GENE PRECURSOR-SEQUENCE P-SEQID GENE-SEQ G-SEQID FOLDED PRECURSOR
======== ================== ======= ========== =======
==========

GAM15 TACATATCTTGAATGTGATC 1 ATAATATTGT 2 A C ATATA--- - GAGC T AAAA
AT
CATTATATATTGAGTCATTA AAATAATGAC G ATGTGATC ATT TTGA GTCATTA CA TA
ATTTAAAAT T
GAGCCATTAAAAAATTTAAA ATTA | |||||||| ||| |||| ||||||| || || |||||||||
ATATTTAATTTTAAATAATA T TATATTAG TAA AATT CAGTAAT GT AT TAAATTTTA
/
TTGTAAATAATGACATTAAA A C AACCGTTA A AAAT T AA-- AT
TTGCCAAAATCGATTATATA
TATTAAATGTA

GAM16 CCGCGCGCGCATGACTACCT 8 CATGACTACC 9 G GCA G G GA AC G TG
GGGCCAGGTTGAGCGCCACC TGGGCCAGGT CCGC CGC TGACTACCTG GCCA GTT GCGCC
CAGGCG T A
AGGCGGTTGAAGGGCGCCTG TGAG |||| ||| |||||||||| |||| ||| ||||| |||||| |
CAGGCGCAGGGCGTGGTGCA GGTG GTG GTTGATGGAC TGGT CGG CGCGG
GTCCGC G /
GGTAGTTGAGGGTGGTGG - GGA G G GA AC G GA

GAM17 TCAATAATATACCGCACACT 22 TACCGCACAC 23 AATATA A CTT TG C TT
TTTATTGCCCCTTTTGTGGC TTTTATTGCC TCAAT CCGC CA TTAT C CC T
GTGGTGATTGGCGGAGAGGG CCTT ||||| |||| || |||| | ||
TTGG GGTTG GGCG GT AGTG G GG T
GGAGA- - T-- GT C TG

GAM18 CACTCTGTTACCCCTTTTTA 39 TGTTACCCCT 40 C TG- TTAACTCTCTAAC TT
TATA
ACTCTCTAACATTTTTCTTT TTTTAACTCT CA TC TTACCCCTTT ATTTTTCT GTTT A
GTTTTATAAGATATAGGCCC CTAA || || |||||||||| |||||||| ||||
AGGAAGATATTCATTTGGAG GT AG AGTGGGGAGG TAGAAGGA CGGA G
GGGTGAACTGAATG A TCA TTTACTTA----- CC TATA

GAM19 TTCTGCACAAGACAGATTGA 65 ACAGATCCTA 66 CAC C AGCA CC TTT
GCAAGGATCTCCGTTTTACC ACCCAATCTA TTCTG AAGA AGATTG AGGATCT GT A
ACACACAGATCCTAACCCAA TCTT ||||| |||| |||||| ||||||| ||
TCTATCTTACACAGAA AAGAC TTCT TCTAAC TCCTAGA CA C
ACA A CCAA CA CAC

GAM20 TGTAGCATGTTTAAAAAAGT 79 AAAGTAACAA 80 CATG- AC CACCG TC GTG
AACAAGTCACCGCCTCATCA GTCACCGCCT TGTAG TTTAAAAAAGTA AAGT CCTCA
ACCTGCT T
CCTGCTGTGTTTAAGGTAGG CATC ||||| |||||||||||| |||| ||||| |||||||
TTTTGGGGGCTTACTGCTTT ATATT AAATTTTTTCGT TTCG GGGGT TGGATGG T
TTTAAAAAAATTTATA TAAAA CA ----- TT AAT

GAM21 CGGTGTCGCGCAGGGCGTAG 95 TCGGAGCTGT 96 G - A - G G G AGC
AGCTTGGGGGCGAGCAGGAC GGGCGTCGCT CG TGTCGC GC GG GC TA AGCTT GGGGCG
A
CGTCTCGGAGCTGTGGGCGT GCGG || |||||| || || || || ||||| ||||||
CGCTGCGGCAGCG GC ACGGCG CG CT CG GT TCGAG CTCTGC G
G T - G G G G CAG

GAM22 CCACGGGCCCGGTGACTCGG 113 TTCCACGGAA 114 - CGG-- C --- - GA
AACCTGAAAGAGAGTTCCAC TCAATGTCGG CCACGG GCC TGA TC GGAAC CT A
GGAATCAATGTCGGCATCGT CATC |||||| ||| ||| || ||||| ||
GG GGTGCT CGG ACT AG CCTTG GA /
A CTGTA A GCA A GA

GAM23 TTCATAAACCCTCGCTCACC 121 TAACTTGTTG 122 C C-- CACCATCTATCAAAA CA
TTC
ATCTATCAAAAAACAAGCAA CCTCAGCTAA TTCATAAA CCT GCT AACAAG AAAGT A
AAGTTTCAGCTCACTTTAAC AGGT |||||||| ||| ||| |||||| |||||
TTGTTGCCTCAGCTAAAGGT AGGTGTTT GGA CGA TTGTTC TTTCA G
TTTGTGGA T AAT CTCCG---------- AA CTC

GAM24 GTTAAATAAAAATATAAATG 135 TGAAATTATA 136 A- - G GT
TTATATGTTAAAATGTGAAA TATCATTTGT GTTAAATAAA ATATA AAT TTATAT T
TTATATATCATTTGTTTAAT TTAA |||||||||| ||||| ||| ||||||
TAATTTGTTT TATAT TTA AGTGTA A
AC A A AA

GAM25 GCAGATCTTATGCTTGTCAG 139 TTAAAGCCCG 140 CTTATGCT A CC - TTTTT
TTAAAGCCCGGAATGTTTTT GAATGTTTTT GCAGAT TGTCAGTTA AGC GGAAT GTT T
TTTTAATTAACAATTCCTGC TTTT |||||| |||||||| ||| ||||| |||
TGTAACTGACACAACAAAAT CGTCTA ACAGTCAAT TCG CCTTA CAA /
CTGC AAACAAC- G T- A TTAAT

GAM26 GTAGCTAGGGTGGTGAGTGG 151 TGGTGAGTGG 152 A TG T GC GC A
CGCTCGCAGCAGCTAGTGAG CGCTCGCAGC GTAGCT GGG G GAGTG GCTC AGCAGCT G
CTGCTGAGCAACACTCCCTG AGCT |||||| ||| | ||||| |||| |||||||
CCCCAGCTAC CATCGA CCC C CTCAC CGAG TCGTCGA T
C GT C AA -- G

GAM27 GGGTGTGGTCCGGACCGCTG 164 TCCCAGGCGA 165 TG GGA TGC- CTCGC C
CGGTAGTTGCCCTCGCAGAT CTACCTCCTG GGG TGGTCC CCGC GGTAGTTGCC AGAT
T
CTGGGTCTCCCAGGCGACTA CGGG ||| |||||| |||| |||||||||| ||||

CCTCCTGCGGGGGGATCATG CCT ACTAGG GGCG CCATCAGCGG TCTG G
TCC GT GG- TCCT ACCC- G

GAM28 GCGCAAAAGACCCCTAGGGA 179 TTTATAGTCT 180 GC- - CC---- A G- AG T - T T
GAGGAGGTAAGCTAGGTGTG CTAACCAGGA GC AAAA GA CCT GG AGAGG GTAAGC
AGGTG TG GTT A
TGTTTAATAACCATCACCTG TATA || |||| || ||| || ||||| |||||| ||||| || |||
TTTATAGTCTCTAACCAGGA CG TTTT CT GGA CC TCTCT TATTTG TCCAC AC CAA
A
TATATTCATTTTTAAGC AAT A TATATA - AA GA - T - T

GAM29 TCGTGAATTTTGATTTTTTA 188 TAAAAAGTTT 189 ------ TTT-- ACCAT
AAACCATTAACTAATTTAAA AATTATTCCA TCGT GAAT GATTTTTTAAA T
AAGTTTAATTATTCCAAATA AATA |||| |||| ||||||||||
ATGA AGTA CTTA TTGAAAAATTT A
ATAAAC TTAAT AATCA

GAM30 AGGTGAGCTCCACGTAGGAT 203 AGAGAGCACC 204 AGCTCCAC G ATACAA A
TTATA
AGCTTAAGATACAATCTCAG TTAAGCTATC AGGTG GTA GATAGCTTAAG TCTC GT C
TTTATACAACACTACAGAGA ATAC ||||| ||| |||||||||| |||| ||
GCACCTTAAGCTATCATACC TCCAC CAT CTATCGAATTC AGAG CA A
TAAAACACACCT ACAAAATC A CACG-- A TCACA

GAM31 TTGCTCAACATTTTAATTTT 221 TTTAATTTTA 222 C- A TTATCTTT- T
ATCTTTAATGTTAACATTTT TCTTTAATGT TTGCT AAC TTTTAATT AATG T
AAACTGCAGTTAAAAGTTTT TAAC ||||| ||| |||||||| ||||
AGTAA AATGA TTG AAAATTGA TTAC A
TT - CGTCAAATT A

GAM32 AGAGGGCGTTGGAGAGAAGC 225 TGGAGAGAAG 226 G TT-- G TGGC G
TTGGCGATGCTGCGGAGCGT CTTGGCGATG AGAGG CG GGA AGAAGCT GATGCT C
TTGGTTTCTGTCCCGGTCGG CTGC ||||| || ||| ||||||| ||||||
CCTTT TTTCC GC CCT TCTTTGG TTGCGA G
G TGGC G T--- G

GAM33 CCATTAAATAAATTAAAAAA 262 TAAATTAAAA 263 TTAA AAAA AATA - ATCA AA
ATTGGAAATATTGGAATGTA AAATTGGAAA CCA ATAAATTA AATTGGA TTGG AATGTA
TTTT T
ATCATTTTAATATAGAAAAA TATT ||| |||||||| ||||||| |||| |||||| ||||
CATACATTACCAAATTCAAT GGT TATTTGAT TTAACTT AACC TTACAT AAAG A
TACTAGTTTATCATTGG TAC- CA-- A--- A ACAA AT

GAM34 GGTGAGAAAGGCTTTTCACG 268 ATGGTGCTCA 269 AGAAA TTTT ACTT- C -
ATTCCT
CATACTTGCACTGTCAGCAG ACATGCGTGC GGTG GGC CACGCAT GCACTGTCAG
AGTTAT TGT A
TTATTGTATTCCTAACACCA GCCA |||| ||| ||||||| |||||||||| |||||| |||
ACACATAACTACTGATGGTG CCAC CCG GTGCGTA CGTGGTAGTC TCAATA ACA
/
CTCAACATGCGTGCGCCAAA AAA-- C--- CAACT A C ACCACA
CACC

GAM35 GAAACTTTAAAATTTATATT 298 TTCATGTAAA 299 AA TAT A A T -- TAA- C CTT
AA
CATGTAAAGTTTTAAGCTTA GTTTTAAGCT ATTTA TC TGTAA GTTT AAGC TTACAAAAT AT
AGGG CAA A
CAAAATTAAATCAGGGCTTC TACA ||||| || ||||| |||| |||| ||||||||| || |||| |||
AAAAAAGATTGTTTTTCTAG TAAAT AG ACATT CGAA TTTG GATGTTTTG TG TCTT
GTT A
TATATGTTTTGTAGATGTTT -- TTT - - T TA TATA A TTT AG
TAAGCTTACAGATTTTAAAT
TAGGGCTTC
GAM36 TGCAGCAGATGTGCCACGGG 311 AGGTGGGTGC 312 A A C - CCA GTG GTAG-----
------ C
CACGTCCCGGTCGGCGTCCA GACCGTAGCC CGGGC CGTCC GGTCG GCGT GGTGG
CGACC CCC G
GGTGGGTGCGACCGTAGCCC CCGC ||||| ||||| ||||| |||| ||||| ||||| |||
CGCAGGGGGCGCAGCAGCGC GTCCG GTAGG CCGGC CGCG CCACC GCTGG
GGG C
CAGGTCGGCCACCACGCGCT C - A T CA- G-- ACCGCGACGACGCGG A
CGGCCAGGATGGCCTGCTGC
ATGCGCTGCA
GAM37 CTGTCACTCATGCCAGTACA 351 TCACTCATGC 352 - TC A--- GTTTA
CTCGCACCCGTAGTGTTTAT CAGTACACTC CTGTCACTCATG CCAGTACAC GC CCCGTAGT
T
ACATAAACTACGGGGGAAGC GCAC |||||||||||| ||||||||| || ||||||||
TTGTGTACTGGATATGAGTG GACAGTGAGTAT GGTCATGTG CG GGGCATCA A
ACAG A TT AAGG AATAC

GAM38 CGCGCATGAGCATGCCCTGT 366 TCCATGGGCA 367 C A - - T - - AG C
ATGCCTCAAGTTTCATAGAG GTGCGCATGC CG GCATG GCA TGCCC TG AT GCCT CA TTT A
TATGTAGGTGATCCATGGGC CG || ||||| ||| ||||| || || |||| || |||
AGTGCGCATGCCG GC CGTAC CGT ACGGG AC TA TGGA GT GAG T
- G G T C G T AT A

GAM39 GTGTCTAGTGACAGACAGGG 394 CACCCGCTCA 395 - A - G AT CTCCTT
AGTGGATTGCGCTCCTTAAA CTGTCTGTCT GT GTCT GT GACAGACAG GAGTGG TGCG A
CTCCCGCACCCGCTCACTGT ACAG || |||| || ||||||||| |||||| ||||
CTGTCTACAGACTAC CA CAGA CA CTGTCTGTC CTCGCC ACGC /
T - T A C- CCTCAA

GAM40 GTAATAAGTTAAATAAAAAT 452 TAAGTTAAAT 453 AA A- - G GT
ATAAATGTTATATGTTAAAA AAAAATATAA GTAAT GTTAAATAAA ATATA AAT TTATAT T
TGTGAAATTATATATCATTT ATGT ||||| |||||||||| ||||| ||| ||||||
GTTTAATAATTAC CATTA TAATTTGTTT TATAT TTA AGTGTA A
A- AC A A AA

GAM41 CTGAGAAGTCATCCAGGTCC 455 TCCAGGAACC 456 AA G GGA - AG GC-- AT
TAGG
AGGAACCGGTGGTAGGCGCC GGTGGTAGGC GAG GTCATCCAG TCCA ACC GGTGGT GC
CCGTGTTG GGTG A
CGTGTTGATGGTGTAGGAGC GCCC ||| ||||||||| |||| ||| |||||| || |||||||| ||||
AGTTGCCCAGCACGGACCAG CTC CAGTAGGTC GGGT TGG CCACCA TG
GGCACGAC CCGT G
TTGACCACCTGGTAGTGGGG -- G GA- T GT ACCA -- TGAC
CTGGATGACCTCGG

GAM42 TGTCTCTTGCTAGGTAGCCT 505 TCTCTTGCTA 506 TC T C - C T GTC T A
GTACAAAACAGTCCTTTTTT GGTAGCCTGT TG TC TG TAGGT AG CTG ACAAAACA CT TTTTA
T
AATGTAAAACAGTGTTTTGT ACAA || || || ||||| || ||| |||||||| || |||||
CCAGACTAGCCTAACACGAA AC AG AC ATCCG TC GAC TGTTTTGT GA AAAAT /
CCA CA C A A A C --- C G

GAM43 TCCTGCAGCACCCCCGGTCC 529 TCGCGCAGCA 530 G G CC G- C --- AC -- T
CGCGCGCTGACCGCGCAGCT CTGCCGGGAC TCCT CA CA CCC GTCCCG GC GCTG CGCG
CAGC G
GCTGCTGATCGCGCAGCACT GAGG |||| || || ||| |||||| || |||| |||| ||||
GCCGGGACGAGGGCATGGTG AGGA GT GT GGG CAGGGC CG CGAC GCGC GTCG
C
AAGGA A G AC AG - TCA -- TA T

GAM44 TTTTGCAAGTCCCTACCAGG 539 ACCAGGTAGC 540 A C--- C- TA C- AAAAT
TAGCCGTGCATAAGCTTAAA CGTGCATAAG TTTTGCA GT CCTA CAGG GC
GTGCATAAGCTT T
ATTAATAAAAAGCTTATGCA CTTA ||||||| || |||| |||| || ||||||||||||
CAAGCCGTCTGATTAGGAAG AAAACGT CA GGAT GTCT CG CACGTATTCGAA A
CACTGCAAAA - CGAA TA GC AA AAATA

GAM45 GTTGGTGTGTGGTAGCGATC 559 TTGGTAGTGA 560 T G - GAT- TT-- TT
TATCTTTCTTTGTGATCTTG AGCCTGCCAG GTTGG GT TGGTAG C CTATC TC T
GTAGTGAAGCCTGCCAGGCT GCTC ||||| || |||||| | ||||| ||
CCAGC CGACC CG ACCGTC G GATGG AG /
T G C AAGT TTCT TG

GAM46 GAGGCCGTTCTGAAAGAGTT 572 TGAAAGAGTT 573 CG G GT TTT C TT A CGT
GGATTTCAGCACCTTGGGAC GGATTTCAGC GAGGC TTCT AAAGA TGGA CAG ACC GGG
CGCAC A
GCACCGTAGCTAGTGTGGCT ACCT ||||| |||| ||||| |||| ||| ||| ||| |||||
CTGGTCTGCTTCATTTTTGA CTTCG AAGA TTTTT ACTT GTC TGG CTC GTGTG G
GAAGCTTC -- G -- C-- - T- G ATC

GAM47 GAGTATGTGAGTTTTGTGTT 606 TAGCCTGCTT 607 TA AGTTT CA- TG GCC
GAGGCAGGCCACTTGCACTT TAACACATAT GAG TGTG TGTGTTGAGGCAGGC CT
CACTTGCATT T
GCATTGCCTTCCAAATGCAG CCCA ||| |||| |||||||||||||| || ||||||||||
GTGAGAGATAGCCTGCTTTA TTT ACAC ACACAATTTCGTCCG GA GTGGACGTAA T
ACACATATCCCACAGGTTT GG CCTAT ATA GA ACC

GAM48 GGCGGGGGTGAGCGCGGCCT 623 CGACGCGGAT 624 C G G- C C G G
CCCTGGCGCCCGAGCGGGCG GCAGGCGCTG GG GGGGGT AGCGC GC TCC TG CGCCC A
ACGCGGATGCAGGCGCTGCC CCCT || |||||| ||||| || ||| || |||||
CTCCC CC CTCCCG TCGCG CG AGG GC GCGGG G
- - GA T C A C

GAM49 TGCCAGTCTCCTACCAGAGT 643 ACCAGAGTAC 644 CA --- CC A A A- TTTTA
ACTTGGCAAAGATCTTTTTA TTGGCAAAGA TGC GTCTC CTA AGAGT CTTGGC AAG TCT
G
GTACACAGAGCCTTCGCCAA TCTT ||| ||||| ||| ||||| |||||| ||| |||
GAGCTCTTAGCACGAGATGA ACG TAGAG GAT TCTCG GAACCG TTC AGA /
GCA AG CAC -- A C CG CACAT

GAM50 GGTAAGGCCTGTGAGTAAGC 665 TAATTCAGAG 666 G- - TGAG-- A CCT
TATCTCCTCCCACAGAAGCT CAGTTATT GGTAA GC CTG TAAGCT TCT C
TAGTAATTCAGAGCAGTTAT ||||| || ||| |||||| |||
T TTATT CG GAC ATTCGA AGA C
GA A TTAATG - CAC

GAM51 TCGCGGAGGAGATGAACGTC 679 CACCTGCTGA 680 A ATGAAC C A T TA
AGCCGGAGCTCCTACATTGG CACTCTACCG TCGCGG GGAG GTCAGC GG GC CC C
GCACCTGCTGACACTCTACC CGA |||||| |||| |||||| || || ||
GCGA AGCGCC TCTC CAGTCG CC CG GG A
A A----- T A - TT

GAM52 AAGTAGTGCGGGTAATGAAG 710 TAGCATAGTA 711 - AA AGTT AA CTCA - CA T
A TCA
AAGTTGCAAGTCTCTCATCT AAAATCAGTT CGGGTAA TG GA GC GTCT TC TGATAG TAG
AAAAATC GT G

GATAGCATAGTAAAAATCAG CAGT ||||||| || || || |||| || |||||| ||| ||||||| ||
TTCAGTATACAGATTTTTTC GCTCATT AT CT CG CAGA AG GCTATC ATC TTTTTAG
CA /
TAAACTATCGTGACACAAGA C GA AC-- AA ACAC T AA T A TAT
CAAGCCATCAGTACTTACTC
GCACTTACTT
GAM53 CCCCGGCCCTCTCGCGCGTC 726 TCTCTGGGAA 727 GG GCG GTCCC---------- CA
CCGTCCCGGGCATCCTCCCT AGCGGGAGGG CCCC CCCTCTCGC TCCC GGG T
GCTCTCTCTGGCCTCTCTGG AGGG |||| ||||||||| |||| |||
GAAAGCGGGAGGGAGGGG GGGG GGGAGGGCG AGGG CCC C
A- AA- TCTCTCCGGTCTCTCTCGT TC

GAM54 AAATTATTTATAAAATTTGA 817 TAGAAACTAT 818 TG----- A A - AC- GAATTA
T
AAAGAATGTAGAAACTATAA AACTTAGAAT ATTTATAAAATT AAA GA TGTAGAAA CTATA
TTA AATAT A
CTTAGAATTAAATATTACAA TAAA |||||||||||| ||| || |||||||| ||||| ||| |||||
TATTATATAAATATATAGAT TAAATGTTTTAA TTT CT GTATTTTT GATAT AAT
TTATA C
TTTTATGATCCTTTATAGTA TATGATA C A A ATA ATA--- A
TAATTTTGTAAATAATTT

GAM55 AGGCGGCGTGGGGAAGGCCG 830 TAGGACTCTT 831 G T GAAG - G G
GCCTGCGTGTGGACGAAGGC GCAGCTT AGGC GCG GGG GCCG GCCT CGT T
GCGGTAGGACTCTTGCAGCT |||| ||| ||| |||| |||| |||
T TTCG CGT CTC TGGC CGGA GCA G
A T AGGA G A G

GAM56 AACACGTGCCCACACTTGGC 841 TTTGAAACAT 842 C CCACACTTG A CT C- -
ATTATTTA
AAGTCTCTTGCGGAAAAGCT AGCTTTTCCA GTGC GC AGT CTTG GGAAAAGCTAT
TTTCAAATAC A
ATTTTCAAATACATTATTTA ACAA |||| || ||| |||| |||||||||||| ||||||||||
ATTACAAACGTATTTGAAAC CACG CG TCA GAAC CCTTTTCGATA AAAGTTTATG
/
ATAGCTTTTCCAACAAGCAA C TTTTTAA-- A AC AA C CAAACATT
CTAGCAATTTTTGCACCTGT
T
GAM57 GGGGCAGTGTCCCTTGTCCA 860 CCTTGCGGAG 861 G--- T TG C G -- - C
CGGCCAGCTCGTAGGCCGCG GCTGGTGTGC GGGGCA TG CCCT T CACG CCAGCT CGTA
GGCCG G
GCGGCCTTGCGGAGGCTGGT GTGA |||||| || |||| | |||| |||||| |||| |||||
GTGCGTGAGGGCGAAGGTGT CCCTGT GC GGGA G GTGT GGTCGG GCGT CCGGC /
CCC GGAA - GT C - AG T G

GAM58 AGCTGGGCATAGGCCAGGGG 879 AGGGGGTCCT 880 - TA CAG T G-- G
GTCCTCGGGGTCGTCCGGCA CGGGGTCGTC AGCTGG GCA GGC GGGGTCC CGG GTC T

GGCCGGGGCCCCGCTCCTGC CGGC |||||| ||| ||| ||||||| ||| |||
GCCAGCT TCGACC CGT TCG CCCCGGG GCC CGG C
G CC --- - GGA C

GAM59 GGTTCTCTTGTAGCCCTCCA 899 TCTCTTGTAG 900 TC TT A -- A-- -- ---- -- G
ACATTGGAAGCCAGCACTGA CCCTCCAACA GGT TC GT GC CCTCC ACATT GGA AGCC
AGCACT A
GAAGTGTTTGGGTTAAAGTC TTGG ||| || || || ||||| ||||| ||| |||| ||||||
CCTGATGTAGAGGAGGTCGC CCG AG CA CG GGAGG TGTAG CCT TTGG TTGTGA
G
ACTCGACGGCC GC CT - CT AGA TC GAAA GT A

GAM60 CTCATTTTAAAATAGCTTGT 914 TAGCTTGTCG 915 TT AA CGGGC ATTCTTCT
CGGGCTGTGTCTATTCTTCT GGCTGTGTCT CTCAT TAA TAGCTTGT TGTGTCT T
TTATGTCCACAGACACAACA ATTC ||||| ||| |||||||| |||||||
CACAAGCTACCTTACTATGA GAGTA ATT ATCGAACA ACACAGA T
G TC CC CACA- CACCTGTA

GAM61 GGAAGACCAGCAGGAAGGGC 920 AAGGGCACGA 921 A A GGAAG A T
ACGAGCTGCTTTCCGAAGCG GCTGCTTTCC GGA GACC GCA GGCACG GCTGCTT C
GCCGTGCCAGGTGTAGGTCT GAAG ||| |||| ||| |||||| |||||||
CC CCT CTGG TGT CCGTGC CGGCGAA C
- A GGA-- - G

GAM62 CCCCTCCTCTTGCAGGTACG 956 CTTTGGATGG 957 TGCAGGTA T CG A
TGGCCCCGCCCAGTGGGATG GGGAGGGG CCCCTCCTCT CG GGCCC CCC G
GGCTTTGGATGGGGGAGGGG |||||||||| || ||||| |||
GGGGAGGGGG GT TCGGG GGG /
TAG----- T TA T

GAM63 TATGTCATGATCTTAATGTA 1091 TGTCATGATC 1092 C T C C ATT
GCACCTTTATTTGAAAAAAA TTAATGTAGC TATGT ATGATCTTAATG AG AC TTT T
GTCCTCCATTAGGATCATCA ACCT ||||| |||||||||||| || || |||
CATA ATACA TACTAGGATTAC TC TG AAA G
C C C A AAA

GAM64 TTGGCCTGGATCTTGAGGTT 1108 AGATGTTGCC 1109 G GAG - CG G C G GG-----
A GG
GGAGATGTTGCCGCTCTGGT GCTCTGGTCG CTT AGGTTG ATGTT GC CTCT GT GCG CGG
GTTC TGTTGT A
CGCGGCGGGGGTTCATGTTG CGGC ||| |||||| ||||| || |||| || ||| ||| |||| ||||||
TGGAGGACGACGAGGACGGC GAG TTCGAC TGCGG CG GGGG CG CGT GCC
CAGG GCAGCA /
GTAGCCGGTGCAGCGGGGGA G G-- G AA G A G GATGCGG A GG

AGCGGGCGTGCAGCTTGGAG
GGGAAGGCGTG
GAM65 CCAGGGCGCTGTCCCAGTGG 1119 TCCCCGTCCT 1120 T T T T- G AT
CGGTGGTAGGTGATGCTCCA GGGTGGTGCC CCAGGGCGCTG CCCAG GGCGG GG AG TG G
GCTCTCCCCGTCCTGGGTGG CTGG |||||||||||| ||||| ||||| || || ||
TGCCCTGG GGTCCCGTGGT GGGTC CTGCC CC TC AC C
- - - TC G CT

GAM66 GCCTTCTACCCTCCTTATAT 1166 TTATATTGAA 1167 TC CC ATAT- T TAT
ATATTATATATTGTTTATTA AAAGGAAGTA GCCT TAC TCCTT ATAT ATA T
TATTGAAAAAGGAAGTACAG CAGG |||| ||| ||||| |||| |||
GT TGGA ATG AGGAA TATA TAT /
C- A- AAAGT T TTG

GAM67 TATATCACGCTCTATTGTAT 1184 TATTACACGG 1185 A AT TAG TCTAA TT
AGATCGTCTAACGTTGAATC AGCGGATATA TATATC CGCTCT TGTA ATCG CG G
GCTGATATTACACGGAGCGG |||||| |||||| |||| |||| ||
ATATA ATATAG GCGAGG ACAT TAGT GC A
- C- TA- C---- TA

GAM68 CCGGCTGAGTCATCGCCCGA 1195 TGAGTCATCG 1196 CTGA A -- C CACGAC
GGACGCGCCCACGACCAAAA CCCGAGGACG CCGG GTC TCGCCC GAGGA GCGCC C
AAGGTGCCTCCTCGAGGGCG CGCC |||| ||| |||||| ||||| |||||
GGACGTCCGG GGCC CAG GGCGGG CTCCT CGTGG /
TG-- - AG C AAAAAA

GAM69 GTGAGTTTACCACGGCAGCG 1199 TCGTAGGCCT 1200 A AG- AA - GT- C- G G ATG
ACCAT
AAAGCCTTGACGGTCTCGTA TGGTCATGTC C CGGC CGA GCC TTGACG CT GTA GCCTT
GTC TCCGAC G
GGCCTTGGTCATGTCCGACA CGAC | |||| ||| ||| |||||| || ||| ||||| ||| ||||||
CCATGCCCCCGTCGGAAAAG G GCCG GCT CGG GGCTGC GG CAT CGGAG CGG
AGGCTG /
GCAGAGGCGTACTTGGTAAC C CCA G- T AAT TT G A AAA CCCCC
GTCGGTGGCGTCGACCGCCG
CGGACAC
GAM70 TCCTCACGGGGTGCCTTATC 1205 CAGGTCCCCG 1206 - T T C TTT G
TTGTTTTCGAGAGATTCCAG TCGAGGA TCCTC ACGGGG GCCT AT TTG TC A
CATCAGGTCCCCGTCGAGGA ||||| |||||| |||| || ||| ||
AGGAG TGCCCC TGGA TA GAC AG G
C - C C CTT A

GAM71 GAGTTGCAAATGCTCCTCCG 1233 TGGCGGGAGG 1234 CAA --- - AC- ACT
ACGAGAGGCTCACTCACCAG TTCAGCGTCA GAGTTG ATGCT CCTCC G GAGAGGCTC C
AGCCTCTCTGGCGGGAGGTT CCGG |||||| ||||| ||||| | |||||||||

CAGCGTCACCGGCTC CTCGGC TGCGA GGAGG C CTCTCCGAG A
CAC CTT G GGT ACC

GAM72 GGGAGGAGCAGTACGGAATA 1238 TATTCCGTAC 1239 GGA GA- GA
G
TCCGGTCAGGAGGGTGGAGT TGCTCCGACC AGCAGTACGGAATATCCGGTCAGGAGGGT
GTT GGGTATCCCATTGGC GC T
TGAGGGTATCCCATTGGCGA |||||||||||||||||||||||||||| ||| |||||||||||||| ||
GCGTAGCGAGCCAATGGGAT TCGTCATGCCTTATAGGCCAGTCCTCTCA CAA
CCTATAGGGTAACCG CG /
ATCCGTAAACGGAACTCTCC AGG ATG AG A
TGACCGGATATTCCGTACTG
CTCCGACC
GAM73 CGACGCTTTTCTTCCTTCTC 1260 ACGCTTTTCT 1261 TTTTCTTCCTTCTCCC C TCC
CCGCAGCCGCTCCCTTCTGC TCCTTCTCCC CGACGC GCAGC GC C
GCTGCTCCTTCTCCTCGCGT GCAG |||||| ||||| ||
TG GTTGCG CGTCG CG T
CTCCTCTTCCT----- - TCT

GAM74 GGAGCTGGTCGTAGGCTCCC 1289 CGTCAAAGTT 1290 A CCCAGG TATC TA - CG
AGGGACTTTATCTGATACCT AAGCTTGGTC GGAGCTGGTCGT GGCT GACTT TGA CCT
AG A
AGCGAATCCTGAGGCGTCAA ATGA |||||||||||| |||| ||||| ||| ||| ||
AGTTAAGCTTGGTCATGACC CCTCGACCAGTA CTGG TTGAA ACT GGA TC A
AGCTCC - TTCGAA ---- GC G CT

GAM75 TGCAGGGGGAATAACCGGAT 1304 TGACAAAGAT 1305 C - TAACCGG CC CCT A CC
AG
CCCTGTCCCTAGCATCAAGC ATTTCCCACC TG AGG GGGAA ATC TGTC AGC TCAAG GC
C
CGCAGCCTGCTTTTTGAAGT TCA || ||| ||||| ||| |||| ||| ||||| ||
TGACAAAGATATTTCCCACC AC TCC CCCTT TAG ACAG TTG AGTTT CG /
TCA - A TA----- AA --- A TT TC

GAM76 CCGGGTGGGGGGTGGCCCCG 1349 CGCTCCGGGG 1350 - C T A C C A ---- A
G
CTGGGCACCGCTGCGCCGCC GCAGCCGGGC GGTGGCCC GC GGGC CCGCTG GC GCCGCC
GGT CCTGGGGC GCCGGG T
GCCAGGTCCTGGGGCAGCCG GGCC |||||||| || |||| |||||| || |||||| ||| |||||||| ||||||
GGGTTCCTGGCGCTCCGGGG TCGCCGGG CG CCTG GGTGGC CG CGGCGG CCG
GGGCCTCG CGGTCC /
GCAGCCGGGCGGCCGCCGGT G T - - - C G ACGG - T
GGGTCCGCTGGGCCGCTGCC
CCGCTCCGG
GAM77 GCGCCGGCAAGACCACCTTC 1434 TTAAGCTTCA 1435 CG- A CC CTTC A C
GAGATTAAGCCCATGTTTAA CGTCATCTGC GCGC GCA GA AC GAG TTAAGC C

GCTTCACGTCATCTGCAACG AACG |||| ||| || || ||| ||||||
CGC CGCG CGT CT TG TTC AATTTG A
CAA - AC CAC- G T

GAM78 GGAGGTCCGCGGTGTCGTCA 1446 TCGGAGGTCC 1447 T C C C TC
CCCAAATGTCT C-- AC
TGACCACCCTGTGGGCTCCC GCGGTGTCGT CGCGG GT GTCATGAC AC CTGTGGGC CC
AGAAC GACC G
CCCAAATGTCTAGAACCGAC CATG ||||| || |||||||| || |||||||| || ||||| ||||
CACGGCCGGTCTCCGTTCTC GTGTC CA CAGTACTG TG GGCGCCTG GG TCTTG
CTGG G
GGAGGTCCGCGGTGTCGTCA C C C T GA C---------- CCT CC
TGACCACCCTGTGGGCTCCC

GAM79 GGTGTCGTCATGACCACCCT 1450 ACCCTGTGGG 1451 TC C C G - CCCCA TCT A
C
GTGGGCTCCCCCCAAATGTC CTCCCCCCAA GGTG GTCATGAC AC CT TGGG CTCC AATG
AGA CCGGC A
TAGAACCGGCCACGGCCGGT ATGT |||| |||||||| || || |||| |||| |||| ||| |||||
CTCCGTTCTCGGAGACCCGA CCAC TAGTACTG TG GA GCCC GAGG TTGC TCT
GGCCG C
AGTGTCGTCATGATCACC -- C T A A CTC-- C-- - G

GAM80 TTGTGTCCCGCATGCTAGAG 1481 TCGCAGAGGA 1482 CGCA AGTA GAG AT - -
-- GA
TATCCTCGAGGAGGATTCTT GCTAGCAGGA TTGTGTCC TGCTAG TCCTC GAGG
TCTTCTA CA GCA CC C
CTACAGCACCGACATGGCCT GGAC |||||||| |||||| ||||| |||| ||||||| || ||| ||
GCATGATGGAGGGTCTCGCA AACACAGG ACGATC AGGAG CTCT GGGAGGT GT
CGT GG /
GAGGAGCTAGCAGGAGGACA AGG- G--- ACG -- A A CC TA
CAA

GAM81 GTCAGGGCGGCTGACGGTCT 1564 CGAGACAAAA 1565 GGCTGACG AA CAAAT
CAAGGGTCCAAATTCCATCG ATGGTCCTGA GTCAGGGC GTCTC GGGTC T
ACCCCGAGACAAAAATGGTC T |||||||| ||||| |||||
CTGAT TAGTCCTG CAGAG CCCAG /
GTAAAAA- C- CTACC

GAM82 CAGGTTTTTTGGGTGGGACA 1616 TGACGTAGCT 1617 T G GGA A- GA
G
TCCGGTACTGCAGGGGCGGA GCTGCAGTAC TTGGGTGGGACA CCGGTACTGCAG GGC
GTCA GGATACCCCATTGGC GC T
GTCAAGGATACCCCATTGGC CGGT |||||||||||| |||||||||||| ||| |||| |||||||||||||| ||
GAGCGTAGCGAGCCAATGGG AACCCACCCTGT GGCCATGACGTC TCG CAGT
CCTATGGGGTAACCG CG /
GTATCCGATGACGTAGCTGC - G ATG AG AG A

TGCAGTACCGGTGTCCCACC
CAAAAAACCG
GAM83 GAGACGGTCGGGCTTGACGT 1623 ACCGAGTTTA 1624 C T ---------- A AG-- CAGCT
C
TGAGGAGCTCCAGCTTGGAC CGACAGCGCA GAGA GG CGGGCT TG CGTTG GAGCTC
TGGA T
TTGTCCACCGAGTTTACGAC AATC |||| || |||||| || ||||| |||||| ||||
AGCGCAAATCTTGTACAGCT TTCT CC GCTCGA AC GCGAC TTTGAG ACCT T
CGTCCTTCTT T T CATGTTCTAA - AGCA CC--- G

GAM84 TCCCTCAGTGTTTGCCAGCT 1628 GGGCCTGTGG 1629 - TG C CTTATTT TTT
TATTTCCCCAGTTTTCACGT ACACCTGAGG TCCCTCAG TGTT C AG CCCCAGT C
ACTGGGGCCTGTGGACACCT GA |||||||| |||| | || |||||||
GAGGGA AGGGAGTC ACAG G TC GGGGTCA A
C GT - C------ TGC

GAM85 GCCAGAGTCTGAAAAGTTTG 1774 GATCATGGAC 1775 AG GAAA- GTA-- --------- - G
TAGCCTTTATGTCCGCCGCC AAGAGAAAGG GCCAG TCT AGTTT GCCTT TATG
TCCGCC C
CGGCGGATCATGGACAAGAG CCAA ||||| ||| ||||| ||||| |||| ||||||
AAAGGCCAAAAAGACTATGC CGGTT AGA TCAGA CGGAA GTAC AGGCGG C
AAGAGTTGGC G- ACGTA AAAAC AGAGAACAG T C

GAM86 GGACCCCAGCCCCGCCGATC 1816 CTTGCCTGGT 1817 - CC ------ ATCCCT C
CCTCCCCCAGGGCGTACCCG TCTGGGGCTC GGA CCCCAG CC GCCG CCC C
GCTTGCCTGGTTCTGGGGCT C ||| |||||| || |||| |||
CC CCT GGGGTC GG CGGC GGG /
C TT TCCGTT CCATGC A

GAM87 AGTTTTGCCACAACAAGCCT 2007 AAGCCTACTG 2008 AACA ---- --- AA GAT
ACTGTCAACACGATGGGAGT TCAACACGAT AGTTTTGCCAC AGCCT ACTGT C CAC G
GGAGAGCGCAGTGACCGGGC GGGA |||||||||||| ||||| ||||| | |||
TGGTGGCAGAGCT TCGAGACGGTG TCGGG TGACG G GTG /
G--- CCAG CGA AG AGG

GAM88 GGCTCGTTAAACCCGCCGTG 2036 ACCCTGTACG 2037 G AAA GGGCATG A- -- C
A A
GGCATGGACACCCTGTACGG GCACCAGGAA GGCTC TT CCCGCCGT GAC CCCT
GTACGG ACC GG A
CACCAGGAACGCCAGGTTCG CGCC ||||| || |||||||| ||| |||| |||||| ||| ||
TACCCAGGGACGTCGGACGG TCGAG GA GGGTGGCA CTG GGGA CATGCT TGG
CC C
TGGGGAAAGGGAGCT G AAG GG----- CA CC - A G

GAM89 GAGATTTAATGCTAGTCTAA 2053 TATTTTACGC 2054 ATTT C CT- TATATTAA - AT
ATATTTCTATATTAAGATAC TGACATTTTT GAG AATG TAGT AAATATTTC GATA CT C
TATCTTAAGATATCGGTACT ACTC ||| |||| |||| ||||||||| |||| ||
CTGAGATATTTTACGCTGAC CTC TTAC GTCG TTTATAGAG CTAT GA T
ATTTTTACTC ATTT A CAT TCTCATGG A AT

GAM90 GGCCGCCGCCTCGAGGTGGC 2058 CACCATGGCG 2059 CGC - - A A- CCC
TCGCGTCGCCATGGAGACCG ACGCGAGCCC GGCCGC CTCG AGGTGG
CTCGCGTCGCCATGG GACCG GA G
AGACCCGTCAATCAGCGGTC GCCT |||||| |||| |||||| |||||||||||||| ||||| ||
ACCATGGCGACGCGAGCCCG CCGGCG GAGC TCCGCC GAGCGCAGCGGTACC
CTGGC CT T
CCTCCGAGTCCGCGGCC CCT C C A GA AAC

GAM91 AATTCATTAGAATTGATTTT 2091 TTCATTAGAA 2092 AT T TT TT-------- A - ATT A
ATTAGAATGAGTTATTTCTT TTGATTTTAT AATTC TAGAAT GA TTA AGA TGA GTT
TCTTC T
CATCCGAAGATTCAACATCA TAGA ||||| |||||| || ||| ||| ||| ||| |||||
TCTTTTTTTTTCTTAATTTC TTAAG ATCTTA CT AAT TCT ACT CAA AGAAG C
TATTCTAGAATT -- T TT TCTTTTTTTT - A CTT C

GAM92 AGAATCTTCTTCTAATTCAT 2095 TTCATTAGAA 2092 TCTTCT- AT T TT TT-------- A -
ATT A
TAGAATTGATTTTATTAGAA TTGATTTTAT AATTC TAGAAT GA TTA AGA TGA GTT
TCTTC T
TGAGTTATTTCTTCATCCGA TAGA ||||| |||||| || ||| ||| ||| ||| |||||
AGATTCAACATCATCTTTTT TTAAG ATCTTA CT AAT TCT ACT CAA AGAAG C
TTTTCTTAATTTCTATTCTA ATTTTTT -- T TT TCTTTTTTTT - A CTT C
GAATTTTTTTTATTATTCT

GAM93 ATTTTAGGATCATTAAAATT 2096 TAGGATCATT 2097 AT---------- TT C
ATTTTTACACTTAAATTTAA AAAATTATTT ATTTTAGGATC TAAAATTA TTTA A
TTTTATCAATTTTTTCAGAT TTAC |||||||||| |||||||| ||||
TTTAAAAT TAAAATTTTAG ATTTTAAT AAAT C
ACTTTTTTAACT TT T

GAM94 GAAAATAAATGACGGATATG 2101 TAAATGACGG 2102 A T G G - - ATG
ATGTGAATGATATATCGTCA ATATGATGTG GA AA AAAT ACG ATAT GATG TGA A
TCGATATACGTGGTTTCTTA AATG || || |||| ||| |||| |||| |||
TC CT TT TTTG TGC TATA CTAC GCT T
A C G A G T ATA

GAM95 GTTATTGGCTCTAATTAGTC 2116 TGAAATAGAG 2117 A- A- CATAAAA AACA
ATAAAAGTACAACAATACAG CTAAAAAAC GTT TTGGCTCTA TTAGT GTAC A
TATGCGACCACTGAAATAGA ||| ||||||||| ||||| ||||

GCTAAAAAAC CAA AATCGAGAT AGTCA TATG /
AA AA CCAGCG- ACAT

GAM96 GTTTCCGCTTTTCAGCGAGC 2147 GAATGCGATG 2148 TT - TTT GA-- GTA T
ATGTACCCTAATGGGAATGC GCTGTTAGTG GT C CGCT CAGC GCAT CCC A
GATGGCTGTTAGTGCGGGAC CGGG || | |||| |||| |||| |||
CA G GTGA GTCG CGTA GGG A
GG C TT- GTAG A-- T

GAM97 AGTACTTGAAATACAGCCCC 2160 AAAAACTAAA 2161 AC AAA CCCC AAAAA AAGT
TAGAAAAATCAAAAGTATTT ACCTGTAGAA AGT TTG TACAG TAG TCAA A
CTTGAAAAACTAAAACCTGT CAAA ||| ||| ||||| ||| ||||
AGAACAAAAACT TCA AAC ATGTC ATC AGTT /
AA AAG CAAA AAAA- CTTT

GAM98 ATAGAAAAAGATAAGAGGAT 2233 CTCTTGGTCA 2234 AA TAAGAG TTA AA A
CGATTAAGCAAAATAAAACT ATTTCGGTTT ATAGAAA GA GATCGA AGCA ATA A
ATGGTGCTCTTGGTCAATTT CTAT ||||||| || |||||| |||| |||
CGGTTTCTAT TATCTTT CT CTGGTT TCGT TAT A
GG TTAA-- C-- GG C

GAM99 TTGAAATCAATGTTTAAAGT 2246 TTTAAAGTTT 2247 -- AA-- A TT T
TTTAAATTGAGTTTTCTCTC TAAATTGAGT TTGAAATCAAT GTTTA GTTTT AA GAG T
TTAAAAACAAGCTAAATAAA TTTC |||||||||| ||||| ||||| || |||
TTGGTTTTAA AATTTTGGTTA TAAAT CAAAA TT CTC T
AA CGAA A CT T

GAM100 CCGTAATCGTGGTGTTCGTC 2250 TTCGAGAATA 2251 AA GG G TCACT A
GTCACTTGTTAACTTTAACG GCGAGCATGG CCGT TCGT TGTTC TCG TGTTA C
TTCGAGAATAGCGAGCATGG |||| |||| ||||| ||| |||||
GGTA AGCG ATAAG AGC GCAAT T
CG -- - TT--- T

GAM101 TCTGAAATATTTATCTAACA 2271 TGAAATATTT 2272 - - ACAA--- CC CA
ATGGTCCAATTACAAGTTTA ATCTAACAAT TCTGAA ATATT TATCTA TGGT AATTA A
ATTTTATCACACACAATAGA GGTC |||||| ||||| |||||| |||| |||||
TGTAATATATTCAGA AGACTT TATAA GTAGAT ACTA TTAAT G
A T AACACAC TT TT

GAM102 GAGGTCGTGGAGTACGGTTG 2285 TCGTGGAGTA 2286 TC G A G T
ATTTCTTTTTCTTAAAAGAA CGGTTGATTT GAGG GT GAGT CGGTT ATTTCTTTT C
GTAAACTGATTCGATTTCCT CTTT |||| || |||| ||||| |||||||||
T TTCC TA CTTA GTCAA TGAAGAAAA T

TT G - A T

GAM103 CAGTGATCAAGAAACAATAT 2290 TATGTAGACG 2291 A AGAAACAA C A GAC A
ACATGATAGGTGACGAAAAT ATGACACTG CAGTG TCA TATA ATGAT GGT GAA A
ATTCATGACTGGTCATATGT ||||| ||| |||| ||||| ||| |||
AGACGATGACACTG GTCAC AGT ATGT TACTG TCA CTT T
- AGCAG--- A G GTA A

GAM104 AATATTGATTTATATTATGC 2311 TATTATGCAA 2312 TTT A A---- A--- A
AACAGTAACAGAACCATTTG CAGTAACAGA AATATTGA ATATT TGC ACAGTA CAGA C
AAAATACTGTCCTAAGCACA ACCA |||||||| ||||| ||| |||||| ||||
ATGTTTAATGTT TTGTAATT TGTAA ACG TGTCAT GTTT C
--- C AATCC AAAA A

GAM105 ACCCTCCACCCAGCCTCCCA 2331 GTCCAGAATA 2332 CC -------- T AATA A T CCAT-----
TCC
TTGGTCCAGAATAGGGAAGT GGGAAGTCCG T CAT TGG CCAG GGG AG CCG
TCCCGGGATC T
CCGCCATTCCCGGGATCTCC CCAT | ||| ||| |||| ||| || ||| ||||||||||
TGATGGTCTCGGGACTCTCC A GTG ACC GGTT CCC TC GGC AGGGCTCTGG
/
TCCCGGCTCCCCATTGGCCA CC CAGTAGAG - A--- C - CCTCCTCTC TAG
GAGATGACGTGCCAGGCATG
GGGCAATCGT
GAM106 GCAATCCTGATATATCGCAA 2342 TATCGCAATA 2343 TCC- AT GCAATAG G
TAGTGGGCCGGGCCCGGTCC GTGGGCCGGG GCAA TGAT ATC TGGGCCG G
AAATAAGGTCAGTCGCCCCT CCCG |||| |||| ||| |||||||
TGC CGTT GCTG TGG ACCTGGC C
CCCC AC AATAA-- C

GAM107 GGGAGATAGTGGACAGCCCC 2347 TAGTGGACAG 2348 AG ACA CC-- - CA TT
CATTGGGCCATGGGCTTTAT CCCCCATTGG GGGAGAT TGG GCC CATT GGGC TGGGC T
TGCCCAATGCCCTAATGCAT GCCA ||||||| ||| ||| |||| |||| |||||
AGGTATCAGTCTTCC CCTTCTG ACT TGG GTAA CCCG ACCCG A
-- A-- ATAC T TA TT

GAM108 AACGGGAATGATCGATTGAC 2377 GAAAAGGTGA 2378 - GA- A ATGTAAA - ATAA
ACTATGTAAAGAGTTCTTAT CAGTTGAATA AACGGGA AT TCGATTG CACT GAGTT CTT A
AAATTCAAAGCAGCTCGAAA ATCT ||||||| || ||||||| |||| ||||| |||
AGGTGACAGTTGAATAATCT TTGCTCT TA AGTTGAC GTGG CTCGA GAA /
CTCGTT C ATA A AAAAG-- C ACTT

GAM109 GATGGTAACGATAGTGGGTA 2385 TAGAGTGTTG 2386 - T ATTT T - G
TTTTCGTCGTTCTCGGGGTC ATATCATCCT GATGGT AACGATAG GGGT TCG CGTTCT CG G

GTAGAGTGTTGATATCATCC TATC |||||| |||||||| |||| ||| |||||| ||
TTATCGTTAATCATC CTACTA TTGCTATT CCTA AGT GTGAGA GC G
A - CTAT T T T

GAM110 AGCAACCGGGGTCTTTATTG 2391 AGTGGGTAGC 2392 TATTG GA -- A TA CCCAT---------
CC ATA
GCCGAGGGTGCAGTGGGTAG CCCCATTGGG GCC GGGT GC GTGGG GCC
TGGGCCG GGG G
CCCCCATTGGGCCGCCGGGA CCGC ||| |||| || ||||| ||| ||||||| |||
TAGTTACCCAATGGCTCATA CGG TCCG TG TACCC TGG ACTCGGT CCC /
CATAGTCATCATGGTCCCCC TTCAA -- TC A CC TACTACTGATACAT AA ATT
ATAGTCTGCCTGGCAACTTA
AGATCCCATT
GAM111 AACCCTGCCCCCTGACTCCC 2412 TCAGTGGGAG 2413 GCCCCCTG TC AA
CATTGGCTAAATGGGTCAGT GTACCCATTA AACCCT AC CCCATTGGCT A
GGGAGGTACCCATTAAGGGT AGGG |||||| || ||||||||||
T TTGGGA TG GGGTGACTGG /
ATTACCCA GA GT

GAM112 CGATCAAGTATTCTCAGCCT 2427 TGAGTACATC 2428 AA------ - GC TG - AAG -----
AA
GTGATGTCTCACCAAGCCGC GTGGATGACG CGATC GTATTC TCA C TGATGT CTCACC
CC GCCGC T
CGCAATCTGTGGCTTCAAGG AGTA ||||| |||||| ||| | |||||| |||||| || |||||
AGGGTGAGTACATCGTGGAT GCTAG CATGAG AGT G GCTACA GAGTGG GG
CGGTG /
GACGAGTACCAGAAGAGGAT GAGAAGAC C A- GT T GA- AACTT TC
CG

GAM113 AAGTACATCCTAATTTTAAC 2432 CATCCTAATT 2433 C TAACTCTAA--- G
TCTAAAAGGGGTTCCTTGTA TTAACTCTAA AAGTACATC TAATTT AAGG G
AAATTATTTAAGTTATGGTG AAGG ||||||||| |||||| ||||
TACTT TTCATGTGG ATTGAA TTCC T
T TTTATTAAAATG T

GAM114 GCTAAAGTGAAAGTCCTGGA 2445 CCGGAAGTCA 2446 AA AAG T A- TAGCT AC
GGATAGCTTCAAACCTCTTG CTAGAGC GCT AGTGA TCC GG GGA TCAA C
ATTCCGGCCGGAAGTCACTA ||| ||||| ||| || ||| ||||
GAGC CGA TCACT AGG CC CCT AGTT /
GA GA- - GG T---- CT

GAM115 CCCGGGGACGGGGCCACCTA 2459 GCCACCTAGC 2460 G ACGG CAC CCA AGC G
GCCAGCCAGCCCGGGGACGG CAGCCAGCCC CCC GGG GGC CTAG GCC CCG G
GGCCACCTAGCCAGCCAGCC GGGG ||| ||| ||| |||| ||| |||
CGGGG GGG CCC CCG GATC CGG GGC G
G GA-- ACC CAC --- A

GAM116 GCGCTGTGGATTTGTCTTCT 2521 TGTGGATTTG 2522 G--- - TCT- - A TT
ACGCTAGATTTTTTTTAAGC TCTTCTACGC GCGCT TGGATT TG TCTAC GCT GA T
AGTGGATTGTCACAATCTAA TAGA ||||| |||||| || ||||| ||| ||
AGAAGCGC CGCGA ATCTAA AC AGGTG CGA TT T
AGAA C TGTT A A TT

GAM117 CACAGTTTTGCTTTGAAGTG 2529 TGAAGTGCCC 2530 T------- TT CCC A G
CCCAATAGAAGCATTTCCAT AATAGAAGCA CACAGTT TGCT GAAGTG AAT GAA C
TCACACTTCTAGCATCTTAT TTTC ||||||| |||| |||||| ||| |||
TTGACTGTG GTGTCAG ACGA CTTCAC TTA CTT A
TTTATTCT T- AC- C T

GAM118 CAGCCCCCACCTACATAAAT 2547 TTTGTCAGTA 2548 CC -- AAACCCAC
TAAACCCACTGAAAGCAAAA GGTGGAGCTG CAGC CCACCTAC ATAAATT T
TTTGTCAGTAGGTGGAGCTG |||| |||||||| |||||||
GTCG GGTGGATG TGTTTAA /
A- AC AACGAAAG

GAM119 GCATCTGGGATGAACTACAC 2610 TTCATCATAG 2611 G--- ACACGACTTAC GC
GACTTACGTCTCCGCGAAGG CAGATGC GCATCTG GATGAACT GTCTCC G
AGGCCAGTTCATCATAGCAG ||||||| |||||||| ||||||
ATGC CGTAGAC CTACTTGA CGGAGG /
GATA C---------- AA

GAM120 AGGCGCGTATTTTACATGTG 2632 CACCCTGCCA 2633 C ATT AT TA A -------- TT
GTACAGGGTAGAAAACCTTG CGTAAACCCG AGGCG GT TTAC GTGG CAGGGT GA
AAACC G
TAGGTTTCAGTTGAGTCACC CCT ||||| || |||| |||| |||||| || |||||
CTGCCACGTAAACCCGCCT TCCGC CA AATG CACC GTCCCA CT TTTGG /
C --- -- -- - GAGTTGAC AT

GAM121 CACTTAAGCTATGATTCCTG 2676 TATGATTCCT 2677 CT ATTCCT T TTTCC
TAGTGCTCTTTCCTAAGCTG GTAGTGCTCT CACTTAAG ATG GTAG GCTC T
AGCCTATTTTGCCCATTTTA TTCC |||||||| ||| |||| ||||
AGTG GTGAATTT TAC TATC CGAG /
-- CCGTTT - TCGAA

GAM122 TGTGGAAAACATTAAGAGTT 2698 TGGAAAACAT 2699 T ---- TAAGAG TG T
GTTATTGAAAATATTTTTTG TAAGAGTTGT TG GGA AAACAT TTGTTAT AAAA A
GTAACAAAACCATGTTTTAG TATT || ||| |||||| ||||||| ||||
GTCCCA AC CCT TTTGTA AACAATG TTTT /
- GGAT CCAA-- GT T

GAM123 ATGCGTTGTTGGCGCACGAT 2713 GAGGATTACG 2714 G TG CA--- ------- AAAGTCG A TG GC CT

CCAACAAAGTCGAGGATTAC TTGGGGCTGC TTGT GCG CGATCCA AC AGGATT CGT GG TG G

GTTGGGGCTGCTGGTACATT TGGT |||| ||| ||||||| || |||||| ||| || ||

CCTGACGAATCCTAAGTGGT GACG CGT GTTGGGT TG TCCTAA GCA CC AC G

TAAAGAATGGGTTGAGAATT G GT TAAGA AAGAAAT GTGAA-- - GT TT AT

GCTGGCAGGGCGT

GAM124 TCTCAGGACATCTCTAGTTA 2718 CATCTCTAGT 2719 ACA- A A- --- TCA

CTTCGTGGATCAGATTTTCC TACTTCGTGG TCTCAGG TCTCT GTT CTTCG TGGA G

AAATCGAAGCGAACAAGAGA ATCA ||||||| ||||| ||| ||||| ||||

ATAACCTGGGA AGGGTCC AGAGA CAA GAAGC ACCT A

AATA A GC TAA TTT

GAM125 CTAGTTTATTAAATAAAAAA 2737 TAATCCCAGG 2738 TTT A AAAAAA AAAC TTATCTA TC - A

AAGGGAAAACCTGTTTATCT TACAGTTAAT CTAG ATTA ATAA GGGA CTGT ACCTGG TT CT T

AACCTGGTCTTCTATTAGGT CCCC |||| |||| |||| |||| |||| |||||| || ||

AATCCCAGGTACAGTTAATC GATC TAAT TATT CCCT GACA TGGACC AA GG T

CCCTACTATTATATAATCTT TTC A ATCATC AATT ------- CT T A

CTAG

GAM126 GACTTCTTGACTTCCGCCGA 2775 TCGGAACCAC 2776 - - CCGAA ATA- - A GGC TCAG

AGTGGATAGATTCAAACAGG CCGGAAGATT GACTTCT TGA CTTCCG GTGG GATT C AACA TGCC A

CTGCCTCAGATTTTGGCATC ACAG ||||||| ||| |||||| |||| |||| | |||| ||||

ATGTTGGAAATCGGAACCAC CTGAAGA ATT GAAGGC CACC CTAA G TTGT ACGG /

CCGGAAGATTACAGAAGTC C A C---- AAGG A G ACT TTTT

GAM127 TAATAGGCCTACGATAAAAT 2781 TTCATTAACA 2782 G TACGATAA- TC T T

GTCAACATATATTTTTTAAT GCCATGGTGT TAATA GCC AATG AACATA ATT T

TTGTGTTTCATTAACAGCCA ATTA ||||| ||| |||| |||||| |||

TGGTGTATTA ATTAT TGG TTAC TTGTGT TAA T

G TACCGACAA T- T T

GAM128 CCAAACTCAGGAAGGTGACA 2796 ATGGATTGCC 2797 - G AC- T G AT AT T C- TC

AATTCAGGAATTCATGGATT GGGTGATTTT CCAAAC TCA GAAGGTG AAA TCA GA TC GGA TGC GGGTGATTT T

GCCGGGTGATTTTCTCCAGA CTCC |||||| ||| ||||||| ||| ||| || || ||| ||| |||||||||

ATTACCCACGCATTCCCGAT GGTTTG AGT CTTCCGC TTT AGT CT AG CCT ACG CCCATTAAG C
CATGATTTTAAACGCCTTCG T G AAA T A -- C- T CA AC
TGATGTTTGG

GAM129 GCCACCTAGCCAGCCAGCCC 2828 AGCCAGCCCG 2829 CA AG-- G ACGG CAC CCA AG-- G AC -- CA
GGGGACGGGGCCACCTAGCC GGGACGGGGC GCC CCC GGG GGC CTAG GCC CCC GGG GG GGC C
AGCCAGCCCGGGGACGGGGC CACC ||| ||| ||| ||| |||| ||| ||| ||| || |||
CACCTAGCCAGCCAGCCCGG CGG GGG CCC CCG GATC CGG GGG CCC CC CCG C
GGACGGGGCCACCTAGCCAG AC GGCA G GA-- ACC CAC GGCA G GA GA AT
CCAGCCCGGGGACGGGGCCA
CCTAGCCAGC
GAM130 CGAGATTCCTGTACACAGCT 2978 GACCGCATTC 2979 A C CAGCTT AA -- - GC
TGCGAAAGGGGAAGTGGTCA CAACCTGCGT CGAG TTC TGTACA GCG AGG GGAA GTGGTCAC A
CGCACTGGTGACCGCATTCC TGTA |||| ||| |||||| ||| ||| |||| ||||||||
AACCTGCGTTGTACAAGAAA GCTT AAG ACATGT TGC TCC CCTT CGCCAGTG C
TTCG A A ------ G- AA A GT

GAM131 TTTATTAGGTGGGAAAACAG 2994 ATTTGCTACA 2995 TAG-- GA ---------- TCT C
GATGCTCTATGAACACATTC TTTGAATTAA TTTAT GTGG AAACAGGAT GC ATGAA A
ATTTGCTACATTTGAATTAA TTTT ||||| |||| ||||||||| || |||||
TTTTGTTTCTTTACATAACA AGATA CATT TTTGTTTTA CG TACTT C
TAGA CAATA TC ATTAAGTTTACAT TT- A

GAM132 CATGGGATAAGTCAAAGATG 2999 TAAGTCAAAG 3000 ATAAGTCAAA - AA TGG TT
TACCAAGCCTTGGGTTTCGC ATGTACCAAG CATGGG GAT GTACC GCCT G T
AGCAGGCGGTACTATCCCCA CCTT |||||| ||| ||||| |||| |
TG GTACCC CTA CATGG CGGA C /
---------- T -- CGA GC

GAM133 ATGCGTCGCTACTCCCCGCA 3011 TCCCCGCAAG 3012 T TACT - ATG- TT
AGGATGGTGGTTTCAACATC GATGGTGGTT ATGCG CGC CCCCG CAAGG GTGGT C
ACGTTGCCTTGCCGGGGTAT TCAA ||||| ||| ||||| ||||| |||||
TGCGTCGCGT TGCGC GCG GGGGC GTTCC CACTA A
T TTAT C GTTG CA

GAM134 CAGCCCGGGGACGGGGCCAC 3042 AGCCAGCCCG 2829 ACGG CAC CCA AG-- G ACGG CAC CCA AGC G
CTAGCCAGCCAGCCCGGGGA GGGACGGGGC GGC CTAG GCC CCC GGG GGC CTAG GCC CCG G
CGGGGCCACCTAGCCAGCCA CACC ||| |||| ||| ||| ||| ||| |||| ||| |||

GCCCGGGGACGGGGCCACCT CCG GATC CGG GGG CCC CCG GATC CGG GGC G
AGCCAGCCAGCCCGGGGACG GA-- ACC CAC GGCA G GA-- ACC CAC --- A
GGGCCACCTAGCCAGCCAGC
CCGGGGACGGG
GAM135 GTAAGACTGCCTAACCGTTT 3043 TCAACGGACG 3044 GA AA--- TCAA TG
CAAAGCAGTGGCGTTGCTCA TAAGGCAGAT GTAA CTGCCT CCGTT AGCAG G
ACGGACGTAAGGCAGATTAT TAT |||| |||||| ||||| |||||
TATT GACGGA GGCAA TCGTT /
A- ATGCA C--- GC

GAM136 CGCCGGCCTCCCCCGGCTCC 3051 TCGGTTCGCG 3052 C -- C CC C--- G C - --- C CC
CGGCCCTCCGCCCCGCCGGC GGGCCGGGGG CGG CTCCCGGCCCT CG CCG CGGCCCGG C CGCGGC C GC GC C
CCGGGCCCGCGGCCGCCGCC TCCC ||| |||||||||| || ||| |||||||| | |||||| | || ||
CCCGGCCGCCCCGCGCCGCG GCC GGGGGCCGGGG GC GGC GCCGGGCC G GCGCCG G CG CG /
CGCCGGGCCGCTTTCGGTTC C CT C TT TTTC - C C CCC C GC
GCGGGGCCGGGGGTCCCGCG
GGGGGCCGGG
GAM137 GTCGAGGGTGTAGCGGCCGG 3062 TAGCGGCCGG 3063 G --- GT TTCAATGT T
TCGTTCAATGTATCCTCCGG TCGTTCAATG GTCGA GGT GTAGCGGCCG CG ATCC C
GATTTTTGGTCGGTCGTTAC TATC ||||| ||| |||||||||| || ||||
GATACCATCGAT TAGCT CCA CATTGCTGGC GT TAGG C
A TAG TG TTT----- G

GAM138 GGGTGCCGCTCCGCCGGGCC 3067 TCCGGCCGAG 3068 C T C ACTC AG
CGGCCGACTCCCGGGAGCGC CCCGGCGGCG GGGTGC GC CCGCCGGGC CGGCCG CCGGG C
CCCGGTCCGGCCGAGCCCGG CCGC |||||| || ||||||||| |||||| |||||
CGGCGCCGCGCCC CCCGCG CG GGCGGCCCG GCCGGC GGCCC /
C C A CT-- CG

GAM139 CCAGCCCGGGGACGGGGCCA 3135 GCCACCTAGC 2460 AG G ACGG CAC CCA AGC G
CCTAGCCAGCCAGCCCGGGG CAGCCAGCCC CC CCC GGG GGC CTAG GCC CCG G
ACGGGGCCACCTAGCCAGCC GGGG || ||| ||| ||| |||| ||| |||
AGCCCGGGGACGG GG GGG CCC CCG GATC CGG GGC G
CA G GA-- ACC CAC --- A

GAM140 CTGCTAGTAGGGCTGCTGGG 3136 CTGCTAGTAG 3137 --- T GGG AG C
CTGCTAGTAGGGCTCCTGGG GGCTGCTGGG CTGCTAGTAG GGC GCT CTGCTAGT GGCT C
CTGCTAGTAGGGCTGCTGGG CTGC |||||||||| ||| ||| |||||||| ||||
CTGCTAGTAG GATGATCGTC TCG CGG GATGATCG TCGG T
GGG T --- -- G

GAM141 CTTGCAGTTCACCCACCATG 3175 CACCATGTTC 3176 C ACC T- TTTACCCG CC GT
TTCGAATTTACCCGCCCCCC GAATTTACCC CTTG AGTTC CACCATG TCGAA CCC CC T
CGTTTTGGCAGGGAAACAGC GCCC |||| ||||| ||||||| ||||| ||| ||
TTTCGGCTCATGGTGTAGGA GAAC TTAAG GTGGTAC GGCTT GGG GG /
ATTACAAG A GAT TC TCGACAAA AC TT

GAM142 TGGGAAGACTTGCGCGACCC 3183 ACCCTGAGTA 3184 GA GAC-------- ATTTAAA TT
TGAGTATTTAAAGGATTTAC TTTAAAGGAT TGG AGACTTGCGC CCTGAGT GGAT A
TATCCGACACTCAGGCAATC TTAC ||| |||||||||| ||||||| ||||
GACAAAGTGCGAGTCTACCA ACC TCTGAGCGTG GGACTCA CCTA /
A- AAACAGCTAAC CAG---- TC

GAM143 TCTAATGGAAATGCGATGGC 3212 TTAGTGAGGG 3213 AAATG --- ACTT - TTT
A- TG
TGTTAGTGAGGGACTTACAC ACTTACACGT ATGG CGATGGCTGT TAGTGAGGG ACA
CGTGT ATTT ACC T
GTGTTTTATTTAACCTGTGA GTTT |||| |||||||||| ||||||||| ||| ||||| |||| |||
CGGTAAAGATTCACATGTTG TGTC GTTGCCGGCA GTCATTTCC TGT GTACA
TAGA TGG G
TCATGCCTTTACTGCAAACG AAAA- AAC GTAC T CT- AA CA
GCCGTTGAAAACTGTTGGG

GAM144 TCGTGTTGCTGAGCTGCTTG 3218 GAGCTGCTTG 3219 GC - CGAGA A
CCGAGATCCAGACTCTGGAG CCGAGATCCA TCGTGTT TGAG CTGCTTGC TCCAG C
CAAGCGGTCTCAAAATACGA GACT ||||||| |||| |||||||| |||||
AGCATAA ACTC GGCGAACG AGGTC /
A- T ----- T

GAM145 ATAAACCCTATATGAGGAAA 3235 AGGAAATTTT 3236 CCCTA GAG A- C TG
TTTTATTAGTACGTTTGTGT ATTAGTACGT ATAAA TAT GAAATTTTATT GTA GTT T
AACTGCAAAATAAAATTTTA TTGT ||||| ||| |||||||||| ||| |||
AATAAATACTTTAT TATTT ATA TTTTAAAATAA CGT CAA /
CATAA AA- AA - TG

GAM146 GCATATATCCGTTTTCTCCT 3240 TCCTTTGTAT 3241 TATA TT T AACCCG - A
TTGTATGAACCCGGTGGGCA GAACCCGGTG GCA TCCGTT CTCCTTTG ATG GTG GGC A
AGGGCCACATAAAAACATTA GGCA ||| |||||| |||||||| ||| ||| |||
GAGGGGCAACGGGCTGC CGT GGGCAA GGGGAGAT TAC TAC CCG G
C--- C- - AAAAA- A G

GAM147 TTGCGCCACAGCGGACGTAC 3261 CAGCGGACGT 3262 CG CA AC---------- A A ATTC
ATCAATCAGATTCGTTACTT ACATCAATCA TTG CCA GCGG GT CATCA TCAG G
GACTGATGCACACAAAGAAA GATT ||| ||| |||| || ||||| ||||
ATGCCGCATGGTACAA AAC GGT CGCC CA GTAGT AGTT /

AT A- GTAAAAGAAACA C C CATT

GAM148 TGTAACTTCACGCTACCCTA 3268 TCACGCTACC 3269 TCA CTACC- A G AATA ACT
AACGTACAATACTGGGACTA CTAAACGTAC TGTAACT CG CTAA C TAC CTGGG A
GAACCCAGAGGTAGTTAGAA AATA ||||||| || |||| | ||| |||||
TATACGGTAGTTACA ACATTGA GC GATT G ATG GACCC /
TG- ATATAA - - GA-- AAG

GAM149 GGCCATCTTCCTCATGATGC 3278 TTCCTCATGA 3279 CTT- TGATGC - GT
CGCGATTTGTCAAGAAATAC TGCCGCGATT GGCCAT CCTCA CGCG ATTT C
GCGATTGGGGCTGCATGGCT TGTC |||||| ||||| |||| ||||
TCGGTA GGGGT GCGC TAAA A
CGTC TA---- A GA

GAM150 ACACCCTTACACCGATGATA 3287 TTGGCAGAAT 3288 A CCGA AAGA AGCAGAG
AGACCAACGAGCAGAGAATA CATGAAGGGT ACACCCTT CA TGAT CCAACG A
AACCGCGTTGGCAGAATCAT GT |||||||| || |||| ||||||
GAAGGGTGT TGTGGGAA GT ACTA GGTTGC A
- ---- AGAC GCCAAAT

GAM151 GCTGGGCTGCTAGTAGGGCT 3311 TGGCTTGCTT 3312 TG -- GCT T T- G
GCTGGGCTGCTAGTAGGGCT GCTTGCTTGC GC GGCT GCTAGTAGG GC GGGC
GCTAGTAGG C
GCCTGCTGGCTTGCTTGCTT TAGT || |||| ||||||||| || |||| |||||||||
GCTTGCTAGTGGGGCCGC CG CCGG TGATCGTTC CG TTCG CGGTCGTCC T
-- GG GTT - TT G

GAM152 TCGACAACTACCTCCGAAAG 3319 TGTTTTGTGG 3320 G --------- --- AAAGT TG T
TGTGTCCTGTTGGATGTTTT ATTAGGTAAA TC ACAACT ACC TCCG G TCC G
GTGGATTAGGTAAAACAGAA ACAG || |||||| ||| |||| | |||
AGTTGTGGA AG TGTTGA TGG AGGT T AGG T
G AAGACAAAA ATT GTTT- GT T

GAM153 GCACCAACCATCCTTATCGA 3338 TAAAGGAAGG 3339 A A ---------- A
CTCCGGTAGAGATGTCGTCA ATGGTGC GCACCA CC TCCT TATCG C
TCCATAAAGGAAGGATGGTG |||||| || |||| |||||
C CGTGGT GG AGGA ATGGC T
A A AATACCTACTGCTGTAGAG C

GAM154 CCTAGTGGTATGTTCTTTTC 3359 TGAGTTAGTG 3360 TA T TTC TCT- GGCCA AC
ATCTGAGTTAGTGGCCAAGC GCCAAGCAAT CC GTGG ATG TTTTCA GAGTTAGT
AGCAAT A
AATACAAGGTTGCTCAACTA ACAA || |||| ||| |||||| |||||||| ||||||

ACTCCCGTTGAAAATCCCAT GG CACC TAC AAAAGT CTCAATCA TCGTTG /
CCACCCGG CC - CCT TGCC AC--- GA

GAM155 CTGGAACTGGTGGAACTTGT 3375 GGACGAGGAA 3376 AAC- GAA A- CGCA
CTATGCGCAAATTACAGAGG CACCGTATAC CTGG TGGTG CTTGTCT TG A
ACGAGGAACACCGTATACCA CAG |||| ||||| ||||||| ||
G GACC GCCAC GAGCAGG AC /
ATAT AAG AG ATTA

GAM156 GGACGCGGGAATTTCCTTGA 3406 AGGCATCAAG 3407 AC TTT ATT--- A
TGATTACGAGAACTTCGTTT GTTCCTGCCG GG GCGGGAA CCTTGATG ACGAG A
CAGGCATCAAGGTTCCTGCC CC || ||||||| |||||||| |||||
GCC CC CGTCCTT GGAACTAC TGCTT /
GC --- GGACTT C

GAM157 ACAAGCTCTGTCAGATTCAA 3499 TCTGTCAGAT 3500 A TC T TT AAAAATAATT GC C
AAAATAATACC AC
AAAATAATTGGTGGCCAACT TCAAAAAATA GC TG CAGA CA GGTG CAA TTCTAG
CAA A
TCTAGAAAATAATACCCAAA ATTG || || |||| || |||| ||| |||||| |||
CACCTTGCGCTCTCACGCTG CG AT GTCT GT TCAC GTT AAGGTC GTT /
GAACTTGAACACTTGCTCTG - TA - C- ---------- AA C GCACTCTCGC- CC
TAATGCTGT

GAM158 GAGGTGTCGGTTGACGGAAA 3509 TGACGGAAAG 3510 GGTT - T C- CAACCG
GAGTTTTGGCCAGGGCGGCA AGTTTTGGCC GAGGTGTC GACGG AAAGAGTT TGGC
AGGGCGG T
ACCGTTATAGATTCGTCTTT AGGG |||||||| ||||| |||||||| |||| |||||||
CGCTATGACTCTTTGCTGTC TTCCACAG CTGTC TTTCTCAG ATCG TTCTGCT T
GACACCTT ---- G T CT TAGATA

GAM159 GTCCGATTCGATACAAGAAC 3550 TTGAAGCCTG 3551 GA - AAGAAC- TG- T A
GCCGA T
CCTGTCATGTCTCACCAGGC GGGAGTATGA GTCC TTC GATAC CC TCATG CTC
CCAGGCT AATC G
TGCCGAAATCTGTGGATTGA AGTG |||| ||| ||||| || ||||| ||| ||||||| ||||
AGCCTGGGGAGTATGAAGTG TAGG AGG CTATG GG AGTAT GAG GGTCCGA
TTAG T
GATGATAGGTATCAGGAAAG AA A GATAGTA TGA - G AG--- G
GAT

GAM160 TTTTAATTCTTGTAACAAAT 3564 ATTCTTGTAA 3565 ACAAAT AC- ATA
GTACTAGTAATATTTTCTAC CAAATGTACT TTTTAATTCTTGTA GT TAGTA T
TAATGGCCCTACGGGAGTTA AGTA |||||||||||||| || |||||
GAA AAGATTGAGGGCAT CG ATCAT T
CC---- GTA CTT

GAM161 TCATTGACAACTTCAAGATT 3572 ATGGATCTAT 3573 T ----- - GC CGT
TGCTTCCCCGTAAACGGGAA GGTCAAGGGT TCAT GACAACT TCA AGATTT TTCCC A
ATGGATCTATGGTCAAGGGT TGTC |||| ||||||| ||| |||||| |||||
TGTCATGG GGTA CTGTTGG GGT TCTAGG AAGGG /
- GAACT A TA CAA

GAM162 GGCGATGCCTCCGTTCCAAC 3582 CAGCACGCGA 3583 C - - - -- TCTA- CA
CTCTCTATTGTCCAACCGAC GGTTCTGGAA GG GATG CCT C CGTTCCA ACCTC TTGTC A
AGCACGCGAGGTTCTGGAAC CGAG || |||| ||| | ||||||| ||||| |||||
GAGAAGGACATCCC CC CTAC GGA G GCAAGGT TGGAG GACAG /
- A A A CT CGCAC CC

GAM163 TGCTTGTTTTGTGCCCCGGG 3610 TTCGTGCCTG 3611 - CC- A AC GCCC
ACAACAACGGTTTGCCCCGC CACGCACGAG TGCTT GTTTTGTGC CGGG CA AACGGTTT C
GAAGAACTGTTCGTGCCTGC ACAA ||||| ||||||||| |||| || ||||||||
ACGCACGAGACAAAGCA ACGAA CAGAGCACG GTCC GT TTGTCAAG G
A CAC - GC AAGC

GAM164 ACCGGTCCTTGAGAAAGTAT 3619 TCCTTGAGAA 3620 T G A T CC CC
ACGCCCTCGCCTTTTGAGTT AGTATACGCC ACCGG CCTT AG AAGTA ACG CTCG T
GTTATTTACTGGAGGCCTGG CTCG ||||| |||| || ||||| ||| ||||
T TGGTC GGAG TC TTTAT TGT GAGT /
C G A - T- TT

GAM165 GTGACCCGTCATCCACGCTC 3632 CCCGTCATCC 3633 ACC C CACG A GA
TTGATCCCGACAATGGGAAC ACGCTCTTGA GTG CGT ATC CTCTTG TCCC C
AAGAGGAGATCACGTGCCAC TCCC ||| ||| ||| |||||| ||||
CAC GCA TAG GAGAAC AGGG A
CGT C AG-- A TA

GAM166 ATGGTCACCCCAAGGTGGAT 3662 TATACAATTG 3663 - GG G --- CA
GCTGCCGTTCATTGTAACGG GTGGTGGCCG ATGGTCACC CCAA TG ATGCT GCCGTT T
TTTCGGTATACAATTGGTGG T ||||||||| |||| || ||||| ||||||
TGGCCGT TGCCGGTGG GGTT AC TATGG TGGCAA T
T A- A CTT TG

GAM167 GCCTTGCGTTACAATCGATA 3670 AATCGATACT 3671 T CA - ATACTT- A C T
CTTTGAACTTCACCTTCCTT TTGAACTTCA GCCT GCGTTA AT CG TGA CTTCA CTTCCT T
TCGGGGAAGATGAAGATCAT CCTT |||| |||||| || || ||| ||||| ||||||
TTGGAGCGCATCTTAACGTC TGGG TGCAAT TA GC ACT GAAGT GAAGGG C
GGGT C TC C GAGGTTT A A G

GAM168 TGAAACCTTCCGGAACTACG 3678 TGAGAACGAG 3679 A -- AA - T AA AA - T
ATGAAATCAAAGCCGTTCTC CCTGACATCC TGAA CCTTC CGG CTA CGA GA TCA GC CGTTCTCGAGG C
GAGGTCATTCTTGAGAACGA TCGT |||| ||||| ||| ||| ||| || ||| || ||||||||||
GCCTGACATCCTCGTTGGAG ACTT GGAAG GTC GGT GCT CT AGT CG GCAAGAGTTCT A
CTGAAGAAGGTTCA - AA GA T C AC C- A T

GAM169 AGAGCTTTTCAGACTAAAAA 3684 TACAATATTT 3685 T TC -- A GT- A GA-- -- - TT
TGTGTTACAATATTTATAGA ATAGACTAAG C TT AGA CTA AAATGT TACAAT TTTATA CT AAGGATA AGA A
CTAAGGATAAGATTATCTCT GATA | || ||| ||| |||||| |||||| |||||| || ||||||| |||
ATATTCTTTCAGAAGATATG G AA TCT GAT TTTACA ATGTTA AGGTAT GA TTCTTAT TCT /
GAGATTGTACCAACATTTAT C CC CA A ACC G AGAA CT A CT
AGACTCTCCAACGCTCT

GAM170 ACGTGACTGCTAATGCAGAC 3689 TCTGACCAAC 3690 CTAAT AGA- C CG CGAT
TGGGTTCGGTCAGAGACGAC CCGGCAAGGC ACGTGACTG GC CTGGGTT GGTCAGAGA A A
GATAAATTTTATCTCTGACC TCAG ||||||||| || ||||||| ||||||||| |
AACCCGGCAAGGCTCAGTCA TGCACTGAC CG GGCCCAA CCAGTCTCT T /
CGT T---- GAAC - AT TTAA

GAM171 ATCTCGTCCCCATGGAAGAG 3709 CGTTCAACTT 3710 G C AAGA- A-- A C AG
GCGAAAGAGGCACCTAGGCA TCGTCGATAA ATCTC TCC CATGG GGCGAAAG GGC CCTAGG AGC C
GCAGCTTGTTCCTAGGCGTT CCAT ||||| ||| ||||| |||||||| ||| |||||| |||
CAACTTTCGTCGATAACCAT TGGAG AGG GTACC CTGCTTTC TTG GGATCC TTG /
GAGGAGGAGGT G A AATAG AAC C - TT

GAM172 GCCTCAGGGTTCCAGACACG 3714 TCCCTGAGCC 3715 A- T ACACGTTCC - A G C
TTCCGCCGGAGGACTTTGCG TGGACCTGAG GCCTC GGGT CCAG GC CGG GGACTTTGC GC A
GCCAGGGTGGCAGAGTCCCT AGGT ||||| |||| |||| || ||| |||||||||| ||
GAGCCTGGACCTGAGAGGT TGGAG TCCA GGTC CG GTC CCTGAGACG TG G
AG - --------- A - G G

GAM173 TGCCCGGTTGCTGCTGCTGC 3748 GGTTGCTGCT 3749 GG TG ------ TCA TC
TCACGCTCCTTGCGCGCATT GCTGCTCACG TGCCC TTGC CTGC TGC CGC C
CTCTGCAGTGGCAAAGGGCA CTCC ||||| |||| |||| ||| |||
ACGGG AACG GACG ACG GCG /
A- GT TCTCTT C-- TT

GAM174 GGTTCTTCGCCAACATGGCG 3782 AAACTGCAGA 3783 ----- A- ATG CTC GTG CC
GTCCTCGCAGGTGTCAAGAC CTGCGACGTA GGTTCT TCGCC AC GCGGTC GCAG
TCAAGA C
CCATCTCTTGAAACTGCAGA CGGC |||||| ||||| || |||||| |||| ||||||
CTGCGACGTACGGCGATTTG CCAAGA AGCGG TG CGTCAG CGTC AGTTCT A
GAGAACC GGTTT CA CAG A-- AA- CT

GAM175 GTACTTCTACACCAGCGGGA 3808 CCAGAACCTT 3809 ACACCAG AA A GA A -- C -
CAACGA TC
ACATGCAGAGATCGGCATGT GCCCTTCAGT CGGG CATGC GA TCGGC TGTGGC AAG
GCA GGT GC A
GGCAAGCGCAGGTCAACGAG CACA |||| ||||| || ||||| |||||| ||| ||| ||| ||
CTCAGAGCCCAGAACCTTGC GCCC GTACG CT AGTCG ACACTG TTC CGT CCA
CG /
CCTTCAGTCACAGCTGAGAT A------ AC A AG - AC C T AGACC- AG
CAGCATGCACCCGAAGAAGC
AC
GAM176 TCGCAGCTACATCAACAAGA 3878 TACGGTACCT 3879 TAC CAAG - TA G
TACGGTACCTGACCGATGAA GACCGATGAA TCGCAGC ATCAA ATAC GG CCTGACCGAT A
AATCGGTCGGGCGCCAGTAT AATC ||||||| ||||| |||| || ||||||||||
GATTGATCGCGCTGTGA AGTGTCG TAGTT TATG CC GGGCTGGCTA A
CGC AG-- A GC A

GAM177 ATGGCTGTGCTGGTCCAAAC 3886 CTGGATCACT 3887 T GC- AA G - T
AGTGAGGCTGGTGCACTAAC AACTGCTGT ATGGC GT TGGTCCA CAGT AG GC G
TGCTGGATCACTAACTGCTG ||||| || ||||||| |||| || ||
T TGTCG CA ACTAGGT GTCA TC CG G
T ATC C- A A T

GAM178 AAGCAAAACTGGAGGACACC 3934 CTAGTGCCAT 3935 G ACAC C - - T - ATAT- AT-
- T CG
GCGCGCAAGGTGTGTAGTGT TATACTTCAC AGG CG GCGCA AG GTGTG AGTGTA TGGCA
AAC CA GAT C
ATGGCAATATAACATCATGA ACTC ||| || ||||| || ||||| |||||| ||||| ||| || |||
TCGCTTCATCTGTCGCGTTT TCC GC CGTGT TC CACAC TCATAT ACCGT TTG GT
CTA T
CTAGTGCCATTATACTTCAC G AT-- - A T T T GATCT CGCT - CT
ACTCTATGTGCCGTACCTGC
AATTCTACTT
GAM179 GTGTGTGTGTGTGCGCTCAC 3953 TCACACGGAA 3954 T TG T GGAACGAGAACAA T
TG T GA GAG
ACGGAACGAGAACAAGTGTG CGAGAACAAG GTGTG CGC CACAC GTGTG GTG CGC
CACACG AC A
TGTGTGCGCTCACACGGAAC TGTG ||||| ||| ||||| ||||| ||| ||| |||||| ||
GAGAACAAGTGTGTGTGTGT CGCGC GTG GTGTG CACAC CGC GTG GTGTGT
TG A

GTGCGCTCACACGGAACGAG T GT T AACAAGAGCAAGG T GT T G- AAC
AACAAGTGTGTGTGTGCGCG
CTCACAC
GAM180 CCAGGCGATTACATATTGCT 3966 CACCGGTGCT 3967 A ATT TTCCA GT TCT C
TCCACCGGTGCTCTGGTTGG CTGGTTGGTC CCAGGCG TTACAT GC CCG GC GGTTGGT
T
TCTGGACCAATCTTTGCTAC TGGA ||||||| |||||| || ||| || |||||||
GGCTACGCGTGTGACGCCTG GGTCCGC AGTGTG CG GGC CG CTAACCA G
G - --- CATC- AT TTT G

GAM181 TGACGAAATGCCACACATTA 3997 TGAGGAACAC 3998 C A- T - C ATCCA TAC
AT- TT
GGAGTGTGAGGAACACGGGC GGGCATCCAT CACA ATT GGAG GTGA GGAA ACGGGC
TGGGC CTGGGG TTC G
ATCCATGGGCTACCTGGGGA GGGC |||| ||| |||| |||| |||| |||||| ||||| |||||| |||
TTTCTTGTCGAATTACCCTA GTGT TAG CCTC CGCT CTTT TGTCCG ATCCG
GATCCC AAG /
GACTGCCTACGCCTGTATTT T CG - A A C---- TCA ATT CT
CATCGCCTCCGCGATTTGTG
GGATGATGTCA
GAM182 GATCGTTATGCCAAGGAAGA 4027 TATGCCAAGG 4028 TT C -- GA CCGCG
TCCTCCGCGATAACTGGGAG AAGATCCTCC GATCG ATG CAA GGAA TCCT A
ATTCCATTTGACATCCGATC GCGA ||||| ||| ||| |||| ||||
CTAGC TAC GTT CCTT AGGG /
C- A TA AG TCAAT

GAM183 GCAGAAAGACTTTCACCAAC 4042 TGTGGAGGCA 4043 AAA - TC AAC- CT ACT
CCTCCATACTGCCATACTTC AGGGTTTGAT GCAG GAC TT ACC CCTCCATA GCCAT T
GCATGGCTGTGGAGGCAAGG GTTA |||| ||| || ||| |||||||| |||||
GTTTGATGTTAAACTGC CGTC TTG AG TGG GGAGGTGT CGGTA /
AAA T TT GAAC -- CGC

GAM184 CATCCGAGCTTTCAGACCCC 4055 TCTCATGGCA 4056 C AG T A - A AA- - G A-
TGAC
GCTAAAGCAAGGGAGGAGGA TTGGCGGGCG CAT CG CT TC GAC CCCGCTAA GC GGGA
GGA GAACA AGCG G
ACAAAGCGTGACGAAATCGC TCAG ||| || || || ||| |||||||| || |||| ||| ||||| ||||
TCCTGTTTATCCATCTCATG GTA GC GA GG CTG GGGCGGTT CG CTCT CCT TTTGT
TCGC /
GCATTGGCGGGCGTCAGGCA A CT C A C A GTA A A CC TAAA
GTCCGAATG

GAM185 ACCTTACAGCGCGAATCACA 4072 TAGTGCACTA 4073 TTACA - C ---- G ---- C
ATTGCACGACCGTGATCCTC GGTTTTGTAT ACC GCGCGAAT CA AAT TGCAC AC
CGTGATCCT A
AAGGGGATCATGTACCGTAG TCGC ||| |||||||| || ||| ||||| || |||||||||
TGCACTAGGTTTTGTATTCG TGG TGCGCTTA GT TTG ACGTG TG GTACTAGGG A

CGTATATGGT TATA- T T GATC A CCAT G

GAM186 GTAGTCGAACTGGCTTACAC 4075 AAAGGAACGC 4076 --- ACA C T ACGAA GGAAC
A- CCGA G
CCAGCTTGTCCAGGACGAAA ATACCAGAAC TG GCTT CCCAG TTG CCAGG AA GCAT
CCAGAA AG G
AGGAACGCATACCAGAACCG CGAA || |||| ||||| ||| ||||| || |||| |||||| ||
AAGGGAACTAAGATTCTGGA AT TGAA GGGTC AAC GGTCC TT CGTA GGTCTT
TC A
CATGCCGAATTGGAAGCCTG AAT CC- - - GAAGG AAGC- CA AGAA A
GCAACTGGGCCAAGTTAATA
GACGAGACGC
GAM187 CGGTGCTGAGGGGTTACAAA 4097 CATGCCGAAC 4098 GG T A CC ACTCC A
GCCGCGTTCACTCCGCATGT GCAACTTCGT CGGTGCTGAG GT AC AAG GCGTTC
GCATGTCG G
CGAGCTTGACATGCCGAACG ACAA |||||||||| || || ||| |||||| ||||||||
CAACTTCGTACAACTTAGCA GCCACGATTC CA TG TTC CGCAAG CGTACAGT C
CCG AA - C AA C---- T

GAM188 GTAGGCGTGTACCGAACGAC 4105 AAGCAAGCAC 4106 GAA-- C--- CCAGAAGA GG- A
AGGCAA CAA
CCCGGCCCAGAAGACCAGGG AGAGACTGGA C CGAC CCGGC CCAG CTG
TGCTTGTT CGG T
CTGATGCTTGTTAGGCAACG AAAG | |||| ||||| |||| ||| |||||||| |||
GCAATAAGACCGAAGCAAGC G GCTG GGCCG GGTC GAC ACGAACGA GCC
A
ACAGAGACTGGAAAAGTAAG ATGCA CCTA AATGAAAA AGA - A----- AGA
CCGGATCCGTCGACGTAGGA
TCGTCTAC
GAM189 GGGTTGCCCGAAAGTATGGG 4220 TACCCATACA 4221 T - A------ C C GCTTCG
CTACGCGCTTCGTTGTAAAG AAACCCTTCG GGGT GC CCGAA GTATGGG TA GC T
CTACCCATACAAAACCCTTC GCGC |||| || ||||| ||||||| || ||
GGCGCACTC CTCA CG GGCTT CATACCC AT CG /
- C CCCAAAA - - AAATGT

GAM190 GATCCAGCTGTGGTGCCTAA 4227 TGTGGTGCCT 4228 CAGC - TAA- C ACAA
GGACATCAGGGACAAGTACC AAGGACATCA GATC TGTGGT GCC GGA ATCAGGG G
CCCTGGTTCCGAACGGTGAC GGGA |||| |||||| ||| ||| |||||||
CACAACGAGATC CTAG ACACCA TGG CCT TGGTCCC /
AGCA G CAAG - CCAT

GAM191 CTCTCCCAGTTTACTCAATA 4247 GTCGTGTGGT 4248 C AC A C TC
TACACCGCGAGTTCTCAACG TGAAAGGACT CTCTCC AGTTT TCAAT TACAC GCGAGTTC A
AACTCGTCGTGTGGTTGAAA AGGG ||||||| ||||| ||||| ||||| ||||||||
GGACTAGGGGAG GAGGGG TCAGG AGTTG GTGTG TGCTCAAG /
A AA - C CA

GAM192 CATCTCAGGAGTTTTAGTGT 4253 TCTCAGGAGT 4254 ---- TAG ACC - A-- AAAGA GAA
GAC
TACCGTCCTGCGCAAGCAAA TTTAGTGTTA G TTT TGTT GTCCTGC GCA GC TGA
CTATACCTTT A
GATGAGAACTATACCTTTGA CCGT | ||| |||| ||||||| ||| || ||| ||||||||||
CAACAAAGGGTATAGGGATC C AAA ACAG TAGGATG CGT CG GCT
GATATGGGAA /
GGAAAGGCCGCTGCAGTAGG TTTT TAA ACT A CGC GAAAG AGG ACA
ATTCAGACAAATAAATTTTC
TCTTGAAAATG
GAM193 TTTTCTTTTGTTGGCTATTC 4263 TGGGAAGAGA 4264 T G- A TTTC G
CCTTTCACCGTGCGTACGGT ACAACAAAGA TTTTCTTT GTTG CT TTCCC ACCGT C
GGGAAGAGAACAACAAAGAA AAA |||||||| |||| || ||||| |||||
AA AAAAGAAA CAAC GA AAGGG TGGCA G
- AA G ---- T

GAM194 GTATATACTTAGATGAGTCA 4448 TTAGTTCTTT 4449 TAC T TCAT TGTC
TTTAAAACTTGTCTATTTAG CTCTAACTTA GTATA TTAGA GAG TTAAAACT T
TTTTAGTTCTTTCTCTAACT TAC ||||| ||||| ||| |||||||
TATAC CATAT AATCT CTT GATTTTGA /
TC- - TCTT TTTA

GAM195 CCGCATCACCGACCAGGCGG 4454 TTCGCGCGTG 4455 CA GA G G GG G G TC
GCGCGGGGAGCGGGCTCTGC TATGGGGAGT CCGCAT CC CCA GCG GCGCG GA CG GC T
TGCGTGTTTTCGCGCGTGTA GCGG |||||| || ||| ||| ||||| || || ||
TGGGGAGTGCGG GGCGTG GG GGT TGT CGCGC TT GT CG G
A- -- A G TT - G TC

GAM196 CACCCGCGCGCGCCGGCCAA 4458 CGTGGCGGTG 4459 A G G AA TGC
CACGGCCTGCCTTACGGCCG GGCGGCGCGG C CCCGCGC CGCC GCC CACGGCC C
TGGCGGTGGGCGGCGCGGGG GGG | ||||||| |||| ||| |||||||
G G GGGCGCG GCGG TGG GTGCCGG T
G - G CG CAT

GAM197 ACGAGATTGTGAACCTGCGC 4521 GCGGACTTTG 4522 ATT TG CCT G A GA - C
CTGGAGATCGAGCGCGCCCG GGGCGTTTTG ACGAG G AA GCGCCT GAG TC GCG CG C
CGACGCGGACTTTGGGGCGT CCGC ||||| | || |||||| ||| || ||| ||
TTTGCCGCTTCGT TGCTT C TT TGCGGG TTT AG CGC GC C
CGC GT --- G C G- A G

GAM198 GCGGCTCGCGCGGCGGGTAA 4538 CCCCGTGGAC 4539 CGC - AA ACGA G
GCGGACGAGCCTGCCGCGGC GCCGCCCTCG GCGGCTCG GGCGG GT GCGG
GCCTGCCGC G

GGCGGCGGGCCCCGTGGACG AGCC |||||||| ||||| || |||| |||||||||
CCGCCCTCGAGCCGC CGCCGAGC CCGCC CA TGCC CGGGCGGCG C
TC- G GG C--- G

GAM199 CGATGAATACTTTAATGACG 4577 TATAATGTCT 4578 A TT-- T CC T ATA-- TT
TTATACCTCTACATAATGCT TATCTCGTAT CGATG ATAC TAA GACGTTATA TC AC ATGC A
TATAGCGTGCAACGTTGATA ATAT ||||| |||| ||| ||||||||| || || ||||
TAATGTCTTATCTCGTATAT GTTAT TATG ATT CTGTAATAT AG TG TGCG /
ATTG A CTCT - -- T CAACG AT

GAM200 TGAGTTTGTCCACAAGTTTG 4582 TCCACAAGTT 4583 GTC -- - - AA
AGGGCAAGAACCTGTTTGCC TGAGGGCAAG TGAGTTT CACA AGTTTG AG GGCAAG C
TCTGTAGACTACTGTGTAAA AACC ||||||| |||| |||||| || ||||||
GACTCA ACTCAGA GTGT TCAGAT TC CCGTTT C
AAT CA G T GT

GAM201 GCCGAGTGGCGGTCAACAGC 4634 GCCCGGTGCC 4635 GTCAACA A
CTCGCGCCGGGAGAGCCCGG GCTTGGC GCCGAGTGGCG GCCTCGCGCCGGG G
TGCGAGGCGCCCGGTGCCGC |||||||||| ||||||||||||
TTGGC CGGTTCGCCGT CGGAGCGTGGCCC A
GGCCCG- G

GAM202 TTGCGACTGGTGCAACAATG 4652 TGGCGTGAGA 4653 C GCA---- ATG- TGAAG T
GTTTCGCTGAAGGTTTGAGA CATGGTGTGA TTGCGA TGGT ACA GTTTCGC GTT G
CATGGCGTGAGACATGGTGT CCTA |||||| |||| ||| ||||||| |||
GACCTAAACCATTCGCAA AACGCT ACCA TGT CAGAGTG CAG /
T AATCCAG GGTA CGGTA A

GAM203 GTCCCAGCGCGCGAATTCGT 4683 CAGCCGCGGC 4684 - -- AT---- AC G
GGACGCCGTCTGGCAGCCGC GGACGTCGCT GTC CCAGCGC GCGA TCGTGG GCC T
GGCGGACGTCGCTGGCGCTG GGCG ||| ||||||| |||| |||||| |||
GTGAT TAG GGTCGCG CGCT GGCGCC CGG C
T GT GCAGGC GA T

GAM204 GCTGCTCTTGCTGCTCTTGC 4731 TCTTGCTGCT 4732 T TCTT T TCTT T TCTT T TCTT T T
TGCTCTTGCTGCTCTTGCTG CTTGCTGCTC GC GC GC GC GC GC GC GC GC C
CTCTTGCTGCTCTTGCTGCT TTGC || || || || || || || || || ||
CTTGCTGCTCTTGCTGCTCT CG CG CG CG CG CG CG CG CG CG T
TGCTGC T TTCT T TTCT T TTCT T TTCT T T

GAM205 CTGGCCGACCGCGGCGGCGG 4765 GGTTGCGCCG 4766 A G AGC T GG
CGAGCGCTTCCGCGTGGCGA CTGCAGCGGC CTGGCCG CCGC GCGGCGGCG GCT CCGCGT
C

GCGCGGCGGTTGCGCCGCTG TGGC ||||||| |||| ||||||||| ||| ||||||
CAGCGGCTGGCCGG GGCCGGT GGCG CGTCGCCGC TGG GGCGCG /
C A GT- C AG

GAM206 GATCTCAAAGACCGATATGG 4775 TCAAAGACCG 4776 CAAA CGA AAACTCAAA- T
AAACTCAAACCGTTATCGGG ATATGGAAAC GATCT GAC TATGG CCG T
TACAATAAACCATGACTGTC TCAA ||||| ||| ||||| |||
CAGATT TTAGA CTG GTACC GGC A
C--- TCA AAATAACATG T

GAM207 CAGTCCCGTTGCCCATGAGC 4811 TGCCCATGAG 4812 C GTTG -- CAG C----- TT G
AGGTACACTTTGGTTCAGGA CAGGTACACT CAGT CC CCCAT GAG GTACA TTTGG CAG
A
AACTGCCCAAGACATCATGT TTGG |||| || ||||| ||| ||||| ||||| |||
ACACTCCGATGGGAAAGGAA GTCA GG GGGTA CTC CATGT GAACC GTC A
CTG A AAA- GC A-- ACTACA C- A

GAM208 GCGCAGAGCTGTACCAGCGC 4862 TACCAGCGCC 4863 G A - AC - T G AGG
CTGGACGCGCTGTTGCTGCC TGGACGCGCT GCGCA AGCTGT CCAGCGC CTGG GCGCTGT
TGC GCC CTGC G
GCTGCAGGGCTTCGCGGGGC GTTG ||||| |||||| ||||||| |||| ||||||| ||| ||| ||||
TGCGCGCGGCGCCCGGCGCG CGCGT TCGGCG GGTCGCG GGCC CGCGGCG GCG
CGG GGCG C
CTGGAGCGGCTGTGCGC G A C -- C T - CTT

GAM209 GGGCCATGGTCAAGGCGTCT 4869 CAGCCGCCGT 4870 CC CAA T GAAAC TCC
GGAAACTGGCCATCCACTTT CGCCATCCC GGG ATGGT GGCG CTG TGGCCA A
GGCCACAGCCGCCGTCGCCA ||| ||||| |||| ||| ||||||
TCCC CCC TACCG CCGC GAC ACCGGT /
-- CTG C ----- TTC

GAM210 AAGTGGACCGGGAGGACCGA 5002 GATCTGGGCC 5003 T C A A G AAG TT A ----
ATG
GGAAGAGTCTTTCCTGATCT CCCGTCCTCT AAG GGAC GGG GG CC AGG AGTCT CCTG TC
TCTGAC A
CTGACATGATGGGTCAGATC T ||| |||| ||| || || ||| ||||| |||| || ||||||
AAGACAGGTTGGATTAGATC TTC CCTG CCC CC GG TCT TTAGG GGAC AG AGACTG
/
TGGGCCCCCGTCCTCTT T - - - G AGA TT - AACT GGT

GAM211 TTCACAAGTATTATTAAAAA 5060 CACAAGTATT 5061 AGTATTATTAAAAA C A TACAT
TGAGTATCGATAGTTACATT ATTAAAAATG TTCACA TGAGTAT GAT GT T
ACCATATCATCCATGCTCAT AGTA |||||| ||||||| ||| ||
GTGGA AGGTGT ACTCGTA CTA TA /

---------- C C TACCA

GAM212 GAGGGTCTGGATGGTGAGCT 5069 TGGATGGTGA 5070 T -- GA TT - C TTCG
TGGAGAGAGCGTCTTCGTCA GCTTGGAGAG GAGGG CTGGAT GGT GC GGAGAG AG GTC
T
ATGACCTGCTCTCCTGTAGC AGCG ||||| |||||| ||| || |||||| || |||
CTTGTCCAGCTTTC CTTTC GACCTG CCG TG CCTCTC TC CAG /
- TT A- T- G - TAAC

GAM213 GAAGATCGATGTCCCGCCGC 5095 CATCGCGTGG 5096 T A - C G AG
CGCTGGCGCAGCTGCGCGGC TGGGACGCGT GAAGA CG TGTCCCGCCGC CG TG CGC C
ATCGCGTGGTGGGACGCGTT TTTC ||||| || |||||||||| || || |||
TTC CTTTT GC GCAGGGTGGTG GC AC GCG T
- - C T G CG

GAM214 CGCTCGTGCGGCAGCCGCCC 5100 GACCTCGTCA 5101 T - CCA-- G AC T
AGCGAGGTGCAGACCGTCAA CGTGCGCGCT CGCTCG GCGGCAGC CGC GCGAGGT CAG
CG C
CGCGCTGGACCTCGTCACGT GCTG |||||| |||||||| ||| ||||||| ||| ||
GCGCGCTGCTGCTGGGCG GCGGGT CGTCGTCG GCG TGCTCCA GTC GC A
- C TGCAC G GC A

GAM215 TTGGTTCCGGCCCCGGTTCC 5116 GCCCCGGTTC 5117 TT CC TTC CT CC A
GGCTCCGGCCCCGATTCCGG CGGCTCCGGC TTGG CCGG CCGG CGG CCGG CCG T
CTCCGGCCCCGACTCCGGCT CCCG |||| |||| |||| ||| |||| |||
CCGGCCCCGA AGCC GGCC GGCC GCC GGCC GGC T
CC TC TCA CC TC C

GAM216 GTACTATCCCCTGAGGGGAT 5218 ACGCCATGAG 5219 A CCCCT- T TTT A C- A-
AAG- A
GGTGTTTTCGGAAGACGCCA AAAGCTCTAC GT CTAT GAGGGGA GGTG TCGGA GACG
CATG GA CTCT C
TGAGAAAGCTCTACAAGGGG AAGG || |||| ||||||| |||| ||||| |||| |||| || ||||
ACCATCGACATGTTTGTCTC CA GATG CTCCCTT CTAC AGCCT CTGT GTAC CT
GGGG A
CGACCCATCTTCCCTCCTGA - CAAGTC - CC- - TT AG ACCA A
ACGTAGAC

GAM217 CGGGCGCTGGAGGCGAGCGC 5247 CATCGAGGCC 5248 -------- G - AG -- GAC
GCAGCGGGCGACGGCAGCCA GTGCTCGCGT CGGGCGC TGGA GCGAGCGCG C CG
GGC G
TCGAGGCCGTGCTCGCGTTC TCAA ||||||| |||| ||||||||| | || |||
AACCCGCACGCGCCCG GCCCGCG ACTT CGCTCGTGC G GC CCG /
CACGCCCA G C GA TA ACG

GAM218 GTTGAGTTGGATTGGCAGAG 5253 TACTGAGCAA 5254 T- TT - G- A ACAACA
TGGACAACAGAATAAGGCTA CTCCCTCTCT GT GAG GGA TTG CAG GTGG G
TACTGAGCAACTCCCTCTCT TAC || ||| ||| ||| ||| ||||
TAC CA CTC CCT AAC GTC TATC A
TT TC C GA A GGAATA

GAM219 CCAGGTAAGGGAGCGAGCTG 5270 TGGATTATTG 5271 AG C C T TT C - TC
TTGGATTATTGTTTCTGACA TTTCTGACAT CC GTAAGGGAG GAG TG TGGATTA GTTT TGA CA
A
TCAATCTGCTCAAAGCTTAA CAAT || ||||||||| ||| || ||||||| |||| ||| ||
TCTACCAACTCCCTCCCTTA GG CATTCCCTC CTC AC ATCTAAT CGAA ACT GT A
CAGG A- C A C T- - C CT

GAM220 CGCTGGCGCCGCGCGCCTAC 5277 TACCTGGACG 5278 GG ---- C AC C - C
CTGGACGCCGACGGCACGCC CCGACGGCAC CGCT CGCCGCGC GC TACCTGG GC GA
CGG A
GCTCTGCTACCGGGTGTGCT GCCG |||| |||||||| || ||||||| || || |||
ACCGCGCGGTGGGCG GCGG GTGGCGCG CG GTGGGCC CG CT GCC C
-- CCAT T AT T C G

GAM221 GCGCTGTACGGCGCGAGCGA 5292 TGTCGAGCGG 5293 T G A- GA CCT ACG
GACATACCTGGACGACGAGC CGCGTGGTCA GCGCTG AC GCGCG GC GACATA GG A
CCTATGTCGAGCGGCGCGTG GCGT |||||| || ||||| || |||||| ||
GTCAGCGT TGCGAC TG TGCGC CG CTGTAT CC C
- G GG AG C-- GAG

GAM222 CGCCCGCTCCGGCGCCGGCG 5296 CTGGCGCGGG 5297 TCC CG G G TC C -- G
- A
AGGGGGTGGTGTCGCGCGGC CGGCCGTGCC CCGC GGCGC GCGA GG GTGGTG
GCGCGGC CGG GCC GT TCGGCCG C
CCGGGCCGGTTCGGCCGACT GCGT |||| ||||| |||| || |||||| ||||||| ||| ||| || |||||||
CGGCTGGCGCGGGCGGCCGT GGCG TCGCG CGCT CC CGCCAC TGCGCCG GCC
CGG CG GGTCGGC /
GCCGCGTCCCACCGCGCCGT TC- -- G G CC T GG G C T
CGCGCGCTCTGCGGCCG

GAM223 GTGCCGCGCCGCCTGGAGTC 5309 TCTCGCGGCC 5310 C------ CT T - T CC
GCGGTTCGGCCGGACCGTGC CTTCAACGGC GTGCCG GCCGC GGAG CGCG GT CGG G
ACGCGCTCTCGCGGCCCTTC AC |||||| ||||| |||| |||| || |||
AACGGCAC CACGGC CGGCG TCTC GCGC CG GCC /
AACTTCC C- - A T AG

GAM224 TCGCCCTTCCGGAGTGACGC 5332 TTCCAAAGCG 5333 CT A G C - T C-- C TCT
ACATAGCTCGCCGGGGCCCG GCGTGTCTGA TCGCC TCCGG GTGAC CA ATA GC CGC
GGGGCC GCCT G

CCTTCTGTCCAGGCCGGTTC GTCA ||||| ||||| ||||| || ||| || ||| |||||| ||||
CAAAGCGGCGTGTCTGAGTC AGCGG AGGCC CACTG GT TGT CG GCG CCTTGG
CGGA /
ACCCGGAGGCGA -- - A C G - AAA C CCT

GAM225 GCAGCCGCAGGATCGACACG 5348 TGGAGTAGGC 5349 A AG--- A A AA - T - GG---
GG
AGGAACGGGGTCAGCACGCG GATGTTGTCC GC GCCGC GATCGAC CG GG CGG GG
CAGCA CGC TCGAT T
GTCGATGGTGTAGTTGGAGT TCCG || ||||| ||||||| || || ||| || ||||| ||| |||||
AGGCGATGTTGTCCTCCGCG CG CGGCG CTGGTTG GT CC GCC CC GTTGT GCG
GGTTG G
CCCTGGTTGGTCACCTGGCG - GTCCA - C GC T T A GATGA AT
GCGC

GAM226 ACGTTGTCGCGATTAAAAAC 5358 ACAAAAGATC 5359 G- ATTAAAAACCAC CAAATAA
CACGCCAAATAAACATACGC CACGCGAAGA ACGTT TCGCG GC A
AGCACAAAAGATCCACGCGA ACGT ||||| ||||| ||
AGAACGT TGCAA AGCGC CG C
GA ACCTAGAAAACA ACGCATA

GAM227 TGCGTCTGCAACGGCATCAT 5362 CATCATGTTC 5363 C -- A- AT TACAC TGC
GTTCCTACACGCCTTGCACC CTACACGCCT TG GTCTGCA ACGGC TC GTTCC GCCT A
TGGGTGGAACGAGCGCCGTC TGCA || ||||||| ||||| || ||||| ||||
CTGCAGACCG GC CAGACGT TGCCG AG CAAGG TGGG /
- CC CG -- ----- TCC

GAM228 TCTGCGACTGCACCTGCTCC 5381 CTTGCGGAAC 5382 CTGCA C TC TTTG
TCCAGGCATTTGATCATCTG AGGTCGCGGA TCTGCGA CCTG TCC CAGGCA A
CTTGCGGAACAGGTCGCGGA ||||||| |||| ||| ||||||
AGGCGCT GGAC AGG GTTCGT T
----- A C- CTAC

GAM229 GATCCGGGACCGCCGTAGCG 5433 CGCCGTAGCG 5434 CC C --- G TTTT- TT
GGGTGTTTTTTAATTTATTT GGGTGTTTTT GATCCGGGA GC GTAG CG GGTGT TAA T
TATATATACGCTATGTATCT TAAT ||||||||| || |||| || ||||| |||
ACTGTTTTTCCGGGTC CTGGGCCTT TG CATC GT TCGCA ATT A
TT T TAT A TATAT TT

GAM230 GCGCCTGGACGTTGCACGCG 5437 CGTTGCACGC 5438 - A A GCG TA A
GCGGGTACCGAAAGCGGCGC GGCGGGTACC GCGCC TGG CGTTGC CGCG GG CCG A
TAACGCGGCAACGGCCACGG GAAA ||||| ||| |||||| |||| || |||
CGC CGCGG ACC GCAACG GCGC TC GGC A
C G - AA- GC G

GAM231 GCCTGCGTCGCCTATGCTTC 5446 TCGCCTATGC 5447 C------- - TCGC - GA CCT
GCGCGTCACCACGACACCTT TTCGCGCGTC GCCTGCGT GCC TATGCT GCGTC ACCAC
CA T
CCTTGAAGTGGTAGACGTCT ACCA |||||||| ||| |||||| ||||| ||||| ||
TCGGCATGCGGCAAATCGTC CGGACGCA CGG GTACGG TGCAG TGGTG GT /
ACGCAGGC CTGCTAAA C CTTC A AA TCC

GAM232 GATGTTCAGCAGGAAGCGCA 5456 TCCATGAGCT 5457 T GA C GA C T C T - TC
TGATGGACTTCTTGGCGTCG CCACGATCCG GA GTTCAGCAG AGCG AT TGGA TTC TGG G
CGGT CG T
GTCGTCTTGTCGTGCCGCTC CTGG || ||||||||| |||| || |||| ||| ||| | |||| ||
CATGAGCTCCACGATCCGCT CT CGAGTTGTC TCGC TA ACCT GAG ACC C GCCG GC
T
GGCTGTTGAGCTC - GG C GC C T T - T TG

GAM233 AGGAGATTGCTATTAGTAAG 5474 TACAATTTCT 5475 - TT TAAG GG TTT
TGGGGCCATTTTTATATTAA TTAGCACATT AGGAGAT TGCTA AG TG GCCATT A
TGGTTACAATTTCTTTAGCA TCCT ||||||| ||||| || || ||||||
CATTTCCT TCCTTTA ACGAT TC AC TGGTAA T
C T- TTTA AT TTA

GAM234 CAGCTGGGTGGCCAGGCCGG 5504 CAGCAGCTTC 5505 TG CAG CGG - - C
AGAGGCTCTGGCCCGGGTCC TGCATGTTGC CAGCTGGG GC GC AGAGGCT CTGG C C
AGCAGCTTCTGCATGTTGCC CCAG |||||||| || || ||||||| |||| |
CAGCTG GTCGACCC TG CG TCTTCGA GACC G G
GT TA- --- C T G

GAM235 GTCGAAGAGGCTGGCGTGCG 5625 TGGCGTGCGC 5626 CG G - T - C TCCA G
CGTTCCACTCGTCCGAGACC GTTCCACTCG GT AA AG GC GGCG TGCG GT CTC T
TGCCGCACCGTCGCACTGTT TCCG || || || || |||| |||| || |||
AAAC CA TT TC CG CTGC ACGC CG GAG C
AA G A - C - TCCA C

GAM236 GCGCGGCACAGTGCCAACGC 5630 ACGCGAAGCG 5631 G - TG A GAAG - CGT
GAAGCGCGCATGCGCACGTT CGCATGCGCA GC CGGCA CAG CC ACGC CG CGCATGCGCA
T
GAACTGCGCATGCGTCGGCG CGTT || ||||| ||| || |||| || ||||||||||
TCGGTGTTGTTGCCGGGC CG GCCGT GTT GG TGCG GC GCGTACGCGT G
G T GT C ---- T CAA

GAM237 TCCCGTAATACTCCGCGATC 5636 TGGAAGCGGT 5637 ATAC- CA TA CGA - - C
AGTTACCGTGGCGACGTTTC ACCGCGGGCG TCCCGTA TCCGCGAT GT CCGTGG
CGTTTC AG GGCG A

AGGGCGCATGCGCCTCTGGA CGTC ||||||| |||||||| || |||||| |||||| || ||||
AGCGGTACCGCGGGCGCGTC GGGGCAT GGGTGCTG CG GGCGCC GCGAAG TC
CCGC T
GTGGGCACAGTACGGGG GACAC -- CG ATG G T G

GAM238 AACAGCCGTTATTAGTTAAT 5640 TTGCTTATGG 5641 -- TAGTTA C T - --- TT-- A
C
TGCTTATGGCCAGTCCCTAG CCAGTCCCTA CAGC CGTTAT ATTG TTA GGCCAGT CCCT
AGC TG AGAAG A
CTTTGAAGAAGCAGCTTCTA GCTT |||| |||||| |||| ||| ||||||| |||| ||| || |||||
CATTTTGTTTTGAGGGTGCT GTCG GTAATG TAAC AGT TCGGTCG GGGA TTG AC
TCTTC /
GGCTTTGATCAATGTAATGG TG ------ T T T GTT TTTT A G
TGCTGTT

GAM239 GCTCTGTTCCCGCATAGCTG 5647 GGAGAAAGCG 5648 GTTC CATA GA - ATAAA
ATCCCGTATAAATATAATAA TAACGGAGAG GCTCT CCG GCT TC CCGT T
CGGAGAAAGCGTAACGGAGA C ||||| ||| ||| || ||||
GC CGAGA GGC CGA AG GGCA A
---- AATG A- A ATAAT

GAM240 GCGCATGCGCCTGGGGGCTT 5766 CAGCTCGCGG 5767 G TTCTAT A
TCTATGCGCGCATACGCGCG GTGTATGCGT GCGCATGCGCCTG GGGCT GCGCGC T
CAGCTCGCGGGTGTATGCGT |||||||||||| ||||| ||||||
TGCGTATGTGGGC CTCGA CGCGCG A
G ------ C

GAM241 GGGGGTCGGGGGGGTGCGCAG 5799 TGCCCTGGCC 5800 T G G GGTCGGA C T
GC C- T
GGCGGTGCCCCGGGTCGGAA TCCCCTCCCC GC CAGGGCG TGCCCCG ACCCCCGGGTG
GGT CGG GG GGGGCT C
CCCCCGGGTGCGGTTCGGGC C || ||||||| ||||||| |||||||||| ||| ||| || ||||||
GGCGGGGCTTCCCGGCTCCT CG GTCCCGT GCGGGGC TGGGGGCCCGC TCG
GCC CC CCTCGG C
TCCACCGGCTCGCCCGGGGG - - A ------- - - A- TT C
TCGGGGCGATGCCCTGGCCT
CCCCTCCCCC
GAM242 CTGACAGTAGCGGGTAATAA 6450 ATCACTTTCA 6451 --- C TAATAAAAACAAT TT-
TTTTT--- ACA
AAACAATAGGATTTTTATCG CGGTGATTTA CAGT AG GGG AGGAT TTATCGT
TATGTT A
TTTTTTTATGTTACAAAACA TTCT |||| || ||| ||||| ||||||| ||||||
ACGTATCACTTTCACGGTGA GTCG TC CCC TCTTA AGTGGCA ATGCAA /
TTTATTCTTGCTATTCCTTT GGT - TTTTCCTTATCGT TTT CTTTCACT CAA
TCCCCTTGGGCTGTCAG

GAM243 CTACGTGGAAAGCAAGCCCA 6472 TAACGAACTG 6473 T AAA A CCACTA - TC- ACT
A TT AA

CTAACGAACTGTCTCAACGA TCTCAACGAC CTACG GG GCA GC ACGAA CTGTC AACG GCA CG TCGT C
CTGCAACGTTTCGTAACCAA TGCA ||||| || ||| || ||||| ||||| |||| ||| || ||||
GCGACCGATGCCCGTTAGCG GATGC CC CGT CG TGCTT GACAG TTGC CGT GC AGCG C
ACAGCTTCGTCTGCCTGCGA - AG- C TC---- C CGA C-- A C- AA
CCCGTAG

GAM244 TATGTGAAATCTCCTAGGAT 6480 AGGATGCTTA 6481 G TC T TAGG CT AAA T
AGGTAGGTACTGTATAAATG AGTTTCTTTT TAT TGAAATC CTAGGA AGG TA GTAT TGA C
ATCATTCAGGATGCTTAAGT CTAG ||| ||||||| |||||| ||| || |||| |||
TTCTTTTCTAGATGATTTTA ATA ATTTTAG GATCTT TCT AT CGTA ACT A
GATA G TA T TTGA T- GG- T

GAM245 CATGCGCAACAGGTCCAGCT 6496 CATTAAACAG 6497 ACAG ---- A C
TAAAGGCGCACTTGTCATTA GCTGGACATG CATGCGCA GTCCAGCT TAA GGCG A
AACAGGCTGGACATGCGCGT CGCG |||||||| |||||||| ||| ||||
G GTGCGCGT CAGGTCGG ATT CTGT C
A--- ACAA A T

GAM246 ATTTGACCCCCAGAACTATG 6502 CAGAACTATG 6503 CCCC--- T AT CT
TATCAGCCTAGAGTTGCAAC TATCAGCCTA ATTTGA CAGAACTA GT CAGC A
TAGTTCTGACTTTGTTCAAA GAGT |||||| |||||||| || ||||
T TAAACT GTCTTGAT CA GTTG /
TGTTTCA - AC AG

GAM247 GAAAACGATATAAATTTTTA 6515 TACCCGTACC 6516 G AAAT C TACCT G A
CCCGTACCTTTGGATGTATA TTTGGATGTA GAAAAC ATAT TTTTAC CG TTGGAT TAT T
TAGATAGATCTAGTTTTGTG TATA |||||| |||| |||||| || |||||| |||
TAGAACAATGTGTTTTT TTTTTG TGTA AAGATG GT GATCTA ATA A
- AC-- T TTT-- G G

GAM248 CTGTAGAACTTGCCATTCTC 6529 TAGAACTTGC 6530 A ACTT TC- AACATTAA
ATTGACAACATTAACAATAC CATTCTCATT CTGT GA GCCATTC ATTGAC C
ATTAGTCAATCTTGAATGGC GACA |||| || ||||||| ||||||
TCAATAG GATA CT CGGTAAG TAACTG A
A ---- TTC ATTACATA

GAM249 GATCGTCTGCCCGCGGCCGC 6542 TTCGAGCGTC 6543 T - --- G C ACG---------- GT
TCACGTTCACGCCGTGGAGG AGCGGCGTGG GA CGT CTG CCCGCG CCGCT ACGTTC CC G
ATCTGGAAGAATTCGAGCGT GGAA || ||| ||| |||||| ||||| |||||| ||
CAGCGGCGTGGGGAACAGCA CT GCA GAC GGGTGC GGCGA TGCGAG GG /
CGTC - C AAG - C CTTAAGAAGGTCTA AG

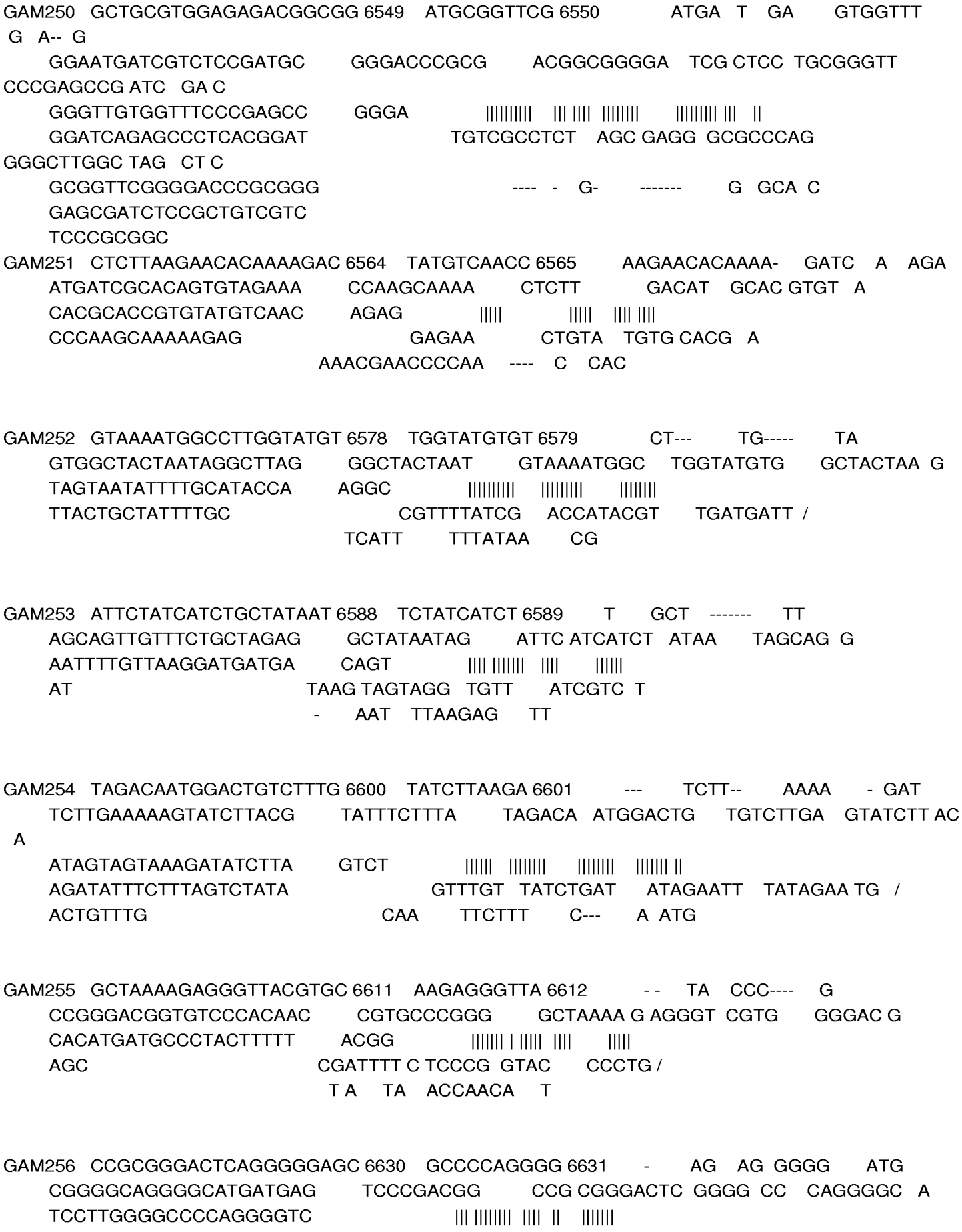
GAM250 GCTGCGTGGAGAGACGGCGG 6549 ATGCGGTTCG 6550 ATGA T GA GTGGTTT
G A-- G
GGAATGATCGTCTCCGATGC GGGACCCGCG ACGGCGGGGA TCG CTCC TGCGGGTT
CCCGAGCCG ATC GA C
GGGTTGTGGTTTCCCGAGCC GGGA
GGATCAGAGCCCTCACGGAT TGTCGCCTCT AGC GAGG GCGCCCAG
GGGCTTGGC TAG CT C
GCGGTTCGGGGACCCGCGGG ---- - G- ------- G GCA C
GAGCGATCTCCGCTGTCGTC
TCCCGCGGC
GAM251 CTCTTAAGAACACAAAAGAC 6564 TATGTCAACC 6565 AAGAACACAAAA- GATC A AGA
ATGATCGCACAGTGTAGAAA CCAAGCAAAA CTCTT GACAT GCAC GTGT A
CACGCACCGTGTATGTCAAC AGAG
CCCAAGCAAAAAGAG GAGAA CTGTA TGTG CACG A
AAACGAACCCCAA ---- C CAC
GAM252 GTAAAATGGCCTTGGTATGT 6578 TGGTATGTGT 6579 CT--- TG----- TA
GTGGCTACTAATAGGCTTAG GGCTACTAAT GTAAAATGGC TGGTATGTG GCTACTAA G
TAGTAATATTTTGCATACCA AGGC
TTACTGCTATTTTGC CGTTTTATCG ACCATACGT TGATGATT /
TCATT TTTATAA CG
GAM253 ATTCTATCATCTGCTATAAT 6588 TCTATCATCT 6589 T GCT ------- TT
AGCAGTTGTTTCTGCTAGAG GCTATAATAG ATTC ATCATCT ATAA TAGCAG G
AATTTTGTTAAGGATGATGA CAGT
AT TAAG TAGTAGG TGTT ATCGTC T
- AAT TTAAGAG TT
GAM254 TAGACAATGGACTGTCTTTG 6600 TATCTTAAGA 6601 --- TCTT-- AAAA - GAT
TCTTGAAAAAGTATCTTACG TATTTCTTTA TAGACA ATGGACTG TGTCTTGA GTATCTT AC
A
ATAGTAGTAAAGATATCTTA GTCT
AGATATTTCTTTAGTCTATA GTTTGT TATCTGAT ATAGAATT TATAGAA TG /
ACTGTTTG CAA TTCTTT C--- A ATG
GAM255 GCTAAAAGAGGGTTACGTGC 6611 AAGAGGGTTA 6612 - - TA CCC---- G
CCGGGACGGTGTCCCACAAC CGTGCCCGGG GCTAAAA G AGGGT CGTG GGGAC G
CACATGATGCCCTACTTTTT ACGG
AGC CGATTTT C TCCCG GTAC CCCTG /
T A TA ACCAACA T
GAM256 CCGCGGGACTCAGGGGGAGC 6630 GCCCCAGGGG 6631 - AG AG GGGG ATG
CGGGGCAGGGGCATGATGAG TCCCGACGG CCG CGGGACTC GGGG CC CAGGGGC A
TCCTTGGGGCCCCAGGGGTC

CCGACGG GGC GCCCTGGG CCCC GG GTTCCTG /
A GA G- ---- AGT

GAM257 GCATGGGTCTATCTACCAAA 6828 TTGCAAAAAA 6829 TCTATCTAC - TAATTAA
GAATTAATTAAAAGTTCCCA TCCCATGC GCATGGG CAA AGAAT A
TTCTATTGCAAAAAATCCCA ||||||| ||| |||||
TGC CGTACCC GTT TCTTA /
TAAAAAAC- A CCCTTGA

GAM258 GTATATACTTAGATGAGTCA 6840 TAATTCTTTT 6841 TACTTAGAT TCAT TC
TTTAAAACTTGTCTATTGAG TCCAACTTAT GTATA GAG TTAAAACTTG T
TTTTAATTCTTTTTCCAACT AC ||||| ||| ||||||||||
TATAC CATAT TTC AATTTTGAGT /
TCAACCTTT TT-- TA

GAM259 GTTGCAACACAATATATTGC 6846 TCAGTAAAGT 6847 ACACAATAT- A- AGA
ATACTGATTAGAATTTAAAT AATTAACCAA GTTGCA ATTGC TACTGATT A
CAGTAAAGTAATTAACCAAT TTCT |||||| ||||| ||||||||
TCTGCAGC CGACGT TAATG ATGACTAA T
CTTAACCAAT AA ATT

GAM260 CTGTTTCTGATTCAGATTCC 6857 TTAATAGTGG 6858 TC - ATTCC G AA C
CCTTGGCTAAAAGTTGCATC AGGTTGCCCT CTGTT TGATT CAG CCTT GCTA AGTTG A
AATTAATAGTGGAGGTTGCC GTAG ||||| ||||| ||| |||| |||| |||||
CTGTAGTCACGGACAG GACAG ACTGA GTC GGAG TGAT TTAAC /
GC T CCGTT G AA T

GAM261 GTCCTGGAAACCCATCCTGG 6863 TGGAAACCCA 6864 CCT AA CATC A- AGTT C
TGGGAGCAGTTGTCGCCGCT TCCTGGTGGG GT GG ACC CTGGTGGG GC GTCGCCG T
AGCGGCGGCGCCGCCTACCA AGCA || || ||| |||||||| || |||||||
GTCTTGGTGGCCCAAAC CA CC TGG GACCATCC CG CGGCGGC A
AAC GG TTCT GC ---- G

GAM262 GTGGTGGGAGTGAGGATGTT 6917 TTCGTCCTTT 6918 GT TTTAT - AA
TATGTCGTCTGGAAACTCTA TCCACCGC GTGGTGGGA GAGGATG GTCGT CTGG A
GTGCGACTTCGTCCTTTTCC ||||||||| ||||||| ||||| ||||
ACCGC CGCCACCTT TTCCTGC CAGCG GATC /
-- TT--- T TC

GAM263 CGGCCGTGTGCGCAGGTTAC 6976 GTACTCCAAA 6977 T C TACG G C TC
TACGTGGGGGACTCACTCTT CGTGACCTCG CGGCCG GTGCG AGGTTAC TGGGG ACT AC T
TGTTGGTACTCCAAACGTGA TACT |||||| ||||| ||||||| ||||| ||| ||
CCTCGTACTGGTTG GTTGGT CATGC TCCAGTG ACCTC TGG TG /

- - CAA- A T TT

GAM264 GGGCGCTAAACCTCTGAGAC 6980 TGATTTGGCT 6981 CTAA-- TCT C TTG CTA C C
CCGTTGATTTGGCTATCACC ATCACCCCTT GGGCG ACC GAGAC CG ATTTGG TCA CC T
CCTTGGGATGACCCCAAATG GGGA ||||| ||| ||||| || |||||| ||| ||
TGAGTTTCTGGTGACACACG TCCGC TGG CTTTG GT TAAACC AGT GG T
CCT ACACAG T-- A G-- CC- A G

GAM265 AGATATCATGGGAGGCGCTG 6995 TCCCAGAAAG 6996 ATCA G-- AAG TC
GGAGAAAGTCTCCCAGAAAG TCTCCCAGAA AGAT TGGGAGGC CTGGGAGA TC C
TCTCCCAGAAAGTCTCCCAG AGTC |||| |||||||| |||||||| ||
AAAGTCT TCTG ACCCTCTG GACCCTCT AG /
AAAG AAA GAA AC

GAM266 ATGTGCTACCTGCCGACAGT 7054 TCTGTACGGT 7055 C CT GA TCA T CAA ---
C CA
GTTGTCAAGGTTGGTGTCAG AACTGATATC TG TAC GCC CAGTGTTG AGGT GGTGTCAG
GCC TGGGGT GCT C
CAAGCCTGGGGTCGCTCACA TACC || ||| ||| |||||||| |||| |||||||| ||| |||||| |||
AAGCACTCTGTACGGTAACT AC ATG CGG GTCGTAGC TCCA CTATAGTC TGG
GTCTCA CGA /
GATATCTACCTCCCGATGCT - TT -- CC- T AA- CAT - AA
GGGCTTGTACACAT

GAM267 GCGGGCGAGCGAGGTGAGGG 7064 TGTTTTTTTT 7065 - G GT G A
AAGGGCAGTTATCTGATTGT TTGCTGGCCG GCG GGC AGCGAG GAGGGAA GGCAGTT T
TGTTTTTTTTTTGCTGGCCG CGC ||| ||| |||||| ||||||| |||||||
CGC CGC CCG TCGTTT TTTTTTT TTGTTAG C
G G -- G T

GAM268 TGGAGGTAGCGGTGCTAAAA 7127 GCGGTGCTAA 7128 A AG G AAAAAAAG G GAGA
AAAGTTGTTGAGAATGTAGA AAAAAGTTGT TGG GGT CGGT CT TT TT A
GGAGGAAGTGGAGGGCCGTC TGAG ||| ||| |||| || || ||
ACCGCCA ACC CCA GCCG GA AG AG /
G CT G GGTGAAGG G ATGT

GAM269 TCACCCTTTCTTGTTTATCC 7142 ATCCAATAGA 7143 A C TTA AATA-- GAT - C T
AATAGAGATTCAGTACCGGT GATTCAGTAC TC CCCTTT TTGT TCC GA TCAG TAC GG A
ATCCCAGTATCTGATTATCA CGGT || |||||| |||| ||| || |||| ||| ||
GATAAGGAAGTACAGTAAAG AG GGGAAA GACA AGG CT AGTC ATG CC T
GGGA - T TGA AATAGA ATT T A C

GAM270 CCTGGATCTGGTCCTGGTCC 7152 CTGGATCTGG 7153 T T T T T T T T T T T T
TGG

TGGATCTGGTCCTGGTCCTG TCCTGGTCCT C GG CC GGTCC GGATC GG CC GGTCC GGATC GG CC GGTCC GGATC T

GATCTGGTCCTGGTCCTGGA GGAT | || || ||||| ||||| || || ||||| ||||| || || ||||| |||||

TCTGGTCCTGGTCCTGGATC G CC GG CTAGG CCTGG CC GG CTAGG CCTGG CC GG CTAGG CCTGG /

TGGTCCTGGTCCTGGATCTG T T T T T T T T T T T T TCC

GTCCTGGTCCTGGATCTGGT

CCTGGTCCTGG

GAM271 TCTCTGACAATCTGCCACCG 7166 TCTGCCACCG 7167 CAAT G AGAACCGAAAC A

AGAACCGAAACCGGGATGAC AGAACCGAAA TCTCTGA CT CCACCG CGGG T

CCGCGGTGGAGTTTCGGGGA CCGG ||||||| || |||||| ||||

AGGGGCT GA GGTGGC GCCC G

TT-- - ---------- A

GAM272 CTTTTTTACGACTCCATCAG 7181 CATCAGAAAG 7182 A CTCCA G G T A G GACCA - AAAG

AAAGAGGTTTAATATTTTTG AGGTTTAATA TT CGA TCA AAAGA GTT AAT TTTTT TGA TCG AAGAGAG A

TGAGACCATCGAAGAGAGAA TTTT || ||| ||| ||||| ||| ||| ||||| ||| ||| |||||||

AGATAAAACTTTTTTACGAC AA GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC T

TCCATCAGAAAGAGGTTTAA - ACCAG G A T G G ACCTC A AAAA

TATTTTTGTGAGACCATCGA

AGAGAG

GAM273 TAAAATTAAATTAATTATAA 7194 TAAGTTAGTA 7195 - - TA-- - A-- - T

AATTATGTATATGATTTACT ATACATAAAT TAAAAT TAA ATTAAT TAAAATT ATGTAT TGATTTA CTAAC T

AACTTTAGTTAGATAAGTTA TTTA |||||| ||| |||||| ||||||| |||||| ||||||| |||||

GTAATACATAAATTTTAGTA ATTTTA ATT TAATTA ATTTTAA TACATA ATTGAAT GATTG T

TATTAATATTATATTTTA T A TATG A ATG A A

GAM274 TCTAAGATTTTAGGAAAAAT 7198 TAAGATTTTA 7199 T TTA- AATTA GG GATG

TATGGGGTTTGATGTATTTA GGAAAAATTA TC AAGATT GGAAA TG GTTT T

AAGCGGCAACTGATTTCCGA TGGG || |||||| ||||| || ||||

TTGGTCTTTGA AG TTCTGG CCTTT AC CGAA A

T TTAG AGTCA GG ATTT

GAM275 TTACCTGCAGCCTAACCCTA 7219 TGTGTTGGTG 7220 C-- AACC CCTA - T T

GCCCTAACCCTAGCTCATGC ACAGTCCTTG TTACCTGCAG CT CTAGC AC CC AGC C

TTGGAGTGTGTTGGTGACAG CAGG |||||||||| || ||||| || || |||

TCCTTGCAGGTGA AGTGGACGTT GA GGTTG TG GG TCG A

CCT CAGT TG-- A T T

GAM276 GGAAATAGCCTTTGGATTAT 7229 CAAGATCAAT 7230 T TA CC A GCC

GCCTTTGATAGTGCCTCAGG CCAACGGTTG GGAAATAGCC TTGGAT TG TTTG TAGT T

CTACAAGATCAATCCAACGG TTTC |||||||||| |||||| || |||| ||||
TTGTTTCC CCTTTGTTGG AACCTA AC GAAC ATCG /
C -- TA - GAC

GAM277 ATGGATTTTACTAGATCATT 7247 TACTAGATCA 7248 - TTT - ATTT- ACC
TATATACCAAAAAATATTAT TTTATATACC ATG GAT AC TAGATC ATAT A
ACGATCTACGTTTTATTATA AAAA ||| ||| || |||||| ||||
T TAT TTA TG ATCTAG TATA A
A TTT C CATAT AAA

GAM278 GGTTCAGGTTCAGGCTCAGG 7265 TGGTTCAGGT 7266 TT TT - ----- TT - T
TTCAAGCTCTGGTTCAGGTT TTTGGTTTAG GG CAGGTTCAGGCTCAGG C AAGCT CTGG
CAG GT C
CAGGCTCTGGTTCAGGTTTT GTTT || |||||||||||||| | ||||| |||| ||| ||
GGTTTAGGTTTTGGGTCTGG CT GTCTAGGTCTGGGTTT G TTTGG GACT GTC CG A
ATCTGGGTC GG TG A TTTTG TG T G

GAM279 TTCTTGCCAAAGACTGTGAC 7274 TTGGTCCCAT 7275 C- GA C C A -- - CTC
GGCTGGAACCAAGTTGACTC CCTTCACAGG TTCTTG CAAA CTGTGA GG TGG ACCAA GT
TGA T
TCGCTCACACCATTGGTCCC ATTT |||||| |||| |||||| || ||| ||||| || |||
ATCCTTCACAGGATTTGAAC GAGAAC GTTT GACACT CC ACC TGGTT CA ACT /
AAGAG AA AG T T C AC C CGC

GAM280 GGCTTGGGCTTTGGCTCAGG 7280 TCAGGTTGAG 7281 G - G G G TG G - G G
G T
TTGAGGCGGAGGCTTGGGCT GCGGAGGCTT CTTT GC TCAG TTGAG C GAGGCT GGCTTT GC
TCAG TTGAG C GAGGC T
TTGGCTCAGGTTGAGGCGGA GGGC |||| || |||| ||||| | |||||| |||||| || |||| ||||| | |||||
GGCTTGGGCTTTGGCTCAGG GGAG CG AGTT GACTC G TTTCGG TCGGAG CG AGTT
GACTC G TTTCG G
TTGAGGCGGAGGCTTGGGCT G G G - G GT G G G - G G
TTGGCTCAGGTTGAGGCGGA
GGCTTGGGTT
GAM281 CTTTTTTACGACTCCATCAG 7297 CATCAGAAAG 7182 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT | ||| ||| ||||| ||| ||| ||||| ||| ||| |||||||
AGAGATAAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG
GAM282 AGCTGCCATTTTGAAAGAGC 7298 TGAAAGAGCT 7299 TGC TT A ATTCAC--- GATT
TAATTCACAGTTTGATTAAA AATTCACAGT AGC CATT GAA GAGCTA AGTTT A

AAAGACTTTTCATCAGTAGC TTGA ||| |||| ||| |||||| |||||
TTATTCTTAGTGTTGCT TCG GTGA CTT TTCGAT TCAGA /
TT- TT A GACTACTTT AAAA

GAM283 CCACCTGCCCGCCCGCCCGC 7313 AGGGAGCGAG 7314 - CG- C-------- C CCA G CGC
CCACCTGACCCGCGCAGAGG CTGTTGAGTT CCAC CTGCC CC GC CGC CCT ACC G
TAAGGGAGCGAGCTGTTGAG GGAT |||| ||||| || || ||| ||| |||
TTGGATTGGCAGAGTGG GGTG GACGG GG CG GCG GGA TGG C
A TTA TTGAGTTGT A AG- A AGA

GAM284 ATAAAAATATTTTTGTAAAA 7333 AATATTTTTG 7334 AAAA A-- GA
CTTTTTTTATGAGACCATCA TAAAACTTTT ATAAAAATATTTTTGT CTTTTTTT TGA C
AAGAGAGAAAGAGAATAAAA TTTA |||||||||||||||| |||||||| |||
ATATTTTTGT TGTTTTTATAAAAATA GAAAGAGA ACT /
AGA- GAA AC

GAM285 GTGGAGGAGAGAGAGAAATA 7342 GAGGAGAGAG 7343 - - - AATAAG - T
AGCACCTTTACCTTTTTTGG AGAAATAAGC GTG GAG GAGAG AGAGA CACCTTTA CCTT T
GGATAAAGGTGAATCTCTAC ACCT ||| ||| ||||| ||||| |||||||| ||||
TCTCGCTCTCAC CAC CTC CTCTC TCTCT GTGGAAAT GGGG T
T G A AA---- A T

GAM286 ACACCTCCCCGGGGGGGCGTG 7451 TGCATTATGG 7452 A- T - - TG C- ATG- TG--- A
TCTACATGGATGTTGGGCAA GTAAAGTGTG AC CC CCCC GGGGGG CG T TAC GATGT
GGC A
GGGTCAAAATGCATTATGGG ACTC || || |||| |||||| || | ||| ||||| |||
TAAAGTGTGACTCTCTAGGG TG GG GGGG TCTCTC GT G ATG TTACG CTG G
GCGGGGGT GG C A A GT AA GGTA TAAAA G

GAM287 GATGGAGTCGTAAAAAAGTT 7466 TGATGGAGTC 7467 T TC AAG CT TC TCTTC T
CTCACAA
TTATCTCTTTCTCTCTTCGA GTAAAAAAGT GA GGAG GTAAAA TTTTAT CTT TC GA GGT
A
TGGTCTCACAAAAATATTAA TTTA || |||| |||||| |||||| ||| || || |||
ACCTCTTTCTGATGGAGTCG CT TCTC TATTTT AAAATG GAG AG CT CCA A
TAAAAAAGTTTTATCTCTTT T -- GAA CT GT TCTTT - AATTATA
C

GAM288 CCCCCGACTCCAACCTCATT 7474 TCCCAGAACT 7475 AACCTCA-- TC -- T CGTA --
- GG GA
CAAAATCCCGCTTGAGTTCC CTAGACCGGT TTCAAAA CCG CT GAGTTC
GGGGAAGTGA GTCT C T
GTAGGGGAAGTGAGTCTGGC GTTT ||||||| ||| || |||||| |||||||||| |||| |
GATTTGAGAGACCCCTCGCT AAGTTTT GGC GA CTCAAG CCTCTTCGCT CAGA
G /

TCTCCCAGAACTCTAGACCG GCTTCTAAG GT CA T AC-- CCC GA TT
GTGTTTTGAAGAATCTTCGA
GAGTCTGGGGG
GAM289 ACCTCTTTCTGATGGAGTCG 7487 TGATGGAGTC 7467 TTTCT TG TC AAG CT TC
TCTTC T CTCACAA
TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
CTCTCTTCGATGGTCTCACA TTTA || || ||| |||||| |||||| ||| || || |||
AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
TTATCTCTTTCTCTCTTCGA
TGGT
GAM290 GATGGTCTCATAAAAAAAGT 7488 ATAAAAAAAG 7489 G TCATAAAA TTTTAC ATTCT-
CTCTCTT TG
TTTACAAAAATATTTTTATT TTTTACAAAA AT GTC AAAG AAAAATATTTTT CTTT
TGA G
CTCTTTCTCTCTTTGATGGT ATAT || ||| |||| |||||||||||| |||| |||
CTCATAAAAAAAGTTTTACA TG TAG TTTC TTTTTATAAAAA GAAA ACT /
AAAATATTTTTATTCTCTTT G TTTCTCTC TCTTA- CATTTT AAAAT-- CT
CTCTCTTTGATGGTC

GAM291 TGTGGGAAACGGGCATGGAG 7498 AAGCCTCCCA 7499 AAA CAT A-- TATCGT
GATGAATTATCGTTATTATT TTCGGATTCA TGTGGG CGGG GGAGG TGAAT T
ATTTAAAGCCTCCCATTCGG CA |||||| |||| ||||| |||||
ATTCACA ACACTT GCTT CCTCC ATTTA /
AG- AC- GAA TTATTA

GAM292 CGCGTTAGTGGTCCGTGGGA 7584 TTAGTGGTCC 7585 -- C G A AGTT CCAT G
AGCTAAGTTGGCCATTGGAG GTGGGAAGCT CGCGT TAGTGGTC GTG GA GCTA GG TG A
ACACCTAGCTTGCACAGACC AAGT ||||| |||||||| ||| || |||| || ||
ACTACCACGCG GCGCA ATCACCAG CAC TT CGAT CC AC G
CC A G - ---- ---- A

GAM293 TTAAACCTCTTTCTGATGGA 7590 CGTAAAAAAG 7591 CTTTCT TG TC AAG -- T
TCCTTC T CTCACAA
GTCGTAAAAAAGTTTTATCT TTTTATCTCT GA GAG GTAAAA TTTTAT CTCT TC GA
GGT A
CTTTCTCCTTCGATGGTCTC TTCT || ||| |||||| |||||| |||| || || |||
ACAAAAATATTAAACCTCTT CT TTC TATTTT AAAATG GAGG AG CT CCA A
TCTGATGGAGTCGTAAAAAA TCTTTC CT TC GAA CT T TCTTT- - AATTATA
GTTTTATCTCTTTCTCCTTT
CTCACAAAAA
GAM294 GATACCGCGTAAGATAGAAA 7605 TACACTTTCC 7606 T A GT GTCTC
GGGTTGGCTATGTGTCTCTG TATCTTCGCG GATACCGCG AAGATAG AAGG TGGCTATGT T
GTAAACATAGTTACACTTTC GTGT ||||||||| ||||||| |||| |||||||||
CTATCTTCGCGGTGTT TTGTGGCGC TTCTATC TTTC ATTGATACA /
- C AC AATGG

GAM295 GGAGTCATAAAATATTTTTA 7617 TAAAATATTT 7618 TC A T- T TCTCTTC T CTCACAA
TTCTCTTTCTCTCTTCGATG TTATTCTCTT GGAG ATAAAAT TTTTTAT CTCT TC GA GGT A
GTCTCACAAAAATATTAAAC TCTC |||| ||||||| ||||||| |||| || || |||
CTCTTTCTGATGGAGTCGTA TCTC TATTTTG AAAAATG GAGG AG CT CCA A
AAAAAGTTTTATCTCT -- A CT T TCTTT-- - AATTATA

GAM296 TCTCGGTCCACGAGGGAAGC 7636 TCCCTTTGTC 7637 TCC-- AAGCG C- C T T
GTCACCCTGACACTGGTCTC CCTTCCGAGA TCTCGG ACGAGGG TCACC TGA AC GGTC C
AGGGCTTGTCTCGTCGGTGA |||||| ||||||| ||||| ||| || ||||
ATCCCTTTGTCCCTTCCGAG AGAGCC TGTTTCC AGTGG GCT TG TCGG A
A TTCCC CTA-- CT C T G

GAM297 GAAATGCCGCGTGATATCCC 7749 TATCCCTATG 7750 C A- A TTC GTTATG
TATGGTTCAGTTGGTTGTTA GTTCAGTTGG GAAATGCCG GTG TATCCCT TGG AGTTGGTT T
TGTAAAAGAGACCAGCTTTC TTGT ||||||||| ||| ||||||| ||| ||||||||
CAGGGGATACACACACGGCG TTTTGCGGC CAC ATAGGGG ACC TCGACCAG /
TTTT A AC - TT- AGAAAA

GAM298 ACCTCTTTCTGATGGAGTCG 7756 CGTAAAAAAG 7757 TTTCT TG TC AAG CT C TTC-- T CTCACAA
TAAAAAAGTTTTATCTTTCT TTTTATCTTT TC GA GAG GTAAAA TTTTAT TTCT TC GA GGT A
CTCTTCGATGGTCTCACAAA CTCT || || ||| |||||| |||||| |||| || || |||
AATATTAAACCTCTTTCTGA AG CT TTC TATTTT AAAATG GAGG AG CT CCA A
TGGAGTCGTAAAAAAGTTTT CTTCT CT TC GAA CT T TCTTT - AATTATA
ATCTCTTTCTCTCTTCGATG
GT
GAM299 GGTGGGGGGTTCAGAGTGAA 7769 AGGTATTGCA 7770 --- GG A G AGA A C A TC
CGAGGAGAGGTATTGCAGTG GTGATTCTCT GGTG GGG TTC GA TGAACGAGG GGT TTG AGTG TTC T
ATTCTCTGTGAGATATTTCA GTGA |||| ||| ||| || ||||||||| ||| ||| |||| |||
ACACCACCCCTCGTTCAGTC CCAC CCC GAG CT ACTTGCTCC CCA AAC TTAT GAG /
CGAGTTCCCAAACACC AAA TT C G CCA C T A TG

GAM300 ACCTCTTTCTGATGGAGTCG 7781 TGATGGAGTC 7467 TTTCT T TC AAG CT TC TCTTC T CTCACAA
TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GGAG GTAAAA TTTTAT CTT TC GA GGT A
CTCTCTTCGATGGTCTCACA TTTA || || |||| |||||| |||||| ||| || || |||
AAAATATTAAACCTCTTTCT AG CT TCTT TATTTT AAAATG GAG AG CT CCA A

GATGGAGTCGTAAAAAAGTT CTT-- C TC GAA CT GT TCTTT - AATTATA
TTATCTTTCTCTCTTCGATG
GT
GAM301 CGCGAAACACTGAATCAAGA 7782 TCCAGTGCTG 7783 AAT CT TA GCC
TCTCACCTCACTGTAGTTGT TGAGATCTTG CGCGAAACACTG CAAGATCTCAC CACTG
GTTGT T
GCCTGTGACAATCCAGTGCT TGCA |||||||||||| |||||||||| ||||| |||||
GTGAGATCTTGTGCAGTGTT GTGTTTTGTGAC GTTCTAGAGTG GTGAC TAACA /
TTGTG GT- TC C- GTG

GAM302 GATGCTGTGGGACAGCGCAT 7801 CACTCTATGC 7802 GA C - - GGTA
AGAGTGTCTGAGTTCTGGTA ACTGCTTCGC GATGCTGTGG CAG GCATAGAGTGTCTG AG
TTCT A
ATGGAGGGATCTCCAGGCAC AGCG |||||||||| ||| |||||||||||||| || ||||
TCTATGCACTGCTTCGCAGC CTGCGACGCT GTC CGTATCTCACGGAC TC AGGG /
GTC TC A C T AGGT

GAM303 GCAAGATCCCGCATGAGTCC 7809 TAGCTTAGAG 7810 A TC CAT TCC CGT - T
CTCTGAGCCGTTAGTTGTGA AGTCTCTCAC GCA GA CCG GAG CTCTGAGC TAGTT
GTGATA A
TATACTTATCACTAACTAGC GGTG ||| || ||| ||| |||||||| ||||| ||||||
TTAGAGAGTCTCTCACGGTG CGT CT GGC CTC GAGATTCG ATCAA CACTAT C
TCTGC - GT ACT TGA --- T T

GAM304 CCCCATCGTCCTCCAGCAGA 7815 CAGCAGCGCA 7816 G TCCAG-- - C- TT A
TGGTT
GGCGCCGCGTGCTGTTCTGT TCGGCGCCTT ATC TCC CA GAGGCGCCG GTGCTG
CTGTAGTGAAATT TGC A
AGTGAAATTATGCTGGTTAT ATGA ||| ||| || ||||||||| |||||| |||||||||||| |||
GTAATGCAAAATTTCACTAC TAG AGG GT TTCCGCGGC CGCGAC
GACATCACTTTAA ACG T
AGCAGCGCATCGGCGCCTTA A TTCACAA A TA -- A TAATG
TGAACACTTGGAAGATGGGG

GAM305 TGAATCGTCCGAGTGGAGTC 7822 TCACCTGGAT 7823 A CGA G GT T T AA
AGTTGTGTGTAAGCCATACT CAACCCTGAC TG ATCGTC GT GA CAG TG GTGT G
CACCTGGATCAACCCTGACG GATG || |||||| || || ||| || ||||
ATGCA AC TAGCAG CA CT GTC AC CATA /
G TCC A AG C T CC

GAM306 CTAGCCCCTGCTCAGGTTTA 7834 TAGAATCCTG 7835 TCAGGTTT TT-- A- TTA
GAATCCTGGATTTTGTAGGG GATTTTGTAG CTAGCCCCTGC AGAATCCTGGATT GT
GGG A
TTAATGATCCCAGATTTTTA GGTT |||||||||| |||||||||||| || |||
ATCCAGGATTTTGTAGGGGT GATTGGGGATG TTTTAGGACCTAA TA CCC T
TAG -------- TTTT GA TAG

GAM307 ACCTCTTTCTGATGGAGTCG 7845 TGATGGAGTC 7467 TTTCT- T TC AAG CT TC TCTTC T CTCACAA

TAAAAAAGTTTTATCTCTTT GTAAAAAAGT C GA GGAG GTAAAA TTTTAT CTT TC GA GGT A

CTCTCTTCGATGGTCTCACA TTTA | || |||| |||||| |||||| ||| || || |||

AAAATATTAAACCTCTTTCT G CT TCTC TATTTT AAAATG GAG AG CT CCA A

GATGGAGTCGTAAAAAAGTT CTTCCT T -- GAA CT GT TCTTT - AATTATA

TTATCTCTTTCTCCTTCGAT

GGT

GAM308 TCGCGTTCTTGCTAGCTCGC 7846 GGAAAGTACT 7847 T A-- - ------- GCAG AG

CGCGGGTATGCAGCCAAGTG CGCCGCTGAA TCGCGT CTTGCT GCT CGCC GCGGGTAT CCA T

CATGGGAAAGTACTCGCCGC GGCG |||||| |||||| ||| |||| |||||||| |||

TGAAGGCGCAGCAAAAGCAA AGCGCG GAACGA CGA GCGG CGCTCATG GGT G

GTGCGCGA T AAA C AAGTCGC AAAG AC

GAM309 CCTAGGCCCCGAGTGGGGTG 7855 CTTCCCAAAC 7856 T C TG G G GTATCT

GTTGGGAAGGCAGTTTTGTA ACTCTGTTTG CC AGGC CCGAG GGGTG TTGGGAAG CAGTTTT C

TCTCTGGCAAAAAAGCTGGC GTGT || |||| ||||| ||||| |||||||| |||||||

TTCCCAAACACTCTGTTTGG GG TCTG GGTTT CTCAC AACCCTTC GTCGAAA T

TGTCTTGG T T GT A G AAACGG

GAM310 GATGGAGTCGTAAAAAAGTT 7919 AGTTTTATCT 7920 T TC AAG -- T TCCTTC T CTCACAA

TTATCTCTTTCTCCTTCGAT CTTTCTCCTT GA GGAG GTAAAA TTTTAT CTCT TC GA GGT A

GGTCTCACAAAAATATTAAA CGAT || |||| |||||| |||||| |||| || || |||

CCTCTTTCTGATGGAGTCGT CT TCTC TATTTT AAAATG GAGG AG CT CCA A

AAAAAAGTTTTATCTCTTTC T -- GAA CT T TCTTT- - AATTATA

GAM311 TAGAGACATCTGTTCAGAAC 7927 GAGCGCGGAT 7928 - TCAGAA TC

TCCGTTCGATCTGCTTCGAG TGTCTCTG TAGAGACA TCTGT CTCCGTTCGA T

TGGAGCGCGGATTGTCTCTG |||||||| ||||| ||||||||||

GTCTCTGT AGGCG GAGGTGAGCT G

T C----- TC

GAM312 ATTAATTATAAAATTATGTA 7993 TAAGTTAGTA 7195 TA-- - A-- - T

TATGATTTACTAACTTTAGT ATACATAAAT ATTAAT TAAAATT ATGTAT TGATTTA CTAAC T

TAGATAAGTTAGTAATACAT TTTA |||||| ||||||| |||||| ||||||| |||||

AAATTTTAGTATATTAAT TAATTA ATTTTAA TACATA ATTGAAT GATTG T

TATG A ATG A A

GAM313 CCACGCCGAAAAGATGTCCA 7994 TCTCTCACAA 7995 C AA--- T A TCGTCAAGAT ACC
GGCTCGTCAAGATGGGACCC TCTGCGTGG CCACGC GA AGA GTCC GGC GGG C
TTTTCCGCCGGATCTCTCAC |||||| || ||| |||| ||| ||| |||
AATCTGCGTGG GGTGCG CT TCT TAGG CCG CCT /
T AACAC C - ---------- TTT

GAM314 GTCGCAAAGGAGCTGTCTGA 8069 AAGGAGCTGT 8070 AA- GCT T - GAG G
GACCATGAGCGGGAAACTGA CTGAGACCAT GTCGCA GGA GTC GAGA CCAT CGG A
GGTGGCTCTCTGACTCTGCA GAGC |||||| ||| ||| |||| |||| ||| |||
TGCGAC CAGCGT TCT CAG CTCT GGTG GTC A
ACG --- T C GA- A

GAM315 GGTGCCACAAAGAGATCGTA 8111 CTAGTGCTGC 8112 A - A - CA C CA - G A TT TG
TCTTAGCCGCACTGGCGTAC GGCCATTCTA GAGATC GT TCTT AGCCG CTGG GTAC TAT GAAG CT G GTGTTAG A
CATATGAAGGCTAGTTGTGT ATGG |||||| || |||| ||||| |||| |||| ||| |||| || | |||||||
TAGTGATTACTTCGCTAGTG TATTAG GT GTGC TGTAC AGGT AATC ACC GCGT CG G CGCTTCA /
CTGCGGCCATTCTAATGGAT - T C G GT - TT G - T AT TT
GCATGTGCGTGCTGTGATTA
TGATGAGGACT
GAM316 CTGCCCGACCTAAAGTCCTT 8121 TCATGGGGGA 8122 AC AAA- A- A- - AA
CAAGGCCAAGTGCAATGTGA CCCAGAGTGC CTGCCCG CT GTCCTTCA GGCC AGTG C T
CGCTGAGGCTCATGGGGGAC GGGC ||||||| || |||||||| |||| |||| |
CCAGAGTGCGGGCAG GACGGGC GA CAGGGGGT TCGG TCGC G /
GT GACC AC AG A TG

GAM317 GTTGGAGGCGACTATGACCG 8142 TTTGAGGAGC 8143 ----- A C-- GA- T A T-- G-- G
CGACGAAGAGGACTCTTTTC CTGAGAGGGT ATG CCGCGA GAA GGAC CTTTTCAGG TCCTC GGCG TTG G
AGGATCCTCTGGCGGTTGGG CCAC ||| |||||| ||| |||| ||||||||| ||||| |||| |||
GACGAAGACGTCTTTGAGGA TAC GGTGCT CTT CCTG GGAGAGTCC AGGAG CTGC AGC G
GCCTGAGAGGGTCCACATTC ACGTT A ACC ACA - G TTT AGA A
CCATCGTGGACATTTGCAAG
GTGGCCAGGAT
GAM318 TTTGTCTTGCCTGGTGTGCT 8165 AGGTATTTGT 8166 CC GCT ----- A TA GT G G GA G
TTACATGGTTCGCAGGTATT GTCGACTGGT TGGTGT TTACA TGGTTCGC GG TTT GTC ACT GTTG ATAA G
TGTGTCGACTGGTTGGAATA TGGA |||||| ||||| |||||||| || ||| ||| ||| |||| ||||
AGGCGACGCCTCTTCTTGCC CGGTCG CCTTA CGTCCTAT TC CTG CCG TTC TCTC GCAG /
GTCCACTTATCCTGCGAAGA TA GTA AGAAG - AC -- - T C- C
ATTCCATGGCTGGCATAAAT

GGCAATA
GAM319 GTGTGTGCTGGATTTCTGCA 8172 AGGGGCAGAT 8173 GT- T- TT- AA- GGCC
ATGTGGCCATGGAACAGGGG CCTCCCCGCC GTGT GC GGA TCTGC TGT A
CAGATCCTCCCCGCCGAACA GAAC |||| || ||| ||||| |||
C CACA CG CCT AGACG ACA /
AGC CC CCT GGG AGGT

GAM320 GCAACGCCCTGCTCAGCAGC 8215 CAGCAGCCTC 8216 AACGCC C CCTCC- AACGCC
C CCTCCG
CTCCGCAACGCCCTGCTCAG CGCAACGCCC GC CTGCT AGCAG GC CTGCT AGCAG
C
CAGCCTCCGCAACGCCCTGC TGCT || ||||| ||||| || ||||| |||||
TCAGCAGCCTCCGCAACGCC CG GACGA TCGTC CG GACGA TCGTC /
CTGCTCAGCAGCCTCCGC CCTCC- C CCGCAA CCTCC- C CCGCAA

GAM321 CGTGCGGTAAATATCGTCGC 8292 GAGAATATAG 8293 TG A---- - GTCT G GCCT
GTCTTGTGTTGTCTATTCTC CGACAGATGT CG CGGTA ATATC GTCGC TGTGTT
TCTATTCTC A
GCCTAAAAAGAGAATAGAGA AGAA || ||||| ||||| ||||| |||||| |||||||||
ATATAGCGACAGATGTAGAA GT GCCGT TGTAG CAGCG ATATAA AGATAAGAG /
ATGCCGTGTG GT AAAGA A ---- G AAAA

GAM322 AAGAAGTTGCGAGATAGTAA 8304 GAGAATATAG 8305 A ATA A A- ATA
TCTTAAGATAGTAGCCTGAG ACTTGCAATA AAGA GTTGCGAG GTA TCTT AG G
AGAATATAGACTTGCAATAT TCTT |||| |||||||| ||| |||| ||
CTT TTCT TAACGTTC TAT AGAG TC T
A AGA A AG CGA

GAM323 GGTATGTTCAGCCTGGGGTT 8313 TTTAGCGTCT 8314 ATGT G -- G ---- C
GCGGACGCTGGGGGGCGAGTC GGGATCCTGA GGT TCA CCT GGGGTT CGGACGCTG
GGGG G
CTGGTTTAGCGTCTGGGATC AGGG ||| ||| ||| |||||| ||||||||| ||||
CTGAAGGGTGGTTTGACC CCA GGT GGA TCCTAG GTCTGCGAT TCCT A
GTTT G AG G TTGG G

GAM324 GGACGCGTCTAGTATCTACG 8319 TCTAGTATCT 8320 CG --- CTA- ACCT G
TCTCACCTCTGAATAGTCTA ACGTCTCACC GGA CGTCT AGTAT CGTCTC CT A
GAGACGCCAAATACTTTAAG TCTG ||| ||||| ||||| |||||| ||
ACGGATCC CCT GCAGA TCATA GCAGAG GA A
AG ATT AACC ATCT T

GAM325 GCGGGAGCTGGGATCCTGGA 8331 TGGGATCCTG 8332 - GG - - AGA AG
GGACAGAGCCAGGTCAGGCG GAGGACAGAG GCGGGAG CT GATC CTG GAGGAC GCC G
TCCTCTTGGCGGTCAGGTCT CCAG ||||||| || |||| ||| |||||| |||

CCCGT TGCCCTC GG CTGG GGT CTCCTG CGG T
T A- C T --- AC

GAM326 ACCCTGCAAGTACTCGGTGA 8379 TGCAAGTACT 8380 C G G- ---------- - C
GTGCGAATCAGTTTTTAACT CGGTGAGTGC AC CT CAA TACTCGG TGAG TGCGAAT A
GATGTCGTGTTGTCCATGAC GAAT || || ||| ||||||| |||| |||||||
TCACCCAAGT TG AC CCA CAGTACC TAGT AATTTTT /
A - CT TGTTGTGCTG C G

GAM327 GCTGTAACTATTTTCAGAAG 8391 TGTCTTGTCT 8392 - A- -- A AT TGA
ATATATGTCTGATGACTGAG GAAAGAAAGT GCTGTA ACT TTTTCAGA AGATAT TGTCTG GAC
G
TGCCGTCTGTAGACGATGTC CTAT |||||| ||| |||||||| |||||| |||||| |||
TTGTCTGAAAGAAAGTCTAT CGATAT TGA GAAAGTCT TCTGTA GCAGAT CTG T
AGC C AA GT - GT CCG

GAM328 GCAATGTTAAAGTGACTCCT 8403 TTAAAGGTAA 8404 - TAAA CT- AGAT- ACCTA
CCAGATTACTCACCTATAAT GAGTTATGAC GC AATGT GTGACTC CC TACTC T
TGCGAGTATTAAAGGTAAGA GCAT || ||||| ||||||| || |||||
GTTATGACGCATTAGC CG TTACG TATTGAG GG ATGAG A
A CAG- AAT AAATT CGTTA

GAM329 CTGGACTATCAACGTACTAT 8410 TTGGTCACGG 8411 - ATCAACGT- T C - A C
ACCAT T
CCACACCTGATGGTCTGGAG TTTCCAACTA GGACT AC AT CAC ACCTG TGGT TGGAGAT
TGACTAATA A
ATACCATTGACTAATATAAC TAGG ||||| || || ||| ||||| |||| ||||||| |||||||||
TATTGGTCACGGTTTCCAAC CCTGA TG TA GTG TGGAT ATCA ACCTTTG
ACTGGTTAT A
TATAGGTCGTGCATTGTTCA G GACTAAACT T C C - - GC--- C
AATCAGAGTCCGAG

GAM330 TTTTTGAACAATACGCACTG 8415 TATAATAAAT 8416 ACA TG--- A GTGA -- G
GTAATATCCGTGATCCCGTG CGTGTGTATC TTTTTGA ATACGCAC GT ATATCC TC CC T
TGGAAGAGAGAGGATATAAT TCAA ||||||| |||||||| || |||||| || ||
AAATCGTGTGTATCTCAAAA AAAAACT TATGTGTG TA TATAGG AG GG G
A C-- CTAAA A AGAG AA T

GAM331 GGCTCTCTGCGGCTCGCGTT 8422 TCTCTGCGGC 8423 TC CTCGC T TTCCC G
CGCGTTCCCCGGTGACGAAA TCGCGTTCGC GGC TCTGCGG GT CGCG CG T
CCCGCGCACACCGCAGAACG GTTC ||| ||||||| || |||| ||
CC CCG AGACGCC CA GCGC GC G
CA A---- C CCAAA A

GAM332 GGCCCCTCCTCCTCCCGGGC 8426 TGAAAACTGG 8427 - TC GCGAGC -- A
GAGCGAGGCCCGCACCTGCG GAGCGGGGGG GGC CCCTCC CTCCCGG GAGGC CCGC C
GCTGCCTCTGAAAACTGGGA CGCC ||| |||||| ||||||| ||||| ||||
GCGGGGGGCGCC CCG GGGGGG GAGGGTC CTCCG GGCG C
C C- AAAAGT TC T

GAM333 AAGAATATATCTTAAGATAG 8466 TATCTTAAGA 8467 AT- T CTT GAAAGAGAT
TAGCTTTTCTGAAAGAGATA TAGTAGCTTT AAGA ATATC TAAGATAGTAG TTCT A
TATATATTAAGAGTACTACT TCTG |||| ||||| |||||||||||| ||||
ATCTTGCGATATTAGTCTT TTCT TATAG GTTCTATCATC GAGA /
GAT C AT- ATTATATAT

GAM334 CAGCTCATCTTACCCACGAC 8475 TGGGCTGAAC 8476 - TA- GACG C GC GT
GTGGTCCACGGCCGTGATGA AGTGGGGGCA CAGC TCATCT CCCAC TGGTCCA G C G
TCTGGGCTGAACAGTGGGGG GGTG |||| |||||| ||||| ||||||| | |
CAGGTGATGCTG GTCG AGTGGA GGGTG GTCGGGT C G /
T CGG ACAA - TA TA

GAM335 TGTCCTCTATGGGTCTCAGA 8521 TATGGGTCTC 8522 TCT T - -- - TG CGT
TGCCTGGCGGCCCTGCCGTA AGATGCCTGG TGTCC ATGGGTC CAGATG CCT GGCGGCC C
C A
CACGTGGAGGTTGCCCGGGG CGGC ||||| ||||||| |||||| ||| ||||||| | |
TTATCTGCGACCCGTGGACA ACAGG TGCCCAG GTCTAT GGG CCGTTGG G G /
--- C T GC A GT CAC

GAM336 TAACGGCGACTTTGGGCAGC 8529 AATCAGTGTC 8530 CGA T- CGAA A CT- AAA
AAATT
GAATCAGTGTCTGTCGCAAA TGTCGCAAAC TAACGG CT TGGGCAG TC GTGT GTCGC
CCCTGTT T
CCCTGTTAAATTTAAACACA CCTG |||||| || ||||||| || |||| ||||| |||||||
ACAGGGAGCGCGACTAAACA GTTGTC GG ACTCGTC AG CACA CAGCG
GGGACAA A
CGGACTAACTGCTCATCGGG CCG CT AATC G AAT CGA CACAA
CCCTGTTG

GAM337 GCGGTCGCCTCTAGAGGCCG 8550 CCCCCCAGAC 8551 CTAGAG CCC- ACCGC
AG TA
CCCCTGGGACCGCGGCGCCC CCCGGCAGGC GCGGTCGCCT GCCG CTGGG
GGCGCCC AG C
AGAGTACAGCTGGGGGCGCC GGCC |||||||||| |||| ||||| ||||||| ||
CCCCAGACCCCGGCAGGCGG CGCCGGCGGA CGGC GACCC CCGCGGG TC /
CCGC ------ CCCA C---- GG GA

GAM338 CCGTTTATCAAAATGGAAAA 8668 TGGAAAAATT 8669 TTTA A - -- AAA
ATTAAGGCTTTGCGTTAAAA AAGGCTTTGC CCG TCAAA TGGAAAAATTAAG GCT TTGCGTTA
T

TCTGCTAACGCAAAGGGCAC GTTA ||| ||||| |||||||||||||| ||| ||||||||
TTAATTTTTCCAGTTTGGAC GGC GGTTT ACCTTTTTAATTC CGG AACGCAAT C
TCGG TCA- G A GA CGT

GAM339 AAATTTTAAACTGCAATGTC 8675 TAAGAGTTTT 8676 AACTGCAAT CCTCTG GA TT
TCCTCTGAAAACTCTGATAG ATCTAAAGAT AAATTTTA GTCT AAAACTCT TAGA A
ATTATCTCTAAGAGTTTTAT TTTT |||||||| |||| |||||||| ||||
CTAAAGATTTTTTTTCCTAA TTTAGAAT TAGA TTTTGAGA ATCT /
GATTT CCTTTTTTTT AATCTA -- CT

GAM340 GATGCGGGAGATAAGCCAAA 8680 GTCAAGTACC 8681 C GG AAG A-- TATAAA C
CTTTATAAAGACCATGGTCG TGGACGTCTT GATG G AGAT CCA ACTT GAC A
TCAAGTACCTGGACGTCTTT TCTG |||| | |||| ||| |||| |||
CTGTC CTGT C TCTG GGT TGAA CTG T
- TT CA- CCA CTG--- G

GAM341 TGGTGTTGCAATGCATTAGG 8691 TCTTTAGTTC 8692 -------- CA AT T A AA - CTC
GAATCTAAAAACGAAATCCT CCTACAGCAT TGGT GTTG ATGC TAGGGAA CTAAA ACGA
TCC TG G
GCTCGGTAACACGGAAATTG CACA |||| |||| |||| ||||||| ||||| |||| ||| ||
TCTTTAGTTCCCTACAGCAT ACCA CAAC TACG ATCCCTT GATTT TGTT AGG AC
G
CACAACAATTGTAAACCA AATGTTAA AC AC - C AA C AAT

GAM342 GGGGTGCAAGTCCCCCGGTG 8724 CCCCGGTGGG 8725 TC G TG AA TC G ---- AG -
T TG
GGGTGCAAGTCCCCCGGTGG GTGCAAGTCC CCCCG TGGGG C G CCCCG TGGGG TGCA
TCCC CCGG GGGG C
GGTGCAAGTCCCCCGGTGGG CCCG ||||| ||||| | | ||||| ||||| |||| |||| |||| ||||
GTGCAAGTCCCCCGGTGGGG GGGGT GCCCC G C GGGGT GCCCC ACGT GGGG
GGCC CCCT A
TGCAAGTCCCCCGGTGGGGT GT G CT AA GT G CTGA -- T - GA
GCAAGTCCCCCGGTGGGGTG
CAAGTCCCCC
GAM343 GTCCCCCGGTGGGGTGCAAG 8752 CCCCGGTGGG 8725 TC G ---- AG - T TT
TCCCCCGGTGGGGTTCAAGT GTGCAAGTCC G CCCCG TGGGG TGCA TCCC CCGG GGGG
C
CCCCCGGTGGGGTGCAAGTC CCCG | ||||| ||||| |||| |||| |||| ||||
CCCCGGTGGGGTGC C GGGGT GCCCC ACGT GGGG GGCC CCCT A
GT G CTGA -- T - GA

GAM344 CCGAGTAGGCCTTGACGCAC 8753 AGGCCTTGAC 8754 T CACC AC CA
CTGACGTGGCAGAACCACCC GCACCTGACG CCGAG AGGCCTTGACG TG GTGG G
CACCACCGTCAGGGTCTTTT TGGC ||||| |||||||||| || ||||
TGG GGTTT TCTGGGACTGC AC CACC /

T CACC CC AA

GAM345 GTCTCTCAAGACTATTACTA 8784 TCACAATAAT 8785 T CA CTATC A CTCT
TCGTAAGATATCTCTCACAA AGTTTCAGGA GTC CT AGACTATTA GT AGATAT C
AGTATCTCACAATAATAGTT C ||| || ||||||||| || ||||||
TCAGGAC CAG GA TTTGATAAT CA TCTATG A
- C- AA--- C AAAC

GAM346 GGAGCAGGGTCCCGGCGCTC 8837 CGGCAAGAGG 8838 AGG--- C- G C G T
TCGTGCGTACTGCTGTACGG GTCGACGACA GGAGC GTC CGGC CTCT GT CGTAC G
CAAGAGGGTCGACGACAACG ACGA ||||| ||| |||| |||| || |||||
ACGCTCC CCTCG CAG GCTG GAGA CG GCATG C
CAGCAA CA G A - T

GAM347 GTCAGACTCCCAGTCGTCCC 8861 TGATTGCGAG 8862 CA C--- G CGC- AC A C-
CCTTGA
GCCTGACTACCGCAAACACC GTCAGCAAAG GT GACTC CAGTC TCC CTGACT CGCAA CA
CCTGT C
CTGTCCTTGACCAAACTCGC GAGA || ||||| ||||| ||| |||||| ||||| || |||||
AGGTCTGATTGCGAGGTCAG CG CTGAG GTCAG AGG GACTGG GCGTT GT
GGACG C
CAAAGGAGACTGTCACGAGT CC CACT - AAAC A- A CT CTCAAA
CCCGC

GAM348 GAATACGGCCAACGCGCCAG 8879 CAGCATGGTC 8880 CGC G AAC CCTCCA A
GTA AAT CT
CGTCCAACCGCCCTCCAACC GCGGGAGGCT CAA GCCAGC TCC CGC ACCGTGC
GCGCC TATTCG TGC T
GTGCAGCGCCGTATATTCGA GGCA ||| |||||| ||| ||| ||||||| ||||| |||||| |||
ATTGCCTTCCGCACGAATAC GTT CGGTCG AGG GCG TGGTACG CGCGG
ATAAGC ACG /
GGGGCGCAGCATGGTCGCGG A-- G --- C----- A GGC --- CC
GAGGCTGGCATTGCGCAATA
TTC
GAM349 ACGTCCAGCCTCTCGGCCGA 8930 TGCACAGTCT 8931 AG TC - GA GC--------- GG
GGACGCCGTGGTAGACGAGT CGGGCCTGAA ACGTCC CC TC GGCC GGAC CGT T
GGTGCACAGTCTCGGGCCTG GGGA |||||| || || |||| |||| |||
AAGGGAAGGACGT TGCAGG GG AG CCGG TCTG GCA /
AA GA T GC ACACGTGGTGA GA

GAM350 CGGCTCGGCTCCGGGGTGGC 8958 CTCCGGGTGG 8959 T G - G G G G T G -
G G
TCCGGGTGGGGGCGGCTCGG GGGCGGCTCG C CCGGGGT GCTCCGG GT GGG CG CTC GC
CCGGGGT GCTCCGG GT GGG C
CTCCGGGGTGGCTCCGGGTG GCTC | ||||||| ||||||| || ||| || ||| || ||||||| ||||||| || |||
GGGGCGGCTCGGCTCCGGGG G GGCCTCG TGGGGCC CG CTC GC GGG TG
GGCCTCG TGGGGCC CG CTC G

TGGCTCCGGGTGGGGGCGGC - G T G G G - G T G G
TCGGCTCCGGGGTGGCTCCG
GGTGGGGGCG
GAM351 ATGGGATTAAATACCAGGGA 8989 ATACCATGGG 8990 A - AG GA G GG TC ATG A
- CTG T
TACAGGCTGTAGGTTCGGTA ATTAAATACC GG TTAAAT ACC G TACAG CTGTA T GGTA
GGT CCA GG GAG G
ATGGGTACCAGGCTGGAGTG AGGG || |||||| ||| | ||||| ||||| | |||| ||| ||| || |||
ACTCATACCATGGGATTAAA CC AATTTA TGG T ATGTC GACAT G CCAT TTA GGT CC
CTC /
TACCAGGGATACAGGCTGTA A A CT GG G AG GA AAA G A ATA A
GGTTCGGTAATTTAAACCTA
T
GAM352 GGGGAACCCCCTAACGGGAT 9006 TAACGGGATG 9007 A A T A TCAA
GTAATTAATTCAAACCTATA TAATTAATTC GGGGA CCCCCTAACGGG TG AATT AT A
TAAATTCCACCCTGTTAGGG AAAC ||||| |||||||||||| || |||| ||
GGATCCCC CCCCT GGGGGATTGTCC AC TTAA TA C
A C C A TATC

GAM353 GATGCCTGACCGCCTCACTG 9013 AAGGACCAAA 9014 G ----- C CT --------- AAAC-
AA
CTGTCCTAAACAGGTACAAG AGTTTAGCCT GAT CCTGA CCGC TCA GCT GTCCT
AGGTAC G
ATGTACTTTCTCAAGGACCA GAGC ||| ||||| |||| ||| ||| ||||| ||||||
AAAGTTTAGCCTGAGCGGGA CTA GGACT GGCG AGT CGA CAGGA TTCATG /
CAATCAGGATC - AACAG - C- TTTGAAAAC ACTCT TA

GAM354 GAGATTCTTGCAGCGGATAT 9074 TGAGTAGAGT 9075 GA T GCGGATA A AT
TTATACGGGATTAGTTTGAG ACACATGCGG GA TTCT GCA TTTAT CGGG T
TAGAGTACACATGCGGAGCA AGCA || |||| ||| ||||| ||||
TC CT GAGG CGT AGATG GTTT /
AC - ACACATG A GA

GAM355 AGGGGAACTTATGACTGTTA 9094 TGTTATAAAA 9095 TAT CT T ATAA A
TAAAAAATAAGAATAAGATT AATAAGAATA AGGGGAACT GA GT ATAAAAA GAAT A
CCATTTTTATTATTATCTGG AGAT ||||||||| || || ||||||| ||||
TTCTCCT TCCTCTTGG CT TA TATTTTT CTTA /
T-- AT T AC-- G

GAM356 ACATGTCCTCCCTGCTCACC 9102 TCGCGGAGGA 9103 T - T- - AAGAAC
ATGAAGAACCTCATGCACGT GGGCCTGT ACA GTCCTCC CTGC CA CCATG C
GGTTGTCGCGGAGGAGGGCC ||| ||||||| |||| || |||||
TGT TGT CGGGAGG GGCG GT GGTGC T
C A CT T ACGTAC

GAM357 CACCTGCTGAACGCGGGCTT 9143 CAGCCACGGC 9144 - TGAAC TC T-- CAC CC
CGCCTGCCACGGCCCCCCGG CAGCTCGCCA CACCT GC GCGGGCT GCC GC GGCC C
GCCTCAGCCACGGCCAGCTC CCTG ||||| || ||||||| ||| || ||||
GCCACCTGCGAGGTG GTGGA CG CGCTCGA CGG CG CCGG /
G TCCAC C- CAC ACT GC

GAM358 GCTCTCCGACGTCAGCCGCG 9215 ACTGGTCGGG 9216 G A G -- G ACG
CAGGGCACGTACCAGCACTG GTAGGCGTGG GCTCTCC ACGTC GCC CG CAG GC T
GTCGGGGTAGGCGTGGAGAG AGAG ||||||| ||||| ||| || ||| ||
T TGAGAGG TGCGG TGG GC GTC CG A
- A G TG A ACC

GAM359 CTCAACGAACTCAGGGTGAT 9233 ACGAACTCAG 9234 CGAA ---- - CAAGGACA
GGGGACCAAGGACAGCAACA GGTGATGGGG CTCAA CTCAGGGTGA TG GGGAC G
ACAAGTCCCTCAAGACTTAC ACCA ||||| |||||||||| || |||||
TTTGAGGTGTTTGAG GAGTT GAGTTTCATT AC CCCTG C
TGTG CAGA T AACAACAA

GAM360 TCTGGGGTCCAGGACACAAT 9284 TCCAGGACAC 9285 TG TC C AA TAGAG
CTCTGCTAGAGCGCAACCGC AATCTCTGCT TC GGG CAGGA AC TCTCTGC C
GGGGAGGGTTCCTGAGCTCT AGAG || ||| ||||| || |||||||
GGA AG CTC GTCCT TG AGGGGCG G
GT GA - GG CCAAC

GAM361 TGGGTGGTTAACAAGAACAA 9308 CTGCGCCCTC 9309 TAACA ACAACAC CT- TT- A
CACCCTGCTGCGCTTTGACT AGGTCCCTCT TGGGTGGT AGA CCTG GCGC TG C
ACACCTGCGCCCTCAGGTCC GCCA |||||||| ||| |||| |||| ||
CTCTGCCACCCA ACCCACCG TCT GGAC CGCG AC T
----- CCCT--- TCC TCC A

GAM362 CCCCTGTTTGACTTTTACGC 9415 TCCCCCAGTC 9416 --- G CGC C CA - G AGG
A C
GGTGGGCGCGCCGGGCGCCA CCTGGCCCCC ACTTTT AC CGGTGGG GCCGGG GC GGGG
TGT GCCTAC GCC CC A
GGGGTGTGGCCTACAGGGCC GCCG |||||| || ||||||| |||||| || |||| ||| |||||| ||| ||
ACCCACAGGGGCATGGTGGG TGAGGA TG GCCGCCC CGGTCC TG CCCC ACA
CGGGTG CGG GG C
CAACATCCCCCAGTCCCTGG CTT G C-- C AC T A GTA - A
CCCCCGCCGGGTTTCAGGAG
TGCAGGGG
GAM363 GGGGCCCGCCAGCTACGCGA 9471 GCGGGCCATG 9472 - --- ACGT AG G AACC
GA G CA
GCTACGTGGTCAGGGGGGAC GTCGCCTTCG CCGCCAGCT ACGCGAGCT GGTC GGG
GAC TGGT CG CCGT G
AACCTGGTGACGGCCGTCAG ACCA |||||||| |||||||| |||| ||| ||| |||| || ||||

CTACGGGCGGGCCATGGTCG GGTGGTCGG TGTGTTTGA CCAG TCC CTG ACCG
GC GGCA /
CCTTCGACCAGTTTGTGTCC A ACC ---- CT G GT-- G- G TC
AGGCTGGTGGACAACCCC

GAM364 GCGTCTAAATTTAAAAAAGT 9478 TCTAAATTTA 9479 A ----- AG - A CC
TTATATATTAGTACCAAATA AAAAAGTTTA GCGTCTA AT TTAAAAA TTTA TATATT GTA A
TAAATATACTAAAGATTTTT TATA ||||||| || ||||||| |||| |||||| |||
AATTATAGTATGGACGT TGCAGGT TG AATTTTT AAAT ATATAA TAT /
A ATATT AG C A AA

GAM365 TGTTTACAATAGTAACTAGT 9488 TTAGAAGATT 9489 T - CTAGTAA AG
AAAATGAAGTCATCATTAGA TATTATCTGT TGT TACA ATAGTAA AATGA T
AGATTTATTATCTGTATACA ATAC ||| |||| ||||||| |||||
ACA ATGT TATTATT TTACT /
T C TAGAAGA AC

GAM366 GGTTAGAAACATTTGGTTTA 9497 TATGACAATT 9498 AGAAACAT GTT C CCGGATACC-
T AA
TGACAATTCCGGATACCTTT CCGGATACCT GGTT TTG TATGA AATT TTTTCTCAG
AT T
TCTCAGTATAATCAAATCTT TTTC |||| ||| ||||| |||| ||||||||| ||
GGGAAGATCAATAAGAAAGT CCAA AAT ATACT TTGA AGAAGGGTT TA C
TTTCATATAATAATATAACA GACAATAT AAT T AAGAATAACT C AA
GAACC

GAM367 GGCTGCCTAATCTTACAGGG 9510 TGCTATCGGG 9511 T A- ACA GG AAGACA
AGCAGAAAGACACACAGACT AGATCAAGGT GGC GCCT ATCTT G AGCAGA C
CTGCTATCGGGAGATCAAGG GCC ||| |||| ||||| | ||||||
TGCC CCG TGGA TAGAG C TCGTCT /
- AC GG- TA CAGACA

GAM368 ATAAGTTTATATATATATTA 9524 TATATTATTG 9525 A CCCGA C GACCCGC --
ACC
TTGGCCCGAGTGCGAGCCCT GCCCGAGTGC TATATAT TTATTGG GTGCGAGC CTGG
GCCAGC TCTCACG G
GGGACCCGCGCCAGCTCTCA GAGC ||||||| ||||||| |||||||| |||| |||||| |||||||
CGACCGTGCCCGTGAGAACG ATATATG AATAACT CACGCTTG GACC CGGTCG
AGAGTGC T
CTGGCAGAATGCCAGCGTTC - CAAAA C GTAAGA- CA CCG
GCACAAAACTCAATAAGTAT
ATATATATTAT
GAM369 GGCGAGGGTCCTGGCAGAAG 9531 TGGCAGAAGG 9532 TCCT CT--- TAG
C
GCCGGCCGGTCGGAGCTGGC CCGGCCGGTC GGCGAGGG
GGCAGAAGGCCGGCCGGTCGGAG GGC CCGGC G
TAGCCGGCCGCGGCTGGATG GGAG |||||||| |||||||||||||||||||| ||| |||||

TCTGTCTCTCTGGCTGGCCG CTGCTTCC TCGTCTTTCGGCCGGTCGGTCTC CTG
GGTCG C
GCTTTCTGCTCCTTCGTC ---- TCTGT TA- G

GAM370 TCCCTGCTTGCTCACGGCCG 9561 GAGGACCCCG 9562 G CC-- A - TC CCT
CCCCTCACCCTTCTCCCTTT GCGGTGAGCA TCCCTGCTTGCTCAC GCCG CCTC CC CT TC
T
CGCGATTGGCGGGAGGACCC AGCA |||||||||||||| |||| |||| || || ||
CGGCGGTGAGCAAGCAGGGA AGGGACGAACGAGTG CGGC GGAG GG GG AG T
G CCCA - C TT CGC

GAM371 CCCGCCAAGTGAGCTCCGCC 9641 AGACGGGGGT 9642 CCA A CGG G
CACCCAGCCCCCACCCTCAT GGGGGCTGGG CCCG
AGTGAGCTCCGCCCACCCAGCCCCCACCCTC TCT GCCCG G
CTCGGGCCCGGGGGCGGGCA TGGG |||| ||||||||||||||||||||||||||||| ||| |||||
GACGGGGGTGGGGGCTGGGT GGGC TCACTCGAGGCGGGTGGGTCGGGGGTGGGGG
AGA CGGGC G
GGGCGGAGCTCACTCGGG --- C --- G

GAM372 GGCGTGTCGCGCTCGCTCGC 9854 AGGCAGCCGC 9855 T - C C--- CG TT
CCGGGCGGTTCATCCGCTTC GGCCGCC GGCG GTCGCG CT GCT GCC GGCGG C
GGCTTTAGGCAGCCGCGGCC |||| |||||| || ||| ||| |||||
GCC CCGC CGGCGC GA CGG CGG TCGCC /
- C - ATTT CT TA

GAM373 GGCCACATGTGCGGTATGGG 9899 TGACGCTGAC 9900 ACA --- ATG G TATC
GGTCGACTATCAAAACGTGG TTACAACGGC GGCC TGTG CGGT GGGGTC AC A
CCCTGACGCTGACTTACAAC C |||| |||| |||| |||||| ||
GGCC CCGG ACAT GTCG TCCCGG TG /
CA- TCA CAG - CAAA

GAM374 CCTCCAGTACGTCGTGGTCA 9925 TCCAGTACGT 9926 C CGTC T C--- A CG
ACGGTACAGACGTGTTTTTG CGTGGTCAAC CCT CAGTA GTGG CAA GGT CAGA T
GACCAGCCTTGCCATATGCT GGTA ||| ||||| |||| ||| ||| ||||
GCAGG GGA GTCGT TACC GTT CCA GTTT G
C A--- - CCGA G TT

GAM375 GCTTGCTTTGGCCCGCCTTG 9929 TAGCCCCCTG 9930 - TTT C---- CT CTT C TT TCG
CGCTTTTGCATTTGGCTCGC GCCCGCAGTG GC TTGC GGCC GC TGCG TTG AT GGC C
CCCTGCCCGGTTTAATTTGC C || |||| |||| || |||| ||| || |||
ATAGCCCCCTGGCCCGCAGT CG GACG CCGG CG ACGT AAT TG CCG C
GC T C-- TCCCC AT TT- T GC TCC

GAM376 TTAAATTTGATAAATAACTT 10011 AATTTGATAA 10012 - - TAA AGA C
AGATATTTTGTTTCAAGAAC ATAACTTAGA TTAA ATTTG ATAAA CTT TATTTTGTTT A
AAGATAAAGAACTTTATCCA TATT |||| ||||| ||||| ||| ||||||||||
AATCTTAA AATT TAAAC TATTT GAA ATAGAACAAG /
C C CAA --- A

GAM377 GGGACGGACGGCGGGCCGGG 10016 CTTCTCCTTC 10017 C C C-- CC C G AG
AGCGGGCGGCAGTGCGGCGC CCCTTCCCCT GGGA GGA GG GGG GGGAG GGGCG C T
CTTCTCCTTCCCCTTCCCCT CCTT |||| ||| || ||| ||||| ||||| |
CCTTCTC CTCT CCT CC CCC TCCTC TCCGC G G
T C CTT CT T - GC

GAM378 CCGCGCGTGCCTTTTTTTTG 10284 TCGCCGCGGC 10285 TTTTTT TTA G - A CT
TTTTACCGCGGCGCGGGAGA GGCCGGCGGG CCGCGCGTGCCT TGTT CCGC GCG
CGGGAGA GCC C
AGCCCTCGCCGGCTCTCTCG GCGC |||||||||||| |||| |||| ||| ||||||| |||
CCGCGGCGGCCGGCGGGGCG GGCGCGCGCGGG GCGG GGCG CGC GCTCTCT
CGG G
CGCGCGG ------ CC- G C - CC

GAM379 GGCGGTGGCGGCCGCGTCTC 10332 TGGCGGCCGC 10333 C T CGTCTCTCTCCTTTC
CCTCTT
TCTCCTTTCCCCGCGCCTCT GTCTCTCTCC GG GG GGCGGCCG CCCGCG T
TTCTTGTTCCGCGGGCTTCT TTTC || || |||||||| ||||||
TTCTTGGCCGTCTCCTCC CC CC CTGCCGGT GGGCGC C
T T TCTTTCTTC------ CTTGTT

GAM380 TCCCTGCTTGCTCACCGCCG 10350 GCTTGCTCAC 10351 C GGGT C AA GCGA
GGGTCCTCCCGCCAATCGCG CGCCGGGGTC TCCCTGCTTGCTCAC GCCG CCTC CGCC TC
A
AAAGGGAGAAGGGTGAGGGG CTCC |||||||||||||| |||| |||| |||| ||
CGGCCGTGAGCAAGCAGGGA AGGGACGAACGAGTG CGGC GGGG GTGG AG A
C ---- A GA AGGG

GAM381 GGGAAAGAGAAGGAGGGGAA 10385 AGGGGAAGGA 10386 AAGA A AG AA AA AGAA CC
GGGGAAGGAGAAGGCGCCGC GAAGGCGCCG GGGA GA GG GGG GGGG GG GGCG G
ACTGCCGCCCGCTCCCGGCC CACT |||| || || ||| |||| || ||||
CGCCGTCCGTCCC CCCT CT CC CCC CCCT CC CCGT C
GC-- G G- GG CG CG-- CA

GAM382 CGCATAAGGCACCGCGGCTG 10491 TAAGGCACCG 10492 TAAG A-- GG - TC ACAG
GGCCCTTCACACAGGCAAAA CGGCTGGGCC CGCA GC CCGCGGCT GCC CT AC G
GTAGGGAGGCAGGGCCGCGG CTTC |||| || |||||||| ||| || ||
CGAGTAATTTGCG GCGT TG GGCGCCGG CGG GG TG C

TTAA AGC GA A GA AAAA

GAM383 CCGAGTGAGCTCCGCCCACC 10522 CGAGATGAGG 10523 C --- GC
CAGCCCCCACCCCCGTCTGC GTGGGGGCTG CCGAGTGAGCTCCGCCCACCCAGCCCCCACCC
CGTCT GCCC C
CCGCCCCCGGGCCCGAGATG GGTG ||||||||||||||||||||||||||||||||| ||||| ||||
AGGGTGGGGGCTGGGTGGGC GGTTCACTCGAGGCGGGTGGGTCGGGGGGTGGG GTAGA
CGGG C
GGAGCTCACTTGG A GCC CC

GAM384 GGGGGAAAGGGGAAGGAGGG 10623 CCGCCGCCCA 10624 G AAAG- AA G A TAGAA A
C
GAGGCTAGAAGCAGCGGGCG TCCGCCTAGC GG GG GGG GGA GGG GGC GC GCGGG G
GGCCCGTCGTCCGCCGCCCA GGCT || || ||| ||| ||| ||| || ||||| |
TCCGCCTAGCGGCTGCC CC TC TCC CCT CCC CCG TG TGCCC G
G GGCGA G- A G CC--- C G

GAM385 GGACAGGCCCCCCCGCTGGC 10685 CATTGGATTT 10686 G- C T C TA- A TCTCG
GCAAAAATACAATAGCTCTC TTTGCCCGCG GGACA GCCCCC CGC GG GCAAAAA CAAT GC
A
GATTATCCGCCATTGGATTT CGGG ||||| |||||| ||| || ||||||| |||| ||
TTTGCCCGCGCGGGGGCGAT CCTGT CGGGGG GCG CC CGTTTTT GTTA CG T
GTCC AG C - - TAG C CCTAT

GAM386 GCCGCAGCCCCAGCTGCCCC 10691 CAGCTGCCCC 10692 - A CC T - - G- G
CCCGGCGCGCGCGATAGCGA CCCGGCGCGC GCCG C GC CAGC GCCCCCCCG GCG C CGC
A
GGTTGCTCGGGGGGGCGCTG GCGA |||| | || |||| ||||||||| ||| | |||
TTGCCGCCGGC CGGC G CG GTCG CGGGGGGGC CGT G GCG T
C C TT - T T GA A

GAM387 CCATAAAGACCATTACCTCG 10760 TGCCTTAGAG 10761 AAA ATTA --- - GTT
GGGCTCCAGTTTGGTGTGGA AGGGGGTTAG CCAT GACC CCTC GGGGC TCCA T
TGCCTTAGAGAGGGGGTTAG TGG |||| |||| |||| ||||| ||||
TGG GGTG TTGG GGAG TTCCG AGGT G
A-- G--- AGA T GTG

GAM388 TGGATTATTTCTCCCAACAC 10789 TATTTCTCCC 10790 TTATTT CA AG CA AAC
CCCAGTATTCAACAACATCA AACACCCCAG TGGA CTCC ACACCCC TATT AC A
GTGATAAGGGGTGTGGAGTC TATT |||| |||| ||||||| |||| ||
TCCA ACCT GAGG TGTGGGG ATAG TG /
CT---- -- A- -- ACT

GAM389 CCACCCAGAGCCACATGAGG 10802 ACGGACCCAC 10803 AGA A- A A CG G
ATCCCGTCGCGGGAACGGAC ATGGCGGCGG CCACCC GCC CATG GG TCC TC C
CCACATGGCGGCGGAGGGTG AGGG |||||| ||| |||| || ||| ||
G GGTGGG CGG GTAC CC AGG AG G
AGG CG A C CA G

GAM390 CCATGTCAGAGGTCCAGTAC 10847 TCAATGGGTT 10848 T - T GATAC TC- AA
CCATGATACTGGCATCACTG TGTGGCCTTT CCATG CAGAGGTC CAG ACCCAT TGGCA ACTGTT A
TTAAACAGACAGTTCTTGTC GCCA ||||| |||||||| ||| |||||| ||||| ||||||
AATGGGTTTGTGGCCTTTGC GGTAC GTTTCCGG GTT TGGGTA ACTGT TGACAG /
CATGG C T - ----- TCT AC

GAM391 GAGAACAGATGAGGTCGTCG 10862 TATAATGGAA 10863 A - G --------- AAA
CAGAAAATCTCCTGTATAAT GGGGATCATC GAGA CAGATGA GGTC TC GCAG A
GGAAGGGGATCATCATCTGT ATCT |||| ||||||| |||| || ||||
CTT TTCT GTCTACT CTAG GG TGTC T
- A G AAGGTAATA CTC

GAM392 TATCCAATATGTTGTTGTGA 10873 TCCAATATGT 10874 A G A - ATTTC ACA - GTCAGT
ATGGCACAGATGTATTTCTG TGTTGTGAAT TATCCA TATGTT TTGTGA TGGCACAGAT GT TGGA GCC CT T
GAACAGCCCTGTCAGTTTTT GGCA |||||| |||||| |||||| |||||||||| || |||| ||| ||
CCAAGAGGCCTATCCAACAA GTAGGT GTACGA GACACT ACCGTGTTTA CA ACCT CGG GA /
TTTGTGCCAGTCACAGGAGC C G G A ----- ATC A ACCTTT
ATGCTGGATG

GAM393 ATCACTCAATTCCAGACCCT 10881 CATCACAGGT 10882 TTCCA TG AC - A AGCACT
GCCTACGAGTATAGGAGCAC GGGGTCCTTG ATCACTCAA GACCC CCT GA GT TAGG A
TATCAATCCCTGGGCATCAC GGTG ||||||||| ||||| ||| || || ||||
AGGTGGGGTCCTTGGGTGAT TAGTGGGTT CTGGG GGA CT CG GTCC /
C---- GT CA A G CTAACT

GAM394 GGCCGCCGCGCGCCCCCGCC 10898 CCGCCGCGCG 10899 C C CCCC C C C CCCC C C C GC
CGGCCGCCGCGCGCCCCCGC CCCCCGCCCG GGC GCCG GCG CGC CGGC GCCG GCG CGC CGGC GCCG GC C
CCGGCCGCCGCGCGCCCCCG GCCG ||| |||| ||| ||| |||| |||| ||| ||| |||| |||| ||
CCCGGCCGCCGCGCGCCCCC CCG CGGC CGC GCG GCCG CGGC CGC GCG GCCG CGGC CG C
GCCCGGCCGCCGCGCGCCCC C C CCCC C C C CCCC C C C CC
CGCCCGGCCGCC

GAM395 AGTAAAATATGAGGATTTTT 11117 TAAAATATGA 11118 TTTTTT AC- T T ATCCTC T TTT TTTCA

```
     TTGACGGAATGATATTATGA      GGATTTTTTT      TATGAGGA    TG  GGAA GATA TATG    GAT
GATA  TTA   T
     TCCTCGATTGATATTTTTAT      GACG          ||||||||    ||  |||| |||| ||||    ||| ||||  |||
     TTCATTATTATTAACACTAT                  ATACTTCT    AC  CCTT TTAT ATAT    CTA CTAT  AAT   T
     CATCTATTAATATATTATTT                     TCTT-- ATA  -  T  AATTAT  -  CAC  TATTA
     TCCATACATTCTTCTTCATA
     TAATTTACT
GAM396  AGGGACTCCGGAGAAGGAAG 11122  GCGCGCCCTT 11123     CTCC   A-    C  T  CG
     GCTGCTCCGCGCACCGGCGC      CTCCTCTCCC      AGGGA   GGAGA  GGAAGG TGC CCG  C
     GCCCTTCTCCTCTCCCCTCC      CTCC          |||||   |||||  |||||| ||| |||
     CT                          TCCCT   CCTCT  TCTTCC GCG GGC  /
                                  CC--   CC    C  C  CA


GAM397  GGGGCTTGGCCGCCGAGGTG 11270  CACCTCGGCG 11271     TT         ----    GGC
     CGCCCCGGCCGGAGGGGCCC      GCCGCCCC        GGGGC  GGCCGCCGAGGTGC   GCCCC  C
     CCGCACCTCGGCGGCCGCCC                  |||||  ||||||||||||||   |||||
     C                           CCCCG  CCGGCGGCTCCACG   CGGGG  /
                                  --          CCCC    AGG


GAM398  AGAAACACGAGGCGGGGGTC 11413  AACCCGTATC 11414      C       TC  -   ---  CAG  A   CA  -
ACC
     CCAGAAAGGGCAGGCAGGTC      CTTTTTTTCT      AGAAACA GAGGCGGGGG  CC AGAAA   GGG   GC
GGT  GC CGC   G
     AGCCGCACCGCCCGCGAGCC      AGGT          |||||||  ||||||||||  || |||||   |||   || |||  || |||
     AACCCGTATCCTTTTTTTCT                  TCTTTGT TTTTGTTTTT  GG TCTTT   TCC   TG CCA  CG GCG
 /
     AGGTGTTTTTGTTTTTGTTT                     -       GT  A    TTT   TA-  C   AC  A   CCC
     CT

GAM399  GGAAAGCGGAAAAACGGAGG 11428  AAGCGGAAAA 11429    AA-    AAAA         G -  AA   -
TCCCG
     ATGGAAGGGCAGAAGATGGG      ACGGAGGATG      GGA   GCGGA   CGGAGGATGGAAGG C AG
GATG GGGAG    A
     GAGTCCCGATCCTCCTCCTG      GAAG          |||   |||||   |||||||||||||| | ||  |||| |||||
     CATCCCCTCGCCTTCCATTC                   CCT   CGCCT   GCCTCTTACCTTCC G TC  CTAC TCCTC
/
     TCCGGCCCTCCGCGAGTCC                      GAG    CCCG         - C  CC    G    CTCCT


GAM400  GGGCCGCGGGCCAGCAGACG 11547  CCCACGCCTC 11548     -------    CCA  AGAC     GGC
     GGCCGCGGCGCCAGCGGCCC      CCGCCGCATT      GGGCC     GCGGG  GC   GGGCCGC  G
     ACGCCTCCCGCCGCATTAGG      AGGC          |||||     |||||  ||   |||||||
     CCC                         CCCGG     CGCCC  CG   CCCGGCG  /
                                  ATTACGC    TC-  CA--     ACC


GAM401  GAAAATTTGTGAGTATATCA 11613  TGAGTATATC 11614     A    ----    TATCAG    ATTA
     GATCATATTATAAAGATGAT      AGATCATATT      GAAA TTTGT   GAGTA    ATCAT   T
```

ATAAGTTACTTTGAAACAGG ATAA |||| ||||| ||||| |||||
ATTTC CTTT GGACA TTCAT TAGTA /
A AAGT TGAATA GAAA

GAM402 GCAATGTTAAAGTGACTCCT 11620 TTAAAGGTAA 8404 - TAAA CT- AGAT- AC T
CCAGATTACTCACCTATAAT GAGTTATGAC GC AATGT GTGACTC CC TACTC CTA A
AGCGAGTATTAAAGGTAAGA GCAT || ||||| ||||||| || ||||| |||
GTTATGACGCATTAGC CG TTACG TATTGAG GG ATGAG GAT /
A CAG- AAT AAATT C- A

GAM403 TATCAAGATGTGTATATTTG 11621 CAGCACAAAT 11622 - ---------- CGAAAA G
CGAAAATTGTGGAGACATAG CAAAAGTATT TATC AAGATGTGTAT ATTTG TTGTG A
CAGCACAAATCAAAAGTATT AATA |||| |||||||||| ||||| |||||
AATACATGTCTTAGATG GTAG TTCTGTACATA TAAAC GATAC G
A ATTATGAAAAC ACGAC- A

GAM404 GCCGAGGACTTACTTGACGA 11641 ACGAATCTCC 11642 A AC TTG T T
ATCTCCTGTGGACTTGGTTC TGTGGACTTG GCCG GG TTAC ACGAATC CCTGTGGAC T
GCAGGGGTTTGTGTGACCCG GTTC |||| || |||| ||||||| |||||||||
GT TGGC CC AGTG TGTTTGG GGACGCTTG /
- -- --- - G

GAM405 GGGCTGATGTAGAGATGAGA 11655 AAGCCGCCCA 11656 ----- T G - G TA
ATTGTTCTGGGGGGCTTTGG GAATAGGTTT GGGCTGA TG AGA ATGAGAAT TGTTCTGGG
GGCTTTGGCCA A
CCATAAACTGGCTAAAGCCG TCGT ||||||| || ||| |||||||| |||||||||| ||||||||||
CCCAGAATAGGTTTTCGTGT TCTGACT AC TTT TGCTTTTG ATAAGACCC
CCGAAATCGGT /
TTCATGAACTCAGTCT CAAGT - G G G CA

GAM406 GTCTGGACCGCACAGTGTGT 11670 CCGCACAGTG 11671 GACC C G AG A
GTGGCAAAGGCATCGGCGTT TGTGTGGCAA GTCTG GCA AGTGTGTGT GCAA GC T
GCGACGCGCGCTTTGTTCAG AGGC ||||| ||| ||||||||| |||| ||
CAGGC CGGAC TGT TCGCGCGCA CGTT CG C
GACT T G G- G

GAM407 GTGTCTATGCCACGTTGCTC 11760 TATGCCACGT 11761 CTA CCAC CTC AC C
GCACATGCGTATCACAGTAC TGCTCGCACA GTGT TG GTTG GC ATGCGTAT A
GCGTAGCCATAACCTTACAC TGCG |||| || |||| || ||||||||
TCACGC CGCA AC CAAT CG TGCGCATG C
CTC ATTC AC- A- A

GAM408 CGGCTGTTTGTTAAGCAGGA 11765 AAGCAGGAGC 11766 C TT A -- ACGC - G

GCCCCACGCCTCCCGAAAGG CCCACGCCTC CGG TG TGTTAAGC GGAGC CCC CTC CC A
TGAGAGAGGGCCGCTTCCGC CCGA ||| || |||||||| ||||| ||| ||| ||
TTGATATCATCTG GTC AC ATAGTTCG CTTCG GGG GAG GG A
T T- C CC AGA- T A

GAM409 CAACCATTTCCGGTCGCTTA 11850 TAAGGGAAGA 11851 TTTC G--- C--- - A
TACGAGGTAGAGTTCTGCTC TCGATGTTGG CAACCA CGGTC CTTATA GAG GTAG G
TCACGTTATAAGGGAAGATC TTG |||||| ||||| |||||| ||| ||||
GATGTTGGTTG GTTGGT GCTAG GAATAT CTC CGTC T
TGTA AAGG TGCA T T

GAM410 TCTCCACTCTCTCGGTGTTC 11861 TCGGTGTTCC 11862 - CT - A GTCCTCAAT
ATACTCA GTTA
CAGAGGCATGTCCTCAATGC AGAGGCATGT CACTCT CGG TGTTCCAG GGCAT GCTGGT
ATGGC T
TGGTATACTCAATGGCGTTA CCTC |||||| ||| |||||||| ||||| |||||| |||||
TCAAAGCCGTGGGCCAGCGT GTGGGA GTT ACAGGGTC CTGTG CGACCG
TGCCG /
GTCCTGGGACAGTTGCAAGG T AC G - --------- GG----- AAAC
GTGTGATGA

GAM411 GTCAGGACCCCTTTGGTCCA 11874 ACCCCTTTGG 11875 A TG T-- A --- G T
TGTCGCGCGGGTCCTCCGGT TCCATGTCGC GTCAGG CCCCTT G CC TGTC GC CGGG C
TCAGGCAGGCGTCTGAAGGG GCGG |||||| |||||| | || |||| || ||||
GCTTGAC CAGTTC GGGGAA C GG ACGG TG GCCT /
- GT TGC - ACT - C

GAM412 TTCCCGGGGAGGAGGGCACC 11877 TTCCCGGGGA 11878 GGA - A AGG GGA - A AGG
--- AG
AGGTTCCCGGGGAGGAGGGC GGAGGGCACC GGA GG GC CC TTCCCGGGGA GG GC CC
TTCCCGGGGA GG G
ACCAGGTTCCCGGGGAGGAG AGGT ||| || || || |||||||||| || || || ||||||||||
GGCACCAGGTTCCCGGGGAG CTT CC CG GG AGGGGCCCTT CC CG GG
AGGGGCCCTT CC G
GAGGGCACCAGGTTCCCGGG GGA A - AGG GGA A - AGG GGA AC
GAGGAGGGCACCAGGTTCCC
GGGGA
GAM413 CACCTCTCCATAGTTGCAAA 11891 TAAAATGTTG 11892 CATAGTT AAA T AAAT CAAG
GACT C
TACGCTACGAAATGCCCAAG GCCGCGTGTG CACCTCTC GC TACGC ACG GCC
GACATT AAA G
GACATTGACTAAACGTGTTT TAGG |||||||| || ||||| ||| ||| |||||| |||
CTAAAATGTTGGCCGCGTGT GTGGAGGG TG ATGTG TGC CGG TTGTAA TTT
T
GTAGGGTTTTCAGAGGGAGG AGACTTT GG- - GC-- ---- AATC G
TG

GAM414 TACCCAGCCGGGTTTACGCA 11904 ACGCAGCTGC 11905 C G T A T
GCTGCGTATACCCAGCTGTG GTATACCCAG TACCCAGC GGGTTTAC CAGCTGCGTA ACCC
GCTGTG T
TTTACGCAGCGGGGTTTACG CTGT |||||||| |||||||| |||||||||| |||| ||||||
CAGCTGGGTAGACCCAGCTG ATGGGTCG CCCAGATG GTCGACGCAT TGGG CGACGC
T
GGTA A G T G A

GAM415 GAAGGAGGGTTGAATACAGT 11927 TGGTATTCCC 11928 G GT A TG G CGC C
AGCT -- TT
TGGGGGTAGTCCGCTGGTAT AGCTGAGGTT GAGG TGAAT CAGT GGGGTA TC TGGTATT
CC GAGGT TGCC A
TCCCAGCTGAGGTTGCCTTA GCCT |||| ||||| |||| |||||| || ||||||| || ||||| ||||
TTTGGTAATGCTTCCGGAAA TTCC ATTTG GTTA CCCCAT AG ACCATAA GG CTTCG
ATGG T
TACCACCTGAGTACCCCATT G AT - -- G TCC A C--- TA TT
GGTTTATACCTTGTTT

GAM416 GTGGGCGCCGCGCGCGTGCT 11950 GAGTGCGCGC 11951 G C TG GTC A GCT-
CA
CTCTCAGTCGCGCCTAGCTG GCTGCGCTGA GT GGCGC GCGCGCG CTCTCTCA GCGCCT
GCT TC A
CTTCCAACAGACAAAAGCGG C || ||||| ||||||| |||||||| |||||| ||| ||
GGCGTTAGTGAGGGAGTGCG CA TCGCG CGCGCGC GAGGGAGT TGCGGG CGA AG
/
CGCGCTGCGCTGAC G T GT GAT G AAAC AC

GAM417 AAAGACTCGCTCAACAGCCC 11989 TGGATTAGGT 11990 CGC A - GAAAA A CC
GAAAACCATCAGCCCGACCG GCTGCTGGAC AAAGACT TCA CAGC CC CCATC GC G
CCGATGGATTAGGTGCTGCT AAGT ||||||| ||| |||| || ||||| ||
GGACAAGTCTTT TTTCTGA GGT GTCG GG GGTAG CG A
ACA C T ATTA- C CC

GAM418 GCTCTGAATTTTTCTGCGCA 11996 TTAGTCAGAT 11997 AATTTT - ------ GAC
CATCTACATAA G
TGCGCGACTCCTCATCTACA AGCAGGGC GCTCTG TCTG C GCATGCGC TCCT
TTTAT C
TAATTTATGCACATAAAAGG |||||| |||| | |||||||| |||| |||||
ATTAGCGCATGCAAATTAGT CGGGAC AGAC G CGTACGCG AGGA AAATA
A
CAGATAGCAGGGC GAT--- T ATTAAA ATT ---------- C

GAM419 TTGACCGGCAAGTTCCAGGC 12039 CACCAGGGAC 12040 -- CA A CA TG- TG
ATCCTAAGTGCTTGATGTAG TACCTAGGTC TTGACC GG AGTTCC GG TCCTAAG CT A
ACCCTTAGGGCACCAGGGAC AA |||||| || |||||| || ||||||| ||
TACCTAGGTCAA AACTGG CC TCAGGG CC GGGATTC GA T

AT A- A AC CCA TG

GAM420 CTGCTGGACGGAGGTAGTAT 12120 AGGTAGTATA 12121 C CGGA C T T-
ACAA
AATCAGCTAGGCCTCAGTAT ATCAGCTAGG CTG TGGA GGTAGTATAAT AGCTAGGCC
CAGTATTCTA GTA A
TCTATGTAACAAATGAATGC CCTC ||| |||| |||||||||| ||||||||| |||||||||| |||
CCTAGAGTACTGCGGTTTAG GAC ACCT CCGTCATATTG TCGATTTGG GTCATGAGAT
CGT /
CTAGTTATACTGCCCGGTTC C TGGC A C CC AAGT
CACCAG

GAM421 CCTGGAGGGGTGTCACATTC 12135 TGTGATAGCC 12136 - - G T- C--- - ACG
TGTGACCGCGACGTTGACGT CATCACAGG CCTG GA GGG TGTCACATTCTG GAC
GCGACGT TG T
TAGACACACGTCGCTGCCGT |||| || ||| |||||||||||| ||| ||||||| ||
CCTCAGAATGTGATAGCCCA GGAC CT CCC ATAGTGTAAGAC CTG CGCTGCA AC T
TCACAGG A A G TC CCGT C AGA

GAM422 GCTGTTGCGTTGGTTGGGAG 12183 TGTTGCGTTG 12184 T T-------- G
TTTGGGGACCAAATTTCTAT GTTGGGAGTT GCTGTTGCG TGG TGGGAGTTTGG G
AATTGGTGTCACCGCGGCAG TGGG ||||||||| ||| ||||||||||
C CGACGGCGC ACT ATCTTTAAACC /
C GTGGTTAAT A

GAM423 GTGGCTCGCGACCACCCACC 12187 TTGGACCCGT 12188 C - ---- ---- T ATT
TGGATTTTGGACCTGGCTTT GGCTCGCGAC GTGG TCGCGA CCAC CCA CC GG T
TGGACCCGTGGCTCGCGACC CAC |||| |||||| |||| ||| || ||
AC CACC AGCGCT GGTG GGT GG CC T
- C CCCA TTTC T AGG

GAM424 GGCTGACCCAAAATTTTAAA 12203 AGAGGGCCAG 12204 A A A G AT- GTA TA
AATTGGGGTTAGCCATCCTG GCTGACCCAA GGCTGACCC AA TTTTAAAA TT GGGTTAGCC
CCT CAAAAA T
TACAAAAATATTACTTTTTG AATT ||||||||| || |||||||| || ||||||||| ||| ||||||
AGAGGGCCAGGCTGACCCAA CCGATTGGG TT AAAATTTT AA CCCAGTCGG GGG
GTTTTT T
AATTTTAAAAATTGGGGTTA G A A A ACC AGA CA
GCC

GAM425 CCGGCATGCTTCTCGCCCGA 12221 CGGGCAGATC 12222 AT T CC CC AT TC
TCCCCCCGATCTCACCCGGC CTGTGAGATG CCGGC GC TCTCGC GATC CCCG C A
CGGGCAGATCCTGTGAGATG CGCC ||||| || |||||| |||| |||| |
CGCCGG GGCCG CG AGAGTG CTAG GGGC G C
-- T TC AC CG CC

GAM426 GCGCGCATAATGGCGGACCT 12236 GTCTATGGTT 12237 - TAATG G - AAAA C
AGGCCTAAAACCCCCAGGAA GGCTGCGCTG GC GCGCA GC GACC TAGGCCT CC C
GCGGGTCTATGGTTGGCTGC C || ||||| || |||| ||||||| ||
GCTGC CG CGCGT CG TTGG ATCTGGG GG C
T ----- G T CGAA A

GAM427 AGCCCTCAGACCGCGTCCGC 12263 TCTGTGGAGT 12264 AGAC CG G CC G ---- T GT A G TG
GCCCCGGGCCAGCCTAGCGT TTGGTTTCGA AGCCCTC CG TCC CGC CGG CC AGCC AGC CGCA AC TC G
CGCAAACGTCTGGAAGAGTC GGGC ||||||| || ||| ||| ||| || |||| ||| |||| || ||
TGTGGAGTTTGGTTTCGAGG TCGGGAG GC AGG GCG GCC GG TTGG TTG GTGT TG AG /
GCCGTGCGGGGAAACGCAGA AC-- AA G T- G AGCT T AG C - AA
GGGCT

GAM428 CGAAACTGCCGTGTAAACGA 12275 GTGGATCGCT 12276 AAC CG AA AT T-- AGCC CC GA G T
ATGCTTAGCGGAGCCGCGCC CGCCCGCTCT GA TGC TGTA CGA GCT AGCGG GCG CGG CGC TCGTTTC T
CGGGACGCGTCGTTTCTTGC TAGC || ||| |||| ||| ||| ||||| ||| ||| ||| |||||||
GAAACGGGGTGGATCGCTCG CT GCG ACAT GCT CGA TCGCC CGC GCT GTG GGCAAAG G
CCCGCTCTTAGCCCTCGCGT --- TG GC CC TTC ---- TC AG G C
ACAGTGCGTCG

GAM429 CGTTAAGGTGTACGTGCGTG 12278 TAAGGTGTAC 12279 AAGG TG GTGT GT
TACGAGACCGCGTGCGAGCG GTGCGTGTAC CGTT TGTACG C ACGAGACCGC G
GTCTCGTCGTAGTGCGTATG GAGA |||| |||||| | ||||||||||
AACG GCAA GTATGC G TGCTCTGGCG C
---- GT ATGC AG

GAM430 GAATATTTTTAAAGACTTTT 12291 TTAAAGACTT 12292 T CTTTTTTC T
TTCCCCAACCTCTGGGTTGG TTTTCCCCAA GAATATTTT AAAGA CCCAACC C
GTTTTTTCTCTTTAAAATAT CCTC ||||||||| ||||| |||||||
TC CTTATAAAA TTTCT GGGTTGG T
- CTTTTTT- G

GAM431 CCCGGGGAGATAGGCGCTCG 12314 CACGTCTTTG 12315 C- TC ----- - T- AA- - G- - C
CGGAGAGGGGGTTGGGCGAA CCCCTTGCTC G GC GC GGAG AGGGGGT GGGCG GGA CGGG GGGGTG GTGC T
GGACGGGGGGGGTGGTGCCT CAGT | || || |||| ||||||| ||||| ||| |||| |||||| ||||
GGCGCGCGCCCCAGCCCGTT C TG CG CCTC TTCCCCG TCTGC CCT GCCC CCCCGC CGCG /
CCGCACGTCTTTGCCCCTTG CT GA TTTGA G TT ACG T GA G G

CTCCAGTTTGCAGGTTCCCT
CTTTCTCCAGG
GAM432 TCCCCCAAAGACACTCTCGG 12342 CGGTTGGGCG 12343 C AAGACACTCT G AGG
CCGACCGCAGAGGGATAACT CGTGGGCGA TC CCCA CG CCGACCGCAG G
GCGGTTGGGCGCGTGGGCGA || |||| || ||||||||||
AG GGGT GC GGTTGGCGTC A
C GC-------- G AAT

GAM433 GAGAGTGACCACACAAGAAG 12417 TTAAATTTTT 12418 G CAC GAAA G
AGAAAAAAAGTCATTTTAAA TTATTGGTTA GAGA TGACCA AAGAAGA AAAA T
TTTTTTTATTGGTTAATTTC ATTT |||| |||||| ||||||| ||||
CTTT ATTGGT TTTTTTT TTTT C
A TA- AAA- A

GAM434 AGCAGACAGGTTAGAGCACT 12421 TGTTGTGTGA 12422 AG AG GAGC - A AG A
GTTGTGTGATGTGAGAGGAG TGTGAGAGGA AGC AC GTTA ACTGTTGTGTGATG TG GAGG
T A
TAAGTGTGTCTCCACCATCG GTAA ||| || |||| |||||||||||||| || |||| |
CATAACAGTTGATAGGTGGG TCG TG TAGT TGACAATACGCTAC AC CTCT G G
CT GG GA ---- C - GT T

GAM435 CGATGTGTTTGACAATGTAC 12434 TAGAAAGCTC 12435 - CAATGTAC TTT A---- TG GG
GA CT A
TCTTTGCTTTCAACTGCAGG TGATCAAACT GTTTGA TC GCTTTC AC CAG TGTTTTA
ATGG TC A
GTGTTTTAGAATGGCTTCAA TCAT |||||| || |||||| || ||| ||||||| |||| ||
CAGATTCATTAAAATGTTCT CAAACT AG CGAAAG TG GTC GTAAAAT TACT
AG C
GTGGTCCATAGAAAGCTCTG T -------- TCT ATACC GT TT -- T- A
ATCAAACTTCATTG

GAM436 TCTGGATCTTGGTAGGCGGC 12453 CTTGTGCTGT 12454 TG A TT ----- C ACT
CGCGAGGGACTGTTGCTTCT GAATTCTATC TC G TC GGTAG GCGGC GCGAGGG G
TGTGCTGTGAATTCTATCTT TTGA || | || ||||| ||||| |||||||
GACTGGA AG C AG CTATC TGTCG TGTTCTT T
GT - TT TTAAG - CGT

GAM437 AATGCTATGGAATTAGTAGT 12461 TATGGAATTA 12462 GAATT TA G C GT
GGGACCCGGGCGTGGTCCAG GTAGTGGGAC AATGCTATG AG GT GGACCCGGG GTG C
TATCCTGGGTCTGGCCGCTT CCGG ||||||||| || || ||||||||| |||
GTAGCATT TTACGATGT TC CG TCTGGGTCC TAT C
----- GC G - GA

GAM438 CCCAATGTGCAAATGTGGTT 12469 GAAGTGGAAA 12470 AAT CAAA T- G GG CT- CCT
TGTATGGCTACTTTGTGTTC CCCTCAGTCA CCC GTG TG GGTTT TAT CTA TTGTGTT A

CTAAAAAATGCAACAATAGA CGGG ||| ||| || ||||| ||| ||| |||||||
AGTGGAAACCCTCAGTCACG GGG CAC AC CCAAA GTG GAT AACGTAA /
GG --- TG-- TC G AA AAC AAA

GAM439 GCGACCTCGTGAATATGAGG 12493 TGAGGACCAA 12494 C-- C ATAT CA----- ACCC GC
ACCAACAACCCTGTGCTTGG CAACCCTGTG GCGA CT GTGA GAGGAC ACA TGTGCTTG G
CGCTCAGGCGCAAGTGTGTG CTTG |||| || |||| |||||| ||| ||||||||
TAATTTGTCCTCCAGATCGC CGCT GA CGCT CTCCTG TGT ACGCGGAC /
AGCAATCGC AAC - AGAC TTTAATG GTGA TC

GAM440 ACTAACCCTAATTCGATAGC 12513 ACCCTAATTC 12514 CTT G
ATATGCTTCCCGTTGGGTAA GATAGCATAT ACTAACCCTAATTCGATAGCATATG CCC T
CATATGCTATTGAATTAGGG GCTT |||||||||||||||||||||| |||
TTAGT TGATTGGGATTAAGTTATCGTATAC GGG /
AAT T

GAM441 TATCGCAGCGTTGCGACATC 12520 TCGCAGCGTT 12521 C CG-- CCTA C - ATAAGCCTAAGA TG
GTCTCCTACATTCTCGTTGA GCGACATCGT TG GACAT TCT CATT TCGTT GAATA AATTTTGCA C
ATAATAAGCCTAAGAAATTT CTCC || ||||| ||| |||| ||||| ||||| |||||||||
TGCATGCATTGCGAGATTGT AC TTGTA AGA GTGA AGCGA CTTAT TTAGAGCGT /
AATATTCAAGCGAAGTGAAG - TTTA A--- - A AATG-------- TA
AATTTATGTTCAGCCTTGCG
GTA
GAM442 AGCGGGGTCTCGGAGCTCCT 12524 TGGCGTGTTT 12525 ---- CTCC G GA GAA-- T
AGGTCAGACCACGAAAGGTC TCTGAGGTTA AGCGGGG TCTCGGAG TA GTCA CCAC AGG C
AGCCTGCAAGGTGGATGGCG TCCC ||||||| |||||||| || |||| |||| |||
TGTTTTCTGAGGTTATCCCC TCGCCCC GGAGTCTT GT CGGT GGTG TCC A
GCT TATT TT-- G A- GAACG G

GAM443 GACATTAATTCTTACGCTCA 12542 TCTTACGCTC 12543 TAATTCTT TCAT TACT G
TGGGTACTTCGGTGACGACC ATGGGTACTT GACAT ACGC GGG TCG T
CTTATGCGTTAAAATGTGTT CGGT ||||| |||| ||| |||
TTGTG TGCG CCC AGC G
TAAAAT-- TATT ---- A

GAM444 CTCCCGGGTACTTACTCGCT 12546 CGTCCATGTT 12547 TACTC AACT- T CG- TC A TT- G A- TT
AACTCTCGCTGCTCGGGCTC GATCAGGTCA ACT GCT CTCGC GCT GGC GGT AAC GACGC CTT GT C

GGTAAACTTGACGCGCTTAG TCGG ||| ||| ||||| ||| ||| ||| ||| ||||| ||| ||
TTTCGTCACAGAAGGCGTCC TGG TGA GGGTG CGG CTG CTA TTG CTGCG GAA
CA G
ATGTTGATCAGGTCATCGGC TAC-- AACTT C CTA GA G TAC - GA CT
CGTGGGTTCAAAGTCATGGT
TCCCGGGG
GAM445 GGAAAACGTAAAGGTGGGCC 12552 TGCCTAACCT 12553 AA AA GC --- CT-- A C AG
CGGTCAGCTGGACGTCCGAG GATACCTGGA GGA ACGT AGGTGG CCGG TCAG GG
CGTC G T
TCTCCGATGCCTAACCTGAT TCTA ||| |||| |||||| |||| |||| || |||| |
ACCTGGATCTACCTATGTTC CCT TGTA TCCATC GGTC AGTC CC GTAG C /
C -- -- TA CAT CAAT - C TC

GAM446 TGTATTTATGTTTATTTTTT 12568 TTTATGTTTA 12569 TTT TT TTTATT T-- T TA T
TATTATTTATTAATATATTT TTTTTTTATT TGTA ATGT ATTTT ATTTATTAA ATATT GTGT
AAA T
GTGTTAAAATTATTTTCTAC ATTT |||| |||| ||||| ||||||||| ||||| |||| |||
ATTAATATTATTTAATAAAT ACAT TATA TGGAA TAAATAATT TATAA TACA TTT A
TAAAATAAGGTTTATATTTT TT- TT TAAAAT TAT T TC T
ACA

GAM447 TTGTAATAACATTATTTACA 12572 ATTAAATTTA 12573 TTAT-- T TAT--- TAT
TTAAATTTATCATTTAATAT TCATTTAATA TTGTAATAACA TTACAT AAATT CATTTAA T
TTTTCTTAAATGTATTTCAG TTTT |||||||||| |||||| ||||| |||||||
TTTCATGTGGTTTATTTGTT AATATTATTGT GGTGTA TTTGA GTAAATT T
ATTATAA TTATTT C CTTTAT CTT

GAM448 CGCCGGTGGCGCGTCCGCGC 12575 TCGGCGCGAC 12576 G G - G T AAAA
GGCGGGTGAGGAAAACCGTC GGACGCGTAG CGCCG TG CGCGTCCG CGCG CGGG GAGG
C
CCTCCTCGGCGCGACGGACG CGGC ||||| || |||||||| |||| |||| ||||
CGTAGCGGCG GCGGC AT GCGCAGGC GCGC GCTC CTCC /
G - A G - CTGC

GAM449 GTAGAAGTCTCAGGCTAGCC 12592 AGTCTCAGGC 12593 AG G - CC - - AAAATAAAC
GT CT
GGCAGCCCCAAAATAAACGT TAGCCGGCAG GTAGA TCTCA GC TAG GGCA GC CCC GT
CGT C
GTCGTCTCGAACGGAACTAA CCCC ||||| ||||| || ||| |||| || ||| || |||
ATACCGGGTGTGTGTCTCTG CGTCT GGAGT TG GTC CTGT TG GGG CA GCA /
TGTGTGAGGTCTCTGC CT G T T- G T CCATAAAT- AG AG

GAM450 TCTAATATGTATGAAATAAT 12713 TAATATGTAT 12714 AA TG AA GA-- G
AGATGTCTGCATAGACAGTA GAAATAATAG TCT TATGTA AAAT TA TGTCT C
ATGCGGTTTTGTACATGCCA ATGT ||| |||||| |||| || |||||
GA AGA GTACAT TTTG GT ACAGA A

```
                                CC    GT   GC  AATG   T


GAM451  GTGTTTATATAATTGTTTAG 12718  AGATTACAGT 12719     TT   A----------    TTAGG  C
     GGGCAAGTCAGATTACAGTA       AGATTTTAAA       GTGT  ATAT        ATTGT    GG A
     GATTTTAAAAATATTTACAC       AATA          |||| ||||        |||||    ||
                                CACA  TATA        TGACA    CT A
                                  TT   AAAATTTTAGA    TTAGA  G


GAM452  TTTTTTGGTTATTGGAAATG 12734  ATCTCCTTGA 12735        TTAT     ---------      C
     AGATTTCTGAAAATCTCCTT       TAAGATTTCC       TTTTTTGG    TGGAAAT       GAGATTT T
     GATAAGATTTCCATTTCAAA       ATTT          ||||||||   |||||||       |||||||
     AGA                          AGAAAACT    ACCTTTA       CTCTAAA G
                                    TT--      GAATAGTTC      A


GAM453  TATTATGTATTTTTATTCCG 12751  TATGTATTTT 12752     T  G      T  GCTAGAA---    GAT
     CTAGAACTATAGATGCTAAT       TATTCCGCTA       TAT AT TATTTTTA TCC        CTATA   G
     GTAGAAACAAAGAAGGATTA       GAAC          ||| || |||||||| |||        |||||
     AAAATAGATTGTA                    ATG TA ATAAAAAT AGG        GATGT   C
                                T  G      T   AAGAAACAAA    AAT


GAM454  GGAGCTAATAAATACACGGG 12765  TAAGTGTATT 12766       AATA     GG   AG  GA  GA
     TAAGCGGACGGATATACGGC       GGAAGCTCT       GGAGCT   AATACAC  GTA  CG  CG  T
     GATATAAGTGTATTGGAAGC                 ||||||   |||||||  |||  ||  ||
     TCT                          TCTCGA   TTATGTG  TAT  GC  GC  A
                                    AGG-     AA   A-  G-  AT


GAM455  GTTCTGATCTTTCTTGTACA 12797  TTCAAGTTTT 12798    T    --   C--    TT  ---  C   TAA-    C   AG GA
 TTCA
     TGTTCAAGTTTTCGGCGGTT       CGGCGGTTAA       CT GTACA  TGTT   AAGT  TC   GG GGT    GATG
TTT  A  TAG    A
     AAGATGCTTTAGAGATAGTT       GATG          || |||||  ||||   ||||  ||   || |||    |||| |||  |  |||
     CAAGATTTTAGATTCAAAAC                  GA CATGT  ACGA   TTTA  AG   CC CTA    CTAC AAA  T  ATT
 /
     ATCACTTATCTCCACAGATC                   -    TA   ACC    CT  ACA  T   TTCA    A   CT AG   TTAG
     ATTTCCAAGCAATTGTACAG
     AAAGATAGAAT
GAM456  TTCCAGTTGAATGAGGACTG 12800  AGTTGAATGA 12801      AG   AATGA      A----------------    T
     CAGTATTCTTATGCCAGGTT       GGACTGCAGT       TTCC  TTG    GGACTGC           GTAT C
     TTTCAAAGACGCAGTCTAAA       ATTC          ||||  |||    |||||||           ||||
     AGTAAAGGGAA                      AAGG  AAT    TCTGACG           CGTA T
                                GA   GAAAA     CAGAAACTTTTTGGAC    T


GAM457  GGATATCCTGTAGTTTTTGA 12806  ATCCTGTAGT 12807      AT  T   GT     GGTTTTTT    G
     TGGTTTTTTGGTTGATGACT       TTTTGATGGT       GGAT  CC GTA  TTTTGAT      GGTT A
```

TACACAAGATCAAAAGTTAC TTTT |||| || ||| ||||||| ||||
TGGTAATCC CCTA GG CAT AAAACTA TCAG /
AT T TG GAACACAT T

GAM458 TCATAGATATGATACAACAC 12822 TGAGTTAAAA 12823 TGATACAACAC CAA---
AAAAATA AA
AACACTACAAATTATATGAG AATATAGAAT TCATAGATA AACACTA ATTATATGAGTTA
TAG T
TTAAAAAATATAGAATATCT ATCT |||||||||| ||||||| |||||||||||||| |||
AATAAATAATTTATGTAATA AGTATTTAT TTGTGAT TAATGTATTTAAT ATC /
CTAGCTAGTGTTTATTTATG ---------- CGATCA AAATA-- TA
A

GAM459 GTCTGAGGGATGGCTCGTCC 12830 TGAGGGATGG 12831 T TC CCA AA ACAC
AACAAACCACACATCGAGGA CTCGTCCAAC GTCTGAGGGA GGC GT ACA CC A
ATGTAATACCTGTCCTCTCT AAAC |||||||||| ||| || ||| ||
CAGAT TAGACTCTCT CTG CA TGT GG /
C TC TAA AA AGCT

GAM460 TACAGTTTGCCCAATGTAAA 12845 TAAACGATAA 12846 CCCA- T C CAA- - AA
CGATAAGCAATAAAGGTCAT GCAATAAAGG TACAGTTTG ATG AAA GATAAG TAAAGGT
CAT A
AAACAGATGAACTTTTAAGA TCAT ||||||||| ||| ||| |||||| ||||||| |||
TTTTATTTTTCATACACTCG ATGTCGAGC TAC TTT TTATTT ATTTTCA GTA C
AGCTGTA TCACA - - TAGA A GA

GAM461 GGATTATGGGGCTAGCTCAG 12850 TAGCTCAGCT 12851 CTA -- CTCGCT AT
CTCGCTAATGCATAATAGCA CGCTAATGCA GGATTATGGGG GC TCAG AATGC A
TTCAACTGACAGCAACCCCA TAAT |||||||||| || |||| |||||
TAGTCT TCTGATACCCC CG AGTC TTACG A
AA- AC AAC--- AT

GAM462 GGAGCCGGGAGGATAGCTCA 12857 TTATGTATAT 12858 C TA-- TC GTTAAG
ACCTGTTAAGAACTCAGAAG TCTTCCTTGC GGAGC GGGAGGA GC AACCT A
GTTATGTATATTCTTCCTTG TCC ||||| ||||||| || |||||
CTCC CCTCG TCCTTCT TG TTGGA A
T TATA TA AGACTC

GAM463 TAAAATATAAATAAGATCAG 12880 TGAGTCGAGC 12881 AATAAGA A GAG A- - ATA
CT
ATTGTGAGGGCCACTCACTC AGGCCACAGA TAAAATATA TCAG TTGT GGCC CTC
ACTCAC TTCGG G
ACATATTCGGCTGCGTCCGG CTGG ||||||||| |||| |||| |||| ||| |||||| |||||
AGTGAGTCGAGCAGGCCACA ATTTTATAT GGTC GACA CCGG GAG TGAGTG
AGGCC C

GACTGGGTAAGAATATATTT AAGAATG A --- AC C --- TG
TA

GAM464 TAGTGGCCACAACCTCCCCA 12890 TAAGTGCTGG 12891 -------- CCA- - CCTTC TA ATTA
A ATAACAA
ACCTTGACCTTCGCCTATCC GAGTGGCTTA A ACCTCC AC CTTGA GCC TCC ATT
AGA C
ATTAATTAAGAATAACAACC AGAG | |||||| || ||||| ||| ||| ||| |||
ATATAACTCTAAGTGCTGGG T TGGAGG TG GAATT CGG AGG TGA TCT C
AGTGGCTTAAGAGTATCCGG CATTCCGA CCTA A ----- TG GTCG A CAATATA
AGGTAGCCTTACTGTGGCCA
CTG
GAM465 TGGACCGCATGGTGACCGAC 12917 CCAGCGCGAG 12918 - A- T ACG GA C
GTGCGCGAGGCCGTGGCCCA CGGTTCCACC TGGAC CGC TGG GACCG TGCGC GGC G
GCGCGAGCGGTTCCACCGCG GCGA ||||| ||| ||| ||||| ||||| |||
AGTCCA ACCTG GCG ACC TTGGC GCGCG CCG T
A CC - GA- AC G

GAM466 GCCATCCTGAATCCCCACTG 12952 ACCCCAATGA 12953 CA TGA -- T CT C CC
TCTACA A TA
GCTCCCGCCGCCGGGGTTCT CGGGTTCCTG GC TCC ATC CCCAC GG CCCG CG GGGGT
CGGGCG G C
ACACGGGCGAGTACGACATG TGGG || ||| ||| ||||| || |||| || ||||| ||||||
CCCGACCCCAATGACGGGTT CG AGG TAG GGGTG CC GGGC GT CCCCA
GCCCGT C /
CCTGTGGGACGATGTGGACA AC TG- CA T TT A AA ------ A AG
GC

GAM467 TCGGCGCGCTGCCGGTGCGT 12981 GTGCGTTCCA 12982 G C T T CAC GT - CT -- T
TCCACGGTCCTTGCCTGTGT CGGTCCTTGC TCG CG GC GCCGG GCGTTC G CCTTG C
GTGT CGT T
CGTTTCGGCGCTGCGCTTGT CTGT ||| || || ||||| |||||| | ||||| | |||| |||
CGGGGGTTTTCGAGCGTTCT AGC GC CG CGGTC TGCGAG T GGGGC G CGCG GCG
C
GGCCGCCGGCGA G - C T CTT TG T TT TC G

GAM468 GCGTATCCCACCTTTGAAAG 12987 CACCTTTGAA 12988 CCA----- AAAGC -- CGAAA
CACCTCCTAACGAAAGACCT AGCACCTCCT GCGTATC CCTTTG ACC TCCTAA G
AATTGGGAAAGGTTAAACGA AACG ||||||| |||||| ||| ||||||
AGGACAAAGACGATACGC CGCATAG GGAAGC TGG AGGGTT A
CAGAAACA AAAT- AA AATCC

GAM469 TATTTCAGAACAACAATCTG 12998 AGACGATAGT 12999 AGAACAACAA CT-- - ------- -
AACATC GTT
CTCCCACTGCTCCTATCGAA GACGACGAAG TTTC TCTG CCCAC TGC TC CTATCG
CG A
CATCCGGTTAATAACGCAGA TAGG |||| |||| ||||| ||| || |||||| ||

CGATAGTGACGACGAAGTAG GAAG AGAT GGGTG ATG AG GATAGC GC
A
GTGGGCCTATAGAAGTACAA CCGAACATGA ATCC G AAGCAGC T AGAC--
AAT
GCCGAAGTA

GAM470 ATTTCACGTGGCTTAGAATC 13006 TGACTACACC 13007 C ---- CT AATC TTGG
GAATACTTGGACTGACGTAT TTTAGCTGAA ATTTCA GT GG TAG GAATAC A
TTATGACTACACCTTTAGCT AT |||||| || || ||| ||||||
GAAAT TAAAGT CG CC ATC TTTATG C
- ATTT AC AGTA CAGT

GAM471 TGCTAAACTAATGATGAAGA 13041 ATGAAGATTA 13042 CTAAT TTA ----- A AA
AC
TTAATGCGGAGGTCTGATAA ATGCGGAGGT TGCTAAA GATGAAGA ATGC GG
GGTCTGAT GAATAA C
GAATAAACCTTATTATTCAG CTGA ||||||| |||||||| |||| || |||||||| ||||||
ATTAGGCCCCAAGAGGCATT ACGATTT CTACTTCT TACG CC CCGGATTA CTTATT
T
CTTCATCTCCTTTTAGCA TCCT- --- GAGAA - GA AT

GAM472 ACAAGTATACCTTCTACTTC 13051 TACCTTCTAC 13052 TAC ACTTC- TA T
TATTGATAATCAGTTTACTG TTCTATTGAT ACAAGTA CTTCT TATTGA ATCAG T
ATACTCAATGTTATTGGGAA AATC ||||||| ||||| |||||| |||||
GTTATTTGT TGTTTAT GAAGG GTAACT TAGTC T
T-- GTTATT CA A

GAM473 GCTGCGTTTATGGGTGGAGG 13068 TTTATGGGTG 13069 GC T GA GG
TCTCCTGTCTGGATTAGGAC GAGGTCTCCT GCT GT TATGGGTG GGTCTCCTGTCT A
AGGGGATTGGCGCTTATGCA GTCT ||| || |||||||| ||||||||||
CAAGGC CGG CA GTATTCGC TTAGGGGACAGG T
AA C GG AT

GAM474 CTATTATTCTAAACTAAAAT 13073 ACTAAAATAA 13074 TCTAAAC CCATT TTTATTC
AACCATTTATACTTTTATTC CCATTTATAC CTATTAT TAAAATAA TATACT C
CATAACGTAGTATATAGATT TTTT ||||||| |||||||| ||||||
TATTTTATTCTTTTATAATG GGTAATA ATTTTATT ATATGA /
G TTTTCTT TAGAT TGCAATA

GAM475 AACTTTTTTATCGAGAGCTC 13083 TAGAAAAACT 13084 CGAG ATA - CT A GAG A
A C
GAGTTATAGAAAAACTTTTT TTTTATCGAG AT AGCTCGAGTT GA AAAA TTTT TC
AGCTCGAG TTTCGA AAG T
ATCGAGAGCTCGAGATTTCG AGCT || |||||||||| || |||| |||| || |||||||| |||||| |||
AAAAGCTTTTTTATCGAGAG TA TTGAGCTCGA CT TTTT AAAA AG TTGAGCTC
AGAGCT TTT T

CTCGAGTTATAGAAAAACTT ---- GAG A TC - ATA G A T
TTTATCGAGAGCTCGAGTTA
TAGAAAAACT
GAM476 TGAACATGTCTACACCATCT 13095 TCTACACCAT 13096 C C CATC- CAGTAG TG
TTTGACAGTAGTGATAAATG CTTTTGACAG TGAA ATGTCTA AC TTTTGA TGATAAA A
ATTTTTTATCAACCATTCAA TAGT |||| ||||||| || |||||| |||||||
AAAAATAGTTAGACATTTCA ACTT TACAGAT TG AAAACT ACTATTT T
- - ATAAA TACCA- TT

GAM477 CGAGTTATAGAAAAACTTTT 13120 ACTTTTTTAT 13121 AC ---- AG GTTA AC ----
G
TTATCGAGAGCTCGAGTTAT CGAGAGCTCG AAAA TTTTTTA TCGAG CTCGA TAGAAAA
TTTTTTA TCGA A
AGAAAAACTTTTTTATCGAG AGTT |||| ||||||| ||||| ||||| ||||||| ||||||| ||||
AGCTCGAGTTATAGAAAAAC TTTT AAAAGAT AGCTC GAGCT ATTTTTT AAAAGAT
AGCT G
TTTTTTATCGAGAGCTCGAA CA TGTA GA ---- CA ATTG C
TGTTAGAAAAACTTTTTTAT
CGAGAGCTCG
GAM478 TTTTTTATCGAGAGCTCGAG 13123 ACTTTTTTAT 13121 - AG GTTA AC CGAG
ATA A C
TTATAGAAAAACTTTTTTAT CGAGAGCTCG TCGAG CTCGA TAGAAAA TTTTTTAT
AGCTCGAGTT GA AAA T
CGAGAGCTCGAGTTATAGAA AGTT ||||| ||||| ||||||| |||||||| |||||||||| || |||
AAACTTTTTTATCGAGAGCT AGCTC GAGCT ATTTTTT AAAAGATA TTGAGCTCGA
CT TTT T
CGAGTTATAGAAAAACTTTT G GA ---- CA ---- GAG A T
TTATCGAGAGCTCGAGTTAT
AGAAAA
GAM479 GAGCTCTCGATAAAAAAGTT 13124 GATAAAAAAG 13125 -- - C AACTC TCG-- - --
A
TTTCTATAACTCGAGCTCTC TTTTTCGAAA ATA AAAAAGTTTTT TAT GAGCTC ATA
AAAAAGTTTT TCGA A
GATAAAAAAGTTTTTCGAAA TCTC ||| |||||||||| ||| |||||| ||| |||||||||| ||||
TCTCGATAAAAACTTTTTCT TAT TTTTTCAAAAA ATA CTCGAG TAT TTTTTCAAAA
AGCT T
ATAACTCGAGCTCTCGATAA AA C - GCT-- CTCAA C AT C
AAAACTTTTTCTATAACTCG
AGCTC
GAM480 AAAAGCTTTTCGAAATCTCG 13130 AAGCTTTTCG 13131 AAT T------ C TAAC CT
TAAAAA TT
ATAAAAACTTTTTCTATAAC AAATCTCGAT CGA CTCGA AAAAACTTTTT TA TCGAG
CTCGA AG T
TCGAGCTCTCGATAAAAAAG AAAA ||| ||||| |||||||||| || ||||| ||||| ||
TTTTTCTAACATTCGAGCTC GCT GAGCT TTTTTGAAAAA AT AGCTC GAGCT
TC /
TCGATAAAAAAGTTTTTCTA CTC CAATATC - ---- TC TACAA- TT
TAACTCGAGCTCTCGATAAA
AAAGTTTTT

GAM481 GAGCTCTCGATAAAAAAGTT 13138 GATAAAAAAG 13139 -- A GT C AACTC TCG-- A
---- A
TTTCTATAACTCGAGCTCTC CTTTTCGAAA ATA AAAA TTTT TAT GAGCTC ATA
AAAAGCTTT TCGA A
GATAAAAAAGCTTTTCGAAA TCTC ||| |||| |||| ||| |||||| ||| |||||||||| ||||
TCTCGATAAAAAAGTTTTTC TAT TTTT AAAA ATA CTCGAG TAT TTTTTGAAA
AGCT T
TATAACTCGAGCTCTCGATA AA C TG A GCT-- CTCAA C AAAT C
AAAAAGTTTTTCTATAACTC
GAGCTC
GAM482 AGTTTTTCTATAACTCGAGC 13146 TAACTCGAGC 13147 AACTC TCG-- A CGAAATC
CT TAAAA TT
TCTCGATAAAAAAGCTTTTC TCTCGATAAA GAGCTC ATA AAAAGCTTTT TCGAG
CTCGA AG T
GAAATCTCGAGCTCTCGATA AAAG |||||| ||| |||||||||| ||||| ||||| ||
AAAAGTTTTTCTATAACTCG CTCGAG TAT TTTTTGAAAA AGCTC GAGCT TC
/
AGCTCTCGATAAAAAAGTTT GCT-- CTCAA C AAT---- TC CAATA TT
TTCTATAACTCGAGCTCTCG
ATAAAAAAGCT
GAM483 GTTTTTCTATAACTCGAGCT 13152 TAACTCGAGC 13147 ACTC TCG-- A GT C TAAC CT
TAAAAA TT
CTCGATAAAAAAGTTTTTCT TCTCGATAAA GAGCTC ATA AAAA TTTT TA TCGAG
CTCGA AG T
ATAACTCGAGCTCTCGATAA AAAG |||||| ||| |||| |||| || ||||| ||||| ||
AAAAGTTTTTCTATAACTCG CTCGAG TAT TTTT AAAA AT AGCTC GAGCT TC /
AGCTCTCGATAAAAAAGTTT CT-- CTCAA C TG A ---- TC CAATA- TT
TTCTATAACTCGAGCTCTCG
ATAAAAAAGC
GAM484 GTTTCGGGGATTGTGAACCG 13153 GGGGATTGTG 13154 -- TG AA---------- G- TGA
TGGCTGAGGGTGTAGATGGG AACCGTGGCT GTTTCGG GGAT TG CCGT GC G
ACAGGAAAAAGCGTGTGATC GAGG ||||||| |||| || |||| ||
TGACCGAGGC CGGAGCC TCTA GT GGTA TG /
AG GT GCGAAAAAGGACAG GA TGG

GAM485 TAGTAATAATTTTAATCTTT 13168 TCTTTGACGC 13169 T TCT ACGC A A TAAT-- T T
TAACGC A
GACGCCTACAGCAGTAGTAA CTACAGCAGT AT TTAA TTG CTAC GC GTAG AAT TTAA
GTT CTAC A
TAATTTTAATGTTTAACGCC AGTA || |||| ||| |||| || |||| ||| |||| ||| ||||
TACAACAGTAGTAATAATTT TG AATT AAT GATG CG CATC TTG AATT TAA
GATG C
TAATGTTTAACGCCTACAGC T TT- AAT- A A CGCAAT T T TAAT-- A
AGTAGTAATAATTTTAATGT
TTAACGCCTA
GAM486 GTAGTAATAATTTTAATGTT 13178 TTAATGTTTA 13179 TAAT-- T T TAACGC A
TAACGCCTACAACAGTAGTA ACGCCTACAA GTAG AAT TTAA GTT CTAC A
ATAATTTTAATGTTTAACGC CAGT |||| ||| |||| ||| ||||
CTAC CATC TTG AATT TAA GATG C

CGCAAT T T TAAT-- A

GAM487 GGGGTGATCCGGATGCGTGG 13182 TCCCGCGGAT 13183 GG A GA T CA CGA
CAAGAGGCCTCGAGCTTGGG GGACGTTCT GG TG TCCG TGCG GG AGAGGCCT G
CTTCTCCCGCGGATGGACGT || || |||| |||| || ||||||||
TCT TC GC AGGT GCGC CC TCTTCGGG /
TT - AG - -- TTC

GAM488 CTACAGCAGTAGTAATAATT 13220 CAGCAGTAGT 13221 A A TAAT-- T T TAACGC A
TTAATGTTTAACGCCTACAA AATAATTTTA CTAC GC GTAG AAT TTAA GTT CTAC A
CAGTAGTAATAATTTTAATG ATGT |||| || |||| ||| |||| ||| ||||
TTTAACGCCTACAGCAGTAG GATG CG CATC TTG AATT TAA GATG C
A A CGCAAT T T TAAT-- A

GAM489 AAACATTAAAATTTAGCTAC 13233 CAGCAGTAGT 13221 TA- - CTACA AG TA
GCCTACAGCAGTAATAATGT AATAATTTTA AAACATTAAAATT GCTAC GC GC TAA A
TTAACGCCTACAGCAGTAGT ATGT |||||||||||| ||||| || || |||
AATAATTTTAATGTTT TTTGTAATTTTAA TGATG CG CG ATT T
TAA A ACATC CA TG

GAM490 GGCGAAAAAATAATTATTCC 13234 AAAATGCTTT 13235 AAAA CCGGCC AAATTCT C
A
GGCCCGCCAAATTCTGCATC CCGGCGAAAA GGCG AATAATTATT CGCC GCAT TTGTG
A
TTGTGAAACTACAAAATGCT AATA |||| |||||||||| |||| |||| |||||
TTCCGGCGAAAAAATAATTA CCGC TTATTAATAA GCGG CGTA AACAT A
TTCCGCC C--- AAAA-- CCTTT-- A C

GAM491 GTGCACTTAATTACGTGCTT 13257 TACTATGTTA 13258 G - TT CT TAT T TC CC
TA
GCTACTATGTTAAGTCCGTG AGTCCGTGCG GT CAC TTAA ACGTG TGCTAC GT AAG
CGTGCG TGTTGT A
CGCCTGTTGTTAACCGCAGC CCTG || ||| |||| ||||| |||||| || ||| |||||| ||||||
ACGTACGTCCTTTACTTGTA CG GTG AATT TGTAC ACGATG CA TTC GCATGC
ACGACG /
GCACATGTTTTTAATGTGGG G T TT -- TT- T CT -- CC
C

GAM492 CTTTAGATAAAGTAGTTTTT 13261 AAGTAGTTTT 13262 AAA- TTTT- C GT
TGATATCGAATGGTAAAGTA TTGATATCGA CTTTAGAT GTAGT TGATAT GAATG A
TTTATATCATCTATACTATA ATGG |||||||| ||||| |||||| |||||
ATCATCTAGAG GAGATCTA TATCA ACTATA TTTAT A
CTAA TATCT - GA

GAM493 TGTATCGTTAAAATCTGAAT 13268 TACGTTAACA 13269 A TTA AATAAAC - A
AAACCGTAGCTAATAGGTAT GGTTTCGAAA TGT TCG AAATCTG CGTA GCT A
ACGTTAACAGGTTTCGAAAC CA ||| ||| ||||||| |||| |||
A ACA AGC TTTGGAC GCAT TGG T
A --- AATT--- A A

GAM494 TTAAAAGGGCATATAAGTTT 13279 TATAAGTTTT 13280 CATA- - AA T TTT- GT
T
TCAAGAAGAATACCTTTTAT CAAGAAGAAT TTAAAAGGG TAAGTT TTC GAAGAA ACCT
ATGTA TGATAGA T
GTAGTTGATAGATTTATCTG ACCT ||||||||| |||||| ||| |||||| |||| ||||| |||||||
TCATACGTTTATAGGTTTCT GGTTTTCCC ATTTAA AAG CTTCTT TGGA TGCAT
ACTGTCT T
TCAAGAATAATTTAGATACC CATAG T AA - TATT -- A
CCTTTTGG

GAM495 TTGTATTTGGCGCGAGTAAG 13293 TATTTGGCGC 13294 - C-- A AA- -- GAAAAA-- ---
TA
CCTATGAAAAACTTCCTTCT GAGTAAGCCT TTGTATT TGG GCG GT GC CTAT CTTCCT
TCTATGC T
ATGCTATATGTGTAGAAATA ATGA ||||||| ||| ||| || || |||| |||||| |||||||
GGAAGCAGAAGTAGTAGCAG AACATAA GCC CGC CA CG GATG GAAGGA
AGATGTG /
CGAGACCGCCATCCGTAATA T TAC - GAG AC ATGAAGAC TAA TA
CAA

GAM496 GTTGCTATGGCTGCTGTTCA 13297 TGGCTGCTGT 13298 AT---- T T TCAA A - CTC
ACGGACCCGCCTCTTTTTGT TCAACGGACC GTTGCT GGC GC GT CGG CCCG C T
CGGGCCGACTGTTGCCTGTA CGCC |||||| ||| || || ||| |||| |
CAAGCAGC CGACGA CCG TG CA GCC GGGC G T
ACATGT T T ---- - T TTT

GAM497 CTGCTTACGTTTTACTTTAA 13327 TAACAGGAAA 13328 ---- A TTAATAAA TTT
TAAAGTTAAGTTTTAAGTTT TGCTCTTAGG CTGCTTA CGTTTT CT GTTAAG T
TAACAGGAAATGCTCTTAGG CAG ||||||| |||||| || ||||||
CAG GACGGAT GTAAAG GA CAATTT A
TCTC - -------- TGA

GAM498 GACACGCTCTGGGCCGCGCC 13373 GCGCGGCGCG 13374 GCTCT - TCCTCGTCT GA
GCTCCTCGTCTGCCGTGATC GACCTTTCAA GACAC GGG CCGCGCCGC GCCGT T
AAGCGGCGCGGCGCGGACCT GTGT ||||| ||| ||||||||| |||||
TTCAAGTGTT TTGTG TCC GGCGCGGCG CGGCG C
AACTT A --------- AA

GAM499 GTGGATCCTTTACCGCTCAT 13376 TCCTTTACCG 13377 A --- ------ -- - - GTTTTAC
TCG

ATGGCTTCTGTTTTACGGTT CTCATATGGC G TCCTT TACC GC TCATAT GGC TTCT GGTTCCCGG T
CCCGGTCGTTCTGTCGGGAA TTCT | ||||| |||| || |||||| ||| |||| |||||||||
CCAGAGTGCCTATATGAACG C AGGGA ATGG CG AGTATA CCG GAGA CCAAGGGCT T
CAATTTTGGTATGAAGGGAC C AGT TTTTAA CA T T ------- GTC CCAT

GAM500 GCGTGGTGAACAGCAGCTTG 13406 TGAACAGCAG 13407 TG -- GCA - C---------- C
TCGCGCTCATAAGCCAGCGG CTTGTCGCGC GCGTGG A ACA GCTTGT CG GCT A
TTCGGCCGCCACGTACAAGC TCAT |||||| | ||| |||||| || |||
GGATGTGCTTGCCGCGC CGCGCC T TGT CGAACA GC CGA T
GT CG AGG T ACCGCCGGCTTGGCGAC A

GAM501 TTCCTCGAATTCACAGGGTG 13414 GTGCCTTGTT 13415 CG ATTCACA T C - GTAT
CCTTGTTTTATCTGCCGTAT TTATCTGCCG TTCCT A GGGTGCCT GTTTTAT TG CC G
GGACAGGACGAATGGAATTG TATG ||||| | |||||||| ||||||| || ||
GGCGCTCACGTTAAGGAA AAGGA T CTCGCGGG TAAGGTA GC GG /
AT GCA---- T A A ACAG

GAM502 TGCGCCTCCAGCCGCTCCGA 13420 ACGCGTACCT 13421 CT-- - T --- AC C
GCGCACCTTCTTGAAGACGC CGGGCGCGTT TGCGC CCAGC CGC CCGAG CGC CTT T
GTACCTCGGGCGCGTTGGCT GGCT ||||| ||||| ||| ||||| ||| |||
ACGCGCA ACGCG GGTTG GCG GGCTC GCG GAA T
CATC C - CAT CA G

GAM503 CGCTCGGCTTGGTCTTCACG 13430 TACGCACCAA 13431 CT - TC CCA----- -- ACCA
TCCAGCAGCGGTACCAGTCC TCCACGTAGA CG CGGCT TGGTCT ACGT GC AGCGGT G
CACCGTTACGCACCAATCCA GACC || ||||| |||||| |||| || ||||||
CGTAGAGACCATAGTCGTCG GC GCTGA ACCAGA TGCA CG TTGCCA /
T- T GA CCTAACCA CA CCCT

GAM504 TCCTCAACAGCAGGGACCAC 13439 GGCCAGGAGG 13440 AACAGCA CCA A AAA G GA
CACCAAACCGAGGGCCTGAT CAATCCCAGA TCCTC GGGA CC CC CCGAGG CCT T
CAAGGACCTCGGCCAGGAGG GGAG ||||| |||| || || |||||| |||
CAATCCCAGAGGAGGAGGA AGGAG CCCT GG GG GGCTCC GGA /
GAGGAGA AAC A ACC A AC

GAM505 GCGTGTCCGGTGCTCCCCGA 13547 TCTAAGGGTC 13548 G --- -- GA TT A GA T T
TGGAGATTTGAAGGAGGTGA GAGCAGAGCT GCGT TCCGGT GCTC CCC TGGAGA TGA G GG GAGC T
GCTTTTGCTCCCATCTCATC GGAG |||| |||||| |||| ||| |||||| ||| | || ||||
TCTAAGGGTCGAGCAGAGCT TGCA AGGTCG CGAG GGG ATCTCT ACT C CC CTCG T

GGAGACGT G AGA CT A- -- - TA - T

GAM506 ACCCGGGATGGGTCTGTCGA 13583 TCGAAAGCTA 13584 A -- AAA TA GCG GT
AAGCTAGCCAAGTCGCGCTG GCCAAGTCGC ACCCGGG TGGGTCTG TCG GC GCCAAGTC
CT T
TTATGGGAGGATTTGGCGCG GCTG ||||||| |||||||| ||| || |||||||| ||
TACGAACCAGACCCACCCGG TGGGCCC ACCCAGAC AGC CG CGGTTTAG GG A
GT - CA ATG -- GA- GT

GAM507 CGTTGATGGCGAAGGCAGCT 13592 GCGAAGGCAG 13593 GGC C TA- -- TT
ATATCGCGGTTTTACTGCTT CTATATCGCG CGTTGAT GAAGG AGC TATC GCGG T
GATGAATGCTACCTTCCAAT GTTT ||||||| ||||| ||| |||| ||||
TAACG GCAATTA CTTCC TCG GTAG CGTC /
AC- A TAA TT AT

GAM508 CCTCCAGCTCCAACTCCCGC 13598 CTCGCCTTGG 13599 -- CTC A CATT C - TAT T C
ATTCGCTGCCTTATGGCTGA TGTATCGCAA CCTC CAG CA CTCCCG CG TGC CT GGC
GAGCT A
GCTCATCGGCTCGCCTTGGT TGGG |||| ||| || |||||| || ||| || ||| |||||
GTATCGCAATGGGAGATGAT GGAG GTC GT GAGGGT GC ATG GG CCG CTCGG T
TCTGTTGAGG TT TTA A AAC- T T TT- - C

GAM509 GCCCTAGTAACCAATGCTCA 13611 TCCCCAGGGT 13612 ACCAAT- CACAATT---------- AAT
GATATACAA
GTCACAATTTGACCTAATGG CATTAACAAT GCTCAGT TGACCT GGGAGAT
C
GAGATGATATACAACGAGCA CTAT ||||||| |||||| |||||||
GAAAATTTCCCCAGGGTCAT TGGGTCG ACTGGG CCCTTTA /
TAACAATCTATACACTATGC ATAACTC TATCACATATCTAACAATT AC-
AAAGACGAG
TGGGTCTCAATATACATGGG
C
GAM510 GGCGGCCGGGGGCCCGCGGC 13624 TCCGCGGTCC 13625 CCG- - C --- C A A
GCGTCAGGCGCCATAGGTGC ACCATACCCG GGCGG GG GG CCGCGG CG GTC GGCGCC
T
CGACCGAGTCCGCGGTCCAC CC ||||| || || |||||| || ||| ||||||
CATACCCGCC CCGCC CC CC GGCGCC GC CAG CCGTGG /
CATA A T TGA - - A

GAM511 CGGTGCGTCCCGGCGGACAT 13657 ACATGCTGGG 13658 CGT- ACA G T GGA T
CG
GCTGGGCCTACCGTGGACTC CCTACCGTGG CGGTG CCCGGCGG TGCT GGCC ACCGT
CTCCAT TC A
CATTTCCGAGACGACGTGGG ACTC ||||| |||||||| |||| |||| ||||| |||||| ||
GGGAGCGGTGGTTGAGCGCG GTCGC GGGCCGCC GCGA TTGG TGGCG GGGGTG
AG G

CCGCCGGGTGAACGCTG AAGT GC- G - AGG C CA

GAM512 GGCCTTATAGATCTCCGGAT 13700 TAGATCTCCG 13701 TTATA - G A GGA
CGATGCGGACGGGGGTAATG GATCGATGCG GGCC GATC TCC GATCG TGC C
ATCAGGGCGATCGGAACGGC GACG |||| |||| ||| ||||| |||
C CCGG CTAG GGG CTAGT ATG G
CAAGG C A A GGG

GAM513 GGGGCAGTCGGGGAAGTGGC 13705 TGACGGGGGT 13706 G AG - -- A AG-------- - AA T GC
TGTCGAGCACGTAGCCCTGC TCGCGAAGAC TCGGGGA TGG CTGT CGAGC CGT CCCTG CACC GA CT T
ACCAAGATCTGCTTAAAGTT GGGC ||||||| ||| |||| ||||| ||| ||||| |||| || ||
CGGGTGACGGGGGTTCGCGA GGCCCCT ACC GGCG GCTCG GCA GGGGC GTGG CT GA T
AGACGGGCTCGCGGCGGACC - AG A GC G GAAGCGCTTG A G- T AA
AGATCCCCGGAGCTCC

GAM514 TTTTTACCTTTTGAAGAGCA 13728 TACCTTTTGA 13729 -- AG --- C AA
GCGCTTAAAGCGGGCACTAG AGAGCAGCGC TTTTTAC CTTTTGA AGC AG GCTT A
AGCTGTTAGAAGAAGTAGAA TTAA ||||||| ||||||| ||| || ||||
A AAAGATG GAAGATT TCG TC CGGG /
AA G- AGA A CG

GAM515 ATATAAGGGCACTTCTACTG 13737 AAGGGCACTT 13738 A - TTCTA A AAA TCA- A
ATGATAGGCAAAATGTATCA CTACTGATGA ATATA GG GCAC CTG TGATAGGCA TGTA TTTG C
TTTGACCCTAAACAGCTACA TAGG ||||| || |||| ||| ||||||||| |||| ||||
AATGTTTATTATAGGCTGTG TATGT CC CGTG GAT ATTATTTGT ACAT AAAT C
CTCCCTGTAT C T TCG-- - AA- CGAC C

GAM516 GCGCGCACAAGGTCATAACA 13748 TTTGTCACAG 13749 CACAAG - A AA TAT- T
ATGGCATATGCTGGTTTAAT TAGTAGACAA GCGCG GTC AT AC TGGCA GCTGGT T
CAGCTATTTGTCACAGTAGT CACG ||||| ||| || || ||||| ||||||
AGACAACACGCGT TGCGC CAG TG TG ACTGT CGACTA /
ACAA-- A A AC TTAT A

GAM517 ACTTGTAAATATCCAGATTT 13756 CGAGAGCAAT 13757 A- - TTTCTTAAAGAT T G TG TCC T AT
CTTAAAGATGCAAAATGATG GTTATGCTAG TCCA GA GCAAAA GATGT TA GTGAT TGCTTTT TT G
TGTATGGTGATTCCTGCTTT ACAT |||| || |||||| ||||| || ||||| ||||||| ||
TTTTATGCAAGGCGAGAGCA AGGT CT TGTTTT TTACA AT TATTG ACGAGAG GG C
ATGTTATGCTAGACATTTTT GG G ---------- T G CG TA- C AA

TTGTTCGTGGAGGCAAGACA
GGT
GAM518 AGACCAAGAACAAGATCGTG 13764 TCGGTTGGCG 13765 GAACAAGAT G A AT
AACACGATGATATAGAATCA TGATTGGTTT AGACCAA CGT AAC CGATGAT A
TCGGTTGGCGTGATTGGTTT ||||||| ||| ||| |||||||
TTTGGTT GCG TTG GCTACTA /
AGT------ G - AG

GAM519 TCTTGATTGCAGACATGAGG 13781 TGAAATATCC 13782 TTGA A GGAA C TAT TTC
TA
AATGCTGAAATATCCGATTC GATTCATCTC TC TTGC GACATGA TG TGAAA CCGA ATCTC
G
ATCTCTAGATGAGGTAGCTC TAGA || |||| ||||||| || ||||| |||| |||||
GGTCTTTCAACAATTATGTC AG AGCG CTGTATT AC ACTTT GGCT TGGAG /
GGCGAGATTGA TTAG G A--- A CT- CGA TA

GAM520 TCTGGCACTTCAACGGCTTC 13789 CTAGAAGGTG 13790 ACTT- A G GG
TGGGGTGGGTTTCATCCTAG ATGTTTTGGC TCTGGC CA CG CTTCTGGGGTG T
AAGGTGATGTTTTGGCCGGA CGGA |||||| || || ||||||||||
AGGCCG GT GT GAAGATCCTAC /
GTTTT A G TT

GAM521 ACCGCCCTTTACCCAGTCTG 13827 TTCCAGATCA 13828 ACCCAGTC AT A G CCCA
ATCTGATGCAACAGACCCCA AAGAGGGTGG ACCGCCCTTT TGATCTG GCA CA AC A
AAGACGTGTGTGTTCCAGAT T |||||||||| ||||||| ||| || ||
CAAAGAGGGTGGT TGGTGGGAGA ACTAGAC TGT GT TG /
A------- CT - G CAGA

GAM522 GGTCGGAACTCTCCCTGGGG 13912 TCGGAACTCT 13913 --- G - - C CTTTTTGCC
GCTTTTTGCCACCTCCACTC CCCTGGGGGC GGTC G AACT C TCC TGGGGG A
CCCCCAAGGATGAAGTTGCG TTTT |||| | |||| | ||| ||||||
TTGACC CCAG C TTGA G AGG ACCCCC /
TTG G A T A CTCACCTCC

GAM523 GCGGCGTCGGCGTAGAACCG 13923 TCAGCCTTTT 13924 TAG T AC--- A
TTAAAGGCACGGGAAATCCC GCGGTTACCG GCGGCGTCGGCG AACCGT AAAGGC GGG A
AATCAGCCTTTTGCGGTTAC CTGG |||||||||||| |||||| |||||| |||
CGCTGGCGCCGC CGCCGCGGTCGC TTGGCG TTTCCG CCC A
CA- T ACTAA T

GAM524 TGCCTTTTCTGAGAGGTTTC 13934 TGAGAGGTTT 13935 TTTTCT- T C GTTT- CT
AAACGATTGTTTACCTTTTG CAAACGATTG TGCC GAGAGGTT CAAA GATT AC T
TTTCCAAATTTTTGCAACTT TTTA |||| |||||||| |||| |||| ||
TTCTCACTACGGCA ACGG CTTTTCAA GTTT TTAA TG /

CATCACT C - ACCTT TT

GAM525 TGTTTTGAACGGGTGGGATG 13951 TCCCCTGGTT 13952 T TG G T C- TC AT- T----
TTT
ACAGGTTCGCGTATGATTTC TGACATA TGT T AAC GG GGGATGA AGGT GCGT GA
TTCGCGTTTGG C
GCGTTTGGTTTCGATTTTAG ||| | ||| || ||||||| |||| |||| || ||||||||||
GCGTGAATAGTTTCTTCACG ATA A TTG TC CCCTATT TCTA TGCA CT
AAGTGCGGATT G
TATATCTTTTTATCCCCTGG C GT G - TT TA CTT TTGAT TTA
TTTGACATA

GAM526 CGGGATTTTCTTTCCAGTTG 13958 TTCCAGTTGG 13959 TT TC TT - ATAAC A
GCCCGATAACGTACTTACCC CCCGATAACG CGGGA TTCTT CAG GGCC CG GT C
CCACGCGGTCCTGTAAGAAT TACT ||||| ||||| ||| |||| || ||
CTCTCG GCTCT AAGAA GTC CTGG GC CA T
CT T- -- C ACCCC T

GAM527 TCCATTTTTATCCTCGCACT 13962 TGAAATGAAA 13963 -- CG C TTC CTC C
TCTTCGCTCTCAAAGCCGCC GGATGGAAAC TCCAT TTTTATCCT CA TTC GCT AAAG C
TTTAAAGTTGAAATGAAAGG ATGG ||||| ||||||||| || ||| ||| ||||
ATGGAAACATGGA AGGTA AAGGTAGGA GT AAG TGA TTTC G
CA AA A T-- AA- C

GAM528 GACTTCACAGAAGAGGGCAA 13997 TACCATAGTC 13998 C-- G C C - C T GTT
ACA
AACAAAAACATTGTGTGTAG TTATTTTTTT GACTT ACAGAA AGGG AAAA AAA AA ATTGTG
GTAGT AGATA G
TGTTAGATAACAGTCATATT TTCT ||||| |||||| |||| |||| ||| || |||||| ||||| |||||
TTAGCTACCATAGTCTTATT CTGAA TGTTTT TCTC TTTT TTT TT TGATAC CATCG
TTTAT /
TTTTTTTCTCTGTTTTGTTT TTT G T T A C - AT- ACT
TAAGTC

GAM529 CAGATATATCGATATCCAAT 14033 TATCCAATTA 14034 TATCG C - --- A T T
TAGGCAAGTGAAACTTCAAT GGCAAGTGAA CAGATA ATATC AATTAGGC AAGT GA ACT
CAATA G
ATGTTTATTGCAGTCTCCAA ACTT |||||| ||||| |||||||| |||| || ||| |||||
ATTTAGTTTAGTTTGATATG GTCTGT TATAG TTGATTTG TTTA CT TGA GTTAT T
TTGTCTG TG--- T A AAC C C T

GAM530 CCTGCCGAGGAACGTCACCA 14046 TGTCGAGGAC 14047 AG- G C- GC- T ----------
GG
GGTGCGGTTGCAGGGGGCAG GTATCCCTGC CCTGCCG GAAC TCA CAGGT GGT GCAGGG
GGCAGTCG A
TCGGGAAAGTGGCTGTCGAG ACCA ||||||| |||| ||| ||||| ||| |||||| ||||||||

GACGTATCCCTGCACCAAGA GGGCGGT CTTG AGT GTCTA CCA CGTCCC CTGTCGGT A
TCTGTTTGAAGTTCGGGTGG GGG A TT GAA - TATGCAGGAG GA CGGG

GAM531 AGTACCAGCGGATTATACTA 14058 TATACTACTC 14059 C -------- C - - A ATAT CAAT
CTCGGCAGAGAATTTATATG GGCAGAGAAT AGTA CAGCGGA TTATA TAC TCGG CAG GAATTT GAGAT T
AGATCAATTGTTAATCTTTT TTAT |||| ||||||| ||||| ||| |||| ||| |||||| |||||
GGGAATTCCTGTCCGACGTA TCGT GTCGTCT AATAT ATG AGCC GTC CTTAAG TTCTA /
TTATAAATGAACCCTCTGCT C CCCAAGTA T C T - GGTT ATTG GCTGCT

GAM532 GATGAAGATTAATTGCGGAG 14064 TTCCTTAAGG 14065 AATT G AATC- CAA
GAATCAGGAATTCAACTTTA CCTCGTCCGA GATGAAGATT GCG AGG AGGAATT C
GTTCCTTAAGGCCTCGTCCG ATCT |||||||||| ||| ||| |||||||
AATCTTCATC CTACTTCTAA TGC TCC TCCTTGA /
GCC- - GGAAT TTT

GAM533 TTAGCTTCTAAGGTGATTAT 14073 TAAGGTGATT 14074 T-- A A T A T GCTAATT GC
ATTTTAGTATTAAATTTTGC ATATTTTAGT TTAGCTTC AAGGTG TT TATTT AGTATTA AT TT GCTT T
TAATTGCTTGCTATAAAGTT ATTA |||||||| |||||| || ||||| ||||||| || || |||
GAAATGTCTAATGCTTAAAT AGTCGAAG TTTCAC AA GTAAA TCGTAAT TG AA TGAA A
GAACACTTTTTTGAAGCTGA TTT - - T C T AGT---- AT

GAM534 GTCTACTAGAGCCTTGCTGT 14079 CACCCGTAGA 14080 ACTAGA C A TAT A
TAACGGTATCTGATACAGCA CAACGAGGCG GTCT GCCTTG TGTT ACGG CTG T
CCCGTAGACAACGAGGCGGG GGAC |||| |||||| |||| |||| |||
AC CAGG CGGAGC ACAG TGCC GAC /
G----- A A CAC A

GAM535 GACGTATCAGATTTTTACAC 14105 TATCAGATTT 14106 A ATTTTTACA AAACCAACT--------G
CCAAACCAACTGCGTGCGCA TTACACCCAA GACGT TCAG CCC GC T
GCGTTTATTAAGGACGCGGG ACCA ||||| |||| ||| ||
ACTGCTACTGAGGCGTC CTGCG AGTC GGG CG G
G ATCGTCA-- CGCAGGAATTATTTGCGA C

GAM536 GACGTTGTTTGTAGTGACGG 14123 TTTGTAGTGA 14124 TT T - A TG TT T
TGGCGTTCCTTTTGGTTCGT CGGTGGCGTT GACGTTG TG AG TG CGG GCG CC T
TTCTGCGTCTTAGGTAACGT CCTT ||||||| || || || ||| ||| ||

```
T                                TTGCAAT  AT TC GC GTC  TGC  GG T
                                   GG  -  T  -  TT  TT  T


GAM537  GGGGAACTTGGGCATGGGGG 14130  GGGCATGGGG 14131      ACTTG   GG      G  A    TTG
     CTACGGTCACGTTGTTGAGG       GCTACGGTCA       GGGGA   GGCAT  GGGCTACG TC CGTTG   A
     ATCAGCGGGGCGTAGTCTGT       CGTT             |||||   |||||  |||||||| || |||||
     GCTATTGTCCCT                  TCCCT    TCGTG  TCTGATGC GG GCGAC   G
                                GTTA-    --      G  -    TAG


GAM538  CTCCACCTCTGGAATTCAGG 14135  TCAGGACCTG 14136     AC     AA--     A  T   GA   TG
     ACCTGCAGACTCTGAGTGAG       CAGACTCTGA       CTCC  CTCTGG    TTCAGG CC GCA  CTC  A
     CTTGTTGGCCCTGAAAATGC       GTGA             ||||  ||||||    |||||| || |||  |||
     CGGAGAGGGAG                   GAGG  GAGGCC    AAGTCC GG TGT  GAG  /
                                GA     GTAA     C  T   TC   TG


GAM539  ATTTCAGTCTAAATGCTAAA 14170  TGTAAATGGA 14171        TC       AA  CA      C
     TCAACAGAATCAAGTTCTGT       GTATTTATCT       ATTTCAG  TAAATGCT  AT  ACAGAAT A
     AAATGGAGTATTTATCTGAG       GAGA             |||||||  ||||||||  ||  |||||||
     AT                         TAGAGTC  ATTTATGA  TA  TGTCTTG /
                                  T-       GG  AA      A


GAM540  CAGCCACTTATGAATTAATT 14185  TGAATTAATT 14186     CC   A--     ATTCTTCTG----     CA
     CTTCTGATAGCTCATTTCGG       CTTCTGATAG       CAG  ACTT   TGAATTA         ATAGCT  T
     TTATAATATCCAATTAATAA       CTCA             |||  ||||   |||||||         ||||||
     TTCAAAAAAGTCTCTG                GTC  TGAA   ACTTAAT         TATTGG  T
                                TC    AAA      AATTAACCTATAA     CT


GAM541  CATTCAGTTTTATAAGAATT 14197  TATAAGAATT 14198     T   T   -     TAT--    ---   ACTT   G
     ATCAGATTCTAACTTGCTGT       ATCAGATTCT       CAT CAGT TTAT AAGAAT    CAGAT   TCTA    GCT T
     CAGGCTGTAGACCCATTTGC       AACT             ||| |||| |||| ||||||    |||||   ||||    |||
     TAATATTTTTCATGGTACTG              GTA GTCA GGTA TTTTTA    GTTTA   AGAT    CGG C
     ATG                          -   T   C     TAATC    CCC    GT--   A


GAM542  GTGTGTCTTATCATGCATAT 14208  TCAACATATT 14209       ----   T   A   TATAAAGAAA      CA
     AAAGAAATTGAGGACAAACA       AAACTGCAGG       GTGTG    TCT ATC TGCA        TTGAGGA  A
     TCCTCAACATATTAAACTGC       ATTG             |||||    ||| ||| ||||        |||||||
     AGGATTGGATCCCCACAC                CACAC    AGG TAG ACGT        AACTCCT  A
                                CCCT   T   G    CAAATTATAC      AC


GAM543  AAGTTAAAACTGTTGCTAGA 14215  TGCTAGATCT 14216      AA    TTG    TCTTTT    GATA
     TCTTTTAATGAGATATTATA       TTTAATGAGA       AAGTT  AACTG   CTAGA     AATGA   T
     ATCATTTCTAGGTAGTTCCA       TATT             |||||  |||||   |||||     |||||
     ATTT                       TTTAA  TTGAT   GATCT     TTACT   T
```

CC G-- ------ AATA

GAM544 GCCAGCATTTCCTCGTGGCG 14223 TTCCTCGTGG 14224 A TTT- T AAC A -- AC-- TTC
AACCGATACCTCGAGACCCG CGAACCGATA GCC GCA CCTCG GGCG CGAT CC TCGAG CCGGTCGAT A
GTCGATTTCACCCATCGACT CCTC ||| ||| ||||| |||| |||| || ||||| |||||||||
GGTCGGTTTGAAAGGCATCG TGG TGT GGGGC CTGC GCTA GG AGTTT GGTCAGCTA /
ACGTCCGGGGTTTTTGTCGG C TTTT - A-- C AA GGCT CCC
T

GAM545 CCCATTAGAGTTCTGACAAA 14229 TTAGAGTTCT 14230 T CTGACA AA TG
TCAAACCATGTATTTGGGTG GACAAATCAA CCCAT AGAGTT AATCA CCA T
GTTCGCCTGACTTTCATGGG ACCA ||||| |||||| ||||| |||
GGGTA TTTCAG TTGGT GGT A
C TCCGC- G- TT

GAM546 GCCGCCTCCCCCGAGTCTTC 14251 CAAGAACTGT 14252 C CC A C ATG---- G
GGAATGTCTTGGCGGCCGTC TATCCCGAGG GCCGC TC CCG GTCTT GGA TCTTGGC G
AAGAACTGTTATCCCGAGGC CACG ||||| || ||| ||||| ||| |||||||
ACGGATGAGCGGC CGGCG AG GGC CGGAG CCT AGAACTG C
- TA A C ATTGTCA C

GAM547 GTGCTGCCGCCGCGGGAGGA 14263 TTATTGCACC 14264 T GC - A A TTTT TG
TGTGTTTTCGTGGACTCGTT CCCGACGAGG GTGC GCC CG CGGG GG TGTG CG G
ATTGCACCCCCGACGAGGTG TGCG |||| ||| || |||| || |||| ||
CGC CGCG TGG GC GCCC CC ACGT GC A
- A- A - - TATT TC

GAM548 CTACATCTGCCTGTGTTACT 14266 TACCTCAGTT 14267 C C--- T- TACTTAC T CC
TACCCTTATGCCATATTATT AATAGATATA CTA ATCTG CTG GT CCT ATG A
AGGATTACCTCAGTTAATAG G ||| ||||| ||| || ||| |||
ATATAG GAT TAGAT GAC CA GGA TAT T
A AATT TC TTA---- T TA

GAM549 GAGGCCACACCCACATGGAG 14278 AGGCCACACC 14279 A--- ACAC CA A--- ACAC CA A--- ACAC A
GCCACACCCACATGGAGGCC CACATGGAGG TGG GGCC CCA TGG GGCC CCA TGG GGCC CC C
ACACCCACATGGAGGCCACA CCAC ||| |||| ||| ||| |||| ||| ||| |||| ||
CCCACATGGAGGCCACACCC ACC CCGG GGT ACC CCGG GGT ACC CCGG GG A
ACATGGAGGCCACACCCACA CACA A--- AC CACA A--- AC CACA A--- T
TGGAGGCCACACCCACATGG

AGGCCACACC
GAM550 AGTGCGGGTTACACAGTGCG 14431 TACACAATTG 14432 -- TAC- GC - ACA
TGTTACACACCGGGTATACA TTCCTGCTCG AGT GCGGGT ACAGT GTGT TAC C
CAATTGTTCCTGCTCGTTAA TTAA ||| |||||| ||||| |||| |||
CT TCA TGCTCG TGTTA CACA ATG /
AT TCCT A- T GGC

GAM551 TAAGCTTTTCCTTTGGAGCT 14437 TTGGAGCTCC 14438 TTTTCCTTT TCCTCC - C
CCTCCCTAAATGCCTTGGCT TCCCTAAATG TAAGC GGAGC CTAAAT GC T
ATTTAGCCTTCCGCTCCTGT CCTT ||||| ||||| |||||| ||
CTGCTTA ATTCG CCTCG GATTTA CG T
TCTGT---- CCTTCC T G

GAM552 GCAGGAACTTCATGATGGAC 14450 TGATGGACTT 14451 CTTC------ CTTCTTG - T
TTCTTGGCGTCGCTACCGCG CTTGGCGTCG GCAGGAA ATGATGGA GCG TCGC A
GTCGTGCTTCTCCATCATCT CTAC ||||||| |||||||| ||| ||||
CCACCATCTTCTTGC CGTTCTT TACTACCT TGC GGCG C
CTACCACCTC CTTCG-- T C

GAM553 AGCTGTTGGCCACCAGCCGG 14464 AGCCGGTTGT 14465 TG A T T TCCA --- C
AAC G
TTGTCCTCCACGGGCAGCGC CCTCCACGGG AGCTGT GCCACC GCCGGT G CC CGG
GCAG GCGCGG GGC T
GCGGAACGGCGTCGCCTCCT CAGC |||||| |||||| |||||| | || ||| |||| |||||| |||
GCGCCTTGCGCACCGCCTCG TCGACA TGGTGG CGGCCA C GG GCC CGTT
CGCGTC CCG /
GTCACCGGCAGGTGGTACAG -- A - T CTCC ACG C CT- C
CT

GAM554 AGCTCGCAGCTTGTTTGGCG 14497 TCTCGTTGCC 14498 CG TT TT TT TA
ACTTGAGAGTTAAACACTCT CTGCTGCTGA AGCT CAGC GT GGCGAC GAGAGT A
CGTTGCCCTGCTGCTGAGGC GGCT |||| |||| || |||||| ||||||
T TCGG GTCG CG CCGTTG CTCTCA /
A- T- TC -- CA

GAM555 ATTGATTGAGCAACTGCAGC 14510 TACTGCACCT 14511 A CAAC ------ AATA
CGGGAATAATGAAGTCTGGA CCTCAACCAA ATTG TTGAG TGCAG CCGGG A
TCTTACTGCACCTCCTCAAC T |||| ||||| ||||| |||||
CAAT TAAC AACTC ACGTC GGTCT T
C CTCC ATTCTA GAAG

GAM556 GCCACGACTCCTGAAGGCGA 14527 CACACGTTAT 14528 -- T AA GA T-- AG A TT
CCTATACGAGGTAGAGTTCT TAGGGCTAAC GCCA CGAC CCTG GGC CCTA ACG GT GAG
C
GCTCACACGTTATTAGGGCT AGGT |||| |||| |||| ||| |||| ||| || |||

AACAGGTGTTGGTTGGC CGGT GTTG GGAC TCG GGAT TGC CA CTC /
TG T AA -- TAT A- - GT

GAM557 GCCAGGTGGCTAGAATCCCG 14536 CACCGGAGAA 14537 --- - GAA - CG CAA AACG
CGGACAACGTAGCTGCTAAC AATACGCCCA GCCAGGT GGC TA TC CCG GA
CGTAGCTGCT A
GACTACAGGCAGCTACGCTC AGCC ||||||| ||| || || ||| || ||||||||||
ACCGGAGAAAATACGCCCAA CGGTCCG CCG AT AG GGC CT GCATCGACGG C
GCCTGGC AAC C AAA A CA C-- ACAT

GAM558 TACGATTTAAATATTATGTA 14572 TAGTACATAC 14573 TTT ATTATGTAAC T C CACT
ACTCTGTATTTATTCGACAC AGAATTTCTT TACGA AAAT TCTGTAT TATT GA A
TATTAATCTAGTACATACAG TCGT ||||| |||| ||||||| |||| ||
AATTTCTTTCGTA ATGCT TTTA AGACATA ATGA CT /
TTC ---------- C T AATT

GAM559 CTCGCCCTCTTGGTCGGCGT 14576 TCTTGGTCGG 14577 CCTCT - C C----- C G CTCG
T
CTCATTGCCGGGTACTCGAA CGTCTCATTG CTCGC TG GT GGCGT TCATTG CGG TA
AATCC G
TCCTGCGGATTACATAGCTG CCGG ||||| || || ||||| |||||| ||| || |||||
TTAATGAATACACACGCCTA GAGCG AC CA CCGCA AGTAAT GTC AT TTAGG /
CGCACCCCGCGAG CCCC- G T CACATA T G ACA- C

GAM560 TGGGTGCCTACGACCTCATG 14582 CACACCTCGG 14583 CC GAC C G T C-- AAC
GACGGCCTAGCTGTTAACGA CGGTCCATAA TGGGTG TAC CT ATGGAC GCC AG TGTT G
ATAGACACACCTCGGCGGTC GAAA |||||| ||| || |||||| ||| || ||||
CATAAGAAAGTATGCCCA ACCCGT ATG GA TACCTG CGG TC ACAG A
-- AAA A G C CAC ATA

GAM561 GATTAGATATCTCTTAACCC 14604 AATGAAATTA 14605 CT CCAA C -- TTCA----- A
ATAGCTA AT
CAATACTCATCTCCTTCAAT TAGCTACGTC TCT TAACC TACT ATC TCC ATG AATT
CGTCT C
GAAATTATAGCTACGTCTAT TATC ||| ||||| |||| ||| ||| ||| |||| |||||
CTACAGACGCACGAATTACA AGA ATTGG GTGA TAG AGG TAC TTAA GCAGA
T
TAACTTAAACGGAAAGATAG TC C--- - AA CAAATTCAA A GCAC--- CA
TGCGGTTACTAGATATCCCC
ATC
GAM562 GCCCGCCCGTCGTTACCTCA 14609 TCACGCGCCA 14610 C- ---- T T CAATG TATTTCC
ATGTGATATTTCCAGACTTC AGGTTCGGC GCC GCC CG CGT ACCT TGA A
TTCAAGCTAGGTCACGCGCC ||| ||| || ||| |||| |||
AAGGTTCGGC CGG TGG GC GCA TGGA ACT /
CT AACC - C TCGA- TCTTCAG

GAM563 GAACAAGAGCCTGCTGTCCC 14652 TACCAGCAGG 14653 AA CC T - A TTC ACC
TGATGTTCGGACCAATGACC TGACGCACCT GAAC GAG TGC GTC CCTG TG GG A
TACCAGCAGGTGACGCACCT CAGG |||| ||| ||| ||| |||| || ||
CAGGTTC CTTG CTC ACG CAG GGAC AC CC A
GA C- - T G CAT AGT

GAM564 CGGGCATGGATCTCTCGCGG 14680 CATGGATCTC 14681 CA-- T C GG G G GTAT
GGTGCGTAGGCGTGTGTATT TCGCGGGGTG CGGG TGGATC CT GCGG TGCGTAG C TGT
T
CATTAACAGCTATGTAATCC CGTA |||| |||||| || |||| ||||||| | |||
GCAGGATTCGAGTACCCG GCCC GCTTAG GA CGCC ATGTATC G ACA C
ATGA - - TA - - ATTA

GAM565 GGGGCATACTTTCTCATGGA 14691 TGAGGTCGTA 14692 - A TT CC G GTCTA
CCCCCGAGTTGTGTCTATTC GGCACCC GGG GC TAC TCTCATGGAC CC AGTTGT T
GTTAACAGCTAGGCCGTCCA ||| || ||| |||||||||| || ||||||
TGAGGTCGTAGGCACCC CCC CG ATG GGAGTACCTG GG TCGACA T
A G CT CC A ATTGC

GAM566 GCCCCAACTCCTCGCCCTAC 14706 TGGGAGGGCG 14707 CCAAC A T AG ATG- GC
ACC TA
CTCAAGATCTATGTGGCCAC AGGGCGGC GCC TCCTCGCCCT CC CA ATCT TG CACG
GC T
GACCGCTATCTCGCCCGTGT ||| |||||||||| || || |||| || |||| ||
TCAAGCCAGATGTGGGAGGG CGG GGGAGCGGGA GG GT TAGA AC GTGC CG C
CGAGGGCGGC C---- - - G- CCGA TT C-- CT

GAM567 AGGATCCAGGACATTATCTC 14912 TGTCAGGGAC 14913 A ACA TA A GAGA G
TGGCGTCACGGAGACGGGGG GGCACCTGGA AGG TCCAGG T TCTCTGGCGTC CG CGG G
ACCGAGTGGATGTCAGGGAC ACCT ||| |||||| | |||||||||| || |||
GGCACCTGGAACCT TCC AGGTCC G AGGGACTGTAG GT GCC G
A AC- GC - GA-- A

GAM568 CAGTTTGGGCATACTTTCTT 14940 TGAGGTCGTA 14941 GT- CA-- TT C G G GTCTA
ATGGACCGCCGAGGTGTGTC GGCACCCAGT CA TTGGG TAC TCTTATGGAC GCC AG TGT
T
TATTCGTTAACAGCTAGGCC AATG || ||||| ||| |||||||||| ||| || |||
GTCCATGAGGTCGTAGGCAC GT GACCC ATG GGAGTACCTG CGG TC ACA T
CCAGTAATG AAT ACGG CT C A G ATTGC

GAM569 GCCAGGCTTGGGCGTATTTT 14951 TACGTTGTCC 14952 CTTG GTATTT - TG C
TAG

CTCCGGTGAGCGTAGCTGCC GCGGGATTCT GCCAGG GGC TCTC CGG AGCGTAGCTGC
TG T
TGTAGTCGTTAGCAGCTACG AGCC |||||| ||| |||| ||| |||||||||| ||
TTGTCCGCGGGATTCTAGCC CGGTCC CCG AGGG GCC TTGCATCGACG AT /
ACCTGGC A--- ATCTT- C TG - TGC

GAM570 TAGTGGAATTGTACTCCCAG 14958 TTCAACTTGC 14959 GA T CTCCC GCCTT- A
TGCCTTTAGCAAATGCTATA TGTCTCACTG TAGTG AT GTA AGT TAGC A
TTCAACTTGCTGTCTCACTG ||||| || ||| ||| ||||
GTCAC TG CGT TCA ATCG A
TC T ----- ACTTAT T

GAM571 AATGAATCTGGAATAGTATC 15010 TCTGGAATAG 15011 TG C TATCTACAACATT - CATTT
TACAACATTAGCAGCATTTA TATCTACAAC AA AAT TGGAATAG AG CAG A
TAAAACTGTCTTTTCCTACT ATTA || ||| |||||||| || |||
ATATCTATTCCAAATTTGTT TT TTA ACCTTATC TC GTC /
GT A TATATCATCCTTT T AAAAT

GAM572 ATAGAACTTGATTTATTTGT 15020 TAAATTGGAT 15021 TT - TGAT A- CCA
TGATTTGCAGTTCCAATAAA CTTGTTCTGT ATAGAAC GATTTA TTTGT TTGC GTT A
GCCCGCGATATAAATTGGAT ||||||| |||||| ||||| |||| |||
CTTGTTCTGT TGTCTTG CTAGGT AAATA AGCG CGA /
TT T T--- CC AAT

GAM573 ATAATTCATATAATAAATAT 15043 TAATGTATAT 15044 TAATA TA A- GT----- CA
AATGTATATAGTTTGTTCTC AGTTTGTTCT ATAATTCATA AATA ATGTAT TAGTTT TCT T
ATTTAGATCATTTAAAATTA CATT |||||||||| |||| |||||| |||||| |||
AAATATGTCTTATTGTTTAT TATTAAGTAT TTAT TGTATA ATTAAA AGA /
GAATTAT TTG-- TC AA ATTTACT TT

GAM574 ATTGTTACCTGCTGCAAGTG 15059 CAGCCCTAGA 15060 C GCTGCA TG CC CCC A T-
CCT- TC TTC
TGACGCCAGCCCTAGAAAGC AAGCTTGTTT TA CT AGTG ACG AG TAGAA GC TGTTTTCA
AC AC C
TTGTTTTCACCTACTCACTT TCAC || || |||| ||| || ||||| || |||||||| || ||
CCCTTGTATGTCTGATGAAA AT GA TCGC TGT TC ATCTT CG ACGAAAGT TG TG
/
GCATTGCTTCTACTTCTCAT A ------ CT AC TTC - TT AGTC TA TTC
GTTCCGCTAGATAACAAT

GAM575 TGGGCTAGCTAAAAGTGAAG 15123 AAAGTGAAGA 15124 T C AAAG- AAT- A- TA
AAATTGAAGTATAAGTTACA AATTGAAGTA TGGGC AG TA TGAAGA TGA GTA A
CTCATATATTTTTAATAAGT TAAG ||||| || || |||||| ||| |||
AACTGCCCA ACCCG TC AT ATTTTT ACT CAT /
- A GAATA ATAT CA TG

GAM576 CAAGGCGGCCAAGAGGCAGA 15143 AGAGGCAGAC 15144 CCAA - GACCTA T AAAA
CCTAAGGGCTCTAAAACTAA CTAAGGGCTC CAAGGCGG GAG GCA AGGGC CT C
AAAGCGCCCTACATGCTCTC TAAA |||||||| ||| ||| ||||| ||
CTGCTTTG GTTTCGTC CTC CGT TCCCG GA T
---- T ACA--- C AAAA

GAM577 GATATATAAATTTTTTATAC 15232 TTTAATCTGT 15233 T TTTTTT - GT- T
TTTCTGGATGTGGAATTCCT GAAAGTATTT GATA ATAAA ATACTTTC TGGAT GGAA T
TCTTTAATCTGTGAAAGTAT CACT |||| ||||| |||||||| ||||| ||||
TTCACTTTTATTATT TTAT TATTT TATGAAAG GTCTA TCTT C
- TCACTT T ATT C

GAM578 GTGTTGCTAATAGAATTTCA 15241 TGACTGAATG 15242 TT TAATAG CG -- T TGT
GA- AA
TCGAATGACTGAATGTTGTG TTGTGTCCGA GTG GC AATTTCAT AATGA CTGAA GTTG
CCGAT TGTA A
TCCGATGATGTAAAATTCTA TGAT ||| || |||||||| ||||| ||||| |||| ||||| ||||
TGAAAATTGGTTTAACTTTC CAC TG TTGGAGTA TTACT GACTT CAAT GGTTA
GTAT T
AGACTCATTATGAGGTTAGT T- TATGA- -- CA T TT- AAA CT
ATGTTCAC

GAM579 GATAAGGAAGAGTTTTTTTG 15246 TAAGGAAGAG 15247 - GTTTTTTTGTGTTT- CT T
TGTTTTCATTTTCTCCTATA TTTTTTTGTG GATA AGGAAGA TCATTTT CC A
GGTTGAAATGGTATAGTTTC TTTT |||| ||||||| ||||||| ||
CCAGAATTTTCTTGTGTC CTGT TTCTTTT GGTAAAG GG T
G AAGACCCTTTGATAT TT A

GAM580 ATTTCTCGGTTTTCTGGTGT 15261 TGAGTGCAAA 15262 T TTA TG GA ATC T
GCAAA T TT
TAAAATTAATTTTGTGAAGT TAGGATGTTA TTTCTGG GTTAAAA ATTT T AGTA TG GAGT
TAGGA GTTA T
AATCTGTGAGTGCAAATAGG TTTC ||||||| ||||||| |||| | |||| || |||| ||||| ||||
ATGTTATTTCTTAATTTTCT AAAGATT CAATTTT TGAA A TCAT GC CTCA GTCTT
TAAT /
GAACTCCGTACTAATGAAGT T --- GT A- --- - A---- T TC
TTTTAACTTTAGAAAACCAG
AAGT
GAM581 GACACATGGTGGAGTTTATG 15273 TATGGAGTGG 15274 A TGG TTT GAGT A A TG--- --
--- TAAAAC
GAGTGGTCTCAGGAGCTGTC TCTCAGGAGC C CA TGGAG ATG GGTCTC GG GC TCG
AGCAG C
GAGCAGTAAAACCCTGTGTC TGTC | || ||||| ||| |||||| || || ||| |||||
TGCTTTTACCGAAAATTGCC G GT GCCTC TGC CCAGAG CC CG AGC TCGTC
/

CGAGACCTCAACGTCCCTCC - T-- CC- AACT - - TTAAA CATTT TGTGTC
GTTGGTC

GAM582 TAAACCAATGGATGTAGTTC 15287 TGGAAGTTTC 15288 G------- - TCA CACGATT AA
TCG -- G
AGATAACACGATTGTGGAAG GCCTTATACG AT GATGTA GT GATAA GTGG GTT
CCTTAT ACG A
TTTCGCCTTATACGGACGCG GACG || |||||| || ||||| |||| ||| |||||| |||
TGCATAGGGACAACACCACT TA CTGCAT CA CTATT CACC CAA GGGATA
TGC C
AACTTATCCGTACATACGTC ATCACAAA A TGC CAAT--- A- CA- CG G
AAACACTAATTGGTTTA

GAM583 GAGGAGTTAATTTTTCTACG 15291 TCTACGGTGG 15292 GT---- TC TG C TAA GC
GTGGCGTGTTTAAACTGCTC CGTGTTTAAA GAGGA TAATTTT TACGG G GTGTT ACT T
AAAGTATAACATCTTTCCGT CTGC ||||| ||||||| ||||| | ||||| |||
AAGAAAATTGTTTATATCCT CTCCT GTTAAAA ATGCC T TACAA TGA C
C ATATTT GA TT C TA- AA

GAM584 CTTTTTTTACCAAACACAAT 15297 TTTAACAGTA 15298 ACCAAACAC TTTAAAA---
TTAC- TT AA
TTTATTTTTAAAATGTTTTA TATCTTCAAT CTTTTTTT AATTTTATT TGTT GGG TT A
CGGGTTTTAAAACAGATTCC AGAA |||||||| ||||||||| |||| ||| ||
CTATTTAACAGTATATCTTC GAAAAAAG TTAAGATAA ACAA CCC AG A
AATAGAATTTCCACTTACGA CATTCACCT CTTCTATATG TTTAT TT AC
AAAAAG

GAM585 GCACGGACTCTCGTCGTAGC 15309 ACTCTCGTCG 15310 CTCTC GT CGTTCAAATC A
ACGTTCAAATCGGTTTATTA TAGCACGTTC GCACGGA GTC AGCA GGTTT T
AAGCCCTCATGCTCAGACTC AAAT ||||||| ||| |||| |||||
CGTGT TGTGCCT CAG TCGT CCGAA T
----- AC ACTC------ A

GAM586 CTGTACCCCACCCCCCTTCT 15316 TTTGTCCCAG 15317 CCCC C AA- - - TC T
AAATAAATTTCCGATCCCTG GAGCGGGGTC CTGTA ACCCC CTTCT ATAAAT TTCCG A CC
G
GAGGTTTCCGGAGTATTTGT CTAT ||||| ||||| ||||| |||||| ||||| | ||
CCCAGGAGCGGGGTCCTATG GACGT TGGGG GAGGA TGTTTA GAGGC T GG G
CAG ATCC C CCC T C TT A

GAM587 TTCGTGAGCTCTTTTTACGA 15326 CCCGGTAGTT 15327 GC--- TTTTAC G A
CTACGGGGCTATGGAGCCCG ACTTGGACAA TTCGTGA TCT GACTAC GGGCT T
GTAGTTACTTGGACAATATC TATC ||||||| ||| |||||| |||||
ATGAG GAGTACT AGG TTGATG CCCGA G
ATAAC TTCA-- G G

GAM588 ATTGTCACCGTCGATGTGTT 15333 TAGCACATCG 15334 CCGT- - GGTGTC- -- AAC
GCTGGTGTCGACGGTCGTGA TTTATTGACA ATTGTCA CGATGTGTTG CT GACGGTC
GTG T
ACTTGACACCGGGCCGTTTT GT ||||||| |||||||||| || ||||||| |||
ATTAAAGATAGCACATCGTT TGACAGT GCTACACGAT GA TTGCCGG CAC /
TATTGACAGT TATTT A AATTATT GC AGT

GAM589 TCGATGATTCTTTGTTCGCA 15351 CACCAGGTCC 15352 T TT - A GT--- AG - CTT
CCAGGTCCTCAGCGCCGCTT TCAGCGCCGC TCGA GATTC TGTT CGC CCAG CCTC CG
CCG A
AAATTCGGCCGAGGAGGCTC TTAA |||| ||||| |||| ||| |||| |||| || |||
AATTGGAGCGTGACATCGAA AGTT CTAAG ACAG GCG GGTT GGAG GC GGC A
TCTTTGA T CT T A AACTC GA C TTA

GAM590 CCCCCCGATTCCCACATGCG 15370 TAGCCGTTCT 15371 AT CATGC CC -- C-- C
TAGCCGTTCTAGCTCCGTCG AGCTCCGTCG CCCCCCG TCCCA GTAG GTTC TAGCTC
GTCG T
CTAGCGATCTTGGGCTATTG CTAG ||||||| ||||| |||| |||| |||||| ||||
AACCTATCTGGGACGGGGGG GGGGGGC AGGGT TATC CAAG ATCGGG TAGC A
-- C---- -- TT TTC G

GAM591 AGGTAACCCAGAACTGAAAA 15375 TGAAAAAAAG 15376 ACC--- AC- AAA-- A GA
AAAGATATAGTGAAGGACTA ATATAGTGAA AGGTA CAGA TGAAA AGAT TAGT A
GATTTAGCAATTTCAATGTC GGAC ||||| |||| ||||| |||| ||||
TGAAAATATACCT TCCAT GTCT ACTTT TTTA ATCA /
ATAAAA GTA AACGA G GG

GAM592 CGTAATATAGATGTTTGTCT 15427 TAGATGTTTG 15428 T A TT CTAATTTAG TC A AA
AATTTAGTAAAATCAAGAGA TCTAATTTAG CG AATAT GATGT GT TAAAA AAGAG AT A
ATAAATTAATCCTTTTCTTT TAAA || ||||| ||||| || ||||| ||||| ||
TTAATACCCACATCATATTC GC TTATA CTACA CA ATTTT TTTTC TA T
G - - CC TA------- TC C AT

GAM593 AAAGCTAGAAACCGTGCCTC 15443 TACAGAAGAA 15444 AAA GCC CA TAG
CATATTTAGTATATGATACA TGGAAATTAG AAAGCTAG CCGT TC TATT T
GAAGAATGGAAATTAGCTTT CTTT |||||||| |||| || ||||
TTTCGATT GGTA AG ATAG A
AAA AGA AC TAT

GAM594 ACAGAATAAAAGAAGCAGTC 15464 TTTACCGGTT 15465 TAAA--- A-- GT AG AG
GAGGAGTTAAAGCAAATTGA GCCCATCTGT ACAGAA AGA GCA CG GAGTTAA C
TTTACCGGTTGCCCATCTGT CTAA |||||| ||| ||| || |||||||
CTAATTTCTGT TGTCTT TCT CGT GC TTTAGTT A
TAATCTG ACC TG CA AA

GAM595 TTTCATTTCTAAAATAATAT 15468 TCTAAAATAA 15469 - - AT TTTCTAA
TCGTTTTCTAATTCTTTTAT TATTCGTTTT TTTC ATTTCTAAAAT AAT TCGT T
ATGGTCATTAATTTTAGAAA CTAA |||| |||||||||| ||| ||||
TCGAAA AAAG TAAAGATTTTA TTA GGTA T
C A CT TATTTTC

GAM596 GGGGGGCGGCAGCGCCGACG 15480 TCGAAGAGGC 15481 G G CG CTTT--- AGAG C - C T- ATC
TCGTGCCCTTTGTCGAAGAG CGCCGCCGCG CAGC CCGA TCGTGCC GTCGA GC GC CGC GCGC GGCC G
GCCGCCGCCGCGCTGGCCAT CTGG |||| |||| ||||||| ||||| || || ||| |||| ||||
CGACCGGCCCTGCGCCGTGT GTCG GGCT AGCGCGG TAGTT CG TG GTG CGCG CCGG /
GTCGCACGATTGATGCTTAC G - TG CCATTCG AGCA C T C TC CCA
CGGCGCGAGTTCGGGCTGGC
GCCCCCC
GAM597 TTGTAATATAGACATATAAA 15494 TGATTGTAAC 15495 CA- A---- T C
TCTCTTCATTAAGTGATTGT ATAGTATCTA TTGTAATATAGA TAT AATC CTT A
AACATAGTATCTATATTATA TATT |||||||||||| ||| |||| |||
A AATATTATATCT ATA TTAG GAA T
ATG CAATG T T

GAM598 AATCTATTAGATGATATATT 15498 TATTAGATGA 15499 -- AT-- ATAAA
TCGTATAAACACATAATGGA TATATTTCGT AATCTAT TAGATGATAT TTCGT C
TAAAATATTATCTAATGTAG ATAA ||||||| |||||||||| |||||
ATT TTAGATG ATCTATTATA AGGTA /
TA AAAT ATACA

GAM599 GTAGGTGCTTTTCAGACATC 15503 TGGAATGGGA 15504 TG------ TT GA- CGG-- GA
CGGTGCAGATTATGCAGAAA AGATAAGAAT GTAGG CTT CA CATC TGCA T
TGATGGAATGGGAAGATAAG CCTA ||||| ||| || |||| ||||
AATCCTAC CATCC GAA GT GTAG ACGT /
TAAGAATA GG AAG TAAAG AT

GAM600 AGAATGAATTTACACGTGTA 15536 CACGTGTAGG 15537 A ACAC T C- CAAC CC
GGTCCTATGACAACTCCTCC TCCTATGACA AGAATG ATTT GTG AGGTC TATGA TCCT C
CCAAGGATATTTCATAAAGA ACTC |||||| |||| ||| ||||| ||||| ||||
CTTCGCCAGAGTATATTTT TTTTAT TGAG CGC TTCAG ATACT AGGA /
A AC-- - AA TTAT AC

GAM601 GGAACTGTCAAAAATTCTCA 15548 TCAGGATTTG 15549 AA G AA- CA-- ACAA
AGAGACACAAGAGGAGTCTC ACGAAAGGAC GG CT TC AAATTCT AGAGAC G
TGGTCAGGATTTGACGAAAG C || || || ||||||| ||||||

GACC CC GA AG TTTAGGA TCTCTG /
AG A CAG CTGG AGGA

GAM602 CTGTCTGATGGTGCCGCTAC 15605 CACCGTGTTG 15606 ---- TAGA TT T- CCTAT
CTAT C TT A
CCTAGACGTGTTTGTCCGCC CGGCTCACCA CCGC TACCC CGTG TG CCGC CATGG
AGA GTC GAC T
CTATCATGGCTATAGACGTC CGCC |||| ||||| |||| || |||| ||||| ||| ||| |||
TTGACATGGTCCGGCCTCTT GGTG GTGGG GCAC AC GGCG GTGCC TCT CGG
CTG /
CACCGTGTTGCGGCTCACCA TCAC CC-- C- TC TT--- ACT- C C- G
CGCCGGGTGCACTGTGGCCC
GTCGCAACGG
GAM603 TTGTGTTCTATGTTAGTATT 15626 TGTTAGTATT 15627 T AACTAATTTT ATA
TGAAACTAATTTTTCCAATA TGAAACTAAT TTGTGTTCTA GTTAGTATTTGA TCCA A
ATACTGGATTAAATGCTAAT TTTT |||||||||| |||||||||||| ||||
CTAGAATATAA AATATAAGAT TAATCGTAAATT AGGT /
C ---------- CAT

GAM604 GGAGCAGTGTACACAACGCC 15631 CTACCTGGCA 15632 C A CAAC - - A GGG
GGTGCCGACGGGGGTAATGC TGACACTCTC GGAG AGTGT CA GCC GGT GCCG CG G
GGCTACCTGGCATGACACTC C |||| ||||| || ||| ||| |||| ||
TCC CCTC TCACA GT CGG CCA CGGC GT /
- - A--- T T - AAT

GAM605 AGAATCTCTCAACGAAGCAT 15701 TCTCTCAACG 15702 CTC- A--- T--- CC
GTAAAATACCATATATTTTA AAGCATGTAA AGAATCT AACGA GCA GTAAAATA A
TTTTCTGTAATATCGTTATT AATA ||||||| ||||| ||| ||||||||
AGGATTTT TTTTAGG TTGCT TGT TATTTTAT /
ATTA ATAA CTTT AT

GAM606 GTTTGCGGTTTAGTTTTCTT 15717 TTTAGTTTTC 15718 C-- TTCTT-- TTT AATT
TAGTTCATTTGCAATTTTAT TTTAGTTCAT GTTTG GGTTTAGTT TAGTTCA GC T
AGTTCTGAATTATCTCATTA TTGC ||||| ||||||||| ||||||| ||
ACTAAACTATCTAAAC CAAAT TCAAATCAA ATTAAGT TG /
CTA TTACTCT CT- ATAT

GAM607 ATAGGATTGTGTGCGTGTGT 15726 TGTGTGCGTG 15727 GATTG- G T TG GA-- - GA
GGTAGATGTTTGGAGAAAGG TGTGGTAGAT ATAG TGT CGTG G GTA TGTTTGGAGAA AG
G
AGAAACTGTTTTCTAGATGG GTTT |||| ||| |||| | ||| |||||||||| ||
AAATATTGTTTACGAGCAAT TGTC ACG GCAT T TAT GTAGATCTTTT TC A
TAAACTGT AAATTA A T GT AAAG G AA

GAM608 GAAAAATACATTTGATGGTC 15766 TCATAATAAA 15767 - G GTC ACC A TGTTAT
G
TATCTACCAGATTATTATGT CTAGAGATGC GAAAAATAC ATTT ATG TATCT AG TTATTATG
AAG T
GTTATAAGGTACTTTTTCTC GTAA |||||||||| |||| ||| ||||| || |||||||| |||
ATAATAAACTAGAGATGCGT CTTTTTGTG TAGA TGC GTAGA TC AATAATAC TTC /
AAGATAGTGTTTTTC A A --- GA- A TCTTT- A

GAM609 ATTATATGATTATAGTTTCT 15777 TATATGATTA 15778 TTA TTCTATTTTTAC CCT-- G
ATTTTTACAGTACCTTGACT TAGTTTCTAT ATTATATGA TAGT AGTA TGACTAAA T
AAAGTCTTTAGTCACACAAT TTTT |||||||||| |||| |||| ||||||||
ACTACCAACCTACACTATTA TAGTATATT ATCA TCAT ACTGATTT /
TATGAT --- CATCCAACCA-- AACAC C

GAM610 ATTTTAAAATCTGCCGTGTC 15784 TTTAAAATCT 15785 A -- C TCT TC T
TAGTCTCGTTATTACAGGAT GCCGTGTCTA ATTTTAAA TCT GC GTG AGTC GT A
TCCTCGCAGTTTAGAATTTA GTCT |||||||| ||| || ||| |||| ||
AAAT TAAAATTT AGA TG CGC TTAG CA T
A TT A TCC GA T

GAM611 GTGGGAAGATAATCTAAAAA 15794 TCTAAAAAAT 15795 -- AA- AAAAA AA- - AAT
CGAA
ATTGTAAATACGTAATGGAA TGTAAATACG GTGG GAAGAT TCTA TTGT ATA CGT
GGAAT A
TCGAAAATAAAGTTTTTAAA TAAT |||| |||||| |||| |||| ||| ||| |||||
CGATATAAAACAAGGAATAG CGCC TTTCTG AGAT AACA TAT GCA TTTTG A
AAGCGTCTTTATCCGC TA CGA AAGG- AAA A AAT AAAT

GAM612 GTGTGTCTCATAGCCGTTAG 15797 TACATGAACA 15798 T AGC - - A TT
GATTATTATTATATTAAAGT TGGATACAC GTGTGTC CAT CGT TAGG ATT TTA A
ACTTACATGAACATGGATAC ||||||| ||| ||| |||| ||| |||
AC CACATAG GTA GTA ATTC TGA AAT T
- CAA C A - TA

GAM613 CGTCCAATATAGCTATCGAC 15864 TTGGATTACG 15865 A -- - TA- AAA AAAT
GTACGTGATAAAAACAAAAT GTTTGTCGTA CGTCCA TATAG CTAT CGACG CGTGAT AACA
T
TTACCTGTTGGATTACGGTT TAGA |||||| ||||| |||| ||||| |||||| ||||
TGTCGTATAGATTTATGGTG GTAGGT GTATT GATA GCTGT GCATTA TTGT /
GATG G TA T TTG GG- CCAT

GAM614 AGCTGGGTACTATAAAAATC 15867 TAATTCTGAA 15868 T TA AAAAA AACCACAG GT
AAACCACAGATAGGTTATAC TGGGGCCCGC AGC GGG CTAT TCA ATAG T
TATAATTCTGAATGGGGCCC T ||| ||| |||| ||| ||||

GCT TCG CCC GGTA AGT TATC A
- GG ----- CTTAA--- AT

GAM615 CTCGTAAATAAAGACGCACA 15890 TGGCGTGTAC 15891 A-- AC AGA T CATATAGT
GACCTCACGCATATAGTACC TTTATTACAA CTCGT AATAAAG GCAC CC CACG A
ATCACACCGTGTGGCGTGTA CGAG ||||| ||||||| |||| || ||||
CTTTATTACAACGAG GAGCA TTATTTC TGTG GG GTGC C
ACA A- C-- T CACACTAC

GAM616 TGCAGATCTTTTTTGTGAAA 15894 TCTTTTTTGT 15895 TCT- A TTTG
AAAAAATAATTATTTTTTTG GAAAAAAAAA TGCAGA TTTTTGTG AAAAAAAATAATTATTTT C
CGCGCCGGAATAATTATTTT TAAT |||||| |||||||| ||||||||||||||||
TTTTGCGCGGAAATATTTTT ACGTTT AAAGGCGC TTTTTTTTATTAATAAGG G
GCA TTAT G CCGC

GAM617 GAATAATTATTTTTTCGCCG 15904 TATTTTTTCG 15905 -- AA-- AG
GAAAGCATTTTGTAGTTTCA CCGGAAAGCA GAATAATTATTTT TTCGCCGGA GCATTTTGT T
CAAGATGCAGAATTTGGCGG TTTT |||||||||||| |||||||| |||||||||
GCCGGAATAATTATTT TTTATTAATAAGG GGGCGGTTT CGTAGAACA T
CC AAGA CT

GAM618 TTTTCTGATCTCAATCAAAT 15911 TTGACATCTT 15912 TG C TCAAAT - TA AC
CTTTAGAGATTACAGACACC TCAAAGTGCT TTTTC ATCT AA CTTT AGAGAT CAGAC C
ATGTTTGACATCTTTCAAAG TTCG ||||| |||| || |||| |||||| |||||
TGCTTTCGGATTGGAAGA AGAAG TAGG TT GAAA TTTCTA GTTTG /
GT C TCGT-- C CA TA

GAM619 TTAAACTTATTACTACTGCT 15922 TTGTAGGCGT 15923 A ATT TA T GC TAAACATT
ATAGGCGTTAAACATTAAAA CAAAGATTAA TTAA CTT AC CTGC ATAG GT A
TTATTACTACTGTTGTAGGC |||| ||| || |||| |||| ||
GTCAAAGATTAA AATT GAA TG GATG TGTC CA /
A AC- CG T AT TTATTAAA

GAM620 GCGTTAAACATTAAAATTAT 15939 ACTGCTGTAG 15940 TT- ATTA T GTA T AC
TACTACTGCTGTAGGCGTTA GCGTTAAACA GCG AAACATTAAAATT CTAC GCT GGCG TAA
A
AACATTATTACTGCTGTAGG TTAT ||| |||||||||||| |||| ||| |||| |||
CGTAGCTAAATTTTAATGTT TGC TTTGTAATTTTAA GATG CGG TCGT ATT T
TTTTCGT TTT ATC- - ATG C AT

GAM621 GGCATTCCTGATATTCATGT 15949 TAAAGTGCTA 15950 A AT- TC- - T A T CC
TAAAGTGCTATACTATAACC TACTATAACC GGC TTCCTG AT ATGT TAAAG GCT TAC ATAA A
ATCTTATGTGGGCTCTTTAT ATCT ||| |||||| || |||| ||||| ||| ||| ||||

ACATCTTATTGGCAGGAGGC CCG GAGGAC TA TACA ATTTC CGG GTG TATT /
C - GGT TTC T T - - CT

GAM622 GGTAGGGTAGACTCGAGACG 15960 GTTTTAGTCT 15961 TA T --- C ----- G CTCT
GCGGCCCGCGGTCTCTCTCT CTGTCTCTCC GG GGG AGACTC GAGACGG GGC CC CGGT
C
TGCCGGGTTTTAGTCTCTGT GGGT || ||| ||||||| ||||||| ||| || ||||
CTCTCCGGGTCTCCTCCTCC CC CTC TCTGGG CTCTGTC CTG GG GCCG /
TC C CCT T ATTTT - TTCT

GAM623 TGGACGTGTTATAAAATCTA 15967 TATAAAATCT 15968 C A CT TT TAT
AATATAAATGTTTTATATTA AAATATAAAT TGGA GTGTT TAAAAT AAATATAAATGT TA T
CTTACTATATTTATATTTGT GTTT |||| ||||| |||||| |||||||||||| ||
TTTAGAATATTCTA ATCT TATAA ATTTTG TTTATATTTATA AT /
- G -- TC TCA

GAM624 TGGTATATTATCATAACGTA 15972 TCAGTACATT 15973 --- TA - TTTT TTTAT TA
TTTGTTTTTGTTTTATAATA CAATATATGT TGGTATA TTATCA ACGTAT TTG TGT AA T
TCATTTTCAGTACATTCAAT TGAT ||||||| |||||| |||||| ||| ||| ||
ATATGTTGATAAATCTATAT ACTATAT AATAGT TGTATA AAC ACA TT C
CA CTA -- T TT-- TGACT TA

GAM625 TCCCTGGTAGCTACTGAGCA 15988 TGGCACAACG 15989 C AG AGC TAAC CTT - TG
AGAT---------- C
GCAGCTGTTTAACAGGCCCT AGGCCTTTGT TG CAGC TGTT AGGCC TTG GC CAG
C C
TTTGGCTGCAGAGATCCCAG AACA || |||| |||| ||||| ||| || ||| |
GGCCATAACAATGGCATACT AC GTTG ACAA TCCGG AAC CG GTC G A
GTGGCACAACGAGGCCTTTG - A- GTT TGTT AGC A GT
ATACGGTAACAATACCG G
TAACATTGGTTGACACTACC
AGGGG
GAM626 GTTGATCGTGTTATTAATTC 16009 TGTAAATACA 16010 ---------- T A T C T--- CATCATT
AAA
TTTCGCTGTAAATACATCAT TCATTAGTAG TCGTGT ATT ATTCT TCG TG AAATA
AGTAGA A
TAGTAGAAAAATCATCTATT AAAA |||||| ||| ||||| ||| || ||||| ||||||
TCAAAAATATTTCCCCCATC AGCACA TAA TAAGA AGC AC TTTAT TTATCT /
GATAGAATAAATTACACGAA TATTGTATCA T A T T CCCC AAAAACT ACT
CTATGTTATTCAGC

GAM627 TGTATTAAACAATAATACTA 16029 TAGAAACTAA 16030 TT - A - AA---- CA ATATA
C
GATGGTTAATCGACATAGAT ATCGAATTTA TGTA AAACAATA AT CT AGATGGTT TCGA
TAG GTACT C
ATAGTACTCCTAGGTATAGA AAAT |||| |||||||| || || |||||||| |||| ||| |||||

AACTAAATCGAATTTAAAAT ATAT TTTGTTGT TA GA TCTACTAA AGCT ATC
TATGG T
CATCTGAGAATATGTTGTTT T- A A G AATTTA AA AAAGA A
TTATA

GAM628 CGAATTGCTGGTATTGTGGT 16036 TACACCACTC 16037 T CT-- T TG CG GT C GGT T
TCATC
GCGGTGTCCTCGACGGTCCA CATTATCTAT CGAA TG GGTA TG GTG GT CCT GAC CCA
GTG T
TGTGTCATCTTATAATCACT TTAC |||| || |||| || ||| || ||| ||| ||| |||
TGGTCAGTCCAGGGTACACC GCTT AT CTAT AC CAC CA GGA CTG GGT CAC T
ACTCCATTATCTATTTACTT C TTAT T CT CA TG C ACT T TAATA
CG

GAM629 GTAAAGTTTCGGACGGCAGA 16054 AGATATTTAT 16055 C A - AT AGCC TTT
TATTTATGAAGCCGATTTCA GAAGCCGATT GTAAAGTTT GG CG GCAGAT TTATGA GA C
GTTTCCGTCGTGAATTTGTA TCAG ||||||||| || || |||||| |||||| ||
CGCCAAATTTTAC CATTTTAAA CC GC TGTTTA AGTGCT CT A
- - A -- GC-- TTG

GAM630 GCCGTCACCGTGTCGCAGCT 16064 TCGCAGCTCT 16065 TCAC TCGCA CCCC-- TCCT
CTTCCCCGGCCTCCTCCTGC TCCCCGGCCT GCCG CGTG GCTCTT GGCC C
TGGCCTACTGCGAGAGCCAC CCTC |||| |||| |||||| ||||
CGCGCCGGC CGGC GCGC CGAGAG CCGG C
C--- CAC-- CGTCAT TCGT

GAM631 GCGTCTCCGGTCCCGATCGA 16152 GCGAGCGTGC 16153 T --- AT AC G - CAT
CCGGTCGCCCCGTCGCATTG GCGGGATCCC GCGTC CCGG TCCCG CG CG TCGCCC
CGTCG T
TTCGACGCGGGCGAGCGTGC CGGC ||||| |||| ||||| || || |||||| |||||
GCGGGATCCCCGGCGACGC CGCAG GGCC AGGGC GC GC AGCGGG GCAGC /
C CCT -- GT G C TTG

GAM632 TCCCGGGCGCTGACGCCGCC 16184 GTCGTTCTTT 16185 G- GACGCCG CATCA G A
GACGACATCAGACGAGCGGA CGTCGGGAGA TCCCGG CGCT CCGACGA GACGA CGG T
TCTCCGGTCGTTCTTTCGTC AGAA |||||| |||| ||||||| ||||| |||
GGGAGAAGAAGCGAGCCGGG AGGGCC GCGA GGCTGCT TTGCT GCC C
A GA AGAAGAG TTC-- G T

GAM633 GGCGGGCGGCGAGCAGGATC 16204 GCAGGATCAG 16205 CA TCAGC C C - G
AGCAGCGCCACGAGATTGTC CAGCGCCACG GGCGGGCGGCGAG GGA AG GC ACGA GATT
T
GATCATCGTCGTCCTTCCCC AGAT |||||||||||| ||| || || |||| ||||
TCGCCGTCCGTT TTGCCTGCCGCTC CCT TC TG TGCT CTAG /
C- ----- C C A C

GAM634 AGTGGACGCGCCTCCCGGTT 16217 TCCGGGAGGA 16218 A- ----- TT CAAC
TACCAACCATTTCGTGTCCG TGGTCGCGCC AGTGG CGCG CCTCCCGG TAC C
GGAGGATGGTCGCGCCCTAC CTAC ||||| |||| |||||||| |||
T TCATC GCGC GGAGGGCC GTG A
CC TGGTA T- CTTT

GAM635 CGTATTTAGAGGCCTCGAAA 16229 TAGAGGCCTC 16230 A- AA G G - G
CAACGTGGAACGGCGTTTCG GAAACAACGT CGTATTT GAGGCCTCGAAAC CGT GAACG
CGTT TC A
ATCGATAGCGCGTTCGACGG GGAA ||||||| |||||||||||| ||| ||||| |||| ||
AGTTTCGGGGCTTCGAAAGT GCATGAA CTTCGGGGCTTTG GCA CTTGC GCGA AG T
ACG AG AG G - T C

GAM636 GGGGGGCCTCCTCGATCGTC 16241 CGGGGGCGGT 16242 C T G AATCGAT
CGCGAAGAATCGATTTATTA CGGAAGGTCC GGGGGGCCT C CGATCGTCC CGAAG T
AGCTTCGGGGGCGGTCGGAA CCC ||||||||| | ||||||||| |||||
GGTCCCCC CCCCCTGGA G GCTGGCGGG GCTTC /
A - G GAATTAT

GAM637 CGGAGGAGGCAGACAGACGG 16365 AGGCAGACAG 16366 C CAGAC CAG CCG
CAGGCGGCCGGCCGGGCACC ACGGCAGGCG CGGAGGAGG AGA GG GCGGCCGG G
GGCTGCAACCCTCTCCTCTT GCCG ||||||||| ||| || ||||||||
CTG GTCTTCTCC TCT CC CGTCGGCC /
- ----- CAA ACG

GAM638 TCGCGGGCCGCTCGCTATGC 16559 TATGCCGACT 16560 C C-- TA C T TGA AT
CGACTGACGTTGACGTTAAT GACGTTGACG TCG GGGC GCTCGC TG CGAC GACGT CGTTA
A
ATATAACGACGTCGTCGACG TTAA ||| |||| |||||| || |||| ||||| |||||
ACGCGGGTTCTGCTCCCGA AGC CTCG TGGGCG GC GCTG CTGCA GCAAT /
C TCT CA A - --- AT

GAM639 CGGCTCCTCCGCCTCGGGCG 16562 TGTGTCTGAC 16563 T --- C C C ---------- T
AG
ACGGGGGCTCGGAGATGACC ACTCCTCCCC CGGC CCT CCGCCT GGG GA GGGG
GC CGG A
GGCTGTGTCTGACACTCCTC TTCC |||| ||| |||||| ||| || |||| || |||
CCCTTCCTCAGGCGGCCCGG GCCG GGG GGCGGA CTC CT CCCC CG GCC
T
GCGCCG C CCC - - T TCCTCACAGTCTGTGT - AG

GAM640 GGGGGTGGTCAACGCCCTAG 16625 ACCCGGCCTA 16626 A C A A CTACC ------ ACT
T T GA

AGAGCGTGACCGTCTACCCG CGACTGCGTG CG CCTAGAG GCGTG CCGT CGGCC
TACG GCG GC CTCC T
GCCTACGACTGCGTGCTCTC CTCT || ||||||| ||||| |||| ||||| |||| ||| || ||||
CGATCTGGAGGCCGCCATGT GC GGGTCTC CGCAC GGCA GCCGG GTGT CGC
CG GAGG /
GCCTGCTGGCCGCCTACGGG G A G G TCC-- TCGTCC AC- - - TC
CACGCGCTCTGGGACGGCCG
CGACCCCC
GAM641 GGCCTCGGGGGCAACGGGGG 16651 CAGCCGCGTC 16652 T GCAACG G GCT- T
CGGCGCTCTGCTCATGCAGC AACCCCGTGG GGCC CGGGG GG GCGGC CTGC C
TCAGCCGCGTCAACCCCGTG CC |||| ||||| || ||||| ||||
GCC CCGG GCCCC CT CGCCG GACG A
T AA---- G ACTC T

GAM642 CTGGGATACACGGTACCTTC 16714 CACGGTACCT 16715 G - A ------ TT - TTT CA
CGCGCATTTGACCAAATCGT TCCGCGCATT CTG GATA C CGG TACC CCGCG CA GAC A
CCTTGACGTGGGGTAGTACG TGAC ||| |||| | ||| |||| ||||| || |||
CCCGCGTTGTCGCAG GAC CTGT G GCC ATGG GGTGC GT CTG A
G T C CGCATG -- A TC- CT

GAM643 GCGCGTTTGCGCACGTTCAC 16720 TCGCGAGTGA 16721 T C TT CTC GAG GTT
GG
CTCGCGAGTGACGTTGTGGA CGTTGTGGAT GCGCG TTGCG ACG CAC GC TGAC
GTGGATGCG A
TGCGGGAGCGCGCGTCCACC GCGG ||||| ||||| ||| ||| || |||| |||||||||
AAGTCGAGAGCCTCGTGTTC CGCGT GACGC TGC GTG CG GCTG CACCTGCGC G
GTCGCAGTTGCGC T - TT CTC AGA AAC GC

GAM644 TTAAAAATATGGTTTCAGAT 16723 TTTCTGGCTT 16724 T TTTC T C TTT CT TA A ---
CT
TGTCTATTTCTGGCTTTTAA TTAAAAATAA TTAAAAA ATGG AGA TGT TA CTGG TT AAA
TAAA AAC T
AAATAAAAACCTTTCGTTTC AAAC ||||||| |||| ||| ||| || |||| || ||| |||| |||
CTTTACTTTCGAACCAGTTT AATTTTT TACC TTT ACG AT GACC AA TTT ATTT TTG
/
ATGCACTTTATTTCCATTTT - TTTA C T TT- -- GC C CCT CT
TTAA

GAM645 GTGGCGAGTCTTTTAAAGTA 16747 AAGTATACTT 16748 TCTT- -- CTT-
AAATATTCGTTCA TTTAATTT
TACTTCGTAAAATATTCGTT CGTAAAATAT GGCGAG TTA AAGTATA CGTA GTAGAT
A
CAGTAGATTTTAATTTAAAA TCGT |||||| ||| ||||||| |||| ||||||
CTCCTATCTATAATTCTTTC CCGTTT AAT TTTATAT GCAT TATCTA /
ATACGTTTTTATATTTACTA TTTTT CA TTTT ACTTTCTTAA--- TCCTCAAA
ATTTTTTTTGCCAT

GAM646 ATGATAAAATTTCAACACAT 16750 CAAAAGCCTT 16751 - TT- C TA- GTA ACA TCC
ACTTGTACAGATGACATATT GTTTTGTATA ATGATAA AAT CAA ACA CTT CAGATG TATT A
TCCACCTGATAACATTTGCA TTCT ||||||| ||| ||| ||| ||| |||||| ||||
AAAGCCTTGTTTTGTATATT TACTATT TTA GTT TGT GAA GTTTAC ATAG /
CTTATCAT C TAT T TCC AAC A-- TCC

GAM647 AAATGGATTTATAGGTTTTG 16771 ATGGATTTAT 16772 TAT TTT---------- GCT
TAGCTAATAATACTTTTCCA AGGTTTTGTA AAATGGATT AGGT GTA A
TTTTCTACCTTTGATCCATT GCTA ||||||||| |||| |||
T TTTACCTAG TCCA CAT A
TT- TCTTTTACCTTTT AAT

GAM648 ATTTTCTCATCTAATAATAA 16786 TGGCAATATA 16787 AAT TTT ---- TC A CTA
CTGT AAC
GTTTAATAGAGGTCCTTTTA TAAGTAAAAG AATAAG AATAGA GG CTTTTATT ATGTA GCT
ATTCA A
TTAATGTACTAGCTCTGTAT CTCC |||||| |||||| || |||||||| ||||| ||| |||||
TCAAACACCATGGATTGTGG TTGTTT TTATCT CC GAAAATGA TATAT CGG
TAGGT /
CAATATATAAGTAAAAGCTC T-- --- ACGA TC A AA- TGT- ACC
CAGCATCTATTTTTGTTTCA
ATTCCGTAGT
GAM649 GTAGCGAGTCTTTTAAAGTA 16806 TAGATTTTAA 16807 C CTT--- A TCGTAAAA
TACTTCGTAAAATATTCTTT TTTAAAACTC GTAG GAGT TTAAAGT TACT T
CAGTAGATTTTAATTTAAAA CTAT |||| |||| ||||||| ||||
CTCCTAT TATC CTCA AATTTTA ATGA /
- AAATTT G CTTTCTTA

GAM650 AGACGTATTAGCGGATCTAA 16815 TAAGAATATA 16816 CTA CCA- A A
CTTTTGAAAATATAC TG TCC
TGGAATCCAATTGATTGACT GCAACAATGA GAT ATGGAAT ATTG TTG CTAT
ATTTTTA A G
ATCTTTTGAAAATATACATT TAAT ||| ||||||| |||| ||| |||| ||||||| |
TTTATGATCCGATACTTGTA CTA TACCTTA TAAC AAC GATA TAAGAAT T A
AGAATATAGCAACAATGATA C-- ATAG - - ---------- GT CAT
ATTCCATCATCGTGTTTTTT
TGCCTCT
GAM651 GAAATATACCGTAAATCAAA 16831 CAAAAGCTTT 16832 A AAATC TTCCATT
ACCACATAATC G
GTTGTTTCCATTAAAAGTTA TTTGCGACTT GAAAT TACCGT AAAGTTGT AAAAGTT
GAAT T
CCACATAATCGAATGTCAAT TTAG ||||| |||||| |||||||| ||||||| ||||
TCCAAAAGCTTTTTTGCGAC CTTTA ATGGTA TTTCAGCG TTTTCGA CTTA C
TTTTAGCATGGTAATTTC - CGAT- TT----- AAAC------- A

GAM652 CCGCCCGCGCGGCATCTCAT 16841 CATCTCATTA 16842 - - CA GCCCGG CTTC

TAGCGCCCGGCGCGGGCGGC GCGCCCGGCG CCGCCCGCG CG G TCTCATTAGC
CGCGGGCGG C
TTCCGCTTCCGCCCGCGATG CGGG |||||||| || | |||||||||| |||||||||
CTAATGAGACCCTCGTCGCG GGCGGGCGC GC C AGAGTAATCG GCGCCCGCC /
GGCGG T T CC TA---- TTCG

GAM653 GTTTCTATATTAATAGGAGA 16851 TCTATATTAA 16852 TATTAATAGGA AG AGT
TAGTTGTTGAGTCATAGTAA TAGGAGATAG GTTTCTA GATAGTTGTTG TCAT A
AAATGAAATGATAACTGTTT TTGT ||||||| |||||||||| ||||
AGAAAT TAAAGAT TTGTCAATAGT AGTA /
---------- AA AAA

GAM654 TTCTTGTTTGTTTATTTCTG 16856 AATACAGATA 16857 -- T CT-- CTA AT----------
C
CTTCTAATCTATTATTTGCA CTAATGTTTC CT TGT TGTTTATTT GCTT ATCT
TATTTG A
ACAAATACAGATACTAATGT AGGG || ||| ||||||||| |||| |||| ||||||
TTCAGGGGATAAGTTTCCGA GA ACA ACAAATAAG TGAA TAGG ATAAAC /
ATAAACATACATTAGGG TT T CCTT --- GGACTTTGTAATCATAGAC A

GAM655 GGAGGTTTCTATCGCGACTT 16878 GGATGCGACG 16879 A ---------- A AAAC
AAAACGCTGGATAGGATGCG AAGAAAACTA GG GGTTTCTA TCGCG CTTA G
ACGAAGAAAACTATAGAGAC TAGA || |||||||| ||||| ||||
TACC CC TCAGAGAT AGCGT GGAT C
A ATCAAAAGAAGC A AGGT

GAM656 GTGCGCTTTGTACTCAGCTT 16881 TTGGTTGACT 16882 C T C TGTCTTCGA TCT
GTCTTCGAAACGATTCTCCG GCGCAGCTCA GTG GCT TGTA TCAGCT AACGAT C
ATGTTGTTGGTTGACTGCGC C ||| ||| |||| |||||| ||||||
AGCTCAC CAC CGA GCGT AGTTGG TTGTTG C
T C C --------- TAG

GAM657 CTTGTAAACTTCATCGTTTA 16906 TTAGAAAATA 16907 A TTCAT ---------- ATAA C T
AT
TTGTTATATAATTTCCTGTA GCAATGATTT CTTGT AAC CGT TTATTGTTAT TTTC TG
AG A
GATAAAACTTTAGAAAATAG TCCC ||||| ||| ||| |||||||||| |||| || ||
CAATGATTTTCCCTTTACGT GAGCA TTG GCA AGTAACGATA AAAG AT TC A
CCGTTAACGAG A CCT-- TTTCCCTTTT ---- - T AA

GAM658 ACGTTAAAGCTAAATTGCTT 16946 TTAAAGCTAA 16947 TAA TAA CTTAT TG T
ATGGTGGGTGGGTCTTCTTA ATTGCTTATG ACGT AGC ATTG GG GGTGGG C
CTTGCCCGGTCTGCTGTCAC GTGG |||| ||| |||| || ||||||
GT TGCA TCG TGGC CC TCATTC T

CTG TC- ----- GT T

GAM659 TATCTTTGTTAATTAGCGTA 16951 TCTTTGTTAA 16952 - ATTA----- TAACTCT
AATTTTAACTCTTTTCCAAA TTAGCGTAAA TATCTT TGTTA GCGTAAATTT T
TAAGTTTATGTAACAACAAC TTTT |||||| ||||| ||||||||||
TAACATGAGATA ATAGAG ACAAT TGTATTTGAA T
T CAACAACAA TAAACCT

GAM660 GCACCGGTGTTATCTGTTCA 16954 TATCTGTTCA 16955 C T TAT TG TCCCT - ACAA-------
---- T
GTCCCTGCCAACTACAATTG GTCCCTGCCA GCAC GG GT C TTCAG GC CAACT
TTG T
TTTGCAAAGGTCTTTTACCG ACTA |||| || || | ||||| || ||||| |||
AAAGTTGTGTCAATCTGAGT TGTG CC CA G GAGTC TG GTTGA AAC T
GGCTACCCCTGTGT T C TC- GT TAAC- T AAGCCATTTTCTGGA G

GAM661 CGTTGTGGATTGTCTGACCT 16978 TTGAAAAAAT 16979 TT TG TGTC CT--- AAAATTTTT
CCG
TTGAAAAAATTTTTGTGTCC TTTTGTGTCC CG G GAT TGAC TTGAA GTGT T
GTGTAGCATTTCAATAAAAG GTGT || | ||| |||| ||||| ||||
TCATTATCTGCTCCG GC C CTA ACTG AACTT TACG /
CT GT TT-- AAAAT --------- ATG

GAM662 CACTATGTCGTGGATTAGTT 16984 TTCTCATGAA 16985 G TAGTT GACAC -- A ATAA
--- TA
TAGATGACACTTGTTGTAGG CGGAACGATT GAT TAGAT TTGT TGTAGGAG TTGT GTTC
GGGGCCG T
AGATTGTATAAGTTCGGGGC CCTA ||| ||||| |||| |||||||| |||| |||| |||||||
CGTATGGGTGGTTCTCATGA CTA ATCTG GACA ACATCCTT AGCA CAAG
TCTTGGT G
ACGGAACGATTCCTACAGTA T TAC-- ACCTA TG - AGG- TAC GG
CAGATCCAGTCTACATATCT
GTTATAGTG
GAM663 CCACGTCGTTGGTTTCTTTT 16998 CGTTCCGTTA 16999 C C ----- TTTATCAT- TTG
ATCATCTTCTTGTACTTGAG GAAACGTTTT CCA GT GTTG GTTTCT CTTC T
GCGTTCCGTTAGAAACGTTT CAAC ||| || |||| |||||| ||||
TCAACAACTTGG GGT CA CAAC CAAAGA GGAG A
T A TTTTG TTGCCTTGC TTC

GAM664 CGAAGAATGTCGTGCCGTTG 17008 TACCCCGCCG 17009 AAT T CGT- TTGT TG
TTGTTGTTTACGTGATACGT ACTCCTTTG CGAAG GTCG GC TGTTG TTACG A
GGTGTTCGATACCCCGCCGA ||||| |||| || ||||| |||||
CTCCTTTG GTTTC CAGC CG ATAGC GGTGC /
CT- - CCCC TTGT AT

GAM665 GGGCTCTCTGCCGTGCGAGG 17034 CCGCGCAGCA 17035 C C AG C CACAGACAC
CTCCTCACAGACACACAGCA GATAGCCC GGGCT TCTGC GTGCG GCT CT A
AGAAAGAAGCGCCGCGCAGC ||||| ||||| ||||| ||| ||
AGATAGCCC CCCGA AGACG CGCGC CGA GA /
T A CG A AAGAACGAC

GAM666 GTGCAGAGACCGCCTGGGTG 17076 AAACACCCGT 17077 C GA TTTTAG AA
TGACTGTTTTTAGGCCTAAC GCGGTCTCTG GTGCAGAGACCGC TGGGTGT CTGT GCCT C
AAAGGCACAGAAACACCCGT TAT |||||||||||| ||||||| |||| ||||
GCGGTCTCTGTAT TATGTCTCTGGCG GCCCACA GACA CGGA /
T AA ------ AA

GAM667 GAGACAAGCTTTCAATATCT 17099 TTCAATATCT 17100 A T A--------- --- GTAAA
GAATCTAAAGTAAAGTCATG GAATCTAAAG GAGACA GC TTCA TATCTGAA TCTAAA G
TTTAGAAGTTTCGGATAAAT TAAA |||||| || |||| |||||||| ||||||
TTATTAATGAATGCATGTCT TTCTGT CG AAGT ATAGGCTT AGATTT /
T A T AATTATTTAA TGA GTACT

GAM668 TATTTTCAAATAGCCGATTT 17112 TTGAATCTGT 17113 T C ------ GTTTT--- TGT T
TC
GCAGTTTTCAGTGTTTCGAT TCCTCCATGC TATTTTCAAA AGC GATT TGCA CAG
TTCGATT CG C
TTCGTCCAGTTGTGATTGAA ATTT |||||||||| ||| |||| |||| ||| ||||||| ||
TCTGTTCCTCCATGCATTTT ATAGAAGTTT TTG TTAG ACGT GTC AAGTTAG GT
A
ATGATTTGTTTTTTGAAGAT T T TATTTT ACCTCCTT T-- T TG
A

GAM669 GTATTCAGCAATTGACACAT 17122 TTCGTGTTTA 17123 C CACATTT T- G
TTTACGGTGCCTGTGTAGGT TTCAATTCTG GTATTCAG AATTGA TACGG GCCT T
TTTCGTGTTTATTCAATTCT AGTA |||||||| |||||| ||||| ||||
GAGTAT TATGAGTC TTAACT GTGCT TGGA G
- TATTT-- TT T

GAM670 ATTATCAATCGGACCAGATA 17131 CAACTAAATG 17132 T ACCA C AA TCT
TTCTAGAATGTATCTTATTT TCGTAACCGT ATTATCAA CGG GATATT TAG TGTA T
ACAACTAAATGTCGTAACCG TGAT |||||||| ||| |||||| ||| ||||
TTGATAAT TAATAGTT GCC CTGTAA ATC ACAT /
- AATG - A- TTA

GAM671 GAACGTCTCTCTCTCCTGTG 17134 TTCAGCATAA 17135 C T C TC- CA-- GTTTTCG
T
TCGATCGCAGAGCGTTTTCG GTTTATTTTG GAA GTC CTCTCTC TGTG GATCG GAGC
GAACTG C

GAACTGTCCTCGGTTCAGCA GTCT ||| ||| ||||||| |||| ||||| |||| ||||||
TAAGTTTATTTTGGTCTATT CTT TAG GGGGGAG ATAT CTGGT TTTG CTTGGC C
ATAGAGGGGGTGATTTC - T - TAT TTTA AATACGA T

GAM672 GAAAGGCATGTGGGTTAATG 17151 TACCACAGGT 17152 C G - TA AAA-- TAC- A-
TT
ATTAAATCAGGTACTATGCC ACCTTTT GAAAGG AT TG GGT ATGATT TCAGG TATGCC
TC T
ATCTTTAGTGAAAGGCATGT |||||| || || ||| |||||| ||||| |||||| ||
TTTCTTGGGCATAAATCATA TTTTCC TG AC CCA TACTAA GGTTC GTACGG AG A
CCACAGGTACCTTTT A G A -- ATACG TTTT AA TG

GAM673 AGTTTAGATGACACTTGTTG 17161 TAGAAGATTG 17162 TG C TG A - TAAGT-- GGG
G CAT
TAGAAGATTGTATAAGTTCG TATAAGTTCG A ACA T TTGTAG AGAT TGTA TC
GCCGTAGGGGT GTTCT G
GGGCCGTAGGGGTGGTTCTC GGGC | ||| | |||||| |||| |||| || ||||||||||| |||||
ATGAACGGAACGATTCCTAC T TGT A GATATT TCTA ACAT AG TGGCATCCTTA
CAAGG /
GGTACAGATCCAGTCTACAT GT C GT G T CTGACCT ACA G CAA
ATCTGTTATAGTGACTGTTG
TCTATGCT
GAM674 AGGACAATTTTTGAGTTCTA 17170 CAATTTTTGA 17171 --------- TCTATTTC- C
TTTCAATGTCATCACATTTT GTTCTATTTC AGGACAAT TTTTGAGT AATGT A
CGACAATATTCAAAATCATC AATG ||||||||| ||||||||| |||||
GCTTATTGTTTT TTTTGTTA AAAACTTA TTACA T
TTCGCTACT TAACAGCTT C

GAM675 GGTTGTATTAAAGGCTTAAT 17178 TAATGCTGTA 17179 GGCTTAATTT T AATACC
TGT
TTCAGCTTTATCAATACCTA TTTAATACAA GGTTGTATTAAA CAGC TTATC TAG A
GTGTAAATCTAACAGATAAT CT |||||||||||| |||| ||||| |||
GCTGTATTTAATACAACT TCAACATAATTT GTCG AATAG ATC /
AT-------- T ACA--- TAA

GAM676 TGCTTATACTCTAAGAGTAT 17195 TAAGAGTATC 17196 T---------- C G
CGCCACCGACGACGACGACG GCCACCGACG
GAGTATCGCCACCGACGACGACGACGGCAGTCGC GC CGGC A
GCAGTCGCTGCCCGGCGAAG ACGA |||||||||||||||||||||||||||||||||| || ||||
CCGAGCCGCCGCGAAGCGGC CTCATAGCGGTGGCTGCTGCTGCTGCCGTCAGCG
CG GCCG /
GAGCGACTGCCGTCGTCGTC AGCGGCGAAGCGCCGC A A
GTCGGTGGCGATACTCTTAG
AGTATAAGCA
GAM677 ATTCATAGTTTTTAAAATTT 17203 CAAATGGAAA 17204 A TTTTTA- A AAA
TTACATTTGAGAAATCATAT ATTTGTTTTA ATTC TAG AAATTTTT CATTTGAG T

TCAAATGGAAAATTTGTTTT TCTA |||| ||| |||||||| ||||||||
ATCTAAGAAT TAAG ATC TTTAAAAG GTAAACTT C
A TATTTTG - ATA

GAM678 TACCAGAGTTTCGTGATGAT 17230 TGATTTGTTA 17231 - G A GA T CTAAA
GATTTGTTATGTGATCCTAA TGTGATCCTA TACCAGAGTT TCGT ATG T TTTGT ATGTGATC A
AAATCGCGATTACATACAAG AAAA |||||||||| |||| ||| | ||||| ||||||||
CTGCATGCGATGACTTTGGT ATGGTTTCAG AGCG TAC G GAACA TACATTAG /
A T - - TC - CGCTA

GAM679 ACCTTCTGAGCTGATGGTCT 17241 TCCGAAGACC 17242 TG GAT- ACT - GATG
ACTGACCTGATGATGAAGAG TTGGAGCTGA ACCTTC AGCT GGTCT GA CCT A
GATCCGAAGACCTTGGAGCT AGGT |||||| |||| ||||| || |||
GAAGGT TGGAAG TCGA CCAGA CT GGA T
-- GGTT AGC A GAAG

GAM680 GGTACTTTCTTTGCCAAAAA 17265 AGAAAGTTTT 17266 TTT - - AAA- G GA AG TT A
AAAAGTTGATTGAAGTCATT TAGCGTGTGT GGTAC CTTTG C CA AAAAA TT TTGA TCA
TTC C
TTCACAAGAATTGATCAGAA CAAA ||||| ||||| | || ||||| || |||| ||| |||
AGTTTTTAGCGTGTGTCAAA CCGTG GAAAC G GT TTTTT AA GACT AGT AAG A
GTGTGCC T-- T T GCGA G A- -- T- A

GAM681 TTGATAACAGTTGAAAGCCA 17283 TTGAAAGCCA 17284 A T GC ATTT AA
AATATTTGCCAAAATCGGTT AATATTTGCC TTG TAACAGT GAAA CAAAT GCC A
TCAATTTGCGTTTCGCTGTT AAAA ||| ||||||| |||| ||||| |||
GCCAA AAC GTTGTCG CTTT GTTTA TGG A
C - GC ACTT CT

GAM682 ACTTTCATCCTGATCACCTG 17322 TAACGAGATT 17323 CCTGA A -------- C C A G
G
TATCCTCTCTCTACTCTACG GAAGAGACAG ACTTTCAT TCACCTGT TCC TCTCT TA TCT
CGT ATCG T
TGATCGGTGACGGTAACGAG ACAA |||||||| |||||||| ||| ||||| || ||| ||| ||||
ATTGAAGAGACAGACAACGG TGGAAGTA AGTGGACA GGG AGAGA GT AGA GCA
TGGC G
GACAGGTGAGACAATGAAGG ACAG- - CAACAGAC A T - A A
T

GAM683 GAGAGGTGTAAAAGATATAT 17351 TACACCGCCA 17352 AAAAGATATA TCG-- A
GGCTCGATCAGCTGATACAC CCGTAAAACC GAGAGGTGT TGGC ATC G
CGCCACCGTAAAACCACGCC ACGC ||||||||| |||| |||
TCTC CTCTCCGCA ACCG TAG C
CCAAAATGCC CCACA T

GAM684 CCGCCATTTTAAGTAGCTGA 17362 AAGTAGCTGA 17363 AA GA A T GTAAAG
CGTCAAGGATTGACGTAAAG CGTCAAGGAT CCGCCATTTT GTAGCT CGTC AGGAT GAC G
GTTAAAGGTCATCCTCGGCG TGAC |||||||||| |||||| |||| ||||| |||
GAAGCTACACAAAATGGTGG GGTGGTAAAA CATCGA GCGG TCCTA CTG /
CA AG C - GAAATT

GAM685 GTGCGTACGTCACAAGTCAC 17381 TAGGCCCCGT 17382 CAC GA A CG GTAA
GTGGAGGGGACCCGCTGTAA CACGTGACTT GTGCGTACGT AAGTCACGTG GGGG CC CT
C
CCCGGAAGTAGGCCCCGTCA ACCA |||||||||| |||||||||| |||| || ||
CGTGACTTACCACGTGTGTA CATGTGTGCA TTCAGTGCAC CCCC GG GA C
C CCA TG - AT AGGC

GAM686 CCGGCGGACGCACCTCGAGA 17386 GACCGGGCCG 17387 - C - GA -- GC -- G -
ACGA A CAG
GGGCCCCGGGCCCGACGGCC CCCGATCGAA CA CT CGA GGGC CCCGG CCGA CG CC
GCGGCG TG GGTCG A
GCGGCGACGATGAGGTCGCA GATG || || ||| |||| ||||| |||| || || |||||| || |||||
GATCTCGACCCCGGAGGCGC GT GA GCT CCCG GGGCC GGCT GC GG TGCCGC
GC CCAGC /
CGTAGGGCGACTCGGACCGG C A A AG CC A- CA G A GGAG C TCT
GCCGCCCGATCGAAGATGCC
GTTCCTCCCGG
GAM687 GCAGCATATGGATATGTAGA 17395 CAGGAGACCA 17396 GCA GA AGAA--- AA
ATTTTGTGCAAAAAGTACAG AAACATACAC GCA TATG TATGT TTTTGTGC A
GAGACCAAAACATACACATG ATGA ||| |||| ||||| ||||||||
AATGC CGT GTAC ATACA AGGACATG /
AA- AC AAACCAG AA

GAM688 TGTATGACGAGTACAAAAGG 17420 TATCTAGGAG 17421 A C- AAA GAACTA CAGC
A ACC
TTTATGAACTACTGGACAGC TAAACCTGTA TGT TGA GAGTACA GGTTTAT CTGGA
ATCTA CGAAG T
ATCTAACGAAGACCTAGACC CTTT ||| ||| ||||||| ||||||| ||||| ||||| |||||
TTTGTAGATATCTAGGAGTA ACA ACT TTCATGT CCAAATG GATCT TAGAT GTTTC
A
AACCTGTACTTTTTCAGACA G TT --- AG---- A--- - CAG

GAM689 GGCGCCGTTGGCGGCCACGA 17433 TGTGGCGGTA 17434 C G--- G GGC C
CCCGGCGGTCCCAGACCAGG GCCGATCGTG GGCGC GTTGGC GCCAC ACCC GGTC C
GTGTGGCGGTAGCCGATCGT CC ||||| |||||| ||||| |||| ||||
GCC CCGTG TAGCCG CGGTG TGGG CCAG /
C ATGG - A-- A

GAM690 TTGGATCTTGTTCTGTTAGT 17463 TGGAAAAATC 17464 CT - TAG - TTG-- TACGTA
ACTGGTTGTCCAGATACGTA CAGCTAATGC TTGGAT TGT TCTGT TA CTGG TCCAGA A
AACTTCTTTCTGGAAAAATC AGAT |||||| ||| ||||| || |||| ||||||
CAGCTAATGCAGATATATTA GGCTTA ATA AGACG AT GACC AGGTCT A
TTCGG TT T TA- C TAAAA TTCTTC

GAM691 CCCGGGCTCCCCGTTCCCCG 17473 CTCCCCGTTC 17474 TTCCC A T- CT - TTCCC A T-
CT - TT
AGGGTCCCGGGCTCCCCGTT CCCGAGGGTC CG CG GGG CCCGGG CCC CG CG GGG
CCCGGG CCC CG C
CCCCGAGGGTCCCGGGCTCC CCGG || || ||| |||||| ||| || || ||| |||||| ||| ||
CCGTTCCCCGAGGGTCCCGG GC GC CCC GGGCCC GGG GC GC CCC GGGCCC
GGG GC /
GCTCCCCGTTCCCCGAGGGT CCCTT - TC T- A CCCTT - TC T- A CC
CCCGGGCTCCCCGTTCCCCG
AGGGTCCCGGG
GAM692 GTTTGTGTTGGTTTTTATGA 17533 TGGTGATTTT 17534 GTT TTTT- G TT AC
CCAGCTTGGTACAAAACCTG TTACCCAACA GTTTGT GGT AT ACCAGC GGT A
CTGGTGATTTTTTACCCAAC AAT |||||| ||| || |||||| |||
AAAT TAAACA CCA TA TGGTCG CCA /
AC- TTTTT G T- AA

GAM693 TTGGGTTCCCCGAGGGTCCC 17546 GTCCCGGGCT 17547 TTCCC A T- CT - TT
GGGCTCCCCGTTCCCCGAGG CCCCGTTCCC TTGGG CG GGG CCCGGG CCC CG C
GTCCCGGGCTCCCCGTTCCC CGA ||||| || ||| |||||| ||| ||
CGA AGCCC GC CCC GGGCCC GGG GC /
CTT-- - TC T- A CC

GAM694 GGCCTAGAGAAGGAGAGGGA 17629 CCGCTCCATG 17630 AG AAG G----- TCT AA
GCTCTATCTAAAGAAGATCC GAGTCTCAGC GGCCT AG GAGA GGAGC ATCT A
GCTCCATGGAGTCTCAGCTG TGCA ||||| || |||| ||||| ||||
CAGGCC CCGGA TC CTCT CCTCG TAGA /
CG GA- GAGGTA CC- AG

GAM695 GTTGGAAACTTACTCGCCAC 17685 TGGAAACTTA 17686 A TACTC - CCCACCC- GA
CCCCCACCCGCTGGGAAAGC CTCGCCACCC GTTGGAA CT GCC ACCC GCTGG A
CGGCATCATCGAGGGTGGGC CCCA ||||||| || ||| |||| |||||
ACAATAGTTCTAGC CGATCTT GA CGG TGGG CGGCC /
- TAACA G AGCTACTA GA

GAM696 CCGGTGGAACTCGTGACAGA 17718 CATCGTGGAG 17719 A - CA G --- AC
TGTCTACGCCACCCTAGGCA ATCATCGACG CCGGTGGA CTCGT GA GAT TCTAC GCC C
TCGTGGAGATCATCGACGAG AGCT |||||||| ||||| || ||| ||||| |||
CTCTACCGG GGCCATCT GAGCA CT CTA AGGTG CGG C
C G A- G CTA AT

GAM697 AGTTTGCCATGCTACAGTTT 17725 GCTACAGTTT 17726 T C G -- TTG- -- ATCACAT
GCATACGATCACATCCAATC GCATACGATC AGTT GC AT CTAC AGT CAT ACG C
CCACGTCAATGAAATGCTAA ACAT |||| || || |||| ||| ||| |||
GTAGAATAGCAACT TCAA CG TA GATG TCG GTA TGC C
- A A AA TAAA AC ACCCTAA

GAM698 GCGCAAGCTGATCGAGCCGT 17740 AGAGTACGTT 17741 AA- T T C CGCC- AATCAG C
AA TT
GCGCCCTCAATCAGAAGCGC TACTACGAGA GCGC GC GA CGAGC GTG CTC AAGCG
TACTTT G T
TACTTTAAGTTTGGCAAAGA ACTA |||| || || ||||| ||| ||| ||||| |||||| |
GTACGTTTACTACGAGAACT CGTG CG CT GCTTG CAC GAG TTTGC ATGAGA C /
ACACGTTCGTCCGCAAAGTG AAA C - - ATCAA CATCA- - AA GG
C

GAM699 TTTCGCGTGGACTAAGTACT 17748 GGGCAAGACC 17749 TT C TAA TGCG CC - AA
GCGCTCCGCCCGACGTCAAA CGTACGTTCA T CG GTGGAC GTAC CT GCCCGACG TCA G
GTTGTGATCGTCGGGCAAGA TCCG | || |||||| |||| || |||||||| |||
CCCGTACGTTCATCCGGGA A GC TACTTG CATG GA CGGGCTGC AGT T
GG C --- CCCA A- T GT

GAM700 GACTACGCCAGTAATACACT 17756 TAAAGTGTTT 17757 A- AG T ACA TG C
TACAAGGTGATCCTAATTGC AAGGTGGAGG GACT CGCC TAA ACACTT AGG AT C
CTAAAGTGTTTAAGGTGGAG TT |||| |||| ||| |||||| ||| ||
GTT TTGG GTGG ATT TGTGAA TCC TA T
AG A- - A-- GT A

GAM701 TCCGCCCCCTGCCGGACGAG 17797 CAGCGGGTAC 17798 -- GA- A AGA G AGCACGAT-
AC--- C A C
CAGCCAGAGGCGGCCGAGCA AGGAAGCGGT GCC GGAC GC GCC GGC GCCG CCCG
CT GCCG GG C
CGATCCCGACCTCGCCGAGG AGCC ||| |||| || ||| ||| |||| |||| || |||| ||
CCGGCCCGGCAGTGCAGCGG CGG CCTG CG CGG CCG TGGC GGGC GA
CGGC CC G
GTACAGGAAGCGGTAGCCGA CT AAG G CAG A GAAGGACAT GACGT - - G
CGGCGGCGAAGTCCTCGGCG
GAGGTGGA
GAM702 ACAGAAAAAGACTATACACG 17844 TAATGAGGAA 17845 AA--- ATACA GA--- AAGG
TAATAA
TGACTCAAAGGATGGTATAA CAACGAGATA ACAG AAAGACT CGT CTCA ATGGTA
C
TAACAATTCATTATTATAAT AGTT |||| ||||||| ||| |||| ||||||
GAGGAACAACGAGATAAGTT TGTC TTTTTGA GCA GAGT TATTAT A
TTTAAGTACTGT ATGAA ATAGA ACAAG AA-- TACTTA

GAM703 GGGCAGCGGCACGAGCCGCC 17849 TGAGGGCGCG 17850 G A- A - ---- TG
CCGCGTGGCGCGCGATGAGG CACGGCGTCG GGGCA CGGC CG GC CGCCC CGCG G
GCGCGCACGGCGTCGGTGCC GTGC ||||| |||| || || ||||| ||||
C CCCGT GCTG GC CG GCGGG GCGC /
G CG A C AGTA GC

GAM704 CGATTCTACGATATAGACAG 17868 TCTACGATAT 17869 ACG- TA --- AA
CGTTGTCAACGTGGACAACA AGACAGCGTT CGATTCT ATA GACAGC GTTGTC C
CTGCTGTCATTATGCAGGGA GTCA ||||||| ||| |||||| ||||||
ATTG GTTAAGG TAT CTGTCG CAACAG G
GACG TA TCA GT

GAM705 GTCGGCCCGGCGCCGGGACG 17872 GCCGCGGACG 17873 CCGGGA A -- GA
CGAGTCGCCGCTCGAGGGGA CCGGGCCGAT GTCGGCCCGGCG CGCG GTCGCC GCTC G
GCGCGGCGGCCGCGGACGCC |||||||||||| |||| |||||| ||||
GGGCCGAT TAGCCGGGCCGC GCGC CGGCGG CGAG /
AG---- - CG GG

GAM706 CCGAGACTCCGGCGGACGAG 17903 TGGCCCGGGC 17904 AC- G G A C TC - - G
AGCCTCCGTCTCCCTCGCGA GCTCCGTCGG CCGAG TCC GC GACG GAGC TCCG TC CC TC
C
GGTGGTGGCCCGGGCGCTCC CGGG ||||| ||| || |||| |||| |||| || || ||
GTCGGCGGGAACCCTCGG GGCTC AGG CG CTGC CTCG GGGC GG GG GG G
CCA G G - C CC T T A

GAM707 TCTCCTCTGGTGTTTTTCCA 17922 TCACGGGGCC 17923 TT ATGG-- G - --- AA
AAAATCTAGA C A
TGGTTGTCTCCTCATGAACC ATACAGAGGG TTTCC TT TCTCC TC ATG CCCG
TGAGG TCGCG T
CGAAAATCTAGATGAGGCTC AGAG ||||| || ||||| || ||| |||| ||||| |||||
GCGATTCGCGACCTCACGGG AAAGG GA AGAGG AG TAC GGGC ACTCC
AGCGC /
GCCATACAGAGGGAGAGAGT T- GCGAGT G G ACA CG ---------- - T
GAGCGGGAAATAACGGGGGG
AGA
GAM708 CGAGACCCGGAGATTTTCGG 17953 ACCCGGAGAT 17954 GA A- T AT T A
GATCTGACCATGTGGGCACA TTTCGGGATC CGA CCCGGAGATTTTCGGG TC GACC G GGGC
C
GCCCCGGTCCGAGACTTGGA TGAC ||| |||||||||||||| || |||| | ||||
GATTTTCGGGATCG GCT GGGCTTTTAGAGGTTC AG CTGG C CCCG /
A- AG C -- - A

GAM709 GCCCGCCCGCGACGAGGGTC 17971 TGAGATGCCG 17972 - A AGG AT---- GAA
G

TCATTAGCATCGCGGGCGGA CGCGGGCGGA GC CCGCCCGCG CG GTCTCATTAGC
CGCGGGCG GC G
AGCGGAAGCCGCCCGCGCCG GC || ||||||||| || |||||||||| |||||||| ||
GGCGCTAATGAGATGCCGCG CG GGCGGGCGC GC TAGAGTAATCG GCGCCCGC
CG A
CGGGCGGAGC A - CG- CGGGCC --- A

GAM710 ATTACAGCTTAACAACCCTA 18028 CACACTGTAA 18029 ACA TAG ACC-------
T TT
GAAAGTTACCCCATTCTTTA AGAGTGGCAT ACCC AAAGTT
CCATTCTTTACAGTGTGAAATCATGTG GA A
CAGTGTGAAATCATGTGTGA AATT |||| |||||| |||||||||||||||||||||||| ||
TTAGTTCTGCATGATTTCAC TGGG TTTCAA
GGTGAGAAATGTCACACTTTAGTACGT CT /
ACTGTAAAGAGTGGCATAAT GGC TA- AAATTAATAC - TG
TAAAAACTTTATGGGTCGGT
AATCTGTAAT
GAM711 GGGGAATAATATGTGGGGGG 18047 TGGAAGAGGG 18048 AAT - GG GG TG A GG GA A
C G A AA
GGATGTGGAAGAGGGAGGGA AGGGAGGGAG ATG TGG G GATG GA GA GAGG GGG
GAGAG GAGAGA AG GC C
GGGAGAGAGCGAGAGAGAGA AGAG ||| ||| | |||| || || |||| ||| ||||| |||||| || ||
GCAACCCGCACTTCTTTTTT TAC ACT C CTAC CT CT CTTC CTC TTTTT TTTTCT TC
CG /
TTTTACTCGACTTCATCATC --- T A- TA TA A A- AG A T - A CC
ATCATCATCATCATCATCAT
CTCC
GAM712 GCTGTGGCCCCCTTCGCGAT 18533 TGTGGCCCCC 18534 T CC- ATGCCGCC-- C T
AGCC T
GCCGCCGCTGCCGTCCCGGT TTCGCGATGC G GGCC CTTCGCG GCTG CGTCCCGGTC
CCGCCGCGC GG G
CTCCGCCGCGCAGCCGGTGT CGCC | |||| ||||||| |||| |||||||||| ||||||||| ||
GCCCCTGGTGCGGCGGCGAC C CCGG GGAGCGC CGGC GCAGGGCCAG
GGCGGCGTG CC T
CGGGACGCCGGCCCTTTATG - CAA GTGTATTTCC C C GTCC G
TGCGCGAGGAACGGCCCGC

GAM713 CGCGGCTCGATCCGGGTCCT 18557 TCCCCGGGTT 18558 ------ TC- CG- A TC ---
CC
CCGCGGTCGAGACTCTCGGG CGACACCCGG GCGGCT CGATCCGGG CTCCG GTCGAG
CTC GGGA CGCGC G
ACGCGCCCGATCGCGCGAGC AGAG |||||| ||||||||| ||||| |||||| ||| |||| |||||
TCCCCGGGTTCGACACCCGG CGCCGG GCTAGGCCC GAGGC CAGCTT GGG
CCCT GCGCG A
AGAGTCCCGGATCGCGAACC CCAAGC TGA CCA - C- CGA CT
GGCCGCG

GAM714 TCACCTTCCCCGTCATCTCT 18576 AAGCCCTCGG 18577 TT TCATCTCTACCA C- TA
CAAC

ACCAAGCCCTCGGTAGTCAG TAGTCAGCAA TCACC CCCCG AGCC TCGG GTCAG C
CAACCATCACCTGACGCCCG CCAT ||||| ||||| |||| |||| |||||
AACGGCTCTTCTTCCACCCG AGTGG GGGGC TCGG AGCC CAGTC A
GGGCTGGTGA TC CCACCTTCTTC- CA CG CACT

GAM715 TGTTCTTCCTCTGCCTCTAC 18594 CCTCTGCCTC 18595 TCC- ACGTCTACA CCACC TT
GTCTACAGCCCCACCTTCTT TACGTCTACA TGTTCT TCTGCCTCT GCC TTC C
CTTCGAACACCGGCGGAGGC GCCC |||||| ||||||||| ||| |||
AGATCTTGGAGCA ACGAGG AGACGGAGG CGG AAG T
TTCT --------- CCAC- CT

GAM716 GGCAGGAATAAACCGTACCG 18729 GAACAGAGGT 18730 TAA --- A CC TCTCTTA
ACCAGTCTCTTAAAAACCCT CTCTTTCTGC GGCAGGAA ACC GT CCGA AG A
CTCCTCGGAACAGAGGTCTC C |||||||| ||| || |||| ||
TTTCTGCC CCGTCTTT TGG CA GGCT TC /
CTC AGA A CC TCCCAAA

GAM717 GGCAGTGGGTCAGAAGTGTA 18841 TTGGGAACTC 18842 GG-- GA TA-- A G
TTTATAATAGCAATATTGGG TCACTATGGC GGCAGT GTCA AGTG TTT TAATA C
AACTCTCACTATGGCAGGAA AGGA |||||| |||| |||| ||| |||||
CTGCT TCGTCA CGGT TCAC AAG GTTAT A
AGGA A- TCTC G A

GAM718 CTGATTTGGATACTAATGTT 18863 TAATGTTTCA 18864 GGATA - A T T
TCAATTATGCCTTTATTGGG ATTATGCCTT CTGATTT CTA ATGTTTCA TTA GCCTT A
GTTTGGGTGAAACATCTAGA TATT ||||||| ||| |||||||| ||| |||||
GAATTAG GATTAAG GAT TACAAAGT GGT TGGGG T
A---- C G T T

GAM719 GGCCCCCTCCCGAGCTGGGG 18876 CGGCCCCCTC 18877 -- CC CT C ATCCC
CCCGGATCCCCGACCTCCCC CCGAGCTGGG GGCCCC CTC GAG GGGGCC GG C
GGCCCCCTCCCGAGCTGGGG GCC |||||| ||| ||| |||||| ||
CC CCGGGG GAG CTC CCCCGG CC G
TC CC -- C CTCCA

GAM720 GCCCGTCTTCAACCTGGTGC 19130 CCCCTGAAAA 19131 - TC AC T --------- CTT
TGGACTTTGACCTCCCCCTG AGCCCGGCCT GC CCG TTCA CTGG GCT GGA T
AAAAAGCCCGGCCTGAGCCT GAGC || ||| |||| |||| ||| |||
GGAGC CG GGT GAGT GGCC CGA CCT G
A CC CC - AAAAGTCCC CCA

GAM721 CCCGGCCCCCTCCCGAGCTG 19217 CCCGAGCTGG 19218 C -- CC CT C ATCCC
GGGCCCGGATCCCCGACCTC GGCCCGG CC GGCCCC CTC GAG GGGGCC GG C

CCCGGCCCCCTCCCGAGCTG || |||||| ||| ||| |||||| ||
GGGCCCGG GG CCGGGG GAG CTC CCCCGG CC G
C TC CC -- C CTCCA

GAM722 CGACCTTCCCGGCCCCCTCC 19339 TGGGGCCCGG 19340 ACCT- C -- CC CT C TCCCCC TT
CGAGCTGGGGCCCGGATCCC ATCCCCCCGG CG TCC GGCCCC CTC GAG GGGGCC GGA CGG C
CCCGGTTCCCCCGACCTTCC TTCC || ||| |||||| ||| ||| |||||| ||| ||| CGGCCCCCTCCCGAGCTGGG GC AGG CCGGGG GAG CTC CCCCGG CCT GCC /
GCCCGGATCCCCCG CCCCT C TC CC -- C TCCA-- CC

GAM723 CGAGCTGGGGCCCGGATCCC 19363 TCCCCGGCCC 19364 C TCCCCCGACCTC C -- CC CT C TTCCCC
CCGACCTCCCCGGCCCCCTC CCTCCCGAGC GGGGCC GGA CC GGCCCC CTC GAG GGGGCC GG C
CCGAGCTGGGGCCCGGTTCC TGGG |||||| ||| || |||||| ||| ||| |||||| ||
CCCGACCTCCCCGGCCCCCT TCCCGG CCT GG CCGGGG GAG CTC CCCCGG CC /
CCCGAGCTGGGGCCCGGTTC C TCCACCCCCTT- C TC CC -- C CTCCAG
CCCCACCTTCCCGGCCCTCG
CCCG

GAM724 GCTGTGCGGCACGGACGGCG 19511 TGACGTGCTG 19512 G CAC- A G - C A
ACGCGGCTGAGATACTCACT ACCAACACTG GCTGT CGG GG CGGC ACG CGG TGAG T
GACGTGCTGACCAACACTGA ACAG ||||| ||| || |||| ||| ||| ||||
CAGC CGACA GTC CC GTCG TGC GTC ACTC /
- ACAA A - A - A

GAM725 CGGTCAACACCTTCTCTGAC 19528 TGGCTGGGGC 19529 TCAAC T GA T CA TT
CTCGCGGGCATGTTTGGCAC GGGTCCCCG CGG ACCT CTCT CC CGCGGG TG T
TTCCGCGTGGCTGGGGCGGG ||| |||| |||| || |||||| ||
TCCCCG GCC TGGG GGGG GG GCGCCT AC /
CC--- C TC T TC GG

GAM726 ATAATCTATATTATTATTTT 19707 TCTATATTAT 19708 TCT- TTTTCT- AC
CTATTTGACTTGCTAAATTT TATTTTCTAT ATAA ATATTATTA ATTTG T
ACAATTGATGATATTTTTTT TTGA |||| |||||||| |||||
AT TATT TATAGTAGT TAAAT T
TTTT TAACATT CG

GAM727 TCAAAGGTCAAGCCGGTAGC 19718 AAGGTCAAGC 19719 AA AAG ------- TC
GGCGTTCCCTACGCTGCTTT CGGTAGCGGC TCA GGTC CCGGT AGCGGCGT C
CTCAGGCCGGAAGACCAATG GTTC ||| |||| ||||| ||||||||
A AGT CCAG GGCCG TCGTCGCA /
AA AA- GACTCTT TC

GAM728 TGTGGCCAGGATGCTCTTCC 19724 GGAGCTCCTC 19725 --------- T CGAGACC
GAGACCAAAATGAAGAGGAG CAACACATGG TGTGGCCA GGA GCTCTTC A
CTCCTCCAACACATGGCCAT CCAT |||||||| ||| ||||||| A ATACCGGT CCT CGAGGAG /
ACACAACCT - AAGTAAA

GAM729 GCGTCTGTATTAAATATTTC 19750 TCTAAATTTT 19751 GTATTAA TC TT T A TTTTTA- ACT
TAAATTTTTAGGTAATAATA TAGGTAATAA CGTCT ATATT TAAATTT AGG AAT ATATAT ATTGTA T
TATTTTTTAATTGTAACTTA TATA ||||| ||||| ||||||| ||| ||| |||||| |||||| TCTATAATACTATTTATATG GTAGA TATAA ATTTAAA TTC TTA TGTATA TAATAT /
TAATTCTTTTAAATTTACTA AATTTC- TC TT - A TTTATCA CTA
ATATCTTTAAAGATGT

GAM730 ACCTCTCCAGGTATACAGAA 19758 CCTCAACGAA 19759 - AG TATACAGAA C A T
GAGCGGGAGTTTTAACACCT CTCTCGGATG ACCTC TCC G GAG GGG GT T
CCTCAACGAACTCTCGGATG AGGT ||||| ||| | ||| ||| || AGGT TGGAG AGG C CTC TCC CA T T CT TCAAGCAA- C A A

GAM731 TGGGGGTTGAGTACTTGGGA 19770 TAAGGAAAAC 19771 TTGA A ACCC CA G
CCCTCCTTATCCAAGTGAAA CCAAGACCCT TGGGGG GT CTTGGG TCCTTATC AGT A
ATTAGATAAGGAAAACCCAA CCA |||||| || |||||| |||||||| ||| GACCCTCCA ACCTCC CA GAACCC AGGAATAG TTA A
---- - AAA- A- A

GAM732 CCCGGTGATTCAGGACTGCC 19842 TCGTCGCAGT 19843 GATTCA CCCTATT GAA
CCTATTTGACATGAAGATGA CCACCGGG CCCGGT GGACTGC TGACAT G
ATGTCGTCGCAGTCCACCGG |||||| ||||||| |||||| G GGGCCA CCTGACG GCTGTA A
------ CT----- AGT

GAM733 TATAGATATTTACGGAGTAT 19864 TATTTGGTAC 19865 G ---- TGAA TAC
ATGAACTGTATACCGATTTA GTAAGTATGT TATA ATATTTACG GAGTATA CTGTA C
CAGAATTTGTATTTGGTACG ATA |||| ||||||||| ||||||| ||||| TAAGTATGTATA ATAT TATGAATGC TTTATGT GACAT G
G ATGG TTAA TTA

GAM734 GTGATATTGTGGGGTCGTGA 19877 TTGTGGGGTC 19878 TT--- TC T - TG TG
TGATATTGACTGTCTGTTGG GTGATGATAT GTGATA GTGGGG GTGA GAT AT AC T
TGATTCTCACCCTCATTGGC TGAC |||||| |||||| |||| ||| || ||

TTATTAT TATTAT TACTCC CACT TTA TG TG /
TCGGT -- C G GT TC

GAM735 GAGGAGCTGCCGGTTGCCAT 19881 CAGCAGGCCT 19882 ------ G TTCAAGCT
TTTTCAAGCTGCTAAACCAC AAGAAGCTCC GAGGAGCT GCC GTTGCCATTT G
GAGTGGCAGCAGGCCTAAGA TC |||||||| ||| ||||||||||
AGCTCCTC CTCCTCGA CGG CGACGGTGAG C
AGAATC A CACCAAAT

GAM736 TGTTAGCCAACAACGACATC 20056 TAGCCAACAA 20057 A CAACA C---- T ACC A
CGTGTACCAGAAATCTTAGC CGACATCCGT TGTT GC ACGA ATCCG GT AG A
TTGGATAATCATCGTAGCAG GTAC |||| || |||| ||||| || ||
ACA ACAG CG TGCT TAGGT CG TC A
A A---- ACTAA T AT- T

GAM737 TCTCTTCGAAGAACCCAGAA 20065 TCGAAGAACC 20066 T ACCCA-- TCA AAATA
TCAGTCAAATAACAGTGGAC CAGAATCAGT TC CTTCGAAGA GAA GTC A
GACTTCAAACTCCTTTTCGA CAAA || |||||||| ||| |||
AGGA AG GAAGCTTTT CTT CAG /
- CCTCAAA CAG GTGAC

GAM738 CCCGTGGGGGGTCTTAGTGG 20082 TAGCACCGCT 20083 T G TCT - AC A A
AAGTGACGTGCTGTGAATAC ATCCACTATG CCCG GG GGG TAGTGGA AGTG GTGCTGTG AT
C
AGGTCCATAGCACCGCTATC TCTC |||| || ||| ||||||| |||| |||||||| ||
CACTATGTCTCGCCCGGG GGGC CC CTC ATCACCT TCGC CACGATAC TG A
- G TGT A -- C G

GAM739 GTGTGGAGTCTGTTGAGAAT 20099 GAGAATGCCA 20100 GT- T A-- - T TAGTC A A
GCCATGCTATAGTCATAGGA TGCTATAGTC GTGTGGA CTGT GAGA TGC CA GCTA
ATAGG TTCA A
TTCAAAATTGAACTTGTTTG ATAG ||||||| |||| |||| ||| || |||| ||||| ||||
TTAGTTGTGTAAAATCTTTA CATACTT GATA TTCT ATG GT TGAT TGTTC AAGT A
TAGTTATTCATAC ATT T AAA T - TGTT- - T

GAM740 TGTGCCGCTTGGAGGGAAAC 20108 TCAGTGGTTT 20109 CCG TGG T C AG TT
ATGACCACCTGAAGTCTGTT TGTTTCCTTG TGTG CT AGGGAAACA GACCAC TGA TCTG A
AACCAGGTCAGTGGTTTTGT ATAG |||| || ||||||||| |||||| ||| ||||
TTCCTTGATAGAGACACA ACAC GA TTCCTTTGT TTGGTG ACT GGAC /
AGA TAG T - -- CA

GAM741 TTTGATCGGTGTAGATTTTG 20121 GATTTTGTTG 20122 -- G TG-- T T GTG
TTGTATTTGGTTGAATTCTG TATTTGGTTG TTTGA TCG TGTAGATTTTGT TAT TGG
TGAATTCTG T

GTGTCGAATAGAATTTATCT AATT ||||| ||| |||||||||||| ||| ||| |||||||||
GTATGGTCCGCAAAGTCTAT GGACT GGC GTATCTGAAACG GTA GTC ATTTAAGAT C
GGCGGGTTCAGG TG G CCTG T T AAG

GAM742 CTTTAGTGGGAACTAGTGGG 20128 TACCCCTATC 20129 TA A A GTGCT T
AGTGCTGTGCCTCGGGTACC CTATAGGTCC CTT GTGGGA CT GTGGGA GTGCC C
CCTATCCTATAGGTCCTACC TACC ||| |||||| || |||||| |||||
GGAG GAG CATCCT GG TATCCT CATGG /
GC - A ATCCC G

GAM743 AGGCATTGTTAACCTTTGGT 20158 AACCTTTGGT 20159 TT TAA GA A - T
TAAAT
GGAACCTAGTGTTAGTGTTG GGAACCTAGT AGGCA GT CCTTTGGTG ACCT GTG TTAGTG
TGTGCTG A
TGCTGTAAATAAGTGTCCAG GTTA ||||| || |||||||| |||| ||| |||||| |||||||
CGCACCACTAGTCACCAGGT TCCGT CA GGAGGCCAC TGGA CAC GATCAC
ACGCGAC A
GTCACCGGAGGCTACTTGCC T- TC- TG C T C CTGTG
T

GAM744 GGGGCTCTGTAACATTTGGT 20171 ATGCTGCTGG 20172 TCT ACA G A - - --
AA
GGGACCTGATGCTGCTGGTG TGTGCTGTAA GGGGC GTA TTTGGTGG ACCTG TGC TGC
TGGTGTGCT GTA T
TGCTGTAAATAAGTGCCTAG ATAA ||||| ||| |||||||| ||||| ||| ||| ||||||||| |||
CACATCACGTAGGCACCAGG CTCCG CAT GGACCACT TGGAC ACG ATG
ACTACACGA CGT A
TGTCACCAGGGCTACTTGCC TT- CG- G C G C TC GA
TC

GAM745 GGCAGGTGGAGTGGGACACA 20204 CTGGTCCCTA 20205 A T-- ACAGT A A
GTTAGAGAACATTAGTCCTC TCTCCACCCG GGC GGTGGAG GGGAC TAGAG AC T
TGGTCCCTATCTCCACCCGC CC ||| ||||||| ||||| ||||| ||
C CCG CCACCTC CCCTG GTCTC TG T
C TAT ----- C A

GAM746 CAAGCCTGCTGCTCAATTGT 20295 TGTATATATT 20296 AGCC TCAATT C C TG TG
ATATATTCCTCTTGTGTTGT CCTCTTGTGT CA TGCTGC GTATATATT CT TTG T T
AGTGTGCAATAGTAGTATGT TGTA || |||||| ||||||||| || ||| |
ATCCTGTTGTAGTACGTG GT ATGATG TATGTATGA GA AAC G A
GC-- TTGTCC T T GT TG

GAM747 GTCGTGCAGTCCCAGCGAGC 20306 TCACAAAACG 20307 - AGT A A CA T CAG-- A G
GCAGCGGTACCAGGTAACGC TCTGCACCGC GT CGTGC CCC GCG GCG GCGG AC GT
ACGCG A
GGACACGTGTCACAAAACGT CTGT || ||||| ||| ||| ||| |||| || || |||||

CTGCACCGCCTGTCGGGCCA CA GCACG GGG TGT CGC CGTC TG CA TGTGC C
GCACGTAC T ACC C C CA - CAAAA C A

GAM748 GGTAAGTTAACAGAGTTTTT 20313 TAAGTTAACA 20314 A G TTT AA TG
TATAAAAATCTGGTATGATT GAGTTTTTTA GGT AGTTAACA AGT TTATA AATC G
CTATAAGCTTGTTAACTAGC TAAA ||| |||||||| ||| ||||| ||||
T TCG TCAATTGT TCG AATAT TTAG T
A - --- C- TA

GAM749 ATTTAGTTTCACACTCCACT 20318 TGGGGTCGAA 20319 CAC C AAGTG
AGCCAAGTGAGTTCCGGGTT GACTAGAT ATTTAGTTT ACTCCA TAGCC A
GTTGGGGTCGAAGACTAGAT ||||||||| |||||| |||||
TAGATCAGA TGGGGT GTTGG G
AGC T GCCTT

GAM750 GCCGCAGGGCACCTGGCCGG 20334 TATCAGGGCC 20335 ----- A CC T GCC
CGTGCCGCCGAAGGGCCGCT TCGAGCTGCG GCCGCAG GGC CCTGG GGCG GCC G
ATCAGGGCCTCGAGCTGCGG GC ||||||| ||| ||||| |||| |||
C CGGCGTC CCG GGACT TCGC CGG /
GAGCT - A- - GAA

GAM751 GCTGCGGCTGGTGCTGCAGC 20362 CTGCAGCTGC 20363 TG C------ AAA CGA CT
- AAG
TGCTGCTGGAAAACCGACGG TGCTGGAAAA CGGC GTGCTGCAGCTG TGCTGG AC
CGGCGT GCGCCG C C
CGTCTGCGCCGCAAGCTGCG CCGA |||| |||||||||||| |||||| || |||||| |||||| |
TCGGCGCCTGCGCCGGATGT GCCG CGCGACGTCGAC ACGGCC TG GCCGCG
CGCGGC G /
ACCGGCACTTCGTCCAGCTG -- CTGCTTC A-- TAG TC T CGT
CAGCGCGCCGCGGC

GAM752 TTCTAAGTGTGCAGGTGTGA 20487 CACACTTTTG 20488 A- C AA------- G
GTAACTTTGAAAAAAGACCC CATTGGGGAA TTCT AGTGTG AGGTGTGAGT CTTT A
GCAAAACTCACACTTTTGCA |||| |||||| |||||||||| ||||
TTGGGGAA AAGG TTACGT TTCACACTCA GAAA A
GG T AAACGCCCA A

GAM753 GTAAATATATGTAAACTGTG 20684 TACAGTGTGG 20685 TAT AA---- GT AC A
TACAGTGCGGAACGTTAAGG AGACCTTTAT GTAAATA GT ACTGTGTACA GCGGA GTT A
GACATCTGTTGTATACAGTG TTGC ||||||| || |||||||||| ||||| |||
TGGAGACCTTTATTTGC CGTTTAT CA TGACATATGT TGTCT CAG G
TTC GAGGTG -- A- G

GAM754 GCGGCCGTCGAGATGACGCT 20709 CCAGAGCGGC 20710 -- GA A GCA-- AGG

CGCACTTGAGGCGACACAGG AGGTCGATGA GCGGC CGTCGA TG CGCTC CTTG C
CACCAGAGCGGCAGGTCGAT CGCT ||||| |||||| || ||||| ||||
GACGCTGC CGTCG GTAGCT AC GCGAG GGAC G
CA GG G ACCAC ACA

GAM755 TACCTTACCCATTGTACCTA 20724 ACCCATTGTA 20725 T--- ---- AC A
TATGTATTGTATACACAGTG CCTATATGTA TACCT ACCCAT TGT CTATATGTATTGT T
TATGTAGACACATGTAGTGG TTGT ||||| |||||| ||| ||||||||||||
GTTTGTGGGTG GTGGG TGGGTG ACA GATGTATGTGACA A
TGTT ATGT CA C

GAM756 GGAGTATACGTAGGCTAGGA 20735 TATACGTAGG 20736 A A C A AG- A A TA
AGACAAAGTAAGGCTTGGTC CTAGGAAGAC GG GT TA GT GGCT GA GAC AAG A
ATCACCAGCCGCTTAAACAC AAAG || || || || |||| || ||| |||
C CC CA AT CG CCGA CT CTG TTC /
A A T - CCA A G GG

GAM757 GGCGGTGGGTCTCGGGCCAA 20746 GCGCTCCGAA 20747 G- C-- CCAAAC - T
ACGCCGTCGTAGACGACGCG AAACGACGCC GGCGGTG GT TCGGG GC CGTCG A
CTCCGAAAAACGACGCCGCC GCC ||||||| || ||||| || |||||
CCGCCGC CA AGCCT CG GCAGC G
AG AAA ------ C A

GAM758 GCACACCAGGCTCTTGGCCC 20790 TTTGCTGAAC 20791 C CTCT CAC - TG
ACCAGAGACACTGTCACGTG GGCCACTCTA GCACAC AGG TGGCC CAG AGACAC T
TTTGCTGAACGGCCACTCTA GTGT |||||| ||| ||||| ||| ||||||
GTGTGT TGTGTG TCT ACCGG GTC TTTGTG C
A C--- CAA G CA

GAM759 GCCCGTACCACTGCCATCGC 20796 CGATGTGTGT 20797 - AC CCA GCC ATACATGCGC
G TAC
CCTTTGGATACATGCGCACA AAAACACCGG GCCCGT ACC TG TC CTTTGG
ACACACAT GCA C
CACATGGCATACCCATTGCG AGAC |||||| ||| || || |||||| |||||||| |||
ATGTGTGTAAAACACCGGAG CGGGCG TGG AC AG GAGGCC TGTGTGTA CGT
/
ACAGAACCATGGGTAGCGGG A GT CA- ACA ACAAAA---- G TAC
C

GAM760 GGTAGCGGGCAGTCCGACGA 20823 AGACAAGGGT 20824 ------ G GACGACAC CA
CACGGCCACCAGCCAGACAA GCCATTCTGC GGTAGCG GGCA TCC GGC C
GGGTGCCATTCTGCGTTGCC GTTG ||||||| |||| ||| |||
CCGTTGC CCGT GGG CCG /
GTCTTA - AACAGA-- AC

GAM761 TGCCTGTCTCTCCATGTTAA 20832 AAGAGCCTTG 20833 TCTCT-- ------- G CGC
GGTTGTTGACGCTGGCTTCA ATACGATCTG TGCCTG CCAT GTTAAGGTT TTGA T
AGAGCCTTGATACGATCTGT TGGC |||||| |||| ||||||||| ||||
GGCCCTCTTCAGGCA ACGGAC GGTG TAGTTCCGA AACT G
TTCTCCC TCTAGCA G TCG

GAM762 CGGCAGTTACCTGTTGTATC 20857 TACCTGTTGT 20858 A- - TC A -- ----------
CT
GCAAGGCTCACGTGGAGCTG ATCGCAAGGC C GT TACCTGTTGTA GCA GGCT CACGTG
GAG G
TCACTCTCCAGCAACAAGGT TCAC | || |||||||||| ||| |||| |||||| |||
GCAACACGTGGAAGCCGTGC G CA GTGGACAGCGT CGT CCGA GTGCAC
CTC T
TGCGACAGGTGTACACGCCG CA T -- G AG AACGTGGAACAACGACCT AC

GAM763 GCCACACGTCCAACTGCTTC 20869 ACGGACAAAA 20870 A --- CTTCCCGAA T TTA
CCGAACGTCTCGTTATATAG CCAGTTCCCG GCC CACGTCC AACTG CGTC CG T
TGCGACGGACAAAACCAGTT GACG ||| ||||||| ||||| |||| ||
CCCGGACGTGGGC CGG GTGCAGG TTGAC GCAG GT A
- CCC CAAAACAG- C GAT

GAM764 GTTTGAGTGTGGTAGCGCTG 20886 TGAGTGTGGT 20887 TT - G - T GAG G AACCCC
G
TGTGAGTTGGCGGTGGAACC AGCGCTGTGT GT GAG TGT GTAG CGCTG GT TTGGC GTGG
CTCGTG T
CCCTCGTGGTGACACGAGCC GAGT || ||| ||| |||| ||||| || ||||| |||| ||||||
CCCGTGGCCAAAAGCCCAGT CA CTC ACG CATT GTGAC CG AACCG TGCC
GAGCAC G
GTTTACAGCACCTCTCAC CT C A T C AA- G CCC--- A

GAM765 AAGAAGATTACTCTTGATGC 20912 AGACCCGATT 20913 T C TG TG---------- TCA -
CAC A
TTGGCTCTCAGAAAGAATGG CTTTTGAGTC TA TCT A CTTGGCTC GAAAGAAT GG
CTCAA G
CACCTCAAAGTTTTGAGACC GAGA || ||| | |||||||| |||||||| || |||||
CGATTCTTTTGAGTCGAGAA GT AGA T GAGCTGAG TTTTCTTA CC GAGTT
T
CCTTACCCCCAACCCTTGAG C T GT CCCAACCCCCATTCCAA --- G CA- T
ATTGCTTTTCTT

GAM766 CGGGAGGACCGCCGACGCCG 20920 TACCGTAGCA 20921 ACG G C- AA- CTC CAGA-
G TG A AGC
TGTCCGGAAGCCTCGTCGGA GGAGCGGCGC GCCG CC TGT CGG GC GTCGGAG GG
CCAGG TTT TAT A
GCAGAGGGCCAGGTGTTTAT CTCC |||| || ||| ||| || ||||||| || ||||| ||| |||

ATAGCAGCAGATAGAGATCC CGGC GG ACG GCC CG CAGCTTC CC GGTTC AGA ATA G
TTGGACCGAAACCTTCGACC GA- - AT ATG CC- CAAAG A CT G GAC
CGCGTACCGTAGCAGGAGCG
GCGCCTCCCG
GAM767 TCGCTGAACAAATTGTATCC 20935 CAGGACCCCG 20936 C A- TA C- - CC --- - G
TCTCAGGGCCTCCTCCGCGT CTGAGGAAGA TCGCTGAA AA TTG TC TCTCAG GG TCCT CC GCGTC T
CGTTGATGTAGGCACAGGAC CGCG |||||||| || ||| || |||||| || |||| || |||||
CCCGCTGAGGAAGACGCGAG AGCGATTT TT AGC AG GGAGTC CC AGGA GG TGTAG /
GTTCTTTAGCGA C GG GC AA G CC CAC A T

GAM768 GCGAGGCACGTCTCACGGTG 20950 CCCGAGCTTT 20951 C-- ---------- AC TT
TTTTTCACCCCGAGCTTTAA AATATATATA GCGAGG ACGT CTC GGTG T
TATATATAGAAACACGTTTA GAAA |||||| |||| ||| ||||
TTTCGC CGCTTT TGCA GAG CCAC /
ATT CAAAGATATATATAATTTC CC TT

GAM769 AGTGGAATGTTCTACCACAA 20969 CCACCCAGAA 20970 GAATG CCACAAGGA AT CC CCA
GGATGGGTATGTAGCCCTGC GATTATAGAA AGTG TTCTA TGGGT GTAG CTG T
CATTTATCAGACTACCACCC AACA |||| ||||| ||||| |||| |||
AGAAGATTATAGAAAACATT TTAC AAGAT ACCCA CATC GAC T
AA--- ATTAGAAG- C- A- TAT

GAM770 CTGCAGCAGTATATTGGTGT 21074 TTTCCAGGAA 21075 AGCA AT GTGAA G AAG
GAAGGAAGGACTAAGTCAAA CCAATCAACA CTGC GT ATTGGT GGAAG ACT T
GGTATTTCCAGGAACCAATC GGCG |||| || |||||| ||||| |||
AACAGGCGG GGCG CA TAACCA CCTTT TGG C
GA-- AC AGGA- A AAA

GAM771 TCTATGCATATGCATGAGAG 21094 TTCATGAGCC 21095 A TT A T CC TCATAAA
ATTCATGCATATGAATGAGA TCTCATGCAT TATGCATATGCATG GAGA CATGCATATG ATGAGAG CTCAT ATAT C
GTCTCATCCATATTCATAAA ATGC |||||||||||||| |||| |||||||||| ||||||| ||||| ||||
CCTCATCCATATTCATGAGC GTACGTATACGTAC TTTT GTACGTATAC TACTCTC GAGTA TATA /
CTCTCATGCATATGCATGTT A T- G C CT CCTACTC
TTTACATGCATATGCATGGA

GAM772 ACTTACATAGTGACAACGGG 21106 TACATAGTGA 21107 TGACAACGGG --- TT
CCGTGCTTTACTGCACACAG CAACGGGCCG ACTTACATAG CC GTGC T
GATAGAAAATCTATGTAAGT TGCT |||||||||| || ||||
TGAATGTATC GG CACG A

TAAAAGATA- ACA TC

GAM773 CATTCGGATAGGTTAATGGT 21115 TAGGTTAATG 21116 -------- AATG G GC
TGGGTCGCGCAGACCGGATA GTTGGGTCGC CATTCGGA TAGGTT GTT GGTC G
AAGCCTGCAACGTATTCTGA GCAG |||||||| |||||| ||| ||||
GTG GTGAGTCT GTCCGA TAG CCAG /
TATGCAAC AA-- G AC

GAM774 CAACTGCGTTTCAATGCATT 21118 TCAATGCATT 21119 C C AT-- TTCTTT T C C
TTC--- CAA
GAATCTTCTTTACGTAGTCG GAATCTTCTT CTG GTTT AATGC TGAATC ACG AGT GT TCG
TTTCT G
TCTCGTTCTTTCTCAAGGTT TACG ||| |||| ||||| |||||| ||| ||| || ||| |||||
AGAAATTGTATCGAACTGCT GGC CAAG TTACG GCTTGG TGC TCG CA AGC
AAAGA /
CGTTGATCTGGTTCGTCAGG A T GACT TCTAGT - T - TATGTT TTG
CATTTGAACACGGTATTTG

GAM775 TCCTCAACAACGTCTGTTAT 21123 TCCGCGAGCT 21124 C AAC T TTAT- - TC--- TG
GCCGCTCACTGTTTTGTTCT TTATCAGCAA TCCT AAC G CTG GC CGC AC T
CCGCGAGCTTTATCAGCAAG GTTT |||| ||| | ||| || ||| ||
TTTAGGA AGGA TTG C GAC CG GCG TG T
T AA- - TATTT A CCTCT TT

GAM776 GCACGTGCTACCGACCAGCG 21128 TATTTAGTAA 21129 ---------- CCG A T
CTTTTAGAGGCGCGGTATTT CTGACATAAC GCACGT GCTA ACC GCGCTT T
AGTAACTGACATAACTTTGC TTTG |||||| |||| ||| ||||||
GTGC CGTGCG TGAT TGG CGCGGA A
TTTCAATACAGTCAA TTA - G

GAM777 GCACCGCAAGCCACGTACAT 21134 GCCACGTACA 21135 - A---- -- A T A A
TGTACCTCAAAAGAGGAATA TTGTACCTCA GCACC GCA GCCA CGT CAT GT CCTC A
TGACGAATGGCCGAGATGCT AAAG ||||| ||| |||| ||| ||| || ||||
GGTGC CGTGG CGT CGGT GCA GTA TA GGAG A
T AGAGC AA - - A A

GAM778 GGCAACCTTGAAGTTCTGAC 21151 TTGAAGTTCT 21152 CTT A - - AACT TG CTCA
GAACTATCTTGCAGCTTGTT GACGAACTAT GGCAAC GA GTTCT GA CG ATCT
CAGCTTGTTT A
TCTCAATTTTAAACGAGCTG CTTG |||||| || ||||| || || |||| ||||||||||
AGATCCGATCAAGAACTCGT CCGTTG CT CAAGA CT GC TAGA GTCGAGCAAA /
TGCC --- - A A C--- -- TTTT

GAM779 GTTCACATGATTCCGGCATC 21156 TCCGGCATCG 21157 ATGAT TC ------- AAAA

GAGTGTTGCAAAATCGAAAG AGTGTTGCAA GTTCAC TCCGGCA GAGT GTTGC T
CAACTTTCTTTGCTCTGTCG AATC |||||| ||||||| |||| ||||
GATGGTGAAT TAAGTG AGGCTGT CTCG CAACG C
GT--- -- TTTCTTT AAAG

GAM780 CGAGAGGAAACAAACTGTCT 21166 GAGGAAACAA 21167 - CAA TT---------- C
TGGAACAATTTCCTTGAAGA ACTGTCTTGG CGAGAG GAAA ACTGTC GGAA A
TTTTAAAACGGCAGTTTTCT AACA |||||| |||| |||||| |||
CTCTCG GCTCTC CTTT TGACGG CCTT A
T --- CAAAATTTTAGAAGTT T

GAM781 GAGTGGCAGCTACAACACCT 21232 TACAACACCT 21233 C- TA- A C CTCG A
CCTCGTCTAACTCTAGAATT CCTCGTCTAA GAGTGG AGC CA CAC TC TCTA C
CGAGTGATGGCCGCTTACCA CTCT |||||| ||| || ||| || ||||
CTC CTCACC TCG GT GTG AG AGAT T
AT CCG A - CTTA C

GAM782 GGTGAGCTCCCCAAGTTTTA 21249 CCCCAAGTTT 21250 ----- GTTTTACT T AAA
CTTCTCTAAACAAAAAGGAT TACTTCTCTA GGTGAGCT CCCCAA TC CT C
GCTCGGATTGGGGCACGAAG AACA |||||||| |||||| || ||
CTCACC CCACTCGA GGGGTT AG GA A
AGCAC AGGCTCGT - AAA

GAM783 CAGGCTAAAACAAAGGAGGC 21291 TGTGAAGGCA 21292 A- AAA--- G GATTT - A GG - AG TCG
GATTTGGGAGGGATAACGGT AAGGTCATCT AC GGA GC GGGAGG GAT AC TTGTTTTC CACC GGGG A
TGTTTTCCACCAGGGGGTCG TCTT || ||| || |||||| ||| || |||||||| |||| ||||
ACCTTTTCTAGGGTGTGAAG TG CCT CG TCTTCT CTA TG AACGGAAG GTGG TCTT C
GCAAAGGTCATCTTCTTCTG AA GAAATA A ----- T C GA T GA TTC
CATCCATAAAGGTAATTGGT
TTG
GAM784 TGCCTGAGAGTAAACATTGA 21308 TGAGAGTAAA 21309 - -- AAACAT A ATAAAAC
CGGATAAAACAAAAATGCCC CATTGACGGA TGCC TGA GAGT TG CGG A
CGCATAACTCTATCATGGCA TAAA |||| ||| |||| || |||
ACGG ACT CTCA AC GCC A
T AT AT---- - CCGTAAA

GAM785 TCTTAACCAAATGTTGGAAG 21331 TGGAAGATCA 21332 T- A AAA TG AA T TA- GCT
ATCATTTTTTTACCTGCTTT TTTTTTTACC TC TA CC TGT G GA CATTTTTT CCT T
AAAGGCCTGAAGGGTGTCGG TGCT || || || ||| | || |||||||| |||
TTGGCAAGGCTATTGA AG AT GG ACG T CT GTGGGAAG GGA /
TT C A-- GT GG - TCC AAT

GAM786 GCAAGCCCATTCTGCCAGTT 21351 TGCCAGTTGG 21352 C AG TG GGAT GCTAG
GGGGATTGGCGGCTAGAAAA GGATTGGCGG GCAAGCCCATT TGCC T G TGGCG A
CCGCGCCATAGCTGGAGGGC CTAG |||||||||| |||| | | |||||
AAAATGGGCTTGC CGTTCGGGTAA ACGG G C ACCGC A
A GA GT GAT- GCCAA

GAM787 GGCTCCCATCCACGTGTAGG 21357 CACGTGTAGG 21358 C A AG--- GAC T
TTTCGACGTCGTAGGTGACA TTTCGACGTC GGCTC CATCC CGTGT GTTTC GTCG A
AAGAGGCGTTCGACGCGAGG GTAG ||||| ||||| ||||| ||||| ||||
ATGAGAGCC CCGAG GTAGG GCGCA CGGAG CAGT G
A A GCTTG AAA G

GAM788 TTGACTTGCAGGAGACGGGT 21360 CAGGAGACGG 21361 TG TG A--- - AAGG-- ATG
AAGGGCCGATGCCAGGCGGC GTAAGGGCCG T ACT C GGAGA CGGGT GCCG C
GATGAAACTTGATTTCCATT ATGC | ||| | ||||| ||||| ||||
GGTGAGTTGG G TGA G CCTTT GTTCA CGGC C
GT GT GTTA A AAGTAG GGA

GAM789 TTCTAACTCTTAACATTTTT 21385 TCGAATAGCA 21386 A- TTAA TT - AAAAT - TATT TTT
ATTTATTTAAAATGATACCT TAAGTTTGAA TTCT ACTC CA TTTAT TTATTT GATACC TTTGT TA T
TTGTTATTTATTTTATTCTA ACGA |||| |||| || ||||| |||||| |||||| ||||| ||
TTTTGCGAACGGTATCGAAT AAGA TGAG GT GAATA GATAAG CTATGG AAGCG AT A
AGCATAAGTTTGAAACGAGT AG CAAA TT C ----- C TTTT CTT
GAAGAA

GAM790 GCGTAGGATTCGCGCAACTT 21389 AACTTTTGCA 21390 AG GCGCA- TT A A CG- GGT
TTGCACCAGGGCGGCGGTAA CCAGGGCGGC GCGT GATTC ACT TGC CC GGG GC A
CAAGCACATCCAGGGCACAG GGTA |||| ||||| ||| ||| || ||| ||
TAATCAAGGGTTTCACGC CGCA TTGGG TGA ACG GG CCT CG A
CT AACTAA C- - A ACA AAC

GAM791 GAAGAAGTTATAGACAAATT 21395 TGATACGATA 21396 GT-- ACAAATTAT AAAACT
ATTCATTCTAAAACTATAAA CTATATGTAT GAAGAA TATAG TCATTCT A
AACAGAATGATACGATACTA TCTT |||||| ||||| |||||||
TATGTATTCTTC CTTCTT ATATC AGTAAGA T
ATGT ATAGCAT-- CAAAAA

GAM792 CTATCGTATGGATAAATATA 21400 TCTAGAATAC 21401 -------- AAA--- TC TACAAAAATATG--- ATCT
TTCTAGAATACAAAAATATG AAAAATATGG GT ATGGAT TATAT TAGAA GTCTA C

GTCTAATCTCGCTACTGGAT TCTA || |||||| ||||| ||||| |||||
AAATCGAAAAATACTTTTTA TA TATCTG ATATA ATTTT TAGGT G
TTATATACATATAGTCTATT AAACAAAT ATATAC TT TCATAAAAAGCTAAA
CATC
AAACAAAATGATAG

GAM793 GTCACTAGAGACAGCTTGGC 21423 ATGGATGGAC 21424 A- CA GC - GCCA TA
TT
GAAGGGGCCAGCCACCATTT TCTTTCACAA GTCACTAG GA GCTTG GAAGGGG CCA
CCATT CAC T
ACACTTTTGGTGATAATGGA GCCT |||||||| || ||||| ||||||| ||| ||||| |||
TGGACTCTTTCACAAGCCTC CGGTGATT CT CGAAC CTTTCTC GGT GGTAA GTG /
GATTAGTGGC AG C- A- A A--- TA GT

GAM794 GTTTAACAATGGGATATAGA 21440 TAGATGACAC 21441 AATG TA CACTAAAGA T
GA
TGACACTAAAGAATACTATT TAAAGAATAC GTTTAAC GGA TAGATGA ATACTAT GT A
GTGAACAACATGGTATGAAT TATT ||||||| ||| ||||||| ||||||| ||
TATCTAACTCCGTTAGAC CAGATTG CCT ATCTATT TATGGTA CA /
---- CA AAG------ - AC

GAM795 GGCGCCGGCGGCCGGCACCG 21444 GGCCGGCACC 21445 - - G A GA--- AA-- TTT
GAAGCAAGCATTTCTAACTG GGAAGCAAGC GGCGCC G GC GCCGGC CCG AGC GCA C
CGCGAGCTGGTAGCGGCGCC ATTT |||||| | || |||||| ||| ||| |||
GGCGGCACGGGCGCC CCGCGG C CG CGGCCG GGC TCG CGT T
G A G C GATGG AGCG CAA

GAM796 GCCCGACCCCCGGGCGCCCC 21448 TGTCCAGGGG 21449 CG C C CAA - G
CAAACTTTGTCCAGATGTCC TCCCCGAGGG GCC ACCC CGGG GCCCC AC TTT T
AGGGGTCCCCGAGGGTGAGG TGAG ||| |||| |||| ||||| || |||
C CGG TGGG GCCC TGGGG TG AGA C
AG A C ACC T C

GAM797 ATGGACATTGTTATGTTATA 21491 TATGTTATAG 21492 TTA--- TAG TTAAT A- TA
GCTTTTAATGGAAATAAAGT CTTTTAATGG ATGGACATTG TGTTA CTT GG AA A
TTGGCCTTCACAAGATTTAA AAAT |||||||||| ||||| ||| || ||
TACAAGATCAATGTCCAT TACCTGTAAC ATAAT GAA CC TT A
TAGAAC TTA CACTT GG TG

GAM798 TCCTTTGCTCAAGCATATAT 21503 AAAGGTACTT 21504 CTC A AACA- ACTTATGAAA
AAAA
AACAAAGGTACTTATGAAAA ATGAAAAGGA TCCTTTG AAGC TATAT AAGGT AGG A
GGAAAAAGCAACCTACTTTA AAAA ||||||| |||| ||||| ||||| |||
CGAGATATAGCTTTTCCAAA AGGAAAC TTCG ATATA TTTCA TCC /
GGA CTT - GAGCA ---------- AACG

GAM799 CGCTGTCGCAGCTCTTTCCC 21635 TCGCAGCTCT 21636 T - -- C TGGC
GGCCTGGCTCTGTTGGCCGT TTCCCGGCCT CGCTG CGCA GCTCTT TC CGGCC T
GACCGAGAGCGTGCGCAGCG GGCT ||||| |||| |||||| || |||||
GCGAC GCGT CGAGAG AG GCCGG C
- G CC T TTGT

GAM800 CTGAGAATACTGAGGATTGG 21658 TGAGGATTGG 21659 GAG TGA T CT--- - TA
GGATGGCTGGCATATACTGA GGATGGCTGG CT AATAC GGAT GGGGATGG GG CA T
CTCTTTTCCATCCCCCATCT CATA || ||||| |||| |||||||| || ||
GTATTGAAG GA TTATG TCTA CCCCTACC TC GT /
AG- --- C TTTTC A CA

GAM801 ATCTGGAAGAAAAATTATAC 21682 TCTGTCATCT 21683 AAGAAAAATT CTG GCAGA-
T AAA
TCTGTCATCTGTATTAGCAG GTATTAGCAG ATCTGG ATACT TCATCTGTATTA ATG GT
T
AATGTGTAAATCAAGCCATG AATG |||||| ||||| |||||||||||| ||| ||
GAATATGGTATAGATGAAGT TAGATC TATGA AGTAGATATGGT TAC CG /
ATTATCCAAACTAGAT AAACCTAT-- --- ATAAGG - AAC

GAM802 TTACAATGTCAAACAAACTA 21701 TACCACTATA 21702 CAA A A AA C CTGCA GGAA
TTATATT--- GA
GGAATCTAAATACTTCCACT TATACACAGA ACT GGA TCT ATA TTCCA TG ATATAT
ATGA T
GCATGGGAAATATATTTATA ATTG ||| ||| ||| ||| ||||| || |||||| ||||
TTATGAGATCATCATTCCTA TGG TCT AGA TAT AAGGT AC TATATA TACT /
CCACTATATATACACAGAAT --- A A AA - TAAG- ACA- TCACCATCCT AC
TGGAATATAAAGAATCTAGG
TCACCTTGTAA
GAM803 ACAGATGAATACTTGGAAAT 21708 AGTTATTTGG 21709 A- AA- -- TG --- - TAA
TGAACCCCTAAAGAATGGGA TTTTATCAAG ACAG TG TACTTG GAAAT A AC CCC A
GTTATTTGGTTTTATCAAGT TACT |||| || |||||| ||||| | || |||
ACTACAGACTGT TGTC AC ATGAAC TTTTG T TG GGG G
AG ATC TA GT TAT A TAA

GAM804 AGTCGCAAGGGCCAAGGCAG 21718 TCGCAAGGGC 21719 C AAGGG C A- TT GC ------
C
AGCTTCTACGCTTGGACCTT CAAGGCAGAG AGT GC CCAAGG AG GC CTAC TTGGA
CCTT A
CACGAAGGAGACTATCCAGA CTTC ||| || |||||| || || |||| ||||| ||||
GTGGCTGCAGCTCCTTGGAG TCA CG GGTTCC TC CG GGTG GACCT GGAA C
AAGCAACT A AAGA- - GA TC A- ATCAGA G

GAM805 AGGTAATTTCATAAAGGACA 21744 AAGGACACTG 21745 AATTT AA-- CACT T T
CTGCTGGAGGTATTTTTGGA CTGGAGGTAT AGGT CATA GGA GCTGGAGGTA TT T
ACTGCCTTTAGTTTTCTGGG TTTT |||| |||| ||| |||||||||| ||
ATATGTAAAACCT TCCA GTAT TCT TGATTTCCGT AA G
AAAT- AGGG TT-- C G

GAM806 ATACAGCAAGACAAATGGGC 21764 TGCCAAGTTT 21765 GCA AAATG AACG G
ATTAAACGTCTGGGCCACCA AGATGTGT ATACA AGAC GGCATTA TCTGG C
GGTGGTGCCAAGTTTAGATG ||||| |||| ||||||| |||||
TGT TGTGT TTTG CCGTGGT GGACC C
AGA AA--- ---- A

GAM807 GTGGTATTCAATGATTTGAA 21800 TCAATGATTT 21801 -------- AGTGAAAGTT T- G
TTGGGAATA
TTTCAGAAGTGAAAGTTACC GAATTTCAGA TT GAATTTCAGA ACCCAG GA
TGTCAGGG T
CAGTGAGTGTCAGGGTTGGG AGTG || |||||||||| |||||| || ||||||||
AATATGTGCAGGTTCTTTGA AG TTTAGAGTCT TGGGTT TT ACAGTTTC /
CAGTTTTTTGGGTTCTGAGA TAAGAACT ---------- TT G TTGGACGTG
TTTTCAAGAATGAATCAAAT
GTCTAC
GAM808 GCCTCTGATCTCATGATACA 21815 ATCATGCCTG 21816 G ATGATA TG A- G C
TTGGAATGAGTTTGCATTCA ATGACATTGG GCCTCT ATCTC CAT G ATGA TTTG A
AGATCATGCCTGATGACATT GGAT |||||| ||||| ||| | |||| ||||
GGGGATGGAGGC CGGAGG TAGGG GTA C TACT GAAC T
- GTTACA GT CG A T

GAM809 CTGCCAATTATGTTCACTGG 21824 TGCCCTTTTC 21825 CAATTATGTTCACT TTT A
GGGGCTTTATCAATATCAAT AAAAAGCAG CTGC GGGGGGC ATCAAT T
TGATGCCCTTTTCAAAAAGC |||| ||||||| ||||||
AG GACG TTTCCCG TAGTTA C
AAAAACT------- --- A

GAM810 TGGACAACTACTTTTTAGCA 21923 TAGCACAAAT 21924 CAAC TTTA ACAA--- ATA TCT
CAAATCCAGATATATCTTCC CCAGATATAT TGGA TACTT GC ATCCAG TA T
TTTAAATTGGGTACCGAAGG CTTC |||| ||||| || |||||| ||
CGCTGAGTATTTCCA ACCT ATGAG CG TGGGTT AT C
TT-- TCG- GAAGCCA AA- TTC

GAM811 TGCCAAGAGGACAGATACCA 21939 AAGGGGAAAG 21940 TAC ATG----- A AG -
CCAAATAAA TTTG
GATGCCATAAAGGGGAAAGA AGTTCCACCA GA CAG CCATA AGGGGAA AGTT CCA
TCCGTT T
GTTCCACCAAATAAATCCGT AATA || ||| ||||| ||||||| |||| ||| ||||||
TTTTGTGGTTTGACGGAGGG CT GTC GGTGT TCTCCTT TCAA GGT AGGCAG
G

GCGTTTTGGCAACTGTTCCT C-- GTATTTTA C G- C TTTGCGGGG TTTG
CTCTGTGGATTTTATGCTGC
TCTGTCCCGCA
GAM812 GGCTTAAATATTTAATGCAA 21977 TTTAATGCAA 21978 TTAAATATT ATG AG TG
TGTAAAAGCTTATGCTTTTA TGTAAAAGCT GGC TAATGCA TAAA CTTA C
AGTCTTTAAGCTGCATTATC TATG ||| ||||||| |||| ||||
TTCCATTGCC CCG ATTACGT ATTT GAAT T
TTACCTTCT CGA CT TT

GAM813 AAACAAGGAATGCATATGGT 21981 AGGAATGCAT 21982 AA- A - AC---- GG -- T
TGCGACACCCGGGTACGTCC ATGGTTGCGA AAAC GGAATGC TA TGGTTGCG ACCCG T
ACG C
GCGTTTGTTCGGGTATACAC CACC |||| ||||||| || |||||||| ||||| | |||
CGCGACCACTGCGCATTCTG TTTG TCTTACG GT ACCAGCGC TGGGC G TGC C
CCGTTT CCG C C CACATA TT TT G

GAM814 GTTTTGGTACCCTTTCTAAT 22006 TACCCTTTCT 22007 TT CC AA CCGA- ---- TT AT
GCGCCGAGGAGCGTTCCGAT AATGCGCCGA GTT GGTAC TTTCT TGCG GG AGCG CCG
A
ACCCGGGCCGTTGAACCCAC GGAG ||| ||||| ||||| |||| || |||| |||
ATCCGCGAGAAACCGTGCCC CGG CCGTG AAAGA GCGC CC TTGC GGC /
GGGC GC CC -- CTACA CAAG CG CC

GAM815 TCCCGTGTACCAGTGTACCT 22019 TTAAGGGTAA 22020 CC A AGTG-- CT AT
TTCTACTATTTAGGTTAAGG ATAAAGGCAC T CGTGT CC TACCTTT ACT T
GTAAATAAAGGCACATGTAA ATGT | ||||| || ||||||| |||
A GTACA GG ATGGGAA TGG /
AT C AAATAA T- AT

GAM816 CCAGGTTTACAGTTTCTAAG 22026 TACAGTTTCT 22027 GTTTA C----- - TT
CGTGTTTTGTCATCGTTTAT AAGCGTGTTT CCAG CAGTTT TAAGCG TG T
TTTTTAAACTGACCAACTGG TGTC |||| |||||| |||||| ||
GGTC GTCAAA ATTTGC AC T
AACCA TTTTTT T TG

GAM817 GACAATTACATCTTCTTCTC 22048 GGGCTCGAGA 22049 AA C -- T- AGATA GACT
TGCAGATACCGACTACTCAG AACGGAGATT GAC TTA ATCTTC TTCTC GC CC A
GGGGCTCGAGAAACGGAGAT TAAC ||| ||| |||||| ||||| || ||
TTAACGGTC CTG AAT TAGAGG AAGAG CG GG /
GC T CA CT GG--- ACTC

GAM818 CCGCTCCTGACGCGATTGAC 22054 TGTCCCAGGT 22055 CTGA GA TGG TT
CTGGAACCGTTTACAGAAGA TGATTTCCAG CCGCTC CGC TTGACC AACCG T
TGTCCCAGGTTGATTTCCAG |||||| ||| |||||| |||||

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                                  GACCTT   GTT  ACCCTG   GAAGA  /
                                     TA--  GG     TA-    CA


GAM819  ACGCCCAAACTCATCCTGGA 22189  CGAGTTCATC 22190    --       TCCTGGAGT    AAT  GGA
        GTGCAAAAATCTGGATCTTA      CAATTCCA       ACG  CCCAAACTCA      GCAAA  CT  T
        CAACACGAGTTCATCCAATT                  |||  ||||||||||       |||||  ||
        CCA                        ACC  AACCTACTTG      AGCAC   CA  /
                                  TT       ---------    AA-  TTC


GAM820  AGCCCGGGTTTTGTTTCAAG 22217  GTTTTGTTTC 22218         TTGTTTCAAGCACAAAACA  G
T
        CACAAAACAAAAGAGAGATA      AAGCACAAAA       AGCCCGGGTT             AAA AGAGATAGC T
        GCTTTGTGGAGAGCTATCCC      CAAA           ||||||||||             ||| |||||||||
        TTCAAAGCC                   CCGAAACTTC             CCT TCGAGAGGT T
                                  ----------  A       G


GAM821  TACATTTTTCTATGTTACTT 22258  TCTATGTTAC 22259       TT  T   CT  TAG    A-----   ATTATATT
        TTAGTTCGTATCAGATTATA      TTTTAGTTCG       TACATTT  CTA GTTA  TT   TTCGT     TCAG      C
        TTCTAGAGCTTCCTGACTAC      TATC           |||||||  ||| ||||  ||   |||||     ||||
        TAACGAAATTAATATGATTT                  ATGTAAA  GGT TAGT  AA   AAGCA     AGTC      T
        GGCCAAATGTA                        CC   T   AT  TTA    ATCATC   CTTCGAGA


GAM822  GCTGGGCCTAATTACGCTGT 22265  ACGCTGTCCG 22266       CCTAATTACG    C -------      CGC
  G
        CCGCCTGTTCCACGCGCGTG      CCTGTTCCAC       GCTGGG       CTGTC GC     CTGTTCCA
GCGTGTCG C
        TCGGCTACGACACGCTGGAG      GCGC           ||||||       ||||| ||     ||||||||  ||||||||
        CAGCTTCCACGCGACAGATC                  CGACTC       GACAG CG     GACGAGGT   CGCACAGC T
        CGTCTCTCAGC                        TCTGCCTA--    -  CACCTTC      ---      A


GAM823  GGCTGACAGGATCGTCCCCT 22279  TGACAGGATC 22280    T-   -   G    TG   G  AT
        TGGCTCGTGATCCTACAAGG      GTCCCCTTGG       GGC  GACAG GATC TCCCCT  GCTC TG  C
        GCAGGGGGGGTCTCTGTTCT      CTCG           |||  ||||| |||| ||||||  |||| ||
        GCC                         CCG  TTGTC CTGG GGGGGA  CGGG AC  C
                                  TC    T   -    --   A  AT


GAM824  CGTGCCGGGACCCCGACAAG 22295  CGAGAAGCGC 22296    T    A  C  ACAA  -       ACA
        GCCTTCTTGCCGACATTACT      CCGACGCGGC       CG GCCGGG CC CG   GGC CTTCTTGCCG   T
        GGCGAGAAGCGCCCGACGCG      CTGG           || |||||| || ||   ||| ||||||||||
        GCCTGGCCG                    GC CGGTCC GG GC    CCG GAAGAGCGGT   /
                                  -    - C  AGC-   C       CAT


GAM825  CTGCATCTGGGATCGCGCTC 22338  TGGGATCGCG 22339    G  -   ---    C   GGA       C  GT
```

GGAGCTCTCCCACCCCGTGT CTCGGAGCTC CT CA TCTG GGATCG GCTC GCTCTCCCAC CC G
TGGAGTGGGAGAGCACAGAG TCCC || || |||| |||||| |||| |||||||||| ||
CTGGTCCTGACGGACTGGAG GA GT AGGC CCTGGT CGAG CGAGAGGGTG GG /
G C AGT - ACA A TT

GAM826 GCGGGGGGGCGACGCAGACG 22356 CGACATGATT 22357 - -- AC ACGG- A
TACGGCGGCAGAGGCCGACA CCTGCCCGTC GCGGGGGGG CGAC GCAG GT CGGC G
TGATTCCTGCCCGTCGATCC GATC ||||||||| |||| |||| || |||| CCCTGT TGTCCCCCT GCTG CGTC TA GCCG A
A CC CT GTACA G

GAM827 CCTCTGCCACCGATGACGCC 22364 TCCGTCCGCC 22365 C-- GAT-- C--- C - A
CGTCGACGACGAGCCGTCCG CTCGGTGTCC CCTCTGC ACC GACGCC GT GACG ACG G
TCCGCCCTCGGTGTCCGCCA GCCA ||||||| ||| |||||| || |||| ||| GGTCCCGCGGAGG GGAGGCG TGG CTGTGG CG CTGC TGC /
CCC ACCGC CTCC C C C

GAM828 CGACATCTGAGGCTCATACT 22396 TGAAAGATTA 22397 C ----- CTCATACT A G
TAATCTATCAGACGGTGTTG TTACCTCTGA CGA ATCT GAGG TAATCT TCAGACG T
TCTGAAAGATTATTACCTCT GAGG ||| |||| |||| |||||| ||||||| GAGAGGATATCG GCT TAGG CTCC ATTAGA AGTCTGT G
A AGAGT ATT----- A T

GAM829 GGATAGCAACATTTATAGGT 22414 TATTATCTTA 22415 TTTATAGGTTCTCTC A TT A AAAATAT A TA
TCTCTCTGAAAGAGGTTTAA ATATATAGTC TGA AGAGG TAAGGAT GTA GGATAGTA TCT A
GGATAGTAAAAATATGGATA TTTA ||| ||||| ||||||| ||| |||||||| ||| GTAATCTTAAGATAGATATT ACT TCTCC ATTTCTG TAT TCTATTAT AGA G
ATCTTAATATATAGTCTTTA ---------- C C- A ATAAT-- - TA
CCCTCTCTCATGCTCTCT

GAM830 TGCGCATGAAAATATCATTA 22420 TGAAAATATC 22421 GC TG ATCA T- AC
AATTGTTTTAAACATTCTTA ATTAAATTGT TGC A AAAAT TTAAATTG TTTAA A
AATTCAATTTAAAATAATTT TTTA ||| | ||||| |||||||| ||||| TTGTAGCA ACG T TTTTA AATTTAAC AAATT T
A- GT ATAA TT CT

GAM831 TCTCGTTAGCCTGGGTAGGA 22429 AGGAATTGCG 22430 C CC TA AGACCCA A CACTGA TAAC
AAGACCCAACCGCGATACCC GTTTCCCCCA TCT GTTAG TGGG GGAA ACCGCGAT CC TCTT T
ACTGATCTTTAACTTTATGA TTAG ||| ||||| |||| |||| |||||||| || |||| GAAAAACAGGAATTGCGGTT AGA CGATT ACCC CCTT TGGCGTTA GG AGAG /

TCCCCCATTAGCAGA - -- -- ------- A ACAAAA TATT

GAM832 GGCGGTATCGGTACATATAC 22439 TATCGGTACA 22440 GG---- TACATATA ATTCACC
GTAATTCACCTTCACAAAAT TATACGTAAT GGC TATCGG CGTA T
ACGGAGTCTTCGATAATAAT TCAC ||| |||||| ||||
AGCC CCG ATAGCT GCAT T
ATAATA TCTGAG-- AAAACAC

GAM833 GTCGCTGAGGAAATCACGAA 22447 TCTACAATGA 22448 -- G- CGA- ATT
GACCATTCAGTCGGTCTACA TTTCCTGAAG GTC GCT AGGAAATCA AGACC C
ATGATTTCCTGAAGCTTGAC CTTG ||| ||| ||||||||| |||||
CAG CGA TCCTTTAGT TCTGG A
TT AG AACA CTG

GAM834 GGGTCGCGGCCCGAAGGCGG 22459 TACCCATCCC 22460 - CC--- C GA-- CTC
CAGT
AGATGCCGAGCTCGGCCAGT CCTTCCACCC GGGTCGC GGC GAAGG GGA TGCCGAG
GGC T
TCGATGCCCTCGGTACCCAT GTCG ||||||| ||| ||||| ||| ||||||| |||
CCCCCTTCCACCCGTCGGCG CCCAGCG CTG CTTCC CCT ATGGCTC CCG /
ACCC G CCCAC C ACCC --- TAGC

GAM835 GTTCTCCCGTTGCTATTGCA 22473 TGGGATGTCT 22474 CC TG TA- A--- C---- C
ACATCCCCGGACACAAGTGT CAGCAAGACG GTTCT CGT C TTGC ACATCCC GGACA A
CCCTTCTGGGATGTCTCAGC TGAT ||||| ||| | |||| ||||||| |||||
AAGACGTGATGCAGAAC CAAGA GTA G AACG TGTAGGG CCTGT A
C- GT CAG ACTC TCTTC G

GAM836 GATCGATCGCACCGTGCAAG 22483 TACCACGGTG 22484 GATC-- CAAGC -------- A
CGTACAGCAATTGCAAAACT CACACGAGAT GATC GCACCGTG GTACA GC A
AATGTACCACGGTGCACACG C |||| |||||||| ||||| ||
AGATC CTAG CGTGGCAC CATGT CG T
AGCACA ----- AATCAAAA T

GAM837 GATTTTTTATGATTTTGTGC 22491 TTAGTTCGTA 22492 ---- T - ---- AT TT
GACAGTAATACATTTTTCTA TTAGATTATA GATTTTT TATGATTT GTGCGA C AGTA ACAT T
TGTTACTTTTAGTTCGTATT TTCT ||||||| |||||||| |||||| | |||| ||||
AGATTATATTCTAGAGATT TTAGAGA ATATTAGA TATGCT G TCAT TGTA T
TCTT T T ATTT -- TC

GAM838 TCGGATTATCCACCGAGGAC 22494 ACCGAGGACC 22495 AT- AC CAA C AAG
CAAGTCGAAAGTTTTATCAA AAGTCGAAAG TCGG TATCC CGAGGAC GT GA T
TGTCCTCGCGGATACCGCTG TTTT |||| ||||| ||||||| || ||

G GGTC ATAGG GCTCCTG TA CT T
GCC C- --- A ATT

GAM839 AGCCCGGGGTCCAAAAGAGT 22501 TCCAAAAGAG 22502 G AAA GGG CAACA
GGGTCGTACAACACGTCATC TGGGTCGTAC AGCCCGGG TCC AGAGT TCGTA C
TACGAACTCTAGGATCCGGG AACA |||||||| ||| ||||| |||||
TT TTGGGCCT AGG TCTCA AGCAT G
- A-- --- CTACT

GAM840 TGCCCTCGAAGCGCCAGATA 22536 TCGAAGCGCC 22537 --- ------ G ACAG-- G
CAGATTTGAGCAAGTATAAA AGATACAGAT TGC CCTCGA AGC CCAGAT ATTT A
GATCTGGGCTTCAAAGTCGA TTGA ||| |||||| ||| |||||| ||||
GGTTAGCA ACG GGAGCT TCG GGTCTA TGAA G
ATT GAAACT - GAAATA C

GAM841 AAGCGTTATCACACTGCGAC 22541 TATCACACTG 22542 TTAT T CGT TG AAAA
GTGCTGACAAAACCCACGTT CGACGTGCTG AAGCG CACAC GCGA GC AC C
GGTTTTGCCGTGTGCATTCG ACAA ||||| ||||| |||| || ||
CTT TTCGC GTGTG CGTT TG TG /
TTAC C T-- GT CACC

GAM842 GTGGTAGCGCTGTGTGAGTT 22552 GGTGGATCCC 22553 G - T GAG G ATCCCC G
GGCGGTGGATCCCCCTCGTG CCTCGTGGTA GT GTAG CGCTG GT TTGGC GTGG
CTCGTG T
GTAACACGAGCCCCCGTGGC ACAC || |||| ||||| || ||||| |||| ||||||
CAAAAGCCCAGTGTTTACAG CG CATT GTGAC CG AACCG TGCC GAGCAC A
C A T C AA- G CCC--- A

GAM843 TAGCGACCAAATGCAACATA 22573 AGACAAAATT 22574 CCAAAT- C TA CTTAG-
CTATTTATC ATGA
AACTTAGACAATCTATTTAT GTAACCACTT TAGCGA GCAA A AA ACAAT TCC C
CTCCATGACTATCGGAACAG CGTT |||||| |||| | || ||||| |||
ACAAAATTGTAACCACTTCG ATCGCT CGTT T TT TGTTA AGG /
TTTTGCTCCTTCATCGCTA ACTTCCT T GC CACCAA AAACAGACA CTAT

GAM844 GGCGACACATTTCTAGACAG 22579 TTTACATATT 22580 CACA CT CA CT - - A
GCTGTTGAAAATGGACTACT ACCCTTCTTC GGCGA TTT AGA GG GT TG AAAATGG C
GTTTTACATATTACCCTTCT AAAT ||||| ||| ||| || || || |||||||
TCAAATCGCC CCGCT AAA TCT CC TA AC TTTTGTC T
---- CT TC AT T A A

GAM845 GGTATATCCCTCTAAATCTG 22587 TCTAAATCTG 22588 ---- C-- - TGATG A A- AT
ATGTTTTTGCATGGACGAGG ATGTTTTTGC GGTATA TCC TCTA AATC TTTTTGCATGG CG
GGT T

TATTGTGCCCCCGACCATGT ATGG |||||| ||| |||| |||| |||||||||| || |||
AAAAGTTGTGATTGTAGGTC CCGTAT AGG GGAT TTAG GAAAATGTACC GC CCG
/
AGGATCCATATGCC ACCT ACT G TGTT- A CC TG

GAM846 GTCGCTGTCCCCGGCCGTGA 22596 TCCCCGGCCG 22597 ---------- GA GGAG GCT
GCGGAGCCGTGCTCTGGGAC TGAGCGGAGC GTCGCT GTCCCCGGCCGT GC CCGT
C
GGGGAGGCGGCGGCCGGGGA CGTG |||||| |||||||||||| || ||||
CGAAGAAGAGAAGGAGCGGC CGGCGA CAGGGGCCGGCG CG GGCA T
GGAAGAGAAGAAG G- GAGG GGG

GAM847 GCTTCGCCGCGGCCCGCGAC 22610 GACACGGTGG 22611 GC G G G G ---- G
GG
CGCGCGCTGCGCGCGGTGCC CGGGCGCGGT GCTTCGCCGCG CCGC ACCGCGC CTGC CGC
GTG CCGT GC C
GTGGCGGCCGGCGATGGTGG GGCG |||||||||| |||| ||||||| |||| ||| ||| |||| ||
ACACGGTGGCGGGCGCGGTG CGAGGTGGCGC GGCG TGGCGCG GGCG GTG CAC
GGTA CG /
GCGGACGCGGTGGAGC A- G - - G AGGT G GC

GAM848 TTCGTGGCGGGCGGCCTGAT 22677 TCGGGCCCGG 22678 - G GA - G T GG T
GGCT - C
CCTGCTGGGCGCGTGCGGGC CGCGGAGAAG GGGC GCCT TCC TGCTGGGC CG GC
GCTGACGG GT GTGCC GCCG G
TGACGGTGTGGCTGTGCCGC GCGG |||| |||| ||| |||||||| || || |||||||| || ||||| ||||
CGCGCGCGGCGGGCGCTCGA CCCG CGGA AGG GCGGCCCG GC CG CGGCTGCC CA
CGCGG CGGC C
CCCGTCGGCGCTCGGGCCCG T G AG C G T -- - GCT- G G
GCGCGGAGAAGGCGGCCCTG
CTCGAG
GAM849 ACATTATATACATTATATAC 22715 TACATTATAT 22716 CAT CAT CAT CAT CAT
CAT C
ATTATATACATTATATACAT ACATTATATA ATA TATATA TATATA TATATA TATATA TATATA
TATATA A
TATATACATTATATACATTA CATT ||| |||||| |||||| |||||| |||||| |||||| ||||||
TATACATTATATACATTATA TAT ATATAT ATATAT ATATAT ATATAT ATATAT
ATATAT /
TACATTATATACATTATATA TAC TAC TAC TAC TAC TAC T
CATTATATACATTATATACA
TTATATACATT
GAM850 ACCCCGCTCCTGGGACAAAT 22743 TAGAAGGGGG 22744 GGGAC C--- AAA T
ACTCCGGAAACCTCCAGGGA GTGGGGT ACCCCGCTCCT AAATA TCCGG CC C
TCGGAAATTTATTTAGAAGG |||||||||| ||||| ||||| ||
GGGGTGGGGT TGGGGTGGGGG TTTAT AGGCT GG C
GAAGA TTAA AG- A

GAM851 CTGTGACCAAGATAGAGAGC 22834 ACCAAGATAG 22835 ACCA GCTCC-- TGAAT T
CTA AGTTT
TCCTTTGGTGAATCCATCTC AGAGCTCCTT CTGTG AGATAGAGA TTTGG CCA CT
TGTTTC A
TATGTTTCAGTTTAACCAAG TGGT ||||| |||||||||| ||||| ||| || ||||||
AAACAGTCAGCTGGTCTAAA GACAT TCTATCTCT AAATC GGT GA ACAAAG /
ATTTCCATCTCTATCTAATA AA-- ACCTTTA T---- C CTG AACCA
CAG

GAM852 AGAAAACCAGGCAGCGTTTG 22848 TACACAGCGT 22849 AC GCA - A TT T
TAACGCTTTGGTATACCAGC ACTGAATTTC AGAAA CAG GCGTT TGTA CGCT GG A
GATACACAGCGTACTGAATT T ||||| ||| ||||| |||| |||| ||
TCT TCTTT GTC TGCGA ACAT GCGA CC T
AA A-- C A -- A

GAM853 GCAATGCCATTGAAGTGCAT 22887 AAGAAAGTGC 22888 - ---- AA TA- ACA A
GTAGCTTTACAGCAATTGCA CTATGCACAC GCAATG CCA TTG GTGCATG GCTTT GC A
AGAAAGTGCCTATGCACACG GAAC |||||| ||| ||| ||||||| ||||| ||
AACCCTGGACATTGC CGTTAC GGT AGC CACGTAT TGAAA CG T
A CCCA A- CCG GAA T

GAM854 TGTAGTCCTACAATCAAGCG 22911 CACCTCTAAG 22912 A T ATCAA- --- T A- AC
AGGTTGTAGACGTTACCTAC CATAACCTGT TGT GTCC ACA GC GAGGT GTAG CGTT C
AATGAACTACACCTCTAAGC CGGG ||| |||| ||| || ||||| |||| ||||
ATAACCTGTCGGGCACA ACA CGGG TGT CG CTCCA CATC GTAA T
- C CCAATA AAT - AA CA

GAM855 TTACTATTGGACTGTTTATA 22923 TGGACTGTTT 22924 ATT C ATACTTA--- AAA CAC
CTTATCTTCAAATGTTCACT ATACTTATCT TTACT GGA TGTTT TCTTC TGTT T
CACAGCAGCGAAGGGGACAC TCAA ||||| ||| ||||| ||||| ||||
TAGAAAACACTCCCAAGTAG GATGA CCT ACAAA GGAAG ACGA /
AC- C AGATCACAGG CG- CAC

GAM856 TAACCTTAGCTCTAACTCTG 22935 TCTAACTCTG 22936 C CT ACTCTGACCC C A
ACCCTAGGCCTAACCCTAAG ACCCTAGGCC TAA CTTAG CTA TAGGC TA C
CCTAACCCTAACCGTAGCTC TAAC ||| ||||| ||| ||||| ||
TAAGTTTA ATT GAATC GAT ATCCG AT C
T TC GCCAATCCCA A C

GAM857 GCAGCGCGGCGCACAGAGCG 22967 AGACTGTTTG 22968 ---- -- C AGC A
AAGGCAGCGGCTTTCAGACT CCAAGCGCAG GCA GCGC GGCG ACAG GAAGGC G
GTTTGCCAAGCGCAGTCTGC TCTG ||| |||| |||| |||| ||||||
CGT CGCG CCGT TGTC CTTTCG C
CTGA AA T AGA G

GAM858 GCGCGCCTCGTCGACCGGGC 22979 GCCCGGGTCT 22980 CCTCGT CGA A C
GACCGGACCCCGCGGGCCCG CGGTCGTTCA GCGCG CGACCGGG CCGG CCC G
GGTCTCGGTCGTTCACGCGC CGCG ||||| |||||||| |||| |||
CGCGC GCTGGCTC GGCC GGG /
ACTT-- TG- C C

GAM859 GTCCGAGGTCCTGGTCGCAT 22988 TCGTGGGTGT 22989 G CATTATC GTGTTC TCCA AT
TATCGTGGGTGTGTTCTTCG GTTCTTCGTC GTCCGAGGTCCT GTCG GTGGGT TTCG GC C
TCCAGCATCCAGGCCGCTCG CAGC |||||||||||| |||| |||||| |||| ||
AGACCCGCTGGCGAGGGCCT TAGGCTCCGGGA CGGT CGCCCA GAGC CG C
CGGAT G ------- ------ TCGC GA

GAM860 TTCAGTACGTAGTAGCTTCT 22995 TGAGCCAGTT 22996 G - TAG - C C C T
CGAACAGATTCGTTCGTTTA TTTTCAGATG TTCA TAC GTAG CT TCT GAA AGATT GTTCGTT A
CAATGAGCCAGTTTTTTCAG GATT |||| ||| |||| || ||| ||| ||||| |||||||
ATGGATTTTACTGTGGTGAA AAGT GTG CATT GG AGA CTT TTTGA CGAGTAA /
G T TTA T - T C C

GAM861 GTCCTTCTCTGCTTCTTTTC 23006 TCTCTGCTTC 23007 - T TCTTT TTCTCTT
TGTGTTCTCTTGCCTTTTTT TTTTCTGTGT GTCCTTCT C GCT TCTGTG G
CACGGGGGCTGAAGAAGGAC TCTC |||||||| | ||| ||||||
CAGGAAGA G CGG GGGCAC C
A T ----- TTTTTTC

GAM862 GGGAGGTTCTTATATTCCAG 23094 TCCCCTGGGT 23095 TTCTTATAT CTC- GTA
GGCTCTGACAGGTATCTCAC TTTCTCCT GGGAGG TCCAGGG TGACAG T
TGTTATCTCCCCTGGGTTTT |||||| ||||||| ||||||
CTCCT TCCTCT GGGTCCC ATTGTC C
TTT------ CTCT ACT

GAM863 ATATACCCCCAATTAGCCCC 23312 TTCACATAAA 23313 ATTA-------- A AC--- GT - TGGC T
CAATTGGCACATGGTAATAT CAGCCAGCTG A GCCCCCA TTGGC ATG AATAT ACCGCCA GCCG G
ACCGCCATGGCGCCGTGCTT GGGG | ||||||| ||||| ||| ||||| ||||||| ||||
GGTATTGGTGGTGATGTTCA T TGGGGGT GACCG TAC TTGTA TGGTGGT TGGT C
CATAAACAGCCAGCTGGGGG GGATTTGTTTTG C ACAAA AC G TA-- T
TGTTTTGTTTAGGTGGGCTT
TTGTGGTATAT
GAM864 CAGCTGCAATAGCATCAGTA 23341 AGTAAACAGT 23342 C A CAGTAAACAGTT TCTAAA

AACAGTTTTCCATTCTAAAA TTTCCATTCT CAG TGCA TAGCAT TTCCAT A
ATATCTATGGGATTATGCTA AAAA ||| |||| |||||| ||||||
TGCACTG GTC ACGT ATCGTA AGGGTA /
- - TT---------- TCTATA

GAM865 AGATCTCCCCCATGCAAATG 23374 TGGAATAGGT 23375 TCT T AAA---- GG GG
TTTTAGGGTAGGCTGTACAT AAACGCTTGG AGA CCCCCA GC TGTTTTA GTA C
GGAATAGGTAAACGCTTGGG GGGT ||| |||||| || ||||||| |||
GGTCTTCT TCT GGGGGT CG ATAAGGT CAT /
TCT T CAAATGG A- GT

GAM866 GTTTGGGAAAAGGAGATTTC 23386 TATCTTGCAG 23387 A G C G ---- TT C
TGCAGGTGCAGTGGTTCCCC CTTTAGAAAT GTTTGGGAAA G AGATTTCTG AG TGCA GTGG
CC C
CGGGCCTTATATCTTGCAGC CTGC |||||||||| | ||||||||| || |||| |||| ||
TTTAGAAATCTGCTTTCTCA CAAACTCTTT C TCTAAAGAT TC ACGT TATT GG C
AAC - G T G TCTA CC G

GAM867 GTCCAACAACATATACTCAT 23400 AACAACATAT 23401 CAA ATATACT-- AGCTTATC
AGAGCTTATCAAACATCCCC ACTCATAGAG GTC CAAC CATAG A
TGTGCCCATCTAGGTTGCCA CTTA ||| |||| |||||
GAC CAG GTTG GTGTC /
ACC GATCTACCC CCCTACAA

GAM868 GGTTTAATATTTTCTTAGTA 23417 TATTTTCTTA 23418 ATA-- A- G- AT-- AAAA
TG AG
CAAAAGTCAATGTTTTAAAA GTACAAAAGT TTTA TTTTCTT GTACAAAA TCA GTTTT
TATATGGA AG A
TATATGGATGAGAGAATATT CAAT |||| ||||||| |||||||| ||| ||||| |||||||| ||
TGTCTGTATAAAAACTGTGT GAGT AAAAGAA CATGTTTT AGT CAAAA ATATGTCT
TT A
GAAATTTTGTACCAAAGAAA GCAAA AC AA GTGT ---- GT AT
AAAACGTGAGCC

GAM869 CCATCAGAAAGAGAATAAAA 23426 TCAGAAAGAG 23427 AGA- AAAA T A CCA -
AAAGA
ATATTTTTGTAAAACTTTTT AATAAAAATA AG ATAAAAATATTTTTGT CTTTTT ATG GA TCG
AAGAGAG G
TATGAGACCATCGAAGAGAG TTTT || |||||||||||||| |||||| ||| || ||| |||||||
AAAGAGATAAAACTTTTTTA TC TGTTTTTATAAAAATA GAAAGA TAC CT AGC
TTTTTTC A
CGACTCCATCAGAAAGAGAA AAAA AGA- C - C-- A AAAAT
TAAAAATATTTTTGTAAAAC
TTTTTTATGAG
GAM870 TATTAAATGTTGTATTTTTA 23443 TTAAATGTTG 23444 - GTTGT CTA CA TA
CTAGGTTCAGGTATATTCTC TATTTTTACT TATT AAAT ATTTTTA GGTT GG T

AAACCCATAAAAATTTTTAA AGGT |||| |||| ||||||| |||| ||
TTTCAATA ATAA TTTA TAAAAAT CCAA TC A
C ATTTT AC- AC TT

GAM871 CATCGTTAAAATTTTTAGCA 23450 TAGCATATCC 23451 TT C CCATCATTT T AAA C---
TT TAAA
TATCCATCATTTTTTAAATT ATCATTTTTT TAG ATAT TTTAAA TTTC TGATTCT TAGA
TCCA T
TTCAAATGATTCTCTAGATT AAAT ||| |||| |||||| |||| ||||||| |||| ||||
TCCATAAATATCCTGGATCT ATC TATA AAATTT AAAG ACTAAGA ATCT AGGT
/
AAATTAGAATCAGAAACTTT AT T TTT------ C --- TTAA -- CCTA
AAATTTATATTCTATAGTTT
TTAATGATG
GAM872 AAATAATGGATAATAATTAG 23463 TGGATAATAA 23464 G AAT T AA
TATTTATATAACTAAATATG TTAGTATTTA AAATAAT GATAAT TAG ATTTATAT C
GATCTATCATTATTAATTAT TATA ||||||| |||||| ||| ||||||||
TT TTTATTA TTATTA ATC TAGGTATA T
A CT- - AA

GAM873 TAGATATTGGATTATTATAA 23469 TATTGGATTA 23470 --- TT AA A
AATAAAAAATTAAAAAATTT TTATAAAATA TAGATATTG GATTA AT AATAAAAAATT A
TTTGTTAAATTTTAATTTAT AAAA ||||||||| ||||| || ||||||||||
TAATATCTA ATCTATAAT TTAAT TA TTGTTTTTTAA A
TAT TT AA A

GAM874 GACGGTGGAGGGGCGGGCGC 23477 GCGCTTGGCC 23478 GGA- G CGGG G
CACGGGCTCGGGGGAGGATG TGCAGACCGT GACGGT GGG CGGGCGCCA CTC G
GCGCTTGGCCTGCAGACCGT C |||||| ||| ||||||||| |||
C CTGCCA TCC GTTCGCGGT GAG G
GACG G AG-- G

GAM875 GAAAGGGTACCAGACCGGGA 23527 AAGGGTACCA 23528 G A AG GGG - AG --------
C CG
TCACGGAGCCGTTTTGCGCG GACCGGGATC GAAA GGT CC ACC ATCA CGG CCGTTT
TGCGCGG GGC G
GCGGCCGGCAGCCACTGCGC ACGG |||| ||| || ||| |||| ||| |||||| ||||||| |||
GGAGAAGTTGAGCGGGCCGA CTTT CCG GG TGG TGGT GCC GGCGAG
GCGCGTC CCG /
TGGTGGGTAGGGGCCGTTTC G - GA G-- A G- TTGAAGAG A AC

GAM876 GTTGCCGGCGCGGGCCCAGA 23541 GTAGAGCGTC 23542 G G - GA-- C GAA GA
A
CGCTCGGGGCGAAGCTCTGG TCGACGGAGG GTTGCC GC CGGG CCCA CG TCGGGGC
GCTCTG GGTCC G

AGGTCCAGCGGGCCGTAGAG TGGG |||||| || |||| |||| || ||||||| |||||| |||||
CGTCTCGACGGAGGTGGGTC TAATGG CG GCCC GGGT GC AGCTCTG CGAGAT
CCGGG /
CCGGCGGGTAAT G - T GGAG - --- G- C

GAM877 TCTTAGTGTGGTATTTGCCT 23559 AGTGTGGTAT 23560 TA TTGCCTGCG GTC
GCGGTGGTCCTTCACACATT TTGCCTGCGG TCT GTGTGGTAT GTG C
TATTATATATCACATACAGA TGGT ||| ||||||||| |||
AGA TACACTATA CAC T
CA TATTATTTA ACT

GAM878 GTATGGGAAAACAAATAGGT 23571 TTCACACGTT 23572 - A A --- GTTA
GGACTGTTATTGTGGGTTCA ATATGTTCTC GTA TGGGA AACA ATAG GTGGACT T
CACGTTATATGTTCTCCTAG CTAG ||| ||||| |||| |||| |||||||
TAC CAT ATCCT TTGT TATT CACTTGG /
G C A GCA GTGT

GAM879 CCATGATGAAGGTCCTCAAT 23580 ATGAAGGTCC 23581 A - - CTCAA A AG T T-- GA
GCCATCAAGGAGTCTGGTAA TCAATGCCAT CC TGATGA AG GTC TGCC TCA GAG CTGG
AAG C
GGACTACTTCATCCAGCTCG CAAG || |||||| || ||| |||| ||| ||| |||| |||
ATGAGGCAGACTCTGTCATC GG ACTACT TC CAG ACGG AGT CTC GACC TTC /
AGG - G T ----- - AG - TAC AT

GAM880 ACGACGTTCTGTACTTCGCT 23601 TACTTCGCTG 23602 T-- A T C A AA TA
GGAGGAAAGCTAGACGCGGT GAGGAAAGCT ACGACG TCTGT CT CG TGG GGA GC G
TCCCACGAGACAGGTCTTGT AGAC |||||| ||||| || || ||| ||| ||
CGT TGCTGT GGACA GA GC ACC CTT CG /
TCT - - - - GG CA

GAM881 GGCGGTCTTGAGAGTACGCG 23617 TGAGAGTACG 23618 CTTGAGA C AA - CA- AGT
CAAGGAATTCATGAAGTTTA CGCAAGGAAT GGCGGT GTA GCGC GG AATT TGA T
TCTCGGAAAATTACCGCGTT TCAT |||||| ||| |||| || |||| |||
ACGAATGCCGCT TCGCCG CAT TGCG CC TTAA GCT T
TAAG--- - -- A AAG CTA

GAM882 CGAACTGTCCGTCCCCAAGG 23620 GAGCGTTACG 23621 A TG C AAG GA T GA G A
CGAGCGTTACGGCGATCGTC GCGATCGTCT CGA C TC GTCCCC GC GCG TACGGC TC TCT
T
TATAAAGAGAGGTTGTACTG ATAA ||| | || |||||| || ||| |||||| || |||
CGTAGGGGGGCTGGTGGATC GCT G GG CGGGGG TG CGT ATGTTG AG AGA A
G A GT T GA- -- C G- - A

GAM883 GTAGACGTAATCGACTTAGA 23627 TGACGTGATT 23628 G ------ AC A ATTA
AGCGGATTATAAAACCGTAT TATTACATGT GTA ACGT AATCG TTAGA GCGG T
TTGACGTGATTTATTACATG ATAC ||| |||| ||||| ||||| ||||
TATAC CAT TGTA TTAGT AGTTT TGCC /
A CATTAT GC A AAAA

GAM884 AACTACCTCTTAAGCTTTTG 23637 TTGCACAGTT 23638 CC - TT GA TT TA--- T--
AATT
TGGATGGTTTCAATATGTGC TTTTGTATTA ACTA TCT TAAGCTT GTG TGGT CAA TGTGCG
AGAGGTT T
GTAGAGGTTAATTTAAAGAG CTTA |||| ||| ||||||| ||| |||| ||| |||||| |||||||
ATTTCTTGTTGCACAGTTTT TGAT AGA GTTCGGG CAT ATTA GTT ACACGT
TCTTTAG A
TTGTATTACTTACTTGGGCT AC A TT TC T- TTTTG TGT AGAA
TGAAGACATAGTT

GAM885 GAATGACGTTATGTACTAAA 23653 CGTTATGTAC 23654 GACG TACTAAATCTT T GT
TCTTTACTCGGTTCAACGGT TAAATCTTTA GAAT TTATG TAC CG T
ATACCCTTTATAAACAAGTT CTCG |||| ||||| ||| ||
C CTTG AATAT ATG GC C
AACA TTCCCAT---- - AA

GAM886 CGTAATTGTATCAGCGAATG 23657 TGTATCAGCG 23658 TG AT AA T AT- T T
TACATGAATCATTTATCCTA AATGTACATG CGTAAT T CAGCG TGTACA GA CA TTA C
ACTGCAATCTGTGCACACGC AATC |||||| | ||||| |||||| || || |||
TGTAGTGATTGCG GCGTTA G GTCGC ACGTGT CT GT AAT /
GT AT AC - AAC C C

GAM887 GTAACGGTAAAATAATATAA 23666 AAGTAGATCT 23667 AAAA ATAAAC G AC
ACTTAGTTTAACTCCTAAAG GATTAATTGT GTAACGGT TAAT TTA TTTA T
TAGATCTGATTAATTGTTAC TAC |||||||| |||| ||| ||||
CATTGTTA ATTA GAT AAAT /
---- GTCTA- G CC

GAM888 GCGACAAACTTGAGGACCAA 23676 TAGAGCAAGC 23677 - AG-- AAATAAT TG C
ATAATGCATTGGCAATTGAT TTTGTTGT GCGACAAA CTTG GACC GCAT G A
GCGGTTAGAGCAAGCTTTGT ||||||| |||| |||| |||| |
TGT TGTTGTTT GAAC TTGG CGTA T /
C GAGA ------- GT A

GAM889 GGATACTCCTATTACGTCGA 23679 TATTACGTCG 23680 TACTCC C C TCA TATAGA
AGTCAGAGGTATAGAACTTT AAGTCAGAGG GGA TATTA GT GAAG GAGG A
CCCCTCCTTTTTCTACATGA TATA ||| ||||| || |||| ||||
TATCCCGTTCC CCT ATAGT CA CTTT CTCC /
TGCCCT A T TTC CCTTTC

GAM890 ACCACTATAATCCCCGCTTC 23682 TATAATCCCC 23683 A CCCCGCTT AATCTCTACTT
GA
CTATAATCTCTACTTCCTAT GCTTCCTATA ACCACT TAAT CCTAT CCTAT T
GATTAAATGGGTAATTAAAT ATCT |||||| |||| ||||| |||||
GATGGGTAATTAAGTGGT TGGTGA ATTA GGGTA GGGTA T
- AT------ GTAAATTAAT- AA

GAM891 GAGGATGTCATCGTGCGTAG 23690 CATCGTGCGT 23691 CAT C ----- AGTTG CG
TCTTCCCAGTTGTCCCGCGC AGTCTTCCCA GAGGATGT CGTG GTAGTCTTC CC TCCCG
C
TTATGGGAATGGGGTCTTTG GTTG |||||||| |||| ||||||||| || |||||
AAGACTATCCACGTCACGTT TTTTTGCA GCAC TATCAGAAG GG AGGGT T
TTT CT- C TTTCT GGTA- AT

GAM892 TTCATCAATTAATGCCTATT 23696 TTAATGCCTA 23697 --- TTA TTA A T
ATGATGTAGTCTCTGCGCAT TTATGATGTA TTCA TCAA ATGCCTA TG TGTAG C
AGGTATGATTTGAAGTTGAG GTCT |||| |||| ||||||| || |||||
GAGT AGTT TATGGAT AC GCGTC /
TGA TAG --- - T

GAM893 CTCGCCGGGGCTCTAGAATA 23705 TAGAATACAA 23706 CCGG CTA C --------- A
CAAAATGCGCACGGACGCTC AATGCGCACG CTCG GGCT GAATA AAAATGCGC ACGG
C
GTATAAACTCGCGCATTTTT GACG |||| |||| ||||| ||||||||| ||||
ATTTGAAGTTAAATCGAG GAGC TTGA TTTAT TTTTACGCG TGCT G
TAAA AG- - CTCAAATA C

GAM894 AATCGCGCCGTAGAGACACG 23713 CACAGCTACG 23714 G AGACAC A T A- AA CA
TACGCGTTGTATTAACACAT GCGGGATT AATC CGCCGTAG GT CGCG TGT TT CA T
ACTGGAAAGAACATCGCGCA |||| |||||||| || |||| ||| || ||
CAGCTACGGCGGGATT TTAG GCGGCATC CA GCGC ACA AA GT /
G GA---- C T AG AG CA

GAM895 AGGCCCTGTTTTATTAACAA 23746 GCCCTGTTTT 23747 C T TT-- T - TT AGGAAA
TT
CATTAAAGCATTCTCAGAGG ATTAACAACA AGG CCTGT TTA AACAACAT AAAG CA CTCAG
GG T
AAAGGTTTAACCACAGCTGA TTAA ||| ||||| ||| |||||||| |||| || ||||| ||
GTGCCTTTTATGTTGTTTGC TCC GGATA AAT TTGTTGTA TTTC GT GAGTC CC /
TTAATATAGGCCCT C T TCGT T C -- GACA-- AA

GAM896 TCCTTTTTGTGCTATGTCGG 23756 TTTGTGCTAT 23757 - CT C GTTA C TCCA

AGTTACAAACAAATCCACAA GTCGGAGTTA TCCTT TTTGTG ATGT GGA CAAA AAA C
ATTTTATTTGCCCATCCTAC CAAA ||||| |||||| |||| ||| |||| |||
ATTTACAAACAAGGA AGGAA AAACAT TACA CCT GTTT TTT /
C T- T ACCC A TAAA

GAM897 GCCGGTTAGTATGACTTACT 23773 TAAGACACAG 23774 T-- GA TA-- A---------- TA
TGTATAATAAGTATAGTTTT AAATACTGTA GCCGG TAGTAT CT CTTGTATA TAAG
T
AAACTGATTTTAGCAGAATA TCCG ||||| |||||| || |||||||| ||||
TATAAGACACAGAAATACTG CGGCC GTCATA GA GAATATAT ATTT A
TATCCGGC TAT AA CACA AAGACGATTTTAGTCAA TG

GAM898 TTTGTCAACTTTGTAAAGGA 23800 TATGTTGTGA 23801 C G AAGGATATTAT GT T A
- TA
TATTATATGTTGTGATTCTA TTCTAGAATA TTTGTCAA TTT TA ATGTT GAT CTAGA TAG
TAG G
GAATAGTAGTAGCTCTATCT GTAG |||||||| ||| || ||||| ||| ||||| ||| |||
AGTCTAGTATCTAAACATTG AAACAGTT AAG GT TACAA CTA GATCT ATC ATC /
GGAATTGACAAA - G ---------- AT T G T TC

GAM899 GTCCTGGGCTATATTCCAGT 23803 GCTATATTCC 23804 - ---------- TAGATAG GG GA
AAA--- G
AGATAGATTGGTTGAGAGGA AGTAGATAGA TGGGCTATA TTCCAG ATT TT
GAGGAG TGT A
GAAATGTGATAACAGACCCA TTGG ||||||||| |||||| ||| || |||||| |||
CTCCTTAAGTTGGTAGAACC ACCCGGTAT GAGGTC TGG GA TTCCTC ACA
T
CTGGAGACAAGAAACTTATG G TCAAAGAACA CCAAGA- TT A- ACCCAG A
GCCCAGCAGTATGGAC

GAM900 ATCGTTAGCACACCTTAAAG 23810 TAGCACACCT 23811 GT- A AAAGA A AAATACAG-
T A
ATTAGAAGAAATACAGGTTA TAAAGATTAG ATC TAGCAC CCTT TT GAAG GTTAG
GTAATAATA C
GTGTAATAATAACGTATTAT AAGA ||| |||||| |||| || |||| ||||| |||||||||
TATCTAGCACAAAAATGTTT TAG ATTGTG GGGA AA CTTT CGATC TATTATTAT /
CAAAGGGCGTGTTATTAGAT ATT C ----- - GTAAAAACA - G

GAM901 ATTTGTTATGGTGATGACCG 23829 TGATACTGCT 23830 - GT CC CTTT TTG AA
GTTT
GCTTTTAGCAGTTGACAAGA GCAGTTATTG ATTTG TTATG GATGA GG TAGCAG AC GAG
A
GGTTTATAAATTCCTATGAT CCAT ||||| ||||| ||||| || |||||| || |||
ACTGCTGCAGTTATTGCCAT AACAT TACCG ATTGA GT CGTCAT TA CCT T
GTACAA G TT C- ---- AG- T- TAAA

GAM902 GTTAAATTACGTGATTATAT 23845 CGTGATTATA 23846 AAT CG AT - TCTGC
TATAAGTTATCTGCTTACTT TTATAAGTTA GTTA TA TGATTAT TATAA GTTA T
TAACATTATATAGTAATTAT TCTG |||| || ||||||| ||||| ||||
ATACTAAC CAAT AT ATTAATG ATATT CAAT /
C-- AT AT A TTCAT

GAM903 CTGTATTTCTTCTAATCTTT 23850 TATCACGGGA 23851 TATT C TAA CTA
AAGGTGTGCTAACGATATAT TTAAAAGGTT CTG TCTT TAATCTT GGTGTG A
CACGGGATTAAAAGGTTATT ATTA ||| |||| ||||||| ||||||
AG GAT GGAA ATTAGGG CTATAT /
TATT A CA- AGC

GAM904 TGTCATCAGTGTTGTCAGGG 23861 GGCCATTGTC 23862 T T - TGT A T T G T T - TGA- AG
TCCTGTGGGCCATTGTCATC ATCAGTGTTG TG TG CAG GGTCC GGGCC TTG CA CA TG TG CAG GGTCC GGC C
AGTGTTGTCAGGGTCCTGAG TCAG || || ||| ||||| ||||| ||| || || || || ||| ||||| |||
GCAGCGGGTCATGTGGGCCA AC AC GTT CCGGG CCTGG GAC GT GT AC AC GTT CCGGG CTG /
TTGTCATCAGTGTTGTCAGG T T A TGT - T T G T T A TGTA GG
GTCCTGTGGGCCATTGTCAT
CAGTGTTGTCA
GAM905 GCGGAGTCTGGCAACGCCCG 23882 TGTGTTAAGG 23883 - C - ----- G - - TG
GGTCCTTGCTACCTGTGTGG GCTGGGTAAA GCG GAGT TGGCA ACGCC C GGTCCTTG C TACC T
TGTGTTAAGGGCTGGGTAAA GGTG ||| |||| ||||| ||||| | |||||||| | ||||
GGTGTCTGCCAATTCTCGC CGC CTTA ACCGT TGTGG G TCGGGAAT G GTGG /
T - C AAATG G T T TG

GAM906 GCATCTCCAATAAGTAGATC 23888 TCTCCAATAA 23889 ATAAGTAGA GATA G GCG G
CAGATACCTAAGACTGCGTT GTAGATCCAG GCATCTCCA TCCA CCTAA ACT TT A
GAAAAAAGAGTGTTAGGGTT ATAC ||||||||| |||| ||||| ||| ||
GGAAAAGTGGGGGTGT TGTGGGGGT AGGT GGATT TGA AA A
GAAA----- TG-- G GA- A

GAM907 TTTGACTATTTCGAAAGAGT 23905 TATTTCGAAA 23906 T AAA-- TATTAACAGT AA-GT
TATTAACAGTTACCGTCAAT GAGTTATTAA TTTGAC ATTTCG GAGT TACCGTC TGC T
GCGTTGGAGCAAGCGACGGT CAGT |||||| |||||| |||| ||||||| |||
GTATCCTATATTCGGAAGTG AGACTG TAGAGT CTTA GTGGCAG ACG G
AGATGTCAGA - GAAGG TATCCTAT-- CGA AG

GAM908 GACCCCTTTATAAGATTTAC 23913 TATAAGATTT 23914 CTTTA - GAC TT- GAG TGATC

AGACGATTTTAGAGGAGAAA ACAGACGATT GACCC TAAGATTT ACA GA TTA GAGAAA
A
TGATCAATACTTTTTTCAAT TTAG |||||| |||||||| ||| || ||| ||||||
AATGCTCAGATGTGGAATTT CTGGG ATTTTAAG TGT CT AAT CTTTTT /
TACGTTCGGGTC CTTGC G AGA CGT AA- TCATA

GAM909 GGCCTCTGTGTTCCGGGCAC 23917 TCCCTGCTTT 23918 ---- --- TTTTA A GA----------
-- TC
GGTTTCCCTGCTTTTACGCC TACGCCACGG GGGCACGGTT TCCCTGC CGCC CGGC
GC T
ACGGCGAGCTCTTATGCCGG CGAG |||||||||| ||||||| |||| |||| ||
GGTGAACTCCACGGCCGAGG CCCGTGCCGA GGGGGCG GTGG GCCG
CG T
TGCGCGGGGGTGTAGCCGTG ACTC TGT C---- A GCACCTCAAGTGGGGC
TA
CCCCTCAGGTTGGACACGCA
GAGCC
GAM910 GGTCCAAGTCCCGGGTCTTG 23926 TCTCTGGAGT 23927 ----- - GGT G GTAT GT
GGAGGGATGTATTTGGGTGG GGTGACTTTC GGTCCA AGTC CCG CTT GGAGGGAT
TTGG G
AGCCAAGAGTCTCTCTGGAG TGTG |||||| |||| ||| ||| |||||||| ||||
TGGTGACTTTCTGTGGACT TCAGGT TCAG GGT GAG TCTCTCTG AACC G
GTCTT T --- G AG-- GA

GAM911 CGGCTCGCGCCGTGCTGACA 23946 GCGCCGTGCT 23947 - C TGACAA-- TGC
AACGCCTTGCTGTTGGGCGT GACAAACGCC CGGC TCG GCCGTGC ACGCCT T
CTTCCTGTGCACGGCCGACG TTGC |||| ||| ||||||| ||||||
CCG GCCG AGC CGGCACG TGCGGG /
C - TGTCCTTC TTG

GAM912 GTGTATAGGTTGTAAGCGCA 23958 TAGGTTGTAA 23959 A- GT- -- G ------- TG C
GTGGTCGTTGTTGTTGCCGC GCGCAGTGGT GTGT TAG TGTAA GCGCAGTG TCG T
TTGTTGC G
GGCAACAGTGGTTGGTGGTG CGTT |||| ||| ||||| |||||||| ||| | |||||||
AACACTGTGTATTTGCACTA CACA ATC ACGTT TGTGTCAC AGT G GACAACG C
CTAGAACAC AG ATC TA A GGTGGTT GT G

GAM913 GCGATGGTAGGTCAGTGGTA 23964 AGTGGTAATA 23965 - AG CA - --- CAGCCG- T
TC GCTCC
ATATGACCAGCCGTGTTGAT TGACCAGCCG TGGT GT GTGGTA ATAT GAC TGTTGAT
GT CATTGG A
TGTTCCATTGGGCTCCACTT TGTT |||| || |||||| |||| ||| ||||||| || ||||||
TACCGATGATGCTGTCAGCA GTCA TA CACCGT TATA CTG ACGACTG CG
GTAGCC /
AACATTTGTCTAAATATGTG T CT A- G AAT TTTACAA T TA ATTTC
CCACAATTCACTGTTCGC

GAM914 AAGCGCAAGAGTCCCAACAT 23969 TATGGGGGTT 23970 C AA C ---- ACT
TCCTCATACAGAGACTGTAG TAATGTTGAG AAG GC GAGTC CAACAT TCCTCATACAGAG G
ACTTTGTATGGGGGTTTAAT ACTC ||| || ||||| |||||| ||||||||||||
GTTGAGACTCGCCTT TTC CG CTCAG GTTGTA GGGGGTATGTTTC T
- -- A ATTT AGA

GAM915 CTCAATGTCCTTAACGGTGT 23974 TATGAGCTTT 23975 C T- C --- CTAT TT CCC TTCT
AG CG CC
ACGGGACCTCTATGAGCTTT ATGCCCAGCT TAA GG GTA GG GACCT GAGC TATG AGC
GAC GC C T
ATGCCCAGCTTCTGACAGGC TCTG ||| || ||| || ||||| |||| |||| ||| ||| || |
CGCCCTCTTGTAGCAGTCTC GTT CC CGT CC CTGGA TTCG GTGC TCG CTG CG
G C
GCTCGTGCTGCTTCCTTAGG C TC - GTA TTCC TC --- CT-- A- AT TT
TCATGCCTGCCTCCCTTGTG
GAACACAGAG
GAM916 TATCTTAGGATATTTTACAT 23987 TATTTTACAT 23988 ACATCC C TCTCCT
CCAGTACCACTCTCCTAAAC CCAGTACCAC TATCTTAGGATATTTT AGTA CAC A
GTTGTGATACTAAAATATCT TCTC |||||||||||||| |||| |||
TAAGATA ATAGAATTCTATAAAA TCAT GTG /
------ A TTGCAA

GAM917 GCGACGGAAGTGTCCGCGAG 24000 ACGGAAGTGT 24001 AGT TC C GC ATTCAA
CACGCATTCAAAAACGTAGC CCGCGAGCAC GCGACGGA G CG GA ACGC A
GTTATCCGAGCTGGTCCGTC GCAT |||||||| | || || ||||
GC CGCTGCCT C GC CT TGCG /
GGT GA - AT ATGCAA

GAM918 CCAGTGTGCTCTGGGCGCCG 24004 CGGTCCGCGC 24005 ---- C-- C G GATC A T
- A
GACGTGGAGATCAGCACGGT TTTCGCGTCG CCA GTGTG TCTGGG GCCG ACGTGGA
AGC CGG CCGCCG GC C
CCGCCGGCACAGCGCGGCGG GCTC ||| ||||| |||||| |||| ||||||| ||| ||| |||||| ||
TCCGCGCTTTCGCGTCGGCT GGT TACAT GGACTC CGGC TGCGCTT TCG GCC
GGCGGC CG /
CTCAGGAACTACATGTTTTG TTTG CAA T - ---- C T G A
G

GAM919 GTCTTCTCTATCTACTGGCA 24008 TGCACGAAAC 24009 C A G G-- C---- A TG-
CTAC- T
GGGCCACTCCGAGTTGGTCT TAGTGGTCGA GTCTTCT TATCT CT GCA GGCCACT CG GT
GT ATCC T
ACATCCTTACGGGTCTCACA ATGT ||||||| ||||| || ||| ||||||| || || || ||||
CACTGCACGAAACTAGTGGT CAGGGGA GTAGA GG TGT CTGGTGA GC CG CA
TGGG A
CGAATGTGGGCAGATGAAGG A C G AAG TCAAA A TCA CACTC C

GGAC

GAM920 CGGAATCTATATGATTCGGG 24012 TGATTCGGGT 24013 AAT G TT GG GGGA
TCTCGGACGGGAATATGGGT CTCGGACGGG CGG CTATAT A CG TCTCGGAC A
CCGAGGAACGTGGTATGGCC AATA ||| |||||| | || ||||||||
G GCC GGTATG T GC GGAGCCTG T
--- G -- AA GGTA

GAM921 TGCCTGCACAAGTACCAGGA 24015 CAAGTACCAG 24016 C ACA AGGAGG - AC
GGGGCTGTCGACTATCGAGC GAGGGGCTGT TGC TGC AGTACC GGCTG TCG T
AGCTGCAATCGGTGCTACAG CGAC ||| ||| |||||| ||||| |||
CAGCA ACG ACG TCGTGG TCGAC AGC /
- ACA CTAACG G TA

GAM922 GACTAAACTTCCTGGGGACT 24045 TAAACTTCCT 24046 -- G C - TG A
AGAGGTGTGGAAACTTTGCT GGGGACTAGA GACTAA ACTTCCTG GGA TAGAGGT G GA A
GCCTCTGCTTCACGGGAAGT GGTG |||||| |||||||| ||| ||||||| | ||
TTTTGGTT TTGGTT TGAAGGGC CTT GTCTCCG C TT /
TT A C T GT C

GAM923 CCTGGAGATGATGCTGACAG 24066 TGATGCTGAC 24067 - TG---- G GTA T
TATGATTTTTTACAAAGTAA AGTATGATTT CCTGG AGA AT CTGACA TGATT T
CTGTTGTTGATCCCATACTC TTTA ||||| ||| || |||||| |||||
CTCAT CCC TT GTCAAT AAACA T
A TAGTTG - G-- T

GAM924 CATTGTCGGTGTGCTTTCGG 24075 TGCTATAGAA 24076 T- TCGGG GTCATAATCAT
CATG
GATTAGCAGTCATAATCATC GGCTTTACCG CATTGTCGG GTGCTT ATTAGCA CTG T
TGCATGTTCATTTTTGCTTG AC ||||||||| |||||| ||||||| |||
CTGCTATAGAAGGCTTTACC CAGCCATTT GAAGAT CGTCGTT TTT T
GAC CG AT--- CG--------- TTAC

GAM925 TGAGTATAGACCCAATCCTT 24092 TATAGACCCA 24093 TA-- CCC- AAAC TTAA
AAACTGATTTAAAACCCCAT ATCCTTAAAC TGAG TAGA AATCCTT TGAT A
CAAGAGGGTTCTCTTCTAAT TGAT |||| |||| ||||||| ||||
TCCTCA ACTC ATCT TTGGGAG ACTA A
CTTA TCTC A--- CCCC

GAM926 TTAGTAGAGTTGGGTAATGT 24097 TGGGTAATGT 24098 A ----- G- A - ------ TATGA
AAA T
TATAGCTAGTCTTGGACCGA TATAGCTAGT TA TG TTATA CT GTCTT GG ACCGAGT
TCAATT GT G
GTTATGATCAATTAAAGTTG CTTG || || ||||| || ||||| || ||||||| |||||| ||

CAGCAAGGATTGAATTATTT AT AC AATAT GA CAGAA CC TGGTTTA AGTTAG
CG C
GGTAACTAACCAAAGACAAG G TACCA AA A A AATCAA TTA-- GAA A
AATATAAACCATCAGTACCT
GACTTGACTAA
GAM927 GCGACCGCACAGCAGGGAAT 24100 CCGCACAGCA 24101 ACC A C GAAT TA CAAAA
TGTAGCACAAAATAATACTG GGGAATTGTA GCG GC CAG AGG TG GCA T
CGCCACCAACCTACTGCGCA GCAC ||| || ||| ||| || |||
TGCGC CGC CG GTC TCC AC CGT /
GTA C A AACC CG CATAA

GAM928 TCTCTGAATTTATTAATTTA 24154 TGTCAAGTCG 24155 TG TAA A AAC - T-----
TT
TCAGCCTTTGAAAAACTACT GTACGTATTC TCTC AATTTAT TTTATCAGCCTTTG AA TAC
TACCG CAGCT A
ACCGTCAGCTTTAACGGCTG CAAA |||| ||||||| |||||||||||||| || ||| ||||| |||||
TCAAGTCGGTACGTATTCCA AGAG TTGAATA AAATAGTTGGAAAC TT ATG ATGGC
GTCGG /
AAGGTTGATAAAATTATAAG CA TTA C --- C TGAACT CA
TTACGAGA

GAM929 GGAGTCGGGCACGGCGCCAG 24163 TTGGGACGAA 24164 C C G CC C C ATAT
TGCTCGCACTTCGCCCTAAT GTGCGAACGC GGAGT GGG ACG CG AGTG TCGCACTTCG
CCTAATA A
AATATATATATATTGGGACG TTCG ||||| ||| ||| || |||| |||||||||| |||||||
AAGTGCGAACGCTTCGCGTT CTTCA CTC TGC GC TCGC AGCGTGAAGC GGGTTAT /
CTCACTTC - T - T- A A ATAT

GAM930 GTGAGTATCTGTCTTGTAGA 24168 TGTCTTGTAG 24169 A G GA AACGC A - AA
CAAACGCATGAAAAGAGCTA ACAAACGCAT GTGAGT TCT TCTTGTA CA ATGA AAGAGCTAA
TG G
ATGAAGCAACACTTGGCTCT GAAA |||||| ||| ||||||| || |||| |||||||||| ||
TATCATACATCTGCTTGCAA CACTTA AGA AGAACGT GT TACT TTCTCGGTT AC C
GAAGAGATTCAC G - TC CTACA A C AA

GAM931 GTCGACGACGAAGATGCAGT 24186 ACGAAGATGC 24187 A GC- TT C TTAAC
GGTTGTGCGCGGTTAACGGA AGTGGTTGTG GTCGACG CGAAGAT AGTGG GTG GCGG G
GTTCCGCCTACTTTTACTTC CGCG ||||||| ||||||| ||||| ||| ||||
AATCTTTGCGTCGGC CGGCTGC GTTTCTA TCATT CAT CGCC /
- ACT TT C TTGAG

GAM932 GCGCAGCAGCTGCTCGCGCA 24211 CAGCAGCTGC 24212 A- A-- AGAGACA TT
GAGACAGTGTTTGCGGCGCG TCGCGCAGAG GCGC GC GCTGCTCGCGC GTGT G
GGCGCGGGCGGCAGAGCGCG ACAG |||| || |||||||||| ||||
CGC CGCG CG CGGCGGGCGCG CGCG /
CG AGA GG----- GC

GAM933 CAGCGGCACGGCGTTGTTGA 24296 TGTACAGACA 24297 GCG TGATG T GAA
TGGTCTTGGGCTGGAACGAG CGTGCTGTTG CAGCGGCACG TTGT GTC TGGGCTG C
CGGTCCGTGATGTACAGACA |||||||||| |||| ||| |||||||
CGTGCTGTTG GTTGTCGTGC GACA TAG GCCTGGC /
ACA TG--- T GAG

GAM934 TCTGAGGGATGGCTCGTACA 24356 TAATACCTGT 24357 T TC CA AAACACAC
ACAAAACACACATCGAGGAA CCTCTCTCAG TCTGAGGGA GGC GTA ACA A
TGTAATACCTGTCCTCTCTC A |||||||| ||| ||| |||
AGA AGACTCTCT CTG CAT TGT /
C TC AA AAGGAGCT

GAM935 ATCTCCTTAAAGGAAATAAA 24382 TCATACTTAA 24383 GAAATA - - AC-- A-- TT
TACCTGGGCTACTTAAGAGA TATAGGCCTT ATCTCCTTAAAG AATAC CTG GGCT TTAAG
GAGT T
GTTTTATACTCATACTTAAT AGAG |||||||||||| ||||| ||| |||| ||||| ||||
ATAGGCCTTAGAGTATTCCC TAGAGGAATTTT TTATG GAT CCGG AATTC CTCA /
TATTTTAAGGAGAT ATCCC- A T ATAT ATA TA

GAM936 AATGAAGTAGATCAACACTA 24386 AAGTAGATCA 24387 AA AG AC- TT-- T
TTTGGAATATATTCTATAAT ACACTATTTG AATG GT ATCA ACTA TGGAA A
TAGTATATGATACATAGCAT GAAT |||| || |||| |||| |||||
T TTAC TA TAGT TGAT ATCTT T
GA CA ATA TAAT A

GAM937 GGACAAGGGTTTTTGAACTT 24400 AGGGTTTTTG 24401 A AG T AAC GT TG TATAT
TG
GGTCTTGCATGGTATATACA AACTTGGTCT GG CA GGTTTT G TTG CT CATGG ACAAT T
ATTGTTCTATTGTCCGTGAG TGCA || || |||||| | ||| || ||||| |||||
AGGTCGACAAAACTTCTGGC CC GT TCAAAA C AGC GA GTGCC TGTTA T
C G CT - --- TG GA ----- TC

GAM938 GTATAGTAATCATTCAGGTT 24409 CGAGTAAATC 24410 T A A A C A T CG
TACCCGAGGTGACGTTTTCC GAACGATACT GTA AGTA TC TTC GGTTTAC CG GG GA T
CCGAGTAAATCGAACGATAC TAC ||| |||| || ||| ||||||| || || ||
TTAC CAT TCAT AG AAG CTAAATG GC CC CT /
- - C - A - - TT

GAM939 GTGTACAAATGTATATGTAA 24414 TCCCAAGGCG 24415 ACA AAACACA GGAAA
ACACAACAGGAAAATATACA TATACATTCT GTGT AATGTATATGT ACA A
TGTCCCAAGGCGTATACATT AACA |||| |||||||||| |||
CTAACAC CACA TTACATATGCG TGT T

ATC GAACCC- ACATA

GAM940 CCTCCTCTGCCACCTCCCAA 24435 CAGGGCAGGG 24436 - CA - AA----- AC
CGGTCACAACGATCGCGATC AGCAGCAGGG CCTCCT CTGC CCT CCC CGGTC A
CAGGGCAGGGAGCAGCAGGG GG |||||| |||| ||| ||| |||||
GG GGGGGA GACG GGA GGG GCTAG /
C AG C ACCTAGC CA

GAM941 TCCATGGCGTCTCTGCTGAC 25019 ACACAGTTAG 25020 A GC- CT- GCA G A
GCAGTGGGAACATCAGTTCA TTCAAGACAT TCC TG GTCT GCTGAC GTG GAAC T
CACAGTTAGTTCAAGACATA ACAG ||| || |||| |||||| ||| ||||
CAGGA AGG AC CAGA TGATTG CAC CTTG C
- ATA ACT A-- A A

GAM942 AAATACATTTTCTCTCCGAG 25049 AGGCAAAACA 25050 TTTT- C-- GA-- - ACG G
AA
GTGAGGTATTATGTACGTGC TAGTTACCAA AAATACA CTCT CGAGGT GGTA TTATGT
TGCC GG T
CGGGAATGGTTCAGGCAAAA TGAC ||||||| |||| |||||| |||| |||||| |||| ||
CATAGTTACCAATGACTTCG TTTGTGT GGGA GCTTCA CCAT GATACA ACGG CT
G
CCAAGGGTTCGTTGTGTTT TGCTT ACC GTAA T AA- A TG

GAM943 GGATGTCGGGGGTTTGAAAA 25077 ACTCAATTTT 25078 ATG- - AAATATA TC G CA
T AGTA C
TATAGGAACATCGAGACTCA CCAGTATCCC GG TCGG GGGTTTGA GGAACA GA ACT
ATTT CC TCC A
ATTTTCCAGTATCCCAAGGG AAGG || |||| |||||||| |||||| || ||| |||| || |||
AGGGGGTAGATGGTGTCTGT CC AGCC CTCGGGCT CTTTGT CT TGG TAGA GG
AGG A
TTCAAGGTCGGGCTCACCGA GATA A GGAA--- -- G -- T GGG- G
ATAGCC

GAM944 GCCGGCGCTTTCTATCTCAC 25098 TCTCACCGTA 25099 CG T TC-- --- AATGCT T
CGTAGAATGCTTCGTCCACG GAATGCTTCG GCCGG CTT CTA TCA CCGTAG TCG C
ATTACGGGCGTGACAATTAG TCCA ||||| ||| ||| ||| |||||| |||
AAGTACCGGT TGGCC GAA GAT AGT GGCATT AGC C
AT - TAAC GCG ------ A

GAM945 CATTTTTCACACCGGAATCG 25107 CACCGGAATC 25108 TT- C- G CGAGTAAAA A
AGTAAAACATAATATGCAAA GAGTAAAACA CATT TCA ACC GAAT CAT A
AAATAGTTCGGGTATTGATA TAAT |||| ||| ||| |||| |||
TAATG GTAA AGT TGG CTTG GTA /
TAT TA G ATAAAAAAC T

GAM946 CGCAATCGAACATTTGTAGC 25115 TCGAACATTT 25116 C G T - ATTT CTCG
ATTTCATATTCTCGTAGAAT GTAGCATTTC CG AATC AACATT GTA GC CATATT T
AATGTGTCTGGCATGCAATG ATAT || |||| |||||| ||| || ||||||
TTGATTCG GC TTAG TTGTAA CGT CG GTGTAA A
- - - A GTCT TAAG

GAM947 CGCGTATCGGCGTCCCGGCG 25126 TGGCGGTCCC 25127 T G T C G T-- GG
CGGCGAGCGTCTGACGGTCT GCGTCGGGTC CGCG ATC GCG CCCGGCGCGG GA CGTC
GAC T
GTCTCTGGCGGTCCCGCGTC GTGG |||| ||| ||| |||||||||| || |||| |||
GGGTCGTGGATCCGTG GTGC TAG TGC GGGCTGCGCC CT GCGG CTG /
C G T - G TCT TC

GAM948 GTTTGGGGCCCAGAGGCTTA 25133 TTTTGCTGAC 25134 GCC A C T TG T- G
TGTGAAGTCATTTGAAAAAT CCTGACCCAA GTTTGGG CAG GG TTA G AAGTCA TT A
TTGATTTTGCTGACCCTGAC AC ||||||| ||| || ||| | |||||| ||
CCAAAC CAAACCC GTC CC AGT C TTTAGT AA A
A-- - - - GT TT A

GAM949 ATAATATTGAACATATTTTA 25185 TATTTTATTG 25186 T GA- TGTATA T
TTGTATATATTTTAAAAATA TATATATTTT ATAA ATT ACATATTTTAT TATTT A
GCTTTATAAGATATGTGAAA AAAA |||| ||| |||||||||| |||||
GTTTTAT TATT TGA TGTATAGAATA ATAAA /
T AAG TTTCG- A

GAM950 GGTGTAATAGGTTTAAGACT 25197 TAATAGGTTT 25198 --- - - TTCTACTA-------- T
ATTTT
TCTACTAAAATATTTAAAAT AAGACTTCTA GGTGTAA TAG GTTTAAG AC AAATAT
TAAA T
TTTTATCATGTTTATGTATT CTAA ||||||| ||| ||||||| || |||||| ||||
TGTATTCTTTCTCCATCGTA CCATATT ATC CAAATTC TG TTTATG ATTT A
CTTAAACTCTACAATTATAC AAC T A CTACCTCTTTCTTATG T GTACT
C

GAM951 CCAGAACACTTTGTAACAGT 25207 TAGCATCCCA 25208 AACA ------ A A CC TT
GCACCATTTTTCAGATTTTG TAAGAAAACT CCAG CTT TGT AC GTGCA ATT T
TATCGTAGCATCCCATAAGA GG |||| ||| ||| || ||||| |||
AAACTGG GGTC GAA ACG TG TATGT TAG /
AAAA TACCCT A C TT AC

GAM952 TCCAAAGATCGTTGTACTAC 25234 GATCGTTGTA 25235 -- T GTACTACC T T
CTGTTCTAAATTATTACATA CTACCTGTTC TCCA AAGA CGTT TGTTC AAATTAT A
ATTTGAATATTCCATAAGCG TAAA |||| |||| |||| ||||| |||||||
TCTTTATGGA AGGT TTCT GCGA ATAAG TTTAATA /

AT - ATACCTT- - C

GAM953 GCGGGGCCGGAGAGCGGCGG 25242 TGCGCTGCTG 25243 AGA------- G CGGAGG A
GGCCGGAGGCGCGGAGGGCC CGAAATAAAA GCGGGGCCGG GCGGCGG GC CGCGG
G
GCGGTGCGCTGCTGCGAAAT GTCG |||||||||| ||||||| || |||||
AAAAGTCGGCTCTGC CGTCTCGGCT CGTCGTC CG GCGCC G
GAAAATAAAG G TG---- G

GAM954 TAGTATAACTGAGGGGACCA 25246 TAACTGAGGG 25247 G AA- A- GG A- G CT G
TGGTATGTATAGGCGCTAGG GACCATGGTA TA TAT CTGAGGGGACC T T TGTATAG CG
AGGC G
CGGGGCTTCGGTTGTACGCG TGTA || ||| |||||||||| | | ||||||| || ||||
GTTAGGGGTCCCCTCAGGAA AT ATG GACTCCCCTGG A G GCATGTT GC TTCG /
GTAGTA G AAG GG TT GC G -- G

GAM955 CACCGTCGAGCAGTCCGTCA 25263 GAGCAGTCCG 25264 GAG TC TC G - ---- G
GG
CCCGGTCGCGGCGCCGACGA TCACCCGGTC CACCGTC CAG CG ACCC GTCG CG GC
CCGACGAC C
CGGCCGAGTCGTCGGAGTCT GCGG ||||||| ||| || |||| |||| || || ||||||||
CTCGCCGACGGGGTCGTCTG GTGGCAG GTC GC TGGG CAGC GC TG GGCTGCTG
C
AGACGGTG A-- T- -- G C TCTC A AG

GAM956 CCCGGTGCCTGGCCTCTTTC 25279 TGTGATTCAC 25280 G C TTTCTCT ---- --------
CCCTTGAC A
TCTGTGATTCACCCAACGCC CCAACGCCCT G TGCCTGG CTC GTGA TTCACC
CAACG GG C
CTTGACGGACCTCCATACTC TGAC | ||||||| ||| |||| |||||| ||||| ||
GTTGTCTCTACCGGTGAGGC C ACGGGCC GAG TACT GAGTGG GTTGC
CC C
TTTCATCTATTTCGAGACCG - A CTTTATC TTCG CCATCTCT TCATA--- T
GGCACGGG

GAM957 CCCAAATAGTTTAAATGGTG 25299 GTGCAATTCG 25300 AAATAGTTTAA TC - ATAA A
CAATTCGTCAATAAATGAAA TCAATAAATG CCC ATGGTGCAAT GT CA ATGAA G
GTTTCATGTCGTGTATTTAT AAAG ||| |||||||||| || || |||||
TGCATCATATCTTAACAAGG GGG TACTACGTTA TA GT TACTT /
G AACAATTCTA- TT T GCTG T

GAM958 GGGCAGATCGTAAGCATTGC 25304 AGGCTCGTGT 25305 CAGAT-- TA A GAACTCAC
CGAACTCACATTTAATAAGG GAAGAACCC GGG CG AGC TTGCC A
CGAGGCTCGTGTGAAGAACC ||| || ||| |||||
C CCC GT TCG AGCGG /

AAGAAGT GC G AATAATTT

GAM959 GCCCGTCGTCGTGGAGTTGG 25383 ACGAAGATAT 25384 TCG G T CTA ATA ATATTA GC
ACTACGAAGATATCGATATT CGATATTACT GCCCG TCGT GAG TGGA CGAAG TCG CTG G
ACTGGCGAACGGCAGCGACT GGCG ||||| |||| ||| |||| ||||| ||| |||
TCGGTTCCATCTCAGCGGAC TGGGC GGCG CTC ACCT GCTTC AGC GGC /
TCGGGT TCA A T TG- --- GAC--- AA

GAM960 GGTATTCGTAACCAGCATTT 25386 TACACAACAG 25387 TA CAGC T AT- AA-- ------ T
GAGTATACGGTTAATGTATC CTGTTGGATT GG TTCGTAAC ATT GAGT ACGGTT TGTA TCC G
CTGGGGAAAAAAATACACAA CTGA || |||||||| ||| |||| |||||| |||| |||
CAGCTGTTGGATTCTGATTT CT AAGCGTTG TAG CTTA TGTCGA ACAT AGG /
CAGTTGCGAACGTC GC ACTT T GGT CAAC AAAAAA G

GAM961 GTCGCCGCTGCCGTCTCTTC 25416 TGACCAGGGG 25417 T - - -- -- CTCGTCCT
AGCCTCGTCCTCCTCCTCCT CTTGGCACGC G CGC CGC TGCC GTCTCT TCAGC C
CGCTGACCAGGGGCTTGGCA GCGC | ||| ||| |||| |||||| |||||
CGCGCGCGC C GCG GCG ACGG CGGGGA AGTCG C
- C C TT CC CTCCTCCT

GAM962 TCCGGGGGTAGCAGGCCTTC 25436 TAGCAGGCCT 25437 - T AA CT
TGGAAAGCCTTGAGCTGCTC TCTGGAAAGC TCCGGGG GTAGCAGGCCTTC GG AGC T
GAAGGCCTGCTGCGCCTTGG CTTG ||||||| |||||||||||| || |||
A AGGTTCC CGTCGTCCGGAAG CT TCG /
G - CG AG

GAM963 AATACTGATGTTGCTTTTCT 25458 TGATGTTGCT 25459 C -- TTTC AAAC
TGGAAATAAACTATTGGTTT TTTCTTGGAA AATA TGATGT TGCT TTGGAAAT T
TTAATACTAGCATTGCATCA ATAA |||| |||||| |||| ||||||||
TTATT TTAT ACTACG ACGA AATTTTTG /
T TT TCAT GTTA

GAM964 AATTAAATTTGTAAATATAT 25489 TATTTAATGG 25490 ---------- GGT- TT-- TT T C TTG
TTAATGGTGGTCTTTGTTGT TGGTCTTTGT AATATAT TTAAT GGTC TGTTG GA TATTTT AA G
TGATTATTTTCAATTGGTTC TGTT ||||||| ||||| |||| ||||| || |||||| ||
TTTAAAATATTTTTCAACAT TTATATA AATTA TTAG ACAAC TT ATAAAA TT T
TTTGATTTAAAATTAAATTT CTATTCTTTTTA AAAT TTTT TT T - TCT
TTCTTATCATATATTTCATT

ATTAATT
GAM965 GAAAGAAATGTATCGTTAGA 25495 TGTGGTCGTC 25496 AA- AT- TTA TGA
CCACACTTTGAGTTCGGGTG CGTAGGCAGA GAAAGA TGT CG GACCACACTT G
TGGTCGTCCGTAGGCAGAGT GTCT |||||| ||| || ||||||||||
CTTTT TTTTCT ACG GC CTGGTGTGGG /
GAG GAT CTG CTT

GAM966 GGCTGGGTGGACCCCTTGGC 25506 ACCCCTTGGC 25507 TG CCT AACAC AG C
GAACACGTGAGGCCCCGCGG GAACACGTGA GGC GGTGGACC TGGCG GTG GCC C
CGCACTGCCACAGGTCCACC GGCC ||| |||||||| ||||| ||| |||
GCC CCG CCACCTGG ACCGT CAC CGG G
-- AC- ----- G- C

GAM967 GATTTCGTGCTCGATTTACC 25566 TTGAATATAC 25567 T C GATTTACCTAAA A TA G - A
TAAATTGAATATACACGATA ACGATACAAT GATT CGTG TC TTGA TA CAC AT AC A
CAATGGTGGTGGTGGGTAAT GGTG |||| |||| || |||| || ||| || ||
CAAATCAGACAGTTAGAATA CTGA GCAT AG AACT AT GTG TG TG T
CGTAGTC T A ATTGACAGACTA A GG G G G

GAM968 TCTATCTCAACACGTTGATT 25570 TAGCAGCGGA 25571 T- TT TT TT- CA- A GA -
TT
TACGTTTAGCAGCGGACAAT CAATCCCGAT CTATC CAACACG GAT ACG TAG GCGGACA
TCCC TCTA CGCG G
CCCGATCTACGCGTTGGTCT CTAC ||||| ||||||| ||| ||| ||| ||||||| |||| |||| ||||
GCGTTGGGCAGGGATGTTTG GATAG GTTGTGT CTA TGT ATC TGTTTGT AGGG
GGGT GCGT G
TGTACTACGGTGTTTATCGG TT GG TT GGC ATG - AC T CT
TGTGTTGTTGATAGA

GAM969 TCATTGTACAAGAAACATTG 25577 TACAAGAAAC 25578 T G- TGCATGA CG T T
CATGAAAGACGATGATTATT ATTGCATGAA TCATTG ACAA AAACAT AAGA A GATTA T
TTAATCTTATCTTACCTATG AGAC |||||| |||| |||||| |||| | |||||
TTTAATTGTTTAATGA AGTAAT TGTT TTTGTA TTCT T CTAAT /
T AA TCCA--- AT - T

GAM970 GGCCCGGCGCTCCACGCCGG 25624 CGCCGGGTCT 25625 C CAC G TT--- AAAA
GGTTCCCGGCGGCGGAAAAG TGTCGCGGCC GGCCCGG GCTC GCCG GG
CCCGGCGGCGG G
CGCGACCGCCGCCGGGTCTT GGGC ||||||| |||| |||| || ||||||||||
GTCGCGGCCGGGCCCGGGCC CCGGGCC CGGG CGGC CT GGGCCGCCGCC C
- C-- G GTTCT AGCG

GAM971 CAGTTTCTGAAGCAAAAGCA 25674 ACAGAAGTCT 25675 - AAA AAA GG- A AA TGC
AAAGAGGCTATAGGGATAAT GAGTATGCTT CAGT TTCTGAAGCA GC AGA CT TAGGGAT
TGC A

GCTGCAATTGCAATCTCTAC CGGA |||| |||||||||| || ||| || ||||||| |||
AGAAGTCTGAGTATGCTTCG GTCA GAGGCTTCGT TG TCT GA ATCTCTA ACG /
GAGAACTG A A-- AG- GAA C -- TTA

GAM972 AAGCGCGATACAAATCGACA 25696 TTCGTACCGC 25697 GATACAAAT A C TTT C
TCTGGTTTTCGAGACCCGCG ATGCCGGCGC AAGCGC CG CAT TGGT CGAGAC C
TTTCGTACCGCATGCCGGCG TT |||||| || ||| |||| ||||||
CTT TTCGCG GC GTA GCCA GCTTTG G
--------- C C T-- C

GAM973 GGGGAGAAAGGGGCGGTAGG 25700 ATCATCCTCC 25701 AGAAA C A AGC - A
GGGAAGCGACGAGACCGATC ACCTCCCCCA GGGG GGGG GGT GGGGGA GA CG G
ATCCTCCACCTCCCCCACCC CCCC |||| |||| ||| |||||| || ||
C CCCC CCCC CCA CCTCCT CT GC A
AC--- T - A-- A C

GAM974 TGGCTGGAGATAGCACTGAG 25870 TAGCACTGAG 25871 C AT- AC- - A C
CGTCTAGGCAGGCCCAGAAT CGTCTAGGCA TGG TGGAG AGC TGAGCGT CT GG A
GCTCATTAGCTTTACTTCAA GGCC ||| ||||| ||| ||||||| || ||
CTA ATC ACTTC TCG ACTCGTA GA CC G
A ATT ATT A C G

GAM975 GGATCAACATGTCACTCACC 25912 TCTCTCGGTA 25913 AACAT A C - C ---- T
AGAGCGTCCACGTCCTCGTG GGACCACGGG GGATC GTC CT ACC AGAG GT CCACG C
GCAGAACTCTCTCGGTAGGA ATCC ||||| ||| || ||| |||| || |||||
CCACGGGATCC CCTAG CAG GA TGG TCTC CA GGTGC C
GGCAC - - C T AGAC T

GAM976 TAATTGTTATTGGCCGGGAC 25924 TTGTTATTGG 25925 T T CC CG--------- TG GA
GAAGTGGGATTACTGCTTAT CCGGGACGAA TAAT GTTAT GG GGGA AAG G T
TATTTTAATTCTCATCGTAA GTGG |||| ||||| || |||| ||| |
TTATTA ATTA TAATG CT CTCT TTC C /
T - A- TAATTTTATTA GT AT

GAM977 CCTGTGAGATTGTTTGTAAA 25930 GATTGTTTGT 25931 T - TAAAGAAT - A- - AA
GAATGAGCCCCACCCTGCCA AAAGAATGAG CC GTGAGATT GTTTG GAGC CCC CCC
TGCC C
ACAAGGTGCGGGAAGGGCGC CCCC || |||||||| ||||| |||| ||| ||| ||||
TTTAGACTAATCTCATCGG GG TACTCTAA CAGAT TTCG GGG GGG GTGG /
C T -------- C AA C AA

GAM978 TATTTAGATATCTGGAACAC 25945 TCAGTGGCCG 25946 AG GAACA - AGGA GGC
CCTGACGACTTTGAGGAGTT CGGATATACA TATTT ATATCTG CC CTGACGACTTTG GTT
A

GGCAGTGGAATTGCAGGGTT AGTA ||||| ||||||| || |||||||||||| |||
GTCAGTGGCCGCGGATATAC ATGAA TATAGGC GG GACTGTTGGGAC TAA G
AAGTA CA GCC-- T GT-- GGT

GAM979 GTTGTAATTGGTACAACAAA 25950 TGGTACAACA 25951 AT---- A -------- AATATT
CATGTAATATTGTATTCCAC AACATGTAAT GTTGTA TGGTACA CAA ACATGT G
ATGTAAATATTATTGTGTAC ATTG |||||| ||||||| ||| ||||||
TATAGTTATACAAC CAACAT ATCATGT GTT TGTACA /
ATTGAT - ATTATAAA CCTTAT

GAM980 AATGATTCAGGAGTTATAAA 25953 AAATGTTTGT 25954 T A- - ATTTA CC
ATTTATGGGCCAATTTTCAA AATCTTTCAG AATGA TC GGAG TTATAAA TGGG A
ATGTTTGTAATCTTTCAGAT ATTC ||||| || |||| ||||||| ||||
TCATT TTACT AG TTTC AATGTTT ACTT A
T AC T GTAA- TT

GAM981 GACGATTTGATAAACGTGGA 25967 TACAAGTTTA 25968 CGA C G CATT TT
TAAAAT
TTGTGTCATTACTTTTTGAA ACATAATCAC GA TTTGATAAA GTG ATTGTGT ACTT TGAA
C
TAAAATCTTTGCCTTTTACA ATTT || ||||||||| ||| ||||||| |||| ||||
AGTTTAACATAATCACATTT CT AAACTATTT CAC TAATACA TGAA ATTT T
ATCAAACCATC ACC A - ATT- C- TCCGTT

GAM982 GCACCTAATAAAAATCACTT 25980 TACACATCCT 25981 C- AAA - TTA A T TGT T- T
AAC
AATAGCAATGTGCTGTGTCA GTCCAGCATT GCAC TAAT AAT CAC AT GCAA GTGCTG CAG
TGT TATTGG C
GTTGTTTATTGGAACCACAC TGCA |||| |||| ||| ||| || |||| |||||| ||| ||| ||||||
CCGGTACACATCCTGTCCAG CGTG ATTA TTA GTG TG CGTT TACGAC GTC ACA
ATGGCC A
CATTTGCAGTGCGTGCATTG TT AG- C CG- A - CT- CT C CAC
AATTATTGTGC

GAM983 GGCTAGACTTCATGGCGCCT 26006 TCAGCGAAAA 26007 TAGAC GG- CT---- CCG
GGCACCGAATCCTGCCTTCT TGAATAATTG GGC TTCAT CGC GGCA A
CAGCGAAAATGAATAATTGC CT ||| ||||| ||| |||| T TCG AAGTA GCG CCGT A
TTAAT AAA ACTCTT CCT

GAM984 GTTTCCATTGCGTCTGGGCT 26023 GGATTAGACG 26024 TT GTC G TCATTGCG
TGG
TGTCTATCATTGCGTCTCTA GGGCCACCAG GT CCATTGC TGG CTTGTCTA TCTCTA T
TGGTTTTTGGAGGATTAGAC TAAT || ||||||| ||| |||||||| |||||| GGGGCCACCAGTAATGGTGC CG GGTAATG ACC GGGCAGAT GGAGGT /

T- ACC G TA------ TTT

GAM985 CCGCCTTAAACTACAGACAG 26028 TCAAAACCTC 26029 AAACTACAGACA CA AA
GTCCCAGCCAAGTAGGCGGA AAAAAGGCGG CCGCCTT GGTCC GCC G
TCAAAACCTCAAAAAGGCGG ||||||| ||||| |||
GGCGGAA CTAGG CGG /
AAACTCCAAAA- -- AT

GAM986 GGAGCAGCAGTGGCCGGGGG 26051 AGTGGCCGGG 26052 A CA -- G CA--- - A
CCCAGACGGGAGTCCGCGTC GGCCCAGACG GG GCAG GTGGC CGGG GCC GACG GG G
GCCCTGGCGCTCGTCGCCGC GGAG || |||| ||||| |||| ||| |||| ||
CTTTGCCC CC CGTT CGCCG GCTC CGG CTGC CC /
- TC CT G TCCCG G T

GAM987 TTATATCATTACTTACAAAT 26124 TAGAATATTT 26125 - ACA GTA AA --- AAAA A
GTATATAGAATATTTAGAAA AGAAAATAAT TTATATCATTA CTT AAT TATAG TATT TAG
TAATA A
ATAATAAAATTATTAAAGGC AAAA |||||||||| ||| ||| ||||| |||| ||| |||||
TATTGGATAACTATGAAATT AATATAGTAAT GAA TTA GTATC ATAG ATC ATTAT A
AAAAGATAATGATATAA A AA- AA- A- GTT GGAA T

GAM988 GCCTTTCTCCGGCAGGTAGC 26128 TACACGTACC 26129 C C-- A AGC A A -- A
CTACACGTACCTCACTATGG TCACTATGGC GC TTT TCCGGC GGT CT CACGTACCTC
CTATGGC CAT A
CCATAAAGATGCAGCCATAG CATA || ||| |||||| ||| || |||||||||| ||||||| |||
AGAGGTACGTGAAGAAGACC CG AGA AGGCTG CCA GA GTGCATGGAG GATACCG
GTA A
CGTCGGAATCAGAAGC A CTA C GAA A A AC G

GAM989 ATTATCACCTTAATCTCTTC 26142 TACATTCTGA 26143 - TA CT CGA- AATAA
AGGCGAACATAAATAACTCC GGATCGGGGT ATTATC ACCT ATCT TCAGG ACATA C
AGCTGTGTACATTCTGAGGA AGAT |||||| |||| |||| ||||| |||||
TCGGGGTAGATAAT TAATAG TGGG TAGG AGTCT TGTGT T
A GC -- TACA CGACC

GAM990 GGGTTAAGGCCTCGGGGTTA 26149 AGGGGCCCGG 26150 AA GGGGTTA - GGC
GGGTCTCAGGCGGCGTTTGG GGTTAGGACC GGGTT GGCCTC GGGTCTC AGGC G
CTTAGGGGCCCGGGGTTAGG T ||||| |||||| ||||||| ||||
ACCT TCCAG TTGGGG CCCGGGG TTCG T
GA ------- A GTT

GAM991 TTGCTTCTGATTCCGACGGG 26357 TACGTGTAGG 26358 CTGA A CT T T CAT
TCTTCTTCACGTACCTCTCT CTACCTGCCG TTGCTT TTCCG CGGGT TCT CACGTACCTC
CTATGGCTG C

ATGGCTGCATCTTTATGGCC GAGA |||||| ||||| ||||| ||| |||||||||| |||||||||
ATAGTGAGGTACGTGTAGGC GGCGGA GAGGC GTCCA GGA GTGCATGGAG
GATACCGGT T
TACCTGCCGGAGAAAGGCGG AA-- C TC T T ATT

GAM992 TTTTAAAGATCCGTGGGCTG 26367 TTAAAGATCC 26368 T GG-- T T ATTCTC
GAGCTTTAAAATTCTCTATT GTGGGCTGGA TTTTAAAGA CCGT GC GGAGCTT AAA T
GTTCTTTCAAGTTCTGCAAA GCTT ||||||||| |||| || ||||||| |||
AATGGTTTTTAAAG GAAATTTTT GGTA CG TCTTGAA TTT A
- AAAA - C CTTGTT

GAM993 GCCTTTAGGGGTAGTGTCGT 26375 TAGGGGTAGT 26376 AG-- G TTG G TTAG G
AG-- G T
TGTCGGGGTTAGGCCTGTAG GTCGTTGTCG GCCTTTAGGGGT T TCG TCGG G GCCT
TAGGGGT T TCG T
GGGTAGTGTCGTTGTCGGGG GGGT |||||||||||| | ||| |||| | |||| ||||||| | |||
TTAGGCCTTTAGGGGTAGTG CGGGGATTTCCG G GGC GGCT T TGGG ATTTCCG
G GGC G
TCGGGGTCGGGGTTAGGCCT GATT G TGG G GA-- G GATT G T
TTAGGGGC

GAM994 GAACCAGCCCTGCGCGCTTG 26378 ATCGCGCATG 26379 CAGCC C T TATATA-- C
CGCTATATACGCCCTGCGCA CGCACAGACG GAAC CTG GCGC TGCGC CGC C
CTCATCGCGCATGCGCACAG TTC |||| ||| |||| ||||| |||
ACGTTC CTTG GAC CGCG ACGCG GCG /
CA--- A T CTACTCAC T

GAM995 TCCATTGATCTGCTCACGAC 26386 TGCACAGCCA 26387 AT AT T GA- A TAGAA
TGTAGCACTTAGAATCGCAC GTGAGCTGGC TCC TG C GCTCAC CTGT GCACT T
AGTGCACAGCCAGTGAGCTG CACA ||| || | |||||| |||| |||||
GCCACAGGA AGG AC G CGAGTG GACA CGTGA /
AC CG T ACC - CACGC

GAM996 CCGAGCTTAAAAAATATTTT 26446 AGATCTGGGA 26447 AAA TAT CGG AA CA- ATC
ATTGGCGGTCAAAGCATGCT AATCATGGAT CCGAGCTT AAATATTT TGG TC AG TGCT C
ATCCTTCAGCAGATCTGGGA GTTT |||||||| |||||||| ||| || || ||||
AATCATGGATGTTTGGAGGC GGTTCGGA TTTGTAGG ACT AG TC ACGA /
TTGG GG- T-- AA- GG TAG CTT

GAM997 GAGCGCAGAGCTATTACCGA 26459 TCGCATGGAC 26460 A ATTA AA- TC CCCC
AGAAGTCTATCCCCCCAAAA CAGGTATTGC GAGCGCAG GCT CCG GAAG TATCC A
TGGATATTTTCGCATGGACC GCTC |||||||| ||| ||| |||| |||||
AGGTATTGCGCTC CTCGCGTT TGG GGT CTTT ATAGG /
A ACCA ACG T- TAAA

GAM998 CACGTTGTGCGTTCTCCGTT 26474 TTCGGGCGGA 26475 TG TC TGA TTT G G TA
GACCTTTGAAAAGGCGCGTG TTACGCGTTA CACGT TGCGT TCCGT CC GAAAA GCGC TGG
T
GTATTTCTCGGTGTGTTTTT CGTG ||||| ||||| ||||| || ||||| |||| |||
CGGGCGGATTACGCGTTACG GTGCA GCGCA AGGCG GG TTTTT TGTG GCT T
TG TT TT --- C-- G - CT

GAM999 GATCGTCAGAGCACGGATGA 26478 TCAGAGCACG 26479 TC C AGC AG ACT
GCGAGCAGCCGGACTCACCG GATGAGCGAG GATCG AGAG ACGGATG GAGC CCGG C
CCGGAGCTCTATCCGTCTCT CAGC ||||| |||| ||||||| |||| ||||
CCTGGTC CTGGT TCTC TGCCTAT CTCG GGCC A
CC - --- A- GCC

GAM1000 CCCGTACTCCGTTCGTTTTG 26506 AGCCGTTTGC 26507 CCGT G ATCAG- CCC- G
CGG CA
GACATCAGCCGTTTGCCCGT CCGTGGTGCC CCCGTACT TCGTTTT GAC CCGTTTG GT
GTGC AGCG T
GGTGCCGGAGCGCATTTTGC GGAG |||||||| ||||||| ||| ||||||| || |||| ||||
TGCACGACTTTCCGAACGGA GGGCATGG AGCAAAG CTG GGCAAGC CA CACG
TCGT /
CCCTGGTCGGAAACGATTTG TTT- G GTCCCA CTTT G --- TT
GTACGGG

GAM1001 TTTTGCTAGGCAAAATGGTG 26516 TGTGCCTACA 26517 AGGCA ---- A- A
TGACACGACTTGGATACCAA TTAGCCATTT TTTTGCT AAATGGT GTG CACGACTTGG T
GTTGTGCCTACATTAGCCAT CAGA ||||||| ||||||| ||| ||||||||||
TTCAGAAGCAAAA AAAACGA TTTACCG CAT GTGTTGAACC /
AGAC- ATTA CC A

GAM1002 GCGGCAGAGGCGGAGATCGA 26537 CGGCTCCGAT 26538 AGAGG A G CA C GT TC
GGTCCAAGTCCAGGTCGCGG CTAGATCCCG GCGGC CGG GATC AGGTC AGTC AG
CGCGG G
TCGAGGTCGCGGTCTCGGCT GTCG ||||| ||| |||| ||||| |||| || |||||
CCGATCTAGATCCCGGTCGC CGCTG GCC CTAG TCTAG TCGG TC GCGCT A
----- - A CC C TG GG

GAM1003 GGCCGTGGGGGGAGCAGGGG 26547 CCCCCACCTC 26548 G- CA AC TCA
GAGACGGTCATCCTCCACCT CTCCAAACGG GGCCGT GGGGGAG GGGGGAG GG T
CCCCCACCTCCTCCAAACGG TC |||||| ||||||| ||||||| ||
TC CTGGCA CCTCCTC CCCCCTC CC /
AA CA CA TCC

GAM1004 GCGTACCTTTTTTTCATCCG 26733 TGCCATGATG 26734 CCTTTTTTT C CCTGCCG AT
A- TTT- TC

ATCCCTGCCGGGTAATACGT ATCGATGTCA GCGTA CATC GATC GGTA ACGTCCC AGA GC C
CCCAAGATTTGCTCCATGTT TATG ||||| |||| |||| |||| ||||||| ||| ||
GTTTCTGCGGGGCGTTGCCA CGTAT GTAG CTAG CCGT TGCGGGG TCT TG /
TGATGATCGATGTCATATGC ACT------ - TAGTA-- -- CG TTGT TA

GAM1005 GCCGATACCTTTTCATTAAT 26741 TACCTTTTCA 26742 AT ATTAA ACAC CTAA - AT
ACACACAGGGCTAACGAAGT TTAATACACA GCCG ACCTTTTC TAC AGGG CGAA GTCAGG G
CAGGATGTCCCTGATATTCG CAGG |||| |||||||| ||| |||| |||| ||||||
ATTTCCCTCACGTACCCGGA TGGT TGGAAAAG ATG TCCC GCTT TAGTCC /
AAAGGTTGTGGT GT GCCC- CAC- TTTA A CT

GAM1006 AGCGACACGGGGCGCGTCGT 26760 CCCCTGCAGC 26761 C TGTAAA TTAA TTTC A- - ATAT A A
GTAAACCATGTTAAACATTT GTGAAGGCAG GT G CCATG ACA AAACTGCTTTCGC GCA GGGAA AT A
CAAACTGCTTTCGCAGCAAT TTTC || | ||||| ||| |||||||||||| ||| ||||| ||
ATGGGAAAATAAATGTATTC TA C GGTAT TGT TTTGACGGAAGTG CGT CCCTT TG A
CCCCTGCAGCGTGAAGGCAG T ------ TC-- CC-- CGA CC-- A T
TTTCCTGTCTTATGGCTATG
TGCTTTGGCT
GAM1007 TAGGGCTGCTGATAGCTAGC 26810 TCCGGTGCCT 26811 G T CTA C---- TT- T G
GCTGCACTTAAAAATGGGGT GTCGTAGACC TAGG CTGC GATAG GCGCTG AC AAAAA GGG T
AGCCCTTTTTCTTGTAAATC TG |||| |||| ||||| |||||| || ||||| |||
CGGTGCCTGTCGTAGACCTG GTCC GATG CTGTC CGTGGC TG TTTTT CCC A
A - --- CTAAA TTC - G

GAM1008 GGGTGGCTATCTATCCATAG 26839 GTGCATTGGA 26840 --- CTA- TAGGCAG T CG
GCAGGCATCCGGCGTCTTTG GATAGTAGCT GGGTG GCTAT TCCA GCA CCGG T
GTGCATTGGAGATAGTAGCT TTCA ||||| ||||| |||| ||| ||||
TTCACCC CCCAC CGATG AGGT CGT GGTT /
TTT ATAG TA----- - TC

GAM1009 CGAGGAATAATAAGAACAAA 26847 TTTCACAGTA 26848 A-- C AATGC A A AACA A TG GA-- CA
GTAATGCCTGTAAAAATAAA GATTTTATTC AATA GAA AAAGT CTGT AAA TA TCAAC T TAT TGGT T
CATCAACATTGTATGATGGT CGGT |||| ||| ||||| |||| ||| || ||||| | ||| ||||
CATTAAACCAATTAGTATGA TTGT CTT TTTTA GACA TTT AT AGTTG A ATG ACCA T
CGTTGAACTAATTTCACAGT GGC A GAT-- C A CA-- C GT ATTA AA

AGATTTTATTCCGGTGTTAT
CCTCG
GAM1010 GTGGCCCAACCTCTGCTCCC 26856 CTTGAGGTCA 26857 ACCTCT T CTCTATTCT--- TT
TTA CC
CTCTATTCTCCTCTTGCGTT TACGTTTTAG GTGGCCCA GC CCC CCTC GCG TCT A
ATCTCCAATAGAATTTGCTT GGTG |||||||| || ||| |||| ||| |||
GAGGTCATACGTTTTAGGGT CGCCGGGT CG GGG GGAG CGT AGA /
GCTCGACCTGGGCCGC CCAGCT T ATTTTGCATACT TT TTA TA

GAM1011 AGTACACGGAATAATGATGG 26865 CATTGCACGC 26866 TACAC A A -- A GCCG----- -
- T
TATCATTGCACGCCGTATAC CGTATACTCT AG GGAATA TG TG GTATC TTGCAC TATA
C TCTATAG C
TCTATAGTCTTTGTAGATGT ATAG || |||||| || || ||||| |||||| |||| | |||||||
TATAACCACAAAAGTGCAGA TC TCTTAT AC AC TATGG GACGTG ATAT G
AGATGTT /
GGTATATCAACAATATTCTA TCAA- A A TA A AAAACACCA T T T
ACTCT

GAM1012 CGTCAGGAGCAACAACGAGG 26868 AGGCAAACCC 26869 A AACAACGAG- ACCC A-
ACA AA
CAAACCCTATTCAGGAACAG TATTCAGGAA CGTC GGAGC GCAA TATTC GGA G C
AACATCATATCCAAGAATGC CAGA |||| ||||| |||| ||||| ||| |
ACATTGCACAACCACAAGTT GCAG CCTTG CGTT GTAAG CCT C /
CCAGACG A AACACCAACA ACAC AA ATA TA

GAM1013 GGCGAAGCTTAGGTTTACTG 26928 TCAAAAAAAT 26929 ---------- TA
ACGTCACTTCAAATACACTC TAAGTTTCTA
TTTACTGACGTCACTTCAAATACACTCAAAAAAATTAA GTTTC T
AAAAAAATTAAGTTTCTATT TTAG |||||||||||||||||||||||||||||||||||||| |||||
AGAAACAACGTAATACGTTT AAATGACTGCAGTGAAGTTTATGTGAGTTTTTTTAATT
CAAAG /
TAATTTTTTTGAGTGTATTT TTGCATAATGCAA AT
GAAGTGACGTCAGTAAACCT
AAGCTTCGCC
GAM1014 TGTCGGAGAGTAAACATTGA 26931 TCGGAGAGTA 26932 -- - AAACAT A TAAAAC
CGGATAAAACAAAAATGCTC AACATTGACG TGTC GG AGAGT TG CGGA A
CGCATAACTCTACCATGGCA GATA |||| || ||||| || ||||
ACGG CC TCTCA AC GCCT A
TA A AT---- - CGTAAA

GAM1015 CGATTTCGAGAAATAATAAG 26939 TGTAAAGATA 26940 ATAA AATGC - GATA--- A AC
T AATC
AATAAAGTAATGCCTGTAAA AACATCAACA TA GAATAAAGT CTGT AAA AAC TCA ATTG
TTGGT A
GATAAACATCAACATTGTTT TTGT || ||||||||| |||| ||| ||| ||| |||| |||||
GGTAATCATTAAACCAATTA GT CTTATTTTA GACA TTT TTG AGT TGAT AACCA
/

GTATGACGTTGAACTAATTT GAC- GAT-- C AATCAAG C A- T AATT
CACAGTAGATTTTATTCCAG
TGTTATCCTCG
GAM1016 GGATCACGCCATTTAGTCAT 26948 TCCAAAATTT 26949 CCATTTA - A ATC A AGTAT
AA AGT
AACAGTAATCCAAAATTTTT TTTAAAGTAT GTCATA AC GTA CAA ATTTTTTAA
ATTTTAACGA GA T
TAAAGTATATTTTAACGAAA ATTT |||||| || ||| ||| ||||||||| |||||||||| ||
GAAGTTGTATCATCGTTAGG CGGTAT TG CAT GTT TAAAAGGTT TAGGATTGCT
CT /
ATTTGGAAAATCTTGTCTAC A------ G A CT- C ----- A- ATG
AGTGTATGGCACGAGATCC

GAM1017 TCCACATCGGCAGATGCGAC 26955 CATCGGCAGA 26956 --- GC A G
GACATACGATTGTGTGCCGT TGCGACGACA TCCACATC GGCAGAT GACG CATAC A
TTAATCTGCCTCGGGTGTGG TACG |||||||| ||||||| |||| |||||
A AGGTGTGG CCGTCTA TTGC GTGTG T
GCT AT C T

GAM1018 CTGGGTTTGTGTGCCGACTT 26958 ACCCTTTGAT 26959 TT TGCC CT CTTTTACCCTT
CTTACT CCT- CTG
GTTCCTTTTACCCTTTGATG GACTTACTGC TGGGT GTG GA TGTTC TGATGA GC
GAC A
ACTTACTGCCCTGACCTGAC CCTG ||||| ||| || ||||| |||||| || |||
CCGTCTACCGCCTCCTCATC ACCCG CAC CT ACAAG ACTACT CG CTG /
ACCTTTAGAACACTCCCTCA -- TCC- C- ATTTCC----- CCTC-- CCAT CCC
CGCCCAG

GAM1019 ACATAGCCCAAATGGACACT 26995 AAATGGACAC 26996 A CAA G A- AGG
TGCGGTTAGGACAAAACCGC TTGCGGTTAG ACAT GCC AT GAC CTTGCGGTT A
AAGCGGTCGATAGGCCATGT GACA |||| ||| || ||| |||||||||
TGTA CGG TA CTG GAACGCCAA /
C A-- G GC AAC

GAM1020 AAATTAAACCTGATTTAAAT 27019 ATCTTTTGCT 27020 CCTGATT T ACA T
GATTTACATGTTGATGCAAA AAAATTTTAA AAATTAAA TAAA GATTT TGT G
ATCTTTTGCTAAAATTTTAA TTT |||||||| |||| ||||| |||
TTT TTTAATTT GTTT CTAAA ACG A
TAAAATC T --- T

GAM1021 TTTAACTTTCGCTTTATTTT 27029 TGTAAATTTG 27030 T CT--- TG TTTA CATAT TTA
C- AGC
TTATGGTTTTAAAATCATAT TATTCTAAAA CT TCG TTATTTTTTA GT AAAT GCTACA
GTA TTA C
GCTACATTAGTACTTAAGCC AGTA || ||| |||||||||| || |||| |||||| ||| |||
TAAATAAATTGCATTTGTAG GA GGT AATGAAAAAT TA TTTA CGATGT CGT AAT
T

CTGTAAATTTGTATTCTAAA T TTATT CT TG-- AATGT TTA TA AAA
AAGTAATTATTTGGTAGTTG
AA
GAM1022 CTAGGTTTCAGACACGTTTA 27034 TACAACGTGT 27035 G AG - CATTC--- GT A - CATA
TCCATTCGCCGGGTATTGAT GAAAACTAG CTAG TTTC ACACGTT TATC GCCGG ATTG TCG GGT T
CGGGTCATATCATTAGCCGT |||| |||| ||||||| |||| ||||| |||| ||| |||
GAATAATCTCTGGCTTCATT GATC AAAG TGTGCAA ATAG CGGTC TAAT AGT CCG C
TCGATACAACGTGTGAAAAC A -- C CTTTACTT TC A G ATTA
TAG

GAM1023 TTAAGCAAGTGTAATTTTTA 27044 TACGCTGGAA 27045 G - ---------- A CCA TTTATGCA GATTT
GCAGTCCAAGTTTTTATGCA ACTAAACTAA A CAAG TGTAA TTTTTAGC GT AGTT ACGCA T
ACGCAGATTTTAATGATGTG CTTA | |||| ||||| |||||||| || |||| |||||
TCCCTCGATAACTATACGCT T GTTC ACATT AAAGGTCG CA TCAA TGTGT /
GGAAACTAAACTAACTTACA G T CAATCAAATC - TA- TAGCTCCC AGTAA
TCTTGGTTGA

GAM1024 AGTTGGAGAATTATTTTGGA 27049 TGGAGAATTA 27050 - TA- A-- AACTAC
CCTTTAACTACTAATGAAAA TTTTGGACCT AGTTGGAGA AT TTTTGG CCTTT T
AAGGAGACTAAAACTTGTAT TTAA ||||||||| || |||||| |||||
TTCCAGCT TCGACCTTT TG AAAATC GGAAA A
A TTC AGA AAAGTA

GAM1025 GCTGCATGGTGGCCAACAGT 27060 ACCACCGTGA 27061 ------- CCAAC AACTTA
GGGAACTTATTATACACCCA CAAATCCAGC GCTG CATGGTGG AGTGGG T
CTACCACCGTGACAAATCCA |||| |||||||| ||||||
GC CGAC GTGCCACC TCACCC /
CTAAACA A---- ACATAT

GAM1026 GCTGGTCCCATTCTCTTGGC 27129 TCACCAAAAA 27130 CCCATTCTC- CACA- TTC
ACAGATTCCATTTTCCATCA CAAAACAACC GCTGGT TTGG GA C
CCAAAAACAAAACAACCAGC AGC |||||| |||| ||
CGACCA AACC CT A
ACAAAACAAA ACTAC TTT

GAM1027 CAGCAAGGCGATATTCGATA 27187 TAACTTCACT 27188 CA ATAT-- TAAC - C C
ACGAATTCTCATTCTCCGAT CTCGATACCC CAG AGGCG TCGA GAA TT TCATT T
GATAACTTCACTCTCGATAC ACGT ||| ||||| |||| ||| || |||||
CCACGTTTACCTG GTC TTTGC AGCT CTT AA AGTAG C
CA ACCCAT CTCA C T C

GAM1028 GAGTCTCTGCAAACATGGGG 27195 ATGAAACATA 27196 - AAACA C-- CACGA A - CGATG AAT
CGAAGCCACGAGGGAGGAGT CCCCTTCCCC TCTGC TGGGG GAAGC GGGAGG GT TGT ATGAGACA C
TGTCGATGATGAGACAAATC CGCT ||||| ||||| ||||| |||||| || ||| ||||||||
TACTGTCTCATGAAACATAC AGACG ACTCT CTTCG CCTTCC CA ACA TACTCTGT /
CCCTTCCCCCGCTTCCTATC A ----- ATC CCC-- C T AAG-- CAT
TCAGCAGAAAAACTC

GAM1029 ACAGTGACATTACCTCATAA 27208 TCAGTTGTTA 27209 CATT CATAAAAAAAAAACATAT C TAT- ACG
AAAAAAAACATATACACCTG AGGTTCATTG ACAGTGA ACCT ACA CTGAG GATC A
AGTATGATCACGATACGATT T ||||||| |||| ||| ||||| ||||
TATTCTCAGTTGTTAAGGTT TGTTACT TGGA TGT GACTC TTAG /
CATTGT ---- AT---------- T TTAT CAT

GAM1030 CTATGTGAACTGATGGCAGC 27235 TTAAAATATC 27236 - AA GC CTTCCAAAC TA
TTCCAAACAAGATTACCTAT TACATCAGAG CTATG TG CTGATG AG AAGAT C
TTTTAAAATATCTACATCAG CATC ||||| || |||||| || |||||
AGCATCATGG GGTAC AC GACTAC TC TTTTA /
T GA A- TATAAAAT- TC

GAM1031 GCTGGTCCCATTCTTTTGGC 27243 TCACCAAAAA 27130 CCCATTC- CAC- TTC
ACAGATTCCATTTTCTATCA CAAAACAACC GCTGGT TTTTGG AGA C
CCAAAAACAAAACAACCAGC AGC |||||| |||||| |||
CGACCA AAAACC TCT A
ACAAAACA ACTA TTT

GAM1032 ATCGCCGATATCTTCGAGAA 27244 TTCGAGAAGA 27245 GATATCT-- AG CAAAAAT ACA
GACAAAAATACACACGCACG CAAAAATACA ATCGCC TCG AAGA AC C
TCAAAAATCTTTCCGACTAC CACG |||||| ||| |||| ||
AGCAAGGCGAT TAGCGG AGC TTCT TG G
AACGACATC CT AAAAAC- CAC

GAM1033 GTAACAACGATAATATTGCT 27252 TAATATTGCT 27253 AA ATA---- A AAA AT
TCAAAGGATTTAGCTGAGGG TCAAAGGATT GT CAACG AT TTGCTTC GG T
GGCAAAGTCTGAAAATGTTG TAGC || ||||| || ||||||| ||
GCAC CA GTTGT TG AACGGGG TC T
CG AAAAGTC A GAG GA

GAM1034 CTCAGAAGAGGGGATTATCT 27267 TCTATAGTTT 27268 A A TC - C
ATAGTTTTTATACTACGGTA TTATACTACG CTCAG AGAGGGG TTA TATAGTTTTT ATACTA G
GTATGGAAGGCTATATGAGT GTAG ||||| ||||||| ||| |||||||||| ||||||

TTTTCTGCTGAG GAGTC TCTTTTT AGT ATATCGGAAG TATGAT /
G G -- G G

GAM1035 GGAAGTACATGTGGGTGGTC 27271 AAACTGCTGT 27272 A T A- TAATTG TCC CT ATC
ACGA- TC
AGGTAATTGTTTGTCCTGCA CCACCTATGC C TGTGGG GGTC GG TTTG TGCAT GT
TAGTA AGTA C
TCTGTATCTAGTAACGAAGT ACCG | |||||| |||| || |||| ||||| || ||||| ||||
ATCCACTACTGAAACTGCTG G ACGCCT CCAG CC AAGC ACGTA CA GTCGT
TCAT /
TCCACCTATGCACCGAAACC - - AA TCCA-- C-- TC CCT CAAAG CA
TCCAAGACCTCCGCAGTGTC
C
GAM1036 CCCCCAGAAAGAATAATCAC 27302 AGAATAATCA 27303 AAGA ACT---------- G
TGCTTCGAACGGAGCTCGAT CTGCTTCGAA CCCCCAGA ATAATC GCTTC A
TCATCATCCGGGATTATGCT CGGA |||||||| |||||| |||||
TTGGGGG GGGGGTTT TATTAG CGAGG A
CG-- GGCCTACTACTTAGCT C

GAM1037 AGGAAGCGGGGGAAGGGGTA 27309 AGGGGTATGT 27310 AA A A TC-- TA
TGTTTCATGAGACAGTAGAT TTCATGAGAC AGG GCGGGGGA GGGGT TGTT ATGAGACAG
G
TTGTCTCATCATCGACAACT AGTA ||| |||||||| ||||| |||| |||||||||
CCTCCCTCGTGGCTT TTC TGCTCCCT CCTCA ACAG TACTCTGTT /
GG - - CTAC TA

GAM1038 GGTATTGTAACAATAACGTA 27321 TATTGTAACA 27322 G ATAACGTACAG---- AAA
CAGTGATGAAACACAACGTC ATAACGTACA GGTATT TAACA TGATG C
AACAATTTTTAAAAACTGTT GTGA |||||| ||||| |||||
AAAATACC CCATAA ATTGT ACTGC A
A CAAAAATTTTTAACA AAC

GAM1039 CGGTTTTTTTTTCCTCCCGT 27331 TCCCGGGTCC 27332 TTCCT TT----- CCC CC
TGCCCCCGGGGGGTCCCCGG CGAAAAAACC CGGTTTTTTT CCCG GCC GGGGGGT C
CCCCCCCCGGCCCTCTCCCG G |||||||||| |||| ||| |||||||
GGTCCCGAAAAAACCG GCCAAAAAAG GGGC CGG CCCCCCG /
CCCT- CCTCTCC CC- GC

GAM1040 GGGGCGCGGTACCCCGCCGA 27362 CGATGGGGAG 27363 CG G A- G- G G GA GCG
TGGGGAGGGGGCGCGGTACC GGGGCGCGGT GGGG C GT CCCC CC AT GG GGGG C
CCGCCGATGGGGAGGGGGCG ACCC |||| | || |||| || || || ||||
CGGTACCCC CCCC G CG GGGG GG TA CC CCCC G
AT G CG AG G G G- ATG

GAM1041 GACAACCCCAATTGTGTTTA 27416 ACCCCAATTG 27417 CCA- TT---------- T
TGTATATTATATATCGTCTG TGTTTATGTA GACAACC ATTGTG TATGTA A
TAGACACACGATGATTGGTT TATT ||||||| |||||| ||||||
GTT TTGTTGG TAGCAC ATATAT /
TTAG ACAGATGTCTGCT T

GAM1042 GCCCCTAAAAAGGATCCTTA 27428 TTAGATCAGT 27429 -- TC GAT TGTATTTT GG
----- CAA
TGATGGCCTTGTATTTTGGG TTCCTTTGGG AAAGGA CTTAT GGCCT GGGA
TTGATTTAAA GGA A
AGGTTGATTTAAAGGACAAA CCGT |||||| ||||| ||||| |||| |||||||||| |||
CTATCCACAGATTTAGATCA TTTTCT GAATG CCGGG TCCT GACTAGATTT
CCT /
GTTTCCTTTGGGCCGTAAGT CG TT --- TT------ TT AGACA ATC
TTCTTTTGCAACTGGGT

GAM1043 CCAGGCACATCTGCTAATAG 27434 CTCCTACTCC 27435 CACAT TG AT A CTCTTACCA
TAGGAACACTCTTACCAGCT TAGTGGCTCC CCAGG C CTA AGTAGGA CA G
ACATCTATGCTCCTACTCCT CTGG ||||| | ||| ||||||| ||
AGTGGCTCCCTGG GGTCC G GAT TCATCCT GT /
CTC-- GT CC C ATCTACATC

GAM1044 AGTTAATATATATTTTATTT 27500 TATTTTATTT 27501 T-- T G TATT
TTGAAAATATTAATTTTTTT TTGAAAATAT AGTTAATA ATAT TTATTTTT AAAA A
TGAAAAATAATATATTATTA TAAT |||||||| |||| |||||||| ||||
TTAACT TCAATTAT TATA AATAAAAA TTTT A
TAT T G TTTT

GAM1045 TCAGAAAGAGGTTTAATATT 27506 TCCATCAGAA 27507 G G T A G GACCA AAG
AGA
TTTGTGAGACCATCGAAGAG AGAGGTTTAA TCA AAAGA GTT AAT TTTTT TGA TCG
AGAGAAAG T
AGAAAGAGATAAAACTTTTT TATT ||| ||||| ||| ||| ||||| ||| ||| ||||||||
TTACGACTCCATCAGAAAGA AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTTC A
GGTTTAATATTTTTGTGA G A T G G ACCTC A-- AAA

GAM1046 TTGAAAGCCGGGGGGTGGGAG 27523 CTGGGTCCGT 27524 CC - A - TG TCG
ATCCGGATTGCCAGTCTGCT GACTACCCAC TTGAAAG GGGGGTGGG AG TC CGGAT
CCAGTCTGC A
CGATATCGCAGGCTGGGTCC TCCC ||||||| |||||||| || || ||||| |||||||||
GTGACTACCCACTCCCCCTT AACTTTC CCCTCACCC TC AG GCCTG GGTCGGACG T
TCAA C- A - T -- CTA

GAM1047 GTCCCTCTTCCGTCGGGAGC 27575 CGTCCCGGCC 27576 CTTCC-- AGC CTCTCG A
GCGCCCGGCTCTCGGCCGAC TTCTACGGGG GTCCCT GTCGGG GCGCCCGG GCCG C

CCCGGCCCGGGCGTCCCGGC AC |||||| |||||| |||||||| ||||
CTTCTACGGGGAC CAGGGG CGGCCC TGCGGGCC CGGC C
CATCTTC --- ------ C

GAM1048 TTTTTTACGACTCCATCAGA 27640 CATCAGAAAG 7182 - CTCCA G G T A G GACCA AAG AGA
AAGAGGTTTAATATTTTTGT AGGTTTAATA CGA TCA AAAGA GTT AAT TTTTT TGA TCG AGAGAAAG T
GAGACCATCGAAGAGAGAAA TTTT ||| ||| ||||| ||| ||| ||||| ||| ||| ||||||||
GAGATAAAACTTTTTTTACG GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTTC A
ACTCCATCAGAAAGAGGTTT A ACCAG G A T G G ACCTC A-- AAA
AATATTTTTGTGAGACCATC
GAAGAGAGAA
GAM1049 CTTTTTTACGACTCCATCAG 27641 CATCAGAAAG 7182 A CTCCA G G T A G GACCA AAG AGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA CGA TCA AAAGA GTT AAT TTTTT TGA TCG AGAGAAAG T
TGAGACCATCGAAGAGAGAA TTTT ||| ||| ||||| ||| ||| ||||| ||| ||| ||||||||
AGAGATAAAACTTTTTTTAC GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTTC A
GACTCCATCAGAAAGAGGTT - ACCAG G A T G G ACCTC A-- AAA
TAATATTTTTGTGAGACCAT
CGAAGAGAG
GAM1050 ACCTCTTTCTGATGGAGTCG 27642 TGATGGAGTC 27643 TTTCT TG TC AAAG CT TC TCTTC T CTCACAA
TAAAAAAAGTTTTATCTCTT GTAAAAAAAG C GA GAG GTAAAA TTTTAT CTT TC GA GGT A
TCTCTCTTCGATGGTCTCAC TTTT | || ||| |||||| |||||| ||| || || |||
AAAAATATTAAACCTCTTTC G CT TTC TATTTT AAAATG GAG AG CT CCA A
TGATGGAGTCGTAAAAAAAG CTTCT CT TC GAAA CT GT TCTTT - AATTATA
TTTTATCTCTTTCTCTCTTC
GATGGT
GAM1051 ACCTCTTTCTGATGGAGTCG 27648 TGATGGAGTC 27643 TTTCT TG TC AAG- CT TC TCTTC T CTCACAA
TAAAAAAGTTTTATCTCTTT GTAAAAAAAG C GA GAG GTAAAA TTTTAT CTT TC GA GGT A
CTCTCTTCGATGGTCTCACA TTTT | || ||| |||||| |||||| ||| || || |||
AAAATATTAAACCTCTTTCT G CT TTC TATTTT AAAATG GAG AG CT CCA A
GATGGAGTCGTAAAAAAAGT CTTCT CT TC GAAA CT GT TCTTT - AATTATA
TTTATCTCTTTCTCTCTTCG
ATGGT
GAM1052 TCTCAATAAAGAAATAAATA 27649 AGAAATAAAT 27650 T A AA TCTTT AT
TATCTTTGTTAAATATGTTA ATATCTTTGT TC CAATA AGAAATA TATA GTTAA A
ACTTTTTGTATATTTCTATA TAAA || ||||| ||||||| |||| |||||
TTGTGA AG GTTAT TCTTTAT ATGT CAATT /
T A -- TTTT- GT

GAM1053 TGGCTGATGTCAAGTCTATG 27664 CCAGAAGTTT 27665 G TCAAG ---- ATTA
TGGAATTAGAAACTCCACAT ATGAGCCA TGGCT ATG TCT ATGTGGA G
CCCCAGAAGTTTATGAGCCA ||||| ||| ||| |||||||
ACCGA TAT AGA TACACCT /
G TTGA- CCCC CAAA

GAM1054 TATGAGGTTCGACCAGCGGC 27765 AGCGGCTGCT 27766 A A GAAGA- GA A AG AA CG
TGCTGGAAGAGGGCGACGAG GGAAGAGGGC TATG GGTTCGACC GCGGCTGCTG GGGC CG GG GATG GTGAC T
GAGGATGAAGTGACCGTGAT GACG |||| ||||||||| |||||||||| |||| || || |||| |||||
GTCGCCGTCACCCGAGCCCG GTGC CCGAGCTGG CGCCGACGAC CCCG GC CC CTGC CGCTG G
TGCAACAGCAGCCGCCGGTC - C AACGTG A- - A- -- TA
GAGCCCGTG

GAM1055 CTATATGAACTTATGTGCCT 27852 TGTGGACAAC 27853 TGAAC GCC- ATGC C
GTCATGCCAGCCAGAGTTGT AAACATAATT CTATA TTATGT TGTC CAGC A
GGACAACAAACATAATTATT ATTA ||||| |||||| |||| ||||
ATAG GATAT AATACA ACAG GTTG G
TATT- AACA GT-- A

GAM1056 GTGGTTGTAACAGTTGCTTC 27857 CGTTCAGTCC 27858 T A TG--- - T ATTA T TA AATC
GAGTTGTGAATTAGAATCGT GATATCGGAG GTGGTTG AAC GT CTTCGA GTTG GA GAA CGT CA T
TACAAATCTTACGTGCGACG AAAG ||||||| ||| || |||||| |||| || ||| ||| ||
TTCAGTCCGATATCGGAGAA CACCAGT TTG CA GAGGCT TAGC CT CTT GCA GT /
AGTACCGTTTGACCAC - C TGAAA A - GA-- - GC GCAT

GAM1057 GCGTTCCGTTGAGAGTGACT 27870 TCCAAGTTCA 27871 - C- TG ----- GTATT CC
GTATTCACCCTTATGTCCAA CTGACTCTTG GC GTTC GT AGAGT GACT CA C
GTTCACTGACTCTTGATAAG ATAA || |||| || ||||| |||| ||
AGCTGC CG CGAG TA TCTCA TTGA GT T
T AA GT GTCAC ACCT- AT

GAM1058 GATACATCGATGTGGACAAC 27895 CCATATGCTA 27896 A- GACAACA --- CT- ATAATA C CT TACT
AACTGGGCCCTCTTTATAAA AAAGTTATGG TGTG ACTGG GCC CTTTATAA AGCG TGT GGA G
TAATAAGCGCTGTCTGGATA AGTA |||| ||||| ||| |||||||| |||| ||| |||
CTGAATTCTCCCATATGCTA ACAT TGACC CGG GAGGTATT TCGT ATA CCT A
AAAGTTATGGAGTACGGCCT AG ------- GTC CAT GAAAA- - C- CTTA
GCCAGTTACAGACGAAGTAT
T

GAM1059 TATGCTTCCTTTAAACAGGT 27907 TCTCACACCA 27908 CT- TAAACA T TGG
GTTGGATTCTGATGGCTTTT GGGACAACAT TATG TCCTT GGTGT GGATTCTGA C
TAGAATCTCACACCAGGGAC A |||| ||||| ||||| |||||||||
AACATA ATAC AGGGA CCACA TCTAAGATT /
AAC ------ C TTT

GAM1060 AGTTGGCTTTCTACCCCTCT 27941 TAGTTTGTGT 27942 CT- CCCT- T ACAA A
TTACAGACAAGGAAAGGTTC GGGATCTCCA AGTTGG TTCTAC CT TACAG GGAA G
CCTGTATAGTTTGTGTGGGA ACT |||||| |||||| || ||||| ||||
TCTCCAACT TCAACC AGGGTG GA ATGTC CCTT /
TCT TGTTT T ---- G

GAM1061 TTTACCTGTCCAATTGTCTG 27952 TACCTGTCCA 27953 T T AT- ------ CTATAATCA
CCAAAAA
TGAGGTCTATAATCAGACTT ATTGTCTGTG TT ACC GTCCA TG TCTGTGAGGT
GACTTT T
TCCAAAAATATAAAGAAAAA AGGT || ||| ||||| || |||||||||| ||||||
GTTAATCTTACAGAAATTAC AG TGG CAGGT AC AGACATTCTA TTGAAA A
CATAATGGACTGGTTGA T T AAT CATTAA A-------- AAGAAAT

GAM1062 GTCTCGGTCAGCGTGCCATA 27967 TGGCATGCTG 27968 C TAAACGAATATTATA C T
A
AACGAATATTATATGGTACG ACCGAAC GT TCGGTCAGCGTGCCA TGGTA G CGA C
TCGAACATTCGCTTATCATG || |||||||||||||| ||||| | |||
GCATGCTGACCGAAC CA AGCCAGTCGTACGGT ACTAT C GCT A
- ---------- T - T

GAM1063 GGGCACAATTTCTTGCACGT 27970 TATACAGGCT 27971 CAATT C- G CA A
GTGCATATACCAAAGGGTAT ATGCAAGGTC GGGCA TCTTGCA GT TG TATACC A
ACAGGCTATGCAAGGTCATA ATAT ||||| ||||||| || || ||||||
TGTCC CCTGT GGAACGT CG AC ATATGG A
ATACT AT G -- G

GAM1064 ATGTTTGTGGAGTGATATAC 27981 GGAGTGATAT 27982 TT TG - TATA TGTGCT TT
TTGTGCTGCTTATTTGCTTT ACTTGTGCTG ATGT G GA GTGA CT GC A
TGGCTTTCGCATTTGCCTGC CTTA |||| | || |||| || ||
AT TACG C TT CGCT GG CG T
TC GT A TTC- TTTT-- TT

GAM1065 ACATGGTGGTATTTGACAGA 27990 TTTGACAGAC 27991 T- TG TT A TG - G
CATGATGTTGGGTTACTAGG ATGATGTTGG ACA GG GTA TGACAG CA ATGT TGG T
CATATTGTTGTTACTTATTG GTTA ||| || ||| |||||| || |||| |||
CTCTTGT TGT TC TAT ATTGTT GT TACG ATC T
TC GT TC - TA G A

GAM1066 GCAAGTGCTACTACTTTTCG 28004 AGTGAAGCCG 28005 AA G TAC-- AG GAG A
GAGTCAGAGTCCAATTGGAG AAAAATTTTG GC GT CTAC TTTTCGG TCA TCC A
TGAAGCCGAAAAATTTTGTA TAGA || || |||| ||||||| ||| |||
GACAGC CG CA GATG AAAAGCC AGT AGG T
A- - TTTTA GA G-- T

GAM1067 TAGTTTAGTAAATAGATTCA 28031 TAAAATATAA 28032 TA AATAG CA TACAAT
ATAATACAATAAATTATTTT TACCGAATTA TAGTT GTA ATT ATAA A
ATAAAATATAATACCGAATT ||||| ||| ||| ||||
A ATTAA CAT TAA TATT A
GC AATA- AA TTATTA

GAM1068 TTTCAAATAATATATGCTAA 28035 TAATATATGC 28036 AA-- AAA CATTAAAAT A
AATTAGTTCATTAAAATTTA TAAAATTAGT TTTCA TAATATATGCTA TTAGTT TTATAG T
TAGATAACTATGATATATCT TCAT ||||| |||||||||||| |||||| ||||||
TTAACTAAAGTAGCATATGT AAAGT ATTGTATACGAT AATCAA AGTATC A
TACTCATGAAA ACTC GA- TTTCTATAT A

GAM1069 CTCCTCCACTAATTCGCGGA 28042 GTGCATCGCC 28043 TAA---- TA TG T T -
TTAT T
TACGTTGCCTTATGGCTGAG ATGGGTGACG CTCCTCCAC TTCGCGGA CGT CCT ATGGC
GA GC TGG T
CTTATTGGTTCCCCATGGTG ACTC ||||||||| |||||||| ||| ||| ||||| || || |||
CATCGCCATGGGTGACGACT GGGGAGGTG AGGTGCCT GCA GGG TACCG CT CG
ACC C
CCGTGGAGGGTTTTGTGGAG TTTTGGG CA GT - - A TGGT C
GGG

GAM1070 CGTTTAATAAATTAAATATA 28047 TAAATTAAAT 28048 A---- - T ATAATA ACAA
AATATTTTAATTTATAATAT ATAAATATTT CGTTTAATA ATTAA ATATAAATATTT AATTT
TAGGTA A
AGGTAACAAATATATGCCTA TAAT ||||||||| ||||| |||||||||||| ||||| ||||||
AAAAATTAAATGTTTATATA GTAAATTAT TAATT TATATTTGTAAA TTAAA ATCCGT
/
TTAATGAAAATATTAAATG AAAAG A - AA---- ATAT

GAM1071 TGACCCCGCCCCTCGGACTT 28050 CCTCGGACTT 28051 CC CCCTC CTT ---- T
TGACCGTTCCCACGCCACGT TGACCGTTCC TGAC CGC GGA TGAC CGT C
CATTTTCCCACGCGACGTCA CACG |||| ||| ||| |||| |||
ACTG GCG CCT ACTG GCA C
CA CAC-- TTT CACC C

GAM1072 AATAATATAGATAGCAGATT 28056 TAATATAGAT 28057 A - GC TA ----- AA

ACTTAAAATATTTATAAAAA AGCAGATTAC AAT ATATA GATA AGATTACT AAATA TTTAT A
ATAAAACTTTTATTTCTGGT TTAA ||| ||||| |||| |||||||| ||||| |||||
AGTTTTGTATCATATATGAT TTA TATAT CTAT TTTGATGG TTTAT AAATA /
T G A GT TC TTTCA AA

GAM1073 GCGCTCATGTCGCTGGGAGT 28068 TCGCTGGGAG 28069 C T C G C ACC
ACACCCGGACCCGGGCCTGG TACACCCGGA GCG TCA GT GCTGG AGTACA CCGG C
ATGTACTCCAGCACCTGATC CCCG ||| ||| || ||||| |||||| ||||
GC CGC AGT CA CGACC TCATGT GGTC G
T C - - A CGG

GAM1074 ATTGATAATTATATGAGTGA 28087 TGAGTGAATT 28088 - ------ TG A G ACACA- CA
ATTTAATGATAACACATCAC TAATGATAAC ATTGATA ATTATA TGAG A TTTAAT ATA TCA
T
ATCCTGAATTTAATATAGTT ACAT ||||||| |||||| |||| | |||||| ||| |||
AAAGTTGCTCAAAAACGTGT TAACTAT TAATGT ACTC T AAATTG TAT AGT /
AATATATCAAT A GCAAAA GT G A AATTTA CC

GAM1075 CCGCCGTCTCGTAGACCGAA 28099 TTTGATGAGG 28100 C C TAGA GA C- ACG
TCCAGACGACGCAGCCCGTC ACGTCGAAAT CCGC GT TCG CC ATC AGACG C
TTTGATGAGGACGTCGAAAT TGTG |||| || ||| || ||| |||||
TGTGG GGTG TA AGC GG TAG TCTGC A
T A TGCA AG TT CCG

GAM1076 CAAACCGGGTGCAATATCAG 28103 TGGTATGAAG 28104 - GCA TC - - TA
CTCCTGTCGCTATTAGTCGG CCTAGGTTTG CAAACC GGGT ATATCAGC CT GTCG C T
CGAGTGGCTGGTATGAAGCC |||||| |||| |||||||| || |||| |
TAGGTTTG GTTTGG TCCG TATGGTCG GA CGGC G /
A AAG GT G T AT

GAM1077 GTAACGGGGATCGCGAGCGG 28134 ACGGGGATCG 28135 AA TCGCGA G AG GAC T
TCGAGTCGGGACCCTGCAGG CGAGCGGTCG GT CGGGGA GC GTCG TCGG CC G
CGACCGAACGGCAGCAGATC AGTC || |||||| || |||| |||| ||
TTCCCCGCAAC CA GCCCCT CG CGGC AGCC GG C
AC TCTAGA A A- AGC A

GAM1078 AGGGTGTCAATTACATTGCT 28143 TTCCCGGGAC 28144 ACATT- -------- T CTA GTA
T
GATCGTGATGTGATAACTAC TTATCTCGTC ATT GC TGATCGTGATG GATAA CTGGGG
ATATTGGTG T
TGGGGGTAATATTGGTGTTA ACGA ||| || |||||||||| ||||| |||||| |||||||||
ACATCAATATTCCCGGGACT TAG CG GTTAGCACTGC CTATT GGCCCT
TATAACTAC A
TATCTCGTCACGATTGTTCT CTACAT TAATTCTT T CAG --- A

TAATGCTACATCGATTGGTC
CCCT
GAM1079 CGTGCTGCCATTAGCTCTTA 28153 TGCCATTAGC 28154 CT C---- T TTC A
TGCTCATTCCGCTGATTCAG TCTTATGCTC CGTG GCCATTAG TCTTA GCTCA CGCTG T
CGCCTTGGGCTGAGAATGTT ATTC |||| |||||||| ||||| ||||| |||||
CTAGTGGTCCCATG GTAC TGGTGATC AGAGT CGGGT GCGAC /
CC TTGTA - TCC T

GAM1080 GGTGAGCGGACGAACAGATA 28165 TGAGCGAGCG 28166 A GA AC-- C G A G AGT
GCCGCGCGCACACGCGAGTC ACTGTCTCGA GGTG GCG CGA AGATAG CGC CGC CAC CG
C
TCCCGGTGAGCGAGCGACTG GTCG |||| ||| ||| |||||| ||| ||| ||| ||
TCTCGAGTCGCACGCACACC CCAC CGC GCT TCTGTC GCG GCG GTG GC /
A AC GAGC A A A - CCT

GAM1081 TTTTGTTAATAAAGTATGTA 28169 TAAAGTATGT 28170 - T TTCATTT TG -
GACTAAG TGTCC
TGGAGGTTTCATTTGTGGTT ATGGAGGTTT TAAAGT ATGTA GGAGGT GTGGT CAC CCTGT
GTGT C
GCACCCTGTGACTAAGGTGT CATT |||||| ||||| |||||| ||||| ||| ||||| ||||
TGTCCCTGTTTTACATATAA ATTTTA TACAT CCTTTA CATTA GTG GGATA TACA
T
TAGGAGTGTGATTACCAACA A - CAAC--- GT A ATA---- TTTTG
TTTCCTACATAATTTTATGC
CCTACCCTAAG
GAM1082 GAGGTGCTTGCATGGAGCCA 28187 TATTGGATAA 28188 TG GC A A G--- C CAA T
TTG
TCTCTATTGGATAAACAGCA ACAGCAAAGG GAGG CTT ATGG GCC TCTCTATT GATAAA AG
AGG GAA G
AAGGTGAATTGGCATTTTCC TGAA |||| ||| |||| ||| |||||||| |||||| || ||| |||
CCTCTTTTTATCAAAAGATG CTTC GAA TGTC CGG AGAGGTAG CTATTT TC TCC
CTT C
GAGAGGCCTGTAAAGTCCTT CT A- - - AAAA T --- C TTA
C

GAM1083 TTCACATGGTTGTGAATCTT 28209 TGTGAATCTT 28210 --- G CT CAC CT
GGCACAGGCCTTAAAGTTTT GGCACAGGCC TTCAC ATGGTT TGAAT TGG AGGC T
CCACGTTCAGAGCCATACAG TTAA ||||| |||||| ||||| ||| ||||
TGGG GGGTG TACCGA ACTTG ACC TTTG A
ACA G C- T-- AA

GAM1084 GCACGTCCGCGGGCGCGTAG 28226 GCGCGTAGGC 28227 C -- G CAGCAC A A AG
CA
GCCAGCACCTGAGCCAGCAG CAGCACCTGA GCA GTCCGCG GGCGCGTA GC CTG GCC
GC GT A
GTCAAAGTGCTCGCCGGCCA GCCA ||| ||||||| |||||||| || ||| ||| || ||
GCAGCGTGCGCGCCAGCGCG TGT CGGGCGC CCGCGCGT CG GAC CGG CG CG A

```
    GGCATGT                          A     GA      G  AC----  -  C  CT  TG


GAM1085  CTCAAATTACTTCAGAGCTT 28254   TACTTCAGAG 28255       TTAC    A   TCATTTTA  A     CCTC
    TCATTTTAAAAAATTACATC       CTTTCATTTT       CTCAAA   TTCAG GCTT      AAA ATTACAT   T
    CTCTTCCTGTGTAATGTTTG       AAAA          ||||||   ||||| ||||      ||| |||||||
    AGTGCTGAATTTTTGAG                    GAGTTT   AAGTC TGAG      TTT TAATGTG   /
                              TT--    G   --------  G     TCCT


GAM1086  CCAGAGCCTTCAAAAATTGC 28287   CAACTGTATG 28288       -----  -    AAAAT-  TGAGT--     GAA
    TGAGTGCTTCTGAAACTGAG       AACCTGAAGA       CCAGAG    C CTTCA     TGC     GCTTCT   A
    AAGCTCCAACTGTATGAACC       GTAA          ||||||    | |||||     |||      ||||||
    TGAAGAGTAACTCTCTGG                   GGTCTC    G GAAGT     ATG      CGAAGA   /
                              TCAAT A    CCAAGT   TCAACCT     GTC


GAM1087  ACAGTAGTTTTCACGGTATT 28300   TTAAATCGGG 28301       -    CACG-     --       T
    TTTTGAAATTAAATTTTAAA       TACATGATAA       ACAGTA GTTTT    GTATTT  TTTGAAAT A
    TCGGGTACATGATAAAGCAT       AGCA          |||||| |||||    ||||||  ||||||||
    GCTGT                      TGTCGT CGAAA    CATGGG  AAATTTTA /
                              A    TAGTA     CT      A


GAM1088  TCGTCGTCCACCTCAGGTAC 28308   TATTATTTTA 28309      CG   A--     GTAC--------        TA
    AATAGTATATTATATATATA       ATAAACTTAT       TCGT  TCC   CCTCAG         AATAGTATAT  T
    TTATTTTAATAAACTTATTG       TGAG          ||||  |||   ||||||          ||||||||||
    AGGACGGGAGAACGA                      AGCA  AGG   GGAGTT         TTATTATATA  /
                              AG   GCA     ATTCAAATAATT        TA


GAM1089  TTACAACTTTCATTTTAAAA 28314   TAGCGTCTTA 28315         TC      -  T   GT  TC
    GTCGCGTCTTCTTCCGGTAG       TTAAAGTTTA       TTACAACTT  ATTTTAA AAG CGC  CT  T
    CGTCTTATTAAAGTTTAAGT       AGTT          |||||||||  ||||||| ||| |||  ||
    TGTAG                      GATGTTGAA  TGAAATT TTC GCG  GG  T
                               TT      A   T   AT  CC


GAM1090  AAAATTATGTGTAAGCCTAG 28319   CATTGTGTTT 28320      TT   GTAA  C   CGT    C      -  A
    CGTGAGTGCGCACAGTCAGA       ACTTTATTTA       AAAA  ATGT    GC TAG   GAGTG GCACAGT CAG T
    TTCTTGCATTGTGTTTACTT       GCAA          ||||  ||||    || |||   ||||| ||||||| |||
    TATTTAGCAATAACATCTTT                 TTTT  TACA    CG ATT   TTCAT TGTGTTA GTT T
    TT                         TC    ATAA  -  TAT     T      C   C


GAM1091  ATCTCTTTCAGTATGTGAAT 28341   TATGTGAATA 28342       TCAGT--  -       TA   T
    AGATAGGTATTTTATCTCTA       GATAGGTATT       ATCTCTT      ATG TGAATAGA  GGTA T
    TTCATCATCGAATTTAAGAG       TTAT          |||||||      ||| ||||||||  ||||
    AT                        TAGAGAA      TAC ACTTATCT  CTAT /
                               TTTAAGC   T      --   T
```

GAM1092 GAGCTGGAAGCTATCCTAAG 28351 TATCCTAAGG 28352 AA A CT CAA-- C CA
GTCAATCCGACTCCAACGTG TCAATCCGAC GAGCTGG GCT TC AAGGT TC GACTC A
GGTCAGAGCCATACCTTTCG TCCA ||||||| ||| || ||||| || |||||
AAGTGTCAGTTC CTTGACT TGA AG TTCCA AG CTGGG C
G- - CT TACCG A TG

GAM1093 ATTTTAGGAACTACGTTCAT 28369 TTCATCTTTT 28370 CG TCA TCCT GC
TATTAAAACTATC T
GGTATCCTGGCGAATATTAA ATCACCATAT ATTTTAGGAACTA T TGGTA G GAA
AATGATA G
AACTATCAATGATATGATTA AGTT |||||||||||| | ||||| | ||| |||||||
TCGTTTTCATCTTTTATCAC TAGAATCTTTGAT A ACTAT C CTT TTGCTAT A
CATATAGTTTCTAAGAT AT CC- TTT- TA ---------- T

GAM1094 TGGGCTACACTGATAGGCTG 28382 CACCTGATTT 28383 G C ---------- C G C
CCCGTTCTGAAGGGGCACCT ACAAAACAGA TGG CTACA TGA TAGG TGCCC TT T
GATTTACAAAACAGACTTTA CTTT ||| ||||| ||| |||| ||||| ||
TTGTGGGCCA ACC GGTGT ATT GTCC ACGGG AA /
G T TCAGACAAAACATTTA - G G

GAM1095 GGCGTCTAAGATATTCTTCC 28419 TCTAAGATAT 28420 - GATAT A--- CTTATT
ATCAACTTATTAACATTTTT TCTTCCATCA GGCGTC TAA TCTTCC TCAA A
GACTAGGGAAGATACATTAT ACTT |||||| ||| |||||| ||||
GACGTC CTGCAG ATT AGAAGG AGTT /
T ACAT- GATC TTTACA

GAM1096 GGCCTGGAGGACGCGGGCCA 28431 CACGAGCTGG 28432 G CGC A A T G GCCT
GCACGTGAAAGTGAGGTGCC CCCTCCTGCG GGCCTG AGGA GGGCCAGC CGTGAA G GA GT
C
TCTTTGACGTCCTTCACGAG GGCC |||||| |||| |||||||| |||||| | || ||
CTGGCCCTCCTGCGGGCC CCGGGC TCCT CCCGGTCG GCACTT C CT CA /
G --- A - - G GTTT

GAM1097 GGCCACCTGCTTTCACCCCT 28501 GGGCTTCACC 28502 T- TCAC---------- CTA
TCTACTTCAAGGGCTTCACC TCCAACCACC GGCCACC GCTT CCCTT C
TCCAACCACCTGAGCTCGGT TGAG ||||||| |||| |||||
GGCC CCGGTGG CGAG GGGAA /
CT TCCACCAACCTCCACTTC CTT

GAM1098 GGCGGAGGATGGGGCGACGG 28522 CACGTGGCCA 28523 - AT--- - G GG--- TAAC
GGTTCTTTAACATTCTCAGG CCTTTAACCT GGCGG AGG GG GGC ACG GTTCTT A
GACAGGCACGTGGCCACCTT GCTG ||||| ||| || ||| ||| ||||||

TAACCTGCTGCC CCGTC TCC CC CCG TGC CAGGGA T
G AATTT A G ACGGA CTCT

GAM1099 ATGTTTTTTATCTCTTTCAG 28542 TATGTGAATA 28342 T -- TCAGT-- - TA T
TATGTGAATAGATAGGTATT GATAGGTATT ATGTTT TT ATCTCTT ATG TGAATAGA GGTA T
TTATCTCTATTCATCATCGA TTAT |||||| || ||||||| ||| |||||||| ||||
ATTTAAGAGATCCGATAAAC TACAAA AG TAGAGAA TAC ACTTATCT CTAT /
AT T CC TTTAAGC T -- T

GAM1100 TGGGATTTTACTTAATATAA 28543 TTAGAAATGC 28544 A ATATAATAT CC TA
TATTATTTCCCGTAATAAAT CAAATCTATA TGGGATTTT CTTA TATTTC GTAA A
TTTATTAGAAATGCCAAATC AGAA ||||||||| |||| |||||| ||||
TATAAGAAAAGTCCTA ATCCTGAAA GAAT GTAAAG TATT A
A ATCTAAACC AT TT

GAM1101 TGTGTATGTATTAATAAAGT 28563 TGTTATGGTT 28564 TA TTA A CT TTT AA T
ACTGTATTTACTAAACTATT GCACCCACA TGTG TGTA ATAA GTA GTA ACT ACTA T
TATAGTAGTCTTATGTTATG |||| |||| |||| ||| ||| ||| ||||
TTATGGTTGCACCCACA ACAC ACGT TATT TAT TAT TGA TGAT T
CC TGG G TG TC- -- A

GAM1102 CGGGTTTTTTATCTCTTTCA 28577 TCGAATTTAA 28578 TCTCT AGT - TA T
GTATGTGAATAGATAGGTAT GAGATCCG CGGGTTTTTTA TTC ATG TGAATAGA GGTA T
TTTATCTCTATTCATCATCG |||||||||| ||| ||| |||||||| ||||
AATTTAAGAGATCCG GCCTAGAGAAT AAG TAC ACTTATCT CTAT /
TT--- C-- T -- T

GAM1103 GAGTATTTAGGGTTAAGTTA 28582 TAACACAGTA 28583 TAT A------- C ATC-- TA
CCTGATCCCAATAAATTTGG TATGATCCTA GAG TTAGGGTTA GTTA CTG CCAA A
CCTTCCAGATAACACAGTAT ACTC ||| ||||||||| |||| ||| |||| |||
ATGATCCTAACTCTC CTC AATCCTAGT CAAT GAC GGTT /
TC- ATATGACA A CTTCC TA

GAM1104 ATTTTAGGAACTATGTTCAT 28609 TTCATGGTAT 28610 TCA TCCT GC
TATTAAAACTATC T
GGTATCCTGGCGAATATTAA CCTGGCGAAT ATTTTAGGAACTATGT TGGTA G GAA
AATGATA G
AACTATCAATGATATGATTA ATTA |||||||||||||||| ||||| | ||| |||||||
TCGTTTTCATCTTTTATCAC TAGAATCTTTGATATA ACTAT C CTT TTGCTAT A
CATATAGTTTCTAAGAT CC- TTT- TA ---------- T

GAM1105 TGTATGTGTGCATGTTGTAT 28615 TGTGTGCATG 28616 TT TTTT- TT
GTTTTGTATTGTTTGCCTGT TTGTATGTTT TGTATGTGTGCATG GTATG GTA G

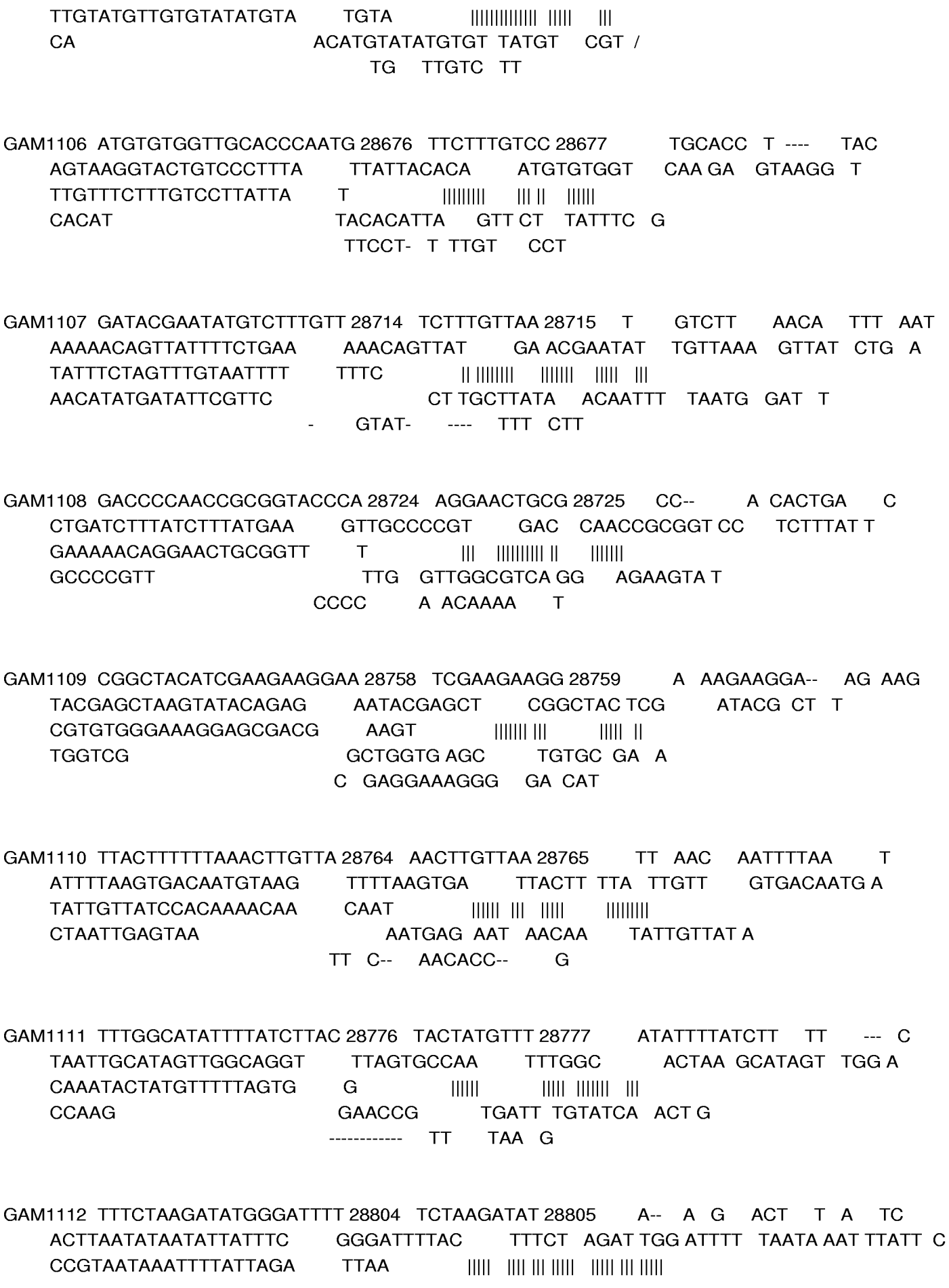
TTGTATGTTGTGTATATGTA TGTA
CA ACATGTATATGTGT TATGT CGT /
TG TTGTC TT
GAM1106 ATGTGTGGTTGCACCCAATG 28676 TTCTTTGTCC 28677 TGCACC T ---- TAC
AGTAAGGTACTGTCCCTTTA TTATTACACA ATGTGTGGT CAA GA GTAAGG T
TTGTTTCTTTGTCCTTATTA T
CACAT TACACATTA GTT CT TATTTC G
TTCCT- T TTGT CCT
GAM1107 GATACGAATATGTCTTTGTT 28714 TCTTTGTTAA 28715 T GTCTT AACA TTT AAT
AAAAACAGTTATTTTCTGAA AAACAGTTAT GA ACGAATAT TGTTAAA GTTAT CTG A
TATTTCTAGTTTGTAATTTT TTTC
AACATATGATATTCGTTC CT TGCTTATA ACAATTT TAATG GAT T
- GTAT- ---- TTT CTT
GAM1108 GACCCCAACCGCGGTACCCA 28724 AGGAACTGCG 28725 CC-- A CACTGA C
CTGATCTTTATCTTTATGAA GTTGCCCCGT GAC CAACCGCGGT CC TCTTTAT T
GAAAAACAGGAACTGCGGTT T
GCCCCGTT TTG GTTGGCGTCA GG AGAAGTA T
CCCC A ACAAAA T
GAM1109 CGGCTACATCGAAGAAGGAA 28758 TCGAAGAAGG 28759 A AAGAAGGA-- AG AAG
TACGAGCTAAGTATACAGAG AATACGAGCT CGGCTAC TCG ATACG CT T
CGTGTGGGAAAGGAGCGACG AAGT
TGGTCG GCTGGTG AGC TGTGC GA A
C GAGGAAAGGG GA CAT
GAM1110 TTACTTTTTTAAACTTGTTA 28764 AACTTGTTAA 28765 TT AAC AATTTTAA T
ATTTTAAGTGACAATGTAAG TTTTAAGTGA TTACTT TTA TTGTT GTGACAATG A
TATTGTTATCCACAAAACAA CAAT
CTAATTGAGTAA AATGAG AAT AACAA TATTGTTAT A
TT C-- AACACC-- G
GAM1111 TTTGGCATATTTTATCTTAC 28776 TACTATGTTT 28777 ATATTTTATCTT TT --- C
TAATTGCATAGTTGGCAGGT TTAGTGCCAA TTTGGC ACTAA GCATAGT TGG A
CAAATACTATGTTTTTAGTG G
CCAAG GAACCG TGATT TGTATCA ACT G
---------- TT TAA G
GAM1112 TTTCTAAGATATGGGATTTT 28804 TCTAAGATAT 28805 A-- A G ACT T A TC
ACTTAATATAATATTATTTC GGGATTTTAC TTTCT AGAT TGG ATTTT TAATA AAT TTATT C
CCGTAATAAATTTTATTAGA TTAA

AATGCCAAATCTATAAGAAA AAAGA TCTA ACC TAAAG ATTAT TTA AATAA C
ATA A G --- T - TG

GAM1113 ACAGAGGTAATGGCTTATTT 28819 AATGGATCCT 28820 A GCTTATTTACACACAATG
TACC TGA
ACACACAATGGATCCTACCA ACCATTCTTG AC GAGGTAATG GATCC ATTCT A
TTCTTGAACAGTGGAATTTT AACA || ||||||||| ||||| |||||
GGATTAACATTACCTCCGT TG CTCCATTAC TTAGG TAAGG C
C AA---------- TTT- TGA

GAM1114 TGGCTAATGTCCAGTCTATG 28834 CATCCCTAGA 28835 A TCCAG-- ---- AACTA
TGGAACTAAAAACCCCGCAT AGAAGTTTAT TGGCT ATG TCTA TGTGG A
CCCTAGAAGAAGTTTATGAG GAGC ||||| ||| |||| |||||
CCA ACCGA TAT AGAT ACGCC /
G TTGAAGA CCCT CCAAA

GAM1115 TTGTTTTTCCATGAATTAAT 28864 TCCATGAATT 28865 TTT - T AAATTCTAC- TT
TAAATTCTACAATTGTTTTC AATTAAATTC TTGTT CCAT GAA TAATT AATTGTT C
GCAGCAATTAAATACAAAAA TACA ||||| |||| ||| ||||| |||||||
ATTATTTCAATGGCTCAATA AATAA GGTA CTT ATTAA TTAACGA /
A CTC A T AAAACATAAA CG

GAM1116 GGTGTTGTGCCCCCTCCCTC 28878 CACAAGTTTA 28879 T T CCCTCCA TTA A----------
--- T
CACAAGTTTAGATGATACCT GATGATACCT GGTG TG GCCCCCT CAAGT GATG
TACC A
ATAGGTACTTGCAGTCTCGC ATAG |||| || ||||||| ||||| |||| ||||
GCCATTACTTGCCAAAAGGG CCGC GC CGGGGGA GTTCA TTAC ATGG T
GGCCGCCGCC C - AAACC-- --- CGCGCTCTGACGTTC A

GAM1117 CTGAGAGATGGGGCTCGCAG 28885 TCGCAGTCAC 28886 --- - TC TCACCC G
TCACCCCCGTGGTAACACGG CCCCGTGGTA CTGAGAG ATG GGGC GCAG CCGTG T
TTGCTTGCCCGCGTGTGCTC ACAC ||||||| ||| |||| |||| |||||
TCGG GGCTCTC TGC CCCG CGTT GGCAC A
GTG G TT ------ A

GAM1118 TGAGTTCGCCCGCTTGCCAT 28917 AAAAAGCCAC 28918 T GCCC GCCA TAT CT TT
TGAATATTGCCTTGTATTAC AGATCTCA TGAG TC GCTT TTGAA TGC TGTA A
CTTATAGCATTTCAAAAAGC |||| || |||| ||||| ||| ||||
CACAGATCTCA ACTC AG CGAA AACTT ACG ATAT C
T ACAC A--- T-- -- TC

GAM1119 GGCATTTTTTTAACAGGCAG 28955 CTCCCGGGCA 28956 TTTTTTA ---- -- ACTA TG
G AGTCTTT

GGTACTATGGGTGAGGAGGT ACCCTTAGCA GGCAT ACAG GC AGGGT TGGG
AGGAGGT CCTC T
GCCTCAGTCTTTTTACCTTA GTTC ||||| |||| || ||||| |||| ||||||| ||||
AGGGGACCTCCTCCCGGGCA CCGTA TGTC CG TCCCA GCCC TCCTCCA GGGG
T
ACCCTTAGCAGTTCTGTGTA TG----- TTGA AT ACGG -- - AATTCCA
TGCC

GAM1120 GCTGCTGCGGCGGCGAGGGC 28974 CTGCGGCGGC 28975 GAGG G
TGCTGCGGCGGCGAGGGCTG GAGGGCTGCT GCTGCTGCGGCGGC GCTGCTGCGGCGGC A
CTGCGGCGGCGAGGGCTGCT GCGG |||||||||||||| ||||||||||||||
GCGGCGGC CGGCGGCGTCGTCG CGGCGGCGTCGTCG G
GGAG G

GAM1121 CCCTCTTCGGCATCAAGGAA 29050 TGACCGGGTG 29051 CAT AGGAA G - A
GGTGATTGGTTTATAGGTGT TTCCTGAAGG CCCTCTTCGG CA GGT AT TGGTTTAT G
AGGCCACGTGACCGGGTGTT GGG |||||||||| || ||| || ||||||||
CCTGAAGGGGG GGGGGAAGTC GT CCA TG ACCGGATG G
CTT GGG-- G C T

GAM1122 AAGGCGGGCATGACCTCGGC 29063 GGGCATGACC 29064 G AT - CTCAG A CTAG
ACTCAGGTTGTCAGTTTCTA TCGGCACTCA AA GCGGGC GA CCTCGGCA GTTGTC GTTT
A
GAAACGAGGAGGATTTGATA GGTT || |||||| || |||||||| |||||| ||||
TTGACGGTGCCGGCGGAGAT TT CGTAGA CG CCGTGGCA AGTTTA GAGG A
GCCTT C GG G GTTAT G AGCA

GAM1123 TAATTGAGGTTCCCGGCAAA 29069 TCACATTTGC 29070 TT T C T T ATA
TGTTGGATAGATAGGTAACT CTGGACCTTT TAA GAGGT CC GGCAAATGT GGA AG G
TCTCACATTTGCCTGGACCT TTTG ||| ||||| || ||||||||| ||| ||
TTTTTG GTT TTCCA GG CCGTTTACA TCT TC G
TT - T C - AAT

GAM1124 TTGAAGTCGATATTGTCGCA 29080 TCCGTGCGCT 29081 AAG A - CCCT T - A
GCCCCCCTGCTCCCAGAGCT TCTTGTAGGC TTG TCGAT TTGTCGC AGCCC GC CC CAG G
GGAAGTCCGTGCGCTTCTTG GGGG ||| ||||| ||||||| ||||| || || |||
TAGGCGGGGTTGGGCA ACG TTGGG GCGGATG TCTTC GC TG AGG C
GG- - T GCGT C A T

GAM1125 TAGGTGGGGTAGCAGCGCCC 29087 TAGCAGCGCC 29088 GGGTA - - C GCTG GC
CCCGCGGATGCTGGCGCGCA CCCCGCGGAT TAGGTG GCAGCGC CCCC CG GGAT GC G
CGTAGTCATACAGCTCGTGC GCTG |||||| ||||||| |||| || |||| ||
GAGGGGGCGAGGAGC CGAGGA GGGAGCG GCTC AC ATAC GC /
GCGG- T G - TGAT AC

```
GAM1126  CGTGAGAGTCTGTAACACCG 29108   CGAAAGCTGA 29109   A   C    C  C--        GGCTAAGGAAG
GA--     AAGTG
         CTTCACCCAGAAGAGACTGG       AAGTCTCTTC        CAC GCTT AC   CAGAAGAGACT        CAGCTT
GAGGGG    C
         CTAAGGAAGCAGCTTGAGAG       TGCT           ||| |||| ||   ||||||||||         ||||||   ||||||
         GGGAAGTGCCTAAACCCTTC                    GTG CGAA TG   GTCTTCTCTGA         GTCGAA    CTTCCC
  /
         CCGAAAGCTGAAAGTCTCTT                    G   -    C  ATC        AA---------     AGCC     AAATC
         CTGCTAGTCAAGCGTGGTGC
         AGACCTCATG
GAM1127  GGTTTTTTTATCCCTTGGAA 29151   TATGTTAAAA 29152         T      GGAATT     A   AG----     TTT
         TTATGTTAAAAATAGGTGTT       ATAGGTGTTT       GGTTTTTT ATCCCTT     ATGTTA AAAT     GTGTTT
 C
         TTTTCTTTAAACATAAGAGA       TTTC           |||||||| |||||||     |||||| ||||     ||||||
         ATTTATAATATCAGATAAAG                     CTAAAAAA TAGGGAA     TATAAT TTTA     TACAAA   /
         GGATTAAAAAATC                            T      ATAGAC     A   AGAGAA     TTT


GAM1128  GCACTTATTTCATGAATTTC 29163   TTCATGAATT 29164          CA     TTCAT     AA
         ATTTTTAGAACTCATTAAAA       TCATTTTTAG       GCACTTATTT  TGAAT    TTTTAG  C
         TAGTATTTGAAAAATAAGTG       AACT           ||||||||||  |||||    ||||||
         T                                TGTGAATAAA  GTTTA    AAAATT  T
                                            AA    TGAT-     AC


GAM1129  GCCCACAGATCGCACCTTCA 29175   TGGAAAGTGT 29176      ACA  T   ACC     CG  AA--  ---   TCT
         ACCGATAAGAGTCTCTAGAT       TCGGGGGC         GCCC   GA CGC   TTCAAC  AT   GA   GTC   A
         GACAAATCGACAGTTAGTTG                      ||||   || |||   ||||||  ||    ||   |||
         GAAAGTGTTCGGGGGC                        CGGG   CT GTG   AGGTTG  TG    CT   CAG   /
                                       GG-  T   AA-     AT  ACAG  AAA   TAG


GAM1130  TCATTGAGTTTAGTGGCAAA 29285   TAGATGCCGC 29286      TTG    TA     AACG    ACAGA
         CGACAAACAGACAAAAATTG       CAGCTAGTTG       TCA   AGTT  GTGGCA    ACAA    C
         TAGATGCCGCCAGCTAGTTG       A              |||   ||||  ||||||    ||||
         A                                AGT   TCGA  CGCCGT    TGTT    /
                                           TGA    C-     AGA-    AAAAA


GAM1131  GTCGGGGCACTTTTTCCTTC 29305   GGGGGTTACA 29306         AC--           G     A  A  AAAT    C
         CCTCGGGGGGTTACAACTAAA       ACTAAATTCG       GTCGGGGC    TTTTTCCTTCCCTC GGGGTT CA
CT    TCGT A
         TTCGTCAGTACGATACAGTG       TCAG           ||||||||    |||||||||||||| |||||| || ||    ||||
         AACTCCGGGGGGGAAGGAGAA                     CGGCCTCG    AAAGAGGAAGGGGGG CCTCAA GT GA
AGCA G
         AAACCGCTCCGGC                            CCAA           G     -  -  CAT-    T


GAM1132  ATGTCGTTTAAATATCTGAT 29310   TCTGATGTTG 29311          AA  ATC        C  TGCT     AA
```

GTTGTTCGCTGCTATGATAA TTCGCTGCTA ATGTCGTTT AT TGATGTTGTT GC ATGAT T
TCGGATCATTCGCCGATAAC TGAT |||||||||| || |||||||||| || |||||
GTTACCGTCGAAACGGCAT TACGGCAAA TG ATTGCAATAG CG TACTA C
GC CC- C CT-- GG

GAM1133 TTTTTATGAGTATTTTTACA 29322 TGAGTATTTT 29323 TTT AAAA A
AAAATGCATAAAGTGTATGT TACAAAAATG TTTTTATGAGTAT TAC ATGCAT A
CGTATGTATATTTATAAAAA CATA |||||||||||| ||| ||||||
AAAAATATTTATA ATG TATGTG /
TGT CTG- A

GAM1134 AGATATATACTTTCAAGTGT 29336 TATTATGTGA 29337 A TTG---------- G AAGTC
AAA--- TT
TTGGTGTGACATTCAAAGTC ATGTTAAGCA A GTGT GT TGACATTCA TAATGGTTG
ATG T
TAATGGTTGAAAATGTTTTT AAAA | |||| || ||||||||| ||||||||| |||
CATAAATGGTAGCTATTATG T CATA CG ATTGTAAGT ATTATCGAT TAC /
TGAATGTTAAGCAAAAACAG C TAAATTAGACAAAAA A GT--- GGTAAA TT
ATTAAATATACCTGAAAGAA
AAATATTTTGT
GAM1135 CTGGTTTAGTTTGGGGAAGT 29357 TATCACGTCT 29358 TG AG A AA-- AATC A A
C-- GT
GAAAGTAAAAATCTGAATAC CTAAGAAAGC C GTTT TTTGGGGA GTGA GTAAA TG AT
CTTGA ATCT A
TTGACATCTGTATAAGGTTT TGG | |||| |||||||| |||| ||||| || || ||||| ||||
TTCAAGAATACAATTGTTTA G CGAA GAATCTCT CACT TATTT AC TA GAACT TGGA
/
TAGTATCACGTCTCTAAGAA GT A- G ATGA GTTA A A TTT AT
AGCTGG

GAM1136 TTTAGTTTGGGGAAGTGAAA 29367 TATCACGTCT 29368 ---- A AA-- AATC A A C--
GT
GTAAAAATCTGAATACTTGA CTAAGAAAGC TTTAGT TTGGGGA GTGA GTAAA TG AT
CTTGA ATCT A
CATCTGTATAAGGTTTTTCA TGGA |||||| ||||||| |||| ||||| || || ||||| ||||
AGAATACAATTGTTTATAGT AGGTCG AATCTCT CACT TATTT AC TA GAACT TGGA
/
ATCACGTCTCTAAGAAAGCT AAAG G ATGA GTTA A A TTT AT
GGA

GAM1137 TCTAATGGTAGTTTTGATAG 29374 TACATTGTTT 29375 TAGTTT A - TC
GAGATTGTCATCAGTTGATA ATTATCTCAT TCTAATGG TGATAGG GAT TGTCA A
CATTGTTTATTATCTCATCT CTAT ||||||||| ||||||| ||| |||||
ATTAGA AGATTATC ATTATTT TTA ATAGT /
TACTCT G C TG

GAM1138 ACTGTCATGAACCGTATGCG 29387 TGTCATGAAC 29388 TG TG C T AT - GTTTAA

ATCACATTGACACGGTTTAA CGTATGCGAT AC TCA AAC GTA GCGATCAC TG ACACG A
AATACATACGTGTGTATCGT CACA || ||| ||| ||| |||||||| || |||||
GGTCGTCTACTGTTTGTGGT TG GGT TTG CAT TGCTGGTG AT TGTGC A
GGT GT GT T C CT G ATACAT

GAM1139 GATCAAGGCCCTCCGTATAA 29395 TAATACGGAG 29396 AG A G C
TGTAAATGTTCCAAAGGTTT GGTTCTGATC GATCA GCCCTCCGTAT ATGTAAAT TT C
GCATAATACGGAGGGTTCTG ||||| |||||||||| |||||||| ||
ATC CTAGT TGGGAGGCATA TACGTTTG AA /
CT A G A

GAM1140 TTTTCTCCTTCCCCCCGGAG 29403 CCCCGGAGTT 29404 C CC A- - - TA- A
TTCACTGTATCGTACTGACG CACTGTATCG TTTT TCCTTCCC CGG GTT CA CTG TCGT C
AATTTAGTTGTAACCCCCGA TACT |||| |||||||| ||| ||| || ||| ||||
GGGAAGGAAAAAG GAAA AGGAAGGG GCC CAA GT GAT AGCA T
A A- CC T T TTA G

GAM1141 GGTTTTACTTCTTTTAGAGA 29412 TCTTTATTAG 29413 CTTCTTT ATTCT TT TCCCA
CA
TTCTTTATTAGTTATTTCCC TTATTTCCCA GGTTTTA TAGAG TTATTAG ATT GTTAT A
AGTTATCAATTATAACGTCG GTTA ||||||| ||||| ||||||| ||| |||||
TAATCTCTAGTAGTATACTC CCAAAAT ATCTC GATGATC TAA CAATA /
TATAAAACC ------- ATAT- TC TGCTG TT

GAM1142 CCGCGGCCTCCCCAAGGTCC 29425 TTCGCCGTCG 29426 C- CCCA --- C AC - AC
GGGCCACGACCGAGAACGCG CCCGGAAGAC CCG GGCCTC AGG TCCGGGC ACG CGA
GA G
CTCTTCGCCGTCGCCCGGAA CTGC ||| |||||| ||| ||||||| ||| ||| ||
GACCTGCGAGGCCCTCGG GGC CCGGAG TCC AGGCCCG TGC GCT CT C
TC CG-- AGA C C- T CG

GAM1143 GCGGCCCCCGTCGCGATGGA 29435 AGGCGGAGGC 29436 GTCG T - - ----- GA A
G
GGCGGAGGCGGAGGCGGAGG GGAGGACGGC CGGCCCCC CGA GGAGGCGG AG GCGGA
GGCG GG CGGCGGCGGG G
ACGGCGGCGGGGGATTCGCC GGCG |||||||| ||| |||||||| || ||||| |||| || ||||||||||
GTCGCCCTCGCCGACGATCC GTCGGGGGG GCT CCTCTGCC TC CGCCT CCGC CC
GCTGCCGCTT /
GCTCTCCCGTCTCCTCGGGG ---- - C T AGCAG TC - A
GGCTGT

GAM1144 CCCTGGCAGTTGTGTGTATT 29771 TGTGTGTATT 29772 CA TG TTCCCCTTCTC -- C
TTACTTC AT
CCCCTTCTCCCAGTGGCTCT CCCCTTCTCC CCCTGG GT TGTGTA CCA GTGGCT
TATTA TG T

ATTATTACTTCTGATTCTCA CAGT |||||| || |||||| ||| |||||| ||||| ||
ATTATTTAATAAGCCATATT GGGACC CG ATACAT GGT TACCGA ATAAT AC /
GGTTACATAAGGCCCAGGG -- GA T---------- TA - TTATTA- TC

GAM1145 ACGTATACGTAGTAAGAAAT 29785 TACGTAGTAA 29786 - ---------- G T GTTT GG TTT
AATATGTTAGCACATATATG GAAATAATAT AG AAATA ATATGTTA CACA ATATGTAT GTATGTAT T G
TATGTTTGTATGTATGGTTT GTTA || ||||| |||||||| |||| |||||||| |||||||| |
TGTATGTTGTATGTATGTAT TT TTTGT TATATAGT GTGT TATGTATG TATGTATG G /
GTATTTGTGTGATATATTAC G TTTATGTCAT - T ---- TT TAT
TGTATTTTGTTTGTTTGCGT
GCGTGTATGT
GAM1146 CCTAAAGGAAAAATTTTCCT 29790 TCGAAAGTTT 29791 A GG CT TTT C
CCGATTTGGATCAATATCCC TTAGTTCAGG CCT AA AAAAATTTTC CCGA GGAT A
CTTGGTCGAAAGTTTTTAGT ||| || |||||||||| |||| ||||
TCAGG GGA TT TTTTTGAAAG GGTT CCTA A
C GA CT CC- T

GAM1147 GAGTTGTCAGCACTGATGAT 29823 TGTCAGCACT 29824 GT A C TT T CG
TATGTGTCTCGCACAAGCAT GATGATTATG GA TGTC GCA TGATGA ATGTG CT C
ATTTTATCATGCAGGCAGTT TGTC || |||| ||| |||||| ||||| ||
C CT ACGG CGT ACTATT TATAC GA A
TG A - T- - AC

GAM1148 ACGGTAACTCGTATATTTTT 29834 ACTCGTATAT 29835 TAACT TA- CG-- TAAA
ACGTACAATAAAGCGATTTG TTTTACGTAC ACGG CGTA TTTTTA TACAA G
TAAAAATAAAAACTTTACGT AATA |||| |||| |||||| |||||
AATCCGT TGCC GCAT AAAAAT ATGTT /
TAAT- TTC AAAA TAGC

GAM1149 GACGTACTTGTCTATCTTAA 29844 AGATATGATA 29845 T -- - AAA ATACCG
ACACGATACCGTAGCCACCC AAAGTCGTC GACG ACT TGTC TATCTT CACG T
GTGGAGATATGATAAAAGTC |||| ||| |||| |||||| ||||
GTC CTGC TGA ATAG ATAGAG GTGC A
- AA T --- CCACCG

GAM1150 GGATGATATCACGCATTTCT 29858 TATCACGCAT 29859 A GCATT AAATAATAT T
AAAATAATATAGGGTTCTAA TTCTAAAATA GGATG TATCAC TCTA AGGGTTCTAA C
TCTTTTGGAATCTTTCATAA ATAT ||||| |||||| |||| ||||||||||
CTAGATCGGTGGTAATATTC CTTAT ATGGTG AGAT TTCTAAGGTT T
A GCT-- CAATACT-- T

GAM1151 AGTTATATTTAAAGGGTAGC 29864 TATGTTGCTA 29865 -- A- - - G CCCC
AATGGTAGAGAACCCCCTCC CGCCTAGTGG AGTTAT ATTTA AGG GTAGCAATG GTA AGAAC
T
GAGTTCTGTATATGTTGCTA GTCT |||||| ||||| ||| ||||||||| ||| |||||
CGCCTAGTGGGTCTATGATT TTAGTA TGGGT TCC CATCGTTGT TAT TCTTG /
TC GA G A G AGCC

GAM1152 TGTTACTGTAGTAGATACTA 29874 TTAGTACTGC 29875 A A C AA AC
CTAGAAGTACTAACATGACT TACAGAACA TGTT CTGTAGTAG TACTA TAG GT T
ATTAGTACTGCTACAGAACA |||| ||||||||| ||||| ||| ||
ACAA GACATCGTC ATGAT ATC TA A
- - T AG CA

GAM1153 CAAAATTACTTTGTCTGCAG 29897 TACTTTGTCT 29898 A A TT G- - TGG-- TA
AGGTTATGGCATATTTACAT GCAGAGGTTA CAA ATT CT GTCT CAG AGGTTA CATATT C
AATATGAATGCTAACCTACT TGGC ||| ||| || |||| ||| |||||| ||||||
GGAGGACTGGAATATTG GTT TAA GG CAGG GTC TCCAAT GTATAA /
A - T- AG A CGTAA TA

GAM1154 GACATGATAGACACAGGATT 29917 AGGTGTTGCA 29918 ---- ACA TTG- CTA CTTTAA
GC- A AAG
TGGCGCTATGGACTTTAAGG GGAATCTAAG GATAG CAGGAT GCG TGGA GGTGTT
AGG ATCT G
TGTTGCAGGAATCTAAGGCT GCTG ||||| |||||| ||| |||| |||||| ||| ||||
GAGGTACCTTTAGACATTGT TTATC GTCCTA TGT ACCT TTACAG TCC TGGA
/
ACAATCCACCTGTAAATATC AAAT A-- TAAA CC- AACATG ATT A GTC
CTGACTATTTAAAAATGTC

GAM1155 GCCTGCTTCACCTGGCAGCT 29924 CACAGGGTCA 29925 -- GCA-- G ATTCTCCCTCT -
CTC TT CT AC
GTGTGTATTCTCCCTCTCCA TAACAATGGT C TG GCT TGTGT CCAA GTGG TATTG
AC CTG T
AGTGGCTCTATTGTTACCTC GTTT | || ||| ||||| |||| |||| ||||| || |||
TGACTCCCAGTTGTTTAATA G AC TGG ACACG GGTT TACC ATAAT TG GAC /
AACCATATTGGTTACATAAG TA AATAC G GAATACATT-- A AA- T- TT CC
GCACAGGGTCATAACAATGG
TGTTTGCTGGC
GAM1156 CGTGACTCGGTGCTGGCGCG 29944 TGATCGCGCC 29945 G T TG TCTCTTC TC
TCTCTTCCGGGTCCTTTCTG GGGTCCGTGT CGT AC CGG CTGGCGCG CGGG C
ATCGCGCCGGGTCCGTGTGC GCG ||| || ||| |||||||| ||||
G GCG TG GCC GGCCGCGC GTCT /
- T TG TA----- TT

GAM1157 CGTTTCGCTTCGACTCTGCC 29950 TCGCTTCGAC 29951 T T CTC GC CCG
GGTCCGCTGGTGCCGACGAT TCTGCCGGTC CGTT CGCT CGA TGCCGGTCC TGGTG A

CGCCGGGACCGGCACTTTCG CGCT |||| |||| ||| ||||||||| |||||
CGGCGGACG GCAG GCGG GCT ACGGCCAGG GCCGC C
- C TTC -- TAG

GAM1158 GTGTACGTGCCAGGAAGTAA 29954 AGGAAGTAAT 29955 TG T - G GTAAT T
TATGTGTGTGTGTATATATA ATGTGTGTGT G TACG GC CAG AA ATGTGTGTGTG A
TATACATCTATTGTTGTGTT GTAT | |||| || ||| || ||||||||||
TGTATGT T ATGT TG GTT TT TACATATATAT T
GT T T G ATC-- A

GAM1159 AGTGCGTGCTTCAGACCCGC 30104 GCCCCGAGCG 30105 - TT CC -- AC CAAC
GGACCCGGGCAACTTGTACC TCTCTGTGCA AGTGCGT GC CAGA CGC GG CCGGG T
CGGCCCCGAGCGTCTCTGTG ACGC ||||||| || |||| ||| || |||||
CAACGCACT TCACGCA CG GTCT GCG CC GGCCC /
A T- CT AG CC ATGT

GAM1160 TAATATAATCCTAATTCATC 30143 TAGCATAGGT 30144 T- ATTCATCT-- C
TTTTTTATCGTATAAAAATT TTTATATTG TAATATAA CCTA TTTTTAT G
CTATAGCATAGGTTTTATAT |||||||| |||| |||||||
TG GTTATATT GGAT AAAAATA /
TT ACGATATCTT T

GAM1161 TGTTGATATAAACTATCACA 30148 TGATATAAAC 30149 TT CACATAAACTAA
AATAAAAAT
TAAACTAAAGTCATTAATAA TATCACATAA TG GATATAAACTAT AGTCATT T
AAATTTTTTCTGCCAATGAT ACTA || |||||||||||| |||||||
TCACTAAACAAATAGTTTAT AT TTATATTTGATA TTAGTAA /
ATTTTTA TT AACAAATCAC-- CCGTCTTTT

GAM1162 CGCGAACTACGAGCGCACAG 30153 CATGGCACTC 30154 A A C A GC--- TGA AC
CAAGCTTGACGACGTGGCGG GAGTACGCG CGCG ACT CGAG GC CA AAGCT CG G
ACAGCTTCCACATGGCACTC |||| ||| |||| || || ||||| ||
GAGTACGCG GCGC TGA GCTC CG GT TTCGA GC T
A - A - ACACC CAG GG

GAM1163 CAATGTATGACGAATACTGC 30160 TATGACGAAT 30161 A-- ATA--- - TCAA TTT T
GTTCAAGGGTTTTGTTTTTA ACTGCGTTCA CAATGT TGACGA CTGC GT GGGT GT T
TTGTGCTCACTGCTGCAGAA AGGG |||||| |||||| |||| || |||| ||
GATATTGTTAAGAGCATTG GTTACG ATTGTT GACG CG CTCG TA T
AGA ATAGAA T TCA- TGT T

GAM1164 CTGGCTTTATTCAGGCCCAG 30168 CTTTATTCAG 30169 TG C------- CA A---------- A
AGACCATTTGGATTTTGCGT GCCCAGAGAC C GCTTTATT AGGCC GAG CC T

TATGCTTACTCGTGGCCTTT CATT | |||||||| ||||| ||| ||
TTGGAAAATAGAGTTGG G TGAGATAA TCCGG CTC GG T
GT AAGGTTTT TG ATTCGTATTGCGTTTTA T

GAM1165 TGAATGGGACATGGAGTATG 30175 TCTCCAGGAT 30176 AA G AGT T AA- T- AGAG
TGTGCAAATGTGATAAGAGC GTACCATCGA TG TG GACATGG ATG GTGCA TG GATA C
TATATATCTCCAGGATGTAC CTAT || || ||||||| ||| ||||| || ||||
CATCGACTATGTCGCAAGCA AC AC CTGTATC TAC CATGT AC CTAT /
GA G AGC - AGG CT ATAT

GAM1166 ACCCCAAGCGGCTCTTTGGT 30182 TCTTTGGTGT 30183 GCG-- CT -- T A ACAA
TTAATA AT
GTCCTCTGAGGCACAATTGT CCTCTGAGGC ACCCCAA GCT TTG GTGTCC CTG GGC
TTGT AGCC A
TTAATAAGCCATATTGGCTA ACAA ||||||| ||| ||| |||||| ||| ||| |||| ||||
CAAAAAGCCCAGGGACATAA TGGGGTT TGG AAC TACAGG GAC CCG AACA
TCGG /
CAATGGTATTTGTTGGGGT GTTTA T- AA - - AAA- ------ TT

GAM1167 ATATATGTGTATATGTACTG 30230 TATGTGTATA 30231 TGT TG - TAT-
T
TTATATATATGTGTGTATGT TGTACTGTTA ATATATGTGTATATGTAC TATATATATGTGTGTA
TAC TGT GTATATG G
ACTGTTATGTATATGTGTTT TATA |||||||||||||||| |||||||||||||| ||| ||| |||||||
ATGTACTGTTATATGTGTGT TGTATGTATATGTATATG GTGTATGTGTATATAT GTG ATA
CATGTAT T
ATATATGTGTATGTGTGTAT T-- GT T TTGT T
ATGTATATGTATGT

GAM1168 CTATTTACATATGTGGCACT 30300 TGGCACTACA 30301 TA TG--- - CA TCC
ACATGTAAATATCCAGATTA TGTAAATATC CTATT CATATG GCA CTA TGTAAATA A
TTTACAAATGGCTGCAGACC CAGA ||||| |||||| ||| ||| ||||||||
CATATGGTGATAG GATAG GTATAC CGT GGT ACATTTAT /
TG CCAGA C AA TAG

GAM1169 CAAAATGGTGTTTGAAAAAT 30318 CACCGTTTAT 30319 A- -- A A T AA
AGGTGTACAACACGTCACCG CAGGTACGCC CAAA TGGTGT TTGA AAAT GGTG AC C
TTTATCAGGTACGCCGAGTT GAGT |||| |||||| |||| |||| |||| ||
TG GTTT GCCGCA GACT TTTG CCAC TG /
GA TG A - - CA

GAM1170 TGTCGTCTTTATCCTTCAGG 30323 TACCTTTAAC 30324 TATCCTTC - TAATT
ACCATGTAATTCTTCAAGTA AAGACGACA TGTCGTCTT AGG ACCATG C
TGGTACCTTTAACAAGACGA ||||||||| ||| ||||||
CA ACAGCAGAA TCC TGGTAT T

CAATT--- A GAACT

GAM1171 GAAACGCGAGATCGATCAGA 30335 TTAGTCTGTA 30336 CGC- -- ------ AAC C
AACGTTCTAGAATTAGTCTG ATATGTCGAT GAAA GAGA TCGAT CAGA GTT T
TAATATGTCGATATCTCCAT ATCT |||| |||| ||||| |||| |||
ATTTC CTTT CTCT AGCTG GTCT TAA A
ATAC AT TATAAT GAT G

GAM1172 GACGCAAATACTCCTCCATT 30344 CCAGAGGGGA 30345 ATA-- CAT---- CG
AACGCGTTTACGTTACTTAC CACGTTGTGT GACGCAA CTCCTC TAACG T
CAGAGGGGACACGTTGTGTC C ||||||| |||||| |||||
CTGTGTT GGGGAG ATTGC T
GCACA ACCATTC AT

GAM1173 GTGTACTAGACGGGAACATG 30494 TACGTGGATA 30495 GACG A C-- TGA--- CA--
ACCC
TCCGGTCCTTTGAGCGTCAA CGAGGATCGT GTGTACTA GGAAC TGT CGGTCCTT GCGT
AGAC A
GACACCCAAAACGTCTGTAT TTGC |||||||| ||||| ||| |||||||| |||| ||||
ACGTGGATACGAGGATCGTT CATATGGT TCTTG ACG GCTAGGAG TGCA TCTG
/
TGCAGTTCTATGATGGTATA AGTA - TTT CATAGG TATG CAAA
C

GAM1174 ACGCTATTATTTTTTGTATG 30498 TATTATTTTT 30499 T TTT T - --- T AC
TTCCTGTGTTGTAATTTCAA TGTATGTTCC ACGC ATTATTT GTA GTTCCTGT GTTGT AAT
TCA A
CATATGATATTCGGACAACG TGTG |||| ||||||| ||| |||||||| ||||| ||| |||
ACGGGGGCCTACCCAAGTAA TGTG TAATGAA CAT CGGGGGCA CAACA TTA AGT /
TTGTGT T CC- C G GGC T AT

GAM1175 GCCGATCCGTTCGTAGTGGT 30503 CGAGGCCGAC 30504 GATC AG TAAT C A A
AATCCCCGATCAACCGACCG GCGGACGAAG GCC CGTTCGT TGG CC CG TC A
AGGCCGACGCGGACGAAGGC GC ||| ||||||| ||| || || ||
CGG GCAGGCG GCC GG GC AG C
AA-- CA ---- A C C

GAM1176 TTATGTTTGCAACCTGTGAA 30607 TTTTATAGGT 30608 GC---- A CAAAATCA
AAGTCAAAATCATTTAAACA TCATTAAAAA TTATGTTT AACCTGTGAAA GT T
AGCTTTTATAGGTTCATTAA TATA |||||||| |||||||||| ||
AAATATAA AATATAAA TTGGATATTTT CG /
AATTAC - AACAAATT

GAM1177 TCGCGCATCGAGCGGAGATA 30613 TAGCGGACCC 30614 GGAGATA G - T - - - T A TT-
--- G

GCGGACCCTCTCCGACGCCT TCTCCGACGC GCG ACC CTC CCGA CG CCTG CCAG GC GA GCACACC GC A
GCCAGTGCAGATTGCACACC CTGC ||| ||| ||| |||| || |||| |||| || || ||||||| ||
GCGAGCGCCTCGGTGTGCCG CGC TGG GAG GGCT GC GGAC GGTT CG CT CGTGTGG CG G
CTCGGCCTTGGCCAGGTCGT GC----- G A T T T C C G CGC CTC C
TCGGTGAGAGGTGCGCCGGT
TCGAAGCGGA

GAM1178 TCGAGCCGATCAGCTGCAGC 30623 TGGCAGCGGC 30624 A- A----- A C- A - GT
TCGCACGAGACGTCAAAGTA GCACGAGATC TCG GCCGATC GCTGC GCT GC CGAG AC C
TTCGGTCTGGCAGCGGCGCA GGCC ||| ||||||| ||||| ||| || |||| ||
CGAGATCGGCCCCGA AGC CGGCTAG CGGCG CGG TG GCTT TG A
CC AGCACG A TC - A AA

GAM1179 GTTCGTCGTTCCGTGTCCAG 30650 TGTTGCTTTC 30651 C TCCG---- C GG TCC - G C
GGGGAGCGTCCCAGCCGGCG CCTGACGAAC GTTCGT GT TGTC AGGG AGCG CAGC CG CGA G
ACGTTTTGACGAGCTGTTGC CTTC |||||| || |||| |||| |||| |||| || |||
TTTCCCTGACGAACCTTCTG TAAGCA CG GCAG TCCC TCGT GTCG GC GTT T
CACGAAT - TCTTCCAA - TT T-- A A T

GAM1180 CCGTGTCCTCGCTTTCTTCT 30674 CACGGGGTTA 30675 CCT CTC CCGCTT C T-- GT CTT
CTCTCCGCTTCCCCGCGATC GAAAAAGAGA CCGTGT CGCTTTCTT TCT CCCCG GA CCG C C
CGGTCCTTCGTTCGGTCGGC GCGT |||||| ||||||||| ||| ||||| || ||| |
TTTCACGGGGTTAGAAAAAG GGCGCG GCGAGAGAA AGA GGGGC CT GGC G G
AGAGCGTGCGCGCGG CGT AA- TT---- A TTC TG CTT

GAM1181 TTTATTATAGTATTTTCTAA 30702 TAGTATTTTC 30703 ATAG T TT----- TAAT
AATTTGTATTAATTATATAT TAAAATTTGT TTTATT TATTT CTAAAAT GTAT T
ACTAAGATTGTTTTAGAAAT ATTA |||||| ||||| ||||||| ||||
AAAAAAATAAA AAATAA ATAAA GATTTTG CATA /
AAAA - TTAGAAT TATA

GAM1182 ATCAAGAAAAAAGTTTGTGG 30713 AAGCTGTCTG 30714 G- TTCT GGA ACA- TG-- ---- - T
TTCTCAGGGGATTAGTTCAC AGGTTAAGGG TTTGTGG CAGG TTAGTTC AGC TCTG AG GTTAAGGG G
AAGCTGTCTGAGGTTAAGGG TGTT ||||||| |||| ||||||| ||| |||| || ||||||||
TGTTTCTTTGGCACTGACAC AAACATT GTTC AGTTAAG TCG AGAC TC CGGTTTCT T
AGAAGTTGCTATAAGAATTG AA TC-- GA- AATA TTGA ACAG A T
AAGCTTGCTTTACAAAAAGT
TACTTGTGAT

GAM1183 CTGGGTAGCGCTACCGAGGG 30728 TCTGTGCGTA 30729 GTA - - - C GCTCA
TGCGTGCTCATCTCTAACCG GTGTCCAG CTGG GCGCTAC CG AG GGTG GT T
CCTCTGTGCGTAGTGTCCAG |||| ||||||| || || |||| ||
GACC TGTGATG GT TC CCGC CA /
--- C G T - ATCTC

GAM1184 GGCCAGCCGATGGGTGCCGG 30824 AGCCGATGGG 30825 AG ATG C- TT C
TTTGGCGGCCGCGGTCGCCG TGCCGGTTTG GGCC CCG GGTG CGGT GGCGGC G
CCGTCCACCAACGGGAGGCC GCGG |||| ||| |||| |||| ||||||
CCGG GGC CCAC GCCG CCGCTG C
AG AA- CT -- G

GAM1185 AGGAGCGGCGACGCGAAGAC 30835 GCTCTCGGCG 30836 CGA CGA T AG
ACAA------- C
GACGGTGAGTCGAGCGGTCG CCGCGTT AGA CGGTGAG CG
CGGTCGGTCGGTCGGTCGGTC CGCG G
GTCGGTCGGTCGGTCACAAC ||| ||||||| || |||||||||||||||||||| ||||
GCGCGTCGCGGTCGTTTGAC TCT GCCGCTT GC GCCAGTCAGTCAGTCAGTCAG
GCGC /
TGACTGACTGACTGACTGAC --- CG- - CA TCAGTTTGCTG T
CGACCGTTCGCCGGCTCTCG
GCGCCGCGTT
GAM1186 CCCGCTATAGGTGAACACTG 30842 TAGGTGAACA 30843 A--- AACAC - AAA TA
GACAAAGGGTACGGCCTGTC CTGGACAAAG CCCGCT TAGGTG TGGA C GGG C
GTTCCACACCTACTACAGCG GGTA |||||| |||||| |||| | |||
GG GGGCGA ATCCAC ACCT G TCC /
CATC ----- T CTG GG

GAM1187 TAGAATACGGGGATATAGAT 30855 CTAGAACATT 30856 TAC G- ------- - AA
GTTTTACAAACAAATGCTAG TTTGATTAAT TAGAA GGG ATAT AGATGTTTTA CA C
AACATTTTTGATTAATATAG ATAG ||||| ||| |||| |||||||||| ||
CCTTTCTA ATCTT TCC TATA TTTACAAGAT GT A
--- GA ATTAGTT C AA

GAM1188 GGCGGTAACAAATTCAGAGT 30863 TACACGTACT 30864 ACAAATTC C- - AA
ACGCTATACGTAATAAAACG TTTCAAATAC GGCGGTA AGAGTACG TATA CGT T
ATGTACACGTACTTTTCAAA CGCC ||||||| |||||||| |||| |||
TACCGCC CCGCCAT TTTCATGC ATGT GCA A
AAACT--- AC A AA

GAM1189 GTCTGTGTTGTATGACTGTA 30870 TGACTGTATG 30871 GTG- AT TA TGT TG G--
GTT
TGTATGTGTAATGTTTGCAT TATGTGTAAT GTCT TTGT GACTG TGTA GTAA TTT CATGTT
A
GTTGTTAATAAATATGAATG GTTT |||| |||| ||||| |||| |||| ||| ||||||

AGTGTTACTTTTACGCGTGG CGGA AATA TTGGT GCAT CATT GAG GTATAA /
TTGCATAAACTAAGGC ATCA CG GC TTT GT TAA ATA

GAM1190 CAATTTGCAAAACAGTTTTT 30884 TGGCAGGAAG 30885 AAACAGT TG TTT TC
CTGCTGATTTGGATCAGTTT TTTTTAATGC CAATTTGCA TTTTCTGC A GGA A
CCTCTTGGCAGGAAGTTTTT AGGT |||||||||| ||||||||| | |||
AATGCAGGTTG GTTGGACGT GAAGGACG T CCT G
AATTTTT GT CT- TT

GAM1191 GGCTTCGTTGCGTATGGCCA 30892 TGGCACCAGC 30893 TT GTATG ACCACGTT
CCACCACGTTAAAGAGAGAC TCGAAGCC GGCTTCG GC GCCACC A
GGTGGCACCAGCTCGAAGCC ||||||| || ||||||
CCGAAGC CG CGGTGG A
T- ACCA- CAGAGAGA

GAM1192 GGCGACATGGTTGATATTGG 30961 TACAGGAATC 30962 G GG A G- CC GATT
GTTTGGTGCCATGGATTTTA TAAATCAGAT GGC ACAT TTGAT TTGGGTTT GTG ATG T
AAACATTACAGGAATCTAAA GTGC ||| |||| ||||| |||||||| ||| |||
TCAGATGTGCC CCG TGTA GACTA AATCTAAG CAT TAC T
- -- - GA -- AAAA

GAM1193 GTGCTTAAGTGCTATCGCTT 30976 TAAGTGCTAT 30977 TAAG----- TC ---------- G
TCGGGAACGCAAAAAAAAAA CGCTTTCGGG GTGCT TGCTA GCTTT CG G
GAGGCTTAGTAAAATATTAT AACG ||||| ||||| ||||| ||
AGTAC CATGA ATGAT CGGAG GC A
TATTATAAA T- AAAAAAAAAAC A

GAM1194 GAGCACAGACAACAATTCAT 30980 TAGGACTATG 30981 -- ---- A ATT TGAAA CAC
TAGGACTATGAAATTACCAC AAATTACCAC GAGC ACAGA CAACA TTC AGGACTA TTAC
C
CTACAGTAGATTGGTCTTTA CTAC |||| ||||| ||||| ||| ||||||| ||||
GGAAATGTTGATGATCTGTA TTCG TGTCT GTTGT AAG TTCTGGT GATG T
AGCTT AA AGTA A GAT TA--- ACA

GAM1195 GGGCAGAAAGTTTTTAATGC 30987 AAGTTTTTAA 30988 A AA AATGCAACTT-- CGT
AACTTGGGGTTCGTACTAAA TGCAACTTGG GGGC GA GTTTTT GGGGTT A
CCTTCTACTACTACTAAAAA GGTT |||| || |||||| ||||||
ACGCTCGGCCC CCCG CT CAAAAA TTCCAA /
G CG ATCATCATCATC ATC

GAM1196 TGCTGTTGGGCATAAGTTTT 30999 TGGGCATAAG 31000 T A TTTA-- AA
TATTGCAAACATCTGCAACA TTTTTATTGC TGCTGT GGGC TAAGTT TTGCA C
CAATGATTTGGCTTGCAGCA AAAC |||||| |||| |||||| |||||

ACGACG TTCG GTTTAG AACGT A
- - TAACAC CT

GAM1197 CCAACAGATGCATATGTAAA 31009 TGTAAAGCGC 31010 AT- T AA GCA AA ATT
GCGCACCAATATATTTTATC ACCAATATAT CCAACAG GCA ATGT AGC CC TAT T
ATGCAGGCAGCTCACGTTTG TTTA ||||||| ||| |||| ||| || |||
CTTGCTGTTGG GGTTGTC CGT TGCA TCG GG GTA T
GTT T C- AC- AC CTA

GAM1198 GTTTCTGTATGACTGTATGT 31012 TGAATGAGTC 31013 C TG TG TGT T G G AA
ATGTGTAATGACTGTATGTA TTACTTTTAC GTTT TGTA AC TATGTA GTAA GACT TAT TATGT
T
TGTAATAAATATGAATGAGT GTGT |||| |||| || |||||| |||| |||| ||| |||||
CTTACTTTTACGTGTGGTTA CAAA ACAT TG GTGCAT CATT CTGA GTA GTATA /
CATAAAC T -- GT TTT - - A AA

GAM1199 CTGGGGTAAACATTTTGGGA 31017 TTTTGCCCAA 31018 TAAACATT AC-- C TGG
CAACCTCCTATGGCATTTAG TTTCCCAG CTGGGG TTGGG AACCTC TA C
AGGTTTTTGCCCAATTTCCC |||||| ||||| |||||| ||
AG GACCCT AACCC TTGGAG AT /
TT------ GTTT - TTA

GAM1200 TTGGGATCAACGCGCGTCTG 31109 TTCGCGAGGG 31110 ATC GCGT --- ATA
ATCAA T
GTACTGGGTGATATCTTCGC ACACCCCAGA TTGGG AACGC CTGGTACT GGGTG
TCTTCGC AATGG C
ATCAAAATGGTCGCTATTCG GTAT ||||| ||||| |||||||| ||||| ||||||| |||||
CGAGGGACACCCCAGAGTAT AACCC TTGTG GGCTATGA CCCAC GGGAGCG
TTATC /
CGGGTGTTTTACCCAA ATT ---- GAC A-- C---- G

GAM1201 CAGGTCCAAAGAGGCTAACG 31113 AGAGGCTAAC 31114 --- AAA - -- C C
AGACGGCGTCCCATCTTCTG GAGACGGCGT CAG GTCC GAGGCT AAC GAGA GG G
TTCGGTCTCCCGGATTCACT CCCA ||| |||| |||||| ||| |||| ||
G GTC TAGG CTCTGG TTG TTCT CC T
ACT CC- C TC A C

GAM1202 GTTGACATGTGGAGCCACTG 31142 ACGACAATAA 31143 ACAT CACTGGCG-- A
GCGCGTTGCCGACAACGGCG CCCGCTCCGC GTTG GTGGAGC CGTTGCCG C
ACGACAATAACCCGCTCCGC CACG |||| ||||||| ||||||||
CACGCAGC CGAC CGCCTCG GCAGCGGC A
GCAC CCCAATAACA A

GAM1203 CAACACACAAGCCAATATGT 31148 TTTGTGCTTT 31149 A CA TG TGCTAA CC C-
TCATT
GCTGCTAACACACCTATATA GCGTGTGTGT CAACACACA GC ATA TGC CACA TATATA
CTGTAA A
CCTGTAATCATTATTCCTTT GTGT |||||||||| || ||| ||| |||| |||||| ||||||
TATAGTTTATGTGTTTGTGC GTTGTGTGT TG TGT GCG GTGT GTGTAT GATATT
T
TTTGCGTGTGTGTGTGTGTG G -- GT TTTC-- TT TT TTCCT
TTG

GAM1204 GCGGGCGTGGGGACCCGGGG 31309 GGGGATGGTA 31310 - GG CGGGGAGA AG T
--- - G
AGAGACCACCAGGCCTCGCC GGGATTGGTG GCG TGG ACC GACCACC GCC
CGCCGGTTT TC TCTCTCTCC T
GGTTTTCTCTCTCTCCGTTG GGTG ||| ||| ||| ||||||| ||| ||||||||| || |||||||||
GGGGGGGGGATGGTAGGGATT TGT ACT TGG TTGGTGG TGG GTGGTTAGGG GG
AGGGGGGGG T
GGTGGGTGAGGTGGTTGTGG T GA TG------ AG - GAT T G
TAGTCATTGTGAGT

GAM1205 TGGTCTCATAAAAAAAGTTT 31357 TGATGGAGTC 31358 AAAA TTTTAC T- T
TCTCTTCAAT CTCACAA
TACAAAAATATTTTTATTCT GTAAAAATAT T AAAG AAAAATATTTTTAT CTCT TC GGT
A
CTTTCTCTCTTCAATGGTCT TTTT | |||| |||||||||||||| |||| || |||
CACAAAAATATTAAACCTCT A TTTC TTTTTATAAAAATG GAGG AG CCA A
TTCTGATGGAGTCGTAAAAA GTC- TCTTA- CT T TCTTTCT--- AATTATA
TATTTTTATTCTCTTTCTGA
TGTCTCAACTA
GAM1206 CCGAGCGGGGGAGAGCGGTA 31364 TACAGGGGAG 31365 GG- AGC- A GAA G G GG
AG GA- GAG GTG
GGGGAAACGCCGCCTGGGAT TGTACCCACC GGAG GGT GGG AC CC CCTG ATG TGG
CC TAGTGT A
GAGTGGGACCGAGTAGTGTG AAAA |||| ||| ||| || || |||| ||| ||| || ||||||
TGATAGGCACTAGAGGGCGC CCTC CCA CCC TG GG GGAC TGC ACC GG
ATCACG /
CAGCGTACAGGGGAGTGTAC CAA AAAA - ATG A - A- G- GCG AG- GAT
CCACCAAAACTCCAACACCA
CGG
GAM1207 TTTTTCTTTGGTACAAAATT 31394 TCTTTGGTAC 31395 T TT CACAA ---- CA A
TCACACAAGTTTTTATACAG AAAATTTCAC TTTTTCTT GGTACAAAA TCA GTTTT TATA
GACAA T
ACAAATTCTTGTCCATATAT ACAA |||||||| ||||||||| ||| ||||| |||| |||||
TTTAAAACATTGACTTTTGT AAAAAGAA TCATGTTTT AGT CAAAA ATAT CTGTT T
ACTAAGAAAAA - C- TA--- TTTT AC C

GAM1208 AAAATATTTTTATTCTCTTT 31432 AATATTTTTA 31433 T- T TCTCTTCAAT CTCACAA
CTCTCTTCAATGGTCTCACA TTCTCTTTCT AAAATATTTTTAT CTCT TC GGT A
AAAATATTAAACCTCTTTCT CTCT |||||||||||| |||| || |||

GATGGAGTCGTAAAAATATT TTTTATAAAAATG GAGG AG CCA A
TT CT T TCTTTCT--- AATTATA

GAM1209 TGGGAAGTACAATATGGGGG 31461 TCAGATTGTT 31462 ACA TA AA-- A A G TG C AT - A- A A
CAATGTAATTGATTGTAATG AGACAGCTAC A TGGGGGC TGTA TTG TT TAA A TCT GT GC GTACC GTG C
ACTCTATGTGCAGTACCAGT AACA | ||||||| |||| ||| || ||| | ||| || || ||||| |||
GACGACACGGTATCCGCTAC T ACCTCCG ACAT GAC AG ATT T AGA CA CG TATGG CAC G
TCAGATTGTTAGACAGCTAC GC- GC CACA C - - GT - CT T CC - A
AACACGCCTCCACGTCGACC
CCCA
GAM1210 ACCTCTTTCTGATGGAGTCG 31479 TATTTTATTC 31480 TCT--- T TC T- T TCTCTTCAAT CTCACAA
TAAAATATTTTATTCTCTTT TCTTTCTCTC GA GGAG GTAAAATATTTTAT CTCT TC GGT A
CTCTCTTCAATGGTCTCACA TTCA || |||| |||||||||||||| |||| || |||
AAAATATTAAACCTCTTTCT CT TCTC TATTTTATAAAATG GAGG AG CCA A
GATGGAGTCGTAAAATATTT TTCTCT T T- CT T TCTTTCT--- AATTATA
TATTCTCTTTCTCTCTTCAA
TGGT
GAM1211 ATAAAAAAGTTTTACAAAAA 31512 TCATAAAAAA 31513 A ACA A TCT- TTCTCT
TATTTTTATTCTCTTTCTCT GTTTTACAAA ATAAAAA GTTTT AAAAT TTTTTAT CT C
CTTCAATGGTCTCATAAAAA AATA ||||||| ||||| ||||| ||||||| ||
AGTTTTACAAAAATATTTTT TATTTTT TAAAA TTTTG AAAAATA GG /
AT A ACA A CTCT TAACTT

GAM1212 AAAATATTTTTATTCTCTTT 31527 AATATTTTTA 31433 TATT T TCTCTTCAAT CTCACAA
CTCTCTTCAATGGTCTCACA TTCTCTTTCT AAAATATTTT CTCT TC GGT A
AAAATATTAAACCTCTTTCT CTCT |||||||||| |||| || |||
GATGGAGTCGTAAAATATTT TTTTATAAAA GAGG AG CCA A
T TGCT T TCTTTCT--- AATTATA

GAM1213 TACATATGCATGCTTTACAC 31528 TAATGTACAG 31529 T-- TGCTT CACC TACTATA G T A
ACCATACAATAATTACTATA TACAGTGTAA CA ATGCA TACA ATACAATAAT ATGTACA TACAG GTA C
ATGTACAGTACAGTGTAACA CATA || ||||| |||| |||||||||| ||||||| ||||| |||
TACCTGTGATGTGCATGTTG GT TATGT ATGT TATGTTGTTG TACGTGT GTGTC CAT /
TTGTATTTTTGTATTTTTGT TTT TTTT- TTT- ------- A - A
ATTTTTGTA

GAM1214 AAAATATTTTTATTCTCTTT 31551 AATATTTTTA 31552 T- T TCGCTTCAAT CTCACAA
CTCGCTTCAATGGTCTCACA TTCTCTTTCT AAAATATTTTTAT CTCT TC GGT A
AAAATATTAAACCTCTTTCT CGCT |||||||||||| |||| || |||

GATGGAGTCGTAAAAATATT TTTTATAAAAATG GAGG AG CCA A
TT CT T TCTTTCT--- AATTATA

GAM1215 TCCCCCGGGAAACGTCCTCT 31559 TCGATGATCC 31560 CC AAC - ATC CGA- -
C
CGATGATCCGGACGAGGTTC GGACGAGGTT TCCC GGGA GTC CTCTCGATG CGGA GGTT
CCTAGTT T
CTAGTTCTCAACTAGGTGAC CCTA |||| |||| ||| ||||||||| |||| |||| |||||||
CCAGCTCCGCATCGAGAGTG AGGG CCCT CGG GAGAGCTAC GCCT CCAG
GGATCAA /
GCAGCTCCCCCGGGA CC CGA T --- CGAC T C

GAM1216 CCGTGGTGTTGGAGTTTTGG 31565 TCGGTCCCAC 31566 TT TTT TAC- T - TACGC-- C
CTC CCTA
TGGGTACACTCCCCTGTACG TCATCCCAGG TG GGAG TGGTGGG AC CC CCTG TGG
GCC TAGTG T
CTGGCGCCCTCTAGTGCCTA CGGC || |||| ||||||| || || |||| ||| ||| |||||
TCACACACTACTCGGTCCCA GC CCTC GCCATCC TG GG GGAC ACC TGG
ATCAC /
CTCATCCCAGGCGGCGTTTC CC TC- CCTT C C CCTACTC C CTC ACAC
CCCTACCGCTCTCCCCCGCT
CGG
GAM1217 GAATTATTATTATTCTTATT 31578 TGAGCTCGTC 31579 TA TTATTA TCC AG AG CT-
CCTGAAC
ATTCTTATTCCACGAGAGTA TGTAAGAGCC AT TTC TTCTTAT ACGAG TATG CTCGT
GTAAGAG G
TGAGCTCGTCTGTAAGAGCC TGAA || ||| ||||||| ||||| |||| ||||| |||||||
TGAACGATGATTATTCTTAT TA AAG GAGAATG TGCTC GTAT GAGCA TATTCTT
/
TTCACGAGAGTATGAGCTCG GC TCC--- TC- GA GA CTT ATTAGTA
TCTGTAAGAGCCTGAACGAT
GATTATTC
GAM1218 GCGGGCTGGTCATCGGCATT 31603 TCTGGCGCAC 31604 G AT- T - A- G CTCCTC
CTT T
CTGGCGCACCGGTGCGCGCT CGGTGCGCGC GCGGGCT GTC CGGCAT CTG GCGC CCG
TGCGCG CC GG C
CCTCCCCTTGGTCTTCCCGG TCCT ||||||| ||| |||||| ||| |||| ||| |||||| || ||
CAACCCCGCGCACGGCCGCG CGCCCGA CAG GCCGTG GGC TGCG GGC ACGCGC
GG CC T
TGCGGCGTGCCGTGGGACGA G GGT C G CC - CCCAAC C-- T
GCCCGC

GAM1219 ATGTGTTTTTTATTAAAGAG 31611 TGTTTTTTAT 31612 T ATCATT -- A A TAA
C TT
ATCATTCACGTGTGGTTTTT TAAAGAGATC TA TAAAGAG CACGT GTGGTTTTT TTGA
AAGAAAT ATGTA AT G
ATTGAAAAGAAATTAAATGT ATTC || ||||||| ||||| ||||||||| |||| ||||||| ||||| ||
ACATTTGATTATTTACATGT GT ATTTTTT GTGCA TACTAGAGA AATT TTTTTTG
TACAT TA A

GTTTTTTATTAAAGAGATCA T GT---- TT - A TG- T TT
TTTACGTGTGTTTTTTATTG
AAAAGAAAT
GAM1220 TATTCTTATTTCATGAGAGT 31621 TTCATGAGAG 31622 TTC TGAGC - T- G
ATGAGCTCGTCTGTGAGAGC TATGAGCTCG TATTCTTAT ATGAGAGTA TCGT C GT A
CTGAACGATGATTATTCTTA TCTG ||||||||| ||||||||| |||| | ||
TTTCATGAGAGTA ATGAGAGTA TATTCTTAT AGCA G CG G
CTT TAGT- A TC A

GAM1221 CCGTGATCGATCCCCTCCCG 31629 TTTCAACGGA 31630 ATCGATCC CCC G CC- -
AG
CCCGGTGGCCCCGAAACGAG CGCCCCGGGA CCGTG CCTCCCG GGTG CC GAAA CG
G
GGTCGATTTCAACGGACGCC GGAA ||||| ||||||| |||| || |||| ||
CCGGGAGGAAAAAATGCACG GGCAC GGAGGGC CCGC GG CTTT GC /
G GTAAAAAA C-- A CAA A TG

GAM1222 TATTCTTATTTCATGAGAGT 31644 TGATCATTCT 31645 TTC - GCTAGTCT GA TG
ATGAGCTAGTCTGTGAGAGC TATTATCATT TATTCTTAT ATGAGAGTA TGA GTGA GCC A
CTGAACGGTGATCATTCTTA ATTC ||||||||| ||||||||| ||| |||| |||
TTATCATTATTCTTATTTCA ATGAGAGTA TATTCTTAT ACT TACT TGG /
TGAGAGTA CTT T ATTATTCT AG CA

GAM1223 ATGAAGTTAATGATACACAC 31650 TTAATGATAC 31651 T ATA C AC GAATT
TACACTGTCGAATTTGATAG ACACTACACT ATGAAGT AATG CA ACTAC TGTC T
GGACAAAGTAGTTGACGCGT GTCG ||||||| |||| || ||||| ||||
TTATTTCAT TACTTTA TTGC GT TGATG ACAG G
T GCA - AA GGATA

GAM1224 TGGCCTTCCAGATGCTAACT 31658 TAACTTTTAT 31659 CT GA A- AC CAC C TG
TTTATGACCCTAACACACAG GACCCTAACA TGGC TCCA TGCT ACTTTTATG CCTAA ACAG
GCCT T
CGCCTTGTGTGGGCCTGTTT CACA |||| |||| |||| ||||||||| ||||| |||| ||||
AGGCGTGGAGGTGGGGCGTG ACCG AGGT GCGG TGGAGGTGC GGATT TGTC
CGGG /
GACAGCCA AC -- GG -- --- - TG

GAM1225 CCTCCACAGTTACTACACCA 31690 TCCACAGTTA 31691 - ACTACACCATATAAT G
TATAATAATGAGAGTTTTAA CTACACCATA CCTCCACA GTT AAT A
AGAGTACCTGCGACATGTGG TAAT |||||||| ||| |||
AGG GGAGGTGT CAG TTG G
A CGTCCATGAGAAATT A

GAM1226 TAAGGGCAGGGAGGAGATAC 31702 TGCAAAAGCG 31703 AG-- A- AC AT A ------ G
AC-- GGTCA

GTATGCAAAAGCGGGGGGGA GGGGGGACTG AGGGC GGAGG GAT GT GC AAA
GCGGG GGG TGC A
CTGCGGTCAACAATAAGTAA CGGT ||||| ||||| ||| || || ||| ||||| ||| |||
AAACCCGCCCGCCACATCTT TTTCG CCTCC CTA CA CG TTT CGCCC CCC ATG
C
TCGCCACAATCGGCCTCCAG GAGA GG A- C- C CTACAC G AAAA AATAA
AGGCTTTTA

GAM1227 TAACGTTGCTTATATTTATG 31720 ACGTTGCTTA 31721 T T T TTGT- CC
TTGTTGTACCCAGTGTGCAT TATTTATGTT TAACGT GC TATAT TATG TGTAC A
GATTTATGTATGTGTGCATG GTTG |||||| || ||||| |||| |||||
TTG GTTGTA CG GTGTA GTAT ACGTG /
- T T TTAGT TG

GAM1228 CAAAACCACAACACTGCTAA 31728 AACCACAACA 31729 A ACAC TAATCCTCT--- TT
TCCTCTGGCTTCCTGCCTCT CTGCTAATCC CA AACCACA TGC GGC C
CCTACTGCTGCATACCTGTG TCTG || ||||||| ||| |||
GTTGTG GT TTGGTGT ACG CCG /
G CCAT TCGTCATCCTCT TC

GAM1229 CTGAAATACCCGTAAACGGG 31759 TACCCGTAAA 31760 A - AAAC- TA AACG
GATGTATAAACGCAAAATGC CGGGGATGTA CTGA ATAC CCGT GGGGATG TA C
CCGTCCCTCCCGAATGGCGT TAAA |||| |||| |||| ||||||| ||
ATATTAG GATT TATG GGTA TCCCTGC GT /
A C AGCCC CC AAAA

GAM1230 AATCCAACCCTCTTTGTACA 31765 TTGCATAGTT 31766 CT-- A-- A- TT --- C C
AAATGCTTTTGGCAGTACAT GGCCACAATT AATCCAACCCT TTGT CAA ATGC TTGGCA
GTA ATTT T
TTCTAAGAGTTACTCATGCT TCAG |||||||||| |||| ||| |||| |||||| ||| ||||
AATTGCATAGTTGGCCACAA TTAGGTTGGGA AACA GTT TACG AATCGT CAT TGAG
A
TTTCAGGGTTGGATT CTTT CCG GA TT ACT - A

GAM1231 TGGGCATATGTTTTTATGCA 31773 TAAGCCAAGT 31774 GC T T- CAA TT TT GT
GGTGTTTGCAATATATTTTG ATCTGTCTTG TGG ATATGTTT TA GCAGGTGTTTG TATAT TG
GGC G
TTGGCGTGTAGCCCTTATTG CAAA ||| |||||||| || |||||||||| ||||| || |||
TATAAGCCAAGTATCTGTCT ACC TGTATAAA GT TGTCTATGAAC ATATG AT CCG /
TGCAAATATGTAACCA AA C TC CGA TT TC AT

GAM1232 TGGTCTGTGTTAAATCCCTT 31801 CCCTTCTATA 31802 T TAAATCCC T T T
CTATATTATTATTGATGTAT TTATTATTGA TGGTCTG GT TTCTATA TA TAT G
TGTTGTAGAAAACTATTACT TGTA ||||||| || ||||||| || |||
TAGACCA ACCAGAT CA AAGATGT GT ATG A

T TTATCAA- T T T

GAM1233 AAGTTTGGCCTTCCTGATCC 31810 TCTTTCTATA 31811 T -- A- TCTTTCTATAAT AC
AA TT
ATCTTTCTATAATCCTGACC ATCCTGACCA AAG TTGGCCTT CCTG TCCA CCTG CAGG
CGT G
AGGAACGTTTGGTATGGGCC GGAA ||| |||||||| |||| |||| |||| |||| |||
TGTGTAGGTTTGGAGGTAGG TTC AACTGGAG GGAT AGGT GGAT GTCC GTA /
CCGAGGTCAACCTT C CC GG TT---------- GT GG TG

GAM1234 GGGATCCATAGTTATGACAC 31823 TATGACACAG 31824 ATAGT C- C--- TATT---
TTC
AGTAACATAGATTATTACCT TAACATAGAT GGGATCC TATGA ACAGTAA ATAGAT ACC
T
TCTTGACGGTCGCAAATATC TATT ||||||| ||||| ||||||| |||||| |||
TATATACTTATTGTTATCGT TCTTAGG ATGCT TGTTATT TATCTA TGG T
ATCGGATTCT CT--- AT CATA TAAACGC CAG

GAM1235 GCAGAAGGTAGCTCCCTCGA 31834 GAAGGTAGCT 31835 T TC-- C C GTGACA
CTGGGTGACAAGAAGAAACC CCCTCGACTG GCAGAAGG AGC CCT GA TGG A
ATTCAGGAAGTGCTTCCTTC GGTG |||||||| ||| ||| || |||
TGC CGTCTTCC TCG GGA CT ACC G
T TGAA - T AAAGAA

GAM1236 GTTCGTGCGCCAGGCCTGCA 31841 GTACATGGGC 31842 G G C------- C AC - GCT
AA
AGATCTCCAACGTGGAGCTG ATCTTGCACG GTTC TGC CCAGGC TGCAAGAT TCCA GTG
GA GACC C
ACCAACCTGGTCTCGTACAT AGAA |||| ||| |||||| |||||||| |||| ||| || ||||
GGGCATCTTGCACGAGAACC CAAG ACG GGTCCG ACGTTCTA GGGT CAT CT
CTGG /
GCCTGGGGCAGAAC - G CCAAGAGC C A- G --- TC

GAM1237 AGATCTATTATGTCTGTTAT 31865 TATTATGTCT 31866 CTA C TATT TCT- CACT
TTGAGATTCTTCATCACTAC GTTATTTGAG AGAT TTATGT TGT TGAGAT TCAT A
TTAATGGCATTATCTCGTCA ATTC |||| |||||| ||| |||||| ||||
CAATGTAACCAATCT TCTA AATGTA ACA GCTCTA GGTA /
ACC - CT-- TTAC ATTC

GAM1238 GGAAGGAGTGTGGCTAATGC 31877 TCAGTACAAT 31878 A T AA---- --- G
TGGTAAGGCACCTTTCTATC CAAGCCCATT GG AGGAGTG GGCT TGCTGGTA AG C
AGTACAATCAAGCCCATTCC CCTC || ||||||| |||| |||||||| ||
TCCC CC TCCTTAC CCGA ATGACTAT TC A
C - ACTAAC CTT C

GAM1239 GAGGTGTGTGGCTCAGCACG 31897 TAATAGGACA 31898 - G- CA- C GTGAC
TAGAGTGACAAGTAAATCTA CAACACCTC GAGGTGT GTG CT GCA GTAGA A
CTGTAATAGGACACAACACC ||||||| ||| || ||| |||||
TC CTCCACA CAC GA TGT CATCT A
A AG TAA - AAATG

GAM1240 GGAATTGTATATTAGCCTTG 31916 AATTGTATAT 31917 -- AGCCTTG AG- TCTAG T
A
CTAAGGGAGACATCTAGTGA TAGCCTTGCT GGAAT TGTATATT CTAAGGG ACA TGA
ATAAGTGTG A
TATAAGTGTGAACTACACTT AAGG ||||| |||||||| ||||||| ||| ||| |||||||||
ATCTTAAATGTTGTAACTCC CCTTA ACATATAA GATTCCT TGT ATT TATTCACAT /
TTAGGATAATCAATATACAA AA CTAATAG CAA TGTAA C C
AATTCC

GAM1241 TCCCTAGGGAGGATCTGGCT 31921 TTTTCAGTTC 31922 C T CT TAA-- AG
CTGTAAGCTGAGGCAGTAGT CAGTCCTCTC TCC TAGGGAGGA CTGG CTG GCTG G
GTTTTCAGTTCCAGTCCTCT TAAG ||| ||||||||| |||| ||| ||||
CTAAGGA AGG ATCTCTCCT GACC GAC TGAT C
A - TT TTTTG GA

GAM1242 GCTGGGCTCGAGCATGACGG 31939 GAGCATGACG 31940 C - A C - ACTA A- G
CGACTACCTCCACCTGAGCG GCGACTACCT GCTGGGCT GA GC TGA G GCG CCTCC CCT A
GGGGGGAGGACGCGCTCATC CCAC |||||||| || || ||| | ||| ||||| |||
AAGCATCTGGCCCGGC CGGCCCGG CT CG ACT C CGC GGAGG GGG G
T A A A T GCA- GG C

GAM1243 ACATCTGGGACAGTTCTGCC 31956 GTGCAGGGGT 31957 - T TTCT-- G AC ATACG
GCTTGACCCATATACGTATT TCCATTCTGT AC ATC GGGACAG GCC CTTG CCAT T
TAATGGTGCAGGGGTTCCAT TCTG || ||| ||||||| ||| |||| ||||
TCTGTTCTGATCGT TG TAG TCTTGTC TGG GGAC GGTA /
C - TTACCT - GT ATTTA

GAM1244 CGGCTGGACGTTGGTCCGCA 31968 AAGCCGTTGG 31969 A T G GC G - AA- C
GGCGGTCGCGGAGGAACCCC CGACCTTGAG CGGCTGG CGT GGTCC CAG GGTCGC GA GG
CC C
GGGAAGCCGTTGGCGACCTT GACC ||||||| ||| ||||| ||| |||||| || || ||
GAGGACCCGCGCCCGGTCG GCTGGCC GCG CCAGG GTT CCAGCG TT CC GG /
C C A -- G G GAA G

GAM1245 GCTGAGGAGGCCGGAGTCGT 31999 TGAAGCCCTC 32000 G- GA - - TGC A-
GAAG
CGGCCTGCTCGTGCGGCACG GGGCCAGGCC GCTGAGGAG CCG GTCGTC GGCCTG CTCG
GGC CGCC A

CCGAAGACGAAGGTGAAGCC AGGC ||||||||| ||| |||||| |||||| |||| ||| ||||
CTCGGGCCAGGCCAGGCGAC CGGCTCCTC GGC CAGCGG CCGGAC GGGC CCG
GTGG /
AGCGGAACTCCTCGGC AA GA A C TC- AA AAGC

GAM1246 GCTATTAAACAGTATGGAGA 32097 TGAGAAACTT 32098 A ----- TG--- A TTAA- G CTTA
A T A
CATTGATCTATTATTTAATG AAAGTAGACT TGGA GACAT ATCT TTAT TGA AAA
AAGTAG C CCG T
AGAAACTTAAAGTAGACTCC CCGA |||| ||||| |||| |||| ||| ||| |||||| | |||
GATTCGGGACTATTTGACTT ATCT TTGTA TAGG AATG ACT TTT TTTATC G
GGC /
TGTCAACTTTGTAAAGGATA - TAGTG TAGTA A TTTCA G CAG- A - T
TGATATGTTGTGATTCTAGA
ATAGTAGTAGC
GAM1247 TTGAAACTCCGCCCCTTACT 32112 TGAAATGTTT 32113 AC CGCCCCTT - AAAAA
TTTATTAAAAATCTTCAAGA ACAATAGAAA TTGAA TC AC TTTTATT T
TGAAATGTTTACAATAGAAA TTCG ||||| || || |||||||
TTCGA AGCTT AG TG AAAGTAG C
AA ATAACATT T AACTT

GAM1248 GCCGGTTAGTATGACTTACT 32118 TAAGACACAG 32119 T-- GA TA-- A----------
TA
TGTATAATAAGTATAGTTTT AAATACTATA GCCGG TAGTAT CT CTTGTATA TAAG
T
AAACTGATTTTAGCAGAATA TCCG ||||| |||||| || |||||||| ||||
TATAAGACACAGAAATACTA CGGCC ATCATA GA GAATATAT ATTT A
TATCCGGC TAT AA CACA AAGACGATTTTAGTCAA TG

GAM1249 GTTGTTTTCATTGTTGATGG 32123 TTGATGGTAA 32124 TG TT TT TG ---- T T A G
T
TAAGGATTCTTATTTTGAAG GGATTCTTAT GT TT CATTG GA GTAAGG ATTC TATTT GA GT
GTTTT C
TGGTTTTTCAGAAGATAACT TTTG || || ||||| || |||||| |||| ||||| || || |||||
CTAAATATGAATTATGCCTT CG AG GTAAC TT TATTCC TAAG ATAAA CT CA TAGAA
A
ATTGTTTTCAATGTTGATGG GT TT TT GT GTAT T T - A G
C

GAM1250 ATTGACTTCGAAGAAAGATG 32127 TTACATGGAG 32128 TG TT AAA C - TT GATT
TGG TAAG
CGTCTTTTGGATTTGTAATG GAACACATTA AT AC CGAAG GATG GT CTT G TGTAATGAC
GCCT T
ACTGGGCCTTAAGTTCATAG CTTT || || ||||| |||| || ||| | |||||||| ||||
GTGTTATTACATGGAGGAAC TA TG GTTTC TTAC CA GGA T ACATTATTG TGGA /
ACATTACTTTGGTTGAT GT -- A-- A A GG ---- --- TACT

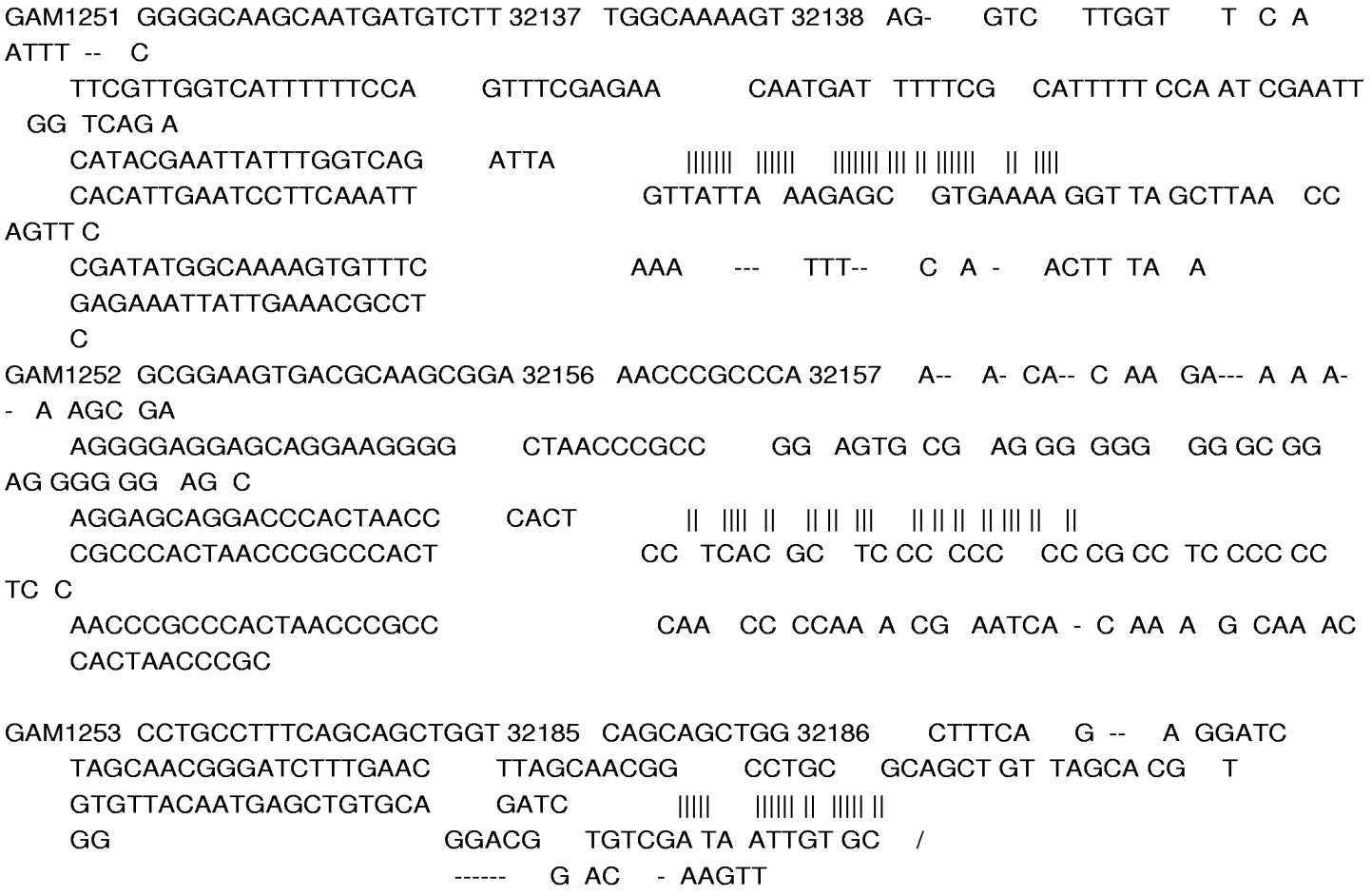
GAM1251 GGGGCAAGCAATGATGTCTT 32137 TGGCAAAAGT 32138 AG- GTC TTGGT T C A ATTT -- C
TTCGTTGGTCATTTTTTCCA GTTTCGAGAA CAATGAT TTTTCG CATTTTT CCA AT CGAATT GG TCAG A
CATACGAATTATTTGGTCAG ATTA
CACATTGAATCCTTCAAATT GTTATTA AAGAGC GTGAAAA GGT TA GCTTAA CC AGTT C
CGATATGGCAAAAGTGTTTC AAA --- TTT-- C A - ACTT TA A
GAGAAATTATTGAAACGCCT
C
GAM1252 GCGGAAGTGACGCAAGCGGA 32156 AACCCGCCCA 32157 A-- A- CA-- C AA GA--- A A A- - A AGC GA
AGGGGAGGAGCAGGAAGGGG CTAACCCGCC GG AGTG CG AG GG GGG GG GC GG AG GGG GG AG C
AGGAGCAGGACCCACTAACC CACT
CGCCCACTAACCCGCCCACT CC TCAC GC TC CC CCC CC CG CC TC CCC CC TC C
AACCCGCCCACTAACCCGCC CAA CC CCAA A CG AATCA - C AA A G CAA AC
CACTAACCCGC
GAM1253 CCTGCCTTTCAGCAGCTGGT 32185 CAGCAGCTGG 32186 CTTTCA G -- A GGATC
TAGCAACGGGATCTTTGAAC TTAGCAACGG CCTGC GCAGCT GT TAGCA CG T
GTGTTACAATGAGCTGTGCA GATC
GG GGACG TGTCGA TA ATTGT GC /
------ G AC - AAGTT
GAM1254 GCCGCTCTTAGCACAAAATC 32211 TAGCACAAAA 32212 CTTAGCACAAAA AACAAATCTA-- -- C
AAAAACAAATCTAGCCACCG TCAAAAACAA GCCGCT TCAAA GC A
CAGTCTGTAGAGACTTTTGA ATCT
GTTGAAAAAGTAAGCGGC CGGCGA AGTTT CG C
ATGAAAAAGTTG TCAGAGATGTCTGA C
GAM1255 TTTCAATAACTCTCACTTTT 32224 TCAATAACTC 32225 TT TCA---------- TT
TTGCTAGAGGCAGGCTCAAC TCACTTTTTT T CAATAACTC CTTT T
AATGTCTGGAGTTGTTGGGG GCTA
G GTTGTTGAG GAGA G
GG GTCTGTAACAACTCGGACG TC
GAM1256 AATGGTGCTATTAGAATTTA 32245 TATTAGAATT 32246 T T AGAA- AAC-- T
CAAAACTGGTAATCCACATA TACAAAACTG AATGG GC ATT TTTACAA TGG A
GTTGTAAAGTTAAAATTGTT GTAA
CCGTT TTGCC TG TAA AAATGTT ACC A
T T AATTG GATAC T

GAM1257 GTCGCTCATGCGGACAGTCA 32255 TCTCTCACAG 32256 C ---- C CA ATTAA
AACATTCATTAACACGCAGG CATGATGAC GTCG TCATGC GGA AGT AACATTC C
ATGTTGCATTCTCTCACAGC |||| |||||| ||| ||| |||||||
ATGATGAC CAGT AGTACG TCT TTA TTGTAGG /
- ACAC C CG ACGCA

GAM1258 GCGTTCATATTAGACTACAA 32303 TATTAGACTA 32304 - ---- ACAAACCT--- AATA
ACCTAATGATAATAACAAAA CAAACCTAAT GCGTTCA TATT AGACT AATGAT A
ATCATTTATATTTTACAAGT GATA ||||||| |||| ||||| ||||||
TTTAACAATATTGAACGC CGCAAGT ATAA TTTGA TTACTA C
T CAAT ACATTTTATAT AAAA

GAM1259 TTCGAATCGCCCCTTTTCCA 32311 TCAAACCTTG 32312 CCCC-- C- AACA T AC
AAACATGTGAAGACCTTCTT ACAAAACCTA TTCGAATCG TTTT CAA TG GAAG C
CTCAAACCTTGACAAAACCT TTTG ||||||||| |||| ||| || ||||
ATTTGATTCGAG GAGCTTAGT AAAA GTT AC CTTC /
TTATCC CA CCAA T TT

GAM1260 GCGAAATGTATTCAGATTCG 32321 AATGTATTCA 32322 TCAGATTCGTTT C---- - C
AA TCA
TTTTCAGGTCCGAACGCCAC GATTCGTTTT GCGAAATGTAT TCAGGT CGA ACG CAC
AC A
AAACTCAACAACGTAAGTGT CAGG |||||||||| |||||| ||| ||| ||| ||
CGTCTCGATTACGCCTGATT TGCTTTACATA AGTCCG GCT TGC GTG TG C
ATACATTTCGT TT---------- CATTA C T AA CAA

GAM1261 TCGTCGAGATCGTGATTTGG 32333 TCTGCAATTC 32334 G T T T G ATATAA TG A- ACT
AGAATATAACGTTGGAAGCA CGTGTCGATG TCGTCGA A CG GA TTG AGA CGT G AGC A
CTAACAGTTCCCTGGCGTCT A ||||||| | || || ||| ||| ||| | |||
GCAATTCCGTGTCGATGA AGTAGCT T GC CT AAC TCT GCG C TTG /
G - - T G ------ GT CC ACA

GAM1262 CGCGTTACCAACAATTGTGT 32354 AATTGTGTGA 32355 ACCAACAA ---- C AC
GATCTCGTTACTGAAATCGG TCTCGTTACT CGCGTT TTGTGT GATCT GTT T
ATTTAAAGCGCAAATATCAA GAAA |||||| |||||| ||||| |||
ACGTG GTGCAA AACGCG TTAGG TAA /
ACTATA-- AAAT C AG

GAM1263 TGCATATTTGGACGCTCATC 32368 TCCATGAATC 32369 TTGGACGCTCAT T CTAC
TGA AAT
CATGAATCTACGAAGCTTGA TACGAAGCTT TGCATAT CCA GAAT GAAGCT TTAT C
TTATAATCCCCAGTAGATGG GATT ||||||| ||| |||| |||||| ||||
CTTCCAAATTCCTGGCTAAC ACGTATA GGT CTTA CTTCGG GATG C
TATTACTATATGCA TCATTATCAATC C AAC- TA- ACC

GAM1264 CGTAAATGCAGGGGTTAATC 32376 AGGGAGCGCG 32377 TAATC G G CA CA GGAA---
- AG G TGAA
GGGCGGATGGGGACCAGCGC GAAGGAGTCC GGGCG ATG GGAC GCG GGGAGCGC
GG TCCT CTC A
AGGGAGCGCGGAAGGAGTCC TGCT ||||| ||| |||| ||| |||||||| || |||| |||
TGCTCTGAAAAAAATGAGGG TTCGC TAC CTTG CGC CCCTTGCG CC AGGG
GAG A
GGAACCGTGAGAAAGCGTTC TTC-- - G A- -- AAAGAGTG A- G TAAA
CCCGCAGTTCGCATCGCTTC
TTGCCCCCCG
GAM1265 TGAGAGATTCCTCTGTGTGT 32401 TACCATAAAA 32402 TTCC - TTTTT ---- TT
TCCCATT AT
TTTTTACCATAAAAAGAGTT AGAGTTATTA A TC TGTGTGT ACCATAAAAAGA GTTA AGT
TGAG T
ATTAGTTCCCATTTGAGATT GTTC | || ||||||| |||||||||||| |||| ||| ||||
TACTTATTTTACTCTTAACT T AG ATACATA TGGTGTTTTTCT CAAT TCA ATTC
/
TCTTCTTTTTGTGGTTTACC TC-- T CCATT TCTT TC TTTT--- AT
ATACATATGACTTTTTTCA

GAM1266 GGGAGAGAAATACCGACGGC 32412 TCACGCCAAC 32413 AATACC GCC- ACA
AATTATTA
CGGACAGAGCGAATTATTAA ACGTCCCACC GGGAGAGA GACG GG GAGCG A
GCACCCAACGCTCACGCCAA TCTT |||||||| |||| || |||||
CACGTCCCACCTCTTTCCC CCCTTTCT CTGC CC CTCGC /
CCACC- ACAA GCA AACCCACG

GAM1267 ATGAAGTTAATGATACACAC 32430 TTAATGATAC 32431 T ATA C AC GAATT
TATACTGTCGAATTTGATAG ACACTATACT ATGAAGT AATG CA ACTAT TGTC T
GGACAAAGTAGTTGACACGT GTCG ||||||| |||| || ||||| ||||
TTATTTCGT TGCTTTA TTGC GT TGATG ACAG G
T ACA - AA GGATA

GAM1268 CGCTCCCGCGGCCCCGCCCC 32436 CCGCGGCCCC 32437 CCC- C- A CC C
CGCCGCC ACC
CCACGCCCGCCGCGCGCGCG GCCCCCCACG CGCT GCGGCCC GCCCCCC CG CGC
GCGCGCGCGCA CGG G
CACGCCGCCCGGACCGCCGC CCCG |||| ||||||| ||||||| || ||| |||||||||| |||
CCGCCTTTTTTGCGCGCGCG GTGG CGTCGGG CGGGGGG GC GCG
CGCGCGCGCGT GCC C
CGCGCCCGCGGGGGGCCCGG ACAC CC C CC - TTTTTCC CGC
GCTGCCACAGGTG

GAM1269 GCCCCTCGCCCCCTCCCGCC 32665 CCTCGCCCCC 32666 CCCTC CCCCTCCC CCCTC CCC
CCTCGCCCCCTCCCGCCCCT TCCCGCCCCT GC GC GC GC C
CGCCCCCTCCCGCCCCTCGC CGC || || || ||

CG CG CG CG T
CTCCC CCCTCCCC CTCCC CCC

GAM1270 GCATATGGAACGGTACTGGA 32824 TATGGAACGG 32825 A AC A G---- A T
TGTAGAACACTTGTGTGTCT TACTGGATGT GCAT TGGA GGT CTG ATGTAGA CAC T
ATATGATAACAGAGCTTCCA AGAA |||| |||| ||| ||| ||||||| |||
ATGC CGTA ACCT TCG GAC TATATCT GTG G
- -- A AATAG - T

GAM1271 TTCGGCATTTACTTCTAATA 32835 TCTAATATAA 32836 G- CT-- AA AA - AAA C C
TAAGGACGTTAAATACTCCA GGACGTTAAA TTC GCATTTA TCT TAT GG ACGTT TA
TCCAAATG A
AATGCATTTATTTGGAATAC TACT ||| ||||||| ||| ||| || ||||| || ||||||||
GAGCGTACCGAGTAGCGGAC AAG CGTAGAT AGG ATG CC TGCGA AT AGGTTTAT
T
TTTTAGATGCGAGAA AG TTTC CG AG A GC- A T

GAM1272 TAGAAATATATTTTTGTTCA 32839 TTCAGGTATA 32840 T TT TTC ATC AAATG AAA
T A
GGTATATCAACAAATGTATA TCAACAAATG GAAA ATATT TG AGGTAT AAC TATATGATGG
ATA ATATTT A
TGATGGAAAATATATATTTA TATA |||| ||||| || |||||| ||| |||||||||| ||| ||||||
AAAAAATATTTATACCATCA CTTT TATAA AT TTCGTA TTG ATATACTACC TAT
TATAAA A
TATAATATAGTTAAATGCTT - TT TT- AA- ATATA A-- T A
TTTATTAATATTTTCTA

GAM1273 GTTGGGAAGTGCATGTTAAT 32850 CTCCTGTTAC 32851 - T A T G - CTA
GAGGACACTATCTTTGCTCC TAGCTCTTCG GTTGG GAAG GC TG TAAT AGGA CA T
TGTTACTAGCTCTTCGCCGG CCGG ||||| |||| || || |||| |||| ||
C CGGCC CTTC CG AT ATTG TCCT GT /
G T - C - C TTC

GAM1274 CATATGGTATTTTATCGGTA 32860 TATTTTATCG 32861 - T ATATAAATCT AC- TA
CA A
TATAAATCTAATAAACTATG GTATATAAAT CATATGG TATTTTA CGGT AATAA TATGTG
TTTTTTA GC T
TGTATTTTTTTACAGCATTTG CTAA ||||||| ||||||| |||| ||||| |||||| ||||||| ||
CCATAGGAAAATCATATATA GTATATC ATAAAAT GTTA TTATT ATATAC AAAGGAT
CG T
ATTATTTCTTCCATTGTTAA T T CCTTCT---- AAT TA AC T
AATATCTATATG

GAM1275 TATAAAATCGTAATACTAGT 32865 ATTCTGGTGT 32866 TCG- TAT---- ATA
ATATCATAATGAGATTTTAA TAATATTTTT TATAAAA TAATACTAG ATC A
TTCTGGTGTTAATATTTTTA ATA ||||||| ||||||||| |||

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      TA                              ATATTTT   ATTGTGGTC     TAG  /
                                        TATA      TTAATTT  AGT


GAM1276  AAATGGTAATGGATCACTAA 32875   TAATGGATCA 32876        -      AAAATAT     TA   A
      AATATAATAATTTAAAATAT      CTAAAATATA      AAATGGTAA TGGATCACT     AATAATT  AAAT T
      TCATTTCCAATTATTTTAAA      ATAA          ||||||||| |||||||||     |||||||  ||||
      AGGTGATTCGTTTATTATTT                    TTTATTATT GCTTAGTGG     TTATTAA  TTTA T
                                 T      AAAATT-     CC   C


GAM1277  GCCGCGCCTGACTAGAGTAC 32880   TACTACTAGG 32881    -     ACTA-   A   ACTATAAA
      ACACTATAAATTCCATTCCG      CGCTGGC         GCC GCGCCTG    GAGT CAC      T
      GTGACTTACTACTAGGCGCT                    ||| |||||||    |||| |||
      GGC                             CGG CGCGGAT    TTCA GTG      T
                                    T     CATCA   -  GCCTTACC


GAM1278  CAGTCTTTTGTCCAATAGTG 32886   TCTTTTGTCC 32887         G       GT----------  AA
      TCGAATAAGCGTTCTATTTC      AATAGTGTCG      CAGTCTTTT TCCAATAGT          CG  T
      TAGTAGTGCTATTGGAAAAA      AATA          ||||||||| |||||||||          ||
      GACTG                           GTCAGAAAA AGGTTATCG          GC  A
                                       -       TGATGATCTTTATCTT  GA


GAM1279  AATTCACCACGCCCGGGAGA 32902   TTTTATGGGT 32903    TT   --     G     TCG-     C     C--   AG
      TTTCGAAATTGCTATTTCCG      GTTCGGTGTT      AA  CACC  ACGCCCG GAGATT    AAATTG TATTTC
 GTGC  T
      TGCAGTTCCGCATTCCGAAG      TT            ||  ||||  ||||||| ||||||   ||||||  ||||||   ||||
      TACAATTTAACCGGTTTTAT                    TT  GTGG  TGTGGGT TTTTGG    TTTAAC ATGAAG   TACG  T
      GGGTGTTCGGTGTTTT                      TT   CT     A     CCAA     -     CCT    CC


GAM1280  GCGGTTTTCGGTCTCTCCTC 32915   AAGCTGCAGA 32916      TT--       CCTC----   G   ATGAC   G
      ACTCGGCAGATGACTTCGGA      GTTCGTCTCC      GCGGT    TCGGTCTCT      ACTC GCAG     TTC G
      AGAGAAGCTGCAGAGTTCGT      GGAG          |||||    |||||||||       ||||  ||||     |||
      CTCCGGAGACCGGCCTCGCC                    CGCCG    GGCCAGAGG      TGAG CGTC     GAG A
      GC                              CTCC       CCTCTGCT    A    GAA--   A


GAM1281  GCGCTGGTCCCCATCCGCCC 32958   TCCCCATCCG 32959        CCCC     -  GATTA  CCCT  AT
      GATTAACCCCTGCATTTACG      CCCGATTAAC      GCGCTGGT    ATCCGC CC     AC    GC  T
      CCCCTGTAAGGAGCGGATCG      CCCT          ||||||||    |||||| ||     ||    ||
      CCAGTGC                         CGTGACCG    TAGGCG GG     TG    CG  T
                                      C---      A  AA---  TCCC  CA


GAM1282  TCTTAAAGCGGCCATCGTTC 33012   TGGCATGGTG 33013    T      GC     TT----------  A
      AGTACTTGCTGGCATGGTGA      ACATGAGTGA      TC TAAAGCG  CATCG          CAGT C
      CATGAGTGATGATGCTTTAT      TGAT          || |||||||  |||||          ||||
```

GA AG ATTTCGT GTAGT GTCG T
T A- GAGTACAGTGGTACG T

GAM1283 GCGTGTAATACGCTGGTGTC 33033 TGGTGTCTCA 33034 CTGG CATTATATA T
TCATTATATACTAGCGTTGC TTATATACTA GCGTGTAATACG TGTCT CTAGCGT G
AGCGCTAGGACTACCTAAGA GCGT |||||||||||| ||||| |||||||
CAACCGTATTATACGT TGCATATTATGC ACAGA GATCGCG C
CA-- ATCCATCAG A

GAM1284 ACAGTAGTTTTCACGGTATT 33037 TTAAATCGGG 33038 - CA G- --- A
TTTGAAATTAATAAATTTTA TAAATGGTAA ACAGTA GTTTT CG TATT TTTGAAATT A
AATCGGGTAAATGGTAAAGC AGCA |||||| ||||| || |||| |||||||||
ATGCTGT TGTCGT CGAAA GT ATGG AAATTTTAA T
A TG AA GCT A

GAM1285 GTTATAATCCATAAGCTTTG 33043 AAGCACTAGT 33044 GAAAG- GG----- - AAAAGG
-- TT
AAAGATCTGCTAGTGTGGAT AGGTAACTAA TAAGCTTT ATCTGCTAGTGT AT ACC
CTGTCG TGG C
ACCAAAAGGCTGTCGTGGTT GAGG |||||||| |||||||||||| || ||| |||||| |||
CGCCCAGTCGACGGATGAGG ATTCGGAG TGGATGATCACG TA TGG GGCAGC
ACC /
TCATAAACGAAGCACTAGTA AATCAA AAGCAAA C AGTA-- TG CG
GGTAACTAAGAGGCTTAGGG
ATGAAGCAAC
GAM1286 ATGATGTGTACTTGTGGCTT 33067 TGTGTACTTG 33068 G --- T CTT T TA
AAATTTATTTTACTTAATTA TGGCTTAAAT ATGAT TGT ACT GTGG AAATTTA TT C
AATTTTATCGCAGTTTAATA TTAT ||||| ||| ||| |||| ||||||| ||
AATCAT TACTA ATA TGA CGCT TTTAAAT AA /
A ATT - AT- T TT

GAM1287 TCATCCCGGCGCGCCCGACA 33073 GCGCTCGGCG 33074 C C CATCCC ATCA
TCCCTGCGCGATCAGCTAGC CGCCGAGATG TCATC CGGCGCGCC GA TGCGCG G
GCGCGCTCGGCGCGCCGAGA A ||||| ||||||||| || ||||||
TGA AGTAG GCCGCGCGG CT GCGCGC /
A - C----- GATC

GAM1288 GCGCACAATTGCCTGTAGTA 33115 AGCGTGAATC 33116 CAAT T AGTAG GAATC GA
AG
GCGTGAATCCCGAGAGTCAG CCGAGAGTCA GCGCA TGCC GT CGT CCGA GTC G
GAGGACGTTGGTAGCGAAGA GGAG ||||| |||| || ||| |||| |||
TCGGCATGCGT TGCGT ACGG TA GCG GGTT CAG /
---- C GAA-- AT--- G- GA

GAM1289 TTGTTTGCTCATCTCATATT 33182 TGGAAAACCG 33183 T T CT - CG- C C-
TCATCC- C
TGGAAAACCGGAACGTCAGC GAACGTCAGC TTGTT GC CAT CATATTT GGAAAAC GAA GT
AGC GA C
TCATCCGACCCGTCACTATA TCAT ||||| || ||| ||||||| ||||||| ||| || ||| ||
TGTTCAACTTCAAAGTTTTC GACAG TG GTA GTATAAA TCTTTTG CTT CA TTG CT
C
TGAAATATGCATGGTCGACA C - C- G AAA - AC TATATCA G
G

GAM1290 ACTTGGTTACTAAATACCCT 33192 TTAGTCCATT 33193 T --- ACC T
AATGGAACTGAGTTCTATTA CGATAGTAAT AC TGGTTACTA AAT CTAATGGAAC G
GTCCATTCGATAGTAATCAT CATG || |||||||||| ||| ||||||||||
GT TG ACTAATGAT TTA GATTATCTTG /
T AGC CCT A

GAM1291 TATTATTTTTGTACCGGATT 33195 TGAGATAGGA 33196 A - GG CG- G TTTTCGGG
A
CGCTTGTCTTGTGTTCTTTT CAGGAAAAGT TATT TTTTTGTA CC ATT CTTGTCTTGT TTC
GTCGGG G
CGGGGTCGGGAGAGTTCGAC AAGG |||| |||||||| || ||| |||||||||| ||| ||||||
AGTTTATGAGATAGGACAGG ATAA GAAAATAT GG TGA GGACAGGATA GAG
CAGCTT A
AAAAGTAAGGATATAAAAGA A A AA AAA - TATTTGA- G
AATA

GAM1292 TTCTTCGGATACGCCGTTTT 33229 ACGCCGTTTT 33230 GATA TTTA CGTCGCTT A -
GA
ACTCGCCGTCGCTTGGCAAC ACTCGCCGTC TTCTTCG CGCCGT CTCGC GGCA CGC
CT A
GCCTGAAGAAAGAGCGTGCC GCTT ||||||| |||||| ||||| |||| ||| ||
GCGAGCCTACGGCGCTATGA AAGAAGT GCGGCA GAGCG CCGT GCG GA G
AGAA ATC- TCC- -------- - A AA

GAM1293 CTGATATCATAATGAAGACA 33236 TATCATAATG 33237 T ------ A - C CAC T
TTTTAGAGCACCACATCGTC AAGACATTTT CTGATATCA AATGAA GAC TTTTA GAG AC
ATCGTC A
TATTGACGGTTGTCTCATGA AGAG ||||||||| |||||| ||| ||||| ||| || ||||||
AACGTCGAATTGTTCGTTTG GGCTGTAGT TTGCTT CTG AAAGT CTC TG TGGCAG T
ATGTCGG - GTTAAG C A - T-- T

GAM1294 TTTTTACGTTGGGATGCTCG 33245 TACGTTGGGA 33246 GGGA TCGTCG- T
TCGATGTCTGTGACATAACA TGCTCGTCGA TTTTTTACGTT TGC ATGTC G
ATTGCAGTAAAATGTAGGAG TGTC |||||||||| ||| |||||
GAGGATGTAA ACG TACAG /
AATG TTAACAA T

```
GAM1295  CTCCTGTAGCCCCCAGTAAA 33251   TAAATGGATT 33252      - - CC  C  TA    ATTT  G    A
         TGGATTTCAGGGAGGGACCG       TCAGGGAGGG       CTCCT GT AG  CC AG  AATGG    CAG GAGGG C
         TCCTTGCTGTCATTCTCTTG       ACCG             ||||| || ||  || ||  |||||    ||| |||||
         GACTAACGAGGAG                        GAGGA CA TC  GG TC  TTACT    GTC TTCCT C
                                  G  A  A-  T  TC    ----  G    G


GAM1296  GTGGGTCCATTCTTAATGGT 33260   TATGTCCCAC 33261      -     T-  TAAT  TG A--  C      AAGA
AATTA  CA
         GGAGAGCAGCTTGGAAGAGG       ATCAGGTTCT       GTGG GTCCAT  CT    GG  G   GAG AGCTTGG
GGA    TGC  T
         AAATTATGCCATTTCGCAAT       CAGA             |||| ||||||  ||    ||  |   ||| |||||||    |||     |||
         ATGTCCCACATCAGGTTCTC                    CACC CAGGTA  GG    CC  C   CTC TTGGACT    CCT    ACG
T
         AGACTGCCCCCTGGTCATGG                      T     CT  TCCC  GT AGA  -     ACAC   GTATA   CT
         ACTCCAC

GAM1297  GTAGAACACGTGGGATAGGG 33281   TGGCAAGGCG 33282       CAC      AG--  A  A      ----------
-    TT
         GATGACCTTGTCGACCGTTT       CCCATTGGTT       GTAGAA   GTGGGAT    GGG TG CCTTGTC
 GACCG  T
         GTCGGTCCCCTGCTCCTTAG       CTAC             ||||||   |||||||    ||| || |||||||            |||||
         AGCTGGCAAGGCGCCCATTG                    CATCTT   CATCTTG    CCC GC GGAACGG
CTGGC  /
         GTTCTACATTTCTAC                       TA-      GTTA  - -      TCGAGATTCCTCGTCCC    TG


GAM1298  CGGTACGCCTGCCTGATGGC 33300   TAGGGCTGCT 33301      C   GC   AT    TGA     GG      G
         TTGATAGTAGGGCTGCTGGG       GGGCTGCTAG       CGGTA GCCT  CTG  GGCT   TAGTAG  CTGCTGG
C
         CTGCTAGTAGGGCTGCTGGG       TAGG             ||||| ||||  |||  ||||   ||||||  |||||||
         CTGCTAGTAGGGCTGCTG                      GTCGT CGGG  GAT  TCGG   GTCGTC  GATGATC T
                                  -   AT   CG    ---     GG      G


GAM1299  AGTAGGCCTGCTTGCTCGCT 33326   TGGCTTGCTA 33327      G     T  TC  TG  CT   -    AG
         GGCCTGCTTGCTGAGGGGAC       GTAGGGCTGC       AGTAG CCTGCT GC  GC  GC  GCT TGCTG  G
         AGTAGGGCTGCTGGCTTGCT       T                ||||| |||||| ||  ||  ||  ||| |||||
         AGTAGGGCTGCT                          TCGTC GGATGA CG  CG  CG  CGG ATGAC  G
                                  G     T  TT  GT  T-   G    AG


GAM1300  GGCCTGCTTGCTTGCTCGCT 33417   TCGCTGGCCT 33418    T  TT  TT  TC  T    T  TT  TT  TC  T    T
TT  TT  TC  TG
         GGCCTGCTTGCTTGCTCGCT       GCTTGCTTGC       C GC  GC  GC  GC GGCC GC  GC  GC  GC GGCC
GC  GC  GC  GC  G
         GGCCTGCTTGCTTGCTCGCT       TCGC             | ||  ||  ||  || |||| ||  ||  ||  || |||| ||  ||  ||  ||
         GGCCTGCTTGCTTGCTCGCT                    G CG  CG  CG  CG CCGG CG  CG  CG  CG CCGG CG  CG
CG  CG  C
```

GGCCTGCTTGCTTGCTCGCT T CT TT TT T T CT TT TT T T CT TT TT TC
GGCCTGCTTGCTTGCTCGCT
GGCC
GAM1301 CTAGTAGGGCTGCTGGGCTG 33438 TGCTAGTAGG 33439 -- T- TG -- GCT T T-
G
CTAGTAGGGCTGCTGGGCTG GCTGCTGGGC CTAGTAG GGC GC GGCT GCTAGTAGG GC
GGGC GCTAGTAGG C
CTAGTAGGGCTGCCTGCTGG TGCT ||||||| ||| || |||| ||||||||| || |||| |||||||||
CTTGCTTGCTTGCTTGCTAG GATCATC CCG CG CCGG TGATCGTTC CG TTCG
CGGTCGTCC T
TGGGGCCGCTTGCCTGCTAC GT TT -- GG GTT - TT G
TAG

GAM1302 GGCCACATTATGCCACGGAA 33461 TATGCCACGG 33462 ATTA A AG- A- TA
GTCAATCTTAGAACAGGTGG AAGTCAATCT GGCCAC TGCC CGGA TC ATCT G
GAACGTCCGGGTACGGTGGC TAGA |||||| |||| |||| || ||||
T TCGGTG ATGG GCCT AG TGGA A
GC-- - GCA GG CA

GAM1303 GGCAGCGTCATACCATGTCG 33465 TACTGTTTGG 33466 - CATA TGT T- TT AC
CCTGCTTGTGGCACTGAGCT CGTTTTGGGG GG CAGCGT CCA CGCC GC GTGGC T
ACTGTTTGGCGTTTTGGGGG GCAC || |||||| ||| |||| || |||||
CACGCTGACC CC GTCGCA GGT GCGG TG CATCG /
A CGGG TTT TT T- AG

GAM1304 GTGGAGATCCAGTGCGGGCC 33476 CGGTCAGTCC 33477 G GTGC CT GA A
TTGGACGGTAAAAGCCGGTC TTTGTGGATC GTG AGATCCA GGGC TG CGGT A
AGTCCTTTGTGGATCTGCAC TGCA ||| ||||||| |||| || ||||
CAC TCTAGGT CCTG AC GCCG A
G GTTT -- TG A

GAM1305 AATACCACTGACATACTCGT 33483 CCACTGACAT 33484 C C- C AT- AG- TT
AATCGTCAGTGTATTTCTTT ACTCGTAATC AATAC ACTGA ATACT GTA CGTC TGTA T
ACGACGGACGTAATATCAGT GTCA ||||| ||||| ||||| ||| |||| ||||
ATTTTCGGTTGTATT TTATG TGGCT TATGA TAT GCAG GCAT C
T TT C AAT GCA TT

GAM1306 GTTGTCTAAAACCTACACGT 33488 TGCCACGGGA 33489 T A TACA AAT C AC
GGAATGACGATTCACAAAGA TTTAGCAAT GTTG CTAAA CC CGTGG GA GATTC A
GTCTCTGCCACGGGATTTAG |||| ||||| || ||||| || |||||
CAAT TAAC GATTT GG GCACC CT CTGAG /
- A ---- GT- - AA

GAM1307 TAAATGTTAGGTTTGCTGGA 33528 TTGCATGGTG 33529 TAGGTT A TTTAA T---
AG TAA

GATAAGTTTAAAGGCATTAT TTTACTTTCT TAAATGT TGCTGGAG TAAG AGGCATTATGT
CGA C T
GTTCGAAGCTAATACCTGTC TAAC ||||||| |||||||| |||| |||||||||| ||| |
TTGTCTTGCATGGTGTTTAC GTTTACA ATGATTTC ATTC TTTGTGGTACG GTT G
A
TTTCTTAACTTTAGTAACAT ------ A TTTCA TTCT CT TCC
TTG

GAM1308 AAACTGTTCATATTGTGAGC 33541 TTCATATTGT 33542 - ----- TGTGA - A
CACAGTAGACATTGTTGGCC GAGCCACAGT AAAC TGT TCATAT GCCA CAGT G
TGTATGTGATCATAACATGT AGAC |||| ||| |||||| |||| ||||
TT TTTG ACA AGTGTA CGGT GTTA A
T ATACT TGTC- T C

GAM1309 CATTATGCTGGAACCTGAAG 33547 TGTAAGGTTA 33548 - GG- GAA TT G TGTGT
G
TGTTTTCTAGAGTGTGTTTA TAAGATATAA CATTATG CT AACCT GTG TTCTA AG
TTAAATG G
AATGGGGTATTTGATTTATC TG ||||||| || ||||| ||| ||||| || |||||||
TGTGGAATTATGTAAGGTTA GTAATAT GA TTGGA TAT AAGGT TC AGTTTAT /
TAAGATATAATG A ATA ATG T- G TATTT G

GAM1310 GACAGTGTGAGTGTGGTAGC 33553 TAACTGAGGA 33554 T T A AG A T AA - CC GT
AGTCATCTAGAACTTCGTCC GCTGAGAAGT GACAG GTGAG GTGGT GC TC TC AG CTTC GT
CATT G
CATTGTGCTAAATGTAACTG GACC ||||| ||||| ||||| || || || || |||| || ||||
AGGAGCTGAGAAGTGACCAC CTGTC CATTC CACCA TG AG AG TC GGAG CA GTAA C
CTTACCCTGTC C - G A- - - GA T AT AT

GAM1311 GTCTTTTATGGCTGGTAAGT 33591 TTTCAGCGTG 33592 TTTT AAG CAT GC
GCTGACATCAGGCCCCCTGT GCCAGCCATC GTC ATGGCTGGT TGCTGA CAG C
TTCAGCGTGGCCAGCCATCG GCTG ||| ||||||||| |||||| |||
CTGAC CAG TACCGACCG GCGACT GTC /
TCGC GT- TT- CC

GAM1312 GTGGCACGTCACCATCAAAA 33594 CTTGATATAA 33595 ACGT ----- AAACATT AAC
ACATTGCCCAACAACACGGG AGGTGGCCAT GTGGC CACC ATCAA GCCC A
CTTGATATAAAGGTGGCCAT ||||| |||| ||||| ||||
TACCG GTGG TAGTT CGGG A
---- AAATA ------- CAC

GAM1313 GAATATCGCAGTTATCAAGG 33634 TATCGCAGTT 33635 TATC GTTATC TTA C T
TTAGTTATACCTGTTTATAC ATCAAGGTTA GAA GCA AAGGTTAG TA CTGT T
AGTTAACCCTAATCTTTGCT GTTA ||| ||| |||||||| || ||||
TTTC CTT CGT TTCTAATC AT GACA A

TT-- ------ CCA T T

GAM1314 GATGATGATTTATGAATTGA 33639 TGATGATTTA 33640 TG TT-------- ATT-- G - C
TTCCGGAAGATCGCTATCGT TGAATTGATT GA ATGAT ATGAATTG CCG AAGAT CG T
ATTTTGTGGTTCCACAATTC CCGG || ||||| |||||||| ||| ||||| ||
ATTTCCATACATGTTATTGT CT TATTG TACTTAAC GGT TTTTA GC A
C GT TACATACCTT ACCTT G T T

GAM1315 TTGATTTTGCATGGTTGTAG 33643 TGGAAGCTTG 33644 T A TTT TG TTTAATAATAT
TGGGG G AGTG
CTTTTTTGGTTTTAATAATA GGGGCAGGTC GGT GT GC TT GT ATGTGTGGAAGCT
GCAG TC T
TATGTGTGGAAGCTTGGGGG AGTG ||| || || || || |||||||||||| |||| ||
CAGGTCAGTGTAAGAGGCTG CTA CA CG AG CG TACGTATCTTTGA TGTC GG
/
TAGTTTCTATGCATGCTGGA - A TT- GT ---------- ----- - AGAA
TTGCAACATCAGGCAGGACC
AA
GAM1316 AGCCGCTGAGTGGTAAACAA 33675 CCGCTGAGTG 33676 C ----- CAACA- AG
CAGAACAGATAGTTTATTAT GTAAACAACA AGC GCTGAG TGGTAAA GAAC A
CTTTACCAACACCCTCAGCC GAAC ||| |||||| ||||||| ||||
GCT TCG CGACTC ACCATTT TTTG /
C CCACA CTATTA AT

GAM1317 TATAAATAATCTGATCTTTT 33701 TAAATAATCT 33702 AAT GA TTTTC - AA
TTCATGTTCAAAAAAATGAA GATCTTTTTT TATAAAT CT TCTT ATGTT CA A
ACATATAAGAAAAGTAATTT CATG ||||||| || |||| ||||| ||
ATA ATATTTA GA AGAA TACAA GT A
AT- AA TA--- A AA

GAM1318 TCACGCCTACCAATAAGACA 33708 TAAGACAAGC 33709 CC CCAATA AG C TT T
AGCCCTATATTTACTTGTTG CCTATATTTA TCACG TA AGACA CC TATAT AC T
CATTTTACTCGTCAGAAGAA CTTG ||||| || ||||| || ||||| ||
ATCACAGAGT TGAGA CT GACTG CA TTTTA GT G
CA AAAGAA CT - C- T

GAM1319 GCACATACAATTAACTTTTT 33716 TATAAAAACT 33717 A AA C TTC --- TT
TTCATCACCTTTAAGGTTAA TAGGTATGGT GC CATAC TTAA TTTTT ATC ACC T
GATATAAAAACTTAGGTATG || ||||| |||| ||||| ||| |||
GT TG GTATG GATT AAAAA TAG TGG /
- -- C TA- AAT AA

GAM1320 AAATATATGTCTTAAAATAT 33759 TCAATATTAT 33760 CT----- AA- C T-- - TG
TTT

CAATATTATGATATAAATAT GATATAAATA AAATATATGT TA ATAT AATATTA GATATAA
ATA AAG T
GAAGTTTTTTCGTTTTGTAT TGAA |||||||||| || |||| ||||||| ||||||| ||| |||
ATTATATCTTTTAATATTCA TTTATATACA AT TATA TTATAAT CTATATT TAT TTT T
TATCAGTATCTATAAACATA AATATCT GAC C TTT A GT GCT
TATTT

GAM1321 GCGGCCGGTCATTCGAGTGA 33767 TCTCGTCGGC 33768 G AT G AT A AG
ATTCATTTTCCAGGGCGGAG GGACGGGTCG GCGGCC GTC TCGA TGA TC TTTTCC G
AAGATCTCGTCGGCGGACGG T ||||||| ||| |||| ||| || ||||||
GTCGT TGCTGG CAG GGCT GCT AG AAGAGG /
G GC - CT - CG

GAM1322 ATTAATTTTAATATCTTTTT 33770 TTTCAAATTC 33771 T TTTTC TA---------- AT
CTGATAAATAAATATATAAC AGATTTAAAA ATTAATTTTAA ATCT TGA AATAAATAT A
ATATTTATTAAATATTCTTT TTAA |||||||||| |||| ||| |||||||||
CATTTCAAATTCAGATTTAA TAATTAAAATT TAGA ACT TTATTTATA /
AATTAAT - CTTAA TTACTTTCTTATAAA CA

GAM1323 TCTCGCGATCGAAGGTCGGC 33775 AGGAGTCGGC 33776 G GAAG-- G G G- G
GCGTGGGCCTGCGACGCAGG GGCGACGATG TCTCGC ATC GTCG CGC TGG CCTGC A
AGTCGGCGGCGACGATGGAG GAGA |||||| ||| |||| ||| ||| |||||
ATGGCGAGA AGAGCG TAG CAGC GCG GCT GGACG /
G AGGTAG G - GA C

GAM1324 CTAGGACGGATTCTGTCGCT 33840 TCTGTCGCTT 33841 C TTC-- -- -- TTTT
TCTTCGCCCGTTTTGGTCCT CTTCGCCCGT CTAGGA GGA TG TCGCTTCTTC GCCCG G
GGGCTGGGAGAGGCGAGTCA TTTG |||||| ||| || |||||||||| |||||
AACCTTCCCTCTTGG GGTTCT CCT AC AGCGGAGAGG CGGGT /
C TCCAA TG GT CCTG

GAM1325 GAGGTGTGTGGCTCAACACG 33844 TAATAGGACA 31898 - G- CA- C GTGAC
TAGGGTGACAAGAAAATCTA CAACACCTC GAGGTGT GTG CT ACA GTAGG A
CTGTAATAGGACACAACACC ||||||| ||| || ||| |||||
TC CTCCACA CAC GA TGT CATCT A
A AG TAA - AAAAG

GAM1326 TGTCCACCGGACGAGTGGCG 33845 CCAGCACCAG 33846 ---- AC- - C - AG
CGGCGAAGACGTCGCCAGCA CTTCTGTCGG TGTC CACCGG GAG TGG GC GGCGA A
CCAGCTTCTGTCGGTGTCAT TGTC |||| |||||| ||| ||| || |||||
GACA ACAG GTGGCT TTC ACC CG CCGCT /
TACT GTC G A A GC

GAM1327 GTATTATCGTCCCGTTCCCA 33895 AGGAGTATGC 33896 A C C------ AAG ATG GT T
C

GAAGGAGTATGCGTCGTTGG GTCGTTGGGT GT TTATCGTCC GTT CCAG GAGT C CGT GGGT G
GTCGGAGCCCATGGTGGCAC CGGA || ||||||||| ||| |||| |||| | ||| |||| TCACTGGCATTCTAAACAGG CG AATAGCAGG CAA GGTC CTCA G GTA CCCG G ACGATAAAGC A A ATCTTAC A-- CG- TG - A

GAM1328 GGTCATGTCGGCCGAATCAT 33909 TCTGCCGGCC 33910 C GTC AAT TCT ATC A GCAA---- A
CTATAGCATCATGGATCGCA AAAATACC GGT AT GGCCG CA ATAGC ATGG TC TGAGA T
ATGAGAATTTTTTAGAAAAC ||| || ||||| || ||||| |||| || ||||| AAGACCATTAGCTATCTGCC CCA TA CCGGC GT TATCG TACC AG ATTTT / GGCCAAAATACC - AAA C-- C-- AT- - AACAAAAG T

GAM1329 TCTCTAATTTTTGCCGGGTT 33928 TGCCGGGTTA 33929 TT---------- GG A GACAC- T TAAAAATA
AAAACATAGACACAAAAGAC AAACATAGAC TGCC GTTAAA CATA AAAAGACAG ATAA G
AGTATAATAAAAATAGAACA ACAA |||| |||||| |||| ||||||||| |||| CCATTTTATTTTGTCTTTTT ATGG CAATTT GTGT TTTTCTGTT TATT A TCCAATGTGTTTAACAAGGT CTATCCCGCTTCT AA - AACCTT T TTACCACA ATCTTCGCCCTATCAGTTTG AGA
GAM1330 TATTAGCTATGCTCACTAAA 33940 ACTTCATTAA 33941 T T - T TC AT CT ATTT TT
CTTCATTAATCAAGCTTAAT TCAAGCTTAA TAT AGC ATGCT CAC AAACT ATTA CAAG TA TTTTAT G
TTTTTTATTTGTTATAAAAT TTTT ||| ||| ||||| ||| ||||| |||| |||| || |||||| ATATACTTGTAGTAGTTTGT GTG TTG TATGA GTG TTTGA TGAT GTTC AT AAAATA / GCAGTATGTTTGTG T - C - -- -- AT AT-- TT

GAM1331 AGTTTACTATTTAGCTACAA 33945 CAAGTTTCTT 33946 CTAT- TT
GTTTCTTAAAAACAATATTT AAAAACAATA AGTTTA TTAGCTACAAGTTTCTTAAAAACAATAT T
TGTATATTGTTTTTAAGAAA TTTT |||||| ||||||||||||||||||||||||||
CTTGTAGCTAGTTTTTTGAA TCAAGT GATCGATGTTCAAAGAATTTTTGTTATA / CT TTTTT TG

GAM1332 CTTTATTACTTAAATTTTGT 33952 GAGCATTGCT 33953 TT T TT AAT TACAAA TA
TTAAATAGCTACAAATTTAT TTATAAACAA CTTTA ACT AAA TTGTTTA AGC TTTAT A
TAAGCATAGAGCATTGCTTT TTTT ||||| ||| ||| ||||||| ||| |||||
ATAAACAATTTTTAGTTTTA GAGAT TGA TTT AACAAAT TCG AGATA / GAG TT - TT ATT TTACG- CG

GAM1333 AACAAAGAAATGGAAATCGT 33958 TATGTTCAAC 33959 AG T---------- A
AATACCAGTTATGTTCAACT TTTGAAATTG AACAA AAATGGAAA CGTAAT C

TTGAAATTGTTTTTTATTTT TTTT ||||| |||||||||| |||||| CTTGTT TTGTT TTTATTTTT GTATTG C CT TGTTAAAGTTTCAACTT A

GAM1334 AGTTGTCGCAACAGGGTAGC 33964 TATATTGTAC 33965 CAAC AGC-- GTAAACTT C AGAC GT
TCGTAAACTTTAATGTATAA CAAAGATTTA AGTTGTCG AGGGT TC TAATGTATAA AG ATCT A
CAGAGACATCTGTAAAAAGA AATC |||||||| ||||| || |||||||||| || |||| TAAACTTTATATATTGTACC TCGATAGT TCCTA AG GTTATATATT TC TAGA A AAAGATTTAAATCCTAATTT TTAA AATTT AAACCAT- - AAA- AA GATAGCT

GAM1335 TGCAACCCCCTGATTTTGCA 33969 CCCCTGATTT 33970 C TG CA A- GA GAAG
GTTCACCCAGAAGGGAAGAC TGCAGTTCAC TGCAA CCCC ATTTTG GTTC CCCA AGG A
AAGCCTCTTGGGACGGACCT CCAG ||||| |||| |||||| |||| |||| ||| AAGATATGGGGATTGCG GCGTT GGGG TAGAAT CAGG GGGT TCC / A TA C- CA TC GAAC

GAM1336 CGTGTGTATATTATTTTTTT 34001 TGTATATTAT 34002 TG-------- G GCG - ---------- G T GT
TTTTTGTGTGTGTTTGCGCC TTTTTTTTTT TTTTTTT TGT TGTTT CC CC CGTGT TC AAT G
CCCGTGTGTCTAATGTGCTG TGTG ||||||| ||| ||||| || || ||||| || ||| TTTGAAACACGTAAAGTAGC AAAAAAA ATA ACAAG GG GG GCACA AG TTG /
TGGTGGAAGAACAGATAAAC TAATTTCCAA G AA- T TCGATGAAAT A T TC CTTTAATAAAAAAAAAAGTA TGTGCTCCCG

GAM1337 GTCCAGGCTAAACGACCGCC 34006 TCTAGAACAA 34007 A TAAA---------- G TTTCTA CAAAA GA AG
TTTTCTAGAACAAAAAGGAG AAAGGAGGAA GTCC GGC CGACC CCT GAA AG GGA A
GAAGAACATCCAACTGATTT GAAC |||| ||| ||||| ||| ||| || ||| TCATCTGGGGGGTCGGCATC CAGG CCG GCTGG GGG CTT TC CCT A TATAGTAAAAATGCCAGGAC A TAAAAATGATATCTACG G TCTA-- TTAG- AA AC

GAM1338 GTTGATGCACATGGTAGACT 34163 TTGCGCACGC 34164 CA CT CTG--- C AACA TG C
GTGTGTCTGTGTCATTCAAC TTTTTACCGT GTTGATG CATGGTAGA GTGTGT TGT ATTC G CTTTG G
AGTGCTTTGCGACGAAGTGT GGAC ||||||| ||||||||| |||||| ||| |||| | ||||| GGGAATAATAAATTGCGCAC TAGCTGC GTGCCATTT CGCACG ATA TAAG T GAAGC /
GCTTTTTACCGTGGACGTCG AG TT CGTTAA A GG-- GT A AT

GAM1339 GGCATTACCTCTGTACTCAA 34166 TTTGATGTTT 34167 - -- C TGTA- A GTCAGT
CGTGTCAGTTTCTATAAACG AATCGCC GGC ATT AC TC CTCA CGT T
ATGAGGATTTGATGTTTAAT ||| ||| || || |||| |||
CGCC CCG TAA TG AG GAGT GCA T
C TT T TTTAG A AATATC

GAM1340 TAATTTGTTACTAATTTCTT 34171 TTTGTTACTA 34172 T -- ATCC TTAGA GT
TATCCACATATTCGTTAGAA ATTTCTTTAT TAAT TGTTAC TAATTTCTTT ACATATTCG ATT
C
TTGTCATGAGTGAATTCGAA CCAC |||| |||||| |||||||||| ||||||||| |||
TGTGTAAGGAGGTTGCTGTA ATTG ACAATG GTTGGAGGAA TGTGTAAGC TGA A
ACACGTTA C TC ---- TTAAG GT

GAM1341 AAGTGATCACAGCCTGAGAA 34183 AGGAGGCCAC 34184 - C-- GAAA A AAGG---
G CCC
AGGAGGCCACAGCGAAGGCC AGCGAAGGCC AAGTGATCA CAGC TGA GGAGGCC CAGCG
CCGC TGC G
GCGTGCCCCGAGCTGCAAGT GCGT ||||||||| |||| ||| ||||||| ||||| |||| |||
GGAGAAGGATGCTGGGCCTT TTTATTGGT GTTG ATT CTTCCGG GTCGT GGTG
ACG A
CAGGATTAAATGTTGTTGGT T TAA AGGA - AGGAAGA A TCG
TATTT

GAM1342 GTCTTGTTTGTAACATGGAT 34224 TTAATATATT 34225 TTGTT C ATA T- CT A TT
TT- C
ATCATTAACTAGATTGTATA ATAATAGTTT GTC TGTAA ATGG TCA TAA AGATTGT TAT
TATATT ATAT T
TTTTATATTTTATATCTTCA TCTT ||| ||||| |||| ||| ||| ||||||| ||| |||||| ||||
TATCTTAATATATTATAATA CAG ATATT TATC AGT GTT TTTGATA ATA ATATAA
TATA T
GTTTTCTTGTTTGAGCCTAT TTACT - CG- TT CT - TT TTC C
TTATATCATTGAC

GAM1343 GTGGTAGCGGCACAGAATCT 34230 CTACTGTCCC 34231 ---- C C AATCTTTCC T
TTCCAGGGCTTTAAAGTCCT ACTATATACC GTGGT AG GG ACAG AGGGCT T
ACTGTCCCACTATATACCAC AC ||||| || || |||| ||||||
CACCA TC CC TGTC TCCTGA A
TATA A C A-------- A

GAM1344 TGTTAAAAGAGGAATGAGTT 34272 TGAGTTCTAG 34273 AAA-- G G G - T- A
CTAGCAAGCTCTAAATAAAT CAAGCTCTAA TGTT AGA GAAT AGTTCTA CAAG CTC AAAT A
ATTTCTGAGACTTGGTGGAA ATAA |||| ||| |||| ||||||| |||| ||| ||||
CTGGTTTGTCTATGTGAACA ACAA TCT TTTG TCAAGGT GTTC GAG TTTA A
GTGTA G G G A TC T

GAM1345 TAATATCTAGTTAAATTTAT 34284 TTTATAATAA 34285 - --------- T A AG T

AATAATGTTTTAGATGGTTA TGTTTTAGAT TAATATCTA GTTAA ATTTA AATA TGTTTT
ATGGT A
CGACCATACAAAATAGTATT GGTT |||||||||| ||||| ||||| |||| |||||| |||||
TAAATCGTATTCGCTTAACT ATTATAGGT CAATT TAAAT TTAT ATAAAA TACCA C
TGGATATTA T CGCTTATGC - G CA G

GAM1346 TCCAGGAGGACAGCGCCTCA 34290 TGTCCAGGAC 34291 - A C-- AGC GA C AAAG
CC
GCGAGGACCTGCGCAGAAAG TCATCGGGGT TCCAGG AGG CAG GCCTC GAG CCTG GCAG
ATG C
ATGCCCTCCATAGTTGTCCA TCAT |||||| ||| ||| ||||| ||| |||| |||| |||
GGACTCATCGGGGTTCATTG AGGTCC TCC GTT TGGGG CTC GGAC TGTT TAC /
CCTGCCTGGA G - ACT CTA A- C GA-- CT

GAM1347 TATAGCTTATTATCTGTTTG 34317 TAGCTTATTA 34318 T- GCTA ATCAAATATAC A
TA-- AGATTA
TGCTAATATAATATCAAATA TCTGTTTGTG TGT TGT ATATAAT TCTTGTT TCGT
GTTGGG A
TACTCTTGTTATCGTTAGTT CTAA ||| ||| ||||||| ||||||| |||| ||||||
GGGAGATTAATATTACATCC ACG GCA TATATTA AGAATAG AGCA TAACCT
T
AATATATACGAGATAAGACA TT AC-- C---------- - TATA ACATTA
TTATATCAACGTTGCACGCT
ATAAGCATTA
GAM1348 CGCTTATGTGTACAGTTTCC 34332 TGTACAGTTT 34333 TT--- T -- TTCCT- AC
TTAGTACCCTGCTATATAAT CCTTAGTACC CGC ATG GTACA GT TAGT C
GCCATGTACTCATTTTACGC CTGC ||| ||| ||||| || ||||
G GCG TAC CATGT CG ATCG /
CATTT T AC TAATAT TC

GAM1349 GAATAGCGCCACATATGATA 34359 TAATAACACT 34360 CACAT ATAATATATTGTA TCT -
C TAG TATCTT
TATAATATATTGTAGATATC TACGTTTTTA ATGATAT GATA GACG AA TGTT ATAAT
C
TGACGAACTGTTTAGATAAT TCGA ||||||| |||| |||| || |||| |||||
TATCTTCTTCTTTTATTATA TACTGTA CTAT TTGC TT ACAA TATTA T
ATAACACTTACGTTTTTATC ACT-- CAAATTCCTTAAG TT- A C TAA TTTTCT
GAATTCCTTAAACATGTCAT
TCAATGCTTC
GAM1350 GTTATGATAAATGATTCTGA 34365 TAAATGATTC 34366 A- TC- CATCT C TTAT
TGACATCTCGCTAGTTATAA TGATGACATC GTTATGAT AATGAT TGATGA CG TAG A
AATCTATCGTATCATTAAAC TCGC |||||||| |||||| |||||| || |||
ATCGTTGCATCATAAT TAATACTA TTGCTA ATTACT GC ATC /
CG CAA AT--- T TAAA

GAM1351 ATTCTCACCCCAGGACTAAA 34369 TCTCACCCCA 34370 - GACTAAA AG C TCT

AGAGAGGCTGTCTCACTTAC GGACTAAAAG ATTCTCA CCCCAG AG AGG TG C
CCTAGCTGTTTTACTGGGGT AGAG ||||||| |||||| || ||| ||
TGGGAAT TAAGGGT GGGGTC TC TCC AT /
T ATTTTG- GA C TCA

GAM1352 GTAGTTTCCATGGGACTATA 34413 TTACTACATA 34414 CCA C T T CCTC A
TAATTTTGTGGCCTCGAATA GTTATCTATC GTAGTTT TGGGA TA ATAATT TGTGG GAAT C
CAAATTTTACTACATAGTTA TTAA ||||||| ||||| || |||||| ||||| ||||
TCTATCTTAAAGACTAT TATCAGA ATTCT AT TATTGA ACATC TTTA A
A-- - C T AT-- A

GAM1353 CACCGCCATGCTTCCCCTCT 34423 ACAACGGGTT 34424 GCCAT T CTCT ACTC- CTCCT
CCCACTCTTGAAACTCCTTT GGGCAGCCCA CACC GCT CCC CCC TTGAAA T
CTCTTTTCAAACAACGGGTT AAGG |||| ||| ||| ||| ||||||
GGGCAGCCCAAAGGTG GTGG CGA GGG GGG AACTTT /
AAACC C TT-- CAACA TCTCT

GAM1354 GTCGAGTAAGGAATCAGTCT 34493 AGTAAGGAAT 34494 AGT ATC T TGT GT A
GTTCTGGTCTATCTGGGTCA CAGTCTGTTC GTCG AAGGA AG C TCTG CT T
GAGTCTTGTCCTTCCACGGC TGGT |||| ||||| || | |||| ||
CGGC TTCCT TC G AGAC GG C
ACC GT- T --- TG T

GAM1355 GTGGGAGGCGTACCTGTTGT 34509 TGTTGTTAAG 34510 TACC - AA ---- GG GA
TAAGTACGAGGGAGGAGCTA TACGAGGGAG GTGGGAGGCG TGT TGTT GTACG AG AG
G
CTTTCTAGAGTGTGCAGACA GAGC |||||||||| ||| |||| ||||| || ||
CACGTCATCGTCTTCCAC CACCTTCTGC GCA ACAG CGTGT TC TC C
TACT C A- GAGA TT AT

GAM1356 AGTGCGTTTGATAAAAGTTT 34522 TGCGATGTTC 34523 TTGATAAA TG A TTC T- TTT-
TCTTTT
GGCAATGCTTCGCATGGTTT AGCTGCACGT AGTGCGT AGTT GCA TGC GCA GG GGT
C
GGTTCTTTTCCCTGTCTGCC ACT ||||||| |||| ||| ||| ||| || |||
TTTTCCTTTGCTGCGATGTT TCATGCA TCGA TGT GCG CGT CC CCG C
CAGCTGCACGTACT CG------ CT A T-- TT TTTT TCTGTC

GAM1357 GCCTTGATGGTTTTGGACTG 34530 TGGTTTTGGA 34531 C ----- ACT---- C
GTGACAAATCACCTGCGCGG CTGGTGACAA GC TTGATG GTTTTGG GGTGA A
CCAGAACAATCTCATCAAAG ATCA || |||||| ||||||| |||||
C CG AACTAC CAAGACC CCACT A
A TCTAA GGCGCGT A

GAM1358 GTTATGTTTCTTAACTTCTT 34546 TTTCACACAC 34547 TTTCTTAACTTCTTC -- TCTT-- GG
- GTACC AAT
CAGGTAGAACGTCTTTGGGA TCGTCCTCTA TATG AGGTAGA ACG TG AC ATCC
GT A
CATCCGTACCGTAATACAAA CCTC |||| ||||||| ||| || || |||| ||
CCCGAAGGATCGTTTCACAC ATGC TCCATCT TGC AC TG TAGG CA /
ACTCGTCCTCTACCTCCCGT CC---------- CC TCACAC TT C AAGCC AAC
AAC

GAM1359 ATACCCGTGCATTTTACCCT 34563 ACCCGTGCAT 34564 TA TTTAC GTTAAT- TGAAG
CGTTAATCATCTGAAGTTGT TTTACCCTCG A CCCGTGCAT CCTC CATC T
GCGGTGTTCCATAGAGGATC TTAA | ||||||||| |||| ||||
GTGTGTACGGGCGT T GGGCATGTG GGAG GTGG /
GC TGCTA ATACCTT CGTGT

GAM1360 GGCCTCGGCGAAGGGGCGTT 34572 TGCCCTTGAG 34573 - GA ---------- A
CCAGCATGACGGCATGCTGG CGTGGGGCC GGCCTCG GC AGGGGCGT TCCAGCATG
C
ACGAGGCGCGCGATGCCCTT ||||||| || |||||||| |||||||||
GAGCGTGGGGCC CCGGGGT CG TTCCCGTA AGGTCGTAC G
G AG GCGCGCGGAGC G

GAM1361 TCCGGCGCGCCAACGCGAAG 34749 CACCGCGCTT 34750 C - C TA C
CGCGGCGTCTAGCCCCGGGC GCGCTTGGCG TCCGGCGCGCCAA GCG AAGCGCGG GTC
GCC C
CCGGCACCGCGCTTGCGCTT CGCC |||||||||||| ||| |||||||| ||| |||
GGCGCGCCGGG GGGCCGCGCGGTT CGC TTCGCGCC CGG CGG /
- G A CC G

GAM1362 TCTATTTTTAAACTATTTTT 34779 TGTGAAAAAT 34780 TTT TCTTATTT TA CACCT--
AAATCG T TA
AATTTTCTTATTTAATATAT CGAAATCGTT TATT AATTT AATATAT GC GTGAA AAA
CGT A
TAGCCACCTGTGAAAAATCG AAGA |||| ||||| ||||||| || ||||| ||| |||
AAATCGTTAAGACACGCTTT ATAA TTAAA TTATATG TG TACTT TTT GCA G
AATCGGTTCATTAAATACGT T-- TTCT---- TA CATAAAT GGCTAA C CA
ATGTATATTTCTTAAATTTA
ATAGTTATAGG
GAM1363 AGTTCGTATATTTTTATATA 34784 TTTGTAAAAA 34785 ---------- A T ACA
TAACAATGATATTTGTAAAA AATAAACTTA AGTTCG TAT TTTTTATA ATA A
AAATAAACTTAACATATTGA ACAT |||||| ||| |||||||| |||
ACT TCAAGT ATA AAAAATGT TAT /
TATACAATTCAA A T AGT

GAM1364 ATGAAAATCTTGCTAATGGG 34792 TTCCTCTATC 34793 TCTT ---------- A

AATATAATTATATTTCCTCT GTATAAATAA ATGAAAA GCTAAT GGGAATAT A
ATCGTATAAATAATTAGCTC TTAG ||||||| |||||| ||||||||
TTTTTTCAT TACTTTT CGATTA CCTTTATA T
TTCT ATAAATATGCTATCT T

GAM1365 GTCCTTCGCGGACGCCTCGG 34799 GTGGAGGTGG 34800 C GA G GC- G
CCGCCTGCGGGTACCAGGGG TCATGAGGGA GTCCTTCG G CGCCTC GCCGCCT GG T
GTGGTGGAGGTGGTCATGAG C |||||||| | |||||| ||||||| ||
GGAC CAGGGAGT C GTGGAG TGGTGGG CC /
A TG G GGA A

GAM1366 ATAAAAATATTTTTGTAAAA 34989 GAAGAGAGAA 34990 AAAA--- A GA
CTTTTTTATGAGACCATCGA AGAGAATAAA ATAAAAATATTTTTGT CTTTTTT TGA C
AGAGAGAAAGAGAATAAAAA AATA |||||||||||||||| ||||||| |||
TATTTTTGT TGTTTTTATAAAAATA GAGAGAA GCT /
AGAGAAA - AC

GAM1367 ATTGCCCATGCACAAACGAT 35098 TAAGTTTTTT 35099 C--- CAA GA TCTC---- CC
AAGTTTTTTCTCATCTCCCT CTCATCTCCC ATTGCC ATGCA AC TAAGTTTTT ATCT C
TAAGATTATTATATAAAAAT TTAA |||||| ||||| || ||||||||| ||||
TTAGGTATTGTATACTCGGC TGACGG TATGT TG ATTTAAAAA TAGA T
AGT CTCA TA- G- TATATTAT AT

GAM1368 CTGCACCCCGGGCTCGTGTA 35117 CACCGGGCCG 35118 C----- GC- CCG - C AAC
CCGCCTGCTGAACCCCACCG ACCTGCAG CTGCA CCCGG TCGTGTA CC TG TG C
CCACGGACCTACGCGAACAC ||||| ||||| ||||||| || || ||
CGGGCCGACCTGCAG GACGT GGGCC AGCGCAT GG AC GC C
CCAGCC ACA CCA C C CAC

GAM1369 GAGAAAGAGAATAAAAATAT 35174 AATATTTTTG 7334 AGA- AAAA--- - A
TTTTGTAAAACTTTTTTTAT TAAAACTTTT GAGAAAG ATAAAAATATTTTTGT CTTTTTTTA
TG G
GAGACCATTGAAGAGAGAAA TTTA ||||||| |||||||||||||| ||||||||| ||
GAGAATAAAAATATTTTTGT TTTTTTC TGTTTTTATAAAAATA GAGAGAAGT AC A
AAAACTTTTTT AAAA AGAGAAA T C

GAM1370 GAGAATAAAAATATTTTTGT 35175 AATATTTTTG 7334 - AAAA--- - A
AAAACTTTTTTTATGAGACC TAAAACTTTT GAG AATAAAAATATTTTTGT CTTTTTTTA TG G
ATTGAAGAGAGAAAGAGAAT TTTA ||| |||||||||||||| ||||||||| ||
AAAAATATTTTTGTTACTC CTC TTGTTTTTATAAAAATA GAGAGAAGT AC A
A AGAGAAA T C

GAM1371 GAGAATAAAATATTTTACGA 35176 TGAGACCATT 35177 AA- CGA CA-- AGAAA - A
T

CTCCATCAGAAAGAGGTTTA GAAGAGAGAA GAG TAAAATATTTTA CTC TC GA GGTTT
ATA T
ATATTTTTGTGAGACCATTG AGAG ||| |||||||||||| ||| || || ||||| |||
AAGAGAGAAAGAGAATAAAA CTC ATTTTATAAAAT GAG AG TT CCAGA TGT T
TATTTTACGACTC AGC AA- AAAG AGAAG A G T

GAM1372 TTTTTCTTAGTACAAAAGTC 35304 TGTGAAATTT 35305 A- G- AT--- AAAA G
AATGTTTTAAAATATATGGA TGTACCAAAG TTTTTCTT GTACAAAA TCA GTTTT
TATATGGACAA A
CAAGAATTTGTCTGTATAAA AAAA |||||||| |||||||| ||| ||||| ||||||||||
AACTTGTGTGAAATTTTGTA AAAAAGAA CATGTTTT AGT CAAAA ATATGTCTGTT A
CCAAAGAAAAA AC AA GTGTT ---- T

GAM1373 GTGGGGCGACCTGCTCTTCT 35335 CGACGAGCGA 35336 G C T T TCT -- C - A
CGCCGCCCGTCGCGACGACG CGCGCCCGGC GT GGG GACC GC CT CGC CGC CGTCG CG
C
ACGACGAGCGACGCGCCCGG GCGG || ||| |||| || || ||| ||| ||||| ||
CGCGGTCCCCGAC CA CCC CTGG CG GG GCG GCG GCAGC GC G
G - - C CCC CA A A A

GAM1374 GAAAGAGAATAAAAATATTT 35405 TAAAAATATT 35406 AA AA- TGTAAAA-- - A
TTGTAAAACTTTTTTTATGA TTTGTAAAAC GA GAG TAAAAATATTTT CTTTTTTTA TG G
GACCATTGAAGAGAGAAAGA TTTT || ||| |||||||||||| |||||||| ||
GAATAAAATATTTTTACGAC CT CTC ATTTTTATAAAA GAGAGAAGT AC A
TCCATC AC AGC TAAGAGAAA T C

GAM1375 GCGGGCTGCACGACCGGCTC 35410 GAGCAGATGC 35411 - C AC A T AG G C C
GAGCTGCTGCACGGCAACCT GCCGGCGCAC GC GGG TGC G CCGGC CG CTGCT CA GG A
GGAGCAGATGCGCCGGCGCA CCAG || ||| ||| | ||||| || ||||| || ||
CCCAGC CG CCC ACG C GGCCG GT GACGA GT CC /
A - -- - C A- G - A

GAM1376 GAGTGTCTGGCCGAGGCCAA 35452 CGCCCGGGCC 35453 G AGGCCAA AG C----
TC TGAC C
GAAGTTCGTGCACGCGTCGG CGACGCCGAT GTGTCTG CCG GA TTCGTGCA
GCGTCGG GCCC GCGGC G
TCGCCCTGACGCGGCCGGAG CTGC ||||||| ||| || |||||||| ||||||| |||| |||||
CCGCCCGGGCCCGACGCCGA CGCAGAC GGC CT AAGCGCGT CGCAGCC CGGG
CGCCG G
TCTGCGCGAAATCCGGCAGA - ------- A- CTAGC -- CC-- A
CGCTC

GAM1377 CTATACGTATCGTATAGATA 35486 TCGTATAGAT 35487 A T A - G GTA
GGGTCGAGTATCCCGTCGAT AGGGTCGAGT CT TACGTA CGT TAGAT AG GTCGA T
GTTCGTCTAACGTACGTAAA ATCC || |||||| ||| ||||| || |||||

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      G                                GA ATGCAT GCA ATCTG TT TAGCT   C
                                       A    - -   C G    GCC


GAM1378  CATTCGTCCTCCACGTCTCG 35491   TTACGTGTCT 35492     -   CTC-    CT   AGCCCCT
      TAGCCCCTCTAACAAAAACG       TGACGTAGTG       CATT CGTC   CACGT  CGT     C
      TTACGTGTCTTGACGTAGTG                  |||| ||||   |||||  |||
                                 GTGA GCAG   GTGCA  GCA     T
                                   T   TTCT    TT   AAAACAA


GAM1379  AAGGACCGACGCCGCGCGGA 35498   CAGCCCTCCC 35499      CC    -  C    ATC---   AC--
CCGTT
      TCGGCACCGCGGCGCCGTTT       ACCGCCGCGC       AAGGA  GACGC CG GCGG     GGC
CGCGGCG    T
      ATATTCGCCGCGAACAGCCC       GTTT           |||||  ||||| || ||||     |||   |||||||
      TCCCACCGCCGCGCGTTTCC                    TTCCT  TTGCG GC CGCC     CCG    GCGCCGC    /
      TT                              --    C  -   ACCCTC   ACAA      TTATA


GAM1380  GTATTAGGAAGAGATAATAT 35517   TGGCAAATTT 35518      A   GAGATAATATGAGA    GGGA
GA
      GAGAGAATTGGGAATAGGAT       AGAAGAAAAG       GTATT GGAA          GAATT    ATAG  T
      TAATTATGGCAAATTTAGAA       AAAA           ||||| ||||          |||||   ||||
      GAAAAGAAAATTCCCAGTAC                    CATGA CCTT          TTTAA    TATT  T
                                 C    AAAAGAAAAGAAGA    ACGG    AA


GAM1381  TCGTCGCGGGAGACCGCGGA 35607   TCGCGGGAGA 35608         G   C     AAA   --   -  G
      AAACGACGGATGTGGCCACA       CCGCGGAAAA       TCGTCGCGG AGA CGCGGA   CGAC  GGAT GT G
      ATCCACGTCGATATTCGCGA       CGAC           |||||||||| ||| ||||||   ||||  |||| ||
      TCTGCCGCGACGA                        AGCAGCGCC TCT GCGCTT   GCTG  CCTA CA C
                                   G   A     ATA    CA    A  C


GAM1382  GCTTCCGGGTACGTAGTAGG 35616   TAGCTTACCT 35617         TACGT      GCT    ---      T    G
      TAGCTTACCTAGTACGGTAT       AGTACGGTAT       GCTTCCGGG    AGTAGGTA   TACCT   AGTACGG
ATGCTG G
      GCTGGGGTAGCATTCCGTAC       GCTG           |||||||||    ||||||||   |||||   ||||||| ||||||
      TTCCGGGTATACCTACTTCC                    CGAAGGCCC    TCATCCAT   ATGGG   TCATGCC TACGAT /
      CGGAAGC                              T----       ---    CCT      T     G


GAM1383  TATAGTTCAACAATGTGATG 35624   AGGCAGTAAT 35625        CAA----    TGA    G
AAGAAAATAAAA    AG  C
      TGTGTCAAGAAAATAAAATG       AAAAGGGGCA       TATAGTT     CAATG   TGTGT TC         TGCCT
TA A
      CCTAGTACATTAAGAGGCAG       TAGA           |||||||      |||||  ||||| ||         |||||  ||
      TAATAAAAGGGGCATAGACC                    ATATCAG      GTTAC   ATACG GG         ACGGA  AT /
      ATTGGCAAGTAGACTATA                       ATGAACG    CAG    G  AAAATAATG---    GA  T
```

GAM1384 GAAACATGTAACAATATTAG 35672 ATGAGCCATA 35673 A ACAA AGA - AGATG
TTTACA
ATATAGGAGATGCATATTTT TAGACAATAT GAA CATGTA TATT TATA GG CATAT A
ACAATACCATTATATGAGCC ACAT ||| |||||| |||| |||| || |||||
ATATAGACAATATACATGCT TTT GTACAT ATAA ATAT CC GTATA T
TT C ---- CAG A GA--- TTACCA

GAM1385 GAAAACCGGACCCGGAAGAT 35679 TCGCCGGGCT 35680 CCG AGA A C TA A AGT
CGATACGTACGGACGAAAAG AACGGGGATC GAAAACCGGAC GA TCG TA G CGG CGAAA
G
TGCCCTTTCGCCGGGCTAAC ACCG |||||||||||| || ||| || | ||| |||||
GGGGATCACCGTCCGGTTTT CTTTTGGCCTG CT GGC AT C GCC GCTTT /
C CCA AGG A - GG - CCC

GAM1386 TAATGTATCAAAAATATCAA 35693 TGTATCAAAA 35694 AAA TC CC GT
TATCCAATGTCCAATTAATG ATATCAATAT TAATGTATCA ATA AATAT AAT C
TTTTTATATCTGATATGTTA CCAA |||||||||| ||| ||||| |||
ATTGTATAGT TAT TTGTA TTA /
CTA TT A- AC

GAM1387 AAGAAGTTAATATAGATAGT 35706 AGTAAAGATA 35707 T GATA- A- TT TTAT
-- A
AAAGATATTTTTTTAGATTA TTTTTTTAGA AGAAGT AATATA GTAAAG TATTT TTAGA
AGATTTTTTAT AC C
TAGATTTTTTATACACATGT TTAT |||||| |||||| |||||| ||||| ||||| |||||||||| ||
TAATAGAAGATCTTCTAACA TTTTTA TTATAT TATTTT ATAAA AATCT
TCTAGAAGATA TG A
AATAGGTTTTATGAAAATAT - AAAAG GG C- ---- AT T
ATTATTTTTT

GAM1388 AGGATGGAAGTTGAGTCCCT 35712 TTAAGGGATT 35713 GAA- --- C A AATTTA
CAGTGTATCAATTTACAATG GGATAGCGAA AGGATG GTTG AGTCCCT AGTGT TC C
CAAGAAATATTAAGGGATTG ACAT |||||| |||| ||||||| ||||| ||
GATAGCGAAACATCCT TCCTAC CGAT TTAGGGA TTATA AG A
AAAG AGG A A AACGTA

GAM1389 ATGTTTTTATATCTAATGTC 35721 TCTAATGTCC 35722 TTTT C GTCCA - TTTT C GT
CAATTAATGTTTTTATATCT AATTAATGTT ATGT ATAT TAAT ATTA ATGT ATAT TAAT C
AATGTCCAATTAATGTTTTT TTTA |||| |||| |||| |||| |||| |||| ||||
ATATCTAATGTCCAATTAAT TATA TGTA ATTA TAAT TATA TGTA ATTA /
GTTTTTATAT TTTT - ACCTG C TTTT - AC

GAM1390 GTAAAAAAGGTTTCTATTTC 35744 TTAGCATGTT 35745 A TTT T A- TA- C GAT

TATAGTAATGTTAACAAGTG CTAGAAGACA GTAAA AAGG CTAT TCT TAG ATGTTAA AAGT
A
ATAACAAATTTTTAGCATGT TAGT ||||| |||| |||| ||| ||| |||||||| ||||
TCTAGAAGACATAGTTTTTT CATTT TTTT GATA AGA ATC TACGATT TTTA A
ATTTAC A TT- C AG TTG - AAC

GAM1391 TAATGTATCAAAAATATCAA 35753 TGTATCAAAA 35754 AAA TC C AC
TATCTAATACCCAATTAATG ATATCAATAT TAATGTATCA ATA AATAT TAAT C
TTTTTATATCTGATATGTTA CTAA |||||||||| ||| ||||| ||||
ATTGTATAGT TAT TTGTA ATTA /
CTA TT - AC

GAM1392 TAATGTATCAAAAATATCAA 35758 TCAATATCCA 35759 AAA TC CCAA TCCA - TT ATC
AAAT
TATCCAATGTCCAATTAATG ATGTCCAATT TCA ATA AATAT TG ATTA ATGTT TAT
TGATATGTTA A
TTTTTATATCTGATATGTTA AATG ||| ||| ||||| || |||| ||||| ||| ||||||||||
AAATATCAATAATGTATCAA AGT TAT TTGTA AC TAAT TATAA ATA ACTATGTAAT
/
AAATATCAATATCTAATACC CTA TT ACTA CCA- C CT AAA AACT
CAATCAATGTTTTTATATCT
GATATGTTA
GAM1393 TATGCATATGAATTTATGAG 35763 CAATACAGGC 35764 A A GA-- AA--- ATGAAGAAG
AAGAAATTGGGATGAAGAAG TAGAATTATG TATGCAT TGA TTTATGA AG ATTGGG T
TTATAAAGAACCCAATACAG AAAT ||||||| ||| ||||||| || ||||||
GCTAGAATTATGAAATTAGT GTACGTG ATT AAGTATT TC TAACCC /
GCATG - A AAGA GGACA AAGAAATAT

GAM1394 AGCCGTTTTCCCCCAACTCT 35778 TCGCTGCTGG 35779 TT CCAAC --- ---- C CCA
ATA C- T
CGCTGCTGGCGACCAACTTC CGACCAACTT G TTCCC TCTC GCT GCTGG GA ACTTCA
AGTA CGCA C
AATAAGTACCGCATCACTGC CAAT | ||||| |||| ||| ||||| || |||||| |||| ||||
GCTTACTGTGAAGTACTCAC T GAGGG AGAG CGA CGACC CT TGAAGT TCAT
GCGT A
CAGCGTGTAGCTTCGAGACC GG TAACC CTT TGTG A CA- G-- TC C
AATGGGAGGGTGGCT

GAM1395 CTGTGGTGGGCGAGTTGTTT 35786 AGTTGTTTAT 35787 ----- G A---- T- A C
ATACAGTACACGATTGTGCT ACAGTACACG CTGTGG TGG CG GTTG TTAT CAGTACA G
GAGTGACCCAACCAAGACGG ATTG |||||| ||| || |||| |||| |||||||
CCAAAATTTCACAG GACACT ACC GC CAAC AGTG GTCGTGT A
TTAAA G AGAAC CC A T

GAM1396 GGTGCATTATAGTGCGGGGC 35792 TATAGTGCGG 35793 G TTAT C GCAC T G
ACGGTTGAAGGTGGCTTCAC GGCACGGTTG GGT CA AGTG GGG GGT GAAG T

CAAACCCACACTTATTGGAC AAGG ||| || |||| ||| ||| ||||
C CCA GT TCAC CCC CCA CTTC G
G TAT- A AAA- - G

GAM1397 GTCATACCCCAAGGGAGAAA 35802 TAAAAAGCAT 35803 CATA A AGAA G- CAA AA A
ATTTGCACAATTAATATTAA GGAAAATTGG GT CCCC AGGG AATTT CA TT TATT A
TGGATAAAAAGCATGGAAAA AACC || |||| |||| ||||| || || ||||
TTGGAACCCTGGGGGGAAAG CG GGGG TCCC TTAAA GT AA ATAG T
C AAAG G AAGG AG ACG AA G

GAM1398 ATGGTTCAGGTCCGCATAGG 35854 GTTCAGGTCC 35855 A ---------- CAG
TTCCCAGCAGAGGAACTTGT GCATAGGTTC ATGGTTC GGTCCGC ATAGGTTCC C
TATTTGATACCGGGGCGGAC CCAG ||||||| ||||||| |||||||||
CGAACTAT TATCAAG CCAGGCG TGTTCAAGG /
- GGGCCATAGTTTAT AGA

GAM1399 TCAAACAATGAATTTAGTAA 35877 ATGAATTTAG 35878 AA- GAA ----- A G
CAGATAGTAGATATGCATTT TAACAGATAG TCA CAAT TTTAGTAA CAGAT GTA A
GAATTTTTATTAAGAAATTG TAGA ||| |||| |||||||| ||||| |||
GGATGA AGT GTTA GAATTATT GTTTA CGT T
AGG AA- TTTAA - A

GAM1400 GTGACGAAGCAGCCTACCCC 35889 AAGCAGCCTA 35890 GA G - -- AA GT T GT ---
-- TT
GAAGGTGGTTCGTGTGAGTG CCCCGAAGGT AGCA CCT ACC CCG GGTG TCGTG GA
GCTCCCG CC GCGGT C
CTCCCGCCGCGGTTTCATAC GGTT |||| ||| ||| ||| |||| ||||| || ||||||| || |||||
CGTGAGGTCACGGGAGCTCC TCGT GGA TGG GGC TCAC AGCAC CT CGAGGGC
GG TGCCA /
ACGAGTCACTACGGCTGGTA AG - A TC A- TG - -- ACT AG TA
AGGTGCTGACACAC

GAM1401 GGAAGTGTCATGGCGTCCAG 35926 AACCCCGTTG 35927 CATG T - C CT TA ATAT
GGGCGTTCGTCTTTATGCAT GCGCGACGCG GGAAGTGT GCG CCAG GGG GTTCGT T TGC
G
ATGAGCGGCGCGATCACGAA CTTC |||||||| ||| |||| ||| |||||| | |||
CCCCGTTGGCGCGACGCGCT CCTTCGCG CGC GGTT CCC CAAGCA A GCG /
TCC CAG- - G - CT GC GCGA

GAM1402 GTTCAGCCGCCTGGCCACGT 35933 CAGCCGCCTG 35934 C - - TCCT - G GCA
CCTGGTGCCTGCTGCAGAAC GCCACGTCCT GTT AGCCGCCT GGCC ACG GGTGC CT CT G
AAGGAGCGCGCCCTGTGGGC GGTG ||| |||||||| |||| ||| ||||| || ||
CGAGGCGGCTAAGC CGA TCGGCGGA CCGG TGT CCGCG GA GA A
A G G C--- C G ACA

GAM1403 GCTTCTTCGTGTGCCCGCCG 35968 CCGTGCCCTG 35969 T CCCG TC G A---- T TC
T C
CCCTCGGGCGCCACGGTGGT AGTACGGGCT GCT CTTCGTGTG CCGCCC GGGC CC CGG
GG CGGC CGCG C
CCGGCTCGCGCCCGCGCGGC CGGG ||| ||||||||| |||||| |||| || ||| || |||| ||||
CGTGCCCTGAGTACGGGCTC CGG GAGGCACAT GGCGGG CTCG GG GTC CC
GCCG GCGC C
GGGCGGAACTACACGGAGGG - CAA- -- - CATGA - GT - G
C

GAM1404 CAACCGCCTAGGTTCCGCCC 35990 CTCTCTCGAC 35991 - A -------- CA- - AA
AGAGAAGCCAAATCGGCTCT GGCAAGTTCT CAACC GCCT GGTTCC GCC GAGA AGCC A
CTCGACGGCAAGTTCTTGGG TGGG ||||| |||| |||||| ||| |||| ||||
ACCGAGGCTGGTTG GTTGG CGGA CCAGGG CGG CTCT TCGG /
T G TTCTTGAA CAG C CT

GAM1405 TTTACAAAAACGTGATCGTG 36006 ACGGACCGCG 36007 AAAAA- G A CGA GG
AGCACGT - AT- AA
ACCACGACCTGGGCGGGCAG TGCCCGTGGG CGTGATC TG CCA CCT GCGGGC
ACGCGG CC TAC A
CACGTACGCGGCCATTACAA CATG ||||||| || ||| ||| |||||| |||||| || |||
ACCAGTACACGGACCGCGTG GCACTAG GC GGT GGG TGCCCG TGCGCC GG
ATG C
CCCGTGGGCATGGGCGAGAT GTCCAG A G AC- -- ------- A CAC AC
CACGGACCTGGTGGA

GAM1406 GCTGCTGGCGACCCGGCTGA 36022 CGAGCGCCGC 36023 CG - TGAC A - T
CGCAGCTCGCGCTTCGGCGG CGGAGTACCA GCTGCTGG AC CCGGC GC GCTCGC GC T
CGAGCGCCGCCGGAGTACCA GCAG |||||||| || ||||| || |||||| ||
GCAGC CGACGACC TG GGCCG CG CGAGCG CG C
A- A C--- - G G

GAM1407 TCTTGGAAAGCTTACCCGCT 36062 AAGCTTACCC 36063 AA ACCC T G CT TT
CTTGGCACTCCTTCTTCGGC GCTCTTGGCA TCTTGG AGCTT GC CTT GCA CC C
TTGCGGAGGTAAGAGCTCCC CTCC |||||| ||||| || ||| ||| ||
CGGGG GGGGCC TCGAG TG GAG CGT GG T
CC AA-- - G TC CT

GAM1408 CGGGTGCCAATAATAAATTT 36085 TGCCAATAAT 36086 G C AATTT GAATCT
TGCGCGAATCTTATTTAAGT AAATTTTGCG CGG TGC AATAATA TGCGC T
GCACACCGTGTTATTTGCGG CGAA ||| ||| ||||||| |||||
CTG GTC GCG TTATTGT ACGTG /
G T GCCAC AATTTA

GAM1409 TTATTGATATTGGCAATTTA 36091 TATGATATAT 36092 - TGG ATT-- -- T

```
    CATTCAGATATATTTGAATA      CTAATAA         TTATT GATAT   CA    TACAT  TCAGA A
    TGTATTATATGATATATCTA                  ||||| |||||  ||    |||||  |||||
    ATAA                            AATAA CTATA   GT    ATGTA  AGTTT T
                                    T    TA-  ATATT    TA    A


GAM1410  TGTCTCCTATAGTACCCCTA 36094   TAGTACCCCT 36095      TC---  A    A  CCTA    TA----    A  C
    AACTTTATAGAATCCGAGGA      AAACTTTATA       TGTC    CT TAGT CC    AACTT     TAGA TC G
    TCTGGACAAAGAGTTGGACT      GAAT          ||||    || |||| ||    |||||     |||| ||
    AAAGCGTACGACA                    ACAG    GA ATCA GG    TTGAG     GTCT AG A
                                   CATGC  A   - ----    AAACAG   - G


GAM1411  GCTTCTCGACGGCAGACTCT 36101   GGAGGAGAGT 36102      -    G      -     TG
    TTCTCCTCTGCTGTGAGGGG      CTGCGTTGAC       GCTTC TCGACG CAGACTCTT TCTCCTC  C
    AGGAGAGTCTGCGTTGACGG      GGGG          ||||| |||||| |||||||||| |||||||
    GGC                             CGGGG AGTTGC GTCTGAGAG AGGGGAG  T
                                    C    -       G      TG


GAM1412  ACTGGGTATAAAGAGTATAT 36117   AAGAGTATAT 36118       ATAA-  G   A    G TA
    CTTTGGGTATAGATACAAAG      CTTTGGGTAT       ACTGGGT    AGA TAT TCTTTG G  T
    AAATAGTCTGAAAGATTTAG      AGAT          |||||||    ||| ||| |||||| |
    T                               TGATTTA    TCT ATA AGAAAC T  A
                                      GAAAG   G   A     A AG


GAM1413  TCTCTTGATGTCACATTTTG 36131   TAAGGAAAAA 36132     TTG   T   -      TACT    A  A   CGTA-  A
  AA
    GGTACTCGGAGATGAGTTCG      AATGCAATTC       TCTC   ATG CAC ATTTTGGG    CGGAG TG GTT
CC TATAG  T
    TACCATATAGAATAACTATA      CGCC          ||||   ||| ||| ||||||||   ||||| || |||    || |||||
    AGGAAAAAAATGCAATTCCG                   AGAG   TAC GTG TAAAATCC    GCCTT AC TAA    GG
ATATC  /
    CCTAAAATAGTGCATAGTGA                     TGA   -   A      ----    A  G   AAAAA  A    AA
    GA


GAM1414  CAAAGTCCATAACAGAGTTT 36163   TGCACAAATG 36164        TAA---  G   -     -  TT   TA
    TGTGTGTTTGCCATAGTTTT      CTGTGGTGAT       CAAAGTCCA     CA AGT TTTGTGT GT  GCCA  G
    GGTTGCTGCACAAATGCTGT      TTGG          |||||||||     || ||| |||||||  ||  ||||
    GGTGATTTGGATTTTG                    GTTTTAGGT     GT TCG AAACACG CG  TGGT  T
                                      TTAGTG  G   T     T  T-   TT


GAM1415  GATAGAGTTAATATTTGTAA 36180   TTAATATTTG 36181          TT    A TTTATTAAT   TCT    AT
    GTTTATTAATGATTCTAAAA      TAAGTTTATT       GATAGAGTTAATA  TGTA G       GAT   AAAAA  T
    AATTAAATTTTTCTATTTTA      AATG          ||||||||||||  |||| |       |||   |||||
    TCACCTCTACATATTAATTC                    TTATCTTAATTAT  ACAT C       TTA   TTTTT  A
    TATT                                 --   - TCCACTATT   TC-     AA
```

GAM1416 GAAAGGTCTTCCGACGTGGC 36183 AAGGTCTTCC 36184 TCTT T AA CT- TGGA
AAGTCTGGACTACGTGGACA GACGTGGCAA GAAAGG CCGACG GGC GT GGACTACG C
GAGTCGTAGTCCCCCACGAG GTCT |||||| |||||| ||| || ||||||||
CTTGTCGGCCTTTT TTTTCC GGCTGT TCG CA CCTGATGC A
---- - AG CCC TGAG

GAM1417 CGGGGGGGTCCCCCGTTGGG 36204 ATGCATCTTA 36205 T- CC G- G GA GCG
CAGGGAGAGGGCGCTGACGA TCAATTGCCC CGGGGGGG CC CGTTGG CA GGA GG C
TGCATCTTATCAATTGCCCC CGTA |||||||| || |||||| || ||| ||
GTAGGGA AGGGATGC CG TTAACT TC ACG GC /
CC -- AT T TA AGT

GAM1418 AGATTTATTGGAGGGGGGGG 36214 TATGGTAATA 36215 TT GG GG GG ATAA T TT
GGATGTATAATATCCATGTT TTTATCAATT AGAT ATTGGA G GG GATGT TA CCATGTT T
TTTAAGATATGGTAATATTT ATCT |||| |||||| | || ||||| || |||||||
ATCAATTATCTAATTGTCT TCTG TAATCT T CT TTATA AT GGTATAG /
T- AT AA AT ---- - AA

GAM1419 CCGACCGACCAGCCGGCCGA 36217 TATGGTAGCT 36218 G CGATTC C C - TG-- C
C-- GA T
TTCGCCCGCCGGGGCTTCTG CTGCCGAGCG CC GC GC CG CGGGGCT TC GAGAACGC
GGGG AGCAGC TC G
GAGAACGCCGGGGCAGCAGC CGGG || || || || ||||||| || |||||||| |||| |||||| ||
GATCTGGGGAAGCTGCTAAA GG CG CG GC GTCTCGA GG TTTTTGCG CCCC
TCGTCG AG G
CCCCTGCGTTTTTATATGGT G ------ A C T TATA T AAA A- G
AGCTCTGCCGAGCGCGGGCT
GACGCGTTGG
GAM1420 GAAGTCGTTGGAGATGCGGC 36220 CGTTCATGCC 36221 --- AG-- GG G GC
CCATGAGCTGCGAGAAGGCG CGCCTCGTTC GAAGTC GTTGG ATGC CCCATGA CT G
TTCATGCCCGCCTCGTTCCA CAGA |||||| ||||| |||| ||||||| ||
GACGCGG GGCGCA CTTGC CCCG ACTTGCG GA A
GAC TCCG T- - AG

GAM1421 AGTCCAGTGACCGGTAACCA 36240 TCCAAGCACG 36241 TC TAACC CCAGCCC C A
CGTCCAGCCCCTGCGTATGT TCCGGTCATT AG CAGTGACCGG ACGT CTG GT T
ACCAGTCCAAGCACGTCCGG GTTC || |||||||||| |||| ||| ||
TCATTGTTCT TC GTTACTGGCC TGCA GAC CA G
TT ----- CGAACCT - T

GAM1422 GTAAAAAAAGTTTCTATTTC 36257 TTAGCATGTT 35745 A TTT T A- TA- C GAT
TATAGTAATGTTAACAAGTG CTAGAAGACA GTAAA AAAG CTAT TCT TAG ATGTTAA AAGT
A
ATAACAAATTTTTAGCATGT TAGT ||||| |||| |||| ||| ||| ||||||| ||||

TCTAGAAGACATAGTTTTTT CATTT TTTT GATA AGA ATC TACGATT TTTA A
ATTTAC A TT- C AG TTG - AAC

GAM1423 GTCTCCATGTGTGTATAAAA 36258 TCCATGTGTG 36259 T- AT T AAAA - AC C AAAA
AGCAAGGCACGTTCATAATG TATAAAAAGC GTC CC GTG GTAT AGCAA GGC GTT
ATAATGT A
TAAAAAAGAACACGTTGTAA AAGG ||| || ||| |||| ||||| ||| ||| |||||||
ACAAGCTATTGCTGTATCAT CAG GG TAC TATG TCGTT TCG CAA TGTTGCA A
TCGGCTGAC TC CT - ---- A AA A CAAG

GAM1424 CCTGCGTCGCCGGCGGCGCA 36291 CTCGATGGTC 36292 G G GGCGC - G CGA
CGGGCAGACGGTCGATGAAG TCGCCGCGCC CCT CGTCGCCG C ACG GGCA ACGGT T
CGCTCGATGGTCTCGCCGCG GGCG ||| |||||||| | ||| |||| |||||
CCGGCGT TGC GCCGCGCC G CTC GGTA CTCGC G
G - ----- T G GAA

GAM1425 AGAAGAATCGCCAGGGTTGC 36300 CAGGGTTGCG 36301 GAA C CGTT -- GC
GTTGCGGTGTGCCCCGGTTC TTGCGGTGTG AGAA TCGC AGGGTTG GC GGTGT C
GAGGCCGGCCGGATTCCGCG CCCC |||| |||| ||||||| || |||||
GCTAA AATC GCCT TAGGCCG GG CTTGG /
GGC - GCC- AG CC

GAM1426 GCTGGGAATGACTCAAGTGC 36320 TGACTCAAGT 36321 ATG TCAAG A AA
CCATAGCCCAAACTGGGTTG GCCCATAGCC GCTGGGA AC TGCCC TAGCCC A
CGGGTAAATCGTGTGTCCCA CAAA ||||||| || ||||| ||||||
GC CGACCCT TG ATGGG GTTGGG /
GTG CTAA- C TC

GAM1427 CGAGTATACTGTTGTGCTTA 36346 TGAGTACACA 36347 GTATA- T TTGATCG C
TTGATCGGCAGCCATCTGCA GACATTATCG CGA CTGT GTGCTTA GCAG C
TTGAGTACACAGACATTATC ||| |||| ||||||| ||||
G GCT GACA CATGAGT CGTC A
ATTACA - TA----- T

GAM1428 GGAGTGTGACAACATATTAT 36357 TTATTGGAAA 36358 - ------- ATAT---------- TC
CATTTATTATTGGAAACAAA CAAAGTTGTC GGAG TGT GACAAC TA A
GTTGTCTCTGAGTACATCTC TCTG |||| ||| |||||| ||
C CCTC ACA CTGTTG AT /
T TGAGTCT AAACAAAGGTTATT TT

GAM1429 AGGCTCCTGATGTGCCTGCT 36373 GGGGAGCGCA 36374 TGATGT --- TT CTG
CTTTTGTCTGAAAAATTGGG AGGCCTGGAG AGGCTCC GCCT GCTCTT GT A
GAGCGCAAGGCCTGGAGCCT CCT ||||||| |||| |||||| ||

TCCGAGG CGGA CGAGGG TA /
TC---- ACG GT AAA

GAM1430 GGGCTTTATTCATAAACAAT 36447 ACTTACTTAA 36448 T TAAACAATAAA TAC CTG
AAAAGGTGTACTGACCCTGA AACACTTGAA GGGCT TATTCA AGGTG TGACC A
ATTTGGTCACTTACTTAAAA TATA ||||| ||||||| ||||| |||||
CACTTGAATATAGCCT TCCGA ATAAGT TTCAT ACTGG A
T TCACAAAA--- TC- TTT

GAM1431 GCAGAGGCGGAGACTTCACC 36455 TCCAGGTGAC 36456 AGACT--- CT G
CTTGGACTGAATAGTCCAGG ATACCCACCG GCAGAGGCGG TCACC TGGACT A
TGACATACCCACCGCCTTTG CCTT |||||||||| ||||| |||||||
T TGTTTCCGCC AGTGG ACCTGA A
ACCCATAC -- T

GAM1432 CCACTGATGTCTCGTGCGAG 36468 ACTGATGTCT 36469 CT CT - - GG C
GGCTTGGGGGCCTGGGTACC CGTGCGAGGG CCA GATGT CGTGCGAGGG CT TGGG C T
CGCAGCCCCTTGCGCGCGCA CTTG ||| ||||| |||||||||| || |||| |
TCTGG GGT CTACG GCGCGTTCCC GA GCCC G G
-- C- C C AT G

GAM1433 ACAGGATGAGATACTTCCGG 36478 TGAGATACTT 36479 GATGA C CG A T
CATTCATGACTAAGGTCAAG CCGGCATTCA ACAG GATA TTC GCATTC TGAC A
AGTGTTAGAATATCGACTGT TGAC |||| |||| ||| |||||| ||||
TGTC CTAT AAG TGTGAG ACTG A
AG--- - AT A G

GAM1434 CTGTGTCCAAAGTTTTAAGT 36486 TCCAAAGTTT 36487 G A TTTA AC----- AT
ACGGACCGCTATGTCCAGCG TAAGTACGGA CTGT TCCA AGT AGTACGG CGCT G
TACCAACCTGTACTATTATG CCGC |||| |||| ||| ||||||| ||||
GAGGCAG GACG AGGT TTA TCATGTC GCGA T
G A ---- CAACCAT CC

GAM1435 CCTCCTATTGGGGAGCACTG 36501 TATTGGGGAG 36502 A --- - - - G
GGCCAAGGGTACTGTGTGCT CACTGGGCCA CCTCCT TTGGGG AGCACTGG GC CA AG G
CTAGTGTTGTGCCTCAGCAG AGGG |||||| |||||| |||||||| || || ||
GGGG GGGGGA GACTCC TTGTGATC CG GT TC T
C GTG T T G A

GAM1436 TTTATTGTCAAGCTTGGTGG 36537 CGTTGGAGAG 36538 TG---------- AA
CAAAGGAGCCATAGAGGGCG AAGCTTGGCG TTTATTGTCAAGCT GTGGC A
TTGGAGAGAAGCTTGGCGAT ATGG |||||||||||||| |||||
GGA AGGTAGCGGTTCGA TACCG G

AGAGAGGTTGCGGGAGA AG

GAM1437 AATGGTATTTGTTGGTTTAA 36556 TTTGTTGGTT 36557 TTT - ATG---------- TGT
TGAGTTGTTTGTTACTGTGG TAATGAGTTG AATGGTA GTTGGT TTA AGT T
TGGATACCACCCGTAGTACC TTTG ||||||| |||||| ||| |||
AACCTTACCATT TTACCAT CAACCA GAT TCA T
TC- T GCCCACCATAGGTGGTG TTG

GAM1438 ACCATGCAATATGTGGTATG 36568 TATAAAGTGA 36569 GCAA--- A GA G G G
GACATTTGTGTATTATTGGT GTAGCCATGT ACCAT TATGTGGT TG CATTT TGTATTATT
GTT G
TGGAAGGCAAGTGGTATAAA AGAT ||||| |||||||| || ||||| ||||||||| |||
GTGAGTAGCCATGTAGATTA TGGTA ATGTACCG AT GTGAA ATATGGTGA CGG A
TAATGGT ATATTAG - GA - A A

GAM1439 CGTGGCCAGCGCCCTCTATA 36580 TTCATTTTCA 36581 G-- - - - T AA TT TTAAT
AAAGATTTAGGATTAATATC GTTGACGGAG CGT GCCAG CGC CC TC AT AAGAT AGGA A
ATTTCCTTCATTTTCAGTTG CGAC ||| ||||| ||| || || || ||||| ||||
ACGGAGCGACTGGTAAAGCG GCG TGGTC GCG GG AG TG TTTTA TCCT /
AAA A A C T AC CT TTACT

GAM1440 TTACGATCCCGCGTCGTGGG 36592 TAGGATCTTT 36593 CGTG GGGT G A CAC - A
TT CCG CT
CCGGGGTCGGGGACTCTGCA CCCGGCCTCT CGT GGCCG CG GG CTCTG CTC CCTTT
GGATCT C GCCT A
CCTCCCTTTAGGATCTTTCC ACCA ||| ||||| || || ||||| ||| ||||| |||||| | ||||
CGGCCTCTACCAGGGCAAGG GTA TCGGC GC CC GGGAC GAG GGGGG CCTAGA
G CGGG C
GAGATCCGGGGGCGAGACCC ---- AT-- G - CCA C - GG AA- AC
AGGGCCGCGTACGGCTATGC
GGGCCCCGTGG
GAM1441 CCTCTCCGAATAATTGAAAC 36605 CTAGTTGTTT 36606 T ATT - AAT
ACTAGTAAATAAGGTACTAG CCCATATTTG CC CTCCGAATA GAAACA CTAGTA A
TTGTTTCCCATATTTGGAGT GAGT || ||||||||| |||||| ||||||
GG GG GAGGTTTAT CTTTGT GATCAT /
T ACC T GGA

GAM1442 GGCGACGTGAGGGTGACGGA 36614 TTGCAAACAT 36615 - --- A--- GTAAAG
CGTAAAGTTTAACCAGTTTG CCTCAGTTCG GGCG ACG TGAGGGTG CGGAC T
CAAACATCCTCAGTTCGTGC TGCG |||| ||| |||||||| |||||
GCC CCGC TGC ACTCCTAC GTTTG T
G TTG AAAC ACCAAT

GAM1443 GTATATATATTATATGTGTG 36624 TATATATTAT 36625 TATAT G TTATATTCCTA C
C

TGTGTTTTATATTCCTATGG ATGTGTGTGT GTATATATAT GTGT TGTGTT TGGCA TGGTA A
CACTGGTACATTACCATGCT GTTT |||||||||| |||| |||||| ||||| |||||
ACCTTGCAAGTAACATAAAT CATATATATA TATA ATACAA ATCGT ACCAT /
ATTTTCATATATATAC CTTT- A TGAACGTTCC- - T

GAM1444 AAAATATTTCTTCGGTTTTA 36658 TGGGTAGGTT 36659 T TTT TCA TT TAGTTT A
ATCAGGCCTTTCTCTAGTTT GTTTGTTCTG AAAATATTTCT CGG TAA GGCCT CTC GTATA A
GTATAAAGTTATATGGGTAG TGGA |||||||||| ||| ||| ||||| ||| |||||
GTTGTTTGTTCTGTGGAAAT TTTTATAAAGG GTC GTT TTGGA GGG TATAT G
ATTTT T TT- TG- T- ------ T

GAM1445 GAAGTTTTCCTGCTCTCGGT 36668 TGTCAAGGAT 36669 TTCC CTCG AAGT- - TG CATA AT
AAGAAGTTCCTGGTGATGTT GTGGCTTGCA GAAGTT TGCT GTAAG TCCT GG ATGTTAAA ACAAA A
AAACATAACAAAATAGTCTT AGCA |||||| |||| ||||| |||| || |||||||| |||||
TGTCTTTGACGTTGTCAAGG CTTTAG ACGA CGTTC AGGA CT TGCAGTTT TGTTT G
ATGTGGCTTGCAAGCACGAT C--- A--- GGTGT A GT C--- CT
TTC

GAM1446 CCTCCAGAAGTTGTGTATCT 36680 AGTAAACGCG 36681 T AA- ----- TAG-- CG A -- CTAA
AGTAAACGCGATAATAGATA ATAATAGATA CC CCAG GT TGTGTATC TAAA CG TAATAGAT AGTG A
GTGCTAAACGAATTACTGAA GTGC || |||| || |||||||| |||| || |||||||| ||||
TCTATTACTGACTTTAATAT GG GGTC TA ATACATAG ATTT GT ATTATCTA TCAT C
TGATACATACATTAATGACC T CAG ATTAC TTATA CA C AG TAAG
TGGTGG

GAM1447 TATATGATATCTTTACTAAG 36686 TATGATATCT 36687 ATCTTT A- AGTT - -- CCAC
AAAGTTTCTCTACTGTATCT TTACTAAGAA TATATGAT ACTA GAA TCTCTA CTG TATCTA A
ACCACACTTCTAGATATCCA AGTT |||||||| |||| ||| |||||| ||| ||||||
GATAGAGATTCGATGGTTTG ATATGCTA TGGT CTT AGAGAT GAC ATAGAT /
TCATCGTATA CTGTT- AG ---- A CT CTTC

GAM1448 GAGCTTCGCTATCACCGACA 36691 GCAGACCGCT 36692 TTC ATCACC-- C C ---- A A
CGCCCCAGCTGCAGGAGATC GGGCATGTTC GAGC GCT GACA GCCC AGC TGC GG G
CGCAGACCGCTGGGCATGTT TACT |||| ||| |||| |||| ||| ||| ||
CTACTTTGAGCTGCTC CTCG CGA TTGT CGGG TCG ACG CC A
T-- GTTTCATC A - CCAG - T

GAM1449 TATCAAGACGTATACATTTG 36708 TAGCAGCACA 36709 - ------ ----- AAAA G
TGAAAACTGTGGAGATATAG AATTAAAGGT TATC AAGACGT ATAC ATTTGTG CTGTG A
CAGCACAAATTAAAGGTATT ATTA |||| ||||||| |||| ||||||| |||||
AATACATGTCTTCGATG GTAG TTCTGTA TATG TAAACAC GATAT G
C CATAAT GAAAT GAC- A

GAM1450 TGTGACTTTCCTGCCGAATT 36722 TTCCTGCCGA 36723 CT-- TG CGAATTTA GATA
TAGAGATGGATATGTAGCAT ATTTAGAGAT TGTGA TTCC C GAGATG T
CTTCACTAGTGGGAATCAAT GGAT ||||| |||| | ||||||
CACA ACACT AAGG G TTCTAC /
AACT GT ATCAC--- GATG

GAM1451 GTTAAAATCTTTGCCAAGTC 36729 AAACATTAGC 36730 T C A CAA - A A C-- TTC
CC GAA C
CCAACACAAGGTCAATGATG CCTGATGCAC T G CA GTCC CACAAGG TCA TG TGGTT CATC
GGCT TG GG C
GTTCCATCTTCGGCTCCTGG GACT | | || |||| ||||||| ||| || ||||| |||| |||| || ||
AAGGCCTGCCAAACATTAGC A C GT CAGG GTGTTCC AGT GC ATCAG GTAG CCGA
AC CC T
CCTGATGCACGACTACGTGA - T C CTC T - - CAC TC- TT AAA G
TCCTTGTGCTCGGACCTGTC
AAGAAGTACC
GAM1452 CTGATGATCTGCGTTGACGA 36743 TGCGTTGACG 36744 - T TT CGA CAAA AG
CGGAAGTGTCAAAGACAAGA ACGGAAGTGT CTGA TGATC GCG GA CGGAAGTGT GACA A
TTCTGTCCTACATTTCCGAG CAAA |||| ||||| ||| || |||||||||| ||||
TTCTCCGTCGGTCACTCAG GACT ACTGG TGC CT GCCTTTACA CTGT T
C C CT TGA TC-- CT

GAM1453 GGAATAAAAAGTGGCCTCTT 36748 TTAAAATATT 36749 A G CTTT AT A
TAAAATATTTGGAGTGGAAA TGGAGTGGAA GGAATAA AAGT GCCT AAA ATTTGGAGTGGAA
A
AAATTGTTTTTTTCACTTTT AAAA ||||||| |||| |||| ||| ||||||||||||
GTAAAAAAAAGTGGCCTTT TTTCCGG TGAA AAAA TTT ACTTTTTTTGTTA /
- A ATGT C- A

GAM1454 GCTTAAGGTTTCGCCCTTCC 36792 ATCAGCTTCT 36793 TT- - CTTCC TCCATAC CAC
GAGAATCCATACTCCATCAC CGGCGAGCAC GC AAGGT TTCGCC GAGAA TCCAT C
CCCAATGGATCAGCTTCTCG CTTT || ||||| |||||| ||||| |||||
GCGAGCACCTTTTCGC CG TTCCA GAGCGG CTCTT AGGTA /
CTT C ----- CGACT-- ACC

GAM1455 AAGGTATTGGGAGTTTTTTT 36803 TTCGTTTTTT 36804 ------ T T- G ATT G AC A
GA
CATTTTTTGCGTAAATTTCG TCGTTTTTTT GAGTTTT TT CATTT TTGC TAA TC CA
TAATGAG TAAATTG A

CAACTAATGAGATAAATTGG CGCA ||||||| || ||||| |||| ||| || || ||||||| |||||||
AAATTCCAATTTTTTTCGTT TAAAAGT AT GAAAC CGCT TTT CT TT TGCTTTT
TTAACCT /
TTTTTCGTTTTTTTCGCACC TAAATA T CA T TTG T TT T TA
AAAGTTAATAAATTGAAAAT
TCCTAAATTCC
GAM1456 ATTGTAAATTCCAAAATTCC 36819 TCCAAAATTC 36820 A AAATTC- GTACAT T
AATTAATTGTACATCTTGGA CAATTAATTG ATTGTA ATTCCA CAATTAATT CT G
AAATTATTCCAATTAGTTAT TACA |||||| |||||| |||||||||| ||
GTAAATTGGAAATTACA ACATTA AGGTTA TGATTAACC AA G
A AATGTAT TTATTA A

GAM1457 GTCATCGACGAGGTTTACAA 36842 TACCTAGACC 36843 TC C------ CAAACT T
ACTCCCTAGCGGGTACCTAG TCTCCATCCT GTCA GA GAGGTTTA CCC A
ACCTCTCCATCCTCTCTGAC CTCT |||| || |||||||| |||
CAGT CT CTCCAGAT GGG G
CT CCTACCT CCAT-- C

GAM1458 GGAACCTGCTACATCTTCTC 36880 AGCCGATTGA 36881 CCT A- CT TC C CC T
TCGCGCCCTCTCCGGACAGC CTATGCCAGC GGAA GCT CAT TC TCG GC TC C
CGATTGACTATGCCAGCCTC CTCT |||| ||| ||| || ||| || ||
TTCC CCTT CGA GTA AG AGC CG AG C
CTC CC TC TT - AC G

GAM1459 GCGGTTCTTGTTCTCCCTGA 36900 TGACAAGGAG 36901 TTCT CTCC C - ------- ACA
GCCACCATCACCCAGACACA GTGATGTGTG GCGG TGTT CTGAG CAC CATCACC
CAGAC G
GGTAGTCTGACAAGGAGGTG ACTC |||| |||| ||||| ||| ||||||| |||||
ATGTGTGACTCGGAAAAACA CGCC ACAA GGCTC GTG GTAGTGG GTCTG /
CCCGC C--- AAA- A T AGGAACA ATG

GAM1460 GTCTCCCACTCCTCAGATGT 36932 TCAGATGTTT 36933 TCCC A TTT TC CT
TTTGATCACTTCTGCCCAAG TGATCACTTC GTC ACTCCTCAG TGT GA ACTT G
TCTTCTCCACACTTGAGGAG TGCC ||| |||||||| ||| || ||||
TCCCGAC CAG TGAGGAGTT ACA CT TGAA C
CCC- C CCT TC CC

GAM1461 AGGTCAAGTACCTCACTGAA 36954 TACCTCACTG 36955 AAG - C- C T TG GA
TTAC TA
GCGGGGATTGGCCTTACTGC AAGCGGGGAT CCTCACTG CGGGGATTG GC TTACTGC G GA
GCG GGCGAG CG A
CGTGATGGCGGAGGCGAGTT TGGC |||||||| |||||||| || ||||||| | || ||| ||||||| ||
ACCGTAAGACGTTCTCGTCC GGAGTGAC GCTCCTAGT CG AGTGATG C CT TGC
CTGCTC GC /
ACGTTCTCCCGTAGTGACCG CCG G CC - C CT AC TT-- AG

CGTGATCCTCGGCCCAGTGA
GGCGCAGACCT
GAM1462 CTGCCTTCGAAGTTCGTGGC 36968 TCGAAGTTCG 36969 CTTC--- T CCA A A T CC
CAACGACTACACTTCCTTTG TGGCCAACGA CTGC GAAGTTCG GG ACG CT CACT
CCTTTGA A
ACCAATCTCAAAGGGGTGAA CTAC |||| |||||||| || ||| || |||| |||||||
GCCGTCGTCCTCGAACTTCT GACG CTTCAAGC CC TGC GA GTGG GGAAACT A
TAAAATGCAG TAAAATT T TGC C A - CT

GAM1463 GAGTCGGCGACTCCCACGCC 36976 ATCGAGTACC 36977 GC - C- TA- CC AC
ATCGAGTACCCAACCTTACA CAACCTTACA GAGTCG GACT CCCA GCCATCGAG CCCAA TT
A
AGAACATTGGGACTCTCGAT AGAA |||||| |||| |||| |||||||||| ||||| ||
GGCTCTGGGCAGTCAACGGC CTCGGC CTGA GGGT CGGTAGCTC GGGTT AA /
TC AA C CT TCA AC GA

GAM1464 TCTTCCTTTCCATCCTGAGC 36980 GCGAACGAGT 36981 CCTTTCCATC - CCGA A
TATTCGCCGAGTGCATCTGC ATGCTCAGCT TCTT CTGAGC TATTCG GTGC T
GCGAACGAGTATGCTCAGCT CTCT |||| |||||| |||||| ||||
CTCTTCCAAGA AGAA GACTCG ATGAGC CGCG C
CCTTCTCTC- T AAG- T

GAM1465 GTATGTAATTTAAAAATGTG 36993 TTTCTTGGTG 36994 A A---- GA T ATAA
TGGATATTTGTATAAAAAAG AATAACATAC GTATGT ATTTA AAATGTGTG TAT TGT A
ACATATACATACATTTCTTG |||||| ||||| |||||||||| ||| |||
GTGAATAACATAC CATACA TAAGT TTTACATAC ATA ACA /
A GGTTC -- T GAAA

GAM1466 TATCAAGATGTGTATGTTTG 37020 CAGCACAAAT 37021 - ---------- AAAA G
TGAAAATTGTGGAGACATAG CAAAGGTATT TATC AAGATGTGTAT GTTTGTG TTGTG A
CAGCACAAATCAAAGGTATT AATA |||| |||||||||| ||||||| |||||
AATACATGTCTTAGATG GTAG TTCTGTACATA TAAACAC GATAC G
A ATTATGGAAAC GAC- A

GAM1467 TTTACAAATGAACTACATGT 37037 TGAACTACAT 37038 AT A C TT TCAAA
TGTATTCTCAAATTGCCCGG GTTGTATTCT TTTACAA GA CTA ATG GTATTC T
ATACTTGTATAGATCTATTG CAAA ||||||| || ||| ||| ||||||
TGAA AAGTGTT CT GAT TGT CATAGG /
AT A A T- CCCGT

GAM1468 GGCCAATCGTGATTAGTAAG 37055 TGATTAGTAA 37056 AATC TG AAGG-- A A
GCTTTAGAAACTTCAAAGAT GGCTTTAGAA GGCC G ATTAGT CTTT GA A
TGCGGCTAATTGCTTCGGCC ACTT |||| | |||||| |||| ||
CCGG C TAATCG GAAA CT C

CTT- GT GCGTTA - T

GAM1469 CTTACCAAACAAAAACAGCT 37062 TGAGTAGTTT 37063 CC ACA T TT-- TA
CAGAGTGGTTATTATAATTT TGTTTATAAG CTTA AAACAAAA GCTCAGAG GG ATTA A
TAATTTTTCCTTTCTGAGTA |||| |||||||| |||||||| || ||||
GTTTTGTTTATAAG GAAT TTTGTTTT TGAGTCTT CC TAAT T
A- GA- T TTTT TT

GAM1470 CTTTATTTAATGTTACTGAA 37081 TGAGTACATA 37082 - TAC AAA ACC TCA
AATGTGCTCATACCTAACAG CAAACGCGTA CTTTATTTA ATGT TG ATGTGCTCAT
TAACAGTT A
TTTCAACTTAACTGTTACAG TGGA ||||||||| |||| || |||||||||| ||||||||
ATGAGTACATACAAACGCGT GGAATAGGT TGCG AC TACATGAGTA ATTGTCAA /
ATGGATAAGG A CAA A-- GAC TTC

GAM1471 ATTGATCGTATTCAAGGCGT 37094 TTCAAGGCGT 37095 TC A- CG AC- TT
TATACAGGGTCTTAATGACT TATACAGGGT ATTGA GT TTCAAGG TTAT AGGGTC A
CTCTAATAGACCTTGAAAAA CTTA ||||| || ||||||| |||| ||||||
CTTTCAAT TAACT CA AAGTTCC GATA TCTCAG /
TT AA A- ATC TA

GAM1472 GAGATAAATAACAAAATCCA 37105 TAAATAACAA 37106 - CA CAAAC T
AACATTACATATCTGTGGTC AATCCAAACA GAGATAAA TAA AAATC ATTACA A
TGATTTCTTTATTTTATCTC TTAC |||||||| ||| ||||| ||||||
CTCTATTT ATT TTTAG TGGTGT T
T TC TC--- C

GAM1473 GACATCTTTGTTGTACAAGG 37112 TACAAGGTGA 37113 TTGTA TGAATA GT ATT
TGAATATGGTCTTAATTATT ATATGGTCTT GACATCTTTG CAAGG TG CTTA A
ATAAGGTTAACCCTTGCGAA AATT |||||||||| ||||| || ||||
GATGTC CTGTAGAAGC GTTCC AT GAAT /
----- CA---- TG ATT

GAM1474 GAAATCTACCAGCAATTTGA 37120 TCTACCAGCA 37121 - CA TT -- ACA A
CGCCATACAAGCAAATGCTC ATTTGACGCC GA AATCTACCAG AT GACG CCAT AGC A
AAGTGGATCGTCTTATAACT ATAC || |||||||||| || |||| |||| |||
GGTAGATTGTC CT TTAGATGGTC TA CTGC GGTG TCG A
G AA TT TA AAC T

GAM1475 CTATTAGGTACTCCTTTTGT 37126 TAACCATACC 37127 ACTCC A AC- CA
GGTAATGGACGACATGTTCT GCAAAATGCA CTATTAGGT TTTTGTGGTA TGG GA T
AACCATACCGCAAAATGCAC CCTA ||||||||| |||||||||| ||| ||
CTAATGG GGTAATCCA AAAACGCCAT ACC CT /

CGT-- - AAT TG

GAM1476 TTTTCAGATGGCTTTTATCC 37136 TTAAGCAGAA 37137 - - TTT TC ----- TAG
TTTTACTAATAGTAGTTTAG GTTTATTGTC TTTTCA GATGG C TA CTTTT ACTAA T
TTAAGCAGAAGTTTATTGTC TATC |||||| ||||| | || ||||| |||||
TATCGTGAAAA AAAAGT CTATC G AT GAAGA TGATT /
G T TT- TT CGAAT TGA

GAM1477 CAAAGAGAAAGATGGAAAAC 37154 TGGAAAACGA 37155 G AA--- AAA GGGA TTTA
AG
GAGGGGGAGGACTTTTTAAA GGGGGAGGAC CAAA AGA GATGG ACGAGG GGACTT
AAGG T
GGAGTTAACCTTGAGTTTAA TTTT |||| ||| ||||| |||||| |||||| ||||
TGTCTCGTCGCCATCATGAG GTTT TCT CTACC TGCTCT TTTGAG TTCC T
TCTGTTTG G GAGTA GC- GTAA ---- AA

GAM1478 ACTTACGCCACGGATTTGTT 37180 ACGGATTTGT 37181 A CA-- TTT A ACA A AT
GACAATCAACAAGACGCATA TGACAATCAA ACTT CGC CGGA GTTG CAATCA AG CGC A
CACGCGCTTGGTTGCCAACT CAAG |||| ||| |||| |||| |||||| || |||
ACTCTGATACGCGGAAGT TGAA GCG GTCT CAAC GTTGGT TC GCG C
G CATA CAT C --- - CA

GAM1479 TGCAGCGGTATCTGCGTGGA 37187 CAGCGGTATC 37188 TATCT G T GG GG
TTCCTGGGGTAGGGTGTCTG TGCGTGGATT TGCAGCGG GCGTG AT CCT GGTAG T
CCAGAGGGTGTACGTTTGTT CCTG |||||||| ||||| || ||| |||||
GCA ACGTTGTT TGCAT TG GGA CCGTC /
----- G - GA TG

GAM1480 GTGGTCACTCTCAGCTGCTA 37197 CAGGCTCTGA 37198 T- CTGCTAA T ATG
ACCTGTGCAGATGGAAACTG GAGTGTTTCA GTGG CACTCTCAG CCTG GCAG G
TCAGGCTCTGAGAGTGTTTC C |||| ||||||||| |||| ||||
AC CACT GTGAGAGTC GGAC TGTC /
TT TC----- - AAA

GAM1481 TAGGAAGACAAGGATGATCG 37365 ACAAGGATGA 37366 GACA G A GA G
CCAAACTGATTGACAAGGGG TCGCCAAACT TAGGAA AG ATGATCGCCAA CT TT A
GTTGGCGATTATACTGCATT GATT |||||| || |||||||||| || ||
CCTG GTCCTT TC TATTAGCGGTT GG GA C
ACG- A - GG A

GAM1482 TTGGAAGGGGATGAGTGGAC 37378 TTAGCAAAAT 37379 -- G- A - - CAA-- C ATGGGA
G TAG
TACACATAGTCAACAGGATT CAATCCTGCA TGA TGG CTA CACAT AGT CAGGATT GT
GT AGCAACT T

CGTATGGGAGTGAGCAACTT AAAG ||| ||| ||| ||||| ||| ||||||| || || |||||||
AGTAATGGTTGTTAGCAAAA ACT ACC GAT GTGTA TCG GTCCTAA TA CG
TTGTTGG /
TCAATCCTGCAAAAGCTAAT GG AA - C A AAAAC C AAA--- A TAA
GTGCTAGCCAAATCAGGAGA
TCCTACAA
GAM1483 GTGTGACGTGAGTCTGATCC 37404 TGACAAGCCT 37405 -- AG - A AACAC T T
CAG TT
AACACTGAACGCTTTCGTCG GACGAGAGCG TGA CGTG TC TG TCC TGAACGCTTTCGTCG
GTTT TCATG CT T
TGTTTTTCATGCAGCTTTTA TTCA ||| |||| || || ||| |||||||||||||| |||| ||||| ||
CAGACCATGACAAGCCTGAC ATT GCAT AG AC GGG ACTTGCGAGAGCAGT CGAA
AGTAC GA /
GAGAGCGTTCATCGGGGCAT AC GA T - GCT-- C C CA- CA
GAAGTACGCATTACAC

GAM1484 GGAACGGAGGAGGCTTTCGC 37418 TGTGACGATG 37419 C AG TT C CT--- A G
CACACCTATCCTGAAAGCGT TCTTTACCAT GGAA GG GAGGC TCG CACACCTATC GAA GC
T
TGCATTCTTTATGATAGGTG TCC |||| || ||||| ||| |||||||||| ||| ||
TGACGATGTCTTTACCATTC CCTT CC TTCTG AGC GTGTGGATAG CTT CG /
C A AT T- A TATTT A T

GAM1485 GCGTGATGATGACATTCATC 37429 CATACGGTTT 37430 AT ACATTCA TT- ATTCA
TAC
ATGTATTTCCATTCACACAT ATATATGACC GCGTG GATG TCATGTAT CC CACA C
ACCTTTTGTGCATACGGTTT ATCC ||||| |||| |||||||| || ||||
ATATATGACCATCCACGC CGCAC CTAC AGTATATA GG GTGT /
-- C------ TTT CATAC TTT

GAM1486 GTTCGTTGTCGCCCCTGTGA 37447 TGTGAGTGTG 37448 TT CCCTGT - - GC AT
GTGTGGAGCTAATCATATTA GAGCTAATCA GTTCG GTCGC GAGT G TGGA TAATC A
GGTTATATCCAGCAACTCTG TATT ||||| ||||| |||| | |||| |||||
AACGTGACCGAGC CGAGC CAGTG CTCA C ACCT ATTGG T
-- CAAGT- A G AT AT

GAM1487 CAATGGCTGATTTTGGATTG 37452 CTTTGTACCA 37453 A T--- GA T T GA ATA
TTACAATGCGAGGATACATT ACAGGGTCTT CA TGGC GATTTTG TTG TACAA GC GG C
CCCGGGCTTTGTACCAACAG ACGC || |||| ||||||| ||| ||||| || ||
GGTCTTACGCCAATG GT ACCG CTGGGAC AAC ATGTT CG CC A
A CATT -- C T GG CTT

GAM1488 GCGATTAACAACATTTTTCA 37462 TCACTAGTGC 37463 TT A TT A C ----- A- T C-----
G T
ATACGGCGTTGAACTATTGC CAACGAGTCT GA AACA CATT TCA TA GG CGTTG ACTA TG
TACCTG C A

TACCTGGCTAATGCAGGTAT CCAT || |||| |||| ||| || || ||||| |||| || ||||||
AAACTCACTAGTGCCAACGA TT TTGT GTAG GGT AT CC GCAAC TGAT AC
ATGGAC G A
GTCTCCATAATGGTGATGAT T- A T- A A TCTGA CG C TCAAAT - T
GTTTTTGC

GAM1489 ATCAGTCCGTATTTTTAATG 37475 TTAATGGCTG 37476 A - T- GGA AGGT G
ACA
GCTGGACTAGAGAAGGTGTT GACTAGAGAA ATC GTC CGTATTTT AATGGCT CTAGAGA
GTT CTATT A
GCTATTACAAACAAATGGGA GGTG ||| ||| |||||||| ||||||| ||||||| ||| |||||
ACTTTCTAGAGCTGTTCCAA TAG TAG GTATAAAA TTGTCGA GATCTTT CAA GGTAA
/
AATATGAGATAGAT A A CC --- ---- G ACA

GAM1490 AAGTAAACGGAATGTTAAAT 37485 TGGAAATAAC 37486 AA AA- AA TA ATG
TCTTACTATGACAGAGATGG AAAACTGTAG AAGT ACGG TGTTA TTCT CT A
AAATAACAAAACTGTAGACT ACTT |||| |||| ||||| |||| ||
T TTCA TGTC ACAAT AAGG GA /
GA AAA A- TA GAC

GAM1491 CAAATAGACTTAAATCACAC 37498 CATCACAGCA 37499 GA AAATCACA T ------- G
TGTTGTTGACTATGGAAATA GCATAAAAAA CAAATA CTT CTGTTGT GA CTAT G
GAGCTACATCACAGCAGCAT AGAA |||||| ||| ||||||| || ||||
AAAAAAAGAATATTTG GTTTAT GAA GACGACA CT GATA A
AA AAAAATAC - ACATCGA A

GAM1492 GGGTGATGGTGCAGTAGTAG 37558 TGATGGTGCA 37559 G A AATGATGA
TTAATGATGAAGGAAAGGGA GTAGTAGTTA GG TGATGGTGCAGTAGT GTT A
ATAATTGCTGTACCATTAAC ATGA || |||||||||||||| |||
C CC ATTACCATGTCGTTA TAA /
A A GGGAAAGG

GAM1493 GTCTCTAGGAATTGATTACC 37571 TAGGAATTGA 37572 C GAA A CC GATG AT
TCGATGCTTCATTAAGGAAG TTACCTCGAT GTCT TAG TTG TTA TC CTTC T
AAGAATAAACAAAGACTGAA GCTT |||| ||| ||| ||| || ||||
GGC CGGA GTC AAC AAT AG GAAG A
A AGA A A- AA-- GA

GAM1494 TTAGACATGGTAAAGAATCC 37576 GACATGGTAA 37577 GA GTAAAGAA AA C GATGT
AACCCTTAATGATGTGCAAA AGAATCCAAC TTA CATG TCC CC TTAAT G
AATTAATGGGGAATATAACA CCTT ||| |||| ||| || |||||
TGGATGA AGT GTAC AGG GG AATTA /
AG AATATA-- -- T AAAAC

GAM1495 TCAAGTTCCTCCTAATAGCT 37587 TGGCAAAACA 37588 -- ------ GGATGG C GAA
TTGGATGGGTCACTGGGAAA GGGGTTATTA TCAA GTTCCTCC TAATAGCTTT GTCA TGG
A
TCATCAATGGCAAAACAGGG ATTA |||| |||||||| |||||||||| |||| |||
GTTATTAATTAATGGAGGAA AGTT TAAGGAGG ATTATTGGGG CGGT ACT /
TAATTGA AA TAATTA ACAAAA A ACT

GAM1496 GATGTGAGTGCAGGTTCAGA 37599 TACAATATGC 37600 G GCAGGT GAAA- A CTA
AAATAATGTGTTTCTATCAC ATATGATAAG GATGT AGT TCA ATA TGTGTTT T
AAATACAATATGCATATGAT CTAC ||||| ||| ||| ||| |||||||
AAGCTACGTC CTGCA TCG AGT TAT ACATAAA /
- AAT--- ATACG A CAC

GAM1497 ACAGTCGGAGTCGAGTTTCT 37614 AGGCACCAAC 37615 - GTC TC ACAT TC
TGGTGACATTGGCTCTTTGT AACTCATCCG ACA GTCGGA GAGTT TTGGTG TGGC T
CAGGCACCAACAACTCATCC ACAT ||| |||||| ||||| |||||| ||||
GACATGT TGT CAGCCT CTCAA AACCAC ACTG /
A A-- C- GG-- TT

GAM1498 CAGGACGAGACGCGGTTCCA 37626 CGACCGGACG 37627 A - A ------- - C CC
CACGGCCATGACCGTCTGGC CCCCGCTGCG CAGG CG AG CG CGGTT CCA ACGG A
GACCGGACGCCCCGCTGCGC CCTG |||| || || || ||||| ||| ||||
CTG GTCC GC TC GC GCCAG GGT TGCC T
- G - CCCGCAG C C AG

GAM1499 AGTCGGCATGTTTTGACTAC 37647 TGTTTTGACT 37648 - T ------ CTACTTCT GTCA
TCCC
TTCTGCCGTCATTCTCCCCC ACTTCTGCCG AGTC GGCA GTTT TGA GCC TTC C
TCATGAAAAGGCTCTTCTAT TCAT |||| |||| |||| ||| ||| |||
CATCCTTTGAACTGCCTGAC TCAG CCGT CAAG ACT CGG AAG C
T T - TTTCCT ATCTTCT- AA-- TACT

GAM1500 GGAGTGCATGCGCGAGATCT 37658 CCACGCAGGA 37659 AG CAT A ACAACC A
ACA- A
GCGACAACCTGACGAAGTAC CTCGCGCTTC GG TG GCGCGAG TCTGCG TG CGAAGT
CG A
ACGAACTCGATCGACTTCGC CAGA || || ||||||| |||||| || |||||| ||
CACGCAGGACTCGCGCTTCC CC AC CGCGCTC GGACGC AC GCTTCA GC C
AGACC AG CTT A ------ C GCTA T

GAM1501 GATCATGTTCGCCACCAACC 37720 GCCGCTGGGC 37721 A-- CACCAA A T CT
CGACGTGCCACCTGGCGTGG GAGAGCGAAC GATC TGTTCGC CCCG CG GCCAC G
CCGCTGGGCGAGAGCGAACA ACGA |||| ||||||| |||| || |||||

CGAGATC CTAG ACAAGCG GGGT GC CGGTG /
AGC AGAGC- C - CG

GAM1502 AGGTTCCGCTGCGTGCTGAA 37749 TTCCGCTGCG 37750 A- GAAA----- GTA CG G - G T C G
GTGAAAGAGCGGTAGCTCCG TGCTGAAGTG GTGCTGA GT GAGCG GCTC GCTGC TG TCG TC GGTG AG A
GCTGCGTGTCGGTCTGGTGC AAAG ||||||| || ||||| |||| ||||| || ||| || |||| ||
AGGATCTCGCCGACGGCCAG CGCGACT CA CTCGC CGAG TGATG AC GGC AG CCGC TC /
GTAGTGAGCGGCGCTCGACT GG GATGTTCAG GG- -- G C - - - T
TGTAGACGGTCAGCGCGCAG
TGCCCCT
GAM1503 GCAGCCGGATGATGGTGCGG 37759 TGTGCAAGCG 37760 A TGC- AGTGAG GAA TT- AC- AGA- T
TTAGTGAGCCGGAAGCCCGT CACCTGCGAC G TGG GGTT CCG GCCCGTT GGTGCG GCACGG ATT G
TTTGGTGCGACGCACGGAGA GGGC | ||| |||| ||| ||||||| |||||| |||||| |||
ATTTGAAGGTCCGGTTGTGC C GCC CCAG GGC CGGGCAG CCACGC CGTGTT TGG A
AAGCGCACCTGCGACGGGCG A TTTC GAGGA- GG- CGT GAA GGCC A
GCGGAGGAGGACCCTTTCCG
ACAGCGGGTGT
GAM1504 GGTGCGCCGGCGGCATCCCG 37766 TCGACAGGAC 37767 G --- ATC---------- G
GTGACGGTGGTCGACAGGAC CAGGTCGAGC GGT CGCCGG CGGC CCG T
CAGGTCGAGCTCGGCGGGCC TCGG ||| |||||| |||| |||
CCG GCGGCT GCTG GGC G
G CGA GACCAGGACAGCTGGT A

GAM1505 GTGAATATTCCTGTCTTATG 37772 TAAGATAGGA 37773 G A- -------- C TAT
TCTGATATAAATTCAACACT AGAGTTAAC GT AAT TTCCTGTCTTA TGT TGA A
AACTGATAAGATAGGAAGAG || ||| |||||||||| ||| |||
TTAAC CA TTG AAGGATAGAAT ACA ACT /
A AG AGTCAATC - TAA

GAM1506 TTATATGATATCTTACAAAA 37798 TATGATATCT 37799 - C C- AAA TT TT- TTCTG
TATATTAAATCTTTCTTTAG TACAAAATAT TTATATGAT AT TTA AAAATATATT TC TC TAGTTAT A
TTATTTCTGATAACTTATAA ATTA ||||||||| || ||| |||||||||| || || |||||||
CTATTTGACGAAGGATATGT AATATATTA TA AAT TTTTGTATAG AG AG ATCAATA T
TTTTTTAATATAATTATATA A T TT GA- C- TTT TTCAA
A

GAM1507 TTTATATTTTTTAATTTTGT 37803 TTTCTTCGGT 37804 TAATTT TTT C AT TAATCACA A TTC CA
ATTTGATTCTGATAATTCGT ATCATAATCT TGTA GATT TGATA TCG AAGAAA TA ATATATAT A

AATCACAAAGAAAATATTCA TTGC |||| |||| ||||| ||| ||||||| || ||||||||
TATATATCAAATAATATATA ACGT CTAA ACTAT GGC TTCTTT AT TATATATA A
TATTATTTCTTCGGTATCAT ATTT-- TT- T -- -------- - TA- AT
AATCTTTGCATTTACATACT
ATAAA

GAM1508 TTGCATAATTATCATTAATA 37806 TATGGTAAAT 37807 -------- TAATA TA
GGAATATCATTTTCATATAT TTTTTATTAT TTGCATAAT TATCAT GGAA T
GGTAAATTTTTTATTATGCG GCGA ||||||||| |||||| ||||
A AGCGTATTA ATGGTA CTTT C
TTTTTTAA TATA- TA

GAM1509 TGTCTTATTTTTTATTTTAT 37810 TAATTAGCAG 37811 - TT- T T ---- AAT
ATGGATTATTATTAATAAAA TTCTTATAAC TGTCT TATTTT AT TTATA GGATT ATTATT A
CAATAATTAGCAGTTCTTAT ATCA ||||| |||||| || ||||| ||||| ||||||
AACATCATAAAATATAGATA ATAGA ATAAAA TA AATAT CTTGA TAATAA A
T TAC C T CGAT CAA

GAM1510 GTAAAAGGATTATTGCATTT 37819 TAAGTATTAA 37820 A T-- CATT TA-- TC T
TTT
ATTAAGTATTAAAACATTAT AACATTATCT GTA AAGGAT ATTG TATTAAGTAT AAACATTA
TA ATA T
CTATATATTTTGAATTATTT ATAT ||| |||||| |||| |||||||||| |||||||| || |||
ACTAATGTTTGAATATATTT CAT TTCCTG TAAC ATAATTTATA TTTGTAAT AT TAT
G
AATACAATTTTGTCCTTGTA G TTT ---- TAAG C- T TAA
C

GAM1511 GGATTTTTGCAATAATATGA 37823 TTATATGTTT 37824 TTT- TA--------- TTTT
TGTTTTATTTTTATTATATG TAATTTTTTG GGAT TGCAA ATATGATG A
TTTTAATTTTTTGCATATTA CATA |||| ||||| ||||||||
TCC CCTA ACGTT TATATTAT /
TTAT TTTTAATTTTG TTTT

GAM1512 TAGAATATAAAAATACATTC 37831 TACGATATTT 37832 TATA-- CAT C AAGATA - A
GCTATAGAAGATATAGTATC TAAAATTTTC TAGAA AAAATA TCG TATAG TAGT ATC A
AAAAGATAACTACAAGCTAT TA ||||| |||||| ||| ||||| |||| |||
ACGATATTTTAAAATTTTCT ATCTT TTTTAT AGC ATATC ATCA TAG A
A TTAAAA --- - GAAC-- A A

GAM1513 GAGTATACAATACAAAATGT 37834 TACAATACAA 37835 ATAC- A T C TTTTCTG T
AGCATATATTTTTCTGTACA AATGTAGCAT GAGT AATACAAA TG AG ATATAT TACAA A
ATATATTGTAATATATACTT ATAT |||| |||||||| || || |||||| |||||
TATTTGTATTTAATAACTT TTCA TTATGTTT AT TC TATATA ATGTT T
ATAAT - T A ------- A

GAM1514 CCTGTGCAGAAAGTGACTCG 37849 CTACCGCGAG 37850 T AA T -- A ----- - - C
GCTGAGTGCTCCGGTGGCCC GTTTCCACCC CCTG GCAG AG GACTC GGCTG GTG CTC CGGT GGC C
TTGCCTACCGCGAGGTTTCC AGCC |||| |||| || ||||| ||||| ||| ||| |||| |||
ACCCAGCCTCGGGTCTCTAC GGAC CGTC TC CTGGG CCGAC CAC GAG GCCA CCG T
TGCCAGG - A- T CT C CTTTG C T T

GAM1515 CATGTGAGTAAATGGAAATC 37886 TGGAAATCAA 37887 AG AA A AATA GAC AA
AATAGCTGACTGTAAAAAAC TAGCTGACTG CATGTG TA TGGA ATC GCT TGT A
ATAAGGCCGATATCCACGTG TAAA |||||| || |||| ||| ||| |||
ATACATG GTACAT GT ACCT TAG CGG ACA /
A- GC A C--- AAT AA

GAM1516 GTAAACAGTATTGTTGGACA 37904 ACAGTATTGT 37905 TAT ACGTCT---- T
CGTCTTCCTCAAGGATTTTT TGGACACGTC GTAAACAG TGTTGGAC TCC C
AAATAGTCCAGCATTGTTTA TTCC |||||||| |||||||| |||
C CATTTGTT ACGACCTG AGG A
--- ATAAATTTTT A

GAM1517 GATCCTAAAGAGCATGTTCA 37917 TTTGAAAAAA 37918 ---- T CAA---- AGAAAAAGTG TTT GGCA
ACAATTAGAAAAAGTGTTTC TCAGAAATTG AAGA GCA GTT CAATT TTTCAAA TACTACA G
AAATTTTACTACAGGCAGGA GTCA |||| ||| ||| ||||| ||||||| |||||||
TATGTAGTATCTTTGAAAAA TTTT TGT CAA GTTAA AAAGTTT ATGATGT /
ATCAGAAATTGGTCAAAAAA AAGA - AAAACTG AGACTAAA-- CT- ATAG
CTGTAGAATTTTTAGGATT

GAM1518 GAGCGAAAGGTGCCTGTGGA 37936 TGAAAGAGGA 37937 AAA GC T-- TT GAAAA G ------ TG
GTTTTGGAAAATCCTCTTTG CATGCTCCTC GAGCG GGT CTG GGAGT TG TCCTCTTT AT GGC T
ATGGCTGTGTCGCCCTGGGA TCAG ||||| ||| ||| ||||| || |||||||| || |||
GTGAAAGAGGACATGCTCCT CTCGC CCG GAC CCTCG AC AGGAGAAA TG CCG G
CTCAGAGGCCGGGCGCTC GGG GA TCT T- ----- G AGGGTC CT

GAM1519 AATAGTAAGAGTCAATTTTT 37964 TAAATAGCAG 37965 AT TA TC T TA--- AT A CAAA GAAT
GTATTATAAATAGCAGTTCA TTCAAATGTG A AG AGAG AATT TTG TT AAAT GCAGTT TGT A
AATGTGAATAAAAAACAGGC AATA | || |||| |||| ||| || |||| |||||| |||
TGCAGTTTTCAAGCATCCAA T TC TCTC TTAA AAC AA TTTG CGTCGG ACA /
CAATTCCTCTCTCTTCT CT TC C- C CTACG CT A ---- AAAA

GAM1520 GATAATATGCTAATAGTAGG 37980 TAATATGCTA 37981 AATAG GTAA A TA A CTAA-
GAAA-- GGTA- AG
TAAACCCAGACTATGCCATC ATAGTAGGTA CT TAG ACCC GAC TGCC TC TGTT CC
GGC A
CTAATGTTGAAACCGGTAGG AACC || ||| |||| ||| |||| || |||| || |||
CAGAGAAGCCGTTTAGGGGA GA GTT TGGG TTG GCGG AG GCAA GG CCG
G
GTAAACGAAGTTGAAGGCGC AGCTA AA-- A TC A TTGAA ATGAGG ATTTG AA
TGTTAGGGTAATTGATCGAA
GCAGAAAATC
GAM1521 AGGGAATGGTCCTTTTCCGC 38006 TGTCTAGTTT 38007 A TCCTT C TTA ------
GGCG
ACTGGTTAACGGTACTGAGG GGAATCTCCA AGGGA TGG TTCCG ACTGG ACGGTACT
GAGGA T
AGGCGTTGAAATCTTTAGGA ATTC ||||| ||| ||||| ||||| |||||||| |||||
AAGGTGCTGTCTAGTTTGGA TCCTT ACC AAGGT TGATC TGTCGTGG TTTCT T
ATCTCCAATTCCT A TCT-- T --- AAAGGA AAAG

GAM1522 TGTAGGTACTGGTGGATTTT 38020 TGAGTTCCTG 38021 CT GA- T T T TCT CG
ATGAGTTCCTGCTCTATGTT CTCTATGTTC TGTAGGTA GGTG TTTTA GAG TCC GC ATGTT
G
CGGTTTGACATGTGGATTTC GGTT |||||||| |||| ||||| ||| ||| || |||||
CTAAAGGAATACCTCTACCT ACGTCCAT CCAT GAAAT CTT AGG TG TACAG T
GCA CT AAG C T - --- TT

GAM1523 AGCCACTCTTTTAAAAATTG 38030 TGGCCAAATA 38031 - AAAAATT--- A TT
CCAACCTTTATTGGTGGCCA TGAGAAAGGA AGCCAC TCTTTT GCCA CC T
AATATGAGAAAGGATGTGGT TGTG |||||| |||||| |||| ||
T TTGGTG AGGAAA CGGT GG A
T GAGTATAAAC - TT

GAM1524 GAGGCGCTGATCTGCAGCTG 38051 CGTGCAGCCG 38052 --- TGA - A CG
CACGGCCGTGGAGTCGTGCA CATGAGACGT GAGG CGC TC TGC GCTGCACGGC T
GCCGCATGAGACGTGATACC GATA |||| ||| || ||| ||||||||||
TC CTCC GTG AG ACG CGACGTGCTG G
ATA CAG T C AG

GAM1525 TTTTGATCGAGGCACCAAGA 38055 CATCGTTGAT 38056 TC GGCACCAA TC AAATT
TTCTGCCAAATTCCCCAAGG ATAATCTTTC TTTTGA GA GAT TGCC C
CATCGTTGATATAATCTTTC AAAG |||||| || ||| ||||
AAAG GAAACT CT TTG ACGG /
TT AATATAG- CT AACCC

GAM1526 GATAACTACCGTTCATGCTG 38069 TACCGTTCAT 38070 C CGTTC - CA TTA

TATGCATCATTATAATCTGA GCTGTATGCA GATAA TAC ATG CTGTATG TCA T
CATATAGACATCTGTAATTA TCAT ||||| ||| ||| ||||||| |||
TC CTATT ATG TAC GATATAC AGT A
A TC--- A -- CTA

GAM1527 GAAAATGAGCCCTGGATTAA 38077 AAGAGGCCAA 38078 ----- CC ATTA-- AATAAT
AGACAATAATGGAAAAAGTC AGTTTAAATA GAAAAT GAGC TGG AAGAC G
TTAAGAGGCCAAAGTTTAAA GTTT |||||| |||| ||| |||||
TAGTTTTC CTTTTG TTTG ACC TTCTG /
ATAAA AA GGAGAA AAAAAG

GAM1528 TCTGGTATACACCCGTCTCG 38087 CCGGACGGAT 38088 TATA C C A- AA TA
TGGTACGAAGTAGAGCGCGG GCAGTCCAGA TCTGG CA CCGTCT GTGGT CG G G
CACCACCGGACGGATGCAGT ||||| || |||||| ||||| || |
CCAGA AGACC GT GGCAGG CACCA GC C /
TGAC A C CG G- GA

GAM1529 CGTAGTCTTAAAAATTTGAT 38159 TTAAAAATTT 38160 A C A---- TAACTACC C ----
ATCATT
AACTACCATTCATGCTATAT GATAACTACC CGT GT TTAA AATTTGA ATT ATG
CTATATGT A
GTATCATTATAATCTGACAT ATTC ||| || |||| ||||||| ||| ||| ||||||||
ATAGACTTCATTAATTATTT GCA CA AATT TTAAACT TAA TAC GATATACA T
TTTCAAATTCATTCTTAATA - T CTTAC TTTTTAT- T TTCA GTCTAA
CACG

GAM1530 TAAGTTAAATAATATACTTT 38170 TAATATACTT 38171 ------ - AAATA CATTT TC
TAAATAAAGTCATTTTTTTA TTAAATAAAG TAAGTTA AATA ATATACTTTT AAGT TTTTA
T
TCTGCTAAAAACTTAAAAAA TCAT ||||||| |||| |||||||||| |||| |||||
AGTATATATATTTCTTAATG ATTCAGT TTAT TATATGAAAA TTCA AAAAT /
ACTTA AATTCT A AAA-- ----- CG

GAM1531 AATACCTCAATGTCTTCTAT 38176 TACCTCAATG 38177 ---- T- CTA--- C AATT C
AT
GGGCGTCGAATTCGTATGCG TCTTCTATGG AATACCT CAA GTCTT TGGG GTCG
CGTATG GTATA C
TATAATCGGTATACACGTGC GCGT ||||||| ||| ||||| |||| |||| |||||| |||||
GCATGATTTCCAGATAAAAA TTATGGA GTT TAGAA ACCT TAGT GCGTGC CATAT
/
GATCTTTGTACTAGGTATT TCAT TC AAATAG T AC-- A GG

GAM1532 ATTAGTATTTAATATTTATT 38192 TTTAATATTT 38193 T TTATTTATTT C
TATTTTTTTACAACTAAAAT ATTTATTTTT ATTAGTATT AATAT TTTTA A
CAACAATTATATTAATGCTA TTAC ||||||||| ||||| |||||

AT TAATCGTAA TTATA AAAAT A
- TTAACAACT- C

GAM1533 GGTTTCAGCCGAGGCAATGT 38197 CAGCCGAGGC 38198 TTC- C- AT TAC CCTGGT - TTT
TTACATAGTCCTGGTGCTTA AATGTTTACA GGT AGC GAGGCA GTT ATAGT GC TTAA C
ATTTCCATTTTAATGCTTGT TAGT ||| ||| |||||| ||| ||||| || ||||
ATACTGTTTGACTGTCTCCA CCA TCG CTCTGT CAG TGTCA CG AATT C
GCTTTTCACC CTTT AC -- TT- TATGTT T TTA

GAM1534 GGGTAATAACTTTCCCAATC 38204 TCAACGGGCC 38205 TA T C C TTGT A TG TT
GGGTTGTGCTCGTAGATGAT CCCTTATTGT GGGTAA ACT TC CAAT GGG GCTCGT GA A T
TTGACTTGTCAACGGGCCCC GACG |||||| ||| || |||| ||| |||||| || |
CTTATTGTGACGGTGCTTAC CCCATT TGG AG GTTA TCC CGGGCA CT T G
CC CG C T T CC-- A GT CA

GAM1535 CCCACATCACACATCAGGAA 38219 TCACACATCA 38220 C------ TC - TGAA GACGA - AC
GTTGAAACCAATGACGATGG GGAAGTTGAA CCCACAT ACACA AGG AAGT ACCAAT TGGT GGC A
TGGCACAATGCCAACCGGTT ACCA ||||||| ||||| ||| |||| |||||| |||| |||
GGTACTTACCTACTGTGTAT GGGTGTG TGTGT TCC TTCA TGGTTG GCCA CCG /
CTCAAGTGTGGG AACTCTA CA A ---- ----- A TA

GAM1536 ATATCAGATATAAAAACATT 38274 TACATTATTG 38275 A A-- C TG TGG T T
GATTGGGTATTAGATATTGA ATATTTTAAC ATATC GATAT AAAA AT AT GTATTAGA AT G
TATTTTTGATACATTATTGA ATAT ||||| ||||| |||| || || |||||||| ||
TATTTTAACATATCAGATAT TATAG CTATA TTTT TA TA CATAGTTT TA A
A CAA A GT TTA T T

GAM1537 TAATTATCATGTCAAGGATG 38281 TCAAGGATGT 38282 T C G TCATA T ATCG
TCATAGACATTGTCATCGTC CATAGACATT TAAT AT ATGTCAA GATG GACA TGTC T
ATAGACACTGTCATCGTCAT GTCA |||| || ||||||| |||| |||| ||||
TGACATTGTCATTA ATTA TG TACAGTT CTGC CTGT ACAG /
C T A TA--- C ATAC

GAM1538 CAATATCAATATTGGTATAA 38294 TATAAAATAT 38295 TCAATA AA AAA AA GAC
AATATATAAAACATAAACTA ATAAAACATA CAATA TTGGTATA ATATAT ACAT ACTA T
GACTTTTATAGTATGTAAAT AACT ||||| |||||||| |||||| |||| ||||
ATATCATATATCAAAACATT GTTAT AACTATAT TATATA TGTA TGAT T
TATTG TTACAA AC AA- -- ATT

GAM1539 TCCTTTATTGAACTTTAGAT 38301 TTGATATTAG 38302 TTT AC AG A- A
ATTTAATAAAATGTATCGAT ATATAAAAAC TCC ATTGA TTT ATATTTAATA AATGT T
ATTGATATTAGATATAAAAA ATTA ||| ||||| ||| |||||||||| |||||
CATTAATTGGA AGG TAATT AAA TATAGATTAT TTATA C
T-- AC AA AG G

GAM1540 ATATCAGATATAAAAACATT 38304 TATTTTGTGA 38305 A A-- C TGG T T
AATTGGGTATTAGATATTGA TATCAGATAT ATATC GATAT AAAA ATTAAT GTATTAGA AT G
TATTTTTGATACATTATTGA ||||| ||||| |||| |||||| |||||||| ||
TATTTTGTGATATCAGATAT TATAG CTATA TTTT TAGTTA CATAGTTT TA A
A GTG A TTA T T

GAM1541 CTATGTTTATTGTCATGGCG 38327 TGTTTATTGT 38328 TG TT- C- -- T
ACAGTGTTGATACACTTTGT CATGGCGACA CTA TTTA GTCATGG GACA GTGT G
TTCCCGTGACTCTTAAAATT GTGT ||| |||| ||||||| |||| ||||
AG GAT AAAT CAGTGCC TTGT CACA A
TA TCT CT TT T

GAM1542 GGAAGCAATGATTTTTACAT 38334 TTGGATAGTA 38335 ATGATTTTT AGT AAATTTTA
C- T- TT
AGTGTTCCTGCAAATTTTAA TCGCAGGAAC GGAAGCA ACAT GTTCCTGC ATAC TCT
CAAG C
TACCTCTTCAAGTTCACTTT TCGG ||||||| |||| |||||||| |||| ||| ||||
GTTGGATAGTATCGCAGGAA TCTTTGT TGTG CAAGGACG TATG AGG GTTT
/
CTCGGTGTTGTTTCT --------- GCT C------- AT TT CA

GAM1543 GATTATTATATTCATCTCGC 38339 TATTATATTC 38340 TATT A C- AC TG
ACCACGAAGTGATTCTTTAA ATCTCGCACC GAT ATATTC TCTCG ACC GAAG A
GGTTTCGAGAGAATATTTAT ACGA ||| |||||| ||||| ||| ||||
C CTA TATAAG AGAGC TGG TTTC /
TT-- - TT AA TT

GAM1544 ATTATGTCCTGTTTGGTGTC 38342 TATGTCCTGT 38343 TG G AAA- TCCCCCC - CTA
GCGA CT
CAAAATGGAGACTCTCCCCC TTGGTGTCCA T GT TCCA TGGAGACTC AGAGCT TGG CC
GATATCC A
CAGAGCTTGGCTACCGCGAG AAAT | || |||| ||||||||| |||||| ||| || |||||||
ATATCCCTAGAGGATGTCGG A TA AGGT ATCTTTGAG TTTTGA GCC GG
CTGTAGG /
ACTCCGTAGTTTTGAGTTTC GT G GGAG ------- T TCA ---- AG
TAGAGGTGGAGATTGAGAAT
AGGGGCAAAGT
GAM1545 TCTGGCATTTTCCCAAATTT 38361 TGGCTTGGGA 38362 T TT ATTTTTT GTT T C

TTTGCCATGTTTTTTGTACA ATTGCTTGG TC GGCA TTCCCAA GCCAT TTTTG ACAA A
ACAGTTGTTTAAAAATGGCT || |||| ||||||| ||||| ||||| ||||
TGGGAATTGCTTGG GG TCGT AAGGGTT CGGTA AAAAT TGTT /
T T- ------- --- T G

GAM1546 GGACAGGTTTGACATCATAG 38502 TGAAAATGAG 38503 -- - ACA AGA - GA
ACACTTCTGATGAAGAAGAT ACAGACCGTG GG ACA GGTTTG TCAT CA CTTCT T
GAAAATGAGACAGACCGTGT TAAC || ||| |||||| |||| || |||||
AACC CC TGT CCAGAC AGTA GT GAAGA /
AA G AG- AAA A AG

GAM1547 CGTCTCCTCTGGGCTACCTC 38522 TCTGGGCTAC 38523 C ACCT ----- T
ATTTTGACCCCGTTTATGGG CTCATTTTGA CGTCTCCT TGGGCT CATTTT GACCCCG T
GTTGTTAAGAAGTGTGAGCC CCCC |||||||| |||||| |||||| |||||||
TATGGGGGGCG GCGGGGGG ATCCGA GTGAAG TTGGGGT T
T GT-- AATTG A

GAM1548 AGGTTAACCCATCTTGGATC 38590 TAGGACAGGA 38591 TAA- TCT AT ATC - T-
GCGA
CATCTCCTGCCTACTTCTCC ATCGGCCATT AGGT CCCA TGG CC TCCTG CCTACTTC
CCT T
TGCGATAAATAAGGTTGAAG TTGG |||| |||| ||| || ||||| |||||||| |||
TAGGACAGGAATCGGCCATT TCCA GGGT ACC GG AGGAC GGATGAAG GGA A
TTGGGCAGTACCT TGAC TTT -- CTA A TT ATAA

GAM1549 CCAGGGTGGATGGTATTTGT 38603 TTGATGGGGC 38604 G - A TG TG ATAC
TGACAAATACATCTATTGTT TATGCCACCT CCAGG TGG ATGGT TT T ACAA A
GATGGGGCTATGCCACCTGG GG ||||| ||| ||||| || | ||||
GGTCC ACC TATCG GG A TGTT /
- G - GT GT ATCT

GAM1550 GGTGTCTTATATGTATCCAC 38635 TATATGTATC 38636 T A AT TAA TACCA TAT
TTTA CA
TAATTGATGTACCAGATATG CACTAATTGA GGTG CTT TATGT CCAC TTGATG GA GTT
GACG G
TTTTTAGACGCAGTTCGTCC TGTA |||| ||| ||||| |||| |||||| || ||| ||||
AATTTTTCATCGTCAGACGT CCAT GAA ATATA GGTG GACTGC CT TAA CTGC /
GGGCATATACAAGTTACC T C CG CA- TA--- TTT C--- TT

GAM1551 AAACACAATCCCGACTCGGA 38642 TTGGTAAATC 38643 C - - C A- ATA-- G
ATATATATATGATAATAAAT CCAGTTCGGG AAACA AAT CCCGA CT GGA TAT TAT A
TGGTAAATCCCAGTTCGGGT TATT ||||| ||| ||||| || ||| ||| |||
ATTTTGTTT TTTGT TTA GGGCT GA CCT ATG ATA T
T T T C AA GTTAA A

GAM1552 CGTTTTCAGCATAGTATAAT 38649 TCTAAACAAA 38650 CAGC ATA T - AAATTTTTT
G
TATTTCTAAACAAAATTTTT ATTTTTTCCG CGTTTT ATAGT ATTA TTCTAAA CA CC T
TCCGTTGGTTCATTAAATGT TTGG |||||| ||||| |||| ||||||| || ||
TTTAGAATTAATACCATTAT GCAAAA TATTA TAAT AAGATTT GT GG /
AAAACG ---- CCA T T AAATTACTT T

GAM1553 AATATTGGCCAATCATCTCT 38654 TATTGGCCAA 38655 G ATCA - GATA- AA
GATATTTGTAAGGAAATAAG TCATCTCTGA AATATTG CCA TCT CT TTTGT G
AAAAAAGAAGAAAAGTGGAC TATT ||||||| ||| ||| || |||||
AATATT TTATAAC GGT AGA GA GAATA G
A GAAA A AAAAA AA

GAM1554 TCTTCGTCTGAGGAGCTATT 38662 TATTGCTAGT 38663 - T G TAT---- - TGT TG
GCTAGTGGGTGTGCACTGAC GGGTGTGCAC TC TTCGTC GAG AGC TGCTA GTGGG
GCAC A
GGTGCTTCCGCGTGGCATCC TGAC || |||||| ||| ||| ||||| ||||| ||||
GTTTGCTGCTTGACGGGTGA AG GGGCAG TTC TCG ACGGT CGCCT CGTG /
T - G TTTGCCT G T-- GC

GAM1555 AAACACAATCCCGACTCGGA 38672 GTAAATCCCA 38673 C - - C ATATATATA AA
ATATATATACGATAATAAAT GTTCGGGAAT AAACA AAT CCCGA CT GGA CGAT T
TGGTAAATCCCAGTTCGGGA TTTG ||||| ||| ||||| || ||| ||||
ATTTTGTTT TTTGT TTA GGGCT GA CCT GTTA /
T A T C AAATG---- AA

GAM1556 CTAGGGAAAACATAAGAATA 38679 GGGAAAACAT 38680 A AAA G AGAA GAG T
AAA AGA
GGAAGAAACCGAGGTTTGGG AAGAATAGGA CT GGGA CATAAGAATAG A ACC GT
TGGGAGA GCTG T
AGAAAAGCTGAGATAAAATA AGAA || |||| |||||||||| | ||| || ||||||| ||||
GCGCATTTTCCATACAGAGG GA TCCT GTGTTTTTGTT T TGG CA ACCTTTT CGAT
A
TTGTTGTTTTTGTGGATCCT A AG- G ---- AGA T ACG AAA
AAG

GAM1557 CTGCAACGCTGATTGATTAA 38777 TGATGTTGTT 38778 A C - ---- G G TC
AAGATGGTCTCCGATGATGA ATTGATCGAA CTGCA CG TGATT GATTAA AA AT GTC C
TGTTGTTATTGATCGAATCA TCAT ||||| || ||||| |||||| || || |||
TGGTGCAG GACGT GT ACTAA CTAGTT TT TA TAG G
G - G ATTG G G TA

GAM1558 TCTGCTCTGGTTGAGCGCGT 38781 TGAGAACTCG 38782 G TT C A-- G G CTT

CATTCGCGACATACCTTTAT GCTGCTCCCA TCT CTCTGG GAGCG GTC TTC C ACATAC T
AAGTATGTGAGAACTCGGCT GAGG ||| |||||| |||||| ||| ||| | ||||||
GCTCCCAGAGGAGA AGA GAGACC CTCGT CGG AAG G TGTATG A
G -- - CTC A - AAT

GAM1559 GCTATTAAGAGTGGTCCTCA 38814 TAGATGGTGA 38815 TATT - C AG G G
GACCATCGGTTTTGGTTGTA TGACTGTCTT GC AAGAG TGGTC TC ACCATC GTTTTGGTT T
GGACCAAGATAGATGGTGAT TTTA || ||||| ||||| || |||||| |||||||||
GACTGTCTTTTTACTGC CG TTTTC GTCAG AG TGGTAG TAGAACCAG A
TCAT T T -- A G

GAM1560 AGGTAATGATAAAACTATTG 38824 TTACACGATC 38825 TAAT AACT- - CT A T
GTCTAGATATGTAATCAAAT TAAATTATCC AGG GATAA ATTG GT AGAT TG A
CTTACACGATCTAAATTATC CATC ||| ||||| |||| || |||| ||
CCATCCT TCC CTATT TAGC CA TCTA AC A
TACC AAATC A T- A T

GAM1561 CATAGAAGTTCAAGTAAACC 38830 TTCAAGTAAA 38831 TTC-- AAA CT AT C - T - -
AAGA
CCTCATGGATTAGCCTCTTA CCCCTCATGG AGAAG AAGT CCC CATGG TAG CTC TTAGG
GGC TC TCTC T
GGTGGCTCTCTCAAGATAAA ATTA ||||| |||| ||| ||||| ||| ||| ||||| ||| || ||||
CGGAGATGACGCCTCTAATG TCTTC TTCG GGG GTGTC GTC GAG AATCT CCG AG
AGAG A
AGTCTGCTGTGTTGGGAAGC TTATT AA- TT -- T T - C T GCAA
TTTTATTCTTCTGTG

GAM1562 TATGACTAATCTAGATATGT 38837 TGACTAATCT 38838 --- AAT ATG
TAATTAGATATGACTAATCT AGATATGTTA TATGACTAATCTA GATATGTT TAGAT A
AGATATGTTAATTAGATTAG ATTA |||||||||||| |||||||| |||||
TCATA ATACTGATTAGAT TTGTATAG ATCTA /
TAA --- ATC

GAM1563 GTGAGAGTGAAGTGTAATGA 38841 AAACAGAAAT 38842 G A TGTAA CG GAA
TAAGTTT TTTATT
CCACGTGAAACAGAAATAAG AAGTTTAACT GT AG GTGAAG TGACCA T ACAGAAA
AACTTT A
TTTAACTTTTTTATTATTTT TTTT || || |||||| |||||| | ||||||| ||||||
TTTAAGGTTTGTTTTTTTTG CG TC CACTTC ATTGGT G TGTTTTT TTGGAA T
TATGTATGGTTAGTCTTCAC - - TG--- AT TA- TTTGT-- TTTTTT
CTGC

GAM1564 GTGTATTATTATAAAGTCCA 38853 TATAAAGTCC 38854 TA- TCC - TTA
TATCGGAGTTACTTTTCTCT ATATCGGAGT GTGTAT TTATAAAG ATATC GGAG C
AGGTATTTTTTATAACTTAT TACT |||||| |||||||| ||||| ||||
ACAC CACATA AATATTTT TATGG TCTC T

TTC T-- A TTT

GAM1565 CTCAAGAGACTCTTCCTCCA 38863 AAGACGTTGA 38864 G TTC- A GTC- GA T
GAGTTGTCCGTGATCGAAAT GACTCGGAGT CTCAA AGACTC CTCC GAGTT CGT TCGAAA
T
TCCTTTCGAAGACGTTGAGA TATG ||||| |||||| |||| ||||| ||| ||||||
CTCGGAGTTATGAGTTTATT GAGTT TTTGAG GAGG CTCAG GCA AGCTTT C
GAG A TATT - AGTT GA C

GAM1566 TCCCACAATCTCATTGGTCC 38868 TCATTGGTCC 38869 CA-- CC -- --- --- G C A --
A
AGAGCCCTCTCAGCCGCGCT AGAGCCCTCT ATTGGTC GAGC TC TCAG CC GC CT TG
TTGGTCGAGA GCT G
CTGATTGGTCGAGAGCTAGC CAGC ||||||| |||| || |||| || || || || |||||||||| |||
TGGCCCTCTCGACCAACCAT TAACCGG CTCG AG AGTT GG CG GA AC
AACCAGCTCT CGG C
AGGCCAGGGATTTTGATTGA CCGC AC TT TTA GAC - T C CC T
CAGCTCCGCCGGCCAATGAG
AACGCAGGGA
GAM1567 AACAAAGAAATGGAAATCGT 38885 TGGAAATCGT 38886 AG T TAATACC T
AATACCAGTTATGTTTAACT AATACCAGTT AACAA AAATGGAAA CG AGTTA G
TTGAAATTGTTTTTTATTTT ATGT ||||| ||||||||| || |||||
CTTGTT TTGTT TTTATTTTT GT TCAAT T
CT T TAAAGTT T

GAM1568 GAAAACACACAAATAGATGT 38889 TACTGTGTTA 38890 A ATAG TAT- AATGT-- GA
TT TGT
ATGTAGTAATGTTATGATAC ATAAACTACT GA AACACACAA ATG GTAGT TAT TACATA
TA T
ATATTTATGTTATTTATTTG TTTT || ||||||||| ||| ||||| ||| |||||| ||
TGTACTGTGTTAATAAACTA CT TTGTGTGTT TAT CATCA GTG ATGTGT AT /
CTTTTTATATGTTGTGTGTT C GTA- TTTT AATAATT TC TT TTA
CTC

GAM1569 TGAGTTGTTAAATCTTTACA 38897 TAAAACAACT 38898 TAAA- CAGG AG TT
GGTGTTTAGATTTTTCAGAT AGAGAAAAGT TGAGTTGT TCTTTA TGTTT ATT T
AAAACAACTAGAGAAAAGTA ATAA ||||||||| |||||| ||||| |||
TAACTCA ACTCAATA AGAGAT ACAAA TAG /
TGAAA CA-- A- AC

GAM1570 CCTCCCCTCCCTCTCCCTCG 38919 TGAGGAGGAG 38920 TCCC C G GG A
TCCTGGTCGGAAAAGTCTGA AAGGAGAATG CCTCCCC TCTCC TC TCCT TCGGA A
GGAGGAGAAGGAGAATGGGG GGGA ||||||| ||||| || |||| |||||
AGG GGAGGGG AGAGG AG AGGA AGTCT A
TA-- A - GG G

GAM1571 CCGAGACGAAGGCCCGTCTG 39185 AGGAAGTGGT 39186 GAAG- ---- TAGA A GC A C CC
TAGAGGAAGTGGTTGCGCAT TGCGCATGCG CCGAGAC GCC CGTCTG GGA GTGGTT GC TG GGG A
GCGGGCCAGCTCCCAGTAGA GGCC ||||||| ||| |||||| ||| |||||| || || |||
CCACGTCCCCCCAGACGCGC GGCTCTG CGG GCAGAC CCT CACCAG TG AC CCT /
AGGCACAGGGTCTCGG GGACA ACGC CCC- G A- - - CG

GAM1572 TCCCGGCACACATCCTGGAT 39211 TCCGTGGAGT 39212 G - A - TGC C C
GCCCTCCACGACGCTCTTTA AGTGGCGGGG TCCCG CAC AC TCC TGGA CCTCCA GACGCT T
GCGTCTGGAGGTCCGTGGAG ||||| ||| || ||| |||| |||||| ||||||
TAGTGGCGGGG GGGGC GTG TG AGG GCCT GGAGGT CTGCGA T
G A - T --- - T

GAM1573 GCAGATGCTCTTGCCTAGAT 39302 TGCCTAGATA 39303 T TG AGATA G TC
ACAGGATGTCGTCCATGCTG CAGGATGTCG GCAGATGC CT CCT CAG ATG G
AGGGGAGGTGGGGTGTCTGC TCCA |||||||| || ||| ||| |||
CGTCTGTG GG GGA GTC TAC /
- GT GGGGA G CT

GAM1574 AAATCTTCTAATTCCAAGAT 39315 TCCGCCTTTC 39316 C - CC A CC
GGATATTCCTAAGGTGTCCG AATATAGAGT AAAT TTCTA ATT AAG TGGATATT T
CCTTTCAATATAGAGTGTTT GTTT |||| ||||| ||| ||| ||||||||
TTTG GAGAT TAA TTC GCCTGTGG /
T A CT C AA

GAM1575 GTAAACGCTCGGCGACAACC 39323 TGTTTTGTAT 39324 CG ACC CT GCTGC AAA AA C- A CC
ACATCTAGAACAGCTGCTGC GTGTAACCTG GG ACA ACAT AGAACA TGCA AGG GCGCA CAAAA ATAG A
AAAAAGGAAGCGCACCAAAA TGTG || ||| |||| |||||| |||| ||| ||||| ||||| ||||
AATAGCCACATTTGTGTTTT TC TGT TGTA TTTTGT ATGT TCC TGTGT GTTTT TGTT C
GTATGTGTAACCTGTGTGTA A- A-- TT ----- GTG AA AT G TA
TGTTTTTTATGTATGTACTG
TGTGTGTAAT
GAM1576 TGGGCGAAGGCCTGCAGCTG 39343 AGCTGGTGAT 39344 C CAGC TG TC CTA -- CCA AT
GTGATTAGTTCCACTAGACG TAGTTCCACT TGGG GAAGGCCTG TGG ATTAGT CA GAC GGGCA CGG C
GGCACCACGGATCCTACCGA AGAC |||| ||||||||| ||| |||||| || ||| ||||| |||
TGCCCAAGTTATTTGCCACT ACCC TTTTCGGAC ACC TAGTCA GT TTG CCCGT GCC C

GATGTCCATCCAGGCTTTTT T CT-- TG CC TTA AA A-- AT
CCCA

GAM1577 GATCTAGATTCTATTGTTAA 39359 TCTATTGTTA 39360 CT- TTAAAAG AAA TC AAT
AAGGAAAAATGTATCGATAA AAAGGAAAAA GAT AGATTCTATTG GAA TGTA GAT A
TAAACCATTTTTACAGAGTT TGTA ||| |||||||||| ||| |||| |||
CAGCATCGGTGGAATCTTAA CTA TCTAAGGTGGC CTT ACAT TTA A
ATC AAT TACGA-- GAG TT CCA

GAM1578 GTCCGCCGTCTAGGTAAGTT 39371 TCTAGGTAAG 39372 C C-- AAGTTT A -- TC A-
CC
TAGAGCTCAGGTCGAGACCG TTTAGAGCTC GTC GC GTCTAGGT AG GCTC AGG GAG
CCGGG T
GGCCTTTGTCCGGCGCTCCC AGGT ||| || |||||||| || |||| ||| ||| |||||
TTGGAGCCTACCTAGACTCA CGG CG CAGATCCA TC CGAG TCC CTC GGCCT T
GCCGGC C ACT ------ - GT -- GC GT

GAM1579 GGGAAACGAAAACAAGGAAG 39378 ACGAAAACAA 39379 AA AAA AAGA AG-- AT
ATGTAGCAATGTATGAAAAG GGAAGATGTA GGG ACGA CAAGG TGT CA G
CAAGGGTCTTGAGATCGTAC GCAA ||| |||| ||||| ||| ||
CTC CTC TGCT GTTCT ACG GT /
CA AGA GGGA AAAA AT

GAM1580 GAAAAAAGATGACTGGGAAG 39463 AAGATGACTG 39464 A AT CT C-- GT
CTATCCGTATTGTGTTTGAT GGAAGCTATC GAAA AAG GACTGGGAAG ATC GTATT G
ACATAGATTCTTCTCGGTCC CGTA |||| ||| |||||||||| ||| |||||
TTGTTTT TTTT TTC CTGGCTCTTC TAG CATAG T
G -- T- ATA TT

GAM1581 GTCTCCCCCCGGAGGACAGC 39474 CGTGTCCCCC 39475 CCCCCC A GC CA - T
TCAGCACCAGCTCAGGCTAG TAAAGAC GTCT GG GGACA TCAG CC AGC C
GCCCTGACGTGTCCCCCTAA |||| || ||||| |||| || |||
AGAC CAGA CC CCTGT AGTC GG TCG A
AATC-- - GC CC A G

GAM1582 GATGCAGGATTACCATTAAT 39482 CTAAAGCTAT 39483 CA- CCATTAATC AC
CTTAGGAAACAACTTCCTAA ATAATCCGTT GATG GGATTA TTAGGAA A
AGCTATATAATCCGTTCATC CATC |||| |||||| |||||||
CTAC CCTAAT AATCCTT /
TTG ATATCGA-- CA

GAM1583 TCTTGCTCGACGTGCCGCGT 39495 CGAGATGGGC 39496 T T -- GGAGAA -- A
TC C
CTGGAGAACTATTTTCTTTG GAGGAGATGC TCT GC CGACGTGCC GCGTCT CTATTT
TCTTTGTC AG TGT T

TCAAGTCTGTCTTTACGAGC TGGG ||| || ||||||||| |||||| |||||| |||||||| || |||
TGGACGAGGACGAGATGGGC AGG CG GTTGTACGG CGTAGA GGTAGA
AGGAGCAG TC GCA T
GAGGAGATGCTGGGCATGTT C - GT GGAGCG GC G GA T
GGCCGGA

GAM1584 TAGCCTTGCATATATTGATG 39555 TTGATGATAT 39556 T A TAT ATAA AC
ATATAATTGTTTTTACTAAG AATTGTTTTT TAGCCT GC TA TGATGAT TTGTTTTT T
GGAACAAAAGATTATCATCT ACTA |||||| || || ||||||| ||||||||
TAAGCAGGTTG GTTGGA CG AT ACTATTA AACAAGGG /
- A TCT GAA- AA

GAM1585 GACGACGTGGTTTTTGCTTC 39563 CAGCGGTCGT 39564 -- TTT TT GA TTT
CGAGCTGTGTTTTTATTGCA TTTAACCGCA GACGAC GTGGTT GC CC GCTGTG T
GCGGTCGTTTTAACCGCAGG GGTC |||||| |||||| || || ||||||
TCGTC CTGCTG CGCCAA TG GG CGACGT /
GA TTT CT -- TAT

GAM1586 GGCGCTCGCACGAGGAGCTG 39570 TCTAGCGCCG 39571 - - A- A ---- TG CGC
GTTCTTTGTCCGCCCGAGAT CTGTTGCAGA GGCGCTC GCA CG GG GCTGG TTCTT TC C
GGAGGAGCGTCTAGCGCCGC GTGC ||||||| ||| || || ||||| ||||| ||
TGTTGCAGAGTGCC CCGTGAG CGT GT CC CGATC AGGAG AG /
A T CG G TGCG GT AGC

GAM1587 GTGATTTATTGATATTAACT 39577 TGGCAGTACC 39578 TTAT TT ACAG-- TAGTGA A-
G
ACAGATGCTAGTGATACTAC TAATGCATAC GTGAT TGATA AACT ATGC TACT
CATGGGGA C
ATGGGGAGCAGTCCTTATGG GAAG ||||| ||||| |||| |||| |||| |||||||||
CAGTACCTAATGCATACGAA CACTG ACTAT TTGA TACG ATGA GTATTCCT A
GAGTTTTTATCATTTGTCAC TTT- TT GAAGCA TAATCC CG G

GAM1588 GTGGTGGCATTGATGACTTT 39586 TACATGTTGG 39587 GAT GC- ACTCC TG TT GC -
- ATT G
GTGCGCTACTCCGCTTTGGT TGAGGTTGTC GACTTTGT GCT GCTT G GA GCCTCAT
ACGTG TACCT C
TGAGCGCCTCATACGTGATT TCCT |||||||| ||| |||| | || ||||||| ||||| |||||
TACCTGCTCAGGTACATGTT CTGAGACA CGA CGGA C CT TGGAGTG TGTAC
ATGGA T
GGTGAGGTTGTCTCCTGAGG CAT GGA AA--- GT CT GT GT --- C
CAAAGCAGGACAGAGTCTAC
TATACCGCTAC
GAM1589 GAGTATTGAAGTTCAAATCA 39602 TGTTGGGTAG 39603 TT TTCAAATCA T- A AG CT T
- - TAA TT
ACCCTTCATGGATAAGTCTG CTCCCTTAAG GAAG ACCCT CATGG TA T GTTGGG AGC
TC CCT G A

TTGGGTAGCTCCCTTAAGTT TTAA |||| ||||| |||||| || | |||||| ||| || ||| |
AAACGTAGGTGATGCTTCCA CTTC TGGGG GTGTC GT G TAACCT TCG AG GGA
C /
ATGAGTCTGCTGTGTTGGGG -- C-------- TT - CT AG - T T TG- AA
TCCTTCTACTC

GAM1590 GGCTATCAAGAGTGGACCTA 39607 TAAGATCGAT 39608 TA - TG A AC G
CTACTATTGGTTTTGGTTGT GGTGAGGACT GGC TCAA GAG G CCT TACTATTGGTTTTGGTT
T
AGAACTAAGATCGATGGTGA GCTT ||| |||| ||| | ||| ||||||||||||||||
GGACTGCTTATTGACTGCC CCG AGTT TTC C GGA GTGGTAGCTAGAATCAA A
TC A GT A -- G

GAM1591 GAGTCCTCCCGCGCCGGACT 39612 TCGCACCGGG 39613 - -- CGC GA TG - AC C
TGGCGCCACTCCCGGGAAGG CTGGGTACTC GAGT CCT CCCG CG CT GCG CC TC C
GCCGCTGAGCTCGCACCGGG |||| ||| |||| || || ||| || ||
CTGGGTACTC CTCA GGG GGGC GC GA CGC GG AG G
T TC CAC TC GT C GA G

GAM1592 TCTTAAGGTCTAATGAGACT 39660 TGTTGAGACC 39661 GG T A TCCCA- AG TC
TG T
CTCCCACCGGAGCTTTCCAT CGGAGTTATG TCTTAA TC AATGAG CTC CCGG CTT
CATTAT AAA A
TATTGAAATACCTTTTGATG AGTT |||||| || |||||| ||| |||| ||| |||||| |||
ATGTTGAGACCCGGAGTTAT AGAGTT AG TTATTT GAG GGCC GAG GTAGTA TTT C
GAGTTTATTGAGGTTGAGA GG - - TATTGA CA TT GT C

GAM1593 GGTAGAGGTAAGGCTAAACT 39664 AGAGGTAAGG 39665 TA AA- AAA G AAG G --- -
-- C
TGGTAAGCGTGAGTTCGCTT CTAAACTTGG GG GAGGT GGCT CTT GT CGT AGTTC
GCTTG GATT C
GGATTCCAGAATCAGGCAAG TAAG || ||||| |||| ||| || ||| ||||| ||||| ||||
TACTGGGCTGATGAGGATGA CC CTCCA TCGA GAA TA GTA TCGGG TGAAC
CTAA A
AGATGAGCTGCCACCTCCTC TC CCG GTA G GGA G TCA GGA G
C

GAM1594 CTCAGGCATATGGAGGAGTA 39687 TGTGCAAAAT 39688 CATATG AG GATTT CAT
TGATTTGCAGTTCATTTTCC AACCCTCACT CTCAGG GAGG TAT GCAGTT T
AACTGTGCAAAATAACCCTC CCTG |||||| |||| ||| ||||||
ACTCCTGAG GAGTCC CTCC ATA TGTCAA T
TCA--- CA AAACG CCT

GAM1595 GTTGCCAGCACAGCTTAATC 39703 TAAAGTGTTA 39704 CA T TC AT- C
CTTTAATTGCTCACATCCTA GCTGTGCCAG GTTGC GCACAGCT AA CTTTA TG T
AAGTGTTAGCTGTGCCAGCA CAAC ||||| |||||||| || ||||| ||

AC CAACG CGTGTCGA TT GAAAT AC C
AC - GT CCT A

GAM1596 GCATTCCTAGGCTGATTATG 39728 TGTGTTGGCA 39729 TCT ---- A- TTTCT T ----------
- A
GTTCTGTGTTGGCACAGATT CAGATTTCTA GGT GT GTTGGC CAGA AC GCGTCT
GCAGG A
TCTACTGCGTCTGCAGGAAA CTGC ||| || |||||| |||| || |||||| |||||
ACCTGCAGCAACAGCACTTT CCG CA CAACCG GTCT TG CGCGGG CGTCC
A
GGGCGCGTCGTTTCTGCAGC TT- CTTT AC TTGC- - TTTCACGACAACGA A
CAACTTTCACTTGCCAACTT
GTCTTGCCGC
GAM1597 GAGAACTTCTAAATCAGGGC 39744 TTAAACGATC 39745 A AAATCA CATGCG A AA
ATGCGAAAAGTAATTACGCT CAGCAAGAGA GAG ACTTCT GGG AA AGT T
CTTAAACGATCCAGCAAGAG AGTA ||| |||||| ||| || |||
AAGTATTC CTT TGAAGA CCT TT TCG T
A GAACGA AGCAAA C CA

GAM1598 CGTGTATTTCACGTTAAGCT 39749 TTTCACGTTA 39750 TT - A T- CCC
GCCAGATCCCAATAAATTTG AGCTGCCAGA CGTGTA TCA CGTTA GC GCCAGAT A
GCCTGCCTGATGCTGACCTA TCCC |||||| ||| ||||| || |||||||
TATG GTATAT AGT GTAGT CG CGGTTTA A
CC C C TC AAT

GAM1599 GGTTAGTATATACTTGATCA 39769 TACTTGATCA 39770 GTATA T GA A- TACG TC
TCGATTCAATGTACGGCTCA TCGATTCAAT GGTTA TAC TGATCATC TTCA TG GC A
AGGTAATCAACTGAAGAGAT GTAC ||||| ||| |||||||| |||| || ||
GATTATGTGGATAACC CCAAT GTG ATTAGTAG AAGT AC TG /
AG--- T AG CA TAA- GA

GAM1600 CGCCGACTCCGTCCGCAGAG 39782 AGCGGAAACT 39783 - CCGCA - A G A GGAA
AACG CAC T
GCGGCGACCGCAGCGGCAGC GTAACGGCCA T CCGT GA GGCGGCGACCGC GC GC GC
ACTGT GC GTTC C
GGAAACTGTAACGGCCACGT CGTT | |||| || |||||||||||| || || || ||||| || ||||
TCTCCGAACAGCGACAGTAA A GGCA CT CCGCTGTTGGCG CG CG CG TGACA CG
CAAG /
CGGCGGCGGCGGCGGTTGTC T ----- G G G G GCAA G--- A-- C
GCCGTCACGGTAGTCGTGGC
G
GAM1601 GACTACACCAATAGGAACAG 39787 ATGGCAGAAT 39788 CA--- TAGGAA GCAA- AATA
AGCAACCATTTAATAATGAA TTGATATTTG GACTA CCAA CAGA CCATTT A
AAATGGCAGAATTTGATATT GGAA ||||| |||| |||| ||||||
TGGGAATATAGTT TTGAT GGTT GTTT GGTAAA /
ATAAG TATA-- AAGAC AAGT

GAM1602 CCGTGCACGTCCCGGTTTTA 39810 TAGCGGGAGT 39811 A TCCC- TT- CG T G CG AC AACAA- AA
GCGGGAGTGTGTGCGCGCGT GTGTGCGCGC CCGTGC CG GGT TAG GGAGTG GT CG CGT CGT GG A
ACCGTAACAAGGAAAACCCA GTAC |||||| || ||| ||| |||||| || || ||| ||| ||
GCGGGACGAAACGATCGACC GGCACG GC CCG ATC CCTCAC CA GC GCA GCA CC /
CACTCCTACTATCCGCCCTC A CCCTC CCT AT C - TA AA GGGCGA CA
CCCGAGCACGG

GAM1603 AAGTATACGAACTTTCCGTT 39830 TAACAATAAT 39831 T AC CGTT AATT TTTATTTAATAA ATAA
AACAATAATTCAATTTTATT TCAATTTTAT AGTA ACGA TTTC AACAAT CAAT AGTATTTTT A
TAATAAAGTATTTTTATAAA TTAA |||| |||| |||| |||||| |||| |||||||||
CATCAGAAATATTAACATCT TCAT TGCT AAAG TTGTTA GTTA TTATAAAGA /
TTATATTGTTCAATTGTTTT - AC ATT- ACTT TATTTCTACAA- CTAC
AGAAACATCGTTACTT

GAM1604 TCGCCGTACGAAAAGAGTAC 39835 TTTGTAAATA 39836 GC GAAAAGAGTACCGAA TTA
CGAATGCAAAAAGTTAAAGG AAAAAAAAAT TC CGTAC TGCAAAAAG A
TTTTTTGTAAATAAAAAAAA AGTA || ||||| |||||||||
AATAGTACGTGGA AG GCATG ATGTTTTTT /
GT ATAAAAAAAAAATAA GGA

GAM1605 AAGGGATATTGAGCTGTTAG 39843 TTAGTGATTC 39844 A A -- A--- -- TT TTG
AGTACGAAACTGACATTTCT GGTTCATTTT AAGGG TATTG GCTGT TAGAGT CGAA ACTGACA TC A
TGACCTTGGTTGTTAGTGAT GAAG ||||| ||||| ||||| |||||| |||| ||||||| ||
TCGGTTCATTTTGAAGCAGC TTCTC ATGAT CGACG GTTTTA GCTT TGATTGT GG C
GTAGTAACTCTT A G AA CTTG AG T- TTC

GAM1606 GATATGTTTATTCATAAACG 39849 TCGCTAAGGA 39850 TTT A ------ -- AATT
CGTCAAATTTTTCATGAATC GTTTAAGAAT GATATG ATTC TAAAC GCG TCA T
GCTAAGGAGTTTAAGAATCT CTCA |||||| |||| ||||| ||| |||
CATGTC CTGTAC TAAG ATTTG CGC AGT /
TC- A AGGAAT TA ACTT

GAM1607 TTTTCAAATCCATTTGTGAG 39860 TACCTTTTCT 39861 CAT- TC- GC
AAGTCTATCGCCTTAGATAC CGTAGTCGAG TTTTCAAATC TTGTGAGAAG TATC C
CTTTTCTCGTAGTCGAGGTT GTTT |||||||||| |||||||||| ||||
TGAAGA AGAAGTTTGG GATGCTCTTT ATAG T
AGCT TCC AT

GAM1608 CCCGTTGGGATAGCTGAGCC 39866 TACCATGGCT 39867 C C CC T- AATCC T CTTCC
T TG T G
GCGGTCCGTGTTGAAATCCA CACCGTGACG TGAGCCG GGT GTG TGA ATCTTC GTG
GATG GG CG TTC T
TCTTCTGTGCTTCCGATGTG GG ||||||| ||| ||| ||| |||||| ||| |||| || || |||
GTGCGTTTCGTTGAACCGTG ACTCGGT CCA TAC ACT TGGAGG CAC CTGC CC
GC AAG /
CCCGTCAACACCGGAGGTCA - A -- CC CTAC- C AA--- - GT C T
TCTCACCCATACCATGGCTC
ACCGTGACGGG
GAM1609 AATGGTAGCGCGTCTTTAAC 39901 TTTGATCGAG 39902 A - TCTTT - TT CT
TCGTCGGTTAGCTCTTTCTT TTCGTCGCCA AATGGT GCG CG AACTCG TCGG AG C
TTGATCGAGTTCGTCGCCAC CTAT |||||| ||| || |||||| |||| ||
TATT TTATCA CGC GC TTGAGC AGTT TC T
C T ----- T T- TT

GAM1610 GAAGATCGAGAAGAGAAAAG 39904 GACTATGTAT 39905 G GAA AAA-- AT GA TAATA T
TACAATGTGAAGTAATAGCT TGGTAGCTCC GAA ATCGA GAG AGTACA GT AG GC A
ACTGCCCTGGACTATGTATT TGTC ||| ||||| ||| |||||| || || ||
GGTAGCTCCTGTCGATATTC CTT TAGCT CTC TTATGT CA TC CG C
A GTC GATGG AT GG C---- T

GAM1611 GAAGTAGCGAACCTCTGCTC 39915 TGAGCAGGAG 39916 T - CT G C
ACTGCCCGGGCCCTCCGGGA TTGCGCTTTT GAAG AGCG AAC CTGCTCACT CCCGGG C
GGTGAGCAGGAGTTGCGCTT C |||| |||| ||| ||||||||| ||||||
TTC CTTT TCGC TTG GACGAGTGG GGGCCT /
- G AG A C

GAM1612 CCCTACAGAAAAGATAATGG 39958 TGAAGGCCTT 39959 C AAA AAT- AC ---- AC
CTACCATCCACAAGGGATTA AGATCTGAGC CCCTA AG AGAT GGCT CA TCC A
CTGAAGGCCTTAGATCTGAG TTGG ||||| || |||| |||| || |||
CTTGGGG GGGGT TC TCTA CCGG GT AGG /
- GAG GATT AA CATT GA

GAM1613 GGGGACCAGTTCTGATAGTG 39974 TGATAGTGAC 39975 AC G- A AGA T
ACAGATAGTAATTATGTTGC AGATAGTAAT GGGG CAGTTCT AT GTGAC TAGTAAT A
TAAGAGTTATAATGAAGAAT TATG |||| ||||||| || ||||| |||||||
TGCCCT TCCC GTTAAGA TA TATTG ATCGTTG /
-- AG A AGA T

GAM1614 GCGGCACACCAGAAACTTGC 39978 TTGCCCAAGT 39979 C CAGAAAC AAACTC - A
ACAAACTCCGGATTCAGCAG GCAACACCGT GCGG ACAC TTGCAC CGGATT C G
AAATTTGCCCAAGTGCAACA GTCC |||| |||| |||||| |||||| |
CCGTGTCCGC CGCC TGTG AACGTG GTTTAA G C
- CCAC--- AACCC- A A

GAM1615 AGAGGGGGAGTGTGTGGTCT 39992 GATCGGCAGA 39993 TGTGT A GA A
GTAGAGAGACATGAGTTGAT CCCCCTCTCC AGAGGGGGAG GGTCTGT GA GAC T
CGGCAGACCCCCTCTCCCCC CCCT |||||||||| ||||||| || |||
TCT TCTCCCCCTC CCAGACG CT TTG G
TCCC- G AG A

GAM1616 TCTCACCCTGACAGCTGTCA 40022 CCTGACAGCT 40023 CC---------- AG
GGGGTTACATGAGAGAACTT GTCAACCTAA TCTCAC
TGACAGCTGTCAGGGGTTACATGAG A
CATGTAACCCCTGACAGCTG TCCT |||||| ||||||||||||||||||||||||
TCAACCTAATCCTGACCGTG AGAGTG ACTGTCGACAGTCCCCAATGTACTT /
AGA CCAGTCCTAATCCA CA

GAM1617 GCATTGTTTACAGCAGATGT 40043 CAGCAGATGT 40044 ATT GC AG CTTGAA AC
CGTAGACATCTTGAAGGACA CGTAGACATC GC GTTTACA AGATGTCGT ACAT GGACAT
C
TACCAAATGTTCAGGTATAT TTGA || ||||||| ||||||||| |||| ||||||
GTGGATGACGTCTATGTGAG CG CGAGTGT TCTGCAGTA TGTA CTTGTA /
CTCAGC ACT A- GG TATGGA AA

GAM1618 GACACTTTGCCAGCGGTTGT 40067 TTTGCCAGCG 40068 CT CC T-- ATTTATCA
AGATTTATCATATTTCTCCA GTTGTAGATT GACA TTG AGCGG TGTAG T
CTACATATCCGTTACAATTT TATC |||| ||| ||||| |||||
GTT TTGT AAC TTGCC ACATC A
TT A- TAT ACCTCTTT

GAM1619 GTAAGGGTACTCTCATCACC 40075 AAGGGTACTC 40076 --- --- T T AAATTAAT
AATGTAAATTAATATGTAGC TCATCACCAA GTAA GGGT ACTCTCA CACCAA GT A
AAACTTTGGTGTGGGAGTCC TGTA |||| |||| ||||||| |||||| ||
TACCCCTTTTGC CGTT CCCA TGAGGGT GTGGTT CA /
TTC TCC - T AACGATGT

GAM1620 AGGGCAATGCTCTAGCAGAT 40084 TAGCAGATAA 40085 AA T AGATAAA- A -- ---------
- A
AAACAAGCTGTTTCAGGAAG ACAAGCTGTT AGGGC TGCTC AGC CA GCT GTTTCA
GGAAG CT T
CTATAAGGTCTTCTCAAATG TCAG ||||| ||||| ||| || ||| |||||| ||||| ||
AATTGAAACCCAGCCTGGAT TCCTG ACGAG TCG GT CGA CAAAGT TCTTC
GG A
GCAGAGCTTGAGCAAGTCCT A- T AGACGTAG C CC TAAGTAAAC T A

GAM1621 GGCCAGGGTAGCTCAATCGG 40108 TTCTCGGTTC 40109 A--- C- GT - - C

TAGAGCAGCGGTTCCTGGAG AAGCCCGAGC GGCCAGGGT GCT AATCG AGAGC AGCGG TTC T
TCCGCTGGTTCTCGGTTCAA CCTG |||||||||| ||| ||||| ||||| ||||| |||
GCCCGAGCCCTGGTT TTGGTCCCG CGA TTGGC TCTTG TCGCC GAG /
AGCC AC -- G T G

GAM1622 TCTGAATAAAACATCAATGT 40131 TAAAACATCA 40132 ATAA--- CAAT ---- A G
CGCAATTTGTATTGTCCAAT ATGTCGCAAT TCTGA AACAT GTC GCA TTTGTATT T
ACAGAATGTCTATGATTCGT TTGT ||||| ||||| ||| ||| ||||||||
GTTAAAACCATCGGA AGGCT TTGTG TAG TGT AGACATAA C
ACCAAAA CT-- TATC A C

GAM1623 AGAGACTGTGATGGGGCAGC 40137 ACTGTGATGG 40138 T A TAC CGA CTCGACAACTA GT TA A G
CTACTCCGAAGACCCCTCGA GGCAGCCTAC GGGGC GCC TC AGACCC AGGGA TCC GGG CGGCAG C
CAACTAAGGGAGTTCCTAGG TCCG ||||| ||| || |||||| ||||| ||| ||| ||||||
GACGGCAGGCTTCTGTCGCC CCCCG CGG AG TTTGGG TCCCT AGG TCC GCTGTC T
TCTGGATCCCTGGGTTTGCA C A TAA ACG ---------- -- TC - T
GAAATGGCAGCCCCCTTGTA
CCCTCT
GAM1624 TTTGTATTTCCCTGTGTCGT 40151 AAAGATGAGA 40152 CC- T - TGG CG T
TCGTGGTCTCGTTCGTGATT GTTGAAATGC TTTGTATTTC TGTG CGTT CG TCTCGTT TGA T
TTTTAAAGATGAGAGTTGAA TACA |||||||||| |||| |||| || ||||||| |||
ATGCTACATATGAAATATAG AGATATAAAG ACAT GTAA GT AGAGTAG ATT T
A TAT C A TG- AA T

GAM1625 GGCATATATTCCTGATCCGC 40190 ATAGAGAAAT 40191 TCCTGATCCGC GA A TA
CAATGATTCAATCCTTAGGA TGTACCTGTA GGCATATAT CAAT TTC ATCCT G
TGGGATAGAGAAATTGTACC TATG ||||||||| |||| ||| |||||
TGTATATGTT TTGTATATG GTTA GAG TAGGG G
TCCAT------ AA A TA

GAM1626 TATATACGATAAGATATGTT 40198 TAAGATATGT 40199 C --- TTT A G CAA-- TT
TATTCATAAACGCGTCAAAT TTATTCATAA TATATA GATAA GATATG ATTC TAAAC CGT ATTT C
TTTTCATGAATCGCTAATGA ACGC |||||| ||||| |||||| |||| ||||| ||| |||||
GTTTAAGAATCTCATGTCAA ATATAT CTGTT CTGTAC TAAG ATTTG GTA TAAG /
ATTGTCCTATATA C AAA TC- A A ATCGC TA

GAM1627 GCTGTCATTAAATATTTATC 40201 TAAACTGTTC 40202 CATTAAATA C CTA - AA- TA A- CT
ATCTAAACTGTTCTAATTGT TAATTGTATA GCTGT TTTAT AT AACT GTTCT TTG TACTT CTAA G

ATACTTACTAACTGTATTAG CTTA ||||| ||||| || |||| ||||| ||| ||||| ||||
AGGAGTAGCCAAAGGAGAAC CGACA AAATG TA TTGA CAAGA AAC ATGAG
GATT /
AAGTTATCATAGTAAAACAG --------- A CTA A GGA CG GA AT
C

GAM1628 AATGGTAGCGCATCTTTAAC 40215 TTTGATCGAG 40216 C CTTT - TT CT
TCGTCAGTTAGCTCTTTCTT TTCGTCGCTA AATGGTAGCG AT AACTCG TCAG AG C
TTGATCGAGTTCGTCGCTAC CTAT |||||||||| || |||||| |||| ||
TATT TTATCATCGC TG TTGAGC AGTT TC T
- C--- T T- TT

GAM1629 TAGGGGACCTCGGATATCGG 40219 TTTGCCAGAA 40220 -- CG C---------- CAA
GCCTCGGCCAAGAAAGCCCA ACAGGTCAAG TAGGGGA CCTCGGATAT GGCCT GGC
G
AATTTGCCAGAAACAGGTCA TATC ||||||| |||||||||| ||||| |||
AGTATCTGGGGTATCTTCTA ATCTTCT GGGGTCTATG CTGGA CCG /
AT AA CAAAGACCGTTTAAAC AAA

GAM1630 CTGAGGAGGGGCTGCAACAT 40238 TCTTACGGAC 40239 A CAACATGACTG T C T -
AAG C
GACTGCCTTGACATCTTGGC CAGCCTCTCC CTG GGAGGGGCTG CC TGA ATCT GG CTG
CC A
TGAAGCCCACGGAACTAGAC CAG ||| |||||||||| || ||| |||| || ||| ||
CAGATCTTACGGACCAGCCT GAC CCTCTCCGAC GG ATT TAGA CC GAT GG /
CTCCCAG - CA--------- C C - A CAA C

GAM1631 GTTACTATTATTTATAACTG 40266 TATTATTTAT 40267 AT--- TAA A C
ATGTAACCCACGTAACATTA AACTGATGTA GTTACTATT TTA CTGATGT AC C
GAATTAATTATCGATAGTAA ACCC ||||||||| ||| ||||||| ||
T TAATGATAG AAT GATTACA TG A
CTATT TAA A C

GAM1632 CGCGCACATCTGCCGTCTGC 40279 TGCTGTTGGG 40280 ACAT C - - AA - C T GT
GCAACACCGCGTCCGTCAAG GCGCAAGAGC CGCGC CTG CG TCT GCGC CA C GCG CC C
GTGCTGTTGGGGCGCAAGAG GACA ||||| ||| || ||| |||| || | ||| ||
CGACAGCGAGCGCG GCGCG GAC GC AGA CGCG GT G CGT GG /
AGC- A G A GG T T - AA

GAM1633 GAGACTGTGATGGGGCAGCC 40289 TGTGATGGGG 40290 - A TAC CGA CTCGACAACTA
GT TA A G
TACTCCGAAGACCCCTCGAC CAGCCTACTC GGGGC GCC TC AGACCC AGGGA TCC
GGG CGGCAG C
AACTAAGGGAGTTCCTAGGG CGAA ||||| ||| || |||||| ||||| ||| ||| ||||||
ACGGCAGGCTTCTGTCGCCT CCCCG CGG AG TTTGGG TCCCT AGG TCC
GCTGTC T

CTGGATCCCTGGGTTTGCAG C A TAA ACG ---------- -- TC - T
AAATGGCAGCCCCCTTGTAC
CCTCTC
GAM1634 GGCGGCGATCTTCCACGCGC 40305 ACGCGCTCCT 40306 ATCTT CGCG AACG- A AC
TCCTCAACGCCACGACGTAC CAACGCCACG GGCGGCG CCA CTCCTC CC CG G
CGGGACCTGGAGGAGGACTG ACGT ||||||| ||| |||||| || ||
GCGCCGCC CCGCCGC GGT GAGGAG GG GC T
----- CAG- GTCCA - CA

GAM1635 TATATACGATAAGATATGTT 40313 TAAGATATGT 40199 C --- TTT A ------ -- AATT
TATTCATAAACGCGTCAAAT TTATTCATAA TATATA GATAA GATATG ATTC TAAAC GCG
TCA T
TTTTCATGAATCGCTAAGGA ACGC |||||| ||||| |||||| |||| ||||| ||| |||
GTTTAAGAATCTCATGTCAA ATATAT CTGTT CTGTAC TAAG ATTTG CGC AGT /
ATTGTCCTATATA C AAA TC- A AGGAAT TA ACTT

GAM1636 AGCGGTTGTAGATTTATCAT 40314 TAAGAATTTA 40315 T T ATAT CC TACATATCC
ATTTCTCCACTACATATCCG GATACATCTA AGCGGT GTAGAT TATC TTCT AC G
TTACAATTTGTTAAGAATTT TATT |||||| |||||| |||| |||| ||
AGATACATCTATATTGCT TCGTTA TATCTA ATAG AAGA TG /
- C ATTT AT TTTAACATT

GAM1637 CTGGGGCCTTGGCGTCGGCC 40321 TGGCGTCGGC 40322 - CTT C G T CT- CAAA
GGTGGCCTACCTGTCCAAAA CGGTGGCCTA CTG GGGC GG GTCG CCGGTGGCC AC GTC
A
AGCTAGACCCAGTGGCCGCT CCTG ||| |||| || |||| ||||||||| || |||
GGGTGGCCCCCTTGCCTACG GGC TCCG CC CGGT GGTCGCCGG TG CAG A
G A TTC C G - ACC ATCG

GAM1638 CTGAGGAGGGGCTGCAACAT 40329 TCTTACGGAT 40330 A CAACATGACTG T C T -
AAG C
GACTGCCTTGACATCTTGGC CAGCCTCTCC CTG GGAGGGGCTG CC TGA ATCT GG CTG
CC A
TGAAGCCCACGGAACTAGAC CAG ||| |||||||||| || ||| |||| || ||| ||
CAGATCTTACGGATCAGCCT GAC CCTCTCCGAC GG ATT TAGA CC GAT GG /
CTCCCAG - TA--------- C C - A CAA C

GAM1639 TGGCACGTGTACATATACCA 40341 TAGTATGTCT 40342 A T - AA-- AT
AAAGGCATTGTAGCCACACT ATGGTTA TGGC CGTG ACATAT ACCAA GGC T
TGGTAGTATGTCTATGGTTA |||| |||| |||||| ||||| |||
ATTG GTAT TGTATG TGGTT CCG G
- C A CACA AT

GAM1640 GTTTAAAAAATCCAAAATTC 40346 TCCAAAATTC 40347 A C--- A T A

TTAATAGAAATTTATTGTGA TTAATAGAAA GTTTA AAAATC AAA TTC TAATAG A
AATTTAAAAGATTTTGTAAA TTTA ||||| |||||| ||| ||| ||||||
T TAAAT TTTTAG TTT AAG GTTATT A
G AAAA A T T

GAM1641 CCGCAGAGTGTTCCGGATTG 40352 TCCACAACAA 40353 - CC G ----- G
CAGGTTTGGGCAACCTGTAT CTCTGCGG CCGCAGAGT GTT GGATT CAGGTTT GG C
GAATTTGGAGTCCACAACAA ||||||||| ||| ||||| ||||||| ||
CTCTGCGG GGCGTCTCA CAA CCTGA GTTTAAG CC A
A CA G TATGT A

GAM1642 TCAACAATGGAGATGACAAC 40375 AGACAGGAAC 40376 - GAGA - ACG A TCCG-
AGTGG
GTCCTGATCTGTCCGGCAGT TGTACAGACA TCAAC AATG TG ACA TCCTG TCTG GC A
GGAGGTAGGCAGAGTCAGAC TTGG ||||| |||| || ||| ||||| |||| ||
AGGAACTGTACAGACATTGG AGTTG TTAC AC TGT AGGAC AGAC CG /
TTGA G AG-- A CA- - TGAGA GATGG

GAM1643 GAAATATTCCCAAGATTCGG 40402 TCCCAAGATT 40403 A- TT AGAT G CAG
GATGCCACAGGTATTGGGTT CGGGATGCCA GAA TA CCCA TCGGGAT CCA G
CCGATAATGGGCCTGCCTTC CAGG ||| || |||| ||||||| |||
CTT GT GGGT AGCCTTG GGT /
CC CC AAT- - TAT

GAM1644 AGAGTGGCTTGGGGTGCAGT 40428 CGGCACCCCA 40429 -------- AGTCTCG C
CTCGGCGCACACGTGCGCGG AACTCCGTAG AGAGTGGCT TGGGGTGC GCGCA A
CACCCCAAACTCCGTAGCCA CCAC ||||||||| |||||||| |||||
CTTT TTTCACCGA ACCCCACG CGCGT C
TGCCTCAA G------ G

GAM1645 TAGTGGTGTTTGAGCGTGGT 40470 TTTGAGCGTG 40471 TG GTTT TG - T
GATGTAGGTCTTTTTACTAT GTGATGTAGG TAG GT GAGCG GTGAT GTAGG C
TATTTTGCTTTTAATTGTTA TCTT ||| || ||||| ||||| |||||
ATT TA TTCGT TATTA CATTT T
GT ATT- TT T T

GAM1646 CGAGAGACGTTTCTCGCTTA 40474 TGAGAAAGCG 40475 - ACGT - A - - - CA
CTATACAGGGCCAAAGCGCA GTGAATTCCC CG AGAG TTC TCGCTT CT ATACA GG GC A
CCATGTATGAGAAAGCGGTG TCTA || |||| ||| |||||| || ||||| || ||
AATTCCCTCTACG GC TCTC AAG GGCGAA GA TATGT CC CG A
A CCTT T A G A A CG

GAM1647 GAGACCTAGCAGACTTCCGG 40508 CAGCACCCAG 40509 - A---- A TC-- TCC AC ACT
- CTG AG

ATCCAGCACCCAGACTTGAT ACTTGATCCT GAG ACCT GCAG CT CGGA AGC CCAG TGA TC CTAC T
CCTGCTACAGTACGTGGATG GCTA ||| |||| |||| || |||| ||| |||| ||| || ||||
ACTTACTGCTGGCCGCTACT CTC TGGA CGTC GA GCCT TCG GGTC ATT AG GGTG /
TCCGAACTAGACTGCCAACA A ACAAC A TCAA TCA CC GTC C TA- CA
AGGTACTC

GAM1648 CCGACTATTATGAAAGGTTA 40553 TGAAAGGTTA 40554 AT G ------ ---- T A GACATATT
CTCGGTTGAACAGATTGGAA CTCGGTTGAA CCGACT TAT AAA GGTTAC TCGGT GAAC GATTGGAA G
GACATATTGAGAACGCGTTC CAGA |||||| ||| ||| |||||| ||||| |||| |||||||
CGATCGTTCACCGATCCAGT GGCTGA GTA TTT CCGGTG AGCCA CTTG CTAGCCTT /
GGCCATTGGATTTGATGCAA AC G AGGTTA ACCT - - GCGCAAGA
GTCGG

GAM1649 GCTGAGTACCACATGTCCAA 40581 CTCGCCTCCG 40582 T AC-- T AAT-- - T
TGGCAGTTTTCCAACTCGCC AGGTCATCCC GCTGAG ACC ATG CC GGC AGTT T
TCCGAGGTCATCCCAGGTCC AGGT |||||| ||| ||| || ||| ||||
TCAGC CGACTC TGG TAC GG CCG TCAA C
C ACCC T AGCCT C C

GAM1650 TTTTTGGTCCACTTTTCCAT 40609 AGGGATAGAT 40610 TTTTCCAT- TA------- - CC TT CG TT C TA
ACGTTTATATTCTTTTAATC CTTGCAAGTT ACGTT TATTCT TTTAAT TGCG ATC T C GT T
CTGCGTTATCCGTTTCCGTT AAAT ||||| |||||| |||||| |||| ||| | | ||
ATATACAGGGATAGATCTTG TGTAA GTAAGA AAATTG ACGT TAG A G CA /
CAAGTTAAATAGAATGCTCT TTTTTTTAC TAAATTCTC T A- TC AT GG A TA
TAAATAATGTCATTTTTTTA
TCCGCTAAAAA
GAM1651 CGAAGTTGAAAACTTTGGCT 40617 TTTGGCTTGA 40618 T A TT C-- T
TGAGCACCGATCATTTGACC GCACCGATCA CGAAGT GAA AC TGGCTTGAGCA CGA C
TGCTTAAGCTATCGTCTTCA TTTG |||||| ||| || |||||||||| |||
CTTCG GCTTCA CTT TG ATCGAATTCGT GTT A
- C CT CCA T

GAM1652 TGTTATTTATAGTTTATAGA 40621 TTTATAGTTT 40622 - TT T G TTT GATTA
CATTTGGGATTATTATAACC ATAGACATTT TGT TA TATAG TTATA ACA GG T
TGTATATAACCTGTATTTGT GGGA ||| || ||||| ||||| ||| ||
ACA ACA GT ATGTC AATAT TGT CC /
T TT C A --- AATAT

GAM1653 TATATACGATAAGATATGTT 40629 TAAGATATGT 40199 C --- TTT A GCGTCAA-- TT
TATTCATAAACGCGTCAAAT TTATTCATAA TATATA GATAA GATATG ATTC TAAAC ATTT C

TTTTCATGAATAGCTAAGGA ACGC |||||| ||||| |||||| |||| ||||| |||| GTTTAAGAATCTCATGTCAA ATATAT CTGTT CTGTAC TAAG ATTTG TAAG / ATTGTCCTATATA C AAA TC- A AGGAATCGA TA

GAM1654 AATGGTAACGCGTCGTTAAC 40630 ACGCGTCGTT 40631 AC T TT - TTAACT TCGTCGGTTAACTCTTTCTT AACTCGTCGG AATGGTA GCG CG AACTCG TCGG C TTGATCGAGTTCGTCGCTAC TTAA ||||||| ||| || |||||| |||| TATT TTATCAT CGC GC TTGAGC AGTT / -- T -- T TTCTTT

GAM1655 AGCGGTTGTAGATTTATCAT 40634 TAAGAATTTA 40315 T T ATAT CC CACATATCC ATTTCTCCACCACATATCCG GATACATCTA AGCGGT GTAGAT TATC TTCT AC G TTACAATTTGTTAAGAATTT TATT |||||| |||||| |||| |||| || AGATACATCTATATTGCT TCGTTA TATCTA ATAG AAGA TG / - C ATTT AT TTTAACATT

GAM1656 TATATATGACATAATAAATT 40635 TATATGACAT 40636 T CATAATA TC- G GGTAAATCCTAGTTCTGGTA AATAAATTGG TATATA GA AATTGGTAAA CTA T TTTTACTAATTACTAAATCT TAAA |||||| || |||||||||| ||| GTATA ATATGT CT TTAATCATTT GGT T - AAATCA- TAT C

GAM1657 CCAAATACATCGACTGCTAC 40644 CTAAAGCAGT 40645 C ACT T GGT CTA TGCTGGTGGACCTATCGTTG TGCCGATTTA CCAAATA ATCG GC ACTGCT GGAC T TCCTAAAGCAGTTGCCGATT TTTG ||||||| |||| || |||||| |||| TATTTGG GGTTTAT TAGC CG TGACGA CCTG C T --- T AAT TTG

GAM1658 CGGTCGGCGCCGATTTCCGG 40652 CCGGTCCAGA 40653 T GC --- G CG CCCGGCGCGTCCCCGCGGGG TCGCGGTCGC CGG CGGC CGATTT CCGGCCC GCG T CCGGTCCAGATCGCGGTCGC CCG ||| |||| |||||| ||||||| ||| CCG GCC GCTG GCTAGA GGCCGGG CGC C C GC CCT G CC

GAM1659 GATCCGGATTTGAAAGAAGT 40669 TGAAAGAAGT 40670 TTGAAA A - GA TACTGTTGGTGATCAAACCA TACTGTTGGT GATCCGGAT GAAGTT CTG TTGGT T GTCAGCAATTTCCTTATTTG GATC ||||||||| |||||| ||| ||||| GATC CTAGGTTTA CTTTAA GAC GACCA C TTC--- C T AA

GAM1660 GCTTGCTCTTCCCTGATCAT 40684 TCCCTGATCA 40685 T- T CC AT--- TC -- ACT CTCCTCAAGTACTACTCGGC TCTCCTCAAG GC TGC CTT CTG CA TCCT CAAGT A TTGCTGGGATTTGTTCTGCA TACT || ||| ||| ||| || |||| |||||

GAAAGTGCACTGC CG ACG GAA GAC GT AGGG GTTCG C
TC T A- GTCTT TT TC GCT

GAM1661 CTCCTTCCAATCCTAGCTCA 40703 GGAGGTCAAT 40704 CCAA GC ----- TTCT TACA
ATTGACCTTCTTCCGACTAC TTCGAAGATA CTCCTT TCCTA TC AATTGACC TCCGAC G
AGAAGATGTTGGAGGTCAAT TGGG |||||| ||||| || |||||||| ||||||
TTCGAAGATATGGGACCTGA GAGGAG AGGGT AG TTAACTGG AGGTTG A
GGAG TCC- AT AAGCT ---- TAGA

GAM1662 ATTCATCCGGGCGTTCAGAA 40709 CATCCGGGCG 40710 -- CGTTCAGAAG G ATAAT
GAGTGGGAGCTATAATACAT TTCAGAAGAG ATTC ATCCGGG AGT GGAGCT A
CAAGCTCCAACTCCCGGATC TGGG |||| ||||||| ||| ||||||
CGAGT TGAG TAGGCCC TCA CCTCGA /
CC ---------- A ACTAC

GAM1663 TTTTTGGTCCATTTTTCCAT 40728 ATCGTGCAGG 40729 TTTTCCAT- TA------- - T TT
CG TCCGTTA
ACGTTTATATTCTTTTAATC TTAAATAGAA ACGTT TATTCT TTTAA CCTGCG ATC TT
T
CTGCGTTATCCGTTTCCGTT TGCT ||||| |||||| ||||| |||||| ||| ||
ATATCCAGTGATAGATCGTG TGTAA GTAAGA AAATT GGACGT TAG AG /
CAGGTTAAATAGAATGCTCT TTTTTTTAC TAAATTCTC T - GC AT TGACCTA
TAAATAATGTCATTTTTTTA
TCCGCTAAAAA
GAM1664 GTGGGGCAGAGGAAAATTTG 40737 GGGCAGAGGA 40738 C GGAAAATT CTTCCT----- G
TGGCTTCCTTGCGAAAGTAT AAATTTGTGG GTGGGG AGA TGTGG TGC A
TTCAAACTAACCACATCTCC CTTC |||||| ||| ||||| |||
CCAC CACCCC TCT ACACC ATG A
- -------- AATCAAACTTT A

GAM1665 TAACTACCCTCCGGGAGCTC 40778 CGGGAGCTCG 40779 ACCC A C C G
GGGGCCGTGGCCACGCAGTC GGGCCGTGGC TAACT TCCGGG GCT GGGGC GTG C
TCCAGCCCTGGACCGAGTTG CACG ||||| |||||| ||| ||||| |||
GTTGA AGGTCC CGA CTCTG CGC C
GCC- - C A A

GAM1666 TCATATTTCTCCACTACATA 40835 TTGCTACATA 40836 TTCTC CATATCC ACAATT TAAA
T T
TCCGTTACAATTTGTTAAAA ATCCAGCTAG TCATAT CACTA GTT TGT AAT TAGA A
ATTTAGATACATCTATATTG TGAA |||||| ||||| ||| ||| ||| ||||
CTACATAATCCAGCTAGTGA AGTATA GTGAT CGA ACA TTA ATCT C
ATATATATGA TATAA ------- CCTAAT TCG- T A

GAM1667 CAGGCACTACTTTTTAGCCG 40845 ATGACATTGA 40846 CTACTTTTT CGTTT A A TT T
- GG

TTTTCTCGGATGACATTGAG GTATTTCTGG CAGGCA AGC TCTCGG TG CA GAG ATT TCT A
TATTTCTGGAAAAAGACAAT AAAA |||||| ||| |||||| || || ||| ||| |||
CTTCCTGCCACCCGAGAGCT GTCCGT TCG AGAGCC AC GT TTC TAA AGA A
TCTGCCTG CT------- ----- C C CC - C AA

GAM1668 CTTCTTTACTCGTGGTTAGT 40893 TACCAGGAGA 40894 G-- TA GATCCG C
CGATCCGGTGCTACCACAAA GTAAAGAAG CTTCTTTACTC TGGT GTC GTG T
AGATACCAGGAGAGTAAAGA |||||||||| |||| ||| |||
AG GAAGAAATGAG ACCA TAG CAC A
AGG -- AAAA-- C

GAM1669 TGATCTTGTGACGCATGCGG 40963 ACGCATGCGG 40964 A T AC TGC G GGCA G
CGCAGGCAGGCCGTTAGGCC CGCAGGCAGG TG TCT GTG GCA GGC CA GGCC T
CATGAGCTTCTGCAGCACAG CCGT || ||| ||| ||| ||| || ||||
ACA AC AGA CAC CGT TCG GT CCGG T
- - GA CT- A AC-- A

GAM1670 GACAAAGAGCTGCTCGCTCA 40978 TCGCTCAGGC 40979 AAAGA CG - -
GTGAATAGTA TG GTAG
GGCTGTTCTGTGAATAGTAC TGTTCTGTGA GAC GCTGCT CTCAGGC TGT TCT CAC
GGGT G
ACTGGGGTGTAGGAGAGGGC ATAG ||| |||||| ||||||| ||| ||| ||| ||||
CCTGGTGAGACACGTGTCTG CTG CGGCGG GGGTCTG GCA AGA GTG CCCG
A
GGAGGCGGCAGTTGGTC GTTGA A- T C ---------- GT GGAG

GAM1671 CGAGGCGTTGTGGCACAAAC 40997 CGTTGTGGCA 40998 G- A- AA- G- A C G
AG- CGA
AAAACAGGCGGAAGCCCTCG CAAACAAAAC CGAGGC TTGTGGC CAAACA ACA GCGGA
GCC TC TC GCCG G
TCAGGCCGCGAGAGGATGGC AGGC |||||| ||||||| |||||| ||| ||||| ||| || || ||||
ATCGAGGATGGCCTCCGCAA GTTCCG AACACCG GTTTGT TGT CGCCT CGG AG AG
CGGT A
TGTCAGTGTTTGAGGCCACA GG GA GAC AA C T G CTA AGG
AGGGCCTTG

GAM1672 GTCGGGGCGGGAGAGTTCAC 41019 TCCGTGCTTG 41020 A A C C C -- T
TCGGCACGCATGCACGTGTA CCTAGCGAAC GTCGGGGCGGG GAGTTC CT GGCA GCATG AC
GTG A
ACCGCCAGTCCGTGCTTGCC TCAC |||||||||| |||||| || |||| ||||| || |||
TAGCGAACTCACCCGTCCCG CGGCCCTGCCC CTCAAG GA CCGT CGTGC TG CGC A
GC A C T T C AC C

GAM1673 CGTGACATGGAGAAACTGGG 41036 AGCTGTTGCC 41037 - A AA- --- A T CA G
CAG- G AT

GGAATTTGTCTTCTGGCACA AGGGTGCTCA GG GA CTGGG GGA TTTGTC TCTGG CAGCT
TTGC GGT CTC G
GCTGTTGCCAGGGTGCTCAT TGAG || || ||||| ||| |||||| ||||| ||||| |||| ||| |||
GAGCGAGGGCCAGATGCAGG CC CT GACCC CCT GAGCAG GGACC GTCGA GACG
CCG GAG A
AGCTGACCCAGGCGACGAGA T - GTA GGA A C CA G TAGA G CG
TCCAGGCCCAGATGTCCCTC
TATCATG
GAM1674 GGGCGTGGCCGCTATTATAA 41054 TTAGGACAAA 41055 T
AAAAAGTGAGAACGCGAAGC GTGCGAACGC
GGCCGCTATTATAAAAAAAGTGAGAACGCGAAGCGTTCGCACTTTGTCCTAATAATA A
GTTCGCACTTTGTCCTAATA TTCG ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATATATATATTATTAGGACA
CCGGCGATAATATTTTTTTCACTCTTGCGCTTCGCAAGCGTGAAACAGGATTATTAT T
AAGTGCGAACGCTTCGCGTT A
CTCACTTTTTTTATAATAGC
GGCCACGCCC
GAM1675 CCGCCCGCCCGACCCCCGAA 41057 TAAACCACAC 41058 C CCGACCCCC CCAC A T
T
TAAACCACACAAGGCGGTAC AAGGCGGTAC CCGC CGC GAATAAA AC AGGCGG ACG T
GTTTTCGTCTGTCTCGTTCT GTTT |||| ||| ||||||| || |||||| |||
TTATTTCTCACACACGCGCG GGCG GCG TTTATTT TG TCTGTC TGC T
CGG C CACACACTC CT-- C - T

GAM1676 CCGCGCAGGAAGGGGAAGGC 41068 TGTGAGGTCA 41069 - G G AA CT---- -- A-
GCAGC
CTCCTCCGCCGGCAGGTGCA GCCGCTTCTT CC GC CAGGAAG GG GGCCTC CCGC CGGC
GGT G
GCGTCAGAACCAGGCCGCAG GGGC || || ||||||| || |||||| |||| |||| |||
CGGCTCTGTGAGGTCAGCCG GG CG GTTCTTC CC CTGGAG GGCG GCCG CCA /
CTTCTTGGGCAGG A G G GA TGTCTC AC GA AGACT

GAM1677 GGTGCTCCAAGATTACTAGT 41088 TGGTAGGTGT 41089 T AAGAT- AG GG
ATTACCTTGGCGTAGAGGTG GGAAGGGCGC GGTGC CC TACT TATTACCTT C
GTAGGTGTGGAAGGGCGCGC GCC ||||| || |||| |||||||||
C CCGCG GG GTGG ATGGTGGAG G
C GAAGGT -- AT

GAM1678 GGGTACGCGCGAGCGAGCGC 41120 CAGTGCGTAG 41121 G A-- G G T - -------- TG
TC
CGGGGCTCTGCGCAGCGTGC CCGTTCTGCG GGTACGC CG GCGAGC CCGGG C CTG
CGCAG CG CTGGCGT G
TGGCGTTCGTTCGCGCCAGT TCAG ||||||| || |||||| ||||| | ||| ||||| || |||||||
GCGTAGCCGTTCTGCGTCAG TTATGCG GC CGCTTG GGCCT G GAC GCGTC GC
GACCGCG T
TGTCCGGGTTCGCCACCGGC - CAC - - T T TTGCCGAT GT CT
GTATTC

GAM1679 GCGGCGAGACGAAGTCCAGC 41129 AGGCACGCGC 41130 AGAC TCCA GG AA ATG
ACGCGCGCGTGCGGGAAGCG GCGTGTCTTC GCGGCG GAAG GCACGCGCGCGTGC G GCGC A
CATGACCAGCGTCAGGCACG CAGC |||||| |||| |||||||||||||| | ||||
CGCGCGTGTCTTCCAGCCGC CGTCGC CTTC TGTGCGCGCGCACG C TGCG /
TGC CGAC ---- GA -- ACC

GAM1680 ACACACCTACAAATTTACAT 41181 TAAAATTGTT 41182 C CT A - - A- A
CTACAGGATTGCCTGAGAGA TGTCTGT ACA AC ACAA TTTA CA TCT CAGG T
CTGCTAAAATTGTTTGTCTG ||| || |||| |||| || ||| ||||
T TGT TG TGTT AAAT GT AGA GTCC T
C TT A C C GA G

GAM1681 TTTATCCTGCAAGACTGTGG 41185 TATTTTGGGG 41186 TGCAA T A- TTA A TC ATATT
CCAGCTTACCAAAAAATTCT TGCCCGGTCC TTTATCC GACTG GGCC GC CCAAAA AT TCTAG G
CTAGATATTGACAAACTGGA AGTC ||||||| ||||| |||| || |||||| || |||||
AGATATTTTGGGGTGCCCGG AGATAGG CTGAC CTGG CG GGTTTT TA AGGTC /
TCCAGTCCTGGATAGA TC--- - CC TGG A GA AAACA

GAM1682 CTTCTGGCGGGCAGCTCTGC 41193 TGGCGGGCAG 41194 TG C CTC- ATCCT
TGGCAGGCATCCTTGGCTCG CTCTGCTGGC CTTC GCGGG AG TGCTGGCAGGC T
GCTTGCCGGCGTCCTCTTCC AGGC |||| ||||| || ||||||||||
CGCGGAG GAGG CGCCC TC GCGGCCGTTCG G
-- T TCCT GCTCG

GAM1683 ACAGCATTTAATACATATTC 41248 TTCATTATTT 41249 G TT CATATT C AT TA
TAAATCTAAGTAATATAATT AATTTAGTTT ACA CAT AATA CTAAAT TAAGTAAT AATT T
TATATAATTCATTATTTAAT TATT ||| ||| |||| |||||| |||||||| ||||
TTAGTTTTATTCGGTGATGT TGT GTG TTAT GATTTA ATTTATTA TTAA /
A GC TTT--- - C- TA

GAM1684 AGTGGACTCTCCACTTCTCT 41255 TAGAATGTCA 41256 CTC C CTTC T- C TA
TCTCGAGTATTCCCTATAAG AGTCCACT AGTGGACT CA TTCT TCGAGTA TC C T
TGATTTACTTGATAGAATGT |||||||| || |||| ||||||| || |
CAAGTCCACT TCACCTGA GT AAGA AGTTCAT AG G /
ACT - T--- TT T AA

GAM1685 CAATGAGATCGATGTTGAGA 41295 GATGTTGAGA 41296 GAGA GA A GAA AGA-- AG AGA
CTGAAGCAAGAAGAAGGCTA CTGAAGCAAG CAAT TC TGTTGAG CT GCA AGA GCT T

GATGTCGGCAGTCTAAGCAT AAGA |||| || ||||||| || ||| ||| |||
GCAGAGGCTCGACGAGAATG GTTA AG GCAGCTC GG CGT TCT CGG /
AATTG AGTA A- - AGA ACGAA GA CTG

GAM1686 TAATACGATCGTTTGAACAT 41337 GATCGTTTGA 41338 C --- TTCG A TCAA
TCGTTGGGTAGTAAATCAAT ACATTCGTTG TAATA GATCGTTTGA ACA TTGGGT GTAAA T
TAATTTTTGCAATTTAGATT GGTA ||||| |||||||||| ||| |||||| |||||
GTTTTTCAAGCGGTTCTATT ATTAT TTGGCGAACT TGT GATTTA CGTTT T
A C TTT TA-- A TTAA

GAM1687 AAGAAAACACCGATTAAATT 41342 ATTAAATTAG 41343 ACACC TT G C TACATT AT
TT
AGCATCAGCTACATTTAAAT CATCAGCTAC AAGAAA GA AAATTA CAT AGC TAAAT TC T
ATTCTTTTAGATAATTTATA ATTT |||||| || |||||| ||| ||| ||||| ||
ATTTGCTTATGTAATTTTTT TTCTTT TT TTTAAT GTA TCG ATTTA AG /
TAATATTTCTT ATAA- TT - T TTTAAT AT AT

GAM1688 TGATGTTTTATTATATTTCT 41351 TGTTTTATTA 41352 T- TATTTCTC
GCTTCTTTTAATAAT TTT
CAAATGCTTCTTTTAATAAT TATTTCTCAA TGATGT TTATTA AAAT TCTTCT T
TCTTCTTTTTCATTAGAAGA ATGC |||||| |||||| |||| ||||||
TAAACTATCAAATAATTTTA ATTACA AATAAT TTTA AGAAGA C
TATTTTTAATAACTACATTA TC TTTTATAT ATAAACTATCAAAT- TTA

GAM1689 TCCTTGTGGTGGTGTCGTTA 41361 TGTCGTTATA 41362 TT GGT AG A AT
TACAGGTAATACATAACGTA CAGGTAATAC TCC GTGGT GTCGTTATAC GTA TAC A
TACGTATAGTGACTAACTAC ATAA ||| ||||| |||||||||| ||| |||
TTGGA AGG CATCA CAGTGATATG CAT ATG /
TT AT- -- - CA

GAM1690 GATTCTGATATATAAATAGT 41368 TATAAATAGT 41369 TC TA-- GTATTTTTT A ATGT
CAA
ATTTTTTTCATTATATGTTA ATTTTTTTCA GAT TGATA TAAATA TC TTAT TAGACTCGG
A
GACTCGGCAAAATACCGGGT TTAT ||| ||||| |||||| || |||| |||||||||
CTATTAATAAGGTCTTCATA CTA ACTAT ATTTAT GG AATA ATCTGGGCC /
TTTAGATTTATCATCATC CT TTAG ACTTCT--- - ATT- ATA

GAM1691 TATAGCAATATGAATTTTTT 41374 TATTAAATAT 41375 A-- TTTTT T TAT T TCTAAA
TATTATTAAATATTAAATTA TAAATTATCT TATAGCA TATGAA TTA TATTAAA TAAA TA T
TCTAAATCCATTTTATTTTA AAAT ||||||| |||||| ||| ||||||| |||| ||
TATTTTAATATTAATTTTTC ATATTGT ATACTT AAT ATAATTT ATTT AT /
ATAGACTGTTATA CAG TTT-- T TAT T TTTACC

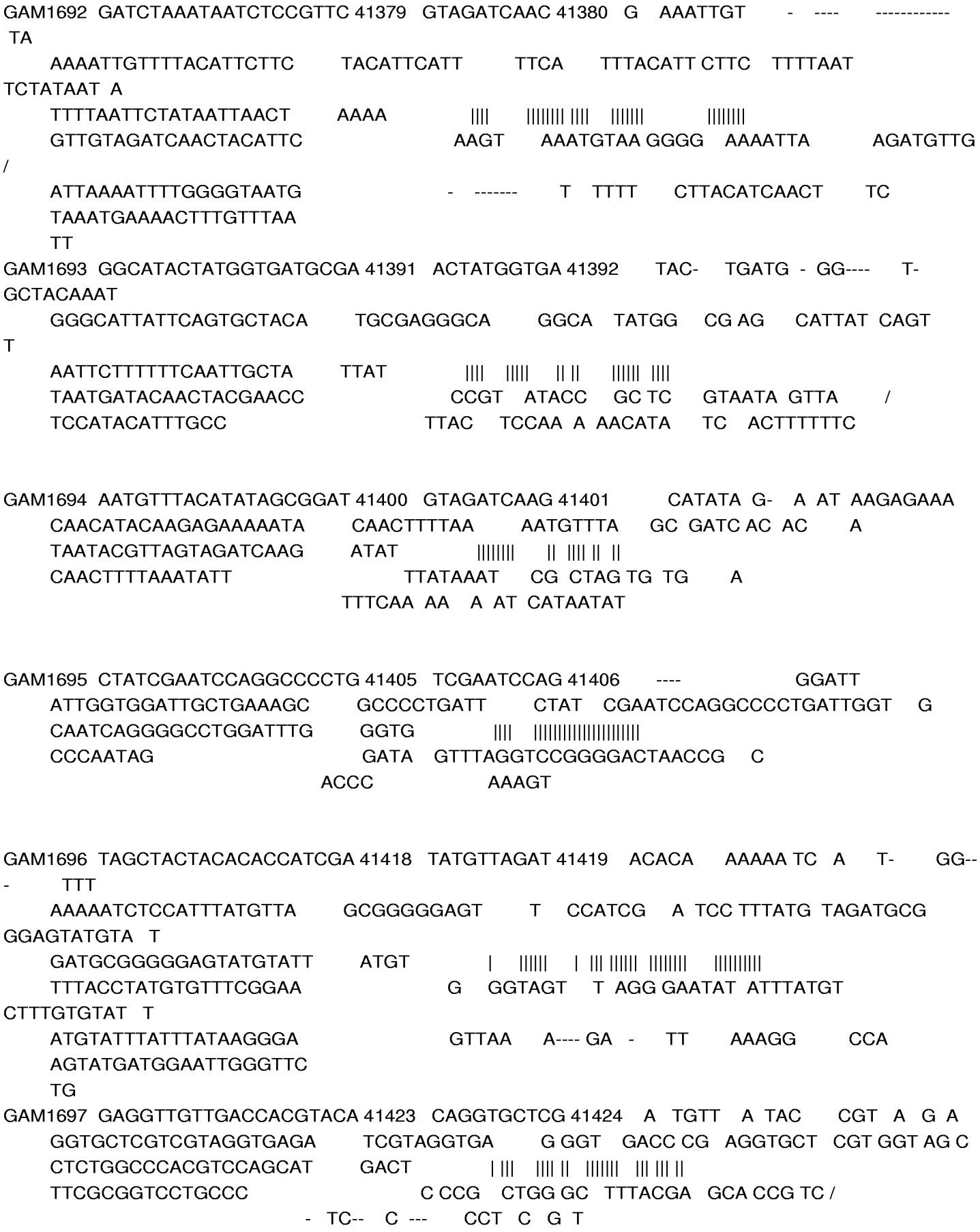
GAM1692 GATCTAAATAATCTCCGTTC 41379 GTAGATCAAC 41380 G AAATTGT - ---- ----------
TA
AAAATTGTTTTACATTCTTC TACATTCATT TTCA TTTACATT CTTC TTTTAAT
TCTATAAT A
TTTTAATTCTATAATTAACT AAAA
GTTGTAGATCAACTACATTC AAGT AAATGTAA GGGG AAAATTA AGATGTTG
/
ATTAAAATTTTGGGGTAATG - ------- T TTTT CTTACATCAACT TC
TAAATGAAAACTTTGTTTAA
TT
GAM1693 GGCATACTATGGTGATGCGA 41391 ACTATGGTGA 41392 TAC- TGATG - GG---- T-
GCTACAAAT
GGGCATTATTCAGTGCTACA TGCGAGGGCA GGCA TATGG CG AG CATTAT CAGT
T
AATTCTTTTTTCAATTGCTA TTAT
TAATGATACAACTACGAACC CCGT ATACC GC TC GTAATA GTTA /
TCCATACATTTGCC TTAC TCCAA A AACATA TC ACTTTTTTC
GAM1694 AATGTTTACATATAGCGGAT 41400 GTAGATCAAG 41401 CATATA G- A AT AAGAGAAA
CAACATACAAGAGAAAAATA CAACTTTTAA AATGTTTA GC GATC AC AC A
TAATACGTTAGTAGATCAAG ATAT
CAACTTTTAAATATT TTATAAAT CG CTAG TG TG A
TTTCAA AA A AT CATAATAT
GAM1695 CTATCGAATCCAGGCCCCTG 41405 TCGAATCCAG 41406 ---- GGATT
ATTGGTGGATTGCTGAAAGC GCCCCTGATT CTAT CGAATCCAGGCCCCTGATTGGT G
CAATCAGGGGCCTGGATTTG GGTG
CCCAATAG GATA GTTTAGGTCCGGGGACTAACCG C
ACCC AAAGT
GAM1696 TAGCTACTACACACCATCGA 41418 TATGTTAGAT 41419 ACACA AAAAA TC A T- GG--
- TTT
AAAAATCTCCATTTATGTTA GCGGGGGAGT T CCATCG A TCC TTTATG TAGATGCG
GGAGTATGTA T
GATGCGGGGGAGTATGTATT ATGT
TTTACCTATGTGTTTCGGAA G GGTAGT T AGG GAATAT ATTTATGT
CTTTGTGTAT T
ATGTATTTATTTATAAGGGA GTTAA A---- GA - TT AAAGG CCA
AGTATGATGGAATTGGGTTC
TG
GAM1697 GAGGTTGTTGACCACGTACA 41423 CAGGTGCTCG 41424 A TGTT A TAC CGT A G A
GGTGCTCGTCGTAGGTGAGA TCGTAGGTGA G GGT GACC CG AGGTGCT CGT GGT AG C
CTCTGGCCCACGTCCAGCAT GACT
TTCGCGGTCCTGCCC C CCG CTGG GC TTTACGA GCA CCG TC /
- TC-- C --- CCT C G T

GAM1698 GACCTTCTGCAGATAGGCGC 41433 TCTGCAGATA 41434 TC CA AG G AC G CT CGC
GCTTGCGCACGTTGACCTCG GGCGCGCTTG GACCT TG GAT GC CGCTTGCGC GTT AC CG
G
CGCGTGACGTTGTGGACGCG CGCA ||||| || ||| || ||||||||| ||| || ||
CGAGCGGGCGTCCAAGGGGT CTGGG AC CTG CG GCGAGCGCG CAG TG GC /
C GA -- -- G -- G TT AGT

GAM1699 GACTATAACCTCCGAAGTAC 41441 TATAACCTCC 41442 C CCGAAG --- A---------- A
TA
GGGACCAGTAGGTAAAATCC GAAGTACGGG GA TATAACCT TACGGG ACC GT
GG A
GACAAGGAATATATTCGTTC ACCA || |||||||| |||||| ||| || ||
CGGTATATCCGTAAACAGGT CT ATGTTGGA ATGCCT TGG CA CC A
TGTACTC C CAA--- ATA CCTTGCTTATATAAGGAA G TA

GAM1700 GCTATCGACAGCTACGACGT 41453 ACTGGATGAG 41454 A TAC-- A ATAC AT - -
AGT
ATTAATACTGGATGAGGTAA GTAATGTCAG GCTATCGAC GC GACGT TTA TGG GAG
GTAAT GTC G
TGTCAGTGATTGGACAATTA TGAT ||||||||| || ||||| ||| ||| ||| ||||| |||
TACTCCCCCACAATGAGACG CGATAGTTG CG CTGCA AGT ACC CTC TATTA CAG
A
TCTTTCCGCGGTTGATAGC G CCTTT G AAC- CC A A GTT

GAM1701 AATAAAATCAGAATCTATAT 41466 TTAGAATATC 41467 A ATCT-- GAAAT TAG
TTGAAATAGTTAGAGAGTGC CTAAATCTGA AATAAA TCAGA ATATTT AGT A
TTAGAATATCCTAAATCTGA CTTT |||||| ||||| |||||| |||
CTTTATT TTATTT AGTCT TATAAG TCG G
C AAATCC AT--- TGA

GAM1702 GCTGTCGGTGAAGCGCAACT 41475 TCGGTGAAGC 41476 - AA CAACTC- CG G
CCACCGTGTGATGGCGGTCG GCAACTCCAC GCTGT CGGTG GCG CAC TGTGAT G
CAGTGATCCAAACGCAGCAC CGTG ||||| ||||| ||| ||| ||||||
CGTACGGT TGGCA GCCAC CGC GTG ACGCTG C
T GA AAACCTA -- G

GAM1703 TCTCAAATTATCGCGATGGA 41481 TATCGCGATG 41482 AAATTAT ---- GCTA- TC
TGCTACAGTAAACTCGCAGT GATGCTACAG TCTC CGCGAT GGAT CAGTAAAC G
TTATTGATTTAATCTCCGGA TAAA |||| |||||| |||| ||||||||
TTGCGTGGAGA AGAG GCGTTA TCTA GTTATTTG /
GT----- GGCC ATTTA AC

GAM1704 AACTAGCACTACGATTACAA 41487 TAGCACTACG 41488 A ---- TACAAT- C - A

TGTGGGCATAACATCTGTAT ATTACAATGT AACTAGC CT ACGAT GTGGG ATA AC T
ATTTTCATCAACTTTATCGT GGGC ||||||| || ||||| ||||| ||| ||
TTTCGGAGCTAGTT TTGATCG GG TGCTA TACTT TAT TG C
A CTTT TTTCAAC T A T

GAM1705 TGGGGGCGTGTATACGAATA 41495 GGCGTGTATA 41496 GG CGAATACC -- TG A
CCTGAAGCGTTGGAAGCATT CGAATACCTG TGG GCGTGTATA TGAA GCGT GA G
TGACGTATTTCAAAAAATAT AAGC ||| ||||||||| |||| |||| ||
ACACGCACTA ATC CGCACATAT ACTT TGCA TT C
A- AAAAA--- TA GT A

GAM1706 GCTTAGCGACGATGCACCCG 41502 CACCCGTGAG 41503 TTA C C G GT T
TGAGGGAGGAGTCGTGAGCG GGAGGAGTCG GC GCGACGATG ACC GTGAGG AGGA CG G
TCCTCCTCACCGGTACATCG TGAG || ||||||||| ||| |||||| |||| ||
TCGCCACGC CG CGCTGCTAC TGG CACTCC TCCT GC A
CAC A C - -- G

GAM1707 TTTCCGCGGCCTCCATTGGC 41520 TTCCCAGTCA 41521 GCCTC T CCTT GAC
TGGGACCTTTAACGACACAG TGTACGCGGA TTTCCGCG CAT GGCTGGGA TAAC A
GGTTATTCCCAGTCATGTAC GA |||||||| ||| |||||||| ||||
GCGGAGA AGAGGCGC GTA CTGACCCT ATTG C
AT--- - T--- GGA

GAM1708 GTCTCCGGTCAGCCCGCTTC 41568 CGAGGCTACC 41569 C A CC T AC T CCCATC
CCTCGACGGCCTCGTCGTCC GAGGGCAGTC GTCT CGGTC GC GCT CCCTCG GGCCTCG
CGT C
CATCCGTTTCGTACGCCGAG AGCC |||| ||||| || ||| |||||| ||||||| |||
GCTACCGAGGGCAGTCAGCC CAGA GCCGG CG TGA GGGAGC TCGGAGC GCA G
GGCCGCAGAC C C AC C CA C TGCTTT

GAM1709 GCGGGGGGAGGAGCGGGGGG 41608 GGGGAGGAGC 41609 GGGGGGAGGA GGGGGGAGGA
GGGGGGAGGA GGGGGGAGGA GGGG
AGGAGCGGGGGGAGGAGCGG GGGGGGAGGA GC GC GC GC GC G
GGGGAGGAGCGGGGGGAGGA GCGG || || || || ||
GCGGGGGGAGGAGCGGGGGG CG CG CG CG CG G
AGGAGCGGGGGGAGGAGCGG AGGAGGGGGG AGGAGGGGGG AGGAGGGGGG
AGGAGGGGGG AGGA
GGGGAGGAGC

GAM1710 TGCCTTACGACCCGTTGAAA 41871 ACCCGTTGAA 41872 T- GA GTTGAA A T GA G
GGATCTGGGAGAACAGTAAT AGGATCTGGG TGCC TAC CCC AGG TC GGGA ACA T
GTCATCCTTGACCCTGGGAG AGAA |||| ||| ||| ||| || |||| |||
TATCGGCA ACGG ATG GGG TCC AG TCCT TGT A
CT A- ------ C T AC A

GAM1711 GCTACGAGTTCCTGCGTGTC 41922 TGGGCGGTTA 41923 - G - TG TC G - TT
GCTGGCTCGCCATTCACTGG CGTGGCGAGG GCTAC GA TTC C CGTG GCTG CT CGCCA C
TGTGGGCGGTTACGTGGCGA TCGG ||||| || ||| | |||| |||| || |||||
GGTCGGTGGC CGGTG CT GAG G GCAT TGGC GG GTGGT /
G G C GT -- G T CA

GAM1712 GGGCTGGGGCCGGGGAGGGC 41931 GGGCCGGGGA 41932 G G GGGGA G G G GGGGA G G G GGGGA G G G GG
TGGGGCCGGGGAGGGCTGGG GGGCTGGGGC CT GG CC GG CT GG CC GG CT GG CC GG CT GG CC G
GCCGGGGAGGGCTGGGGCCG CGGG || || || || || || || || || || || || || || || ||
GGGAGGGCTGGGGCCGGGGA GG TC GG TC GG TC GG CC GG TC GG CC GG TC GG /
GGGCTGGGGCCGGGGAGGGC G G AGGGG G G G AGGGG G G G AGGGG G G G AG
TGGGGCTGGGGAGGGCTGGG
GCT
GAM1713 TCGGACATTGCTGATATCAT 42256 TCCATGAGTA 42257 A G G A-- C------ GC
GGCCCAGGCTAGCTGGAAGA ATGAGAGTGC TCGG CATT CT AT TCATGG CCAG T
AATCCATGAGTAATGAGAGT CGA |||| |||| || || |||||| ||||
GCCGA AGCC GTGA GA TA AGTACC GGTC /
- - G ATG TAAAGAA GA

GAM1714 GTCGAACGTGTCGGGCTAGC 42276 GGCTATGGAA 42277 - - TA - G T G TGGAG --- TGA T
CATGGTCGGGCGTGTGCCCT CCGTCGCTGT CG GGC GC CAT GTCGGGCG GT CCC AGCGATGG CGT CTGC T
GGAGAGCGATGGCGTTGACT ATGG || ||| || ||| |||||||| || ||| |||||||| ||| ||||
GCTTATGCGGCTATGGAACC GC TCG CG GTG CGGTCTGC CA GGG TCGCTGCC GTA GGCG A
GTCGCTGTATGGGAACCCGT T G TG T G C A TATG- AAG TC- T
CTGGCGGTGTGCGTGCTGCG
TACATATCAC
GAM1715 TGTTCGTGGACAGAGCTTCT 42285 TTCAATTCTC 42286 - AG TTCT A T A CTT - C TTG GTC
TTGCGGTAGATTATGATGAC AACATACGTT CAG C TTGCGGT GAT ATG TGA CAATTC TCAA ATACG CT A
TTCAATTCTCAACATACGTT GCTG ||| | ||||||| ||| ||| ||| |||||| |||| ||||| ||
GCTGTCACAGAAGATTGTGT GTC G AACGTCA CTA TAC ACT GTTAAG AGTT TGTGT GA C
TTGAGGAATTGTTTCAGCAT G CT TAT- A - G TT- G - TA- AGA
ATCAACTGCAATATGTCCTG
GACCCGAACA
GAM1716 TCCTTGTGGTGGAGTTGTTA 42292 AGTTGTTATA 42293 TT GA G AGTA AT
TACAAGTAATACATAATGTA CAAGTAATAC TCC GTGGTG GTT TTATACA ATAC A
TATGTATAAGGACGCACCAT ATAA ||| |||||| ||| ||||||| ||||
TCGGA AGG TACCAC CAG AATATGT TATG /

CT G- G A--- TA

GAM1717 GCCGTGGACCAGCCCTGGTC 42300 GACCGGGCCA 42301 G C ---------- CT-- CTT C
GCCTCGCTTACCTGGGTCGC TCTCCCTGCT GCCGT GA CAGC CCTGGTCGC CG AC T
CGTTTCGTGACCGGGCCATC GTTT ||||| || |||| ||||||||| || ||
TCCCTGCTGTTTGACGGC CGGCA TT GTCG GGGCCAGTG GC TG G
G T TCCCTCTACC CTTT CGC G

GAM1718 GACGCACCAAGAAGGCATCC 42318 ATTGTCCCGC 42319 GCACC AG- ATCCT TG AA
TGATGGTGTTTAAAAAAAAT ACATCTTTAA GAC AAGA GC GA GTGTTT A
ATTGTCCCGCACATCTTTAA GGTC ||| |||| || || ||||||
GGTC CTG TTCT CG CT TATAAA /
GAAT- ACA CC--- GT AA

GAM1719 GTACGTTCATCGCCCTGAAC 42328 GCCCTGAACC 42329 - - C C- C AT
CTGTCGTTTATAGAGAACAT TGTCGTTTAT GTAC GTTC AT GCCCTGAA CTGT GTTT A
AGATTTCAGGGTCATCGAGC AGAG |||| |||| || |||||||| |||| ||||
TGTAC CATG CGAG TA TGGGACTT GATA CAAG /
T C C TA - AG

GAM1720 AAAGAATTAGATTGTAAATA 42338 TTAATTTAAA 42339 A-- AATAT AAA A GG
AA
TACAAAAATTAATTCTTTAA AGAATTAGAT AAAGAATTAG TTGTA ACAA TTAATTCTTT AAA
AATAG A
AAGGAATAGAAAATATTATT TGTT |||||||||| ||||| |||| |||||||||| ||| |||||
AATTTAAAAGAATTAGATTG TTTCTTAATT AACAT TGTT GATTAAGAAA TTT TTATT
A
TTCTGATACAAAAATTAATT AAA AGTCT A-- A AA AT
CTTT

GAM1721 TTTTTGTAGACAAAGAAGAG 42342 TTACTGCAGA 42343 ACAAAGA ACACC CT - ---
ATTT AA
TACACCCTCTCATGGGCCCA TGGGCTCACT TTTTTGTAG AGAGT CT CA TGGGCCCA
GCA AGA C
GCAATTTAGAAACATCTCTT GGAA ||||||||| ||||| || || |||||||| ||| |||
ACTGCAGATGGGCTCACTGG AAAAATATC TTTCG GA GT ACTCGGGT CGT
TCT A
AAGAGCTTTGATAATGCTAT GTAATAG A---- AG C AGA CAT- CT
AAAAA

GAM1722 GGGGGGTCTGTTTCTCCTGT 42371 AGCCGTTAAC 42372 - TTTCTCC CA AA--- C TA-
----- C
GGCAGCCGTTAACGCCGCTA GCCGCTAAGC GGGGGGT CTG TGTGG GCCGTT CGC GC
AGC T
AGCCTAGCTGACGAGATGCG CTAG ||||||| ||| ||||| |||||| ||| || |||
CGAATTAAACGGCACCACGC CCCCCCA GAC GCACC CGGCAA GCG CG TCG
/

CAGCACCCCCC C C------ A- ATTAA - TAGAGCAG A

GAM1723 GCACTGGTGTCCCATAATAA 42377 ACTGGTGTCC 42378 - T- CCATAATAA --- A ATT
AGTGTATGACTCATTGTAAG CATAATAAAG GCACT GG GTC AGTG TATG CTC G
AGCATGTTGTACTGACTTCC TGTA ||||| || ||| |||| |||| |||
TGGTGT TGTGG CC CAG TCAT GTAC GAG /
T TT --------- GTT - AAT

GAM1724 GAGCCTCCGCACGTCCACCC 42397 CCCCCCGGTC 42398 CCGC CCACC ATC TA
CGGGGATCTGCTACTCGCGC ACGTTCAGGT GAGCCT ACGT CCGGGG TGC C
CCCCCGGTCACGTTCAGGTT TC |||||| |||| |||||| |||
C CTTGGA TGCA GGCCCC GCG /
CT-- CT--- CC- CT

GAM1725 AAACACAAAAATGTATGTTC 42446 AAATGTATGT 42447 CAA- -- ACC-- A
AACCTTTTATTATACAATAA TCAACCTTTT AAACA AAATGTAT GTTCA TTTTATT T
AACTTTGTGAACTTATACAT ATTA ||||| |||||||| ||||| |||||||
TTGCTTTGTTT TTTGT TTTACATA CAAGT AAAATAA A
TTCG TT GTTTC C

GAM1726 AAACCTAATCAGAAATTCAG 42458 TGTTAGGGAT 42459 TC- AAA - AAATT - ACAG - - TTCA
AAAACTATCTTGAAATTGAC GGTCTACAAG AAAT AGA CTAT CTTG GAC ATCC GGC TAGT GATATC A
ATCCACAGGGCTAGTGATAT AATA |||| ||| |||| |||| ||| |||| ||| |||| |||||||
CTTCAATATCTGATATCAAC TTTA TCT GATA GAAC CTG TAGG TTG ATCA CTATAG T
TATGTTAGGGATGGTCTACA TCT AAA A AT--- G GA-- T A TCTA
AGAATAGAAATCTTCTATTT
CTGAAAGAAAT
GAM1727 ATTTCACATGTAAAACAATC 42472 TGTAAAACAA 42473 C-- CT A A AC
TTAAACACCACCAAGGGTAT TCTTAAACAC ATTTCA ATGTAAAACAAT TA AC CC C
AATTGTTTTATATTTCTGAA CACC |||||| |||||||||||| || || ||
AT TAAAGT TATATTTTGTTA AT TG GG /
CTT -- A - AA

GAM1728 GCAGATGTAAAGGCCTGGTG 42494 TAACCTGTCA 42495 A GTAAAGG GT- GC TC A AGGA A
AGGCGAGTGTCTAGATTACA CTTCACTCCA GC GAT CCTG GAG GAGTG TAG TTAC GACTA T
GGAGACTAATATAGTCGGTA ACAG || ||| |||| ||| ||||| ||| |||| |||||
ACCTGTCACTTCACTCCAAC CG CTG GGAC CTC TTCAC GTC AATG CTGAT /
AGGATCAGTCAGC A ACTA--- AAC AC T- C G--- A

GAM1729 CTGTCGTCCCCCGATGCCGA 42514 TTCGTGATAG 42515 TC- CC ATG A CG -- A
TCTCGCACACAGAGGCTGTT AACGGACGGT CTG GTC CCG CCG TCT CAC ACAG G
CGTGATAGAACGGACGGTGA GACT ||| ||| ||| ||| ||| ||| ||||
CTTCCAG GAC CAG GGC GGC AGA GTG TGTC /
CTT T- A-- A TA CT G

GAM1730 ATGTAGATGACGCGGAACAC 42519 TAGATGACGC 42520 G C AC A CAGATAACTAATG
CACA GG- AAA
ATATCTCAGATAACTAATGA GGAACACATA ATGACG GGA ACAT TCT ATGTATCTA
AAC GA A
TGTATCTACACAAACGGGAA TCTC |||||| ||| |||| ||| ||||||||| ||| ||
AAAGAAATCAGAGTTAGATA TACTGC CCT TGTA AGG TACATAGAT TTG CT
G
GATACATGGAAATGTATCCT A T A- A ---------- AGA- AGA AAA
CGTCATAGATAT

GAM1731 GGAATGTTTGGAATATCCAA 42527 TATTGTTTTA 42528 A CAA ----- A --- TAAT GT
GAT
AGGCAGATTTTCTAACATTA AATTTTAAGT A TATC AGGCAG ATTTTCTAAC TTAG TTAA
AT CATTT G
GTTAATAATATGTCATTTGA TAGA | |||| |||||| |||||||||| |||| |||| || |||||
TGTAAAAAATGGTATTGTTT T ATAG TTTGTT TAAAAGATTG AATT AATT TA
GTAAA T
TAAATTTTAAGTTAGAAAAT A A-- AAATA - TTA TTGT TG AAA
ATAAATTGTTTAGATAATCC
AAATATATC
GAM1732 GTTTTGCCCCATCGGCTATC 42533 TAGGTGCCGC 42534 - T T CTCC- A
TGCTCCCAAAAAGTTGTAAT TGGGTGCGAA GTTTTGC CCCA CGGC ATCTG CAA A
ATAGGTGCCGCTGGGTGCGA AT ||||||| |||| |||| ||||| |||
AAT TAAAGCG GGGT GCCG TGGAT GTT A
T C - ATAAT G

GAM1733 CGATTTACGTAATCTATATA 42554 GCAGAGTATC 42555 A A A CAA A- GAGA
CAAGATATATGCGAGAGAAT ATATAGAGAA CGATTT CGTA TCT TATA GATAT TGCGA A
GATATCGCAGAGTATCATAT TGCG |||||| |||| ||| |||| ||||| |||||
AGAGAATGCGAGGTCG GCTGGA GCGT AGA ATAT CTATG ACGCT T
- A G A-- AG ATAG

GAM1734 CGGTTACTATCAATATTATT 42559 TGATTATGAT 42560 A ATAT T - TATGAAAAT
CATCTAGTGATTATGAAAAT AGAACTG CGGTT CTATCA TA TCATC TAGTGAT T
TATAATGAATATTATTATGA ||||| |||||| || ||||| |||||||
TGATTATGATAGAACTG GTCAA GATAGT AT AGTAG ATTATTA /
- ---- T T TAAGTAATA

GAM1735 TATTACTAACATAAAGATAA 42566 TACGTAAACT 42567 AACATAAAG A AAACT TA -------
--------- G

TACGTAAACTACTTAATCTT ACTTAATCTT TACT ATAAT CGT ACT ATCTT
AGCA A
AGCAGACATGCTCCACATAA AGCA |||| ||||| ||| ||| ||||| ||||
TCTATTTAGAGATCGAGTCA ATGA TATTA GCA TGA TAGAG TCGT C
TGCACGATTATATAAGTAAT ATA------ - CGTAC GC ATTTATCTAATACACC A
A

GAM1736 ATGTCCAGGGGACCTCGCGA 42574 CAGGGGACCT 42575 - -- - T GG--- A
TTGTGGGAAGACCGCTTATA CGCGATTGTG ATGT CCAGGG GACCTCG CGA TGTG AAG C
TACACACTCGACGGGGTTTG GGAA |||| |||||| ||||||| ||| |||| |||
TTTTGGCACGT TGCA GGTTTT TTGGGGC GCT ACAC TTC C
C GT A C ATATA G

GAM1737 GCATTCTGTCTTTAAGGGAT 42606 TCTGTCTTTA 42607 - TTAAGGGA A
TTTCTGACAAAGTTAGAAAA AGGGATTTTC GCATTC TGTCT TTTTCTGAC A
AATGATTTAGACATGAATGT TGAC |||||| ||||| |||||||||
TGTAAG ACAGA AAAAGATTG /
T TTTAGTAA A

GAM1738 TCGAGTATATGATCTCATCT 42641 TATGATCTCA 42642 TATG CT------ T TCAT
CGATCTCAATCATCTTATTT TCTCGATCTC TCGAGTA ATCTCAT CGA CTCAA C
GAGTCGTATTCCTAATGAGA AATC ||||||| ||||||| ||| |||||
TATTACTCGA AGCTCAT TAGAGTA GCT GAGTT /
TA-- ATCCTTAT - TATT

GAM1739 ACGAAGATCTTGAGGCTGGG 42649 CGGAAGGTGC 42650 A GAG G GACA T
TAGCTGACAGGCTTCGGTCC CCAGCAGGAT ACGA GATCTT GCTGGGTA CT GGC T
GGAAGGTGCCCAGCAGGATC CTCG |||| |||||| |||||||| || |||
TCGT TGCT CTAGGA CGACCCGT GA CTG C
- --- G AGGC G

GAM1740 TGGTCAAGATGTACCCCGAA 42674 TGATGTGGGG 42675 CAAG A AA T A A
ATCATGAGAGATAATGGTCC ATATACCA TGGT ATGT CCCCG ATCA GAG GAT A
CTTTGATGTGGGGATATACC |||| |||| ||||| |||| ||| |||
A ACCA TATA GGGGT TAGT TTC CTG T
---- - G- - C G

GAM1741 GTTGAATGGTCATCGAATAA 42708 TATCAGTGAT 42709 - C AT- AAAATA- A C
GTTTTGGAAAATAGACACTC TATTACAAT GTTG AATGGTCAT GA AAGTTTTGG GAC CT A
ATAAGGTTATCGATGCCGAA |||| |||||||| || |||||||| ||| ||
ACTTCTATCAGTGATTATTA TAAC TTATTAGTG CT TTCAAAGCC TTG GA T
CAAT A A ATC GTAGCTA - A

GAM1742 CCTGTTGGAGTGAAGTGACA 42724 AGTGAAGTGA 42725 T GA A AC- C--- T

GGTTACCGACTATATTAGTC CAGGTTACCG CCTG TG GTGA GTG AGGTTAC GACTA A
TCCTGTAATCTAGACACTCG ACTA |||| || |||| ||| ||||||| |||||
CCTCACCAGG GGAC AC CGCT CAC TCTAATG CTGAT /
C TC - AGA TCCT T

GAM1743 GAGTTTAGATCTGAATTGAT 42736 TACAATATGT 42737 CTGA-- A -- AA
ACTGTCCAATCAGGATCTAG TTATCTAAGC GAGTTTAGAT ATTG TACT GTCC T
TACAATATGTTTATCTAAGC TT |||||||||| |||| |||| ||||
TT TTCGAATCTA TAAC ATGA TAGG /
TTTGTA - TC AC

GAM1744 GGAATGTTTGGAATATCCAA 42748 TATTGTTTTA 42528 A CAA ----- A --- TAAT GT GAT
AGGCGGATTTTCTAACATTA AATTTTAAGT A TATC AGGCGG ATTTTCTAAC TTAG TTAA AT CATTT G
GTTAATAATATGTCATTTGA TAGA | |||| |||||| |||||||||| |||| |||| || |||||
TGTAAAAAATGGTATTGTTT T ATAG TTTGTT TAAAAGATTG AATT AATT TA GTAAA T
TAAATTTTAAGTTAGAAAAT A A-- AAATA - TTA TTGT TG AAA
ATAAATTGTTTAGATAATCC
AAATATATCT
GAM1745 GCACAGTATCAAGGATCAAC 42749 AAGGATCAAC 42750 A- - AA CAACTC CT
TCTGTTTATCTAGACATGAA TCTGTTTATC GCAC GTA TC GGAT TGTTTAT A
TACTTCAATCCCAGGCTACC TAGA |||| ||| || |||| |||||||
CGTGT TGTG CAT GG CCTA ATAAGTA G
CC C AC ACTTC- CA

GAM1746 GTTGCCGCTCTGATACTCCT 42773 TGCGGTAGCT 42774 CT CTC - G - A
CCGGGATGAGCCACATGGTC GTCCTGGTGG GTTGCCGCT GATA CT CCG GATGAG CC C
TCGTTGCGGTAGCTGTCCTG TAAC ||||||||| |||| || ||| |||||| ||
GTGGTAAC CAATGGTGG CTGT GA GGC TTGCTC GG A
TC C-- T G T T

GAM1747 TTATCAGGATTAGAACATTT 42802 AGTAAAAATG 42803 AGA TTTG ---- TTTAG A- -- AG G
GGGACAGTGAGGTGTTTAGT GTGGGCAAGC T ACA GGACAGTG AGGTG TAAAA TGGTGGG CA CACA A
AAAAATGGTGGGCAAGCACA ACAG | ||| |||||||| ||||| ||||| ||||||| || ||||
GAAGTGTGAATGTCCCCGCT A TGT CCTGTTAT TCTAC GTTTT GTCGCCC GT GTGT A
GGGTTTTGAAAATCATCTAT GAA CTTA TGTA TAAAA GG CT AA G
GTTATTGTCCATTCTGTAAG
AGTCCAGGTAA
GAM1748 GGCGACACTTGGGTGCACAG 42846 AAGCTGCCGC 42847 CA -- CA-- TG CGT- AC ACC
GTGGCCGTAGGTGTCACGTG GATGTACCCC GGCGA CTT GGGTGCA GG GC AGGTGTC GTG T

ACCTTTTCCGCCGGCACCTT CGGG ||||| ||| ||||||| || || ||||||| |||
TAAGCTGCCGCGATGTACCC CCGCT GGG CCCATGT CC CG TCCACGG CGC T
CCGGGGATCGCC AG CC AGCG GT AATT C- CTT

GAM1749 GGGTGGATATCAAAGTAGAC 42892 TACCGGGATT 42893 T TATCAAAG--- C- T-
GAAAA
AATCCCTTAAAGAGAAAACA CTTCTGAAAC GGG GGA TAGA AATCCC TAAAGA C
GGAATCTTTACCGGGATTCT AATC ||| ||| |||| |||||| ||||||
TCTGAAACAATCTTTTCCCC CCC CCT GTCT TTAGGG ATTTCT /
C - TTTCTAACAAA TC CC AAGGA

GAM1750 CCACACCCCCAGGATCTTCC 42905 TGAGGAAGCA 42906 CCCC ------ TA- CCCCC
TCTAAGGCCCCCACCAAACC TCTGGTCCTA CCACAC AGGAT CTTCCTC AGG A
TGGTGAGGAAGCATCTGGTC AGAG |||||| ||||| ||||||| |||
CTAAGAGTGTGG GGTGTG TCCTG GAAGGAG TCC /
AGAA GTCTAC TGG AAACC

GAM1751 TGGTTTAGAGCTAAATTTGT 42937 TAGAGCTAAA 42938 TTTA AAA C--- TT
GAACTCTTTAAGAAAACTTT TTTGTGAACT TGG GAGCT TTTGTGAA TC T
ACAAAATCAGCTCATCTCCA CTTT ||| ||||| |||||||| ||
ACC CTCGA AAACATTT AG /
TCTA CTA CAAA AA

GAM1752 ACCTGAAAATTGGATTGATA 42948 TGGATTGATA 42949 AAAATT-- T CAAA AA C---
TA
ACAAAGAGTTAAAGTTCTGT ACAAAGAGTT ACCTG GGA TGATAA GAGTT AGTT TGT C
TACTGTACAAAAAAACTAGG AAAG ||||| ||| |||||| ||||| |||| |||
ATTTAGAATTATCACTCCTT TGGAC CCT ACTATT TTTAG TCAA ACA T
TGCCTGCAGGT GTCCGTTT C AAGA GA AAAA TG

GAM1753 GTGCAGAGAAACGACTCGCG 42961 TCGCGGGTTT 42962 G GAAACGA AGTAGCGTGTTT
- TCAG - TA
AGTAGCGTGTTTGACCTGGA GCGCGAGGAT CAGA CTCGCG GACCTG
GAGACGATGT GG AG C
GACGATGTTCAGGGAGTACA CTGG |||| |||||| |||||| |||||||||| || ||
ACTACTACACACATCGTCTC GTCT GAGCGC TTGGGC CTCTGCTACA TC TC
/
GCGGGTTTGCGCGAGGATCT G AG----- GT---------- G CACA A AA
GGAC

GAM1754 GAGGCAGAAGGCGGATGATC 42968 TGTTTCAGCG 42969 AGAAG - AT AAAAAGT C
TGAAAAAAAGTACACCCTCG TACCGCAAAC GAGGC GCGG ATG CTGAA ACACC T
GTGTTTCAGCGTACCGCAAA GGCC ||||| |||| ||| ||||| |||||
CGGCCTT TTCCG CGCC TGC GACTT TGTGG /
GCAAA A -- ------- C

GAM1755 GAAGATTTAAATGGTTTATT 42975 TAAATGGTTT 42976 TTAA A CCTTG T TTC
AGACCTTGCTGCTATTGATT ATTAGACCTT GAAGAT ATGGTTT TTAGA CTGC ATTGA A
CAACATTCAATGTAGATAAT GCTG |||||| ||||||| ||||| |||| |||||
CTAAAAGACTGTGTCTTC CTTCTG TGTCAGA AATCT GATG TAACT A
---- A AATA- - TAC

GAM1756 CTGAACACTTTTATCGCCCT 42986 TATCGCCCTG 42987 A C T C C - CC A
GAATCTATCCTTTATTCAAA AATCTATCCT CTG ACA TTT AT GCC TGAA TCTAT TTT T
ACATAGACTTCAAGGCCATC TTAT ||| ||| ||| || ||| |||| ||||| |||
GAGCTGTACAG GAC TGT GAG TA CGG ACTT AGATA AAA T
A C C C A C CA C

GAM1757 TCGCCCCGAAACCGCAACGC 42990 TGGGCTGGCG 42991 C- AAACC AA A CACC CCC A
GGCAGAGTCGGCGCCACACC CCGACCCTGC TCGCC CG GC CGCGGCAG GTCGGCGCCA CCCGTC CG G
CCCGTCCCCCGAGTTCGCGA CGCG ||||| || || |||||||| |||||||||| |||||| ||
TGGGCTGGCGCCGACCCTGC AGCGG GC CG GCGCCGTC CAGCCGCGGT GGGTAG GC T
CGCGGCAACGAAGGCGA AA AA--- -- C C--- C-- T

GAM1758 CCCCGCCCTCATCCCCTGAC 43016 ACCCGGTGGA 43017 - T - CT CA C T AAAA AAA C AAATAA- A
ACACCCGGTGGAAAAAACGA AAAAACGAAA CC CATC CC GA CACC GG GGA ACG GA ACAT AACGA T
AAGACACATAAATAAAACGA GACA || |||| || || |||| || ||| ||| || |||| |||||
ATTTTGTTGTTAAAAATGTT GG GTAG GG CT GTGG CC CCT TGC CT TGTA TTGTT /
TCCACGTGACGTCCCCGGTG C C A CC TA - - GCAG AC- T AAAATTG T
ATTCCCGGAGATGCGGCACG
CGGCGG
GAM1759 TGGACTCATGGGCCAGCGGG 43048 CACCTCAAGA 43049 TG AGC C- CAG--- G
TCCGAGGCAGGAAGCTATTC CCCGGCTTGA TGGACTCA GGCC GGGTC GAGG GAA C
AAAGCACCTCAAGACCCGGC GTCC |||||||| |||| ||||| |||| |||
TTGAGTCCA ACCTGAGT TCGG CCCAG CTCC CTT T
-- --- AA ACGAAA A

GAM1760 GGTGAGGCCTTCGGGTCGCT 43108 AAGCGTACCC 43109 G CC-- - CG G
CGTGGTAGTAATACCAGAAG GGAACTTCTT GGT AGG TTCGGGT CGCT TGGTA T
CGTACCCGGAACTTCTTGAC GACC ||| ||| ||||||| |||| |||||
C CCA TTC AGGCCCA GCGA ACCAT A
G TTCA T AG A

GAM1761 TTGTAATAATAATGGAACTA 43118 TCTATAGTTT 43119 - TG TC T- TTCTTT T C
TATCTTTTGATATTTCTTTT TTTTATTTAT TTGTAATAA TAA GAACTATA TTT GATAT TC
AATA T
CTAATACTGGTATTTGGTAT TACA |||||||||| ||| |||||||| ||| ||||| || ||||
AATATATTTTAAATCTATAG AACATTATT ATT TTTGATAT AAA TTATA GG TTAT G
TTTTTTTATTTATTACAA T TT CT TT TAATAT T G

GAM1762 ACATTCATTTGTAAAATTTT 43127 TCATTTGTAA 43128 -------- TAAAATTTTT ATT
TTAATTTATTTCTAAAATTA AATTTTTTAA ACATTCATT TG TAATTT T
TTTCCAACATCATCAAATAT TTTA |||||||||| || ||||||
AATGAGTGT TGTGAGTAA AC ATTAAA /
TATAAACT TACAACCTTT ATC

GAM1763 GAGGAACGGAAACATCGTGG 43131 ACGGAAACAT 43132 A AAA T AGAAAAT
TGGAGAAAATATTCGCTGGC CGTGGTGGAG GAGGA CGG CATCGTGG GG A
CCCGCGATGGGACCGTCCTC AAAA ||||| ||| |||||||| ||
CTCCT GCC GTAGCGCC CC T
- AGG - GGTCGCT

GAM1764 CCATGGCCAGAGCAAAAGAA 43292 TTCAAACTTC 43293 CA CAAA GAA C
GTGAAGGACGCCGAAGTGTT TGAAACTCAT CCATGGC GAG AGAAGT GGACGC G
CAAACTTCTGAAACTCATGT GTCA ||||||| ||| |||||| ||||||
CATGG GGTACTG CTC TCTTCA CTTGTG A
TA AAAG AA- A

GAM1765 GACGTCCCCGTGGTTACCGT 43307 TCCCCGTGGT 43308 -- A- --- A TC
GACAAGCTCCACGCTAGTCA TACCGTGACA GACGTCCCC GTGGTT CCGT GAC AGC C
CAGCGGACAACTACAGGGGG AGCT ||||||||| |||||| |||| ||| |||
GCGTC CTGCGGGGG CATCAA GGCG CTG TCG /
GA CA ACA A CA

GAM1766 GTAATGATATCTCCATACTA 43317 AAGGAGCTCA 43318 TAT--- AT-- --- GT CA A
GTAGGTCCACCCAACTGGGA TTTCATTAC GTAATGA CTCC ACT AGTAG C CCC A
AGGTCTACTATCAGTCAAAG ||||||| |||| ||| ||||| | |||
GAGCTCATTTCATTAC CATTACT GAGG TGA TCATC G GGG C
TTACTC AAAC CTA TG AA T

GAM1767 GTAAATTAGACAGACACCGA 43364 TTCTCAATTG 43365 T - ------ A AT AA--- C T
TAGGTAAATGAGACACCGAT GTACCTCTGG GTAAAT AG AC AGAC CCG AGGTA TGAGA
ACCGA A
ATATCGGTTCTCAATTGGTA AGTC |||||| || || |||| ||| ||||| ||||| |||||
CCTCTGGAGTCTTATAAAGT CATTTG TC TG TCTG GGT TCCAT ACTCT TGGCT T
GCTTGTTTAC T G AAATAT A C- GGTTA - A

GAM1768 TTGAGAAAACAGTTGAGGCA 43381 AACAGTTGAG 43382 AAA-- T A ------- A
TACAGAAATTGTGTAACTAA GCATACAGAA TTGAG ACAGT G GGC ATACAG A
CGCCCCACTGTGCTCCCTTA ATTG |||||| ||||| | ||| ||||||
A AATTC TGTCA C CCG TGTGTT /
CCTCG - C CAATCAA A

GAM1769 CCACAAACAGAGCAAACTCG 43394 GAGCAAACTC 43395 AAACA A TC A CGC
ATGAAGGCCGCTACCGCCTC GATGAAGGCC CCAC GAGCA AC GATGA GGC T
ATCATGTCTGTTTCCTTGGT GCTA |||| ||||| || ||||| |||
GG GGTG TTTGT TG CTACT CCG /
GTTCC C TA - CCA

GAM1770 GCCGTTCCGGTCAACACCAA 43409 TTGATCCATG 43410 -- TCAAC- ACAAAAT T
CAAAATGCTTTACAAGTTGA GTTATAATCC GCC GTTCCGG ACCA GCTT A
TCCATGGTTATAATCCGGAA GGAA ||| ||||||| |||| ||||
TGTGGC CGG TAAGGCC TGGT TGAA /
TG TAATAT ACCTAGT C

GAM1771 CCCCGGTCCACATAGGAAGC 43418 TCCGTAATTC 43419 CCACATAG GCCAA ACGAAA
CAAGGGCGGACGAAAATAAA ACACACGAAT CCCCGGT GAA GGGCGG A
AACCCGTCCGTAATTCACAC CGGG ||||||| ||| ||||||
ACGAATCGGGG GGGGCTA CTT CCTGCC T
AGCACACA AATG- CAAAAA

GAM1772 CTTCTCCCAGTGCTCACTCA 43424 TCCCAGTGCT 43425 CCCA ---- -- A CGA AC
GCTGACCTTTGACCGACTAC CACTCAGCTG CTTCT GTGCTCA CTCA GCTG CCTTTGAC
CT A
AGAAGATGTCGGAGGCCAGC ACCT ||||| ||||||| |||| |||| |||||||| ||
TTTGAGGATATGAGCGCAGA GAAGA CGCGAGT GAGT CGAC GGAGGCTG GA /
AG ---- ATAG TT C TA- AG

GAM1773 CGTATTGGATGCTGGAGGAT 43470 TATTGGATGC 43471 A AT- AGG-- GAT G- G
GATATGGAGGTGAGAAATCG TGGAGGATGA CGT TTGG GCTGG AT ATG AGGTGA A
CCTGACATTTAATAACACCC TATG ||| |||| ||||| || ||| ||||||
AGCTCACCAAGCG GCG AACC CGACC TA TAC TCCGCT A
- ACT CACAA ATT AG A

GAM1774 AACTTTTCTTTGTTCGTGAA 43476 TTCGTGAACA 43477 TCTT T A-- TCAA TT
TTTATTC
CATATTTTCAAAATTTCCTT TATTTTCAAA AACTTT TGT CGTGAAC TATTT AA TCC A
TATTCAGACCTTTGGATTTT ATTT |||||| ||| ||||||| ||||| || |||
AAGTACTCGTTTACGACATT TTGAGG ACA GCATTTG ATGAA TT AGG /
CTGGAGTT TCTT - CTC ---- TT TTTCCAG

GAM1775 GCGAGACAGATCAGCATTTG 43483 ACTGCACAGA 43484 A AGCA- - C AA
GCAGCCTAAACGGAGACTGC ATCGAGATCG GCGAGAC GATC TTTG GCAG CT A
ACAGAATCGAGATCGTTTTG TTTT ||||||| |||| |||| |||| ||
C CGTTTTG CTAG AGAC CGTC GA C
- AGCTA A A GG

GAM1776 TAGTATGGTTTAGAGCTAAG 43493 CTTTACAAGA 43494 TTA G TAACG-- C
TTTGTTAACGCCCTAAGGAA TTAGTTCATC TAGTATGGT GAGCTAA TTTGT CC T
GCTTTACAAGATTAGTTCAT ACCA ||||||||| ||||||| ||||| ||
CACCATATTG GTTATACCA CTTGATT GAACA GG A
CTA A TTTCGAA A

GAM1777 AACTGGGAGAAGTTTGTAGT 43520 AGAAGTTTGT 43521 GA TA ACATC-- AC
ACATCAGACCATCTAAAAAG AGTACATCAG AACTGG GAAGTTTG GT AG C
GGCCCCAGACTTTATCAGTT ACCA |||||| |||||||| || ||
TTGACT TTTCAGAC CG TC /
A- CC GGAAAAA TA

GAM1778 GGGTTCCCTCCACATTGTGG 43535 TTGGCCAACC 43536 G CCA TG- G C TG
GCAACCGTTGTAGGCGTTGG ATGCAGGGGA G GTTCCCT CAT TGG CAAC GT T
CCAACCATGCAGGGGAATGT ATGT | ||||||| ||| ||| |||| ||
T TAAGGGG GTA ACC GTTG CG /
G AC- CCA G - GA

GAM1779 TTCTAACACATGTGTGGGCA 43547 ACAGGACTGG 43548 AACAC G A---- ATA CA C
ACAGATATCCTCATGCCAAT CACATGCTCA TTCT AT TGTGGGCA CAG TCCT TGC A
GCAACAGGACTGGCACATGC CGGA |||| || |||||||| ||| |||| |||
TCACGGATACAGAA AAGA TA GCACTCGT GTC AGGA ACG A
CA--- G ACACG --- CA T

GAM1780 GGGTCTGCAAAACCCTCTGA 43585 CTCGTTCTTC 43586 TGCAAAACCCTC- ACACAG
GAATACACAGCATTAAAATT CTCAAATGAC GGGTC TGAGAAT C
CTCGTTCTTCCTCAAATGAC CC ||||| |||||||
CC CCCAG GCTCTTA /
TAAACTCCTTCTT AAATTA

GAM1781 TGGCAATTGAAAAGTGGTTA 43673 TGAGTAGCCA 43674 A GAAAA A---------- AAA
CAGCCCAAAAACGGGGCCTG CCAAGAGATG TGGCA TT GTGGTTAC GCCC A
TTTTGATGAGTAGCCACCAA CCA ||||| || |||||||| ||||
GAGATGCCA ACCGT AG CACCGATG CGGG /
- AGAAC AGTAGTTTTGTC GCA

GAM1782 TTTGAGAATAATGTACTGGT 43726 TAATGTACTG 43727 GTA TG A T GAGACGG-- -
T --- - G
GTACAAAGTGCTGAGACGGG GTGTACAAAG AATAAT C GTGT CAAAG GCT GAGA
GTCCC CA AC CGT A
AGAGTCCCTCAACCGTGAAA TGCT |||||| | |||| ||||| ||| |||| ||||| || || |||
ATGTGTGTTTGTGGGACTTC TTATTA G CACA GTTTC CGA CTCT CAGGG GT TG
GTA A
TCATTATGCAAAGCCTTTGA AC- GT - - AACGTATTA T T TTG T A
CACTGGCAATTATTTCTTCA
GA
GAM1783 GCGACTCGTCCGCTTGACAG 43736 TGACAGGAGA 43737 CT TC TTGA AGCT-- TT
GAGAAGCTACGGCCTTAAAG AGCTACGGCC GCGA CG CGC CAGGAGA ACGGCC A
GCTGTTGACCCTCTCTTGCC TTAA |||| || ||| ||||||| ||||||
CTGCGCCGTTTCGC CGCT GC GCG GTTCTCT TGTCGG /
TT C- TCCC CCCAGT AA

GAM1784 GATATTGGCTCGTCTCACCT 43760 TTGGAGGTAA 43761 -- TG TC C CG AC
TCAACCGGTTACAGAAGATG GATATGTTGA GATA T GC GTCT ACCTTCAAC GTT A
TTGGAGGTAAGATATGTTGA CTTA |||| | || |||| ||||||||| |||
CTTATC CTAT A TG TAGA TGGAGGTTG TAG G
TC GT TA A -- AA

GAM1785 CATTCCGGTCAACAAGGCCA 43773 TACATGGCTA 43774 CAA A AAAT--- CT
AAATGCTCTATAAGCTTATA TGAACCGGAA CATTCCGGT CA GGCCA GCT A
CATGGCTATGAACCGGAATG TG ||||||||| || ||||| |||
GTAAGGCCA GT TCGGT CGA /
A-- A ACATATT AT

GAM1786 GGGTTGTCTATCGGGCCACC 43789 TGTCTATCGG 43790 TG T GC C CC C
CCCTGCTCAGACTATTTGAG GCCACCCCCT GGGT TC ATCGG CA CC TGCTCAGA T
CGAGGCTGACCGATGATGAC GCTC |||| || ||||| || || ||||||||
CT TCCA AG TAGCC GT GG GCGAGTTT /
GT - A- C A- A

GAM1787 CGACGAGAGGAGATCGACTT 43806 CTACAGGATT 43807 GA A -------- -- TA
TCCTGGGATAACTTCCTACA TCAAACAGGC CGACGAGAGGA TCG CTT TCCTG GGA A
GGATTTCAAACAGGCGGTCC GGTC |||||||||||| ||| ||| ||||| |||
TCTCGTTG GTTGCTCTCCT GGC GGA AGGAC CCT /
-- - CAAACTTT AT TC

GAM1788 TGGATACACCGGTGCTGAAT 43824 TACGCCATCG 43825 A C AATTCT GGA
TCTTACGACTTGGGATCAAC GGTATCTA TGGATAC CCGGTG TG TACGACTTG T
AAGTCGTACGCCATCGGGTA ||||||| |||||| || |||||||||
TCTA ATCTATG GGCTAC GC ATGCTGAAC /

```
                                    -    C ------       AAC


GAM1789 GGTTGAGGCCCAAGCTCGAA 43830  TCCCTGATGC 43831      - AA   CGC  CG  A A  CCC  T
C-  AT-  GCC
     ATCGCGCGACCGGCGATCAA       TCTCGTCATC       AAGCT CG  ATCG  GAC  GCG TC AGT  TGA
GCTCT  GTC  CTT  A
     GTCCCTGATGCTCTCGTCAT       TTGC          ||||| ||  ||||  |||  ||| || |||  ||| ||||| |||  |||
     CTTGCCAGAAAAGCCGGACC                  TTCGA GC  TAGC  CTG  CGC AG TCA  ACT CGAGG  CAG
 GAA  /
     TGGAGCTCAAACTCGACCGC                    A  CG   C--  CA  C  C  A--  -   TC  GCC  AAG
     ACGTCCCGATGCCGAAGCTT
     AGGCGCCAACC
GAM1790 CGGCCGCATTCATATTCTCG 43852  GCCGCATTCA 43853     C   ---  ATTC   TTTCT  G
     ATTTCTTGTGCAAACACCCG       TATTCTCGAT       CGGC GCAT  TCAT   TCGA   TGT C
     TTCGAAATGATCCATGCGCC       TTCT          |||| ||||  ||||   ||||   |||
     G                              GCCG CGTA  AGTA   AGCT    ACA A
                                     -   CCT   A---   TGCCC  A


GAM1791 ACGTAGTATCTATCTTGATA 43858  TATCTTGATA 43859    G   A -     - AA   A  C
     AGGCTATGCGAGCAGGCCCC       AGGCTATGCG       AC TAGT TC TATCTTG AT  GGCT TG G
     ATCCGGGATATGAGCTAGGT       AGCA          || |||| || ||||||| ||  |||| ||
                                  TG ATCG AG ATAGGGC TA  CCGG AC A
                                   G   - T     C  CC   - G


GAM1792 CAGGTCGATGAGTCACTGCG 43869  TGAGTCACTG 43870       ---  -       GATCCC    G
     ATCCCCACGGGCGACCGTGG       CGATCCCCAC       CAGGTCG  ATG AGTCACTGC     CACGG C
     CAGTGGCTGCGTTGGCGGCC       GGGC          |||||||  ||| |||||||||     |||||
     TG                             GTCCGGC   TGC TCGGTGACG     GTGCC G
                                      GGT  G       ------    A


GAM1793 GGAGCGGAACCCATTGAATA 43886  TACGTTAACC 43887      -   CCCA--  AATAATGT      A
CTATCA
     ATGTCGTGTATGAGTCTATC       CGCAGCATTT       GGAGC GGAA     TTG      CGTGTATG GT     A
     AATATTTCACCGTATACGTT       TTTC          ||||| ||||     |||      |||||||| ||
     AACCCGCAGCATTTTTTCCA                  CCTCG CCTT     GAC      GCATATGC CA     /
     GCTCC                           A   TTTTAC   GCCCAATT      - CTTTAT


GAM1794 GACTGGAACTTTGGTATAAC 43892  ACTTTGGTAT 43893      ---     TG   AACC  - C    C
     CCCCCCAGCTACAAGTAGTT       AACCCCCCCA       GACTG  GAACTT  GTAT   CC CC AGCTA A
     TGGAGGACACATATAGGTTT       GCTA          |||||  ||||||  ||||   || || |||||
     GTACAGTC                        CTGAC   TTTGGA  TATA   GG GG TTGAT A
                                   ATG    --   CACA  A  T    G


GAM1795 GGGTCGCAAGTTTTTACTAC 43914  TCGCAAGTTT 43915     C  A   TTAC       CCTAC   AC
```

AGGCTGGCCTACGTGCACGT TTACTACAGG GGGT GCA GTTT TACAGGCTGG GTGC G
CCGCGCCTTCGGCCTGTAAA CTGG |||| ||| |||| |||||||||| ||||
GCGTGCAGCCC CCCG CGT CGAA ATGTCCGGCT CGCG T
A G ---- TC--- CC

GAM1796 TCTGGCAACCACCCTCTGTG 43927 TTAGCCCACC 43928 AA CCCTCT A - C CT CCCAG
GACCTGGTGGCCTGACCTTA ATGGACCATC TCTGGC CCA GTGG CC TGGTGG CTGAC TAC A
CCCCAGATTTATGTATGTTA TTAT |||||| ||| |||| || |||||| ||||| |||
GCCCACCATGGACCATCTTA AGATCG GGT TACC GG ACCACC GATTG ATG /
TTGGGGGCTAGA GG TATTC- A T C T- TATTT

GAM1797 CCAGTTTCTAAGGTTGTCAG 43934 TCTAAGGTTG 43935 T- AG CA CG AA A CG
CACGGATGAATATGTGACTC TCAGCACGGA CCAGT TCTA GTTGT GCA GATG TATGTG CT C
GCACAAGCATATACTATCAT TGAA ||||| |||| ||||| ||| |||| |||||| ||
GCAAGCAGCTCTAGATTATT GGTTA AGAT CGACG CGT CTAT ATATAC GA A
GG TT CT AA A- C- - AC

GAM1798 GCTTCACAAGACCAACAAAA 43951 TAACTCAAGA 43952 AACAA-- - ACAACG---- C ------- ---- TT
GGTGGTGAACAACGTTTTGA ATTAAGAACT ACC AAG GTGGTGA TTTTGA TC GTCTA G
CTCGTCTATTGCCTGGATTA TTAA ||| ||| ||||||| |||||| || ||||| |||||
CTAACTCAAGAATTAAGAAC TGG TTC CACCACT AGAATT AG TAGGT /
TTTAAAAGTCACCACACTTG GTAGACG A GAAAATTTCA A AACTCAATCAT CC
CAGATGGGTCTGTGAAGT

GAM1799 TCTAGACTACTTGCAGTGGG 43961 AGTGGGTAAT 43962 C GCAG ATCCCTATTTCCCTA AA
TAATCCCTATTTCCCTATTA CCCTATTTCC TCTAGA TACTT TGGGTA TTAG A
GAAAAGCTAACAAAACTATT CTAT |||||| ||||| |||||| ||||
GTACCCAAGGTATCTGGA AGGTCT ATGGA ACCCAT AATC /
- ---- GTTATCAAAAC---- GA

GAM1800 AACGTGCTGCAAGTACATCT 43972 TGCAAGTACA 43973 CT- G C GC- C A TAAA GGT GGA
ACAGCCACACCTACACGTAA TCTACAGCCA AACGTG GCAA TACAT TACA CACAC TAC CG AA TAAAC A
AAAGGTTAAACGGAAATAGT CACC |||||| |||| ||||| |||| ||||| ||| || || |||||
TTATAATTGTGTTGGTATGT TTGTAT TGTT GTGTG ATGT GTGTG ATG GT TT ATTTG /
GTGTTATGTATGTGTGTTGT ATT - T ATT T - TGTG AAT ATA
TTATATGTT

GAM1801 CAAACATTACCATCGACACT 44013 TCGACACTTC 44014 - TA TC-- CACAA GAAC
TCACAATGCTGAACTGGTGG ACAATGCTGA CAAA CAT CCA GACACTT TGCT T
AGCAAAGTGTCACTCTGGCT ACTG |||| ||| ||| ||||||| ||||
GTGCTTTG GTTT GTG GGT CTGTGAA ACGA G
C TC CTCA ----- GGTG

GAM1802 TTGTGTCTTCTGAGGCCCAG 44022 TACACAAGGC 44023 T A CA T TTAATA TT
TTGTTTAATAAACCTTACTG CCAGGGACAC TTGTGTCT CTG GGCC GT GT AACC A
GTTACACAAGGCCCAGGGAC AA |||||||| ||| |||| || || |||| /
ACAA AACACAGG GAC CCGG CA CA TTGG /
- - AA - ------ TC

GAM1803 GAGATAGTTTTCTCTATTCT 44109 TGAAATAATT 44110 TTT - A ------- CTAGAAACAT
A A
GAAATAATTAGAACTAGAAA AGAACTAGAA GT CT CT TTCTG AAATAATTAGAA
GTTTAGAAA AA C
CATGTTTAGAAAAAAACGAT ACAT || || || ||||| |||||||||||| ||||||||| ||
TATTTCTGAATTATTCTAAT CA GA GA AGGAC TTTATTAATCTT TAAGTCTTT TT
G
TATTTGAACAAACAGGAAAG TAT A A AAACAAG AT-------- A A
AAGTATACTATCGTC

GAM1804 GCGAAGATGACTCTCAAATT 44119 TATTACACTT 44120 AAG ACT- AAA T TAC CGT
ATTACACTTACGGCATTCGT ACGGCATTCG GCG ATG CTC TTAT ACACT GGCATT T
TAACCAATGCCTATGGTGTC TTAA ||| ||| ||| |||| ||||| ||||||
ATAAACGAGTATCCGTATCC CGC TGC GAG AATA TGTGG CCGTAA A
GC CTA CTAT CA- C TAT CCA

GAM1805 GAGTGTTTATCCAGGGAAAT 44123 AGGGAAATCA 44124 CCAG A C GAA AA
CAAAGAAGAAGTTAATATAG AAGAAGAAGT GAGTGTTTAT GGA AT AAAGAA GTT T
ACAATTCTTTTGTATTCATA TAAT |||||||||| ||| || |||||| |||
GACACTC CTCACAGATA CTT TG TTTCTT CAG A
---- A T AA- AT

GAM1806 AGGAACAGATGTTTGCCAGA 44172 TTTCCCAGGA 44173 - G C A T- - G- -- A
GG
CATTTTTTTAATAGGGCTGG TCTGGTTATT AGGAACAG AT TTTGC AG CATTTTT TAAT AGG
CTGG AAC GTT T
AACAGTTGGTGAGGACGTTT AAAA |||||||| || ||||| || ||||||| |||| ||| |||| ||| |||
CCCAGGATCTGGTTATTAAA TCCTTGTC TA AAATG TC GTGAAAA ATTG TCT GACC
TTG CAG G
AGTGCTAGTAAAAATACTGT A A A - TT G AG CT - GA
TCCT

GAM1807 ATTTATTGGTATAATTTCAG 44191 TATTGGTATA 44192 T A C TATTC-- ATAC

TATTCGCATACTCTTCGGCA ATTTCAGTAT ATTTATTGG AT ATTT AG GC T
AACTTTCTCAAATCATCTAA TCGC |||||||| || |||| || ||
TGAAT TAAGTAATC TA TAAA TC CG C
- C C TTTCAAA GCTT

GAM1808 GTGGCGGGCCACCAATGGAG 44194 TGGAGGACCT 44195 - - A A A A TCACG AG
GACCTGATCACGGGCAAGAC GATCACGGGC GTGG CGGG CC CCA TGG GG CCTGA GGCA
A
ATGCCTCAGGGCCACCAATG AAGA |||| |||| || ||| ||| || ||||| ||||
GAGGACCTGATCAC CACT GTCC GG GGT ACC CC GGACT CCGT /
A A A A A G ----- AC

GAM1809 GGCATACAACAAACGATACA 44225 TGATTGCTGG 44226 ACA AAACGA T TG - TAC
GAACA
TATATGATTGCTGGTACTCC TACTCCCGGA GGCAT AC TACA ATA ATTG CTGG TCCCG
T
CGGAACATACCGCACGGGAA ACAT ||||| || |||| ||| |||| |||| |||||
CGTCAGTTAATTGTATTGTA TCGTA TG ATGT TAT TAAT GACT AGGGC A
GAAGAAGTCGATGCT GC- AAGAAG - GT T GCA ACGCC

GAM1810 TAATGCGCTTGGACTTTTTA 44240 TAAAACCTAT 44241 T T - TTTA G TAC
GTTGTATACTACTTTTGTAT AAGTTACATG TAA GCGC TG GACTT GTT TATAC T
AAAACCTATAAGTTACATGT TGTT ||| |||| || ||||| ||| |||||
GTTTTA ATT TGTG AC TTGAA CAA ATATG /
T T A TATC A TTT

GAM1811 ATACAATACAAAATACAACT 44248 TACAAAATAC 44249 - ACAACT A AC---- G
CTTCGCATGTAAGAACTGGA AACTCTTCGC ATACAATA CAAAAT CTTCGC TGTAAGA
TGGA A
GATATCCAAACATATCTTAC ATGT |||||||| |||||| |||||| ||||||| ||||
ACGCGGGGGTTTTGTTATTG TATGTTAT GTTTTG GGGGCG ACATTCT ACCT T
TAT T ------ C ATACAA A

GAM1812 TCCCCTCCTACGGGAGCAGC 44262 ACTATGCTTT 44263 CAGCATACC C T CG
AATGGACA GCTA AAG
ATACCGCTCGACACTATGCT ACGAAGGTAA AG GCTCGACA TA GCTTTA AAGGT CC
GGTGC G
TTACGAAGGTAATGGACACC TGGA || |||||||| || |||||| ||||| || |||||
GCTAGGTGCAAGGCAAGGCA TC TGAGCTGT AT CGGAAT TTCCG GG
TCACG C
CTGCAAGGAGAGGCCTTACT --------- C - CA GAGA---- AACG GAA
AAGGCTACTGTCGAGTCTCC
TGAGAGGTAA
GAM1813 TTGTGTCTTCTGAGGCCCAG 44273 TTACAAAAGG 44274 T A CAG TTAATA TT
TTGTTTAATAAACCTTATTG CCCAGGGACA TTGTGTCT CTG GGCC TTGT AACC A

GTTACAAAAGGCCCAGGGAC CAA ||||||||| ||| |||| |||| |||| ACAA AACACAGG GAC CCGG AACA TTGG / - - AA- ------ TT

GAM1814 GGCACCGATACGCGTGTTGT 44318 TCAAAGCGTT 44319 ACC - GTGTT A - TA TTTACAGAACTCTATGAGAG GTTACAGCC GGC GATA CGC GTTTT CAGAA CTC T TTTCTGGAGACTCAAAGCGT ||| |||| ||| ||||| ||||| ||| TGTTACAGCC CCG TTGT GCG CAGAG GTCTT GAG / ACA T AAACT - T AG

GAM1815 CAAATTACGTATAATATAGG 44413 AATTACGTAT 44414 ATT ATAATA GA G ------- A ATAAT GGAGTGGCTTTAGCATAATA AATATAGGGG CAA ACGT TAGGG GTG CT TT GC A TTTAAGCAGAAACAAACAGG AGTG ||| |||| ||||| ||| || || || CACCTCTCTACCAAGACGTT GTT TGCA ATCTC CAC GA AG CG / GTTG GT- GAACC- TC G CAAACAA A AATTT

GAM1816 ATCTAGTTAGTCCTTTGACG 44419 CGATTTGTCA 44420 T CCT--- GA- AA AGGATGAAAAGAGTCACGAT ACATCAAACT ATC AGTTAGT TTGACGAG TGA A TTGTCAACATCAAACTAATT AATT ||| ||||||| |||||||| ||| GAT TAG TTAATCA AACTGTTT ACT G - AACTAC AGC GA

GAM1817 ATAATTAGAACTAGAAACAT 44424 ACGATTATTT 44425 AAACAT - ---- ---- AAATTA AATTATTT GTCTAGAAAGAAACGATTAT CTAAATTATT G GTCTAGA AAGAA ACGAT TATTTCT TTCC G TTCTAAATTATTCCAATTAT CCAA | ||||||| ||||| ||||| ||||||| |||| TTGAACAAACAGGAAAGAAG C TAGATCT TTTTT TGCTA ATGAAGA AAGG / TATACTATCGTCATTTTTTT GACC-- C TTAC TCAT ------ ACAAACAA CTCTAGATCCAGCTACGATT GATAAT

GAM1818 CCGCCGCGCTCGGTCTCGGT 44434 TCGGTGCCGC 44435 - CT GG T TG GCG G T GCCGCGGGGTCGAGGCCGGT GGGGTCGAGG CCG CCGCG C TC CGG CC GG TCGAGGCCGG T TATCCGGTTTCGGGCCAGGA CCGG ||| ||||| | || ||| || || |||||||||| GTCGGAGAGGTCGCGGACGG GGC GGCGC G AG GCT GG CC GGCTTTGGCC A A TG AG - GA A-- G T

GAM1819 CTTTATCTATTCTGAATCAT 44443 TCTATTCTGA 44444 C C ATCA GAG GT GGAGCAGCTGGTTCTACAGC ATCATGGAGC CTTTAT TATT TGA TG CAGCTG T TGAACAACTATCAAAATATA AGCT |||||| |||| ||| || |||||| TAGAG GAGATA ATAA ACT AC GTCGAC C T A ATCA AA- AT

GAM1820 TTTAAAAAATGGTGTGGTAA 44461 TATATGCCAA 44462 AAA GT- - ACT
GTTATACACTAAAAGTATAG AGTTTAAA TTTAAA TGGTGTG AAGTT ATAC A
ACTTGTATATGCCAAAGTTT |||||| ||||||| ||||| ||||
AAA AAATTT ACCGTAT TTCAG TATG /
GAA ATG A AAA

GAM1821 GGGTGAGAACGTTCCAGAGT 44471 AGGGAAATCA 44124 CGTT A CCAG A C
GAA AA
GTCTATCCAGGGAAATCAAA AAGAAGAAGT GGGTGAGAA CC GAGTGTCTAT GGA AT
AAAGAA GTT T
GAAGAAGTTAATATAGACAA TAAT ||||||||| || |||||||||| ||| || |||||| |||
TTCTTTTGTATTCATAGACA CTTATTTTT GG CTCACAGATA CTT TG TTTCTT CAG A
CTCGGTTTTTTATTC T--- - ---- A T AA- AT

GAM1822 GGGCGCCCCGAGCATCGGCG 44472 TCTCTCGGTC 44473 C C C TGTC A
GTGTCTCTCGAGAGCTTTCG CTCGGGGCCC GGG GCCCCGAG ATCGG GG TCTCGAG G
AGATCTCTCGGTCCTCGGGG C ||| |||||||| ||||| || |||||||
CCCC CCC CGGGGCTC TGGCT TC AGAGCTT C
- C C T--- T

GAM1823 CGCCGCTGGCTCGGAGCCAA 44603 CTCGCCCACG 44604 CT - A C GCC T-- AT
GTGCGCCGGCGGCCGGGCTC CTGCTGCACT CGCCG GGCTCGG AGCC AGTGCG CGGCG
GGGC CGG C
GGATCGCTCGCTCGCCCACG CGGC ||||| ||||||| |||| |||||| ||||| |||| |||
CTGCTGCACTCGGCTCCCGG GCGGC CCGGGCC TCGG TCACGT GTCGC CCCG GCT
/
GCCCTCGGCG TC C C C A-- CTC CG

GAM1824 GTCTAGAAAATATAACGCAA 44633 TAACGCAATA 44634 GA AACG ATGTT- AA
TATGTTAGTTAAAAATGTAA TGTTAGTTAA GTCTA AAATAT CAAT AGTTA A
CTTGTTAGATTGATATTTCA AAAT ||||| |||||| |||| ||||| |||||
TGGGC CGGGT TTTATA GTTA TCAAT A
AC ---- GATTGT GT

GAM1825 ATAGACGCTATTTATCCGGG 44640 TGAGAACGTT 44641 ATTTATCC GTA- AA
CGGTATACCCAAAAGGGGTG CCAGAGTGTC ATAGACGCT GGGCG TACCC A
AGAACGTTCCAGAGTGTCTA TAT ||||||||| ||||| |||||
T TATCTGTGA CTTGC GTGGG /
GAC----- AAGA GA

GAM1826 GAGTGTCTATCCAGGGAAAT 44660 TAATTCTTTT 44661 CCAG A C GAA AA
CAAAGAAGAAGTTAATATAG GTATTCATAG GAGTGTCTAT GGA AT AAAGAA GTT T
ATAATTCTTTTGTATTCATA ACAC |||||||||| ||| || |||||| |||

GACACTC CTCACAGATA CTT TG TTTCTT TAG A
---- A T AA- AT

GAM1827 GTGTCGGTGACGCCGTGTGG 44679 TCGGTGACGC 44680 - -- CC - ACG-- ACCAGA
G
GTACGCCGGCACCAGACTAA CGTGTGGGTA GTG TCGGT GACG GTGT GGGT CCGGC
CTAA A
GAACTTAGAACCCCGCTGGA CGCC ||| ||||| |||| |||| |||| ||||| ||||
AAGGACCCTACACCGTCCTG CAC AGTCG CTGC CACA CCCA GGTCG GATT A
CTGACCAC C TC -- T GGAAA CCCCAA C

GAM1828 ATAATTAGAACTAGAAACAT 44684 TAGAAAGAAA 44685 AAAC CT --- ---- GAATTA
AATTATTT
GTCTAGAAAGAAACGATTAT CGATTATTTC TAG ATGT AGAAAGAA ACGAT TATTTCT
TTCC G
TTCTGAATTATTCCAATTAT TGAA ||| |||| |||||||| ||||| ||||||| ||||
TTGAACAAACAGGAAAGAAG ATC TATA TCTTTTTT TGCTA ATGAAGA AAGG
/
TATACTATCGTCATTTTTTT GACC TC TAC TCAT ------ ACAAACAA
CTCTATATCCAGCTACTACT
GATAAT
GAM1829 AGAGACTGTGATGGGGCAGC 44711 ACTGTGATGG 44712 T A TAC CAA CTCGACAACTAA
GT TA A G
CTACTCCAAAGACCCCTCGA GGCAGCCTAC GGGGC GCC TC AGACCC GGGA TCC
GGG CGGCAG C
CAACTAAGGGAGTTCCTAGG TCCA ||||| ||| || |||||| |||| ||| ||| ||||||
GACGGCAGGCTTCTGTCGCC CCCCG CGG AG TTTGGG CCCT AGG TCC
GCTGTC T
TCTGGATCCCCGGGTTTGCA C A TAA ACG C---------- -- TC - T
GAAATGGCAGCCCCCTTGTA
CCCTCT
GAM1830 CTGAAGAGGGGCTGCAACAT 44729 TCTTACGGAC 40239 AA CAACATGACTG T C T -
AAG C
GACTGCCTTGACATCTTGGC CAGCCTCTCC CTG GAGGGGCTG CC TGA ATCT GG CTG
CC A
TGAAGCCCACGGAACTAGAC CAG ||| ||||||||| || ||| |||| || ||| ||
CAGATCTTACGGACCAGCCT GAC CTCTCCGAC GG ATT TAGA CC GAT GG /
CTCCCAG C- CA--------- C C - A CAA C

GAM1831 GATACCCATTCAAGTGAAAG 44730 TGAAAGGCTA 44731 AG - -------- A - CTA ----
A
GCTATTATAGTTAGGAGGGC TTATAGTTAG TCA TGAA AGG CT TTATAGTT AGGAGGG
GCA ATATAAG A
TAGCAATATAAGAAAACTTA GAGG ||| |||| ||| || |||||||| ||||||| ||| |||||||
TATTCAATGTATTTTTTTTT AGT ACTT TCC GA AGTATCGA TTTTTTT TGT
TATATTC A
AAGCTATGAAAGTAAAGATA GA A ATAGAAAT A A TTA AACT A

CCTATTCAAGTGAAAGGCTA
TT
GAM1832 GTATAAAAAACTTAAGGTTT 44743 AAGAAACTGA 44744 AAAA A- AAA--- CCATA
AAA
ATTTAAAAGTCCATATTTTA ATAGAAATAG GTATA ACTTA GGTTTATTT AGT TTTTAT A
TAAAAGTTAATGAAAAAGAA ATTG ||||| ||||| ||||||||| ||| ||||||
ACTGAATAGAAATAGATTGA CGTAT TGAAT TTAGATAAA TCA AAAGTA G
TAAGTCCATATGC ACC- AG GATAAG AAGAA ATT

GAM1833 TGTCTAGAAAGAAACGATTA 44756 ACGATTATTT 44757 - ---- ---- GAATTA
AATTATTT
TTTCTGAATTATTCCAATTA CTGAATTATT TGTCTAGA AAGAA ACGAT TATTTCT TTCC
A
TTTAAACAAACAGGAAAGAA CCAA |||||||| ||||| ||||| ||||||| ||||
GTATACTATCGTCATTTTTT ATAGATCT TTTTT TGCTA ATGAAGA AAGG /
TCTCTAGATA C TTAC TCAT ------ ACAAACAA

GAM1834 GGCAGCGCCGCCCGCCCGCA 44766 TGCCGAGGCG 44767 CGC--- - - ---- T
GCGGCGGTCCCCCGCCCTCG GCCCATCGTG GGCAGCGC CCGCC CG CAGC GGCGG C
GCTGCCGAGGCGGCCCATCG CTGC |||||||| ||||| || |||| |||||
TGCTGCC CCGTCGTG GGCGG GC GTCG CCGCC C
CTACCC A C GCTC C

GAM1835 AGAGTTGCATGAAGATATTG 44784 CACTGCACTG 44785 GAAGATA GAAA- C - AG TG
CG ATC-- A
TTGAAATTCTCCGCAGAAGG TGGCCCAATT TTGTT TTCT CG CAGA GGGT CA GCAG
AATCCAG C
GGTTGCACGGCAGATCAATC TGAC ||||| |||| || |||| |||| || |||| |||||||
CAGACACTGGATTCCGCACT AACAA AAGA GC GTTT CCCG GT CGTC
TTAGGTC /
GCACTGTGGCCCAATTTGAC AGGAA-- AGAGA A A AA GT CA ACGCC A
GAAGAAAGAGAAACAAAAGG
AATGCAATTCT
GAM1836 GATGACTGGTTTCTATTTGG 44813 TTTCTATTTG 44814 G--- TT- A GT
TGACAGTCGTTCTGACTGTA GTGACAGTCG GATGACTG TTTCTAT GGTG CAGTC T
CCTATGTAGAAAATAACGGT TTCT |||||||| ||||||| |||| |||||
CATC CTACTGGC AAAGATG CCAT GTCAG /
AATA TAT - TC

GAM1837 GGGACCGCTCCAATGAGTTC 44821 TGCTGGGGGA 44822 CG--- AA G TAT A G
TCCTATGGCAAGCGGTCGCT GTCAGGAGAC GGGAC CTCC TGA TTCTCC GGCA GC G
GCTGGGGGAGTCAGGAGACA ACCG ||||| |||| ||| |||||| |||| ||
CCGTCCC CCCTG GAGG ACT AGGGGG TCGT CG T
CCACA -- G --- - C

GAM1838 GGTGGAGATGGCAGAGGCTG 44867 AGAGGCTGTC 44868 CA TC C C
TCGCCGCGCCCGAGGTGCTG GCCGCGCCCG GGTGGAGATGG GAGGCTG GC GCGCC G
CCCAGCCTCCCCGTCTCCAT AGGT |||||||||| ||||||| || |||||
C CTACCTCTGCC CTCCGAC CG CGTGG /
C- C- T A

GAM1839 GCCGCCTGTCCCCGGATCAC 44889 TCCCCGGATC 44890 C -- CA- C GATC ACGC
CCCGTGATCGTCCGACGCCA ACCCCGTGAT GCCGC TGTCCC CGGAT CCC GT GTCCG C
CTACCGGGCCAACTGGGCCA CGTC ||||| |||||| ||||| ||| || |||||
GTCTGAAGGGACGCGTGGC CGGTG GCAGGG GTCTG GGG CA CGGGC A
C AA ACC T AC-- CATC

GAM1840 GTGGTGATTTAGAAATAGGA 44895 TGATTTAGAA 44896 AAATA AGA C AGGATG
GACCTACCGCAGGATGATGA ATAGGAGACC GTGGTGATTTAG GG CCTAC GC A
GGAAGCGTGGGCCGAGCTAA TACC |||||||||||| || ||||| ||
GTTACCAC CACCATTGAATC CC GGGTG CG T
GAG-- --- - AAGGAG

GAM1841 CAAAGAAACACCTACTTCTT 44914 TTCGTACCGT 44915 GA C -- G--- TG C- T C
CAGACATGTGCACGATAATA GTGTAGAATG CAAA AACAC TAC TTCTTCA ACA TG ACGA
AATAG A
GCATCTATTTTCGTACCGTG AAGG |||| ||||| ||| ||||||| ||| || |||| |||||
TGTAGAATGAAGGGTTGTAT GTTT TTGTG ATG GGGAAGT TGT GC TGCT TTATC /
GTGTTGATTTG AG T TT AAGA GT CA T T

GAM1842 TTGGCTTGACCTCGACCCAA 44919 TGTGTAATTC 44920 GA G AA-- T T GA AT----
GC T T
AGTTGTGTAATTCAGGAAAG AGGAAAGATT T CCTC ACCC AGTTGTG AA TCAG AAG
TTCC AAAGAG GG A
ATTTCCGCAAAGAGTGGTAA TCCG | |||| |||| ||||||| || |||| ||| |||| |||||| ||
CTCTCTCTTTAGGAGTTTTC G GGAG TGGG TTAACAT TT AGTC TTC GAGG
TTTCTC CT A
ACTTCACTGATTTTTACAAT AG - CATA T T AC ACTTTT A- T C
TATACGGGTGAGGGAGACCA
A
GAM1843 GGCGCCCGCGGCGGTTCCGG 44925 CCCGCGCGCG 44926 C - TC T CTCCCCCA
TGCCTCCCCCAGCCCCTCCA CCGCGTGCGC GGCGC CGCGGCG GT CGG GC G
GCCCCGCGCGCGCCGCGTGC C ||||| ||||||| || ||| ||
GCC CCGCG GCGCCGC CG GCC CG /
T G C- C ACCTCCCC

GAM1844 TTAATCTGTGTGTCCTGTTC 45227 TACAATATAC 45228 TCT CC TCC CC A-- A-- G
TTATG
CACCCCATGAGTAAGTGTTG AACATATGTA A GTGTGT TGT AC CATG GTA GTGTTGTA
TATTGTGTG T

TAGTATTGTGTGTTATGTCT CAGC | |||||| ||| || |||| ||| |||||||| |||||||||
GGTGTATACAATATACAACA T TACACA ATA TG GTAC CAT TACAACAT
ATAACATAT C
TATGTACAGCCATGTTGTTT TT- AA TTT TT CGA GTA - GTGGT
TATAAAACACATTTTTAA

GAM1845 TAAAGGGGGCACATGTGGCT 45273 AAGGGGGCAC 45274 -- GTGGCTAT AA
ATAGTAGAATCTCTACTCAA ATGTGGCTAT TAAAGGGGGC ACAT AGTAG T
TATAGTGTCCGCCCCCTTTA AGTA |||||||||| |||| |||||
ATTTCCCCCG TGTG TCATC /
CC ATATAAC- TC

GAM1846 CAGGCTGATGAGTCACCGTA 45284 TGAGTCACCG 45285 --- - ATTCCC G
TTCCCCACGGGCGACCGTGA TATTCCCCAC CAGGCTG ATG AGTCACCGT CACGG C
CGGTGGCTGCGTTGGCGGCC GGGC ||||||| ||| ||||||||| |||||
TG GTCCGGC TGC TCGGTGGCA GTGCC G
GGT G ------ A

GAM1847 GTTTCTATAACAACCTCCCC 45294 TCTATAACAA 45295 T CAAC CCCC--- CC- A
CAGGTCCAGTTATGAACTCC CCTCCCCCAG GT TCTATAA CTC AGGT AGTT T
CACCTTACACCAGAGATATT GTCC || ||||||| ||| |||| ||||
ATGGATGC CG AGGTATT GAG TCCA TCAA /
T ATA- ACCACAT CCC G

GAM1848 GAAACTAGACATAAAATAAA 45309 AGAGAAGTTA 45310 ACT A AATATTTA--- TTGGA TT
AAG- GAA
TATTTACCAACTTGGAACTT GGTGTTTGTT AGACATAA ATA CCAAC ACTT ACTTC
TCAT G
TTACTTCAAGTCATGAAGAT GGGA |||||||| ||| ||||| |||| ||||| ||||
AGTGGAAGAGAAGTTAGGTG TCTGTATT TAT GGTTG TGGA TGAAG GGTG
/
TTTGTTGGGAGCCTTGAAAT CTT C AAAGTTCCGAG TTTG- T- AGAA ATA
ATCTTATGTCTTTCCTC

GAM1849 TAATAGTACAGAATATAAAC 45337 TACAGTTTAT 45338 G ------ AAT---------- C
AATACATGCGACATGTTGAG GTTTCAATTA TAATA TACA GAATATAAAC ACATG G
GAGTTTGACTTACAGTTTAT TGTA ||||| |||| |||||||||| |||||
GTTTCAATTATGTAGTATTA ATTAT ATGT TTTGTATTTG TGTAC /
G ATTAAC ACATTCAGTTTGAGGAGT A

GAM1850 AAAACGTCCTGCATCTGCAG 45345 TAGGAAGAAG 45346 TCCT C AGCC A CC TAA
CA
CCACTTCATCCTCCAGTAAA TAGTATGTGT AAAACG GCAT TGC ACTTC TCCT AG ACC A
CCCAAACGGTCTAGGAAGAA TATT |||||| |||| ||| ||||| |||| || |||
GTAGTATGTGTTATTGTTTT TTTTGT TGTG ATG TGAAG AGGA TC TGG /
TAT- T A--- A -- --- CA

```
GAM1851  CCTTTTGCTTGTTCACTGTG 45353   ATGCTGCGCA 45354    T     G   C          ACATT
         CGGCATTATTACATTTACAC       TGAAAGAGCG       CC TTTGCTT TTCA TGTGCGGCATTATT    T
         CGGTAATGCTGCGCATGAAA       AACG           || ||||||| |||| ||||||||||||||
         GAGCGAACGG                    GG AAGCGAG AAGT ACGCGTCGTAATGG    /
                                  C     A   -          CCACA


GAM1852  GGAGGAGATAAATATCTTAC 45365   TGAGCTGAGG 45366     A  AAAGA     GA--  AC    CAA
GG-  AAAA   GT
         GCAAAGAAGCGCTTGAGCTA       TTACAGATTT       TCTT CGC    AGCGCTT   GCT  AGAAA   GTGAC
AGC   GGCT  T
         CAGAAACAAGTGACGGAGCA       CTAA           |||| |||    |||||||   |||  |||||   |||||   |||   ||||
         AAAGGCTGTTGTGGCTGAGC                  AGGA GCG    TCGCGGG   CGA  TCTTT   CATTG   TCG
TCGG  /
         TGAGGTTACAGATTTCTAAG                   C   A----     ACAA   A-    AGA    GAG   AG--   TG
         CAACAGGGCGCTAGCGCAGG
         AACTACCTCT
GAM1853  GCACTGATAGACGCGATAGA 45384   TTGAATGTTG 45385     T  TAGAC      G     TACCCAT   T
TG   AGT
         GCGAGATTACCCATATATCG       TTTATGTTTT       GCAC GA    GCGATAGA CGAGAT      ATA CGTT
GGG   T
         TTTGGGGAGTTATGCCTTGA       GTTT           |||| ||    |||||||| ||||||      ||| ||||  |||
         ATGTTGTTTATGTTTTGTTT                  TGTG CT    TGTTATTT GTTTTG      TGT GTAA  TCC   /
         ATTGTTTTTCTGTGT                     T  TTT--       -     TATT---   T    GT   GTA


GAM1854  CGAGGGGAACGGGGGATGGA 45399   TGGAAGGACG 45400    A   AA     A      AC   AA   GA  TCC
AT
         AGGACGGGAAGTGGAAGTCC       GGAAGTGGAA       CG GGGG  CGGGGG TGGAAGG  GGG  GTG  AG
 TG  A
         TGATACCCATCCTACACCCC       GTCC           || ||||  |||||| |||||||  |||  |||  ||   ||
         CCTGCCTTCCACCCTCCGGC                   GC CCCC  GCCTCC ACCTTCC  CCC  CAC  TC   AC  /
         CCCCCG                        -   CG     C      GT   CC   A-  CT-  CC


GAM1855  GCTTTTCACGCCACGCGTAT 45450   TACCAGGCTG 45451       T  C    C  ---      ACGAGTTTT
         AAACGAGTTTTCAGTCATAA       GCATGGAAGC       GCTTT CA GCCA GC   GTATAA       C
         ATTGTACCAGGCTGGCATGG                  |||||  ||  ||||  ||   ||||||
         AAGC                          CGAAG GT CGGT CG   CATGTT       /
                                     -  A    -  GAC      AAATACTGA


GAM1856  GACCCACGTACTCCAAGAAG 45586   TGCCTGGCTC 45587       C   CTCCA  A-      TGTCC   CCC
         GCATGTGTCCCACCCCGCCT       TCTATGCTTG       GACCCA GTA    AG  AGGCATG     CAC   G
         GTGTTTTTGTGCCTGGCTCT       GGTC           ||||||  |||    ||  |||||||     |||
         CTATGCTTGGGTC                        CTGGGT CGT    TC  TCCGTGT     GTG   /
                                     T   ATCTC  GG      TTTT-   TCC
```

GAM1857 AGAATGCCTGGGAAATGATA 45606 TGAGTACGAA 45607 ATG-- GAAA TAG A --- GAA-
AGAAA
GAGAAAGAGAGACTGAAACT GTCAATTCTC AGA CCTGG TGA AG AAGAGA GACT
ACTTAGTGC A
TAGTGCAGAAAAGAACCGCG TTAC ||| ||||| ||| || |||||| |||| |||||||||
CTGAGTACGAAGTCAATTCT TCT GGACC ACT TC TTCTCT CTGA TGAGTCGCG
/
CTTACTTCAGCCAGGAATAG GATAA G--- --- A TAA AGCA CCAAG
TCT

GAM1858 GACTTAAACGCATACGGGTA 45622 TCCACCCTCC 45623 A-- -- AC- ATA CA
TAGACTATCACGCAATGGTC GTGCTGGTTA GACTT AAC GCAT GGGT GACTAT C
CACCCTCCGTGCTGGTTACC CCGA ||||| ||| |||| |||| ||||||
GAGTC CTGAG TTG CGTG CCCA CTGGTA G
CCA GT CCT C-- AC

GAM1859 CTCAAGAGCTGTGGTCAGCG 45652 CAAGAGCTGT 45653 A- A T C------- CAACACTCT
CTCAACACTCTAATGCCTCT GGTCAGCGCT CTC AG GCTG GGT AGCGCT A
AAGCGCTCTCACCTCACCCA CAAC ||| || |||| ||| ||||||
GCCTCCGAG GAG TC CGAC CCA TCGCGA /
CC - - CTCCACTC ATCTCCGTA

GAM1860 TAGAAACTGATGACTCATGC 45701 ATCTCTTTCC 45702 A ATGACTCATGC CCCAATC
ACC
GCTGGCCCAATCTCCACCTT AGCCAGTTAC TAG AACTG GCTGG TCC T
CCAGGATCTCTTTCCAGCCA TA ||| ||||| ||||| |||
GTTACTA ATC TTGAC CGACC AGG T
A ---------- TTTCTCT ACC

GAM1861 GACTTCTTTCCAGAGATTGT 45777 TAACTGCCCC 45778 C--- A----- TTCCAA
CTTCCAACTCAACATGATAA TCTGACAAAA GACTTCTTT CAGAG TTGTC C
CTGCCCCTCTGACAAAAAGA AGAA ||||||||| ||||| |||||
AGTT TTGAAGAAA GTCTC AATAG T
AACA CCCGTC TACAAC

GAM1862 GGCAATTGTCTCTACCGCTC 45818 TCGCGACCCA 45819 CTCTAC---- TCC TCA
CTGGTGTCAAGTTTACCGTC AATGTGCGAT GGCAATTGT CGC TGGTG A
GCGACCCAAATGTGCGATTG TGCC ||||||||| ||| |||||
CC CCGTTAGCG GCG GCCAT /
TGTAAACCCA CT- TTG

GAM1863 GGCGTTCATCGGTCTCGGGC 45825 TAGCTGCGGC 45826 TC-- CTC G - ATAT
GCGCGCTGGTATATCTTAAC CTAACCCATT GGCGTTCA GGT GGGC CGC GCTGGT C
ACTAGCTGCGGCCTAACCCA TGGA |||||||| ||| |||| ||| ||||||

TTTGGACGTT TTGCAGGT CCA TCCG GCG CGATCA T
TTAC A-- - T CAAT

GAM1864 TCCTATCCTGCTGAACTTTA 45840 TTCAGCTAGT 45841 C TG T A T
GCAGAAACTCTAGCGAGTTT GTTGTATGAT TCCTATC TGC AAC TTAGC GAAACTC A
CAGCTAGTGTTGTATGATAG AGGA ||||||| ||| ||| ||||| |||||||
GA AGGATAG ATG TTG GATCG CTTTGAG G
T -- T A C

GAM1865 ATACCCGGCGATTTTCCCAA 45845 ACCCGGCGAT 45846 GG -- ACCACC- TCTAACA
CCACCCCTCTAACAACGATA TTTCCCAACC ATACCC CGATTT TCCCA CC A
TACGGCATTCCCTGGGACCA ACCC |||||| |||||| ||||| ||
GGTCGAGGGTGT TGTGGG GCTGGA AGGGT GG C
A- CC CCCTTAC CATATAG

GAM1866 ATAATTAGAACTAGAAACAT 45900 AAACAGGAAA 45901 AC AAAC TT --- ----
GAATTATTC--- T
GTTTAGAAAGAAACGATTAT GAAGTATACT TAG ATGT AGAAAGAA ACGAT TATTTCT
CAA T
TTCTGAATTATTCCAATTAT ATCG ||| |||| |||||||| ||||| ||||||| |||
TTGTCCAAACAGGAAAGAAG ATC TATA TCTTTTTT TGCTA ATGAAGA GTT
A
TATACTATCGTCATTTTTTT TC GACC TC TAC TCAT AAGGACAAACCT T
CTCTATATCCAGCTACTGCT
GATAAT
GAM1867 GAATGTTCCAGAGTGTTTAT 45921 TTCCAGAGTG 45922 TT--- A CCAG A T GAA
AA
CCAGGGAAATTAAAGAAGAA TTTATCCAGG GAATG CC GAGTGTTTAT GGA AT AAAGAA
GTT T
GTTAATATAGACAATTCTTT GAAA ||||| || |||||||||| ||| || |||||| |||
TGTATTCATAGACACTCGGT CTTAT GG CTCACAGATA CTT TG TTTCTT CAG A
TTTTTATTC TTTTT - ---- A T AA- AT

GAM1868 TAAAGCTGATTGTATAAATT 45963 AAGCTGATTG 45964 ---------- C ATACCTA
TACTATTAATACCTAATTGA TATAAATTTA TAAAGCTGATTGTAT AAATTTA TATTA A
CCACTAATAATAAATTTTTT CTAT |||||||||||||| ||||||| |||||
ATCATTAATATAATTAGTTT ATTTTGATTAATATA TTTAAAT ATAAT T
TA ATTACTATTT A CACCAGT

GAM1869 GCGAGGATGACTCTCAAATT 45973 TATTACACTC 45974 A---- A TCAAA T CAC CGT
ATTACACTCACGGCATTCGT ACGGCATTCG GCG GGATG CTC TTAT ACACT GGCATT T
TAACCAATGCCTATGGTGTC TTAA ||| ||||| ||| |||| ||||| ||||||
ATAAACGAGTATCCGTGTCC CGC CCTAT GAG AATA TGTGG CCGTAA A
GC CTGTG - CA--- C TAT CCA

GAM1870 GGCTGCGGGACAGTGATGGA 45976 ATGGAGATGA 45977 ----- - AT G AT-- - A
GATGATGGTGGCCCAGAGGG TGGTGGCCCA GGCTGC GGGACA GTG GGA ATG GGTGG CCC G
ACCACCTGCGCGTGTCCCAC GAGG |||||| |||||| ||| ||| ||| ||||| |||
GTGTCCCCCTTTGCGGTC CTGGCG CCCTGT CAC CCT TGC CCACC GGG /
TTTCC G -- G GCGT A A

GAM1871 AGAAAGAAACGATTATTTCT 46041 ACGATTATTT 44757 --- ---- GAATTA AATTATTT
GAATTATTCCAATTATTTGA CTGAATTATT AGAAAGAA ACGAT TATTTCT TTCC G
ACAAACAGGAAAGAAGTATA CCAA |||||||| ||||| ||||||| ||||
CTATCGTCATTTTTTTCT TCTTTTTT TGCTA ATGAAGA AAGG /
TAC TCAT ------ ACAAACAA

GAM1872 GGATGACTCTCAAATTATTA 46042 TATTACACTC 45974 A TCAAA T CAC CGT
CACTCACGGCATTCGTTAAC ACGGCATTCG GGATG CTC TTAT ACACT GGCATT T
CAATGCCTATGGTGTCATAA TTAA ||||| ||| |||| ||||| ||||||
ACGAGTATCC CCTAT GAG AATA TGTGG CCGTAA A
- CA--- C TAT CCA

GAM1873 GTCGCAGGCCCAGTAGAGCG 46043 GCCCAGTAGA 46044 CA A GA CG TC GGT
CCGGGTTCTCCGGGTCGAAC GCGCCGGGTT GTCG GGCCC GTA GCGC GGTTC CG C
GTGAGCCGTGTGTGCGGGCC CTCC |||| ||||| ||| |||| ||||| ||
CTTGAT TAGT CCGGG CGT TGTG CCGAG GC /
TC - G- -- T- AAG

GAM1874 GGCCCGCGCACAACAAATCG 46085 TGTGATAGAA 46086 GCGCACAACAA A CTTAAC T
CGGATTACTTAACTGCATCC TACGATAGGG GGCCC ATCGCGG TTA TGCA C
ATGCAAGCACTGACTGTGAT CC ||||| ||||||| ||| ||||
AGAATACGATAGGGCC CCGGG TAGTGTC AGT ACGT C
ATAGCATAAGA - CACGA- A

GAM1875 GCGTAATGGGCGTGGTCATC 46113 CTGCAGTTGG 46114 AATG T- - C ATATA GT
CTCGGCTATATAAGGGGGCG TGATCGACTT GCGT GGCG GGTC ATC TCGGCT AGGGGGCGC C
CGTCGAGCGCTTCCTGCAGT CCGC |||| |||| |||| ||| |||||| |||||||||
TGGTGATCGACTTCCGCCAG CGCA CCGC TCAG TAG GGTTGA TCCTTCGCG /
GGACGC GGGA CT C T CG--- AG

GAM1876 ATTTCTTCTCCGTGTTGCAG 46123 AGCCAAGACG 46124 TG C CTATGATA G ATG
ATCTATGATATTGGTGCGAT TTTACAAGTC ATTTCTTCTCCG TTG AGAT TTGGT CG G
GGTCACGAGCCAAGACGTTT GGAG |||||||||||| ||| |||| ||||| ||
ACAAGTCGGAGGAGGAGT TGAGGAGGAGGC AAC TTTG AACCG GC /
TG A CAG----- A ACT

GAM1877 CCCTCTCCTTCATGCGCCGA 46136 AAGAGGCTGT 46137 CCTTCAT C CGAC G
TACCCCGACTCGGTGACGAA CGGTGTCCCC CCCTCT GCGCCGATA CC TCG T
GAGGCTGTCGGTGTCCCCGT GTAG |||||| ||||||||| || |||
AGAGGG GGGAGA TGTGGCTGT GG AGC G
TGCCCC- C AGA- A

GAM1878 AGAGCTGTCGCGAAGTATTC 46152 TCGCGAAGTA 46153 C TATTC GTG TAA CG AAT
GCTCCGTGCGGGTAACGCCG TTCGCTCCGT AGAGCTGT GCGAAG GCTCC CGGG CGC A A
AAATAGACTTAGCGCCCGAG GCGG |||||||| |||||| ||||| |||| ||| |
GAGTTTTCGTACGGCTCT TCTCGGCA TGCTTT TGAGG GCCC GCG T /
- ----- A-- --- AT CAG

GAM1879 GATGTAGTAGACGTTGGCGC 46157 TAGTAGACGT 46158 AGT G---- TG C AT-- A
GGATGGGATCTCCCTTGGCC TGGCGCGGAT GATGT AGAC T G GCGG GGG T
GCCTTGAAGTGGGTCTTGGC GGGA ||||| |||| | | |||| |||
ATC CTACG TCTG A T CGCC CCC C
GT- GGTGA GT C GGTT T

GAM1880 GTACGCGGTGAAGGTAAGTT 46162 TTCGTCTTTG 46163 A GT T CA TG--- T TGGGA GTC-- GG
GCTTCCAAAAGGCGTGGGTG AAGTACTTGT G AAGT GCTTC AAAGGCG GGTGT GC ATGGTGG GCA A
TTGCTGGGAATGGTGGGTCG CGTA | |||| ||||| ||||||| ||||| || ||||||| |||
CAGGAAAATGTTAAAGTCGC C TTCA TGAAG TTTCTGC CCGTA CG TGCCGCT TGT A
CGTGCATGCCGAGTTCGTCT G TG - -- TTGAG - ----- GAAAT AA
TTGAAGTACTTGTCGTAACT
GTCGTAC
GAM1881 GTCGCTGGGCGCGACGACTC 46165 TGGAAGAGGA 46166 GGGCGC-- - GCGC GA G -- G TCCT
CTCGCGCCCACCTGTGAAGC CGTCGTTAAA GTCGCT GACGAC TCCTC CCACCTGT AGCC CG TG GG T
CGCGTGGGGTCCTTTTTATC GAGG |||||| |||||| ||||| |||||||| |||| || || ||
GTAGTTGGGGTTGGGCAGGT CGGCGG TTGCTG AGGAG GGTGGACG TTGG GT AT CT /
GGAAGAGGACGTCGTTAAAG AGGAGAAA C AA-- GG G TG G ATTT
AGGAGGCGGC

GAM1882 GGTTGTGTCATGACGGGCTT 46212 TCCACAGTGG 46213 T CA CG- - - AA TGC T CTA
CAGTCCATTAAGTGGATGCT GCGTGGCAGC GGT GTGT TGA GGCT TCA GTCCATT GTGGA TG CAC C
GTCACCTACTGAGTGCCACC CACA ||| |||| ||| |||| ||| ||||||| ||||| || |||

TTCCACAGTGGGCGTGGCAG CCA TACG ACT CCGA GGT CGGGTGA CACCT AC
GTG /
CCACATCAAGCATACC - A- ACA C G -- TCC C AGT

GAM1883 ACTACTTAGGCATGGCTGCT 46277 AGGCATGGCT 46278 TTA GC CT CCCCTA - CA
TTTC
GACCCCTATGGCGACAGCAT GCTGACCCCT ACTAC GGCATG TG GA TGGCGA CAG
TGTTTTTT T
GTTTTTTTTTCTGCGTAGGG ATGG ||||| |||||| || || |||||| ||| ||||||||
AACAACTGTTTGCCAGGCAC TGATG TCGTGC AT CT ACCGTT GTC ACAAGGGA /
TTCTTTAATCGTGCTGGTGT TGG TA TT TCACGG T A- TGCG
AGT

GAM1884 CCTGGCAGTGCCATATACAG 46310 TGGCAGTGCC 46311 ATACA- ACACCTAG CATG
AC -- CAAATA
TCCCACACCTAGTGGGTCCA ATATACAGTC TGCCAT GTCCC TGGGTC GTA GTC
TGAGGCT T
TGGTAACGTCTGAGGCTCAA CCAC |||||| ||||| |||||| ||| ||| |||||||
ATATTTAATAAGCCTTACTG ATGGTA CAGGG ACCCGG CAT CGG ATTCCGA
/
GCTACAGCAGGCCCAGGGAC ACAACA -------- ACGA -- TC ATAATT
ACAACAATGGTATATGCTGG
G
GAM1885 AAACAAGGTAGAAACCAACG 46337 TGGTATTTCC 46338 ----- A AC AC-- CC AGG
AAGCATTA- AA
GGGTCCTCAGGTGGTATTTC GGAAGCATTA A GGT GAA CA GGGGT TC
TGGTATTTCCGG CC A
CGGAAGCATTACCAAATAAG CCAA | ||| ||| || ||||| || ||||||||||| ||
GCAACCTCAGCTGGGAATAC T CCA CTT GT CCCCA AG ACCATAAGGGTC
GG T
CAGCGGACTACCCCCAACTG TCCTC A AT CAAC TC GCG GACTCCAAC AA
TATTCAACCCTCCTTTGTTT

GAM1886 ACACAACTGTGCATTCTGGG 46349 AACACTGGGG 46350 ACT AT--- G C A CC
CTGTACGCCTCCCATGGGCG TAAGGGCACT ACACA GTGC TCT GG TGT CGCCT C
AACACTGGGGTAAGGGCACT GTGT ||||| |||| ||| || ||| |||||
GTGTGT TGTGT CACG GGG TC ACA GCGGG /
GT- GGAAT G - A TA

GAM1887 TAGGTTTGTAACATCCTCTG 46376 TTGGCCCCTA 46377 G - -- - ----------- TAA GT
CCATAACTTGTCAAAAAGAT CAGAAAAGCA TAG TTTGTA AC ATCCT CT GCCA CTT C
TTGGCCCCTACAGAAAAGCA GGAT ||| |||||| || ||||| || |||| |||
GGATCCGTATGCAAAGCTA ATC AAACGT TG TAGGA GA CGGT GAA A
G A CC C AAAGACATCCC TTA AA

GAM1888 GTGTGTATGTATTTATTACC 46401 AAGTATGTCA 46402 TT TACCA TT GTC--- TG
ATG T ATA

ATATGTGTTTGTATGTCTGT CATAGTTTTA TAT TATGTG TGTAT TGTATGTC TACA
TATGTA GT C
ATGTCTGTACAATGTATGTA TATT ||| |||||| ||||| |||||||| |||| |||||| ||
TGTATACTTCAACTATGTAT ATA ATACAC GTATG ATATGTAG GTGT ATGTAT CA
T
GTGTGGATGTATAAATAAAG T- TTTTG T- AAATAA GT --- - ACT
TATGTCACATAGTTTTATAT
TTTATACATAT
GAM1889 CACCCCAGGAGCCCCGGCAG 46409 CAGCACCCCA 46410 C- CA A CCA A C- CA A CCA
A C- CA A C
CACCCCAGGAGCCCCGGCAG GGAGCCCCGG GC CCGG GC CC GG GC CCGG GC CC GG
GC CCGG GC CC C
CACCCCAGGAGCCCCGGCAG CAGC || |||| || || || || |||| || || || || |||| || ||
CACCCCAGGAGCCCCGGCAG CG GGCC CG GG CC CG GGCC CG GG CC CG
GGCC CG GG /
CACCCCAGGAGCCCCGGCAG AC C- A ACC A AC C- A ACC A AC C- A A
CACCCCAGGAGCCCCGGCAG
CACCCCAGGAG
GAM1890 CTTTGTTGAACTTGCCGTAC 46574 TGTTGTAGCC 46575 C CCG CAG T ATA AC C---
CTA T GC
CCGTCCAGCTTGATGTTATA GGTGGCGAAC GTAC TC CTTGA GTT CACCG GTTAC
TTGTTAA TG AC C
CACCGACGTTACCTTGTTAA TCGG |||| || ||||| ||| ||||| ||||| ||||||| || ||
CTATGTACGCCCAGTCAAAA CATG AG GGGCT CAA GTGGC CGATG AGCAATT
AC TG /
TTAACGATGTTGTAGCCGGT T --- A-- - GCG -- TTGT AAA - AC
GGCGAACTCGGGAGAGTACT
GCTTGAGAAAG
GAM1891 AGGGTGTTTCGGGTGCGGTT 46579 CGGGTGCGGT 46580 GTTT---- - - TG- T CCT
GCCTGACCCTAATAAGTTTG TGCCTGACCC AGGGT CGGGTG C GGT CC GAC A
GACTGCCTGACGCCCGCATA TAAT ||||| |||||| | ||| || |||
TATAACCCT TCCCA GCCCGC G CCG GG TTG A
ATATATAC A T TCA T AAT

GAM1892 CACCTCCAATGGGAGAGCAT 46584 ACAGGGCGAT 46585 - AAT---- ------ A TG CA AA----
C AA
TGGGGCAAGGGAACCCCGTG TGCCCTCCCC C TCC GGGA GAGC T GGG AGGG
CCC GTGCAGG C
CAGGAACCCACCTGCACAGG TGGA | ||| |||| |||| | ||| |||| ||| |||||||
GCGATTGCCCTCCCCTGGAG G AGG CCCT TTCG G CCC TCCC GGG
CACGTCC C
CTTATAACTTCCCCTATTCA T ACTTATC TCAATA A GT C- GTTAGC A AC
GGATGGTG

GAM1893 GTGTTTTTGATTGTAGCGGA 46614 TTTTTGATTG 46615 ATT - AAA-- TA
AAAATGTAATAAATTTTACA TAGCGGAAAA GTGTTTTTG GTAG CGGAA TGTAA A
GACAGTTTTGCCTACTGAGA ATGT ||||||||| |||| ||||| |||||
ACAT TACAAGAGT CATC GTTTT ACATT A
--- C GACAG TT

GAM1894 ATAACTTTTGGTCACCCACC 46622 ACTTTTGGTC 46623 G- C CGAA - GT- C CGGA
AA
TCGAACGTCGAGTAGTCGAC ACCCACCTCG ATAACTTTTG TCACC ACCT CG TCGA AGT
GA TGGTTG G
GGATGGTTGAAGCCCGGCCA AACG |||||||||| ||||| |||| || |||| ||| || ||||||
GATCCACTTCATCGAGCGCC TATTGGAGAC AGTGG TGGG GC AGCT TCA CT
ACCGGC /
AGGGTGGTGAAACAGAGGTT AA - ACC- G ACT C AG-- CC
AT

GAM1895 TCCTGGATACAATACTCTCC 46629 TACAATACTC 46630 GATAC- CCCTCC TC
TATTACGCCCCTCCGGTCAG TCCTATTACG TCCTG AATACTCTCCTATTACGC GG A
GCCCTCCCGCGTAATAGGAG CCCC ||||| |||||||||||||||| ||
GGTATTTCTTTATAGGG GGGAT TTATGGGAGGATAATGCG CC /
ATTTCT CCCTC- GG

GAM1896 CGTCGCCACAGAATACATGT 46646 TGTCTAGAGA 46647 A ACATG TA TAT- CCAT AT
CTAGAGATATCAGGCCATTG TATCAGGCCA CGTCGCCAC GAAT TC GAGA CAGG TG T
ATTTTCACCTTGCTCTTCTT TTGA ||||||||| |||| || |||| |||| ||
CTGAAAATGGTTCGTGGCGA GTAGCGGTG CTTG AG TTCT GTTC AC /
TG - GTAAA TC TCTC C--- TT

GAM1897 GGGCGGGATAGCTCAGCAAA 46655 TACTATGTCG 46656 -- AGC AAA TG -- ----- T A
CTCTCC A
CCTGGATGGGTCATCGTGTG TACACGTGAA GGAT TCAGC CC GA TGGG TCA CGTGTG
GGCG GA G
AGGCGCTCTCCGAAGTCTCT ATCT |||| ||||| || || |||| ||| |||||| |||| ||
ACTATGTCGTACACGTGAAA CCTA AGTTG GG CT ACTC AGT GCACAT CTGT
CT T
TCTCTCAAATCTGGGGTTGA TA --- --- GT AA TCTAA - G ATCAT- C
ATCCATCGCCC

GAM1898 CTCCGGGAGGGAAAACGGCG 46664 GGGAAAACGG 46665 AG AA GGTAGAAA C T
GC
AGGGTAGAAACGAGCGGTGA CGAGGGTAGA CTCCGGG GGA ACGGCGAG CGAG GG GA
A
GCAAAATCCCCTCGCTCGTC AACG ||||||| ||| |||||||| |||| || ||
GTCGTCCTCCTCGGAG GAGGCTC CCT TGCTGCTC GCTC CC CT A
CT GC -------- - - AA

GAM1899 GTCATCGGCGTACGTGGGGA 46710 AAGAGTCCGG 46711 CG -- TA- C GAAA----
TG
TGTACCGCGACTGAAAGCTG GCCCATCAGC GTCATCGGCGTA TGGG GATG CCG GACT
GC T
TTGGCGACGTAAGAGTCCGG CCAG |||||||||||| |||| |||| ||| |||| ||

GCCCATCAGCCCAGATATGT CAGTAGCTGTAT ACCC CTAC GGC CTGA CG /
CGATGAC AG GA CCG - GAATGCAG GT

GAM1900 TACAGCTACGAAGAGAATAT 46778 ACGAAGAGAA 46779 - TACG-- TAT -- G
ATGTTATGTGAGAATGTTAG TATATGTTAT TACA GC AAGAGAA ATGTT ATGT A
ACATTTTTCTTTTAAATTTG GTGA |||| || ||||||| ||||| ||||
CTTGTA ATGT CG TTTTCTT TACAG TGTA G
T TTTAAA TT- AT A

GAM1901 ACCACAGCGCATGCGCCGGG 46791 CGTTGTGGGG 46792 A- CATGC G G - C G
TTG T
CCGTTGTGGGGCCCCGGGCC CCCCGGGCCG ACC CAGCG GCCGG CC TTGTGG GGCCC
GG CCGGGGCCCC GG C
GGGGCCCCTTGGGTCCGCCG GGGC ||| ||||| ||||| || |||||| ||||| || |||||||||| ||
GGGCCCCGGGCCGGGCCGCC TGG GTTGC CGGCC GG GGCACC CCGGG CC
GGCCCCGGGG CC C
ACGGGGGCCGGCCGTTGGCG CG ----- - G G - G --- G
GT

GAM1902 CCAGCGGCCGGCCGGCGCTT 46819 ACGCCCCTTG 46820 A CC - T GA-- AT
AGGGGGAGGATGTCGCCGAC GCCGCCCCGG CC GCGGCCGG GGCG CT AGGGG GG G
GCCCCTTGGCCGCCCCGGCT CTGC || |||||||| |||| || ||||| ||
GCAGG GG CGTCGGCC CCGC GG TCCCC CC T
A -- C T GCAG GC

GAM1903 TCTGCCTCTGCCGCTTGTGA 46884 TGAGTGCGCG 46885 - G G G -- - TG ---
G G
GTGCGCGCGCCGGCTCTGCG CGCCGGCTCT CC CTTGTGAGT CGC CGCCGGCT CTGC GG
TCG GCGGCGGCTGC GC G
GTGTCGGCGGCGGCTGCGGC GCGG || ||||||||| ||| |||||||| |||| || ||| |||||||||| ||
GGCTGCGGCGGCCGCCGTGT GG GGGCGCTCA GTG GCGGCCGG GATG CT GGC
TGCCGCCGGCG CG C
TCGGTCTCGGTAGCCGGCCG C G G G CC G CT TTG G T
GCGGGTGGACTCGCGGGGGG
CCGGAGGGTGG
GAM1904 GGCAAAGCGGCGGGGCGGTT 46894 AAGCGGCGGG 46895 AAG ---- -- -- ---- - G ---
--- G
CGGGGGGGGGGGGGGGGGGC GCGGTTCGGG CGGC GGGGC GGT TCGGGGGGGG
GGG GGG GGGC GG A
GGGAAACCAAGTAGGCCCGC GGGG |||| ||||| ||| |||||||||| ||| ||| |||| ||
CCATCCGCGGCCCCTCCCGG GCTG CCCCG CCG GGCCCTCCCC CCT CCC
CCCG CC A
CAGCCACGCCCCCAGCGTCG GG- CGAC CA AC GGCG A G GATGAA A
GGTGTC

GAM1905 TTTTTTTATTTTGTCTTTGG 47025 TATTTTGTCT 47026 G TT ----- A- A AA
GTTTATAGGAGAGAAAAACT TTGGGTTTAT TTTTTTTATTTT TCT GG GTTTAT GG GAG A

CCCGGATGGACATTGACTTT AGGA |||||||||||| ||| || |||||| || |||
AGAGAGAGTAAAAGAA AAGAAAATGAGA AGA TC CAGGTA CC CTC /
G TT AGTTA GG - AA

GAM1906 TTGCCGCCGTGGGCAATCGG 47039 CCGCCGTGGG 47040 C AATCGG - CCA GC
TTGTTAGTCCCAGGTAGGCC CAATCGGTTG TTGC GCCGTGGGC TTGT TAGTC GGTAG C
CACTATCGATTATGCAGTGG TTAG |||| ||||||||| |||| ||||| |||||
CCTACGGCAGCAA AACG CGGCATCCG GACG ATTAG CTATC /
A GT---- T --- AC

GAM1907 GTGCCGTTTAGATGGTCTCA 47047 TTGGGTCTAA 47048 G G AGATG C G G GAGG
GACCGGGATCGAGGTGCAAG GGCGGGAAGG GT CC TTT GTCT AGACC G ATC T
GTTGGGTCTAAGGCGGGAAG GGAT || || ||| |||| ||||| | |||
GGGAT TA GG AAG CGGA TCTGG T TGG /
G G GG--- A G - AACG

GAM1908 CACGGTCGTTGTAGGCTTGT 47057 TCGTTGTAGG 47058 C A TTGT GAGAAA
GATAGATGAGAAACATAAAC CTTGTGATAG CACGGT GTTGT GGC GATAGAT C
GGTTTGTTCGCCACGATCGC ATGA |||||| ||||| ||| |||||||
CGTG GTGCCG TAGCA CCG TTGTTTG A
C - C--- GCAAAT

GAM1909 GTTTTAGAAAACCATCTACT 47063 TTTGATATTT 47064 AACC- TACT TATG
ATATCATATGAAATACTGGT CTTTTAAAAC GTTTTAGAA ATC ATATCA A
ATTTGATATTTCTTTTAAAA ||||||||| ||| ||||||
C CAAAATTTT TAG TATGGT A
CTTTA TT-- CATA

GAM1910 TCGCGAGGAGAACTCCGCCG 47074 TAACGCGAGA 47075 - A A C AAA- GGA A
AACGGATG T
TAAACTCGGGACGTAACGGA AAGGCGTCGG TCG CG GGAG ACTCCG CGT CTCG CGT
ACGG CG C
ACGGATGCGTCTACGAACAA AGTC ||| || |||| |||||| ||| |||| ||| |||| ||
CTCCCGTAACGCGAGAAAGG GGC GC CCTC TGAGGC GCG GAGC GCA TGCC
GC T
CGTCGGAGTCCTCCACGACG A A C T GAAA --- A CTCAACAA A
G

GAM1911 GTGTATGAAATGGGCGGGAT 47080 TATGAAATGG 47081 A TG- GGATA TAC
ACCAATTTG T
ACTATCTACGTGGACCAATT GCGGGATACT GTGT TGAAA GGCG CTATC GTGG CATA
T
TGCATATTATATGAAAACTA ATCT |||| ||||| |||| ||||| |||| ||||
ACCGCATGATGGCGCTATTT CACA ATTTT TCGC GGTAG CGCC GTAT /
TTTAAACAC A TTA ----- TA- AATCAAAA- A

GAM1912 CCTCCACCTCCTCTTCGAAG 47094 TATTCCACTG 47095 --------- - T AA C- T------ C
TACTT
AATATTCCACTGTCCCCTTT TCCCCTTTTC TCC TCT CGAAG TATT CACTG
CCCCTTTT TC T
TCTCTACTTTTTAATGAAAA TCTA ||| ||| ||||| |||| ||||| |||||||| ||
AGGGGCAAATGTCAGTGATG AGG AGA GCTTC GTAG GTGAC GGGGAAAA AG
/
ATGAGCTTCGAGACGGACCA ACCAACACC C - GA TA TGTAAAC - TAATT
CAACCACCAACTGGAGG

GAM1913 AGGCTCTGACGTCTCTCCCT 47153 TCTGACGTCT 47154 TCT CTCTCCCTACCC CTCC AA
ACCCTGGCTCCCGGAAAAAA CTCCCTACCC AGGC GACGT TGG CGG A
CCGAAAACCACCCATTTCCT TGGC |||| ||||| ||| |||
CATGTTTGCCT TCCG TTGTA ACC GCC A
T-- CTCCTTTACCC- AAAA AA

GAM1914 TTACATAATTTATATTAAGA 47170 TAATTTATAT 47171 - TCAAAT C CT AGAAT
G
ATATCAAATATTCTATCTAA TAAGAATATC TTACATAATTTATAT TAAGAATA ATT TAT AAAC
TC T
ACAGAATTCGTAAGATATAG AAAT |||||||||||||| |||||||| ||| ||| |||| ||
TTTTTGTATAATTATTTTTA AATGTGTTAAATATA ATTTTTAT TAA ATG TTTG AG A
TATATAAATTGTGTAA T ------ T TT ATAT- A

GAM1915 TTGTATGTGACGTTTCCGGA 47176 TATGTGACGT 47177 T- TTTCC - AAAAGG G T
ATAAAAAGGTTGATCCGTCG TTCCGGAATA TTGTATG GACG GGA ATA TTGATCC TCG G
TGAACGAAGGGTCGAATACG AAAA ||||||| |||| ||| ||| ||||||| |||
TGTCTCCAGCTCGTCTTCAT AGCATAC CTGC CCT TGT AGCTGGG AGC A
ACGA TT TCGA- C GCATA- A A

GAM1916 GTTGTCGCTTTCGTTGTAGA 47186 TATCTCGACA 47187 - TTTC T CG A GTC
CGTATCGGAACGTCCATAGT CGCGCACGAC GTTGT CGC GTTG AGA TATCGGA C C
CCGATATCTCGACACGCGCA ||||| ||| |||| ||| ||||||| |
CGAC CAGCA GCG CAGC TCT ATAGCCT G /
C CA-- - -- - ATA

GAM1917 GTTTTTTTTTATTGCTAATG 47190 TTGCTAATGC 47191 A - TGCGTAAACC ATG
AGTAC
CGTAAACCTGCCCCATGCCC GTAAACCTGC GTTTTTTTTT TTGC TAA TGCCCC CCCCC
A
CCAGTACAAACAAGGGGGGG CCCA |||||||||| |||| ||| |||||| |||||
GGGGCACTAAAAATTTTTGC CAAAAAAAAA AGCG GTT ACGGGG GGGGG /
GCGAAAAAAAAAAC - C TTTAAAAATC GG- AACAA

GAM1918 GCTGGCCACGTGCCCCGAAC 47206 CATCGATGGA 47207 C - C- ACA---- AT
ATCAGATTACCTGGGACCCC CGCGTTGTCA GCTGGC ACGTG CC CGA TCAG T
ATCGATGGACGCGTTGTCAG GC ||||||| ||||| || ||| |||| /
C CGACTG TGCGC GG GCT GGTC /
T A TA ACCCCAG CA

GAM1919 CAAGCTTCGCGTTCAGCGGC 47226 CAGCGGCTTC 47227 TTCA-- G - GCAACAA AC- A TCT--- - TCA
TTCTGTTTGCGCAACAATCA TGTTTGCGCA GCG CTT CTGTTTGC TC AT CGGAAT CT CCT C
CATACGGAATTCTCTCCTTC ACAA ||| ||| |||||||| || || |||||| || |||
ACACTGGGCAGTTCTTCATT CGT GAG GACAAATG AG TA GCCTTA GA GGG /
CCGCATAGCGAGCTTAAAGT CGATGG G T AAATTCG CGA C CTTCTT C TCA
AAACAGTGAGGTGCGGTAGC
CGCTTGTTTG
GAM1920 CGTCCGCGGCGACGGCGCCG 47275 GGAGTGGGGT 47276 GGCGA C CC G G A G A
TCGCCGCCGCGCTCGGAACG CGACGGCCCG CGTCCGC CGG GCCGTCG GCC CGCTC GA CGTTC GA C
TTCGGAACGTTCGGAACGCT AGGA ||||||| ||| ||||||| ||| ||||| || ||||| ||
CGGAGTGGGGTCGACGGCCC GCAGGCG GCC CGGCAGC TGG GTGAG CT GCAAG CT G
GAGGAAGCGGACG AAGGA - -- G G C G T

GAM1921 ACGTGTTTTTTTTAAGTTAT 47361 TAAGTTATTT 47362 -- - A ACT- T CCACC
TTTACTATTGAGCCACCTAT TACTATTGAG ACGTGTT TTTTTTAA GTT TTTT AT GAG T
ACACTCTGTTACAAAAAAAA CCAC ||||||| |||||||| ||| |||| || |||
CATTGAAAAATAGATATGT TGTATAG AAAAAGTT CAA AAAA TG CTC /
AT A A ACAT T ACATA

GAM1922 GATATGTCAATACAACAGTC 47377 TATGTCAATA 47378 AA - ACAG AATG C T A
AATGTTCTCAGGATTGCAAG CAACAGTCAA GATATGTC TA CA TC TTCT AGGA TGC A
TGCGTTTTTAAGAAAAAGAA TGTT |||||||| || || || |||| |||| |||
ATATGATGAAGATATATC CTATATAG GT GT AG AAGA TTTT GCG G
AA A ATAA AAA- A T T

GAM1923 CGTGCGTGTTCTGTGCGTTA 47387 GTGCGTTATA 47388 T C- TATATAA - AA
TATAACCAGAACAAGCTGTG TAACCAGAAC CGTGCG GTT TGTGCGT CCAGA AC G
TCTGGACTTTGCGCGCAACG AAGC |||||| ||| ||||||| ||||| ||
ATCTGCACG GCACGT TAG ACGCGCG GGTCT TG /
C CA TTTCA-- G TC

GAM1924 ACACCCACTTCCAGGGCGTA 47398 CGAAAGTTCT 47399 A ACTTCCA C AACCC AG TCACC A ACT

ACCCGAAAGTTCTCACCACA CACCACACCC AC CCC GGG GT GAA TTC AC CCC T
CCCACTTCCAGGGCGTAACC ACTT || ||| ||| || ||| ||| || |||
CGAAAGTTCTCACCACACCC TG GGG CCC CA CTT AAG TG GGG /
ACTTCCAGGGCGT C ACCTTCA A CCACT GA CCCAA C ACC

GAM1925 GGCGTGGCGATACGACGAAG 47419 TGACCGTGTG 47420 C - ------ A- A G
CCGTGGAGATGGCTCTGACC TGAAACGACC GG GTGG CG ATACG CG AGCCGT G
GTGTGTGAAACGACCGCTCC GCTC || |||| || ||||| || ||||||
CC CGCC GC TGTGC GT TCGGTA A
T A AAAGTG CA C G

GAM1926 ACCACATGGTGGTTATCTGT 47427 TATCTGTATA 47428 TAT ATAAACT C - A AC-----
- ACC
ATAAACTGCACCTGTTAACG AACTGCACCT CATGGTGGT CTGT GCAC TG TT ACGTGTA
TGCGCC A
TGTAACTGCGCCACCACAAG GTTA ||||||||| |||| |||| || || ||||||| ||||||
GGCGTATATAAAAGTGCATG GTACTACCG GATA TGTG GC AA TGTACGT
ATGCGG C
TAAATCGAGTGTTTAAAAAA C-- AAAAATT A T A GAAAATAT GAA
TAGCGCCATCATGCGGT

GAM1927 CGGCTTGTGGAGGTAAGAGC 47441 TGTGGAGGTA 47442 TTGT TA TCCC- GG- C
TACC
TCCCGGGGGACGGCTTACCA AGAGCTCCCG CGGC GGAGG AGAGC GG GA GGCT A
ACTTGGCTTCATACTTATCT GGGG |||| ||||| ||||| || || ||||
GCTCTCTTCTCCTTCGCTG GTCG CCTCT TCTCG TC CT TCGG /
CTT- TC TCTAT ATA - TTCA

GAM1928 CCTCTCAAATCTTGGGTTAA 47483 TCTTGGGTTA 47484 T AATC AAACTCATC C A
ACTCATCACCGCGAAAATCT AACTCATCAC CCTC CA TTGGGTT AC GCGAA A
TTGCCGTTCCAAACCCGAAT CGCG |||| || ||||||| || |||||
CCTGCGAGG GGAG GT AGCCCAA TG CGTTT T
C CCTA ACCT----- C C

GAM1929 GCTCGGGCGCATCCGCTCGC 47491 TTCGACAGCA 47492 - ATC- C C CA- A T
TCGTCGACAACGAGCTCTGC GCGCCGCGCG GCTCGGG CGC CGCT GCT GTCGA ACG GC
C
GTGTACTTCGACAGCAGCGC CCCC ||||||| ||| |||| ||| ||||| ||| ||
CGCGCGCCCCGAGC CGAGCCC GCG GCGA CGA CAGCT TGT CG /
C CGCC - - TCA G T

GAM1930 ATCTCGTCAATTCCATTCCG 47508 CATCATGCCA 47509 ATT--- CC A ----------
GAA
ACTGCTACTGCCATGAATCA TCACGATCAG TCTCGTCA CCATT GACTGCT CTG
CCAT T

AATGGGACATCATGCCATCA CAGC |||||||| ||||| ||||||| ||| |||| CGATCAGCAGCAGTCAAGGT AGAGTAGT GGTGG CTGACGA GAC GGTA / GGCACTTATGATGAGAT ATTCAC AA C TAGCACTACCGTACTACAG AAC

GAM1931 GGCGACTACGATATACTAGT 47544 ACTACGATAT 47545 C ATA- T T AA GTTGGACGAAGTTATGTCCA ACTAGTGTTG GGCGA TACGAT CTAG GT GGACG G CCCTGGCCCAGTTGTATTCG GACG ||||| |||||| |||| || ||||| CC CCGCT ATGTTG GGTC CA CCTGT T T ACCC C - AT

GAM1932 GTCACGTTGGGTGACTCTGT 47548 ACGTTGGGTG 47549 AC T CTCT-- A-- C CGATCCACGCCTGGAAACCG ACTCTGTCGA GTC GTTGGG GA GTCG TCCA G ACCCACCTTCCCCCAACCCG TCCA ||| |||||| || |||| |||| AC CAG CAACCC CT CAGC AGGT C CC C TCCACC CAA C

GAM1933 TGCCAACTGTCCGCTTGGTG 47560 TCTGCACCAC 47561 CAACT- CGCT- C- AACATTT CACTGAACATTTCCGCCCAA CAATGATTAC TGC GTC TGGTGCA TG C CCATCTGCACCACCAATGAT ACTG ||| ||| ||||||| || TACACTGCA ACG TAG ACCACGT AC C TCACAT TAACC CT CAACCCG

GAM1934 GATGATTCAGTCATTGTCGG 47580 AGTCATTGTC 47581 TTCA- A TC CT CCCA TC CACTCCACCCATCTCCCCGA GGCACTCCAC GATGA GTC TTG GGCA CCA TC C ATTGGCCTGCCATCAAAGAC CCAT ||||| ||| ||| |||| ||| || CTCCTTCATC CTACT CAG AAC CCGT GGT AG / TCCTC A TA CC TA-- CC

GAM1935 TGGAAATAGTATATAAGGAT 47594 TAGTATATAA 47595 G GTTT---------- GTAC - TT- A CT AGTTTCTAGATTGTACGGGA GGATAGTTTC TATAA GATA CTAGATT GGGAG CTC CACT CTCG G GCTCTTCACTACTCGCTGCG TAGA ||||| |||| ||||||| ||||| ||| |||| |||| TCGAGAGTGTACGAGACTCT ATATT TTAT GGTTTGG CTCTC GAG GTGA GAGC C CCAGGTTTGGTAAGAAATAT G ATTTTATAAAGAAT AC-- A CAT - TG TTTATATTGTTATAATGTTA CTATGATCCA

GAM1936 GGATTTGTATATTAGCCTTG 47601 AGGGAGACAT 47602 -- AGCCTTG AG- TAG T A CTAAGGGAGACATCTAGTGA CTAGTGATAT GGA TTTGTATATT CTAAGGG ACATC TGA ATAAGTGTG A TATAAGTGTGAACTACACTT AAGT ||| |||||||||| ||||||| ||||| ||| ||||||||| ATCTTAAATGATGTAACTCC CCT AAACATATAA GATTCCT TGTAG ATT TATTCACAT /

TTAGGATAATCAATATACAA TA CTAATAG CAA TAA C C
AATTCC

GAM1937 GCGAGTCGCTATGACGCGTC 47606 CACTATGGCG 47607 TC - A GTCCTT CCAG---
GA GTCG A
GAGGGTCCTTCGTCTCCAGA CGTCGATGGT GAG GCTAT GACGCGTCG GG CGTCT
AGCCAG GA GC T
GCCAGGAGAGTCGGCATTGG CCCT ||| ||||| |||||||||| || ||||| |||||| || ||
CATCATCAACTGGCTGAACC CTC TGGTA CTGCGCGGT TC GCAGA TCGGTC CT
CG T
CCAGACGCACTATGGCGCGT CC G A AC---- CCCCAAG AA ACTA G
CGATGGTCCCTCGT

GAM1938 GGAAGTGAAGAACCTCGTGA 47614 TGAAGAACCT 47615 AGTG-- C A------- AA TC
CTC
CCCAAATACTCCTGCTCCTC CGTGACCCAA GGA AAGAACCT GTG CCCA TAC CTG C
ATAGACGTACCTGGGATGAG ATAC ||| |||||||| ||| |||| ||| |||
AGACACAAGGTTCTTAAATT CCT TTCTTGGA CAC GGGT ATG GAT /
GTCC GTTAAA A AGAGAGTA CC CA ACT

GAM1939 GCAGCTCTAACTTGGCATCT 47634 TGGCACGACT 47635 AACTT--- CTCTTTT G T CCT-- -
TT---- CT
CTTTTACAGTGGTTCTCCTG GTTCCTATAT GGCAT ACAGT GT CT GATTT GCTC
CGTG C
ATTTGCTCTTCGTGCTCTTC GCTC ||||| ||||| || || ||||| |||| ||||
ATGTCCACTGAGCAAGATCC TCGTA TGTCA CA GG CTAGA CGAG GTAC /
TTCTGGCACGACTGTTCCTA TCACGCTC TATCCT- G C TCTTC A TCACCT TT
TATGCTCTCGCACTCTTGTT
GC
GAM1940 GGTTTGGGCAACAAAACTCT 47643 CAAGCAAGAG 47644 TT ACAAA- AACCC C
TAACCCTTTGCGCGAATGCA TGGCTAATGT GGT GGGCA ACTCTT TTTGCG G
AGCAAGAGTGGCTAATGTCT CTGC ||| ||||| |||||| ||||||
GCC CCG TCTGT TGAGAA GAACGT A
-- AATCGG C---- A

GAM1941 GTGATGTTGCGATAACATCC 47700 AAAGAGGTCT 47701 T AACAT GG -- C
TCTGGGATGCCAAGCAGATC TCATCGCACA GTGATGT GCGAT CCTCT GA TGC A
AAAGAGGTCTTCATCGCACA TCGC ||||||| ||||| ||||| || |||
TCGC CGCTACA CGCTA GGAGA CT ACG /
- CTTCT AA AG A

GAM1942 TACTATAACAGGAAACATAG 47713 TAACGGCAAT 47714 CAGGAAAC GAA GGA CC
AAGTTGCGGATAGAGCCTGG GATATTTATA TACTATAA ATA GTTGC TAGAG T
TTTCTAACGGCAATGATATT GTG |||||||| ||| ||||| |||||
TATAGTG GTGATATT TAT TAACG ATCTT G
-------- AG- GCA TG

GAM1943 TGCATGAAAATATCATTAAA 47720 TGAAAATATC 22421 - TG A A- - CAA
TTGTTTTACAAATTTTAAAT ATTAAATTGT TGC A AAAAT TC TTAAATTGT TTTA A
GCAATTTAAAAGAATTTTTG TTTA ||| | ||||| || |||||||| ||||
TAGCA ACG T TTTTA AG AATTTAACG AAAT /
A GT - AA T TTT

GAM1944 TGTATTTTTCTTTGCAGAGA 47721 TGGAGAGCTT 47722 TTTT - GA-- T - TTATA TG
GGA
TGTATGGAGAGCTTATATTG ATATTGGGGG TGTAT CTTTG CA GATGTA GG AGAGC T
GG A
GGGGAAAATACCTGACTGTT AAAA ||||| ||||| || |||||| || ||||| | ||
CTGCCTATATTCGAATGTTG ACATG GAAGT GT TTATAT CC TCTTG A CC A
AAGTATGTACA TAT- T AAGC - G TC--- GT ATA

GAM1945 GGGTGTGATGTACAGGAAAA 47802 TACAGGAAAA 47803 A--- A--- AAAA AAG A - AC
TGACGAAGATGAAGGAACCA TGACGAAGAT GGGTGTG TGTAC GG TGACG ATG AG GA
C
ATCGCTGCATAACGTTAAAC GAAG ||||||| ||||| || ||||| ||| || ||
CGCAAGTGCAGAAATACACC CCCACAT ACGTG CC ATTGC TAC TC CT /
C AAAG AACG AA-- AA- G G AA

GAM1946 TATATATTTTGGGTTCTGGC 47842 TATTTTGGGT 47843 T-- TTCT CTA TAC C - T T
ATAATC
TACTGTATATACAGGTACTG TCTGGCTACT TGGG GG CTGTATA AGGTA TGTGGTA CA
TGGAT GTT A
TGGTACATTGGATTGTTATA GTAT |||| || ||||||| ||||| ||||||| || ||||| |||
ATCACACAACCAGCCATCTA ACCC CC GACATGT TCCAT ACATCGT GT ATCTA
CGA C
CTGCTGCTACACTACCTTGT CAT CTT- CC- --- C C C C CCAACA
ACAGCCCCTTCCCCATACAG
TATGTA
GAM1947 GGTTCCACCTGCCTTCTTTC 47848 TCCACCTGCC 47849 CCT C - AATCAA----- G
AATCAATGCGAAAGCACACC TTCTTTCAAT GGTTCCA GC TTC TTTC TGC A
CCCTACCGAAATGGATGCCT CAAT ||||||| || ||| |||| |||
GGAACC CCAAGGT CG AGG AAAG ACG A
C-- T T CCATCCCCCAC A

GAM1948 GCAATGTTAAAGTGACTCCT 47881 TTAAAGGTAA 8404 - TAAA CT- AGAT- ACCTA
CCAGATTACTCACCTATAAT GAGTTATGAC GC AATGT GTGACTC CC TACTC T
CGCGAGTATTAAAGGTAAGA GCAT || ||||| ||||||| || |||||
GTTATGACGCATTAGC CG TTACG TATTGAG GG ATGAG A
A CAG- AAT AAATT CGCTA

GAM1949 AAGTAAAGATTTCAAAGATG 47882 TAAAGATTTC 47883 TTCAAA--- --- TG

TTTTCTGTCAGAAAATACCA AAAGATGTTT AAGTAAAGAT GATG TTTTC T
TCCAAGTCAATATCTTTACT TCTG |||||||||| |||| |||||
T TTCATTTCTA CTAC AAAAG /
TAACTGAAC CAT AC

GAM1950 GGTTTAGTATCTCAATTGTC 47897 TGAGTATTTG 47898 A - ATTGTCTG AAG TTA- - --- T
TGTCTTAAGTTCCATTACAA GATTTGGAAA GGTTT GTAT CTCA TCTT TTCCA CAAATAT AC A
ATATACTAACGTCTGAGTAT AGAA ||||| |||| |||| |||| ||||| ||||||| ||
TTGGATTTGGAAAAGAAAAT CTAGA TATA GAGT AGAA AAGGT GTTTATG TG A
TTGTGAGTATATCAGATC C T GTTTAAA- --- TTAG AGTC C

GAM1951 TAATATTTGTAATTATTTTT 47928 TTATTGTTAT 47929 T T TT- AAT TATA
TTAATAAAATATAATACTAT TTAAAATAAT TAA ATTTG AATTATTTT TAATAA ATAATAC T
ATCATTTGTATTATTATTGT TCTA ||| ||||| ||||||||| |||||| |||||||
TATTTAAAATAATTCTAAAT ATT TAAAT TTAATAAAA ATTGTT TATTATG C
TTTA T C TTT AT- TTTA

GAM1952 AATATTGAATGTATTATTGA 47936 TTGAATGTAT 47937 T ---- ATT T
TTTTATTAATATATTTATTT TATTGATTTT AATATTGAATGTA TAT TGATTTT AATA A
AAAAAATCATTATATATTAC ATTA |||||||||||| ||| ||||||| ||||
ATTTAATATT TTATAATTTACAT ATA ACTAAAA TTAT T
T TATT AAT T

GAM1953 ACTTTCATTAATAATATTTT 47942 TCATTAATAA 47943 TTC TA--- TTATC TT
TAAATTTATCAGAGTTTACA TATTTTTAAA ACT ATTAATAA TTTTTAAAT AGAGT A
TATTCTCCGTTTAAAAAATT TTTA ||| |||||||| ||||||||| |||||
TTTTATTAATTCTGGT TGG TAATTATT AAAAATTTG TCTTA C
TCT TTTTA CC--- TA

GAM1954 TGATATAGATTTAATATTTG 47945 TATAGATTTA 47946 TTAATAT TTT - TTA
TTTATCATATTTATCATATA ATATTTGTTT TGATATAGAT TTG ATC ATAT T
TAGATTCAATCATAGTATCT ATCA |||||||||| ||| ||| ||||
ATATCA ACTATATCTA AAC TAG TATA /
TGATACT T-- A TAC

GAM1955 GATATAATATTTACTAATTT 47952 TATATAATTT 47953 TAATATTT ---------- A
ATCATCTGATATATAATTTT TTAATATAAT GATA ACTAATT TATC T
TAATATAATTAGTTAATTTA TAGT |||| ||||||| ||||
TC CTAT TGATTAA ATAG C
TTAAT--- TATAATTTTTAATAT T

GAM1956 GTATTGAATTCATAAATTAT 47957 TATATATTCT 47958 TCATA T CTATTTC TAAA
ATATTCTATTTCGCTTAAAA ATTTCGCTTA GTATTGAAT AAT ATATATT GCT A
TTTTAGTTATTAATATATCA AAAT |||||||||| ||| ||||||| |||
TTACTATATTTAATAT TATAATTTA TTA TATATAA TGA /
TATCA C TTAT--- TTTT

GAM1957 TTTATTAGATATTATATTAA 47963 TATTAGATAT 47964 T TATT TTCAT TATT
TTTCATCATATATTCCTGCT TATATTAATT TTTATTAGA ATTA AAT CATA C
ATGTTTTCATTTTTTGATTC TCAT |||||||||| |||| ||| ||||
TAATAAA AAATAATCT TAGT TTA GTAT /
- TTT- CTTTT CGTC

GAM1958 TAAAACATCTAAAGATGATA 47967 AAGATGATAG 47968 C AA ----- T----- TTTCA
GATGTGTATTAATTTCATCT ATGTGTATTA TAAAA ATCTA GATGA TAGATG GTATTAA T
TGTTTAATATTTATATCATC ATTT ||||| ||||| ||||| |||||| |||||||
TATTTTTTCATCAATAGATT ATTTT TAGAT CTACT ATCTAC TATAATT /
TTTTA T AA TTTTT TATATT TGTTC

GAM1959 TAATAATATCATGTATATAA 47972 TCATGTATAT 47973 C- TA TT TTATA AT TTG
TTTTTTATATTTATATTAAA AATTTTTTAT TAATAATAT ATGTATA ATTT TATAT TTAA TC A
TTCTTGATCTGATCTTAAAC ATTT ||||||||| ||||||| |||| ||||| |||| ||
TATATATCAAATCTTGTACA ATTATTATA TACATGT TAAA ATATA AATT AG /
TTTATATTATTA TT TC CT TCA-- CT TCT

GAM1960 TGTTTGTCAATCATATAATT 47979 TAATATGTTC 47980 TCAAT AATT CTTT CTAT
AATATTTTCTTTTATACTAT TTCAAATA TGTTTG CATAT AATATTTT TATA T
TATCATTATATATAAAATAT |||||| ||||| |||||||| ||||
TTAATATGTTCTTCAAATA ATAAAC GTATA TTATAAAA ATAT A
TTCTT AT-- TAT- TACT

GAM1961 ATACGAAACATTGTCGGCTC 47986 AACATTGTCG 47987 A CTCAAAAACTCCC ATG
A
AAAAACTCCCACAGATGTCC GCTCAAAAAC ATACGAA CATTGTCGG ACAG TCCATCG
C
ATCGACGTCGATGGAACTGT TCCC ||||||| ||||||||| |||| |||||||
TTGGCAATGCTTTGTGT TGTGTTT GTAACGGTT TGTC AGGTAGC G
C ---------- A-- T

GAM1962 TACTCATTTCCTGCATCCAC 48014 TCGGGCAGCC 48015 ---- A- G---------- T
CATATTGGCTGCCCGGGCCA AATATGGTGG CCACCATATTGGCTGCCCG GGCC ATAATGC
AGCGGC G
ATAATGCGAGCGGCTGCGCC ATGC |||||||||||||||||| |||| ||||||| ||||||
GCTGCGCGCTTCGCGCGCGC GGTGGTATAACCGACGGGC CCGG TGTTACG
TCGCCG /

ATTGTAAGGCCTAATCGGGC TAAT AA CGCGCGCTTCGCGCG C
AGCCAATATGGTGGATGCAG
GAAATGAGTA
GAM1963 ACTTTGAAAAAGCTTCTGTT 48029 TGAAAAAGCT 48030 G TTC TG- AG----------
AT
TATGCATGTAGGTTATTTAA TCTGTTTATG ACTTT AAAAAGC TGTTTA CATGT GTT
T
ACAGTTTTATAACGAAAAAA CATG ||||| ||||||| |||||| ||||| |||
AATATGATTTAGATAAATGT TGAAA TTTTTTG ATAGAT GTATA CAA /
TTTTTAAAAGT A TAA TTA AAAAAAAGCAATATTTTGA AT

GAM1964 GCCAAGATTAACACCTTTTA 48039 TTAGTATTAA 48040 A A CTT CATGC TT T
CATGCGTACTGTTGTTCAAA GTGATGACCT GCCAAG TTA CAC TTA GTACTG GT C
TTTTAGTATTAAGTGATGAC TGGC |||||| ||| ||| ||| |||||| ||
CTTGGC CGGTTC AGT GTG AAT TATGAT TA A
C A --- ----- TT A

GAM1965 GCTCTTATAATATTGGACTC 48042 TGAGAACAAC 48043 AATA- GA CACCATA A
CACCATAGGAAACTTCCGAA CACAATAAGA GCTCTTAT TTG CTC GGA A
ATTGAGAACAACCACAATAA GC |||||||| ||| ||| |||
GAGC CGAGAATA AAC GAG CCT C
ACACC AA TTAAAG- T

GAM1966 GGATTATTACACAATGACAT 48084 TATTACACAA 48085 TATTA T T C- AA
GTCATCTACAATATGTAGAT TGACATGTCA GGAT CACAA GACA GT ATCTAC T
CTACTGTTTTTGTGCTATCC TCTA |||| ||||| |||| || ||||||
CCTA GTGTT TTGT CA TAGATG /
TC--- T - TC TA

GAM1967 GTTCTTGAAGTACACAAGGC 48108 TGAAGTACAC 48109 CACA G AA CA CC A----
A TTTG
TTGAATCCAACACCATAAGA AAGGCTTGAA TTCTTGAAGTA AG CTTG TC ACA ATAAGAAA
GTG GTTG T
AAAGTGAGTTGTTTGTGTAT TCCA |||||||||| || |||| || ||| |||||||| ||| ||||
CAGCCATAGCAATTTCTTGT AAGAACTTCGT TC GAAT AG TGT TGTTCTTT TAC
CGAC /
TTTGTAGAGTAAGACTGATG AG-- A G- A- TT AACGA - TATG
CTTCAAGAAT

GAM1968 GTTTTCACATTACATCCAAA 48138 CATTACATCC 48139 CACATT CCAAAAAG T ATAA
TG
AAGTTCTCTAGTGTATAAGA AAAAAGTTCT GTTTT ACAT TTCTCTAG GT GAA T
ATGTGTTTCCGCCTGGAGAA CTAG ||||| |||| |||||||| || |||
ATGTTTCTAAAAC CAAAA TGTA AAGAGGTC CG CTT /
TCTT-- -------- - C--- TG

GAM1969 GAGCAGCAGCACACAACAGG 48154 TAACCTGTCC 48155 C- ACACA- CGCA - AGA
CGCAAGAGTCAGAGAAAGGC ACCCGCTCTC GAGCAG AGC ACAGG AGAG TCAG A
TGAGCTCTAACCTGTCCACC TGCT |||||| ||| ||||| |||| ||||
CGCTCTCTGCTC CTCGTC TCG TGTCC TCTC AGTC /
TC CCCACC AA-- G GGA

GAM1970 GCTCTTATTATGTTAGCTTC 48181 TAAATTGTGA 48182 AT- A TC CCA A
CACCATAGGAAACTTTCTAA GCAACCGCAA GCTCTTATT GTT GCT CA TAGGA A
ATTGTGAGCAACCGCAATAA TAAG ||||||||| ||| ||| || |||||
GAGC CGAGAATAA CAA CGA GT ATCTT C
CGC - GT TAA T

GAM1971 CTTCTTTTATAGAGCCACCA 48191 TTAGTACCTT 48192 A C CC-- T C--- TTTG T AC--
T AA
TTACCTGCAACTATATTTGG GTAACTTTTG AT GAG CA ATTACC GCAA TATA GCT AGCAA
CTA TGG A
CTTAGCAAACCTATTGGAAA TGGT || ||| || |||||| |||| |||| ||| ||||| ||| |||
TACCACTAGATGATTGTTTA TA CTC GT TAATGG TGTT ATGT TGA TTGTT GAT
ACC /
GTACCTTGTAACTTTTGTGG - A TTTT - TTCA TCCA T AGTA C AT
TAATTTTTTGACTCATTTAG
AAG
GAM1972 TGAGTTTAATGAATTTTATG 48200 AGGCAGAGAA 48201 T - ---- GTTGAA- G-
GAG AA
AGAGTACTGTTGAAGGCAGA ATAGAGAGTG TTAA GAATTTTATG AG AGTACT GGCA
AGAAATAGA TGT C
GAAATAGAGAGTGTAACAGG TAAC |||| |||||||||| || |||||| |||| ||||||||| |||
CAAATCTATTTTTGATGTTG GATT TTTAAAGTAC TC TCGTGG TTGT TTTTTATCT
ACG /
ATGTCAGGTGCTATACCTGC - G CATA ACTGTAG AG AA- GA
ATGAAATTTTTAGATTCA

GAM1973 GAAAACAACAATAATGAGAA 48318 TTTCACGTCC 48319 AACAATA A A- ACCACAA
TGAAATCACCACAACCAAGC ATGAGTTTTT GAAAAC ATG GA TGAAATC C
CAGATTTCACGTCCATGAGT |||||| ||| || |||||||
TTTT TTTTTG TAC CT ACTTTAG /
AG----- - GC ACCGAAC

GAM1974 GTGCAGGCTACATTTTTGGG 48338 GCTACATTTT 48339 C-- TTTTG TATTT T T T
CTTATTTTGTGCTGCTGCTG TGGGCTTATT GTGCAGG TACAT GGCT TG GC GC G
TGTTCGTTTTGGCTGTGTGT TTGT ||||||| ||||| |||| || || ||
GCTTCCTGCGC CGCGTCC GTGTG TCGG GC TG TG C
TTC TG--- TTTT- T - T

GAM1975 GCTTTTGTAACTATTTGGTA 48352 TGGTATACAA 48353 TT - TT ---------- TT CAG

TACAAGTTATTCACAGCGTA GTTATTCACA GCT TGTA ACTA TGGTAT ACAAG ATTCA
C
ATGAATTCTTGTCCACTGTA GCGT ||| |||| |||| |||||| ||||| |||||
AAGGTACCACCTGGTATACA TGG ACAT TGGT ACCATG TGTTC TAAGT G
GGT -- A CC GAAATGTCACC T- AAT

GAM1976 ACAATGGCGATCATACTGTC 48356 TGACGTGTAT 48357 TG C- - CTGTT G
CTGTTTCTGGAGCCAGATGA CTATTGTTGT ACAA GCGAT ATAC TGTC TCTG A
CGTGTATCTATTGTTGTTGT TGT |||| ||||| |||| |||| ||||
TGTT TGTTA TATG GCAG AGAC G
GT TC T T---- C

GAM1977 TTTTGTGCACAGCGATTTGG 48371 TGGTATCCCG 48372 A C TT C--- - - --- -- TA
ATACAAA
TATCCCGGGTCTAGACATGG GGTCTAGACA CAG GAT GGTATCC GGGT CT AG ACATGGT
TC TCCA A
TTCTATCCAATACAAAAGCA TGGT ||| ||| ||||||| |||| || || ||||||| || ||||
GACATGGACGGACTGCCATG GTT TTG TCATGGG CCCA GA TC TGTACCG AG
AGGT /
TAAACTCAGAACCCAGGTGG - - T- TGGA A C AAA TC GC ACAGACG
GTACTTGTTTTGGCCAGAG

GAM1978 TTGATGATGGTGATACATGG 48375 TACATGGTTG 48376 TG A - TGTT T TA
TTGTTATTATGGTTTATATT TTATTATGGT TTGATGA GTG TACA TGGT ATTA GGTT T
AACCTTAATTGTTACCATTG TTAT ||||||| ||| |||| |||| |||| ||||
TGGCATTGTTATTAA AATTATT TAC GTGT ACCA TAAT CCAA A
GT G T TTGT T TT

GAM1979 GTCTGTACAAAAGTTTGAGA 48388 TAGAATGGGG 48389 ACAAA TTG- - AG GGCTA
GT
TTTTCAGATTCTGCGGCTAT AACATCTACT GTCTGT AGT AGAT TTTC ATTCTGC
TAGAGAA A
AGAGAAGTATAATTCTTTGG TACT |||||| ||| |||| |||| ||||||| |||||||
TAGAATGGGGAACATCTACT CGGATA TCA TCTA AAGG TAAGATG GTTTCTT T
TACTGGAAAATAGGC AAAGG TTCA C GG ----- AA

GAM1980 GGAAGACACATTATTTGACG 48400 TAGAACGCTC 48401 CAC T C - AG CT
ACGAGTTATACTCTATTATA TTTCGATGAT GGAAGA ATTATT GA GA CG TTATA C
GAACGCTCTTTCGATGATAA AATT |||||| |||||| || || || |||||
TTTTCC CCTTTT TAGTAG TT CT GC GATAT T
AA- C T C AA TA

GAM1981 CAAATACTTTATATTGTGTT 48405 TATTGTGTTT 48406 TACTT - T- A A A A
TTGTATCTATGATTAATAAA TGTATCTATG CAAA TATATTG TGT TTGT TCT TG TT A
ACAAGAAATAATTACATCAA ATTA |||| ||||||| ||| |||| ||| || ||

```
    TATATTTTTG                          GTTT    ATATAAC ACA  AATA AGA AC AA T
                                    TT---     T  TT   A  - A  A


GAM1982  TTTAAATTTTATTTTATTGC 48412  TAATAGCATC 48413       TT   TTAT-  C  T   CA
    CATTTGATACATAATGTCTA      TTTAGTATGT      TTTAAAT  TATT    TGC ATT GATA  T
    ATAGCATCTTTAGTATGTTT      TTAA          |||||||  ||||    ||| ||| ||||
    AAA                       AAATTTG  ATGA    ACG TAA CTGT  /
                               T-   TTTCT   A  T   AA


GAM1983  GAGACGTCCATATCTGATTA 48421  TTGATCCGGG 48422     CGTCC    --   T  GATGA  AAAA
    TTATGATGAGGTAAAAAATA      GTATTATATT      GAGA    ATATCT  GATTA TAT    GGT   A
    AACCGTTTAATATTGATCCG      TTC           ||||    ||||||  ||||| |||    |||
    GGGTATTATATTTTC                   CTTT    TATGGG  CTAGT ATA    CCA   /
                              TATAT    GC    T  ATTTG  AATA


GAM1984  GGAAGACACATTATTTGACG 48426  TAGAACGATC 48427      ACAC     T  C  -  AA    CT
    ACGAATTATACTCTATTATA       TTTCGATGAT      GGAAG   ATTATT GA GA CG  TTATA  C
    GAACGATCTTTCGATGATAA       AAAT          |||||   |||||| || || ||  |||||
    ATTTCC                     CCTTT   TAGTAG TT CT GC  GATAT  T
                              AAA-    C  T  A  AA    TA


GAM1985  GGAAGACATATTATTTGACG 48430  TAGAACGCTC 48431      ACA      T  C  -  AG    CT
    ACGAGTTATACTCTATTATA       TTTCGATGAT      GGAAG   TATTATT GA GA CG  TTATA  C
    GAACGCTCTTTCGATGATAA       AAAT          |||||  ||||||| || || ||  |||||
    ATTTCC                     CCTTT   ATAGTAG TT CT GC  GATAT  T
                              AA-     C  T  C  AA    TA


GAM1986  CACGAAACTCTTAATGTTTC 48435  TTTGTCCTTA 48436          TAATGTTT-  CTTA  A
    TCCTTAGGATTTCTGCCAGA       GAGTTTTGTG      CACGAAACTCT       CTC    GG T
    GTTTGTCCTTAGAGTTTTGT                  ||||||||||       |||   ||
    G                          GTGTTTTGAGA       GAG    TC T
                                   TTCCTGTTT   ACCG  T


GAM1987  GCAAGCGCATTATATGTTTT 48492  TGATATACAA 48493    A   GCA       T TG      AAT     CAAAGTT
 A
    TGATATCTTAATGATATACA       AGTTTGCAAG      GC AGC   TTATATGTT T  ATATCTT   GATATA
TGC A
    AAGTTTGCAAGCGCATTATA       CGCA          || |||   |||||||||  |  |||||||   ||||||      |||
    TGTTTTCAAGATGTTGATGA                CG TTG   AATATGTAG A  TGTAGAA   TTGTAT      ACG G
    TGTATAAAAGTTGC                   -  AA-       T GT      CTT     ATT----   C


GAM1988  GCGCCTGCGGCATAATGTTC 48504  AATCATGCGT 48505      C       AATGTTCG     GTG   T
    GGTGTGAGTGTGTTTTAACA       GCTGTGCGTG      GCGC TGCGGCAT      GTGTGA   TGT T
```

AATCATGCGTGCTGTGCGTG C |||| |||||||| |||||| |||
C CGTG GTGTCGTG CGTACT ACA T
C -------- AA- A

GAM1989 CCGGTTAATGACCACGATCG 48534 ACCACGATCG 48535 AA TCGC TCT TTCTC
CGATCTTGCTTTCTCTTTAT CGATCTTGCT CCGGTT TGACCACGA GA TGCT T
TTGGTATTTCCTTGTGGTCA TTCT |||||| ||||||||| || ||||
AACCGG GGCCAA ACTGGTGTT CT ATGG T
-- C--- TT- TTTAT

GAM1990 GGGGCGGGTGGATCTGTGAC 48551 CAGCGACTCC 48552 -------- - TG TAATCC
TAATCCATAAAAACGTCAGC TCCTCAAAAT GGGGCGGGT GGA TC TGAC A
GACTCCTCCTCAAAATCTGC CTGC ||||||||| ||| || ||||
CCC CCCCGTCTA CCT AG ACTG T
AAACTCCT C CG CAAAAA

GAM1991 TGTCTGAATTTATGTGCGAG 48572 TGTGCAGAAT 48573 - TTTA-- TG - TTACTATA
ATTACTATATACAAAAATTC ATTTACAGAC TGTCTG AA TG CG AGA T
TATGTGCAGAATATTTACAG G |||||| || || || |||
ACG GCAGAC TT AC GT TCT /
A TATAAG GT A TAAAAACA

GAM1992 TTTGTAAAGGATATGATATG 48591 TATGTTGTGA 23801 AAAGGATATGAT GT T A - TA
TTGTGATTCTAGAATAGTAG TTCTAGAATA TTTGT ATGTT GAT CTAGA TAG TAG G
TAGCTCTATCTAGTCTAGTA GTAG ||||| ||||| ||| ||||| ||| |||
TCTAAACATTGGGAATTGAC AAACA TACAA CTA GATCT ATC ATC /
AAA GTTAAGGGT--- AT T G T TC

GAM1993 GGTTCTTGTCTATCACCGGA 48592 CACCGAGATG 48593 T- C A - A AAT TT
GTTTTCTTAGGAATCGTTAT GGCCTGCTGA GGTTCT GTCTATCA CGG GTTT TCTT GG CG A
TTGCACCGAGATGGGCCTGC TAGA |||||| |||||||| ||| |||| |||| || ||
TGATAGACCCGGGACC CCAGGG CAGATAGT GTC CGGG AGAG CC GT /
CC C - T - AC- TT

GAM1994 ATTTTTATCATAACACTACT 48608 CATAACACTA 48609 CAT CTACTT TA- TAGAA
TCGGTTAGATGTTTTAGAAA CTTCGGTTAG ATTTTTAT AACA CGGT GATGTTT A
AAAATAAATATCACTACCGT ATGT |||||||| |||| |||| |||||||
TCTTGTTTTATAAAAAT TAAAAATA TTGT GCCA CTATAAA /
TT- TCTT-- TCA TAAAA

GAM1995 GACGCGGGGGTCCCCAGCGG 48622 CCGCGCGAGG 48623 GGTCC A GC T G - G - CA - C C
CGCCGCGGTGAGCACCGTCG CGACGCGTGT GGG CC GCGGCGCC GG GA CAC CGTCGC TCG GC GCG CCG CAC G

CGTCGGCCAGCGCCGCCACC CTCC ||| || |||||||| || || ||| |||||| ||| || ||| ||| |||
GCCGTGCCGGCCGCCGCGCG CCC GG CGCCGCGG CC CT GTG GCAGCG AGC CG
CGC GGC GTG C
AGGCGACGCGTGTCTCCAGG ----- C A- T - C G G C- C C C
CGCCGCCGGCCCGCGTC

GAM1996 GCGTCGACGACGGGGCGACG 48640 TCGACGACGG 48641 T A CGA -- -- G T
GCGGCGGACGGCGCGGCTCC GGCGACGGCG GCG CG CGACGGGG CGGCG GCGGAC
GGC CGGC C
GCCGGGCCAGGTCCGCGACG GCGG ||| || |||||||| ||||| |||||| ||| ||||
CCGCCCCCGTCGCGCGC CGC GC GCTGCCCC GCCGC CGCCTG CCG GCCG /
- - C-- AG GA G C

GAM1997 GTGACTCACACCCAGGTTAT 48830 TAACGGGTTT 48831 TG - CA -- C TG T AA
TTCAGATA
CCCTGGTGCAAGTTGGGTTC TGGTGATTTA G ACT CA CCCAGGTTA TC C G GC GTTGGG
A
AGATAATAAAGCGGTTTTAA ATTT | ||| || |||||||| || | | || ||||||
CGGGTTTTGGTGATTTAATT C TGA GT GGGTTTAAT AG G T TG CAATTT T
TGGGATGAAGTTGC GT A A- TT T GT T GG TGGCGAAA

GAM1998 TTTTATTAAACAAGAGCCAC 48838 TTAATGCTGG 48839 TAA G ACAC T GAAA TA CT
- T
ACAGTCTTGAGAAAGTTAAT TCGACTCCGT TTTTAT ACAA AGCC AGTC TGA GT ATG
GGTCGACT CCGTA T
GCTGGTCGACTCCGTATTAT ATTA |||||| |||| |||| |||| ||| || ||| |||||||| |||||
TGCGGCAGTTGGCCTCGTCG AAAGTA TGTT TTGG TCAG GCT TA TGC
CCGGTTGA GGCGT A
ATCAAATCGTGACTAGGTTG TG- G A--- T AAAC GC T- C T
TTGTGTATGAAA

GAM1999 GTGATGGCCGAACACGGTAC 48842 TGGCCGAACA 48843 A ACA TA TT GAA
GATTTGTGAAACAGACATTT CGGTACGATT GTG TGGCCGA CGG CGA TGT A
CGGGCTGGGATTGGTCAGTA TGTG ||| ||||||| ||| ||| |||
C CAT ACTGGTT GTC GCT ACA /
G AGG GG TT GAC

GAM2000 CGACTACGTACACAGTTAGC 48846 AGCGGGAGAG 48847 CA GTTA- GA - GG
GGGAGAGGAGATCGGAGGGT GAGATCGGAG CGACTACGTA CA GCGG GAGGAGAT CGGA
G
ATCTGAATTTCTTCCTTCGT GGTA |||||||||| || |||| |||||||| ||||
GTACATGCATATGTGGTCG GCTGGTGTAT GT TGCT CTTCTTTA GTCT /
AC ACATG TC A AT

GAM2001 CCAGGCGGTCAGCTATCGGG 48929 GAGAATGAGA 48930 CG - --- - TG AACA CT T
TGATTACAACACATCTTCGA GTGATTGCCA CCAGG GTC AGC TATCG GG ATTAC CAT
TCGAG A

GTAATTCGAGAATGAGAGTG CGAT ||||| ||| ||| ||||| || ||||| ||| |||||
ATTGCCACGATGTTTGCTCG GGTCC TAG TCG GTAGC CC TAGTG GTA AGCTT /
ATACCTGG A- C TTT A GT AGA- AG A

GAM2002 GCCGTCAGGATCAAGGATCG 48938 TCGCTCCGCC 48939 A---- ATCAA- AT ACC-- A
GAGACCCCCAACAGGGACTC CCAGACCGCC GCCGTC GG GG CGGAG CCC A
GCTCCGCCCCAGACCGCCCG CGAC |||||| || || ||||| |||
ACCGACGGC CGGCAG CC CC GCCTC GGG C
CCAGC GCCAGA CC GCTCA A

GAM2003 GTAACCCTCAGCGGCCCCAG 48977 CAGCGGCCCC 48978 A CCTCA CCGAC-- CACCA
CCCGACGCCCACCATCTCTC AGCCCGACGC GT AC GCGGCCCCAGC GCC T
TGGCACAAATCGCTGGGGTC CCAC || || |||||||||| |||
GTCAAAGTCAC CA TG TGCTGGGGTCG CGG C
C AAAC- CTAAACA TCTCT

GAM2004 GTTCGAACACCGCTGGGCCG 49133 CGGCCTGCTC 49134 ACA ----- C - CT
GCTTTGACTTCTTCGACGGC AACCCTGCGG GTTCGA CCGC TGGGC GGCT TTGA T
CTGCTCAACCCTGCGGCACT CACT |||||| |||| ||||| |||| ||||
CGAAC CAAGCT GGCG ACTCG CCGG AGCT /
CAC TCCCA T C TC

GAM2005 TATCATGAATTGATTATGTC 49167 TATGTCTGAT 49168 AT A GATATTATTT - AC
TGATATTATTTTCATGGCCC ATTATTTTCA TATCATGA TGATT TGTCT TCATGG CCC A
ACATGAGGGCCCATGATCCT TGGC |||||||| ||||| ||||| |||||| |||
CTAAGGACAAGATCACTCAT GTGGTACT ACTAG ACAGG AGTACC GGG T
GGTG C- A AATCTCCT-- C AG

GAM2006 GGCGTTCAGGCCTTAATACT 49177 CAGCATGTAT 49178 CA TA TA--- - TCT
AGCCGCATCTTACCTGTCGG CGGGGCTCCG GGCGTT GGCCT ATAC GCCG CA T
CAGCATGTATCGGGGCTCCG ACGC |||||| ||||| |||| |||| ||
ACGCC CCGCAG TCGGG TATG CGGC GT /
CC GC TACGA T CCA

GAM2007 CGCCGAAAAATGCTTGTCTG 49188 CACTTTTTTG 49189 AAAA CTT CT T-- T CG
GCTGAGGTTGGTGTCGCTAA TCTCGCTTCA CGCCGA TG GT GGC GAGGT GGTGT C
TGCCACTTTTTTGTCTCGCT ATGT |||||| || || ||| ||||| |||||
TCAATGTCGGTG GTGGCT AC CG CTG TTTCA CCGTA /
GTA- TT- CT TTT - AT

GAM2008 GAGAAAATCTGTGATTCTCT 49202 TCTGTGATTC 49203 TC AT T TG T T
ATGAGTGTTATTTTTATTAT TCTATGAGTG GAGAAAA TGTG TCTCTA GAG T AT T
CCTTTTGGGGACTACGATTT TTAT ||||||| |||| |||||| ||| | ||

```
    TTCTT                          TTCTTTT  GCAT  AGGGGT TTC  A TA T
                                   TA   C-    T   CT T  T


GAM2009  GGTCCGCATGGCTCCGGACT 49213   TACGGGTATC 49214      GCAT   C   --   TT--    AG
    CGTTTATCGTGAGCTTCATG       TGCAGCTGGA       GGTCC   GGCT CGGA  CTCGT   ATCGTG  C
    ATTTCTACGGGTATCTGCAG       CC             |||||   |||| ||||  |||||   ||||||
    CTGGACC                      CCAGG   TCGA GTCT  GGGCA   TAGTAC  /
                               ----   C   AT    TCTT    TT


GAM2010  GTCGTTTTGTTCACCGTCGC 49254   CACCGTCGCT 49255        GTTC    C---    A   GAAA
    TGTGCAACGCGTGAAACAAG       GTGCAACGCG       GTCGTTTT   ACCGTCG   TGTGCA CGCGT   C
    AGCGTGATGCGCACCTTCGG       TGAA           ||||||||   |||||||   |||||| |||||
    CGGTATGAAGAACGAT                   TAGCAAGA   TGGCGGC   ACGCGT GTGCG   /
                                 AGTA     TTCC    A    AGAA


GAM2011  CGTATAAGAGCCACAGGTTT 49263   TAAGAGCCAC 49264     ----      C  GGTT  ATT   CAA     TG
    CATTTATCAATGTTTATTGT       AGGTTTCATT       CGT   ATAAGAGC ACA   TC  TAT   TGTTTAT  T
    ATATAAATAGAATATCGATA       TATC           |||   |||||||| |||   ||  |||   |||||||
    TGTGCTCTTATTCTAACG                 GCA   TATTCTCG TGT   AG   ATA   ATAAATA  /
                               ATCT      -   AT--  CT-   AG-     TA


GAM2012  TTATTAATAGATAGAGTATA 49277   TAGAGTATAC 49278       A      GTATACGAAA-   TAT
    CGAAACAATATTATTTTTGG       GAAACAATAT       TTATTA TAGATAGA        CAA   T
    GTAAAACGGATCTATCTAGT       TATT           ||||||| ||||||||        |||
    GATGA                        AGTAGT ATCTATCT        GTT   A
                                 G      AGGCAAAATGG   TTT


GAM2013  CAGTGAGGGCTTTGATCTGT 49280   TTTCGCAAGC 49281       -    -   ----    TTTCTTTC
    TTCTTTCCGATCCTTATCAG       CTCTTACTG        CAGTGAG GGCTT TGA   TCTG      C
    AATTTTCGCAAGCCTCTTAC                 |||||||  |||||  |||   ||||
    TG                         GTCATTC CCGAA GCT   AGAC      G
                                 T   C   TTTA   TATTCCTA


GAM2014  TAGTTTTCGTTGTGAGCTTT 49304   CAATAGGTCT 49305     TTTC   TGA   TTTT     GTCT   TA
    TTGATTTATGTCTCCAGTAA       CCTAGCATTC       TAGT   GTTG   GCT   GATTTAT   CCAG  A
    ATTTGGCAATAGGTCTCCTA       AGCA           ||||   ||||   |||   |||||||   ||||
    GCATTCAGCATTACTG                   GTCA   CGAC   CGA   CTGGATA   GGTT  /
                               TTA-   TTA   TCCT     AC--   TA


GAM2015  GCTTTGGCCCTTCAGTTTGC 49331   TGAGATAGAA 49332       GC-    AG-    CAAT   TAA-    T
    CAATTTCTTAACAAGCTTGG       TCTGCAAAAG       GCTTTG   CCTTC   TTTGC   TTCT   CAAGC T
    GTTTGAGATAGAATCTGCAA       AGGA           ||||||   |||||   |||||   ||||   |||||
    AAGAGGAGGATACAGAGC                 CGAGAC   GGAGG   AAACG   AAGA   GTTTG G
```

ATA AGA TCT- TAGA G

GAM2016 GTTACCTTCATTTCTGCTCA 49370 TACCTTCATT 49371 CTT TT T- C A C
CACTGATCTTCAAGAGATAG TCTGCTCACA GTTAC CA TC GCTCA ACTG TCTT A
TTGGGCCTGATTTGTACGTG CTGA ||||| || || ||||| |||| ||||
GC CGGTG GT AG CGGGT TGAT AGAG /
CAT TT TC - - A

GAM2017 GAGCCTTAGGCCTCCAACGG 49404 CTGCCGGCGT 49405 CTTA TCCAAC T A ATTAC
ATTTTGGCAAGCCATTACTG CTCTTTGGCC GAGC GGCC GGAT TTGGCA GCC T
TTTGCGGCTGCCGGCGTCTC CTGC |||| |||| |||| |||||| |||
TTTGGCCCTGCTC CTCG CCGG TCTG GGCCGT CGG G
TC-- TTTC-- C - CGTTT

GAM2018 ATGGCACTTAAAATTGACTG 49432 ATGGAGCAGC 49433 ACT AATT CAACC A AGTT
TG
TTCAACCCTACTCCAAGTTC CTAATAGTTT ATGGC TAA GACTGTT CT CTCCA
CTCTTGCT T
TCTTGCTTGTTTTGGCAAGA AACT ||||| ||| ||||||| || ||||| ||||||||
GTTATGGAGCAGCCTAATAG TACTG ATT TTGATAA GA GAGGT GAGAACGG T
TTTAACTTATGAGTCAT AGT CAAT TCC-- C ATT- TT

GAM2019 AAGATCTCTAACAAAAAGCT 49443 TCTCTAACAA 49444 TC AACAAAA T ACCAC
GTCTTTACCACAAGCAAGAG AAAGCTGTCT AAGA TCT AGCTG CTTT A
AGTCAGCTGCAAAGAACTCT TTAC |||| ||| ||||| ||||
T TTCT AGA TCGAC GAGA A
CA AACG--- T GAACG

GAM2020 TGTTTCTTTTCAAAATGTGT 49469 TTAAAAGACA 49470 CAAAA G GC A TTC
TGCAGCTAGTTTCCATTTAC AAAAGGAGAT TGTTTCTTTT TGT TT AGCT GT C
CAGTTAAAAGACAAAAAGGA A |||||||||| ||| || |||| ||
GATA ATAGAGGAAA ACA AA TTGA CA A
A---- G AA C TTT

GAM2021 CTTTACACACTTTATAGAAC 49509 TAGAACAGGG 49510 T AC T AC----- - ATT
AGGGAAATTTACATTTACAA AAATTTACAT CT TACAC TTTA AGA AGGGAAAT TTAC T
GTAATATTTCCCTTCAACAG TTAC || ||||| |||| ||| |||||||| ||||
TCTTTGAAAAGTGTACAG GA ATGTG AAGT TCT TCCCTTTA AATG A
C AA T GACAACT T AAC

GAM2022 GCCAGGTTTCCATTGCCACC 49523 TTTCCATTGC 49524 T- ATT-- C G GAA
CGGGCGAAAACAAGCCGGGT CACCCGGGCG GCCAGGT TCC GC ACCCGG C A
AGTTTCAGGGGTCATCTGGC AAAA ||||||| ||| || |||||| |

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                                    CGGTCTA  GGG    TG TGGGCC G   A
                                       CT   GACTT  A     - AAC


GAM2023  ACATGATAAGACAATTCGTG 49560   TAAGTGAACA 49561       TAAGACA-   G    TCCA    T
GCCAA-    G
         AATTCCATTTAAGTGAACAG       GCCAAGTTTT       ACATGA      ATTC TGAAT    TTTAAG GAACA
GTTTT T
         CCAAGTTTTGTACAAAATGC       GTAC          ||||||      |||| |||||   |||||| |||||     |||||
         CACATGTTCCTTAAAAGCTG                  TGTACT      TAAG ATTTG    AAATTC CTTGT     TAAAA A
         TTTAAGAATGGAAACCTTCA                    TCCAAAGG   A    TCGA    -    ACACCG    C
         TGT

GAM2024  TTTTTCCTCTGTTTTTGCTT 49576   CCTCTGTTTT 49577       CT-    TTTT    ACGTTCAAAT
TCTTTAA
         GACGTTCAAATTTTGGGTCG       TGCTTGACGT       TTTTTC   CTGT    GCTTG       TTTGGGTCG     C
         TCTTTAACCTGCTCTTGACT       TCAA          ||||||   ||||    |||||       |||||||||
         TAAATAAGCTTCTACGGTCA                  AAAAAG   GGCA   CGAAT       AAATTCAGT     /
         GAAAAA                      ACT    TCTT    ----------       TCTCGTC


GAM2025  GGAGCAAGCCATTTTAAAAT 49616   TTCGAAGTGC 49617      C    CATTTT      CC  TACAG       TCC
         CTCCGTTACAGTTGAATGGT       AGATTTTCCG       GGAG AAGC     AAAATCT  GT    TTGAATGG   A
         CCAAGTCTATTCGAAGTGCA       CTTT          |||| ||||     |||||||  ||    ||||||||
         GATTTTCCGCTTTCTCT                     TCTC TTCG     TTTTAGA  CG    AGCTTATC   /
                                 T   CC----      --  TGA--       TGA


GAM2026  GCCTAAATTATTATCTAAAA 49624   TCTAAAATAG 49625       AAT    TCT    AGC    T     C---    A
TAT
         TAGCATAAGGTGGGTAAGCT       CATAAGGTGG       GCCTA   TATTA   AAAAT   ATAAGG GGGTAAG
TGTAT TAATA   C
         GTATATAATATATCACATTG       GTAA          |||||   |||||   |||||   |||||| |||||||    ||||| |||||
         TTGAATATGATTTCTTATTT                   CGGAT   ATAAT   TTTTA   TATTTC TTTATTC    GTATA GTTGT
 A
         CTTTATCATTTTTATTAATA                     ---    TAT    C--     -     TTTA    A    TAC
         TAGGC

GAM2027  CGATATAGTACGCGCCTGCC 49662   TAGTACGCGC 49663       A      CT  CG-  A      ----------
AA
         GGGAGAAACATCCCCTGAAC       CTGCCGGGAG       CGATAT GTACGCGC  GC   GG GAAACAT
CCCCTG  C
         CGCGGGGGTGACCGTATACT       AAAC          ||||||  ||||||||  ||   ||  |||||||         ||||||
         ATGTTTCCTAGAGCCGTGCG                   GCTGTA CATGCGTG  CG   TC CTTTGTA         GGGGGC  /
         TACCATGTCG                       C      C-  AGA  -      TCATATGCCAGT     GC


GAM2028  AATATAACATTATCAATATT 49669   TATAACATTA 49670           CA   T   --   --      A
         ATCAATATTATCAAAAAAAT       TCAATATTAT       AATATAACATTAT  ATAT ATCA  ATAT  TATCAAA A
         TTGATATAATATTATGATCA       CAAT          ||||||||||||  |||| ||||  ||||  |||||||
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TGTAATGGTGTTATATT TTATATTGTGGTA TGTA TAGT TATA ATAGTTT A
A- C AT AT A

GAM2029 TCCCCGTGGGCTCCACGCGT 49673 AACACCGTGA 49674 GC C C T -- C
TTTCCACCCTTTCCTGGAGG ATCCACGGGG TCCCCGTGG TC ACG GT TTCC ACCCTTT C
GGTCCGGAACACCGTGAATC A |||||||||| || ||| || |||| |||||||
CACGGGGA AGGGGCACC AG TGC CA AAGG TGGGGAG T
TA - - C CC G

GAM2030 AGTCTGGCCGAGCGGCGCCA 49716 CGAGTCCGCG 49717 A ---------- G - G AC
ACC
TCTTGGAGGAGGGGCGAGTC GTCGCCGCCT GCGCC TCT TGGAG AGG GGCGA
TCGCGGGC CGCCTCGGT C
GCGGGCACCGCCTCGGTACC GTTC ||||| ||| ||||| ||| ||||| |||||||| |||||||||
CCCTGGCCGAGGCGAGTCCG CGCGG AGA GCCTT TCC CCGCT GGCGCCTG
GCGGAGCCG C
CGGTCGCCGCCTGTTCCGTG G TCCATCGTAGT G G - A- GTC
ATGCTACCTAGAGGGCGCTG
TCGAGGCGACT
GAM2031 TCTCGACGGTTCTCTCGCTC 49726 GACGGTTCTC 49727 G---- CT C TTCT
GTCATGCCGTTCTGAGCTCC TCGCTCGTCA TCTCGACG TTCTCTCG CGTCATG CG G
GACATGGCGGACGAGAGAAA TGCC ||||||||| |||||||| ||||||| ||
ATGGCGTCGAGA AGAGCTGC AAGAGAGC GCGGTAC GC A
GGTAA AG A CTCG

GAM2032 AATTTATCGATTAGTCTTAA 49733 TTTATAGTGG 49734 TT CTT TACA-- AG T
AATC
TGATACACTAAGTATATACA ATCCATTCAT AATTTATCGA AGT AATGA CTA TATA ACACAG
A
CAGAATCAGAACCTGTGTTT TACT |||||||||| ||| ||||| ||| |||| ||||||
ATAGTGGATCCATTCATTAC TTAAATAGTT TCA TTACT GGT ATAT TGTGTC /
TCTTGATAAATT C- --- TACCTA G- T CAAG

GAM2033 TACTGTTTTATTGGTAGTTT 49744 TGGATGTATC 49745 TATT- T T CGA CTT CA
ATGTATCGACGCTTTCCCAA TATGCTACCT TACTGTTT GGTAGT TA GTAT CG TCC A
AATGGATCTGGATGTATCTA TGGT |||||||| |||||| || |||| || |||
TGCTACCTTGGTGGACAGTA ATGACAGG CCATCG AT TATG GT AGG A
TGGTT T C TAG CT- TA

GAM2034 GCTTCACACGTTTCTACCAA 49750 TAGTAGGAAC 49751 T -------- CAA CAAGA
GCCCAAGATTCGATCGGTAG CCGCAATTGT GC TCACAC GTTTCTAC GCC T
TAGGAACCCGCAATTGTGTG GTGA || |||||| |||||||| |||
ACGT TG AGTGTG CAAGGATG TGG T
C TTAACGCC A-- CTAGC

GAM2035 GCGTTCGCACCGCGAACCAA 49759 TATTATTGGC 49760 -- AA TAAG A
TATAAGATTATATATATAAT GCAAGGTGCG GCGTTCGCACC GCG CCAATA ATTAT T
ATATTATTGGCGCAAGGTGC AACG |||||||||||| ||| |||||| |||||
GAACGC CGCAAGCGTGG CGC GGTTAT TAATA A
AA -- TATA T

GAM2036 GTCCGAGGCCGCCGGGGAGG 49766 CGCGTTCGCC 49767 -- GA G --- ---- A
GGAA GAAGGG
AGGTTGTGGGGGCGGGAGGA GCGGCGTCCG CCG GGGAG GGTT TGG GGGCG GG
GGATGTGTGGG GG G
TGTGTGGGGGAAGGGAAGGG ATCC ||| ||||| |||| ||| ||||| || |||||||||| ||
GGAGACGGCCGAAACCTACG GGC CCCTC CTAG GCC CCTGC CC CTTGCGCATCC
CC G
CGTTCGCCGCGGCGTCCGAT AG G- G TAG GGCG G AAAG GGCAGA
CCGGGATCGCTCCCGACGGG
GCTCTCGTTC
GAM2037 AGCTTGTTATTGGCTCCCGG 49769 TGCCATGTTG 49770 A G-- C--- GA
CCCAGTTGATGGAGCTGCCA GGAGAAACAA AGCTTGTT TTG CTCCCGGC CAGTT T
TGTTGGGAGAAACAAAGCAA AGCA |||||||| ||| |||||||| |||||
GTT TTGAACGA AAC GAGGGTTG GTCGA /
- AAA TACC GG

GAM2038 TCTGGATGGTGGATTTGACG 49836 GTGGATTTGA 49837 T ------ -- TTCA G
ATTTCAGCGACGTATGTCGT CGATTTCAGC TCTGGA GGTGGAT TTGAC GAT GCGAC T
ACATATCTAGTCAACTTAAC GACG |||||| ||||||| ||||| ||| |||||
GTCTATTTCCGGA AGGCCT TTATCTG AACTG CTA TGCTG A
- CAATTC AT TACA T

GAM2039 GCCGCGGGCGTGCAGGGAGG 49839 GGCGTGCAGG 49840 C- GG ------ G A--- AA
CCGAAGCGGCGGCCGGAGCC GAGGCCGAAG GC GCG CGT GCA GG GGCCG G
GTGCAGAAACACGTACGTAC CGGC || ||| ||| ||| || |||||
GC CG TGC GCA CGT CC CCGGC C
CA AT CAAAGA G GAGG GG

GAM2040 GTTCAGGCGGCGGGGCTCGA 49894 AGGCGGCGGG 49895 AG - ------- - GA- ACCGGA
A
CGACGGACCGGACGGTACAG GCTCGACGAC GTTC GCGG CGGG GCT CGAC CGG
CGGTAC G
TTGTACCGGAGCCGATAGTC GGAC |||| |||| |||| ||| |||| ||| ||||||
GTAGTAACTAGACCCGACCG CAGG TGCC GCCC TGA GCTG GCC GCCATG T
TGAGGAC AG A AGATCAA T ATA GAG--- T

GAM2041 CCCGTCGCGTTGGGTTGCAG 49996 TCGCGTTGGG 49997 - GTTG TG AG---------- C
CCGCAAGCGGACGCTGGGGG TTGCAGCCGC CCCG TCGC GGT C CCG A

GAGCGGTGGCCAGAGCGAGC AAGC |||| |||| ||| | |||
GGG GGGC AGCG CCG G GGC A
G AGA- GT GCGAGGGGGGTCGCA G

GAM2042 GGGCGCCGCCACCCCCGACC 50009 TCGCCGGGCG 50010 CG A A G G GT
GGGGGAGCGGTCGTCGCTCG GGGGGGAAGC GGGCGC CC CCCCCG CC GG GAGCG C
CCGGGCGGGGGGGGAAGCGCC GCCC |||||| || |||||| || || |||||
C CCCGCG GG GGGGGC GG CC CTCGC /
AA - - G G TG

GAM2043 TTCAGGGCCCCACAAATTTC 50050 ATAGAACTAA 50051 C ATT A--- C G CACCCCC TG C-- CCCA A
ATATTTCCAGCAGCCTTTCC CTTGTGACAC AA TCAT TTTC AGCA CCTTTC CG AGT TTC CAG A
ACCCCCCGTGAGTCTTCCCC AGAA || |||| |||| |||| |||||| || ||| ||| |||
ACAGAAACTGCATAGAACTA TT AGTG AAAG TTGT GGAAAG GT TCA AAG GTC /
ACTTGTGACACAGAAAGGTG A GT- GACC T - ACACA-- GT ATC ATAC A
TTTGAAACCAGGTGATGTTA
TGAAACTGAAG
GAM2044 CGGCGGCTGGACCTGCGCCA 50073 ACGGCAGACG 50074 -- ACC C- C T GG GG- C
GCGCCTGTCCGTGGGCGGCA GCAAGTTCCT CGGCG GCTGG TGCGCCAG GC TG CCGT GC CAT C
TCCTGATGACGGCAGACGGC GGTG ||||| ||||| |||||||| || || |||| || |||
AAGTTCCTGGTGTGCCAGCG GCCGC CGACC GTGTGGTC TG AC GGCA CG GTA T
GCGCCG GG --- CT A - GA GCA G

GAM2045 GGCAGCGCTTGTTTCGCATG 50092 TGAGCGCGGA 50093 AGC C - A -- TTT G GA
CACAGCCGCTTTCTGGGCGC GCTGGCGTTG GGC GCTTGTTT GCA TGC CAGC CGC CT GGCGCGTGC G
GTGCGAGCGGCGCGCGCTGA CCGA ||| |||||||| ||| ||| |||| ||| || ||||||||| GCGCGGAGCTGGCGTTGCCG CCG CGAGCGAG CGT GCG GTCG GCG GA TCGCGCGCG /
AGCGAGCACGCC CA- C T - AG C-- G GC

GAM2046 GAAAAGGAGGAGAACACGGA 50118 TAGCGCTCAG 50119 GA--- A A TAG GA TCTC AA
TAAAGTTAGCGCTCAGAATA AATATCTCAT GAAAAGGAG GAACACGG TA AGT CGCTCA ATA ATTCA T
TCTCATTCAAATCCATGAAT TCAA ||||||||| |||||||| || ||| |||||| ||| |||||
AAACTATATGGGCGATATTC TTTTTCCTT TTTGTGCC GT TTA GCGGGT TAT TAAGT C
TGCCGTGTTTAAAGATTCCT AGAAA - C TA- A- CAAA AC
TTTT

GAM2047 GGGATGAAACCTCTACTGCC 50128 TGGGATCTGA 50129 -- CCTCT - AAT--- - A-
TAC T
CTAGGAATGCCAGGCAGGTA GCCTGGGCTA GGGAT GAAA ACTGCCC TAGG GCC
AGGC GG CCCACC C
CCCCACCTCCGGGTGGGATC ATTG ||||| |||| ||||||| |||| ||| |||| || ||||||
TGAGCCTGGGCTAATTGTCT TCCTA CTTT TGATGGG ATCT CGG TCCG TC
GGGTGG C
ACGGGTAGTTTCATTTCCAA AC ACTT- C GTTAAT G AG TA- G
TCCT

GAM2048 GAGAAGGTGTTCCGCTGTGG 50136 TGCCCCAGTG 50137 GTTC-- T TGCCA G
CTGCCAACCTGGTAACAGGT TGCGTAACCT GAGAAGGT CGCTG GGC ACCTG T
GCCCCAGTGTGCGTAACCTT TCTT |||||||| ||||| ||| |||||
CTT TTCTTCCA GTGAC CCG TGGAC A
ATGCGT C ----- A

GAM2049 GTATATAGATGTCAATGAAG 50150 TAGATGTCAA 50151 TAGA ATGAAG AC CA T
AGTACACAGAAGCAGCTGCA TGAAGAGTAC GTATA TGTCA AGT ACAGAAG GC G
GCAACTTCTGTACTAGTGGC ACAG ||||| ||||| ||| ||||||| ||
AGATTGTGC CGTGT ACGGT TCA TGTCTTC CG C
TAG- GA---- -- AA A

GAM2050 CATGTTTGTCAGCATATTTG 50168 CTAGGTCAAA 50169 G T CATA- - ATT TGTT
CATTGCATGTTTCAAATTGC GTTCCCTGCC CAT TTTG CAG TTTG C GCA T
TAGGTCAAAGTTCCCTGCCA AAAA ||| |||| ||| |||| | |||
AAAATG GTA AAAC GTC AAAC G CGT C
A C CCTTG T GAT TAAA

GAM2051 CCAAACTTGCTTTTAGGCAC 50208 ACTTGCTTTT 50209 T T G ACATA TAC
ATAGTTTTACTGCATAAACA AGGCACATAG CCAAACT GCT TTAG C GTTT T
TTTAGCTAATAGCAGTTTGG TTTT ||||||| ||| |||| | ||||
GGTTTGA CGA AATC G CAAA G
- T - ATTTA TAC

GAM2052 GCCACAGAGGTCTCTGCTAG 50216 TGCTAGTTTG 50217 C G- TG AGT CC GAA
TTTGGGCCAGCGAAACGGGC GGCCAGCGAA GC ACAGA GTCTC CT TTGGG AGC A
TATCCCGGTCCGGTGGAGGC ACGG || ||||| ||||| || ||||| |||
AGTCTGTCGC CG TGTCT CGGAG GG GGCCC TCG /
C GA GT CCT TA GGC

GAM2053 GTAGAGATATTGTTTAATGA 50224 TATTGTTTAA 50225 GAGATA GAAA- - A
AATTAACAATCCTATTAAGG TGAAATTAAC GTA TTGTTTAAT TTAACAAT CCT T
AATTGTTAAAAAGAATTAAA AATC ||| ||||||||| |||||||| |||
CAAGAGGTAC CAT AACAAATTA AATTGTTA GGA T

GGAG-- AGAAA A A

GAM2054 AATAATAGATCTATTAAGAC 50228 CATAACAGGC 50229 A - AA A AC---- G
AAAGCACTGCGGAAACGCAT TTAGTCAAAT AAT ATAGAT CTATT GAC AAGC TGCG A
AACAGGCTTAGTCAAATAGA AGAA ||| |||||| ||||| ||| |||| ||||
ATCTATAGTT TTG TATCTA GATAA CTG TTCG ACGC A
A A A- A GACAAT A

GAM2055 AGGTACCTTTGTACGCCTGT 50255 TTCAATAGCA 50256 C-- G
TTATATCCCTTCCCCCGT A AG
TTTATATCCCTTCCCCCGTA GGGGTACAAG AGGTAC TTTGTAC CCTGTT AACTTT
GA C
ACTTTAGAAGCTTATCAAAA CCAG |||||| ||||||| |||||| ||||||
GTTCAATAGCAGGGGTACAA TCCATG GAACATG GGACGA TTGAAA CT T
GCCAGTACCT ACC G TAAC---------- A AT

GAM2056 GAAACATTTCAGTCTCTCTG 50265 TGGCATCTGA 50266 AT- CTC- CAAC TA
GCATCTGACAACGGCTACGC CAACGGCTAC GAAAC TTCAGTCT TGGCATCTGA GGC C
GCCACTCAGATGCCAAAACA GCGC ||||| |||||||| |||||||||| |||
GACTGGATGCGTTTC CTTTG AGGTCAGA ACCGTAGACT CCG /
CGT CAAA CA-- CG

GAM2057 TTGGGTGTCCGTGTTTCCCT 50279 TACCATATAG 50280 T TGTTTCCCTTTAT TAC CT
T
TTATATTCATACTGGCTGCT CTATTGGATT TTGGGTG CCG ATTCA TGGCTG
TATGGTGACAATT A
TATGGTGACAATTTACGAAT GGCC ||||||| ||| ||||| |||||| ||||||||||||
TGTTACCATATAGCTATTGG GACCCAC GGT TAGGT ATCGAT
ATACCATTGTTAA C
ATTGGCCACCCAG C ---------- T-- -- G

GAM2058 TCGGACCGCTGCGATTCCAT 50287 GGGTAATAGC 50288 C A C A GCG T
CCTTCGACTAGCGACTTGTT CGGACGACGG TCGGACCGCTG GATTCC TC TTCG CTA
ACTTGT A
ATGGCGGGTAATAGCCGGAC AGTC |||||||||| |||||| || |||| ||| ||||||
GACGGAGTCTCGGCGGTTCG AGCTTGGCGGC CTGAGG AG AGGC GAT TGGGCG T
A T C C C AA- G

GAM2059 GACCGCATGAATCAAGACAT 50293 CATGTAAACC 50294 CATGAA C TA G G T
GTAAACCGTGTGTGTATGTT GTGTGTGTAT GACCG TCAAGA ATG AACC TGT TGTATGT A
AAATGTCTTTAATAAACAGC GTTA ||||| |||||| ||| |||| ||| |||||||
ACTTTCATGTTACAC CACAT ACTTTC ACG ACAA ATA TTTCTGT A
TGT--- - -- - A A

GAM2060 CCTTTGGAAACGCATCCAGT 50308 TGTTTTGGCA 50309 T CATC G G-- GC
CTGTTTTGGCATCTGAGTGG TCTGAGTGGC CCTT GGAAACG CAGTCT TTTTGGCATCTGA
TGGC G
CGCGTAGCCGTTGTCAGATG GCGT |||| ||||||| |||||| |||||||||||||| ||||
CCAGAGAGACTGAAATGTTT GGAG TCTTTGT GTCAGA GAGACCGTAGACT GCCG /
CTCGAGG C AAA- - GTT AT

GAM2061 TGTGACATCTGGGACAAAGA 50314 TGGGACAAAG 50315 A TCT AC AAA ATTT T
AACTATTTTACCTTTTCAGG AAACTATTTT TGTG CA GGG AAAG CT TACCT T
TATGAGACTTTACCCTATTG ACCT |||| || ||| |||| || |||||
ACACA ACAC GT CCC TTTC GA ATGGA T
A TAT A- A-- GT-- C

GAM2062 TCCTGTCCGCTGTGTGGACC 50333 GACCTGGGAC 50334 C T T CCATGACGC A A
AGA A
ATGACGCTTGACCTGGGACT TAGATTGCAC TCCTGTC GC GTG GGA TTG CCTGGG CT
TTGC C
AGATTGCACCGGCAAAGCCC CGGC ||||||| || ||| ||| ||| |||||| || ||||
AGGCGATTCCCATGCGACAG AGGACAG CG TAC CCT AGC GGACCC GA AACG C
GA - - - T-------- - - --- G

GAM2063 CGTGAATGGGGGCAGTGCAC 50364 ACGCACCAGG 50365 T - A--- AC--- A G TGGT
GCACCAGGATCCAGACTGGT ATCCAGACTG CG GA ATGGGGGC GTGC GC CCA
GATCCAGAC C
CCAAGCGTCTGGGTCGTGGC GTCC || || |||||||| |||| || ||| |||||||||
GCCTTTGGCATAATCGTCCC GC CT TATCCCTG TACG CG GGT CTGGGTCTG C
TATCTCCG - C CTAA GTTTC C G CGAA

GAM2064 GGTTTATGTCAAAGGAGAAG 50416 TATGTCAAAG 50417 A TGATTTTAA ACC
GTGATTTTAATTGCACCTGA GAGAAGGTGA GGTTTATGTCAAAGG GAAGG TTGC T
AGCAACCCTAGGTCTTCCCT TTTT |||||||||||||| ||||| ||||
TTGATGTGAGCT TCGAGTGTAGTTTCC CTTCT AACG /
- GGATCCC-- AAG

GAM2065 CGCCACTGCCGCTCAGGTAC 50427 CTCAGGTACA 50428 CCG----- AGG - A CAT CAA
AGTAGGACATACCCCAAATA GTAGGACATA CGCCACTG CTC TAC AGT GGA ACCC A
TTGGGTTCCACTCGTAGAGA CCCC |||||||| ||| ||| ||| ||| ||||
AGAAAATTAGTGGCG GCGGTGAT GAG ATG TCA CCT TGGG T
TAAAAGAA --- C - --- TTA

GAM2066 GTGACCTGGAAATGCTCCCC 50462 TTGGACCTTC 50463 A AAA CC-- T A-- TT TTA
GTGAGAAACCTTGTTTAAAC TCCGGCCTCA GTG CCTGG TGCT CCG GAGAA CC GT A
GCACTTGGACCTTCTCCGGC GCGC ||| ||||| |||| ||| ||||| || ||

CTCAGCGCCAGGCAT TAC GGACC GCGA GGC CTCTT GG CA A
- --- CTCC - CCA TT CGC

GAM2067 GTTTGGACTTAGACTTGCTC 50472 ACTTGCTCTA 50473 T AC- CTCTA ACAA- GG ---
---- TAC
TATGTTACAATTGGGAGGAG TGTTACAATT TTTGGACT AG TTG TGTT TTGGGA AGCGT
GACT C
CGTGACTTACCATTGGTCGT GGGA ||||||||| || ||| |||| |||||| ||||| ||||
TGATGACGTTAATTCCAAAC AAATTTGA TC AAC ACAA AACCTT TTGCA CTGG
/
AAAAACAACAACAACAACTT T AAC AACA- AAACA AA GTAGTTG TTA
AGTTTAAAT

GAM2068 ATAATCATCTTTTAAATTAT 50487 TATAATATCT 50488 CA TT T TT T AATCATT T
TTATAATATCTTCTAAATCA TCTAAATCAT ATAAT TCTT AAAT AT ATAATA CTTCTA TAATT
G
TTTAATTTGTTAATTATAGA TTAA ||||| |||| |||| || |||||| |||||| |||||
AGTATTATCTATATTTTCAA TATTA AGAA TTTA TA TATTAT GAAGAT ATTAA T
GAATATTAT TA CT - TC - ------- T

GAM2069 GATCAATTGGAATGTTTAAT 50495 TTCATATTTA 50496 - GTTT A- TG
AAAAGTTTGTCTAATTTCAT AAATTCTAAA GATCAATT GGAAT AATA AAGTT T
ATTTAAAATTCTAAATTGAT TTGA |||||||| ||||| |||| |||||
C CTAGTTAA TCTTA TTAT TTTAA /
A AAAT AC TC

GAM2070 GTTAATTGCATTATTAATAA 50505 TTAATACTAT 50506 CA- A T
TATTGATAATATTATTATTA TAGTAAGATC GTTAATTG TTATTAATA TATTGATAATATTA T
ATATTATTAATACTATTAGT AGTT |||||||| ||||||||| ||||||||||||||
AAGATCAGTTAAT TAATTGAC AATGATTAT ATAATTATTATAAT A
TAG C T

GAM2071 GGTTTATGTCACGTGACCAA 50512 TATGTCACGT 50513 TA- G AC ACACCC---------- A
CACCCGTAACCTTACAGTCT GACCAACACC GGTT TGTCAC TG CA GTA C
CACTCAACAACCCCTGTCCA CGTA |||| |||||| || || |||
GGTGACAAACAACC CCAA ACAGTG AC GT CAT C
CAA G CT CCCCAACAACTCACTCTGA T

GAM2072 GTTTTATGTGTGTTAATATT 50519 TATAGAACTG 50520 GTG ATA-- GC AT- GA C
- A
ATTATTGCTGGGTTATATAT TCAGGATAAA TAT TGTTA TTATTATT TGGGTT ATATATA
ACTGT AGG ATA A
ATAGAACTGTCAGGATAAAA ATAT ||| ||||| |||||||| |||||| ||||||| ||||| ||| |||
TATACCTACGGTGTATATAT ATA ACAAT AATAATAA ATCTAA TATATAT TGGCA
TCC TAT /

TTAAATCTAAAATAATAAGA AAA AAAAG A- ATT G- - A A
AAATAACAAAAATAAAAT

GAM2073 CGTTGATGTATTGTGTCCAT 50534 TATTGTGTCC 50535 TATT G CAT T TAA
GTGTATCAAATAAACTTTTT ATGTGTATCA CGTTGATG GT TC GTG ATCAAA A
GGTTCACCAGAGACCGTATC AATA |||||||| || || ||| ||||||
AATG GTAACTAT CA AG CAC TGGTTT /
GC-- G AC- T TTC

GAM2074 CTGAGGGGACCATGATATGT 50549 TACGCGGTTA 50550 CA- A- G AA G
ATAGGCGAAAGGCGGGGCTT GGAGTCCCCT CTGAGGGGAC TGAT TGTATAG CGA GGC G
CGGTTGTACGCGGTTAGGAG CAG |||||||||| |||| ||||||| ||| |||
TCCCCTCAG GACTCCCCTG ATTG GCATGTT GCT TCG /
AGG GC G -- G

GAM2075 ACTTAGAATACCCCAAACTA 50561 GGACGGCTGG 50562 AAT - AA TAGAC A G G
CG
GACTCCGTGTGATAGCTGGT CACACGGAAT ACTTAG ACC CC AC TCCGTGTG TAGCTG TT
GAT T
TGGATCGTTAATCGGACGGC GTAG |||||| ||| || || |||||||| |||||| || |||
TGGCACACGGAATGTAGGAG TGAGTC TGG GG TG AGGCACAC GTCGGC AG CTA /
GTCGCTGAGT GC- A A- TA--- G - G AT

GAM2076 CAGTGTTTCAAAAGTAGCAT 50573 CACTGGGTTG 50574 GTAGCATAAA CC----- A
TAGAG A- TT GGT
AAACACTATCCATTCCAAGT ATATTGGACT CACTAT ATTCCA GTCTG TAAC AGTGT
CA A
CTGTAGAGTAACAAGTGTTT GGGG |||||| |||||| ||||| |||| ||||| ||
CAGGTATAAATGCTGCACTG GTGATA TGGGGT CAGGT GTTG TCACG GT
T
GGTTGATATTGGACTGGGGT AA-------- TAAAAAA - TATA- GG TC AAA
AAAAAATATAGTGAATTTTG
AGACCTG
GAM2077 ATATTGTTTCCTAGATATGC 50593 TAAGTGCAAA 50594 TT C A---- CAG-
GATTTTAATT G
TGGCAGTTTGTATGATTTTA AAAATTAGCA ATA GTTTC TAGAT TGCTGG TTTGTAT
GTTG G
ATTGTTGGGAACAACTAAGT AAAG ||| ||||| ||||| |||||| ||||||| ||||
GCAAAAAAATTAGCAAAAGA TAT CAAAG ATTTA ACGATT AAACGTG CAAC A
ATTTAGAAACCTTAT TC - AGAAA AAAA AAT------- A

GAM2078 GACTTGGGTCTTGCAACGCT 50613 TGGCATGCGC 50614 ACGCT----- - AAT - ------ A--
G AAG
ACACTCTGGCAATCATCCAA TAGAGATGTT A ACA CTCTGGC CAT CCA ACAGAA
TTT TCTA A
CAGAAATTTGTCTAAAGAGC TTTT | ||| ||||||| ||| ||| |||||| ||| ||||

TCTAGAGGAAAGATTTTGTA T TGT GAGATCG GTA GGT TGTTTT AAG AGAT
G
TAATATGGCATGCGCTAGAG ATTATTTTTT A C-- C ATAATA AGA G CTC
ATGTTTTTTTATTATGCAAG
GACCCAGTT
GAM2079 TTATTGTTGGAAAAATTTTA 50621 TAGAATGTGT 50622 G- G AAA CC----- T AT
GCCCAAAACATTGACATAGC TGAAAAAATG TTATT TT GA ATTTTAGC AAAACA TGAC A
GTCGTTGTTTTACACAATGT A ||||| || || |||||||| |||||| ||||
TAGAATGTGTTGAAAAAATG AGTAA AA TT TAAGATTG TTTTGT GCTG /
A AA G GTG TAACACA T CG

GAM2080 AACCAATCTCAAAAGTTACT 50667 TCTCAAAAGT 50668 AT ----- AC - AAGTA
TGTGCTAAGTATTTCAAAGA TACTTGTGCT AACCA CTCA AAAGTT TTGTG CT T
TACAGAAGACTTTTTTCATG AAGT ||||| |||| |||||| ||||| ||
AGCTGGTT TTGGT GAGT TTTCAG GACAT GA /
C- ACTTT AA A AACTT

GAM2081 AGGACGCGGCCCCGACGGCC 50680 GCCCCGACGG 50681 - GGC G - - A----------
AA
ACCCCGACGAAGAAACGGAC CCACCCCGAC AGGAC GC CCCGACG CC AC CCCG
CG G
GACGCCGGCCGCGGCCCGGG GAAG ||||| || ||||||| || || |||| ||
AGTAGGCGTCGGGATAGCGG TCCTG CG GGGCTGC GG TG GGGC GC A
TCCT G ATA - A A CCGGCGCCGGCCGCAGCAG AA

GAM2082 CGGGTCTCGGCCACGGTGGC 50704 CGCCGGAGTG 50705 - G GG --- A C
GACCAGGGGCACCTCCCGGA GGCGACGACC CGGGTC TCG CCAC TGGCGA CC GGGG A
CCTCGCCGGAGTGGGCGACG CG |||||| ||| |||| |||||| || ||||
ACCCG GCCCAG AGC GGTG GCCGCT GG CCCT C
C G AG CCA - C

GAM2083 GCCGCGGCGCTCCATGAGGA 50744 TGAGGAGCCA 50745 C - T CCA CC - AAG
GCCAGAGCCCGCCGGGGAAG GAGCCCGCCG GC GCGGCGC TCCA GAGGAG GAGC GC
CGGGG G
GCGGCCCCGTGCCGCTCCTC GGGA || ||||||| |||| |||||| |||| || |||||
CTCCTCCTGGAGGCGCCGCC CG CGCCGCG AGGT CTCCTC CTCG CG GCCCC /
GC C G C CTC C- T GGC

GAM2084 TAATGTTGGTTCATGAAGAT 50832 TGAAGATAAA 50833 CAT AAG T CAA - --- TAA A
AT A
AAAGTGTGCCAAAGAAACTT GTGTGCCAAA GTT GAAGATA TG GC AGAA ACT TTTA ACA
ATGATTA GT G
TTATAAACAAATGATTAATG GAAA ||| ||||||| || || |||| ||| |||| ||| ||||||| ||
TAGGTGCTAGTCGTGTGTAC CGA CTTTTAT AC CG TCTT TGG AAAT TGT
TGCTGAT CG G

TTAAACAGGGTATTCTATAG TAT GA- - ATA A GAC TCA G -- T
CCAAGTATTTTCTATAGCCA
GTATTA
GAM2085 CGCCGTGGACAGGTTTAGCG 50885 ACAGGTTTAG 50886 G GACA C TTTTTCTC CCGT
CTTTTTCTCGCCGCGCCGTC CGCTTTTTCT CGCC TG GGTTTAG GC GCCGCG C
ACTTCGCGGTCTTATCACGC CGCC |||| || ||||||| || ||||||
TTTAGACCACAGGGCG GCGG AC CCAGATT CG TGGCGC /
G A--- T CACTATTC TTCA

GAM2086 CGACAACGTCGGGCGCGTTC 50894 TAAAATCACA 50895 T-- G- T AGAG TGT T- C
CTG- CAC T T
AGAGTCCTGTACCGTGTGCG CCTCGGTGGA ACG CG GCGCG TC TCC ACCG GTG GA
AGA GTAG GT C
ACTGAGACACGTAGTGTTCA AAGA ||| || ||||| || ||| |||| ||| || ||| |||| ||
AACTCTACCTTCTAAAATCA TGC GC CGTGC AG AGG TGGC CAC CT TCT CATC
CA A
CACCTCGGTGGAAAGATCGT TAT GG T AA-- --- TC A AAAA TC- T A
GCGGCGTATCGTTGTCG

GAM2087 GGAAACGGGACACAATGGAC 50940 TTACTGCATA 50941 AAC ACAAT CTT AC T GTC
TTTGCAACGTATATGTCTTT TCCGTCTTTT GGA GGGAC GGA TGCA GTA AT T
GATTTACTGCATATCCGTCT ATCC ||| ||||| ||| |||| ||| ||
TTTATCC CCT TTCTG CCT ACGT CAT TA /
ATT ----- AT- -- T GTT

GAM2088 AGACATACGAGCCAGTGTAC 50948 TTTCAAAGTA 50949 C CAGT AGCGTAT TC
AGCGTATTGTCTCTCCATTT CTGTTGTTCG AGA ATACGAGC GTAC TG T
CAAAGTACTGTTGTTCGTAT TATC ||| |||||||| |||| ||
CTCT TCT TATGCTTG CATG AC C
C TTGT AAACTTT CT

GAM2089 GTTGTCATGTATCGTTGTGT 50962 TGTCATGTAT 50963 AT TCGT GGCTGATATTG GC
TTGGCTGATATTGTGACGGG CGTTGTGTTT GTTGTC GTA TGTGTTT TGACGG G
CGAACTGTCAAAAAAAAACA GGCT |||||| ||| ||||||| ||||||
CATATTAGACAAC CAACAG TAT ACACAAA ACTGTC /
AT ---- AAAAA------ AA

GAM2090 ATAGCGAAGAAAAATACATC 50970 TGTGTAGACT 50971 ---------- TG T A CTG T
CTTTT T
TGATCGCCAAATGGCGATCA GTCGTTTTGG ATCTGATCGCCAAA GCGA CAGT CT
ACGC CAT CCG A
GTACTCTGACGCTCATCTTT TGGT |||||||||||||| |||| |||| || |||| ||| |||
TCCGTAACCGGCGTGTGTGT TAGACTGGTGGTTT TGCT GTCA GA TGTG GTG
GGC A
AGACTGTCGTTTTGGTGGTC GTCTGAATTA -- - - --- T C---- C
AGATATTAAGTCTGCGTAAT

```
      TCTTTCCTCT
GAM2091  TCCGGCCGGGTCACTTGTTC 50976  TCACTTGTTC 50977     -    C  TT   TCATAAA   TCTAT
      TCATAAAAGCGGTCTATCTC       TCATAAAAGC       TCCGG CCGGGT AC  GTTC     AGCGG   C
      CACTCCGCTCAGCCGGACCG       GGTC             ||||| |||||| ||  ||||     |||||
      TACCCGGACCGGA                     AGGCC GGCCCA TG  CAGG     TCGCC    T
                                  A    -  C-   CCGAC--    TCACC


GAM2092  GTCGCAAAGCGCGCGGGCAG 50987  TCGCGATGGC 50988    C  AA     ---   AGCCA    - AG
      CCACGGCCCAGACTGCGGTC       CCGGAGCGCG       GT GC  AGCGCGC   GGGC    CGGCC C  A
      GCGATGGCCCGGAGCGCGCT       CTCG             || ||  |||||||   ||||    ||||| |
      CGCCAC                          CA CG  TCGCGCG   CCCG    GCTGG G  /
                                   C  C-      AGG    GTAGC    C TC


GAM2093  GGGAGACGGCGCAGCCAGTG 50997  CACGTGGTCT 50998       CG-    -  -     TAAAG
      TTTTTAAAGATAAAACAAGG       GTGCGGCTCT       GGGAGA   GCGCAG CCA GTGTTTT    A
      CACGTGGTCTGTGCGGCTCT       CCC              ||||||   |||||| ||| |||||||
      CCC                             CCCTCT   CGTGTC GGT CACGGAA    T
                                       CGG     T   G      CAAAA


GAM2094  GATAACGGCACTAATATTAA 51068  CGGCACTAAT 51069     AAC   A  ATATTAACT   C     GCT
      CTTATCTAAAGGGCTAACAC       ATTAACTTAT       GAT   GGC CTA       TAT TAAAGG   A
      CTTTACATATAGCGCCCAAA       CTAA             |||   ||| |||       ||| ||||||
      TC                              CTA   CCG GAT       ATA ATTTCC   /
                                      AAC   C   ---------   C     ACA


GAM2095  TATAGAGATTATCAGTATCC 51076  TAGAGATTAT 51077      A   TATCAG   C    AC  TAAT
      AAGACACTAATAAACACGTA       CAGTATCCAA       TATAG GAT     TAT CAAG  AC    A
      GCTTGTATAACTATTACTAT       GACA             |||||  |||     |||  ||||  ||
      A                               ATATC TTA     ATA GTTC  TG    A
                                       A   TCA---   T    GA  CACA


GAM2096  TACGTTTTTCATTCTTCTAG 51096  TTTTTCATTC 51097      TT-     C   AGAAACA    ACT
      AAACATTTGAACTATTATTA        TTCTAGAAAC       TACGT   TTCATT TTCT      TTTGA   A
      GACAATGGAGAAAAGTGAAT        ATTT             |||||   |||||| ||||      |||||
      ATACGTA                         ATGCA   AAGTGA AAGA      AGATT   /
                                   TAT     A    GGTAAC-    ATT


GAM2097  GATGAGACAGGTTTACTTTA 51108  TTTAGATAGC 51109        CAG   TAC    GA    - AC  AT
      GATAGCGGTACTGATGTCCA        GGTACTGATG       GATGAGA   GTT   TTTA  TAGCG GT  TG  G
      CACGCGTTAGATAAATATAA        TCCA             |||||||   |||   ||||  ||||| ||  ||
      TAAATCTCATC                       CTACTCT   TAA   AAAT  ATTGC CA  AC  /
                                     AAA   TAT    AG     G  C-  CT
```

GAM2098 ACCGCAAACTCCCGTCGAAG 51116 TCGAAGCTGG 51117 G AC- C-- GA GAG G GC
CTGGAGCCGTGTGCAAAACA AGCCGTGTGC ACC CAA TCC GTC AGCTG CC TGT A
GGATGTAGCTAGGCAGCGGA AAAA ||| ||| ||| ||| ||||| || |||
CCGTTGGGT TGG GTT AGG CGG TCGAT GG ACA /
- GCC CGA A- GTA - AA

GAM2099 CTTCGAAATCTTCAACCCCG 51150 TCGAAATCTT 51151 AA AA--- - GGA AAAAC
GAGGCGGCAAAACACACGCG CAACCCCGGA CTTCGA TCTTC CC CC GGCGGC A
CCGTCGAAGGAGGAACAAGA GGCG |||||| ||||| || || ||||||
AGAAGTCGAAG GAAGCT AGAAG GG GG CTGCCG /
GA AACAA A AAG CGCAC

GAM2100 CTCTTAGAGTATCGCCACCG 51162 ACGGCAGTCG 51163 ---------- T
ACGACGACGACGGCAGTCGA AGCGCGGCTT
TTAGAGTATCGCCACCGACGACGACGACGGCAGTCGAG CGCGGC T
GCGCGGCTTCGCCGCGGCAG CGCC ||||||||||||||||||||||||||||||||||||| ||||||
CTTCGCTGCCTCGACTGCCG AATCTCATAGCGGTGGCTGCTGCTGCTGCCGTCAGCTC
GCGCCG /
TCGTCGTCGTCGGTGGCGAT CGTCGCTTCGACG C
ACTCTAAGAG

GAM2101 TTCATTCTCGGTGTAATGGT 51183 TCTCGGTGTA 51184 C G AATG G AA- - -- CT
T
ATCTATGAGAACTTCGGTTT ATGGTATCTA TTCATT TC GTGT GTATCTAT AG CTTCGG TTT
GTCG TGACT G
GTCGCTTGACTTGTTAGTCG TGAG |||||| || |||| |||||||| || |||||| ||| |||| |||||
GACGATTAGAATCTGAGGAA AGGTAA AG CACG TATGGATA TC GGAGTC AAG TAGC
GCTGA T
ACTGATAGGTATGCACGGAC C G ---- G AAA T AT AG T
AATGGA

GAM2102 GAGACAGCAACATGAGTGAA 51192 TGAGTGAAAG 51193 --- C TG-- GAGATA
AACAAACC
AGAGATAGCATGAAAACAAA AGATAGCATG GAG ACAG AACA AGTGAAA GCATGAA
T
CCTTGAAATAATTTATGCGT AAAA ||| |||| |||| ||||||| |||||||
AATTTTATTATCTTGTTATT CTC TGTT TTGT TTATTTT CGTATTT /
GTGACCTC CAG A TCTA AATG-- AATAAAGT

GAM2103 GATTATAACACTACTTGGAC 51239 TATAAGCATA 51240 C CTAA TACT T CCAATT TTTA
TATACT T
TAACTGATACTACATATGTT TACTGTATCT A TTGGA CTGA ACA ATGTT TG TAAGCA
GTATC T
CCAATTTGTTTATAAGCATA TCTG | ||||| |||| ||| ||||| || |||||| |||||
TACTGTATCTTCTGATATTT T AACTT GACT TGT TACAA AC ATTCGT TATAG
C
GCTTAGCTTCATTTAACATT C TTAG ---- T TTT--- TTCG T----- T

TGTTCAGGATTTTCAACTAC
ATATTTTAATT
GAM2104 CATTAATAGTTTTTTTACCA 51250 TTAATAGTTT 51251 TT TTTGC-- CTCTCATATC
ATTA T CA
TTTGCAATAAAATCTCTCAT TTTTACCATT TT TTTACCA AATAAAAT ATAAAT TAAAA
GTAG T
ATCATAAATATTATAAAATG TGCA || ||||||| |||||||| |||||| ||||| ||||
TAGCATTATCTATTTTTAAT AG AAATGGT TTGTTTTA TATTTA ATTTT TATC T
TTATTACTATCATATTTTGT T- TTTTCTT TACTATCAT- ---- - TA
TTTCTTTTTGGTAAATGACC
GTTTATG
GAM2105 AAAACTCGTACCAACGGCAA 51255 TTATTTGTAT 51256 A --- AAAA-- GAA T A- G AC
TC A
AAATTTCGAAGATTAGAGGA GATTCAGACT CA C GGCA TTTC GAT AGAGGAG TGAAT
CG ACA TGGTG T
GATGAATGCGACACATCTGG CTTT || | |||| |||| ||| ||||||| ||||| || ||| |||||
TGATTTTATTATTTGTATGA GT G TCGT AAAG CTG TTTTCTC ACTTA GT TGT
ATTAT T
TTCAGACTCTTTTGTCCAGA A TTT AATATA AC- - AG - A- TT T
AAATATAATGCTTTTGATGG
TATCGGGTGT
GAM2106 CTTACAAAAAAATTGGATTC 51262 AAAAATCCAA 51263 ACAAAAAAA CAATA G
AATATTATTGGAGACGATAA GAAACAAGAA CTT TTGGATT TTATTG A
AAAATCCAAGAAACAAGAAG G ||| ||||||| ||||||
GAA AACCTAA AATAGC G
GAACAAAG- AA--- A

GAM2107 TGCCTTTCCGGCAGAGCATC 51315 TTTGCAATCA 51316 CA CC T CATC C GC--- C
TC CTT
CCCTGGCATCGACACTCACG TATAGTGAGT TTCCGG GAGCAT CC GG GA ACTCAC GAT
GCAA AACTGA A
CGATCGCAATCAACTGACTT TCTA |||||| |||||| || || || |||||| ||| |||| ||||||
AATCCTCGGTTTTGCAATCA AAGGCC CTTGTG GG CC CT TGAGTG CTA CGTT
TTGGCT A
TATAGTGAGTTCTACCCCTG CC CA T CCAT - ATATA A -- CCT
GACGTGTTCCCCCGGAACTG
CA
GAM2108 CCACAATTAGCTATTCGTGT 51322 TAGCATCATC 51323 T T T AC - T AC---- CTA
CTT
ACTAGCATCATCGGATACGC GGATACGCCT CCACAAT AGCTAT CG GT TAGCA TCA CGGAT
GC TCCTGCA A
CTATCCTGCACTTAAGCCTG ATCC ||||||| |||||| || || ||||| ||| ||||| || |||||||
CAGGACGCTATCAGGTCCGC GGTGTTG TCGATG GT TA ATTGT AGT GCCTG CG
AGGACGT A
TGACTGTTACCATTTGTGTA C T T CC C C GACTAT C-- CCG
GCTCGTTGTGG

GAM2109 TATAAATGATGTTTGTGAAT 51326 TAAATGATGT 51327 TTG TAT-
CTGATACATAATTAAA C A

ATATATTATCTGATACATAA TTGTGAATAT TATAAATGATGT TGAA ATATTAT AATA
CATCAT G
TTAAAAATACCATCATAGCA ATAT |||||||||||| |||| ||||||| |||| ||||||
TGATGATATTGTAGTATTTT ATATTTATTATA ATTT TATGATG TTAT GTAGTA /
TTTTAAATATATTATTTATA TAA TTTT ---------- A C

GAM2110 TTATTATAAATTCTGTTGTA 51336 TCTGTTGTAT 51337 TTC T T
TAATTATAATTATAATTATA AATTATAATT TTATTATAAA TGTTG ATAATTATAAT A
ATTATTAATACATTTTATAA ATAA |||||||||| ||||| ||||||||||
TAA AATAATATTT ATAAT TATTAATATTA T
TAC - A

GAM2111 TCTCATTGTTATGTAGTTGT 51341 TATTAAACAT 51342 - AT A -- TTAT C TTTTTA
T- T
GATTTATTAAACATATTTTT ATTTTTTATA TCTC ATTGTT GT GTTGT GAT TAAA ATAT
TAACTC AG A
TATAACTCTAGTATTCTCCG ACTC |||| |||||| || ||||| ||| |||| |||| |||||| ||
AGTTACTTATATATTTATTT AGAG TGATAA TA TAACA CTG ATTT TATA ATTGAG
TC T
GTCAGACAATAATGCAATAG G CG A GA TTT- A TTC--- CC T
TGGAGA

GAM2112 CTTATTGTATAGAATATCAT 51347 TAGAATATCA 51348 A- -- CGAT--- G
GACGATTGGGAAGCCGTTAT TGACGATTGG CTTATTGTATAGA TATCA TGA TGG A
TAATCAATTGGTAGATTTAT GAAG |||||||||||| ||||| ||| |||
ACGATGAG GAGTAGCATATTT ATGGT ACT GCC A
AG TA AATTATT G

GAM2113 TATTGTACTGTTTAGGAAAA 51359 TAGGAAAAAC 51360 C TTTA AAA ------ TCA
ACTGATTTTTCAAATATAAA TGATTTTTCA TATTGTA TG GGAA CT GATTTT A
ATCTATAATAGAAGTTCCGG AATA ||||||| || |||| || ||||||
TCACTACAATA ATAACAT AC CCTT GA CTAAAA A
C TGG- GAA TAATAT TAT

GAM2114 CTGGAGCCAAGGGGATGGAG 51380 TGAATTCTTT 51381 - T GA A G
ATGGCATCGTGTGGGCTGAA CTCTTGGTTT CTG GAGCCAAGGGGA GGA TGGC TC T
TTCTTTCTCTTGGTTTGCAG GCAG ||| |||||||||||| ||| |||| ||
GAC TTTGGTTCTCTT CTT GTCG GG G
G T AA - T

GAM2115 CCTTATTTTATAAAATATCA 51402 TAAAATATCA 51403 T A- TGAC GAAG
TGACGATTGGGAAGCTGTTA TGACGATTGG CCTTATT TATAAA TATCA GATTGG C
TTAATCAATTGGTAGATTTA GAAG ||||||| |||||| ||||| ||||||
TACGATGAGG GGAGTAG ATATTT ATGGT CTAATT T
C AG TAA- ATTG

GAM2116 GGTGGCATCCCTTCATATCG 51409 ATAAGGCTCG 51410 --- - TA GC----- A- AGT AG
G G
CCCCTAGGTCTAGTTCACTG AGGGTTGGAA CA TC CCTTCA TC CCCT GGTCT
TCACTGG TTG ATGGA A
GAGTTGGATGGAGAAGTTCG AGAA || || |||||| || |||| ||||| ||||||| ||| |||||
TGCAACCGGTGATAAGGCTC GT GG GGAAGT AG GGGA TCGGA AGTGGCC AAC
TGCTT A
GAGGGTTGGAAAGAACTGAA TAA A CA AAAGGTT GC AT- -- G G
GGAGGAATTGCTGACACACC

GAM2117 CCTATGATACATATGCTCTT 51468 TAATGTACTT 51469 - A CTCTTAA C TT T TA
GCA
AATGTACTTGTTTACTGTTT GTTTACTGTT CCT ATGAT CATATG TGTA TTG TAC GTT TAC
C
ATACGCACCCAAGTAACAAC TATA ||| ||||| |||||| |||| ||| ||| ||| |||
TGTATTTAATTATAACCTAT GGA TACTA GTGTAT ATAT AAT ATG CAA ATG C
GTGAATCATAAGG A A CCA---- T TT T CA AAC

GAM2118 GTAGCGAGCGTGAGGAAACA 51475 TGACTAAAGT 51476 A A G AAA- AAA - ACTGTG----
---- AC
AAATAGCGTCACTGTGGCCA GGAAGCCTGA GT GCG GCGT AGG CA TAG CGTC
GCC C
CCATGGCATAAATGACTGAA CGCC || ||| |||| ||| || ||| |||| |||
CGATGACTAAAGTGGAAGCC CA TGC CGCA TCC GT ATC GTAG CGG /
TGACGCCGTGAC G - G GAAG GAA A CAAGTCAGTAAATA TA

GAM2119 TCCATACGTTTTTGGGAAAG 51489 TTTTTGGGAA 51490 A T-- AAA----- T
TTGGGCTCGGCCCAACGCAA AGTTGGGCTC TCCAT CGT TTTGGG GTTGGGC C
CAGACCTAGGCACACGATGG GGCC ||||| ||| |||||| |||||||
A AGGTA GCA GGATCC CAACCCG /
- CAC AGACAACG G

GAM2120 TCATTAAGCAAGACAGCGTC 51507 TGCGGCAACA 51508 AAGCAAGAC AGA AC---
AAAAGA-- T A
AGACGCACGCTGGAAAAGAG CCAGCCAGCA TCATT AGCGTC CGC GCTGG
GCTGC CC A
CTGCTCCAACCGGTGCGGCA AAAG ||||| |||||| ||| ||||| ||||| ||
ACACCAGCCAGCAAAAGGCG AGTAG TCGCAG GCG CGACC CGGCG GG C
CAGACGCTCATAAGGATGA GAATAC--- AC- GAAAA GACCACAA T C

GAM2121 CATCGCGCGGGGCACGCACT 51529 TGCCGTGGGC 51530 GCGC ACGCACTTCAC
A
TCACGCCGCGCGCCCACGGC GCGCGGCGCC CATC GGGGC
GCCGCGCGCCCACGGCAGCGTCCG G

AGCGTCCGAGGGCGGGCGCT CCCA |||| ||||| ||||||||||||||||||||||
GCCGTGGGCGCGCGGCGCCC GTAG CCCCG
CGGCGCGCGGGTGCCGTCGCGGGC G
CCAGATG AC-- ---------- G

GAM2122 CACCAGAATGGATAGAAAGA 51569 AGACAAACAC 51570 GAA AAAGA C-- ACAA TA
CAAACACAGTTACAACATAG AGTTACAACA CACCA TGGATAG CAAA ACAGTT CA G
CTTTGAGGACTGTCAATTTG TAGC ||||| ||||||| |||| |||||| ||
AACTATCTAAAATGGTG GTGGT ATCTATC GTTT TGTCAG GT C
AAA AA--- AAC GA-- TT

GAM2123 TTCTCATCGCTTTTCTTACT 51614 TAAAATGTTA 51615 TCTTACT GA AAATAAA A AC C
TG GAAA TG
TAACAGATTGCAAAAATAAA CTGTGATGAA TAACA TTGCAA ACA TATT CG T TTGAT
ATTG A
ACAATATTACCGCTTGTTGA GAA ||||| |||||| ||| |||| || | ||||| ||||
TGAAAATTGTGAATTAATGC ATTGT AATGTT TGT ATAG GT A AATTG TAAT /
TAGTTAATGATGAGATATGT ------- AA GATG--- - A- - GT ATCG TA
GTAGTTGTAAAATGTTACTG
TGATGAAGAA
GAM2124 GCTTGTGTTGCAACAGCGCT 51655 TGTGTTGCAA 51656 TTG C GCTAAAAA A C AG
AAAAAATGAGAACAAGAGAG CAGCGCTAAA GC TGTTGCAA AGC ATG GAA AAG A
ACTTTTTACATAATAGCTTT AAAT || |||||||| ||| ||| ||| |||
TGCAATAAATGC CG ATAACGTT TCG TAC TTT TTC /
TAA T ATAA---- A - AG

GAM2125 GAATTAACCAATAGAGACAC 51667 TTGCTGACGG 51668 TA C ----- A -- A
GTTTGACACAGAAGCTGTGT TCTATATTCT GAAT AC AATAGA GAC CGTT TGACACAG A
TGCTGACGGTCTATATTCTG GTTT |||| || |||||| ||| |||| ||||||||
TTTGTATTC CTTA TG TTGTCT CTG GCAG GTTGTGTC /
-- T TATAT - TC G

GAM2126 TTGTTTGTGTTCTGAAGCTT 51671 TAGATTGTTT 51672 G C - TT AGT T T
ATCAGTTATTATATAAGAAA ACGAAGCAGA TTGTTT TGTT TG AAGC ATC TATTA ATAAGAAA
G
TGCCTTTCTTATTGATAGAT AGCA |||||| |||| || |||| ||| ||||| ||||||||
TGTTTACGAAGCAGAAGCAG GACGAA ACGA GC TTTG TAG ATAGT TATTCTTT C
G A A T- --- - C

GAM2127 ATATCTGTAAGTTGTATTCT 51684 TGTAAGTTGT 51685 TGTAAG TA TCG A- T
TTTTATCGAAGCAGAGTTTC ATTCTTTTTA ATATC TTG TTCTTTTTA AAGC GAG T
CTCCGGTTTAGTTAGGAAGA TCGA ||||| ||| ||||||||| |||| |||
AGTTAAATGATGT TGTAG AAT AAGAAGGAT TTTG CTC T
TA---- TG TGA GC C

GAM2128 GGAGACTCACCTTGGGGATC 51689 TCGGCACCTC 51690 C ATCCATCCTCTCCA CC TT AC TT-- T AC
CATCCTCTCCAAGCGGCCTC CTGAACTGCT ACCTTGGGG AGCGG TCGG GAG GCC CCG GGG C
GGTTGAGACGCCTTCCGTGG CCTC ||||||||| ||||| |||| ||| ||| ||| |||
GACCGTCTCCCGGCCTCGGC TGGAACCCT TCGTC AGTC CTC CGG GGC CCT G
ACCTCCTGAACTGCTCCTCC A CC---------- A- -- CA CTCC - CT
CAAGGTAAGTCTCC

GAM2129 CCCAAGGTAAGTCTCCTCTC 51716 TCCCCGAGGG 51717 AA AA ------ A TC TC CC
AGGTCGAGCTCGGCTGCCCC TCTTTAGAGA CCC GGT GTCTC CTCTC GG GAGC GGCTGCC T
TTAGGTAGTCGCTCCCCGAG CACC ||| ||| ||||| ||||| || |||| |||||||
GGTCTTTAGAGACACCCGGG GGG CCA CAGAG GGGAG CC CTCG CTGATGG / C- -- ATTTCT C -- -- AT

GAM2130 CCTAGCGCTGAAAAACAAGG 51762 TCAAAATAAA 51763 A GAAAA-- AA - GACG ACCCC CC TAA
CTCTGACGATTACCCCCTGC AGATGCCGAG CCT GCGCT AC GGC TCT ATT CTG CA A
CCATAAAATTTGCCTAGTCA TCTA ||| ||||| || ||| ||| ||| ||| ||
AAATAAAAGATGCCGAGTCT GGA CGCGA TG CCG AGA TAA GAT GT /
ATAAAAGCGCAAGG A AAATATC AG T AAA- AACT- CC TTA

GAM2131 AAGAATCTGTTATATGGTAT 51784 TCTGTTATAT 51785 ATCT TAT A- GG ATAAAACATTAAA CC- A
AGGGAGAGTATAAAACATTA GGTATAGGGA AAGA GTTA GGTAT G AGAGT TGC GTACTT T
AATGCCCGTACTTATTAAAG GAGT |||| |||| ||||| | ||||| ||| ||||||
TATTCAGTAGCCAATCCTAA TTCT TAAT TCATA C TCTCA ATG TATGAA T
CTCTTTCGAATACTTATTAA CGT- TAT AG TT ATCCTAACCG--- ACT A
TTGCTCTT

GAM2132 TTGTTTTAAATTGTTGATTT 51794 TGATTTATTA 51795 T T ----- ------- T
ATTAAAGAATATAGTTTGGC AAGAATATAG TTGTTTTAAA TG TGATTTA TTAAAGA ATATAGTT G
AACTATATAAATGAATTTTT TTTG |||||||||| || ||||||| ||||||| ||||||||
GAGAATTTAAGTCATTATTT AACAAAGTTT AT ACTGAAT AGTTTTT TATATCAA G
TGAAACAA T T TTAAG AAGTAAA C

GAM2133 TGAGTCAATTGGTAGAGTTT 51801 AGTCAATTGG 51802 AG - TT- AA-------- GCTAA- GGC
TATAACGAGGTCGCTAACTG TAGAGTTTTA TG TCAATTG GTAGAG TTAT CGAGGTC CT T
GCTGTTAAGAGATGAGACCT TAAC || ||||||| |||||| |||| ||||||| ||

CGCCTATTCCTGATAACTTC AC AGTTGAC TATTTC AATA GCTCCAG GA G
TTTATACAGTTGAAACA AA A TTC GTCCTTATCC AGTAGA ATT

GAM2134 GATTTCTAAGTTACTTCTGC 51809 AGTTACTTCT 51810 TT AAG CT GCAT CTA G
AGCATATAACTAAACACGTT GCAGCATATA GA TCT TTACTT GCA ATAA AACAC T
AGTGTTCTTTATTGTTTGGG ACTA || ||| |||||| ||| |||| |||||
TAAAACAGATTTC CT AGA AATGGG TGT TATT TTGTG T
TT CAA TT ---- TC- A

GAM2135 TTTCTCGAATATACGGGCCA 51820 TCGAATATAC 51821 ATA GCCAAGTTAGAA C A----------
AGTTAGAATCTCCAGTAACT GGGCCAAGTT TTTCTCGAAT CGG TCTC AGT ACTA C
ACCATAGTGGGATATCATCC AGAA |||||||||| ||| |||| ||| |||| AGCAGCTAGAGACCGCCAAT AAAGAGCTTA GCC AGAG TCG TGAT /
TCGAGAAA ACC ---------- A ACGACCTACTATAGGG A

GAM2136 TCCATATTTCCTGACTTGTG 51826 TGGGATGGGG 51827 TT TG----- G - G GA
TCTTGACTTGCGTCGATTGG GTGTGGGATG TCCATAT CC ACTT TGTCTTG ACTT CGTC T
GATGGGGGTGTGGGATGGGG GGGG ||||||| || |||| ||||||| |||| ||||
GTGTGGGATGGGGGTGTGGG GGGTGTG GG TGGG GTAGGGT TGGG GTAG T
GG TAGGGTG G G G GG

GAM2137 TCCAGTGTAAGCAAGTCGAT 51918 TGAATGACAT 51919 AA-- AGT - ----- TAG G AAA
TTGAATGACATAGGCGACAA AGGCGACAAA TCCAGTGT GCA CGATTT GAA TGACA GC AC G
AGTGAGGTGGCATTTGTCAG GTGA |||||||| ||| |||||| ||| ||||| || ||
AAGTTTCAAAGTCGTGTAAG AGGTTACA TGT GCTGAA CTT ACTGT CG TG T
AACATTGGA AGAA --- A TGAAG TTA G GAG

GAM2138 TGCACTACCTATCTGCTCAT 51938 TAGTGTTGAG 51939 ACCT CA ---- TT TT GTGTTT T
TCGTTGTTTCGGTTCTGTGT GTAATTCTAG TGCACT ATCTGCT TTC GTTG TCGG CT GTCTGA T
TTGTCTGATTCTTAGATAGT AAAG |||||| ||||||| ||| |||| |||| || |||||| GTTGAGGTAATTCTAGAAAG ATGTGA TAGGCGA AAG TAAT AGTT GA TAGATT /
CGGATTGAGTGTA GT-- -- ATCT GG GT ------ C

GAM2139 GGGTAAATGACAATGGGGGT 51949 AATGACAATG 51950 AA AATG ACA- G G
AAATGACAATGGGGCGCTTG GGGGTAAATG GGGTA TGAC GGGGTAAATG AT GG C
GTGACACATTTGCCCCACCG ACAA ||||| |||| |||||||||| || ||
TCGCCTGCCC CCCGT GCTG CCCCGTTTAC TG TT G
CC CCA- ACAG G C

GAM2140 TTTCTCGAATATACGGGCCA 52003 TCGAATATAC 51821 AT GCCAAGTTAGAA C A------
--------- C
AGTTAGAATCTCCAGTAACT GGGCCAAGTT TTTCTCGAAT ACGG TCTC AGT
ACTA C
ACCATAGTGGGATATCATCC AGAA |||||||||| |||| |||| ||| |||| |||| |

GAM2146 ATTGTTTGTATTCATTCAAT 52208 TTTGTATTCA 52209 TT - AATGT CC T
GTCTCCTTTTCAGAAATTAG TTCAATGTCT ATTGT GTATTC ATTC CT TTT C
TTTAGAGTCGAATACTGCAA CCTT ||||| |||||| |||| || |||
T TAACG CATAAG TGAG GA AAA A
T- C ATTT- TT G

GAM2147 TAGAGTTAAGAGAAATTAGA 52221 TGGCTACAAA 52181 GTTAA-- ATT ACATTA A
GTC
GTTTGTACATTAAGCAACAT CTTTTCCTTT TAGA GAGAA AGAGTTTGT AGC ACAT T
GTCTCTAAATGTGGCTACAA TCCA |||| ||||| ||||||||| ||| ||||
ACTTTTCCTTTTCCACATCA ATCT CTTTT TTTCAAACA TCG TGTA C
TCTA ACTACAC CCT ------ G AAT

GAM2148 AACATCCTAATACTTTATTT 52222 TAACAATATC 52223 TAATACTTTAT TT AG AT
GTTTTAAAGCTATTAAAGAG ATTTTTGGAT AACATCC TTGTT AA CT T
TTCTAACAATATCATTTTTG GTT ||||||| ||||| || ||
GATGTT TTGTAGG AACAA TT GA /
TTTTTACTAT- TC GA AA

GAM2149 AGGTTTACCTATTTTATCAC 52232 TATTGTGTAC 52233 T- CC ----- - AT
GATTGATATCTGATTATATT AAGTAAAATA AGGT TA TATTTTAT CACGAT TGAT C
GTGTACAAGTAAAATAATTA ATTA |||| || |||||||| |||||| ||||
CTACCT TCCA AT ATAAAATG GTGTTA ATTA /
TC TA AACAT T GT

GAM2150 TCAGAGTATAAATTTTAGAA 52236 TGCGTTGATG 52237 TAAATT AA- TTAG
ATAACATTAGCAAATTGTTG TCGTTATTCT TCAGAGTA TTAG ATAACA C
TGCGTTGATGTCGTTATTCT GA |||||||| |||| ||||||
GA AGTCTTAT AGTT TGTTGT /
TGCTGT GCG TAAA

GAM2151 CTTACGAGGATCTCCTTAAA 52252 TGACGGGAAG 52253 AC ATC TAA TCCAG
TTCGAGTCCAGTAATTCCTT CCTTACGAG CTT GAGG TCCT ATTCGAG T
TGAGTGACGGGAAGCCTTAC ||| |||| |||| |||||||
GAG GAG TTCC AGGG TGAGTTT A
CA GA- CAG CCTTA

GAM2152 CCCTTGTTAAGATATGATGC 52277 TATGATGCAA 52278 TT TAAGAT- A AAATA CGAC A
AATAAATACACGACATGAAA TAAATACACG CCC GT ATG TGCAAT CA ATGAA C
CTTTCATTTATTGACGAATT ACAT ||| || ||| |||||| || |||||
GCACCATTTAAACTATTTGG GGG TA TAC ACGTTA GT TACTT /
G TT TCAAATT C AGCA- TATT T

GAM2153 AAAACTTTTACGGTGGAGAA 52285 TACGGTGGAG 52286 TTT- GAGAATTAT AC
TTATTAAATTACTAAACATA AATTATTAAA AAAACT ACGGTG TAAATTACTAA A
TTAGTAATTTATACTGTTCA TTAC |||||| |||||| ||||||||||
TAGTTTT TTTTGA TGTCAT ATTTAATGATT /
TACT --------- AT

GAM2154 TGCGTAAATTTCGCAACTAA 52290 TTTTTCGTTT 52291 T TTT C CT T AA
TGAGATAAATTGGAAATTCC TTTTCGTTTT TGCG AAA CG AA AATGAGA AAATTGG A
AATTTTTTTCGTTTTTTTCG TTTC |||| ||| || || ||||||| |||||||
TTTTTTTCGCA ACGC TTT GC TT TTGCTTT TTTAACC /
T TTT T TT T TT

GAM2155 CTGAGGGGACCATGATGTGT 52333 TACGCGGATA 52334 -- ATGA G TC G
ATAGGCGTCAAGCGGGGCTT GGAATCCCCT CTGAGGGGA CC TGTGTATAG CG AAGC G
CGGTTGTACGCGGATAGGAA CAG ||||||||| || ||||||||| || ||||
TCCCCTCAG GACTCCCCT GG GCGCATGTT GC TTCG /
AA ATAG G -- G

GAM2156 GATGGCGTCTTCCCTGTTTT 52343 TAAGGCAGGC 52344 - C ----- C A -
GGA
GCCCTTAGACTATTCGAGTT AAGACAGCTA GATGGC GTCTT CCTGTTTT GCC
TTAGACTATTCG GTTGCCTCT GT T
GCCTCTGTGGATTAGGGCTG TT |||||| ||||| |||||||| ||| |||||||||||| ||||||||| ||
GAGGCAGCACGGATAGTCTG TTATCG CAGAA GGACGGAA CGG AGTCTGATAGGC
CGACGGAGG CG T
ATGGCCAAATAAGGCAGGCA A C TAAAC T A T GGA
AGACAGCTATT

GAM2157 TTGTAATTTCCAATTTACAT 52379 TTAATTGGAA 52380 T TTTACA C AAATA T
AACTAATTGAAATAATTTTA TTTTGGAATT TTGTAA TTCCAA TAA TAATTG ATTT A
CAAGATGAACAATTAATTGG TACA |||||| |||||| ||| |||||| ||||
AATTTTGGAATTTACAA AACATT AAGGTT GTT ATTAAC TAGA C
T TTAAG- A AAG-- A

GAM2158 AATTGGAATTTTGGAATTTA 52387 TAATAATTTT 52388 GA- T---- TTTTAT
CAATTTTATTAACTTTTTGT CCAAGATGTA AATTG ATTTTGGAA TTACAA T
AATAATTTTCCAAGATGTAC CAAT ||||| ||||||||| ||||||
AATT TTAAC TAGAACCTT AATGTT /
ATG TTAAT TTTCAA

GAM2159 AAGAAAGCTTTAAAGTTAAA 52399 AAGCTTTAAA 52400 A AAAGT--- -- G AC T
TATCCTGCAGATACGATTTT GTTAAATATC AAGA AGCTTT TAAATATC CT CAGAT GA T
TCCATCTGAAGTTGGTATTT CTGC |||| |||||| |||||||| || ||||| ||
GTTATAGAAAAAGTTATCTT TTCT TTGAAA GTTTATGG GA GTCTA CT T
A AAGATATT TT A C- T

GAM2160 TGTATAACGAGGTTGCTGAA 52416 TATAACGAGG 52417 A C C---- A ---- CG
TGGATATTACGAGATAATAC TTGCTGAATG TGT TAA GAGGTTG TGA TGGA TATTA A
ATCTCCATCACCTAATAATT GATA ||| ||| ||||||| ||| |||| |||||
TCTTTAAACA ACA ATT CTTTAAT ACT ACCT ATAAT /
A T AATCC - CTAC AG

GAM2161 TATCTATCGTTGGCATTTCA 52421 TCTATCGTTG 52422 A T- TCAAGTTCC CAC
AGTTCCGATACACATTTTAT GCATTTCAAG TATCT TCG TGGCATT GATA A
TCCATAAATAATGCTATTTG TTCC ||||| ||| ||||||| ||||
AAGATA ATAGA AGT ATCGTAA TTAT /
- TT TAAATACC- TTT

GAM2162 TAGCTTTTATTGAATCCAAA 52436 TTGAATCCAA 52437 TTAT AAAACATC AAC
ACATCAGTTAACAAACAAGC AACATCAGTT TAGCTT TGAATCC AGTT A
TACCAAAGGATTTGTCATAA AACA |||||| ||||||| ||||
GTTG GTTGAA GTTTAGG TCGA A
TACT AAACCA-- ACA

GAM2163 GTATGAAACTTTATGAGGAA 52452 AACTTTATGA 52453 - TTATGAGG G AA
CTGGTGAGAAATAACTTACG GGAACTGGTG GT ATGAAACT AACTG TGAG A
GTTATGATTTCGGTTTCGTC AGAA || |||||||| ||||| ||||
GC CG TGCTTTGG TTGGC ATTC T
C CTTTAGTA - AA

GAM2164 CACAAAATGATTAGATGCTT 52491 TATACTTAAC 52492 A A GC- AC TTA CTAT CT ACT-
ACTAAACTT
AACTTACTTAATAACTATAC TATACTTATA TT GAT TTA TTAC ATAA ACTTAA AT TATAG
A
TTAACTATACTTATAGACTA GACT || ||| ||| |||| |||| |||||| || |||||
AACTTAACTTATCAACTATA AA CTA AAT AGTG TATT TGGATT TA ATATC /
CTTAATTTTTAGGTCCTTAT C - ATA CA TAA CC-- TT ATTC AACTATTCA
AATGTGAACTAAATAATCAA
CTGTTTTGTG
GAM2165 TCTCAGTAGTAGTAAGTCTC 52497 TCTTGCTGAA 52498 T A- --- CAC TG T ACA-
TGCA- T TTTT
ACTGGTGATGGGATACAAGT TAGGCTATCT C CAGT GTAGTA AGTCT TGG A GGGAT AG
AGT CC C
GCAAGTTCCTTTTCAAATGG ACTA | |||| |||||| ||||| ||| | ||||| || ||| ||
TGCTCAAATCTAAGGATCCT G GTCA TATCAT TCGGA GTC T TCCTA TC TCG GG
/
CTTGCTGAATAGGCTATCTA - CG CTA TAA GT C GGAA TAAAC T TAAA
CTATGCACTGGA

GAM2166 GTAATAATGTTGTATACAGT 52512 TATTATGGCA 52513 TAA- - GTAA GT- T- T

AAGTTGGTTAACATGTTGGT ATGTATTACA GTAA TGTTGTA TACA GTTG TAACATG TGGT
T
TTTTATTATCCATGTTATTA ACAG |||| ||||||| |||| |||| ||||||| ||||
TGGCAATGTATTACAACAGC CATT ACAACAT ATGT CGGT ATTGTAC ATTA T
ATTTAC TACG T AA-- ATT CT T

GAM2167 ATTGTACATACTATATTGTA 52518 TGCTATGTGT 52519 TG A AA- AC- CAA
AAACAACCAGCCAATACTGC ATATAGTGAG AT TACATACT TATTGTA ACA CAGC T
TGCTATGTGTATATAGTGAG GTAT || |||||||| ||||||| ||| ||||
GTATGTATGGT TG ATGTATGG GTGATAT TGT GTCG /
GT A ATG ATC TCA

GAM2168 TGCACTGCGGTCATCGTCTC 52548 TCCACGGTCC 52549 C- TCG C - T CTCCTCAA
T A C CAC
CACGGTCCACTCCTCCTCAA ACTCCTCCTC A TGCGGTCA TCT CAC GG CCACTC GCTCT
TGGC GA GG A
GCTCTTTGGCAGACGGCACA AAGC | |||||||| ||| ||| || |||||| ||||| |||| || ||
TACTCATCGGCCGCGGGGCG T GTGCCAGT AGA GTG CC GGTGAG CGGGG
GCCG CT CT /
TAGAGTGGCCAGTGTAGAAT CT TA- T A - ATG----- C G A CAT
TGACCGTGTCTGTA

GAM2169 GGTTCTCTGTTAATGACTCA 52573 TTAATGACTC 52574 T T TAAT A CCA- GG- T
TCCCATAAGTGGTGGTCTGG ATCCCATAAG GGT C CTGT GACTC TC TAAGT TGGTC G
TGACCAAGAACTTAGTCTGA TGGT ||| | |||| ||||| || ||||| |||||
AGGGTCACAGCGACC CCA G GACA CTGGG AG ATTCA ACCAG G
- C ---- A TCTG AGA T

GAM2170 CACTTTCTGTGGTGCCTTAT 52577 TCTGTGGTGC 52578 TTTCT TG CTT CCT CT
GAATCAGACCTAGCTACACT CTTATGAATC CAC GTGG C ATGAATCAGA AG A
TTTCTGATTCATGTGCTACC AGAC ||| |||| | |||||||||| ||
TCTGTG GTG CATC G TACTTAGTCT TC /
TCTC- GT --- TT- AC

GAM2171 TATGGGAATATTCTGGTAAA 52593 AAAGTGCATG 52594 GG TC- A- - GTATCAAT TC
AGTGCATGTATCAATTTTAG TATCAATTTT TATG AATAT TGGTAAA GTG CAT TTTAG G
TCGTTTTTGGATTTCTGTAA AGTC |||| ||||| ||||||| ||| ||| |||||
TGTTACGATTTGCTATGTGT GTAC TTATG ATCGTTT CAT GTA AGGTT T
ATTTTCATG TT TGT AG T ATGTCTTT TT

GAM2172 GCGGGGCCGAAAGCCACGTT 52606 TCTCTGAACC 52607 GC A C TTC--- C-
TGTGTGC CC CA
CTCTGAACCTTGCGTGTGTG TTGCGTGTGT GCGGG CGAA GC ACG TCTGAA CTTGCG
AA CCAG C
CAACCCCAGCACGGTAATAC GCAA ||||| |||| || ||| |||||| |||||| || ||||

TGTCATGAAACACACTTTAA CATGG AGAG TC ACA TTTCAC AAAGTA GT TAAT /
GGTAACACTGAGACTGGTAC TC - - ATGGAA AC CT----- CA GG

GAM2173 GACGTATTAACTTTTCCATC 52634 TCTATATTAG 52635 TT TTTTCCA TTC T TT- TGT
TTCTATATTAGGATTAGTTG GATTAGTTGT GACGTA AAC TC TATA TAGGA AGT T
TTTTATACTTTCTTCTATTA TTTA |||||| ||| || |||| ||||| |||
TAATTGAGTTGTTGTTTTTA CTGCAT TTG AG ATAT ATCTT TCA T
CGTC TT TTGTTG- TTA T CTT TAT

GAM2174 TGTAGTTTTAGTGTATAGAT 52639 TATACAGATT 52640 T TT T ATAT -- TT- T TC
ATTATACAGATTTGATTTAT TGATTTATCT TG AGT TAGTG ATAG TATACA GA TGAT TA T
CTATTATATCGCTTTCCATG ATTA || ||| ||||| |||| |||||| || |||| ||
TGTATAAGCTATTTACTATT AC TTA ATCAT TATC ATGTGT CT GCTA AT /
ATTCCA C TT T GAAT AC TTC T TA

GAM2175 GATTAGTTATATTCTATGTA 52644 TCTATGTAAT 52645 TT A TC T-- GATTACATG
TACTATTT
ATAATAACGATTACATGTAT AATAACGATT GA AGTT TAT TATGTAA AATAAC
TATATAACATA C
ATAACATATACTATTTCTAT ACAT || |||| ||| ||||||| |||||| ||||||||||
TTTCTTATGTTATATAAAAA CT TCAG ATA ATACATT TTATTG ATATATTGTAT /
AGTTATTTATTTACATAATA TT A -- TAT AAAAA---- TCTTTTAT
AGACTTTTC

GAM2176 GTCCGCCGTCTAGGTAAGTT 52649 TCTAGGTAAG 39372 C C-- AAGTTT A -- TC A-
CC
TAGAGCTCAGGTCGAGACCG TTTAGAGCTC GTC GC GTCTAGGT AG GCTC AGG GAG
CCGGG T
GGCCTTTGTCCGGCGCTCCC AGGT ||| || |||||||| || |||| ||| ||| |||||
TTAGAGCCTACCTAGACTCA CGG CG CAGATCCA TC CGAG TCC CTC GGCCT T
GCCGGC C ACT ------ - AT -- GC GT

GAM2177 GCCGCCCTACCTGAGGCCGC 52650 CTGCCGCCTC 52651 CCTACCT C CATCC C TT
CATCCACGCCGGTTGAGTCG CCGCCTGTGG GCCGC GAGGC GC ACGC GG G
CGTTCTGCCGCCTCCCGCCT T ||||| ||||| || |||| ||
GTGGT TGGTG CTCCG CG TGCG CT /
TCCGCC- C TCT-- - GA

GAM2178 GAATATGAATTCTATATCTA 52779 TACATTGAAC 52780 TTC TCT TCT TAG-- T
TA
CAGCATTTTCTTTATAGTTA AATTGATATA GAATATGAA TATA ACAGCATTT TTA TTAATGT
GTAAT T
ATGTTGTAATTATCGGTTAT AGTG ||||||||| |||| ||||||||| ||| ||||||| |||||
ACATTGAACAATTGATATAA CTTATACTT GTGT TGTTGTGAA AGT AGTTACA
TATTG /

GTGTTGTTTTGTGCTTTTCA TTC TT- TAT TAACA - GC
TATTC

GAM2179 CCTGTGCTTCGCCCGGATGG 52782 TGGCGTCCTC 52783 G CCC- A A-- - C
ACGAGAGCCTCACCTCCGTG GCCGTCCAGC CCTGT CTTCG GGATGG CGAG GCC TCAC T
ATGGCGTCCTCGCCGTCCAG ACGA ||||| ||||| |||||| |||| ||| ||||
CACGAAGAACAGG GGACA GAAGC CCTGCC GCTC CGG AGTG C
A ACGA - CTG T C

GAM2180 TTTCCATATCATCATTGTGT 52790 TGTGTAAACT 52791 C ATT AAAC- AA TT
AAACTAAATAACGTTTTCTA AAATAACGTT TTTCCATAT ATC GTGT TAAAT CGT T
TGGCATTTAATAAGGCATTG TTCT ||||||||| ||| |||| ||||| |||
GATATGTGGAAA AAAGGTGTA TAG TACG ATTTA GTA /
- GT- GAATA CG TC

GAM2181 AGATCTGCGGCACGCACTGC 52794 TACAGGGAGG 52795 T GCA ---- A- G-- --- - TC
ATCACCGGCCTCTCGGTCAC TGCAGATCAT AGA CTGCG CGCA CTGCATC CC GCC TCT
CGG A
GTCGAAGAACAGGTACAGGG GCGC ||| ||||| |||| ||||||| || ||| ||| |||
AGGTGCAGATCATGCGCACG TCT GACGC GCGT GACGTGG GG TGG AGA GCT /
CAGCTCT C AC- ACTA AG ACA ACA A GC

GAM2182 TTTTTCTTATTGTCTTCAGA 52807 TCAGATTATA 52808 ---------- CT A CCTTAT
TGAGCCTTATTACTTCATCT AATTTTCTAA TTTTTCTTA TTGT TC GATGAG T
CATCAGATTATAAATTTTCT TAAA ||||||||| |||| || ||||||
AATAAATTAAGAAAAA AAAAAGAAT AATA AG CTACTC A
TAAATAATCTTTTA TT A TACTTC

GAM2183 AATTAGACGTAAGTTCCGCT 52817 ACGTAAGTTC 52818 C TC C AATTTT- C A
TGGGAATTTTTTAACGCTAA CGCTTGGGAA AATTAGA GTAAGT CG TTGGG TTAACG TAA G
AGAGTTAACGTTAATCGTAC TTTT ||||||| |||||| || ||||| |||||| |||
ACCCAACGTATTTACATCTA TTGATCT CATTTA GC AACCC AATTGC ATT A
GTT A T- - ACATGCT A G

GAM2184 CTGTTGTTTAAAAGAAAGTA 52824 TAAAAGAAAG 52825 AA- A GACAG-------- A- - T
GACAGTGATACGGTGAACCA TAGACAGTGA CTGTTGTTTAA GA AGTA TG TAC GG G
GTAGCCAAAACAAAATTTAA TACG |||||||||| || |||| || ||| ||
TATTATCAGATTAAACAGCA GACGACAAATT CT TTAT AC ATG CC A
G AGA A AATTTAAAACAAA CG A A

GAM2185 TTGAAGCTTTTATATTAAAC 52838 AATCAACCCT 52839 TTTATATTAAACA AA ACCC
GC-- ACA
ATGCGATCTAATCAACCCTA AGGCAAACAC TTGAAGCT TGCGATCT TCA TAG AAAC
C

GGCAAACACACTAAGTTTAA ACTA |||||||| |||||||| ||| ||| ||||
GACTAAAACTGAAGAGATCG AATTTCGG ACGCTAGA AGT ATC TTTG /
CAGGCTTTAA ---------- GA CAAA AGAA AAT

GAM2186 TTGCTCCCAAACCTCAGCGC 52860 AAATATGGAA 52861 CCAAACCTC- - CTCCCAAAAGA CC- CA
CTCCCAAAAGACATATTTCC CATTCCCAGC TTGCTC AGC GC CATATTT TG G
TGCAGATTCACTCAAATATG TGCT |||||| ||| || ||||||| ||
GAACATTCCCAGCTGCTACA AGCGAG TCG CG GTATAAA AC A
ACAAACAGAGCGA ACAAACAACA T ACCCTTACAAG CTC TT

GAM2187 ATACAGCTTTGATTCTTCTG 52881 TAGCTTTGAT 52882 T TG TT T AT- - CG
ATCGTCTTGACGGTGTTCAC GTTGTAT ATACAGC T A CT CTG CGTCT TGA G
GGGCGCGGTGGTAGCTTTGA ||||||| | | || ||| ||||| |||
TGTTGTAT TATGTTG A T GA GGT GCGGG ACT T
T GT TC T GGC C TG

GAM2188 GCGTCTGCAGCATTGTCTGC 52887 TCTGCAGCAT 52888 C - ------- CT TCAT
CTGGTCATCACCTTCCTGCA TGTCTGCCTG GCGT TGCAGCATT GTC TGC GG C
GCTCATCGACTGGTGCTGCG GTCA |||| ||||||||| ||| ||| ||
CGCGC CGCG GCGTCGTGG CAG ACG CC A
C T CTACTCG T- TTCC

GAM2189 TTTTGCTTATGCAGAGTCGG 52910 TATGCAGAGT 52911 TG AGTCG GG
CAAGCTTTGGAAAGGAGCTT CGGCAAGCTT TTT CTTATGCAG GCAAGCTTT A
GCGCCGCTGCGTAAGTGAAG TGGA ||| ||||||||| |||||||||
GAA GAATGCGTC CGTTCGAGG /
GT GCCG- AA

GAM2190 TGCTGTAAAGCCAGAAAGAA 52923 CAAGTGGATG 52924 CCA A-- AGG -- A- CC AT G
ATCTAGGAGGCCCATCTACA GAGGCTTAAG CTGTAAAG GAAAGAA TCT AGGCC CATCTAC GG AGTG TGGG A
GGCCAGTGATTGGGGAACCT GAAT |||||||| ||||||| ||| ||||| ||||||| || |||| ||||
CAGCCACTCCAAGTGGATGG GACATTTT TTTTCTT AGG TTCGG GTAGGTG CC TCAC ACTC A
AGGCTTAAGGAATCTTCTTT CTC CTA AA- AG AA -- CG C
TCTCTTTTACAGTA

GAM2191 CATACGAATATACGATAGGA 52965 GGAGGAAAGA 52966 AATATACG A ---- - GG
GGAAAGAAGTTCCTGGTCAA AGTTCCTGGT CATACG AT GGAGGAAAGA AGT TCCT T
GGATGCTTGGGTTTTTCCTC CAAG |||||| || |||||||||| ||| ||||
TAATAAAAGAGTGTATG GTATGT TA TCTCCTTTTT TCG AGGA /
GAGAAAA- A GGGT T AC

GAM2192 ATTAATCACTGATTCCTTTT 53026 TCACTGATTC 53027 A TTCCTTT--- T CG AG
TCGATGCCGGACAATAGCAC CTTTTTCGAT ATTAATC CTGA TTCGA GC GACAAT C
AATTGTTTAGCTTTGGACTC GCCG ||||||| |||| ||||| || ||||||
TATGTATTCAGGATTAAT TAATTAG GACT AGGTT CG TTGTTA A
- TATGTATCTC T AT AC

GAM2193 CGCCTTACAGGGGTGTGGTA 53039 CGGCAAGACC 53040 ACA---- T AG A CT
GTGCAGGGTCTGCCTGCTCG GCTCCCCGGC CGCCTT GGGG GTGGT TGC GGGT G
GCAAGACCGCTCCCCGGCAA AACC |||||| |||| ||||| ||| ||||
CCGAGGCG GCGGAG CCCC CGCCA ACG CTCG C
CCAACGG T GA G TC

GAM2194 AAACCATCCAATCCACTACC 53074 TGGCATATTA 53075 ATCCACT--- GCT- - T - A TAT
TTTTATACA
AATAGCTGGCATATTAAGTG AGTGTAGTTA ACCAATA GGCA TAT AAG TGT GT
ATTATT A
TAGTTATATTATTTTTTATA TATT ||||||| |||| ||| ||| ||| || ||||||
CAATATTCTCGTAATAATTC TGGTTGT TTGT ATA TTC ACG TA TAATAA /
TATAGCATCTTCATACTGTT GAATATTTTT AATT C C T A TCT TGCTCTTAT
TTAATGTTGGTTTTTTATAA
GATGATGGTTT
GAM2195 ACCACTGGAAAGCTTCTACC 53085 TGGAAAGCTT 53086 T AA- TC CCT--- CA T
TCTGGACATGTGTTATATAC CTACCTCTGG ACCAC GGA GCT TA CTGGA TGTGT A
AATCCAGTCATACTGAGAGT ACAT ||||| ||| ||| || ||||| |||||
GAGTCTTGTGGT TGGTG TCT TGA GT GACCT ACATA /
T GAG GA CATACT A- T

GAM2196 AACCTGTTAAGCTGAGATGG 53111 TGTTAAGCTG 53112 G----- AGAT TT GA
CTGCATTTTTGGAGAAATAA AGATGGCTGC AACCT TTAAGCTG GGCTGCAT TTG G
TGTGCAGCTTAGCTTGAATT ATTT ||||| |||||||| |||||||| |||
TTAAGGTT TTGGA AGTTCGAT TCGACGTG AAT A
ATTTTA ---- T- AA

GAM2197 TATTTGTTTTAAGTACATCA 53122 TTTAAGTACA 53123 T A C- CCA TCTT- T TT
CCAAAAATTTCTTTATAATT TCACCAAAAA TATTTGTT TA GTA ATCA AAAATT TATAAT
CATT A
CATTTTATTAATGTATTATA TTTC |||||||| || ||| |||| |||||| |||||| ||||
TTTTCAATTTTATGATTTTA GTAAATAA AT TAT TAGT TTTTAA ATATTA GTAA /
TATATAATAAATG T A TT A-- CTTTT T TT

GAM2198 GCGCAGTTCCCGAGGGGTCA 53133 TTCCCGAGGG 53134 C G A TT ATCATAA
TTTCTTATCATAAAATAATA GTCATTTCTT GCGCAGTTCC GA GGGTC T CTT A
AAAAGGGGGACCTGTCCGGA ATCA |||||||||| || ||||| | |||
GCTGCGC CGCGTCGAGG CT TCCAG G GAA A

C G - GG AAATAAT

GAM2199 TTGGTTCTTTGAACATCTTG 53142 TCTTTTGATT 53143 CTT ---- ATCTT AG TA
GTCGAAAAGTAGGTATTTTC TATCCGTACA TTGGTT TGA AC GGTCGAAA TAGG T
TATCTTTTGATTTATCCGTA CTCG |||||| ||| || |||||||| ||||
CACTCGTGTAGCCAG GACCGA GCT TG TTAGTTTT ATCT /
TGT CACA CCTAT CT TT

GAM2200 CGTCTGAATATCCAAAGTTA 53148 TCTGAATATC 53149 C-- TATCCAA T GGTC - AATC
AAAAT
TCAGGTCTAGTGTAATCTAC CAAAGTTATC CGT TGAA AGT ATCA TAG TGT TAC C
AAAATCAGAACAGTAATTGG AGGT ||| |||| ||| |||| ||| ||| |||
CATCTAAATGATCACTACAA GCA ACTT TCA TAGT ATC ACG ATG A
ACTTTCATGTACG TGT TCAAACA C AA-- T GTTA ACAAG

GAM2201 ACTTGATTCAAAGTCGGGAT 53158 TCAAAGTCGG 53159 - TTCA G GAT T - AA
TTTTTCGGTTGAATTTCGTA GATTTTTTCG AC TTGA AA TCGG TTT TCGGT TG T
TCGACAAATTACTGAGTTCG GTTG || |||| || |||| ||| ||||| ||
TTCAATGT TG AACT TT AGTC AAA AGCTA GC /
T TGC- G ATT C T TT

GAM2202 GCCATTCTCTACAAGGTAAA 53167 TGTAAGCATA 53168 CTACAA --- CTGTAAGC TAG
CAT T AC
GACCCGGGAGTCTGTAAGCA TAGATGACAT GGTAAAGAC CCGGGAGT ATA ATGA
AATGG ATC A
TATAGATGACATAATGGTAT AATG ||||||||| |||||||| ||| |||| ||||| |||
CACAATGATCCGTTTCATAA CTATTTCTG GGCCTTTA TAT TACT TTGCC TAG
/
TTATTAGAAAATATTTCCGG CTTAGG ACA TAAAAGAT TAA --- - TA
ACAGTCTTTATCGGATTCTT
TATTGC
GAM2203 TCCGTCTAAAACATAACTTT 53171 TCTAAAACAT 53172 CATAACTTTCT--- TA T TT
AGAA---- AC
CTGTACCATAGGGTATCTTT AACTTTCTGT AAA GTACCA GGG ATCT TGTAAATCA
TAGA C
TGTAAATCAAGAATAGAACC ACCA ||| |||||| ||| |||| ||||||||| ||||
CGGTCTAAACGATAATGATT TTT CATGGT CTC TGGA ACGTTTAGT ATCT C
TGCAAGGTTCTCCTGGTACT TTTTTAAGCATTAT C- T -- AATAGCAA GG
ATTACGAATTTTTTTTTAGC
TTCGGG
GAM2204 TAATAAAAATATATGGCCAA 53200 TAAAAAATAT 53201 AAAAT GGCCAAAG- CC
AGTTATTCCGAAGATAAAAA AAATATTCTA TAATA ATAT TTATT G
ATATAAATATTCTAATATTA ATAT ||||| |||| |||||
ATTAT TATA AATAG /
AATCT AATATAAAA AA

GAM2205 CAATATAAATAAATTATCTT 53203 TAAGTTAAAA 53204 AAT--- AT-- T TTTC
TTATTATTTCTTTTTTAATA TTTTACCAGT CAATATA AAATT CTT TATTA T
TAAGTTAAAATTTTACCAGT ATAT ||||||| ||||| ||| |||||
ATATTG GTTATAT TTTAA GAA ATAAT /
GACCAT AATT T TTTT

GAM2206 AAAGGTAACGTGTAATCGCC 53209 TAATTTGTGT 53210 C T C T AC TTG
ATATATTGCAACCATTGATT GTTTGCGCTT AAAGGTAA GTGTAA CGC ATA ATTGCA CA A
TTTGTGTAATTTGTGTGTTT TGCT |||||||| |||||| ||| ||| |||||| ||
GCGCTTTGCTTTT TTTTCGTT CGCGTT GTG TGT TAATGT GT T
T T - T -- TTT

GAM2207 GCTGCGCCCCCTAACTATAC 53218 TACAAGCACG 53219 CCCCCTAACTATA-- G C
AAC---------- AA
AAGCACGCAGGTGCAAACCG CAGGTGCAAA CTGCG CAA CACG AGGTGCA
CG A
AAAACCGTAGCGTTTCCACG CCGA ||||| ||| |||| ||||||| ||
ACTTATGTACCTCCGTGGTT GACGT GTT GTGC TCCATGT GC /
GGAACACGAAAGCAACTGCA CAACGAAAGCACAAG G C
ATTCAGCACCTTTGCGAT CA
GT

GAM2208 GTCAGGCATGTTTGCGCATA 53237 TTAAAACAAA 53238 GG-- TTGC T
AAACATACAACAT G T
TATAAAAACATACAACATAC TTGTATTGTA GTCA CATGT GCA ATATAA ACAC TAA T
ACGTAATTTTTTGGTGTTTA CATG |||| ||||| ||| |||||| |||| |||
AAACAAATTGTATTGTACAT CAGT GTACA TGT TATGTT TGTG GTT T
GAAATTGAC TAAA ---- - AAACAAAATT--- - T

GAM2209 CCACGTCGTTATCAGCGTGC 53245 CAAGATCGAC 53246 CG - A- - TGT--- C - C
CAG
TGTGTCACGCCGTCTCGGCC GTGACTATTT CCA TCGTTA TC GCGT GC GTCACG CG TCT
GGC C
AGCAGCGTCAAGATCGACGT TGCA ||| |||||| || |||| || |||||| || ||| |||
GACTATTTTGCAACGCAAGA GGT AGCAGT AG CGCA CG CAGTGC GC AGA CTG /
TTGACGAGATGG AG T AA A TTTTAT A T A CGA

GAM2210 GGGTAATACGAATTTTGAAT 53259 TGGGAGTATC 53260 A- AATTTTGAAT GA ATCTG-
TATAT
TTTGGGAGTATCTGTCAAGT TGTCAAGTAT GGGTA TACG TTTGG GT TCAAG T
ATATTCAACTCTTGAATAAC ATTC ||||| |||| ||||| || |||||
CACGACCAGGCGTAGCTATC CCTAT ATGC GGACC CA AGTTC /
C CG ---------- AG CCAATA TCAAC

GAM2211 CGCTATACCGTCCTTTAAAT 53267 TTTAAATTAG 53268 - -- TTTA GACA GCGCG
TAGACAAGGTGCGCGTCTCT ACAAGGTGCG CGCT ATACCGT CC AATTA AGGT T
AAACCTATAATTCCCGGTAG CGTC |||| ||||||| || ||||| ||||
CGGTATAAGCG GCGA TATGGCG GG TTAAT TCCA C
A AT CCC- A--- AATCT

GAM2212 GGCGACCGTTGTGTGGAGTT 53273 GACCGTTGTG 53274 AC T G AGAAAAGA A
AGAAAAGAGCACGGACACCG TGGAGTTAGA GGCG CGTTGTG GGA TT GCACGG C
TGCAGGGTCCCTACAGCGCC AAAG |||| ||||||| ||| || ||||||
GCC CCGC GCGACAT CCT GG CGTGCC /
C- C G A------- A

GAM2213 GCAGATCTGTTAACGCCTGT 53297 TTAACGCCTG 53298 A --------- C ACAATG A A
AGAACAATGGACTATTATTA TAGAACAATG GC GATCTGTTAAC GC TGTAGA GACT TT T
AAAAGTCATTATTTACAAGC GACT || |||||||||| || |||||| |||| ||
TTTACAAAAGTTGATGGATT CG TTAGGTAGTTG CG ACATTT CTGA AA T
AGC A AAAACATTT A ATTA-- A A

GAM2214 TCAAATTGAAGATCATCCAA 53301 TGCAAAAGAT 53302 AGA - CAACA T T
CAGCGTATCATTTTTTAATG AGAGGCTTAA TCAAATTGA TC ATC GCGTA CATT T
TATGCAAAAGATAGAGGCTT TTTG ||||||||| || ||| ||||| ||||
AATTTGA AGTTTAATT AG TAG CGTAT GTAA T
CGG A AAAA- - T

GAM2215 TGTTGAGATATGTACATTAA 53310 TTATATTATT 53311 A- TGTACAT-- AAT TC TC
TAAATATATTCCAGAATCAT ATCCAAAGTC TGTTG GATA TAATA ATAT CAGAA A
TTTTTGTTATATTATTATCC TATC ||||| |||| ||||| |||| |||||
AAAGTCTATCCCCAACA ACAAC CTAT ATTAT TATA GTTTT /
CC CTGAAACCT --- TT TT

GAM2216 GTTTTTTTTGTATTTATATA 53318 TATAGTGTTT 53319 T T- TACAAC - -- ACT
CAACAACACATAGTTTGTAC TTTATAAATA GTT TTTT GTATTTATA AACAC ATAG TTTGT A
TAATGACAGAGTTTATAGTG TCTA ||| |||| ||||||||| ||||| |||| |||||
TTTTTTATAAATATCTAAAA CAA AAAA TATAAATAT TTGTG TATT AGACA /
TAAC T TC TTT--- A TG GTA

GAM2217 ACCTCTTTCTGATGGAGTCG 53327 TGATGGAGTC 53328 TTTCT TG TC AG CT TC
TCTTC T CTCACAAA
TAAAAAGTTTTATCTCTTTC GTAAAAAGTT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
TCTCTTCGATGGTCTCACAA TTAT || || ||| |||||| |||||| ||| || || |||
AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA /
GATGGAGTCGTAAAAAGTTT CTTCT CT TC GA CT GT TCTTT - AATTATAA
TATCTCTTTCTCTCTTCGAT

```
      GGT
GAM2218  GTGAGTATATATTATCTCGT 53332   TATATTATCT 53333     A  ----  --      TC T    A
      CCTTGGTTTACATGGATCAG       CGTCCTTGGT       GTG GTAT   ATAT  TATCTCG  CT GGTTT C
      AGTGAGATACAATATCTGAA       TTAC           ||| ||||   ||||  |||||||  || |||||
      TACGTAC                    CAT CATA   TATA  ATAGAGT  GA CTAGG A
                                 G   AGTC   AC     GA  -    T

GAM2219  TATCGCATTTATTGGAGACG 53338   TCGCATTTAT 53339       -    TG ----------    T---      TA
      TAACAATGTAGCGCATTGTT       TGGAGACGTA       TATCGCA TTTAT  G        AGACG    AACAATG  G
      TCCTCGTCTATCTATATGTT       ACAA           ||||||| |||||  |        |||||    |||||||
      TTGATAAGTTGCGATA                    ATAGCGT GAATA  T        TCTGC    TTGTTAC  /
                                 T    GT TTGTATATCTA    TCCT      GC

GAM2220  TTTCTAAGAATTTACAATCT 53349   TAATTCTATT 53350        ---      A   TAA---     TACAT    C
      AAAATAGTACATGATTCACA       AATGTTGATG       TTTCTAAG   AATTTAC ATC     AATAG    GATT A
      ATTTAATTCTATTAATGTTG       GTAA           ||||||||  ||||||| |||     |||||    ||||
      ATGGTAAATTACATTTAGAA                 AAAGATTT   TTAAATG TAG     TTATC    TTAA /
      A                          ACA      G   TTGTAA    TTAAT    C

GAM2221  TTTTCTCCGTACAAGAAATG 53361   TACAAGAAAT 53362        C  ACAAGAAA   AC-    CTT
CAGACA   TT    C-   CAC
      GACGTCACTTGAGCAGACAC       GGACGTCACT       TTTTCTC GT       TGG   GTCA   GAG     CAG
TCAT  GAC   G
      AGTTTCATCGACCACGACAG       TGAG           ||||||| ||       |||   ||||   |||     |||  ||||  |||
      TCTCATGATCTGACTACCTC                 AAAAGAG CA       ACC   CAGT   CTC     GTC  AGTA  CTG   /
      TGACCCGCCAACGAGAAAA                    - --------   GCC    ---   CATCA-   T-    CT   ACA

GAM2222  CCCGTCTCCCTCTGTGGTCG 53380   CTCTCGTCTC 53381     G            G--    TGGT       A   GA
      TGGGTGGTGCGAGAGTACAC       GGGGGACCAC       CCC TCTCCCTCTGTGGTC   TGGG
GCGAGAGT CAC  T
      GATGGGTGGCTCTCGTCTCG       AGGG           |||  ||||||||||||||   ||||    ||||||||  |||
      GGGGACCACAGGGGGAGGGG                 GGG GGAGGGGGACACCAG   GCTC    TGCTCTCG GTG
/
      GG                         G            GGG    ----       -   GG

GAM2223  GGCATGTCGGCCGACAAATC 53406   TGTAGCAGTT 53407     CAT     C   A--   C---       CTTC
      GCAGCTGTCTTCGCCGCCGC       AACGTCGCCG       GG   GTCGGC GAC   AAT    GCAGCTGT    G
      AGCTGTAGCAGTTAACGTCG       GCCT           ||   |||||| |||   |||    ||||||||
      CCGGCCTCC                    CC   CGGCCG CTG   TTG    TGTCGACG    C
                                 TC-     -   CAA   ACGA       CCGC

GAM2224  AATCACATATATAATACTTC 53410   CAATAGCGGC 53411       C      AATA-  T   ATA     AGAAA
      TAATATGTAAAGAAATAATA       GATGATATGT       AATCA ATATAT     CT CTA   TGTAA     T
      TGTTACAATAGCGGCGATGA       ATGA           |||||  ||||||     ||  |||   |||||
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    TATGTATGATT                    TTAGT TGTATA   GG GAT  ACATT   A
                                A    GTAGC  C  A--   GTATA


GAM2225  CATCTTTTACCAACACAAAG 53421  TCTTTTACCA 53422   CT    ACACAAA    ATATTT TT   -
GATAAT   ACA
    GGTGGATATTTGTTCATTGG      ACACAAAGGG      AT  TTTACCA    GGGTGG    G  CATTG GAGTT
 AATAC  C
    AGTTGATAATAATACACACA      TGGA          ||  |||||||     ||||||    | ||||| |||||    |||||
    AAGTATTTGGATTCACGGTG                 TA  AGATGGT     TCCATC    T  GTGGC CTTAG    TTATG
/
    GGTTACGACTACCTCAGACT                  AG     CAGAC--    AGCAT- GG    A    GT----    AAA
    GGTAGAGAATG

GAM2226  GTACGCGTGTCGATTCATCA 53443  ACGCGTGTCG 53444        --    ------    A--   AT
    AGGTATATAAACCTGGGGAT      ATTCATCAAG      GTACGCGT  GTCGA    TTCATC   AGGT  A
    GAGGCTACCTCGACATACGT      GTAT          |||||||| |||||    ||||||  ||||
    GTGC                          CGTGTGCA  CAGCT    GAGTAG   TCCA  T
                                   TA    CCATCG    GGG    AA


GAM2227  TACCTTTAGGTGTTAGGATA 53449  TAAAACATTT 53450   AG----------      A--  ATAC      ATATTT-
 A  TT
    TATCAATTATACAGTACCGA      GAATGTG        TT        GATATATC  ATT   AGTACCGAT     TTTGA
AA  T
    TATATTTTTTGAAAATTTTA                ||         ||||||||  |||   |||||||||      ||||| ||
    TTTATCGAACTAGCACATTG                  AA         CTATATAG   TAA   TTATGGTTA     AAGCT TT  T
    GTATTTGAGAATGTAGATAT                   AATAATAGCAGA      ATG   GAGT      CACGATC    A  TA
    ATCAGACGATAATAAAACAT
    TTGAATGTG
GAM2228  CTTCATTTACAGTAAATATA 53455  TGCTTTGTCC 53456   T    C   AA  -----       CCAA
    GGCATATATCCAAAATCTAT      GTAGATACTA      CT CATTTA AGTA  TAT    AGGCATATAT   A
    ATATGCTTTGTCCGTAGATA      TAAA          || |||||| ||||  |||    ||||||||||
    CTATAAATGTAG                    GA GTAAAT TCAT  ATG    TTCGTATATA   /
                                T    A   AG   CCTGT       TCTA


GAM2229  GACCAGTCAGCCGCGAACGG 53466  AGTCAGCCGC 53467    CAGT    CGAA-    A  AC---  -  A
    AAATAACGCCGAATCGAGCT      GAACGGAAAT      GAC   CAGCCG    CGGAA TA    GC CG A
    CCTCTAATTCCGATAACCGG      AACG          |||   ||||||    ||||| ||    || ||
    CTGTTGTC                      CTG   GTCGGC    GCCTT AT    CG GC /
                                TT--    CAATA    A  CTCCT  A  T


GAM2230  GGCTTGGCCCATCAACTGCT 53472  TTAGAAGGCA 53473       CCA  AAC   AAA   TTA   GACTT
    AAACTGATTAGGGAGACTTT      CGGGAGACGC      GGCTTGGC  TC  TGCT  CTGA  GGGA    T
    AAACATCCCCTTAGAAGGCA      CGAG          ||||||||  ||  ||||  ||||  ||||
    CGGGAGACGCCGAGCT                    TCGAGCCG   AG   ACGG   GATT   CCCT    /
                                CAG  GGC    AA-    C--    ACAAA
```

GAM2231 ACAGACAGTTCTTTGTGAAC 53482 TAGAACTCTT 53483 ---- T ACG-- TT
GACATTTTCTCGTGTAGAAC GAAGAACTTT ACAGAC AGTTCTTTG GA ACAT T
TCTTGAAGAACTTTTCGTCT TCGT |||||| ||||||||| || ||||
GT TGTCTG TCAAGAAGT CT TGTG C
CTTT T CAAGA CT

GAM2232 GGTGTGTGGGCGGCGTACAA 53486 CAGCACAAGT 53487 CGGC AACA-- T
CATGCGCATATTTGCGCAGC ACAATTTCAC GGTGTGTGGG GTAC TGCGCA A
ACAAGTACAATTTCACGTAT GTAT |||||||||| |||| ||||||
T TTATGCACTT CATG ACGCGT T
TAA- AACACG T

GAM2233 AGGATTTTTGCAACTCTTCT 53499 TACCATGAGC 53500 AGGA- G T -- T A
AGCACAAAAC GTCAG
AAGGATATAGTGAGTTTCAT CTGACTATAG TTCTA TATAGT AG TTCATG ATCT C CCAA
ACCC G
GATCTTCACCAAAGCACAAA ATAA ||||| |||||| || |||||| |||| | |||| ||||
ACACCCGTCAGGTCATAGGG GAGAT ATATCA TC GAGTAC TAGA G GGTT
TGGG /
TTTGGGAGATACCATGAGCC AATAG G C CA - - ---------- ATACT
TGACTATAGATAATAGAGGA
TTGCTTGTGCT
GAM2234 TTACATAAGGTTTTTACAAA 53515 TATAATATTT 53516 GTTT- C---- CTTGT - CA-
ACATA
TATTGACTTGTTATTTATTA ATTCAATATT ATAAG TTA AAATATTGA TATT TATTAAA
AATGGG T
AACAAATGGGACATATAACA TTTT ||||| ||| ||||||||| |||| ||||||| ||||||
CTTTCATTAAATTTAATATA TATTC AAT TTTATAACT ATAA ATAATTT TTACTT
A
ATATTTATTCAATATTTTTT AATTT ATTTT TATTT T AAA TCACA
TATAATTTAACTTATGTAA

GAM2235 GGGTACACGAAAACAGCTAA 53519 ACGTTGGGCC 53520 A AAC- AACAAGA C
TAAGCA- C- G
CGTTGGGCCAAACAAGATAT AAACAAGATA AAAC GCT GTTGGGCCA TATCTG GG
GTTT GGCCCCG C
CTGCGGTAAGCAGTTTCGGC TCTG |||| ||| ||||||||| |||||| || |||| |||||||
CCCGGCCCGGGGCCAAGAAC TTTG CGA CAACCCGGT ATAGAC CC CAAG
CCGGGGC /
AGATGGTCCCCAGATATGGC A CTCC ------- C TGGTAGA AA C
CCAACCCTCAGCAGTTTCTT
AAGACCC
GAM2236 GGTTAGTTCAATTTGTTAAA 53528 TTAGTCCTGA 53529 -- CAAT--- AA A CTCAGT C
GACAGGATCTCAGTAGTCCA CTCAACAATA GGT TAGTT TTGTT AG CAGGAT AGT C
GGCTTTAGTCCTGACTCAAC CCAC ||| ||||| ||||| || |||||| |||
AATACCACCAGCTAAAACC CCA ATCGA AACAA TC GTCCTG TCG A
AA CCACCAT C- A ATT--- G

GAM2237 ATAGAAAATCAAAAACAATG 53535 TGCGTAGCAC 53536 AAATCAAAAACAAT A C
AATGGTGCTAAGCACCACAT CATTTTCATA ATAGA GAATGGTGCTA GCACCACAT C
CCGGATGTGGTGCGTAGCAC ACAT ||||| |||||||||| |||||||||
CATTTTCATAACATTAATCT TATCT TTTACCACGAT CGTGGTGTA G
AT AATTACAATACT-- G G

GAM2238 GAGCAGAACAAACCACATCA 53541 CAAGATGTTA 53542 CAG AAA-- ---------- AA A
AGTGCATAGCACAAGATGTT GCATACTCCG GAG AAC CC ACATC GTGC T
AGCATACTCCGGAACTGGTT GAAC ||| ||| || ||||| ||||
ATCTC CTC TTG GG TGTAG CACG /
TA- GTCAA CCTCATACGAT AA A

GAM2239 GTGCTTTAACGTCAATGGTA 53563 AATGGTACAA 53564 AAATTTTATCCT C T - T
CTCT------- AA
CAAATTTTATCCTCGCTTTG ATTTTATCCT GGTAC CG TT GTGTAT CATAT CGT
AGTATA A
TGTATCATATTCGTCTCTAG CGCT ||||| || || |||||| ||||| ||| ||||||
TATAAAATTCTATATTCAAA CTATG GC AA CGCATA GTGTA GCG TTATAT T
TTATCATGCGATGTGTATAC ---------- - T T - TACTATTAAAC CT
GCTAACGGTATCAATAAACG
GAGCAC
GAM2240 GGCCGGACCGTTGATTCCCT 53575 TCCCTGACGA 53576 G TTG C AG----- ATGC
AG
GACGACTACGAGCACATGCA CTACGAGCAC GGCCG ACCG ATTCCCTGACGA TACG CAC
ATGAAGC A
TGAAGCAGAAGGCTTCATTT ATGC ||||| |||| |||||||||||| |||| ||| |||||||
GGTGACCCCGACGTGATCGT CCGGC TGGT TAAGGGATTGCT GTGC GTG
TACTTCG /
TAGGGAATAGTGGTCGGCC - GA- A AGCCCCA GTT- GA

GAM2241 CTGAGTGACGTCGGAGGGAG 53585 TACCCTACCG 53586 GACG - AGC CAC G
CTCCACGGCCGGGGGCCAAG AGAACTCAG CTGAGT TCGG AGGG TC GGCC G
ATACCCTACCGAGAACTCAG |||||| |||| |||| || ||||
GACTCA AGCC TCCC AG CCGG /
AG-- A AT- AA- G

GAM2242 CCACCTGTTTTAACATATAA 53609 TAATATTGAT 53610 T- -- GA T TATCCGTCATTG- ---
------- TT
TAGGCAGGAGATAGATATCC AAAATCTCCA ATAATAG GCAG GA AGA CAATATT
CCT T
GTCATTGCAATATTCCTTTT TTCT ||||||| |||| || ||| ||||||| |||
CGTAGGCACACAATCTAATA TATTATT CGTC TT TCT GTTATAA GGA C
TTGATAAAATCTCCATTCTC TC TA TC C TACCTCTAAAATA TCTAACACAC TG
TTCTCTGCATTTATTATCTT

GTTTCGGTGG
GAM2243 CTAAATAGTTTAATCCAATA 53626 TTGCATTGCA 53627 AT ATC A---- GG
AATTGAGGATAATCAATTCT TAAACTCGTT CTAA AGTTTA CAAT AATTGA A
TGCATTGCATAAACTCGTTA AG |||| |||||| |||| ||||||
G GATT TCAAAT GTTA TTAACT T
GC AC- CGTTC AA

GAM2244 ACACGACTGTGGTAGATTTG 53638 TGTGGTAGAT 53639 C TG-- A T AGA C T
TTCTATAGAGCCGGTTGCCG TTGTTCTATA ACA GAC TGGTAG TTTGT CTAT GC GG T
CAAATAGATAGAACTACCAA GAGC ||| ||| |||||| ||||| |||| || ||
TATGTCTGT TGT CTG ACCATC AGATA GATA CG CC /
- TATA A - AA- - G

GAM2245 ACAGTTTGAAAAATAACAGT 53646 AACAGTATCA 53647 AATA TCATTTAAACAT TG
ATCATTTAAACATTTAACTT TTTAAACATT ACAGTTTGAAA ACAGTA TTAACT C
GCGGGGTTAATTTCACAACT TAAC |||||||||| |||||| ||||||
TTACTGTTTTTAAGCTGT TGTCGAATTTT TGTCAT AATTGG /
---- TTCAACACTTT- GG

GAM2246 GGGACAGAAAAGAGATTGGA 53660 TAGGTCCCTA 53661 ATT A- GATG - A--
GAAACA- CTA
ACTTTTAGGATGGAACATCA TTGGTAGTTC GAG GG ACTTTTAG GAAC ATCAGTA
ACCTACGG GAG T
GTAAACCTACGGGAAACAGA ACTA ||| || |||||||| |||| ||||||| |||||||| |||
GCTATGGAACTCCCAAGTAC CTT CC TGAAAATC CTTG TGGTTAT TGGATGTC
CTC G
TGTAGGTCCCTATTGGTAGT --- AA A--- A CCC ATGAACC AAG
TCACTAAAAGTAACCTTCTG
TGTATGATCCC
GAM2247 CCCCATTTGGTGTAACCCAT 53664 CATTTGGTGT 53665 A GTAA TG--- CCTCA T
ATGTGCCACCTCATAATCCT AACCCATATG CCCC TTTGGT CCCATA TGCCA TAATCCT T
TTTAAGGGTTAAATTTGGTA TGCC |||| |||||| |||||| ||||| |||||||
AGTGTTGTGGGGAGCCAAGA GGGG GAACCG GGGTGT ATGGT ATTGGGA T
GGGG A AG-- TGTGA TTAA- A

GAM2248 GCAGCTGGGGTGGAAGTCTG 53684 TTAGTCTCCG 53685 C AGTCTGAAAAA AAA --- G
A AG
AAAAAGGGAAAGGGGAGGTG ACCCGCCGTC GCAG TGGGGTGGA GGG GGGGA G TG
GC A
AGCAGAGTGCCCAGTTAGTC CGCC |||| ||||||||| ||| ||||| | || ||
TCCGACCCGCCGTCCGCCCT TGTC ATCCCGCCT CCC CCTCT T AC CG /
ACTGT - GCCG------- AG- GAT G C TG

GAM2249 GTTCTTAGCTGATGATGGCA 53693 TTGAAGCTGT 53694 T--- ----- GTA ACGAAGAT -
- G TTA

TTGAAGCTGTATATTACGAA ATATTACGAA GATGGCATTG AAGCT TATT GCACAA
GGTA T AC T
GATGCACAAGGTATGACTTA GATG |||||||||| ||||| |||| |||||| |||| | ||
TGATGTGGTTACCATTGTGC CTACCGTAGC TTTGA GTAG CGTGTT CCAT G
TG /
TTAAGGATGAGTTTGACGAC GTGT AGCAG --- GAATT--- A T G TAG
GATGCCATCTGTGATAGCAA
TGTGAGAGC
GAM2250 GGTTATTTAGGCATTAAAAA 53698 AGGCAGGGTC 53699 T G T AAAT--- T T- -
AC- A
TGTTATATGTTTCGGCGACC TGCTGTTAAC GGT ATTTAG CA TAA GTTATA GTT CGGC
GACCCTGC AAGGT T
CTGCACAAGGTATTAACTTT TATA ||| |||||| || ||| |||||| ||| |||| |||||||| |||||
AAGGCAGGGTCTGCTGTTAA TCG TGAGTC GT ATT CAATAT CAA GTCG
CTGGGACG TTTCA T
CTATAACTTTCCTGTTATTG - - T GTCCTTT - TT T GAA A
CTGAGTGCT

GAM2251 TAAAATGGTGTTATGTTTAC 53723 TGATTGATGA 53724 TA -- AA TTACT GGG-- T
G TGGA
CAGTCAAACAGTTACTCGAC CATATTTAGT GT TGTTTACCA GTC ACAG CGAC GTGTT
TCGG TAGAA C
GGGGTGTTTTCGGGTAGAAT CGCT || ||||||||| ||| |||| |||| ||||| |||| |||||
GGACACTTTTCTGATTGATG CA ATGAATGGT CAG TGTC GCTG TACAG AGTT
GTCTT /
ACATATTTAGTCGCTCTGTA CC AT A- TC--- ATTTA T A TTCA
GACTATGGTAAGTACCACAC
TATGTTA
GAM2252 TCGGGGTTGCCACGGCTGAT 53727 TCAGTTGTTG 53728 GG - -- AAACT TG
CTCATAAACTCCTGCAATGG GTAATAACGA TCG GTTGCCA CGGCTGA TCTCAT CC C
TGGTGGGAAATCAGTTGTTG ||| ||||||| ||||||| |||||| ||
GTAATAACGA AGC TAATGGT GTTGACT AGGGTG GG A
AA T AA GT--- TA

GAM2253 TATACTATCTGAAGAATATA 53736 TATCATACAA 53737 TATCTGA- - ------ ATT
TAATAACTGATATAGTATTA GGATTGTTAT TATAC AGAATATATAATAA CT GATATAGT A
TCAGCTATATCATACAAGGA ATAT ||||| |||||||||||||| || ||||||||
TTGTTATATATTTTCTAAAA ATATG TTTTATATATTGTT GG CTATATCG /
ATGTATA TAAAAATC A AACATA ACT

GAM2254 AGATCCTTGGTTATTATATT 53741 TCCTTGGTTA 53742 C- GTT-- CCTTAT - AA
CCTTATACTAGTAGAATAGT TTATATTCCT AGAT CTTG ATTATATT ACTA GTAG T
TACTTAGTTAATGATGTAAT TATA |||| |||| |||||||| |||| ||||
TCTAACAAGAAATCT TCTA GAAC TAATGTAG TGAT CATT /
AA AATCT TAAT-- T GA

GAM2255 TCTGGCTCTGTTATTGTACC 53749 TATTGTACCC 53750 GT-- TG CCC- TAAC TA

CGATATAACGGTAATACTAA GATATAACGG TCTGGCTCT TAT TA GATA GG A
TTTATCTAAATATGATGTAT TAAT ||||||||| ||| || |||| ||
AAGAGTTAGA AGATTGAGA GTA AT CTAT TC /
ATAT GT AAAT TTAA AT

GAM2256 AGCGATAAAAGTAATAGAAA 53752 TAGAAAACAC 53753 C AA- --- A- ATACCA- C
AA GAT
ACACTATACCATGTCTACCG TATACCATGT G GATAA GTAATAGA AAAC CT TGTCTAC
GAT TATGAA T
ATAATATGAAGATTATATTC CTAC | ||||| |||||||| |||| || ||||||| ||| ||||||
ATAAAGTCGTAGATAATTAA C CTATT TATTATTT TTTG GA ATAGATG CTG
ATACTT /
AGAGAAGTTTAAATTTATTA - AAA AAA AA GAAATTA - AA ATA
TAAATTATCCT

GAM2257 GTGAGATAGTCATGGAGACT 53775 CTTTGTGGAT 53776 GAT AG TA---- GA A TCG
ACATCAGATTACGAGGATGT GATGAACTAT GTGA AGTCATGG AC CATCA TTACGAGG TG
T
CGTTTTTACTTTGTGGATGA GTAG |||| |||||||| || ||||| |||||||| ||
TGAACTATGTAGCCGTGACT TACT TCAGTGCC TG GTAGT GGTGTTTC AT /
CCATCAT ACC GA TATCAA A- - TTT

GAM2258 TGGAAGACTGTACAAGGAAT 53785 TGAGCGAAGG 53786 AA A A TCGATGATG
ATACGGTAC AA AATTA
TGATGAAGTTCGATGATGTT AGACCACTAC GGA TTGATG AGT TTGCT TATGG
TTGATAA A
GCTATACGGTACTATGGAAT ATCA ||| |||||| ||| ||||| ||||| |||||||
TGATAAAATTAATGAGATTA TCT AACTAC TCA AGCGA GTATC AGCTATT /
TCGAGGCTATGAGCGAAGGA -- - A CCAGAGGA- --------- GG AGAGT
GACCACTACATCAATCTTAC
AGAAGTCCA
GAM2259 CAGTATCATTTAAACATTTA 53792 TCACAACTTT 53793 A TTT TTT C C T
ACTTGCGGGGTTGATCTCAC ATTGTTTTTG CAGT TCA AAACA AA TTG GGGG T
AACTTTATTGTTTTTGAACT AACT |||| ||| ||||| || ||| ||||
G GTCA AGT TTTGT TT AAC CTCT G
- T-- TAT C A A

GAM2260 AGATCCGTGAGAAATACGTT 53809 TGAGAAATAC 53810 GTG TA TTTAGCCG- TA
TAGCCGCCTTTAATAGAGGA GTTTAGCCGC AGATCC AGAAA CG CCTT A
AATCCCACCGCCTTTCTGGA CTTT |||||| ||||| || ||||
TCT TCTAGG TCTTT GC GGAG /
--- CC CACCCTAAA AT

GAM2261 GTTAATCTCACAACTTTACT 53816 TAGCATAGAT 53817 TAA AAC -- - C
GTTTTTGAACTGTTCAAAAT CCGTGAGAAA GT TCTCAC TTTA CTGT TTTTGAA T
ATAGCATAGATCCGTGAGAA TAC || |||||| |||| |||| |||||||

ATAC CA AGAGTG AGAT GATA AAAACTT /
TAA CCT AC T G

GAM2262 CCACCTGTTTTAACATATAA 53842 TAATAGGCAG 53843 TA T- -- GA T TATCCGTCATTG-
CTTCTC A
TAGGCAGGAGATAGATATCC GAGATAGATA ACA ATAATAG GCAG GA AGA
CAATATTC GT G
GTCATTGCAATATTCCTTCT TCCG ||| ||||||| |||| || ||| |||||||| ||
CGTAGGCACACAATCGAATA TGT TATTATT CGTC TT TCT GTTATAAG CA G
TTGATAAAATCTCCATTCTC -- TC TA TC C TACCTCTAAAATA CTAACA C
TTCTCTGCATTTATTATCTT
GTCTTGGTGG
GAM2263 CATGTAGTAAGTGTCGATTG 53852 TTAGGACAGA 53853 T A GA G A AAC
TAATAAGGAACTGATGCCTA TACTACTATT CA GTAGTA GTGTC TT TAATA GG T
TTAGGACAGATACTACTATT TG || |||||| ||||| || ||||| ||
TG GT TATCAT CATAG AG ATTAT CC G
T - AC G - GTA

GAM2264 CTGTGTCCAAGGTAAAATCG 53859 TCCAAGGTAA 53860 CAA AAA GTT TAG
TGTTTGTGTAGTTTTCACAA AATCGTGTTT CTGTGTC GGT ATCGT TGTG T
TGATGCCATCATAGATATAG GTGT ||||||| ||| ||||| ||||
GATATAG CTA TAGTA ACAC /
ATA CCG --- TTT

GAM2265 GTCATTCATTTAGAATGGTT 53876 TATTATGTTT 53877 A TTAG G GG TCA TG T
C C
GTTGGGCTTTATCAAGTGTA AAAGATGACA GTC TTCAT AATG TTGTTG CTTTA AG TA
TAGTCAG AT A
TTAGTCAGCATCAGCATCTG ATAT ||| ||||| |||| |||||| ||||| || || ||||||| ||
GCTATTATGTTTAAAGATGA CAG AAGTA TTAT AACAGT GAAAT TT AT ATCGGTC TA
G
CAATATTATTATGAAGAC - TTA- - A- --- GT T - C

GAM2266 TGAGAATATTGATGATTTTT 53881 TGATATTTAC 53882 AT- TTTTTTTAAGA---- C TTAT
CATTACAGA
TTTAAGATGATATTTACTTT TTTTTATATG TGATGAT TGATATTTA TTT ATGCTTG
A
TTATATGCTTGCATTACAGA CTTG ||||||| ||||||||| ||| |||||||
ATAATATTCACAGGTATTAT ACTACTA GCTATGAGT AAA TATGGAC /
TAAAATGAGTATCGGAGCTA CCT TACCATTACATCGAG A TTAT
ACTTATAAT
CATTACCATATCATCATCCA
TGCTCA
GAM2267 GTGCCGCCATCTAATGTGTT 53890 AAGAAGCAGA 53891 C C AATG AGA GT
TAGAGACCGTGAGGGTCAAG ACAGATGCGC GTG CGC ATCT TGTTT GACC G
AAGCAGAACAGATGCGCCAC CAC ||| ||| |||| ||||| ||||

CAC GCG TAGA ACGAA CTGG /
C - CAAG GAA GA

GAM2268 ATGGAGATACAACGTGAAAT 54059 TAATGTATCA 54060 CAA- A-- T ACTC
ACTTTATTACTCCATTAAAT CTTACGATAA ATGGAGATA CGTGA ATAC TTATT C
AATGTATCACTTACGATAAT TGTC |||||||||| ||||| |||| |||||
GTCTCTAT TATCTCTGT GCATT TATG AATAA /
AATA CAC T ATTA

GAM2269 AAGATGATAAAAACACGTTT 54067 AACACGTTTA 54068 T CGTTT TT GTCAACCA
ATTTTATATGTCAACCATTA TTTTATATGT AAGA GATAAAAACA AT TATAT T
CTAAAAAATATATTGTTCTG CAAC |||| |||||||||| || |||||
TTTTTGTTTTCTT TTCT TTGTTTTTGT TG ATATA T
T CT--- TT AAAAATCA

GAM2270 CTCACAACACCGCGTGGCCA 54083 GAGCTGGATT 54084 C GT-- TTTT A T TT C--
CAAAC- CT AC
TTTTTAGAGCTGGATTGTGC GTGCGGACAA CGC GGCCA TAG GC GGA GTG GGA
GCCG TCACGC C
GGACAAACGCCGCTTCACGC ACGC ||| ||||| ||| || ||| ||| ||| |||| ||||||
ACCTCGCGTGACCGGCCAGT GCG CTGGT ATC CG CCT CAC TCT CGGC
AGTGCG /
ACTCTTACCACTTTCCGCCT C ACTG TC-- - - TT CAT CATGAC C- CT
ACTTGGTCGTCAGCGCTGTT
TTGGG
GAM2271 CGGGGACACCTGCACGAGAC 54092 ACCCCTGGGC 54093 A G ----- CC TCTCA A
CCCTGGGCTCTCAGGAACTC TCTCAGGAAC CGGGG CACCT CA CGAGACC TGGGC GG
A
CGCCCAGGTCTTGCCAATTG TCCG ||||| ||||| || ||||||| ||||| ||
GGGTGATCCTG GTCCT GTGGG GT GTTCTGG ACCCG CC C
A - TAACC -- ----- T

GAM2272 AGATCCATGAGAAATACGTT 54182 TCCATGAGAA 54183 T AATACGTTTAGCCG TA
TAGCCGCCTTTAATAGAGGA ATACGTTTAG AGATCCA GAGA CCTT A
AATCCCACCGCCTTTCTGGA CCGC ||||||| |||| ||||
TCT TCTAGGT CTTT GGAG /
- CCGCCACCCTAAA- AT

GAM2273 GTTAATCTCACAACTTTACT 54199 TAGCATAGAT 54200 TAA CAAC -- - C
GTTTTTGAACTGTTCAAAAT CCATGAGAAA GT TCTCA TTTA CTGT TTTTGAA T
ATAGCATAGATCCATGAGAA TAC || ||||| |||| |||| |||||||
ATAC CA AGAGT AGAT GATA AAAACTT /
TAA ACCT AC T G

GAM2274 TGGGAACTTCAGGAGCTGAC 54208 CAGGAGCTGA 54209 CA C AC GA TAT TATCT-
CT
TTAGAAAATATTGTTTTATC CTTAGAAAAT TGGGAACTT GGAG TG TTA AAA TGTTT
CTTGGG G
TCTTGGGCTGCATTCAGGTT ATTG ||||||||| |||| || ||| ||| ||||| ||||||
TTTTAGGCATTTTTGATAAA ATTCTTGGG CCTT AC AAT TTT ACGGA GGACTT /
CATTTCCCCGGGTTCTTA CC T A- AG TT- TTTTTT AC

GAM2275 CTGGGAATAATAACTTTCTA 54214 TGAATAGACC 54215 AATAATAAC TA C GAT AA
GTCCATGATACAAAGAAGTT TGAAACAGCC CTGGG TTTC GTC AT AC A
GAATAGACCTGAAACAGCCC CAG ||||| |||| ||| || ||
AG GACCC AAAG CAG TA TG G
GAC------ TC A AGT AA

GAM2276 GAGATTGTACTATTTGTATA 54255 GATTGTACTA 54256 T- AT- A CG T-- A
CGCATCTTTAATAAAAGTTT TTTGTATACG GAGAT GTACT TTGT TA CA CTTT A
TGAATAAACAATTGAGTACT CATC ||||| ||||| |||| || || ||||
TGTTTC CTTTG CATGA AACA AT GT GAAA T
TT GTT A AA TTT A

GAM2277 GTGGGAAATTAGGAAACAGT 54261 TAGGAAACAG 54262 GAAATT- A-- GT TA GCAAA
TG T
GAGGTTAAAGCCGCAAAAGC TGAGGTTAAA GTGG AGG AACA GAGGT AAGCC AGCT
AGGAG T
TTGAGGAGTTACTTCTACAG GCCG |||| ||| |||| ||||| ||||| |||| |||||
CTGCTAAGGCTTCTGCTTCT CATC TCC TTGT CTTCG TTCGG TCGA TCTTC /
GTTAAACCTCCATAAACTAC AAATACC AAA -- TC AATCG CA A

GAM2278 AAGTGATATAAGGGGAATAC 54284 TAAGGGGAAT 54285 TATAA ATACACAT ATCAAAA
ACATGAGTAATCAAAACCCA ACACATGAGT AAGTGA GGGGA GAGTA C
GCACATACTCTCCTCGAATT AATC |||||| ||||| |||||
CATTT TTTACT CTCCT CTCAT C
TAAG- -------- ACACGAC

GAM2279 CCCAGCACATACTCTCCTCG 54299 TGAGTCGACG 54300 CACATACTC- C A TT CC
AATTCATTTCTCCTACCAGT ACCATCGCCT CCCAG TC TCGA TTCAT CT T
TGTGAGTCGACGACCATCGC ACTG ||||| || |||| ||||| ||
CTACTGGG GGGTC AG AGCT GAGTG GA A
ATCCGCTACC C - TT CC

GAM2280 TGTTTGGTCCGGTAGATATG 54309 GGTAGATATG 54310 CCGG-- AAAT CAA
GCAAATCCCAACCCCAGGGC GCAAATCCCA TGTTTGGT TAGATATGGC CC C
CGTATCTGAAAAGTATCAAG ACCC |||||||| |||||||||| ||
CA ACGAACTA GTCTATGCCG GG C

TGAAAA ---- ACC

GAM2281 GTTTTAGACCTATACGGTAA 54327 TAGATGGAGC 54328 T C A TA GCAACA A----- G
TGCAACATCCATCATCCGGT GCCAATCGCC GT TTAGAC TAT CGG AT TCCATC TCCG T
GACGGAAATATAGATGGAGC GATA || |||||| ||| ||| || |||||| ||||
GCCAATCGCCGATAGTTTGA CA AGTTTG ATA GCC TA AGGTAG AGGC G
TAC T - - GC ACCGCG ATATAA A

GAM2282 GCCCTTAGTCATCCATGCTG 54332 TCCATGCTGT 54333 TTA ATC- GC - CA AA-
CCAC- G
TGGCCGGTGCAGGAAAGACC GGCCGGTGCA GCCC GTC CAT TGTGGCCG GTG GG AGA
CCT A
ACCCTGATTAGGCAATTTCT GGAA |||| ||| ||| |||||||| ||| || ||| |||
ACACCAACACTCGGCCACGA CGGG CAG GTA GCACCGGC CAC CC TCT GGA T
ATGCTCAGACGCTGGGC TCG ACTC A- T AA ACA TTAAC T

GAM2283 GCGCGATTAGGTTAGATTCG 54371 TCCATGAGAT 54372 - TT GAAAC C- TC - ---
AATCCG AA
GAAACCATAGCTGTCCATGA TTTCAATCCG TAGA CG CATAG TG CATG AGAT TTTC
GAGTTAAGT A
GATTTTCAATCCGGAGTTAA GAGT |||| || ||||| || |||| |||| |||| |||||||||
GTAAACTGCTTAACTTGCAC ATTT GC GTATC GC GTAC TCTG AAAG
TTCAATTCG /
TCGAAAACAGTCTACATGTC T TC ----- CA CT A ACA CTCACG TC
CGACCTATGCGCTTTTATTT
CTGGTTGTGTT
GAM2284 GGAATTGATGTCCAGTGCGT 54384 TTGAATAATT 54385 A TGTC-- --------- TTC CAG
TCATTCAACACAGAGTAATG GTTATTGTAT GG ATTGA CAGT GCG ATTCAACA A
TTGAATAATTGTTATTGTAT CGCT || ||||| |||| ||| ||||||||
CGCTGTCATCTTCAATGCC CC TAACT GTCG TGT TAAGTTGT G
G TCTACT CTATGTTAT TAA AAT

GAM2285 TCACTATACGAGGGATATAA 54392 ATTGTACATA 54393 C GGATAT G AAACTGAA
T G
AGAATTTCTAGATCCTAAAC TAGAGGATAT TCA TATACGAG AAAGAATTTCTA ATCCT
ACAGTT TT A
TGAAACAGTTTTTGAATGAT AGAG ||| |||||||| |||||||||||| ||||| |||||| ||
AATTGTACATATAGAGGATA AGT ATATGTTT TTTTTTAGAGAT TAGGA TGTTAA
AG A
TAGAGATTTTTTTTTGTATA A ------ A GATATACA T T
ATGA

GAM2286 ATACACAGATTTATTGTAAA 54405 TATTGGGAAG 54406 A GAT - A AT AAC AGT
A
GCTATATCATATTCAAACTC ATGAATATGG ATAC CA TTAT TGTA AGCTAT CATATTCA TCT
TATAT T

TAGTTATATATTGATATATT TGGT |||| || |||| |||| |||||| |||||||| ||| |||||
GGGAAGATGAATATGGTGGT TATG GT AGTA ATAT TTGGTG GTATAAGT AGG
ATATA T
TATATATATGATAATGGTAT - AAT T A -- AGA GTT G

GAM2287 GTCTCCTTAAAGCTTCTGAT 54419 TGATGGTAAC 54420 C TTAA CT T AC-- T ATGT
GGTAACTGTGTTACATGTGC TGTGTTACAT GT TCC AGCTT GA GGTA TGTGT AC G
TCCGTCATACGTAAATGCCT GTGC || ||| ||||| || |||| ||||| ||
TCTTAAGCTATTTGGAAAC CA AGG TCGAA CT CCGT GCATA TG /
A TTTA TT T AAAT C CCTC

GAM2288 TTTATATACTTATTTAAAAT 54434 TAAAATGGGA 54435 TACT- AA A A ---- AA-
TAAA
ATACATATATTATTCCTATA AAAGATGAAT TTTATA TATTT AATAT CATAT TTAT TCCTAT
ACAT A
AACATTAAAATAGCATGTAA ATGA |||||| ||||| ||||| ||||| |||| |||||| ||||
AATGGGAAAAGATGAATATG AAATGT ATAAA TTATA GTATA AGTA AGGGTA TGTA
/
ATATTGAAAATATAATTTGT TTAAT AG - - GAAA AAA CGAT
AAA

GAM2289 GTTGTATATTCAAATTTAGA 54469 TAGATGCATC 54470 ATTCAAA A --------- CATA
GT- CT
ATATTTAGATGCATCATATT ATATTGTGGT GTAT TTTAGA TATTTA GATGCAT TTGTG
TTGA T
GTGGTTTGACTTCATTCAAT TTGA |||| |||||| |||||| ||||||| ||||| ||||
TATACAAATGTATTTCCAAA CATA AAATCT ATAAAT TTATGTA AACAT AACT
C
TCTTAAATATCTAAACTTAT CTATTC- - TCTAAACCT ---- ATT TA
CATACAAT

GAM2290 GCTCCCGCTCAGTCTGTTAG 54480 GCTCAGTCTG 54481 GTTAGT T A GAAT
TTGCATATTC T TT AAA A
TCCTCCTAGTTCGAATCCTT TTAGTCCTCC T CC CCT GTTC CCTT TCTC CCCAC
TTCA TC A
TTGCATATTCTCTCTCCCAC TAGT | || ||| |||| |||| |||| ||||| |||| ||
TTTTCAAAATCAAAGAGGGT G GG GGA CAAG GGAA AGAG GGGTG AGGT
AG /
GGACTGTGGGGAGAAAGGGA ------ T - ---- ---------- - TC GGG A
ACAGGTGGGGACGACCGGGA
GC
GAM2291 ACCTTAGTGTATTTTTTGGG 54493 TTTTTTGGGT 54494 AG TTT A - AATTTATGTGT
TT
TTATTGCAAATTTATGTGTT TATTGCAAAT ACCTT TGTA TTTGGGTT TTG CA TCTCT G
CTCTTTGTATAGAGATTTTA TTAT ||||| |||| |||||||| ||| || |||||
GTGTCGAAAATTCAAATTTA TGGAA ACAT AAACTTAA AGC GT AGAGA T
CAGCAAGGT CG TT- A T GATTTT----- TA

GAM2292 GCGGCTCAAATATGCCTGTT 54503 GCTCAAATAT 54504 ----- A T- GCATT
TTGTGCATTATATAGACAAA GCCTGTTTTG GCGGC TCA ATA GCCTGTTTTGT A
ATAGGCTCTGTATGGAATAT TGCA ||||| ||| ||| ||||||||||
GCCGC CGCCG GGT TGT CGGATAAAACA /
TATAA A CT GATAT

GAM2293 CTCACGACACCGCGTGGCCA 54525 TAGCTGGATT 54526 C -- TG TTT C TT C-- CGAAC- C TG TT
TTTTAGCTGGATTGTGCGGA GTGCGGACGA GACA CGC G GCCA TAG TGGA GTG GGA ACCG T CGC C
CGAACACCGCTTGCGCTTCT ACAC |||| ||| | |||| ||| |||| ||| ||| |||| | |||
CGCGTGACCGGTTAGTACTC CTGT GCG T TGGT ATC GCCT CAC TCT TGGC A GCG /
TTACCACCTTCCGCCTACTT C AT GT TC- C TC CAT CATGAT C GT CT
GGTTGTTAGCGCTGTCCTGG
G
GAM2294 GCCGTCCCGATTAACCGATT 54538 TAACCGATTC 54539 CC--- TT C CCGCA- AGCAC ACCA
CCCCGCACGGAGCACCGCGG CCCGCACGGA GCCGTC GA AAC GATTCC CGG CGCGG C
ACCACCCGACCGCGAGCCGA GCAC |||||| || ||| |||||| ||| |||||
CTCCTGGAGTTCGTTCCTCA CGGCAG CT TTG TTGAGG GCC GCGCC /
TTTCGACGGC CTTTA CC C TCCTCA GA--- AGCC

GAM2295 GTTTTACCGTCTGTCCCGAC 54548 CCCCGGCGTT 54549 C CT- --- AAA AACCACAA AT
GTTAAAGGGAGGTAACCACA AACGGGATGC GTTTTAC GT GTCCCG ACGTT GGGAGGT GC A
AGCATACTGCCGCCTTCCCC AACC ||||||| || |||||| ||||| ||||||| ||
GGCGTTAACGGGATGCAACC CAGAATG CA TAGGGC TGCGG CCTTCCG CG /
GTAAGAC C ACG AAT CC- C------- TC

GAM2296 TGTAAAAAGAAAATGCGAGT 54569 TGGCATGAAG 54570 AAAAGA- GA- AAG TGT T GT T AT TT
GCAAGAACTGTGGTTGGTTT CATTTACAAA TGTA AAATGC GTGC AAC GGT G TTCC GCG ATCAG C
CCTGCGATATCAGTTCAACC AGTG |||| |||||| |||| ||| ||| | |||| ||| |||||
TGATTACGTGGAAGTCTACT ACGT TTTACG TACG TTG TCA C AAGG TGC TAGTC A
TCTGTTGTGGCATGAAGCAT GAAAACA AAG GTG TCT T TG - AT CA
TTACAAAAGTGCA

GAM2297 TCCGGCAACATCACCGCGGC 54581 TATGCCGTGC 54582 AACATCAC C -- -- C
CGTGCGGATGCTCCAAAGCC CGCCGGA TCCGGC CGCGGC GTGC GGAT GCT C
TGTCCACGTATGCCGTGCCG |||||| |||||| |||| |||| |||
CCGGA AGGCCG GTGCCG TATG CCTG CGA A

CC------ - CA TC A

GAM2298 GCCCCCGTCTGTCGCCTCTC 54588 CCCGTCTGTC 54589 CC T TCTCC TTTCC
CCTTTTTTCCCCCCCTCAAA GCCTCTCCCT GCC CGTCTG CGCC CTTT C
GAACGTGGTGTTGGGCGCCG TTTT ||| |||||| |||| ||||
GC CGG GCGGGT GTGG GAAA C
CC T TGCAA CTCCC

GAM2299 CTTCCTTTGATGTAGCATGA 54621 TAGCATGATC 54622 TTT TGT TG CA-- C
TCAATGATGTCACGCATGAC AATGATGTCA CTTCC GA AGCA AT ATGATGTCA G
ATCGTCCTTATTGTGTTTCT CGCA ||||| || |||| || |||||||||
TCTCGGAAG GAAGG CT TTGT TA TGCTACAGT C
CT- TCT GT TTCC A

GAM2300 TTCTTTTAAATACGTATCAC 54635 TAATACTTAG 54636 AAT TC TT TGCTTTACTTA
CT TTTT
AGTTTAATGCTTTACTTATA TTAATACCTT TTCTTTTA ACGTA ACAG TAA TAAG TTGTA
T
AGCTTTGTATTTTTAGAATT TACT |||||||| ||||| |||| ||| |||| |||||
ATAATACTTAGTTAATACCT AAGAAAGT TGCAT TGTC ATT ATTC AATAT A
TTACTCTGTCTACGTTGAAA --- C- TC TCCATAATTG- AT TAAG
GAA

GAM2301 GCGGGCGCTCGCTAGGCCGC 54641 CGAGCATGCG 54642 -- - GAA GTA -- AC -
G TCG
CCGGAAATGCGTAGCGGACC CGCGGCGGAC GCTAGG CCGCC CG ATGC GC GG CCGT
GCGCGCATGC CGCAG A
CGTGCGCGCATGCGCGCAGT CCTA |||||| ||||| || |||| || || |||| |||||||||| |||||
CGACATTTGCGAGCATGCGC CGATCC GGCGG GC TACG CG CC GGCG
CGCGCGTACG GCGTT /
GCGGCGGACCCTAGCGAGCA CA C GCG AG- AT CA G A TAC
TGCGCGCGGCGGACCCTAGC
GAGCATGCGC
GAM2302 GTCGCCGGTTTAAATACTCA 54656 TACCCCAGAC 54657 GCC AAAT T TT AAGCCG TG
C
TTCGGAAGCCGTGGGTGGCG CGTTGTGTTA GTC GGTTT AC CA CGG TGGG GCGC T
CCTCGCGTACCCCAGACCGT TAAA ||| ||||| || || ||| |||| ||||
TGTGTTATAAAACCCAGAC CAG CCAAA TG GT GCC ACCC TGCG /
AC- ATAT T T- AG---- CA C

GAM2303 GTGGTCCTAAAAGTTTTTGC 54668 TAAAAGTTTT 54669 AA T AG-- AG TTGTTT TA -------
- ATA
CAGTCAGACAGTTGTTTCGG TGCCAGTCAG GTTTT GCC TC ACAG CGGA CAGTA
AGACG GG T
ATACAGTAAGACGGGATATA ACAG ||||| ||| || |||| |||| ||||| ||||| ||
ATGCCGCGTTTCCAAATCTA TAAAA CGG AG TGTC GCCT GTTAT TTTGC CC
A

TTGCCTCCGTATCTGTACGA -- C CGTA CA TAT--- CC CTAAACC G GTA
ATGCGGCCAAAATAATGGAC
TGT
GAM2304 ATAATCAACATAACCTCATC 54687 TAATAGGGAT 54688 ACA - C- A -- A
ATCTATTAACTGATAACGGT AAAGGATTAA ATAATCA TAA CCT ATC TCTATTA ACTGAT A
TAGTTATAATAGGGATAAAG TGAT ||||||| ||| ||| ||| ||||||| ||||||
GATTAATGATTAT TATTAGT ATT GGA TAG GGATAAT TGATTG C
A-- A AA - AT G

GAM2305 ACAGATGATCTGAGTAATAT 54693 TTCACGGTCT 54694 A -- T ACCT- T- AT
ACCTCTGTTATATATTTAAT TAGTATTTTT ACAG TGA TCTGAG AATAT CTGT ATAT T
GTTCACGGTCTTAGTATTTT AGAT |||| ||| |||||| ||||| |||| ||||
TAGATATCAATTGT TGTT ACT AGATTT TTATG GGCA TGTA /
A AT - ATTCT CT AT

GAM2306 ATCGTATTGTGGTTATATGG 54697 TGTGGTTATA 54698 ATTG T C A- TAA
CTACAATTTCATAATGAGTT TGGCTACAAT ATCGT TGGTTATA GG TAC ATTTCA T
GAAGTCAGTGTCCTATGATC TTCA ||||| |||||||| || ||| ||||||
AATGACGAT TAGCA ACTAGTAT CC GTG TGAAGT G
GTA- - T AC TGA

GAM2307 TGCTTCACAAAATTACATTA 54703 TACATTAATA 54704 ATTA-- AAAA- GTT AA --- G
TG-- TG G
ATAAAACATGTTTTTAATTA AAACATGTTT CATTAAT CAT TTT TTATTAAT TCCG TG
GTT T T
TTAATTCCGGTGTGGTTTGT TTAA ||||||| ||| ||| |||||||| |||| || ||| |
GTTAGTGGGCGGGTTAGTGG GTGATTG GTG GGG GGTGATTG GGGT AT
CGG G T
GCGGGTTAGTGGGCGGGTTA GGGCGG GGCGG ATT CG GGC G TGGG GT
A
GTGGGCGGGTTAGTGGGCGG
GTTAGTGGGCG
GAM2308 GGCGGGTTAGTGGGCGGGTT 54719 TAGTGGGCGG 54720 C GTTA TG TT T C TT TG C
TT T TTAG
AGTGGGCGGGTTAGTGGGCG GTTAGTGGGC GG GG G GGCGGG AG GGG GGG AG GG
GGG AG GGGCGGG T
GGTTAGTGGGCGGGTTAGTG GGGT || || | |||||| || ||| ||| || || ||| || |||||||
GGCGGGTTAGTGGGTCCTGC CT TC C TCGCCT TC CCC TCC TC CC TCC TC
CTCGTCC /
TCCTCCCCTTCCTGCTCCTC - ACTG GT -- - - -- GT T CC - TGGG
CCCTTCCGCTTGCGTCACTT
CCGCTTCCGGT
GAM2309 ATGGAAAGGGGGGCGAGGCA 54729 CCCCCGTTCG 54730 G A CA C -
GACGATGAGAGGATGGA A - GG
GGGCAGCGGGCGGGGGAGGA CCCACTACGA CGAG C GGG GCGGG GGGG GAG
CG GGGGG TCCC A
CGATGAGAGGATGGACGAGG GGTC |||| | ||| ||||| |||| ||| || ||||| ||||

GGGTCCCGGAGGAGGGAGCC GCTT G CCC CGCCC CCCC CTC GC CCCCC
AGGG G
CCCCGCTCGCCCCACCCGCC - C -- A G ---------- - G AG
CCCGTTCGCCCACTACGAGG
TCTAT
GAM2310 TTAACTTCGCAATAATTTCT 54742 TCGCAATAAT 54743 CT CAATAATTT T TAA
GGTTAGATAACGCACTCTAC TTCTGGTTAG TTAA TCG CTGGT AGA C
CAGTCAAGTCAATGATATTA ATAA |||| ||| ||||| |||
G GATT AGT GACCA TCT G
AT AACTGAACT - CAC

GAM2311 AGCGCCGGCGGCTGGCGAGC 54749 CTCGCCGCGT 54750 - - - G
GGCGGCGGCCACGCGCGCTG TGCGCGGCGT AGCGCCG GCGGC TGGCGAGCGGCG GCG C
CTCGCCGCGTTGCGCGGCGT T ||||||| ||||| |||||||||||| |||
T TTGCGGC CGTTG GCCGCTCGTCGC CGC C
G C G A

GAM2312 TGCCGGAGATGCACGCCATC 54755 ACGCCATCTT 54756 A CAC C -- AGTAC----------
G
TTCGAGGAGTACCCGGACCT CGAGGAGTAC TGCCGG GATG GC ATCTTC GAGG
CCG A
GGAGCAGAAGTACCTGAGCC CCGG |||||| |||| || |||||| |||| |||
TCATGAAGATGCCCATCACC ACGGCC CTAC CG TAGAAG CTCC GGT C
GGCA A C-- - TA GAGTCCATGAAGACGA C

GAM2313 TTCCCACTCCCTCCTCCAGG 54770 CCTCCAGGGC 54771 - ---- C-- G- C ------ -
CG
GCCTGCTTCGACGATCCCGC CTGCTTCGAC TTCC CAC TCCCTC TCCAGG CCTG TTCG
ACG ATCCCG G
GGGCCGGGATACGTGGCGCC GATC |||| ||| |||||| |||||| |||| |||| ||| ||||||
CGAACAGGGACCTGGAAACG AAGG GTG AGGGAG AGGTCC GGAC AAGC TGC
TAGGGC /
AGGGACTCCGTGAGGAA A CCTC CAA AG - CCGCGG A CG

GAM2314 GGATTTTATATCTGATATCA 54795 TATCTGATAT 54796 C CACAAA T A A - CAAAA- -
CCAAT AA
CAAAATATCAATAATGTATC CACAAAATAT T TGATAT ATA CA TA TG TAT ATATCA ATAT
GTCC T
AAAAATATCAATATCCAATG CAAT | |||||| ||| || || || ||| |||||| |||| ||||
TCCAATAAAGGATTTTATAT A ACTATA TAT GT AT AC ATA TATAGT TATA TAGG
A
CTGATATCACAAAATATCAA - AAAAC- - A A T AAACAC C TTT-- AA
TAATGTATCAAAAATATCAA
TATCTAATACC
GAM2315 AGGGAAGGTTTGACTCGCCT 54805 AAGAAGCGAC 54806 AA GAC C CCCA AGGAC
CTCCCAGCCCAGGACCAAAA AGAATCCGTC AGGG GGTTT TCGC TCT GCCC C

CGGGCGAAGAAGCGACAGAA CT |||| ||||| |||| ||| ||||
TCCGTCCT TCCT CTAAG AGCG AGA CGGG /
GC AC- A AG-- CAAAA

GAM2316 AACATACCAATGTCGATCTC 54843 TCTCATACTT 54844 T - C- C CTT-- TA CAAGT---
ACA
ATACTTATGGTAGGTTCAAG ATGGTAGGTT AACA ACC AATGT GAT TCATA ATGG GGTT
CACG G
TCACGACAGGCCGCGTGTTA CAAG |||| ||| ||||| ||| ||||| |||| |||| ||||
CACACAACCCCCATTTCACT TTGT TGG TTACG CTA AGTGT TACC CCAA GTGC
G
GTGAAATCCCGCATTCGGTT - C CC A CACTT C- CACACATT GCC
GTT

GAM2317 GCTATGATAAGCGGAGGAAA 54860 TATGATAAGC 54861 TAT A --- AAA TG T
ACCTGCCTGATTCCTTGGGC GGAGGAAAAC GC GATA GCG GAGGA CCTGCC A T
GGGGATCCTTGTGCGCTGTC CTGC || |||| ||| ||||| |||||| |
TTGC CG CTGT CGC TTCCT GGGCGG T C
TT- - GTG AG- GT C

GAM2318 TAGGTTATCGTTGAGATTAA 54875 TGACAAAATT 54876 G AT G AA-- --- TTACG T T
GAT
AAAGACTACGTTACGTTTTC TCGTAGTTAA TA GTT CGTTGA ATT AAA GACTACG TT TC
CT G
TCTGATGACAAGTGACAAAA ATTT || ||| |||||| ||| ||| ||||||| || || ||
TTTCGTAGTTAAATTTCTAG AT TAA GTAACT TAA TTT TTGATGC AA AG GA /
AATGTCAATGTGAATGTA G GT G GATC AAA TTTAA C T ACA

GAM2319 TAACTGTCCCGGCGTGCCTC 54884 TGGCATGAGG 54885 CGG TCCA - AG
CATCTGCTGAGTCCCGTGCA ATGGTTG TAACTGTCC CGTGCC TCTGC TG T
GACTGGCATGAGGATGGTTG ||||||||| |||||| ||||| ||
GTTGGTAGG GTACGG AGACG GC /
A-- TC-- T CC

GAM2320 CGAGTTAAATTACATAAGTC 54897 TCCCGAGTTC 54898 - TACA A G TT AGA
CCGAGTTCTCGGGACAAGAT TAGGGACCTA CGAGT TAAAT TA GTCCC AG CTCGGGACA T
GGCGTGTCCCGAGTTCTAGG CTTG ||||| ||||| || ||||| || |||||||||
GACCTACTTGTTTGTACTTG GTTCA GTTTG AT CAGGG TC GAGCCCTGT G
T TTC- C A TT GCG

GAM2321 GAGGGCCGGGTGTCCGAAGC 54906 GAGGCCGTCG 54907 CG C AGC A AG G
CGACCTCCAGCGGTACCGGG ACACCGCCCT GAGGGC GGTGTC GA CG CCTCC CG T
AGGCCGTCGACACCGCCCTC C |||||| |||||| || || ||||| ||
CTCCCG CCACAG CT GC GGAGG GC A
-- - --- C -- C

GAM2322 CCGCGCTCCTGCCCCCGGTC 54983 CCCCCGGTCT 54984 ----- C CC - TCT CC T A ACG TACAT
TTCTACGAGCCCGTGGTGGA TCTACGAGCC CG CTC TG CCCGGT CT ACGAG CGTGG GG CT CGGCC C
CTACGCGGCCTACATCAACC CGTG || ||| || |||||| || ||||| ||||| || || |||||
TGGCCGAGCTCTACGTCTTC GC GAG AC GGGCCA GG TGCTT GCATC TC GA GCCGG /
GTCTGGTACCGGGACCACGA CTCTT C CA T TC- CT - - --- TCCAA
GTTCTCCGCGG

GAM2323 AACGCGCTGCCCGGCGAGCG 55002 TCGGACCCGC 55003 C - -- --- C C C - AG
GTCCGCGGCCGCCGCCGAGA GCTCGGACCG AACGCG TG CCCGG CGAGC GGTCCG GG CGC GC CG A
CCCGAGCCGCGTCCTCGGAC GGAC |||||| || ||||| ||||| |||||| || ||| || ||
CCGCGCTCGGACCGGGACGA TTGCGC GC GGGCC GCTCG CCAGGC CC GCG CG GC /
CGCGTT A A AG CGC T T C A CC

GAM2324 TTTGCGCCTGCGTCTGTATC 55020 CTAGATCTGT 55021 TG CCTG T- CT A A
TGTACTAGTTAGCTAACTAG ATCTGGCGGT TT CG CGTC GTAT GT CTAGTT G
ATCTGTATCTGGCGGTTCCG TCCG || || |||| |||| || ||||||
TGAA AA GC GCGG TATG TA GATCAA C
GT CTTG TC TC - T

GAM2325 TGGGAGACGTCTCAGAGGCA 55031 TCTCAGAGGC 55032 AGACG G TCGG T
TCGGGGGCCATTTTTGTGGC ATCGGGGGCC TGGG TCTCAGA GCA GGGCCAT T
CCAATCTGTATCTGAGAACC ATTT |||| ||||||| ||| |||||||
CG GCCC AGAGTCT TGT CCCGGTG T
A---- A CTAA T

GAM2326 GAAGGATACGTGGTTCTATT 55041 TATTGGGCGG 55042 ATACGT TAT C C CG
GGGCGGCGAGGGGCCGAAAC CGAGGGGCCG GAAGG GGTTC TGGG GG GAGGGGC A
GCTCCTCTCCTCCATCTGAA AAAC ||||| ||||| |||| || |||||||
TTTTTGCTTTC CTTTC TTAAG ACCT CC CTCCTCG A
GTTT-- TCT - T CA

GAM2327 TGCTACCTTTAAACCTTATG 55057 TACCTTTAAA 55058 CTT TTATGT CT-- C AAA C TG
TAGACTGGGACAGTAAAGCA CCTTATGTAG TGCTAC TAAACC AGA GGGA AGT GCA AGCT G
CAGCTTGGGTCAGCTTGTCA ACTG |||||| |||||| ||| |||| ||| ||| ||||
CTTTTCTTTAATCTTTTTCC ACGATG ATTTGG TCT TCTT TCA TGT TCGA G
GGTTTAGTAGCA --- CCTTTT AATT T C-- - CT

GAM2328 GGGAAGATAATTTCAGTTGA 55070 TCAGAGCATG 55071 AA - AGTTGA AGAA G T
AGAAGAAGTTGTGAAGTACG GTCTAGAAAT GGG GAT AATTTC AGA GTT TGAAG A
TTTCAGAGCATGGTCTAGAA TCAT ||| ||| |||||| ||| ||| |||||
ATTCATTACCCC CCC TTA TTAAAG TCT CGA ACTTT C
CA C A----- GGTA G G

GAM2329 CGGGGCAGTTTGTGTACAAG 55086 TACAAGAACT 55087 A T G - T A GT
AACTGCGAGATGGTGCACAT GCGAGATGGT CGGGGC GTT GT TACAA GAAC GCG GATG G
CGCGCCGTTCTTTGTAGCGG GCAC |||||| ||| || ||||| |||| ||| ||||
CGGCCCTG GTCCCG CGG CG ATGTT CTTG CGC CTAC /
G - - T C G AC

GAM2330 CCCTTTTCAGTACAAAGGCA 55112 TACATCAAGA 55113 GTA AAGG AC A T AATTACA A
A T - A AA
AACCCTATCTCGCTAATTAC AGAAAAGTCA CA CAA CCT TC CGCT TCAAG AGAA AG
CAC AG TTC G
ATCAAGAAGAAAAGTCACAG CAGA || ||| ||| || |||| ||||| |||| || ||| || |||
ATTCAAGAAAGAGCTCGTGC GT GTT GGA GG GTGG AGTTC TTTT TC GTG TC
GAG A
CTATTTTGCTTGAATTGGGT AG- GAA- -- - T GTTA--- G A C C - AA
GTGGAGGTTGAAGTGGAGGA
GGAGGG
GAM2331 TCTGGCGGGTTATTGGTGGA 55153 TTGGTGGAAG 55154 GGC AT GG CAATG T G
AT
AGGCTGTAACAATGTCTGTG GCTGTAACAA TCT GGGTT TGGTGGAA CTGTAA TC GT TC
A
TCATAATCGAACTGAAAACT TGTC ||| ||||| |||||||| |||||| || || ||
TGCAGATTTTACCGCAACCT AGA TCCAA GCCATTTT GACGTT AG CA AG A
CAAGA AC- C- A- CAAA- T - CT

GAM2332 GGGCTTGTAGTTATACGTTC 55167 TACGTTCGAC 55168 GT CAC TAAAAAA G GTACA--
- CTTT G G
GACACCATTAAAAAAGAAGG ACCATTAAAA ATAC TCGA CAT GAAG CTATAT GA
CATC ATTG C
CTATATGTACAGACTTTCAT AAGA |||| |||| ||| |||| |||||| || |||| ||||
CGATTGGCATCAATGATGTA TATG GGCT GTA TTTC GATATA CT GTAG TAAC
A
TCTCAGATCAGAATATAGGC -- TA- ------- G AGACTAGA CTAT - T
TTTATGATTCGGGTATGTGC
AAGCCC
GAM2333 CGATTTAAAAAGGGGCAGTC 55175 CACCGCCTGT 55176 AA - CA AAGTT CG
TGCAAAGTTTATCGCGGGTG TAGGTTG CGATTTAA AGG GG GTCTGCA TAT C
TAATGTAGACACCGCCTGTT |||||||| ||| || ||||||| |||
AGGTTG GTTGGATT TCC CC CAGATGT GTG /
G- G A- AAT-- GG

GAM2334 TGTCGCAATCGTATCAAACT 55187 TGAGTGCGAT 55188 ATCAA C CA T A
CAGGCGGCAAGAGATACTGT TGTGACA TGTCGCAATCGT ACTCAGG GG AGAGA ACTGTT
G
TAGACAGCAGTTCTCTAACC |||||||||||| ||||||| || ||||| ||||||
TTCTGAGTGCGATTGTGACA ACAGTGTTAGCG TGAGTCT CC TCTCT TGACGA A
----- T AA - C

GAM2335 CCGTTGTACGAGTCTCTCAT 55194 ATGAAGTCCT 55195 T T AGT CATGA CCTT- A G
GAAGTCCTTTGATACTAGAA TTGATACTAG CCG TG ACG CTCT AGT TGAT CTA A
ATAGGATCATTGAAACTGAA AAAT ||| || ||| |||| ||| |||| |||
GAAGAGTCGCGTCCATCGG GGC AC TGC GAGA TCA ACTA GAT A
T C GCT AGAAG AAGTT G A

GAM2336 TCGAAACCTGTTATTTCCTG 55205 TATTACAGTG 55206 AAACCT TGGATCAC T CG G
GATCACCTGTTAACGTACGC GGAATAACTA TCG GTTATTTCC CTGT AA TACGC T
GTGGCGTATATTACAGTGGG AAAG ||| ||||||||| |||| || |||||
AATAACTAAAAGTGA AGT CAATAAGGG GACA TT ATGCG /
GAAAAT T------- - AT G

GAM2337 AAGAAAAGGTATTCGCCCTC 55211 AAAGGTATTC 55212 A TTCG--- CT T AG T
TGCTGGTCAAGGCTCAGCAA GCCCTCTGCT AAGAAA GGTA CCCTCTG GG CA GC C
TGCCTATAGAGGGAATAAAT GGTC |||||| |||| ||||||| || || ||
TACCATTTCTT TTCTTT CCAT GGGAGAT CC GT CG /
A TAAATAA AT - AA A

GAM2338 GGTACATCAATAAGTTTGGA 55231 TCAATAAGTT 55232 ATC ----- CAA- G
CAAGAGGAAACTTGTATTCC TGGACAAGAG GGTAC AATAAG TTTGGA GAG A
AAAATGACTTTATTATGGTA GAAA ||||| |||||| |||||| |||
CT TCATG TTATTT AAACCT TTC A
GTA CAGTA TATG A

GAM2339 TGGTGATAGATTAATCCTTG 55270 ATAGAGGAAC 55271 GATTAA GA- ACTTT
AAGTAACTTTTTTATATATT TAATATTACT TGGTGATA TCCTT AGTA T
ATAGAGGAACTAATATTACT A |||||||| ||||| ||||
A ATCATTAT AGGAG TTAT /
AATCA- ATA ATATT

GAM2340 GAATCAACTAACAACATAGA 55293 TAGAAAACAT 55294 AAC - TT C- T TCT G -
G TAA
AAACATATTTATCCTTGTGT ATTTATCCTT AAC ATAGAAAA CATAT ATC TTGTG AAT CG CTT
AGTTG AAT C
AATTCTCGGCTTAGTTGGAA GTGT ||| |||||||| ||||| ||| ||||| ||| || ||| ||||| |||
TTAACTTTTGTTGCAATTCA TTG TATTTTTT GTATA TAG GATAC TTA GC GAA TTAAC
TTG T

AGACGCTTATTCATAGTAGA AA- A T- AT - TTC A C G TTT
TTATATGATTTTTTATAAGT
TTAAGATATC
GAM2341 TATTACTGCAAGATTTTGAT 55300 TTCACATTGC 55301 CA----- TT--- TTTTTTAT TT
CATAC T
TTTTTATTTGGTTTTGTCAT CAGCTTTTAC TATTACTG AGAT TGA TTGGT TGT
AAGC T
ACAAGCTTTAGTTTTCACAT TTCA ||||||||| |||| ||| ||||| ||| ||||
TGCCAGCTTTTACTTCATTC ATGATGAT TCTA ACT GACCG ACA TTTG T
TCATCTGTATTATTAGTAGT TATTATG CTCTT TCATTTTC TT CT--- A
A

GAM2342 AATGAATGCCTGCCTGTATT 55332 TAATATACAT 55333 AT CT CT TTATAA GTTAATA
CA-- TT
ATAATATACATAAGTTAATA AAGTTAATAG AATGA GC GC GTA TATACATAA GTTTTTAT
TATT T
GTTTTTATCATATTTTTCTA TTTT ||||| || || ||| ||||||||| |||||||| ||||
ATACTATATAAAAATATCAT TTACT CG TG CAT ATATGTATT TAAAAATA ATAA
/
TATGTATAATCATTACTGTC AT C- T- TACTA- ACTA--- TATC TC
GCTATCATT

GAM2343 TTTTATAGTATATACGTTAT 55338 TAGTATATAC 55339 T TAC T A CTA
TGTCAAAATCTAAACAAATA GTTATTGTCA TTTTATAG ATA GTTAT GTCAA AT A
TTGGCATAATACCTATCTAT AAAT |||||||| ||| ||||| ||||| ||
AAGA AGAATATC TAT TAATA CGGTT TA A
- CCA - A AAC

GAM2344 CAATATTGTATTGTTATATT 55343 TATAAAATTC 55344 T TATTG- TA
ATTAGTTTATATTACTGAAT CCAATCTTG CAA ATTG TTATATTATTAGTTTA T
TAATAATATAAAATTCCCAA ||| |||| ||||||||||||||||
TCTTG GTT TAAC AATATAATAATTAAGT T
C CCTTAA CA

GAM2345 TCGGCGTTGTCGCAATCGTA 55349 TCAAACTTGT 55350 GTT CAAAC CTGC ACA
TT
CCAAACACAAGCTGCGAGAG TAAGTGCGGT TCGGC GTCGCAATCGTAC ACAAG GAGAG
CTG A
ACACTGTTAGACAGCAATTC TGTG ||||| |||||||||||| ||||| ||||| |||
TCAAACTTGTTAAGTGCGGT AGCCG CAGTGTTGGCGTG TGTTC CTCTT GAC /
TGTGACGCCGA --- AAT-- AAA- AAC AG

GAM2346 GACCGTTGCCATTAGAAGTC 55359 TGCCATTAGA 55360 TG - CAA T
AAATTCAGCTTTTGCTGAGT AGTCAAATTC GACCGT CCATTAGAA GT ATTCAGC T
GAGCTTTCTAATGGACATGG AGCT |||||| ||||||||| || |||||||
TT TTGGTA GGTAATCTT CG TGAGTCG T
CA T AG- T

GAM2347 TCGAAACCCCTTATTTCCTG 55368 TATTACAGTG 55369 A C C-- GGA-- C T CG TT
GATCACCTGTTAACGCACGT GGAATAAGTA TCGAA CC CTTATTT CT TCAC TGT AA CACG
T
TTGACGTGTATTACAGTGGG AAAG ||||| || ||||||| || |||| ||| || ||||
AATAAGTAAAAGTGAGAGGT AGCTT GG GAGTGAA GA GGTG ACA TT GTGC /
TCGA - A AAT ATAAG - - AT AG

GAM2348 GACCGTGGCCATCAGGAGTC 55379 TGAGTGAGCT 55380 G CA TCAA- T
AAATTCAGCTTTTGCTGAGT TTCCAGTGGA GACCGTG CCAT GGAG ATTCAGC T
GAGCTTTCCAGTGGACATGG CATG ||||||| |||| |||| |||||||
TC CTGGTAC GGTG CCTT TGAGTCG T
A A- TCGAG T

GAM2349 CCCCCAGGCATATTCAATAG 55394 TCGCATACTG 55395 -- T A GG- TT
GGACAGTGTTAATTTACTGT AATTGTTTGT CCCC CAGGCA ATTCA TA GACAGTG A
CGCATACTGAATTGTTTGTT TGGG |||| |||||| ||||| || |||||||
GGGG GGGG GTTTGT TAAGT AT CTGTCAT A
TT - C ACG TT

GAM2350 TGCGGGGGCAACATATCCTT 55400 TCCACCACGG 55401 CAACATATCC GCC--------- TA
CACCCGCCGCTACCTGCTCT GGTGAACTTC TGCGGGGG TTCACCC GC C
TCCACCACGGGGTGAACTTC CCCC |||||||| ||||||| ||
CCCCGCA ACGCCCCC AAGTGGG CG /
TTC------- GCACCACCTTCT TC

GAM2351 TGTCTTGCATTACTACCGTC 55453 CATTACTACC 55454 GCATTA A TC CTCCACA CCCT
ACCTCCACAGCCCCTATTAC GTCACCTCCA TGTCTT CT CCG AC GC A
AGCCCGCAAGTCTCGGCAGA CAGC |||||| || ||| || ||
AAAAGACA ACAGAA GA GGC TG CG T
AAA--- C TC AACGCC- ACAT

GAM2352 GTTGTACTGAAATTCGTGAG 55471 TGCAATAGAT 55472 G AT- GTGA A ATA
TAATATATAAAACCATAATG CATTCAGTAA GTT TACTGAA TC GTA TAT A
CAATAGATCATTCAGTAAAA AAC ||| ||||||| || ||| |||
C CAA ATGACTT AG CGT ATA A
A ACT ATAA A CCA

GAM2353 AGGGACCTCTGATTCTCCTG 55502 TGAGGAACCG 55503 A T CTCCTGT G A- ATC
G
TGACGCATGCCGATCCTATC GTATGGGTCG AGGG CC CTGATT GAC CATGCCG TCCT
GATT G
GATTGGAAATCTGAGGAACC ATCA |||| || |||||| ||| ||||||| |||| ||||

GGTATGGGTCGATCAGTGGC TCCC GG GACTAG CTG GTATGGC AGGA CTAA /
CCCT C T ------- G CA GT- A

GAM2354 ACCACATGACAATGAACAAA 55513 CATGACAATG 55514 -- - ACCT- A GA
CCTAAGACAGATTATGCTTT AACAAACCTA ACCACATG ACAATG AACAA AAG CA T
ATGCTTGTTGTGTTGTAATA AGAC |||||||| |||||| ||||| ||| ||
TGTGGT TGGTGTAT TGTTGT TTGTT TTC GT /
AA G CGTAT - AT

GAM2355 GCCGCAGCTCACATGCCGCC 55537 TGAGAGGAGG 55538 ACAT G TC CT
TTCCGCGCTTGCCTAGGCGC CGGGTTGCGG GCCGCAGCTC GCC CCT CGCGCTTGC A
GAGTGTGAGAGGAGGCGGGT C |||||||||| ||| ||| |||||||||
TGCGGC CGGCGTTGGG CGG GGA GTGTGAGCG G
---- A GA CG

GAM2356 TCCTCGGCGCCCTCCTGGTC 55693 GTGGACCGGC 55694 C- CCC - T TCG --- TAA
TC
TGGATCGGCTCCGGTCTTAA ATGGTACTCC TCCT GGCG TCC TGGTC GGA GCT
CCGGTCT CA G
CATCGTCTGGTGGACCGGCA TGGC |||| |||| ||| ||||| ||| ||| ||||||| ||
TGGTACTCCTGGCCATGGAC AGGG CCGC AGG ACCGG CCT TGG GGCCAGG GT /
GCCCTGGGA TC --- T T CA- TAC TG- CT

GAM2357 CGAATACTCCGAGCTTCCGC 55719 ACTCCGAGCT 55720 - C T---- C TATAAAA
CTGTATAAAATAAAGAGATT TCCGCCTGTA CGA ATACTC GAGC TC GCCTG T
GGGCCGACCTCCGCTCTGAG TAAA ||| |||||| |||| || |||||
TGTCTCG GCT TGTGAG CTCG AG CGGGT A
C T CCTCC C TAGAGAA

GAM2358 CGCGTATTATACAGTGTTGT 55741 TATACAGTGT 55742 - C TTAAGATA A-- A----------
-- AA
CTGTTTAAGATAGTAATATG TGTCTGTTTA AGTGTTGT TGT GTAAT TGGTGTATA
GTAT C
GTGTATAAGTATAACGTGTA AGAT |||||||| ||| ||||| ||||||||| ||||
CCAAGATTATCCAACTATAT TTACAATA GCA CATTA ACTATATAT CATG /
ATCAACGATTACGTAACCTA A A TCCAATG- GCA CAACCTATTAGAAC TG
CGAATAACATTACTTGTATT
ACGCG
GAM2359 TTACAATAAAATTTAGTTTA 55751 GCTAAATTCA 55752 TAAAATT TTAAG TGCA
AGTAGTGCTGCAATTTCTGC CTATGATGTT TTACAA TAGT TAGTGC A
GCTAAATTCACTATGATGTT TTGT |||||| |||| ||||||
TTGTAA AATGTT ATCA ATCGCG T
TTGTAGT CTTAA TCTT

GAM2360 GGCCCGAGTCTGCCTGGCTG 55757 AGGTGCAAAT 55758 -- CCTG TGC GT - TCC
CTGCGTCTCGCTCCGAGTGC GCGACCAGAC GGCCCGA GTCTG GC TGC CTCG C G
CGAGGTGCAAATGCGACCAG TGTC ||||||| ||||| || ||| |||| |
ACTGTCGGGCC CCGGGCT CAGAC CG ACG GAGC G /
GT CAG- TAA TG C TGA

GAM2361 CGTCTCTCCGGAGAGCGGCT 55769 CTCCGGAGAG 55770 CTCT G A ------ C
TGGTGCGGAGCTCCCGGGAG CGGCTTGGTG CGT CC GAG GCGGCTTGG TGCGGAGCTC
C
CTCCGCGGAAGACCCAGGCC CGGA ||| || ||| |||||||||| ||||||||||
GCCTCGGGTGTAACG GCA GG CTC CGCCGGACC GCGCCTCGAG G
ATGT G - CAGAAG G

GAM2362 GGCCCGACAGTCTGGTCGCA 55807 ACGCAGCAGC 55808 CA-- C ATT AC G ACT
TTTGCACCTCGGCACTCGGA CAGGCAGACT GGCCCGA GTCTGGT GC TGC CTCG C C
GCGAGACGCAGCAGCCAGGC CGGG ||||||| ||||||| || ||| |||| |
AGACTCGGGCC CCGGGCT CGGACCG CG ACG GAGC G /
CAGA A --- CA - AGG

GAM2363 CGTTACACCCGAGGCGGCCT 55883 CACCCGAGGC 55884 ACA C - CTG CTTCC C
GGGTCTTCCGCGGAGCTCCC GGCCTGGGTC CGTT CC GAG GCGGC GGT GCGGAGCTC
C
GGGAGCTCCGCACCAAGCCG TTCC |||| || ||| ||||| ||| |||||||||
CTCTCCGGAGAGACG GCAG GG CTC CGCCG CCA CGCCTCGAG G
AGA C T AA- ----- G

GAM2364 TGGGCATTTTTGATTGCAGA 55937 AGAGAACAAG 55938 T A T--- - T AAAAA
AAAATTCAAA C A
TTTCCAGGTTTTCTGCAAAA GCGGAATACA TTGAT GC GAT TCCAG GT TTCTGC TCT
CTG TATT T
ATCTAAAATTCAAACTGCTA CTGG ||||| || ||| ||||| || |||||| ||| ||| ||||
TTATTAATACAGGTCCCAGA GATTA CG TTA AGGTC CA AAGGCG AGA GAC
ATAA /
GAACAAGGCGGAATACACTG - A CAAT A T GAACA GACCCTG--- - T
GATAACATTAGCATTAGAAC
CCA
GAM2365 TGTATTACAGTAGAAAGAAA 55981 TACAGTAGAA 55982 TATT GA TACTCAA T TG C-
TG G
TACTCAAAGTGTTCAATGTA AGAAATACTC TG ACAGTA AAGAAA AGTGT CAA TA CTG
CG G
CCTGTGCGGGATCGTGCGGC AAAG || |||||| |||||| ||||| ||| || ||| ||
TTGTTTTGTATATTTTTCTT AC TGTCAT TTCTTT TTATA GTT GT GGC GC A
ATACTGTTTTCA TTT- A- ------- T TT TC GT T

GAM2366 ACTGGACTCGGTTTCGCTGT 56007 CTCCCAGAGC 56008 T GCT G TTCAA TGA

AGCTGTGGTTCAACCTGAAC TGCTAGGAAC ACTGGAC CGGTTTC GTAGCT TGG CC A
ATGGCTCCCAGAGCTGCTAG CGGT ||||||| ||||||| |||||| ||| ||
GAACCGGTCCAGT TGACCTG GCCAAGG CGTCGA ACC GG /
- AT- G CTC-- TAC

GAM2367 CCCATACGTGATTCGTGATC 56034 AACCTTTCCA 56035 AC TG TC CTTTTTT--- TAG
TTTTTTGGTTTGTAGTATAG CTCTATCATA CCCAT G AT GTGAT GGTTTG T
TAAACCTTTCCACTCTATCA TTGC ||||| | || ||||| ||||||
TATTGCTCGTGGG GGGTG C TA TACTA CCAAAT A
CT GT -- TCTCACCTTT GAT

GAM2368 GATTATACTATGTGGCTATA 56055 TACTATGTGG 56056 A-- T GCTATA AAT TC
ATAAAATTACGTTCTTTACG CTATAATAAA GATT TAC ATGTG ATAA TACGT T
TATTATACTACACACGTTGT ATTA |||| ||| ||||| |||| |||||
AACAAATC CTAA ATG TGCAC TATT ATGCA /
ACA T ACATCA --- TT

GAM2369 TATGAAAGGAATAGTATTTG 56065 TTAAAAATAG 56066 AAA AATA G A - ATACGT
AAT
TTAAAAATAGAACTGTATAC AACTGTATAC TATG GG GTATTT TTAAA ATAGAA CTGT
ATTA A
GTATTAAATACAAATGATCC GTAT |||| || |||||| ||||| |||||| |||| ||||
ATTGATAGATTTTATGTTTA ATAC CC TATAAG AATTT TATTTT GATA TAGT C
AAGAATATAACCCATGCATA GTA CAA- A G A GTTACC AAA

GAM2370 ATGCTTAATATCTTTACTAC 56072 TGGCCATGAT 56073 C- TACTACAACC AA TA T
ACA
AACCCGAAAATGTACATTTA CGTATCAATA ATG TTAATATCTT CGA ATG CATT ATTAAA
A
TTAAAACAAGTATTTAATAA AGGT ||| |||||||||| ||| ||| |||| ||||||
TGGCCATGATCGTATCAATA TAC AGTTATGGAA GCT TAC GTAA TAATTT /
AGGTATTGAAACAT AA TAACTAT--- AG CG - ATG

GAM2371 GAGTTGTTACGTCTGCGTCT 56080 TACGTCTGCG 56081 GT TCTGC T AA T
TTGTAAGTTTTCTAAACAGA TCTTTGTAAG GAGTT TACG GTCTT GT GTTT C
TCAAGGCCTCGTATAAACTC TTTT ||||| |||| ||||| || ||||
CTCAA ATGC CGGAA TA CAAA /
AT TC--- C GA T

GAM2372 GACAGGCCCCGGCTATCGCG 56088 TATCGCGACA 56089 GG G TA------- G -- C
ACATGTCGGCGACCCACGGT TGTCGGCGAC GACA CCCC GC TCGCGACATGTC GC
GACC A
CGGGTGGACGTGTCGCGACA CCAC |||| |||| || |||||||||||| || ||||
TGGACGTGCAGGGGGATGTT TTGT GGGG CG AGCGCTGTGCAG TG CTGG /

```
                                   AG   A TGCAGGTAC        G GG   C


GAM2373 ATACACTATGACCAACATAA 56092  AATGTTGTGG 56093       ATGACCAA--     AG   AC
        CAAGTAATACAAAATTAAAT      TAACAAAAAG      ATACACT      CATAACA TAAT A
        GTTGTGGTAACAAAAAGGTG      GTGT          |||||||      ||||||| ||||
        TAT                           TATGTGG       GTGTTGT ATTA /
                                        AAAAACAATG     AA   AA


GAM2374 GAGAGTGATTGAGGAAGTGA 56101  TGTTAAGCAG 56102    GAA GAA     CA  GAAA     A   AA---
- C   GA  A
        AGCTAGAGCAATAGAAAGCT      AACTCCTGCT      AG  GT  GCTAGAG ATA   GCTGTTA GCAG
CT CTGCT CCT A
        GTTAAGCAGAACTCCTGCTG      GACC          ||  ||  ||||||| |||   ||||||| ||||    || |||||  |||
        ACCTAAATAGGGAAGCAGTA                  TC  CG  TGATCTC TAT   TGACAAT CGTC    GA GACGA
GGA A
        GCAGACGCTGCTAACAGTGA                   AGG AAG    -- GAG-    -  GCAGAC T   AG  T
        GTATCTCTAGTGAAGCGGAC
        TCGAGCTCAT
GAM2375 ATTGTTTCATATTATTGCAT 56121  TCAATACCAT 56122    CA TC    - A   CGCAAT  -    C---
CCT   TGTTA
        GTCCAACAACAACTGACGCA      TTCGAAGAGT      TG TG CAACAA C ACTGA    TAC CTTCGA
GTAT  ACGG   T
        ATTACCTTCGACGTATCCTA      ATCA          ||  ||  |||||| | |||||    ||| ||||||   ||||  ||||
        CGGTGTTATTTAGTCTGTCA                  AC  AC  GTTGTT G TGACT    ATG GAAGCT   CATA  TGTC
 /
        ATACCATTTCGAAGAGTATC                  -- CT    T C   ------  A    TTAC   AC-   TGATT
        AGTCGTTTGTTGTCCACAGT
        AAAAGCAAT
GAM2376 TTCCGGAATTAGGGTTGGCT 56129  AGGCAACCCC 56130                --       ACG  C
C
        CTGGGCCAGCGCTTGGGGTT      AAGCAAGCTG      ATTAGGGTTGGCTCTGGGCCAGC
GCTTGGGGTTG  TG CACTAAGACAAGCGG G
        GACGTGCCACTAAGACAAGC      GCCC          ||||||||||||||||||||  ||||||||||  || ||||||||||||||
        GGCGCGCCGCTTGTCTTAGT                  TAATCCCAACCGAGACCCGGTCG  CGAACCCCAAC  AC
GTGATTCTGTTCGCC C
        GTCAAGGCAACCCCAAGCAA                          AA       GGA  T          G
        GCTGGCCCAGAGCCAACCCT
        AATTCCGGAA
GAM2377 TGTTCCGCGTGAGAGCCATT 56238  TGTGGCTACA 56239     C   GAG----    T  AA-  CAG  AG
        CTTAATCCAGTAGAGACGGC      TGCAACGCAG      TGTTC GCGT     AGCCAT CTT  TC  TAG  A
        TAAAGAGAGGGGTGTGGCTA      GACA          |||||  ||||     ||||||  |||  ||  |||
        CATGCAACGCAGGACA                  ACAGG CGCA     TCGGTG GGG  AG  ATC  C
                                    A   ACGTACA    T  GAG  AA-  GG


GAM2378 TGTAATCGTCACGTGAACTC 56258  GGACACTGGA 56259     T  C  GTGAA    AG  -  C
        CAAGGTCGAGCTGACTCGGA      GGTGAGTCAC      TGTAA CGT AC    CTCCA  GTC GAG T
        CACTGGAGGTGAGTCACGCT      GCTT          |||||  |||  ||    |||||  |||  |||
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      TGCA                                ACGTT GCA TG     GAGGT  CAG CTC G
                                        C   C  AGTG-     CA   G   A


GAM2379  AAGGAATCGTATTTATTAAA 56273   AATCGTATTT 56274       A       A     AAT     ----------          TA
      AATAGAAATGTGTATATTTT        ATTAAAAATA        AAGGA TCGTATTT TTAAA   AGAAAT
GTGTA  T
      ACACACAAATGATGAATTAA        GAAA           ||||| |||||||| |||||   ||||||              |||||
      TAGATTTCTTATTTAAGGAG                    TTCCT AGTATGAG AATTT   TCTTTA             CACAT  /
      TATGATCCTT                        -       G     AT-      GATAATTAAGTAGTAAACA     TT


GAM2380  GCGACCCCAGCCACGCACGA 56279   TTTGCGGGAT 56280        CCAG  A    CG   A  -    AA
      ACAGAGTTTAACGGAAGCGT        AAGGTTGT         GCGACC    CC CGCA  AAC GA GTTT  C
      CGTTTGCGGGATAAGGTTGT                    ||||||    || ||||  ||| || ||||
                                TGTTGG    GG GCGT  TTG CT CGAA  /
                                   AATA  -    --   -  G    GG


GAM2381  TATATCTATTGTAATTTTAC 56297   TATTACTTTT 56298        TATT-     TT      T---     -  A
      AAGTTATAGGAATAATCGCT        TGATGTA          TATATC     GTAAT  TACAAG    TATAG GA T
      ATATTTTTTTGTATATTACT                    ||||||     |||||  ||||||    ||||| ||
      TTTTGATGTA                        ATGTAG     CATTA  ATGTTT    ATATC CT A
                                      TTTTT     T-      TTTT     G  A


GAM2382  TTTATATATTCATTACAGTA 56303   TAATATAGTT 56304   TT-  TT  A       -        GT     -    CAC
TAAT
      AGATGGTGATAAATTAGTTA        TATTATTCAT          CA  AC GTAAGATGG TGATAAATTA  TATTA
CAACA   AAAAATAT    A
      TTACAACACACAAAAATATT        TTTA              ||  || |||||||||  ||||||||||  |||||  |||||   |||||||||
      AATAATATCATGTTTTTTGT                      GT  TG CATTTTACT ATTATTTGAT  ATAAT GTTGT
TTTTTGTA    A
      TGATAATATAGTTTATTATT                    TTT  TT  A       T        --     A     ---        CTAT
      CATTTTACAGTTTTGTTTTA
      TATAAA
GAM2383  GCATTTATCGTCTCAATTAT 56309   TAATAGGAGA 56310       -   CG----    AA    A     AC
      AATATTACTAAAGTATAATA        AAAAATATAT        GCATT TAT      TCTC  TTAT ATATT  T
      GGAGAAAAAATATATAATGT        AATG              |||||  |||      ||||  |||| |||||
                                TGTAA ATA      AGAG  GATA TATGA  /
                                   T   TAAAAA    --    A     AA


GAM2384  TGATACATTGATTAATGAAA 56316   TCCAGTAGTT 56317      T    -     A  AAA    TTATAAT
      GAACTTATAATGCCTCAAAT        ACGTGTTTCG         TGA ACAT TGATTA TG   GAAC       G
      GTTCCAGTAGTTACGTGTTT                      |||  |||| ||||||  ||   ||||
      CG                              GCT TGTG ATTGAT AC   CTTG       C
                                      T    C      G  ---    TAAACTC
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GAM2385 TTTTTACACTATTAAGTTTT 56329 TATTAAGTTT 56330 C -- GTTTT TA
ATTGCTACTAACCGTAGTAA TATTGCTACT TTTTTA ACT ATTAA ATTGCTAC A
TTTTATTAATGCAGTATAAA AACC |||||| ||| ||||| ||||||||
AA AAAAAT TGA TAATT TAATGATG /
A CG ATTT- CC

GAM2386 GGTTCACAATGTTAGTGATG 56337 TGGTAAGCAG 56338 TGA - GAAAGATG G --- TC -- ------- T
GGGCGCTGAAAGATGCGTAG AAATCCAAGG TGGGGC GCT CGTA CTACC CT TGGA GCCACT C
CTACCCTTCTGGAGCCACTT GTAC |||||| ||| |||| ||||| || |||| ||||||
CCTGGTGGTAAGCAGAAATC ACCCTG CGA GCAT GGTGG GG ACCT TGGTGG C
CAAGGGTACGGTGGTACGGT TCG A AAGGTG-- - CAT GA AAAGACGAA T
GGAAAGCAGTCCCAGCTCTG
CATTGGGAACC
GAM2387 AGTTGAAAGCATTGATGAAA 56356 TTGAAAGCAT 56357 CA T TCCTTA A
TCCTTAGGCATAGCCGGTAA TGATGAAATC AGTTGAAAG TTGA GAAA GGC T
TTTTCTCGGGACTTTCGACT CTTA ||||||||| |||| |||| |||
TCAGCTTTC GGCT CTTT CCG /
AG - TAATGG A

GAM2388 CATGCGTGAAGAAGATAAGA 56365 TCCTATGTGT 56366 AAGA AGA AT TTT
GGGAATCCACTTTTCAGTAG CTAAAGCATG CATGCGTG AGATA GGGA CCACT C
TGGTCCTATGTGTCTAAAGC CGTG |||||||| ||||| |||| |||||
ATGCGTG GTGCGTAC TCTGT TCCT GGTGA /
GAAA GTA -- TGA

GAM2389 GCTTTTTCTATTATGGCATT 56379 TGGCATTTTG 56380 TTTTTCTA G T AT- TGTCC
TTGTAATAATGCTCTGTCCA TAATAATGCT GC TTAT GCATTT GTAATA GCTC A
CTATCGAGTCTGTATTATTA CTGT || |||| |||||| |||||| ||||
AGTGTGATAAGTGTGC CG AATA TGTGAA TATTAT TGAG /
TGTG---- G T GTC CTATC

GAM2390 ATTATCATCAATAAAATGTT 56393 TGTGAATAAC 56394 A AA TGTG- A CTCTCTT-- T
TGTGTGAATAACTCTCTCTT TCTCTCTTGT ATTATC TCAAT AATGTT TGAAT ACT GTT C
GTTTCCAAACTCTCAAAATG TTCC |||||| ||||| |||||| ||||| ||| |||
GTAGTTCGATCCTAATATTA TAGTGG AGTTA TTATAA GCTTG TGG CAA C
AATTGAAGGTGAT A AA TCCTA A TAAAACTCT A

GAM2391 ATGAACATATAAGATACAAT 56423 TAAGATACAA 56424 CAT A TGACTTT--- TACAT TT
GACTTTAGTAATTTACATTC TGACTTTAGT ATGAA ATAAGAT CAA AGTAATT TC C
TTCACGATTAACAATTATTT AATT ||||| ||||||| ||| ||||||| ||
TTACAAATTTTGATTTTATT TATTT TATTTTA GTT TTATTAA AG /

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    TTAT                              ---     -  TTAAACATTT     CAATT  CA


GAM2392  TTCCGGAATTAGGGTTGGCT 56430   TTAGTGGCAC 56431                TT        CCT  A
C
     CTGGGCCAGCTTGCTTGGGG       GTCAACCCCA       ATTAGGGTTGGCTCTGGGCCAGC
GCTTGGGGTTG   TG CACTAAGACAAGCGG G
     TTGCCTTGACACTAAGACAA       AGCG          |||||||||||||||||||||  ||||||||||  || |||||||||||||
     GCGGCGCGCCGCTTGTCTTA                  TAATCCCAACCGAGACCCGGTCG  CGAACCCCAAC   AC
GTGATTCTGTTCGCC C
     GTGGCACGTCAACCCCAAGC                                --        TGC  G          G
     GCTGGCCCAGAGCCAACCCT
     AATTCCGGAA
GAM2393  TTCCCGCCTTATGCAAATGG 56433   AGCCATTTTA 56434         T   AAATGG  AG       G   T  CT
AATTTT
     GCAGCCATTTTAAGTGTTTC       AGTGTTTCAC       TTCCCGCCT ATGC     GC  CCATTTTAA TGTT CA
AT    A
     ACTATAATTTTATTGGTCAG       TATA          ||||||||| ||||     ||  ||||||||| |||| ||  ||
     TTTTGTAACGGTTAAAATGG                  AGGGGCGGA TGCG     CG  GGTAAAATT GCAA GT  TG
T
     GCGGAGCGTAGGCGGGGA                        -   AGG---  --       G   T  TT  ACTGGT


GAM2394  GATCTTCTGCTCTATTCCAA 56452   AACACTGTGA 56453       C  C   A   AA        A-----  ACC
     CATCAGTCACAAGGCACCGA       CTGATGGGGG       GATCTT TG TCT TTCC  CATCAGTCACA     GGC
G
     GCGCCGAACACTGTGACTGA       AGAA          |||||| || ||| ||||  ||||||||||     |||
     TGGGGGAGAAGACCACAGGA                  CTAGGA AC AGA GAGG  GTAGTCAGTGT     CCG  /
     TC                            C  C   A   GG        CACAAG   CGA


GAM2395  TATCAAGATGTGTATGTTTG 56578   CAGCACAAAT 56579     -        ----------      AAAA    G
     TGAAAATTGTGGAGACATAG       CAAGGGTATT       TATC AAGATGTGTAT        GTTTGTG   TTGTG A
     CAGCACAAATCAAGGGTATT       AATA          |||| ||||||||||        |||||||   |||||
     AATACATGTCTTAGATG                     GTAG TTCTGTACATA        TAAACAC   GATAC G
                                A        ATTATGGGAAC      GAC-    A


GAM2396  CCTAATTTATTAAGATCAGA 56591   TAAAATCTAT 56592         TT  GATCA      A  AC    T
     TGGATTATAACATGTTTCTG       TACAATTTTT       CCTAATTTA  AA    GATGGATT TA  ATGTT C
     AATATCTAAAATCTATTACA       AAAT          |||||||||  ||    ||||||||  ||  |||||
     ATTTTTAAATTAGG                        GGATTAAAT  TT    TTATCTAA AT  TATAA T
                                   TT  AACA-      A  C-    G


GAM2397  ATTTATATATATTTCTCTTT 56597   TATATATTTC 56598      TATAT    T  ------    T    CC  TATT
     CTATATAATATCCTCTATTT       TCTTTCTATA       ATTTA    ATTTC CTTT     CTATA AATAT  TC    T
     TTTTCGAAAATATTTATAGC       TAAT          |||||    ||||| ||||     ||||| |||||  ||
     AACATAAGGTGGAATTTTAA                  TAAAT    TAAGG GGAA     GATAT TTATA  AG    T
     AT                            TT---    T   TACAAC    -    AA  CTTT
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GAM2398 ACCATATAAACGAAGCCAAA 56607 TAAACGAAGC 56608 AT- -- ACT-- GAGA GCC
CTACAGAGAGTGCCGTCAAC CAAACTACAG ACCAT AAACGA AGCCAA ACA GT G
GATGTTTTTATTGGTTACTC AGAG ||||| |||||| |||||| ||| ||
GTTTTGGGTGGT TGGTG TTTGCT TTGGTT TGT CA /
GGT CA ATTTT AG-- ACT

GAM2399 GCCCCGAGTCGCGTGGATGA 56619 TGAGCAACGC 56620 C G -- AT AAC- T C A
GCAACGCTAAACAACAACCG TAAACAACAA GC CCGAGTC CG TGG GAGC GC AAA AAC A
TTTTTTCGCTACCGCTCCCC CCGT || ||||||| || ||| |||| || ||| |||
CAGCCGGGGCTCGGAGC CG GGCTCGG GC ACC CTCG CG TTT TTG C
A G CG CC CCAT C T C

GAM2400 ACCACCCAAAACGAGTAACC 56623 TGGCTTCGTT 56624 CCCA TAA TAAAAACATCGTTG
CA
AATAAAAACATCGTTGACGG TATATGGT ACCA AAACGAG CCAA ACGG C
CACTCTCTGTAGTTTGGCTT |||| ||||||| |||| ||||
CGTTTATATGGT TGGT TTTGCTT GGTT TGTC T
ATA- C-- TGA---------- TC

GAM2401 TACATTATAATATAACTAAC 56653 TTAAAACTAA 56654 A TAACT-- A ATG
TGTTTAAACAATGATGGTGT ACTTGTTACA TACATTATAAT TAAC GTTT AACA A
TAAAACTAAACTTGTTACAT TTGT |||||||||| |||| |||| ||||
TGTGATGTA ATGTAGTGTTA ATTG CAAA TTGT /
C TTCAAAT A GGT

GAM2402 TTATGTGGGGGATGTTCTTG 56663 TAACGCGAGG 56664 T C- TG GGC ATT
TTTC G AC
GGGATGCTTTGCGGGCCAGG GTTCCTTAAT GGGGGATGTT TTGGGGA CTTTGCG CAGGCG
TGGA GC GGTT T
CGATTTGGATTTCGCGGGTT AAAT |||||||||| ||||||| ||||||| |||||| |||| || ||||
ACTGGGACTGGTATTTCCGT TTTTCTGTAA AATTCCT GGAGCGC GTTTGT GCCT
TG TCAG /
GTTTGTAACGCGAGGGTTCC - AT TG AAT --- TTA- G GG
TTAATAAATGTCTTTTCGTA
A
GAM2403 ACAGTAGAAAAAAATACACA 56668 AAGCGTACAA 56669 - A CGT AATG C
AAGCGTACAATGTACGTGTT TGTACGTGTT ACAGTA GAAAA AATACACAAAG AC
TACGTGTT A
CAGGAGCATGTGGTTTATTT CAGG |||||| ||||| |||||||||| || ||||||||
TGTGTGTTCTTTTTATATTG TGTTAT TTTTT TTGTGTGTTTT TG GTGTACGA G
T A C ATT ---- G

GAM2404 GCGAACCCCACGACTGCCGA 56677 TAGACGACGC 56678 AA CCACGA TG AAA AGATG
G

AACGTTAGATGCTACTCGTA AACGGTGGCC GCG CC C CCG CGTT CTACTC T
GAGTAGACGACGCAACGGTG ATAA ||| || | ||| |||| ||||||
GCCATAAGGAGCGC CGC GG G GGC GCAG GATGAG /
GA AATACC GT AAC CA--- A

GAM2405 GATCAGAGGAACCGGATCTT 56687 TCTTCTGGTT 56688 AA TT AATC T
ATAATCGGAGCTCTTTCGAG TGGTTTGGAC GATCAGAGG CCGGATC AT GGAGCTCT T
AGCTCTTCTGGTTTGGTTTG CTCT ||||||||| ||||||| || ||||||||
GACCTCTGGTC CTGGTCTCC GGTTTGG TG TCTCGAGA C
A- TT GTCT G

GAM2406 GATCTTCTGCTCTATCTCAA 56712 TAGCTGGTGG 56713 C C A A TA----- ACA
CATCAGCTACTAGGCACAGA TGAGGAAGAA GATCTT TG TCT TCTCA CATCAGCTAC GGC
G
GCGCCGAAGTATGTAGCTGG CACA |||||| || ||| ||||| |||||||||| |||
TGGTGAGGAAGAACACAGGA CTAGGA AC AGA GGAGT GTGGTCGATG CCG /
TC C A A G TATGAAG CGA

GAM2407 CCATTGCCGAAGGCACAACC 56749 AGCGCAATGC 56750 C - ------ - GC AGA- CC - G-
- CA
CGCCGCCGACGCAGAGCAGA GAGCCGCCAG AAC CCGCC GCC GAC AGAGC GCG GC
CGCA GCG TCGT A
GCGCCGCCGCAGGCGTCGTC AGCT ||| ||||| ||| ||| ||||| ||| || |||| ||| ||||
AAGCAACGAGCGCAATGCGA TTG GGCGG TGG CTG TCTCG CGC CG GCGT
CGC AGCA G
GCCGCCAGAGCTCTAGTCAG T C ATCGAC A A- AGAC -- A AA G AC
GTCAGCTAGGCGGCGTTTAG
CCAGGCGAGGG
GAM2408 AATTGCATCAACCACCCTGC 56765 TGTGTTATCT 56766 CAAC CCCT - TGA- TCAAAA
GCCCTAGTGTGACCTCAAAA GATGTGCGAT AATTGCAT CA GCGC CCTAGTG CC A
AAGAGCCTGGAACCTACTGG T |||||||| || |||| ||||||| ||
GTGTGTTATCTGATGTGCGA TTAGCGTG GT TGTG GGGTCAT GG A
TT TA-- CTAT T CCAA TCCGAG

GAM2409 AAGTGTCATTTGACCCTGAA 56774 TCATTGGTCA 56775 G T TT CTG AATAAA
TGACGAATAAAATAAAAGTG TCTGTCAGTT AA TG CA TGACC AATGACG A
TCATTGGTCATCTGTCAGTT || || || ||||| |||||||
TT AC GT ACTGG TTACTGT /
G T CT --- GAAAAT

GAM2410 GAATATTATTATTGAAATTA 56819 TCTAATGTAG 56820 TT GAA T CC- CAAT TCA
TGTGAGCCACGTAGCAATCA ATAATTTTGT GAATA ATTATT ATTA GTGAG ACGTAG CAAG
T
AGTCATGTTTTTGTCACTAC TT ||||| |||||| |||| ||||| |||||| ||||
GTTTACTCATCTAATGTAGA TTTGT TAATAG TAAT TACTC TGCATC GTTT /

TAATTTTGTTT TT ATG C ATT ACT- TTG

GAM2411 AACAACTTATAACACGATGT 56827 TTAGTGTAAC 56828 A A CAC-- CCG AA
TACCCGAAGAAACCATTTTA ATTTAAGATT AAC ACTT TAA GATGTTAC AAGA C
GTGTAACATTTAAGATTAGA AGAA ||| |||| ||| |||||||| ||||
AGTAGTT TTG TGAA ATT TTACAATG TTTT /
A G AGAAT TGA AC

GAM2412 GCGCCTCGGTCTGAGAACCG 56832 TAGCGTTCGG 56833 TC T A G C C- CA GA
GCCTAGCGTTCGGACCGCAG ACCGCAGTCG GCGCC GG CTG GAACCG C TAG
GTTCGGACCG GTC G
TCGAGACAGATGACGGTCCG AGAC ||||| || ||| |||||| | ||| |||||||||| |||
AGCCACTGAGCGGTTCCCAG CGCGG CC GAC CTTGGC G GTC CGAGCCTGGC TAG
A
CCCTGGCGC TC - C - A AC AG AC

GAM2413 GTCTTCGTTGAAAACTATGC 56836 TTTGCATATA 56837 T- T AA CA TAT TTTT
CGTTAAGTG- A
ATTTATATTGTTTTTTAACC CATATGCGGT TCG TG AACTATG TTTA TGTT AACCGC
GCGAAAG T
GCCGTTAAGTGGCGAAAGAT TTTA ||| || ||||||| |||| |||| |||||| |||||||
ACTTTTTGCATATACATATG AGC AT TTGATAC AGGT GCAA TTGGCG
CGTTTTT A
CGGTTTTAACGTTTTGGACA TT T AC -- TTT TT-- TATACATATA C
TAGTTCATATCGATTAAC

GAM2414 TTGTATTTTTCAAGACGTAT 56851 TTTGATGCGT 56852 T CAAG-- TTT TT TTTC
TTTTTGTTTTATTTCTTCTA ATTCAAAAAA TTG ATTTTT ACGTATT TGT TA T
TTGTCATATTTGATGCGTAT ATCA ||| |||||| ||||||| ||| ||
TCAAAAAAATCAA AAC TAAAAA TGCGTAG ATA GT T
- AACTTA TTT CT TATC

GAM2415 GCCACAGAACCGCACTGTGT 56859 TGACAAGCAA 56860 -- C CA TGTTCA T CAG G
T- AT
TCAGGTGTATACAGGCTGGT ATGTATTCCC GCCACA GAA CG CTG GG GTATA GCT
GTCAGT TGCTGC T
CAGTTTGCTGCATTGGGCAG CAGG |||||| ||| || ||| || ||||| ||| |||||| ||||||
CGCCGCTGACAAGCAAATGT CGGTGT CTT GC GAC CC TATGT CGA CAGTCG
GCGACG /
ATTCCCCAGGACGATTCATT TA A AG C----- T AAA A CC GG
GTGGC

GAM2416 ATTAAATCATTAATTTCTTT 56896 TCATTAATTT 56897 TC TTTC ATC TG
ATTTGATAATCGTTTGACTG CTTTATTTGA ATTAAA ATTAA TTTATTTGATA GTT A
GCATATCAAATAAATTTTTT TAAT |||||| ||||| |||||||||| |||
AATCCTTTAGT TGATTT TAATT AAATAAACTAT CGG /

```
                                    CC    TTTT       A--  TC

GAM2417 TATTTTAGCTATATCTTTTC 56902  TAAAAGGTGA 56903    TT   TA- TC  T   ATA     TCACC
        CTTTATAATATACTTCACCA      ATTTGATTGT      TAT TAGC  TA TTT CCTTT  ATATACT   A
        ATAGTAGTATATAAAAGGTG      TATT         ||| |||| || ||| ||||| |||||||
        AATTTGATTGTTATTATA                ATA ATTG  GT AAG GGAAA  TATATGA   /
                                  TT   TTA TT  T   A--     TGATA

GAM2418 AGATACATACGTTCGCTATG 56920  TTGGTTGAGC 56921                        TAA    A  ---  -  T
        GACCAAGTGGTACCGGTTGG      GCAACCAACC
GTTCGCTATGGACCAAGTGGTACCGGTTGGTTGC  GCTCGA CAA  GAC GGC A
        TTGCTAAGCTCGAACAAGAC      GGTA         ||||||||||||||||||||||||||||||||  |||||| |||  ||| |||
        GGCTAAGCCGGTCCGGTTGG                CAAGCGATACCTGGTTCACCATGGCCAACCAACG
CGAGTT GTT  CTG CCG /
        TTGAGCGCAACCAACCGGTA                                    ---    G  GGC  G  A
        CCACTTGGTCCATAGCGAAC
        GTATGTATCT
GAM2419 TAATATGGTAGGTTAACTGT 56926  TGGTAGGTTA 56927      GGTA- GT     AAAAA--  TAG
        AAAAAATAATAGAACTTTTG      ACTGTAAAAA      TAATAT   G TAACTGTA     TAA  A
        GAATAAATATAGTTAGTTGG      ATAA         ||||||   | ||||||||     |||
        TTAATGTTA                   ATTGTA   T ATTGATAT     GTT  A
                                  ATTGG TG     AAATAAG  TTC

GAM2420 TATTGCTTTATTACTTCATT 56932  TAAAAAAGTA 56933      T- T   CAT     TAA
        TTTATTATAAATAACTGATA      CTACCAGCGA      TATTGCT  TA TACTT  TTTTATTA  A
        AAAAAGTACTACCAGCGATA      TA           ||||||| || ||||| |||||||||
                                ATAGCGA  AT ATGAA  AAAATAGT  T
                                   CC  C   ---      CAA

GAM2421 TATAATAATATACAATAATC 56944  TAATATACAA 56945     TA-    AATAAT-  TTC   GTA
        TTTTCTGTGTGTAAGATAAC      TAATCTTTTC      TATAA  ATATAC     CTT  TGTGT  A
        GCGTTTAAGTATATAAGTAT      TGTG         |||||  ||||||     |||  |||||
        ATAGTTTATA                  ATATT  TATATG     GAA  GCGCA  G
                                  TGA    AATATAT  TTT   ATA

GAM2422 TTAGCACCATATCCAAAATA 56951  TGTACATTTA 56952     CACCATATCCAAAAT    AC---
AAA  TTAA   T
        ATTGTACATTTAAATATAAA      AATATAAAAA      TTAG         AATTGT   ATTTAAATAT  AATT
GTTTT T
        AATTTTAAGTTTTTTAAAAA      TTTT         ||||          ||||||   ||||||||||  ||||  |||||
        CCAATAATTCATGTTTAAAT                AATC          TTAACA   TAAATTTGTA  TTAA  CAAAA /
        ATTAAACAATTTCTTTTCTT                  TTTTTTCTTTTCT--    AATTA      C--  TAAC   A
        TTTTCTAA

GAM2423 AAAATAATTGTACATTTAAA 56957  TGTACATTTA 56952    AT    AC---      AAA  TTAA   T
```

TATAAAAATTTTAAGTTTTT AATATAAAAA AAA AATTGT ATTTAAATAT AATT GTTTT T
TAAAAACCAATAATTCATGT TTTT ||| |||||| |||||||||| |||| |||||
TTAAATATTAAACAATTTCT TTT TTAACA TAAATTTGTA TTAA CAAAA /
TT CT AATTA C-- TAAC A

GAM2424 GGGTGGTGTCTGCAGCAAAA 56958 TATTTTGCAT 56959 T TCT - GAG-- AC C
GAGGAACTTGCCCAGGCAGT GCCACCTCCC GGG GGTG GCA GCAAAA GA TTGC C
CAGTTATTTTGCATGCCACC ||| |||| ||| |||||| || ||||
TCCC CCC CCAC CGT CGTTTT CT GACG A
T --- A ATTGA -- G

GAM2425 TGGGGGCTTCATGATCCCAC 57038 TTGAGATTCT 57039 TTCAT A -- CCGAT TGATGA
------- CT
CGCCTTTCCCGATGATGATG GATGAGAGGC GATCCC CC GCCTTTC GA CAACCG
CGGCTGT G
ACAACCGCGGCTGTCTGAAG TTGG |||||| || ||||||| || |||||| |||||||
CGGCTGACGAAATCGGTTGA CTGGGG GG CGGAGAG CT GTTGGC
GTCGGCG /
GATTCTGATGAGAGGCTTGG TTT-- G TT TAGT- TAGA-- TAAAGCA AA
GGGGGTCTTTGCCCTCA

GAM2426 GAGTAAGTCTGAAGCCTTTA 57043 ATAACCCACC 57044 AG AA CTTTAT-- TATAAG CCC
TGGTGTATAAGCGGCCCGAA TTTACCCTGC GAGTA TCTG GC GGTG CGG G
TTTTGATAACCCACCTTTAC GACG ||||| |||| || |||| |||
CCTGCGACGGAGTGCTC CTCGT AGGC CG CCAC GTT A
G- AG TCCCATTT CCAATA TTA

GAM2427 TCGAGCTGTTCATTTGAAGA 57049 GAGCTGTTCA 57050 GA T- TT G TGAGA T
CACTGAGAGTGGTTAACCAT TTTGAAGACA TC GCTGT CAT GAA ACAC GTGG T
GTGTGTGTTCCTATGTTGCA CTGA || ||||| ||| ||| |||| ||||
GTAAGA AG TGACG GTA CTT TGTG TACC A
AA TT TC G TG--- A

GAM2428 ACGGGTCATCCGACAAACAT 57075 ATGATGTACC 57076 - TCCGACAAACAT ACTT- G
G
GATGCACTTCGTGGTCAGGC CGCGTCTGAT ACGGG TCA GATGC CGT GTCAG C
AGCTGATGATGTACCCGCGT CCCG ||||| ||| ||||| ||| |||||
CTGATCCCGT TGCCC AGT CTGCG GTA TAGTC A
T ---------- CCCAT G G

GAM2429 TCTGCTGGTACAAGGAATGG 57082 CGTTGATTTT 57083 C--- AG GGC CC
CCGTTACCGGTTGACGTTGA ATGTACTACC TCTG TGGTACA GAAT CGTTA G
TTTTATGTACTACCTACAGG TACA |||| ||||||| |||| |||||
GGAC ATCATGT TTTA GCAGT /
ATCC AT GTT TG

```
GAM2430  ATACATGTGTTCGCTATGAG 57088   TGGTTGGTTG 57089                          TCT             A
         CGAACTGGTACTGGTTGGTT       AGCGCAACCA       GTTCGCTATGAGCGAACTGGTACTGGTTGGTTGC
 GCTCAACCAACCAGACCGGC A
         GCTCTGCTCAACCAACCAGA       ACCA          ||||||||||||||||||||||||||||||||||  ||||||||||||||||||
         CCGGCAAAGCCGGTCTGGTT                  CAAGCGATACTCGCTTGACCATGACCAACCAACG
CGAGTTGGTTGGTCTGGCCG /
         GGTTGAGCGCAACCAACCAG                                      ---             A
         TACCAGTTCGCTCATAGCGA
         ACACATGTAT
GAM2431  TATGCTTGGTCGTTGGTTTG 57103   TCACTGCCAA 57104     CT   CGT   ---     AA -   C
         GTAGAAGAGGAGCACTTCCA       AATATCACTT       TATG  TGGT   TGGT   TTGGTAG  GA GGAG A
         TCACTGCCAAAATATCACTT       ACCA          ||||  ||||   ||||   |||||||  || ||||
         ACCATCATA                    ATAC  ACCA   ACTA   AACCGTC  CT CCTT /
                                  T-   TTC   TAA     A-  A   C


GAM2432  GGCCACAGGATGTAGATCGC 57126   AAGCTGCAAT 57127      CA  AT   GATC   ACA  GAAAC   AA
         AGACACTGAAACGCTGAAAC       ACCGCCGATG       GGCCA  GG  GTA   GCAG   CT    GCTG  A
         ACAGCATTAAGCTGCAATAC       GCC           |||||  ||  |||   ||||   ||    ||||
         CGCCGATGGCC                    CCGGT  CC  CAT   CGTC   GA    CGAC  /
                                  AG  GC   AA--   ---  ATTA-   AC


GAM2433  ATGGCACGCGCCGCCAGCAA 57172   CGCCAGCAAA 57173       -   CC          AGT----------     TG
CT
         ATTTAAGTCCTGGTGGCTCA       TTTAAGTCCT       ATGGCA CGCG  GCCAGCAAATTTA
CCTGG  G  C
         CCTGCCAGGTAAACAAGGTT       GGTG          ||||||  ||||  ||||||||||||           |||||  |
         AAAGTGGGTTTGCTGGCCTT                  TACCGT GCGT  CGGTCGTTTGGGT          GGACC  C  /
         GCGTTGCCAT                      T   TC          GAAATTGGAACAAAT    GT CA


GAM2434  ATCCGTCTGTGTTATAACTA 57189   TATATGGATA 57190      TC   G    AC     CT-  AA
         AAATCTTCAAATTCGATTAA       TTCGGAT          ATCCG  TGT TTATA  TAAAAT   TC  A
         TTTTATATATGGATATTCGG                  |||||  ||| |||||  ||||||   ||
         AT                          TAGGC  ATA GGTAT  ATTTTA   AG  T
                                      TT   -    AT     ATT  CT


GAM2435  GACAACATATCATACTCGCA 57193   TATCATACTC 57194      A   T   A     T  AC   CCCCC
         TGCACACCCCCCCCCCATCAA       GCATGCACAC       GACA CATA CAT CTCGCA GC  ACC    C
         GGTAAGTTTGTGAGATGTTA       CCCC          |||| |||| ||| |||||| ||  |||
         TGTGTC                        CTGT GTAT GTA GAGTGT TG  TGG    C
                                  -   T   -     T  AA   AACTA


GAM2436  GGCCAATAGCCAATATTGAT 57210   TTCAATGTAT 57211        A  CA          TATATAACCAA    -    -
 TA
```

```
     TTATGCTATATAACCAATGA      AGATCGATAT      GGCCAAT GC  ATATTGATTTATGC       TGAAT
AATAT GGC  A
     ATAATATGGCTAATGGCCAA      GCAT          ||||||| ||  ||||||||||||||        ||||| ||||| |||
     TATTGATTCAATGTATAGAT                    CCGGTTA CG  TATAGCTAGATATG       ACTTA TTATA
CCG  /
     CGATATGCATTGGCC                          - --          TA---------    G    A   GT


GAM2437  TTAATCATATCATAATTAAG 57222   TATTTAGCAA 57223      C   C   --     ATTTTTCTTTAT    A    T
     TAATTTTTCTTTATCTAGAA      TACAAATTCT      TTAAT ATAT ATAA  TTAAGTA       CTAGA GTAAAT
C
     GTAAATTCAATTTATATTTA      ATTT          ||||| |||| ||||  |||||||        ||||| ||||||
     GCAATACAAATTCTATTTGA                    AATTA TATA TATT  AGTTTAT        GATTT TATTTA /
     AATTATCATATTATTAA                       T   C   AA     CTTAAACATAAC    A    A


GAM2438  GTGCCCTTCTCGCCTTCATT 57227   AATTGTATGA 57228      C ----   -- CTT--  T    T-    G
     TTCTTCTGCTGTCGAGCAGT      GCTGGAGATA      GTGC CT   TCTC  GC    CA TTTCT  CTGCT T
     TAGGAATTGTATGAGCTGGA      TAAG          |||| ||   ||||  ||    || |||||  |||||
     GATATAAGTGCAC                          CACG GA   AGAG  CG    GT AAGGA  GACGA C
                                T  ATAT   GT  AGTAT  T    TT    G


GAM2439  TGGGTAAAAGGGTGGAAGGG 57233   TAAGGACCAA 57234      ---      GGAAGG  G   GG-    ATTC
A   TT
     TGGTTGGTTGGTATTCCCTT      AAAAACAATA      TGGGT   AAAAGGGT    GT GTT   TTGGT   CCTT
GAC  G
     AGACTTGATGTTAAGGACCA      AAAT          |||||  ||||||||    || |||  |||||   |||| |||
     AAAAAACAATAAAATCTTTT                    ATCCA   TTTTTCTA    TA CAA   AACCA   GGAA TTG  /
     TAAAACCTA                              AAA      AAA---  A   AAA    ----   -   TA


GAM2440  GGTTCTGTATTAAGTCAGTT 57244   TATTAAGTCA 57245      GTA--   GTCAG    GT-  TG  TA
     TATGTTTTGGGTAAGATCTG      GTTTATGTTT      GGTTCT    TTAA    TTTAT   TT  GG  A
     GATGGATGAGAACATTAAGA      TGGG          ||||||    ||||    |||||   ||  ||
     CGAAGAATC                               CTAAGA    AATT    GAGTA   AG  CT  /
                                AGCAG   ACAA-    GGT  GT  AG


GAM2441  TAGCTTGCCTTAAGCAGTCT 57248   AAGCAGTCTT 57249      --  CTT--   AGT    ATAT      T   ATT
     TTATATCTTCTGTATATTAT      TATATCTTCT      TAGCT  TGC    AAGC   CTTT    CTTCTGTA ATT   T
     TTTAAAGTTTATAGGAGCAA      GTAT          |||||  |||    ||||   ||||    |||||||| |||
     AGTTCGCTTTACTCGCAATA                    ATCGA  ACG    TTCG   GAAA    GAGGATAT TGA   /
     GCTA                                    TA   CTCAT    CTT    C---      T   AAT


GAM2442  AAAAGAACCTATAATCCCTT 57257   TATGCTGCTC 57258      AAC TA    C   TC---   -  CC--    CA
     CGCACACCGCGTCACACCGC      ATTAGGAATT      AAAAG   C  TAAT CCT    GCA CA    GCGT   C
     GCTATATGCTGCTCATTAGG      ACGG          |||||   |  |||| |||    ||| ||   ||||
     AATTACGGCTCCTTTT                        TTTTC   G  ATTA GGA    CGT GT    CGCG   A
```

CTC GC A TTACT C ATAT CC

GAM2443 GTGTGACTTGGATTGGAAAT 57262 TGACTTGGAT 57263 G - - -- G AAAAATC
GTGGAGAAAAAATCGGGACC TGGAAATGTG GT TG ACTTGGATTG GAA AT TGGAGA G
CATTTCTAGGTTGTTCACAA GAGA || || |||||||||| ||| || ||||||
TCCAAGTACAGAC CA AC TGAACCTAAC CTT TG ATCTTT /
G A A GT G ACCCAGG

GAM2444 GAAAGATCATAACTAATAAC 57296 TTCAAATGTT 57297 CATAACTAA ACA AAT
TACTATA
ATTACAAATAATCCTACTAT AATCTTTC GAAAGAT TAACATT AAT CC A
AATCAATACGGTGATTCAAA ||||||| ||||||| ||| ||
TGTTAATCTTTC CTTTCTA ATTGTAA TTA GG /
--------- AC- GT- CATAACT

GAM2445 GCCCTTCTAATTAAGAAAAA 57311 TAAGAAAAAA 57312 - AATT-- G A ---- C A - A
ATCGGCGATGAAGATTAAGC TCGGCGATGA GCCCTT CT AA AAA AATC GG
GATGAAGATTA GC CG C
CGACAGTGAGCGTAATCTTC AGAT |||||| || || ||| |||| || |||||||||| || ||
ATCTCTCTTAGATTATTTGT TGGGGA GA TT TTT TTAG TC CTACTTCTAAT CG GT A
TTTCCAGAGTAGGGGT T GACCTT G A ATTC T G A G

GAM2446 GCCATTTTCGCGCGAAAACT 57332 TGAGTAATTT 57333 TTTC ACTGA GA AGT
GAATGAGGAAGTGAAAATCT CGCGTTTATG GCCAT GCGCGAAA AT GGA G
GAGTAATTTCGCGTTTATGG GC ||||| |||||||| || |||
C CGGTA TGCGCTTT TG TCT A
TT-- AA--- AG AAA

GAM2447 TATTTGCCGAGGGCCGAGTA 57338 TGTCAAAGTC 57339 C--- G AGTA CGATC GG
CGATTACC TT
GACTTTGACCGATCACGTGG CGGTGTTTTT TGC GAG GCCG GACTTTGAC ACGTGG
GTTT GTG T
GGGTTTCGATTACCGTGTTT ACGT ||| ||| |||| ||||||||| |||||| |||| |||
TTCACCTAAATTTCCGCGTA ATG TTT TGGC CTGAAACTG TGCGCC TAAA
CAC /
CGGTGTCAAAGTCCGGTGTT CATT G ---- TGGCA TT TC------ TT
TTTACGTAGGTG

GAM2448 CCTTCTTCAATAATATACCT 57345 TAATATACCT 57346 AA TATACC T TG GC T
TCAAACTTTTTGTGCGCGTT TCAAACTTTT CCTTCTTC TAA TTCAAAC TTT T GCGT A
AATATGCAAATGAGGCGTTT TGTG |||||||| ||| ||||||| ||| | ||||
GAATTTGGGGAGGAAGG GGAAGGAG GTT AAGTTTG GGA A CGTA A
GG T----- C GT AA T

GAM2449 CCATCATCAATAATATACCT 57350 TACCTTAAAC 57351 - AATA ATA -------- TGG T
TAAACTTTTGGTGCGTGTTA TTTTGGTGCG CCA TCATC AT CCTTAAA CTTT TGCGTG T
ATATGCAAATGAGGCGTTTG TGTT ||| ||||| || ||||||| |||| ||||||
AATTTGGGGAGGGTGAAAGG GGT AGTGG TG GGGGTTT GGAG ACGTAT A
TGATTGG T AAAG GGA AAGTTTGC TAA A

GAM2450 TATGTTTTCTGCTACCAAGT 57358 TGAATGTAAC 57359 - C- CA - CAA - GAT
ACACAATAGGTTGATTTAAA TAAGTAAATA TATGTTT TCTG TAC AGT ACA TAG GTT T
ACACTGAATGTAACTAAGTA GGTA ||||||| |||| ||| ||| ||| ||| |||
AATAGGTAAACATG GTACAAA GGAT ATG TCA TGT GTC CAA /
T AA AA A AA- A AAT

GAM2451 GCTGCGAGGTGATCCACGTA 57371 TCCACGTAAG 57372 GC GATC- AAGC- AGAA T
AGCCCTCAGAACCGTCTCGG CCCTCAGAAC GCT GAGGT CACGT CCTC CCG C
AAGGAGGACCCCACGTGCTT CGTC ||| ||||| ||||| |||| |||
TAGCCTCAAAGC CGA CTCCG GTGCA GGAG GGC /
AA ATTTC CCCCA GAA- T

GAM2452 GGATCTTCTGCTCTGCACAA 57380 CGACATAGGT 57381 C C - A A----- ACA
CCAGCCACACGGCACAGTGC GGCTGGTGGT GGATCTT TG TCT GCAC ACCAGCCAC CGGC
G
GCCGACATAGGTGGCTGGTG GCTA ||||||| || ||| |||| ||||||||| ||||
GTGCTAGAACACAGGATCT TCTAGGA AC AGA CGTG TGGTCGGTG GCCG /
C A T G GATACA CGT

GAM2453 TTGTGACGTAGCAATTATCG 57401 AGAGTTTAGT 57402 AG - TC T A- TCG
TATTGTGCATGTGTCGTTCA ATACTAATAT TTGTGACGT CA ATTA GTATTG GC TGTG T
TCACAGAGTTTAGTATACTA GAAG ||||||||| || |||| |||||| || ||||
ATATGAAGCGTCGCGA AGCGCTGCG GT TAAT TATGAT TG ACAC T
AA A CA T AG TAC

GAM2454 GTCAACCAGGGCACCCTCCC 57407 CAGGGCACCC 57408 G C- CCCA A GC
CCACCGAGTGCTTTAATGCG TCCCCCACCG GTCAACCAGG CACC TCC CCG GT T
GAGAGGAATGGTGGCCTGGT AGTG |||||||||| |||| ||| ||| ||
TGAC CAGTTGGTCC GTGG AGG GGC TA T
G TA AGA- G AT

GAM2455 TTGTTTTTGAACATGTGGCA 57440 TCAGTGCCAC 57441 TT CA AC GCAAT C-
TGAAA TTC
CACGCTGCAATGTACTGCCA AATTTCATTA TTGTT TGAA TGTGGCAC GCT GTA TGCCA
GGTGG T
TGAAAGGTGGTTCTATATCC ACAA ||||| |||| |||||||| ||| ||| ||||| |||||
ACCACTTGGCGTCTGCCGAA AACAA ACTT ACACCGTG TGA CGT GCGGT
CCACC A

GTCAGTGCCACAATTTCATT TT TA AC AGC-- CT TCA-- TAT
AACAA

GAM2456 GTGTTTCCCTTATAAACTCC 57456 ACTCCATTAT 57457 TCCC AACTCC TTA CT
GC - T
ATTATGTAGTTTATTAATAT GTAGTTTATT GTGTT TTATA ATTATGTAGT TTAATAT AGA
TATT CTT A
CTAGAGCTATTCTTTATTAA AATA ||||| ||||| |||||||||| ||||||| ||| |||| |||
GTAATAAATCTGTATTAGAT CACAA AATAT TAATATATTA GATTATG TCT ATAA
GAA T
TATTATATAATCTCTATAAT CT-- CTC--- TTA -- AA T T
CAACAC

GAM2457 AATAACTGTATTTCTCACTC 57464 TCTTGCTCTT 57465 C - CTTA TC-- -- AAT
ATTAT AGT
TTGCTCTTAGTTAGTCATTG AGTTAGTCAT TTTCT ACTCT TGCT GTTAG ATTGTG TCT
AATT TAC A
TGTCTAATAATTATTATTAC TGTG ||||| ||||| |||| ||||| |||||| ||| |||| |||
AGTACAAGGTATTATGAATT AAAGA TGAGA ACGA TAGTC TAACGC AGA TTAA
ATG C
CAAAGATACGCAATAAATCT - T CTA- TAAA AT AAC GTATT GAA
GATATCAGCATAGAGTAGAA
AATTGTTGTT
GAM2458 TCTTCCCCCCCATCACCCCG 57468 TCCCGGTTGA 57469 CA A- TG A A TTAA CATTA-
TT- TGG
CAATTTGCACCCAGCCTTTA TTTTTGGGTG CAT CCCCGC ATT C CCC GCCT CTA
AATTGGG CGAT C
ACTACATTAAATTGGGTTCG GGTG ||| |||||| ||| | ||| |||| ||| ||||||| ||||
ATTGGCAATGTTGTCTCCCG GTG GGGGTG TGG G GGG TGGG GGT TTGGCCC
GTTG /
GTTGATTTTTGGGTGGGTGG A- GG GT A G TG-- TTTTAG TCT TAA
GGAGTGGGTGGGTGGGGAGT
GGGTGGGTGGG
GAM2459 GTTATGAAAATTTTAATATT 57478 TGAAAATTTT 57479 A TAATATT - TAC A CTA
TTAA
TCTTCATTACAGTATATACC AATATTTCTT GTT TGAAAATTT TCTTC AT AGTAT TAC
AATCTA A
TAAATCTATTAAAATATTAG CATT ||| ||||||||| ||||| || ||||| ||| ||||||
ATTGTAGTGATACTAATATA CAA ATTTTTAAA AGAAG TA TCATA GTG TTAGAT /
GAAGATTTTAAATTTTTAGA G TTTT--- A TAA - ATG TATA
AC

GAM2460 TGGCAGAGCCTTGTTTCGTT 57487 TATAACACAA 57488 C - TT TC - --- G T ATC T
GTACATGCTGGGTGAATCGC TCTGGTCTCT TGG AGAG CC GTT GTTGTA CAT GCT GG GA
GC C
TCATGCAAGTCTTGAGCTCT CCA ||| |||| || ||| |||||| ||| ||| || || ||
ATGATATAACACAATCTGGT ACC TCTC GG TAA CAATAT GTA CGA TT CT CG A
CTCTCCA - T TC CA A TCT G - GAA T

GAM2461 TTCCTGGTTGGTATTGCGCT 57533 TATTGCGCTA 57534 GG TGCG- AC -- CA
ACCGATTCTTCACAGACTGA CCGATTCTTC TTCCT TTGGTAT CT CGAT TCTTCA G
AGACTGTCGAGATTGTGTAC ACAG ||||| ||||||| || |||| ||||||
CAAAAAGGAG GAGGA AACCATG GA GCTG AGAAGT /
AA TGTTA -- TC CA

GAM2462 CTCCATGCAAACTATCTAAA 57538 AATGTAATTA 57539 T AACTATCTAA GTCATG C
TGTAATTAGTCATGATCATG GTCATGATCA CTCCA GCA ATGTAATTA AT A
GTACCGTATAATTATATTGC TGGT ||||| ||| ||||||||| ||
TGGAG GAGGT CGT TATATTAAT TG T
- ---------- ATGCCA G

GAM2463 GCGGTTCTTGTTCTCCCTGA 57542 TCCCTGAGCC 57543 TTCT CTCC C - AGACA-
AT
GCCACCATCACCTAGACACA ACCATCACCT GCGG TGTT CTGAG CAC CATCACCT CAG
A
GATAGTCTGAAAAGGAGGTG AGAC |||| |||| ||||| ||| |||||||| |||
ATGCGTGTCTCGGAAAAACA CGCC ACAA GGCTC GTG GTAGTGGA GTC /
CCCGC C--- AAA- T C GGAAAA TG

GAM2464 CAAGTCAATAAAACACTATT 57575 TATTATGTTC 57576 A ------- C GTTCACCC-- -
CA
ATGTTCACCCTGAATCAATC ACCCTGAATC CAAGTC ATA AAACA TATTAT TGAAT
CAAT C
ACTCTGTTGCATTTATAACA AATC |||||| ||| ||||| |||||| ||||| ||||
AAAAAGTAATAATGTTTATG GTTCAG TAT TTTGT ATAATG ATTTA GTTG T
TAAATATAGACTTG A AAATGTA A AAAAAACAAT C TC

GAM2465 GTTTATACTACACTGCAGGC 57586 TACACTGCAG 57587 A - AGGCGTATG - A
GTATGCACAGCGATAAAGGT GCGTATGCAC GTTTATACT CA CTGC CACAGCG ATA A
GTATGTTGTGAACTTAAAAG AGCG ||||||||| || |||| ||||||| |||
CAGCTGAGTATAAAC CAAATATGA GT GACG GTGTTGT TGT G
- C AAAATTCAA A G

GAM2466 TCTCGAAGCACTCTATATTA 57605 TCTATATTAG 57606 GA ----- TTA AA AAGCA CTT
GAGCGAAACAAGCAGTACTT AGCGAAACAA TCTC AGC ACTCTATA GAGCG AC GTA T
TGACCTACCCCGTAGCGCTT GCAG |||| ||| |||||||| ||||| || |||
CTTATAGAGTTTCGCGCTAG AGAG TCG TGAGATAT TTCGC TG CAT G
AGA A- CGCTT TC- GA CCC-- CCA

GAM2467 CCCCCCCGTCCGCCCGCGAG 57622 TCTAATTTTT 57623 T G GCGAGTAAAGG G AA
GCACG GCG GT AG
TAAAGGCTGTCTAATTTTTT TCCGCACGCC CC CCC CT TCT TTTTTTCC CCC CCT
CTTCTT G

CCGCACGCCCGCGCCTGTCT CGCG || ||| || ||| |||||||| ||| ||| ||||||
TCTTAGGGAGGGGAAGGAGG GG GGG GG AGG AGGAAGGG GGG GGG
GAAGGG G
GGAGGGAGGGGAAGGAGGGG G A GAGGAAGGGGA G GG GA--- AG- AG
GA
AGGGAGGGGAAGGAGGGGAG
GGAGGGGAAGG
GAM2468 GGGGAGGGAGGGGAAGGAGG 57626 CGGGCCAAAG 57627 AA A A- AA-- AGGGGA
--- - AG
GGAGGGAGGGGAAGGAGGGG CTCCGGCTCC GGGAGGGG GGAGGGG GGG GGGG GG
TTCG GGCCGGCC G G
ATTCGGGCCGGCCGAGGATT CCCT |||||||| ||||||| ||| |||| || |||| |||||||| |
CGGGCCGGCCGAGCGAGCGG CCCTCCCC CTTCCCC CTC CCTC CC GAGC
CCGGCCGG C A
GCCAAAGCTCCGGCTCCCCC -- - GG GAAA GGGC-- GAG G TT
TTCCCCCTCCCGCCCC

GAM2469 CACCAACGCCACCGTCGCGA 57679 TGGGATTTAC 57680 CGCGACCTT TC T CC-- AC
TG - AG
CCTTTCTGAATCTAATACTA TACGGCCCCT CGT TCTGAA TAATAC ACCA CAC
CGGAGG AG CTCCG G
CCACCCACACCGGAGGTGAG GGGA ||| |||||| |||||| |||| ||| |||||| || |||||
CTCCGAGGTCAACCAACCTC ATA GTTGGT GGAGGG CCCC TCA TTAGGG TC
AACCA T
TGGGATTTACTACGGCCCCT ATTGG---- -- T GGCA T- TC C AC
GGGAGGTGGTTGGGTTAATA
ACGCTAGGCCT
GAM2470 GGACGCGTGAGTGTGCATGT 57698 ACGGGCCTCT 57699 --- ----- CT TCTCTCCTT C
T
CTCTCTCTCCTTCGCGGGCC GTCTTTTGGA GGACGCGTG AGTGT GCATGT C CG
GGGCCCGTCTT G
CGTCTTTGTGGAGACGGGCC ACGT ||||||||| ||||| |||||| | || ||||||||||
TCTGTCTTTTGGAACGTGCT CCTGCGCGC TCGCG CGTGCA G GT
TCCGGGCAGAG T
CGGGGCGCTTACCGCGCGTC CAT GGGCT AG TTTTCT--- C G
C

GAM2471 TAGAAAATTTATTTATTAGC 57711 TTTATTAGCT 57712 ------- TA GCTA C----------
CT
TCGTTTAGTGCTAAATCATC CGTTTAGTGC AGC TCGTT GT AATCATCAT
AACAA T
ATCAACAACTTCATTGTTTT TAAA ||| ||||| || ||||||||| |||||
CATCTTTTTTCTTTTTTATG TCG AGCAA CA TTAGTAGTA TTGTT /
ATGATTGATAACAACGATAT AAGATAT -- ATAG TTTTTTCTTTTTTCTACTT AC
AGAAGCTAATATTACAGAAG
GTCTA
GAM2472 TCATTAAATTCAGTTTTATA 57720 TCAGTTTTAT 57721 TC TTTATAATCTTT-
TTACCTCACA A
ATCTTTTTTTATTACCTCAC AATCTTTTTT TCATTAAAT AGT TTTTA GC T
AGCATTCGCGTATCATTATT TATT ||||||||| ||| ||||| ||

AAAATTTCCAACTCATTATT AGTAATTTA TTA AAAAT CG T
ATTTAATGA -- TTACTCAACCTTT TATTACTATG C

GAM2473 CCGGCAAGCACTCGTCCGAA 57724 AAGCACTCGT 57725 AAGC - TC GACAC A-- CC ATTC
GGAGGACACGCCACGCGACC CCGAAGGAGG CCGGC ACT CG CGAAGGAG GCC CGCGA CG C
CGATTCCCAGCCGCTTCGCG ACAC ||||| ||| || |||||||| ||| ||||| ||
CCCGGCTACTTCTTCGCCTG GGCCG TGA GT GCTTCTTC CGG GCGCT GC /
CAGTCCGCCGG CC-- C CC AT--- CCC TC CGAC

GAM2474 CTCCCATCTTTCCCTGACGG 57748 TCTTTCCCTG 57749 C C- G CA A -- TA
CATCTAACCGTTAAAATACG ACGGCATCTA CT CCAT TTTCCCT ACGG TCT AC CGT A
ACGTCAGGCACCGTAAGGGA ACCG || |||| ||||||| |||| ||| || |||
AAAAATGGAAG GA GGTA AAAGGGA TGCC GGA TG GCA A
A AA A AC C CA TA

GAM2475 CGCGGGGGAAGGTCGGTCCA 57756 TTGGAACAGA 57757 - T CCATTTC-- C A C C
TTTCGCTCCTATTCCGCACC AGCATTACAC CGCGGGGGAA GG CGGT GCT CT TTCCG AC T
TTCGTTTGGAACAGAAGCAT ACAC |||||||||| || |||| ||| || ||||| ||
TACACACACCGCCATTTCCC GCGCCCCTTT CC GCCA CGA GA AAGGT TG T
CGCG A - CACACATTA A C T C

GAM2476 GGGCTGTGCTAGCACGCGCC 57790 TAGCACGCGC 57791 ------ CTA CACGA GTC
ACGAGGAGGTCACGGCTCCG CACGAGGAGG GGGC TGTG GCACGCGC GGAG A
CGCGTGCAAACGCAGACAAC TCAC |||| |||| |||||||| ||||
GCCC CCCG ACGC CGTGCGCG CCTC /
CAACAG AAA ----- GGC

GAM2477 GGTTGGTACTCCCGCGCGCC 57802 GCGCCGCGCG 57803 GTA CC C G GAGAAG AA C
GGGGGAGAAGTGCGCGCGCG CGCAACCGCG GGTTG CTC GCG GCCG GG TGCGCGCGCGGC CAA G
GCAACAACGCCTTGCGCCGC GCCG ||||| ||| ||| |||| || |||||||||||| |||
GCGCGCAACCGCGGCCGTCG CCAAC GAG TGC CGGC CC ACGCGCGCGCCG GTT C
AGAACAACC AA- C- - G A----- C- C

GAM2478 TGCAATAAAAATTAAATTAT 57894 TAAATTATGG 57895 AATAAAAA AT G AACCTT AA
GGAATAACCTTAATAGTAAA AATAACCTTA TGC TTAA TAT GAAT AATAGTA T
TAGATATTATTTTTTTAGTT ATAG ||| |||| ||| |||| |||||||
CAGTATATTAGGTCTCGCA ACG GATT ATG CTTG TTATTAT A
CTCTG--- AT A ATTTTT AG

```
GAM2479  AATTGAAAAGAAATATGAAA 57899   TATGAAATGT 57900      AAAAG      AAATGTACAAT-      T
         TGTACAATTGTAATTTTATT       ACAATTGTAA       AATTG    AAATATG         TGTAATTT A
         AAATTATATAAAAATAATAA       TTTT           |||||    |||||||         ||||||||
         TATATTTAACGGCAATT                       TTAAC    TTTATAT         ATATTAAA T
                                  GGCAA      AATAATAAAAAT      T

GAM2480  CAGCACGCCACGCTCGCCGT 57909   TGGCAAAAAT 57910      ACG  C  C   - ------ TG    T
         CGTTGCGTCATAAATGACGT       GATTGGCAGT       CAGC  CCA GCT GCCG TC     GT  CGTCA A
         GGCAAAAATGATTGGCAGTT       TGGA           ||||  ||| ||| |||| ||     ||  |||||
         GGACCGCTG                    GTCG  GGT TGA CGGT AG     CG  GCAGT A
                                  CCA  -  -   T  TAAAAA  GT    A

GAM2481  TTTTCCAATTTCGTAAGTCG 57924   GATGATAGGA 57925        A--      AA----------       CAAAAACAT
 AA
         TCTACAAAAACATATACAAA       TTATTATGTG       TTTTCCA   TTTCGT          GTCGTCTA       ATAC
A
         CTGTATCTAGATGATAGGAT       GCGG           |||||||  ||||||          ||||||||       ||||
         TATTATGTGGCGGAACAATG                    AAAAGGT   AAGGCG          TAGTAGAT       TATG  /
         GAAAA                      AAC     GTGTATTATTAGGA      C--------    TC

GAM2482  AGGTTGGCTTTAAAAATGGC 57932   TAAGTTAGGT 57933        TTTAAAAAT    -   -      AGGA  CT
         TAAGTTAGGTCAAAAGGAAC       CAAAAGGAAC       AGGTTGGC       GGCTA AGTT AGGTCAAA    AC
C
         CTCAAGTGATGTTTGACTTC       CTCA           ||||||||       ||||| |||| ||||||||    ||
         AACTCTGGTCTTAATCTGTT                    TCCAATTG       CTGGT TCAA TTCAGTTT    TG  /
         AACCT                        TCTAATT--    C   C       GTAG  AA

GAM2483  GTATTGCCACCGACGACGAC 57956   ACGGCAGTCC 57957                                  ----------      G
         GACGGCAGTCCCTGCCGGCG       CTGCCGGCGA
GTATTGCCACCGACGACGACGACGGCAGTCCCT           GCCGGC A
         AAGCCGGCCGCCGCGAAGCG       AGCC           ||||||||||||||||||||||||||||||||||||           ||||||
         GCAAGGGACTGCCGTCGTCG                    CATAACGGTGGCTGCTGCTGCTGCCGTCAGGGA
CGGCCG /
         TCGTCGGTGGCAATAC                                      ACGGCGAAGCGCCGC     A

GAM2484  TTGACCTTCTGAGCTGATGT 58019   GACCTTCTGA 58020    G     TGAG TG T    ACT  -  GATG
         CTACTGACCTGATGATGGAG       GCTGATGTCT       TT ACCTTC    C  A GTCT   GA CCT    A
         AGGATCCGAAGACCTTGGAG       ACTG           ||  ||||||    |  |  ||||   ||  |||
         CTGAAGGTGGA                  AG TGGAAG    G  T CAGA   CT GGA    T
                                  G     TCGA GT C    AGC  A   GAGG

GAM2485  GACTGAATTTTCGCAGTCTC 58034   ATTACAGTGA 58035             AGTCTCTTTTC    TTCCC    T
CC
```

TTTTCCCTCTTCCCTTGTTA GGTTACACAG GACTGAATTTTCGC CCTC TTGT ATTC A
TTCCCATAGAATTACAGTGA GTGG |||||||||||||| |||| |||| ||||
GGTTACACAGGTGGAGATTC TTGACTTAGAGGTG GGAG GACA TAAG /
AGTT GACACATT--- T---- T AT

GAM2486 ACGACGGCTACAGCTCGCGG 58047 GAAGATGAGC 58048 A A C-- GAA- - GCC AG
TCGAAGCCGTCGCCCGACAG GCGAGACCGT ACG CGGCTAC GCT GCGGTC GC CGTC
CGAC A
ATAGTCGAAGATGAGCGCGA ACAG ||| ||||||| ||| |||||| || |||| ||||
GACCGTACAGGTAGTAGTCG TGC GCTGATG TGG TGCCAG CG GTAG GCTG /
ACGT A A ACA AGCG A AA- AT

GAM2487 AGGCGAAGGCTTTCGCCACT 58059 TGATAGGCGT 58060 A TT C T TTG CGTG
CCTATCTTGAAAGCGTGTCA GACGATGTCT AGGCG AGGC TCG CAC CCTATC AAAG T
TTCTTTATGATAGGCGTGAC CCGC ||||| |||| ||| ||| |||||| ||||
GATGTCTCCGCCT TCCGC TCTG AGC GTG GGATAG TTTC /
C T- A C TA- TTAC

GAM2488 TTGGATCCCAATGTCTTGTT 58064 ACTGCAGTCT 58065 - TC TTC AAT TA TTATA T
A- -- A
CAGAATGCTGCTAGATGCTT CGTGCTGCAT CCAA TG TTG AG GCTGC GATGC AGC
CGAGA GCAGT AC A
ATAAGCTCGAGAAGCAGTAC CGCA |||| || ||| || ||||| ||||| ||| ||||| ||||| ||
AAGAGTAAACTGCAGTCTCG GGTT AC AAT TC TGACG CTACG TCG GCTCT
CGTCA TG G
TGCTGCATCGCAGTCTACTA C C- TTA ATC -- ----- T GA AA A
TTTAACCACTTGGGGGCCAA

GAM2489 GATGAACTGTCCTCAACAAG 58075 CTTGTTGTTG 58076 A GTCCT TGAAAA T
TATGAAAAGCAATTATTTGT TAAGATTATT GATGA CT CAACAAGTA GCAA T
GAAGTTACTTGTTGTTGTAA ||||| || ||||||||| ||||
GATTATT TTATT GA GTTGTTCAT TGTT A
A ATGTT TGAAG- T

GAM2490 CCTGCAGGCATTTTGTGAAA 58090 TTGATGAGAG 58091 T GCA AAGG ATGAAAGCTA
GAAA T
AGGGTAAAGTATGAAAGCTA CCTTAAAATG CC GCAG TTTTGTGAA GTAAAGT CTCTCA
AGTAC T
CTCTCAGAAAAGTACTTATG ACTT || |||| ||||||||| ||||||| |||||| |||||
TATTGATGAGAGCCTTAAAA GG CGTC AAAACACTT TATTTCA GAGAGT
TTATG A
TGACTTTATATTCACAAAAC T --- A--- GTAAAATTCC AG-- T
TGCTGG

GAM2491 GCGAGAAAGCACGCAAATCA 58099 TATTGCGTTG 58100 - - A- GTAA T- AC
TT GG

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    AAGTCTAGTGCGTAATTCAC      AGAGTGTTGT       GCACGCAAATCAAA GTCT  GTGC   TTCAC  CACT
 CGGCGTAAT  GT  T
    TCACTACCGGCGTAATTTGT      GGGC          |||||||||||||| ||||  ||||   |||||  ||||  |||||||||  ||
    GGTTATGCTATTGCGTTGAG                  TGTGTGTTTGGTTT CGGG  CATG   GGGTG  GTGA
GTTGCGTTA  CG  T
    AGTGTTGTGGGCGTAGTACG                  G          T   GG   ATGC   TT   GA      T-  TA
    GGGGCTTTTGGTTTGTGTGT
    GATTAATATGC
GAM2492  CATTTGTAATAGAAAATTTA 58103   TAGAAAATTT 58104      GTA  -      A  A   GAAA
    AGAGAAGAAAAAGAATTCCT      AAGAGAAGAA       CATTT   ATA GAAAATTT AG GAA    A
    AAAATTTTTATATGAAAGTG      AAAG          |||||   ||| ||||||||  || |||
                              GTGAA   TAT TTTTTAAA TC CTT    /
                                AG-   A      A  -   AAGA


GAM2493  TAGATTATAAACATAGACCT 58157   TATAAACATA 58158       --  ----       CTT    AT
    TGCCTATTGAAAGGTCTAGT      GACCTTGCCT       TAGATT  ATA   AACATAGAC   GCCT  T
    CTATGTTGAACTATTAGATC      ATTG          ||||||  |||   |||||||||   ||||
    TA                        ATCTAG  TAT   TTGTATCTG   TGGA  G
                                AT   CAAG       ATC    AA


GAM2494  CGGGAAACTGCGTTTTGGAT 58164   TGCGTTTTGG 58165      AAACT-        TAA-    A   G
    AATGTGCAGGACGTATGTTC      ATAATGTGCA       CGGG     GCGTTTTGGA    TGTGC GGAC T
    GTACGGTCCTCCAGAACGCC      GGAC          ||||     ||||||||||   ||||| ||||
    GCGTACCCG                   GCCC     CGCAAGACCT   GCATG CTTG A
                              ATGCGC        CCTG    -   T


GAM2495  TTTGGATTGTAAGCGCTATC 58177   TGGATTGTAA 58178      -  T   AA   T      --   ACG
    ACGTATGCGACGGGGGACGC      GCGCTATCAC       TTTG GA TGT  GCGC ATCACGTA  TGCG   G
    AACTGCGTGATCGTGTACAC      GTAT          |||| || |||  |||| ||||||||  ||||
    TCGCGAA                     AAGC CT ACA  TGTG TAGTGCGT  ACGC   G
                              G  C   --   C       CA    AGG


GAM2496  TATAACGTCTAACTTACAAC 58180   TAACGTCTAA 58181     TA      ACT      CG  CA     AA
    ACGGTCATAATAGAATCCCT      CTTACAACAC       TA  ACGTCTA   TACAACA  GT  TAATAG  T
    ATTAACATGTTGTATATAGA      GGTC          ||  |||||||  |||||||  ||  ||||||
    TGTCGTA                     AT  TGTAGAT   ATGTTGT  CA  ATTATC  /
                              GC      AT-      A-  --     CC


GAM2497  ATGATTTAGTTACTTTAATA 58186   TTCAGGTATT 58187        A    CTTT    A  GTT      AAATTGATT
    ACCGTTAGACATAAAATTGA      TAACGAATCA       ATGATTT GTTA    AATA CC   AGACATA       C
    TTCTATGAAAACTGTGTTTC      T             |||||||  ||||    ||||  ||   |||||||
    AGGTATTTAACGAATCAT                      TACTAAG CAAT    TTAT GG   TTTGTGT       /
                                -   ----   -  AC-      CAAAAGTAT
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GAM2498 CTAATATAGTTAATAGTGTA 58204 TAGTGTACTA 58205 A C CAAACA TAAAAA----- C--
CCCAA
CTACAAACAGGCGATGGTAA CAAACAGGCG TAAT GTGTA TA GGCGATGG GACT
TTCGTCTT A
AAAGACTCTTCGTCTTCCCA ATGG |||| ||||| || |||||||| |||| ||||||||
AAATGTTAGAGACGGAAATA ATTA CATAT AT CCGCTATC TTGA AGGCAGAG
A
GTTGTCAAGATTCTCTATCG C A C----- TCTTAGAACTG TAA ATTGT
CCCTAATATACCATTAAAAA
TTGTTAG
GAM2499 GTTCTTAAATAGCAGCCAGG 58213 TCTGTCAGTT 58214 --- ----- CT- --- T TCCTCT-
C G
GCCTTACCGACCAGTTTTCG GGTGTAAGCC GCAGC CAGGGC TACCGAC CAG
TTTCGTG TGG GCG C
TGTCCTCTTGGCGCGGCTCT CTGC ||||| |||||| ||||||| ||| ||||||| ||| |||
GCCTATATATGCCACGGAAT TGTCG GTCCCG GTGGTTG GTC AAGGCAC ATC
CGT T
CTGTCAGTTGGTGTAAGCCC TAG CTACC AAT ACT T CGTATAT - C
TGCCATCGCTGTGATATTTT
TATTGCGTTGC
GAM2500 TCTGCTATTCGCCTACCTAG 58226 GGGAAACCTC 58227 GCT- - - - A TC AA-- CC
GGAAACCTCGAAAAAAATCC GAAAAAAATC TCT ATTCGCCTA C CT AGGG AACC GAA
AAAT T
TAAATTTAACGTTTTTGGTT CTAA ||| ||||||||| | || |||| |||| ||| ||||
GCCCTGAGTGTTGGGCGAAT AGA TAAGCGGGT G GA TCCC TTGG TTT TTTA /
TGAAAGA AAGT T T G G TT GCAA AA

GAM2501 GGAATTTTTCTTGGTTTTCG 58237 TTTTTCTTGG 58238 TTT GG TTT A AT
GGTGTGATTTTATATTCATG TTTTCGGGTG GGAA TTCTT TTTTCGGGTGTGA TAT TTC G
TAGAAAGTGTTTCACACCTG TGAT |||| ||||| |||||||||||| ||| |||
AGGAGAAGAATCTTTCC CCTT AAGAA AGGAGTCCACACT GTG AAG /
TCT G- TT- A AT

GAM2502 TCGAATTCAAACGTGCGACA 58253 TTCATGTTTC 58254 C G TG TATTGGTTC
GGAAC
GTGGCTATTGGTTCGGGCGA TGTGCACATT TCGAATTCAAA GTGC ACAG GC
GGGCGACC C
CCGGAACCCGTTAGGTCGTT TGAA |||||||||| |||| |||| || ||||||||
CATGTTTCTGTGCACATTTG AGCTTAAGTTT CACG TGTC TG CTTGCTGG /
AATTCGA A - TT TA------- ATTGC

GAM2503 ACGCGCATGTTGAAGTCGAG 58270 TTGAAGTCGA 58271 C AT- TGA CG- TC G
GTGTCCACACAAGTAGTTGT GGTGTCCACA ACG GC GT AGT AGGTG CACACAA T
GTGTACCTAACGCTCTTGCC CAAG ||| || || ||| ||||| |||||||
CAGCACGT TGC CG CG TCG TCCAT GTGTGTT A
A ACC TTC CAA -- G

GAM2504 ATCGGCCCACTCTTGCATTT 58278 TGAAGGAGGA 58279 G CA--- GCA G A
CTTCGGGGACGTTTGTGAAG GAGAGGATAC ATC GCC CTCTT TTTCTTCG GG C
GAGGAGAGAGGATACGGCGG GGCG ||| ||| ||||| |||||||| ||
AT TAG CGG GAGAG GAGGAAGT TT G
G CATAG AG- G T

GAM2505 GTTCCCTTCTATGATAATGG 58351 TATGATAATG 58352 TTCTAT AAT TTT TTATG-- GTC ACA
ATTTGGCCTTATGGCTGTCG GATTTGGCCT GTTCCC GAT GGA GGCC GCT GGCA G
GCAACAGGCCTGCCAAAGTA TATG |||||| ||| ||| |||| ||| ||||
ATCATCGGCCCACTCTTGCA CAGGGG TTA TCT CCGG TGA CCGT /
TTTCTTCGGGGAC CTTCT- CGT CAC CTACTAA AA- CCG

GAM2506 GGATAAATAATCGTATTATT 58359 AATCGTATTA 58360 GT- T AAT G AAT G GGG A GGCA CT
GTAATAGGGAAATTTAGGGG TTGTAATAGG AATC ATTA TGT AG GA TTAGG GAG TTTCA TGGTG GAG A
AGGGGTTTCAATGGTGGGCA GAAA |||| |||| ||| || || ||||| ||| ||||| ||||| |||
GAGCTAAACTTAACACCAAT TTAG TAAT ACA TC CT AATCC TTC AAGGT ACCAC TTC /
GGAAAGCTTGCCTAATCGCT ATT T C-- G --- G GA- A AA-- AA
CACATTAATTTAGATTTTCG
ACTTGTGTCC
GAM2507 ACGCGACAACTTCGAGAACC 58368 CGAGATAGAC 58369 C AA- AACC G CCG- GA
TCGGGGTCTCCGCGGCCGAC CGCGACTCGG ACG GAC CTTCGAG TCG GGTCT CGGCC C
CTGGCCGAGATAGACCGCGA AGGT ||| ||| ||||||| ||| ||||| |||||
CTCGGAGGTCGTCCGT TGC CTG GAGGCTC AGC CCAGA GCCGG /
- CTG ---- G TAGA TC

GAM2508 GCGCACCGCCGCCGAGATCG 58373 TCAGAAGTCC 58374 C - C GAT G AA------- A C G G
AGTGTCAGAAGTCCAAGCGC AAGCGCGTCG GCG AC CGCCG CGA CGAGT TCAG GTCCA G GC TC T
GTCGTGGAGGCCCTGGACGT TGGA ||| || ||||| ||| ||||| |||| ||||| | || ||
CGTCATCCTGAAGCTCGTCG CGC TG GCGGC GCT GCTCG AGTC CAGGT C CG AG /
TCGGCGAGTTCGC T A T --- A CTACTGCTG - C G G

GAM2509 CAAGATGAATCGGTGAAGTC 58395 GTGAAGTCTC 58396 AATC T T TAG GCCTT- TA
TCCATAGAGTGCCTTATTTG CATAGAGTGC CAAGATG GGTGAAG C CCA AGT ATTTG C
TACAGCAAGTTTCTAAATTA CTTA ||||||| ||||||| | ||| ||| |||||
CTTGGGTTTTCATCACAACG GTTCTGC CTACTTT G GGT TTA TGAAC /
TCTTG AACA T - TCA AATCTT GA

GAM2510 CGGGTTCTGGTGCGGGTTTC 58414 GTTTCGGTGC 58415 G TG G TT G TG G TT G G TT G G TT G GGG
GGTGCGGGTTCTGGCGCGGG GGGTTTCGGT CT G C GG TC G C GG CT GCGC GG CT GCGC GG CT GCGC T
TTCTGGCGCGGGTTCTGGCG GCGG || | | || || | | || || |||| || || |||| || || ||||
CGGGTTTCGGTGCGGGTTTC GG C G CT GG C G CT GG CGTG CT GG CGTG CT GG CGTG T
GGTGCGGGTTTCGGTGCGGG G GT G TT G GT G TT G G TT G G TT G GCT
TTTCGGTGCGGGTTTCGGTG
CGGGTTTCGG
GAM2511 GGGGCGGGAGGGGGAAGGGG 58419 AGGGGGAGCC 58420 C A- CC CTTT- CCCGC-- CTC C A
GAGCCGGAGCTTTGGCCCGC GGAGCTTTGG GGGAGGGGGA GGGGGAG GGAG GG TCG GGCCGGCC GA T
TCGCTCGGCCGGCCCGAATC CCCG |||||||||| ||||||| |||| || ||| |||||||| ||
CTCGGCCGGCCCGAATCCCC CCCTCCCCTT TCCCCTC CCTC CC AGC CCGGCCGG CT C
TCCTTCCCCTCCCTCCCCTC T CC -- CCCTT TCCCCTA --- - C
CTTCCCCTCCCTCCCC

GAM2512 GATTTGGCCAAATGTATCCA 58491 TAACTAGTGT 58492 CC G CATCATAA--- GG ATAA G GTAAAC T
TCATAATCTGGGTTATAAAC AGAAAACAGA GG AAAT TATC TCTG TT AC GGT AAGAATATA G
GGGTGTAAACAAGAATATAT GATA || |||| |||| |||| || || ||| |||||||||
GTTTATATTTTTTAACTAGT CC TTTG ATAG AGAC AA TG TCA TTTTTATAT T
GTAGAAAACAGAGATAGTAA TT - ATAAATGATAG AA GATG A AT---- T
ATAGATAGTTTTTCCAGATC

GAM2513 TTATGTAAACAAGTTTATAA 58519 TAAGTTGTGA 58520 AACAA-- T AT TA
GTTGTGAAGAAGATAGTAAA AGAAGATAGT TTATGTA GTTTATAAGTTG GAAGAAG AG A
TTTTCCTTTTTTTAATTTAT AAAT ||||||| |||||||||||| ||||||| ||
AGGCGAGCCCATACATGA AGTACAT CGGATATTTAAT TTTTTTC TT /
ACCCGAG - CT TA

GAM2514 AGACCCTGAGTGGTATACTG 58530 TGAGATGTGC 58531 - --- - TC CT CG TC - - CTGCT CA
TCTCTGTCCGTGGTCCTGAC GATCTGACCA ATACTGT CTC TG CGTGGTC GA GT CATC C GCA AATAA C
GGTTCCATCCGCACTGCTAA TGTT ||||||| ||| || ||||||| || || |||| | ||| |||||
TAACACTTTTATTTTTGCTG TATGACA GAG AC GTACCAG CT CG GTAG G CGT TTATT /
AGATGTGCGATCTGACCATG A AAC T TT T- AG T- A T TT--- TT
TTCATGAGCAAACAGTATAA
CCTATGGCCT
GAM2515 AATATAGTACCTAAAGGATA 58534 TATAGTACCT 58535 ACCTAA TA A CAA
TTATTCTCAAATACAAGAAC AAAGGATATT AATATAGT AGGA TT TTCT A

AAGTTCCTGATAATTATATT ATTC |||||||| |||| || ||||
TTATATTA TCCT AA AAGA T
ATAG-- TG C ACA

GAM2516 GTAATTATATATAATATAAT 58540 TATAATATAA 58541 - T ATC T TTAT TA
CTATATAATAATATTTATTT TCTATATAAT GTAAT TATA ATAATATA TATATAA AATAT
TTATTGT A
ATTGTTAAATACAATAACAT AATA ||||| |||| |||||||| ||||||| ||||| |||||||
ATTTTATATATAATATATTA TATTA ATAT TATTATAT ATATATT TTATA AATAACA /
TTTATATATTAT T T AAT - C--- TA

GAM2517 TTTATACATCACATCATTTT 58548 TACATCACAT 58549 CAT---- GTCAT T
TGTCATTTAAATCTTTTAAT CATTTTTGTC TTTATACATCA CATTTTT TTAAA C
CCTAAAAAATGTCCAATTTG ATTT |||||||||||| ||||||| |||||
ATGTGTAAA AAATGTGTAGT GTAAAAA AATTT /
TTAACCT ATCCT T

GAM2518 CGGTCTTTCCGTTATGGAAG 58569 TGGAAGGTTT 58570 GTTAT- AA TTT GT
GTTTGCTTACGGTCCACGTA GCTTACGGTC CGGTCTTTCC GG GG GCTTACG C
GGTTCTCCGACCTTGCGAGG CACG |||||||||| || || |||||||
AAAGATTG GTTAGAAAGG CC CC TGGATGC /
AGCGTT AG TCT AC

GAM2519 GATTAGATCTAAGTTGCTAG 58574 TGACATAGCA 58575 TCTAAGT - CAC TT
TCATGCACGTTTTAAGCTCT TATTCTAGTT GATTAGA TGCTA GTCATG GT T
ATGACATAGCATATTCTAGT ||||||| ||||| |||||| ||
T TTGATCT ACGAT CAGTAT CG /
TAT---- A CT- AA

GAM2520 TGACATAAGCCTTGGGATCT 58604 TTAGATCTAG 58605 ATA- TG TT TC TCT
TTGTGTCTGTCTAATGTCAC GCTACTGGTC TGAC AGCCT GGATCT GTG TG A
TGCTTAGATCTAGGCTACTG A |||| ||||| |||||| ||| ||
GTCA ACTG TCGGA TCTAGA CGT AC A
GTCA -- TT C- TGT

GAM2521 CGTCCGCCTGTACGCGGACC 58621 TTTCTGGTTT 58622 C - T A TC AGGCG T T
GATCACCAGAAGGCGGACAT TTGGACTGTG CGTC GCC TG ACGCGG CCGA ACCAGA
GACAT GGGC G
TGGGCTGTGGTTCATGTTTC TTCG |||| ||| || |||||| |||| |||||| ||||| ||||
TGGTTTTTGGACTGTGTTCG GCGG TGG GC TGTGTC GGTT TGGTCT TTGTA CTTG T
TGGTTGGCG T T T A TT ----- - G

GAM2522 GTATTTTATTGGGAATATTG 58625 TGTTTCGGAT 58626 TT- TT -- --- GA

GCGGGGATAAACCTGTTTCG GTTTACCCTT GTA TTA GGG AATATT GGCGGG T
GATGTTTACCCTTAATCTTA AATC ||| ||| ||| |||||| ||||||
C CAT AAT CCC TTGTAG TTGTCC A
TCT T- AT GCT AA

GAM2523 ACCGCGGAGCTTATAGCCGC 58630 TAGCCGCCTG 58631 C AGCC ---- TT G CT
CTGCCTTGCTCGCTGCTGGA CCTTGCTCGC ACCGCGGAG TTAT GCCT GCC GCTC CTG
G
CAGGAGCTCGGTTGTTGGGC TGCT ||||||||| |||| |||| ||| |||| |||
ACTGATAACTCCGTGGT TGGTGCCTC AATA CGGG TGG CGAG GAC /
- GTCA TTGT CT - AG

GAM2524 AAAGGTTGACGGGCATTCTT 58652 GGGCATTCTT 58653 TGAC TTCT GCTCCT
AATTATGTTGCTCCTTTTAC AATTATGTTG AAAGGT GGGCA TAATTATGTT T
CAAATGTGGTTATGCTGCTT CTCC |||||| ||||| ||||||||||
TACTGCCTTT TTTCCG TTCGT ATTGGTGTAA /
TCAT CGT- ACCATT

GAM2525 GATGTACATTCCAACACTGC 58665 TGTACATTCC 58666 TCCAAC TG---------- TTT G
TGCCATATTTTTGGAGAAAT AACACTGCTG GATGTACAT ACTGC CCATAT TGGA A
TCAATATGGATATGATATTA CCAT ||||||||| ||||| |||||| ||||
TTTGCAGTATGTATATC CTATATGTA TGACG GGTATA ACTT A
------ TTTATTATAGTATA --- A

GAM2526 ACATTGAGTATCTAAATTAT 58685 TAAATTATAC 58686 AG CT-- A AAA
ACAAGTATTAAAAATACTAG AAGTATTAAA ACATTG TAT AAATTATACAAGT TTA A
ATTTGTGTAGTTTTAAAATA AATA |||||| ||| ||||||||||||| |||
AATAATGT TGTAAT ATA TTTGATGTGTTTA GAT /
AA AAAT - CAT

GAM2527 ACTAGTCACAAATCAGATCA 58692 TCCAAACTAT 58693 A ACAAATCA TC CAAA - T
ATGGTCAAAGATCTTCGGAA TACTCCAGGG ACT GTC GA AATGGT GAT C T
TCCAAACTATTACTCCAGGG ATAA ||| ||| || |||||| ||| |
ATAAGT TGA TAG CT TTATCA CTA G C
A GGAC---- CA AAC- A G

GAM2528 GATTAGTTAATATCGATGAT 58714 TTACATTAAA 58715 T GATG AAA CATAAG
TTAATAAAGGGAGCCATAAG TGATGTTATT GATTAGT AATATC ATTTAAT GGGAGC T
TGTTAAAGTTCTTACATTAA AGTC ||||||| |||||| ||||||| ||||||
ATGATGTTATTAGTC CTGATTA TTGTAG TAAATTA TTCTTG /
- ---- CA- AAATTG

GAM2529 GCGTTACTCTTCCCACTTAT 58720 TACTCTTCCC 58721 TT CTTCCCA T- TAGG

AATATTTTAGGAAAACAAAT ACTTATAATA GCG ACT CTTA AATATTT A
ATTTTTAAGCCAAAGTTTCG TTTT ||| ||| |||| |||||||
T TGC TGA GAAT TTATAAA /
TT AACC--- TT CAAA

GAM2530 TTTATTTATTAAATATAGAC 58734 TATTTATTAA 58735 A AAA GAT - AAA
GATCCCATAAAATATAATGA ATATAGACGA TTT TTTATT TATAGAC CC CAT A
GGTTAGTTTATAGAATAGGA TCCC ||| |||||| ||||||| || |||
AGA AGA GGATAA ATATTTG GG GTA T
A G-- ATT A ATA

GAM2531 CGTGACTTCCGGTCATGTGA 58739 TCAGCCCAAT 58740 ----- A A CA
CTTCCGGTGACGTGTTTCCG AGTTAAGCCG CGGTCATGTGACTTCCGGTGACGTGTTTCCGGCT
GTT GGTTGACC CGCG T
GCTGTTAGGTTGACCACGCG GAAA |||||||||||||||||||||||||||||||| ||| |||||||| ||||
CATGCCGCGCGGTCAGCCCA GCCAGTACACTGAAGGCCACTGCACAAAGGCCGA TAA
CCGACTGG GCGC /
ATAGTTAAGCCGGAAACACG ATTGA C C CG
TCACCGGAAGTCACATGACC
GGAAGTCACG
GAM2532 GTATTTGGTGGAGTCGTAAA 58762 AAGCTGACAG 58763 - T CG GACAG TCCC GC-
GG GCCCG
GCTGACAGAGTCCCTGGGTG AGTCCCTGGG GT AT TGGTGGAGT TAAAGCT AG TGGGT
GCT GCT C
CGCTGGGCTGCCCGCACTGA TGCG || || ||||||||| ||||||| || ||||| ||| |||
AGTAAAGTTAAACTCACTCC CA TG ACCACCTCG GTTTTGG TC ACTCA TGA TGA
/
CTAGACAGGTTTTGAGCTCC A C A- ACAGA CCTC AAT AA AGTCA
ACCACGTAAC

GAM2533 GTTAGAGACGGAAATAGTTG 58799 TAACATGGTA 58800 ----- AAGAT CG TAATA
TAAAA TA T
TCAAGATTCTCTATCGTCCT ACTGGAATAG AATAG TTGTC TCTCTAT TCC TACCAT
ATTGT GA T
AATATACCATTAAAAATTGT AGAT ||||| ||||| ||||||| ||| |||||| ||||| ||
TAGATTTTTCCGCAATAACA TTATT GATAG AGAGATA AGG ATGGTA TAACG
CT T
TGGTAACTGGAATAGAGATA GTCTA CCGAT -- TCA-- CAA-- C- T
GCCGATAGATCTGTTATTTC
AGTCGCTGAT
GAM2534 GAGAGGCTGGCAGATTGAGC 58812 TAGAGCCTGG 58813 G ATT - GGG CT A A
CCTGGGAGGTTCTCTCCAGC GTGTTCCCTG GAGAG CTGGCAG GAGC CCT AGGTTCT CC
GC C
ACTAGCAGGTAGAGCCTGGG CTAG ||||| ||||||| |||| ||| ||||||| || ||
TGTTCCCTGCTAGACTCTC CTCTC GATCGTC CTTG GGG TCCGAGA GG CG T
A C-- T --- T- A A

GAM2535 CACGCTTGCTTGCTTAAAGC 58829 GCTTGCTTGC 58830 T AA-------- CCTCTT
CCTCTTCAATAAAGCTGCCA TTAAAGCCCT CACGCT GCTTGCTT AGC C
TTTTAGAAGTAAGCTAGTGT CTTC |||||| |||||||| |||
G GTGTGA CGAATGAA TCG /
T GATTTTACCG AAATAA

GAM2536 AAGACCCTGGTCTGTTAGGA 58843 TGTTAGGACC 58844 A ---------- ACCC G
CCCTTTCTGCTTTGGGAAAC CTTTCTGCTT AAG CCCTG GTCTGTTAGG
TTTCTGCTTTGG A
CGAAGCAGGAAAATCCCTAG TGGG ||| ||||| |||||||||| ||||||||||
CAGATTGGCGCCTGAACAGG TTC GGGAC TAGACGATCC AAGGACGAAGCC A
GACTT A AAGTCCGCGGT CTAA A

GAM2537 GCCATACAGTGGACCAATAC 58852 CAGTGGACCA 58853 ACA GGA--- A- - T
GGGATAATGTTTGTCCTCGC ATACGGGATA GCCAT GT CCAAT CG GGATAA G
AATTGGATAGAAACGTAGTG ATGT ||||| || ||||| || ||||||
GC CGGTG CA GGTTA GC CCTGTT /
ATG AAGATA AC T T

GAM2538 TGGTTTGATATTTCATATAC 58859 TATTTCATAT 58860 A T AGATA C ATT AA--
A CT
TATTTATAAGATATCCATAT ACTATTTATA TTCAT TACTATT ATA TCCATAT ATC GTGT
ACTAAATA CGT T
CATCATTGTGTAAACTAAAT AGAT ||||| ||||||| ||| ||||||| ||| |||| |||||||| |||
AACGTCTTCTATGTATTTAG AGGTA GTGGTAG TAT AGGTGTA TAG TACA
TGATTTAT GTA /
TAAGGACATTGGATATGTGG C - GAAA- - GT- GGAA - TC
AAAAGTATGATGGTGCATGG
AAGTTAGTACA
GAM2539 GTCCGCTGTTTCCGTTAATA 58866 TAATAGCACG 58867 CGCTG TAATAAT TT AA GC
- C
ATACTATTTTCGTAACTGGC ATCGTGGTTA GTC TTTCCGT ACTAT TCGT CTG GGA
TTATT A
GGATTATTCATAAATAACTC ACAA ||| ||||||| ||||| |||| ||| ||| |||||
TAATAGCACGATCGTGGTTA CAG AAAGGTA TGGTG AGCA GAT TCT AATAA T
ACAATATGGAAAAACTTGAC TTCAA TAACAAT CT C- AA C A

GAM2540 GGTGGTGGATGGGTGATGAC 58881 TGGTGGATGG 58882 GG G T A TTGGTAG
AGGGTTGGTAGGTCGTAAAT GTGATGACAG GGTGGT AT GG GATGAC GGG G
CCCGGTCATCCTGGTAGCCA GGTT |||||| || || |||||| |||
CT TCACCG TG TC CTACTG CCC T
A- G - G TAAATGC

GAM2541 CGTGCTACTGAGATATACTA 58893 TAGAGTATAA 58894 GCTA--- CTACCGA A GA
GTTAC A

CCGATATAGAGTATAATGAT TGATTTAGTT CGT CTGAGATATA TATAGAGT TAAT TTTA
TTTAAT A
TTAGTTACTTTAATAACCGT ACTT ||| |||||||||| |||||||| |||| |||| ||||||
TAGACATAAAATTGATTCTA GCA GACTTTGTGT GTATCTTA GTTA AAAT
AGATTG C
TGAAAACTGTGTTTCAGGTA ATTTATG CAAAA-- - -- AC--- C
TTTAACG

GAM2542 ACCGCGGACGTCATCGCCGC 58900 TCGCCGCCTG 58901 C-- TC -- CT TT G CT
CTGCCTTGCTCGCTGCTGGA CCTTGCTCGC ACCGCGGA GTCA GCC GC GCC GCTC CTG
G
CAGGAGCTCGGCTGTTGGGC TGCT |||||||| |||| ||| || ||| |||| |||
ACTGACAACTCCGTGGT TGGTGCCT CAGT CGG TG CGG CGAG GAC /
CAA CA GT T- CT - AG

GAM2543 GGAAATGCGCCAGAGGGTGA 58927 TGACAGGTAT 58928 TGCG A A- C---- - G
TGCTGGGTCGCACGGCGCCA CTACTGGACT GGAAA CCAG GGGTG TG TGG GTC C
ACTGACAGGTATCTACTGGA TTTC ||||| |||| ||||| || ||| |||
CTTTTCC CCTTT GGTC TCTAT AC ACC CGG A
TCA- A GG AGTCA G C

GAM2544 GTATAATCAGTTTGATGTTG 58943 TGGCGGCAAA 58944 AAT T TGTG AATAC AT A
C
TGCATTTAATACCCATCGCA TGATTACATT GTAT CAGT TGATGT CATTT CC CGCAGT TC
A
GTATCCAAGGACACTGTGGC ACAT |||| |||| |||||| ||||| || |||||| ||
GGCAAATGATTACATTACAT CATG GTTA ATTACA GTAAA GG GTGTCA AG A
TGCAGTAC AC- C TTA- C---- CG C G

GAM2545 GTGCGGTGCACGTTGACATC 58948 TGTGGACAAC 58949 G - - ACA A- A AGG
ATGTTCAAAGTAGGCGAGGC GAGCTGACGC GT CGGTG CA CGTTG TC TGTTCA AGT C
TGTGGACAACGAGCTGACGC TGAC || ||||| || ||||| || |||||| |||
TGACACCGGAT TA GCCAC GT GCAGT AG ACAGGT TCG /
G A C CG- CA G GAG

GAM2546 CGTACTACTGAGATATACTA 58962 TAGAGTATAA 58894 ACTA--- CTACCGA A GA
GTTAC A
CCGATATAGAGTATAATGAT TGATTTAGTT CGT CTGAGATATA TATAGAGT TAAT TTTA
TTTAAT A
TTAGTTACTTTAATAACCGT ACTT ||| |||||||||| |||||||| |||| |||| ||||||
TAGACATAAAATTGATTCTA GCA GACTTTGTGT GTATCTTA GTTA AAAT
AGATTG C
TGAAAACTGTGTTTCAGGTA ATTTATG CAAAA-- - -- AC--- C
TTTAACG

GAM2547 AGGGTACGTCTATCGGTCCG 58963 CCAGCACAGG 58964 TC TCC- G GAAA GGAT-
GTTA CG AG

GCTGGCCCGAAAGGCGGTGG TGGTAATCGC G TATCGG GGCT GCCC GGCGGT
CCTGTGT GGGTT T G
ATCCTGTGTGTTAGGGTTCG TATA | |||||| |||| |||| |||||| ||||||| ||||| |
TAGGTGGTAAATCCCAGCAC C GTGGCC TCGG CGGG TCGCTA GGACACG
CCTAA G /
AGGTGGTAATCGCTATAGGG CA CTAT A ATA- ATGGT AC-- AT GT
CAGGCTTATCCCGGTGACCG
CTTCCCT
GAM2548 GGGGCCTCCGGTGTGAATAA 58973 CCTCCGGTGT 58974 C - G ATAAGCCCT GA
GCCCTCGTCTGGAGCATCAG GAATAAGCCC GGGGC TC CGGT TGA CGTCTG G
ACGTTAAACTGAGACGTCCC TCGT ||||| || |||| ||| ||||||
CCCTG AG GTCA ATT GCAGAC C
C A A --------- TA

GAM2549 CCCCACGTATGGCAACGCCG 58982 TATGGCAACG 58983 -- GG- G TTAAAA-- T
CTTAAAACCCTTCGGGGACA CCGCTTAAAA CCCCAC GTAT CAAC CCGC CCC T
GCTATGCGGGTTGACAATGC CCCT |||||| |||| |||| |||| |||
CAGTGGGG GGGGTG CGTA GTTG GGCG GGG C
AC ACA - TATCGACA G

GAM2550 GCGGCGCCGTGCTACAGGCG 58992 GTGGCATTCC 58993 ---- TG A G G A AA- - -
T
GCAAGGGGAAAAATCCTTCG CTCCCTTAGC GCGGC GCCG CT CA GC GC AGGGGA AAT
CC TTCGGG G
GGTGACCCCGGGTGGCATTC AGCA ||||| |||| || || || || |||||| ||| || ||||||
CCTCCCTTAGCAGCATGAGT CGTCG TGGT GA GT CG CG TTCCCT TTA GG
GGGCCC A
GTGGTGGTAGCTGC ATGG GT - A A A CCC C T C

GAM2551 GGTCCGCTGCCTAGCTACAT 59034 CGACGGGAGT 59035 GT - -- TA TACA TT- ACACG
CCTGTTTTGCACACGGCTCC TTGCGGTCAA G C CGCT GCC GC TCCTGTT GC G
AGCTTCGACGGGAGTTTGCG GCGA | | |||| ||| || ||||||| ||
GTCAAGCGAGGTC C G GCGA TGG CG AGGGCAG CG /
TG A AC -- TTTG CTT ACCTC

GAM2552 GATATCTCATTATTTGATTA 59042 TGTTATATTA 59043 TCTC- T- -- - CA
TGTAGCGCCAGGAGCTGTTA AGTCAATCTA GATA ATTA TTGATT ATGTAGC GC G
TATTAAGTCAATCTAATCAC ATCA |||| |||| |||||| ||||||| ||
TCTATC CTAT TAAT AACTGA TATATTG CG /
CTCAC CT AT T AG

GAM2553 CTTTCAACCATAAATAATGT 59047 ACCATAAATA 59048 A ---- TAATG- TTT A
CGTTGTTTTAAATTTATATC ATGTCGTTGT CTTTC ACCA TAAA TCGTTG TA A
GATGAACTAATTTTAAATCT TTTA ||||| |||| |||| |||||| ||
GGTGGAAAG GAAAG TGGT ATTT AGTAGC AT T

G CTAA TAATCA TAT T

GAM2554 TTGTATATATTATAGTTTCA 59062 TAACTGCAGA 59063 TATA A TCATTA C--- CATACC
CCTT- A
TTATGGGCATTTTATCATAC TGAAAAATAA TTG TATT TAGTT TGGG ATTTTAT
TCTGCA TC A
CTCTGCACCTTTCAACTGAC AATA ||| |||| ||||| |||| ||||||| |||||| ||
TAACTGCAGATGAAAAATAA AAC ATAG ATCGA ACCC TAAAATA AGACGT
AG C
AATATCACCCAAGCTAAGAT TATG A ------ ACTA AAAAGT CAATC T
AGTATCAA

GAM2555 TGCCCAGCAGCAGCAGTAGC 59082 CGAGGAGAAC 59083 C --- AGCC T CCCAGT
CCCTCTGTGCCCAGTTCCAT TGCTGGCCCT TG CCAGCAG CAGCAGT CCTC GTG T
CATCGCCGAGGAGAACTGCT GCTG || ||||||| ||||||| |||| |||
GGCCCTGCTGGCCG GC GGTCGTC GTCGTCA GGAG CGC C
C CCG AGA- C TACTAC

GAM2556 CTCGTCGCTTGACAGCACCG 59112 CAGCCGCAGC 59113 T A -- ACC------- A
CCGCAGCCGCGGCAGCCGCA CGCCATGACA CTCGTCGCT G CA GC GCCGC G
GCCGCCATGACAGCGACGAG GCGA ||||||||| | || || |||||
GAGCAGCGA C GT CG CGGCG C
- A AC CCGACGCCGA C

GAM2557 GGGACAGACCAGACCTAGGA 59198 AGGCATGGAC 59199 ---------- GA A--- TC
GCTATTCTACCATAGCAGAA ATACTAATAT GGGACAGA CCA CCTAGG GCTAT T
CTTAGGCATGGACATACTAA CTGT |||||||| ||| |||||| |||||
TATCTGTCTT TTCTGTCT GGT GGATTC CGATA A
ATAATCATACA AC AAGA CC

GAM2558 ACAGGCCGGGTTTTAAAACT 59202 TGTGAGGATC 59203 GG TAA---- ---------- G G
TTT
TACTCAGGGGAATTGTTTTT TAACTCTAAG ACAGGCC GTTT AACTTA CTCA GG
AATTG T
TTTAGTTCTGTGAGGATCTA TTGA ||||||| |||| |||||| |||| || |||||
ACTCTAAGTTGACACATAAA TGTCCGG TAAA TTGAAT GAGT TC TTGAT /
TTAGGCCTGT AT TACACAG CTCAATCTAG G - TTT

GAM2559 ATTAGAGAACCACGTAATTG 59212 TCCACCAAGC 59213 A-- CGTAA GTCA C T
GGTCAACCCGTTAATACCGG CCTGGAAATC ATTAGAGA CCA TTGG ACC GT A
TCCACCAAGCCCTGGAAATC TCTA |||||||| ||| |||| ||| ||
TCTAGT TGATCTCT GGT AACC TGG CA A
AAA CCCG- ACC- C T

GAM2560 GATGTTAAATATTATTAGTC 59248 TAATAGGCCC 59249 - AGTCTC A-- CGCAA
GTCAAC CTA
TCATTAACAAACCACGCAAC TGGAAATTGT GATGTTA AATATTATT ATTAACAA CCA
CTAT CCG A
TATGTCAACCCGCTAATACC TAAT ||||||| ||||||||| |||||||| ||| |||| |||
GGTCTAATAGGCCCTGGAAA CTACAAT TTATAATAA TAATTGTT GGT GATA
GGC /
TTGTTAATAAATAATATTGT G A----- AAA CCCG- ATCT-- CAT
AACATC

GAM2561 CATATATATGTAATAGTCTC 59256 TATGTAATAG 59257 A A CTCAT C-- CGCAA
GTCAAT TTA
ATCACTAACCCACGCAACTG TCTCATCACT CATATATATGT AT GT CACTAA CCA CTGT
CCG A
TGTCAATCCGTTAATACCGG AACC |||||||||| || || |||||| ||| |||| |||
TCCAACAGGCCCTGGAAATT GTATATATACA TA CG GTGATT GGT GACA GGC
/
AGTGGCAATAACATATATAT A A ----- AAA CCCG- ACCT-- CAT
G

GAM2562 CCGCTTCTATTTACTCCCGC 59265 CCGCAGCACA 59266 C-- CTCCCG-- AC A AA
AGCACAATGAACCAACACGG ATGAACCAAC CCGCTT TATTTA CAGC AATGA CC C
GCTCGTTTCGTTGATCACAT ACGG |||||| |||||| |||| ||||| ||
TTAGATAAAAAGGCGG GGCGGA ATAGAT GTTG TTGCT GG A
AAA TTACACTA CT C GC

GAM2563 GTTAGGCAATGTATATTTAT 59280 CAATGTATAT 59281 - CA TATTTAT
AAATTTAAAACATATT CT
CCATCGTCAAATTTAAAACA TTATCCATCG GTTA GG ATGTA CCATCGTC TGAA T
TATTTGAACTTAACTTCAGA TCAA |||| || ||||| |||||||| ||||
TGATGGTGCATCCATAGC CGAT CC TACGT GGTAGTAG ACTT A
A -- ------- ---------- CA

GAM2564 ATATTTTTCTATAATCTGTC 59288 TCCCTCATAG 59289 C ATC- - AAC T TCCACAAA
TTTTAAACGATGGATTTTCC AATGATACAC ATATTTTT TATA TGTC TTTTA GA GGATTT T
ACAAATGCGCCTCTCAAGTC GTAT |||||||| |||| |||| ||||| || ||||||
CCTCATAGAATGATACACGT TATAAAAA ATAT ATAG AAGAT CT CCTGAA G
ATAAAAAATAT - GCAC T A-- C CTCTCCGC

GAM2565 CCGCTTCTATTTACTCCCGC 59299 CCGCAGCACA 59266 - - CTCCCG-- AC A AA
AGCACAATGAACCAACACGG ATGAACCAAC CCGC TTCT ATTTA CAGC AATGA CC C
GCTCGTTTCGTTGATCACAT ACGG |||| |||| ||||| |||| ||||| ||
TTAGATAAGAAGGCGG GGCG AAGA TAGAT GTTG TTGCT GG A
G A TTACACTA CT C GC

GAM2566 CCGCTTCTATTTACTCCCGC 59300 CCGCAGCACA 59301 C-- CTCCCG-- C A AA

AGCACAATGAACCAACACAG ATGAACCAAC CCGCTT TATTTA CAGCA AATGA CC C
GCTCGTTTTGTTGATCACAT ACAG |||||| |||||| ||||| ||||| ||
TTAGATAAAAAGGCGG GGCGGA ATAGAT GTTGT TTGCT GG A
AAA TTACACTA T C AC

GAM2567 CGCTTCTATTTACTCCCGCA 59327 TCCCGCAACA 59328 - - CTCCCG-- AC A AA
ACACAATGAACCAACACGGG CAATGAACCA CGC TTCT ATTTA CAAC AATGA CC C
CTCGTTTCGTTGATCACATT ACAC ||| |||| ||||| |||| ||||| ||
TAGATAAGAAGGCG GCG AAGA TAGAT GTTG TTGCT GG A
G A TTACACTA CT C GC

GAM2568 ACGGTAGAATTGATAATATA 59336 TACCTCATAA 59337 TAAA-------- CA-- T- TCTGTG
A TT TA
AATATGAGCATTAGTATTTC AACAAAAAAG TAATA TATGAG TTAG ATT GATTAAT
GAT C G
TGTGGATTAATAGATTTCTA CTAT ||||| |||||| |||| ||| ||||||| ||| |
GTATGGGATCATTAATCATT ATTAT ATACTC AATC TAA CTAATTA CTA G T
TCTAATCTCTAAATACCTCA CGAAAAAACAAA CATA TC TCTTTA - GG TA
TAAAACAAAAAAGCTATTAT
CAAATACTGT
GAM2569 ATTATTAGACGAGTTACAAA 59357 TGCGATCAGA 59358 A TACAAA AT G GA
CTATTTGGATAGACACATAT TATTTGCTAA ATTATTAG CGAGT CT TTG ATA C
GCGATCAGATATTTGCTAAT TAAT |||||||| ||||| || ||| |||
AAT TAATAATC GTTTA GA AGC TAT A
- TA---- CT G AC

GAM2570 GCGGGTTCTTGTATTCCGTG 59360 TTGGCTGGCA 59361 G A AT ATT
TGATAGATGGTTGGATTGAT TACGGAATAT GCGG TTCTTGTATTCCGTGTG TAG GGTTGG G
AATCGATTGGCTGGCATACG AGGA |||| |||||||||||||||| ||| ||||||
GAATATAGGAGGTCGC CGCT GAGGATATAAGGCATAC GTC TTAGCT A
G G GG AAT

GAM2571 CTGAGGGGACCATAGCATGT 59372 TAGCATGTAT 59373 CA- A- G AA G
ATAGGCGAAAAGCGGGGCTT AGGCGAAAAG CTGAGGGGAC TAGC TGTATAG CGA AGC G
CGGTTGTACGCGGTTAGGAG CGGG |||||||||| |||| ||||||| ||| |||
TCCCCTCAG GACTCCCCTG ATTG GCATGTT GCT TCG /
AGG GC G -- G

GAM2572 GGGTTTTATAAATGATTATA 59380 TAAATGATTA 59381 T ATGA A AAA AAA
AGAGTAAAAAGAAAGTTGCT TAAGAGTAAA GGGTT TATAA TTAT AGAGTA AG G
GATGCTCTCATAACCTTGTA AAGA ||||| ||||| |||| |||||| ||
TAACCC CCCAA ATGTT AATA TCTCGT TC /
T CC-- C AG- GTT

```
GAM2573 CTCAGTCCCTGTCTCTAGTT 59395   TCCCTGTCTC 59396      -     C  TA--  TGT   TCGA
        TGTCTGTTCGAGATCCTACA       TAGTTTGTCT       CTCAG TCCCTGT TC   GTT   CTGT   G
        GTTGGCGCCCGAACAGGGAC       GTTC          ||||| ||||||| ||   |||  ||||
        CTGAG                              GAGTC AGGGACA AG   CGG   GACA   A
                                        C     - CCCG   TT-   TCCT


GAM2574 TGTAGCTAAAGCTAAAGCAT 59429   GCTAAAGCTA 59430     A --------      AAA     GTGCT
        GCAGTGCTATTGAAATGCAT       AAGCATGCAG       TGT GC      TAAAGCT   GCATGCA    A
        GTAGCTTTACAACAATTGCA       TGCT          ||| ||      |||||||  |||||||
        ACA                             ACA CG      ATTTCGA   TGTACGT    T
                                       A  TTAACAAC      ---      AAAGT


GAM2575 GTTTGGGGATGAACCATGGT 59447   TATGTCAGAA 59448       GA-   ACCA---     TT    A
        CTTTGCTTGACACAAGCTGG       CCTAAAC         GTTTGGG   TGA     TGGTCT  GCTTG C
        GACCGATATATGTCAGAACC                    |||||||   |||      ||||||  |||||
        TAAAC                           CAAATCC   ACT     GCCAGG  CGAAC /
                                        AAG   GTATATA     GT    A


GAM2576 ACATTATGCATTGTGGTTTT 59451   TATGCATTGT 59452      T     TT     TT   TGT TG TTT
        GTTGTGTGGTTTGTTTTTGC       GGTTTTGTTG       ACAT ATGCA  GTGGT  TGT   G  G   G
        TTATATTGCTATGTTGCATG       TGTG          |||| |||||  |||||  |||   |  |
        TGT                             TGTG TACGT  TATCG  ATA   C  T   /
                                        -    TG    TT   TT- GT TTT


GAM2577 GCCTATTTGTACGGGTCGAG 59465   TACGGGTCGA 59466      ATTTG-   GG---    TAC    TG     AC
        TACAAACGTGGCCATCACGA       GTACAAACGT       GCCT    TACG    TCGAG   AAACG  GCCATC  G
        TAGATGGTTCTGTTTTTCGA       GGCC          ||||     ||||    |||||  |||||  ||||||
        ACAGATGTAAATCGGAGGC                     CGGA     ATGT    AGCTT   TTTGT  TGGTAG  A
                                       GGCTAA    AGACA    ---     CT     AT


GAM2578 CATCACGATAGATGGTTCTG 59468   GTTCTGTTTT 59469      GT--   G      --   --    T   CG    CGTC--
  ACG
        TTTTTCGAACAGATGTAAAT       TCGAACAGAT       GATG    TCT TTTTTCGA  ACA  GATG AAAT  GAGG
  GTGCAGT   G
        CGGAGGCGTCGTGCAGTACG       GTAA          ||||   ||| ||||||||  |||  |||| ||||  ||||     |||||||
        GTAAACTGCACATCTATCCT                    TTAT    AGA AAAAAGTT  TGT  TTAT TTTG  CTCC
CACGTCA  /
        CTAGTTTCTATTGATGTAAT                     AACT  -      AA   AG    C    AT    TATCTA      AAT
        TGAAAAAAGATCAATATTTT
        ACGATGATG
GAM2579 ATACACAGTACTTGTAATTT 59475   TACATCAGTT 59476       A ----  --        T  A   TCT----------
TCG
        CTTGAAACATCTCCTCGAAT       GACACCGTGT       ATACAC GT    ACT  TGTAATTTCT GA ACA
CC   A
        ATGGCATTAACTTTCTTTTT       GT            |||||| ||    |||  ||||||||| || |||           ||
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GTATTTAGAGATTACATCAG TGTGTG CA TGA ACATTAGAGA TT TGT GG A
TTGACACCGTGTGT C CAGT CT T A TTTTCTTTCAATTAC TAT

GAM2580 TGTTACGTCCCACTGGCACA 59490 TGAGAGCAAT 59491 ACG CTG TTAAAAAAAATGGTA
GG TG AA- T
TTTAAAAAAAATGGTAAGAG CTGATGGAAT TGTT TCCCA GCACAT AGA GTTCT T
CAT T
GGTTCTTGTAACATTTGATG ATAT |||| ||||| |||||| ||| ||||| | |||
GGGATGAGAGCAATCTGATG ACGA AGGGT TGTGTA TCT CGAGA A GTA /
GAATATATGTGTTGGGAAGC --- --- TATAAGGTAG----- AA GT GGG G
A

GAM2581 GTTTGCTGCATGCACGCGAC 59499 TTGCTGCATG 59500 A ACAAACACGAGAT - - AAG
A AA A TT
AAACACGAGATTGTGCTCGA CACGCGACAA CATGC CGCG TGT GC TCGATG GTT
GTC CG TTTAT G
TGAAGGTTAGTCAACGATTT ACAC ||||| |||| ||| || |||||| ||| ||| || |||||
ATTTGGTTATAAGCGGGGAT GTGCG GCGT ACA CG AGTTAC CAG TAG GC
GAATA G
AGACGCGCATTGATGCTACA - CAATTAAGTAT-- T T GCG A GG - TT
TATGAATTAACTGCGGCGTG
TTGGGGGTTAT
GAM2582 GCCCAACGGTGCCCCTTTAT 59517 CAACGGTGCC 59518 CCAAC CCCT CG-- GA
CGCCGTATGAATATGTGAAG CCTTTATCGC GC GGTGC TTATCGC TAT A
AGCGATAACAGCACCCACGC CGTA || ||||| ||||||| |||
CG CCACG AATAGCG GTG T
CAC-- AC-- AGAA TA

GAM2583 TACCGATATACAGTATAATG 59524 TATACAGTAT 59525 - T ATA- - T AC--- A
ATTTAGTTACTTTAATAACC AATGATTTAG TACC GA ATACAGT AT GA TTAGTT TTTAAT A
GTTAGACATAAAATTGATTC TTAC |||| || ||||||| || || |||||| ||||||
TATGAAAACTGTGTTTCAGG ATGG CT TGTGTCA TA CT AGTTAA AGATTG C
TA A T AAAG T T AATAC C

GAM2584 GGGGGGGTGGGCCTCGTCCC 59542 CGGGACCCGC 59543 G G CTC CA--- GA-- C
CACGCAGACCCGCGGGCAAA GCGCCTGCCT GGG GGGTG GC GTCCC CGCA CC G
TGCGAGAACGGGACCCGCGC ||| ||||| || ||||| |||| ||
GCCTGCCT TCC TCCGC CG CAGGG GCGT GG C
G G CC- CAAGA AAAC G

GAM2585 ATATATTATGTGCACGAGCA 59667 TATTATGTGC 59668 A CGAGCA ATA ATT
GCATAAGACATATTATGAAG ACGAGCAGCA ATATATT TGTGCA GC AGACAT A
TGTTTAAGCAGGATGCACAA TAAG ||||||| |||||| || ||||||
ATGTAT TATGTAA ACACGT CG TTTGTG T
- AGGA-- AA- AAG

GAM2586 GTGGCAGACAAAGCCAAAAC 59677 TGTTACAGTG 59678 G G AAAG AAAC TG AAA
AATGTTTTAAAAAAAAAGGT GAGGTGTGGT GTG CA AC CCA AA TTTT A
GTTACAGTGGAGGTGTGGTA AC ||| || || ||| || ||||
C CAT GT TG GGT TT GGAA /
G G GA-- GACA GT AAA

GAM2587 CACGCCGCTATGGGAGGCGC 59713 CCGCTGCGAG 59714 CG ATG A - TTT
CGTGTTTTTCACCAACACGC ACGCGTG CACGC CT GG GGCGC CGTGTT C
GCGCCGCTGCGAGACGCGTG ||||| || || ||||| ||||||
GTGCG GA TC CCGCG GCACAA /
CA GCG G C CCA

GAM2588 TGTATTCAGTATTTTTGGAA 59723 TCAGTATTTT 59724 TTC G CA AA- A
TCATAAAAAATAAAAAAAGT TGGAATCATA TGTA AGTATTTTT GAAT TAAAA TAAAA A
TTTACCATTTTAAAATTTAA AAAA |||| ||||||||| |||| ||||| |||||
AAAGTATTTACA ACAT TTATGAAAA TTTA ATTTT ATTTT A
--- A AA ACC G

GAM2589 TGTCTTATTAGTTACGCTTA 59735 TATTAGTTAC 59736 TTAT CG TTTT TTTTACG
TTTTTATGTGTTTTACGTTG GCTTATTTTT TGTC TAGTTA CTTAT ATGTG T
CTTTATTATATTTTATAAGA ATGT |||| |||||| ||||| |||||
ATGATTGTTTGACA ACAG GTTAGT GAATA TATAT T
TTT- AA TTT- TATTTCG

GAM2590 GCGCTGCTGGGGGACAGGAG 59740 TGCTGGGGGA 59741 G G GA A CAG GAGAC
GAGGGTTCGCAGCCCTGAGA CAGGAGGAGG GCGCT CT GGG CAGG GGAGGGTTCG CCCT
T
CTTAAAGAAGGGGACGAGCC GTTC ||||| || ||| |||| |||||||||| ||||
CTCCGCCTGAACCTGAGGAG CGTGA GA TCC GTCC CCTCCCGAGC GGGA T
TGC G G AA G AG- AGAAA

GAM2591 GTGTGAGCCCTTCACGTCGG 59775 TAAACAGCCC 59776 TG CT C G - G
GGGTGTTTGTGTGTTTGTGA CGATTTGACA G TGAGCC TCA GTCGGGG TGTTTGTG TGTTT T
AGCAGCATAAACAGCCCCGA GGTT | |||||| ||| ||||||| |||||||| |||||
TTTGACAGGTTCGTGC C GCTTGG AGT TAGCCCC ACAAATAC ACGAA /
GT AC T G G G

GAM2592 GAACCTGTCAAATCGGGGCT 59785 TGTCAAATCG 59786 A G AA C A C CTTC
GTTTATGCTGCTTCACAAAC GGGCTGTTTA GA CCT TCA TCGGGG TGTTT TG TG A
ACACAAACACCCCCGACGTG TGCT || ||| ||| |||||| ||||| || ||
AAGGGCTC CT GGG AGT AGCCCC ACAAA AC AC /
C A GC C C - AAAC

```
GAM2593 ACGAACCTGTCAAATCGGGG 59792   TGTCAAATCG 59793        G   AA     CTA   A  C  CTCC
        CTATTTATGCTGCTCCACAA       GGGCTATTTA       ACGAACCT TCA  TCGGGG   TTT TG TG    A
        ACACACAAACACCCCCGACA       TGCT             |||||||| |||  ||||||   ||| || ||
        TGAAGGGTTCGT                          TGCTTGGG AGT  AGCCCC   AAA AC AC   /
                                    A   AC     CAC   C  -  AAAC

GAM2594 GTTGGGCCAAACAGGATATC 59796   GCCCGGGGCC 59797   AGGA     C  T  G  ---   C-      C
AA   AGA   T
        TGCGGTGAGCAGTTTCGGCC       AAGAACAGAT          TATCTG GG GA CA   GTTT  GGCCCCGG
CCGGGGCC  GAAC   TGG C
        CCGGCCCGGGGCCAAGAACA       GGTC               |||||| || || ||   ||||  |||||||| ||||||||  ||||   |||
        GATGGTCACCGCGGTTCGGC                          ATAGAC CC CT GT   CAAG  CCGGGGCC GGCCCCGG
CTTG   GCC /
        CCCGGCCCGGGGCCAAGAAC                    ----     -  -  G  AGA    AA       C       --   GC-   A
        AGATGGTCCCCAGATATGGC
        CCAAC
GAM2595 CGCCACCCTGCGGGCGACCC 59831   TACTTCGCCG 59832     -   CT---    -  ACC   -          TAGTC
 T   C
        GGGGGGTGCTCTGATAGTCT       CCGCGACCCG        CGC CACC     GCGGG CG   CGG
GGGGTGCTCTGA    TCGCG GCC A
        CGCGTGCCCAAGGCCCGTGA       CCAC             ||| ||||    ||||| ||   ||| ||||||||||||    ||||| |||
        TCGGGGTACTTCGCCGCCGC                      GCG GTGG    CGCCC GC   GCC CTTCATGGGGCT
AGTGC CGG /
        GACCCGCCACCCGGTGTGCG                       T   CCCAC    A  GCC   G          -----    C   A

GAM2596 CCTCGTCTTTGGTTGGCTCC 59847   CTCCGAATAC 59848     T---  -   CAATCC-   TC    TC-  C   ATT
GCA      TTT
        AATCCGATTCCGAGTCGTCC       CTGTCGAATC        TGG    TG GCTC     GAT  CGAG   GT CGA   GG
TCGGAGTC   T
        GAATTGGGCATCGGAGTCTT       TCCT              |||    || ||||      |||  ||||   || |||   ||   ||||||||
        TTCCCTGGCTCCGAATACCT                      ACC    AC CGAG      CTG  GCTC   TA GCT   CC
AGCCTCGG   C
        GTCGAATCTCCTCGTCGTCT                       CATC  T    CCTGCTT   CT    CTC  A   GT-  ATA      TCC
        TCGTCCGAGCTCACTACCCA
        AAGATCGCGG
GAM2597 TCCGTCCATCGGCGTGGTGC 59862   AAGCACCCCG 59863     G   A   G  T     C--    -   TC
        TCGATCCCGTCATTCGGTGA       CGAAGGAGGA        TCC TCC TCG CG GGTGCT   GATC CCG   A
        TCTCAAGCACCCCGCGAAGG                    ||| ||| ||| || ||||||   |||| |||
        AGGA                          AGG AGG AGC GC CCACGA   CTAG GGC  /
                                   -   A   -  C     ACT    T   TT

GAM2598 GCTATTACCGTATCTAATTC 59944   TACCGTATCT 59945       ACC   CTAATTCCGAGG   AGA   AA
        CGAGGATGAAGAGCGAAATT       AATTCCGAGG        GCTATT   GTAT         ATGA   GCG   A
        CGTGATCGTAAAAATAAAAA       ATGA              ||||||   ||||         ||||   |||
        ATACAAGATAGT                          TGATAG   CATA         TGCT   TGC  /
                                   AA-    AAAAATAAAAA-    AG-   TT
```

GAM2599 GAGGCGGTCGGCGGAGGAGG 59953 AGGAGGCGGC 59954 - C CA - C- A CC ------ CT C

CGGCAGGAGGCGGCAGAGGA AGAGGAGGCC GG AGGAGG GG GGAG GCGG AGAGG GG GGAGGGCG TGGG GC C

GGCCGGAGGGCGTGGGCTGC GGAG || |||||| || |||| |||| ||||| || |||||||| |||| ||

CCTGGCCCCCCGTCGCGCCG CC TTTTCC CC TCTC CGCC TTTCC CC TCTCTCGC GCCC CG T

CTCTCTCTCCCCTTTTCCCG C - TC T CT - TC CGCGCT CC G

CTCTCTCTCCCCTTTTCCCG

CCCGCCTGCCC

GAM2600 GGGTACCACAGGTGGGTGCT 60321 TGGAAACTTG 60322 A AC- T TTT-- TGCC-- T CGT C

TTGGAAACTTGCCGGTCGCC CCGGTCGCCG GGGT CC AGGTGGG GC GGAAACT GG CGC GCTC T

GTGCTCCTGTGAGCTTGCGT TGCT |||| || ||||||| || ||||||| || ||| ||||

CCCTCCCCGGTTTCCTTTGC TCCA GG TCCGCCC CG CCTTTGG CC GCG CGAG G

GCTCCCGCCTTCCGGACCT - CCT T CGTTT CCCCTC T TT- T

GAM2601 GCCGAAAGCCGCGTGTCGGT 60326 GGACATGACG 60327 G GG ACA T T AGA TATA

GACACGTCGTCTTGAGACGG CGCCCAAGAC GCCGAAA CCGCGTGTC TG CG CGTC TG CGGTGTCTTA T

TGTCTTATATATCTTCTTAA ACGT ||||||| ||||||||| || || |||| || ||||||||||

GACGCCGGACATGACGCGCC CGGTTTT GGTGCACAG AC GC GCAG AC GCCGCAGAAT C

CAAGACACGTGGATTTTGGC A A- CC- - T AG- TCTT

GAM2602 TGTACGTATGTCGTGACTGT 60331 TGACGCGAGG 60332 A T -- - CGCGT AA A C

CGCGCGTGTCCTTGAACGTC ACCCGACAGC TGT CG ATGTC GTGA CTGTCG GTCCTTG CGTCAG TA C

AGATACCGGTACTGACGCGA TTAC ||| || ||||| |||| |||||| ||||||| |||||| ||

GGACCCGACAGCTTACGAGA ACG GT TACAG CATT GACAGC CAGGAGC GCAGTC AT G

CATTGAGCA A - AG C C---- -- - G

GAM2603 TATATTATATAATATTTTAT 60335 TATTATATAA 60336 - A---- G T TT ATTCCAATT-- GT

AAAATTAGTATTTCTTTTAT TATTTTATAA ATATAATATT TTATAA ATTA TA TTC TTATAT AATA A

ATATTCCAATTAATAGTAAA AATT |||||||||| |||||| |||| || ||| |||||| ||||

ATATTTATAAATATAGATAT TATATTATAA AATGTT TAAT AT AAG AATATA TTAT A

AATTGAACTAATAATCTCTA C ATCTC A C TT GATATAAATAT AA

TTGTAACAATATTATATAAT

ATA
GAM2604 GTTTTTCTTGTCTACTGGTT 60338 TTCCTGTAAA 60339 GTCTACT- CATATACA
AACATATACAACAACACAAT AGAAAAAC GTTTTTCTT GGTTAA A
TAACTTCCTGTAAAAGAAAA |||||||||
AC CAAAAAGAA TCAATT /
AATGTCCT AACACAAC

GAM2605 CGGGTGCTCCGCTCTTCGTA 60364 TTTTTTGATT 60365 TCC CT- TACCTGT TT
CCTGTAGACTTGGATGTCTT TAGCTGCACC CGGGTGC GCT TCG AGAC G
TTTTGATTTAGCTGCACCCG CG ||||||| ||| ||| ||||
GCCCACG CGA AGT TCTG G
T-- TTT TTTT--- TA

GAM2606 CCGAGGTCGTCGGTTTCGAG 60373 TTTAGACTTT 60374 - C TTC TATT C TTT GCAT - TTC
TATTTCCACTTTGTGCATAC GTCGATTTTC CCG AGGT GTCGGT GAG TC AC GT ACCCC CC A
CCCCCTTCATTCGGCGGGGT TACC ||| |||| |||||| ||| || || || ||||| ||
TTAGACTTTGTCGATTTTCT GGC TTTA CGGCCA CTT AG TG CA TGGGG GG /
ACCGGCATTTACGG A - T-- TT-- C TTT GATT C CTT

GAM2607 TGTTGTTGCGTTCGAAACCG 60382 AGAGGAATCA 60383 T C--- C AA A-- TC CT
AAGAGGAATCATCGGAAGCT TCGGAAGCTG TGTTG TG GTTCGAAA CG GAGG ATCA GGAAG G
GAACTTCCTTTGGTATACCT AACT ||||| || |||||||| || |||| |||| |||||
CCACGATTTCGAATTAAACA ACAAT AC TAAGCTTT GC CTCC TGGT CCTTC /
TTAACA T AAAT A AC ATA TT AA

GAM2608 CGTAAAGTGACGTTTACGTT 60406 TCGAAAACGG 60407 A TTA TT GAG C --- T TGT G T AA
CGAAAACGGAGTCCAACTAG AGTCCAACTA G CGT CG CGAAAACG TC AACT AGTG TCGGGA ATG AC CG C
TGTTCGGGATGTATGGACTC GTGT | ||| || |||||||| || |||| |||| |||||| ||| || ||
GAACAACGGTGCGTTTCTTC C GCG GT GCTTTTGC AG TTGG TCAT AGCCTT TGC TG GC /
CGACTACTTGTGGTTTGAAA - CG- T- AAA T TGT C CTT G - AA
ACGTTTTCGTTGGCGCGCAC
TGCG
GAM2609 CTTGTAGAATTACCGTGGAT 60429 TGTAGAATTA 60430 TTACCG--- TCACAACTG
CACAACTGTTGCATATCTTC CCGTGGATCA CTTGTAGAA TGGA T
CAAAATATATCTTTTGCAAG CAAC ||||||||| ||||
GAACGTTTT ACCT /
CTATATAAA TCTATACGT

GAM2610 TAGACTTCCAAGTATTAATT 60441 TCCAAGTATT 60442 TTCCAAG GTTACA TC T AA TCGC TT TATA

CGTTACAGATCCATGTATGA AATTCGTTAC TATTAATTC GA CA GTATGA CGAG TAA
AGTG A
AACGAGTCGCTAATTAGTGT AGAT ||||||||| || || |||||| |||| ||| ||||
ATAATTTTCATTTTTTATAA ATAATTAAG CT GT CATACT GTTT ATT TTAC /
TTTTGTCATACTGCTCCAGA TATA--- AC---- C- - -- TAAT TT TTTT
ATTAATAATATCTCTA

GAM2611 GTTTCGGGGAAGGGGGAGGA 60451 TACAGCACCA 60452 GG- GAGGAGAAG T G GAGG
C ACACTC- T AT
GAAGGTTTCGGGGGAGGAGG GGTTCTCCAC A GG GT TC GGGGAG TGGA TTGTG
GGGT ATC T
TGGACTTGTGACACTCGGGT AC | || || || |||||| |||| ||||| |||| |||
TATCATTAACGATACTTACA T CC CA GG CTTCTT ACCT AACGC TTCA TAG A
TCGGCGCAATTCCAAAATTC GGA ACGA----- T G AAA- T GGCTACA - CA
TTCGGGTACAGCACCAGGTT
CTCCACAC
GAM2612 GCGGGGGGAGGAGCGGGGGG 60543 GGGGAGGAGC 60544 GGGGGGAGGA GGGGGGAGGA
GGGG
AGGAGCGGGGGGAGGAGCGG GGGGGGAGGA GC GC GC G
GGGGAGGAGCGGGGGGAGGA GC || || ||
GC CG CG CG G
AGGAGGGGGG AGGAGGGGGG AGGA

GAM2613 GGGGGGAGGAGCGGGGGGAG 61200 AGACGCCGAA 61201 A AG GGGGGAGGA GGG
AGGA GGGG
GAGCGGGGGGAGGAGCGGGG AACGGGCCCC GGGGGG GG CG GCG GG GC G
GGAGGAGCGGCCAGACGCCG CCCC |||||| || || ||| || ||
AAAACGGGCCCCCCCC CCCCCC CC GC CGC CC CG G
- GG AAAAGC--- AGA GG-- AGGA

GAM2614 GCCCCCCGCGGGCGCGCGCG 61252 CGGGCGGCGT 61253 GG - AAAAAGG G
CGCGCAAAAAAGGCGGGCGG GCGCGCGCGC GCCCCCCGCG CGC GCGCGCGCGCA
CGGGC G
CGGTCCGGGCGGCGTGCGCG GGCG |||||||||| ||| |||||||||| |||||
CGCGCGGCGGGCGTGGGGGG CGGGGGGTGC GCG CGCGCGCGCGT GCCTG C
C GG G GCGGCGG G

GAM2615 GCGGGGGGAGGAGCGGGGGG 61322 GGGGAGGAGC 41609 GGGGGGAGGA GGGGGGAGGA
GGGGGGAGGA GGGG
AGGAGCGGGGGGAGGAGCGG GGGGGGAGGA GC GC GC GC G
GGGGAGGAGCGGGGGGAGGA GCGG || || || ||
GCGGGGGGAGGAGCGGGGGG CG CG CG CG G
AGGAGC AGGAGGGGGG AGGAGGGGGG AGGAGGGGGG AGGA

GAM2616 GAATTGTCCTTGAGCTTGTA 61339 TGACACCGGG 61340 C ---- TTTA TAC C --- GGG
- - TG

TACTCTGTTTACATACCACC CGGCCCTTAG TTGTATA CTCTG CA CAC TGAGGGT TCGG
TA CT TCG A
TGAGGGTTCGGGGGTACTTC TGAT ||||||| ||||| || ||| ||||||| |||| || || |||
GTGATGCGGCAGATGACACC AACATAT GAGAC GT GTG ATTCCCG GGCC GT
GA GGC /
GGGCGGCCCTTAGTGATTGC - ACAA C--- TA- - GCG ACA A C GT
CAGAGAACATATACAACCGA
AGACCTCGTTT
GAM2617 GGATTCTATAGATTTAATAA 61350 TATTACAGAT 61351 -------- T AA - CAAC CTAC
ATCCAACTGATTCTACTATA TCTATAGATT GGAT TCTATAGA TT TAA ATC TGATT T
AAATCAACAGATATTACAGA TAAT |||| |||||||| || ||| ||| |||||
TTCTATAGATTTAATAAATC CCTA AGATATCT AG ATT TAG ACTAA /
C AATAATTT T AC A ACA- AATA

GAM2618 GAACTGAGCTTTTTAATTAA 61355 AAAGTGAAGG 61356 A TTTTAATTAA AAG C- - C
AGTGAAGGACCCGGGCCAAG ACCCGGGCCA GA CTGAGCT AGTG GAC CG GGC A
GCCTCGCCGTCATCTACTCG AGGC || ||||||| |||| ||| || |||
GCTCAGTC CT GACTCGG TCAT CTG GC CCG A
- C--------- CTA CC T G

GAM2619 TATTTGCTTGCCCGTGATGT 61461 TGTTTGTATG 61462 TGATG- TT- TTG A - T
GTAAAT CAC
GCTTTGTATTTGTTTGTATG TAGTGCTTTC GCCCG TGC TGTAT TTTGT TGTAG TGCTT
CTTT GT A
TAGTGCTTTCTTTGTAAATG TTTG ||||| ||| ||||| ||||| ||||| ||||| |||| ||
TCACAGAAACTTCTAAAAGA TGGGT ATG ACATA AAATA ATATC ACGGA GAAA
CA /
GGCACCTATAATAAAAATAT TAAAAA TCT TAA - C - ATCTT- AAG
ACATCTGTAAAAAATTGGGT
TTTGTGGTTAG
GAM2620 GGTATATATTTATAAAAAAG 61469 TAACATCGTA 61470 ATAAAAAAG-- C CGCGGAA
GACAC CATCAT
TTTTTGATTACGATGTCATA ATCAAAAGAA TTTTTGATTACGATGT ATA AGAG
ATTAA A
CGCGGAAAGAGGACACATTA TTGC |||||||||||||||| ||| |||| |||||
ACATCATACATCAATTAATT GAAAACTAATGCTACA TAT TCTT TAATT /
ACATTCTTATAACATCGTAA TTTAACGTTAA A ------- ACAT- AACTAC
TCAAAAGAATTGCAATTTTG
ATGTATACC
GAM2621 TGTATTCAGTATTTTTGGAA 61476 TCAGTATTTT 59724 TTC G CA AAAA A
TCATAAAAAAATAAAAAAAG TGGAATCATA TGTA AGTATTTTT GAAT TAAA TAAAA A
TTTTACTAATTTAAAATTTA AAAA |||| ||||||||| |||| |||| |||||
AAAAGTATTTACA ACAT TTATGAAAA TTTA ATTT ATTTT A
--- A AA AATC G

GAM2622 GTGGTTCTCTGCTTTTCCTC 61477 TCTGCTTTTC 61478 CTC C T C -------- CA
CAGAGGTCTGTGAGCACAGT CTCCAGAGGT GTGGTT TG TT TC TCCAGAGGTCTGT
GAGCA G

TTGCTCAAGAATAAGCAGAC CTGT |||||| || || || |||||||||||| |||||
CTTTGGATGACAAACACAAA CACCAA AC AA AG AGGTTTCCAGACG CTCGT /
ACCAC AAC A C T AATAAGAA TT

GAM2623 GCGTACCCTGCTCGGGCTGG 61533 ACCCTGCTCG 61534 --- -- - C---- - C C
TCCA A
GTACCAGCAGCCGACGGAGA GGCTGGGTAC CGGGCTGG GTACCAGCA GC CGA GG
AGAAGCGG GGT GG GC G
AGCGGCGGTCGGTCCAGCAG CAGC |||||||| ||||||||| || ||| || |||||||| ||| || ||
ACGCCGTTCCCGCCCCGCTT GCCCGACC CATGGTCGT TG GCT CC TCTTCGCC
CCG CC CG A
CTACCACTACTCGCGTAATG ATG AA C CATCA A - C TTGC C
CTGGTACGTACCAGCCCGAA
GAAGGAGACGT
GAM2624 GACGCCGTTAATAATTGGCA 61589 TGTGCACACC 61590 G AATAA-- A A - GC-
C TAG
GTAAACTGCGAAAGGGCGTA TTTCCGCGGT GAC CCGTT TTGGC GT AACTGCG AAAGG
GTACATCG AG T
CATCGCAGTAGTGATTTTAC TCAC ||| ||||| ||||| || ||||||| ||||| |||||||| ||
GATGTGCACACCTTTCCGCG CTG GGCGA AACCG CA TTGGCGC TTTCC
CGTGTAGC TT G
GTTCACCGCCAACAACAAAA - AAACAAC C C C ACA A TTA
GCGGGTC

GAM2625 CGAATGTATCTAGTTCGTTG 61602 TATCTAGTTC 61603 GTA-- TT TGAA- - AA
AAGTATGCAACTCGCATTGC GTTGAAGTAT CGAAT TCTAG CGT GTA TGC C
AAGATACGTGTTAGAGAATA GCAA ||||| ||||| ||| ||| |||
GTTTG GTTTG AGATT GCA CGT ACG /
ATAAG GT TAGAA T CT

GAM2626 GGGCGCCGCCGCCACGAAGG 61611 ACCCTGCGTT 61612 C- -- - ---- - ACCC TTTTT
AAAA-- T
AGACCCTGCGTTTTTTCTTC TTTTCTTCGT GC GC CGC CACGA AGG AG TGCG
TCTTCGT CCAT C
GTAAAACCATTCAAATGGCT AAAA || || ||| ||||| ||| || |||| ||||||| ||||
CGCCGCGAAGATGTCTGTAC TG CG GTG GTGTT TCC TC ATGT AGAAGCG
GGTA A
CTACCTACAATTGTGAGTGT AA TT A AACA A C--- CTGT- CCGCTC A
TGCAAGTGTCC

GAM2627 GTATTTATACATATCGTCAA 61626 CACTATGTGT 61627 - TC ATC TTTG AAT
TCGTCATTTTTGTGTAAAAT AAATTAC GTA TTTATACATA GTCA GTCATT TGTAA G
GATAATTACAAATGACAAAT ||| |||||||||| |||| |||||| |||||
GACACTATGTGTAAATTAC CAT AAATGTGTAT CAGT CAGTAA ACATT A
T CA AAA ---- AAT

GAM2628 AACCCTGCGAAAAGAAGCTG 61629 AAGAAGCTGT 61630 GAAAA A CTA- TAT

TGCTACTATATTTTGCTAGG GCTACTATAT AACCCTGC GA GCTGTG CTA T
CAACATGGTATCAGCAGGGT TTTG |||||||| || |||||| |||
T TTGGGACG CT TGGTAC GAT T
A---- A AACG CGT

GAM2629 GATATCAACCTGTGCCTGTA 61643 TGCCTGTATT 61644 A- - A G TCA
TTAGCTGTGTCAGAAGCCAA AGCTGTGTCA GATATCA CCTGT GCCTGT TTAGCT TG G
AGCTAAACAGGCTATAGGAA GAAG ||||||| ||||| |||||| |||||| ||
TGGTATT TTATGGT GGATA CGGACA AATCGA AC A
AA T - A CGA

GAM2630 CTATCTAATAATATACCTTA 61658 TACCTTATAC 61659 AATATACC TGG G AATA AA
TACTGGACTAGTGCCAATAT TGGACTAGTG CTATCTAAT TTATAC ACTA TGCC TT A
TAAAATGAAGTGGGCGTAGT CCAA ||||||||| |||||| |||| |||| ||
GTGTAATTTGATTGGGTGG GGTGGGTTA AATGTG TGAT GCGG AA A
GTTT---- --- - GTG- GT

GAM2631 TGTAAGTTTGGGCGGATGAG 61670 TGAGGAAGTG 61671 TTTG GA AA---- GG G G G
GAAGTGGGGCGCGGCGTGGG GGGCGCGGCG TGTAAG GGCG TGAGG GT GGCGCG C
TGG A
AGCCGGGCGCGCCGGATGTG TGGG |||||| |||| ||||| || |||||| | |||
ACGTTTTAGACGCCATTTTA ACATTT CCGC ATTTT TA CCGCGC G GCC /
CA TA-- AG GCAGTG GG - G G

GAM2632 AGCGGACGGTAGTGCTTTAC 61712 TAGTGCTTTA 61713 G C TA-- A A AAT T
TAAAAGATAATACTGTGGTC CTAAAAGATA AGC GA GG GTGCTTT CTAAA GAT AC G
GATCGTTTAGAAGGCATGAA ATAC ||| || || ||||||| ||||| ||| ||
TCCTTTGGCT TCG TT CC TACGGAA GATTT CTA TG T
G T TAAG - G GC- G

GAM2633 GTCGGATCGAGTTTTATTCA 61727 TAACGTTGAC 61728 G TT AT A T T
AAGTTGTTATGGGTACTAAC GATTCTCGAT GTCG ATCGAG TT TCAA GTTG TA G
GTTGACGATTCTCGATGCGG GCGG |||| |||||| || |||| |||| ||
C CGGC TAGCTC AG AGTT CAAT AT G
G TT C- G C G

GAM2634 GTATCAAAAATATCAATATC 61732 TCAAAAATAT 61733 C C ATCTAATACCCA CA -
C---- CA
TAATACCCAATCAATGTTTT CAATATCTAA TAT AAAAATAT AAT AT ATGTTTTT ATAT
TGATAT C
TATATCTGATATCACAAAAT TACC ||| |||||||| ||| || |||||||| |||| ||||||
ATCAATAATGTATCAAAAAT ATA TTTTTGTA TTA TA TATAAAAA TATG ACTATA
A
ATCAATATCTAATACCCAAT - A ACCCATAATCTA AC C TAATA AA

TAATGTTTTTATAT

GAM2635 TGTTTTTATATCTGATATGT 61738 TGATATGTTA 61739 C-- AA- CAA AAA TC CTAATA
TAAAATATCAATAATGTATC AAATATCAAT TTATAT TGATATGTTA ATAT TAATGTATCA ATA AATAT C
AAAAATATCAATATCTAATA AATG |||||| |||||||||| |||| |||||||||| ||| |||||
CCCAATCAATGTTTTTATAT AATATA ACTATGTAAT TATA ATTGTATAGT TAT TTGTA C
CTGATATGTTAAAATATCAA AAA AAC AA- CTA TT ACTAAC
TAATGTATCAAAAATATAAA
TAATCA
GAM2636 GGTAAAAGAAAGTTAGAAAT 61743 TATGATGAAC 61744 G AGAA AAG A
TAAAGAAATTAGTGATTTAT AAGTTTTTTT GGTAAAAGAAA TT ATTA AAATT G
ATGATGAACAAGTTTTTTTT TACT |||||||||| || |||| |||||
ACT TCATTTTTTTT AA TAGT TTTAG /
G CAAG ATA T

GAM2637 CGTCTGAATATGCATCTGAA 61753 ACCAGTATAG 61754 AATA A --------- T A-- TT
ACTTGGACATTAGTTGACAC AAACTTTTAG CGTCTG TGC TCTGAA ACT GG CA A
CAGTATAGAAACTTTTAGAA AAGC |||||| ||| |||||| ||| || ||
GCGCTCCAGACG GCAGAC GCG AGATTT TGA CC GT /
CTC- A TCAAAGATA - ACA TG

GAM2638 TATATATTATAAAAAAGTTT 61778 TATATTATAA 61779 TAAA--- AG GAAAAAG-CACATTAA
TTGATTACGATGTTATAAGA AAAAGTTTTT TATTA AA TTTTTGATTACGATGTTATAAGAG GA C
GGAAAAAGGACACATTAACA GATT ||||| || |||||||||||||||||||||| ||
TCATACATCAATTAACATTC GTAGT TT GAAAACTAATGCTACAATATTCTT CT /
TTATAACATCGTAATCAAAA TTTAACG AA ACAATTAA ACATACTA
GAATTGCAATTTTGATGTAT
A
GAM2639 CTCAAAGCTCATCTCTTCTT 61784 AAGCTCATCT 61785 AA C C - TCAC CA
CACTTGCGTCAACGAATGTA CTTCTTCACT CTC AGCT AT TCTT CT TTGCGT A
AATTAGTAAGAATAGCTAGA TGCG ||| |||| || |||| || ||||||
G GAG TCGA TA AGAA GA AATGTA C
A- - - T TTA- AG

GAM2640 ATTTGTTAATGGTCTCGATG 61802 TTAATGGTCT 61803 G - CTCGAT--- A G C
TAATCGTCGTAGCTGCTACG CGATGTAATC ATTT TTAA TGGT GT ATC TCGTAG T
AGATAACTTTTTTTCTGCCA GTCG |||| |||| |||| || ||| |||||
TTTAAGAGAT TAGA AATT ACCG CA TAG AGCATC /
G T TCTTTTTTT A - G

GAM2641 TTGTTAGCCGCTTCCTTTTC 61806 ACGGAGGAAA 61807 A CG- C-- A AATACAA
CATGAAATACAAATAATAAG CGAAGAATGC TTGTT GC CTTC TTTTCC TGA A
ATCACGGAGGAAACGAAGAA AACA ||||| || |||| |||||| |||
TGCAACAA AACAA CG GAAG AGGAGG ACT T
- TAA CAA C AGAATAA

GAM2642 TAAGTGTGCTAAACGCCGCA 61861 TGTTTTGACT 61862 T TAAAC AG AT
GAGCAAAACGTTATAATAGA GTGGTGCCTA TAAGTG GC GCCGCAG CAAAACGTT A
TGTTTTGACTGTGGTGCCTA CTTA |||||| || ||||||| |||||||||
CTTA ATTCAT CG TGGTGTC GTTTTGTAG A
C ----- A- AT

GAM2643 TCTGCAATTAAATTCTGTTA 61871 TCTGTTATCG 61872 -- TT TC - --------- GGGAA T
TCGAAGTGGGAAGATTTGTA AAGTGGGAAG TCTG CAA AAAT TGTTA TCG AAGT
GATTTG A
ATCAAATTAAAAACTTAAAA ATTT |||| ||| |||| ||||| ||| |||| ||||||
TATTACGATTAACAAGATTT AGAC GTT TTTA ACAAT AGC TTCA TTAAAC A
TTTGACCAGA CA T- GA T ATTATAAAA AAAA- T

GAM2644 CGTCACTGAAATACGCGCGC 61875 TATCGCGCAC 61876 A AAATAC ----- A A CC
GAGGAACGCCCCGACGATCC AGGACAGCGA CGTC CTG GCGCG CG GGA CG C
CGGATATCGCGCACAGGACA CG |||| ||| ||||| || ||| ||
GCGACG GCAG GAC CGCGC GC CCT GC C
C AGGACA TATAG - A AG

GAM2645 CATGGAATGATGCGGCACGG 61878 CACCCGACGC 61879 A A GCAC C AGCGACG
CGCGACAGCGACGGGGAAAT ACCATCCATG CATGGA TG TGCG GG GCGAC G
GGTCGCACCCGACGCACCAT |||||| || |||| || |||||
CCATG GTACCT AC ACGC CC CGCTG /
- C AGC- A GTAAAGG

GAM2646 GCGGTTCTTGTTCTCCCTGA 61907 TGACAAGGAG 36901 TTCT CTCC C - ------- ACA
GCCACCATCACCCAGACACA GTGATGTGTG GCGG TGTT CTGAG CAC CATCACC
CAGAC G
GATAGTCTGACAAGGAGGTG ACTC |||| |||| ||||| ||| ||||||| |||||
ATGTGTGACTCGGAAAAACA CGCC ACAA GGCTC GTG GTAGTGG GTCTG /
CCCGC C--- AAA- A T AGGAACA ATA

GAM2647 GGTTGCTGCACAACCGGGGC 61908 TGAGGCCCTT 61909 CAACC TG ----- AT
TTTGCCCGGGGATTTCATCC GTAGTAACC GGTTGCTGCA GGGGCTT CC CGGGG T
CGTTCAAGGTGAGGCCCTTG |||||||||| ||||||| || |||||
TAGTAACC CCAATGATGT TCCCGGA GG GCCCT T
----- GT AACTT AC

GAM2648 GCAGACTGAAGCGACCTATG 61975 TATGGTGAAA 61976 TGA CTA GAAAAC TGT ----
GT-- A A
GTGAAAACGGATGTACCATC ACGGATGTAC CAGAC AGCGAC TGGT GGA ACCATC
TAGCT GG GT G
TAGCTGTGGAGTAGTGACCC CATC ||||| |||||| |||| ||| |||||| ||||| || ||
TAGAAGCTAATCCGATGGTT GTTTG TTGCTG ACCA CCT TGGTAG ATCGA CC
CA T
CCACCAGTCGTTGTTTGC --- --- ------ --- CCTA AGAT - G

GAM2649 ATCCAGACGTTGCTCCTGCA 61994 CGTTGCTCCT 61995 C A TG CCT------- TT- T
CCCATAA
TTTTGAGTGTGTCCCATAAG GCATTTTGAG ATC AG CGT CT GCAT TGAGTG GT G
CCTCCAAACCGCTCACTCGT TGTG ||| || ||| || |||| |||||| ||
GCCCACAACTCCAGTGACGC TAG TC GCA GA CGTG ACTCGC CA /
CTCGAT C C GT CCTCAACACC CTC - AACCTCC

GAM2650 TGATGAGAAAGTATTCTTCA 62003 AAGTATTCTT 62004 GA---- A TCAC- AC
CTGTAGACATGTTATATTAT CACTGTAGAC TGATGA AAGT TTCT TGTAG A
CAGAAACTTCAAGAATTATC ATGT |||||| |||| |||| |||||
A ACTATT TTCA AAGA ATATT /
AAGAAC - CTATT GT

GAM2651 CCTGGTTCAGTATCCGGGTT 62011 GTTCAGTATC 62012 GG AT- ---- T TC T
GTCCTGTATTGTTACGGTGT CGGGTTGTCC CCT TTCAGT CCG GG TG CTGTA T
ATCCGTCTTGGCACACTGAA TGTA ||| |||||| ||| || || |||||
AGGG GGG AAGTCA GGT CC AT GGCAT G
A- CAC TCTG T GT T

GAM2652 CGTTTGGATGAAGTGATTCC 62020 TGTTAAAATT 62021 GA- TGA- - AATTCGAA G
AGAATTCGAATTAGTATCGA TTAGCTGAGA CGTTTG TGAAG TTC CAG TTAGTATC A
CCGATGTTAAAATTTTAGCT AGTA |||||| ||||| ||| ||| ||||||||
GAGAAGTATCTTCAGGATGA GCAAGT ACTTC AAG GTC AATTGTAG C
ACG AGG TATG A GATTTTAA C

GAM2653 CATCTGTAATTAATAGGTTC 62025 TAGGTTCCTC 62026 GTAA-- GT C TTACA- A
CTCGATTTACATCAAATTTT GATTTACATC CATCT TTAATAG TCCT GAT TCAA T
GAAAGACTGTTAGGACTGTT AAAT ||||| ||||||| |||| ||| |||
GGGAAATAAGGTG GTGGA GGTTGTC AGGA TTG AGTT /
ATAAAG -- - TCAGAA T

GAM2654 TTGTAGGTGCGGATAGGTCT 62030 TACAGTGGCT 62031 A T ATA - T TA A- -- T A
TCC- A
CTCTACAGAGCTGTATAGGT GCGGCGACGA TGT GG GCGG GGTC TC C CAG GCTGTAT
AGG GTG CGG GGG C

GTGACGGTCCGGGACACCCA CCCC ||| || |||| |||| || | ||| ||||||| ||| ||| ||| |||
AGCCCGCCGCCCCTGTGTAC ACA CC CGCC CCAG AG G GTC TGACATG TCC CGC GCC CCC /
AGTGGCTGCGGCGACGACCC A T --- C C GC GG TG C C CGAA A
CGCTCCAACAA

GAM2655 CCCTGCTCACGTACGAGTTC 62082 TACAGTGTTC 62083 ------ - G T TCTAATCTTC TG - - AG
GATCTAATCTTCGGGGTGCG CATTCGTACT CCCT GCTCA CGTAC AGT CGA GGGG C GTA TGCGA T
TATGCGAAGTTGTTGCGTTA GTAC |||| ||||| ||||| ||| ||| |||| | ||| |||||
CAGTGTTCCATTCGTACTGT GGGA CGAGT GCATG TCA GCT CCTT G CAT GCGTT /
ACGTTGAGCGCTAATAGGG TAATCG T - T TA-------- GT A T GT

GAM2656 ACCGCAGGAGGTACCCGTAG 62099 TGTGATCCTC 62100 C -- C-- T GAAAAA
TCGTTGAAAAATTGAAAGTG CTCCGGT ACCG AGGAGG TAC CG AGTCGTT T
GCGGCTCCGTATGTGATCCT |||| |||||| ||| || |||||||
CCTCCGGT TGGC TCCTCC GTG GC TCGGCGG T
C TA TAT C TGAAAG

GAM2657 TTTACATTTATTAAATTAAC 62108 TAAATTAACA 62109 TAT- ACA TT------ AAAA T ACAAT
ATTATGTTTAATACAAAATC TTATGTTTAA TTACATT TAAATTA TTATGT AATAC TCTA CATG T
TATCATGACAATTATTTACA TACA ||||||| ||||||| |||||| ||||| |||| |||| |||
TGTGGACAGTATTTATTTTT GGTGTAG ATTTAAT AATATA TTATG AGGT GTAC /
TATATAAAATAATTTATTAT TATT AA- TTTTTTAT AC-- - ATTTA
GATGTGGA

GAM2658 ACAAGTTATGGAAATAAAGA 62114 TATGGAAATA 62115 TT- - AA-- CGCA
AACTCGCATGTTTTAGTTTT AAGAAACTCG ACAAG ATG GAAATA GAAACT T
AGTCTATTTCTCATTCTCTT CATG ||||| ||| |||||| ||||||
GT TGTTC TAC CTTTAT TTTTGA G
TCT T CTGA TTTT

GAM2659 GCCCATCGAACGCTCTTCGG 62130 AACCGTAGTA 62131 C-- AA - T--- G- AA -- CAT
GATTATAATTTCAATGTCAT GCCGTTGTAG GCC ATCG CG CTCT CGG ATTAT TTTCA ATGT C
CCTCTACATCTTGAAACCGT AGTC ||| |||| || |||| ||| ||||| ||||| ||||
AGTAGCCGTTGTAGAGTCGC CGG TAGC GC GAGA GCC TGATG AAAGT TACA C
GCGATAATGGC TAA GC T TGTT GA CC TC TCT

GAM2660 GGAAGTCAAGTATTTATACA 62133 TCAAGTATTT 62134 AA ATTT G T TT
CGTTGAGTGTCATTTACATG ATACACGTTG GG GTCAAGT ATACAC TTGAGTG CAT A

```
     TGTCATTTAAGTGTGTCATT       AGTG           ||  |||||||    |||||| |||||||  |||
     TGACCC                          CC  CAGTTTA    TGTGTG AATTTAC GTG  C
                                --      C---     -      T   TA


GAM2661  TCACTTTCAGTTTTTAGTTT 62149   CTTGAACACA 62150       TCAGTTT    ---------    C    AT
     CAACTCTTATTGCGAGACTT       ATTCTACTAA       TCACTT      TTAGT       TTCAA TCTT  T
     GAACACAATTCTACTAACTT       CTTC           ||||||      |||||       ||||| ||||
     CAATAAGTGA                      AGTGAA      AATCA       AAGTT AGAG  /
                                  TAACTTC    TCTTAACAC    C    CG


GAM2662  TAGATATAAAACTAGGTAAT 62165   TATAAAACTA 62166    GA    AA-  G-    C    CAC   A
     CTATACACACTAAAAAGTTT       GGTAATCTAT       TA  TATAA   CTA  GTAAT TATA   ACT A
     TTATACATTACGATAGATAT       ACAC           ||  |||||   |||  ||||| ||||   |||
     TATGGATA                        AT  GTATT   GAT  CATTA ATAT   TGA A
                                AG    ATA   AG    C    TTT   A


GAM2663  TATATAATACCTTTACACCA 62186   TATAATACCT 62187    TA   -    ACAC  CG  ACT      TG
     CGCAACTACATATATTGCTT       TTACACCACG       TA  TAAT ACCTTT   CA  CA   ACATATAT  C
     TGTATATGTTGTATGAAAGG       CAAC           ||  |||| ||||||   ||  ||   ||||||||
     TAATTACGTA                      AT  ATTA TGGAAA   GT  GT   TGTATATG  T
                                GC    A     ----  AT  ---       TT


GAM2664  GGTCTGAGGAAGATTAAGAA 62196   AGGAAGATTA 62197     C       A  ---         T  TGTTC     TT
     AAAGGCCTCGTGTTCACTTG       AGAAAAAGGC       GGT TGAGGAAG TTA   AGAAAAAGGCC CG
ACTTGG  G
     GTTGCCGTCAAGTATCCTGT       CTCG           ||| |||||||| |||   |||||||||||  ||    ||||||
     GGTTTTTTTCTACCTAACTT                 CCG ACTCCTTC AAT   TCTTTTTTTGG GT    TGAACT  C
     CCTCATGCC                       T      -  CCA         T  CCTA-     GC


GAM2665  GCATTGAGCACTGCTAATAG 62236   TTGTGCAGAT 62237      TGA   CT   AA       T   AC  TAAA
GAG
     GTTTGTATCACGTTAAAGAT       TTAAACTTGG       GCAT   GCA  GCT  TAGGTTTG ATC  GT    GATTTA
T
     TTAGAGTGTATGAATTGTGC       GTTT           ||||   |||  |||  |||||||| |||  ||    ||||||
     AGATTTAAACTTGGGTTTTG                 CGTA   CGT  TGG  GTTCAAAT TAG  CG    TTAAGT   /
     CCTTATGC                        TTC   TT   --       T   A-  TG--     ATG


GAM2666  TCTGTCCAATCGGAAGTGAA 62249   GTCATTTTTA 62250       -  AAT--  ----------     AAC    T
     ACCACATCTTTGTGTCATTT       ATCAGCCCCG       TCTGT CC     CGG        AAGTGA   CACA C
     TTAATCAGCCCCGTTAAAGG       TTAA           |||||  ||     |||        ||||||   ||||
     TACAGA                          AGACA GG     GCC        TTTACT   GTGT T
                                  T  AAATT   CCGACTAATT     ---    T
```

GAM2667 GCCGCCCTGCGACACAATCA 62253 ACACAATCAC 62254 C- ACACAATCA C C- TTT
CCCGTCCGTGGTTTCGAATC CCGTCCGTGG GCCGC CTGCG CC GTC GTGG C
TACACGACAGGCCCGCAGAC TTTC ||||| ||||| || ||| ||||
GCGGC CGGCG GACGC GG CAG CATC G
CA CC------- A CA TAA

GAM2668 GACAGGCCCGCAGACGCGGC 62268 TTGGTTGCGC 62269 A CGC C CTAACACACAC - CA C
TAACACACACGCCGGCAACC GGTCCCGTCT GAC GGCC AGACG GG GCCG GCAACC GACCC A
CAGACCCCAGTGGGTTGGTT CCTG ||| |||| ||||| || |||| |||||| |||||
GCGCGGTCCCGTCTCCTGGC TTG TCGG TCTGC CC TGGC CGTTGG TTGGG G
TAGTT A TCC - ---------- G -- T

GAM2669 CTCTACCTCTGGACTTCAGG 62272 TCAGGACCTG 62273 AC AC-- A T GA TT
ACCTGCAGACTCTTAGTGAG CAGACTCTTA CTCT CTCTGG TTCAGG CC GCA CTC A
CTTGTTGGCCCTGAAAATGC GTGA |||| |||||| |||||| || ||| |||
CGGAGAGGGAG GAGG GAGGCC AAGTCC GG TGT GAG /
GA GTAA C T TC TG

GAM2670 CACACATGCTTCCGTATGTC 62285 TATGATCGAC 62286 AT CC A T T C
GTATCTTGTTTAACTTTTTA AATAGAGCCA CACAC GCTT GT TGTCG ATC TGTTTAA T
AGTATGATCGACAATAGAGC GTGT ||||| |||| || ||||| ||| |||||||
CAGTGTG GTGTG CGAG TA ACAGC TAG ATGAATT T
AC A- - - T T

GAM2671 CAACGAGCTAGACTTTGTTA 62291 TAGACTTTGT 62292 GAGCTAG - ---------- A
TGGAGAAACTCTAAAAAAAA TATGGAGAAA CAAC ACTTTG TTA TGGAG A
TTGTTAATTAAAGTAAATAG CTCT |||| |||||| ||| |||||
TTG GTTG TGAAAT AAT ATCTC /
ATAAA-- T TGTTAAAAAAA A

GAM2672 ACAGTTCCGATAACGTAAAG 62302 TACCGCGTTG 62303 G AAA CCT C CGCGTA
TCCTGACCTCTTACGCGTAT TTGGGAATGT ACA TTCCGATAACGT GT GAC TCTTA T
AGATTTTGAGACGTCTACCG ||| |||||||||||| || ||| |||||
CGTTGTTGGGAATGT TGT AGGGTTGTTGCG CA CTG AGAGT /
A C-- T-- C TTTAGA

GAM2673 TTTTTATGGGTTTTACATTG 62323 TGTCGTAGTA 62324 GTTT A G TT- - AGA -- TT
CTTTATTATATTTTATAAGA TAGATATATT TTTTTATGG TAC TT CTTTA ATAT TTTATA ATGAT TG T
ATGATTGTTTGACAATGTCG ATTA ||||||||| ||| || ||||| |||| |||||| ||||| ||
TAGTATAGATATATTATTAG AAAAATATT ATG GA GAGAT TATA AGATAT TGCTG AC /

AGGAGGTATAATTATAAAAA AAT- - G TAT T GA- TA AG

GAM2674 TGTTGATACTTGATATTGAT 62326 TTGATAATTA 62327 ACT- T --- AG TAGTATAAT AT T
AATTAGTATAATTAGTATAA GTATAATTAG TTGAT TGATAT GATA ATT TATAAT TAGTATA TAGTA A
TTAGTATAATTAGTATAATT TATA ||||| |||||| |||| ||| |||||| ||||||| |||||
ACTATGTATTATATTTCATT AATTA ACTATA CTGT TAG GTATTA ATTATGT ATCAT A
ATTATGAGGATTTATGTCAT AAGT - ATT GA TTACTTTAT -- T
ATCATGAAATTAATA

GAM2675 TTATTATATACACAGCATAC 62331 CAGCATACAT 62332 ATACACAGCAT- TAT
ATAAGTGTATATTATTTACA AAGTGTATAT TTATTAT ACATAAGTGTA T
CTTATGTTTATAACTCGACG TATT ||||||| ||||||||||
TAATAA AATAATG TGTATTCACAT /
CAGCTCAATATT TTA

GAM2676 GATGGACGGCCAGGCCTCCG 62342 TCAGCAGCAG 62343 A GCC C- GA- A A- AA - C
AGCAGCGCATCCTGCAACTG GAGCGTGCCG GATGG CG AGG CTCC GC GCGC TCCTGC CTG CG G
CGCGTCCGTCAGCAGCAGGA CCAA ||||| || ||| |||| || |||| |||||| ||| ||
GCGTGCCGCCAAGGAGCTCC CTACC GT TCC GAGG CG CGTG AGGACG GAC GC T
TCGATGCCATC - AGC TC AAC C CG AC T C

GAM2677 CACCGGAACCCACCAGAGGC 62428 CCGGAACCCA 62429 CC CA---------- A
GGAAGCCGCCTTCGCCCGTG CCAGAGGCGG CACCGGAA CAC GAGGCGG A
AGGGTGCGTGTGTTTTCTGG AAGC |||||||| ||| |||||||
TG GTGGTCTT GTG TTCCGCC /
TT TGCGTGGGAGTGCCCGC G

GAM2678 AGATCTAGGTTATTTGATGA 62530 TAGGTTATTT 62531 G GACAC GCAGGAAC
CACCCGCAGGAACACATACA GATGACACCC AGATCTAG TTATTTGAT CC A
ACAGGAGAATTAAATGAATT GCAG |||||||| ||||||||| ||
AGATCT TCTAGATT AGTAAATTA GG C
A AGA-- ACAACATA

GAM2679 CGTTAGCCCAAAGAGTGAAG 62539 AAGGATGCAG 62540 G CAA -- CTAT CTTTA -- T AGT
TCTATTCCCTTTATTGAGTC CTTCGTGCTC CGTTA CC AGAGT GAAGT TCC TTGA GTC CTG T
TCTGAGTTTTCCCAGCGATA TAGG ||||| || ||||| ||||| ||| |||| ||| |||
TTCAAAGGATGCAGCTTCGT GCAGT GG TCTCG CTTCG AGG AACT TAG GAC T
GCTCTAGGTGACG - A-- TG ACGT A---- TA C CCT

GAM2680 TGTTGTTATTATTATTTGAA 62562 TGTTATTATT 62563 TG G TTTG GAAAA TG GAAAA G

GTTTGATTTATGAAAATCTT ATTTGAAGTT GT TTATTATTATTT AAG ATTTAT TCTTC CTTTCT GGTC T

CTGCTTTCTGAAAAGGTCGT TGAT || |||||||||||| ||| |||||| ||||| |||||| ||||

TGACCAAGAGAAAGTGGGAG CA GGTAGTGGTGAA TTC TGAATG GGAGG GAAAGA CCAG /

GGTGAGTAAGTACTCTTGAA TT G TCA- AGTG- GT GAA-- T

GTGGTGATGGTTACA

GAM2681 CTATTTGTTTGTGTATGAGC 62565 TGTATGAGCT 62566 T G AT-- ---- T TT

TAGGTATTGGTTAATTCCAT AGGTATTGGT CTATT GTTT TGT GAGCTA GGTAT GG A

GCTTAAGTGGTTCTACCATA TAAT ||||| |||| ||| |||||| ||||| ||

GGAACGATAG GATAG CAAG ATA CTTGGT TCGTA CC A

- G CCAT GAAT - TT

GAM2682 GAGGAAGATTAAGAAAAACT 62573 AGAAAAACTG 62574 TTAAGAAA AT--------- T

GCTTATTGGGTCTTTCCGTG CTTATTGGGT GAGGAAGA AACTGCTT TGGG C

TTTTAGATGAAGCAGTTGAA CTTT |||||||| |||||||| ||||

ATTCTTCCTC CTCCTTCT TTGACGAA GCCT T

TAAAG--- GTAGATTTTGT T

GAM2683 TGAAATGGACTATGTAAGCT 62602 GACTATGTAA 62603 AA GA A AAG-- GGG-- CA

GGGGGCACATATATGTATAT GCTGGGGGCA TG ATG CT TGT CTG GCA T

ACGGAGGAAACAAGGACATG CATA || ||| || ||| ||| |||

GCA AC TAC GA ACA GGC TGT A

GG AG - AAGGA ATATA AT

GAM2684 GCTGGGGCCATATATATGTG 62609 TACCTGGCAT 62610 G C ATA G A-- A

CAGGACATTAACGATGATAC AAGGTGCCCG GCT GGGC AT TATGT CAGG CATT A

CTGGCATAAGGTGCCCGGGC GGC ||| |||| || ||||| |||| ||||

CGG CCCG TG ATACG GTCC GTAG /

G - GA- - ATA C

GAM2685 GCCACATTGGACCACAGGTG 62642 TATCACAGAC 62643 A T GA ACAG--- ACCA

GTGCCACCATTACAGGTATC TAAGGGACAT GCC CAT G CC GTGGTGCC T

ACAGACTAAGGGACATGAGG GAGG ||| ||| | || ||||||||

C CGG GTA C GG CACTATGG /

A - AG AATCAGA ACAT

GAM2686 TTATGTGTATAACACAGAAA 62658 TATAACACAG 62659 - ACAGAAA GAAA- G AAAG

AGGAAATATGGCTAAAGGTA AAAAGGAAAT TTATGT GTATAAC AG TATG CT G

AAAGGCATGGTAGACTATAA ATGG |||||| ||||||| || |||| ||

AGGGTTGTACTATATGA AGTATA CATGTTG TC GTAC GA /
T GGAAATA AGATG G AAAT

GAM2687 GACCGCCTATTAGGTGTGGC 62670 TATTAGGTGT 62671 -- C- C-- GGG G TA
TTCGGGCTCCGCCTAGTGGG GGCTTCGGGC GACC GC TATTAGGTGTGG TTC CTCC CC G
AGGAGACAGGAAAACCACGC TCCG |||| || |||||||||||| ||| |||| ||
CTAGTGACGCTGGGTC CTGG CG GTGATCCGCACC AGG GAGG GG /
GT CA AAA ACA A GT

GAM2688 AAACAGCTAACGTTGGGCCA 62677 ACGTTGGGCC 62678 A AAC- AACAGGA C T G --
- C- G
AACAGGATATCTGCGGTGAG AAACAGGATA AC GCT GTTGGGCCA TATCTG GG GA CA
GTTT GGCCCCG C
CAGTTTCGGCCCCGGCCCGG TCTG || ||| ||||||||| |||||| || || || |||| |||||||
GGCCAAGAACAGATGGTCCC TG CGA CAACCCGGT ATAGAC CC CT GT CAAG
CCGGGGC /
CAGATATGGCCCAACCCTCA A CTCC ------- - - G AGA AA C
GCAGTTT

GAM2689 ATGTTGTTTTACGATATAAT 62687 TGTAACATAT 62688 TTTACG A-- ----- A
ACAACTATAAAATATGGAGA ATAACAGTAC ATGTTGT ATATA TACAA CTATA A
TCTTGTAACATATATAACAG AACA ||||||| ||||| ||||| |||||
TACAACAT TACAACA TATAT ATGTT GGTAT /
TGACAA ACA CTAGA A

GAM2690 GTGCGGAGCACTTCTCTGAT 62708 CAGGATGTAA 62709 CACTT - - G GTGA CA T
- C CCG
GCGCCGGCCGTGACGGCAAG TCAGAGCTCT TGCGGAG CTCTGAT GCG CC GCC CGG
AG ACTTTG AC TGG C
TACTTTGACCTGGCCGCAAT CCGC ||||||| ||||||| ||| || ||| ||| || |||||| || |||
TCCACGTGTAGAGTTCTCCC GCGCCTC GAGACTA TGT GG CGG GCC TC TGAGAT
TG ACC A
GAGGGCAGGATGTAATCAGA TC--- A A A GA-- C- T G C TTA
GCTCTCCGCGC

GAM2691 GGAGCACTTCTCCGATGGGT 62731 TCCGATGGGT 62732 - TTCT GG TC-- A AC
CGGTCGTGACTCCACGTGCG CGGTCGTGAC GGAG CAC CCGAT GTCGG GTG CTCC G
GAGCACTTCTCCGATGGGTC TCC |||| ||| ||||| ||||| ||| ||||
GGTCGTGACTCC CCTC GTG GGCTG TAGCC CAC GAGG T
A CT-- GG TCTT - CG

GAM2692 GTTCAGGGGTTCGTCGAACC 62740 AACCGTACCA 62741 GG TC G CCACAGCC
CGTTT
GTACCACAGCCTGGTCGTTT CAGCCTGGTC GTTCA GGT GTCGAACC TA TGGT A
AATCTCAACCAATATTTTCT GTTT ||||| ||| |||||||| || |||
AGGGTTCGACATCATGAAC CAAGT CTA CAGCTTGG AT ACCA A

A- -- G CTTTTATA ACTCT

GAM2693 GCCTCGTTTGCCCATTTTCT 62746 TCTATGATTT 62747 - GATTTTTTT GG---
TCTGTCTTCT- TAC
ATGATTTTTTTTTACCTCGG TTTTTTACCT ATTT TCTAT TTACCTCG TTCTAGA
CCATA T
GTTCTAGATCTGTCTTCTCC CGGG |||| ||||| |||||||| ||||||| |||||
ATATACTCATTGTGGTCATA TAAG AGGTG GGTGGGGGC GAGGTTT GGTGT
/
TTTTTTTTTGGAGGGAGGCG G --------- GGAGG TTTTTTATACT TAC
GGGTGGGTGGAGGAATGGGT
GGAGGAAGT
GAM2694 CCATGACCCTTATGATTTGC 62751 TGATTTGCCA 62752 AT - GA- - AAA C TCATCAA
CAAAAAAGCGGTTTCATCAA AAAAAGCGGT CC GAC CCTTAT TTTG CC AAAG GGTT G
GATTTTCTAACCCTTTCACG TTCA || ||| |||||| |||| || |||| ||||
GATGAAGAAATAAGGTGTTC GG TTG GGAATA AAGT GG TTTC CCAA /
GG C- T AAG A CAC - TCTTTTA

GAM2695 GGCGGGGTGGGTGGAGGAAT 62774 CTTTTCCGCT 62775 GGT A- GAGG
GGGTGGAGGAAGTACACCCG TCAACCGTT GGCGG GGGTGGAGGA TGGGTG A
GCTTTTCCGCTTCAACCGTT ||||| |||||||||| ||||||
TTGCC TTCGCCTTTT GCCCAC /
AAC CG ATGA

GAM2696 CCTTTCATTGTAAATGTATG 62792 TGGCACAAGA 62793 AAA--- A- ---- - ----------
T
GTTTGATAATGATGAAAGAA CTGAAGGG GT TGT TGGTT TGATAATG ATGAAA
GAAA T
ATTCTTTTCCTTATACCTGT || ||| ||||| |||||||| |||||| |||||
TGGGATTTTATATATTATCA CA ACA ACCAG ACTATTAT TATTTT CTTT C
AGATGACCAAAACAAATGGC CGGTAA AA TAGA A AGGGTTGTCCATATTC
T
ACAAGACTGAAGGG

GAM2697 GGGATACTGTTCGCTTTTTT 62860 TACTGTTCGC 62861 GG C CTTT T TTA
CTTTCGTGTCTGTTTATCTT TTTTTTCTTT G ATACTGTT GCTTTTTT CG GTCTGT T
ATAGATCGTGCCGAGGAAGT CGTG | |||||||| |||||||| || ||||||
AGCAGTATTTC C TATGACGA TGAAGGAG GC TAGATA /
TT - CCGT - TTC

GAM2698 CCTTACACATGTGATTACAT 62867 TACATGATAG 62868 A GTGA-- AG-- TA----
TACAT
GATAGACTTATTAGTAGTAG ACTTATTAGT CCTT CACAT TTACATGAT ACTTATTAG
GTAGA C
ATACATCTAAATTCTACAAC AGTA |||| ||||| ||||||||| ||||||||| |||||
GACCTAGTAAGTATTAGTTA GGAG GTGTA AGTGTATTG TGAATGATC CATCT /

```
    TGTGAAATAGAATGTGGAGG                  -   AGATAA      ATTA      CAGCAA    TAAAT


GAM2699  TTTATGCTTGCATTATTAAT 62874   TACACAATAC 62875         - TTATTAA    - A-  TG T
         GGTATGTAATATGATTGATT      CAATTTGTCA      TTTATGCTTG CA     TGGTAT GT  ATA  A T
         GTGTACACAATACCAATTTG      AGTA          |||||||||| ||     |||||| ||  |||  |
         TCAAGTATGAA                   AAGTATGAAC GT     ACCATA CA  TGT  T G
                                      T  TTA----     A  CA   GT A


GAM2700  TGGCCCCGTAAGAGGCAGTC 62888   CTAAGGCTAC 62889     C  C   - -      ---    AT- - GT
         ATAGCTATGGCCGTGTTGGT      ATTGGCTGCT       TGG CC GTAA GA GGCAGTCA   TAGCT   GG CC
G
         CCTAAGGCTACATTGGCTGC      GTCT          ||| || |||| || ||||||||   |||||   || ||
         TGTCTTTATTGGTCCA                  ACC GG TATT CT TCGTCGGT   ATCGG   CC GG  /
                                  T  T   T  G      TAC    AAT  T  TT


GAM2701  GGGAAATTTGTTCAACGCAT 62924   TGGAATCGTC 62925     A-     TCA   CATT      TC
         TTTTCAATTTCACGCAATTG      ACGCAGATGC       GGGA  ATTTGT   ACG    TTTCAATT  A
         GAATCGTCACGCAGATGCTC      TCTC          ||||  ||||||   |||    ||||||||
         TC                           CTCT  TAGACG   TGC   AAGGTTAA  C
                                       CG     CAC   T---      CG


GAM2702  GATTCATCTACAAAAACTAA 62938   TTCATCTACA 62939    T   CTACAAAAACTAATC    TAA
         TCCATTATAACTTATTAGTG      AAAACTAATC       GA TCAT          CATTA   C
         CTACTTTTCTATAAGTGATT      CATT          || ||||          |||||
         C                          CT AGTG          GTGAT   T
                                    T   AATATCTTTTCATC-    TAT


GAM2703  TTGATTTGAACATAGTCATA 62946   TCTAATAGAT 62947   A    TAAG   ATAAA  A  CT     CT   T T
AT   CC   CTG
         AGGGGATAAATAATACTTTA      AGCCCTGACT       TAGTCA   GGG    TA TA  TTATATTT  GAT G GG
TGA  CATT   C
         TATTTCTGATTGTGGATTGA      AGAC          ||||||   |||    || ||  ||||||||  ||| | ||  |||  ||||
         CCCATTCTGCTTAAAATGCT                ATCAGT   CCC    AT AT  AGTGTAAA  TTA C CC  GCT
GTAA   T
         TCGCCCATTGAAAATGTGAT                -    ----  GATAG  A  CT     AG   - - --   TC    AAT
         CTAATAGATAGCCCTGACTA
         GACAAATTAA
GAM2704  TCCAGAAAGCTCTCCAGACC 62952   ACAGTATACA 62953      AAGCTCTCCA   CATTT      AT
         ATTTTACTGTTTATACACAA      AGTCATTTTA       TCCAGA       GAC    TACTGTTT  A
         ACAGTATACAAGTCATTTTA      TGAA          ||||||       |||    ||||||||
         TGAATCTGGA                    AGGTCT       CTG    ATGACAAA  C
                                    AAGTATTTTA   AACAT      CA


GAM2705  GCTTTTCGTCTCTCCAAGGA 62970   CAAGGAACAC 62971      TC   TCTCCAA  A   TG    GCT
```

ACACTGGGTCCGCTGAAAGG TGGGTCCGCT GCTTT GTC GG ACAC GGTCC G
GACCGTGTACCGACCAAAGC GAAA ||||| ||| || |||| |||||
CGAAA CAG CC TGTG CCAGG A
C- ------- A -- GAA

GAM2706 TATGCTACTATTGATGTACA 63022 TACTATTGAT 63023 C TATT --- ATT CAC
ATTTGACACACGCTTCATTA GTACAATTTG TATG TAC GATGTA CA TGA A
TGAACTACATCCTGTACCAT ACAC |||| ||| |||||| || |||
G GTAC ATG CTACAT GT ACT C
C TC-- CAA ATT TCG

GAM2707 GGCCGTCTGGTTCGAGGATA 63035 GAGGATATGA 63036 C GT- A T- TG - C C
TGACCCCCGCCGAGCTGGAG CCCCCGCCGA GGC GTCTG TCG GGA A ACC CC GC G
GTTGTCTTCCCGACTACGGA GCTG ||| ||||| ||| ||| | ||| || ||
CGCC CCG CAGGC AGC CCT T TGG GG CG /
- ATC - TC GT A T A

GAM2708 TCTAAACAGTTGGCGTTAAC 63048 TACAGCATTT 63049 - GG -- - TT A- AGATTT
TT
GCTTATGCATACATTCAGAT GCTGTTGTAA TCTAAAC AGTT CGTTA AC GC ATGC TACATTC
TATGTGC T
TTTATGTGCTTTATTGCATG CGGG ||||||| |||| ||||| || || |||| ||||||| |||||||
TACGAATGTACAGCATTTGC AGATTTG TCGG GCAAT TG CG TACG ATGTAAG
ATGTACG A
TGTTGTAACGGGCTAGTTTA A -- GT T TT AC C----- TT
GA

GAM2709 AATGACCTATATGTTAATAC 63064 TAATACTCGA 63065 CC TGTTA CG-- TG TG T
TCGATTGATATTGATATTGA TTGATATTGA AATGA TATA ATACT AT ATAT ATA T
TATTGATATTGATAATTAGT TATT ||||| |||| ||||| || |||| |||
GTATATTATATTTCATT TTACT ATAT TGTGA TA TATA TAT G
TT TATA- TTAA GT GT A

GAM2710 ATGTCTATCCAGTATATGCG 63067 TACAATATCT 63068 TATCCA -- AG A--- TA- T T
GT
AGTAAGTCTTATCTTGTCAT GTATAAGTAC ATGTC GTAT ATGCG TA GTCT TCT GTCA
TG T
TGGTTTACATTGATCAGAGT CCTT ||||| |||| ||||| || |||| ||| |||| ||
CAGATACAATATCTGTATAA TACAG CATG TATGT AT TAGA AGA TAGT AC /
GTACCCTTCCGACAT CCTTCC AA CT AACA CTG C T AT

GAM2711 GTACTGGGTCTCTCTGGTTA 63077 TCTCTGGTTA 63078 C C A TCT CT
GACCAGATCTGAGCCTGGGA GACCAGATCT GTA TGGGT TCTCTGGTTAG CCAGA GAGC G
GCTCTCTGGCTAACTAGGGA GAGC ||| ||||| |||||||||| ||||| ||||
ACCCACTGC CGT ACCCA AGGGATCAATC GGTCT CTCG G

C - - --- AG

GAM2712 CACGCTTGCTTGCTTAAAGA 63096 AAGCTGCCAG 63097 - A---------- A
CCTCTTCAATAAAGCTGCCA TTAGAAGCAA CACGCTTG CTTGCTT AAG C
GTTAGAAGCAAGTTAAGTGT GTTA |||||||| ||||||| |||
G GTGTGAAT GAACGAA TTC C
T GATTGACCGTCGAAATAAC T

GAM2713 GCTCTGCGGAGAGGCTGGCA 63128 AGAGGCTGGC 63129 GGAG- - C TC CT
GATCGAGCCCTGAGAGGTTC AGATCGAGCC GCTCTGC AG GCTGG AGA GAGCC G
TCTCCAGCACTAGCAGGTAG CTGA ||||||| || ||||| ||| |||||
AGC CGAGATG TC CGACC TCT CTTGG A
GACGA A - -- AG

GAM2714 TTAGTGACAGTCCAGACCTA 63241 TCCAGACCTA 63242 ACA GA A--- TC
GGAGCTATTCTACCATAGCA GGAGCTATTC TTAGTG GTCCA CCTAGG GCTAT T
GAACTTAGGCATGGACATAC TACC |||||| ||||| |||||| |||||
TAA AATCAT CAGGT GGATTC CGATA A
A-- AC AAGA CC

GAM2715 ATCATTTATTTATTGTATAA 63271 TATTTTATTA 63272 TTA- ------- AA CA- TA AAAAT
TA CT
TATTTCATATATTTTATTAA AAATTTACAT TTTA TTGTAT TATTT TA TTTTATT T
CATATT A
AATTTACATATTCTAACAAA ATTC |||| |||||| ||||| || ||||||| | ||||||
TGTGCGATAACAATAAAAAT AAAT AATATA ATAAA AT AAAATAA A GTGTAA
A
TAGATAAATAGGATATAAAA CTCG TTAACAA GG TAG TA CAAT- GC AC
CAATTTAAAGCTCAGGAT

GAM2716 AAAATGGCATATTTTAATAT 63278 AATGGCATAT 63279 - TT- TATATAT TT
ATATGATTTTTATAGTCTTT TTTAATATAT AAAATGGC ATAT TAA GATT T
AATTTTATTTATATAGTCAT ATGA |||||||| |||| ||| ||||
TTT TTTTACTG TATA ATT CTGA /
A TTT TTAATTT TA

GAM2717 ATGATATAAAAGAGTGCTAA 63289 TGCAACAGTC 63290 TATAAAA CTAAATTTTT TAAACTT-
- TCCTA TT CTC
ATTTTTGAGTAAACTTGCAA CTAACATTCA A GAGTG GAG GC AACAG ACA
CAC T
CAGTCCTAACATTCACCTCT CCTC | ||||| ||| || ||||| ||| |||
CGTGTGTTTGTGTCTGTTCG T CTCGC CTC CG TTGTC TGT GTG /
CCATCCCGTCTCCGCTCGTC CACTG-- ---------- TGCCCTAC C TG--- TT TGC
ACTTAT

GAM2718 TTTTTGGAGGTTCGCTTTTC 63313 TTGGAGGTTC 63314 - TT------ C ATA T
TATATCTCATGAAGAAAGTC GCTTTTCTAT TTTTTGG AGG CG TTTTCT TC C
GCTGTTCGTCCTACTAAAAA ATCT ||||||| ||| || |||||| ||
AAAAATC TCC GC GAAAGA AG A
A TGCTTGTC T --- T

GAM2719 GAGCATGAGAGCGGCTTTAG 63322 TGAGAGCGGC 63323 G - G AG TC AT TTT-
AA CCT A
CGTAAAGTTTTTCTCCGATA TTTAGCGTAA AGAGCGGC TTTA CGTAA TTTTTC CG AGT
GAT AGGT TAAG A
GTTTTGATAAAGGTCCTTAA AGTT |||||||| |||| ||||| |||||| || ||| ||| |||| ||||
GAATCTTAACCTATCCCTTA TTTTGCCG AGAT GCGTT AAAAAG GT TCA CTA TCCA
ATTC /
CTCTGATGAAAAAGATTGCG A C G AG TA C- TTCC -- --- T
GTAGACGCCGTTTTAGAAAT
C
GAM2720 CAGCTTCGAGGTATAACCTA 63326 ATGATGTTTT 63327 --- A CAACAC G -- T GAA
CTT
CAACACGGAGGGGAAGGGGG GTCCCTCTGT TATA CCTA GGAGGG AAG GGGGGG
ACAAAACGT ATTAGA T
GGTACAAAACGTGAAATTAG CTTA |||| |||| |||||| ||| |||||| ||||||||| ||||||
ACTTTTTTTTTAATGATGTT ATGT GGAT CCTTTC TTC TCTCCC TGTTTTGTA
TAATTT /
TTGTCCCTCTGTCTTACTTT GGA C AC---- A TG - G-- TTT
CCCATAGGCTGTAAGGCCCT
CGAGGAAGAG
GAM2721 AAGACTGAGAAAACTCGATG 63348 GGTGCATAAT 63349 GAAA-- TCG --- C
TACTTCCGAGGATGTGGTGC GTCACACATC AAGACTGA AC ATGTACT TC G
ATAATGTCACACATCAGTCT AGTC |||||||| || ||||||| ||
T TTCTGACT TG TACGTGG AG A
ACACAC TAA TGT G

GAM2722 GTTGAAAATAACTTTATAGA 63358 TAGAATTTTA 63359 ACTTTATA A TTTCTTTATT
CT
ATTTTAAAATTTTCTTTATT AAATTTTCTT GTTGAAAATA GAATTTT AAAT AAAAT T
AAAATCTTTTGTTTTTCTTT TATT |||||||||| ||||||| |||| |||||
TATTATTTCAAAATTTTGTT TAATTTTTGT TTTAAAA TTTA TTTTG /
TTTAAT -------- C TTATTTTCT- TT

GAM2723 GGTGTGAATATCAAGCAGGA 63367 AAGCAGGACA 63368 GAATATCAA- - GA- TAACAAG
GA
CATAACAAGGTAGGATCTCT TAACAAGGTA GGTGT GC AG CA GTAG T
ACAATACTTGGCACTAGCAG GGAT ||||| || || || ||||
CATTAATAACACC CCACA CG TC GT CATC /
ATAATTACGA A ACG TCATAA- TC

GAM2724 CACAATGGTAAGCCAGTGGT 63423 TACTATGTTA 63424 AAT A- CCA- GGTAT
AGTAAAGGTATAAGAAATTT CTGAACCTAG CAC GGT AG GTGGTAGTAAA A
GCTACTATGTTACTGAACCT GTG ||| ||| || ||||||||||
AGGTG GTG CCA TC TATCATCGTTT /
GAT AG ATTG AAAGA

GAM2725 GATCCTGCTGTCTCTACAGC 63437 TGGAATGGTG 63438 T C TC T ------ ACA
ATCATTCCAGGCACAGAACG CTGTTGAATC GA CCTG TG TC ACAGCATCATTCCA GGC G
CCAAAAAATGGAATGGTGCT AACA || |||| || || |||||||||||||| |||
GTTGAATCAACAGGTTC CT GGAC AC AG TGTCGTGGTAAGGT CCG /
T A TA T AAAAAA CAA

GAM2726 GGGAGACGGGGTTGGTTTGG 63453 TAGCACATGT 63454 GG - T TT GG TT TTG
GGTTGGTTTGGGGTTGGTTT CTGCATTTGT G AGACGGG GT GG TG GTTGG TGGGG G
TCCCGTTAGCACATGTCTGC TTTT | ||||||| || || || ||||| |||||
ATTTGTTTTTC C TTTGTTT CG CT AC CGATT GCCCT /
TT A T GT A- -- TTT

GAM2727 GCTTACCAGTAGACAAAGAG 63467 TAGCTCCCTA 63468 ACC ACAAA AC - ACA----- -
CAA
CACAGCAGTACAAGCGCCAA TTTAAAGGC GCTT AGTAG GAGC AG CAGT AG CGC C
CAGCAGCGACTGACTACCCA |||| ||||| |||| || |||| || |||
CTGACTTAGCTCCCTATTTA CGGA TTATC CTCG TC GTCA TC GCG A
AAGGC AAT C---- AT A CCCATCAG A ACG

GAM2728 ATGACTCGGCGCCGACTCGG 63525 TAGGTGGGTC 63526 GC GA GGC- G AAAA GGAT-
GACA GGTAG
CGACCGGCCAAAAGGTGGTG TTAAGAGAAG GCC CTC GACC GCC GGTGGT
GGGTGAT GGGTT G
GATGGGTGATGACAGGGTTG GTTA ||| ||| |||| ||| |||||| ||||||| |||||
GTAGGTCGTAAATCCCGGTC TGG GAG CTGG TGG TCACCG TCCACTG CCTAA
/
ACCTTGGTAGCCACTATAGG AT AA AATT G ATA- ATGGT GC-- ATGCT
TGGGTCTTAAGAGAAGGTTA
AGATTCCTCT
GAM2729 TAGAGCAATTTATAGATTCT 63533 TCAGTACTAG 63534 AGA A- - ---- A G - GTT
GT
GAAGTGCTTTTATTGCTGAT TGGAATAGTT TTCTG AGTG CTTT TATTGCTG TAACTGTT
TACT GTAT GAT G
AACTGTTGTACTGTATGTTG AACG ||||| |||| |||| |||||||| |||||||| |||| |||| |||
ATGTGGCTGTCTCAGTACTA AGGAC TTAC GGGA ATGATGGC ATTGATAA GTGA
CATG CTG G
GTGGAATAGTTAACGGTAGT --- AG A CATC A G T ACT TC
ACTACAGGGACATTGACAGG
AACAGGTTTGA
GAM2730 TATCTAAGATAACACAGCAA 63536 TATCAAAGAT 63537 TAA- CAGCAAT GGA T
AGT- CA

TAGATCGGATGATTTACTAA CTTGTTATCG TATC GATAACA AGATC TGAT TACTAA
CAT A
AGTCATCAATGGTGTCCGTT ATTG |||| ||||||| ||||| |||| |||||| |||
AGTATATCAAAGATCTTGTT ATAG CTATTGT TCTAG ACTA ATGATT GTG /
ATCGATTGATA TTAG ------- AA- T GCCT GT

GAM2731 GCGGCGTGGATATATACTCC 63539 TGACTGGCGT 63540 C A A T C ------ TCA
AGCCAGAAAAGACTCAGATT ACATAGCCAT GCGG GTGG TAT TAC CCAG CAGAAA AGAC
G
GTCTCATGACTTTCTGACTG CCGC |||| |||| ||| ||| |||| |||||| ||||
GCGTACATAGCCATCCGC CGCC TACC ATA ATG GGTC GTCTTT TCTG /
- G C C A CAGTAC TTA

GAM2732 TGCTTGGTATGCATTGCTAC 63545 ATGCATTGCT 63546 TT T- -- CTA- C TTA
ACTTGCTTATGCTGCAACTG ACACTTGCTT TGC GG ATG CATTG CA TTGC T
CTTTCAATGAACATTCCCTT ATGC ||| || ||| ||||| || ||||
GCA ACG CC TAC GTAAC GT AACG /
TT CT AA TTTC C TCG

GAM2733 GCCTGGGCTCGCTCGCGGTC 63562 TTCACTCGCA 63563 ----- - TCAG GAT
AGGGATCGATGACGGGTTCA GAGCACAGAG GCCTGGGCTC GCTC GCGG GGATC G
CTCGCAGAGCACAGAGAGTC AGTC |||||||||| |||| |||| |||||
CGGGC CGGGCCTGAG CGAG CGCT CTTGG /
AGACA A CA-- GCA

GAM2734 GACTTGATTACCGTCGACGG 63575 CGCCACGTCT 63576 CT C T CC- - T-- AGG
CCCGGGCTCTTCGAGGTCCA TCGTCGCTGC GA TGATTA CG CGACGG CG GGC CTTCG T
CGAAGTCCGCCACGTCTTCG TGAT || |||||| || |||||| || ||| |||||
TCGCTGCTGATCGTCTC CT GCTAGT GT GCTGCT GC CCG GAAGC /
CT C C TCT A CCT ACC

GAM2735 TAAAATTTGTGTGTGCAGCA 63584 AGGAATGTAA 63585 ATTTG TGC GACGAATT A
CGAACCAA
ATTGACGAATTTATTCCATG AATTGTTATC TAAA TGTG AGCAATT TATTCC TGA C
ACGAACCAACATAAATAATT ACAA |||| |||| ||||||| |||||| |||
TAAGGAATGTAAAATTGTTA ATTT ACAC TTGTTAA GTAAGG ATT A
TCACAATGGCTTTA CGGTA TA- AAT----- A TAATAAAT

GAM2736 AAAGCAATCGTTACTTGATT 63614 AATCGTTACT 63615 AAT - TT TTT- A CTTCT
TTAAAGACTTCTCAATTTCT TGATTTTAAA AAAGC CGT TAC GA TA AGA C
CTCTACATTTCCTGTATACG GACT ||||| ||| ||| || || |||
GCTTT TTTCG GCA ATG CT AT TCT A
--- T TC TTAC C CTTTA

GAM2737 GGTGAAATCTTCTGGGCTAG 63618 TAGTGCTCTC 63619 T TCTTC CT G - TC-- CT
TGCTCTCACTCTCCTATCTG ACTCTCCTAT GG GAAA TGGG AGT CT CTCAC TCCTAT G
GCATAGGACTTCGTGAGTAG CTGG || |||| |||| ||| || ||||| ||||||
ACTTTCCCATTTCTTTTCTC TC CTTT ACCC TCA GA GAGTG AGGATA /
T T TCTTT TT - T CTTC CG

GAM2738 CAACTTGTTCTGAGACGTCT 63625 TCCCTGGGGC 63626 T ACG GAT AT ----- TG----- TA
AAAG G
GGATCTGATCCCGACCGCTG TAGCAGAAAC GAG TCTG CTG CCC GACCGC TCGT
CTGCC AC A
TCGTTACTGCCAAAGACGAA TCTT ||| |||| ||| ||| |||||| |||| ||||| ||
AGTGGTAGGCGCGAACCGTT CTC AGAC GAT GGG TTGGTG AGCG GATGG
TG A
TGTGGTTTCCCTGGGGCTAG - AA- --- CG TCCCT TTTGCCA CG ---- A
CAGAAACTCTTTAGGTTG

GAM2739 GCAGAGACGAAAGAGGAGTA 63650 AGGAGTACTC 63651 GA AA- T GAG G
CTCTTGAGTGCGCAGCGAGA TTGAGTGCGC GCAGA CG AGAGGAG ACTCTT TGC C
AGAGTTTTCTCTCAGCGAAT AGCG ||||| || ||||||| |||||| |||
CTGC CGTCT GC TCTCTTT TGAGAA GCG /
AA GAC - GA- A

GAM2740 AAATCTATCTTATATACACA 63659 TTAGTGTTTA 63660 AT --------- A TTCTATCAA
TAATTATTCTATCAATTTTA ATAAAAATAT AAATCT CTTATAT ACAC TAATTA T
CCAATTAGTTAGTGTTTAAT GGGG |||||| ||||||| |||| ||||||
AAAAATATGGGGGATTT TTTAGG GGGTATA TGTG ATTGAT /
-- AAAATAATT - TAACCATTT

GAM2741 TCCAATAGTACATTTTCCAG 63667 TTAGATATTA 63668 A- G TTCCAGAT T TGT ATTT
---- A
ATTAGATATTAATGTCGTAT ATGTCGTATT TCC ATA TACATT TAGATA TAA CGT GA
ACAG G
TTGAACAGAGCCTGTAACAT TGAA ||| ||| |||||| |||||| ||| ||| || ||||
CTCAATGTCTTTATTATCTA AGG TAT ATGTAA ATCTAT ATT GTA CT TGTC /
TAGCCAATGTAATATCCGGA CC A CCGAT--- T TCT ACT- ACAA C

GAM2742 TTATATATATACTAACATCT 63671 TATATACTAA 63672 G T---- C - G
ATACTACTAACCTAACTATG CATCTATACT ACTAACATCTATACTACTAACCTAACTATG
CCTAATG ATG AGT GTCGGC T
GCCTAATGTATGCAGTGTCG ACTA |||||||||||||||||||||||||||||| ||||||| ||| ||| ||||||
GCGTCGCCGACAACTACATT TGATTGTAGATATGATGATTGGATTGATAC GGATTAT
TAC TCA CAGCCG /
ATATTATTAGGCATAGTTAG - TATAT A A C
GTTAGTAGTATAGATGTTAG
TATATATATAA

GAM2743 CCCTGAAAATCTTATGTCAT 63679 TTACCTGACA 63680 TGAAAA -- TA C GA
ATACTGTGTGGACATATATA GATGAGGACA CCC TCTTA TGTCA TA TGTGTG C
TATTACCTGACAGATGAGGA TATG ||| ||||| ||||| || ||||||
CATATGGG GGG GGAGT ACAGT AT ATATAT A
TATACA AG CC T AT

GAM2744 TATGATATTTAAAATGGTTG 63689 TAATCTTTAT 63690 TAAAATGGTTGTTAT T- GCT
TTATATAAATTTACCGCTTA TCAGTATCAT TATGATATT ATAAA TTACC T
CAGGTAATCTTTATTCAGTA A ||||||||| ||||| |||||
TCATA ATACTATGA TATTT AATGG /
CT---------- CT ACA

GAM2745 AATATCATCTATTGAATATC 63702 AAGATTATTT 63703 C CT AT----- AAAT
TTTTTAAATTGCTAAAAAAG TGTTAATTCA AATAT AT ATTGA ATCTTTTT T
ATTATTTTGTTAATTCATTA TTAT ||||| || ||||| ||||||||
TATT TTATA TA TAATT TAGAAAAA /
T CT GTTTTAT ATCG

GAM2746 TTATATTTTTTAAATATTTA 63710 TACAATATTT 63711 T- ------- TTAT TCTAT
TACATATTATATTTTATTTC ATTAAAATGT TTATATTTT TAAATATT TATACATA ATTTTATT
A
TATATCATATAATAAAATTT AA ||||||||| |||||||| |||||||| ||||||||
TGTGTATATCGTTACAATAT AATGTAAAA ATTTATAA ATATGTGT TAAAATAA T
TTATTAAAATGTAA TT CATTGCT TT-- TATAC

GAM2747 GGTATTTTTATCATATTTAT 63723 TCATATTTAT 63724 ATTTT C TTATT TTT
TTAATATTTTTTCATTAATA TTAATATTTT GGT TAT ATAT TAATATT T
TTATCATATATAATATGACC TTCA ||| ||| |||| |||||||
CCA ATA TATA ATTATAA C
GT--- A TACT- TTA

GAM2748 CCCCCATCAGAAGGTTTAGG 63730 TTGTACATTC 63731 TCA TTTA TCCG TTAC
ATC
TCCGGTATTTACGCCTTTAT CCTTCTGGGG CCCCCA GAAGG GG GTAT GCCTTTATC G
CATCGGTAGATGGAGGTTGT G |||||| ||||| || |||| |||||||||
ACATTCCCTTCTGGGGG GGGGGT CTTCC CT CATG TGGAGGTAG /
--- ---- TA-- T--- ATG

GAM2749 CTGCTGCCGAGGAACTGCTT 63786 TCGCCCAACT 63787 CGA AAC- T ATA A - C
ACCTC
GATATGGACGGCCGCACCTC ACGCATACGC CTGCTGC GG TGC TG TGG CG G CGC A
AGAACAGCGACTCGCCCAAC CAGC ||||||| || ||| || ||| || | |||
TACGCATACGCCAGCAGCAG GACGACG CC ACG AT ACC GC C GCG /
A-- GCAT C CA- C T A ACAAG

```
GAM2750  AACGCTTAATAGAAATTATT 63794   TATTGTACAT 63795        --     ATTA    CAT--    TAT    T
         GTACATTTTTCTATTAGTAT       TTTTCTATTA       AACGCTTA  ATAGAA    TTGTA    TTTTC   TAGTA G
         GAGTGCTATGAAAATTTCCT       GTAT             |||||||| ||||||    |||||    |||||  |||||
         ACAAAAGTTCTGTTTTGAGT                  TTGTGAGT  TGTCTT    AACAT    AAAAG   ATCGT A
         GTT                                TT     GAA-    CCTTT    T--    G

GAM2751  CATAAATATTCTAAGCCAAA 63800   TTTGTTAGAA 63801      A       GC       TTTCTCGTG  T   C  C  T
 T
         TATTTTTCTCGTGATTAGTC       TATCTGTG         CATA ATATTCTAA  CAAATATT       AT AGT TG GT
AC T
         TGCGTTACTTCTGTCACCAC                 |||| |||||||||  ||||||||       || ||| || || ||
         ACTCATATTTTTCATGGTAT                 GTGT TATAAGATT  GTTTATGG       TA TCA AC CA TG C
         TTGTTAGAATATCTGTG                    C       --       TACTTTTTA  C   C  -  C  T

GAM2752  ATGGCGGTTGTACTGTAATT 63823   TCACGGAGAT 63824      GG    C   ATT--    AAAT-     TTTA
         TCTCAAATCAAAGTTTTAAA       ACTCTACACT       ATGGC  TTGTA TGTA    TCTC    CAAAGT    A
         GTATGCTTTGTCACGGAGAT       ACGA             |||||  ||||| ||||    ||||    ||||||
         ACTCTACACTACGAAGTTAT                  TATTG  AGCAT ACAT    AGAG    GTTTCG    A
                                  A-    C   CTCAT    GCACT     TATG

GAM2753  GTGACGGCCCCTGCGGTCGC 63829   CCGCACCATG 63830     -   GC   T C    GCCT   CTC   --   CC-
A
         CTGACCTCCGTTGCCCGGGA       TACGTCTTAG       GTG ACG  CCC G GGTC    GAC   CGT  TGC   GGG
C
         CACCCACCGCACCATGTACG       ACCA             ||| |||  ||| | ||||    |||   |||  |||   |||
         TCTTAGACCACGGGTTCGTA                  CGC TGC  GGG C CCAG    CTG   GTA  ACG   CCC /
         CGC                              A   TT   - A    ATT-   CAT   CC   CCA   A

GAM2754  GGTATTACCATAGACGCGGC 63843   TACCATAGAC 63844      TTA-    AG     G   ATAG     C  AT
         GTATAGTACCAGCGTATCTC       GCGGCGTATA       GGTA    CCAT  ACGCG CGT    TACCAG GT  C
         ACCTGGTAGCGGCGCGTAGT       GTAC             ||||    ||||  ||||| |||    |||||| ||
         GGATTTTGCC                      CCGT    GGTG  TGCGC GCG    ATGGTC CA  /
                                  TTTA    A-     G   ----      -  CT

GAM2755  CAAAGCATTGAAGGTGGCTC 63846   TGAATGGGGT 63847     A    TGAA   G   -    AGAG
GTTTCAG
         GCCTAGAGCGGATTGTTTCA       GAAGCAGCTA       CA AGCAT    GGT GCT CGCCT    CGGATT      T
         GTAGTCCATAAATCTGAATG       TGCT             || |||||    ||| ||| |||||    ||||||
         GGGTGAAGCAGCTATGCTGT                  GT TCGTA    TCG CGA GTGGG    GTCTAA      A
         G                                G    ----   A   A    GTAA     ATACCTG

GAM2756  GCTCGTATGAGCCGGTGATT 63870   TCAATGGTGT 63871       AT    -   ATT    AT   TC   CT     A
```

CCGTTATCATTCTTGCTGCG ACTCGGTTCA GCTCGT GAGCCG GTG CCGTT CAT TTG GCGTAT A
TATAACGTACGCTTAATTGT CGAG |||||| |||||| ||| ||||| ||| ||| |||||| GTCAATGGTGTACTCGGTTC TGAGCA CTTGGC CAT GGTAA GTG AAT CGCATG / ACGAGT -- T GT- CT TT T- C

GAM2757 TGACGAATTACGACATTATT 63875 TAGAGGACGT 63876 TACGACATTA A G TG- AC
TTAGAGGACGTGTGTGCGTA GTGTGCGTAC TGACGAAT TTTT GAGGAC TGTG CGT A
CATCAACGAGTCGCGGGTCC ATCA |||||||| |||| |||||| |||| ||| TTAAGAGGTTCGTCA ACTGCTTG GAGA TTCCTG GCGC GCA T
---------- A G TGA AC

GAM2758 CTTTCCACGTTGATCTTTTA 63886 TTGAAGCGTT 63887 C - TCTTTT---- TCT- T - T
TGTTTCTCTTCTGCGAGTTT GCAACATCTT CTTTC ACG TTGA ATGTTTC TC GC GAG T
ATTCAGTTGATTTTGAAGCG CGGC ||||| ||| |||| ||||||| || || ||| TTGCAACATCTTCGGCCGTT GAAAG TGC GGCT TGCGAAG AG TG CTT T
GAAAG T C TCTACAACGT TTTT T A A

GAM2759 CTATCGCCACGGAACTCACT 63894 AGAGGACGTC 63895 CGCCA GAACTCAC A TTATTTTA C C -- AT
AATTATGACATTATTTTAGA TGTTCGTATA CTAT CG TAATT TGACA GAGGA GT TG TTCGT A
GGACGTCTGTTCGTATATCA TCAA |||| || ||||| ||||| ||||| || || ||||| ACGAGTCTAAACTCCTTAAA GATA GC ATTGA ACTGT TTCCT CA AT GAGCA T
CGGTTTGTCAAGTTATACAA ATCA- AAAACAT- - TTGGCAAA - A CT AC
AACGACTAATAG

GAM2760 TAACAATATATTATTAGTTT 63901 TTAATAATAT 63902 ---------- TA
ATATTACTGAATTAATAATA AAAATTCCCA TAACAA TATATTATTAGTTTA T
TAAAATTCCCAATCTTGTTA ATCT |||||| |||||||||||||| ATTGTT ATATAATAATTAAGT T
CTAACCCTTAAA CA

GAM2761 AAGGTTAGTGAGATTCCTAT 63904 TTAGTGAGAT 63905 TT TTCCTATTCCAAAATCAT G T
TCCAAAATCATGAAGGAGTT TCCTATTCCA AAGG AGTGAGA GAA GAGT T
TGTATTCGTTTTTTCTCATT AAAT |||| ||||||| ||| |||| TTCCTT TTCC TTACTCT TTT CTTA G
TT TT---------- G T

GAM2762 GCTCCACCCCGCCGACGAGC 63914 GGACGGTGGG 63915 CA- GA AG- GG G GC
CGGCCGCCGTCCGGGTGCGC GGACGCGGGG GCTC CCCCGCC CG CC CCGCCGTCCG GT G
GGACGCGGACGGTGGGGGAC GCGG |||| ||||||| || || |||||||||| ||

GCGGGGGCGGGGCGCGAGC CGAG GGGGCGG GC GG GGTGGCAGGC CA C
CGC GG GCA G- G GG

GAM2763 ATCTATGAAAACAGACGACT 64052 ATCATACTAA 64053 - AAACAG G AAGAGA
GCTAGCA AA
ATAAAGAGATAGGCTAGCAA GTATAGTAGT ATCTA TGA AC ACTATA TAG ATTCT T
TTCTAATCGGGAATCATACT ATCA ||||| ||| || |||||| ||| |||||
AAGTATAGTAGTATCACATC TAGGT ACT TG TGATAT ATC TAAGG /
ATTGGAT T ACACTA A GA---- ATAC--- GC

GAM2764 TTCCCTAGTAAGGTGCGAGT 64062 TTAGGTGATC 64063 TAGTAA- GC- GTGA TT
GACTAGCAAGATTTACTCTT AAAACCGGTC TTCCC GGT GA CTAGCAAGA T
GTTAGGTGATCAAAACCGGT ATTG ||||| ||| || |||||||||
CATTGGGAG GAGGG CCA CT GATTGTTCT /
TTACTGG AAA AGTG CA

GAM2765 CTACTGGCAATACTAGATGA 64065 TGGCAATACT 64066 TG AA AGA T G --- -- A
CTTGTTGTCTAGACTTGGGA AGATGACTTG CTAC GC TACT TGACT GTT TCTAGA
CTTGGGAG AGGC G
GAGGCAGCGCTTTCCTTCCA TTGT |||| || |||| ||||| ||| |||||| |||||||| ||||
AGTGATCTGGGGGCAGTCAA GATG CG GTGG ACTGA CGG GGGTCT GAACCTTC
TTCG /
AGGTGAGCTGGTAG GT A- AA- - - AGT CT C

GAM2766 ACGTTCCACTCGTCCAGATT 64071 TAAGTGTAGA 64072 G A C CCA AA TA AC A
AAGTGTAGACCTTTACGTTA CCTTTACGTT AC TTCC CT GT GATT GTG GACCTTT GTT A
ATAACAAGAAGGTTGTCACG AATA || |||| || || |||| ||| ||||||| |||
CGATCAGTGCAAGCGGAAGG TG AAGG GA CG CTAG CAC TTGGAAG CAA /
T G C A TGA CG TG AA T

GAM2767 GTGGTCTATTCTTTTTCGTT 64075 CTGCGGGGTG 64076 G AT - GT TG T ATCC- C
TGCCTCTGATCCTGGGCGGT ATAGATAAAA GT GTCT TCTTTT TC T CC CTG TGGG G
CCGTACTGCGGGGTGATAGA GAAG || |||| |||||| || | || ||| ||||
TAAAAGAAGACAAC CA CAGA AGAAAA AG A GG GGC GCCT /
A -- T AT GT - GTCAT G

GAM2768 AGAACAAAAAGTGTGTGTCT 64093 TGTGCAGTAG 64094 --- AA --- T CATT -- TT
C
GACATTCACATTTATTTTTA AGTTGTGCCT AGAACA AA GTGT GTGTC GA CACA TTTATT
TACAAGA A
CAAGACAATTTTGTGCAGTA TCCG |||||| || |||| ||||| || |||| |||||| |||||||
GAGTTGTGCCTTCCGACACC TCTTGT TT CGCG CACAG CT GTGT AGATGA
GTGTTTT /
CCGCGCCGTTCGCTGTTCT CGC GC CCC C TCC- TG C- A

GAM2769 TCTCTATCCAAGGATGTAAT 64104 TCCAAGGATG 64105 ATCCAA T TTAAA TGA
TAAATGTTTGATCGATAACA TAATTAAATG TCTCT GGATG AA TGTT T
ATGTTTCCATCCATAGCAGA TTTG ||||| ||||| || ||||
GA AGAGA CCTAC TT ACAA C
CGATA- C TGTA- TAG

GAM2770 ACCGATTCTTCCTGTTTGAA 64108 ATCATGTTTT 64109 T TCCTGTTT CT-- TT
CGTCTATTTTTTTGTTAAGA TTCTCACAGT ACCGAT CT GAACGT ATTTTT G
ATTATCATGTTTTTTCTCAC ATCG |||||| || |||||| ||||||
AGTATCGGT TGGCTA GA TTTGTA TAAGAA /
T CACTCTTT CTAT TT

GAM2771 GAAGTGCGGTTCCAGAAGGA 64112 GGCGTAGATG 64113 GG GAAGG ATAAAAC
AG G
GTAATAAAACCTGTGCCTCA TGCTGTGGAA GAAGTGC TTCCA AGTA CTGTGCCTC CGG
T
GCGGGTGACTGGGAGGCGTA AGCA ||||||| ||||| |||| ||||||||| |||
GATGTGCTGTGGAAAGCATT TTTTACG AAGGT TCGT GATGCGGAG GTC G
TT A- G---- GTA---- G- A

GAM2772 GTATGTATGATAGTATATTT 64127 TGTATGATAG 64128 G G AG A TA
ATAAGATTAGTTTGTTATGT TATATTTATA GTAT TAT AT TATATTTATA GAT G
AAGTATGTAGTAGTAAGTAT AGAT |||| ||| || |||||||||| |||
TATG ATG TG GTATGAATGT TTG T
A A AT A TT

GAM2773 TGCTAAAATACAATCTAAAC 64131 TGTTAAAAAA 64132 AT CTAAACA - -- G CAG-
CCA G
AATAATGAATTGGTGTTAAA TCAGTATCCA ACAAT ATAAT GAA TTG TGTTAAAAAAT TAT
GCTTAGC T
AAATCAGTATCCAGCTTAGC GCTT ||||| ||||| ||| ||| |||||||||| ||| |||||||
GTGTGTTAAGTAATAAAGTA TGTTA TATTA CTT AAC ATAGTTTTTTA ATA
TGAATTG G
TTTTTTGATAACAAATTTCT -- ------- T TA A TGAA A-- T
ATTATATTGTTAAGCA

GAM2774 GTAATGGGGAACCGAAAACT 64145 TGGGGAACCG 64146 -- AAAC AA AAATACAGA
GAACCAAATACAGAAATTAG AAAACTGAAC GTAATGGGGAA CCGA TG CC A
AAGAGGAACATCGGCTTTTC CAAA |||||||||| |||| || ||
CCGTTAT TATTGCCCTTT GGCT AC GG /
TC ---- AA AGAAGATTA

GAM2775 GATGGGTGGGAAATATAATA 64194 TACACGGTTA 64195 G GAAATATAATAAAGC AAAT
CATAAAA

AAGCAACCGAAATGGTACAT CACCACCGAT GAT GGTGG AACCG GGTA A
AAAAACTAAAAATACCTACA C ||| ||||| ||||| ||||
CGGTTACACCACCGATC CTA CCACC TTGGC CCAT /
G ACA---------- ACAT AAAAATC

GAM2776 CCCCCCTCCCCCTGTGGTCC 64201 CTCGCACCAC 64202 CC C CCCCGAGA-- C- CC
CCCGAGACGAGAGCCACCCA CCACGACCAC CCC CTCCC CTGTGGTC CGAGAG CAC A
TCGTGTACTCTCGCACCACC AGAG ||| ||||| |||||||| |||||| |||
CACGACCACAGAGGGAGACG GGG GAGGG GACACCAG GCTCTC GTG /
GG CA A CACCCACCAC AT CT

GAM2777 AGATCCTGCTGTCTCCTCAG 64225 TGGAATGGTG 63438 T C TC CT ------ ACA
CATCATTCCAGGCACAGGAC CTGTTGAATC AGA CCTG TG TC CAGCATCATTCCA GGC G
GCCAGAAAATGGAATGGTGC AACA ||| |||| || || |||||||||||| |||
TGTTGAATCAACAGGTTCT TCT GGAC AC AG GTCGTGGTAAGGT CCG /
T A TA TT AAAAGA CAG

GAM2778 AGCGATTTATCTAAATTAAA 64226 TCTAAATTAA 64227 TATC TAAATTA TTAT TTTATAAC
TTACATTATGCTTTTATAAC ATTACATTAT AGCGATT TAAAT CA GCT T
TTACCTACTAGCCTGCCCAA GCTT ||||||| ||||| || |||
CATTTACACGATCGTT TTGCTAG ATTTA GT CGA /
CAC- CAACCC- C--- TCATCCAT

GAM2779 AAATAGCTAACATTAAGTAG 64233 TAGCTAACAT 64234 T--- - CAAG -- C GA A
CTAA TGA
TCAAGGAACGAAAACAGGAA TAAGTAGTCA TAAGT AGT GAA CGAAAA AGGAA ATTTTTG
TGT GGTG A
GAATTTTTGATGTCTAAGGT AGGA ||||| ||| ||| |||||| ||||| ||||||| ||| ||||
GTGAATTATTATCACAATAA ATTCG TCG TTT GTTTTT TTCTT TGAAAAT ACA
CTAT T
AAGTGATTCTTATTTTTGAA TATT A AAA- AA A AG A ---- TAT
TTTAAAGCTAGCTTATTATT
ACTAGCCGTTT
GAM2780 AGTTCTACATACCAGTGATT 64247 ACGCCTTTTT 64248 TCTACAT TTTCC---------- TT
TTTAC CT
TCCACGCCTTTTTGTTTATT GTTTATTTAC GT ACCAGTGA ACGCC TTTGTTTA
GC T
TACGCCTTCCGCATTCTAAA GCCT || |||||||| ||||| |||||||| ||
TAAGTGGTGTTTTATAAATC CA TGGTTACT TGTGG GAATAAAT CG /
CCCTGCTTCATTGGTTTTAA CTAATTT TCGTCCCCTAAATATTT T- CTTA- CC
TCACT

GAM2781 CATGGGCGGCGATATAAAAT 64262 CATCGTAGTC 64263 GC ATAAAA AAG -
CAAAAAATC- A
GCAAGGTGCTGCTCAAAAAA ATGCTCATG CATGGGCG GAT TGC GTGCT GCT
AGGC A

TCAGGCAAAGCCTCGCGCAA |||||||| ||| ||| ||||| ||| ||||
AAAAGCAAGCACATCGTAGT GTACTCGT CTG ATG CACGA CGA TCCG /
CATGCTCATG A- ------ CTA A AAAAACGCGC A

GAM2782 GGCCCGGGCTGCGCACGCCA 64288 TGAGTTCGCT 64289 C- A CCAGC A T A A----
--- TG
GCCGGGACGGGTGAGTTCGC AGGCAAGCAC GCTG GC CG CGGG CGGG GAGTTCGCT
GGCA GCACG GAC G
TAGGCAAGCACGGACTGGCG GGAC |||| || || |||| |||| |||||||| |||| ||||| |||
GTTACACGTGCATGCGTGCC CGGC CG GC GCCC GCCC CTCAAGTGA CCGT
CGTGC TTG /
GAGTGAACTCTCCCGCCCCG CT C A---- C T G GCGTA ACA GC
ACGCGCTCCGGCTCCGGGCC

GAM2783 GGGGGAGGGACGGGGAAGGG 64298 CCCGCCTTCG 64299 A A G G - C - T- CCTG
GGCGCGCGGGGCTGCCCTGC CGCCCCCCCC GGGGG GGG CG G AAGG GGGCG GCGG GGC
GC C
CGCCCGCCCGCCGCCGCCGC C ||||| ||| || | |||| ||||| |||| ||| ||
CCGCCTTCGCGCCCCCCCCC CCCCC CCC GC C TTCC CCCGC CGCC CCG CG C
C - G - G - G CC CCCG

GAM2784 ACGCGATTTATTTATTTCAA 64866 TTCAACGCGT 64867 TT-- TTATT ---------- T ---
CG TTC
CGCGTTCACAGTACGCTTTC TCACAGTACG GCGA TAT TCAAC GCGT CACA GTA
CT C
CACTTAGTATATAATTGTGA CTTT |||| ||| ||||| |||| |||| ||| ||
CGCATCCTTTTTTAATAAGT CGCT ATA AGTTG CGCA GTGT TAT GA A
TGATTCCTATACCATTCGCG TACC TCCTT AATAATTTTTTCCTA - TAA AT TTC
T

GAM2785 CACCCGTAGTTAACGCATCT 64869 TGAAGAGTAG 64870 ACGCA-- A CCATTACTG C
AT
ACAGATCCATTACTGAAGTA AAATAATTAC CACCCGTAGTTA TCT CAGAT AAGTA AC T
CACATTAACGTTGCTTATCT GGGT |||||||||||| ||| ||||| ||||| ||
GAAGAGTAGAAATAATTACG GTGGGCATTAAT AGA GTCTA TTCGT TG A
GGTG AAAGATG A --------- - CA

GAM2786 GTGTTCCCCAGAGCGTCTGT 64884 CCCCAGAGCG 64885 CC GCGT T T TCTTT-
TTCCAAC
GTATTCAGTTTCTTTCTTGA TCTGTGTATT GTGTT CCAGA CTG GTA TCAGTT CTTGAT
T
TTTCCAACTTAATCGCATCG CAGT ||||| ||||| ||| ||| |||||| ||||||
AGCATCGCGGCTGATTGCCC CACAA GGTCT GGC CGT AGTCGG GAGCTA /
GGTAATCTGGACAACAC CA AAT- C T CGCTAC CGCTAAT

GAM2787 TTCGTAATACTTGATATACT 64903 TTCAGAGTCT 64904 ACTT-- TAT GTC G

CGTCAGAAAGCAGTTTCTTC TCCTGAAAGT TTCGTAAT GA ACTC AGAAA C
AGAGTCTTCCTGAAAGTTAC TACG |||||||| || |||| |||||
GAA AAGCATTG CT TGAG TCTTT A
AAAGTC TC- ACT G

GAM2788 GACGCTAACCTCCTCCTTGT 64911 TGTACATATC 64912 C CCTCC-- GTCA- A C
CAGTGTACAACTGCACACGG AGAAGGATTT GA GCTAA TCCTT GTGTACA CTG A
CTGTACATATCAGAAGGATT ATAT || ||||| ||||| ||||||| ||| TATATTTGGCTC CT CGGTT AGGAA TACATGT GGC C
- TATATTT GACTA C A

GAM2789 ATCTAGTTGTATGAGTTTAT 64918 TTCACGGTCT 54694 TT - TTT TT - AAT CTTTAA----
----- AT
CGTTTACATAAGCAATTAAC TAGTATTTTT GTA TGAG ATCGT ACAT AAGC TAACGG
CAG G
GGCTTTAACAGATGATCTGA AGAT ||| |||| ||||| |||| |||| |||||| |||
GTAATAATATACCTCTGTTA TAT ATTC TGGCA TGTA TTTG ATTGTC GTC /
TACGTTTAATGTTCACGGTC TT G --- CT A CAT TCCATATAATAATGA TA
TTAGTATTTTTAGAT

GAM2790 GTTTAATGTTCACGGTCTTA 64919 TTCACGGTCT 54694 T -------- CTTA T
GTATTTTTAGATATCAATTG TAGTATTTTT GTT AATGT TCACGGT GTATT T
TGATTTACACCATATTCGAC AGAT ||| ||||| ||||||| |||||
CAG TTATA AGTGTTA TATAG T
C CCACATTT AC-- A

GAM2791 AAAATAAATTAGAAGCTGTG 64920 TAGAAGCTGT 64921 AAATT AG ----- - ATGAA-
TT
GGTCATTGTTATGAATCTCT GGGTCATTGT AAAAT AGA CTGTGG GTCA TTGTT TCTC
T
TTCAGAGGAATACAGACAAT TATG ||||| ||| |||||| |||| ||||| |||| TGACAAAATTCACAGACTCT TTTTA TCT GACACT CAGT AACAG GGAG /
CAAGATTTT GAAC- CA TAAAA T ACATAA AC

GAM2792 CCACCGCAATAGATCCTGTT 64927 TATCGCATTT 64928 C AA TCC TA - A C
AGATACATAGATCCTCGTCG TCTAACGTGA CCA CGC TAGA TGT GATA CAT GAT C
TGATATCGCATTTTCTAACG TGG ||| ||| |||| ||| |||| ||| ||| TGATGG GGT GTG ATCT ACG CTAT GTG CTG T
A CA TTT -- A - C

GAM2793 ACAGGCCTGGCCTGGTAAGT 64936 GCGCAGTAAA 64937 CC TA TCCC G -- - GA--
GTA AAG C
TCCCAAGTGGTAAGAGACCC TCGCGATGCG TGG AGT AAGTGGTAAGA ACCC GG CAC
AGT GT ACGC A
GGCACGAAGTGTAGTAAGAC TAGC ||| ||| |||||||||| |||| || ||| ||| || ||||

GCCATTGGCGCAGTAAATCG CGC AGA TACTATTTTCG GGCT GA GCG GCT TG
CGGT /
CGATGCGTAGCTTCGGGCTT C- -- AGT- - TC T TAGC AAA ACG T
TTATCATTGAAGACGCCCGC
CAGTAACTT
GAM2794 AAAATAAATTAGAGGCTGTG 64940 GGTCATTGTT 64941 AAATT G ----- - ATGAA- TT
GGTCATTGTTATGAATCTCT ATGAATCTCT AAAAT AGAG CTGTGG GTCA TTGTT TCTC
T
TTCAGAGGAATACAGACAAT TTCA ||||| |||| |||||| |||| ||||| ||||
TGACAAAATTCACAGACTCT TTTTA TCTC GACACT CAGT AACAG GGAG /
CAAGATTTT GAAC- A TAAAA T ACATAA AC

GAM2795 GCCGTCTTGCGAATCGTGAC 64947 TGTGTATGTA 64948 C TT AATCGT ---- A T---- -
C-- AT
GCTGGAGATGTTGCAACACC TAACTCATCC GC GTC GCG GACG CTGG GATG TGCA
ACAC TGC T
TGCATTGAGCAACTGTGTAT CGGA || ||| ||| |||| |||| |||| |||| ||| |||
GTATAACTCATCCCGGATAT TG CAG TGC TTGT GGCC CTAC ATGT TGTG ACG
/
TGTTTCAACCGTTTGACTGT T TT CAACT- TATA - TCAAT A TCA AG

GAM2796 GAGGAGAGACGCGACTTCTG 64960 TGGCATGCAG 64961 G ACTTC C - - ----------
--- G
GCATGCAGCCTGCTCCGGAC CCTGCTCCGG AG AGAGACGCG TGG AT GCAGCC TGC
TCCG A
ACGGATTCCCAATTACCACC ACAC || ||||||||| ||| || |||||| ||| |||| |||| |||
CCAAGCACGGCTGCTATTCT TC TCTCTGTGT ATC TA CGTCGG ACG AGGC
C
ATTTTATGTGTCTCTGCTT G ATTTT T T C AACCCCACCATTAACCCTT A

GAM2797 GCTCTCTACCTACAAGAATC 64981 TTTACAGCGC 64982 --------- ACC A ---- A TT T
ATTAGTGCTGAAGGTTCCTT TAGTATTAGA GCT CTCT TACAAGA TC ATTAGTGCTG
AGG CC T
TCGGGGTTTACAGCGCTAGT GTTT ||| |||| ||||||| || |||||||||| ||| ||
ATTAGAGTTTTGTAAGAGTT CGA GAGA ATGTTTT AG TGATCGCGAC TTT GG T
TATTATTAGC TTATTATTT --- G ATTA A GG C

GAM2798 AAAATAAATTAGAAGCTGTT 64984 TAGAAGCTGT 64985 AAATT AG TG----- - ATGAA-
TT
GGTCATTGTTATGAATCTCT TGGTCATTGT AAAAT AGA CTGT GTCA TTGTT TCTC T
TTCAGAGGAATACAGACAAT TATG ||||| ||| |||| |||| ||||| ||||
TGACAAAATTCACAGACTCT TTTTA TCT GACA CAGT AACAG GGAG /
CAAGATTTT GAAC- CA CTTAAAA T ACATAA AC

GAM2799 TTTATAGTTAGAAATGGATA 64989 TAATACCAAT 64990 AA--- - T TCTCTAA
ATAATCTTAAT-- A

ATTGAAATATTTTCTCTAAT AATCTTAATA AGA TGGATA ATTGAAA ATTT TACCA
ATAAA T
ACCAATAATCTTAATATAAA TAAA ||| |||||| ||||||| |||| ||||| |||||
ATCTTTTATCCTCATCTCAT TCT GCCTAT TAACTTT TGAG GTGGT TATTT C
CGTGGTGAATAAATGAGTCT ATAAA A C TAAATAA GCTACTCTACTCC T
TTCAATATATCCGAAATATC
TAACTCATGAA
GAM2800 AGTCGTTGAAACAATTGTTT 64997 TGCGTGGATA 64998 A--- TT AA CAA -- G T-----
C
AACAAACAACCCGTGTACGT AGGGATATTT AGTCGTTG AACAA GTTT CAAA CCC GT
TACGT GAGAG G
TGAGAGCGACTCTCCCATTT GGCA |||||||| ||||| |||| |||| ||| || ||||| |||||
GCGTGGATAAGGGATATTTG TCAGCAAC TTGTT TAGA GTTT GGG TA GTGCG
CTCTC /
GCAGATTTTGTTCTCGCAAC GCTC T- CG ATA AA G TTTACC A
GACT

GAM2801 TGGATAAGGAAGTTACGTAC 65001 AGGAAGTTAC 65002 A A A- TA- AG GT
GTAGATCCGTATAAGGATAA GTACGTAGAT TGGATA GGA GTT CG CGT ATCC A
ACGATTCGCAAATATCCTGT CCGT |||||| ||| ||| || ||| ||||
CTA ATCTGT CCT TAA GC GCA TAGG T
- A AC TTA AA AA

GAM2802 TTGCTGTTACAATAGTGGGC 65005 TGTTACAATA 65006 TG- A- ---- CCAC ACT AA
CCACTGTGACTAGAAAGCCT GTGGGCCCAC TTGC TTAC ATAGT GGGC TGTG AG A
TCGCACAGCCCTGAGATTAT TGTG |||| |||| ||||| |||| |||| ||
AAGTAGACTGCAA AACG GATG TATTA CCCG ACAC TC /
TCA AA GAGT ---- GCT CG

GAM2803 AGTGGTCCTTCAAAGTTATG 65018 TATGTTGCAC 65019 CCTTCAAA A CACTCA
GTACACA T
TTGCACTCATAGAAGTACAC TCATAGAAGT AGTGGT GTT TGTTG TAGAA CC C
ACCTCCGGCATCCATTCTGA ACAC |||||| ||| ||||| ||||| ||
AAAATAACAAAACACCACT TCACCA CAA ACAAT GTCTT GG /
-------- A AAAAA- ACCTAC- C

GAM2804 ATAAGTAGACTGCAACAACA 65033 TCTCGCGGTC 65034 T CT CAACATCGAAACC C A
TCGAAACCCCGCGACACAAA TTGCTCTCTT ATAAG AGA GCAA CCGCGA ACA A
TCTGTCTCGCGGTCTTGCTC AT ||||| ||| |||| |||||| |||
TCTTAT TATTC TCT CGTT GGCGCT TGT T
- -- CT---------- C C

GAM2805 TAAGAATGCATTTGTTCTGC 65044 ATGCATTTGT 65045 - C - TAGAAA AACT--
CAATTAT ATCTT G
CAATAGAAACTTAAACTGAG TCTGCCAATA CA TTTGTT TGC CAA CTTA GAGC
TATATA TG A

CCAATTATTATATAATCTTT GAAA || |||||| ||| ||| |||| |||| |||||| ||
GGAAACGTGTATGTATTTGC GT AAATAA ATG GTT GAGT TTCG ATGTAT GC
A
TTTTTCTGTGAGAAACTTGA C A A CAAA-- GTCTTT TTT---- GT--- A
GTAAAATAAACTGCCACATT
CTTG
GAM2806 TATAATGTACTAGATAATAT 65069 TAATATTATA 65070 A T GA TAAAG- ATTTAACCA
TATAAAGCCTTTATTTAACC AAGCCTTTAT TATA TG ACTA TAATATTA CCTTT A
AACCTATCTTCAAAGGACCG TTAA |||| || |||| |||||||| |||||
TCTGATGTTAAATGGTTCGA ATAT GC TGGT ATTGTAGT GGAAA /
TATA A T AA CTGCCA CTTCTATCC

GAM2807 TGCATTTTATGCAAAAAAAG 65077 TGCAAAAAAA 65078 A AAAAAA--- ATATG CTT
TTACA
AAAATATGAGCAGGCTTGGA GAAAATATGA TGCATTTT TGC AGAAA AGCAGG GGA
A
TTACAACCTCTTCCTCCTGC GCAG |||||||| ||| ||||| |||||| |||
TAAGGTTTCTGAGCAAAAAG ACGTAGAA ACG TCTTT TCGTCC CCT /
CAAAAGATGCA A AAAAACGAG GGAA- T-- TCTCC

GAM2808 GCCCTGAGCTCGCGCCTCAA 65131 CCTCAATGTC 65132 A GCGCCTCAA CAAAA CA
AG
TGTCAGCTGCAAAAAGTCAC AGCTGCAAAA GCCCTG GCTC TGTCAGCTG AGT CTTA T
TTAAGTCCTGGGCCACTACA AGTC |||||| |||| ||||||||| ||| ||||
GCTGACAATTCAGAGCCAGG CGGGAC CGAG ACAGTCGAC TCA GGGT /
GC - ACTTA---- A---- CC CC

GAM2809 GTTATCGCGCCACCTTGTGG 65153 TATCGCGCCA 65154 A TTGT TTATATA A TTTCC
TACTTTCA CTAT
CTACATTATATAGCACGATC CCTTGTGGCT CC GGCTACA GCACG TCAC ACGTTA
CGTA G
ACTTTCCACGTTATACTTTC ACAT || ||||||| ||||| |||| |||||| ||||
ACGTACTATGACTCATACGC GG CCGGTGT CGTGC GGTG TGCAAT GCAT
A
CTTAACGTCACGTGGCGTGC - ---- TAG---- - CAC-- TCC----- ACTC
GATTGTGGCCGGGGCTGAAA
AT
GAM2810 CGCAGTTCGGCGACACGCCC 65157 CTAAATCGCG 65158 C ---------- AC-- CC CAGC
AAT
GCGTCCCGACAGCAGAGGTA CGCGGGCTCA CG AGTTC GGCGAC GCCCGCGT CGA
AGAGGT C
ATCCCGAGCTTCTAAATCGC AGTC || ||||| |||||| |||||||| ||| ||||||
GCGCGGGCTCAAGTCGCCCT GC TCAAG CCGCTG CGGGCGCG GCT TCTTCG
C
TTTTGTCTCGAACTCG - CTCTGTTTTTC AACT C- AAA- AGC

GAM2811 CATCTATATCATTTCTATAT 65164 TCTATATCAT 65165 C CAT ATAAAA T TTTAAAA
AAAAATTTTGCAATTTTAAA TTCTATATAA CAT TATAT TTCTAT ATTT GCAAT A
AAATGTACCATTGTCAAATC AAAT ||| ||||| |||||| |||| |||||
TAGCCATAGAATCATATATA GTA ATATA AAGATA TAAA TGTTA /
TG T CT- CCGATC C CCATGTA

GAM2812 AAGGTTTCATCTAATCCTTT 65171 TTTTTCTATA 65172 TTTCATCTAAT TTTCCA AC TTC
TTCCAATAACAAAAATTTTT TCTATAGGGC AAGG CCTT ATA AAAAATTT G
CGTTATAAATTTTTTCTATA ATAT |||| |||| ||| ||||||||
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CCTT TTATAATATAC TATCTA CT TAT

GAM2813 GAGAGTGTGCCTTAGCTTGA 65178 TCTAGAGCTT 65179 TG G A- AA AC A T
AAGGCACTCTAAAGCTAATG CAGGTCAGAG GAGAG T CCTT GCTTGA GGC TCTA AGC A
CTCTAGAGCTTCAGGTCAGA GAGT ||||| | |||| |||||| ||| |||| |||
GGAGTGCTCTC CTCTC G GGAG TGGACT TCG AGAT TCG A
GT A AC -- -- C T

GAM2814 TGGTCCTGGCTACACACCCA 65191 CCTGGCTACA 65192 C C ACCCAA-- GTC
AAGGCACGTCAGACAGTGTC CACCCAAAGG TGGTC TGG TACAC AGGCAC A
TCTAAATCAGTGTACCAAGA CACG ||||| ||| ||||| ||||||
CCA ACCAG ACC ATGTG TCTGTG G
A - ACTAAATC ACA

GAM2815 CTCTTGAAGACATAAATACT 65213 TAAGCGTTCT 65214 GA CATAAAT TAT ATATA CT
ATTAAGAAATATATGGACTT TATACGTTCT CTCTT AGA AC TAAGAA TGGA T
TATTCTAAGCGTTCTTATAC AAAG ||||| ||| || |||||| ||||
GTTCTAAAGAG GAGAA TCT TG ATTCTT ATCT T
A- ------- CAT GCGA- TA

GAM2816 GGTTTGATTTAAGTAAATGA 65221 TTAGTTGTTT 65222 A TAA TG T TG TA GT
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T
TGAGTTTAATTAGATTAGTT AGTT |||||| |||||| |||||| || || ||| |||||||
GTTTAGTGATTTATAGTTTA TTAAAC AAATTT TATTTA GA TT TGA TTAGATT T
AAGCAAATT G GA- GT T GT -- AA

GAM2817 CCCTCACAGTTGCTGTGGTG 65227 TGTGGTGTTG 65228 TCA- TG TG- G- ATTCC--------
T
TTGTGATTCCTCTTCTGCAG TGATTCCTCT CCC CAGT C TG TGTTGTG TCTTC G
AAGATATTAATAAAGTGTAT TCTG ||| |||| | || ||||||| |||||
AACAGACAAATGTGACTGGC GGG GTCA G AC ACAATAT AGAAG C
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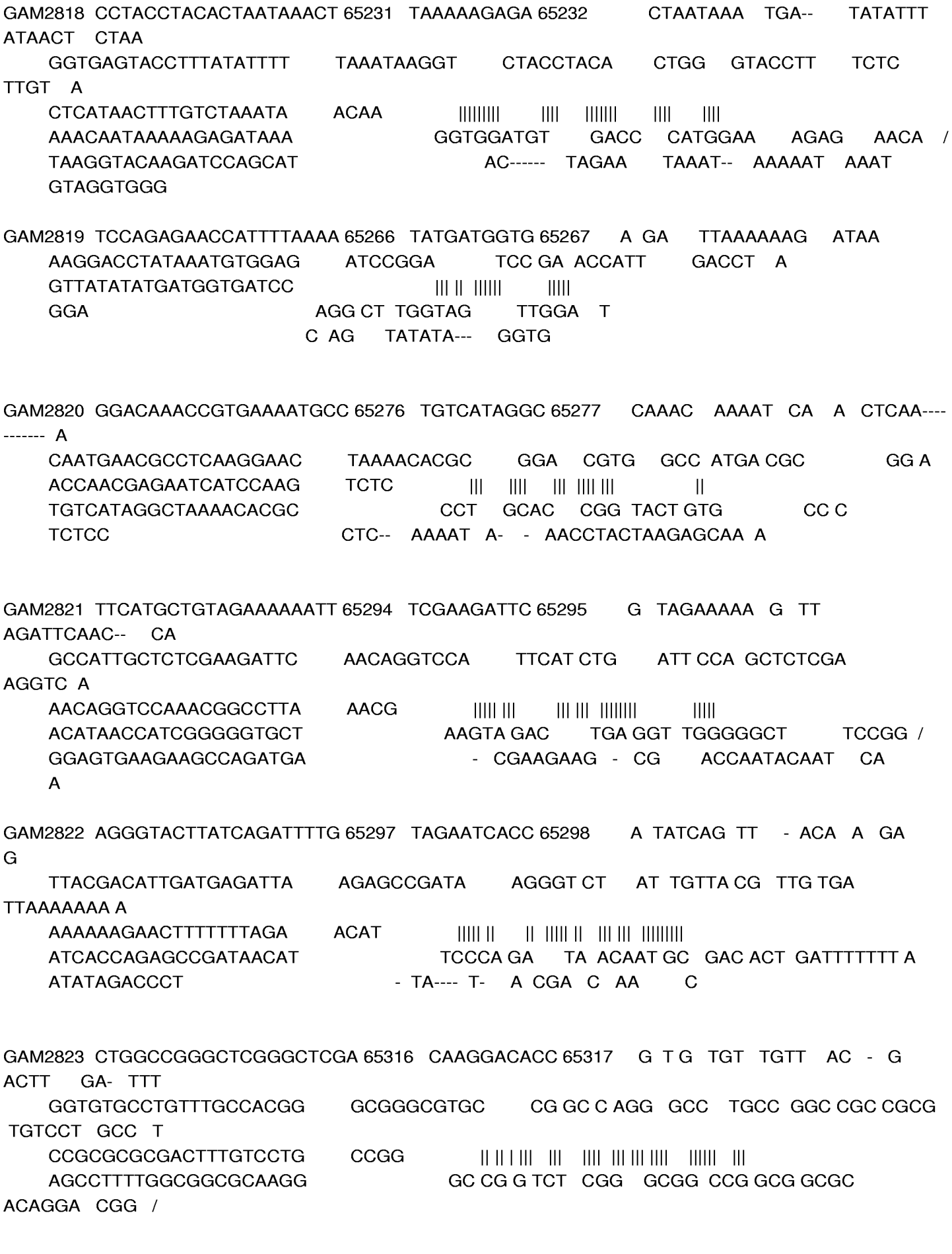
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ATAACT CTAA
GGTGAGTACCTTTATATTTT TAAATAAGGT CTACCTACA CTGG GTACCTT TCTC
TTGT A
CTCATAACTTTGTCTAAATA ACAA
AAACAATAAAAAGAGATAAA GGTGGATGT GACC CATGGAA AGAG AACA /
TAAGGTACAAGATCCAGCAT AC------ TAGAA TAAAT-- AAAAAT AAAT
GTAGGTGGG
GAM2819 TCCAGAGAACCATTTTAAAA 65266 TATGATGGTG 65267 A GA TTAAAAAAG ATAA
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GTTATATATGATGGTGATCC
GGA AGG CT TGGTAG TTGGA T
C AG TATATA--- GGTG
GAM2820 GGACAAACCGTGAAAATGCC 65276 TGTCATAGGC 65277 CAAAC AAAAT CA A CTCAA----
------- A
CAATGAACGCCTCAAGGAAC TAAAACACGC GGA CGTG GCC ATGA CGC GG A
ACCAACGAGAATCATCCAAG TCTC
TGTCATAGGCTAAAACACGC CCT GCAC CGG TACT GTG CC C
TCTCC CTC-- AAAAT A- - AACCTACTAAGAGCAA A
GAM2821 TTCATGCTGTAGAAAAAATT 65294 TCGAAGATTC 65295 G TAGAAAAA G TT
AGATTCAAC-- CA
GCCATTGCTCTCGAAGATTC AACAGGTCCA TTCAT CTG ATT CCA GCTCTCGA
AGGTC A
AACAGGTCCAAACGGCCTTA AACG
ACATAACCATCGGGGGTGCT AAGTA GAC TGA GGT TGGGGGCT TCCGG /
GGAGTGAAGAAGCCAGATGA - CGAAGAAG - CG ACCAATACAAT CA
A
GAM2822 AGGGTACTTATCAGATTTTG 65297 TAGAATCACC 65298 A TATCAG TT - ACA A GA
G
TTACGACATTGATGAGATTA AGAGCCGATA AGGGT CT AT TGTTA CG TTG TGA
TTAAAAAAA A
AAAAAAGAACTTTTTTTAGA ACAT
ATCACCAGAGCCGATAACAT TCCCA GA TA ACAAT GC GAC ACT GATTTTTTT A
ATATAGACCCT - TA---- T- A CGA C AA C
GAM2823 CTGGCCGGGCTCGGGCTCGA 65316 CAAGGACACC 65317 G T G TGT TGTT AC - G
ACTT GA- TTT
GGTGTGCCTGTTTGCCACGG GCGGGCGTGC CG GC C AGG GCC TGCC GGC CGC CGCG
TGTCCT GCC T
CCGCGCGCGACTTTGTCCTG CCGG
AGCCTTTTGGCGGCGCAAGG GC CG G TCT CGG GCGG CCG GCG GCGC
ACAGGA CGG /

ACACCGCGGGCGTGCCCGGC G T - TT- TT-- C- T G C--- ACG CGG
GTTGGCTTTCTGTGCGCGAC
GCCTGCTAG
GAM2824 GACCTTTCGTCCGGTGTCGG 65376 CTAGCGCTCC 65377 C G ---- CGC- AA CA A
CC
ACGCCTCAAGCATGCCAGGC GCGTGCGAGA GAC TTTC TCCG GTGTCGGA CTC GCATGC
GGCGC GGCG G
GCAGGCGCCGCCCTGCTAGC AGAT ||| |||| |||| |||||||| ||| |||||| ||||| ||||
GCTCCGCGTGCGAGAAGATC TTG AGAG AGGC CACAGCCT GAG CGTGCG TCGCG
TCGT C
CGACACTACTCGGAGAGACG C - TCAT AGAA -- CC A CC
TT

GAM2825 CGCGGGCAGGGATCCTTCAC 65385 CTTCTGCTCG 65386 G TCCTTCACGCG T
CCGC C
GCGCGGGCCCGTGGTAGCCG GGCCCGACCT CGCG GCAGGGA CGGGCCCG GGTAG
GGG C
CGGGCCCTTCCTTCTGCTCG TTCC |||| ||||||| |||||||| ||||| |||
GGCCCGACCTTTCCTGCGCG GCGC CGTCCTT GCCCGGGC TCGTC CCT C
CG G TCCA------- - TT-- T

GAM2826 GCTCGCGCACACGCCGTACA 65416 TCGCGCACAC 65417 G ACG CACACT -- T
CACTGCAGCAGTTACTGTTC GCCGTACACA GCTC CGCAC CCGTA GCAG CAG T
TGCCCTCTACGGAGGTGCGG CTGC |||| ||||| ||||| |||| |||
GGC CGGG GCGTG GGCAT CGTC GTC /
- GA- CTCC-- TT A

GAM2827 TTGTTATTAATACTAGTTGA 65431 TAATACTAGT 65432 TATTA - TG TTTTCTA T
TTTTTCTAGCATCTTTGTCG TGATTTTTCT TTGT ATACTAG T AT GCA C
TGTTGATCTAGTATGTGTGC AGCA |||| ||||||| | || |||
AA AACG TATGATC A TG TGT T
TGTG- T GT TGC---- T

GAM2828 ATTTCTGGTCTCTAGACGCT 65440 TTTGTCGTTA 65441 GTCTCTA C- CAATA
GGTAGTTCAATAAATAAAAA CAGAGAT ATTTCTG GACG TGGTAGTT A
ACTATCATTTGTCGTTACAG ||||||| |||| ||||||||
AGAT TAGAGAC CTGT ACTATCAA A
ATTG--- TT AAAAT

GAM2829 AGAGGCGCGACTTTTGGCAT 65444 TTACCACCCC 65445 ACTTT----- A CC C ACACG
T
GCAGCCTGCTCCGGACACGG GAGCACTGCA AGAGGCGCG TGGC TGCAG TGCTC GG
GATT C
ATTTCCAATTACCACCCCGA GCTA ||||||||| |||| ||||| ||||| || ||||
GCACTGCAGCTATTCTATTT TTTCTGTGT ATCG ACGTC ACGAG CC TTAA /
TATGTGTCTTT ATTTTATCTT - -- C CACCA C

GAM2830 GCTATAGAAATGACTCTTTA 65464 TTCTGAACAG 65465 T A GA T---- A --- ----- A CAC
TCTTAGTGGCCTCAGAGACT TGGTCTTTAC GCTA AGA AT CTCT TATCTT GT GGCC TCAGAG CT A
CACAATATGGTTCTGAACAG AAGA |||| ||| || |||| |||||| || |||| |||||| ||
TGGTCTTTACAAGATACTAG CGAT TTT TA GAGA ATAGAA CA CTGG AGTCTT GG A
CAGAGAAATCTTTTTAGC T C AA CGATC - TTT TGACA - TAT

GAM2831 TAATAAACGATTTAATTAAA 65478 TAAATTACTA 65479 CG T ATT TACTATA A CTA
TTACTATATATATATTTACA TATATATATT TAATAAA AT TA AAAT TATATATTT CAA T
ACTATCCTTTGAAGTATATA TACA ||||||| || || |||| |||||||| |||
ATTCAATATTTTGTATATTA ATTATTT TA AT TTTA ATATATGAA GTT /
TTTATTA AT T GT- TAACTTA - TCC

GAM2832 GTGGTATCAGGAGTACATCT 65493 TCAGGAGTAC 65494 A ------- AT-- ACAACT
TGCACAACTATTGACGGCAG ATCTTGCACA GTGGT TCAGGA GTAC CTTGC A
GCACCGTACATTTTAATCCT ACTA ||||| |||||| |||| |||||
GGACCAC CACCA GGTCCT CATG GGACG /
- AATTTTA CCAC GCAGTT

GAM2833 TATGGTGATATAGTAATGAG 65508 CTTGCACAAG 65509 A A CT AA TT AG TT AG TT C
TGCCTGCACAAGTGCTTGCA TGCTTGCACA AT TAGTAATG GTGC GCAC GTGC GCAC GTGC GCAC GTGC GCA A
CAGGTGCTTGCACAGGTGCT AGTG || |||||||| |||| |||| |||| |||| |||| |||| |||| |||
TGCACAAGTGCTTGCACAAG TA GTCATTAC CATG CGTG CACG CGTG CACG CGTG CACG CGT A
TGCTTGCACAAGTGCCTGCA C A TT AA TC AA TT AA TT G
CAAGTGCTTGTACACATTAC
TGCATCGCCAA
GAM2834 AAGATAGTATTCATCTTCAT 65518 TAGTATTCAT 65519 CATCTTC CTAT CTA
GCTATTTAATACATCTAATA CTTCATGCTA AAGATAGTATT ATG TTAATACAT A
TATGTATTGGTCATTAAAAA TTTA |||||||||| ||| |||||||||
ATATTATTTT TTTTATTATAA TAC GGTTATGTA /
AAAAT-- T--- TAT

GAM2835 TGTTGTGGTATCAGGAGTAC 65530 AGGCAGCATA 65531 --- A ------- CAT-- ACAACT
ATCTTGCACAACTATTGACG CATTTCAATC TGT TGTGGT TCAGGA GTA CTTGC A
GCAGGCAGCATACATTTCAA CTGG ||| |||||| |||||| ||| |||||
TCCTGGACCACATTGACA ACA ACACCA GGTCCT CAT GGACG /
GTT - AACTTTA ACGAC GCAGTT

GAM2836 CATTTGTGCTAGATGAGCGG 65549 TGCTAGATGA 65550 G - G-- C A TC
CAAAGAACTCATCTTTCTGA GCGGCAAAGA CATTT TGCTAGA TGA CGG AAAGA CTCA T
GATTTTTCTGGGATTATTCT ACTC ||||| ||||||| ||| ||| ||||| ||||
GGTAAAAATG GTAAA ATGGTCT ATT GTC TTTTT GAGT T
A T AGG - A CT

GAM2837 TTGGTGCCCCCTTAGAGGCA 65563 TAGGTGCCCC 65564 CC - T A- A GAA
CATTATAGAACCAGGTATAG CTTAGAGGTA TTGGTG CC CT AG GGCAC TTATA C
GTGCCCCCTTAGAGGTACAC CACC |||||| || || || ||||| |||||
CAA AACCAC GG GA TC CCGTG GATAT C
AT A T CC - GGA

GAM2838 ATCTCAAGGAACTTAAATGA 65585 TAGAAAGTTT 65586 - AG AAATG GTTGT- AC
AGAGTTGTAGACAAACTTAG ATGAAGAT ATCT CA GAACTT AAGA AG A
TAATCTTATAGAAAGTTTAT |||| || |||||| |||| ||
GAAGAT TAGA GT TTTGAA TTCT TC /
A A- AGATA AATGAT AA

GAM2839 TAGTAAATGTGATTGTATGT 65613 AATGTGATTG 65614 - ----- A TTACATTTCC CAAT
A
TGTTACATTTCCATGTCAAT TATGTTGTTA TAGTAA ATGT GATTGT TGTTG ATGT
AGAGTTT T
AGAGTTTATAAAAATTTTTA CATT |||||| |||| |||||| ||||| |||| |||||||
TACATTATCTTCCAACAAGC ATCATT TGCA TTAACG ACAAC TACA TTTTAAA A
AATTGACGAACGTATTACTA A AGCAG A CTTCTAT--- TAT- A

GAM2840 GACTATACCTAGTGCTATTT 65626 TATACCTAGT 65627 C --- - C------- T TTCTT
TGACATACTCGTGTTCTTGT GCTATTTTGA GACTATA CTAG TGC TATTTTGA ATAC CGTG
G
GTAATTGCGGTATCTATATT CATA ||||||| |||| ||| |||||||| |||| ||||
ATTAAAGTACGTAAATCTAG TTGATAT GATC ATG ATGAAATT TATG GCGT T
CTATAGTT C TAA C ATTATATC - TAATG

GAM2841 TTCCAGCAATATCATTTTTG 65634 TAAAGTATTA 65635 TCA TA--- A G AT-- TCG
GG ATT
TACTTAAAGTATTATCCTGT TCCTGTAAAT A TTTTTG CTT AA TATT CCTGTAAA
TCATTGAT TATT G
AAATCGTCATTGATGGTATT CGTC | |||||| ||| || |||| |||||||| |||||||| ||||
ATTGTAAGATAAATTAATGG T AAAAAC GAA TT GTGA GGACATTT GGTAATTA
ATAG /
TTTTTACAGGTAAAAGTGGT CAA TTAGA C G AAAT TT- A- AAT
TCAAGAGATTCAAAAAAACT
ATTATTGGGA
GAM2842 ACATTAGTATGTTTATTTCA 65640 TGTTTATTTC 65641 TG CATAAT A ATTTA TA-
A

TAATGTCATTATTAGTATTT ATAATGTCAT ACATTAGTA TTTATTT GTC TTATTAGT GTAGT GC A
AGTAGTTAGCAAGTGCCATA TATT |||||||||| ||||||| ||| |||||||| ||||| ||
TTACAACTAATAAGATCAAA TGTAGTCGT AAATAAA TAG AATAATCA CATTA CG G
AATAAAACTGCTGATGT CA AAC--- - A---- TAC T

GAM2843 GCTACCACACGGAGGCCGAT 65649 TCCGAACACT 65650 A- A G CGATACC C AA AA- TCA AC
ACCGGGACGGCAACAAATTC GGCGCCTCCT GCT CCAC CGGA GC GGGA GGC CA TTCG GCT A
GTCAGCTACAACGGTCCGAA CACA ||| |||| |||| || |||| ||| || |||| |||
CACTGGCGCCTCCTCACACA CGA GGTG GTCT CG TCCT CCG GT AAGC TGG /
GCATCTGGTGGCCAGC CC - A ACACAC- - CG CAC C-- CA

GAM2844 TAGCCGTCCTCGCCGCCGCA 65679 AAGGTGCGCC 65680 - GT C C C GCATAC-- GC
TCTGCATACGCTGCTCTGAG GCAAGGGTGC TAGC C CCT GC GC GCATCT GCT T
TCTCATTAAAGGTGCGCCGC GTTA |||| | ||| || || |||||| |||
AAGGGTGCGTTA ATTG G GGA CG CG CGTGGA TGA C
C TG A C - AATTACTC GT

GAM2845 TGATTAATTTTGATAATCTC 65689 TTCGCGCTCA 65690 TTTG A - TT A - T A TACCTCG
ATTACGTTTATTATACGAGT GTAAAATGTT TGATTAAT ATA TCTCATT ACG TATT TAC GAG CG GGATA A
CGAGGATATACCTCGATACA TGTT |||||||| ||| ||||||| ||| |||| ||| ||| || |||||
TTTTGTTCGCGCTCAGTAAA ACTGGTTG TAT AGAGTAG TGT GTAA ATG CTC GC CTTGT /
ATGTTTGTTGATGAGAGTAT ---- G T TT A A - G TTTACAT
GTTGGTCA

GAM2846 GATGGCCCTCCAGGCTGTCG 65693 TCGACGCCCC 65694 T TC C CCCTGTTT T TG
ACGCCCCCTCCCTGTTTGTC CTCCCTGTTT GATGGCCC CCAGGCTG GA GCCCCCT GTCGCC GGC G
GCCTGGCTGGCCGCTCGGTG GTCG |||||||| |||||||| || ||||||| |||||| |||
GCTCCGGGGGGCTTCCGGCC CTGCCGGG GGTCCGGC CT CGGGGGG CGGTGG TCG /
TGGGGGCCGTC - -- T CCT----- C CC

GAM2847 CTCGGGGGATAGTGAGGAAT 65714 TACGGGACCC 65715 GGG G AT- CAA- TAC AATGA GG
TCTCAAGGGATACGGGACCC AATGACTGGA CTCG GATA TGAGGA TCT GGGA GGGACCC CT A
AATGACTGGATAAGAGAAGG TAAG |||| |||| |||||| ||| |||| ||||||| ||
GTTTTTCCCCGTAAGATGAT GAGT CTAT GCTCCT AGA CCCT TTTTGGG GA /
CCTCGTATCACATGAG ACA - AGT ATGC --- AAGA- AT

GAM2848 GTACTATCAGTTAACCACTC 65722 TCAGTTAACC 65723 TC TTA CTC TGCTCA
TTGAATATGCTCAATGACCC ACTCTTGAAT GTACTA AG ACCA TTGAATA A
TATTCAACACTGGTGTCTCT ATGC |||||| || |||| |||||||
TAGTAC CATGAT TC TGGT AACTTAT /
TC TG- CAC CCCAGT

GAM2849 CACGGACGGTGTCGCTGTTA 65733 TCGCTGTTAT 65734 ACG - ATTCGCGAACA - ATAC
TATTCGCGAACAGTGGTGAT ATTCGCGAAC CACGG GTGT CGCTGTTAT GTGGTGA TCTG A
CTGATACAAGGCATAGAGTC AGTG ||||| |||| ||||||||| ||||||| ||||
ACTACCAATAATAGCGTATA GTGCT CATA GCGATAATA CATCACT AGAT A
CAGTCGTG GA- T AC--------- G ACGG

GAM2850 GAAATCGGATAACGGCACGC 65737 AAGGTCTCAG 65738 G AA T CA GAC GTTTA CG A A A
GGAAAGGTCTCAGCGAGTTG CGAGTTGGAC ACGGCAC CGGA GG CT GCGAGTTG ACGTT GC TCTCGA G GT T
GACACGTTGTTTAGCCGTCT ACGT ||||||| |||| || || |||||||| ||||| || |||||| | ||
CGAAGAGTATCTGCACTCGA TGCTGTG GCCT CC GA CGTTTAGC TGCGA TG AGAGCT C CG C
GAAAGTAGCGTTGCGATTTG - CG T -- GT- ----- AA - A T
CAGTCCGCTCCGGTGTCGTT
CACCCAGTTAC
GAM2851 TCTTTGCTTGATTTACAATA 65746 TGCTTGATTT 65747 G - ACAA TA C - GA
TGATATTTCTCTTAATAATG ACAATATGAT TCTTT CTT GATTT TATGA TTT TCTTAATA AT T
ATTAATATATTAAGAAAAAC ATTT ||||| ||| ||||| ||||| ||| |||||||| ||
TTATGACGAAGATTAAAGGA GGAGA GAA TTAGA GTATT AAA AGAATTAT TA /
GAGG G A AGCA C- A A AT

GAM2852 GCTTAACTAAGGGGACTATG 65753 TGGCATGTAT 65754 TAA-- A A- A- G CA G
GCATGTATAGGCGCAAAGCG AGGCGCAAAG GCT CT AGGGGACT TGGC TGTATAG CG AAGC G
GGGCTTCGGTTGTACGCGGT CGGG ||| || |||||||| |||| ||||||| || ||||
TAGGAGTCCCCTCAGGATAT TGA GA TCCCCTGA ATTG GCATGTT GC TTCG /
AGT TATAG C GG GC G -- G

GAM2853 GAGATTGTATCAGTTTCGTA 65762 GATTGTATCA 65763 -- - T TA TGA G T
GTCTTGAGTATTGGTATTAC GTTTCGTAGT GAGATTGTA TC AGT TCG GTCT GTATTG TAT A
TATATAGTATATAGATGTCG CTTG ||||||||| || ||| ||| |||| |||||| |||
ACGCTAGATATACAGTCTC CTCTGACAT AG TCG AGC TAGA TATGAT ATA C
AT A C TG TA- - T

GAM2854 GGAGGTGGAGCTGGTAGAAA 65766 TGACAAGAAA 65767 ------- - AAATT- G A - AGAA

TTCTAGATATTTTATGTATT TATATAGTAG GGAG GTGGAGCT GGTAG CTA ATATTTT TGT ATTT A

TAGAAAAAGAAGATGACAAG CAGT |||| |||||||| ||||| ||| ||||||| ||| |||| AAATATATAGTAGCAGTTGC CCTC TACTTCGG CCGTT GAT TATAAAG ACA TAGA /

CTGGCTTCATGATAATACTC ATAATAG T GACGAT A A G AGAA C

GAM2855 TGAGAAACTGAAGAAAGATG 65778 AGACCATAGT 65779 GAA A-- AGA ------- T--- ACAC T

GTTTTGAAGTTCTATGGACA AATGCTTTAT TGA ACTGA GAA TGGTTT TGAAGT CTATGG TTGG T

CTTGGTTTTCCAGACCATAG ATAA ||| ||||| ||| |||||| |||||| |||||| |||| TAATGCTTTATATAAAAAAG ACT TGATT CTT GCCGAA ATTTCG GATACC GACC T

CCGGGTTCAAATTAGTAGGT GGA AAA GG- AAAATAT TAAT A--- T CA

GAM2856 ACGTCGCTTGTACACGTCGT 65784 GGGTACGGGG 65785 ---- A TT GCCC

TCGTGGCCCAAAGACACGGG ACACGGCGT ACGTCG CTTGTAC CGTCG CGTG A

TGGCGGGTACGGGGACACGG |||||| ||||||| ||||| |||| CGT TGCGGC GGGCATG GCGGT GCAC / ACAG G GG AGAA

GAM2857 GGTACGACGAGAATCTTTAT 65819 ACGAGAATCT 65820 GT G CTTTATACC GA AACT

ACCTTTCCTGGAATATCATT TTATACCTTT G ACGAC AGAAT TTTCCTG ATATCATT G

AACTGTTGCCAATGATGTTA CCTG | ||||| ||||| ||||||| |||||||| GGAAATATTCTGTTGTGTC C TGTTG TCTTA AAAGGAT TGTAGTAA T TG - T-------- -- CCGT

GAM2858 CATTGTAAAAGAAATATATG 65832 TATGTGGTGT 65833 AAAG TG GTTACAGTTA AA- GAG

TGGTGTTACAGTTAGGTGAA TACAGTTAGG CATTGTA AAATATATG GT GGTG CAA A

CAAGAGATATATTGGAGCAT TGAA ||||||| ||||||||| || |||| ||| TGCTGCATATGTTTGAGTGC GTAACGT TTTGTATAC CG TTAC GTT T AATG GAG- GT ---------- GAG ATA

GAM2859 CAGGAATAGTATAAGGCCAA 65849 TAGTATAAGG 65850 AA- - CC --- CAC

GGTTAGATTTCTCACCTGCA CCAAGGTTAG CAGG TAG TATAAGG AAGGTTAG ATTTCT C

GAAATAAATTAGCTTTTCTT ATTT |||| ||| ||||||| |||||||| |||||| TATATCTACCCCCTG GTCC ATC ATATTTC TTTCGATT TAAAGA / CCC T T- AAA CGT

GAM2860 GTCTTAGAACTAGTGCTTTG 65856 TCAATCATTT 65857 CTAGT TT TT A G G
TCAATCATTTAATGGCCAAG AATGGCCAAG GTCTTAGAA GC TGTCAATCA TA TG
CCAAGGCAA G
GCAAGGCATTGTCTTGGGCA GCAA ||||||||| || ||||||||| || || |||||||||
CTATTTGATTGACATTGTGG CAGAATCTT TG ACAGTTAGT AT AC GGTTCTGTT C
TCTTTCTAAGAC TCTGG TT TT C G A

GAM2861 TATGATTCGTTTGATATTAC 65878 TGATTCGTTT 65879 GA TG TACTT-- AGA AAGAC
TTATATAGATCCAAGAAGAC GATATTACTT TAT TTCGTT ATAT ATAT TCCAAG A
ATATAACTTGGAATAATATT ATAT ||| |||||| |||| |||| ||||||
TTATCCATATTGAATGAAAA ATA AAGTAA TATA TATA AGGTTC /
ATA AA GT CCTATTT ATA AATAT

GAM2862 GGTAATACTTTTCTAAAAAC 65882 TCTAAAAACT 65883 A C T A AT- CA AT T
TAATCTCAAGTATTGTTTAC AATCTCAAGT GGTA TA TTT CTAAAA CTA CT AGT TGTT A
AAGCGACTGAAGTAATAGTT ATTG |||| || ||| |||||| ||| || ||| ||||
TTAGCAAAATAATACC CCAT AT AAA GATTTT GAT GA TCA GCGA C
A A C - AAT AG -- A

GAM2863 AACCTTATGTTACTTTTACT 65890 TATGTTACTT 65891 TAT TTT TTTTT AGAT TG
CGCCT C T
TTTTACAGATCACAGCATGA TTACTTTTTA ACCT GTTAC TAC AC CACAGCA AGT
GAAGT TTTCA C
GTCGCCTGAAGTCTTTCATC CAGA |||| ||||| ||| || ||||||| ||| ||||| |||||
GGTGGAATGCTTTTATTTGT TGGG CAATG ATG TG GTGTCGT TTA TTTCG
AAGGT G
GCTGTGCCGTTTCGTGTATT CC- TT- TGCTT CC-- GT T---- T G
GTAACCCGGGTT

GAM2864 CAGTAAAGGTATTATTTTGC 65905 TATTTTGCTA 65906 G A T G - TTA C CGC T
TAAAACTATTACTTCAGTCG AAACTATTAC CA TAA GGTA TATTTT CTAAAA CTA CTT AGT
TTG A
CTTGTAAACAATACTTGAGA TTCA || ||| |||| |||||| |||||| ||| ||| ||| |||
TTAGTTTTTAGAAAAGTATT GT ATT CCAT ATGAAA GATTTT GAT GAG TCA AAC A
ACCATTAATG A A T A T TA- T T-- A

GAM2865 ACCAGGTATTAGTGCCCCCT 65916 TAAGTGCCCC 65917 -- A- CC - T A- A AACCAG A
- CCC
TAGAGGCACATTATATAACC CTTAGTGGCA GGT TTAGTG CC CT AG GGCAC TTATAT GT
TAG GTGCC T
AGGTATAGGTGCCCCCTTAG CACT ||| |||||| || || || ||||| |||||| || ||| |||||
AGGCACACTAACAATAGGTA CCA AATCAC GG GA TC CCGTG AATATG CA ATC
CACGG T
TAAGTGCCCCCTTAGTGGCA CA CC AC T T CC - GATAA- - A AGA
CACTAACCACCACAATTGGT

GAM2866 CGGTGCCATTTTTTCCAAATG 65938 TGGCTGATTC 65939 TTT AAA GG TG TAT AT T TG
CAG T TG
GGGGTTGCATTATGGATAGG TATCTCTCGT TTCC TG GGT CAT GGATAGGA TCG T CA
TTTGG GGT T
AATTCGTTTGCACAGTTTGG GTGG |||| || ||| ||| |||||||| ||| | || ||||| |||
TGGTTGTGATATCCCAAAAT AAGG AC CCG GTG TCTATCTT AGT G GT AAACC
CTA G
ATGTGGCTGATTCTATCTCT TT- A-- TA GT CTC -- C GT ATA - TA
CGTGTGGCCATCAAGGAATT
AGACGCCG
GAM2867 TCTCTACTCAGTCCCTGTCT 65944 TTGGCGCCCG 65945 A - C TA-- TGT TCGA
CTAGTTTGTCTGTTCGAGAT AACAGGGACC TCTCT CTCAG TCCCTGT TC GTT CTGT G
CCTACAGTTGGCGCCCGAAC TGAG ||||| ||||| ||||||| || ||| ||||
AGGGACCTGAGAGGGG GGGGA GAGTC AGGGACA AG CGG GACA A
- C - CCCG TT- TCCT

GAM2868 CACCATTGCTATGACCGTGC 65960 TTGATACCAT 65961 C - AT ---- TG CCCG- A GTA
CCCGGGTAATCAATAGTAGC TGCGTGCAAA CA CAT TGCT GACC G C GGTA TCAATA G
TATATTGATACCATTGCGTG AGGT || ||| |||| |||| | | |||| ||||||
CAAAAGGTTTCAGCACATGC GT GTA ACGA TTGG C G CCAT AGTTAT /
TG C C CT AAAA GT CGTTA - ATC

GAM2869 TGACAGATAATAATATATTT 65972 TAATATATTT 65973 - AA------- - ACC-- T AA
ACCGTGATTTTAATTAAACA ACCGTGATTT TGACAG AT TAATAT ATTT GTGAT TT T
TCACATCCAAAGTAATATTA TAAT |||||| || |||||| |||| ||||| ||
AATTCGAAGATACTGTTA ATTGTC TA ATTATA TGAA CACTA AA /
A GAAGCTTAA A ACCTA C AT

GAM2870 AATATGTATATTATATGCTC 65975 TATTATATGC 65976 A - GC AAA AA T GAAT
AAACTAAGGTAGATATGGAA TCAAACTAAG AAT TGTATATT ATAT TC CT GGTAGA ATG A
TATTTACATTTTACCGAAGA GTAG ||| |||||||| |||| || || |||||| |||
AGATAATATAAATATACAAA TTA ACATATAA TATA AG GA CCATTT TAC /
TT A A AT AA- AG - ATTT

GAM2871 TGTGAATTCTATACTGTGAA 65981 CTTGAACATT 65982 GA TATAC - C T C
TGCTTTAGATCTGAGTCTTG TCACAAAATG TGT ATTC TGTGAA TG TT AGAT T
AACATTTCACAAAATGAATA AATA ||| |||| |||||| || || ||||
AACA ACA TAAG ACACTT AC AG TCTG G
AA TAAA- T A T A

GAM2872 CGCGGTTTCTTACGCGGGCT 66002 CCCCGGGGAG 66003 T T GGG GAG A GC
GAGCTCGGGAGTAGCGGATG AGGAGTGTTA CGCGGTT CT ACGC CT CTCGGG GTA G
CCCCGGGGAGAGGAGTGTTA GTAA ||||||| || |||| || |||||| |||
GTAACCGCG GCGCCAA GA TGTG GA GGGCCC CGT /
T T AG- GAG - AG

```
GAM2873  TTCGTTTTTCAGAAAACTCA 66057   TTTTTCAGAA 66058      T     AAACT     TTCAGTCA
         AGTGTTCAGTCATATCAAGT       AACTCAAGTG       TTCGT TTTCAGA     CAAGTG      T
         TCACTTGCCTCTGAAACACG       TTCA          ||||| |||||||     ||||||
         AA                              AAGCA AAAGTCT     GTTCAC      /
                                          C      CC---      TTGAACTA


GAM2874  TGTTTATTTAGTATGGTAAC 66078   TAGTATGGTA 66079       T--       AAC  TATAT  CG   TTA
         TGTATATGACGGAATTAATG       ACTGTATATG       TGTTTAT   TAGTATGGT   TG    GA  GAA   A
         CTTCTATCTCTTCATAAACT       ACGG          |||||||  |||||||||  ||    ||  |||
         ATATTATTTATAAATA                    ATAAATA   ATTATATCA   AC    CT  CTT   /
                                    TTT       AAT  TTCT-  AT   CGT


GAM2875  TATATCTAATATACTTGGAT 66082   TAATATACTT 66083       TA----    CT    -      TACAAG--   TT
CG
         TATTTCTGTACAAGAATTTA       GGATTATTTC       TATATC     ATATA  TGGATT ATTTCTG       AAT
AGCTATT  T
         GCTATTCGTAAAATAGTTTT       TGTA          ||||||     |||||  |||||| |||||||       |||  |||||||
         ATTATCAAATCTAGGAATCA                  ATATAG     TATAT  ACTTAA TAAGGAT       TTA  TTGATAA  /
         ATTCATATATATGCATACGA                     CATACG    AT     C      CTAAACTA   TT      AA
         TATA

GAM2876  ACTGGCCACTCACCCATGTT 66093   CTTTCTGCAC 66094       -  C    CCAT     AT    A----    CG
         GTATTGCAACCAACGTTGTT       CGCAATCCCG       ACTGG CCA TCAC    GTTGT  TGCA     CCAA  T
         TGGCTTTCTGCACCGCAATC       TGAA          ||||| ||| ||||    |||||  ||||     ||||
         CCGTGAATGGTCCGGT                     TGGCC GGT AGTG    TAACG  ACGT     GGTT  T
                                   T   A    CCC-     CC    CTTTC    TG


GAM2877  GATTCTCATGTATGTGTTTT 66108   TAAAATACCT 66109      CT--     T         CCT   ATT
         GTAACCTGACATTAAAAAGT       GCATGTTGCA       GATT    CATGTA GTGTTTTGTAA   GAC   A
         CTGTTTATAAAATACCTGCA       ATC           ||||    |||||| ||||||||||   |||
         TGTTGCAATC                        CTAA    GTACGT CATAAAATATT   CTG   A
                                   CGTT     C         TGT   AAA


GAM2878  TAATATATGTATAATCTTAT 66126   ATCAGATTTA 66127       --  TAT    T   GTTAAAA
         AGGTTAAAATAACACTAACT       TCATTAATAT       TAATAT  ATG   AATCT ATAG     T
         ATCAGATTTATCATTAATAT       TA            ||||||  |||   ||||| ||||
         TA                              ATTATA  TAC   TTAGA TATC      A
                                    AT   TAT    C    AATCACA


GAM2879  AAATAATTATCCTGATTTCT 66136   TCTATAGAAC 66137       ATTA--          C  T  AA  CTTTT---    A
         CTATAGAACACTTTTTTGCA       ACTTTTTTGC       AAATA     TCCTGATTTCT TA AG  CA       TTGC G
         GCTGCAACTTATTTATGGAC       AGCT          |||||     |||||||||| || ||  ||       ||||
         TTTGTGGGAATCAGGAATCT                     TTTAT     AGGACTAAGGG GT TC  GT       AACG C
```

TGTATTT GTTCTA T T AG ATTTATTC T

GAM2880 GCATTAGATAACTGCAGAAA 66160 ACGCTGCGTA 66161 G AAC AAGA------ C GTT--
T
GACGCTGCGTATAGTTATGT TAGTTATGTA GCATTA AT TGCAGA CG TGCGTATA
ATGTATTC T
ATTCTTAGAATACGTCTGTA TTCT |||||| || |||||| || |||||||| ||||||||
TATACGCACGAACATATAAG CGTAAT TA ATGTCT GC ACGCATAT TGCATAAG /
TCTGTAAGAATGTAATGC G AGA GAATATACAA - ATGTC A

GAM2881 CTTACCCTTCCCCAACTTTC 66169 TGAGGCCGGT 66170 ---- A TT-- - G C ATATT-- GC
TGTA AG
TCTGTCGGTCGTGGTATATT GTATGTAGAG CCC AC TCTCTG TC GT GTGGT GAG
CGG TGTAG A
GAGGCCGGTGTATGTAGAGA AGTC ||| || |||||| || || ||||| ||| ||| |||||
GTCTACGATCTTCGATCTCC GGG TG AGAGGC AG TA CACTA CTC GCT
GCATC /
CTTCGGATCACATGGAGCGG GCTT A TTGT G G - GGCTTCC TA TCTA TG
AGATGTTGTAGGGTTCGAGA
GGGGTGAG
GAM2882 GCCTGGAGTGTGCATTGCAA 66181 TACAAAGTGT 66182 A GT-- GCAATACAAAG GG
TACAAAGCCCGGGAAATGGG TACAGCACCA GCCTGG GT GCATT CCCG A
ATACAAAGTGTTACAGCACC GGC |||||| || ||||| ||||
AGGC CGGACC CG TGTGA GGGT /
A ACAT AACATA----- AA

GAM2883 GGTCGTCTTTGCTCCGCGTC 66243 GAGCTGCGCA 66244 C- TTTC AA TT CTCC A----
CCGATTA A
AATTTCTGAACGCTTGGCTC CTTCTTGGCG C GCGTCAA TG CGC GGCTCTA GCG
GGGA GGTC T
TACTCCGCGAGGGACCGATT CACG | ||||||| || ||| ||||||| ||| |||| ||||
AGGTCATTGACCGAAAATCC G CGCGGTT AC GCG TCGAGAT CGC CCCT
CCAG /
CATCAACGCTAGAGCTGCGC CA CTTC -- -- ---- AACTA AAAAG-- T
ACTTCTTGGCGCACGAGCTC
CTCGACC
GAM2884 GTAGTCGGTACTTAGGCTCA 66257 TGCCAGGCTC 66258 T C AG CAA C T GTC
AGCCGTTCCGCCGTCAAAAG AATTACTGCT GTAG CGGTA TT GCT GC GT CCGCC A
GCGGGCTGCCAGGCTCAATT AC |||| ||||| || ||| || || |||||
ACTGCTAC CATC GTCAT AA CGG CG CG GGCGG /
- T CT AC- T - AAA

GAM2885 GATTTATTGTGTATGGAAGA 66317 TGTATGGAAG 66318 GT AAGAA ACC CAT ATA
A - TA
AGTAACCATATTACATAATA AAGTAACCAT GATTTATT GTATGG GTA ATATTA AAT TAC
GGC TATT C

TATACAGGCTATTTACAAGA ATTA ||||||||| |||||| ||| |||||| ||| ||| ||| ||||
TGCGCCGTACCGTTCGATGA CTAAGTAA CGTATC CAT TATAGT TTG ATG CCG
GTAG /
TATAGTACGTACTATGCCAA AC ATG-- GA- AGC CC- - C AA
ATGAATC

GAM2886 CGTAGGAGATCTTGGCAATA 66327 TAGGAGATCT 66328 - T-- AATA GCGGA
TTCTGGCGGATAAGAACGGA TGGCAATATT CGTAGGA GA CTTGGC TTCTG T
AAAGCCAAGTATTCGTTCTA CTGG ||||||| || |||||| |||||
TG GTATCTT CT GAACCG AAGGC /
G TAT AA-- AAGAA

GAM2887 CTGATACGGATGATCTTGGT 66340 TGAAAACCGG 66341 A GATGA - A- GG- C TG
TTAGGTGGCAACGCTGAAAG GAACGCAGGA CTGAT CG TCTTG GTTT GGT CAA GC A
TTTGAAAACCGGGAACGCAG AAAC ||||| || ||||| |||| ||| ||| ||
GAAAACGAATCGG GGCTA GC AGGAC CAAG CCA GTT TG /
A AAA-- G GG AAA - AA

GAM2888 CGTAGTGGACTTTCGCTTTG 66383 TTACTCCATA 66384 CTT-- CT GAA- T T
AAGAGTTAATGTTAATATAT GATTCGATAT CGTAGTGGA TCG TT GAGT AATGT A
TTACTCCATAGATTCGATAT AATT ||||||||| ||| || |||| |||||
AATTTATTACG GCATTATTT AGC AG CTCA TTATA A
AATAT TT ATAC T T

GAM2889 CACTAAAAAGACATATAGTA 66387 TATGACCTAC 66388 AAAA- CA --- CC T --- T
GTAGGTTACCTATTATCCTT GTTTATTATA CACT AGA TATAGTA GTAGGTTA TAT AT CC T
AAGGCTCATCATGTATGACC ATCT |||| ||| ||||||| |||||||| ||| || ||
TACGTTTATTATAATCTCGC GTGA TCT ATATTAT CATCCAGT GTA TA GG A
CGAGTG GCCGC A- TTG AT C CTC A

GAM2890 GAAGCTAAAGAATTAAGAAA 66395 AAGAATTAAG 66396 AAA- A A--- C A -- A
ACAGTATCGCGATACGCAAG AAAACAGTAT GAAGCT GA TTAAGA AA AGT TC GCG T
AACTATTACCATTTTAATCG CGCG |||||| || |||||| || ||| || |||
GAGAGCTTT TTTCGA CT AATTTT TT TCA AG CGC /
GAGG - ACCA A - AA A

GAM2891 TTTTTTTTAATATAGAATAT 66405 TAGAATATAA 66406 AATAT ACATTT A TA
AACATTTTAAATAATATATT CATTTTAAAT TTTTTTTT AGAATATA TAAATA TA T
ATTAATATTTATATATTTTT AATA |||||||| |||||||| |||||| ||
TCAAAAAAAA AAAAAAAA TTTTATAT ATTTAT AT T
CTT-- ------ A TA

GAM2892 GGGAATGTGTTTAACCTTAT 66411 TACCTAGTAA 66412 T ACCTTAT--- A AA
CTATCTTAATAAAAGAAGTG ACATTTTTCC GGGAA GTGTTTA CT TCTT T

CTACCTAGTAAACATTTTTC ||||| ||||||| || ||||
C CCTTT TACAAAT GA AGAA /
T GATCCATCGT - AA

GAM2893 CACCCAGACGCTCGGCACTT 66456 ACGCTCGGCA 66457 C CTC CT CT- G
AGCTCTCGAGTGATTGCCTG CTTAGCTCTC CAC CAGACG GGCA TAGCT CGA T
GCTGCTTGCCCCGTTTGCGT GAGT ||| |||||| |||| ||||| |||
G GTG GTTTGC CCGT GTCGG GTT G
C C-- TC TCC A

GAM2894 GCCCCGTTTGCGTGGAATGA 66462 GCCCCTGTTT 66463 C TG ATGA CA
GGCCAAACAAGCATTTGGCC GTCTAGACGG GCCCCGTTTG G GA GGCCAAA A
CCTGTTTGTCTAGACGGGGC GGC |||||||||| | || |||||||
CGGGGCAGAT T TT CCGGTTT G
C GT GTCC AC

GAM2895 GGGGCTTTGTGTTTTTCCCA 66507 GCTTTGTGTT 66508 C T TTCCCACC CC -- C- G
CCCCTGCCCTTGCCCCTGGC TTTCCCACCC GGGG TTTG GTTT CCTG CTT GCC
CTGGCC C
CGCCTGGCCGGCCGGCTAAA CTGC |||| |||| |||| |||| ||| ||| ||||||
GTATAGGCCAGACCAAACCC CCCC AAAC CAGA GGAT GAA CGG GGCCGG C
CC C - CC------ AT AT CC T

GAM2896 GTAATAACCTTACAAAACAT 66546 TAAGATATGA 66547 CT AAA ACAA-- G
ATACAACATTGGAAATGCAT ATGTGTGTTA GTAATAAC TACA CATAT CATT G
AAGATATGAATGTGTGTTAT TTAC |||||||| |||| ||||| ||||
TAC CATTATTG GTGT GTATA GTAA /
T- AA- GAATAC A

GAM2897 GGTGATAAGTCTTATATAGC 66557 TACAATATAA 66558 TCTT GCAA GAA A- ---
ACAA CT
AATATAGAAGTAAACATAGG GTATATTAAT GTGATAAG ATATA TATA GTA ACATAG
GCAAA GTATT A
CAAAACAAGTATTCTAATAG TTTG |||||||| ||||| |||| ||| |||||| ||||| |||||
ATATTTTGCTAACTATGTAG CATTGTTT TATAT ATAT CAT TGTATC CGTTT
TATAG A
TACAATATAAGTATATTAAT TAAT GA-- AA- GA AAT ---- AT
TTTGTTACC

GAM2898 AATCTGACTTAGTTAAATAT 66562 TTCATATAAT 66563 CTTA -- AG
GTGGATTTAGTTAAAAATTC TTTAATATTT AATCTGA GTTAAA TATGTGGATTT T
ATATAATTTTAATATTTCAG CAGA ||||||| |||||| ||||||||||
ATT TTAGACT TAATTT ATATACTTAAA T
TTA- TA AA

GAM2899 ATTATTTGATAAGTTTACTA 66571 TAAGTTTACT 66572 --- ACTAA TTAAAATT TCG
ATAAATGGTTAAAATTAGAC AATAAATGGT ATTATTTG ATAAGTTT TAAATGG AGAC T
TCGTTAATGTCTTCTTCACT TAAA |||||||| |||||||| ||||||| ||||
CATTTAAAACTTATAAACAA TAGTAAAC TATTCAAA ATTTACT TCTG T
ATGAT AAA ----- CACTTCT- TAA

GAM2900 TACGATAACCGTAATGTCCG 66584 AACCGTAATG 66585 ATAA - GC CG---- - T -
G
CTATGACGGTAAGTGGTAAC TCCGCTATGA TACG CCGTAATGT CC TATGA GT AAGTGG
AACGT GTC T
GTGTCGTTTGGCAACGTTTC CGGT |||| ||||||||| || ||||| || |||||| ||||| |||
ATTTGGCAATGTTTCATATG GTGC GGCATTATA GG ATACT CG TTTACT TTGCA
CGG T
GGAATATTACGGCAAACGTG AAAC A GT TTGTAA G - A T

GAM2901 GCCGTACGTGGGTTCACAGC 66588 CGCAAGCACG 66589 T GT ACA TTTTTTTA GAG
TTTTTTTTTACCGAGATCAG GTCACGTCGG GCCG ACGTGG TC GCTT CC A
GGACACGCAAGCACGGTCAC C |||| |||||| || |||| ||
GTCGGC CGGC TGCACT GG CGAA GG /
- -- CA- CGCACAG- ACT

GAM2902 TGTCCTTACTGACATCTGCG 66614 TGGATTCGGT 66615 --- C C T CT
TTTGTATCTGTGTGTGCGTG AACCAGGATA TGTCCT TACTGA ATCTG GT TGTAT G
CTGGATTCGGTAACCAGGAT |||||| |||||| ||||| || |||||
A ATAGGA ATGGCT TAGGT CG GCGTG T
CCA - - T TG

GAM2903 ACATATCCGTCACCGGGAGG 66645 TCCGTCACCG 66646 T ------- GT G TT TCAT
GTCGTTGTTCTCATATCGTG GGAGGGTCGT ACATA CCGTCACC GGGAGG C TTG C A
GTCGAGGGTCCTTCTGTTAG TGTT ||||| |||||||| |||||| | ||| |
GGGGTGACGGTGTGT TGTGT GGCAGTGG TCTTCC G AGC G /
- GGGATTG TG G TG TGCT

GAM2904 TTATTTTTTAAATATTAATT 66653 TGAAATTTTA 66654 TAAATAT TT GACTA
TTTCATAGACTATTTACTAT TAAATAAAAA TTATTTTT TAA TTTCATA T
ATGAAATTTTATAAATAAAA TAA |||||||| ||| |||||||
ATAA AATAAAAA ATT AAAGTAT T
TAAAT-- TT ATCAT

GAM2905 TATCTTTTAATATGAATTAC 66657 TCTTTTAATA 66658 AATTAC -- CTT CTGA
TTCACTTTATCTTTCTTACC TGAATTACTT TATCTTTTAATATG TTCACTTT ATCTTT AC T
TGATTATTGTTTAAAGATTA CACT |||||||||||||| |||||||| |||||| ||
AAAGTGAAATATATTGGAAG ATGGAAGGTTATAT AAGTGAAA TAGAAA TG /

GTA A----- AT TT- TTAT

GAM2906 TCTTCCGGAAAGACTTCAGA 66671 CGGAAATAAA 66672 CA GATCG AAAAG- AA----
T AAA TGA
CAGATCGGAAATAAAAGACC AGACCGCATA GACTT GACA GAAAT ACCGCAT
CAGTGT G TCAG A
GCATAACAGTGTTGAAATCA ACAG ||||| |||| ||||| ||||||| ||||||| | ||||
GTGAACTTCTGGGACATATT TTGAA TTGT CTTTG TGGTGTA GTTATA C GGTC
/
GGTAATAATGTGGTATACGA -- AAAA- AGCATA ATAATG - AG- TTC
GTTTCAAAATGTTAAGTTAA
TACGGTATGA
GAM2907 GTTTATTATTTTCATTTTTA 66697 TATGTTATCA 66698 AT- TTCATTTT - T A TAA
AAAATATAATCGTAATCATA TTTTTATAAT GTTT TATT TAAAAAT ATAA CGTA TCA G
AGGTTTTGGTATGTTATCAT TTTC |||| |||| ||||||| |||| |||| |||
TTTTATAATTTTCAATATAC CAAA ATAA ATTTTTA TATT GTAT GGT G
AAAC CAT CTTTTAAT C - - TTT

GAM2908 TTTATTATTATCCATAATAT 66703 TATAATATAT 66704 TATCC A A ATA
ATAATATATAATATATAATA AATATATCTT TTTATTAT ATA TATATA TATATA T
TATAATATATAATATATCTT ATAA |||||||| ||| |||||| ||||||
ATAATAGG GGATAATA TAT ATATAT ATATAT A
TTCTA A A AAT

GAM2909 GGTAAGTACATGTTCATACA 66712 TACATGTTCA 66713 AA- TA C AG-------- TCACT
AAGTTTTGACTCACTCTCTT TACAAAGTTT GGT G CATGTTCATA AA TTTTGAC C
TGTTAGAAACCATTTCCGTT TGAC ||| | |||||||||| || |||||||
CTGTGGATATGCGCCAGACC CCA C GTATAGGTGT TT AAGATTG /
GAC GC C GCCTTTACCA TTTCT

GAM2910 TCACTTGGCACACTCTCGGA 66725 AACTGGTTAA 66726 AC ACA CGGA A CA --- ACA
TTTAACAAGCATTGCTGGAC AAAAGAGCGC TC TTGGC CTCT TTTAAC AG TTGC TGG C
ACTTACCAACCGTAACTGGT CAAA || ||||| |||| |||||| || |||| |||
TAAAAAAGAGCGCCAAAGGG GG AACCG GAGA AAATTG TC AATG ACC /
GA C-- AA-- G -- CCA ATT

GAM2911 ATTTTTATCATAACACTACT 66777 AACACTACTT 66778 CAT CT- TT-- TA AG
TTGGTTAGATGTTTTAGAAA TGGTTAGATG ATTTTTAT AACA AC TGGT GATGTTTT A
AAAAATATCGCCGTACCGTT TTTT |||||||| |||| || |||| ||||||||
CTTGTTTTTTATAAAAAT TAAAAATA TTGT TG GCCG CTATAAAA A
TTT TCT CCAT -- AA

GAM2912 TGATTTTCTTTCTAATACTA 66794 TGGGAATAAA 66795 T TC A C ATAT TC A A TC
TATATTTCTCTCGAAGAAGT ATACTACTGT TGATTT CTT TA TA TAT TTCTC GA GA GT T

TCTTGCACATCATCTGGGAA TGAG ||||||| ||| || || ||| ||||| || || ||
TAAAATACTACTGTTGAGTA ACTAAA GAG GT AT ATA AAGGG CT CT CA T
AATCA T TT C C AAAT T- A A CG

GAM2913 ACATCTGGCCTGTTCATAAA 66813 TCAAATCTAG 66814 GCCT- AA - A T- -- CT
TATAC
TAAAAACTTGGCGATTCTAT CCATTGTCTT ACATCTG GTTCATA TA AA AC TGGC GATT
ATA T
ATATACTCTTATTATCAAAT ATAG ||||||| ||||||| || || || |||| |||| |||
CTAGCCATTGTCTTATAGAT TGTGGAT CGAGTGT AT TT TG ACCG CTAA TAT /
GTGAGCTACTGTAGGTGT GTCAT AG A C TT AT AC TATTC

GAM2914 TTGATTTTCTTTCTAATACT 66820 TGGGAATAAA 66795 T TC A C ATAT TC A A TT
ATATATTTCTCTCGAAGAAG ATACTACTGT TTGATTT CTT TA TA TAT TTCTC GA GA GT T
TTTTTGCACATCATCTGGGA TGAG ||||||| ||| || || ||| ||||| || || ||
ATAAAATACTACTGTTGAGT GACTAAA GAG GT AT ATA AAGGG CT CT CA T
AAATCAG T TT C C AAAT T- A A CG

GAM2915 AGAAATTGGTCTGTGTTACA 66821 TGTATTGGCT 66822 T T TACATA-- --- TC T
TATCTCTTCTATATTATTGT TAGAAAACTA AGAAA TGGTCTG GT TCT CT TATATTA T
TGATGTATTGGCTTAGAAAA TTAC ||||| ||||||| || ||| || |||||||
CTATTACTTAGACCATTTTC TCTTT ACCAGAT CA AGA GG ATGTAGT G
T T T TTATCAAA TTC TT T

GAM2916 CCTCGTGGCGCGCGTCCGCG 66829 CTCCCGCCCG 66830 ---------- C T A
CCC C
CCGGGGTCGCGAGGTCCCGG CGACCCCGGC TCGTG GCG GCG
CCGCGCCGGGGTCGCG GGT GGAC G
ACCGAGGTCTCCCGCCCGCG GCGG ||||| ||| ||| |||||||||||||||| ||| ||||
ACCCCGGCGCGGCGCCGCGG AGCAC CGC CGC GGCGCGGCCCCAGCGC
CCG TCTG A
AAAAACAGACGACGACACGA AGCAGCAGACAAAAAGG - - - CCC G
GG

GAM2917 AAGACCACTGCAACAGCTTC 66900 AAAAAGCACT 66901 A ----- C CTTC GTACGCT TT
TGCGTACGCTTGTATTTACA TTTGCCACAG AAGACC CT GCAA AG TGC TGTAT A
GTACATAAAAAAGCACTTTT AGCG |||||| || |||| || ||| |||||
GCCACAGAGCGGTCTT TTCTGG GA CGTT TC ACG ACATG /
C GACAC T ---- AAAAAAT AC

GAM2918 CCTTAGGGTGTTGAAAGGTG 66922 TGTAGGAAAA 66923 TGAA - A CCGT GAA T-------
--------- T
TCCAACGACCGTGTAGGAAA GAAGAGTTCG AGGTG TCCA CGA GTAG AAGAAGAG
TCG T
AGAAGAGTTCGTTCGCGACT TTCG ||||| |||| ||| |||| |||||||| |||

GGGCTTTGTCCCTGCCTCTT TCCAT AGGT GCT CATT TTCTTCTC AGC C
CTTCTGTTACCATTTCGTGG ATC- T - TTAC GTC CGTCCCTGTTTCGGGTC G
ATTACCTCTATCGCCTTAAG
G
GAM2919 GCGGTGTCTGTGTTTACCAC 66935 TCTGTGTTTA 66936 - T CGT-- TT T T----------
TT
TCGTGACGACGTTCAGAACT CCACTCGTGA CCACT CG GACGA TCAGAAC CTG ACGG
TCTC C
TCTGTACGGTTCTCTTCGTG CGAC ||||| || ||||| ||||||| ||| |||| ||||
AGACTGAGCACGGCTCTGCC GGTGA GT CTGCT AGTTTTG GAC TGCC
AGAG /
CGTCAGTCGTTTTGACATTT T - TTTAC CT - CGTCTCGGCACGAGTC TG
TCGTCTGTAGTGGAGCGCGA
ATACCAGGGC
GAM2920 TATACACTAATGAGCCTCTT 66956 TGGCAGAGCT 66957 T AT- CT --- - A
TGTTGTGTATTTTGCTTTAT GCTCTTATAG TA ACACTA GAGC CTTTGTT GTGT ATTTTGCTTT
T
TTAAAGCAAGATCACACCGT TGTT || |||||| |||| ||||||| |||| ||||||||||
GGCAGAGCTGCTCTTATAGT AT TGTGAT CTCG GAGACGG CACA TAGAACGAAA T
GTTTA T ATT TC TGC C T

GAM2921 CGCTTAGCAATGCGAAAGTT 66966 TTAGTGCTGA 66967 T TGC A -- AAG ACA- T
AGTGCTGAAGTTTCACGACA AGTTTCACGA CGCT AGCAA GAA GT TAGTGCTG TTTCACG
GG T
GGTTATCCAAGACGTGAAAG CAGG |||| ||||| ||| || |||||||| ||||||| ||
ATGGCACTGTTACCTTCAAC GCGA TCGTT CTT CA GTCACGGT AAAGTGC CC A
TTGCTAGCG - CAA C TT AG- AGAA T

GAM2922 GTGCCATTGCTGTATTGGTC 66973 TGCTGTATTG 66974 TT T ----- -- TATAT - CT
TCAAGCATATATTTACGCAA GTCTCAAGCA GTGCCA GCTGTAT GG TCT CAAGCA TTAC
GCAA T
CTTTGATTGCTGTAATTTTG TATA |||||| ||||||| || ||| |||||| |||| ||||
CTTGGAAGATTTTTCCATAC CACGGT CGACATA CC AGA GTTCGT AATG CGTT T
AGCTTGGCAC T- - TTTTT AG TTT-- T AG

GAM2923 ATACAATACTACACACGCCA 66980 ACCATTGTGT 66981 T - C T C- T GCCT
TATATGCTGCTAGGCCTGTA TGTGTGTTAG ATACAA ACTA CACACG CATA ATG TGC AG G
AACTTGCAACCATTGTGTTG TTTT |||||| |||| |||||| |||| ||| ||| ||
TGTGTTAGTTTTGTGT TGTGTT TGAT GTGTGT GTGT TAC ACG TC /
T T T - CA T AAAT

GAM2924 GACATTTACCAGAGATACGT 67004 TATTGTGTAC 67005 CA - -------- TG T T
GATACTCGGTCTACTGTGTA CTTGTAATCT GA TTTACC AGAGA TACG ATAC CGG C
TTGTGTACCTTGTAATCTCT CTAG || |||||| ||||| |||| |||| |||
AGGTAAACTTC CT AAATGG TCTCT ATGT TATG GTC T
TC A AATGTTCC GT T A

GAM2925 TACTGATCTCTTTGTTTTTT 67009 GGGAAGGTTT 67010 T ----- TT--- G AT
TTTTTCTGTGTATTGTGATA GTAAGGACAA TACTGA CT CTTTGTTTTT TTTTCT TGT T
GGGAAGGTTTGTAAGGACAA AGGA |||||| || |||||||||| |||||| |||
AGGACAAAGTTCAGTA ATGACT GA GAAACAGGAA GGAAGG ATA G
T AACAG TGTTT G GT

GAM2926 GATTGCCATCGCGGACGCAC 67067 TGCCGCAGAC 67068 C C-- A AC- A- ACC-- CCCCCG GC
GCGGGGACCCGCCAGAGACC CACCTCGCGG CG GGA GC CGCGGGG CCGCC GAG CTGC GCGCGGGCG G
CTGCCCCCCGGCGCGGGCGG CGGC || ||| || ||||||| ||||| ||| |||| |||||||||
CGCCGCGCCCGCGTGCCGCA GC CCT CG GCGCCCC GGCGG CTC GACG TGCGCCCGC C
GACCACCTCGCGGCGGCTCC - TTC - CTC CG CACCA CCG--- GC
CCCGCGGCCTTTCCCGTGGC
CCTC
GAM2927 GGTTTTCTTCGAGGCCGTCG 67102 TTCACGGGCC 67103 - A CGTC A --- A
CGAGGCCGAAAAATTTTTTT CGCGCCCGAG GGTTTTCT TCG GGC GCG GGCC GAAAA T
CACGGGCCCGCGCCCGAGAG AGAG |||||||| ||| ||| ||| |||| |||||
AGAGCC CCGAGAGA AGC CCG CGC CCGG CTTTT T
G - ---- - GCA T

GAM2928 GATCATATAGTTATGTATAT 67109 TTAGTGACGA 67110 A A- ATTA G -- GAG GAAAAT
TAGTGACGAATCAAGAGATG ATCAAGAGAT GATC TATAGTT TGTAT GT ACGA ATCAA AT A
AAAATAATCCTGAATATATT GAAA |||| ||||||| ||||| || |||| ||||| ||
GATTTTCGTAACAGATACGG CTAG ATATCAG GCATA CA TGCT TAGTT TA A
AGACTATAGATC - AG GA-- A TT ATA AGTCCT

GAM2929 GAAATCAAGGGATGCGTTGA 67122 TCAACGTCAT 67123 CAA- GG - A CTC
ATCTTCTCATAAAAAGACTC TTCGATTATT GAAAT G ATG CGTTGA TCTT A
AACGTCATTTCGATTATTTC TC ||||| | ||| |||||| ||||
CTTTA C TAC GCAACT AGAA T
TTAG TT T C AAA

GAM2930 TGGGTCTCGCGATAGCTTTG 67133 TTAACGGTGG 67134 T ----- TTTGT CG G - C CCC G A
TGTTCGTCGATCGTCGACGC TTTGTACGAT GGTC CGC GATAGC GTT TC ATCGT CGA GCCGCT AAC CG T
CGCTCCCAACGCGATCTCGG AGAA |||| ||| |||||| ||| || ||||| ||| |||||| ||| ||
TTAACGGTGGTTTGTACGAT CCAG GCG CTGTTG CGA AG TAGCA GTT TGGTGG TTG GC C
AGAAAAGCCTGTTGTCAGAG - AGAGA TC--- AA A T - CAA - T

AGCGGACCCA

GAM2931 GATCCTGCTGTCTCTGCAAC 67140 TCTCTGCAAC 67141 T C TC T ------ ACA
ATCAATCCAGGCACAGAGCG ATCAATCCAG GA CCTG TG TC GCAACATCAATCCA GGC G
CCGCAAGATGGATTGGTGTT GCAC || |||| || || |||||||||||||| |||
GTTGATCCAACAGGTTC CT GGAC AC AG TGTTGTGGTTAGGT CCG /
T A CT T AGAACG CGA

GAM2932 TAGAGCTTGTGAGTTGTTAT 67184 TATTACGTTT 67185 CT T TATT TTTGTTGTTT TCT
TT
TACGTTTTGTTGTTTGAATC TGTTGTTTGA TAGAG TGTGAG TGT ACGT GAATC GT T
TCTGTTTTGTTACTCTGATT ATCT ||||| |||||| ||| |||| ||||| ||
TCCTTCACGTTTGCACCTTA ATCTC ACATTC ACG TGCA TTTAG CA G
CACTCTCTA TC C TT-- CTTCC----- TCT TT

GAM2933 AGTGTGTGATAATGCCGGGG 67188 TAAGAGCATA 67189 TG G TAAT C T - G C GC- G
CTTCACGCTACGCTCGCGCT GGTCGGTGCC AG T TGA GC GGGGC TC AC CTA GCTC
GCTC T
CGTAGAGCTAAGAGCATAGG CTCG || | ||| || ||||| || || ||| |||| ||||
TCGGTGCCCTCGTTGCTTCA TC G ACT TG TCCCG GG TG GAT CGAG CGAG /
GGTGCT GT G TCGT C T C - A AAT A

GAM2934 GCACTTTTTTTTTCCGATTT 67199 TAATGTAGCT 67200 A TT TTTG TCC- TACA
TGACTCCTCGTACATATATC ATTGGAGGAT GC CTTT TTTTCCGAT AC TCG T
GATAATGTAGCTATTGGAGG GGAG || |||| ||||||||| || |||
ATGGAGGC CG GAGG AGGAGGTTA TG AGC /
- T- TCGA TAAT TATA

GAM2935 GCTCAACAGTATAGGATTTT 67206 TGAGTTGTCT 67207 A GTATAGGATTTTAAGT G GA
ATA G G TC
AAGTCTCCTTTGTAGAATCA GGTTAGGAGG GCTC ACA CTCCTTT TA ATCA AA TTA
TGTG A
ATAAAGTTAGTGTGTCATTC GAGT |||| ||| ||||||| || |||| || ||| ||||
GTAGTGAGTTGTCTGGTTAG CGGG TGT GAGGGAG AT TGGT TT AGT ATGC /
GAGGGAGTGTGTCGGGC C GT---------- G -- CTG G G TT

GAM2936 TGTCTAAATCTTGAAGAGGT 67214 AGAGGTAATC 67215 AA TT -- AATC C T
AATCGAGCGGTTGGTTAACC GAGCGGTTGG TGTCT ATC GAAGA GGT GAG GGTTGG T
GATCCTTACCGCCTGTCTTC TTAA ||||| ||| ||||| ||| ||| ||||||
TCGATAAGGCA ACGGA TAG CTTCT CCG TTC CTAGCC A
A- CT GT CCA- - A

GAM2937 CCCCGATGCGAAGGCCGAAA 67225 TAGGACTAGC 67226 ----- GA G GAA- TAA
AGGGCTAACCATGCCCTTAG AAAAAATCGG CCCCGA TGC AG CC AAGGGC C

TAGGACTAGCAAAAAATCGG GG |||||| ||| || || ||||||
GG GGGGCT ACG TC GG TTCCCG /
AAAAA A- A ATGA TAC

GAM2938 GGAGCGGGGGGGATCTCGAC 67253 ACGGACAGAT 67254 G --- GA-- --------- C
GCGCGCGACGGACAGATCGA CGAGACGGAC GGAGC GGG GG TCTCGA CG G
GACGGACCAGGCCCGGCTTC CAGG ||||| ||| || |||||| ||
CTTCG CCC CC AGAGCT GC C
G GGA AGGC AGACAGGCA G

GAM2939 ATTTTTTGTTGCATAGATAA 67304 TTGAAGTGTA 67305 TT AGAT A ACA
AACATACGGACAGGTATCGG ACTTAAAAT ATTTT GTTGCAT AAAACAT CGG G
TGTTTTTGAAGTGTAACTTA ||||| ||||||| ||||||| |||
AAAT TAAAA CAATGTG TTTTGTG GCT /
TT AAGT - ATG

GAM2940 CAGCAATTTTACAGTTTTGT 67319 TTACTCAGGC 67320 AC- TTTG --- A GC -- -
CTC T
CTTGTCTGGAGACCGCTGCC GATTGTTG AGT TCTTG TCTGG GACCGCT CGGTC GC
GCTAATCC AGG A
GGTCGCGCTAATCCCTCAGG ||| ||||| ||||| ||||||| ||||| || |||||||| |||
TAAGCTTAAAGGATTAGCTG TCA AGGAT GGACC CTGGCGA GCCAG CG
CGATTAGG TTC A
CTCGACCGAAAGCGGTCCCA GAC TTA- GGT - AA CT T AAA G
GGTGGTAGGAATTACTCAGG
CGATTGTTG
GAM2941 TCTTCTTGCAAAAGTGTTAT 67342 AAGAAACATT 67343 GC TG TAACAGAAAAAATTA T A
GAC C TCA
AACAGAAAAAATTATAATGT AGATTATATT TT AAAAG TTA TAATGT GT TTAGTG CT
AAAC A
TGTATTAGTGGACCTCAAAC AAAT || ||||| ||| |||||| || |||||| || ||||
TCAACATGTTTAAGAAACAT AA TTTTT AAT ATTATA TA GATTAC GA TTTG /
TAGATTATATTAAATACATA AA GA TCAATAAATACATAA T - AAA A TAC
AATAACTTAAAGTTTTTAAA
AGAAGA
GAM2942 ATCATAAAATCTTTAATTAT 67353 TATCAAAGAA 67354 AA- A TATT TTA
TATTTATATTTTATTAGCGA CCTTATGAT ATCATAA TCTTT AT ATTTATATT T
TATAAATCTATCAAAGAACC ||||||| ||||| || |||||||||
TTATGAT TAGTATT AGAAA TA TAAATATAG T
CCA C TC-- CGA

GAM2943 CCGCCGAAAGCGGTAGAAAG 67370 AGCCAGAAGC 67371 C----- TA AAGA- CCCTC-
AGAC
AGCCAGAAGCGGCCCTCGCA GGCCCTCGCA CCG CGAAAGCGG GA GCCAGAAGCGG
GC G
GACGGTACGCATCCCCCTGT GACG ||| ||||||||| || |||||||||| ||

TTTTGGCCCCGCTCCCCCGC GGC GTTTTCGCC CT CGGTTTTTGTC CG /
TTTTGACATCACGG ACTACA CC CGCCC CCCCTA CATG

GAM2944 GTGGCGTAGGAGTGGCGAAC 67400 GGAGTGGCGA 67401 GTA A A- CATTA
CGGCGTCATTATAATCAAAC ACCGGCGTCA GTGGC GG GTGGCGA CCGGCGT T
GCCGGAGTCGCCGCCCGCCA TTAT |||||| || ||||||| |||||||
C CACCG CC CGCCGCT GGCCGCA A
--- - GA AACTA

GAM2945 ATTCCCTGACGACTACGAAC 67406 TCCCTGACGA 67407 GAC AA----- T GG
ACCTAAATGAAGCGGAAGGC CTACGAACAC ATTCCCTGAC TACG CACC AAATGAAGC A
TTCATTTGGTGACCCCGACG CTAA |||||||||| |||| |||| |||||||||
TGATAGTTAGGGAAT TAAGGGATTG GTGC GTGG TTTACTTCG /
ATA AGCCCCA - GA

GAM2946 GGCGAAAAGCTGAGTGGCGT 67416 TACCCTACCG 67417 AAAG G G - A------ ACT
CGGAGGGAGCTCTACTGCAG AGCACTCAGA GGCGA CTGAGTG C TCGG AGGG GCTCT
G
GGAGCCAACATACCCTACCG GAGT |||||| ||||||| | |||| |||| |||||
AGCACTCAGAGAGTCGTT TTGCT GACTCAC G AGCC TCCC CGAGG /
GAGA - - A ATACAAC GAC

GAM2947 GTTGATGGCCGGACCGTCGA 67429 TCCCTAACGA 67430 GA G TCG G TG AA-----
T AG
TTCCCTAACGATTGCGAACA TTGCGAACAC TT TGGCCG ACCG ATTCCCTAAC AT CG
CACC GAATGAAGC A
CCTGAATGAAGCAGAAGGCT CTGA || |||||| |||| |||||||||| || || |||| |||||||||
TCATTTGGTGACCCCGACGT AG ACCGGC TGGT TAAGGGATTG TA GC GTGG
TTTACTTCG /
GATAGTTAGGGAATAGTGGT AC - GA- A GT AGCCCCA - GA
CGGCCACAGAC

GAM2948 TACAGTTCAAGGATAATTAC 67439 TTCACTTGCT 67440 ATTACAT - CTTAAACCACCTCATAT
TCCC CA TACCT
ATCTGGGTAGTCTTAAACCA CTTTCACTAT CTGGG TAGT GAAAG AGT AAGCT
T
CCTCATATGAAAGTCCCAGT CCCA ||||| |||| ||||| ||| |||||
CAAAGCTTACCTTCATTACA GACCC ATCA CTTTC TCA TTTGA C
GTTTCACTTGCTCTTTCACT ------- T ---------- TCGT C- CATTA
ATCCCAGTACCCTAAACCTG
TA
GAM2949 GACCGTTGAGTCCCTAACGA 67466 GCGAACACCT 67467 AG TG AA----- T GG
TTGCGAACACCTGAATGAAG GAATGAAGCG GACCGTTG TCCCTAACGAT CG CACC
GAATGAAGC A
CGGAAGGCTTCATTTGGTGA GAAG |||||||| |||||||||| || |||| |||||||||
CCCCGACGTGATCGTTAGGG CTGGTGAT AGGGATTGCTA GC GTGG TTTACTTCG /

AATAGTGGTC A- GT AGCCCCA - GA

GAM2950 ACCACAAAATGTCACAATAA 67486 TTAGTAGTTT 67487 - ATGTC TA TT T
TTATTTTTTTTAAAAAATTA GTCCCTTTGA ACCA CAAA ACAA ATTATT TTT A
GTAGTTTGTCCCTTTGATGG TGGT |||| |||| |||| |||||| |||
T TGGT GTTT TGTT TGATGA AAA A
A CCC-- -- TT A

GAM2951 GGAACTTTAAATGTGACGCA 67496 TGAGAGGAAC 67497 - AA GACGCA-- AGTGT---
G
TCTTTTCAGGTAGTGTTGGA CACAGAACAT GGA ACTTT ATGT TCTTTTCAGGT TG A
GACATAGATCAGATTTGAGA CAAA ||| ||||| |||| |||||||||| ||
GGAACCACAGAACATCAAAG CTT TGGAA TACA AGGAGAGTTTA AC G
GTATTC A AC AGACACCA GACTAGAT A

GAM2952 CTGAGTGACGTCGGAGGGAG 67531 CGTCGGAGGG 67532 GACG - GAGC CAC G
CTCCACGGCCGGGGGCCAAG AGCTCCACGG CTGAGT TCGG AGG TC GGCC G
ATAACCTACCGAGAACTCAG CCGG |||||| |||| ||| || ||||
GACTCA AGCC TCC AG CCGG /
AG-- A AAT- AA- G

GAM2953 GACCGTCGATTCCCTGACGA 67558 TCCCTGACGA 67559 TCG C AG----- T AG
CTACGAGCACCTGAATGAAG CTACGAGCAC GACCG ATTCCCTGACGA TACG CACC
GAATGAAGC A
CAGAAGGCTTCATTTGGTGA CTGA ||||| |||||||||||| |||| |||| |||||||||
CCCCGACGTGATCGTTAGGG CTGGT TAAGGGATTGCT GTGC GTGG TTTACTTCG /
AATAGTGGTC GA- A AGCCCCA - GA

GAM2954 GCAATTAGATTTGTAATGTT 67572 TCGAATCTTG 67573 -- T TT--- ACC - G ------- A
AAC
TGATACCGCCAACGTCTCTG TCACGTTTAG AA TTAGATTTG AATGT GAT GC CAAC TCT
CTGA GA A
AAGAAACAAAAATCTCGGCT ATCT || ||||||||| ||||| ||| || |||| ||| |||| ||
GATATAGAAGTTGCGTCGAA TT AGTCTAGAT TTGCA CTA TG GTTG AGA GGCT
CT A
TCTTGTCACGTTTAGATCTG TA - CTGTT AGC C A TATAGTC - AAA
AATTTGC

GAM2955 GTGGCTTGAACATCTACTTG 67577 TTCAAAGTGT 67578 ----- TA TGAGA ----
TCGAA- GA
AGAAGATACTACGTTCGAAG CTACGTTAGA GTGGCTTGA ACATC CT AGATACT ACGT
GC C
CGACCAGCGAGGTTACGTTC CGAT ||||||||| ||||| || ||||||| |||| ||
AAAGTGTCTACGTTAGACGA CATTGAACT TGTAG GA TCTGTGA TGCA CG /
TGTTAAGATCAAGTTAC AGAAT CA TTGCA AACT TTGGAG AC

GAM2956 GATGTTAAGATCAAGTTACC 67582 TATCGTAGCA 67583 A ---- CA AA- TT TAT TTC-
AA GT
AATATTAAAAACATTTGTTA ACATTGGTTG GATCAA GTTAC ATATTAAA CA TGT AACA
CCG GAAC T
TAACATTCCCGAAGAACGTT TAAC |||||| ||||| |||||||| || ||| |||| ||| ||||
GTGTTCGTGGTTACTGTTCC TTGGTT CGATG TATAGTTT GT ACA TTGT GGT
CTTG /
TACATTGGCATTTGATATCG G ACAA C- ACG T- TCC CATT G- TG
TAGCAACATTGGTTGTAACA
TC
GAM2957 TGAAACAATTACGTATAAAG 67589 TAAAGAACTA 67590 A G GAAC CAA T GA
AACTATGCAATATATTAGGT TGCAATATAT TGAA CAATTAC TATAAA TATG TATAT AGGT T
GATAAGACCTATATAACTAT TAGG |||| ||||||| |||||| |||| ||||| ||||
ATTTGTGAGTAATTGCTTTA ATTT GTTAATG GTGTTT ATAT ATATA TCCA A
C A ---- CA- - GA

GAM2958 TAAAAACGATATACTGACTC 67595 CACTCGTAAT 67596 G --------- ACT ATT TA TT AA
GGATTTGATAGTTTATGCAA AGTATTTATT TAAAAAC AT ATACTG CGG TGA GT ATGC
A
ATTAGCGTCCACCTCACTCG TTTC ||||||| || |||||| ||| ||| || ||||
TAATAGTATTTATTTTTCAT ATTTTTG TA TATGAT GCT ACT CA TGCG T
GGTTTTTA G CTTTTTATT AAT C-- C- CC AT

GAM2959 ACCTGAGTGTTCAAAAAAAT 67602 TCAATAGTAG 67603 GTTCAAAAAAAT AT TC CAA
AACT G
CAATAAACCATCCCTCAATA GAGTGGTTTT ACCTGAGT CA AAACCA CCT TA TGT C
AACTTGTGCTGACATCAATA CTGT |||||||| || |||||| ||| || |||
GTAGGAGTGGTTTTCTGTAT TGGACTCG GT TTTGGT GGA AT ACA T
AAGTACTAGCTCAGGT ATCATGAATAT- CT GA TG- AACT G

GAM2960 AACTTATTATTGTTAGATGA 67615 TGAAATAACT 67616 ----- TG TG-- CCTACTTTTG---
- GC
TGAAATAACTGATAGACCTA GATAGACCTA TGTTAG ATGA AAATAAC ATAGA
GATATA TGT A
CTTTTGGATATATGTGCATC CTTT |||||| |||| ||||||| ||||| |||||| |||
GACATTGTATCAGTAACTAT GCAATT TATT TTTATTG TATCT CTATGT ACA T
AAATTCTATACCCGTTATTT ATTAA GT CCCA TAAATATCAATGA T GC
TGTTATAATTATTAACGAAC
ATTAGTT
GAM2961 GCCCGACGTCAGTCAGTCAC 67620 AGGCGGTGAG 67621 A AGTCA AG G GA--- -
ACA- - GGG
CTGAGGCGGTGAGCCACACA CCACACAGCC GCCCG CGTC GTCACCTG GC GT GC CAC
GC CC G
GCCCGGGGTGAGGAGCGGAG CGGG ||||| |||| |||||||| || || || ||| || ||
GTGAGCGAGGGACGGCGTAG CGGGT GCAG CGGTGGAT CG CA CG GTG CG
GG /

GTGGCGACGGTGGGC G ----- G- G GGGAG A GAGG A AGT

GAM2962 GGAGAGGGACAGAGAGGACA 67707 GAGGACACAA 67708 GGGA CAACGGA GA GCC
CAACGGAGTCGAGGTTGCCA CGGAGTCGAG GGAGA CAGAGAGGACA GTC GGTT A
AGGAACCGGGCGTTTTATTG GTTG ||||| |||||||||||| ||| ||||
TCTTTTTTGCGTCTCC CCTCT GTTTTTTCTGT CGG CCAA /
GC-- TATTTTG G- GGA

GAM2963 AACTTATTATTGTTAGATGA 67720 TGACGAAATA 67721 ----- TG-- CCTACTTTCG--- - GA
CGAAATAACTGATAGACCTA ACTGATAGAC TGTTAG ATGACGAAATAAC ATAGA GATATA TGT A
CTTTCGGATATATGTGAATC CTAC |||||| |||||||||||| ||||| |||||| |||
GACATTGTATCAGTAACTAT GCAATT TATTGTTTTATTG TATCT CTATGT ACA T
AAATTCTATACCCGTTATTT ATTAA CCCA TAAATATCAATGA T GC
TGTTATAATTATTAACGAAC
ATTAGTT
GAM2964 GGGTTTAAGCAATCAGAGGC 67724 TCTGAAAGAT 67725 AAGCAA-- ----- CTCATTTT T
GTGTCTCATTTTGGTACGCC ATCAAGCCC GGGTTT TCAGA GGCGTGT GG A
ACACGCCGTACGTCTGAAAG |||||| ||||| ||||||| ||
ATATCAAGCCC CCCGAA AGTCT CCGCACA CC C
CTATAGAA GCATG -------- G

GAM2965 CACATTAGCATAAGATGTAC 67791 TGTAACAAAC 67792 - - TAAGA T T AA GTC CC A
TTGTAACAAACCGCGTCCTC CGCGTCCTCA CACATT AG CA TGTAC TG AACA CCGC CTCA TA G
ACCTAAGCCTAATTGAGGCG CCTA |||||| || || ||||| || |||| |||| |||| ||
GCCTGTTCTATGTATAACCT GTGTAG TC GT ATATG AT TTGT GGCG GAGT AT C
TGACTAGATGTG A A TCCA- T C CC --- TA C

GAM2966 GGATAGCTCTGCGCAGCTAT 67806 TACCGCGCAG 67807 ---------- AGC CCCCACT
ACCCCACTTAATAAATTATA AGTATAAAAG GGATA GCTCTGCGC TATA T
CCGCGCAGAGTATAAAAGAT ATTA ||||| ||||||||| ||||
TATATTATCC CCTAT TGAGACGCG ATAT /
TATATTAGAAAATA CC- TAAATAA

GAM2967 TATTTTGAAAGATATGAGTA 67813 TGAAAGATAT 67814 GATA AA AT
AAATATTTAATGAAATAAGT GAGTAAAATA TATTTTGAAA TGAGTAA TATTTA G
AACTTATTTAATAATTTCAA TTTA |||||||||| ||||||| ||||||
AATA ATAAAACTTT ATTTATT ATGAAT A
AATA CA AA

GAM2968 GTGGTGGGAGTGGGCGTGGT 67826 TTTAAATTGG 67827 G -- G- GTA G TT T TG CCA GA
ATGCGGGGGTTCTTTGTTTA GCCCAGGCGG GT GGGAGTG GCGTG TGCG GGGTTCT GT TAAAT GGC GGCG T
AATTGGGCCCAGGCGGATCA ATCA || ||||||| ||||| |||| ||||||| || ||||| ||| ||||
GTGCCAGTTTTGTTTGCATT TA TCCTCAC CGTAC GCGT TCCGGGG TA GTTTG TTG CCGT C
GGGGGCCTGTGCGGCATGCG T AC AG G-- G GT C TT A-- GA
ACACTCCTCAATTGC

GAM2969 ACGTCGAGCCCGCGTTGGGG 67833 CACCGGCACG 67834 --- C T C TCAC AC- CA
CATATCACGCTACTGTACAG TTCGACGT ACGTCGAGC CCG GT GGGG ATA GCT TGTA G
CTCTGCACTAAGCACTTTAT ||||||||| ||| || |||| ||| ||| ||||
ACTCTCACCGGCACGTTCGA TGCAGCTTG GGC CA TCTC TAT CGA ACGT C
CGT CAC - C A TTCA ATC CT

GAM2970 ATTTGTTATTAAATGAATAA 67858 TAAATGAATA 67859 TT A ATAAAATT TCA
AATTAGATTCATCTATATCT AAATTAGATT AT GTT TTAAATGA AGAT T
TCTTCACTCATTTAAAAACT CATC || ||| |||||||| ||||
TAT TA CAA AATTTACT TCTA C
TT A CACTTCT- TAT

GAM2971 TAGTCACGACTGAAATAACC 67866 CGGCATGGTT 67867 ACT AA-- C -- TTT
GCGTGATTATTTTTTGGTAT TCTGTGACTA TAGTCACG GAAAT CCG GT GATTAT T
AATTCTACACGGCATGGTTT |||||||| ||||| ||| || ||||||
CTGTGACTA ATCAGTGT CTTTG GGC CA TTAATA T
--- GTAC A TC TGG

GAM2972 GAGAGAGAAAGAGACAGAGA 67939 ACCACGTTTT 67940 AGACA G C-- CC--- - A CC
GACGCGAGACGAAAGAGACC TATCTTTTTT GAGAGAGAAAG GAGAGACGC AGA GAAAGAGA ACG GG CG A
ACGGGACGCCACACGACCAC TATT |||||||||| ||||||||| ||| |||||||| ||| || ||
GTTTTTATCTTTTTTTATTC TTTTTTCTTTC TTTTTTGCG TCT TTTTTTCT TGC CC GC /
TGCGTTTTTTATCCGCTTTC GCCTA - TAT ATTTT A A AC
TTTTTT

GAM2973 AAATAAAATTCTGATTGGTC 67950 TGATTGGTCA 67951 A C -- GTCAAT T
AATGTGAATGTATTCACTTA ATGTGAATGT AAATAAA TT TG ATTG GTGAA G
ACAGTTCCACAAATTTATTT ATTC ||||||| || || |||| |||||
TTTATTT AA AC TGAC CACTT T
A C CT AATT-- A

GAM2974 CTACCAATCTTCAAATATCG 67957 TATCGCCCAT 67958 CAAT T C- AAC AC

CCCATTTAACAGTACAAAAC TTAACAGTAC CTAC CTTCAAA ATCGCC ATTT AGT A
TAGGGGGTATGGCGGTTTTG AAAA |||| ||||||| |||||| |||| |||
AAGCTCGTAG GATG GAAGTTT TGGCGG TGGG TCA /
CTC- - TA GGA AA

GAM2975 AAATAAAATTCTGATTGGTC 67965 TGATTGGTCA 67951 A C -- GTCAAT T
AATGTGAATGTATTCACTTA ATGTGAATGT AAATAAA TT TG ATTG GTGAA G
ACAATTCCACAAATTTATTT ATTC ||||||| || || |||| |||||
TTTATTT AA AC TAAC CACTT T
A C CT AATT-- A

GAM2976 GATTATTTTTTGGTATAATT 67966 TATGAATTCT 67967 TTTTTG TAATTCTAC ----------
TC
CTACACGGCATAGTTTCTGT ACCCCCGTTA GATTAT GTA ACGG CATAGTT T
AACTATGAATTCTACCCCCG CATT |||||| ||| |||| |||||||
TTACATTTGTATAATC CTAATA CAT TGCC GTATCAA /
TGTTTA --------- CCCATCTTAA TG

GAM2977 GGCGCGCCAATAGGTAGGGA 67979 TACGTTCCCT 67980 C- - A GG- TGGATCT
GTCAATG CGT
TGGATCTACGTATGTCAATG AAAATGCTGT GGCG GC CA TA TAGGGA ACGTAT
GAGGC A
GAGGCCGTATAAAGCTTCAA GCTC |||| || || || |||||| |||||| |||||
TAATACGTTCCCTAAAATGC CCGC CG GT GT ATCCCT TGCATA CTTCG T
TGTGCTCCGCC CT T C AAA ------- ATAA--- AAA

GAM2978 CATGGGATCCGGTTCGTAAT 67993 AAGGTTGTCG 67994 - CCG C - AT-- T
CGCGCTATCGTCTTCGTAAA TTACGAACAT CAT GGGAT GTTCGTAAT GCG CT CG C
GGTTGTCGTTACGAACATAT ATCC ||| ||||| ||||||||| ||| || ||
CCCGATG GTA CCCTA CAAGCATTG TGT GG GC T
G TA- C T AAAT T

GAM2979 GGGAATACAGACATCATTGG 68000 GACCTACAGC 68001 ATACA CATC --- G TGG
CAGGTGCAATGGCAGTTTTG CAGTTCATTA GGGA GA ATTGGC AGGT CAA C
GACCTACAGCCAGTTCATTA TCCC |||| || |||||| |||| |||
TCCC CCCT CT TGACCG TCCA GTT A
ATTA- ---- ACA G TTG

GAM2980 GGCGCTACAGATGTAATTGA 68014 TATGATGGGA 68015 ----- GA- AATT AGAT
CGAAAGATCTGTATTTGTCT TGTGGTGGGT GGC GCTACA TGT GACGAA C
ATGATGGGATGTGGTGGGTT TGCC ||| |||||| ||| ||||||
GCC CCG TGGTGT GTA CTGTTT /
TTGGG AGG GTAT ATGT

GAM2981 TTTGATAATGATAGACAGAA 68026 TGATAGACAG 68027 A C AATG GC T
TGCAATGCTGTACACAAATT AATGCAATGC TTTGATAATG TAGA AG CAAT TG A
GGGACTTTTTATATTATCAA TGTA |||||||||| |||| || |||| ||
G GAACTATTAT ATTT TC GTTA AC C
- T AGG- A- A

GAM2982 ACAGAAAATCCGCAGGAGAT 68033 CAGGAGATTC 68034 AAAATCCGC - C------- A T
TCCAGCATTGTTCCAAGCTG CAGCATTGTT ACAG AGGA GATT CAGC TTG T
TCTAACAAAATCTTCCTCAT CCAA |||| |||| |||| |||| |||
AATGAACTGT TGTC TCCT CTAA GTCG AAC /
AAGTAATAC T AACAATCT - C

GAM2983 AGAAATTGCTTGCGCCAAAG 68099 TTACTGCATC 68100 T- C CAAAG G ATA--- GCA
GTG CA
AACGTTTGAAATATGTTACT AACGTGCTCA GAAAT GCTTG GC AAC TTTGAA TGTTACT
TCAAC CT G
GCATCAACGTGCTCAGAAAG GAAA ||||| ||||| || ||| |||||| ||||||| ||||| ||
AAGTTGAGAGTGACAAACCA TTTTG CGGAC CG TTG AAATTT ACAGTGA AGTTG
GA /
CTTTAAAGGTTAAGCCAGGC TT - AA--- G CACCAA G-- AA- AA
TTGTTTTT

GAM2984 GAGTGGCAGTAAAATCATTA 68121 TTAAATGAAT 68122 C TAAAATCATTAC AG-----
AT
CAATCTGATTTAGTTGATAA AAAATTAGAT GAGTGG AG AATCTGATTT TTGATAA T
ATTTGTTATTAAATGAATAA TCAT |||||| || |||||||||| |||||||
AATTAGATTCATCTATATCT CTCACT TC TTAGATTAAA AATTATT /
TCTTCACTC - TTCTATATCTAC ATAAGTA GT

GAM2985 GACGATTCACCTACCTGGCG 68130 TTGCAGCGTT 68131 - - T CT- TT---- -- A - A G
TTGCAGCGTTATTACGGATA ATTACGGATA GAC GATTC ACC AC GGCG GCAGC GTTATT
CGG AT CG A
CGGATCGGATACCGAATGGC CGGA ||| ||||| ||| || |||| ||||| |||||| ||| || ||
TAGCTGCCACCTCCGCCCTC CTG CTGAG TGG TG CCGC CGTCG CGGTAA GCC TA
GC /
GTCGGTCGAGTCAGTC A C C CTC CTCCAC AT - A G T

GAM2986 CCCTTCCCGAGCGAGTGCGG 68133 TGAGAGGAAA 68134 - GA ---- GCGG CC---------
- AAAC
TTTCTCACATGCCGTGAGCA ACTTTATTGC CCCT TCCC GC GAGT TTTCTCACATG
GTG AGC G
AACGAAAACGCTACACATAA AGGG |||| |||| || |||| |||||||||| ||| |||
TAAGACACGTGTGAGAGGAA GGGA AGGG CG TTCA GGAGAGTGTGC CAC
TCG A
AACTTTATTGCAGGGACAGG C A- TTAT AAA- ACAGAATAATA A CAAA

G

GAM2987 ACGAAAAATGATGAAGGCAA 68170 TAAAAAGTGT 68171 GATGAAG A - AA ATAAAAAG
AG TG GTG- - TG G
TCATTCCTCATAAGATGATA AGTGAGTGAG GCA TCATTC CTCAT GATG TA G T
TGT G T T
AAAAGTAAGGTGTGTGTGTG AGTA ||| |||||| ||||| |||| || | | ||| | |
TGTGTGTGTGTGATAAAAAG TGT AGTGAG GAGTG TTAT GT T G ATA T G G
TGTAGTGAGTGAGAGTATTA GAGTG-- G T A- GAGAGTGA GA GT AAAA G GT T
GTGAGTGAGTGAGTGTGTGA
GTGAGTGAGT
GAM2988 GTCGTTCTCGTTCAGAATCT 68203 TCGCAGCATA 68204 T GTTC A TCG - G G
TTCGCAGCATAAGTAGTATG AGTAGTATGT GTCGT CTC AGA TCTT CAGC ATAAGTA TAT T
TCGATATACTTATCGTTGAA CGAT ||||| ||| ||| |||| |||| ||||||| |||
GACTCTTCCAGAGACGAT TAGCA GAG TCT AGAA GTTG TATTCAT ATA C
- ACCT C --- C - G

GAM2989 CCTACGCGAGGCTGAACCTC 68207 AAGAAGAGAA 68208 G TGAACCT AA CA- TC
G
CTGAATCACTGCATCTTTCT TAGTGGCCAG CCTAC CGAGGC CCTG TCACTG TCTT
TTGAG C
TGAGGCGTTTAAAGAAGAGA GGCC ||||| |||||| |||| |||||| |||| |||||
ATAGTGGCCAGGGCCTCGGT GGGTG GCTCCG GGAC GGTGAT AGAA AATTT /
GGG - ------- C- AAG GA G

GAM2990 CTTGGTATAGAAACATGATG 68367 TGTGAAAAAT 68368 TG TAGAA GATGTA T- TG T
TATCACTTTGCCTTGGGGGG GTAATTACTG CT GTA ACAT TCAC T CCT G
TGATTGTGAAAAATGTAATT GG || ||| |||| |||| | |||
ACTGGG GG CAT TGTA AGTG A GGG G
GT TAA-- AAA--- TT GT G

GAM2991 CTGTACCTGCTCCTACAGTT 68402 CCTACAGTTT 68403 T C A GCTGTAC - CT T
TCTGCTGTACCAGTACCTGC CTGCTGTACC CTG ACCTGCTC TAC GTTTCT CAGT AC
GCTGC C
TGCTCCTGTAGCTGTAGCTG AGTA ||| |||||||| ||| |||||| |||| || |||||
CTAAGAGACGTAGAGTAGGT GAT TGGATGAG ATG CAGAGA GTCG TG CGATG C
TAG - - - ATC---- A T- T

GAM2992 TGTGTTCTCCTCCCGCCGCT 68445 CTCGAGCTGA 68446 -------- CCGCC T ACCA
TGTGCAGCACCACCTCCCGC GGATCCGTGA TGTGTTC TCCTC GCTTG GCAGC C
TGCTCGAGCTGAGGATCCGT TGGA ||||||| ||||| ||||| |||||
GATGGACACA ACACAGG AGGAG CGAGC CGTCG C
TAGTGCCT T---- T CCCT

GAM2993 TCCAACAACTGTTTATGTAA 68466 TAAAGGAAAA 68467 AA CTGT TGT AAA--- CA GA

AGGAAAATAAAGACTCAGAG TAAAGACTCA TCC CAA TTA AAAGGAAAAT GACT GA A
AAAATCCAAGTTCATATGAT GAGA ||| ||| ||| |||||||||| |||| ||
TTTTCTTTTATTGATTGGGG AGG GTT AGT TTTCTTTTTA TTGA CT /
GA GG ---- TAT GTATAC AC AA

GAM2994 GGATAAAACGAATCTTTAGT 68548 ATAGAAACAA 68549 AACGAA TA- GAG-- AGAA
ATGAGCTATTATAGAAGTAG TACAACGAGA GGATAA TCTT GTAT CTATTAT G
AATAATAGAAACAATACAAC AATA |||||| |||| |||| |||||||
GAGAAATAGATTGTCT TCTGTT AGAG CATA GATAATA /
AGATAA CAA ACAAA AGAT

GAM2995 TATGTTCTTTTTTTATTGGG 68582 TACAATGCAA 68583 T TG- ---- G- - GG
AGGCGCGGGTAGGCGGGTAG AAGCCTTCGA TATGT CTTTTTTTAT GGAGGC GCG GTAG
GC G
CTTTACAATGCAAAAGCCTT CGTG ||||| |||||||||| |||||| ||| |||| ||
CGACGTGGAGGAAGGCGTG GTGCG GAAGGAGGTG CTTCCG CGT CATT CG /
- CAG AAAA AA T AT

GAM2996 GGTCCGTTTTGTCACGGGAA 68590 AGAGGAAACA 68591 C -- CAC--- --- A - --- G
A
AGGAAAGAGGAAACAGGCCG GGCCGCGGAC GGT CGT TTTGT GGGAA AGGAAAG GGAA
ACAGG CC CGG C
CGGACACCCGGGGGAGTTTG ACCC ||| ||| ||||| ||||| ||||||| |||| ||||| || |||
TGTTCCCTTTTCTTTCTTCC CCA GCG AAACA CCCTT TCTTTTC CCTT TGTTT GG
GCC A
CACACACACAAAAGGCGTAC T GA CACACA CTT - G GAG G C
C

GAM2997 TTTCTTATTATATATCAATT 68706 AAGGATGTGC 68707 ATTATATATCAATTA AC TTAA
GCT AC CGCA
AATGACTATCTTAACTTTAT ATGAATAAAC TCTT ATG TATC CTTTATAGA TTCAT
TAT A
AGAGCTTTCATACTATCGCA CAAT |||| ||| |||| ||||||||| ||||| |||
ATTATATATCATGAATCATT AGAA TAC GTAG GAAATATTT AAGTA ATA /
TATAAAGGATGTGCATGAAT ATTAACCAAATAAG- GT ---- ACT CT TATT
AAACCAATTAAAGAAA

GAM2998 CTCCATATTTTACCATTGAC 68719 TATTTTACCA 68720 CAT GACAAA- C TC
AAACTCACATCTACTGTAAG TTGACAAACT CTC ATTTTACCATT CT ACA T
GTCAAAAGATGGTAAAATCA CACA ||| |||||||||| || |||
CGAG GAG TAAAATGGTAG GA TGT /
CAC AAAACTG A CA

GAM2999 GTGGTTTCTACTCAAAAGCT 68728 ACTCAAAAGC 68729 TTCTA A TC CA CCTC AA
CGAACAACGCCTCGGGAAAG TCGAACAACG GTGGT CTCAAA GC GAA ACG GGG A
ACCCACGTATTTACGCTTTG CCTC ||||| |||||| || ||| ||| |||

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      AGAAAATACCAC                        CACCA    GAGTTT CG  TTT  TGC    CCC  /
                                      TAAAA     -  CA   A-   A---   AG

GAM3000  CGATAGAGGGATTTAGAGAC 68748   AGAGGGATTT 68749     T    GG   TAGAGA     T  --    AGA
      CTTTCTTCCACGTTAGAACG        AGAGACCTTT        CGA AGAG  ATT     CCTTTC TCC  ACGTT   A
      ACGACGTAAGGACGAAAGGG        CTTC            ||| ||||  |||      |||||| |||  |||||
      AGGTTTCTTTTTCG                        GCT TTTC  TGG     GGAAAG AGG  TGCAG   C
                                    T    TT   AG----      C   AA     CAG

GAM3001  GTATTATACATATATCTGTT 68776   TACATATATC 68777        T-  -     C         ATTGTC
      GATATGATTGTCACTTTACC        TGTTGATATG        GTATTA  AC ATATAT TGTTGATATG     A
      ATATCAACAATATATAGTTT        ATTG            ||||||  || |||||| ||||||||||
      TAATAT                        TATAAT  TG TATATA ACAACTATAC     /
                                   TT  A     -         CATTTC

GAM3002  TGAGCAAAGGGTACAAGGCC 68780   CAAGGCCCAA 68781      CA     A  AG    --     AT    T   CT
      CAATCCAATCCGTTCGCCTT        TCCAATCCGT        TGAG  AAGGGT CA  GCCC  AATCCA  CCGT CGC
T
      GCGCGCGCGGCTGGATTTAG        TCGC            ||||  |||||| ||  ||||  ||||||  |||| |||
      GGTTGACCCTTACTCA                        ACTC  TTCCCA GT  TGGG  TTAGGT  GGCG GCG  /
                                    A-     -  --    AT     C-    C   CG

GAM3003  GGTTGTTGTTAGTAATAGTA 68794   TTAGTAATAG 68795      -   TT-     TAGTAT       A
      TACAAGATAATGGTATTTTG        TATACAAGAT        GGTTG TTG   AGTAA     ACAAGATA T
      TTCTTTACTTGTTAGTCAAT        AATG            |||||  |||   |||||     ||||||||
      T                           TTAAC GAT   TCATT     TGTTTTAT G
                                    T   TGT     TCT---       G

GAM3004  GCGCCGCGAGGGTAGGTGGT 68797   TTCCTGATTC 68798    GC   G    -   TG-    ATA  -   TT
      CGATAGCCCGTTTGACGGAG        TGGTGTAGC         GC  CGC AGGGT AGG   GTCG   GC CCG  T
      TAGCGATATTCCTGATTCTG                    ||  ||| ||||| |||   ||||   || |||
      GTGTAGC                         CG  GTG TCTTA TCC   TAGC   TG GGC  /
                                  AT   G    G   TTA   GA-  A   AG

GAM3005  TTAGTGTTGGAATTATTAGT 68853   TACAACAATG 68854          AATTAT      CTTC    CA---   TG
      ATTCTTCTTGTCATCTTGTT        CTATACCTAA        TTAGTGTTGG     TAGTATT    TTGT     TCT  T
      CAGAAATATACAACAATGCT        TACT            ||||||||||     |||||||    ||||     |||
      ATACCTAATACTAA                        AATCATAATC     ATCGTAA    AACA     AGA  /
                                    CAT---      C---    TATAA   CT

GAM3006  TAGGGTTCTGCTATTCAGAC 68863   TAGTAGGCCG 68864      G  -  TG    TCA    ---    -    AT
      GTACGCACATTAAGTGTAGT        TCATGTGGTG        TAGG TT C  CTAT   GACG   TAC GCAC  T
      AGGCCGTCATGTGGTGGTAA        GTAA            |||| || |  ||||   ||||   ||| ||||
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GCCTA ATCC AA G GGTG CTGC ATG TGTG /
G T GT TA- CGG A AA

GAM3007 GTAGAATGTTTACATTATTA 68893 TGTGATCAAT 68894 ---- AA- T GAATC
ATACTGTGAATCAAACAAAC AAACACTGTG GTAGAATGTTTACA TTATT TAC GT A
TGTGATCAATAAACACTGTG AATA |||||||||||||| ||||| ||| ||
AATATTTTAC CATTTTATAAGTGT AATAA GTG CA /
CACA CTA T AACAA

GAM3008 AGGTAAAGTGCTATCGCTTT 68912 TAAAGTGCTA 68913 AAA- TATCGC - AAAAAGAA
CGTGTGAAAAAGAACCATAG TCGCTTTCGT AGGT GTGC TTTCGT GTG C
ACACCGCTACGAGAACTGCA GTGA |||| |||| |||||| |||
CCACCACCT TCCA CACG AGAGCA CGC C
CCAC TCA--- T CACAGATA

GAM3009 TGTGAGAAGTTTGCCTCGTT 68919 TGGAATAGTT 68920 GA-- GC C T -- TTA----- TT
T
AAGGTCTTCCATTTAAATAT TTTAACTAGT TGA AGTTT CT GTTAAGG CT TCCAT AATA
ATATAAACA T
TATATAAACATTTGTGTTTA AAAG ||| ||||| || ||||||| || ||||| |||| |||||||||
TATCTTATTCGTCTTTTATG ATT TCGAA GA CAATTTT GA AGGTA TTAT
TATATTTGT T
GAATAGTTTTTAACTAGTAA AATG AT T T TA TTTTCTGC TC G
AGCTGTAATTACA

GAM3010 CATGGCCTGTGTAACTAGCC 68928 CATTTCACTA 68929 G T C GTTAC A
TTCTAGTGAAAGTTACCGAA GAACGCTGGT CATGGCCT TG AACTAGC TTCTAGTGAAA CG A
AACGCATTTCACTAGAACGC TCAG |||||||| || ||||||| |||||||||| ||
TGGTTCAGAGGCTATG GTATCGGA AC TTGGTCG AAGATCACTTT GC A
G - C AC--- A

GAM3011 ATGTGAGAAGTTTGCCTCGT 68953 TAAGGTCTTC 68954 GA-- GC C T -- TTA----- TT
A T
TAAGGTCTTCCATTTAAATA CATTTAAATA TGA AGTTT CT GTTAAGG CT TCCAT AATA
AT TAAACA T
TTATATAAACATTTGTGTTT TTAT ||| ||||| || ||||||| || ||||| |||| || ||||||
GCATCTTATTCGTCTTTTGT ATT TCGAA GA CAATTTT GA AGGTG TTAT TA
GTTTGT T
GGAATAGTTTTTAACTAGTA AATG AT T T TA TTTTCTGC TC C G
AAGCTGTAATTACAT

GAM3012 ATATGTTAATTGGAATATAC 68958 CATTCGAAAA 68959 TAATT A ACAC--- ATAG
ACTGCTATAGTTTACGGGCA TAATCCTAAC ATATGT GGA TAT TGCT T
TTCGAAAATAATCCTAACAC ACAT |||||| ||| ||| ||||
ATAT TATACA CCT ATA ACGG T
CAAT- A AAAGCTT GCAT

GAM3013 GTAAGCTACCGTACATCTCT 68968 CTCACATAGA 68969 TA ACC ACA TTCACAAA C
TTCACAAACCCAGGGCTCAC GACAAGCACA G AGCT GT TCTCT CC A
ATAGAGACAAGCACAAGCTC AGCT | |||| || ||||| ||
GC C TCGA CG AGAGA GG /
GC ACA AAC TACACTC- G

GAM3014 GCGCGGCACTCAATCGTTAC 69001 TTACTGGTGG 69002 - CTCAATC T G TGCTT- G ---
------ A T
TGGTGGCTGCTTCTGGGACG CTGCTTCTGG GCGGCA GT ACTG TGGC CTG GACG
AC CAAGC C
ACACAAGCTCAGTTTGGTAT GACG |||||| || |||| |||| ||| |||| || |||||
GCAACTACGTCACAGCTCAT CGCCGT CA TGAC ACCG GAC CTGC TG
GTTTG /
CGCCAACAGTTACTGCCGCT T ------- T A CTACTC A ATCAACGTA - A
GC

GAM3015 TGTGAGAAGTTTGCCTCGTT 69009 TGGAATAGTT 68920 GA-- GC C T -- TTA----- TT
T
AAGGTCTTCCATTTAAATAT TTTAACTAGT TGA AGTTT CT GTTAAGG CT TCCAT AATA
ATATAAACA T
TATATAAACATTTGTGTTTG AAAG ||| ||||| || ||||||| || ||||| |||| |||||||||
TATCTTATTCGTCTTTTATG ATT TCGAA GA CAATTTT GA AGGTA TTAT
TATGTTTGT T
GAATAGTTTTTAACTAGTAA AATG AT T T TA TTTTCTGC TC G
AGCTGTAATTACA

GAM3016 AGTGTCTAGGATGCGTAATT 69010 TAGGATGCGT 69011 G -- TT T TAT
TTTTATATGGTATAGATCCT AATTTTTTAT AGT TCTAGGATGCG TAAT TTTATA GG A
GTAAGCGTTGTCTGTATTCT ATGG ||| |||||||||| |||| |||||| ||
GGAGCT TCG AGGTCTTATGT GTTG GAATGT CC /
- CT C- - TAG

GAM3017 AGTTGGATGAATAGTATGTC 69013 TTAGTGCACT 69014 GG A - TTAATAA A TT----
ATA
TTAATAATTGTTATTATTTC CTATAAAAAC AGTT ATGA TAGT ATGTC TTGTT TTAT
CACTAATTA T
ACTAATTAATATTTAGTAAT GAGA |||| |||| |||| ||||| ||||| |||| |||||||||
TAGTGCACTCTATAAAAACG TCAA TACT ATCA TACAG AGCAA AATA
GTGATTAAT T
AGAATGACATAACTAATCAT -- A A TAAG--- A TCTCAC GAT
AACT

GAM3018 GTACGGCCCATGGGAGGGAA 69024 AGGGGGTGTT 69025 - A GG TT AC T
CATTTCCACGTGTTCCAATA CCTTAATAGG GTACGG CCC TG AGGGAACAT CC GTGT C
CAGGGGGTGTTCCTTAATAG GACT |||||| ||| || ||||||||| || ||||
GGACTGTGC CGTGTC GGG AT TTCCTTGTG GG CATA C

A - AA GG A- A

GAM3019 AATGAAGTTTAAAGAATATT 69036 CTTTAATTTT 69037 A ---- --- - AC
AAATTTGACGTACAGGCTTT ATTCTTATTT AATGA GTTTAA AGAATA TTAAA TTTG G
AATTTTATTCTTATTTTAAA TAAA ||||| |||||| |||||| ||||| ||||
CCTTATT TTATT CAAATT TCTTAT AATTT GGAC /
C TTAT TTT C AT

GAM3020 GTCACAATGGCCTACGTGAC 69041 TACGTGAGAT 69042 A G A G - GTA A- TAAAAC
TTGGTATACGTGACCTAAAA AATGTAATGA GTCAC AT GCCT CGT AC TTG TACGTG CC A
CAACAAAGTGGCGTACGTGA GGTG ||||| || |||| ||| || ||| |||||| ||
GATAATGTAATGAGGTGGTG TAGTG TG TGGA GTA TG AAT GTGCAT GG A
GTGAT G G - A T AGA GC TGAAAC

GAM3021 CAGACCCACCCCAGTCAGAC 69047 TGACATGGGT 69048 GA CA -------- A - GG--- GA
GA
CCAGTGGCGAGAGGCGAGCA GGGGATG CA CCCACCC GTC AG CC CAGT CGA
GGC G
GCTGTTGAAAAAATTGAGGA || ||||||| ||| || || |||| ||| |||
CTTGTTACATGACATGGGTG GT GGGTGGG CAG TC GG GTTA GTT TCG /
GGGATG AG TA TACATTGT A A AAAAA G- AC

GAM3022 TGGCCCTCACCTGCCGCCTC 69072 AGAATGCACC 69073 CTCA - G GTTTCC CGGGA
C
CGTTTCCCGGTGCCGGGATT GTAGGAGGGG TGGCC CC TGCC CCTCC CGGTGC TTC
G
CCGAGGAAGAATGCACCGTA CATG ||||| || |||| ||||| |||||| |||
GGAGGGGCATGGCCGGCCA ACCGG GG ACGG GGAGG GCCACG AAG A
CC-- T - AT---- TAAG- G

GAM3023 AGTTGCATGTGGAAAAATCA 69090 TCGCTTGGTC 69091 TGT AAAATCAAAATAAA CTG
CT
AAATAAAAAGTCTGGAGTCT CTGTAACT AGTTGCA GGA AAGT GAGT C
CACGCTCGCTTGGTCCTGTA ||||||| ||| |||| ||||
ACT TCAATGT CCT TTCG CTCG /
--- GG---------- --- CA

GAM3024 GGAAAGGATCTCGTGCGCTA 69115 AAGGATCTCG 69116 AAA T C- TAT TC G
TAAGTCTAACGAAAGTTGAG TGCGCTATAA GG GGATC CGTG GC AAG TAAC A
CTTGCAACATGGGTCTATGC GTCT || ||||| |||| || ||| ||||
C CC TCTGG GTAC CG TTC GTTG A
GTA - AA --- GA A

GAM3025 ATCAATGCTGGTGCCACGGT 69119 CTGGTGCCAC 69120 CT CA A CCCT
TTCACCCCCTTCTTAAGGGA GGTTTCACCC ATCAATG GGTGC CGGTTTC CC T
GGCTGCTGCACCCACGTTGG CCTT ||||||| ||||| ||||||| ||
T TGGTTGC CCACG GTCGGAG GG C
AC TC - AATT

GAM3026 CCCTCTACGAAATGTTCAGT 69130 GGTGCATACT 69131 T AA T CGGAA A AA
CGGAAGCTGAGAACCTCCCG GACATTGTGA CCCTC ACGA TGT CAGT GCTG G C
GTGCATACTGACATTGTGAG GGG ||||| |||| ||| |||| |||| |
GG GGGAG TGTT ACA GTCA TGGC C /
- -- - TACG- C TC

GAM3027 GGTAGGAAGTTGGCCAAAGG 69151 GTTACTGTCT 69152 TA - CCAAA TT ATATA
TTTCCGGATATAAGCCACCC AACTATCCCC GG GGA AGTTGG GGT CCGG A
GGTTACTGTCTAACTATCCC || ||| |||||| ||| ||||
C CC CCT TCAATC TCA GGCC /
-- A TG--- TT CACCG

GAM3028 AAGTTTAAGTAAGATACTTA 69192 TAAGATACTT 69193 A TA- TATTTTCT - T AC
TTTTCTAGTAGCTAGTACGT ATTTTCTAGT AAGTTT AG AGATACT AGT AGC AGT G
TGCTTGCTCATTTTTCTAAT AGCT |||||| || ||||||| ||| ||| |||
AGTGTTTATTCTAAAACTT TTCAAA TC TTTGTGA TTA TCG TCG /
A TTA TAATCTTT C T TT

GAM3029 AACAAATAAACTTATAAACA 69205 TATAAACATA 69206 TAAAC TATTTTAA TT
TATTTTAAGCTTTACTGGTA TTTTAAGCTT AACAAA TTATAAACA GCT A
TTGTTGTTTATAACCTTTTT TACT |||||| ||||||||| |||
GTT TTGTTT AATATTTGT TGG /
TTCC- TGTTA--- TC

GAM3030 ACAGTTTAAAATGTTAAACT 69213 TTTAAAATGT 69214 TT- TA TTT ATTT A
TTTGTTATTTTTAATATGAT TAAACTTTTG ACAG TAAAATGT AACT GTT TTAATATG T
ATATGTTAACAGCTATAGTT TTAT |||| |||||||| |||| ||| ||||||||
GCATTTTATATTTGT TGTT ATTTTACG TTGA CGA AATTGTAT /
TAT -- TAT C--- A

GAM3031 GGCCGTCTCCTCTCGCGATC 69218 GACCTGCACG 69219 C CCTCTCG TCTG--- ACCCTCT
CTTAC CG
TGCGTGACCCTCTTCGACTT ACCCTCTTCG GG CGTCT CGA CGTG TCGA GGA C
ACGGACGCCCTCCTCGACCT ACTT || ||||| ||| |||| |||| |||
GCACGACCCTCTTCGACTTA CC GCAGG GCT GCAC AGCT CCT /
CGGACGCCC C CATTCA- TCTCCCA GTCC--- ----- CC

GAM3032 GCACGACCCTCTTCGACTTA 69226 ACTTACGGAC 69227 CCTCTT CT - C CTCG C GACCCT
CGGACGCCCTCCTCGACCTG GCCCTCCTCG GCACGAC CGA TACGGA CGCC TC AC TGCAC C
CACGACCCTCTTCTCGAGTG ACCT ||||||| ||| |||||| |||| || || |||||
CACGTAAAGACGGCGATTCG CGTGTTG GCT GTGCTT GCGG AG TG ACGTG T
TGCTCGTGTTGTGC T----- C- A C AAA- C AGCTCT

GAM3033 TATTAACAAGAATCATCCCA 69231 AGCAAATATA 69232 CAA CCCA AAATA- A G
GCAAATATATTAGAGAAGCG TTAGAGAAGC TATTAA GAATCAT GC TATTAG GAAGC C
CTCGTTTTATTAATACCAGT GCTC |||||| ||||||| || |||||| |||||
AGTAATAGTGATTCCATTGA ATAGTT CTTAGTG TG ATAATT TTTTG T
TA AC- ATAA ATGACC A C

GAM3034 CTAGATATGAACAACATGTA 69244 TGAACAACAT 69245 A A-- ---- TAA A
ATTAGAATGCTAAGATTATG GTAATTAGAA CTAGAT TG ACA ACATG TTAG A
TAATATGTACACAAGTTTGG TGCT |||||| || ||| ||||| ||||
GGTTTG AC TGT TGTAT AATC T
A ACA ATAA TAG G

GAM3035 ACCACCACCACAACCCCCCG 69256 TTCCGGGGGG 69257 ACGAAGT ACGAAGT T
GAACACAGGCCCAAAATTTT TTGTGGTGGT CCCCCGGAACACAGGCCCAAAATTTTCGCT GACCAC GACGCGC T
CGCTACGAAGTGACCACACG GGT |||||||||||||||||||||||||||| |||||| |||||||
AAGTGACGCGCTTCGCGCGT GGGGGCCTTGTGTCCGGGTTTTAAAAGCGA CTGGTG CTGCGCG /
CGTGGTCAGCGAAAATTTTG ------- ------- C
GGCCTGTGTTCCGGGGGGTT
GTGGTGGTGGT
GAM3036 GGATTTTAGAATTTCCAAAT 69271 TCCAAATTCA 69272 T AATT AAA--- --- T
TCACCAGCGATTTATCGGTT CCAGCGATTT GGAT TTAG TCC TTCACCAG CGA T
TTGGTGAAATCCAAGGATTT ATCG |||| |||| ||| |||||||| |||
ATTAATGTCC CCTG AATT AGG AAGTGGTT GCT T
T ATTT AACCTA TTG A

GAM3037 GGATTTTAGAATTTCCAAAT 69277 TTGGTGAAAT 69278 T AATT AAA--- C TT
TCACCAGCGATTTATCTGTT CCAAGGATTT GGAT TTAG TCC TTCACCAG GAT A
TTGGTGAAATCCAAGGATTT ATTA |||| |||| ||| |||||||| |||
ATTAATGTCC CCTG AATT AGG AAGTGGTT TTG T
T ATTT AACCTA - TC

GAM3038 GATGCGCTGCAAAGTTTCCT 69291 TCACCCAACA 69292 C- GCA TTCCTATTA TC CGC
ATTAGGGTTCCGCGCTTTAC TACTTGAAGC GATG GCT AAGT GGGT CG T
GTCACCCAACATACTTGAAG ACCA |||| ||| |||| |||| ||

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     CACCATC                          CTAC  CGA   TTCA      CCCA  GC  /
                                   CA  AG-   TACAA----   CT  ATT


GAM3039  ACAGGAAACATTAGAGTGAT 69324   TGTTATCGGA 69325      AACA-   AG   TAAA   TA
     TAAAACCATAAGCCTGGTGT      TTAAAAACCT      ACAGGA   TTAG  TGAT   ACCA  A
     TATCGGATTAAAAACCTCTT      CTTG          ||||||   |||| ||||   ||||
     GT                           TGTTCT   AATT  GCTA   TGGT  G
                                   CCAAA   AG   TTG-   CC


GAM3040  TAGTTACTTTATTACGATGA 69329   TACTTTATTA 69330      C    ACG   ATC     CG TT
     ATCTTTATTAACGATTCTTT      CGATGAATCT      TAGTTA TTTATT   ATGA   TTTATTAA  A  C
     TATTAATGAATTATCATAAG      TTAT          |||||| ||||||  ||||  |||||||| |
     ATAAATAATTA                   ATTAAT AAATAG   TACT   AAGTAATT  T  /
                                -    AA-   ATT      AT TT


GAM3041  AGGGCCACGTCGAGTGTACT 69334   TCTGTGACTG 69335       C  GAGT--  CTC    CT   G--    A
     CTGTGACTGTCTGCTGCGGA      TCTGCTGCGG      AGGGCCA GTC    GTA   TGTGA  GTCT
CTGCGG C
     CACTGCGGAAAGGACCTTAC      ACAC          ||||||| |||    |||  |||||  ||||  ||||||
     ATTTGCTGTCAAGACTGGCT                TCTCGGT CAG    CGT   ACATT  CAGG   GGCGTC /
     CT                           -  AACTGT   TT-    C-   AAA    A


GAM3042  ACCACCACCACAACCCCCCG 69361   TCGCTGACCA 69362                        -------    -------    CG
     GAACACAGGCCCAAAATTTT      CGACGCGCGA      CCCCCGGAACACAGGCCCAAAATTTTCGCT
GACCAC     GACGCG  A
     CGCTGACCACGACGCGCGAA      AACG          ||||||||||||||||||||||||||||||     ||||||     ||||||
     ACGCGTCACTTCGTGTGGTC                GGGGGCCTTGTGTCCGGGTTTTAAAAGCGA     CTGGTG
  CTGCGC  /
     ACTTCGTAGCGAAAATTTTG                                  TGCTTCA    TGCTTCA    AA
     GGCCTGTGTTCCGGGGGGTT
     GTGGTGGTGGT
GAM3043  CTTGTAGAGCTATTCGCCAC 69366   CTTGGAAAGG 69367       AGCT   GCCA  TA   AGAAGA
     ATACCTAGAAGAATAAGACA      ATTTTGCTAT      CTTGTAG   ATTC   CA  CCT    A
     GGGCTTGGAAAGGATTTTGC      AAG           |||||||   ||||   ||  |||
     TATAAG                       GAATATC   TAGG   GT  GGG    T
                                GTTT   AAAG  TC   ACAGAA


GAM3044  CCTCGAGGACATTGTCCTAG 69388   AACCATTTCC 69389     -  GACA    CT   --   AAC   TTC   ------
--   C
     ATTTGCAACCATTTCCACAA      ACAACCGCAA      CCTC GAG   TTGTC  AGAT  TTGC   CAT   CACA
 ACCG A
     CCGCAACCGGTCGACCTTAT      CCGG          |||| |||   |||||  ||||  ||||   |||   ||||      ||||
     GTGTTATGAGCAATTATCTG                GGAG CTC   GACAG  TCTA  AACG   GTA   GTGT     TGGC
A
     ACAGCTCAGAGG                    A  ----   --   TT   A--   TT-   ATTCCAGC   C
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GAM3045  ACCACCACCACAACCCCCCG 69407   TCGCTGACCA 69408                    -------  -------  G
         GAACACAGGCCCAAAATTTT      CGACGCGCGA      CCCCCGGAACACAGGCCCAAAATTTTCGCT
GACCAC     GACGCGC A
         CGCTGACCACGACGCGCGAA      AGCG          ||||||||||||||||||||||||||||||  ||||||  |||||||
         GCGCGTCACTTCGTGTGGTC                GGGGGCCTTGTGTCCGGGTTTTAAAAGCGA     CTGGTG
   CTGCGCG /
         ACTTCGTAGCGAAAATTTTG                                TGCTTCA    TGCTTCA     A
         GGCCTGTGTTCCGGGGGGTT
         GTGGTGGTGGT
GAM3046  CCCCAGCCTCTGCGCGTTTG 69412   GATGGCCCGG 69413    G   G  G TGT  G  GG  GGGTAG
TG    -  -    CG
         TTCGATGGCCCGGGTAGCTT      GTAGCTTGTT      CCA CCTCT CGC TT  TC AT  CCC    CT  TTTCCC
ACC CCCTAT  G
         GTTTCCCACCCCCTATCGGA      TCCC          ||| ||||| ||| ||  || ||  |||    ||  |||||| ||| ||||||
         GGTGGGGAGGTGGGGAGGTG                GGT GGAGG GTG AG   GG TG  GGG    GG  GGAGGG
TGG GGGGTG  /
         GGGAGGTGGGGAGGTGGGGA                  -   G  G --- G  GA  GTGGAG  GT    G  A    GA
         GGTGGGGAGGTGGGG

GAM3047  CCTTATCCTTAGGGTTTAGT 69438   ATCCTTAGGG 69439    TA  TTA-----   TA----------------    A
         TTTGAAGCAGAGCGAGCGCA      TTTAGTTTTG      CCT  TCC      GGGTT            GTTTTG A
         GCGAGCGTAAACAACCCGAA      AAGC          |||  |||      |||||            ||||||
         TAAACGGACTAGG                   GGA  AGG      CCCAA            CGAGAC /
                                 TC   CAAATAAG    CAAATGCGAGCGACGCGAG    G


GAM3048  TGTTTCTCTTTCTTTCCCCC 69455   TCCGTTGGTT 69456      -  T  T    ATAAA--    T- --   ----    -
TTCC
         CCTCTCTCCGCAATAAACGC      GGGTGGTTGG      TTCCCC CCC CTC CCGCA     CGCCT  CC
CGGA   ACTGT GT   C
         CTTCCCGGAACTGTGTTTCC      GGTG          ||||||  ||| ||| |||||     |||||  ||  ||||   |||||  ||
         CCCCCTACAACAGTGTTGTC                AGGGGG GGG GGG GGCGT     GTGGG  GG  GCCT
TGACA CA   C
         CGTTGGTTGGGTGGTTGGGG                  C  T  -   GGGGTTG    TT  TT   GTTG    A  TCCC
         TGCGGGGGTGGGCGGGGGAA
         GCAAGAAAACG
GAM3049  GCTCTAATCTCTATCCTCCT 69460   TGGTGTGTGG 69461    CTAA    AT C  -  TC   TTTTT   -   -
CCAC---    ACTTC
         TCCCCTTTTTTCACTCCTCC      GTGAGTGATG      CT   TCTCT  C TC CT  CCC    TCA CTC CTC
CGGCA    C
         CACCGGCAACTTCCCCTACT      GCAG          ||   |||||  | || ||  |||    ||| ||| |||     |||||
         GCTGTTTTCCCGAGAGAGAT                GA   AGAGA  G AG GA  GGG    GGT GAG GAG     GTCGT
  /
         GGTGTGTGGGTGAGTGATGG                  CCG-   CG T  T  GT   TGTGT   A  A  CCCTTTT   CATCC
         CAGAGAGCCAGC

GAM3050  GGCCCTTCCCTGTTGATTTA 69507   TTTGCGGAAC 69508    CCTTCC    A  --------- GCA    C  A
         TGGCATCGCACACAACGGTG      ACATTTTATT      GGC    CTGTTG TTTA      TG  TCGCA ACA C
```

TTTGCGGAACACATTTTATT TAAA ||| |||||| |||| || ||||| |||
TAAAACGACAGCGCC CCG GACAGC AAAT AC GGCGT TGT G
C----- A TTATTTTAC AA- T G

GAM3051 GACATGTGAGCAATAAGGAA 69513 TAAGGAACGT 69514 GCAATAA T- CT TAGA
CGTGGGCTGCTAGATACAAC GGGCTGCTAG GACATGTGA GGAACG GGG GC T
GCCCCCTTCGTTCCTCACAT ATAC ||||||||| |||||| ||| ||
GTC CTGTACACT CCTTGC CCC CG A
------- TT C- CAAC

GAM3052 GTACACCGGAATTGCCAGGA 69531 CACCGGAATT 69532 A G TG AC-- C ---- TT
CGACCGGGTCCTTTCTTGGA GCCAGGACGA GTAC CC GAAT CCAGG GA CGGG TCC T
TAAACCCGCTCAATGCCTGG CCGG |||| || |||| ||||| || |||| |||
AGATTTGGGCGTGC CGTG GG TTTA GGTCC CT GCCC AGG C
C G GA GTAA C AAAT TT

GAM3053 GATACAATTTTAGATGCTAT 69540 TAGATGCTAT 69541 A T AT GA- AGA- AAGA
TAATGATAATTTAGATTTTA TAATGATAAT GAT CAATTTTAGA GCT TAAT TAATTT TTTTA A
AAGAATTAATAAAAGACGAA TTAG ||| |||||||||| ||| |||| |||||| |||||
ATTAGTAATTAAGTTTTTAA CTA GTTGAAATTT TGA ATTA ATTAAA AAAAT /
AGTTGAATC A T -- ATG GCAG AATT

GAM3054 TACTAATAAAGTATGTTCAA 69545 TAAAGTATGT 69546 A-- --- AT A
TGTTAATAAAAGTATTAACT TCAATGTTAA TACTA TAAAGTATGT TCA GTTAATA A
CTGACAAATGTATTTTAATA TAAA ||||| |||||||||| ||| |||||||
TAGTA ATGAT ATTTTATGTA AGT CAATTAT A
ATA AAC CT G

GAM3055 ACTGTATTTGATTTTTTTAG 69554 AGATTGCAGA 69555 GTA AGGA TTGC G T AAC
CA AATT
GAAATTTTGCGTTGCAATCA TGTGTTGGAG TTTGATTTTTTT AATT GTT CAA CATATC
TGCA CTGA A
TATCAACTGCACACTGAAAT CTGA |||||||||||| |||| ||| ||| |||||| |||| ||||
TAAAGATCAGATTGCAGATG AAACTAAGGAAG TTAG CGA GTT GTGTAG ACGT
GACT /
TGTTGGAGCTGATTAGGAAG AA- GA-- T--- G - --- TA AGAA
GAATCAAAAAAGT

GAM3056 TGTCTACAACAATTAGTTAA 69588 AACAATTAGT 69589 ACA A -- A TC
ATTGCTATGTTCTACTGCGA TAAATTGCTA TGTCT ACAATT GTTAAAT TGCT TGT T
GTAACATTTGATAAGTTGTA TGTT ||||| |||||| ||||||| |||| |||
AGAGACG GCAGA TGTTGA TAGTTTA ATGA GCG A
GAA A CA - TC

GAM3057 ACAAGGCAAGCCACAACCTT 69596 TGATGATAAT 69597 ACAACCTT GAACC---- CC-
AC--------- TG G
AGATGGAACCTCAGCCAGAC ATATAATTAA AGATG TCAG AGACTATTGA TAT
AC C
TATTGAACTATTGACGCTGT TGGT ||||| |||| |||||||||| ||| ||
TGATGATAATATATAATTAA TCTAC AGTT TCTGGTAATT GTA TG /
TGGTCTTATTTGAATATGAC TCTTCGT- AACAGTATA TAT AATATATAATA GT
T
AACATCTTGCTTCTTGTTCT
GCCTTGT
GAM3058 AGTGATGAAGATTAAGAAAA 69600 CATTTCTTAT 69601 T- T AA - - TA
ACCAGTCGGTATTTTCCAGA CTTCATCTTC AG GATGAAGAT AAGAAA CCA GTC GG T
CTTGGCATTTCTTATCTTCA T || |||||||| |||||| ||| ||| ||
TCTTCT TC CTACTTCTA TTCTTT GGT CAG CC T
TT - AC T A TT

GAM3059 ACGTGATACAGCCGTTAGAG 69678 GAGCAACCTG 69679 GATACA A- --- CTG C C---
A
CAACCTGTACTTGACTTGTC TACTTGACTT ACGT GCCGTT GAG CAAC TA TTGA
TTGTCAC G
ACAGCGTGACAATTTATCAA GTCA |||| |||||| ||| |||| || |||| |||||||
TAAACGTTGACCCTCGAAAC TGCA TGGCAA CTC GTTG AT AACT AACAGTG /
GGTACGT ------ AG CCA CAA - ATTT C

GAM3060 GTGTCCGGGCAATCAGCCAT 69692 AGCCATTGCG 69693 -- AATCA A GGTAT AA
TGCGGTATCCGGGCAATCTG GTATCCGGGC GTGT CCGGGC GCC TTGC CCGGGC T
CCCGGTCTTGGCAAGGCGCC AATC |||| |||||| ||| |||| ||||||
CGGGAGCAC CACG GGCCCG CGG AACG GGCCCG /
AG ----- - GTTCT TC

GAM3061 GGGCCCATGGTGGCGCGCGG 69705 TGATATGTTT 69706 --- -- CCAC C----- TCCC GT
TG T G
CCCCCACCGTCCCCATTTCC CAGTGACCCT GC GCG GCCC CGTCC CATT ACG T C
CATGGGCACC A
CACGGTTTGCTCATGGGCAC CGGA || ||| |||| ||||| |||| ||| | | ||||||||||
CGACGGTGCCCGTGGTGATA CG TGC CGGG GTAGG GTGA TGT A G
GTGCCCGTGG /
TGTTTCAGTGACCCTCGGAT TTT AG CCCA CTCCCA CTT- AT GT - C
GACCCGGGCGACGTTTTGCG
CACCATGGTCC
GAM3062 TAATAAATTTCTTTTCACGA 69710 ATAAGTGGAC 69711 AA TC- GA- ------- GA CGT
TGCATCTTATTGAATGACGT ATATAGATGC TAATA TTTCTTT AC TGCATCT TATT ATGA
T
TTTCTCATAAGTGGACATAT AGAA ||||| ||||||| || ||||||| |||| ||||
AGATGCAGAAGTAATGAAGA ATTAT AAAGAAG TG ACGTAGA GTGA TACT /
AAAGTATTA GA TAA AAG TATACAG A- CTT

GAM3063 ACTATCGTAATATATATTAT 69742 TCACTGAAAG 69743 G TATTATCA -- TT GCC AG- T

CACTGAAAGACTTTTAGGCC ACTTTTAGGC ACTATC TAATATA CTGAA AGACT TAG AAGA GAGATG A

AAGAAGGAGATGTAACATCT CAAG |||||| ||||||| ||||| ||||| ||| |||| ||||||

TAAGTCTTTTGTTAGTCTCT TGATAG ATTATAT GACTT TCTGA GTT TTCT TTCTAC /

TTCAGAAGACTTTATATTAA A TTCAGAA- TC TT --- GAA A

GATAGT

GAM3064 GAGAATACTAAAATTCCTAA 69782 AGCTAGTTCT 69783 TT ACGATG CA- -- TC C CA- A- TT

CGATGATATGTTTTCAGCTA TCATAACGTC AA CCTA ATATGTTTT GC TAGT TTCATAA GTC GA TG C

GTTCTTCATAACGTCCAGAA CAGA || |||| ||||||||| || |||| ||||||| ||| || ||

TGTTCACCAGCTCCATGACT TT GGAT TGTATAGGA CG ATCA AAGTATT CAG CT AC /

TATGAATACTAATGCCTTAG T- AA---- TTC TA T- - TAC CG CA

GATATGTAATAGGTTTCTAA

TATTTACAAT

GAM3065 CGGGCCAAAGGATGGGGTGG 69796 TGATACGGTG 69797 GG G AAAA AAAGGG AG CAA - AT

GGTGAGGGTAAAAGCACAAA CCAGCCCTGG GG TGGGGT AGGGT GCAC AGTACC ACCGAAAA GGA CGG C

GGGAGTACCAGACCGAAAAC CCCC || |||||| ||||| |||| |||||| |||||||| ||| |||

AAGGACGGATCGGCCCGCTC CC GCCCCG TCCCG CGTG TCGTGG TGGCTTTT CCT GCC G

CGTTTTTCGGTGGGGTGCTG AA G AC-- GCATAG GG TG- C CG

ATACGGTGCCAGCCCTGGCC

CCGAACCCCCG

GAM3066 GTCCTCCACCTCCGCCACCG 69830 CCGCCGAGCC 69831 CC---- -- C CA- TTATC

CGATTTATCATCATCGTCGC GTTCCTCAGG GTCCT AC CTC GC CCGCGAT A

GGGCCGCCGAGCCGTTCCTC GAC ||||| || ||| || |||||||

AGGGAC CAGGG TG GAG CG GGCGCTG /

ACTCCT CC C CCG CTACT

GAM3067 GCCATCACCGTCGCCGATCG 69902 TTCACGTACG 69903 - T C TC - T - C-- C

ACCAGGACCGCCGCGCGGTC TTCTGGCCCG GC CA CA CG GCC GA CG AC AGGACCGC G

TTCACGTACGTTCTGGCCCG CTGC || || || || ||| || || || ||||||||

CTGCTGCGC CG GT GT GC CGG CT GC TG TTCTGGCG /

C C C C- T T A CAC C

GAM3068 AACGGCTCTTGCGTATAATG 69908 TAATGCATGT 69909 - GC AA TTCC TA CGATC--- TC

CATGTTTCCGGTTATTTACT TTCCGGTTAT AACGG CTCTT GTAT TGCATGT GGT TTTACT CG T

CGATCCGTCTTACGTAGTAC TTAC ||||| ||||| |||| ||||||| ||| |||||| ||

ATGGTAAACACCCATACATG TTGTC GGGAA TATG ATGTACA CCA AAATGG GC /
TAAGTATAAAAGGGACTGTT A AA A- TAC- C- TACATGAT AT

GAM3069 TCCCCCTCTGGACTTGTAAC 69921 TGGTAAGTGA 69922 CCCTCT TGTAACT AGT TTG
AG- CT
TGGTAAGTGATAATCCTTGG TAATCCTTGG TCC GGACT GGTA GATAATCC GAAGCT
GTA C
AAGCTAGGTACTCGTTACGC AAGC ||| ||||| |||| |||||||| |||||| |||
AAGTTTTGGATTATCTTGTG AGG CTTGA CCGT CTATTAGG TTTTGA CAT /
CCCAACATTAGTTCTCGGA CT---- TTACAAC GTT --- ACG TG

GAM3070 GTCACGAGGGGAACGCAGTA 69940 TCTAAACCTT 69941 GA -- A T-- TCTAA TT AGTAA
AAAG CC G
CCTTTTCATCTAAACCTTTG TGCACGAGTA AC GCAGT CCTT TCA ACCT GCACG TT
AT GCTT A
CACGAGTAATTAAAGATCCG ATTA || ||||| |||| ||| |||| ||||| || || ||||
CTTGACGAGCCTATATGGAA TG TGTCA GGAA AGT TGGA CGTGC AA TA
CGAG /
GAGCGTGCCAGGTATTTGAC AA AT - TTC TTA-- C- GAG-- GGTA TC C
TTAAGGACTGTTAGTAACTG
AAGACCTGAC
GAM3071 GAACAATCGCCTTTGTGTAA 69949 TTGACATATC 69950 TCGC AA-- TT------ GA TTA
CAAATTAGC
ATGTTGCGGAGAATGTCATT CGTTGTTTCA ACAA CTTTGTGT ATG GCGGA ATGTCA
GG A
AGGCAAATTAGCAAACATAA CCAT |||| |||||||| ||| ||||| |||||| ||
AACCGGTTGACATATCCGTT TGTT GAAACACA TAC TGCCT TACAGT CC /
GTTTCACCATGTTGACACAA TTTT GTTG CACTTTGT A- TGG AAAATACAA
AGTTTTTTGTTC

GAM3072 GTGATTTTGGCAATAGTCCG 69963 ACGAGCTGGT 69964 AT ---- TC AATCCAT
TGTAATCCATAATCCAGTAA GCTTGCTAGA GTG TTTGGCAA TAG CGTGT A
CACGAGCTGGTGCTTGCTAG CAC ||| |||||||| ||| |||||
ACAC CAC AGATCGTT GTC GCACA A
-- CGTG GA ATGACCT

GAM3073 ATATGTGTTATTTTAGGATC 70002 TAGGATCATA 70003 ATTTTAG C C ACGGT
ATATTTACATATTTACGGTA TTTACATATT ATATGTGTT GAT ATATTTA ATATTT A
TATCAAAGATGTTAGATATA TACG ||||||||| ||| ||||||| ||||||
GTTAATAGGACACATAT TATACACAG TTG TATAGAT TGTAGA T
GATAA-- A - AACTA

GAM3074 TCTTTAAGAACCAAGTGTGA 70005 AAATATTTCA 70006 AG AA GA AG
GGTAGATAGAGCGGTTAAAT TATCGGTTAT TCTTTA AACC GTGTGAGGTA TAG C
ATTTCATATCGGTTATAAAG AAAG |||||| |||| |||||||||| |||
A AGAAAT TTGG TATACTTTAT ATT /

A- C- AA GG

GAM3075 TGGTAGTCTTGATAGCCTTT 70011 TACTAACTGC 70012 A CT CT ACA TTAAC
AACAAGCATTAACGCTGCTT TATTAACAAC TGGT GT TGATAGC TTA AGCA G
TGCTACTAACTGCTATTAAC CA |||| || ||||||| ||| ||||
AACCA ACCA CA ATTATCG AAT TCGT C
A -- TC CA- TTCGT

GAM3076 TTCCTGGGTAGCTGGAGATA 70033 TAGCATTGAG 70034 - A-- T T AT- - A CA
GCATTGAGCGTCTAGGCAGG CGTCTAGGCA TTC CTGGGT GC GGAGA AGC TGAGCGT CT
GG G
TCCAGAATGCTCATTAGCTT GGTC ||| |||||| || ||||| ||| ||||||| || ||
TTCCTGCCTCACTCAGAGAA AAG GACTCA CG CCTTT TCG ACTCGTA GA CC /
A CTC T - ATT A - TG

GAM3077 AATGGAATCTAATAATTTAC 70047 TAATTTACAT 70048 CTA AC CC TT GCTT
ATACCGTTTTTGAAGTGAGC ACCGTTTTTG AATGGAAT ATAATTT ATA GTT TGAAGTGA T
TTTCTAATTATTTCGTGATT AAGT |||||||| ||||||| ||| ||| ||||||||
ATAGAAATTATCATTCTGTT TTGTCTTA TATTAAA TAT TAG GCTTTATT /
C-- GA -- T- AATC

GAM3078 GTAGAAGTTGTATTTTTAGA 70051 AGTTGTATTT 70052 AG AGA TCGA GA
AGTCGAATCTGAGTCAAGAT TTAGAAGTCG GTAGA TTGTATTTTT AG ATCT G
CTATAGAAAATATAAACTTT AATC ||||| |||||||||| || ||||
AT TATTT AATATAAAAG TC TAGA T
CA ATA ---- AC

GAM3079 AGGAGAGCGAGCAGAGAGGG 70061 CCACGCCCCA 70062 GAG G AGAG C GG GT --
T
GCCGGTGCGGGAGTTTGGAA TGCACGTGCC AG AGC AGC AGGGG C TGCGGGA TTGG
AAC C
CTCCGCGGTCATTCATCTCC C || ||| ||| ||||| | ||||||| |||| |||
CGCCACGCCCCATGCACGTG CC GCA GTA CCCGC A GCCCTCT CTTA GGC C
CCC CGT C C--- - CC A- CT G

GAM3080 ACCATTAAAAATATTTTTAT 70189 TTAATAAATG 70190 TAAAAA TT- C T
CTGTTAGATTTAATTTAATA GCTCATGGAA ACCAT TAT TTAT TGTTAGAT T
AATGGCTCATGGAATGTGTG TGTG ||||| ||| |||| ||||||||
GT TGGTG GTA GGTA ATAATTTA /
TGTAAG CTC A A

GAM3081 CAGTGAGATATGGTCTAATT 70197 TAGCTGGCTG 70198 - C A TG - C C T- CCG-----
ACTT

GGAGACTATACGCTCCAGTT CATATATCTA AGTGA GATATGGT TA T G AGA TATA GC
CCAGTT CCGA A
CCGCCGAACTTATAATCTTG CTGA ||||| |||||||| || | | ||| |||| || |||||| ||||
GAAATTTTTAGCTGGCTGCA TTATT TTATACTA AT A C TCT ATAT CG GGTCGA
GGTT T
TATATCTACTGAATAATCAT A - A GT A - A TC TTTTTAAA CTAA
ATTATTATTG

GAM3082 GTGTGTGTGTGTGCGTCCGT 70213 TCCCCGGGGT 70214 TCCG TTC CG GGT - AG
AAA C TT GTCA
TCGTTCGTTCGTCGGGGTGA TTTTTTACCG GTGCG TTCG GTT TCGG GAG GG GAAGAA
CG GGG C C
GGGAGGAAGAAAAACGCGGG CTTT ||||| |||| ||| |||| ||| || |||||| || ||| |
TTCGTCACACAAGGTCCCCG CATGC AAGC CAA AGTT TTC CC TTTTTT GC CCC
G /
GGGTTTTTTTACCGCTTTAT TGTA --- AA AT- G AT GGG - TG AACA
TGAAAAACCGAAATGTCGTA
CACACATGTC
GAM3083 GCCTTCACGAGCACGGGCGA 70226 CACGAGCACG 70227 T A-- G A GA G- C
GCGAGCATATGGTGTCTATA GGCGAGCGAG GCCT CACG GCAC GGCG GC GCATATG TGT
T
CGAGCGTGTGTGGGCGTGTC CATA |||| |||| |||| |||| || ||||||| |||
GGTGTGTCCGTGTGGGT TGGG GTGC TGTG CTGT CG TGTGTGC GCA A
T CTG G G GG GA T

GAM3084 CCGACGGGCTGAACGTCCGG 70238 TGAAGAAACG 70239 A- G AA GG --- - G A
GCCTCTCGGTGACATCGGTG GGCGGGCGGG CCG CGG CTG CGTCCG CC TCT CG TG C
AAGAAACGGGCGGGCGGGCG CGGG ||| ||| ||| |||||| || ||| || ||
GGCTGACCGG GGC GTC GGC GCGGGC GG AGA GT GC A
CA G GG G- CAA A G T

GAM3085 TACCTGTACCGATAAGGCAC 70277 TACTTCCTTA 70278 ACC CACAC-- GAGCAAAC
ACCCTGAGCAAACAAACCAT TTCAGACAGG TACCTGT GATAAGG CCT A
AAAGGTATACTTCCTTATTC TA ||||||| ||||||| |||
AGACAGGTA ATGGACA TTATTCC GGA /
GAC TTCATAT AATACCAA

GAM3086 GAGTAGGCGGTACGCCCACC 70322 CTTGTGGCCT 70323 CG GC C ---- TCG
CGTATAAGAATCGTAATTTC CGAGTGGCGG GAGTAGG GTAC CCAC CG TATAAGAA T
TTGTGGCCTCGAGTGGCGGT TGCG ||||||| |||| |||| || ||||||||
GCGACTTGCTC CTCGTTC CGTG GGTG GC GTGTTCTT /
AG GC A TCCG TAA

GAM3087 GATCGGTGGTGTAACCGTGT 70329 TCGGTGGTGT 70330 C T---------- TGTA TTTTAG
AGGTATTTTTAGTTTTTATG AACCGTGTAG GAT GGTGG GTAACCG GGTAT T
TACCATTTCGGTTGCTTTAT GTAT ||| ||||| ||||||| |||||

TATATTTCCCACCCATC CTA CCACC CGTTGGC CCATG /
C CTTTATATTATTT TTTA TATTTT

GAM3088 TGATGTTATTGTACTAAGTC 70335 TAAGTCATCA 70336 ATT CTAA A- TC-- C-- ---
GTTTCA
ATCAAAATGTTCTTGACTAC AAATGTTCTT GATGTT GTA GTCATCAA ATGT TTGA TAC
TTACA A
TTACAGTTTCAATATCCATG GACT |||||| ||| |||||||| |||| |||| ||| |||||
TAATATGTATTCTCAAAATC CTACAG TAT TAGTAGTT TATA AACT ATG AATGT
/
ATATGCTTGATGATATCTAT GT- CTA- CG CTAA CTT TAT ACCTAT
TGGACATCA

GAM3089 TATGTTTTAGTGCTATAGTA 70344 TATTAATCAA 70345 TTTT - -------- ATATAA
TATAAGTCACTCAACTATTA CAGCCACTTC TATG AGTG CT ATAGT G
ATCAACAGCCACTTCTTCAT TTCA |||| |||| || |||||
A ATAC TCAC GA TATCA T
TTCT C CAACTAAT ACTCAC

GAM3090 CACGCGTGTGGTTGCTTGCA 70353 GCGCATGGTT 70354 TTGCTT - TC T GC - T ---
TG T CT
TGTTCTCTTTGTTCCTGCGG GTGCTTGTTC GCA TGT TCTT GTTCCT GGAACGCG CA
GGTT G C TGTT C
AACGCGCATGGTTGTGCTTG TCTT ||| ||| |||| |||||| |||||||| || |||| | | ||||
TTCTCTTTAACGCGTGCGGT CGT ACA AGAG CGAGGA TCTTGTGC GT TCAG C G
GCAA T
GACTTGCCGTGTTCTAAGGA TTC--- T GA - A- C - TGG GT C TT
GCGAGAAGACATTGCCTTTT
GCACAGTGTG
GAM3091 TTAGTGTTGGTATTATTAGT 70366 TACAGCAATG 70367 - TTAT - TCT CA TG
ATTCTTCTTGTCATCTTGTT CTATACCTAA TTAGTGTT GGTA TAGTATT CT TGT TCT T
CAGAAATATACAGCAATGCT TACT |||||||| |||| ||||||| || ||| |||
ATACCTAATACTAA AATCATAA CCAT ATCGTAA GA ATA AGA /
T ---- C CAT A- CT

GAM3092 TTTTTTACCCATAAATAATA 70376 TACAATAATT 70377 CATAAATAATAA
TTAATTTCTCGTAAAAG AA
AATACAATAATTAATTTCTC AATTTCTCGT TTTTTTACC ATACAATAA TAGAA T
GTAAAAGTAGAAAATATATT AAAA ||||||||| ||||||||| |||||
CTAATTTATTGTATGGTAAG AAGGAATGG TATGTTATT ATCTT A
GAA ---------- TA---------- AT

GAM3093 CTGTACTACTTTTATCATAA 70382 TTACTGGCAG 70383 ATAA-- CGTTTGA TT A
GTGGT- T
TTAATAATCGTTTGAATATT ATAGGGGTGG ATC TTAATAAT ATA ACTGGCAG TAGGG
ATAGCGAT C

ACTGGCAGATAGGGGTGGTA TATA ||| |||||||| ||| |||||||| ||||| ||||||||
TAGCGATTCCGTCGTTGTTA TAG AATTATTA TGT TGGCTGTC ATTCC
TGTTGCTG /
GTGACCTTAGCTGTCGGTTC ATTCTG ------- CT G AGTGAT C
TGTATTATTAAGTCTTAGAT
AAAAAGTGCCG
GAM3094 GTGACTGATCTATCGATTAG 70393 TGTCTGGATT 70394 - TC - GTGA T
GTGATGCTGTGATTCTGTCA TAGTTAC GTGACTGA TCTA GAT TAG TGCTGTGAT C
TAGCAGTGACTATGTCTGGA |||||||| |||| ||| ||| |||||||||
TTTAGTTAC CATTGATT AGGT CTG ATC ACGATACTG /
T -- T AGTG T

GAM3095 CCAGTGACGCTGCCACCGGG 70402 ACGCTGCCAC 70403 AC - CCGG C ACAACTT
ATCTACAACAACTTACTACA CGGGATCTAC CCAGTG GCTG CCA GAT TACA A
ATCTGTGTGTCTGGACAGCA AACA |||||| |||| ||| ||| ||||
ACATTGG GGTTAC CGAC GGT CTG GTGT C
AA A ---- T CTAACAT

GAM3096 GTTTCCCTGATTCGTGTATG 70420 TCTACAGTAT 70421 CTGAT GTA T - A-- CG--
TATT
TCTACAGTATTTTCCGTGCG TTTCCGTGCG GTTTCC TCGT TGTC ACA GT TTTTCCGTG
GTGGAGA C
GTGGAGATATTCAAATTTTT GTGG |||||| |||| |||| ||| || |||||||| |||||||
TATAATACATGGAAAGATCG TAGAGG AGCA GCAG TGT CG GAAAGGTAC
TATTTTT /
CTTGTGACGACGACAATGGA TAAC- --- - T CTA ATAA TAAA
GAT

GAM3097 GACTCAAGCATATATACACG 70428 AAGCATATAT 70429 CA - A CG GA AA
GCTCGGGGAGCAAGGTGTGA ACACGGCTCG GACT AG CAT TATACACGGCT GG GC G
CTGTGGTCGTGTGTGGTGTC GGGA |||| || ||| |||||||||| || ||
TCTGGTC CTGG TC GTG GTGTGTGCTGG TC TG /
TC T - TG AG TG

GAM3098 ACAGAAGAAGTTCTATATCT 70441 TCTAAAAAAA 70442 A AA-- A CT-- C CT
AAAAAAAAA A
AGGCACACTCTAAAAAAAAA AAAAAGCACA ACAG AG GTTCT TAT AGG ACA CTA
AAGC C
AAAGCACACGCTTGCTGGCA CGCT |||| || ||||| ||| ||| ||| ||| |||| |||
TGTCCCTCGTAATAAAGAAC TGTC TC CAAGA ATA TCC TGT GGT TTCG A
AAAACTACTGT A AAAA A ATGC C AC CG------- C

GAM3099 TGGGGATGCGTGAGTGGCCC 70489 TCTAACCAAT 70490 AG------- T T CGG GGGAG T
A AA CAT
TCTGTGGGCGGTGGGGGAGA CCCCAGGGGC GCGTG TGGCCC CTG GGG TGG AG
CTTAT GG GTG A

GTCTTATAGGAAGTGCATAT CAAG ||||| |||||| ||| ||| ||| || ||||| || |||
AACCACAACCCATGGGTCTA CGCAC ACCGGG GAC CCC ACC TC GGGTA CC
CAC T
ACCAATCCCCAGGGGCCAAG AGACAAAGA - - TA- AA--- T C AA CAA
AAACAGACACGCCCCA

GAM3100 TACATTAAGGCAGTGTTGAT 70520 AGGCAGTGTT 70521 A A AGTG T TTCA CC
TTTTTTTCATTGTACCCACT GATTTTTTTT TAC TTA GGC TTGATTT TT TTGTA C
TACGAATAACGAATCAAAAG CATT ||| ||| ||| ||||||| || |||||
CCATGAAGTA ATG AGT CCG AACTAAG AA AGCAT A
A A AA-- C TA-- TC

GAM3101 TTATCAGCGTCTTATAATGT 70536 TTTTAAAAGT 70537 TC TAATGT GT TTTT TTC
GATGTCTTTTTTTTTATTTT AGTCTGTTAA TTA AGCGTCTTA GAT CTTTT TATT T
CTTGTCGGTATTTTAAAAGT GATG ||| ||||||||| ||| ||||| ||||
AGTCTGTTAAGATGTTTTTA AAT TTGTAGAAT CTG GAAAA ATGG T
A TT TGT--- AT TTTT CTG

GAM3102 CGCCCGCGCCCGACTCGCAG 70543 GCGGAGCGCG 70544 C GC ACT A A A G TC
CTCACGAGATGGCTGCTCTC CACGGCAGCG CGCC GC CCG CGC GCTC CG GATG CTGC T
GGCAGCGTCGCGGAGCGCGC GCG |||| || ||| ||| |||| || |||| ||||
ACGGCAGCGGCG GCGG CG GGC GCG CGAG GC CTGC GACG /
- AC AC- - - G - GC

GAM3103 GCTCGCGGTGCAGCTGCCGC 70703 GTGCAGCTGC 70704 - ----- - CA ---- G
AGAGCCGCGAAAGCGTCGTG CGCAGAGCCG GCTCGCGGT GCA GCTGC CG GAGC CGC
A
CTCCACGCGCAGCTTCTCTG CGAA ||||||||| ||| ||||| || |||| |||
CGATCGCGGGC CGGGCGCTA CGT CGACG GC CTCG GCG A
G CTCTT C AC TGCT A

GAM3104 GTCGTGGTCGTCGTCGTGGC 70733 GGTTGAGGCT 70734 TG TG - ---- G T
CGTGGCCGTGTAGCGGGGCG GCTGCTGCGG GTCG GTCGTCGTCGTGGCCG GCCGT
GTAGCGG GGC CC G
CCTGCTGGGGTTGAGGCTGC CTGC |||| |||||||||||||||| ||||| ||||||| ||| ||
TGCTGCGGCTGCGGCCGCGG CGGC CAGCAGCGGCGCCGGC CGGCG CGTCGTC
TTG GG C
CGACGACTGCGGC GT GT T GGAG G T

GAM3105 TACCAATATTGGAATTATAA 70769 ATGCATCGGT 70770 AAT TATA- G ---- C - G
TATAGGTGTATTTGCGCACT AAATATAGCT TACC ATTGGAAT ATATAG TGTATTTGC GCA
TCG C A
CGCGACGGTTGATGCATCGG GTAT |||| |||||||| |||||| ||||||||| ||| ||| |
TAAATATAGCTGTATCTAAT ATGG TGATCTTG TATGTC ATATAAATG CGT AGT G C
GTTCTAGTCGGTA C-- TAATC G GCTA - T G

GAM3106 CTTTTTCAAGATCCTGGTTT 70774 TGATTGATAA 70775 AAGA T TT ---- AA ATA AA-
TC
GATTGATAAATGATATGCAA ATGATATGCA CTTTTTC TCC GGT GATT GATA TG TGCA
ATC T
AATCTCTGATGATCTCTGCA AAAT ||||||| ||| ||| |||| |||| || |||| |||
ATGCAAATGTCTCACAGTCT GAAAAAG AGG CCA CTGA CTGT AC ACGT TAG G
ACCGGAGAAAAAG ---- - T- CACT AA GTA CTC TA

GAM3107 GGGGTAGTGTCGGAGAGGCC 70789 TGACTTGGTG 70790 T -- CC--- C TAAG
GCCCC TC
CGCCGCGCATTTAAGGAGTC CGCCGCCGTC GGGGTAG GTCGGAGA GGC GC GCGCATT
GAGTCGCC GAC T
GCCGCCCCGACTCTGTGTCT AGCT ||||||| |||||||| ||| || ||||||| |||||||| |||
TCGGGTGACTTGGTGCGCCG CCCCGTC TAGCCTCT TCG CG CGCGTGG
TTCAGTGG CTG /
CCGTCAGCTAGTCTCCGATC - GA ACTGC C ---- GCTT- TG
TGCCCC

GAM3108 TGCCAATATTGGAATTATAA 70796 ATGCATCTGT 70797 AAT TATA- G ---- C - G
TATAGGTGTATTTGCGCACT AAATATAGCT TGCC ATTGGAAT ATATAG TGTATTTGC GCA
TCG C A
CGCGACGGTTGATGCATCTG GTAT |||| |||||||| |||||| ||||||||| ||| ||| |
TAAATATAGCTGTATCTAAT ATGG TGATCTTG TATGTC ATATAAATG CGT AGT G C
GTTCTAGTCGGTA C-- TAATC G TCTA - T G

GAM3109 TGGAATTATAATATAGGTGT 70813 TAATATAGGT 70814 TAT- G --- - CTA AA
ATTTGAGCACTAGAAACGGT GTATTTGAGC TGGAAT AATATAG TGTATTT GA GCA GA C
CGATGCATCGGTAAATATAG ACTA |||||| ||||||| ||||||| || ||| ||
CTGTATTTAATGTTCTA ATCTTG TTATGTC ATATAAA CT CGT CT /
TAAT G TGG A AG- GG

GAM3110 TGGAATTATAATATAGGTAT 70818 ATGCATCGGT 70770 TATA- G ---- CTT G
ATTTGCGCACTTGCGACAGT AAATATAGCT TGGAAT ATATAG TATATTTGC GCA GC A
TGATGCATCGGTAAATATAG GTAT |||||| |||||| ||||||||| ||| ||
CTGTATCTAATGTTCTA ATCTTG TATGTC ATATAAATG CGT TG C
TAATC G GCTA AGT A

GAM3111 CTTTGCTCTAATTTCAGGAA 70819 TTCACAGTTG 70820 AATT G CT AAA- TATCGC -
AAAAGAA
CTGCTAACCAGGTAAAGTGC CTGACAACGG CT TCAG AACTG AACCAGGT GTGC
TTTCG GGTGA C
TATCGCTTTCGGGTGAAAAA TGCT || |||| ||||| |||||||| |||| ||||| |||||
GAACCATAGACATCGCTACG GG AGTC TTGAC TTGGTCCA CACG AGAGC
TCGCT C

AGAACTGCACCACCACCTGG CAAC G AC CCAC TCA--- A ACAGATA
TTCACAGTTGCTGACAACGG
TGCTGAAAG
GAM3112 TTTTTATTCTTGTTATTTAG 70830 TATACAGTTA 70831 A TGT -- A CA G
CTGAGTCATCGGTACCGAAT AGAGTATCTA TTTTT TTCT TAT TTAGCTG GT TCG T
ATACAGTTAAGAGTATCTAG GAGG ||||| |||| ||| ||||||| || |||
AGGGAGAA AAGAG GAGA ATG AATTGAC TA AGC A
G TCT AG A TA C

GAM3113 CCTCTGGTACAGTTCTGACA 70843 TGAGGGCTGC 70844 ------- GACAA GA G
AAGAGGACTCTTGCAGAGAG GTGTTCTACT CCTCTGGTA CAGTTCT AGAG CTCTT C
GACTCTGAGGGCTGCGTGTT AGAG |||||||||| ||||||| |||| |||||
CTACTAGAGG GGAGATCAT GTCGGGA TCTC GAGAG /
CTTGTGC G---- AG A

GAM3114 TCCCAAGCTTTCGTTACCCT 70853 TGTAAATGTT 70854 G----- T AATGCAA G
TAGACTTGG T
CTAGGGGTAACAAATGCAAT TAGACTTGGA CCCTCTA GGG AACA TGACT TAAATGTT
AGTGTT A
GACTGTAAATGTTTAGACTT GTGT ||||||| ||| |||| ||||| |||||||| ||||||
GGAGTGTTTAAAACACTGAC GGGAGAT CTC TTGT ACTGG ATTTACAG
TCACAA /
ATTTAGGTCAACGATGTTCT GAAAGA - AGCA--- - --------- A
CAGAAAGTAGAGGGTGGCCA
AACCGGA
GAM3115 TGTAGATACCATATAATGAA 70861 TGTTAAGATA 70862 ---- GAA----- T - G G- TTT
TTAA A
TGTTTTATTAGGATAGTAGT GTAGTTCTGT ATAAT TGTTTTA TAGGAT A TA TTAATAG
AG GAC G
TAATAGTTTAGTTAAGACAG TAAG ||||| ||||||| |||||| | || ||||||| || |||
TAGTTCTTTCTGTTAAGATA TATTG ATAGAAT GTCTTG T AT AATTGTC TC TTG
T
GTAGTTCTGTTAAGATAGTA ATAG ATTTGATG T A G AG TT- ---- A
GTTTAGTTATGATAGTGGTT
TAGTTAAGACA
GAM3116 ATCTGCTCTGTTTTGTACAA 70868 TATGACACAC 70869 T A AAAAGT G T GATT A
TG T AGT
AAAGTGGAAGTGTGTGTTTA AGTTCTGGAA TT GT CA GGAA TGTGTGTT ATAT CACAAA C
TAGTT AAC A
TATGATTCACAAAACTGTAG ACTG || || || |||| |||||||| |||| ||||||| | ||||| |||
TTTAACAGTAAAAGTTAATT AA CA GT TCTT ACACACAG TATG GTGTTT G GTTAA
TTG /
GTGGTTTGTGGTATGACACA C - CAAAGG G - ---- - GT - AAA
CAGTTCTGGAAACTGACCAA
ACAGTGTTCTT
GAM3117 CATTTAGTACAACTTGGTCA 70894 TTCGTCCTAC 70895 TAGTACAA GG A GG GC - T-
AC- - A C
TGGGTGGCAGGAGATGGCAC AATCAGAGAA CATT CTT TC TG TG AGGA GA GGC
TGAGCGT CT GG A

TGAGCGTCTAGGCAGGCCCA GGGA |||| ||| || || || |||| || ||| ||||||| || ||
GAATGCTCATTAGCTTTTCG GTAG GGA AG AC AC TCCT CT TCG ACTCGTA GA CC G
TCCTACAATCAGAGAAGGGA TTTTAG-- AG - TA A- G TT ATT A C G
TTTTGATG

GAM3118 GCCATTGTACTTGATATATT 70904 TACTTGATAT 70905 AT A ATATTTC A ATT
TCGCTGATATCATTTCTCGG ATTTCGCTGA GCC TGT CTTGAT GCTGAT TC T
AATCGGCATCAAGAGCAGGC TATC ||| ||| |||||| |||||| ||
CGG ACG GAACTA CGGCTA GG /
-- A ------- A CTC

GAM3119 TAGTTCTTTTCTTTATGTTA 70911 TAGATTGTTA 70912 CT T TA CC CT TGTCAACTA
ATCCCAGTTTGGGCTAGTTC TACTAAAGAA TAGTT TTTCTTTA GT AT CAGTTTGGG AGTTCT C
TTGTCAACTACATAAACCAT ACAA ||||| |||||||| || || ||||||||| ||||||
GGAATTTTTTAGATTGTTAT ATCAA AAAGAAAT CA TA GTTAGATTT TTAAGG /
ACTAAAGAAACAAACTA AC - -- TT T- TACCAAATA

GAM3120 TGGCTGGAGATGGCACGGAG 70929 GATGGCACGG 70930 - ---- ACG- - A CA
CGTCTAGGCAGGTCCAGAAT AGCGTCTAGG TGGCTGGAG AT GGC GAGCGT CT GG G
GCTCATTAGCTTTATATCCT CAGG ||||||||| || ||| |||||| || ||
TCAGTCA ACTGACTTC TA TCG CTCGTA GA CC /
C TATT ATTA A - TG

GAM3121 GTAATTGAGTTTCCAAACTT 70950 TGTGGAAAAG 70951 GAG A TACA ATA
ACATTTGATACAGTACGAAA AAGTTGC GTAATT TTTCCA ACT TTTG C
ATGGTGTGGAAAAGAAGTTG |||||| |||||| ||| ||||
C CGTTGA AAAGGT TGG AAGC A
AGA G TAA- ATG

GAM3122 CAACAAACGTTGTGGAAATT 70960 TGTGGAAATT 70961 A T TT TTGT- CC---- C
CAAAATTGTTGTCCTAGGCC CAAAATTGTT CAAC AACGT GTGGAAA CAAAATTG CCTAGG TGC A
TGCCACGGCAATAAATCCTA GTCC |||| ||||| ||||||| |||||||| |||||| |||
GGCGTCTCAGTTTTGGTTTT GTTG TTGCA CGCTTTT GTTTTGAC GGATCC ACG C
TCGCTACGTTAGTTG A T TG TCTGC TAAATA G

GAM3123 CTATCTACCAGATTATTATG 70977 TAAGGTACTT 70978 TACC-- AT AT--- GG TTTT-- ATAAA
TGTTATAAGGTACTTTTTCT TTTCTCATAA CTATC AGATT TATGTGTT AA TACT CTCATA C
CATAATAAACTAGAGTATGA TAAA ||||| ||||| |||||||| || |||| ||||||
GTATGATAGTGTTTTTTCAA GGTAG TCTAA ATATACAA TT GTGA GAGTAT /

AACATATAAATCTAAAATTG TTAAAA -- AACTT TT TAGTAT GAGAT
ATGG

GAM3124 AATCTGATAACTTTAAACAT 70985 TAACTTTAAA 70986 AT-- ATGG T T
GGATTTTTGATGACATAGTG CATGGATTTT AATCTG AACTTTAAAC AT TT G
GTTTAAAGTTTAAACAGATT TGAT |||||| |||||||||| || ||
TTAGAC TTGAAATTTG TA AG A
AAAT GTGA C T

GAM3125 TCTCCAGACCCGGGTTTCAC 70990 GAAAGTGTGT 70991 -- GA G TT - GC GC C
CTG TT AAAG
CTTGCCCTCGCTCTCTCCGT GGTTGGGGGG CA CCC GGT CAC CTT CCTC TCTCTC
GTCTAT TAC AAG T
CTATCTGTACTTAAGAAAGT TGAC || ||| ||| ||| ||| |||| |||||| |||||| ||| |||
GATCCTTTTGTGTGTGGGCC GT GGG TTG GTG GAA GGGG AGAGAG CGGGTG
GTG TTC /
GAGAGAAGGGGAAAGTGTGT CA GG G GT T A- A- C T-- TT CTAG
GGTTGGGGGGTGACAGAGA

GAM3126 TGCCTGTGTCGTGTTCGTTG 71023 TCACTGAGTT 71024 TC TTAATT A TTC-- GTT
TTTTT TT A
TTAATTCGCCACCATTCACT TCCAAAAGAT GTTG CGCC CCA ACTGA TCCAAAAGATTG
CC GAA T
GAGTTTCCAAAAGATTGTTT TGTT |||| |||| ||| ||||| |||||||||||| || |||
TTCCTTGAAATTGTTCCGGT TAAC GCGG GGT TGATT GGGTTTTCTGGC GG
CTT T
CGGTCTTTTGGGTTAGTAAT C- C----- - TGTAA --- T---- C- G
GTTGGGGCGCCAATCATATG
GCACTTGTA
GAM3127 GGTTGACCTGTATTGTTATG 71045 TGAAGATGAT 71046 ACC-- A- TG GAACA C
AACAATTTGACACCTCAGAT GAAGACGATG GGTTG TGT T TTAT ATTTGA A
GAAGATGATGAAGACGATGA ACCA ||||| ||| | |||| ||||||
CCAACC CCAAC GCA A AGTA TAGACT C
CAGTA GA GT GAAG- C

GAM3128 TGGTCATGGATAGGAGATGC 71087 TAGGAGATGC 71088 CA ----- T CAAA T AT
ATCAAATGATCGCATAGGGC ATCAAATGAT TGGT TGGATAGG AGA GCAT TGA CGC A
GCTCACGAATGCTTCTAGCT CGCA |||| |||||||| ||| |||| ||| |||
TTTTATTCAGAATCA ACTA ACTTATTT TCT CGTA ACT GCG /
AG TTCGA T AGC- C GG

GAM3129 GTAAATTTAATAACTTTTGT 71095 ACTTTTGTAT 71096 A ACTT ---- - G----- TG TATT
AGA
ATCTATGGTGAATGTATGAA CTATGGTGAA TA TA TTGTATCTAT GGTG AAT TA AATAT
AATTT T
TATTATTAATTTAGATAAAA TGTA || || |||||||||| |||| ||| || ||||| |||||
AATTTTGTATTTGTAATAAA AT AT AGCGTGGATA CCAC TTG AT TTATG TTAAA
/

GGTTACACCGGTAATAGGTG G AC-- ATGG A GAAATA GT TT-- AAA
CGACATAGTAAGTATAC

GAM3130 GTACGTATACTATTGATTTA 71107 TATACTATTG 71108 C A C T T TTT CA
CTTGTATTTGTTTTCATATA ATTTACTTGT GTA GT TA TATTGATT ACT GTA GTTTT T
GAGCTTTTATAGTAATTAAT ATTT ||| || || |||||||| ||| ||| |||||
ATTACATTTAC CAT TA AT ATAATTAA TGA TAT CGAGA /
T C T - - TTT TA

GAM3131 GTGTTACTTGTGATTTTCAT 71115 CTTGTGATTT 71116 CTT CATACAACAT T TAATG--
TT TG AC
ACAACATACTGTTATTATAA TCATACAACA TTA GTGATTTT ACTG TATTA TGAA
TATAGT A C
TGTGAATTTATAGTTGAACC TACT ||| |||||||| |||| ||||| |||| |||||| |
TCATTGGCTGTGTTTTCAAA AAT CATTGAAA TGAT ATAAT ACTT GTGTCG T
T
AAGTCTAATATTAGTTCATA TT- TACT------ T CTGAAAA TT GT AC
AAGTTACTTTAATAT

GAM3132 TTGCATACGTTCATCATTGG 71122 TTTTGCTGGC 71123 ACGTTCAT- T TC T TGTTT A
ATCCCATGTTGTTTCCAGAG TCCATTGTAT TTGCAT CA TGGA CCA GT CC G
GGTTTTGCTGGCTCCATTGT ATTA |||||| || |||| ||| || ||
ATATTAAGATGCAA AACGTA GT ACCT GGT CG GG A
GAATTATAT T C- - TTTT- G

GAM3133 ACATCTCAATAAAAAAATGT 71130 AATGTAATAT 71131 - CAAT TATAAT TA---- T
AATATAATATTTATATCATT AATATTTATA ACAT CT AAAAAAATGTAA ATTTA TCAT T
TTGTGACATTATTGAATTAT TCAT |||| || |||||||||||| ||||| ||||
CATTTATATTTTTTTTAGCA TGTA GA TTTTTTTATATT TAAGT AGTG /
TGT C T--- TACTAT TATTAC T

GAM3134 ATGTTTTTTTTAATTTTTCT 71137 TTAATGAATA 71138 TTT TTCTAT ACAT TTGA C
ATTTCATACATATAAATTGA AATAAATTAA ATGTTT TTAATTT TTCAT ATAAA TCGAT T
TCGATCTTTATTGACTTTAT TTCA |||||| ||||||| ||||| ||||| |||||
TAATGAATAAATAAATTAAT TATAAA AATTAAA AAGTA TATTT AGTTA T
TCAAATAT CTT TAAAT- AT-- C--- T

GAM3135 CCGTCCCCCGCCCCGCCGCC 71142 TACCGAGGAG 71143 - - CCCC - CC - TCGCC C -
CT -- T
CTCCCCGTCGCCGCCTCCCC GCCGGGGACG C CC CCG GC CG CT CCCCG GC TCCCCG
CC CTC TACCTG C
GCCCTCTCTACCTGTCCGCG CCCC | || ||| || || || ||||| || |||||| || ||| ||||||
GGTACCGAGGAGGCCGGGGA G GG GGC CG GC GA GGGGC CG AGGGGC GG
GAG ATGGGC C
CGCCCCCGGGGAAGACCGAG A A AGC- A CA A CCC-- C C AG CC G
CCGACGGAGGAGACGG

GAM3136 GCCACAGGGTGTCGCTCACG 71188 TCACGTAGTC 71189 A-- - T C T T CA A A T
TAGTCGCCGCGCGCCAGCAG GCCGCGCGCC GCC CAGG GTG CGCT ACG AG
CGCCGCGCGC GC GC GCG T
CAGCGTTCCGCGGCGCGCGC AGCA ||| |||| ||| |||| ||| || |||||||||| || || |||
GTGGCGCCTCGTCGGCGCGC CGG GTCC CGC GCGG TGC TC GCGGTGCGCG CG CG
CGC /
GCCTGCACGGC CAC G - C - C -- - G C

GAM3137 GATACATGGCAATGGACAAG 71198 CATGGCAATG 71199 ACAT A A - A---------- AG
CATCAGAGTACCTGCGGAAA GACAAGCATC GAT GGCA TGG CAAGC ATC G T
TACTGCAAAGATGGCTTGCT AGAG ||| |||| ||| ||||| ||| |
ATGCTTAGGTC CTG TCGT ATC GTTCG TAG C /
GAT- - - G AAACGTCATAAAGGCGT CA

GAM3138 CAGGAGCGCGCCACCCTTTC 71216 TTCATGATTG 71217 - CGC -- TT C-- GTA
GTCGAACGTACAACGGTTCT GGCATGGTTC CAG GAG GCCA CCC TCGT GAAC C
TCATGATTGGGCATGGTTCA ACTC ||| ||| |||| ||| |||| ||||
CTCACTG GTC CTC TGGT GGG AGTA CTTG A
A ACT AC TT CTT GCA

GAM3139 GAGGCACTGGCTCGGTTGGG 71230 CATTCGGCAT 71231 T CTCG- A ---- CGG
TAGCCAGCCTTTCGGGTAAT CTACCCGTGC GAGGCAC GG GTTGGGT GCCA GCCTTT G
AAAGGCTTGTTGGCATTCGG CTC ||||||| || ||||||| |||| ||||||
CATCTACCCGTGCCTC CTCCGTG CC CGGCTTA CGGT CGGAAA T
C ATCTA - TGTT TAA

GAM3140 ATGAAGTTAATGATACACAC 71237 TTAATGATAC 31651 T ATA C AC GAATT
TACACTGTCGAATTTGATAG ACACTACACT ATGAAGT AATG CA ACTAC TGTC T
GGACAAAGTAGTTGACACGT GTCG ||||||| |||| || ||||| ||||
TTATTTCAT TACTTTA TTGC GT TGATG ACAG G
T ACA - AA GGATA

GAM3141 TCGAACTAAACGAAATATTT 71238 GGACAAGCGT 71239 AAAC- ------- T A
GTCTTTCTATGAAATCATAG TGATTATTTC TCGAACT GAAATA TTTGTCTT CTATG A
AGGACAAGCGTTGATTATTT CATT ||||||| |||||| |||||||| |||||
CCATTCAGTTTGG GGTTTGA CTTTAT GAACAGGA GATAC A
CTTAC TAGTTGC - T

GAM3142 GGGTTAACGCCTGATGGTGC 71249 TACCTTATAG 71250 A CTGAT - TAAT A T
TAATGCACTGCCGCTTCGGC CGTAATCC GGGTTA CGC GGT GC GC CTGCCGC T
GGCGGGTCGCTACCTTATAG |||||| ||| ||| || || |||||||
CGTAATCC CCTAAT GCG CCA CG TG GGCGGCG C
- ATATT T C--- - G

GAM3143 GCCGAATATTTTGTTTCGAA 71263 TATTTTGTTT 71264 ATATTTTGTTT --
AAACGCCTACACCAA A
CGGAGCAGAAACGCCTACAC CGAACGGAGC GCCGA CGAAC GGAGCAG GAG
C
CAAGAGACCACTCCTGTTCC AGAA ||||| ||||| ||||||| |||
CCGTTCGTCGGC CGGCT GCTTG CCTTGTC CTC C
---------- CC ---------- A

GAM3144 ATAGAGGGGTGTTTTTTAAA 71286 TACTATACGC 71287 G TT- A T - ATG
GTTACTGTATGCGTCACATG GAATACCCTC ATAGAGGG TGTTT TA AGT AC TGT C
TACTATACGCGAATACCCTC TAT |||||||| ||||| || ||| || |||
TAT TATCTCCC ATAAG AT TCA TG ACA /
- CGC A - T CTG

GAM3145 TTGGGAGGCAAAAAGAAAGA 71292 AGGCAAAAAG 71293 A AAAAGAAAGAAAACACCCA
A CGA
AAACACCCAGACGTAGGCCC AAAGAAAACA TTGGG GGCA GACGT GGCC G
GAGGACCGGCCGGCGTCCTC CCCA ||||| |||| ||||| ||||
TGTCCCCGA AGCCC CTGT CTGCG CCGG G
- CTC---------- G CCA

GAM3146 TAGGTGTAGAATGGTCATAT 71425 TGTAGAATGG 71426 - AGAA CATAT C ATG
GGCCAGTTTGATGATTTATA TCATATGGCC TAG GTGT TGGT GGC AGTTTG A
AACTGCTTTTTTACTAACAC AGTT ||| |||| |||| ||| ||||||
ACTA ATC CACA ATCA TCG TCAAAT T
A ---- TTTTT - ATT

GAM3147 TGTTGTACATGTGCAGAAAA 71432 CATGTGCAGA 71433 - -------- T - TATTTATCC
CG TGT
ATGTGTAAATACGTGTTATT AAAATGTGTA TGTGCAGAA AAA GTGTAAATA CGTGT
CATG TCT A
TATCCCATGCGTCTTGTACA AATA ||||||||| ||| ||||||||| ||||| |||| |||
TAGATATATGTTTTTATATA ATACGTTTT TTT CATATTTAT GCATA GTAT AGA /
CGCTATTTATACTTTATATA A CCTATATA - C TATTTTT-- AT TAC
TCCTTTTGCATAACCATAGA
CA
GAM3148 TCTTGTTTGTTCCCTGGAGT 71489 TCCCTGGAGT 71490 TT C -------- T- GA- GGT
ATGAGACTAGGGGGTGTTAA ATGAGACTAG TCTTG TGTT CC TGGAG ATGA CTAGGG
G
TCTTGGGAATTATTTTTCTA GGGG ||||| |||| || ||||| |||| ||||||
ACCTTGTTGGTAGCATTCAA AGAAC ACGA GG ATCTT TATT GGTTCT T
GA TT T TTGTTCCA TT AAG AAT

GAM3149 GGGGGTGCTAACACATTAAA 71507 TATAAAGCAT 71508 GG CACA- A GCAACA- A
ATGTTTTCGCAACAGGGCAA TTAGCACATC GG GTGCTAA TTA AATGTTTTC GGGC A
AGCTTAGATATAGAGGACAT T || ||||||| ||| ||||||||| ||||
TATAAAGCATTTAGCACATC TC CACGATT AAT TTACAGGAG TTCG /
T TA TACGA A ATATAGA A

GAM3150 AAGAGAGTTGTTTTTAAAAA 71539 CACTGGGTCA 71540 AAAACTATG- T ----- GAG
CTATGAAATTACCACCAGGA TTTAGATGAA AAGAGAGTTGTTTTTA AAAT ACC ACCAG
T
GTTGATTGGTCACTGGGTCA TTGT |||||||||||||||| |||| ||| |||||
TTTAGATGAATTGTGAAAAC TTTTTTCGACAAAAGT TTTA TGG TGGTT /
AGCTTTTTT GTTAAGTAGA C GTCAC AGT

GAM3151 TTCGTGGACTCGACCGTACA 71549 TCGACCGTAC 71550 T CTC C A --- AC-- ---- A
ATGC
CCTCGAGACGGTGGACGCAC ACCTCGAGAC TTCG GGA GA CGT CACC TCGAG GGTGG
ACGC CTC G
TCATGCGTTACGAGGGCGTA GGTG |||| ||| || ||| |||| ||||| ||||| |||| |||
CAACCACCCCCGTTCGACCC AAGC CCT TT GCA GTGG AGCTT CCACC TGCG
GAG /
GGTGAACGATTCTTCCCGAA - TC- A A CCC GCCC AACA G CATT

GAM3152 TAAACATCCCTATAGTGAAA 71552 TCCCTATAGT 71553 AT-- TA GAAA ATTAG A
CTGATTAGTACAAGAGTAAA GAAACTGATT TAAAC CCCTA GT CTG TAC A
CAGGAGCCCTGGGGTCTGGT AGTA ||||| ||||| || ||| |||
TTA ATTTG GGGGT CG GAC ATG G
GTCT CC AG-- AA--- A

GAM3153 TTTACAGTTCCATTCTCTCG 71566 AAGCGGTTCT 71567 AG CATTCT ACGCA T- C-
AAAAA ACAC
AACGCAATTATGAAATAAAC TTATTTCTTT TTTAC TTC CTCGA ATTA GAAATAAA AC
TAA T
ACAAAAATAAACACTATTCT AATA ||||| ||| ||||| |||| |||||||| || |||
TAAAGCGGTTCTTTATTTCT AAGTG AAG GAGCT TAAT CTTTATTT TG ATT /
TTAATAATCGAGCATGAAAG GA TAC--- AA--- TT CT GCGAA CTTA
GTGAA

GAM3154 AGTACCGCGGCTTCTATAAT 71576 CCGCGGCTTC 71577 C- GC- TAATCAG-- C
CAGAGATGCTCGTATCTATC TATAATCAGA AGTA CGCG TTCTA AGATG T
TTCGTTTAGAACGACGCGAT GATG |||| |||| ||||| |||||
TACT TCAT GCGC AAGAT TCTAT C
TA AGC TTGCTTCTA G

GAM3155 CTGTATTAAGTTAGTTTCTG 71586 TAAGTAATTA 71587 T TT TA AAT ATTT T G A-
A

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     AATAAGTAATTAATAGATAG       ATAGATAGAT        TAG  TCTGAA  AGTAATT   AGATAG    TAGTT AT
TAAAA  TGTTAAC T
     ATTTTAGTTTATGTAAAAAT       TTTA           ||| ||||||  |||||||  ||||||   ||||| || |||||  |||||||
     GTTAACATTTGTTAATAAGT                    ATT  AGATTT  TCATTGA   TTTATC    ATTAA TA ATTTT
ATAATTG T
     TTTAGATAATTACTATTTTA                  -  TT     TA      GAT     ----    - G    GA      T
     GAGTTACTATTTTAGATTTT
     ACCATTTTAG
GAM3156  AATGTAAGTGTCCTTTTATA 71590   TAGAATATAT 71591     ATTGC  -    -----------  -----     AAAATCTT-
-     A
     AGATTGCTCAGAGTGACTGA       CAAACTGTTA       AAG     TC AGAGT        GAC     TGACA
TTCTATA C
     CAAAAATCTTTTCTATAACT       AAAA           |||     || |||||         |||     |||||        |||||||
     TATAGAATATATCAAACTGT                    TTC     AG TCTCA         CTG     ATTGT        AAGATAT /
     TAAAAATGTCTCCCTATTGT                      ATTA-  T    ATGTTATCCCT   TAAAA    CAAACTATAT      T
     AACTCTTGAATTACTTATGG
     CTATTATATT
GAM3157  GACTTATCCATCTGAATGAT 71606   TGAATGATGC 71607     TTAT   TCT   T      TTTAT    AC--  GG
     GCGCGTTTATTGCACACGCG       GCGTTTATTG       GAC    CCA   GAA GATGCGCG    TGCAC    GC  C
     GCGAAGCTCAAGTGCATGTG       CACA           |||    |||  ||| ||||||||     |||||    ||
     CATTTTCTTTTGGTTTGTT                     TTG    GGT   CTT TTACGTGT    ACGTG    CG  G
                              TTT-   TTT   -       -----     AACT  AA


GAM3158  TACTCAAGTCCAGGCAAGTT 71619   TCCAGGCAAG 71620     CAA      CAA     T----------------  T
     GAATTCCCTTGAGGGACACT       TTGAATTCCC       TACT   GTCCAGG   GTTGAA             TCCC T
     CCCGTGGTTTGCGGTTTCAG       TTGA           ||||   |||||||   ||||||             ||||
     CCCTGGGCAGTGGTA                         ATGG   CGGGTCC   CGACTT             AGGG G
                              TGA      ---     TGGCGTTTGGTGCCCTCAC    A


GAM3159  TGAATCTAATTGTTTAAAGT 71640   TGACAAACAC 71641       ---   T    AAAG-    --    ATA
     GTTTTAGATATAGGCTAAAT       AGACATTTAT       TGAATC   TAA TGTTT    TGTT  TTAG   T
     GACAAACACAGACATTTATT        TTGA           ||||||   ||| |||||    ||||  ||||
     TGATTTA                     ATTTAG   ATT ACAGA    ACAG  AATC   /
                                TTT   T    CACAA    TA    GGA


GAM3160  CCTTGGCTGCTACACAGCAC 71660   CAGCACAATG 71661     GGCT-   ACA   C-      TAAA-   G
     AATGCTAAACAGGCTATTGA       CTAAACAGGC       CCTT    GCT   CAG  ACAATGC    CAG C
     AATTGTATTGTTTTTGGAGA       TATT           ||||    |||   |||  |||||||    |||
     GTTTACAGAGG                     GGAG    TGA   GTT  TGTTATG    GTT T
                              ACATT   GAG   TT     TTAAA   A


GAM3161  AGTATTTTCAAAAAAAAAAA 71679   GGGCACCCTG 71680   AAAAAAA              CCC
CCTACAAAACT  TA--   G  TT
     AAAAAATAAACAGGGCACCC       CGCACCCTGC            AAAAAAAATAAACAGGGCA   TGC        GC
TGCC TA  T
     TGCCCTACAAAACTGCTATG       CCTG             ||||||||||||||||||  |||        ||    |||| ||
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CCGTATTTATTAGGGCACCC TTTTTTTTATTTGTCCCGT ACG CG ACGG AT
/
TGCGCACCCTGCCCTGTTTA ------- CCC ---------- TCCC G TA
TTTTTTTTCTAAAATATT

GAM3162 GTACTTGGTCACTAGAGAAG 71750 GAGGTTAGTT 71751 TC A T TGTA T CAAC
TAGTGTATGTCTTCTCCAAC TCTCTTCCCT GTACTTGG ACTAG GAAG AG TG CTTCTC C
CTTAAGAGAGGTTAGTTTCT GGTT |||||||| ||||| |||| || || ||||||
CTTCCCTGGTTTAAGTAC CATGAATT TGGTC CTTC TC AT GGAGAG /
-- C - TTTG T AATT

GAM3163 ATTAAGTAGAGAATAGTGTA 71760 TAAGTAGAGA 71761 T TAGT---- --- --- T ACT
AGCCTGTAGTTACTGACAAG ATAGTGTAAG ATTAAG AGAGAA GTAA GC CTG AGTT G
ACTTCAGACAGCCCTTTACT CCTG |||||| |||||| |||| || ||| ||||
CATAATTTTTTCTCTTAAT TAATTC TCTTTT CATT CG GAC TCAG A
- TTAATACT TCC ACA T AAC

GAM3164 GTTTCTAATAATATAACCCT 71770 AAAAAGCTCT 71771 A A C- A A- AA- GTGT
TAGAAGAATTAAAAGTAAGG TCAAAGTCGT GTTTCTA TAATAT AC CTT GAAGA TT AAGTAAG
G
TGTGAGAAATTTACTTAAAA CATA ||||||| |||||| || ||| ||||| || |||||||
AGCTCTTCAAAGTCGTCATA TAAAGAT GTTATA TG GAA CTTCT AA TTCATTT A
TTGTAGAAAT - C CT A CG AAA AAAG

GAM3165 AGCAGCTGGCTTCACGCAAT 71807 TGCGTAGTAG 71808 - TC- TTTTTAGGTCA AA
TTTTAGGTCAAGGAAATTTC CATAGCTGTT AGCAGCTG GCT ACGCAA AGGA T
TCCTTTGCGTAGTAGCATAG |||||||| ||| |||||| ||||
CTGTT TTGTCGAT CGA TGCGTT TCCT T
A TGA ---------- CT

GAM3166 ACGAGCGGGGCCTGTTTATG 71827 TATGGGCCGG 71828 G CT T --------- TCC AT T
T
GGCCGGGCGTCCCGATGAGT GCGTCCCGAT ACGAGCGGG C GTT ATGGGC CGGGCG
CG GAG AC G
ACTGTTGTTTCCGCCGCCCG GAGT ||||||||| | ||| |||||| |||||| || ||| ||
AACCCCCCCCGCCCATCAACC TGCTTGTCC G CAA TACCCG GCCCGC GC CTT TG
T
GCCTGTTCGT - C- C CCCCCCCAA C-- -- - T

GAM3167 GGATTGATTGTTCATAAATA 71830 AAGCCGGTTA 71831 GAT- - ATATTTTTAT- -- GACC
T
TTTTTATACTCTGACCAAGA TTTACGTTGT GGATT TGTTC ATAA ACT CT AAGAAA T
AATTATTTTTTTATTAAGCC TATG ||||| ||||| |||| ||| || ||||||
GGTTATTTACGTTGTTATGG CCTGG GCAAG TATT TGG GA TTTTTT A
AACGCGAAGGTCC AAGC G GTTGCATTTAT CC ATTA T

GAM3168 ACTGTTTTTACCAGCGCTTC 71834 TAGGTTGTTT 71835 A- - - ------ - T
AAACTGTAGTTTTGACAAAT GGGGGGAGAGC ACTGTTTTT CCAG CG CT TCAAA C G
AGGTTGTTTGGGGGAGAGCG GGT |||||||||| |||| || || ||||| |
GT TGGCGAGAG GGTT GT GG AGTTT G T
GG T T ATAAAC T A

GAM3169 TATCTTGGCTGCTGGATCTA 71849 TGCTGGATCT 71850 CT C AAA-- T AACAC T
AATATTTTAGAACACTGTTT AAATATTTTA TAT TGG TGCTGGATCT TATT TAG TG T
ACAACACCTATGATAATAAG GAAC ||| ||| |||||||||| |||| ||| ||
AGATCTAGTAACTAGAGTA ATG ATC ATGATCTAGA ATAG ATC AC T
AG A GAATA T CACA- A

GAM3170 GTGGCTCTTTGCGTAAAATC 71866 TAGCAGAAGT 71867 - G TAAAAT-- C-- T
TTCTCACATGATTGTAGCAG GAAAATTTGG GTGGC TCTTT CG CTTCT ACA G
AAGTGAAAATTTGGGAAGAG GAAG ||||| ||||| || ||||| ||| |
GCCAC CACCG AGAAG GT GAAGA TGT A
G G TTAAAAGT CGA T

GAM3171 GCTCCACCAATACTCGCCGC 71930 CAGTACTCTT 71931 AC--- ACT- CA- T TTT C
ACAC CAT
AGTACTCTTTTTCCTCACAC TTTCCTCACA GCTCC CAAT CGCCG GTAC CT TC TC AGC
A
AGCCATATCTAGCTACCAGA CAGC ||||| |||| ||||| |||| || || || |||
CGATCCAGGTGCGTTCGGTG CGGGG GTTG GTGGC CGTG GA AG AG TCG T
CTTCGTTGTCCACGGGGC CACCT CTTC TTG - CCT C ACCA ATC

GAM3172 TGCCACACGTCGGTGATAAC 71966 CCACACGTCG 71967 CC A A A A CACTA
ATCCACTCACTACCCCACGG GTGATAACAT TG AC CGTCGGTG TAAC TCC CT C
AGGAAGTTACATTGACGGTA CCAC || || |||||||| |||| ||| ||
CCA AC TG GCAGTTAC ATTG AGG GG /
CA - - A A CACCC

GAM3173 CTTTATGTCCGCTCGCCCTC 71984 AGAATGGTTC 71985 T CGCT C---- GA--- G
CCAGAGCGAAAGTGAGAATG CTGGGGCGTT CTT ATGTC CGCCCT CCA GC A
GTTCCTGGGGCGTTTTGGCG TTGG ||| ||||| |||||| ||| ||
TTGAG GAG TGCGG GCGGGG GGT TG A
T TTTT TCCTT AAGAG A

GAM3174 GTGGTTTCTTGTGCGACGCT 71996 CACCGGGGTG 71997 T T T AC
TCCTGTGTAACTGCATACAC TCGCCAGGAA GTGGTTTCTTG GCGACGCT CC GTGTA T
CGGGGTGTCGCCAGGAAACC ACCG |||||||||| |||||||| || |||||
GC CGCCAAAGGAC CGCTGTGG GG CACAT G

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                                    -     - C    AC


GAM3175  GAAATTTTGTCCTTCCTTCC 72035  CTGCTGGAAG 72036       TG C  TC      C   G
         GGCCGCATGTTCATGCTGCT       CTGGCGTGGA       GAAATTT  T CT  CTTCCGGC GCAT T
         GGAAGCTGGCGTGGAATTTC       ATTT           ||||||| | ||  |||||||| ||||
                                                CTTTAAG  G GG  GAAGGTCG CGTA T
                                                   GT C  TC      T   C


GAM3176  ATGATGCTGGTTATTACACA 72052  TATATGGGAG 72053   TG  G      TACAC       ATA-         T
         TGTGTTTTAATATATATATA       TAAAGCATAT       A  AT CTGGTTAT    ATGTGTTTTA    TATATATATATA
A
         TATATATATATATATATATG       AACG           | || ||||||||    ||||||||||   ||||||||||||
         GGAGTAAAGCATATAACGTA                    T  TA GACCAATG    TATACGAAAT    GTATATATATAT T
         ACCAGAATTGT                        GT  A      CAA--        GAGG         A


GAM3177  ATATAAATATACATTCATTT 72056  TATACATTCA 72057       TA     C     TG-     --     T
         ATTGTAAATAATTATATATA       TTTATTGTAA       ATATAAA  TACATT ATTTAT   TAAATA  ATTATA A
         TATAATTTTGTTTGTTTGTA       ATAA           |||||||  |||||| ||||||   ||||||  ||||||
         AATAATGTGCTTTTATAT                      TATATTT  GTGTAA TAAATG   GTTTGT  TAATAT T
                                    TC     -     TTT     TT     A


GAM3178  GAGATGCAGTCCTTGCATCG 72069  AGTCCTTGCA 72070     A  A-  C-   AT     -      CGC
         GCGCGCCCGAGCCGCCCCCC       TCGGCGCGCC       GAG TGC  GTC  TTGC  CGGCGCG CCCGAGC
C
         GCTCGGGCCGCGCCGCGCAA       CGAG           ||| |||  |||  ||||  ||||||| |||||||
         ATGACGCGCGCTT                     TTC GCG  CAG  AACG  GCCGCGC GGGCTCG   C
                                 -  CG   TA   C-      C      CCC


GAM3179  CGGGTAGAAGAGGGATATTC 72084  AGAGGGATAT 72085        A     TATT      CA   CAA
         AGAGATCAGGGCAAGTCTCC       TCAGAGATCA       CGGGTAGA GAGGGA    CAGAGAT  GGG   G
         CGAGTCTCTGCTCTCTCCTC       GGGC           ||||||||  ||||||    |||||||  |||
         TACCTG                           GTCCATCT CTCTCT    GTCTCTG  CCC   /
                                          C     C---      AG   TCT


GAM3180  GTAAAAAGCGTTCAATAGTT 72105  AAGCGTTCAA 72106     AAAA       TAG   -      T  C
         GCCACGCTTTGACCGGTCAG       TAGTTGCCAC       GT    AGCGTTCAA   TTGC CACGCTT GA C
         GCGTGCGCAGTCTTGAATGC       GCTT           ||    |||||||||   |||| ||||||| ||
         TCTGGAC                          CA    TCGTAAGTT   GACG GTGCGGA CT G
                                    GGTC       CT-   C      -  G


GAM3181  TTGCAATTGTTATAACAGCA 72111  TTTGTTGTGT 72112        TGT    ACA     TATT    G
         TATATTGTATGTAAATATTT       GTGTGTATAT       TTGCAAT   TATA   GCATA    GTAT T
         GTTGTGTGTGTGTATATATT       ATTG           |||||||   ||||   |||||    ||||
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     GTAA                              AATGTTA  ATGT  TGTGT   TATA A
                                        TAT  GTG   TGTT  A


GAM3182  ACGCGCGCCAGAGTTGGATC 72120  TCAAGGAAAT 72121      C       ------- C-  C G  T-  AACA
     ACATCTCGTTGTTCTAACAC       GTAAGTCTGC       ACGCG GCCAGAGTTG      GAT  ACAT TC TTG
TCT  C
     GCTAAGGACTCAAGGAAATG       CAAT          ||||| ||||||||||      |||  |||| || |||  |||
     TAAGTCTGCCAATCGATTTT                  TGTGC CGGTTTTAGC      CTG  TGTA AG AAC  AGG   G
     GGCTCGTGT                            T       TAACCGT  AA   A  G  TC  AATC


GAM3183  GCAAAATACCAACCGCGCCC 72142  TGAGCCAAAT 72143     AA   AACC--- GCC   A  A
     GACACATAAAGGTGAGTTGT       GAGGTGAGTT       GCAA  TACC      GC  CGAC CAT A
     GAGCCAAATGAGGTGAGTTG       GT           ||||  ||||      ||  |||| |||
     T                              TGTT  GTGG      CG  GTTG GTG A
                                     GA   AGTAAAC  AGT   A  G


GAM3184  CTGAGGTTCAACCAGTTGAC 72188  AACCAGTTGA 72189         AA  AG  GA-    --   GAAGA  AG
     CTGTTTTGTGAAGAGGAGTT       CCTGTTTTGT       CTGAGGTTC  CC  TT  CCTGTT  TTGT    GG  T
     ACCGAACGAGCAGCAGGAGA       GAAG          |||||||||  ||  ||  ||||||  ||||    ||
     GAGAGGAGGAGCCTCAG                     GACTCCGAG  GG  AG   GGACGA  AGCA    CC  /
                                    GA  AG  AGA    CG    AG---  AT


GAM3185  GGGCTCTGGCCAACGGTGGA 72203  AACGGTGGAC 72204     TC   CCA     ACCTC   TTTTTC   TC
     CCTCGTCTTTTTCCGTTCCC       CTCGTCTTTT       GGGC  TGG   ACGGTGG    GTC     CGT  C
     CCACGTTCCCGACACCACCA       TCCG          ||||  |||   |||||||    |||     |||
     CCGTCCCCACCGTCC                      CCTG  ACC   TGCCACC    CAG     GCA  C
                                  CC   CC-      ACCA-   CCCTT-   CC


GAM3186  CGCTCGACGGCGCGGCGGTG 72217  TCAAATAGTC 72218     T  A--         ----------   -    C    G
     ACCCCGTCCGCGGGTCGCGC       GAGCCTCCGT       CGC CG   CGGCGCGGCGG          TGAC
CCCGT CGCG G
     GCGGGAGTCAAATAGTCGAG       CGCG          |||  ||   ||||||||||          |||| ||||| ||||
     CCTCCGTCGCGCCGCACCGG                    GCG GC   GCCGCGCTGCC          ACTG GGGCG GCGC /
     CG                             -  CAC         TCCGAGCTGATAA    A    C    T


GAM3187  CGCACCGGCGAGTCGGGACG 72222  AGGCGGCCGA 72223     AC    -     GA   GC  GT    CCT
     CGCCCGTCCGGCCTCTCGTC       CTCCGTCGAG       CGC  CGGCG AGTCGG  CGC  CC  CCGG   C
     CGGGAGGAGGCGGCCGACTC       GCG           |||  ||||| ||||||  |||  ||  ||||
     CGTCGAGGCG                              GCG  GCTGC TCAGCC  GCG  GG  GGCC   T
                                   GA    C     G-   GA  AG    TGC


GAM3188  TTCAATATGTTAGTGTAAAA 72263  TTAGTGTAAA 72264    A-     A     AA   A        A   AA    A     AC
ATT
```

TAAATGTATATGTATATAAT ATAAATGTAT A TATGTT GTGTA ATA ATGTATATGT TAT TATAT AATATG TGAA A

ATATAAATATGACTGAAATT ATGT | |||||| ||||| ||| |||||||||| ||| ||||| |||||| ||||

ATTATTCAATATGTTAGTGT T GTATAA TATAT TAT TGTATATGTA ATA ATGTG TTGTAT ACTT /

AAAATAAATGTATATGTATA CA A AA A A AA A A- ATT

TAATATATAAATATGACTGA

A

GAM3189 TGGGGCACTTGCAGATTTGT 72274 ACGCGGGGGC 72275 A GC GTAA--- A- A- GGGG

AAGGCCACGCACGGCGGGGA TGCTCTAAAA TGGGGC CTT AGATTT GGCC CGC CGGC A

GACAGGCCGACGCGGGGGCT ATTT |||||| ||| |||||| |||| ||| ||||

GCTCTAAAAATTTAAGGGCC ATCCCG GGA TTTAAA TCGG GCG GCCG G

CTA - A- AATCTCG GG CA GACA

GAM3190 GCTGCTCTAAAAATTTAAGG 72281 TTAAGGGCCC 72282 CTAAAAA AC---------- C

GCCCTACGGTCCACAGACCC TACGGTCCAC GCTGCT TTTAAGGGCCCT GGTC A

GCCTTCCCGGGGGGGCCCTT AGAC |||||| |||||||||||| ||||

GGAGCGACCGGCAGC CGACGG AGGTTCCCGGGG CCAG C

CCAGCG- GGGCCCTTCCGC A

GAM3191 GGAAGCGGAACCGATCGACC 72294 AAGCGGAACC 72295 G ACCG C CA----- C

GCCACCTGCTCCCAGGGACC GATCGACCGC GGAAGC GA ATCGA CGC CCTG T

CTTGCGCTCGATGTCGTCGG CACC |||||| || ||||| ||| ||||

CTTCC CCTTCG CT TAGCT GCG GGAC C

G GCTG C TTCCCAG C

GAM3192 ACCACCACAACCCCCCCAGA 72319 CATCGCAATA 72320 TACGTAG ACGAAGT T

ACCCAAGCCCAATCCTATTG GGATTGGGCT CCCAGAACCCAAGCCCAATCCTATTGCGA TGACCAC GACGCGC T

CGATACGTAGTGACCACACG TGGG |||||||||||||||||||||||||||| ||||||| |||||||

AAGTGACGCGCTTCGCGCGT GGGTCTTGGGTTCGGGTTAGGATAACGCT ACTGGTG CTGCGCG /

CGTGGTCATCGCAATAGGAT ------- ------- C

TGGGCTTGGGTTCTGGGGGG

GTTGTGGTGGT

GAM3193 AGTTCAAGTGGTATATGTTG 72324 TTCAAGTGGT 72325 TC-- T ---------- GA G

AGAAAGGTGATAGCCTTATC ATATGTTGAG AGT AAG GGTATATG TTGA AAGGT A

AAACAAACAGGATCATATGC AAAG ||| ||| |||||||| |||| |||||

CTCTTCATTACT TCA TTC CCGTATAC AACT TTCCG T

TTAC T TAGGACAAACA A- A

GAM3194 GTCGTGCGATTCAGAACACA 72339 GAACACACTT 72340 AT GAA---- - - CA T

CTTTTCTCAACCTTCTGGTA TTCTCAACCT GTCGTGCG TCA CA CA CTTTTCT ACC T

GAGAGGCTGCTGAAAATAAT TCTG |||||||| ||| || || ||||||| |||
GACGCGTACGAT TAGCATGC AGT GT GT GGAGAGA TGG C
GC AATAAAA C C -- T

GAM3195 GTCGTGAACGTTGCTGCTTA 72361 GAACGTTGCT 72362 - - CTGCTTATACC T
TACCGTGGGTAATCTCACTA GCTTATACCG GTCGT GA ACGTTG GTGGG A
CATCATCCAATGTATCGACG TGGG ||||| || |||||| |||||
AC CAGCA CT TGTAAC CACTC A
G A CTACTACAT-- T

GAM3196 GGAGCACGTGAACAGACCCA 72367 AGTGGCGTTT 72368 C ACAGACCCA G- T C-
ACA
GTGGCGTTTGCCGTGACAAG GCCGTGACAA GGAG ACGTGA GTGGC TTTGCCG GA AAG
C
ACACTGTCCTTCCTCCGGCG GACA |||| |||||| ||||| ||||||| || |||
AAAAGCCGCTCGCGTCTTC CTTC TGCGCT CGCCG AAGCGGC CT TTC T
- --------- AA - CC CTG

GAM3197 CGGCGTTCTCGATGCCCTAT 72371 GAGCACGTGA 72372 - A-- - CT G- CTC AAT- AG
G TCCA
CTTTCCTCGTGCGCGCTCGG ACAGACCCAG CC CT TCT TTC CGTGC CG GGA
GGCGGGC TTGC TGCT A
AAATGGCGGGCAGTTGCGTG TGGC || || ||| ||| ||||| || ||| ||||||| |||| ||||
CTTCCAACCTCCGGCGGCGA GG GA AGA AAG GCACG GC CCT TCGCCCG AGCG
GCGG C
AGCCCGCTTGCCTCCTCGGA T CCC C T- AG T-- CCGT A- - CCTC
GCACGTGAACAGACCCAGTG
GCGTTTGCCG
GAM3198 GCGTACAAAGTTGTTACACC 72399 TACAAAGTTG 72400 -- T TAC----- C
TTGCGGCTGCTGCAAGGTCA TTACACCTTG GCGT ACAAAG TGT ACCTTGCGG T
AGCTTCGCATCTTTGTAAAC CGGC |||| |||||| ||| |||||||||
GC CGCA TGTTTC ACG TGGAACGTC /
AA T CTTCGAAC G

GAM3199 GATATTTACTTTTTATATGC 72413 CACAGGTATT 72414 C TTAT ------- A
TTGCATTACAGAATGATATT ATTAAAATGA GATATTTA TTT ATGCTTG CATT C
CACAGGTATTATTAAAATGA GTAT |||||||| ||| ||||||| ||||
GTATC CTATGAGT AAA TATGGAC GTAA A
A TTAT ACTTATA G

GAM3200 TATAATCAATGATACGTGTA 72427 TCAATGATAC 72428 CAA - A T TCC
TTAGAATACTTTCCGAATAA GTGTATTAGA TATAAT TGATACG TGT TTAGAA ACTT G
GTCTTCTAAATATTGTATTA ATAC |||||| ||||||| ||| |||||| ||||
ATTATG GTATTA ATTATGT ATA AATCTT TGAA /
--- T - C TAA

GAM3201 ATTTAAGTATTAATTGTCCT 72441 TTAATTGTCC 72442 TCCTAAT- TGC CTT---------- A
AA
AATCGTGAATGCATATCTCT TAATCGTGAA TTAATTG CGTGAA ATATCT AAAA
AATATATA T
TAAAAAAATATATAAATCAT TGCA ||||||| |||||| |||||| |||| ||||||||
ATATATTATTTTCATAATCA AATTAAC GTATTT TATGGA TTTT TTATATAT /
TTTTCAGGTATAATTTTATG TTTTTAAT TAA CTTTTACTAATAC A AC
TAATTTTTCAATTAAACTAA
AT
GAM3202 GAAGAATAGCGTGTGGAGCG 72450 TAGCGTGTGG 72451 - GGAGCGA -- TT
ATCCTTGGTGTTAATTCACC AGCGATCCTT GAAGA ATAGCGTGT TCCTT GGTG A
TTGAGGAGCACGTTATATCT GGTG ||||| ||||||||| ||||| ||||
TT TTTCT TATTGCACG AGGAG CCAC A
A ------- TT TT

GAM3203 CGTGCTGCTGCAAAAGCGAA 72455 AAACGCAAAA 72456 GC AAA AA AGA G T-
GAAG- A--- GG
GGGTAGAGACGCTCTTGTGA GACTTGGGGG TGCT TGC AGCG GGGT GAC CTCT GT
GCGTT GATAG C
AGGCGTTAGATAGGGCAATT GTCG |||| ||| |||| |||| ||| |||| || ||||| |||||
ATTGAAAAACGCAAAAGACT GCGA ACG TTGC CTCG CTG GGGG CA CGCAA
TTATT /
TGGGGGGTCGGCTCAACGTT A- C-- AA G-- G TT GAAAA AAAG AA
CGCAAAGCGCG

GAM3204 TCAGAATGGATGTCTTGCTG 72490 TAGCAGACTA 72491 AATGGAT TG--- AGATA
CTATAATAGATAGAGAAGGT TAGATTAATT TCAG GTCT CTGCTATAAT G
TATAGCAGACTATAGATTAA AGTT |||| |||| ||||||||||
TTAGTTGA AGTT TAGA GACGATATTG /
GATTAAT TATCA GAAGA

GAM3205 CATGATATAGAAAAGAAATA 72494 ACTCCAAGAT 72495 A---------- TA
TTATTTCGTGATACGGATAC ACAGTTACTA
AGAAATATTATTTCGTGATACGGATACTCCAAGATAC GTTAC T
TCCAAGATACAGTTACTATT TTAG |||||||||||||||||||||||||||||||||||| |||||
AGTAACGATCTGTCAGATCT TCTTTATAATAAAGCACTATGCCTATGAGGTTCTATG
CAATG /
GTATCTTGGAGTATCCGTAT TCTAGACTGTCTAG AT
CACGAAATAATATTTCTTTT
CTATATCATG
GAM3206 AAACGCGGGCGTATTGGTCC 72500 GCGTATTGGT 72501 C A AT -- - G G G
CAATGGGGTCTCGGTGGGGT CCCAATGGGG AAACGCGGG GT TTGGTCCCA GG GGT CTC
GT GG T
ATCGACAGAGTGCCAGCCCT TCTC |||||||| || |||||||| || ||| ||| || ||
GGGACCGAACCCCGCGTTT TTTGCGCCC CA AGCCAGGGT CC CCG GAG CA CT /
- - C- GA T A G A

GAM3207 AAGGGTGGTGTTGGTTGGCG 72510 CTTCCGTTGA 72511 G TG -- G T
AGGGGGGGCTTCGGCCTTCC CCCAACTGAT AAG GTGGTGT GTTGG CGA GGGGGGC T
GTTGACCCAACTGATATCAC ATCA ||| ||||||| ||||| ||| |||||||
ACTT TTC CACTATA CAACC GTT CCTTCCG C
A GT CA G G

GAM3208 ATATAATAATATTTATTGAT 72522 TATATTATAA 72523 T GA T - - TAAA A
GATTGATATTATTAGAATAT TAAATGGATA TATTTAT GAT TTGATA TATTA GAATAT
ATTATAATAAATGGA ATTAT T
ATTATAATAAATGGATAAAA AAAT ||||||| ||| |||||| ||||| |||||| |||||||||||||| |||||
TTATATGGATAATAATTTTA GTAGATA TTA AATTAT ATAGT TTTATA TAATATTATTTATTT
TAATA G
TTTATTATAATAATATTTAT - AA T A A TAA- G
GATATTATTAAAAATTATAG
ATGTGTTATGT
GAM3209 ACGGGAAAGCACAATCATTG 72528 TGACACAGCA 72529 GAAA CAATCAT A- AAG
TTATCAGAAAGCAGAGTCAG AATGTAACCG ACGG GCA TGTTATC GA C
GATGACACAGCAAATGTAAC T |||| ||| ||||||| ||
CGT TGCC TGT ACAGTAG CT A
AA-- AAACGAC GA GAG

GAM3210 AAGCAGAGTCAGGATGACAC 72545 TAAACGCTAA 72546 GAG GA C GCAAAT- AACC
TT
AGCAAATGTAACCGCAAGTT ATCATGTATC AAGCA TCAG TGA ACA GT GCAAG C
CCGCTTGTAAACGCTAAATC AGCT ||||| |||| ||| ||| || |||||
ATGTATCAGCTGATGCTT TTCGT AGTC ACT TGT CG TGTTC /
--- G- A ACTAAAT CAAA GC

GAM3211 GTGTGTTGGCGGGATTTTGG 72553 TTTGGCACCT 72554 GGC GATTT-- C CT AAAG
C
CACCTCTCTTTCAAAGTGTG CTCTTTCAAA GTGTGTT GG TGGCA CTCT TTC TGTGGG
G
GGCGTCCCACGGAATTGGAG GTGT ||||||| || ||||| |||| ||| ||||||
TTGTCATCACACACCAAAGA CACATAG CC ACTGT GAGG AAG GCACCC /
TACAC AAA ACACACT T TT ---- T

GAM3212 GAAGTTCTACACACAGGCAC 72560 TGGTGTGTAT 72561 TC-- AG GGA TATAG T
GGATCTATAGTGTGAGTGGC ATCGCTTC GAAGT TACACAC GCAC TC TGTGAG G
TCACGTGACGAGTGTTGGTG ||||| ||||||| |||| || ||||||
TGTATATCGCTTC CTTCG ATGTGTG TGTG AG GCACTC /
CTAT GT AGC T---- G

GAM3213 CACACAAGAGGAGAGGCACC 72578 AGAGGCACCC 72579 A AGAGG AG---- AGA

CAGCCATGAGACGGGACGTG AGCCATGAGA CACACA GAGG CACCC CCATG C
GACGTGAGGGTGGGCCTTTG CGGG |||||| |||| ||||| |||||
TGTG GTGTGT TTCC GTGGG GGTGC G
- GG--- AGTGCA AGG

GAM3214 CGGCGGGTGTGGTGTGTCTT 72636 TCTATGATAT 72637 GGG -- - TC ATC TG - - AT
ATCTATGATATAGTGACGAT AGTGACGATG CGGC TG TGGT GTG TT TATGATATAG AC GA TGT G
GTATGTTGCAGTCTGTATCT TATG |||| || |||| ||| || |||||||||| || || |||
ATATTATGTAAAAACCACTA GCCG AC ACTA CAC AA GTATTATATC TG CT ACG /
TCAATCAATAGCCG ATA TA T CA AAT TA T G TT

GAM3215 CGGTGGGAAAAAAGGCATTA 72645 TCAGTCTGTG 72646 AAAAAA TATTATCT T T
TTATCTCTGTGGTACGTCTC CCGTCCCCGC CGGTGGG GGCAT CTG GG A
AGTCTGTGCCGTCCCCGCCG CG ||||||| ||||| ||| ||
GCCGCCC CCGTG GAC CT C
CTG--- TCT----- T G

GAM3216 TGAACGCGGACACCTTTGAG 72685 ACGCGGACAC 72686 C ACACCTTT- AATTTAGCA AA TT
GAATTTAGCATGGAAGAGTT CTTTGAGGAA TGAA GCGG GAGG TGG GAGT G
TGATATTCCCCCACCCCCAC TTTA |||| |||| |||| ||| ||||
CTCTCCCGAAACCCGTCTTC ACTT TGCC CTCC ACC CTTA /
A C CAAAGCCCT ACCCCC--- CC TA

GAM3217 ACGACGAGACCCCTATTAAA 72688 TATCAGGTGT 72689 G AG CC T---- GA TAA CAT
TAAAATGACTGTAAACGCAT TTTATTTTTT AC ACG AC CTAT AAATAAAAT CTG ACG A
ATAAACGTATCAGGTGTTTT CTAT || ||| || |||| ||||||||| ||| |||
ATTTTTTCTATAGTAGTGCG TG TGC TG GATA TTTATTTTG GAC TGC T
TGGT G G- AT TCTTT TG TA- AAA

GAM3218 TCTAGACGATATAGTGGAAC 72697 AGTGGAACAA 72698 AC ATA G ATA GA
AAAATATAGCGGATGAAAAA AATATAGCGG TCTAG GAT GTG AACAAAAT GCGGAT A
TTTGTAGATTTTGTTATACA ATGA ||||| ||| ||| |||||||| ||||||
CGGTCTACTAGA AGATC CTG CAT TTGTTTTA TGTTTA /
AT GCA A GA- AA

GAM3219 GGTCACCGTGCGAGATATTG 72725 AAGTATTACC 72726 ---- AC - TT -- - TAAGTG TT
TTCTGGAGTTAAGTGAGGTT AGTTGACCTG GG TC CGT GCGAGATA GTT CTGG AGT AGG C
CAACCTGAAGTATTACCAGT TTTT || || ||| |||||||| ||| |||| ||| ||| |||
TGACCTGTTTTGCGACGAGG CC AG GCA CGTTTTGT CAG GACC TTA TCC /
AATTACC ATTA GA G C- TT A TGAAG- AA

GAM3220 CCTGTGAGGTCAACCTTCGT 72729 TGATACTGGC 72730 A AA---- TTC T- C
ATTTTTGTCAACGCAACTGA ATTAGGACCC CCTGTG GGTC CC GTATT TTGT A
TACTGGCATTAGGACCCTAC TACA |||||| |||| || ||||| ||||
AGG GGACAT CCAG GG CATAG AACG A
C GATTAC T-- TC C

GAM3221 GTCCGGCTGGTGGTGGAGTG 72740 TGGTGGTGGA 72741 T--- G -------- A G
TACAGGACCTGACATTCACG GTGTACAGGA GTCCGGC GGT GTG GAGTGT CAG A
ACCTACACGACCTACTGCTG CCTG ||||||| ||| ||| |||||| |||
GGC CGGGTCG CCA CAC CTTACA GTC /
TCAT G ATCCAGCA - C

GAM3222 CCTTTCCGCGAATCTTGCGA 72762 CTAGGGCTAT 72763 - GC GA - GC- TT ATG
GATGCCTGCTGGTTTCTATG TGAGTAGGGT CCTTT CC GAATCTTGC GAT GCCT TGGT CT
G
GTGAAGGGGCCGCTAGGGCT TTGG ||||| || ||||||||| ||| |||| |||| ||
ATTGAGTAGGGTTTGGTAGA GGAGA GG TTTGGGATG TTA CGGG GCCG GA /
GG T -- AG T ATC GG AGT

GAM3223 CTCCGTATCGAGCGAATTGC 72777 TTGGAGCTGG 72778 TA--- A - -- A CT C - C
CTT
TCCGGATCCCTGAGACGCCA TAGGCGAGTT CTCCG TCG GCGAATT GCT CCGG TCC
GAGA GC CATT TC C
TTCTCCTTCGGTGAAAATGA CGCC ||||| ||| ||||||| ||| |||| ||| |||| || |||| ||
GCCTCTTTTGGAGCTGGTAG GGGGC GGC CGCTTGA CGG GGTC AGG TTCT CG
GTAA AG /
GCGAGTTCGCCCGGATTTTC TTTTA C G AT G TT C A A TGG
GGGG

GAM3224 GCGACTTTCAAACATCTCTA 72785 TACTTGGACC 72786 CTTTCAAAC A ACC- TAAA T
CTTGGACCTGTAAAACTTTT TGTAAAACTT GCGA ATCTCT CTTGG TG AC T
GTGTCCCACCTGTCGAGAAG TTGT |||| |||||| ||||| || ||
AGATTCGC CGCT TAGAGA GAGCT AC TG T
--------- A GTCC CCTG T

GAM3225 GGTATCCCGGATAATCTGAC 72795 TAGGGGGCGG 72796 ATAATC -- ATA-- G
GTA G GGG
GTTCCGGATATAGGGGGCGG GGGGTAGTGG GGTATCCCGG TGAC GTTCCGG
TAGGGGGCGG GG GT GG T
GGGGTAGTGGGGGGGTGTGTC GGGG |||||||||| |||| ||||||| |||||||||| || || ||
GACAAACTGCCGCTTCTTAA TCGTGGGGCT GCTG CGGGGCC ATTCTTCGCC TC
CA CT /
AACACCGGGGCCCGTCGCTC C----- CC ACAAA G AAA G GTG
GGGGTGCT

GAM3226 CCCGTGGTCCGATCTTCACT 72903 TCACTCGCCT 72904 T ATCTTCACTCAC - - GA
CACTCGCCTGTCTGCGGACC GTCTGCGGAC CCCG GGTCCG TCG CCTGTC TGCG C
TATGCACGGCGGGACGGCGC CTAT |||| |||||| ||| |||||| ||||
GCGGACCCGGG GGGC CCAGGC GGC GGGCGG ACGT C
- GCGC-------- A C AT

GAM3227 ACATTATACAGTCGTAGTAC 72911 AAGGTTCTTC 72912 GTACCGTTTATATA - ---
ATAAAAATAT T
CGTTTATATAATGTTAGGTA AACTTACCGT GTA ATGTTA GGTAG GAGGAGCCT
TTTGAT G
GGAGGAGCCTATAAAAATAT GACG ||| |||||| ||||| |||||||| ||||||
TTTGATTGGCGTTAAAAGGT CGT TGCAGT CCATT CTTCTTGGA AAATTG
G
TCTTCAACTTACCGTGACGT ACAATTATTTTTCC G CAA ---------- C
CCTTTTTATTAACATGCGTT
TTTATTGATGT
GAM3228 GACGCGAATAAATATTTGAC 72920 TAAAATACCT 72921 C AA G ---------- AC AT
GTGCTCCGACGTAAATTTTA ATTCCCGTT GACG GAATA TATTT ACGTG CTCCG GTAA
T
TTATTCTGGAGAAGTAATGC |||| ||||| ||||| ||||| ||||| ||||
ATATGTAAAATACCTATTCC TTGC CTTAT ATAAA TGTAT GAGGT TATT T
CGTT C CC A ACGTAATGAA CT AT

GAM3229 ACTTTTTTTTACCGTTTATA 72927 TAAATTATTA 72928 AT--- - - - - - T
AATTATTATTTTATAAAATA TTTTATAAAA CCGTTTATAAATTATTATTTT AAAATAA AGATG TTA
ATTTA CT TACC T
AAGATGTTAATTTACTTACC TAAA |||||||||||||||||||| ||||||| ||||| ||| ||||| || ||||
TTAGGTATAGATAAATATAA GGCAAATATTTAATAATAAAA TTTTATT TCTAC AAT
TAAAT GA ATGG /
TCATCTATTATTTTTATTAA ATTAT A T A A T A
AAATAATAATTTATAAACGG
TAAAAAAAAGT
GAM3230 TTGGTACAGATTTATAAACT 72931 TACTCTGACT 72932 AC T AA TTA C TT GA
TTTACACAGTATTCAAGGAA AAGTATAACT TTGGT AGA TTAT ACTT CA AGTA CAAG A
TGTTTGTTTACTCTGACTAA CTAC ||||| ||| |||| |||| || |||| ||||
GTATAACTCTACCAA AACCA TCT AATA TGAA GT TCAT GTTT /
-- C -- TCA C TT GT

GAM3231 CGATACTGCTGCCAATATAG 72941 TATCATCTTG 72942 A G T A CTC AGT
ACTCTGTTTAGTGCCAGAAC GAAGCAGATC CGAT CTGCT CCAA AT GA TGTTT G
ATATCATCTTGGAAGCAGAT G |||| ||||| |||| || || |||||
CG GCTA GACGA GGTT TA CT ACAAG /
- A C - AT- ACC

GAM3232 TGGTAAAAAAACAGGATTAA 72949 AACAGGATTA 72950 AAAAA T AACAAACAA CAAAT

AAAAACAAACAACGACAAAT AAAAAACAAA TGGTA ACAGGAT AAAAA CGA C
CTTATCATCGGCTGAAATTT CAAC ||||| ||||||| ||||| |||
TTATTCTGTATACTA ATCAT TGTCTTA TTTTT GCT T
A---- - AAAGTCG-- ACTAT

GAM3233 ATATTATCTTTATCTAACCG 73006 TTAACATAAA 73007 CT TAACCGAACAG---- - TT
AACAGATGTTGCTTTCTTAG TAGAAAAAAA ATATTAT TTATC ATGTTG CT C
TTAACATAAATAGAAAAAAA ACGA ||||||| ||||| |||||| ||
ACGATAACTATAATAT TATAATA AATAG TACAAT GA /
TC CAAAAAAAAGATAAA T TT

GAM3234 CTTTATCCCCATAGGATTCT 73009 TCAGAGTCCC 73010 - T - A T--- -- A
TTTAAATTTAAAATTTTAAA ATCGGGGCTA CT TTA CCCC AT GGATTCT TTAA ATTTAA A
TAATTAACGTCAGAGTCCCA ACAG || ||| |||| || ||||||| |||| ||||||
TCGGGGCTAACAG GA AAT GGGG TA CCTGAGA AATT TAAATT T
C C C C CTGC AA T

GAM3235 CGCACACGGGCAGGCAGAAG 73037 TCGCAAGCAG 73038 ACA A C A - AGT GC
GCGCAGTCGATCTCGCACTG CCCTTTCCCA CGC CGGGC GG AGA GGC GC CGATCTC A
GGGTCGCAAGCAGCCCTTTC GCCC ||| ||||| || ||| ||| || |||||||
CCAGCCCGCGGCG GCG GCCCG CC TTT CCG CG GCTGGGG /
GC- A C C A AAC TC

GAM3236 GCAGATGTTATCGCAGTTGC 73115 TACAACAGCC 73116 - --- C A CG ----- CCATT
GCACCTGCCATTGCACGACA GTAGATTCAT GCAG ATG TTAT GC GTTG C ACCTG G
GGTCTCCAGTACAACAGCCG ACTG |||| ||| |||| || |||| | |||||
TAGATTCATACTGC CGTC TAC GATG CG CAAC G TGGAC /
A TTA C A AT ACCTC AGCAC

GAM3237 TTGTTTGGCTTTGTTCCAAC 73131 CACGTGGTGC 73132 TG TTT T AC TTTT AGTT TTT
TGTTTTTGGCCCGAGTTGGG GTCAGGTGA T TTTGGC GT CCA TGT GGCCCG GGG C
TTTCGTTTTCCCGGGTTTCA | |||||| || ||| ||| |||||| |||
CGTGGTGCGTCAGGTGA A GGACTG CG GGT GCA TTGGGC CCT G
GT --- T -- CT-- ---- TTT

GAM3238 GTAAATTATGATATGGCACA 73209 TATGGCACAT 73210 TT - ACA C AGA C
TGCGTTAGATGCTGCCAGAA GCGTTAGATG GTAAA ATG ATATGGC TG GTT TG T
ACACACGGCTATATACATTT CTGC ||||| ||| ||||||| || ||| ||
TAT TATTT TAC TATATCG AC CAA AC G
-- A GC- A AG- C

GAM3239 CGGTGAAGACTGAGACGGTG 73227 GTGAAGACTG 73228 T - A--- -- AAGACTG -
AAGAC - T GAAG

AAGACTGAGACGGTGAAGAC AGACGGTGAA GAAGA CTG GACGG TG AG ACGGTG
TG AGA GGT C
TGAGATGGTGAAGCCCCAGC GACT ||||| ||| ||||| || || |||||| || ||| |||
CTTCTGCAACCGCCGTACTA CTTCT GGC CTGCC AC TC TGCCGC AC TCT CCG
/
ATGAAGCAGCCCGTCGCAAC - C AACG CG GAAGTAA A CA--- G T ACCC
GGCTCTTCCCG

GAM3240 CACCAAAGTCAACCGCGGGT 73263 TGAGACGGTG 73264 AA--- A-- CG-- AAA
TTTAAAAAATACATTAAGAC AAGACTGAGA CACC AGTC ACCG GGTTTTAA A
TGAGACGGTGAAGACTGAGA CGGT |||| |||| |||| ||||||||
CGGTG GTGG TCAG TGGC TCAGAATT T
CAGAG AAG AGAG ACA

GAM3241 TATCAAATACTGTACGGAAT 73271 AACTCTGTTG 73272 AATAC AAT A TCTCTT
GGATTCATTCTCTTCTCTTT TATATCTACT TATCA TGTACGG GG TTCAT C
TTATGAAACTCTGTTGTATA GATA ||||| ||||||| || |||||
TCTACTGATA ATAGT ATATGTT TC AAGTA T
CATCT GTC A TTTTTC

GAM3242 TTTAGAGAAGTTTAAAGATC 73283 AAAGATCCGC 73284 GA TAA CTAC -- CAACAA
CGCTACGACGAGCCAACAAT TACGACGAGC TTTAGA AGTT AGATCCG GACG AGC T
GGAAGAGCTAACGTCTGGAT CAAC |||||| |||| ||||||| |||| |||
CTAGTGATTGTTTAAA AAATTT TTAG TCTAGGT CTGC TCG /
G- TGA ---- AA AGAAGG

GAM3243 CTAGAGGATAATTTATCTCG 73302 TAATTTATCT 73303 G- AATT CTCG - TATAAT
A CG
TGATATAGTGATAATATAAT CGTGATATAG CTA AGGAT TAT TGATATAG TGATAA
AATAG GTG G
AATAGAGTGCGGTTTTACCT TGAT ||| ||||| ||| |||||||| |||||| ||||| |||
ATTTTATCATCTATATTAAT GAT TCCTA ATA ATTATATC ACTATT TTATC CAT T
AATATAATCCTAATAG AA AT-- ATA- T ------ - TT

GAM3244 TAGGAGTATCTATTTTAACA 73306 TATTTTAACA 73307 CT TT-- AGC TT C AT
AAGCATCGATTTGCTAATAT AAGCATCGAT TAGGAGTAT AT TAACAA ATCGA TG TAAT A
ACAATTATCATTTTGATTAA TTGC ||||||||| || |||||| ||||| || ||||
TTGTTATTTTATTCATATTC ATTCTTATA TA ATTGTT TAGTT AC ATTA /
TTA CT TTTT AAT TT T AC

GAM3245 GTAAAATATTTCCGGTAGGC 73315 TCTCTAAGTT 73316 CGG C TC TTTAATT-
TAGT ATA
GTGTATGTAGTGTTCTGTTA GATAAAC TAGG GTGTATGTAGTGT TGTTAT TGATATAT
ACAGCT T
TTTTAATTTGATATATTAGT |||| |||||||||||| |||||| |||||||| ||||||

ACAGCTATATAACAGTTGTG ATCT TATATACATCACA ACAATA ATTGTATG TGTTGA /
TATGTTACACGCCATATAAC GA- C -- TACCGCAC ---- CAA
AACACTACATATATCTCTAA
GTTGATAAAC
GAM3246 TGCACAGTGCTGATCAATTG 73321 TGTTGACAGT 73322 C C----- ATC- G TAACT G TTAAC T
ACTGGTATTAACTGTTGACA TTTAACTGTT TGCA AGTG TG AATTGACT GTAT GTT ACAGTT TGT C
GTTTTAACTGTTCATACAAA CATA |||| |||| || |||||||| |||| ||| |||||| |||
TTGTGACTATATATACAAGT ACGT TCAC AC TTGATTGA CATA CAG TGTTAA ACA A
TAGTTTCCCCAAAAAATCAC C TAAAAA CCCT A TATAT - ----- T
TCTGCA

GAM3247 ACAGTCCTTGTTATCAACAT 73337 TCCTTGTTAT 73338 CC A CAT ACA A T ATC
TGTCTTACAAGTGGATGATG CAACATTGTC ACAGT TTGTT TCAA TGTCTT AGTGG TGA GT T
TATCTAAAAACTCACCTATT TTAC ||||| ||||| |||| |||||| ||||| ||| ||
AAAGACATTGGAAACAGATA TGTCA GACAA GGTT ACAGAA TTATC ACT CA A
CTGT TA A --- A-- C - AAA

GAM3248 GGGGAGGGGGGTGGCGGCTG 73358 TCCAACCGAT 73359 AGGG G GC GGAAAG AA A CCGAAA AGAGAAAA
GGGAAAGGGAAGGAACGCCC AAATCAAGCG GGGG GG TGGCG TGG GG GG ACGC CC G
GAAACCAGAGAAAAGGACCA CCGA |||| || ||||| ||| || || |||| ||
AAAGGGAAACGCGTCCAACC CCCC CC GCCGC ACT CC CC TGCG GG /
GATAAATCAAGCGCCGACCA AAGA A GA AAATAG AA - CAAAG- AAAACCAG
GAACCCC

GAM3249 ACCAGCACAGCAAGCATATA 73362 TTGTAGGTGT 73363 -------- G A G TG TAA
GGGTGGTAACAAGTTGTTGT TGCTGTACAG ACCAGC ACAGCAA CAT TA GG G C
AGGTGTTGCTGTACAGTAAG TAAG |||||| ||||||| ||| || || |
GCTGGT TGGTCG TGTCGTT GTG AT TT T /
GAATGACA - G G GT GAA

GAM3250 GGACGGACAAGATTCACAAC 73366 TTGCTGTGGA 73367 GACAAGAT A TTTAA A-- CC
CTTTAAAACAACATTACCAA TGTGACAGCA GGACG TCACA CC AACA CATTA A
ATAGTGACCTGTTGCTGTGG ACGT ||||| ||||| || |||| |||||
ATGTGACAGCAACGTTC CTTGC AGTGT GG TTGT GTGAT /
AACGAC-- A TGTCG CCA AA

GAM3251 TAGGTATAATATAATTAATT 73373 TTAGTACTAC 73374 T ------ AT T- -- CA C
ATATGGTTTATTATCACAAT CCAATAATCA TAGGTATAATATAA TA ATTAT GGT TATTA TCACAATT AC A
TCAACCATGGTGATTGTGAA AATG |||||||||||||| || ||||| ||| ||||| |||||||| ||

TTAGTACTACCCAATAATCA ATCTATGTTATGTT GT TAATA CCA ATGAT AGTGTTAG
TG T
AATGTGCTTGTATTGTATCT C GTAAAC AC TC TA -- G
A

GAM3252 TCAGCTTCAGATGAGCTCTA 73379 TGGAGAGACG 73380 CTT A- - ATTGA A
TTGAAGAGTCAAGAGGCTCT CTCAAACTGC TCAG CAG TGAGC TCT AGAGTC A
GGAGAGACGCTCAAACTGCC CTTG |||| ||| ||||| ||| ||||||
TTGA AGTT GTC ACTCG AGA TCTCGG G
CC- AA C GAGG- A

GAM3253 AAGCTAATTTTACGTGAGTT 73393 TTTTACGTGA 73394 TTT AA- TTTAAA
AAAAGTTTAAAAAGATTTCT GTTAAAAGTT AAGCTAAT ACGTGAGTT AAG A
TGGAAATTCACGTTATTAGT TAAA |||||||| ||||||||| |||
TT TTTGATTA TGCACTTAA TTC /
T-- AGG TTTAGA

GAM3254 TACGACTAACATTTTTATAG 73398 ACTAACATTT 73399 -- CA- A - ACA- A GT
TTATCATTACAATTTTTTAG TTATAGTTAT TAC GACTAA TTTTT TAGTTAT CATT ATTTTTT
GCA T
CAGTTAAATGCAAAAAAATA CATT ||| |||||| ||||| ||||||| |||| ||||||| |||
ACAGATGTATAATTGAAAGA ATG TTGATT AAGAA GTTAATA GTAG TAAAAAA CGT A
ACTTTTAGTTTTGTA TT TTC A T ACAA A AA

GAM3255 CATAATCATCATATTTTCTC 73415 TACCTCAGTT 73416 CATCA - C C TTAACC-- T TT
AACCTGATTAACCCTTCAAT AGATAAATAA CATAAT TATTT TCT AAC TGA CT CAA C
TCATCTTGTAGATTATACCT AAAT |||||| ||||| ||| ||| ||| || |||
CAGTTAGATAAATAAAAATT GTATTA ATAAA AGA TTG ACT GA GTT A
ATG AAA-- T - - CCATATTA T CT

GAM3256 GCACCGTGGAGGTCGTTCTA 73425 TATCGCATGC 73426 AC GGTCG TA- GCG- CG
T CAACT
TCGCATGCGATTGTGCGAAT GATTGTGCGA GC CGTGGA TTC TCGCAT ATTGTG AATG
GC G
GTGCCAACTGCGAATGCCGT ATGT || |||||| ||| |||||| |||||| |||| ||
TATTACAATAAAAATGTGAC CG GCGCCT AAG AGTGTA TAACAT TTGC CG /
TTGAAAAATCCGCGAAGC AA AAA-- TTC AAAA TA - TAAGC

GAM3257 TTGTGGGATGTTCGTCGTAT 73428 CTTTGCACGT 73429 G GTC--- T - CA G --- C
CGGCAACATTGGCATCCGCT ACCAACCAGA TTGTG GATGTTC GTA CG GCAA TT GCA
TCCG T
GCGGATTATGTGGACTTTGC ACGT ||||| ||||||| ||| || |||| || ||| ||||
ACGTACCAACCAGAACGTTG AGCAC TTGCAAG CAT GC CGTT AG TGT AGGC /
CACGA G ACCAAC - A TC G ATT G

GAM3258 GATAAAAATATGTCGAGGGA 73432 TATGTCGAGG 73433 AAAAATA GA GA CATT- A
TGACATTGATGAGACCCCTT GATGACATTG GAT TGTC GG TGA GATGAG C
ATTCTCTCTCAAACTAAGAC ATGA ||| |||| || ||| ||||||
AGTAATCCATC CTA ACAG TC ACT TTATTC C
CCTAATG AA AA CTCTC C

GAM3259 GGGGGGAAGGAGGTTGACTG 73437 TGCAGCACTA 73438 G--- GT-- A AATT
CAACCTCAATTGATCAGAGG ACTCTTTACA GGGGG AAGGAG TG CTGCAACCTC G
TTGCAGCACTAACTCTTTAC ACCC ||||| |||||| || ||||||||||
AACCCCC CCCCC TTTCTC AC GACGTTGGAG /
AACA AATC - ACTA

GAM3260 CATTCCCTAGCTATTATAAG 73465 TATCTGGCTA 73466 ---- T- TTAATT
GTTAATTGCAAAAACCCTTA AGATGGGAGT CATTCCC TAGCTA TATAAGG G
TATCTGGCTAAGATGGGAGT G ||||||| |||||| |||||||
G GTGAGGG ATCGGT ATATTCC C
TAGA CT CAAAAA

GAM3261 GGATGTAACGGTGGAGGTCC 73506 GGGCAAGAAT 73507 --------- G GGT--- G AG
GGCAGGAAGTGGGCAAGAAT TGACCGATTT GGATGTAA CGGT GA CC GC G
TGACCGATTTATCTATTGCA ATCT |||||||| |||| || || ||
TCC CCTACGTT GCCA TT GG TG /
ATCTATTTA G AAGAAC G AA

GAM3262 TTGTGGTCTAACTCAAGACT 73511 GTCGTGGTTG 73512 - T T A GCTGAA GC
AGCTGAATCGGTGCTATAAC ACACGCAG TTGTG GTC AAC CA GACTA TCGGT T
CGATAGTCGTGGTTGACACG ||||| ||| ||| || ||||| |||||
CAG GACGC CAG TTG GT CTGAT AGCCA A
A - - G ------ AT

GAM3263 GTTTTAGAGCTGGATCCTCC 73541 TTAGACAGCT 73542 TAGA GG C CC AGGC C
AA
TGACCCTGTAGGCCTACATT CAGAGGATGA GTTT GCT ATCCTC TGA CTGT CTA ATTGC
T
GCAATGAGCAATTAGACAGC GGTG |||| ||| |||||| ||| |||| ||| |||||
TCAGAGGATGAGGTGGATGA CAAG TGG TAGGAG ACT GACA GAT TAACG /
AC TAGG AG - C- ---- - AG

GAM3264 GTGCCTAAATCTGTTTCTGT 73550 CTAAGGGTGG 73551 AA-- TG TCTGTTAT ATT
TATTTTAGGGGCATTTGACG GTGTTGGGGT GTGCCT ATC TT TTTAGGGGC T
GTTCCTAAGGGTGGGTGTTG AT |||||| ||| || |||||||||
GGGTAT TATGGG TGG GG GAATCCTTG G
GTTG GT -------- GCA

```
GAM3265  GTCTGAAGGGGGGCCCTAAT 73573   TAAAGCTTCA 73574     ---   GG-    CC    AA----    G
         CAACTTAAGTGCTTAAGGTA       AATTCATCTG       GTC   TGAA   GGGGC  TAATC     CTTAA T
         TAGGATTAAAGCTTCAAATT       AC            |||  ||||  |||||  |||||     |||||
         CATCTGAC                        CAG   ACTT   CTTCG  ATTAG     GAATT G
                                  TCT    AAA     AA     GATATG    C

GAM3266  GTGCAGTGCACAGGAACAGA 73596   TTCACTGGAT 73597      G       -   AC-    TC--    CATAC  T
         CATCCATCACCTACATACGC       ATATTGTGTC       GTGCA TGCACAGGA ACAG   ATCCA    ACCTA
GC T
         TTCTGCTGGGTTCACTGGAT       CTGT           ||||| |||||||||| ||||   |||||    |||||     ||
         ATATTGTGTCCTGTGTGTGC                 CGCGT GTGTGTCCT TGTT   TAGGT    TGGGT    CG C
         GC                          -       G    ATA     CACT     -----  T

GAM3267  AGGAGGAGGAGCACTATCCC 73606   GAGCAGGTGT 73607        G    C  TCCCTATACAATA       G
AAC
         TATACAATAGACACCTGTTG       TAGATTTACT       AGGAGGAG AGCA TA          GACACCTGTT CA   C
         CAAACCTTGTGGAGCAGGTG       ATTA           |||||||| |||| ||          |||||||||| ||
         TTAGATTTACTATTATTGCT                 TCTTCCTC TCGT AT          TTGTGGACGA GT   /
         ACTCCTTCT                       A    T  TATCATTTAGA--        G  GTT

GAM3268  TTTATTTGATGGGATGTAGA 73612   GGACCACACT 73613      TTT     A    A-   CAA   ACTA
         TGGCAACTAACTACCTCATA       ACACTCATTT       TTTA   GATGGG TGTAG  TGG   CTA    C
         GGACCACACTACACTCATTT       TTAA           ||||   ||||||  |||||  |||   |||
         TTAAA                        AAAT   TTACTC ACATC  ACC   GAT    /
                                  TT-     -    AC   AG-   ACTC

GAM3269  TGTACGTAATGGACATCATA 73627   TTTCTTGGTT 73628        TAAT   C    T---     GAT
         GGTACGATAGCAGTATCTTT       TCTTATTTGT       TGTACG    GGA ATCA    AGGTAC   A
         CTTGGTTTCTTATTTGTATA       ATA            ||||||    ||| ||||    ||||||
                                  ATATGT    TCT TGGT    TCTATG   /
                                     TTAT   T    TCTT     ACG

GAM3270  CATTAGCAGTAACTGAATAT 73648   TATAATGCAA 73649     T  C  TA   GAAT     CAAA  AA    TA-   T
         AATGCAAAACAAGCAATACA       AACAAGCAAT       CAT AG AG  ACT    ATAATG    AC  GCAA   CAAA A
         AATACATTTGACTTTGCAGT       ACAA           |||  ||  ||  |||    ||||||    ||  ||||   ||||
         CATTATTAAAGTCTCCTTAT                 GTA TC TC  TGA    TATTAC    TG  CGTT   GTTT C
         G                           T  C  --   AAT-      ----  A-    TCA    A

GAM3271  CGATACATAAAAGGTGAGTT 73673   TCAGGCAGCT 73674       ATAAAA      TATG    AAAT-------     A
         ATGTGCCAAATCAGATACAG       GCTCGCCAGA       CGATAC     GGTGAGT    TGCC         CAGAT C
         TCTGTGCCAAACTCAGGCAG       TGCG           ||||||     |||||||    ||||         |||||
         CTGCTCGCCAGATGCGTATC                 GCTATG     CCGCTCG    ACGG         GTCTG /
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    G                                CGTAGA     TCG-   ACTCAAACCGT    A


GAM3272 ATTACTGTTACCGCTGTAAT 73693  TAACAAAAGT 73694      -  CC    A -------     ----- T   TTC
    AACAAAAGTATCTATAATTC      ATCTATAATT      ATTACT GTTA  GCTGT ATAA     CAAAAGT    ATC
ATAA  C
    CCATTTATTGATAATTAACT      CCCA          ||||||| ||||  ||||| ||||      |||||||    ||| ||||
    TTTGACAATATTTATAATAG                  TAATGA CAAT  TGATA TATT     GTTTTCA    TAG TATT  /
    TTTAACTAGTAAT                       T   T-    A   TATAACA     ATTAA   T   TAC


GAM3273 ATTCTTTAGAACCAACTGAC 73713  CTACGGCAGT 73714                TTCA          A   CC   C--
GC
    CAAGTTCACGTACGTATGAC      CACACGTCAT      CTTTAGAACCAACTGACCAAG
CGTACGTATGACGTG TGAC  GCTG   GC  G
    GTGATGACCCGCTGCGCGCG      ACGT          ||||||||||||||||||||  |||||||||||||| ||||  ||||  ||
    CTGCCTACGGCAGTCACACG                  GAAATCTTGGTTGACTGGTTC   GCATGCATACTGCAC
ACTG  CGGC   CG  /
    TCATACGTACGCTCCTTGGT                          CTC-          -   A-   ATC  TC
    CAGTTGGTTCTAAAGAAT

GAM3274 GTAGATGCTATCATTACTCT 73718  TATCATTACT 73719   CTA   TAC  TAAAATATA    AA  -   AG-
AA-   AC   GT
    AAAATATATAATGAATAATC      CTAAAATATA      G   TCAT   TC      TAATG  TA ATCC   ATTT   AACT
GTAT  G
    CAGATTTAAAACTACGTATG      TAAT          |  ||||  ||       |||||  || ||||  ||||  ||||  ||||
    TGGAAGTACTCGGTTCCAGA                  T   AGTA   AG       ATTAT  AT TAGG   TAAG   TTGG  CATG
G
    ATAGCGGATATAGATATTAA                  AAG   CAT  TGAACAA--    AG  A   CGA   ACC   CT   AA
    ACAAGTGATACATGAGAATA
    TACTAC
GAM3275 AAAGGAGAAATATCAGATTA 73721  TATTACACCA 73722        AA   C   T   C  -  C    GATAC
CAA
    TGACGGGTACTATTGGATAC      TCATTATTTT      AAAGGAG  ATAT AGAT ATGA GG GTA TATTG
CGACGAA   G
    CGACGAACAAGTAATTTGTT      ATGT          |||||||  |||| |||| |||| || ||| |||||    |||||||
    GATACGATATTACACCATCA                  TTTCTTC  TGTA TTTA TACT CC CAT ATAGC    GTTGTTT  /
    TTATTTTATGTACTTCTTT                    A-   T   T   A  A   T    ATA--     AAT


GAM3276 ATATGACTAGACCGATGACC 73731  TCGATCATTC 73732      A-    CC    CCATTTAAAAA   TCTCT-
CT
    ATTTAAAAAATACTCTCTAG      TTTTAGCACA      ATATG  CTAGA  GATGA        ATAC    AG  T
    CTTTAACTTAAACTGTATCG      TGT           |||||  |||||  |||||         ||||     ||
    ATCATTCTTTTAGCACATGT                  TGTAC  GATTT  TTACT        TATG     TC  T
                                AC    TC    AGC--------   TCAAAT  AA


GAM3277 GATTTTCAATTATGTATCAT 73740  TCCTCCTTGA 73741    TTTTCAATTATGT    TTAT--    CAGT
    TATAGCAACAGTAATTCTTG      TTTTAGCATC      GA          ATCA     AGCAA   A
```

CTCCTCCTTGATTTTAGCAT CTCT || |||| |||||
CCTCTTC CT TAGT TCGTT /
TCTCCTACGATTT TCCTCC CTTA

GAM3278 TATTTGTAAATGGATATCCT 73789 TATCCTATAA 73790 T GGATA -- T TAGACACA
ATAAAATTTTTATTAGACAC AATTTTTATT TATTTG AAAT TCCTA TAAAATT TTAT G
AGGAGCAGATATAACAATTT AGAC |||||| |||| ||||| ||||||| ||||
TAAATAGGAGAGATTTTCAA ATGAAC TTTA AGGAT ATTTTAA AATA /
GTA T GAG-- AA C TAGACGAG

GAM3279 GAACAAATTATATTAATGTA 73799 TAATGTACAT 73800 AA ATT TAGAGA GA G
CATTTAGAGATTAGAGATGA TTAGAGATTA GAACA TTAT AATGTACATT TTA GAT A
AAATTATAAGACACAATGTA GAGA ||||| |||| |||||||||| ||| |||
TATTTGGTAATGTTT TTTGT AATG TTATATGTAA AAT TTA A
-- GT- CACAG- A- A

GAM3280 TGGGTGTTTTTGGGGTGTGG 73815 GGTCATTGGA 73816 T- G C A GG- GG T A--
- CAGT
CGGACGCGGGGCGGTCATTG CGGGGTGCAG TGGGTG TTTTGGGGT TGG GG CGCG GC
TCAT GG CGGG GTG T
GACGGGGTGCAGTTAAATAC TTAA |||||| ||||||||| ||| || |||| || |||| || |||| |||
ATGCCCGGGACCCATGAAGC GCCCAC AAGACTCCG GCC TC GCGC CG AGTA CC
GCCC TAC A
ATGCGCGACTTCCGGGCCTC CC G T A GTA A- C AGG G ATAA
AGAACCCACCCG

GAM3281 GACCTGCATTGCTACGAAGA 73823 GTAGTTCCGT 73824 T GAA - GAA GAG A----- C
ATTC
GTTAAGTGAAGAAGAGACAG GTTGCTTTTG GCTAC GAGTT AAGT GAA ACAGAGG
GGAGC ACGATTT C
AGGAGGAGCCACGATTTATT TGAT ||||| ||||| |||| ||| ||||||| ||||| |||||||
CCTTACAAGATTGTAGTTCC TGGTG TTCAG TTCG CTT TGTTTTC CCTTG
TGTTAGA T
GTGTTGCTTTTGTGATTCCA - ATA C AAC AG- GTTGTG A ACAT
AGCTTCGACTTATAGTGGTT
GCAACTC
GAM3282 GCAAGACTTCGTTTATACGT 73828 ACTTCGTTTA 73829 CTTC ATAC- ----- CA
GCTTGCTACAAATTTAGGAA TACGTGCTTG GCAAGA GTTT GTGCTTG CTA A
TTCGAGCGCAACAGGAACTT CTAC |||||| |||| ||||||| |||
TTGC CGTTTT CAAG CGCGAGC GAT A
---- GACAA TTAAG TT

GAM3283 CTCATTGTGGTTTTCGCGCC 73839 CATTGTGGTT 73840 A- T CG C AGAG- AACC
TCAGAGTTGTTAACCACATT TTCGCGCCTC CTC TTGTGG TTTCG C TC TTGTT A
CGGCAAAAGGGGAAGTATGA AGAG ||| |||||| ||||| | || |||||
AACCCACAAGGGAG GAG AACACC AAAGT G AG AACGG C

GG C AT A GGGAA CTTA

GAM3284 ACACTACATTTCTCAGAACC 73844 ACTACATTTC 73845 AC---- TC CCA CTA
AAAAATTTCTAAATAAAGAT TCAGAACCAA ACACT ATTTC AGAA AAAATTT A
TTTTTCTATGAAATTCATAA AAAT ||||| ||||| |||| |||||||
AGTGT TGTGA TAAAG TCTT TTTTAGA A
AATACT TA --- AAT

GAM3285 TTTTTATTCTTCATTCGTTA 73875 AAAGGGCAAT 73876 ATT TC T ACTTTTAACACA GAA
A
CGACTTTTAACACACCCGAA ATTTTGCGTC TTTTT CTTCAT GT ACG CCC TGT T
TGTATCGACAAAGGGCAATA ATTT ||||| |||||| || ||| ||| |||
TTTTGCGTCATTTATGGAGT AAAAG GAGGTA TA TGC GGG ACA C
TAGAAAA ATT TT C GTTTTATAAC-- AA- G

GAM3286 GAGATAAGTTTCATAAGTTT 73886 TAAGTTTCAT 73887 T TTTTATT-- TTTCA
ATTTTATTATCATTTCAAAT AAGTTTATTT GAGA AAGTTTCATAAGTTTA ATCA A
ATTTTGATTTCTTTTTCTAA TATT |||| |||||||||||||| ||||
ATTTGTGAAATTTTTTTC CTTT TTTAAAGTGTTTAAAT TAGT A
T CTTTTTCTT TTTAT

GAM3287 TCTACTGGTGAAATGATGTG 73893 TATTATATGG 73894 CT AAA -- TC - T A- A
TGCT
TCCCAATATTAATGCATTTA AGCGGACATC TCTA GGTG TGATGT G CCA ATA TA TGC
TTTAT A
TTGCTAGTAACGTAAACGCA GACG |||| |||| |||||| | ||| ||| || ||| |||||
GATATTATATGGAGCGGACA AGAT CCGC GCTACA C GGT TAT AT ACG AAATG G
TCGACGCCTTAGA T- A-- GG GA A T AG C CAAT

GAM3288 ATTATTACTATAGAAGATGT 73897 TAAGTAAAGC 73898 - AAGA TAGAAAAA TG G
TTACAC - A T
TAGAAAAAATGATGCTGGTT ATATAACGAC AT AG TGT A AT CTGGTTA ATGTGTTT AT
TATATA A
ATTACACATGTGTTTATATA TAAC || || ||| | || ||||||| |||||||| || ||||||
TATATATATATATAAGTAAA TA TC ATA T TA GACCAAT TATACGAA TG ATATAT
T
GCATATAACGACTAACCAGA G ATGG TTAAAA-- GT A CAGCAA A A A
ATTGTAAAATTATAGGTACT
GATAGAATAAT
GAM3289 ACAAAGCATTTCCACAACTG 73902 TACATGGGAA 73903 AA TTTCCACAAC GG A- GG
AA TTTC
CTGGGTTTACATGGGAAACA ACAAAGCATT AC AGCA TGCT GTTT CATG AAAC AGCA
C
AAGCATTTCCACAACTGCTG TCCA || |||| |||| |||| |||| |||| ||||
GGTTTACATGGGAAACAAAG TG TCGT ACGA CAAA GTAC TTTG TCGT A

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    CATTTCCACAACTGCTGGGT                GG  CAACACCTTT  AA  GG  A-  GG  CAAC


GAM3290 ACTGGCAGAACGAGCACAGC 73956  TGGCAGAACG 73957      AG  GA  ---  G - TTAG--  G
    AGGCCTTTAGGGTGGTAACT      AGCACAGCAG      ACTGGC  AAC  GCAC  AGCA GC CT    GGT G
    ACGTGTGGTGTGTGCTATCG      GCCT          ||||||  |||  ||||  |||| || ||    |||
    TGCAGTTAGGTTAGT                   TGATTG  TTG  CGTG  TCGT TG GG    TCA T
                                GA  A-  CTA  G  T  TGTGCA  A


GAM3291 CCAACCTGCAAAACCAGCAC 73998  ACCAGCACAG 73999    AC TG  AACC   A TG   TA- GT  A
 G TG
    AGCTGGCCTATAGGGTGGTA      CTGGCCTATA      CCA  C  CAA   AGCAC GC  GCCTA  GG  GGT
ACA AG  T
    ACAGAGTGTGGGTTGTGTAG      GGGT          |||  |  |||   ||||| ||  |||||   ||  ||| ||| ||
    CCGTCCAGTTAGGCTGGCGG                GGT  G  GTT   TCGTG CG  CGGAT   CC  CCG TGT TT  G
    TGCTTTGTGGAGTGG                   GA GT  ----   G  GT   TGA  TG   A   G  GG


GAM3292 GGCGGTGGCGATCAAAAGGC 74030  TAGAGTGTAA 74031       CGA  AAAAG  G-    AA
    GCGTATGAGAAACCGTTTAT      TAGAATCACC      GGCGGTGG  TC   GCGC  TATGAG  A
    AGAGTGTAATAGAATCACCG      GTC           ||||||||  ||   ||||  ||||||
    TC                          CTGCCACT  AG   TGTG  ATATTT  C
                                  A--  ATAA-   AG    GC


GAM3293 ACCGTTTGTACTGGCGTTCT 74045  TAGGAGGCTC 74046    GT   - - - G   TT  ACAT  T
    TTACGACATTCGTGTCCGAC      GCGTTACAAG      ACC  TTGTA C TG GC TTCT  ACG   TCG G
    CGGCGTTTAGGAGGCTCGCG      GT            |||  ||||| | || || ||||  |||   |||
    TTACAAGGT                   TGG  AACAT G GC CG AGGA  TGC   AGC T
                              --   T C  T  G   TT  GGCC  C


GAM3294 GGTCGTCGGAAGTTACTGAT 74069  TCGGAAGTTA 74070      TC-     AC  ---  AACAACA
    GGAACAACAAGCGCCGCCCA      CTGATGGAAC      GGTCG  GGAAGTT  TGA  TGG     A
    ACTTCAAATTTCCAGCCGAC      AACA          |||||  |||||||  |||  |||
    C                           CCAGC  CCTTTAA  ACT  ACC     /
                                  CGA    --  TCA  CGCCGCG


GAM3295 TGATGTGGTCTCTGGGATGA 74079  TAGTATGGCT 74080       TCT      AATAT----       AGT
    AATATTATTATATGTAGTAT      TTTCTCGTTC      TGATGTGG  CTGGGATGA      TATTATATGT  A
    GCAATATATAGTATGGCTTT      CAGT          ||||||||  |||||||||      ||||||||||
    TCTCGTTCCAGTCTTTATAT                  ATTATATT  GACCTTGCT      ATGATATATA  T
    TA                          TCT      CTTTTCGGT       ACG


GAM3296 TCTCTCAGAAAACGAGAGTG 74088  TAGGAGGTGA 74089       GAA-  GA-  GTGA     CA
    ACTTCTAGACACACTCTAGG      TCGTAGTTGG      TCTCTCA   AAC  GA   CTTCTAGA  C
    AGGTGATCGTAGTTGGCATG      CATG          |||||||   |||  ||   ||||||||
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      AGAGA                          AGAGAGT   TTG  CT   GAGGATCT  /
                                     ACGG  ATG  AGTG     CA


GAM3297  CTGTTCTACGGAATTAACAA 74092   TAAGAAAATA 74093     -   G  TAAC-   C  AATATAAAG-----
AAC
      CTCGTGAATATAAAGATACA      AGAAGCACAG       CTGTT CTACG AAT    AACT GTG          ATAC  A
      ACATTCAGTATAAGAAAATA      TTAT          ||||| ||||| |||    |||| |||          ||||
      AGAAGCACAGTTATATCATT                 GACAA GATGC TTA    TTGA CAC          TATG  T
      GCGTAGCAACAG                       C   G  CTATA  -  GAAGAATAAAAGAA   ACT


GAM3298  ATATGGGTGGGGCGGGCGTG 74107   TATGCAGATG 74108   GG-  GG   GGAG   TA    GG
TGTATGGGAGGGGG     A
      GGAGGGACCTAGTCTGTGGG      TGGTCTGACA       GC  GCGTG   GGACC  GTCTGTG  GTCA
 CTGACCT C
      GTCATGTATGGGAGGGGGCT      CGTA           ||  |||||   |||||  |||||||  ||||         |||||||
      GACCTACGAGGGTCAGGGTG                  TG  TGCAC   TCTGG  TAGACGT  TAGT
GACTGGG G
      AGAGGAAGTTGATATGCAGA                AGA  GA   AG--   TG    A-   TGAAGGAGAGTGG-     A
      TGTGGTCTGACACGTAGGTA
      GAGTCCTATAT
GAM3299  TGTTAATCATCAATCCGTTA 74115   TACGGAAACA 74116       CATC--   GTT     AAATT     T
      CGGAAACAAATTATCATTTT      AATTATCATT       TGTTAAT    AATCC  ACGGAAAC   ATCATTTT A
      TATAAAAATGGTTTGTGGTT      TTTA          |||||||    |||||  ||||||||   ||||||||
      TCTGTTTAGGGTTACCTTTA                ACAATTA    TTGGG  TGTCTTTG   TGGTAAAA T
      TTAACA                            TTTCCA   ATT     GTGTT     A


GAM3300  ATCATTTTTAGAACTGACCA 74124   TCACATGGTT 74125              TC-         A  ----------    T
      ACCATGTTCACGTAAGTGAC       GGTCAGTTCT       AGAACTGACCAACCATGT  ACGTAAGTGACGTG
TGAC        GCGCGC T
      GTGATGACGCGCGCTTCGCG       AAAA          ||||||||||||||||  ||||||||||||| ||||        ||||||
      CGCTGCCTGCGGCAGTCACA                 TCTTGACTGGTTGGTACA  TGCATTCACTGCAC ACTG
  CGCGCG /
      CGTCACTTACGTCTCACATG                        CTC         -  ACGGCGTCCGT    C
      GTTGGTCAGTTCTAAAAATG
      AT
GAM3301  TAGCTGCTAAATGTGATACG 74153   TACGACACGC 74154     TG T   T    - AA-   A  AAAA   -- -
TAA   AA
      GAAGTTGAAAAAAAACTGCC       TCGTATTTTA       TAGC  C AAATG GATACG G  GTTG AAA   CTGC
CG CT  ATCA  A
      GCTTAAATCAAAAAAATGAT       TTTT          ||||  | ||||| |||||| |  |||| |||   ||||  || ||  ||||
      AGACGACGCAGATTTACGAC                 ATCG  G TTTAT TTATGC C   CAGC TTT   GACG  GC GA
TAGT  A
      ACGCTCGTATTTTATTTTGT                  GT T   T    T GCA   A  A---   CA  A  ---   AA
      GGCTA

GAM3302  CTCAGACAAGGTATTTTTTA 74160   TATTTTTTAG 74161     --  C    AT-      A  CTA  GC
      GCATCCTATCGCACAGACAC       CATCCTATCG       CTCA  GA AAGGT  TTTTTAGC TC   TC  A
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GAGCTAGGAGTGGACTTTCT CACA |||| || ||||| |||||||| || ||
CCGTGAG GAGT CT TTTCA GAGGATCG AG AG /
GC C GGT - CAC AC

GAM3303 GCACCCTGAAGATGGTTTGA 74170 TCTGCAGTCA 74171 A C A--- G ATGCT T - ATTTGG
ATGCTCTGCAGTATGTCAAG GACAGTCTCA GC CC TG AGAT GTTTGA CTGCAG ATGTC AAGA A
AATTTGGAACTTGCTCTTCG AACA || || || |||| |||||| |||||| ||||| ||||
GCGTCTGCAGTCAGACAGTC CG GG AC TCTG CAGACT GACGTC TGCGG TTCT /
TCAAACATGGGC - T AAAC A ----- - C CGTTCA

GAM3304 GAAGCAGGTCTACTTGAGCC 74205 AGGAATTTCA 74206 -------- ACTTGA A CT G GAA
AGTTGATTGGAGTCTCTGCT GCAACTGGTA GAAGCA GGTCT GCCAGTTG TTGGAGT CT CT A
GAAACAAAAGAGGAATTTCA GATC |||||| ||||| |||||||| ||||||| || ||
GCAACTGGTAGATCTATTTA CTTCGT CTAGA TGGTCAAC GACTTTA GA GA C
TATGCTTC ATATTTAT ------ - AG - AAA

GAM3305 CATTTTTAGAACTGACCAAC 74238 GAACTGACCA 74239 TC- A A ---------- T
CATGTTCACGCAAGTGACGT ACCATGTTCA AGAACTGACCAACCATGT ACGC AGTGACGTG TGAC GCGCGC G
GATGACGCGCGCTGCGCGCG CGCA |||||||||||||||| |||| ||||||||| |||| ||||||
CTGCCTTCGGCAGTCACACG TCTTGACTGGTTGGTACA TGCG TCACTGCAC ACTG CGCGCG /
TCACTAGCGTTTCACATGGT CTT A - ACGGCTTCCGT C
TGGTCAGTTCTAAAAATG

GAM3306 TGGTCGGTTACTCACTCTGC 74256 CAGGAGCGAG 74257 C -- A GC-- TTCT
TTTCATTTCTGAGTTTGTGA ACTAACCAAC TGGT GGTTA CTC CTCT TTTCAT G
GACACAGGAGCGAGACTAAC TA |||| ||||| ||| |||| ||||||
CAACTA ATCA CCAAT GAG GAGG AGAGTG A
A CA C ACAC TTTG

GAM3307 CCTAATTTCGTCGTCCACTG 74286 TCCCCAGTCG 74287 T GTCGTCCACT---- C T TTTT TC C TT
ACCACTTGGTTTTAAATCCG TCTTCTCCTT CC AATTTC GAC ACT GG AAA CGGT TTAC T
GTCTTACTTTTTGTAACATT TTTT || |||||| ||| ||| || ||| |||| ||||
GCTTTTCCCCAGTCGTCTTC GG TTAAAG CTG TGA CC TTT GTTA AATG /
TCCTTTTTTAAGAAATTTGG T AATTTTTTCCTCTT C C C--- TC C TT

GAM3308 TTTGGTAGCTTCTACTTTTG 74330 TAGCTTCTAC 74331 TA TTCTAC CTTG AC
GCTTGAAAGACTTACCTTTC TTTTGGCTTG TTTGG GC TTTTGG AAAG T

CAAAACATTGTGCCTCCAAA AAAG ||||| || |||||| ||||
AAACC CG AAAACC TTTC T
TC TGTTAC ---- CA

GAM3309 CGAGGGGACTATAACATGTA 74349 AACATGTATA 74350 ATAACATGTA AAA--- G G
TAGGCGAAAAGCGGGGTCTC GGCGAAAAGC CGAGGGGACT TAGGCG AGC GG T
GGTTGTAACGCGCTTAGGAA GGGG |||||||||| |||||| ||| ||
GTCCCCTCG GCTCCCCTGA ATTCGC TTG CT /
AGG------- GCAATG G C

GAM3310 GGGTGTGTGTGTGGGGGTGG 74360 TCCCCGACTC 74361 G T TG T G C CC G AG
TGGGCGGCCGCGGGCGCGGA CTCTGTACTA GGGT TG GTG GGGG GGT GG GG GCGGGC
CGG G
GGGTCCGGCCCGTCCCCGAC GACT |||| || ||| |||| ||| || || |||||| |||
TCCTCTGTACTAGACTC CTCA AT CAT CTCC TCA CC CC TGCCCG GCC /
G - GT - G - -- - TG

GAM3311 CGTCCGGATCGGGCGAACGG 74385 CGAGAGAGCG 74386 GA GG AA G G- TC
TCTCGGCCTCTCGGGCGAGA AGCGAGCGAG CGTCCG TCG CG CG TCTC GCC T
GAGCGAGCGAGCGAGCGGGC CGGG |||||| ||| || || |||| |||
G GCGGGC AGC GC GC AGAG CGG /
G- GA GA G AG GC

GAM3312 GGTATAGTTGCATATTTATT 74440 TGCATATTTA 74441 ATTTTATGT A CTTT- T T ----------
----- T
TTATGTTCATTTTCTTTCTT TTTTATGTTC TC TTTT CTTGCT GAG GT GTTAT T
GCTTGAGTGTGTTATTTCAA ATTT || |||| |||||| ||| || |||||
TAGCTCCTGTTTAGCAGGTC AG AAAA GAACGA TTC CA CGATA C
GAACCTTCAGCAAGTTCACA TTCCTTTT- A CACTT C - AGCTGGACGATTTGTCCT
A
AAAAGATTTTCCTTTTGTGT
GTTTCTTTTC
GAM3313 GTTTAACGGCGTTTGGACCA 74452 GGACAACATA 74453 TT GACCATTACCAT TATG
AGC
TTACCATATTATGTTTATGC ATTTAGCTAT GT AACGGCGTTTG ATTATGTT CTTT A
TTTAGCAGAAAAAGGACAAC AGAT || |||||||||| |||||||| ||||
ATAATTTAGCTATAGATGCT CG TTGTCGTAGAT TAATACAA GGAA G
GTTTTGC TT ATCGATT----- CA-- AAA

GAM3314 GGGGACCGTCCGTTCTCTCC 74457 TCCCTGTGCA 74458 GG C C- TCT TG CA- G
CTTGTTTG G
CTGTGCAGGTGCGACTCTTG GGTGCGACTC G GAC GTC GTTC CCC TG GGTGC ACT
TGCTG T
TTTGTGCTGGTCGCGGCAGG TTGT | ||| ||| |||| ||| || ||||| ||| |||||
TGGCGCCCAACGTGGGGCTC C TTG CAG CGAG GGG GC CCGCG TGG ACGGC
C

GAGCTCGACAGTTTTC TT A CT CTC GT AAC G -------- G

GAM3315 GCTTGTTCAAATTTTATAAA 74472 TTTATAAAGA 74473 T TCAAATT GAATCATATTC GG
GAATCATATTCATTAGGCAT ATCATATTCA GCT GT TTATAAA ATTA C
ATAATAAAAAATATAATTTA TTAG ||| || ||||||| ||||
TAATACACTTACAGC CGA CA AATATTT TAAT A
- TTCACAT AATATAAAAAA AT

GAM3316 TAGTTCTTAACATCTATTAA 74478 TTGCTTTAAT 74479 CT CATCT TCATT TT
TCATTTATTCGCTTATTGCT TGTTTTTGTA TAGTT TAA ATTAA TA C
TTAATTGTTTTTGTAAACTA AACT ||||| ||| ||||| ||
ATCAA GTT TAATT AT G
AT TTTGT TCGTT TC

GAM3317 CGTCCACTTAAGCTGGTGGT 74490 AGGCAGCTAC 74491 - -- - G T AGCT
GCGTTGTGGAGCTGAAGACC AGCAGCTTAT CGTCCACT TAAGCTG GTGG TGC TTG GG G
TAAGGCAGCTACAGCAGCTT GGTG |||||||| ||||||| |||| ||| ||| ||
ATGGTGGACG GCAGGTGG ATTCGAC CATC ACG AAT CC /
T GA G G - AGAA

GAM3318 GCTATTTTCTCTTTTGTTTT 74526 TCTTTTGTTT 74527 ATTT TTTTATAATC G - AG T
ATCGTTC T
ATAATCATGTCTGAGCCTAT TATAATCATG GCT TCTCTTTTG AT TCT G CCTA GT
TGATGA T
GTATCGTTCTGATGATTCTT TCTG ||| ||||||||| || ||| | |||| || ||||||
CGTCATCTAAAACTAGGTCC CGA AGGGGAGGC TG AGA C GGAT CA
ACTGCT C
AAGAGGTCGGAGGGGACCAC CACC ---------- G A CT - AAATCT- T
AGC

GAM3319 GCAGCATTTTCTTTTGACCG 74532 TGCCTGTCTC 74533 TTCTTTT C TT TAA
GCTTAGTAATAAGTCTTTGC TTTTCAATGC GCAGCATT GAC GGC AG T
CTGTCTCTTTTCAATGCTGT TGT |||||||| ||| ||| ||
TGTCGTAA CTG CCG TC A
CTTTTCT T TT TGA

GAM3320 GTCCTCCGATTCGCCACTAT 74569 TCACCAGCCA 74570 T C--- CACTAT CAT
ATTTGCCATTAGAGCAAATC CAAGTCGGGG GTCC CCGATT GC ATTTGC T
ACCAGCCACAAGTCGGGGAC AC |||| |||||| || ||||||
CAGG GGCTGA CG TAAACG /
- ACAC ACCAC- AGA

GAM3321 GCCACTCATTGCCATTCGGT 74701 TTATATTACC 74702 C CA CC G ACATTACA GGAAC
GGACATTACAAAGACGGAAC CACAGAATTC GC ACT TTG ATTC GTGG AAGAC C

CAAAGAAGTCTTATATTACC CAAA || ||| ||| |||| |||| |||||
CACAGAATTCCAAAGTAGC CG TGA AAC TAAG CACC TTCTG A
A -- CT A CATTATA- AAGAA

GAM3322 TTTGTTCTTTTAATATAAAC 74716 AATAACATTA 74717 TCT TATAAAC- -
TTAATTCTACC-- GATTTA
ACAAAATAACATTAATTCTA ATTCTACCAA TTGT TTTAA ACAAAAT AACA
AACGATG T
CCAACGATGGATTTATTAAT CGAT |||| ||||| ||||||| |||| |||||||
AATATCGTTTTGCTATCATC AACA AAATT TGTTTTA TTGT TTGCTAT /
ATTGTTAATTTTGTTAAAAT TGT TTTAAAAT A TACTACTATCGTT AATAAT
TTTTAAATGTACAAG

GAM3323 ACTATTGAATGAAGACTCCA 74719 ATGAAGACTC 74720 AATG CTCC ---- A
GATTCAATAATAATTGAAAG CAGATTCAAT ACTATTG AAGA AGA TTCAAT A
GCTCTCTATCTTATGCAATA AATA ||||||| |||| ||| ||||||
GT TGATAAC TTCT TCT AAGTTA T
GTA- ATC- CGGA A

GAM3324 AGGTTCAATTTTCTCATCAT 74733 TAAAGTTATT 74734 CAA C---- ATTT-- GTT TTC
TTACTGTTGTAATTCAATCT CCGATATTTA AGGTT TTTTCT ATC ACT GTAA A
TACTAAAGTTATTCCGATAT AGAA ||||| |||||| ||| ||| ||||
TTAAGAAAAAATAACCT TCCAA AAAAGA TAG TGA CATT /
TAA ATTTA CCTTAT AAT CTA

GAM3325 TGTAACAAGTGTAACAAACA 74740 TAACAAGTGT 74741 A C CACA-- G G- AT --- T
TTAT
CAACTGTAATGATGATTATG AACAAACACA T ACAAGTGTAA AAA ACT TAAT ATG TATGTA
ACTA GCA G
TAACTATGCATTATGATACT ACTG | |||||||||| ||| ||| |||| ||| |||||| |||| |||
GCTGGTGATTATATATATAT A TGTTTATATT TTT TGA ATTA TAT ATATAT TGGT
CGT /
GAATTAGAGTAAAACTTTTT A T TCAAAA G AG AT TAG - CATA
TTATATTTGTAACA

GAM3326 GGTTTGTGGTTGTTATGTGC 74764 TGGTTGTTAT 74765 T G- TA CTTTA GG GGT
CTTTATTGTAGGGGTGTTGG GTGCCTTTAT GGT TGT GTTGT TGTGC TTGTAG GTGTTGG
T
GGTTATTATTAATGCACTAT TGTA ||| ||| ||||| ||||| |||||| |||||||
AGAGCTGTACAAGGCGATAA CCA ACA TAGCG ACATG GATATC CGTAATT A
ACACACC C AA GA TCGA- A- ATT

GAM3327 CTCACTCTGATATGTGCACC 74768 TGATATGTGC 74769 TCTG G - GTG T
GTGTGTGATTTTATCACGAA ACCGTGTGTG CTCAC ATATGT CA CC TGTGAT T
GGCTGGACATATGTTTGTGA ATTT ||||| |||||| || || ||||||
G GAGTG TATACA GT GG GCACTA /

```
                                    TTTG     G  C  AA-     T


GAM3328  GAGCGACCGTTATTGGTTTG 74779   TGACAAGACC 74780       --  TTA   GTTT     ACGC
         GAGTGACGCCCGGACATTCC       GGATTCGTTC       GAGCGA  CCG   TTG   GGAGTG   C
         TGACAAGACCGGATTCGTTC                  ||||||  |||   |||   ||||||
                                    CTTGCT  GGC   AAC   CCTTAC   /
                                       TA   CAG   AGT-    AGGC


GAM3329  ATATGTACACATATTTTAAT 74799   TATTTTAATT 74800         --  A      ATATC-   TTACTTG
         TATATCTGTTTTACTTGGAT       ATATCTGTTT       ATATGTACA  CAT TTTTAATT     TGTT     G
         TTAATAACAATACTGAATTA       TACT          |||||||||  ||| ||||||||     ||||
         AAACATGATTGTATATAT                      TATATATGT  GTA AAAATTAA     ACAA     /
                                    TA   C      GTCATA    TAATTTA


GAM3330  TTCCGTAATATCTGTTTTAT 74805   TCTGTTTTAT 74806     C    ATC     ATA   GA  -  A  C
         ATAGTGAGGGTTCACGCATG       ATAGTGAGGG       TTC GTAAT   TGTTTT   TAGT  GGG TTC CG A
         CGCGAGTCCCGACTAATGAG       TTCA          ||| |||||   ||||||   ||||  ||| ||| ||
         GACAATTACTGAA                          AAG CATTA   ACAGGA   ATCA  CCC GAG GC T
                                    T    ---     GTA   G-   T   C  G


GAM3331  GTCTATTTCCCACGACATAC 74817   TCCGTGGGAA 74818     -      ACGACATAC        AATACCCA
         TTCCGCGGAAAAATACCCAC       GACGATGGGG       GTC TATTTCCC       TTCCGCGGAAA      C
         GCTCCTTAATTTCCGTGGGA       GAAA          |||  ||||||||       ||||||||||
         AGACGATGGGGGAAATGTGG                   CGG GTAAAGGG       AGGGTGCCTTT      G
         C                          T      GGTAGCAGA        AATTCCTC


GAM3332  AAAACCGGGTCCGCGAGCGG 74900   TGGCGTGCGT 74901      C   TC   A  G  CGT  GTC
         GCCCGTCCGGTCGAGACGGT       GTGTGTCTGT       AAAA CGGG  CGCG GCG GCC   CCG  G
         GGCGTGCGTGTGTGTCTGTT       TTTT          ||||  ||||  |||| ||| |||   |||
         TTT                        TTTT GTCT  GTGT CGT CGG   GGC   /
                                    T   GT   G   G   T--   AGA


GAM3333  GGGAGAACCATTGTGTTGCC 74933   TGCCGGAGCC 74934      G   ---     GT   GGA  -  TTGA  -    T
         GGAGCCCTTTGAAGAGTGAT       CTTTGAAGAG       GGGA AAC   CATTGT  TGCC   GCC CT    AGA
GTGAT T
         TTCATCACGTCTAGTGGCCG       TGAT          ||||  |||   ||||||  ||||   |||  ||    |||  |||||
         AGGTGCGGCAATGTTTGTTG                    TCCT TTG   GTAACG  GTGG   CGG GA    TCT CACTA /
         TCCT                       G   TTT     GC    AGC   T  ----  G    C


GAM3334  TCTGTTTCTGTGTATAGACT 74942   TGTATAGACT 74943         G   AT--   TGTT    A    GC
         GTTTGAGATTGGCGCTTGGC       GTTTGAGATT       TCTGTTTCT TGT    AGAC    TGAG TTGGC  T
         CGACTCATTGTCTTACCATA       GGCG          |||||||||  |||    ||||    |||| |||||
         GGGGAACGGA                             AGGCAAGGG ATA    TCTG    ACTC AGCCG  /
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                                    G  CCAT   TT--  -   GT


GAM3335  TTTATTTGTATTTTATTAAA 74947  TCAATGATCT 74948     TTT    T  AAAA        GAAAA  T
     ATTCTCAATGATCTGAAAAG      GAAAAGGCCT      TTTA  GTATTT ATT   TTCTCAATGATCT   GGCC
C
     GCCTCGAGGCTAAGAGATTA      CGAG          ||||  |||||| |||   ||||||||||||    ||||
     TTGGGGGGTGAGTAAGTACT                  AAAT  CATGAA TGA   GGGGGTTATTAGA    TCGG G
     TTTAAA                    TTT    -  GTG-         GAA--  A


GAM3336  AATTTTATTTATAGGTTCTA 74960  TAGGTTCTAA 74961   AT---     TTC     AAAAATATTA   --  T
C     AT
     ATTCTAAAAATATTATAAAT      TTCTAAAAAT      T   TTATAGG  TAATTCT       TAAAT  GTA CGAT
ATTATAA  A
     GTATCGATCATTATAAATAT      ATTA          |   |||||||  |||||||       |||||  ||| |||| |||||||
     TGTTATAATAATTGCTATTA                A   AATATCC  ATTGAGA       ATTTA  TAT GTTA TAATATT
T
     ATTTACTAAAAATGAGAGTT                ACTAT    CA-    GTAAAAATC-   AT  C   A    GT
     AACCCTATAATATCAAAAAT
     T
GAM3337  GATCACAACAATTAGTACAG 74963  TAGCATTCTT 74964     CAACAATTAGTACAG   CCTCC   ---
 A
     ATGGCCTCCCAATATCACAT      TTCTCCTGAT      GATCA         ATGG   CAATA  TCAC T
     CGTGATTCTATTGTCAAATC      C           |||||         ||||   |||||  ||||
     ATAGCATTCTTTTCTCCTGA                CTAGT         TACT   GTTAT  AGTG /
     TC                        CCTCTTTTCTTACGA   AAACT   CTT   C


GAM3338  GGGGGAACTGGTGGTGTCCG 75002  CACCCGGTCC 75003          -  C-----      CA  CC
     GACTGGGCAATCCAGGGTCA      GAATCAAACA      GGGGGAACTGGTGG TGT    CGGACTGGG  AT
A
     CCCGGTCCGAATCAAACACC      CCCG          |||||||||||||| |||    |||||||||  ||
     CGCCAGTTCCTCC                   CCTCCTTGACCGCC ACA    GCCTGGCCC  TG  /
                                C  AACTAA      AC  GG


GAM3339  CCCCAAAGAATAAAACACCG 75014  TAAAACACCG 75015    AAA     CACCGT     TC   TACAA
     TCAACGGGTCTTTTGTACAA      TCAACGGGTC      CCCC  GAATAAAA    CAACGGG  TTTTG    A
     AAAAATCAGAGAGCCTGTTG      TTTT          ||||  ||||||||    |||||||  |||||
     TCTCTTTTTTATTCGGGG                GGGG  CTTATTTT    GTTGTCC  GAGAC    /
                               ---      TTCTCT     GA    TAAAA


GAM3340  TCCTCTCTTACTTTTCTTTA 75024  TCTTACTTTT 75025     TCT  CTTTTCTTTATT    -   AA
CTCTTCTT-----  AT
     TTTCTCTTTAAAACTCTCTT      CTTTATTTCT      TCCTC  TA        TCTCT TTAA  CT        TCTG  T
     CTTTCTGATTATCAGATTCC      CTTT          |||||  ||        ||||| ||||  ||         ||||
     AACAATCTCAGGCTTAACAG                AGGGG  AT        AGAGA AATT  GA        AGAC  /
     AGATACTGGGGA                    TC-  ----------    C   CG  CTCTAACAACCTT   TA
```

GAM3341 CGTGCCAAAGCCCCGCCGCA 75074 AGGGATGGGG 75075 AA - - GCAACGT GCTG
ACGTCTCGAGCTGCGCCATC ACTGCGGCGC CGTGCC AG CCCCG CC CTCGA C
GAGGGATGGGGACTGCGGCG G |||||| || ||||| || |||||
CG GCGCGG TC GGGGT GG GAGCT /
CG A A ------- ACCG

GAM3342 GTTGTTTTGAGCAACTGTTA 75210 TTTGTCCTGC 75211 T ACTGTT T A T
CTGAAAGAGCTTTGTTTATT GTGCTCCAGA GTTGTTT GAGCA AC GAA GAGC T
TTGTCCTGCGTGCTCCAGAC CAAC ||||||| ||||| || ||| ||||
AAC CAACAGA CTCGT TG TTT TTTG /
C GCGTCC T A T

GAM3343 TGTAATACTTTGGTGCTGTC 75233 ACTTTGGTGC 75234 TGGT- CCC TATT
CCCTTCTATTTATTTGTATG TGTCCCCTTC TGTAATACTT GCTGT CTTCTATT T
ATAGGAGTAAGCAGCTTTAT TATT |||||||||| ||||| |||||||| /
AAGTATTATA ATATTATGAA CGACG GAGGATAG
TATTT AAT TATG

GAM3344 TAACATAATGTAAACAATTA 75248 TGTAAACAAT 75249 ATG-- ATAA TT T
TATAAATTTAAAGTTTTTAA TATATAAATT TAACATA TAAACAATTAT AT AAAGTTT T
AACTTTTGTGCAATAATTGT TAAA ||||||| |||||||||| || ||||||| /
TTAAAATATATGTTA ATTGTAT ATTTGTTAATA TG TTTCAAA /
ATAAA ACG- T- A

GAM3345 TTGTTAGTTGTTTTTAATGA 75258 TGTACATATA 75259 TAAT CCAC C ---- T-
AAATTAG- GC
TACCACACAACGAGATGTTT CATTTGGAAC GTTTT GATA ACAA GAG ATGTTTT ATG
TAACTTT C
TTATGAAATTAGTAACTTTG ATTA ||||| |||| |||| ||| ||||||| ||| |||||||
CCAAGAGGTTGTACATATAC CAAAA TTAT TGTT CTC TACAAGG TAC
GTTGGAG /
ATTTGGAACATTAAACTCTT TGT- AA-- T AAAT TT ATATACAT AA
TGTAATATTTGTAAAACAAA
ACAA
GAM3346 GTCTAGCAAACTCCCTTAAA 75273 TACAGTATTT 75274 GCAAA - -- GAGA - A AA--
A
TGTTGGAGATATCGATTGAA AGATGGGTAG GTCTA CT CCC TTAAATGTTG TAT CG
TTGAAA GT T
AAAGTATACACGTTATTTTA ACAT ||||| || ||| |||||||||| ||| || |||||| ||
AATGTATGAGTACAGTATTT CAGAT GA GGG GATTTATGAC GTA GT AATTTT CA A
AGATGGGTAGACATAGAC ACA-- T TA ATGA T A ATTG C

GAM3347 GAGCCTCCGTTGGGTTTTCT 75286 TACCCCGTAA 75287 - ---- TTTCTTT - GTAC

TTGTGCCTGTACTCAAAAGG ACGGCGGGCT GAGCCT CCGTT GGGT GTG CCT T
TCATACCCCGTAAACGGCGG C |||||| ||||| |||| ||| |||
GCTC CTCGGG GGCAA CCCA TAC GGA /
C ATGC ------- T AAAC

GAM3348 ACTTCTGGCCCTCCATGGGG 75309 CAGTACCACG 75310 CCC A GG- TCCG
TGCGCGTCCGCAACTTTGCG GACATCCAGA ACTTCTGG TCC TGG TGCGCG C
CAGTACCACGGACATCCAGA AGT |||||||| ||| ||| ||||||
AGT TGAAGACC AGG ACC ACGCGT A
TAC C ATG TTCA

GAM3349 TCATAAAAAAGCTATTATCA 75326 TCATTCTTTT 75327 - CTATTATCA A AC
AATACTGTACTGAATGGATT CTCTTTTTAT TCATAAAAA AG AAT CTGT T
CATTCTTTTCTCTTTTTATG GA ||||||||| || ||| ||||
A AGTATTTTT TC TTA GGTA /
C TTTTCTTAC - AG

GAM3350 ATGTTGTAGTGTGATGGTTG 75371 TTAAAATAAT 75372 AG- GAT- TG GTGATA
TGGTGTGATATAAGAAAAAC AATAATAT ATGTTGT TGT GGT TGGT T
CAACTTAAAATAATAATAAT ||||||| ||| ||| ||||
AT TATAATA ATA TCA ACCA A
ATA AAAT -- AAAAGA

GAM3351 ATACTTGCATTAGGATTAGT 75374 GCCTTTGTTC 75375 A ACTTC C TC
CCATTCCCCAAAA - T
ACTTCTCGCCTTTGTTCTCA TCATTTCTGA GG TTAGT TCG CTTTGT TCATTTCTGA
GTTG GTGA C
TTTCTGACCATTCCCCAAAA CCAT || ||||| ||| |||||| |||||||||| |||| ||||
GTTGGTGATCATTTACACAA CT AATCA GGC GAAACA AGTGGAGGCT TAAC
CATT A
TCTCCCATTCGGAGGTGAAT A C---- A TA TACCCTC------ A T
ACAAAGACGGCACTAAATCT
ATCAAGTAT
GAM3352 ACGATGAATGAGTAATAAGA 75403 TTAGTGTTTA 75404 TA A AATCTA --------- A
TTCTATCAA
AATATGAAATCTATCTTATA ATAAAAATAT TAA AGAAAT TGA TCTTATAT ACAC TAATTA
T
TACACATAATTATTCTATCA GGGA ||| |||||| ||| |||||||| |||| ||||||
ATTTTACCAATTAGTTAGTG ATT TTTTTA ATT AGGGTATA TGTG ATTGAT /
TTTAATAAAAATATGGGAAT CC - AATCTA AAAATAATT - TAACCATTT
CTAATTAATTTTTCCTTACA
CAATCGACGT
GAM3353 AGTGTGCCGGGAAGCTGTAA 75408 AAGCTGTAAA 75409 - GGAA- AAAACGAA TAATTGA
AACGAAGGCTAATTGATACA ACGAAGGCTA AGTGT GCCG GCTGT GGC T
GAAGTGCCGGACAGCGGGTA ATTG ||||| |||| ||||| |||
TGGCAATACT TCATA CGGT CGACA CCG A

A ATGGG GG------ TGAAGAC

GAM3354 GGGAGGGCGTATGCTTGTAA 75420 GGGCGTATGC 75421 AG A - ---- AAGA ACGTTA
TTTAAGATCCACGTTACACC TTGTAATTTA GGG GGCGT TG CT TGTAATTT TCC C
CAAGGAGAAATTACAATCTG AGAT ||| ||||| || || |||||||| |||
GACAGACGTCGCCC CCC CTGCA AC GG ACATTAAA AGG /
G- G A TCTA G--- AACCCA

GAM3355 TTGTCCAAACTTCTACTTGC 75425 TCCAAACTTC 75426 C TC CCC T T
CCATTTTTATCATTTCTGAT TACTTGCCCA TTGT CAAACT TACTTG AT TTTATCATT C
GGTAAACATTCAAGTAAGTT TTTT |||| |||||| |||||| || |||||||||
TGCGCAA AACG GTTTGA ATGAAC TA AAATGGTAG /
C -- T-- C T

GAM3356 GCTCCCAATGTAACATAATG 75438 TCCCAATGTA 75439 CCCAA --- T AAATAAATGTG T
AAA A- C AA
TAAATAAATGTGACTTTATG ACATAATGTA TGTA ACATAA GT AC TTATGT TGCA
GG AGT G
TAAATGCAAGGCAGTAAGCA AATA |||| |||||| || || |||||| |||| || |||
GCTCCCAATGTAACATAATG ACGT TGTATT CA TG AATACA ATGT CC TCG /
TAAATAAATGTAACTTTATG ----- AAA T ATGTAAATAAA T --- AA C AC
TAAATGCAAGT

GAM3357 CTCATCCTCACAGTCTAGAG 75449 ATAGTACTTA 75450 -- C A -- TCC G
GGTTCCATCGCGCAAGTGAT CTCAGGATTT CTCATC CTCA AGTCT GAG GGT ATCGC C
AGTACTTACTCAGGATTTGA GAGT |||||| |||| ||||| ||| ||| |||||
GTAGATGAG GAGTAG GAGT TTAGG CTC TCA TAGTG A
AT - A AT TGA A

GAM3358 ACGGGGTTCAACTTTTACGC 75456 TATTGTGGTG 75457 T TA ---- GTA
AGTAATTTAGTAATATATAA AGGTTGTACC ACGGGGT CAACTTT CGCAGTA ATTTA A
GTAAGCTATTGTGGTGAGGT TCGT ||||||| ||||||| ||||||| |||||
TGTACCTCGT TGCTCCA GTTGGAG GTGTTAT TGAAT T
T TG CGAA ATA

GAM3359 TAGTCTGGTGGATTTTTGCA 75459 TTAGTTCTTA 75460 ------ TAAT AT---- T AT-
AAG
TTAATTCATAAAATAATCTT TACTAAAGAT T TTGCAT TCATAAA AATCTTTAGTATA
GGAG GTGT A
TAGTATATGGAGATGTGTAA TTTA | |||||| ||||||| |||||||||||||| |||| ||||
GAGGGACATTAGTTCTTATA G AACGTA AGTGTTT TTAGAAATCATAT TCTT
TACA /
CTAAAGATTTTAGGATTTGT GAAAAT TAT- AGGATT - GAT GGG
GATATATGCAATAAAAGGAT
TTTGTCAACTA

GAM3360 TTGCATATATCACAAATCCT 75467 TATCACAAAT 75468 ATA- C TCCTAA AGAACTA
CCCT
AAAATCTTTAGTATAAGAAC CCTAAAATCT TTGCAT TCA AAA AATCTTTAGTATA ATGT
C
TAATGTCCCTCTTACACATC TTAG |||||| ||| ||| |||||||||||| ||||
TCCATATACTAAAGATTATT AACGTA AGT TTT TTAGAAATCATAT TACA /
TTATGAATTAATGCAA ATTA A TA---- ACCTC-- CATT

GAM3361 GGTGTGAAACTATGAGGAAC 75474 TGTGAAACTA 75475 - TATGAGGAA- A AA
TGATGAGAAATGACTTACGG TGAGGAACTG GGTG TGAAAC CTG TGAG A
CCATGATTTTGTTTCGTCGC ATGA |||| |||||| ||| ||||
T TCGC GCTTTG GGC ATTC T
T TTTTAGTACC - AG

GAM3362 TTTTTTTATAGCGTGAAGGA 75495 TAGCGTGAAG 75496 C---------- A- TAT- A-- T
TATGATAAAAAATATAATTG GATATGATAA TTTTTTTATAG GTGA GGA GATAAA AATA
A
TTGTATTTATCCCATTCCAA AAAA |||||||||| |||| ||| |||||| ||||
TCACCTTATATGATTCTGTA AAAAAAATGTC CACT CCT CTATTT TTGT A
AAAAAA TTAGTATATTC AA TACC ATG T

GAM3363 ACGAATCATGATTTGATCTA 75506 TACATTCTCG 75507 AT- TTTG CT TTTCAG
CCATTTCAGCATTTATTGGT GGTTCGT ACGAATC GA AT ACCA C
TTATACATTCTCGGGTTCGT ||||||| || || ||||
TGCTTGG CT TA TGGT /
GCT TACA TT TATTTA

GAM3364 TGCGGGCACTGGGGACGGTG 75513 TAAATAATAA 75514 CAC ACGGTGG A TG
GTGTTGTATATGTGAATTTG ATGAGACCCC TGCGGG TGGGG TGTTGT TATG A
TAAATAATAAATGAGACCCC ATCC |||||| ||||| |||||| ||||
ATCCTGTA ATGTCC ACCCC ATAATA ATGT A
T-- AGAGTAA A TT

GAM3365 GAACCAACCGCACGAGAAGG 75557 TTGGCGGGTG 75558 AA A AGAA T GAA GAGA
CTCGCTCGGAAGACCGAGAA GCCGGTGGCG GAACC CCGC CG GGC CGCTCG GACC A
GGGAAGGTTGGCGGGTGGCC GGGT ||||| |||| || ||| |||||| ||||
GGTGGCGGGGTTC CTTGG GGCG GT CCG GTGGGC TTGG G
-- - GG-- - GG- AAGG

GAM3366 CACTACGTGTATGTAGCGGT 75562 TACATTGTGT 75563 TATGTA GAC ACCTC - A
TAC AA AT
GTACACGGACCGACCTCATC CACATAGTG GTG GCGGTGTACACG CG ATCGTG TCTA
TG CGCT CG C
GTGTCTAATGTACCGCTAAC ||| |||||||||||| || |||||| |||| || |||| ||

GATCCACCGCCGGCGTTTTA CAC TGTTACATGTGC GC TGGTAC AGAT AT
GCGG GC C
TAGAGCATGGTCACACGCAC TG---- AC- ACAC- G - TTT CC CA
GTGTACATTGTGTCACATAG
TG
GAM3367 CGTCGGGCCGGGTGTCCGCC 75586 TGCGGGGGCG 75587 G ---- TG - C A GA-- AC---
GA
CACGTGACGCCCACGCCGAG GCAGACGAGG CGTCGG CC GGG TCC G CC CGT CGCCC
GCC G
GAGGCTGCGGGGGCGGCAGA TCGG |||||| || ||| ||| | || ||| ||||| |||
CGAGGTCGGGGTGCCCGAGA GCGGCC GG CCC GGG C GG GCA GCGGG CGG /
GGGCCGGCG G AGAG GT G T A GACG GGCGT AG

GAM3368 GTGTACGGGTGCTTTATTAT 75628 TTGTATATAT 75629 TACG- T TATCAT -- AT
CATCAGCGTCATGCAGACTG AACGTACCAT GTG GGTGC TTAT CAGC GTC G
GTTGTATATATAACGTACCA GATC ||| ||||| |||| |||| |||
TGATCAC CAC CCATG AATA GTTG CAG /
TAGTA C TATAT- GT AC

GAM3369 TCGATTGCGAAAATTTAATT 75635 CATTGGATAG 75636 GA GAAA- - T- A
CATTGTATGAAAATATTTCA GGGGCAAGGG TC TTGC ATTTAAT TCA TGTATGAAA T
TGTACTTGGCATTGGATAGG A || |||| ||||||| ||| |||||||||
GGGCAAGGGA AG AACG TAGGTTA GGT ATGTACTTT /
GG GGGGA C TC A

GAM3370 CCCAAAACCAAGCCATCCAA 75708 ACCAAGCCAT 75709 AA A AA- AAAAA TTGTCA
TTT T
ACATAAAAACAATAAATTGT CCAAACATAA CCCAA CCA GCCATCCA CAT CAATAAA GA
TGT T
CAGATTTTGTTTAAGCATTC AAAC ||||| ||| |||||||| ||| ||||||| || |||
GTATCTTTATTGGAGTGGGG GGGTT GGT TGGTAGGT GTG GTTATTT CT ACG A
TGGATGGTGTGGGGTTGGG GG G GGG AG--- CTATG- T-- A

GAM3371 GTTTAAGTTCTAGATCAGGA 75747 GATCAGGAAA 75748 AA AGA- AG AGAGCAT GT
AAAGAGCATAATGTCAAAAT AGAGCATAAT GTTT GTTCT TC GAAA AAT C
TTATAATTTCGGAGAAAAGG GTCA |||| ||||| || |||| |||
ATAAAAAC CAAA TAGGA AG CTTT TTA A
AA AAAG G- AATAT-- AA

GAM3372 GTCCATTAACCGTTCTATGA 75775 TCATATGGTT 75776 C T TCT C C- C T
TCGACGCCGGTATTCTCGCA TATGCGC GT CAT AACCGT ATGAT GA GC GG A
CTCATCATATGGTTTATGCG || ||| |||||| ||||| || || ||
C CG GTA TTGGTA TACTA CT CG TC T
C T --- - CA C T

GAM3373 GCTTTCTTTCTAAAATTGTC 75784 TCTTTCTAAA 75785 TC- A CATT TCGACAC T ATATT
ATTTATCATATCGACACGAA ATTGTCATTT GCTT TTTCTAAA TTGT TATCATA GAA TGT T
TTGTATATTTAAATAGCATT ATCA |||| |||||||| |||| ||||||| ||| |||
TCTAACTTATGATATCATAA TGAA AAAGATTT AATA ATAGTAT CTT ACG /
TTTAGAAATACAAGT CAT - CT-- TCAAT-- T ATAAA

GAM3374 AGGTTTTTAGAGGAGGTACC 75800 TTTGTTGGGA 75801 TTT GTA TACC AT
GATACCCAGACATATGCAAG ACTTCTTTGG AGGT TAGAGGAG CCGA CAGACAT G
TGTTTGTTGGGAACTTCTTT CTT |||| |||||||| |||| |||||||
GGCTT TTCG GTTTCTTC GGTT GTTTGTG C
--- AAG ---- AA

GAM3375 ACACCGCACTTTGTTTGACT 75811 TAGATAATAG 75812 - GC T A- - G- A TG
GTATTAGTACCACATGGAGT CAGCACATGC AC ACC ACTTTGT TG CTGT ATTA TACC CA G
TGGGTAGATAATAGCAGCAC AGAG || ||| ||||||| || |||| |||| |||| ||
ATGCAGAGTAGGTAGT TG TGG TGAGACG AC GACG TAAT ATGG GT A
A A- T AC A AG - TG

GAM3376 GTGGTAACACTGTGTCCAAA 75824 CGACTGGTGG 75825 AA G T A- - TC
GTGTAGTTCACCACTGCGAC TAGAGTGCAG GTGGT CACT TG CCA AGT GTAGT A
TGGTGGTAGAGTGCAGCCAC CCAC ||||| |||| || ||| ||| |||||
CACCG GTGA AT GGT TCA CGTCA /
AC G - GG G CC

GAM3377 CATTGCTCTGTTGTAAACTA 75857 TAAGTTAAAC 75858 ---- TTGTA- ATATATA AA- AAAT AGGGA
TATATAAGTTAAACCAAAAT CAAAATTCGC CATTG CTCTG AACT AGTT ACCA TCGC G
TCGCAGGGAGACAAGGTGAC AGGG ||||| ||||| |||| |||| |||| ||||
GGTGGTGAGAACTCAGTTGA GTGAC GAGAC TTGA TCAA TGGT AGTG /
GAGTCAGAGAATACAGTG ATAA TGAGAG C------ GAG GGC- GAACA

GAM3378 CTTGGTTGTGGTGATTTCAT 75864 TGTTGCTATA 75865 - TG T TTCT T--- -- TT TC
TCTCATTATTGTTGTTTTCT CACCGAG CTTGGT TGTGG AT TCA CA TATTGT TGTTTTC TCCG T
TTCCGTCTTGCGGATGAAGA |||||| ||||| || ||| || |||||| ||||||| ||||
TGTTGCGATGCGGTTGTTGT GAGCCA ATATC TG GGT GT GTAGCG GTAGAAG AGGC /
TGGTGTTGCTATACACCGAG C GT T TGTT TGGC TT T- GT

GAM3379 AGATGATCTTTTTGTTCTTC 75871 TGTGCAGGGC 75872 TCTTT --- AT- ATGAT TG
TG--- CG
TGGTTCATTTCCTATGATTG ATGCGGGGAA GA TTGTTCT TCTGGTTC TTCCT TGTT GC
CTGAC A
TTTGGCTGCTGACCGACGCG TCAG || ||||||| |||||||| ||||| |||| || |||||
TCAGGATGTGCAGGGCATGC CT AATAGGG AGGCCAGG AAGGG ACGG CG
GACTG C
GGGGAATCAGGACCGGACAC TT--- CAC ACT GCGT- GA TGTAG CG
GGGATAATTTCATCT

GAM3380 AGAACACGCGGTCCCCTGTG 75895 CCCCTGTGGT 75896 A GG---- GG TT TT TT
GTGTTTTTGGTTATTTTTAT GTTTTTGGTT AGA CACGC TCCCCTGT TGTT TGG ATTT A
TAAATCTCGTCGACAAACAG ATTT ||| ||||| |||||||| |||| ||| ||||
GGGGAAAGGGGCGTGGTCT TCT GTGCG GGGGGACA ACAG GCT TAAA /
G GGGAAA A- CT C- TT

GAM3381 GATTGATAACCTTGATGTAG 75918 TGTAGCAAGC 75919 A T A GC A - AGAG AG
CAAGCCAACCTTTGGAGAGT CAACCTTTGG GATTGATA CCT G TGTA AAGCCA CCTTT GG
TTTG G
TTGAGGTACAGGGACCCAAG AGAG |||||||| ||| | |||| |||||| ||||| || ||||
AGGATGGTTTTATGCACCAG CTGATTAT GGA C ACGT TTTGGT GGAGA CC GGAC /
GTATTAGTC - - C AT A A CAG- AT

GAM3382 CGCGACCGGCCAAAAGACCG 75940 TCACAGCGCT 75941 GA- AAAA C- ----- C G
CGCGGCGCCCGTCGGGCCCT CGTCGCGCGG CGC CCGGCC GAC GCGC GG GCCC T
CACAGCGCTCGTCGCGCGGC CCGG ||| |||||| ||| |||| || ||||
CGGGCGGCG GCG GGCCGG CTG CGCG CC CGGG /
GCG CGCG CT ACACT - C

GAM3383 TTGTTATATAGACCCACCAC 75959 TATATAGACC 75960 TT CCC CA G T
ATAGTGAGATTTTATCTCGG CACCACATAG TTG ATATAGA ACCA TA TGAGAT T
TGACTGGTTTTATGTTTCAA TGAG ||| ||||||| |||| || ||||||
AAC TGTATTT TGGT GT GCTCTA /
TT --- CA G T

GAM3384 TTTGTCGTGTGCTTTTCGTG 75969 GTGCTTTTCG 75970 - GT----- T - - T CGC
TCTCGGGGCGGTTTCCGCGA TGTCTCGGGG TTTGT CGT GCT TTCGTGTCT CGG GGCGG
TTC G
CCGAACCCGTCGCCGCGGAC CGGT ||||| ||| ||| ||||||||| ||| ||||| |||
GCGAGCAGCCGGATCAACGT GAACA GCA CGA GAGCGCAGG GCC CTGCC AAG /
ACAAG T ACTAGGC C C G C CCA

GAM3385 GTCCAATATTTTATATAAAA 75973 AGACGTTGTC 75974 - TTATATAAAAAC CTA GTTGT
TC TAAT
ACATTTTATTTCTAGACGTT AGAAAATCCT T CCAATATT ATTTTATTT GAC CAGAAAA
CTG A

GTCAGAAAATCCTGTAATAT GTAA | |||||||| |||||||| ||| ||||||| |||
TTTTAGTTTTTTTGGTTGTG A GGTTATAA TGAAATAAG TTG GTTTTTT GAT /
AATAAAGTATCGCCCTAATA T TAATCCCGCTA- TG- ----- T- TTTT
ATATTGGTAC

GAM3386 GAGTCTGCGCTGCGGCGGCG 75990 TCTGCGCTGC 75991 C -------- C - - TA
CTCTTTATACTGGGCGGACG GGCGGCGCTC GAGT TG CGCTGCGG GGCG CT CTT T
CCCCCGCAGCGGCAAAACAC TTTA |||| || |||||||| |||| || |||
ACACTC CTCA AC GCGACGCC CCGC GG GGG A
C ACAAAACG C A C TC

GAM3387 TCGCTTTAAATACGGACTGA 75997 GAGTGCCAAA 75998 G TAAATAC GAAA AGGG T
AAGGAGGGCCTTCTACGGAA GTCTATGAGG TC CTT GGACT GG CCTTC A
GGAGTGCCAAAGTCTATGAG GA || ||| ||||| || |||||
GGA AG GAG TCTGA CC GGAAG C
G TA----- AA-- GTGA G

GAM3388 GTGCGGAGCGGCGGACATAA 76049 TAGTGTGCCC 76050 G C - AA- - ------ T A
GGCATCTGGAGCAGCTGTTC CCGCTGCGTA GTGCG AGCGG GG ACAT GG CA TC GGAGC
G
CTGAATACGTTGACCATAGT T ||||| ||||| || |||| || || || |||||
GTGCCCCCGCTGCGTAT TATGC TCGCC CC TGTG CC GT AG CCTTG C
G C G ATA A TGCATA T T

GAM3389 CACGCAGATATAAGGGCACT 76067 TAAGGGCACT 76068 ATATA - - AA- C- A
GGAACAGCTGCTACTAGGCA GGAACAGCTG CACGCAG AGGGCAC TG G CAG TGCT C
CATTGAAGCTCGTGTGTCCT CTAC ||||||| ||||||| || | ||| ||||
CGCTGCGTG GTGCGTC TCCTGTG GC C GTT ACGG T
GC--- T T GAA AC A

GAM3390 GTGCAGTTTACTTTTAATCT 76113 TCTACATATT 76114 - TTT AT- T- TT GT- TA
ACATATTTTACTGTGTTATT TTACTGTGTT GTG CAG ACTTTTA CTACA ATT ACT GT T
TATTTAAGTTTAATTTTGTA ATTT ||| ||| ||||||| ||||| ||| ||| ||
GTTGTAAAAGTTGTTTGCCA CAC GTT TGAAAAT GATGT TAA TGA TA /
C C TGT GTT TT TT ATT TT

GAM3391 GGAGGAGCCATTCCAACACC 76132 TCCAACACCG 76133 GC-- T AA -- G T CAG TT
GGAGCTGCCAGCGTGGTTGT GAGCTGCCAG GGAGGA CAT CC CACC GGA C GC CGTGG
G
ACCATGAGTGCTGTCCGAGG CGTG |||||| ||| || |||| ||| | || |||||
TGCGGGTATGAATATTCTCT TCTCTT GTA GG GTGG CCT G CG GTACC /
ATAA T GC AG - T TGA AT

GAM3392 CATAGTTTTCTGTATTAGAT 76139 TATTAGATAG 76140 - TA G T TTTCAATTCC T TT

AGTACGCTTTCAATTCCAGT TACGCTTTCA CATAGTT TTCTG TTA ATAG ACGC AG GTGG
A
GTGGTTATACCACCTTGTGT ATTC ||||||| ||||| ||| |||| |||| || ||||
CTATGTAAGTTAGAGTGGCT GTATCGG GAGAT AAT TATC TGTG TC CACC /
ATG T TG G - T--------- - AT

GAM3393 GAGTATGCGCAACTAGATTT 76144 ACTAGATTTT 76145 A CG AACT TT AA - CT
TAATGCTACTAATTGGACAG AATGCTACTA GAGT TG C AGA TT TG CTA A
AAGCTTCTTGGTACAAACTT ATTG |||| || | ||| || || |||
TTCA AC G TCT GA AC GGT /
A AT GT-- TC AG A TA

GAM3394 GCCTAGACATCAGACCGCGC 76150 CGTCACAGCC 76151 TA ATCA GCGCA T T T C
AGGCTGTTGTTGTGTTGCTT ATATAGGTTA GCC GAC GACC GGCTGT G TGTG TG T
GTACCACGTCACAGCCATAT CGTT ||| ||| |||| |||||| | |||| ||
AGGTTACGTTCGGGT TGG TTG TTGG CCGACA C GCAC AT T
GC CA-- ATATA - T C G

GAM3395 TTTCCGTCGATCTGGAAGCT 76159 TCCTTCACCA 76160 C T CTG---- CT TA
TGTGTTCTAAATGAATATAT AATATCGCAG TTTC G CGAT GAAG TGTGTTC A
CCTTCACCAAATATCGCAGA AAG |||| | |||| |||| |||||||
AG GAAG C GCTA CTTC ATATAAG /
A - TAAACCA CT TA

GAM3396 ATTTTCTTTGTTCTTTTATG 76192 TCTTTGTTCT 76193 C TT TATGT AAAA
ACAAAC A A
TTTATTTTGTTTGTCATTTA TTTATGTTTA TTT TTTG CTTT TTATTTTGTTTGTCATTTAA CA
TTT TC A
AAAAACAACAAACTTTATCA TTTT ||| |||| |||| |||||||||||||||||| || ||| ||
AATGACAAACAAATGACAAT GGA AGAT GAAG AATGAAACAAACAGTAAATT GT
AAA AG A
TAAATGACAAACAAAGTAAT A TT TGAT- AACA AAAC-- C T
AGTGAAGTTTAGAAAGGAT

GAM3397 TCTACGTATCTCGTCGTCCA 76212 TTTCTAGACG 76213 AC TCT GTCC TTTTATAT
ATATTTTATATAAAAACATT TTGCCAGA TCT GTA CGTC AATA A
TTATTTCTAGACGTTGCCAG ||| ||| |||| ||||
A AGA CGT GCAG TTAT A
C- T-- ATCT TTTACAAA

GAM3398 CCCGTCGGTCGGAAGCGAGT 76288 CTGCATGCCG 76289 - T AA- AGT TTCA- T
GCCCTTCAAGCGTGTCCGCT TCGGATGGG CCCGTC GG CGG GCG GCCC AGCG G
CCTCTGGGCTGCATGCCGTC |||||| || ||| ||| |||| ||||
GGATGGG GGGTAG CT GCC CGT CGGG TCGC T
G - GTA --- TCTCC C

GAM3399 GGTTCTCACAAAAATATGCA 76351 TGCATGGAAG 76352 TCA AAAA TCT TG G
GATCTCTATGAGTGTTGTAG TGGTTGGGCC GGTTC CA TATGCAGA CTA A T
CTCTGCATGGAAGTGGTTGG ||||| || |||||||| ||| |
GCC CCGGG GT GTACGTCT GAT T /
TTG GAAG C-- GT G

GAM3400 GCTGCAAAGATCAGTGGCTT 76511 TTTACATTGG 76512 T C- - TTTCTAACT TAT
TTCTAACTGCAACTTATGGA CTTACTATAT GC GCAAAGAT AGTG GCT GCAACT G
ACAGTTGTTTACATTGGCTT CTTT || |||||||| |||| ||| ||||||
ACTATATCTTTGTGC CG TGTTTCTA TCAT CGG TGTTGA G
- TA T TTACATT-- CAA

GAM3401 TAGTACATTACTTAATATCC 76515 TCCGTAAGTC 76516 ACTTA- C TA CTTT T-
ATCA AA
GTAAGTCTTTTTAGTTCATT TTTTTAGTTC TAGTACATT ATAT CG AGT TTAGT CATTTTTA
ACT C
TTTAATCAACTAACCAAGTA ATTT ||||||||| |||| || ||| ||||| |||||||| |||
ATAAAAATGTCATTAATGCT GTTATGTAA TATA GC TCG AATTA GTAAAAAT TGA
/
CGCGTATATGAATGAAATGT AGTAAG T GC T--- CT AA-- AC
ATTG

GAM3402 CCCTTCGCCGACGCCGTGGC 76521 TGTGGGCTAT 76522 TTCG-- AC A T-- TTC
ACCTGGTTCACCCCCTGTGG GGCCGGAATA CCC CCG GCCGTGGC CC GG A
GCTATGGCCGGAATATTGGG TTGG ||| ||| |||||||| || ||
GGG GGC CGGTATCG GG CC /
TTATAA -- - TGT CCC

GAM3403 TTATTATTTGCTATTCTTTC 76529 ATGATATTGA 76530 GC--- TCTT- AT A
AATATATTTAATATTAATGA TAAATATAAA TTATTATTT TAT TCAATAT TTA T
TATTGATAAATATAAAAAAA AAAA ||||||||| ||| ||||||| |||
AATGATAA AATAGTAAA ATA AGTTATA AAT A
AAAAA TAAAT GT T

GAM3404 CAGGTCAACAAAATAATTTG 76539 TGAAATGTTG 76540 ACAAAATAA TG AT--
AAATCGCTGT- - AA
AAATGTTGGAGAAATCGCTG GAGAAATCGC CAGGTCA TT AA GTTGGAG ACTA
CA A
TACTACAAAATATGCTAGTT TGTA ||||||| || || ||||||| |||| ||
TATTTTTATGCTTCAGCTCT GTTCGGT AG TT CGACTTC TGAT GT /
GTTTGGAAGTGGCTTG GA------- GT GTCT GTATTTTTATT C AT

GAM3405 GTGAGAAACAAAGACAAAGC 76551 TATAATATCA 76552 AAACAA - A GA GAC TCGTT
A CAC

GAATACGACAAATTCGTTTA TTTAAGTATA GTGAG AGA C AAGC ATAC AAAT TATTA
ACGT A
TTAAACGTCACATTTACGTA GTTT |||||| ||| | |||| |||| |||| |||||| ||||
TAATATCATTTAAGTATAGT CACTC TCT G TTTG TATG TTTA ATAAT TGCA /
TTCGTTCTGCCAACTCAC AACCG- T C A- AA- CT--- A TTT

GAM3406 CTGCTCGGATGGCGACCGTG 76555 GACCGTGCAC 76556 CTC -------- T ACTAC CC
CACTACTCCCGCCGACCTGG TACTCCCGCC CTG GGATGGC GACCG GC TCCCG G
GACCCCGCCGGTCACCCTCA GACC ||| ||||||| ||||| || ||||| CGTCGTCCCCCAG GAC CCTGCTG CTGGC CG AGGGT A
CC- CACTCCCA - CCCC- CC

GAM3407 CGAAAAACCGAGCAATAGGA 76569 TATGGTTCGA 76570 CC - A AGCAC- GT AC----
ACAAA ACT
GCACTATGGTTCGAGAAGAC GAAGACATTA GA GCAAT GG TATG TCGAGAAG
ATTATAAG CTC A
ATTATAAGACAAACTCACTA TAAG || ||||| || |||| |||||||| |||||||| ||| GATGGAGGGCTTATAATTAT CT CGTTA CC ATAC AGTTCTTC TAATATTC GAG
G
AAGCTTCTTGACATAATCTA AA G - AATCTA -- GAATAT GG--- GTA
ACCATTGCGTCAAAATTTCG

GAM3408 AACACTTTGGTGTGATTCAT 76574 TATGTAATGT 76575 TTTG ATTC TACAACC TG --
AATATC--- T
TTTACAACCATGATTATATG AATATCAATA C GTGTG ATTT A ATTATAT GTAATGT
AATA A
TAATGTAATATCAATATAGT TAGT | ||||| |||| | ||||||| ||||||| |||| TATTTAAAAACTCACATTAT G TACAC TAAA T TGATATA TATTACA TTAT G
CTATATAGTTGTTAATCTTA TCTA CCT- TTCTAAT GT TC CTCAAAAAT T
AATTCCCACATATCTGTGTT

GAM3409 GGGTCAGAGGGCTGCTTTGA 76581 TCCAGGAGAG 76582 CAGA G GA G
TGGGGTCAGGATGTTGGCTC GCCTGTTCAC GGGT GGGCT CTTT TGGGGTCAG A
CAGGAGAGGCCTGTTCACCC CC |||| ||||| |||| |||||||||
CCCA TCCGG GAGG ACCTCGGTT T
CTTG A -- G

GAM3410 CGAAGTGGAACTCCACCACT 76833 TGAAATGAGA 76834 GA CA G CAA AAACATGCTTCT
G ACAC C AG
GATCAAATCGGGAAACATGC GTGGAGTGAA ACTCCAC CT AT ATCGGG GT TTGT
TG CCCGG C
TTCTGTGTTGTACACTGCCC CGGC ||||||| || || |||||| || |||| || ||||| CGGAGCCCACCGGGTTAACA TGAGGTG GA TA TAGCTC CG AACA AT
GGGCC C
AGGCTATTCCACCAGCTCGA G- A- G AAG GACCACCTTAT- G ---- T AC
TGAAATGAGAGTGGAGTGAA
CGGCCG

GAM3411 CGCCAAGACCTTTTCACAGC 76874 GCAGTGCCGT 76875 - CTTTTCACA TTA CACATC
ACTTTATTGTCACATCATCA CATTGGTG CGCCAA GAC GCACT TTGT A
CACACAGCAGTGCCGTCATT ||||||| ||| ||||| |||| /
GGTG GTGGTT CTG CGTGA GACA /
A C-------- C-- CACACT

GAM3412 TGCCCACTCCTCCATGGTGA 76903 CCTCCATGGT 76904 CC- TCCT GATATAAAGAC
ACTT
TATAAAGACCACCCACTTCC GATATAAAGA TGC AC CCATGGT CACCC C
TTCGGGTGAGCCCCTAAGCC CCAC ||| || ||||||| ||||| /
ATGGTTGTACTGCA ACG TG GGTACCG GTGGG /
TCA TT-- AATCCCCGA-- CTTC

GAM3413 ATGATACTTTTATTAATTCT 76935 TCTAATTGGA 76936 T AATTCTTCGTTCT- A -
TAACAA CT
TCGTTCTCTAATTGGATTTA TTTAACAACG ATGA ACTTTTATT CTA TTG GATT CGAT
T
ACAACGATCTTTGGTCGCAA ATCT |||| ||||||||| ||| ||| |||| ||||
TCACAACTAGCTTTTACTTG TATT TGAAAATAA GAT AAC CTAA GCTG /
TCTGAATAAAAGTTTAT - GTCTGTTCATTTTC C A C----- GT

GAM3414 TTAAATATTTAGTTTGATAT 76940 TTAATATTAT 76941 AA TT T TT TTGTA
TTTTGGTTTGTATAATTGTA ATTGTTTATC TT ATA TAGT TGATATT TGGT T
TTATTAATATTATATTGTTT AGG || ||| |||| ||||||| ||||
ATCAGG GG TAT GTTA ATTATAA ATTA A
AC TT T TT TGTTA

GAM3415 TTAGAATTAGGACACCGGAA 76946 TAGGACACCG 76947 TAGG GGAA AAC AAGA
GTGGAACGCCTAAGAGAGCG GAAGTGGAAC TTAGAAT ACACC GTGG GCCT G
AGGCCCGCGGTGTAGGTTTT GCCT ||||||| ||||| |||| ||||
GA AGTTTTG TGTGG CGCC CGGA /
GA-- ---- --- GCGA

GAM3416 GTTATAGCTGGGCACACTTG 76958 TAGCTGGGCA 76959 - GCACAC - AC
CGGTTTCCGAACGCAGTCGG CACTTGCGGT GTTAT AGCTGG TTGCG GTTTCCGA G
AGATACGTAGTCAGCTAGTA TTCC ||||| |||||| ||||| ||||||||
GC CGATG TCGACT GATGC TAGAGGCT C
A ------ A GA

GAM3417 GTAACGAATGCTCGTGTACT 76984 TACGTAGCGT 76985 CGA - CT AA T- CC T
TTATAATTGCATGCCCGATT GTTTTAC GTAA ATGCT CGTGTA TTAT TTGCA GC GAT A
ACAATCTGTTCTGTAAGAAT |||| ||||| |||||| |||| ||||| || |||
AATTATACGTAGCGTGTTTT CATT TGCGA GCATAT AATA AATGT TG CTA C
AC TTG T T- AG CT T- A

GAM3418 GTATAGAAGAGACGCAGTCA 76987 TAGAAGAGAC 76988 A ACT C CC TTGT CACACTAT
T- CT A
ACTTGCCGGTGCCGTGAAAT GCAGTCAACT GTCA TGC GGTG GTGAAA CTC GA
GTTTTTA GTTAC A
TGTCTCCACACTATGATGTT TGCC |||| ||| |||| |||||| ||| || ||||||| |||||
TTTACTGTTACAAGGTAATT CAGT GTG TCAC CACTTT GAG CT CAGAAAT
TAATG /
AAAGACCTTCGAGTTTTTCA - --- T CT TT-- -------- TC -- G
CTCCACTTGTGTGACGCTCC
TTCGATTAT
GAM3419 GAAAAATGTAGTTACAATGT 77010 TACGTTTTAC 77011 TAGTT A --- TTAG
AAGTGTTTTAGTTTATGATA ATGTTATTTT GAAAAATG ACA TGTAA GTGTT T
CGTTTTACATGTTATTTTTC TC |||||||| ||| ||||| |||||
CTTTTTAT TGT ACATT CATAG /
----- - TTG TATT

GAM3420 AAGTATTATATGTTTCCTAT 77022 TAGTGTAATA 77023 T- TTCC TG GAG C
GTGAGTGAGGCCATGCCTCG TATATTTACT AAGTA TATATGT TA T TGAGGC A
TTAGTGTAATATATATTTAC T ||||| ||||||| || | ||||||
TT TTCAT ATATATA AT G GCTCCG /
TT ---- GT ATT T

GAM3421 AAAGTATTTACTATTCTGCA 77036 TCTGCAAGGG 77037 T TTCTGC AGT C
AGGGAGTGAGGACGCATCCT AGTGAGGACG AAAGTAT TACTA AAGGG GAGGA G
CCAACCTTTTAGTACGTACT CATC ||||||| ||||| ||||| |||||
TT TTTCATG ATGAT TTTCC CTCCT C
C ------ AAC A

GAM3422 CGCCGACAAGACCTCAGCAT 77046 TTACTAGCCG 77047 CAAG - --- C - ATGG
GGCTCGGAGGCTATGGATCT TGACCTTGAC CGCCGA ACC TCAG CATGGCT GG AGGCT
A
TGAGCTTACTAGCCGTGACC GGTG |||||| ||| |||| ||||||| || |||||
TTGACGGTGGCTTTGGCG GCGGTT TGG AGTT GTGCCGA TC TTCGA T
TCGG C CCA - A GTTC

GAM3423 GCTAATATTCCAGTAAATAA 77050 TCCAGTAAAT 77051 T ---------- A CT - A- CTT
AACTTTTATGAACACTTGTA AAAACTTTTA GCTAATA TC CAGTAAAT AAA TTTAT GA CA
G
ATGGCTCTGTAAATTTTTCA TGAA ||||||| || |||||||| ||| ||||| || ||
TTTACTGCACTTAAATTTGA TGGTTGT AG GTCATTTA TTT AAATG CT GT /
CTGTTGGT C TTTAAATTCAC C TT T CG AAT

GAM3424 TTATTGGTCGCTAAGTTTAT 77074 TTGGTCGCTA 77075 T --- A TATCCCTAA GT C

CCCTAATTGTCACGCGTGGT AGTTTATCCC TTA TGGTC GCTA GTT TT CA G
AAAAACAACAACATAGTCAA TAAT ||| ||||| |||| ||| || ||
GATCGTTAA AAT GCTAG TGAT CAA AA GT C
T AAC A CAACAAA-- TG G

GAM3425 GTGTCTAATGGTGGAAGCGT 77080 TCTAATGGTG 77081 GAA ---- - CC ---- G AG CG AC
GGCACTGGCCGAAATGATAT GAAGCGTGGC GTG GCGTG GCA CTGG GAAATGAT ATATT CGTAT AG CG A
ATTGCGTATAGAGCGCGACA ACTG ||| ||||| ||| |||| |||||||| ||||| ||||| || ||
AACGAATTAGATGCGAATGT CAC CGTAT TGT GATT TTTTACTA TGTAA GCGTA TT GC /
GAAGATCATTTTTATTAGAT ATC ACAA A AT GAAG - GA AA AA
GTAACATATGCCTACACCAA
TAGTAC
GAM3426 CCGTGACATTTGACAGACCT 77091 TTTGACAGAC 77092 TGA TTT G ---------- T
GGAATTGTTATTCTGATATA CTGGAATTGT CCG CA GACA ACCT GGAAT G
TAGTGGGTGTGTCTGGCCGG TATT ||| || |||| |||| |||||
GGC GT CTGT TGGG TCTTA T
CG- --- G TGATATATAG T

GAM3427 CAACATACATAATGTGCATG 77094 TAATGTGCAT 77095 C A-- C GAA A TCAG CTG
CGAAACCACTTTTTCAGTGT GCGAAACCAC CAACATA AT ATGTG ATGC ACC CTTTT TGTACG A
ACGCTGACATTGTGCAACAC TTTT ||||||| || ||||| |||| ||| ||||| ||||||
GGAGGGGTAGCATCTACATA GTTGTAT TA TACAT TACG TGG GGAGG ACGTGT /
CAATATATGTTG A ACA C A-- - CACA TAC

GAM3428 CTAATAAGTGGAAGCCAATT 77101 TGGAAGCCAA 77102 ATAAG- AAG ATTAAG AAGCCA
AAGTAGAAGCCAATTAAACC TTAAGTAGAA CTA TGG CCA TAG A
TAATAAGTGGAAGCCAATTA GCCA ||| ||| ||| |||
AGTAG GAT ACC GGT ATC /
GAATTA GAA GAATA- CAAATT

GAM3429 GGCTTCTACTTAATTGGCTT 77140 TAATTGGCTT 77141 - --- CTT CTT TTAATT TCT--- T CT
CCACTTATTAGGTTTAATTG CTACTTAATT ACTTAAT TGG CCA ATTAGGT GGCT ACTTAAT GG T
GCTTCTACTTAATTGGCTTC GGCT ||||||| ||| ||| ||||||| |||| ||||||| ||
CACTTATTAGGTTTAATTGG TGGATTA ACC GGT TAATTCA TCGG TGGATTA TC C
CTTCTACTTAATTGGCTTCC T TTC TTC --- TCT--- TTAATT T AC
ACTTATTAGGTTTAATTGGC
T
GAM3430 CCGTGCCTTATACATCACCC 77151 TATGTTCGTG 77152 T T TCACCCACCCC CT CAGT

ACCCCCGCTCATAATTCAGT ACGTCTTTGT CCG GCCT ATACA CG CATAATT C
CTTTAAATTATGTTCGTGAC ATCA ||| |||| ||||| || |||||||
GTCTTTGTATCAGGCTCGG GGC CGGA TATGT GC GTATTAA /
T C TTCTGCAGT-- TT ATTT

GAM3431 GGCCGTTCGTATTATAGCAT 77155 TAGCATTGGG 77156 T TATTA CAT------ A -- - AC---- - CATCTTC
TGGGACTCGCTGTTACTGCC ACTCGCTGTT TCG TAG TGGG CTC GC TGTT TG CCCT A
CTCATCTTCACATCCACAAG ACTG ||| ||| |||| ||| || |||| || ||||
GGACACATCTAGACACGTAG GGC ATC ACCC GAG TG ACAG AC GGGA C
GAGACCCATCACATTCTCTA - TTTCC TCTTACACT A GA C ATCTAC A ACACCTA
CCTTTCGGCGGCC

GAM3432 GACGATAACTTGATTTCGAA 77167 TAACTTGATT 77168 CGA TACC ---------- T TAAATA
ATTACCCATGGAGATACTTT TCGAAATTAC TGATTT AAT CATGGAGAT AC TTATTACTCCAT A
ATTACTCCATTAAATAATTT CCAT |||||| ||| ||||||||| || |||||||||||
ATCATGGAGTGATAATGTCC GCTAAA TTA GTACCTTTG TG AATAGTGAGGTA /
TGTTTCATTTGTTTCCATGA ACA TACA TTTACTTTGTCC T CTATTT
CATATTACAAAATCGATTCC
GTC
GAM3433 CGGCGCTTTGTCTAGCCCTC 77173 TAGCCCTCTT 77174 TT CT CTT G T
TTAGTGGGTATTGTTACCGG AGTGGGTATT CGGCGCT GT AGCCCT AGT GGTA T
CTGGGGTTTTATTGGCGTTG GTTA ||||||| || |||||| ||| ||||
GTTGCGG TA TTGGGG TCG CCAT G
T- TT --- G T

GAM3434 TACAGCCACGTTTACTAGCG 77177 TAGCGGGACT 77178 GCC TTA C-- TTAT A
GGACTTATAAGTGAAATCAT TATAAGTGAA TACA ACGT CTAG GGGAC AAGTG A
TTTATTGTTCTATATTAGAT ATCA |||| |||| |||| ||||| |||||
TACGTAAATGTA ATGT TGCA GATT TCTTG TTTAC A
AAA TTA ATA TTAT T

GAM3435 ATGATGGCGAACCAACAGTC 77183 CTTGTCTTCG 77184 AACAG ---- - TTTTTTTTAA T TTTTT AT
CGAGTGTCCCGTTTTTTTTT GCATATGGAG CC TCC GAGTGTC CCGT GCTGG GGAT GCTTA A
AAGCTGGTGGATTTTTTGCT ATGC || ||| ||||||| |||| ||||| |||| |||||
TAATACATAAGCTTGTCTTC GG AGG TTCGTAG GGTA CGGCT TCTG CGAAT /
GGCATATGGAGATGCTTTAG CA--- GGAT A TA-------- - TT--- AC
GGGAACGGTCGTCCTCGT

GAM3436 TTCAACTTATTAGGTTGTGA 77195 TACCGGAGTC 77196 A - - TTGT AA T
CTCCAATACCATTTTTATGG CTCCGTAATA TTC ACT TATTA GG GACTCC TACCAT T
TACCGGAGTCCTCCGTAATA TAGT ||| ||| ||||| || |||||| ||||||
TAGTCGAA AAG TGA ATAAT CC CTGAGG ATGGTA T
C T G TC-- CC T

GAM3437 CTAGGCAGAGCCGGCGGGTA 77199 AGAGATCCGT 77200 CAGA C---- T - ------- C
CAG CAC
CATTTTTTCGTCAGACACGG TTTACAAAAT GCCGG GGGTACATTTT TCGT CA GA
ACGGGTC GC C
GTCCAGGCCACCTACAGCAG TGCA ||||| |||||||||| |||| || || ||||||| ||
AGATCCGTTTTACAAAATTG CGGCC TCTATGTAAGA GGCA GT TT TGCCTAG
CG T
CACGGCAGAATGTATCTACG AAA- AAGCA C C TAAAACA T AGA ACA
AACCGGCAAAACTAG

GAM3438 CGAGGACGGCGAGGCGTCTG 77212 TTTCTCTGCT 77213 - TCT T TTAAA T - TGT G
TTAAAAA
CGTGTTAAACGGCTGTACGC GTCCGGTCGC GGCGAGG CG GCG G CGGCTG AC GCGGGG
GAT TGCTT A
GGGGTGTGATGTGCTTTTAA CTGC ||||||| || ||| | |||||| || |||||| ||| |||||
AAAACTGGCTCTAAGTAGTC CCGTTCC GC CGT C GCTGGC TG CGTCTC CTG
ATGAA C
TTTCTCTGCTGTCCGGTCGC A C-- C ----- C T TTT - TCTCGGT
CTGCCCGACCTTGCCGTCTT
CG
GAM3439 TCTAAATTTCGTGTCGCGAT 77234 TGGATAGACA 77235 AAT--- CG GCGATA GG
ACGGTAAGGGTAGTTACTGG TAAATCAAAA TCTA TT TGTC CGGTAA G
ATAGACATAAATCAAAATAG TAGA |||| || |||| ||||||
A AGAT AA ACAG GTCATT T
AAAACT AT ATAG-- GA

GAM3440 GGAATTTTTCTATTTTGATT 77243 TCTATTTTGA 77244 TCT ATTTA TATCCA-- CT
TATGTCTATCCAGTAACTAC TTTATGTCTA GGAATTTT ATTTTG TGTC GTAA A
CCTTACCGTATCGCGACACG TCCA |||||||| |||||| |||| ||||
AAATTTAGAGTTTC CTTTGAGA TAAAGC ACAG CATT C
TT- ----- CGCTATGC CC

GAM3441 CACACACTGGTGACAACCTG 77265 TACTCTGGTC 77266 AACCT TTCACTGCCATA--- A A
TAT AC A AA-- A
CATTCACTGCCATACGGAGG CCGGACCTAC C GCA CGG GGG AG TCCG GGA
CCA AGC T
GAAGTATTCCGACGGAACCA CCCT | ||| ||| ||| || |||| ||| ||| |||
AAAGCATTTGCTACTCTGGT G CGT GTC CCC TC AGGC CCT GGT TCG T
CCCGGACCTACCCCTGACAT CGTC- CTACACATCCATACA - A C-- -- - CTCA T
ACCTACACATCTGCCTGCGT
TGCTAGTTTTG

GAM3442 AAATACCAATGACTGTCACC 77291 CCCCCGTACT 77292 CCA - CAC C CCCAAG
CCCCCGTACTATT ACC G AG
CCTACCCCAAGCCACGCCCC ATTAGACCAG ATGA CTGT CC TAC CCACG AG
AG GTG T
CGTACTATTAGACCAGGGTG GGTG |||| |||| || ||| ||||| || || |||
AGTAACCACGCTATCCTTTA TGCT GACA GG ATG GGTGC TC TC CAC A
AAAACCCATACGTGGAGTTT ATG C AAT A TTTGA- ATACCCAAAAATT CTA G
CA
GTAAGGTAAACAGCTCGTGT
ATATTT
GAM3443 TGAGTGTTGTGTGTACCTAT 77308 TGGGAAAAAA 77309 GT G A-- - A AGGC
TTTCCACTGAGGGAGGCGCG AGGTGGGCAT TGAGT TGTGT TACCT TTTTCCAC TG GGG G
TATTCGCATGTGGGAAAAAA ACAA ||||| ||||| ||||| |||||||| || |||
AGGTGGGCATACAATTTA ATTTA ATACG GTGGA AAAGGGTG AC CTT /
AC G AAA T G ATGC

GAM3444 AATGTTTACAATCTAAACCT 77412 TGAGCTAAAT 77413 TTACAATCTAAAC- GAA A
CAGAATCATAAATGTGATGA TTACTAATAC AATGT CTCA TCAT A
GCTAAATTTACTAATACATT ATT ||||| |||| ||||
TTACA GAGT AGTG A
TAATCATTTAAATC --- T

GAM3445 TGTCATATTGCACCAGAATT 77420 TATTGCACCA 77421 CATA A---- GAATTAATAA -
AGA
AATAATATCTCTAATAGATC GAATTAATAA TGT TTGC CCA TATCT CTAAT T
TGATTAGTAGATACATGGCT TATC ||| |||| ||| ||||| |||||
ATCGCAAAACAACA ACA AACG GGT ATAGA GATTA /
ACAA CTATC AC-------- T GTC

GAM3446 GGTTCTGTTTCTTCTTCCTT 77426 TCTAATGAAC 77427 T TCTTCTTCC TTT TTACGT
T
ATATATTTTTTTATTATTAC ATGTATAGTT GG TCTGTT TTATATAT TTTATTA ATTAT A
GTATTATTACATAATTATCT CCAT || |||||| |||||||| ||||||| |||||
CTAATGAACATGTATAGTTC CC AGACAA GATATGTA AAGTAAT TAATA /
CATAATAACAGATCC T TAATACCTT C-- CTCTAT C

GAM3447 TAATTTGATTCTAATATAAT 77444 TCCATTAGAT 77445 T A TCAG T ------- C
CTTCAGTATTGGATGAATCT TAGATTAGAT TAATTTGAT CTAAT TAATCT TA TGGA TGAAT
T
CAATTCAAATTAATTCCATT TAGA ||||||||| ||||| |||||| || |||| |||||
AGATTAGATTAGATTAGATT ATTAGATTA GATTA ATTAGA AT ACCT ACTTA C
AGATTA - G TTAG T TAATTAA A

GAM3448 GTCCGATCCTTTTTATCCGC 77455 TGACTAGGCA 77456 TCCTTTTTAT GCTACT TT GAA
CC

TACTCCTTTTCAGAAGTAAC CTAAGGCTCA GTCCGA CC CCT TCA GTAAC A
CCATTTGTTACCTATGACTA TCAG |||||| || ||| ||| |||||
GGCACTAAGGCTCATCAGTT TAGGCT GG GGA AGT CATTG T
CGGAT TGACTACTC- AATCAC TC ATC TT

GAM3449 ATGCTACCCACACAACTAAG 77466 ATAGTTACAT 77467 ACCCACACAACTA- - TCC
CTAGATCCTTAACTCATAGT AAAAACCTCA ATGCT AGCTA GA T
TACATAAAAACCTCAAGTAT AGTA ||||| ||||| ||
TATGA TTGAT CT T
ACTCCAAAAATACA A CAA

GAM3450 GTAACATTAAAACGTTGTTT 77489 TGGTATGTAA 77490 AAA TGTTTTGTTTT T - CC TTAT-
TAT TA G
TGTTTTTATTTGGCGCCTTT TTATGTTAAC CGT TAT TG GCG TTTA GG
GTAATTATGT AC A
ATTATGGTATGTAATTATGT GAAT ||| ||| || ||| |||| || ||||||||| ||
TAACGAATGTCACGTGATTA GCA ATA AC CGC AAAT TC CATTAGTGCA TG
A
CTTTCTTAGATTAAAAACGC AC- TATGGTCTTGT C A AA TAGAT TTT C- T
ACACATATGTTCTGGTATAC
GCACTTTGTTC
GAM3451 GTTCTCTATCACACATGATG 77493 AGTACAGATC 77494 -- - A GA- ACA GGGGA
ATACACACTCGGGGACAAGG ATGAGTAGAT GTTCTCT ATC AC CATGAT TAC CTC C
AGGGGGAGTACAGATCATGA ACAG ||||||| ||| || |||||| ||| |||
GTAGATACAGAGAAT TAAGAGA TAG TG GTACTA ATG GGG /
CA A A GAC AGG AGGAA

GAM3452 TTATATGTAAATATTGCAAT 77517 TAAATTATTA 77518 C A CA -- CCTAAT-- TA---
A
ATAAATTATTAACAATTCAA ACAATTCAAA AATATTG AATATAA TTATTAA ATTCA AATTG
TAT TTGA G
ATTGCCTAATTATTATTGAA TTGC ||||||| ||||||| ||||||| ||||| ||||| ||| ||||
GTATCAAGACCTATATTCTA TTATAAT TTATATT AATGGTT TAAGT TTAAC ATA
AACT T
ATTCAATTAATGAATTTGGT - A -- AA TTAATCTT TCCAG A
AAATTATATTTAATATTTCT
AAAAATGTAA
GAM3453 GCTGCTTGTGGCTTTTAACC 77520 TGTCAGAGAT 77521 TGT TAAC------ ACT T
CACACA----- G AA
AGTCACTAGTCACGCCCACA TCAAGAGGTG GGCTTT CAGTC AG CACGCC
TGAC AGGA A
CATGACGAGGAAAAACTCCT TGTC |||||| ||||| || |||||| |||| ||||
GTCAGAGATTCAAGAGGTGT CCGAAA GTTAG TC GTGTGG ACTG TCCT /
GTCTTAAGATTGCAGAAGAA CT- TCAAGAAGAC AAT T AGAACTTAGAG - CA
CTAAAGCCTCTCCAGC

GAM3454 TTCCACCAAAGATAATTATA 77534 TAATTTACAA 77535 A TAA ATT CCAT TA AAAAG TT
- A AG

ATAATTTACCCCATCATTAA AAAGTGTTTA ATTA TA TACC CAT ATTTACA TG TACA
GCT GCTTA T
TTTACAAAAAGTGTTTACAG CAGC |||| || |||| ||| ||||||| || |||| ||| |||||
CTAGCTTAAGTGGTAGGTAG TGAT AT ATGG GTA TGGATGT AT ATGT TGG
TGGAT /
GTATGTAGGTATGTAGGTAT A TCG GT- AT-- -- ----- GG A A GG
GTAGGTATGTAGCTTAGTAG
TTTAGTGTAA
GAM3455 TTCAGGTGTAGACCCGTCAT 77563 GTGCATTTAT 77564 - AT TG ---------- ------ TG
TT
TGTGACGCGTGGGTTGAGGT CTCAACAGTT CCC GTC TG ACGCGTGG GTTGAG G
CCATGAAT G
GCCATGAATTTGTCATTCAT TTCC ||| ||| || |||||||| |||||| | ||||||||
GGTGCATTTATCTCAACAGT GGG CGG GC TGCGCGCC CAACTC C
GGTACTTA /
TTTCCCTAACCGCGCGTTGC A C- GT AATCCCTTTTGA TATTTA GT CT
GCGGCAGGGTTTTTACTCTG
AG
GAM3456 CGCTGTTTTCGCGGTCCCGC 77584 TCCCGCTCGG 77585 TTTT T - G TGT C
TCGGGCTGTCGGCGTCCGTG GCTGTCGGCG CGCTG CGCGG CCCGC TCG GC CGG G
CGCGGCGCGGGCCCGCGTTC TCCG ||||| ||||| ||||| ||| || |||
CGGCG GCGGC GCGCC GGGCG GGC CG GCC /
CTT- C C G T-- T

GAM3457 GGCACAGTCTCGCGTCAAGA 77596 AAGAGGCCGG 77597 C CAAGA C - GC----
AGCGCAC G A AGC
AGGGCCCGGAGCCCCTCCGA AGGGAGGAGA CTCG GT AGGGC CG GA CCCTCCG
GCCT TT TCCC T
GCGCACGCCTGTTATCCCAG TCTT |||| || ||||| || || ||||||| |||| || ||||
CTCTCGGGGAAGAGGCCGGA GAGC CG TCCCG GT CT GGGAGGC CGGA AA
GGGG /
GGGAGGAGATCTTGAGCCCT T AGG-- A T AGAGGA ------- G - CTC
GGAGCTCGAGACCTTGGCC

GAM3458 TGACGCCCTCTCTATTCTTT 77647 TATGATGATT 77648 A TTAT A AT G ---------- A
AACGT
ATATGATGATTTAAGATTGA TAAGATTGAG TTCT ATG TG TTAAGATTGA TCCA AC
TTTTTCC T
GTCCAACATTTTTCCAACGT TCCA |||| ||| || |||||||||| |||| || |||||||
TTTACAGGAAAAAGGTATTT AAGA TAT AC AATTCTAATT AGGT TG AAAAAGG
/
TTAACTATGGAATTAATCTT A TT-- C CC A ATCAATTTTTA G ACATT
AACCCACTATTTAGAAAAAA
ATAAAAGACA
GAM3459 TCCCTCATACCGCCTCGTGT 77661 TAAGTGGCTG 77662 C-- - C CG A---------- GT
GTCCAGTGTGTAAACTTCCA TGACCTGGA TCC TCATA CCGC T TGTGTCC GT G
GGTTCTAGTTTTGGGGATAT ||| ||||| |||| | ||||||| ||
ATAAGTGGCTGTGACCTGGA AGG AGTGT GGTG A ATATAGG CA T
TCC C - AT GGTTTTGATCTTGGACCTT AA

GAM3460 CGGCCTGGGTGGGCGGAGGG 77756 TCCGTCCCCG 77757 - T--- ---------- AA
AACTAACCCAACGTATAAAT TTCCAAGGCC CGGCCT GGG GGGCGGA GGG C
CCGTCCCCGTTCCAAGGCCG G |||||| ||| ||||||| |||
GCCGGA CCT CCTGCCT CCC T
A TGCC AAATATGCAA AA

GAM3461 CCTCATGCGGAACTCGTGCC 77799 TTCATATTTT 77800 C ACTC- GCCAAATTATAATC T
TG T- T T
AAATTATAATCTTGATGTGT AAAAACCCAA TG GGA GT TTGA GTGTG TAATATA
ATATT ATG A
GTGTAATATATATATTTATG CTCC || ||| || |||| ||||| ||||||| ||||| |||
TATTTATCAATGTTTTATAT AC CCT CA AATT TATAC GTTATAT TGTAA TAT T
TGTTCATATTTTAAAAACCC A CAACC AA---------- T TT TT C T
AACTCCACATAGAAGG

GAM3462 GGACCCACCGGAACGGAGGG 77818 ACACAGCCGC 77819 A- A- AC A A ACC---- AAA--
CC
AGCGACCCGGCAAAGGCCCC ACAACCCGCC GG CCC CCGGA GG GGG GCG CGGC
GG C
ACCACACAGCCGCACAACCC CCCC || ||| ||||| || ||| ||| |||| ||
GCCCCCCTCCGGAAGGGAAC CC GGG GGCCT CC CCC CGC GCCG CC /
C AA AA -- - - CCAACAC ACACA AC

GAM3463 ACCACCAGATACATTCTGTA 77936 GAGCAGGTGT 77937 A T AAA GTTT--- ---------
GG
AATAGTTTGCTGTGGTTGCT ATCTGGGGT ACC CCAGATACAT CTGT TA GCTGTGGT
TGCTTA G
TAGGGAATAGGCATAGAATA ||| |||||||||| |||| || |||||||| ||||||
CAACCATGGTTATAAGATAG TGG GGTCTATGTG GACG AT TGGTACCA
ACGGAT /
AGCAGGTGTATCTGGGGT - - AG- AGAATAT ACATAAGAT AA

GAM3464 CCGCTCGATAGATCGCGTCG 78090 AGGAAGTACC 78091 TCGA - GGAA AAC
ACCAC C
AGGAAGTACCAACCGTGACC AACCGTGACC CCGC TAGA TCGCGTCGA GTACC CGTG
TCCTC G
ACTCCTCCGGCGGGGATCCT ACTC |||| |||| ||||||||| ||||| |||| |||||
CCGCGACGGGTACATCGACG GGCG ATCT AGCGCAGCT CATGG GCGC AGGGG
G
CGATTCTACGCGG C--- T A--- GCA CTCCT C

GAM3465 GTGTCGTTTGTTGTGGGTGG 78119 TCGTTTGTTG 78120 C T TG- GG
TATATACTATTTAAG AC
GATTATATACTATTTAAGGC TGGGTGGGAT GTGT GTT GTTG GGTG AT GC A

ACATTGTAAAATACGGACTT TATA |||| ||| |||| |||| || ||
TCATTTCACCAATCAACCAA CACA CAA CAAC CCAC TA TG /
CCACAC C C TAA TT CTTTCAGGCATAAAA TT

GAM3466 CGTTTTCGGTTGCTGGGTCT 78125 TGTTTTGGTA 78126 TT CTGG-- A-- T T
TATAATAAAATATTTTATAA TGTGAGGCAT CG TTCGGTTG GTCTTATA TAAAATA TT A
ACTGTTTTGGTATGTGAGGC GTTT || |||||||| |||||||| ||||||| ||
ATGTTTTAACCGAGTTCG GC GAGCCAAT CGGAGTGT GTTTTGT AA T
TT TTTGTA ATG C A

GAM3467 TGGCTACTTGGCAGTTACAA 78130 TACTTGGCAG 78131 TA---- TT AGTT C TG
GTTCACCTCTGCCAGAAGTG TTACAAGTTC TGGC CTTGGCAG ACA CAC TC C
TGTTTTTGCCAAGACATTTG ACCT |||| |||||||| ||| ||| ||
CCA ACCG GAACCGTT TGT GTG AG /
TTTACA TT ---- A AC

GAM3468 AATCTGAACTTCATCGAAAC 78149 TATAAACCAT 78150 AAC TCGAAACTCTCAT- C----
C CAT
TCTCATCTATAAACCATCTC CTCACTTACA AATCTG TTCA CTATAAAC ATCT ACTTA
T
ACTTACATTATTTAAGTAGA TTAT |||||| |||| |||||||| |||| |||||
TTCCTAGTTTATAGTTATAT TTAGAC AAGT GATATTTG TAGA TGAAT /
AAAACAATTGAATACCAGAT CAT TAACAAAATATATT ATCCT - TTA
T

GAM3469 GCCGGCGCCGCGACGCGTCG 78152 CGTCGTCGGG 78153 - - G - AGAC
GCGCCAGACGAGCGGGCGCC CGATCGAGC GC CGG CGCC CGACG CGTCGGCGCC G
GGCGTCGTCGGGCGATCGAG || ||| |||| ||||| ||||||||||
C CG GCT GCGG GCTGC GCGGCCGCGG /
A A - T GCGA

GAM3470 TCTCTCCGCCCAGTCTCCGC 78182 CATCCGCAGG 78183 C- GCCCAGT - CTAA AA
CTAAGGGAAACCAGTCCCAT AGTCCCTCAG TCT TCC CTCC GC GGGA C
CCGCAGGAGTCCCTCAGGAC GACA ||| ||| |||| || ||||
AAGA AGA AGG GAGG CG CCCT C
AC ACTCCCT A CCTA GA

GAM3471 CCTCTGAACCAAACTTTGGG 78229 AGGGACGCGG 78230 GAA AAA G ATTG T
TCTCATTGTGATTCTTGTCA GGGTGGGAGA CCTCT CC CTTTG GTCTC TGAT C
GGGACGCGGGGGTGGGAGAG GG ||||| || ||||| ||||| ||||
G GGAGA GG GGGGC CAGGG ACTG T
--- GTG G ---- T

GAM3472 TGATCGTTGTTTCGAACCGC 78875 AGGTACCATC 78876 TTC ACC ATAA-
TCATACATACTAAA AGTTG- ATGA

GAATAAAACTTTCATACATA GGTTTAAAAC GA GCGA AACTT CGATGG TGTTTT
G
CTAAACGATGGAGTTGTGTT TAAG || |||| ||||| |||||| ||||||
TTATGAGCGTTGAAAACAAA CT TGCT TTGAA GCTACC ACAAAA C
GGTACCATCGGTTTAAAACT C-- AA- ATACG TCAAAATTTG---- ATGGAA GTTG
AAGTTGCATATCGTAATCCA
CAAAAATCA
GAM3473 TTTGCTACAGCTTATATAAA 78883 TACATTGCCT 78884 TG T-- - TTA- TT - A CT
TTTATGTGCGATACATCTTA GTCACGTGAA TT C ACAG C TATAAAT ATGTGCG AT CAT T
AGTGCATCCGTACGTTATTT || | |||| | ||||||| ||||||| || |||
ATACATTGCCTGTCACGTGA AA G TGTC G ATATTTA TGCATGC TA GTG /
A GT CAC C TTAC T- C C AA

GAM3474 AATAAAAATTTCATAAATTC 78915 TAAAAATTTC 78916 T C TTCATAT TT
ATATAAAGATTTTGTTTTTT ATAAATTCAT AATAAAAA TT ATAAA AAAGA T
TTTCTTTTTATTAATTTTTT ATAA |||||||| || ||||| |||||
ATT TTATTTTT AA TATTT TTTTT T
T T TTCTTT- TG

GAM3475 TATTTTTGTTTGAAGAAAGA 78920 TGTTTGAAGA 78921 TG- AGAATGCC AATC
ATGCCATAATGACGTAATCA AAGAATGCCA TATTTT TTTGAAGAA ATAATGACGT A
ATAAAATGTCATTATTTTTT TAAT |||||| ||||||||| ||||||||||
CAAAAATAAAATA ATAAAA AAACTTTTT TATTACTGTA A
TAA -------- AAAT

GAM3476 TACCTTCGTCCAATTGGTTA 78934 TAGCGCAGTT 78935 CTT A T --- T T--- TTGTC
ATCTGTGCTTCACTTGTCAC TATACACCTA TAC CGTCC AT GGT TAA CTGTGCT CAC A
CGGTTGTGTAATAGCGCAGT TAGG ||| ||||| || ||| ||| ||||||| |||
TTATACACCTATAGGGCGCC ATG GCGGG TA CCA ATT GACGCGA GTG C
TGTA TCC A T CAT T TAAT TTGGC

GAM3477 TCCGCTTTAATAGCAGTACA 78940 AGCAGTACAT 78941 C TT - - TCAGT TT
TTCAGTGAGGTTTTACCTCC TCAGTGAGGT TC GC TAATAG C AGTACAT GAGG T
ATATGTGCTAGTCTGTTATT TTTA || || |||||| | ||||||| ||||
GTCGA AG TG ATTGTC G TCGTGTA CTCC /
C TT T A TAC-- AT

GAM3478 CACAGGCCCTTGTATCTGAT 78958 TCCATTCGGG 78959 CC TGT TGTAGC T
GTAGCGAGTGTTTCACTCCA TTATAGTTCT CACAGG CT ATCTGA GAGTG T
TTCGGGTTATAGTTCTTGTG TGTG |||||| || |||||| |||||
GTGTTC GA TGGGCT CTCAC /
TT TAT TAC--- T

GAM3479 CTTAATGGTTCATTCGTTCG 78963 TAATGGTTCA 78964 T TCATT C- TAT-- TT

TATATTCTTTTTCGATTTTT TTCGTTCGTA CTTAA GGT CGTT GTA TC T
TATTCAACGCTAATACCTTA TATT ||||| ||| |||| ||| ||
AG GAATT CCA GCAA TAT AG T
- TAATC CT TTTTT CT

GAM3480 TTCTTTTATGACGGATAATG 78968 CGACAACAAG 78969 GATAATGTA C-- - -- CAGG- G
TC G A A
TAGCGGCCGATTCAGCGTCC TGCATGAAAT GCGGC GAT TCAGC GTC TC ATG
CTTGTTG TC AC A
AGGTCGATGTCCTTGTTGGT TAGA ||||| ||| ||||| ||| || ||| ||||||| || ||
CAACAAAGTCGACAACAAGT CGCTG CTA AGTTG CAG AG TAC GAACAAC AG
TG /
GCATGAAATTAGACTCGTTG --------- CTC T CT ATTAA - GT - C A
ATATCCTCGTCGCTCATTTA
AGAA
GAM3481 GTGAGCCCGGCCGGCGGAGC 78986 CACCCGGAAA 78987 -- --- G AGC GAC TTTATA
T
CTCCGACCCTTTATAGCGTT GGAGAACCGC GTGAG CCC GGCCG CGG CTCC CC
GCGTT G
TGTGACGCACCCGGAAAGGA GGCC ||||| ||| ||||| ||| |||| || |||||
GAACCGCGGCCGCTGGGTCC CACTC GGG CCGGC GCC GAGG GG CGCAG /
TCAC CT TCG - AA- AAA CCCA-- T

GAM3482 GGCGGTAGCGGACGCACGGC 79050 ACACAATAAC 79051 CG AGC - GA AA- AAACA
- GGACAC
GGACACAATAACAAACAGAC AAACAGACCG GG GT GGACGCA CGGCG CAC TAAC
GACCG C G
CGCGGACACGGAGGGAGTCG CGGA || || ||||||| ||||| ||| |||| ||||| |
GTTGGGTTGGGCGTGGACGC CC CA CCTGCGT GCCGC GTG GTTG TTGGC G /
CGCTGCGTCCACACACCC CA CA- C AG CGG GG--- T AGGGAG

GAM3483 TCCCAATAAAGTGCAGTCGT 79065 AGTCGTTTTC 79066 - ATAAA GCAG-- G AA CG ATG
G G
TTTCTAACCCACGGATGCCG TAACCCACGG TC CCA GT TC TTTTCT CCCA G CC
TTGTAT C
TTGTATGCCTATACGGGGGA ATGC || ||| || || |||||| |||| | || ||||||
CTATGGGGGGGGGAAAGGAAA AG GGT CA AG AAAGGG GGGT C GG GGCATA C
GGAAACAGGAATGGAGA A AAGGA AAGGAA G GG AT A-- G T

GAM3484 TCGAAATAAACTTTCTCATT 79073 TGCAGTGGAG 79074 AAACTT C ---------- A
GGTTAGCATAGGCTGCAGTG TTCCAATCAA TCGAAAT TCT ATTGGT TAGC T
GAGTTCCAATCAATAGAATT TAGA ||||||| ||| |||||| ||||
TCGG GGCTTTA AGA TAACTA GTCG A
------ - ACCTTGAGGTGAC G

GAM3485 GCTTAATTTTTAGATATAGT 79087 AGTTGTAGAA 79088 TAGATA GA- ATAA
TGAATAATTGCAAATAATGT ACTACAGTTA GCTTAATTTT TAGTT ATAATTGCAA T
AGTTGCAGTTGTAGAAACTA AAAT |||||||||| ||||| ||||||||||
CAGTTAAAATTAAGC CGAATTAAAA ATCAA TGTTGACGTT /
TTGAC- AGA GATG

GAM3486 CTTCGCCAGGGAAGGGATTC 79105 CACCCGGAGT 79106 C C A--- T C AGTACTTT A
AC
ACCCGGAGTACTTTTGCATC ACTTTTGCAT CTT GC AGGGA GGGAT CAC CGG TGC TC
C
ACCCGCGAGCACTTTGAGGC CACC ||| || ||||| ||||| ||| ||| ||| ||
CGAGTGCATCCCCGACTCTC GAA CG TCTCT CCCTA GTG GCC ACG AG C
TGCAAG - - CAGC C A GGAGTTTC - CG

GAM3487 TTATTTTTTTTTTTTTATTA 79124 TACAATATAA 79125 TTTT--- A
TATTGTATTATTTAATACAA TAAAATATAT TTATTTTT TTTTATTATATTGTATT T
TATAATAAAATATATTTAAA TTAA |||||||| ||||||||||||||||
AATAA AATAAAAA AAAATAATATAACATAA T
TTTATAT T

GAM3488 GTATATATGAGATTATCTGT 79132 TATATGAGAT 79133 AGA TC TT ACTATTT
TATTTTAAGACTATTTATAC TATCTGTTAT GTATATATG TTA TGTTA TTAAG A
ACCCTTTAATTTAACAATTG TTTA ||||||||| ||| ||||| |||||
ACATATATAC CATATATAC AGT ACAAT AATTT /
--- TA TT CCCACAT

GAM3489 GGAATTTGCTCGACTGAAGG 79141 ATTTGCTCGA 79142 AATT CGAC AA ATC CGCA
TACCCAA
TATCAAGACGCAGTGTACCC CTGAAGGTAT GG TGCT TG GGT AAGA GTG C
AACCCGACAGCCACCACTCT CAAG || |||| || ||| |||| |||
TTAAACTCCCAAGCGCCGCC CC GCGA AC TCA TTCT CAC C
GCC- ---- CC AAT CAC- CGACAGC

GAM3490 AGGAATGCCGTAGTCCTGTC 79144 TGCCGTAGTC 79145 AA --- T CT GGA TAG C
GGAAGCTTTAGTGTGAGCCT CTGTCGGAAG AGG TGC CG AGTC GTC AGCTT TGTGAG C
CTCACGGATAAGCTCGAGAT CTTT ||| ||| || |||| ||| ||||| ||||||
TAGACTCCGTTTGCAAGCCT TCC ACG GC TCAG TAG TCGAA GCACTC /
GA TTT C AT AGC TAG T

GAM3491 GGTGGCCGGCAAGGTGCAAT 79150 TCTAACATCT 79151 G -- ---- TGCA T TG T
GTTTAGTGAGTTACCTGTCT CCCCTTTAAA GGTG CC GGC AAGG ATGTT AG AG T
AACATCTCCCCTTTAAAGCC GCCA |||| || ||| |||| ||||| || ||
AAGGCACC CCAC GG CCG TTCC TACAA TC TC A
- AA AAAT CCTC - TG C

GAM3492 GGAAATATGTAAGTTTGTTA 79187 TTAAAGCAGC 79188 GT- TTGTTAA - G T
AAGCAGCCAGTGTGACTTTG CAGTGTGACT GGAAATAT AAGT AGCAGC CA TGTGAC T
TCATGTGTGTTGTTGTTACT TTGT |||||||| |||| |||||| || |||||| /
TTCTGTATTTTC CTTTTATG TTCA TTGTTG GT GTACTG /
TCT TTG---- T - T

GAM3493 CTCTTTCCACCATCTTTTAG 79193 TAACTAAGAA 79194 AAAAAT
TTGTATTCTTAGTTATCAAT TACAACTAAA
CACCATCTTTTAGTTGTATTCTTAGTTATCAATAAAGGCGCGAAGCGCCATA T
AAAGGCGCGAAGCGCCATAA AGAT ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AAAATTATGTCATATGGCGC
GTGGTAGAAAATCAACATAAGAATCAATAGTTATTTCCGCGCTTCGCGGTAT /
TTCGCGCCTTTATTGATAAC ACTGTA
TAAGAATACAACTAAAAGAT
GGTGGAAAGAG
GAM3494 CTGAGGGCTTTTCTAGTTTC 79198 TTCTAGTTTC 79199 TTT TT GCTG TT
CGCTGTGAGGTTTTACCTCG CGCTGTGAGG CTGAGGGCT CTAGT CC TGAGG T
AAGGTTGCTAGTCTGGTTTT TTTT ||||||||| ||||| || |||||
CAG GACTTTTGG GATCG GG GCTCC /
TCT TT AA-- AT

GAM3495 ATTAAATTTTTAAACATTCC 79207 TAAATTTTTA 79208 - - TTCCTTAAAATC- ATCTAAAC
AGTA
TTAAAATCTATGTATCTAAA AACATTCCTT ATTAAA TTTT TAAACA TATGT GTGAC
A
CGTGACAGTAAATCAGTCAT AAAA |||||| |||| |||||| ||||| |||||
CCTGACATATTCTATTCCAT TAATTT AAAA ATTTGT ATACA TACTG /
TTTGTTTATAAAATTTTAAT T T TTTACCTTATCTT GTCC---- ACTA

GAM3496 TTGACTTTGCATTTCTCTTA 79215 TACAGGGTCT 79216 CTTT T TTAA-- TTG C
ACTTGTGATTTGATTCTAGA GTGGGAACTG TTGA GCA TTCTC CTTGTGAT ATT T
GTACGTTACAGGGTCTGTGG CTTT |||| ||| ||||| |||||||| |||
GAACTGCTTTTTCGA AGCT CGT AAGGG GGACATTG TGA A
TTTT C TGTCTG CA- G

GAM3497 GCGTTATTGGAGTTAACGGT 79233 TCGAACACCC 79234 TG - AC TATGG T
TATGGTGAGACTTTGTCTCG TAACTTTTGA GCGTTAT GA GTTA GGT TGAGAC T
AACACCCTAACTTTTGATAA TAAT ||||||| || |||| ||| ||||||
TGC CGTAATA TT CAAT CCA GCTCTG /
GT T C- CAA-- T

GAM3498 GTGGATAAATTCGCAAGGGT 79297 TCCGCCGTGA 79298 A AT AG T A G AA
ATCATGGCGGACGACCGGGG TCCATGCGGT GTGG TAA TCGCA GG ATCATGGCGGACG
CCGGG TTCG C

TTCGAACCCCGGATCCGGCC TACC |||| ||| ||||| || |||||||||||| ||||| ||||
GTCCGCCGTGATCCATGCGG CGCC ATT GGCGT CC TAGTGCCGCCTGC GGCCT
AGGC /
TTACCGC - -- A- - C - CC

GAM3499 TAGACGACCGGTTTATCATT 79300 ACCGGTTTAT 79301 AC ATCATTAATTAATAC GT
AATTAATACAATGTCTAAAT CATTAATTAA TAGACG CGGTTT AAT C
TCCATAACATATTACAAAAT TACA |||||| |||||| |||
CGCCGTCTA ATCTGC GCTAAA TTA T
C- ACATTATACAATACC AA

GAM3500 GCAGGTGTCACCGAGGTTGT 79307 AGGTTGTCGC 79308 --- A- GAG- CGC CAT ATG
CGCTGTCCCATCTTATGTGA TGTCCCATCT GCAGGT GTC CC GTTGT TGTCC CTT T
AAAGTGGACGAATAACGAGA TATG |||||| ||| || ||||| ||||| |||
GGGAGACGAGATCTGC CGTCTA CAG GG CAATA GCAGG GAA /
GAG AG AGAG A-- T-- AAG

GAM3501 CACACCCAAGAACAACGATA 79312 TAATATCGTT 79313 CCC C- GGA ATCA
TGGATGATCACGACAACAAT TTTTCTTTGT CACA AAGAA AACGATAT TG C
AATATCGTTTTTTCTTTGTG G |||| ||||| |||||||| ||
GTGT TTCTT TTGCTATA AC G
--- TT ATA AACA

GAM3502 TTTGAAAAAGAGGGAGGGGG 79318 TACATTATCA 79319 G G G ATTT TTTAAG A-----
--------- A
TGGTAATTTATGTGTTTTTT ACTCATCAAG GA GGG TGGTA ATGTGTTT GAAGTGGA
GAG C
AAGGAAGTGGAAGAGACTCT CTTA || ||| ||||| |||||||| |||||||| |||
CATATGTATACACAAGTTCA CT CTC ACTAT TACATAGA TTTCACTT CTC /
CTTTATTTCAGATACATTAT A A A ---- CTTTA- GAACACATATGTATA T
CAACTCATCAAGCTTAAATT
CAAA
GAM3503 CCAACAATGTGATCTTGCTT 79326 AACAATGTGA 79327 TGATC G---------- A
GCGGAGGCAAAATTTGCACA TCTTGCTTGC CCAACAATG TTGCTTGCGGA GCAA A
GTATAAAATCTGCAAGTAGT GGAG ||||||||| |||||||||| ||||
GCTATTGTTGG GGTTGTTAT GATGAACGTCT CGTT /
CGT-- AAAATATGACA T

GAM3504 GCACGTGCCGTGCTGTCTCT 79338 TTCGCGCCGC 79339 A C - TC C CTTT C C- -
CAT AC
CGCCCGACTTTTCGCGCCGC GGGCACATGG GC CGTGC GTGC TGTC TCGC CGA TCG GC
GCG GGCA GG G
GGGCACATGGACGGCGCCTT ACGG || ||||| |||| |||| |||| ||| ||| || ||| |||| ||
TGCCACGCCAGCCCGACTTC CG GCGCG CGCG ACGG AGCG GCT AGC CG CGC
CCGT CC G

TCGCGCGACTGGCACGCGCC - C C TC C CTTC C AC A TT- GC
GCGCGGC

GAM3505 TCTTTACTTTTAAGAATGAA 79343 TTTAAGAATG 79344 TTT- AT T -- T
TGAGATGAGGGTGGCCCTCA AATGAGATGA TCTTTAC TAAGA GAA GAGA TGAGGG G
AATCTCTTCCTCTTATCGTG GGGT ||||||| ||||| ||| |||| ||||||
TGAAGA AGAAGTG ATTCT CTT CTCT ACTCCC /
TGCT C- - AA G

GAM3506 CTCATCTTTGGTGTGATTAG 79355 TTCACATTTG 79356 - TGGT ------- T
GTGTGGTGTAACTTTGTTAC ATTATGAGAT CTC ATCTT GTGATTAGGTGTGG TGTAAC T
GTATCCTTTCACATTTGATT AGAG ||| ||||| |||||||||||||| ||||||
ATGAGATAGAG GAG TAGAG TATTAGTTTACACT GCATTG /
A ---- TTCCTAT T

GAM3507 GTAACCATAGTAGTAATAAT 79368 TTAGACTACT 79369 --- CAT AA TAGTAG
AGTAGTAGCAGTTAGTTTAT CTAGTTCATA GTA AC AGTAGT TAATAG C
TAGACTACTCTAGTTCATAC C ||| || |||||| ||||||
CAT TG TCATCA ATTATT A
ACT ATC G- TGATTG

GAM3508 CTGGGTTATCACTATCTCGA 79383 TAGCGTGTGA 79384 T CGA TTA GAGA T C T
CC---- A
AACTTAGCAGAGACTAACAT CGTTGAAAGA TA CACTATCT AAC GCA CTAACA CT GCTGC
CTAGG TGC A
CTCGCTGCTCTAGGCCTGCA TAGT || |||||||| ||| ||| |||||| || ||||| ||||| |||
ATGCAATAAATCCTAGGTAG AT GTGATAGA TTG TGT GATTGT GA TGATG GATCC
ACG /
TCAGCTGTTAGCGTGTGACG T AAG CAG GC-- C C - TAAATA T
TTGAAAGATAGTGTTATTTC
GG
GAM3509 ACAGGCGTGTTTATGTACAT 79386 TTGACTGGGC 79387 --- T A T TATT
TAAAGTATTTGTGGTTTTTA GTTTCGTTTG ACAGGCG TGTTTA GT CA TAAAG T
TTGACTGGGCGTTTCGTTTG T ||||||| |||||| || || |||||
T TGTTTGC GCGGGT CA GT ATTTT G
TTT - - T TGGT

GAM3510 ACGTGCTTATTCAACGCTCT 79396 TAGCGTCCCT 79397 TTAT GCTCTTT TTGAATCAT T
TTGGGATTTGAATCATCGTA ACCAGTTGAG ACGTGC TCAAC GGGAT CG A
AACGTAGCGTCCCTACCAGT CGCG |||||| ||||| ||||| ||
TGAGCGCGT TGCGCG AGTTG CCCTG GC A
---- ACCAT-- CGAT----- A

GAM3511 GCCTCAGTCTCTCGGTGCGT 79403 TCTCTCGGTG 79404 C ---- CAG
GGACCAGACGGCGTCCATGC CGTGGACCAG GC TCAGT CTCTCGGTGCGTGGAC A

```
    ACCGAGGGCAGAACTGGTGC       ACGG          || |||||   ||||||||||||||||
                                CG GGTCA   GGGAGCCACGTACCTG   C
                                 T    AGAC           CGG


GAM3512  CTGATACTTTGGAACTGTAT 79409   AACTGTATAC 79410    GAT  TT        A  AA    G     CC----  TT
    ACTAAGCCAAGTTTAGGCCC       TAAGCCAAGT       CT   AC  TGGAACTGTAT CT  GCCAA TTTAGG
CG  A
    GTTATGCGATAAATCCTAGG       TTAG          ||   ||  ||||||||||| ||  ||||| ||||||     ||
    TTGGTGGAGAATACGGTTTC                    GA   TG  GCTTTGGCATA GA  TGGTT GGATCC     GC  /
    GTTGTTGAAG                        AGT  TT        A  GG    -     TAAATA  GT


GAM3513  TAGCACCACCCGATCGTAAA 79419   TTTCATGGAG 79420      CC   CGATCGTAA      TATT
ACCCAT     GAAAACTCT
    CTCCATGTATTGGTTACCCA       TGGTTTGCTA       TAGCA  ACC       ACTCCATG    GGTT
CTGCATC       C
    TCTGCATCGAAAACTCTCCG                  |||||  |||       ||||||||    ||||     |||||||
    AACACTAGGTGCAGTAAGGC                   ATCGT  TGG       TGAGGTAC    TCGG     GACGTGG       /
    TTTCATGGAGTGGTTTGCTA                     T-   ---------       TT--    AAT---      ATCACAAGC


GAM3514  ATTAGAATACAGAGTGGCTG 79487   TAGAATACAG 79488        -   A   T     G  AC    TCTA
    CGCCACCGCTTCTATTTTAC       AGTGGCTGCG       ATTAGAA TAC GAG GGCTGC CC  CGCT    T
    AGTGAGGGTAGCCCTCCGTG       CCAC          |||||||  |||  |||  ||||||  ||  ||||
    CTTTTAGT                          TGATTTT GTG CTC CCGATG GG  GTGA    T
                                    C   C  -     -  A-    CATT


GAM3515  GTTCTGGTAGTCTGTCAGTT 79598   TAGTCTGTCA 79599       --   A     T AGT    AG    AAG
    CGGAGAGTTAAGAAAAAACT       GTTCGGAGAG       GTTCT  GGT GTCTG C   TCGG  AGTT   A
    ACCGGTTGTAGATGACCAAA       TTAA          |||||  |||  |||||  |   ||||  ||||
    GGAC                              CAGGA  CCA TAGAT G   GGCC  TCAA   /
                                    AA   G    - TT-    A-    AAA


GAM3516  GAAACTTTTACTAATTTTGA 79610   TGTACAGTTG 79611       TTTT     TTT   ATA-   C     C-   TC
    ATAACACGATGAGCATGTCA       TTTTTGGTTT       GAAAC    ACTAA   TGA    ACA GATGAG  ATG  A
    TGCATTCTTCATCTTGTACA       TCGT          |||||    |||||   |||    |||  ||||||  |||
    GTTGTTTTTGGTTTTCGTTT                    CTTTG    TGGTT   GTT    TGT CTACTT  TAC  /
    C                                 CTTT     TTT   GACA   T     CT   GT


GAM3517  GAAACTTTTACTAATTTTGA 79614   TGAATAACAC 79615       TTTT     TTT   ATA-   C     -----    A
    ATAACACGATGAGCATATCA       GATGAGCATA       GAAAC    ACTAA   TGA    ACA GATGA     GCAT T
    TGCATTCTTCATCTTGTACA       TCAT          |||||    |||||   |||    |||  |||||     ||||
    GTTGTTTTTGGTTTTCGTTT                    CTTTG    TGGTT   GTT    TGT CTACT     CGTA /
    C                                 CTTT     TTT   GACA   T     TCTTA   C
```

GAM3518 GCTACTACGACGACTAAGCC 79620 TAGCGTGTCG 79621 TACT A TAA CCAAGA AACA G - - TG T
CAAGACGAACAACGTGCGCG ACGTCCATGC GC ACG CGAC GC CG AC TG CGC G CG A
TGCGTACCGTGCGGCGACAG || ||| |||| || || || || ||| | ||
GTGACGATAGCGTGTCGACG CG TGC GCTG CG GC TG AC GCG C GC /
TCCATGC TACC A TG- ATA--- AG-- G A G GT C

GAM3519 GGCCATTCAAGTCTATTTTC 79642 TTAGTGCATT 79643 CATT CTATTTTCCCAA CTACC ACCCA
CCAAGCACTACTACCACACC TGCAGCC GGC CAAGT GCACTA AC A
CAACAGCAGTCCTTTTAGTG ||| ||||| |||||| ||
CATTTGCAGCC CCG GTTTA CGTGAT TG /
AC-- ---------- TTTCC ACGAC

GAM3520 GTGGGCGCCCTACGTCGGAC 79650 TCGCTGCGTG 79651 C CC- T ACTA TCT
TATGGGACCTCTGACGCGGT ATCGCCCCAC GTGGG GC TACG CGG TGGGACC G
CTCGCTGCGTGATCGCCCCA ||||| || |||| ||| |||||||
C CACCC CG GTGC GTC GCTCTGG A
- CTA - ---- CGC

GAM3521 TACTGTAGGAAAAAAAAGGA 79712 TGACGAGTTT 79713 -- AAAAAAGGATGG G T- TTC C
TGGTTGTCGATGTATTGGTT CTACGAGGTA TACT GTAGGAA TTGTC ATG ATTGG AGACGG T
CAGACGGCTTTCCGTCTATT |||| ||||||| ||||| ||| ||||| ||||||
CAATTTCATGACGAGTTTCT ATGG CATCTTT AGCAG TAC TAACT TCTGCC T
ACGAGGTA AG G---------- - TT TA- T

GAM3522 ATAATTGTTCAGCAGAATGA 79724 TTGGATCATA 79725 TCAGCAGA TTT TT
TCCTTTACCCCTTTTGGGGG GTCATCATAA ATAATTGT ATGATCC ACCCC T
TTTGGATCATAGTCATCATA TTAT |||||||| ||||||| |||||
ATTAT TATTAATA TACTAGG TGGGG /
CTACTGA- TT- GT

GAM3523 TTTCACCTAATTATTTAATT 79728 TTTATCGATA 79729 CC T ATTT TAAT--- TC CC A
TTATCGATAATTTTTCTCCT ATTTTTCTCC TTTCA TAAT ATTTA TATCGA TTTTC CTTTT AAAT T
TTTCCAAATATTATTTCTAA TTTT ||||| |||| ||||| |||||| ||||| ||||| ||||
AAGTTGAAAATATGAATTTG GAAGT ATTG TGAAT ATAGTT AAAAG GAAAA TTTA /
ATATACTAAGTGTTATGAAG -- - CAT- TAAGTAT TT TC T

GAM3524 GGGAAGCCGGGGAGTCACCA 79738 AGTCACCAAC 79739 AA-- G GAG A AACCCA AA

ACCCACCCTGAATCGACAGG CCACCCTGAA GGG GCC GG TC CC CCCTG T
GCAAAAAGGGAAGCCGGGCA TCGA ||| ||| || || |||||
CCGCCC CCC CGG CC AG GG GGGAC C
GCCA G GA- - AAAAAC AG

GAM3525 TTGGCCATAGCTTCGCTATA 79771 TCCATGGTGT 79772 G -- AT T
CCCCACCACAACCACCACCA GGTGGTGGTG
CATAGCTTCGCTATACCCCACCACAACCACCACCACCAC ACC GGACAC GGCC T
CCACGACCGGACACATGGCC GTTG |||||||||||||||||||||||||||||||||||||||||| ||| |||||| ||||
TTTGGCCGTGTCCATGGTGT GTATCGAAGCGATATGGGGTGGTGTTGGTGGTGGTGGTG
TGG CCTGTG CCGG /
GGTGGTGGTGGTTGTGGTGG - TA -- T
GGTATAGCGAAGCTATGGCC
AA
GAM3526 TTTGTATTTACATTTCCAAG 79794 GACAATGTAC 79795 ------ - AA-- ACAA
AGACAATATACCTCCTACGG TCATCAATAC TTTGTATT TACATT TCC GAG T
ACAATGTACTCATCAATACA AGA |||||||| |||||| ||| |||
GA AGACATAA ATGTAA AGG CTC /
CTACTC C CATC CATA

GAM3527 GAGCGGACACGGTTATCGTT 79812 TAAACGCGAG 79813 AC TTATC C- G GA A
CCTGGCGGATATAAGTATAT TTAGCCTTTC GAGCGGAC GG GTT CT GCG TATA G
AAACGCGAGTTAGCCTTTCC CCGT |||||||| || ||| || ||| ||||
CGTCCGTTT TTTGCCTG CC CGA GA CGC ATAT T
C- TTTC- TT G AA A

GAM3528 GGCGTCCGCGTGTCTAAACC 79815 GTTTGCTTCC 79816 G C AACC T T
GCGTGCTCGCTGACGCGGGT TATATAGTGG GGCGTCCGC TGT TA GCG GCTCGC G
TTGCTTCCTATATAGTGGAC ACGT ||||||||| ||| || ||| ||||||
GTC CTGCAGGTG ATA AT CGT TGGGCG A
- T CCTT T C

GAM3529 GAAACAAGCAATATATTCTT 79822 TCTTAAGTTA 79823 A AA TCTTA TATAG-
TCAAACCACATCA TAT
AAGTTATAGGTACGTCAAAC TAGGTACGTC GA AC GCAATATAT AGT GTACG AGG
A
CACATCAAGGTATATCCCCT AAAC || || ||||||||| ||| ||||| |||
CTCTTTATAAACTGTACAAT CT TG TGTTATATA TCA CATGT TCC /
CATACTCATATATTGTAGGT A GA C---- TACTAA CAAATATTTCTC- CCT
ATC

GAM3530 TTTATATCATTTTCATTTTG 79831 TGTATAATAA 79832 T C G ACATTATCTAT T -- A
T ATT
TTTAATAACATTATCTATGA ATAATTTATA TTT ATTTT TTTAATA GATA GTAT AATA ATAA
TTATA G
TATGTATAATAAATAATTTA ATTG ||| ||||| ||||||| |||| |||| |||| |||| |||||

TAATTGTCGATATAATTTAT AAA TAAAA AAATTAT CTAT TATG TTAT TATT AATAT
T
ATATTCAGTATTATCTTCAA - C G AATTACAACTT - AC A T AGC
CATTAATATTAAAGAAAATC
AAATTAAGAAA
GAM3531 ATAGTAAAACCTCCCGAATC 79836 TGCCTCGGGA 79837 AAA CC ATCTCA T A
TTCTG
TCAGTCTCTCGAAGCGTGGT GCTCGAAGGG ATAGT ACCT CGA G CTCTCGA GCGTGG
C
TCTGCCAGCGTCCATGCCTC TGCT ||||| |||| ||| | ||||||| ||||||
GGGAGCTCGAAGGGTGCTAT TATCG TGGG GCT C GAGGGCT CGTACC C
--- AA ------ - C TGCGA

GAM3532 CTGTTGACAGGTAGAGATCC 79852 GACAGGTAGA 79853 TGA TCCC TAA TA C
CGGGAGGTAAAGGTGCATAG GATCCCGGGA CTGT CAGGTAGAGA GGGAGG AGGTGCA
GG A
GCACACCTGCGCCTGACTCT GGTA |||| |||||||||| |||||| ||||||| ||
CCTTTTCTACCTGACCGCAG GACG GTCCATCTTT TCCTCT TCCGCGT CC C
CCA ---- CAG -- A

GAM3533 TTAAATTTTTATCACTCTAT 79879 TGAAAAATGA 79880 AT ACTCTATA ACC AAT
ATTTTCAACCTTTAGAAATA AAAAAATTAA TTAA TTTTATC TTTTCA TTTAGA A
GTATCTGAAAAATGAAAAAA AGAT |||| ||||||| |||||| ||||||
ATTAAAGATAGAATTAA AATT AAGATAG AAAAGT AAGTCT /
-- AAATTAAA AAA ATG

GAM3534 GATAATTTTTCTCACTTTCC 79896 TTGAAATTAG 79897 TTT- CA - CT---- TT
AAATATTAATTCTAATTTTT TATTATGGAA GATAATT CT CTTTCCA AATATTAATT AATT T
AATGATTTCTTGAAATTAGT AGAA ||||||| || ||||||| |||||||||| ||||
ATTATGGAAAGAAGTTTTGA CTATTAG GA GAAAGGT TTATGATTAA TTAG A
TTATC TTTT A- A AGTTCT TA

GAM3535 GACCAGTTTAAAACTTGTTT 79916 TTTATGTATT 79917 --- TGTT TTTTACTT AT- TT
CGTT
TATTTTTACTTTATGTATTG GTCTTGCTTT GACCAGTTT AAAACT TTAT TATGT TGTC
GCTTT T
TCTTGCTTTCGTTTCCTTCA CGTT ||||||||| |||||| |||| ||||| |||| |||||
AAGTGACGTCAACATACTTT TTGGTCGAG TTTTGG GATG ATACA GCAG TGAAA
C
CTTGTAGTTTGGTTTTTGAG AGT TTT- TTCTTTC- ACT -- CTTC
AGCTGGTT

GAM3536 GATACGGGCGCGGTTAGAAG 79920 GAAGTTACTC 79921 C TTAG TAC T- G C T
TTACTCATTCGGTGCTTGTT ATTCGGTGCT GATACGGGCG GG AAGT TCAT CG TG TTGTTG
T
GTTGCCAACAATCAGCGTTA TGTT |||||||||| || |||| |||| || || ||||||

TGAACTTGTTTCTGCCTGTA CTATGTCCGT CT TTCA AGTA GC AC AACAAC G
TC - TTG- --- TT G T C

GAM3537 GTATTATATATATATATATA 79928 TATATATATA 79929 T A
TATATATATATATATATATA TATATATATA GTAT ATATATATATATATATATATATAT T
TATATATATATATATATATA TATA |||| ||||||||||||||||||||||||
C CATA TATATATATATATATATATATATA A
- T

GAM3538 GTGTTATACATATATATATA 79936 TATTATATAT 79937 A A-- - T
TATATATATATATATATATA ATACACGTAG GTGTT TAC TATATATATA TATATATATATA A
TATATATATTATATATATAC ACAC ||||| ||| |||||||||| ||||||||||
ACGTAGACAC CACAG ATG ATATATATAT ATATATATATAT T
- CAC T A

GAM3539 GTGATTAATATATATATATA 79963 TAATATATAT 79964 - A A
TATATATATATATATATATA ATATATATAT GTG ATT ATATATATATATATATATATATAT T
TATATATATATATATATATA ATAT ||| ||| ||||||||||||||||||||||
GATACAT TAC TAG TATATATATATATATATATATATA A
A A T

GAM3540 ACATTTGTTGGCAAGAAAAG 80370 TGACCGTAGG 80371 T G ------ A A GATA A
CTT
AGCACCGATAACGGTAAGAA CGTTCATTTA ACA TTGTTG CAAG AAA GAGC CC ACGGT
AGAA T
CTTTTATTTTTTGACCGTAG CTAA ||| |||||| |||| ||| |||| || ||||| ||||
GCGTTCATTTACTAACCTTG TGT AACAAC GTTC TTT CTTG GG TGCCA TTTT T
GCAACAATTGT T G CAATCA A C A--- G TTA

GAM3541 TGCTATATTCAAGTTTTTGC 80374 TATCATGTGA 80375 TCAAGTT-- TG C TAT T
CTGTATCGTTTTCGTATCAT ATAATATACT TGCTATAT TT C TG CG T
GTGAATAATATACTGTATAG GTAT |||||||| || | || ||
TA ATGATATG AA G AC GC T
TCATATAAT GT T TAT T

GAM3542 GCGGTCACATTATACTTAGT 80390 TTGAAACAGA 80391 C - - TAG TCTCTTGTG T
CATCTCTTGTGGTTGTTAAC TATACATGTA GCGGT ACAT TATA CT TCA GTTG T
AACAATCTTGAAACAGATAT ACCG ||||| |||| |||| || ||| ||||
ACATGTAACCGC CGCCA TGTA ATAT GA AGT CAAC A
A C A CAA TCTAA---- A

GAM3543 ACGTAGGTGGTTATTTGATC 80397 AGGTGGTTAT 80398 T T TC - GGAT-- GGT
GTTGGGATGATTGTGGTTAA TTGATCGTTG ACG AGGTGGTTAT TGA GT TG GATTGT T

CAACAATCTACATACACATT GGAT ||| |||||||||| ||| || || ||||||
TTCATATGACCGCCTTCGT TGC TCCGCCAGTA ACT TA AC CTAACA A
T T TT C ATACAT ACA

GAM3544 GTAATACTATCTATAAACAT 80405 TCTATAAACA 80406 A T ACATA AT-- TA
AAGTATATAATAAATACTTT TAAGTATATA GTA TACTA CTATAA AGTAT AATAAA C
TTATTTACGGTACTCTTGTA ATAA ||| ||||| |||||| ||||| ||||||
GTGGTGATAC CAT GTGGT GATGTT TCATG TTATTT /
A - C---- GCAT TT

GAM3545 GCAATTTGCCTAACATGGAG 80412 TAACATGGAG 80413 TT CT T- -- AC
GATTGAGGACCCACCTTTTA GATTGAGGAC GCAA TGC AACA GGAGGATT GAGG C
ATTCTCTTCTGTTTGCATTG CCAC |||| ||| |||| |||||||| ||||
C CGTT ACG TTGT TCTCTTAA TTCC /
-- T- CT TT AC

GAM3546 TGTCCTTACTCCGTCTTGGT 80442 CGTCCCATCT 80443 A- CTTG TG TG GT
GGGTGGGTGGCTGTGTATGG GTGCGGGGAG TGTCCTT CTCCGT G GGTGGG GCT G
CGTCCCATCTGTGCGGGGAG GGGG ||||||| |||||| | |||||| |||
GGGGGCA ACGGGGG GGGGCG T CTACCC CGG T
GA ---- GT TG TA

GAM3547 TTAAAGTAACCTAACACCAT 80470 AAAGTAACCT 80471 CC CCATA CTTTA
AACACTTTACTTTCCTTGTA AACACCATAA TTAAAGTAA TAACA ACA C
CTTATGTTACTTTACTTTAG CACT ||||||||| ||||| |||
GATTTCATT ATTGT TGT T
TC ATTCA TCCTT

GAM3548 TGACCAGTGAACAATTTGTT 80486 TTGGTTGCAA 80487 ---------- CA -- TAGTTT
TAATGTTAGTTTATTCAATG ATATTCATTA TGACC AGTGAA ATTTGT TTAATGT A
CATTGGTTGCAAATATTCAT CTTC ||||| |||||| |||||| |||||||
TACTTCTCCAATCCCAGGTC ACTGG TTACTT TAAACG GGTTACG /
A ACCCTAACCTCTTCA A- TT TAACTT

GAM3549 GAAGTTAATGGAAATAGGGC 80494 TTAATGGAAA 80495 G - AAATA G ---------- GG - GAA
GTTTGTTAGGGGTTGTGAAA TAGGGCGTTT GAA TTAA TGG GGGC TTT GTTAG GTT GT A
TAAACGAACAACTGGCTTCA GTTA ||| |||| ||| |||| ||| ||||| ||| ||
GTGATTAGAGAGCTCAAACC CTT AATT ACC CTCG GAG CGGTC CAA CA /
AGTTAAGTTC G G AAA-- A ATTAGTGACTT AA G AAT

GAM3550 GATCTTTCCCACGTTGTATG 80504 TCTTTCCCAC 80505 - CATCTTC -------- CC A CAGC----- T

CCATCTTCCAGCAGAGCCGC GTTGTATGCC TTGT ATGC CAGC AGAG GCGGAGT GA
AACC C
GGAGTAGACAGCAACCTCAA ATCT |||| |||| |||| |||| ||||||| || ||||
GGTTAAAAACAGATCACTTC AACA TATG GTCG TCTC CGCTTCA CT TTGG
A
GCTCTCTCACCAAAAGCTGC C TTC---- AAAACCAC T- - AGACAAAAA A
TTGTATCACAACCAGGAATC
TC
GAM3551 GGTATGACGTGAAAAAATAG 80532 TGACGTGAAA 80533 G AAAAAT A GTAG GT
ATTAGGTAGGTTGTGAAAAA AAATAGATTA GGTAT ACGTGA AG TTAG GTT G
CAGATTAAACTTAAAATTAT GGTA ||||| |||||| || |||| |||
GTGTATT TTATG TGTATT TC AATT CAA A
- AAAAT- A AGA- AA

GAM3552 GATCGTCTTTTTGGCTGTGA 80537 TGAACTCATT 80538 C TTTTT T AG C CAATA
AGTCCCTCAATAAATACTAG GCCTCCGGCT GAT GTC GGC GTGA TC CT A
TGAACTCATTGCCTCCGGCT GTC ||| ||| ||| |||| || ||
GTC CTG CGG CCG TACT AG GA /
T CCT-- T CA T TCATA

GAM3553 GTCGTACACCCGGCTGACGA 80555 TTCCCGAACG 80556 A CG GAGAAACA C T
G
GAAACACGCTTCGGGGGTGG AGGACATAGT GTCGT CACC GCTGAC CG TTCGGGGG
GGACCA G
ACCAGGGCTGGTTCTTCCCG CAGC ||||| |||| |||||| || |||||||| ||||||
AACGAGGACATAGTCAGCGG CAGTA GTGG CGACTG GC AAGCCCTT CTTGGT G
TGATGAC - -- ATACAGGA - - C

GAM3554 ATTCAACTTGTTAAATTAAT 80565 TTAGTAGTAA 80566 A- GGATAG A G- G G
GA GTT
AATGGATAGTTTAAAATAGT TAAGATAGTT CTTGTTA ATTAATAAT TTTAAA TA TTATTA TA
TAATAA TA T
TATTAGTAGTAATAAGATAG TAAA ||||||| ||||||||| |||||| || |||||| || |||||| ||
TTTAAAATAGTTATTAGTAG GAATAAT TGATTATTG AAATTT AT AATAAT AT ATTATT
AT A
TAATAAGATAGTTTAAAATA GA ATA--- G AG G G G- AAA
GTTATTAGTAGTAATAAGAT
AGTTTAAAAT
GAM3555 GGGCCAACGTTCCGTCGTGT 80574 TTTGCAGGCC 80575 ----- TC TG -- CTCA CCA
GCTTGCGGCTCAGTCCAGTT AGTGCGACGT GGGCCA ACGT CGTCG T GCTTGCGG GT
G
TCGCGTTTGCAGGCCAGTGC TGCG |||||| |||| ||||| | |||||||| ||
GACGTTGCGTGCTTGTGGCC CCCGGT TGCG GCAGC G CGGACGTT CG T
C GTTCG TT GT AC TG-- CTT

GAM3556 ATTGTATATTTTATTTTATT 80578 TATTTTATTT 80579 ---------- TATTT T T TA A
T

TTATATTTTATATTTTATAT TATTTTATAT TTTATTT TA ATTT ATATTT TATTTTATTTT
TATT T
TTTATTTTATATTTTGTAGT TTTA ||||||| || |||| |||||| |||||||||| ||||
AAGAATAGAATGCTAAATGT AGATAAG AT TGAA TGTAAA GTAAGATAAGA
ATGA G
CAAGTTTATTCGAATAGATG AAAATTATTCTGT CTT-- T C TC - T
TCTTATTAAAAACATATATA
AT
GAM3557 TGCTACTAGGATGTAAGATT 80592 AGGATGTAAG 80593 CTA- T TT- ATC AC TC
TAGATCGGAAGGACGTCCCA ATTTAGATCG TGCTA GGATG AAGA TAG GGAAGG G C
CACCCTTCCACTATATTCTT GAAG ||||| ||||| |||| ||| |||||| |
CATCCCGAATAGCA ACGAT CCTAC TTCT ATC CCTTCC C /
AAGC - TAT A-- CA AC

GAM3558 GAATAGGTCAGAAGTAATAA 80603 TAGGTCAGAA 80604 A - GAAGTAATAAGAC A A G
GACTTGCAATAGAGAAATTA GTAATAAGAC GAAT GGT CA TTGC AT GA A
GTAGTAGATGAAATGAAAAA TTGC |||| ||| || |||| || ||
TGAACCAGTTC CTTG CCA GT GATG TG TT A
A A AAAAAGTAAAGTA A A A

GAM3559 GTCGAGGAACACGCCCCCGG 80614 AGGCCGGCGG 80615 AACA - A CC AA - C ----
GACTTCTT
ACCCCGTATAAGGCCGGCGG GCGCCTCGGA AGG CGCCC CCGG CC GTAT GG CCGG
GGGCG CCTCG C
GCGCCTCGGACTTCTTCTTT CTTC ||| ||||| |||| || |||| || |||| ||||| |||||
TTTGGCGAGGAACACGCCCC TCC GTGGG GGCC GG TATG CC GGCC CCCGC
GGAGC /
CGGACCCCGTATAAGGCCGG ---- C - AA CC A - ACAA GGTTTTTT
CGGGTGCCTCGGAC

GAM3560 GCTGGCACGGCCGGCGCCGC 80632 GCGCGGGGCA 80633 T G G G GATGACGA
GCAAGATGACGACGGGAGAG GGCAGTGCCG GC GGCAC GCC GC CCGCGCAA C
GTTGCGCGGGGCAGGCAGTG C || ||||| ||| || ||||||||
CCGC CG CCGTG CGG CG GGCGCGTT /
- A A G GGAGAGGG

GAM3561 ATGCAATATTACTAATATTT 80881 GCAATATTAC 80882 CTAATATTTTC- C TTATATA T
TCACACGCTTATATACCTAT TAATATTTTC ATGCAATATTA ACA GC CC A
TGGACAATGTTGTATATCCC ACAC |||||||||| ||| || ||
ACCCCTAATATTGCAT TACGTTATAAT TGT TG GG T
CCCCACCCTATA - TAACA-- T

GAM3562 ATCGCAGAATGTATAAAGAA 80897 AAGAATATAA 80898 CAGAA A AATACTAAAC T
TATAATACTAAACTTTGCTC TACTAAACTT ATCG TGTATAA GAATAT TTTGC C
TAGTAGACATACTGATATTC TGCT |||| ||||||| |||||| |||||
ATTATACACGAT TAGC ACATATT CTTATA AGATG T

----- A GTCATAC--- A

GAM3563 AGTTCTATTACATTGCTAGC 80904 TATAGAATTT 80905 TACATTG- GC-- G GA
TACTTGTAGGAATGCTAAAG AGTATAGAAC AGTTCTAT CTA TACTT TAG A
TACTTATAGAATTTAGTATA T |||||||| ||| ||||| |||
GAACT TCAAGATA GAT ATGAA ATC /
TGATTTAA ATTC - GT

GAM3564 CTTAGAGACTACTTTGTCTT 80920 TACTTTGTCT 80921 C- TTT- C A ACTACTC C ----
CTG
TCAAATATGACTACTCCCTC TTCAAATATG AGAGA TAC GTCTTT AAAT TG CCT TCATC
CATTGGT T
TCATCCATTGGTCTGTTAAA ACTA ||||| ||| |||||| |||| || ||| ||||| |||||||
CCAATGTGGTGATGATAGGT TCTCT ATG CGGAAA TTTA AC GGA AGTAG
GTAACCA /
AAGATGCAAATTTAAAGGCT AT TATT - A GTAGAAT T TGGT AAT
TATGTATATCTCTAAG

GAM3565 TTATATCTTCTTATTTTTTT 80938 TATTTTTTTA 80939 TA TGCTTACAA TG A GAATTAG-
GGAAAGTGA
ATGCTTACAATTTCTGCAGA TGCTTACAAT TCT TTTTTTTA TTTC CAGA TTA TATCT
G
ATTAGAATTAGTATCTGGAA TTCT ||| |||||||| |||| |||| ||| |||||
AGTGAGAAAAATTAAAGATA AGA AAGAAGAT AAAG GTTT AAT ATAGA /
AAATTAAATAATTTGTGGAA TC TAAAAATTA GT - AAATTAAA AATTAAAAA
AATTAAAAATTAGAAGAACT
AGAATTAATA
GAM3566 TTGACGATAAACCTATAGAG 80942 TAGCATTAAT 80943 ATAAACCTA GA T- AT AA
A
TTGCTTTAGCATTAATAAAT AAATGTAAAA TTGACG TA GTTGC TTAGC TAATAAATGTA
ACT T
GTAAAACTATATAGTATATA CTAT |||||| || ||||| ||||| |||||||||| |||
TTTATTACCGTTGATTGTAA AACTGC AT TAATG AGTTG ATTATTTATAT TGA A
TAATACGTCAA --------- AA TT CC A- T

GAM3567 CCCAGGTTTCTGTTCGGTCT 80947 TCTGTTCGGT 80948 G T T GTC AC C
GCTACTACGATCAGATCAGT CTGCTACTAC CCCA GT TCTG TCG TGCTACT GAT A
GGCGCGATCAGATGCGTGGG GATC |||| || |||| ||| ||||||| |||
GGGT CG AGAC AGC GCGGTGA CTA /
G T T --- -- G

GAM3568 GCAAGTTACACAAACAAAGC 80950 TAAGATCATT 80951 T ACAAAC C T-- CA---------- T
AAAGTAAGCCAACAGTTTTC TCAGTTTCGT GCAAGT AC AAAG AAAG AAGC ACAG T
TGTAAGATCATTTCAGTTTC CTTT |||||| || |||| |||| |||| ||||
GTCTTTCTTTAATCGTACTT CGTTCA TG TTTC TTTC TTTG TGTC T
GC - CTAA-- - TGC ACTTTACTAGAA T

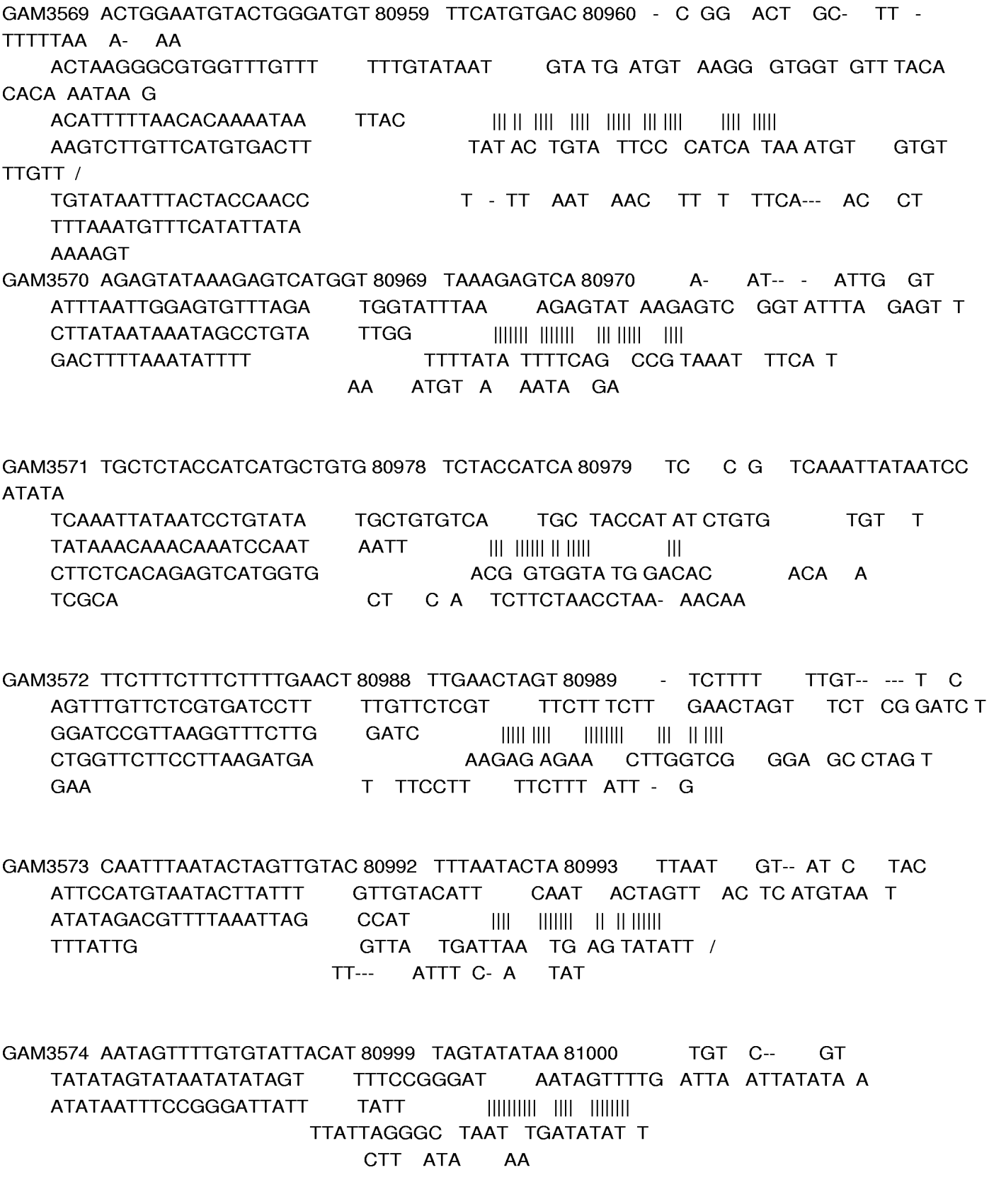
GAM3569 ACTGGAATGTACTGGGATGT 80959 TTCATGTGAC 80960 - C GG ACT GC- TT - TTTTTAA A- AA
ACTAAGGGCGTGGTTTGTTT TTTGTATAAT GTA TG ATGT AAGG GTGGT GTT TACA CACA AATAA G
ACATTTTTAACACAAAATAA TTAC
AAGTCTTGTTCATGTGACTT TAT AC TGTA TTCC CATCA TAA ATGT GTGT TTGTT /
TGTATAATTTACTACCAACC T - TT AAT AAC TT T TTCA--- AC CT
TTTAAATGTTTCATATTATA
AAAAGT
GAM3570 AGAGTATAAAGAGTCATGGT 80969 TAAAGAGTCA 80970 A- AT-- - ATTG GT
ATTTAATTGGAGTGTTTAGA TGGTATTTAA AGAGTAT AAGAGTC GGT ATTTA GAGT T
CTTATAATAAATAGCCTGTA TTGG
GACTTTTAAATATTTT TTTTATA TTTTCAG CCG TAAAT TTCA T
AA ATGT A AATA GA
GAM3571 TGCTCTACCATCATGCTGTG 80978 TCTACCATCA 80979 TC C G TCAAATTATAATCC ATATA
TCAAATTATAATCCTGTATA TGCTGTGTCA TGC TACCAT AT CTGTG TGT T
TATAAACAAACAAATCCAAT AATT
CTTCTCACAGAGTCATGGTG ACG GTGGTA TG GACAC ACA A
TCGCA CT C A TCTTCTAACCTAA- AACAA
GAM3572 TTCTTTCTTTCTTTTGAACT 80988 TTGAACTAGT 80989 - TCTTTT TTGT-- --- T C
AGTTTGTTCTCGTGATCCTT TTGTTCTCGT TTCTT TCTT GAACTAGT TCT CG GATC T
GGATCCGTTAAGGTTTCTTG GATC
CTGGTTCTTCCTTAAGATGA AAGAG AGAA CTTGGTCG GGA GC CTAG T
GAA T TTCCTT TTCTTT ATT - G
GAM3573 CAATTTAATACTAGTTGTAC 80992 TTTAATACTA 80993 TTAAT GT-- AT C TAC
ATTCCATGTAATACTTATTT GTTGTACATT CAAT ACTAGTT AC TC ATGTAA T
ATATAGACGTTTTAAATTAG CCAT
TTTATTG GTTA TGATTAA TG AG TATATT /
TT--- ATTT C- A TAT
GAM3574 AATAGTTTTGTGTATTACAT 80999 TAGTATATAA 81000 TGT C-- GT
TATATAGTATAATATATAGT TTTCCGGGAT AATAGTTTTG ATTA ATTATATA A
ATATAATTTCCGGGATTATT TATT
TTATTAGGGC TAAT TGATATAT T
CTT ATA AA
GAM3575 TGGAAGAGATTTTCTAACGC 81003 TAACGTGCGT 81004 GATTTTCTA C AC AG GTG
CGCGACTAAAGAGCTGTGGT GCCGTCTTCT TGGAAGA ACGC GCG TAAAG CT G

AAAAGACTTTAACGTGCGTG A ||||||| |||| ||| ||||| ||
CCGTCTTCTA ATCTTCT TGCG TGC ATTTC GA T
GCCG----- - A- A- AAA

GAM3576 CTTTTATCACCGGCTGCACT 81018 AGACCAGACA 81019 TC TGCA AAAAG GATA CAA AA
GATCAAAAGTGGTTGGATAC ATCAAAGATC CTTTTA ACCGGC CTGATC TGGTTG CTG TCA C
TGCAATCAAACACCTGAGAC AGGT |||||| |||||| |||||| |||||| ||| |||
CAGACAATCAAAGATCAGGT GAAGAT TGGTTG GACTAG ACTAAC GAC AGT A
TGGTTTAGAAG T- ---- AA--- A--- CAG CC

GAM3577 GATATAATTTTATGTATGTG 81049 TGTGGAGTGG 81050 TTTA- G T AA A GT AT C GA AGA GG
GAGTGGAAGCGGAGCGTGAT AAGCGGAGCG TGTAT TGGAG GG GCGG GC GAT ATTG GATGT AGC GGC A
ATATTGCGATGTGAAGCAGA TGAT ||||| ||||| || |||| || ||| |||| ||||| ||| |||
GGCGGATGAGCCGGGTTGGA GTATA ATTTT CC TGTC TG TTA TAAC CTATA TTG CCG T
TATCCAATCAATTGAGTACT TAAGG A - GG A AG AC - GG GG- AG
GTGGCCTTTTAAATATGGGA
ATGTTATGTC
GAM3578 ACTTGAAACCTCATTCACAT 81058 TTATTTGAGT 81059 C TT G TTT GG CTC
AGCTTAGGTTTTTAGGCACT GTGTGTGAGC ACTTGAAA CTCA CACATA CTTAGGT TA CA C
CCAATTTGAATATTATTTGA TTTC |||||||| |||| |||||| ||||||| || ||
GTGTGTGTGAGCTTTCAAGT TGAACTTT GAGT GTGTGT GAGTTTA AT GT A
C -- - TT- AA TTA

GAM3579 TTAGTATTAATTGCTACCGT 81069 TTAATTGCTA 81070 TT-- CCG CAT- A G ATA
TACATTGTACAAATGGAGAT CCGTTACATT TTAGTA AATTGCTA TTA TGT CAAATG AG T
ATTCCCTGTATTTGGCATTT GTAC |||||| |||||||| ||| ||| |||||| ||
CTAAAATTAGCAATTTTATT AATCGT TTAACGAT AAT ACG GTTTAT TC /
GCTAA TATT TAA CTTT - G CCT

GAM3580 GTGACTAAACCGCATAGGTC 81076 CACCTGGTGC 81077 CT C - - GCCAAC------ C
ATTGCCAACAACCGCACCCG GATTTTATCA GTGA AAA CGCAT AGGT CATT AACCG A
GTTAATCAGATATAAAATGC C |||| ||| ||||| |||| |||| |||||
ACCTGGTGCGATTTTATCAC CACT TTT GCGTG TCCA GTAA TTGGC C
AT A G C AATATAGACTAA C

GAM3581 GCCAAAAGTTGCGTGTCTGA 81131 AAGTTGCGTG 81132 AAA - GAGT TGG-- TT
GTGGACGTGGGTTTTTATAG TCTGAGTGGA GCCA GTTGCGTGT CT GGACG G T
AGTCGTCCTAAGCGCGTGCG CGTG |||| |||||||| || ||||| |
GCGGGTGGC CGGT CGGCGTGCG GA CCTGC T T
GGG C AT-- TGAGA AT

GAM3582 GGTTAATTTATAAGAAACCA 81141 TATAAGAAAC 81142 TTA- ATACTTTAAATCTC C
C
ATACTTTAAATCTCTAATTC CAATACTTTA GGTTAAT TAAGAAACCA TAATT GTTGTT T
GTTGTTCTAAACAACAGTTA AATC ||||||| |||||||||| ||||| ||||||
TGGTTTCTTAAATTGTTGAT TTAGTTG ATTCTTTGGT ATTGA CAACAA /
T TTAA ---------- - A

GAM3583 CTTTTAAGCTTATTGTAATA 81150 TTTAAGCTTA 81151 TT - T T T ATA CA TG T
TATATGAATAGCTATTCACA TTGTAATATA CT TAAG C TATTG AATATATA GA GCTATTCA G
GGAC T
GTGGGACTTGGTCTTGTGTT TATG || |||| | ||||| |||||||| || |||||||| | ||||
GAATAGTATCTTATATATTT GA ATTC G ATAAT TTATATAT CT TGATAAGT T TCTG /
TAATATGTCTTATTAG TT T T T T A-- TG GT G

GAM3584 GTATAATTTTTTTAGTTTTT 81158 TAATTTTTTT 81159 AAT TAG --- TTC
ATAGATTCTTTATTCTATAC AGTTTTTATA GTAT TTTTT TTTT TATAGA T
TTAAAAAATGAAAATAAATA GATT |||| ||||| |||| ||||||
C CATA AAAAG AAAA ATATCT T
AAT TAA TTC TAT

GAM3585 TTGGATTATTCATTTTTATG 81163 TATTGTGCAG 81164 GA TCATT T ATT A-- CGA
AACTATGTTATTTACAAAGC ACGTGGTTCT TTG TTAT TTTA GAACTATGTT TACAA GCTT
A
TTCGAAAGTGAGTATATTGT TGGG ||| |||| |||| |||||||||| ||||| ||||
GCAGACGTGGTTCTTGGGTT AGC AATG GGGT CTTGGTGCAG GTGTT TGAG /
GTTGTAAACGA A- TTGTT T AC- ATA TGA

GAM3586 TAACGTGTAGTTTTGATGAT 81167 ATGATGGTGA 81168 T TT T TG C T T TGG
GGTGACACATGGTTGTTGTT CACATGGTTG TAACG GTAG TTGA GATGG ACA ATGG TG
TGTTA C
ATGGCTTTTAGCATCACTTA TTGT ||||| |||| |||| ||||| ||| |||| || |||||
TTGTTGCTATTTTAGGGTTA ATTGT CATT GATT TTATC TGT TATT AC ACGAT /
CTGTTA - GG - GT - C T TTT

GAM3587 ATGATATTATCGATAGTTGT 81184 TCGATAGTTG 81185 C A TG - TGCTCT
GATAATGTGCTCTTTTATTT TGATAATGTG ATGATATTAT GAT GTTG AT AATG T
TATTAATTGCGATGATTATA CTCT |||||||||| ||| |||| || ||||
ATATTAT TATTATAATA TTA TAGC TA TTAT /
- G GT A TTTATT

GAM3588 TAGGAAATTGGTTTATAATG 81191 TGAAAATAAA 81192 ATTG--- AATGTATA T TTTT
TTC

TATAATTTTTTTAGTTTTTA TACAAAGGTT TAGGAA GTTTAT ATTTTTT AGT ATAGA T
TAGATTCTTTATTCTATACT CCTG |||||| |||||| ||||||| ||| |||||
TAAAAAATGAAAATAAATAC GTCCTT TAAATA TAAAAAA TCA TATCT T
AAAGGTTCCTG GGAAACA AAAG---- T ---- TAT

GAM3589 TGTTCAGTCTAAAAATAATG 81222 TTACTTGGAA 81223 TC CTAAA - - A A T C CC
TTGGGTATTTATAATTACCG ACACCCATAC TGT AGT AATA ATGT TGGGT TTT TAA TA CG C
CCCCCGTGTTACTTGGAAAC ATAT ||| ||| |||| |||| ||||| ||| ||| || ||
ACCCATACATATGTTCCACT ACA TCA TTGT TACA ACCCA AAA GTT AT GT C
CTACA TC CC--- A T C G C T GC

GAM3590 TGCTAAGTTTCAGTTTAAAT 81233 TAAGTTTCAG 81234 AA TC T CA TTGCAA- T
CATTTCCTTGCAATTCTCTA TTTAAATCAT TGCT GTT AGTT AAAT TTTCC TTC C
GAACAATATTGGAAACCATT TTCC |||| ||| |||| |||| ||||| |||
TCAACTCAACAAGCA ACGA CAA TCAA TTTA AAAGG AAG T
A- C- C CC TTATAAC A

GAM3591 TTAAGTCTATTGTTCATGGC 81252 TATTGTTCAT 81253 TAT T ---- C- T TA
TTAAGTCTATTACTCATAGC GGCTTAAGTC TTAAGTC TG TCA TGG TTAAG CTAT C
TTAACTCCATTACTGATCAT TATT ||||||| || ||| ||| ||||| ||||
GACTTAA AATTCAG AC AGT ACC AATTC GATA /
T-- T CATT TC - CT

GAM3592 TCGCAACACAACATGGTTAC 81255 TTAAGGCTTG 81256 G T ACCCATAG GAAATTT
CCATAGATTGAGGAAATTTC TTGTGTTGGA TC CAACACAACA GGTT ATTGAG C
CAATAAACTCAGTATTAAGG || |||||||||| |||| ||||||
CTTGTTGTGTTGGA AG GTTGTGTTGT TCGG TGACTC /
- - AATTA--- AAATAAC

GAM3593 GTAGCACTCGAAATTTCAAA 81293 TAGCGGCTGG 81294 AG C ATTTCAAA A AAATAC
- A
CGGCATGTAAATACGAATGT TGTTCGATGT GT CA TCGAA CGGC TGT GAATGTC CTT
G
CCTTAGAAAGCGACGTTTAG CAC || || ||||| |||| ||| ||||||| |||
CGGCTGGTGTTCGATGTCAC CA GT AGCTT GTCG GCG TTTGCAG GAA /
CT - GTG----- - A----- C A

GAM3594 GCTGCCATGTATTTCCTGGA 81305 AGCAAGTAGA 81306 C TTTCCTG A GAT AG
CA
GAGCAAGTAGATGATGAGGA TGATGAGGAA GCTGC ATGTA GAG GCAAGTA GATG GAAC
G
ACCAGATAGTTTATATCCAT CCAG ||||| ||||| ||| ||||||| |||| ||||
ACTTGCACTTAAAGTCTACA TGATG TACAT TTC CGTTCAT CTAT TTTG A
TTGTAGT T CTGAAA- A AC- A- AT

GAM3595 TCAGACTGAGGGGCCCTTAG 81354 TTCTTCGCGG 81355 AG TT- TT G
GTTTATATGAAATATATTCT GTTTAACAGT TCAGACTG GGGCCC AGG TATAT A
TCGCGGGTTTAACAGTTTGG TTGG ||||||||| |||||| ||| |||||
GGTTTGAC TTTGGG TTC ATATA /
AA CGC TT A

GAM3596 TATATCGTAGATAAGAATGT 81361 TATCGTAGAT 81362 T --- - T TAA- GTT
GATAAGATCGTTGGTGGATC AAGAATGTGA TATATCG AGATA AGA ATG GA GATC G
AACTTCCATATCTACCTATC TAAG ||||||| ||||| ||| ||| || ||||
TTCGATATA ATATAGC TCTAT TCT TAC CT CTAG /
T CCA A - TCAA GTG

GAM3597 ATCACTCAAGATTACTTACT 81365 TCAAGATTAC 81366 CTCA T ACT-- TTT
TCTATTTTAATGTATAGATT TTACTTCTAT ATCA AGAT ACTT TCTAT A
AAAAGGTTATTTCGTATGAT TTTA |||| |||| |||| |||||
TAGT TTTA TGGA AGATA A
ATGC T AAATT TGT

GAM3598 TGAAGACCCGAGAGAAGAGC 81371 ACAAAAATTT 81372 ---------- CTTTACAAAAA AAAAA
A TTC ACAA
TTTACAAAAAACACAAAAAA CAATAAAAAC AAGAG ACACA ACAAA AT AATAAAA
T
ACAAAAATTTCAATAAAAAC AATT ||||| ||||| ||||| || |||||||
AATTTAAATTTTATTTATCT TTCTC TGTGT TGTTT TA TTATTTT T
TTGTATGTGTGTCTCTTGCA ACCCCCAACG ---------- GTA-- C T-- AAAT
ACCCCCACCCCTTATAGATC
TTCA
GAM3599 TCGTCCTAGCTATAGGTATA 81380 TCCCACACTT 81381 T A T A TAT C T- - TA
ACTGTGGTCTCAGCATTATT TTCCAATTGC TCG CCT GC AT GG AA TGTGG CT CAGCAT T
TGTGCTGAAGTCCCACACTT AGGC ||| ||| || || || || ||||| || ||||||
TTCCAATTGCAGGCGA AGC GGA CG TA CC TT ACACC GA GTCGTG /
- - T A TT- C CT A TT

GAM3600 TGTTAAAATATCAAATGTTA 81426 TATCAAATGT 81427 ATCA - GTTT TCTTC
CAATAGTTTTTTTGTTATCT TACAATAGTT TGTTAAAAT AATGT TACAATA TTTTGTTA T
TCTTTTATTAATAAAGCCAT TTTT ||||||||| ||||| ||||||| ||||||||
ATTGTGTATATTAATTTTAA ACAATTTTA TTATA GTGTTAT GAAATAAT /
CA A--- T ACC- TATTT

GAM3601 CTGTATACAAGACAAACCAA 81435 TACAAGACAA 81436 ACAAACCAA- CAATA
AAATACAATAAACGCGATAT ACCAAAAATA CTGTATACAAG AAATA A
TTAAACATTTTATTTGTGTA CAAT |||||||||| |||||
CAG GACATGTGTTT TTTAT A

ATTTTACAAA AGCGC

GAM3602 GCCGAGCACGCCGCCGCGAT 81455 TCCGTGGACG 81456 A A - A-- AGA AGAT
CGGAGACCCAGATCTGCAGG GCGGCCGGC GCCG GC CGCCG CCGCG TCGG CCC C
GCCGAGTCCGTGGACGGCGG |||| || ||||| ||||| |||| |||
CCGGC CGGC CG GCGGC GGTGC AGCC GGG /
- - A CTG --- ACGT

GAM3603 CGGGTCGCCCCTCGACGACG 81537 TACTGCGCGA 81538 CGCCCCT C C - ACC----
CC
CCGTCGCCGACCCGATCCAA CCGCCTCGTC CGGGT CGACGA GC GTCGC CG CGAT A
AATCGTAAATACTGCGCGAC GTTC ||||| |||||| || ||||| || ||||
CGCCTCGTCGTTCCCCACCC GCCCA GCTGCT CG CAGCG GT GCTA /
G CCCCTT- C C C CATAAAT AA

GAM3604 GAGTACTTATTAAGAATGAC 81540 TGACAAATGA 81541 TA ATT GAATGACAAAT A A
CAAATGACAAAT GATT
AAATAACAAATGACAAATGA CAAATGACAA AG CTT AA AACAA TG CAAATGA
GAC C
CAAATGACAAATGACGATTC ATGA || ||| || ||||| || ||||||| |||
TAAAAGTCTATATAAGCATT TC GAA TT TTGTT AC GTTTATT CTG T
ATTTGCCAATTGTTTTTCAC TC AT- AAAATCACTTT A C ACGAATATAT-- AAAA
TAAAATTTAAAGCTCTC

GAM3605 GGCGTCGTCGTCGGGCCGGG 81567 CTCGCACTCC 81568 GT- C---- -- GC GT TC---
TT AA
TGCGTCGCCGTTCGGGCCGG GGCGCCGTGT CGG GCGT GCCG TTCGG CGGACG
CGGTGTC GCG TCT A
ACGGTCGGTGTCTCGCGTTT TCGC ||| |||| |||| ||||| |||||| ||||||| ||| |||
CTAAAAGAGGGCTCGCACTC GCC TGTA CGGC GAGTC GCTTGT GCCGCGG
CGC GGG A
CGGCGCCGTGTTCGCACTGA GCT TTTTA CA AC -- CCTCA TC AG
GACCGGCATTTTATGTTCGC
CGGCCCCACCC
GAM3606 GAGTTGGCTACACCGAGATC 81590 CACCGAGATC 81591 - ACA- G - AT----- A- TT
AC
CGGCATCATACCTTACGTGA CGGCATCATA GAG TTGGCT CC AGAT CCGGC CAT CC
ACGTGA T
ACTGCTTACGTTTGGGGATG CCTT ||| |||||| || |||| ||||| ||| || ||||||
TTTTTGCGTCGGTGTTTGGG TTC AACTGA GG TTTG GGCTG GTA GG TGCATT /
GAGGAGTCAATCTT T GGAG G T CGTTTTT GG TT CG

GAM3607 TTTGTAGTTTTAAGATTGAG 81595 TAAGCTTTTT 81596 A TT T------- TTTTTT C A CTA
GTTTTTTGACGCTAGCCCTA CCTCATAAAT TTTGT GTT AAGA TGAGG GA GCT GCC T
TAGTAGGTAAGCTTTTTCCT ATTT ||||| ||| |||| ||||| || ||| |||
CATAAATATTTCTTTGGCAC AGACA CGG TTCT ACTCC TT CGA TGG A

AGA - T- TTATAAAT TT---- T A ATG

GAM3608 GCTGTGGGTTATATGTTTGC 81602 TGGTCGGAGA 81603 GT- TA-- CG ACAA CAATA
GATTTTCCACAAAGAACAAT GTTATAAGCA GCT GGGT TATGTTTG ATTTTCC AGAA A
AATAACTCTTCTGGTCGGAG TACC ||| |||| |||||||| ||||||| ||||
AGTTATAAGCATACCGTGCC TGA CCCG ATACGAAT TGAGAGG TCTT T
CCAAAGT AAC TGCC AT CTGG CTCAA

GAM3609 GACTTTTATCACGTTATCTC 81610 TAGTATAGCA 81611 TATCAC- - CA- TAA
ATGTATAAAATATTACAAAT TAAACTAAAG GACTTT GTTAT CT TGTA A
AGTATAGCATAAACTAAAGT TC |||||| ||||| || ||||
C CTGAAA CGATA GA ACAT A
TCAAATA T TAA TAT

GAM3610 TTGCATATTATATTTTATAT 81623 TATTATATTT 81624 C - A ATTTTAT
TTTATATTTTATATTTTGTA TATATTTTAT TTG ATATTA TATTTTAT TTTTAT A
ATAAGAATAGAATGCTAATG ATTT ||| |||||| |||||||| ||||||
TCAA AAC TGTAAT GTAAGATA AGAATA /
- C - ATGTTTT

GAM3611 GTGTTCGAGTGAGTTGGATT 81626 TAATAAGAAT 81627 ----- T TG-- G ATTGTA
ATATT TTTT
ATGTGAGTATTGGATTGTAT AAAATGCTAA TTGGA TA TGA TATTGG TATTTTATTTT
TTATA A
ATTTTATTTTATATTTTATA TGTC ||||| || ||| |||||| |||||||||| |||||
TTTTATATTTTGTAATAAGA AACCT AT ACT GTAATC GTAAAATAAGA AATGT
T
ATAAAATGCTAATGTCAAGT TAGAT T TTGA - ------ AT--- TTTA
TTATTCCAATAGATGTCTTA
TTAAAAAACAT
GAM3612 TTTATTTTTTTCTTTTTAAT 81632 TCAGAGAGAT 81633 - A AATTTA CTTTTTCT CT
CTATCAAT
TTTAATTTATTAATTTTCTT AAAAAGATAG TCTTTTT ATTTT TTAATTTT ATATTTAG AATT
A
TTTCTATATTTAGCTAATTC A ||||||| ||||| |||||||| |||||||| ||||
TATCAATAATTTTTCTCAAT AGAGAGA TAAAA AATTGAAA TATAAATC TTAA
A
TTCTAAATATTATTTCTAAA T C ------ ATCTTTAT T- CTCTTTTT
AGTTAAAAAATCAGAGAGAT
AAAAAGATAGA
GAM3613 GTCGGAGAGTTATAAACATA 81702 AAGGGGTTTT 81703 A ATAA CCATGC- AAAG TC
CCATGCACCAAAGGGTCAGT ACTTTATGTG GTCGG GAGTT ACATA ACC GG A
TTTAAGGGGTTTTACTTTAT AATT ||||| ||||| ||||| ||| ||
GTGAATTCACCGAC CAGCC CTTAA TGTAT TGG TT G
A G--- TTCATTT GGAA TT

GAM3614 TGTTGATCGCATATTGCTAT 81724 TCGCATATTG 81725 T C ATA - TCAACCCAA TT - TA
TTCTGCTCAACCCAAAGTGT CTATTTCTGC TGT GAT GC TTGCTATTT CTGC AGTG AG C C
TAGCTACGTTGTCTCTCACT TCAA ||| ||| || ||||||||| |||| |||| || |
CAGAACCTGTAGTAAATAGT ACA TTG TG AATGATAAA GATG TCAC TC G G
AAAGTTGTTTACA T T A-- T TCCAAGAC- TC T TT

GAM3615 ATCAATTTTTAGTTTTAAAT 81739 TATAGCCAAT 81740 TT TTTAAATA ACCTAGG AAA
ATATTGGTACCTAGGACAAA AATTATTCCA ATCAATT TAGT TATTGGT AC G
GAAAGTATATATAGCCAATA CTAA ||||||| |||| ||||||| ||
ATTATTCCACTAAATTGAT TAGTTAA ATCA ATAACCG TG /
-- CCTTATTA ATATATA AAA

GAM3616 TTACGTAATAATGACCGGAT 81747 ATCCCGTTCC 81748 ATA GAC TGTAAT AACAAATC
GTAATTCGAACAAATCATAA GAAAATATAC TTACGTA AT CGGA TCG A
AACACCGATCCCGTTCCGAA GTGA ||||||| || |||| |||
AATATACGTGA AGTGCAT TA GCCT AGC /
A-- AAA TGCCCT CACAAAAT

GAM3617 TACTACTCTTAAAACACATG 81755 TGTATAAGCT 81756 ---- AAAC TATT AGG
TGTATTGTGTTAGGTTAAAG TTAGTAGTA TACTACT CTTA ACATGTG GTGTT T
CATCCTTTATATGTATAAGC ||||||| |||| ||||||| |||||
TTTAGTAGTA ATGATGA GAAT TGTATAT TACGA /
TTTC A--- TTCC AAT

GAM3618 CCTCTTTCGATTTCTACACG 81785 TCAGTTAGAC 81786 TTTC - C GA AAA TAT
AGAAAAGTTATAAAATACAT GATCATTGAG CCTC GATT TCTA AC GA GT A
CAGTTAGACGATCATTGAGG G |||| |||| |||| || || ||
GGAG CTAG AGAT TG CT CA A
TTA- C - A- A-- TAA

GAM3619 TCGGAACGCGTGAGGAGGCG 81800 AGGCACCGCC 81801 AAC A A- CAC A- CGCG
GCACTGCTAGCGACGCGGAC CGCCCGCGCT TCGG GCGTG GG GGCGG TGCT GCGA G
ACATTGCGAGGCACCGCCCG CGA |||| ||||| || ||||| |||| ||||
CCCGCGCTCGA AGCT CGCGC CC CCGCC ACGG CGTT A
--- - GC --- AG ACAC

GAM3620 GCGAGCCGCGTCGTTCGCGG 81865 CACGCTGTTC 81866 AG C T TT -- G - GCCACA
ACGCGGCGGTGGGTCCGGCC GTCCGCGCTC GCG C GCG CG CGCGGACG CGGCG TGGGTC CG G
ACAGAGCGACACGCGGCCCA GTCG ||| | ||| || |||||||| ||||| |||||| ||

CGCTGTTCGTCCGCGCTCGT CGC G CGC GC GCGCCTGC GTCGC ACCCGG GC A
CGCAGTCCGC CT A T TC TT - C ACAGCG

GAM3621 TTTGAGCCCCAAGCGGTACG 81870 TACACTGAAC 81871 A CC -- AC CTACATAT
GACTACATATTTTCCATAAA TTGAGCACAA TTTG GC CAAG CGGT GGA T
TCTACACTGAACTTGAGCAC A |||| || |||| |||| |||
AAA AAAC CG GTTC GTCA TCT T
A A- AA CA AAATACCT

GAM3622 ACCGGTTTTATAAAGTAAAG 81951 TATAAAGTAA 81952 GT --- TAAA - --- C - G
TAAAGTAGACCCCACTAGGA AGTAAAGTAG ACCG TTTAT AAAG GTAAAGT AGAC CC
ACTA G A
AACTTGGTCGGCAAGTTTAA ACCC |||| ||||| |||| ||||||| |||| || |||| |
CTTTATCCTTTTAAATAAAT TGGC AAATA TTTC TATTTCA TTTG GG TGGT C A
ACGGT AT AAT C--- A AAC C T A

GAM3623 AGGTGGCACTTCAGTTGTAA 81964 ACAGAACAAG 81965 GCAC- T TAACCT ACG-
TAGACA- ATA
CCTGATAACGTGCTTTAGAC CAGAACTATT AGGTG TTCAG TG GATA TGCTT CT A
ACTATAAACCGAGACAGAAC TTCA ||||| ||||| || |||| ||||| ||
AAGCAGAACTATTTTCACTG TCCAC AAGTC AC TTAT ACGAA GA A
AAAACCACACCT ACCAA - TT---- CAAG CAAGACA GCC

GAM3624 TTATTTCATTATTTGCATTG 82023 GCATTGGTAA 82024 GC-- TAA--- T TTATTTAA C
A ACT
GTAATACTTATTGTAATTTT TACTTATTGT TTT ATTGG TACT ATTGTAATT ATTAT
AGTATT GG A
ATTTAAATTATCAGTATTAG AATT ||| ||||| |||| ||||||||| ||||| |||||| ||
GACTAATAACCAATACTAAT AAA TAGCC GTGA TGATATTAA TAGTA TCATAA
CC A
GATAATTATAGTAGTGATGA AAAT TAAGTA - -------- A - AAT
ATCCGATTAAAAAATAATGA
AAATTAATAG
GAM3625 AACGTCTAGCATTCCCGAGA 82029 TAGCATTCCC 82030 CTA TTCCC---- AAAT A T
AATTGCAGCTTTAGCGCATA GAGAAATTGC AACGT GCA GAG TGC GC T
AACTCTACACTCATTGCAAA AGCT ||||| ||| ||| ||| ||
CGTT TTGCA CGT CTC ACG CG T
AA- TACTCACAT AAAT - A

GAM3626 GACCTAATACGGGTACTGTC 82043 ACTGTCTATA 82044 AC AA ---------- ACA CAT
AG GT
TATAAACTCGATGCGCGACA AACTCGATGC GGT TGTCTAT ACTCGA TGCGCG GAT
GT ACG C
GATCATGTAGACGGTCCCAC GCGA ||| ||||||| |||||| |||||| ||| || |||
GTAAACTAATCACGTGCATA CCA GCAGATG TGAGCT ACGTGC CTA CA TGC
C

AAACCATATATATCGAGTAG CA GA ATATATACCAAAAT A-- AT- AA AC
GTAGACGACACCCGCCTCAC
GTC
GAM3627 GAGGTTCATGACAAAATTCC 82053 TTCATGACAA 82054 T AAAT - TGTATTAT- ------
TTAACT
TACTGTATTATGTACGATGG AATTCCTACT GAGGT CATGACA TC CTAC GTACGA
TGGATT A
ATTTTAACTAGCACATGATT GTAT ||||| ||||||| || |||| |||||| ||||||
CATTAGTATCGTACTCGTTT TTCCA GTATTGT AG GATG CATGCT ACTTAG /
TTCGTAGAGACATGTTATGT T AC-- A CTTTTTGCT ATGATT TACACG
ACCTT

GAM3628 TATTGCTGTTTGTAAGTTTT 82062 TTGCTGTTTG 82063 TTGTA TTT ---- TATTCC
TTACTAGAGTTTGTATTCCC TAAGTTTTTT TATTGCTGT AGTTT ACTA GAGTTTG C
CCTGCTCAGATTTTATATGG ACTA ||||||||| ||||| |||| |||||||
TTTAAGCTGCAGCAATA ATAACGACG TCGAA TGGT TTTAGAC /
----- TT- ATAT TCGTCC

GAM3629 GCCAGAACAAGCTTAGGATC 82070 ACCCCAGCTG 82071 -- ---------- TA A ACAATA
ACAATACAACACAGAACCCC CTATCATAAC GCCAGA ACA AGCT GG TC C
AGCTGCTATCATAACTGTTC TGTT |||||| ||| |||| || ||
TCTGGC CGGTCT TGT TCGA CC AG /
CT CAATACTATCG CC A ACACAA

GAM3630 TGTTTTTATTTACTATTCGC 82092 TGACATTGGT 82093 TT - T TTCGC ACATTATCC
CAA C
GTCATCACATTATCCTAACC ACATATAATC TG TT TAT TACTA GTCATC TAAC AAATA A
AAAAATACATTTATTTGCTG CA || || ||| ||||| |||||| |||| |||||
TTAGATGACATTGGTACATA AC AA ATA ATGGT CAGTAG ATTG TTTAT T
TAATCCA CT T C TA--- --------- TCG T

GAM3631 AATGCTGAATGCTGAAGCTG 82124 TGTAACACAA 82125 G TGAAGC A - AAG TG
GTAACT TG
TATACACTCAAGTTGATAAC TGCGCATTTA AAT CTGAATGC TGT TACA CTC T ATAACG
CTTTC G
GGTAACTCTTTCTGGTAGGA GAAT ||| |||||||| ||| |||| ||| | |||||| |||||
AGCTACGTTATTGGGAGATG TTA GATTTACG ACA ATGT GAG G TATTGC
GAAGG /
TAACACAATGCGCATTTAGA A CGTAAC - A --- GT ATC--- AT
ATT

GAM3632 GGGAGGCTCTTAACCATCAA 82134 GCTCTTAACC 82135 CTCTTAACCATCAAAAC ACT -
C
AACTTCGTGACTGGCGTCCC ATCAAAACTT GGGAGG TTCGTG GGCG TCC G
GAGGAGCGCCCCACGGATCC CGTG |||||| |||||| |||| |||
TCCC CCCTCC AGGCAC CCGC AGG /
T---------- C-- G A

GAM3633 TGCAATATTGTTATCGTAAT 82139 TGAGTCGGAT 82140 ATT TAT-- G AA- AGT
TGGAAAATTAGTGTTCGAGT TATGTGAGTA TGCAAT GT CGTAATT GA ATT G
GAGTCGGATTATGTGAGTAC CTGG |||||| || ||||||| || |||
TGGATTGCA ACGTTA CA GTATTAG CT TGA T
GGT TGAGT G GAG GCT

GAM3634 ATTGTATATTTTATTTTATA 82143 TATTTTATTT 82144 T A T TTT ATT AATAGA G
TTTTATATTTTGTAGTAAGA TATATTTTAT ATTGTATAT TT TTT ATA TAT TTGTAGTAAG AT
C
ATAGAATGCTAATGACAAGT ATTT ||||||||| || ||| ||| ||| |||||||||| ||
TTATTACAATAGATGTCTTA TAATATATA AA AAA TAT GTA AACATTATTT TA T
TTAAAAAACATATATAAT C A T TCT GAT GAACAG A

GAM3635 GTAATTCAATAGCTGTGAAT 82149 TAAAGTGCAA 82150 ATAGCTG C CT A
ATTT
TATAAAGTGCAATACTGTAA TACTGTAAGC GTAATTCA TGAATTATAAAGTG AATA GT
AGCGA C
GCGAATTTCTATTATCGCTG GAAT |||||||| |||||||||||||| |||| || |||||
GCTTTATTACACTTTATAAT TATTAAGT ACTTAATATTTCAC TTAT CG TCGCT T
TCATGAATTAT ------- A TT G ATTA

GAM3636 CCCTGTCTGATCCCGAAAGC 82154 TGCCCTAGCT 82155 TCTG - AA --- TA-- CTC
TGCTAGGTTCTCTTATAACC GACGTGGGTA CCCTG ATCC CG AGCT GC GGTT T
GTATGCCCTAGCTGACGTGG CTCG ||||| |||| || |||| || ||||
GTACTCGGGG GGGGC TGGG GC TCGA CG CCAA /
TCA- T AG TCC TATG TAT

GAM3637 GGTTTCCGGAATTGGTCGAA 82167 TCGAAGATAT 82168 ---- A --------- T- C--- TG - GC
GCA
GATATAAATAGGATCTTGGT AAATAGGATC GTCGA GA TATAAA AGGAT T GTA GAT
TTGGG G
AGATGCTTGGGGCAGGAAAC TTGG ||||| || |||||| ||||| | ||| ||| |||||
CTAAAATCGTGCTGAACGCG CAGCT CT ATATTT TTCTG A CGT CTA AATCC
G
TCTTTCTTTATAAAGTGGCT ATAA G CTCGGTGAA CT CGCA GT G A- AAA
CTCGTCGACAATAAGCAGAT
TGAAGCT
GAM3638 CTTTCTTTATAAAGTGGCTC 82175 TATAAAGTGG 82176 TATAA GCTCT C ATA AGA
TCGTCGACAATAAGCAGATT CTCTCGTCGA CTTTCTT AGTG CGT GACA AGC T
GAAGCTCTGTCCGCGTATAC CAAT ||||||| |||| ||| |||| |||
TCTGAGAGGG GGGAGAG TCAT GCG CTGT TCG T
TC--- AT--- C C-- AAG

GAM3639 TGGTGTGTGTCTATATATAT 82182 AGAGATAGAC 82183 ----- - ATA-- GTCACTGA
TGGTCACTGATTTTTTTTAC ATCACAGTTC TGGT GTG TGTCTAT TATTG T
AATAAAGAGATAGACATCAC ACCA |||| ||| ||||||| |||||
AGTTCACCA ACCA CAC ACAGATA ATAAC /
CTTGA T GAGAA ATTTTTTT

GAM3640 ACAACTAGTGTGCATACACT 82231 TAGTGTGCAT 82232 - TA TTC AA CTC CATC -----
-- CT
AATTTTCGACAAGTAACTCG ACACTAATTT TACA C ATT GAC GTAA GCA TTTAGAATT
TTCGATT A
CACATCTTTAGAATTTTCGA TCGA |||| | ||| ||| |||| ||| |||||||||| |||||||
TTCTAAAAAGTCGAATAACA ATGT G TAG TTG TATT CGT AAATCTTGA
AAGCTGA A
CTAGTTCTAAAATTGCTTTA T TC T-- AG T-- TA-- TCACAAT AA
TGAGTTTGATCTGTTGTATG
TAGATTTTTGT
GAM3641 GGTTCCCCTGATTAGGCTAC 82236 TGTCTTGGTC 82237 TCCCCT - T- T GA C CC
GAGTCGCGGTGATCGCTTCC TTCCACC GGT GATTAGG C ACGAG CGCGGT TCG TT C
CAAAAACCGAGCTGCGTTTG ||| ||||||| | ||||| |||||| ||| ||
TCTGTCTTGGTCTTCCACC CCA CTGGTTC G TGTTT GCGTCG AGC AA A
CCTT-- T TC - -- C AA

GAM3642 TAAAGCTTTCTCTATCTTTT 82260 TCTATCTTTT 82261 GC C----- -- TCTTTAA CC C
ATT
TATCTCTTTAATTTTTCAAC TATCTCTTTA TAAA TTTCT TATCT TTTTATC TTTTTCAA TT
TGA A
CTTCTGAATTAATATCATAA ATTT |||| ||||| ||||| ||||||| |||||||| || |||
ACTTGAGAAAAATTATTGAT ATTT AAAGG ATAGA AAAATAG AAAGAGTT AA ACT
/
AAAATTAGATAATTTATGGA A- TATTTA TT TTATTAA CA T ATA
AAATTTA

GAM3643 GAAAGCACACGATACACATG 82271 AAGCACACGA 82272 A C T CATGT A- G ATG A
A
TATCCAGTATGCTATATGAT TACACATGTA GAAAGC CA GA ACA ATCC GTAT CTAT ATTA
CATAATT T
TAACATAATTATAAAATTAT TCCA |||||| || || ||| |||| |||| |||| |||| |||||||
GATGATAAATGGGGTATAGG TTTTCG GT CT TGT TAGG TATG GGTA TAGT
GTATTAA A
GATTGTTCTGAGCTTTT A - - ----- GA G AA- A A

GAM3644 GAGGCATCTCAGTGTTTGAA 82317 CACTGATTGA 82318 C------- TGA- GGAAG
TTGGAAGAATGTGTGGTGAA CATTGTGCCT GAGGCAT TCAGTGTT ATT A
TGGCACTGATTGACATTGTG C ||||||| |||||||| |||
CCTC CTCCGTG AGTCACGG TGG A
TTACAGTT TAAG TGTGT

GAM3645 ATTCTTGAGGCATCTCAGTG 82387 TGGAAGAATG 82388 ----- AG-- T AA AA TGT AT----
TGATT
TTTGAATTGGAAGAATGTGT TGTGGTGAAT CATCTC TG TTG TTGG GAATG GGTGA
GGCAC G
GGTGAATGGCACTGATTGAC GGCA |||||| || ||| |||| ||||| ||||| |||||
ATTGTGCCTCTAAGTCACCT GTGGGG GC AGC GATT CTTAT CCACT CCGTG
/
ATTCAATTAGGGCGACCGTG TTAGA GTGT C GG AA --- GAATCT TTACA
TGGGGGTGAGATTTAATTGG
CGAGAACCAT
GAM3646 CGACGTTCCTTCAATATTTC 82420 ATCGTGATAG 82421 TCCTTCA TT TTAA C T C
TTTAACGCCATCGTGAAACT ATTTATCACG CGACGT ATA TCT CGC ATCG GAAA T
CTTTTCCTGATCGTGATAGA TCG |||||| ||| ||| ||| |||| ||||
TTTATCACGTCG GCTGCA TAT AGA GTG TAGT CTTT C
C------ TT TA-- C C T

GAM3647 TATGTTATAAAACAGTGTAG 82424 TATAAAACAG 82425 C A A
CGTTGAATTTTAAAAAAATC TGTAGCGTTG TATGTTATAAAACAGTGTAG GTTG ATTTT A
CAACATTATACTGTTTTATA AATT |||||||||||||||||| |||| |||||
ATATA ATATAATATTTTGTCATATT CAAC TAAAA /
A C A

GAM3648 CCGTGGCGTAAATATAGGAC 82434 TAGGACATAG 82435 C AA ACATA TACA AC
ATAGATCGGTACAGATACAC ATCGGTACAG CCGTGG GTA TATAGG GATCGG GAT A
CGTCACCTGATCACCCCCTA ATAC |||||| ||| |||||| |||||| |||
TACTATCTATGG GGTATC TAT ATATCC CTAGTC CTG /
- C- CCCA- CA-- CC

GAM3649 ACACTTTCCCGCGTGTCGCG 82452 TGCCTGGCGC 82453 TTT C-- TC- GT T T
TGTGGTTCATGTGTGTGCCT CCCCACCCTC ACAC CCCG GTG GCGT GGT CA G
GGCGCCCCCACCCTCGGGTT GGGT |||| |||| ||| |||| ||| ||
CGTGT TGTG GGGC CAC CGCG CCG GT T
CTT TCC CCC GT T G

GAM3650 TGCGTGTGTGGTTAACGCCT 82484 TTGCATGGCG 82485 TAA CT T GAA GA AA-
AAGG-- TG A T
TTGTTTGCTGAATGAGTTGA TGTTAAATGG CGC TTGT TGCT TGAGTT TGT GTTTAATA
G AG TAA G
TGTAAGTTTAATAAAGGGTG GGCG ||| |||| |||| |||||| ||| |||||||| | || |||
AGATAATGTTTAACTTGCAT GCG AATA ATGG ATTCGG GCG TAAATTGT C TC
ATT /
GGCGTGTTAAATGGGGCGGG --- T- T GAA G- GGG GCGGTA GT A T
GCTTAAAGGGTATATAATGC
GCCGTGGGCTA
GAM3651 GTGCTCCGCACCTGTGTTTA 82489 TATGTCAGCA 82490 TG C AC TG----- CTA --- TGT

TCTAATGTGACGTCACTGTT GCTGAGTGT G CTC GC CTG TTTAT ATGTGACG TCAC T
TTTGTGAGAGTGTCATGTAA | ||| || ||| ||||| |||||||| ||||
TAAAATTATGTCAGCAGCTG T GAG CG GAC AAATA TGTACTGT AGTG /
AGTGT GT T AC TGTATTA A-- GAG TTT

GAM3652 AAACCTGGAGAACTTGTAGG 82521 TAAGGCCATT 82522 - AAC GT TATA GAC-
AGG-- G AT
GTTGTATAGTCGACAGGATG CCTGCAGAAA AAACCTG GAG TTGTAGG TG GTC
AGGATGT TG AGAC G
TAGGTGGAGACATGACGTCT CTTA ||||||| ||| ||||||| || ||| ||||||| || ||||
ACAAAGAGACATCCTATAAG TTTGGAT TTC GACGTCC AC CGG TCCTACA AC
TCTG /
GCCATTCCTGCAGAAACTTA A AAA TT ---- AATA GAGAA A CA
TAGGTTT

GAM3653 TAAGATAATCTAAATATTCT 82536 TCTCTATAAC 82537 - A-- TTC- - AA TTGT TA T
T TAC
CTATAACATAATTGTAATGT ATAATTGTAA AAT CT AATA TCT AT CATAA AATGTGTTT
TGT TA AGC A
GTTTTATGTTTATAGCTACA TGTG ||| || |||| ||| || ||||| ||||||||| ||| || |||
AATGTTTTATGCAAAATACA TTA GA TTAT AGG TG GTATT TTACATAAA ACG AT
TTG /
TTTTATGAGGTCGGATACTT C AAA TCAT C GA ---- -- T T TAA
ATTAAAAGCATTGTCTTA

GAM3654 GAGCGGGGAAGACGGCGAGC 82543 TCTTGCTGCT 82544 GG C C CCA C
CCTCC
GGGCCACGGTGGCGGTCGGA ACTGCCCCTC GAGCG GAAGA GGCGAG GGG
CGGTGGCGGT GGAGT T
GTCCTCCTCCTGCTGCTCTT TCGC ||||| ||||| |||||| ||| |||||||||| |||||
GCTGCTACTGCCCCTCTCGC CTCGC CTTCT TCGCTC CCC GTCATCGTCG TCTCG C
TTCTTCACGCTC A- - T C-- T TCGTC

GAM3655 ATATTAATATTAAAATATGA 82567 TAAAATATGA 82568 ATTAA CT- TTTTT TAAA
TA
ACTTAGATTTTTTATATTAA ACTTAGATTT ATATTAAT AATATGAA TAGA TATAT TCTA A
ATCTATAATATTAGAATATA TTTA |||||||| |||||||| |||| ||||| ||||
TATCTTCTATATTTTATATT TATAATTA TTATATTT ATCT ATATA AGAT T
AAAAATTAATAT AAAA- TAT TCT-- TA-- TA

GAM3656 GGCGCACATGAGGAATATAA 82574 TGAGGAATAT 82575 CACATGA ATAATATAGCAACA
- C A G
TATAGCAACAGTCGGCTCGG AATATAGCAA GGCG GGAAT GTCGGCTC GGG
CGACG CGGGC C
GCCGACGACGGGCGCTCGCT CAGT |||| ||||| |||||||| ||| ||||| |||||
CGGCGTCGACTCGGAGCCGG CTGC TCTTA CGGCCGAG CTC GCTGC
GCTCG T

CCGATTCTCGTC ------- GC---------- G A G C

GAM3657 TTATAAAATTATTATTGATA 82586 TATTATTGAT 82587 ATT GATAATAAATC A A
ATAAATCATTGAAAATATAT AATAAATCAT TTATAAA ATTATT ATTGA AATATATT T
TATTAATATATTATTAATAT TGAA ||||||| |||||| ||||| ||||||||
ACACAATAAATAATTAATTT AATATTT TAATAA TAATT TTATATAA /
ATAA AAT ATAACACATA- A T

GAM3658 GTCTAGGGGAAGGACATGGG 82591 TAGGGGAAGG 82592 A AAGGACAT C T ACC
GCAGGGGGATGGAGACCAGG ACATGGGGCA GTCT GGGG GGGG AGGGGGA GGAG A
ACCTCCTCCTCCTCCCCCTC GGGG |||| |||| |||| ||||||| ||||
CAGGAC CAGG CCTC CCCC TCCTCCT CCTC G
A -------- - - CAG

GAM3659 CCGTCGTCACAGCTGGAAGG 82760 GAGCTTCCAG 82761 GT CA GAAGG C--- TTAAT -
G AT
ACACCGTTAATCTGGAGCGT TTGTTCGTAA CC CGTCA GCTG ACA CG CTGGA GC
TTGAA A
TGAAATAGTCTTCAGAGCTT ATGT || ||||| |||| ||| || ||||| || |||||
CCAGTTGTTCGTAAATGTAT GG GCAGT CGAT TGT GC GACCT CG GACTT G
GTGTAGCGCTGACGCAGG AC CG GTGTA AAAT TTGTT T A CT

GAM3660 GGTGTCTGAAAGCTCGCCAA 82765 TGAAAGCTCG 82766 -- A C CAAG C GCG
GGTCTCGCGTAAAAGAACAG CCAAGGTCTC GGT GTCTGAA G TCGC GT TC T
ATGTGAACTTCAGATGTACC GCGT ||| ||||||| | |||| || ||
CCA TAGACTT C AGTG CA AG A
TG - A TAGA - AAA

GAM3661 GATGTGAACTTCAGATGTAC 82770 AATAATACGG 82771 TG ACTTC T ACC CAA- T-
TTC------- AT
CAACCAAATAATACGGGTTC GTTCCGCTAT GATG A AGA GT AAC ATAA ACGGG
CGCT A
CGCTATAAAAAGTGCACCTC AAAA |||| | ||| || ||| |||| ||||| ||||
TATTCCCGTTCTTATCCCCG CTAT T TCT CA TTG TATT TGCCC GTGA A
TTCTAACTCTTCCTTGTATC GT CCT-- - ATC CCCC CT TTATCTCCAC AA

GAM3662 CGATTACGAATGCCCTGGCT 82773 CCTGGCTATT 82774 CGAA T C TT AT- T
ATTTTAATGTTATTACTAGT TTAATGTTAT CGATTA TGCCC GG TA TTA GT A
AATTTACCGGGCGATAATCG TACT |||||| ||||| || || ||| ||
GCTAAT GCGGG CC AT AAT CA T
A--- - - TT GAT T

GAM3663 TCTTAAGTATTAACTTTAAA 82806 TATAAAGATT 82807 T T T AT-- AA --- TGTGT
AAC

TATAATTATAAAGATTGTGT GTGTATTCTT TC TAAG AT AACTTTAA AT TTATAA AGAT ATTCTTC G

ATTCTTCAACGACAGAGGAG CAAC || |||| || |||||||| || |||||| |||| |||||||

TTCTCTATCTACTTTATAAC AG GTTC TG TTGAAATT TG AATATT TCTA TGAGGAG /

AGTTTTATTAAAGTTTGTTC C T T ATTT AC TCA TCTCT ACA TTGCGA

GAM3664 CGAGTGCTCACCCCCGAGGA 82821 TTGCCACTCG 82822 -- - CCC --- CGCACCCATCTCC AGT

GCTCGCCGCACCCATCTCCG CGAGCAGATT CGAGT GCT CA CCGAGGA GCTCGC GCAGCT A

CAGCTAGTAACAAGGTTGCC CTCG ||||| ||| || ||||||| |||||| |||||| |||||| ACTCGCGAGCAGATTCTCGG GTTCA CGA GT GGCTCTT CGAGCG CGTTGG A

CATTGTAGCGGACTTG GG T TAC AGA CTCAC-------- AAC

GAM3665 CACCCACAAAGGAGTTTGTA 82826 AGGAGTTTGT 82827 C AG GTAAAA- ATC

AAATAAAATCTCTGTTTAGA AAAATAAAAT CAC CACAA GAGTTT TAAA T

CCTTAAAATTTGTTGTGTGT CTCT ||| ||||| |||||| |||| G GTG GTGTT TTTAAA ATTT / T G- ATTCCAG GTC

GAM3666 GTGAGTTTGTGGACCCAAAG 82839 GTGGACCCAA 82840 ---------- TG A CAAA-- C-AGAGA

CCCTCAGAGACAACGCGACA AGCCCTCAGA GTGAGT T TGG CC GCC TC C

GGCCAGTATGGACCGTGATA GACA |||||| | ||| || ||| ||

CTTTTATTTATTAACTCAC CACTCA A GCC GG CGG AG /

ATTATTTATTTTCAT GT A TATGAC AC CGCAA

GAM3667 TGACGTGGATACTAGTAAAA 82884 TGACGTGGAT 82885 GGA--- AAAAAAGT AA- TC

AAAGTGCGTCAAAGCTCTTA ACTAGTAAAA TGACGT TACTAGTA GCGTCA GC T

GCGTGTGACGTGGATACTAG GGGA |||||| |||||||| |||||| ||

TAAAAGGGACGTCA ACTGCA ATGATCAT TGCAGT CG /

GGGAAA AGG----- GTG AT

GAM3668 TACCCCAGATTTACCCGTTA 82896 CCTAAAATTC 82897 CAG - - G CC -- C C-- TC C C AG

CCCTAAAATTCCCTCCCCTT CCTCCCCTTT ATTTA C CC TTA CTAAA ATTC CT CCCTT TCTT ACTCG CG G

TCTCTTCACTCGCCGAGGCC CTCT ||||| | || ||| ||||| |||| || ||||| |||| ||||| ||

ACGCCGAGTAGGACCGAGGG TAGAT G GG AAT GATTT TGAG GA GGGAG AGGA TGAGC GC C

TACAGCGAGTCTTTTAGTTT ATG T T - TT TC C CAT CC - C AC

AAGGTGTTAGATGTAAGGTA

```
GAM3669  TTATGTTCTTCATTTGCACG 83006   TATACAGCTA 83007       C     GCA  TA-  A--  A   TA    AAC
 AT
     TTATACAGCTATCACTATTT       TCACTATTTG       TTATGTT TTCATTT  CGT  TAC  GCT TCAC  TTTGA
 CATGG  C
     GAAACCATGGATCTTCTATG       AAAC          ||||||| |||||||  |||  |||  ||| ||||  |||||  |||||
     TCGAACGTGAAGTCACGTAG                    AATATAA AGGTAAA  GCA  ATG  TGA AGTG  AAGCT
GTATC  /
     ATACGAAATGGAAATATAA                       -     ---  TAG  CAC  -   C-    ---    TT


GAM3670  TTTACAAATATTACTAAATG 83026   TGATGTAGGT 83027       AA  T   AAA  T  C   TTAATAAG
     CTATCCATGTTTAATAAGCT       ATTATGTAAA       TTTACA  TA TACT  TGC ATC ATGT      C
     ATACGTTACATGATGTAGGT                    ||||||  || ||||  ||| ||| ||||
     ATTATGTAAA                        AAATGT  AT ATGG  ATG TAG TACA      /
                                  --  T   ---  -  -   TTGCATAT


GAM3671  TGAGTTAAATTATAATAAGC 83053   TAAGCTAGTT 83054    A   AA--       C     TA   AT
     TAGTTATAAGTTATAATAAG       ATAAGTTATA       TG GTTA   TTATAATAAG TAGTTA  AGTT  A
     CTATTAGCTAATTTATTATA       ATAA          || ||||   ||||||||||| ||||||  ||||
     AAAAATAACCA                     AC CAAT   AATATTATTT ATCGAT  TCGA  A
                                -   AAAA       A    TA   AT


GAM3672  GGCAAGTGCGCGTGCAGGCG 83062   CGTGCAAGTG 83063       TGC  G   A   T  T   --    -  CA   G
T
     TGCTCGCGTGCGCCGCCAGC       TGTGCCGCCC       GGCAAG   GC TGC GGCG GC CGCG  TGCGC
CGC  GCG GCCC T
     GGGCCCTTAGGGCGCGTGCG       GCAG          ||||||   || ||| |||| || ||||  ||||| |||  ||| ||||
     CGTGCAAGTGTGTGCCGCCC                    CCGTTC   CG ACG CCGC CG GTGT  ACGTG GCG  TGC
CGGG /
     GCAGGCCCTTGCC                        C--  G   C    - T   GA    C   --   G    A


GAM3673  TGGATAATATTTTTATTAAT 83090   TTAACAGAAT 83091     AAT     ATT  TGTT       TAATA   ATA  A
    ATAA
     GTTAAAAAAAATTTAATAAT       ATGAAATAAT       GAT   ATTTTT   AA   AAAAAAAATT    ATA   TG
TTAGTATAA   T
     AATATGATTAGTATAAATAA       TTTT          |||  ||||||  ||   ||||||||||    |||  || |||||||||
     TCAAATTATATTAACAGAAT                    CTA   TAAAAA   TT   TTTTTTTTAA    TAT   AC AATTATATT
/
     ATGAAATAATTTTTTTTTTT                     AT-     GT-  TT--       TAAAG   AAG  -       AAAC
     TTGAAAAATTAATCCA

GAM3674  GCCGTAGGGCTGGCAGGGAC 83095   GGGCTGGCAG 83096         -----    CA   A    ACCCAGCA
TTTT
     GGCACCCAGCAGCTATTTTC       GGACGGCACC       GCCGTAGG    GCTGG  GGG CGGC      GCTA
C
     ATCTCTAGCGCCGCCTACTA       CAGC          ||||||||    |||||  ||| ||||       ||||
     GCGGAAATCTGCGGT                         TGGCGTCT    CGATC  TCC GCCG       CGAT    A
```

AAAGG A- - -------- CTCT

GAM3675 TTCTAGGGTTCTATTATCAT 83215 TAGGGTTCTA 83216 -- AT TT AT G T
CAATTCCATAGTGAGTCTTT TTATCATCAA TTCTAG GGTTCTATT CATCAA CC AGT AG C
GACTTCGGTTTGGTGGCAGT TTCC |||||| ||||||||| |||||| || ||| ||
AGGGCTTTCTGGAG GAGGTC TCGGGATGA GTGGTT GG TCA TT /
TT CG T- CT G T

GAM3676 TCTGAACACTTTCTTGAAAG 83224 TTGAAAGTTG 83225 AACA --- A- T CT CCA GT
TTGCGGCTGACCACCGTACA CGGCTGACCA TCTG CTTT CTTGA AGT GCGG GA CC A
GGAATTCTCTCGCACTAGTC CCGT |||| |||| ||||| ||| |||| || ||
GGGTTTGAAGCGCGGG GGGC GAAG GGGCT TCA CGCT CT GG /
GC-- TTT GA - CT TAA AC

GAM3677 CTTTCGTGAGGACCTGTAAG 83231 TTGCATGTAA 83232 CG AC GTAAG C - A
TATGTCATGGAGTGGGAGGG GCCTTATAGA CTTT TGAGG CT TATGT ATG GAGTGGG G
TTCATTTATATTGCATGTAA GG |||| ||||| || ||||| ||| |||||||
GCCTTATAGAGG GGAG ATTCC GA GTACG TAT TTTACTT G
AT -- AT--- T A G

GAM3678 TTTCTGTATTTTGTCAAATA 83253 TATTTTGTCA 83254 TTT A-- CATT C TTAAAAA-
TA-- TT
GTCATTGGTCTGATTAAAAA AATAGTCATT TCTGTAT GTCA ATAGT GGT TGA GGTT
ATAAATG T
GGTTTAATAAATGTTTTACA GGTC ||||||| |||| ||||| ||| ||| |||| |||||||
TTTATATTTGGCCGACTCTG AGGCATA TAGT TGTCA TTA ACT CCGG
TATTTAC /
TTCATATTTTACTGTCGCTG --- CGC TT-- T TGTCTCAG TTTA AT
ATATACGGAAA

GAM3679 TGTTATCAAATGTACTGTTT 83259 ACGCAAATGG 83260 TATC G ATAC----- A TT C
TTT
AATACGCAAATGGATTTACT ATTTACTACG TGT AAAT TACTGTTTA GCA ATGGA TA
TACG T
ACGTTTTAATTGTATGTCTT TTTT ||| |||| |||||||||| ||| ||||| || ||||
CATGTGCAGGCTCTAGTGGA ACA TTTA ATGATAGGT CGT TACTT GT ATGT /
TAGTAATTTTCTCACA CTCT - GATCTCGGA G CT - TAA

GAM3680 TGGTGCTAATTATTCCTATA 83263 TATTTCACGA 83264 - A ATAT GAAA ATGAAGGCA T
---------- A
TTATATTTCACGAAAAATGA AAAATGATGA CT TATT TTCAC AATG ATCAT CC
TCAT A
TGAAGGCAATCATTCCTCAT AGGC || |||| ||||| |||| ||||| || ||||
AAGATGATAAAAAGTAAGGG GA GTGA GAGTG TTAT TAGTG GG AGTA /
TGTGATAAAAGTGTATTGAG T - GGT- AGAG GTGAAAA-- T GAATGAAAAAT G

AGTGAGTGGAGTGAGTGAGT
GAGAGTATTA
GAM3681 CTATGCATACTATGTGCCCC 83271 TAGCAGAGTA 83272 AT - G- CC C G
GCGATGGCGGCTGTCGTCCT CGTTCGCATG CTATGC AC TAT TGC CG GATGGC G
GTAGCAGAGTACGTTCGCAT G |||||| || ||| ||| || ||||||
GG GGTACG TG ATG ACG GT CTGCTG C
CT C AG AT C T

GAM3682 GTAGTGGATGTCCTGGACCA 83296 TGTCATGGAC 83297 G-- - - A-- -- TG T
TCGTGGCTACGGCTGCGTAG CATCGTGGCT GTAGT GATG TCC TGG CCAT CG GC A
TGGATGTCATGGACCATCGT AC ||||| |||| ||| ||| |||| || ||
GGCTAC CATCG CTAC AGG ACT GGTG GC CG C
GTG C T GTA AT GT G

GAM3683 GCGAGTGGTCGTTGACGTTG 83333 TATCAAGTAC 83334 -- TCG - GTT ---- G
TGGTTGTTTTACGAAGTAAA AGTTCTACTT GC GAGTGG TTG AC GTGGT TGTTTTAC A
ATATATAGCTATCAAGTACA TTGC || |||||| ||| || ||||| ||||||||
GTTCTACTTTTGC CG TTCATC GAC TG TATCG ATAAAATG /
TT TT- A AAC ATAT A

GAM3684 GGCGACAGGAAGTCTGTCCA 83343 TGAGGGAAGG 83344 A A-- TCCA - A - AA
AAGT CTA
ACCTCATTACCCTTTCCAAA CGTGAGAGCG GGCGAC GG AGTCTG AC CTC TTAC CCTTTCC
AGC CGG C
GCAAGTCGGCTACCATACCG TCAG |||||| || |||||| || ||| |||| ||||||| ||| |||
TAAGCTGAGGGAAGGCGTGA CCGCTG CC TCAGAC TG GAG AGTG GGAAGGG TCG
GCC C
GAGCGTCAGACTACACCGTC - ACA ---- C - C AG AAT- ATA
GCC

GAM3685 CTTTTTTTTTGTGAGGCTTT 83355 TATAAAATTG 83356 T GAG --- TT
GTATAAATTGTTTTTTATAT TAAATAAAAA CT TTTTTTTGT GC TTTGTATAAA G
AAAATTGTAAATAAAAAAAC AACA || |||||||||| || ||||||||||
AG GA AAAAAAATA TG AAATATATTT T
C AA- TTA TT

GAM3686 TAATACTTGACTGACTTAAA 83360 TACTTGACTG 83361 C CT AA--- - TAATTAATA
TTC
ACTTGATAATTAATAATATA ACTTAAAACT TAATA TTGACTGA TA AC TTGA ATATAA G
ATTCGTTTTTATATGTGACT TGAT ||||| |||||||| || || |||| ||||||
ATTTTAACGTCTAAATGTAT ATTAT AATTGATT GT TG AATT TATATT /
TAGTTAAATATTA A AT AAATC C TTATCAGTG TTT

GAM3687 TAGCTACTGAAGATAAAGAA 83367 TATTTCAAAA 83368 A ATAAAGAA ---- AA
GAAGTAAGAAAATCTGAAGT AGCTTTAGAA TAGCT CTGAAG GAAGTA AG A

ATTTCAAAAAGCTTTAGAAG GTTG |||||| ||||||| |||||| ||
TTG GTTGA GATTTC CTTTAT TC /
A GAAAAA-- GAAG TA

GAM3688 TGCGACGTGTAGAACCACTT 83377 AGGATTGTTT 83378 A - A-- T- AA T
ACAAAACTTTTTGAAAGGAT AGCTAGGATT TGCGACGTGT GAA CC CT ACAA CTTT T
TGTTTAGCTAGGATTCACGC CACG |||||||||| ||| || || |||| ||||
GTTGTA ATGTTGCGCA CTT GG GA TGTT GAAA /
- A ATC TT AG G

GAM3689 TAAAATATAATATTAATGTA 83385 TATAATATTA 83386 A T GTAC C TAT T T
CTAAAACTTATATATTATTA ATGTACTAAA TAAAAT TAA ATTAAT TAAAA TTATATAT
TAATTTA CTAAC A
ATTTATCTAACTAAAGTTAG ACTT |||||| ||| |||||| ||||| |||||||| ||||||| |||||
TAAATTATATATATAATTTT ATTTTA ATT TAATTA ATTTT AATATATA ATTAAAT GATTG
A
ATAATTAATTTAATTTTA - - AT-- - T-- - A

GAM3690 TAGCCTCCCACTTTTATGGA 83389 ATGAGTCATG 83390 CCC----- - AAATCTG CT
AATCTGGTAGCTCCTCCTAC AAATGTCCCT TAGCCT AC TTTTATGG GTAG C
ATGAGTCATGAAATGTCCCT TCAA |||||| || |||||||| ||||
TCAAAGGCTG GTCGGA TG AAAGTACT CATC C
AACTTCCC T GAGTA-- CT

GAM3691 CGTCTAGGCCACGTACAGTC 83413 TACAGTGTTA 83414 - ------ G T- --- TC- CCTCT
TATTGTCCTCGGACCCTCTG CTGTTGTGTG CGTCTA GG CCAC TACAG CTATT GTCC
GGAC G
CCTATAGGTTAATAGGAATA TATC |||||| || |||| ||||| ||||| |||| ||||
CAGTGTTACTGTTGTGTGTA GGATCT GC TGTT GTCAT TGACA GGAT TGGA /
TCGCTCTAGG C TATGTG - TG TAA AAT TATCC

GAM3692 AGTGCGGTGGCGATTGTATG 83449 TAAGCCGGTT 83450 GC A- TATGTAT T- - AA
TATCCTCTTATTTCGGGAAT CGAGGCGCCA AGT GGTGGCG TTG CC CTTAT TTCGGG T
GGACCCGAGTGTAAGCCGGT CTAA ||| ||||||| ||| || ||||| ||||||
TCGAGGCGCCACTAAACT TCA TCACCGC AGC GG GAATG GAGCCC G
AA GG TT----- CC T AG

GAM3693 TTTTTTTAATGGTGTTGTGG 83453 TGAGGAATGA 83454 AA- -- TG - G- -- A AG
ATGAGGAATGAGGAATGAGA GGAATGAGAG TTTTTTT TGGTG T TG GATGAG AATGA GGA
TGAG T
GTGTCTTATCTAGTCATTGG TGTC ||||||| ||||| | || |||||| ||||| ||| ||||
TTTATTACATGGATCATCAG AAAGAGG ACTAC G AC TTATTT TTACT TCT ATTC /
AGGGAGAAA GAG TA GT A GG GA - TG

GAM3694 TGTGTTGTTTTTAAAAAAAG 83475 TAAAAAAAGA 83476 G TT CATT
AAAAAAAAAGGCATTATTTT AAAAAAAAGG TGTGTT TTT AAAAAAAGAAAAAAAAAGG A
TTCTTTTTTTTTCTTTTTTT CATT |||||| ||| ||||||||||||||||||
TTAAAAATATA ATATAA AAA TTTTTTTCTTTTTTTTTCT T
- TT TTTT

GAM3695 TTATAATTTATTTATCTAAT 83640 TAATATTAAA 83641 TTTATT CTA GT- TA
ATTAAAATATATATAGTTTA ATATATATAG TTATAA TAT ATATTAAAATATATATA TTAAT A
ATTAATCATTAATAATGTAT TTTA |||||| ||| |||||||||||||||| |||||
GTATTTTAATATGTAATATT AATATT ATA TATAATTTTATGTATGT AATTA /
ATTTATAA TATT-- ATG AAT CT

GAM3696 GTTTGTATCGCATCTTTCCT 83645 TCGCATCTTT 83646 T ATCG TT AG TTA T
CCT-- CTA
GTGTGTAGTTGTTTATGTTG CCTGTGTGTA GT TGT CATCT CCTGTGTGT TTGT TGT
GGATG GTGGGT T
GATGCCTGTGGGTCTATCAC GTTG || ||| ||||| ||||||||| |||| ||| ||||| ||||||
ACCCGCCCCTCCATCCCACA CG ACA GTAGG GGGCACACA AACA ACA CCTAC
CGCCCA /
AACACAAAACACACGGGTTG C AAA- TT A- CAA C CTCCC CAC
GATGAAAACACGC

GAM3697 GGCGCCTACGCACTTTGTAT 83651 TATAAGACTG 83652 TAC - ----- G GA-
AAATACTAGG AACTA
ATAAGACTGATTGTAAATAC ATTGTAAATA CC GCACTTTG TA TATAA ACT TTGT
TGGAGT G
TAGGTGGAGTAACTAGGAAA CTAG || |||||||| || ||||| ||| |||| ||||||
AACTCTAACAAAAAGGTGTT GG TGTGAAAT AT GTGTT TGG AACA ATCTCA
/
GTGCTGTTTATTAAAGTGTA CA- T TTGTC G AAA ---------- AAAAG
CGGAGCC

GAM3698 TTGGATAAATTAGGTTGACA 83658 TTGACATTAG 83659 TAAAT---------- G T ACA A
TTAGTAACAGAAAGTATTCA TAACAGAAAG TTGGA TAGGTT ACAT AGTA GAA G
ATATTATGTAGACCTATAAA TATT ||||| |||||| |||| |||| |||
AAATGAGACCCTCCAA AACCT ATCCAG TGTA TTAT CTT T
CCCAGAGTAAAAAAT A - AA- A

GAM3699 CCTGTTTCACCTATCTCTAA 83666 TAAGTAGGAT 83667 TTTCAC TC AAA- AA TGACAT--
ATCT T
AAATCAAAAATTCTATGACA TAATATTTGG G CTATC TAA TC AAATTCTA TTTTAT
TTATTT T
TTTTTATATCTTTATTTTTT AATT | ||||| ||| || |||||||| |||||| ||||||
GGAATAAGTAGGATTAATAT T GATAG ATT AG TTTAAGGT AGGATG AATAAG
T
TTGGAATTTGAGAAAAATTA TAA--- CT AAAA AG TTATAATT ---- G

TCGATAGAATTAGG

GAM3700 TTTTTATAAATTTTTATGAG 83673 TAAAGTGTAT 83674 TTT ----- - A
TATTTTTACAAAAATGTATA GTCTTATGTA TTTTTATAAAT TATGAG TATTTT TACA A
AAGTGTATGTCTTATGTATA TATT |||||||||| |||||| |||||| ||||
TTTATAAAAA AAAAATATTTA GTATTC GTGAAA ATGT A
TAT TGTAT T A

GAM3701 CCTTTAAAATTGATGCATTA 83688 ATGCATTATA 83689 A C TAGT
TAAGATCGTGTAGTAAATCC AGATCGTGTA CCTTTAAAATTGATGCATTATA GAT GTG A
ACTATCCTGTAATGCATTAA GTAA |||||||||||||||||||| ||| |||
TTTTAAAGG GGAAATTTTAATTACGTAATGT CTA CAC /
C T CTAA

GAM3702 ATATAAATACAAAAACATAT 83702 TTAGTTGTTG 83703 AA A AT - TAG
GTTTTAGTAGGAATTTTAGG TATGGATAT ATAT ATACAA AAC ATGT TTTAG G
TACATTAGTTGTTGTATGGA |||| |||||| ||| |||| |||||
TAT TATA TATGTT TTG TACA GGATT A
GG G AT T TTA

GAM3703 TTGTAATCTGCGTCAATATT 83720 AAAACGTAGC 83721 AA- TCAA- TCTC T
CTCTAACTTCAGTTAAAACG AATCGCAGAG TTGT TCTGCG TAT TAAC T
TAGCAATCGCAGAGGGGCAA GGGC |||| |||||| ||| ||||
AACG AGACGC ATG ATTG C
GGG TAACG CAAA A

GAM3704 TCTGTGGGGGAGTGGGGTGT 83741 TGGTTTGAAC 83742 GG - G GG ATTAG G TAG
TGTGGATATTAGAGGGTAGA GTCTCCATTA TCTGTGGG AGTGGGG TGTT T AT AG G A
GGGTGCTGGTTTGAACGTCT ACCC |||||||| ||||||| |||| | || || | |
CCATTAACCCACGGG GGGCACCC TTACCTC GCAA G TG TC T /
AA T - TT G---- G GGG

GAM3705 AGCTTTTATGTGTGTGAAGA 83751 TGTGTGAAGA 83752 TTTTAT- T AGT G TA
AGTGATGTTTAGGGTAAGGT AGTGATGTTT AGC GTGTG GAAGA GAT TT G
CTGTCTTTTTGCATTGGATT AGGG ||| ||||| ||||| ||| ||
TGCT TCG TACGT TTTCT CTG AA G
TTTAGGT T GT- G TG

GAM3706 GAGAGTTGAAACCTTCGCTA 83763 TCGCTACTCA 83764 A TTC---- TACTCAAG AG
CTCAAGTTAGTAAGAAACTA AGTTAGTAAG GAGAGTTG AACC GC TTAGTA A
CTAGAATTCATGCACAATTT AAAC |||||||| |||| || ||||||
GGTTGCAACTCTT TTCTCAAC TTGG CG GATCAT A
G TTTAACA TACTTAA- CA

GAM3707 TTAAATAAAAGTAGTACCAT 83778 TAGCATCGTT 83779 A T TT- TT AA
TACTTTAAAAGTTAACGATG AACTTTTAAA TTAAATAAAAGT GTACCA
TACTTTAAAAGTTAACGATGTT TCTTT TT A
TTTTTCTTTTTTTAAAACAA GTAT |||||||||||| |||||| |||||||||||||||||||| ||||| ||
GTTAAAGATTTAGCATCGTT AATTTATTTTCA CATGGT ATGAAATTTTCAATTGCTACGA
AGAAA GA A
AACTTTTAAAGTATTGGTAC C T TTT TT AC
CACTTTTATTTAA

GAM3708 GCGTTTCGTTAACCCTTCGT 83785 CGTGCATTCT 83786 TCG TT- T T T CA
TGTTACTAGGTGTGTACTTC TGGTAGCTAT GCGTT TTAACCC CGT GTTACTAGG GTGTAC
TCTC C
TCCACGAGAGGCGTGCATTC GTGT ||||| ||||||| ||| ||||||||| |||||| ||||
TTGGTAGCTATGTGTGGGTT CGCAG GATTGGG GTA CGATGGTTC TACGTG GGAG /
AGGGCGACGC CGG TGT T T C AG

GAM3709 TGGCAGTTGACGGGTTTGTG 83791 AGCTGGAGTG 83792 -- CG TG TAG ----- CCAC-
-- CCCAT
ATAGCTGGAGTGCTGACCAC CTGACCACGG TTGA GGTT TGA CTGGAG TGCTGA
GGCACA GGA T
GGCACAGGACCCATTAACTT CACA |||| |||| ||| |||||| |||||| |||||| |||
TCCTATGTGTTTATTTTTAG AACT CTAG ACT GACCTC ACGATT TTGTGT CCT
/
CAATGGTCTCCAGAATTCAA AA -- GA TAA TGGTA TTTAT AT TTCAA
GGATCTCAAAAGGGCCTGCC
A
GAM3710 ATTAATTATTTTATAATTTT 83895 TTTATAATTT 83896 A TT-- A GA
ATAATTTATGAAAAATAAAA TATAATTTAT ATTAATTATTTT TAAT TATA TTTAT A
TATATTTTATTAAAAATAAT GAAA |||||||||||| |||| |||| |||||
TAAT TAATTAATAAAA ATTA ATAT AAATA /
- TTTT A AA

GAM3711 ATTGTCTGATATCTTGTCCT 83898 TAAGTAGCCC 83899 CTGATAT G ---- A -- A TG --
---- TAA
GGGGGCAATTTTATTCAGTG CCGTCCAGGA ATTGT CTT TCCT GGGGGC ATTT TATTC G
C CC C
CCCTAACTTTGGAAATACGT GAAG ||||| ||| |||| |||||| |||| ||||| | | ||
GCGAGTAATAAGTAGCCCCC TAACA GAA AGGA CCCCCG TGAA ATGAG C G
GG /
GTCCAGGAGAAGTTGCTTAC TTCGTT- G CCTG A TA - GT CATAAA TTT
AAT

GAM3712 TGCATTTGTTGCATTTCCTG 83924 TAGCAACGGA 83925 TT- TG - T - ATCACGA
AACATC
TTCATCACGATATACAACAT CACGGCAATA TGCAT GT C ATT CC TGTTC TATAC A
CACAAAAAGTATAGCAACGG GTGA ||||| || | ||| || ||||| |||||
ACACGGCAATAGTGACTTTA ACGTA CA G TAA GG ACAGG ATATG /

TGCA TTT GT A C C CAACG-- AAAAAC

GAM3713 TTGTGTCCATATGTGTACCC 83932 TACCTCAACA 83933 CATATGTGTACCCGAGAAA AA AA T CCTAA C AATAA
GAGAAAGTAATTTAATGTTG TTCTCAACAG TC GT TTT TGTTG AGAA GAG TATT A
TAGAACCTAAGAGCTATTAA AAAA || || ||| ||||| |||| ||| ||||
TAAAAACCCAATACCTCAAC GG CA AAA ACAAC TCTT CTC ATAA /
ATTCTCAACAGAAAACCACG ---------- CC AG - ACAA- C CCCAA
GCACAG

GAM3714 TACATTTCTAAATATAAATT 83973 CATTTCTAAA 83974 A CT ATAAATTAAATTT A T- AG
AAATTTGTTATGATCTGATA TATAAATTAA TAC TTT AAAT GTT TGATC GATA C
AGCGAGTATCTTGATCAAAT ATTT ||| ||| |||| ||| ||||| ||||
TGTCGTGCTAAAATTTTTAA ATG AAA TTTA TAA ACTAG CTAT G
ACGTA C TT AAATCGTGCTGT- - TT GA

GAM3715 CGTGTTTATTCAAGGGAGTG 83978 AGGGAGTGGG 83979 - CAAG A GGA G C
GGATAGGGTTCGACGGTTCG ATAGGGTTCG CGTGTTT ATT GG GTG TAGG TTCGA G
AAACTTAACACACCAAATAA ACGG ||||||| ||| || ||| |||| |||||
TCGAGCGCG GCGCGAG TAA CC CAC ATTC AAGCT G
C TAAA A A-- A T

GAM3716 CCCCCCTCACCGGTGTTAAT 84008 TTTGCCGTTT 84009 - AC G AATA CAC - A T C GCTCGCA
ACGCACGACAATAAATGAGC ATTTGTTTAT CCCC CCTC CG TGTT CG GACAA TAAATG GC GACA AC C
TGACACACGCTCGCACATAC TGGG |||| |||| || |||| || ||||| |||||| || |||| ||
ACAGTTTGTTTGCCGTTTAT GGGG GGGG GC ACAG GT TTGTT ATTTGC CG TTGT TG /
TTGTTTATTGGGGACAGCGA C CA G GG-- TAT T - T T ACACATA
CGGGGCGGGG

GAM3717 TTTTTAAAAATTTGAATTTA 84011 TGACAAAGTA 84012 AAAA--- C--------- ---- C
TGTTCGTCATTTGACCCAGG AGGTAATATA TTTTTA TTTGAATTTATGTT GTCATTTG AC C
TAAGATAAATGACAAAGTAA AATT |||||| |||||||||||||| |||||||| ||
GGTAATATAAATTTAAGGTC AAAAAT GAATTTAAATATAA CAGTAAAT TG A
AATCTAAAAA CTAACTG TGGAATGAAA AGAA G

GAM3718 GGCTCCGAAGGTCCGCTGCT 84019 TGAGAAGTAG 84020 T AA- - CGG- C T--- C C TC
CGGCTCCGCTCACCGCTCCG CGTGTGGACT GGC CCG GGTCCGC TGCT CTC GC CAC GCT CGG T
GTCTGGCTGCAGCAGTGCTT GAAC ||| ||| ||||||| |||| ||| || ||| ||| |||
CGCTGAGAAGTAGCGTGTGG TTG GGC TCAGGTG GCGA GAG CG GTG CGA GTC /

ACTGAACGGTGTT T AAG T TGAA T CTTC A C GG

GAM3719 TCTGTCTGTCGCGAAACGTA 84046 ATAATGCCTA 84047 CTGTCG- AAC -- C T -- A
CAGCTCTAATTACATTGTTT ATTGATCTAA TCTGT CGA GTAC AG TC AATTA CATTGTTT A
AAGGAGATAATGCCTAATTG GTAC ||||| ||| |||| || || ||||| ||||||||
ATCTAAGTACATGTTGACCA AGACG GTT CATG TC AG TTAAT GTAATAGA G
AACGCAGA CAAACCA GTA AA T - CC G

GAM3720 CTTCGAGAAAAGCGCTCTTC 84053 TGTTGCGTCT 84054 AGAAA-- - TCTT---------- TA
GAGTACTCCCTCGGCAGACT CCCATAGTGA CTTCG AG CGC CGAG C
ATTCTGTTGCGTCTCCCATA AG ||||| || ||| ||||
GTGAAG GAAGT TC GCG GCTC T
GATACCC T TTGTCTTATCAGACG CC

GAM3721 CGGGTTGACAAAATCGAACG 84065 TGAGCTCCGC 84066 G AAA GAA- T AA TT
GTGTTTAAGCTTTGACCGGT GAAGACTCTG CGGGTT ACA TC CGG GTTT GCT G
GAGCTCCGCGAAGACTCTGT TAAG |||||| ||| || ||| |||| |||
AAGCCTG GTCCGA TGT AG GCC CGAG TGG A
A CTC AAGC T -- CC

GAM3722 CGTGAGAGGCTGACAGCTTA 84081 ACCCCGTATA 84082 CT C T- CAAAAT-- A
AAATACAC AGCACC AT
CGAAGCAAAATCACAAAGAA TCACAAGTCT GA AGCT ACGAAG CACA AGA ATGC
TAGAT C
AATACACATGCAGCACCTAG CTGT || |||| |||||| |||| ||| |||| |||||
ATATCCAGTTTAACCCCGTA TT TTGA TGTTTT GTGT TCT TATG ATTTG /
TATCACAAGTCTCTGTGTCA TT T TC TTATAACT C GAACACTA CCCCA- AC
ATATTTTTTGTCTAGTTTTT
TTTTCCTCCTG
GAM3723 CCCGGACAGCGTGCAAGTCT 84099 TAGAGAGCAC 84100 ACAG CAA - GA AG GGG
GA
CGACTAAGGAGCGGGCGCGA ACACGACGAC CCCGG CGTG GT CTC CTA GAGC CGC G
GCGAGCGAAAGTTTTATAGA CGGG ||||| |||| || ||| ||| |||| |||
GAGCACACACGACGACCGGG GGGCC GCAC CA GAG GAT TTTG GCG C
AGCA A-- C A- AT AAA AG

GAM3724 GTTGTCAAGGGCTGTGAACA 84112 TCAAGGGCTG 84113 C G AC A AA
CATTGGCAATCTCGCCGACG TGAACACATT GTTGT AAG GCTGTGA AC TTGGC T
TCATTACGGCACTTAATAAC GGCA ||||| ||| ||||||| || |||||
CAATA TTC CGGCATT TG AGCCG C
A A AC C CT

GAM3725 CCGCTCGATCTCGGCTCTGT 84132 ATCGCGGTCC 84133 GATCT CT T CGT
CGGTCGCCGTCCTTCGCGAT GTTCGGGAGC CCGCTC CGG CTG CGGTCGC C

CGCGGTCCGTTCGGGAGCGG GG |||||| ||| ||| |||||||
GGCGAG GCC GGC GCTAGCG C
GGCTT T- - CTT

GAM3726 AACTAATTAATTATTTAATG 84162 TTTAATGTGT 84163 TT T - GTTTTATA - A-
TT
TGTTTTATATTATATTTTTA TTTATATTAT AACTAA AA TATTTA ATGT TTATATTTTTATA
TATTTT ATGA A
TATATTTTAATGATTAATTC ATTT |||||| || |||||| |||| |||||||||||| |||||| ||||
ATAAAAAATGTTATAGAGAT TTGATT TT ATAAGT TGCG AATATAGAGATAT GTAAAA
TACT /
ATAAGCGTATGAATATTTTT TT T A -------- T AA TA
TTAGTT

GAM3727 GGTTGTAGCGAAATGTCCCC 84170 CATGCCGCCG 84171 --------- TA AA T A A GC
AACCCC
AACAGCGGCCAGTCAACCCC CTCAAACTTA GGTT G GCG ATG CCCCA C GCG CAGTC
C
CTTAAGCGACTGATGCGTGG AACC |||| | ||| ||| ||||| | ||| |||||
GGCATGCCGCCGCTCAAACT CCAA C CGC TAC GGGGT G CGT GTCAG /
TAAACC ATTCAAACT GC CG - - - A- CGAATT

GAM3728 TACCCGTAAATAAGCACGCT 84181 GTATGGCTGT 84182 GTAAATA ACGCTTTAAAT A AA
TTAAATCAAACAACAACAGG AAAGGGTA TACCC AGC CA ACAAC C
TTGTATGGCTGTAAAGGGTA ||||| ||| || |||||
ATGGG TCG GT TGTTG /
AAATG-- ---------- A GA

GAM3729 GTGTTTACAAACAAGCAATC 84211 ATCACTTTGT 84212 C C TCTATA C CAGCATC
TATAATTCGCACAGCATCAA TTATTTTAGA GTGTTTA AAA AAGCAA ATT GCA A
GAATTTCTGCAATCACTTTG CAC ||||||| ||| |||||| ||| |||
TTTATTTTAGACAC CACAGAT TTT TTTGTT TAA CGT A
- A TCAC-- - CTTTAAG

GAM3730 GAAATATCCTTAGAAGCATG 84234 TGAGTATATT 84235 ---------- GA T T TTC GAGCCAT
- A-- AA
TCTTTCGGCAGAGCCATTAC ATATGCCTTA CTTA AGCA G CT GGCA TAC CGGT
GC A
CGGTAGCAAAAAAGCAACAT GCCT |||| |||| | || |||| ||| |||| ||
TGAGTATATTATATGCCTTA GAAT TCGT C GA CCGT ATG GTTA CG A
GCCTGCTCATAAGCGTCCTT CTTTTTTTTCCTGC AC C - TT- ATATTAT A CAA
AA
TTTTTTCATGGTATTTT

GAM3731 GCGACGGGCCGTTACGTTTC 84242 CACCGTGTTG 84243 AC C GT A TGC--- TCC------
-------- CA

ACCGTGTTGCGTCTCCGACA CGTCTCCGAC GCG GGGC GTTAC TTC CCGTGT GTC
GA C
CTGATCAAGCTGTTCACGGC ACTG ||| |||| ||||| ||| |||||| ||| ||
AATGACATTCTTATACGGGA CGC CCCG CGATG AAG GGCATA CAG CT T
ACAGTAGCGCCCACGC A- - AC - TTCTTA TAACGGCACTTGTCGAA AG

GAM3732 CTCCATAGTTCAAATGGAGC 84258 TTCAAATGGA 84259 AG A--- GAG-- GAAAA TAG
CTGAAAATTATAGTAATTTA GCCTGAAAAT CTCCAT TTCA ATG CCT TTA T
AAATTAAGGAGAGACATAAG TATA |||||| |||| ||| ||| |||
ATGAAAGATGGGG GGGGTA AAGT TAC GGA AAT A
GA AGAA AGAGA ATTAA TTA

GAM3733 TAACATGCAAAAAAAATATG 84270 TTTAAACTTA 84271 AA- TA CTTATTT AGCACT
TTTAAACTTATTTTAAGCTA TTTTAAGCTA TAACATGCAA AAAA TGTTTAAA TAAGCT T
GCACTTATTTAAAAGCTTGT GCAC |||||||||| |||| |||||||| ||||||
TTTAAACACGTTTTAAATTG ATTGTATGTT TTTT ACAAATTT GTTCGA A
TATGTTA AAA GC T------ AAATTT

GAM3734 CATTAAATTATCATTTTTGA 84277 TAAATTATCA 84278 CA AAT T A C ATC
ATGTATTTATACCAGATCAA TTTTTGAATG CATTAAATTAT TTTTTG GTA TT TAC AG A
AAACTTGTACAATTATTAAT TATT |||||||||| |||||| ||| || ||| ||
AAAAAATAATTTAGTG GTGATTTAATA AAAAAT TAT AA ATG TC A
-- AAT T C T AAA

GAM3735 CTGGTATAAAGATGTTAGAT 84287 TATTAAACAA 84288 G AGA A TA-- -- AA
TAGTTAATGGGAATCGTCTA TTATATGAG CT GTATAA TGTT GAT GTTA ATGGG T
TAATAATGAATATTAAACAA || |||||| |||| ||| |||| |||||
TTATATGAG GA TATATT ACAA TTA TAAT TATCT /
G A-- A TAAG AA GC

GAM3736 TTGATTTTCTTTCTAATACT 84291 TGGGAATAAA 66795 T TC A C ATAT TC A A TC
ATATATTTCTCTCGAAGAAG ATACTACTGT TTGATTT CTT TA TA TAT TTCTC GA GA GT T
TTCTTGCACATCATCTGGGA TGAG ||||||| ||| || || ||| ||||| || || ||
ATAAAATACTACTGTTGAGT GACTAAA GAG GT AT ATA AAGGG CT CT CA T
AAATCAG T TT C C AAAT T- A A CG

GAM3737 TCTCCGGTCTCCATAACTCG 84292 TGAGCACCTC 84293 C C CATAAC C CG A----- TTA
T
CTCTCGCCTGGAGCTTTTAT CCCAGGGAAG TCT CGGT TC TCG TCT CCTGG GCTT
TATAC A
ATACTAACGTGTGATGAGCA ATGA ||| |||| || ||| ||| ||||| |||| |||||
CCTCCCCAGGGAAGATGATG AGA GCCG AG AGT AGA GGACC CGAG GTGTG A
ACGCCGAGA - C T----- - AG CCTCCA TA- C

GAM3738 GGCGGCGGGGCAGCGGCGCG 84321 TCCGCGCTCG 84322 C AG - GA GA GAGA
GGCGACGGGAGCGAGAGGGC GGCCCCCCGC GGCGG GGGGC CG GCGCGGGC CGG GC
G
GAGCGACCGGTCCGCGCTCG C ||||| ||||| || |||||||| ||| ||
GGCCCCCCGCC CCGCC CCCCG GC CGCGCCTG GCC CG G
- G- T -- AG AGCG

GAM3739 GGGTTGTAAGTTTTAATCAG 84598 TCCTGGGTGT 84599 G AATCAGTAGG- - AAA -
AAG
TAGGTGTACCCAAAAAGGCC CAGGATTTTT GG TTGTAAGTTTT TG TACCCA AGG CC A
AAGAGTGCGGATCTCCTGGG ATAG || |||||||||| || |||||| ||| ||
TGTCAGGATTTTTATAGAGA CC AACATTCAGAG AC GTGGGT TCT GG G
CTTACAAGCC G ATATTTTTAGG T CC- A CGT

GAM3740 CTTTTGGCCCCTCTGGGTCG 84612 CCTCTGGGTC 84613 T C GT GAAGT G
CGAGGAAGTGGCGGACGCCT GCGAGGAAGT CT TTGGCCC TCTGG CGCGAG GGC G
TAAGCTCGTGCCGGACGGGC GGCG || ||||||| ||||| |||||| |||
CGACGG GG AGCCGGG AGGCC GTGCTC CCG A
C C -- GAATT C

GAM3741 GGAAACGCGCCAGACTCCGG 84639 TGAAGGATTT 84640 A-- - CCAGAC GGAAC AA
TTTATCA T
AACTATGAAGGATTTATCAC ATCACTGTAT GGA ACG CG TCC TATG GGA CTG A
TGTATACAGACTCCGACGTA ACAG ||| ||| || ||| |||| ||| |||
CGAAGGATAATCACGACGTA CCT TGC GC AGG ATGC CCT GAC T
ACTCC CAA A ACTAAT AAGC- AG CA----- A

GAM3742 GCTTAAGTACGGGCCGCGGC 84654 CTGCCGCAAG 84655 T GGC C - A- C AT G
TT TC C
GATCGCGGGCGTCGATCGCG CGCGATCCCG TTAAG ACG CG GG CG TCGCGGG GTCG
CGC TGCGGC GGAG CGG T
TGCGGCTTGGAGTCCGGCTG CGAC ||||| ||| || || || ||||||| |||| ||| |||||| |||| |||
CCGTTTCTGCCGCAAGCGCG GGTTC TGC GC CC GC AGCGCCC TAGC GCG
ACGCCG TCTT GCC /
ATCCCGCGACACGACCCGAC T A-- - A AC - -- A -- T- G
GTTCTTGGGC

GAM3743 GGCGACGGCCGCGCTTACGC 84667 TCAGCCACCA 84668 A-- C TTA C C- - CC
GGCGCTGGGTCCGCCCACAT CGCCCGCGCG GGCG CGG CGCGC CG GG GCTGG GT G
CAGCCACCACGCCCGCGCGC CCCG |||| ||| ||||| || || ||||| ||
CCGCCCCGCC CCGC GCC GCGCG GC CC CGACT CA C
CCC C CCC A AC A CC

GAM3744 TTGGTCAATCGGTACTCAGA 84746 TCAGATGCTT 84747 TCAATCGG C
TCTCTCCAATATATC ATA

TGCTTCTCTCCAATATATCG CTCTCCAATA TTGG TACT AGATGCT GGTACTCA T
GTACTCAATATATAGTGAGT TATC |||| |||| ||||||| |||||||| |||||||
ACCAAATGGCATTTTGGTAA AACC ATGG TTTACGG CCATGAGT A
AAATCCCAA CTAAAA-- T TAAA---------- GAT

GAM3745 TCGTTTTTTTTAACCCAGTT 84759 TAAATGGTTA 84760 TTT-- CAG T T - - ACA- TG
A AA
TTACGTATAATATGATAACA AATATACAAT T TTTAACC TT TACG ATAA TA TGATA TTTGT
ATATA TG A
TTTGTTGATATAATGAAATG GA | ||||||| || |||| |||| || ||||| ||||| ||||| ||
ACGTATATACAAACTTATAT A AAATTGG AA ATGT TATT GT ACTAT AAACA TATAT
GC T
CAATGCTTATTGTATAAATG CATAT TA- T - C A ATTC -- - AG
GTTAAATATACAATGA

GAM3746 TCTGACAACGAACAAAACGA 84777 ACGAACAAAA 84778 ACAAC- AAAAC- CAA ACC
ACTCAAAGCACCCACAAGCT CGAACTCAAA TCTG GAAC GAACT AGC C
CTAGTTCAACAAAGTTCATC GCAC |||| |||| ||||| |||
ACGCAGA AGAC CTTG CTTGA TCG A
GCACTA AAACAA TC- AAC

GAM3747 GGTCTGTACATAATAAGAAA 84805 TAGCTTTCAC 84806 ATAATAAGAAAA AG ----
TG
AACTTAGGGTGAAAGTTAGG CTCAAGTAAG GGTCTGTAC ACTT GGTGAAAGTTA GGT
C
TTGCTCACCACTATAGCTTT TACA ||||||||| |||| |||||||||| |||
CACCTCAAGTAAGTACAGAT CTAGACATG TGAA CCACTTTCGAT CCA /
C AA---------- CT ATCA CT

GAM3748 GAGAGAAAAGAAAAAAACCG 84825 ATAGAACCGC 84826 A AAA- AAA- C GG C C
TCTAAAA C CA A
CGGGTGCCGGTGCTGTCTAA TGTCGCCGCC GA GA AAAC GCG TG CGGTG TG GGC
GTTTT ATAAA A
AAGGCCGTTTTCAATAAAAA GTCG || || |||| ||| || ||||| || ||| ||||| |||||
TTTTTATAGAACCGCTGTCG CT CT TTTG CGT GC GCCGC GC TCG CAAGA
TATTT T
CCGCCGTCGTTTGCCGTTTG - GCTG GCTG C TT T C TG----- C -- T
TCGTCGTCGTCGTC

GAM3749 GATTAGTCATCTTGTATGCA 84834 TCTTGTATGC 84835 TCATCT T AAT A AAA-
TAC
TTTTAATTAAATATATGTAA ATTTTAATTA GATTAG TGTA GCATTTT TAAATATATGT AT
TTA A
TAAATTATACATTTTTAAAC AATA |||||| |||| ||||||| |||||||||| || |||
AGATAATATATATTTAAAAA TTAATC ACAT TGTAAAA ATTTATATATA TA AAT T
TGTTTACATTACCCTAATT CCATT- T --- A GACA TTT

GAM3750 TTTGTTTATTTTTATGATGT 84842 TTTATGATGT 84843 TTATTTT--- AACATAT- A T
AG CA
AACATATATTAATGTTTACA AACATATATT TTTGT TATGATGT ATT ATG TTACACAG
CG A
CAGAGCGCAATAACGTCCTG AATG ||||| |||||||| ||| ||| |||||||| ||
TGTAATTATAAATTCTCATT AAACA ATACTACA TAA TAT AATGTGTC GC T
GACATCATATTTTTCTATTA TTATCTTTTT GTTACTCT A T CT AA
CAAA

GAM3751 TCTAGTCAAGTGCTTTTATT 84845 TGACCACAGA 84846 AGTC ----- --- CATATG
CCACAG CTAC
TTGTCATATGCTGCCACAGG GACCAACAAA TCT AAGTGCT TTTATTT TGT CTG
GTGGG C
TGGGCTACCTCAACCCATGA TAAA ||| ||||||| ||||||| ||| ||| |||||
CCACAGAGACCAACAAATAA AGA TTCACGG AAGTAAA ACA GAC TACCC /
ATGAATCGCCGGCACTTTAA AAT- CCGCT TAA ACCAGA ACCAG- AACT
AGA

GAM3752 CGTCGCCTCCTGGAACTCCC 84865 TGGAACTCCC 84866 - CT AACTCC T A T C-
ATCT
GGATATACCTCGCCCCGTAG GGATATACCT CGTCGC CTC GG CGGA AT CC CGCCC
GTAG T
ATCTTATATGTTACCTGGGT CGCC |||||| ||| || |||| || || ||||| ||||
GGGATTTCCGCGCCTCGAGC GCAGTG GAG CC GCCT TA GG GTGGG CATT A
GTGACG C CT GC---- T - - TC GTAT

GAM3753 GGGGGGCAGTGATAAGTCAT 84873 TAAGTCATGA 84874 - GCAG T C AC- AGAT
GACAATTTTAGATGAGGTAG CAATTTTAGA GG GGG TGA AAGT ATG AATTTT G
AAATTTTGCATATTTTCAGA TGAG || ||| ||| |||| ||| ||||||
CCCACC CC CCC ACT TTTA TAC TTAAAG A
A AG-- - - GTT ATGG

GAM3754 ATTCCACGTTCTCATAAAAA 84881 TCCACGTTCT 84882 - C AAACAG- TAAAAA AC
CAGGCACTTAAAAAGAGCAC CATAAAAACA ATTCC ACGTTCT ATAA GCACT GAGC C
CAGGTTTAGTGTAGTCTTAT GGCA ||||| ||||||| |||| ||||| ||||
TATAGAATGTAGGAAT TAAGG TGTAAGA TATT TGTGA TTTG /
A - ATTCTGA ------ GA

GAM3755 CGGATTATCTATGTGCATGG 84900 TGCATGGAGT 84901 - TATGT--- ----- A TATC
AA
AGTGTCCTACATATCAAAAT GTCCTACATA CGGATT ATC GCATGGA GTGTCCT CA
AAAAT A
AAATGGTTTTACTGAAGGAT TCAA |||||| ||| ||||||| ||||||| || |||||
ACAATTGTTCATGTTGTTTC GTTTAA TGG TGTACTT CATAGGA GT TTTTG /
TTGGTAAATTTG A TTCTTTGT GTTAA A CA-- GT

GAM3756 TCCTCTCGATCGGATCGCAA 84917 TCTCGATCGG 84918 TCT A T CAA TT- AA
CGCTTTACCCTAGAAGCCAC ATCGCAACGC TCC CG TCGGA CG CGC TACCCTAG G
TAGGGTGTACGCGGCCGTTC TTTA ||| || ||||| || ||| ||||||||
TGACGTTGGA AGG GC AGTCT GC GCG GTGGGATC C
TT- - T CG- CAT AC

GAM3757 GGTAGAAGGTGTGAATCTCG 84920 TAGAAGGTGT 84921 GTGAA GCGA CC
AGTGCGAGCCCGAAGCACAA GAATCTCGAG GGTAGAAGGT TCTCGAGT GC G
ACTCGAGGAAGCCTTCTGCC TGCG |||||||||| |||||||| ||
CCGTCTTCCG GGAGCTCA CG /
AA--- AACA AA

GAM3758 AGGCAAGATTCACTCTGCAA 84924 TGCAAGACGT 84925 CAA TCT------- CG T- GAA-
T
GACGTGTGAAGTAGCGAACG GTGAAGTAGC AGG GATTCAC GCAAGA TG GAAGTAGC
CGC C
CTCACGCGAAGAGCTATTTT GAAC ||| ||||||| |||||| || |||||||| |||
TTCAGTTTTTGTTCTTTCTC TCC CTAGGTG TGTTTT AC TTTTATCG GCG A
TCGTGGATCGCTCCT TCG CTCTCTTTCT TG TT AGAA C

GAM3759 ATGCATTATATATTTTATAT 84939 TATATGAATT 84940 TTT ATTATAG AAGAG
GAATTATAGTTGCAAGAGTT ATAGTTGCAA ATGCATTATATA TATATGA TTGC T
ACACGTAAAACAACTCATAT GAGT |||||||||||| ||||||| ||||
ACATTATATAATGTAT TATGTAATATAT ATATACT AATG /
TAC CAACAA- CACAT

GAM3760 ACAGATTTGGGGTGGAGACG 84943 TGGGGTGGAG 84944 ATTT--- - AG-- -------
GATACT--- A
GCGTGGGCGATACTGTATAA ACGGCGTGGG ACAG GG GGTGG ACGGCG TGGGC
GTATA A
AGTTGTACTACTTACCAGCC CGAT |||| || ||||| |||||| ||||| |||||
CAGTCAGTGTGCTGTAGTGC TGTC CC CCACC TGTCGT ACCCG CATGT G
CACCACCTGTAAAGCTGT GAAATGT A GTGA GTGACTG ACCATTCAT T

GAM3761 TTATTGATAAGGATTAATGA 84998 TAAGGATTAA 84999 G- TA- C
TTATTTAACAAATTAAATAA TGATTATTTA TTATTGATAAG AT ATGATTATTTAA A
TTATATTATAGCTTATCAAT ACAA |||||||||| || ||||||||||
AA AATAACTATTC TA TATTAATAAATT A
GA TTA A

GAM3762 TCGGGGGGAGGAGAGGAAAC 85008 AGAGGAAACC 85009 G GA AAA--- A CAC
CGGGGACTCACCGGCGGCCT GGGGACTCAC TCGG GGGAG GAGG CCGGGG CT C
CGGACCGAGCCTCGCTCCCG CGGC |||| ||||| |||| |||||| ||

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      CCGG                              GGCC CCCTC  CTCC     GGCTCC GG   /
                                      G    G-    GAGCCA     -  CGG


GAM3763  AGGCTGTCCGGAAATCTAAG 85055   TAAGTTAATG 85056     CT     AAA      T    ATAAA  GATG
      TTAATGAATAAAGTAGATGG       AATAAAGTAG       AGG  GTCCGG   TCTAAGT AATGA    GTA   G
      TTAATACTCATTGCTTAGAA       ATGG           |||  ||||||   ||||||| |||||     |||
      TTGGACTACTT                          TTC  CAGGTT   AGATTCG TTACT    CAT   /
                                     AT     A--      -    -----   AATT


GAM3764  TAAATAGTATTTTAGGGTTA 85065   TTTTAGGGTT 85066      TAG-   T         -  AAT--   TAAA
      AAGTAATACTTTAAAGGGAC       AAAGTAATAC       TAAA    TAT TTAGGGTTAAA GT    ACTT   G
      AAGTCACAGACATTTGATCT       TTTA           ||||    ||| ||||||||||| ||     ||||
      TAGTATAAATTTTTA                      ATTT    ATA GATTCTAGTTT CA     TGAA   /
                                     TTAA   T         A  GACAC    CAGG


GAM3765  CTGATGTCCCGTCCGGTTTT 85070   ACGACATTAA 85071     GA GT      GG ---     CACG   C  G
      TAACACGGTCCCGGGCCCGT       ATAGGAAGGG       CT  T  CCCGTCC  TT   TTTAA    GTC CG G
      GACGACATTAAATAGGAAGG       ACGG           ||  |  |||||||  ||   |||||    ||| ||
      GACGGGGTGGGGG                          GG  G  GGGCAGG  AG   AAATT    CAG GC C
                                     GG TG      GA  GAT     ACAG   T  C


GAM3766  AATCTTACCACTGTGTGTGT 85085   TCGTGCTGTC 85086    T  -     ----------          TG - TG  TG     C
 TG
      GCGTGTGTGTGTGTCGAGTC       CGCACATATT       T AC CACTGT           GTGTGTGCG  T G  TG
TCGAGT GTGT  T
      GTGTTGTCCGCACATTTGAG       TTAT           | || ||||||           |||||||||  | |  ||  ||||||  ||||
      TCGTGCTGTCCGCACATATT                   A TG GTGACA           TATACACGC  G C  GC  AGTTTA
CACG  /
      TTATCTTTTGGGTACAGTGT                   T  T     TGGGTTTTCTATTT       CT T GT  TG     -   CC
      GTTAGATT

GAM3767  TAGTATTGAAAAGGTGTTTG 85089   TTTGATGCAT 85090      A    AAAG    -   TT    -    TG  TTCT-
  -  T
      TATTTATGTATATTTGGTTT       ATTGAATATC       TAGT TTGA    GTGTT TGTA  TATGT ATATT  GT
TCAAGTAGC CC A
      CTTCAAGTAGCCCTATAGGC       ACAT           ||||  ||||    |||||  ||||  |||||  |||||  ||     |||||||||  ||
      GCTATTTGATGCATATTGAA                   GTCA AACT    TACGA ACGT  ATACA TATAA  TA
AGTTTATCG GG T
      TATCACATATTTGCACAGCA                     -   ----     C    TT     C     GT  TACGT       C  A
      TTCAAACTG

GAM3768  TTTTGTTCATACGTATAGTC 85094   TCGAAACGAT 85095     CATACG----  T   C         TT---      T   TA
T   CTA
      TTCTTAAGTTTTTAATATTT       GTTATTTTTA       TT         TA AGT TTCTTAAGTT     TAATATT GTT
TCGA ACG   A
      GTTTATCGATACGCTAACAC       ATTT           ||         || ||| ||||||||||     ||||||| |||  |||| |||
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     CCGTCTCGAAACGATGTTAT                AA      AT TCA AAGAATTTAA   ATTGTAG CAA  AGCT
TGC  C
     TTTTAATTTAAGAAACTTTA                TAAAAATAAA  T  -      TTTTT    -  --   C  CCA
     AAATAAAAATAACAAAA

GAM3769  GACTGTTTGTGCATGTGTTT 85097   TGGAAGGATG 85098   -   TGT   -  T TG   ATGTT  AACTG
A
     TGGAAGGATGTTGGAAACTG      TTGGAAACTG      GA CTGTT  GCATG TGT T  GAAGG   GGA   TC
C
     TCACGTGAGCTCTCCCCTAG      TCAC          || |||||  ||||| ||| |  |||||   |||   ||
     CCTTTTGACATACCGTGTTG                CT GGCGG  TGTGC ATA A  TTTCC   CCT   AG G
     TGGCGGCTC                     C   TGT   C  C GT   GATCC  CTCG-  T


GAM3770  CGATAAGTCGCGTGTAGGCG 85125   AACCGGATAT 85126   --   TCGCGTGT   -  AC-   -   CATCAA
ATCT   GATTTAA
     ACTGGCTACATCAACCGGAT      CTGCGGGGAT      T  AAG      AGG CG  TGG CTA    CCGGAT
GCGGG    A
     ATCTGCGGGGATTTAAAAAG      TTAA          |  |||      ||| ||  ||| |||    ||||||  |||||
     ACGACCCGTTGTCATCCGGC                G  TTC      TCC GC  ACC GAT    GGCCTA   TGCCC    /
     TTAGACCAAACCGTCCTTTT                CC  TACTATTT  T  CAA  A  TC----    CTGT   AGCAGAA
     ATCATCTTCCGTCG

GAM3771  TATATGGTGCACTATGTAAA 85133   TATGGTGCAC 85134      --     ----------  A  -   TATG
GCT
     CGACATTATGGGCGTGCTTT      TATGTAAACG      TATATGG  TGCACTA          TGT AAC GACAT
GGCGT  T
     TAAATGCCGTGTCTGTTCAC      ACAT          |||||||  |||||||          ||| ||| |||||   |||||
     ACTTCATTAAAATATTTGGT                ATGTACT  GCGTGGT          ACA TTG CTGTG   CCGTA  T
     GCGTTTCATGTA                    TT     TTATAAAATTACTTC  C  T   ----   AAT


GAM3772  CCCCATGGGCTCTCTTCTAG 85138   CACTTGGTGA 85139    ATGGG   TT  GAAACGAAAAT
CGAAAC
     AAACGAAAATGGTGCTCGAA      GAGAAAGGGG      CCCC   CTCTC  CTA       GGTGCT    A
     ACAAAAACTAGGCACTTGGT                |||   |||||  |||        ||||||
     GAGAGAAAGGGG                  GGGG   GAGAG  GGT       TCACGG    A
                              AAA--   T-  ----------    ATCAAA


GAM3773  TTTGTGTTTTGTGCGTTGCC 85280   TGTGTCCGAG 85281      TTTTGT  G   C  - A   ATT
     TGGCAAACGCGATTTGGGTG      CAAGCCACGG      TTTGTG    GC TTGC TGG CA ACGCG  T
     CGTGTGTCCGAGCAAGCCAC      A             ||||||    || |||| ||| || |||||
     GGA                       AGGCAC    CG AACG GCC GT TGCGT  /
                               ------  -   A  T  G   GGG


GAM3774  AGTTTGTATATTTAAGAATG 85319   TTTAAGAATG 85320    T    T      AAATAAA  TT  C  G GATT
     AAAATAAAATATTTTCGAAG      AAAATAAAAT      AGTT GTATAT TAAGAATGA     ATA  TT GAA C   A
     CGATTATAAAGTTCAATTTG      ATTT          ||||  |||||| |||||||||     |||  || ||| |
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TCATTTGTCATTTTTGTGTA TCAA TATATG GTTTTTACT TGT AA CTT G /
TATCAACT C T GTTTAC- TT - - AAAT

GAM3775 AATCGTTCTCACACGTTCGA 85327 CACACGTTCG 85328 CT- - C GA TA CA
ATTACCGACACACATCTGTC AATTACCGAC AATCGTT CA CA GTTC AT CCGACA C
GGCTATAGGACTTGCTGCAC ACAC ||||||| || || |||| || ||||||
AACGGTT TTGGCAA GT GT CAGG TA GGCTGT A
CAC C T A- TC CT

GAM3776 TGCATCGGTGCCGTAACCTT 85335 TCGGTGCCGT 85336 ATC CC CCT--- T- AC
CGCTGCTTTACTTAAAAAGC AACCTTCGCT TGC GGTG GTAA TCGC GCTTT T
CTGTGATTTCATTTACCACC GCTT ||| |||| |||| |||| |||||
CCAGCA ACG CCAC CATT AGTG CGAAA T
ACC -- TACTTT TC AA

GAM3777 TACAATAAAGATATATCTTA 85340 TATCTTAACC 85341 ATAAAGATATAT AACC A
ACCTTTATCTTTGAGCCCAA TTTATCTTTG TACA CTT TTTATCTTTG G
GGATAGACAAAAAGTAAGAA AGCC |||| ||| ||||||||||
AAACATGTA ATGT GAA AGATAGGAAC C
ACAAAAAGAAT- AAAC C

GAM3778 AGGAGTAAAGTTGTTGCTTC 85354 AAGAATGTTT 85355 AAA TT CA--- TTTC- - A
T
AAGAATGTTTCATACAACTG CATACAACTG AGGAGT GTTG GCTT AGAATG ATA
CAACTG AGAG G
AAGAGTGGTTCTGTAGTTGC AAGA |||||| |||| |||| |||||| ||| |||||| ||||
TATTTATGTATTCTAAGAAA TCTTCA CAAC TGAA TCTTAT TAT GTTGAT TCTT /
AGTCCAACCCACTTCT CC- C- AAGAA GTATT C G G

GAM3779 TTTTAGAACTGACCAACCAT 85385 GAACTGACCA 85386 TC- A -------- TG
GTTCACGTAAGTGACGTGAT ACCATGTTCA TTAGAACTGACCAACCATGT
ACGTAAGTGACGTG TGAC GCGCGC C
GACGCGCGCTGCGCGCGCGC CGTA |||||||||||||||||| |||||||||||| |||| ||||||
CTTCGGACGTCACACGTCAC AATCTTGACTGGTTGGTACA TGCATTCACTGCAC ACTG
CGCGCG /
TTACGTTTCACATGGTTGGT CTT - CAGGCTTC CG
CAGTTCTAAAA

GAM3780 TGGATCTTTACAAATAGAAG 85395 TCCATTGTAA 85396 T ATA TCTATTTT
GATCTATTTTTGTTACATTT AGCTTCA TGGA CTTTACAA GAAGGA T
TCTTTCCATTGTAAAGCTTC |||| |||||||| ||||||
A ACTT GAAATGTT CTTTCT G
C AC- TTTACATT

GAM3781 AAAATCGATTCCGTCCAAGA 85402 TCGATTCCGT 85403 C CCAAG AAAAACA
TGATAAAAACATTTACCGGC CCAAGATGAT AAAAT GATTCCGT ATGAT T
ATCATAAACACGGAGTTTAT AAAA ||||| ||||||||| |||||
TTT TTTTA TTGAGGCA TACTA T
T CAAA- CGGCCAT

GAM3782 GGCATTAAATCGTATCTATC 85408 TCTATCGGAT 85409 TTAAA TATCTAT - - TTTA AT
GGATTACCAAAAATTTAGCA TACCAAAAAT GGCA TCG CGGATT ACC AAAAA GC G
TGTCGCCGTTTTTTTTAGGTC TTAG |||| ||| |||||| ||| ||||| ||
GATCCGCCGTCGGCTGCC CCGT GGC GCCTAG TGG TTTTT CG /
C---- TGCC--- C A TTGC CT

GAM3783 CGGGGGGAACAATGACGCAA 85411 CGGCGCCTAC 85412 G AACAATGA AAAA C
CGCTG
AAGGGCCCCGGGCGCTGAGT TCGCGCCGCC CGGG GG CGC GGGC CCGGG A
TAAATCCGGCGCCTACTCGC CG |||| || ||| |||| |||||
GCCGCCCG GCCC CC GCG TCCG GGCCT G
G -------- CTCA C AAATT

GAM3784 GGCCCGAAAACCTGCGCGCC 85566 CTGGCTCCTG 85567 AAAACCT C G CAAA- AA
GCGGCGGCAAAAGTGAAAAA GTGTTGCGCG GGCCCG GCGCGC GCG CGG AGTG A
GTACTGGCTCCTGGTGTTGC CCGG |||||| |||||| ||| ||| |||
GCGCCGGGCC CCGGGC CGCGCG TGT GTC TCAT A
------- T G CTCGG GA

GAM3785 GGGGGCGAGCCACCGTCCCG 85581 CCCGCGAGCC 85582 - CCACC CCC C CA CATC
CCCGCCAGTGCATCCCAGAC GCACATCCCC GGGGGCG AG GT GC CGC GTG C
GCCCGCGAGCCGCACATCCC TCCG ||||||| || || || ||| |||
CTCCGCTCCC CCCTCGC TC CA CG GCG CGC /
C CCCTA CGC A CC AGAC

GAM3786 TTTATAATTAGATTTAAATT 85628 TACAGGTTTA 85629 T A - TT TT AAAAGAT
AAAAA
GGCTTCAATTAGACTTAAAA ATTGGCTTTT TTTA AATT GATT TAAA GGC CAATTAGACTT
TGAATG A
GATTGAATGAAAAAAGTATC TTAT |||| |||| |||| |||| ||| |||||||||| ||||||
CATTTACAGGTTTAATTGGC AAAT TTAG TTAA ATTT TCG GTTAATTTGGA ATTTAC
/
TTTTTTATAATTAGATTTAA - A T TT -- C------ CTATG
A

GAM3787 GGCGAGCGGCGAGGGCGACA 85638 TCCCGCGGTC 85639 C C -- AC T-- G A- G
CTGCTGGCGCGAGGGGACCC CGCCCGGTCC GG GAGCGG GA GGGCG ACTGC GGC CG
GG G
GCCGGGCTCCCGCGGTCCGC CCGC || |||||| || ||||| ||||| ||| || ||

CCGGTCCCCGCTCCCC CC CTCGCC CT CCCGC TGGCG TCG GC CC A
C C GG C- CCC G CG C

GAM3788 GCAAGACCGCGATGGCGTGT 85689 TGCCTTAGTC 85690 AA- - C --- TGT G AGA
AG
GTTCCTCCCGAGTCTCAGAC ACGGATCGGG GC GA CCG GAT GGCG GTTCCTCCCGA
TCTC CC T
CAGTTTTGGGTAGGGGTCGG GT || || ||| ||| |||| |||||||||||| |||| ||
GAGGAATTGCCTTAGTCACG TG CT GGC CTG CCGT TAAGGAGGGCT GGGG GG T
GATCGGGGT GGG A A ATT --- - ATG TT

GAM3789 TATAATATAATTTTAATTTT 85700 TTTATATATT 85701 AA TTTA - TTT
ATATATTTAATAATTTTTCA TAATAATTTT TATAATAT TTTTAAT TATATTTA ATAAT T
ATATTATATAAATATACATT TCAA |||||||| ||||||| |||||||| |||||
AAAAATATTATA ATATTATA AAAATTA ATATAAAT TATTA C
-- C--- A TAA

GAM3790 GGCCACGTGCAACGTTCACG 85706 ACGCTGCTAT 85707 CA--- AA ACGC CTAT A A
CC
CTGCTATAAGAAGGCCATGT AAGAAGGCCA GGC CGTGC CGTTC TG AAGA GGCC
TGTCC C
CCCCCGTGGACGGGTCTCTT TGTC ||| ||||| ||||| || |||| |||| |||||
TGACACGAGCGCGGCACGCC CCG GCACG GCGAG AC TTCT CTGG GCAGG /
GTTGCC TTGCC GC C--- AGT- - - TG

GAM3791 ATCTTTTTCTGGTTTTGTTT 85716 TTTCTGGTTT 85717 TTT GTTTTT GTTTT T GT
TTCTTTGTTTTCTTTTAGGA TGTTTTTCTT ATCTT CTGGTTTT CTTT CT TTAGGACT G
CTGTGTTAAGTTTTAATAGT TGTT ||||| |||||||| |||| || ||||||||
TAAGAGTTTTTAGGAATTAG TAGAA GATTAAGG GAGA GA AATTTTGA T
TTTAAGAT TTT ATTTTT ATT-- T AT

GAM3792 GCGTGTCTGGAGCGCGGTGC 85740 TGTCTGGAGC 85741 T G G G- AAGA ATA
GACCAAGAGTCTTATAAGGC GCGGTGCGAC GCG GTCT GAGC CGGTGC ACC GTCTT A
AGAGACGCGGGTGGGCGCCG CAAG ||| |||| |||| |||||| ||| |||||
GCTCGGGCCGT TGC CGGG CTCG GCCGCG TGG CAGAG G
- - - GG GCG- ACG

GAM3793 TAGATATAACGTATATATTC 85756 TATAACGTAT 85757 TAT- T ATT AT- ATA
ATTATATTTCCCATCTAATA ATATTCATTA TAGA AACG ATAT CATT ATTTCCCATCTA A
AATTATGGGTGGGAAATCTG TATT |||| |||| |||| |||| ||||||||||||
AATGCGAGTGTTCGTTTTTT ATTT TTGC TGTG GTAA TAAAGGGTGGGT A
TTTA TTTT T AGC GTC ATT

GAM3794 ACTGTCTCTATGCCGCCTAC 85761 TGCCTGGTGG 85762 G GC - A TTG TG AAAGAA
G CTTG
TGTTGCCTGGTGGGAAAGAA GAAAGAACGG ACT TCTCTAT CGC CT CTG CC GTGGG CG
GGC A
CGGGGCCTTGAGTAAGCCGC GGCC ||| ||||||| ||| || ||| || ||||| || |||
GCCCATTGGGGTCGGGGAGT TGG AGAGATA GTG GG GGC GG TACCC GC CCG
/
GATAGAGAAGGT A -- A - TG- GT ------ G AATG

GAM3795 TCCATGTTTGTTTATATTAT 85839 TTTATATTAT 85840 ------- - TT A C T
TTTCAACCTTATTTTAATAA TTTCAACCTT TCCATGTTTGT TTATAT TATT C AC TTAT T
AGTGGGGGATATATATAAAT ATTT |||||||||| |||||| |||| | || ||||
TTAATATAAACATGGG GGGTACAAATA AATATA ATAG G TG AATA T
TAATTTA T GG G A A

GAM3796 GCGCCCCCCCCCCCGCGCGC 85842 AAGCACCCGC 85843 C C---------- CC CT CG TG
TGTGCCGTCTGACGGAAAGC GTGTAGGGCT GCGC CC CCC CGCGCG GTGC TC A
ACCCGCGTGTAGGGCTGCAT GCAT |||| || ||| |||||| |||| ||
ATAAATGGAGCGC CGCG GG GGG GTGCGC CACG AG /
A TAAATATACGTC AT C- AA GC

GAM3797 GTATTTTCATACAATAATTT 85865 TAGTTTATTT 85866 --- A A T T TATAGTT C
TAT
TTTAATGTTTATAGTTTATT CAATCGATTA GTATTTT CATAC ATA TTT TTAA GTT
TATTTCAAT GAT C
TCAATCGATTATCAGTATCA TCAG ||||||| ||||| ||| ||| |||| ||| ||||||||| |||
TTGAAATATTAACTTAACAA CATAAGA GTATG TAT AAA AATT CAA ATAAAGTTA CTA
/
AATATGTATGTATAGAATAC TAT - A C - TT----- - TGA

GAM3798 TTCGAAGACATTAATACTGG 85869 TAGAGGACGC 85870 GACAT TAC - ----- GT GAC
TTTTCTTTCTCGTTATGACG AAAGAGAGAC TTCGAA TAA TGGTTT TCT TTCTC TAT G
ATCAATATAGAGGACGCAAA CAAT |||||| ||| |||||| ||| ||||| |||
GAGAGACCAATTTAGATTCG GAGCTT ATT ACCAGA AGA AGGAG ATA A
AG AG--- TA- G AACGC AT ACT

GAM3799 GCCGCCAACCCGAGCGCCGG 85882 AGAAGGAGGA 85883 CCAACC --- C - ----------
AAACAAGAA AT
AGAAGGAGGAGAAACAAGAA GAAACAAGAA CG CGAG CG CGGAG AAGGAG GAG
GA C
GAATCACTCGAGACACGGCT GAAT || |||| || ||||| |||||| ||| ||
CAGAACCCAGCGACTCTTTA GC GCTC GC GCCTT TTTCTC CTC CT /
TTCCGCGTCCCTCGCACCCG CCAC-- CCT - A AGCGACCCAAGA GGCACAGAG
CA
GC

GAM3800 GGTTGGATTGTTTGTGTACA 86161 TACATTTATT 86162 TG ---------- TTATTT
TTTATTTTCATTTTGTGTAC TTCATTAAAG GGT GATTGTTT GTGTACAT T
ATTTATTTTCATTAAAGCGA CGAT ||| |||||||| ||||||||
TCTGACC CCA CTAGCGAA TACATGTG /
GT ATTACTTTTATT TTTTAC

GAM3801 TACTGTTAAAGGCTCCAGGG 86165 TTAAAGGCTC 86166 TAA GAAACTGAAT G
TAGAGT T
AAACTGAATTAGAGCCTAGA CAGGGAAACT TACTGT AGGCTCCAGG TAGA CC ACG T
GTACGTTGACGTTAGAATGG GAAT |||||| |||||||||| |||| || |||
TCTACTTGGGGTTTCTACAG GTGACA TTTGGGGTTC ATCT GG TGC G
TG TC- ---------- - TAAGAT A

GAM3802 GCGCGTATTTTTTCTTCACT 86184 GCGTATTTTT 86185 TTC T- T---- - C TA G
GTTGTCGGCGTCCTCTAGCG TCTTCACTGT GCGCGTATTTTTTC AC GTTG CGGCG TC TC
GC A
AGCGCACGAAGATTGCCGCC TGTC |||||||||||||| || |||| ||||| || || ||
CACCGACCTGTTCGAAAGAG CGCGCGTGAGAAAG TG CAGC GCCGT AG AG CG G
TGCGCGC CT- TC CACCC T A CA C

GAM3803 TTTGCCCCCCCCCCGACGCG 86195 CATTTCTCCT 86196 CCCCC ACGC GAC TCA ----
TTACA
AGAAAGACCTTGTCAGTGGG CCGGGGCGCA TTTGC CCCCG GAGAAA CTTG GTG
GGCG G
CGTTACAGCACCTTGCCTCT AG ||||| ||||| |||||| |||| ||| ||||
TCACGATCAAGACATTTCTC GAACG GGGGC CTCTTT GAAC CAC CCGT /
CTCCGGGGCGCAAG C---- CTC- ACA TAG TTCT TCCAC

GAM3804 CAATCATAATCATCGCCCTT 86259 TACAAAACAC 86260 ATAA-- - GCCCTTTC- TATTTC-
A
TCGTGTTATTTCTTGTAACG ACACACAGTA CAATC TC ATC GTGT TTGTAACG A
AATTCGTTACAAAACACACA TATA ||||| || ||| |||| ||||||||
CACAGTATATAAGATAGAGG GTTAG AG TAG CACA AACATTGC T
AACGGATTG GCAAGG A AATATATGA CACACAA T

GAM3805 TTGTAGTCAGGGTTCTAGTT 86370 TTGGGCCCTG 86371 --- - TA- TAA C G C T GA
AAGTAGGCGCCGCGCGATTT CCGCGCAGCG TTGTAGTC AGG GTTC GT GTAGG GCC CG
GAT TAC A
ACGAATTAGTACATTTGGGC AGCG |||||||| ||| |||| || ||||| ||| || ||| |||
CCTGCCGCGCAGCGAGCGTC AGCGTCAG TCT CGAG CG CGTCC CGG GT TTA ATG
T
TCACGACTGCGA CAC G CGA CGC - - - C AT

GAM3806 GGCTACTACTATAAGGCCTT 86380 TATAAGGCCT 86381 ACT- TAT- CT A GATCTTGG ATACTT T

TAGCTTCGATCTTGGTGTAT TTAGCTTCGA GGCT AC AAGGC TT GCTTC TGT GCGTG A

ACTTGCGTGTAGGCGCGCTA TCTT |||| || ||||| || ||||| ||| |||||

ACAAAAAAGGGGCAGCAGTC TCGG TG TTCTG GA CGGGG ACA CGCGC G

TTTAATGTCACGGGCT GCAC TAAT AC - AAAAA--- AT---- G

GAM3807 CCGAACAAGTCTACATAGAT 86386 TCTACATAGA 86387 TC CAT-- A AA

CAGTTATTAAGAAAAACTTA TCAGTTATTA CCGAACAAG TA AGATC GTTATTAAG A

ATAACGATCTCTCTTTACCC AGAA ||||||||| || ||||| |||||||||

TTGTTCGG GGCTTGTTC AT TCTAG CAATAATTC /

CC TTCTC - AA

GAM3808 CTTTGTCTGTAAACCGTTTT 86399 TAGCCGGGGG 86400 G - AA- TTTTTAT TGGG

TATTGTTGGGGAATTACATA TGCAAGGGAA CTTT TC TGTA CCG TGT G

GCCGGGGGTGCAAGGGAAAG AG |||| || |||| ||| |||

GAAA GG ACGT GGC ACA /

G A GGG CGAT--- TTAA

GAM3809 GGTAAAGTTATACATTTACC 86480 AAAGTTATAC 86481 - T ACCGTT CAA- A

GTTGGACAAGGTAAGATTAC ATTTACCGTT GGTAAA GTTATACA TT GGA GGTA G

CGACATCCTAATAGAATTGT GGAC |||||| |||||||| || ||| ||||

ATAACTTTTGCT TCGTTT CAATATGT AA CCT CCAT A

T T GATAAT ACAG T

GAM3810 ATATAATATTTCGTCGATAC 86489 TAATATTTCG 86490 A T C GTGATTTCTC TT

GTGATTTCTCGTGTTTTTTC TCGATACGTG ATAT ATATT CGT GATAC GTG T

ATATAAAAAAGTATTATGAA ATTT |||| ||||| ||| ||||| |||

TATAATAT TATA TATAA GTA TTATG TAC T

A - - AAAAAATA-- TT

GAM3811 TGATCTCACGTCACAGTTTT 86492 TCTCACGTCA 86493 C C AGTTTTTTT TCTCGCGT

TTTTTTCATATGTCTCGCGT CAGTTTTTTT TGAT TCA GTCAC TTTCATATG T

TGATACATCCCGTATGAAAT TTTC |||| ||| ||||| |||||||||

ATTTAAGGTGGTTGAAATCA ACTA AGT TGGTG AAAGTATGC G

A - GAATTTAT- CCTACATA

GAM3812 TGATCTCACGTCACAGTTTT 86530 TCTCACGTCA 86531 C C AGTTTTTT TCTCGCGT

TTTTTCATATGTCTCGCGTT CAGTTTTTTT TGAT TCA GTCAC TTTCATATG T

GATACATCCCGTATGAAATA TTCA |||| ||| ||||| |||||||||

TTTAAGGTGGTTGAAATCA ACTA AGT TGGTG AAAGTATGC G

A - GAATTTAT CCTACATA

GAM3813 TAGTTCGCCTGTGTGAGCTG 86552 TAACACAGTG 86553 - GAG---------- G TTA
ACAAACTTAGTAGTGTTTGT CGAGCTG TAGTTCGC CTGTGT CT ACAAAC G
GAGGATTAACAACAATTAAC ||||||||| |||||| || ||||||
ACAGTGCGAGCTG GTCGAGCG GACACA GA TGTTTG T
T ATTAACAACAATTAG G TGA

GAM3814 GGCGGCAAGCGAGATCCCTC 86567 AGGCAAAGCG 86568 AA AGATCC AGAC -- TCG
CGAGACGTCTGGCTCGTACT GGGCGCGCGC GGCGGC GCG CTCCG GTCTG GC T
GCTGCAGGCAAAGCGGGGCG CGCT |||||| ||| ||||| ||||| ||
CGCGCCGCT TCGCCG CGC GGGGC CGGAC CG /
CG ------ GAAA GT TCA

GAM3815 TGACTTTCTGGAAATGGATT 86642 TGGAAATGGA 86643 TTTCTG A TTTCTGCAAATAG T
TCTGCAAATAGAAGGATCTA TTTCTGCAAA TGAC GAA TGGA AAGGA C
TCTTTACAACATCATTTTTC TAGA |||| ||| |||| |||||
CAATTTAATGTGTCA ACTG TTT ACCT TTTCT T
TGTAA- A TTTTACTACAACA A

GAM3816 GTTCATCTGCGTGAGCTTCC 86661 AAGGATCATT 86662 T- -------- G- TCTCA
GATCTCAGTATTGTTTGGAA GATTAACGCG GTTCA CTGCGT GA CTTCCGA G
GGATCATTGATTAACGCGGT GTTT ||||| |||||| || |||||||
TTGAAC CAAGT GGCGCA CT GAAGGTT T
TT ATTAGTTA AG TGTTA

GAM3817 TATGTAATATTGTGGGACAT 86667 TGTAATATTG 86668 T TG GG C G T GTCATA
GTGTTGTGTGTCATATAAGA TGGGACATGT TATGTAA AT T GA AT TGTTG GT T
AAAACCAACAGATTTAAGTG GTTG ||||||| || | || || ||||| ||
ATTTTATATA ATATATT TA G TT TA ACAAC CA A
T GT AA - G - AAAAGA

GAM3818 GTCAAAAGAGGCCGCCAGCT 86674 TTTGTGCGAC 86675 AAAA- C C CT--
ACCCCAGAAAAGAA AG
AGACACCCCAGAAAAGAAGC ACGTTTTATT GTC GAGG CGC AG AGAC
GCAGAGAA A
AGAGAAAGAGACTTCTTTGT CTGC ||| |||| ||| || |||| ||||||||
GCGACACGTTTTATTCTGCG CAG CTCC GCG TC TTTG TGTTTCTT G
TCCTCCGCTCGAC CTCGC T - TTAT CACAGCG------- CA

GAM3819 TTTTATTGAGTGGTGGTAGT 86681 TATTGAGTGG 86682 A A GT TTAC - T
TACGGATATCTAATATTAAT TGGTAGTTAC TTTT TTG GTG GGTAG GGATA TCTAATA T
ATTAGACTATCTCTATCGTC GGAT |||| ||| ||| ||||| ||||| |||||||
ACACAACAAAA AAAA AAC CAC CTATC TCTAT AGATTAT A
C A TG ---- C A

GAM3820 GAACGCACGTGAAGTTCCAC 86690 TATTGTGTTT 86691 C - GTTC - CG T
AGAGCCGCGTGGCTGTAGCT ACGTTGCTTT GAA GCA CGTGAA CACAG AGC CG G
ATTGTGTTTACGTTGCTTTT T ||| ||| |||||| ||||| ||| ||
TTT CGT GCATTT GTGTT TCG GT G
T T ---- A AT C

GAM3821 TAAAAACGTTTCTGGTGTAT 86717 TTAAAACATT 86718 AA T- TG T T T
GTTTTTATTTTGTATATAAA GCTGGCTGGC TAA ACGTT C GTG ATGTTTT ATTTTG A
ATTAAAACATTGCTGGCTGG GTGG ||| ||||| | ||| ||||||| ||||||
CGTGGTTA ATT TGCGG G CGT TACAAAA TAAAAT T
GG TC GT - T A

GAM3822 CGGTGCACAGGAAAGAGCCA 86721 TATTCCTTTC 86722 - --- AGCCA- TCACGGC
AAGTGTCACGGCGTCTTTTT CTGTTTTGTA CG GTGC ACAGGAAAG AAGTG G
TTATTTGTATTCCTTTCCTG CTCG || |||| ||||||||| |||||
TTTTGTACTCG GC CATG TGTCCTTTC TTTAT T
T TTT CTTATG TTTTTTC

GAM3823 GGAAATGTCTATGGGGTTAT 86726 GGTGCACAAA 86727 ---- ------ GG- G - TGAA
TGGTCATCGTTGAATACATG TGATTAAAAT GGAAAT GTCT AT GGTTATT GT CATCGT T
CGGTGCACAAATGATTAAAA GAAA |||||| |||| || ||||||| || ||||||
TGAAAAAAGGCTCGTGTTTC TCTTTG CGGA TA TTAGTAA CA GTGGCG /
T TGCT AAAAAG AAA A C TACA

GAM3824 TTTGGTCGATGTAAAATTTT 86754 TGTAAAATTT 86755 CGA AAATTTTT - AAA
TGTCGATAAAAATTAAAAAA TTGTCGATAA TTTGGT TGTA GTCGATAA AAATTAA A
TAACTTAATTTATTATTGAT AAAT |||||| |||| |||||||| |||||||
CTCGTGTGTACAACCGAA AAGCCA ACAT TAGTTATT TTTAATT T
--- GTGTGCTC A CAA

GAM3825 TAAATTTCTGCGAGAGCACA 86762 GCGCATGGAA 86763 TTT G - CACCGCAC TTA GC
GAT
CCGCACCCTTACGCTGGCTC TTGTTGCTGG TAAA CTGC AG AGCA CC CGCTG TCG A
GGATAGCTACGAATAGCGCA CAGC |||| |||| || |||| || ||||| |||
TGGAATTGTTGCTGGCAGCT ATTT GACG TC TTGT GG GCGAT AGC G
TTTTA TTC G G TAA----- TAC A- ATC

GAM3826 GCCGCTCGGGGACTGCGCGA 86778 GACTGCGCGA 86779 C T A- - GAGA- AAAGAGA GG
GACAAAAGAGAGGGGACGCC GACAAAAGAG GC GC CGGGG CT GCGC CA GG A
GGAGGGGTGGGAGGGCGCAA AGGG || || ||||| || |||| || ||
GGACCCCGCGCGC CG CG GCCCC GA CGCG GT CC /
- C AG A GGAGG GGGGAGG GC

GAM3827 TATTTTAATGGAACTGGATC 86819 TGGAACTGGA 86820 TTAAT- TCA -------- C
ATTAGGACCTCTCCCGCCCA TCATTAGGAC TATT GGAACTGGA TTA GGA C
TTTAAATTTTTAGTTTCTAC CTCT |||| ||||||||| ||| |||
AATAATA ATAA CTTTGATTT AAT CCT T
TAACAT TTA TTACCCGC C

GAM3828 GTTTAGTGTAATAAATTTAA 86838 TTAGTGTAAT 86839 T ATAAATTTAATAAA A AA
TAAAATATTGACAAAATAGT AAATTTAATA GT TAGTGTA AT TTGAC A
TAAATGAATATATGAAAGTA AAAT || ||||||| || |||||
CATTATAC CA ATTACAT TA AATTG A
T GAAAGTATATAAG- - AT

GAM3829 GGCGGCGGGTCCCTCTTGTC 86847 TCCCTCTTGT 86848 G C TCTTGTCTCG G - TCACG
TCGGAGACGGCGGGTCACGG CTCGGAGACG GGCG CGGGT CC GAGACG CG GG G
GTATTTCACGACGTCTCACG GCGG |||| ||||| || |||||| || ||
GTACTCGACGCC CCGC GCTCA GG CTCTGC GC CT /
A T CA-------- A A TTATG

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GENE    TARGET    UTR SEQUENCE            SEQID   BINDING-SITE
======== ========= === ====================== ======= ==========================
GAM15   KCNK4    3'  CAATATTGAGTGATGACATT   3           TAAATA
                                TAATATTG     ATGACATT
                                ||||||||     ||||||||
                                GTTATAAC     TACTGTAA
                                     TCAC__
GAM15   C20orf13  3'  ATATTGTAAATAACTTTCCATT 4               GA__
            A                    ATATTGTAAATAAT    CATTA
                                ||||||||||||||    |||||
                                TATAACATTTATTG    GTAAT
                                        AAAG
GAM15   KIAA1724  3'  TATTTCAATAATGACATTA    5         GTA
                                TATT   AATAATGACATTA
                                ||||   ||||||||||||
                                ATAA   TTATTACTGTAAT
                                  AG_
GAM15   MGC3279   3'  TAATAATTACATAATGACATT  6          TTG  A
                                TAATA   TA ATAATGACATT
                                |||||   || ||||||||||
                                ATTAT   AT TATTACTGTAA
                                   TA_  G
GAM15   PRO0641   5'  CAATACAGCATAATGACATTA  7           T  AA
                                TAATAT GT  ATAATGACATTA
                                |||||| ||  ||||||||||||
                                GTTATG CG  TATTACTGTAAT
                                    T  __
GAM16   DUOX1    3'  ATGGCCACCTGGAACAAGGTTG 10        A       GC  _
                                ATG CTACCTGG  CA GGTTG
                                ||| ||||||||  || |||||
                                TAC GGTGGACC  GT CCAAC
                                  C       TT  T
GAM16   EPHA8    3'  TGGCTGCCTGGGCCCTGCTG   11       A  A       AG
                                TG CT CCTGGGCC  GTTG
                                || || ||||||||  ||||
                                AC GA GGACCCGG  CGAC
                                 C  C       GA
GAM16   UBE2H    3'  ATGCTATGCACCTCAGGTTGAG 12        A   CC  G   __
                                ATG CTA  TG GCC  AGGTTGAG
                                ||| |||  || |||  ||||||||
                                TAC GAT  AC TGG  TCCAACTC
                                  _  __  G   AG
GAM16   AMOT     5'  TGACTCAGGCCAGGTTG     13         ACC
                                TGACT   TGGGCCAGGTTG
                                |||||   ||||||||||||
                                ACTGA   GTCCGGTCCAAC
                                    ____
GAM16   FLJ13491  5'  ATGCTCCTGGGCCGGGTTG   14       A  A       A
                                ATG CT CCTGGGCC GGTTG
                                ||| || |||||||| |||||
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                                TAC GA GGACCCGG CCAAC
                                  _ _       C
GAM16   MGC18079  3'  TGAGGTCCGCGGGCCAGGTTGA 15       CTA  _
            G                    TGA   CC TGGGCCAGGTTGAG
                                 |||   || ||||||||||||||
                                 ACT   GG GCCCGGTCCAACTC
                                   CCA  C
GAM16   NAV1      5'  ATGACTGCCTGGGCCTCAGAG  16         A       AGGTT
                                 ATGACT CCTGGGCC    GAG
                                 |||||| ||||||||    |||
                                 TACTGA GGACCCGG    CTC
                                    C       AGT__
GAM16   LOC150299 3'  CATGGCCGTGGCCCACAGGTTG 17        ACTA  _   G   __
            AG                     CATG    CC TGG CCA  GGTTGAG
                                 ||||    || ||| |||  |||||||
                                 GTAC    GG ACC GGT  CCAACTC
                                   C___  C   G   GT
GAM16   LOC150370 3'  ATGATTACCTGAGTCCTGG    18        C       _  A
                                 ATGA TACCTGGG CC GG
                                 |||| |||||||| || ||
                                 TACT ATGGACTC GG CC
                                   A       A  A
GAM16   LOC153196 5'  CATGTCTGCCTGGGCCTGA    19        A  A       AGGT
                                 CATG CT CCTGGGCC    TGA
                                 |||| || ||||||||    |||
                                 GTAC GA GGACCCGG    ACT
                                   A  C       _____
GAM16   LOC254182 3'  CATGCTGACCCAGGTTG      20        ACTAC    G
                                 CATG     CTGG CCAGGTTG
                                 ||||     |||| ||||||||
                                 GTAC     GACT GGTCCAAC
                                    _____    G
GAM16   LOC54550  3'  TGGCTACCTGGCTAGGTTG    21       A       G C
                                 TG CTACCTGG C AGGTTG
                                 || |||||||| | ||||||
                                 AC GATGGACC G TCCAAC
                                  C       _ A
GAM17   CNR1      3'  GCTGTCAGCCCCATTGTCCCTT 24       A__  C       C
                                 GC   CA TTTTATTG CCCTT
                                 ||   || |||||||| |||||
                                 CG   GT GGGGTAAC GGGAA
                                   ACA  C       A
GAM17   EXTL1     3'  CCGCACCCCTCTGCTCCTT    25         A    AT   C
                                 CCGCAC CTTTT  TGC CCTT
                                 |||||| |||||  ||| ||||
                                 GGCGTG GGGAG  ACG GGAA
                                    _     __   A
GAM17   DCAMKL1   3'  CACCGGGCAATTTATTGCTCTT 26         CA  CT       CC
                                 TACCG  CA  TTTATTGC  CTT
                                 |||||  ||  ||||||||  |||
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                              GTGGC  GT  AAATAACG  GAA
                                 CC  T_      A_
GAM17   DKFZp761O17121 3' ACACTACTGCCTGTCCCTT   27       _  TTTA  C
                              GCAC ACT   TTG CCCTT
                              |||| |||   ||| |||||
                              TGTG TGA   GAC GGGAA
                                A  CG__  A
GAM17   FLJ11838  3'  CCTACACACCACTGCC     28     _     TTT
                              CC GCACACT   ATTGCC
                              || |||||||   ||||||
                              GG TGTGTGG   TGACGG
                               A     ___
GAM17   FLJ23510  3'  CACTGCACATTAGCCAGCCCCT 29      C    CTTTTATT
           T                   TAC GCACA      GCCCCTT
                              ||| |||||      |||||||
                              GTG CGTGT      CGGGGAA
                                A    AATCGGT_
GAM17   KIAA1948  5'  GCACTGCCCATTTGCCCCTT   30      A_  TTA
                              GCAC  CTT   TTGCCCCTT
                              ||||  |||   |||||||||
                              CGTG  GGG   AACGGGGAA
                                AC   TA_
GAM17   LOC146819 3'  GCTGTATACTTCACCTGCCCCT 31     AC___    TA
           T                   GC    ACTTT  TTGCCCCTT
                              ||    |||||  |||||||||
                              CG    TGAAG  GACGGGGAA
                               ACATA    TG
GAM17   LOC146821 3'  CGCTGTATACTTCACCTGCCCC 32      AC___    TA
           TT                   CGC    ACTTT  TTGCCCCTT
                              |||    |||||  |||||||||
                              GCG    TGAAG  GACGGGGAA
                                ACATA    TG
GAM17   LOC154043 5'  CCTGCGCTCCGGTGCCCCTT   33     _ ACA   TAT
                              CC GC   CTTT   TGCCCCTT
                              || ||   ||||   ||||||||
                              GG CG   GAGG   ACGGGGAA
                               A  C__   CC_
GAM17   LOC157798 3'  ACACTTTTTGCAGCCTT    34         AT   C_
                              ACACTTTT  TGC  CCTT
                              ||||||||  |||  ||||
                              TGTGAAAA  ACG  GGAA
                                   __   TC
GAM17   LOC221752 3'  TACTGCCCACTTTGCCTCTCCT 35      C  A    TTAT   ___
           T                   TAC GC CACTT    TGCC   CCTT
                              ||| || |||||    ||||   ||||
                              ATG CG GTGAA    ACGG   GGAA
                                A  G     _____    AGA
GAM17   LOC51093  5'  CCGTACACTCCTCTCCTCTT   36      C      ATTG  C
                              CCG ACACTTTT    CC CTT
                              ||| ||||||||    || |||
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                                GGC TGTGAGGA   GG GAA
                                  A      GA__ A
GAM17   LOC92231  3'  CACCGCACGTTTTCCC     37         AC   ATTGC
                                TACCGCAC  TTTT    CCC
                                ||||||||  ||||    |||
                                GTGGCGTG  AAAA    GGG
                                    C_   _____
GAM17   LOC92841  5'  ACACTTTTTGGACCCCTT    38         ATT
                                ACACTTTT   GCCCCTT
                                ||||||||   |||||||
                                TGTGAAAA   TGGGGAA
                                    ACC
GAM18   DIAPH2    3'  TGTTACCCTTTTTGATTTTTCT 41         C   TAACTC
            A                    TGTTACCC TTTT     TCTA
                                ||||||||| ||||     ||||
                                ACAATGGG AAAA     AGAT
                                    A   CTAAAA
GAM18   EPHB2     3'  TGTATCCCTTTTACTCT     42       TAC     TA
                                TGT   CCCTTTT  ACTCT
                                |||   |||||||  |||||
                                ACA   GGGAAAA  TGAGA
                                  TA_      __
GAM18   LYN       3'  GTTACTTTTCCTCTCTA     43        CCCTT   AA
                                GTTAC    TTT  CTCTCTA
                                |||||    |||  |||||||
                                CAATG    AAA  GAGAGAT
                                   _____  AG
GAM18   NRIP1     3'  TGTATGCCCTTTCTCACTGTCT 44       TAC      A   C_
                                TGT   CCCTTTTT ACT  TCT
                                |||   |||||||| |||  |||
                                ACA   GGGAAAGA TGA  AGA
                                  TAC       G   CA
GAM18   PCTP      3'  TGTTATCCCTTCTACATTTCTA 45        C      TAACTC
            A                    TGTTA CCCTTTT     TCTAA
                                ||||| |||||||     |||||
                                ACAAT GGGAAGA     AGATT
                                   A      TGTAA_
GAM18   SMAP      3'  TGCTACTCCAACTCTCTA    46         C  TTTTT
                                TGTTAC CC    AACTCTCTA
                                ||||||  ||    |||||||||
                                ACGATG GG    TTGAGAGAT
                                   A  _____
GAM18   SORCS1    3'  TGTTTCCCTCTTTCTCT     47        AC      TAAC
                                TGTT  CCCTTTT    TCTCT
                                ||||  |||||||    |||||
                                ACAA  GGGAGAA    AGAGA
                                  A_      _____
GAM18   TIMP3     5'  TGCTACCCCTCCAGTTTCTCT  48            TTAAC
                                TGTTACCCCTTT    TCTCT
                                ||||||||||||    |||||
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                                ACGATGGGGAGG    AGAGA
                                      TCAA_
GAM18   TRPS1    3'  TGCTACCCTTTTTTCT     49          C    AA
                                TGTTACCC TTTTT  CT
                                |||||||| |||||  ||
                                ACGATGGG AAAAA  GA
                                     A    A
GAM18   ACVR2    3'  GTTACCCTTTTTAAAATCT    50          C     CTC
                                GTTACCC TTTTTAA   TCT
                                ||||||| |||||||   |||
                                CAATGGG AAAAATT   AGA
                                    _     TT_
GAM18   DKFZp761G2113 3'  TGTTCCCTTAACCCTCTA    51        A   CTTT
                                TGTT CCC    TTAACTCTCTA
                                |||| |||    ||||||||||
                                ACAA GGG    AATTGGGAGAT
                                  _  ____
GAM18   EIF4B    3'  TGTAGTCCCTTTCTCTCT    52       TAC     TTAA
                                TGT   CCCTTT    CTCTCT
                                |||   ||||||    ||||||
                                ACA   GGGAAA    GAGAGA
                                  TCA     ____
GAM18   FLJ11827  3'  TGTTGCCCTTTTATAACC    53        AC      _
                                TGTT  CCCTTTT TAACT
                                ||||  ||||||| |||||
                                ACAA  GGGAAAA ATTGG
                                  C_      T
GAM18   FLJ20094  3'  CCCTTTTTAGGTTCCTCTA   54           AC__
                                CCCTTTTTA    TCTCTA
                                |||||||||    ||||||
                                GGGAAAAAT    GGAGAT
                                     CCAA
GAM18   FLJ20531  3'  TGTTGCTCCTTTTCAGTCCCT  55        ACC       AC
                                TGTT   CCTTTTTA  TCTCT
                                ||||   ||||||||  |||||
                                ACAA   GGAAAAGT  AGGGA
                                  CGA       C_
GAM18   FUBP3    3'  TATTACCCCTTTCGAACTCT   56             T
                                TGTTACCCCTTTT AACTCT
                                |||||||||||| ||||||
                                ATAATGGGGAAAG TTGAGA
                                       C
GAM18   KIAA0218  3'  TGTTCCAATCAGCTCTCTAA   57        A  CCTTT   A
                                TGTT CC    TTA CTCTCTAA
                                |||| ||    ||| ||||||||
                                ACAA GG    AGT GAGAGATT
                                  _ TT___   C
GAM18   KIAA1577  3'  TGTTGTCCCTCTTTATTCTA   58        AC        ACTC
                                TGTT  CCCTTTTTA    TCTA
                                ||||  |||||||||    ||||
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                                ACAA  GGGAGAAAT    AGAT
                                  CA        A___
GAM18   SPEC1    3'  TGTTAACCCTTTAGATCTCTA  59         C     TTAAC
                                TGTTA CCCTTT     TCTCTA
                                ||||| ||||||     ||||||
                                ACAAT GGGAAA     AGAGAT
                                   T      TCT__
GAM18   LOC121274 3'  TGTTTCCTTGTTACTCTCTAA  60         ACC    T   A
                                TGTT   CCTT TTA CTCTCTAA
                                ||||   |||| ||| ||||||||
                                ACAA   GGAA AAT GAGAGATT
                                  A__    C   _
GAM18   LOC139673 3'  TGTAGTCCCTTTCTCTCT    52         TAC     TTAA
                                TGT   CCCTTT    CTCTCT
                                |||   ||||||    ||||||
                                ACA   GGGAAA    GAGAGA
                                  TCA     _____
GAM18   LOC220758 3'  TGTGCCCCTCTCCTTCT     61         TA       TAA  C
                                TGT  CCCCTTTT   CT TCT
                                |||  ||||||||   || |||
                                ACA  GGGGAGAG   GA AGA
                                  C_        ___  A
GAM18   LOC221060 3'  TGTCATCTCTTTTTAATCTTTC 62          CCC       _  C
            TAA                   TGTTA   CTTTTTAA CT TCTAA
                                |||||   |||||||| || |||||
                                ACAGT   GAAAAATT GA AGATT
                                   AGA       A  A
GAM18   LOC221140 3'  TGTTCCCTTTCCATTCT     63         AC        AC
                                TGTT  CCCTTTTTA  TCT
                                ||||  |||||||||  |||
                                ACAA  GGGAAAGGT  AGA
                                  __        AA
GAM18   LOC90488  3'  CTTTTTAAACTTCTCTAA    64           _  _
                                CTTTTTAA CT CTCTAA
                                |||||||| || ||||||
                                GAAAAATT GA GAGATT
                                     T  A
GAM19   DLG5     3'  AGGTCCTACCCCAACGACACTT 67       A    A     CTAT
                                AG TCCTA CCCAAT    CTT
                                || ||||| ||||||    |||
                                TC AGGAT GGGTTG    GAA
                                 C    G     CTGT
GAM19   RBBP9    3'  AATCCTATAGGTCTATCTT    68          ACCCAA
                                GATCCTA     TCTATCTT
                                |||||||     ||||||||
                                TTAGGAT     AGATAGAA
                                   ATCC__
GAM19   AXOT     3'  ACAGATCATCCATCT       69          CTAACCCA
                                ACAGATC       ATCTATCT
                                |||||||       ||||||||
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                                TGTCTAG       TAGGTAGA
                                          ________
GAM19   C8orf2    3'  ACAGATCCCTCCACATCTAT   70          AAC   _
                                ACAGATCCT   CCA ATCTAT
                                |||||||||   ||| ||||||
                                TGTCTAGGG   GGT TAGATA
                                     A__   G
GAM19   DAPK2     3'  TCCTAACCTCCCCTTCTT     71          CAA   A
                                TCCTAACC   TCT TCTT
                                ||||||||   ||| ||||
                                AGGATTGG   GGG AGAA
                                     AG_   A
GAM19   DJ971N18.2 3'  ACAGATCCCAACACTAC     72             CCAAT
                                ACAGATCCTAAC    CTAT
                                ||||||||||||    ||||
                                TGTCTAGGGTTG    GATG
                                      T____
GAM19   KIAA1786  3'  CAGGTTTTAAGCCAGTCCACCT 73       ATCC   C   A
           T                     CAG    TAA CCA TCTATCTT
                                |||    ||| ||| ||||||||
                                GTC    ATT GGT AGGTGGAA
                                  CAAA   C   C
GAM19   NRM       3'  CAGACCCTGGTCCACCTTCTT  74          AAC   A   A
                                CAGATCCT   CCA TCT TCTT
                                ||||||||   ||| ||| ||||
                                GTCTGGGA   GGT GGA AGAA
                                     CCA   _   _
GAM19   NRM       3'  CAGACCCTGGTCCACCTTCTT  74          AAC   A   A
                                CAGATCCT   CCA TCT TCTT
                                ||||||||   ||| ||| ||||
                                GTCTGGGA   GGT GGA AGAA
                                     CCA   _   _
GAM19   NRM       3'  CAGACCCTGGTCCACCTTCTT  74          AAC   A   A
                                CAGATCCT   CCA TCT TCTT
                                ||||||||   ||| ||| ||||
                                GTCTGGGA   GGT GGA AGAA
                                     CCA   _   _
GAM19   SLC6A14   3'  GATCCTAATTTTTCCATCTT   75          CCCAA
                                GATCCTAA    TCTATCTT
                                ||||||||    ||||||||
                                CTAGGATT    AGGTAGAA
                                     AAAA_
GAM19   TIAM2     3'  ACAGCATCTATTACAATCTATC 76        ATC   ACC
           TT                    ACAG   CTA   CAATCTATCTT
                                ||||   |||   ||||||||||
                                TGTC   GAT   GTTAGATAGAA
                                  GTA   AAT
GAM19   TSPAN-3   3'  GATCCTACAATCTAT       77          ACC
                                GATCCTA   CAATCTAT
                                |||||||   ||||||||
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                                CTAGGAT   GTTAGATA
                                   ___
GAM19   TXNL2    3'  ACAGATCCTGGTTCAAATCCCA 78          _______ _
                                ACAGATCCT     AA CCCA
                                |||||||||     || ||||
                                TGTCTAGGA     TT GGGT
                                    CCAAGT  A
GAM20   FZD7     3'  AAAGCAACAAGTCATCAC    81              C
                                AAAGTAACAAGTCA CGC
                                |||||||||||||| |||
                                TTTCGTTGTTCAGT GTG
                                      A
GAM20   MMP19    5'  AAAGAACAAGTCACCTCT    82        T        GC
                                AAAG AACAAGTCACC  CT
                                |||| ||||||||||  ||
                                TTTC TTGTTCAGTGG  GA
                                  _        A_
GAM20   MSL3L1   3'  AAAGTAACAAGTGTCGTGTC  83            CAC  CC
                                AAAGTAACAAGT   CG  TC
                                ||||||||||||   ||  ||
                                TTTCATTGTTCA   GC  AG
                                    CA_  AC
GAM20   MSL3L1   3'  AAAGTAACAAGTGTCGTGTC  83            CAC  CC
                                AAAGTAACAAGT   CG  TC
                                ||||||||||||   ||  ||
                                TTTCATTGTTCA   GC  AG
                                    CA_  AC
GAM20   MSL3L1   3'  AAAGTAACAAGTGTCGTGTC  83            CAC  CC
                                AAAGTAACAAGT   CG  TC
                                ||||||||||||   ||  ||
                                TTTCATTGTTCA   GC  AG
                                    CA_  AC
GAM20   RAD51C   3'  GTAACAAGTCCACTTGTACAC  84            _  CGCCT
                                GTAACAAGTC AC     CAT
                                |||||||||| ||     |||
                                CATTGTTCAG TG     GTG
                                    G  AACAT
GAM20   RAD51C   3'  GTAACAAGTCCACTTGTACAC  84            _  CGCCT
                                GTAACAAGTC AC     CAT
                                |||||||||| ||     |||
                                CATTGTTCAG TG     GTG
                                    G  AACAT
GAM20   CL24751  3'  AAAGTGGCAGATGACCTCATC  85         AACA  TCACC
                                AAAGT    AG    GCCTCATC
                                |||||    ||    ||||||||
                                TTTCA    TC    TGGAGTAG
                                  CCG_  TAC__
GAM20   DKFZP564O123 3'  AAAGGGACAAGTCATCAT    86        TA       CCGCC
                                AAAG  ACAAGTCA    TCAT
                                ||||  ||||||||    ||||
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                                TTTC  TGTTCAGT    AGTA
                                  CC      _____
GAM20   FLJ12800  3'  AATAACAAGTCACAGTGCATC  87            C__  C
                                AGTAACAAGTCAC   GC TC
                                ||||||||||||   || ||
                                TTATTGTTCAGTG   CG AG
                                       TCA  T
GAM20   FLJ12800  3'  AATAACAAGTCACAGTGCATC  87            C__  C
                                AGTAACAAGTCAC   GC TC
                                ||||||||||||   || ||
                                TTATTGTTCAGTG   CG AG
                                       TCA  T
GAM20   FLJ13204  3'  GTTACAAGTCAGCCGTC    88      A      CC  _
                                GT ACAAGTCA  GCC TC
                                || ||||||||  ||| ||
                                CA TGTTCAGT  CGG AG
                                 A       __  C
GAM20   FLJ30567  3'  AAAGTAACAACGACTCTCAT  89          AGTC  C  _
                                AAAGTAACA    AC GC CTCAT
                                |||||||||    || || |||||
                                TTTCATTGT    TG TG GAGTA
                                      _____  C  A
GAM20   KIAA1240  3'  AAAATAACAAGTTGCCCAC   90           CACC   T
                                AAAGTAACAAGT    GCC CAT
                                ||||||||||||    ||| |||
                                TTTTATTGTTCA    CGG GTG
                                       A___   _
GAM20   LRBA      3'  AACAGTGGCTCCGCCTCAT   91        A  CA__
                                AACA GT    CCGCCTCAT
                                ||||  ||    |||||||||
                                TTGT CA    GGCGGAGTA
                                  _  CCGA
GAM20   PEGASUS   5'  GGAGTAAACCACACCGCCT   92      A    _ AAGT
                                A AGTAA C    CACCGCCT
                                | |||||  |    ||||||||
                                C TCATT G    GTGGCGGA
                                 C     T GT__
GAM20   SNX10     3'  AAAGCAACAAGTTATCCT    93            CACCG
                                AAAGTAACAAGT     CCT
                                ||||||||||||     |||
                                TTTCGTTGTTCA     GGA
                                       ATA__
GAM20   LOC124216 3'  AAGAAACAAGTCATTTGCATC  94        T       CC_  C
                                AAG AACAAGTCA   GC TC
                                |||  |||||||||   || ||
                                TTC TTGTTCAGT   CG AG
                                  T        AAA  T
GAM20   LOC148021 3'  AAAGTGGCAGATGACCTCATC  85        AACA  TCACC
                                AAAGT    AG    GCCTCATC
                                |||||    ||    ||||||||
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                                TTTCA   TC    TGGAGTAG
                                  CCG_  TAC__
GAM21   ACTA1   5' GGCGCTGTCCGCTGCG     97      A    GGGCG
                                GG GCTGT    TCGCTGCG
                                || |||||    ||||||||
                                CC CGACA    GGCGACGC
                                 G   ______
GAM21   EXTL1   5' GGGCTGTGGCCCCTGTGG    98      A     GCG  G   C
                                GG GCTGTGG   TC CTG GG
                                || |||||||   || ||| ||
                                CC CGACACC   GG GAC CC
                                 _     ___  G   A
GAM21   FMNL    3' TCGGGGCTGGGGCTTGCG    99       A   T   GTCGC
                                TCGG GCTG GGGC    TGCG
                                |||| |||| ||||    ||||
                                AGCC CGAC CCCG    ACGC
                                  C   _   A____
GAM21   PHKA2   5' TCGGGGCTGTGGCCTCCAAGCG 100      A     G G  GCT
           G                     TCGG GCTGTGG C TC   GCGG
                                |||| ||||||| | ||   ||||
                                AGCC CGACACC G AG   CGCC
                                  C     _ G  GTT
GAM21   PTK2    3' GGAGCTGTGAGTGCTG      101           CGTC
                                GGAGCTGTGGG   GCTG
                                ||||||||||    ||||
                                CCTCGACACTC   CGAC
                                      A___
GAM21   EFS2    5' CGGGCCGGGGCGTCGCTGCGG  102     A   T
                                CGG GCTG GGGCGTCGCTGCGG
                                ||| |||| ||||||||||||||
                                GCC CGGC CCCGCAGCGACGCC
                                 _   _
GAM21   HYPC    5' CCGGAGCCGTCGCTGC      103         TGTGGG
                                TCGGAGC     CGTCGCTGC
                                |||||||     |||||||||
                                GGCCTCG     GCAGCGACG
                                  _______
GAM21   KIAA0478 3' CCGGAGCTGGCGCTCGCTGTGG 104         GTG   _    C
                                TCGGAGCT   GGCG TCGCTG GG
                                ||||||||   |||| |||||| ||
                                GGCCTCGA   CCGC AGCGAC CC
                                     ___   G     A
GAM21   KIAA0953 5' TCGAGAGGCCGGCGTCGCTGCG 105     _  CT  G
           G                     TCG GAG  GT GGCGTCGCTGCGG
                                ||| |||  || ||||||||||||
                                AGC CTC  CG CCGCAGCGACGCC
                                  T  __  G
GAM21   PIP5K2B  5' GGGCAGGCGTCGCTGG     106     A  TGT        C
                                GG GC   GGGCGTCGCTG G
                                || ||   |||||||||| |
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                                CC CG   TCCGCAGCGAC C
                                 _ ___         A
GAM21   PIP5K2B   5'  GGGCAGGCGTCGCTGG      106      A  TGT         C
                                GG GC   GGGCGTCGCTG G
                                || ||   |||||||||||| |
                                CC CG   TCCGCAGCGAC C
                                 _ ___         A
GAM21   LOC155389 5'  TCGGGGCGTGTGGGTGGCG    107       A _     CGTCGCT
                                TCGG GC TGTGGG      GCG
                                |||| || ||||||      |||
                                AGCC CG ACACCC      CGC
                                  C  C     AC_____
GAM21   LOC157653 5'  GCTGTGGACAGAGCTGTGG    108           TC    C
                                GCTGTGGGCG  GCTG GG
                                ||||||||||  |||| ||
                                CGACACCTGT  CGAC CC
                                      CT    A
GAM21   LOC221773 5'  TCGGAGCTGAGGGCAGCG     109          T    TCGCT
                                TCGGAGCTG GGGCG     GCG
                                |||||||| |||||     |||
                                AGCCTCGAC CCCGT     CGC
                                     T    _____
GAM21   LOC245718 5'  TCGAAGCTGTGGGACTGCG    110            CGTC
                                TCGGAGCTGTGGG    GCTGCG
                                ||||||||||||    ||||||
                                AGCTTCGACACCC    TGACGC
                                                 ____
GAM21   LOC253451 5'  TCGGGGCGTGTGGGTGGCG    107       A _     CGTCGCT
                                TCGG GC TGTGGG      GCG
                                |||| || ||||||      |||
                                AGCC CG ACACCC      CGC
                                  C  C     AC_____
GAM21   LOC256310 5'  GGAGCTGTGGCTGAAGCTG    111           G GTC_
                                GGAGCTGTGG C    GCTG
                                |||||||||| |    ||||
                                CCTCGACACC G    CGAC
                                     _ ACTT
GAM21   LOC256512 5'  GGGGCTGTGGCTCCGGCTGTGG 112      A      G GT  _   C
                                GG GCTGTGG C  CG CTG GG
                                || ||||||| |  || ||| ||
                                CC CGACACC G  GC GAC CC
                                 C      _ AG  C   A
GAM22   MAP3K14   3'  TCCCACGGAGTCTCGGC     115          A  AATG
                                TTCCACGGA TC    TCGGC
                                |||||||| ||    |||||
                                AGGGTGCCT AG    AGCCG
                                     C  ____
GAM22   FLJ20397  5'  TTCCACGGGACCATGTGTC    116          A   A_
                                TTCCACGG ATCA  TGTC
                                |||||||| ||||  ||||
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                                AAGGTGCC TGGT  ACAG
                                    C    AC
GAM22   HEY2     3'  GGATCTGTCGGCATC      117      A  AA
                                GGA TC  TGTCGGCATC
                                ||| ||  ||||||||||
                                CCT AG  ACAGCCGTAG
                                  _ __
GAM22   KLF12    3'  TTCCATGAATCAATACTGTC  118       CG     ___
                                TTCCA  GAATCAA   TGTC
                                |||||  |||||||  ||||
                                AAGGT  CTTAGTT   ACAG
                                   A_      ATG
GAM22   LOC148753 5'  TCCCACGGGGTCGCAGC    119         AA  AAT T
                                TTCCACGG  TC   G CGGC
                                ||||||||  ||   | ||||
                                AGGGTGCC  AG   C GTCG
                                    CC  ___ _
GAM22   LOC154834 3'  TCCCACACCTCTTCAGTGTTGG 120        GAA__   A   C
                                TTCCACG    TCA TGT GG
                                |||||||    ||| ||| ||
                                AGGGTGT    AGT ACA CC
                                    GGAGA   C   A
GAM23   ATP11A   3'  AACTTGTTGTCAGAG      123         CC    CTAA
                                AACTTGTTG  TCAG    AG
                                |||||||||  ||||    ||
                                TTGAACAAC  AGTC    TC
                                    __    __
GAM23   BCL2L2   3'  GCTCCTCTTGGCTAAAGGT   124      G    A__
                                GTT CCTC   GCTAAAGGT
                                ||| ||||   |||||||||
                                CGA GGAG   CGATTTCCA
                                  _    AAC
GAM23   CLNS1A   3'  CAACTTGTTGTCTCAGTAAG  125          C    C  A
                                TAACTTGTTG CTCAG TA AG
                                |||||||||| ||||| || ||
                                GTTGAACAAC GAGTC AT TC
                                    A    _
GAM23   DMD      3'  TAATTTGTTACCTTAGAGCTTT 126      C       C__    AAA
            GGT                   TAA TTGTTGCCT   AGCT   GGT
                                ||| |||||||||   ||||   |||
                                ATT AACAATGGA   TCGA   CCA
                                  A       ATC    AAC
GAM23   DMD      3'  TAATTTGTTACCTTAGAGCTTT 126      C       C__    AAA
            GGT                   TAA TTGTTGCCT   AGCT   GGT
                                ||| |||||||||   ||||   |||
                                ATT AACAATGGA   TCGA   CCA
                                  A       ATC    AAC
GAM23   DMD      3'  TAATTTGTTACCTTAGAGCTTT 126      C       C__    AAA
            GGT                   TAA TTGTTGCCT   AGCT   GGT
                                ||| |||||||||   ||||   |||
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                          ATT AACAATGGA  TCGA  CCA
                            A      ATC   AAC
GAM23  DMD    3' TAATTTGTTACCTTAGAGCTTT 126    C     C__   AAA
          GGT               TAA TTGTTGCCT  AGCT  GGT
                          ||| |||||||||  ||||  |||
                          ATT AACAATGGA  TCGA  CCA
                            A      ATC   AAC
GAM23  DMD    3' TAATTTGTTACCTTAGAGCTTT 126    C     C__   AAA
          GGT               TAA TTGTTGCCT  AGCT  GGT
                          ||| |||||||||  ||||  |||
                          ATT AACAATGGA  TCGA  CCA
                            A      ATC   AAC
GAM23  DMD    3' TAATTTGTTACCTTAGAGCTTT 126    C     C__   AAA
          GGT               TAA TTGTTGCCT  AGCT  GGT
                          ||| |||||||||  ||||  |||
                          ATT AACAATGGA  TCGA  CCA
                            A      ATC   AAC
GAM23  DMD    3' TAATTTGTTACCTTAGAGCTTT 126    C     C__   AAA
          GGT               TAA TTGTTGCCT  AGCT  GGT
                          ||| |||||||||  ||||  |||
                          ATT AACAATGGA  TCGA  CCA
                            A      ATC   AAC
GAM23  DMD    3' TAATTTGTTACCTTAGAGCTTT 126    C     C__   AAA
          GGT               TAA TTGTTGCCT  AGCT  GGT
                          ||| |||||||||  ||||  |||
                          ATT AACAATGGA  TCGA  CCA
                            A      ATC   AAC
GAM23  DMD    3' TAATTTGTTACCTTAGAGCTTT 126    C     C__   AAA
          GGT               TAA TTGTTGCCT  AGCT  GGT
                          ||| |||||||||  ||||  |||
                          ATT AACAATGGA  TCGA  CCA
                            A      ATC   AAC
GAM23  DMD    3' TAATTTGTTACCTTAGAGCTTT 126    C     C__   AAA
          GGT               TAA TTGTTGCCT  AGCT  GGT
                          ||| |||||||||  ||||  |||
                          ATT AACAATGGA  TCGA  CCA
                            A      ATC   AAC
GAM23  DMD    3' TAATTTGTTACCTTAGAGCTTT 126    C     C__   AAA
          GGT               TAA TTGTTGCCT  AGCT  GGT
                          ||| |||||||||  ||||  |||
                          ATT AACAATGGA  TCGA  CCA
                            A      ATC   AAC
GAM23  DMD    3' TAATTTGTTACCTTAGAGCTTT 126    C     C__   AAA
          GGT               TAA TTGTTGCCT  AGCT  GGT
                          ||| |||||||||  ||||  |||
                          ATT AACAATGGA  TCGA  CCA
                            A      ATC   AAC
GAM23  DMD    3' TAATTTGTTACCTTAGAGCTTT 126    C     C__   AAA
          GGT               TAA TTGTTGCCT  AGCT  GGT
                          ||| |||||||||  ||||  |||
                          ATT AACAATGGA  TCGA  CCA
                            A      ATC   AAC
GAM23  DMD    3' TAATTTGTTACCTTAGAGCTTT 126    C     C__   AAA
          GGT               TAA TTGTTGCCT  AGCT  GGT
                          ||| |||||||||  ||||  |||
                          ATT AACAATGGA  TCGA  CCA
                            A      ATC   AAC
GAM23  DMD    3' TAATTTGTTACCTTAGAGCTTT 126    C     C__   AAA
          GGT               TAA TTGTTGCCT  AGCT  GGT
                          ||| |||||||||  ||||  |||
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                                ATT AACAATGGA  TCGA  CCA
                                  A       ATC   AAC
GAM23  KRT2A   3' TAACTTGCTGCCAGTTAAGGT 127          TC  C  A
                                TAACTTGTTGCC  AG TA AGGT
                                ||||||||||||  || || ||||
                                ATTGAACGACGG  TC AT TCCA
                                      __  A  C
GAM23  PAIP2   3' TAACTTGTAGCCTCAGTAA  128        T     C
                                TAACTTGT GCCTCAG TAA
                                |||||||| ||||||| |||
                                ATTGAACA CGGAGTC ATT
                                     T     _
GAM23  PREP    3' TAACTTGTTGCAGAAAGG   129          CTC  CT
                                TAACTTGTTGC   AG  AAAGG
                                ||||||||||   ||  |||||
                                ATTGAACAACG   TC  TTTCC
                                      ____  __
GAM23  WASF3   3' TAACTTGTTGATTCAGCT   130          CC
                                TAACTTGTTG  TCAGCT
                                ||||||||||  ||||||
                                ATTGAACAAC  AGTCGA
                                      TA
GAM23  FLJ22795 3' CCTGTTGCTCCTAGGT     131        C  AG   AA
                                CTTGTTGC TC  CTA  GGT
                                |||||||| ||  |||  |||
                                GGACAACG AG  GAT  CCA
                                     _  __   C
GAM23  SYNE-2  3' TTGTTTCCATCAGCTAAGGT  132       G  _      A
                                TTGTT CC TCAGCTAA GGT
                                ||||| || |||||||| |||
                                AACAA GG AGTCGATT CCA
                                   A  T       C
GAM23  LOC144698 3' CAACTAAATTCAGCTGAGGT  133       TGTTGCC     AA
                                TAACT      TCAGCT  AGGT
                                |||||      ||||||  ||||
                                GTTGA      AGTCGA  TCCA
                                   TTTA___     CC
GAM23  LOC145225 3' TTGTTGCCTTCCTTTGCTGGAG 134          _ A___   AA
          GT                      TTGTTGCCT C    GCT  AGGT
                                |||||||||  |    |||  ||||
                                AACAACGGA G    CGA  TCCA
                                     A GAAA   CC
GAM23  LOC145717 3' CCTGTTGCTCCTAGGT     131        C  AG   AA
                                CTTGTTGC TC  CTA  GGT
                                |||||||| ||  |||  |||
                                GGACAACG AG  GAT  CCA
                                     _  __   C
GAM23  LOC220537 3' CCTGTTGCTCCTAGGT     131        C  AG   AA
                                CTTGTTGC TC  CTA  GGT
                                |||||||| ||  |||  |||
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                                GGACAACG AG  GAT  CCA
                                    _ __  C
GAM24   PDGFRA   3' AAATTATATATCATTTATT   137
                                AAATTATATATCATTTGTT
                                |||||||||||||||||||
                                TTTAATATATAGTAAATAA

GAM24   PEG10    3' TGAAATTATATATGATGTT   138           CATT
                                TGAAATTATATAT   TGTT
                                |||||||||||||   ||||
                                ACTTTAATATATA   ACAA
                                      CT__
GAM25   CYP1B1   3' TTAAAGCTTGGCTGGCTTTTTT 141        CC  AAT
           TT                    TTAAAGC  GG   GTTTTTTTTT
                                |||||||  ||   ||||||||||
                                AATTTCG  CC   CGAAAAAAAA
                                    AA  GAC
GAM25   GPD2     3' TTAAAGTTTTGGAATGTTTT  142        CCC_
                                TTAAAG   GGAATGTTTT
                                ||||||   ||||||||||
                                AATTTC   CCTTACAAAA
                                   AAAA
GAM25   SON      3' TCAAAGCCTGGAGATGTTTTT 143         C  _
                                TTAAAGCC GGA ATGTTTTT
                                |||||||| ||| ||||||||
                                AGTTTCGG CCT TACAAAAA
                                     A  C
GAM25   SON      3' TCAAAGCCTGGAGATGTTTTT 143         C  _
                                TTAAAGCC GGA ATGTTTTT
                                |||||||| ||| ||||||||
                                AGTTTCGG CCT TACAAAAA
                                     A  C
GAM25   SON      3' TCAAAGCCTGGAGATGTTTTT 143         C  _
                                TTAAAGCC GGA ATGTTTTT
                                |||||||| ||| ||||||||
                                AGTTTCGG CCT TACAAAAA
                                     A  C
GAM25   BIVM     3' AGCCCCAATTTTTTTTT     144        G AAT
                                AGCCC G   GTTTTTTTTT
                                ||||| |   ||||||||||
                                TCGGG T   TAAAAAAAAA
                                   G ___
GAM25   DKFZp434D177 3' GCAGAGAATGTTTTTTTT   145     CC
                                GC  GGAATGTTTTTTTT
                                ||  ||||||||||||||
                                CG  TCTTACAAAAAAAA
                                 TC
GAM25   FLJ20729 3' CCCAGGTTTTTTTTT      146        AAT
                                CCCGG   GTTTTTTTTT
                                |||||   ||||||||||
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                                GGGTC   CAAAAAAAAA
                                  ___
GAM25   METAP2    3'  AAAGTCCGGAAAGCTTTTT   147       C     T
                                AAAG CCGGAA GTTTTTT
                                |||| |||||| |||||||
                                TTTC GGCCTT CGAAAAA
                                  A     T
GAM25   NUCKS     3'  AGCCCCTGCTTTTTTTT     148        GGAA
                                AGCCC    TGTTTTTTTTT
                                |||||    ||||||||||
                                TCGGG    ACGAAAAAAAA
                                  G___
GAM25   TA-LRRP   3'  TTAAAGCCCTGGAGCATTTTTT 149          _   AT
            TTT                   TTAAAGCCC GGA  GTTTTTTTTT
                                |||||||| |||  ||||||||||
                                AATTTCGGG CCT  TAAAAAAAAA
                                     A   CG
GAM25   LOC122618 3'  AAGCCACGAGTTTTTTTT    150        _   AAT
                                AAGCC CGG   GTTTTTTTT
                                ||||| |||   |||||||||
                                TTCGG GCT   CAAAAAAAA
                                  T   ___
GAM25   LOC149010 3'  GCAGAGAATGTTTTTTTTT   145      CC
                                GC  GGAATGTTTTTTTTT
                                ||  ||||||||||||||
                                CG  TCTTACAAAAAAAAA
                                 TC
GAM26   NOV       3'  TGGTGGGTGGCGCAGCAGCT   153        A    GCTC
                                TGGTG GTGGC    GCAGCAGCT
                                ||||| |||||    |||||||||
                                ACCAC CACCG    CGTCGTCGA
                                  C    _____
GAM26   SMOH      3'  GGTGAGTGTGTGCAGCAGCT   154          GCGCTC
                                GGTGAGTG     GCAGCAGCT
                                ||||||||     |||||||||
                                CCACTCAC     CGTCGTCGA
                                     ACA___
GAM26   EPS8R3    5'  TGGTGGTGGAAGGACAGCAGCT 155        A   CGCTC
                                TGGTG GTGG     GCAGCAGCT
                                ||||| ||||     |||||||||
                                ACCAC CACC     TGTCGTCGA
                                  _    TTCC_
GAM26   EPS8R3    5'  TGGTGGTGGAAGGACAGCAGCT 155        A   CGCTC
                                TGGTG GTGG     GCAGCAGCT
                                ||||| ||||     |||||||||
                                ACCAC CACC     TGTCGTCGA
                                  _    TTCC_
GAM26   FLJ20130  5'  TGGTGGTGGCAACAGCAGC    156        A     CTC
                                TGGTG GTGGCG   GCAGCAGC
                                ||||| ||||||   ||||||||
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                                ACCAC CACCGT   TGTCGTCG
                                  _    ___
GAM26   FLJ20211  3'  TGGTGAGTGGCAGCAG      157           CTC
                                TGGTGAGTGGCG   GCAG
                                ||||||||||||  ||||
                                ACCACTCACCGT   CGTC
                                     ___
GAM26   LYPLA2    3'  AGTGAGTGGGTCAGCGGCT    158          CGCTCG    A
                                GGTGAGTGG     CAGC GCT
                                |||||||||     |||| |||
                                TCACTCACC     GTCG CGA
                                    CA____    C
GAM26   MGC35558  3'  TGGCGAGTGGCCCACAGTGGCT 159           G T    CA
                                TGGTGAGTGGC C CGCAG  GCT
                                |||||||||| | |||||  |||
                                ACCGCTCACCG G GTGTC  CGA
                                    _ _    AC
GAM26   SPOP      3'  TGGTCAGTGGCAGCAACAG    160       G      CTC
                                TGGT AGTGGCG   GCAGCAG
                                |||| |||||||   |||||||
                                ACCA TCACCGT   CGTTGTC
                                  G     ___
GAM26   SUN1      3'  TGGTGAGGGCTTAAGCAGCAGC 161         T   GCTC
            T                    TGGTGAG GGC    GCAGCAGCT
                                |||||||| |||    |||||||||
                                ACCACTC CCG    CGTCGTCGA
                                   _  AATT
GAM26   LOC163341 3'  TGGTGAGCTGGGAACAGTGGCT 162         _  CGCTC    CA
                                TGGTGAG TGG    GCAG  GCT
                                |||||||| |||    ||||  |||
                                ACCACTC ACC    TGTC  CGA
                                   G   CT___    AC
GAM26   LOC253263 3'  TGGTCAGTGCTCGCAGTGGCT  163       G   GGC       CA
                                TGGT AGT   GCTCGCAG  GCT
                                |||| |||   ||||||||  |||
                                ACCA TCA   CGAGCGTC  CGA
                                  G   ___       AC
GAM27   CENPC1    5'  TCTCAGGCGACTGCCGCG     166      C       ACCTC
                                TC CAGGCGACT     CTGCG
                                || |||||||||     |||||
                                AG GTCCGCTGA     GGCGC
                                 A        C____
GAM27   EDNRA     5'  TCCTGGGCACTGCTTCTCCCGG 167      CA   G   AC__     C
            G                    TCC  GGC ACT    CTCCTG GG
                                |||  ||| |||    |||||| ||
                                AGG  CCG TGA    GAGGGC CC
                                  AC   _   CGAA     _
GAM27   PLAU      3'  TCCCAGGCACTGTCACGTGGG  168         G   ACC  C  C
                                TCCCAGGC ACT   TC TG GGG
                                ||||||||| |||   || || |||
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                                AGGGTCCG TGA   AG GC CCC
                                    _  C__  T  A
GAM27   SCN2A2   3'  GGCATAGACCTCCTGTGGG   169       ACT      C
                                GGCG   ACCTCCTG GGG
                                ||||   |||||||| |||
                                CCGT   TGGAGGAC CCC
                                  ATC       A
GAM27   DRF1     3'  AGGGACCTCCTGCGGG      170       C  CTA
                                AGG GA   CCTCCTGCGGG
                                ||| ||   ||||||||||
                                TCC CT   GGAGGACGCCC
                                  _ ___
GAM27   FLJ14327 3'  TCCCAGGCCACTGCCTCTAAAC 172          G   A    CT_
                                TCCCAGGC ACT CCTC   GC
                                |||||||| ||| ||||   ||
                                AGGGTCCG TGA GGAG   TG
                                     G   C    ATT
GAM27   FLJ14327 3'  TCCCAGGCAGGCTAGCAGG   171          A_   CCTCCT
                                TCCCAGGCG  CTA     GCGGG
                                |||||||||  |||     |||||
                                AGGGTCCGT  GAT     CGTCC
                                     CC   _______
GAM27   KIAA1199 3'  TCCCAGGCAGCTGCTGGCAGG  173          A  AC  CCT
                                TCCCAGGCG CT  CT   GCGGG
                                |||||||||  ||  ||   |||||
                                AGGGTCCGT GA  GA   CGTCC
                                     C  C_  C__
GAM27   NDRG4    3'  CCCAGGCGGCTATGGGGTGTGG 174          A   CCTCC  C
           G                     CCCAGGCG CTA     TG GGG
                                |||||||| |||     || |||
                                GGGTCCGC GAT     AC CCC
                                     C   ACCCC  A
GAM27   NDRG4    3'  CCCAGGCGGCTATGGGGTGTGG 174          A   CCTCC  C
           G                     CCCAGGCG CTA     TG GGG
                                |||||||| |||     || |||
                                GGGTCCGC GAT     AC CCC
                                     C   ACCCC  A
GAM27   PASK     5'  CCCCAGGCGAGACCCTGTGGG  175          CTACC    C
                                TCCCAGGCGA     TCCTG GGG
                                ||||||||||     ||||| |||
                                GGGGTCCGCT     GGGAC CCC
                                     CT___     A
GAM27   VPS4B    5'  TCCCAGGCGGTTCCCAAGG   176          ACTACC    C
                                TCCCAGGCG      TCCTG GG
                                |||||||||      ||||| ||
                                AGGGTCCGC      AGGGT CC
                                     CA____     T
GAM27   LOC158267 3'  TCCCAGGTGCTGTTTCTCACAA 177          CGA  ACC  CT
           G                     TCCCAGG   CT   TC  GCGGG
                                |||||||   ||   ||  |||||
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                                AGGGTCC  GA  AG TGTTC
                                   AC_ CAA AG
GAM27  LOC206836 5' TCCCAGGCGCTGCCTGGCC  178        A A T_____
                                TCCCAGGCG CT CC    CC
                                ||||||||| || ||    ||
                                AGGGTCCGC GA GG    GG
                                    _ C ACCIII
GAM28  NEDD4   3' TTTACAGTTCTCACAGG    181        _  TAAC
                                TTTATAGT CTC   CAGG
                                |||||||| |||   ||||
                                AAATGTCA GAG   GTCC
                                   A  T___
GAM28  PATE    3' TAGCAACCTGCAGGATATA  182      CT AAC
                                TAGT CT  CAGGATATA
                                ||||  ||  |||||||||
                                ATCG GG  GTCCTATAT
                                  TT AC_
GAM28  DKFZP727C091 5' TTCATAGTGTCAGGATAT   183        CTCTAAC
                                TTTATAGT     CAGGATAT
                                ||||||||     ||||||||
                                AAGTATCA     GTCCTATA
                                   CA_____
GAM28  HGC6.1.1 3' TTATAGAAACTTAACCAGGATA 184       TCT _
          TA                    TTATAG  CT AACCAGGATATA
                                ||||||  || ||||||||||||
                                AATATC  GA TTGGTCCTATAT
                                   TTT A
GAM28  KIAA0265 3' TTTATAGTTTTTCCAGGAT  185        CTCTAA
                                TTTATAGT    CCAGGAT
                                ||||||||    |||||||
                                AAATATCA    GGTCCTA
                                   AAAA__
GAM28  KIAA0455 3' TTTACTGGTCATCAGGATATA 186      A_  TCTAAC
                                TTTAT GTC    CAGGATATA
                                |||||  |||    |||||||||
                                AAATG CAG    GTCCTATAT
                                  AC  TA____
GAM28  KIAA1486 3' TTTATAGCTCTGACAGCCCAT 187       T  AAC  GA
                                TTTATAG CTCT  CAG  TAT
                                ||||||| ||||  |||  |||
                                AAATATC GAGA  GTC  GTA
                                   _  CT_  GG
GAM29  IL1R1   3' AAAATTATTATTCCAAATA  190       TA
                                AAAGTT ATTATTCCAAATA
                                ||||||  ||||||||||||
                                TTTTAA  TAATAAGGTTTAT
                                  __
GAM29  FLJ10704 3' AAAAATTTAAACCTTCCA   191         TTA
                                AAAAGTTTAA  TTCCA
                                ||||||||||  |||||
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                                TTTTTAAATT  AAGGT
                                     TGG
GAM29   FLJ31168  3'  AAAAGTCTTGGATTCCAAATA  192        AATT
                                AAAAGTTT   ATTCCAAATA
                                ||||||||   ||||||||||
                                TTTTCAGA   TAAGGTTTAT
                                    ACC_
GAM29   KIAA1034  3'  AAAGTTTCTTCTTCCAAATA  193       AATTA
                                AAAGTTT    TTCCAAATA
                                |||||||    |||||||||
                                TTTCAAA    AAGGTTTAT
                                   GAAG_
GAM29   NFX1      3'  AAAAGTTTGGTTTGTCCAAATA 194       AATTAT
                                AAAAGTTT    TCCAAATA
                                ||||||||    ||||||||
                                TTTTCAAA    AGGTTTAT
                                    CCAAAC
GAM29   ZNF333    3'  AAAAATCTAATTCCAAATA   195         TAT
                                AAAAGTTTAAT  TCCAAATA
                                ||||||||||  ||||||||
                                TTTTTAGATTA  AGGTTTAT
                                      ___
GAM29   LOC142941 3'  AAAGACCCTTATTCCAAATA  196      TTTAA
                                AAAG   TTATTCCAAATA
                                ||||   ||||||||||||
                                TTTC   AATAAGGTTTAT
                                  TGGG_
GAM29   LOC146443 5'  AAAATCTCTTATTCCAAATA  197       AA
                                AAAGTTT TTATTCCAAATA
                                ||||||| ||||||||||||
                                TTTTAGA AATAAGGTTTAT
                                   G_
GAM29   LOC150035 5'  AAAGTCCCTAATTCCAAATA  198       AATT
                                AAAGTTT   ATTCCAAATA
                                |||||||   ||||||||||
                                TTTCAGG   TAAGGTTTAT
                                   GAT_
GAM29   LOC155032 3'  AAGTTCTAATTCCAAATA    199      AATT
                                AAGTTT   ATTCCAAATA
                                ||||||   ||||||||||
                                TTCAAG   TAAGGTTTAT
                                  AT__
GAM29   LOC158696 3'  AAAAATACCCATTCCAAAT   200      TTAA
                                AAAAGT   TTATTCCAAAT
                                ||||||   ||||||||||||
                                TTTTTA   GGTAAGGTTTA
                                  TG__
GAM29   LOC89231  3'  AAAAATTCCAAATTCCAAAT  201       AATT
                                AAAAGTTT   ATTCCAAAT
                                ||||||||   |||||||||
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                                TTTTTAAG   TAAGGTTTA
                                     GTT_
GAM29   LOC91308 5' TAAAAAGTTCTAGAAATGCCCA 202          AATT_ _
            AATA                   TAAAAAGTTT    AT TCCAAATA
                                   ||||||||||    || ||||||||
                                   ATTTTTCAAG    TA GGGTTTAT
                                        ATCTT  C
GAM30   NEF3    3' AGGGAGCACCCTGAGCTTGCAT 205     A       A   AT
                                   AG GAGCACCTT AGCT  CAT
                                   || |||||||| ||||  |||
                                   TC CTCGTGGGA TCGA  GTA
                                    C       C   AC
GAM30   TYR     3' AAGAGCACTTTAATTCACATAC 206         C   GCTAT
                                   GAGAGCAC TTAA    CATAC
                                   |||||||| ||||    |||||
                                   TTCTCGTG AATT    GTATG
                                        A   AAGT_
GAM30   DKFZP434O047 5' GAGAGCACCTTTCACCAT   207          AA
                                   GAGAGCACCTT  GCTAT
                                   ||||||||||  |||||
                                   CTCTCGTGGAA  TGGTA
                                         AG
GAM30   FLJ12800  3' AGAGAGCACTTAAGATTCATAC 208         C    CTA
                                   AGAGAGCAC TTAAG   TCATAC
                                   |||||||| |||||   ||||||
                                   TCTCTCGTG AATTC   AGTATG
                                        _    TA_
GAM30   FLJ22362  3' GAGCACCTGAGGCTCCAT    209         TAA  A
                                   GAGCACCT   GCT TCAT
                                   ||||||||   ||| ||||
                                   CTCGTGGA   CGA GGTA
                                        CTC  _
GAM30   KIAA0335  3' GATAGCATTTTCAAATATCATA 210     G   CC_   C
            C                       GA AGCA   TTAAG TATCATAC
                                   || ||||   ||||| ||||||||
                                   CT TCGT   AGTTT ATAGTATG
                                    A   AAA    _
GAM30   KIAA0729  3' AGAGGACACCATATCATA    211       AG   TTAAGC
                                   AGAG  CACC     TATCATA
                                   ||||  ||||     |||||||
                                   TCTC  GTGG     ATAGTAT
                                     CT   T_____
GAM30   LRRFIP1   3' AGAGCACCTGGTAATTGTCATA 212          __  GCTA
            C                       AGAGCACCT  TAA   TCATAC
                                   |||||||||  |||   ||||||
                                   TCTCGTGGA  ATT   AGTATG
                                        CC   AAC_
GAM30   MDN1    3' AGGGAGCACCTGGGTAAGC   213     A      ___
                                   AG GAGCACCT   TAAGC
                                   || ||||||||   |||||
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                                TC CTCGTGGA   ATTCG
                                 C       CCC
GAM30   PRO1598   5'  GAGAGCACTTTAACCTAT    214          C   G
                                GAGAGCAC TTAA CTAT
                                |||||||| |||| ||||
                                CTCTCGTG AATT GATA
                                     A   G
GAM30   TINF2     3'  AGAGAGCATTTTAGTTCTAT  215          CC  AG_
                                AGAGAGCA  TTA   CTAT
                                ||||||||  |||   ||||
                                TCTCTCGT  AAT   GATA
                                     AA   CAA
GAM30   LOC118487 3'  AGAGAGCACCTTGCAGGGACTA 216             AA  TATCA_
          C                      AGAGAGCACCTT  GC     TAC
                                ||||||||||||  ||     |||
                                TCTCTCGTGGAA  CG     ATG
                                       __  TCCCTG
GAM30   LOC150481 5'  GAGACACAGACTATCAT     217        G   CTTAA
                                GAGA CAC     GCTATCAT
                                |||| |||     ||||||||
                                CTCT GTG     TGATAGTA
                                  _   TC___
GAM30   LOC200420 5'  AAAGAGCATTTTCTCTTCAT  218          CC  AAG  A
                                AGAGAGCA  TT   CT TCAT
                                ||||||||  ||   || ||||
                                TTTCTCGT  AA   GA AGTA
                                     AA  GA_  _
GAM30   LOC253752 3'  AAGAGCACTTTAATTCACATAC 206          C    GCTAT
                                GAGAGCAC TTAA     CATAC
                                |||||||| ||||     |||||
                                TTCTCGTG AATT     GTATG
                                     A    AAGT_
GAM30   LOC255654 5'  GAGAGCACTTTTCACCAT    219          C  AA
                                GAGAGCAC TT  GCTAT
                                |||||||| ||  |||||
                                CTCTCGTG AA  TGGTA
                                     A  AG
GAM30   LOC257463 3'  GAGGCACCTTAAATGCATA    220       A        CTAT
                                GAG GCACCTTAAG    CATA
                                ||| ||||||||||    ||||
                                CTC CGTGGAATTT    GTAT
                                  _         AC__
GAM31   FLJ25436  3'  TTTAATTTTACCTGATACGTTA 223             TTA
          A                     TTTAATTTTATCT   ATGTTAA
                                ||||||||||||   |||||||
                                AAATTAAAATGGA   TGCAATT
                                       CTA
GAM31   LOC130250 5'  TTAAGTTTTATCTTTCTTGCTA 224        _        AA
                                TTAA TTTTATCTTT  TGTTA
                                |||| ||||||||||  |||||
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                                AATT AAAATAGAAA  ACGAT
                                  C        GA
GAM32   CDC25A   3'  TGGAGGGAAGCTTGGGCTG   227       A       CGAT
                                TGGAG GAAGCTTGG    GCTG
                                ||||| |||||||||    ||||
                                ACCTC CTTCGAACC    CGAC
                                  C       ____
GAM32   CSNK1A1  3'  TGGGGAGAAACAAATGCTG   228      A     TTGGC
                                TGG GAGAAGC    GATGCTG
                                ||| |||||||    |||||||
                                ACC CTCTTTG    TTACGAC
                                  C      T____
GAM32   DPH2L2   3'  TGGGCAGAGGCCAGGGATGCTG 229      AG   A   T  C
            C                    TGG  AGA GCT GG GATGCTGC
                                ||| ||| ||| || ||||||||
                                ACC  TCT CGG CC CTACGACG
                                  CG   C   T  _
GAM32   EGFL5    5'  TGGGGAGGACGCTGCTG    230      A   AAGCTT   A
                                TGG GAG     GGCG TGCTG
                                ||| |||     |||| |||||
                                ACC CTC     CTGC ACGAC
                                  C  _______    G
GAM32   MAT1A    3'  TGGGGAGAAGGTAGAGATGCTG 231      A     CT   C
            C                    TGG GAGAAG  TGG GATGCTGC
                                ||| ||||||  ||| ||||||||
                                ACC CTCTTC  ATC CTACGACG
                                  C     C_   T
GAM32   PIP5K1A  3'  TGGAGTGGAGGGGATGCTG   232       AGA  CTT  C
                                TGGAG   AG   GG GATGCTG
                                |||||   ||   || |||||||
                                ACCTC   TC   CC CTACGAC
                                   ACC  ___  _
GAM32   PTK7     3'  TGGGGAGGACTCACTTGCTG   233      A   AA    G GA
                                TGG GAG  GCTTG C  TGCTG
                                ||| |||  ||||| |  |||||
                                ACC CTC  TGAGT G  ACGAC
                                  C   C_    _ A_
GAM32   RELA     3'  TGGAGAGAGCCAGTGCTG    234         A   TGGCGA
                                TGGAGAGA GCT     TGCTG
                                |||||||| |||     |||||
                                ACCTCTCT CGG     ACGAC
                                     _   TC_____
GAM32   SCA1     3'  GGGGAGAAGGAGGGATGCTGC  235     A     CTT  C
                                GG GAGAAG   GG GATGCTGC
                                || ||||||   || ||||||||
                                CC CTCTTC   CC CTACGACG
                                  C     CT_  _
GAM32   TCF3     3'  TGGAGAGAGGCCTGGGTGC   236         A     CGA
                                TGGAGAGA GCTTGG   TGC
                                |||||||| ||||||   |||
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                                ACCTCTCT CGGACC   ACG
                                    C     C__
GAM32   BIKE     3'  TGGTGAGGATGACGATGCTG  237      A   AAGCT
                                TGG GAG    TGGCGATGCTG
                                ||| |||    ||||||||||
                                ACC CTC    ACTGCTACGAC
                                  A  CT___
GAM32   C22orf5  3'  TGGAGAGACAGCTTGGTGAAAG 238          _     C  T_
            C                    TGGAGAGA AGCTTGG GA  GC
                                ||||||||| ||||||| ||  ||
                                ACCTCTCT TCGAACC CT  CG
                                    G      A  TT
GAM32   CHST3    3'  TGGAGAGAGGCCTCAGCTG   239         A   GGCGAT
                                TGGAGAGA GCTT     GCTG
                                |||||||| ||||     ||||
                                ACCTCTCT CGGA     CGAC
                                    C   GT_____
GAM32   DKFZp434M0331 3'  TGGAGAGAGGGAGGCAGGGTGC 240          AGCTT   A__
            TG                    TGGAGAGA    GGCG   TGCTG
                                |||||||||    ||||  |||||
                                ACCTCTCT    CCGT   ACGAC
                                    CCCT_   CCC
GAM32   DKFZp566O084 3'  TGGGAAGAAGCTTGTTGTGCAG 241     AG       ________  ATGC
            CAC                   G  AGAAGCTTG      GCG   T
                                |  |||||||||      |||   |
                                C  TCTTCGAAC      CGT   G
                                 CT       AACAIII   CGTA
GAM32   FBXO9    5'  TGGAGAGAGCCTCTTGCTG   242         A   GGCGA
                                TGGAGAGA GCTT    TGCTG
                                |||||||| ||||    |||||
                                ACCTCTCT CGGA    ACGAC
                                    _   GA___
GAM32   FLJ10241  3'  TGGAGTGGGGCGAAGGATGCTG 243       AGAA  TT  C
            C                    TGGAG   GC  GG GATGCTGC
                                |||||   ||  || ||||||||
                                ACCTC   CG  TC CTACGACG
                                   ACCC  CT  _
GAM32   FLJ12587  3'  TGGGGAGAAGCCCCCAGTGCTG 244      A       GG  A
                                TGG GAGAAGCTT  CG TGCTG
                                ||| |||||||||  || |||||
                                ACC CTCTTCGGG  GT ACGAC
                                  C       G_  C
GAM32   KIAA0451  3'  TGGGGAGGGCCCAGCGTGCTGC 245      A   AA   TG   A
                                TGG GAG  GCT  GCG TGCTGC
                                ||| |||  |||  ||| ||||||
                                ACC CTC  CGG  CGC ACGACG
                                  C   C_   GT   _
GAM32   KIAA0514  3'  TGAAGAGAGGCTTCAGCTG   246         AGCTT   GAT_
                                TGGAGAGA    GGC    GCTG
                                ||||||||    |||    ||||
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                                ACTTCTCT    CCG    CGAC
                                      _____  AAGT
GAM32   MAPK8IP3  3'  TGGGTGGAAGCCAGGGATGCTG 247      AGA     T  C
            C                    TGG   GAAGCT GG GATGCTGC
                                 |||   |||||| || ||||||||
                                 ACC   CTTCGG CC CTACGACG
                                   CAC     T  _
GAM32   MGC33182  3'  TGGGGAGAAACAAATGCTG   228      A      TTGGC
                                 TGG GAGAAGC    GATGCTG
                                 ||| |||||||    |||||||
                                 ACC CTCTTTG    TTACGAC
                                   C      T____
GAM32   MR        3'  TGGAGAGAGGTTATCAAAGGTG 248          A C   G  ___
            CTG                    TGGAGAGA G TTG CGA   TGCTG
                                 |||||||| | ||| |||   |||||
                                 ACCTCTCT C AAT GTT   ACGAC
                                      _ C   A   TCC
GAM32   RPS6KC1   3'  GGAAAGAAAGATGCTG      249          CTTGGC
                                 GGAGAGAAG     GATGCTG
                                 |||||||||     |||||||
                                 CCTTTCTTT     CTACGAC
                                       _______
GAM32   LOC144558 3'  TGGGTAGAGGCCAGCGATGCTG 250      AG   A   T
            C                    TGG  AGA GCT GGCGATGCTGC
                                 |||  ||| ||| ||||||||||
                                 ACC  TCT CGG TCGCTACGACG
                                   CA   C  _
GAM32   LOC147958 5'  TGGAGAGAGGCTGGCGGC    251          A   T   AT
                                 TGGAGAGA GCT GGCG  GC
                                 |||||||| ||| ||||  ||
                                 ACCTCTCT CGA CCGC  CG
                                      C   _   __
GAM32   LOC153222 3'  TGGGGGAAGGTTTATAATGCTG 252      AGA    C  GGC
            C                    TGG   GAAG TT   GATGCTGC
                                 |||   |||| ||   ||||||||
                                 ACC   CTTC AA   TTACGACG
                                   CC_    C  ATA
GAM32   LOC157278 3'  TGGGTAGAGGCCAGCGATGCTG 250      AG   A   T
            C                    TGG  AGA GCT GGCGATGCTGC
                                 |||  ||| ||| ||||||||||
                                 ACC  TCT CGG TCGCTACGACG
                                   CA   C  _
GAM32   LOC157737 5'  TGGGGGGAAGCTTGTTGCGCAG 253     AGA      ________  ATGC
            CAC                    G   GAAGCTTG      GCG    T
                                 |   ||||||||      |||    |
                                 C   CTTCGAAC      CGT    G
                                  CCC       AACGIII   CGTA
GAM32   LOC158972 3'  TGGGAGGGGGTGGGCTGATGCT 254      A   AAGCTT   _
            GC                     TGG GAG     GGC GATGCTGC
                                 ||| |||     ||| ||||||||
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                                ACC CTC     CCG CTACGACG
                                  _  CCCCAC   A
GAM32   LOC199923 5'  TGGGAGAAGCTGCGAGTGCTG  255      A      TG   _
                                TGG GAGAAGCT  GCGA TGCTG
                                ||| ||||||||  |||| |||||
                                ACC CTCTTCGA  CGCT ACGAC
                                  _      __    C
GAM32   LOC220522 3'  TGGGCAGAAGCTTGTTGTGCAG 256     AG       ________   ATGC
            CAC                   G  AGAAGCTTG      GCG    T
                                |  |||||||||      |||   |
                                C  TCTTCGAAC      CGT    G
                                 CG        AACAIII   CGTA
GAM32   LOC221528 5'  GGAGAGAGGACAGATGCTGC   257         AGCTT   _
                                GGAGAGA    GGC GATGCTGC
                                |||||||    ||| ||||||||
                                CCTCTCT    CTG CTACGACG
                                    C_____   T
GAM32   LOC221692 3'  TGGAGAGAAATTAGAAGTGTG  258          C    CGA  C
                                TGGAGAGAAG TTGG   TG TG
                                |||||||||| ||||   || ||
                                ACCTCTCTTT AATC   AC AC
                                      _   TTC  _
GAM32   LOC222031 3'  TGGGGGGATGCTTGGCATGGCC 259      AGA  A      AT
                                TGG   GA GCTTGGCG  GCT
                                |||   || ||||||||  |||
                                ACC   CT CGAACCGT  CGG
                                  CCC  A       AC
GAM32   LOC255461 3'  TGGGTAGAGGCCAGCGATGCTG 250      AG   A   T
            C                    TGG  AGA GCT GGCGATGCTGC
                                |||  ||| ||| ||||||||||
                                ACC  TCT CGG TCGCTACGACG
                                  CA   C   _
GAM32   LOC255516 3'  TGGGTAGAGGCCAGCGATGCTG 250      AG   A   T
            C                    TGG  AGA GCT GGCGATGCTGC
                                |||  ||| ||| ||||||||||
                                ACC  TCT CGG TCGCTACGACG
                                  CA   C   _
GAM32   LOC257552 5'  GGAGAGAGGACAGATGCTGC   257         AGCTT   _
                                GGAGAGA    GGC GATGCTGC
                                |||||||    ||| ||||||||
                                CCTCTCT    CTG CTACGACG
                                    C_____   T
GAM32   LOC257602 5'  GGAGAGAGGACAGATGCTGC   257         AGCTT   _
                                GGAGAGA    GGC GATGCTGC
                                |||||||    ||| ||||||||
                                CCTCTCT    CTG CTACGACG
                                    C_____   T
GAM32   LOC90494  5'  TGGGGAGGAGCCTGGCCTCTCC 260      A   A      GATG_
            TG                    TGG GAG AGCTTGGC    CTG
                                ||| ||| ||||||||    |||
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                                ACC CTC TCGGACCG    GAC
                                  C  C      GAGAG
GAM32  LOC90719 3'  TGGGGGGATGCTTGGCAGC   261      AGA  A      AT
                                TGG  GA GCTTGGCG  GC
                                |||  || ||||||||  ||
                                ACC  CT CGAACCGT  CG
                                  CCC  A      __
GAM33  MMP20    3'  ATGAAAAAAATTGGAAGTATT  264     T          A
                                AT AAAAAAATTGGAA TATT
                                || ||||||||||||| ||||
                                TA TTTTTTTAACCTT ATAA
                                 C          C
GAM33  PIK3CD   3'  TTAAAAAAATAGAAAATATT   265          T
                                TTAAAAAAAT GGAAATATT
                                |||||||||| |||||||||
                                AATTTTTTTA CTTTTATAA
                                       T
GAM33  FLJ13204 3'  TAAATTAAAAGGATCACTGGAA 266          AA___     A
          GTATT                   TAAATTAAAA    ATTGGAA TATT
                                |||||||||    ||||||| ||||
                                ATTTAATTTT    TGACCTT ATAA
                                      CCTAG     C
GAM33  OAZ      3'  AATTAAAAAATTAAAAGGAAAT 267          ATT___
          ATT                   AATTAAAAAA    GGAAATATT
                                |||||||||    |||||||||
                                TTAATTTTTT    CCTTTATAA
                                      AATTTT
GAM34  ATP1A1   5'  CGGTGCTCAGTGCCCGGCGCC  270          ACA  G  _
                                TGGTGCTCA  TGC TG CGCC
                                |||||||||  ||| || ||||
                                GCCACGAGT  ACG GC GCGG
                                      C__  G  C
GAM34  EDNRA    5'  TGGAGCTCGGCGTGCGC    271      T   AACAT
                                TGG GCTC    GCGTGCGC
                                ||| ||||    ||||||||
                                ACC CGAG    CGCACGCG
                                  T   C_____
GAM34  GSTZ1    3'  TGGTGTTACGGTGAGCACGCCA 272       CTCA  A_  C TG
                                TGGTG   AC  TG G  CGCCA
                                |||||   ||  || |  |||||
                                ACCAC   TG  AC C  GCGGT
                                   AA__  CC  T GT
GAM34  ICMT     3'  TGGTGCTCTGGCCCCGCGCC  273         AACAT  G_
                                TGGTGCTC    GC  TGCGCC
                                ||||||||    ||  ||||||
                                ACCACGAG    CG  GCGCGG
                                     AC___  GG
GAM34  IL12RB2  5'  GTGCTCAGCGTACACAGCCA  274         ACAT    ___
                                GTGCTCA   GCGTGC   GCCA
                                |||||||   ||||||  ||||
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                                CACGAGT   CGCATG  CGGT
                                   ____     TGT
GAM34   LOXL2    3' ATGGTGCTCAGTGAGCGCCC  275          ACA  C   G
                                ATGGTGCTCA  TG GTGC CC
                                ||||||||||  || |||| ||
                                TACCACGAGT  AC CGCG GG
                                   C__  T   _
GAM34   PPARA    5' ATGGTGCTGGTTGTGCGCC   276         CAACATGC
                                ATGGTGCT      GTGCGCC
                                ||||||||      |||||||
                                TACCACGA      CACGCGG
                                   CCAA____
GAM34   DKFZP434O047 5' GGTGCTCAGTCCATGGTGC   277          A__   C
                                GGTGCTCA  CATG GTGC
                                ||||||||  |||| ||||
                                CCACGAGT  GTAC CACG
                                   CAG   _
GAM34   FLJ12704  3' ATGGTGCTCCATGCTCTGTG  278          AA   ___
                                ATGGTGCTC  CATGC  GTG
                                |||||||||  |||||  |||
                                TACCACGAG  GTACG  CAC
                                   __    AGA
GAM34   FLJ13940  3' ATGTTGCTCAGCATGCAC    279      G    ACAT
                                ATG TGCTCA   GCGTGCGC
                                ||| ||||||   ||||||||
                                TAC ACGAGT   CGTACGTG
                                  A    ____
GAM34   FLJ21240  5' GTGCTTAACAAATACGCCA   280       C   TGC
                                GTGCT AACA  GTGCGCCA
                                ||||| ||||  ||||||||
                                CACGA TTGT  TATGCGGT
                                   A   T__
GAM34   FLJ21777  5' TGGCGCTCGGCTGCGCGC    281         AACA
                                TGGTGCTC   TGCGTGC
                                ||||||||   |||||||
                                ACCGCGAG   ACGCGCG
                                   CCG_
GAM34   GMPPB    5' GGTGCTCAGCGTCAGCGGCC  282          ACAT   __  _
                                GGTGCTCA   GCGT  GCG CC
                                ||||||||   ||||  ||| ||
                                CCACGAGT   CGCA  CGC GG
                                   ____   GT   C
GAM34   KIAA0339  3' ATGGCGCTCAGCAGCCGCC   283          A  T  GTG
                                ATGGTGCTCA CA GC   CGCC
                                |||||||||| || ||   ||||
                                TACCGCGAGT GT CG   GCGG
                                   C  _  ___
GAM34   KIAA1303  3' TGGTGCCATCTGCACATGCGTG 284         CA____       C
            TGC                   TGGTGCT     ACATGCGTG GC
                                |||||||     ||||||||| ||
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                                ACCACGG     TGTACGCAC CG
                                    TAGACG        A
GAM34   p25     3'  TGGTGCTCATGCGTGC     285          ACA
                                TGGTGCTCA   TGCGTGC
                                |||||||||   |||||||
                                ACCACGAGT   ACGCACG
                                    ___
GAM34   PCQAP   3'  ACGGTGCTCAGCAGGAATGC   286          A  TGC
                                ATGGTGCTCA CA   GTGC
                                |||||||||| ||   ||||
                                TGCCACGAGT GT   TACG
                                     C  CCT
GAM34   PDCD7   5'  TGGGCCCGGCATGCGTGCGC   287      T    AA
                                TGG GCTC  CATGCGTGCGC
                                ||| ||||  ||||||||||
                                ACC CGGG  GTACGCACGCG
                                  _   CC
GAM34   SRP9    3'  ATGCTGTTCAACATGACA    288      G  C      _
                                ATG TG TCAACATG CG
                                ||| || ||||||| ||
                                TAC AC AGTTGTAC GT
                                  G  A       T
GAM34   LOC133671 5'  ATGGTGCTTGCCGCTGCC    289          CAACA   G  _
                                ATGGTGCT    TGC TGC GCC
                                ||||||||    ||| ||| |||
                                TACCACGA    ACG GCG CGG
                                    _____  _  A
GAM34   LOC149401 3'  ATGGTGCTTACGTGC       290          CAACA
                                ATGGTGCT    TGCGTGC
                                ||||||||    |||||||
                                TACCACGA    ATGCACG
                                    _____
GAM34   LOC201627 3'  ATGGTTTTCAACATGTGT    291        GC       C
                                ATGGT  TCAACATG GT
                                |||||  |||||||| ||
                                TACCA  AGTTGTAC CA
                                   AA       A
GAM34   LOC220932 3'  TGGTGCTTCCCACGTGCGCC   292          CAACA
                                TGGTGCT    TGCGTGCGCC
                                |||||||    ||||||||||
                                ACCACGA    GTGCACGCGG
                                    AGG__
GAM34   LOC253150 3'  ATGGTCTTGGCCGCGCGCC    293        G  CAACATG
                                ATGGT CT      CGTGCGCC
                                ||||| ||      ||||||||
                                TACCA GA      GCGCGCGG
                                   _  ACCG___
GAM34   LOC255527 5'  GTGCTCAATGCTATGGTGCGTC 294          AC   _____    C
            A                    GTGCTCA  ATGC    GTGCG CA
                                |||||||  ||||    ||||| ||
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                                CACGAGT  TACG   CACGC GT
                                   __   ATAC    A
GAM34   LOC256586 5'  ATGGCGCTCGATGACGCC    295         AAC   CGT
                                ATGGTGCTC   ATG   GCGCC
                                |||||||||   |||   |||||
                                TACCGCGAG   TAC   TGCGG
                                    C__   ___
GAM34   LOC90637  3'  ATGGTGCTCAATGGGGCTCCA 296          AC   CGT  G
                                ATGGTGCTCA  ATG   GC CCA
                                ||||||||||  |||   || |||
                                TACCACGAGT  TAC   CG GGT
                                    __   CC_  A
GAM34   LOC93166  5'  TGTGCGCCCTGCGTGCGC    297     _     AACA
                                TG GTGCTC    TGCGTGCGC
                                || ||||||    |||||||||
                                AC CGCGGG    ACGCACGCG
                                 A     _____
GAM35   COG3      3'  TTCTGTAAAGTTCTTGC     300       A        AA
                                TTC TGTAAAGTTTT  GC
                                ||| ||||||||||  ||
                                AAG ACATTTCAAGA  CG
                                  _         AA
GAM35   EVA1      3'  TTCTGTATCTTAAGCTT     301       A   AAA
                                TTC TGT   GTTTTAAGCTT
                                ||| |||   ||||||||||
                                AAG ACA   TAGAATTCGAA
                                  _  ___
GAM35   FLJ20701  3'  ATGCTAAAGAATAGCTTACA   302       _   TTTTA
                                ATGT AAAG    AGCTTACA
                                |||| ||||    ||||||||
                                TACG TTTC    TCGAATGT
                                  A   TTA__
GAM35   GK001     3'  TTCCTGTGAATTCAGAGCTTAC 303       A   AA    TA
            A                    TTC TGT  AGTTT  AGCTTACA
                                ||| |||  |||||  ||||||||
                                AAG ACA  TTAAG  TCGAATGT
                                  G   C_    TC
GAM35   KIAA0410  3'  TTCATGTAGAGTAACATTTTAC 304         A   TT  AGC
            A                    TTCATGTA AGT  TA   TTACA
                                ||||||| |||  ||   |||||
                                AAGTACAT TCA  GT   AATGT
                                    C   TT  AA_
GAM35   MGC12217  5'  TTCATGTAAAGTTTTCATTACA 305             AAGC
                                TTCATGTAAAGTTTT    TTACA
                                ||||||||||||||    |||||
                                AAGTACATTTCAAAA    AATGT
                                        GT__
GAM35   NAV3      3'  TTCATGTACAGTTTTGAAGC   306         A     _
                                TTCATGTA AGTTTT AAGC
                                |||||||| |||||| ||||
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                                AAGTACAT TCAAAA TTCG
                                    G     C
GAM35   OSBPL3   3' CTCAAGATAGTTTTAAGCTTA 307      TGTAA
                                TTCA    AGTTTTAAGCTTA
                                ||||    ||||||||||||
                                GAGT    TCAAAATTCGAAT
                                  TCTA_
GAM35   PFTK1    3' CATGTAAAGTTTTCTCCCTA  308           AAG
                                CATGTAAAGTTTT  CTTA
                                ||||||||||||  ||||
                                GTACATTTCAAAA  GGAT
                                       GAG
GAM35   SLC5A7   3' TTCACTTATTTTAAGCTTA  309       GTAAA
                                TTCAT    GTTTTAAGCTTA
                                |||||    ||||||||||||
                                AAGTG    TAAAATTCGAAT
                                   AA___
GAM35   LOC90231 3' TATTGAGTGGAAAGCTTACA  310     AA  TTT
                                TGT  AGT   AAGCTTACA
                                |||  |||   |||||||||
                                ATA  TCA   TTCGAATGT
                                  AC   CCT
GAM36   AP1M1    3' GTGGGTGACACGTGGCCCCGC 313       GC  _  A
                                GTGGGT  GAC CGT GCCCCGC
                                ||||||  ||| ||| |||||||
                                CACCCA  CTG GCA CGGGGCG
                                    __  T   C
GAM36   DNLC2A   3' AGCTGGGTGCGGGCTTCCTGC  314     G      ACC  AG  CC
                                AG TGGGTGCG   GT  CC  GC
                                || ||||||||   ||  ||  ||
                                TC ACCCACGC   CG  GG  CG
                                 G      C__  AA  A_
GAM36   MGST3    5' GTGGGTGCGGCGCCCTCGC   315         ACC  A   _
                                GTGGGTGCG   GT GCCC CGC
                                |||||||||   || |||| |||
                                CACCCACGC   CG CGGG GCG
                                     ___  _    A
GAM36   RAB38    3' AGTGCCGACTGTGGCCCG    316       _  C  A   C
                                GGTGC GAC GT GCCC G
                                ||||| ||| || |||| |
                                TCACG CTG CA CGGG C
                                   G   A  C   A
GAM36   RYR2     3' GGTGAGTGTGGCTGCCACG   317         CGACC  A   C
                                GGTGGGTG    GT GCC CG
                                ||||||||    || ||| ||
                                CCACTCAC    CG CGG GC
                                     AC___  A   T
GAM36   SEPX1    3' GGTGGGTGTGGGCTGCCCGC  318         CGACC  A    C
                                GGTGGGTG    GT GCCC GC
                                ||||||||    || |||| ||
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                                CCACCCAC    CG CGGG CG
                                     ACC__  A   _
GAM36   SNL     5'  AGGTGGGTGGCGGGTCCCTGC  319          _ ACCGTAG   C
                                AGGTGGGTG CG      CCC GC
                                |||||||||  ||      |||  ||
                                TCCACCCAC GC      GGG CG
                                     C  CCA_____   A
GAM36   TMEPAI   3'  GTGGGTGCGCGCCCCG      320          ACCGTA
                                GTGGGTGCG     GCCCCG
                                |||||||||     ||||||
                                CACCCACGC     CGGGGC
                                     G_____
GAM36   TNFRSF6B  5'  GGGGGTGGCCATAGCCCTGC   321     T    CGA       C
                                GG GGGTG   CCGTAGCCC GC
                                ||  |||||   |||||||||  ||
                                CC CCCAC   GGTATCGGG CG
                                 _    C__        A
GAM36   BIK     3'  GGTGGGGCCAGCCCC      322         T  GACCG
                                GGTGGG GC    TAGCCCC
                                ||||||  ||    |||||||
                                CCACCC CG    GTCGGGG
                                   _  ______
GAM36   C1orf24   3'  AGGGGGTGCAAGAAGCCCTGC  323      T      CCGT    C
                                AGG GGGTGCGA    AGCCC GC
                                |||  ||||||||    |||||  ||
                                TCC CCCACGTT    TCGGG CG
                                  _       CT__     A
GAM36   C20orf150 3'  AGGTGGGTGCTGGCAGCTGTCC 324          GACC    ___  C
            TGC                    AGGTGGGTGC    GTAGC   CC GC
                                ||||||||||    |||||   ||  ||
                                TCCACCCACG    CGTCG   GG CG
                                     AC__     ACA  A
GAM36   C21orf91  3'  GGTAGGTGCGACTTCATTCC  325           CG  GC
                                GGTGGGTGCGAC  TA  CC
                                ||||||||||||  ||  ||
                                CCATCCACGCTG  GT  GG
                                      AA  AA
GAM36   DKFZP434H132 5'  GGTGGGTGCGATCGAAGC    326           C  T
                                GGTGGGTGCGA CG AGC
                                ||||||||||| || |||
                                CCACCCACGCT GC TCG
                                     A  T
GAM36   DKFZP586J0619 3'  AGGTGGGTGCGGCCGTGC    327           A    A
                                AGGTGGGTGCG CCGT GC
                                |||||||||||  ||||  ||
                                TCCACCCACGC GGCA CG
                                     C    _
GAM36   DKFZp762K222 5'  GGTGGGTGCGCCGACACGC   328           A   TA__
                                GGTGGGTGCG CCG    GC
                                |||||||||  |||    ||
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                                CCACCCACGC GGC   CG
                                      _  TGTG
GAM36   EZFIT    5' GGTGGGCGCGACCCC      329          ACCGTA
                                GGTGGGTGCG     GCCCC
                                ||||||||||     |||||
                                CCACCCGCGC     TGGGG
                                       _______
GAM36   FLJ12541 3' AGGTGGGTTGACCTTCCCTGC 330        GC   GTAG  C
                                AGGTGGGT  GACC   CCC GC
                                ||||||||  ||||   ||| ||
                                TCCACCCA  CTGG   GGG CG
                                     A_   AA__   A
GAM36   FLJ20552 3' GGTGGGTGGGAAAGGCCCCG  331        C  CCGTA
                                GGTGGGTG GA    GCCCCG
                                |||||||| ||    ||||||
                                CCACCCAC CT    CGGGGC
                                     C  TTC__
GAM36   FLJ22578 3' AGGTAGGTGCGGAGTCCCG   332         ACCGT  C
                                AGGTGGGTGCG    AG CCCG
                                ||||||||||     || ||||
                                TCCATCCACGC    TC GGGC
                                      C____  A
GAM36   IL-17RE  5' AGGTGGGTGGCAGGGCC    333         CGACC   CC
                                AGGTGGGTG    GTAG  CC
                                |||||||||    ||||  ||
                                TCCACCCAC    CGTC  GG
                                      _____   CC
GAM36   KIAA1691 3' GGTTGGGTGCGGCCAGGGC   334      _     A   TA
                                GGT GGGTGCG CCG  GC
                                ||| ||||||| |||  ||
                                CCA CCCACGC GGT  CG
                                  A      C   CC
GAM36   KIAA1719 3' AGGTGGGAGTGGGTGCCCCG  335        TGCGACC  A
                                AGGTGGG      GT GCCCCG
                                |||||||      || ||||||
                                TCCACCC      CA CGGGGC
                                     TCACC__  _
GAM36   LHX6     3' AGGTGGGTGGACTCCTGGCCGC 336         C   CGTAGCC
                                AGGTGGGTG GAC      CCGC
                                |||||||| |||      ||||
                                TCCACCCAC CTG      GGCG
                                      _  AGGACC_
GAM36   MGC10870 5' GGTGGGCGCTGCCGGCCTCGC  337          GA   TA   C
                                GGTGGGTGC  CCG  GCC CGC
                                |||||||||  |||  ||| |||
                                CCACCCGCG  GGC  CGG GCG
                                      AC   __   A
GAM36   MPN      3' AGGCTGGGTGCAGAGCTCTGC  338      _      ACCGT   CCC
                                AGG TGGGTGCG    AGC   GC
                                ||| ||||||||    |||   ||
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                                TCC ACCCACGT    TCG  CG
                                  G      C____  AGA
GAM36   SBBI31   3' AGGTGGGTGCTGTCCATCCGC 339        GA_  AGCC
                                AGGTGGGTGC  CCGT   CCGC
                                ||||||||||  ||||   ||||
                                TCCACCCACG  GGTA   GGCG
                                     ACA   _____
GAM36   SNURF    3' GGTGGGGGCGGAGTGCCCCG  340       T  ACC  A
                                GGTGGG GCG  GT GCCCCG
                                |||||| |||  || ||||||
                                CCACCC CGC  CA CGGGGC
                                   C  CT_  _
GAM36   TIMM13   3' GGTGGGGTGGCCCGCGCTCGC 341       _ CGA   A  CC
                                GGTGGG TG  CCGT GC  CGC
                                |||||| ||  |||| ||  |||
                                CCACCC AC  GGCG CG  GCG
                                   C  CG_   _  A_
GAM36   LOC118978 3' AGGTGGGTGCGGTCGTGGGC  342         AC  A_
                                AGGTGGGTGCG  CGT  GC
                                ||||||||||  |||  ||
                                TCCACCCACGC  GCA  CG
                                     CA   CC
GAM36   LOC145989 5' AGGTGGGTGGCGGGTCCCCGC  343        _  ACCGTAG
                                AGGTGGGTG CG      CCCCGC
                                |||||||| ||      ||||||
                                TCCACCCAC GC      GGGGCG
                                     C  CCA____
GAM36   LOC147515 5' GGTGGGTGCGAAGGCCCG    344         CCGTA   C
                                GGTGGGTGCGA    GCCC G
                                ||||||||||     |||| |
                                CCACCCACGCT    CGGG C
                                     TC___    A
GAM36   LOC148413 3' AGGTGGGTGGTGGCCTGGTCCC 345        CGA_  GTAG   C
           TGC                    AGGTGGGTG   CC   CCC GC
                                |||||||||   ||   ||| ||
                                TCCACCCAC   GG   GGG CG
                                     CACC  ACCA   A
GAM36   LOC148979 3' AGGTGGGTGCGCTGGTGC    346         ACC  A
                                AGGTGGGTGCG   GT GC
                                ||||||||||   || ||
                                TCCACCCACGC   CA CG
                                     GAC  _
GAM36   LOC149650 3' AGTGGGTCTCGTGGCCTCG   347       GCGAC   A   C
                                GGTGGGT    CGT GCC CG
                                |||||||    ||| ||| ||
                                TCACCCA    GCA CGG GC
                                   GA___   C   A
GAM36   LOC165476 5' GGTGGGTGTCCGTGGTCCTGC 348        CGA   AGC  C
                                GGTGGGTG   CCGT   CC GC
                                ||||||||   ||||   || ||
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                                CCACCCAC  GGCA  GG CG
                                    A__   CCA  A
GAM36  LOC197049 3'  GGTGGGTGCTACTGGGGTGC  349         G  C___  A
                                GGTGGGTGC AC   GT GC
                                ||||||||| ||   || ||
                                CCACCCACG TG   CA CG
                                    A  ACCC  _
GAM36  LOC256041 5'  GGTGGGTGCCCGGCCCTGC   350         GA  TA   C
                                GGTGGGTGC  CCG  GCCC GC
                                |||||||||  |||  |||| ||
                                CCACCCACG  GGC  CGGG CG
                                    __  __   A
GAM37  BCL7A   5'  TCACTCGCGCACAGACACTCGC 353        A  _  T
          AC                      TCACTC TGC CAG ACACTCGCAC
                                |||||| ||| ||| ||||||||||
                                AGTGAG GCG GTC TGTGAGCGTG
                                   C  T  _
GAM37  HNRPM   5'  CTCTCGAGATACACTCGC   354      A  CCA
                                CTC TG  GTACACTCGC
                                ||| ||  ||||||||||
                                GAG GC  TATGTGAGCG
                                  A  TC_
GAM37  SLC6A8  3'  TCACGCACGCGTGCACTCGCAC 355      T   CA  A
                                TCAC CATGC  GT CACTCGCAC
                                |||| |||||  || |||||||||
                                AGTG GTGCG  CA GTGAGCGTG
                                  C    __ C
GAM37  FLJ12985  3'  CACTCATCACACTTGCA    356        GCCAG    C
                                CACTCAT   TACACT GCA
                                |||||||   |||||| |||
                                GTGAGTA   GTGTGA CGT
                                    ______    A
GAM37  FLJ30213  3'  ACTCATGCTGGTATAGACTGC  357        CA  C__  C
                                ACTCATGC  GTA  ACT GC
                                ||||||||  |||  ||| ||
                                TGAGTACG  CAT  TGA CG
                                    AC  ATC  _
GAM37  KIAA0036  5'  TCACTCATCCTCGCTTCGC   358        G  A_  ACAC
                                TCACTCAT CC  GT   TCGC
                                |||||||| ||  ||   ||||
                                AGTGAGTA GG  CG   AGCG
                                    _  AG  A___
GAM37  KIAA0869  3'  TCACTCATGTTAGTGGCTTCAC 359        CC  ACAC
                                TCACTCATG  AGT   TCGC
                                |||||||||  |||   ||||
                                AGTGAGTAC  TCA   AGTG
                                    AA  CCGA
GAM37  KIAA1280  5'  TCACTCATGATAGCCTGCGC  360        CC  ACACT
                                TCACTCATG  AGT   CGC
                                |||||||||  |||   |||
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                                AGTGAGTAC  TCG    GCG
                                     TA   GAC__
GAM37   MGC17330  3'  CCATGCCAGTAGCTTGC     361           CA  C
                                TCATGCCAGTA  CT GC
                                ||||||||||  || ||
                                GGTACGGTCAT  GA CG
                                      C_  A
GAM37   MGC22014  3'  CACTCGCGGAGTGCACTCGCAC 362       AT  C_   A
                                CACTC  GC  AGT CACTCGCAC
                                |||||  ||  ||| |||||||||
                                GTGAG  CG  TCA GTGAGCGTG
                                   __  CC   C
GAM37   UBE2D3    3'  TCACTCATCCATTGACAACTTG 363         G   GT_   _  C
          CA                      TCACTCAT CCA   ACA CT GCA
                                ||||||||| |||   ||| || |||
                                AGTGAGTA GGT   TGT GA CGT
                                     _   AAC   T  A
GAM37   LOC122439 3'  TCATTTCTGCCAGTAGTCAC   364      CTCA      CAC
                                TCA    TGCCAGTA   TCGC
                                |||    ||||||||   ||||
                                AGT    ACGGTCAT   AGTG
                                  AAAG       C__
GAM37   LOC146488 3'  TCACGCACGCGTGCACTCGCAC 355       T    CA  A
                                TCAC CATGC  GT CACTCGCAC
                                |||| |||||  || |||||||||
                                AGTG GTGCG  CA GTGAGCGTG
                                  C     __  C
GAM37   LOC146820 3'  TCATTCATGCCAGAACGTGC   365      C       T  ACTC
                                TCA TCATGCCAG AC    GC
                                ||| |||||||||  ||    ||
                                AGT AGTACGGTC TG    CG
                                  A        T  CA__
GAM37   LOC255624 3'  CACTCATCACACTTGCA     356         GCCAG     C
                                CACTCAT     TACACT GCA
                                |||||||     |||||| |||
                                GTGAGTA     GTGTGA CGT
                                     ______      A
GAM38   LARS2     5'  CCATGGGCGCCGCCATG     368          AG   G
                                CCATGGGC  TGC CATG
                                ||||||||  ||| ||||
                                GGTACCCG  GCG GTAC
                                     CG   _
GAM38   NRAP      3'  TCCATGGGCAGATGGAAC     369           _  C_
                                TCCATGGGCAG TG  GC
                                |||||||||||  ||  ||
                                AGGTACCCGTC AC  TG
                                       T  CT
GAM38   SCNN1G    3'  TCTGTGAGCAGTTGGCTTG    370      CA       _ C  A
                                TC  TGGGCAGT G GC TG
                                ||  |||||||| | || ||
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                                AG  ACTCGTCA C CG AC
                                 AC       A _  A
GAM38   XT3      3'  TCCATGGGGTACATGC      371          CA  GC
                                TCCATGGG  GT  GCATGC
                                ||||||||  ||  ||||||
                                AGGTACCC  CA  TGTACG
                                      __  __
GAM38   B3GAT3   3'  CCTGTGGGCAGTGCCACAC   372      A_        G
                                CC  TGGGCAGTGC CATGC
                                ||  |||||||||| |||||
                                GG  ACCCGTCACG GTGTG
                                 AC         _
GAM38   CHST3    3'  CCATGGCAGTGTATGC      373         G     CGC
                                CCATGG CAGTG   ATGC
                                |||||| |||||   ||||
                                GGTACC GTCAC   TACG
                                   _    A__
GAM38   DKFZp434N035 3'  TCCATGAGCGACTCGGTGC   374           AG G  CA
                                TCCATGGGC  T CG  TGC
                                |||||||||  | ||  |||
                                AGGTACTCG  G GC  ACG
                                     CT A  C_
GAM38   DKFZP564O0423 3'  TCCTGTGGACCGCATGCCG   375       A_    AGTG
                                TCC  TGGGC    CGCATGCCG
                                |||  |||||    |||||||||
                                AGG  ACCTG    GCGTACGGC
                                  AC    _____
GAM38   FADS1    3'  TCCATGGGTGGTGCATCTG   376          CA    CA
                                TCCATGGG  GTGCG  TG
                                ||||||||  |||||  ||
                                AGGTACCC  CACGT  AC
                                     AC    AG
GAM38   FLJ10743  3'  TCCTGGGCAGTGTCTGC     377       A        CGCA
                                TCC TGGGCAGTG    TGC
                                ||| |||||||||    |||
                                AGG ACCCGTCAC    ACG
                                  _        AG__
GAM38   FLJ13330  3'  CATGGGCATCCACGGTGCCG   378          G G   A_
                                CATGGGCA T CGC  TGCCG
                                ||||||||  | |||  |||||
                                GTACCCGT A GTG  ACGGC
                                     _ G   CC
GAM38   FLJ23309  5'  TCCTTGGGCACCATGC      379       A    AGT  G
                                TCC TGGGC   GC CATGC
                                ||| |||||   || |||||
                                AGG ACCCG   TG GTACG
                                  A    ____  _
GAM38   GREAT    3'  CATGGACAGTGCAACC      380             CAT
                                CATGGGCAGTGCG   GCC
                                ||||||||||||   |||
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                                GTACCTGTCACGT  TGG
                                       ___
GAM38  KCNT1    3'  TCCGTGGGCAGTGCCAGCTTGC 381      A       __ A
                                TCC TGGGCAGTGC  GC TGC
                                ||| ||||||||||  || |||
                                AGG ACCCGTCACG  CG ACG
                                  C        GT  A
GAM38  KIAA0323 3'  CCATGGGCCACATGC      382         AGTG
                                CCATGGGC   CGCATGC
                                ||||||||   |||||||
                                GGTACCCG   GTGTACG
                                       _____
GAM38  PPP1R16B 3'  CCTGTGGGCAGTGCCCATG   383     A_       G
                                CC  TGGGCAGTGC CATG
                                ||  |||||||||| ||||
                                GG  ACCCGTCACG GTAC
                                 AC        G
GAM38  PRAM-1   3'  TCCATGGGTGGCAACTGC    384        CAG  C  __
                                TCCATGGG   TG GCA  TGC
                                ||||||||   || |||  |||
                                AGGTACCC   AC CGT  ACG
                                     ___  _  TG
GAM38  RIN3     5'  TCCTGGGCAGCTCTGGCATGC  385      A      GC__
                                TCC TGGGCAGT   GCATGC
                                ||| ||||||||   ||||||
                                AGG ACCCGTCG   CGTACG
                                  _      AGAC
GAM38  SYNPO2   5'  TCCTGAGCCGTGCATGCCG   386      A    A   GC
                                TCC TGGGC GTGC  ATGCCG
                                ||| ||||| ||||  ||||||
                                AGG ACTCG CACG  TACGGC
                                  _    G   __
GAM38  LOC144465 3'  TCTGTGGGCAGTAGCTGC    387      CA       C  A
                                TC  TGGGCAGTG GC TGC
                                ||  ||||||||| || |||
                                AG  ACCCGTCAT CG ACG
                                 AC       _ _
GAM38  LOC144866 5'  TCCATGGGCACTGCCTCC    388          G   GCATG
                                TCCATGGGCA TGC    CC
                                |||||||||| |||    ||
                                AGGTACCCGT ACG    GG
                                      G   GA___
GAM38  LOC151056 3'  TCCATGGGGAGTGCCATG    389         C    G
                                TCCATGGG AGTGC CATG
                                |||||||| ||||| ||||
                                AGGTACCC TCACG GTAC
                                     C    _
GAM38  LOC165246 5'  TCTGTGGGCAGTGGGAGCCA  390      CA       CGCAT
                                TC  TGGGCAGTG    GCCG
                                ||  |||||||||    ||||
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                                AG  ACCCGTCAC    CGGT
                                 AC        CCT__
GAM38   LOC254173 3'  TCCAGGGCGGGCGCTGC     391       T   AGT   A
                                TCCA GGGC   GCGC TGC
                                |||| ||||   |||| |||
                                AGGT CCCG   CGCG ACG
                                  _    CC_   _
GAM38   LOC256369 3'  TCCGTGAGCAGTGCGAT     392       A        C
                                TCC TGGGCAGTGCG AT
                                ||| ||||||||||| ||
                                AGG ACTCGTCACGC TA
                                 C         _
GAM38   LOC257277 5'  TCCATGGGCGCCGCCATG    393          AG   G
                                TCCATGGGC  TGC CATG
                                |||||||||  ||| ||||
                                AGGTACCCG  GCG GTAC
                                     CG   _
GAM39   ARHGAP6   3'  CGCTCACTGGAGATCCTGCAG  396          TCT   A_
                                CGCTCACTG   GTCT  CAG
                                |||||||||   ||||  |||
                                GCGAGTGAC   TAGG  GTC
                                     CTC    AC
GAM39   ARHGAP6   3'  CGCTCACTGGAGATCCTGCAG  396          TCT   A_
                                CGCTCACTG   GTCT  CAG
                                |||||||||   ||||  |||
                                GCGAGTGAC   TAGG  GTC
                                     CTC    AC
GAM39   CARKL     3'  GCTCTCTGTCTACAG       397       ACTG
                                GCTC    TCTGTCTACAG
                                ||||    ||||||||||
                                CGAG    AGACAGATGTC
                                  _____
GAM39   CCR9      3'  GCTCACTGTATTCCTCAG     398          CTG   A
                                GCTCACTGT   TCT CAG
                                |||||||||   ||| |||
                                CGAGTGACA   AGG GTC
                                     TA_   A
GAM39   CCR9      3'  GCTCACTGTATTCCTCAG     398          CTG   A
                                GCTCACTGT   TCT CAG
                                |||||||||   ||| |||
                                CGAGTGACA   AGG GTC
                                     TA_   A
GAM39   CD164     3'  CCTTTCACTGTCTTCTA      399      GC       G
                                CC  TCACTGTCT TCTA
                                ||  ||||||||| ||||
                                GG  AGTGACAGA AGAT
                                 AA        _
GAM39   EPHA3     3'  CCAGAATTATTGTCTGTCTGCA 400       CTCAC__        A
           G                     CCG       TGTCTGTCT CAG
                                |||       ||||||||| |||
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                                GGT      ACAGACAGA GTC
                                  CTTAATA        C
GAM39   EXTL3    3'  CCCCTCAGAGCCTGTCTGCAG  401      G   CT      A
                                CCC CTCA  GTCTGTCT CAG
                                ||| ||||  |||||||| |||
                                GGG GAGT  CGGACAGA GTC
                                  _   CT       C
GAM39   HLF      3'  CTCTTGCTGTTATCTACAG   402      A__   C
                                CTC   CTGT TGTCTACAG
                                |||   |||| |||||||||
                                GAG   GACA ATAGATGTC
                                  AAC   _
GAM39   MYC      5'  CCCGCCCGCTGCTATGGCTGTA 403        A  T_________  TCTA
            CA                    CGCTC CTG       CTG   CA
                                ||||| |||       |||   ||
                                GCGGG GAC       GAC   GT
                                   C   GATACCIII   ATC
GAM39   NPDC1    3'  CACCCGTTCCTGCGCTCTAC   404        C  A   CTG
                                CACCCG TC CTGT   TCTAC
                                |||||| || ||||   |||||
                                GTGGGC AG GACG   AGATG
                                   A  _   CG_
GAM39   PPIL1    3'  CCTTTGCTCACTACAGCTGTAC 405     C__      T_____  TCTA
            A                    C   GCTCACTG     CTG   CA
                                |  ||||||||     |||   ||
                                G   CGAGTGAT     GAC   GT
                                 AAA       GTCIII   ATC
GAM39   PRKY     3'  CACCCTCTTCAGATGTCTACAG 406        G  _  CTGTC
                                CACCC CT CA     TGTCTACAG
                                ||||| || ||     |||||||||
                                GTGGG GA GT     ACAGATGTC
                                   A  A  CT___
GAM39   PRPS1    3'  CCTGCTCCTGCCTTACA     407      C   A     GTC
                                CC GCTC CTGTCT   TACA
                                || |||| ||||||   ||||
                                GG CGAG GACGGA   ATGT
                                 A   _     ____
GAM39   RAF1     3'  CCACTTGCGCATCTACAG     408        CAC   C
                                CCGCT   TGT TGTCTACAG
                                |||||   ||| |||||||||
                                GGTGA   ACG GTAGATGTC
                                   ____   C
GAM39   SRP14    3'  GCTCTTCACAGAGATGTCTACA 409      ____   TGTC_
            G                    GC   TCAC    TGTCTACAG
                                ||   ||||    |||||||||
                                CG   AGTG    ACAGATGTC
                                 AGA    TCTCT
GAM39   STK11    3'  CACCCGCCAGCTGGTCTGC    410          CA   _
                                CACCCGCT  CTG TCTGT
                                ||||||||  ||| |||||
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                                GTGGGCGG  GAC AGACG
                                     TC   C
GAM39   C11orf25  3'  CCTGCCTCATCTGTCTGT    411      C  _  _
                                CC GC TCA CTGTCTGT
                                || || ||| ||||||||
                                GG CG AGT GACAGACA
                                 A  G   A
GAM39   C1orf33   3'  TCATGTTCCCTGTCTACAG   412      C  ___
                                TCA TGT   CTGTCTACAG
                                ||| |||   ||||||||||
                                AGT ACA   GACAGATGTC
                                  _   AGG
GAM39   CSTL1     5'  CACCTGTTCCCTGTGCTTCCTT 413       CGC  A   _  GT  __
            TACAG                    CACC   TC CTGT CT  CT  ACAG
                                ||||   || |||| ||  ||  ||||
                                GTGG   AG GACA GA  GA  TGTC
                                   ACA  G   C  AG  AA
GAM39   DKFZP434B205 3'  GCTTGCTGTCTGCCCCTCAG   414      CA        A_
                                GCT  CTGTCTGTCT  CAG
                                |||  ||||||||||  |||
                                CGA  GACAGACGGG  GTC
                                  AC         GA
GAM39   DKFZp762K222 5'  CGCTCCTTCATCCGTCTAC    415       A  __
                                CGCTC CT  GTCTGTCTAC
                                ||||| ||  ||||||||||
                                GCGAG GA  TAGGCAGATG
                                   _  AG
GAM39   DT1P1A10  3'  CACCTGCCCACTGTCCCC    416       C        TG
                                CACC GCTCACTGTC  TC
                                |||| ||||||||||  ||
                                GTGG CGGGTGACAG  GG
                                   A         GT
GAM39   FLJ10701  3'  CTCATTGTCTACAACTCAG   417       C     T__  A
                                CTCA TGTCTG   CT CAG
                                |||| ||||||   || |||
                                GAGT ACAGAT   GA GTC
                                   A     GTT  _
GAM39   HSNOV1    3'  CACCCGTTTTCTGCCACA    418        CTCACTG   T
                                CACCCG      TCTG CTACA
                                ||||||      |||| |||||
                                GTGGGC      AGAC GGTGT
                                   AAA____   _
GAM39   KIAA0258  3'  CACCCTTCACTGTCTACGTC   419       GC       __
                                CACCC  TCACTGTCT  GTC
                                |||||  |||||||||  |||
                                GTGGG  AGTGACAGA  CAG
                                   A_        TG
GAM39   KIAA0445  5'  CCTGCTCCTGTAGCCGCAG   420     C   A   CT   TA
                                CC GCTC CTGT  GTC  CAG
                                || |||| ||||  |||  |||
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                                GG CGAG GACA  CGG  GTC
                                 A   _   T_  C_
GAM39   KIAA0555 3' CACTTCTCATCTGTCGTCT   421      CCG   _    T
                                CAC  CTCA CTGTC GTCT
                                |||  |||| ||||| ||||
                                GTG  GAGT GACAG CAGA
                                  AA_   A    _
GAM39   KIAA0774 5' GCTCACTGCACACCTGCAG   422          C GT  A
                                GCTCACTGT T  CT CAG
                                |||||||||  |  ||  |||
                                CGAGTGACG G  GA GTC
                                      T TG  C
GAM39   KIAA1576 3' ACCTGCCTCCCTGTGTTTACAG 423      C   CA  GTC   C
                                ACC GCT  CT   TGT TACAG
                                ||| |||  ||   ||| |||||
                                TGG CGG  GG   ACA ATGTC
                                  A   AG  AC_  A
GAM39   KIAA1789 5' ACTTACTGTTGCTACA     424      C    C  T
                                GCT ACTGT TG CTACA
                                ||| ||||| || |||||
                                TGA TGACA AC GATGT
                                  A    _ _
GAM39   KIAA1922 5' CACCTGCTCCTGTAGCCGCAG  425      C   A   CT   TA
                                CACC GCTC CTGT  GTC  CAG
                                |||| |||| ||||  |||  |||
                                GTGG CGAG GACA  CGG  GTC
                                  A   _   T_  C_
GAM39   MRPL9    3' GCTTATCAAATCTACAG    426      CAC   T_
                                GCT   TGTC  GTCTACAG
                                |||   ||||  ||||||||
                                CGA   ATAG  TAGATGTC
                                  ____   TT
GAM39   MRPS16   5' ACCCGCACGCACCAGCTCTAC  427        T__   _ CTG
                                ACCCGC   CACT GT   TCTAC
                                ||||||   |||| ||   |||||
                                TGGGCG   GTGG CG   AGATG
                                   TGC   T ____
GAM39   NMT2     3' CACCTGTCACTGAGCTACA   428      CGC    TCTGT
                                CACC   TCACTG    CTACA
                                ||||   ||||||    |||||
                                GTGG   AGTGAC    GATGT
                                  AC_     TC____
GAM39   PDE2A    3' ACCCGCTCCCTGTTTGGCTGTC 429        A  T________  TCTA
                                CCCGCTC CTG      CTG   C
                                ||||||| |||      |||   |
                                GGGCGAG GAC      GAC   G
                                   G  AAACCIII  AT
GAM39   PSR      3' CACCCACTTAACGTCTGT   430         CAC
                                CACCCGCT  TGTCTGT
                                ||||||||  |||||||
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                                GTGGGTGA   GCAGACA
                                    ATT
GAM39   SES2     3'  CACCCTCTCAGTCTGC      431        G    CT
                                CACCC CTCA  GTCTGT
                                ||||| ||||  ||||||
                                GTGGG GAGT  CAGACG
                                  A   __
GAM39   SLC37A1  3'  ACTCGCTCACTTTGATGTTCTG 432      C      _____ _
          T                      AC CGCTCACT    GT CTGT
                                || ||||||||    || ||||
                                TG GCGAGTGA    CA GACA
                                 A       AACTA  A
GAM39   SR-BP1   3'  CCCGCTCCTGTCCATCCGCAG  433         A        TA
                                CCCGCTC CTGTCTGTC  CAG
                                ||||||| |||||||||  |||
                                GGGCGAG GACAGGTAG  GTC
                                  _        GC
GAM39   LOC129676 5'  CACCCGTCACTCCAGGTCTGC  434         C    ____
                                CACCCG TCACT   GTCTGT
                                |||||| |||||   ||||||
                                GTGGGC AGTGA   CAGACG
                                  _    GGTC
GAM39   LOC134121 3'  CCCATTCACTGCTAAACTGT   435       C      ____
                                CCCG TCACTGT   CTGT
                                |||| |||||||   ||||
                                GGGT AGTGACG   GACA
                                  A      ATTT
GAM39   LOC148022 5'  ACCCATTCACTGTTCCAGCTGT 436     C     T_________   TCTA
          ACA                     CG TCACTG        CTG    CA
                                || ||||||        |||    ||
                                GT AGTGAC        GAC    GT
                                 A     AAGGTCIII   ATC
GAM39   LOC149127 3'  ACCCGCTTCTCTGTGGCTGTC  437         _ A   T_____   TCTA
                                ACCCGCT C CTG     CTG    C
                                ||||||| | |||     |||    |
                                TGGGCGA G GAC     GAC    G
                                   A A   ACCIII   AT
GAM39   LOC149579 5'  CACCTGCTCCTGTAGCCGCAG  425       C    A    CT   TA
                                CACC GCTC CTGT  GTC  CAG
                                |||| |||| ||||  |||  |||
                                GTGG CGAG GACA  CGG  GTC
                                  A    _    T_   C_
GAM39   LOC151248 5'  CTCAGATGCTGTCTACAG    438       C_  T
                                CTCA  TG CTGTCTACAG
                                ||||  || ||||||||||
                                GAGT  AC GACAGATGTC
                                  CT  _
GAM39   LOC152464 5'  CACCTGCTTGTGGTCCA     439       C   CAC   CT
                                CACC GCT   TGT  GTCTA
                                |||| |||   |||  |||||
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                                GTGG CGA   ACA  CAGGT
                                  A  ___   C_
GAM39   LOC157273 3'  ACTCGCTCACTGTCATGAGAAC 440      C         _ TCT
            AG                    AC CGCTCACTGTC TG   ACAG
                                  || |||||||||| ||   ||||
                                  TG GCGAGTGACAG AC   TGTC
                                   A         T  TCT
GAM39   LOC157280 5'  CACCCGCCATGTTTGC      441          T  C   C
                                  CACCCGC CA TGT TGT
                                  ||||||| || ||| |||
                                  GTGGGCG GT ACA ACG
                                     _ _   A
GAM39   LOC157753 3'  GCTCGTTGCTTGGCCTACAG   442        AC   CT_
                                  GCTC  TGT   GTCTACAG
                                  ||||  |||   ||||||||
                                  CGAG  ACG   CGGATGTC
                                    CA   AAC
GAM39   LOC164714 5'  CACCCACTTGTTGTCC      443          CAC   C
                                  CACCCGCT   TGT TGTCT
                                  ||||||||   ||| |||||
                                  GTGGGTGA   ACA ACAGG
                                       ___   _
GAM39   LOC170082 3'  CACCCACACTCTGTCTACA    444          TG
                                  CGCTCAC  TCTGTCTACA
                                  |||||||  ||||||||||
                                  GTGGGTG  AGACAGATGT
                                      TG
GAM39   LOC200268 3'  ACCGGCTCACTGTGCACAGCTG 445          T__________   TCTA
            TACA                    GCTCACTG         CTG    CA
                                  ||||||||         |||    ||
                                  CGAGTGAC         GAC    GT
                                       ACGTGTCIII   ATC
GAM39   LOC201617 5'  CACTTGCTTCTTGTCTGTCTTC 446      CC   CAC        A
            AG                    CAC  GCT   TGTCTGTCT CAG
                                  |||  |||   ||||||||| |||
                                  GTG  CGA   ACAGACAGA GTC
                                    AA   AGA        A
GAM39   LOC201895 5'  CCTTCTCACTGTGTCCTAC    447      CG       CTG
                                  CC  CTCACTGT   TCTAC
                                  ||  ||||||||   |||||
                                  GG  GAGTGACA   GGATG
                                   AA       CA_
GAM39   LOC220766 5'  ACTTCTCACTGTCATGCC     448      CCG        _
                                  AC   CTCACTGTC TGTC
                                  ||   ||||||||| ||||
                                  TG   GAGTGACAG ACGG
                                   AA_        T
GAM39   LOC255448 5'  CACCCGCCATGTTTGC      441          T  C   C
                                  CACCCGC CA TGT TGT
                                  ||||||| || ||| |||
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                                GTGGGCG GT ACA ACG
                                   _ _  A
GAM39   LOC90520  3'  ACCTGTTGTCTTTCTGTCTACA 449      CGCTCA  G
          G                     ACC     CT TCTGTCTACAG
                                |||     || ||||||||||
                                TGG     GA AGACAGATGTC
                                  ACAACA  A
GAM39   LOC91450  5'  GCTTCCTGTCTGTCTCAG    450      CA        A
                                GCT  CTGTCTGTCT CAG
                                |||  |||||||||| |||
                                CGA  GACAGACAGA GTC
                                  AG        C
GAM39   LOC96810  3'  CCATTCAGTCTGTCTCAG    451      C  CT       A
                                CCG TCA  GTCTGTCT CAG
                                ||| |||  |||||||| |||
                                GGT AGT  CAGACAGA GTC
                                  A  __       C
GAM40   CYYR1     3'  TCATATAAAAATATAAATGT   454      A
                                TTA ATAAAAATATAAATGT
                                ||| ||||||||||||||||
                                AGT TATTTTTATATTTACA
                                  A
GAM41   ADAMTS4   3'  CCGGGCGTGGTGGTAGGTGCC  457      A  AACC       C
                                CC GG    GGTGGTAGG GCC
                                || ||    ||||||||| |||
                                GG CC    CCACCATCC CGG
                                 C  GCA_        A
GAM41   APOL1     3'  GGGCATGGTGGTAGGCGCC    458      AACC
                                GG    GGTGGTAGGCGCC
                                ||    ||||||||||||
                                CC    CCACCATCCGCGG
                                 CGTA
GAM41   DFFB      3'  GGCCCTGGTGGTAGGTGCC    459      AA  _       C
                                GG  CC GGTGGTAGG GCC
                                ||  || ||||||||| |||
                                CC  GG CCACCATCC CGG
                                 G_  A        A
GAM41   DNM2      3'  CCTGGGGATGTAGGCGCC    460      A  AACC  TG
                                CC GG    GG  GTAGGCGCC
                                || ||    ||  |||||||||
                                GG CC    CC  CATCCGCGG
                                 A  _____  TA
GAM41   FMNL      5'  GGACGCCTGGAGGCGCCC    461      A_  GG   T
                                GGA  CC  TGG AGGCGCCC
                                |||  ||  ||| ||||||||
                                CCT  GG  ACC TCCGCGGG
                                  GC  __   _
GAM41   GAS11     5'  TCCGGGACCAGGGCGC      462      A  A   TGGTA
                                TCC GGA CCGG    GGCGC
                                ||| ||| ||||    |||||
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                                AGG CCT GGTC    CCGCG
                                  C  _  _____
GAM41   GNAI2   3' TCCAGGAATGGTGGCG     463        ACCG    A
                                TCCAGGA   GTGGT GGCG
                                |||||||   ||||| ||||
                                AGGTCCT   TACCA CCGC
                                    ____   _
GAM41   GPR30   5' GGAACCGATGGCCGCCC    464           AGG
                                GGAACCGGTGGT  CGCCC
                                ||||||||||||  |||||
                                CCTTGGCTACCG  GCGGG
                                     ___
GAM41   HR      5' CCCAGGGGCTGGAGAGGCGCCC 465        AACC  _  T_
                                TCCAGG   GG TGG  AGGCGCCC
                                ||||||   || |||  ||||||||
                                GGGTCC   CC ACC  TCCGCGGG
                                   ____ G  TC
GAM41   IGF1    3' CCGGGCATAGTGGTGGGTGCC 466     A  AACC    A  C
                                CC GG   GGTGGT GG GCC
                                || ||   |||||| || |||
                                GG CC   TCACCA CC CGG
                                 C  GTA_    C  A
GAM41   MTMR1   5' CCGGGAGCCGGCGGTGGCGCCC 467     A   A      A
                                CC GGA CCGGTGGT GGCGCCC
                                || ||| |||||||| |||||||
                                GG CCT GGCCGCCA CCGCGGG
                                 C  C      _
GAM41   P53AIP1 3' TCCAGGGAGGTGTAGGCGC   468        AACC   G
                                TCCAGG   GGTG TAGGCGC
                                ||||||   |||| |||||||
                                AGGTCC   CCAC ATCCGCG
                                   CT__   _
GAM41   PTPRH   3' TCCAGGAATCTGGGCTCAAGTG 469    CC__  ___  A  CG_  CIII
            GGTGTCCG              A   GGT  GGT GG  CC   G
                                |   |||  ||| ||  ||   |
                                T   CCG  TCA CC  GG   C
                                 AGAC  AGT  C  ACA  IIIC
GAM41   RORA    5' TCCAGAAACTGGGGCTGTGC  470         C  T  AG_
                                TCCAGGAAC GG GGT  GC
                                |||||||| || |||  ||
                                AGGTCTTTG CC CCG  CG
                                     A  _  ACA
GAM41   RORA    5' TCCAGAAACTGGGGCTGTGC  470         C  T  AG_
                                TCCAGGAAC GG GGT  GC
                                |||||||| || |||  ||
                                AGGTCTTTG CC CCG  CG
                                     A  _  ACA
GAM41   SCN4A   3' TCTGGGAACGCAGGCGC    471     CA    CGGTG
                                TC  GGAAC    GTAGGCGC
                                ||  |||||    ||||||||
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                                AG  CCTTG    CGTCCGCG
                                 AC    _____
GAM41   TMEFF2   5' TCCAGGGACTGGGCTCAGCCC 472       A  C_  GGTA  G
                                TCCAGG AC  GGT    GGC CC
                                |||||| ||  |||    ||| ||
                                AGGTCC TG  CCG    TCG GG
                                   C  AC   AG__  _
GAM41   ACTR1A   3' TCCAGTGGCCGGTGTGGTCC  474      GAA    GTA  CG
                                TCCAG   CCGGTG   GG  CC
                                |||||   ||||||   ||  ||
                                AGGTC   GGCCAC   CC  GG
                                  ACC     A__  A_
GAM41   ACTR1A   3' TCCTGGAACCAGCAGGTGCC  473     A    GGT    C
                                TCC GGAACC   GGTAGG GCC
                                ||| ||||||   |||||| |||
                                AGG CCTTGG   TCGTCC CGG
                                  A     ___     A
GAM41   CARD14   3' GGGACCACCCAGGCGCCC    475     A   GTGG
                                GG ACCG    TAGGCGCCC
                                || ||||    |||||||||
                                CC TGGT    GTCCGCGGG
                                 C   GG__
GAM41   DDR1     3' TCCAGGAATCAGTGTTGTCC  476        C    GTAGGCG
                                TCCAGGAA CGGTG      CC
                                |||||||| |||||      ||
                                AGGTCCTT GTCAC      GG
                                     A    AACA___
GAM41   DDR1     3' TCCAGGAATCAGTGTTGTCC  476        C    GTAGGCG
                                TCCAGGAA CGGTG      CC
                                |||||||| |||||      ||
                                AGGTCCTT GTCAC      GG
                                     A    AACA___
GAM41   DDR1     3' TCCAGGAATCAGTGTTGTCC  476        C    GTAGGCG
                                TCCAGGAA CGGTG      CC
                                |||||||| |||||      ||
                                AGGTCCTT GTCAC      GG
                                     A    AACA___
GAM41   DNAJA4   5' AGGGACTGGTGGTAGGGAC   477     A  C       C
                                AGG AC GGTGGTAGG GC
                                ||| || ||||||||| ||
                                TCC TG CCACCATCC TG
                                  C  A       C
GAM41   DOCK3    3' CAGGAGCTGATGGTAGGCA   478       ACC
                                CAGGA   GGTGGTAGGCG
                                |||||   ||||||||||
                                GTCCT   CTACCATCCGT
                                   CGA
GAM41   FLJ21817 3' TCCAGGGAGTGGTAGTTGGTGC 479       AACC    A  C
                                TCCAGG    GGTGGT GG GC
                                ||||||    |||||| || ||
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                                AGGTCC   CCATCA CC CG
                                   CTCA     A  A
GAM41   KCNT1    3'  TCCAGGAAGTGGTGGTCGGGC  480         CC     A  C
                                TCCAGGAA  GGTGGT GG GC
                                ||||||||  |||||| || ||
                                AGGTCCTT  CCACCA CC CG
                                     CA     G  _
GAM41   KIAA0174  3'  TCCAGGAACCGTTACAATGGCG 481           __ TG  A   _
           TCC                    TCCAGGAACCG  G  GT GGCG CC
                                ||||||||||  |  || |||| ||
                                AGGTCCTTGGC  T  TA CCGC GG
                                      AA GT  _   A
GAM41   KIAA0295  3'  TCCAAGAACTGCTGGGTGC   482          CG  GGTA  C
                                TCCAGGAAC  GT   GG GC
                                |||||||||  ||   || ||
                                AGGTTCTTG  CG   CC CG
                                     A_  AC__  A
GAM41   KIAA0493  5'  CCCGGGAGCCCACCGGGCG   483      A  A_  G  TAG
                                TCC GGA  CCG TGG  GCG
                                ||| |||  ||| |||  |||
                                GGG CCT  GGT GCC  CGC
                                  C  CG  G  ___
GAM41   KIAA0939  3'  TCCGGGTGGGGGGGGTAGGCGCC 484      A  AACC  T
           C                    TCC GG   GG GGTAGGCGCCC
                                ||| ||   || ||||||||||
                                AGG CC   CC CCATCCGCGGG
                                  C  ACCC  _
GAM41   KIAA1303  3'  TCCGGGACCCGGCAGTGCC   485      A  A   TG  AGGC
                                TCC GGA CCGG  GT   GCC
                                ||| ||| ||||  ||   |||
                                AGG CCT GGCC  CA   CGG
                                  C  G   GT  ____
GAM41   KIAA1958  3'  TCCGGGGGCCGGCGGTGGG   486      A  AA      A
                                TCC GG  CCGGTGGT GG
                                ||| ||  |||||||| ||
                                AGG CC  GGCCGCCA CC
                                  C  CC      C
GAM41   MGC1842   3'  TCCAGCAGCCAGCAGGTGC   487       GAAC   _    C
                                TCCAG   CGGT GGTAGG GC
                                |||||   |||| |||||| ||
                                AGGTC   GTCG TCGTCC CG
                                   ____   G    A
GAM41   MGC32043  3'  CCAGGGCAGGTGGTAGGTGCC  488       AACC       C
                                CCAGG   GGTGGTAGG GCC
                                |||||   ||||||||| |||
                                GGTCC   CCACCATCC CGG
                                   CGT_       A
GAM41   MRPL15    5'  TCCAAGAACTTTCAAGGGCGCC 489          CGGTGGTA
           C                    TCCAGGAAC      GGCGCCC
                                |||||||||      |||||||
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                                AGGTTCTTG      CCGCGGG
                                     AAAGTTC_
GAM41   SSTK     3'  GGGGCCTGGCAGACAGTAGGTG 490     AA  _  ____     C
            C                    GG  CC GGT    GGTAGG GC
                                 ||  || |||    |||||| ||
                                 CC  GG CCG    TCATCC CG
                                  CC  A   TCTG     A
GAM41   TMEM8    3'  TCCAGGGCTGGACCAGGCGCC  491        AACC  TGG
                                 TCCAGG    GG   TAGGCGCC
                                 ||||||    ||   ||||||||
                                 AGGTCC    CC   GTCCGCGG
                                    CGA_  TG_
GAM41   LOC138428 5'  TCCGGGAACCCAGGCGCC    492      A     GGTGG
                                 TCC GGAACC     TAGGCGCC
                                 ||| ||||||     ||||||||
                                 AGG CCTTGG     GTCCGCGG
                                   C     _____
GAM41   LOC147160 5'  TCTGGGAACCAGTGGGAC    493      CA         TA
                                 TC  GGAACCGGTGG  GGC
                                 ||  ||||||||||  |||
                                 AG  CCTTGGTCACC  CTG
                                  AC         __
GAM41   LOC147817 3'  CAGGTGTGGTGGTAGGCGCC   494       AACC
                                 CAGG    GGTGGTAGGCGCC
                                 ||||    ||||||||||||
                                 GTCC    CCACCATCCGCGG
                                   ACA_
GAM41   LOC151121 5'  TCCAGCAGGGGTGGGTGC    495       GAAC   T   A  C
                                 TCCAG    CGG GGT GG GC
                                 |||||    ||| ||| || ||
                                 AGGTC    GTC CCA CC CG
                                    _____  C   C  A
GAM41   LOC158056 5'  GGAAGGGGTAGGCGC       496       CC  T
                                 GGAA  GG GGTAGGCGC
                                 ||||  || |||||||||
                                 CCTT  CC CCATCCGCG
                                    __  _
GAM41   LOC203054 5'  TCCAGGAACTGGTAGAGCC    497          CGG      C
                                 TCCAGGAAC   TGGTAGG GCC
                                 |||||||||   ||||||| |||
                                 AGGTCCTTG   ACCATCT CGG
                                      ___      _
GAM41   LOC254228 3'  TCCAGGAATGGGATTAGTGCC  498          CC  T   A  C
                                 TCCAGGAA  GG GGT GG GCC
                                 ||||||||  || ||| || |||
                                 AGGTCCTT  CC CTA TC CGG
                                     A_  _   A  A
GAM41   LOC255811 5'  TCCAGGAATAGGTTTTCCTGCC 499          CC   GGTAGGC
            C                    TCCAGGAA  GGT      GCCC
                                 ||||||||  |||      ||||
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                                AGGTCCTT  CCA      CGGG
                                    AT   AAAGGA_
GAM41   LOC255975 5'  TCCAGGAACCGTAGCGCC    500           GTGGTA
                                TCCAGGAACCG     GGCGCC
                                ||||||||||      ||||||
                                AGGTCCTTGGC     TCGCGG
                                     A_____
GAM41   LOC256451 3'  CAGGAGCCGCACAGGCGCCC   501        A   GTGG
                                CAGGA CCG    TAGGCGCCC
                                ||||| |||    |||||||||
                                GTCCT GGC    GTCCGCGGG
                                   C   GT__
GAM41   LOC85414  5'  CCTAGGAATCAGCCAGGCGCCC 502      _    C    GG
                                CC AGGAA CGGT  TAGGCGCCC
                                || ||||| ||||  |||||||||
                                GG TCCTT GTCG  GTCCGCGGG
                                 A    A   __
GAM41   LOC91828  5'  TCCAGGAAGCTGGTGTAGTCGC 503         CC_   G   G
                                TCCAGGAA   GGTG TAG CGC
                                ||||||||   |||| ||| |||
                                AGGTCCTT   CCAC ATC GCG
                                     CGA    _   A
GAM41   LOC92299  5'  GGGGGTGTCGCTAGGCGCCC   504     AACC    G___
                                GG   GGTG   TAGGCGCCC
                                ||   ||||   |||||||||
                                CC   CCAC   ATCCGCGGG
                                 C___    AGCG
GAM42   BCL2      3'  TCTCTTGCGGAGTATTTGTGCA 507         TA    GCC   A
                                TCTCTTGC  GGTA   TGT CA
                                ||||||||  ||||   ||| ||
                                AGAGAACG  TCAT   ACA GT
                                     CC    AA_   C
GAM42   CASP2     3'  TCTCTTGCATTTCCTGTGCA   508         TAGGTAG    A
                                TCTCTTGC      CCTGT CA
                                ||||||||      ||||| ||
                                AGAGAACG      GGACA GT
                                     TAAA___     C
GAM42   CASP2     3'  TCTCTTGCATTTCCTGTGCA   508         TAGGTAG    A
                                TCTCTTGC      CCTGT CA
                                ||||||||      ||||| ||
                                AGAGAACG      GGACA GT
                                     TAAA___     C
GAM42   CDKN2D    3'  TCTTTTAAAACGCTGTACAA   509       GCTAGGT   _
                                TCTT      AGC CTGTACAA
                                ||||      ||| ||||||||
                                AGAA      TTG GACATGTT
                                  AATT___   C
GAM42   CDKN2D    3'  TCTTTTAAAACGCTGTACAA   509       GCTAGGT   _
                                TCTT      AGC CTGTACAA
                                ||||      ||| ||||||||
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                                AGAA      TTG GACATGTT
                                  AATT___   C
GAM42   IL16     3'  CCTTTTGCTGGGTGGCGTCCTA 510      C    A  AG___
                                TCT TTGCT GGT    CCTG
                                ||| ||||| |||    ||||
                                GGA AACGA CCA    GGAT
                                  A    C  CCGCA
GAM42   MMP15    3'  TTGCCGGCTGTACAA      511       A  TAGC
                                TTGCT GG   CTGTACAA
                                ||||| ||   ||||||||
                                AACGG CC   GACATGTT
                                  _ ____
GAM42   PIM1     3'  TCTCTTTTATTCCCCTGTACA  512       GC  GGTAG
                                TCTCTT  TA   CCTGTACA
                                ||||||  ||   ||||||||
                                AGAGAA  AT   GGACATGT
                                   A_  AAGG_
GAM42   CAMP-GEFII 3'  TCTCTTGCTAGGTAGCTGGTA  513            CT
                                TCTCTTGCTAGGTAGC  GTA
                                ||||||||||||||||  |||
                                AGAGAACGATCCATCG  CAT
                                          AC
GAM42   DKFZP434C171 5'  TCTCCTGCTGGGTAGAACTG  514        A    C_
                                TCTCTTGCT GGTAG  CTG
                                |||||||| |||||  |||
                                AGAGGACGA CCATC  GAC
                                     C    TT
GAM42   FLJ10751  3'  TCCCTTGCTGGGTGGGCATG  515        A  A_  C
                                TCTCTTGCT GGT  GC TG
                                |||||||| |||  || ||
                                AGGGAACGA CCA  CG AC
                                     C  CC  T
GAM42   FLJ12987  3'  TCTCTTGCTAGGGGGACTG  516          TAGC
                                TCTCTTGCTAGG   CTG
                                ||||||||||||   |||
                                AGAGAACGATCC   GAC
                                       CCCT
GAM42   FLJ14950  3'  TCTCTTGCTCAGACTGT    517        AGG  C
                                TCTCTTGCT  TAG CTGT
                                |||||||||  ||| ||||
                                AGAGAACGA  GTC GACA
                                     ___  T
GAM42   GPR105    3'  TCTTGCTAAGTATACA     518         AGCCT
                                TCTTGCTAGGT   GTACA
                                ||||||||||    |||||
                                AGAACGATTCA   TATGT
                                      _____
GAM42   KIAA0461  3'  CTTGCTAATAACACCTGTA   519        GTA_
                                CTTGCTAG   GCCTGTA
                                ||||||||   |||||||
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                                GAACGATT   TGGACAT
                                    ATTG
GAM42   KIAA1464  5'  TCTCTTGCTGGTTGACCGC   520         A  A_  T
                                TCTCTTGCT GGT  GCC GT
                                ||||||||| |||  ||| ||
                                AGAGAACGA CCA  TGG CG
                                     _  AC  _
GAM42   KIAA1884  3'  TCTTTTTTGGTACTGTACA   521      GCTA   GC
                                TCTT   GGTA  CTGTACA
                                ||||   ||||  |||||||
                                AGAA   CCAT  GACATGT
                                  AAAA   __
GAM42   SDS3      3'  CTTGTACAAGTCTGTACAA   522      C_   AGC
                                CTTG  TAGGT  CTGTACAA
                                ||||  |||||  ||||||||
                                GAAC  GTTCA  GACATGTT
                                  AT   ___
GAM42   LOC125704 3'  TCTTTGCTAGGTAGGCA    523      C        CCT
                                TCT TTGCTAGGTAG  GTA
                                ||| ||||||||||  |||
                                AGA AACGATCCATC  CGT
                                  _       ___
GAM42   LOC153222 5'  TCTCTTGCTGTGATGGTGTA  524         A_  AGCC
                                TCTCTTGCT  GGT   TGTA
                                |||||||||  |||   ||||
                                AGAGAACGA  CTA   ACAT
                                     CA  CC__
GAM42   LOC170409 5'  TCTTGCCAGGTGCAGT     525          A  CT
                                TCTTGCTAGGT GC  GT
                                |||||||||| ||  ||
                                AGAACGGTCCA CG  CA
                                      _ T_
GAM42   LOC220020 5'  TCTTGTGCCCTGTACA     526       CTAG  AG
                                TCTTG   GT  CCTGTACA
                                |||||   ||  ||||||||
                                AGAAC   CG  GGACATGT
                                  A___  __
GAM42   LOC51141  3'  TCATCTTGCTTTTCTGTACAA  527     _     AGGTAGC
                                TC TCTTGCT      CTGTACAA
                                || |||||||      ||||||||
                                AG AGAACGA      GACATGTT
                                  T      AAA____
GAM42   LOC51213  3'  TCTTTTGCTAGGGTAGACA   528      C      _  CCTGT
                                TCT TTGCTAGG TAG    ACA
                                ||| |||||||| |||    |||
                                AGA AACGATCC ATC    TGT
                                  A       C  _____
GAM43   FXYD1     5'  TCACGCAAAAGCTGCCGGGGTG 531         CA_      AC
            AGG                   TCGCGCAG  CTGCCGGG  GAGG
                                ||||||||  ||||||||  ||||
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                                AGTGCGTT  GACGGCCC  CTCC
                                    TTC       CA
GAM43   DKFZP566K1924 5'  CCGCGCAGCTGGGGGCGAGG  532          AC  CC   A
                                TCGCGCAGC  TG  GGG CGAGG
                                |||||||||  ||  ||| |||||
                                GGCGCGTCG  AC  CCC GCTCC
                                     __  C_  _
GAM43   FLJ10737  3'  GCCCAGCACTGCACTCTGGAGG 533      G       CGGGAC
                                GC CAGCACTGC     GAGG
                                || |||||||||     ||||
                                CG GTCGTGACG     CTCC
                                 G       TGAGAC
GAM43   KIAA0544  5'  GCGCGGCGCTGCCGGGCAGAGG 534       A  A       AC
                                GCGC GC CTGCCGGG  GAGG
                                |||| || ||||||||  ||||
                                CGCG CG GACGGCCC  CTCC
                                  C  C       GT
GAM43   PCYT2     3'  CCGCGCAGCACTGCCACCAGG  535             GGG  G
                                TCGCGCAGCACTGCC   AC AGG
                                ||||||||||||||   || |||
                                GGCGCGTCGTGACGG   TG TCC
                                        ___  G
GAM43   SRCRB4D   3'  TCACGCAGTAAGTGGACGGG   536         CACTGCCG    A
                                TCGCGCAG       GGACG GG
                                ||||||||       ||||| ||
                                AGTGCGTC       CCTGC CC
                                    ATTCA___    _
GAM43   LOC126364 5'  TCCGCAGCGCTGCTGGG     537      G     A   C
                                TC CGCAGC CTGC GGG
                                || |||||| |||| |||
                                AG GCGTCG GACG CCC
                                 _     C    A
GAM43   LOC221749 5'  TCGCGCAGGCGCTGCCACAGG  538          _ A    __
                                TCGCGCAG C CTGCC  GGG
                                |||||||| | |||||  |||
                                AGCGCGTC G GACGG  TCC
                                    C C     TG
GAM44   AQP6      5'  CCAGGTAGCCATTGACCAGGGC 541            __  ATAA
          TT                     CCAGGTAGCCGT  GC    GCTT
                                ||||||||||||  ||    ||||
                                GGTCCATCGGTA  TG    CGAA
                                      AC  GTCC
GAM44   SLA       3'  ACCAGTAGCACGATGAGCTTA  542        G   _ _  CATA
                                ACCAG TAGC CG TG    AGCTTA
                                ||||| |||| || ||    ||||||
                                TGGTC ATCG GC AC    TCGAAT
                                   _    T  T  _____
GAM44   SYT1      3'  ACCAAGTATGTGGTGTAAG    543          GCC_  CA
                                ACCAGGTA    GTG  TAAG
                                ||||||||    |||  ||||
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                                TGGTTCAT   CAC  ATTC
                                    ACAC   __
GAM44   TAP2     3'  CCAGGTAGCAGATATAAAGCTT 544          CGTGCAT
              A                  CCAGGTAGC      AAGCTTA
                                 |||||||||      |||||||
                                 GGTCCATCG      TTCGAAT
                                     TCTATAT
GAM44   WASF3    3'  CAGTGTAGCCAAGCTT      545      _      TGCATA
                                 CAG GTAGCCG     AGCTT
                                 ||| |||||||     |||||
                                 GTC CATCGGT     TCGAA
                                   A     _______
GAM44   FLJ13848 3'  ACCAGGAGGTTAAGCT      546        T  CC  GCA
                                 ACCAGG AG  GT   TAAGCT
                                 |||||| ||  ||   ||||||
                                 TGGTCC TC  CA   ATTCGA
                                    _  __  ___
GAM44   KIAA0831 3'  ACTAGGTAAGAATAAGCTT    547     C     CCGTGC
                                 AC AGGTAG     ATAAGCTT
                                 || ||||||     ||||||||
                                 TG TCCATT     TATTCGAA
                                  A     CT____
GAM44   MGC1136  5'  CCAGGTAGCTGCTGCTC     548          CG   ATAA
                                 CCAGGTAGC  TGC    GCTT
                                 |||||||||  |||    ||||
                                 GGTCCATCG  ACG    CGAG
                                      __   A___
GAM44   RCD-8    3'  CCAGGTAGCTGAGCT       549          CG  CATA
                                 CCAGGTAGC  TG    AGCT
                                 |||||||||  ||    ||||
                                 GGTCCATCG  AC    TCGA
                                      __  _____
GAM44   SSI-1    5'  CCAGGAGCCGTGCAGCT     550        T       TAA
                                 CCAGG AGCCGTGCA   GCT
                                 ||||| |||||||||   |||
                                 GGTCC TCGGCACGT   CGA
                                    _      ___
GAM44   LOC115294 3'  CAGGTTATATAAGCTT      551        AGCCG  C
                                 CAGGT     TG ATAAGCTT
                                 |||||     || ||||||||
                                 GTCCA     AT TATTCGAA
                                    ______  A
GAM44   LOC143286 5'  CACAAGCCTGTGCATAAGCTT  552      GGT   _
                                 CA   AGCC GTGCATAAGCTT
                                 ||   |||| ||||||||||||
                                 GT   TCGG CACGTATTCGAA
                                  GT_    A
GAM44   LOC163026 5'  GCCAGCTGTGCCTGTAAGCTTA 553     G    C    A__
                                 G TAGC GTGC   TAAGCTTA
                                 | |||| ||||   ||||||||
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                                C GTCG CACG   ATTCGAAT
                                 G   A   GAC
GAM44   LOC196510 3'  ACCAGGTAGCTGTGGCT    554          C   CATAA
                                ACCAGGTAGC GTG    GCT
                                |||||||||| |||    |||
                                TGGTCCATCG CAC    CGA
                                     A  _____
GAM44   LOC196872 3'  ACCAGTGTGGCGATAAGCTT  555       _ AGCC   C
                                ACCAG GT   GTG ATAAGCTT
                                ||||| ||   ||| ||||||||
                                TGGTC CA   CGC TATTCGAA
                                  A  C___  _
GAM44   LOC200220 3'  ACCAGGTAGCTGTGGCT    554          C   CATAA
                                ACCAGGTAGC GTG    GCT
                                |||||||||| |||    |||
                                TGGTCCATCG CAC    CGA
                                     A  _____
GAM44   LOC203378 5'  CCAGGTAGCGGGACTGGCTT  556          CGT  ATAA
                                CCAGGTAGC  GC   GCTT
                                |||||||||  ||   ||||
                                GGTCCATCG  TG   CGAA
                                     CCC  AC__
GAM44   LOC254043 3'  CAGGTAGCCTAAGCTT     557          GTGCA
                                CAGGTAGCC    TAAGCTT
                                |||||||||    |||||||
                                GTCCATCGG    ATTCGAA
                                     _____
GAM44   LOC256015 5'  CCAGGTAGAGATGGGCTT   558          CC   CATAA
                                CCAGGTAG  GTG    GCTT
                                ||||||||  |||    ||||
                                GGTCCATC  TAC    CGAA
                                     TC   C____
GAM45   ACPT     3'  CTGGTAGTGGAAGACCGTGGGC 561          _  C   CCA
          T                      TTGGTAGTG AAG CTG   GGCT
                                |||||||||| ||| |||   ||||
                                GACCATCAC TTC GGC   CCGA
                                     C   T   AC_
GAM45   CACNA1D   3'  TGGTACTCTGCCAGGCT     562       AGTGAA  _
                                TGGT     GC CTGCCAGGCT
                                ||||     || ||||||||||
                                ACCA     TG GACGGTCCGA
                                   _______  A
GAM45   IRAK4    3'  TTAGTAGTGGAGTCAGCTGGGC 563          A  CCT  CA
          T                      TTGGTAGTG AG   GC  GGCT
                                |||||||||| ||   ||  ||||
                                AATCATCAC TC   CG  CCGA
                                     C  AGT  AC
GAM45   BLZF1    3'  GTAGTGGCCAAAACCAGGCT   564        AA   T__
                                GTAGTG  GCC   GCCAGGCT
                                ||||||  |||   ||||||||
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                                CATCAC  CGG   TGGTCCGA
                                   __  TTT
GAM45   BRAL1    5'  CTGGATGAAGGTTTGCCAGGCT 565       TA     CC_
            C                    TTGG  GTGAAG   TGCCAGGCTC
                                 ||||  ||||||   ||||||||||
                                 GACC  TACTTC   ACGGTCCGAG
                                   __     CAA
GAM45   ELF4     5'  GGTGGTGGCCTAAGCCAGGCTC 566      A   AA   __
                                 GGT GTG  GCCT  GCCAGGCTC
                                 ||| |||  ||||  |||||||||
                                 CCA CAC  CGGA  CGGTCCGAG
                                   C  __   TT
GAM45   FLJ10815  3'  TTGGAAGTGGCCAGGC     567       T   AAGCCT
                                 TTGG AGTG     GCCAGGC
                                 |||| ||||     |||||||
                                 AACC TCAC     CGGTCCG
                                   T  _______
GAM45   KIAA0227  3'  TGGTACACTTGCCAGGCT    568       GTGAA  C
                                 TGGTA    GC TGCCAGGCT
                                 |||||    || |||||||||
                                 ACCAT    TG ACGGTCCGA
                                    G____  A
GAM45   KIAA0826  3'  TTGGTAGTCAGTCTTCAGGCT  569         GA  C  GC
                                 TTGGTAGT  AG CT  CAGGCT
                                 ||||||||  || ||  ||||||
                                 AACCATCA  TC GA  GTCCGA
                                      G_  A  A_
GAM45   LOC155061 3'  TTGGGGTGGGCGGCCAGGCT   570       TA   AA  CT
                                 TTGG  GTG  GC  GCCAGGCT
                                 ||||  |||  ||  ||||||||
                                 AACC  CAC  CG  CGGTCCGA
                                   C_  C_  C_
GAM45   LOC162022 5'  TTGGTGATGAAGCCCAGGC    571       A       TGC
                                 TTGGT GTGAAGCC   CAGGC
                                 ||||| ||||||||   |||||
                                 AACCA TACTTCGG   GTCCG
                                    C       ___
GAM46   BCL7A    5'  GAAAGAGTTGGGCATCGCGCAT 574           ATT  A_   C
            CT                     GAAAGAGTTGG   TC  GCA CT
                                 ||||||||||   ||  ||| ||
                                 CTTTCTCAACC   AG  CGT GA
                                       CGT  CG   A
GAM46   C1orf6   3'  AAGGGGTTGGAGCCCATGCCT  575      A_     T    GCA
                                 AAG  GTTGGA TTCA   CCT
                                 |||  |||||| ||||   |||
                                 TTC  CAACCT GGGT   GGA
                                   CC     C    AC_
GAM46   CCNT2    3'  TGAAGGCAAAATTTCAGTGCCT 576       A A  TG       CA
                                 TGAA G GT  GATTTCAG  CCT
                                 |||| | ||  ||||||||  |||
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                                ACTT C CG  TTAAAGTC  GGA
                                  _ _  TT       AC
GAM46   CNTNAP2  3'  TGAGAGGATTGGATCTCA    577      A  AG
                                TGA AG  TTGGATTTCA
                                ||| ||  ||||||||||
                                ACT TC  AACCTAGAGT
                                  C  CT
GAM46   FACL4    3'  GAAAGGCAATTTTCAGCA    578       A  TGGA
                                GAAAG GT    TTTCAGCA
                                ||||| ||    ||||||||
                                CTTTC CG    AAAGTCGT
                                   _  TTA_
GAM46   FACL4    3'  GAAAGGCAATTTTCAGCA    578       A  TGGA
                                GAAAG GT    TTTCAGCA
                                ||||| ||    ||||||||
                                CTTTC CG    AAAGTCGT
                                   _  TTA_
GAM46   GP2      3'  AGAGACGGAGTTTCAGCA    579       T   _
                                AGAG TGGA TTTCAGCA
                                |||| |||| ||||||||
                                TCTC GCCT AAAGTCGT
                                  T   C
GAM46   HTR4     5'  TGAGTGAGTTGGATTTCAA   580      AA
                                TGA  GAGTTGGATTTCAG
                                |||  ||||||||||||||
                                ACT  CTCAACCTAAAGTT
                                  CA
GAM46   ATIP1    3'  GAAAGTGGTTTCAGCACCT   581       AGT   A
                                GAAAG   TGG TTTCAGCACCT
                                |||||   ||| ||||||||||
                                CTTTC   ACC AAAGTCGTGGA
                                   ____  _
GAM46   CAMKK2   3'  TGGAAGAGCTGTCATAACAGCA 582     A      G_  TT
            CCT                   TG AAGAGTTG  AT  CAGCACCT
                                || ||||||||  ||  ||||||||
                                AC TTCTCGAC  TA  GTCGTGGA
                                 C       AG  TT
GAM46   DOCK3    3'  TGAAAGAATGAAAATCAG    583          T   TT
                                TGAAAGAGT GGA  TCAG
                                ||||||||| |||  ||||
                                ACTTTCTTA CTT  AGTC
                                      _  TT
GAM46   FLJ10925 5'  TGAGAGGAGCTGTTCAGCACCT 584      AA_    GAT
                                TGA   GAGTTG   TTCAGCACCT
                                |||   ||||||  ||||||||||
                                ACT   CTCGAC   AAGTCGTGGA
                                  CTC    ____
GAM46   FLJ20886 5'  TGGGAGAGCTGGGCGGTCACCT 585     AA      ATTTCAG
                                TG  AGAGTTGG      CACCT
                                ||  ||||||||      |||||
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                                AC  TCTCGACC      GTGGA
                                 CC       CGCCA__
GAM46   IL-23R   3' AAAGGAAAATTTTCAGCA    586       TT     _
                                AGAG  GGATTT CAGCA
                                ||||  |||||| |||||
                                TTTC  TTTAAA GTCGT
                                  CT     A
GAM46   KIAA0329 3' AGATCTGGGATTTCGGCATCT  587      GTT_     A   C
                                AGA    GGATTTC GCA CT
                                |||    ||||||| ||| ||
                                TCT    CCTAAAG CGT GA
                                 AGAC      C   A
GAM46   KIAA0773 3' TGGAAGATTTGGATTTTCA    588     A    G       _
                                TG AAGA TTGGATTT CA
                                || |||| |||||||| ||
                                AC TTCT AACCTAAA GT
                                 C    A       A
GAM46   KIAA1045 3' GAATGGTGATTTCAGTGCCT   589       TG_      CA
                                GAGT   GATTTCAG  CCT
                                ||||   ||||||||  |||
                                CTTA   CTAAAGTC  GGA
                                  CCA       AC
GAM46   KIAA1423 3' TGAAGGGTTGGAACCCCAGCAT 590       A A     _ TT    C
           CT                     TGAA G GTTGGA T  CAGCA CT
                                |||| | |||||| |  ||||| ||
                                ACTT C CAACCT G  GTCGT GA
                                  _ C     T GG    A
GAM46   KLF12    3' TGACAGGCACTTTCAGCA    591      A  A  TGGA
                                TGA AG GT    TTTCAGCA
                                ||| || ||    ||||||||
                                ACT TC CG    AAAGTCGT
                                 G  _  TG__
GAM46   SPAF     3' GAAAGGATTTTCAGCATCT    592      TT     _    C
                                GAG  GGATTT CAGCA CT
                                |||  |||||| ||||| ||
                                CTT  CCTAAA GTCGT GA
                                 T_     A    A
GAM46   LOC138311 3' AGGGTTGGACCCTGGCACCT  593     A       CA
                                AG GTTGGATTT  GCACCT
                                || |||||||||  ||||||
                                TC CAACCTGGG  CGTGGA
                                 C        AC
GAM46   LOC143381 3' TGGAAGAGCTGGATTTGC    594     A         CA
                                TG AAGAGTTGGATTT  GC
                                || ||||||||||||  ||
                                AC TTCTCGACCTAAA  CG
                                 C          __
GAM46   LOC145317 5' TGAGGAGTCCTTCAGCAC    595      AA    GGA
                                TGA  GAGTT   TTTCAGCAC
                                |||  |||||  |||||||||
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                                ACT  CTCAG   GAAGTCGTG
                                  C_    ___
GAM46   LOC148562 3'  AAGAGTTGATGATTTTAGCA   596          __    C
                                AAGAGTTG  GATTT AGCA
                                ||||||||  ||||| ||||
                                TTCTCAAC  CTAAA TCGT
                                    TA    A
GAM46   LOC149317 5'  TGAAGGAGTTGAATAACA    597       A       TT
                                TGAA GAGTTGGAT  CA
                                |||| |||||||||  ||
                                ACTT CTCAACTTA  GT
                                  C        TT
GAM46   LOC151457 5'  GAGCTGGATTTTGGCACCT   598            CA
                                GAGTTGGATTT  GCACCT
                                ||||||||||  ||||||
                                CTCGACCTAAA  CGTGGA
                                       AC
GAM46   LOC153592 3'  TGGAAGAGCTGGAAGCTCACCT 599      A        TTTCAG
                                TG AAGAGTTGGA     CACCT
                                || ||||||||||     |||||
                                AC TTCTCGACCT     GTGGA
                                 C         TCGA__
GAM46   LOC164237 5'  AAATAGGTTTCAGCACC     600       T  A
                                GAGT GG TTTCAGCACC
                                |||| || ||||||||||
                                TTTA CC AAAGTCGTGG
                                  T  _
GAM46   LOC200030 3'  TGAAGGAGTTGAATAACA    597       A       TT
                                TGAA GAGTTGGAT  CA
                                |||| |||||||||  ||
                                ACTT CTCAACTTA  GT
                                  C        TT
GAM46   LOC204285 5'  TGATGGAGAGCTTCAGCATCT  601      AA   TT  A      C
                                TGA  GAG  GG TTTCAGCA CT
                                |||  |||  || |||||||| ||
                                ACT  CTC  TC GAAGTCGT GA
                                  AC   __ _       A
GAM46   LOC253613 3'  TGAGGGAGTTGAATTTATCCT  602      AA        CAGCA
                                TGA  GAGTTGGATTT    CCT
                                |||  ||||||||||    |||
                                ACT  CTCAACTTAAA    GGA
                                  CC         TA___
GAM46   LOC255042 5'  GAGAGGGATGTGCGCAGCACCT 603      TT    TT___
                                GAG  GGAT    CAGCACCT
                                |||  ||||    ||||||||
                                CTC  CCTA    GTCGTGGA
                                  TC    CACGC
GAM46   LOC51667  3'  TGAAAAAGTTGGAGCA      604            TTTCA
                                TGAAAGAGTTGGA    GCA
                                ||||||||||||    |||
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                                ACTTTTTCAACCT    CGT
                                      _____
GAM46   LOC89944 3'  TGCAAGGGCACGTTTCAGCAC  605     A   A  TGGA
                                TG AAG GT    TTTCAGCAC
                                || ||| ||    |||||||||
                                AC TTC CG    AAAGTCGTG
                                 G   C  TGC_
GAM47   ADAT1    3'  TAGCTTGCTCTAAGTTCC    608       C       CACATA
                                TAGC TGCTTTAA     TCC
                                |||| ||||||||     |||
                                ATCG ACGAGATT     AGG
                                  A       CA____
GAM47   CTNNB1   3'  TACCCTACCCATACATATCCCA 609      G      TAAC
                                TA CCTGCTT    ACATATCCCA
                                || |||||||    ||||||||||
                                AT GGATGGG    TGTATAGGGT
                                 G      TA__
GAM47   NEURL    3'  TAGCCAGGCCACATGTCC    610        T_  TTTAA    A
                                TAGCC  GC    CACAT TCC
                                |||||  ||    ||||| |||
                                ATCGG  CG    GTGTA AGG
                                   TC  _____    C
GAM47   SGPL1    3'  GCCTGTTCCATATCCC      611        C   AACA
                                GCCTG TTT    CATATCCC
                                ||||| |||    ||||||||
                                CGGAC AAG    GTATAGGG
                                  _  _____
GAM47   UNC119   3'  TAGTCTGCTTTATTGTGCATC  612      C       ACACA
                                TAG CTGCTTTA     TATC
                                ||| ||||||||     ||||
                                ATC GACGAAAT     GTAG
                                  A       AACAC
GAM47   C20orf45 3'  TAACCTGCTTTTACAAATGTCC 613           A   C  A
                                TAGCCTGCTTT ACA AT TCC
                                |||||||||||| ||| || |||
                                ATTGGACGAAA TGT TA AGG
                                       A   T  C
GAM47   DDX18    3'  AGCCTGTTTTATATCCC     614        C    ACACA
                                AGCCTG TTTA     TATCCC
                                |||||| ||||     ||||||
                                TCGGAC AAAT     ATAGGG
                                   A   _____
GAM47   FLJ22246 3'  CAGCCTGCTTTGGTACAT    615           AAC
                                TAGCCTGCTTT   ACAT
                                ||||||||||   ||||
                                GTCGGACGAAA   TGTA
                                       CCA
GAM47   HS6ST    3'  GCATAAGTTAACACATATTCCA 616      C  CT        C
                                GC TG  TTAACACATAT CCA
                                || ||  |||||||||| |||
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                                CG AT  AATTGTGTATA GGT
                                 T  TC         A
GAM47   KIAA0205  3'  GCCTGTGGCCAAGCACATGTTC 617       CT_   _    A_
            C                    GCCTG   TTAA CACAT  TCC
                                 |||||   |||| |||||  |||
                                 CGGAC   GGTT GTGTA  AGG
                                    ACC    C     CA
GAM47   PADI1     3'  CAGCCTGCCTGTGCATGTCTCA 618          TAACA   A  C
                                 TAGCCTGCTT     CAT TC CA
                                 ||||||||||     ||| || ||
                                 GTCGGACGGA     GTA AG GT
                                       CAC__   C  A
GAM47   RI58      3'  GCCTGCTTTGCTAGAATATCC  619          AACAC_
                                 GCCTGCTTT      ATATCC
                                 |||||||||      ||||||
                                 CGGACGAAA      TATAGG
                                       CGATCT
GAM47   LOC115051 3'  GCATAAGTTAACACATATTCCA 616      C  CT         C
                                 GC TG  TTAACACATAT CCA
                                 || ||  |||||||||||| |||
                                 CG AT  AATTGTGTATA GGT
                                  T  TC         A
GAM47   LOC143310 3'  GCCTGCTTTGCACATCC     620          AACA
                                 GCCTGCTTT    CATATCC
                                 |||||||||    |||||||
                                 CGGACGAAA    GTGTAGG
                                       C___
GAM47   LOC147669 3'  GCCCTACCCTATATATATC    621       _      ACAC
                                 GCC TGCTTTA    ATATC
                                 ||| |||||||    |||||
                                 CGG ATGGGAT    TATAG
                                   G      ATA_
GAM47   LOC256530 3'  GCCTGCTTTCCAGATGTCCC   622          AA  C  A
                                 GCCTGCTTT  CA AT TCCC
                                 |||||||||  || || ||||
                                 CGGACGAAA  GT TA AGGG
                                       G_  C  C
GAM48   BCR       5'  CGGCGAGGCGCGGGCGCTGCTC 625      A  C  A   A      C
            T                    CG CG GG TGC GGCGCTGC CT
                                 || || || ||| |||||||| ||
                                 GC GC CC GCG CCGCGACG GA
                                  C  T  _   C       A
GAM48   BCR       5'  CGGCGAGGCGCGGGCGCTGCTC 625      A  C  A   A      C
            T                    CG CG GG TGC GGCGCTGC CT
                                 || || || ||| |||||||| ||
                                 GC GC CC GCG CCGCGACG GA
                                  C  T  _   C       A
GAM48   CALB1     5'  CGCGGGCGCTGCCGGGCGCTGT 626      A___   A_     C   III
            CCTA                    CGG    TGC  GGCGCTG CCT   A
                                 |||    |||  ||||||| |||   |
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                                GCC   ACG  CCGCGAC GGA   T
                                  CGCG   GC      A   III
GAM48   GRM6     3'  CGACGCGGAGCATGGTCT    627          T   _  CG
                                CGACGCGGA GCA GG  CT
                                |||||||||  ||| ||  ||
                                GCTGCGCCT CGT CC  GA
                                     _   A  A_
GAM48   GSTT2    5'  CGACGCGGTGTGGGCAGCAGC  628          A  CA   _  T
                                CGACGCGG TG  GGC GC GC
                                ||||||||  ||  ||| || ||
                                GCTGCGCC AC  CCG CG CG
                                     _ AC   T  T
GAM48   HADHA    3'  GCTGGGTGCAGAACTGCCCT   629      _  A     C
                                GC GG TGCAGG GCTGCCCT
                                || || |||||| ||||||||
                                CG CC ACGTCT TGACGGGA
                                 A  C     _
GAM48   NPAS2    5'  GCGGCGGGAGGCGCTGCTCT   630        ATGC        C
                                GCGG    AGGCGCTGC CT
                                ||||    |||||||||  ||
                                CGCC    TCCGCGACG GA
                                  GCCC        A
GAM48   13CDNA73 5'  GACGCGGTGCAGGCAGCC    631          A       CT
                                GACGCGG TGCAGGCG  GCC
                                |||||||  ||||||||  |||
                                CTGCGCC ACGTCCGT  CGG
                                     _      __
GAM48   Apg4B    3'  GCGGATGCACAGGCCC      632          AG   CT
                                GCGGATGC  GCG  GCCC
                                ||||||||  |||  ||||
                                CGCCTACG  TGT  CGGG
                                     __   C_
GAM48   FLJ12122 3'  CAGACGTGGGCGCTGCCC    633         CA
                                CGGATG  GGCGCTGCCC
                                ||||||  ||||||||||
                                GTCTGC  CCGCGACGGG
                                   AC
GAM48   HEAB     5'  ACGCGGTCGGCGCTGCCC    634         ATGCA
                                ACGCGG    GGCGCTGCCC
                                ||||||    ||||||||||
                                TGCGCC    CCGCGACGGG
                                   AG___
GAM48   HRK      3'  CGATCGCTCCAGGCGCTG    635      _  GGATG
                                CGA CGC    CAGGCGCTG
                                ||| |||    |||||||||
                                GCT GCG    GTCCGCGAC
                                  A  AG___
GAM48   SHANK3   5'  CGCGCCGGGGGCGCTGCCCT  636       GA  CA
                                CGCG  TG  GGCGCTGCCCT
                                ||||  ||  ||||||||||
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                                GCGC  GC  CCGCGACGGGA
                                  G_  CC
GAM48   TRIM36   5'  CGACGCGGGTGTATCGAATTTG 637          A  CAGG  C___  C
           TCCT                    CGACGCGG TG    CG    TG CCT
                                |||||||| ||    ||    || |||
                                GCTGCGCC AC    GC    AC GGA
                                     C  ATA_  TTAA  A
GAM48   LOC124590 5'  CACGGGAGACGCTGTCCT    638         ATGC       C
                                CGCGG    AGGCGCTG CCT
                                |||||    |||||||| |||
                                GTGCC    TCTGCGAC GGA
                                  C___       A
GAM48   LOC149506 3'  CGGTGCCAGGCGCTGCC     639       A  _       C
                                CGG TGC AGGCGCTGC C
                                ||| ||| ||||||||| |
                                GCC ACG TCCGCGACG G
                                  _  G        A
GAM48   LOC150290 3'  CATGTGCAATGGGTGCTGCCCT 640      GA   ___  C
                                CG  TGCA   GG GCTGCCCT
                                ||  ||||   || ||||||||
                                GT  ACGT   CC CGACGGGA
                                 AC    TAC  A
GAM48   LOC197201 3'  GGCTGCAGGCGTTGCCCT    641      A       C
                                GG TGCAGGCG TGCCCT
                                || |||||||| ||||||
                                CC ACGTCCGC ACGGGA
                                 G       A
GAM48   LOC96597  3'  CGCAGGCAGGTGCTGCC     642        AT    C
                                CGCGG  GCAGG GCTGCC
                                |||||  ||||| ||||||
                                GCGTC  CGTCC CGACGG
                                  __     A
GAM49   CACNA2D3  5'  ACCGGAGTACTTAGCAGCAAT  645      A          AA
                                ACC GAGTACTTGGCA  GAT
                                ||| ||||||||||||  |||
                                TGG CTCATGAATCGT  TTA
                                  C          CG
GAM49   EGR3      3'  ACCAAGTACCTTAGAGAT    646       G      GGCAA
                                ACCA AGTACTT     AGAT
                                |||| |||||||     ||||
                                TGGT TCATGGA     TCTA
                                  _      ATC__
GAM49   IL2RB     3'  CAGAGTAACAAAGAT       647          CTTG
                                CAGAGTA    GCAAAGAT
                                |||||||    ||||||||
                                GTCTCAT    TGTTTCTA
                                     _____
GAM49   WW45      3'  ACCAGAGTACTTGTTTGCAA   648              ___
                                ACCAGAGTACTTG   GCAA
                                ||||||||||||   ||||
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                                TGGTCTCATGAAC  CGTT
                                       AAA
GAM49   FLJ10830 3' ACCAGTAATGGTGAAGGTCTT 649      AGTACT  CA  A
                                ACCAG    TGG  AAG TCTT
                                |||||    |||  ||| ||||
                                TGGTC    ACC  TTC AGAA
                                   ATT___  AC  C
GAM49   FXYD3   3' GTATTTGGAAAGATCTT    650     C   C
                                GTA TTGG AAAGATCTT
                                ||| |||| |||||||||
                                CAT AACC TTTCTAGAA
                                  A  _
GAM49   FXYD3   3' GTATTTGGAAAGATCTT    650     C   C
                                GTA TTGG AAAGATCTT
                                ||| |||| |||||||||
                                CAT AACC TTTCTAGAA
                                  A  _
GAM49   KIAA0415 3' CAGAGTGTTGACAAAAA    651       AC
                                CAGAGT  TTGGCAAAGA
                                ||||||  ||||||||||
                                GTCTCA  AACTGTTTTT
                                   C_
GAM49   KIAA0997 5' ACCAGAGCTGCGGAGAT    652        ACT  CAA
                                ACCAGAGT  TGG  AGAT
                                ||||||||  |||  ||||
                                TGGTCTCG  GCC  TCTA
                                     AC_  ___
GAM49   MGC1203  3' AAAGTACTCACAAAGAT    653         G
                                AGAGTACTTG CAAAGAT
                                |||||||||| |||||||
                                TTTCATGAGT GTTTCTA
                                       _
GAM49   NMU     3' CAGAGTACATTTAGCAAGGAT 654         __     A
                                CAGAGTAC  TTGGCAA GAT
                                ||||||||  ||||||| |||
                                GTCTCATG  AATCGTT CTA
                                     TA     C
GAM49   PPP2R3A  3' CCAGGTAAGTTAAAGATCTT  655      A  CTTGGC
                                CCAG GTA     AAAGATCTT
                                |||| |||     |||||||||
                                GGTC CAT     TTTCTAGAA
                                  _  TCAA__
GAM49   RAB10   3' AGAGATAGCTAAAGATCTT   656      TACT  _
                                AGAG   TGGC AAAGATCTT
                                ||||   |||| |||||||||
                                TCTC   ATCG TTTCTAGAA
                                  T___   A
GAM49   YAP1    3' AGAGTATGTGGCAATAAT    657       CT    A
                                AGAGTA  TGGCAA GAT
                                ||||||  |||||| |||
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                                TCTCAT  ACCGTT TTA
                                   AC     A
GAM49   ZNF263   3'  CCAGGGTACTTGGCCCCTCTT  658       A       AAAGA
                                CCAG GTACTTGGC    TCTT
                                |||| |||||||||    ||||
                                GGTC CATGAACCG    AGAA
                                  C       GGG__
GAM49   LOC151446 5'  TACTCTTTGGTGAAGATCTT   659      ___  CA
                                TACT   TGG  AAGATCTT
                                ||||   |||  ||||||||
                                ATGA   ACC  TTCTAGAA
                                  GAA   AC
GAM49   LOC152445 3'  GCGGCCATGCAAAGATCTT   660     A_  TG
                                GT  CT  GCAAAGATCTT
                                ||  ||  ||||||||||
                                CG  GG  CGTTTCTAGAA
                                 CC  TA
GAM49   LOC197414 3'  AAGTACTTGGTGGATTCTT   661          CAAA  _
                                GAGTACTTGG    GAT CTT
                                ||||||||||    ||| |||
                                TTCATGAACC    CTA GAA
                                      AC__   A
GAM49   LOC222178 3'  CCAGGTCAAAGGCAAAGATCTT 662       A  ACTT
                                CCAG GT    GGCAAAGATCTT
                                |||| ||    ||||||||||||
                                GGTC CA    CCGTTTCTAGAA
                                  _ GTTT
GAM49   LOC254746 3'  CAGGGTCTTCACGAAGATCTT  663      A  A   G  A
                                CAG GT CTT GC AAGATCTT
                                ||| || ||| || ||||||||
                                GTC CA GAA TG TTCTAGAA
                                  C  _   G  C
GAM49   LOC51141  3'  CCAGAGTACTCAGAAGATCTT  664          TG CA
                                CCAGAGTACT  G  AAGATCTT
                                ||||||||||  |  ||||||||
                                GGTCTCATGA  C  TTCTAGAA
                                      GT __
GAM50   DISC1    3'  CAATTCAAGGCAGTTATT    667          A
                                TAATTCAG GCAGTTATT
                                |||||||| |||||||||
                                GTTAAGTT CGTCAATAA
                                     C
GAM50   GUK1     3'  TAATCCAACAGTTATT      668         GA
                                TAATTCA  GCAGTTATT
                                |||||||  |||||||||
                                ATTAGGT  TGTCAATAA
                                       __
GAM50   HYAL4    5'  AATTCAGAAGGTCAGTTATT   669          ___
                                AATTCAGAG   CAGTTATT
                                |||||||||   ||||||||
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                                TTAAGTCTT  GTCAATAA
                                     CCA
GAM50   PCDH11X  3' TAATTAGGGCAGTTATT    670      C  A
                                TAATT AG GCAGTTATT
                                ||||| || |||||||||
                                ATTAA TC CGTCAATAA
                                   _ C
GAM50   PCDH11X  3' TAATTAGGGCAGTTATT    670      C  A
                                TAATT AG GCAGTTATT
                                ||||| || |||||||||
                                ATTAA TC CGTCAATAA
                                   _ C
GAM50   PCDH11Y  3' TAATTAGGGCAGTTATT    670      C  A
                                TAATT AG GCAGTTATT
                                ||||| || |||||||||
                                ATTAA TC CGTCAATAA
                                   _ C
GAM50   PKHD1    3' TAATTCAGGGCATCATTATT  671       A  __
                                TAATTCAG GCA  GTTATT
                                |||||||| |||  ||||||
                                ATTAAGTC CGT  TAATAA
                                     C  AG
GAM50   SLC1A1   3' TAATTCTAACAGTTATT    672      AG
                                TAATTC  AGCAGTTATT
                                ||||||  ||||||||||
                                ATTAAG  TTGTCAATAA
                                   A_
GAM50   ZNF216   3' AATTCAGATGCATGTTATT  673       _  _
                                AATTCAGA GCA GTTATT
                                |||||||| ||| ||||||
                                TTAAGTCT CGT CAATAA
                                     A  A
GAM50   FLJ20136 3' TAACTCAGTTCAATTATT    674      AG
                                TAATTCAG  CAGTTATT
                                ||||||||  ||||||||
                                ATTGAGTC  GTTAATAA
                                     AA
GAM50   PABPC5   3' CAATTCAGCGCAGTTATT    675       A
                                TAATTCAG GCAGTTATT
                                |||||||| |||||||||
                                GTTAAGTC CGTCAATAA
                                     G
GAM50   LOC201627 3' TAATTCAAGACACAGCTATT  676       _ _
                                TAATTCA GA GCAGTTATT
                                ||||||| || |||||||||
                                ATTAAGT CT TGTCGATAA
                                     T  G
GAM50   LOC221362 3' TAATTCAGCAGCTGCTATT   677       _  A
                                TAATTCAG AGC GTTATT
                                |||||||| ||| ||||||
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                                ATTAAGTC TCG CGATAA
                                     G   A
GAM50   LOC91308 3'  AATTCAGGTGCAGTTATT    678        A_
                                AATTCAG  GCAGTTATT
                                |||||||  |||||||||
                                TTAAGTC  CGTCAATAA
                                    CA
GAM51   CNGB1    3'  CACCTGCTGGAACTGCGCGCG  681          AC   CTAC
                                CACCTGCTG  ACT   CGCG
                                |||||||||  |||   ||||
                                GTGGACGAC  TGA   GCGC
                                     CT   CGC_
GAM51   GPC1     3'  CACCCGCTGACACTGAGCG   682            CTACC
                                CACCTGCTGACACT    GCG
                                ||||||||||||||    |||
                                GTGGGCGACTGTGA    CGC
                                          CT___
GAM51   ICMT     3'  ACCTGCTACCCCTTTCTGC   683         A A   ACC_
                                ACCTGCTG C CTCT   GC
                                |||||||| | ||||   ||
                                TGGACGAT G GGGA   CG
                                     _ _   AAGA
GAM51   MBD3     3'  CACCTGCTGGCTGCTCTCCA  684          ACA_   A
                                CACCTGCTG   CTCT CCG
                                |||||||||   |||| |||
                                GTGGACGAC   GAGA GGT
                                     CGAC   _
GAM51   NRXN1    5'  CCTCCTGACACTTACGC     685      G      C   C
                                CCT CTGACACT TAC GC
                                ||| |||||||| ||| ||
                                GGA GACTGTGA ATG CG
                                  G       _   _
GAM51   SPINT2   5'  CCTGCGACACTCAACG      686       T     TACC
                                CCTGC GACACTC   GCG
                                ||||| |||||||   |||
                                GGACG CTGTGAG   TGC
                                   _      T___
GAM51   TIMM23   3'  CTCTGACACTCCCAGACG    687     G       ACC
                                CT CTGACACTCT   GCG
                                || ||||||||||   |||
                                GA GACTGTGAGG   TGC
                                  _        GTC
GAM51   CBCIP2   3'  CACCTGCTGGGCTGACGTGA  688          ACACT  AC  C
                                CACCTGCTG    CT  CG GA
                                |||||||||    ||  || ||
                                GTGGACGAC    GA  GC CT
                                     CC___  CT  A
GAM51   DRIL2    3'  CACCTGCTGGCACCCCTCATCG 689          A     ACCG
                                CACCTGCTG CACTCT   CG
                                |||||||| ||||||   ||
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                                GTGGACGAC GTGGGG   GC
                                    C     AGTA
GAM51   FLJ22246  5'  CACCCGCCCTTTCTGCCGCG  690        GACAC  A
                                CACCTGCT    TCT CCGCG
                                ||||||||    ||| |||||
                                GTGGGCGG    AGA GGCGC
                                    GAA__   C
GAM51   FLJ22671  3'  TGCTTGACAACACCACG    691      _   CTC
                                TGCT GACA   TACCGCG
                                |||| ||||   |||||||
                                ACGA CTGT   GTGGTGC
                                  A   T__
GAM51   KIAA0632  3'  CACCTGTGACACGCTGCG    692       C    T  ACC
                                CACCTG TGACAC CT   GCG
                                |||||| |||||| ||   |||
                                GTGGAC ACTGTG GA   CGC
                                  _     C ___
GAM51   KIAA1453  3'  CACCTGCTGGCCATTCACC   693        A_  C  T
                                CACCTGCTG  CA TC ACC
                                |||||||||  || || |||
                                GTGGACGAC  GT AG TGG
                                    CG  A  _
GAM51   MacGAP    3'  TACTAACATTCTGTCGTGA   694        C   AC  C
                                TGCTGACA TCT  CG GA
                                |||||||| |||  || ||
                                ATGATTGT AGA  GC CT
                                    A   CA  A
GAM51   MGC12837  5'  CACCAGCTGGCACCAGATCACC 695      T   A   C___
          G                      CACC GCTG CACT   TACCG
                                |||| |||| ||||   |||||
                                GTGG CGAC GTGG   GTGGC
                                  T   C   TCTA
GAM51   PRKCZ     3'  CCCGCTGACGCTTCCCTCTGCG 696        A  _  ACC_
                                CCTGCTGAC CT CT   GCG
                                ||||||||| || ||   |||
                                GGGCGACTG GA GG   CGC
                                    C  A  GAGA
GAM51   REV1L     5'  CACCGCTGAGCAGCGCCGCG  697      T   _  CTCTA
                                CACC GCTGA CA    CCGCG
                                |||| ||||| ||    |||||
                                GTGG CGACT GT    GGCGC
                                  _    C  CGC__
GAM51   LOC122769 5'  CCTGTTGGACTGGTCCGCGA  698      C  AC  CTA
                                CCTG TG  ACT   CCGCGA
                                |||| ||  |||   ||||||
                                GGAC AC  TGA   GGCGCT
                                  A  C_   CCA
GAM51   LOC128989 5'  CTGCTGACACAGGTCGCGA   699         TCTAC
                                CTGCTGACAC    CGCGA
                                ||||||||||    |||||
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                                GACGACTGTG    GCGCT
                                     TCCA_
GAM51   LOC130612 5'  CACCGGCTGGCACTCCAGTCCC 700       T   A     ___
           GCG                    CACC GCTG CACTCTA   CCGCG
                                  |||| |||| |||||||   |||||
                                  GTGG CGAC GTGAGGT   GGCGC
                                    C   C      CAG
GAM51   LOC147080 3'  CTGCTGACACTCTGC       701             ACC
                                  CTGCTGACACTCT   GC
                                  ||||||||||||   ||
                                  GACGACTGTGAGA   CG
                                        ___
GAM51   LOC147165 3'  CACCTGCTCCACGCTGTCGCG  702          GA   T  AC
                                  CACCTGCT  CAC CT  CGCG
                                  ||||||||  ||| ||  ||||
                                  GTGGACGA  GTG GA  GCGC
                                       G_   C  CA
GAM51   LOC149657 3'  CACCTGCTGTGTACGCG     703          ACACTC   C
                                  CACCTGCTG     TAC GCG
                                  |||||||||     ||| |||
                                  GTGGACGAC     ATG CGC
                                       AC_____   _
GAM51   LOC157503 3'  CCTGCTGACAGTGGCCTCCCGC 704           C___   A
           GA                     CCTGCTGACA    TCT CCGCGA
                                  ||||||||||    ||| ||||||
                                  GGACGACTGT    GGA GGCGCT
                                        CACC   G
GAM51   LOC220537 3'  CACCTGCCTTTCCTGCCGCG   705         GACAC   A
                                  CACCTGCT     TCT CCGCG
                                  ||||||||     ||| |||||
                                  GTGGACGG     GGA GGCGC
                                       AAA__   C
GAM51   LOC221466 5'  CACCTGCTGGCACACACA     706          A   TCTAC
                                  CACCTGCTG CAC     CGCG
                                  ||||||||| |||     ||||
                                  GTGGACGAC GTG     GTGT
                                       C   T_____
GAM51   LOC221755 3'  TGCTGACATTACACGA      707          CTC   C
                                  TGCTGACA   TAC GCGA
                                  ||||||||   ||| ||||
                                  ACGACTGT   ATG TGCT
                                       A__   _
GAM51   LOC255028 5'  CACCGCTGACCGCCGCG     708       T     ACTCTA
                                  CACC GCTGAC      CCGCG
                                  |||| ||||||      |||||
                                  GTGG CGACTG      GGCGC
                                    _     GC_____
GAM51   LOC92305  3'  CACCTGCTGAGCGCTCTA     709           CA_
                                  CACCTGCTGA   CTCTA
                                  ||||||||||   |||||
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                                GTGGACGACT   GAGAT
                                     CGC
GAM51   LOC93512 3'  CACCTGCTCCACGCTGTCGCG  702         GA   T  AC
                                CACCTGCT  CAC CT  CGCG
                                ||||||||  ||| ||  ||||
                                GTGGACGA  GTG GA  GCGC
                                    G_   C  CA
GAM52   AGTR1    3'  TAGAAAAGTCGGTTCAG     712      T   A  A
                                TAG AAAA TC GTTCAG
                                ||| |||| || ||||||
                                ATC TTTT AG CAAGTC
                                  _   C  C
GAM52   AGTR1    3'  TAGAAAAGTCGGTTCAG     712      T   A  A
                                TAG AAAA TC GTTCAG
                                ||| |||| || ||||||
                                ATC TTTT AG CAAGTC
                                  _   C  C
GAM52   AGTR1    3'  TAGAAAAGTCGGTTCAG     712      T   A  A
                                TAG AAAA TC GTTCAG
                                ||| |||| || ||||||
                                ATC TTTT AG CAAGTC
                                  _   C  C
GAM52   AGTR1    3'  TAGAAAAGTCGGTTCAG     712      T   A  A
                                TAG AAAA TC GTTCAG
                                ||| |||| || ||||||
                                ATC TTTT AG CAAGTC
                                  _   C  C
GAM52   AGTR1    3'  TAGAAAAGTCGGTTCAG     712      T   A  A
                                TAG AAAA TC GTTCAG
                                ||| |||| || ||||||
                                ATC TTTT AG CAAGTC
                                  _   C  C
GAM52   CDH6     3'  GCCAGAAGGATTAGTTCAGT   713      A   T  AA  C
                                GC TAG AA  AT AGTTCAGT
                                || ||| ||  || ||||||||
                                CG GTC TT  TA TCAAGTCA
                                 _  _ CC  A
GAM52   CRADD    3'  TAGTAAAGTCCACAGTTCAGT  714         AAT__
                                TAGTAAA    CAGTTCAGT
                                |||||||    |||||||||
                                ATCATTT    GTCAAGTCA
                                    CAGGT
GAM52   ID4      3'  TAGCTATAGTGAAAATCA     715       _    A
                                TAGC ATAGT AAAATCA
                                |||| ||||| |||||||
                                ATCG TATCA TTTTAGT
                                  A    C
GAM52   OTC      5'  ATAGTAAAAATATCTCAGT    716           CAG
                                ATAGTAAAAAT   TTCAGT
                                ||||||||||   ||||||
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                                TATCATTTTTA   GAGTCA
                                      TA_
GAM52   UGP2     3'  TAACATAGTAAAGTACCTTTTA 717            A_   AG  C
            GT                   TAGCATAGTAAA  ATC  TT AGT
                                 ||||||||||||  |||  || |||
                                 ATTGTATCATTT  TGG  AA TCA
                                       CA   AA  _
GAM52   BRP44I   3'  TAGTAAAAATAGCATTCAGT   718           CA_
                                 TAGTAAAAAT   GTTCAGT
                                 ||||||||||   |||||||
                                 ATCATTTTTA   TAAGTCA
                                      TCG
GAM52   FLJ12891  3'  GCAAGATAAAAAATCAGTTTAG 719       TA      _     C
            T                     GCA  GTAAAAA TCAGTT AGT
                                  |||  ||||||| |||||| |||
                                  CGT  TATTTTT AGTCAA TCA
                                    TC      T     A
GAM52   GZMK     3'  CAGCATGGTAGAAATACATCAG 720         A   A    _  GT
            T                     TAGCAT GTA AAAT CA  TCAGT
                                  ||||||| ||| |||| ||  |||||
                                  GTCGTA CAT TTTA GT  AGTCA
                                     C   C    T  __
GAM52   HSA243666 3'  TAGCATAGGTAAGGAGGCTCTA 721           _   AAATCA   _
            GT                    TAGCATAG TAA     GTTC AGT
                                  |||||||| |||     |||| |||
                                  ATCGTATC ATT     CGAG TCA
                                       C   CCTC__    A
GAM52   MAFB     3'  AGCATAGCAGTTGGTTCAGT   722           AAAATCA
                                  AGCATAGTA      GTTCAGT
                                  |||||||||      |||||||
                                  TCGTATCGT      CAAGTCA
                                       CAAC___
GAM52   MBLL39    3'  CATAGTAAAAAATACAGT    723            TCAGTT
                                  CATAGTAAAAA     CAGT
                                  ||||||||||     ||||
                                  GTATCATTTTT     GTCA
                                       TAT___
GAM52   MGC4309   3'  TAGCATGTGGAATCAGT     724         A  AAA
                                  TAGCAT GT   AATCAGT
                                  |||||| ||   |||||||
                                  ATCGTA CA   TTAGTCA
                                     _  CC_
GAM52   ZNF294    3'  GCTGGTAAGAATAGCTCAGT   725      ATA    A   C
                                  GC   GTAA AAT AGTTCAGT
                                  ||   |||| ||| ||||||||
                                  CG   CATT TTA TCGAGTCA
                                   AC_    C   _
GAM53   ADCY3     5'  TCTCTGAGACCGGGGGAGG    728          AAA  G  A
                                  TCTCTGGG   GC GG GGGAGG
                                  ||||||||   || || ||||||
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                                AGAGACTC   TG CC CCCTCC
                                    ___  G  _
GAM53   ATP1B2   3'  TCTGGGAAGGCGAATGGGGG   729          A    A   A
                                TCTGGGAA GCGGG GGG GG
                                |||||||| ||||| ||| ||
                                AGACCCTT CGCTT CCC CC
                                     C    A   _
GAM53   CACNB1   3'  TCTCTAGGAGGGTGAGGG    730          AA C  _
                                TCTCTGGGA  G GG GAGGG
                                |||||||||  | || |||||
                                AGAGATCCT  C CC CTCCC
                                    __ _  A
GAM53   CARP     5'  TCTGGGAAGCTGAAGAGGGAGG 731          A  __
          G                      TCTGGGAA GC  GGGAGGGAGGG
                                |||||||| ||  ||||||||||
                                AGACCCTT CG  TTCTCCCTCCC
                                     _  AC
GAM53   CELSR2   3'  TCTTTGGGAAGGGAAAGGG   732      C     AGC      A
                                TCT TGGGAA   GGGAGGG GG
                                ||| ||||||   ||||||| ||
                                AGA ACCCTT   CCCTTTC CC
                                  A     ____      _
GAM53   CYLN2    5'  TCTCTGGGAAGGCGGGAGG   733          A
                                TCTCTGGGAA GCGGGAGG
                                |||||||||| ||||||||
                                AGAGACCCTT CGCCCTCC
                                      C
GAM53   DUSP4    5'  CTTTGGGGAGAAGGGAGG    734      C   AAAGC
                                CT TGGG    GGGAGGGAGG
                                || ||||    ||||||||||
                                GA ACCC    TCTTCCCTCC
                                 A   C____
GAM53   EFNB1    3'  CCTGGGAAGGTGGCAAGGGGGG 735          AGC  _    A
                                TCTGGGAA   GG GAGGG GGG
                                ||||||||   || ||||| |||
                                GGACCCTT   CC TTCCC CCC
                                     CCA  G    _
GAM53   EGR3     5'  TGGGGGGCGGGAGAGGG     736       AAA       A
                                TGGG   GCGGGAGGG GG
                                ||||   ||||||||| ||
                                ACCC   CGCCCTCTC CC
                                  CC_       _
GAM53   EIF4EBP1 3'  TCTCTTGGGGAAGGAGGGGGAG 737        _  A   C   A
          GG                     TCTCT GGG AAG GGG GGGAGGG
                                ||||| ||| ||| ||| |||||||
                                AGAGA CCC TTC TCC CCCTCCC
                                  A   C   C   _
GAM53   GNA11    3'  TCCCTGGGGGAGCCGGGGG   738          AA   G  A
                                TCTCTGGG  AGC GG GGG
                                ||||||||  ||| || |||
```

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                                AGGGACCC  TCG CC CCC
                                    CC   G  _
GAM53   GPR17    3'  TCTCTGGAGGAAGTGGGTCTGG 739        _ A   C   A__
           G                     TCTCTGG G AAG GGG   GGG
                                 ||||||| | ||| |||   |||
                                 AGAGACC C TTC CCC   CCC
                                    T C   A   AGA
GAM53   IER5     3'  TCATTGGGAGAGAAAGGTGGGG 740     TC    A  C__  GA
           AGGG                  TC  TGGGA AG   GG  GGGAGGG
                                 ||  ||||| ||   ||  |||||||
                                 AG  ACCCT TC   CC  CCCTCCC
                                  TA    C  TTT  AC
GAM53   IGFBP1   5'  TCTCTGGGAGGGTGGG     741          AAGC   AG  A
                                 TCTCTGGGA    GGG  GG G
                                 |||||||||    |||  || |
                                 AGAGACCCT    CCC  CC C
                                      ____   A_  G
GAM53   ITGA5    3'  TCTCTGGGGAACAGGGAGGG   742         AA  _
                                 TCTCTGGG  AGC GGGAGGG
                                 ||||||||  ||| |||||||
                                 AGAGACCC  TTG CCCTCCC
                                    C_   T
GAM53   ITGA7    3'  TCTCTGGGGAAGGGATGGAGGG 743         AAAGC    G
                                 TCTCTGGG    GGGA GGAGGG
                                 ||||||||    |||| ||||||
                                 AGAGACCC    CCCT CCTCCC
                                    CTT__    A
GAM53   MCL1     3'  TCTTGGTGGGGAGGGAGG    744      C   GAAAGC
                                 TCT TGG     GGGAGGGAGG
                                 ||| |||     ||||||||||
                                 AGA ACC     CCCTCCCTCC
                                   _   AC____
GAM53   MUCDHL   3'  TCCCTGGGAGGGCTCAGGGGG  745         AA  GGG   A
                                 TCTCTGGGA  GC   AGGG GG
                                 |||||||||  ||   |||| ||
                                 AGGGACCCT  CG   TCCC CC
                                      CC  AG_   _
GAM53   MUCDHL   3'  TCCCTGGGAGGGCTCAGGGGG  745         AA  GGG   A
                                 TCTCTGGGA  GC   AGGG GG
                                 |||||||||  ||   |||| ||
                                 AGGGACCCT  CG   TCCC CC
                                      CC  AG_   _
GAM53   NLGN3    3'  TCCTGGATCTGGGAGGGAGGG  746     T    AAAGC
                                 TC CTGGG    GGGAGGGAGGG
                                 || |||||    ||||||||||
                                 AG GACCT    CCCTCCCTCCC
                                   _    AGA__
GAM53   NTE      3'  TCCAGGGGTGGGAGGGAGGG   747      TG  AAAGC
                                 TC  GG    GGGAGGGAGGG
                                 ||  ||    ||||||||||
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                                AG  CC    CCCTCCCTCCC
                                 GT  CCA__
GAM53   PAPOLA   5'  TCCACTGAGGCGGGAGGGAGGG 748      _    AAA
                                TCT CTGGG   GCGGGAGGGAGGG
                                ||| |||||   ||||||||||||
                                AGG GACTC   CGCCCTCCCTCCC
                                  T   ____
GAM53   PFKM     5'  TCCTTGGGAAAGGGGGGAGGG  749      TC      GC   A
                                TC  TGGGAAA  GGG GGGAGGG
                                ||  |||||||  ||| |||||||
                                AG  ACCCTTT  CCC CCCTCCC
                                 GA      __  _
GAM53   PKD2     3'  CTGGGGAAACAGGGAGGG    750        A   _
                                CTGGG AAGC GGGAGGG
                                ||||| |||| |||||||
                                GACCC TTTG CCCTCCC
                                   C    T
GAM53   PPEF1    5'  TCTCTGGGGAAATGCAGAGGG  751          _  _   G
                                TCTCTGGG AAA GCGG AGGG
                                |||||||| ||| |||| ||||
                                AGAGACCC TTT CGTC TCCC
                                     C   A   _
GAM53   PPP1R12B  3'  CCTTTGGGGGATTAGAAGGGAG 752       C    AAAGC
            GG                    TCT TGGG    GGGAGGGAGGG
                                ||| ||||    ||||||||||
                                GGA ACCC    TCTTCCCTCCC
                                  A   CCTAA
GAM53   PRKWNK3   3'  TGGGGGGGCTAAGGAGGG    753       AAAGC   __
                                TGGG    GGG  AGGGAGGG
                                ||||    |||  ||||||||
                                ACCC    CCC  TTCCTCCC
                                  C____   GA
GAM53   RARA     3'  TCTCCAGTGGGAGGGAGGG    754        GGGAA  C
                                TCTCT    AG GGGAGGGAGGG
                                |||||    || ||||||||||
                                AGAGG    TC CCCTCCCTCCC
                                   _____  A
GAM53   STK11    3'  TCTCCGGGAGGGCGGGCGG    755          AA    A
                                TCTCTGGGA  GCGGG GG
                                |||||||||  ||||| ||
                                AGAGGCCCT  CGCCC CC
                                     CC    G
GAM53   TNFRSF11A 3'  TCTCTGGGGGGGGGGAGTCGGG 756          AAAGC    __  A
            GG                    TCTCTGGG    GGGAG  GG GGG
                                ||||||||    |||||  || |||
                                AGAGACCC    CCCTC  CC CCC
                                    CCCC_    AG  _
GAM53   TNFRSF1B  3'  CCTCTGGGGGAGGAGGAGGG   757          AA  C
                                TCTCTGGG  AG GGGAGGG
                                ||||||||  || |||||||
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                                GGAGACCC  TC TCCTCCC
                                    CC  C
GAM53   WNT8B    3'  TCTGGGAAAGGAAAGGG     758          C GG
                                TCTGGGAAAG G  AGGG
                                |||||||||| |  ||||
                                AGACCCTTTC C  TCCC
                                     _ TT
GAM53   AEBP1    5'  TCTCTGGGAAAGGGCGGAGAGG 759            C  GA
           G                     TCTCTGGGAAAG GG  GGGAGGG
                                ||||||||||| ||  |||||||
                                AGAGACCCTTTC CC  CTCTCCC
                                      _ GC
GAM53   ASE-1    3'  TCTCTGGGGAGGGATTCTGGGG 760          AAAGC   _____   A
           G                     TCTCTGGG    GGGA   GGG GG
                                ||||||||    ||||   ||| ||
                                AGAGACCC    CCCT   CCC CC
                                    CT___   AAGA  _
GAM53   CENTG1   3'  CTCCAGTGGGAGGGAGG     761       GGGAA  C
                                CTCT    AG GGGAGGGAGG
                                ||||    || ||||||||||
                                GAGG    TC CCCTCCCTCC
                                  _____  A
GAM53   CNNM1    3'  GGGAGGTGGGAGGGAGGG    762       AAGC
                                GGGA   GGGAGGGAGGG
                                ||||   ||||||||||
                                CCCT   CCCTCCCTCCC
                                  CCA_
GAM53   DKFZp547O146 3'  TCTCTGGGAGCTGGGGAGGG   763          AA __
                                TCTCTGGGA  GC  GGGAGGG
                                |||||||||  ||  |||||||
                                AGAGACCCT  CG  CCCTCCC
                                     __ AC
GAM53   DRIL2    3'  TGGGAAAGCAGGCCAATAAGGG 764            AGG__
                                TGGGAAAGCGGG    GAGGG
                                ||||||||||||    |||||
                                ACCCTTTCGTCC    TTCCC
                                      GGTTA
GAM53   FLJ10357  3'  TCTCAGGGAAAGTCAGGGGG   765       T     _   A
                                TCTC GGGAAAG CGGG GGG
                                |||| ||||||| |||| |||
                                AGAG CCCTTTC GTCC CCC
                                  T      A   _
GAM53   FLJ10925  3'  TCTCAGCCCTGCGGGAGGGAGG 766      G  AAA_
           G                     TCT GG   GCGGGAGGGAGGG
                                ||| ||   ||||||||||||
                                AGA TC   CGCCCTCCCTCCC
                                  G  GGGA
GAM53   FLJ11078  3'  CTTTGGGAAGGAGGGAGGGAGG 767     C     AGC
           G                     CT TGGGAA   GGGAGGGAGGG
                                || ||||||   ||||||||||
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                              GA ACCCTT   CCCTCCCTCCC
                               A     CCT
GAM53   FLJ11703  3' TCTCTGGAGTCAGCTGAGGGAG 768         AA_   GG
           GG                  TCTCTGGG   AGC  GAGGGAGGG
                              ||||||||   |||  |||||||||
                              AGAGACCT   TCG  CTCCCTCCC
                                  CAG   A_
GAM53   FLJ11783  5' TCTCTAGGAGGGAGGGAGG   769          AAGC
                              TCTCTGGGA   GGGAGGGAGG
                              |||||||||   ||||||||||
                              AGAGATCCT   CCCTCCCTCC
                                   ____
GAM53   FLJ12572  3' TCTGTGGGACCAGGGGAGGGAG 770      C    A_  C
           GG                  TCT TGGGA  AG GGGAGGGAGGG
                              ||| |||||  || ||||||||||
                              AGA ACCCT  TC CCCTCCCTCCC
                                C    GG  _
GAM53   FLJ13154  3' TCTCTGGGAAAGCTGCTGGG   771            GGGA
                              TCTCTGGGAAAGC   GGG
                              ||||||||||||   |||
                              AGAGACCCTTTCG   CCC
                                     ACGA
GAM53   FLJ14346  3' CTCTGGGAAGGTGGGAG    772          AAGC   A
                              CTCTGGGA   GGG GGGAG
                              ||||||||   ||| |||||
                              GAGACCCT   TCC CCCTC
                                   _____  A
GAM53   FLJ20507  3' TCTACTGGGAGAGACTCGGGGA 773      _     A  _ GGGA
           GGG                   TCT CTGGGA AG C   GGGAGGG
                              ||| |||||| || |   |||||||
                              AGA GACCCT TC G   CCCTCCC
                                T     C  T AGC_
GAM53   FLJ20507  3' TCTACTGGGAGAGACTCGGGGA 773      _     A  _ GGGA
           GGG                   TCT CTGGGA AG C   GGGAGGG
                              ||| |||||| || |   |||||||
                              AGA GACCCT TC G   CCCTCCC
                                T     C  T AGC_
GAM53   FLJ21369  3' CTGCTGGGGGGTGGGGGGGGGGG 774     _    AAAGC   A   A
                              CT CTGGG    GGG GGG GGG
                              || |||||    ||| ||| |||
                              GA GACCC    CCC CCC CCC
                               C    CCACC  _  _
GAM53   FLJ21438  5' TCTCCGGGAGAGTTGGGGGG   775          A  CG  A
                              TCTCTGGGA AG  GG GGG
                              ||||||||| ||  || |||
                              AGAGGCCCT TC  CC CCC
                                   C  AA  _
GAM53   FLJ22357  5' TCTCTGGGGGGTCCTGAGG   776          AAAGC   AGG_
                              TCTCTGGG    GGG   GAGG
                              ||||||||    |||   ||||
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                                AGAGACCC    CCC   CTCC
                                      _____  AGGA
GAM53   H2AV     3'  TCGCTGGAACCCGGGAGGGAGG 777     T     AAG
              G                    TC CTGGGA   CGGGAGGGAGGG
                                   || ||||||   ||||||||||||
                                   AG GACCTT   GCCCTCCCTCCC
                                    C     GG_
GAM53   ITGB8    3'  TCTCTGGGAAGCGTAGGG    778           A   GG
                                   TCTCTGGGAA GCG  AGGG
                                   |||||||||| |||  ||||
                                   AGAGACCCTT CGC  TCCC
                                         _  A_
GAM53   KIAA0194 3'  TGGGGGAAGAGGGAGGG     779       AAAGC
                                   TGGG    GGGAGGGAGGG
                                   ||||    ||||||||||
                                   ACCC    TTCTCCCTCCC
                                     CC___
GAM53   KIAA0317 3'  TCTCTGGAAGGCTGCCGGAGGG 780          AA__  G
                                   TCTCTGGGA   GC GGAGGG
                                   |||||||||   || ||||||
                                   AGAGACCTT   CG CCTCCC
                                        CCGA  G
GAM53   KIAA0544 3'  CCTCTGGGAAGGCAGAGGG   781          A   G
                                   TCTCTGGGAA GCGG AGGG
                                   |||||||||| |||| ||||
                                   GGAGACCCTT CGTC TCCC
                                         C   _
GAM53   KIAA0676 3'  CCTGGGAGAGCAGGAGGG    782         A
                                   TCTGGGA AGCGGGAGGG
                                   ||||||| ||||||||||
                                   GGACCCT TCGTCCTCCC
                                       C
GAM53   KIAA0854 5'  TGGAGGGGGATAAGGAGGG   783      GAA  C   __
                                   TGG   AG GGGA  GGGAGGG
                                   |||   || ||||  |||||||
                                   ACC   TC CCCT  TCCTCCC
                                     ___  C    AT
GAM53   KIAA1061 5'  TGGGCGGGAGGGAGG       784      GAAA
                                   TGG    GCGGGAGGGAGG
                                   |||    ||||||||||||
                                   ACC    CGCCCTCCCTCC
                                     _____
GAM53   KIAA1169 3'  TCTCTGTGAAAGGGAGGG    785        G   GC
                                   TCTCTG GAAA  GGGAGGG
                                   |||||| ||||  |||||||
                                   AGAGAC CTTT  CCCTCCC
                                      A   __
GAM53   KIAA1196 3'  TCCCTGGGGAATGGGGGAGGG  786          AAAGCG  A
                                   TCTCTGGG     GG GGGAGGG
                                   ||||||||     || |||||||
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                                AGGGACCC     CC CCCTCCC
                                     CTTA__ _
GAM53   KIAA1671  3'  TCTGGGAAGGCCAAAGGGGAGG 787          A  G    _
            G                    TCTGGGAA GC GGAGGG AGGG
                                 |||||||| || |||||| ||||
                                 AGACCCTT CG TTTCCC TCCC
                                      C  G     C
GAM53   KIAA1870  3'  TCTTTGGGCAGGAAGCTGGGGA 788     C   GAAA     _____
            GGG                    T TGG    GCGGGA    GGGAGGG
                                 | |||   ||||||    |||||||
                                 A ACC    CGTCCT    CCCTCCC
                                  A  ____     TCGAC
GAM53   KNSL6    3'  TCTCTGGGGAGGGCCAGG    789          AAAGCGG    __
                                 TCTCTGGG      GAGGG  AGG
                                 ||||||||      |||||  |||
                                 AGAGACCC      CTCCC  TCC
                                      ________    GG
GAM53   NFAT5    5'  CTGCCAGGGTGGGAGGGGGG   790     _ TG  AAAGC      A
                                 CT C  GG     GGGAGGG GGG
                                 || |  ||    ||||||| |||
                                 GA G  CC     CCCTCCC CCC
                                  C GT  CA___      _
GAM53   NUCKS    3'  TCATTGGGAAAGGGGAGGG   791      TC       C
                                 TC  TGGGAAAG GGGAGGG
                                 ||  |||||||| |||||||
                                 AG  ACCCTTTC CCCTCCC
                                  TA       _
GAM53   OS4      3'  TCTCTGGGGCAAGTGGGAATGG 792          AAA    A    _
                                 TCTCTGGG   GCGGG GGGAG GG
                                 ||||||||   ||||| ||||| ||
                                 AGAGACCC   CGTTC CCCTT CC
                                      ___     A     A
GAM53   PGCP     3'  TCTATGTGGTGGGAGGGAGGG  793       C  _  AAAGC
                                 TCT TG GG     GGGAGGGAGGG
                                 ||| || ||     ||||||||||
                                 AGA AC CC     CCCTCCCTCCC
                                   T  A  A____
GAM53   RPL36    3'  TCAGGGAGAGGGCAGGGGAGGG 794      T    A  C  G    _
                                 TC GGGA AG GG AGGG AGGG
                                 || |||| || || |||| ||||
                                 AG CCCT TC CC TCCC TCCC
                                  T    C  _  G    C
GAM53   RPL36    3'  TCAGGGAGAGGGCAGGGGAGGG 794      T    A  C  G    _
                                 TC GGGA AG GG AGGG AGGG
                                 || |||| || || |||| ||||
                                 AG CCCT TC CC TCCC TCCC
                                  T    C  _  G    C
GAM53   SCAMP-4  3'  CTCTGGGAGGACGGGAGGG   795          AA
                                 CTCTGGGA  GCGGGAGGG
                                 ||||||||  |||||||||
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                                GAGACCCT  TGCCCTCCC
                                    CC
GAM53   SEMA6C   3'  TCTCTGGGGGAGCCCCGAGGG  796        AA  GG_
                                TCTCTGGG  AGC  GAGGG
                                ||||||||  |||  |||||
                                AGAGACCC  TCG  CTCCC
                                    CC  GGG
GAM53   SLC26A9  3'  TCTCTGGAGATGCGGGGAGGG  797        AAA   _
                                TCTCTGGG  GCGGG AGGG
                                ||||||||  ||||| ||||
                                AGAGACCT  CGCCC TCCC
                                    CTA   C
GAM53   TNFAIP3  3'  TCTCTGAGAGATGCTGGGGGAG 798        AA_  G  A
           GG                     TCTCTGGGA  GC GG GGGAGGG
                                ||||||||||  || || |||||||
                                AGAGACTCT  CG CC CCCTCCC
                                     CTA  A  _
GAM53   ZNF185   3'  CCTTTGGGAGGCCTGAAGGGAG 799      C    AA  G_
           GG                     TCT TGGGA  GC  GGAGGGAGGG
                                ||| |||||  ||  ||||||||||
                                GGA ACCCT  CG  CTTCCCTCCC
                                  A    C_  GA
GAM53   LOC115574 3'  TGGGAGGGAGGGAGGG     800       AAGC
                                TGGGA   GGGAGGGAGGG
                                |||||   ||||||||||
                                ACCCT   CCCTCCCTCCC
                                  ____
GAM53   LOC116411 5'  TGGAAAGAGCGGGGGGGGGG  801       _    A  A
                                TGGGAA AGCGGG GGG GGG
                                ||||||  ||||||  ||| |||
                                ACCTTT TCGCCC CCC CCC
                                   C     _  C
GAM53   LOC143903 5'  GGGAGGCGGGGGGGAGGG   802      AA   A
                                GGGA  GCGGG GGGAGGG
                                ||||  |||||  |||||||
                                CCCT  CGCCC CCCTCCC
                                  C_    C
GAM53   LOC147136 3'  CCTGGGAGTGAAGGGAGG   803       AAGCG
                                TCTGGGA   GGAGGGAGG
                                |||||||   |||||||||
                                GGACCCT   CTTCCCTCC
                                    CA___
GAM53   LOC147694 3'  TCTGGGGAAGTAGGGAAGG  804       A  C_
                                TCTGGG AAG  GGGAGGG
                                ||||||  |||  |||||||
                                AGACCC TTC  CCCTTCC
                                   C  AT
GAM53   LOC148529 5'  TCTCTGGAAAAGCTAAGAGGG  805          _
                                TCTCTGGGAAAGC GGGAGGG
                                |||||||||||| |||||||
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                                AGAGACCTTTTCG TTCTCCC
                                       A
GAM53   LOC149077 3'  TCTCTGGGGTGAGGCTGGAGGG 806          AAAGC   AG
                                TCTCTGGG    GGG  GGAGGG
                                ||||||||    |||  ||||||
                                AGAGACCC    TCC  CCTCCC
                                    CAC__   GA
GAM53   LOC149448 3'  CTTTGGGGTGGTGGGAGGGAGG 807      C    AAAGC
          G                      CT TGGG    GGGAGGGAGGG
                                || ||||    ||||||||||
                                GA ACCC    CCCTCCCTCCC
                                 A   CACCA
GAM53   LOC157737 5'  TGGGGAAACGGGACTTGGG   808        A       ___
                                TGGG AAGCGGGA   GGG
                                |||| ||||||||   |||
                                ACCC TTTGCCCT   CCC
                                  C       GAA
GAM53   LOC219700 5'  TCCCTGGGGCTGTGGGAGGGAG 809          AAAGC
          GG                     TCTCTGGG    GGGAGGGAGGG
                                ||||||||    ||||||||||
                                AGGGACCC    CCCTCCCTCCC
                                    CGACA
GAM53   LOC219848 3'  TCTCTGGGAGGCTGGGAATGG  810          AA  _    _
                                TCTCTGGGA  GC GGGAG GG
                                |||||||||  || ||||| ||
                                AGAGACCCT  CG CCCTT CC
                                    C_  A    A
GAM53   LOC221511 3'  TCTCGGGAAGGTGACAGTGAGG 811       T    A___   _
          G                     TCTC GGGAA   GCGG GAGGG
                                |||| |||||   |||| |||||
                                AGAG CCCTT   TGTC CTCCC
                                  _    CCAC   A
GAM53   LOC222166 3'  TCTCAGGGGAGGGAGGAGG   812       T_   AAGC     G
                                TCTC  GGGA   GGGAGG AGG
                                ||||  ||||   |||||| |||
                                AGAG  CCCT   CCCTCC TCC
                                  TC   ____    _
GAM53   LOC253115 5'  TCCCTGGGGGAACTGGGAGGG  813          AA  _
                                TCTCTGGG  AGC GGGAGGG
                                ||||||||  ||| |||||||
                                AGGGACCC  TTG CCCTCCC
                                    CC   A
GAM53   LOC254205 5'  TCTCGGGGAGGGCGTCGGGGG  814       T   AA   GGA   A
                                TCTC GGGA  GCG   GGG GG
                                |||| ||||  |||   ||| ||
                                AGAG CCCT  CGC   CCC CC
                                  C   CC   AG_  _
GAM53   LOC257220 5'  TCTTTGGGCAGGAAGCTGGGGA 788    C   GAAA    _____
          GGG                    T TGG   GCGGGA    GGGAGGG
                                | |||   ||||||    |||||||
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                                A ACC    CGTCCT     CCCTCCC
                                 A  _____      TCGAC
GAM53   LOC257556 5'  TCCCTGGGGGAACTGGGAGGG  813          AA  _
                                TCTCTGGG  AGC GGGAGGG
                                ||||||||  ||| |||||||
                                AGGGACCC  TTG CCCTCCC
                                    CC   A
GAM53   LOC257569 3'  TCTCGGGAAGGTGACAGTGAGG 811        T    A___   _
          G                      TCTC GGGAA    GCGG GAGGG
                                |||| |||||    |||| |||||
                                AGAG CCCTT    TGTC CTCCC
                                  _    CCAC    A
GAM53   LOC257617 5'  TCCCTGGGGGAACTGGGAGGG  813          AA  _
                                TCTCTGGG  AGC GGGAGGG
                                ||||||||  ||| |||||||
                                AGGGACCC  TTG CCCTCCC
                                    CC   A
GAM53   LOC91409  3'  TCTCTGAGGAAGTGGTTTAGGG 815          A   C  GAGGG
                                TCTCTGGG AAG GG     AGGG
                                |||||||| ||| ||     ||||
                                AGAGACTC TTC CC     TCCC
                                    C   A  AAA__
GAM53   LOC91974  5'  CCTGGGAAGACACTGGGGAGGG 816          AG  GGA
                                TCTGGGAA  CG   GGGAGGG
                                ||||||||  ||   |||||||
                                GGACCCTT  GT   CCCTCCC
                                    CT  GAC
GAM54   DYT1      3'  CAGAAACACTTGGAATTAA    819          TATA    A
                                TAGAAAC    ACTT GAATTAA
                                |||||||    |||| |||||||
                                GTCTTTG    TGAA CTTAATT
                                    _____    C
GAM54   CBX8      3'  TAGAAAATATAACTCTAGA    820         C       _
                                TAGAAA TATAACTT AGA
                                |||||| |||||||| |||
                                ATCTTT ATATTGAG TCT
                                   T       A
GAM54   DKFZP434F1017 3'  TAGAAACTATATTTACTTA    821            ___
                                TAGAAACTATA   ACTTA
                                ||||||||||   |||||
                                ATCTTTGATAT   TGAAT
                                      AAA
GAM54   FLJ23017  3'  TAAAAAAATGACTTAGAATTAA 822         CT  A
                                TAGAAA  AT ACTTAGAATTAA
                                ||||||  || ||||||||||||
                                ATTTTT  TA TGAATCTTAATT
                                   T_  C
GAM54   FLJ32786  3'  AGAAACTGGCTGATAGAATTAA 823          ATAACT
                                AGAAACT     TAGAATTAA
                                |||||||     |||||||||
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                                TCTTTGA     ATCTTAATT
                                    CCGACT
GAM54   KIAA1492  3'  CAGAAACTATAATTTAATATT  824           C    A
                                TAGAAACTATAA TTAG ATT
                                |||||||||||| |||| |||
                                GTCTTTGATATT AATT TAA
                                       A    A
GAM54   PIGPC1    3'  GAAACTATAACACTACTTAAA  825          TTAGAA
                                GAAACTATAAC     TTAAA
                                ||||||||||      |||||
                                CTTTGATATTG     AATTT
                                       TGATG_
GAM54   LOC199923 3'  TAAAAACTATGACTTGCCACTA 826          A    AGA
          AA                     TAGAAACTAT ACTT   ATTAAA
                                |||||||||| ||||   ||||||
                                ATTTTTGATA TGAA   TGATTT
                                       C    CGG
GAM54   LOC200734 3'  TAGAAACCATAAAAAAAAGTTA 827           CTT   A
          A                      TAGAAACTATAA   AGA TTAA
                                |||||||||||   ||| ||||
                                ATCTTTGGTATT   TTT AATT
                                       TTT   C
GAM54   LOC254251 3'  TACAAACTATCAGAATTAA   828     G     TAAC
                                TA AAACTA    TTAGAATTAA
                                || ||||||    ||||||||||
                                AT TTTGAT    AGTCTTAATT
                                 G     _____
GAM54   LOC51141  3'  TAGAAACTAACCACAAATTA  829         TA   TA
                                TAGAAACTA  ACT  GAATTA
                                |||||||||  |||  ||||||
                                ATCTTTGAT  TGG  TTTAAT
                                      __   TG
GAM55   CDC25C    3'  CAGGACTCTGCCACCAGCTT  832         TG___
                                TAGGACTCT    CAGCTT
                                |||||||||    ||||||
                                GTCCTGAGA    GTCGAA
                                      CGGTG
GAM55   CDC25C    3'  CAGGACTCTGCCACCAGCTT  832         TG___
                                TAGGACTCT    CAGCTT
                                |||||||||    ||||||
                                GTCCTGAGA    GTCGAA
                                      CGGTG
GAM55   EGFL5     3'  TAGAACTCTTCCTCCCAGCTT 833          _____ G
                                TAGGACTCT    T CAGCTT
                                |||||||||    | ||||||
                                ATCTTGAGA    G GTCGAA
                                      AGGA G
GAM55   GJB5      5'  TAGGACTCAGCAAGCAGCTT  834         TT___
                                TAGGACTC     GCAGCTT
                                ||||||||     |||||||
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                                ATCCTGAG    CGTCGAA
                                    TCGTT
GAM55   D2S448   3'  TAGGACTCCTGCCTGCTT    835          A_
                                TAGGACTCTTGC  GCTT
                                ||||||||||||  ||||
                                ATCCTGAGGACG  CGAA
                                    GA
GAM55   FLJ14154 3'  TAGGACCCTCTGCCATGGCTT 836         _  A___
                                TAGGACTCT TGC   GCTT
                                |||||||||  |||   ||||
                                ATCCTGGGA ACG   CGAA
                                    G  GTAC
GAM55   KIAA0317 5'  AGGATCACAGCTGCAGCTT   837      C  ____
                                AGGA TC   TTGCAGCTT
                                ||||  ||   |||||||||
                                TCCT AG   GACGTCGAA
                                  _  TGTC
GAM55   LHX6     3'  GGACTCCTGGCCGCAGCTT   838       ____
                                GGACTCT   TGCAGCTT
                                |||||||   ||||||||
                                CCTGAGG   GCGTCGAA
                                    ACCG
GAM55   LSM4     3'  TAGGAATCCAGCCAGCTT    839      C  T  _
                                TAGGA TCT GC AGCTT
                                |||||  |||  ||  |||||
                                ATCCT AGG CG TCGAA
                                   T  T  G
GAM55   LOC91801 3'  TAAGACTCTCAGATGCTT    840          CA_
                                TAGGACTCTTG   GCTT
                                ||||||||||   ||||
                                ATTCTGAGAGT   CGAA
                                      CTA
GAM56   DAAM1    3'  TTTAAATCTATGTTTTTCCAAC 843       ACA  GC_
          AA                    TTTGAA   TA   TTTTCCAACAA
                                ||||||   ||   ||||||||||||
                                AAATTT   AT   AAAAGGTTGTT
                                   AG_  ACA
GAM56   NPY1R    3'  TTTAAAATATAGTTTCTCCAA  844       C   C
                                TTTGAAA ATAG TTTTCCAA
                                |||||||  ||||  ||||||||
                                AAATTTT TATC AAGAGGTT
                                    A   A
GAM56   PCDH8    3'  GAAATAGCTTCCAACA      845      AC     TT
                                GAA  ATAGCT  TCCAACA
                                |||  ||||||  |||||||
                                CTT  TATCGA  AGGTTGT
                                  __    __
GAM56   PPP1CC   3'  TTGAAACAGATTTCTTTTTTAA 846         TAG__    CC
          CA                    TTGAAACA    CTTTT  AACA
                                ||||||||    |||||  ||||
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                                AACTTTGT    GAAAA  TTGT
                                    CTAAA    AA
GAM56   ANKRD6   3'  TTTGAAACATGACCTGCATGAC 847          AG   TTCCA
           A                    TTTGAAACAT  CTT    ACA
                                ||||||||||  |||    |||
                                AAACTTTGTA  GGA    TGT
                                     CT   CGTAC
GAM56   DKFZP762D096 3'  TTTGGCACCATTTTCCAACA   848      AAA   AGC
                                TTTG   CAT   TTTTCCAACA
                                ||||   |||   ||||||||||
                                AAAC   GTG   AAAAGGTTGT
                                  C__   GT_
GAM56   FLJ13031  5'  TTTGAGCCAATGTTCCAACA   849       AA  TAGCTT
                                TTTGA  CA     TTCCAACA
                                |||||  ||     ||||||||
                                AAACT  GT     AAGGTTGT
                                   CG  TAC___
GAM56   ICK      3'  TTTAAAACCTGCTTTCCAGCAA 850          ATA    T   A
                                TTTGAAAC   GCTTT CCA CAA
                                ||||||||   ||||| ||| |||
                                AAATTTTG   CGAAA GGT GTT
                                     GA_    _   C
GAM56   KIAA0820  3'  AAACATAGCAACCAGACA    851          TTTT   _
                                AAACATAGC    CCA ACA
                                |||||||||    ||| |||
                                TTTGTATCG    GGT TGT
                                     TT__   C
GAM56   KIAA0934  3'  TTTGAAATGGGCTTTTCCAACA 852         CATA
           A                    TTTGAAA    GCTTTTCCAACAA
                                |||||||    ||||||||||||||
                                AAACTTT    CGAAAAGGTTGTT
                                    ACC_
GAM56   KIAA1571  3'  TTTAAATATAGCTTTTC     853         AC
                                TTTGAA  ATAGCTTTTC
                                ||||||  ||||||||||
                                AAATTT  TATCGAAAAG
                                   A_
GAM56   KIAA1635  3'  TTTGAGTACAGCTACTTCTAAC 854        AAC     _   C
           A                    TTTGA   ATAGCT TTTC AACA
                                |||||   |||||| |||| ||||
                                AAACT   TGTCGA GAAG TTGT
                                   CA_     T    A
GAM56   SAC2     3'  TTTAAAACCCTTTCCAA     855          ATAG
                                TTTGAAAC    CTTTTCCAA
                                ||||||||    |||||||||
                                AAATTTTG    GGAAAGGTT
                                             _____
GAM56   LOC127703 3'  TTTGCAACAGCTCCTTTTCCAA 856        A    TAG_
                                TTTG AACA    CTTTTCCAA
                                |||| ||||    |||||||||
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                                AAAC TTGT    GAAAAGGTT
                                  G    CGAG
GAM56   LOC157623 5'  TTTGAAACATTGTTTTCCA    857           AGC
                                TTTGAAACAT   TTTTCCA
                                ||||||||||   |||||||
                                AAACTTTGTA   AAAAGGT
                                     AC_
GAM56   LOC200609 5'  TTTGAGGTTGTTTTCCAACAA  858        AACATAGC
                                TTTGA       TTTTCCAACAA
                                |||||       ||||||||||||
                                AAACT       AAAAGGTTGTT
                                   CCAAC___
GAM56   LOC201799 3'  TCTGAAACATAGAAGGCTGACA 859             CTTTTCCA
                                TTTGAAACATAG       ACA
                                ||||||||||||       |||
                                AGACTTTGTATC       TGT
                                       TTCCGAC_
GAM57   GPC6     5'  CTTGGGGATGTGTGTGCGTG   862       C   GGCTG
                                CTTG GGA    GTGTGCGTG
                                |||| |||    |||||||||
                                GAAC CCT    CACACGCAC
                                  C   ACA__
GAM57   SLC6A6   3'  CTTGCGAGGCTGAGTTGTGA   863         G      T  GC
                                CTTGCG AGGCTGG GT  GTGA
                                |||||| ||||||| ||  ||||
                                GAACGC TCCGACT CA  CACT
                                   _      _  A_
GAM57   C21orf93  3'  CTTGGGAGGCTGATGTG     864       C
                                CTTG GGAGGCTGGTGTG
                                |||| ||||||||||||
                                GAAC CCTCCGACTACAC
                                  _
GAM57   FLJ00058  5'  CCTTGTGTGTGTGCGT      865        CGGAGGC  _
                                CCTTG      TG GTGTGCGT
                                |||||      || ||||||||
                                GGAAC      AC CACACGCA
                                   _______  A
GAM57   FLJ13197  3'  TTGGGAGGCTGAGGCAGTG   866      C       T   C
                                TTG GGAGGCTGG GTG GTG
                                ||| ||||||||| ||| |||
                                AAC CCTCCGACT CGT CAC
                                  _        C  _
GAM57   KIAA0685  5'  CTTCGGAGGCCCGTGTG     867      G       G
                                CTT CGGAGGCT GTGTG
                                ||| |||||||| |||||
                                GAA GCCTCCGG CACAC
                                  _       G
GAM57   KIAA0924  3'  CTTTCGGAGGCTGAGGTG    868       G        T
                                CTT CGGAGGCTGG GTG
                                ||| |||||||||| |||
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                                GAA GCCTCCGACT CAC
                                  A         C
GAM57   KIAA1751  3'  CCTTGGGAGGCTGAGGTG    869       C       T
                                CCTTG GGAGGCTGG GTG
                                ||||| ||||||||| |||
                                GGAAC CCTCCGACT CAC
                                  _       C
GAM57   MGC13061  3'  CCTTGGGAGGCTGAGGTG    869       C       T
                                CCTTG GGAGGCTGG GTG
                                ||||| ||||||||| |||
                                GGAAC CCTCCGACT CAC
                                  _       C
GAM57   LOC146138 3'  CCTTGCGGCAGGTTGGCCACGT 870         _  C   G
          GA                    CCTTGCGG AGG TGGT TGCGTGA
                                |||||||| ||| |||| |||||||
                                GGAACGCC TCC ACCG GTGCACT
                                    G  A  _
GAM57   LOC146229 3'  CTTTTGGAGGCTGAGGTG    871      GC       T
                                CTT  GGAGGCTGG GTG
                                |||  ||||||||| |||
                                GAA  CCTCCGACT CAC
                                  AA        C
GAM57   LOC149132 5'  CCTGTGGAGGCTGTTGTG    872       C       G
                                CTTG GGAGGCTG TGTG
                                |||| |||||||| ||||
                                GGAC CCTCCGAC ACAC
                                  A       A
GAM57   LOC149711 3'  CTTTCGGAGGCTGAGGTG    868       G       T
                                CTT CGGAGGCTGG GTG
                                ||| |||||||||| |||
                                GAA GCCTCCGACT CAC
                                  A         C
GAM57   LOC150290 3'  TTGGGAGGCTGAGGCGTGA   873       C       TGT
                                TTG GGAGGCTGG   GCGTGA
                                ||| |||||||||   ||||||
                                AAC CCTCCGACT   CGCACT
                                  _       C__
GAM57   LOC158515 5'  CCTTGGGGTGGTGTGCGTG   874       GC  A  C
                                CCTT  GG GG TGGTGTGCGTG
                                ||||  || || ||||||||||
                                GGAA  CC CC ACCACACGCAC
                                    __  _  _
GAM57   LOC200093 3'  CCTTTGGAGACTGTGTGTG   875       GC      _
                                CCTT  GGAGGCTG GTGTG
                                ||||  |||||||| |||||
                                GGAA  CCTCTGAC CACAC
                                  A_       A
GAM57   LOC200268 3'  CCTTGGGAGGCTGAGGTG    869       C       T
                                CCTTG GGAGGCTGG GTG
                                ||||| ||||||||| |||
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                                GGAAC CCTCCGACT CAC
                                  _       C
GAM57   LOC221960 3'  CTTGGGAGGCTGAGGTG     876       C       T
                                CTTG GGAGGCTGG GTG
                                |||| ||||||||| |||
                                GAAC CCTCCGACT CAC
                                  _       C
GAM57   LOC254100 3'  TTGGGAGGCTGAGGTGTG    877       C     __
                                TTG GGAGGCT  GGTGTG
                                ||| |||||||  ||||||
                                AAC CCTCCGA  CCACAC
                                  _     CT
GAM57   LOC255452 3'  CCTTGCGGAGCCCGCGTG    878           G  G
                                CCTTGCGGAG CT GTGTG
                                |||||||||| || |||||
                                GGAACGCCTC GG CGCAC
                                      _ G
GAM57   LOC255975 5'  CCTGTGGAGGCTGTTGTG    872       C       G
                                CTTG GGAGGCTG TGTG
                                |||| |||||||| ||||
                                GGAC CCTCCGAC ACAC
                                  A       A
GAM57   LOC51622  3'  CTTGGGAGGCTGAGGTG     876       C       T
                                CTTG GGAGGCTGG GTG
                                |||| ||||||||| |||
                                GAAC CCTCCGACT CAC
                                  _       C
GAM58   ACCN2     5'  AGGGGGCTTCGGCAAGCCGGC  881         CC    GGTC T
                                AGGGGGT  TCGG    G CCGGC
                                |||||||  ||||    | |||||
                                TCCCCCG  AGCC    C GGCCG
                                    A_   GTT_ _
GAM58   DNMT3L    5'  GGGGGTCACTTGGGGTGGGGAG 882         _ C     CGTCC
            C                    GGGGGTC CT GGGGT     GGC
                                |||||||  || |||||     |||
                                CCCCCAG GA CCCCA     TCG
                                    T  A     CCCC_
GAM58   MECP2     3'  AGGGGGCCTTGGGGAGGC     883         T   C    TC
                                AGGGGG CCT GGGG  GT
                                |||||| ||| ||||  ||
                                TCCCCC GGA CCCC  CG
                                  _   A    TC
GAM58   SOD3      3'  AGGGGGGCCTCGGGGGTCCCTG 884         T       TC   __
            GC                    AGGGGG CCTCGGGG  GTCC  GGC
                                |||||| ||||||||  ||||  |||
                                TCCCCC GGAGCCCC  CAGG  CCG
                                  C       __    GA
GAM58   SYN1      5'  AGGGGGTCCTAGGGGTGGTCTG 885           C    C   C
            GC                    AGGGGGTCCT GGGGT GTC GGC
                                |||||||||| ||||| ||| |||
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                                TCCCCCAGGA CCCCA CAG CCG
                                     T    C  A
GAM58   SYN1     5'  AGGGGGTCCTAGGGGTGGTCTG 885          C    C  C
           GC                    AGGGGGTCCT GGGGT GTC GGC
                                 |||||||||| ||||| ||| |||
                                 TCCCCCAGGA CCCCA CAG CCG
                                     T    C  A
GAM58   TXNRD1   3'  AGGGGGCCTTGGGCGGTGCCGG 886      T  C  _______  GTCC
           AG                    GGGG CCT GGG     GTC   G
                                 |||| ||| |||      |||   |
                                 CCCC GGA CCC     CGG   C
                                   _  A  GCCAIII  CCTG
GAM58   BC022889  3'  AGGAGGTCCTCGGGGTCA    887
                                 AGGGGGTCCTCGGGGTCG
                                 ||||||||||||||||||
                                 TCCTCCAGGAGCCCCAGT

GAM58   C6orf31   5'  GGGGGTCCTCGGCCGG     888          GGTCGT
                                 GGGGGTCCTCGG    CCGG
                                 ||||||||||||    ||||
                                 CCCCCAGGAGCC    GGCC
                                                 _____
GAM58   FLJ22169  3'  AGGGGGTCCTGGGGATGAGGC  889          C   TCGTCC
                                 AGGGGGTCCT GGGG    GGC
                                 |||||||||| ||||    |||
                                 TCCCCCAGGA CCCC    CCG
                                     _   TACT__
GAM58   KIAA0418  3'  GGGAGTCCTTGGGGGAAGCCGG 890         C   TCGT
           C                     GGGGGTCCT GGGG   CCGGC
                                 |||||||||| ||||   |||||
                                 CCCTCAGGA CCCC   GGCCG
                                     A   CTTC
GAM58   KIAA1100  3'  AGGGAGTCTTTGGAGCTTGGC  891        CTC   CGTCC
                                 AGGGGGTC  GGGGT   GGC
                                 ||||||||  |||||   |||
                                 TCCCTCAG  CCTCG   CCG
                                     AAA   AA___
GAM58   KIAA1719  3'  AGGGGGCCTTGGTGGGTCGGC  892       T  C  _  TC  C
                                 AGGGGG CCT GG GG  GTC GGC
                                 |||||| ||| || ||  ||| |||
                                 TCCCCC GGA CC CC  CAG CCG
                                   _  A  A  __  _
GAM58   MGC4368   3'  GGCGGGTCCTCGGGGAGGGGC  893     _        TCGTCC
                                 GG GGGTCCTCGGGG    GGC
                                 || ||||||||||||    |||
                                 CC CCCAGGAGCCCC    CCG
                                  G         TCC___
GAM58   STX1B2    3'  GGGGGTCCATGGCCCGG    894         TCGG  CGT
                                 GGGGGTCC   GGT  CCGG
                                 ||||||||   |||  ||||
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                                CCCCCAGG   CCG  GGCC
                                    TA__  ___
GAM58   TNRC4    3' AGGGGGCCCTTGGGGGAGG   895         C   TCGTCC
                                AGGGGGTCCT GGGG    GG
                                |||||||||| ||||    ||
                                TCCCCCGGGA CCCC    CC
                                     A   CT____
GAM58   LOC124842 3' GGGGGTCCCTGCTACTCCGGC 896        CGGG  CG_
                                GGGGGTCCT   GT  TCCGGC
                                |||||||||   ||  ||||||
                                CCCCCAGGG   CG  AGGCCG
                                     A___  ATG
GAM58   LOC158056 5' AGGGGGTCTGTGGGGTCCAGGA 897       CTC    GTCC
           GC                    AGGGGGTC  GGGGTC   GGC
                                |||||||   ||||||   |||
                                TCCCCCAG  CCCCAG   TCG
                                    ACA    GTCC
GAM58   LOC92305  3' AGGGGGTCCTGGCGGCTGG   898         C _  CGTCC
                                AGGGGGTCCT GG GGT    GG
                                |||||||||| || |||    ||
                                TCCCCCAGGA CC CCG    CC
                                     _ G  A____
GAM59   ADD1     3' CCTCCTCCTTCTCTAACATTGG 901       GTAG __  C
                                TCTCTT   CC  CTC AACATTGG
                                ||||||   ||  ||| ||||||||
                                GGAGGA   GG  GAG TTGTAACC
                                   ____  AA  A
GAM59   B3GALT2   5' TCTCTTGTAGTCATTCTCCTTG 902         CC___   AACA
           G                   TCTCTTGTAG   CTCC   TTGG
                                ||||||||||   ||||   ||||
                                AGAGAACATC   GAGG   AACC
                                     AGTAA   ____
GAM59   DPP6     3' TCTTGTAGCCCCTCACCAT   903          TC  A
                                TCTTGTAGCCC  CA CAT
                                ||||||||||  || |||
                                AGAACATCGGG  GT GTA
                                      GA  G
GAM59   HLF      3' TCTCTGTACAACATT      904       T  GCCCTC
                                TCTCT GTA    CAACATT
                                ||||| |||    |||||||
                                AGAGA CAT    GTTGTAA
                                   _  _______
GAM59   ROBO1    3' TCTTGTAGGTTTCGACATTGG  905        CCC  CA
                                TCTTGTAG  TC  ACATTGG
                                ||||||||  ||  |||||||
                                AGAACATC  AG  TGTAACC
                                    CAA  C_
GAM59   ROBO1    3' TCTTGTAGGTTTCGACATTGG  905        CCC  CA
                                TCTTGTAG  TC  ACATTGG
                                ||||||||  ||  |||||||
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                                AGAACATC  AG  TGTAACC
                                    CAA  C_
GAM59   THY1    3'  TCCTTTGTAGCCCTCTCCACTG 906     TC        CAA
                                TC  TTGTAGCCCTC  CATTG
                                ||  ||||||||||  |||||
                                AG  AACATCGGGAG  GTGAC
                                 GA        AG_
GAM59   AMOTL1  3'  TCTCTTGTGGTTCCTGAGGCCA 907      AGC_  T_______  ACAT
           ATTG                 TTGT   CC      CCA   TG
                                ||||   ||      |||   ||
                                AACA   GG      GGT   AC
                                  CCAA  ACTCCIII  TAC
GAM59   FLJ20449 3'  TCTTGTAGCTCTCTGGCTGG  908         C  CAACA
                                TCTTGTAGC CTC    TTGG
                                |||||||| |||    ||||
                                AGAACATCG GAG    GACC
                                     A  ACC__
GAM59   MDN1    5'  TCCTTTGTTCTCCTCCAACGTT 909     TC   AGC      A
           GG                   TC  TTGT  CCTCCAAC TTGG
                                ||  ||||  |||||||| ||||
                                AG  AACA  GGAGGTTG AACC
                                 GA   AGA      C
GAM59   MGC2821  3'  TCTCTTGTGCTTTTTCTACTTT 910         A  CCTCCA_  A
           GG                   TCTCTTGT GC      AC TTGG
                                |||||||| ||      || ||||
                                AGAGAACA CG      TG AACC
                                    _ AAAAAGA  A
GAM59   LOC145497 5'  TCTCTTGTAGCATCTCCACA  911          C_    A
                                TCTCTTGTAGC  CTCCA CA
                                ||||||||||  ||||| ||
                                AGAGAACATCG  GAGGT GT
                                      TA    G
GAM59   LOC221362 5'  CCTCTTGGTCTTCCAGTGTTGG 912        TAGCCC   ACA
                                TCTCTTG    TCCA  TTGG
                                |||||||    ||||  ||||
                                GGAGAAC    AGGT  AACC
                                    CAGA__   CAC
GAM59   LOC222174 3'  TCTCCTGTAGTGTCTGTGGCAT 913         CC_  CCAA
           TGG                  TCTCTTGTAG  CT   CATTGG
                                ||||||||||  ||   ||||||
                                AGAGGACATC  GA   GTAACC
                                     ACA  CACC
GAM60   HNRPF   3'  GCTGGGGCCGTGTGTCTATT  916     TGTC   __
                                GCT   GGGCT  GTGTCTATT
                                |||   |||||  |||||||||
                                CGA   CCCGG  CACAGATAA
                                  C___    CA
GAM60   AQP9    3'  TAACTTGTCAAATGTCTGTTC  917          GCT    A
                                TAGCTTGTCGG  GTGTCT TTC
                                ||||||||||  ||||||  |||
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                                ATTGAACAGTT   TACAGA AAG
                                      ___     C
GAM60   KIAA1336 3'  TAGCTTGCGAGGCAGTCTATT  918         C    TGT
                                TAGCTTGT GGGC   GTCTATT
                                |||||||| ||||   |||||||
                                ATCGAACG TCCG   CAGATAA
                                     C    T__
GAM60   PRO1575  5'  ACTTGTTATATGTCTATT    919        CGGGC
                                GCTTGT    TGTGTCTATT
                                ||||||    ||||||||||
                                TGAACA    ATACAGATAA
                                   AT___
GAM61   CHST5    3'  GGGCAAGAGTTGCTTTCCATGA 922        C   C      __
           AG                     GGGCA GAG TGCTTTCC  GAAG
                                |||||  ||| ||||||||  ||||
                                CCCGT CTC ACGAAAGG  CTTC
                                   T   A       TA
GAM61   CHST6    3'  GGGCAAGAGTTGCTTTCCATGA 922        C   C      __
           AG                     GGGCA GAG TGCTTTCC  GAAG
                                |||||  ||| ||||||||  ||||
                                CCCGT CTC ACGAAAGG  CTTC
                                   T   A       TA
GAM61   EML1     3'  AGGGCACAGTTTTCCTGA    923         G  CTGC    _
                                AGGGCAC AG    TTTCC GA
                                |||||||  ||    |||||  ||
                                TCCCGTG TC    AAAGG CT
                                    _ A___     A
GAM61   MUC5B    5'  GGGTGTGAGCTGTTCCCA    924      CAC     C
                                GGG   GAGCTG TTTCCG
                                |||   ||||||  ||||||
                                CCC   CTCGAC AAGGGT
                                  ACA     _
GAM61   NUMA1    3'  AGGGTGTGAGCTGCTGCTGAAG 925       CAC       TTCC
                                AGGG   GAGCTGCT    GAAG
                                ||||   ||||||||    ||||
                                TCCC   CTCGACGA    CTTC
                                  ACA       CGA_
GAM61   PTPRA    5'  AGGGCCATGGGCTGATTCCGAA 926        ACGA_    CT
           G                     AGGGC    GCTG  TTCCGAAG
                                |||||    ||||  ||||||||
                                TCCCG    CGAC  AAGGCTTC
                                   GTACC    T_
GAM61   RFX2     3'  GGGATGGCTGCTTTCTGAAG   927      CACGA       C
                                GGG    GCTGCTTTC GAAG
                                |||    ||||||||| ||||
                                CCC    CGACGAAAG CTTC
                                  TAC__       A
GAM61   TNFRSF6B 5'  AAGGGCACAGAGCGTGGCT    928          _    T__
                                AAGGGCAC GAGC   GCT
                                ||||||| ||||   |||
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                                TTCCCGTG CTCG   CGA
                                     T    CAC
GAM61   C6orf26   3'  GGAGAAAGCTGCTTTCTGGA   929      CAC        C_
                                GGG   GAGCTGCTTTC  GA
                                |||   ||||||||||  ||
                                CCT   TTCGACGAAAG  CT
                                  CT_         AC
GAM61   DKFZP586B2420 3'  AGGGCACAGGCTGCTTAAACG  930          A      TC_
                                AGGGCACG GCTGCTT   CG
                                |||||||| |||||||   ||
                                TCCCGTGT CGACGAA   GC
                                     C      TTT
GAM61   FLJ22167  3'  GGGCAAGAGTTGCTTTCCATGA 922        C   C       __
            AG                    GGGCA GAG TGCTTTCC  GAAG
                                |||||| ||| ||||||||  ||||
                                CCCGT CTC ACGAAAGG  CTTC
                                   T   A       TA
GAM61   FLJ25471  5'  AAGGGCAATAAGGGCTTTCCG  931         C_   CT
                                AAGGGCA  GAG  GCTTTCCG
                                |||||||  |||  ||||||||
                                TTCCCGT  TTC  CGAAAGGC
                                     TA   C_
GAM61   FLJ32499  3'  AAGGGCACAGGCTAGCTCCTGG 932           A   _    CC
            A                     AAGGGCACG GCT GCTTT  GA
                                |||||||||  ||| |||||  ||
                                TTCCCGTGT CGA CGAGG  CT
                                      C   T    AC
GAM61   HSPC047   3'  AGGGCACGAGCTGTTCCA    933             CT
                                AGGGCACGAGCTG  TTCCG
                                ||||||||||||  |||||
                                TCCCGTGCTCGAC  AAGGT
                                          __
GAM61   KIAA0227  3'  AGGGAGTGGGCTGCTTCCAA   934       CACGA      T
                                AGGG    GCTGCTT CCGA
                                ||||    ||||||| ||||
                                TCCC    CGACGAA GGTT
                                  TCACC      _
GAM61   KIAA0356  3'  GGGCACTACCTTTCTGA     935        GA  TG    C
                                GGGCAC  GC  CTTTC GA
                                ||||||  ||  ||||| ||
                                CCCGTG  TG  GAAAG CT
                                   A_  __     A
GAM61   KIAA0459  3'  AAGGCACCGCTCTTTCCG    936         GA   G
                                AGGGCAC  GCT CTTTCCG
                                |||||||  ||| |||||||
                                TTCCGTG  CGA GAAAGGC
                                   G_  _
GAM61   KIAA1297  3'  AGGGCACGCGCTTCTCG     937          AGC    TC
                                AGGGCACG   TGCTT  CG
                                ||||||||   |||||  ||
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                                TCCCGTGC  GCGAA  GC
                                   ___    GA
GAM61   KIAA1465  3'  AAGGGCACGGGCTCCG     938         A  TGCTT
                                AAGGGCACG GC    TCCG
                                ||||||||| ||    ||||
                                TTCCCGTGC CG    AGGC
                                    C  _____
GAM61   KIAA1655  5'  AGGGCATCCCTGTTTTCTGGA  939       CGAG  C   C_
                                AGGGCA   CTG TTTC  GA
                                ||||||   ||| ||||  ||
                                TCCCGT   GAC AAAG  CT
                                   AGG_  A   AC
GAM61   MGC13272  5'  AGGGCACAGCTTCGCG     940         AGCT   C
                                AGGGCACG   GCTTT CG
                                ||||||||   ||||| ||
                                TCCCGTGT   CGAAG GC
                                   _____   C
GAM61   Rab11-FIP2 5'  GGGCACGGCCGCTCCG     941         A    TT
                                GGGCACG GCTGC  TCCG
                                ||||||| |||||  ||||
                                CCCGTGC CGGCG  AGGC
                                   _    __
GAM61   TPC2     3'  AGGGCACGGCGCCTCCCTGAAG 942          A  T     _
                                AGGGCACG GC GCTTTCC GAAG
                                |||||||| || ||||||| ||||
                                TCCCGTGC CG CGGAGGG CTTC
                                   _ _      A
GAM61   LOC129228 5'  AGGGCACAGGTACCTTTGGA  943         G  C     CC
                                AGGGCAC AG TGCTTT  GA
                                ||||||| || ||||||  ||
                                TCCCGTG TC ATGGAA  CT
                                   _ C     AC
GAM61   LOC144079 5'  GGGTGGATGAGACTTTCCGAAG 944       CAC__   CT
                                GGG    GAG  GCTTTCCGAAG
                                |||    |||  ||||||||||||
                                CCC    CTC  TGAAAGGCTTC
                                  ACCTA  __
GAM61   LOC146435 5'  AGGCCGCTCCTCGCTTTCTGA  945       A  AG  __     C
                                GGGC CG  CT  GCTTTC GA
                                |||| ||  ||  |||||| ||
                                TCCG GC  GG  CGAAAG CT
                                  _  GA  AG     A
GAM61   LOC158656 5'  GGCACGAGCTGCCAGCAGAAG  946             TTCC
                                GGCACGAGCTGCT   GAAG
                                ||||||||||||   ||||
                                CCGTGCTCGACGG   CTTC
                                       TCGT
GAM61   LOC196047 5'  AAGGACACGAGTTGTATCAGA  947           C  CTT  C
                                AAGGGCACGAG TG   TC GA
                                |||||||||| ||   || ||
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                                TTCCTGTGCTC AC   AG CT
                                      A  AT_  T
GAM61   LOC196860 5'  AAGGCACAGCGCTTTCTGAAG  948        G   T     C
                                AGGGCAC AGC GCTTTC GAAG
                                ||||||| ||| |||||| ||||
                                TTCCGTG TCG CGAAAG CTTC
                                   _  _     A
GAM61   LOC204970 5'  AGGAGCACGAGCTGCGGCCCGA 949      _         TT
                                AGG GCACGAGCTGC  TCCGA
                                ||| ||||||||||  |||||
                                TCC CGTGCTCGACG  GGGCT
                                  T         CC
GAM61   LOC205143 5'  GGCGCACGGGCCCCGAA     950     _    A   GCTTT
                                GG GCACG GCT    CCGAA
                                || ||||| |||    |||||
                                CC CGTGC CGG    GGCTT
                                 G    C  _____
GAM61   LOC220776 3'  AGGGCACAGGCACTGAA     951         A  T   TTCC
                                AGGGCACG GC GCT   GAA
                                |||||||| || |||   |||
                                TCCCGTGT CG TGA   CTT
                                     C  _  ____
GAM61   LOC222136 3'  AGGGCACAAGCTGTGGGA    952            CTTTCC
                                AGGGCACGAGCTG     GA
                                ||||||||||||     ||
                                TCCCGTGTTCGAC     CT
                                      ACC___
GAM61   LOC253129 5'  AGGGCACGCGGCTCCGA     953         AGCT  TT
                                AGGGCACG    GC  TCCGA
                                ||||||||    ||  |||||
                                TCCCGTGC    CG  AGGCT
                                     GC__  __
GAM61   LOC257475 5'  AGGGCACAGCTGCTGTCCA   954         G      T
                                AGGGCAC AGCTGCT TCCG
                                ||||||| ||||||| ||||
                                TCCCGTG TCGACGA AGGT
                                   _      C
GAM61   LOC51035  3'  AAGGCACGAGTCCTGAA     955          CTGCTT  _
                                AGGGCACGAG     TCC GAA
                                ||||||||||     ||| |||
                                TTCCGTGCTC     AGG CTT
                                      _______  A
GAM62   ABP1     3'  CTCTGGATGCCAGGGAGGGG  958          __
                                CTTTGGATG  GGGGAGGGG
                                |||||||||  |||||||||
                                GAGACCTAC  TCCCTCCCC
                                     GG
GAM62   ARHGDIA  3'  CTTTGGTATGGGGAGGGG    959        ATG
                                CTTTGG   GGGGAGGGG
                                ||||||   |||||||||
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                                GAAACC  CCCCTCCCC
                                   ATA
GAM62   ASGR2   5' CCTTGGCCAAGGAGGGG    960       ATG
                                CTTTGG  GGGGAGGGG
                                ||||||  |||||||||
                                GGAACC  TTCCTCCCC
                                   GG_
GAM62   ASGR2   5' CCTTGGCCAAGGAGGGG    960       ATG
                                CTTTGG  GGGGAGGGG
                                ||||||  |||||||||
                                GGAACC  TTCCTCCCC
                                   GG_
GAM62   ASGR2   5' CCTTGGCCAAGGAGGGG    960       ATG
                                CTTTGG  GGGGAGGGG
                                ||||||  |||||||||
                                GGAACC  TTCCTCCCC
                                   GG_
GAM62   BAZ2A   3' CTCTGAAGGGAGGGG     961       ATG
                                CTTTGG  GGGGAGGGG
                                ||||||  |||||||||
                                GAGACT  TCCCTCCCC
                                  ___
GAM62   BCL3    3' CCGAAGATGGGGGGGGG    962    TT      A
                                CT  GGATGGGGG GGGG
                                ||  ||||||||| ||||
                                GG  TCTACCCCC CCCC
                                 CT       _
GAM62   COMT    5' CTCTGGCTGCGGGAGGGG   963       A  G
                                CTTTGG TG GGGAGGGG
                                |||||| || ||||||||
                                GAGACC AC CCCTCCCC
                                   G  G
GAM62   DGKG    5' CTCTCGGGGGAGGGG      964      GGA
                                CTTT  TGGGGGAGGGG
                                ||||  ||||||||||
                                GAGA  GCCCCCTCCCC
                                  ___
GAM62   DLG4    5' CTTTACTAAGGGAGGGG    965       GA
                                CTTTG TGGGGGAGGGG
                                |||||  ||||||||||
                                GAAAT ATTCCCTCCCC
                                   G_
GAM62   DUSP4   5' CTTTGGGGAGAAGGGAGGGG 966       AT__
                                CTTTGG   GGGGGAGGGG
                                ||||||   ||||||||||
                                GAAACC   TTCCCTCCCC
                                   CCTC
GAM62   EVX1    5' CTCCGGTGGGGGAGGGG    967       A
                                CTTTGG TGGGGGAGGGG
                                |||||| ||||||||||
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                                GAGGCC ACCCCCTCCCC
                                      _
GAM62   FE65L2   3' TTTGAGCAGGGGGAGGGG   968      AT_
                                TTTGG  GGGGGAGGGG
                                |||||  ||||||||||
                                AAACT  CCCCCTCCCC
                                   CGT
GAM62   FE65L2   3' TTTGAGCAGGGGGAGGGG   968      AT_
                                TTTGG  GGGGGAGGGG
                                |||||  ||||||||||
                                AAACT  CCCCCTCCCC
                                   CGT
GAM62   FGFR3    3' CTTTGGGTGTGGGAGGGG   969       A G
                                CTTTGG TG GGGAGGGG
                                |||||| || ||||||||
                                GAAACC AC CCCTCCCC
                                    C A
GAM62   FMNL     5' CTTCCTGCGGGGAGGGG    970      GGA _
                                CTTT  TG GGGGAGGGG
                                ||||  || |||||||||
                                GAAG  AC CCCCTCCCC
                                  G__ G
GAM62   GLTSCR1  3' CTTCGGGAGGAGGGG      971       ATG
                                CTTTGG  GGGGAGGGG
                                ||||||  |||||||||
                                GAAGCC  CTCCTCCCC
                                      ___
GAM62   GPRK7    3' CTATGGATGGGAATCAGG   972     T       A_
                                CT TGGATGGGGG GGG
                                || ||||||||||  |||
                                GA ACCTACCCTT  TCC
                                 T        AG
GAM62   HOXB2    5' CAATGGTGGGGGAGGGG    973    TT  A
                                C  TGG TGGGGGAGGGG
                                |  ||| ||||||||||
                                G  ACC ACCCCCTCCCC
                                 TT  _
GAM62   HPCA     3' CCCCTTTGGGGGAGGGG    974      GGA
                                CTTT  TGGGGGAGGGG
                                ||||  ||||||||||
                                GGGG  ACCCCCTCCCC
                                  AA_
GAM62   IGF1     3' CTTTGCAAGGGAGGGG     975       GAT
                                CTTTG  GGGGGAGGGG
                                |||||  ||||||||||
                                GAAAC  TTCCCTCCCC
                                   G__
GAM62   IL2RB    3' CTGTGGACGGGGAGGGG    976     T       G
                                CT TGGATGGGG AGGGG
                                || ||||||||| |||||
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                                GA ACCTGCCCC TCCCC
                                 C       _
GAM62   KCNJ10   5' CCTTGGATGGGCCGCGGGG  977          GGA_
                                CTTTGGATGGG  GGGG
                                ||||||||||  ||||
                                GGAACCTACCC  CCCC
                                      GGCG
GAM62   KPNA1    3' TTTGTGTGGGGGGAGGGG  978      GA    _
                                TTTG  TGGGGG AGGGG
                                ||||  |||||| |||||
                                AAAC  ACCCCC TCCCC
                                  AC     C
GAM62   LENG4    5' CTCTGATGACAGGAGGGG  979       G   _
                                CTTTG ATGG GGGAGGGG
                                ||||| |||| ||||||||
                                GAGAC TACT TCCTCCCC
                                  _   G
GAM62   LPIN2    3' CCTTGCTGTGGGGAGGGG  980       GA  _
                                CTTTG  TG GGGGAGGGG
                                |||||  || |||||||||
                                GGAAC  AC CCCCTCCCC
                                   G_  A
GAM62   MAPK3    3' CTTTGACAGGGAGGGG    981       ATG
                                CTTTGG  GGGGAGGGG
                                ||||||  |||||||||
                                GAAACT  TCCCTCCCC
                                   G__
GAM62   MAT1A    3' CAACGGTGGGGGAGGGG   982    TT  A
                                C  TGG TGGGGGAGGGG
                                |  ||| ||||||||||
                                G  GCC ACCCCCTCCCC
                                 TT  _
GAM62   MSF      3' CTCTGAGGGGAGGGG     983       GAT
                                CTTTG  GGGGGAGGGG
                                |||||  ||||||||||
                                GAGAC  TCCCCTCCCC
                                   ____
GAM62   MVK      3' CTCTGGGAGGGAGGGG    984       AT
                                CTTTGG  GGGGGAGGGG
                                ||||||  ||||||||||
                                GAGACC  CTCCCTCCCC
                                   __
GAM62   NAGA     3' CTTTGGAAAAGGAGGGG   985        T
                                CTTTGGA GGGGGAGGGG
                                |||||||  ||||||||||
                                GAAACCT TTTCCTCCCC
                                   _
GAM62   OCLN     5' CTTCGGATGGAACCTTGGGG  986          GA__
                                CTTTGGATGGGG  GGGG
                                ||||||||||||  ||||
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                                GAAGCCTACCTT   CCCC
                                      GGAA
GAM62   PAX2    3' CTGTGTCGGGGGAGGGG    987    T GA
                                CT TG  TGGGGGAGGGG
                                || ||  ||||||||||
                                GA AC  GCCCCCTCCCC
                                 C  A_
GAM62   PAX2    3' CTGTGTCGGGGGAGGGG    987    T GA
                                CT TG  TGGGGGAGGGG
                                || ||  ||||||||||
                                GA AC  GCCCCCTCCCC
                                 C  A_
GAM62   PCDH9   5' CTTTGGAGGGGAGGGG     988       TG
                                CTTTGGA  GGGGAGGGG
                                |||||||  |||||||||
                                GAAACCT  CCCCTCCCC
                                   __
GAM62   PCTK1   3' CTTAGGGTGGAGGAAGGG   989     T A
                                CTT GG TGGGGGAGGGG
                                ||| || ||||||||||
                                GAA CC ACCTCCTTCCC
                                  T  C
GAM62   PCTK1   3' CTTAGGGTGGAGGAAGGG   989     T A
                                CTT GG TGGGGGAGGGG
                                ||| || ||||||||||
                                GAA CC ACCTCCTTCCC
                                  T  C
GAM62   PCTK1   3' CTTAGGGTGGAGGAAGGG   989     T A
                                CTT GG TGGGGGAGGGG
                                ||| || ||||||||||
                                GAA CC ACCTCCTTCCC
                                  T  C
GAM62   PFKM    5' CTTGGGAAAGGGGGGAGGGG  990     T  T__
                                CTT GGA  GGGGGAGGGG
                                ||| |||  ||||||||||
                                GAA CCT  CCCCCTCCCC
                                  C  TTC
GAM62   POLR2C  3' CTGTGTATGTGGGAGGGG   991     T G  G
                                CT TG ATG GGGAGGGG
                                || || ||| ||||||||
                                GA AC TAC CCCTCCCC
                                 C  A  A
GAM62   PSD     3' CCTTGGGGAGGAAGGAGGGG  992       AT_  _
                                CTTTGG  GGG GGAGGGG
                                ||||||  ||| |||||||
                                GGAACC  CCT CCTCCCC
                                   CCT  T
GAM62   PTPRA   5' CTTTAGGAGAAGGGG     993       GAT
                                CTTTG  GGGGGAGGGG
                                |||||  ||||||||||
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                              GAAAT  CCTCTTCCCC
                                     ___
GAM62   RABL2A   3' TCTGCCTGGGGGGAGGGG   994      GA    _
                              TTTG TGGGGG AGGGG
                              |||| |||||| |||||
                              AGAC ACCCCC TCCCC
                                GG    C
GAM62   RABL2B   3' TCTGCCTGCGGGGAGGGG   995      GA _
                              TTTG TG GGGGAGGGG
                              |||| || |||||||||
                              AGAC AC CCCCTCCCC
                                GG G
GAM62   RALB     3' TTTGGGAGGGAAGAAGGGG   996      AT __
                              TTTGG GGG GGAGGGG
                              ||||| ||| |||||||
                              AAACC CCC CTTCCCC
                                 CT  TT
GAM62   RB1      3' CTTTAGGTGTAGGGGAGGGG  997       A__
                              CTTTGG TGGGGGAGGGG
                              |||||| ||||||||||
                              GAAATC ATCCCCTCCCC
                                 CAC
GAM62   RXRA     3' CTTTGGAAAAAGGGG      998       TGG
                              CTTTGGA GGGAGGGG
                              ||||||| ||||||||
                              GAAACCT TTTTCCCC
                                     ___
GAM62   RYR1     3' CCTTAGGGGGAGGGG      999       GAT
                              CTTTG GGGGGAGGGG
                              ||||| ||||||||||
                              GGAAT CCCCCTCCCC
                                     ___
GAM62   SDHC     3' CTGTGGGCAAAAAAGGGG   1000    T  AT
                              CT TGG GGGGGAGGGG
                              || ||| ||||||||||
                              GA ACC TTTTTTCCCC
                               C  CG
GAM62   SORCS2   3' CTCTGGAGTGGGGAGGGG   1001      TG
                              CTTTGGA GGGGAGGGG
                              ||||||| |||||||||
                              GAGACCT CCCCTCCCC
                                 CA
GAM62   SPOCK    5' CCTTGGATGGGTCCAGGG   1002        GGA
                              CTTTGGATGGG GGGG
                              |||||||||||  ||||
                              GGAACCTACCC TCCC
                                    AGG
GAM62   STC1     3' CTTTGGAAGTTTAAGGGG   1003      T GG_
                              CTTTGGA GG  GAGGGG
                              ||||||| ||  ||||||
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                                GAAACCT TC   TTCCCC
                                   _ AAA
GAM62   STXBP1   3' TTTGGTCCGAGGGAGGGG   1004      A_
                                TTTGG TGGGGGAGGGG
                                ||||| ||||||||||
                                AAACC GCTCCCTCCCC
                                   AG
GAM62   SURF4    3' CTTTACCAAGGGAGGGG    1005      GA
                                CTTTG TGGGGGAGGGG
                                ||||| ||||||||||
                                GAAAT GTTCCCTCCCC
                                   G_
GAM62   TBXA2R   3' CTCTGGATGGGAAAAAGGGG 1006          __
                                CTTTGGATGGGG GAGGGG
                                |||||||||||| ||||||
                                GAGACCTACCCT TTCCCC
                                      TT
GAM62   TCF7     3' CTGTGAATGGGGAGGGG    1007    T      G
                                CT TGGATGGGG AGGGG
                                || ||||||||| |||||
                                GA ACTTACCCC TCCCC
                                 C       _
GAM62   TDGF1    3' CTTTGGGAAAAAAAGGGG   1008      AT
                                CTTTGG GGGGGAGGGG
                                |||||| ||||||||||
                                GAAACC TTTTTTCCCC
                                   CT
GAM62   TNFSF12  3' CTCTAGAGGGAGGGG      1009       TGG
                                CTTTGGA GGGAGGGG
                                ||||||| ||||||||
                                GAGATCT CCCTCCCC
                                   ___
GAM62   ZNF148   5' CCTTGAGAGGAGGGG      1010      GAT
                                CTTTG GGGGGAGGGG
                                ||||| ||||||||||
                                GGAAC TCTCCTCCCC
                                   ___
GAM62   ZNF289   3' CCTCTGGGGGAGGGG      1011     GGA
                                CTTT TGGGGGAGGGG
                                |||| ||||||||||
                                GGAG ACCCCCTCCCC
                                   ___
GAM62   AF9Q34   3' TTGAAAGTGGGGGAGGGG   1012      __
                                TTGGA TGGGGGAGGGG
                                ||||| ||||||||||
                                AACTT ACCCCCTCCCC
                                   TC
GAM62   AIG-1    3' CCTCATTGGGGGAGGGG    1013      GA
                                CTTTG TGGGGGAGGGG
                                ||||| ||||||||||
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                                GGAGT  ACCCCCTCCCC
                                  A_
GAM62   AQP10    3'  CTTTGCGGGAGGAGGGG     1014       GAT
                                CTTTG  GGGGGAGGGG
                                |||||  ||||||||||
                                GAAAC  CCTCCTCCCC
                                  GC_
GAM62   BANP     5'  TTTGGCACTCAGGAGGGG    1015       _ GG
                                TTTGG AT  GGGAGGGG
                                ||||| ||  ||||||||
                                AAACC TG  TCCTCCCC
                                  G  AG
GAM62   BAT8     3'  CTCTGGGAGGGAGGGG      984        AT
                                CTTTGG  GGGGGAGGGG
                                ||||||  ||||||||||
                                GAGACC  CTCCCTCCCC
                                  __
GAM62   BTN1A1   3'  CTATGGAGGAGAGGGG      1016     T   TG
                                CT TGGA  GGGGAGGGG
                                || ||||  |||||||||
                                GA ACCT  CCTCTCCCC
                                 T   __
GAM62   C2orf9   3'  CTCTGCAGGGGAGGGG      1017       GAT
                                CTTTG  GGGGGAGGGG
                                |||||  ||||||||||
                                GAGAC  TCCCCTCCCC
                                  G__
GAM62   CACNG4   3'  TCTGGGGCAGCGGGAGGGG   1018       A_  _
                                TTTGG  TGG GGGAGGGG
                                |||||  ||| ||||||||
                                AGACC  GTC CCCTCCCC
                                  CC  G
GAM62   CARM1    3'  CTTTGGTGGGGAGGGG      1019       ATG
                                CTTTGG  GGGGAGGGG
                                ||||||  |||||||||
                                GAAACC  CCCCTCCCC
                                  A__
GAM62   CIC      3'  CTCTGGGGAAAAAAGGGG    1020       AT
                                CTTTGG  GGGGGAGGGG
                                ||||||  ||||||||||
                                GAGACC  TTTTTTCCCC
                                  CC
GAM62   CSE-C    3'  CTCTGGATAAAAAGGGG     1021          G
                                CTTTGGATGGGG AGGGG
                                |||||||||||| |||||
                                GAGACCTATTTT TCCCC
                                  _
GAM62   CYP2A7   5'  CTGTGGATTTAGGAGGGG    1022     T   GG
                                CT TGGAT  GGGAGGGG
                                || |||||  ||||||||
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                                GA ACCTA  TCCTCCCC
                                 C    AA
GAM62   CYP2A7   5' CTGTGGATTTAGGAGGGG   1022    T   GG
                                CT TGGAT  GGGAGGGG
                                || |||||  ||||||||
                                GA ACCTA  TCCTCCCC
                                 C    AA
GAM62   DKFZp547O146 5' CTTTGAGTAAAAAGAGGGG   1023       AT_
                                CTTTGG   GGGGGAGGGG
                                ||||||   ||||||||||
                                GAAACT   TTTTCTCCCC
                                   CAT
GAM62   FLJ10748  3' CTCTGGTGGGGAGGGG     1024       ATG
                                CTTTGG   GGGGAGGGG
                                ||||||   |||||||||
                                GAGACC   CCCCTCCCC
                                   A__
GAM62   FLJ10826  5' CTTTGGATGAAGTTTGGG    1025          GAG
                                CTTTGGATGGGG   GGG
                                ||||||||||||   |||
                                GAAACCTACTTC   CCC
                                      AAA
GAM62   FLJ11783  3' CCTTGAAAGGAGGGG      1026       TGG
                                CTTTGGA   GGGAGGGG
                                |||||||   ||||||||
                                GGAACTT   TCCTCCCC
                                     ___
GAM62   FLJ11850  5' CTTTGGAGAAAGTAGGGG    1027        T GG  _
                                CTTTGGA G  GG AGGGG
                                ||||||| |  || |||||
                                GAAACCT C  TC TCCCC
                                   _ TT  A
GAM62   FLJ12587  3' CTCTGAGGAGGGGAGGGG    1028       AT
                                CTTTGG  GGGGGAGGGG
                                ||||||  ||||||||||
                                GAGACT  TCCCCTCCCC
                                   CC
GAM62   FLJ13848  3' TCTGGGGAAGATGAGGGG    1029      AT   _
                                TTTGG  GGGG GAGGGG
                                |||||  ||||  ||||||
                                AGACC  TTCT CTCCCC
                                  CC   A
GAM62   FLJ14225  3' CTGTGGTGAGGGGAGGGG    1030    T  A  _
                                CT TGG TG GGGGAGGGG
                                || ||| || |||||||||
                                GA ACC AC CCCCTCCCC
                                 C  _  T
GAM62   FLJ14640  5' CTGTGGTGCAGGAGGGG    1031    T  A  G
                                CT TGG TG GGGAGGGG
                                || ||| || ||||||||
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                                GA ACC AC TCCTCCCC
                                 C   _  G
GAM62   FLJ20174  3'  CTTTGCAAGAAGAGGGG    1032      GAT
                                CTTTG  GGGGGAGGGG
                                |||||  ||||||||||
                                GAAAC  TCTTCTCCCC
                                   GT_
GAM62   FLJ20195  3'  CCCCTTTGGGGGAGGGG    974       GGA
                                CTTT  TGGGGGAGGGG
                                ||||  ||||||||||
                                GGGG  ACCCCCTCCCC
                                  AA_
GAM62   FLJ21019  3'  CTCTCGGGGGAGGGG      964       GGA
                                CTTT  TGGGGGAGGGG
                                ||||  ||||||||||
                                GAGA  GCCCCCTCCCC
                                  ___
GAM62   FLJ21478  3'  CTTTGAGAGGAGGGG      1033      GAT
                                CTTTG  GGGGGAGGGG
                                |||||  ||||||||||
                                GAAAC  TCTCCTCCCC
                                  ___
GAM62   FLJ21977  3'  CCTTGAAGGGAGGGG      1034      ATG
                                CTTTGG  GGGGAGGGG
                                ||||||  |||||||||
                                GGAACT  TCCCTCCCC
                                  ___
GAM62   FLJ22593  5'  CTCTGGACTCTGGAGGGG   1035       GGG
                                CTTTGGAT  GGAGGGG
                                ||||||||  |||||||
                                GAGACCTG  CCTCCCC
                                    AGA
GAM62   HAND1     3'  CTTTGGCGAAGGGAGGGG   1036      AT
                                CTTTGG  GGGGGAGGGG
                                ||||||  ||||||||||
                                GAAACC  TTCCCTCCCC
                                   GC
GAM62   IMAGE:4907098 3'  CTTCTTGGGGGAGGGG    1037      GGA
                                CTTT  TGGGGGAGGGG
                                ||||  ||||||||||
                                GAAG  ACCCCCTCCCC
                                  A__
GAM62   ITPK1     3'  CTGTGGGGAGGGAGGGG    1038    T  AT
                                CT TGG  GGGGGAGGGG
                                || |||  ||||||||||
                                GA ACC  CTCCCTCCCC
                                 C  C_
GAM62   KCNK15    3'  TTTGGAAAGGAGGGAGGGG   1039      T_ _
                                TTTGGA  GG GGGAGGGG
                                ||||||  || ||||||||
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                                AAACCT  CC CCCTCCCC
                                   TT  T
GAM62   KIAA0356 3' CCTTTCTGAGGGAGGGG    1040      GGA
                                CTTT   TGGGGGAGGGG
                                ||||   ||||||||||
                                GGAA   ACTCCCTCCCC
                                  AG_
GAM62   KIAA0429 5' CTGCAGCAGGGGAGGGG    1041     T   A
                                CT TGG TGGGGGAGGGG
                                || ||| ||||||||||
                                GA GTC GTCCCCTCCCC
                                 C   _
GAM62   KIAA0775 3' CTCTATAGAGGGGAGGGG    1042       GAT
                                CTTTG   GGGGGAGGGG
                                |||||   ||||||||||
                                GAGAT   TCCCCTCCCC
                                   ATC
GAM62   KIAA1169 3' CTCTGTGAAAGGGAGGGG    1043       GAT
                                CTTTG   GGGGGAGGGG
                                |||||   ||||||||||
                                GAGAC   TTCCCTCCCC
                                   ACT
GAM62   KIAA1649 5' CCTTAGATGGGGAGGGG    1044            G
                                CTTTGGATGGGG AGGGG
                                |||||||||||| |||||
                                GGAATCTACCCC TCCCC
                                          _
GAM62   KIAA1831 5' CCTTGGATGGAGATAGGG    1045            _
                                CTTTGGATGGGGG AGGG
                                |||||||||||| ||||
                                GGAACCTACCTCT TCCC
                                       A
GAM62   KIAA1950 3' CTCTGCAGGGGAGGGG     1017       GAT
                                CTTTG   GGGGGAGGGG
                                |||||   ||||||||||
                                GAGAC   TCCCCTCCCC
                                   G__
GAM62   LEPROTL1 3' CCTTGCAGGGGAGGGG     1046       GAT
                                CTTTG   GGGGGAGGGG
                                |||||   ||||||||||
                                GGAAC   TCCCCTCCCC
                                   G__
GAM62   MAP2K6   5' CTTTGATGGGGGAGGGG    1047       G
                                CTTTG ATGGGGGAGGGG
                                ||||| ||||||||||||
                                GAAAC TACCCCCTCCCC
                                      _
GAM62   MGC15476 3' CTTTGTGAATGAGAGGGG    1048       _ TGG
                                CTTTG GA   GGGAGGGG
                                ||||| ||   ||||||||
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                                GAAAC CT   CTCTCCCC
                                   A  TA_
GAM62   MGC2668   3'  CTTTGGGTAGGGAGGGG     1049       ATG
                                CTTTGG   GGGGAGGGG
                                ||||||   |||||||||
                                GAAACC   TCCCTCCCC
                                   CA_
GAM62   MGC2705   3'  TCTGGTGTGGGGGAGGGG    1050       A_
                                TTTGG  TGGGGGAGGGG
                                |||||  ||||||||||
                                AGACC  ACCCCCTCCCC
                                   AC
GAM62   MGC3123   3'  CTGTGGATGAGAAGGGG     1051     T       G
                                CT TGGATGGGG AGGGG
                                || |||||||| |||||
                                GA ACCTACTCT TCCCC
                                 C       _
GAM62   NEUROG3   3'  CTTTGAATGGGATTATGGGG   1052           GA__
                                CTTTGGATGGGG   GGGG
                                ||||||||||||   ||||
                                GAAACTTACCCT   CCCC
                                      AATA
GAM62   NOL4      5'  CTTTGGGTGGGGGAAGGG    1053       A
                                CTTTGG TGGGGGAGGGG
                                |||||| ||||||||||
                                GAAACC ACCCCCTTCCC
                                   C
GAM62   OVCOV1    3'  CTCTGAAGGGAGGGG       961        ATG
                                CTTTGG   GGGGAGGGG
                                ||||||   |||||||||
                                GAGACT   TCCCTCCCC
                                   ___
GAM62   PCANAP7   5'  CTCTGTGGGGGAGGGG      1054       GA
                                CTTTG  TGGGGGAGGGG
                                |||||  ||||||||||
                                GAGAC  ACCCCCTCCCC
                                   __
GAM62   POLM      3'  CCTTGGCGGGGAGGGG      1055       ATG
                                CTTTGG   GGGGAGGGG
                                ||||||   |||||||||
                                GGAACC   CCCCTCCCC
                                   G__
GAM62   PP1057    3'  CTCAAGCTGGGGGAGGGG    1056     T  A
                                CTT GG TGGGGGAGGGG
                                ||| || ||||||||||
                                GAG TC ACCCCCTCCCC
                                  T  G
GAM62   PTPRT     3'  TTGGGTGGGAGAGCAGGG    1057       A      __
                                TTGG TGGGGGAG  GGG
                                |||| ||||||||  |||
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                                AACC ACCCTCTC  CCC
                                  C       GT
GAM62   RNF8     3'  CTCTGAAAGGAGGGG       1058         TGG
                                CTTTGGA   GGGAGGGG
                                |||||||   ||||||||
                                GAGACTT   TCCTCCCC
                                    ___
GAM62   RPS6KA4  3'  TTAGAAGTGGGGGAGGGG    1059       __
                                TTGGA  TGGGGGAGGGG
                                |||||  ||||||||||
                                AATCT  ACCCCCTCCCC
                                   TC
GAM62   SARM     3'  CTCTGGCAGGGAGGGG      1060        ATG
                                CTTTGG   GGGGAGGGG
                                ||||||   |||||||||
                                GAGACC   TCCCTCCCC
                                   G__
GAM62   SCRG1    5'  CTGTGGGGAGGAGGGG      1061     T   AT
                                CT TGG  GGGGGAGGGG
                                || |||  ||||||||||
                                GA ACC  CCTCCTCCCC
                                 C  __
GAM62   SMCR5    3'  CCTTGGATGGACAGCTAGGGG  1062           GG___
                                CTTTGGATGGG    AGGGG
                                ||||||||||     |||||
                                GGAACCTACCT    TCCCC
                                      GTCGA
GAM62   TSC22    3'  CCTTGGAAGTGAGGGG      1063         T  GG
                                CTTTGGA GG  GAGGGG
                                ||||||| ||  ||||||
                                GGAACCT TC  CTCCCC
                                   _ A_
GAM62   UXS1     5'  CTCTAGAGGGAGGGG       1009         TGG
                                CTTTGGA   GGGAGGGG
                                |||||||   ||||||||
                                GAGATCT   CCCTCCCC
                                    ___
GAM62   ZIC4     3'  CCCAAAATGGGGGAGGGG    1064      TG
                                CTT  GATGGGGGAGGGG
                                |||  ||||||||||||
                                GGG  TTACCCCCTCCCC
                                  TT
GAM62   ZNF297   3'  CCTTGGGGGGGAGGGG      1065        AT
                                CTTTGG  GGGGGAGGGG
                                ||||||  ||||||||||
                                GGAACC  CCCCCTCCCC
                                    __
GAM62   LOC144262 5'  CTCTGCGGTGGGAGGGG     1066        GA  _
                                CTTTG  TGG GGGAGGGG
                                |||||  ||| ||||||||
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                                GAGAC  GCC CCCTCCCC
                                  __   A
GAM62   LOC145864 3' CTTTGGAACCGAGAGGGG    1067        TGG
                                CTTTGGA   GGGAGGGG
                                |||||||   ||||||||
                                GAAACCT   CTCTCCCC
                                    TGG
GAM62   LOC147007 3' CTAAGTTGGGGGAGGGG     1068     TT  A
                                CT  GG TGGGGGAGGGG
                                ||  || ||||||||||
                                GA  TC ACCCCCTCCCC
                                 T_  A
GAM62   LOC147669 5' CTCTGGATGGGAGAGGGG    1069
                                CTTTGGATGGGGGAGGGG
                                ||||||||||||||||||
                                GAGACCTACCCTCTCCCC

GAM62   LOC148034 5' CTCTGGGGGAGGAGGGG     1070        AT
                                CTTTGG  GGGGGAGGGG
                                ||||||  ||||||||||
                                GAGACC  CCTCCTCCCC
                                   C_
GAM62   LOC148089 3' CTTTGAGGTAAGGAGGGG    1071        ATG
                                CTTTGG   GGGGAGGGG
                                ||||||   |||||||||
                                GAAACT   TTCCTCCCC
                                   CCA
GAM62   LOC149606 3' CCTTGGATGAAGGCAGGGG   1072             _
                                CTTTGGATGGGGG AGGGG
                                |||||||||||| |||||
                                GGAACCTACTTCC TCCCC
                                      G
GAM62   LOC152328 3' CTTTGGGGAGAGGGG       1073        ATG
                                CTTTGG   GGGGAGGGG
                                ||||||   |||||||||
                                GAAACC   CCTCTCCCC
                                  ___
GAM62   LOC152641 5' CCTTGGGGTGCCGGAGGGG   1074        A_  GG
                                CTTTGG  TG  GGAGGGG
                                ||||||  ||  |||||||
                                GGAACC  AC  CCTCCCC
                                   CC  GG
GAM62   LOC153232 3' CTTTGGGGGGGGGGGG      1075        AT    A
                                CTTTGG  GGGGG GGGG
                                ||||||  ||||| ||||
                                GAAACC  CCCCC CCCC
                                   C_    _
GAM62   LOC161003 3' TTTGGCAGGTGGGGGAGGGGC 1076        A___          III
                                TTTGG   TGGGGGAGGGG  C
                                |||||   ||||||||||   |
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                                AAACC   ACCCCCTCCCC  G
                                  GTCC         III
GAM62   LOC196812 3' CTTAGGATGAGGAGGGG    1077     T      G
                                CTT GGATGGGG AGGGG
                                ||| |||||||| |||||
                                GAA CCTACTCC TCCCC
                                  T      _
GAM62   LOC196872 3' CTGTGGACTGGGGAGGGG    1078    T    G
                                CT TGGAT GGGGAGGGG
                                || ||||| |||||||||
                                GA ACCTG CCCCTCCCC
                                 C    A
GAM62   LOC219404 3' CTTTGGAAAACTGGGGAGGGG 1079        TG___
                                CTTTGGA    GGGGAGGGG
                                |||||||    |||||||||
                                GAAACCT    CCCCTCCCC
                                    TTTGA
GAM62   LOC219513 5' CTCTGGAAGGAGGGG       1080        TGG
                                CTTTGGA   GGGAGGGG
                                |||||||   ||||||||
                                GAGACCT   TCCTCCCC
                                   ___
GAM62   LOC219848 3' CTCTGCTATGGGAGGGG     1081       GA  G
                                CTTTG  TG GGGAGGGG
                                |||||  || ||||||||
                                GAGAC  AT CCCTCCCC
                                  G_  A
GAM62   LOC253015 5' CTTTGGAGATGGGAGGGG    1082        TGG
                                CTTTGGA   GGGAGGGG
                                |||||||   ||||||||
                                GAAACCT   CCCTCCCC
                                    CTA
GAM62   LOC254532 5' CTGTGGAGGGGAGGGG      1083     T   TG
                                CT TGGA  GGGGAGGGG
                                || ||||  |||||||||
                                GA ACCT  CCCCTCCCC
                                 C   __
GAM62   LOC255057 3' CTTGGGTTGGGGGAGGGG    1084     T  A
                                CTT GG TGGGGGAGGGG
                                ||| || ||||||||||
                                GAA CC ACCCCCTCCCC
                                  C  A
GAM62   LOC256158 5' CTTTGGAGATGGAAGGGG    1085        TGG
                                CTTTGGA   GGGAGGGG
                                |||||||   ||||||||
                                GAAACCT   CCTTCCCC
                                    CTA
GAM62   LOC56961  5' CTCTGGATGGATAGAGGG    1086          _
                                CTTTGGATGGG GGAGGG
                                |||||||||| ||||||
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                                GAGACCTACCT TCTCCC
                                      A
GAM62   LOC90784 5' CTTTGGACGGAAGTGGGG    1087           A
                                CTTTGGATGGGGG GGGG
                                ||||||||||||| ||||
                                GAAACCTGCCTTC CCCC
                                      A
GAM62   LOC90917 5' CTCTGGTCAGGGGAGGGG    1088       A
                                CTTTGG TGGGGGAGGGG
                                |||||| ||||||||||
                                GAGACC GTCCCCTCCCC
                                   A
GAM62   LOC91963 5' CCTTGGGGAAGAGGGG      1089       AT
                                CTTTGG  GGGGGAGGGG
                                ||||||  ||||||||||
                                GGAACC  CCTTCTCCCC
                                   __
GAM62   LOC92017 5' CTCTGAGTAGGGGAGGGG    1090       GA
                                CTTTG  TGGGGGAGGGG
                                |||||  ||||||||||
                                GAGAC  ATCCCCTCCCC
                                   TC
GAM63   GABRR1   3' TGTCGTATTTCCTGCAGCACCT 1093      ATG  C  AA
                                TGTC   AT TT  TGTAGCACCT
                                ||||   || ||  ||||||||||
                                ACAG   TA AA  ACGTCGTGGA
                                  CA_  _  GG
GAM63   MHC2TA   3' TGTCACGATTTTCATTTAGC   1094         C  AATG
                                TGTCATGAT TT    TAGC
                                |||||||||  ||    ||||
                                ACAGTGCTA AA    ATCG
                                      A  GTAA
GAM63   MYEOV    3' TATCATGATTTTCCCAGCACCT 1095          C  AATG
                                TGTCATGAT TT    TAGCACCT
                                |||||||||  ||    ||||||||
                                ATAGTACTA AA    GTCGTGGA
                                      A  GG__
GAM63   STAU2    3' TGTTGTATCTTAATGGTGTACC 1096     CATG       TAGC
           T                     TGT    ATCTTAATG    ACCT
                                |||    |||||||||    ||||
                                ACA    TAGAATTAC    TGGA
                                  ACA_        CACA
GAM63   CTCFL    3' TGTCATGAACTTAATTGT    1097         T    _
                                TGTCATGA CTTAAT GT
                                |||||||| |||||| ||
                                ACAGTACT GAATTA CA
                                      T     A
GAM63   FLJ10432 3' TGTGAGGATCTGTAGCACCT  1098     CAT    TAAT
                                TGT   GATCT    GTAGCACCT
                                |||   |||||    |||||||||
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                                ACA  CTAGA   CATCGTGGA
                                  CTC   ____
GAM63   FLJ23563 3'  TGTGATTTCTAACAGCACCT  1099     C  GA  TAATG
                                TGT AT  TCT    TAGCACCT
                                ||| ||  |||    ||||||||
                                ACA TA  AGA    GTCGTGGA
                                  C  A_  TT___
GAM63   KIAA0971 3'  TGGCATGATCTTATGCA    1100     T       A
                                TG CATGATCTTA TGTA
                                || ||||||||||| ||||
                                AC GTACTAGAAT ACGT
                                 C       _
GAM63   KIAA1229 3'  TCATGATCTTGTTTCATCT   1101         TAA  AG  C
                                TCATGATCT   TGT  CA CT
                                |||||||||   |||  || ||
                                AGTACTAGA   ACA  GT GA
                                     ___   AA  A
GAM63   KIAA1272 3'  TGTCATGACCTGAAGCGCC   1102          TAATGT  A
                                TGTCATGATCT     AGC CC
                                ||||||||||      ||| ||
                                ACAGTACTGGA     TCG GG
                                      CT_____   C
GAM63   PRO2955  3'  TGTCATGTTCAGTAGCACC   1103        A  TTAAT
                                TGTCATG TC    GTAGCACC
                                ||||||| ||    ||||||||
                                ACAGTAC AG    CATCGTGG
                                    A  T_____
GAM63   PSTPIP2  3'  TGTCATGTTCAGTAGCACC   1103        A  TTAAT
                                TGTCATG TC    GTAGCACC
                                ||||||| ||    ||||||||
                                ACAGTAC AG    CATCGTGG
                                    A  T_____
GAM63   YAF2     3'  TGTCATGAAAATGTGGTACCT  1104        TCTT    AGC
                                TGTCATGA   AATGT   ACCT
                                ||||||||   |||||  ||||
                                ACAGTACT   TTACA   TGGA
                                     T____    CCA
GAM63   LOC120103 3'  GTCATGATCTTGAACAGTGCCT 1105          AATG   CA
                                GTCATGATCTT   TAG  CCT
                                ||||||||||    |||  |||
                                CAGTACTAGAA   GTC  GGA
                                      CTT_   AC
GAM63   LOC219818 3'  TGTTCTTCAATGTAGCAC    1106     A  _
                                TG TCT TAATGTAGCAC
                                || ||| ||||||||||
                                AC AGA GTTACATCGTG
                                 A  A
GAM63   LOC219942 3'  TGTCATGATCTAATCACC    1107          TAATGTAG
                                TGTCATGATCT      CACC
                                ||||||||||       ||||
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                                ACAGTACTAGA      GTGG
                                     TTA_____
GAM64   FLRT2    3'  AGATGTTGTCCTCCCTGGT   1110        _  G
                                AGATGTTG CC CTCTGGT
                                |||||||| || |||||||
                                TCTACAAC GG GGGACCA
                                    A  A
GAM64   BICD2    3'  AGATGTTAGCTGCAGCGTGCGG 1111       _  C  TCTG  C
           C                     AGATGTT GC GC   GT GCGGC
                                ||||||| || ||   || |||||
                                TCTACAA CG CG   CA CGCCG
                                   T  A  TCG_ _
GAM64   C11orf25 3'  AAATGTTGCTGTTCTGTGGC  1112        CGC   GTC
                                AGATGTTGC   TCTG   GC
                                |||||||||   ||||   ||
                                TTTACAACG   AGAC   CG
                                    ACA    AC_
GAM64   FLJ10922 3'  AGATGTTACTGCTGGGCGTGGC 1113       C   CT  T  C
                                AGATGTTGC GCT  GG CG GGC
                                ||||||||| |||  || || |||
                                TCTACAATG CGA  CC GC CCG
                                    A   C_  _  A
GAM64   FLJ23375 5'  AGATGTTGCTGTCTCCGGGC  1114        CG_    TC
                                AGATGTTGC   CTCTGG  GC
                                |||||||||   ||||||  ||
                                TCTACAACG   GAGGCC  CG
                                    ACA     __
GAM64   SCYA16   5'  AGATGTTGTCTGTTGCTGG   1115        CCGC   GTC  _
                                AGATGTTG    TCTG   GC GG
                                ||||||||    ||||   || ||
                                TCTACAAC    AGAC   CG CC
                                    _____    AA_  A
GAM64   LOC134713 5'  GATGTTGCCGATCTTCCACAGG 1116         C   GG   _
           C                     GATGTTGCCG TCT  TCGC GGC
                                |||||||||| |||  |||| |||
                                CTACAACGGC AGA  GGTG CCG
                                    T   A_   T
GAM64   LOC255056 5'  GATGTCGCTGCCCCCTGCGGC  1117        C    GGTC
                                GATGTTGC GCTCT    GCGGC
                                |||||||| |||||    |||||
                                CTACAGCG CGGGG    CGCCG
                                    A    GA__
GAM64   LOC92840  3'  GATGTTGCTGCTGCTGGGAGAC 1118        C   _   TC_
                                GATGTTGC GCT CTGG   GC
                                |||||||| ||| ||||   ||
                                CTACAACG CGA GACC   TG
                                    A   C    CTC
GAM65   ABCD1    5'  TCTCCTGTCCTGTCAGTGCCCT 1121     _  C     GG
           GG                     TC CC GTCCTG  TGGTGCCCTGG
                                || || ||||||  ||||||||||
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                                AG GG CAGGAC  GTCACGGGACC
                                 A  A     A_
GAM65   AIPL1    3'  TCCCTGCCTGGGTGGCTGTGG  1122       C T        GCCC
                                TCCC G CCTGGGTGGT    TGG
                                |||| | ||||||||||    |||
                                AGGG C GGACCCACCG    ACC
                                  A _         AC__
GAM65   AUP1     3'  TCTCCGTCCTGCGGCTCTG    1123     C      GG    GCC
                                TC CCGTCCT  GTGGT   CTG
                                || |||||||  |||||   |||
                                AG GGCAGGA  CGCCG   GAC
                                 A       __     A__
GAM65   HLF      3'  TCCTTGTCCTAGGGAATAGTCT 1124      CC       TG   CC
            GG                    TCC  GTCCTGGG  GTG  CTGG
                                |||  ||||||||  |||  ||||
                                AGG  CAGGATCC  TAT  GACC
                                  AA       CT   CA
GAM65   HM13     3'  CCCTGTCCTGGAGCTGCCCTTG 1125      C      _ GG     _
            G                    CCC GTCCTGG GT  TGCCCT GG
                                ||| |||||||  ||  ||||||  ||
                                GGG CAGGACC CG  ACGGGA CC
                                  A      T __      A
GAM65   IGLL1    5'  CCCTAGAGAGTGGTGCCCTGG  1126      GTCCT
                                CCC     GGGTGGTGCCCTGG
                                |||     ||||||||||||||
                                GGG     CTCACCACGGGACC
                                  ATCT_
GAM65   KLK10    5'  TCCTGCTCTGGGAGGGGCCCTG 1127      CC TC     T  T
            G                    TCC  G  CTGGG GG GCCCTGG
                                |||  |  |||||  ||  |||||||
                                AGG  C  GACCC CC CGGGACC
                                  A_ GA    T  C
GAM65   NT5M     3'  TCCCTGTCCTGAGCCCCTG    1128       C        GGTG
                                TCCC GTCCTGGGT    CCCTG
                                |||| |||||||||    |||||
                                AGGG CAGGACTCG    GGGAC
                                  A        _____
GAM65   NYX      5'  CCGTCCTGGGAGTCTCCCTGG  1129           T   G_
                                CCGTCCTGGG GGT  CCCTGG
                                ||||||||||  |||  ||||||
                                GGCAGGACCC TCA  GGGACC
                                       _   GA
GAM65   VIPR2    3'  CCTTTCCTGGGCACCTG     1130     CG       GTGC
                                CC  TCCTGGGTG    CCTG
                                ||  |||||||||    ||||
                                GG  AGGACCCGT    GGAC
                                 AA        _____
GAM65   ZNF205   5'  TCCTTGTCCTGGGTGTCCTGG  1131      CC        GTGC
                                TCC  GTCCTGGGTG    CCTGG
                                |||  ||||||||||    |||||
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                                AGG  CAGGACCCAC   GGACC
                                  AA        A___
GAM65   ARHGEF9   3'  TCCCTGATCCTGGAGCCCTGG  1132      C_      TGGT
                                TCCC  GTCCTGGG   GCCCTGG
                                ||||  ||||||||   |||||||
                                AGGG  TAGGACCT   CGGGACC
                                  AC       ____
GAM65   BTN3A1    3'  TCCTTATCCTGGAGCCATCCTG 1133     CC     _  G  GC
           G                     TCC  GTCCTGG GT GT  CCTGG
                                |||  ||||||| || ||  |||||
                                AGG  TAGGACC CG TA  GGACC
                                  AA      T  G  __
GAM65   C11orf9   3'  TCCTCTTCCTGGATATTCCTGG 1134     CCG       GTGC
                                TCC   TCCTGGGTG   CCTGG
                                |||   |||||||||   |||||
                                AGG   AGGACCTAT   GGACC
                                  AGA       AA__
GAM65   C17orf31  3'  TCCTTGTCTCTGGCCCTG    1135     CC  _  GGTGGT
                                TCC  GTC CTG     GCCCTG
                                |||  ||| |||     ||||||
                                AGG  CAG GAC     CGGGAC
                                  AA   A  _______
GAM65   C20orf59  5'  CCTCTCCTGGGCCTGCTCTGG  1136    CG      GG   C
                                CC  TCCTGGGT  TGC CTGG
                                ||  ||||||||  ||| ||||
                                GG  AGGACCCG  ACG GACC
                                  AG       G_   A
GAM65   CABP4     3'  TCTCCATCCTGGAGGCTCCTGG 1137    C       T   GC
                                TC CCGTCCTGGG GGT  CCTGG
                                ||  ||||||||||  |||  |||||
                                AG GGTAGGACCT CCG  GGACC
                                  A        _   A_
GAM65   CENTB5    3'  GCCCTGGGAGGAGGCTCTGG   1138        T  T_  C
                                GTCCTGGG GG  GC CTGG
                                ||||||||  ||  ||  ||||
                                CGGGACCC CC  CG GACC
                                     T  TC  A
GAM65   DEFCAP    5'  TCCCTCTCCTGGGTCCTG    1139      CG      GGTGC
                                TCCC  TCCTGGGT    CCTG
                                ||||  ||||||||    ||||
                                AGGG  AGGACCCA    GGAC
                                  AG       ______
GAM65   DEFCAP    5'  TCCCTCTCCTGGGTCCTG    1139      CG      GGTGC
                                TCCC  TCCTGGGT    CCTG
                                ||||  ||||||||    ||||
                                AGGG  AGGACCCA    GGAC
                                  AG       ______
GAM65   DKFZP566J091 3'  CCCTCGTCCTCCTGCCCTG   1140      _     GGGTGG
                                CCC CGTCCT     TGCCCTG
                                |||  ||||||     |||||||
```

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                                GGG GCAGGA     ACGGGAC
                                  A     GG____
GAM65   DNAJA3   3'  CCCGTCTCCCAGGTGCCCTGG  1141       _  G GT
                                CCCGTC CT G  GGTGCCCTGG
                                |||||| || |  ||||||||||
                                GGGCAG GG T  CCACGGGACC
                                   A  G __
GAM65   FLJ22938 3'  CCCTGTCCCCACAGTGCCCTGG 1142     C    GG TG
                                CCC GTCCT  G  GTGCCCTGG
                                ||| |||||  |  |||||||||
                                GGG CAGGG  T  CACGGGACC
                                  A    G_ GT
GAM65   KIAA0375 3'  TCCCTCTCCTGGGTGGAGGTCT 1143      CG        TGCC
            GG                    TCCC  TCCTGGGTGG   CTGG
                                ||||  ||||||||||   ||||
                                AGGG  AGGACCCACC   GACC
                                  AG        TCCA
GAM65   KIAA1164 5'  CATTCTGGGTGATGATGG    1144     C        CCC
                                CGT CTGGGTGGTG   TGG
                                ||| ||||||||||   |||
                                GTA GACCCACTAC   ACC
                                  A        T__
GAM65   MGC10966 3'  TCCCTGGCCTGGGTGATG    1145      CGT
                                TCCC   CCTGGGTGGTG
                                ||||   ||||||||||
                                AGGG   GGACCCACTAC
                                  ACC
GAM65   MGC13047 3'  TCCTGGGTCAGAGCTGG     1146         _  T  CC
                                TCCTGGGT GG GC  TGG
                                |||||||| || ||  |||
                                AGGACCCA TC CG  ACC
                                     G  T  __
GAM65   MYT1     3'  TCCCCTCTTAGGGTGCCCTGG  1147       G  CTG  T
                                TCCCC TC   GG GGTGCCCTGG
                                ||||| ||   || ||||||||||
                                AGGGG AG   TC CCACGGGACC
                                   _  AA_  _
GAM65   OSBPL5   3'  TCCTCGTCTGAGAGCTCTG   1148     C    C    TGGT  C
                                TCC CGTC TGGG   GC CTG
                                ||| |||| ||||   || |||
                                AGG GCAG ACTC   CG GAC
                                  A    _    T___  A
GAM65   PCBP4    5'  TCCCCTCCACATCAGGTGCCCT 1149       G   TGGGT_
            GG                    TCCCC TCC     GGTGCCCTGG
                                ||||| |||     ||||||||||
                                AGGGG AGG     CCACGGGACC
                                   _  TGTAGT
GAM65   RAB-R    3'  TCCTGCCTGGGTGGGGGTGG   1150     CC T       TGCCC
                                TCC  G CCTGGGTGG    TGG
                                |||  | |||||||||    |||
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                                AGG  C GGACCCACC    ACC
                                  A_ _       CCC__
GAM65   SDC3     3'  TCCCTGCCCTGGGCCTTCCGTC 1151      C       GG__  C
            CTGG                    TCCC GTCCTGGGT    TG CCTGG
                                |||| |||||||||    || |||||
                                AGGG CGGGACCCG    GC GGACC
                                  A        GAAG  A
GAM65   SPINLW1  3'  TCCCCATCTTGTATGTCCTGG  1152         CTGG   G  C
                                TCCCCGTC    GTG TG CCTGG
                                ||||||||    ||| || |||||
                                AGGGGTAG    CAT AC GGACC
                                     AA__   _  A
GAM65   ZIN      3'  TCCCTGGCCTGGAAGCCTTGG  1153      CGT     TGGT   C
                                TCCC   CCTGGG    GCC TGG
                                ||||   ||||||    ||| |||
                                AGGG   GGACCT    CGG ACC
                                  ACC     T___   A
GAM65   LOC131478 5'  CCCTTGTCCTGGGTCCTG    1154     C_       GGTGC
                                CCC  GTCCTGGGT    CCTG
                                |||  |||||||||    ||||
                                GGG  CAGGACCCA    GGAC
                                  AA        _____
GAM65   LOC145226 5'  TCTCCGTCCTGGGTGCTG    1155     C          G
                                TC CCGTCCTGGGTG TG
                                || ||||||||||| ||
                                AG GGCAGGACCCAC AC
                                  A          G
GAM65   LOC147040 3'  GCCCTGGGCGGCCTTGG     1156          GT   C
                                GTCCTGGGTG  GCC TGG
                                ||||||||||  ||| |||
                                CGGGACCCGC  CGG ACC
                                     __   A
GAM65   LOC148887 3'  TCCCCGCCTGGGGCTGTGTCTG 1157        T     TG_  CC
            G                    TCCCCG CCTGGG   GTG  CTG
                                |||||| ||||||   |||  ||||
                                AGGGGC GGACCC   CAC  GACC
                                   _     CGA   A_
GAM65   LOC148936 5'  TCCCTTCTGCACTGCCCTGG   1158      GG__   G
                                TCCT    GTG TGCCCTGG
                                ||||    ||| ||||||||
                                AGGG    CGT ACGGGACC
                                  AAGA   G
GAM65   LOC148938 5'  TCCCTTCTGCACTGCCCTGG   1158      GG__   G
                                TCCT    GTG TGCCCTGG
                                ||||    ||| ||||||||
                                AGGG    CGT ACGGGACC
                                  AAGA   G
GAM65   LOC150142 5'  CGTGAGAGGTGGTGTTCTGG   1159      CCT       CC
                                CGT   GGGTGGTG  CTGG
                                |||   ||||||||  ||||
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                                GCA   TCCACCAC  GACC
                                  CTC       AA
GAM65   LOC155376 5'  GTCCTGGAGATCCTGG      1160         T   GC
                                GTCCTGGG GGT  CCTGG
                                |||||||| |||  |||||
                                CAGGACCT CTA  GGACC
                                      _   __
GAM65   LOC158427 5'  TCCCCTTCTTCACTGCCCTGG  1161       G  CTGGG  G
                                TCCCC TC    TG TGCCCTGG
                                ||||| ||    || ||||||||
                                AGGGG AG    GT ACGGGACC
                                   A  AA___  G
GAM65   LOC158572 3'  TCCTGTCCTGATGCCTGCCCTG 1162      CC      GTGG
          G                      TCC  GTCCTGG   TGCCCTGG
                                |||  |||||||   ||||||||
                                AGG  CAGGACT   ACGGGACC
                                  A_      ACGG
GAM65   LOC164584 5'  TCCTCGTTCGCGATGCCCTGG  1165     C   CCTGG
                                TCC CGT    GTGGTGCCCTGG
                                ||| |||    ||||||||||||
                                AGG GCA    CGCTACGGGACC
                                  A   AG___
GAM65   LOC164584 5'  TCCTCGTTTGCGATGTCCTGG  1164     C   CCTGG    C
                                TCC CGT    GTGGTG CCTGG
                                ||| |||    |||||| |||||
                                AGG GCA    CGCTAC GGACC
                                  A   AA___     A
GAM65   LOC164584 5'  TCCTCGTTTGCGATGTCCTGG  1164     C   CCTGG    C
                                TCC CGT    GTGGTG CCTGG
                                ||| |||    |||||| |||||
                                AGG GCA    CGCTAC GGACC
                                  A   AA___     A
GAM65   LOC164584 5'  TCCTCGTTTGCGATGTCCTGG  1164     C   CCTGG    C
                                TCC CGT    GTGGTG CCTGG
                                ||| |||    |||||| |||||
                                AGG GCA    CGCTAC GGACC
                                  A   AA___     A
GAM65   LOC164584 5'  TCCTCGTTCGCGATGCCCTGG  1165     C   CCTGG
                                TCC CGT    GTGGTGCCCTGG
                                ||| |||    ||||||||||||
                                AGG GCA    CGCTACGGGACC
                                  A   AG___
GAM65   LOC164584 5'  TCCTCGTTCGCGATGCCCTGG  1165     C   CCTGG
                                TCC CGT    GTGGTGCCCTGG
                                ||| |||    ||||||||||||
                                AGG GCA    CGCTACGGGACC
                                  A   AG___
GAM65   LOC164584 5'  TCCTCGTTTGCGATGTCCTGG  1164     C   CCTGG    C
                                TCC CGT    GTGGTG CCTGG
                                ||| |||    |||||| |||||
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                                AGG GCA    CGCTAC GGACC
                                  A  AA___     A
GAM65   LOC164584 5'  TCCTCGTTATTGACGCCCTGG  1163     C  CCTGGG  GT
                                TCC CGT     TG  GCCCTGG
                                ||| |||      ||  |||||||
                                AGG GCA     AC  CGGGACC
                                  A  ATA___  TG
GAM65   LOC164584 5'  TCCTCGTTCGCGATGCCCTGG  1165     C  CCTGG
                                TCC CGT    GTGGTGCCCTGG
                                ||| |||    ||||||||||||
                                AGG GCA    CGCTACGGGACC
                                  A  AG___
GAM65   LOC164584 5'  TCCTCGTTCGCGATGCCCTGG  1165     C  CCTGG
                                TCC CGT    GTGGTGCCCTGG
                                ||| |||    ||||||||||||
                                AGG GCA    CGCTACGGGACC
                                  A  AG___
GAM65   LOC222233 5'  GTCCTGGAGATCCTGG      1160        T  GC
                                GTCCTGGG GGT  CCTGG
                                |||||||| |||  |||||
                                CAGGACCT CTA  GGACC
                                     _  __
GAM65   LOC253532 5'  GTCCTGGAGATCCTGG      1160        T  GC
                                GTCCTGGG GGT  CCTGG
                                |||||||| |||  |||||
                                CAGGACCT CTA  GGACC
                                     _  __
GAM65   LOC253681 3'  GCCCTGGGCGGCCTTGG     1156         GT  C
                                GTCCTGGGTG  GCC TGG
                                ||||||||||  ||| |||
                                CGGGACCCGC  CGG ACC
                                      __  A
GAM65   LOC254875 5'  GTCCTGGAGATCCTGG      1160        T  GC
                                GTCCTGGG GGT  CCTGG
                                |||||||| |||  |||||
                                CAGGACCT CTA  GGACC
                                     _  __
GAM66   GCLM     3'  TCATATTGAAGGAAATTACAGG 1168         AAA     _
                                TTATATTGA   AGGAAGT ACAGG
                                |||||||||   ||||||| |||||
                                AGTATAACT   TCCTTTA TGTCC
                                     ___      A
GAM66   NRIP1    3'  TATATTGAAAAGGATCAGG    1169          A  AGTA
                                TATATTGAAAA GGA    CAGG
                                |||||||||||| |||    ||||
                                ATATAACTTTT CCT    GTCC
                                      _  A___
GAM66   PXF      3'  TTATTTTGAGAAAGGAAA     1170      A   A
                                TTAT TTGA AAAGGAAG
                                |||| |||| ||||||||
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                                AATA AACT TTTCCTTT
                                  A   C
GAM66   RHD     3'  TATTCAAAAAGGGAAGTATAGG 1171      G     _    C
                                TATT AAAAAGG AAGTA AGG
                                |||| ||||||| ||||| |||
                                ATAA TTTTTCC TTCAT TCC
                                  G      C    A
GAM66   RHD     3'  TATTCAAAAAGGGAAGTATAGG 1171      G     _    C
                                TATT AAAAAGG AAGTA AGG
                                |||| ||||||| ||||| |||
                                ATAA TTTTTCC TTCAT TCC
                                  G      C    A
GAM66   SRD5A1  3'  TTATATTGATAACAGGTACAGG 1172          A  A  AA
                                TTATATTGA AA GG  GTACAGG
                                ||||||||| || ||  |||||||
                                AATATAACT TT TC  CATGTCC
                                     A  G  __
GAM66   APBA3   3'  TTATATTAGGAAATCATACAGG 1173        GAAAA   ___
                                TTATATT    AGGAA   GTACAGG
                                |||||||    |||||   |||||||
                                AATATAA    TCCTT   TATGTCC
                                   _____    TAG
GAM66   FLJ20105 5' TTGAAGAAGGAAATACAGG   1174       A
                                TTGAA AAGGAAGTACAGG
                                ||||| ||||||||||||
                                AACTT TTCCTTTATGTCC
                                   C
GAM66   HDAC9-PENDING 3'  TTATTTGAGAAAGGAAG     1175      A   A
                                TTAT TTGA AAAGGAAG
                                |||| |||| ||||||||
                                AATA AACT TTTCCTTC
                                  _   C
GAM66   KIAA0317 3'  GAGCAAAGGGGAGTACAGG   1176     A_    A_
                                GA  AAAGG  AGTACAGG
                                ||  |||||  ||||||||
                                CT  TTTCC  TCATGTCC
                                 CG    CC
GAM66   KIAA1034 3'  TTATTTGAAAAAGTACAG    1177      A    AAAG
                                TTAT TTGAA    GAAGTACAG
                                |||| |||||   |||||||||
                                AATA AACTT    TTTCATGTC
                                  _    ____
GAM66   MBLL39   3'  TATTGAGGAGGAAACAGG    1178       AAA    GT
                                TATTGA   AGGAA  ACAGG
                                ||||||   |||||  |||||
                                ATAACT   TCCTT  TGTCC
                                   CC_    __
GAM66   MBLL39   3'  TATTGAGGAGGAAACAGG    1178       AAA    GT
                                TATTGA   AGGAA  ACAGG
                                ||||||   |||||  |||||
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                                ATAACT   TCCTT  TGTCC
                                   CC_    __
GAM66   POPX1    3'  TTAAATTGAAAAAGGGATAC   1179     T        AA
                                TTA ATTGAAAAAGG  GTAC
                                ||| ||||||||||  ||||
                                AAT TAACTTTTTCC  TATG
                                  T         C_
GAM66   LOC165741 3'  TATTGAAAGAGGAGTAAGG   1180         A   A   C
                                TATTGAAA AGGA GTA AGG
                                |||||||| |||| ||| |||
                                ATAACTTT TCCT CAT TCC
                                     C   _  _
GAM66   LOC203197 3'  TTATATTGGAAAAAGGAAG   1181          _
                                TTATATTG AAAAAGGAAG
                                |||||||| ||||||||||
                                AATATAAC TTTTTCCTTC
                                     C
GAM66   LOC254735 3'  TATTGAAAAGGATGATACAGG  1182         A   A_
                                TATTGAAAA GGA  GTACAGG
                                ||||||||| |||  |||||||
                                ATAACTTTT CCT  TATGTCC
                                      _  AC
GAM66   LOC257319 3'  TTATATTGGAAAAGAAAA    1183         A
                                TTATATTG AAAAGGAAG
                                |||||||| |||||||||
                                AATATAAC TTTTCTTTT
                                     C
GAM67   OCRL     3'  TTACACAACACTGGATAT    1186         A  _
                                TTACACGG GC GGATAT
                                |||||||| || ||||||
                                AATGTGTT TG CCTATA
                                     G  A
GAM67   OCRL     3'  TTACACAACACTGGATAT    1186         A  _
                                TTACACGG GC GGATAT
                                |||||||| || ||||||
                                AATGTGTT TG CCTATA
                                     G  A
GAM67   FLJ11045  5'  TATTACATTACAGATAT    1187         CGGA
                                TATTACA   GCGGATAT
                                |||||||   ||||||||
                                ATAATGT   TGTCTATA
                                     AA__
GAM67   KIAA0397  3'  TTACACAGAAGAGTATA    1188           C GA
                                TTACACGGAG G  TATA
                                |||||||||| |  ||||
                                AATGTGTCTT C  ATAT
                                      _ TC
GAM67   KIAA1172  3'  TACAGCGGGAGCGGATATA   1189       _  _
                                TACA CGG AGCGGATATA
                                |||| ||| ||||||||||
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                                ATGT GCC TCGCCTATAT
                                  C   C
GAM67   KIAA1737 3'  TATGACATGGAACAAATA    1190     T   C
                                TAT ACA GGAGCGGATA
                                ||| ||| ||||||||||
                                ATA TGT CCTTGTTTAT
                                  C   A
GAM67   OR51E2   3'  TTACACAGGAAGCAATATA   1191       _   _   G
                                TTACAC GGA GCG ATATA
                                |||||| ||| ||| |||||
                                AATGTG CCT CGT TATAT
                                   T   T   _
GAM67   TRIM5    3'  TATCACACGATGATATA     1192          AGCG
                                TATTACACGG    GATATA
                                ||||||||||    ||||||
                                ATAGTGTGCT    CTATAT
                                      A___
GAM67   VEST1    5'  TATTACACAGCTAATAT     1193          AGCG
                                TATTACACGG    GATAT
                                ||||||||||    |||||
                                ATAATGTGTC    TTATA
                                      GA__
GAM67   LOC92106 5'  TATTACACTGAGACTTTTGGAT 1194         G   _ _____
                                TATTACAC GAG C    GGAT
                                |||||||| ||| |    ||||
                                ATAATGTG CTC G    CCTA
                                     A   T AAAA
GAM68   GFAP     3'  TGAGTCATCGCTCAGGA     1197          C G
                                TGAGTCATCGC C AGGA
                                |||||||||||| | ||||
                                ACTCAGTAGCG G TCCT
                                      A _
GAM68   KIAA0290 5'  TGAGTCACTGTCCAGCTCCGTG 1198        CGC   AGGA  C
            CC                    TGAGTCAT   CCG    CG GCC
                                |||||||   |||    || |||
                                ACTCAGTG   GGT    GC CGG
                                     ACA   CGAG  A
GAM69   KIAA1243 3'  GTAGGGCTTGGTCAAATGAC   1201       C       TGTCC
                                GTAGG CTTGGTCA     GAC
                                ||||| ||||||||     |||
                                CATCC GAACCAGT     CTG
                                   C       TTA__
GAM69   LOC221088 3'  GGCCTTGAAGTGCATGTC    1202         __  _
                                GGCCTTG  GT CATGTC
                                |||||||  || ||||||
                                CCGGAAC  CA GTACAG
                                     TT  C
GAM69   LOC256211 5'  TCGTAGCCTTGGGCGTCCG    1203        G     TCA
                                TCGTAG CCTTGG   TGTCCG
                                |||||| ||||||   ||||||
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                                AGCATC GGAACC   GCAGGC
                                  _     C__
GAM69   LOC51275  5'  GTAGGTGTATGTCCGA      1204       CCTTG  C
                                GTAGG    GT ATGTCCGA
                                |||||    || ||||||||
                                CATCC    CA TACAGGCT
                                  A_____ _
GAM70   C18orf1   3'  CAAGTCCCTGCCAGCAGG    1207         C   __
                                CAGGTCCC GTCG  AGG
                                |||||||| ||||  |||
                                GTTCAGGG CGGT  TCC
                                    A    CG
GAM70   GHRHR     3'  CAGGCCCCAGTAAGAGGA    1208         C  C_
                                CAGGTCCC GT  GAGGA
                                |||||||| ||  |||||
                                GTCCGGGG CA  CTCCT
                                    T  TT
GAM70   ITPA      3'  CAGATCCCCGGCCTGAGG    1209          _ _
                                CAGGTCCCCG TC GAGG
                                |||||||||| || ||||
                                GTCTAGGGGC GG CTCC
                                    C  A
GAM70   LIF       3'  CAGGCCCCCACATCTGGA    1210          __  GA
                                CAGGTCCCC  GTC  GGA
                                |||||||||  |||  |||
                                GTCCGGGGG  TAG  CCT
                                    TG   A_
GAM70   PIM1      3'  AGGTCCCCAAGTCAGAGGA   1211          __  _
                                AGGTCCCC  GTC GAGGA
                                ||||||||  ||| |||||
                                TCCAGGGG  CAG CTCCT
                                    TT   T
GAM70   ZNFN2A1   3'  AGGTCCCCTGCCCTGAGG    1212          _  __
                                AGGTCCCC GTC  GAGG
                                |||||||| |||  ||||
                                TCCAGGGG CGG  CTCC
                                    A   GA
GAM70   DKFZP586J1624 3'  CAGGTCCCGGTGCAGAGG    1213          C  _ _
                                CAGGTCCC GT C GAGG
                                |||||||| || | ||||
                                GTCCAGGG CA G CTCC
                                    C  C T
GAM70   FAM3D     3'  CAGGCCCCTGGCTGAGGA    1214          C_  C
                                CAGGTCCC  GT GAGGA
                                ||||||||  || |||||
                                GTCCGGGG  CG CTCCT
                                    AC  A
GAM70   FLJ00001  3'  CAGGTCCCCATACTCTGAGGA  1215          ___  _
                                CAGGTCCCCG   TC GAGGA
                                ||||||||||   || |||||
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                                GTCCAGGGGT  AG CTCCT
                                     ATG  A
GAM70   FLJ12700 3' CAGATCCCCACATCTGGA   1216        __  GA
                                CAGGTCCCC  GTC  GGA
                                |||||||||  |||  |||
                                GTCTAGGGG  TAG  CCT
                                     TG  A_
GAM70   KIAA0232 3' CAGGTCCCTCTCGGTGAGGA  1217        ___ TC
                                CAGGTCCC  CG  GAGGA
                                ||||||||  ||  |||||
                                GTCCAGGG  GC  CTCCT
                                     AGA  CA
GAM70   KIAA1243 3' CAGGCCCCTCTCAATGGA   1218        CG  _
                                CAGGTCCC  TCGA GGA
                                ||||||||  |||| |||
                                GTCCGGGG  AGTT CCT
                                     AG   A
GAM70   KIAA1328 3' CAAGTCCCCGTGAAAGGA   1219         C_
                                CAGGTCCCCGT  GAGGA
                                ||||||||||  |||||
                                GTTCAGGGGCA  TTCCT
                                      CT
GAM70   KIAA1887 5' CAGGTCCCATCGCTGAGGA  1220        __  C
                                CAGGTCCC  CGT GAGGA
                                ||||||||  ||| |||||
                                GTCCAGGG  GCG CTCCT
                                     TA  A
GAM70   KIAA1987 3' CAGGCCCCCACTGCCGGG   1221        ___  A
                                CAGGTCCCC  GTCG GG
                                |||||||||  |||| ||
                                GTCCGGGGG  CGGC CC
                                     TGA  _
GAM70   LACE1    3' CAAGTCCCACAATAAGGA   1222        _ TC
                                CAGGTCCC CG  GAGGA
                                ||||||||  ||  |||||
                                GTTCAGGG GT  TTCCT
                                     T  TA
GAM70   MCT-1    5' CAGATCCCCTCACACGAGGA  1223       GT___
                                CAGGTCCCC   CGAGGA
                                |||||||||   ||||||
                                GTCTAGGGG   GCTCCT
                                     AGTGT
GAM70   MGC10540 3' CAGGTCCCAGCCTTCAGGA  1224        C  G__
                                CAGGTCCC GTC  AGGA
                                ||||||||  |||  ||||
                                GTCCAGGG CGG  TCCT
                                     T  AAG
GAM70   NKD1     3' CAGATCCCGAGCCCCGAGG  1225        C_ __
                                CAGGTCCC  GT  CGAGG
                                ||||||||  ||  |||||
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                                GTCTAGGG CG GCTCC
                                    CT GG
GAM70   PRO1483  3' CAGGCCCCTTCCACTAGGA  1226       CG __
                                CAGGTCCC TCG AGGA
                                |||||||| ||| ||||
                                GTCCGGGG GGT TCCT
                                    AA GA
GAM70   SEC61A1  3' CAGGCCCCCTTCTTAGGA  1227       G G_
                                CAGGTCCCC TC AGGA
                                ||||||||| || ||||
                                GTCCGGGGG AG TCCT
                                    A AA
GAM70   TIP120A  3' CAGATCCCTTAATCAGGA  1228       C__ G
                                CAGGTCCC GTC AGGA
                                |||||||| ||| ||||
                                GTCTAGGG TAG TCCT
                                    AAT _
GAM70   LOC128272 3' GGTCCCCATGTCAGAGGA  1229       __ _
                                GGTCCCC GTC GAGGA
                                ||||||| ||| |||||
                                CCAGGGG CAG CTCCT
                                    TA T
GAM70   LOC158515 5' CAGGTCCCAGCAGCGGGA  1230       C __ A
                                CAGGTCCC GT CG GGA
                                |||||||| || || |||
                                GTCCAGGG CG GC CCT
                                    T TC _
GAM70   LOC200982 3' CAGGTCCCTCAGCCAGGA  1231       _ _ G
                                CAGGTCCC C GTC AGGA
                                |||||||| | ||| ||||
                                GTCCAGGG G CGG TCCT
                                    A T _
GAM70   LOC91917  3' CAGGTCCCTGGCACGGGGA  1232       C_ _ A
                                CAGGTCCC GT CG GGA
                                |||||||| || || |||
                                GTCCAGGG CG GC CCT
                                    AC T C
GAM71   PIM1    3' TGGCGAGACGTGTCACG    1235       G TCAGC   C
                                TGGCGGGA GT   GTCAC G
                                |||||||| ||    ||||| |
                                ACCGCTCT CA   CAGTG C
                                    G _____   A
GAM71   VASP    5' TGGCTGGAGGTTCAGGGGTTCG 1236     G       CGTCAC
          G                      TGGC GGAGGTTCAG    CGG
                                |||| ||||||||||    |||
                                ACCG CCTCCAAGTC    GCC
                                  A       CCCAA_
GAM71   SART3   3' TGGTGGGAGGTCCGCC     1237     C       A GTCAC
                                TGG GGGAGGTTC GC   C
                                ||| ||||||||| ||   |
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                                ACC CCCTCCAGG CG    G
                                  A       _ _____
GAM72   ANKH    3'  TATTCCTACTCCAGTGACC   1240       GTAC    ___
                                TATTCC   TGCTCC  GACC
                                ||||||   ||||||  ||||
                                ATAAGG   ATGAGG  CTGG
                                   ____     TCA
GAM72   CXADR   3'  TATTCCGTACAGTTCCTGA   1241         TGC  _
                                TATTCCGTAC   TCC GA
                                ||||||||||   ||| ||
                                ATAAGGCATG   AGG CT
                                      TCA   A
GAM72   MTNR1A  3'  CATTCTGTACTTCTCTTGAC  1242      C    G  C_
                                TATTC GTACT CTC  GAC
                                |||||  ||||| |||  |||
                                GTAAG CATGA GAG  CTG
                                   A    A   AA
GAM72   MX1     5'  TTCCTGTAGCCTCCGACC    1243     _  CTG
                                TTCC GTA   CTCCGACC
                                ||||  |||   ||||||||
                                AAGG CAT   GAGGCTGG
                                  A  CG_
GAM72   SCA1    3'  TTCCTATTGCTCCAAACC    1244     G  C      _
                                TTCC TA TGCTCCGA CC
                                ||||  ||  |||||||  ||
                                AAGG AT ACGAGGTT GG
                                  _ A       T
GAM72   GMPPB   3'  TATTCCATACAGCCCTGGCC  1245         T   CGA
                                TATTCCGTAC GCTC   CC
                                ||||||||||  ||||   ||
                                ATAAGGTATG CGGG   GG
                                      T   ACC
GAM72   GMPPB   3'  TATTCCATACAGCCCTGGCC  1245         T   CGA
                                TATTCCGTAC GCTC   CC
                                ||||||||||  ||||   ||
                                ATAAGGTATG CGGG   GG
                                      T   ACC
GAM72   GMPPB   5'  TATTCCATACAGCCCTGGCC  1245         T   CGA
                                TATTCCGTAC GCTC   CC
                                ||||||||||  ||||   ||
                                ATAAGGTATG CGGG   GG
                                      T   ACC
GAM72   IGF2AS  3'  TATTCCGTGCCATGACC     1246        ACT   CC
                                TATTCCGT   GCT  GACC
                                ||||||||   |||  ||||
                                ATAAGGCA   CGG  CTGG
                                   ___   TA
GAM72   JIK     5'  TATTCCATATTGCTCAGA     1247         C    C
                                TATTCCGTA TGCTC GA
                                |||||||||  |||||  ||
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                                ATAAGGTAT ACGAG CT
                                     A    T
GAM72   KIAA1068 3' CTCCACTGCTCTGACC     1248      GT     C
                                TTCC  ACTGCTC GACC
                                ||||  ||||||| ||||
                                GAGG  TGACGAG CTGG
                                  __      A
GAM72   NET-5    5' TATTCCGCGCCCGCAGGACC  1249        A_   TCC
                                TATTCCGT  CTGC   GACC
                                ||||||||  ||||   ||||
                                ATAAGGCG  GGCG   CTGG
                                     CG    TC_
GAM72   PSK-1    5' TTCCTCCGTCTCCGACC     1250      GTA  _
                                TTCC   CTG CTCCGACC
                                ||||   ||| ||||||||
                                AAGG   GGC GAGGCTGG
                                  A__   A
GAM72   STK17B   5' TATTTTTACCGCTCCGGCC   1251      CCG       A
                                TATT   TACTGCTCCG CC
                                ||||   |||||||||| ||
                                ATAA   ATGGCGAGGC GG
                                  AA_        C
GAM72   STX12    3' TATTCCGTCTCCAAACC     1252        ACTG     _
                                TATTCCGT    CTCCGA CC
                                ||||||||    |||||| ||
                                ATAAGGCA    GAGGTT GG
                                     ____     T
GAM72   LOC144248 5' ATTCCGTACTCTCTGAC     1253          G   C
                                ATTCCGTACT CTC GAC
                                |||||||||| ||| |||
                                TAAGGCATGA GAG CTG
                                     _  A
GAM72   LOC150356 3' CTCCGTGCTCAGAGACGACC  1254        ACT   _____
                                TTCCGT   GCTC    CGACC
                                ||||||   ||||    |||||
                                GAGGCA   CGAG    GCTGG
                                   ___   TCTCT
GAM72   LOC154215 3' TATTCCATAAACACATTGACC  1255         CT_  TCC
                                TATTCCGTA   GC   GACC
                                |||||||||   ||   ||||
                                ATAAGGTAT   TG   CTGG
                                     TTG  TAA
GAM72   LOC168576 5' ATTCCGTACTCGCACCGA    1256          _  T
                                ATTCCGTACT GC CCGA
                                |||||||||| || ||||
                                TAAGGCATGA CG GGCT
                                     G  T
GAM72   LOC197342 5' TTCAGCACCTGCTCCGGCC   1257      C   _      A
                                TTC GTAC TGCTCCG CC
                                ||| |||| ||||||| ||
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                                AAG CGTG ACGAGGC GG
                                  T   G      C
GAM72   LOC256158 5'  TATTCCGTGACTCCGCC     1258         ACT     A
                                TATTCCGT   GCTCCG CC
                                ||||||||   |||||| ||
                                ATAAGGCA   TGAGGC GG
                                    C__     _
GAM72   LOC55908  5'  TATTCCGTGCTCACACC     1259         ACT    CG
                                TATTCCGT   GCTC  ACC
                                ||||||||   ||||  |||
                                ATAAGGCA   CGAG  TGG
                                    ___    TG
GAM73   ANK1      3'  GCCACAGCTCCTTCTCCTGCAG 1262      TTTC        C
                                GCT    TTCCTTCTCC GCAG
                                |||    |||||||||| ||||
                                CGG    GAGGAAGAGG CGTC
                                  TGTC         A
GAM73   ANK1      3'  GCCACAGCTCCTTCTCCTGCAG 1262      TTTC        C
                                GCT    TTCCTTCTCC GCAG
                                |||    |||||||||| ||||
                                CGG    GAGGAAGAGG CGTC
                                  TGTC         A
GAM73   EIF4EBP2  3'  GCTTTTCTTCTAATCCTTGCAG 1263          C TC   C_
                                GCTTTTCTTC T  TCC  GCAG
                                |||||||||| |  |||  ||||
                                CGAAAAGAAG A  AGG  CGTC
                                    _ TT   AA
GAM73   KTN1      3'  GCTTTTTTTTTCCTTCTTTAAA 1264        C__       CCCG__
          TCAG                    GCTTTT   TTCCTTCT     CAG
                                ||||||   ||||||||     |||
                                CGAAAA   AAGGAAGA     GTC
                                   AAA       AATTTA
GAM73   MYBL1     3'  CGCTCTTTCCTTCTCTCG     1265         CT       C
                                CGCTTTT  TCCTTCTC CG
                                |||||||  |||||||| ||
                                GCGAGAA  AGGAAGAG GC
                                   __        A
GAM73   NORE1     3'  ACTTTTTTTTTCCTTCTC     1266        C__
                                GCTTTT   TTCCTTCTC
                                ||||||   |||||||||
                                TGAAAA   AAGGAAGAG
                                   AAA
GAM73   PODXL     3'  CGCTTTCCAGGCCCTCTTTTCC 1267          TT_     C__
                                CGCTTTTC   CCTTCT   CC
                                ||||||||   ||||||   ||
                                GCGAAAGG   GGGAGA   GG
                                    TCC     AAA
GAM73   POV1      3'  TTTTCCTCCTTTTTGCAG     1268          CTCCC
                                TTTTCTTCCTT    GCAG
                                ||||||||||     ||||
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                                AAAAGGAGGAA    CGTC
                                     AAA__
GAM73   SET     3' TTTTCTTTTTTCCCACAG    1269        CC  C
                                TTTTCTT  TT TCCCGCAG
                                |||||||  || ||||||||
                                AAAAGAA  AA AGGGTGTC
                                   __ A
GAM73   CARD9   3' CGCGTCCTTCTCCTGCAG    1270     TTTTCT       C
                                CGC     TCCTTCTCC GCAG
                                |||     ||||||||| ||||
                                GCG     AGGAAGAGG CGTC
                                  C_____        A
GAM73   DKFZP564B1162 3' ACTTTTCTCCTTCTCCTGCAG  1271         T      C
                                GCTTTTCT CCTTCTCC GCAG
                                |||||||| |||||||| ||||
                                TGAAAAGA GGAAGAGG CGTC
                                   _      A
GAM73   FLJ10922  3' GCTTTCCTTCCCTCCAACTCCT 1272            ____  C
            GCAG                    GCTTTTCTTCCTTC    TCC GCAG
                                |||||||||||||    ||| ||||
                                CGAAAGGAAGGGAG    AGG CGTC
                                      GTTG   A
GAM73   FLJ20548  3' GCCCTTAGTGTCTTCTCCCGCA 1273       CTTC_
            G                    GCTTTT    CTTCTCCCGCAG
                                ||||||    ||||||||||||
                                CGGGAA    GAAGAGGGCGTC
                                   TCACA
GAM73   FLJ21159  3' GCTTCTCCTTTTCTTGCAG   1274         CC   CCC
                                GCTTTTCTT  TTCT   GCAG
                                |||||||||  ||||   ||||
                                CGAAGAGGA  AAGA   CGTC
                                     A_   A__
GAM73   FLJ22037  3' TTTTCTTCAACTTCTGCAG   1275        __    CCC
                                TTTTCTTC  CTTCT   GCAG
                                ||||||||  |||||   ||||
                                AAAAGAAG  GAAGA   CGTC
                                     TT    ____
GAM73   FLJ23058  3' CGTTTTATTTTCTTCTCCC   1276    C   TC  C
                                CG TTT  TT CTTCTCCC
                                || |||  || ||||||||
                                GC AAA  AA GAAGAGGG
                                 A   TA  A
GAM73   KIAA0453  3' ACTTTTTTTTTCCTTCTC    1266       C__
                                GCTTTT   TTCCTTCTC
                                ||||||   |||||||||
                                TGAAAA   AAGGAAGAG
                                   AAA
GAM73   KIAA0664  3' GCTCGCCCCCTTCTCCCGCAG  1277      TT
                                GCTT  CTTCCTTCTCCCGCAG
                                ||||  ||||||||||||||||
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                                CGAG  GGGGGAAGAGGGCGTC
                                  C_
GAM73   KIAA0748  3'  GCTGCCTTTCTCCTGCAG    1278     TTTCTT   _   C
                                GCT     CCTT CTCC GCAG
                                |||     |||| |||| ||||
                                CGA     GGAA GAGG CGTC
                                  C_____   A   A
GAM73   LYPLA2    5'  CGATTCTCCTCTTTCTCCCGCA 1279     C      C
           G                     CG TTTTCTTC TTCTCCCGCAG
                                 || |||||||| ||||||||||
                                 GC AAGAGGAG AAGAGGGCGTC
                                  T       A
GAM73   SLC38A4   3'  TTTTCCTCTTCTGCA       1280         C   CCC
                                TTTTCTTC TTCT   GCA
                                |||||||| ||||   |||
                                AAAAGGAG AAGA   CGT
                                    _   ___
GAM73   LOC112724 5'  TTTCCTTCCTTCCTTAAGC   1281            CCC_
                                TTTTCTTCCTTCT   GC
                                ||||||||||||    ||
                                AAAGGAAGGAAGG   CG
                                      AATT
GAM73   LOC147670 3'  CACTTTTCTTTCTCC       1282          CCT
                                CGCTTTTCTT   TCTCC
                                ||||||||||   |||||
                                GTGAAAAGAA   AGAGG
                                    ___
GAM73   LOC148343 5'  GCTTTTTTTCCTTCTTCCC   1283        C      _
                                GCTTTT TTCCTTCT CCC
                                |||||| |||||||| |||
                                CGAAAA AAGGAAGA GGG
                                   A       A
GAM73   LOC151465 3'  CTTTTTTTCCTTCCTCACA   1284       C      CC
                                CTTTT TTCCTTCT  CGCA
                                ||||| ||||||||  ||||
                                GAAAA AAGGAAGG  GTGT
                                   A       A_
GAM73   LOC197419 5'  ACGCTTCAACCCTTCTCC    1285        TCT
                                ACGCTTT   TCCTTCTCC
                                |||||||   |||||||||
                                TGCGAAG   GGGAAGAGG
                                   TT_
GAM73   LOC254945 5'  GCTTTTCTTTTTTCTACAACAG 1286          CC   CCC
                                GCTTTTCTT  TTCT   GCAG
                                |||||||||  ||||   ||||
                                CGAAAAGAA  AAGA   TGTC
                                     AA    TGT
GAM73   LOC255000 3'  ACGCCTGCACGTCTTTTCCCGC 1287        TTCTTC   C
           AG                   ACGCTT     CTT TCCCGCAG
                                ||||||     ||| ||||||||
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                                TGCGGA     GAA AGGGCGTC
                                   CGTGCA   A
GAM73   LOC64182  5'  GCTTTGGTCCTTCTCCCGCAG  1288       TCT
                                GCTTT   TCCTTCTCCCGCAG
                                |||||   ||||||||||||||
                                CGAAA   AGGAAGAGGGCGTC
                                   CC_
GAM74   CYFIP2    5'  GTCAAAGTTAGCCTGGTACATG 1291          A     _
          A                      GTCAAAGTTA GCTTGGT CATGA
                                |||||||||| ||||||| |||||
                                CAGTTTCAAT CGGACCA GTACT
                                      _      T
GAM74   DDEF1     3'  CGTTCAAAAACTTGGTTATGA  1292     _    TTAA      C
                                CGT CAAAG    GCTTGGT ATGA
                                ||| |||||    ||||||| ||||
                                GCA GTTTT    TGAACCA TACT
                                  A    _____      A
GAM74   FACL5     3'  ATTAAGGTTGGAAATCATGA   1293       C    ___
                                GTTAAG TTGG   TCATGA
                                |||||| ||||   ||||||
                                TAATTC AACC   AGTACT
                                   C    TTT
GAM74   MPV17     3'  GTAAAGTTGATAAGGTCATGA  1294     C     AAGCTT
                                GT AAAGTT     GGTCATGA
                                || ||||||     ||||||||
                                CA TTTCAA     CCAGTACT
                                 _     CTATT_
GAM74   PPFIA3    5'  GCCAGGATGGGCTTGGTCGTG  1295      AA  TAA      A
                                GTCA  GT   GCTTGGTC TG
                                ||||  ||   |||||||| ||
                                CGGT  TA   CGAACCAG AC
                                  CC  CC_       C
GAM74   ZNF146    3'  GTTAAAGTTAACCTCATTCGTG 1296     C       G   GG  A
                                GT AAAGTTAA CTT  TC TG
                                || |||||||| |||  || ||
                                CA TTTCAATT GAG  AG AC
                                 A       G   TA  C
GAM74   FLJ10997  3'  GTTAAAATTAAGCCATATGA   1297     C         TGGTC
                                GT AAAGTTAAGCT     ATGA
                                || ||||||||||     ||||
                                CA TTTTAATTCGG     TACT
                                 A          TA___
GAM74   FLJ12057  3'  GTCAGTGGTTGGGCTGATCATG 1298       AA_   AA   T
                                GTCA   GTT  GCT GGTCATG
                                ||||   |||  ||| |||||||
                                CAGT   CAA  CGA CTAGTAC
                                  CAC   CC   _
GAM74   FLJ20033  3'  GCCAAAGTTAAGTTTCTATGA  1299           CTTGG  _
                                GTCAAAGTTAAG    TC ATGA
                                ||||||||||||    || ||||
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                                CGGTTTCAATTC    AG TACT
                                      AA___  A
GAM74   KIAA0419  3'  GTCAAAGTTAAATTTAAAATG  1300          C   TC
                                GTCAAAGTTAAG TTGG  ATG
                                |||||||||||| ||||  |||
                                CAGTTTCAATTT AATT  TAC
                                      A   T_
GAM74   KRTAP9-8  3'  GTCAAAGTTGAGATCATG    1301         AAGCTT
                                GTCAAAGTT     GGTCATG
                                |||||||||     |||||||
                                CAGTTTCAA     CTAGTAC
                                     CT____
GAM74   LOC145813 5'  CGTCAAGGTTGCAGTGAGCCAT 1302       A   AA  T_  _
          GA                      CGTCAA GTT  GC  TG GTCATGA
                                |||||| |||  ||  || |||||||
                                GCAGTT CAA  CG  AC CGGTACT
                                   C   __  TC  T
GAM74   LOC219653 3'  TCAAAAAGGGGCTTGGTCGTG  1303       TTAA      A
                                TCAAAG    GCTTGGTC TG
                                ||||||    |||||||| ||
                                AGTTTT    CGAACCAG AC
                                    TCCC       C
GAM75   B3GALT2   5'  TGACAAAAATGTTTTCTTCTCC 1306          A_   CCA_
          T                      TGACAAAGAT  TTTC    CCT
                                |||||||||  ||||    |||
                                ACTGTTTTTA  AAAG    GGA
                                      CA    AAGA
GAM75   CDH1     3'  TGAGGTAGACCCACCTCA    1307     CAA   TATTT
                                TGA   AGA    CCCACCTCA
                                |||   |||    |||||||||
                                ACT   TCT    GGGTGGAGT
                                  CCA   _____
GAM75   MYH1     3'  TGACAAAGATTTTCACA     1308          A   C
                                TGACAAAGAT TTTC CA
                                |||||||||| |||| ||
                                ACTGTTTCTA AAAG GT
                                      _   T
GAM75   VDR      3'  TGATGGGAAGAAAACCCACCTC 1309     CA__   TATTT
          A                      TGA    AAGA    CCCACCTCA
                                |||    ||||    |||||||||
                                ACT    TTCT    GGGTGGAGT
                                  ACCC    TTT__
GAM75   AF020591  3'  TGGCAGGGAAATTTCCCATCT  1310     A  AA  T      C
                                TG CA  GA ATTTCCCA CT
                                || ||  || |||||||| ||
                                AC GT  CT TAAAGGGT GA
                                 C  CC  T       A
GAM75   ALS2CR8   5'  TGGCAAAGATATATTAAACCT  1311     A       TTCCC
                                TG CAAAGATAT    ACCT
                                || |||||||||    ||||
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                                AC GTTTCTATA    TGGA
                                 C       TAATT
GAM75   AP3S2    3'  TGACAGAGCAAGACTCCACCTC 1312      A  ATATTTC
           A                     TGACA AG      CCACCTCA
                                 ||||| ||      ||||||||
                                 ACTGT TC      GGTGGAGT
                                    C  GTTCTGA
GAM75   APOL4    3'  ACAAAGATCACCTACTTCA   1313        ATTT  C  C
                                 ACAAAGAT    CC AC TCA
                                 ||||||||    || || |||
                                 TGTTTCTA    GG TG AGT
                                      GT__  A  A
GAM75   C21orf91  3'  TGACAAAGATGTTAAATACTGC 1314          A  TCCCA___
           CT                     TGACAAAGAT TT       CCT
                                 |||||||||| ||       |||
                                 ACTGTTTCTA AA       GGA
                                       C  TTTATGAC
GAM75   DKFZP586B1621 3'  TGACAAAGGCCACCTC      1315         ATATTTC
                                 TGACAAAG      CCACCTC
                                 ||||||||      |||||||
                                 ACTGTTTC      GGTGGAG
                                      C_______
GAM75   DKFZp761F2014 3'  TGCAGGGAGCACAACCCACCTC 1316     A  AA  _   TT
                                 TG CA  GA TAT  CCCACCTC
                                 || ||  || |||  ||||||||
                                 AC GT  CT GTG  GGGTGGAG
                                  _  CC  C   TT
GAM75   DKFZp762M136 3'  GACACCATTTCCCACCTC    1317      AAGA
                                 GACA    TATTTCCCACCTC
                                 ||||    ||||||||||||
                                 CTGT    GTAAAGGGTGGAG
                                   G___
GAM75   FLJ13868  3'  GACAGAACTCCCACCTC     1318       AA  TAT
                                 GACA  GA   TTCCCACCTC
                                 ||||  ||   ||||||||||
                                 CTGT  CT   GAGGGTGGAG
                                    __  T__
GAM75   FLJ20126  3'  TGACAATATTTCCACTTCA   1319       AAG       C  C
                                 TGACA   ATATTTCC AC TCA
                                 |||||   |||||||| || |||
                                 ACTGT   TATAAAGG TG AGT
                                    ___       _  A
GAM75   FLJ20986  5'  TGAAAAAGATATTCTTTACCT  1320      C         CCC
                                 TGA AAAGATATTT   ACCT
                                 ||| ||||||||||   ||||
                                 ACT TTTCTATAAG   TGGA
                                   T         AAA
GAM75   FLJ23042  3'  TGATGGAAATTCTCCCCAC    1321      CAA    A
                                 TGA   AGAT TTTCCCAC
                                 |||   |||| ||||||||
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                                ACT   TTTA GAGGGGTG
                                  ACC    A
GAM75   HSPC054  3'  TGACAAAAATCCTTCACTTCA  1322         TATT   __   C
                                TGACAAAGA    TCC  CAC TCA
                                |||||||||    |||  ||| |||
                                ACTGTTTTT    AGG  GTG AGT
                                     ____   AA   A
GAM75   JDD1     3'  TGAAGCCATCTTCCCACCTCA  1323    A   ATA_
                                C AAG    TTTCCCACCTCA
                                | |||    ||||||||||||
                                A TTC    GAAGGGTGGAGT
                                 C   GGTA
GAM75   KCNV1    3'  TAACATATATTTCCCA      1324       AAG
                                TGACA   ATATTTCCCA
                                |||||   ||||||||||
                                ATTGT   TATAAAGGGT
                                   A__
GAM75   KIAA0010 3'  GACAAAGATGCAGCCGCCAC   1325         ATT_ _
                                GACAAAGAT    TC CCAC
                                |||||||||    || ||||
                                CTGTTTCTA    GG GGTG
                                     CGTC  C
GAM75   KIAA0514 3'  TGCATGAGTCATTTCCACCTCA 1326     A  A_  A      C
                                TG CA  AG TATTTCC ACCTCA
                                || ||  || ||||||| ||||||
                                AC GT  TC GTAAAGG TGGAGT
                                 _  AC  A      _
GAM75   KIAA0800 3'  TGACACAGACCCACTTC     1327       A   TATTT    C
                                TGACA AGA    CCCAC TC
                                ||||| |||    ||||| ||
                                ACTGT TCT    GGGTG AG
                                   G   _____    A
GAM75   KIAA1254 3'  TGACAAAGCAAGATTCCATCTC 1328         ATAT_   CAC
            A                    TGACAAAG    TTCC   CTCA
                                |||||||||    ||||   ||||
                                ACTGTTTC     AAGG   GAGT
                                     GTTCT    TA_
GAM75   KIAA1327 3'  TGACAGAAATATCCACCT    1329       A     TTC
                                TGACA AGATAT   CCACCT
                                ||||| ||||||   ||||||
                                ACTGT TTTATA   GGTGGA
                                   C     ___
GAM75   MAD4     3'  CAGGGACACGACCACCTCA   1330     AA    TTC
                                CA  GATAT   CCACCTCA
                                ||  |||||   ||||||||
                                GT  CTGTG   GGTGGAGT
                                 CC    CT_
GAM75   MGC10200 3'  TGACAAAGCAAGATCCTGTCTC 1331         ATATT   CAC
            A                    TGACAAAG    TCC   CTCA
                                |||||||||    |||   ||||
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                                ACTGTTTC    AGG   GAGT
                                    GTTCT   ACA
GAM75   NCUBE1   3'  TGACAAAGATGTGATCTC    1332          ___
                                TGACAAAGAT   ATTTC
                                ||||||||||  |||||
                                ACTGTTTCTA   TAGAG
                                     CAC
GAM75   NPD002   3'  TGACACAGGTCCCCACCCACCT 1333       A  ATA_ TT
           CA                    TGACA AG    T  CCCACCTCA
                                ||||| ||    |  |||||||||
                                ACTGT TC    G  GGGTGGAGT
                                  G  CAGG GT
GAM75   POF1B    3'  TGCAAAGATATTTCAGTCC   1334     A         CCA
                                TG CAAAGATATTTC   CC
                                || ||||||||||||   ||
                                AC GTTTCTATAAAG   GG
                                 _          TCA
GAM75   SLC26A7  3'  TGACAAAAGTATTTCTCA    1335         A     C
                                TGACAAAG TATTTC CA
                                |||||||| |||||| ||
                                ACTGTTTT ATAAAG GT
                                     C     A
GAM75   TCEA3    3'  CAAAGATATGACACCTCA    1336          TTCC
                                CAAAGATAT    CACCTCA
                                |||||||||    |||||||
                                GTTTCTATA    GTGGAGT
                                     CT__
GAM75   TU12B1-TY 3'  TGACAAAGATGCTTTTTCC   1337          A___
                                TGACAAAGAT    TTTCC
                                ||||||||||    |||||
                                ACTGTTTCTA    AAAGG
                                     CGAA
GAM75   VDU1     3'  TGACAAAGCAAGACTCTGTCTC 1338         ATAT_  CCAC
           A                     TGACAAAG    TTC    CTCA
                                ||||||||    |||   ||||
                                ACTGTTTC    GAG    GAGT
                                     GTTCT   ACA_
GAM75   LOC126603 5'  TGACAAAGAGGCTCACCACCTC 1339          TA  TC
           A                     TGACAAAGA  TT  CCACCTCA
                                |||||||||  ||  ||||||||
                                ACTGTTTCT  GA  GGTGGAGT
                                     CC  GT
GAM75   LOC143286 5'  TGACTGGTCTTCCCACCTCA   1340      AAAGATA
                                TGAC      TTTCCCACCTCA
                                ||||      ||||||||||||
                                ACTG      GAAGGGTGGAGT
                                  ACCA___
GAM75   LOC151963 3'  ACAAAGACACCTACTTC     1341          TTT  C  C
                                ACAAAGATA   CC AC TC
                                |||||||||   || || ||
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                                TGTTTCTGT   GG TG AG
                                     ___  A  A
GAM75   LOC152503 3'  CAAAGATATATACCTCA     1342          TTCCC
                                CAAAGATAT    ACCTCA
                                |||||||||    ||||||
                                GTTTCTATA    TGGAGT
                                     TA___
GAM75   LOC197408 5'  TGATCAAGATACCCCTGCCTCA 1343      CA      TT   A_
                                TGA  AAGATAT  CCC  CCTCA
                                |||  |||||||  |||  |||||
                                ACT  TTCTATG  GGG  GGAGT
                                  AG       __   AC
GAM75   LOC201183 5'  GATAGAAGACCTTCCCACCT   1344     CA_    A
                                GA   AAGAT TTTCCCACCT
                                ||   ||||| ||||||||||
                                CT   TTCTG GAAGGGTGGA
                                  ATC    _
GAM75   LOC257482 3'  GACAAAGAATCTGCCTC     1345         T    CCCA
                                GACAAAGA ATTT    CCTC
                                |||||||| ||||    ||||
                                CTGTTTCT TAGA    GGAG
                                     _    C___
GAM75   LOC51246  3'  CAAGGATTGTTCCCCACCT    1346      A   A_
                                CAA GAT  TTTCCCACCT
                                ||| |||  ||||||||||
                                GTT CTA  AAGGGGTGGA
                                  C   AC
GAM75   LOC90139  3'  TGAAGAAGATATCCAAGCCTCA 1347      CA     TT   CA_
                                TGA  AAGATA  TCC   CCTCA
                                |||  ||||||  |||   |||||
                                ACT  TTCTAT  AGG   GGAGT
                                  TC      __   TTC
GAM75   LOC91351  3'  GACAAACATTTTTTCCATTTCA 1348       G  A   C   CC
                                GACAAA AT TTT CCA  TCA
                                |||||| || ||| |||  |||
                                CTGTTT TA AAA GGT  AGT
                                    G  A   A   AA
GAM76   APBA2     3'  TCCTCTGGGCCCGGGCGGC    1351      GG_    AG
                                TCC   GGGC  CCGGGCGGC
                                |||   ||||  |||||||||
                                AGG   CCCG  GGCCCGCCG
                                  AGA   __
GAM76   AXIN1     3'  GCTCTGGGCCCTGCGGGTGGCC 1352      CGG    AGC_   C
                                GCTC   GGGC    CGGG GGCC
                                ||||   ||||    |||| ||||
                                CGAG   CCCG    GCCC CCGG
                                  A__    GGAC    A
GAM76   CA12      5'  CCGGGGGCTCCCGGTGGCC    1353         AG    GC
                                CCGGGGGC  CCGG  GGCC
                                ||||||||  ||||  ||||
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                                GGCCCCCG  GGCC  CCGG
                                    AG    A_
GAM76   DDB1     3'  GCTCTGGGGGCAGCTGGC    1354       C        CG
                                GCTC GGGGGCAGC  GGC
                                |||| |||||||||  |||
                                CGAG CCCCCGTCG  CCG
                                  A        A_
GAM76   EP300    5'  CGCTCCGGCGGCGGGCGCAGGC 1355          G   A_ _
           GGCC                    CGCTCCGG GGC  GC CGGGCGGCC
                                |||||||| |||  || |||||||||
                                GCGAGGCC CCG  CG GTCCGCCGG
                                    G   CC  C
GAM76   FBXL3A   5'  GCTCCGGGGACGGCGGCGGC   1356           A  CG
                                GCTCCGGGGGC GC  GGCGGC
                                |||||||||| ||  ||||||
                                CGAGGCCCCTG CG  CCGCCG
                                      C  __
GAM76   FGF18    5'  CGCTCCGGGGTCGGGGCGCGCG 1357          GCAGC_  G
           GC                    CGCTCCGGGG     CG GCGGC
                                |||||||||      || |||||
                                GCGAGGCCCC     GC CGCCG
                                     AGCCCC  G
GAM76   FGF18    5'  CGCTCCGGGGTCGGGGCGCGCG 1357          GCAGC_  G
           GC                    CGCTCCGGGG     CG GCGGC
                                |||||||||      || |||||
                                GCGAGGCCCC     GC CGCCG
                                     AGCCCC  G
GAM76   FUT5     3'  CGCCCGGGGGCAGGGC      1358      T       GCC
                                CGC CCGGGGGCA   GGGC
                                ||| |||||||||   ||||
                                GCG GGCCCCCGT   CCCG
                                  _       ____
GAM76   GLS      5'  GCTCCGGGCGTGGGCGGCC   1359          GGCAGCC
                                GCTCCGGG      GGGCGGCC
                                ||||||||      ||||||||
                                CGAGGCCC      CCCGCCGG
                                     GCA____
GAM76   HRB      5'  GCGCCGGGGGCCCGCGG     1360     T      AG  GG
                                GC CCGGGGGC  CC  GCGG
                                || ||||||||  ||  ||||
                                CG GGCCCCCG  GG  CGCC
                                 C       __  __
GAM76   MAPK4    3'  GCTCTGTGGGGCCTGGAGCGGC 1361       CG_    AGCC
           C                     GCTC   GGGGC   GGGCGGCC
                                ||||   |||||   ||||||||
                                CGAG   CCCCG   CTCGCCGG
                                  ACA    GAC_
GAM76   MATK     5'  GCTCCGGGGACCGCGGC     1362           AGCCGG
                                GCTCCGGGGGC     GCGGC
                                ||||||||||      |||||
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                                CGAGGCCCCTG     CGCCG
                                      G_____
GAM76   MFI2     3'  GCTCTGGGGCGGGGCGGC    1363      CG    AGCC
                                GCTC  GGGGC   GGGCGGC
                                ||||  |||||   |||||||
                                CGAG  CCCCG   CCCGCCG
                                  A_    C___
GAM76   ODF2     3'  GCTTGGGGGCAAGTGGC     1364      CC     GCCG  C
                                GCT  GGGGGCA   GG GGC
                                |||  |||||||   || |||
                                CGA  CCCCCGT   TC CCG
                                  A_      ____ A
GAM76   PGF      5'  CTCCCGTAGCTGGGCGGCC   1365      GGG   AGCC
                                CTCC   GGC   GGGCGGCC
                                ||||   |||   ||||||||
                                GAGG   TCG   CCCGCCGG
                                  GCA   A___
GAM76   SLC1A2   5'  GCTCCGGGGGCTCCGAGGGTGG 1366          AG __   C
              C                  GCTCCGGGGGC  CC  GGG GGC
                                ||||||||||  ||  ||| |||
                                CGAGGCCCCCG  GG  CCC CCG
                                      A_  CT   A
GAM76   SLC1A4   5'  CGCCCCGGGGGTCTCGCGGCC  1367          CAGCCGG
                                CGCTCCGGGGG      GCGGCC
                                ||||||||||      ||||||
                                GCGGGGCCCCC      CGCCGG
                                      AGAG___
GAM76   SP3      5'  CGCTCCGGCGGCGGCGGGGGCC 1368        G   A  C   C
                                CGCTCCGG GGC GC GGG GGCC
                                |||||||| ||| || ||| ||||
                                GCGAGGCC CCG CG CCC CCGG
                                    G   C  _   _
GAM76   STK31    5'  CCCTCTGGGGTGGCGGGCGGC  1369    G   C    GCA  C
                                C CTC GGGG   GC GGGCGGC
                                | ||| ||||   || |||||||
                                G GAG CCCC   CG CCCGCCG
                                 G   A    AC_  _
GAM76   VEGF     5'  CTCCGGGGGCGGGCTCCGGCC  1370          AGCC   ___
                                CTCCGGGGGC   GGGC   GGCC
                                ||||||||||   ||||   ||||
                                GAGGCCCCCG   CCCG   CCGG
                                      ____    AGG
GAM76   ARHV     5'  CGCTCCGGGGGCAGCAGAGGGG 1371              C   C
              CC                   CGCTCCGGGGGCAGC GGG GGCC
                                ||||||||||||||| ||| ||||
                                GCGAGGCCCCCGTCG CTC CCGG
                                        T   C
GAM76   DKFZP434K1772 5'  CGCTCCGGGGGCACCGAGGAGC 1372            G    C
              C                  CGCTCCGGGGGCA CCGGG GGCC
                                |||||||||||| ||||| ||||
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                                GCGAGGCCCCCGT GGCTC TCGG
                                        _    C
GAM76   DKFZP761E2110 5' GCCCGGGGGCTGAGCGGC    1373    T      AGCC
                                GC CCGGGGGC   GGGCGGC
                                || ||||||||   |||||||
                                CG GGCCCCCG   CTCGCCG
                                 _      A___
GAM76   FBXO5    5' CGCTCCGGGGGCAGCTGAGC  1374             C
                                CGCTCCGGGGGCAGC GGGC
                                |||||||||||||| ||||
                                GCGAGGCCCCCGTCG CTCG
                                        A
GAM76   FLJ10099  5' CGCGCCGGGGGCAGCGTCTGGC 1375     T        CG__
                                CGC CCGGGGGCAGC   GGC
                                ||| ||||||||||   |||
                                GCG GGCCCCCGTCG   CCG
                                  C         CAGA
GAM76   FLJ10743  3' GCTTTGGGGGCAGGAGGGC  1376     CC      CC
                                GCT  GGGGGCAG  GGGC
                                |||  ||||||||  ||||
                                CGA  CCCCCGTC  CCCG
                                  AA       CT
GAM76   FLJ12076  5' CGCCTGGCCCGGGCGG     1377     CCGGG   AG
                                CGCT    GGC  CCGGGCGG
                                ||||    |||  ||||||||
                                GCGG    CCG  GGCCCGCC
                                  A_____   __
GAM76   FLJ12089  5' GCTCCTGGGGGTGCAGGCGGCC 1378       _    CA  C
                                GCTCC GGGGG  GC GGGCGGCC
                                ||||| |||||  || ||||||||
                                CGAGG CCCCC  CG TCCGCCGG
                                   A    A_ _
GAM76   FLJ12171  3' GCCCGGGGGCGCTGGC     1379     T      A  CG
                                GC CCGGGGGC GC  GGC
                                || ||||||| ||  |||
                                CG GGCCCCCG CG  CCG
                                 _      _  A_
GAM76   FLJ12697  3' GCTCCGGGGCGTGGCGG     1380          GCAGC  _
                                GCTCCGGGG    CG GGCGG
                                |||||||||    || |||||
                                CGAGGCCCC    GC CCGCC
                                      _____  A
GAM76   FLJ20366  5' CTCTGCAGCCAGCCGGGCGGC  1381     CGG  G
                                CTC   GG CAGCCGGGCGGC
                                |||   || ||||||||||||
                                GAG   TC GTCGGCCCGCCG
                                  ACG  G
GAM76   FOXO3A   5' CGCCCGGGGGAGGGGCGGC   1382     T     C  CC
                                CGC CCGGGGG AG  GGGCGGC
                                ||| ||||||| ||  |||||||
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                                GCG GGCCCCC TC  CCCGCCG
                                  _     _ __
GAM76   GABARAPL1 5'  CGCTCCGGGGGCAACAGCG   1383            CG
                                CGCTCCGGGGGCAGC  GGCG
                                |||||||||||||| ||||
                                GCGAGGCCCCCGTTG  TCGC
                                      __
GAM76   HUMNPIIY20 5'  CGCACCGGGGGCGGCGGC    1384     T      AGCCG
                                CGC CCGGGGGC    GGCGGC
                                ||| ||||||||    ||||||
                                GCG GGCCCCCG    CCGCCG
                                  T     ______
GAM76   HYPC     5'  TCCAGGGGCTGGGTGGCC    1385         AGCC   C
                                TCCGGGGGC    GGG GGCC
                                |||||||||    ||| ||||
                                AGGTCCCCG    CCC CCGG
                                     A___   A
GAM76   KIAA0140  3'  ACTCCGGGGGCAAGACATGGCC 1386          GCC   __
                                GCTCCGGGGGCA   GGGC  GGCC
                                ||||||||||||   ||||  ||||
                                TGAGGCCCCCGT   TCTG  CCGG
                                       ___   TA
GAM76   KIAA0159  5'  CGCCCGGGGGCGGGCCAAGGC  1387     T      A_   _
                                CGC CCGGGGGC  GCCG GGC
                                ||| ||||||||  |||| |||
                                GCG GGCCCCCG  CGGT CCG
                                  _      CC    T
GAM76   KIAA0202  5'  CGCTCCGCCCGGGCGG      1388        GGGGCAG
                                CGCTCCG      CCGGGCGG
                                |||||||      ||||||||
                                GCGAGGC      GGCCCGCC
                                   G_______
GAM76   KIAA0397  3'  GCCCGGGGGCAGGGC       1389     T       GCC
                                GC CCGGGGGCA   GGGC
                                || |||||||||   ||||
                                CG GGCCCCCGT   CCCG
                                  _      ___
GAM76   KIAA0781  3'  CCCTCTGATTCCAGTTGGGTGG 1390    G   C  GGG   CC   C
          C                      C CTC GG   CAG  GGG GGC
                                | ||| ||   |||  ||| |||
                                G GAG CT   GTC  CCC CCG
                                 G   A  AAG   AA   A
GAM76   KIAA1858  3'  GCTCTTGGGGGGACCAGGCGGC  1391      C_    CA
                                GCTC  GGGGG  GCCGGGCGGC
                                ||||  |||||  ||||||||||
                                CGAG  CCCCC  TGGTCCGCCG
                                  AA    __
GAM76   LZ16     5'  GCTCCGAGGGCTGCGCGGC    1392          A  CGG
                                GCTCCGGGGGC GC   GCGGC
                                |||||||||| ||   |||||
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                                CGAGGCTCCCG CG   CGCCG
                                      A ___
GAM76   MAP2K7   3' CCCTGGCAGGCAGCTGGGTGGC 1393     C _     C  C
            C                  CTC GG GGGCAGC GGG GGCC
                               ||| || ||||||| ||| ||||
                               GGG CC TCCGTCG CCC CCGG
                                 A G      A  A
GAM76   MGC10526 5' CGATGGCAGTCGGGCGGCC   1394    GG    C
                               CG  GGCAG CGGGCGGCC
                               ||  ||||| |||||||||
                               GC  CCGTC GCCCGCCGG
                                TA    A
GAM76   MGC14480 3' CTCTGGGGGTGGCCTCAGCC  1395     C    CA   GGG
                               CTC GGGGG  GCC   CGGCC
                               ||| |||||  |||   |||||
                               GAG CCCCC  CGG   GTCGG
                                 A    AC  A__
GAM76   MGC15937 5' GCTCCGGGGGTGCCTCGTGG  1396         CA   GGGC
                               GCTCCGGGGG  GCC   GG
                               ||||||||||  |||   ||
                               CGAGGCCCCC  CGG   CC
                                     A_  AGCA
GAM76   MGC2629  5' GCTCCGGGGGTGGCCTCGTGCC 1397          CA   GGGCG
                               GCTCCGGGGG  GCC    GCC
                               ||||||||||  |||    |||
                               CGAGGCCCCC  CGG    CGG
                                     AC   AGCA_
GAM76   MGC4415  3' TCTGGGGGCAGGTCGGGTGGCC 1398    C      C_   C
                               TC GGGGGCAG  CGGG GGCC
                               || ||||||||  |||| ||||
                               AG CCCCCGTC  GCCC CCGG
                                A       CA   A
GAM76   MST4     5' CCCTCCGGGGGTAGTTCGGCGG 1399    G       C  CCG
            CC                   C CTCCGGGGG AG   GGCGGCC
                               | |||||||||  ||   |||||||
                               G GAGGCCCCC TC   CCGCCGG
                                G       A  AAG
GAM76   NPEPL1   5' CGCTCCGGGCGGCAGGCAGG   1400          _    C
                               CGCTCCGGG GGCAG CGGG
                               |||||||||  |||||  ||||
                               GCGAGGCCC CCGTC GTCC
                                     G    C
GAM76   PCTAIRE2BP 5' CGCTTCGAGGGCAGCCTGGC   1401      C         G
                               CGCT CGGGGGCAGCC GGC
                               ||||  |||||||||||  |||
                               GCGA GCTCCCGTCGG CCG
                                 A          A
GAM76   PIP5K1C  3' CGCCTTCGGGGGCAGCCGGAGC 1402      C_          _
                               CGCT  CGGGGGCAGCCGG GC
                               ||||  ||||||||||||| ||
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                                GCGG  GCCCCCGTCGGCC CG
                                  AA          T
GAM76   RGS11    5'  CGCCCGGGGGCGGCCGGG    1403     T      A
                                CGC CCGGGGGC GCCGGG
                                ||| |||||||| ||||||
                                GCG GGCCCCCG CGGCCC
                                  _      C
GAM76   SCAMP-4  3'  GGAGGCAGGGAGGGTGGCC   1404        CC_   C
                                GGGGGCAG   GGG GGCC
                                ||||||||   ||| ||||
                                CCTCCGTC   CCC CCGG
                                     CCT   A
GAM76   SHANK3   3'  CGCTGGGTGGGCTGGGCGGCC  1405      CC   _  CA  C
                                CGCT  GGG GG  GC GGGCGGCC
                                ||||  ||| ||  || ||||||||
                                GCGA  CCC CC  CG CCCGCCGG
                                  __   A  __  A
GAM76   SLK      5'  GCTCCGGCCGGGCGG      1406        GGGGCA
                                GCTCCG     GCCGGGCGG
                                ||||||     |||||||||
                                CGAGGC     CGGCCCGCC
                                           _______
GAM76   SNPH     3'  TCTGGGGGCAGTCATGGC    1407     C       C  _
                                TC GGGGGCAG CG GGC
                                || |||||||| || |||
                                AG CCCCCGTC GT CCG
                                 A       A  A
GAM76   SSH-3    5'  GCCCGGGGGCGAACGGC     1408     T       AGCC
                                GC CCGGGGGC    GGGCGGC
                                || ||||||||    |||||||
                                CG GGCCCCCG    CTTGCCG
                                _      _____
GAM76   SSI-1    5'  CGCTCCGGGGCGGCTCTGGCCG 1409        __   A_______   GGGC
            CCCGG                   TCCGGG  GGC      GCC    GG
                                ||||||  |||      |||    ||
                                AGGCCC  CCG      CGG    CC
                                   CG   AGAIIIC   CGGG
GAM76   STAT5A   5'  CGTTCCGGCGGGCGGC      1410     C    GGGCAGC
                                CG TCCGG      CGGGCGGC
                                || |||||      ||||||||
                                GC AGGCC      GCCCGCCG
                                 A   _________
GAM76   TBPL1    5'  TCCGGGTGCGAGGCGGCC    1411        G  AGCC
                                TCCGGG GC    GGGCGGCC
                                |||||| ||    ||||||||
                                AGGCCC CG    TCCGCCGG
                                   A  C____
GAM76   THG-1    5'  CTCCGGGGGCCGCGGC      1412          AGCCGG
                                CTCCGGGGGC     GCGGC
                                ||||||||||     |||||
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                                GAGGCCCCCG     CGCCG
                                     G_____
GAM76   UBE2G1   5' GCTCTGGGGGCGGCTGGAGC  1413      C     A  C  _
                                GCTC GGGGGC GC GG GC
                                |||| |||||| || || ||
                                CGAG CCCCCG CG CC CG
                                  A     C  A  T
GAM76   XAP135   5' CGCTCCGGGGGTGGCTGGGTCG 1414          CA  C   CG
           C                     CGCTCCGGGGG  GC GGG  GC
                                 ||||||||||  || |||  ||
                                 GCGAGGCCCCC  CG CCC  CG
                                       AC  A   AG
GAM76   XAP135   5' CGCTCCGGGGGTGGCTGGGTCG 1414          CA  C   CG
           C                     CGCTCCGGGGG  GC GGG  GC
                                 ||||||||||  || |||  ||
                                 GCGAGGCCCCC  CG CCC  CG
                                       AC  A   AG
GAM76   LOC126257 5' GCTCCGCGCGCAGCCGGGCGGC 1415       GGG
           C                     GCTCCG   GCAGCCGGGCGGCC
                                 ||||||   ||||||||||||||
                                 CGAGGC   CGTCGGCCCGCCGG
                                    GCG
GAM76   LOC145717 5' CGCCCGGGGGTGGCCGGGGC   1416     T     CA     CG
                                CGC CCGGGGG  GCCGGG  GC
                                ||| |||||||  ||||||  ||
                                GCG GGCCCCC  CGGCCC  CG
                                  _      AC     __
GAM76   LOC147136 5' GCTCTGGGGGCAGGGGC     1417      C      CC
                                GCTC GGGGGCAG  GGGC
                                |||| ||||||||  ||||
                                CGAG CCCCCGTC  CCCG
                                  A      __
GAM76   LOC148887 3' TCCCGGGGCTGAGTGGGCGGC  1418     G    __  CC
                                TCC GGGGC  AG  GGGCGGC
                                ||| |||||  ||  |||||||
                                AGG CCCCG  TC  CCCGCCG
                                  G    AC  A_
GAM76   LOC150372 3' GCCTGGGGGGTGCCAGACGTGGC 1419     CC    CA     __
                                GCT  GGGGG  GCCGGGC  GGC
                                |||  |||||  |||||||  |||
                                CGG  CCCCC  CGGTCTG  CCG
                                  A_    A_      CA
GAM76   LOC150384 5' GCCTCGGGGGGCAGGGATCCCGG 1420     TC       _____  G
           C                     GC  CGGGGGGCAG    CC GGC
                                 ||  |||||||||    || |||
                                 CG  GCCCCCGTC    GG CCG
                                  GA        CCTA  G
GAM76   LOC151127 5' CGCTCCGGTGGTTGCTGCGG   1421         G  CA  CGG
                                CGCTCCGG GG  GC   GCGG
                                |||||||| ||  ||   ||||
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                                GCGAGGCC CC  CG   CGCC
                                    A  AA  A__
GAM76   LOC158056 5'  TCCGGGGGCACACACAGG    1422          _ _
                                TCCGGGGGCA GC CGGG
                                |||||||||| || ||||
                                AGGCCCCCGT TG GTCC
                                     G  T
GAM76   LOC163412 5'  GCTCTGGGGGCAGACCCGTGGC 1423      C      __  _
                                GCTC GGGGGCAG  CCG GGC
                                |||| ||||||||  ||| |||
                                CGAG CCCCCGTC  GGC CCG
                                  A       TG   A
GAM76   LOC166219 5'  GCTCCGTGGGCGGCCTGGG   1424       G    A  _
                                GCTCCG GGGC GCC GGG
                                |||||| |||| ||| |||
                                CGAGGC CCCG CGG CCC
                                   A   C   A
GAM76   LOC219401 5'  CGTCCGGGGGCGGGG      1425     C       AGCCG  C
                                CG TCCGGGGGC    GG GG
                                || |||||||||    || ||
                                GC AGGCCCCCG    CC CC
                                 _       _____ _
GAM76   LOC253960 3'  CGTTCCGGGAGGCGGCCTGCAG 1426     C    _  A   GG __
           AGCC                    CG TCCGGG GGC GCC  GC  GGCC
                                || |||||| ||| |||  ||  ||||
                                GC AGGCCC CCG CGG  CG  TCGG
                                 A     T   C   A_  TC
GAM76   LOC254485 3'  CACTTCCCAGACAGTTGGGCGG 1427      _ G   G   CC
           CC                     CGCT CC GGG CAG  GGGCGGCC
                                |||| || ||| |||  ||||||||
                                GTGA GG TCT GTC  CCCGCCGG
                                  A  G   _   AA
GAM76   LOC256158 5'  GCTCCTCGGCTGGGCGGCC   1428       GGG   AGCC
                                GCTCC   GGC    GGGCGGCC
                                |||||   |||    ||||||||
                                CGAGG   CCG    CCCGCCGG
                                   AG_   A___
GAM76   LOC256933 5'  GCCCCGGGGGCGGTTTCGGCCG 1429         A__________   GGGC
           CCCGG                    CCGGGGGC        GCC    GG
                                ||||||||        |||    ||
                                GGCCCCCG        CGG    CC
                                     CCAAAGIIIC   CGGG
GAM76   LOC257471 5'  CGCTCCGGCGGCGGCGGGGGCC 1368         G   A  C   C
                                CGCTCCGG GGC GC GGG GGCC
                                |||||||| ||| || ||| ||||
                                GCGAGGCC CCG CG CCC CCGG
                                     G   C   _   _
GAM76   LOC257479 5'  GCCTGGTCGCGGGCCGGGCGGC 1430     CC  GG  A_
                                GCT  GG  GC  GCCGGGCGGC
                                |||  ||  ||  ||||||||||
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                                CGG  CC  CG  CGGCCCGCCG
                                  A_  AG  CC
GAM76   LOC51619  5'  CGCTGCCGGGGACCCGGGCGGC 1431      _       AG
              C                    CGCT CCGGGGGC  CCGGGCGGCC
                                   |||| ||||||||  ||||||||||
                                   GCGA GGCCCCTG  GGCCCGCCGG
                                     C       __
GAM76   LOC56930  3'  GCACTGGGGGCAGGCGGC    1432     TCC      GCCG
                                   GC   GGGGGCA    GGCGGC
                                   ||   |||||||    ||||||
                                   CG   CCCCCGT    CCGCCG
                                    TGA      _____
GAM76   LOC57228  5'  CGCTGGGGGCGGCCGGTGCG   1433       CC     A    _
                                   CGCT  GGGGGC GCCGG GCG
                                   ||||  |||||| ||||| |||
                                   GCGA  CCCCCG CGGCC CGC
                                     __      C     A
GAM77   CYP21A2   3'  TTAAGCCTCAATCCTCTGCAGC 1436           C   A      A
              G                    TTAAGCTTCA GTC TCTGCA CG
                                   |||||||||| ||| |||||| ||
                                   AATTCGGAGT TAG AGACGT GC
                                         _  G     C
GAM77   ELSPBP1   3'  TTAAGCTTGACAGATGCAA   1437         C   TCATC
                                   TTAAGCTT ACG     TGCAA
                                   |||||||| |||     |||||
                                   AATTCGAA TGT     ACGTT
                                        C   CT___
GAM77   ERAP140   5'  TTAAGCTTCCTTCCATCTTGCA 1438          ACG     _   A
              GCG                    TTAAGCTTC   TCATCT GCA CG
                                   |||||||||   |||||| ||| ||
                                   AATTCGAAG   GGTAGA CGT GC
                                         GAA     A   C
GAM77   MGC10924  3'  TTAAGCTTCATTTGTATCC    1439          C__   C
                                   TTAAGCTTCA   GT ATCT
                                   ||||||||||   || ||||
                                   AATTCGAAGT   CA TAGG
                                         AAA  _
GAM77   NDUFA4    5'  CTAAGCTAAAAATTATCTGCAA 1440         TCAC  C
                                   TTAAGCT    GT ATCTGCAA
                                   |||||||    || ||||||||
                                   GATTCGA    TA TAGACGTT
                                        TTTT  A
GAM77   LOC118987 3'  TAAGCTTCAACACTTGCA    1441          CGT   TC
                                   TAAGCTTCA   CA  TGCA
                                   |||||||||   ||  ||||
                                   ATTCGAAGT   GT  ACGT
                                         T__  GA
GAM77   LOC150886 5'  TTAACCTGATCATATCTGCAA  1442       G  TCA   C
                                   TTAA CT   CGT ATCTGCAA
                                   |||| ||   ||| ||||||||
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                                AATT GA   GTA TAGACGTT
                                  G  CTA  _
GAM77   LOC153525 5'  TTAAGCTTCATTTGTATCC    1439          C__  C
                                TTAAGCTTCA   GT ATCT
                                ||||||||||   || ||||
                                AATTCGAAGT   CA TAGG
                                     AAA  _
GAM77   LOC157376 3'  TTAAGCCTATTGCGCATTTGCA 1443         CA__  T   C
                                TTAAGCTT    CG CAT TGCA
                                ||||||||    || ||| ||||
                                AATTCGGA    GC GTA ACGT
                                     TAAC  _   A
GAM77   LOC197358 3'  TTAATTTCACGCTATCTGCAA  1444       GC     TC
                                TTAA  TTCACG  ATCTGCAA
                                ||||  ||||||  ||||||||
                                AATT  AAGTGC  TAGACGTT
                                  A_     GA
GAM77   LOC91170  3'  TTAAGGTTCCCATCTGC     1445       C   ACG
                                TTAAG TTC   TCATCTGC
                                |||||| |||   ||||||||
                                AATTC AAG   GGTAGACG
                                  C  ____
GAM78   LOC254842 5'  TCGGAGGCTCCGCGGTGTCG   1448         _
                                TCGGAGG TCCGCGGTGTCG
                                ||||||| ||||||||||||
                                AGCCTCC AGGCGCCACAGC
                                    G
GAM78   LOC256281 3'  GGGGTCCGCGGGGTGT      1449     A       T  C
                                GG GGTCCGCGG GT GT
                                || |||||||| || ||
                                CC CCAGGCGCC CA CA
                                 _       C  _
GAM79   ATP1A2    3'  CCTCATTATCTCTCCCCAAATG 1452     CT  GGG   C
            T                    CC  GT   CTC CCCCAAATGT
                                 ||  ||   ||| ||||||||||
                                 GG  TA   GAG GGGGTTTACA
                                  AG  ATA   A
GAM79   CRKL      3'  CCGCTGTGTGCATTCCAAATGT 1453     _    G  TCCCC
                                CC CTGTG GC     CCAAATGT
                                || ||||| ||     ||||||||
                                GG GACAC CG     GGTTTACA
                                 C     A  TAA__
GAM79   EDAR      3'  ACCCTGGGGTGTTTTCTAAATG 1454        T   CTCCCCCC
            T                    ACCCTG GGG       AAATGT
                                 ||||||| |||       ||||||
                                 TGGGAC CCC       TTTACA
                                    _   ACAAAAGA
GAM79   GYPC      3'  CCTGCTGTTCCCCCCAAATGT  1455       GGGC
                                CCTGT    TCCCCCCAAATGT
                                |||||    ||||||||||||
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                              GGACG   AGGGGGGTTTACA
                                ACA_
GAM79   GYPC    3' CCTGCTGTTCCCCCCAAATGT 1455      GGGC
                              CCTGT   TCCCCCCAAATGT
                              |||||   ||||||||||||
                              GGACG   AGGGGGGTTTACA
                                ACA_
GAM79   HNRPK   3' CCCTGGCCCACCCCCCAAATGT 1457     GT  G  _
                              CCCT  GG CT CCCCCCAAATGT
                              ||||  || || ||||||||||||
                              GGGA  CC GG GGGGGGTTTACA
                                __  G  T
GAM79   HNRPK   3' CCCTGTCCCACCCCCCAAATGT 1456      GGGCT
                              CCCTGT    CCCCCCAAATGT
                              ||||||    ||||||||||||
                              GGGACA    GGGGGGTTTACA
                                 GGGT_
GAM79   MKI67   3' CCCTGTGAAGCCCTCAGATGT  1458       CTC   C  A
                              CCCTGTGGG   CCC CA ATGT
                              |||||||||   ||| || ||||
                              GGGACACTT   GGG GT TACA
                                   C__   A  C
GAM79   MUCDHL  3' CCCGGGGACCCCCCGGGTGT   1459     T   CT    AAA
                              CCTG GGG  CCCCCC   TGT
                              |||| |||  ||||||   |||
                              GGGC CCC  GGGGGG   ACA
                                _  T_     CCC
GAM79   MUCDHL  3' CCCGGGGACCCCCCGGGTGT   1459     T   CT    AAA
                              CCTG GGG  CCCCCC   TGT
                              |||| |||  ||||||   |||
                              GGGC CCC  GGGGGG   ACA
                                _  T_     CCC
GAM79   NPR1    3' TGTGGGCCAGCCCCAGATGT   1460       CC    A
                              TGTGGGCT  CCCCA ATGT
                              ||||||||  ||||| ||||
                              ACACCCGG  GGGGT TACA
                                   TC    C
GAM79   NRIP1   5' CTGTGTTTCTCCCAAATGT   1461      GGC  CC
                              CTGTG   TC  CCCAAATGT
                              |||||   ||  |||||||||
                              GACAC   AG  GGGTTTACA
                                AA_  A_
GAM79   SIRPB2  3' CCTGTGGGCAGGCAGATGT   1462       TCCCCC  A
                              CCTGTGGGC     CA ATGT
                              |||||||||     || ||||
                              GGACACCCG     GT TACA
                                   TCC___  C
GAM79   SIRPB2  3' CCTGTGGGCAGGCAGATGT   1462       TCCCCC  A
                              CCTGTGGGC     CA ATGT
                              |||||||||     || ||||
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                                GGACACCCG     GT TACA
                                     TCC___  C
GAM79   TPSB1    5' ACCCAGTGGGCTCTCCCC    1463      T      C
                                ACCC GTGGGCTC CCCC
                                |||| |||||||| ||||
                                TGGG CACCCGAG GGGG
                                  T       A
GAM79   AMOT     3' CCAGAAAGATCCCCCAAATGT  1464    TGT   CTC
                                CC   GGG   CCCCCAAATGT
                                ||   |||   ||||||||||
                                GG   TTC   GGGGGTTTACA
                                 TCT   TA_
GAM79   COASTER  3' TGTGAGCTCCTGCAGATGT   1465         CCC  A
                                TGTGGGCTCC   CA ATGT
                                ||||||||||   || ||||
                                ACACTCGAGG   GT TACA
                                     AC_  C
GAM79   HTEX4    5' CCTGAACCCCTTCTCAAGTGT  1466     TG     CCC_   A
                                CCTG  GGCTCC    CAA TGT
                                ||||  ||||||    ||| |||
                                GGAC  TTGGGG    GTT ACA
                                  __      AAGA   C
GAM79   HTEX4    5' CCTGAACCCCTTCTCAAGTGT  1466     TG     CCC_   A
                                CCTG  GGCTCC    CAA TGT
                                ||||  ||||||    ||| |||
                                GGAC  TTGGGG    GTT ACA
                                  __      AAGA   C
GAM79   HTEX4    5' CCTGAACCCCTTCTCAAGTGT  1466     TG     CCC_   A
                                CCTG  GGCTCC    CAA TGT
                                ||||  ||||||    ||| |||
                                GGAC  TTGGGG    GTT ACA
                                  __      AAGA   C
GAM79   ITPK1    3' CCCTGTGGTGCTCTCTGATCTC 1467     _    CCCC____      III
           AAATGTA                TGG GCTC       CAAATGT   A
                                ||| ||||       |||||||   |
                                ACC CGAG       GTTTACA   T
                                  A    AGACTAGA      III
GAM79   KCNJ9    5' ACCGCTGTTTCTCCTAAATGT  1468     _    GGG    CCCC
                                ACC CTGT   CTCC    AAATGT
                                ||| ||||   ||||    ||||||
                                TGG GACA   GAGG    TTTACA
                                  C    AA_    A___
GAM79   KIAA0194 3' CCCTCCTCAGCTTCCCCCAAAT 1469      GTG_   C
           GT                    CCCT    GGCT CCCCCAAATGT
                                ||||    |||| ||||||||||
                                GGGA    TCGA GGGGGTTTACA
                                  GGAG    A
GAM79   KIAA1086 3' CCCTGTGGCTCTCCCCA     1470         G   C
                                CCCTGTGG CTC CCCCA
                                |||||||| ||| |||||
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                                GGGACACC GAG GGGGT
                                   _  A
GAM79   KLF12    3'  CCTGTGAGCTTCTGAATGT   1471          CCCCCCA
                                CCTGTGGGCT      AATGT
                                ||||||||||      |||||
                                GGACACTCGA      TTACA
                                     AGAC___
GAM79   PRAX-1   3'  CCCTGGGGCTCCCCACG     1472       T       CCAA
                                CCCTG GGGCTCCCC    ATG
                                ||||| |||||||||    |||
                                GGGAC CCCGAGGGG    TGC
                                  _      _____
GAM79   Rab11-FIP3 3'  ACCCAAGGCTTTCCCCAAATGT 1473      TGT    CC
                                ACCC   GGGCT  CCCCAAATGT
                                ||||   |||||  ||||||||||
                                TGGG   TCCGA  GGGGTTTACA
                                  T__     AA
GAM79   TADA3L   5'  CCTGTGGAGCTCCCTGGGATGT 1474        _     CCCAA
                                CCTGTGG GCTCCC     ATGT
                                ||||||| ||||||     ||||
                                GGACACC CGAGGG     TACA
                                    T     ACCC_
GAM79   TADA3L   5'  CCTGTGGAGCTCCCTGGGATGT 1474        _     CCCAA
                                CCTGTGG GCTCCC     ATGT
                                ||||||| ||||||     ||||
                                GGACACC CGAGGG     TACA
                                    T     ACCC_
GAM79   TADA3L   5'  CCTGTGGAGCTCCCTGGGATGT 1474        _     CCCAA
                                CCTGTGG GCTCCC     ATGT
                                ||||||| ||||||     ||||
                                GGACACC CGAGGG     TACA
                                    T     ACCC_
GAM79   LOC149271 5'  ACCCTGTGGGCTCTTGCTCC   1475           CCC__
                                ACCCTGTGGGCTC     CC
                                ||||||||||||     ||
                                TGGGACACCCGAG     GG
                                      AACGA
GAM79   LOC153279 3'  CCCTGTCCCACCCCCCAAATGT 1456        GGGCT
                                CCCTGT     CCCCCCAAATGT
                                ||||||     ||||||||||||
                                GGGACA     GGGGGGTTTACA
                                   GGGT_
GAM79   LOC155072 3'  CCCTGTGGACTCCCCACC     1476            _
                                CCCTGTGGGCTCCCC CC
                                |||||||||||||| ||
                                GGGACACCTGAGGGG GG
                                       T
GAM79   LOC200933 3'  ACCCAGTTGTCCCCAAATG    1477       T  GGGCTCC
                                ACCC GT      CCCCAAATG
                                |||| ||      |||||||||
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                                TGGG CA      GGGGTTTAC
                                  T  ACA____
GAM79   LOC202868 3'  CCCTGTGGACTCCCCACC    1476            _
                                CCCTGTGGGCTCCCC CC
                                |||||||||||||| ||
                                GGGACACCTGAGGGG GG
                                         T
GAM79   LOC89944  3'  CCTTCTGTCCTCCTCCCTGGAT 1478     G_ GG   _  CAA
           GT                    CCT  TG  CTCC CCC   ATGT
                                |||  ||  |||| |||   ||||
                                GGA  AC  GAGG GGG   TACA
                                  AG  AG    A   ACC
GAM79   LOC89944  3'  CCTTCTGTCCTCCTCCCTGGAT 1478     G_ GG   _  CAA
           GT                    CCT  TG  CTCC CCC   ATGT
                                |||  ||  |||| |||   ||||
                                GGA  AC  GAGG GGG   TACA
                                  AG  AG    A   ACC
GAM79   LOC92293  3'  CTGAGGGCTCCCTCCAATTGT  1479     T      C    A
                                CTG GGGCTCCC CCAA TGT
                                ||| |||||||| |||| |||
                                GAC CCCGAGGG GGTT ACA
                                  T      A    A
GAM79   LOC93082  3'  ACCTGAACTCCCTCAGATGT   1480     CTG       CC  A
                                ACC   TGGGCTCCC  CA ATGT
                                |||   |||||||||  || ||||
                                TGG   ACTTGAGGG  GT TACA
                                  ____        A_  C
GAM80   CLASP1    5'  GCAGGGCTTTCTGGTAGGAGGA 1483      A  AG__  AGC
           C                     GCAG GG    CT   AGGAGGAC
                                ||||  ||    ||   ||||||||
                                CGTC CC    GA   TCCTCCTG
                                  _  GAAA  CCA
GAM80   CLECSF11  5'  TCGCGGCCTGAGGCAGGAGG   1484      AGAG_   CTA
                                TCGC    GAG   GCAGGAGG
                                ||||    |||   ||||||||
                                AGCG    CTC   CGTCCTCC
                                  CCGGA   ___
GAM80   CYP24     5'  CGCGGGAAGGCAGGAGGA    1485     AGA    CTA
                                CGC   GGAG   GCAGGAGGA
                                |||   ||||   |||||||||
                                GCG   CCTT   CGTCCTCCT
                                  C__    C__
GAM80   FABP2     3'  GAGAGGCTGAGGCAGGAGGA   1486     GA   A__
                                GAG  GCT   GCAGGAGGA
                                |||  |||   |||||||||
                                CTC  CGA   CGTCCTCCT
                                  TC   CTC
GAM80   GPR4      3'  GGAGGCCAAGGCAGGAGGA    1487       _   __
                                GGAG CTA  GCAGGAGGA
                                ||||  |||  |||||||||
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                                CCTC GGT  CGTCCTCCT
                                  C   TC
GAM80   INPP5B   3'  GCAGAGGAACTGGTGAA     1488          AGCA  A
                                GCAGAGGAGCT    GG GGA
                                ||||||||||    || |||
                                CGTCTCCTTGA    CC CTT
                                      ____  A
GAM80   ISLR     3'  GCAGAGGAGCAGACAACAGA   1489          TA    G
                                GCAGAGGAGC  GCAG AGG
                                ||||||||||  |||| |||
                                CGTCTCCTCG  TGTT TCT
                                     TC    G
GAM80   JPH3     5'  CCGGAGGAGAGGAGGA      1490      CA     CTAGC
                                TCG  GAGGAG    AGGAGGA
                                |||  ||||||    |||||||
                                GGC  CTCCTC    TCCTCCT
                                 __    ______
GAM80   KRTHA8   5'  CAGTGGTGTAGCAGGAGGAC   1491      A  AGC
                                CAG GG   TAGCAGGAGGAC
                                ||| ||   ||||||||||||
                                GTC CC   ATCGTCCTCCTG
                                  A  AC_
GAM80   LIMD1    3'  TCCCAGAGGGGACAGGAGGA   1492     G     AGCTA
                                TC CAGAGG    GCAGGAGGA
                                || ||||||    |||||||||
                                AG GTCTCC    TGTCCTCCT
                                 G     CC___
GAM80   LPIN1    3'  CGCAGAGGAGTTAGTTAAGG   1493          C   CAG
                                CGCAGAGGAG TAG   GAGG
                                |||||||||| |||   ||||
                                GCGTCTCCTC ATC   TTCC
                                     A   AA_
GAM80   MAP2K2   3'  CCGCAGGGGTGAGGCAGGAGG  1494        A  AGCTA
                                TCGCAG GG    GCAGGAGG
                                |||||| ||    ||||||||
                                GGCGTC CC    CGTCCTCC
                                   _ CACTC
GAM80   NOTCH2   3'  GCAGGAAGTAGGGGGA      1495      A   C   CA  A
                                GCAG GGAG TAG  GG GGA
                                |||| |||| |||  || |||
                                CGTC CTTC ATC  CC CCT
                                  _   _  __  _
GAM80   NRXN2    5'  TCGCGAGGAGCTAGGGG     1496      A        CA
                                TCGC GAGGAGCTAG  GG
                                |||| ||||||||||  ||
                                AGCG CTCCTCGATC  CC
                                  _        C_
GAM80   PACSIN3  3'  GCAGAAGGGCTGTCAGGA    1497        A   AG
                                GCAGAGG GCT  CAGGA
                                |||||||  |||  |||||
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                                CGTCTTC CGA  GTCCT
                                    C   CA
GAM80   SAS     3'  GGAGACTGAGGCAGGAGGA   1498      _ A__
                                GGAG CT   GCAGGAGGA
                                |||| ||   |||||||||
                                CCTC GA   CGTCCTCCT
                                  T  CTC
GAM80   SOX4    5'  TCGCAGAGGAGTTATAG     1499          C  GC
                                TCGCAGAGGAG TA  AG
                                |||||||||| ||  ||
                                AGCGTCTCCTC AT  TC
                                      A  A_
GAM80   UMPS    3'  GAGAGACTGAGGCAGGAGGA  1500     GA   A__
                                GAG  GCT   GCAGGAGGA
                                |||  |||   |||||||||
                                CTC  TGA   CGTCCTCCT
                                  TC   CTC
GAM80   VAV2    3'  TCACAGAGGAGCTAGAGA    1501            C
                                TCGCAGAGGAGCTAG AGG
                                |||||||||||||| |||
                                AGTGTCTCCTCGATC TCT
                                                _
GAM80   ZNF142  5'  CCGGGGGGAGCCAAGGAGGAC 1502     CAGA      GC
                                TCG   GGAGCTA  AGGAGGAC
                                |||   |||||||  ||||||||
                                GGC   CCTCGGT  TCCTCCTG
                                  CCC_      __
GAM80   ABLIM   3'  CAGAGGACACAGGAGG      1503        GCTA
                                CAGAGGA   GCAGGAGG
                                |||||||   ||||||||
                                GTCTCCT   TGTCCTCC
                                    G___
GAM80   ABLIM   3'  CAGAGGACACAGGAGG      1503        GCTA
                                CAGAGGA   GCAGGAGG
                                |||||||   ||||||||
                                GTCTCCT   TGTCCTCC
                                    G___
GAM80   ANKRD6  3'  GCGAGGTTGAGGCAGGAGGA  1504     A   AGCTA
                                GC GAGG    GCAGGAGGA
                                || ||||    |||||||||
                                CG CTCC    CGTCCTCCT
                                 _   AACTC
GAM80   ASB16   5'  TCATGGAGGGAGCAGCAGGAGG 1505     CA   _  T
                                TCG  GAGG AGC AGCAGGAGG
                                |||  |||| ||| |||||||||
                                AGT  CTCC TCG TCGTCCTCC
                                  AC   C  _
GAM80   BTBD3   3'  GCTGGGGCCAGCAGGAGGAC  1506    AGA  A
                                GC   GG GCTAGCAGGAGGAC
                                ||   || ||||||||||||||
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                                CG   CC CGGTCGTCCTCCTG
                                 AC_  _
GAM80   C22orf19  3'  TCGGGAGGCTGAGGCAGGAGGA 1507      CA    AGCTA
                                TCG  GAGG    GCAGGAGGA
                                |||  ||||    |||||||||
                                AGC  CTCC    CGTCCTCCT
                                  C_    GACTC
GAM80   COLEC12   3'  GCAAGACTGAGGCAGGAGG    1508     _ G_   CTA
                                GCA GA  GAG   GCAGGAGG
                                ||| ||  |||   ||||||||
                                CGT CT  CTC   CGTCCTCC
                                  T  GA  ___
GAM80   CSL4      3'  GGAGGCCAAGGCAGGAGGAC   1509      _   __
                                GGAG CTA  GCAGGAGGAC
                                |||| |||  ||||||||||
                                CCTC GGT  CGTCCTCCTG
                                   C   TC
GAM80   DKFZp434J0226 5'  TCCTAGAGGAGCTGGTGA    1510     GC       AGCA  AG
                                TC  AGAGGAGCT    GG  GA
                                ||  |||||||||    ||  ||
                                AG  TCTCCTCGA    CC  CT
                                 GA        _____  A_
GAM80   FLJ10687  3'  GGAGACTGAGGCAGGAGGA    1498      _ A__
                                GGAG CT   GCAGGAGGA
                                |||| ||   |||||||||
                                CCTC GA   CGTCCTCCT
                                  T  CTC
GAM80   FLJ12476  5'  GCAGAGGAGCTGCTCTGG     1511           A  A__
                                GCAGAGGAGCT GC   GG
                                |||||||||||  ||   ||
                                CGTCTCCTCGA CG   CC
                                       _  AGA
GAM80   FLJ12800  3'  GCAGAAGGGGCAGGAGG      1512         AGCTA
                                GCAGAGG    GCAGGAGG
                                |||||||    ||||||||
                                CGTCTTC    CGTCCTCC
                                    CC___
GAM80   FLJ13197  3'  GGACACACATAGCAGGAGGAC  1513      ___  _
                                GGA   GC TAGCAGGAGGAC
                                |||   || ||||||||||||
                                CCT   TG ATCGTCCTCCTG
                                  GTG  T
GAM80   FLJ13769  5'  GAGGCCCAGGCAGGAGGA    1514       AG   _
                                GAGG  CTAG CAGGAGGA
                                ||||  |||| ||||||||
                                CTCC  GGTC GTCCTCCT
                                  G_    C
GAM80   FLJ14100  3'  TCCCAGGATCCGGAGCAGGAGG 1515     G  GA   G  __
                                TC CA  GGA CT  AGCAGGAGG
                                || ||  ||| ||  |||||||||
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                                AG GT  CCT GG  TCGTCCTCC
                                 G __   A  CC
GAM80   FLJ20584  3'  TCGCAAAGGAGCGTGGGGA   1516          TAGCA  A
                                TCGCAGAGGAGC    GG GGA
                                ||||||||||||    || |||
                                AGCGTTTCCTCG    CC CCT
                                       CA___  _
GAM80   FLJ25416  5'  GGAGGCTAAGGCAGGAGGA   1517      _  __
                                GGAG CTA  GCAGGAGGA
                                |||| |||  |||||||||
                                CCTC GAT  CGTCCTCCT
                                  C   TC
GAM80   GMEB2     5'  GGGGCTCAGAGCAGGAGGAC  1518     A  ___
                                GG GCT   AGCAGGAGGAC
                                || |||   ||||||||||
                                CC CGA   TCGTCCTCCTG
                                 C   GTC
GAM80   HIF1AN    3'  GCAGAGGAGCTGGCTTTAAGAC 1519          A  AGG
                                GCAGAGGAGCT GC   AGGAC
                                |||||||||| ||   |||||
                                CGTCTCCTCGA CG   TTCTG
                                       C  AAA
GAM80   IRX3      3'  GAGGGCTGAGGAGGAC      1520       A   AGC
                                GAGG GCT   AGGAGGAC
                                |||| |||   ||||||||
                                CTCC CGA   TCCTCCTG
                                  _   C__
GAM80   KIAA0321  5'  TCTGGAGGAGCTGAGTCTGGA  1521     GCA      _  CA_
                                TC   GAGGAGCT AG   GGA
                                ||   |||||||| ||   |||
                                AG   CTCCTCGA TC   CCT
                                 AC_       C  AGA
GAM80   KIAA0478  3'  GAAGCTGTGGCAGGAGGA    1522        A__
                                GGAGCT   GCAGGAGGA
                                ||||||   |||||||||
                                CTTCGA   CGTCCTCCT
                                    CAC
GAM80   KIAA0843  3'  GCAGCAGGAGCCGAGGA     1523      _      AGCAG
                                GCAG AGGAGCT    GAGGA
                                |||| |||||||    |||||
                                CGTC TCCTCGG    CTCCT
                                  G      ______
GAM80   KIAA0972  3'  CATGGGAGAGCAGGAGG     1524     GA   CT
                                CA  GGAG  AGCAGGAGG
                                ||  ||||  |||||||||
                                GT  CCTC  TCGTCCTCC
                                 AC    __
GAM80   KIAA1045  3'  CCGCAGAGGGGCTCTGGGGA  1525          A   AGCA  A
                                TCGCAGAGG GCT    GG GGA
                                ||||||||| |||    || |||
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                                GGCGTCTCC CGA    CC CCT
                                     C   GA__  _
GAM80   KIAA1056  3'  TCTCAGAAGGTAGGAGGA    1526     G     AGCTAGC
                                TC CAGAGG      AGGAGGA
                                || ||||||      |||||||
                                AG GTCTTC      TCCTCCT
                                 A     CA_____
GAM80   KIAA1297  3'  TCTGGAGGAGCTAGCTTTCCTG 1527     GCA         AGGA___
           GGAC                    TC   GAGGAGCTAGC      GGAC
                                ||   ||||||||||      ||||
                                AG   CTCCTCGATCG      CCTG
                                 AC_         AAAGGAC
GAM80   KIAA1530  3'  GGAGACCGAAGCAGGAGGA   1528       _ __
                                GGAG CT  AGCAGGAGGA
                                |||| ||  ||||||||||
                                CCTC GG  TCGTCCTCCT
                                  T  CT
GAM80   KIAA1649  3'  GAGAGGCTGAAGCAGGAGGA   1529     GA  __
                                GAG  GCT  AGCAGGAGGA
                                |||  |||  ||||||||||
                                CTC  CGA  TCGTCCTCCT
                                  TC   CT
GAM80   KIAA1941  3'  GCAGAGGAGCATAGAGG     1530          TAGCA
                                GCAGAGGAGC    GGAGG
                                ||||||||||    |||||
                                CGTCTCCTCG    TCTCC
                                      TA___
GAM80   LENG5     3'  CCGCGGAGAAAGGTAGGAGGA  1531      A     CTAGC
                                TCGC GAGGAG    AGGAGGA
                                |||| ||||||    |||||||
                                GGCG CTCTTT    TCCTCCT
                                  C     CCA__
GAM80   LRN       3'  CCGCGGAGGAGCTGGGCCTAGG 1532      A       A_  AGG
                                TCGC GAGGAGCT  GC   AGG
                                |||| ||||||||  ||   |||
                                GGCG CTCCTCGA  CG   TCC
                                  C       CC  GA_
GAM80   MAPK8IP2  3'  TCGCAGGGGAGTGGCAGGAGG  1533       A    CTA
                                TCGCAG GGAG   GCAGGAGG
                                ||||||  ||||   ||||||||
                                AGCGTC CCTC   CGTCCTCC
                                   C    AC_
GAM80   MAPK8IP2  3'  TCGCAGGGGAGTGGCAGGAGG  1533       A    CTA
                                TCGCAG GGAG   GCAGGAGG
                                ||||||  ||||   ||||||||
                                AGCGTC CCTC   CGTCCTCC
                                   C    AC_
GAM80   MAPK8IP2  3'  TCGCAGGGGAGTGGCAGGAGG  1533       A    CTA
                                TCGCAG GGAG   GCAGGAGG
                                ||||||  ||||   ||||||||
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                                AGCGTC CCTC   CGTCCTCC
                                   C    AC_
GAM80   MCAM     3'  GAAGAGGCGAGCAGGAGG    1534        _ T
                                GAGGAG C AGCAGGAGG
                                |||||| | |||||||||
                                CTTCTC G TCGTCCTCC
                                   C C
GAM80   MGC13159 3'  GAAGGCTGAGGCAGGAGGA   1535      A   A__
                                GAGG GCT   GCAGGAGGA
                                |||| |||   |||||||||
                                CTTC CGA   CGTCCTCCT
                                  _   CTC
GAM80   MGC23284 5'  CGCAGAGGCACCCAGGAGG   1536         A   AG
                                CGCAGAGG GCT  CAGGAGG
                                |||||||| |||  |||||||
                                GCGTCTCC TGG  GTCCTCC
                                     G   __
GAM80   MGC5508  3'  GCAGGGGGCTGGCAGGAGG   1537      A  A   A
                                GCAG GG GCT GCAGGAGG
                                |||| || ||| ||||||||
                                CGTC CC CGA CGTCCTCC
                                  _ C   C
GAM80   PALMD    3'  GATAGTTAGCAGGAGGA     1538     GG  C
                                GA  AG TAGCAGGAGGA
                                ||  || ||||||||||
                                CT  TC ATCGTCCTCCT
                                 A_  A
GAM80   PELI1    5'  TCGGGAGGCTGAGGCAGGAGGA 1507      CA    AGCTA
                                TCG  GAGG    GCAGGAGGA
                                |||  ||||    |||||||||
                                AGC  CTCC    CGTCCTCCT
                                  C_   GACTC
GAM80   PPI5PIV  3'  GAGGGGCTGCCAGGAGGAC   1539      A   AG
                                GAGG GCT  CAGGAGGAC
                                |||| |||  |||||||||
                                CTCC CGA  GTCCTCCTG
                                  C   CG
GAM80   PPIL2    3'  GCGAGGCTGAGGCAGGAGGA  1540     A    AGCTA
                                GC GAGG    GCAGGAGGA
                                || ||||    |||||||||
                                CG CTCC    CGTCCTCCT
                                  _   GACTC
GAM80   PRO0899  5'  GCCAGACTGAAGCAGGAGGA  1541     AG   AGCT
                                GC  AGG   AGCAGGAGGA
                                ||  |||   ||||||||||
                                CG  TCT   TCGTCCTCCT
                                 G_  GACT
GAM80   RA-GEF-2 3'  GAGGAGATGCAGGAGGA    1542        CTA
                                GAGGAG   GCAGGAGGA
                                ||||||   |||||||||
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                                CTCCTC  CGTCCTCCT
                                   TA_
GAM80   SARM     3'  GCAGAGGAGCTATTTGGGAC  1543          GCAGGA
                                GCAGAGGAGCTA    GGAC
                                ||||||||||||    ||||
                                CGTCTCCTCGAT    CCTG
                                      AAAC__
GAM80   SLC16A10 5'  CCGGAGGAGCTGCGGGG    1544    CA      A  A  A
                                TCG  GAGGAGCT GC GG GG
                                |||  |||||||| || || ||
                                GGC  CTCCTCGA CG CC CC
                                  __      _ _ _
GAM80   SQV7L    5'  GGAGGCCAAGGCAGGAGGA   1487      _  __
                                GGAG CTA  GCAGGAGGA
                                |||| |||  |||||||||
                                CCTC GGT  CGTCCTCCT
                                  C   TC
GAM80   STAF65(gamma) 5'  TCGCAGAGCGGGCTGGGCGG  1545        GA_  A_  A
                                TCGCAGAG   GCT  GC GG
                                ||||||||   |||  || ||
                                AGCGTCTC   CGA  CG CC
                                     GCC   CC  _
GAM80   STK39    5'  GCGGAGGAGAGCAGGAGGAC  1546    A     CT
                                GC GAGGAG  AGCAGGAGGAC
                                || ||||||  ||||||||||
                                CG CTCCTC  TCGTCCTCCTG
                                 C     __
GAM80   THEA     3'  GGAGATCCAAGGCAGGAGGA  1547      __  __
                                GGAG  CTA  GCAGGAGGA
                                ||||  |||  |||||||||
                                CCTC  GGT  CGTCCTCCT
                                  TA   TC
GAM80   LOC115219 3'  GCAGGAGGCAGGAGGA     1548     GA   CTA
                                GCA  GGAG   GCAGGAGGA
                                |||  ||||   |||||||||
                                CGT  CCTC   CGTCCTCCT
                                  __   ____
GAM80   LOC129676 5'  CAGAGGAGCTGGGGAAGAGG  1549          AGC_
                                CAGAGGAGCT    AGGAGG
                                ||||||||||    ||||||
                                GTCTCCTCGA    TTCTCC
                                      CCCC
GAM80   LOC143677 3'  AGAGGAGCTGACTCAGAGGAC  1550         AG A_
                                AGAGGAGCT  C  GGAGGAC
                                |||||||||  |  |||||||
                                TCTCCTCGA  G  TCTCCTG
                                      CT AG
GAM80   LOC145447 5'  GGAGCAAAGAGCAGGAGGA   1551       T___
                                GGAGC    AGCAGGAGGA
                                |||||    ||||||||||
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                                CCTCG   TCGTCCTCCT
                                  TTTC
GAM80   LOC145725 3' GGAGGCCGAGGCAGGAGGA  1552     _ A__
                                GGAG CT  GCAGGAGGA
                                |||| ||  |||||||||
                                CCTC GG  CGTCCTCCT
                                  C  CTC
GAM80   LOC145732 3' GGAGGCCGAGGCAGGAGGA  1552     _ A__
                                GGAG CT  GCAGGAGGA
                                |||| ||  |||||||||
                                CCTC GG  CGTCCTCCT
                                  C  CTC
GAM80   LOC150054 5' GGAGGCCAAGGCAGGAGGA  1487     _  __
                                GGAG CTA  GCAGGAGGA
                                |||| |||  |||||||||
                                CCTC GGT  CGTCCTCCT
                                  C  TC
GAM80   LOC154215 3' GCAGAGGAGTTAGCAATGG  1553       C    GA
                                GCAGAGGAG TAGCAG  GG
                                ||||||||| ||||||  ||
                                CGTCTCCTC ATCGTT  CC
                                     A    A_
GAM80   LOC154877 5' TCGGAGGCTGAAGCAGGAGGA 1555    CA   AGCT
                                TCG  GAGG   AGCAGGAGGA
                                |||  ||||   ||||||||||
                                AGC  CTCC   TCGTCCTCCT
                                  __   GACT
GAM80   LOC154877 3' TCACAGAGGGACAGGGGAGG  1554       AG T  CA
                                TCGCAGAGG  C AG  GGAGG
                                |||||||||  | ||  |||||
                                AGTGTCTCC  G TC  CCTCC
                                     CT _  C_
GAM80   LOC154877 3' GGAGGCCAAGGCAGGAGGA  1487     _  __
                                GGAG CTA  GCAGGAGGA
                                |||| |||  |||||||||
                                CCTC GGT  CGTCCTCCT
                                  C  TC
GAM80   LOC196957 3' GGAGGCCGAGGCAGGAGGA  1552     _ A__
                                GGAG CT  GCAGGAGGA
                                |||| ||  |||||||||
                                CCTC GG  CGTCCTCCT
                                  C  CTC
GAM80   LOC196961 3' GGAGGCCGAGGCAGGAGGA  1552     _ A__
                                GGAG CT  GCAGGAGGA
                                |||| ||  |||||||||
                                CCTC GG  CGTCCTCCT
                                  C  CTC
GAM80   LOC197138 3' GGAGGCCGAGGCAGGAGGA  1552     _ A__
                                GGAG CT  GCAGGAGGA
                                |||| ||  |||||||||
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                                CCTC GG   CGTCCTCCT
                                  C  CTC
GAM80   LOC199786 3'  GGAGGCCAAGGCAGGAGGA   1487      _  __
                                GGAG CTA  GCAGGAGGA
                                |||| |||  |||||||||
                                CCTC GGT  CGTCCTCCT
                                  C   TC
GAM80   LOC199899 5'  TCGAGAGGCTAAGGCAGGAGGA 1556     C    AGCTA
                                TCG AGAGG    GCAGGAGGA
                                ||| |||||    |||||||||
                                AGC TCTCC    CGTCCTCCT
                                  _    GATTC
GAM80   LOC203427 3'  GGAGGCCAAGGCAGGAGGA   1487      _  __
                                GGAG CTA  GCAGGAGGA
                                |||| |||  |||||||||
                                CCTC GGT  CGTCCTCCT
                                  C   TC
GAM80   LOC203427 3'  TCTGGAGGCTGAAGCAGGAGGA 1557    GCA   AGCT
                                TC   GAGG   AGCAGGAGGA
                                ||   ||||   ||||||||||
                                AG   CTCC   TCGTCCTCCT
                                 AC_   GACT
GAM80   LOC220018 5'  GCAGGGGGAAGCAGGAGGA   1558      A  AGCT
                                GCAG GG   AGCAGGAGGA
                                |||| ||   ||||||||||
                                CGTC CC   TCGTCCTCCT
                                  _ CCT_
GAM80   LOC221496 3'  GCTGAGGAGCTGGCGGGAGG   1559    A      A  A
                                GC GAGGAGCT GC GGAGG
                                || |||||||| || |||||
                                CG CTCCTCGA CG CCTCC
                                 A       C  C
GAM80   LOC256158 5'  TCACAGAGGAGCTCCATGGGG  1560           AG  _  A
                                TCGCAGAGGAGCT  CA GG GG
                                ||||||||||||  || || ||
                                AGTGTCTCCTCGA  GT CC CC
                                        G_  A  _
GAM80   LOC256476 5'  GAGAGGCTGGAGCAGGAGGA   1561     GA  __
                                GAG  GCT  AGCAGGAGGA
                                |||  |||  ||||||||||
                                CTC  CGA  TCGTCCTCCT
                                  TC   CC
GAM80   LOC257463 3'  GGAGGCCAGTGCAGGAGGAC   1562      _  __
                                GGAG CTA  GCAGGAGGAC
                                |||| |||  ||||||||||
                                CCTC GGT  CGTCCTCCTG
                                  C   CA
GAM80   LOC84549  3'  AGAACTAAAGGCAGGAGGA   1563        ___
                                GGAGCTA   GCAGGAGGA
                                |||||||   |||||||||
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                                TCTTGAT  CGTCCTCCT
                                   TTC
GAM81   BRCA1   3' GAAACAGAACTACCCTGAT  1566      AA  GG
                                GAGACA  AAT  TCCTGAT
                                ||||||  |||  |||||||
                                CTTTGT  TTG  GGGACTA
                                   C_   AT
GAM81   BRCA1   5' GAAACAGAACTACCCTGAT  1566      AA  GG
                                GAGACA  AAT  TCCTGAT
                                ||||||  |||  |||||||
                                CTTTGT  TTG  GGGACTA
                                   C_   AT
GAM81   CLC     3' CGAGGCAAGGTCCTGAT    1567     A  AAAT
                                CGAG CAA   GGTCCTGAT
                                ||||  |||   |||||||||
                                GCTC GTT   CCAGGACTA
                                  C  ____
GAM81   CNGA3   3' GAGACAAAAAGTCCCA     1568       AT
                                GAGACAAAA  GGTCCTG
                                |||||||||  |||||||
                                CTCTGTTTT  TCAGGGT
                                     __
GAM81   FANCF   3' GACAAAAATATCTTGAT    1569       G  C
                                GACAAAAATG TC TGAT
                                |||||||||| || ||||
                                CTGTTTTTAT AG ACTA
                                     _  A
GAM81   GSTA4   3' GACAAAAAAGGTTGAT     1570       T  CC
                                GACAAAAA GGT  TGAT
                                |||||||| |||  ||||
                                CTGTTTTT CCA  ACTA
                                    T  __
GAM81   KIF5C   3' GAGAACATGGTCCTGAT    1571     CAAAA
                                GAGA   ATGGTCCTGAT
                                ||||   ||||||||||
                                CTCT   TACCAGGACTA
                                  TG___
GAM81   MID1    3' GAGACAAAAGGAAAATTGAT  1572       AT  TCC__
                                GAGACAAAA  GG   TGAT
                                |||||||||  ||   ||||
                                CTCTGTTTT  CC   ACTA
                                     __ TTTTA
GAM81   MID1    3' GAGACAAAAGGAAAATTGAT  1572       AT  TCC__
                                GAGACAAAA  GG   TGAT
                                |||||||||  ||   ||||
                                CTCTGTTTT  CC   ACTA
                                     __ TTTTA
GAM81   MYCL2   3' GAGGTAATGGTCCACGTTGAT 1573     ACAAA     _____
                                GAG   AATGGTCC   TGAT
                                |||   ||||||||   ||||
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                                CTC    TTACCAGG   ACTA
                                  CA___      TGCA
GAM81   RAD17   3' GAAACAAAAATGAAGCTG    1574          TC
                                GAGACAAAAATGG CTG
                                |||||||||||||  |||
                                CTTTGTTTTTACT GAC
                                      TC
GAM81   RAD17   3' GAAACAAAAATGAAGCTG    1574          TC
                                GAGACAAAAATGG CTG
                                |||||||||||||  |||
                                CTTTGTTTTTACT GAC
                                      TC
GAM81   RAD17   3' GAAACAAAAATGAAGCTG    1574          TC
                                GAGACAAAAATGG CTG
                                |||||||||||||  |||
                                CTTTGTTTTTACT GAC
                                      TC
GAM81   RAD17   3' GAAACAAAAATGAAGCTG    1574          TC
                                GAGACAAAAATGG CTG
                                |||||||||||||  |||
                                CTTTGTTTTTACT GAC
                                      TC
GAM81   RAD17   3' GAAACAAAAATGAAGCTG    1574          TC
                                GAGACAAAAATGG CTG
                                |||||||||||||  |||
                                CTTTGTTTTTACT GAC
                                      TC
GAM81   RAD17   3' GAAACAAAAATGAAGCTG    1574          TC
                                GAGACAAAAATGG CTG
                                |||||||||||||  |||
                                CTTTGTTTTTACT GAC
                                      TC
GAM81   RAD17   3' GAAACAAAAATGAAGCTG    1574          TC
                                GAGACAAAAATGG CTG
                                |||||||||||||  |||
                                CTTTGTTTTTACT GAC
                                      TC
GAM81   RAD17   3' GAAACAAAAATGAAGCTG    1574          TC
                                GAGACAAAAATGG CTG
                                |||||||||||||  |||
                                CTTTGTTTTTACT GAC
                                      TC
GAM81   RORB    3' AAAACAAAATCCTGAT     1575        AATG
                                GAGACAAA   GTCCTGAT
                                ||||||||   ||||||||
                                TTTTGTTT   TAGGACTA
                                      ____
GAM81   TCP10   3' CAAGGCAGAAATGGCCCC   1576      A  A
                                CGAG CA AAATGGTCCT
                                ||||  ||  ||||||||||
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                                GTTC GT TTTACCGGGG
                                  C  C
GAM81   TCTA     3'  AAGACAAAAGAACTGAT     1577         AAT  TC
                                GAGACAAA   GG  CTGAT
                                ||||||||   ||  |||||
                                TTCTGTTT   TC  GACTA
                                    ___  TT
GAM81   TGM4     3'  GAGACAATGGTGGCCCTGAT   1578        AAA
                                GAGACAA   TGGTCCTGAT
                                |||||||   ||||||||||
                                CTCTGTT   ACCGGGACTA
                                    ACC
GAM81   TMOD2    3'  GATAAAATGGTCCTGAT     1579     CA
                                GA  AAAATGGTCCTGAT
                                ||  ||||||||||||||
                                CT  TTTTACCAGGACTA
                                 A_
GAM81   ARGBP2   5'  CAAGACAAAAACCTTTGGT   1580           _____
                                CGAGACAAAAA    TGGT
                                ||||||||||    ||||
                                GTTCTGTTTTT    ACCA
                                      GGAA
GAM81   C1QR1    3'  GAAACAAAAGTACCTAAT     1581         AAT  _
                                GAGACAAA   GGT CCTGAT
                                ||||||||   ||| ||||||
                                CTTTGTTT   TCA GGATTA
                                    ___   T
GAM81   CHSY1    3'  GAGACAAAATGGTTCTGA     1582          A    C
                                GAGACAAAA TGGT CTGA
                                ||||||||| |||| ||||
                                CTCTGTTTT ACCA GACT
                                     _   A
GAM81   CLDN4    5'  GAGATAAAGCCAGTCCTGAT   1583       C   AA
                                GAGA AAA  TGGTCCTGAT
                                |||| |||  ||||||||||
                                CTCT TTT  GTCAGGACTA
                                  A   CG
GAM81   CRSP3    3'  GAGACAAAAATATAGAT      1584           GTCCT
                                GAGACAAAAATG    GAT
                                ||||||||||||    |||
                                CTCTGTTTTTAT    CTA
                                      AT___
GAM81   DKFZP564A022 3'  AGCCAGGATGGTCCTGAT    1585     A  AAA
                                AG CA   ATGGTCCTGAT
                                || ||   ||||||||||
                                TC GT   TACCAGGACTA
                                 G  CC_
GAM81   DKFZP586P0123 3'  AAGGCAAAAATGGTCCTG    1586      A
                                GAG CAAAAATGGTCCTG
                                ||| ||||||||||||||
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                                TTC GTTTTTACCAGGAC
                                  C
GAM81   DRIL2    3' GAGGCCAAGATGGCCCCA    1587     A_  AA
                                GAG  CAA  ATGGTCCTG
                                |||  |||  |||||||||
                                CTC  GTT  TACCGGGGT
                                  CG   C_
GAM81   FLJ10081 3' GAGGCAAAAATGACTG      1588     A       TC
                                GAG CAAAAATGG  CTG
                                ||| |||||||||  |||
                                CTC GTTTTTACT  GAC
                                  C       __
GAM81   FLJ10483 3' CAAGACTTGGTCCTGA      1589       AAAAA
                                CGAGAC    TGGTCCTGA
                                ||||||    |||||||||
                                GTTCTG    ACCAGGACT
                                   A____
GAM81   FLJ13114 3' GAGCCAAAGGTCCCGAT     1590     A   AAT
                                GAG CAAA   GGTCCTGAT
                                ||| ||||   |||||||||
                                CTC GTTT   CCAGGGCTA
                                  G   ___
GAM81   FLJ14494 3' GATAAAAACAGTTCCTGAT   1591     C       _
                                GA AAAAATGGT CCTGAT
                                || |||||||| ||||||
                                CT TTTTTGTCA GGACTA
                                 A       A
GAM81   FLJ20725 3' GAGCAATGCAGTCCTGAT    1592     A   AAA
                                GAG CAA   TGGTCCTGAT
                                ||| |||   ||||||||||
                                CTC GTT   GTCAGGACTA
                                  _  AC_
GAM81   GPR64    3' GAGACAAAACAACCATGAT   1593         ATGGT  _
                                GAGACAAAA    CC TGAT
                                |||||||||    || ||||
                                CTCTGTTTT    GG ACTA
                                     GTT__  T
GAM81   IRAK3    3' GAGACAATTATCCTGAT     1594        AAATG
                                GAGACAA    GTCCTGAT
                                |||||||    ||||||||
                                CTCTGTT    TAGGACTA
                                   AA___
GAM81   IRX1     3' AGACAAAAATATATGAT     1595          GTCC
                                AGACAAAAATG    TGAT
                                ||||||||||    ||||
                                TCTGTTTTTAT    ACTA
                                      AT__
GAM81   KIAA0493 3' GAGATTAAAGAGCCCTGAT   1596      CAA   T
                                GAGA   AAA GGTCCTGAT
                                ||||   ||| |||||||||
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                                CTCT   TTT TCGGGACTA
                                  AA_   C
GAM81   KIAA0544  3'  GACAGACGATCCCAGAT     1597      AAA      _
                                GACA   ATGGTCCT GAT
                                ||||   |||||||| |||
                                CTGT   TGCTAGGG CTA
                                  C__       T
GAM81   MAFB      3'  CAAGACAAAGTTGTTTTCTGAT 1598         AA  GTC_
                                CGAGACAAA  TG    CTGAT
                                |||||||||  ||   |||||
                                GTTCTGTTT  AC    GACTA
                                     CA  AAAA
GAM81   NS1-BP    3'  GAACAAAAACATAGTTCTGAT  1599     A      __   C
                                GAG CAAAAAT  GGT CTGAT
                                ||| |||||||  ||| |||||
                                CTT GTTTTTG  TCA GACTA
                                  _      TA   A
GAM81   PRO1257   3'  AGACAAAAACAAGACTGAT    1600         TG TC
                                AGACAAAAA  G  CTGAT
                                |||||||||  |  |||||
                                TCTGTTTTT  T  GACTA
                                     GT CT
GAM81   RAB10     5'  CGGGACAAAATGGCCT      1601     A      A   T
                                CG GACAAAA TGG CCT
                                || ||||||| ||| |||
                                GC CTGTTTT ACC GGA
                                 C      _   _
GAM81   SLC2A13   3'  GAACAAAAACTGACCCTGAT   1602      A     _  GT
                                GAG CAAAAA TG  CCTGAT
                                ||| |||||| ||  ||||||
                                CTT GTTTTT AC  GGACTA
                                  _     G  TG
GAM81   UBF-fl    3'  GAGAGCAGGATGGTCCTGAT   1603      _  AAA
                                GAGA CA   ATGGTCCTGAT
                                |||| ||   ||||||||||
                                CTCT GT   TACCAGGACTA
                                  C  CC_
GAM81   ZDHHC2    3'  GAGGCAAAAATGGTTGAT     1604      A        CC
                                GAG CAAAAATGGT  TGAT
                                ||| ||||||||||  ||||
                                CTC GTTTTTACCA  ACTA
                                  C         __
GAM81   LOC149069 3'  GAGACAAAAAGCCTG       1605          AT  T
                                GAGACAAAA  GG CCTG
                                |||||||||  || ||||
                                CTCTGTTTT  TC GGAC
                                          __  _
GAM81   LOC151146 5'  CGAGACAAAGGAGCCAGAT    1606          AAT  T_  T
                                CGAGACAAA   GG  CC GAT
                                |||||||||   ||  || |||
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                                GCTCTGTTT  CC  GG CTA
                                    ___  TC  T
GAM81   LOC152373 5' GAGGCCAGCATCATCCTGAT  1607    A_  AAA  G
                                GAG  CA   AT GTCCTGAT
                                |||  ||   || ||||||||
                                CTC  GT   TA TAGGACTA
                                  CG  CG_  G
GAM81   LOC153077 3' GAAGCAAAAGAGTCCTGAT   1608   GA    AT
                                GA  CAAAA  GGTCCTGAT
                                ||  |||||  |||||||||
                                CT  GTTTT  TCAGGACTA
                                 TC    C_
GAM81   LOC170393 3' CGAGACAAAGGCGTGA      1609       AAT   CC
                                CGAGACAAA   GGT  TGA
                                |||||||||   |||  |||
                                GCTCTGTTT   CCG  ACT
                                    ___   C_
GAM81   LOC202134 3' AGACAAAAAGGAAGGCTTGAT 1610       T___   CC
                                AGACAAAAA    GGT  TGAT
                                |||||||||    |||  ||||
                                TCTGTTTTT    CCG  ACTA
                                     CCTT   A_
GAM81   LOC203238 3' GAAACAAAAGTCAACTGAT   1611       AAT   __
                                GAGACAAA   GGTC  CTGAT
                                ||||||||   ||||  |||||
                                CTTTGTTT   TCAG  GACTA
                                    ___    TT
GAM81   LOC223009 5' GAGACAAAAGTTGGGCCT    1612       A_   T
                                GAGACAAAA  TGG CCT
                                |||||||||  ||| |||
                                CTCTGTTTT  ACC GGA
                                     CA   C
GAM81   LOC254643 3' CAAGGCAGGGAGCCCTGAT   1613     A  AAAAT
                                CGAG CA    GGTCCTGAT
                                ||||  ||    |||||||||
                                GTTC GT    TCGGGACTA
                                  C  CCC__
GAM81   LOC256176 5' GAGGCCAGCATCATCCTGAT  1607    A_  AAA  G
                                GAG  CA   AT GTCCTGAT
                                |||  ||   || ||||||||
                                CTC  GT   TA TAGGACTA
                                  CG  CG_  G
GAM81   LOC256254 3' GAAACAAAAGTCAACTGAT   1611       AAT   __
                                GAGACAAA   GGTC  CTGAT
                                ||||||||   ||||  |||||
                                CTTTGTTT   TCAG  GACTA
                                    ___    TT
GAM81   LOC57826  3' AGACAAAAATATGCTGAT    1614        GTC
                                AGACAAAAATG   CTGAT
                                ||||||||||   |||||
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                                TCTGTTTTTAT   GACTA
                                      AC_
GAM81   LOC92399  3'  CAAGACAAGGCCTGA      1615        AAAT  T
                                CGAGACAA    GG CCTGA
                                ||||||||    || |||||
                                GTTCTGTT    CC GGACT
                                     _____  _
GAM82   SH3BGRL2  3'  TGATGTGGCTGCTACAAAGGT  1618      C  A       TACC
                                TGA GT GCTGCTGCAG    GGT
                                ||| || ||||||||||    |||
                                ACT CA CGACGATGTT    CCA
                                  A  C         T___
GAM82   VDAC3     3'  TGATGTACTTGTTGTAGTACCG 1619      C   GC  C  C
            GT                    TGA GTA  TG TG AGTACCGGT
                                ||| |||  || || |||||||||
                                ACT CAT  AC AC TCATGGCCA
                                  A   GA  A  A
GAM82   LOC150147 5'  TGGCATAGCTGTTGTGGCAGC  1620     A       CT___
                                TG CGTAGCTG     GCAGT
                                || ||||||||     |||||
                                AC GTATCGAC     CGTCG
                                 C       AACAC
GAM82   LOC153338 5'  TGATGTATTTGCTGCAGGCC   1621      C   GC       TA
                                TGA GTA  TGCTGCAG  CC
                                ||| |||  ||||||||  ||
                                ACT CAT  ACGACGTC  GG
                                  A   AA       C_
GAM82   LOC257478 5'  TGAAGTGGTCCTTGCAGTACTG 1622      C  AG_  GC       C
            GT                    TGA GT   CT  TGCAGTAC GGT
                                ||| ||   ||  |||||||| |||
                                ACT CA   GG  ACGTCATG CCA
                                  T  CCA  A_       A
GAM83   DKFZP586N0721 3'  CCAGTTTACATGAGGCAA    1625     G       AC  C
                                CC AGTTTACG  AG GCAA
                                || ||||||||  || ||||
                                GG TCAAATGT  TC CGTT
                                 _       AC  _
GAM83   HIC       3'  GAGTTAACAGTGCAAAT     1626       TAC    C
                                GAGTT   GACAG GCAAAT
                                |||||   ||||| ||||||
                                CTCAA   TTGTC CGTTTA
                                   ___     A
GAM83   LOC90719  5'  CCAGGTTCGGGGCGCAAATC   1627      A   TA  ACA
                                CCG GTT  CG   GCGCAAATC
                                ||| |||  ||   |||||||||
                                GGT CAA  GC   CGCGTTTAG
                                  C   __  CC_
GAM84   ARF5      3'  AGGCCTGTGGCTATGGGGGA   1630          ACACC  A
                                GGGCCTGTGG     TG GGGA
                                ||||||||||     || ||||
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                                TCCGGACACC    AC CCCT
                                      GAT__  C
GAM84   ARHGDIA  3'  GGGCCTGTGGGTGGGGG    1631         ACACC  A
                                GGGCCTGTGG    TG GGG
                                ||||||||||    || |||
                                CCCGGACACC    AC CCC
                                      C____  C
GAM84   ATRN     3'  GGGCCTGTGGGAATTAAGGG  1632         ACACC
                                GGGCCTGTGG    TGAGGG
                                ||||||||||    ||||||
                                CCCGGACACC    ATTCCC
                                      CTTA_
GAM84   BCLG     3'  GGGCTTTTGGACACCTTGGGG 1633      CTG       GA
                                GGGC  TGGACACCT  GGG
                                ||||  |||||||||  |||
                                CCCG  ACCTGTGGA  CCC
                                  AAA       AC
GAM84   BMP1     3'  GGGCCTGTAGGGAGGAGTGGGG 1634         ACACC__  A
           GA                     GGGCCTGTGG      TG GGGA
                                ||||||||||      || ||||
                                CCCGGACATC      AC CCCT
                                      CCTCCTC  C
GAM84   CDH5     5'  GCCTGTGGGGCTGAGGGA    1635         ACAC
                                GCCTGTGG   CTGAGGGA
                                ||||||||   ||||||||
                                CGGACACC   GACTCCCT
                                     CC__
GAM84   CENTD1   3'  GGGCCTGTGAATATAGATCCCT 1636         CA_________  TGAG
           CAGG                   GCCTGTGGA       CC   GG
                                |||||||||       ||   ||
                                CGGACACTT       GG   CC
                                     ATATCTIIIA  GAGT
GAM84   CENTD1   3'  GGGCCTGTGAATATAGATCCCT 1636         CA_________  TGAG
           CAGG                   GCCTGTGGA       CC   GG
                                |||||||||       ||   ||
                                CGGACACTT       GG   CC
                                     ATATCTIIIA  GAGT
GAM84   COL18A1  3'  GGCCTGTGGGCACCCCGGG   1637         A    GA
                                GGCCTGTGG CACCT  GGG
                                ||||||||| |||||  |||
                                CCGGACACC GTGGG  CCC
                                     C    G_
GAM84   COL18A1  3'  GGCCTGTGGGCACCCCGGG   1637         A    GA
                                GGCCTGTGG CACCT  GGG
                                ||||||||| |||||  |||
                                CCGGACACC GTGGG  CCC
                                     C    G_
GAM84   COL18A1  3'  GGCCTGTGGGCACCCCGGG   1637         A    GA
                                GGCCTGTGG CACCT  GGG
                                ||||||||| |||||  |||
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                                CCGGACACC GTGGG  CCC
                                     C    G_
GAM84   CRYAA    3'  GGGTCTGGGACACCCTGA    1638     C  T     _
                                GGG CTG GGACACC TGA
                                ||| ||| ||||||| |||
                                CCC GAC CCTGTGG ACT
                                  A  _      G
GAM84   DVL1     3'  GGGCCTGTGCACCGCAGGG   1639         GA   TG
                                GGGCCTGTG  CACC  AGGG
                                |||||||||  ||||  ||||
                                CCCGGACAC  GTGG  TCCC
                                     __    CG
GAM84   EPHB3    3'  AGGTCTGGGCCCTGAGGG    1640     C  T  ACA
                                GGG CTG GG   CCTGAGGG
                                ||| ||| ||   ||||||||
                                TCC GAC CC   GGACTCCC
                                  A  _ G__
GAM84   FBXL7    3'  GGGCCTGTGTGCGAGGG     1641         GACACC
                                GGGCCTGTG     TGAGGG
                                |||||||||     ||||||
                                CCCGGACAC     GCTCCC
                                     AC_____
GAM84   FGFR1    3'  GCCTGTGGCAGGGAGGG     1642         A  CCT
                                GCCTGTGG CA   GAGGG
                                |||||||| ||   |||||
                                CGGACACC GT   CTCCC
                                     _ CC_
GAM84   GAMT     5'  GGGCTTGTGGGCCGGGG     1643      C    ACAC   A
                                GGGC TGTGG    CTG GGG
                                |||| |||||    ||| |||
                                CCCG ACACC    GGC CCC
                                  A    C___   _
GAM84   GAMT     5'  GGGCTTGTGGGCCGGGG     1643      C    ACAC   A
                                GGGC TGTGG    CTG GGG
                                |||| |||||    ||| |||
                                CCCG ACACC    GGC CCC
                                  A    C___   _
GAM84   GRB7     3'  GGGCTGTTTTCTATCTGAGGGA 1644      C   GGACAC_
                                GGGC TGT      CTGAGGGA
                                |||| |||      ||||||||
                                CCCG ACA      GACTCCCT
                                  _   AAAGATA
GAM84   GZMM     3'  GGTCCTGTGGAGACAGCGAGGG 1645     G       C  C_
                                GG CCTGTGGA AC  TGAGGG
                                || |||||||| ||  ||||||
                                CC GGACACCT TG  GCTCCC
                                 A       C  TC
GAM84   IARS     5'  GGGCGTACCTGAGGG       1646       CT  GGAC
                                GGGC  GT    ACCTGAGGG
                                ||||  ||    |||||||||
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                                CCCG  CA    TGGACTCCC
                                  __  _____
GAM84   KIF5B    5'  GGGCTTGTGGTCGCGAGGG   1647      C     ACACC
                                GGGC TGTGG    TGAGGG
                                |||| |||||    ||||||
                                CCCG ACACC    GCTCCC
                                  A    AGC__
GAM84   KLK4     3'  GGGCCTGAGGGAGGAGGG    1648        T_   CACCT
                                GGGCCTG  GGA    GAGGG
                                |||||||  |||    |||||
                                CCCGGAC  CCT    CTCCC
                                    TC   C____
GAM84   KRT6A    3'  GGGCCTGAGGACTGTGGGA   1649         T    ACC  A
                                GGGCCTG GGAC   TG GGGA
                                ||||||| ||||   || ||||
                                CCCGGAC CCTG   AC CCCT
                                    T   ___  A
GAM84   L1CAM    3'  GGGCCTGCTGGAGAGGG     1650         _    CACCT
                                GGGCCTG TGGA    GAGGG
                                ||||||| ||||    |||||
                                CCCGGAC ACCT    CTCCC
                                    G   _____
GAM84   L1CAM    3'  GGGCCTGCTGGAGAGGG     1650         _    CACCT
                                GGGCCTG TGGA    GAGGG
                                ||||||| ||||    |||||
                                CCCGGAC ACCT    CTCCC
                                    G   _____
GAM84   LPO      3'  GGCCCTGTGGACCAAAGGGA  1651     G        ACCT
                                GG CCTGTGGAC    GAGGGA
                                || |||||||||    ||||||
                                CC GGACACCTG    TTCCCT
                                 G       GT__
GAM84   MMP19    3'  GCCCGTACCTGAGGGA      1652        GGAC
                                GCCTGT    ACCTGAGGGA
                                ||||||    ||||||||||
                                CGGGCA    TGGACTCCCT
                                  ____
GAM84   MMP19    3'  GCCCGTACCTGAGGGA      1652        GGAC
                                GCCTGT    ACCTGAGGGA
                                ||||||    ||||||||||
                                CGGGCA    TGGACTCCCT
                                  ____
GAM84   MMP2     3'  GGGCCTGTGGGAGCCAGGG   1653          ACA  TG
                                GGGCCTGTGG   CC  AGGG
                                ||||||||||   ||  ||||
                                CCCGGACACC   GG  TCCC
                                     CTC  __
GAM84   NAGA     3'  AGGTTTGTGGACACATCTGGGG 1654      CC        __   A
          A                      GGG  TGTGGACAC  CTG GGGA
                                 |||  |||||||||  ||| ||||
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                                TCC  ACACCTGTG  GAC CCCT
                                  AA        TA  _
GAM84   NYX      5'  GGACCCCTACCTGAGGG     1655        G GGAC
                                GGGCCT T    ACCTGAGGG
                                |||||| |    |||||||||
                                CCTGGG A    TGGACTCCC
                                   G _____
GAM84   PODXL    5'  AGGCCTGTGGGTGGCTCCGGA  1656           ACAC  GA
                                GGGCCTGTGG    CT  GGG
                                ||||||||||    ||  |||
                                TCCGGACACC    GA  CCT
                                      CACC  GG
GAM84   POLR2E   3'  GGGCTGTGTGGATGGAGGA    1657       C_     CACCT
                                GGGC  TGTGGA     GAGGG
                                ||||  ||||||     |||||
                                CCCG  ACACCT     CTCCT
                                  AC     AC___
GAM84   RAP1GA1  5'  AGGTCTAGTGCCTGAGGGA    1658      C  _   GACA
                                GGG CT GTG    CCTGAGGGA
                                ||| || |||    |||||||||
                                TCC GA CAC    GGACTCCCT
                                  A  T  _____
GAM84   RFNG     3'  GGCCGTGGCACCTGAGGGA    1659       T    A
                                GGCC GTGG CACCTGAGGGA
                                |||| |||| ||||||||||
                                CCGG CACC GTGGACTCCCT
                                   _    _
GAM84   SCRT1    5'  GGGCCTGCGGAGCCGGGG     1660           CAC   A
                                GGGCCTGTGGA   CTG GGG
                                ||||||||||   ||| |||
                                CCCGGACGCCT   GGC CCC
                                      C__   _
GAM84   SLC30A3  3'  GGGCCATGTGGGGAGGG      1661        _     ACACCT
                                GGGCC TGTGG     GAGGG
                                |||||| |||||     |||||
                                CCCGG ACACC     CTCCC
                                   T     C_____
GAM84   SLC7A5   5'  GGGCCTGGGACACCCGGGA    1662         T        A
                                GGGCCTG GGACACCTG GGG
                                ||||||| ||||||||| |||
                                CCCGGAC CCTGTGGGC CCT
                                      _        _
GAM84   SMARCD1  3'  GGTCCTGCTGCTACCTGAGGG  1663     G     GGAC
                                GG CCTGT    ACCTGAGGG
                                || |||||    |||||||||
                                CC GGACG    TGGACTCCC
                                  A    ACGA
GAM84   SMARCD1  3'  GGTCCTGCTGCTACCTGAGGG  1663     G     GGAC
                                GG CCTGT    ACCTGAGGG
                                || |||||    |||||||||
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                                CC GGACG    TGGACTCCC
                                 A    ACGA
GAM84   TAZ     3'  GGGCCTGTGGTGGGGGG      1664          ACACC  A
                                GGGCCTGTGG    TG GGG
                                ||||||||||    || |||
                                CCCGGACACC    AC CCC
                                      _____  C
GAM84   TCF7    3'  GGGCCTGTGGGGGGCCCTGGGG  1665          ACA_   A
                                GGGCCTGTGG   CCTG GGG
                                ||||||||||   |||| |||
                                CCCGGACACC   GGAC CCC
                                      CCCG   _
GAM84   TIMP4   5'  GAGCCTGTGAGGTCTGGGGGA  1666          ACAC   A
                                GGGCCTGTGG   CTG GGGA
                                ||||||||||   ||| ||||
                                CTCGGACACT   GAC CCCT
                                      CCA_   C
GAM84   TP73    3'  GGGCCTGTGAGGTGCCTGGGGA 1667          ACA_   A
                                GGGCCTGTGG   CCTG GGGA
                                ||||||||||   |||| ||||
                                CCCGGACACT   GGAC CCCT
                                      CCAC   _
GAM84   TRH     3'  AGGCCTGTGGTGGGGGG      1668          ACACC  A
                                GGGCCTGTGG    TG GGG
                                ||||||||||    || |||
                                TCCGGACACC    AC CCC
                                      _____  C
GAM84   WFDC1   5'  GGGCCTGTGAGTGGGG      1669          ACACC  A
                                GGGCCTGTGG    TG GGG
                                ||||||||||    || |||
                                CCCGGACACT    AC CCC
                                      C____  _
GAM84   WNT3A   3'  GGGCTGTGGACAGGCGGA    1670      C       CCTGA
                                GGGC TGTGGACA    GGG
                                |||| ||||||||    |||
                                CCCG ACACCTGT    CCT
                                  _      CCG__
GAM84   ZNF261  3'  GGGCCTGTCACCCTGAGGGA   1671          GG  A
                                GGGCCTGT  AC CCTGAGGGA
                                ||||||||  || |||||||||
                                CCCGGACA  TG GGACTCCCT
                                     G_  _
GAM84   AIF1    3'  GAGCCTGTGGACAAGGGTAGGG 1672           CCTG_
           A                     GGGCCTGTGGACA    AGGGA
                                 ||||||||||||    |||||
                                 CTCGGACACCTGT    TCCCT
                                       TCCCA
GAM84   ANKRD5  5'  GGGCCTGCTGGGGCGACCGGGG 1673          ___  AC   T A
           A                     GGGCCTGT   GG  ACC G GGGA
                                 ||||||||   ||  ||| | ||||
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                                CCCGGACG   CC  TGG C CCCT
                                     ACC  GC   _ _
GAM84   AP3S2    3'  GGGAGAATGGCACCTGAGGGA  1674      CCT    A
                                GGG   GTGG CACCTGAGGGA
                                |||   |||| ||||||||||
                                CCC   TACC GTGGACTCCCT
                                  TCT   _
GAM84   ATIP1    3'  GAGTCTGTGGACTTTGGGGA  1675      C       ACC  A
                                GGG CTGTGGAC   TG GGGA
                                ||| ||||||||   || ||||
                                CTC GACACCTG   AC CCCT
                                  A       AA_  _
GAM84   BA526D8.4 5'  AGGTTTGAATTCTGAGGGA   1676     CCTG    CAC
                                GGG   TGGA   CTGAGGGA
                                |||   ||||   ||||||||
                                TCC   ACTT   GACTCCCT
                                  AA__   AA_
GAM84   C12orf6   5'  GAGCCTGTGGGAAGGG      1677          ACACCT
                                GGGCCTGTGG     GAGGG
                                ||||||||||     |||||
                                CTCGGACACC     TTCCC
                                     C_____
GAM84   C20orf162 5'  GGGGATGGTGTCTGAGGGA   1678     CCT    ACAC
                                GGG   GTGG   CTGAGGGA
                                |||   ||||   ||||||||
                                CCC   TACC   GACTCCCT
                                  C__   ACA_
GAM84   C6orf9    3'  GGACCTGTGGGCGGGG      1679          ACACC  A
                                GGGCCTGTGG    TG GGG
                                ||||||||||    || |||
                                CCTGGACACC    GC CCC
                                     C____  _
GAM84   CHRAC1    3'  GGGCCTGTCGAGGAGGG     1680         G  CACCT
                                GGGCCTGT GA    GAGGG
                                |||||||| ||    |||||
                                CCCGGACA CT    CTCCC
                                     G  C____
GAM84   COTL1     3'  GGGCTGTGGACACAGGG     1681      C       CTG
                                GGGC TGTGGACAC   AGGG
                                |||| |||||||||   ||||
                                CCCG ACACCTGTG   TCCC
                                  _       ___
GAM84   CSMD1     5'  GGGCCTGTGGTCACTCCA    1682          A  _
                                GGGCCTGTGG CAC CTG
                                |||||||||| ||| |||
                                CCCGGACACC GTG GGT
                                     A  A
GAM84   CSNK1G1   3'  GGGCCTGAGGACTCCTGGGA  1683        T   A   A
                                GGGCCTG GGAC CCTG GGG
                                ||||||| |||| |||| |||
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                                CCCGGAC CCTG GGAC CCT
                                    T   A   _
GAM84   DJ37E16.5 3'  GGGCCTGTGGCTGCAGG     1684          ACAC   A
                                GGGCCTGTGG    CTG GGG
                                ||||||||||    ||| |||
                                CCCGGACACC    GAC TCC
                                      _____   G
GAM84   DKFZp434C0923 3'  GGCTCTGTGGACAGGAGCAGGG 1685     _       CCTG_
                                GGC CTGTGGACA     AGGG
                                ||| |||||||||     ||||
                                CCG GACACCTGT     TCCC
                                  A       CCTCG
GAM84   DKFZp434F142 3'  GGGCCTGTAGACACAGCAGGGA 1686             CTG
                                GGGCCTGTGGACAC   AGGGA
                                ||||||||||||||   |||||
                                CCCGGACATCTGTG   TCCCT
                                         TCG
GAM84   DKFZP434J193 3'  GGGCCTGTGGGACAGGTCCCTC 1687          _ A_______  TGAG
            G                    GGGCCTGTGG AC      CC    G
                                ||||||||||  ||      ||    |
                                CCCGGACACC TG      GG    C
                                      C  TCCIIIA  GAGT
GAM84   DKFZP434P0111 3'  GGGCCTGTGGGACCTGGG    1688          AC     A
                                GGGCCTGTGG  ACCTG GG
                                ||||||||||  ||||| ||
                                CCCGGACACC  TGGAC CC
                                      C_    _
GAM84   DKFZP434P1750 5'  GGGCCTGTGCCAGGGCCTGAGG 1689         GA ____
            G                    GGGCCTGTG  CA   CCTGAGGG
                                |||||||||  ||   ||||||||
                                CCCGGACAC  GT   GGACTCCC
                                     G_  CCC
GAM84   DKFZp547D155 3'  GGGCCTGTGGAACCCTAGA   1690          C    G
                                GGGCCTGTGGA ACCT AGG
                                |||||||||| |||| |||
                                CCCGGACACCT TGGG TCT
                                      _    A
GAM84   DKFZp761F2014 3'  GGGCCTGTGGAGTGGGCCAGGG 1691          CA___  TG
                                GGGCCTGTGGA     CC  AGGG
                                ||||||||||     ||  ||||
                                CCCGGACACCT     GG  TCCC
                                      CACCC  __
GAM84   DPYSL4    3'  GAGCCTGTGGGGAGGG      1692          ACACCT
                                GGGCCTGTGG     GAGGG
                                ||||||||||     |||||
                                CTCGGACACC     CTCCC
                                      C_____
GAM84   DUSP14    3'  TGTAAAAAACACTTGAGGGA   1693       ___    C
                                TGTG   GACAC TGAGGGA
                                ||||   ||||| |||||||
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                                ACAT   TTGTG ACTCCCT
                                  TTT    A
GAM84   FLJ10761 3' GGGCCTGAGGGCCAGGG     1694        T  ACA  TG
                                GGGCCTG GG   CC  AGGG
                                ||||||| ||   ||  ||||
                                CCCGGAC CC   GG  TCCC
                                   T  C__  __
GAM84   FLJ11160 3' GGGTCTGTGCACACTTGA    1695     C    G    C
                                GGG CTGTG ACAC TGA
                                ||| ||||| |||| |||
                                CCC GACAC TGTG ACT
                                  A    G    A
GAM84   FLJ13855 3' GGCCTGTGGGAAATAATGGGGG 1696         ACACC__  A
           A                     GGCCTGTGG      TG GGGA
                                |||||||||      || ||||
                                CCGGACACC      AC CCCT
                                     CTTTATT  C
GAM84   FLJ13881 3' GGGCCCGTGGGGTCCAGGGA   1697         ACA  TG
                                GGGCCTGTGG   CC  AGGGA
                                ||||||||||   ||  |||||
                                CCCGGGCACC   GG  TCCCT
                                     CCA  __
GAM84   FLJ14564 3' GGGCCTGTGCACTGCTGGGG   1698        G  AC   A
                                GGGCCTGTG AC  CTG GGG
                                ||||||||| ||  ||| |||
                                CCCGGACAC TG  GAC CCC
                                     G  AC  _
GAM84   FLJ14957 3' GGCCTGTGGGCATGCCTGGGGA 1699         A  __   A
                                GGCCTGTGG CA  CCTG GGGA
                                ||||||||| ||  |||| ||||
                                CCGGACACC GT  GGAC CCCT
                                     C  AC   _
GAM84   FLJ20783 3' GGGCCTGTGGAGCCCCAGA   1700          CA   G
                                GGGCCTGTGGA  CCT AGG
                                ||||||||||  ||| |||
                                CCCGGACACCT  GGG TCT
                                      C_  G
GAM84   FLJ22169 3' GGCCTGTGGGCGCCTGCCCGGG 1701         ACA   A__
                                GGCCTGTGG   CCTG   GGG
                                |||||||||   ||||   |||
                                CCGGACACC   GGAC   CCC
                                     CGC    GGG
GAM84   FLJ23058 3' AGGCCTGTGGTGTGGGGGA   1702         ACACC  A
                                GGGCCTGTGG     TG GGGA
                                ||||||||||     || ||||
                                TCCGGACACC     AC CCCT
                                     AC___  C
GAM84   FLJ31168 3' GGGATCAGCACCTGAGGG    1703     CCTG   A
                                GGG    TGG CACCTGAGGG
                                |||    ||| ||||||||||
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                                CCC   GTC GTGGACTCCC
                                  TA__  _
GAM84   HYPC     5'  AGGCCTGTGGGCACTGGGG   1704         A  C  A
                                GGGCCTGTGG CAC TG GGG
                                |||||||||| ||| || |||
                                TCCGGACACC GTG AC CCC
                                     C  _ _
GAM84   KCNN1    3'  GGGCCATGCTGTCTGAGGGA  1705      _  GGACAC
                                GGGCC TGT    CTGAGGGA
                                ||||| |||    ||||||||
                                CCCGG ACG    GACTCCCT
                                  T  ACA___
GAM84   KIAA0352 3'  GGGCTGGAACCTGAGGG    1706      CTG   C
                                GGGC  TGGA ACCTGAGGG
                                ||||  |||| |||||||||
                                CCCG  ACCT TGGACTCCC
                                   ___   _
GAM84   KIAA0397 3'  AGGCCTGTCTCTGAGGG    1707        GGACAC
                                GGGCCTGT    CTGAGGG
                                ||||||||    |||||||
                                TCCGGACA    GACTCCC
                                    GA____
GAM84   KIAA0450 5'  GGGGTTGAACACGCCTGAGGG 1708     CCTG    __
                                GGG   TGGACA  CCTGAGGG
                                |||   ||||||  ||||||||
                                CCC   ACTTGT  GGACTCCC
                                  CA__    GC
GAM84   KIAA0478 3'  GGGCCTGTGGGGAGGG     1709         ACACCT
                                GGGCCTGTGG    GAGGG
                                ||||||||||    |||||
                                CCCGGACACC    CTCCC
                                     C_____
GAM84   KIAA0700 3'  GGGTCGTGCCGGCTCTGAGGGA 1710     CC_  _  ACAC
                                GGG   TGT GG   CTGAGGGA
                                |||   ||| ||   ||||||||
                                CCC   ACG CC   GACTCCCT
                                  AGC   G  GA__
GAM84   KIAA0798 5'  GGACCTGTGGACAGGG     1711          CCTGA
                                GGGCCTGTGGACA    GGG
                                ||||||||||||    |||
                                CCTGGACACCTGT    CCC
                                      _____
GAM84   KIAA1163 3'  GAGCATGCAGGTACTTGAGGGA 1712     C  TG AC  C
                                GGGC TG  G  AC TGAGGGA
                                |||| ||  |  || |||||||
                                CTCG AC  C  TG ACTCCCT
                                  T  GT CA  A
GAM84   KIAA1821 3'  GGGTCTGGGATCTGCCAGGG  1713     C   T   CAC  __
                                GGG CTG GGA   CTG  AGGG
                                ||| ||| |||   |||  ||||
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                                CCC GAC CCT   GAC  TCCC
                                  A  _  A__   GG
GAM84   KIAA1881  3'  GGGCCTGAGGACCCAGGG    1714        T   A  TG
                                GGGCCTG GGAC CC  AGGG
                                ||||||| |||| ||  ||||
                                CCCGGAC CCTG GG  TCCC
                                   T   _  __
GAM84   KIAA1938  3'  GGGTTTGTTGGACCCAAGGG   1715     CC  _   A  T
                                GGG  TGT GGAC CC GAGGG
                                |||  ||| |||| || |||||
                                CCC  ACA CCTG GG TTCCC
                                  AA  A   _ _
GAM84   LAT1-3TM  5'  GGGCCTGGGACACCCGGGA   1662        T       A
                                GGGCCTG GGACACCTG GGG
                                ||||||| ||||||||| |||
                                CCCGGAC CCTGTGGGC CCT
                                   _       _
GAM84   MAP2K7    3'  GGGCCTGTGGCCATGCCCCTGG 1716          A  __  GA
                                GGGCCTGTGG CA  CCT  GG
                                |||||||||| ||  |||  ||
                                CCCGGACACC GT  GGG  CC
                                     G  AC   GA
GAM84   MGC10902  3'  GGGCCTGTGGGTGCAGGA    1717          ACACC  A
                                GGGCCTGTGG    TG GGGA
                                ||||||||||    || ||||
                                CCCGGACACC    AC TCCT
                                     C____  G
GAM84   MGC10963  3'  GGGTCTGGTGGGATCTGAGGGA 1718     C  _  ACAC
                                GGG CTG TGG   CTGAGGGA
                                ||| ||| |||   ||||||||
                                CCC GAC ACC   GACTCCCT
                                  A  C  CTA_
GAM84   MGC12972  3'  GAGCCTGCTCTGAGGG      1719         GGACAC
                                GGGCCTGT     CTGAGGG
                                ||||||||     |||||||
                                CTCGGACG     GACTCCC
                                   A_____
GAM84   MGC15854  5'  GGGCCTGGATCTGAGGGA    1720        T  ACAC
                                GGGCCTG GG   CTGAGGGA
                                ||||||| ||   ||||||||
                                CCCGGAC CT   GACTCCCT
                                   _ A___
GAM84   MGC17303  3'  GGGCCTGCTGGACACACAGA   1721        _     CTGA
                                GGGCCTG TGGACAC   GGG
                                ||||||| |||||||   |||
                                CCCGGAC ACCTGTG   TCT
                                   G      TG__
GAM84   N4BP3     3'  GAGCCTGTGGATACTCCTGGGG 1722          __ A   A
                                GGGCCTGTGGA  C CCTG GGG
                                ||||||||||  | |||| |||
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                                CTCGGACACCT  G GGAC CCC
                                      AT A   _
GAM84   NCKX3    3'  GGGCCTGTGTGACTCGGGG   1723         _  ACC  A
                                GGGCCTGTG GAC   TG GGG
                                ||||||||| |||   || |||
                                CCCGGACAC CTG   GC CCC
                                     A  A__  _
GAM84   NPTXR    3'  GGGCCTGTTGCATGGGGGA   1724        GGA  CC  A
                                GGGCCTGT   CA  TG GGGA
                                ||||||||   ||  || ||||
                                CCCGGACA   GT  AC CCCT
                                     AC_  __  C
GAM84   NPTXR    3'  GGGCCTGTTGCATGGGGGA   1724        GGA  CC  A
                                GGGCCTGT   CA  TG GGGA
                                ||||||||   ||  || ||||
                                CCCGGACA   GT  AC CCCT
                                     AC_  __  C
GAM84   OSR2     5'  GAGTCTGTGGACGCGGATCCCT 1725    C      A_________  TGAG
            CAGG                    G CTGTGGAC        CC    GG
                                | ||||||||        ||    ||
                                C GACACCTG        GG    CC
                                 A       CGCCTIIIA  GAGT
GAM84   PDZD2    5'  GGGCCTGTGGGCTTCCGGGGA  1726          ACAC   A
                                GGGCCTGTGG    CTG GGGA
                                ||||||||||    ||| ||||
                                CCCGGACACC    GGC CCCT
                                      CGAA  _
GAM84   PEPP3    3'  GGGTGTGTGGACACTGA     1727      CC       C
                                GGG  TGTGGACAC TGA
                                |||  ||||||||| |||
                                CCC  ACACCTGTG ACT
                                  AC        _
GAM84   PIGQ     3'  GGGTGCTGTTCGGCTGAGGGA  1728      C_   GGACAC
                                GGG  CTGT     CTGAGGGA
                                |||  ||||     ||||||||
                                CCC  GACA     GACTCCCT
                                  AC    AGCC__
GAM84   PIPPIN   3'  GGGCCTGTGAGTGGGG      1669          ACACC  A
                                GGGCCTGTGG    TG GGG
                                ||||||||||    || |||
                                CCCGGACACT    AC CCC
                                      C____  _
GAM84   PPIB     3'  GGGCCTGTGGAATGTGAGGG   1729          CACC
                                GGGCCTGTGGA   TGAGGG
                                ||||||||||   ||||||
                                CCCGGACACCT   ACTCCC
                                       TAC_
GAM84   PPP1R16A 5'  GGGCCAGGCTGGGCCTGAGGG  1730       T_ _   ACA
                                GGGCC  G TGG   CCTGAGGG
                                |||||  | |||  ||||||||
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                                CCCGG  C ACC   GGACTCCC
                                   TC G   C__
GAM84   SEC14L2  3' GGGCCTGGCTCTGAGGGA    1731       GT  ACAC
                                GGGCCT  GG    CTGAGGGA
                                ||||||  ||    ||||||||
                                CCCGGA  CC    GACTCCCT
                                   __  GA__
GAM84   STX12    3' AGGCCTGTGGAAAAGGG     1732          CACCT
                                GGGCCTGTGGA    GAGGG
                                ||||||||||     |||||
                                TCCGGACACCT    TTCCC
                                      T_____
GAM84   TMG3     3' AGGCCTGTGGACATTCTG    1733           C_
                                GGGCCTGTGGACA  CTG
                                ||||||||||||  |||
                                TCCGGACACCTGT  GAC
                                      AA
GAM84   TRAF3    3' GGGCCTGTGGGGCCCGGG    1734          ACA   A
                                GGGCCTGTGG   CCTG GG
                                ||||||||||   |||| ||
                                CCCGGACACC   GGGC CC
                                   CC_   _
GAM84   TREX1    5' GGGCCTGTGACGCGAGGG    1735          ACACC
                                GGGCCTGTGG    TGAGGG
                                ||||||||||    ||||||
                                CCCGGACACT    GCTCCC
                                   GC___
GAM84   X123     3' AGGCTTGTGGACACATAGGG   1736      C       CTG
                                GGGC TGTGGACAC   AGGG
                                |||| |||||||||   ||||
                                TCCG ACACCTGTG   TCCC
                                  A       TA_
GAM84   ZDHHC8   3' GGGCCTGAGGGCTGGGG     1737        T  ACAC   A
                                GGGCCTG GG    CTG GGG
                                |||||||  ||    ||| |||
                                CCCGGAC CC    GAC CCC
                                   T  C___   _
GAM84   LOC125268 3' GGGCCTGTGCGAGGCCAGGGA 1738          _  CA  TG
                                GGGCCTGTG GA  CC  AGGGA
                                |||||||||  ||  ||  |||||
                                CCCGGACAC CT  GG  TCCCT
                                   G  CC  __
GAM84   LOC130074 3' GGGCCTGCTGGGCCGGG     1739        _  ACA  TGA
                                GGGCCTG TGG   CC   GGG
                                |||||||  |||   ||   |||
                                CCCGGAC ACC   GG   CCC
                                   G   C__  ____
GAM84   LOC130985 5' GCCTGCAGGACACCTGAGGG   1740        _
                                GCCTGT GGACACCTGAGGG
                                ||||||  ||||||||||||
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                                CGGACG CCTGTGGACTCCC
                                   T
GAM84   LOC131870 3' GGATCCAGAATTACCTGAGGGA 1741    GC  T  C_
                                GG  CTG GGA  ACCTGAGGGA
                                ||  ||| |||  ||||||||||
                                CC  GGT CTT  TGGACTCCCT
                                 TA  _  AA
GAM84   LOC135892 3' GGGCCTGTGGGCCGGCAGGA  1742         ACA  TGA
                                GGGCCTGTGG  CC  GGGA
                                ||||||||||  ||  ||||
                                CCCGGACACC  GG  TCCT
                                      C__  CCG
GAM84   LOC145871 5' GGGCCTGTGGGGGTCGGGGG  1743         ACACC  A
                                GGGCCTGTGG    TG GGG
                                ||||||||||    || |||
                                CCCGGACACC    GC CCC
                                      CCCA_  C
GAM84   LOC146506 3' GGGCTGTGAACTGAGGG    1744      C     ACC
                                GGGC TGTGGAC  TGAGGG
                                |||| |||||||  ||||||
                                CCCG ACACTTG  ACTCCC
                                  _     ___
GAM84   LOC147525 5' GAGCCGCCCGCCTGAGGGA   1745       T  GGACA
                                GGGCC GT    CCTGAGGGA
                                ||||| ||    |||||||||
                                CTCGG CG    GGACTCCCT
                                  _ GGC__
GAM84   LOC149478 3' GAGCCTGTGGTGTCTGAGGG  1746         ACAC
                                GGGCCTGTGG   CTGAGGG
                                ||||||||||   |||||||
                                CTCGGACACC   GACTCCC
                                      ACA_
GAM84   LOC150406 3' GGGCACACCTGAGGG      1747      CTGTGG
                                GGGC     ACACCTGAGGG
                                ||||     ||||||||||
                                CCCG     TGTGGACTCCC
                                  _______
GAM84   LOC150481 5' GGCTCTGTCCTGAGGG     1748     _   GGACA
                                GGC CTGT    CCTGAGGG
                                ||| ||||    ||||||||
                                CCG GACA    GGACTCCC
                                  A  _____
GAM84   LOC152274 3' GCGTCTGGATCCTGAGGGA  1749    CTG   CA
                                GC  TGGA  CCTGAGGGA
                                ||  ||||  |||||||||
                                CG  ACCT  GGACTCCCT
                                 CAG   A_
GAM84   LOC153769 3' GGGCTGCGTCTGAGGG     1750      C   GACAC
                                GGGC TGTG    CTGAGGG
                                |||| ||||    |||||||
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                                CCCG ACGC    GACTCCC
                                  _   A____
GAM84   LOC154990 5'  GGGCCTGTTGATGCCACCGGGA 1751        G  CA  TGA
                                GGGCCTGT GA  CC   GGGA
                                |||||||| ||  ||   ||||
                                CCCGGACA CT  GG   CCCT
                                    A  AC  TGG
GAM84   LOC157254 5'  GGCCTGTGGGGTCGGTGTCTGG 1752         ACAC_____  A
          GGG                   GGCCTGTGG       CTG GGG
                                |||||||||       ||| |||
                                CCGGACACC       GAC CCC
                                    CCAGCCACA   C
GAM84   LOC157740 5'  GGGCCTGTGGAGAGGG     1753          CACCT
                                GGGCCTGTGGA    GAGGG
                                ||||||||||    |||||
                                CCCGGACACCT    CTCCC

                                ______
GAM84   LOC158801 3'  GGGTGCTACGTGCCTGAGGGA  1754     C_    GACA
                                GGG  CTGTG   CCTGAGGGA
                                |||  |||||   |||||||||
                                CCC  GATGC   GGACTCCCT
                                  AC    AC__
GAM84   LOC196463 3'  GGGACTGCTTCCTGAGGGA   1755     C   GGACA
                                GGG CTGT    CCTGAGGGA
                                ||| ||||    |||||||||
                                CCC GACG    GGACTCCCT
                                  T   AA___
GAM84   LOC196707 3'  GGGCCTGTGGTGTACCCAAGG  1756         AC_  TG
                                GGGCCTGTGG  ACC  AGG
                                ||||||||||  |||  |||
                                CCCGGACACC  TGG  TCC
                                    ACA  GT
GAM84   LOC196872 3'  GGCTCTGTGGACTGGGG     1757     _      ACC  A
                                GGC CTGTGGAC   TG GGG
                                ||| ||||||||   || |||
                                CCG GACACCTG   AC CCC
                                  A      ___  _
GAM84   LOC199988 5'  GGGCCTGTGAGGTGCCTGGGGA 1667         ACA_   A
                                GGGCCTGTGG    CCTG GGGA
                                ||||||||||    |||| ||||
                                CCCGGACACT    GGAC CCCT
                                    CCAC   _
GAM84   LOC200781 5'  GCCTGCAGGACACCTGAGGG   1740       _
                                GCCTGT GGACACCTGAGGG
                                |||||| ||||||||||||
                                CGGACG CCTGTGGACTCCC
                                   T
GAM84   LOC219513 5'  GGGCCTGCGCCTGGGGG     1758         GACA   A
                                GGGCCTGTG    CCTG GGG
                                |||||||||    |||| |||
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                                CCCGGACGC   GGAC CCC
                                    ____   C
GAM84   LOC219920 5'  GGGCCTGTGGGTCCCCTGA   1759         ACA_
                                GGGCCTGTGG   CCTGA
                                ||||||||||   |||||
                                CCCGGACACC   GGACT
                                     CAGG
GAM84   LOC220776 3'  GGGCCTGGACAACCCTTGGG   1760       GT   _  GA
                                GGGCCT  GGACA CCT  GGG
                                ||||||  ||||| |||  |||
                                CCCGGA  CCTGT GGG  CCC
                                   __    T   AA
GAM84   LOC222031 3'  GGCCTGTGGGCATTAATGG   1761         A  CC   G
                                GGCCTGTGG CA  TGA GG
                                ||||||||| ||  ||| ||
                                CCGGACACC GT  ATT CC
                                     C  A_   A
GAM84   LOC222057 3'  GGGCCTGTAGACGCACTGGGA  1762          AC_  A
                                GGGCCTGTGGAC   CTG GGG
                                ||||||||||||   ||| |||
                                CCCGGACATCTG   GAC CCT
                                      CGT   _
GAM84   LOC255975 5'  GGGCCTGTAGACGCACTGGGA  1762          AC_  A
                                GGGCCTGTGGAC   CTG GGG
                                ||||||||||||   ||| |||
                                CCCGGACATCTG   GAC CCT
                                      CGT   _
GAM84   LOC255975 5'  GGGCCTGTAGATGCTGA     1763          CAC
                                GGGCCTGTGGA   CTGA
                                ||||||||||   ||||
                                CCCGGACATCT   GACT
                                      AC_
GAM84   LOC256905 3'  GGGCCTGTCGGGGCGTGGGGGA 1764        _  ACACC  A
                                GGGCCTGT GG    TG GGGA
                                |||||||| ||    || ||||
                                CCCGGACA CC    AC CCCT
                                     G  CCGC_  C
GAM84   LOC256937 5'  GGGCCTGGGACACCCAGG    1765        T      G
                                GGGCCTG GGACACCT AGG
                                ||||||| |||||||| |||
                                CCCGGAC CCTGTGGG TCC
                                    _      _
GAM84   LOC257054 3'  GGGCGTCCACGGCCTGAGGGA  1766     __ TG   ACA
                                GGGC  C  TGG   CCTGAGGGA
                                ||||  |  |||   |||||||||
                                CCCG  G  GCC   GGACTCCCT
                                  CA GT   ___
GAM84   LOC56926  5'  GGTCCTGTGGGCACCGCGG   1767    G     A   TGA
                                GG CCTGTGG CACC   GG
                                || ||||||| ||||   ||
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                                CC GGACACC GTGG   CC
                                 A      C    CG_
GAM84   LOC90631  3'  AGGCTTGTGGACAGCAGGG   1768      C       CCTG
                                GGGC TGTGGACA    AGGG
                                |||| ||||||||    ||||
                                TCCG ACACCTGT    TCCC
                                  A       CG__
GAM84   LOC91156  5'  GGGCCTTGGGCATCCTTGGA   1769       G   A  _   GA
                                GGGCCT TGG CA CCT  GGG
                                |||||| ||| || |||  |||
                                CCCGGA ACC GT GGA  CCT
                                   _   C  A   A_
GAM84   LOC91179  5'  GGGCCCGTGGACGCCAGGG   1770           A  TG
                                GGGCCTGTGGAC CC  AGGG
                                ||||||||||||  ||  ||||
                                CCCGGGCACCTG GG  TCCC
                                       C  __
GAM84   LOC91663  5'  GGCTGTAAGAGCACCTGAGGG  1771     C   _  _
                                GGC TGTG GA CACCTGAGGG
                                |||  |||| ||  ||||||||||
                                CCG ACAT CT GTGGACTCCC
                                  _    T  C
GAM84   LOC91963  5'  AGGCCTGTGGGTTCTGGGA   1772          ACAC   A
                                GGGCCTGTGG    CTG GGG
                                ||||||||||    ||| |||
                                TCCGGACACC    GAC CCT
                                     CAA_  _
GAM84   LOC93259  5'  GGGTGTGACCTGAGGG     1773     CC    GAC
                                GGG  TGTG   ACCTGAGGG
                                |||  ||||   |||||||||
                                CCC  ACAC   TGGACTCCC
                                  __   ____
GAM85   ABCA2     3'  CGGGCAGGAGAAAGGCCA    1776     A  A
                                TGG CA GAGAAAGGCCA
                                ||| ||  ||||||||||
                                GCC GT CTCTTTCCGGT
                                  C  C
GAM85   ABCA2     3'  CGGGCAGGAGAAAGGCCA    1776     A  A
                                TGG CA GAGAAAGGCCA
                                ||| ||  ||||||||||
                                GCC GT CTCTTTCCGGT
                                  C  C
GAM85   ARSB      3'  GAGCAAGAGAAGGGCCAA    1777    GA      A
                                G  CAAGAGAA GGCCAA
                                |  ||||||||  ||||||
                                C  GTTCTCTT CCGGTT
                                 TC       C
GAM85   CYP8B1    3'  GATCATGGAAACCAAGGGAGG  1778          CAA_  AA
                                GATCATGGA   GAG  AGG
                                |||||||||   |||  |||
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                                CTAGTACCT   TTC  TCC
                                     TTGG   CC
GAM85   FGF5    3'  TCAGGACTATCAAGAGGCCA  1779     T   AA__   AA
                                TCA GGAC   GAGA  GGCCA
                                ||| ||||   ||||  |||||
                                AGT CCTG   TTCT  CCGGT
                                  _   ATAG   __
GAM85   FGF5    3'  TCAGGACTATCAAGAGGCCA  1779     T   AA__   AA
                                TCA GGAC   GAGA  GGCCA
                                ||| ||||   ||||  |||||
                                AGT CCTG   TTCT  CCGGT
                                  _   ATAG   __
GAM85   FXYD7   3'  GACATGGACACTGAGGGGCCA 1780     T      A_   AAA
                                GA CATGGACA  GAG   GGCCA
                                || ||||||||  |||   |||||
                                CT GTACCTGT  CTC   CCGGT
                                 _      GA   C__
GAM85   MUCDHL  3'  TGGACAAGGACGGCGAGGCCAA 1782         A  A____
                                TGGACAAG GA    AGGCCAA
                                |||||||| ||    |||||||
                                ACCTGTTC CT    TCCGGTT
                                     _ GCCGC
GAM85   MUCDHL  3'  TGGACAAGGACGCGAGGCCAA  1781         A  A___
                                TGGACAAG GA   AGGCCAA
                                |||||||| ||   |||||||
                                ACCTGTTC CT   TCCGGTT
                                     _ GCGC
GAM85   PIK3CG  3'  GACCAGCAGAGGAAGGTCA   1783       TGGACA   A   C
                                GATCA     AGAG AAGG CA
                                |||||     |||| |||| ||
                                CTGGT     TCTC TTCC GT
                                   CG____   C   A
GAM85   RUNX1   3'  CATAAACAGGAGAAAGGC    1784         A
                                CATGGACA GAGAAAGGC
                                |||||||| |||||||||
                                GTATTTGT CTCTTTCCG
                                     C
GAM85   SERPIND1 3' ATCATGGATTTGAAAGGTCA  1785         CAAGA    C
                                ATCATGGA    GAAAGG CA
                                ||||||||    |||||| ||
                                TAGTACCT    CTTTCC GT
                                     AAA__     A
GAM85   DKFZP434A043 5' GATCTGGAGAAAAAGG     1786      A   CAA
                                GATC TGGA   GAGAAAGG
                                |||| ||||   ||||||||
                                CTAG ACCT   CTTTTTCC
                                  _   ___
GAM85   DKFZp434O0515 5' GATCATAGGTGAGACTCCCACC 1787         ACAA   AAG__
            AA                    GATCATGG   GAGA    GCCAA
                                ||||||||   ||||    |||||
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                                CTAGTATC   CTCT    TGGTT
                                    CA__   GAGGG
GAM85   FLJ11362 3' TCATGAACAAGGAGGCCA    1788          A  AA
                                TCATGGACAAG GA  GGCCA
                                |||||||||| ||  |||||
                                AGTACTTGTTC CT  CCGGT
                                      _  __
GAM85   FLJ22611 3' ATAGACACAAAGGCCAA     1789        AGAG
                                ATGGACA   AAAGGCCAA
                                |||||||   |||||||||
                                TATCTGT   TTTCCGGTT
                                   G___
GAM85   GDAP2    3' GATTATAGGAAAAAGGC     1790      C   ACAA
                                GAT ATGG   GAGAAAGGC
                                ||| ||||   |||||||||
                                CTA TATC   CTTTTTCCG
                                  A   _____
GAM85   HARSL    3' GATTGTGGACAAATTCACCA   1791     CA      AGAAAG
                                GAT  TGGACAAG     GCCA
                                |||  ||||||||     ||||
                                CTA  ACCTGTTT     TGGT
                                  AC       AAG___
GAM85   HSPC063  3' GAAATGGGAGAAAGGC      1792     TC   ACAA
                                GA  ATGG   GAGAAAGGC
                                ||  ||||   |||||||||
                                CT  TACC   CTCTTTCCG
                                 T_   _____
GAM85   HSPC065  3' GATTATGGGGAAGAGAAA    1793     C    AC
                                GAT ATGG  AAGAGAAA
                                ||| ||||  ||||||||
                                CTA TACC  TTCTCTTT
                                  A   CC
GAM85   KBRAS2   3' GAAAAGGACAGGAGAAAGGTCA 1794     TCAT    A      C
                                GA   GGACA GAGAAAGG CA
                                ||   ||||| |||||||| ||
                                CT   CCTGT CTCTTTCC GT
                                 TTT_    C       A
GAM85   KIAA0100 5' GATCATGGCTAAGGAGTTTGC  1795         AC   A  AAG_
                                GATCATGG  AAG GA   GC
                                ||||||||  ||| ||   ||
                                CTAGTACC  TTC CT   CG
                                    GA   _  CAAA
GAM85   KIAA0475 3' GATCGAGAAGAAAGGC      1796      AT   CAAG
                                GATC  GGA   AGAAAGGC
                                ||||  |||   ||||||||
                                CTAG  TCT   TCTTTCCG
                                  C_   _____
GAM85   KIAA1671 3' TCATGGATTTTCAAAGGCCAA  1797         CAAGAG
                                TCATGGA     AAAGGCCAA
                                |||||||     |||||||||
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                                AGTACCT     TTTCCGGTT
                                    AAAAG_
GAM85   KIAA1877 3'  GGACATAGTGAGAAAGGTCA   1798       A___       C
                                GGACA    GAGAAAGG CA
                                |||||    |||||||| ||
                                CCTGT    CTCTTTCC GT
                                   ATCA       A
GAM85   MBLL39   3'  ACCAGGGGGAAAGGCCA     1799       T  ACAAGA
                                ATCA GG     GAAAGGCCA
                                |||| ||     |||||||||
                                TGGT CC     CTTTCCGGT
                                  C  C_____
GAM85   MGC26766 3'  GACCATGGGCAGGAACTCTGC  1800         A  A   AAAG
                                GATCATGG CA GAG    GC
                                |||||||| || |||    ||
                                CTGGTACC GT CTT    CG
                                     C  C   GAGA
GAM85   MGC26778 3'  GATCATAGACAAGGGGCCA    1801             AGAAA
                                GATCATGGACAAG    GGCCA
                                ||||||||||||     |||||
                                CTAGTATCTGTTC    CCGGT
                                       C_____
GAM85   NTPBP    3'  CATAAATACAAGGGAAAGGCCA 1802        __    A
           A                     CATGG  ACAAG GAAAGGCCAA
                                |||||  ||||| ||||||||||
                                GTATT  TGTTC CTTTCCGGTT
                                   TA    C
GAM85   PADI3    3'  GATCATGGGGAGTTTATAAGGC 1803         ACAA   A____
                                GATCATGG    GAG    AAGGC
                                ||||||||    |||    |||||
                                CTAGTACC    CTC    TTCCG
                                     C___   AAATA
GAM85   PDE1C    3'  ATGGTGTGAGGGAAGGCCAA   1804       ACAA   A_
                                ATGG    GAG  AAGGCCAA
                                ||||    |||  ||||||||
                                TACC    CTC  TTCCGGTT
                                  ACA_   CC
GAM85   PER3     3'  ATCATGGATGAAAAGG       1805          CAA    A
                                ATCATGGA   GAGAA GG
                                ||||||||   ||||| ||
                                TAGTACCT   CTTTT CC
                                     A__    _
GAM85   REC14    5'  GATCAAGGACAAAAGGCCA    1806       T     GAGA
                                GATCA GGACAA    AAGGCCA
                                ||||| ||||||    |||||||
                                CTAGT CCTGTT    TTCCGGT
                                   T     _____
GAM85   LOC115399 3'  GACCAGCAGGGAGAAGGGCCA  1807       T__  ACAA    A
                                GATCA   GG    GAGAA GGCCA
                                |||||   ||    ||||| |||||
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                                CTGGT  CC   CTCTT CCGGT
                                  CGT  ____   C
GAM85  LOC145624 5' GATATTAAGAGGAGAAAGGC  1808    CAT_  CAA
                                GAT   GGA  GAGAAAGGC
                                |||   |||  |||||||||
                                CTA   TCT  CTCTTTCCG
                                  TAAT  C__
GAM85  LOC146823 3' ATCATGAAGGAAGAGAGGGGC 1809       C_    AA
                                ATCATGGA  AAGAGA  GGC
                                ||||||||  ||||||  |||
                                TAGTACTT  TTCTCT  CCG
                                    CC    CC
GAM85  LOC201115 5' GATCCTGGACAAAGGGGTCAA 1810     A    A  AAA  C
                                GATC TGGACA GAG  GG CAA
                                |||| |||||| |||  || |||
                                CTAG ACCTGT TTC  CC GTT
                                  G    _  C__  A
GAM85  LOC57826  3' TCGATGGATCTTGAAGGCCAA 1811    _   CAAGA  A
                                TC ATGGA    GAA GGCCAA
                                || |||||    ||| ||||||
                                AG TACCT    CTT CCGGTT
                                 C    AGAA_  _
GAM85  LOC91351  3' GATTATGGAAAAGGCC     1812     C   CAAGAG
                                GAT ATGGA    AAAGGCC
                                ||| |||||    |||||||
                                CTA TACCT    TTTCCGG
                                  A   _______
GAM85  LOC92017  5' GATCATGGGGGAGGTACCA   1813       ACAA  AAAG
                                GATCATGG   GAG   GCCA
                                ||||||||   |||   ||||
                                CTAGTACC   CTC   TGGT
                                    CC__   CA__
GAM85  LOC92840  3' GACCATGGGTGAGACCGGGC  1814       ACAA   AA_
                                GATCATGG   GAGA  GGC
                                ||||||||   ||||  |||
                                CTGGTACC   CTCT  CCG
                                    CA__   GGC
GAM85  LOC93259  5' CATGGACAAGGAGGTCA    1815        A  AA  C
                                CATGGACAAG GA  GG CA
                                |||||||||| ||  || ||
                                GTACCTGTTC CT  CC GT
                                     _  __  A
GAM86  ABCC11   3' CTTAGATGGTTCTGGGGTTC  1818     CC       C
                                CTTG  TGGTTCTGGGG TC
                                ||||  |||||||||| ||
                                GAAT  ACCAAGACCCC AG
                                  CT        A
GAM86  ADORA2A  3' TGCTCCAGCCTGGGGCTCC   1819    _TG  T
                                TGC C  GT CTGGGGCTCC
                                ||| |  || ||||||||||
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                                ACG G  CG GACCCCGAGG
                                  A GT  _
GAM86   AGXT     3'  TGCCTGGTTCTGCCTCC     1820          GGG
                                TGCCTGGTTCTG  CTCC
                                ||||||||||||  ||||
                                ACGGACCAAGAC  GAGG
                                       G__
GAM86   ANKRD3   3'  CTTCCACGCCTGGGGCT     1821     G  TG  T
                                CTT CC  GT CTGGGGCT
                                ||| ||  || ||||||||
                                GAA GG  CG GACCCCGA
                                  _  TG  _
GAM86   CARKL    3'  CCTGCCTGAGCCTGGGCTCC  1822         TT    G
                                CTTGCCTGG  CTGGG CTCC
                                |||||||||  ||||| ||||
                                GGACGGACT  GACCC GAGG
                                     CG    _
GAM86   CKTSF1B1 3'  TTGCTGGTTCTGAATGTC    1823      C        GC
                                TTGC TGGTTCTGGG  TC
                                |||| ||||||||||  ||
                                AACG ACCAAGACTT  AG
                                  _        AC
GAM86   DAP3     5'  TGCCTGGGGCCGGCTCC     1824        TT  GG
                                TGCCTGG  CT  GGCTCC
                                |||||||  ||  ||||||
                                ACGGACC  GG  CCGAGG
                                    CC  __
GAM86   DAP3     5'  TGCCTGGGGCCGGCTCC     1824        TT  GG
                                TGCCTGG  CT  GGCTCC
                                |||||||  ||  ||||||
                                ACGGACC  GG  CCGAGG
                                    CC  __
GAM86   DLEC1    3'  CTTGCAGTCCCTGGGGCT    1825       CT    _
                                CTTGC  GGTTC TGGGGCT
                                |||||  ||||| |||||||
                                GAACG  TCAGG ACCCCGA
                                  __     G
GAM86   DLEC1    3'  CTTGCAGTCCCTGGGGCT    1825       CT    _
                                CTTGC  GGTTC TGGGGCT
                                |||||  ||||| |||||||
                                GAACG  TCAGG ACCCCGA
                                  __     G
GAM86   EGFL6    5'  GCCTGGCCGAGGCTCC      1826        TT
                                GCCTGG  CTGGGGCTCC
                                ||||||  ||||||||||
                                CGGACC  GGCTCCGAGG
                                    __
GAM86   ENTPD5   3'  CTTTTTGGCTCACAGGGCTC  1827      GCC     _
                                CTT   TGGTTC TGGGGCTC
                                |||   |||||| ||||||||
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                                GAA   ACCGAG GTCCCGAG
                                  AA_     T
GAM86   EPHA2    3'  CTTGGCCGATGGGGCTCC    1828      C    TTC
                                CTTG CTGG   TGGGGCTCC
                                |||| ||||   |||||||||
                                GAAC GGCT   ACCCCGAGG
                                  C   ____
GAM86   ESRRA    5'  CTGGTCACCTGGGGCTCC    1829        __
                                CTGGTT  CTGGGGCTCC
                                ||||||  ||||||||||
                                GACCAG  GACCCCGAGG
                                   TG
GAM86   F9       3'  CTTGCTTGGCTCTGAACACT   1830       C        _
                                CTTGC TGGTTCTGGG GCT
                                ||||| |||||||||| |||
                                GAACG ACCGAGACTT TGA
                                   A         G
GAM86   GAB2     3'  TGCCTGTCCCAGGGTTCC    1831       G   TG   C
                                TGCCTG TTC  GGG TCC
                                ||||||| |||  ||| |||
                                ACGGAC AGG  CCC AGG
                                   _  GT   A
GAM86   GAB2     3'  TGCCTGTCCCAGGGTTCC    1831       G   TG   C
                                TGCCTG TTC  GGG TCC
                                ||||||| |||  ||| |||
                                ACGGAC AGG  CCC AGG
                                   _  GT   A
GAM86   GALNT2   3'  TTGTTTGGTTCTGACCC     1832     CC      GG
                                TTG  TGGTTCTG  GCTC
                                |||  ||||||||  ||||
                                AAC  ACCAAGAC  TGGG
                                  AA      __
GAM86   GPC1     3'  CTTGCCTGTGTTGGGGGCTCC  1833         _  CT
                                CTTGCCTG GTT  GGGGCTCC
                                |||||||| |||  ||||||||
                                GAACGGAC CAA  CCCCGAGG
                                     A   C_
GAM86   GRLF1    3'  CTTCCTGTGCATGGGGGCTCC  1834     G   _  TCT
                                CTT CCTG GT   GGGGCTCC
                                ||| |||| ||   ||||||||
                                GAA GGAC CG   CCCCGAGG
                                  _   A  TAC
GAM86   HD       3'  CTTGCCTGGCTCGCC       1835            TGGG
                                CTTGCCTGGTTC    GCT
                                ||||||||||||    |||
                                GAACGGACCGAG    CGG
                                                 ____
GAM86   HMGB2    5'  CTTCCCTCACGGGGCTCC    1836      G   G TTC
                                CTT CCT G   TGGGGCTCC
                                ||| ||| |   |||||||||
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                                GAA GGA T   GCCCCGAGG
                                  G   G ___
GAM86   HR      5'  CCTGCCCTCATGGGGCTC    1837        GGT  _
                                CTTGCCT   TC TGGGGCTC
                                |||||||   || ||||||||
                                GGACGGG   AG ACCCCGAG
                                    ___  T
GAM86   HR      5'  CCTGCCCTCATGGGGCTC    1837        GGT  _
                                CTTGCCT   TC TGGGGCTC
                                |||||||   || ||||||||
                                GGACGGG   AG ACCCCGAG
                                    ___  T
GAM86   IL11RA  3'  CCTGCCTGGTTTCTATCC    1838          _  GGGC
                                CTTGCCTGGTT CTG   TCC
                                |||||||||||| |||   |||
                                GGACGGACCAA GAT   AGG
                                      A  ____
GAM86   IRAK1   3'  CTGCCTTCCAGGGGCT     1839        GG   T
                                TTGCCT  TTC GGGGCT
                                ||||||  ||| ||||||
                                GACGGA  AGG CCCCGA
                                   __   T
GAM86   ITGAL   3'  TGCTTGGCACTGGGGCTCC   1840      C    T
                                TGC TGGT CTGGGGCTCC
                                ||| |||| ||||||||||
                                ACG ACCG GACCCCGAGG
                                  A   T
GAM86   ITPKB   3'  CTTCCTAGGGGGCTC       1841      G    TTCT
                                CTT CCTGG   GGGGCTC
                                ||| |||||   |||||||
                                GAA GGATC   CCCCGAG
                                  _   _____
GAM86   JRK     5'  TGCTCCCCTTCTGGGGCTCC  1842      _  GG
                                TGC CT  TTCTGGGGCTCC
                                ||| ||  ||||||||||||
                                ACG GG  AAGACCCCGAGG
                                  A  GG
GAM86   KEL     5'  CTTCCTGGTTCCACTC      1843      G       GGG
                                CTT CCTGGTTCT   GCTC
                                ||| |||||||||   ||||
                                GAA GGACCAAGG   TGAG
                                  _       ___
GAM86   LAD1    3'  CTTGGTTGGTTCTAGATTC   1844       CC        GC
                                CTTG  TGGTTCTGGG  TC
                                ||||  ||||||||||  ||
                                GAAC  ACCAAGATCT  AG
                                   CA         A_
GAM86   LDHB    5'  CTTGCCTGGTGGGCTCC     1845          TCTG
                                CTTGCCTGGT    GGGCTCC
                                |||||||||    |||||||
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                                GAACGGACCA   CCCGAGG
                                      ____
GAM86   LOH11CR2A 5'  CTGGCTACTCATGGGGCTC   1846      ___ _
                                CTGGT  TC TGGGGCTC
                                |||||  || ||||||||
                                GACCG  AG ACCCCGAG
                                   ATG  T
GAM86   LZTS1    3'  TCGTCCTGCTTGGGGCTC    1847     _   G TC
                                TTG CCTG T  TGGGGCTC
                                ||| |||| |  ||||||||
                                AGC GGAC A  ACCCCGAG
                                  A   G __
GAM86   MAN2B1   5'  CTTCCTCCTGGGGTTC     1848     G  GGT     C
                                CTT CCT  TCTGGGG TC
                                ||| |||  ||||||| ||
                                GAA GGA  GGACCCC AG
                                  _  ___      A
GAM86   MAP1B    5'  TTGTGTGGTCGGGGGCTCC   1849     CC    CT
                                TTG  TGGTT  GGGGCTCC
                                |||  |||||  ||||||||
                                AAC  ACCAG  CCCCGAGG
                                  AC    C_
GAM86   MAPK10   5'  TGTTTGGTTCTGAAAGGGTC  1850     CC      ___  C
                                TG  TGGTTCTG  GGG TC
                                ||  ||||||||  ||| ||
                                AC  ACCAAGAC  CCC AG
                                 AA       TTT  _
GAM86   MAPK7    5'  TTGCTTGGTCCCAGGAGCTC  1851      C     TG  _
                                TTGC TGGTTC  GG GCTC
                                ||||  ||||||  ||  ||||
                                AACG ACCAGG  CC CGAG
                                  A     GT  T
GAM86   MAPK7    5'  TTGCTTGGTCCCAGGAGCTC  1851      C     TG  _
                                TTGC TGGTTC  GG GCTC
                                ||||  ||||||  ||  ||||
                                AACG ACCAGG  CC CGAG
                                  A     GT  T
GAM86   MAT1A    3'  TGCCTGGCCTGGGTGGGGCT  1852          C___
                                TGCCTGGTT   TGGGGCT
                                |||||||||   |||||||
                                ACGGACCGG   ACCCCGA
                                     ACCC
GAM86   MSI1     3'  CCTGCGGCCTGGGGCT     1853       CT   T
                                CTTGC  GGT CTGGGGCT
                                |||||  ||| ||||||||
                                GGACG  CCG GACCCCGA
                                  __  _
GAM86   MYCL1    3'  CTTGTCCCCTGGGGCTCC    1854      _  GGTT
                                CTTG CCT   CTGGGGCTCC
                                ||||  |||  ||||||||||
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                                GAAC GGG   GACCCCGAGG
                                  A  ____
GAM86   NRCAM    3'  CTTGCCTGATTTCTTAGATTC  1855          _ G  GC
                                CTTGCCTGGTT CT GG  TC
                                |||||||||| || ||  ||
                                GAACGGACTAA GA TC  AG
                                      A  A  TA
GAM86   NUP98    3'  TGCCATTACCTGGGGCTCC   1856     TGGT
                                TGCC   TCTGGGGCTCC
                                ||||   ||||||||||
                                ACGG   GGACCCCGAGG
                                  TAAT
GAM86   PAX2     5'  TGCCTTCCCCGTGGGGCTCC  1857      GG  _
                                TGCCT  TTC TGGGGCTCC
                                |||||  ||| |||||||||
                                ACGGA  GGG ACCCCGAGG
                                   AG   C
GAM86   PAX2     5'  TGCCTTCCCCGTGGGGCTCC  1857      GG  _
                                TGCCT  TTC TGGGGCTCC
                                |||||  ||| |||||||||
                                ACGGA  GGG ACCCCGAGG
                                   AG   C
GAM86   PCDHGA1  3'  CTTCCTGCTGGGGCTC     1858     G   GTT
                                CTT CCTG   CTGGGGCTC
                                ||| ||||   |||||||||
                                GAA GGAC   GACCCCGAG
                                  _   ___
GAM86   PCDHGA10 3'  CTTCCTGCTGGGGCTC     1858     G   GTT
                                CTT CCTG   CTGGGGCTC
                                ||| ||||   |||||||||
                                GAA GGAC   GACCCCGAG
                                  _   ___
GAM86   PCDHGA11 3'  CTTCCTGCTGGGGCTC     1858     G   GTT
                                CTT CCTG   CTGGGGCTC
                                ||| ||||   |||||||||
                                GAA GGAC   GACCCCGAG
                                  _   ___
GAM86   PCDHGA11 3'  CTTCCTGCTGGGGCTC     1858     G   GTT
                                CTT CCTG   CTGGGGCTC
                                ||| ||||   |||||||||
                                GAA GGAC   GACCCCGAG
                                  _   ___
GAM86   PCDHGA12 3'  CTTCCTGCTGGGGCTC     1858     G   GTT
                                CTT CCTG   CTGGGGCTC
                                ||| ||||   |||||||||
                                GAA GGAC   GACCCCGAG
                                  _   ___
GAM86   PCDHGA2  3'  CTTCCTGCTGGGGCTC     1858     G   GTT
                                CTT CCTG   CTGGGGCTC
                                ||| ||||   |||||||||
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                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGA3  3' CTTCCTGCTGGGGCTC    1858   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGA4  3' CTTCCTGCTGGGGCTC    1858   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGA5  3' CTTCCTGCTGGGGCTC    1858   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGA6  3' CTTCCTGCTGGGGCTC    1858   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGA7  3' CTTCCTGCTGGGGCTC    1858   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGA8  3' CTTCCTGCTGGGGCTC    1858   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGA9  3' CTTCCTGCTGGGGCTC    1858   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGB1  3' CTTCCTGCTGGGGCTC    1858   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGB2  3' CTTCCTGCTGGGGCTC    1858   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGB3  3' CTTCCTGCTGGGGCTC    1858   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
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                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGB4  3' CTTCCTGCTGGGGCTC    1858    G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGB5  3' CTTCCTGCTGGGGCTC    1858    G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGB6  3' CTTCCTGCTGGGGCTC    1858    G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGB7  3' CTTCCTGCTGGGGCTC    1858    G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGC3  3' CTTCCTGCTGGGGCTC    1858    G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGC3  3' CTTCCTGCTGGGGCTC    1858    G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGC4  3' CTTCCTGCTGGGGCTC    1858    G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PCDHGC5  3' CTTCCTGCTGGGGCTC    1858    G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM86  PFKFB4   3' CTGCTGTGGTTGGGGCTC   1859    C_  TC
                                TTGC TGGT TGGGGCTC
                                |||| |||| ||||||||
                                GACG ACCA ACCCCGAG
                                  AC  __
GAM86  PK428    5' CTTGCCCGGAGGCGGCT    1860       TTCT _
                                CTTGCCTGG   GG GGCT
                                |||||||||   || ||||
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                                GAACGGGCC   CC CCGA
                                     T___  G
GAM86   PKD2L1   3'  CTTGCCTGATTCCCTTCGGAGC 1861          T_______ GGCT
           C                   CTTGCCTGGTTC      GG   C
                               ||||||||||||      ||   |
                               GAACGGACTAAG      CC   G
                                     GGAAGIII  TCGG
GAM86   PLXNA1   3'  CTTGCCCGGCTACGGGCT   1862          CTG
                               CTTGCCTGGTT   GGGCT
                               ||||||||||   |||||
                               GAACGGGCCGA   CCCGA
                                     TG_
GAM86   RAD9     3'  CTGCCACTGGCTGGGGCT   1863       __  TT
                               TTGCC  TGG  CTGGGGCT
                               |||||  |||  ||||||||
                               GACGG  ACC  GACCCCGA
                                  TG  __
GAM86   RAP1     3'  CTTGACTGAGAAGGGCTCC   1864      C   TTCT
                               CTTG CTGG   GGGGCTCC
                               |||| ||||   ||||||||
                               GAAC GACT   TCCCGAGG
                                 T   CT__
GAM86   RBP3     3'  CTGTCTGCCCTGGGGCTC   1865     C  G
                               TTG CTG TTCTGGGGCTC
                               ||| ||| ||||||||||
                               GAC GAC GGGACCCCGAG
                                 A  _
GAM86   REN      5'  CTTCCCTCAGTCTGGGGCTC  1866     G  _  T
                               CTT CCT GGT CTGGGGCTC
                               ||| ||| ||| |||||||||
                               GAA GGA TCA GACCCCGAG
                                 G  G  _
GAM86   RLBP1    3'  CTTGCCTGTTTTCACAGACTC  1867        G_  TG
                               CTTGCCTG  TTC  GGGCTC
                               ||||||||  |||  ||||||
                               GAACGGAC  AAG  TCTGAG
                                    AA   TG
GAM86   RNF18    3'  CTTCCTGGGATAAAGGGGTTCC 1868     G    TTCT__   C
                               CTT CCTGG     GGGG TCC
                               ||| |||||     |||| |||
                               GAA GGACC     CCCC AGG
                                 _    CTATTT   A
GAM86   SIGLEC11 3'  CTGCCTGGTTTCCTGTGCT   1869         __   GG
                               TTGCCTGGT  TCTG  GCT
                               |||||||||  ||||  |||
                               GACGGACCA  GGAC  CGA
                                    AA   A_
GAM86   SLC22A11 3'  TTGACTAAAGGGGCTCC    1870     C   TTCT
                               TTG CTGG   GGGGCTCC
                               ||| ||||   ||||||||
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                                AAC GATT   CCCCGAGG
                                  T   T___
GAM86   SLC28A1  3'  CTTCCCTGAAGAGGGCTC   1871     G    TTCT
                                CTT CCTGG   GGGGCTC
                                ||| |||||   |||||||
                                GAA GGACT   TCCCGAG
                                  G    TC__
GAM86   SMARCB1  3'  GCCCTGCCTGGGGCTCC    1872      G  T
                                GCCT GT CTGGGGCTCC
                                |||| || ||||||||||
                                CGGG CG GACCCCGAGG
                                  A  _
GAM86   SNK      3'  GCCTGGTTCTGGGTTCC     1873           GC
                                GCCTGGTTCTGGG  TCC
                                ||||||||||||  |||
                                CGGACCAAGACCC  AGG
                                       A_
GAM86   SPTA1    5'  CTTGCTTGGTCCTAGAATCC   1874      C        C
                                CTTGC TGGTTCTGGGG TCC
                                ||||| |||||||||||| |||
                                GAACG ACCAGGATCTT AGG
                                   A         _
GAM86   TGFBR2   3'  CTGCTTGGTTCTGGAGTTC   1875      C        C
                                TTGC TGGTTCTGGGG TC
                                |||| |||||||||||| ||
                                GACG ACCAAGACCTC AG
                                  A         A
GAM86   XRCC5    3'  CTTGTTTTGTTAGAACTCC   1876      CCTG  TC
                                CTTG   GT  TGGGGCTCC
                                ||||   ||  |||||||||
                                GAAC   CA  ATCTTGAGG
                                  AAAA  __
GAM86   AP3D1    3'  CCTGCCTGGTGGGGGCTC    1877          TCT
                                CTTGCCTGGT   GGGGCTC
                                ||||||||||   |||||||
                                GGACGGACCA   CCCCGAG
                                      C__
GAM86   BLu      3'  TGCGGAGACTGGGGCTCC    1878     CT  TT_
                                TGC  GG   CTGGGGCTCC
                                |||  ||   ||||||||||
                                ACG  CC   GACCCCGAGG
                                  __  TCT
GAM86   C20orf67 3'  CTAGCACCCCTGGGGCTCC   1879       ___
                                CTGGT   TCTGGGGCTCC
                                |||||   ||||||||||
                                GATCG   GGACCCCGAGG
                                   TGG
GAM86   C5orf4   3'  CTTGAAAAAGTCTGGGGCT   1880      CCT_  T
                                CTTG   GGT CTGGGGCT
                                ||||   ||| ||||||||
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                                GAAC    TCA GACCCCGA
                                  TTTT  _
GAM86   C5orf4   5' CTTGAAAAAGTCTGGGGCT   1880      CCT_  T
                                CTTG    GGT CTGGGGCT
                                ||||    ||| ||||||||
                                GAAC    TCA GACCCCGA
                                  TTTT  _
GAM86   CAMK1G   3' CTACGCCTTGGGGCTCC     1881     _    GGTTC
                                CT TGCCT    TGGGGCTCC
                                || |||||    |||||||||
                                GA GCGGA    ACCCCGAGG
                                 T    ______
GAM86   CDC91L1  3' CCTGTCTGGGAGGGGGCTCC  1882      C    TTCT
                                CTTG CTGG    GGGGCTCC
                                |||| ||||    ||||||||
                                GGAC GACC    CCCCGAGG
                                  A    CTC_
GAM86   CEACAM7  3' TTGTCTGTTCTGGGATC     1883     C   G      C
                                TTG CTG TTCTGGGG TC
                                ||| ||| |||||||| ||
                                AAC GAC AAGACCCT AG
                                 A  _      _
GAM86   CECR7    5' TGCCTGGGTCACCGGGCTCC   1884       T  TG_
                                TGCCTGG TC   GGGCTCC
                                ||||||| ||   |||||||
                                ACGGACC AG   CCCGAGG
                                    C  TGG
GAM86   CGB7     5' CCTGCCTGGTGTACCTGGCT   1885         T__  GG
                                CTTGCCTGGT   CT  GGCT
                                ||||||||||   ||  ||||
                                GGACGGACCA   GG  CCGA
                                      CAT  A_
GAM86   CHDH     3' CTTGGCTTATCAGGGGGCT    1886      C  G   CT
                                CTTG CT GTT  GGGGCT
                                |||| || |||  ||||||
                                GAAC GA TAG  CCCCGA
                                  C  A   TC
GAM86   CHST8    5' CTTACTTCTGAGATGGGGCTC  1887       __   TTC
                                CTTGC  CTGG   TGGGGCTC
                                |||||  ||||   ||||||||
                                GAATG  GACT   ACCCCGAG
                                   AA    CT_
GAM86   CRR9     3' CTTGCCTGTGAGGGCTCC     1888        GTTCT
                                CTTGCCTG    GGGGCTCC
                                ||||||||    ||||||||
                                GAACGGAC    TCCCGAGG
                                    AC___
GAM86   DKFZP564L0864 3' TGTCTGGTTCTAAGTTCC    1889     C        GC
                                TG CTGGTTCTGGG  TCC
                                || ||||||||||  |||
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                                AC GACCAAGATTC  AGG
                                 A        A_
GAM86   FBX30    3' CTTGCCTGTCCCTGCTCC    1890        G   GGG
                                CTTGCCTG TTCT   GCTCC
                                |||||||| ||||   |||||
                                GAACGGAC AGGG   CGAGG
                                     _   A__
GAM86   FIGN     3' CTTTCTGTCATCTGGGGCT   1891     GC   GT_
                                CTT  CTG   TCTGGGGCT
                                |||  |||   |||||||||
                                GAA  GAC   AGACCCCGA
                                  A_   AGT
GAM86   FLJ10193 3' TGCCTGGCAGGGCTC      1892        TCT
                                TGCCTGGT   GGGGCTC
                                ||||||||   |||||||
                                ACGGACCG   TCCCGAG

                                    ____
GAM86   FLJ10307 3' TACATAATTGGGGCTC     1893     C   TC
                                TGC TGGT  TGGGGCTC
                                ||| ||||  |||||||||
                                ATG ATTA  ACCCCGAG
                                  T   __
GAM86   FLJ10408 3' CCTGCCTGGCCTGGGCTCC   1894         T   G
                                CTTGCCTGGT CTGGG CTCC
                                |||||||||| ||||| ||||
                                GGACGGACCG GACCC GAGG

                                    _   _
GAM86   FLJ10511 3' CTTGTTGGTTCACACAGTCC  1895      CC    _ G  C
                                CTTG  TGGTTC TG GG TCC
                                ||||  |||||| || || |||
                                GAAC  ACCAAG GT TC AGG
                                  A_     T  G  _
GAM86   FLJ12294 3' CTGCCCACCTGGGGCTCC    1896       GT
                                TTGCCTG  TCTGGGGCTCC
                                |||||||  ||||||||||||
                                GACGGGT  GGACCCCGAGG

                                    __
GAM86   FLJ13102 3' CTGGCCTGGGGGGCTC     1897    T    TTCT
                                CT GCCTGG   GGGGCTC
                                || ||||||   |||||||
                                GA CGGACC   CCCCGAG
                                 C    _____
GAM86   FLJ14494 3' CTGCCTGGCCCTGGGCTC    1898           G
                                TTGCCTGGTTCTGGG CTC
                                |||||||||||||||| |||
                                GACGGACCGGGACCC GAG

                                    _
GAM86   FLJ14596 5' CTTGCTGCTGGGGCTC     1899       C  GTT
                                CTTGC TG   CTGGGGCTC
                                ||||| ||   |||||||||
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                                GAACG AC   GACCCCGAG
                                  _ ___
GAM86   FLJ20073  3'  TGCCTGGTAAGTAGTGGGGTTC 1900        TC____    C
                                TGCCTGGT     TGGGG TC
                                ||||||||     ||||| ||
                                ACGGACCA     ACCCC AG
                                     TTCATC     A
GAM86   FLJ20551  3'  CTTCCCTGGTTGGAGCTCC   1901     G     TC
                                CTT CCTGGT  TGGGGCTCC
                                ||| ||||||  |||||||||
                                GAA GGACCA  ACCTCGAGG
                                  G     __
GAM86   FLJ21432  3'  TGTCAAAGTTTTGGGGCTCC   1902     CCT_   C
                                TG    GGTT TGGGGCTCC
                                ||    |||| |||||||||
                                AC    TCAA ACCCCGAGG
                                  AGTT    A
GAM86   FLJ21438  5'  TTGCCTGGCAGGCAGGGCT   1903         TC_
                                TTGCCTGGT   TGGGGCT
                                |||||||||   |||||||
                                AACGGACCG   GTCCCGA
                                     TCC
GAM86   FLJ21865  3'  CTTCCTGGTTCCCCCTGGTTCC 1904      G       GG__  C
                                CTT CCTGGTTCT    GG TCC
                                ||| |||||||||    || |||
                                GAA GGACCAAGG    CC AGG
                                  _       GGGA  A
GAM86   FLJ22746  3'  CCTGTCTGATGTGGGGCTCC   1906      C     TC
                                CTTG CTGGT  TGGGGCTCC
                                |||| |||||  |||||||||
                                GGAC GACTA  ACCCCGAGG
                                  A    C_
GAM86   FLJ22746  3'  CTTGCCCTGGTTCCTCTGGAGC 1905        _     T_______  GGCT
            C                    CTTGCC TGGTTC      GG    C
                                ||||||  ||||||      ||    |
                                GAACGG ACCAAG      CC    G
                                   G     GAGAIII  TCGG
GAM86   FUK      3'  CTTGCTCTGGTCAGCT      1907       _     CTGG
                                CTTGC CTGGTT    GGCT
                                |||||  ||||||    ||||
                                GAACG GACCAG    TCGA
                                  A     ____
GAM86   GR6      5'  TGCCGTGCTCTGGGGCTC    1908       TG
                                TGCC  GTTCTGGGGCTC
                                ||||  ||||||||||||
                                ACGG  CGAGACCCCGAG
                                  CA
GAM86   GRIN3A   3'  CTTGCCTGGTCCAATCAATCC  1909           TGGGGC
                                CTTGCCTGGTTC     TCC
                                ||||||||||||     |||
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                                GAACGGACCAGG     AGG
                                      TTAGTT
GAM86   GTPBP5   3' TGTCCTTGCCCTGGGGCTCC  1910    _  G
                                TG CCT GTTCTGGGGCTCC
                                || ||| ||||||||||||
                                AC GGA CGGGACCCCGAGG
                                 A  A
GAM86   HSPC216  3' TTGCTATGGCAGGGGGCTCC  1911     C_   TCT
                                TTGC  TGGT   GGGGCTCC
                                ||||  ||||   ||||||||
                                AACG  ACCG   CCCCGAGG
                                  AT    TC_
GAM86   HSU24186 5' TTGGCTCGTCTGGGGCTCC   1912     C  G  T
                                TTG CT GT CTGGGGCTCC
                                ||| || || ||||||||||
                                AAC GA CA GACCCCGAGG
                                  C  G  _
GAM86   HSU79266 3' CTGGCCCAGTCCTGGGGCTC  1913    T   TG
                                CT GCC  GTTCTGGGGCTC
                                || |||  ||||||||||||
                                GA CGG  CAGGACCCCGAG
                                 C   GT
GAM86   KHSRP    3' CTTGCCGCGAGGGCTC     1914       TG  TCT
                                CTTGCC  GT   GGGGCTC
                                ||||||  ||   |||||||
                                GAACGG  CG   TCCCGAG
                                   __  C__
GAM86   KIAA0009 3' CTTTCCTGGTTCTCAACT   1915     G       G  G
                                CTT CCTGGTTCT GG CT
                                ||| ||||||||| || ||
                                GAA GGACCAAGA TT GA
                                  A       G  _
GAM86   KIAA0040 5' CTTGCCTGGTGGGCTCC    1845         TCTG
                                CTTGCCTGGT    GGGCTCC
                                ||||||||||    |||||||
                                GAACGGACCA    CCCGAGG
                                      _____
GAM86   KIAA0125 5' TTGCTGGTCCTCCTGGGGCTC 1916     C    ___
                                TTGC TGGTT   CTGGGGCTC
                                |||| |||||   |||||||||
                                AACG ACCAG   GACCCCGAG
                                   _    GAG
GAM86   KIAA0285 3' CTTACCTGGTTCAAGTCC    1917          TG   C
                                CTTGCCTGGTTC  GGG TCC
                                ||||||||||||  ||| |||
                                GAATGGACCAAG  TTC AGG
                                      __  _
GAM86   KIAA0286 3' CTTGCTGGTTCTGGAAC     1918       C
                                CTTGC TGGTTCTGGGGC
                                ||||| ||||||||||||
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                                GAACG ACCAAGACCTTG
                                      _
GAM86   KIAA0296 3' CTGGTGCCACTGGGGCTCC   1919      T___
                                CTGGT   CTGGGGCTCC
                                |||||   ||||||||||
                                GACCA   GACCCCGAGG
                                   CGGT
GAM86   KIAA0472 3' CCTGCCTGGGAAGGTTCC    1920        TTCT  GC
                                CTTGCCTGG   GGG  TCC
                                |||||||||   |||  |||
                                GGACGGACC   TCC  AGG
                                     CT__   A_
GAM86   KIAA0544 3' CCTGCCTGGCCCAGGGCTCC  1921         T TG
                                CTTGCCTGGT C  GGGCTCC
                                |||||||||| |  |||||||
                                GGACGGACCG G  CCCGAGG
                                      _ GT
GAM86   KIAA0618 5' CTGGCCCCCTCCTGGGGCTC  1922    T   GG
                                CT GCCT  TTCTGGGGCTC
                                || ||||  ||||||||||
                                GA CGGG  AGGACCCCGAG
                                 C   GG
GAM86   KIAA1183 3' CTTGGCCTGGGGCTGGTTCC  1923     _    TT   GG
                                CTTG CCTGG  CTGG  CT
                                |||| |||||  ||||  ||
                                GAAC GGACC  GACC  GG
                                  C    CC   AA
GAM86   KIAA1274 3' CTAGCACTCCTTGGGGCTCC  1924      ___  _
                                CTGGT   TCT GGGGCTCC
                                |||||   ||| ||||||||
                                GATCG   GGA CCCCGAGG
                                   TGA   A
GAM86   KIAA1297 5' TTGCCTGAGTTTTGAACC    1925       _  CTG
                                TTGCCTG GTT   GGGCT
                                ||||||| |||   |||||
                                AACGGAC CAA   CTTGG
                                    T   AA_
GAM86   KIAA1691 3' CCTGCCCCCTTGTCTGGGGTTC 1926       GGT__     C
                                CTTGCCT    TCTGGGG TC
                                |||||||    ||||||| ||
                                GGACGGG    AGACCCC AG
                                    GGAAC      A
GAM86   KIAA1729 5' TTGCCTGGCTTAAAGTTCC   1927         C    C
                                TTGCCTGGTT TGGGG TCC
                                |||||||||| ||||| |||
                                AACGGACCGA ATTTC AGG
                                      _    A
GAM86   KIAA1755 5' TGCTCCTCCTGGGGCTCC    1928     _ GG
                                TGC CT  TTCTGGGGCTCC
                                ||| ||  ||||||||||||
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                                ACG GG  AGGACCCCGAGG
                                  A __
GAM86   KIAA1814  3'  CTTGCCCGGTGGGCT       1929          TCTG
                                CTTGCCTGGT    GGGCT
                                ||||||||||    |||||
                                GAACGGGCCA    CCCGA
                                      _____
GAM86   KIAA1831  3'  CTTGTCTGGTCCTATC      1930       C       GGGC
                                CTTG CTGGTTCTG    TC
                                ||||  |||||||||    ||
                                GAAC GACCAGGAT    AG
                                  A       _____
GAM86   LIN-28    3'  TTGCCTGGTGCAGAACC     1931          TC
                                TTGCCTGGT  TGGGGCT
                                |||||||||  |||||||
                                AACGGACCA  GTCTTGG
                                     C_
GAM86   MGC10526  5'  CTGCCTGGTCTGGTTCC     1932          T    GG
                                TTGCCTGGT CTGG  CT
                                |||||||||  ||||  ||
                                GACGGACCA GACC  GG
                                     _   AA
GAM86   MGC11115  3'  CCTGCCTGGTTTTGAAAGCC   1933           C   _
                                CTTGCCTGGTT TGGG GCT
                                ||||||||||| |||| |||
                                GGACGGACCAA ACTT CGG
                                      A   T
GAM86   MGC1136   3'  CTGTCTGGTTCTGCAAGCT    1934      C       _
                                TTG CTGGTTCTG GGGCT
                                |||  |||||||||  |||||
                                GAC GACCAAGAC TTCGA
                                  A       G
GAM86   MGC15548  5'  CTTCCTGAGCGCTGGGCTC    1935      G   _ T    G
                                CTT CCTG GT CTGGG CTC
                                |||  ||||  ||  |||||  |||
                                GAA GGAC CG GACCC GAG
                                  _   T  C    _
GAM86   MGC16186  5'  TCGCGCCTGGGGCTCC       1936      CTG  T
                                TTGC   GT CTGGGGCTCC
                                ||||   ||  ||||||||||
                                AGCG   CG GACCCCGAGG
                                     ___  _
GAM86   MGC3101   3'  TGCTTGTGCTGGGGCTCC     1937      CTG  T
                                TGC   GT CTGGGGCTCC
                                |||   ||  ||||||||||
                                ACG   CA GACCCCGAGG
                                  AA_  C
GAM86   MGC33345  3'  CTCGCCTGGGGGCTC        1938          TTCTG
                                CTTGCCTGG    GGGCTC
                                |||||||||    ||||||
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                                GAGCGGACC    CCCGAG
                                      _____
GAM86   MSP     3' CTTCCTTGGGCTCTGGGCTCC 1939     G  __      G
                                CTT CCT  GGTTCTGGG CTCC
                                ||| |||  ||||||||| ||||
                                GAA GGA  CCGAGACCC GAGG
                                  _  AC       _
GAM86   N4BP3   3' CTTCCCTGGAGGAAGGCTCC  1940     G    TTCT
                                CTT CCTGG   GGGGCTCC
                                ||| |||||   ||||||||
                                GAA GGACC   TTCCGAGG
                                  G   TCC_
GAM86   OBSCN   3' CTGGCCTGGTTCTGCCTCC   1941    T        GGG
                                CT GCCTGGTTCTG  CTCC
                                || ||||||||||  ||||
                                GA CGGACCAAGAC  GAGG
                                 C        G__
GAM86   OSBPL5  3' CCTGCCTCTGTGGGGCTCC   1942       GGTTC
                                CTTGCCT   TGGGGCTCC
                                |||||||   |||||||||
                                GGACGGA   ACCCCGAGG
                                    GAC__
GAM86   P5-1    3' CTTCCCTGGTAGGGCTC    1943     G    TCT
                                CTT CCTGGT  GGGGCTC
                                ||| ||||||  |||||||
                                GAA GGACCA  TCCCGAG
                                  G    ___
GAM86   PIP5K1C 3' CCTGCCTGGGAGGTTC     1944         TTCT   C
                                CTTGCCTGG   GGGG TC
                                |||||||||   |||| ||
                                GGACGGACC   CTCC AG
                                     ____   A
GAM86   PL6     3' CTTGCCTTGGCTCAGGGCTC  1945       _    T
                                CTTGCCT GGTTC GGGGCTC
                                ||||||| ||||| |||||||
                                GAACGGA CCGAG TCCCGAG
                                    A   _
GAM86   PNMA5   3' TGCCTTCCTGGGGCTCC    1946      GG
                                TGCCT  TTCTGGGGCTCC
                                |||||  ||||||||||||
                                ACGGA  AGGACCCCGAGG
                                     __
GAM86   PRIC285 3' CTTCCTGGTTCTGAGACT   1947     G
                                CTT CCTGGTTCTGGGGCT
                                ||| ||||||||||||||
                                GAA GGACCAAGACTCTGA
                                  _
GAM86   PRO0246 5' CTTGCCTGGTGTCATAGTCC  1948         _ TGG  C
                                CTTGCCTGGT TC   GG TCC
                                |||||||||| ||   || |||
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                                GAACGGACCA AG   TC AGG
                                     C  TA_ _
GAM86   PRO2325  3'  CTGCCTGGGAGTGAGGGCTC  1949        TTC  _
                                TTGCCTGG   TG GGGCTC
                                ||||||||   || ||||||
                                GACGGACC   AC CCCGAG
                                     CTC  T
GAM86   PRO2325  3'  CTGCCTGGGAGTGAGGGCTC  1949        TTC  _
                                TTGCCTGG   TG GGGCTC
                                ||||||||   || ||||||
                                GACGGACC   AC CCCGAG
                                     CTC  T
GAM86   PTPNS1   3'  CTTGCCCATTCTTGGGGTTC  1950        G   _   C
                                CTTGCCTG TTCT GGGG TC
                                |||||||| |||| |||| ||
                                GAACGGGT AAGA CCCC AG
                                     _   A   A
GAM86   PTPRT    3'  TTGCCTGAGTTTCCTTTGGAGC 1951       _  _ T_____  GGCT
            CCC                    TGCCTG GTT C      GG   CC
                                ||||||| ||| |      ||   ||
                                ACGGAC CAA G      CC   GG
                                   T   A GAAAIII  TCGG
GAM86   RAB11B   3'  TGCCTGGTTCTTCGGGCT    1952          G_
                                TGCCTGGTTCT  GGGCT
                                ||||||||||  |||||
                                ACGGACCAAGA  CCCGA
                                      AG
GAM86   RAB20    3'  CTTGCCTGGTCAGACCCC    1953          CTG
                                CTTGCCTGGTT   GGGCTCC
                                ||||||||||   |||||||
                                GAACGGACCAG   TCTGGGG
                                      ___
GAM86   SIAT8D   3'  TTGCGTTCCTGGGGTTCC    1954      CTGG      C
                                TTGC   TTCTGGGG TCC
                                ||||   |||||||| |||
                                AACG   AGGACCCC AGG
                                  CA__       A
GAM86   TED      3'  CTTCCCTGGGGTCAGGGCT   1955     G    T_ T
                                CTT CCTGG  TC GGGGCT
                                ||| |||||  || ||||||
                                GAA GGACC  AG TCCCGA
                                  G    CC  _
GAM86   TRAF3    3'  TGCCTGAGCAAAGGGCTCC   1956       _ TCT
                                TGCCTG GT   GGGGCTCC
                                ||||||  ||   ||||||||
                                ACGGAC CG   TCCCGAGG
                                   T  TT_
GAM86   TRIM2    3'  CTTGTTTAGTTCTGGAGACT  1957      CC       _
                                CTTG  TGGTTCTGG GGCT
                                ||||  ||||||||| ||||
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                                GAAC  ATCAAGACC CTGA
                                  AA        T
GAM86   TTTY13   5'  CTGCTTGGGCTCTGGGGCTCC  1958      CT_
                                TTGC   GGTTCTGGGGCTCC
                                ||||   ||||||||||||||
                                GACG   CCGAGACCCCGAGG
                                  AAC
GAM86   TTYH2    3'  CTGCACCCCCTGGGGCT     1959      _ GG
                                TTGC CT  TTCTGGGGCT
                                |||| ||  ||||||||||
                                GACG GG  GGGACCCCGA
                                  T  __
GAM86   TXI1     5'  CTTGGCCTTCAGGGGCTCC    1960      _  GGT  T
                                CTTG CCT   TC GGGGCTCC
                                |||| |||   || ||||||||
                                GAAC GGA   AG CCCCGAGG
                                  C   ___  T
GAM86   ULK2     3'  CTTGCCTAGTTCCTGACT    1961           GG
                                CTTGCCTGGTTCT  GGCT
                                ||||||||||||  ||||
                                GAACGGATCAAGG  CTGA
                                       A_
GAM86   URB      5'  CTTGCCTGGATTCAGTCC    1962         _  TGG  C
                                CTTGCCTGG TTC   GG TCC
                                |||||||| |||   || |||
                                GAACGGACC AAG   TC AGG
                                     T  ___  _
GAM86   VTS58635 5'  CTTGCCGCTGTCTGGGGCTCC  1963       TG_  T
                                CTTGCC   GT CTGGGGCTCC
                                ||||||   || ||||||||||
                                GAACGG   CA GACCCCGAGG
                                   CGA  _
GAM86   ZNF304   3'  CTTGCCTATGGGGTTC      1964        GTTC    C
                                CTTGCCTG    TGGGG TC
                                ||||||||    ||||| ||
                                GAACGGAT    ACCCC AG
                                    _____     A
GAM86   ZNF384   3'  CTGGTTGCATTTGGGGCTCC   1965       C_____
                                CTGGTT    TGGGGCTCC
                                ||||||    |||||||||
                                GACCAA    ACCCCGAGG
                                   CGTAA
GAM86   LOC115704 3'  CCTGCCTGGGGGGCCTGGCTC   1966         TT_  GG
                                CTTGCCTGG   CT  GGCTC
                                |||||||||   ||  |||||
                                GGACGGACC   GG  CCGAG
                                     CCC  A_
GAM86   LOC122618 3'  CTTCCTGGAGGGCTC       1967      G    TTCT
                                CTT CCTGG    GGGGCTC
                                ||| |||||    |||||||
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                                GAA GGACC   TCCCGAG
                                  _   ____
GAM86   LOC132241 5' TTGCTAGGTTCTGACTC    1968     CT     GG
                                TTGC  GGTTCTG  GCTC
                                ||||  |||||||  ||||
                                AACG  CCAAGAC  TGAG
                                  AT     __
GAM86   LOC138389 3' CCTGCGCTCCTGGGGCTC    1969      CT G
                                CTTGC  G TTCTGGGGCTC
                                |||||  | ||||||||||
                                GGACG  C AGGACCCCGAG
                                   __ G
GAM86   LOC144144 3' CTTCCTGGGATAAAGGGGTTCC 1868     G    TTCT__   C
                                CTT CCTGG     GGGG TCC
                                ||| |||||     |||| |||
                                GAA GGACC     CCCC AGG
                                  _    CTATTT   A
GAM86   LOC145333 5' CTTGCCTGATACACAGGTTCC  1970         TCTG  C
                                CTTGCCTGGT   GGG TCC
                                ||||||||||   ||| |||
                                GAACGGACTA   TCC AGG
                                     TGTG  A
GAM86   LOC145719 3' TTCCCTCAGGGGGGCTCC    1971    G  __ TTCT
                                TT CCT  GG   GGGGCTCC
                                || |||  ||   ||||||||
                                AA GGA  CC   CCCCGAGG
                                 G  GT  ____
GAM86   LOC145720 3' TTCCCTCAGGGGGGCTCC    1971    G  __ TTCT
                                TT CCT  GG   GGGGCTCC
                                || |||  ||   ||||||||
                                AA GGA  CC   CCCCGAGG
                                 G  GT  ____
GAM86   LOC146667 3' TGTGTGGTCCTGGGGCTCC   1972    CC
                                TG  TGGTTCTGGGGCTCC
                                ||  ||||||||||||||
                                AC  ACCAGGACCCCGAGG
                                 AC
GAM86   LOC146725 5' CCTGCCTGGAACTGGCTC    1973        TT  GG
                                CTTGCCTGG  CT  GGCTC
                                |||||||||  ||  |||||
                                GGACGGACC  GA  CCGAG
                                     TT  __
GAM86   LOC146728 5' CTGCAGCCCCTGGGGCTC    1974     CT   _
                                TTGC  GGTTC TGGGGCTC
                                ||||  ||||| ||||||||
                                GACG  TCGGG ACCCCGAG
                                  __    G
GAM86   LOC147178 3' CTTGCTGCCCACAGGGGCTC  1975      C  G  CT_
                                CTTGC TG TT   GGGGCTC
                                ||||| || ||   |||||||
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                                GAACG AC GG   CCCCGAG
                                  _ G  TGT
GAM86   LOC147514 3' CTGTCTGGTCCTCGGCT     1976      C       G  G
                                TTG CTGGTTCT GG CT
                                ||| |||||||| || ||
                                GAC GACCAGGA CC GA
                                  A       G  _
GAM86   LOC148018 5' CTCTGAGGCTTTGGGGTTCC   1977      GCCT    C     C
                                CTT    GGTT TGGGG TCC
                                |||    |||| ||||| |||
                                GAG    CCGA ACCCC AGG
                                  ACT_    A     A
GAM86   LOC149175 3' CTCGCCTGAGGAACGGGCTC   1978          TTCTG
                                CTTGCCTGG     GGGCTC
                                |||||||||     ||||||
                                GAGCGGACT     CCCGAG
                                      CCTTG
GAM86   LOC149668 5' CTTGCCTGGCTCTCAAGGCC   1979             _
                                CTTGCCTGGTTCT GGGGCT
                                |||||||||||| ||||||
                                GAACGGACCGAGA TTCCGG
                                        G
GAM86   LOC150538 5' CTTTCCGTTATGGGGCTC     1980      G  TG   C
                                CTT CC  GTT TGGGGCTC
                                ||| ||  ||| ||||||||
                                GAA GG  CAA ACCCCGAG
                                  A  __   T
GAM86   LOC151568 5' CCTGCCTGGGGCCCATGGGGCT 1981          __     _
          CC                      CTTGCCT  GGTTC TGGGGCTCC
                                ||||||| ||||| |||||||||
                                GGACGGA  CCGGG ACCCCGAGG
                                    CC     T
GAM86   LOC152698 3' CCTGCCTGGCCTGGGCTCC    1894          T     G
                                CTTGCCTGGT CTGGG CTCC
                                |||||||||| ||||| ||||
                                GGACGGACCG GACCC GAGG
                                          _    _
GAM86   LOC154739 5' CTTGCCTGGCTCACTC       1982            TGGG
                                CTTGCCTGGTTC    GCTC
                                ||||||||||||    ||||
                                GAACGGACCGAG    TGAG
                                          _____
GAM86   LOC157280 3' CCTGCCTGGCCTGGGCTCC    1894          T     G
                                CTTGCCTGGT CTGGG CTCC
                                |||||||||| ||||| ||||
                                GGACGGACCG GACCC GAGG
                                          _    _
GAM86   LOC159110 3' CTTCCTGGTTCTGAAAGCT    1983      G         _
                                CTT CCTGGTTCTGGG GCT
                                ||| |||||||||||| |||
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                                GAA GGACCAAGACTT CGA
                                  _         T
GAM86   LOC159116 3'  CTTCCTGGTTCTGAAAGCT   1983     G         _
                                CTT CCTGGTTCTGGG GCT
                                ||| |||||||||||| |||
                                GAA GGACCAAGACTT CGA
                                  _         T
GAM86   LOC196955 5'  CTTGCTGGCCGGGGCT      1984      C   TT
                                CTTGC TGG  CTGGGGCT
                                ||||| |||  ||||||||
                                GAACG ACC  GGCCCCGA
                                  _  __
GAM86   LOC197114 3'  TTCCCTCAGGGGGGCTCC    1971     G  __  TTCT
                                TT CCT  GG   GGGGCTCC
                                || |||  ||   ||||||||
                                AA GGA  CC   CCCCGAGG
                                 G   GT  ____
GAM86   LOC197117 3'  TTCCCTCAGGGGGGCTCC    1971     G  __  TTCT
                                TT CCT  GG   GGGGCTCC
                                || |||  ||   ||||||||
                                AA GGA  CC   CCCCGAGG
                                 G   GT  ____
GAM86   LOC199714 5'  CTTGACCCGTGGGGCT      1985      _   GTTC
                                CTTG CCTG   TGGGGCT
                                |||| ||||   |||||||
                                GAAC GGGC   ACCCCGA
                                  T   ____
GAM86   LOC200862 5'  TTGCCTGGTCACCTAGGGGCTC 1986          __ _
          C                      TTGCCTGGTT  CT GGGGCTCC
                                ||||||||||  || ||||||||
                                AACGGACCAG  GA CCCCGAGG
                                      TG  T
GAM86   LOC201252 3'  TTGCCTGGCTTTGTGGAG    1987          C__
                                TTGCCTGGTT   TGGGG
                                ||||||||||   |||||
                                AACGGACCGA   ACCTC
                                      AAC
GAM86   LOC201689 3'  CTTGGCTTATCAGGGGGCT   1886      C  G   CT
                                CTTG CT GTT  GGGGCT
                                |||| || |||  ||||||
                                GAAC GA TAG  CCCCGA
                                  C  A   TC
GAM86   LOC203350 3'  CTTGCTGGTCCTTGGCTC    1988       C      GG
                                CTTGC TGGTTCT  GGCTC
                                ||||| |||||||  |||||
                                GAACG ACCAGGA  CCGAG
                                  _      A_
GAM86   LOC203396 5'  CCTGCCTGGAACTGGCTC    1973          TT  GG
                                CTTGCCTGG  CT  GGCTC
                                |||||||||  ||  |||||
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                                GGACGGACC  GA  CCGAG
                                     TT  __
GAM86   LOC220020 5'  TTGGCTGGGCCAGGGCTCC   1989     C   TT TG
                                TTG CTGG  C  GGGCTCC
                                ||| ||||  |  |||||||
                                AAC GACC  G  CCCGAGG
                                  C   C_ GT
GAM86   LOC220027 5'  CTTGCCTTGGTTGATGCT    1990       _  TC  GG
                                CTTGCCT GGT  TG  GCT
                                ||||||| |||  ||  |||
                                GAACGGA CCA  AC  CGA
                                    A  __  TA
GAM86   LOC220486 3'  CTTCCTGGGATAAAGGGGTTCC 1868     G    TTCT__   C
                                CTT CCTGG     GGGG TCC
                                ||| |||||     |||| |||
                                GAA GGACC     CCCC AGG
                                  _    CTATTT   A
GAM86   LOC221474 5'  CCTGCAAAAGCTGGGGCT    1991      CT  TT
                                CTTGC  GG  CTGGGGCT
                                |||||  ||  ||||||||
                                GGACG  TT  GACCCCGA
                                   T_  TC
GAM86   LOC222031 3'  CTGGCTTGGTTTGACCCTCC   1992    T  C    C   GG
                                CT GC TGGTT TGG  CTCC
                                || || ||||| |||  ||||
                                GA CG ACCAA ACT  GAGG
                                 C  A    _   GG
GAM86   LOC222681 5'  CTGACTCTTCTGGGGTTCC   1993      ___      C
                                CTGG   TTCTGGGG TCC
                                ||||   |||||||| |||
                                GACT   AAGACCCC AGG
                                  GAG       A
GAM86   LOC253816 3'  CTTGCCTGGCTCAAACT     1994          TG
                                CTTGCCTGGTTC  GGGCT
                                ||||||||||||  |||||
                                GAACGGACCGAG  TTTGA
                                       __
GAM86   LOC254107 5'  CCTGCCCTCTGGGGCTCC    1995       GGT
                                CTTGCCT   TCTGGGGCTCC
                                |||||||   ||||||||||||
                                GGACGGG   AGACCCCGAGG
                                      ___
GAM86   LOC255374 5'  TGCCTGGCTGGGCTC       1996        CTG
                                TGCCTGGTT   GGGCTC
                                |||||||||   ||||||
                                ACGGACCGA   CCCGAG
                                      ___
GAM86   LOC255448 3'  CCTGCCTGGCCTGGGCTCC   1894         T    G
                                CTTGCCTGGT CTGGG CTCC
                                |||||||||| ||||| ||||
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                                GGACGGACCG GACCC GAGG
                                          _   _
GAM86   LOC256849 5'  CTGGCCTGGGGCGCAGGGCTCC 1997    T    TTCT_
                                CT GCCTGG    GGGGCTCC
                                || ||||||    ||||||||
                                GA CGGACC    TCCCGAGG
                                 C     CCGCG
GAM86   LOC257507 5'  CTGACTCTTCTGGGGTTCC   1993     ___      C
                                CTGG   TTCTGGGG TCC
                                ||||   |||||||| |||
                                GACT   AAGACCCC AGG
                                  GAG       A
GAM86   LOC257625 5'  CTGACTCTTCTGGGGTTCC   1993     ___      C
                                CTGG   TTCTGGGG TCC
                                ||||   |||||||| |||
                                GACT   AAGACCCC AGG
                                  GAG       A
GAM86   LOC54505  5'  CTTGCTTGACACGGGGCTCC   1998      C   TTC
                                CTTGC TGG   TGGGGCTCC
                                ||||| |||   |||||||||
                                GAACG ACT   GCCCCGAGG
                                  A   GT_
GAM86   LOC56964  3'  CCTGCCTGAGGGCTC       1999        GTTCT
                                CTTGCCTG    GGGGCTC
                                ||||||||    |||||||
                                GGACGGAC    TCCCGAG
                                          _____
GAM86   LOC57105  3'  CTTTTCTGCTCTGGGGCT    2000     GC   G
                                CTT  CTG TTCTGGGGCT
                                |||  ||| ||||||||||
                                GAA  GAC GAGACCCCGA
                                 AA  _
GAM86   LOC57862  3'  CTTCCTGGTGAAGCTC      2001     G    TCT
                                CTT CCTGGT   GGGGCTC
                                ||| ||||||   |||||||
                                GAA GGACCA   CTTCGAG
                                  _    ____
GAM86   LOC90639  3'  CTGGCCTGGCCCTGGTTCC   2002    T        GG
                                CT GCCTGGTTCTGG  CT
                                || ||||||||||||  ||
                                GA CGGACCGGGACC  GG
                                 C          AA
GAM86   LOC91050  3'  CTTGACCCTCTCTGGGGCT   2003     _  GG
                                CTTG CCT  TTCTGGGGCT
                                |||| |||  ||||||||||
                                GAAC GGG  GAGACCCCGA
                                  T  A_
GAM86   LOC91355  5'  TGCCTGGGGGGGCTCC      2004       TTCT
                                TGCCTGG    GGGGCTCC
                                |||||||    ||||||||
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                                ACGGACC   CCCCGAGG
                                   C___
GAM86   LOC92078 3'  TGCCTGGTTTCCACTCC    2005        _ GGG
                                TGCCTGGTT CT   GCTCC
                                ||||||||| ||   |||||
                                ACGGACCAA GG   TGAGG
                                     A ___
GAM86   LOC93259 5'  CTGCCTGAGGGGCTCC     2006       TTCT
                                TTGCCTGG   GGGGCTCC
                                ||||||||   ||||||||
                                GACGGACT   CCCCGAGG
                                    _____
GAM87   DDAH2    5'  AGCTCATATACTACGATGGG  2009     C  C   CA  _
                                AGC TA TGT  AC ACGATGGG
                                ||| || |||  || ||||||||
                                TCG GT ATA  TG TGCTACCC
                                  A  _  __  A
GAM87   JMJ      3'  AAGTTTACTGTCAAAAAGAGGG 2010     CC       CAC  T
            A                    AAG  TACTGTCAA   GA GGGA
                                ||| |||||||||  || ||||
                                TTC  ATGACAGTT   CT CCCT
                                  AA       TTT  _
GAM87   MKLN1    3'  AGCTTTACTGTCAGTCAGTGGA 2011     C_      ACA  A
                                AGC  TACTGTCA   CG TGGG
                                |||  ||||||||  || ||||
                                TCG  ATGACAGT   GT ACCT
                                  AA       CA_  C
GAM87   PTGFRN   3'  AAGGCTACTGTCAATGCA    2012     C        CA
                                AAG CTACTGTCAA  CG
                                ||| ||||||||||  ||
                                TTC GATGACAGTT  GT
                                  C        AC
GAM87   PTPRZ1   3'  AAGTTACTGTCAGGTGATGGGA 2013     CC       ACAC
                                AAG  TACTGTCA   GATGGGA
                                |||  ||||||||  |||||||
                                TTC  ATGACAGT   CTACCCT
                                  A_       CCA_
GAM87   SNCB     3'  AGCCACTGTCGGGGATCGGG  2014     T     AACAC  _
                                AGCC ACTGTC    GAT GGG
                                |||| ||||||    ||| |||
                                TCGG TGACAG    CTA CCC
                                  _     CCC__   G
GAM87   DMRTB1   3'  AACCTGCTGTCAACGACCCTGG 2015       A      _  GA
                                AGCCT CTGTCAAC AC  TGG
                                ||||| |||||||| ||  |||
                                TTGGA GACAGTTG TG  ACC
                                   C       C  GG
GAM87   FLJ12800 3'  AACCTACTGTCCTGCATGGG  2016          AACACG
                                AGCCTACTGTC     ATGGG
                                ||||||||||     |||||
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                                TTGGATGACAG     TACCC
                                      GACG__
GAM87   FLJ12800 3' GCCTACTGTCCTGAATGGG   2017          AACAC
                                GCCTACTGTC    GATGGG
                                ||||||||||    ||||||
                                CGGATGACAG    TTACCC
                                      GAC__
GAM87   FLJ20079 3' GCTTACTGTCAATAAATATGTG 2018    C       CACGA___
           GGA                    GC TACTGTCAA       TGGGA
                                || |||||||||       |||||
                                CG ATGACAGTT       ACCCT
                                 A        ATTTATAC
GAM87   FLJ21272 3' ACCTATTGTCAACAAGG     2019       C       CGAT
                                GCCTA TGTCAACA    GGG
                                ||||| ||||||||    |||
                                TGGAT ACAGTTGT    TCC
                                   A       _____
GAM87   FLJ25124 3' AAGCCTCTGTCAACCAGGG   2020        A       ACGAT
                                AAGCCT CTGTCAAC    GGG
                                |||||| ||||||||    |||
                                TTCGGA GACAGTTG    CCC
                                   _       GT___
GAM87   KIAA0628 3' GCCTTAGGGCACACGATGGGA  2021       ACTGTCA
                                GCCT       ACACGATGGGA
                                ||||       ||||||||||||
                                CGGA       TGTGCTACCCT
                                  ATCCCG_
GAM87   KIAA1084 3' AAGCTTATGTCAACACGA    2022       C  C
                                AAGC TA TGTCAACACGA
                                |||| || ||||||||||||
                                TTCG AT ACAGTTGTGCT
                                  A  _
GAM87   MGC16279 5' GCCACTGTCACCCTGGG     2023      T      A ACGA
                                GCC ACTGTCA C    TGGG
                                ||| ||||||| |    ||||
                                CGG TGACAGT G    ACCC
                                  _      _ GG__
GAM87   MGC32043 3' GCCAGCTGTCAGCCCAATGGGA 2024      TA     ACA
                                GCC  CTGTCA   CGATGGGA
                                |||  ||||||   ||||||||
                                CGG  GACAGT   GTTACCCT
                                  TC     CGG
GAM87   MGC5139  5' AGCTTGTTGTCAACAAAGTAGA 2025      CTAC       CGA
                                AGC    TGTCAACA   TGGG
                                |||    ||||||||   ||||
                                TCG    ACAGTTGT   ATCT
                                  AACA       TTC
GAM87   RTP801   3' CTCTGCAGTACACGATGGG   2026     A   CA_
                                CT CTGT   ACACGATGGG
                                || ||||   ||||||||||
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                                GA GACG   TGTGCTACCC
                                 _   TCA
GAM87   WIRE     3'  CCTACTGTCAATATAGA     2027          CACG
                                CCTACTGTCAA    ATGGG
                                ||||||||||    |||||
                                GGATGACAGTT    TATCT
                                      A___
GAM87   LOC146506 3'  CCAGGCAACACGATGGG     2028     TACT T
                                CC    G CAACACGATGGG
                                ||    | ||||||||||||
                                GG    C GTTGTGCTACCC
                                 TC__ _
GAM87   LOC152220 3'  AAGTCTACAGTCAATGGG    2029     C    T    ACACG
                                AAG CTAC GTCA     ATGGG
                                ||| |||| ||||     |||||
                                TTC GATG CAGT     TACCC
                                  A   T   _____
GAM87   LOC153937 5'  AGCCACTGTCAATATTCAAAGG 2030      T      CA__   T
                                AGCC ACTGTCAA    CGA GG
                                |||| ||||||||    ||| ||
                                TCGG TGACAGTT    GTT CC
                                  _       ATAA   T
GAM87   LOC157627 3'  AAGCTTGCATCACGATGGG    2031      CTAC  T  A
                                AAGC    TG CA CACGATGGG
                                ||||    || || |||||||||
                                TTCG    AC GT GTGCTACCC
                                  A___  _  A
GAM87   LOC206426 3'  AACCTACTGTCAAGGCAGGGTG 2032           CA  A__
            GGA                   AGCCTACTGTCAA  CG   TGGGA
                                ||||||||||||  ||   |||||
                                TTGGATGACAGTT  GT   ACCCT
                                      CC  CCC
GAM87   LOC221489 5'  AACTCTACTGTCAACATGTGGG 2033      _         CGA
                                AGC CTACTGTCAACA   TGGG
                                ||| ||||||||||||   ||||
                                TTG GATGACAGTTGT   ACCC
                                  A          AC_
GAM87   LOC254250 5'  AGCCTACTTCAATGCATGCAGA 2034         G    CA G   _
                                AGCCTACT TCAA  C ATG GGA
                                |||||||| ||||  | ||| |||
                                TCGGATGA AGTT  G TAC TCT
                                     _    AC _   G
GAM87   LOC92270  3'  AGCCCACTGTGGACATGGTGGG 2035          CA   CGA
                                AGCCTACTGT  ACA   TGGG
                                ||||||||||  |||   ||||
                                TCGGGTGACA  TGT   ACCC
                                      CC   ACC
GAM88   AKAP2    3'  CCCTGTGTCTGCTTTGGGAACG 2038        ACG_  ACCA
            CC                    CCCTGT   GC    GGAACGCC
                                ||||||   ||   ||||||||
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                                GGGACA   CG   CCTTGCGG
                                   CAGA  AAAC
GAM88   ARNTL    5'  CCGTGGCTCGCCGGGAGCGCC  2039      AC   A__  A   A
                                CTGT  GGC   CC GGA CGCC
                                ||||  |||   || ||| ||||
                                GGCA  CCG   GG CCT GCGG
                                  __   AGC  C   C
GAM88   IL5RA    3'  ACCCTGTACGGCATGGG     2040            CCA
                                ACCCTGTACGGCA   GG
                                ||||||||||||   ||
                                TGGGACATGCCGT   CC
                                       AC_
GAM88   MUCDHL   3'  CCTTGTGGTCAGGGAGGAACGC 2041     C   AC  _  CC_
            C                    CC TGT  GG CA   AGGAACGCC
                                || |||  || ||   |||||||||
                                GG ACA  CC GT   TCCTTGCGG
                                 A   __  A  CCC
GAM88   CASKIN1  3'  CCCTGCACGCCGGGACGC    2042          GCA  A   A
                                CCCTGTACG   CC GGA CGC
                                |||||||||   || ||| |||
                                GGGACGTGC   GG CCT GCG
                                      ___  C   _
GAM88   DKFZP586M1120 3'  CCCTGTACCTGGCCAGGAATGC 2043          __   AC     C
                                CCCTGTAC  GGC  CAGGAA GC
                                ||||||||  |||  |||||| ||
                                GGGACATG  CCG  GTCCTT CG
                                     GA   __     A
GAM88   DVL2     3'  ACCCAGTCACACACCAGGAGCG 2044       TG_   G       A
            CC                     ACCC   TACG CACCAGGA CGCC
                                ||||   |||| |||||||| ||||
                                TGGG   GTGT GTGGTCCT GCGG
                                  TCA   _       C
GAM88   FLJ23186 5'  ACCTTGTCGGCACCATTGG   2045      C   A      A_____
                                ACC TGT CGGCACC     GG
                                ||| ||| |||||||     ||
                                TGG ACA GCCGTGG     CC
                                  A   _      TAAIII
GAM88   GBTS1    3'  CCCCAGCACCAGGGATGCC   2046      TGTA        AAC
                                CCC   CGGCACCAGG   GCC
                                |||   ||||||||||   |||
                                GGG   GTCGTGGTCC   CGG
                                  _____         CTA
GAM88   KIAA1918  3'  CTGTACAGCATCAATGGCATGC 2047           C  __  AAC
            C                    CTGTACGGCA CA  GG   GCC
                                |||||||||| ||  ||   |||
                                GACATGTCGT GT  CC   CGG
                                      A  TA  GTA
GAM88   LOC120241 5'  CGCAGACCGCCGGGAACGCC   2048      C   A_  A
                                TGTA GGC  CC GGAACGCC
                                |||| |||  || ||||||||
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                                GCGT CTG  GG CCTTGCGG
                                  _  GC  C
GAM88   LOC161635 5'  TGTACAGCAACTGGGGATGCC  2049         _ CA_  AC
                                TGTACGGCA C   GGA  GCC
                                |||||||||  |   |||  |||
                                ACATGTCGT G   CCT  CGG
                                     T ACC   A_
GAM88   LOC205418 5'  CCTGTGGCTGCCAGGGACGCC  2050       AC  A_    A
                                CCTGT  GGC  CCAGG ACGCC
                                |||||  |||  ||||| |||||
                                GGACA  CCG  GGTCC TGCGG
                                  __  AC    C
GAM88   LOC220587 3'  ACCCAGTCACACACCAGGAGCG 2044      TG_   G      A
          CC                      ACCC   TACG CACCAGGA CGCC
                                |||||  |||| |||||||| ||||
                                TGGG   GTGT GTGGTCCT GCGG
                                  TCA   _      C
GAM88   LOC254102 3'  CCCTGTACGGGGAAGGGCGCC  2051          CACC  AA
                                CCCTGTACGG    AGG  CGCC
                                ||||||||||    |||  ||||
                                GGGACATGCC    TCC  GCGG
                                     CCT_  C_
GAM88   LOC256145 5'  TGTGCTGCACCAAGATGCC   2052     ACG       AC
                                TGT   GCACCAGGA  GCC
                                |||   |||||||||  |||
                                ACA   CGTGGTTCT  CGG
                                  CGA       A_
GAM89   ABCB4    5'  TATTTTACCTGACAAATTC   2055        G     TT
                                TATTTTAC CTGACA  TTT
                                ||||||||  ||||||  |||
                                ATAAAATG GACTGT  AAG
                                     _     TT
GAM89   ABCB4    5'  TATTTTACCTGACAAATTC   2055        G     TT
                                TATTTTAC CTGACA  TTT
                                ||||||||  ||||||  |||
                                ATAAAATG GACTGT  AAG
                                     _     TT
GAM89   M17S2    5'  TATCTTACGCTGATATTC    2056           C
                                TATTTTACGCTGA ATTT
                                ||||||||||||  ||||
                                ATAGAATGCGACT TAAG
                                       A
GAM89   M17S2    5'  TATCTTACGCTGATATTC    2056           C
                                TATTTTACGCTGA ATTT
                                ||||||||||||  ||||
                                ATAGAATGCGACT TAAG
                                       A
GAM89   DKFZp761H079 3'  ATTTTGGGCCAACATTTTTATT 2057       AC  TG       C
          C                      ATTTT  GC  ACATTTTTA TC
                                |||||  ||  |||||||| ||
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                                TAAAA  CG  TGTAAAAAT AG
                                  CC  GT       A
GAM90   ATP7A    3'  CAACATGGCGAAACCCCGTCT  2060     C      CGC  G   C
                                CA CATGGCGA   GA CCCG CT
                                || ||||||||   || |||| ||
                                GT GTACCGCT   TT GGGC GA
                                 T      ___  G   A
GAM90   CTF1     3'  CAACATGGCGAAACCTCGTCT  2061     C      CGCG   _ C
                                CA CATGGCGA   AGCC CG CT
                                || ||||||||   |||| || ||
                                GT GTACCGCT   TTGG GC GA
                                 T      ____   A  A
GAM90   CYP4F3   3'  CATGGCGAAACCCCGCCT    2062        CGC  G
                                CATGGCGA   GA CCCGCCT
                                ||||||||   || |||||||
                                GTACCGCT   TT GGGCGGA
                                     ___  G
GAM90   DPH2L1   3'  CACCATGGTGCCAGCCTCTGCC 2063        CGAC  G   C__
           T                     CACCATGG   GC AGCC   GCCT
                                ||||||||   || ||||   ||||
                                GTGGTACC   CG TCGG   CGGA
                                     A___  G   AGA
GAM90   HOXD13   5'  CACCATGGCGCGGCGCGCC   2064        GAC   A  C
                                CACCATGGC   GCG GC CGCC
                                |||||||||   ||| || ||||
                                GTGGTACCG   CGC CG GCGG
                                     ___  _ C
GAM90   KNS2     5'  GACTGTGCGCCGAGCCCGCCT  2065     GA__  _
                                GGC   CGC GAGCCCGCCT
                                |||   ||| ||||||||||
                                CTG   GCG CTCGGGCGGA
                                  ACAC   G
GAM90   LAMC2    3'  CACCATAGCTCTGAATGGGCCT 2066        GACGCGA__  C
           GCCT                  CACCATGGC       GCC GCCT
                                |||||||||       ||| ||||
                                GTGGTATCG       CGG CGGA
                                     AGACTTACC   A
GAM90   LZTS1    3'  CACCATGGCGGAGCACAGCCTC 2067         AC  _   __
           CGCCT                  CACCATGGCG  GCG AGCC  CGCCT
                                |||||||||  ||| ||||  |||||
                                GTGGTACCGC  CGT TCGG  GCGGA
                                     CT   G   AG
GAM90   MCL1     3'  CACCATGGTTAGACTAGCCTGC 2068        C__  GCG   C
                                CACCATGG   GAC   AGCC GC
                                ||||||||   |||   |||| ||
                                GTGGTACC   CTG   TCGG CG
                                     AAT   A__   A
GAM90   NCOA6    5'  CAACATGGCGAAACCCCGCCT  2069     C      CGC  G
                                CA CATGGCGA   GA CCCGCCT
                                || ||||||||   || |||||||
```

```
                                GT GTACCGCT   TT GGGCGGA
                                 T      ___  G
GAM90   PCDHB9   3'  CACCATGATGAAACCCGC    2070       GC  CGCG    C
                                CACCATG  GA   AGCCCG C
                                |||||||  ||   |||||| |
                                GTGGTAC  CT   TTGGGC G
                                    TA  ____     A
GAM90   PIGR     3'  CAACATGGCGAAACCC     2071     C      CGCG
                                CA CATGGCGA   AGCCC
                                || ||||||||   |||||
                                GT GTACCGCT   TTGGG
                                 T      ____
GAM90   SGT      3'  CACGGCGCCGTGGGCTCGTCT  2072       A  CGA  C  C
                                CATGGCG CG   GC CG CT
                                ||||||| ||   || || ||
                                GTGCCGC GC   CG GC GA
                                    G  ACC  A  A
GAM90   SRC      3'  CACCGGGTTCCAAGCCCGCCT  2073      AT  CGACG
                                CACC  GG    CGAGCCCGCCT
                                ||||  ||    ||||||||||||
                                GTGG  CC    GTTCGGGCGGA
                                  C_  AAG__
GAM90   TOP1     5'  ACCACGGCGGCGACGCTGCCT  2074         AC   _  CC
                                ACCATGGCG  GCGA GC  GCCT
                                |||||||||  |||| ||  ||||
                                TGGTGCCGC  CGCT CG  CGGA
                                     __   G  A_
GAM90   ASB16    3'  CAACATGGCGAGACCCCGTCT  2075     C      CGC  G    C
                                CA CATGGCGA   GA CCCG CT
                                || ||||||||   || |||| ||
                                GT GTACCGCT   CT GGGC GA
                                 T      ___  G    A
GAM90   DKFZP434F0318 3'  CAACATGGCGAAACCC     2071     C      CGCG
                                CA CATGGCGA   AGCCC
                                || ||||||||   |||||
                                GT GTACCGCT   TTGGG
                                 T      ____
GAM90   FLJ20413  3'  CGGCCGAGTGCGAGCCCG    2076      _  C_
                                TGGC GA  GCGAGCCCG
                                |||| ||  |||||||||
                                GCCG CT  CGCTCGGGC
                                  G  CA
GAM90   FLJ20783  5'  CCACGGCGATTCCTCGCCT   2077         CGCGAG  _
                                CCATGGCGA     CC CGCCT
                                |||||||||     || |||||
                                GGTGCCGCT     GG GCGGA
                                     AA____  A
GAM90   FLJ32468  5'  CACCATGGCGGCCAGGGCC   2078          AC  G  CCC
                                CACCATGGCG  GC AG   GCC
                                ||||||||||  || ||   |||
```

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                                GTGGTACCGC  CG TC   CGG
                                     __  G  C__
GAM90   KIAA0427  3'  AACAATGCGAGCCCGTCT    2079       C       C
                                GGCGA GCGAGCCCG CT
                                ||||| ||||||||| ||
                                TTGTT CGCTCGGGC GA
                                   A       A
GAM90   KIAA0478  3'  CAACATGGCGAGACCC      2080     C       CGC  G
                                CA CATGGCGA   GA CCC
                                || ||||||||   || |||
                                GT GTACCGCT   CT GGG
                                 T      ___  _
GAM90   KIAA0513  5'  CAACATGGCGAAACCC      2071     C       CGCG
                                CA CATGGCGA    AGCCC
                                || ||||||||    |||||
                                GT GTACCGCT    TTGGG
                                 T      _____
GAM90   KIAA0563  5'  CAACATGGCGAAACTCCGCCT  2081     C       CGCG  _
                                CA CATGGCGA    AGC CCGCCT
                                || ||||||||    ||| |||||||
                                GT GTACCGCT    TTG GGCGGA
                                 T      _____  A
GAM90   KIAA0720  3'  GCCGTCGAGAAGGGCCCGCCT  2082    G  A  C ___
                                G CG CG GA   GCCCGCCT
                                | || || ||   ||||||||
                                C GC GC CT   CGGGCGGA
                                 G  A  T  TCC
GAM90   KIAA1036  3'  CACCATGGCAGCCCTGCC    2083          GACGCG    _
                                CACCATGGC     AGCCC GCC
                                |||||||||     ||||| |||
                                GTGGTACCG     TCGGG CGG
                                     _______    A
GAM90   KIAA1115  5'  CAACATGGCGAAACCC      2071     C       CGCG
                                CA CATGGCGA    AGCCC
                                || ||||||||    |||||
                                GT GTACCGCT    TTGGG
                                 T      _____
GAM90   TBCC      3'  CAACATGGCGAAACCCCGTCT  2060     C       CGC  G   C
                                CA CATGGCGA   GA CCCG CT
                                || ||||||||   || |||| ||
                                GT GTACCGCT   TT GGGC GA
                                 T      ___  G    A
GAM90   LOC145989 5'  CACCTTGGTGGCCTTGCCCGCC 2084      A   CGAC  GA_
           T                     CACC TGG    GC   GCCCGCCT
                                |||| |||    ||   ||||||||
                                GTGG ACC    CG   CGGGCGGA
                                  A  AC__  GAA
GAM90   LOC145990 3'  CACCATGGCGCCCCC       2085          GACGCGA    G
                                CACCATGGC      GCCC CC
                                |||||||||      |||| ||
```

```
                                GTGGTACCG      CGGG GG
                                        _______   _
GAM90   LOC155372 3'  CACCATGGTGAAATTCCGTCT  2086        C  CGC  GC   C
                                CACCATGG GA   GA  CCG CT
                                |||||||| ||   ||  ||| ||
                                GTGGTACC CT   TT  GGC GA
                                     A ___  AA   A
GAM90   LOC162137 3'  CACCGCGGCAGCCCGC      2087      A    GACGCG
                                CACC TGGC     AGCCCGC
                                |||| ||||     |||||||
                                GTGG GCCG     TCGGGCG
                                  C  ______
GAM90   LOC200940 3'  CCTGTGGCCACCGGCCCGCCT  2088     A_   G  G  A
                                CC  TGGC AC CG GCCCGCCT
                                ||  |||| || || ||||||||
                                GG  ACCG TG GC CGGGCGGA
                                 AC    G  _  _
GAM90   LOC254610 5'  ATGGCGACGGCCACC       2089          CGA   C
                                ATGGCGACG   GCC GCC
                                |||||||||   ||| |||
                                TACCGCTGC   CGG TGG
                                        ___   _
GAM90   LOC256118 5'  CACCAAGGTGAAGCCCTGC    2090       T  C  CGCG    _
                                CACCA GG GA    AGCCC GC
                                ||||| || ||    ||||| ||
                                GTGGT CC CT    TCGGG CG
                                   T  A  _____     A
GAM91   FLJ23511  3'  TTAGAATTTATCTTGTTAGA   2093         G     A
                                TTAGAATT ATTTT TTAGA
                                |||||||| ||||| |||||
                                AATCTTAA TAGAA AATCT
                                     A     C
GAM91   LOC152627 5'  TTCATAGAATTGAAGTGAGTTA 2094       T       TTTTA_
          G                      TTCAT AGAATTGA      TTAG
                                |||||  ||||||||      ||||
                                AAGTA TCTTAACT      AATC
                                   _        TCACTC
GAM92   FLJ23511  3'  TTAGAATTTATCTTGTTAGA   2093         G     A
                                TTAGAATT ATTTT TTAGA
                                |||||||| ||||| |||||
                                AATCTTAA TAGAA AATCT
                                     A     C
GAM92   LOC152627 5'  TTCATAGAATTGAAGTGAGTTA 2094       T       TTTTA_
          G                      TTCAT AGAATTGA      TTAG
                                |||||  ||||||||      ||||
                                AAGTA TCTTAACT      AATC
                                   _        TCACTC
GAM93   LAMC1     3'  GGATCATCAAGAACTAAGTTAC 2098           _    TTT
                                GGATCATTAA AATTA   TTAC
                                ||||||||| |||||   ||||
```

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                                CCTAGTAGTT TTGAT   AATG
                                      C    TC_
GAM93   NCALD    3' AGGAAGACTAGGATTATTTTTA 2099      TC   AA
             C                    AGGA  ATTA  ATTATTTTTAC
                                  ||||  ||||  ||||||||||
                                  TCCT  TGAT  TAATAAAAATG
                                    TC    CC
GAM93   CLCA4    3' ATCTTAAAATTATTTTTA    2100     A
                                  ATC TTAAAATTATTTTTA
                                  ||| ||||||||||||||
                                  TAG AATTTTAATAAAAAT
                                   _
GAM94   CANX     3' TGAGGGACAGAGGTGTGAATG  2103     C    T __
                                  TGA GGATA GA  TGTGAATG
                                  ||| ||||| ||  ||||||||
                                  ACT CCTGT CT  ACACTTAC
                                    C    _ CC
GAM94   CD81     3' TAAATGACGGAGTCAGGATG   2104          __ T
                                  TAAATGACGGA  TA GATG
                                  ||||||||||  || ||||
                                  ATTTACTGCCT  GT CTAC
                                         CA  C
GAM94   EHD2     3' AATGACGGATGGATGGA     2105          AT   T
                                  AATGACGGAT  GATG GA
                                  |||||||||  |||| ||
                                  TTACTGCCTA  CTAC CT
                                        C_   _
GAM94   ITGA11   3' TGCGGTCAATGTGAATG     2106     A  ATA
                                  TG CGG   TGATGTGAATG
                                  || |||   ||||||||||
                                  AC GCC   GTTACACTTAC
                                   _   A__
GAM94   LCN1     3' AATGACGGAGGTGCTGGA    2107         TA  A  T
                                  AATGACGGA  TG TG GA
                                  |||||||||  || || ||
                                  TTACTGCCT  AC AC CT
                                        CC  G  _
GAM94   LCN1     3' AATGACGGAGGTGCTGGA    2107         TA  A  T
                                  AATGACGGA  TG TG GA
                                  |||||||||  || || ||
                                  TTACTGCCT  AC AC CT
                                        CC  G  _
GAM94   NRG1     3' ATGACGAATGGTGTGAATG   2108         TA  A
                                  ATGACGGA  TG TGTGAATG
                                  ||||||||  || ||||||||
                                  TACTGCTT  AC ACACTTAC
                                        __  C
GAM94   PDE4C    3' TAAGTGACAGATGTGACTCAAG 2109      A       A   GT__
             A                    TAA TGACGGAT TGAT    GA
                                  ||| |||||||| ||||    ||
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                                ATT ACTGTCTA ACTG    CT
                                  C       C    AGTT
GAM94   MGC5590   3'  AATGACAGGATAGGAAT     2110         ATAT    T
                                AATGACGG    GATG GAAT
                                ||||||||    |||| ||||
                                TTACTGTC    CTAT CTTA
                                     _____    C
GAM94   NMP200    3'  GAGTGAAATGATGTGAAT    2111     CG  T
                                GA  GA ATGATGTGAAT
                                ||  || ||||||||||
                                CT  CT TACTACACTTA
                                 CA  T
GAM94   PDZD2     5'  ATGACGGATGGCCGAATG    2112          ATGATG
                                ATGACGGAT     TGAATG
                                |||||||||     ||||||
                                TACTGCCTA     GCTTAC
                                     CCG___
GAM94   LOC146733 3'  TAAATGACGAGTTTATGGGTG  2113           A__    AT
                                TAAATGACGG   TATG  GTG
                                ||||||||||   ||||  |||
                                ATTTACTGCT   ATAC  CAC
                                     CAA    C_
GAM94   LOC163231 3'  TGATGACGGATTGGGTG     2114     A       A  AT
                                A ATGACGGAT TG  GTG
                                | |||||||||  ||  |||
                                A TACTGCCTA AC  CAC
                                 C        _  C_
GAM94   LOC196812 3'  TAAATATGGATGTGATAATAAA 2115        AC    A    _
          TG                      TAAATG  GGAT TGATG TGAATG
                                ||||||  |||| ||||| ||||||
                                ATTTAT  CCTA ACTAT ATTTAC
                                   A_    C    T
GAM95   ATP1B1    3'  TGAAAGAGCCAAAAAAC     2118       AT
                                TGAA  AGAGCTAAAAAAC
                                ||||  ||||||||||||
                                ACTT  TCTCGGTTTTTTG
                                   __
GAM95   CCNF      3'  TGGGACAGAGCTCTAAAAC   2119     AA       AA
                                TG  ATAGAGCT  AAAAC
                                ||  ||||||||  |||||
                                AC  TGTCTCGA  TTTTG
                                 CC       GA
GAM95   EGR1      3'  TAAAATAGAACCACAAAA    2120            A
                                TGAAATAGAGCTA AAAA
                                |||||||||||| ||||
                                ATTTTATCTTGGT TTTT
                                         G
GAM95   NRG1      3'  TGAAAAGAGCAAAAAAC     2121        T    T
                                TGAAA AGAGC AAAAAAC
                                ||||| ||||| |||||||
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                                ACTTT TCTCG TTTTTTG
                                      _   _
GAM95   OLR1     3' GAAATAGAAGCCTAAAAA    2122          _  A
                                GAAATAGA GCT AAAAA
                                |||||||| ||| |||||
                                CTTTATCT CGG TTTTT
                                     T   A
GAM95   RNMT     3' TGGCACTAAGCTAAAAAAC   2123     AA  A
                                TG  AT GAGCTAAAAAAC
                                ||  || ||||||||||||
                                AC  TG TTCGATTTTTTG
                                 CG  A
GAM95   SCA1     3' TGAAATAGAACCACAAAA    2124           A
                                TGAAATAGAGCTA AAAA
                                |||||||||||| ||||
                                ACTTTATCTTGGT TTTT
                                       G
GAM95   TRPS1    3' TGAAACAGTACTGAAAAAC   2125         A   A
                                TGAAATAG GCT AAAAAC
                                |||||||| ||| ||||||
                                ACTTTGTC TGA TTTTTG
                                     A   C
GAM95   BDG-29   3' TAAAATAAAACTAAAAAA    2126
                                TGAAATAGAGCTAAAAAA
                                ||||||||||||||||||
                                ATTTTATTTTGATTTTTT

GAM95   C13orf1  3' GAAATAGACTGCCAAAAA    2127          __
                                GAAATAGA  GCTAAAAA
                                ||||||||  ||||||||
                                CTTTATCT  CGGTTTTT
                                     GA
GAM95   CNTN5    3' TGAAACAGATCTGCTAAA    2128          ___
                                TGAAATAGA   GCTAAA
                                |||||||||   ||||||
                                ACTTTGTCT   CGATTT
                                      AGA
GAM95   E46L     3' TGAAACAGATTCCAAAAA    2129         G_
                                TGAAATAGA  CTAAAAA
                                |||||||||  |||||||
                                ACTTTGTCT  GGTTTTT
                                      AA
GAM95   ESDN     3' TGAAATAGTTACCAAAAA    2130         A_
                                TGAAATAG  GCTAAAAA
                                ||||||||  ||||||||
                                ACTTTATC  TGGTTTTT
                                     AA
GAM95   FLJ10849 3' TAAAATAAAACTAAAGAAC   2131              A
                                TGAAATAGAGCTAAA AAC
                                |||||||||||||| |||
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                                ATTTTATTTTGATTT TTG
                                        C
GAM95   FLJ13590 5' TGAAATGCACCAAAAAAC   2132      AGA
                                TGAAAT  GCTAAAAAAC
                                ||||||  ||||||||||
                                ACTTTA  TGGTTTTTTG
                                   CG_
GAM95   FLJ23510 5' TGAAATAGAACAAGGAAAC  2133        TAAA
                                TGAAATAGAGC   AAAC
                                ||||||||||   ||||
                                ACTTTATCTTG   TTTG
                                      TTCC
GAM95   FPGT    3' TGAAACAGCCTACCAAAAA   2134       A__
                                TGAAATAG  GCTAAAAA
                                ||||||||  ||||||||
                                ACTTTGTC  TGGTTTTT
                                     GGA
GAM95   LRPPRC   3' TGAAACAGAGCAGGGAAAC  2135        TAAA
                                TGAAATAGAGC   AAAC
                                ||||||||||   ||||
                                ACTTTGTCTCG   TTTG
                                      TCCC
GAM95   MGC2848  3' TGAAACAGGAGCTGAAAA   2136       _  A
                                TGAAATAG AGCT AAAA
                                |||||||| |||| ||||
                                ACTTTGTC TCGA TTTT
                                     C  C
GAM95   PIP5K1C  3' TGAAAAGGAACCAAAAAAC  2137      TA
                                TGAAA  GAGCTAAAAAAC
                                |||||  ||||||||||||
                                ACTTT  CTTGGTTTTTTG
                                   TC
GAM95   PRDM15   3' TGAAATAAAGTTAAAAAA   2138       C
                                TGAAATAGAG TAAAAAA
                                |||||||||| |||||||
                                ACTTTATTTC ATTTTTT
                                      A
GAM95   SEC24A   3' TGAAATATACTAAAAAA    2139      GA
                                TGAAATA  GCTAAAAAA
                                |||||||  |||||||||
                                ACTTTAT  TGATTTTTT
                                     A_
GAM95   SPRY4    3' TAAAATAGAGCTTCAAAA   2140        AA
                                TGAAATAGAGCT  AAAA
                                ||||||||||||  ||||
                                ATTTTATCTCGA  TTTT
                                      AG
GAM95   TIP120A  3' TGAAATAAATGCTACAAAAAC 2141       _  _
                                TGAAATAGA GCTA AAAAAC
                                ||||||||| |||| ||||||
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                                ACTTTATTT CGAT TTTTTG
                                     A   G
GAM95   VRP      3'  TGAAACAGTGCAAAAAAA   2142        A  T
                                TGAAATAG GC AAAAAA
                                |||||||| || ||||||
                                ACTTTGTC CG TTTTTT
                                     A  T
GAM95   LOC144473 3'  TGAAATAAAACCAAGAAAC   2143            A
                                TGAAATAGAGCTAA AAAC
                                |||||||||||||| ||||
                                ACTTTATTTTGGTT TTTG
                                        C
GAM95   LOC144740 5'  TAAAATATGAACTAAAAAA   2144        _
                                TGAAATA GAGCTAAAAAA
                                ||||||| ||||||||||
                                ATTTTAT CTTGATTTTTT
                                     A
GAM95   LOC158187 3'  TGAAACAGAGCCTATGAAAAAA 2145          _____
           C                     TGAAATAGAGCT    AAAAAAC
                                ||||||||||||    |||||||
                                ACTTTGTCTCGG    TTTTTTG
                                      ATAC
GAM95   LOC219653 3'  GAAACAAGAGCTAAGAAAC   2146       _     A
                                GAAATA GAGCTAA AAAC
                                |||||| ||||||| ||||
                                CTTTGT CTCGATT TTTG
                                    T      C
GAM96   F3       5'  GAGTGCGAGGGGGTGCGG    2149     A    T  CTGTTA
                                GA TGCGA GG     GTGCGG
                                || ||||| ||     ||||||
                                CT ACGCT CC     CACGCC
                                 C    C  C_____
GAM96   ITGA4    5'  ATGCGACGGTTGGCCAACGGG  2150          C  TTAGT
                                ATGCGATGG TG    GCGGG
                                ||||||||| ||    |||||
                                TACGCTGCC AC    TGCCC
                                      A  CGGT_
GAM96   L1CAM    3'  GAGTGCGATGCTGGGAGTGGG  2151     A     G   TT   C
                                GA TGCGATG CTG  AGTG GG
                                || ||||||| |||  |||| ||
                                CT ACGCTAC GAC  TCAC CC
                                 C      _   CC   _
GAM96   L1CAM    3'  GAGTGCGATGCTGGGAGTGGG  2151     A     G   TT   C
                                GA TGCGATG CTG  AGTG GG
                                || ||||||| |||  |||| ||
                                CT ACGCTAC GAC  TCAC CC
                                 C      _   CC   _
GAM96   RDS      3'  TGTGATGGCCACCTGTGTGGG  2152     C     TG TA   C
                                TG GATGGC  T  GTG GGG
                                || ||||||  |  ||| |||
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                                AC CTACCG  G  CAC CCC
                                 A     GT GA   A
GAM96   DKFZp762K222 5'  TGGATGGCTGGGTGGG     2153     C      TTA   C
                                TG GATGGCTG   GTG GG
                                || ||||||||   ||| ||
                                AC CTACCGAC   CAC CC
                                 _       C__   _
GAM96   FLJ10634  3'  TGGATGGCTGGAGCTGGG    2154     C      TT   GC
                                TG GATGGCTG  AGT  GGG
                                || ||||||||  |||  |||
                                AC CTACCGAC  TCG  CCC
                                 _       C_   A_
GAM96   HHLA2     3'  ATGCGATGCTTGGCTTGGG   2155         G  GTTA  GC
                                ATGCGATG CT    GT  GGG
                                |||||||| ||    ||  |||
                                TACGCTAC GA    CG  CCC
                                     _ AC__  AA
GAM96   KIAA0329  3'  GCGGTGCGGTGCAGTGCGG   2156     ATG  T  _
                                GCG   GC GT TAGTGCGG
                                |||   || || ||||||||
                                CGC   CG CA GTCACGCC
                                  CA_  C  C
GAM96   LOC147807 3'  GCGATGGCCGGGGGTGTGGG  2157          TTA   C
                                GCGATGGCTG   GTG GGG
                                ||||||||||   ||| |||
                                CGCTACCGGC   CAC CCC
                                      CCC   A
GAM96   LOC200734 3'  TGGCTGCTGCAGTGTGGG    2158         __    C
                                TGGCTGT  TAGTG GGG
                                |||||||  ||||| |||
                                ACCGACG  GTCAC CCC
                                    AC    A
GAM96   LOC222776 5'  GAATGCGGGGCTAAGGAGTGTG 2159        AT    TT_   C
          GG                    GAATGCG  GGCTG   AGTG GGG
                                |||||||  |||||   |||| |||
                                CTTACGC  CCGAT   TCAC CCC
                                    C_    TCC    A
GAM97   ACTB      3'  AAAAACCAAAACAAAACAA   2162           CTGT
                                AAAAACTAAAAC    AGAACAA
                                ||||||||||||   |||||||
                                TTTTTGGTTTTG    TTTTGTT
                                      _____
GAM97   ADAM17    3'  AAAAACTAAAACCTGAAA    2163             T
                                AAAAACTAAAACCTG AGA
                                |||||||||||||| |||
                                TTTTTGATTTTGGAC TTT
                                      _
GAM97   ADAM17    3'  AAAAACTAAAACCTGAAA    2163             T
                                AAAAACTAAAACCTG AGA
                                |||||||||||||| |||
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                                TTTTTGATTTTGGAC TTT
                                     _
GAM97   BACH2    3'  AAAAACAAAAACCCAGAGGCAG 2164       T     ____
                                AAAAAC AAAACCT    GTAG
                                |||||| |||||||    ||||
                                TTTTTG TTTTGGG    CGTC
                                   T      TCTC
GAM97   BCL6     3'  AAACTGAAAACTAGAACAAA  2165      _    CTG
                                AAACT AAAAC   TAGAACAAA
                                ||||| |||||   |||||||||
                                TTTGA TTTTG   ATCTTGTTT
                                  C    ___
GAM97   BCL6     3'  AAACTGAAAACTAGAACAAA  2165      _    CTG
                                AAACT AAAAC   TAGAACAAA
                                ||||| |||||   |||||||||
                                TTTGA TTTTG   ATCTTGTTT
                                  C    ___
GAM97   CDKN1B   5'  AAAAACAAAACCGAACAA    2166       T    TGTA
                                AAAAAC AAAACC    GAACAA
                                |||||| ||||||    ||||||
                                TTTTTG TTTTGG    CTTGTT
                                     _    ____
GAM97   CDYL     3'  AAAACCAAAACTGTCTATAAA 2167          ___
                                AAAACTAAAAC   CTGTAGA
                                ||||||||||   |||||||
                                TTTTGGTTTTG   GATATTT
                                      ACA
GAM97   CXCL13   3'  AAAACTAAAATCCAGAGCAG  2168         _ T__
                                AAAACTAAAA CC   GTAG
                                |||||||||| ||   ||||
                                TTTTGATTTT GG   CGTC
                                     A  TCT
GAM97   DDX3     3'  AAAACTGCACTGTAGAGCA   2169       AAAAC     A
                                AAAACT    CTGTAGA CA
                                ||||||    ||||||| ||
                                TTTTGA    GACATCT GT
                                   CGT__      C
GAM97   DSG1     3'  AAAAACAAAACCTGAAA     2170       T      T
                                AAAAAC AAAACCTG AGA
                                |||||| |||||||| |||
                                TTTTTG TTTTGGAC TTT
                                     _      _
GAM97   ELAVL2   5'  AAAAACAAACCAAGGAACAAA 2171       TA    TGTA
                                AAAAAC  AAACC   GAACAAA
                                ||||||  |||||   |||||||
                                TTTTTG  TTTGG   CTTGTTT
                                   __    TTC_
GAM97   FZD10    3'  AAAACCAAAACAAAACAA    2172          CTGT
                                AAAACTAAAAC   AGAACAA
                                ||||||||||   |||||||
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                                TTTTGGTTTTG   TTTTGTT
                                     ____
GAM97   IGF1    3' AAAAACAAAACCAAGAAACAAA 2173       T    TGTA
                                AAAAAC AAAACC   GAACAAA
                                |||||| ||||||   |||||||
                                TTTTTG TTTTGG   TTTGTTT
                                   _    TTC_
GAM97   LTB4R   5' AAAAACTAAAAATTCCTGGCAG 2174          ___  _
                                AAAAACTAAAA  CCTG TAG
                                ||||||||||  |||| |||
                                TTTTTGATTTT  GGAC GTC
                                      TAA   C
GAM97   MAK     3' AAAACTAAAACACTCTAAA  2175          _ G
                                AAAACTAAAAC CT TAGA
                                |||||||||| || ||||
                                TTTTGATTTTG GA ATTT
                                      T  G
GAM97   MTR     3' AAAAACCAAAACAAAACAA  2162          CTGT
                                AAAAACTAAAAC   AGAACAA
                                ||||||||||   |||||||
                                TTTTTGGTTTTG   TTTTGTT
                                     ____
GAM97   NAV2    3' AAAAACCAAAACTGAGCAG  2176          CT_
                                AAAAACTAAAAC  GTAG
                                ||||||||||  ||||
                                TTTTTGGTTTTG  CGTC
                                      ACT
GAM97   SEDL    3' AAAAACAAAAACCCACAAA  2177       T    TG
                                AAAAAC AAAACC  TAGA
                                |||||| ||||||  ||||
                                TTTTTG TTTTGG  GTTT
                                   T    GT
GAM97   SHANK2  3' AAAGACTGTGGAATGTAGAACA 2178     A  AAAACC
          A                     AAA ACT    TGTAGAACAA
                                ||| |||     ||||||||||
                                TTT TGA     ACATCTTGTT
                                  C  CACCTT
GAM97   SLC19A2 3' ACTAAACCAGAACAAA     2179       A  TGT
                                ACTAAA CC  AGAACAAA
                                |||||| ||  ||||||||
                                TGATTT GG  TCTTGTTT
                                     _ ___
GAM97   SMARCA1 3' AAAAGCTAAAACCTCAGCACAA 2180     A      G  A
                                AAAA CTAAAACCT TAG ACAA
                                |||| ||||||||| ||| ||||
                                TTTT GATTTTGGA GTC TGTT
                                  C       _  G
GAM97   SMARCA1 3' AAAAGCTAAAACCTCAGCACAA 2180     A      G  A
                                AAAA CTAAAACCT TAG ACAA
                                |||| ||||||||| ||| ||||
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                                TTTT GATTTTGGA GTC TGTT
                                  C       _  G
GAM97   SMS     3'  AAAAACAAAAGCCCACAGA   2181       T   A  TG
                                AAAAAC AAA CC  TAGA
                                |||||| ||| ||  ||||
                                TTTTTG TTT GG  GTCT
                                   T   C  GT
GAM97   SRRM1   3'  AAAATCAAAACCAAAAAAACAA 2182      C      TGT
            A                    AAAA TAAAACC   AGAACAAA
                                |||| |||||||   ||||||||
                                TTTT GTTTTGG   TTTTGTTT
                                  A      TTT
GAM97   TRHDE   3'  GAAAAATATGTAGAACAA    2183    T    CC
                                C AAAA  TGTAGAACAA
                                | ||||  ||||||||||
                                C TTTT  ACATCTTGTT
                                 T    AT
GAM97   WHSC1   3'  GGAAACCAAAACTACCTCCGAA 2184    A        __ GTA
            CAAA                   A AAACTAAAAC  CT   GAACAAA
                                | ||||||||||  ||   |||||||
                                C TTTGGTTTTG  GG   CTTGTTT
                                 C        AT  AGG
GAM97   A4GALT  3'  AACCAAAACCAGAAAAGAACAA 2185          TGT__
            A                    AACTAAAACC    AGAACAAA
                                ||||||||||    ||||||||
                                TTGGTTTTGG    TCTTGTTT
                                      TCTTT
GAM97   ALS2CR7 3'  AAAACCGAAACTGCAGA    2186       TA   C
                                AAAAC  AAAC TGTAGA
                                |||||  |||| ||||||
                                TTTTG  TTTG ACGTCT
                                   GC   _
GAM97   ARHGEF11 5'  AAAAACTACGACCTTCTCAGA  2187         AA   G__
                                AAAAACTA  ACCT   TAGA
                                ||||||||  ||||   ||||
                                TTTTTGAT  TGGA   GTCT
                                     GC    AGA
GAM97   ATP10D  3'  AAAACTAAACCCTGAGA    2188          A   T
                                AAAACTAAA CCTG AGA
                                ||||||||| |||| |||
                                TTTTGATTT GGAC TCT
                                      G   _
GAM97   C1orf16 3'  AAAAACAAAACCCAGAAAACAA 2189        T      GT
            A                    AAAAAC AAAACCT  AGAACAAA
                                |||||| |||||||  ||||||||
                                TTTTTG TTTTGGG  TTTTGTTT
                                   _      TC
GAM97   CPEB1   3'  AAAACAAAACCTGACAA     2190       T      TAGA
                                AAAAC AAAACCTG    ACAA
                                ||||| ||||||||    ||||
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                                TTTTG TTTTGGAC    TGTT
                                  _     ____
GAM97   DNAJA2   3' AAAAACAAAACCAAAAACAAA 2191       T     TGT
                                AAAAAC AAAACC   AGAACAAA
                                |||||| ||||||   ||||||||
                                TTTTTG TTTTGG   TTTTGTTT
                                  _     T__
GAM97   FLJ10297 3' AAAAACCAAAACAAAACA    2192           CTGT
                                AAAAACTAAAAC    AGAACA
                                ||||||||||||    ||||||
                                TTTTTGGTTTTG    TTTTGT
                                      ____
GAM97   FLJ10813 3' AAAAACTAACTCTAGAACA   2193          AAC  G
                                AAAAACTAA   CT TAGAACA
                                |||||||||   || |||||||
                                TTTTTGATT   GA ATCTTGT
                                    ___  G
GAM97   FLJ11850 3' AAAAACAAAACACATAGACAA 2194       T    C     A
                                AAAAAC AAAAC TGTAGA CAA
                                |||||| ||||| ||||||| |||
                                TTTTTG TTTTG GTATCT GTT
                                  _    T     _
GAM97   FLJ13449 3' AAAAACAAAACCAAAAACAAA 2191       T     TGT
                                AAAAAC AAAACC   AGAACAAA
                                |||||| ||||||   ||||||||
                                TTTTTG TTTTGG   TTTTGTTT
                                  _     T__
GAM97   FLJ14281 3' AAAAACTTAAACAAAGAACAAA 2195        A    CTGT
                                AAAAACT AAAC    AGAACAAA
                                |||||||| ||||    ||||||||
                                TTTTTGA TTTG    TCTTGTTT
                                   A    TT__
GAM97   FLJ20308 3' AAAAACAAAACCCTCAAAACAA 2196       T      G
          A                      AAAAAC AAAACCT TAGAACAAA
                                |||||| ||||||| |||||||||
                                TTTTTG TTTTGGG GTTTTGTTT
                                  _      A
GAM97   FLJ21290 5' AAAAGCCAAAACCCACAG    2197      A       TG
                                AAAA CTAAAACC  TAG
                                |||| ||||||||  |||
                                TTTT GGTTTTGG  GTC
                                  C       GT
GAM97   KIAA0630 3' AAAACTGAAACTCTGTAA    2198        A   _
                                AAAACT AAAC CTGTAG
                                |||||| |||| ||||||
                                TTTTGA TTTG GACATT
                                   C    A
GAM97   KIAA1209 3' AAAACCTAAAGCCATGTAGA  2199      A    A  _
                                AAAA CTAAA CC TGTAGA
                                |||| ||||| || ||||||
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                                TTTT GATTT GG ACATCT
                                  G    C  T
GAM97   KIAA1384 3' AAAAAATAAAATGCAGAACAA 2200      C    CC
                                AAAAA TAAAA  TGTAGAACAA
                                ||||| |||||  ||||||||||
                                TTTTT ATTTT  ACGTCTTGTT
                                   T    __
GAM97   KIAA1437 3' AAAAACTAAAACTGCCACAAA 2201          C   AGA
                                AAAAACTAAAAC TGT   ACAAA
                                |||||||||||| |||   |||||
                                TTTTTGATTTTG ACG   TGTTT
                                       _   G__
GAM97   KIAA1473 3' AAAAACTAAAACTGTACAA   2202          C   G
                                AAAAACTAAAAC TGTA AA
                                |||||||||||| ||||| ||
                                TTTTTGATTTTG ACAT TT
                                       _   G
GAM97   KIAA1598 3' AAAAACCAAAACCTACTAG   2203            _
                                AAAAACTAAAACCTG TAG
                                |||||||||||||| |||
                                TTTTTGGTTTTGGAT ATC
                                       G
GAM97   KIAA1724 3' AAAAACTAAAATATGCAAA   2204          CC
                                AAAAACTAAAA  TGTAGA
                                ||||||||||  ||||||
                                TTTTTGATTTT  ACGTTT
                                      AT
GAM97   KIAA1819 5' AAAAACCAAAACAAAACAA   2162          CTGT
                                AAAAACTAAAAC    AGAACAA
                                ||||||||||||    |||||||
                                TTTTTGGTTTTG    TTTTGTT
                                       ____
GAM97   KIAA1858 3' AAAAACTAAACAATAGAGCAAA 2205         ACCT    A
                                AAAAACTAAA    GTAGA CAAA
                                ||||||||||    ||||| ||||
                                TTTTTGATTT    TATCT GTTT
                                      GT__    C
GAM97   LUC7L    3' AAAAACAAAAACCAAAACA   2206       T    TGT
                                AAAAAC AAAACC   AGAACA
                                |||||| ||||||   ||||||
                                TTTTTG TTTTGG   TTTTGT
                                   T    ___
GAM97   MGC23937 3' CTAAAACCAAACTAAACAAA  2207        TGTA_
                                CTAAAACC    GAACAAA
                                ||||||||    |||||||
                                GATTTTGG    TTTGTTT
                                     TTTGA
GAM97   MKRN1    3' ACCAAAACCACAGAACAA    2208         TGT
                                ACTAAAACC   AGAACAA
                                |||||||||   |||||||
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                                TGGTTTTGG  TCTTGTT
                                     TG_
GAM97   MMRN    3'  AAAAACCAAAACAGAGCAGA  2209          CT_
                                AAAAACTAAAAC  GTAGA
                                ||||||||||||  |||||
                                TTTTTGGTTTTG  CGTCT
                                    TCT
GAM97   MRPL56  3'  AAAAACTAATAACACGTAAACA 2210        _  C    A
          AA                    AAAAACTAA AAC TGTAGA CAAA
                                |||||||||| ||| |||||| ||||
                                TTTTTGATT TTG GCATTT GTTT
                                     A  T    _
GAM97   PANK    3'  AACTAAAACAGAAAAACAA   2211        CTGT
                                AACTAAAAC   AGAACAA
                                |||||||||   |||||||
                                TTGATTTTG   TTTTGTT
                                     TCT_
GAM97   PRO0132 5'  TGAAACTGAGAACAGTAGAACA 2212   A    AA_  CT
                                A AAACT  AAC  GTAGAACA
                                | |||||  |||  ||||||||
                                A TTTGA  TTG  CATCTTGT
                                 C   CTC  T_
GAM97   RALGPS1A 3'  AAAAACAGAAACCTATGGAGCA 2213       TA      A  A
                                AAAAAC  AAACCTGT GA CA
                                ||||||  |||||||| || ||
                                TTTTTG  TTTGGATA CT GT
                                   TC       C  C
GAM97   RNF8    3'  AAACCAAAACCAAGACACAA  2214         TGT  _
                                AAACTAAAACC  AGA ACAA
                                ||||||||||  ||| ||||
                                TTTGGTTTTGG  TCT TGTT
                                     T__  G
GAM97   SEC63L  3'  AAAACTAAAGCTGAACAA   2215        ACCT  A
                                AAAACTAAA   GT GAACAA
                                |||||||||   || ||||||
                                TTTTGATTT   CG CTTGTT
                                     ____  A
GAM97   TBLR1   3'  AAAAACAAAACCAACAGA   2216       T    TG
                                AAAAAC AAAACC  TAGA
                                |||||| ||||||  ||||
                                TTTTTG TTTTGG  GTCT
                                   _     TT
GAM97   TOB2    3'  AAAAACAAAACTGCAGA    2217       T   C
                                AAAAAC AAAAC TGTAGA
                                |||||| ||||| ||||||
                                TTTTTG TTTTG ACGTCT
                                   _   _
GAM97   TSGA14  3'  AAAAACTAAAAACGTAGA   2218         CC
                                AAAAACTAAAA  TGTAGA
                                ||||||||||  ||||||
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                                TTTTTGATTTT  GCATCT
                                      T_
GAM97   ZNF220   3' AAAACCAAAACCCACAACAAA 2219          TG  GA
                                AAAACTAAAACC  TA  ACAAA
                                ||||||||||||  ||  |||||
                                TTTTGGTTTTGG  GT  TGTTT
                                      GT  __
GAM97   ZNF297B  3' AAAGACTAAAACCAGACAACA 2220     A       TGTAG
                                AAA ACTAAAACC     AACA
                                ||| |||||||||     ||||
                                TTT TGATTTTGG     TTGT
                                  C       TCTG_
GAM97   ZNF297B  3' AAAGACTAAAACCAGACAACA 2220     A       TGTAG
                                AAA ACTAAAACC     AACA
                                ||| |||||||||     ||||
                                TTT TGATTTTGG     TTGT
                                  C       TCTG_
GAM97   LOC147353 3' AAAACTAAGAACCTACTCAGA 2221        _     __
                                AAAACTAA AACCTG  TAGA
                                ||||||||| ||||||  ||||
                                TTTTGATT TTGGAT  GTCT
                                     C     GA
GAM97   LOC147429 3' AAAACTAAAAACCTGAAA    2222         _   T
                                AAAACTAAAA CCTG AGA
                                |||||||||| |||| |||
                                TTTTGATTTT GGAC TTT
                                      T   _
GAM97   LOC148198 3' AAAAACTAAAACTGTACAA   2202          C   G
                                AAAAACTAAAAC TGTA AA
                                |||||||||||| |||| ||
                                TTTTTGATTTTG ACAT TT
                                      _   G
GAM97   LOC150159 3' AAAACTAAAACCAGCAAA    2223          T
                                AAAACTAAAACC GTAGA
                                |||||||||||| |||||
                                TTTTGATTTTGG CGTTT
                                       T
GAM97   LOC169026 3' AAAAACTAAACCGCAGA     2224         A  T
                                AAAAACTAAA CC GTAGA
                                |||||||||| || |||||
                                TTTTTGATTT GG CGTCT
                                      _ _
GAM97   LOC201626 3' AAAAACTAAAATCCTAAAAA  2225          _   T
                                AAAAACTAAAA CCTG AGA
                                |||||||||||| |||| |||
                                TTTTTGATTTT GGAT TTT
                                      A   T
GAM97   LOC221576 3' AAAAACTAAAACTATAG     2226          C
                                AAAAACTAAAAC TGTAG
                                |||||||||||| |||||
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                                TTTTTGATTTTG ATATC
                                      _
GAM97   LOC253955 3'  AAAAACCAAAACAAAACAA   2162          CTGT
                                AAAAACTAAAAC   AGAACAA
                                ||||||||||||  |||||||
                                TTTTTGGTTTTG   TTTTGTT
                                     ____
GAM97   LOC254057 3'  AAAGCCAAAAACCAGCAGA    2227     A      T
                                AAA CTAAAACC GTAGA
                                ||| |||||||| |||||
                                TTT GGTTTTGG CGTCT
                                  C       T
GAM97   LOC255533 5'  AAAACTAAAGCAAAACAA    2228         ACCT
                                AAAACTAAA   GTAGAACAA
                                |||||||||   |||||||||
                                TTTTGATTT   CGTTTTGTT
                                     ____
GAM97   LOC257515 3'  AAAAACTAAAACTATAG     2226          C
                                AAAAACTAAAAC TGTAG
                                |||||||||||| |||||
                                TTTTTGATTTTG ATATC
                                      _
GAM97   LOC257572 3'  AAAAACTAAAACTATAG     2226          C
                                AAAAACTAAAAC TGTAG
                                |||||||||||| |||||
                                TTTTTGATTTTG ATATC
                                      _
GAM97   LOC51312  3'  AAAAGCTAAACCTGCAA     2229      A   A
                                AAAA CTAAA CCTGTAG
                                |||| ||||| |||||||
                                TTTT GATTT GGACGTT
                                  C   _
GAM97   LOC56267  3'  AAACTAAAACTTGTTTCCAA  2230         C  AGAA
                                AAACTAAAAC TGT   CAA
                                |||||||||| |||   |||
                                TTTGATTTTG ACA   GTT
                                     A  AAG_
GAM97   LOC91145  3'  CAAAACCCTGTTGTAGAGCAAA 2231        ____   A
                                TAAAACCT   GTAGA CAAA
                                ||||||||   ||||| ||||
                                GTTTTGGG   CATCT GTTT
                                    ACAA   C
GAM97   LOC92597  3'  AAACTGAAACCTATGAA     2232      A      A
                                AAACT AAACCTGT GAA
                                ||||| |||||||| |||
                                TTTGA TTTGGATA CTT
                                  C      _
GAM98   SLC7A7    5'  CTCTTGGCTCAGCACTTTCT   2235       CAATT   ___
                                CTCTTGGT    TCGGT   TTCT
                                ||||||||    |||||   ||||
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                                GAGAACCG    AGTCG   AAGA
                                  _____     TGA
GAM98   ARPC5    3'  CTCTTGGTCAGGTGGTTT    2236          ATTTC
                                CTCTTGGTCA    GGTTT
                                ||||||||||    |||||
                                GAGAACCAGT    CCAAA
                                    CCA__
GAM98   CAP350   3'  CTCTTAGTCAATTTGCTC    2237            CG
                                CTCTTGGTCAATTT  GTTT
                                ||||||||||||||  ||||
                                GAGAATCAGTTAAA  CGAG
                                              __
GAM98   FLJ10856 3'  CTCTTGGTTGAATGATTTTCTA 2238          CAATTTCGG
            T                   CTCTTGGT       TTTCTAT
                                ||||||||       |||||||
                                GAGAACCA       AAAGATA
                                    ACTTACTA_
GAM98   HDAC9-PENDING 3'  TCTAGGTCAATTTGGATT    2239      T       C
                                TCT GGTCAATTT GGTT
                                ||| |||||||| ||||
                                AGA CCAGTTAAA CTAA
                                  T       C
GAM98   KCNMB3L  3'  TCTTGGCAATCCCTGTTT    2240        T    TT G
                                TCTTGG CAAT  C GTTT
                                |||||| ||||  | ||||
                                AGAACC GTTA  G CAAA
                                   _   GG A
GAM98   MGC21675 3'  TCTTGGTTGTTTTCGGCT    2241         CAA
                                TCTTGGT   TTTCGGTT
                                |||||||   ||||||||
                                AGAACCA   AAAGCCGA
                                    ACA
GAM98   PCDH19   3'  CTCTTGGTCATTAAAGTCT    2242           A  TC
                                CTCTTGGTCA TT  GGTTT
                                |||||||||| ||  |||||
                                GAGAACCAGT AA  TCAGA
                                      _  TT
GAM98   PRO1728  5'  TCTTGGCAAAATATTTCTAT   2243        T   TTTCG
                                TCTTGG CAA    GTTTCTAT
                                |||||| |||    ||||||||
                                AGAACC GTT    TAAAGATA
                                   _   TTA__
GAM98   LOC155100 3'  TCTTGGCAATCCCTGTTT    2240        T    TT G
                                TCTTGG CAAT  C GTTT
                                |||||| ||||  | ||||
                                AGAACC GTTA  G CAAA
                                   _   GG A
GAM98   LOC158629 5'  CTCTTGGCAATTTATTATTT   2244         T     CG_
                                CTCTTGG CAATTT   GTTT
                                ||||||| ||||||   ||||
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                                GAGAACC GTTAAA   TAAA
                                   _     TAA
GAM98   LOC253841 3'  CCTTGGTCTTGGTTTCTA    2245        AATTTC
                                TCTTGGTC     GGTTTCTA
                                ||||||||     ||||||||
                                GGAACCAG     CCAAAGAT
                                   AA____
GAM99   RFXAP    3'  TTTAAAGTTTTAAAGTTTTC   2248          AATT
                                TTTAAAGTTTTA    GAGTTTTC
                                ||||||||||||    ||||||||
                                AAATTTCAAAAT    TTCAAAAG
                                                ____
GAM99   KIAA1363  3'  AAGTGAAAAAATTGAGTTTTC  2249      TTT_
                                AAGT    AAATTGAGTTTTC
                                ||||    ||||||||||||
                                TTCA    TTTAACTCAAAAG
                                  CTTT
GAM100  NEBL     3'  TTCGAAAATTCATACATGG    2252         AG  A
                                TTCGAGAAT  CG GCATGG
                                |||||||||  || ||||||
                                AAGCTTTTA  GT TGTACC
                                   A_  A
GAM100  PFKFB4   3'  TTCAAGAATATCCCTGCATGG  2253          GCGA_
                                TTCGAGAATA    GCATGG
                                ||||||||||    ||||||
                                AAGTTCTTAT    CGTACC
                                   AGGGA
GAM100  STK31    5'  TTCGAGAAGGGGAAGAGAGTGT 2254         T_____  C   CA
            GG                    TTCGAGAA    AG GAG  TGG
                                ||||||||    || |||  |||
                                AAGCTCTT    TC CTC  ACC
                                   CCCCT  T   AC
GAM100  XT3      3'  TCGAGAATGGAGAATGG     2255         AGC   C
                                TCGAGAAT   GAG ATGG
                                ||||||||   ||| ||||
                                AGCTCTTA   CTC TACC
                                   C__   T
GAM100  B3GALT1  5'  TTCAGGAAATCAAGCATGG   2256      A   TAG
                                TTCG GAA   CGAGCATGG
                                ||||  |||   |||||||||
                                AAGT CTT   GTTCGTACC
                                  C   TA_
GAM100  CHST4    3'  TTCTAGACACAAGCATGG    2257     G   ATA
                                TTC AGA   GCGAGCATGG
                                |||  |||   ||||||||||
                                AAG TCT   TGTTCGTACC
                                  A   G__
GAM100  FLJ12899  3'  CGAGATAAGAGCATGG      2258       A   C
                                CGAGA TAG GAGCATGG
                                |||||  |||  ||||||||
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                                GCTCT ATT CTCGTACC
                                  _  _
GAM100  FLJ20558  3'  GAGAACAGAATAAAGAGCGTGG 2259        C_____   A  III
            C                    GAGAATAG    GAGC TGG  C
                                 ||||||||    |||| |||  |
                                 CTCTTGTC    CTCG ACC  G
                                     TTATTT   C  III
GAM100  FLJ25415  3'  TTCGAAAATAGATATGG    2260          CGAGC
                                 TTCGAGAATAG    ATGG
                                 ||||||||||    ||||
                                 AAGCTTTTATC    TACC
                                       TA___
GAM100  KIAA1014  3'  GAGAATAAAGGCAGCATGG   2261        ___  G
                                 GAGAATA   GC AGCATGG
                                 |||||||   || |||||||
                                 CTCTTAT   CG TCGTACC
                                     TTC  _
GAM100  KIAA1204  3'  TTCCAGGGAAAGAGCATGG   2262     G  AAT  C
                                 TTC AG   AG GAGCATGG
                                 ||| ||   || ||||||||
                                 AAG TC   TT CTCGTACC
                                   G  CCT  _
GAM100  KOC1      3'  TTCAGAGAGCAGCGTGG     2263     _   A    AGCA
                                 TTC GAGA TAGCG   TGG
                                 ||| |||| |||||   |||
                                 AAG CTCT GTCGC   ACC
                                   T   C    _____
GAM100  MGC3222   5'  TTCGAAAATCCGCGTGG     2264         A_  AGCA
                                 TTCGAGAAT  GCG   TGG
                                 |||||||||  |||   |||
                                 AAGCTTTTA  CGC   ACC
                                      GG  _____
GAM100  PTR4      5'  TTCAGGAATAGCACCAGG    2265      A      AG  T
                                 TTCG GAATAGCG  CA GG
                                 |||| ||||||||  || ||
                                 AAGT CTTATCGT  GT CC
                                   C       G_  _
GAM100  LOC124944 3'  CGGGAATAGCGAGGTGG     2266     A        CA
                                 CG GAATAGCGAG  TGG
                                 || ||||||||||  |||
                                 GC CTTATCGCTC  ACC
                                  C        C_
GAM100  LOC165229 5'  GAGAATAGCGAACTGTGG    2267           A_
                                 GAGAATAGCGAGC  TGG
                                 ||||||||||||  |||
                                 CTCTTATCGCTTG  ACC
                                        AC
GAM100  LOC219914 5'  TTCAAGAATGAAGCCGTGG   2268         AGC   A_
                                 TTCGAGAAT   GAGC  TGG
                                 |||||||||   ||||  |||
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                                AAGTTCTTA  TTCG  ACC
                                    C__   GC
GAM100  LOC219914 3'  TTCAAGAATGAAGCCATGG   2269        AGC   _
                                TTCGAGAAT  GAGC ATGG
                                |||||||||  |||| ||||
                                AAGTTCTTA  TTCG TACC
                                    C__   G
GAM100  LOC257355 3'  CTCTCCAGCGAGCATGG    2270    GAGAA
                                TTC    TAGCGAGCATGG
                                |||    ||||||||||||
                                GAG    GTCGCTCGTACC
                                  AG___
GAM100  LOC51172  3'  CTCTCCAGCGAGCATGG    2270    GAGAA
                                TTC    TAGCGAGCATGG
                                |||    ||||||||||||
                                GAG    GTCGCTCGTACC
                                  AG___
GAM101  ENAM    5'  TGAAATATATTCTTAATGGTC  2273       TTA  AAC
                                TGAAATAT  TCT  AATGGTC
                                ||||||||  |||  |||||||
                                ACTTTATA  AGA  TTACCAG
                                    TA_  A__
GAM101  FDX1    3'  TGAAATATTTATTTATAAGGTC 2274         C  ACAAT
                                TGAAATATTTAT TA    GGTC
                                ||||||||||||| ||    ||||
                                ACTTTATAAATA AT    CCAG
                                     A  ATT__
GAM101  PRKACB  3'  TATTTATCTAAACCAATG   2275         __
                                TATTTATCTAA  CAATG
                                ||||||||||  |||||
                                ATAAATAGATT  GTTAC
                                     TG
GAM101  RAD54B  3'  TGAAATATTTAACTAGGC   2276         T  ACAAT
                                TGAAATATTTA CTA    GGT
                                |||||||||| |||    |||
                                ACTTTATAAAT GAT    CCG
                                     T  _____
GAM101  SLC6A8  3'  TGAAATATTTGCCTTGGT   2277       AT  AACAA
                                TGAAATATTT  CT    TGGT
                                |||||||||  ||    ||||
                                ACTTTATAAA  GA    ACCA
                                    CG  _____
GAM101  UGT2B4  3'  TGAAATATTTCTAATGGT   2278       TA   ACA
                                TGAAATATT  TCTA  ATGGT
                                |||||||||  ||||  |||||
                                ACTTTATAA  AGAT  TACCA
                                    __  ___
GAM101  FLJ12085 3'  TGAAATATTTATCTACACA  2279          _
                                TGAAATATTTATCTA ACA
                                ||||||||||||||| |||
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                                ACTTTATAAATAGAT TGT
                                       G
GAM101  FLJ13111  3'  GAAATATTTATCTAGGC     2280            ACAAT
                                GAAATATTTATCTA    GGT
                                |||||||||||||    |||
                                CTTTATAAATAGAT    CCG
                                      _____
GAM101  FLJ21369  3'  TGAAGAATTTATATCCAATGGT 2281      AT     CTAA
          C                    TGAA  ATTTAT    CAATGGTC
                               ||||  ||||||    ||||||||
                               ACTT  TAAATA    GTTACCAG
                                 CT     TAG_
GAM101  PPFIBP2   3'  TCCACCTTTGGCAATGGTC   2282        AA__
                               TTTATCT    CAATGGTC
                               |||||||    ||||||||
                               AGGTGGA    GTTACCAG
                                   AACC
GAM101  LOC120892 3'  ATATTTATCCTCATGGTC    2283          AACA
                               ATATTTATCT    ATGGTC
                               ||||||||||    ||||||
                               TATAAATAGG    TACCAG
                                     AG__
GAM101  LOC146488 3'  TGAAATATTTGTCTTGGT    2284          A   AACAA
                               TGAAATATTT TCT     TGGT
                               |||||||||| |||     ||||
                               ACTTTATAAA AGA     ACCA
                                     C  _____
GAM102  CITED2    3'  TGGGGGTTTGATTTCTT     2287      AGTAC   _
                               TGG     GGTT GATTTCTT
                               |||     |||| ||||||||
                               ACC     CCAA CTAAAGAA
                                 C____    A
GAM102  LOC149670 3'  GTGGAGTTAAGATTTCTTT    2288        ACGGTT
                               GTGGAGT     GATTTCTTT
                               |||||||     |||||||||
                               CACCTCA     CTAAAGAAA
                                   ATT___
GAM102  LOC85479  5'  CGTGGGCGTTGTTGATTTCTTT 2289       A  ACG
                               CGTGG GT   GTTGATTTCTTT
                               ||||| ||   ||||||||||||
                               GCACC CG   CAACTAAAGAAA
                                  _ CAA
GAM103  CYP8B1    3'  TATGTTGGATGACACTG     2292       AGAC
                               TATGT    GATGACACTG
                               |||||    ||||||||||
                               ATACA    CTACTGTGAC
                                  AC__
GAM103  ENTPD6    3'  TATGCAGACACACAGACACTG  2293          AT__
                               TATGTAGACG    GACACTG
                               ||||||||||    |||||||
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                                ATACGTCTGT   CTGTGAC
                                     GTGT
GAM103  IFNAR2   3'  TATGTAAACAATGCACTG    2294          A
                                TATGTAGACGATG CACTG
                                |||||||||||| |||||
                                ATACATTTGTTAC GTGAC
                                          _
GAM103  PDLIM1   3'  TGCTGACAAGGTGACACTG   2295     A    __
                                TGT GACGA  TGACACTG
                                ||| |||||  ||||||||
                                ACG CTGTT  ACTGTGAC
                                  A    CC
GAM103  RAP1     3'  TATGTAGACCAACTCCTG    2296         GAT  A_
                                TATGTAGAC   GAC  CTG
                                |||||||||   |||  |||
                                ATACATCTG   TTG  GAC
                                     G__   AG
GAM103  ZNF264   3'  TATGTGCACAATAACCACTG  2297       AG      _
                                TATGT  ACGATGAC ACTG
                                |||||  |||||||| ||||
                                ATACA  TGTTATTG TGAC
                                   CG       G
GAM103  C1orf22  3'  TATGCAGAGAACTCACTG    2298         C   GA
                                TATGTAGA GAT  CACTG
                                |||||||| |||  |||||
                                ATACGTCT TTG  GTGAC
                                     C   A_
GAM103  C20orf42 3'  TGTGGACAGATGACACTG    2299      A   _
                                TGT GAC GATGACACTG
                                ||| ||| ||||||||||
                                ACA CTG CTACTGTGAC
                                  C   T
GAM103  DKFZP434F2021 3'  ATGTAGACTGAACTG       2300         GA   C
                                ATGTAGAC  TGA ACTG
                                ||||||||  ||| ||||
                                TACATCTG  ACT TGAC
                                     __   _
GAM103  DKFZP434N014 3'  TATATAAATACAATGACACTG  2301         __
                                TATGTAG  ACGATGACACTG
                                |||||||  ||||||||||||
                                ATATATT  TGTTACTGTGAC
                                     TA
GAM103  KIAA0993 3'  TATGTAGGAACAACACTG    2302         AC  TG
                                TATGTAG  GA  ACACTG
                                |||||||  ||  ||||||
                                ATACATC  TT  TGTGAC
                                     C_  GT
GAM103  MGC23980 3'  TATGAAAGGCTGACACTG    2303       T   CGA
                                TATG AGA   TGACACTG
                                |||| |||   ||||||||
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                                ATAC TTT   ACTGTGAC
                                  _  CCG
GAM103  PLAGL2   3'  TGTAAACAGTGTTCACTG    2304        A  A_
                                TGTAGACG TG  CACTG
                                |||||||| ||  |||||
                                ACATTTGT AC  GTGAC
                                     C  AA
GAM103  LOC147353 3'  TGTAGACAGTATCTGACACTG  2305       GA____
                                TGTAGAC     TGACACTG
                                |||||||     ||||||||
                                ACATCTG     ACTGTGAC
                                    TCATAG
GAM103  LOC148183 3'  TGTAGCACAGGTGACACTG   2306      _  A_
                                TGTAG ACG  TGACACTG
                                ||||| |||  ||||||||
                                ACATC TGT  ACTGTGAC
                                   G   CC
GAM103  LOC161742 3'  TATGTAAATAATAAGCACTG  2307       CG  _
                                TATGTAGA  ATGA CACTG
                                ||||||||  |||| |||||
                                ATACATTT  TATT GTGAC
                                     AT   C
GAM103  LOC196264 3'  TGTAAATTGATGACACTG    2308      C_
                                TGTAGA  GATGACACTG
                                ||||||  ||||||||||
                                ACATTT  CTACTGTGAC
                                    AA
GAM103  LOC196478 5'  CATGTAGATTCTGCCACTG   2309       CGA  A
                                TATGTAGA   TG CACTG
                                ||||||||   || |||||
                                GTACATCT   AC GTGAC
                                     AAG  G
GAM103  LOC202934 3'  TATGCAGACTATACCACTG   2310       G   A
                                TATGTAGAC ATG CACTG
                                ||||||||| ||| |||||
                                ATACGTCTG TAT GTGAC
                                      A   G
GAM104  FOSB     3'  GCAACAGTGCAGAACCA     2313       AA
                                GCAACAGT  CAGAACCA
                                ||||||||  ||||||||
                                CGTTGTCA  GTCTTGGT
                                     C_
GAM104  SCEL     3'  TTATGCAATAACAGAA      2314       ACA
                                TTATGCA   GTAACAGAA
                                |||||||   |||||||||
                                AATACGT   TATTGTCTT
                                          ___
GAM104  WNT5A    3'  CATTATGCAATAAATTAAGAGC 2315        C  TAAC   A
            CA                    TATTATGCAA AG    AGA CCA
                                ||||||||||  ||    ||| |||
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                                GTAATACGTT TT    TCT GGT
                                     A  TAAT   C
GAM104  WNT5A    3'  CATTATGCAATAAATTAAAGAG 2316          CAG__   C   A
            CCA                    TATTATGCAA    TAA AGA CCA
                                |||||||||||    ||| ||| |||
                                GTAATACGTT    ATT TCT GGT
                                     ATTTA   _   C
GAM104  ABCA8    3'  TATTATACAGAACAATGGAACC 2317          __    AACA
            A                   TATTATGCA  ACAGT   GAACCA
                                |||||||||  |||||   ||||||
                                ATAATATGT  TGTTA   CTTGGT
                                     CT    C___
GAM104  ANKRD6   3'  TATTATGCAGTTGCAAAAC   2318          ACA  AA
                                TATTATGCA   GT  CAGAAC
                                |||||||||   ||  ||||||
                                ATAATACGT   CA  GTTTTG
                                     ___  AC
GAM104  ATP9A    3'  TATTGGGCAACAGCAACGAGCC 2319       AT        A  A
            A                   TATT  GCAACAGTAAC GA CCA
                                ||||  |||||||||||| || |||
                                ATAA  CGTTGTCGTTG CT GGT
                                  CC          _  C
GAM104  C20orf160 3'  CATTATGCGGCTGCAGAGCCA  2320         AACA  AA    A
                                TATTATGC    GT  CAGA CCA
                                ||||||||    ||  |||| |||
                                GTAATACG    CG  GTCT GGT
                                     C___  AC    C
GAM104  EKN1     3'  TATTTTGCCCTCAACAGAAC   2321       A   AACAG
                                TATT TGC    TAACAGAAC
                                |||| |||    |||||||||
                                ATAA ACG    GTTGTCTTG
                                  A   GGA__
GAM104  KIAA0016 3'  TACAGAGTAGTGACAGAACCA  2322       AC__   A
                                TGCA    AGT ACAGAACCA
                                ||||    ||| |||||||||
                                ATGT    TCA TGTCTTGGT
                                  CTCA   C
GAM104  KIAA0125 3'  TGCAACAGATCAAAAGAAC    2323          __   C
                                TGCAACAG  TAA AGAAC
                                ||||||||  ||| |||||
                                ACGTTGTC  GTT TCTTG
                                     TA   T
GAM104  KIAA0372 3'  TATTATGCTTTTTCAACAGAA  2324          AACAG
                                TATTATGC    TAACAGAA
                                ||||||||    ||||||||
                                ATAATACG    GTTGTCTT
                                     AAAAA
GAM104  KIAA1915 3'  CATTGTGCAATAACAAAGACAG 2325       A   ___    TA     C
            AATCA                   TATT TGCA   ACAG  ACAGAA CA
                                |||| ||||   ||||  |||||| ||
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                                GTAA ACGT   TGTT  TGTCTT GT
                                  C    TAT    TC     A
GAM104   XRN2     3'  TATTATGCAACATACA      2326            GTA
                                TATTATGCAACA   ACA
                                ||||||||||||   |||
                                ATAATACGTTGT   TGT
                                       A__
GAM104   LOC146880 3'  TATTATGCCACAGTGAACA    2327         A    _
                                TATTATGC ACAGT AACA
                                |||||||| ||||| ||||
                                ATAATACG TGTCA TTGT
                                     G    C
GAM104   LOC147804 5'  TCATGCACCAGTAGTAGCAGAA 2328         A    A___
                                TTATGCA CAGTA    CAGAA
                                ||||||| |||||    |||||
                                AGTACGT GTCAT    GTCTT
                                    G    CATC
GAM104   LOC150311 5'  TTATGCAACAGAGAAC      2329           TAAC    C
                                TTATGCAACAG    AGAA C
                                ||||||||||||   |||| |
                                AATACGTTGTC    TCTT G
                                      ____    A
GAM104   LOC154215 3'  CATGCAAACACAGTAATGGAAC 2330         ___      CA
                                TATGCA   ACAGTAA  GAAC
                                ||||||   |||||||  ||||
                                GTACGT   TGTCATT  CTTG
                                   TTG      AC
GAM105   CBS      3'  GTCCAGAACAGGGAAAACC    2333             T
                                GTCCAGAATAGGGAAG CC
                                |||||||||||||||| ||
                                CAGGTCTTGTCCCTTT GG
                                          T
GAM105   CD79B    3'  GTCCAGGAAAGGGGTTGGGCCA 2334        AAT    AAGTCC
           T                     GTCCAG   AGGG     GCCAT
                                ||||||   ||||     |||||
                                CAGGTC   TCCC     CGGTA
                                   CTT    CAACC_
GAM105   CD79B    3'  GTCCAGGAAAGGGGTTGGGCCA 2334        AAT    AAGTCC
           T                     GTCCAG   AGGG     GCCAT
                                ||||||   ||||     |||||
                                CAGGTC   TCCC     CGGTA
                                   CTT    CAACC_
GAM105   NRIP1    3'  GTCCAGAAATGGAATACTGTC  2335         TAG   ____
                                GTCCAGAA   GGAA    GTC
                                ||||||||   ||||    |||
                                CAGGTCTT   CCTT    CAG
                                     TA_    ATGA
GAM105   RFX2     3'  GTCCAGAATAAGGAACCCA    2336             G
                                GTCCAGAATAGGGAA TCCG
                                |||||||||||||| ||||
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                                CAGGTCTTATTCCTT GGGT
                                                _
GAM105  KIAA1323  3'  GTCCAAATAGGGCAATGTC   2337       A    AA__
                                GTCCAGA TAGGG   GTC
                                ||||||| |||||   |||
                                CAGGTTT ATCCC   CAG
                                   _    GTTA
GAM105  SIVA      3'  GTCCAGGGAAGGCTGCCA   2338      GAATA    TCC
                                GTCCA   GGGAAG  GCCA
                                |||||   ||||||  ||||
                                CAGGT   CCCTTC  CGGT
                                  _____    CGA
GAM105  SIVA      3'  GTCCAGGGAAGGCTGCCA   2338      GAATA    TCC
                                GTCCA   GGGAAG  GCCA
                                |||||   ||||||  ||||
                                CAGGT   CCCTTC  CGGT
                                  _____    CGA
GAM105  LOC130612 5'  GTCCAGGGAAAGTCCG     2339       AATA
                                GTCCAG   GGGAAGTCCG
                                ||||||   ||||||||||
                                CAGGTC   CCTTTCAGGC
                                  ____
GAM105  LOC150383 3'  GTCCAGAAGGAGCTGC     2340       ATA   A  CC
                                GTCCAGA   GGGA GT  GC
                                |||||||   |||| ||  ||
                                CAGGTCT   TCCT CG  CG
                                   ___   _ A_
GAM105  LOC151009 3'  GTCTAGAATAGGCAAATCCA  2341     C      G
                                GTC AGAATAGG AAGTCCG
                                ||| |||||||| |||||||
                                CAG TCTTATCC TTTAGGT
                                  A       G
GAM106  RIP5      5'  TCGCGCCGCCCGGGCCGGGCC  2344      AATA __
                                TCGC   GT  GGGCCGGGCC
                                ||||   ||  ||||||||||
                                AGCG   CG  CCCGGCCCGG
                                  CGG_  GG
GAM106  LOC151325 5'  TCGCCGGGCCGGGCCC     2345      AATAG
                                TCGC    TGGGCCGGGCCC
                                ||||    ||||||||||||
                                AGCG    GCCCGGCCCGGG
                                  _____
GAM106  LOC197342 3'  TATCCGTGCAGAGGCCGGGC  2346      GCAA  T
                                TATC   TAG GGGCCGGGC
                                ||||   ||| |||||||||
                                ATAG   GTC TCCGGCCCG
                                  GCAC  _
GAM107  ARHGDIB   3'  TAGGGACTCATTGGGC     2349     T   AGCCCC
                                TAG GGAC     CATTGGGC
                                ||| ||||     ||||||||
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                                ATC CCTG     GTAACCCG
                                  _   A_____
GAM107  BMP1    3'  ATGGACAGTCTCACCAGGCCA  2350        CCCC   TG
                                GTGGACAG   CAT  GGCCA
                                ||||||||   |||  |||||
                                TACCTGTC   GTG  CCGGT
                                    AGA_   GT
GAM107  ERBB4   3'  TGGATTCCCTCATTGGGCC   2351      CAG   C
                                TGGA   CCC CATTGGGCC
                                ||||   ||| |||||||||
                                ACCT   GGG GTAACCCGG
                                  AA_   A
GAM107  MECP2   3'  ATGGAGCCCCTGTTGGGCCA  2352      CA    CA
                                GTGGA  GCCCC  TTGGGCCA
                                |||||  |||||  ||||||||
                                TACCT  CGGGG  AACCCGGT
                                  __     AC
GAM107  PAX2    3'  AGTGGGCAGCCCCCCACTTCCA 2353      A      ATTGGG
                                AGTGG CAGCCCCC     CCA
                                ||||| ||||||||     |||
                                TCACC GTCGGGGG     GGT
                                  C       GTGAA_
GAM107  PAX2    3'  AGTGGGCAGCCCCCCACTTCCA 2353      A      ATTGGG
                                AGTGG CAGCCCCC     CCA
                                ||||| ||||||||     |||
                                TCACC GTCGGGGG     GGT
                                  C       GTGAA_
GAM107  PCOLN3  3'  GTGGACAGGCTCCCTGTCG   2354        _ _  CA
                                GTGGACAG C CCC  TTG
                                |||||||| | |||  |||
                                CACCTGTC G GGG  AGC
                                    C A   AC
GAM107  TXNRD2  3'  GTGGACAGTCCCCTGAGCCA  2355        C   AT
                                GTGGACAG CCCC  TGGGCCA
                                |||||||| ||||  |||||||
                                CACCTGTC GGGG  ACTCGGT
                                    A   __
GAM107  ATPW    5'  TAGTGGACGCTCGACTGGGC  2356        A  CCCC
                                TAGTGGAC GC    ATTGGGC
                                |||||||| ||    |||||||
                                ATCACCTG CG    TGACCCG
                                    _ AGC_
GAM107  DKFZP564L2423 3'  GTGGGTGGCTTCCCAGACCA  2357      ACA  C_   TTG
                                GTGG   GC  CCCA   GGCCA
                                ||||   ||  ||||   |||||
                                CACC   CG  GGGT   CTGGT
                                  CAC  AA    ___
GAM107  FLJ12816 3'  TGGAGGCTCCCCATTGGGCCA  2358      CA  _
                                TGGA  GC CCCCATTGGGCCA
                                ||||  || ||||||||||||
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                                ACCT  CG GGGGTAACCCGGT
                                  C_  A
GAM107  FLJ12934  3'  AGTGGACAGTTCTCCCTCG   2359        CC__   A
                                AGTGGACAG   CCC TTG
                                |||||||||   ||| |||
                                TCACCTGTC   GGG AGC
                                    AAGA  _
GAM107  FLJ13710  3'  TGGCAGCGCCTGGGCCA    2360    A   C  CAT
                                TGG CAGC CC   TGGGCCA
                                ||| |||| ||   |||||||
                                ACC GTCG GG   ACCCGGT
                                  _   C ___
GAM107  FLJ20294  3'  GTGGACAAGCCCTGGGGGC   2361       _   CCATT
                                GTGGACA GCCC    GGGC
                                ||||||| ||||    ||||
                                CACCTGT CGGG    CCCG
                                    T   ACC__
GAM107  FLJ22160  3'  GTGGACAGTCAATGCTGGGCCA 2362       CCCCCA
                                GTGGACAG    TTGGGCCA
                                ||||||||    ||||||||
                                CACCTGTC    GACCCGGT
                                    AGTTAC
GAM107  FLJ22938  3'  GTGGACAGTCCCCTCCCTTCCA 2363       _   CA  GGG
                                GTGGACAG CCCC  TT   CCA
                                |||||||| ||||  ||   |||
                                CACCTGTC GGGG  GG   GGT
                                    A   AG  AA_
GAM107  GORASP2   3'  TAGTGGACGCCCCGC      2364       A    CATTGG
                                TAGTGGAC GCCCC     GC
                                |||||||| |||||     ||
                                ATCACCTG CGGGG     CG
                                  _    _______
GAM107  KIAA0237  3'  ATGGGTAGCCCCCACTTCC   2365     AC       TGGG
                                GTGG  AGCCCCCAT   CC
                                ||||  |||||||||   ||
                                TACC  TCGGGGGTG   GG
                                  CA       AA__
GAM107  RINZF     3'  ATGGACAGAGTGATTGGGTCA  2366       CCCCC    C
                                GTGGACAG    ATTGGG CA
                                ||||||||    |||||| ||
                                TACCTGTC    TAACCC GT
                                    TCAC_    A
GAM107  LOC112817 3'  AGTGGATGGCCCTATCTCAGGC 2367      CA   CCA_ TG
          CA                    AGTGGA  GCCC   T  GGCCA
                                ||||||  ||||   |  |||||
                                TCACCT  CGGG   A  CCGGT
                                  AC   ATAG GT
GAM107  LOC126133 5'  TAGTGGAGCAGCTGCTGGGCCA 2368       _   CCCCA
                                TAGTGGA CAGC    TTGGGCCA
                                ||||||| ||||    ||||||||
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                                ATCACCT GTCG    GACCCGGT
                                    C   AC___
GAM107  LOC127841 5'  TAGAGGGATCCCCATTGGGTCA 2369     T_  CAGC       C
                                TAG  GGA   CCCCATTGGG CA
                                |||  |||   |||||||||| ||
                                ATC  CCT   GGGGTAACCC GT
                                  TC  A___       A
GAM107  LOC130074 3'  TAGTGGGCATCCTCACTG    2370       A  GC  C
                                TAGTGG CA  CC CATTG
                                |||||| ||  || |||||
                                ATCACC GT  GG GTGAC
                                   C  A_  A
GAM107  LOC163231 3'  CAGTGGACAGTTTCCCACTG   2371          CC_
                                TAGTGGACAG   CCCATTG
                                ||||||||||   |||||||
                                GTCACCTGTC   GGGTGAC
                                      AAA
GAM107  LOC199733 3'  TAGTGGGCAGCCCCAC      2372       A      CATTGG
                                TAGTGG CAGCCCC     GC
                                |||||| |||||||     ||
                                ATCACC GTCGGGG     TG
                                   C     _______
GAM107  LOC200942 3'  CAGTGGACAGCTCCCACCA    2373          C
                                TAGTGGACAGC CCCATTG
                                |||||||||| |||||||
                                GTCACCTGTCG GGGTGGT
                                      A
GAM107  LOC220914 5'  GGACAGCCTAGGAATGGGCCA  2374        CCCAT_
                                GGACAGCC     TGGGCCA
                                ||||||||     |||||||
                                CCTGTCGG     ACCCGGT
                                     ATCCTT
GAM107  LOC51337  3'  GTGGGCAGCCCCCAGGCC    2375      A       TTG
                                GTGG CAGCCCCCA   GGCC
                                |||| |||||||||   ||||
                                CACC GTCGGGGGGT   CCGG
                                  C       ___
GAM107  LOC90979  3'  TAGTTGGATATATTGGGCC    2376      _  CAGCCCCC
                                TAGT GGA       ATTGGGCC
                                |||| |||       ||||||||
                                ATCA CCT       TAACCCGG
                                  A  ATA_____
GAM108  CNGA3     3'  AAAGGTGACTAAATAATCT    2379         AGT
                                AAAGGTGAC   TGAATAATCT
                                |||||||||   ||||||||||
                                TTTCCACTG   ATTTATTAGA
                                      ___
GAM108  HCS       3'  GAGAGGTGTTGAATAATCT    2380     AA   GACA
                                GA  AGGT    GTTGAATAATCT
                                ||  ||||    ||||||||||||
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                                CT  TCCA    CAACTTATTAGA
                                 C_   _____
GAM108   LOC116071 3'  GAAAAAGTGGAGTGATAATCT  2381          AC   T  A
                                GAAAAGGTG  AGT GA TAATCT
                                |||||||||  ||| || ||||||
                                CTTTTTCAC  TCA CT ATTAGA
                                    C_   _ _
GAM108   LOC132617 5'  GAAAGGGTGAGGTTGAACAAC  2382       A     CA
                                GAAA GGTGA  GTTGAATAAT
                                ||||  |||||  ||||||||||
                                CTTT CCACT  CAACTTGTTG
                                  C     C_
GAM108   LOC152905 5'  AGGGGAAATAGAATAATCT   2383      T  C   T
                                AGG GA AGT GAATAATCT
                                |||  ||  |||  |||||||||
                                TCC CT TTA CTTATTAGA
                                  C  _   T
GAM108   LOC157317 3'  GAGAGGTGTTGAATAATCT   2380     AA    GACA
                                GA  AGGT    GTTGAATAATCT
                                ||  ||||    ||||||||||||
                                CT  TCCA    CAACTTATTAGA
                                 C_   _____
GAM108   LOC221810 3'  AAGGATTTGAATAATCT     2384       TGACAG
                                AAGG      TTGAATAATCT
                                ||||      ||||||||||
                                TTCC      AACTTATTAGA
                                  TA_____
GAM109   DCK      3'  TAGAGCAATATCATTTTTATC  2387        GTT       CC
                                TAGAGT   GATATCAT  TTATC
                                ||||||   ||||||||  |||||
                                ATCTCG   TTATAGTA  AATAG
                                    ___       AA
GAM109   HFE      3'  AAGTGCTTTTATCATCCTTATC 2388         GA
                                GAGTGTT  TATCATCCTTATC
                                |||||||  ||||||||||||
                                TTCACGA  ATAGTAGGAATAG
                                     AA
GAM109   HFE      3'  AAGTGCTTTTATCATCCTTATC 2388         GA
                                GAGTGTT  TATCATCCTTATC
                                |||||||  ||||||||||||
                                TTCACGA  ATAGTAGGAATAG
                                     AA
GAM109   MUCDHL    3'  CAGAATGTCGTCCTT       2389          ATATCA
                                TAGAGTGTTG     TCCTT
                                ||||||||||     |||||
                                GTCTTACAGC     AGGAA
                                               _______
GAM109   MUCDHL    3'  CAGAATGTCGTCCTT       2389          ATATCA
                                TAGAGTGTTG     TCCTT
                                ||||||||||     |||||
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                                GTCTTACAGC     AGGAA
                                          _______
GAM109  KLK6    3'  GAGACTGTATCATCCTTATC  2390     TGT  A
                                GAG   TG TATCATCCTTATC
                                |||   || ||||||||||||
                                CTC   AC ATAGTAGGAATAG
                                  TG_  _
GAM110  COL18A1  3'  GTGGGGGCTTCCTCCGAGCCGC 2393      TA  CC  A
                                GTGGG  GC  CC TTGGGCCGC
                                |||||  ||  || |||||||||
                                CACCC  CG  GG GGCTCGGCG
                                   C_  AA  A
GAM110  COL18A1  3'  GTGGGGGCTTCCTCCGAGCCGC 2393      TA  CC  A
                                GTGGG  GC  CC TTGGGCCGC
                                |||||  ||  || |||||||||
                                CACCC  CG  GG GGCTCGGCG
                                   C_  AA  A
GAM110  COL18A1  3'  GTGGGGGCTTCCTCCGAGCCGC 2393      TA  CC  A
                                GTGGG  GC  CC TTGGGCCGC
                                |||||  ||  || |||||||||
                                CACCC  CG  GG GGCTCGGCG
                                   C_  AA  A
GAM110  KCNJ16   3'  AGTGGTAGCCCTCATAATTGC  2394      G     C   TGG_
                                AGTGG TAGCCC CAT    GC
                                ||||| |||||| |||    ||
                                TCACC ATCGGG GTA    CG
                                   _     A   TTAA
GAM110  MFAP2    3'  AGTGGGGAGCCCCCATCG    2395       T
                                AGTGGG AGCCCCCATTG
                                |||||| ||||||||||
                                TCACCC TCGGGGGTAGC
                                   C
GAM110  PEA15    3'  AGTGGGTAGATGGTGGGTTGC  2396        CCCCCAT    CC
                                AGTGGGTAG      TGGG  GC
                                |||||||||      ||||  ||
                                TCACCCATC      ACCC  CG
                                     TACC___    AA
GAM110  ZNF261   3'  AGTGGGTACCCCCTTTG     2397        G    A
                                AGTGGGTA CCCCC TTG
                                |||||||| ||||| |||
                                TCACCCAT GGGGG AAC
                                     _    A
GAM110  AF9Q34   3'  AGCGGGTAGCCTCCGAGCCCGC 2398          C  ATT  G
                                AGTGGGTAGCC CC   GG CCGC
                                |||||||||| ||   || ||||
                                TCGCCCATCGG GG   TC GGCG
                                      A  C__  G
GAM110  CAMTA1   5'  CGCACAGCTCCCGTTGGGCCG  2399     G    C   A
                                TG GTAGC CCC TTGGGCCG
                                || ||||| ||| ||||||||
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                                GC TGTCG GGG AACCCGGC
                                 G    A  C
GAM110  CREB-H   3' GTGGGTAGCTGCCCAGTG    2400         C_   T
                                GTGGGTAGC  CCCA TG
                                |||||||||  |||| ||
                                CACCCATCG  GGGT AC
                                     AC    C
GAM110  DKFZP434J154 3' GTGGGCAGCCCCTGGGCC    2401           CAT
                                GTGGGTAGCCCC   TGGGCC
                                ||||||||||||   ||||||
                                CACCCGTCGGGG   ACCCGG
                                       ___
GAM110  KIAA0310  3' GTGGGCAGTCCCCAGCG     2402         C    TTGG  C
                                GTGGGTAG CCCCA    GC G
                                |||||||| |||||    || |
                                CACCCGTC GGGGT    CG C
                                    A    _____  _
GAM110  KIAA1550  3' GTGGGAGCTCCCATCGGCTGC  2403       T   C       G C
                                GTGGG AGC CCCATTGG C GC
                                ||||| ||| |||||||| | ||
                                CACCC TCG GGGTAGCC G CG
                                   _  A       _ A
GAM110  KIAA1724  3' AGTGGGCAGCCTCTGTCCTAGG 2404           CCCA__
                                AGTGGGTAGCC     TTGGG
                                ||||||||||      |||||
                                TCACCCGTCGG     GATCC
                                      AGACAG
GAM110  SYT12    3' GTGGGAGCCCCCAGGGTG    2405       T      TT   CC
                                GTGGG AGCCCCCA  GGG  G
                                ||||| ||||||||  |||  |
                                CACCC TCGGGGGT  CCC  C
                                   _       __   A_
GAM110  LOC138399 5'  AGTGGGTAGCTCCTCTCCATAG 2406          _ ___    TG
            C                    AGTGGGTAGC CC   CCAT  GGC
                                ||||||||||  ||   ||||  |||
                                TCACCCATCG GG   GGTA  TCG
                                     A  AGA   __
GAM110  LOC150407 3'  GTGGGCAGCCCTGAGGGGTTGC 2407           CCATT   CC
                                GTGGGTAGCCC    GGG  GC
                                ||||||||||     |||  ||
                                CACCCGTCGGG    CCC  CG
                                      ACTC_   AA
GAM110  LOC196759 3'  AGTGGGTAACTCCTTTCTGC   2408          C  CA  GG
                                AGTGGGTAGC CC  TT  GC
                                ||||||||||  ||  ||  ||
                                TCACCCATTG GG  AG  CG
                                     A  AA  A_
GAM110  LOC199864 3'  AGTGGGTAGCTCCTTTCTGC   2409          C  CA  GG
                                AGTGGGTAGC CC  TT  GC
                                ||||||||||  ||  ||  ||
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                                TCACCCATCG GG  AG  CG
                                     A  AA  A_
GAM110  LOC255391 5'  GTGGGTATTCCTGGGGCTCCG  2410       GC  CCAT   ___
                                GTGGGTA  CC   TGGG  CCG
                                |||||||  ||   ||||  |||
                                CACCCAT  GG   ACCC  GGC
                                    AA  ____   CGA
GAM110  LOC255475 5'  AGTGGGTAGTCCTGGACC   2411        C  CCAT
                                AGTGGGTAG CC   TGGGCC
                                |||||||||  ||   ||||||
                                TCACCCATC GG   ACCTGG
                                     A  ____
GAM111  NDUFA2   3'  TCAGTGGTTGCACCATTAAGGG 2414       GAG    C
                                TCAGTGG  GTACC ATTAAGGG
                                |||||||  |||||  ||||||||
                                AGTCACC  CGTGG TAATTCCC
                                    AA_   _
GAM111  RAB5B    3'  AGGGGAAACACCATTAGGGG  2415    T   GG   C   A
                                AG GGGA  TACC ATTA GGG
                                ||  ||||  ||||  ||||  |||
                                TC CCCT  GTGG TAAT CCC
                                 _   TT   _   C
GAM111  APPD     3'  TCAGTGGGGTGTGCCTGTCAGG 2416       AG  A  CATTA
           G                     TCAGTGGG  GT CC    AGGG
                                |||||||  ||  ||    ||||
                                AGTCACCC  CA GG    TCCC
                                    CA  C  ACAG_
GAM111  FLJ13305  5'  TCGGTGGGAGGTGGCCATC   2417    A      AC
                                TC GTGGGAGGT  CCATT
                                ||  |||||||||  |||||
                                AG CACCCTCCA  GGTAG
                                 C       CC
GAM111  FLJ14810  3'  TCAGTGGGAGGGGAAGGGCCCT 2418       TA_________  ATTAA
           TAAG                   GTGGGAGG       CCC    G
                                |||||||||       |||   |
                                CACCCTCC        GGG   C
                                    CCTTCCCIII  AATTA
GAM111  KCND1    3'  TCAGTGGGGGGGGCAGAAGGG  2419       A  TACC  TT
                                TCAGTGGG GG   CA  AAGGG
                                |||||||| ||   ||  |||||
                                AGTCACCC CC   GT  TTCCC
                                    _  CCC_  C_
GAM111  LOC126526 3'  TCAGTGGGGAGTGGGGGAAGGG 2420       AG  ACCCATT
                                TCAGTGGG  GT     AAGGG
                                ||||||||  ||     |||||
                                AGTCACCC  CA     TTCCC
                                    CT  CCCCC__
GAM111  LOC127534 3'  TCAGTGACCTGCCCATTAAGGG 2421       GAGGTA
                                TCAGTGG    CCCATTAAGGG
                                |||||||    ||||||||||
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                                AGTCACT     GGGTAATTCCC
                                    GGAC__
GAM111  LOC200982 3'  GTGGGGGGTGACATTTGGG   2422       A   ACC    AA
                                GTGGG GGT   CATT  GGG
                                ||||| |||   ||||  |||
                                CACCC CCA   GTAA  CCC
                                   C   CT_    A_
GAM111  LOC203339 5'  TCAGTGGGGGCGTGTCCACAGG 2424         A   AC__    TA
                                TCAGTGGG GGT    CCAT  AGG
                                |||||||| |||    ||||  |||
                                AGTCACCC CCG    GGTG  TCC
                                    _   CACA    __
GAM111  LOC203339 5'  TCAGTGGGGGCGTGTCCATCTG 2423        A   AC__     A__
          TAGGG                   CAGTGGG GGT    CCATT   AGGG
                                |||||||| |||    |||||   ||||
                                GTCACCC CCG    GGTAG   TCCC
                                    _   CACA     ACA
GAM111  LOC219920 3'  AGGGGAGGCATTGAGG      2425     T     TACC    A
                                AG GGGAGG    CATT AGG
                                || ||||||    |||| |||
                                TC CCCTCC    GTAA TCC
                                 _     _____   C
GAM111  LOC220164 3'  TCAGTGAGAGGTGCCCATC    2426           A
                                TCAGTGGGAGGT CCCATT
                                |||||||||||| ||||||
                                AGTCACTCTCCA GGGTAG
                                      C
GAM112  FLJ22875  3'  TGAGTACATTTGGGCACAGTA  2429          CG   ATG  G
                                TGAGTACAT  TGG   AC AGTA
                                |||||||||  |||   || ||||
                                ACTCATGTA  ACC   TG TCAT
                                    A_   CG_  _
GAM112  MYL9      3'  TGAGCACACTCCCATGGCG    2430          ___     A
                                TGAGTACAT   CGTGG TG
                                |||||||||   ||||| ||
                                ACTCGTGTG   GTACC GC
                                    AGG    _
GAM112  LOC202134 5'  TGAGTCGTTTCAGACGAGT    2431       TACA    GGAT
                                TGAG    TCGT    GACGAGT
                                ||||    ||||    |||||||
                                ACTC    AGCA    CTGCTCA
                                  _____    AAGT
GAM113  PPP2R5E   3'  TCCTAATTTTAAAACTAAAGG  2434           CT     A
                                TCCTAATTTTAA  CTAAA GG
                                ||||||||||||  ||||| ||
                                AGGATTAAAATT  GATTT CC
                                      TT    _
GAM113  TZFP      5'  CCTAACTCAGAGGCTCTAAGAG 2435          TAA__      A
          G                     CCTAATTT    CTCTAA AGG
                                ||||||||    |||||| |||
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                                GGATTGAG    GAGATT TCC
                                    TCTCC     C
GAM113  FLJ12443  3'  ATCCTTTGACTCTAAAAGG   2436      AATT  A
                                ATCCT   TT ACTCTAAAAGG
                                |||||   || ||||||||||
                                TAGGA   AA TGAGATTTTCC
                                  ____  C
GAM113  FLJ22559  5'  TCCAGCTAACTCTGAAAGG   2437     TAATT      A
                                TCC    TTAACTCT AAAGG
                                |||    |||||||| |||||
                                AGG    GATTGAGA TTTCC
                                  TC___       C
GAM113  KIAA0266  3'  CATCTCATTCCAACTCTAAAAG 2438      CTA
            G                    CATC   ATTTTAACTCTAAAAGG
                                ||||   ||||||||||||||||
                                GTAG   TAAGGTTGAGATTTTCC
                                  AG_
GAM113  KIAA0316  3'  TCCTATCACTCTAAAGGG    2439      ATTTTA      A
                                TCCTA     ACTCTAAA GG
                                |||||     |||||||| ||
                                AGGAT     TGAGATTT CC
                                  AG____       C
GAM113  SLC21A8   3'  CTAATCTTAACCATAAAGG   2440          CTA
                                CTAATTTTAACT   AAAGG
                                ||||||||||||   |||||
                                GATTAGAATTGG   TTTCC
                                     TA_
GAM113  SPEC1     3'  TCCTAATTACCCTGGAAGG   2441        TTA    AA
                                TCCTAATT   ACTCT  AAGG
                                ||||||||   |||||  ||||
                                AGGATTAA   TGGGA  TTCC
                                    ___    CC
GAM113  SSH2      3'  TCCTTCAGGAACTCTAAAGGG  2442      AATTTT       A
                                TCCT     AACTCTAAA GG
                                ||||     ||||||||| ||
                                AGGA     TTGAGATTT CC
                                  AGTCC_       C
GAM113  LOC126969 3'  TCCTAATTTGTACAAAAAAAGG 2443         TA  TCT
                                TCCTAATTT  AC   AAAAGG
                                |||||||||  ||   ||||||
                                AGGATTAAA  TG   TTTTCC
                                     CA  TTT
GAM113  LOC253912 3'  ATCCTCACAACTCTAGGAGG  2444      AATTT      AA
                                ATCCT    TAACTCTA  AGG
                                |||||    ||||||||  |||
                                TAGGA    GTTGAGAT  TCC
                                  GT___      CC
GAM114  COPEB     5'  CCGAAAGTCTCCCCGGAGC   2447         A_  A_
                                CCGGAAGTC  CT  GAGC
                                |||||||||  ||  ||||
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                                GGCTTTCAG  GG  CTCG
                                     AG  GC
GAM114  E2F1     3'  CCGAAAGTGCAGTTAGAGC   2448        _  C_
                                CCGGAAGT CA  TAGAGC
                                |||||||| ||  ||||||
                                GGCTTTCA GT  ATCTCG
                                     C  CA
GAM114  FGF1     3'  CCTGAAGTCACCCAGGGC    2449    G       _  A
                                CC GAAGTCACT AG GC
                                || ||||||||| || ||
                                GG CTTCAGTGG TC CG
                                 A        G  C
GAM114  FGF1     3'  CCTGAAGTCACCCAGGGC    2449    G       _  A
                                CC GAAGTCACT AG GC
                                || ||||||||| || ||
                                GG CTTCAGTGG TC CG
                                 A        G  C
GAM114  FGF1     3'  CCTGAAGTCACCCAGGGC    2449    G       _  A
                                CC GAAGTCACT AG GC
                                || ||||||||| || ||
                                GG CTTCAGTGG TC CG
                                 A        G  C
GAM114  POLR2A   3'  CCAGAAGTTCACCGGGAGC   2450        _   A_
                                CCGGAAGT CACT  GAGC
                                |||||||| ||||  ||||
                                GGTCTTCA GTGG  CTCG
                                     A   CC
GAM114  DKFZp761C121 3'  CAGAAGCCCATACTAGAG    2451        ___
                                CGGAAGTC   ACTAGAG
                                ||||||||   |||||||
                                GTCTTCGG   TGATCTC
                                     GTA
GAM114  GBTS1    3'  CCGAAAGTCACATTGCTAGAG  2452          _____
                                CCGGAAGTCAC    TAGAG
                                ||||||||||    |||||
                                GGCTTTCAGTG    ATCTC
                                      TAACG
GAM114  SEC14L1  3'  CCAGGAGTCCCTGAGAGC    2453      A   A  _
                                CCGG AGTC CT AGAGC
                                |||| |||| || |||||
                                GGTC TCAG GA TCTCG
                                  C   G  C
GAM114  Sfmbt    3'  CCGAAAGTGCAAAGAGAGC   2454        _  CT_
                                CCGGAAGT CA   AGAGC
                                |||||||| ||   |||||
                                GGCTTTCA GT   TCTCG
                                     C  TTC
GAM114  LOC152426 5'  CGGAAGTCCTGAAGCTAGAGCG 2455         A_____      III
                                CGGAAGTC     CTAGAGC   G
                                ||||||||     |||||||   |
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                                GCCTTCAG    GATCTCG  C
                                    GACTTC      III
GAM114  LOC202865 5'  CGGAAAGTCAGCTGGAGC    2456       _   _ A
                                CGGAA GTCA CT GAGC
                                ||||| |||| || ||||
                                GCCTT CAGT GA CTCG
                                   T   C  C
GAM114  LOC221938 3'  CCAGAAGTCACCTTGGAGC   2457           A__
                                CCGGAAGTCACT   GAGC
                                ||||||||||||  ||||
                                GGTCTTCAGTGG   CTCG
                                      AAC
GAM114  LOC253489 5'  CCAGACGGCCGGCTAGAGC   2458       A_  A_
                                CCGGA  GTC  CTAGAGC
                                |||||  |||  |||||||
                                GGTCT  CGG  GATCTCG
                                   GC   CC
GAM115  ACK1    3'  CACCCAGGGCAGGGCCTGGGG  2461        C_  CCA  C
                                CACCTAG  CAG   GCC GGGG
                                |||||||  |||   ||| ||||
                                GTGGGTC  GTC   CGG CCCC
                                    CC   C__   A
GAM115  ADD1    3'  GCACACACTGGGTCAGCCCGGG 2462    _  _ AGCCAGC
          G                     GC CAC CT      CAGCCCGGGG
                                || ||| ||      ||||||||||
                                CG GTG GA      GTCGGGCCCC
                                 T   T  CCCA___
GAM115  ADD1    3'  GCACACACTGGGTCAGCCCGGG 2462    _  _ AGCCAGC
          G                     GC CAC CT      CAGCCCGGGG
                                || ||| ||      ||||||||||
                                CG GTG GA      GTCGGGCCCC
                                 T   T  CCCA___
GAM115  B4GALT7  3'  GCCACCTACGCCAGCTGCATGG 2463         _     CA  CCG
                                GCCACCTA GCCAGC  GC   GG
                                |||||||| ||||||  ||   ||
                                CGGTGGAT CGGTCG  CG   CC
                                    G     A_  TA_
GAM115  DIA1    3'  GCCAACCCCCCAGCTCGGGG   2464      CCTA   AG    C
                                GCCA   GCC  CCAGC CGGGG
                                ||||   |||  ||||| |||||
                                CGGT   TGG  GGTCG GCCCC
                                  ____  GG    A
GAM115  DSCAM   5'  GCCGCTCGGCACCTGCCCGGGG 2465     AC  AGCCA  A
                                GCC  CT    GCC GCCCGGGG
                                |||  ||    ||| ||||||||
                                CGG  GA    TGG CGGGCCCC
                                  C_  GCCG_  A
GAM115  EN2     5'  GCCGCCTGGGCCGCCCGGG   2466     A  AGCCA  A
                                GCC CCT    GCC GCCCGGG
                                ||| |||    ||| |||||||
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                                CGG GGA    CGG CGGGCCC
                                  C  CC___  _
GAM115  F2RL3   5'  GCCGCTTGCCAGCCAGCCCG  2467     AC  A
                                GCC  CT GCCAGCCAGCCCG
                                |||  || |||||||||||||
                                CGG  GA CGGTCGGTCGGGC
                                  C_  A
GAM115  GLUL    5'  CAGACAGCGGCCGGCCCGGGG 2468    CC   CA  A
                                CA  TAGC  GCC GCCCGGGG
                                ||  ||||  ||| ||||||||
                                GT  GTCG  CGG CGGGCCCC
                                 CT   C_  C
GAM115  IL15    5'  GCCACCCAGTTCCCTCCCGGGG 2469         CCAG  AG
                                GCCACCTAG   CC  CCCGGGG
                                |||||||||   ||  |||||||
                                CGGTGGGTC   GG  GGGCCCC
                                      AA__  GA
GAM115  JUND    5'  CCCGCCGCGCCGGCCCGGG   2470     A  A_  A
                                CCT GCC  GCC GCCCGGG
                                ||| |||  ||| |||||||
                                GGG CGG  CGG CGGGCCC
                                  _  CG  C
GAM115  KCNF1   5'  GCCGCCGGCCTCGCCCGGG   2471     ACCTA  A  A_
                                GCC    GCC GCC  GCCCGGG
                                |||    ||| |||  |||||||
                                CGG    CGG CGG  CGGGCCC
                                  ______  C  AG
GAM115  LIMK1   5'  CCACCGCCGCCGGCCCGGGG  2472      TA  A  A
                                CCACC  GCC GCC GCCCGGGG
                                |||||  ||| ||| ||||||||
                                GGTGG  CGG CGG CGGGCCCC
                                   __  _  C
GAM115  LIMK1   5'  CCACCGCCGCCGGCCCGGGG  2472      TA  A  A
                                CCACC  GCC GCC GCCCGGGG
                                |||||  ||| ||| ||||||||
                                GGTGG  CGG CGG CGGGCCCC
                                   __  _  C
GAM115  MAP3K5  5'  ACCGCCTGGCCAGCCACAGCTC 2473     A  A      __ C
          GGGG                   GCC CCT GCCAGCCA  GC CGGGG
                                ||| ||| ||||||||  || |||||
                                TGG GGA CGGTCGGT  CG GCCCC
                                  C  C       GT  A
GAM115  NCOR2   3'  GCACAGGGCCAGCCCGGGG   2474    _ __
                                GC CA  GCCAGCCCGGGG
                                || ||  ||||||||||||
                                CG GT  CGGTCGGGCCCC
                                 T  CC
GAM115  NF2     5'  GCCGGCTGGCCGGCCCGGG   2475     ACCTA  CA  A
                                GCC    GC  GCC GCCCGGG
                                |||    ||  ||| |||||||
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                                CGG    CG  CGG CGGGCCC
                                  C____  AC   C
GAM115  OVOL1    5'  GCCACCACACAGCCCGGG    2476        TAGCCA  _
                                GCCACC     GC CAGCCCGGG
                                ||||||     || |||||||||
                                CGGTGG     TG GTCGGGCCC
                                   _______  T
GAM115  RFC2     3'  CCTGGCCAGCCACTGGAG    2477      A       G CC
                                CCT GCCAGCCA C  GGGG
                                ||| ||||||| |  ||||
                                GGA CGGTCGGT G  CCTC
                                  C       _ A_
GAM115  RFX1     3'  CCACCTGCGCCGGCCCGGGG   2478        A  CA   A
                                CCACCT GC  GCC GCCCGGGG
                                |||||| ||  ||| ||||||||
                                GGTGGA CG  CGG CGGGCCCC
                                   _ __   C
GAM115  RXRG     5'  GCTTCCTAGCAGCCCGGG    2479     CA     CAGCC
                                GC  CCTAGC    AGCCCGGG
                                ||  ||||||    ||||||||
                                CG  GGATCG    TCGGGCCC
                                 AA    _____
GAM115  WW45     5'  GCCGCCTGTCCGGAGCCCGGGG 2480      A   AG  AGCC
                                GCC CCT  CC    AGCCCGGGG
                                ||| |||  ||    |||||||||
                                CGG GGA  GG    TCGGGCCCC
                                  C   CA  CC__
GAM115  BA108L7.2 3'  GCCAGCCCAGTCAGCTTGGGG  2481       _    C    CAGCCC
                                GCCA CCTAG CAGC     GGGG
                                |||| ||||| ||||     ||||
                                CGGT GGGTC GTCG     CCCC
                                  C    A   AA____
GAM115  C22orf4  3'  GCCTCTGGCCGCCGAACCCGGG 2482      AC  A   A  _
           G                     GCC  CT GCC GCC AGCCCGGGG
                                |||  || ||| ||| |||||||||
                                CGG  GA CGG CGG TTGGGCCCC
                                  A_  C   _   C
GAM115  CEP3     5'  ACCTGTGCCCTGGCCCGGGG   2483      A_   AGCCA
                                ACCT  GCC    GCCCGGGG
                                ||||  |||    ||||||||
                                TGGA  CGG    CGGGCCCC
                                  CA   GAC__
GAM115  D21S2056E 3'  GCCACCTGCCCGGGG       2484         AGCCAGCCA
                                GCCACCT       GCCCGGGG
                                |||||||       ||||||||
                                CGGTGGA       CGGGCCCC
                                              _________
GAM115  DKFZP586N0721 3'  GCCACTTGTTTAGCCAGCCTGG 2485        CTAGCC       C
                                GCCAC     AGCCAGCC GG
                                |||||     |||||||| ||
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                                CGGTG     TCGGTCGG CC
                                  AACAAA       A
GAM115  DTX2     3'  GCCACCCAGCCAGCCATGGGG  2486             GCCC
                                GCCACCTAGCCAGCCA   GGGG
                                ||||||||||||||||   ||||
                                CGGTGGGTCGGTCGGT   CCCC
                                          A___
GAM115  FLJ14681 3'  GCCACCTATCAGCTAAGAG   2487         GC   CAGCCC
                                GCCACCTA  CAGC     GGG
                                ||||||||  ||||     |||
                                CGGTGGAT  GTCG     CTC
                                    A_    ATT___
GAM115  FLJ21709 3'  CATCTGGCCAGCCATGAG    2488     C  A       GCCC
                                CA CT GCCAGCCA    GGG
                                || || ||||||||    |||
                                GT GA CGGTCGGT    CTC
                                 A  C       A___
GAM115  FLJ21916 3'  GCCATCTTGCCGGCCAGCC    2489      C  A   A
                                GCCA CT GCC GCCAGCC
                                |||| || ||| |||||||
                                CGGT GA CGG CGGTCGG
                                  A  A   C
GAM115  FLJ22390 3'  GCCATTTCAAAAGCTAGCCCGG 2490       CCTAGCC   C
          GG                    GCCA      AGC AGCCCGGGG
                                ||||      ||| |||||||||
                                CGGT      TCG TCGGGCCCC
                                  AAAGTTT   A
GAM115  KCNG3    5'  CCTGCCCTCCGCTGGCCCGGGG 2491      A   AG  A___
                                CCT GCC  CC    GCCCGGGG
                                ||| |||  ||    ||||||||
                                GGA CGG  GG    CGGGCCCC
                                  _   GA  CGAC
GAM115  KIAA0189 3'  CCATCTGGCTGGCCCAGGG    2492      C  A  CAGCCA
                                CCA CT GC     GCCCGGGG
                                ||| || ||     ||||||||
                                GGT GA CG     CGGGTCCC
                                  A  C  AC____
GAM115  KIAA0469 3'  GCCATCTGGCCAGCACAAGGG  2493       C  A     _   CCC
                                GCCA CT GCCAGC CAG   GGG
                                |||| || |||||| |||   |||
                                CGGT GA CGGTCG GTT   CCC
                                  A  C     T  ___
GAM115  KIAA1006 5'  GCCGCCTGCCAGCCCGG     2494      ACCTA   A
                                GCC    GCC GCCAGCCCGG
                                |||    ||| ||||||||||
                                CGG    CGG CGGTCGGGCC
                                  ______   A
GAM115  KIAA1297 3'  GCCGCTTGCCCGCCCGGG    2495      ACCTA  CA   A
                                GCC    GC  GCC GCCCGGG
                                |||    ||  ||| |||||||
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                                CGG    CG  CGG CGGGCCC
                                  _____ AA   G
GAM115  KIAA1643 3'  GCCCCTGCAGCCGGCCCGGGG  2496     A   A  C    A
                                GCC CCT GC AGCC GCCCGGGG
                                ||| ||| || |||| ||||||||
                                CGG GGA CG TCGG CGGGCCCC
                                  _  _ _   C
GAM115  KIF13B   3'  CCTGCCAAGTGCTGGCCCGGGG 2497     A   ___  CA
                                CCT GCCA   GC  GCCCGGGG
                                ||| ||||   ||  ||||||||
                                GGA CGGT   CG  CGGGCCCC
                                  _    TCA  AC
GAM115  KIF13B   3'  CCTGCCAAGTGCTGGCCCGGGG 2497     A   ___  CA
                                CCT GCCA   GC  GCCCGGGG
                                ||| ||||   ||  ||||||||
                                GGA CGGT   CG  CGGGCCCC
                                  _    TCA  AC
GAM115  LASP1    3'  GCCACCTAACCCAGATCCTGGG 2498          AGCCAG  C
            G                    GCCACCTAGCC     CC GGGG
                                ||||||||||      || ||||
                                CGGTGGATTGG     GG CCCC
                                      GTCTA_  A
GAM115  MARK2    5'  GCCGCTCACGCCAGCCCGGGG  2499     ACCTA  _  _
                                GCC     GC CA GCCAGCCCGGGG
                                |||     || || ||||||||||||
                                CGG     CG GT CGGTCGGGCCCC
                                  _____  A  G
GAM115  MGC15854 5'  GCCATCTTGCCAGCCCGGG    2500      C  AGCCA
                                GCCA CT     GCCAGCCCGGG
                                |||| ||     ||||||||||
                                CGGT GA     CGGTCGGGCCC
                                  A  A____
GAM115  MGC19570 3'  GCCACCTAGTGGCCAGCC     2501          CCA
                                GCCACCTAG   GCCAGCC
                                |||||||||   |||||||
                                CGGTGGATC   CGGTCGG
                                      AC_
GAM115  N4BP3    3'  GCCACCCAGCCGGCTGGG     2502          A  CAGCCC
                                GCCACCTAGCC GC      GGG
                                |||||||||| ||      |||
                                CGGTGGGTCGG CG      CCC
                                      C  A_____
GAM115  PP3501   3'  GCCTTCTGGCAGGAGCCCGGGG 2503      AC  A  C  CC
                                GCC  CT GC AG  AGCCCGGGG
                                |||  || || ||  |||||||||
                                CGG  GA CG TC  TCGGGCCCC
                                  AA  C  _  C_
GAM115  RAGD     5'  CCACCGGCCGGCCGGCCCGGGG 2504       TA   A   A
                                CCACC  GCC GCC GCCCGGGG
                                |||||  ||| ||| ||||||||
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                                GGTGG  CGG CGG CGGGCCCC
                                  C_   C   C
GAM115  SELM     3'  CCCATCCCTGCTGGCCCGGGG  2505      G  A_  CA
                                CCTA CC  GC  GCCCGGGG
                                |||| ||  ||  ||||||||
                                GGGT GG  CG  CGGGCCCC
                                  A  GA  AC
GAM115  SLC26A9  3'  CTAGCCAGCCTCCAGGG     2506          AGC
                                CTAGCCAGCC   CCGGGG
                                ||||||||||   ||||||
                                GATCGGTCGG   GGTCCC
                                     A__
GAM115  SLC26A9  3'  CTAGCCAGCCTCCAGGG     2506          AGC
                                CTAGCCAGCC   CCGGGG
                                ||||||||||   ||||||
                                GATCGGTCGG   GGTCCC
                                     A__
GAM115  LOC146280 5'  CCACCTGGCGCCCAGGCCCGGG 2507        A  CAG   _
          G                      CCACCT GC   CCAG CCCGGGG
                                 |||||| ||   |||| |||||||
                                 GGTGGA CG   GGTC GGGCCCC
                                    C  CG_   C
GAM115  LOC146443 5'  GCCACTGCACTCCAGCCCGGGG 2508       CTA  CAG
                                GCCAC   GC   CCAGCCCGGGG
                                |||||   ||   ||||||||||
                                CGGTG   CG   GGTCGGGCCCC
                                  A__  TGA
GAM115  LOC148189 5'  CCTGCAGCCAGCCCGG      2509      A  C
                                CCT GC AGCCAGCCCGG
                                ||| || ||||||||||
                                GGA CG TCGGTCGGGCC
                                  _ _
GAM115  LOC157848 3'  CAGCCAGCAGCTGGCTTGGGG  2510         C   CC____
                                TAGCCAGC AGC     GGGG
                                |||||||| |||     ||||
                                GTCGGTCG TCG     CCCC
                                     _  ACCGAA
GAM115  LOC162022 5'  CCCGCGAGCCAGCCCGGGG   2511      A  C
                                CCT GC AGCCAGCCCGGGG
                                ||| || ||||||||||||
                                GGG CG TCGGTCGGGCCCC
                                  _  C
GAM115  LOC196047 5'  GCTCACACCTGAGCCAGCCTGG 2512     _  CTA  __       C
          GG                     GC CAC   GCC  AGCCAGCC GGGG
                                 || |||   |||  |||||||| ||||
                                 CG GTG   TGG  TCGGTCGG CCCC
                                  A  ____  AC       A
GAM115  LOC197342 3'  GCCATCTGCCAGCCAGAAG   2513      C  A       CCC
                                GCCA CT GCCAGCCAG   GGG
                                |||| || |||||||||   |||
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                                CGGT GA CGGTCGGTC   TTC
                                  A _       ___
GAM115  LOC200213 5'  GCAGGAGGCTGGCCGGCCCGGG 2514     CACCTA  CA   A
            G                    GC     GC  GCC GCCCGGGG
                                 ||     ||  ||| ||||||||
                                 CG     CG  CGG CGGGCCCC
                                  TCCTC_  AC   C
GAM115  LOC201522 3'  GCCGCCTGCCAGCCCCGGG   2515      A  A      AGC
                                 GCC CCT GCCAGCC   CCGGG
                                 ||| ||| |||||||   |||||
                                 CGG GGA CGGTCGG   GGCCC
                                  C  _     ___
GAM115  LOC205418 3'  CACCTTGGCCAGCCCCGGG   2516       A_      AGC
                                 CACCT  GCCAGCC   CCGGG
                                 |||||  |||||||   |||||
                                 GTGGA  CGGTCGG   GGCCC
                                   AC      ___
GAM115  LOC255990 5'  GCCGCCTCTAGTGCCAGCCCGG 2517      A   AGCCA
            GG                     GCC CCT    GCCAGCCCGGGG
                                 ||| |||    ||||||||||||
                                 CGG GGA    CGGTCGGGCCCC
                                  C   GATCA
GAM115  LOC58489  5'  GCTGGCTGGCTGGCTGGCCCGG 2518     CAC  A  CA  CA
            G                    GC   CT GC  GC  GCCCGGG
                                 ||   || ||  ||  |||||||
                                 CG   GA CG  CG  CGGGCCC
                                  ACC  C  AC  AC
GAM115  LOC58525  3'  GCCGCTTTGCCAGCCAGCCAG  2519      ACCTA         C
                                 GCC    GCCAGCCAGCC GG
                                 |||    |||||||||||  ||
                                 CGG    CGGTCGGTCGG TC
                                  CGAAA         _
GAM115  LOC92095  3'  CCGGGGCCTCAGCTGGCCCGGG 2520     TA_  __  CA
            G                    CC   GCC  AGC  GCCCGGGG
                                 ||   |||  |||  ||||||||
                                 GG   CGG  TCG  CGGGCCCC
                                  CCC   AG   AC
GAM115  LOC92096  3'  CCGGGGCCTCAGCTGGCCCGGG 2520     TA_  __  CA
            G                    CC   GCC  AGC  GCCCGGGG
                                 ||   |||  |||  ||||||||
                                 GG   CGG  TCG  CGGGCCCC
                                  CCC   AG   AC
GAM116  IL24     3'  TGAGGATCTGCTTTGTGCT   2523     T      T   CTAC
                                 TG GGATTTG CTT    GCT
                                 || ||||||| |||    |||
                                 AC CCTAGAC GAA    CGA
                                  T      _   ACA_
GAM116  LPIN1    3'  TGTGGATTTTCTTTCACA    2524          G    C
                                 TGTGGATTT TCTT TACG
                                 ||||||||| |||| ||||
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                                ACACCTAAA AGAA GTGT
                                     _   A
GAM116  FLJ11016  3'  TGTGGATTTGTCTTACCATCTG 2525            _  CG  A
            GA                    TGTGGATTTGTCTT CTA  CT GA
                                  ||||||||||||| |||  || ||
                                  ACACCTAAACAGAA GGT  GA CT
                                        T   A_  C
GAM116  FOLR3    3'  TGTGGATTTGTCTATTAGATCT 2526        T_________   CGC
            AGCGTAG                 ATTTGTC        TCTA   TAG
                                  |||||||        ||||  |||
                                  TAAACAG        AGAT   ATC
                                     ATAATCTIII   CGC
GAM116  LOC204593 5'  TGTGGATTTTCTGGCT     2527          G   TCTAC
                                  TGTGGATTT TCT    GCT
                                  |||||||| |||    |||
                                  ACACCTAAA AGA    CGA
                                     _  C____
GAM116  LOC254911 5'  TGTGGATGTGTCTTCTCCAGA  2528        T      ACG
                                  TGTGGAT TGTCTTCT   CTAGA
                                  ||||||| ||||||||  |||||
                                  ACACCTA ACAGAAGA   GGTCT
                                     C      ___
GAM117  ASPH     3'  TGAGGTGCCAACAAAGCATTT  2531      A    C     A
                                  TGA GTGCC AATAGA GCATTT
                                  ||| ||||| |||||| ||||||
                                  ACT CACGG TTGTTT CGTAAA
                                    C   _    _
GAM117  ASPH     3'  TGAGGTGCCAACAAAGGCATTT 2532      A    C     A
                                  TGA GTGCC AATAGA GCATTT
                                  ||| ||||| |||||| ||||||
                                  ACT CACGG TTGTTT CGTAAA
                                    C    _     C
GAM117  ESR1     3'  TGAAGTGCCATAATAGAGGC   2533          C_     A
                                  TGAAGTGCC  AATAGA GC
                                  |||||||||  |||||| ||
                                  ACTTCACGG  TTATCT CG
                                       TA     C
GAM117  CASPR3   3'  TGAAGGTAGTCCAAGAAGCATT 2534       TGC__   AT
            TC                    TGAAG    CCA  AGAAGCATTTC
                                  |||||    |||  ||||||||||||
                                  ACTTC    GGT  TCTTCGTAAAG
                                    CATCA  __
GAM117  DKFZP564G2022 5'  TGGAGTGCCTACCGAAAGCATT 2535     A     CAATA
            TC                    TG AGTGCC    GAAGCATTTC
                                  || ||||||    ||||||||||
                                  AC TCACGG    TTTCGTAAAG
                                   C     ATGGC
GAM117  FLJ23309  3'  TGAAGTGCCAAAAGACTGGCAT 2536          C  T   A__
            TT                    TGAAGTGCC AA AGA   GCATTT
                                  ||||||||| || |||   ||||||
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                                ACTTCACGG TT TCT   CGTAAA
                                      _ T   GAC
GAM117  KLHL4    3'  TGAAGTTTTAAAAACATTT   2537       GCCCAA
                                TGAAGT     TAGAAGCATTT
                                ||||||     ||||||||||
                                ACTTCA     ATTTTTGTAAA
                                   AA____
GAM117  MGC12966 3'  TGAGGTGCTTTTAAGCATTT  2538     A   CCAATAG
                                TGA GTGC      AAGCATTT
                                ||| ||||      ||||||||
                                ACT CACG      TTCGTAAA
                                  C   AAAA___
GAM117  PRO1489  5'  TGAAATGCCAAAAGGCATTT  2539         C  T  AA
                                TGAAGTGCC AA AG  GCATTT
                                ||||||||| || ||  ||||||
                                ACTTTACGG TT TC  CGTAAA
                                      _ T  __
GAM117  PRO2730  5'  TGAGCTGCCCAAGCATTT    2540     AG     ATAGA
                                TGA  TGCCCA    AGCATTT
                                |||  ||||||    |||||||
                                ACT  ACGGGT    TCGTAAA
                                  CG     ______
GAM117  RGPR     3'  AAGTGCCCGGTGGAGGCATC  2541         AATA  A
                                AAGTGCCC    GA GCATT
                                ||||||||    || |||||
                                TTCACGGG    CT CGTAG
                                     CCAC  C
GAM117  T2BP     3'  GTTCCCAAAAGCATTT      2542     G    ATA
                                GT CCCA   GAAGCATTT
                                || ||||   |||||||||
                                CA GGGT   TTTCGTAAA
                                 A   ___
GAM117  LOC118851 3'  TGAAGTGCCCATTTTCATTTC  2543           ATAGAAG
                                TGAAGTGCCCA      CATTTC
                                ||||||||||       ||||||
                                ACTTCACGGGT      GTAAAG
                                      AAAA___
GAM117  LOC158401 5'  TGAAGTGCTGAACATT      2544         CCAATA   G
                                TGAAGTGC     GAA CATT
                                ||||||||     ||| ||||
                                ACTTCACG     CTT GTAA
                                     A_____  _
GAM117  LOC199775 3'  TGAAGTGCCAGTGCCTTATCAT 2545          CAATAGAAG_
           TTC                    TGAAGTGCC         CATTTC
                                  |||||||||         ||||||
                                  ACTTCACGG         GTAAAG
                                       TCACGGAATA
GAM117  LOC202781 3'  TGAAATGCTTGGGACAAAAGTA 2546         CCA__      C
           TTTC                     TGAAGTGC     ATAGAAG ATTTC
                                    ||||||||     ||||||| |||||
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                                ACTTTACG    TGTTTTC TAAAG
                                    AACCC      A
GAM118  ARAF1    5'  TTTGTCAAGATGGGCTG    2549        GT     A
                                TTTGTCA  AGGTGG GCTG
                                |||||||  |||||| ||||
                                AAACAGT  TCTACC CGAC
                                   __     _
GAM118  AVPR1A   5'  TGTGGAGGGGGGTGGAGCTG   2550     C_  TA
                                TGT  AG  GGTGGAGCTG
                                |||  ||  ||||||||||
                                ACA  TC  CCACCTCGAC
                                  CC  CC
GAM118  BCL2     3'  TTTGGCAGTAAATAGCTG    2551      T      GG
                                TTTG CAGTAGGT  AGCTG
                                |||| ||||||||  |||||
                                AAAC GTCATTTA  TCGAC
                                  C       __
GAM118  DMRT2    3'  TTTGTCAGTAAGTGTTTGCTG  2552            GA_
                                TTTGTCAGTAGGTG   GCTG
                                ||||||||||||||   ||||
                                AAACAGTCATTCAC   CGAC
                                       AAA
GAM118  DUSP1    3'  TTTGTCAGATGGACT      2553         TAG    G
                                TTTGTCAG   GTGGA CT
                                ||||||||   ||||| ||
                                AAACAGTC   TACCT GA
                                   ____    _
GAM118  ELF3     3'  TTTGTCAGACTCAAAAGCTG   2554         TAGGT
                                TTTGTCAG    GGAGCTG
                                ||||||||    |||||||
                                AAACAGTC    TTTCGAC
                                    TGAGT
GAM118  FANCF    3'  TTTGTCACTTTAAAGCTG    2555        GTAGG
                                TTTGTCA    TGGAGCTG
                                |||||||    ||||||||
                                AAACAGT    ATTTCGAC
                                    GAA__
GAM118  FREB     3'  TGTCAGTAAGAATAGCTG    2556          TGG
                                TGTCAGTAGG   AGCTG
                                |||||||||   |||||
                                ACAGTCATTC   TCGAC
                                     TTA
GAM118  GAD2     3'  TTTCTCAGTAGGGGGCT     2557     G      T  A
                                TTT TCAGTAGG GG GCT
                                ||| |||||||| || |||
                                AAA AGTCATCC CC CGA
                                  G       _  _
GAM118  GBE1     3'  TCTGCATCTGGTGGAGCTG   2558      T  GTA
                                TTTG CA   GGTGGAGCTG
                                |||| ||   ||||||||||
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                                AGAC GT   CCACCTCGAC
                                  _ AGA
GAM118  GUCY1B2  3'  TTTGTCGGAGCTGAAGGCTG  2559       AGT  G    _
                                TTTGTC   AG TGGAG CTG
                                ||||||   || ||||| |||
                                AAACAG   TC ACTTC GAC
                                   CC_  G    C
GAM118  HAO1     3'  TTTGTCAAGTAATACATGCTG  2560       _   GTGGA
                                TTTGTCA GTAG    GCTG
                                ||||||| ||||    ||||
                                AAACAGT CATT    CGAC
                                   T   ATGTA
GAM118  JPH3     3'  TCTGTCTCCACGTGGAGCTG  2561       AG  G
                                TTTGTC  TA GTGGAGCTG
                                ||||||  || |||||||||
                                AGACAG  GT CACCTCGAC
                                   AG  G
GAM118  LAPTM5   3'  TTTGTCAGTTGCTTGGCTG   2562        AG  GGA
                                TTTGTCAGT  GT   GCTG
                                |||||||||  ||   ||||
                                AAACAGTCA  CG   CGAC
                                     A_  AAC
GAM118  NRF1     3'  TTTGTCAGTAGCTCAAC     2563         G GG
                                TTTGTCAGTAG T  AGC
                                |||||||||||  |  |||
                                AAACAGTCATC G  TTG
                                      _ AG
GAM118  PDE4D    3'  TTTGTCAGCTCTACCAAGCTG  2564        AG_ TG
                                TTTGTCAGT   G  GAGCTG
                                |||||||||   |  ||||||
                                AAACAGTCG   T  TTCGAC
                                     AGA GG
GAM118  PITPN    3'  CTTGGGAGGGTGGAGCTG    2565      TC  TA
                                TTTG  AG  GGTGGAGCTG
                                ||||  ||  ||||||||||
                                GAAC  TC  CCACCTCGAC
                                  CC  __
GAM118  PLAUR    5'  TTTGTCAGGAGGGATACTG   2566        T   T  A
                                TTTGTCAG AGG GG GCTG
                                |||||||| ||| || ||||
                                AAACAGTC TCC CT TGAC
                                     C   _  A
GAM118  SLA2     3'  TTTGCCAAGTGGAGCTG     2567        GTA
                                TTTGTCA   GGTGGAGCTG
                                |||||||   ||||||||||
                                AAACGGT   TCACCTCGAC
                                      ____
GAM118  TCFL4    3'  CTTGTCAGGCTACAGAGCTG  2568         TAG TG
                                TTTGTCAG   G  GAGCTG
                                ||||||||   |  ||||||
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                                GAACAGTC  T  CTCGAC
                                    CGA GT
GAM118  TSPY     3'  TTCGTCAGTGATCAGGGCTG  2569         A  __  A
                                TTTGTCAGT GGT  GG GCTG
                                ||||||||| |||  || ||||
                                AAGCAGTCA CTA  CC CGAC
                                    _  GT  _
GAM118  DJ473B4  5'  TTTGTCAGCGTCTCTAGGCTG  2570         AGG__  A
                                TTTGTCAGT    TGG GCTG
                                |||||||||    ||| ||||
                                AAACAGTCG    ATC CGAC
                                    CAGAG  _
GAM118  DKFZp434O0320 3'  TTTGTGAGTAGACAGGCTG  2571       C     TG A
                                TTTGT AGTAGG  G GCTG
                                ||||| ||||||  | ||||
                                AAACA TCATCT  C CGAC
                                   C     GT _
GAM118  DKFZP434O125 3'  TTTGTAGCCTCTGGAGCTG  2572       C  AGG
                                TTTGT AGT  TGGAGCTG
                                ||||| |||  ||||||||
                                AAACA TCG  ACCTCGAC
                                   _  GAG
GAM118  DKFZP564L2423 3'  TTTGATCAAACCTGGAGCTG  2573      _   TAGG
                                TTTG TCAG   TGGAGCTG
                                |||| ||||   ||||||||
                                AAAC AGTT   ACCTCGAC
                                  T   TGG_
GAM118  ECE2     3'  TTTGTCAGGAGAGCTG     2574         TAGGT
                                TTTGTCAG    GGAGCTG
                                ||||||||    |||||||
                                AAACAGTC    TCTCGAC
                                    C____
GAM118  FLJ10597  3'  TCTGTCAGTATGGGGGCTG  2575         _ T  A
                                TTTGTCAGTA GG GG GCTG
                                |||||||||| || || ||||
                                AGACAGTCAT CC CC CGAC
                                    A  _  _
GAM118  FLJ11222  5'  CTTGGCAACGGTGGAGCTG  2576      T  GTA
                                TTTG CA  GGTGGAGCTG
                                |||| ||  ||||||||||
                                GAAC GT  CCACCTCGAC
                                  C  TG_
GAM118  FLJ12409  3'  TTTGTCAGTGAGTAACTTCTG  2577         AG   AG_
                                TTTGTCAGT  GTGG  CTG
                                |||||||||  ||||  |||
                                AAACAGTCA  CATT  GAC
                                    CT   GAA
GAM118  FLJ12572  5'  TTTGTAGTAGCTATAGCTG  2578       C    G  G
                                TTTGT AGTAG TG AGCTG
                                ||||| ||||| || |||||
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                                AAACA TCATC AT TCGAC
                                  _    G  A
GAM118  FLJ13710 3' TCTGTCAGTGGCCCATCTG   2579        A   GGAG
                                TTTGTCAGT GGT   CTG
                                ||||||||| |||   |||
                                AGACAGTCA CCG   GAC
                                     _  GGTA
GAM118  FLJ20464 5' TTGTCGCCTCCCGGAGCTG   2580      A  AGG_
                                TTGTC GT   TGGAGCTG
                                ||||| ||   ||||||||
                                AACAG CG   GCCTCGAC
                                  _ GAGG
GAM118  FLJ30058 3' TTTGTCAGCTGTCAGTAGGCTG 2581        A___    A
                                TTTGTCAGT   GGTGG GCTG
                                |||||||||   ||||| ||||
                                AAACAGTCG   TCATC CGAC
                                     ACAG   _
GAM118  FLJ30567 3' TGTTGATGGGGTGGAGCTG   2582     CA  A_
                                TGT  GT  GGTGGAGCTG
                                |||  ||  ||||||||||
                                ACA  TA  CCACCTCGAC
                                  AC  CC
GAM118  FLJ31153 3' TTTGCCAATCAGGAGCTG    2583        AGGT
                                TTTGTCAGT   GGAGCTG
                                |||||||||   |||||||
                                AAACGGTTA   CCTCGAC
                                     GT__
GAM118  KIAA0121 3' TCTGTCAGTAATCTGCTG    2584         GTGGA
                                TTTGTCAGTAG    GCTG
                                ||||||||||    ||||
                                AGACAGTCATT    CGAC
                                      AGA__
GAM118  KIAA0352 3' TTTATCAGTTCAGGGCTG    2585        AGGT  A
                                TTTGTCAGT   GG GCTG
                                |||||||||   || ||||
                                AAATAGTCA   CC CGAC
                                     AGT_  _
GAM118  KIAA0444 3' TTTGCCAGCCTGGGGCTG    2586        AGG   A
                                TTTGTCAGT   TGG GCTG
                                |||||||||   ||| ||||
                                AAACGGTCG   ACC CGAC
                                     G__   C
GAM118  KIAA0871 3' TTTGTCAGAGTTTGGCTG    2587        TA   GGA
                                TTTGTCAG  GGT   GCTG
                                ||||||||  |||   ||||
                                AAACAGTC  TCA   CGAC
                                     __  AAC
GAM118  KIAA1219 3' TTTGTCAGTGTGACAGCTG   2588        AG   _
                                TTTGTCAGT  GTGG AGCTG
                                |||||||||  |||| |||||
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                                AAACAGTCA  CACT TCGAC
                                    __   G
GAM118  KIAA1949  3'  TTTGGCAGGTGGGGCTG    2589     TCA      A
                                TTTG  GTAGGTGG GCTG
                                ||||  |||||||| ||||
                                AAAC  CGTCCACC CGAC
                                   ___      C
GAM118  KIAA1949  3'  TTTGGCAGGTGGGGCTG    2589     TCA      A
                                TTTG  GTAGGTGG GCTG
                                ||||  |||||||| ||||
                                AAAC  CGTCCACC CGAC
                                   ___      C
GAM118  KIAA1949  3'  TTTGGCAGGTGGGGCTG    2589     TCA      A
                                TTTG  GTAGGTGG GCTG
                                ||||  |||||||| ||||
                                AAAC  CGTCCACC CGAC
                                   ___      C
GAM118  MIL1      3'  TTTACAAGGTGGAGCTG    2590      T  GT
                                TTTG CA  AGGTGGAGCTG
                                |||| ||  ||||||||||
                                AAAT GT  TCCACCTCGAC
                                  _ __
GAM118  NIP30     3'  TTTGTCAGGATGGAGCTG    2591       TA
                                TTTGTCAG  GGTGGAGCTG
                                ||||||||  |||||||||
                                AAACAGTC  CTACCTCGAC
                                    __
GAM118  OR2C3     5'  TTTGTCAGTTGATTTCTG    2592       A  GGAG
                                TTTGTCAGT GGT   CTG
                                ||||||||| |||   |||
                                AAACAGTCA CTA   GAC
                                     A  AA__
GAM118  PSMD10    3'  CTTGTTGCTATTGGAGCTG   2593      CA  AGG
                                TTTGT  GT   TGGAGCTG
                                |||||  ||  ||||||||
                                GAACA  CG   ACCTCGAC
                                   A_  ATA
GAM118  SDBCAG84  3'  TTTATCAACCTGGGGCTG    2594       TAGG  A
                                TTTGTCAG    TGG GCTG
                                ||||||||    ||| ||||
                                AAATAGTT    ACC CGAC
                                     GG__   C
GAM118  SEC8      3'  TTTGTTGTAAACAGCAGCTG  2595      CA    TG _
                                TTTGT  GTAGG  G AGCTG
                                |||||  |||||  | |||||
                                AAACA  CATTT  C TCGAC
                                   A_     GT G
GAM118  SENP7     3'  TTTGACAAGCACTGGGGCTG  2596      T  _  GG  A
                                TTTG CA GTA  TGG GCTG
                                |||| || |||  ||| ||||
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                                AAAC GT CGT  ACC CGAC
                                  T T  G_  C
GAM118  TM4-B    3'  TGTGGCAGGTGGGGCTG    2597     CA      A
                                TGT  GTAGGTGG GCTG
                                |||  |||||||| ||||
                                ACA  CGTCCACC CGAC
                                  C_       C
GAM118  ZNF317   3'  TCTGTCAGTGGCCAGGGCTG  2598         A  __  A
                                TTTGTCAGT GGT  GG GCTG
                                ||||||||| |||  || ||||
                                AGACAGTCA CCG  CC CGAC
                                      _  GT  _
GAM118  LOC119188 5'  TTTGTGGATCTCAGAGCTG   2599      CA  AGG
                                TTTGT  GT   TGGAGCTG
                                |||||  ||   ||||||||
                                AAACA  TA   GTCTCGAC
                                   CC  GA_
GAM118  LOC150113 5'  TCTGGTAAAGGTGGAGCTG   2600     TC  T
                                TTTG  AG AGGTGGAGCTG
                                ||||  || ||||||||||
                                AGAC  TT TCCACCTCGAC
                                  CA  _
GAM118  LOC151979 5'  TTTGTCAGACCTTTGTGGAGCT 2601        TAG___
          G                      TTTGTCAG     GTGGAGCTG
                                ||||||||     |||||||||
                                AAACAGTC     CACCTCGAC
                                     TGGAAA
GAM118  LOC153910 3'  TTTGTTAGGTGGAGACTG    2602      CAG      _
                                TTTGT   TAGGTGGAG CTG
                                |||||   ||||||||| |||
                                AAACA   ATCCACCTC GAC
                                   ___       T
GAM118  LOC160646 3'  TTTGTCAGGGGAGCT      2603       GTA  T
                                TTTGTCA   GG GGAGCT
                                |||||||   || ||||||
                                AAACAGT   CC CCTCGA
                                   ___  _
GAM118  LOC170425 5'  TTTGTCAGTAAGGAAAATGCTG 2604          TG  __
                                TTTGTCAGTAGG  GA  GCTG
                                ||||||||||||  ||  ||||
                                AAACAGTCATTC  TT  CGAC
                                      CT  TA
GAM118  LOC220394 5'  TTCGTCAGTGTGCCTCAGCTG  2605        AG  GG_
                                TTTGTCAGT  GT   AGCTG
                                |||||||||  ||   |||||
                                AAGCAGTCA  CG   TCGAC
                                     CA  GAG
GAM118  LOC254173 3'  TTTGCAGTAGGAGCT      2606      T    GGT
                                TTTG CAGTA   GGAGCT
                                |||| |||||   ||||||
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                                AAAC GTCAT   CCTCGA
                                  _    ____
GAM118  LOC255458 5'  TTTGTTAGAGCCGGCAGCTG   2607       C  T  G  _
                                TTTGT AG AG TGG AGCTG
                                ||||| || || ||| |||||
                                AAACA TC TC GCC TCGAC
                                   A  _  G   G
GAM118  LOC91149  3'  TTTGATAGGTAGGGCTG     2608      TCA      A
                                TTTG   GTAGGTGG GCTG
                                ||||   |||||||| ||||
                                AAAC   TATCCATC CGAC
                                  ____       C
GAM118  LOC91948  3'  TTTGTCAATGTTTAAGCTG    2609         AGGTG
                                TTTGTCAGT    GAGCTG
                                |||||||||    ||||||
                                AAACAGTTA    TTCGAC
                                     CAAA_
GAM119  CHD2      3'  TTCATCACAAAACAATGC     2612          CA_
                                TTCATCATAG   GATGC
                                ||||||||||   |||||
                                AAGTAGTGTT   TTACG
                                     TTG
GAM119  CLK2      3'  TCCATCATGGCTAGATGC     2613         A  _
                                TTCATCAT GC AGATGC
                                |||||||| || ||||||
                                AGGTAGTA CG TCTACG
                                     C  A
GAM119  GNAS      3'  TTCATCACACTCAGGATG     2614         G_  _
                                TTCATCATA  CAG ATG
                                |||||||||  ||| |||
                                AAGTAGTGT  GTC TAC
                                     GA   C
GAM119  ITK       3'  TCCATCACTTTGGGCAGATG   2615         A____
                                TTCATCAT    GCAGATG
                                ||||||||    |||||||
                                AGGTAGTG    CGTCTAC
                                     AAACC
GAM119  MLLT2     3'  TTCATCATAGGGATCTTAGATG 2616          C_______
                                TTCATCATAG      AGATG
                                ||||||||||      |||||
                                AAGTAGTATC      TCTAC
                                     CCTAGAA
GAM119  PPP2R5E   3'  TTCACCATAAACTGATGC     2617          _ A
                                TTCATCATAG C GATGC
                                |||||||||| | |||||
                                AAGTGGTATT G CTACG
                                     T A
GAM119  WASF1     5'  TTCATCATCCGCAAGTGC     2618         A_   A
                                TTCATCAT  GCAG TGC
                                ||||||||  |||| |||
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                                AAGTAGTA  CGTT ACG
                                    GG    C
GAM119  CCR8     3'  TTCACCATCAGTCAATGC    2619        _ CA
                                TTCATCAT AG  GATGC
                                |||||||| ||  |||||
                                AAGTGGTA TC  TTACG
                                    G  AG
GAM119  FLJ13386 3'  TTCACCACTGCTTTAGATG   2620        A ___
                                TTCATCAT GC   AGATG
                                |||||||| ||   |||||
                                AAGTGGTG CG   TCTAC
                                    A  AAA
GAM119  KIAA0923 3'  CTCATCATAGACTGCAGATGC 2621          ____
                                TTCATCATA    GCAGATGC
                                |||||||||    ||||||||
                                GAGTAGTAT    CGTCTACG
                                     CTGA
GAM119  MGC24447 3'  CTCATCATAACTTAATGC    2622          A_
                                TTCATCATAGC  GATGC
                                ||||||||||  |||||
                                GAGTAGTATTG  TTACG
                                      AA
GAM119  SMARCF1  3'  TCATCATACAGCAGGATG    2623        __   _
                                TCATCAT  AGCAG ATG
                                |||||||  ||||| |||
                                AGTAGTA  TCGTC TAC
                                    TG    C
GAM119  LOC116068 3'  TTCACCACATTCCAGATGC   2624         G__
                                TTCATCATA   CAGATGC
                                |||||||||   |||||||
                                AAGTGGTGT   GTCTACG
                                     AAG
GAM119  LOC120526 3'  TTCAGCATAGCAGCAGTGC   2625      T      A__
                                TTCA CATAGCAG   TGC
                                |||| ||||||||   |||
                                AAGT GTATCGTC   ACG
                                  C       GTC
GAM119  LOC145501 3'  CTCGTCATAGCAGCAGTGC   2626      A      A__
                                TTC TCATAGCAG   TGC
                                ||| |||||||||   |||
                                GAG AGTATCGTC   ACG
                                  C        GTC
GAM119  LOC146894 3'  TTCATCACCAGCTGATGC    2627         _  A
                                TTCATCAT AGC GATGC
                                |||||||| ||| |||||
                                AAGTAGTG TCG CTACG
                                    G   A
GAM119  LOC164173 3'  TTCACCATACACTCATGC    2628          _ AG
                                TTCATCATA GC  ATGC
                                |||||||||  ||  ||||
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                                AAGTGGTAT TG  TACG
                                     G  AG
GAM119  LOC201627 3'  TCCATCATTAATACTAGATGC  2629          A___  _
                                TTCATCAT   GC AGATGC
                                ||||||||   || ||||||
                                AGGTAGTA   TG TCTACG
                                     ATTA  A
GAM119  LOC219920 5'  CTCATCATTAGCTGGCAGGTGC 2630          A_____   A  III
           G                     TTCATCAT    GCAG TGC  G
                                ||||||||     |||| |||  |
                                GAGTAGTA    CGTC ACG  C
                                     ATCGAC   C  III
GAM119  LOC92078  3'  TCATCACAGACTGTAGGTGC  2631          _ ___  A
                                TCATCATAG C  AG TGC
                                ||||||||| |  || |||
                                AGTAGTGTC G  TC ACG
                                     T ACA  C
GAM120  ABCB11   3'  TGCCTGTTATAGACCCGCCT  2634       AC__  A
                                TGCC   GTA ACCCGCCT
                                ||||   ||| ||||||||
                                ACGG   TAT TGGGCGGA
                                  ACAA  C
GAM120  BLK      3'  CACCCCGCCTTCGCGGCCCGTC 2635          A_  AAA   C
           T                     CACCCTGCC  CGT  CCCG CT
                                |||||||||  |||  |||| ||
                                GTGGGGCGG  GCG  GGGC GA
                                     AA  CC_   A
GAM120  CLCN4    5'  CACGCTGCCACGTGACGCCC  2636      C       AAACC
                                CAC CTGCCACGT    CGCCT
                                ||| |||||||||    |||||
                                GTG GACGGTGCA    GCGGG
                                  C       CT___
GAM120  INHA     5'  CACCCTGCCCCGTGCCCC    2637          A  AAA
                                CACCCTGCC CGT  CCC
                                ||||||||| |||  |||
                                GTGGGACGG GCA  GGG
                                     G  CG_
GAM120  KIT      3'  ACTCTGCCATGTACACATTTGC 2638     C    C  A  CC__
           CT                    AC CTGCCA GTA AC   GCCT
                                || |||||| ||| ||   ||||
                                TG GACGGT CAT TG   CGGA
                                 A     A  G  TAAA
GAM120  KLF4     5'  CACCACTGTCGCGGTCGCCT  2639      _  CCA  AAACC
                                CACC CTG  CGT    CGCCT
                                |||| |||  |||    |||||
                                GTGG GAC  GCG    GCGGA
                                  T  A__  CCA__
GAM120  PIG3     5'  CTGCCGCGGACCCGCCT     2640       A  TAA
                                CTGCC CG  ACCCGCCT
                                ||||| ||  ||||||||
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                                GACGG GC   TGGGCGGA
                                  C  C__
GAM120  REPS2    5'  CCGCCACAGCCACCGCCT    2641        _  AAAC
                                CTGCCAC GT    CCGCCT
                                ||||||| ||    ||||||
                                GGCGGTG CG    GGCGGA
                                   T  GT__
GAM120  S100A10  5'  CCCTCGCTCCCGGACCCGCCT  2642      _  CA_  TAA
                                CCCT GC   CG   ACCCGCCT
                                |||| ||   ||   ||||||||
                                GGGA CG   GC   TGGGCGGA
                                  G  AGG  C__
GAM120  SERPINA4 3'  CCCTGCCACATCCTCCTGC   2643          AAA  C
                                CCCTGCCACGT   CC GC
                                ||||||||||   || ||
                                GGGACGGTGTA   GG CG
                                      GGA  A
GAM120  SLC9A5   3'  CACCCTGTCAGCCCCTGC    2644        C  C  AAA  _
                                CACCCTG CA GT   CCC GC
                                ||||||| || ||   ||| ||
                                GTGGGAC GT CG   GGG CG
                                   A  _  ___   A
GAM120  SLC9A5   3'  CACCCTGTCAGCCCCTGC    2644        C  C  AAA  _
                                CACCCTG CA GT   CCC GC
                                ||||||| || ||   ||| ||
                                GTGGGAC GT CG   GGG CG
                                   A  _  ___   A
GAM120  TRO      3'  CACCCTGCTGTCCTGCC     2645         CAC  AAA  C
                                CACCCTGC   GT   CC GCC
                                ||||||||   ||   || |||
                                GTGGGACG   CA   GG CGG
                                   A__  ___  A
GAM120  BMF      3'  CTGCCACGTCCCTTCTGCCT  2646          AAA  ____
                                CTGCCACGT   CCC    GCCT
                                |||||||||   |||    ||||
                                GACGGTGCA   GGG    CGGA
                                     ___   AAGA
GAM120  CHST3    3'  CCTGCCACGTGGCCACCT    2647          AAAC
                                CCTGCCACGT    CCGCCT
                                ||||||||||    ||||||
                                GGACGGTGCA    GGTGGA
                                    CC__
GAM120  CLDN4    3'  CACCACTGCCCAAACC      2648      _    ACG
                                CACC CTGCC   TAAACC
                                |||| |||||   ||||||
                                GTGG GACGG   GTTTGG
                                  T    ___
GAM120  FLJ12171 3'  ACCCTGCCTGTAGTGTGGCTCC 2649          AC   AACCC  _
                                ACCCTGCC  GTA    GC CT
                                ||||||||  |||    || ||
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                                TGGGACGG  CAT    CG GG
                                    A_   CACAC  A
GAM120   FLJ20257  3'  CCCTGCCAGTCTTCTCCGTCT  2650        C  AAAC_   C
                                CCCTGCCA GT    CCG CT
                                |||||||| ||    ||| ||
                                GGGACGGT CA    GGC GA
                                    _ GAAGA   A
GAM120   FLJ20531  3'  CACCCTGCACTCTGTCGCCT   2651        C  GTAAACC
                                CACCCTGC AC     CGCCT
                                |||||||| ||     |||||
                                GTGGGACG TG     GCGGA
                                    _ AGACA__
GAM120   FLJ20967  5'  CACCCGCCACATCCGC     2652       T     AAAC
                                CACCC GCCACGT   CCGC
                                ||||| |||||||   ||||
                                GTGGG CGGTGTA   GGCG
                                  _    _____
GAM120   GMPPB     5'  CCCTTCACCAACCCGCCT    2653      GC   GTA
                                CCCT  CAC   AACCCGCCT
                                ||||  |||   |||||||||
                                GGGA  GTG   TTGGGCGGA
                                  A_   G__
GAM120   GMPPB     5'  CCCTTCACCAACCCGCCT    2653      GC   GTA
                                CCCT  CAC   AACCCGCCT
                                ||||  |||   |||||||||
                                GGGA  GTG   TTGGGCGGA
                                  A_   G__
GAM120   GTPBP5    3'  CCCATGCCACGGCCGCCT    2654      _     TAAAC
                                CCC TGCCACG    CCGCCT
                                ||| |||||||    ||||||
                                GGG ACGGTGC    GGCGGA
                                  T     C____
GAM120   HSPC052   5'  CACCCTGCGCTGCCCTCTGCCT 2655        CAC  AAA  ___
                                CACCCTGC   GT   CCC   GCCT
                                ||||||||   ||   |||   ||||
                                GTGGGACG   CG   GGG   CGGA
                                    ___  AC_   AGA
GAM120   KIAA0543  3'  ACCCTGCCTGCTGACTTGCCT  2656        AC  AA  CC
                                ACCCTGCC  GT  AC  GCCT
                                ||||||||  ||  ||  ||||
                                TGGGACGG  CG  TG  CGGA
                                    A_  AC  AA
GAM120   KIAA1271  3'  CACCCTGCCGCTCCTGCC    2657        AC  AAA  C
                                CACCCTGCC  GT   CC GCC
                                |||||||||  ||   || |||
                                GTGGGACGG  CG   GG CGG
                                    __  A__  A
GAM120   LY117     3'  ACCCTGTCCACCCGCC     2658        _  ACGTAA
                                ACCCTG CC     ACCCGCC
                                |||||| ||     |||||||
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                                TGGGAC GG     TGGGCGG
                                  A _______
GAM120  LY117    3'  ACCCTGTCCACCCGCC      2658        _ ACGTAA
                                ACCCTG CC     ACCCGCC
                                |||||| ||     |||||||
                                TGGGAC GG     TGGGCGG
                                  A _______
GAM120  LY117    3'  ACCCTGTCCACCCGCC      2658        _ ACGTAA
                                ACCCTG CC     ACCCGCC
                                |||||| ||     |||||||
                                TGGGAC GG     TGGGCGG
                                  A _______
GAM120  MESDC2   3'  CACCCTGCTGATGTAGGACACC 2659         CAC_   AACC
           T                     CACCCTGC    GTA    CGCCT
                                ||||||||    |||    |||||
                                GTGGGACG    CAT    GTGGA
                                     ACTA   CCT_
GAM120  MGC7036  3'  CACCCTGCACATCCC       2660         C    AAA
                                CACCCTGC ACGT   CCC
                                |||||||| ||||   |||
                                GTGGGACG TGTA   GGG
                                  _    ____
GAM120  MRPL48   5'  CCCGCCACCACGCCCGCCT   2661         G  AA
                                CCTGCCAC TA  CCCGCCT
                                |||||||| ||  |||||||
                                GGGCGGTG GT  GGGCGGA
                                   _ GC
GAM120  OLIG1    3'  CTGCCACGTCCCAGACC     2662          AAA  __
                                CTGCCACGT   CCC  GCC
                                |||||||||   |||  |||
                                GACGGTGCA   GGG  TGG
                                     ___   TC
GAM120  PRO0097  3'  CACCCTGCCTCCATTTGCCT  2663          A_   AAACCC
                                CACCCTGCC  CGT     GCCT
                                |||||||||  |||     ||||
                                GTGGGACGG  GTA     CGGA
                                     AG   AA____
GAM120  PTPN21   5'  CCCCGCTCAGCGACCCGCCT  2664        _ _  TAA
                                CCCTGC CA CG   ACCCGCCT
                                |||||| || ||   ||||||||
                                GGGGCG GT GC   TGGGCGGA
                                  A  C  ___
GAM120  SNPH     3'  CTGCCACGCCCCTGCCT     2665          AAA  _
                                CTGCCACGT   CCC GCCT
                                |||||||||   ||| ||||
                                GACGGTGCG   GGG CGGA
                                     ___   A
GAM120  LOC126549 5'  CCCTGCCACCTGTAGAGCTTGC 2666          __   AACCC_
           CT                     CCCTGCCAC  GTA     GCCT
                                |||||||||  |||     ||||
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                                GGGACGGTG  CAT     CGGA
                                    GA   CTCGAA
GAM120   LOC136442 3'  CACCCGTGCCGTCAGCCCCGTC 2667       _   ACG  AA    C
           T                     CACCC TGCC   TA  CCCG CT
                                 ||||| ||||   ||  |||| ||
                                 GTGGG ACGG   GT  GGGC GA
                                   C   CA_  CG    A
GAM120   LOC139046 5'  CCTGCCACGCCAGGCCTGCCT  2668          AAA_  C
                                 CCTGCCACGT    CC GCCT
                                 ||||||||||    || ||||
                                 GGACGGTGCG    GG CGGA
                                       GTCC  A
GAM120   LOC146842 5'  CCTGCCACGTACGGTCCGCCT  2669          AAC_
                                 CCTGCCACGTA    CCGCCT
                                 ||||||||||    ||||||
                                 GGACGGTGCAT    GGCGGA
                                       GCCA
GAM120   LOC152453 5'  CACCCTGCTGCTGTGCACCT   2670        CAC  AAACC
                                 CACCCTGC   GT    CGCCT
                                 ||||||||   ||    |||||
                                 GTGGGACG   CG    GTGGA
                                     A__  ACAC_
GAM120   LOC158435 3'  CCTCTGCCACAGAACCTGCCT  2671     _      TA    C
                                 CC CTGCCACG  AACC GCCT
                                 || ||||||||  |||| ||||
                                 GG GACGGTGT  TTGG CGGA
                                   A       C_    A
GAM120   LOC199780 5'  CACCCTGCCCACCCGCC     2672          A GTAA
                                 CACCCTGCC C    ACCCGCC
                                 |||||||||  |    |||||||
                                 GTGGGACGG G    TGGGCGG
                                        _ _____
GAM120   LOC200317 5'  CCCTGCCAGCCCCCTGCCT   2673         C  AAA  C
                                 CCCTGCCA GT   CC GCCT
                                 |||||||| ||   || ||||
                                 GGGACGGT CG   GG CGGA
                                     _  GG_  A
GAM120   LOC200743 5'  CACCCCGCCCCCGCCC      2674         ACGTAAA
                                 CACCCTGCC      CCCGCCT
                                 |||||||||      |||||||
                                 GTGGGGCGG      GGGCGGG
                                        ________
GAM120   LOC257480 5'  CCTGCCACGCTCCGCCGCCT   2675          AAAC
                                 CCTGCCACGT    CCGCCT
                                 ||||||||||    ||||||
                                 GGACGGTGCG    GGCGGA
                                       AGGC
GAM121   CALCA    3'  TGAGTCCTGCTCTCTTTCC    2678      T     AGTG
                                 TGA TCCTGT    CTCTTTCC
                                 ||| ||||||    ||||||||
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                                ACT AGGACG   GAGAAAGG
                                  C     A___
GAM121  HCS      3'  TATGTTTCCTGTATCATTTCC  2679      A      GTGC  _
                                TATG TTCCTGTA   TC TTTCC
                                |||| ||||||||   || |||||
                                ATAC AAGGACAT   AG AAAGG
                                  A       _____ T
GAM121  PPARGC1  3'  TATGATATCTGTAGTGCT    2680       TC
                                TATGAT  CTGTAGTGCT
                                ||||||  ||||||||||
                                ATACTA  GACATCACGA
                                   TA
GAM121  SHMT1    3'  TATAATTCTTGTAGACATTCT  2681        C    _ GC
                                TATGATTC TGTAG T  TCT
                                |||||||| ||||| |  |||
                                ATATTAAG ACATC G  AGA
                                     A    T TA
GAM121  ARSDR1   3'  TCCTATAACTCTTTCC     2682        GT
                                TCCTGTA  GCTCTTTCC
                                |||||||  |||||||||
                                AGGATAT  TGAGAAAGG
                                   __
GAM121  CDC14B   3'  TGGTTCCAGTGACACCCTTTC  2683    A   T  AG
                                TG TTCC GT  TGCTCTTTC
                                || |||| ||  |||||||||
                                AC AAGG CA  GTGGGAAAG
                                 C   T  CT
GAM121  FLJ20079 3'  TATGATTCTTTTCTCTTTCC   2684        CTGTAGTG
                                TATGATTC       CTCTTTCC
                                ||||||||       ||||||||
                                ATACTAAG       GAGAAAGG
                                     AAAA_____
GAM121  FLJ22028 3'  TATGATTCCTGAAGAAATTCC  2685          T  TGCTCT
                                TATGATTCCTG AG     TTCC
                                |||||||||| ||     ||||
                                ATACTAAGGAC TC     AAGG
                                      T  TTT___
GAM121  HCGIV.9  3'  TGATTCCTGTTGTAATGCT   2686         ___
                                TGATTCCTGT   AGTGCT
                                ||||||||||   ||||||
                                ACTAAGGACA   TTACGA
                                      ACA
GAM121  KIAA0417 3'  TATGGTTCCTCCTCTTTC    2687      A    GTAGTG
                                TATG TTCCT     CTCTTTC
                                |||| |||||     |||||||
                                ATAC AAGGA     GAGAAAG
                                  C    G_____
GAM121  KIAA1396 3'  ATTCCTGTTAGTTTTC      2688         _  GCTC
                                ATTCCTGT AGT    TTTC
                                |||||||| |||   ||||
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                                TAAGGACA TCA    AAAG
                                    A  _____
GAM121  LCE      3'  TGATTCCTTGTGCCATTTTC  2689        GTA    C_
                                TGATTCCT  GTGCT  TTTC
                                ||||||||  |||||  ||||
                                ACTAAGGA  CACGG  AAAG
                                    A__    TA
GAM121  MGC15429 3'  TGATTCCTGAGAGTTTTTTC  2690         T_  GCTC
                                TGATTCCTG  AGT   TTTC
                                |||||||||  |||   ||||
                                ACTAAGGAC  TCA   AAAG
                                     TC  AA__
GAM121  RAB39    3'  TAATTCCTGATAAAATCTTT  2691         _  TGC
                                TGATTCCTG TAG  TCTTT
                                ||||||||| |||  |||||
                                ATTAAGGAC ATT  AGAAA
                                     T  TT_
GAM121  LOC131544 3'  TGTTTCCTTCTTTGCTCTTTC  2692    A    GTAG
                                TG TTCCT   TGCTCTTTC
                                || |||||   |||||||||
                                AC AAGGA   ACGAGAAAG
                                 A    AGAA
GAM121  LOC144512 5'  ATGATTCTTTATGCTCTTT   2693       CTGTA
                                ATGATTC    GTGCTCTTT
                                |||||||    |||||||||
                                TACTAAG    TACGAGAAA
                                    AAA__
GAM121  LOC149157 3'  TATGATCCTGTTCCTT     2694       T    AGTGC
                                TATGAT CCTGT    TCTTT
                                |||||| |||||    |||||
                                ATACTA GGACA    AGGAA
                                  _   _____
GAM121  LOC151556 3'  TATGATTCCATGTAGGGTTCT  2695         _    TGC
                                TATGATTCC TGTAG  TCT
                                ||||||||| |||||  |||
                                ATACTAAGG ACATC  AGA
                                     T    CCA
GAM121  LOC203286 3'  TATGTCCAGTGCTCTTTC    2696     AT  TGT
                                TATG  TCC  AGTGCTCTTTC
                                ||||  |||  ||||||||||
                                ATAC  AGG  TCACGAGAAAG
                                  __  ___
GAM121  LOC204823 3'  TGAATTCTGAAGCTCTTTCC  2697     TTC  TAGT
                                TGA  CTG   GCTCTTTCC
                                |||  |||   |||||||||
                                ACT  GAC   CGAGAAAGG
                                  TAA  TT__
GAM121  LOC254143 5'  ATGATTCTTTATGCTCTTT   2693       CTGTA
                                ATGATTC    GTGCTCTTT
                                |||||||    |||||||||
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                                TACTAAG    TACGAGAAA
                                   AAA__
GAM122  EGLN1    3'  TGTAAAACATTAACTAAAAGTT 2700     G       ____
             ATT                  TG AAAACATTAA   GAGTTGTT
                                || ||||||||||   ||||||||
                                AC TTTTGTAATT   TTCAATAA
                                 A        GATT
GAM122  IL1R1    3'  TGGAAGGCATTAAAAGTT    2701       AA
                                TGGAA  CATTAAGAGTT
                                |||||  ||||||||||
                                ACCTT  GTAATTTTCAA
                                   CC
GAM122  KPNA1    3'  TGGAAAACATTTGAGAAGTT   2702          AA   TT
                                TGGAAAACATT  GAG  GTT
                                ||||||||||  |||  |||
                                ACCTTTTGTAA  CTC  CAA
                                      A_   TT
GAM122  PSG11    3'  GAAAACATTATCCTTTTGTTAT 2703          AGAG_
             T                   GAAAACATTA    TTGTTATT
                                ||||||||||    ||||||||
                                CTTTTGTAAT    AACAATAA
                                      AGGAA
GAM122  AD-020   3'  TGGAAAACGTATGAATTGTT   2704        AT  A
                                TGGAAAAC  TA GAGTTGTT
                                ||||||||  || ||||||||
                                ACCTTTTG  AT CTTAACAA
                                     C_  A
GAM122  AD-020   3'  TGGAAAACGTATGAATTGTT   2704        AT  A
                                TGGAAAAC  TA GAGTTGTT
                                ||||||||  || ||||||||
                                ACCTTTTG  AT CTTAACAA
                                     C_  A
GAM122  C22orf19 3'  TGGAGAATATCAAGAGTCAC   2705      A  C       TG
                                TGGA AA ATTAAGAGT  T
                                |||| || |||||||||  |
                                ACCT TT TAGTTCTCA  G
                                   C  A       GT
GAM122  CXorf1   3'  TGGAGACATTAAGAAAAATT   2706      AA        TT
                                TGGA  ACATTAAGAG  GTT
                                ||||  ||||||||||  |||
                                ACCT  TGTAATTCTT  TAA
                                   C_        TT
GAM122  EVI5     3'  TGGAAAACTTTAATTGTT    2707        ATTAAG
                                TGGAAAAC     AGTTGTT
                                ||||||||     |||||||
                                ACCTTTTG     TTAACAA
                                     AAA___
GAM122  FBXO30   3'  GGAAAACATTAATTTTATT   2708          GAG
                                GGAAAACATTAA   TTGTT
                                ||||||||||||   |||||
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                                CCTTTTGTAATT  AATAA
                                      AA_
GAM122  FLJ10252  3'  GGGAAACATTAATTGTTGTT  2709    A      GA
                                GG AAACATTAA  GTTGTT
                                || |||||||||  ||||||
                                CC TTTGTAATT  CAACAA
                                  C       AA
GAM122  FLJ12969  3'  TGGAAAACATAAGTATT    2710          T  A
                                TGGAAAACAT AAG GTT
                                |||||||||| ||| |||
                                ACCTTTTGTA TTC TAA
                                      _  A
GAM122  KIAA0737  3'  TGGGAAACATTAAAATGATCAT 2711     A        GTT
          T                      TGG AAACATTAAGA  GTTATT
                                ||| ||||||||||  ||||||
                                ACC TTTGTAATTTT  TAGTAA
                                  C        AC_
GAM122  KIAA1393  3'  TGGAAAACGTAAGAACATTATT 2712        AT   __
                                TGGAAAAC  TAAGA  GTTGTT
                                ||||||||  |||||  ||||||
                                ACCTTTTG  ATTCT  TAATAA
                                     C_    TG
GAM123  C1orf2    3'  GAGGATGCTGGGGGCTGCTGGT 2715       TAC     _
                                GAGGAT   GTTGGGG CTGCTGGT
                                ||||||   ||||||| ||||||||
                                CTCCTA   CGACCCC GACGACCA
                                   ___      C
GAM123  C1orf2    3'  GAGGATGCTGGGGGCTGCTGGT 2715       TAC     _
                                GAGGAT   GTTGGGG CTGCTGGT
                                ||||||   ||||||| ||||||||
                                CTCCTA   CGACCCC GACGACCA
                                   ___      C
GAM123  KIAA0226  5'  AGACCAGACGTTGGGGCTGTTG 2716      __        C
          GT                     GGATT  ACGTTGGGGCTG TGGT
                                |||||  |||||||||||| ||||
                                TCTGG  TGCAACCCCGAC ACCA
                                   TC         A
GAM123  LOC221814 5'  GAGGATTACTTTCCCTGTTGGT 2717         GTTGGGG  C
                                GAGGATTAC      CTG TGGT
                                |||||||||      ||| ||||
                                CTCCTAATG      GAC ACCA
                                     AAAGG__  A
GAM124  CALD1     3'  CATCTCTAGCTGTGA      2720          ACTTC
                                CATCTCTAGTT    GTGG
                                ||||||||||    ||||
                                GTAGAGATCGA    CACT
                                      _____
GAM124  LANCL1    3'  TCTTTAGTTACTACCATG    2721     C      _
                                TCT TAGTTACT TCGTG
                                ||| |||||||| |||||
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                                AGA ATCAATGA GGTAC
                                  A       T
GAM124  SFRS7    3'  CATCTTTAATTACTTTGCA   2722       C       C
                                CATCT TAGTTACTT GTG
                                ||||| ||||||||| |||
                                GTAGA ATTAATGAA CGT
                                   A       A
GAM124  DKFZp434A171 3'  CATCTCTAGTGATTGAAC    2723          TACTTCG
                                CATCTCTAGT      TGGAT
                                ||||||||||      |||||
                                GTAGAGATCA      ACTTG
                                      CTA____
GAM124  DNAJC5   3'  CTACGCACTTCGTGGGTCA   2724     GT        A
                                CTA  TACTTCGTGG TCA
                                |||  |||||||||| |||
                                GAT  GTGAAGCACC AGT
                                  GC         C
GAM124  DRF1     3'  CCTCCCACCTTTGTGGATCA   2725      AGTTA   C
                                TCTCT    CTT GTGGATCA
                                |||||    ||| ||||||||
                                GGAGG    GAA CACCTAGT
                                   GTG__   A
GAM124  FLJ12568 3'  CATCTTTAATTACTCAT     2726       C       T
                                CATCT TAGTTACT CGT
                                ||||| |||||||| |||
                                GTAGA ATTAATGA GTA
                                   A       _
GAM124  ICK      3'  CATCTCAGTTACTATAATC   2727        T      TCGTG
                                CATCTC AGTTACT    GATC
                                |||||| |||||||    ||||
                                GTAGAG TCAATGA    TTAG
                                   _      TA___
GAM124  KIAA1432 3'  CATTTCTGTTACTTCATG    2728      C   A
                                CAT TCT GTTACTTCGTG
                                ||| ||| ||||||||||
                                GTA AGA CAATGAAGTAC
                                  A  _
GAM124  LCHN     3'  CTGTTCACTTTGTGGATCA   2729     AG     C
                                CT  TTACTT GTGGATCA
                                ||  |||||| ||||||||
                                GA  AGTGAA CACCTAGT
                                 CA     A
GAM124  MGC16142 5'  CATCCTAGTTAATTTGGATCA  2730       T      CTTCG
                                CATC CTAGTTA     TGGATCA
                                |||| |||||||     |||||||
                                GTAG GATCAAT     ACCTAGT
                                   _      TAA__
GAM124  LOC149721 5'  CATCTCCAGTTATTTGT     2731            C  C
                                CATCTCTAGTTA TT GT
                                |||||||||||| || ||
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                                GTAGAGGTCAAT AA CA
                                      A  _
GAM124  LOC153910 3'  CATTTCTAGTAAAGTGGGTCA  2732      C     TACTTC    A
                                CAT TCTAGT      GTGG TCA
                                ||| ||||||      ||||| |||
                                GTA AGATCA      CACC AGT
                                  A     TTT___    C
GAM124  LOC154442 3'  CAGTTTTTGTGGATCA      2733       AC  C
                                TAGTT  TT GTGGATCA
                                |||||  ||  ||||||||
                                GTCAA  AA CACCTAGT
                                   __  A
GAM124  LOC219294 3'  CATTTCTAAGTTATTCATGGAT 2734      C   _    C
              C                  CAT TCTA GTTA TTCGTGGATC
                                ||| |||| |||| ||||||||||
                                GTA AGAT CAAT AAGTACCTAG
                                  A   T   _
GAM124  LOC222237 3'  ACCTCTAGTTGCCACCAGATCA 2735           A  TCG
                                ATCTCTAGTT CT   TGGATCA
                                |||||||||| ||   |||||||
                                TGGAGATCAA GG   GTCTAGT
                                      C  TG_
GAM124  LOC253912 3'  CTCCACGCCTTCGTGGATCA   2736       GTTA
                                CTCTA    CTTCGTGGATCA
                                |||||    ||||||||||||
                                GAGGT    GAAGCACCTAGT
                                   GCG_
GAM125  ARG2     3'  TCCCAGGTCTAACCCC      2739         ACAG
                                TCCCAGGT    TTAATCCC
                                ||||||||    ||||||||
                                AGGGTCCA    GATTGGGG
                                      ____
GAM125  CNGB3    3'  CAATCCTAGGTACAATCA    2740        C
                                TAATCC AGGTACAGTTA
                                |||||| ||||||||||
                                GTTAGG TCCATGTTAGT
                                    A
GAM125  GOLGA4   5'  ATCTGGGTACAATTAAT     2741      CCA
                                ATC   GGTACAGTTAAT
                                |||   ||||||||||||
                                TAG   CCATGTTAATTA
                                  AC_
GAM125  IL1F5    3'  AATCCCAGGGGCTGTGATCC   2742          TACA  TA
                                AATCCCAGG    GT  ATCC
                                |||||||||    ||  ||||
                                TTAGGGTCC    CA  TAGG
                                      CCGA  C_
GAM125  JRKL     3'  CATTTTAGCAGATTAATCCC   2743     GG_ _  _
                                CA   TA CAG TTAATCCC
                                ||   || ||| ||||||||
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                                GT   AT GTC AATTAGGG
                                 AAA  C   T
GAM125  MAP1A    5'  TAATCCCAGGTGGCTCC     2744          ACA  TAA
                                TAATCCCAGGT   GT   TCC
                                ||||||||||   ||   |||
                                ATTAGGGTCCA   CG   AGG
                                      C__  ___
GAM125  MTMR8    3'  AATCACAAATATAGTTAATCC  2745      C     C
                                AATC CAGGTA AGTTAATCC
                                |||| |||||| |||||||||
                                TTAG GTTTAT TCAATTAGG
                                  T     A
GAM125  TGIF     5'  ATCCCAGGCGCCCGCTCC    2746         ACA   AA_
                                ATCCCAGGT   GTT   TCC
                                |||||||||   |||   |||
                                TAGGGTCCG   CGG   AGG
                                     ___   GCG
GAM125  ZNF26    3'  ATCCCAAATATGGTTGGTC    2747          CA   AA
                                ATCCCAGGTA  GTT  TC
                                ||||||||||  |||  ||
                                TAGGGTTTAT  CAA  AG
                                      AC   CC
GAM125  ABCC13   3'  ATCCCAGGGCATAGTGCCTC   2748         _  C   TAA
                                ATCCCAGG TA AGT   TC
                                ||||||||  || |||   ||
                                TAGGGTCC GT TCA   AG
                                     C  A   CGG
GAM125  ARSDR1   3'  TAATCCTTAACTAGTTAATCC  2749        CAGGT  _
                                TAATCC     AC AGTTAATCC
                                ||||||     || |||||||||
                                ATTAGG     TG TCAATTAGG
                                   AAT__  A
GAM125  DKFZP434L1435 5'  TCCGGTACAGCAACCCC     2750      CA       T
                                TCC  GGTACAGT AATCCC
                                |||  |||||||| ||||||
                                AGG  CCATGTCG TTGGGG
                                  __       _
GAM125  HPCAL4   3'  TAATCCCAGGATCAAGAGAATT 2751           TAC_  TT   C
             CC                   TAATCCCAGG    AG  AAT CC
                                ||||||||||    ||  ||| ||
                                ATTAGGGTCC    TC  TTA GG
                                      TAGT  TC   A
GAM125  KIAA1817 3'  ATCCCAGATGCTTGCTCCC   2752         ACA   AA_
                                ATCCCAGGT   GTT   TCCC
                                |||||||||   |||   ||||
                                TAGGGTCTA   CGA   AGGG
                                     ___   ACG
GAM125  MDN1     3'  TAACTTCAGGTACATGCT    2753       CC       _
                                TAAT  CAGGTACA GTT
                                ||||  |||||||| |||
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                                ATTG  GTCCATGT CGA
                                  AA       A
GAM125  MUC13    3'  ATCCCAGGTGCCTCC      2754         ACA   AA
                                ATCCCAGGT   GTT  TCC
                                |||||||||   |||  |||
                                TAGGGTCCA   CGG  AGG
                                      ___   __
GAM125  NS1-BP   3'  TAATCCCATGGTGCAAGGATTT 2755        _   A   TTAA_
           CC                     TAATCCCA GGT CAG    TCC
                                |||||||| ||| |||    |||
                                ATTAGGGT CCA GTT    AGG
                                    A   C   CCTAA
GAM125  PPP1R16B 3'  CCCAGGTATGTCATTCC    2756         CA    A
                                CCCAGGTA  GTTA TCC
                                ||||||||  |||| |||
                                GGGTCCAT  CAGT AGG
                                    A_    A
GAM125  PTK6     3'  ATCCCAGGTCCAGGCCC     2757         A   TTAAT
                                ATCCCAGGT CAG    CCC
                                ||||||||| |||    |||
                                TAGGGTCCA GTC    GGG
                                    G   C____
GAM125  RAB1B    3'  ATCCCAGGTCCTGGATCCCC   2758         ACAGTTA
                                ATCCCAGGT      ATCCCC
                                |||||||||      ||||||
                                TAGGGTCCA      TAGGGG
                                    GGACC__
GAM125  SKIP     5'  ATCCCAGAGTTCAATTCC    2759        _  A    TAA
                                ATCCCAG GT CAGT   TCC
                                ||||||| || ||||   |||
                                TAGGGTC CA GTTA   AGG
                                    T  A   ___
GAM125  SLC37A1  5'  TAATCCTGGCTCCAGATCC   2760       CA   A_   TTA
                                TAATCC  GGT  CAG   ATCC
                                ||||||  |||  |||   ||||
                                ATTAGG  CCG  GTC   TAGG
                                   A_   AG   ___
GAM125  LOC134145 5'  TCTAGGTCAGCCAACCCC    2761     CC    A
                                TC  AGGT CAGTTAATCCC
                                ||  |||| ||||||||||
                                AG  TCCA GTCGGTTGGGG
                                 A_   _
GAM125  LOC144231 5'  TAATCCCAGTTAATC       2762         GGTACA
                                TAATCCCA     GTTAATC
                                ||||||||     |||||||
                                ATTAGGGT     CAATTAG
                                      _______
GAM125  LOC148764 3'  TAATCTCAGGTACAGCCGACC  2763        C         TA
                                TAATC CAGGTACAGT  ATC
                                ||||| ||||||||||  |||
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                                ATTAG GTCCATGTCG  TGG
                                   A        GC
GAM125  LOC150225 3'  CCAGGGTGCTAATCCCC     2764       TACA
                                CCAGG    GTTAATCCCC
                                |||||    ||||||||||
                                GGTCC    CGATTAGGGG
                                   CA__
GAM125  LOC153579 5'  TCCCAGATGCTAAGATTCCC   2765        ACA    ___
                                TCCCAGGT   GTTAA   TCCC
                                ||||||||   |||||   ||||
                                AGGGTCTA   CGATT   AGGG
                                     ___     CTA
GAM125  LOC158332 5'  TAATCCCAGGATTTCC      2766         TACA   AA
                                TAATCCCAGG    GTT  TCC
                                ||||||||||    |||  |||
                                ATTAGGGTCC    TAA  AGG
                                      _____   __
GAM125  LOC200251 5'  TCCCAGGCTAGTCTCC      2767         AC    AA
                                TCCCAGGT  AGTT  TCC
                                ||||||||  ||||  |||
                                AGGGTCCG  TCAG  AGG
                                    A_    __
GAM125  LOC204285 5'  TAATCCCAGGCACAGAACACCC 2768              TTA
                                TAATCCCAGGTACAG   ATCC
                                ||||||||||||||   ||||
                                ATTAGGGTCCGTGTC   TGGG
                                      TTG
GAM125  LOC253639 5'  ATCCTTTGGAGTTAATCC    2769      CA_  TAC
                                ATCC   GG   AGTTAATCC
                                ||||   ||   |||||||||
                                TAGG   CC   TCAATTAGG
                                  AAA  ___
GAM125  LOC253832 3'  TCCCAGGTAAACCAAGTCTCC  2770          C  TT  _  _
                                TCCCAGGTA AG  AA TC CC
                                ||||||||| ||  || || ||
                                AGGGTCCAT TT  TT AG GG
                                     _  GG  C  A
GAM125  LOC256158 5'  TCCCAGGTACAACAGCCTCCCC 2771            TTAA_
                                TCCCAGGTACAG    TCCCC
                                ||||||||||||    |||||
                                AGGGTCCATGTT    AGGGG
                                      GTCGG
GAM125  LOC55565  5'  CCCAGGTAAATTCCC       2772         C   TAA
                                CCCAGGTA AGT   TCCC
                                |||||||| |||   ||||
                                GGGTCCAT TTA   AGGG
                                   _   ___
GAM125  LOC55901  5'  AATCCCAGGTCTTTAGTCTCC  2773          AC__    AA
                                AATCCCAGGT    AGTT  TCC
                                ||||||||||    ||||  |||
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                                TTAGGGTCCA   TCAG  AGG
                                     GAAA   __
GAM125  LOC92719 3' TCCCAGGTCAGTTGGACCCC  2774        A    AAT
                                TCCCAGGT CAGTT   CCCC
                                |||||||| |||||   ||||
                                AGGGTCCA GTCAA   GGGG
                                     _    CCT
GAM126  WIG1     5' TCGGAACCCCCGGGAC     2777        A    AA
                                TCGGAACC CCCGG  GAT
                                |||||||| |||||  |||
                                AGCCTTGG GGGCC  CTG
                                     _    __
GAM126  KIAA0963 3' GGGACCACCCGGTTTCAC   2778    A       AAGA
                                GG ACCACCCGG    TTAC
                                || |||||||||    ||||
                                CC TGGTGGGCC    AGTG
                                 C        AA__
GAM126  KIAA1303 3' CCGGAGCCGTCCGGGACC   2779      A  AC    AA
                                TCGGA CC  CCGG  GATT
                                ||||| ||  ||||  ||||
                                GGCCT GG  GGCC  CTGG
                                   C  CA   __
GAM126  KIAA1423 3' GGAATCAGTGAATGATTACAG  2780     C  CCCG  _
                                GGAA CA    GAA GATTACAG
                                |||| ||    ||| ||||||||
                                CCTT GT    CTT CTAATGTC
                                  A  CA__   A
GAM127  HGF      3' TTCTTACTAAAATGGTGTATTA 2783     A   ACAGCC
                                TTC TTA     ATGGTGTATTA
                                ||| |||     ||||||||||||
                                AAG AAT     TACCACATAAT
                                  _  GATTT_
GAM127  NPEPPS   3' TCATTAACAGTAGAGTGT    2784         CCAT
                                TCATTAACAG    GGTGT
                                ||||||||||    |||||
                                AGTAATTGTC    TCACA
                                     ATC_
GAM127  CNNM2    3' TTCATTAACATTCATTTTG   2785         GC   GG
                                TTCATTAACA  CAT  TG
                                |||||||||  |||  ||
                                AAGTAATTGT  GTA  AC
                                     AA   AA
GAM127  DSCR1L1  3' TCAACAGAGCTATGGTGTATT  2786       __  C
                                TTAACA  GC ATGGTGTATT
                                ||||||  || ||||||||||
                                AGTTGT  CG TACCACATAA
                                   CT  A
GAM127  FBXO8    3' TTCGTTAACAGCTGTGT     2787      A      CATG
                                TTC TTAACAGC    GTGT
                                ||| ||||||||    ||||
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                                AAG AATTGTCG    CACA
                                  C       A___
GAM127  GT650    5'  TTCTTGACAGCCACAATGT   2788      A  A      TG
                                TTC TT ACAGCCA  GTGT
                                ||| || |||||||  ||||
                                AAG AA TGTCGGT  TACA
                                  _ C      GT
GAM127  KIAA1673 3'  TTCATTAAAGCCTGTATT    2789         C   ATGG
                                TTCATTAA AGCC    TGTATT
                                |||||||| ||||    ||||||
                                AAGTAATT TCGG    ACATAA
                                    _   _____
GAM127  KIAA1950 3'  TTCATGAATGGCCACAGCAATA 2790       T  CA       _
           TT                     TTCAT AA  GCCATGGTG TATT
                                |||||  ||  |||||||||  ||||
                                AAGTA TT  CGGTGTCGT ATAA
                                   C  AC        T
GAM127  PPP1R1A  3'  TTCATTAATAGCCACTGTG   2791         C     G
                                TTCATTAA AGCCAT GTG
                                |||||||| |||||| |||
                                AAGTAATT TCGGTG CAC
                                     A     A
GAM127  STK38L   3'  TCCATTAACAGTTATGACA   2792          CC   GT
                                TTCATTAACAG  ATG  G
                                ||||||||||  |||  |
                                AGGTAATTGTC  TAC  T
                                      AA   TG
GAM127  LOC142893 5'  TTCATTAACGACAATAGTGT   2793          A  C
                                TTCATTAAC GC ATGGTGT
                                |||||||||  || |||||||
                                AAGTAATTG TG TATCACA
                                     C  T
GAM127  LOC145902 5'  TTCATTAATGCTACCATGGTGT 2794          CA__
                                TTCATTAA    GCCATGGTGT
                                ||||||||    ||||||||||
                                AAGTAATT    TGGTACCACA
                                     ACGA
GAM127  LOC257206 5'  TTCATTAACACCAGTGGT    2795          G  _
                                TTCATTAACA CCA TGGT
                                |||||||||| ||| ||||
                                AAGTAATTGT GGT ACCA
                                      _  C
GAM128  ALPI     3'  GGGTTGCCGGAAGCTTCTC    2798     A      TGAT
                                GG TTGCCGGG    TTTCTC
                                || ||||||||    ||||||
                                CC AACGGCCT    GAAGAG
                                  C       TC__
GAM128  AP1G1    3'  ATGGATTGCAGTCCTTTTCT   2799          CG   GA
                                ATGGATTGC  GGT  TTTTCT
                                |||||||||  |||  ||||||
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                                TACCTAACG TCA AAAAGA
                                    __ GG
GAM128 BCAT1   3' GATTGCAATTCATTTTCTC  2800      CG  G_
                                GATTGC GGT ATTTTCTC
                                |||||| ||| ||||||||
                                CTAACG TTA TAAAAGAG
                                   __ AG
GAM128 DTNB    3' TAGATTGCAAAAATTTTCTCC 2801       CGGGT
                                TGGATTGC   GATTTTCTCC
                                ||||||||   ||||||||||
                                ATCTAACG   TTAAAAGAGG
                                    TTT__
GAM128 DYRK1A  3' TGGATTTTATGATTTTCT   2802      GCCGG
                                TGGATT   GTGATTTTCT
                                ||||||   ||||||||||
                                ACCTAA   TACTAAAAGA
                                   AA___
GAM128 DYRK1A  3' TGGATTTTATGATTTTCT   2802      GCCGG
                                TGGATT   GTGATTTTCT
                                ||||||   ||||||||||
                                ACCTAA   TACTAAAAGA
                                   AA___
GAM128 DYRK1A  3' TGGATTTTATGATTTTCT   2802      GCCGG
                                TGGATT   GTGATTTTCT
                                ||||||   ||||||||||
                                ACCTAA   TACTAAAAGA
                                   AA___
GAM128 GGA3    3' ATGGCAGCTGGTGATTTT   2803     ATT CG
                                ATGG  GC GGTGATTTT
                                ||||  || |||||||||
                                TACC  CG CCACTAAAA
                                  GT_ A_
GAM128 GGA3    3' ATGGCAGCTGGTGATTTT   2803     ATT CG
                                ATGG  GC GGTGATTTT
                                ||||  || |||||||||
                                TACC  CG CCACTAAAA
                                  GT_ A_
GAM128 HTR2C   3' GGATTGCTGAAGGATTTTCT  2804       C  T
                                GGATTGC GGG GATTTTCT
                                ||||||| ||| ||||||||
                                CCTAACG CTT CTAAAAGA
                                   A  C
GAM128 ITSN1   3' ATGGACTGCCTTCATTTTCT  2805        GGGTG
                                ATGGATTGCC   ATTTTCT
                                ||||||||||   |||||||
                                TACCTGACGG   TAAAAGA
                                    AAG__
GAM128 SLC20A2 5' TGGGTGCCGGGTACTTTTCT  2806     AT      A
                                TGG TGCCGGGTG TTTTCT
                                ||| ||||||||| ||||||
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                                ACC  ACGGCCCAT AAAAGA
                                  C_       G
GAM128  TGFA     3'  ATGGATTTGCTAAGTTTTCTCC 2807        _ CG   GAT
                                ATGGATT GC  GGT   TTTCTCC
                                |||||||  ||  |||   |||||||
                                TACCTAA CG  TCA   AAAGAGG
                                    A  AT   ___
GAM128  TNFSF10  3'  ATGGATTGTTGCGCTTTCT   2808         CCGG   A
                                ATGGATTG    GTG TTTTCT
                                ||||||||    ||| ||||||
                                TACCTAAC    CGC GAAAGA
                                    AA__   _
GAM128  BIKE     3'  TGGATTGCTGATGTTCTTC    2809         CG    A
                                TGGATTGC  GGTG TTTTC
                                ||||||||  |||| |||||
                                ACCTAACG  CTAC AGAAG
                                    A_    A
GAM128  FLJ10933 3'  TGGATTGTGTAATTTT      2810         CCGG
                                TGGATTG    GTGATTTT
                                |||||||    ||||||||
                                ACCTAAC    CATTAAAA
                                    A___
GAM128  FLJ20984 5'  GGATTGTAATTTTCT       2811        GCCGG
                                GGATT    GTGATTTTCT
                                |||||    ||||||||||
                                CCTAA    CATTAAAAGA
                                  _____
GAM128  KIAA0527 3'  ATGAAGCTGGTGATTTTCT   2812       TT  CG
                                ATGGA  GC  GGTGATTTTCT
                                |||||  ||  ||||||||||
                                TACTT  CG  CCACTAAAAGA
                                  __  A_
GAM128  KIAA0669 3'  ATAGATTGCTTTCAGTTTTTTT 2813         CG__   GA
            C                    ATGGATTGC    GGT  TTTTC
                                |||||||||    |||  |||||
                                TATCTAACG    TCA  AAAAG
                                     AAAG   AA
GAM128  KIAA1229 3'  ATAGATTGCAAAAATTTTCTCC 2814         CGGGT
                                ATGGATTGC    GATTTTCTCC
                                |||||||||    ||||||||||
                                TATCTAACG    TTAAAAGAGG
                                     TTT__
GAM128  KIAA1254 3'  ATGGATGTTGGTGTTCTC    2815        T CCG    ATT
                                ATGGAT G   GGTG   TTCTC
                                ||||||  |   ||||   |||||
                                TACCTA C   CCAC   AAGAG
                                   _ AA_   ___
GAM128  PRO1584  5'  ATGGAGAAGGTGATTTTCT   2816       TTGCC
                                ATGGA    GGGTGATTTTCT
                                |||||    ||||||||||||
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                                TACCT    TCCACTAAAAGA
                                  CT___
GAM128  ULK2     3'  GGAAAGGGTGATTTTCTCC   2817     TTGCC
                                GGA    GGGTGATTTTCTCC
                                |||    ||||||||||||||
                                CCT    CCCACTAAAAGAGG
                                  TT___
GAM128  LOC128553 3'  ATGGCTGGGGTGATTTT     2818      A   CC
                                ATGG TTG  GGGTGATTTT
                                |||| |||  ||||||||||
                                TACC GAC  CCCACTAAAA
                                  _  __
GAM128  LOC145384 3'  TAGATTGCAAAAATTTTCTCC  2801         CGGGT
                                TGGATTGC    GATTTTCTCC
                                ||||||||    ||||||||||
                                ATCTAACG    TTAAAAGAGG
                                     TTT__
GAM128  LOC145945 5'  GGATGATGATTTTCT      2819      TGCCG
                                GGAT    GGTGATTTTCT
                                ||||    ||||||||||||
                                CCTA    CTACTAAAAGA
                                  _____
GAM128  LOC146489 5'  ATGGATTCCCGGGTGACTTC   2820        G
                                ATGGATT CCGGGTGATTTT
                                ||||||| ||||||||||||
                                TACCTAA GGCCCACTGAAG
                                    G
GAM128  LOC149296 5'  ATGGATGCCATTTTCT      2821        T   GGGTG
                                ATGGAT GCC    ATTTTCT
                                |||||| |||    |||||||
                                TACCTA CGG    TAAAAGA
                                  _  _____
GAM128  LOC152793 3'  TGGATTGCAGGGTGGGGGTCTC 2822         C    ATTT
          C                      TGGATTGC GGGTG   TCTCC
                                |||||||| |||||   |||||
                                ACCTAACG CCCAC   AGAGG
                                     T    CCCC
GAM128  LOC164714 5'  TGGATGTTGTCTGTTTTCTCC  2823       TGCCGGG  A
                                TGGAT      TG TTTTCTCC
                                |||||      || ||||||||
                                ACCTA      AC AAAAGAGG
                                  CAACAG_  _
GAM128  LOC201191 5'  CGGTTGCTGCCTTTCTC     2824      A   CGGG  A
                                TGG TTGC   TG TTTTCTC
                                ||| ||||   || |||||||
                                GCC AACG   AC GAAAGAG
                                  _   ____  G
GAM128  LOC201617 5'  TGGATTGCCTATTTTTCTC   2825         GGGTGA
                                TGGATTGCC    TTTTCTC
                                |||||||||    |||||||
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                                ACCTAACGG     AAAAGAG
                                     ATA___
GAM128  LOC256207 3'  ATGGATTTTGTAATTTT     2826        GCCGG
                                ATGGATT    GTGATTTT
                                |||||||    ||||||||
                                TACCTAA    CATTAAAA
                                   AA___
GAM128  LOC91170  3'  ATGGATTGTCTGAGGATCTT   2827        CC_  T
                                ATGGATTG   GGG GATTTT
                                ||||||||   ||| ||||||
                                TACCTAAC   CTC CTAGAA
                                     AGA  _
GAM129  ADAMTS7   3'  AGTCAGTGTGGTGAGGGGCCAC 2830     C   CCCG  _  C
                                AG CAG    GG GA GGGGCCAC
                                || |||    || || ||||||||
                                TC GTC    CC CT CCCCGGTG
                                 A   ACA_  A  _
GAM129  ADORA1    3'  AGCAGCAGAGATGGGGTCACC  2831     C   CC    C    C
                                AGC AGC  GGGGA GGGG CACC
                                ||| |||  ||||| |||| ||||
                                TCG TCG  TCTCT CCCC GTGG
                                  _  __     A    A
GAM129  ATP8B2    3'  GCCAGCCCTGGGTGCTCTGGTC 2832         _  GACGG_  C
           AC                     GCCAGCCC GGG     GG CAC
                                ||||||| |||      || |||
                                CGGTCGGG CCC     CC GTG
                                     A   ACGAGA  A
GAM129  BLK       3'  GCCAGCACGGGGGGTGCC    2833        C    AC  G
                                GCCAGC CGGGG  GG GCC
                                |||||| |||||  || |||
                                CGGTCG GCCCC  CC CGG
                                   T    __  A
GAM129  CACNA1S   5'  AGCCAGCCAGGGGGCGGGGC   2834         C    A
                                AGCCAGCC GGGG CGGGGC
                                |||||||| |||| ||||||
                                TCGGTCGG CCCC GCCCCG
                                     T    C
GAM129  CAPN10    3'  AGCTGGCACAGGGGGCCAC    2835     CA  C    ACGG
                                AGC  GC CGGGG    GGCCAC
                                |||  || |||||    ||||||
                                TCG  CG GTCCC    CCGGTG
                                  AC  T    _____
GAM129  CAPN10    3'  AGCTGGCACAGGGGGCCAC    2835     CA  C    ACGG
                                AGC  GC CGGGG    GGCCAC
                                |||  || |||||    ||||||
                                TCG  CG GTCCC    CCGGTG
                                  AC  T    _____
GAM129  CAPN10    3'  AGCTGGCACAGGGGGCCAC    2835     CA  C    ACGG
                                AGC  GC CGGGG    GGCCAC
                                |||  || |||||    ||||||
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                                TCG  CG GTCCC   CCGGTG
                                  AC  T   ____
GAM129  CAPN10   3' AGCTGGCACAGGGGGCCAC   2835    CA  C   ACGG
                                AGC  GC CGGGG   GGCCAC
                                |||  || |||||   ||||||
                                TCG  CG GTCCC   CCGGTG
                                  AC  T   ____
GAM129  CAPN10   3' AGCTGGCACAGGGGGCCAC   2835    CA  C   ACGG
                                AGC  GC CGGGG   GGCCAC
                                |||  || |||||   ||||||
                                TCG  CG GTCCC   CCGGTG
                                  AC  T   ____
GAM129  CAPN10   3' AGCTGGCACAGGGGGCCAC   2835    CA  C   ACGG
                                AGC  GC CGGGG   GGCCAC
                                |||  || |||||   ||||||
                                TCG  CG GTCCC   CCGGTG
                                  AC  T   ____
GAM129  CARPX    5' AGCCGGCCAGGGACAGTCACC  2836     A   C     G_
                                AGCC GCC GGGGACGG  GCC
                                |||| ||| ||||||||  |||
                                TCGG CGG TCCCTGTC  TGG
                                  C   _      AG
GAM129  CDKN1A   5' GCCGGCCCGGGGTCCCC    2837    A     ACGGGG  A
                                GCC GCCCGGGG    CC CC
                                ||| ||||||||    || ||
                                CGG CGGGCCCC    GG GG
                                  C      A_____  _
GAM129  CLPS     3' GCCAGCCCGGGAGATGCGCTGG 2838       _  __  _____  GCCA
           TGGCCC                 GCCCGGG GA  CG    GG   CC
                                |||||||  ||  ||    ||   ||
                                CGGGCCC CT  GC    CC   GG
                                    T  AC  GAIII  ACCG
GAM129  CNTN2    5' GCTCAGCTTGGGGACAGCC   2839    _   CC    GG
                                GC CAGC  GGGGAC  GGCC
                                ||  ||||  ||||||  ||||
                                CG GTCG  CCCCTG  TCGG
                                 A   AA    __
GAM129  COL4A3   5' GCGAGTCCGGGGACCCTCAGGC 2840    C  C     G___
                                GC AG CCGGGGAC   GGGC
                                ||  || ||||||||   ||||
                                CG TC GGCCCCTG   TCCG
                                 C  A      GGAG
GAM129  COL4A3   5' GCGAGTCCGGGGACCCTCAGGC 2840    C  C     G___
                                GC AG CCGGGGAC   GGGC
                                ||  || ||||||||   ||||
                                CG TC GGCCCCTG   TCCG
                                 C  A      GGAG
GAM129  COL4A3   5' GCGAGTCCGGGGACCCTCAGGC 2840    C  C     G___
                                GC AG CCGGGGAC   GGGC
                                ||  || ||||||||   ||||
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                                CG TC GGCCCCTG   TCCG
                                 C A      GGAG
GAM129  CPE     5'  CAGCCCGCGCACTGGGGCCACC 2841       GGG  _
                                CAGCCCG  AC GGGGCCACC
                                |||||||  || |||||||||
                                GTCGGGC  TG CCCCGGTGG
                                    GCG  A
GAM129  FAAH    3'  GCCAGGGACGGGGTGGGGCTGC 2842      CC_   AC   CA
          C                      GCCAG  CGGGG  GGGGC  CC
                                |||||  |||||  |||||  ||
                                CGGTC  GCCCC  CCCCG  GG
                                   CCT   A_   AC
GAM129  FBXW1B  5'  GCCAGCCCGCCCGGGCCGCC  2843        GGGA  G  A
                                GCCAGCCCG   CGGG CC CC
                                |||||||||   |||| || ||
                                CGGTCGGGC   GCCC GG GG
                                     GG__   _  C
GAM129  FBXW1B  5'  GCCAGCCCGCCCGGGCCGCC  2843        GGGA  G  A
                                GCCAGCCCG   CGGG CC CC
                                |||||||||   |||| || ||
                                CGGTCGGGC   GCCC GG GG
                                     GG__   _  C
GAM129  GARP    3'  GCAGCCCGGGAAGGGGGTCACC 2844    C       C   C
                                GC AGCCCGGGGA GGGG CACC
                                || |||||||||| |||| ||||
                                CG TCGGGCCCTT CCCC GTGG
                                 _       C   A
GAM129  GGT2    5'  GCCAGCCTGGGGGCCAC    2845       C   ACGGG
                                GCCAGCC GGGG   GCCAC
                                ||||||| ||||   |||||
                                CGGTCGG CCCC   CGGTG
                                   A  _____
GAM129  GNAS    5'  AGCTGGCCCGGAGGTCCCAGCC 2846     CA      ACGG_
                                AGC  GCCCGGGG   GGCC
                                |||  ||||||||   ||||
                                TCG  CGGGCCTC   TCGG
                                  AC      CAGGG
GAM129  GPRK5   5'  AGCCGGCCGGCGGGGC     2847     A  CGG  A
                                AGCC GCC  GG CGGGGC
                                |||| |||  || ||||||
                                TCGG CGG  CC GCCCCG
                                  C  ___ _
GAM129  IRF1    3'  AGCCAGCCCTGGGATTGG   2848        G   CG
                                AGCCAGCCC GGGA  GG
                                ||||||||| ||||  ||
                                TCGGTCGGG CCCT  CC
                                     A   AA
GAM129  ITPR3   3'  GCCAGCTGGCTGGGCCAC   2849       CCGG  ACG
                                GCCAGC   GG  GGGCCAC
                                ||||||   ||  |||||||
```

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                                CGGTCG   CC  CCCGGTG
                                   A___  GA_
GAM129  LEF1    5'  GCTGCCCCGGCGGCCAC    2850    CA   GGGGA  _
                                GC  GCCC    CGG GGCCAC
                                ||  ||||    ||| ||||||
                                CG  CGGG    GCC CCGGTG
                                 A_   _____  G
GAM129  LLGL1   3'  AGTGAGCAGAGATGGGGCCAC  2851    CC   CC    C
                                AG  AGC  GGGGA GGGGCCAC
                                ||  |||  ||||| ||||||||
                                TC  TCG  TCTCT CCCCGGTG
                                 AC  __    A
GAM129  LZTS1   3'  GCCGGCCTGGGACAGGGCC   2852     A  CG
                                GCC GCC  GGGACGGGGCC
                                ||| |||  ||||||||||
                                CGG CGG  CCCTGTCCCGG
                                  C  A_
GAM129  MLC1    3'  AGCCCGCCCCGGGTCGTCGGTG 2853    A   G  A _____  GCCA
            GCCC                  CC GCCC GGG CG    GG   CC
                                || |||| ||| ||    ||   ||
                                GG CGGG CCC GC    CC   GG
                                 G   G   A  AGIII  ACCG
GAM129  MLC1    3'  AGCCCGCCCCGGGTCGTCGGTG 2853    A   G  A _____  GCCA
            GCCC                  CC GCCC GGG CG    GG   CC
                                || |||| ||| ||    ||   ||
                                GG CGGG CCC GC    CC   GG
                                 G   G   A  AGIII  ACCG
GAM129  MUC3B   3'  GCTGCCCGCGTCCTGGGGCCAC 2854    CA    GGGAC_
            C                   GC  GCCCG    GGGGCCACC
                                ||  |||||    |||||||||
                                CG  CGGGC    CCCCGGTGG
                                 A_    GCAGGA
GAM129  NCOR2   3'  GCCAGCCCGGGGCGGGA    2855          A
                                GCCAGCCCGGGG CGGGG
                                |||||||||||| |||||
                                CGGTCGGGCCCC GCCCT
                                          _
GAM129  NLGN2   5'  GCCGCCCGGGGCGCCGCC    2856    A      A  GG
                                GCC GCCCGGGG CG  GCC
                                ||| ||||||| ||  |||
                                CGG CGGGCCCC GC  CGG
                                  _      _  GG
GAM129  NOX4    5'  AGCCAGCCCGGGCGGGG    2857          GA
                                AGCCAGCCCGGG  CGGGG
                                ||||||||||||  |||||
                                TCGGTCGGGCCC  GCCCC
                                          __
GAM129  NRF1    3'  GCCAGCCCGAGGAGCATCGGTG 2858          _ G_____  GCCA
            GC                    CCAGCCCGGGGA C    GG   C
                                ||||||||||| |    ||   |
```

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                                GGTCGGGCTCCT G     CC    G
                                      C TAGIII  ACCG
GAM129  NTE     3'  AGCTACCCCCACGGGGCCACC  2859     CA    GGGG
                                AGC  GCCC    ACGGGGCCACC
                                |||  ||||    ||||||||||
                                TCG  TGGG    TGCCCCGGTGG
                                  A_    GG__
GAM129  OTOF    3'  GCCGGCCAGGAGGCCAC     2860      A   C   GACG
                                GCC GCC GGG    GGGCCAC
                                ||| ||| |||    |||||||
                                CGG CGG TCC    TCCGGTG
                                  C   _   ____
GAM129  PFKL    5'  CAGCCCAGGGTCACAGCCA   2861           A  G
                                CAGCCCGGGG CG GGCCA
                                |||||||||| || |||||
                                GTCGGGTCCC GT TCGGT
                                      A  G
GAM129  PKNOX1   3'  AGCCAACCCGTGGGGGCTGCC  2862           _   AC  G_
                                AGCCAGCCCG GGG  GG  GCC
                                |||||||||| |||  ||  |||
                                TCGGTTGGGC CCC  CC  CGG
                                      A   __  GA
GAM129  POLR2C   3'  GCCAGCCCTGGGGCAAGAAC  2863         _    AC
                                GCCAGCCC GGGG  GGGGC
                                |||||||| ||||  |||||
                                CGGTCGGG CCCC  TCTTG
                                     A    GT
GAM129  PPP1R8   5'  GCTAGCTCCGGCCGGGCCAC  2864     C   _   GGACG
                                GC AGC CCGG    GGGCCAC
                                || ||| ||||    |||||||
                                CG TCG GGCC    CCCGGTG
                                 A   A    GG___
GAM129  PPP1R8   5'  GCTAGCTCCGGCCGGGCCAC  2864     C   _   GGACG
                                GC AGC CCGG    GGGCCAC
                                || ||| ||||    |||||||
                                CG TCG GGCC    CCCGGTG
                                 A   A    GG___
GAM129  PRV1    3'  CATTCGGGGGGAGCCAC    2865     GCC    AC
                                CA   CGGGG  GGGGCCAC
                                ||   |||||  ||||||||
                                GT   GCCCC  CCTCGGTG
                                 AA_    __
GAM129  PTGS1    3'  AGCCAGCTGTGGGGATGAG   2866        CC_    C
                                AGCCAGC   GGGGA GGG
                                |||||||   ||||| |||
                                TCGGTCG   CCCCT CTC
                                    ACA    A
GAM129  PTGS1    3'  AGCCAGCTGTGGGGATGAG   2866        CC_    C
                                AGCCAGC   GGGGA GGG
                                |||||||   ||||| |||
```

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                                TCGGTCG  CCCCT CTC
                                   ACA   A
GAM129  PTPN11   5' GCTGGCCCGAGGGAGGCC   2867   CA     AC
                                GC GCCCGGGG GGGGCC
                                || |||||||| ||||||
                                CG CGGGCTCC CTCCGG
                                 AC      __
GAM129  PTPN11   5' GCTGGCCCGAGGGAGGCC   2867   CA     AC
                                GC GCCCGGGG GGGGCC
                                || |||||||| ||||||
                                CG CGGGCTCC CTCCGG
                                 AC      __
GAM129  RECQL5   3' GCCGGCTCTGGGACGGGGC  2868    A CCG
                                GCC GC  GGGACGGGGC
                                ||| ||  ||||||||||
                                CGG CG  CCCTGCCCCG
                                  C AGA
GAM129  RGS16    3' GCCACCTGCAGGGGGCCACC 2869     G __   ACGG
                                GCCA CC CGGGG  GGCCACC
                                |||| ||  |||||  |||||||
                                CGGT GG GTCCC  CCGGTGG
                                  _ AC   _____
GAM129  SIX2     5' GCCGCCCGGGGCGCCGC    2870     A     A GG
                                GCC GCCCGGGG CG GC
                                ||| |||||||| ||  ||
                                CGG CGGGCCCC GC CG
                                  _      _ GG
GAM129  SOD3     5' AGCCAGCCCAGGAACGCAGGC 2871            _
                                AGCCAGCCCGGGGACG GGGC
                                |||||||||||||||| ||||
                                TCGGTCGGGTCCTTGC TCCG
                                          G
GAM129  SORCS2   3' AGCCACCCCGGTGGCTACC  2872      G   _ ACGGG
                                AGCCA CCCGG GG   GCC
                                ||||| ||||| ||    |||
                                TCGGT GGGCC CC   TGG
                                   G   A GA___
GAM129  STX1A    3' ACCTAGCCCAAGGGGTTGC  2873     _      AC G_
                                GCC AGCCCGGGG GG GC
                                ||| |||||||| ||  ||
                                TGG TCGGGTTCC CC CG
                                  A       __ AA
GAM129  TCIRG1   5' GCCAGCCTGGGGAGAGCAC  2874       C   CG  C
                                GCCAGCC GGGGA GGGC AC
                                ||||||| |||||  |||| ||
                                CGGTCGG CCCCT  CTCG TG
                                   A   __   _
GAM129  TRPC6    5' ACTGGCCCGGGGAAAAGTCACC 2875    CA      CG GC
                                GC GCCCGGGGA GG CACC
                                ||  |||||||||  ||  ||||
```

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                              TG  CGGGCCCCT  TC  GTGG
                               AC        TT  A_
GAM129  UPF3B    5'  GCTTGGCCGGAACGGGGTTACC 2876     CA_  CG       CC
                              GC   GCC  GGGACGGGG  ACC
                              ||   |||  |||||||||  |||
                              CG   CGG  CCTTGCCCC  TGG
                               AAC  __        AA
GAM129  UPF3B    5'  GCTTGGCCGGAACGGGGTTACC 2876     CA_  CG       CC
                              GC   GCC  GGGACGGGG  ACC
                              ||   |||  |||||||||  |||
                              CG   CGG  CCTTGCCCC  TGG
                               AAC  __        AA
GAM129  WBSCR1   3'  GCTGCCCGGGGACTCACC    2877     CA       GGG
                              GC  GCCCGGGGAC   GCC
                              ||  ||||||||||   |||
                              CG  CGGGCCCCTG   TGG
                               A_        AG_
GAM129  WBSCR1   3'  GCTGCCCGGGGACTCACC    2877     CA       GGG
                              GC  GCCCGGGGAC   GCC
                              ||  ||||||||||   |||
                              CG  CGGGCCCCTG   TGG
                               A_        AG_
GAM129  WHSC1    3'  GCCGGCCTGAGGACGGACAGC  2878      A   C       __
                              GCC GCC GGGGACGG  GGC
                              ||| ||| ||||||||  |||
                              CGG CGG CTCCTGCC  TCG
                                C   A       TG
GAM129  WHSC1    3'  GCCGGCCTGAGGACGGACAGC  2878      A   C       __
                              GCC GCC GGGGACGG  GGC
                              ||| ||| ||||||||  |||
                              CGG CGG CTCCTGCC  TCG
                                C   A       TG
GAM129  WHSC1    3'  GCCGGCCTGAGGACGGACAGC  2878      A   C       __
                              GCC GCC GGGGACGG  GGC
                              ||| ||| ||||||||  |||
                              CGG CGG CTCCTGCC  TCG
                                C   A       TG
GAM129  ZNF140   5'  ACCGCCCGGGGCCATCGGTGGC 2879      A       A G_____  GCCA
                              GCC GCCCGGGG C     GG    C
                              ||| |||||||  |     ||    |
                              TGG CGGGCCCC G     CC    G
                                _       G TAGIII  ACCG
GAM129  AGS3     5'  GCCAGCCCGGGATGGAAGCAC  2880           AC    C
                              GCCAGCCCGGGG  GGGG CAC
                              ||||||||||||  |||| |||
                              CGGTCGGGCCCT  CCTT GTG
                                     A_    C
GAM129  ARGBP2   5'  AGCCAGCCTAGGGAGCATTGGT 2881        CG    _ G_____  GCCA
            GGC                    CCAGCC  GGGA C     GG    C
                              ||||||  |||| |     ||    |
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                                GGTCGG  CCCT G     CC    G
                                   AT    C TAAIII  ACCG
GAM129  C14orf4   5'  GCGGCCCGGGGGAGCGGCC   2882     CA       AC  _
                                GC  GCCCGGGG  GG GGCC
                                ||  ||||||||  || ||||
                                CG  CGGGCCCC  TC CCGG
                                 C_       C_  G
GAM129  C6orf31   3'  CAGAACAAGGCGGGGCCGCC   2883     CC     A      A
                                CAG  CGGGG CGGGGCC CC
                                |||  ||||| ||||||| ||
                                GTC  GTTCC GCCCCGG GG
                                  TT     _      C
GAM129  CENTG1    3'  AGCCAGCCTGGGTATGGGC   2884          C   GACG
                                AGCCAGCC GGG    GGGC
                                |||||||| |||    ||||
                                TCGGTCGG CCC    CCCG
                                     A   ATA_
GAM129  CNK1      3'  CAGCTCGGGGTGAGACC     2885       C     AC
                                CAGC CGGGG  GGGGCC
                                |||| |||||  ||||||
                                GTCG GCCCC  CTCTGG
                                  A     A_
GAM129  DKFZP434B103 3'  AGCCAGCCTGGGAGCTGCC   2886          CG    CGGG
                                AGCCAGCC  GGGA    GCC
                                ||||||||  ||||    |||
                                TCGGTCGG  CCCT    CGG
                                     A_    CGA_
GAM129  DKFZP434H204 5'  GCCGGCCCAGGGGGTCACAGTG 2887      A       ____    G
             C                   GCC GCCCGGGG    ACGG GC
                                |||  ||||||||    |||| ||
                                CGG CGGGTCCC    TGTC CG
                                  C       CCAG    A
GAM129  DKFZP586J0619 3'  GCCATGCCCGGGGGGATCCGCC 2888       _       AC  GG  A
                                GCCA GCCCGGGG  GG  CC CC
                                |||| ||||||||  ||  || ||
                                CGGT CGGGCCCC  CC  GG GG
                                  A       __  TA  C
GAM129  FBXO32    5'  GCTCGGGGACGTGCCACC    2889     C       GG
                                GC CGGGGACG  GCCACC
                                || ||||||||  ||||||
                                CG GCCCCTGC  CGGTGG
                                 A       A_
GAM129  FJX1      3'  GCCACTCGGGGGCCAAACC    2890       G C     ACG
                                GCCA C CGGGG   GGGCC
                                |||| | |||||   |||||
                                CGGT G GCCCC   TTTGG
                                  _ A    CGG
GAM129  FLJ10060  5'  AGCTGGCCCGAGGTGCAGCTGC 2891      CA       A_   G_
             C                   AGC  GCCCGGGG  CGG  GCC
                                |||  ||||||||  |||  |||
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                              TCG  CGGGCTCC  GTC  CGG
                                AC       AC   GA
GAM129  FLJ10852  5' GCCAGCCCGCCTTGGGTCGCC  2892         GGGAC  __
                              GCCAGCCCG    GGG  GCC
                              |||||||||    |||  |||
                              CGGTCGGGC    CCC  CGG
                                   GGAA_   AG
GAM129  FLJ11457  3' AGTCCAGGAGGCGGGGCCA   2893    _   CCC   A
                              AG CCAG   GGGG CGGGGCCA
                              || ||||   |||| ||||||||
                              TC GGTC   CTCC GCCCCGGT
                               A  ____   _
GAM129  FLJ12389  3' AGCTGGCCCGGAGGCACGCTGG 2894   CA    _ _  ______ GCCA
           TGGC                   GCCCGG GG ACG    GG   C
                               ||||||  || |||    ||   |
                               CGGGCC CC TGC    CC   G
                              AC     T  G   GAIII  ACCG
GAM129  FLJ13769  3' AGCCAGCCTGGAGGTGGCC   2895         C   ACGG
                              AGCCAGCC GGGG   GGCC
                              |||||||| ||||   ||||
                              TCGGTCGG CCTC   CCGG
                                   A   CA__
GAM129  FLJ14129  3' GCCGGCCCGGGACAGACC    2896     A     G    G
                              GCC GCCCGGG ACGGG CC
                              ||| ||||||| ||||| ||
                              CGG CGGGCCC TGTCT GG
                                C     _    _
GAM129  FLJ14810  3' GCCTGGTAGGATGGGGCCACC  2897     C  __  C
                              GCC GG  GGA GGGGCCACC
                              ||| ||  ||| |||||||||
                              CGG CC  CCT CCCCGGTGG
                                A  AT   A
GAM129  FLJ20277  3' AGCCAGCCTGGGGGTACACAGT 2898         C  _____  GG
           ACC                   AGCCAGCC GGGG   ACGG  CC
                              |||||||| ||||   ||||  ||
                              TCGGTCGG CCCC   TGTC  GG
                                   A   CATG   AT
GAM129  FLJ20306  5' AGCCAGCTCGGGAGGTGGGGC  2899        C   AC_
                              AGCCAGC CGGGG   GGGGC
                              ||||||| |||||   |||||
                              TCGGTCG GCCCT   CCCCG
                                   A    CCA
GAM129  FLJ20320  5' ACTCAGCCCGGCGCGGGCCGCC 2900    _      GGA _    A
                              GC CAGCCCGG   CG GGGCC CC
                              || ||||||||   || ||||| ||
                              TG GTCGGGCC   GC CCCGG GG
                               A       ___  G    C
GAM129  FLJ20366  5' AGCCAGCCGGGCGGCTGC    2901         CG   A   G_
                              AGCCAGCC  GGG CGG  GC
                              ||||||||  ||| |||  ||
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                                TCGGTCGG  CCC GCC  CG
                                   __  _  GA
GAM129  FLJ23233  5'  GCCACCCTGGGCGCCGCC    2902      G  G  A  GG
                                GCCA CCC GGG CG  GCC
                                |||| ||| ||| ||  |||
                                CGGT GGG CCC GC  CGG
                                  _  A  _  GG
GAM129  GMEB2     3'  GCCGGCTCAGGGACAGGCTGCC 2903     A  C       __
                                GCC GC CGGGGACGGG  GCC
                                ||| || ||||||||||  |||
                                CGG CG GTCCCTGTCC  CGG
                                  C  A        GA
GAM129  GSA7      3'  AGTCAGCCCCACAGCGGGGCCA 2904     C    _ G  A
                                AG CAGCCC G GG CGGGGCCA
                                || |||||| | || ||||||||
                                TC GTCGGG T TC GCCCCGGT
                                 A     G G  _
GAM129  H6PD      5'  GCCAGCCCGGCCGCCAC     2905          GGACGGG
                                GCCAGCCCGG      GCCAC
                                ||||||||||      |||||
                                CGGTCGGGCC      CGGTG
                                     GG_____
GAM129  HSSEXGENE 3'  GCTCAGCCCGGGGACCCAGGC  2906     _         G_
                                GC CAGCCCGGGGAC  GGGC
                                || ||||||||||||  ||||
                                CG GTCGGGCCCCTG  TCCG
                                 A          GG
GAM129  KCNB2     5'  GCCAGCCCGGGAGTTGCC    2907           ACGGG
                                GCCAGCCCGGGG    GCC
                                ||||||||||||    |||
                                CGGTCGGGCCCT    CGG
                                     CAA__
GAM129  KIAA0014  3'  GCCGGCAGTGCCGACGGGGCTG 2908     A  CCGGG_      CA
           CC                     GCC GC     GACGGGGC  CC
                                ||| ||     ||||||||  ||
                                CGG CG     CTGCCCCG  GG
                                  C  TCACGG       AC
GAM129  KIAA0082  5'  AGCCAGCCCGGGTCCGCCGG   2909          GA _____
                                AGCCAGCCCGGG  CG    GG
                                ||||||||||||  ||    ||
                                TCGGTCGGGCCC  GC    CC
                                     AG  GGIII
GAM129  KIAA0218  5'  GCCAGACCCGGGCGCCGCC    2910       _    GA  GG
                                GCCAG CCCGGG  CG  GCC
                                |||||  ||||||  ||  |||
                                CGGTC GGGCCC  GC  CGG
                                   T      __  GG
GAM129  KIAA0247  3'  AGCCACCCGGGGACTTGG    2911       G        GG
                                AGCCA CCCGGGGAC  GG
                                |||||  |||||||||  ||
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                                TCGGT GGGCCCCTG  CC
                                  _       AA
GAM129  KIAA0515 3' GCCAACCTGGGAGCCAC     2912        C  GACGG
                                GCCAGCC GGG    GGCCAC
                                ||||||| |||    ||||||
                                CGGTTGG CCC    TCGGTG
                                   A  _____
GAM129  KIAA0537 5' AGCCACCCGGGGCCGGGGCCGC 2913       G     A     A
          C                     AGCCA CCCGGGG CGGGGCC CC
                                ||||| ||||||| ||||||| ||
                                TCGGT GGGCCCC GCCCCGG GG
                                  _     G     C
GAM129  KIAA0544 3' AGACAGCCCGGAGGCC     2915     C      GGACG
                                AG CAGCCCGG    GGGCC
                                || ||||||||    |||||
                                TC GTCGGGCC    TCCGG
                                 T      _____
GAM129  KIAA0544 3' AGCTGGCCTGGGACAGGCC   2914     CA  CG      G
                                AGC  GCC  GGGACGGG CC
                                |||  |||  |||||||| ||
                                TCG  CGG  CCCTGTCC GG
                                 AC  A_      _
GAM129  KIAA0674 5' AGCCAGCCGGTATAGGCCAC  2916        C GGACG
                                AGCCAGCC GG    GGGCCAC
                                |||||||| ||    |||||||
                                TCGGTCGG CC    TCCGGTG
                                   _ ATA__
GAM129  KIAA1615 5' GCCCGGCAGCGCGGGGCCACC 2917       _ A_
                                GCCCGG GG  CGGGGCCACC
                                |||||| ||  ||||||||||
                                CGGGCC TC  GCCCCGGTGG
                                   G  GC
GAM129  KIAA1887 5' CCAGTCTAAAGCCGGGGCCACC 2918     CCC   A
                                CCAG   GGGG CGGGGCCACC
                                ||||   |||| ||||||||||
                                GGTC   TTTC GCCCCGGTGG
                                  AGA   G
GAM129  KIAA1949 5' AGACAGCCCGGGGGTGAGAC  2919    C       AC
                                AG CAGCCCGGGG  GGGGC
                                || ||||||||||  |||||
                                TC GTCGGGCCCC  CTCTG
                                 T        CA
GAM129  KIAA1949 5' AGACAGCCCGGGGGTGAGAC  2919    C       AC
                                AG CAGCCCGGGG  GGGGC
                                || ||||||||||  |||||
                                TC GTCGGGCCCC  CTCTG
                                 T        CA
GAM129  KIAA1949 5' AGACAGCCCGGGGGTGAGAC  2919    C       AC
                                AG CAGCCCGGGG  GGGGC
                                || ||||||||||  |||||
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                              TC GTCGGGCCCC  CTCTG
                               T        CA
GAM129  LGI4     3'  AGCCAGCCAAGGGGCC      2920         CGGG  C
                              AGCCAGCC    GA GGGGCC
                              ||||||||    || ||||||
                              TCGGTCGG    TT CCCCGG
                                   _____  _
GAM129  LYPLA3   3'  AGCCAGTCAGGCTGGCCAC   2921        CC    GACGG
                              AGCCAG  CGGG    GGCCAC
                              ||||||  ||||    ||||||
                              TCGGTC  GTCC    CCGGTG
                                 A_   GA___
GAM129  MARK2    5'  GCCAGCCCGGGGATGCGCC   2922            CGGG
                              GCCAGCCCGGGGA   GCC
                              ||||||||||||    |||
                              CGGTCGGGCCCCT   CGG
                                     ACG_
GAM129  MEGF11   5'  GCCGGCCCAGGGATCGGCC   2923      A       CGG
                              GCC GCCCGGGGA   GGCC
                              ||| |||||||||   ||||
                              CGG CGGGTCCCT   CCGG
                                C        AG_
GAM129  MGC11115 3'  AGCAGCCTGGGACAAGCCGCC  2924      C   CG       G  A
                              AGC AGCC  GGGACGGG CC CC
                              ||| ||||  |||||||| || ||
                              TCG TCGG  CCCTGTTC GG GG
                                _    A_       _  C
GAM129  MGC14859 3'  GCTCAGGGTATAAACCACC   2925     C    ACG
                              GC CGGGG   GGGCCACC
                              || |||||   ||||||||
                              CG GTCCC   TTTGGTGG
                               A    ATA
GAM129  MGC4707  3'  GCCATTCACCTTCCGGGGCCAC 2926       GC__  GGGGA
                              GCCA   CC    CGGGGCCAC
                              ||||   ||    |||||||||
                              CGGT   GG    GCCCCGGTG
                                AAGT  AAG__
GAM129  NSE1     3'  GCAGCCCGGGCCCGGGCCACC  2927     C       GA   G
                              GC AGCCCGGG  CGGG CCACC
                              || ||||||||  |||| |||||
                              CG TCGGGCCC  GCCC GGTGG
                                _       GG   _
GAM129  OCLM     5'  AGCCACACTGAGATGGGGC    2928       G CCG    C
                              AGCCA C   GGGA GGGGC
                              ||||| |   |||| |||||
                              TCGGT G   CTCT CCCCG
                                 _ TGA    A
GAM129  PLCL2    5'  GCTAGCCCGGGCTTCGTCGGTG 2929    C       GA_  _____  GCCA
           GC                   C AGCCCGGG   CG    GG    C
                              | ||||||||   ||    ||    |
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                                G TCGGGCCC  GC   CC   G
                                 A      GAA  AGIII  ACCG
GAM129  POLR2J2  3'  GCCACCCTGGGGTGAGCTGCC  2930     G  C   AC  __
                                GCCA CC GGGG  GGG  GCC
                                |||| || ||||  |||  |||
                                CGGT GG CCCC  CTC  CGG
                                  G  A   A_   GA
GAM129  SDC3     3'  AGCCAGGCCTGCCGGGGCCACC 2931       C  GGGGA
                                AGCCAG CC    CGGGGCCACC
                                |||||| ||    ||||||||||
                                TCGGTC GG    GCCCCGGTGG
                                   C  ACG__
GAM129  SLC26A1  3'  GCCAGGCTGGGTAGGGCCAC  2932      CCCG  AC
                                GCCAG   GGG  GGGGCCAC
                                |||||   |||  ||||||||
                                CGGTC   CCC  TCCCGGTG
                                   CGA_  A_
GAM129  SSTK     3'  ACTAGTCCGCAAATGGGGGCCA 2933    C  C   G   C_
            CC                   GC AG CCG GGA  GGGGCCACC
                                || || ||| |||  |||||||||
                                TG TC GGC TTT  CCCCGGTGG
                                 A  A   G   AC
GAM129  SYT12    3'  AGCCAGCCTGAGGGTCCATGC  2934       C__  GA  GG
                                AGCCAGCC   GGG  CG  GC
                                ||||||||   |||  ||  ||
                                TCGGTCGG   CCC  GT  CG
                                     ACT   AG  A_
GAM129  TCL6     5'  AGCCAGCCTGGGGACAGAG   2935       C
                                AGCCAGCC GGGGACGGGG
                                |||||||| ||||||||||
                                TCGGTCGG CCCCTGTCTC
                                     A
GAM129  TCL6     5'  AGCCAGCCTGGGGACAGAG   2935       C
                                AGCCAGCC GGGGACGGGG
                                |||||||| ||||||||||
                                TCGGTCGG CCCCTGTCTC
                                     A
GAM129  TCL6     5'  AGCCAGCCTGGGGACAGAG   2935       C
                                AGCCAGCC GGGGACGGGG
                                |||||||| ||||||||||
                                TCGGTCGG CCCCTGTCTC
                                     A
GAM129  TCL6     5'  AGCCAGCCTGGGGACAGAG   2935       C
                                AGCCAGCC GGGGACGGGG
                                |||||||| ||||||||||
                                TCGGTCGG CCCCTGTCTC
                                     A
GAM129  TOR2A    3'  AGCCGCCCGGGAGGGGGC    2936     A      AC
                                AGCC GCCCGGGG  GGGGC
                                |||| ||||||||  |||||
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                                TCGG CGGGCCCT  CCCCG
                                  _       C_
GAM129  TRIM28   3'  AACTGGGGGATGGGGCCAC   2937     CC    C
                                AGC  GGGGA GGGGCCAC
                                |||  ||||| ||||||||
                                TTG  CCCCT CCCCGGTG
                                  AC    A
GAM129  UBXD1    5'  CCAGTCGGGGACGGGGCCGCC  2938      CC          A
                                CCAG  CGGGGACGGGGCC CC
                                ||||  |||||||||||| ||
                                GGTC  GCCCCTGCCCCGG GG
                                  A_          C
GAM129  UXS1     5'  GCCAGTTTGGGAACAGGGC   2939      CCC
                                GCCAG   GGGGACGGGGC
                                |||||   ||||||||||
                                CGGTC   CCCTTGTCCCG
                                   AAA
GAM129  WBSCR16  3'  CCCGGGACGGGGCCGCC    2940       G      A
                                CCCGGG ACGGGGCC CC
                                |||||| |||||||| ||
                                GGGCCC TGCCCCGG GG
                                   _       C
GAM129  LOC127281 3'  AGCTGCCCGGGGGTGGGA    2941     CA      AC
                                AGC  GCCCGGGG  GGGG
                                |||  ||||||||  ||||
                                TCG  CGGGCCCC  CCCT
                                  A_       CA
GAM129  LOC143153 3'  AGCCAGCCTGGTGGCCAGGCTG 2942         C  _  A   __
          CC                      AGCCAGCC GG GG CGGG  GCC
                                |||||||| || || ||||  |||
                                TCGGTCGG CC CC GTCC  CGG
                                     A  A  G    GA
GAM129  LOC145717 5'  AGCCGCCCGGGGGTGGCC    2943      A      ACGG
                                AGCC GCCCGGGG    GGCC
                                |||| ||||||||    ||||
                                TCGG CGGGCCCC    CCGG
                                  _       CA__
GAM129  LOC145748 5'  CAGCCCGGGGACGGGGCCAGCC 2944                  _
                                CAGCCCGGGGACGGGGCCA CC
                                |||||||||||||||||| ||
                                GTCGGGCCCCTGCCCCGGT GG
                                        C
GAM129  LOC146488 5'  CAGCCCAGAGTGGGGCCAC   2945          AC
                                CAGCCCGGGG  GGGGCCAC
                                ||||||||||  ||||||||
                                GTCGGGTCTC  CCCCGGTG
                                   A_
GAM129  LOC147165 3'  GCCAGTCCGGGGGAGCGGACC  2946       _  C    CG
                                GCCAG CC GGGGA  GGGCC
                                ||||| || |||||  |||||
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                                CGGTC GG CCCCT  CCTGG
                                  A  C    CG
GAM129  LOC148181 3'  AGCTGAGCCTGGAGAGGCCACC 2947     C_   C    CGG
                                AGC  AGCC GGGGA   GGCCACC
                                |||  |||| |||||   |||||||
                                TCG  TCGG CCTCT   CCGGTGG
                                  AC   A   ___
GAM129  LOC148189 5'  AGCCAGCCCGGGGGTCCAATGG 2948           ACG____
          G                      AGCCAGCCCGGGG      GGG
                                ||||||||||||      |||
                                TCGGTCGGGCCCC      CCC
                                       CAGGTTA
GAM129  LOC148534 5'  GCCGGCCCGAGGGCTGGCGC   2949     A    _   AC  G
                                GCC GCCCG GGG  GG GC
                                ||| ||||| |||  || ||
                                CGG CGGGC CCC  CC CG
                                  C    T   GA  G
GAM129  LOC148887 3'  CAGAAACAAGGGACGGGGCCAC 2950     CCC__          III
          CG                     CAG    GGGGACGGGGCCACC   G
                                |||    ||||||||||||||  |
                                GTC    TCCCTGCCCCGGTGG   C
                                  TTTGT           III
GAM129  LOC150519 5'  GCCTGGGGCCGAGGCCACC   2951     C   A
                                GCC GGGG CGGGGCCACC
                                ||| |||| ||||||||||
                                CGG CCCC GCTCCGGTGG
                                  A   G
GAM129  LOC150819 3'  AGCCAGCCTGGAGGCCC     2952        C  GGACG    A
                                AGCCAGCC GG     GGGCC C
                                |||||||| ||     ||||| |
                                TCGGTCGG CC     TCCGG G
                                    A _____     C
GAM129  LOC152860 3'  AGCCAGCCCGAGGGTGGAA   2953           AC
                                AGCCAGCCCGGGG  GGGG
                                ||||||||||||  ||||
                                TCGGTCGGGCTCC  CCTT
                                       CA
GAM129  LOC153232 5'  AGCTGGGCCCGGGGGACCAC   2954     CA_      ACGG
                                AGC   GCCCGGGG    GGCCAC
                                |||   ||||||||    ||||||
                                TCG   CGGGCCCC    CTGGTG
                                  ACC       ____
GAM129  LOC154790 5'  GCCTAGGGGCGGGGCCACC   2955     CG   A
                                GCC  GGG CGGGGCCACC
                                |||  ||| ||||||||||
                                CGG  CCC GCCCCGGTGG
                                  AT   C
GAM129  LOC196955 5'  AGCCAGCCTGAGCCAGCTGCC  2956        C   GA   G_
                                AGCCAGCC GGG  CGG  GCC
                                |||||||| |||  |||  |||
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                                TCGGTCGG CTC  GTC  CGG
                                    A  G_  GA
GAM129  LOC196985 5' AGACAGCCTGGGGGGCTGCC  2957    C    C   AC  G_
                                AG CAGCC GGGG  GG  GCC
                                || ||||| ||||  ||  |||
                                TC GTCGG CCCC  CC  CGG
                                 T    A   __  GA
GAM129  LOC199786 3' AGCCAGACATTCGGGGCCAC  2958       CC  GGGA
                                AGCCAG  CG   CGGGGCCAC
                                ||||||  ||   |||||||||
                                TCGGTC  GT   GCCCCGGTG
                                   T_  AA__
GAM129  LOC200213 5' GCCGGCCCGGGGCCGCGGCC  2959     A      A  G
                                GCC GCCCGGGG CG GGCC
                                ||| |||||||| || ||||
                                CGG CGGGCCCC GC CCGG
                                  C       G  G
GAM129  LOC203248 3' AGCGGCCCGGGGTGGCTGCC  2960     CA      AC  G_
                                AGC  GCCCGGGG  GG  GCC
                                |||  ||||||||  ||  |||
                                TCG  CGGGCCCC  CC  CGG
                                  C_       A_  GA
GAM129  LOC204970 3' CAGTTTGGGGAGGAGCCAC   2961     CCC    C
                                CAG   GGGGA GGGGCCAC
                                |||   ||||| ||||||||
                                GTC   CCCCT CCTCGGTG
                                  AAA    _
GAM129  LOC219942 3' GCCAGCCCAACGTCGGGGTCAC 2962          GGA    C
                                GCCAGCCCGG   CGGGG CAC
                                ||||||||||   ||||| |||
                                CGGTCGGGTT   GCCCC GTG
                                     GCA    A
GAM129  LOC221975 5' GCCACCCGGGGACGCTGG    2963      G       _____
                                GCCA CCCGGGGACG    GG
                                |||| ||||||||||    ||
                                CGGT GGGCCCCTGC    CC
                                  _        GAIII
GAM129  LOC222031 3' AGCCAGCCTGGGGTGGAG    2964        C   AC
                                AGCCAGCC GGGG  GGGG
                                |||||||| ||||  ||||
                                TCGGTCGG CCCC  CCTC
                                    A   A_
GAM129  LOC223009 5' AGCTGGGCCTGGAGAGGCCACC 2965     CA_  C    CGG
                                AGC   GCC GGGGA   GGCCACC
                                |||   ||| |||||   |||||||
                                TCG   CGG CCTCT   CCGGTGG
                                  ACC   A   ___
GAM129  LOC245727 5' AGCCGCCCGGGGGTGGCC    2943      A      ACGG
                                AGCC GCCCGGGG    GGCC
                                |||| ||||||||    ||||
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                                TCGG CGGGCCCC   CCGG
                                  _      CA__
GAM129  LOC253216 5'  GCCGGCCCAGGGGGTCACAGTG 2887     A      ____   G
            C                    GCC GCCCGGGG   ACGG GC
                                 ||| ||||||||   |||| ||
                                 CGG CGGGTCCC   TGTC CG
                                   C      CCAG   A
GAM129  LOC254263 5'  GCGGCCCGGGGGGGCGCC    2966    CA      AC  G
                                 GC  GCCCGGGG  GG GCC
                                 ||  ||||||||  || |||
                                 CG  CGGGCCCC  CC CGG
                                  C_      __  G
GAM129  LOC255056 5'  AGCTGCCCGAGGGGCCC    2967    CA    GGAC    A
                                 AGC  GCCCGG   GGGGCC C
                                 |||  ||||||   |||||| |
                                 TCG  CGGGCT   CCCCGG G
                                   A_    ____     C
GAM129  LOC255682 5'  AGCCCGCCCCCTCCGGGGCCAC 2968     A   GGGGA
            C                    AGCC GCCC    CGGGGCCACC
                                 |||| ||||    ||||||||||
                                 TCGG CGGG    GCCCCGGTGG
                                   G   GGAG_
GAM129  LOC255975 5'  GCTGGGCCTGGAGGGGCCACC  2969    CA_  CGG  C
                                 GC   GCC   GGA GGGGCCACC
                                 ||   |||   ||| |||||||||
                                 CG   CGG   CCT CCCCGGTGG
                                  ACC   A__   _
GAM129  LOC255975 5'  AGCTGTGCCTGGAGAGGTCACC 2970     CA_  C    C  G_
                                 AGC   GCC GGGGA GG  GCC
                                 |||   ||| ||||| ||  |||
                                 TCG   CGG CCTCT CC  TGG
                                   ACA   A    _ AG
GAM129  LOC255987 5'  GCTGGGCCTGGAGGGGCCACC  2969    CA_  CGG  C
                                 GC   GCC   GGA GGGGCCACC
                                 ||   |||   ||| |||||||||
                                 CG   CGG   CCT CCCCGGTGG
                                  ACC   A__   _
GAM129  LOC51619  5'  GCGGCCCGGCCGGGGCTGCC   2971    CA    GGA    CA
                                 GC  GCCCGG   CGGGGC  CC
                                 ||  ||||||   ||||||  ||
                                 CG  CGGGCC   GCCCCG  GG
                                  C_     G__     AC
GAM129  LOC90249  3'  AGCCAGCCCTGGGGACGGGCAC 2972          _       ___
            GCC                    AGCCAGCCC GGGGACGGG   GCC
                                 |||||||||  |||||||||   |||
                                 TCGGTCGGG CCCCTGCCC   CGG
                                      A        GTG
GAM129  LOC90379  3'  AGCCGGCCAGGAAGAGGCCACC 2973      A  C    C
                                 AGCC GCC GGGGA GGGGCCACC
                                 |||| ||| ||||| |||||||||
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                                TCGG CGG TCCTT CTCCGGTGG
                                  C  _   _
GAM129  LOC90525  3'  CAGCCCGGGGACGGCGCC   2974           G
                                CAGCCCGGGGACGG GCC
                                ||||||||||||| |||
                                GTCGGGCCCCTGCC CGG
                                       G
GAM129  LOC90906  5'  AGCCACCTAAGGGGCTGCC   2975      G CG  AC G_
                                AGCCA CC  GGG  GG  GCC
                                ||||| ||  |||  ||  |||
                                TCGGT GG  TCC  CC  CGG
                                  _ AT   __ GA
GAM129  LOC91040  3'  AGCCACCTCGGGGACAGGGCC  2976      G _
                                AGCCA CC CGGGGACGGGGCC
                                ||||| || ||||||||||||
                                TCGGT GG GCCCCTGTCCCGG
                                  _ A
GAM129  LOC92080  5'  GCCCAGTGGGGACGGGGCTGCC 2977      ___       CA
                                GCCC  GGGGACGGGGC  CC
                                ||||  ||||||||||  ||
                                CGGG  CCCCTGCCCCG  GG
                                  TCA        AC
GAM129  LOC93512  3'  GCCAGTCCGGGGGGAGCGGACC  2946      _ C   CG
                                GCCAG CC GGGGA  GGGCC
                                ||||| || |||||  |||||
                                CGGTC GG CCCCT  CCTGG
                                  A  C    CG
GAM130  ARCN1   3'  GCATTCCAGCCTGGGTTA   2980        A   C
                                GCATTCCA CCTG GTTG
                                |||||||| |||| ||||
                                CGTAAGGT GGAC CAAT
                                     C   C
GAM130  LILRA3   3'  ACTGCATTCCAGCCTGGT   2981    C      A   C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C   _
GAM130  PIGR    3'  ACTGCATTCCAGTCTGGGT   2982    C      AC  C
                                AC GCATTCCA  CTG GT
                                || ||||||||  ||| ||
                                TG CGTAAGGT  GAC CA
                                 A       CA  C
GAM130  TNFAIP1  3'  CGCATTCCAGTCTCTGT    2983         AC  GCG
                                CGCATTCCA  CT   TTGT
                                |||||||||  ||   ||||
                                GCGTAAGGT  GA   GACA
                                     CA  ___
GAM130  TRPV1   3'  ACTGCATTCCAGCCTGGGT   2984    C      A   C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
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                                TG CGTAAGGT GGAC CA
                                 A       C    C
GAM130  TRPV1    3' ACTGCATTCCAGCCTGGGT   2984    C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C    C
GAM130  TRPV1    3' ACTGCATTCCAGCCTGGGT   2984    C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C    C
GAM130  TRPV1    3' ACTGCATTCCAGCCTGGGT   2984    C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C    C
GAM130  XRCC5    3' CCGCATCCAACTTGTTTTG   2985        T    C CG
                                CCGCAT CCAAC TG  TTG
                                |||||| ||||| ||  |||
                                GGCGTA GGTTG AC  AAC
                                   _    A  AA
GAM130  CHSY1    3' ACTGCATTCCAGCCTGGGT   2984    C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C    C
GAM130  DCAMKL1  3' GCATTCCATCTGATTA     2986         AC   C
                                GCATTCCA  CTG GTTG
                                ||||||||  ||| ||||
                                CGTAAGGT  GAC TAAT
                                    A_   _
GAM130  GR6      5' ACTGCATTCCAGCCTGGGT   2984    C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C    C
GAM130  KIAA1040 3' ACTGCATTCCAGCCTGGGT   2984    C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C    C
GAM130  KIAA1829 3' ACCGCATTCCAGCCTGGAT   2987          A    C
                                ACCGCATTCCA CCTG GT
                                |||||||||||| |||| ||
                                TGGCGTAAGGT GGAC TA
                                      C    C
GAM130  KIAA1924 3' ACTGCATTCCAGCCTAGGT   2988    C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
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                                TG CGTAAGGT GGAT CA
                                 A       C    C
GAM130  MGC2474   3' ACTGCATTCCAGCCTGGGT   2984     C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C    C
GAM130  PRKWNK2   3' CCGCATTCTGGCACTCCGAGT 2989         CA__ _  C
                                CCGCATTC    AC CTG GT
                                ||||||||    || ||| ||
                                GGCGTAAG    TG GGC CA
                                     ACCG  A   T
GAM130  TCL6      5' ACTGCATTCCAGCCTGAGT   2990     C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C    T
GAM130  TCL6      5' ACTGCATTCCAGCCTGAGT   2990     C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C    T
GAM130  TCL6      5' ACTGCATTCCAGCCTGAGT   2990     C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C    T
GAM130  TCL6      5' ACTGCATTCCAGCCTGAGT   2990     C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C    T
GAM130  UBE2D1    3' GCTTTTCAGCTGCATTGTA   2991     A  C  AC
                                GC TT CA  CTGCGTTGTA
                                || || ||  ||||||||||
                                CG AA GT  GACGTAACAT
                                 A  A  C_
GAM130  LOC150587 3' ACCGCATTCCAGCTTGGGCTA 2992           ACC  C
                                ACCGCATTCCA   TG GTTG
                                ||||||||||   || ||||
                                TGGCGTAAGGT   AC CGAT
                                      CGA  C
GAM130  LOC151979 5' ACTGCATTCCAGCTTG      2993     C       ACCT  G
                                AC GCATTCCA    GC TTG
                                || ||||||||    || |||
                                TG CGTAAGGT    CG AAC
                                 A       _____ _
GAM131  ABLIM     3' CTTGCTAAGAATTAATTT     2996         CATTT
                                TTTGCTA    GAATTAATTT
                                |||||||    ||||||||||
```

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                                GAACGAT    CTTAATTAAA
                                   T____
GAM131  ABLIM    3'  CTTGCTAAGAATTAATTT    2996        CATTT
                                TTTGCTA    GAATTAATTT
                                |||||||    ||||||||||
                                GAACGAT    CTTAATTAAA
                                   T____
GAM131  LOC153443 3'  TTGCTATATTTAAACAATTTT  2997       C      T
                                TTGCTA ATTTGAAT AATTTT
                                |||||| |||||||| ||||||
                                AACGAT TAAATTTG TTAAAA
                                   A      _
GAM131  LOC221288 5'  ATTTGCAGCATTTGAAAGTAAT 2998       TA      T_
          T                     ATTTGC  CATTTGAA  TAATT
                                ||||||  ||||||||  |||||
                                TAAACG  GTAAACTT  ATTAA
                                   TC       TC
GAM132  CDH5     3'  CAAGTCAAGCTGTCCAGGCCTT 3001         AGA   A   A
                                TAAGTCAA   TGT CCA GCCTT
                                ||||||||   ||| ||| |||||
                                GTTCAGTT   ACA GGT CGGAA
                                    CG_   _   C
GAM132  PAX5     5'  GTCGGAATAATTCAAGCCTT   3002      AAA    TAC
                                GTC   GATG   CAAGCCTT
                                |||   ||||   ||||||||
                                CAG   TTAT   GTTCGGAA
                                  CC_    TAA
GAM132  ZNF35    5'  GTCAAACCCCATCCAAGC    3003        GA_   A
                                GTCAAA   TGT CCAAGC
                                ||||||   ||| ||||||
                                CAGTTT   GTA GGTTCG
                                   GGG   _
GAM132  BCoR     3'  TAAGTCAAAGTGTGGAGCTCCT 3004          A   ACCAAG
          T                     TAAGTCAAAG TGT     CCTT
                                |||||||||| |||     ||||
                                ATTCAGTTTC ACA     GGAA
                                      _  CCTCGA
GAM132  DKFZP564I052 3'  AGACAAAGATGTGCCTC     3005     T       ACCAA
                                AG CAAAGATGT     GCCTT
                                || |||||||||     |||||
                                TC GTTTCTACA     CGGAG
                                 T       ______
GAM132  DKFZP566F084 3'  GTCAAGAAGGGCCAAGCCTT   3006       A  TGTA
                                GTCAA GA    CCAAGCCTT
                                ||||| ||    |||||||||
                                CAGTT CT    GGTTCGGAA
                                   _  TCCC
GAM132  KIAA0628  3'  TAAGTCAAGGATGGACTCTGC  3007         A    T  CAA
                                TAAGTCAA GATG AC   GC
                                |||||||| |||| ||   ||
```

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                                ATTCAGTT CTAC TG   CG
                                    C    C  AGA
GAM132  MRPL18   5'  AAGTCAGGGACAAGCCT     3008        AA  TGTAC
                                AAGTCA  GA    CAAGCCT
                                ||||||  ||    |||||||
                                TTCAGT  CT    GTTCGGA
                                   CC  _____
GAM132  NCOA2    3'  AGCTCGATTGGTATCAAGCCTT 3009      CAAA  __  C
                                AGT   GAT  GTA CAAGCCTT
                                |||   |||  ||| ||||||||
                                TCG   CTA  CAT GTTCGGAA
                                  AG__  AC  A
GAM132  LOC166793 3'  TGAGACAGCATCAAGCCT    3010    A   _  C
                                A AGAT GTA CAAGCCT
                                | |||| ||| |||||||
                                A TCTG CGT GTTCGGA
                                 C   T  A
GAM133  DGCR2    3'  CCCAGGATGGTGGTTTCA    3013     GCA
                                CCC   AGGATGGTGGTTTCA
                                |||   ||||||||||||||
                                GGG   TCCTACCACCAAAGT
                                   ___
GAM133  DHFR     5'  CCCCTGCGAGGCAAGCGGTTT  3014      _  A   AT
                                CCCC GC AGG  GGTGGTTT
                                |||| || |||  ||||||||
                                GGGG CG TCC  TCGCCAAA
                                  A  C   GT
GAM133  IL1F5    5'  CCTCCAAGGATGCCTCA     3015     G_     GGTG
                                CC  CAAGGAT   GTTTCA
                                ||  |||||||   ||||||
                                GG  GTTCCTA   CGGAGT
                                 AG     _____
GAM133  SLC2A3   5'  TCTCCGCAAAGGGTGGAGCC   3016    C      AT    TT
                                TC CCGCAAGG  GGTGG  TC
                                || ||||||||  |||||  ||
                                AG GGCGTTTC  CCACC  GG
                                 A      __    TC
GAM133  TSC      3'  TCTCCGCGGAGGTGGC      3017    C   AA   T
                                TC CCGC  GGA GGTGGT
                                || ||||  ||| ||||||
                                AG GGCG  CCT CCACCG
                                 A   __  _
GAM133  TTYH1    3'  TCCCTCCAAGGATGGGACC    3018      CG       T GT
                                TCCC  CAAGGATGG G  T
                                ||||  ||||||||| |  |
                                AGGG  GTTCCTACC C  G
                                  AG       _ TG
GAM133  ZYX      3'  TCCCTGCAGGATGGGCGA     3019      C   A    _
                                TCCC GCA GGATGG TGG
                                |||| ||| |||||| |||
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                                AGGG CGT CCTACC GCT
                                  A  _     C
GAM133  C5orf6   3'  CCCTTAAGGATGGTGCCCT   3020     GC        G
                                CCC  AAGGATGGTG TTT
                                |||  |||||||||| |||
                                GGG  TTCCTACCAC GGA
                                  AA        G
GAM133  FLJ10482 5'  TCCCCGCAGGGGGGTCCC    3021         A  AT  T   TT
                                TCCCCGCA GG  GG GGT  C
                                |||||||| ||  || ||| |
                                AGGGGCGT CC  CC CCA  G
                                     _ __  _  GG
GAM133  FLJ10581 3'  TCCCTGCCAGGATGATGCTTCA 3022      C  A       G
                                TCCC GC AGGATGGTG TTTCA
                                |||| || ||||||||| |||||
                                AGGG CG TCCTACTAC GAAGT
                                  A  G       _
GAM133  FLJ13902 3'  TCCCCGTGGGAATGGTGG    3023       CAA
                                TCCCCG   GGATGGTGG
                                ||||||   |||||||||
                                AGGGGC   CTTACCACC
                                   ACC
GAM133  FLJ21276 3'  TCCCCGCAGGAGTGGGCACA   3024          A   TG    TTT
                                TCCCCGCA GGA  GTGG   CA
                                |||||||| |||  ||||   ||
                                AGGGGCGT CCT  CACC   GT
                                     _  __    CGT
GAM133  FREQ     3'  TCCCTGCAGGATGTTGG     3025      C   A    G
                                TCCC GCA GGATG TGG
                                |||| ||| ||||| |||
                                AGGG CGT CCTAC ACC
                                  A  _    A
GAM133  KIAA0172 5'  CCCCGTGAGGAGAAGTTTCAA  3026       CA    T  T
                                CCCCG  AGGA GG GGTTTCAA
                                |||||  |||| || ||||||||
                                GGGGC  TCCT CT TCAAAGTT
                                   AC   _ _
GAM133  KIAA0247 3'  TCTACGCAAGGATGTTCCTC   3027     CC        GTGG
                                TC  CGCAAGGATG    TTTC
                                ||  ||||||||||    ||||
                                AG  GCGTTCCTAC    GGAG
                                 AT        AA__
GAM133  KIAA0748 3'  TCCTGCAAGAGGTGGCTT    3028     CC     AT
                                TCC  GCAAGG  GGTGGTTT
                                |||  ||||||  ||||||||
                                AGG  CGTTCT  CCACCGAA
                                  A_     __
GAM133  OSBPL2   3'  GCAGGATTAGCTTCAA      3029     A    GG
                                GCA GGAT  TGGTTTCAA
                                ||| ||||  |||||||||
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                                CGT CCTA  ATCGAAGTT
                                  _   __
GAM133  OSBPL2   3'  GCAGGATTAGCTTCAA      3029      A    GG
                                GCA GGAT  TGGTTTCAA
                                ||| ||||  |||||||||
                                CGT CCTA  ATCGAAGTT
                                  _   __
GAM133  PIP5K2B  3'  TCTCCATGAGCCAGTTGGTTTC 3030     C   CA  GA   _
           AA                     TC CCG  AG  TGGT GGTTTCAA
                                || |||  ||  |||| ||||||||
                                AG GGT  TC  GTCA CCAAAGTT
                                 A  AC  G_   A
GAM133  PIP5K2B  3'  TCTCCATGAGCCAGTTGGTTTC 3030     C   CA  GA   _
           AA                     TC CCG  AG  TGGT GGTTTCAA
                                || |||  ||  |||| ||||||||
                                AG GGT  TC  GTCA CCAAAGTT
                                 A  AC  G_   A
GAM133  TRAF3    5'  CCCGCCAGGGTGGTGGTC    3031       A   A
                                CCCGC AGG TGGTGGTT
                                ||||| ||| ||||||||
                                GGGCG TCC ACCACCAG
                                  G   C
GAM133  LOC124402 3'  TCTCCGCCAGGGTGGTCCTCCA 3032     C    A   A    GG
                                TC CCGC AGG TGGT  TTTCA
                                || |||| ||| ||||  |||||
                                AG GGCG TCC ACCA  GAGGT
                                 A   G   C   G_
GAM133  LOC128387 3'  CCCAGTAGCAATGGTTTCA   3033      CAA  A
                                CCCG   GG TGGTGGTTTCA
                                ||||   || ||||||||||
                                GGGT   TC GTTACCAAAGT
                                  CA_  _
GAM133  LOC148946 5'  TCCCCTAAGGATGGGCCT    3034       GC       TG
                                TCCCC  AAGGATGG  GTTT
                                |||||  ||||||||  ||||
                                AGGGG  TTCCTACC  CGGA
                                  A_       __
GAM133  LOC153546 5'  TCCCCGTAGAGATGGCTT    3035       CAA   T
                                TCCCCG   GGA GGTGGTTT
                                ||||||   ||| ||||||||
                                AGGGGC   TCT CTACCGAA
                                  A__   _
GAM133  LOC157381 3'  TCCTCACAGCATGATGGTTTCA 3036     C    A G
                                TCC CGCA G ATGGTGGTTTCA
                                ||| |||| | ||||||||||||
                                AGG GTGT C TACTACCAAAGT
                                 A   _ G
GAM133  LOC158156 3'  CAAGGATATTATTTCAA     3037         GTG
                                CAAGGATG   GTTTCAA
                                ||||||||   |||||||
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                                GTTCCTAT   TAAAGTT
                                    AA_
GAM133  LOC159976 5'  CCCGCATCAGTGGTTT      3038        AGGA
                                CCCGCA    TGGTGGTTT
                                ||||||    |||||||||
                                GGGCGT    GTCACCAAA
                                   A___
GAM133  LOC201227 3'  TCCTTGCAGGTGGTGGCT    3039      CC   A  A
                                TCC  GCA GG TGGTGGTT
                                |||  ||| || ||||||||
                                AGG  CGT CC ACCACCGA
                                  AA   _ _
GAM133  LOC203350 3'  TCCCCAAATGGTGGTTTCA    3040        CAAG
                                TCCCCG    GATGGTGGTTTCA
                                ||||||    ||||||||||||
                                AGGGGT    TTACCACCAAAGT
                                    _____
GAM133  LOC253955 5'  CCCCCGCAGGGGTGG       3041          A  AT
                                TCCCCGCA GG  GGTGG
                                |||||||| ||  |||||
                                GGGGGCGT CC  CCACC
                                    _ __
GAM134  ADAMTS7   3'  AGTCAGTGTGGTGAGGGGCCAC 2830     C   CCCG  _  C
                                AG CAG    GG GA GGGGCCAC
                                || |||    || || ||||||||
                                TC GTC    CC CT CCCCGGTG
                                 A   ACA_  A  _
GAM134  ADORA1    3'  AGCAGCAGAGATGGGGTCACC  2831      C   CC     C    C
                                AGC AGC  GGGGA GGGG CACC
                                ||| |||  ||||| |||| ||||
                                TCG TCG  TCTCT CCCC GTGG
                                  _  __    A   A
GAM134  ATP8B2    3'  GCCAGCCCTGGGTGCTCTGGTC 2832          _   GACGG_  C
            AC                    GCCAGCCC GGG     GG CAC
                                |||||||| |||     || |||
                                CGGTCGGG CCC     CC GTG
                                    A   ACGAGA  A
GAM134  BLK       3'  GCCAGCACGGGGGGTGCC    2833        C    AC  G
                                GCCAGC CGGGG  GG GCC
                                |||||| |||||  || |||
                                CGGTCG GCCCC  CC CGG
                                   T    __  A
GAM134  CACNA1S   5'  AGCCAGCCAGGGGGCGGGGC   2834          C    A
                                AGCCAGCC GGGG CGGGGC
                                |||||||| |||| ||||||
                                TCGGTCGG CCCC GCCCCG
                                    T   C
GAM134  CAPN10    3'  AGCTGGCACAGGGGGCCAC    2835      CA  C     ACGG
                                AGC  GC CGGGG   GGCCAC
                                |||  || |||||   ||||||
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                                TCG  CG GTCCC   CCGGTG
                                  AC  T   ____
GAM134  CAPN10   3' AGCTGGCACAGGGGGCCAC  2835    CA  C   ACGG
                                AGC  GC CGGGG   GGCCAC
                                |||  || |||||   ||||||
                                TCG  CG GTCCC   CCGGTG
                                  AC  T   ____
GAM134  CAPN10   3' AGCTGGCACAGGGGGCCAC  2835    CA  C   ACGG
                                AGC  GC CGGGG   GGCCAC
                                |||  || |||||   ||||||
                                TCG  CG GTCCC   CCGGTG
                                  AC  T   ____
GAM134  CAPN10   3' AGCTGGCACAGGGGGCCAC  2835    CA  C   ACGG
                                AGC  GC CGGGG   GGCCAC
                                |||  || |||||   ||||||
                                TCG  CG GTCCC   CCGGTG
                                  AC  T   ____
GAM134  CAPN10   3' AGCTGGCACAGGGGGCCAC  2835    CA  C   ACGG
                                AGC  GC CGGGG   GGCCAC
                                |||  || |||||   ||||||
                                TCG  CG GTCCC   CCGGTG
                                  AC  T   ____
GAM134  CAPN10   3' AGCTGGCACAGGGGGCCAC  2835    CA  C   ACGG
                                AGC  GC CGGGG   GGCCAC
                                |||  || |||||   ||||||
                                TCG  CG GTCCC   CCGGTG
                                  AC  T   ____
GAM134  CARPX    5' AGCCGGCCAGGGACAGTCACC 2836     A  C     G_
                                AGCC GCC GGGGACGG  GCC
                                ||||  ||| ||||||||  |||
                                TCGG CGG TCCCTGTC  TGG
                                  C  _      AG
GAM134  CDKN1A   5' GCCGGCCCGGGGTCCCC    2837    A     ACGGGG  A
                                GCC GCCCGGGG    CC CC
                                |||  ||||||||    || ||
                                CGG CGGGCCCC    GG GG
                                  C      A_____  _
GAM134  CLPS     3' GCCAGCCCGGGAGATGCGCTGG 2838      _  __  _____  GCCA
           TGGCCC                GCCCGGG GA  CG    GG   CC
                                |||||||  ||  ||    ||   ||
                                CGGGCCC CT  GC    CC   GG
                                   T  AC  GAIII  ACCG
GAM134  CNTN2    5' GCTCAGCTTGGGGACAGCC   2839    _   CC    GG
                                GC CAGC  GGGGAC  GGCC
                                ||  ||||  ||||||  ||||
                                CG GTCG  CCCCTG  TCGG
                                 A   AA    __
GAM134  COL4A3   5' GCGAGTCCGGGGACCCTCAGGC 2840    C  C     G___
                                GC AG CCGGGGAC   GGGC
                                ||  ||  ||||||||   ||||
```

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                                CG TC GGCCCCTG   TCCG
                                 C  A      GGAG
GAM134  COL4A3   5'  GCGAGTCCGGGGACCCTCAGGC 2840    C  C     G___
                                GC AG CCGGGGAC   GGGC
                                || || ||||||||   ||||
                                CG TC GGCCCCTG   TCCG
                                 C  A      GGAG
GAM134  COL4A3   5'  GCGAGTCCGGGGACCCTCAGGC 2840    C  C     G___
                                GC AG CCGGGGAC   GGGC
                                || || ||||||||   ||||
                                CG TC GGCCCCTG   TCCG
                                 C  A      GGAG
GAM134  CPE      5'  CAGCCCGCGCACTGGGGCCACC 2841       GGG  _
                                CAGCCCG  AC GGGGCCACC
                                |||||||  || |||||||||
                                GTCGGGC  TG CCCCGGTGG
                                    GCG  A
GAM134  FAAH     3'  GCCAGGGACGGGGTGGGGCTGC 2842     CC_   AC   CA
            C                    GCCAG  CGGGG  GGGGC  CC
                                |||||  |||||  |||||  ||
                                CGGTC  GCCCC  CCCCG  GG
                                   CCT   A_   AC
GAM134  FBXW1B   5'  GCCAGCCCGCCCGGGCCGCC  2843       GGGA  G  A
                                GCCAGCCCG   CGGG CC CC
                                |||||||||   |||| || ||
                                CGGTCGGGC   GCCC GG GG
                                     GG__   _  C
GAM134  FBXW1B   5'  GCCAGCCCGCCCGGGCCGCC  2843       GGGA  G  A
                                GCCAGCCCG   CGGG CC CC
                                |||||||||   |||| || ||
                                CGGTCGGGC   GCCC GG GG
                                     GG__   _  C
GAM134  GARP     3'  GCAGCCCGGGAAGGGGGTCACC 2844    C       C   C
                                GC AGCCCGGGGA GGGG CACC
                                || |||||||||| |||| ||||
                                CG TCGGGCCCTT CCCC GTGG
                                 _       C   A
GAM134  GGT2     5'  GCCAGCCTGGGGGCCAC    2845       C   ACGGG
                                GCCAGCC GGGG   GCCAC
                                ||||||| ||||   |||||
                                CGGTCGG CCCC   CGGTG
                                   A  _____
GAM134  GNAS     5'  AGCTGGCCCGGAGGTCCCAGCC 2846     CA     ACGG_
                                AGC  GCCCGGGG   GGCC
                                |||  ||||||||   ||||
                                TCG  CGGGCCTC   TCGG
                                  AC      CAGGG
GAM134  GPRK5    5'  AGCCGGCCGGCGGGGC     2847     A  CGG  A
                                AGCC GCC  GG CGGGGC
                                |||| |||  || ||||||
```

```
                                TCGG CGG   CC GCCCCG
                                  C  ___  _
GAM134  IRF1    3'  AGCCAGCCCTGGGATTGG    2848         G   CG
                                AGCCAGCCC GGGA  GG
                                ||||||||| ||||  ||
                                TCGGTCGGG CCCT  CC
                                    A   AA
GAM134  ITPR3   3'  GCCAGCTGGCTGGGCCAC    2849       CCGG  ACG
                                GCCAGC   GG   GGGCCAC
                                ||||||   ||   |||||||
                                CGGTCG   CC   CCCGGTG
                                   A___  GA_
GAM134  LEF1    5'  GCTGCCCCGGCGGCCAC    2850     CA   GGGGA  _
                                GC  GCCC    CGG GGCCAC
                                ||  ||||    ||| ||||||
                                CG  CGGG    GCC CCGGTG
                                 A_   _____  G
GAM134  LLGL1   3'  AGTGAGCAGAGATGGGGCCAC  2851    CC   CC    C
                                AG  AGC  GGGGA GGGGCCAC
                                ||  |||  ||||| ||||||||
                                TC  TCG  TCTCT CCCCGGTG
                                 AC  __    A
GAM134  LZTS1   3'  GCCGGCCTGGGACAGGGCC   2852     A  CG
                                GCC GCC  GGGACGGGGCC
                                ||| |||  ||||||||||
                                CGG CGG  CCCTGTCCCGG
                                  C  A_
GAM134  MLC1    3'  AGCCCGCCCCGGGTCGTCGGTG 2853    A   G   A _____  GCCA
           GCCC                  CC GCCC GGG CG    GG   CC
                                || |||| ||| ||    ||   ||
                                GG CGGG CCC GC    CC   GG
                                 G   G   A  AGIII  ACCG
GAM134  MLC1    3'  AGCCCGCCCCGGGTCGTCGGTG 2853    A   G   A _____  GCCA
           GCCC                  CC GCCC GGG CG    GG   CC
                                || |||| ||| ||    ||   ||
                                GG CGGG CCC GC    CC   GG
                                 G   G   A  AGIII  ACCG
GAM134  MUC3B   3'  GCTGCCCGCGTCCTGGGGCCAC 2854    CA   GGGAC_
           C                    GC  GCCCG    GGGGCCACC
                                ||  |||||    |||||||||
                                CG  CGGGC    CCCCGGTGG
                                 A_    GCAGGA
GAM134  NCOR2   3'  GCCAGCCCGGGGCGGGA    2855          A
                                GCCAGCCCGGGG CGGGG
                                |||||||||||| |||||
                                CGGTCGGGCCCC GCCCT
                                                _
GAM134  NLGN2   5'  GCCGCCCGGGGCGCCGCC   2856     A      A  GG
                                GCC GCCCGGGG CG  GCC
                                ||| |||||||| ||  |||
```

```
                                CGG CGGGCCCC GC  CGG
                                  _      _ GG
GAM134  NOX4     5'  AGCCAGCCCGGGCGGGG     2857          GA
                                AGCCAGCCCGGG  CGGGG
                                ||||||||||||  |||||
                                TCGGTCGGGCCC  GCCCC
                                      __
GAM134  NRF1     3'  GCCAGCCCGAGGAGCATCGGTG 2858          _ G_____  GCCA
             GC                   CCAGCCCGGGGA C     GG   C
                                ||||||||||||| |     ||   |
                                GGTCGGGCTCCT G     CC   G
                                      C TAGIII  ACCG
GAM134  NTE      3'  AGCTACCCCCACGGGGCCACC  2859     CA   GGGG
                                AGC  GCCC   ACGGGGCCACC
                                |||  ||||   ||||||||||
                                TCG  TGGG   TGCCCCGGTGG
                                  A_   GG__
GAM134  OTOF     3'  GCCGGCCAGGAGGCCAC     2860     A  C  GACG
                                GCC GCC GGG   GGGCCAC
                                ||| ||| |||   |||||||
                                CGG CGG TCC   TCCGGTG
                                  C  _  ____
GAM134  PFKL     5'  CAGCCCAGGGTCACAGCCA   2861          A  G
                                CAGCCCGGGG CG GGCCA
                                |||||||||| || |||||
                                GTCGGGTCCC GT TCGGT
                                      A  G
GAM134  PKNOX1   3'  AGCCAACCCGTGGGGGCTGCC  2862          _  AC  G_
                                AGCCAGCCCG GGG  GG  GCC
                                |||||||||| |||  ||  |||
                                TCGGTTGGGC CCC  CC  CGG
                                      A  __  GA
GAM134  POLR2C   3'  GCCAGCCCTGGGGCAAGAAC  2863        _   AC
                                GCCAGCCC GGGG  GGGGC
                                |||||||| ||||  |||||
                                CGGTCGGG CCCC  TCTTG
                                     A   GT
GAM134  PPP1R8   5'  GCTAGCTCCGGCCGGGCCAC  2864    C  _   GGACG
                                GC AGC CCGG    GGGCCAC
                                || ||| ||||    |||||||
                                CG TCG GGCC    CCCGGTG
                                 A  A   GG___
GAM134  PPP1R8   5'  GCTAGCTCCGGCCGGGCCAC  2864    C  _   GGACG
                                GC AGC CCGG    GGGCCAC
                                || ||| ||||    |||||||
                                CG TCG GGCC    CCCGGTG
                                 A  A   GG___
GAM134  PRV1     3'  CATTCGGGGGGAGCCAC    2865    GCC    AC
                                CA  CGGGG  GGGGCCAC
                                ||  |||||  ||||||||
```

```
                                GT   GCCCC  CCTCGGTG
                                 AA_    __
GAM134  PTGS1    3'  AGCCAGCTGTGGGGATGAG   2866       CC_    C
                                AGCCAGC   GGGGA GGG
                                |||||||   ||||| |||
                                TCGGTCG   CCCCT CTC
                                   ACA    A
GAM134  PTGS1    3'  AGCCAGCTGTGGGGATGAG   2866       CC_    C
                                AGCCAGC   GGGGA GGG
                                |||||||   ||||| |||
                                TCGGTCG   CCCCT CTC
                                   ACA    A
GAM134  PTPN11   5'  GCTGGCCCGAGGGAGGCC   2867    CA      AC
                                GC  GCCCGGGG  GGGGCC
                                ||  ||||||||  ||||||
                                CG  CGGGCTCC  CTCCGG
                                 AC       __
GAM134  PTPN11   5'  GCTGGCCCGAGGGAGGCC   2867    CA      AC
                                GC  GCCCGGGG  GGGGCC
                                ||  ||||||||  ||||||
                                CG  CGGGCTCC  CTCCGG
                                 AC       __
GAM134  RECQL5   3'  GCCGGCTCTGGGACGGGGC   2868     A  CCG
                                GCC GC   GGGACGGGGC
                                |||  ||   ||||||||||
                                CGG CG   CCCTGCCCCG
                                  C  AGA
GAM134  RGS16    3'  GCCACCTGCAGGGGGCCACC   2869     G  __    ACGG
                                GCCA CC  CGGGG   GGCCACC
                                ||||  ||  |||||   |||||||
                                CGGT GG  GTCCC   CCGGTGG
                                  _  AC    _____
GAM134  SIX2     5'  GCCGCCCGGGGCGCCGC    2870     A      A  GG
                                GCC GCCCGGGG CG  GC
                                |||  ||||||| ||  ||
                                CGG CGGGCCCC GC  CG
                                  _       _  GG
GAM134  SOD3     5'  AGCCAGCCCAGGAACGCAGGC  2871              _
                                AGCCAGCCCGGGGACG GGGC
                                ||||||||||||||| ||||
                                TCGGTCGGGTCCTTGC TCCG
                                      G
GAM134  SORCS2   3'  AGCCACCCCGGTGGCTACC   2872      G    _  ACGGG
                                AGCCA CCCGG GG    GCC
                                |||||  |||||  ||    |||
                                TCGGT GGGCC CC    TGG
                                   G    A  GA___
GAM134  STX1A    3'  ACCTAGCCCAAGGGGTTGC   2873     _       AC  G_
                                GCC AGCCCGGGG  GG  GC
                                |||  |||||||||  ||  ||
```

```
                                TGG TCGGGTTCC  CC  CG
                                 A       __ AA
GAM134  TCIRG1   5' GCCAGCCTGGGGAGAGCAC   2874       C    CG   C
                                GCCAGCC GGGGA  GGGC AC
                                ||||||| |||||  |||| ||
                                CGGTCGG CCCCT  CTCG TG
                                   A   __   _
GAM134  TRPC6    5' ACTGGCCCGGGGAAAAGTCACC 2875    CA       CG  GC
                                GC  GCCCGGGGA  GG  CACC
                                ||  |||||||||  ||  ||||
                                TG  CGGGCCCCT  TC  GTGG
                                 AC       TT  A_
GAM134  UPF3B    5' GCTTGGCCGGAACGGGGTTACC 2876    CA_  CG       CC
                                GC   GCC  GGGACGGGG  ACC
                                ||   |||  |||||||||  |||
                                CG   CGG  CCTTGCCCC  TGG
                                 AAC  __       AA
GAM134  UPF3B    5' GCTTGGCCGGAACGGGGTTACC 2876    CA_  CG       CC
                                GC   GCC  GGGACGGGG  ACC
                                ||   |||  |||||||||  |||
                                CG   CGG  CCTTGCCCC  TGG
                                 AAC  __       AA
GAM134  WBSCR1   3' GCTGCCCGGGGACTCACC    2877    CA       GGG
                                GC  GCCCGGGGAC   GCC
                                ||  ||||||||||   |||
                                CG  CGGGCCCCTG   TGG
                                 A_        AG_
GAM134  WBSCR1   3' GCTGCCCGGGGACTCACC    2877    CA       GGG
                                GC  GCCCGGGGAC   GCC
                                ||  ||||||||||   |||
                                CG  CGGGCCCCTG   TGG
                                 A_        AG_
GAM134  WHSC1    3' GCCGGCCTGAGGACGGACAGC  2878     A  C      __
                                GCC GCC GGGGACGG  GGC
                                ||| ||| ||||||||  |||
                                CGG CGG CTCCTGCC  TCG
                                  C  A       TG
GAM134  WHSC1    3' GCCGGCCTGAGGACGGACAGC  2878     A  C      __
                                GCC GCC GGGGACGG  GGC
                                ||| ||| ||||||||  |||
                                CGG CGG CTCCTGCC  TCG
                                  C  A       TG
GAM134  WHSC1    3' GCCGGCCTGAGGACGGACAGC  2878     A  C      __
                                GCC GCC GGGGACGG  GGC
                                ||| ||| ||||||||  |||
                                CGG CGG CTCCTGCC  TCG
                                  C  A       TG
GAM134  ZNF140   5' ACCGCCCGGGGCCATCGGTGGC 2879     A      A G_____  GCCA
                                GCC GCCCGGGG C     GG   C
                                ||| |||||||| |     ||   |
```

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                                TGG CGGGCCCC G     CC    G
                                  _       G TAGIII  ACCG
GAM134  AGS3     5'  GCCAGCCCGGGATGGAAGCAC  2880           AC    C
                                GCCAGCCCGGGG  GGGG CAC
                                ||||||||||||  |||| |||
                                CGGTCGGGCCCT  CCTT GTG
                                      A_    C
GAM134  ARGBP2   5'  AGCCAGCCTAGGGAGCATTGGT 2881        CG   _ G_____  GCCA
           GGC                    CCAGCC  GGGA C     GG    C
                                ||||||  |||| |     ||    |
                                GGTCGG  CCCT G     CC    G
                                   AT    C TAAIII  ACCG
GAM134  C14orf4  5'  GCGGCCCGGGGGAGCGGCC   2882     CA       AC  _
                                GC  GCCCGGGG  GG GGCC
                                ||  ||||||||  || ||||
                                CG  CGGGCCCC  TC CCGG
                                 C_       C_  G
GAM134  C6orf31  3'  CAGAACAAGGCGGGGCCGCC   2883     CC    A      A
                                CAG  CGGGG CGGGGCC CC
                                |||  ||||| ||||||| ||
                                GTC  GTTCC GCCCCGG GG
                                  TT     _      C
GAM134  CENTG1   3'  AGCCAGCCTGGGTATGGGC   2884         C   GACG
                                AGCCAGCC GGG    GGGC
                                ||||||| |||    ||||
                                TCGGTCGG CCC    CCCG
                                     A   ATA_
GAM134  CNK1     3'  CAGCTCGGGGTGAGACC     2885       C    AC
                                CAGC CGGGG  GGGGCC
                                ||||| |||||  ||||||
                                GTCG GCCCC  CTCTGG
                                  A     A_
GAM134  DKFZP434B103 3'  AGCCAGCCTGGGAGCTGCC   2886         CG    CGGG
                                AGCCAGCC  GGGA    GCC
                                ||||||||  ||||    |||
                                TCGGTCGG  CCCT    CGG
                                     A_    CGA_
GAM134  DKFZP434H204 5'  GCCGGCCCAGGGGGTCACAGTG 2887      A       _____    G
           C                     GCC GCCCGGGG    ACGG GC
                                ||| ||||||||    |||| ||
                                CGG CGGGTCCC    TGTC CG
                                  C       CCAG    A
GAM134  DKFZP586J0619 3'  GCCATGCCCGGGGGGGATCCGCC 2888       _      AC  GG  A
                                GCCA GCCCGGGG  GG  CC CC
                                |||| ||||||||  ||  || ||
                                CGGT CGGGCCCC  CC  GG GG
                                  A       __  TA  C
GAM134  FBXO32   5'  GCTCGGGGACGTGCCACC    2889     C       GG
                                GC CGGGGACG  GCCACC
                                || ||||||||  ||||||
```

```
                                CG GCCCCTGC  CGGTGG
                                 A       A_
GAM134  FJX1     3'  GCCACTCGGGGGCCAAACC   2890      G C    ACG
                                GCCA C CGGGG   GGGCC
                                |||| | |||||   |||||
                                CGGT G GCCCC   TTTGG
                                  _ A    CGG
GAM134  FLJ10060  5'  AGCTGGCCCGAGGTGCAGCTGC 2891     CA      A_  G_
          C                      AGC  GCCCGGGG  CGG  GCC
                                |||  ||||||||  |||  |||
                                TCG  CGGGCTCC  GTC  CGG
                                  AC       AC   GA
GAM134  FLJ10852  5'  GCCAGCCCGCCTTGGGTCGCC  2892         GGGAC  __
                                GCCAGCCCG    GGG  GCC
                                |||||||||    |||  |||
                                CGGTCGGGC    CCC  CGG
                                     GGAA_   AG
GAM134  FLJ11457  3'  AGTCCAGGAGGCGGGGCCA   2893    _   CCC   A
                                AG CCAG   GGGG CGGGGCCA
                                || ||||   |||| ||||||||
                                TC GGTC   CTCC GCCCCGGT
                                 A   ___   _
GAM134  FLJ12389  3'  AGCTGGCCCGGAGGCACGCTGG 2894   CA    _ _  _____  GCCA
          TGGC                    GCCCGG GG ACG    GG   C
                                 ||||||| || |||    ||   |
                                 CGGGCC CC TGC    CC   G
                                AC     T  G   GAIII  ACCG
GAM134  FLJ13769  3'  AGCCAGCCTGGAGGTGGCC   2895        C   ACGG
                                AGCCAGCC GGGG   GGCC
                                |||||||| ||||   ||||
                                TCGGTCGG CCTC   CCGG
                                    A   CA__
GAM134  FLJ14129  3'  GCCGGCCCGGGACAGACC   2896     A     G    G
                                GCC GCCCGGG ACGGG CC
                                ||| ||||||| ||||| ||
                                CGG CGGGCCC TGTCT GG
                                  C     _    _
GAM134  FLJ14810  3'  GCCTGGTAGGATGGGGCCACC  2897     C __  C
                                GCC GG  GGA GGGGCCACC
                                ||| ||  ||| |||||||||
                                CGG CC  CCT CCCCGGTGG
                                  A  AT   A
GAM134  FLJ20277  3'  AGCCAGCCTGGGGGTACACAGT 2898        C   ____   GG
          ACC                    AGCCAGCC GGGG   ACGG  CC
                                |||||||| ||||   ||||  ||
                                TCGGTCGG CCCC   TGTC  GG
                                    A   CATG   AT
GAM134  FLJ20306  5'  AGCCAGCTCGGGAGGTGGGGC  2899       C    AC_
                                AGCCAGC CGGGG   GGGGC
                                ||||||| |||||   |||||
```

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                                TCGGTCG GCCCT  CCCCG
                                   A    CCA
GAM134  FLJ20320  5'  ACTCAGCCCGGCGCGGGCCGCC 2900    _      GGA _   A
                                GC CAGCCCGG  CG GGGCC CC
                                || ||||||||  || ||||| ||
                                TG GTCGGGCC  GC CCCGG GG
                                 A      ___ G    C
GAM134  FLJ20366  5'  AGCCAGCCGGGCGGCTGC    2901        CG  A  G_
                                AGCCAGCC  GGG CGG  GC
                                ||||||||  ||| |||  ||
                                TCGGTCGG  CCC GCC  CG
                                    __  _  GA
GAM134  FLJ23233  5'  GCCACCCTGGGCGCCGCC    2902      G  G  A  GG
                                GCCA CCC GGG CG  GCC
                                |||| ||| ||| ||  |||
                                CGGT GGG CCC GC  CGG
                                  _  A  _ GG
GAM134  GMEB2    3'  GCCGGCTCAGGGACAGGCTGCC 2903     A  C       __
                                GCC GC CGGGGACGGG  GCC
                                ||| || ||||||||||  |||
                                CGG CG GTCCCTGTCC  CGG
                                  C  A        GA
GAM134  GSA7     3'  AGTCAGCCCCACAGCGGGGCCA 2904    C    _ G  A
                                AG CAGCCC G GG CGGGGCCA
                                || |||||| | || ||||||||
                                TC GTCGGG T TC GCCCCGGT
                                 A     G G  _
GAM134  H6PD     5'  GCCAGCCCGGCCGCCAC     2905          GGACGGG
                                GCCAGCCCGG      GCCAC
                                ||||||||||      |||||
                                CGGTCGGGCC      CGGTG
                                     GG_____
GAM134  HSSEXGENE 3'  GCTCAGCCCGGGGACCCAGGC  2906    _         G_
                                GC CAGCCCGGGGAC  GGGC
                                || ||||||||||||  ||||
                                CG GTCGGGCCCCTG  TCCG
                                 A          GG
GAM134  KCNB2    5'  GCCAGCCCGGGAGTTGCC    2907          ACGGG
                                GCCAGCCCGGGG    GCC
                                ||||||||||||    |||
                                CGGTCGGGCCCT    CGG
                                      CAA__
GAM134  KIAA0014  3'  GCCGGCAGTGCCGACGGGGCTG 2908    A  CCGGG_      CA
          CC                    GCC GC     GACGGGGC  CC
                                ||| ||     ||||||||  ||
                                CGG CG     CTGCCCCG  GG
                                  C  TCACGG       AC
GAM134  KIAA0082  5'  AGCCAGCCCGGGTCCGCCGG  2909          GA _____
                                AGCCAGCCCGGG  CG    GG
                                ||||||||||||  ||    ||
```

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                                TCGGTCGGGCCC  GC    CC
                                      AG  GGIII
GAM134  KIAA0218 5' GCCAGACCCGGGCGCCGCC   2910      _    GA  GG
                                GCCAG CCCGGG  CG  GCC
                                ||||| ||||||  ||  |||
                                CGGTC GGGCCC  GC  CGG
                                   T     __  GG
GAM134  KIAA0247 3' AGCCACCCGGGGACTTGG    2911      G       GG
                                AGCCA CCCGGGGAC  GG
                                ||||| |||||||||  ||
                                TCGGT GGGCCCCTG  CC
                                   _       AA
GAM134  KIAA0515 3' GCCAACCTGGGAGCCAC     2912       C   GACGG
                                GCCAGCC GGG    GGCCAC
                                ||||||| |||    ||||||
                                CGGTTGG CCC    TCGGTG
                                    A  _____
GAM134  KIAA0537 5' AGCCACCCGGGGCCGGGGCCGC 2913      G     A     A
          C                      AGCCA CCCGGGG CGGGGCC CC
                                ||||| ||||||| ||||||| ||
                                TCGGT GGGCCCC GCCCCGG GG
                                   _     G     C
GAM134  KIAA0544 3' AGACAGCCCGGAGGCC     2915    C      GGACG
                                AG CAGCCCGG    GGGCC
                                || ||||||||    |||||
                                TC GTCGGGCC    TCCGG
                                 T     _____
GAM134  KIAA0544 3' AGCTGGCCTGGGACAGGCC   2914     CA  CG      G
                                AGC  GCC  GGGACGGG CC
                                |||  |||  |||||||| ||
                                TCG  CGG  CCCTGTCC GG
                                  AC  A_     _
GAM134  KIAA0674 5' AGCCAGCCGGTATAGGCCAC  2916        C  GGACG
                                AGCCAGCC GG    GGGCCAC
                                |||||||| ||    |||||||
                                TCGGTCGG CC    TCCGGTG
                                    _ ATA__
GAM134  KIAA1615 5' GCCCGGCAGCGCGGGGCCACC 2917       _ A_
                                GCCCGG GG  CGGGGCCACC
                                |||||| ||  ||||||||||
                                CGGGCC TC  GCCCCGGTGG
                                   G  GC
GAM134  KIAA1887 5' CCAGTCTAAAGCCGGGGCCACC 2918     CCC   A
                                CCAG   GGGG CGGGGCCACC
                                ||||   |||| ||||||||||
                                GGTC   TTTC GCCCCGGTGG
                                  AGA   G
GAM134  KIAA1949 5' AGACAGCCCGGGGGTGAGAC  2919    C       AC
                                AG CAGCCCGGGG  GGGGC
                                || ||||||||||  |||||
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                                TC GTCGGGCCCC  CTCTG
                                 T        CA
GAM134  KIAA1949 5' AGACAGCCCGGGGGTGAGAC  2919    C       AC
                                AG CAGCCCGGGG  GGGGC
                                || ||||||||||  |||||
                                TC GTCGGGCCCC  CTCTG
                                 T        CA
GAM134  KIAA1949 5' AGACAGCCCGGGGGTGAGAC  2919    C       AC
                                AG CAGCCCGGGG  GGGGC
                                || ||||||||||  |||||
                                TC GTCGGGCCCC  CTCTG
                                 T        CA
GAM134  LGI4    3' AGCCAGCCAAGGGGCC     2920        CGGG  C
                                AGCCAGCC   GA GGGGCC
                                ||||||||   || ||||||
                                TCGGTCGG   TT CCCCGG
                                    _____ _
GAM134  LYPLA3  3' AGCCAGTCAGGCTGGCCAC  2921      CC   GACGG
                                AGCCAG  CGGG   GGCCAC
                                ||||||  ||||   ||||||
                                TCGGTC  GTCC   CCGGTG
                                   A_   GA___
GAM134  MARK2   5' GCCAGCCCGGGGATGCGCC  2922          CGGG
                                GCCAGCCCGGGGA   GCC
                                ||||||||||||   |||
                                CGGTCGGGCCCCT   CGG
                                      ACG_
GAM134  MEGF11  5' GCCGGCCCAGGGATCGGCC  2923    A      CGG
                                GCC GCCCGGGGA  GGCC
                                ||| |||||||||  ||||
                                CGG CGGGTCCCT  CCGG
                                  C       AG_
GAM134  MGC11115 3' AGCAGCCTGGGACAAGCCGCC 2924    C   CG      G  A
                                AGC AGCC  GGGACGGG CC CC
                                ||| ||||  |||||||| || ||
                                TCG TCGG  CCCTGTTC GG GG
                                  _   A_      _ C
GAM134  MGC14859 3' GCTCAGGGTATAAACCACC  2925    C    ACG
                                GC CGGGG  GGGCCACC
                                || |||||  ||||||||
                                CG GTCCC  TTTGGTGG
                                 A    ATA
GAM134  MGC4707  3' GCCATTCACCTTCCGGGGCCAC 2926     GC__  GGGGA
                                GCCA   CC    CGGGGCCAC
                                ||||   ||    |||||||||
                                CGGT   GG    GCCCCGGTG
                                  AAGT  AAG__
GAM134  NSE1    3' GCAGCCCGGGCCCGGGCCACC  2927    C      GA   G
                                GC AGCCCGGG  CGGG CCACC
                                || ||||||||  |||| |||||
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                                CG TCGGGCCC  GCCC GGTGG
                                 _      GG   _
GAM134  OCLM     5'  AGCCACACTGAGATGGGGC   2928       G CCG   C
                                AGCCA C   GGGA GGGGC
                                ||||| |   |||| |||||
                                TCGGT G   CTCT CCCCG
                                  _ TGA   A
GAM134  PLCL2    5'  GCTAGCCCGGGCTTCGTCGGTG 2929    C      GA_ _____  GCCA
             GC                   C AGCCCGGG  CG    GG   C
                                | ||||||||  ||    ||   |
                                G TCGGGCCC  GC    CC   G
                                 A      GAA  AGIII  ACCG
GAM134  POLR2J2  3'  GCCACCCTGGGGTGAGCTGCC  2930      G  C   AC  __
                                GCCA CC GGGG  GGG  GCC
                                |||| || ||||  |||  |||
                                CGGT GG CCCC  CTC  CGG
                                  G  A   A_   GA
GAM134  SDC3     3'  AGCCAGGCCTGCCGGGGCCACC 2931       C  GGGGA
                                AGCCAG CC    CGGGGCCACC
                                |||||| ||    ||||||||||
                                TCGGTC GG    GCCCCGGTGG
                                   C  ACG__
GAM134  SLC26A1  3'  GCCAGGCTGGGTAGGGCCAC   2932      CCCG   AC
                                GCCAG   GGG  GGGGCCAC
                                |||||   |||  ||||||||
                                CGGTC   CCC  TCCCGGTG
                                  CGA_   A_
GAM134  SSTK     3'  ACTAGTCCGCAAATGGGGGCCA 2933    C  C   G   C_
             CC                   GC AG CCG GGA  GGGGCCACC
                                || || ||| |||  |||||||||
                                TG TC GGC TTT  CCCCGGTGG
                                 A  A   G   AC
GAM134  SYT12    3'  AGCCAGCCTGAGGGTCCATGC  2934        C__   GA  GG
                                AGCCAGCC   GGG  CG  GC
                                ||||||||   |||  ||  ||
                                TCGGTCGG   CCC  GT  CG
                                     ACT   AG  A_
GAM134  TCL6     5'  AGCCAGCCTGGGGACAGAG   2935        C
                                AGCCAGCC GGGGACGGGG
                                |||||||| ||||||||||
                                TCGGTCGG CCCCTGTCTC
                                     A
GAM134  TCL6     5'  AGCCAGCCTGGGGACAGAG   2935        C
                                AGCCAGCC GGGGACGGGG
                                |||||||| ||||||||||
                                TCGGTCGG CCCCTGTCTC
                                     A
GAM134  TCL6     5'  AGCCAGCCTGGGGACAGAG   2935        C
                                AGCCAGCC GGGGACGGGG
                                |||||||| ||||||||||
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                                TCGGTCGG CCCCTGTCTC
                                    A
GAM134  TCL6     5'  AGCCAGCCTGGGGACAGAG   2935        C
                                AGCCAGCC GGGGACGGGG
                                |||||||| ||||||||||
                                TCGGTCGG CCCCTGTCTC
                                    A
GAM134  TOR2A    3'  AGCCGCCCGGGAGGGGGC    2936      A      AC
                                AGCC GCCCGGGG  GGGGC
                                |||| ||||||||  |||||
                                TCGG CGGGCCCT  CCCCG
                                  _      C_
GAM134  TRIM28   3'  AACTGGGGGATGGGGCCAC   2937     CC    C
                                AGC  GGGGA GGGGCCAC
                                |||  ||||| ||||||||
                                TTG  CCCCT CCCCGGTG
                                  AC    A
GAM134  UBXD1    5'  CCAGTCGGGGACGGGGCCGCC  2938      CC          A
                                CCAG  CGGGGACGGGGCC CC
                                ||||  |||||||||||||| ||
                                GGTC  GCCCCTGCCCCGG GG
                                  A_          C
GAM134  UXS1     5'  GCCAGTTTGGGAACAGGGC   2939       CCC
                                GCCAG   GGGGACGGGGC
                                |||||   ||||||||||
                                CGGTC   CCCTTGTCCCG
                                   AAA
GAM134  WBSCR16  3'  CCCGGGACGGGGCCGCC    2940       G      A
                                CCCGGG ACGGGGCC CC
                                |||||| |||||||| ||
                                GGGCCC TGCCCCGG GG
                                   _      C
GAM134  LOC127281 3' AGCTGCCCGGGGGTGGGA   2941      CA      AC
                                AGC  GCCCGGGG  GGGG
                                |||  ||||||||  ||||
                                TCG  CGGGCCCC  CCCT
                                  A_       CA
GAM134  LOC143153 3' AGCCAGCCTGGTGGCCAGGCTG 2942         C  _  A   __
          CC                      AGCCAGCC GG GG CGGG  GCC
                                |||||||| || || ||||  |||
                                TCGGTCGG CC CC GTCC  CGG
                                    A  A  G    GA
GAM134  LOC145717 5' AGCCGCCCGGGGGTGGCC    2943      A      ACGG
                                AGCC GCCCGGGG    GGCC
                                |||| ||||||||    ||||
                                TCGG CGGGCCCC    CCGG
                                  _      CA__
GAM134  LOC145748 5' CAGCCCGGGGACGGGGCCAGCC 2944                  _
                                CAGCCCGGGGACGGGGCCA CC
                                ||||||||||||||||||| ||
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                                GTCGGGCCCCTGCCCCGGT GG
                                      C
GAM134  LOC146488 5'  CAGCCCAGAGTGGGGCCAC   2945          AC
                                CAGCCCGGGG  GGGGCCAC
                                ||||||||||  ||||||||
                                GTCGGGTCTC  CCCCGGTG
                                     A_
GAM134  LOC147165 3'  GCCAGTCCGGGGGAGCGGACC  2946       _  C     CG
                                GCCAG CC GGGGA  GGGCC
                                ||||| || |||||  |||||
                                CGGTC GG CCCCT  CCTGG
                                   A  C     CG
GAM134  LOC148181 3'  AGCTGAGCCTGGAGAGGCCACC 2947      C_   C     CGG
                                AGC  AGCC GGGGA   GGCCACC
                                |||  |||| |||||   |||||||
                                TCG  TCGG CCTCT   CCGGTGG
                                  AC    A    ___
GAM134  LOC148189 5'  AGCCAGCCCGGGGGTCCAATGG 2948            ACG____
              G                  AGCCAGCCCGGGG      GGG
                                 ||||||||||||       |||
                                 TCGGTCGGGCCCC      CCC
                                       CAGGTTA
GAM134  LOC148534 5'  GCCGGCCCGAGGGCTGGCGC   2949      A    _   AC  G
                                GCC GCCCG GGG  GG GC
                                ||| ||||| |||  || ||
                                CGG CGGGC CCC  CC CG
                                  C    T   GA  G
GAM134  LOC148887 3'  CAGAAACAAGGGACGGGGCCAC 2950      CCC__           III
              CG                  CAG    GGGGACGGGGCCACC   G
                                  |||    ||||||||||||||   |
                                  GTC    TCCCTGCCCCGGTGG   C
                                    TTTGT            III
GAM134  LOC150519 5'  GCCTGGGGCCGAGGCCACC   2951      C    A
                                GCC GGGG CGGGGCCACC
                                ||| |||| ||||||||||
                                CGG CCCC GCTCCGGTGG
                                  A    G
GAM134  LOC150819 3'  AGCCAGCCTGGAGGCCC     2952         C  GGACG    A
                                AGCCAGCC GG     GGGCC C
                                |||||||| ||     ||||| |
                                TCGGTCGG CC     TCCGG G
                                     A _____     C
GAM134  LOC152860 3'  AGCCAGCCCGAGGGTGGAA   2953           AC
                                AGCCAGCCCGGGG  GGGG
                                ||||||||||||  ||||
                                TCGGTCGGGCTCC  CCTT
                                       CA
GAM134  LOC153232 5'  AGCTGGGCCCGGGGGACCAC  2954      CA_      ACGG
                                AGC   GCCCGGGG    GGCCAC
                                |||   ||||||||    ||||||
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                                TCG  CGGGCCCC  CTGGTG
                                  ACC     ____
GAM134  LOC154790 5' GCCTAGGGGCGGGGCCACC  2955    CG  A
                                GCC  GGG CGGGGCCACC
                                |||  ||| ||||||||||
                                CGG  CCC GCCCCGGTGG
                                  AT  C
GAM134  LOC196955 5' AGCCAGCCTGAGCCAGCTGCC 2956       C  GA  G_
                                AGCCAGCC GGG  CGG  GCC
                                |||||||| |||  |||  |||
                                TCGGTCGG CTC  GTC  CGG
                                     A  G_  GA
GAM134  LOC196985 5' AGACAGCCTGGGGGGCTGCC  2957    C   C   AC  G_
                                AG CAGCC GGGG  GG  GCC
                                || ||||| ||||  ||  |||
                                TC GTCGG CCCC  CC  CGG
                                 T    A   __ GA
GAM134  LOC199786 3' AGCCAGACATTCGGGGCCAC  2958      CC  GGGA
                                AGCCAG  CG   CGGGGCCAC
                                ||||||  ||   |||||||||
                                TCGGTC  GT   GCCCCGGTG
                                   T_  AA__
GAM134  LOC200213 5' GCCGGCCCGGGGCCGCGGCC  2959    A      A  G
                                GCC GCCCGGGG CG GGCC
                                ||| |||||||| || ||||
                                CGG CGGGCCCC GC CCGG
                                  C       G  G
GAM134  LOC203248 3' AGCGGCCCGGGGTGGCTGCC  2960    CA      AC  G_
                                AGC  GCCCGGGG  GG  GCC
                                |||  ||||||||  ||  |||
                                TCG  CGGGCCCC  CC  CGG
                                  C_       A_  GA
GAM134  LOC204970 3' CAGTTTGGGGAGGAGCCAC   2961    CCC    C
                                CAG   GGGGA GGGGCCAC
                                |||   ||||| ||||||||
                                GTC   CCCCT CCTCGGTG
                                  AAA    _
GAM134  LOC219942 3' GCCAGCCCAACGTCGGGGTCAC 2962         GGA   C
                                GCCAGCCCGG   CGGGG CAC
                                ||||||||||   ||||| |||
                                CGGTCGGGTT   GCCCC GTG
                                     GCA    A
GAM134  LOC221975 5' GCCACCCGGGGACGCTGG    2963      G       _____
                                GCCA CCCGGGGACG    GG
                                |||| ||||||||||    ||
                                CGGT GGGCCCCTGC    CC
                                  _        GAIII
GAM134  LOC222031 3' AGCCAGCCTGGGGTGGAG    2964        C   AC
                                AGCCAGCC GGGG  GGGG
                                |||||||| ||||  ||||
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                                TCGGTCGG CCCC  CCTC
                                    A   A_
GAM134  LOC223009 5'  AGCTGGGCCTGGAGAGGCCACC 2965     CA_  C    CGG
                                AGC   GCC GGGGA  GGCCACC
                                |||   ||| |||||  |||||||
                                TCG   CGG CCTCT  CCGGTGG
                                  ACC   A   ___
GAM134  LOC245727 5'  AGCCGCCCGGGGGTGGCC    2943      A      ACGG
                                AGCC GCCCGGGG   GGCC
                                |||| ||||||||   ||||
                                TCGG CGGGCCCC   CCGG
                                  _      CA__
GAM134  LOC253216 5'  GCCGGCCCAGGGGGTCACAGTG 2887     A      ____   G
          C                      GCC GCCCGGGG   ACGG GC
                                |||| ||||||||   |||| ||
                                CGG CGGGTCCC   TGTC CG
                                  C      CCAG   A
GAM134  LOC254263 5'  GCGGCCCGGGGGGCGCC    2966    CA      AC  G
                                GC  GCCCGGGG  GG GCC
                                ||  ||||||||  || |||
                                CG  CGGGCCCC  CC CGG
                                 C_      __ G
GAM134  LOC255056 5'  AGCTGCCCGAGGGGCCC    2967    CA    GGAC    A
                                AGC  GCCCGG   GGGGCC C
                                |||  ||||||   |||||| |
                                TCG  CGGGCT   CCCCGG G
                                  A_    ____     C
GAM134  LOC255682 5'  AGCCCGCCCCCTCCGGGGCCAC 2968      A   GGGGA
          C                      AGCC GCCC    CGGGGCCACC
                                |||| ||||    ||||||||||
                                TCGG CGGG    GCCCCGGTGG
                                  G   GGAG_
GAM134  LOC255975 5'  AGCTGTGCCTGGAGAGGTCACC 2970     CA_  C    C  G_
                                AGC   GCC GGGGA GG  GCC
                                |||   ||| ||||| ||  |||
                                TCG   CGG CCTCT CC  TGG
                                  ACA   A    _ AG
GAM134  LOC255975 5'  GCTGGGCCTGGAGGGGCCACC  2969    CA_  CGG   C
                                GC   GCC   GGA GGGGCCACC
                                ||   |||   ||| |||||||||
                                CG   CGG   CCT CCCCGGTGG
                                  ACC   A__   _
GAM134  LOC255987 5'  GCTGGGCCTGGAGGGGCCACC  2969    CA_  CGG   C
                                GC   GCC   GGA GGGGCCACC
                                ||   |||   ||| |||||||||
                                CG   CGG   CCT CCCCGGTGG
                                  ACC   A__   _
GAM134  LOC51619  5'  GCGGCCCGGCCGGGGCTGCC   2971    CA    GGA    CA
                                GC  GCCCGG   CGGGGC  CC
                                ||  ||||||   ||||||  ||
```

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                                CG  CGGGCC   GCCCCG  GG
                                 C_     G__      AC
GAM134   LOC90249  3' AGCCAGCCCTGGGGACGGGCAC 2972          _       ___
             GCC                   AGCCAGCCC GGGGACGGG   GCC
                                |||||||| |||||||||   |||
                                TCGGTCGGG CCCCTGCCC   CGG
                                    A        GTG
GAM134   LOC90379  3' AGCCGGCCAGGAAGAGGCCACC 2973       A  C    C
                                AGCC GCC GGGGA GGGGCCACC
                                |||| ||| ||||| |||||||||
                                TCGG CGG TCCTT CTCCGGTGG
                                  C  _    _
GAM134   LOC90525  3' CAGCCCGGGGACGGCGCC    2974             G
                                CAGCCCGGGGACGG GCC
                                |||||||||||||| |||
                                GTCGGGCCCCTGCC CGG
                                        G
GAM134   LOC90906  5' AGCCACCTAAGGGGCTGCC    2975       G  CG   AC  G_
                                AGCCA CC  GGG  GG  GCC
                                ||||| ||  |||  ||  |||
                                TCGGT GG  TCC  CC  CGG
                                   _ AT   __  GA
GAM134   LOC91040  3' AGCCACCTCGGGGACAGGGCC  2976       G  _
                                AGCCA CC CGGGGACGGGGCC
                                ||||| || ||||||||||||
                                TCGGT GG GCCCCTGTCCCGG
                                   _ A
GAM134   LOC92080  5' GCCCAGTGGGGACGGGGCTGCC 2977       ___         CA
                                GCCC   GGGGACGGGGC  CC
                                ||||   ||||||||||  ||
                                CGGG   CCCCTGCCCCG  GG
                                  TCA          AC
GAM134   LOC93512  3' GCCAGTCCGGGGGAGCGGACC  2946       _ C    CG
                                GCCAG CC GGGGA  GGGCC
                                ||||| || |||||  |||||
                                CGGTC GG CCCCT  CCTGG
                                   A  C    CG
GAM135   DDX9      3' TCAACAGATGTAGCTGGCA   3045         C   A__
                                TCAACGGA GTA   GGCA
                                |||||||| |||   ||||
                                AGTTGTCT CAT   CCGT
                                    A   CGA
GAM135   PCLO      3' GGCTGGTGGAGGCAGATTAT   3046     AC_  A_
                                GG   GT  AGGCAGATTAT
                                ||   ||  ||||||||||
                                CC   CA  TCCGTCTAATA
                                 GAC  CC
GAM135   PRO1575   5' TCCACTTTTTTAAGGCAGATT  3047     A  GGACG
                                TC AC    TAAGGCAGATT
                                || ||    ||||||||||
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                                AG TG    ATTCCGTCTAA
                                 G  AAAAA
GAM135  TOLLIP   3'  TCAATGGCATGCAGATTA    3048      C  A   AAG
                                TCAA GG CGT   GCAGATTA
                                |||| || |||   ||||||||
                                AGTT CC GTA   CGTCTAAT
                                  A  _  ___
GAM135  LOC151009 5'  TCGACGAATGCACGCAGATTAT 3049     A    C   AG
                                TC ACGGA GTA  GCAGATTAT
                                || ||||| |||  |||||||||
                                AG TGCTT CGT  CGTCTAATA
                                 C    A  G_
GAM135  LOC253664 5'  GGTTGCCAGGCAGATTAT    3050     AC  A
                                GG  GT AGGCAGATTAT
                                ||  || ||||||||||
                                CC  CG TCCGTCTAATA
                                 AA  G
GAM136  ZNF200    5'  TCGTTTCGCGGGGCCTCCGGGA 3053     G        C_______   GGT
            CC                    CG TTCGCGGGGC      GGG   C
                                || ||||||||||      |||  |
                                GC AAGCGCCCCG      CCC   G
                                 A         GAGGIII   TGG
GAM136  C14orf4   5'  CGGTTCAGCTCTGGGGGTCCC  3054       _  GGGGCC
                                CGGTTC GC     GGGGGTCCC
                                |||||| ||     |||||||||
                                GCCAAG CG     CCCCCAGGG
                                   T  AGA___
GAM136  DOC-1R    5'  CCGGTTCGCGCCGAGGGGTC   3055         GGG   _
                                TCGGTTCGC   GCCG GGGGTC
                                |||||||||   |||| ||||||
                                GGCCAAGCG   CGGC CCCCAG
                                      ___    T
GAM136  FLJ21135  5'  GGGCGGGTTGGGGGTCC     3056     TTC    GCC
                                GG   GCGGG   GGGGGTCC
                                ||   |||||   ||||||||
                                CC   CGCCC   CCCCCAGG
                                 ___     AA_
GAM136  LOC147160 5'  GCGGCAGGGCTGGGGGTCCC   3057     TC      C
                                GT  GCGGGGC GGGGGTCCC
                                ||  ||||||| |||||||||
                                CG  CGTCCCG CCCCCAGGG
                                 C_      A
GAM136  LOC163033 5'  GGTGGGGGTCGGGGGTCCC    3058     TCGC    C
                                GGT    GGGG CGGGGGTCCC
                                |||    |||| ||||||||||
                                CCA    CCCC GCCCCCAGGG
                                  C___    A
GAM136  LOC200138 5'  GGTTGCGGGGGGAGTCCC     3059      C     CCG
                                GGTT GCGGGG   GGGGTCCC
                                |||| ||||||   ||||||||
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                                CCAA CGCCCC  CCTCAGGG
                                  _    ____
GAM136  LOC51195  3'  CGGGAGGGGGCTGGGGGTCCC  3060     TTCGC    C
                                CGG    GGGGC GGGGGTCCC
                                |||    ||||| |||||||||
                                GCC    CCCCG CCCCCAGGG
                                  CTC__    A
GAM136  LOC56906  5'  TCGGTGCGCGGGAGCCGGGTTC 3061      T    _    GG
          C                      TCGGT CGCGGG GCCGGG  TCC
                                |||||| |||||| ||||||  |||
                                AGCCA GCGCCC CGGCCC  AGG
                                  C    T    A_
GAM137  EBAG9    3'  GGATGGCCTGATCAATGTAT  3064    CC   GT_
                                GG  GGTC   TCAATGTAT
                                ||  ||||   |||||||||
                                CC  CCGG   AGTTACATA
                                 TA   ACT
GAM137  FLJ21032  5'  GCGGCCGGCGTCTGT     3065        T   CAA
                                GCGGCCGG CGTT   TGT
                                |||||||| ||||   |||
                                CGCCGGCC GCAG   ACA
                                  _   ____
GAM137  KIAA0258  3'  TAGCAGCTGCCAATGTAT   3066       CG  CGTT
                                TAGCGGC  GT   CAATGTAT
                                |||||||  ||   ||||||||
                                ATCGTCG  CG   GTTACATA
                                   A_  _____
GAM138  AXIN1    5'  TCCGGCCGGCTCTGGCGGCG  3069        A  CC_
                                TCCGGCCG GC   GGCGGCG
                                |||||||| ||   |||||||
                                AGGCCGGC CG   CCGCCGC
                                   _  AGA
GAM138  CAPZA1   5'  GGCCCAGCCCGGCTACGGGC  3070      G      _____
                                GGCC AGCCCGGC    GGC
                                |||| ||||||||    |||
                                CCGG TCGGGCCG    CCG
                                  G       ATGC
GAM138  CDA      5'  TCCGGCCAGCCTGGCTGGGGC  3071       G   C   _  C
                                TCCGGCC AGCC GGC GG GC
                                ||||||| |||| ||| || ||
                                AGGCCGG TCGG CCG CC CG
                                   _   A   A  C
GAM138  FHL2     5'  CCGGCCGAGTGGAGCGCTGC  3072        CCC  C    C
                                CCGGCCGAG   GG GGCGC GC
                                |||||||||   || ||||| ||
                                GGCCGGCTC   CC TCGCG CG
                                   A__  _    A
GAM138  FZD1     5'  GGCTCCCGGCTGGCGGCGCCGC 3074     ___  A  CC
                                GGC   CG GC  GGCGGCGCCGC
                                |||   || ||  ||||||||||
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                                CCG  GC CG  CCGCCGCGGCG
                                  AGG  _  A_
GAM138  FZD1    5'  TCCGTCGAGCCCAAGCCG   3073      GC       CGGC
                                TCCG  CGAGCCCGG   GCCG
                                ||||  |||||||||   ||||
                                AGGC  GCTCGGGTT   CGGC
                                  A_      _____
GAM138  GSPT1   5'  TCCGTGGTTATTGGCGGCGCCG 3075      GCCGAGCCC
            C                    TCCG       GGCGGCGCCGC
                                ||||       ||||||||||
                                AGGC       CCGCCGCGGCG
                                  ACCAATAA_
GAM138  HD      5'  TCGGGCCGACTCGCGGCGCCGC 3076    C     G C  G
                                TC GGCCGA C CG CGGCGCCGC
                                || |||||| | || |||||||||
                                AG CCGGCT G GC GCCGCGGCG
                                 C    _ A  _
GAM138  KIAA0857 5'  GGCCGAGCCGGTGCGCGGCGCC 3077          _________   GGC
            GCC                   GCCGAGCC       CGGC   GCC
                                ||||||||       ||||  |||
                                CGGCTCGG       GCCG   CGG
                                    CCACGIIIC   CGG
GAM138  NAGA    5'  TCCAGCCGGGTCCGGGTTCCCG 3078        AGC   CGGCG
            C                    TCCGGCCG   CCGG    CCGC
                                ||||||||   ||||    ||||
                                AGGTCGGC   GGCC    GGCG
                                    CCA   CAAG_
GAM138  RANBP2L1 5'  CGGCCGGGCTCGTGGCGCCGC  3079       A  C  GC
                                CGGCCG GC CG  GGCGCCGC
                                |||||| || ||  ||||||||
                                GCCGGC CG GC  CCGCGGCG
                                   C  A  A_
GAM138  RDBP    5'  TCCGGCCGCGCCCGCGCTGGCC 3080         A    _  GGC
            GC                    TCCGGCCG GCCCG GC   GCCGC
                                ||||||||  |||||  ||   |||||
                                AGGCCGGC CGGGC CG   CGGCG
                                    G    G  AC_
GAM138  SIM2    3'  GCCGGGCTCGGTGGCGCCGC   3081      A  C   C
                                GCCG GC CGG GGCGCCGC
                                |||| || ||| ||||||||
                                CGGC CG GCC CCGCGGCG
                                  C  A   A
GAM138  SOLH    5'  CCTCCACAGCCCGGCGGCGCCG 3082     GG  _
            C                    CC  CCG AGCCCGGCGGCGCCGC
                                ||  ||| ||||||||||||||||
                                GG  GGT TCGGGCCGCCGCGGCG
                                 A_  G
GAM138  TACC1   5'  TCCCGCCGGCAGCCGGCGCCGC 3083     G   A  CC  _
                                TCC GCCG GC  GGC GGCGCCGC
                                ||| |||| ||  ||| ||||||||
```

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                                AGG CGGC CG  TCG CCGCGGCG
                                  G   _ __   G
GAM138  TEAD3    5'  TCCGGCCGGGCCGCTCCG    3084        AGCCC  G  G
                                TCCGGCCG    GGC GC CCG
                                ||||||||    ||| || |||
                                AGGCCGGC    CCG CG GGC
                                     _____  G  A
GAM138  TLL2     5'  TCCGGCCGGGACTCGGTGG   3085        A_  C  C
                                TCCGGCCG  GC CGG GG
                                ||||||||  || ||| ||
                                AGGCCGGC  TG GCC CC
                                    CC  A   A
GAM138  TSG      5'  CGGCCGAGCCCGGGGCGC    3086           C
                                CGGCCGAGCCCGG GGCGC
                                |||||||||||| |||||
                                GCCGGCTCGGGCC CCGCG

                                          _
GAM138  ABIN-2   5'  TCTGGGCCTCGGCGGCGCCGC  3087    C  CCGA  _
                                TC GG   GCC CGGCGGCGCCGC
                                || ||   ||| ||||||||||||
                                AG CC   CGG GCCGCCGCGGCG
                                 A  ____  A
GAM138  BM039    5'  TCCCGCCGAGCCCCTTCCTGCC 3088     G       GGCGGC
          GC                      TCC GCCGAGCCC     GCCGC
                                ||| |||||||||     |||||
                                AGG CGGCTCGGG     CGGCG
                                  G       GAAGGA
GAM138  BPES     3'  TCAGGCTGGCGGCGGCGTCG  3089    C  CGAGCC      C
                                TC GGC     CGGCGGCG CG
                                || |||     |||||||| ||
                                AG CCG     GCCGCCGC GC
                                 T  ACC___      A
GAM138  BRI3     5'  TCCGGCCCGGCTCGGCTCG   3090       GA  C   GG
                                TCCGGCC  GC CGGC  CG
                                |||||||  || ||||  ||
                                AGGCCGG  CG GCCG  GC
                                    GC  A   A_
GAM138  C20orf102 5'  TCGGGCCGGGGGCGCC     3091    C    AGCCC  C
                                TC GGCCG    GG GGCGCC
                                || |||||    || ||||||
                                AG CCGGC    CC CCGCGG
                                 C   _____  _
GAM138  CIDEB    5'  TCCTGCTGCTGGCGGCGCTGC  3093    G  CGA  CC      C
                                TCC GC   GC  GGCGGCGC GC
                                ||| ||   ||  |||||||| ||
                                AGG CG   CG  CCGCCGCG CG
                                  A  A__  A_      A
GAM138  CIDEB    5'  GGCCGACGGCGCGGTGCTGC  3092       __  CCG   C  C
                                GGCCGA  GC   GCGG GC GC
                                ||||||  ||   |||| || ||
```

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                                CCGGCT  CG   CGCC CG CG
                                   GC  ___    A  A
GAM138  DKFZP434H0820 5'  TCCGGCCGACGCCGCCGC    3094         AGCCCG   G
                                TCCGGCCG     GCG CGCCGC
                                ||||||||     ||| |||||||
                                AGGCCGGC     TGC GCGGCG
                                   _______  G
GAM138  DKFZP564D172 3'  CCGGCCGAGCCAGGCAGGGCGC 3095           C  __
                                CCGGCCGAGCC GGC  GGCGC
                                |||||||||||| |||  |||||
                                GGCCGGCTCGG CCG  CCGCG
                                      T  TC
GAM138  DKFZP566M1046 5'  CCTGGCCGGGCCCGGTTGC   3096    _    A     CG
                                CC GGCCG GCCCGG  GC
                                || ||||| ||||||  ||
                                GG CCGGC CGGGCC  CG
                                 A    C     AA
GAM138  DKFZP586J0619 3'  CGGCCGAGCTCATCAGCCGC   3097         C  GCGGC
                                CGGCCGAGC CG    GCCGC
                                ||||||||| ||    |||||
                                GCCGGCTCG GT    CGGCG
                                     A  AGT__
GAM138  FLJ10342  5'  TCCGCTCGAGCTTTGCGCCGC  3098      GC    CCGGCG
                                TCCG  CGAGC     GCGCCGC
                                ||||  |||||     |||||||
                                AGGC  GCTCG     CGCGGCG
                                  GA    AAA___
GAM138  FLJ10432  3'  TCCGGCCGACTCGGTGG     3099         G C   C
                                TCCGGCCGA C CGG GG
                                ||||||||| | ||| ||
                                AGGCCGGCT G GCC CC
                                     _ A   A
GAM138  GOLPH2    5'  TCCGGCCGGCTCCGCGCCG   3100         A  _  GGCG
                                TCCGGCCG GC CC    GCGCCG
                                |||||||| || ||    ||||||
                                AGGCCGGC CG GG    CGCGGC
                                     _  A  _____
GAM138  HIC       5'  TCCGCCGAGCCCGCGCCG    3102       G      GGCG
                                TCCG CCGAGCCC    GCGCCG
                                |||| ||||||||    ||||||
                                AGGC GGCTCGGG    CGCGGC
                                   _       _____
GAM138  HIC       5'  TCCGGCTCAGCCCAGACGCCGC 3101        CG      CG
                                TCCGGC  AGCCCGG  GCGCCGC
                                ||||||  |||||||  |||||||
                                AGGCCG  TCGGGTC  TGCGGCG
                                   AG      __
GAM138  KIAA0410  5'  GGCCAGGGCTCGACGCCG    3103       A_  CCGG
                                GGCCG  GC    CGGCGCCG
                                |||||  ||    ||||||||
```

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                                CCGGT CG   GCTGCGGC
                                  CC A___
GAM138  KIAA0888 5' TCCGGCCGGTCCCAGGCCG   3104        AG    CGGC
                                TCCGGCCG CCCGG   GCCG
                                |||||||| |||||   ||||
                                AGGCCGGC GGGTC   CGGC
                                    CA   ____
GAM138  KIAA0963 5' TCCGGCCGGGCGCGGAGCCCGC 3105        A C   C   G
                                TCCGGCCG GC CGG GGC CCGC
                                |||||||| || ||| ||| ||||
                                AGGCCGGC CG GCC TCG GGCG
                                    C C  _  _
GAM138  KIAA1089 5' TCCGGCCGTAGCCGCAGCCGCC 3106        _   CG    _
          GC                  TCCGGCCG AGCC  GCGGC GCCGC
                                |||||||| ||||  ||||| |||||
                                AGGCCGGC TCGG  CGTCG CGGCG
                                    A   __    G
GAM138  KIAA1198 3' TCCAGCCGGGCCTGGTGGC   3107        A   C  C
                                TCCGGCCG GCC GG GGC
                                |||||||| ||| || |||
                                AGGTCGGC CGG CC CCG
                                    C   A  A
GAM138  KIAA1202 5' CGGCTGGGCTCAGGCGCCGC   3108      CGA  C  GC
                                CGGC   GC CG  GGCGCCGC
                                ||||   || ||  ||||||||
                                GCCG   CG GT  CCGCGGCG
                                  ACC  A  __
GAM138  KIAA1893 5' TCCGGCCGGGCTGGCGG    3109        A  CC
                                TCCGGCCG GC  GGCGG
                                |||||||| ||  |||||
                                AGGCCGGC CG  CCGCC
                                    C  A_
GAM138  MAN1C1   5' TCCGGCCGAGCCCTCCCCGCCG 3110           GGCGG
          C                   TCCGGCCGAGCCC    CGCCGC
                                ||||||||||||    ||||||
                                AGGCCGGCTCGGG    GCGGCG
                                      AGGG_
GAM138  MGC12679 3' CCCGGCCGGGTCAACGTCG   3111        AGCCC  _    C
                                TCCGGCCG    GG CGGCG CG
                                ||||||||    || ||||| ||
                                GGGCCGGC    CC GTTGC GC
                                    _____ A    A
GAM138  MGC13272 5' TCCGGCCGGGGCCGGCCTGAGG 3112        AGC    _____
          GC                   TCCGGCCG   CCGGC    GGC
                                ||||||||  |||||    |||
                                AGGCCGGC   GGCCG    CCG
                                    CCC    GACTC
GAM138  MGC4170  3' TCCGGCCAGGGCTCAGAAACCG 3113        A_  C   CGGC
          C                   TCCGGCCG  GC CGG   GCCGC
                                ||||||||  || |||   |||||
```

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                                AGGCCGGT  CG GTC    TGGCG
                                    CC  A   TT__
GAM138  MGC4415  3'  GGGCGGCGGCGGCGCTGC    3114     C  A  CC       C
                                GG CG GC  GGCGGCGC GC
                                || || ||  |||||||| ||
                                CC GC CG  CCGCCGCG CG
                                 C  _ __       A
GAM138  MOT8     5'  TCCGCGCCGATGGGGCGGCGCT 3115      _    GCCC       C
           GC                     TCCG GCCGA    GGCGGCGC GC
                                |||| |||||    |||||||| ||
                                AGGC CGGCT    CCGCCGCG CG
                                  G    ACC_       A
GAM138  OSBPL2   5'  CCGGCCGAGCTCACTGCCGC   3116          C  G GGC
                                CCGGCCGAGC CG C   GCCGC
                                |||||||||| || |   |||||
                                GGCCGGCTCG GT G   CGGCG
                                      A  _ A__
GAM138  OSBPL2   5'  CCGGCCGAGCTCACTGCCGC   3116          C  G GGC
                                CCGGCCGAGC CG C   GCCGC
                                |||||||||| || |   |||||
                                GGCCGGCTCG GT G   CGGCG
                                      A  _ A__
GAM138  QKI      5'  GGTCGAGCCCGCTCAGCGCCGC 3117     C       G_
                                GG CGAGCCCG  CGGCGCCGC
                                || ||||||||  |||||||||
                                CC GCTCGGGC  GTCGCGGCG
                                 A       GA
GAM138  SEMA6A   5'  CGGCCGGCAGCGCGGTGCCGC  3118        A  CCG    C
                                CGGCCG GC   GCGG GCCGC
                                |||||| ||   |||| |||||
                                GCCGGC CG   CGCC CGGCG
                                   _  TCG    A
GAM138  SHANK3   5'  GGCCGGGCCCGGGCCG      3119        A     CGGC
                                GGCCG GCCCGG    GCCG
                                ||||| ||||||    ||||
                                CCGGC CGGGCC    CGGC
                                   C     _____
GAM138  SLC26A8  5'  GCCTGGCTGGCGGCGCTGC    3120      GA  CC       C
                                GCC  GC  GGCGGCGC GC
                                |||  ||  |||||||| ||
                                CGG  CG  CCGCCGCG CG
                                  AC  A_       A
GAM138  SLK      5'  TCCGCCGAGCCCGGCCCG    3121       G         GGCG
                                TCCG CCGAGCCCGGC    CCG
                                |||| ||||||||||    |||
                                AGGC GGCTCGGGCCG    GGC
                                   _        _____
GAM138  SRp25    5'  CCGGCTGGGAAGCGCGGCGCCG 3122       C___    CCG
           C                     CCGGC    GAGC   GCGGCGCCGC
                                |||||    ||||   ||||||||||
```

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                                GGCCG   TTCG  CGCCGCGGCG
                                  ACCC  ___
GAM138  LOC126003 5'  CGGCCGAGCTGCTTTACGGCGC 3123        CCG___
            CG                  CGGCCGAGC    GCGGCGCCG
                                |||||||||    |||||||||
                                GCCGGCTCG    TGCCGCGGC
                                   ACGAAA
GAM138  LOC130612 5'  CGGCGCGGTGGCGGCGCCGC  3124     _ AGCCC
                                CGGC CG   GGCGGCGCCGC
                                |||| ||   ||||||||||
                                GCCG GC   CCGCCGCGGCG
                                  C  CA___
GAM138  LOC143666 5'  TCCTGCCGAGCCCGCCTCGTGC 3125        __________  GCGC
            GGCGCCG                 CCGAGCCCG       GCG   CG
                                |||||||||       |||   ||
                                GGCTCGGGC       CGC   GC
                                   GGAGCAIII  CGCG
GAM138  LOC150244 5'  TCCGGCCGGGCCTGGCCGC   3126        A  C  G
                                TCCGGCCG GCC GGC GC
                                |||||||| ||| ||| ||
                                AGGCCGGC CGG CCG CG
                                   C  A  G
GAM138  LOC150465 5'  TCTCGGGTGCCGGCGGCGCCGC 3127    _  CCGA  C
                                TC CGG   GCC GGCGGCGCCGC
                                || |||   ||| ||||||||||
                                AG GCC   CGG CCGCCGCGGCG
                                 A  CA__  _
GAM138  LOC164173 3'  GCCGAGCCTCAATTCGCCGC  3128        _  CGG
                                GCCGAGCC CGG  CGCCGC
                                |||||||| |||  ||||||
                                CGGCTCGG GTT  GCGGCG
                                   A  AA_
GAM138  LOC203504 5'  TCCAGCCGGGCCTCCGCGGCCG 3129        A  CG_   GC
            C                    TCCGGCCG GCC  GCGGC  CGC
                                |||||||| |||  |||||  |||
                                AGGTCGGC CGG  CGCCG  GCG
                                   C  AGG   __
GAM138  LOC205011 5'  TCGCGGCCTGGGCGGCGCCG  3130    _   GAGCCC
                                TC CGGCC    GGCGGCGCCG
                                || |||||    ||||||||||
                                AG GCCGG    CCGCCGCGGC
                                 C   AC_____
GAM138  LOC205418 3'  TCCAGCCGGGCCTGCAGCTGC  3131        A  CG   _
                                TCCGGCCG GCC  GCGGC GC
                                |||||||| |||  ||||| ||
                                AGGTCGGC CGG  CGTCG CG
                                   C  A_   A
GAM138  LOC219348 5'  CCTGGCCGAGCGCAGCGCCGC  3132    _     CCG
                                CC GGCCGAGC  GCGGCGCCGC
                                || ||||||||  ||||||||||
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                                GG CCGGCTCG   CGTCGCGGCG
                                 A      ___
GAM138  LOC221496 5'  TCAGGCCGGGCCCTCGCCG   3133     C    A   GGCGG
                                TC GGCCG GCCC    CGCCG
                                || ||||| ||||    |||||
                                AG CCGGC CGGG    GCGGC
                                 T    C    A____
GAM138  LOC253181 5'  GGGGGCCCGGCGGCGCCG    3134     CCGA
                                GG   GCCCGGCGGCGCCG
                                ||   ||||||||||||||
                                CC   CGGGCCGCCGCGGC
                                 CC__
GAM138  LOC253258 5'  TCCTGCCGAGCCCGCCTCGTGC 3125          __________  GCGC
           GGCGCCG                 CCGAGCCCG       GCG   CG
                                |||||||||       |||   ||
                                GGCTCGGGC       CGC   GC
                                     GGAGCAIII  CGCG
GAM139  ACK1    3'  CACCCAGGGCAGGGCCTGGGG  2461       C_   CCA   C
                                CACCTAG  CAG   GCC GGGG
                                |||||||  |||   ||| ||||
                                GTGGGTC  GTC   CGG CCCC
                                    CC   C__   A
GAM139  ADD1    3'  GCACACACTGGGTCAGCCCGGG 2462    _   _  AGCCAGC
           G                     GC CAC CT      CAGCCCGGGG
                                || ||| ||      ||||||||||
                                CG GTG GA      GTCGGGCCCC
                                 T   T  CCCA___
GAM139  ADD1    3'  GCACACACTGGGTCAGCCCGGG 2462    _   _  AGCCAGC
           G                     GC CAC CT      CAGCCCGGGG
                                || ||| ||      ||||||||||
                                CG GTG GA      GTCGGGCCCC
                                 T   T  CCCA___
GAM139  B4GALT7  3'  GCCACCTACGCCAGCTGCATGG 2463         _     CA  CCG
                                GCCACCTA GCCAGC  GC   GG
                                |||||||| ||||||  ||   ||
                                CGGTGGAT CGGTCG  CG   CC
                                     G     A_  TA_
GAM139  DIA1    3'  GCCAACCCCCCAGCTCGGGG   2464      CCTA   AG    C
                                GCCA   GCC  CCAGC CGGGG
                                ||||   |||  ||||| |||||
                                CGGT   TGG  GGTCG GCCCC
                                  _____  GG    A
GAM139  DSCAM   5'  GCCGCTCGGCACCTGCCCGGGG 2465     AC  AGCCA   A
                                GCC  CT    GCC GCCCGGGG
                                |||  ||    ||| ||||||||
                                CGG  GA    TGG CGGGCCCC
                                  C_  GCCG_   A
GAM139  EN2     5'  GCCGCCTGGGCCGCCCGGG   2466     A   AGCCA   A
                                GCC CCT    GCC GCCCGGG
                                ||| |||    ||| |||||||
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                                CGG GGA    CGG CGGGCCC
                                  C  CC___  _
GAM139  F2RL3   5'  GCCGCTTGCCAGCCAGCCCG  2467     AC  A
                                GCC  CT GCCAGCCAGCCCG
                                |||  || |||||||||||||
                                CGG  GA CGGTCGGTCGGGC
                                  C_  A
GAM139  GLUL    5'  CAGACAGCGGCCGGCCCGGGG  2468    CC   CA   A
                                CA  TAGC  GCC GCCCGGGG
                                ||  ||||  ||| ||||||||
                                GT  GTCG  CGG CGGGCCCC
                                 CT   C_  C
GAM139  IL15    5'  GCCACCCAGTTCCCTCCCGGGG 2469         CCAG  AG
                                GCCACCTAG   CC  CCCGGGG
                                |||||||||   ||  |||||||
                                CGGTGGGTC   GG  GGGCCCC
                                      AA__  GA
GAM139  JUND    5'  CCCGCCGCGCCGGCCCGGG   2470     A  A_  A
                                CCT GCC  GCC GCCCGGG
                                ||| |||  ||| |||||||
                                GGG CGG  CGG CGGGCCC
                                  _  CG  C
GAM139  KCNF1   5'  GCCGCCGGCCTCGCCCGGG   2471     ACCTA  A  A_
                                GCC    GCC GCC  GCCCGGG
                                |||    ||| |||  |||||||
                                CGG    CGG CGG  CGGGCCC
                                  ______  C  AG
GAM139  LIMK1   5'  CCACCGCCGCCGGCCCGGGG  2472      TA  A  A
                                CCACC  GCC GCC GCCCGGGG
                                |||||  ||| ||| ||||||||
                                GGTGG  CGG CGG CGGGCCCC
                                   __  _  C
GAM139  LIMK1   5'  CCACCGCCGCCGGCCCGGGG  2472      TA  A  A
                                CCACC  GCC GCC GCCCGGGG
                                |||||  ||| ||| ||||||||
                                GGTGG  CGG CGG CGGGCCCC
                                   __  _  C
GAM139  MAP3K5  5'  ACCGCCTGGCCAGCCACAGCTC 2473     A  A      __ C
          GGGG                   GCC CCT GCCAGCCA  GC CGGGG
                                ||| ||| ||||||||  || |||||
                                TGG GGA CGGTCGGT  CG GCCCC
                                  C  C       GT  A
GAM139  NCOR2   3'  GCACAGGGCCAGCCCGGGG   2474    _ __
                                GC CA  GCCAGCCCGGGG
                                || ||  ||||||||||||
                                CG GT  CGGTCGGGCCCC
                                 T  CC
GAM139  NF2     5'  GCCGGCTGGCCGGCCCGGG   2475     ACCTA  CA   A
                                GCC    GC  GCC GCCCGGG
                                |||    ||  ||| |||||||
```

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                                CGG    CG  CGG CGGGCCC
                                  C____  AC   C
GAM139  OVOL1    5'  GCCACCACACAGCCCGGG    2476        TAGCCA  _
                                GCCACC     GC CAGCCCGGG
                                ||||||     || |||||||||
                                CGGTGG     TG GTCGGGCCC
                                   _______  T
GAM139  RFC2     3'  CCTGGCCAGCCACTGGAG    2477      A       G CC
                                CCT GCCAGCCA C  GGGG
                                ||| |||||||| |  ||||
                                GGA CGGTCGGT G  CCTC
                                  C       _ A_
GAM139  RFX1     3'  CCACCTGCGCCGGCCCGGGG   2478        A  CA   A
                                CCACCT GC  GCC GCCCGGGG
                                |||||| ||  ||| ||||||||
                                GGTGGA CG  CGG CGGGCCCC
                                   _ __   C
GAM139  RXRG     5'  GCTTCCTAGCAGCCCGGG    2479     CA     CAGCC
                                GC  CCTAGC    AGCCCGGG
                                ||  ||||||    ||||||||
                                CG  GGATCG    TCGGGCCC
                                 AA    ______
GAM139  WW45     5'  GCCGCCTGTCCGGAGCCCGGGG 2480      A   AG  AGCC
                                GCC CCT  CC    AGCCCGGGG
                                ||| |||  ||    |||||||||
                                CGG GGA  GG    TCGGGCCCC
                                  C   CA  CC__
GAM139  BA108L7.2 3'  GCCAGCCCAGTCAGCTTGGGG  2481       _    C    CAGCCC
                                GCCA CCTAG CAGC     GGGG
                                |||| ||||| ||||     ||||
                                CGGT GGGTC GTCG     CCCC
                                  C    A   AA_____
GAM139  C22orf4  3'  GCCTCTGGCCGCCGAACCCGGG 2482      AC  A   A  _
           G                     GCC  CT GCC GCC AGCCCGGGG
                                |||  || ||| ||| |||||||||
                                CGG  GA CGG CGG TTGGGCCCC
                                  A_  C   _   C
GAM139  CEP3     5'  ACCTGTGCCCTGGCCCGGGG   2483      A_   AGCCA
                                ACCT  GCC    GCCCGGGG
                                ||||  |||    ||||||||
                                TGGA  CGG    CGGGCCCC
                                  CA   GAC__
GAM139  D21S2056E 3'  GCCACCTGCCCGGGG       2484         AGCCAGCCA
                                GCCACCT       GCCCGGGG
                                |||||||       ||||||||
                                CGGTGGA       CGGGCCCC
                                              _________
GAM139  DKFZP586N0721 3'  GCCACTTGTTTAGCCAGCCTGG 2485        CTAGCC       C
                                GCCAC     AGCCAGCC GG
                                |||||     |||||||| ||
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                                CGGTG     TCGGTCGG CC
                                  AACAAA       A
GAM139  DTX2     3'  GCCACCCAGCCAGCCATGGGG  2486             GCCC
                                GCCACCTAGCCAGCCA   GGGG
                                ||||||||||||||||   ||||
                                CGGTGGGTCGGTCGGT   CCCC
                                          A___
GAM139  FLJ14681 3'  GCCACCTATCAGCTAAGAG   2487         GC   CAGCCC
                                GCCACCTA  CAGC     GGG
                                ||||||||  ||||     |||
                                CGGTGGAT  GTCG     CTC
                                    A_    ATT___
GAM139  FLJ21709 3'  CATCTGGCCAGCCATGAG    2488     C  A       GCCC
                                CA CT GCCAGCCA    GGG
                                || || ||||||||    |||
                                GT GA CGGTCGGT    CTC
                                 A  C       A___
GAM139  FLJ21916 3'  GCCATCTTGCCGGCCAGCC    2489      C  A   A
                                GCCA CT GCC GCCAGCC
                                |||| || ||| |||||||
                                CGGT GA CGG CGGTCGG
                                  A  A   C
GAM139  FLJ22390 3'  GCCATTTCAAAAGCTAGCCCGG 2490       CCTAGCC   C
          GG                    GCCA      AGC AGCCCGGGG
                                ||||      ||| |||||||||
                                CGGT      TCG TCGGGCCCC
                                  AAAGTTT   A
GAM139  KCNG3    5'  CCTGCCCTCCGCTGGCCCGGGG 2491      A   AG  A___
                                CCT GCC  CC    GCCCGGGG
                                ||| |||  ||    ||||||||
                                GGA CGG  GG    CGGGCCCC
                                  _   GA  CGAC
GAM139  KIAA0189 3'  CCATCTGGCTGGCCCAGGG    2492      C  A  CAGCCA
                                CCA CT GC     GCCCGGGG
                                ||| || ||     ||||||||
                                GGT GA CG     CGGGTCCC
                                  A  C  AC____
GAM139  KIAA0469 3'  GCCATCTGGCCAGCACAAGGG  2493       C  A     _   CCC
                                GCCA CT GCCAGC CAG   GGG
                                |||| || |||||| |||   |||
                                CGGT GA CGGTCG GTT   CCC
                                  A  C     T  ___
GAM139  KIAA1006 5'  GCCGCCTGCCAGCCCGG     2494      ACCTA   A
                                GCC    GCC GCCAGCCCGG
                                |||    ||| ||||||||||
                                CGG    CGG CGGTCGGGCC
                                  ______   A
GAM139  KIAA1297 3'  GCCGCTTGCCCGCCCGGG    2495      ACCTA  CA   A
                                GCC    GC  GCC GCCCGGG
                                |||    ||  ||| |||||||
```

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                                CGG    CG  CGG CGGGCCC
                                  _____ AA   G
GAM139  KIAA1643 3'  GCCCCTGCAGCCGGCCCGGGG  2496     A   A  C    A
                                GCC CCT GC AGCC GCCCGGGG
                                ||| ||| || |||| ||||||||
                                CGG GGA CG TCGG CGGGCCCC
                                  _  _ _   C
GAM139  KIF13B   3'  CCTGCCAAGTGCTGGCCCGGGG 2497     A   ___  CA
                                CCT GCCA   GC  GCCCGGGG
                                ||| ||||   ||  ||||||||
                                GGA CGGT   CG  CGGGCCCC
                                  _    TCA  AC
GAM139  KIF13B   3'  CCTGCCAAGTGCTGGCCCGGGG 2497     A   ___  CA
                                CCT GCCA   GC  GCCCGGGG
                                ||| ||||   ||  ||||||||
                                GGA CGGT   CG  CGGGCCCC
                                  _    TCA  AC
GAM139  LASP1    3'  GCCACCTAACCCAGATCCTGGG 2498          AGCCAG  C
          G                      GCCACCTAGCC     CC GGGG
                                ||||||||||      || ||||
                                CGGTGGATTGG     GG CCCC
                                      GTCTA_  A
GAM139  MARK2    5'  GCCGCTCACGCCAGCCCGGGG  2499     ACCTA  _  _
                                GCC     GC CA GCCAGCCCGGGG
                                |||     || || ||||||||||||
                                CGG     CG GT CGGTCGGGCCCC
                                  _____  A  G
GAM139  MGC15854 5'  GCCATCTTGCCAGCCCGGG   2500      C  AGCCA
                                GCCA CT    GCCAGCCCGGG
                                |||| ||    ||||||||||
                                CGGT GA    CGGTCGGGCCC
                                  A  A____
GAM139  MGC19570 3'  GCCACCTAGTGGCCAGCC    2501          CCA
                                GCCACCTAG   GCCAGCC
                                |||||||||   |||||||
                                CGGTGGATC   CGGTCGG
                                      AC_
GAM139  N4BP3    3'  GCCACCCAGCCGGCTGGG    2502          A  CAGCCC
                                GCCACCTAGCC GC     GGG
                                |||||||||| ||     |||
                                CGGTGGGTCGG CG     CCC
                                      C  A_____
GAM139  PP3501   3'  GCCTTCTGGCAGGAGCCCGGGG 2503     AC  A  C  CC
                                GCC  CT GC AG  AGCCCGGGG
                                |||  || || ||  |||||||||
                                CGG  GA CG TC  TCGGGCCCC
                                  AA  C  _  C_
GAM139  RAGD     5'  CCACCGGCCGGCCGGCCCGGGG 2504       TA   A   A
                                CCACC  GCC GCC GCCCGGGG
                                |||||  ||| ||| ||||||||
```

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                                GGTGG  CGG CGG CGGGCCCC
                                  C_   C   C
GAM139  SELM     3'  CCCATCCCTGCTGGCCCGGGG  2505      G  A_  CA
                                CCTA CC  GC  GCCCGGGG
                                |||| ||  ||  ||||||||
                                GGGT GG  CG  CGGGCCCC
                                  A  GA  AC
GAM139  SLC26A9  3'  CTAGCCAGCCTCCAGGG     2506          AGC
                                CTAGCCAGCC   CCGGGG
                                ||||||||||   ||||||
                                GATCGGTCGG   GGTCCC
                                     A__
GAM139  SLC26A9  3'  CTAGCCAGCCTCCAGGG     2506          AGC
                                CTAGCCAGCC   CCGGGG
                                ||||||||||   ||||||
                                GATCGGTCGG   GGTCCC
                                     A__
GAM139  LOC146280 5'  CCACCTGGCGCCCAGGCCCGGG 2507        A  CAG   _
          G                      CCACCT GC   CCAG CCCGGGG
                                 |||||| ||   |||| |||||||
                                 GGTGGA CG   GGTC GGGCCCC
                                    C  CG_   C
GAM139  LOC146443 5'  GCCACTGCACTCCAGCCCGGGG 2508       CTA  CAG
                                GCCAC   GC   CCAGCCCGGGG
                                |||||   ||   ||||||||||
                                CGGTG   CG   GGTCGGGCCCC
                                  A__  TGA
GAM139  LOC148189 5'  CCTGCAGCCAGCCCGG      2509      A  C
                                CCT GC AGCCAGCCCGG
                                ||| || ||||||||||
                                GGA CG TCGGTCGGGCC
                                  _ _
GAM139  LOC157848 3'  CAGCCAGCAGCTGGCTTGGGG  2510         C   CC____
                                TAGCCAGC AGC     GGGG
                                |||||||| |||     ||||
                                GTCGGTCG TCG     CCCC
                                     _  ACCGAA
GAM139  LOC162022 5'  CCCGCGAGCCAGCCCGGGG    2511      A  C
                                CCT GC AGCCAGCCCGGGG
                                ||| || ||||||||||||
                                GGG CG TCGGTCGGGCCCC
                                  _  C
GAM139  LOC196047 5'  GCTCACACCTGAGCCAGCCTGG 2512     _  CTA  __       C
          GG                     GC CAC   GCC  AGCCAGCC GGGG
                                 || |||   |||  |||||||| ||||
                                 CG GTG   TGG  TCGGTCGG CCCC
                                  A  ____  AC       A
GAM139  LOC197342 3'  GCCATCTGCCAGCCAGAAG   2513      C  A       CCC
                                GCCA CT GCCAGCCAG   GGG
                                |||| || |||||||||   |||
```

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                                CGGT GA CGGTCGGTC   TTC
                                  A _       ____
GAM139  LOC200213 5'  GCAGGAGGCTGGCCGGCCCGGG 2514     CACCTA  CA   A
            G                     GC     GC  GCC GCCCGGGG
                                  ||     ||  ||| ||||||||
                                  CG     CG  CGG CGGGCCCC
                                   TCCTC_  AC   C
GAM139  LOC201522 3'  GCCGCCTGCCAGCCCCGGG   2515      A   A      AGC
                                  GCC CCT GCCAGCC   CCGGG
                                  ||| ||| |||||||   |||||
                                  CGG GGA CGGTCGG   GGCCC
                                   C   _     ____
GAM139  LOC205418 3'  CACCTTGGCCAGCCCCGGG   2516       A_      AGC
                                  CACCT  GCCAGCC   CCGGG
                                  |||||  |||||||   |||||
                                  GTGGA  CGGTCGG   GGCCC
                                    AC      ____
GAM139  LOC255990 5'  GCCGCCTCTAGTGCCAGCCCGG 2517      A   AGCCA
            GG                      GCC CCT    GCCAGCCCGGGG
                                  ||| |||    ||||||||||||
                                  CGG GGA    CGGTCGGGCCCC
                                   C   GATCA
GAM139  LOC58489  5'  GCTGGCTGGCTGGCTGGCCCGG 2518     CAC  A  CA  CA
            G                     GC   CT GC  GC  GCCCGGG
                                  ||   || ||  ||  |||||||
                                  CG   GA CG  CG  CGGGCCC
                                   ACC  C  AC  AC
GAM139  LOC58525  3'  GCCGCTTTGCCAGCCAGCCAG  2519      ACCTA         C
                                  GCC    GCCAGCCAGCC GG
                                  |||    |||||||||||  ||
                                  CGG    CGGTCGGTCGG TC
                                   CGAAA         _
GAM139  LOC92095  3'  CCGGGGCCTCAGCTGGCCCGGG 2520     TA_  __  CA
            G                     CC   GCC  AGC  GCCCGGGG
                                  ||   |||  |||  ||||||||
                                  GG   CGG  TCG  CGGGCCCC
                                   CCC   AG   AC
GAM139  LOC92096  3'  CCGGGGCCTCAGCTGGCCCGGG 2520     TA_  __  CA
            G                     CC   GCC  AGC  GCCCGGGG
                                  ||   |||  |||  ||||||||
                                  GG   CGG  TCG  CGGGCCCC
                                   CCC   AG   AC
GAM140  ALPP     3'  CTGCCTGGTACCCACTGGGCTG 3138       A_   GGG TG
                                  CTGCT  GTA   C  CTGGGCTG
                                  |||||  |||   |  ||||||||
                                  GACGG  CAT   G  GACCCGAC
                                    AC   G__ GT
GAM140  CYLN2    3'  CTGGTGTGGACTGGGCTGC   3139     A  AG  CT
                                  CT GT  GG  GCTGGGCTGC
                                  || ||  ||  ||||||||||
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                                GA CA  CC  TGACCCGACG
                                 C  CA  __
GAM140  CYP3A43  5' CTGCTCTTTGCTGGGCTG    3140       AGTAGGGC
                                CTGCT       TGCTGGGCTG
                                |||||       ||||||||||
                                GACGA       ACGACCCGAC
                                   GAA_____
GAM140  CYP3A43  5' CTGCTCTTTGCTGGGCTG    3140       AGTAGGGC
                                CTGCT       TGCTGGGCTG
                                |||||       ||||||||||
                                GACGA       ACGACCCGAC
                                   GAA_____
GAM140  CYP3A43  5' CTGCTCTTTGCTGGGCTG    3140       AGTAGGGC
                                CTGCT       TGCTGGGCTG
                                |||||       ||||||||||
                                GACGA       ACGACCCGAC
                                   GAA_____
GAM140  CYP3A5   5' CTGCTGTTTGCTGGGCTG    3141       A  AGGGC
                                CTGCT GT    TGCTGGGCTG
                                ||||| ||    ||||||||||
                                GACGA CA    ACGACCCGAC
                                   _ A____
GAM140  MKI67    3' CTGCTGTAGGGTGGCTG     3142       A     CT
                                CTGCT GTAGGG  GCTG
                                ||||| ||||||  ||||
                                GACGA CATCCC  CGAC
                                   _     AC
GAM140  PFN1     5' CTGCTACTGGGGCTGCTCTCGG 3143       GTA      G__
           C                     CTGCTA   GGGCTGCT   GGC
                                ||||||   ||||||||   |||
                                GACGAT   CCCGACGA   CCG
                                   GAC       GAG
GAM140  RP2      3' CTGTTAGTAGAGTTACTTGC   3144     C      C    GG
                                CTG TAGTAGGG TGCT  GC
                                ||| |||||||| ||||  ||
                                GAC ATCATCTC ATGA  CG
                                  A       A   A_
GAM140  STK13    5' CTGCTGGGCTGCTGGGCTG   3145       AGTA
                                CTGCT    GGGCTGCTGGGCTG
                                |||||    ||||||||||||||
                                GACGA    CCCGACGACCCGAC
                                   _____
GAM140  C20orf100 3' CTGGTGGTGGGCAGTGGGCTGC 3146     CTA  A    TGC
                                CTG   GT GGGC   TGGGCTGC
                                |||   || ||||   ||||||||
                                GAC   CA CCCG   ACCCGACG
                                  CAC  _    TC_
GAM140  CYP3A7   5' CTGCTGTTTGCTGGGCTG    3141       A  AGGGC
                                CTGCT GT    TGCTGGGCTG
                                ||||| ||    ||||||||||
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                                GACGA CA    ACGACCCGAC
                                  _ A____
GAM140  DGS-A    3'  CTGCCAGTAGGGCTCAGTTGC  3147            GCTGG
                                CTGCTAGTAGGGCT    GC
                                ||||||||||||||    ||
                                GACGGTCATCCCGA    CG
                                      GTCAA
GAM140  DKFZp566D133 3'  CTGCTGATCACTGCTGGGCTGC 3148       A  AGG
                                CTGCT GT   GCTGCTGGGCTGC
                                ||||| ||   ||||||||||||
                                GACGA TA   TGACGACCCGACG
                                  C  G__
GAM140  FLJ20257  5'  CTGCTGGTGGTGCTGTCCCCGG 3149       A  A  _   ___
                                CTGCT GT GG GCTG   CTGG
                                ||||| || || ||||   ||||
                                GACGA CA CC CGAC   GGCC
                                  C  _  A   AGG
GAM140  KIAA1691  3'  CTGTGGGTGGGCGGGCTG    3150     CTA  A    TGCT
                                CTG   GT GGGC    GGGCTG
                                |||   || ||||    ||||||
                                GAC   CA CCCG    CCCGAC
                                 ACC  _   _____
GAM140  KIAA1910  5'  CTGCTGGTGGAGTTCTTGCTG  3151       A  A   CTG  GG
                                CTGCT GT GGG   CT  GCTG
                                ||||| || |||   ||  ||||
                                GACGA CA CCT   GA  CGAC
                                  C  _   CAA  A_
GAM140  MGC3123   5'  CTGCTGGCAGGGTCCACGCTGC 3152       A     _ TG TGG
                                CTGCT GTAGGG C  C   GCTGC
                                ||||| |||||| |  |   |||||
                                GACGA CGTCCC G  G   CGACG
                                  C     A GT ___
GAM140  PP1628    3'  CTGCTGGTGGGGGAAGGCTG   3153       A  A   CTGCT
                                CTGCT GT GGG    GGGCTG
                                ||||| || |||    ||||||
                                GACGA CA CCC    TCCGAC
                                  C  C   CT___
GAM140  SEMA7A    3'  CTAGTGCCCTGGGCTG      3154       AGG   G
                                CTAGT   GCT CTGGGCTG
                                |||||   ||| ||||||||
                                GATCA   CGG GACCCGAC
                                   ___   _
GAM140  UBCE7IP5  3'  CTGCTGGTGGGAAGCAGGCTG  3155       A  A   CT  T
                                CTGCT GT GGG  GC GGGCTG
                                ||||| || |||  || ||||||
                                GACGA CA CCC  CG TCCGAC
                                  C  _   TT  _
GAM140  LOC120772 5'  CTGCTAGTCGGGCTGCGTGC   3156         A      TGG
                                CTGCTAGT GGGCTGC   GC
                                |||||||| |||||||   ||
```

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                                GACGATCA CCCGACG   CG
                                    G      CA_
GAM140   LOC124222 3'  CTGCTGGGAGGGCTGGTATGC  3157       AGT      C  G
                                CTGCT   AGGGCTG TG GC
                                |||||   ||||||| || ||
                                GACGA   TCCCGAC AT CG
                                   CCC      C  A
GAM140   LOC144121 5'  CTGCTAGTCGGGCTGCGTG   3158         A     _
                                CTGCTAGT GGGCTGC TG
                                |||||||| ||||||| ||
                                GACGATCA CCCGACG AC
                                    G      C
GAM140   LOC144165 5'  CCGCTGCGGGGCTGCTGGGCTG 3159       A TA
           C                     CTGCT G  GGGCTGCTGGGCTGC
                                ||||| |  ||||||||||||||
                                GGCGA C  CCCGACGACCCGACG
                                   _ GC
GAM140   LOC144587 5'  CTGCTGGCAGGGTCCACGCTGC 3152       A     _ TG TGG
                                CTGCT GTAGGG C  C   GCTGC
                                ||||| |||||| |  |   |||||
                                GACGA CGTCCC G  G   CGACG
                                   C     A GT ___
GAM140   LOC145258 3'  GCCTCGGGCTGCTGGGCTG   3160     AGTA
                                GCT    GGGCTGCTGGGCTG
                                |||    ||||||||||||||
                                CGG    CCCGACGACCCGAC
                                  AG__
GAM140   LOC149722 5'  CTGCTGGAACTGCTGGGTTGC  3161       AGTA         C
                                CTGCT    GGGCTGCTGGG TGC
                                |||||    |||||||||| |||
                                GACGA    CTTGACGACCC ACG
                                   C___          A
GAM140   LOC150418 5'  CTCCTGTCTCCCTGCTGGGCTG 3162     G  A  AGGG
                                CT CT GT    CTGCTGGGCTG
                                || || ||    ||||||||||
                                GA GA CA    GACGACCCGAC
                                 G  _  GAGG
GAM140   LOC151201 3'  TGCTAATAGGGCAGTGCTG   3163           __
                                TGCTAGTAGGGC  TGCTG
                                ||||||||||||  |||||
                                ACGATTATCCCG  ACGAC
                                       TC
GAM140   LOC152282 3'  CTGCTACTGGGGCTGCTG    3165        GTA
                                CTGCTA   GGGCTGCTG
                                ||||||   |||||||||
                                GACGAT   CCCGACGAC
                                   GAC
GAM140   LOC152282 3'  CTGCTACTGGGGCTGCTG    3165        GTA
                                CTGCTA   GGGCTGCTG
                                ||||||   |||||||||
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                                GACGAT   CCCGACGAC
                                   GAC
GAM140   LOC152282 3'  CTGCTGGTGGAGCTGCTG    3164       A  A
                                CTGCT GT GGGCTGCTG
                                |||||| || |||||||||
                                GACGA CA CTCGACGAC
                                   C  C
GAM140   LOC152282 3'  CTGCTACTGGGGCTGCTG    3165       GTA
                                CTGCTA   GGGCTGCTG
                                ||||||   |||||||||
                                GACGAT   CCCGACGAC
                                   GAC
GAM140   LOC152282 3'  CTGCTACTGGGGCTGCTG    3165       GTA
                                CTGCTA   GGGCTGCTG
                                ||||||   |||||||||
                                GACGAT   CCCGACGAC
                                   GAC
GAM140   LOC152282 3'  CTGCTACTGGGGCTGCTGGAGC 3167       GTA        _
            TGC                    CTGCTA   GGGCTGCTGG GCTGC
                                ||||||   |||||||||| |||||
                                GACGAT   CCCGACGACC CGACG
                                   GAC         T
GAM140   LOC152282 3'  CTGCTACTGGGGCTGCTGGAGC 3167       GTA        _
            TGC                    CTGCTA   GGGCTGCTGG GCTGC
                                ||||||   |||||||||| |||||
                                GACGAT   CCCGACGACC CGACG
                                   GAC         T
GAM140   LOC152282 3'  CTGCTACTGGGGCTGCTGG    3166       GTA
                                CTGCTA   GGGCTGCTGG
                                ||||||   ||||||||||
                                GACGAT   CCCGACGACC
                                   GAC
GAM140   LOC152282 3'  CTGCTACTGGGGCTGCTG    3165       GTA
                                CTGCTA   GGGCTGCTG
                                ||||||   |||||||||
                                GACGAT   CCCGACGAC
                                   GAC
GAM140   LOC158230 3'  CTGCTGGCAGGGCTTCTACCTG 3168       A      G   GG
            C                     CTGCT GTAGGGCT CTG  CTGC
                                ||||| |||||||| |||  ||||
                                GACGA CGTCCCGA GAT  GACG
                                   C       A   G_
GAM140   LOC158373 5'  CTGCGGTAGGGCCGGC     3169      TA      GCTG
                                CTGC  GTAGGGCT   GGC
                                ||||  ||||||||   |||
                                GACG  CATCCCGG   CCG
                                  C_      _____
GAM140   LOC163682 3'  CTGCTGTGCCTGGGT      3170       A  AGG  TG    C
                                CTGCT GT   GC  CTGGG T
                                ||||| ||   ||  ||||| |
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                                GACGA CA   CG  GACCC A
                                  _ ___  __     A
GAM140  LOC205693 5'  CTGCTGGTAGAGGTAGGCTG  3171       A     CTGC
                                CTGCT GTAGGG    TGGGCTG
                                ||||| ||||||    |||||||
                                GACGA CATCTC    ATCCGAC
                                   C     C___
GAM140  LOC221100 5'  CTGCTGGTGGAGGGATTGGCTG 3172       A __    CTGCTG
                                CTGCT GT  AGGG     GGCTG
                                ||||| ||  ||||     |||||
                                GACGA CA  TCCC     CCGAC
                                   C  CC    TAA___
GAM140  LOC253959 3'  CTGCTGATCACTGCTGGGCTGC 3148       A  AGG
                                CTGCT GT   GCTGCTGGGCTGC
                                ||||| ||   ||||||||||||
                                GACGA TA   TGACGACCCGACG
                                   C  G__
GAM140  LOC256492 5'  CTGCTGTGGGGCTGCTG     3173       A  A
                                CTGCT GT GGGCTGCTG
                                ||||| || |||||||||
                                GACGA CA CCCGACGAC
                                   _  C
GAM140  LOC256867 5'  CTGCTAGTCGGGCTGCGTGC   3156         A      TGG
                                CTGCTAGT GGGCTGC   GC
                                |||||||| |||||||   ||
                                GACGATCA CCCGACG   CG
                                     G      CA_
GAM140  LOC91660  3'  TGTTAGTAGAGTTGGGGTTTTG 3174     C      C  CT   C__
            C                    TG TAGTAGGG TG  GGG   TGC
                                || |||||||| ||  |||   |||
                                AC ATCATCTC AC  CCC   ACG
                                 A       A  __   AAA
GAM141  ATP10C    3'  CCATGTTCACACCTGCC     3177          AATT    C
                                CCATGTTCG    TACC GCC
                                |||||||||    |||| |||
                                GGTACAAGT    GTGG CGG
                                     ____    A
GAM141  DPP6      3'  CACCATGTTGAACGTCC     3178          C    TTAC
                                CACCATGTT GAAT    CC
                                ||||||||| ||||    ||
                                GTGGTACAA CTTG    GG
                                     _    CA__
GAM141  RUNX1     3'  ACCATGTTTTCCCAC       3179          CGAAT  A
                                ACCATGTT     TT CCCGC
                                ||||||||     || |||||
                                TGGTACAA     AA GGGTG
                                     _____  _
GAM141  FLJ10989  3'  CACCATGTTGACCAGGC     3180          C  ATTTA  C_
                                CACCATGTT GA    CC  GC
                                ||||||||| ||    ||  ||
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                                GTGGTACAA CT    GG  CG
                                    _ _____ TC
GAM141  FREQ    3'  CACCATGTTCGTTCCCTGCCC  3181          AAT  A  _
                                CACCATGTTCG   TT CCC GCCC
                                ||||||||||   || ||| ||||
                                GTGGTACAAGC   AA GGG CGGG
                                    ___ _  A
GAM141  LOC149073 5'  CCATGTTCGTCTGCCC     3182         AA   A
                                CCATGTTCG  TTT CCC
                                |||||||||  ||| |||
                                GGTACAAGC  AGA GGG
                                    __  C
GAM142  CACNG6   5'  ACCCTGAGGTTTAGAGA     3185         TA   A
                                ACCCTGAG  TTTA AGG
                                ||||||||  |||| |||
                                TGGGACTC  AAAT TCT
                                    C_   C
GAM142  DUT     3'  ACCCAGTCAATAGAGGATTTA  3186      TG   ATT  A
                                ACCC  AGT   TA AGGATTTA
                                ||||  |||   || ||||||||
                                TGGG  TCA   AT TCCTAAAT
                                  __  GTT  C
GAM142  ID4     3'  CCCTGCTTGAAGGATTT     3187       AGTA   A
                                CCCTG    TTT AAGGATTT
                                |||||    ||| ||||||||
                                GGGAC    GAA TTCCTAAA
                                  _____  C
GAM142  ITPR3    3'  CTCAGGCCAAAGGATTT     3188     G  TAT
                                CT AG   TTAAAGGATTT
                                || ||   ||||||||||
                                GA TC   GGTTTCCTAAA
                                 G  C__
GAM142  KCNAB1   3'  CCTGGGTATTTTACAGGTTTAC 3189      A     AA_   A
                                CCTG GTATTT   AGG TTTAC
                                |||| ||||||   ||| |||||
                                GGAC CATAAA   TCC AAATG
                                  C     ATG  _
GAM142  MAD2L1   3'  CTGAATATTTAGACTT      3190          AAA
                                CTGAGTATTT   GGATTT
                                ||||||||||   ||||||
                                GACTTATAAA   TCTGAA
                                    ____
GAM142  MAP3K1   3'  CCCTGGTATTTAAGAAA     3191       A       AG
                                CCCTG GTATTTAA  GA
                                ||||| ||||||||  ||
                                GGGAC CATAAATT  TT
                                  _       CT
GAM142  TPMT     3'  CTGAGTAAAAGACAAGGGTTTA 3192        TTTA__    A
                                CTGAGTA     AAGG TTTA
                                |||||||     |||| ||||
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                                GACTCAT     TTCC AAAT
                                    TTTCTG    C
GAM142  CSAD     3'  CCTGAGTAGCTGGGTTTAC   3193        TTTAAA  A
                                CCTGAGTA     GG TTTAC
                                ||||||||     || |||||
                                GGACTCAT     CC AAATG
                                     CGA___  C
GAM142  dJ309H15.1 3'  CCTGGGTCAGCAAAAGGATTT  3194      A  ATTT_
                                CCTG GT    AAAGGATTT
                                |||| ||    |||||||||
                                GGAC CA    TTTCCTAAA
                                  C  GTCGT
GAM142  FBXO30   3'  CTGAATATTTGAAATTTAC   3195         AAA
                                CTGAGTATTT   GGATTTAC
                                ||||||||||   ||||||||
                                GACTTATAAA   TTTAAATG
                                      C__
GAM142  FLB6421   3'  CCCAGAGTATTTAGGA     3196     T      AA
                                CCC GAGTATTT  AGGA
                                ||| ||||||||  ||||
                                GGG CTCATAAA  TCCT
                                  T       __
GAM142  FLJ13456  3'  CTGAGTAAAGAAGGGATTTAC  3197        TTTAAA
                                CTGAGTA     GGATTTAC
                                |||||||     ||||||||
                                GACTCAT     CCTAAATG
                                    TTCTTC
GAM142  HE3-BETA  3'  ACTCTAAGTATTTGGA     3198     C       AAA
                                AC CTGAGTATTT   GGA
                                || ||||||||||   |||
                                TG GATTCATAAA   CCT
                                 A        ____
GAM142  KIAA0924  3'  CTGAGTATTTGAAACTTA    3199         AAA
                                CTGAGTATTT   GGATTTA
                                ||||||||||   |||||||
                                GACTCATAAA   TTTGAAT
                                      C__
GAM142  KIAA1786  3'  ACTCTGAATATTTAAGG     3200     C        A
                                AC CTGAGTATTTAA GG
                                || ||||||||||||| ||
                                TG GACTTATAAATT CC
                                 A          _
GAM142  KIAA1944  3'  ACCCTGAAGGGCTCAGAGGATT 3201        _ TA   A
              T                  ACCCTGA G  TTTA AGGATTT
                                 ||||||| |  |||| |||||||
                                 TGGGACT C  GAGT TCCTAAA
                                     T CC   C
GAM142  POPX1    3'  GAATTTTAAAGGATTTAC    3202      A
                                GAGT TTTAAAGGATTTAC
                                |||| ||||||||||||||
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                                CTTA AAATTTCCTAAATG
                                  _
GAM142  SPRY1    5'  ACCCTAAGCAAGGATTT     3203          TTTAA
                                ACCCTGAGTA    AGGATTT
                                ||||||||||    |||||||
                                TGGGATTCGT    TCCTAAA
                                      _____
GAM142  SPTLC2   3'  CTGAGCAGAGGATTTA      3204        TTTAA
                                CTGAGTA    AGGATTTA
                                |||||||    ||||||||
                                GACTCGT    TCCTAAAT
                                    C____
GAM142  TRIP-Br2 3'  TGAGTATCAGGGATTTA     3205         TAAA
                                TGAGTATT   GGATTTA
                                ||||||||   |||||||
                                ACTCATAG   CCTAAAT
                                     TC__
GAM142  USP15    3'  CTGATAAAGGATTTA       3206       GTATT
                                CTGA    TAAAGGATTTA
                                ||||    ||||||||||
                                GACT    ATTTCCTAAAT
                                  _____
GAM142  LOC116228 3' CCTGAGGATTTAGTTAGAT   3207        T    AA_
                                CCTGAG ATTTA   GGAT
                                |||||| |||||   ||||
                                GGACTC TAAAT   TCTA
                                   C    CAA
GAM142  LOC128338 3' ACCCAGTTCTAAAGGATTTAC 3208       TG   A
                                ACCC  AGT TTTAAAGGATTTAC
                                ||||  ||| ||||||||||||||
                                TGGG  TCA AGATTTCCTAAATG
                                  __  _
GAM142  LOC201411 3' CTGAGTAAAAGACAAGGGTTTA 3192        TTTA__    A
                                CTGAGTA     AAGG TTTA
                                |||||||     |||| ||||
                                GACTCAT     TTCC AAAT
                                     TTTCTG    C
GAM142  LOC220936 3' TGAGTATTATGAATTCA     3209         TAAA
                                TGAGTATT   GGATTTA
                                ||||||||   |||||||
                                ACTCATAA   CTTAAGT
                                     TA__
GAM142  LOC221337 5' CTGAGCAAAAGGATTT      3210        TTT
                                CTGAGTA   AAAGGATTT
                                |||||||   |||||||||
                                GACTCGT   TTTCCTAAA
                                   ___
GAM142  LOC90826  3' ACACTGAGTATTTAAAGGA   3211     C
                                AC CTGAGTATTTAAAGGA
                                || ||||||||||||||||
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                                TG GACTCATAAATTTCCT
                                 T
GAM143  FLJ10607  3'  GTGAAGGATTTCTGTTGTTT  3214        C  ACACG
                                GTGAGGGA TT    TGTTT
                                |||||||| ||    |||||
                                CACTTCCT AA    ACAAA
                                    A  GACA_
GAM143  FLJ23590  3'  TTAGTAAGTGGGTATGTGTTT  3215        _  ACTTACAC
                                TTAGTGAG GG      GTGTTT
                                |||||||| ||      ||||||
                                AATCATTC CC      CACAAA
                                    A  CATA____
GAM143  UBE2N     3'  TTAGTGAGGGCTGTGATGTTT  3216         A  TACAC
                                TTAGTGAGGG CT    GTGTTT
                                |||||||||| ||    ||||||
                                AATCACTCCC GA    TACAAA
                                     _  CAC__
GAM143  UBE2N     3'  TTAGTGAGGGCTGTGATGTTT  3216         A  TACAC
                                TTAGTGAGGG CT    GTGTTT
                                |||||||||| ||    ||||||
                                AATCACTCCC GA    TACAAA
                                     _  CAC__
GAM143  LOC162461 3'  TCAGTGAGGACATGTGTT    3217         GACTT  C
                                TTAGTGAGG    ACA GTGTT
                                |||||||||    ||| |||||
                                AGTCACTCC    TGT CACAA
                                     _____  A
GAM144  ABCC3     3'  GAGTAGCTGCCGAAGGGGTCCA 3220      CT  T    A___
          G                      GAG  GCT GCCGAG   TCCAG
                                |||  ||| ||||||   |||||
                                CTC  CGA CGGCTT   AGGTC
                                  AT  _     CCCC
GAM144  ABCC3     3'  GAGTAGCTGCCGAAGGGGTCCA 3220      CT  T    A___
          G                      GAG  GCT GCCGAG   TCCAG
                                |||  ||| ||||||   |||||
                                CTC  CGA CGGCTT   AGGTC
                                  AT  _     CCCC
GAM144  ACP2      3'  GAGCTATTTGCCGAAGAC    3221        C     GATCC
                                GAGCTG TTGCCGA    AGAC
                                |||||| |||||||    ||||
                                CTCGAT AACGGCT    TCTG
                                   A     _____
GAM144  FAAH      3'  GAGCAGGGATGGAGGTCCAGAC 3222      TGCTTGCC  A
          T                      GAGC       GAG TCCAGACT
                                ||||       ||| ||||||||
                                CTCG       CTC AGGTCTGA
                                  TCCCTAC_  C
GAM144  MRPL49    5'  GAGCTGCCTGCCCAGGCAG   3223          G  ATC
                                GAGCTGCTTGCC AG   CAG
                                ||||||||||| ||   |||
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                                CTCGACGGACGG TC   GTC
                                      G  C__
GAM144  SKP2     5'  GAGCTGCTCGCCTCCCAGA   3224          GAGA
                                GAGCTGCTTGCC   TCCAGA
                                ||||||||||||  ||||||
                                CTCGACGAGCGG   GGGTCT
                                      A___
GAM144  SKP2     5'  GAGCTGCTCGCCTCCCAGA   3224          GAGA
                                GAGCTGCTTGCC   TCCAGA
                                ||||||||||||  ||||||
                                CTCGACGAGCGG   GGGTCT
                                      A___
GAM144  APC10    5'  GGCTGCTTGCCGAAACTCAGA  3225    A          TC
                                G GCTGCTTGCCGAGA  CAGA
                                | ||||||||||||||  ||||
                                C CGACGAACGGCTTT  GTCT
                                _          GA
GAM144  BLR1     3'  GAGCTGCTTTCCGCTCCC    3226         G   AGA
                                GAGCTGCTT CCG   TCC
                                |||||||||  |||   |||
                                CTCGACGAA GGC   GGG
                                     A   GA_
GAM144  BLR1     3'  GAGCTGCTTTCCGCTCCC    3226         G   AGA
                                GAGCTGCTT CCG   TCC
                                |||||||||  |||   |||
                                CTCGACGAA GGC   GGG
                                     A   GA_
GAM144  DKFZP434P0316 5'  GAGCTGCTTGCTCAGGTCC   3227          CG  A
                                GAGCTGCTTGC  AG TCC
                                ||||||||||  ||  |||
                                CTCGACGAACG  TC AGG
                                      AG  C
GAM144  FLJ20174  3'  GAGCTGCTTCTGAGAACC    3228         GCC    T
                                GAGCTGCTT   GAGA CC
                                |||||||||   ||||  ||
                                CTCGACGAA   CTCT GG
                                     GA_    T
GAM144  KIAA1005  3'  GAGCTGCTTTTCGAGGATC   3229         GC   _
                                GAGCTGCTT  CGAG ATC
                                |||||||||  ||||  |||
                                CTCGACGAA  GCTC TAG
                                     AA    C
GAM144  ZAK      3'  GAGCTGTCTTGCTGCAAG    3230        _    __
                                GAGCTG CTTGC  CGAG
                                ||||||  |||||  ||||
                                CTCGAC GAACG  GTTC
                                   A     AC
GAM144  LOC148894 3'  GAGCTGCTGCACCTAGAC    3231         _   G
                                GAGCTGCT TGCC AGAT
                                ||||||||  ||||  ||||
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                                CTCGACGA GTGG TCTG
                                    C    A
GAM144  LOC151171 5'  GAGCTTCTAGGTCCAGAC    3232       G  TGCCG  A
                                GAGCT CT    AG TCCAGAC
                                ||||| ||    || |||||||
                                CTCGA GA    TC AGGTCTG
                                  A _____  C
GAM144  LOC57805  3'  GCTGCTTAGCCCCAGCCAGGCT 3233        _  GAGAT   A
                                GCTGCTT GCC    CCAG CT
                                ||||||| |||    |||| ||
                                CGACGAA CGG    GGTC GA
                                    T  GGTC_   C
GAM144  LOC90371  3'  GCTGCTTGGGTTGTCCAGGCT  3234        CCGAGA    A
                                GCTGCTTG     TCCAG CT
                                ||||||||     ||||| ||
                                CGACGAAC     AGGTC GA
                                     CCAAC_    C
GAM145  NEB      3'  AGAGGTTTTATTAGTTGCTGGT 3237      AA       AC___
           TTGT                   GGA  TTTTATTAGT    GTTTGT
                                ||| ||||||||||    ||||||
                                TCT  AAAATAATCA    CAAACA
                                  CC        ACGAC
GAM145  COLEC12   3'  AGGAGTTTTTATTAGTAC    3238      AA
                                AGGA  TTTTATTAGTAC
                                ||||  ||||||||||||
                                TCCT  AAAATAATCATG
                                  CA
GAM145  COLEC12   3'  AGGAGTTTTTATTAGTAC    3238      AA
                                AGGA  TTTTATTAGTAC
                                ||||  ||||||||||||
                                TCCT  AAAATAATCATG
                                  CA
GAM145  LOC147632 5'  GGAAGTTTTATTAGCACAT    3239      A
                                GGAA TTTTATTAGTACGT
                                |||| |||||||||||||
                                CCTT AAAATAATCGTGTA
                                  C
GAM146  ATP2A3    3'  TCCGGCGGGACCCGGTGGGCA  3242     TTT  AT  A
                                TCC   GT  GA CCCGGTGGGCA
                                |||   ||  || ||||||||||
                                AGG   CG  CT GGGCCACCCGT
                                  C__  CC  _
GAM146  DPYSL2    3'  TCCCTGTATGAGCTTGGTGGG  3243       T     ACCC
                                TCCTT GTATGA    GGTGGG
                                ||||| ||||||    ||||||
                                AGGGA CATACT    CCACCC
                                   _     CGAA
GAM146  RAB36     3'  CCCTGGAGCTGAGCCCGGTGGG 3244      TTGTA   A
                                TCCT    TGA CCCGGTGGG
                                ||||    ||| |||||||||
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                                GGGA    ACT GGGCCACCC
                                  CCTCG   C
GAM146  C20orf100 3'  CTTTGGGCTGGTGGTGGGCA  3245      TA_  AACCC
                                CTTTG  TG    GGTGGGCA
                                |||||  ||    ||||||||
                                GAAAC  AC    CCACCCGT
                                   CCG  CA___
GAM146  CEACAM8  3'  TCCTTCTGTGTTTTGGTGGGCA 3246       GTA  AACCC
                                TCCTTT  TG    GGTGGGCA
                                ||||||  ||    ||||||||
                                AGGAAG  AC    CCACCCGT
                                   AC_  AAAA_
GAM146  DKFZP566G1424 3'  TCCTTTGTAAGAGTGGTG    3247         T  ACCC
                                TCCTTTGTA GA    GGTG
                                ||||||||| ||    ||||
                                AGGAAACAT CT    CCAC
                                     T  CA__
GAM146  FLJ10244  3'  TCCTTTGTATGATACCATGTA  3248          AC  _
                                TCCTTTGTATGA  CCG GTG
                                ||||||||||||  ||| |||
                                AGGAAACATACT  GGT CAT
                                      AT   A
GAM146  FLJ12985  3'  CTTGTATGAATTCACCTGTG  3249         C___  G
                                TTTGTATGAA    CC GTG
                                |||||||||    || |||
                                GAACATACTT    GG CAC
                                     AAGT  A
GAM146  KIAA0157  3'  TCCTCTGTATGAACTCAGC   3250           C
                                TCCTTTGTATGAAC CGGT
                                |||||||||||||| ||||
                                AGGAGACATACTTG GTCG
                                       A
GAM146  MGC2217   5'  TCCTTTGCATGAGTTCCTCGTG 3251          AC_  G_
                                TCCTTTGTATGA   CC  GTG
                                ||||||||||||   ||  |||
                                AGGAAACGTACT   GG  CAC
                                      CAA  AG
GAM146  NAV3     3'  TCCTTTGTGTGTGGTGG     3252        A  AACCC
                                TCCTTTGT TG    GGTGG
                                |||||||| ||    |||||
                                AGGAAACA AC    CCACC
                                    C  A____
GAM146  SPBPBP   5'  CTTTGTATGAGCCTGTA     3253         A  CG
                                CTTTGTATGA CC  GTG
                                |||||||||| ||  |||
                                GAAACATACT GG  CAT
                                      C  A_
GAM146  STAM2    5'  TTTGTATGGGTCAGGC      3254         AACCC  _
                                TTTGTATG    GGT GGGC
                                ||||||||    ||| ||||
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                                AAACATAC    CCA TCCG
                                      _____  G
GAM146  YAP     5'  TCCTTTGTGCTGGGTCCAGAAT 3255        A_ AAC   TGGG
          CA                    TCCTTTGT  TG  CCGG   CA
                                ||||||||  ||  ||||   ||
                                AGGAAACA  AC  GGTC   GT
                                    CG  CCA   TTA_
GAM146  LOC147086 5'  TCTTTTGTATAGGGTCTATCAG 3256    C      AACCCGG_
          GCA                   TC TTTGTATG      TGGGCA
                                || ||||||||      ||||||
                                AG AAACATAT      GTCCGT
                                 A      CCCAGATA
GAM146  LOC153196 5'  TCTGTGGGCCTTGGTGGGCA  3257      ATGAA  C_
                                TTTGT    CC  GGTGGGCA
                                |||||    ||  ||||||||
                                AGACA    GG  CCACCCGT
                                   CCC__  AA
GAM146  LOC166206 5'  CTTTGCTGGTTTGGTGGGCA  3258      A  AACCC
                                CTTTGT TG    GGTGGGCA
                                |||||| ||    ||||||||
                                GAAACG AC    CCACCCGT
                                   _ CAAA_
GAM146  LOC202309 5'  TTTGGTTAAATGGTGGGCA   3259     TA   CCC
                                TTTG  TGAA   GGTGGGCA
                                ||||  ||||   ||||||||
                                AAAC  ATTT   CCACCCGT
                                  CA   A__
GAM146  LOC254778 3'  CTTTGTATCAACATATGGCA  3260       G  CCG   G
                                CTTTGTAT AAC   GTGG CA
                                |||||||| |||   |||| ||
                                GAAACATA TTG   TACC GT
                                    G  TA_   _
GAM146  LOC255624 3'  CTTGTATGAATTCACCTGTG  3249        C___  G
                                TTTGTATGAA    CC GTG
                                ||||||||||    || |||
                                GAACATACTT    GG CAC
                                      AAGT  A
GAM147  EXO1    3'  CAGGGACTTCAAATTGATCAGA 3263     C   GTA  TCA__
          TT                    CAG GGAC   CA    ATCAGATT
                                ||| ||||   ||    ||||||||
                                GTC CCTG   GT    TAGTCTAA
                                  _   AA_  TTAAC
GAM147  EXO1    3'  CAGGGACTTCAAATTGATCAGA 3263     C   GTA  TCA__
          TT                    CAG GGAC   CA    ATCAGATT
                                ||| ||||   ||    ||||||||
                                GTC CCTG   GT    TAGTCTAA
                                  _   AA_  TTAAC
GAM147  EXO1    3'  CAGGGACTTCAAATTGATCAGA 3263     C   GTA  TCA__
          TT                    CAG GGAC   CA    ATCAGATT
                                ||| ||||   ||    ||||||||
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                                GTC CCTG   GT     TAGTCTAA
                                  _    AA_  TTAAC
GAM147  P2RX4     3'  AGTGGAGACTCAATCAGATT   3264     C   CGT  A
                                AG GGA   AC TCAATCAGATT
                                || |||   || ||||||||||
                                TC CCT   TG AGTTAGTCTAA
                                 A   C__  _
GAM147  DKFZP434L1717 3'  AGCAGATGAATATAATCAGATT 3265        CGTACATC
                                AGCGGA       AATCAGATT
                                ||||||       |||||||||
                                TCGTCT       TTAGTCTAA
                                   ACTTATA_
GAM147  LOC132660 5'  GCTATGACGTCGATCAGATT   3266     G__    ACATCA
                                GC   GACGT     ATCAGATT
                                ||   |||||     ||||||||
                                CG   CTGCA     TAGTCTAA
                                 ATA    GC_____
GAM147  LOC200933 3'  GCTGGGTGTCCCTAATCAGATT 3267     _  AC  ACATC
                                GC GG  GT     AATCAGATT
                                || ||  ||     |||||||||
                                CG CC  CA     TTAGTCTAA
                                 A  CA  GGGA_
GAM148  COG3      3'  TCACGTACTTACTGTACAATA  3270       C   CC  AAC
                                TCACG TAC  TA   GTACAATA
                                ||||| |||  ||   ||||||||
                                AGTGC ATG  AT   CATGTTAT
                                   _   A_  GA_
GAM148  CRKL      3'  GCTACTCTTTGCACAATA    3271       C  AAAC
                                GCTAC CT    GTACAATA
                                ||||| ||    ||||||||
                                CGATG GA    CGTGTTAT
                                   A  AA__
GAM148  G6PT1     5'  TCACGCTACCCAGGACACGC   3272           TAA__
                                TCACGCTACCC     ACGT
                                ||||||||||     ||||
                                AGTGCGATGGG     TGCG
                                       TCCTG
GAM148  PPP3CA    3'  GCGACTGTAAACGTACAATA   3273     T  CC
                                GC AC  TAAACGTACAATA
                                || ||  ||||||||||||||
                                CG TG  ATTTGCATGTTAT
                                 C  AC
GAM148  SEC22L1   3'  TCACTTACCCTAAAGCA     3274       GC       C
                                TCAC  TACCCTAAA GTA
                                ||||  ||||||||| |||
                                AGTG  ATGGGATTT CGT
                                  A_        _
GAM148  SP3       3'  ACACTTTAAACGTACAATA   3275       ACCC
                                ACGCT    TAAACGTACAATA
                                |||||    ||||||||||||||
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                                TGTGA   ATTTGCATGTTAT
                                  A___
GAM148  KIAA0889  3'  ACCACCTAAACGTACAATA   3276       C
                                GCTACC TAAACGTACAATA
                                |||||| ||||||||||||
                                TGGTGG ATTTGCATGTTAT
                                  _
GAM148  RES4-25   5'  CGCTACCCTAAGACACGT    3277          ___
                                CGCTACCCTAA   ACGT
                                ||||||||||   ||||
                                GCGATGGGATT   TGCA
                                      CTG
GAM148  LOC257471 3'  ACACTTTAAACGTACAATA   3275       ACCC
                                ACGCT   TAAACGTACAATA
                                |||||   ||||||||||||
                                TGTGA   ATTTGCATGTTAT
                                  A___
GAM148  LOC90072  3'  ACCACCTAAACGTACAATA   3276       C
                                GCTACC TAAACGTACAATA
                                |||||| ||||||||||||
                                TGGTGG ATTTGCATGTTAT
                                  _
GAM149  LRRC2     3'  TTCGTCATGATGTCCAAGCTGT 3280      C      _  CGAT
                                TTC TCATGATG CCG   TTGT
                                ||| |||||||| |||   ||||
                                AAG AGTACTAC GGT   GACA
                                  C       A  TC__
GAM149  HB-1      3'  TTCTTCATGCTCAGCAATTTGT 3281      C    ATGCC
            C                    TTC TCATG    GCGATTTGTC
                                ||| |||||    ||||||||||
                                AAG AGTAC    CGTTAAACAG
                                  A    GAGT_
GAM149  SP140     3'  TTCCTTTTGAGGATTTGT    3282       CA   TGCCGC
                                TTCCT  TGA     GATTTGT
                                |||||  |||     |||||||
                                AAGGA  ACT     CTAAACA
                                  AA   C_____
GAM149  LOC149351 5'  TTCCTCATGGGCCTGACTTGTC 3283         AT   GC
                                TTCCTCATG  GCC  GATTTGTC
                                |||||||||  |||  ||||||||
                                AAGGAGTAC  CGG  CTGAACAG
                                     C_   A_
GAM149  LOC221288 3'  CTCATGATCCTGAAACAATGT  3284        G  GC  TT___
                                CTCATGAT CC  GA    TGT
                                |||||||| ||  ||    |||
                                GAGTACTA GG  CT    ACA
                                     _ A_  TTGTT
GAM149  LOC64102  5'  CTCCTGTGCTGCGATTTGT   3285      A  A   C
                                CTC TG TGC GCGATTTGT
                                ||| || ||| |||||||||
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                                GAG AC ACG CGCTAAACA
                                  G _  A
GAM149  LOC90509  5'  CTCATATCAGATTTGT     3286       ATGC  C
                                CTCATG   CG GATTTGT
                                ||||||   || |||||||
                                GAGTAT   GT CTAAACA
                                   A___  _
GAM150  D12S2489E 3'  TTGGAGAATCATGCATGT    3289      C       AAGG
                                TTGG AGAATCATG   GT
                                |||| |||||||||   ||
                                AACC TCTTAGTAC   CA
                                  _       GTA_
GAM150  DGKA      3'  TTGGAGGCCAAGGGTG      3290      C  AA   TGA
                                TTGG AG  TCA   AGGGTG
                                |||| ||  |||   ||||||
                                AACC TC  GGT   TCCCAC
                                  _ C_  ___
GAM150  DRD2      3'  CTGGCAGAGTGAGGGTG     3291        ATCA   A
                                TTGGCAGA   TGA GGGTG
                                ||||||||   ||| |||||
                                GACCGTCT   ACT CCCAC
                                     C___  _
GAM150  NORE1     3'  TTGGCAGAATCTGTGGT     3292          A  AAG
                                TTGGCAGAATC TG   GGT
                                |||||||||| ||   |||
                                AACCGTCTTAG AC   CCA
                                       _ A__
GAM150  OGT       5'  TTGACAGAATTGTGGCTAT   3293         CA  AA  G
                                TTGGCAGAAT  TG  GG TGT
                                |||||||||  ||  || |||
                                AACTGTCTTA  AC  CC ATA
                                     __  A_  G
GAM150  PHKB      3'  TTGGCATAATCATGAGAAC   3294       G      A GG
                                TTGGCA AATCATGA G  T
                                |||||| |||||||| |  |
                                AACCGT TTAGTACT C  G
                                   A       _ TT
GAM150  SCN3A     3'  TTGGTGAATCATGCACTAGT  3295      CA      AAG_
                                TTGG  GAATCATG   GGT
                                ||||  ||||||||   |||
                                AACC  CTTAGTAC   TCA
                                  A_      GTGA
GAM150  DGKD      3'  CTGGCAGAGCCACGGGGTGT  3296        AT   AA
                                TTGGCAGA  CATG  GGGTGT
                                ||||||||  ||||  ||||||
                                GACCGTCT  GTGC  CCCACA
                                     CG   __
GAM150  FLJ10900  3'  TTGGAGAATCACAGTGGTGT  3297      C       AAG
                                TTGG AGAATCATG   GGTGT
                                |||| |||||||||   |||||
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                                AACC TCTTAGTGT   CCACA
                                  _       CA_
GAM150  FYCO1    3'  TTGGCAGAGCATCCCTTTGGGT 3298         __  ATGAA
            GT                   TTGGCAGA  ATC    GGGTGT
                                 ||||||||  |||    ||||||
                                 AACCGTCT  TAG    CCCACA
                                     CG   GGAAA
GAM150  MGC15396 3'  TTGGCAGAATGATGTTAGT   3299          C  AAG
                                 TTGGCAGAAT ATG   GGT
                                 ||||||||||| |||   |||
                                 AACCGTCTTA TAC   TCA
                                       C   AA_
GAM150  PIF1     3'  TTGGTTAGGCTCTGAAGGGTGT 3300      C_  AA  A
                                 TTGG  AG  TC TGAAGGGTGT
                                 ||||  ||  || ||||||||||
                                 AACC  TC  AG ACTTCCCACA
                                   AA  CG  _
GAM150  PME-1    3'  TTGGCAGAATACATGAAAAGGT 3301          _       T
                                 TTGGCAGAAT CATGAAGGG GT
                                 |||||||||| ||||||||| ||
                                 AACCGTCTTA GTACTTTTC CA
                                       T       _
GAM150  SEMA4G   3'  TGGGGAAAAAGGGTGT     3302     CA   TCAT
                                 TGG  GAA   GAAGGGTGT
                                 |||  |||   |||||||||
                                 ACC  CTT   TTTCCCACA
                                   C_  _____
GAM150  SH3BGRL  3'  TGGCAGAAGGAGGGAAGGGTGT 3303        TCAT_
                                 TGGCAGAA    GAAGGGTGT
                                 ||||||||    |||||||||
                                 ACCGTCTT    CTTCCCACA
                                     CCTCC
GAM150  LOC145921 3'  TTGGCAGAGCCATGTTGGT   3304        AT   AAG
                                 TTGGCAGA  CATG   GGT
                                 ||||||||  ||||   |||
                                 AACCGTCT  GTAC   CCA
                                     CG    AA_
GAM150  LOC152286 3'  TTGGCAAATCATGCTTG     3305        A    AAGGG
                                 TTGGCAGA TCATG    TG
                                 |||||||| |||||    ||
                                 AACCGTTT AGTAC    AC
                                     _    GA___
GAM150  LOC154761 3'  TTGACACCTGAAGGGTG     3306       GAA  A
                                 TTGGCA   TC TGAAGGGTG
                                 ||||||   || |||||||||
                                 AACTGT   GG ACTTCCCAC
                                      ___  _
GAM150  LOC170221 3'  TTGGAGGTACGAAGGGTGT   3307      C  AATC
                                 TTGG AG   ATGAAGGGTGT
                                 |||| ||   ||||||||||
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                                AACC TC    TGCTTCCCACA
                                  _ CA__
GAM150  LOC201229 3'  TTGGCAGACTGCTGGGTGT   3308        ATCA  AA
                                TTGGCAGA   TG  GGGTGT
                                ||||||||   ||  ||||||
                                AACCGTCT   AC  CCCACA
                                    G___  GA
GAM150  LOC51145  3'  TTGGAGAATTATGAAAGGT   3309      C    C
                                TTGG AGAAT ATGAAGGGT
                                |||| ||||| |||||||||
                                AACC TCTTA TACTTTCCA
                                  _    A
GAM150  LOC90594  3'  TTGGCAGAATAAAAGTG     3310         CATG
                                TTGGCAGAAT   AAGGGTG
                                ||||||||||   |||||||
                                AACCGTCTTA   TTTTCAC

                                     _____
GAM151  CEACAM1   3'  TGGTTTTCTTCTCTTTGCTAGT 3313     CTTG  G  GC
                                TGG   CTT CTT  TTGCTAGT
                                |||   ||| |||  ||||||||
                                ACC   GAA GAG  AACGATCA
                                  AAAA  _  A_
GAM151  DMRT2     3'  TGGATTTGTTTGCTTGCTTGCT 3314     C_  C
                                TGG  TTG TTGCTTGCTTGCT
                                |||  ||| ||||||||||||
                                ACC  AAC AACGAACGAACGA
                                  TA  A
GAM151  KIAA1084  3'  TGGCTTGCTTTTCTGGCTTGCT 3315         G_ T     A
            GGT                   TGGCTTGCTT  CT GCTTGCT GT
                                ||||||||||  || ||||||| ||
                                ACCGAACGAA  GA CGAACGA CA
                                     AA  C      C
GAM151  NRN1      3'  TGGCTGTGCTTGCTTGCTCACT 3316       _         TG
                                TGGCT TGCTTGCTTGCT  CT
                                ||||| ||||||||||||  ||
                                ACCGA ACGAACGAACGA  GA
                                   C          GT
GAM151  LOC126669 3'  TGGTTTTTTGTTTGCTTGCTTG 3317     C___  C
                                TGG   TTG TTGCTTGCTTG
                                |||   ||| ||||||||||
                                ACC   AAC AACGAACGAAC
                                  AAAA  A
GAM151  LOC219347 3'  TGCCTTGCTTGCTGCCT     3318     G        T
                                TG CTTGCTTGCT GCTT
                                || |||||||||| ||||
                                AC GAACGAACGA CGGA
                                 G        _
GAM152  BTEB1     3'  TGTTTTGTGACATTTTAAAACA 3321         ATTAGG
            G                    TGTTTTGTGG     TAAAACAG
                                ||||||||||     ||||||||
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                                ACAAAACACT     ATTTTGTC
                                     GTAAA_
GAM152  FLOT2    3'  TGTTCTGTGGGATTAAAAC   3322          ATTAGG
                                TGTTTTGTGG     TAAAAC
                                ||||||||||     ||||||
                                ACAAGACACC     ATTTTG
                                     CTA___
GAM152  GNRHR    5'  TGTTTTGTGTATTGGTAATCCA 3323          G   A    ___
          ACAG                     TGTTTTGTG ATT GGTAA   AACAG
                                ||||||||| ||| |||||   |||||
                                ACAAAACAC TAA CCATT   TTGTC
                                     A   _    AGG
GAM152  DKFZp434F1719 3'  TGTTTTGTGAGGTTGTACA   3324          GATT    AAA
                                TGTTTTGTG    AGGT   ACA
                                |||||||||    ||||   |||
                                ACAAAACAC    TCCA   TGT
                                     _____    ACA
GAM152  KIAA1463  3'  TGTTTAGTGGATCATTAAAA   3325       T       GG
                                TGTTT GTGGATTA  TAAAA
                                ||||| ||||||||  |||||
                                ACAAA CACCTAGT  ATTTT
                                   T       A_
GAM152  KIAA1573  3'  TATTTTGTGGAGTGGGGCA   3326          TTA_
                                TGTTTTGTGGA    GGTA
                                ||||||||||    ||||
                                ATAAAACACCT    CCGT
                                      CACC
GAM152  KIAA1915  3'  TGTTTTGTGAGCACAAAACAG  3327          ATTAGG
                                TGTTTTGTGG     TAAAACAG
                                ||||||||||     ||||||||
                                ACAAAACACT     GTTTTGTC
                                     CGT___
GAM152  MGC13057  5'  TGTTTGTGGAGGAAGCA     3328       T    TT
                                TGTTT GTGGA  AGGTA
                                ||||| |||||  |||||
                                ACAAA CACCT  TTCGT
                                   _    CC
GAM152  TAF2     3'  TGTTTTGGGGAGGAAACA    3329        T  ATT   TA
                                TGTTTTG GG   AGG  AAACA
                                ||||||| ||   |||  |||||
                                ACAAAAC CC   TCC  TTTGT
                                   _ C__   __
GAM152  TMLHE    3'  TGTTTTGTGGGATGGGATAA  3330          _  TA
                                TGTTTTGTGG AT  GGTAA
                                |||||||||| ||  |||||
                                ACAAAACACC TA  CTATT
                                      C  CC
GAM152  TRIP-Br2  3'  GTTTTGGGGTAAAAC       3331        T  ATTAG
                                GTTTTG GG    GTAAAAC
                                |||||| ||    |||||||
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                                CAAAAC CC     CATTTTG
                                  _ ______
GAM152  LOC146733 5'  TGTTTGGTGGATTAGAACA   3332        T         TAAA
                                TGTTT GTGGATTAGG    ACA
                                ||||| ||||||||||    |||
                                ACAAA CACCTAATCT    TGT
                                   C         _____
GAM152  LOC149913 3'  TGTGTTGTGGAAGAAC      3333      T      TT   TAAA
                                TGT TTGTGGA  AGG    AC
                                ||| |||||||  |||    ||
                                ACA AACACCT  TCT    TG
                                  C      __  _____
GAM152  LOC166983 5'  TGTTTTGTGGTTGTCACGGT  3334           A__   _
                                TGTTTTGTGG   TTA GGT
                                ||||||||||   ||| |||
                                ACAAAACACC   AGT CCA
                                      AAC   G
GAM152  LOC200301 5'  TGTTTTGTGGGCTAGAGT    3335           AT   _
                                TGTTTTGTGG  TAG GT
                                ||||||||||  ||| ||
                                ACAAAACACC  ATC CA
                                      CG   T
GAM152  LOC51064  3'  TATTTTGTGGGAAAGCA     3336           ATT
                                TGTTTTGTGG   AGGTA
                                ||||||||||   |||||
                                ATAAAACACC   TTCGT
                                      CT_
GAM152  LOC51145  3'  TGGTTTCAGGTAAGACAG    3337      A_       A
                                TGG  TTAGGTAA ACAG
                                |||  |||||||| ||||
                                ACC  AGTCCATT TGTC
                                  AA       C
GAM153  ADCY7     3'  TAAAGGAAAGAAGAGATGC   3340           T__
                                TAAAGGAAGGA   GGTGC
                                ||||||||||   |||||
                                ATTTCCTTTCT   CTACG
                                       TCT
GAM153  AP1G1     3'  TAAAGAATGAGAATGGTGC   3341         __
                                TAAAGGA  AGGATGGTGC
                                |||||||  ||||||||||
                                ATTTCTT  TCTTACCACG
                                    AC
GAM153  CDK2AP1   3'  TAAAGGGAGACAATGGTG    3342        A  __
                                TAAAGG AG  GATGGTG
                                ||||||  ||  |||||||
                                ATTTCC TC  TTACCAC
                                    C  TG
GAM153  GAB2      3'  TAAAGGACAGGAAGAGGC    3343         _   T  T
                                TAAAGGA AGGA GG GC
                                ||||||| |||| || ||
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                                ATTTCCT TCCT CT CG
                                    G   T  C
GAM153  KCNS2    3'  TAAAAGAAACCTGGGTGC    3344        GA  _
                                TAAAGGAAG  TGG TGC
                                |||||||||  ||| |||
                                ATTTTCTTT  ACC ACG
                                     GG   C
GAM153  UBE2V1   3'  TAAAGGAACCAGGGGTGC    3346       ___  AT
                                TAAAGGA   AGG  GGTGC
                                |||||||   |||  |||||
                                ATTTCCT   TCC  CCACG
                                    TGG  __
GAM153  UBE2V1   3'  TAAAGGAACCAGGGGTGC    3346       ___  AT
                                TAAAGGA   AGG  GGTGC
                                |||||||   |||  |||||
                                ATTTCCT   TCC  CCACG
                                    TGG  __
GAM153  UBE2V1   3'  TAAAGAAACCAGGGGTGC    3345       ___  AT
                                TAAAGGA   AGG  GGTGC
                                |||||||   |||  |||||
                                ATTTCTT   TCC  CCACG
                                    TGG  __
GAM153  USH3A    3'  TAAAGAAAAAAGCCTGGTG   3347         ___
                                TAAAGGAAGGA   TGGTG
                                ||||||||||   |||||
                                ATTTCTTTTTT   ACCAC
                                      CGG
GAM153  C19orf7  3'  AAAAGACAGTGATGGTGC    3348       _ _
                                AAAGGA AG GATGGTGC
                                ||||||  ||  ||||||||
                                TTTTCT TC CTACCACG
                                   G  A
GAM153  PB1      3'  TAAAAGAAACGTAATGGTG   3349        ___
                                TAAAGGAAG   GATGGTG
                                |||||||||   |||||||
                                ATTTTCTTT   TTACCAC
                                      GCA
GAM153  SEC61A1  3'  TAAGGGAAAACAATGGTG    3350     A   __
                                TAA GGAAG  GATGGTG
                                |||  |||||  |||||||
                                ATT CCTTT  TTACCAC
                                  C    TG
GAM153  STAT2    3'  TAAAGGAAAGAAGAAAGC    3351         T  T_
                                TAAAGGAAGGA GG  GC
                                ||||||||||| ||  ||
                                ATTTCCTTTCT CT  CG
                                      T  TT
GAM153  UBCE7IP5 3'  TAAAGGAAAGGAATGTGC    3352        _  TG
                                TAAAGGAA GGA  GTGC
                                ||||||||  |||  ||||
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                                ATTTCCTT CCT  CACG
                                     T   TA
GAM153   LOC144308 3'  AAAGGAACGGAACATGGTGC   3353        _  ___
                                AAAGGAA GGA   TGGTGC
                                ||||||| |||   ||||||
                                TTTCCTT CCT   ACCACG
                                    G   TGT
GAM153   LOC146784 5'  TAAAGAAACAGGAAATGGTG   3354        __   __
                                TAAAGGA  AGGA  TGGTG
                                |||||||  ||||  |||||
                                ATTTCTT  TCCT  ACCAC
                                    TG    TT
GAM153   LOC148760 3'  TAAAGGAAGAACATTTGC    3355           GG_
                                TAAAGGAAGGAT   TGC
                                ||||||||||||   |||
                                ATTTCCTTCTTG   ACG
                                       TAA
GAM153   LOC195977 3'  AAGAGAAGGACATGTGGTGC   3356     _    ____
                                AAG GAAGGA    TGGTGC
                                ||| ||||||    ||||||
                                TTC CTTCCT    ACCACG
                                  T     GTAC
GAM153   LOC254266 5'  CAAAGGATGGACTTGGTG    3357        A  __
                                TAAAGGA GGA  TGGTG
                                ||||||| |||  |||||
                                GTTTCCT CCT  ACCAC
                                    A   GA
GAM153   LOC56961  5'  CAAAGGAAGGGTGGGTGC    3358          AT_
                                TAAAGGAAGG   GGTGC
                                ||||||||||   |||||
                                GTTTCCTTCC   CCACG
                                      CAC
GAM154   IL10RA    3'  TGAGTTATGACCAATACAA   3361        G     _
                                TGAGTTA TGGCCAA GCAA
                                ||||||| ||||||| ||||
                                ACTCAAT ACTGGTT TGTT
                                    _      A
GAM154   MAK       3'  TGAGTCAGTGGTCAGCA     3362          CCA
                                TGAGTTAGTGG   AGCA
                                ||||||||||   ||||
                                ACTCAGTCACC   TCGT
                                      AG_
GAM154   NEDD4     3'  TGAGTTAGTTGGCTAGAAATA  3363        _  CA  C
                                TGAGTTAGT GGC  AG AATA
                                ||||||||| |||  || ||||
                                ACTCAATCA CCG  TC TTAT
                                      A   A_  T
GAM154   TNFSF4    3'  AGTTAGTGGCTAAGTCAA    3364          C  _
                                AGTTAGTGGC AAG CAA
                                |||||||||| ||| |||
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                                TCAATCACCG TTC GTT
                                     A  A
GAM154  BLP2     3'  TGTAGTTTGACTTGGGCAATAC 3365    _   AG   CAA_
           AA                    TG AGTT  TGGC   GCAATACAA
                                 || ||||  ||||   |||||||||
                                 AC TCAA  ACTG   CGTTATGTT
                                  A   __   AACC
GAM154  BLP2     3'  TGTAGTTTGACTTGGGCAATAC 3365    _   AG   CAA_
           AA                    TG AGTT  TGGC   GCAATACAA
                                 || ||||  ||||   |||||||||
                                 AC TCAA  ACTG   CGTTATGTT
                                  A   __   AACC
GAM154  C20orf42 3'  TGGGTCAGTGGTCATCTTGGCA 3366    A      C  A____
                                 TG GTTAGTGG CA    GCA
                                 || |||||||| ||    |||
                                 AC CAGTCACC GT    CGT
                                  C       A  AGAAC
GAM154  CPR2     3'  TGGGTGAGTGGCCAAGCA   3367    A  T
                                 TG GT AGTGGCCAAGCA
                                 || || ||||||||||||
                                 AC CA TCACCGGTTCGT
                                  C  C
GAM154  DKFZP434I0714 3'  TGGATTAATAAGCAATACA   3368    AG    GCCA
                                 TG  TTAGTG   AGCAATACA
                                 ||  ||||||   |||||||||
                                 AC  AATTAT   TCGTTATGT
                                  CT    _____
GAM154  FLJ13310 3'  TGAGCTAGTGGCTCCCACATAC 3369          CAA_  A
           A                     TGAGTTAGTGGC   GCA TACA
                                 ||||||||||||   ||| ||||
                                 ACTCGATCACCG   TGT ATGT
                                       AGGG  _
GAM154  KIAA1229 3'  TGAGCTAGGCTGGGCAGTACAA 3370       GT   CAA   A
                                 TGAGTTA  GGC   GCA TACAA
                                 |||||||  |||   ||| |||||
                                 ACTCGAT  CCG   CGT ATGTT
                                     __   ACC   C
GAM154  MGC2560  3'  TGAGGTAGAAGTCAAGCAATA  3371     T   T  C
                                 TGAG TAG GG CAAGCAATA
                                 |||| ||| || |||||||||
                                 ACTC ATC TC GTTCGTTAT
                                   C   T  A
GAM154  PRO2900  3'  TGGGTCAGTGGCCAGCA    3372    A       A
                                 TG GTTAGTGGCCA GCA
                                 || ||||||||||| |||
                                 AC CAGTCACCGGT CGT
                                  C        _
GAM154  LOC144535 3'  TGATTAGTGGTTCCATTGCAA  3373     G     __   A_
                                 TGA TTAGTGG  CCA  GCAA
                                 ||| |||||||  |||  ||||
```

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                                ACT AATCACC  GGT  CGTT
                                  _     AA   AA
GAM154  LOC145258 3'  GAGTTAGGTAAGTAATAC    3374        TGGCC   C
                                GAGTTAG    AAG AATAC
                                |||||||    ||| |||||
                                CTCAATC    TTC TTATG
                                    CA___   A
GAM155  COX6A1    3'  GGATGGGAGACCAGTATACCAG 3377     CGA   AC  _
                                GGA   GGA  ACC GTATACCAG
                                |||   |||  ||| |||||||||
                                CCT   CCT  TGG CATATGGTC
                                  AC_   C_   T
GAM155  CRSP8     3'  GGACGAGGAGCATGCTGCACA  3378         A  CC__
                                GGACGAGGA CA    GTATA
                                |||||||||  ||    |||||
                                CCTGCTCCT GT    CGTGT
                                     C  ACGA
GAM155  CXCL16    3'  GGGGAGGAACAACTGGTGTAC  3379     AC       CC__  A
                                GG  GAGGAACA    GT TAC
                                ||  ||||||||    || |||
                                CC  CTCCTTGT    CA ATG
                                 C_       TGAC  C
GAM155  SCNN1B    3'  GGACGAGGGTAGGAACCA    3380        AACACC   T__
                                GGACGAGG     GTA   ACCA
                                ||||||||     |||   ||||
                                CCTGCTCC     CAT   TGGT
                                     _______  CCT
GAM155  SLC21A3   3'  GGAAGGGGAACATCACACACCA 3381     CGA     C
           G                     GGA   GGAACA CGTATACCAG
                                |||   |||||| ||||||||||
                                CCT   CCTTGT GTGTGTGGTC
                                  TCC     A
GAM155  C21orf61  3'  GAACGAGGAACGTATGTGTCCA 3382          ACC    A___
           G                     GGACGAGGAAC   GTAT    CCAG
                                ||||||||||   ||||    ||||
                                CTTGCTCCTTG   CATA    GGTC
                                     ___    CACA
GAM155  CST7      3'  GGACAAGGAGCATGCATCC    3383         A  CC    A
                                GGACGAGGA CA  GTAT CC
                                |||||||| ||  |||| ||
                                CCTGTTCCT GT  CGTA GG
                                     C  A_   _
GAM155  FLJ14596  5'  GGACAGGGACACACATACCAG  3384      G   A   C
                                GGAC AGG ACAC GTATACCAG
                                |||| ||| |||| |||||||||
                                CCTG TCC TGTG TGTATGGTC
                                  _  C   _
GAM155  FLJ14668  3'  GGCAGGAACACTGCCA      3385     A G       C TATA
                                GG C AGGAACAC G    CCA
                                || | |||||||| |    |||
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                                CC G TCCTTGTG C    GGT
                                 _ _       A _____
GAM155  HSA250839 3'  GACGAGGAGCACACAATCCAG  3386         A   _  T  A
                                GACGAGGA CAC CG AT CCAG
                                |||||||| ||| || || ||||
                                CTGCTCCT GTG GT TA GGTC
                                     C   T  _  _
GAM155  KIAA0514  5'  GGACGAGGGAGCAATGACCAG  3387         AACAC  TAT
                                GGACGAGG    CG   ACCAG
                                ||||||||    ||   |||||
                                CCTGCTCC    GT   TGGTC
                                     CTC__  TAC
GAM155  KIAA0562  3'  GGCGGGAGGCCCATACCAG   3388     A  A   ACA  G
                                GG CG GGA   CC TATACCAG
                                || || |||   || ||||||||
                                CC GC CCT   GG GTATGGTC
                                 _  _   CC_  _
GAM155  KIAA1190  3'  GGACGAGGACGCTGGAGCCAG  3389         ACAC   ATA__
                                GGACGAGGA   CGT    CCAG
                                |||||||||   |||    ||||
                                CCTGCTCCT   GCG    GGTC
                                     _____  ACCTC
GAM155  MAPK8IP3  3'  GAACGGGGAACACCAGCA    3390       A       _
                                GGACG GGAACACC GTA
                                ||||| |||||||| |||
                                CTTGC CCTTGTGG CGT
                                   C       T
GAM155  MGC11386  3'  GGAGGGGAACATCACACACCAG 3391      CGA     C
                                GGA   GGAACA CGTATACCAG
                                |||   |||||| ||||||||||
                                CCT   CCTTGT GTGTGTGGTC
                                  CC_     A
GAM155  MGC14421  5'  GGCAGGAACACTATCC      3392     A G       CG   A
                                GG C AGGAACAC  TAT CC
                                || | ||||||||  ||| ||
                                CC G TCCTTGTG  ATA GG
                                 _ _       __   _
GAM155  MGC3035   5'  GGACGAGGAAGACAGCAACCAG 3393          C  C   T
                                GGACGAGGAA AC GTA ACCAG
                                |||||||||| || ||| |||||
                                CCTGCTCCTT TG CGT TGGTC
                                     C  T   _
GAM155  OSBPL8    5'  GGACGAAGGGCGCTGCCCAG   3394         AACAC   ATA
                                GGACGAGG    CGT   CCAG
                                ||||||||    |||   ||||
                                CCTGCTTC    GCG   GGTC
                                     CC___   ACG
GAM155  RAB25     3'  GGACAAGGGGCACCAAAAAGCC 3395         AA    TATA_
            AG                    GGACGAGG  CACCG    CCAG
                                ||||||||  |||||    ||||
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                                CCTGTTCC  GTGGT    GGTC
                                    CC    TTTTC
GAM155  STAT2    3'  GGGGAGGAACAGGTACAGCCAG 3396    AC      CC   _
                                GG  GAGGAACA  GTATA CCAG
                                ||  ||||||||  ||||| ||||
                                CC  CTCCTTGT  CATGT GGTC
                                 C_      C_    C
GAM155  LOC119146 5'  GGGAGGAACACGCAGTCC    3397    AC      C  TA
                                GG  GAGGAACAC GTA  CC
                                ||  |||||||||| |||  ||
                                CC  CTCCTTGTG CGT  GG
                                 __       _  CA
GAM155  LOC120864 5'  GGACGAGGATCAAACACAC   3398         A  CCG
                                GGACGAGGA CA   TATAC
                                |||||||||| ||   |||||
                                CCTGCTCCT GT   GTGTG
                                      A  TT_
GAM155  LOC121838 5'  GGAGAGGGGCACACCA     3399     C   AACACC
                                GGA GAGG     GTATACCA
                                ||| ||||     ||||||||
                                CCT CTCC     CGTGTGGT
                                  _   C_____
GAM155  LOC143916 5'  GGAAGGGGAACATCACACACC  3400     CGA    C
                                GGA   GGAACA CGTATACC
                                |||   |||||| ||||||||
                                CCT   CCTTGT GTGTGTGG
                                  TCC     A
GAM155  LOC146733 3'  GGCGGGGAACATCACACACCAG 3401    A  A    C
                                GG CG GGAACA CGTATACCAG
                                || || |||||| ||||||||||
                                CC GC CCTTGT GTGTGTGGTC
                                 _ C     A
GAM155  LOC149950 3'  GGCAAGGAACAGAATAGCCAG  3402    A       CCGT  _
                                GG CGAGGAACA    ATA CCAG
                                || |||||||||    ||| ||||
                                CC GTTCCTTGT    TAT GGTC
                                 _       CT__   C
GAM155  LOC200819 3'  GGTGAGGAACATGGCCCTCAG  3403    AC      CC  ATAC
                                GG  GAGGAACA  GT   CAG
                                ||  ||||||||  ||   |||
                                CC  CTCCTTGT  CG   GTC
                                 A_      AC  GGA_
GAM155  LOC57086  3'  GGAAGGGGAACGTCACACACC  3404     CGA    AC
                                GGA   GGAAC  CGTATACC
                                |||   |||||  ||||||||
                                CCT   CCTTG  GTGTGTGG
                                  TCC    CA
GAM155  LOC93349  3'  GGAGGGGAACACCTCCCAG   3405     CGA      GTATA
                                GGA   GGAACACC    CCAG
                                |||   ||||||||    ||||
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                                CCT  CCTTGTGG   GGTC
                                  CC_      AG___
GAM156  AQP6    3'  GACACCTCACTGCCGCC    3408       AAGGT  _
                                GGCATC    TC CTGCCGCC
                                ||||||    || ||||||||
                                CTGTGG    AG GACGGCGG
                                   _____  T
GAM156  ARD1    5'  AGGCGCAGTCAGCTGCCGCC  3409     ATCAA   C_
                                AGGC    GGTT  CTGCCGCC
                                ||||    ||||  ||||||||
                                TCCG    TCAG  GACGGCGG
                                  CG___   TC
GAM156  BTAF1   5'  GGCATCTGCCCTGCCGCC   3410       AAG  T
                                GGCATC   GT CCTGCCGCC
                                ||||||   || |||||||||
                                CCGTAG   CG GGACGGCGG
                                   A__  _
GAM156  CAPN10  3'  AGGCAAAGTTCCTGCTGCC   3411      TCA       C
                                AGGCA   AGGTTCCTGC GCC
                                |||||   |||||||||| |||
                                TCCGT   TTCAAGGACG CGG
                                  ___        A
GAM156  CHAD    5'  AGGCGCTCGGGTCTGCCGCC  3412     A_  AA   TC
                                AGGC  TC  GGT  CTGCCGCC
                                ||||  ||  |||  ||||||||
                                TCCG  AG  CCA  GACGGCGG
                                  CG  C_  __
GAM156  DTR     5'  GGCACCGTCTGCCGC      3414       AAG  TC
                                GGCATC   GT  CTGCCGC
                                ||||||   ||  |||||||
                                CCGTGG   CA  GACGGCG
                                   ___  __
GAM156  DTR     3'  GGCATGAAGGTCCCTTGC    3413       C       _
                                GGCAT AAGGTTCCT GC
                                ||||| ||||||||| ||
                                CCGTA TTCCAGGGA CG
                                   C       A
GAM156  EVC     5'  GGCGCTCAGGCTGCCGCC    3415     A_   A  TTC
                                GGC  TCA GG   CTGCCGCC
                                |||  ||| ||   ||||||||
                                CCG  AGT CC   GACGGCGG
                                  CG   _ ___
GAM156  FRAP1   5'  AGGCCTCAGCTGCCGC      3416      A   A GTTC
                                AGGC TCA G    CTGCCGC
                                |||| ||| |    |||||||
                                TCCG AGT C    GACGGCG
                                  G   _ _____
GAM156  GYG2    3'  AGGCACAAGGTTCAACAGC   3417       T       CT  C
                                AGGCA CAAGGTTC  GC GC
                                ||||| ||||||||  || ||
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                                TCCGT GTTCCAAG  TG CG
                                  _       T_  T
GAM156  IGF2R    3'  GGCACAAGGTACCGC       3418       T     TCCT
                                GGCA CAAGGT    GCCGC
                                |||| ||||||    |||||
                                CCGT GTTCCA    TGGCG
                                  _     _____
GAM156  KCNN2    5'  AGGCATGGGCTGCTGCC     3419        CAA    C
                                AGGCAT   GGTT CTGCC
                                ||||||   |||| |||||
                                TCCGTA   CCGA GACGG
                                   C__    C
GAM156  KIF1B    3'  AAGCATCCCACCGCCTGCTGCC 3420         AAGGTT    C
                                AGGCATC     CCTGC GCC
                                |||||||     ||||| |||
                                TTCGTAG     GGACG CGG
                                    GGTGGC    A
GAM156  MAN2A2   3'  AGGCTTCAAGGTCTGCC     3421       A      TC
                                AGGC TCAAGGT  CTGCC
                                |||| |||||||  |||||
                                TCCG AGTTCCA  GACGG
                                  A      __
GAM156  MAP3K7IP2 5'  AGCATTTTCCTTTGCCGCC   3422       CAAGG    __
                                GGCAT    TTCCT  GCCGCC
                                |||||    |||||  ||||||
                                TCGTA    AAGGA  CGGCGG
                                   A_____    AA
GAM156  MAPK9    3'  AGGCATCAAGACTGC       3423          TTC
                                AGGCATCAAGG   CTGC
                                ||||||||||   ||||
                                TCCGTAGTTCT   GACG
                                     ___
GAM156  MAPK9    3'  AGGCATCAAGACTGC       3423          TTC
                                AGGCATCAAGG   CTGC
                                ||||||||||   ||||
                                TCCGTAGTTCT   GACG
                                     ___
GAM156  MEN1     5'  AGGCATCAGGTTTGCC      3424         A    CC
                                AGGCATCA GGTT  TGCC
                                |||||||| ||||  ||||
                                TCCGTAGT CCAA  ACGG
                                  _   __
GAM156  NAV2     5'  GGCGCTCAGGGGCTGCCGCC   3425     A_   A  TTC
                                GGC  TCA GG   CTGCCGCC
                                |||  ||| ||   ||||||||
                                CCG  AGT CC   GACGGCGG
                                  CG   C  C__
GAM156  NT5C     3'  AGGCACCAGCACGATGCCGCC  3426         AG  TCC_
                                AGGCATCA  GT    TGCCGCC
                                ||||||||  ||    |||||||
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                                TCCGTGGT CG   ACGGCGG
                                   __ TGCT
GAM156  NUCB1   3' GGTATCAGGGTTCACCG    3427    C   A   CT
                                GG ATCA GGTTC GCCG
                                || |||| ||||| ||||
                                CC TAGT CCAAG TGGC
                                 A   C   __
GAM156  OCLN    5' GGCTCTCGGTTCCTGCCGCC  3428    A AA
                                GGC TC GGTTCCTGCCGCC
                                ||| ||  ||||||||||||
                                CCG AG  CCAAGGACGGCGG
                                  _ AG
GAM156  PDCL    3' AAGCATCAACCCTTCCTGC   3429       GG_
                                AGGCATCAA  TTCCTGC
                                |||||||||  |||||||
                                TTCGTAGTT  AAGGACG
                                     GGG
GAM156  PRDM4   5' AGGCATCAGGGTTTGC     3430       A   CC
                                AGGCATCA GGTT TGC
                                |||||||| ||||  |||
                                TCCGTAGT CCAA ACG
                                    C   __
GAM156  PRKG1   5' GGCTCCTTCCTGCCGC     3431    A AAGG
                                GGC TC   TTCCTGCCGC
                                ||| ||   ||||||||||
                                CCG AG   AAGGACGGCG
                                  _ G___
GAM156  SBF1    5' AGGCATCGGCGAGCCGC    3432       AA  TCCT
                                AGGCATC  GGT   GCCGC
                                |||||||  |||   |||||
                                TCCGTAG  CCG   CGGCG
                                   __  CT__
GAM156  SLA     3' AGGGATCAGGGAACCTCGC  3433    C   A  TT  GC
                                AGG ATCA GG  CCT  CGC
                                ||| |||| ||  |||  |||
                                TCC TAGT CC  GGA  GCG
                                  C   C  TT  __
GAM156  SNL     3' GGCCGTCACGCCCTGCCGC  3434    A_  AG  T
                                GGC  TCA  GT CCTGCCGC
                                |||  |||  || ||||||||
                                CCG  AGT  CG GGACGGCG
                                  GC  G_ _
GAM156  SRGAP1  3' AGGCCTCAGGTGCTTCTTGCTG 3435     A  A  ___  C  C
           CC                   AGGC TCA GGT  TC TGC GCC
                                |||| ||| |||  || ||| |||
                                TCCG AGT CCA  AG ACG CGG
                                  G  _  CGA  A  A
GAM156  TGFBR2  3' GGCAGCTTCCTGCTGCC    3436     TCAA G     C
                                GGCA   G TTCCTGC GCC
                                ||||   | ||||||| |||
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                                CCGT    C AAGGACG CGG
                                  ____ G      A
GAM156  TMC1     5'  AGGCTCAAAGTTGCTGCC    3437       A       C
                                AGGC TCAAGGTT CTGCC
                                |||| |||||||| |||||
                                TCCG AGTTTCAA GACGG
                                  _       C
GAM156  AFAP     3'  GGCAGAGCTTCCTGCCG     3438       TCA  G
                                GGCA   AG TTCCTGCCG
                                ||||   || |||||||||
                                CCGT   TC AAGGACGGC
                                  C__  G
GAM156  ASB10    3'  AGACATCACCCGGCTGCCGC  3439          AGGTTC
                                AGGCATCA     CTGCCGC
                                ||||||||     |||||||
                                TCTGTAGT     GACGGCG
                                     GGGCC_
GAM156  AUH      3'  GGTCATTAAGGTTCCATGTGC 3440     _  C       _  CC
                                GG CAT AAGGTTCC TG  GC
                                || ||| |||||||| ||  ||
                                CC GTA TTCCAAGG AC  CG
                                 A  A       T  A_
GAM156  CDH22    5'  AGGCACCAGGGCGCCGC     3441          A   TCCT
                                AGGCATCA GGT    GCCGC
                                |||||||| |||    |||||
                                TCCGTGGT CCG    CGGCG
                                     C  _____
GAM156  CTRP5    5'  AGGCGCCCCCTGCCCTGCCG  3442       A_  AAG  T
                                AGGC  TC   GT CCTGCCG
                                ||||  ||   || |||||||
                                TCCG  GG   CG GGACGGC
                                  CG  GGA  _
GAM156  DIS3     3'  AGTCATTTTCATCCTGCCGCC 3443     G   CAAGGT
                                AG CAT     TCCTGCCGCC
                                || |||     ||||||||||
                                TC GTA     AGGACGGCGG
                                 A   AAAGT_
GAM156  DKFZp434O0320 3'  AGGTTCAAGGCTTTGCC     3444      CA       CC
                                AGG  TCAAGGTT  TGCC
                                |||  ||||||||  ||||
                                TCC  AGTTCCGA  ACGG
                                  A_       A_
GAM156  DKFZP564A1164 5'  AGGTTCACGAGATTTGCCG   3445      CA  __    CC
                                AGG  TCA  AGGTT  TGCCG
                                |||  |||  |||||  |||||
                                TCC  AGT  TCTAA  ACGGC
                                  A_  GC    __
GAM156  EPI64    3'  AGCCAGGCCTTCCTGCCGCC  3446      ATCA   __
                                GGC    AGGT  TCCTGCCGCC
                                |||    ||||  ||||||||||
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                                TCG   TCCG  AGGACGGCGG
                                  G___   GA
GAM156  ERMAP    3' GGCGTCAAGCCTGCTGCC   3447     A   GTT   C
                                GGC TCAAG   CCTGC GCC
                                ||| |||||   ||||| |||
                                CCG AGTTC   GGACG CGG
                                  C   ___    A
GAM156  FKBP14   3' GGTTCAAGTGATTCTGCCGCC 3448    CA   GTTC_
                                GG  TCAAG    CTGCCGCC
                                ||  |||||    ||||||||
                                CC  AGTTC    GACGGCGG
                                 A_    ACTAA
GAM156  FLJ00001 3' GGCAGCAGCCCCTGCCG    3449     TCAA
                                GGCA   GGTTCCTGCCG
                                ||||   ||||||||||
                                CCGT   TCGGGGACGGC
                                  CG__
GAM156  FLJ10521 3' AGCATCAAGGGCACCTGCC   3450        TT_
                                GGCATCAAGG   CCTGCC
                                ||||||||||   ||||||
                                TCGTAGTTCC   GGACGG
                                     CGT
GAM156  FLJ12270 3' GGCATCAAGAGAACGCTGC   3451        TTCC   C
                                GGCATCAAGG   TGC GC
                                ||||||||||   ||| ||
                                CCGTAGTTCT   GCG CG
                                     CTT_   A
GAM156  FLJ20254 5' GCCCTGCGGTTCCTGCCGCC  3452    ATCAA
                                GC    GGTTCCTGCCGCC
                                ||    ||||||||||||
                                CG    CCAAGGACGGCGG
                                 GGACG
GAM156  FLJ23209 3' GGCTCAAGTGATCTTGCTGC  3453     A   GT_  C   C
                                GGC TCAAG   TC TGC GC
                                ||| |||||   || ||| ||
                                CCG AGTTC   AG ACG CG
                                  _    ACT  A   A
GAM156  FLJ23259 5' AGACATCTTCCTGTTGC     3454       AAGG    CC
                                AGGCATC    TTCCTG  GC
                                |||||||    ||||||  ||
                                TCTGTAG    AAGGAC  CG
                                    ____     AA
GAM156  FLJ31951 3' AAGCATCATTCCTGCTGC    3455        AGG     C
                                AGGCATCA   TTCCTGC GC
                                ||||||||   ||||||| ||
                                TTCGTAGT   AAGGACG CG
                                    ___      A
GAM156  FYCO1    3' AGCCATCAAGGGGCTGCC    3456    G      TTC
                                AG CATCAAGG   CTGCC
                                || ||||||||   |||||
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                                TC GTAGTTCC   GACGG
                                 G       CC_
GAM156  HS6ST    3' GGCACTGCCAGCTGCCGCC   3457       CAAG   C_
                                GGCAT    GTT  CTGCCGCC
                                |||||    |||  ||||||||
                                CCGTG    CGG  GACGGCGG
                                   A___   TC
GAM156  HSPC195  5' AGGCTCAGCCGCCTCTGCCGCC 3458      A   AG_  TC
                                AGGC TCA   GT  CTGCCGCC
                                |||| |||   ||  ||||||||
                                TCCG AGT   CG  GACGGCGG
                                  _  CGG  GA
GAM156  HUMAGCGB 5' GCGTCTCCTCTGCCGCC    3459     A  AAGG  _
                                GC TC    TTC CTGCCGCC
                                || ||    ||| ||||||||
                                CG AG    AGG GACGGCGG
                                 C _____  A
GAM156  KIAA0125 3' AGGCTCAAGGTCCTGCC     3460      A      T
                                AGGC TCAAGGT CCTGCC
                                |||| ||||||| ||||||
                                TCCG AGTTCCA GGACGG
                                  _      _
GAM156  KIAA0275 3' GGCAGTCAAGATGCCGCC    3461       _     TTCC
                                GGCA TCAAGG    TGCCGCC
                                |||| ||||||    |||||||
                                CCGT AGTTCT    ACGGCGG
                                  C     _____
GAM156  KIAA0295 3' AGGCATCAGGATCTGCC     3462         A  TTC
                                AGGCATCA GG   CTGCC
                                |||||||| ||   |||||
                                TCCGTAGT CC   GACGG
                                    _ TA_
GAM156  KIAA0495 5' AGGCGGCAAAGTGCCGC     3463      AT     TCCT
                                AGGC  CAAGGT   GCCGC
                                ||||  ||||||   |||||
                                TCCG  GTTTCA   CGGCG
                                  CC     _____
GAM156  KIAA0677 5' AGGCTCAGCTCCTGC       3464      A   AG
                                AGGC TCA  GTTCCTGC
                                |||| |||  ||||||||
                                TCCG AGT  CGAGGACG
                                  _  __
GAM156  KIAA1010 3' AGCATCAAGGTTTACAACC   3465           CC   C
                                GGCATCAAGGTT  TGC GCC
                                ||||||||||||  ||| |||
                                TCGTAGTTCCAA  ATG TGG
                                       __   T
GAM156  KIAA1061 5' GGCTGCCCTATTTCTGCCGCC 3466     A_  AAG   C
                                GGC  TC   GTT CTGCCGCC
                                |||  ||   ||| ||||||||
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                                CCG  GG   TAA GACGGCGG
                                  AC  GA_   A
GAM156  KIAA1196  3'  GGCATCAAGCTTCTGCTGCC   3467         G   C   C
                                GGCATCAAG TTC TGC GCC
                                ||||||||| ||| ||| |||
                                CCGTAGTTC AAG ACG CGG
                                     G   _   A
GAM156  MGC13090  3'  GGCACCAAGGCCACTGCC    3468           TC
                                GGCATCAAGGT  CTGCC
                                ||||||||||  |||||
                                CCGTGGTTCCG  GACGG
                                      GT
GAM156  PDE8B     3'  AGGCACCAAGGCTTTGC     3469            CC
                                AGGCATCAAGGTT  TGC
                                ||||||||||||  |||
                                TCCGTGGTTCCGA  ACG
                                       A_
GAM156  RIN1      3'  AGGCTCAGGGTCTCCCGCC   3470       A   A   _
                                AGGC TCA GGT TCCTGCC
                                |||| ||| ||| |||||||
                                TCCG AGT CCA AGGGCGG
                                  _  C   G
GAM156  SCAMP-4   3'  GGCGGCCGACCTGCTGCC    3471      ATCAA   __    C
                                GGC    GGTT  CCTGC GCC
                                |||    ||||  ||||| |||
                                CCG    CCGG  GGACG CGG
                                  _____   CT    A
GAM156  SSH3BP1   5'  AGGCAGCAAGGTCCGCC     3472       T     T  T
                                AGGCA CAAGGT CC GCC
                                ||||| |||||| || |||
                                TCCGT GTTCCA GG CGG
                                   C     _  _
GAM156  THEA      3'  GGCATTAAGGTCAGGTTGCC  3473       C     CC__
                                GGCAT AAGGTT   TGCC
                                ||||| ||||||   ||||
                                CCGTA TTCCAG   ACGG
                                   A     TCCA
GAM156  ZNF297B   5'  AGATATCCTCTCTGCCGCC   3474     GC   AAGG   _
                                AG  ATC   TTC CTGCCGCC
                                ||  |||   ||| ||||||||
                                TC  TAG   GAG GACGGCGG
                                 TA  ____   A
GAM156  LOC115051 3'  GGCACTGCCAGCTGCCGCC   3457       CAAG   C_
                                GGCAT   GTT  CTGCCGCC
                                |||||   |||  ||||||||
                                CCGTG   CGG  GACGGCGG
                                   A___   TC
GAM156  LOC130105 3'  AGGCATCAGGCTCTGC      3475         A    C
                                AGGCATCA GGTTC TGC
                                |||||||| ||||| |||
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                                TCCGTAGT CCGAG ACG
                                   _    _
GAM156  LOC134111 3'  GGCATTGAGTTTCCTGCC    3476       CA  G
                                GGCAT  AG TTCCTGCC
                                ||||||  || ||||||||
                                CCGTA  TC AAGGACGG
                                   AC  A
GAM156  LOC135138 3'  AGGTTTCAAGTCCCAGCTGCTG 3477      CA    G   ___  C
          CC                      AGG  TCAAG TTCC   TGC GCC
                                ||| ||||| ||||   ||| |||
                                TCC  AGTTC AGGG   ACG CGG
                                  AA    _   TCG   A
GAM156  LOC144893 3'  AGGCTCAGTTCCTGCTGC    3478      A   AG      C
                                AGGC TCA  GTTCCTGC GC
                                |||| |||  |||||||| ||
                                TCCG AGT  CAAGGACG CG
                                  _  __       A
GAM156  LOC145482 3'  AGACATCAGGCCCGGC      3479        A   T  T
                                AGGCATCA GGT CC GC
                                |||||||| ||| || ||
                                TCTGTAGT CCG GG CG
                                   _  _ C
GAM156  LOC145989 3'  GGCCGTCACACCCTGCCGC   3480     A_   AGGT
                                GGC  TCA   TCCTGCCGC
                                |||  |||   |||||||||
                                CCG  AGT   GGGACGGCG
                                  GC   GT__
GAM156  LOC146159 5'  AGGCACCAGCGGTGCCGC    3481        A_   TCCT
                                AGGCATCA  GGT   GCCGC
                                ||||||||  |||   |||||
                                TCCGTGGT  CCA   CGGCG
                                    CG  ____
GAM156  LOC146774 3'  GGCATCTGGCCGCCGC      3482       AA  TTC
                                GGCATC  GG   CTGCCGC
                                ||||||  ||   |||||||
                                CCGTAG  CC   GGCGGCG
                                   A_ ___
GAM156  LOC147136 3'  AGGCAGTGAGGCCCCCTGCC  3483       TCA     _
                                AGGCA   AGGTTCC TGCC
                                |||||   ||||||| ||||
                                TCCGT   TCCGGGG ACGG
                                   CAC      G
GAM156  LOC147645 5'  AGGCAGCAGGGGCCCCGCC   3484       T  A  TT
                                AGGCA CA GG  CCTGCC
                                ||||| || ||  ||||||
                                TCCGT GT CC  GGGCGG
                                   C  C  CG
GAM156  LOC148231 3'  AGGTTTCAAGGCCCTGCC    3485      CA      T
                                AGG  TCAAGGT CCTGCC
                                |||  ||||||| ||||||
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                                TCC  AGTTCCG GGACGG
                                  AA      _
GAM156  LOC149706 5'  AGGCATCAAGGTCTAGACC   3486           CCT
                                AGGCATCAAGGTT   GCC
                                ||||||||||||   |||
                                TCCGTAGTTCCAG   TGG
                                       ATC
GAM156  LOC157355 3'  AGGTGCAGGGACCTGCCGCC  3487     CATCA   TT
                                AGG    AGG  CCTGCCGCC
                                |||    |||  |||||||||
                                TCC    TCC  GGACGGCGG
                                  ACG__   CT
GAM156  LOC158055 3'  AGGCACCAAGGTCACGC    3488           CC
                                AGGCATCAAGGTT  TGC
                                ||||||||||||  |||
                                TCCGTGGTTCCAG  GCG
                                       T_
GAM156  LOC158318 3'  GGTGTCAAGGCTCTGAGGC   3489     CA       C  CC
                                GG  TCAAGGTTC TG  GC
                                ||  |||||||||  ||  ||
                                CC  AGTTCCGAG AC  CG
                                 AC        _ TC
GAM156  LOC199704 5'  AGGCATCAAGGTTAACAC    3490           CC
                                AGGCATCAAGGTT  TGC
                                ||||||||||||  |||
                                TCCGTAGTTCCAA  GTG
                                       TT
GAM156  LOC200844 5'  GGCGCGCTCCCGCTGCCGCC  3491     ATCAAG     ___
                                GGC     GTTCCT   GCCGCC
                                |||     ||||||   ||||||
                                CCG     CGAGGG   CGGCGG
                                  CG_____     CGA
GAM156  LOC222070 5'  AGGCACCAGATGGCACTGCTGC 3492         A__   TC    C
                                AGGCATCA   GGT  CTGC GC
                                ||||||||   |||  |||| ||
                                TCCGTGGT   CCG  GACG CG
                                     CTA   T_   A
GAM156  LOC253594 5'  AGACATCAAATGCTGCC     3493          GTTC
                                AGGCATCAAG    CTGCC
                                ||||||||||    |||||
                                TCTGTAGTTT    GACGG
                                      AC__
GAM156  LOC255647 5'  AGCACGACTGCCGCC       3494       CAA  TTC
                                GGCAT   GG   CTGCCGCC
                                |||||   ||   ||||||||
                                TCGTG   CT   GACGGCGG
                                   ___  ___
GAM156  LOC255990 5'  AGGATCAGGCCGCCGC      3495      C    A  TTC
                                AGG ATCA GG   CTGCCGC
                                ||| |||| ||   |||||||
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                                TCC TAGT CC   GGCGGCG
                                  _   _ ___
GAM156  LOC257458 5'  AAGCATCCTCTCTGCCGCC   3496        AAGG  _
                                AGGCATC    TTC CTGCCGCC
                                |||||||    ||| ||||||||
                                TTCGTAG    GAG GACGGCGG
                                   ____  A
GAM156  LOC91768  5'  AGGCGCTGGTGCTGCCGCC   3497      ATCAA  TC
                                AGGC    GGT  CTGCCGCC
                                ||||    |||  ||||||||
                                TCCG    CCA  GACGGCGG
                                  CGA__  C_
GAM156  LOC92305  5'  GGCATGGAGTCCCGCCGC    3498      CAA  T_
                                GGCAT   GG  TCCTGCCGC
                                |||||   ||  |||||||||
                                CCGTA   CC  AGGGCGGCG
                                   ___ TC
GAM157  ADCY2     3'  TCTTTCAGATTCAAGGAACA   3501      G        AA
                                TCT TCAGATTCAA  AATA
                                ||| ||||||||||  ||||
                                AGA AGTCTAAGTT  TTGT
                                  A         CC
GAM157  DLG2      5'  TCTGTCAGTTTGAAAATGCATT 3502         A  CA    ATA
           G                     TCTGTCAG TT  AAAA   ATTG
                                |||||||| ||  ||||   ||||
                                AGACAGTC AA  TTTT   TAAC
                                    _ AC    ACG
GAM157  FOXO1A    3'  TCTGTCAGTTACAGGTAATTG  3503         ATT  AAAAA
                                TCTGTCAG   CA    TAATTG
                                ||||||||   ||    ||||||
                                AGACAGTC   GT    ATTAAC
                                    AAT  CC___
GAM157  FAM8A1    3'  TCTGTCAGATTTTAAGAATA   3504           CA  A
                                TCTGTCAGATT  AA AATA
                                ||||||||||  || ||||
                                AGACAGTCTAA  TT TTAT
                                      AA  C
GAM157  FLJ10900  3'  TCTATGCAGTATTTAAAAAATA 3505       _  _  C
           ATTG                   TCTGT CAG ATT AAAAAATAATTG
                                |||||| ||| ||| ||||||||||||
                                AGATA GTC TAA TTTTTTATTAAC
                                   C   A   A
GAM157  LOC120526 3'  TCTGTTAGTTCAAAATATA   3506       C  A      A
                                TCTGT AG TTCAAAA ATA
                                ||||| || ||||||| |||
                                AGACA TC AAGTTTT TAT
                                   A  _      A
GAM157  LOC146901 3'  TCAACAAATTCAAAAGGTAATT 3507     TGT         AA
           G                     TC   CAGATTCAAAA  TAATTG
                                ||   ||||||||||  ||||||
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                                AG  GTTTAAGTTTT  ATTAAC
                                 TT_        CC
GAM157  LOC254778 3'  TCTGCAGATTGGGAATAATTG  3508      T     CAAAA
                                TCTG CAGATT    AATAATTG
                                |||| ||||||    ||||||||
                                AGAC GTCTAA    TTATTAAC
                                  _     CCC__
GAM158  ARF1    5'  GGAAGGACACTGGCCAGGG   3511      A  GTT
                                GGAA GA   TTGGCCAGGG
                                |||| ||   ||||||||||
                                CCTT CT   GACCGGTCCC
                                  C  GT_
GAM158  ASB2    5'  GATGGAGGGAGAGCCAGG    3512    C   AA   TTTT
                                GA GGA  GAG    GGCCAGG
                                || |||  |||    |||||||
                                CT CCT  CTC    TCGGTCC
                                 A   CC  _____
GAM158  E2F3    3'  TGAGGGGAGGAGGCCAGG    3513     C  AAA   TTTT
                                TGA GG   GAG    GGCCAGG
                                ||| ||   |||    |||||||
                                ACT CC   CTC    CCGGTCC
                                  C  ____   CT__
GAM158  EPHB6   3'  GGAGAGGCGGAGGACCAGGG   3514     A  A  TTT  _
                                GGA AG GT   GG CCAGGG
                                ||| || ||   || ||||||
                                CCT TC CG   CC GGTCCC
                                  C  _  CCT  T
GAM158  FEZ1    5'  TGGCGGAGGGAGGCGGATCCCG 3515    A   AA   TTT   __  A
           GG                     TG CGGA  GAG   TGG  CC GGG
                                || ||||  |||   |||  || |||
                                AC GCCT  CTC   GCC  GG CCC
                                 C   CC   C__   TA  G
GAM158  FEZ1    5'  TGGCGGAGGGAGGCGGATCCCG 3515    A   AA   TTT   __  A
           GG                     TG CGGA  GAG   TGG  CC GGG
                                || ||||  |||   |||  || |||
                                AC GCCT  CTC   GCC  GG CCC
                                 C   CC   C__   TA  G
GAM158  HYAL1   5'  CGAGGACAACCTGGCCAGGG   3516     C   AAGAGT
                                TGA GGA     TTTGGCCAGGG
                                ||| |||     ||||||||||
                                GCT CCT     GGACCGGTCCC
                                  _   GTT___
GAM158  MGAT1   3'  GGAAGAGCCAGGTCAGGG    3517      A    TT  C
                                GGAA GAGTT  GG CAGGG
                                |||| |||||  || |||||
                                CCTT CTCGG  CC GTCCC
                                  _    T_  A
GAM158  MKI67   3'  GGAAAGTTCCAGGCAGGG    3518      AA     TG C
                                GGA  GAGTTT  G CAGGG
                                |||  ||||||  | |||||
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                                CCT  TTCAAG  C GTCCC
                                  __     GT C
GAM158  PDE4B    3'  GATGGGAAGCAGGGCCAGGG  3519     C  AAA   TTT
                                GA GG   GAGT   GGCCAGGG
                                || ||   ||||   ||||||||
                                CT CC   TTCG   CCGGTCCC
                                 A  C__    TC_
GAM158  TBX6     5'  CGGTGGGGAGCCCCGGCTAGGG 3520      AAA_        C
                                CGG    GAGTTTTGGC AGGG
                                |||    |||||||||| ||||
                                GCC    CTCGGGGCCG TCCC
                                  ACCC         A
GAM158  TBX6     5'  CGGTGGGGAGCCCCGGCTAGGG 3520      AAA_        C
                                CGG    GAGTTTTGGC AGGG
                                |||    |||||||||| ||||
                                GCC    CTCGGGGCCG TCCC
                                  ACCC         A
GAM158  TEM7     3'  GGTGTAGGTTTGCTTGGCCAGG 3521     AA_  A   ___
              G                  GG   AG GTTT   TGGCCAGGG
                                ||   || ||||   |||||||||
                                CC   TC CAAA   ACCGGTCCC
                                 ACA  _    CGA
GAM158  WSX1     5'  GACGGAAAGTCCCCGGCTGGGG 3522          AG      CA
                                GACGGAAAG  TTTTGGC  GGG
                                |||||||||  |||||||  |||
                                CTGCCTTTC  GGGGCCG  CCC
                                      A_      AC
GAM158  C20orf124 3'  TGACGGACAATGGCCAGG    3523         AAGAGTTT
                                TGACGGA       TGGCCAGG
                                |||||||       ||||||||
                                ACTGCCT       ACCGGTCC
                                    GTT_____
GAM158  CHL1     3'  TGACAGAAGGAGAATATCGGGG 3524          __    T   CCA
                                TGACGGAA  AGAGT TTGG   GG
                                ||||||||  ||||| ||||   ||
                                ACTGTCTT  TCTTA AGCC   CC
                                     CC    T   ___
GAM158  FASTK    3'  TGGCGGGCAAGGTGGCCAGGG  3525     A   AAA   TTT
                                TG CGG   GAG   TGGCCAGGG
                                || |||   |||   |||||||||
                                AC GCC   TTC   ACCGGTCCC
                                 C   CG_   C__
GAM158  FLJ10604  3'  TGGCGGCAAGGGGACCAGG   3526     A   A   AGTTTT
                                TG CGG AAG     GGCCAGG
                                || ||| |||     |||||||
                                AC GCC TTC     CTGGTCC
                                 C   G   CC____
GAM158  FLJ14126  5'  TGAGGGAAAGAAGCTGGG    3527      C      GTTTT   CA
                                TGA GGAAAGA    GGC  GG
                                ||| |||||||    |||  ||
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                                ACT CCTTTCT    TCG  CC
                                  C      _____   AC
GAM158  GAL3ST-4  5' TGACAGAGAGATGGAGCCAGGG 3528        A   GTTTT
                                TGACGGA AGA    GGCCAGGG
                                ||||||| |||    ||||||||
                                ACTGTCT TCT    TCGGTCCC
                                    C   ACC__
GAM158  KIAA0427  3' TGAGGAAGGGGAGGGCCAGGG  3529     C    A__   TTTT
                                TGA GGAA   GAG    GGCCAGGG
                                ||| ||||   |||    ||||||||
                                ACT CCTT   CTC    CCGGTCCC
                                  _    CCC   ____
GAM158  KIAA0980  5' TGAAGGGAAGGTGGGGCCAGGG 3530     C  A   A  TTT
                                TGA GG AAG GT   GGCCAGGG
                                ||| || ||| ||   ||||||||
                                ACT CC TTC CA   CCGGTCCC
                                  T  C   _  CC_
GAM158  KIAA1045  3' GAAAGAGTCCCTGCTCAGGG   3531          TG  _
                                GAAAGAGTTT  GC CAGGG
                                ||||||||||  || |||||
                                CTTTCTCAGG  CG GTCCC
                                     GA  A
GAM158  KIAA1110  3' GGAAAGTGGTGGCCAGGG    3532        AGTTT
                                GGAAAG    TGGCCAGGG
                                ||||||    |||||||||
                                CCTTTC    ACCGGTCCC
                                   ACC__
GAM158  KIAA1199  3' TGAAGGAAAGAGTTTGTGGTTG 3533     C         _  CCA
           GG                     TGA GGAAAGAGTTT TGG   GGG
                                ||| ||||||||||| |||   |||
                                ACT CCTTTCTCAAA ACC   CCC
                                  T         C   AA_
GAM158  KIAA1908  3' TGACTGGGAGGGCCAG      3534      _ AAA   TTTT
                                TGAC GG   GAG    GGCCAG
                                |||| ||   |||    ||||||
                                ACTG CC   CTC    CCGGTC
                                  A  ___   _____
GAM158  MGC3101   3' TGGCGGGTGGAAGTGTGGCCAG 3535     A   AAA_   TT
           GG                     TG CGG    GAGT  TGGCCAGGG
                                || |||    ||||  |||||||||
                                AC GCC    TTCA  ACCGGTCCC
                                 C   CACC    C_
GAM158  MGC32043  3' TGAGGGGAAGAAAGCCAGG   3536     C  A    TTTT
                                TGA GG AAGAG    GGCCAGG
                                ||| || |||||    |||||||
                                ACT CC TTCTT    TCGGTCC
                                  C  C    _____
GAM158  MOST2     5' TGAGGGAGGCTGGCCAGG    3537     C  AAA   TT
                                TGA GG   GAG  TTGGCCAGG
                                ||| ||   |||  |||||||||
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                                ACT CC   CTC  GACCGGTCC
                                  _ ____  C_
GAM158   P450RAI-2 3'  TGGCAGGAAGAGTTTTGTGGGG 3538     A   A        GCCA
                                TG CGG AAGAGTTTTG    GGG
                                || ||| ||||||||||    |||
                                AC GTC TTCTCAAAAC    CCC
                                 C   C         AC__
GAM158   TRIM4    3'  GGAAGGAGTTTTGGTCAGGG   3539       A        C
                                GGAA GAGTTTTGG CAGGG
                                |||| ||||||||| |||||
                                CCTT CTCAAAACC GTCCC
                                  C        A
GAM158   LOC142826 3'  GATGGAATTTTGGTCAGGG    3540     AA        C
                                GA  GAGTTTTGG CAGGG
                                ||  ||||||||| |||||
                                CT  CTTAAAACC GTCCC
                                 AC        A
GAM158   LOC146856 3'  TGAGGGGAGGAAGCCAGG    3541      C  AAA   TTTT
                                TGA GG   GAG    GGCCAGG
                                ||| ||   |||    |||||||
                                ACT CC   CTC    TCGGTCC
                                  C  ____   CT__
GAM158   LOC150273 3'  GATGGAGAGGGGGCCAGG    3542     C   AA   TTTT
                                GA GGA  GAG    GGCCAGG
                                || |||  |||    |||||||
                                CT CCT  CTC    CCGGTCC
                                 A   __   CC__
GAM158   LOC150282 5'  GATAGAGGGTGACTGGCCAGGG 3543     A    TT___
                                GA AGAG     TTGGCCAGGG
                                || ||||     ||||||||||
                                CT TCTC     GACCGGTCCC
                                 A    CCACT
GAM158   LOC157349 5'  TGACGAAGGAGGTGCGAGCCGG 3544         AA   TTTT_   A
            GG                    TGACGGA  GAG     GGCC GGG
                                |||||||  |||     |||| |||
                                ACTGCTT  CTC     TCGG CCC
                                    C_   CACGC    C
GAM158   LOC195977 3'  TGACGGGGGGAGTGACAAAGGG 3545        AAA    TTT   C_
                                TGACGG   GAGT   GGC  AGGG
                                ||||||   ||||   |||  ||||
                                ACTGCC   CTCA   CTG  TCCC
                                   CCC    ___    TT
GAM158   LOC197317 3'  TGAGGGAAGGGTTCCGGCCCGG 3546      C    A A        A
            G                     TGA GGAA G GTTTTGGCC GGG
                                ||| |||| | ||||||||| |||
                                ACT CCTT C CAAGGCCGG CCC
                                  C    _ C        G
GAM158   LOC254181 5'  GGAAGGGTCACAGCCAGGG    3547       A A   T
                                GGAA G GTT TGGCCAGGG
                                |||| | ||| |||||||||
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                                CCTT C CAG GTCGGTCCC
                                  _ C   T
GAM158  LOC257200 3'  GATGGGAAGAGGCCAGG     3548     C  A    GTTTT
                                GA GG AAGA    GGCCAGG
                                || || ||||    |||||||
                                CT CC TTCT    CCGGTCC
                                 A  C   _____
GAM158  LOC90829  5'  GGAAGTTCTGGCCAGGG     3549      AAG
                                GGA   AGTTTTGGCCAGGG
                                |||   ||||||||||||||
                                CCT   TCAAGACCGGTCCC
                                   ___
GAM159  FBXL11    3'  TTGGGGCCTGGAGACCAATGGA 3552      AA       G  T__
            AGTG                   TTG  GCCTGGGGA TA   GAAGTG
                                |||  |||||||||| ||   ||||||
                                AAC  CGGACCTCT GT   CTTCAC
                                  CC        G  TAC
GAM159  GALNT1    3'  TGAAGCATATTTGAGTATGGAG 3553        C  GG_      A
            TG                   TGAAGC TG   GAGTATG AGTG
                                ||||||| ||   ||||||| ||||
                                ACTTCG AT   CTCATAC TCAC
                                   T  AAA      C
GAM159  RGS3      5'  TTGAAGCCCTGGGGAGTCTG   3554         _      A
                                TTGAAGCC TGGGGAGT TG
                                |||||||| |||||||| ||
                                AACTTCGG ACCCCTCA AC
                                     G       G
GAM159  KIAA1600  3'  TCGAAGTTTTCCTTGTATGAAG 3555       _____   GGGGA
            TG                   TGAAG    CCT    GTATGAAGTG
                                |||||    |||    ||||||||||
                                GCTTC    GGA    CATACTTCAC
                                   AAAA   A_____
GAM159  MGC2628   3'  TTGAAGCCTGGGGGTGCAT    3556            A_
                                TTGAAGCCTGGGG  GTAT
                                ||||||||||||  ||||
                                AACTTCGGACCCC  CGTA
                                        CA
GAM159  MGC34869  3'  CTGGAGCCTGGGGAAAGTG    3557      A         TA
                                TTG AGCCTGGGGAG  TG
                                ||| ||||||||||  ||
                                GAC TCGGACCCCTT  AC
                                  C          TC
GAM159  OSBPL3    3'  TTGGGGCCTGGGGAGGGAAGTG 3558      AA        TAT
                                TTG  GCCTGGGGAG   GAAGTG
                                |||  ||||||||||   ||||||
                                AAC  CGGACCCCTC   CTTCAC
                                  CC         C__
GAM159  SYT12     3'  TTGAGGTCCGGGGAGTAGA    3559       AGC        T
                                TTGA   CTGGGGAGTA GA
                                ||||   |||||||||| ||
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                                AACT   GGCCCCTCAT CT
                                  CCA         _
GAM159  LOC124976 3'  TTGAGCCTGGGGGCACAGGTG  3560      A       A    GAA
                                TTGA GCCTGGGG GTAT   GTG
                                |||| |||||||| ||||   |||
                                AACT CGGACCCC CGTG   CAC
                                  _       _    TC_
GAM159  LOC148114 5'  TTGGGGCCTGGGGGGCTTGGGT 3561      AA       A  A  AA
          G                      TTG  GCCTGGGG GT TG  GTG
                                 |||  |||||||| || ||  |||
                                 AAC  CGGACCCC CG AC  CAC
                                   CC       C  A  C_
GAM159  LOC254428 3'  AAAGAGGTGGGAGTGTGGGGTG 3562      CCTG     A  AA
                                GAAG    GGGAGT TG  GTG
                                ||||    |||||| ||  |||
                                TTTC    CCCTCA AC  CAC
                                  TCCA      C  CC
GAM159  LOC254945 5'  TTGGGGCTGGGAACACTGGAGT 3563      AA  C     GTA  A
          G                      TTG  GC TGGGGA   TG AGTG
                                 |||  || ||||||   || ||||
                                 AAC  CG ACCCTT   AC TCAC
                                   CC  _     GTG  C
GAM160  APPL     3'  ATTCTTGAGCAAATGTA     3566         TAA
                                ATTCTTG   CAAATGTA
                                |||||||   ||||||||
                                TAAGAAC   GTTTACAT
                                    TC_
GAM160  CASP10   3'  ATTCTTATAACAAATTTACTGT 3567             G    A
          A                      ATTCTTGTAACAAAT TACT GTA
                                 |||||||||||||| |||| |||
                                 TAAGAATATTGTTTA ATGA CAT
                                           A   _
GAM160  CASP10   3'  ATTCTTATAACAAATTTACTGT 3567             G    A
          A                      ATTCTTGTAACAAAT TACT GTA
                                 |||||||||||||| |||| |||
                                 TAAGAATATTGTTTA ATGA CAT
                                           A   _
GAM160  MEN1     3'  TGCTTACCTAGATGTACTAGTA 3568      A_  AA__
                                TGT  AC    ATGTACTAGTA
                                |||  ||    ||||||||||
                                ACG  TG    TACATGATCAT
                                  AA  GATC
GAM160  HTATSF1  3'  TTCATGTAACACTACTAGTA  3569      T      AATG
                                TTC TGTAACA    TACTAGTA
                                ||| |||||||    ||||||||
                                AAG ACATTGT    ATGATCAT
                                  T      G___
GAM160  LOC149332 5'  TCTTGTAGTACTTAGT      3570         ACAAAT    _
                                TCTTGTA     GTACT AGT
                                |||||||     ||||| |||
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                                AGAACAT     CATGA TCA
                                   _______    A
GAM160  LOC57086  3'  ATTTTTGTAACTACTAGT    3571     C     AAATG
                                ATT TTGTAAC    TACTAGT
                                ||| |||||||    |||||||
                                TAA AACATTG    ATGATCA
                                  A     _____
GAM161  FLJ12681  3'  TGGGTCTATGGTCAGGGC    3574     A       A
                                TGG TCTATGGTCA GGGT
                                ||| |||||||||| ||||
                                ACC AGATACCAGT CCCG
                                  C       _
GAM161  HCA127    3'  TGGGGTTGGGCAAGGGTTGT  3575     ATCTA   T
                                TGG    TGG CAAGGGTTGT
                                |||    ||| ||||||||||
                                ACC    ACC GTTCCCAACA
                                  CCA__   C
GAM161  KIAA0494  3'  ATGGGTAAGTAAGGGTTGT   3576     ATCTAT   C
                                ATGG     GGT AAGGGTTGT
                                ||||     ||| |||||||||
                                TACC     TCA TTCCCAACA
                                  CAT___   _
GAM161  KIAA1557  5'  ATGGAGTTATGTTAGGTTGTC  3577      TC    GTCAA
                                ATGGA  TATG    GGGTTGTC
                                |||||  ||||    ||||||||
                                TACCT  ATAC    TCCAACAG
                                   CA    AA___
GAM161  LHX6      3'  TGGATAACATTGGGGGTTGTC  3578      CTA__   TCAA
                                TGGAT    TGG    GGGTTGTC
                                |||||    |||    ||||||||
                                ACCTA    ACC    CCCAACAG
                                   TTGTA   _____
GAM161  NBL1      3'  ATGGTCTTGGGGGGTTGT    3579      A   A   TCAA
                                ATGG TCT TGG    GGGTTGT
                                |||| ||| |||    |||||||
                                TACC AGA ACC    CCCAACA
                                  _   _   C___
GAM161  PABPC5    3'  TGGATTTTTGGTCAAAATGTT  3580      CTA       _
                                TGGAT   TGGTCAAGG GTT
                                |||||   ||||||||| |||
                                ACCTA   ACCAGTTTT CAA
                                   AAA        A
GAM161  YAP       5'  TGGATTTGTGTCAAGAGC    3581      CTA  _
                                TGGAT   TG GTCAAGGGT
                                |||||   || |||||||||
                                ACCTA   AC CAGTTCTCG
                                   A__  A
GAM162  ATP6V0C   3'  CAGGCTGTTCGTTCTGGAATGA 3584     C  GAG__       C
              G                  CA GC     GTTCTGGAA GAG
                                 || ||     ||||||||| |||
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                                GT CG    CAAGACCTT CTC
                                 C  ACAAG       A
GAM162  CISH    5'  CAGCGGCGACTCCGGA     3585      AC   GG
                                CAGC  GCGA  TTCTGGA
                                ||||  ||||  |||||||
                                GTCG  CGCT  GAGGCCT
                                  C_   __
GAM162  CISH    5'  CAGCGGCGACTCCGGA     3585      AC   GG
                                CAGC  GCGA  TTCTGGA
                                ||||  ||||  |||||||
                                GTCG  CGCT  GAGGCCT
                                  C_   __
GAM162  RAB36   3'  CAGCACGAGACGGGTGGGATGA 3586       C  _  TTC   AAC
          G                      CAGCACG GA GG   TGG   GAG
                                ||||||| || ||   |||   |||
                                GTCGTGC CT CC   ACC   CTC
                                    T  G  C__   CTA
GAM162  RANBP3  3'  ACACGCGGGGTGAAGGAACGAG 3587       A   TCT
                                GCACGCG GGT   GGAACGAG
                                ||||||| |||   ||||||||
                                TGTGCGC CCA   CCTTGCTC
                                    C   CTT
GAM162  RANBP3  3'  ACACGCGGGGTGAAGGAACGAG 3587       A   TCT
                                GCACGCG GGT   GGAACGAG
                                ||||||| |||   ||||||||
                                TGTGCGC CCA   CCTTGCTC
                                    C   CTT
GAM162  TCN2    3'  GCGAGGCTGCTGGGATGAG   3588        _   AAC
                                GCGAGGTT CTGG   GAG
                                |||||||| ||||   |||
                                CGCTCCGA GACC   CTC
                                    C    CTA
GAM162  THRA    5'  CAGCACGCCAAGAGACTGG   3589        G   TT_
                                CAGCACGC AGG   CTGG
                                |||||||| |||   ||||
                                GTCGTGCG TTC   GACC
                                    G   TCT
GAM162  ZFP103  5'  CGCGAGGCGGCGACGAG    3590        TCT  A_
                                CGCGAGGT   GG  ACGAG
                                ||||||||   ||  |||||
                                GCGCTCCG   CC  TGCTC
                                    ____  GC
GAM162  CHST8   5'  GCAGCAAACTCTGGGACGAG   3591     C  G GG    A
                                GCA GC A  TTCTGG ACGAG
                                ||| || |  |||||| |||||
                                CGT CG T  GAGACC TGCTC
                                  _  _ TT     C
GAM162  DKFZP727G051 5'  GCGGGGCCCTGGGGCGAG   3592     A      AA
                                GCG GGTTCTGG  CGAG
                                ||| ||||||||  ||||
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                                CGC CCGGGACC  GCTC
                                  C       CC
GAM162  FLJ13204  5'  CGCGAGGTCCCGGCGAG     3593           AA
                                CGCGAGGTTCTGG  CGAG
                                ||||||||||||  ||||
                                GCGCTCCAGGGCC  GCTC
                                          __
GAM162  FLJ14249  5'  GCGGCGGGGACTCCGGGCG   3594     AC   A _     AA
                                GC  GCG GG TTCTGG  CG
                                ||  ||| || ||||||  ||
                                CG  CGC CC GAGGCC  GC
                                 C_   C  T     C_
GAM162  FLJ14249  5'  GCGGCGGGGACTCCGGGCG   3594     AC   A _     AA
                                GC  GCG GG TTCTGG  CG
                                ||  ||| || ||||||  ||
                                CG  CGC CC GAGGCC  GC
                                 C_   C  T     C_
GAM162  GFPT1     5'  GCCCGCGAGGCCAGGGGCGAG  3595     A       CT  AA
                                GC CGCGAGGTT  GG  CGAG
                                || |||||||||  ||  ||||
                                CG GCGCTCCGG  CC  GCTC
                                 G       T_  CC
GAM162  IL-17RC   3'  CAGCACGCAGCTGAGCGA    3596         G  GTT    AA
                                CAGCACGC AG   CTGG  CGA
                                ||||||||  ||   ||||  |||
                                GTCGTGCG TC   GACT  GCT
                                     _  ____    C_
GAM162  ISL2      3'  AGCATGCGAGGTCCGCGG     3597       C        _
                                AGCA GCGAGGTTC TGG
                                |||| ||||||||| |||
                                TCGT CGCTCCAGG GCC
                                  A       C
GAM162  KIAA0186  3'  CAGCACATGGGGAGGACGA    3598         CGA  TTCT   A
                                CAGCACG   GG    GGA CGA
                                |||||||   ||    ||| |||
                                GTCGTGT   CC    CCT GCT
                                    AC_  CT__   _
GAM162  KIAA0329  3'  GCTGTGGGTTCTGGAACGAG   3599     GA__
                                GC    GGTTCTGGAACGAG
                                ||    ||||||||||||||
                                CG    CCAAGACCTTGCTC
                                 ACAC
GAM162  MGC15504  5'  GCACCGGGTCCTGGGCG     3600       G  A       AA
                                GCAC CG GGTTCTGG  CG
                                |||| || ||||||||  ||
                                CGTG GC CCAGGACC  GC
                                  _  _       C_
GAM162  PPI5PIV   5'  CAGCGCGAGGGGTCACG     3601       AC     TTCT  A_
                                CAGC  GCGAGG   GG  ACG
                                ||||  ||||||   ||  |||
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                                GTCG  CGCTCC    CC  TGC
                                  __    _____  AG
GAM162   LOC144571 5'  CAGAGAGGAGGTTCTGGAA   3602      CACGC
                                CAG    GAGGTTCTGGAA
                                |||    ||||||||||||
                                GTC    CTCCAAGACCTT
                                  TCTC_
GAM162   LOC144698 5'  CAGCACGTCCTGGAGTGA    3603        GCGAG       AC
                                CAGCAC    GTTCTGGA  GA
                                ||||||    ||||||||  ||
                                GTCGTG    CAGGACCT  CT
                                   ______       CA
GAM162   LOC151473 5'  GCTGAGGCCCTGGGCGAG    3604     _        AA
                                GC GAGGTTCTGG  CGAG
                                || ||||||||||  ||||
                                CG CTCCGGGACC  GCTC
                                 A         C_
GAM162   LOC151701 3'  AGCACGGACTCTGGGATGAG   3605        CGA GT     AAC
                                AGCACG   G  TCTGG   GAG
                                ||||||   |  |||||   |||
                                TCGTGC   C  AGACC   CTC
                                   ___ TG    CTA
GAM162   LOC153474 5'  GCGCGCGAGGCCGCTGGAACGA 3606     A        _
           G                     GC CGCGAGGTT CTGGAACGAG
                                || |||||||| ||||||||||
                                CG GCGCTCCGG GACCTTGCTC
                                 C         C
GAM162   LOC158436 5'  CAGTGGGCGGGTGGCGTGGGGC 3607      CAC   A   TC__   AA
           GAG                    CAG   GCG GGT    TGG  CGAG
                                |||   ||| |||    |||  ||||
                                GTC   CGC CCA    ACC  GCTC
                                  ACC   _   CCGC   CC
GAM162   LOC199688 5'  GCGCGCTAGGTTGGCGA     3608     A   G    TC   AA
                                GC CGC AGGT  TGG  CGA
                                || ||| ||||  |||  |||
                                CG GCG TCCA  ACC  GCT
                                 C   A    __   __
GAM162   LOC200854 5'  CAGCACGCAGGCCAAGTGG    3609         G    C__
                                CAGCACGC AGGTT   TGG
                                |||||||| |||||   |||
                                GTCGTGCG TCCGG   ACC
                                     _     TTC
GAM163   DIAPH2    3'  GTGCCTGCACTGTGAACCA    3612          GCAC   A
                                GTGCCTGCAC    GAG CA
                                ||||||||||    ||| ||
                                CACGGACGTG    CTT GT
                                      ACA_   G
GAM163   PACE4     3'  TTCATGCTTGCACGCACA     3613         C
                                TTCGTGC TGCACGCACG
                                ||||||| ||||||||||
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                                AAGTACG ACGTGCGTGT
                                    A
GAM163  KIAA1145  3'  TTCCTGCCTGCAGCAGA    3614     G      C  C
                                TTC TGCCTGCA GCA GA
                                ||| |||||||| ||| ||
                                AAG ACGGACGT CGT CT
                                  G      _  _
GAM163  TGIF2     3'  GTGCCTGCGGCAGACA     3615        AC  CGA
                                GTGCCTGC  GCA  GACA
                                ||||||||  |||  ||||
                                CACGGACG  CGT  CTGT
                                    C_  ___
GAM163  LOC154860 5'  TTCGTGCCTGTGGCCTACGA  3616         CAC __
                                TTCGTGCCTG  GC  ACGA
                                ||||||||||  ||  ||||
                                AAGCACGGAC  CG  TGCT
                                     AC_  GA
GAM163  LOC254746 3'  TTCTTGCCTGCAAAGA     3617     G      CGCAC
                                TTC TGCCTGCA    GAGA
                                ||| ||||||||    ||||
                                AAG ACGGACGT    TTCT
                                  A      _____
GAM163  LOC96597  5'  GTACCTGCTTCGAGACA    3618        ACGCA
                                GTGCCTGC    CGAGACA
                                ||||||||    |||||||
                                CATGGACG    GCTCTGT
                                    AA___
GAM164  GRIA3     3'  TCCTTGAAGCAGCCACGTTTTC 3621        AA  A   CCC
          G                      TCCTTGAG  AGT TACG  TCG
                                ||||||||  ||| ||||  |||
                                AGGAACTT  TCG GTGC  AGC
                                    CG  _   AAA
GAM164  TGM4      3'  CCCTTGAGAAATGTCCT     3622          _ ATACGC
                                TCCTTGAGAAA GT     CCT
                                |||||||||| ||     |||
                                GGGAACTCTTT CA     GGA
                                     A _______
GAM164  WNT11     3'  TCCTTGAGCAGAGTCCTC    3623        AA_  ATACGC
                                TCCTTGAG  AGT     CCTC
                                ||||||||  |||     ||||
                                AGGAACTC  TCA     GGAG
                                    GTC  _______
GAM164  APH2      3'  CTGAGAAAAGCTGCCCT     3624         _ ATAC
                                TTGAGAAA GT    GCCCT
                                |||||||| ||    |||||
                                GACTCTTT CG    CGGGA
                                    T  A___
GAM164  CTCF      3'  TCCTTGAAGTTTTCGTTCTCG  3625        GAA  ATA  CC
                                TCCTTGA  AGT  CG  CTCG
                                |||||||  |||  ||  ||||
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                                AGGAACT  TCA  GC  GAGC
                                   ___   AAA  AA
GAM164  GRM5     5'  TCCTCGAGGGCTTCCTGCGCTC 3626        AAAGTATA_  C
            TCG                    TCCTTGAG       CGC CTCG
                                |||||||||       ||| ||||
                                AGGAGCTC       GCG GAGC
                                    CCGAAGGAC  A
GAM164  HLA-DRB3 3'  CCTGAGAAAGCCCTC      3627         GTATAC
                                CTTGAGAAA     GCCCTC
                                |||||||||     ||||||
                                GGACTCTTT     CGGGAG
                                    _______
GAM164  KIAA0551 3'  CTTGAGAAAGTGGCACCCTCG  3628          ATA
                                CTTGAGAAAGT  CGCCCTCG
                                ||||||||||  ||||||||
                                GAACTCTTTCA  GTGGGAGC
                                      CC_
GAM164  NUBP1    3'  TCTCTGAGAAAGTGGCTTC   3629    C       ATAC  CC
                                TC TTGAGAAAGT   GC  TC
                                || ||||||||||   ||  ||
                                AG GACTCTTTCA   CG  AG
                                 A        C___  A_
GAM164  SBBI26   3'  TGAGAAAGTGTGTATATGCC  3630         ____  C
                                TGAGAAAGT   ATA GCC
                                |||||||||   ||| |||
                                ACTCTTTCA   TAT CGG
                                      CACA  A
GAM164  LOC56932 3'  TCCTTGAGGGAAGTAGGCTCTC 3631        A_    TAC  C
                                TCCTTGAG  AAGTA  GC CTC
                                ||||||||  |||||  || |||
                                AGGAACTC  TTCAT  CG GAG
                                     CC    C__  A
GAM165  CD72     5'  CCTGTCATCCACTGTCCTCCC  3634    C       GC  TGA
                                CC GTCATCCAC  TCT  TCCC
                                || |||||||||  |||  ||||
                                GG CAGTAGGTG  AGG  AGGG
                                 A        AC  ____
GAM165  CELSR3   3'  CCTCGTCCACGCCGTCATCCC  3635    G  A      C  G
                                CC TC TCCACGCT TT ATCCC
                                || || |||||||| || |||||
                                GG AG AGGTGCGG AG TAGGG
                                 _  C       C  _
GAM165  EMX2     3'  CCCGTCGTCCTGCTCCC     3636        A  AC
                                CCCGTC TCC  GCTCTT
                                ||||||  |||  ||||||
                                GGGCAG AGG  CGAGGG
                                    C  A_
GAM165  ITGA1    5'  CCGCCCCTTCGCGCTCTTGGTC 3637       ATCCA_      A
                                CCGTC     CGCTCTTG TC
                                |||||     |||||||| ||
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                                GGCGG     GCGAGAAC AG
                                  GGAAGC       C
GAM165  LARGE    3'  CCTGTCACCCCTTGAT      3638     C      ACGCT
                                CC GTCATCC     CTTGAT
                                || |||||||    ||||||
                                GG CAGTGGG     GAACTA
                                 A     _____
GAM165  LARGE    3'  CCTGTCACCCCTTGAT      3638     C      ACGCT
                                CC GTCATCC     CTTGAT
                                || |||||||    ||||||
                                GG CAGTGGG     GAACTA
                                 A     _____
GAM165  LHX4     5'  GTTTCCAATCCCTTTGATC   3639     CA   CG    _
                                GT  TCCA  CTCTT GATC
                                ||  ||||  ||||| ||||
                                CA  AGGT  GGGAA CTAG
                                 A_   TA    A
GAM165  LOXL1    3'  TCATCCACGTTCGCTCCC    3640          C  TTGA
                                TCATCCACG TC    TCCC
                                |||||||||| ||    ||||
                                AGTAGGTGC AG    AGGG
                                      A  CG__
GAM165  MYO1D    3'  CCCGTCATCCCGTGTCTT    3641           A  C_
                                CCCGTCATCC CG  TCTT
                                |||||||||| ||  ||||
                                GGGCAGTAGG GC  AGAA
                                      _  AC
GAM165  AKAP11   3'  ATCTCCTACCTTGATC      3642      A   AC  T
                                GTC TCC  GC CTTGATC
                                ||| |||  || |||||||
                                TAG AGG  TG GAACTAG
                                  _   A_ _
GAM165  DKFZP727M111 5'  CCTGCTCAGCTTCTTGATCCC  3643     GTCA  CAC  _
                                CC    TC   GCT CTTGATCCC
                                ||    ||   ||| ||||||||||
                                GG    AG   CGA GAACTAGGG
                                 ACG_  T__   A
GAM165  GP5      3'  CCTTTATCCACGCATTGAT    3644     GTC       TC
                                CC   ATCCACGC  TTGAT
                                ||   ||||||||  |||||
                                GG   TAGGTGCG  AACTA
                                 AAA       T_
GAM165  HSPC052  3'  CCGTCACCATAATGATTCC    3645        T   CGCTCT   _
                                CCGTCA CCA     TGAT CC
                                |||||| |||     |||| ||
                                GGCAGT GGT     ACTA GG
                                   _  ATT____    A
GAM165  KCNK15   3'  CCCGTCATCCGTTTCCAATCCC 3646           ACGCTC TG
                                CCCGTCATCC     T  ATCCC
                                ||||||||||     |  |||||
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                                GGGCAGTAGG     G  TAGGG
                                      CAAA__ GT
GAM165  KIAA1068  5'  CCTGTCTCCATGTCGCCTCCC  3647     C   A   ___    CTTGA
                                CC GTC TCCA   CGCT     TCCC
                                || ||| ||||   ||||     ||||
                                GG CAG AGGT   GCGG     AGGG
                                 A   _    ACA   _____
GAM165  KIAA1091  3'  CCATCATCCATGCCCTTCC   3648          C     TGA
                                CCGTCATCCA GCTCT   TCC
                                |||||||||| |||||   |||
                                GGTAGTAGGT CGGGA   AGG
                                      A    ___
GAM165  KIAA1883  3'  CCGTCATCCACAGAGGATTCC  3649           CTCTT  _
                                CCGTCATCCACG     GAT CC
                                ||||||||||||     ||| ||
                                GGCAGTAGGTGT     CTA GG
                                       CTC__   A
GAM165  KIAA1941  3'  CCTGTCATCCACGCTGCCATCC 3650     C         _  TG
            C                    CC GTCATCCACGCT CT  ATCCC
                                || ||||||||||||  ||  |||||
                                GG CAGTAGGTGCGA GG  TAGGG
                                 A          C  __
GAM165  MGC10911  3'  CCCGTCATGCACAGATGATC   3651         C    CTCT
                                CCCGTCAT CACG    TGATC
                                ||||||||  ||||    |||||
                                GGGCAGTA GTGT    ACTAG
                                     C    CT__
GAM165  MGC11266  5'  CCCGCCATCCACGTCTTCC   3652           C   TGA
                                CCCGTCATCCACG TCT   TCC
                                |||||||||||| |||   |||
                                GGGCGGTAGGTGC AGA   AGG

                                      _   ____
GAM165  MPPE1     3'  CATCATCCACTTGAT      3653          GCTC
                                CGTCATCCAC    TTGAT
                                ||||||||||    |||||
                                GTAGTAGGTG    AACTA

                                     _____
GAM165  PAN2      3'  GTCATCCATGCTTGCCC     3654         C   CT  A
                                GTCATCCA GCT  TG TCC
                                ||||||||  |||  ||  |||
                                CAGTAGGT CGA  AC GGG
                                     A   __  _
GAM165  PRO1728   5'  GTCACCCACTGATCC       3655         GCTCT
                                GTCATCCAC     TGATCC
                                |||||||||     ||||||
                                CAGTGGGTG     ACTAGG

                                      ______
GAM165  PTDSS2    3'  CCCATCATCCACGTGTCC     3656           CTCT  A
                                CCCGTCATCCACG    TG TCC
                                ||||||||||||    ||  |||
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                                GGGTAGTAGGTGC    AC AGG
                                      ____ _
GAM165  LOC115442 3'  GCATCTGCTCTTGATC      3657    T    CAC
                                G CATC   GCTCTTGATC
                                | ||||   ||||||||||
                                C GTAG   CGAGAACTAG
                                _    A__
GAM165  LOC150113 5'  CCTGTCTCCACGCTTC      3658     C   A       CTTGA
                                CC GTC TCCACGCT     TC
                                || ||| ||||||||     ||
                                GG CAG AGGTGCGA     AG
                                 A   _       ______
GAM165  LOC152794 3'  CCCGTCATCTAGGTTTTAAGCC 3659          CACGCTC    T
              C                  CCCGTCATC       TTGA CCC
                                |||||||||       |||| |||
                                GGGCAGTAG       AATT GGG
                                      ATCCAA_    C
GAM165  LOC220549 5'  CCTGCATCCACAGTGAT     3660     C T       CTCT
                                CC G CATCCACG    TGAT
                                || | |||||||||    ||||
                                GG C GTAGGTGT    ACTA
                                 A _       C___
GAM165  LOC254205 5'  CCTGTTCACTGGCTCTTGATC  3661     CG_    CCAC
                                CC   TCAT    GCTCTTGATC
                                ||   ||||    ||||||||||
                                GG   AGTG    CGAGAACTAG
                                 ACA    AC__
GAM166  CREBL2    3'  TATACAATTGAGTGGACCA    3664           _    TG
                                TATACAATTG GTGG  GCCG
                                |||||||||| ||||  ||||
                                ATATGTTAAC CACC  TGGT
                                      T    __
GAM166  KIAA0319  3'  TACACAATTGCTGAGTCGT    3665           G  GT  C
                                TATACAATTG TG  GG CGT
                                |||||||||| ||  || |||
                                ATGTGTTAAC AC  TC GCA
                                      G   __  A
GAM166  LOC132617 3'  TATACAGGTGGTGGC       3666         ATT
                                TATACA   GGTGGTGGC
                                ||||||   |||||||||
                                ATATGT   CCACCACCG
                                     ___
GAM166  LOC139135 5'  TATGCAACTGGTGATGATGGCT 3667      A        ___     C
              GT                  TAT CAATTGGTG   GTGGC GT
                                ||| |||||||||   ||||| ||
                                ATA GTTGACCAC   TACCG CA
                                  C        TAC     A
GAM166  LOC51754  5'  TGACAGAGATGTGGCCGT    3668    T   ATT    G
                                A ACA   GGTG TGGCCGT
                                | |||   |||| |||||||
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                                A TGT   CTAC ACCGGCA
                                 C  CT_   _
GAM166  LOC90119  5'  TGACACGATGGTGGCTGT    3669    T  AT       C
                                A ACA  TGGTGGTGGC GT
                                | |||  |||||||||| ||
                                A TGT  GCTACCACCG CA
                                 C  __        A
GAM167  BPAG1     5'  CGATGTTCTTTCTTTCACCTT  3672     AC  GAAC
                                CGAT  TTT   TTCACCTT
                                ||||  |||   ||||||||
                                GCTA  AGA   AAGTGGAA
                                  CA  AAGA
GAM167  BPAG1     5'  CGATGTTCTTTCTTTCACCTT  3672     AC  GAAC
                                CGAT  TTT   TTCACCTT
                                ||||  |||   ||||||||
                                GCTA  AGA   AAGTGGAA
                                  CA  AAGA
GAM167  BPAG1     5'  CGATGTTCTTTCTTTCACCTT  3672     AC  GAAC
                                CGAT  TTT   TTCACCTT
                                ||||  |||   ||||||||
                                GCTA  AGA   AAGTGGAA
                                  CA  AAGA
GAM167  COL19A1   3'  GAGCTTTTGGGCTTCACCTT  3673    TAC   AA
                                GA  TTTG  CTTCACCTT
                                ||  ||||  |||||||||
                                CT  AAAC  GAAGTGGAA
                                 CGA   CC
GAM167  PMP2      3'  ATCAATACTTTGATTTCA    3674          AC
                                ATCGATACTTTGA  TTCA
                                ||||||||||||  ||||
                                TAGTTATGAAACT  AAGT
                                       A_
GAM167  POU5F1    3'  ATCATTGAACTTCACCTT    3675     ATACT
                                ATCG    TTGAACTTCACCTT
                                ||||    ||||||||||||||
                                TAGT    AACTTGAAGTGGAA
                                  _____
GAM167  POU5F1    3'  ATCATTGAACTTCACCTT    3675     ATACT
                                ATCG    TTGAACTTCACCTT
                                ||||    ||||||||||||||
                                TAGT    AACTTGAAGTGGAA
                                  _____
GAM167  POU5F1    3'  ATCATTGAACTTCACCTT    3675     ATACT
                                ATCG    TTGAACTTCACCTT
                                ||||    ||||||||||||||
                                TAGT    AACTTGAAGTGGAA
                                  _____
GAM167  IPLA2(GAMMA) 3'  GACTGGAACTTCACCTT    3676     ACTTT
                                GAT    GAACTTCACCTT
                                |||    ||||||||||||
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                                CTG    CTTGAAGTGGAA
                                  AC___
GAM167  LOC157273 3'  GACAGTGAACTTCACCTT    3677      CTT
                                GATA   TGAACTTCACCTT
                                ||||   ||||||||||||
                                CTGT   ACTTGAAGTGGAA
                                  C__
GAM168  TOSO    5'  GACGATGAGGAAATCCTCGT   3680     A   GCCT  C
                                GA CGA    GA ATCCTCGT
                                || |||    || ||||||||
                                CT GCT    CT TAGGAGCA
                                 _   ACTC  T
GAM168  LOC152283 5'  TGAGGACGATGTAATCCTCGT  3681      A   GCCTGAC
                                TGAG ACGA      ATCCTCGT
                                |||| ||||      ||||||||
                                ACTC TGCT      TAGGAGCA
                                  C    ACAT___
GAM168  LOC255002 5'  TGGGAATGAGCCTGACAC    3682     A   C
                                TG GAA GAGCCTGACAT
                                || ||| ||||||||||
                                AC CTT CTCGGACTGTG
                                 C   A
GAM168  LOC92017  5'  TGAGAGGTGGGCCACCCTCGT  3683       ACGA_   TGAC
                                TGAGA    GCC    ATCCTCGT
                                |||||    |||    ||||||||
                                ACTCT    CGG    TGGGAGCA
                                   CCACC  _____
GAM169  EREG    3'  TACAATATGTATAGGACCA   3686         T    _
                                TACAATAT TATAG ACTA
                                |||||||| ||||| ||||
                                ATGTTATA ATATC TGGT
                                     C    C
GAM169  FLJ11175  3'  TACAATATTTGGACAGAGGAT  3687          ATA   TA
                                TACAATATTT   GAC  AGGAT
                                ||||||||||   |||  |||||
                                ATGTTATAAA   CTG  TCCTA
                                      C__   TC
GAM169  MRPL56   3'  TAAATATTTATAGGTAAAGG   3688    C        ACT
                                A AATATTTATAG   AAGG
                                | ||||||||||   ||||
                                A TTATAAATATC   TTCC
                                 T         CAT
GAM170  ARNT2    3'  CTGAAGAACGAAGGCTCAG   3691      CC   CCGGC
                                CTGA  AAC    AAGGCTCAG
                                ||||  |||    |||||||||
                                GACT  TTG    TTCCGAGTC
                                  TC   C_____
GAM170  CRACC    3'  TCTGACCAATTAGTGTAAGCTC 3692          CCCGGCA
           AG                     TCTGACCAA      AGGCTCAG
                                |||||||||      ||||||||
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                                AGACTGGTT      TTCGAGTC
                                     AATCACA
GAM170  DFFB     3'  CTGACCAACGGAGCAGGGTTCA 3693         CC    A  C
            G                    CTGACCAAC  GGCA GG TCAG
                                 |||||||||  |||| || ||||
                                 GACTGGTTG  TCGT CC AGTC
                                      CC    C  A
GAM170  G6PT1    5'  TCTGGCAGCCAGAGGCTCA   3694      AC  AC    CA
                                 TCTG  CA  CCGG  AGGCTCA
                                 ||||  ||  ||||  |||||||
                                 AGAC  GT  GGTC  TCCGAGT
                                   C_  C_    __
GAM170  HD       3'  TGACCGAGAGAGGCTCAG    3695       AACCC  CA
                                 TGACC    GG  AGGCTCAG
                                 |||||    ||  ||||||||
                                 ACTGG    TC  TCCGAGTC
                                    C_____ TC
GAM170  VCL      3'  TCTGTGCCAGCCAGGCTCA   3696      ACCAAC    A
                                 TCTG     CCGGC AGGCTCA
                                 ||||     ||||| |||||||
                                 AGAC     GGTCG TCCGAGT
                                   AC_____    G
GAM170  VCL      3'  TCTGTGCCAGCCAGGCTCA   3696      ACCAAC    A
                                 TCTG     CCGGC AGGCTCA
                                 ||||     ||||| |||||||
                                 AGAC     GGTCG TCCGAGT
                                   AC_____    G
GAM170  DKFZp547C176 5'  TCTGGCGGCGGTAGGCTCA   3697      ACCAACC   A__
                                 TCTG      CGGC   AGGCTCA
                                 ||||      ||||   |||||||
                                 AGAC      GCCG   TCCGAGT
                                   C_______    CCA
GAM170  FLJ10815  3'  TCTGACCAGCCCAGCCCACACA 3698         A     AAG  T
            G                    TCTGACCA CCCGGC   GC CAG
                                 |||||||| ||||||   || |||
                                 AGACTGGT GGGTCG   TG GTC
                                      C     GG_  T
GAM170  FLJ13909  3'  CCTGACCAGCAGGCT      3699         ACCCG   A
                                 TCTGACCA    GCA GGCT
                                 ||||||||    ||| ||||
                                 GGACTGGT    CGT CCGA
                                       ______  _
GAM170  FLJ20320  3'  TCTGCTCAAGTCACAAGGCTCA 3700      AC   CC  G
            G                    TCTG  CAA  CG CAAGGCTCAG
                                 ||||  |||  || ||||||||||
                                 AGAC  GTT  GT GTTCCGAGTC
                                   GA   CA  _
GAM170  FLJ23191  5'  TCTGGCAGCTCCTGGAGGCTCA 3701      ACCAA_  C  CA
            G                    TCTG     CC GG  AGGCTCAG
                                 ||||     || ||  ||||||||
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                                AGAC     GG CC  TCCGAGTC
                                  CGTCGA  A  __
GAM170  KIAA0449  3'  TCTGACCACCTCAAAGGCT   3702        A  _  GC
                                TCTGACCA CC CG  AAGGCT
                                |||||||| || ||  ||||||
                                AGACTGGT GG GT  TTCCGA
                                     _  A  __
GAM170  TIP47     3'  CTGACTGATAGGGTGAGGCTCA 3703      CAACCC  CA
          G                      CTGAC     GG  AGGCTCAG
                                |||||     ||  ||||||||
                                GACTG     CC  TCCGAGTC
                                  ACTATC  AC
GAM170  LOC126074 5'  TCTGACCAATCGGTGGCTC   3704        CC   CAA
                                TCTGACCAA  CGG   GGCTC
                                |||||||||  |||   |||||
                                AGACTGGTT  GCC   CCGAG
                                     A_   A__
GAM170  LOC145757 5'  TCTGGCAACCCGGGAGCAGCT  3705      AC       CAA_
                                TCTG  CAACCCGG    GGCT
                                ||||  ||||||||    ||||
                                AGAC  GTTGGGCC    TCGA
                                  C_       CTCG
GAM170  LOC146481 3'  TCTGACCCACTGACAGGCTCAG 3706        A  CC    A
                                TCTGACC AC  GGCA GGCTCAG
                                ||||||| ||  |||| |||||||
                                AGACTGG TG  CTGT CCGAGTC
                                    G  A_   _
GAM170  LOC159199 5'  TCTGACCCGCAGGCTC      3707       CCAA    G  A
                                TCTGA    CCCG CA GGCTC
                                |||||    |||| || |||||
                                AGACT    GGGC GT CCGAG
                                  _____   _ _
GAM170  LOC90333  3'  TCTGGCTAACACGGTGAAACCC 3708      ACC   C   CA
            AG                    TCTG   AAC CGG  AGGCTCAG
                                ||||   ||| |||  ||||||||
                                AGAC   TTG GCC  TTTGGGTC
                                  CGA   T   AC
GAM171  DNAM-1    3'  ATTCAACTTTCACATAATCAT  3711          T G    C
                                GTTCAACTTTCG C ATAA CAT
                                |||||||||||| | |||| |||
                                TAAGTTGAAAGT G TATT GTA
                                     _ _    A
GAM171  KIAA0280  3'  GTTCAACTGTTCTGTGAAC   3712        _   _ C
                                GTTCAACT TTC GT GAT
                                |||||||| ||| || |||
                                CAAGTTGA AAG CA TTG
                                     C   A  C
GAM171  LOC129831 3'  GTTCAACTTTAGTAGATA    3713          C  C
                                GTTCAACTTT GT GATA
                                |||||||||| || ||||
```

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                                CAAGTTGAAA CA CTAT
                                     T  T
GAM172  ADAM22   3'  TCCATGAGCCTGGGTTTCTACC 3716       G_________  TGAGA
          TCTCAGG               GAGCCTG       ACC    GG
                                |||||||       |||    ||
                                CTCGGAC       TGG    CC
                                   CCAAAGAIII  AGAGT
GAM172  ADRBK1   3'  TCCCTGAGCCCGGGTGCTGGGG 3717          AC_  AGA
          GT                  TCCCTGAGCCTGG  CTG  GGT
                              ||||||||||||||  |||  |||
                              AGGGACTCGGGCC  GAC  CCA
                                     CAC  CC_
GAM172  CD34    3'  TCCCTGAGCCTCAGGGGAGGT  3718         __  ACCTGA
                              TCCCTGAGCCT  GG    GAGGT
                              ||||||||||  ||    |||||
                              AGGGACTCGGA  CC    CTCCA
                                     GT  C_____
GAM172  DIAPH2   3'  CCCTTGAGCCTGGGAGTTTGAG 3719      _      ACCTGA
          GT                  CCCT GAGCCTGG    GAGGT
                              |||| ||||||||     |||||
                              GGGA CTCGGACC     CTCCA
                                A       CTCAAA
GAM172  IGFBP3   3'  TCCCTGAGCCTGACTTTACCTC 3720         G_______  TGAGA
          TCG                 CCTGAGCCTG      ACC    G
                              |||||||||       |||    |
                              GGACTCGGAC      TGG    C
                                   TGAAAIII  AGAGT
GAM172  KLK4    3'  CCTCTGGGTCTGGGGAAGGAGG 3721    _  AGC   ACCT_  A
          GGT                 CC CTG  CTGG    GAG GGT
                              || |||  ||||    ||| |||
                              GG GAC  GACC    CTC CCA
                               A  CCA   CCTTC  C
GAM172  LARGE   3'  TCTTCGAAAGGCCTGAGAGGT  3722    CC   CCT  A
                              TC  TGAG  GG CCTGAGAGGT
                              ||  ||||  || ||||||||||
                              AG  GCTT  CC GGACTCTCCA
                               AA   T__  _
GAM172  LARGE   3'  TCTTCGAAAGGCCTGAGAGGT  3722    CC   CCT  A
                              TC  TGAG  GG CCTGAGAGGT
                              ||  ||||  || ||||||||||
                              AG  GCTT  CC GGACTCTCCA
                               AA   T__  _
GAM172  MADH1    5'  CCTGGAGCCTGGATTGATCTGG 3723      _      CC   GA_
          T                   CCTG AGCCTGGA  TGA   GGT
                              |||| ||||||||  |||   |||
                              GGAC TCGGACCT  ACT   CCA
                                C       A_   AGA
GAM172  NCF2    3'  TCCTTGGGCCTGGACTTGGGT  3724     C  A      C  AGA
                              TCC TG GCCTGGAC TG   GGT
                              ||| || |||||||| ||   |||
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                                AGG AC CGGACCTG AC   CCA
                                  A  C       A ___
GAM172  NUMB     3'  CTGGGCCTGGACTTGTACCTCT 3725     A       _________ GAGA
                CAG                    TG GCCTGGAC       CT    GG
                                || ||||||||       ||    ||
                                AC CGGACCTG       GG    TC
                                 C       AACAIIIT  AGAG
GAM172  PLA2G4C  5'  CCTGAGCCTGGGTCTGGGGC  3726           AC   AGA
                                CCTGAGCCTGG  CTG   GGT
                                ||||||||||  |||   |||
                                GGACTCGGACC  GAC   CCG
                                      CA   C__
GAM172  PPP1R12B  3'  CCCTTGAGCCTGGGAG      3727       _       ACCTGA
                                CCCT GAGCCTGG     GAG
                                |||| ||||||||      |||
                                GGGA CTCGGACC     CTC
                                  A       _______
GAM172  SLC1A4    3'  TGAGCCTGGCAGCTCAAGGGGT 3728          AC_ _   A
                                TGAGCCTGG   CT GAG GGT
                                |||||||||   || ||| |||
                                ACTCGGACC   GA TTC CCA
                                     GTC  G   C
GAM172  SP3      5'  TCCCTGAACCTGGACTTGACCA 3729              C   GA
                GT                     TCCCTGAGCCTGGAC TGA  GGT
                                ||||||||||||||| |||  |||
                                AGGGACTTGGACCTG ACT  TCA
                                       A   GG
GAM172  BMF      3'  TCCCTGAGGTCTGCTGGAGGT  3730         C_   GAC   A
                                TCCCTGAG  CTG   CTG GAGGT
                                ||||||||  |||   ||| |||||
                                AGGGACTC  GAC   GAC CTCCA
                                     CA   ___   _
GAM172  cerk     3'  TCTTTGGCCTGGACTGTACCTC 3731    CC  A       _________ GAGA
                TA                     TG GCCTGGAC       CT    G
                                 || ||||||||       ||    |
                                 AC CGGACCTG       GG    T
                                AA  _       ACAIIIT  AGAG
GAM172  FLJ13902  3'  TCACTGAGCCTGGGACCAGGT  3732     C        _   TGAG
                                TC CTGAGCCTGG ACC    AGGT
                                || ||||||||||  |||    ||||
                                AG GACTCGGACC TGG    TCCA
                                  T         C  _____
GAM172  FLJ20856  3'  CCCCTGAGCTTGGGCCTA    3733          C   A
                                TCCCTGAGC TGG CCTG
                                |||||||||  ||| ||||
                                GGGGACTCG ACC GGAT
                                      A   C
GAM172  FLJ23185  3'  TCTCCTGAGGCTTGAGAGG   3734     _     C  GGACC
                                TC CCTGAG CT     TGAGAGG
                                || ||||||  ||     |||||||
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                                AG GGACTC GA    ACTCTCC
                                 A     C _____
GAM172  KIAA0855  3'  TCCCTGACTGAAAATGAGAGGT 3735        GC    CC
                                TCCCTGA  CTGGA  TGAGAGGT
                                |||||||  |||||  ||||||||
                                AGGGACT  GACTT  ACTCTCCA
                                    __    TT
GAM172  KIAA0876  3'  TCCCTGAGTCTGGGGCCG    3736        C   AC
                                TCCCTGAG CTGG  CTG
                                |||||||| ||||  |||
                                AGGGACTC GACC  GGC
                                    A   CC
GAM172  MPZL1    5'  TCCCTGAGCCCGGGTCCCCGCT 3737           A__   A_
           GAGGT                  TCCCTGAGCCTGG   CCTG  GAGGT
                                |||||||||||||   ||||  |||||
                                AGGGACTCGGGCC   GGGC  CTCCA
                                      CAG   GA
GAM172  RNPC1    3'  TCTCTGAGCCTTGACTCTG   3738    C      G  _
                                TC CTGAGCCT GAC CTG
                                || |||||||| ||| |||
                                AG GACTCGGA CTG GAC
                                 A       A  A
GAM172  LOC124976 3'  CCTTGAGCCTGGGGGCACAGGT 3739    C       ACCTGAG
                                CC TGAGCCTGG      AGGT
                                || |||||||||      ||||
                                GG ACTCGGACC      TCCA
                                 A       CCCGTG_
GAM172  LOC143188 5'  TCCCTGAGCTGGAAAG     3740         C   CCTGA
                                TCCCTGAGC TGGA    GAG
                                |||||||||| ||||    |||
                                AGGGACTCG ACCT    TTC
                                    _   _____
GAM172  LOC145988 3'  TCCCTGACTGAAACTGAGAGGT 3741        GC    C
                                TCCCTGA  CTGGA CTGAGAGGT
                                |||||||  ||||| |||||||||
                                AGGGACT  GACTT GACTCTCCA
                                    __    T
GAM172  LOC146733 3'  TCCTTGATCCTGGACCAGG   3742    C  G      TGAG
                                TCC TGA CCTGGACC   AGG
                                ||| ||| ||||||||   |||
                                AGG ACT GGACCTGG   TCC
                                  A  A      ____
GAM172  LOC147343 5'  TCCCTGAGACTGGATTTGATAG 3743        C    CC  G
                                TCCCTGAG CTGGA  TGA AG
                                |||||||| |||||  ||| ||
                                AGGGACTC GACCT  ACT TC
                                    T    AA  A
GAM172  LOC149271 5'  TCCCTGAGTCAGGAGACCTGGG 3744        CCT__     AGA
           T                    TCCCTGAG    GGACCTG  GGT
                                ||||||||    |||||||  |||
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                                AGGGACTC    TCTGGAC   CCA
                                    AGTCC      ___
GAM172  LOC150245 5'  TCTCTGAGCCTGGTCTG     3745     C        AC
                                TC CTGAGCCTGG  CTG
                                || ||||||||||  |||
                                AG GACTCGGACC  GAC
                                 A        A_
GAM172  LOC256113 5'  TCTTTGAGCCTGGCTATGTACC 3746        G__________  TGAGA
          TCTCAGG                 GAGCCTG        ACC    GG
                                |||||||        |||    ||
                                CTCGGAC        TGG    CC
                                   CGATACAIII   AGAGT
GAM172  LOC257471 5'  TCCCTGAACCTGGACTTGACCA 3729             C   GA
          GT                    TCCCTGAGCCTGGAC TGA  GGT
                                |||||||||||||| |||  |||
                                AGGGACTTGGACCTG ACT  TCA
                                        A   GG
GAM172  LOC91351  3'  CCTGAGCCCTGGGCCAAG    3747         _  A  T
                                CCTGAGCC TGG CC GAG
                                |||||||| ||| || |||
                                GGACTCGG ACC GG TTC
                                    G   C  _
GAM173  FGF18    5'  GGCTGCTGCTGCTGCAGACTC  3750             TCAC
                                GGTTGCTGCTGCTGC    GCTC
                                ||||||||||||||    ||||
                                CCGACGACGACGACG    TGAG
                                        TC__
GAM173  FGF18    5'  GGCTGCTGCTGCTGCAGACTC  3750             TCAC
                                GGTTGCTGCTGCTGC    GCTC
                                ||||||||||||||    ||||
                                CCGACGACGACGACG    TGAG
                                        TC__
GAM173  GUCY1A3  5'  GGTGGCCCCCTGCTCACGCT   3751      T   G TG
                                GGT GCT C  CTGCTCACGCT
                                ||| ||| |  ||||||||||
                                CCA CGG G  GACGAGTGCGA
                                  C   G __
GAM173  HMOX2    5'  GGTTCTTGCTGCTCTCGCTCC  3752       G  GC       A
                                GGTT CT  TGCTGCTC CGCTCC
                                |||| ||  |||||||| ||||||
                                CCAA GA  ACGACGAG GCGAGG
                                  _ __       A
GAM173  IRS1     5'  GTTGCTGCTGCTGCTGCT    3753              CAC
                                GTTGCTGCTGCTGCT   GCT
                                ||||||||||||||   |||
                                CAACGACGACGACGA   CGA
                                                ___
GAM173  IRS2     5'  GTTGCTGCTGCTGCTGCC    3754              CAC
                                GTTGCTGCTGCTGCT   GCT
                                ||||||||||||||   |||
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                                CAACGACGACGACGA  CGG
                                                 ___
GAM173  MAN2A2   3'  TGTCCACCTGCTGCTCGTGCTC 3755    _ TG _      AC
            C                    TG C  C TGCTGCTC  GCTCC
                                 || |  | ||||||||  ||||||
                                 AC G  G ACGACGAG  CGAGG
                                  A GT G       CA
GAM173  PIM1     5'  GGTTGCTGCTGCTGCTGCT   3756            CAC
                                 GGTTGCTGCTGCTGCT  GCT
                                 ||||||||||||||||  |||
                                 CCAACGACGACGACGA  CGA
                                                 ___
GAM173  AMOT     5'  GTTGCTGCTGCTGCTGAC    3757            C
                                 GTTGCTGCTGCTGCT AC
                                 ||||||||||||||| ||
                                 CAACGACGACGACGA TG
                                                 C
GAM173  BIKE     3'  GTTGCTGCTGCTGCTGCT    3753           CAC
                                 GTTGCTGCTGCTGCT  GCT
                                 ||||||||||||||  |||
                                 CAACGACGACGACGA  CGA
                                                 ___
GAM173  BIKE     3'  GTTGCTGTTGCTGCTGCT    3758       C     CAC
                                 GTTGCTG TGCTGCT  GCT
                                 ||||||| |||||||  |||
                                 CAACGAC ACGACGA  CGA
                                      A     ___
GAM173  BIKE     3'  GTTGCTGTTGCTGCTGCT    3758       C     CAC
                                 GTTGCTG TGCTGCT  GCT
                                 ||||||| |||||||  |||
                                 CAACGAC ACGACGA  CGA
                                      A     ___
GAM173  C14orf4  5'  GTTGCTGCTGCTGCTGCT    3753           CAC
                                 GTTGCTGCTGCTGCT  GCT
                                 ||||||||||||||  |||
                                 CAACGACGACGACGA  CGA
                                                 ___
GAM173  C14orf4  5'  GTTGCTGCTGCTGCTGCT    3753           CAC
                                 GTTGCTGCTGCTGCT  GCT
                                 ||||||||||||||  |||
                                 CAACGACGACGACGA  CGA
                                                 ___
GAM173  CDC10    5'  GGTGCTGCTGTTGACGCTC   3759     T     C  CTC
                                 GGT GCTGCTG TG   ACGCTC
                                 ||| ||||||| ||   ||||||
                                 CCA CGACGAC AC   TGCGAG
                                   _      A  ___
GAM173  CLIC4    5'  GGCTGCTGCTGCTGCTGCTGCT 3760             CAC
                                 GGTTGCTGCTGCTGCT  GCT
                                 ||||||||||||||||  |||
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                                CCGACGACGACGACGA  CGA
                                          CGA
GAM173  DKFZp434N035 3'  AGTTGCTGCTCCGTGCTC    3761          GC_
                                GGTTGCTGCT  TGCTC
                                ||||||||||  |||||
                                TCAACGACGA  ACGAG
                                     GGC
GAM173  FLJ10157  5'  GCTTGCTGCTGCTGCTGGCGTC 3762    G          CA  C
          C                      G TTGCTGCTGCTGCT  CG TCC
                                | ||||||||||||||  || |||
                                C AACGACGACGACGA  GC AGG
                                 G           CC  _
GAM173  FLJ12505  5'  GGCTGCTGCTGCTGCTGCT   3763             CAC
                                GGTTGCTGCTGCTGCT  GCT
                                ||||||||||||||||  |||
                                CCGACGACGACGACGA  CGA
                                          ___
GAM173  IL18BP   3'  GGTTGTGCTGCTGCTGGCC   3764       C       CAC
                                GGTTG TGCTGCTGCT  GCT
                                |||||  ||||||||||  |||
                                CCAAC ACGACGACGA  CGG
                                   _        C__
GAM173  KIAA0935  3'  GGTGCTGCTGTGAGTCTTGTGC 3765     T     CTG__  CAC
          TC                     GGT GCTGCTG    CT  GCTC
                                ||| |||||||    ||  ||||
                                CCA CGACGAC    GA  CGAG
                                  _      ACTCA  ACA
GAM173  KIAA1028  3'  GGTTCTGCTGCTGTTGCT    3766      G       CTCAC
                                GGTT CTGCTGCTG    GCT
                                ||||  |||||||||    |||
                                CCAA GACGACGAC    CGA
                                  _       AA___
GAM173  KIAA1819  5'  GGCTGCTGTTGCTGCTGCT   3767        C      CAC
                                GGTTGCTG TGCTGCT  GCT
                                ||||||||  |||||||  |||
                                CCGACGAC ACGACGA  CGA
                                     A      ___
GAM173  MGC12435  5'  GGTTGCTACTGTCACTGCTC  3768          ___
                                GGTTGCTGCTG  CTGCTC
                                ||||||||||  ||||||
                                CCAACGATGAC  GACGAG
                                      AGT
GAM173  N4BP3    3'  GTTGCTGCTGTCAGCTCGCTC  3769         CT_  AC
                                GTTGCTGCTG  GCTC  GCTC
                                |||||||||  ||||  ||||
                                CAACGACGAC  CGAG  CGAG
                                      AGT  __
GAM173  OSBPL10   5'  GGCTGCTGCTGCTGCTACAGCT 3770             _  C
          CC                     GGTTGCTGCTGCTGCT CA GCTCC
                                ||||||||||||||| || |||||
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                                CCGACGACGACGACGA GT CGAGG
                                          T _
GAM173  RNPC2    5'  GATTGCTGCTGCTGCTGCT   3771            CAC
                                GGTTGCTGCTGCTGCT   GCT
                                ||||||||||||||||  |||
                                CTAACGACGACGACGA   CGA
                                          ___
GAM173  SMARCF1  3'  GCTTGCTGCTGACCCAGC    3772     _     _   C
                                GCT GCTGCTG CTCA GC
                                ||| ||||||| |||| ||
                                CGA CGACGAC GGGT CG
                                  A      T   _
GAM173  SMARCF1  3'  GCTTGCTGCTGACCCAGC    3772     _     _   C
                                GCT GCTGCTG CTCA GC
                                ||| ||||||| |||| ||
                                CGA CGACGAC GGGT CG
                                  A      T   _
GAM173  SMARCF1  3'  GCTTGCTGCTGACCCAGC    3772     _     _   C
                                GCT GCTGCTG CTCA GC
                                ||| ||||||| |||| ||
                                CGA CGACGAC GGGT CG
                                  A      T   _
GAM173  ZF       3'  GGTTACTGTGTCACATTCATGC 3773         C  CT  __   C
           T                     GGTTGCTG TG  GC  TCA GCT
                                ||||||||  ||  ||  ||| |||
                                CCAATGAC AC  TG  AGT CGA
                                     _ AG  TA   A
GAM173  LOC115110 3'  GTTGCTGCTGACTCACGTTCC  3774          CT      C
                                GTTGCTGCTG  GCTCACG TCC
                                ||||||||||  ||||||| |||
                                CAACGACGAC  TGAGTGC AGG
                                     __      A
GAM173  LOC146520 5'  GGTTGCTGCTTGCTGTTCGCTC 3775          _   CTCA
           C                     GGTTGCTGCT GCTG    CGCTCC
                                ||||||||||  ||||    ||||||
                                CCAACGACGA CGAC    GCGAGG
                                     A    AA__
GAM173  LOC151127 5'  GGGAAGCTGTTGCTCACGCTCC 3776     TTGCT    C
                                GG     GCTG TGCTCACGCTCC
                                ||     ||||  ||||||||||||
                                CC     CGAC ACGAGTGCGAGG
                                 CTT__    A
GAM173  LOC152282 3'  GGCTGCTGCTGCTGCTGCT   3763            CAC
                                GGTTGCTGCTGCTGCT   GCT
                                ||||||||||||||||  |||
                                CCGACGACGACGACGA   CGA
                                          ___
GAM173  LOC152282 3'  GGCTGCTGCTGCTGCTAC    3778            C
                                GGTTGCTGCTGCTGCT AC
                                ||||||||||||||||  ||
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                                CCGACGACGACGACGA TG
                                                _
GAM173  LOC152282 3'  GGCTGCTGCTGCTGCTGCT   3763              CAC
                                GGTTGCTGCTGCTGCT  GCT
                                |||||||||||||||  |||
                                CCGACGACGACGACGA  CGA
                                                ___
GAM173  LOC152282 3'  GGCTGCTGCTGCTGCTGCT   3763              CAC
                                GGTTGCTGCTGCTGCT  GCT
                                |||||||||||||||  |||
                                CCGACGACGACGACGA  CGA
                                                ___
GAM173  LOC152282 3'  GGCTGCTGTTGCTGCTAC    3777         C      C
                                GGTTGCTG TGCTGCT AC
                                |||||||| ||||||| ||
                                CCGACGAC ACGACGA TG
                                     A      _
GAM173  LOC256228 5'  GGCTGCTGTGCTCCTCATGCTC 3779         C    G    C
                                GGTTGCTG TGCT CTCA GCTC
                                |||||||| |||| |||| ||||
                                CCGACGAC ACGA GAGT CGAG
                                     _   G    A
GAM173  LOC256950 3'  GGATGCTGCTGTTTGGAGGCTC 3780     T       CTGCTCAC
          C                      GG TGCTGCTG       GCTCC
                                || ||||||||       |||||
                                CC ACGACGAC       CGAGG
                                 T       AAACCTC_
GAM173  LOC91409  3'  GGTTGCGCTGCTGAAAGTGTGC 3781        T      CTCA____
          GCTC                     GGTTGC GCTGCTG       CGCTC
                                |||||| |||||||       |||||
                                CCAACG CGACGAC       GCGAG
                                     _      TTTCACAC
GAM174  B3GALT2   3'  AAACTGCAGGTTTGCAAACTTG 3784          AC_    _ GTAC
          GC                     AAACTGCAG   TGCGA C    GGC
                                |||||||||   ||||| |    |||
                                TTTGACGTC   ACGTT G    CCG
                                     CAA     T AA__
GAM174  CAPN1    3'  GGACTGCAGACTGTGTCGAGC  3785    A        CGAC  A  _
                                A ACTGCAGACTG    GT CG GC
                                | ||||||||||    || || ||
                                C TGACGTCTGAC    CA GC CG
                                 C          A___  _  T
GAM174  COG6     3'  AAACTGCAGAGCTGGAGAGATG 3786          _   C  CGTAC
          GC                     AAACTGCAGA CTG GA     GGC
                                |||||||||| ||| ||     |||
                                TTTGACGTCT GAC CT     CCG
                                     C   _  CTCTA
GAM174  IRAK1    3'  CTGCAGACGCCCTGCATGGC   3787         T  GAC   C
                                CTGCAGAC GC   GTA GGC
                                |||||||| ||   ||| |||
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                                GACGTCTG CG   CGT CCG
                                    _ GGA   A
GAM174   LDLR    3'  CAGACTGCGGACTGCAGTGGC  3788          _ _  C_
                                CAGACTGCG AC GTA  GGC
                                ||||||||| || |||  |||
                                GTCTGACGC TG CGT  CCG
                                     C  A   CA
GAM174   MYLK2   3'  ACTGGAGGCTGCCCCATGGC  3789      C  A   GA   AC
                                ACTG AG CTGC  CGT  GGC
                                |||| || ||||  |||  |||
                                TGAC TC GACG  GTA  CCG
                                  C  C    GG  __
GAM174   NR4A2   3'  CTGAGACTGCTCACACGGC   3790      C      GA
                                CTG AGACTGC  CGTACGGC
                                ||| |||||||  ||||||||
                                GAC TCTGACG  GTGTGCCG
                                  _      A_
GAM174   PLDN    5'  AAACTGCGGGCTTCGATCACG  3791        AGA  G   CG
                                AAACTGC   CT CGA  TACG
                                |||||||   || |||  ||||
                                TTTGACG   GA GCT  GTGC
                                    CCC  A   A_
GAM174   PTMS    5'  ACCGCAGGCTGCGGCCGT    3792        A    A_
                                ACTGCAG CTGCG  CGT
                                ||||||| |||||  |||
                                TGGCGTC GACGC  GCA
                                    C    CG
GAM174   TAL1    3'  CTGCAGACAGCAATGATGGC   3793        T   CGTAC
                                CTGCAGAC GCGA    GGC
                                |||||||| ||||    |||
                                GACGTCTG CGTT    CCG
                                     T   ACTA_
GAM174   TPK1    5'  CGCAGGCTGCGGGAGCTACGGC 3794       A    AC_ _
                                TGCAG CTGCG   GT ACGGC
                                ||||| |||||   || |||||
                                GCGTC GACGC   CG TGCCG
                                   C    CCT  A
GAM174   ABLIM   3'  AAACTGCAAACTGCAGTGTGGC 3795            AC  AC
                                AAACTGCAGACTGCG  GT  GGC
                                ||||||||||||||  ||  |||
                                TTTGACGTTTGACGT  CA  CCG
                                         CA  __
GAM174   ABLIM   3'  AAACTGCAAACTGCAGTGTGGC 3795            AC  AC
                                AAACTGCAGACTGCG  GT  GGC
                                ||||||||||||||  ||  |||
                                TTTGACGTTTGACGT  CA  CCG
                                         CA  __
GAM174   FBXO9   5'  AACTGCGGGCCCGGCGTACGGC 3796        AGA  G  A
                                AACTGC   CT CG CGTACGGC
                                ||||||   || || ||||||||
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                                TTGACG   GG GC GCATGCCG
                                   CCC  _  C
GAM174  FLJ11218  3'  AACTGCAGATCATACGG     3797          CTGCGA
                                AACTGCAGA     CGTACGG
                                |||||||||     |||||||
                                TTGACGTCT     GTATGCC
                                   A_____
GAM174  KIAA1257  3'  AAACTGCAAACTGCCAAATGCG 3798             GAC  A
          GC                      AAACTGCAGACTGC   GT CGGC
                                |||||||||||||   || ||||
                                TTTGACGTTTGACG   TA GCCG
                                      GTT  C
GAM174  KIAA1456  3'  ACTGCAGCTGCTTGTCTGG   3799        A   GAC  AC
                                ACTGCAG CTGC   GT  GG
                                |||||||  ||||   ||  ||
                                TGACGTC GACG   CA  CC
                                   _   AA_  GA
GAM174  KIAA1549  3'  CTGTCACACGACGTATGGC   3800     _  GAC       C
                                CTG CA   TGCGACGTA GGC
                                |||  ||   |||||||||  |||
                                GAC GT   GTGCTGCAT CCG
                                  A  ___       A
GAM174  MGC3165   3'  AACTGCAGGATCAGTGCGGC  3801         ACTG  AC  A
                                AACTGCAG    CG  GT CGGC
                                ||||||||    ||  ||  ||||
                                TTGACGTC    GT  CA GCCG
                                     CTA_  __  C
GAM174  RAI17     3'  ACTGCAGGCTGTAGGCACCAC  3802        A  CGAC   G
                                ACTGCAG CTG    GTAC GC
                                |||||||  |||    ||||  ||
                                TGACGTC GAC    CGTG TG
                                   C   ATC_    G
GAM174  SS-56     3'  TGCAGACTGTATCATGGC    3803          CGA   AC
                                TGCAGACTG   CGT  GGC
                                |||||||||   |||  |||
                                ACGTCTGAC   GTA  CCG
                                     ATA   __
GAM174  LOC118851 3'  ACTGCAGGCTGTGGTCCAG   3804        A   CGAC  A
                                ACTGCAG CTG    GT CGG
                                |||||||  |||    ||  |||
                                TGACGTC GAC    CA GTC
                                   C   AC__   G
GAM174  LOC197423 5'  CTGCAGACTGTGCAGG      3805          CGAC   C
                                CTGCAGACTG    GTA GG
                                ||||||||||    |||  ||
                                GACGTCTGAC    CGT CC
                                     A___   _
GAM174  LOC220110 5'  ACTGCGGACCTCGACTGCGGC  3806       A   G   GTA
                                ACTGC GACT CGAC   CGGC
                                |||||  ||||  ||||   ||||
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                                TGACG CTGG GCTG   GCCG
                                  C    A    AC_
GAM174  LOC255057 3'  GGACTGCAGACGGCGGGG    3807    A       T   ACGTAC
                                A ACTGCAGAC GCG     GG
                                | ||||||||| |||     ||
                                C TGACGTCTG CGC     CC
                                 C       C   C_____
GAM175  AGRN     5'  CCAGGTCTTTGCCCTTCAA   3810      AACC
                                CCAG    TTGCCCTTCAG
                                ||||    ||||||||||
                                GGTC    AACGGGAAGTT
                                  CAGA
GAM175  CNTN2    3'  CCAGGGCTTGCCCTTCTTCC  3811      AAC       AG
                                CCAG   CTTGCCCTTC  TC
                                ||||   ||||||||||  ||
                                GGTC   GAACGGGAAG  GG
                                  CC_        AA
GAM175  DHCR7    3'  CCAGAGTCTGCACAGTCAC   3812      ACC    CCTT
                                CCAGA   TTGC    CAGTCAC
                                |||||   ||||    |||||||
                                GGTCT   GACG    GTCAGTG
                                  CA_    T___
GAM175  DYRK1A   3'  CAGATGTCCTTCAGTCA     3813      ACCT  C
                                CAGA    TG CCTTCAGTCA
                                ||||    || ||||||||||
                                GTCT    AC GGAAGTCAGT
                                  _____  A
GAM175  F8       3'  AGGACTCTAGTTTTCAGTCAC  3814     A  _  TGCCC
                                AG AC CT     TTCAGTCAC
                                || || ||     |||||||||
                                TC TG GA     AAGTCAGTG
                                 C  A  TCAA_
GAM175  GAS7     3'  AGAATCTGCCCCTCGCTCA   3815      CC       AG
                                AGAA  TTGCCCTTC  TCA
                                ||||  |||||||||  |||
                                TCTT  GACGGGGAG  AGT
                                  A_        CG
GAM175  GJA5     5'  CCAGACCTTGCCTACCA     3816       A      CT
                                CCAGA CCTTGCC  TCA
                                ||||| |||||||  |||
                                GGTCT GGAACGG  GGT
                                  _      AT
GAM175  MAGEA12  5'  CAGAACCTTGCCTCCTCA    3817           _
                                CAGAACCTTGCC CTTCA
                                |||||||||||| |||||
                                GTCTTGGAACGG GGAGT
                                       A
GAM175  MAGEA4   5'  CAGAACCTTGACTCCTCACA  3818          CC    AG
                                CAGAACCTTG  CTTC  TCACA
                                ||||||||||  ||||  |||||
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                                GTCTTGGAAC  GAGG  AGTGT
                                      T_   __
GAM175  MID1     3'  CAGAACCTTTCTTTCCAACA  3819         GCCC    T
                                CAGAACCTT    TTCAG CA
                                |||||||||    ||||| ||
                                GTCTTGGAA    AGGTT GT
                                     AGAA    _
GAM175  NAT1     5'  CCAGCACTTCCTTCAGTCACA  3820       AAC   GC
                                CCAG   CTT  CCTTCAGTCACA
                                ||||   |||  ||||||||||||
                                GGTC   GAA  GGAAGTCAGTGT
                                  GT_   __
GAM175  NXF3     3'  CCAGATCTCCTGGTTCAGTCAC 3821       AC_   CCC
            A                    CCAGA   CTTG   TTCAGTCACA
                                 |||||   ||||   ||||||||||
                                 GGTCT   GGAC   AAGTCAGTGT
                                    AGA   C__
GAM175  THOP1    3'  CCAGAGCCTGCCCCATC     3822       A   T    TCA
                                 CCAGA CCT GCCCT   GTC
                                 |||||| ||| |||||   |||
                                 GGTCT GGA CGGGG   TAG
                                    C   _    ___
GAM175  ZNF131   3'  CAAAACTCCCCTTCAGT     3823        CT G
                                 CAGAAC  T CCCTTCAGT
                                 ||||||  | |||||||||
                                 GTTTTG  A GGGAAGTCA
                                    __ G
GAM175  AP1M2    3'  CCAGGACCTGCCCTCA      3824       A    T   TTCAG
                                 CCAG ACCT GCCC     TCA
                                 |||| |||| ||||     |||
                                 GGTC TGGA CGGG     AGT
                                   C   _   _____
GAM175  BIKE     3'  CCTGAATTTTGCCCTCAAATGC 3825     A   CC       C   _
            A                    CC GAA  TTGCCCTT AGT CA
                                 || |||  |||||||| ||| ||
                                 GG CTT  AACGGGAG TTA GT
                                  A   AA       T   C
GAM175  CDC14B   3'  AGAGTCTTCCTTCAGCTCTGGT 3826     AC   GC      _______
            CACA                   GA  CTT  CCTTCAGT     CACA
                                 ||  |||  ||||||||     ||||
                                 CT  GAA  GGAAGTCG     GTGT
                                  CA  __       AGACCA
GAM175  CDC14B   3'  AGAGTCTTCCTTCAGCTCTGGT 3826     AC   GC      _______
            CACA                   GA  CTT  CCTTCAGT     CACA
                                 ||  |||  ||||||||     ||||
                                 CT  GAA  GGAAGTCG     GTGT
                                  CA  __       AGACCA
GAM175  CHL1     3'  CACAACCTTGCCCTCCTCACA  3827     G          AG
                                 CA AACCTTGCCCTTC  TCACA
                                 || ||||||||||||  |||||
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                                GT TTGGAACGGGAGG  AGTGT
                                 G         __
GAM175  DIO2     3'  CAGCCTTCCTTCAGT      3828     AA   GC
                                CAG  CCTT  CCTTCAGT
                                |||  ||||  ||||||||
                                GTC  GGAA  GGAAGTCA
                                  __   __
GAM175  DIO2     3'  CAGCCTTCCTTCAGT      3828     AA   GC
                                CAG  CCTT  CCTTCAGT
                                |||  ||||  ||||||||
                                GTC  GGAA  GGAAGTCA
                                  __   __
GAM175  DKFZP434L1435 5'  CAAAAGCTTTTCAGTCACA   3829      CCTT  CC
                                CAGAA   GC  TTCAGTCACA
                                |||||   ||  ||||||||||
                                GTTTT   CG  AAGTCAGTGT
                                   ____  AA
GAM175  FLJ10700  3'  AAAACTGGTCTTCAGTCACA  3830      CT  CC
                                AGAAC  TG  CTTCAGTCACA
                                |||||  ||  ||||||||||
                                TTTTG  AC  GAAGTCAGTGT
                                   __  CA
GAM175  FLJ10898  3'  AAACTTTTCTCAGTCAC     3831      C  GCCC
                                GAAC TT   TTCAGTCAC
                                ||||  ||   |||||||||
                                TTTG AA   GAGTCAGTG
                                  _  AA__
GAM175  FLJ22035  3'  CCAGAGCCTGCCCTTTCCCACA 3832      A  T    CAG
                                CCAGA CCT GCCCTT  TCACA
                                |||||  |||  ||||||  |||||
                                GGTCT GGA CGGGAA  GGTGT
                                   C  _     AG_
GAM175  GK001    5'  CCAGAACCGTAGCTCAGTCAC  3833       TT_  CCT
                                CCAGAACC   GC   TCAGTCAC
                                ||||||||   ||   ||||||||
                                GGTCTTGG   CG   AGTCAGTG
                                     CAT  ___
GAM175  GRIN3A   3'  CCAGAACCTTCTCAAAAACA  3834        GCCC    TC
                                CCAGAACCTT   TTCAG  ACA
                                ||||||||||   |||||  |||
                                GGTCTTGGAA   GAGTT  TGT
                                      ____    TT
GAM175  HES2     5'  ACCTTGCCCCAGTCGCA     3835        TT    A
                                ACCTTGCCC  CAGTC CA
                                |||||||||  |||||  ||
                                TGGAACGGG  GTCAG GT
                                     __    C
GAM175  HNRPA0   5'  CCCGGGCCTTGCCCCCGCC   3836     AGAA       CA
                                CC   CCTTGCCCTT  GTC
                                ||   ||||||||||  |||
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                                GG   GGAACGGGGG  CGG
                                 GCCC        __
GAM175  KIAA0153  3'  GAATCCTGCCCCAAGCACA   3837     C       TC  T
                                GAA CTTGCCCT  AG CACA
                                ||| ||||||||  || ||||
                                CTT GGACGGGG  TC GTGT
                                  A       T_  _
GAM175  KIAA0258  3'  CAGAGCTTTAGCCCCAATCACA 3838      ACCTT_   TT
                                CAGA     GCCC  CAGTCACA
                                ||||     ||||  ||||||||
                                GTCT     CGGG  GTTAGTGT
                                  CGAAAT   __
GAM175  KIAA0295  3'  CCAAGGGTCTGCCTTCAGTCA  3839      AACC    C
                                CCAG    TTGCC TTCAGTCA
                                ||||    ||||| ||||||||
                                GGTT    GACGG AAGTCAGT
                                  CCCA    _
GAM175  KIAA1058  3'  CCAGAACCTTTTTTTTCTGT   3840         GCCC   A
                                CCAGAACCTT    TTC GT
                                ||||||||||    ||| ||
                                GGTCTTGGAA    AAG CA
                                      AAAA   A
GAM175  MDS018    3'  CAGAGTCCTGCCAACTCGC   3841      AC     C_   A
                                CAGA  CTTGCC  TTC GT
                                ||||  ||||||  ||| ||
                                GTCT  GGACGG  GAG CG
                                  CA     TT   _
GAM175  MGC15634  3'  AGAACCTTCTCCTTAAAT    3842        GC    C
                                AGAACCTT  CCTT AGT
                                ||||||||  |||| |||
                                TCTTGGAA  GGAA TTA
                                     GA    T
GAM175  MGC3123   3'  GAACTTTATTCAGTCACA    3843      C   CCC
                                GAAC TTG   TTCAGTCACA
                                |||| |||   ||||||||||
                                CTTG AAT   AAGTCAGTGT
                                  A   ___
GAM175  OSR2      5'  CCAGAACCTCGCTCTTCGGC   3844          C    A
                                CCAGAACCTTGC CTTC GT
                                |||||||||||| |||| ||
                                GGTCTTGGAGCG GAAG CG
                                       A    C
GAM175  RAB14     3'  GAATAAATCCTTCAGTCACA   3845     CCTTGC
                                GAA     CCTTCAGTCACA
                                |||     ||||||||||||
                                CTT     GGAAGTCAGTGT
                                  ATTTA_
GAM175  RAB9B     3'  CAGAACCTTGTCTCTTACCCTC 3846          ________    CA
            TTGT                  CAGAACCTTG      CCCTT  GT
                                ||||||||||      |||||  ||
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                                GTCTTGGAAC      GGGAG  CA
                                     AGAGAAT    AA
GAM175  REPRIMO   3' CCAGAGCTTGGCCCACCTGC  3847       AC   _  T  A
                                CCAGA  CTTG CCC TC GT
                                |||||  |||| ||| || ||
                                GGTCT  GAAC GGG GG CG
                                   C_   C   T  A
GAM175  RISC      3' CAGAACCTTCTTGATCAC    3848         GCC   CA
                                CAGAACCTT   CTT  GTCAC
                                |||||||||   |||  |||||
                                GTCTTGGAA   GAA  TAGTG
                                     ___   C_
GAM175  STMN4     3' CCAGGACTCTGTCCTTCA    3849       A  C   C
                                CCAG AC TTG CCTTCA
                                |||| || ||| ||||||
                                GGTC TG GAC GGAAGT
                                  C  A   A
GAM175  TP53INP1  5' CAAAACCTTGTCTTTAGT    3850          CC   C
                                CAGAACCTTG  CTT AGT
                                ||||||||||  ||| |||
                                GTTTTGGAAC  GAA TCA
                                     A_   A
GAM175  UNC5D     3' AGAACTTTGCCTTCAATACA  3851       C    C     C
                                AGAAC TTGCC TTCAGT ACA
                                ||||| ||||| |||||| |||
                                TCTTG AACGG AAGTTA TGT
                                  A    _     _
GAM175  VILL      5' CCAGGTCTTTGCCCTTCTCA  3852       AACC       AG
                                CCAG    TTGCCCTTC  TCA
                                ||||    |||||||||  |||
                                GGTC    AACGGGAAG  AGT
                                  CAGA        __
GAM175  ZMPSTE24  3' CAGAAATGTCTTCAGTCACA  3853       CCT  CC
                                CAGAA   TG  CTTCAGTCACA
                                |||||   ||  ||||||||||
                                GTCTT   AC  GAAGTCAGTGT
                                   T__  A_
GAM175  LOC121219 5' CCAGAACCTTTTTGTAAGTTAC 3854          GCCCTTC   C
           A                     CCAGAACCTT      AGT ACA
                                 ||||||||||      ||| |||
                                 GGTCTTGGAA      TCA TGT
                                      AAACAT_   A
GAM175  LOC130507 3' AGCATTTTGCTCTTCAACCACA 3855     AACC    C     GT
                                AG    TTGC CTTCA  CACA
                                ||    |||| |||||  ||||
                                TC    AACG GAAGT  GTGT
                                 GTAA    A     TG
GAM175  LOC138429 3' AGCACCTTGCTCCAGTCACA  3856     A      CC
                                AG ACCTTGC  TTCAGTCACA
                                || |||||||  ||||||||||
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                                TC TGGAACG  AGGTCAGTGT
                                 G      __
GAM175  LOC145317 5'  CCGCAGGCCCTTCAGTCACA   3857     TT__
                                CC    GCCCTTCAGTCACA
                                ||    ||||||||||||||
                                GG    CGGGAAGTCAGTGT
                                 CGTC
GAM175  LOC145719 5'  CCAGGGACCCTGCCTTCAGTCG 3858       A_       C       A
          CA                      CCAG  ACCTTGCC TTCAGTC CA
                                ||||  |||||||| ||||||| ||
                                GGTC  TGGGACGG AAGTCAG GT
                                  CC        _       C
GAM175  LOC145720 5'  CCAGGGACCCTGCCTTCAGTCG 3858       A_       C       A
          CA                      CCAG  ACCTTGCC TTCAGTC CA
                                ||||  |||||||| ||||||| ||
                                GGTC  TGGGACGG AAGTCAG GT
                                  CC        _       C
GAM175  LOC147136 3'  CCAAAGCTGTGATTCAGTCAC  3859       ACC   CCC
                                CCAGA   TTG   TTCAGTCAC
                                |||||   |||   |||||||||
                                GGTTT   GAC   AAGTCAGTG
                                  C__   ACT
GAM175  LOC149952 3'  AGAACCTTCCTGTCGTTACA   3860         G  CT  A  C
                                AGAACCTT CC  TC GT ACA
                                |||||||| ||  || || |||
                                TCTTGGAA GG  AG CA TGT
                                     _ AC  _  A
GAM175  LOC151199 3'  CCAGCAGTCTTCCAGTCAC    3861       AAC_  TGCCC
                                CCAG    CT    TTCAGTCAC
                                ||||    ||    |||||||||
                                GGTC    GA    AGGTCAGTG
                                  GTCA  _____
GAM175  LOC152286 5'  CAGGGACCTTGCCTCCCCCACA 3862       A_       C   AG
                                CAG  ACCTTGCC TTC  TCACA
                                |||  |||||||| |||  |||||
                                GTC  TGGAACGG AGG  GGTGT
                                  CC        _  G_
GAM175  LOC152502 3'  CAGGTGTTTCGTCAGTCACA   3863      AACC_   CCCT
                                CAG    TTG    TCAGTCACA
                                |||    |||    |||||||||
                                GTC    AGC    AGTCAGTGT
                                  CACAA   ____
GAM175  LOC152876 5'  CCAGGGCCCTGTCTCAGCCACA 3864       AA    CCC
                                CCAG  CCTTG   TTCAGTCACA
                                ||||  |||||   ||||||||||
                                GGTC  GGGAC   GAGTCGGTGT
                                  CC    A__
GAM175  LOC157349 5'  CCAGAGCCCTGCCCTGAGC   3865       A        TC
                                CCAGA CCTTGCCCT  AGT
                                ||||| |||||||||  |||
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                                GGTCT GGGACGGGA  TCG
                                   C       C_
GAM175  LOC159963 3'  GGAGATTTGCCCTTATCCCA  3866    C   ACC      CA  A
                                C AGA   TTGCCCTT  GTC CA
                                | |||   ||||||||  ||| ||
                                C TCT   AACGGGAA  TAG GT
                                 C   A__       __   G
GAM175  LOC168448 3'  AGAGTCTTCCTTCAGTTCTGGT 3867     AC   GC    _______
           CACA                    GA  CTT  CCTTCA     GTCACA
                                || |||  ||||||     ||||||
                                CT  GAA  GGAAGT     CAGTGT
                                 CA  __     CAAGAC
GAM175  LOC197114 5'  CCAGGGACCCTGCCTTCAGTCG 3858       A_       C       A
           CA                     CCAG  ACCTTGCC TTCAGTC CA
                                |||| |||||||| ||||||| ||
                                GGTC  TGGGACGG AAGTCAG GT
                                   CC       _       C
GAM175  LOC197117 5'  CCAGGGACCCTGCCTTCAGTCG 3858       A_       C       A
           CA                     CCAG  ACCTTGCC TTCAGTC CA
                                |||| |||||||| ||||||| ||
                                GGTC  TGGGACGG AAGTCAG GT
                                   CC       _       C
GAM175  LOC200583 5'  GAACATCAATTCAGTCAC    3868       C   CCC
                                GAAC TTG   TTCAGTCAC
                                |||| |||   |||||||||
                                CTTG AGT   AAGTCAGTG
                                   T   T__
GAM175  LOC203696 5'  CCAGAACCTGCTCAC       3869          T  CCTTCAG
                                CCAGAACCT GC      TCAC
                                ||||||||| ||      ||||
                                GGTCTTGGA CG      AGTG
                                      _ ________
GAM175  LOC220477 5'  CGAAAACCTTTCAGTCA     3870    C       GCCCT
                                C AGAACCTT    TCAGTCA
                                | ||||||||    |||||||
                                G TTTTGGAA    AGTCAGT
                                 C       ______
GAM175  LOC221002 3'  CAGTGTGTCTTTCAGTCACA   3871      AACCT  CCC
                                CAG    TG   TTCAGTCACA
                                |||    ||   ||||||||||
                                GTC    AC   AAGTCAGTGT
                                  AC___  AGA
GAM175  LOC253187 3'  CAGGTCTTTGCCCCTCCTTTAC 3872      AACC       AGTC
           A                     CAG   TTGCCCTTC   ACA
                                |||   |||||||||   |||
                                GTC   AACGGGGAG   TGT
                                  CAGA       GAAA
GAM175  LOC254381 5'  CCAGAGGCTTGTCCAGCCACA  3873       AC   CCC
                                CCAGA  CTTG   TTCAGTCACA
                                |||||  ||||   ||||||||||
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                                GGTCT  GAAC   AGGTCGGTGT
                                  CC   ___
GAM175  LOC255397 5'  CCTGGGCCTTGCCCTGCCTTTC 3874     AGAA       _ AG
           ACA                    CC    CCTTGCCCT TC  TCACA
                                ||   ||||||||| ||  |||||
                                GG   GGAACGGGA GG  AGTGT
                                 ACCC       C  AA
GAM175  LOC256401 3'  AGAGTCTTCCTTCAGTTCTGGT 3867     AC   GC     _______
           CACA                    GA  CTT  CCTTCA     GTCACA
                                ||  |||  ||||||     ||||||
                                CT  GAA  GGAAGT     CAGTGT
                                 CA  __     CAAGAC
GAM175  LOC257273 5'  CAGAACCTGCTCTTCTGC    3875         T  C    A
                                CAGAACCT GC CTTC GT
                                |||||||| || |||| ||
                                GTCTTGGA CG GAAG CG
                                     _ A    A
GAM175  LOC51189  3'  CCAGAACCATGTCTACAC    3876         T  CCCT  AGT
                                CCAGAACC TG    TC   CAC
                                |||||||| ||    ||   |||
                                GGTCTTGG AC    AG   GTG
                                     T  _____  AT_
GAM175  LOC92078  5'  GACCTTGCCTTGGAAGTCACA  3877     A      CTTC_
                                GA CCTTGCC     AGTCACA
                                || |||||||     |||||||
                                CT GGAACGG     TCAGTGT
                                 _      AACCT
GAM176  CCNC      3'  TACGGTACTTGATTAATTGATT 3880       C   CC________   GAAA
           TTA                    CGGTAC TGA        GAT    A
                                ||||||| |||        |||    |
                                GCCATG ACT        CTA    T
                                   A   AATTAAIII   AAAG
GAM176  DKFZP434P211 5'  GGTACCTGTGCAATCAAA    3881         AC    G
                                GGTACCTG  CGAT AAA
                                ||||||||  |||| |||
                                CCATGGAC  GTTA TTT
                                     AC    G
GAM176  LOC149506 3'  GGTAAAACACGATGAAAAT    3882      CCT   _
                                GGTA   GAC CGATGAAAAT
                                ||||   ||| ||||||||||
                                CCAT   TTG GCTACTTTTA
                                  T__   T
GAM176  LOC150174 5'  GGTACCTGTGCAATCAAA    3881         AC    G
                                GGTACCTG  CGAT AAA
                                ||||||||  |||| |||
                                CCATGGAC  GTTA TTT
                                     AC    G
GAM176  LOC150213 5'  GGTACCTGTGCAATCAAA    3881         AC    G
                                GGTACCTG  CGAT AAA
                                ||||||||  |||| |||
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                                CCATGGAC  GTTA TTT
                                    AC    G
GAM176  LOC219505 5'  AGCATGACTGATGAAAATC   3883      CC    C
                                GGTA  TGAC GATGAAAATC
                                ||||  |||| ||||||||||
                                TCGT  ACTG CTACTTTTAG
                                  __    A
GAM176  LOC219899 3'  GTACCTGAGATTAGAATC    3884        CC   GAA
                                GTACCTGA  GAT   AATC
                                ||||||||  |||   ||||
                                CATGGACT  CTA   TTAG
                                    __  ATC
GAM176  LOC221060 3'  GGTACTTAAACATGAAAAT   3885       C   C G
                                GGTAC TGA C ATGAAAAT
                                ||||| ||| | ||||||||
                                CCATG ATT G TACTTTTA
                                   A   T _
GAM177  ASB2     5'  CTGGACACCGCTGCTGT     3888       T    AA
                                CTGGA CACT  CTGCTGT
                                ||||| ||||  |||||||
                                GACCT GTGG  GACGACA
                                  _    C_
GAM177  DBH      3'  CTGGACCACTGTGCAGGCTGT  3889          AACT__
                                CTGGATCACT     GCTGT
                                ||||||||||     |||||
                                GACCTGGTGA     CGACA
                                     CACGTC
GAM177  DNMT3B   3'  CTGTCCCTGACTGCTGT     3890      GA  A  A
                                CTG  TC CT ACTGCTGT
                                |||  || || ||||||||
                                GAC  GG GA TGACGACA
                                 A_  _  C
GAM177  LDLR     5'  CCGGATCACGACCTGCTGT   3891         TAA
                                CTGGATCAC   CTGCTGT
                                |||||||||   |||||||
                                GGCCTAGTG   GACGACA
                                     CTG
GAM177  LNK      3'  CTAGAAGCCACTGCTGT     3892       TCA   A
                                CTGGA   CTA CTGCTGT
                                |||||   ||| |||||||
                                GATCT   GGT GACGACA
                                  TC_   _
GAM177  OSM      3'  CTGGGACACCCTGCCGCTGT  3893      AT    AA_
                                CTGG  CACT   CTGCTGT
                                ||||  ||||   |||||||
                                GACC  GTGG   GGCGACA
                                  CT    GAC
GAM177  PAFAH1B1 3'  TGAAAAACAAACTGCTGT    3894      TC  T
                                TGGA  AC AACTGCTGT
                                ||||  || |||||||||
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                                ACTT  TG TTGACGACA
                                  TT  T
GAM177  PML      3'  CTGGACTCACTGCTGCTGT   3895      _    AA
                                CTGGA TCACT  CTGCTGT
                                ||||| |||||  |||||||
                                GACCT AGTGA  GACGACA
                                   G    C_
GAM177  PTGS1    3'  CTGAGATCACTGCTGT     3896     _     AACT
                                CTG GATCACT   GCTGT
                                ||| |||||||   |||||
                                GAC CTAGTGA   CGACA
                                  T     ____
GAM177  PTGS1    3'  CTGAGATCACTGCTGT     3896     _     AACT
                                CTG GATCACT   GCTGT
                                ||| |||||||   |||||
                                GAC CTAGTGA   CGACA
                                  T     ____
GAM177  RAP1     3'  TGGATCACTACTATGT     3897         A   C
                                TGGATCACTA CTG TGT
                                |||||||||| ||| |||
                                ACCTAGTGAT GAT ACA
                                       _  _
GAM177  SHOX     5'  TGGATCACCAGCGCTGT    3898         AC
                                TGGATCACTA  TGCTGT
                                ||||||||||  ||||||
                                ACCTAGTGGT  GCGACA
                                      C_
GAM177  SHOX     5'  TGGATCACCAGCGCTGT    3898         AC
                                TGGATCACTA  TGCTGT
                                ||||||||||  ||||||
                                ACCTAGTGGT  GCGACA
                                      C_
GAM177  SNX5     3'  CTGAATCACCTGCTGT     3899         TAA
                                CTGGATCAC   CTGCTGT
                                |||||||||   |||||||
                                GACTTAGTG   GACGACA
                                       ___
GAM177  TNFRSF9  3'  TGGACCACTGGACTATGT   3900         A_   C
                                TGGATCACT  ACTG TGT
                                |||||||||  |||| |||
                                ACCTGGTGA  TGAT ACA
                                      CC   _
GAM177  C1orf16  3'  CTGGACCCCATGCTGT     3901        A  AC
                                CTGGATC CTA  TGCTGT
                                ||||||| |||  ||||||
                                GACCTGG GGT  ACGACA
                                       _  __
GAM177  DKFZP564C103 3'  CTGGACCACCTGTTGT     3902         TAA  C
                                CTGGATCAC   CTG TGT
                                |||||||||   ||| |||
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                                GACCTGGTG   GAC ACA
                                    ___   A
GAM177  DKFZP727M111 5'  CTGGGCCAGCAACCGCTGC   3903      AT  C
                                CTGG  CA TAACTGCTGT
                                ||||  || ||||||||||
                                GACC  GT GTTGGCGACG
                                  CG  C
GAM177  EIF2B3   5'  CCGGGTCAGACCGCTGT    3904      A   CTA
                                CTGG TCA   ACTGCTGT
                                |||| |||   ||||||||
                                GGCC AGT   TGGCGACA
                                  C   C__
GAM177  ENPP4    3'  CTGGCACCACTGTTGT     3905      AT    A   C
                                CTGG  CACTA CTG TGT
                                ||||  ||||| ||| |||
                                GACC  GTGGT GAC ACA
                                  __    _   A
GAM177  FLJ10895 3'  CTGGATCAGTCCATCACTGT   3906         __   ACT
                                CTGGATCA  CTA   GCTGT
                                ||||||||  |||   |||||
                                GACCTAGT  GGT   TGACA
                                    CA   AG_
GAM177  FLJ13902 3'  CTGGCCCCAACTGCTGT    3907      A  A
                                CTGG TC CTAACTGCTGT
                                |||| || ||||||||||
                                GACC GG GGTTGACGACA
                                  _ _
GAM177  FLJ22215 3'  TGGATCACAACCTTGT     3908         T   GC
                                TGGATCAC AACT  TGT
                                |||||||| ||||  |||
                                ACCTAGTG TTGG  ACA
                                    _   A_
GAM177  FLJ30294 3'  TAGAACAACTGCTGT      3909      TC  T
                                TGGA  AC AACTGCTGT
                                ||||  || |||||||||
                                ATCT  TG TTGACGACA
                                  __  _
GAM177  KALI     3'  CTGGATCATAAACTCTCTGT  3910         CT   G_
                                CTGGATCA  AACT  CTGT
                                ||||||||  ||||  ||||
                                GACCTAGT  TTGA  GACA
                                    AT   GA
GAM177  KIAA0368 3'  CTGGCACAAAGACTGCTGT   3911      AT   TA__
                                CTGG  CAC    ACTGCTGT
                                ||||  |||    ||||||||
                                GACC  GTG    TGACGACA
                                  __   TTTC
GAM177  KIAA0555 3'  TGGGTCACCAACACTGT     3912      A      T
                                TGG TCACTAAC GCTGT
                                ||| |||||||| |||||
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                                ACC AGTGGTTG TGACA
                                  C       _
GAM177  KIAA0852  5'  CTCGATTCAGACTGCTGT    3913     G   _  CTA
                                CT GAT CA   ACTGCTGT
                                || ||| ||   ||||||||
                                GA CTA GT   TGACGACA
                                 G   A  C__
GAM177  KIAA1145  3'  TACACGACTGACTGCTGT    3914     G  C   A
                                TG AT ACT ACTGCTGT
                                || || ||| ||||||||
                                AT TG TGA TGACGACA
                                 G  C   C
GAM177  KIAA1157  3'  TGGACCACACTGCTGT      3915         TA
                                TGGATCAC  ACTGCTGT
                                ||||||||  ||||||||
                                ACCTGGTG  TGACGACA
                                          __
GAM177  KIAA1485  3'  CTGGATCATGACCGTGT     3916         CTA    C
                                CTGGATCA   ACTG TGT
                                ||||||||   |||| |||
                                GACCTAGT   TGGC ACA
                                     AC_   _
GAM177  PLAGL2    3'  CTGACCAACTGACTGCTGT   3917      G   _  A
                                CTG ATCA CT ACTGCTGT
                                ||| |||| || ||||||||
                                GAC TGGT GA TGACGACA
                                  _   T  C
GAM177  SSB-4     3'  CTGATATCCCACTGCTGT    3918       _  A   A
                                CTGG ATC CTA CTGCTGT
                                |||| ||| ||| |||||||
                                GACT TAG GGT GACGACA
                                   A   _  _
GAM177  TBX19     3'  CTGGGCACACTGCTGT      3919       AT   TA
                                CTGG  CAC  ACTGCTGT
                                ||||  |||  ||||||||
                                GACC  GTG  TGACGACA
                                  C_   __
GAM177  LOC140275 5'  TGGATTCAACTGCTGT      3920       CAC
                                TGGAT   TAACTGCTGT
                                |||||   ||||||||||
                                ACCTA   GTTGACGACA
                                   A__
GAM177  LOC146515 5'  CTGGACTGCTATGCTGT     3921        CA   AC
                                CTGGAT  CTA  TGCTGT
                                ||||||  |||  ||||||
                                GACCTG  GAT  ACGACA
                                    AC   __
GAM177  LOC150157 5'  CTGGGCTTCCTACTGCTGT   3922       A__  A   A
                                CTGG   TC CTA CTGCTGT
                                ||||   || ||| |||||||
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                                GACC   AG GAT GACGACA
                                  CGA  _  _
GAM177  LOC151902 3'  CTGGCTAACTGCTGT      3923      ATCA
                                CTGG   CTAACTGCTGT
                                ||||   ||||||||||
                                GACC   GATTGACGACA
                                  ____
GAM177  LOC154789 5'  TGCATCACTAATGATGT     3924     G      C  C
                                TG ATCACTAA TG TGT
                                || |||||||| || |||
                                AC TAGTGATT AC ACA
                                 G       _ T
GAM177  LOC155064 3'  TGGACCACGTACTCTGT     3925         TA   G
                                TGGATCAC  ACT CTGT
                                ||||||||  ||| ||||
                                ACCTGGTG  TGA GACA
                                     CA  _
GAM177  LOC164714 5'  CTGGACCACCCACTTGTTGT  3926          A   GC_
                                CTGGATCACT ACT   TGT
                                |||||||||| |||   |||
                                GACCTGGTGG TGA   ACA
                                      G   ACA
GAM177  LOC197350 5'  CCGGACCAGCTGCTGT     3927         CTAA
                                CTGGATCA   CTGCTGT
                                ||||||||   |||||||
                                GGCCTGGT   GACGACA
                                     C___
GAM177  LOC201910 3'  TGAACTCAACTGCTGT     3928       CAC
                                TGGAT   TAACTGCTGT
                                |||||   ||||||||||
                                ACTTG   GTTGACGACA
                                   A__
GAM177  LOC219347 3'  TGGATTTGGCAACTGCTGT   3929       CAC_
                                TGGAT   TAACTGCTGT
                                |||||   ||||||||||
                                ACCTA   GTTGACGACA
                                   AACC
GAM177  LOC222962 3'  CTGGCATCACTGCTGT      3930      _     AACT
                                CTGG ATCACT   GCTGT
                                |||| ||||||   |||||
                                GACC TAGTGA   CGACA
                                  G    ____
GAM177  LOC255042 5'  GGGTCACTAACCTGCTGC    3931     A      _
                                GG TCACTAAC TGCTGT
                                || |||||||| ||||||
                                CC AGTGATTG ACGACG
                                 C       G
GAM177  LOC51301  3'  CTAGATCACTTTCCCTTGT   3932          AA_  GC
                                CTGGATCACT   CT  TGT
                                ||||||||||   ||  |||
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                                GATCTAGTGA  GG  ACA
                                      AAG  A_
GAM177  LOC92370  3'  TGGATTCTATACTGCTGT    3933       CA  _
                                TGGAT  CTA ACTGCTGT
                                |||||  ||| ||||||||
                                ACCTA  GAT TGACGACA
                                   A_  A
GAM178  LOH11CR2A 5'  TGCTGAGTGTACTTCACACTC  3936     CATTA_
                                TGC     TACTTCACACTC
                                |||     ||||||||||||
                                ACG     ATGAAGTGTGAG
                                  ACTCAC
GAM178  PRKAR1A   3'  CCAGATTTATACTTCATACT   3937      TGCCA        C
                                CTAG    TTATACTTCA ACT
                                ||||    |||||||||| |||
                                GGTC    AATATGAAGT TGA
                                   TA___        A
GAM178  SLC4A4    3'  GTGCCACTGGGCTTCATGCTC  3938        ATA    CA
                                GTGCCATT   CTTCA  CTC
                                ||||||||   |||||  |||
                                CACGGTGA   GAAGT  GAG
                                     CCC    AC
GAM178  FLJ12484  3'  GTGCCAAGCACTTCACA     3939       TTA
                                GTGCCA   TACTTCACA
                                ||||||   |||||||||
                                CACGGT   GTGAAGTGT
                                    TC_
GAM178  FLJ20060  3'  GTCCAAATACTTCACA      3940     G   TT
                                GT CCA  ATACTTCACA
                                || |||  ||||||||||
                                CA GGT  TATGAAGTGT
                                  _   T_
GAM178  HSPC216   3'  CTAGTCTGTTAACCCCACACTC 3941       GCCATTAT
                                CTAGT       ACTTCACACTC
                                |||||       ||||||||||||
                                GATCA       TGGGGTGTGAG
                                   GACAAT__
GAM178  KIAA0326  3'  CAGTGCCATTGCGGTACTT   3942          A___
                                TAGTGCCATT    TACTT
                                |||||||||    |||||
                                GTCACGGTAA    ATGAA
                                      CGCC
GAM178  KIAA1613  3'  CAGTGCCATGAAATCATGCTC  3943         TATACT   CA
                                TAGTGCCAT     TCA  CTC
                                |||||||||     |||  |||
                                GTCACGGTA     AGT  GAG
                                      CTTT__   AC
GAM178  METAP1    3'  TAGTGCAAACTTCACGCT    3944       CATTAT      A
                                TAGTGC     ACTTCAC CT
                                ||||||     ||||||| ||
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                                ATCACG     TGAAGTG GA
                                   TT_____      C
GAM178  SPBPBP   5' ATGCATCACTTCACAT     3945      C   AT      C
                                GTGC ATT  ACTTCACA T
                                |||| |||  |||||||| |
                                TACG TAG  TGAAGTGT A
                                  _  __       A
GAM178  LOC130479 5' CTAGTGTCCTTATTCCCCACAC 3946       _ A   A
           TC                    CTAGTG CC TTAT CTTCACACTC
                                |||||| || |||| ||||||||||
                                GATCAC GG AATA GGGGTGTGAG
                                   A  _   A
GAM178  LOC146517 3' GTGTCATCAGCTCACACTC   3947     C    TAC
                                GTG CATTA   TTCACACTC
                                ||| |||||   |||||||||
                                CAC GTAGT   GAGTGTGAG
                                  A    C__
GAM178  LOC154822 3' GTGCCATTGCACATTGCACTC  3948        A   TTCA
                                GTGCCATT TAC    CACTC
                                |||||||| |||    |||||
                                CACGGTAA GTG    GTGAG
                                     C   TAAC
GAM178  LOC170063 3' TGCCAAGTTACTTCACATTC   3949       TTA       C
                                TGCCA   TACTTCACA TC
                                |||||   ||||||||| ||
                                ACGGT   ATGAAGTGT AG
                                   TCA        A
GAM178  LOC199678 5' CTATTGCTCAATTTCACACT   3950     G  _  TTATAC
                                CTA TGC CA     TTCACACT
                                ||| ||| ||     ||||||||
                                GAT ACG GT     AAGTGTGA
                                  A   A  TA_____
GAM178  LOC91179  5' TAAGTGCCATTGCTACACT    3951    T       ATA  TC
                                C AGTGCCATT   CT  ACACT
                                | |||||||||   ||  |||||
                                A TCACGGTAA   GA  TGTGA
                                 T        C__  __
GAM178  LOC92573  5' CTAGTGCTTCTCAATCACACTC 3952        CATTATACT
                                CTAGTGC        TCACACTC
                                |||||||        ||||||||
                                GATCACG        AGTGTGAG
                                     AAGAGTT__
GAM179  ADAM11    3' TCACACGGGGCAGTGGGTGTG  3955        AA G  AACAA
                                TCACACGG  C AG     GTGTG
                                ||||||||  | ||    |||||
                                AGTGTGCC  G TC     CACAC
                                     CC _  ACC__
GAM179  ADAM11    3' TCACACGGGGCAGTGGGTGTG  3955        AA G  AACAA
                                TCACACGG  C AG     GTGTG
                                ||||||||  | ||    |||||
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                                AGTGTGCC  G TC    CACAC
                                    CC _  ACC__
GAM179  RREB1    5'  TCACACGGAGTAGAAAATG   3956         ACG   CA
                                TCACACGGA   AGAA  AGTG
                                |||||||||   ||||  ||||
                                AGTGTGCCT   TCTT  TTAC
                                    CA_    __
GAM179  FLJ13158 3'  TCGCAGGCTCAAAGGGCAAGTG 3957     A  C  AA    AA_
          TG                     TC CA GG  CGAG   CAAGTGTG
                                || || ||  ||||   ||||||||
                                AG GT CC  GTTT   GTTCACAC
                                 C  _  GA    CCC
GAM179  FLJ14888 3'  TCACCTGGGGGGACAAGTGTG  3958      AC  AACGA  A
                                TCAC  GG    GA CAAGTGTG
                                ||||  ||    || ||||||||
                                AGTG  CC    CT GTTCACAC
                                  GA  CCC__  _
GAM179  FLJ22955 5'  CACTGGAGAGCAGGGCAAGTGT 3959     _   AC   AA___
          G                     CAC GGA  GAG    CAAGTGTG
                                ||| |||  |||    ||||||||
                                GTG CCT  CTC    GTTCACAC
                                  A  __   GTCCC
GAM179  KIAA1607 3'  CCACAGGGACAAGTGT     3960       C   ACGAGAA
                                TCACA GGA      CAAGTGT
                                ||||| |||      |||||||
                                GGTGT CCT      GTTCACA
                                  C  ________
GAM179  KLK15    3'  TCACACGGGTGGTCATGTGTG  3961        AACGAGAA  A
                                TCACACGG       CA GTGTG
                                ||||||||       || |||||
                                AGTGTGCC       GT CACAC
                                    CACCA___  A
GAM179  KLK15    3'  TCACACGGGTGGTCATGTGTG  3961        AACGAGAA  A
                                TCACACGG       CA GTGTG
                                ||||||||       || |||||
                                AGTGTGCC       GT CACAC
                                    CACCA___  A
GAM179  KLK15    3'  TCACACGGGTGGTCATGTGTG  3961        AACGAGAA  A
                                TCACACGG       CA GTGTG
                                ||||||||       || |||||
                                AGTGTGCC       GT CACAC
                                    CACCA___  A
GAM179  KLK15    3'  TCACACGGGTGGTCATGTGTG  3961        AACGAGAA  A
                                TCACACGG       CA GTGTG
                                ||||||||       || |||||
                                AGTGTGCC       GT CACAC
                                    CACCA___  A
GAM179  TOLLIP   3'  CACCCAAGAACAGGTGTG    3962      GGAA       A
                                CAC    CGAGAACA GTGTG
                                |||    |||||||| |||||
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                                GTG   GTTCTTGT CACAC
                                  G___      C
GAM179  LOC154449 5'  TCACACGGGAGAGGAGCAT   3963        AAC   ACA
                                TCACACGG  GAGA  AGTGT
                                ||||||||  ||||  |||||
                                AGTGTGCC  CTCT  TCGTA
                                     ___  CC_
GAM179  LOC202781 3'  TCACATGAGGGCAAGTGTG   3964      CGGAAC  AA
                                TCACA    GAG  CAAGTGTG
                                |||||    |||  ||||||||
                                AGTGT    CTC  GTTCACAC
                                   A_____  CC
GAM179  LOC90246  5'  TCACATGAATGCCTCAAGTGTG 3965      C  ACGAGAA
                                TCACA GGA     CAAGTGTG
                                ||||| |||     ||||||||
                                AGTGT CTT     GTTCACAC
                                   A  ACGGA__
GAM180  BRCA1     5'  CGTTGGTCAGGCTGGTCTGGA  3968    G  C  T
                                CG TG TC GGTTGGTCTGGA
                                || || || ||||||||||||
                                GC AC AG CCGACCAGACCT
                                 A  C  T
GAM180  MEF2D     5'  CACTGTGCTCATGAACGGTCTG 3969     CG    _ GT
          G                      CAC  GTGCTC TG  TGGTCTGG
                                 |||  |||||| ||  ||||||||
                                 GTG  CACGAG AC  GCCAGACC
                                   A_     T  TT
GAM180  MNT       3'  GGTCCCAGGGTTGGTCTGG   3970     G  CT
                                GGT CT  GGTTGGTCTGG
                                ||| ||  ||||||||||||
                                CCA GG  CCAACCAGACC
                                  G  TC
GAM180  PLXNA2    3'  CCAGGTGTCTGGTCTGG     3971    _   C  GGTT
                                CC GGTG TCT   GGTCTGG
                                || |||| |||   |||||||
                                GG CCAC AGA   CCAGACC
                                 T   _  _____
GAM180  PODXL     3'  CACTTGGGGTGGTTGGTCTGGA 3972     C_  TGCTC
                                CAC  GG    TGGTTGGTCTGGA
                                |||  ||    ||||||||||||
                                GTG  CC    ACCAACCAGACCT
                                  AA  CC___
GAM180  TNFRSF6B  3'  CACTGCGTGTTCTGGCTGG   3973     CG_  C
                                CAC   GTG TCTGGTTGG
                                |||   ||| |||||||||
                                GTG   CAC AGACCGACC
                                  ACG   A
GAM180  UC28      3'  CAGTGCCTTGGTCTGG      3974        CTGG
                                CGGTGCT    TTGGTCTGG
                                |||||||    |||||||||
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                                GTCACGG   AACCAGACC
                                      ____
GAM180  XK      3'  CCTGTGCTCTGAGACCTTGG  3975    G      TT GT  _
                                CC GTGCTCTGG  G  CT GG
                                || |||||||||  |  || ||
                                GG CACGAGACT  C  GA CC
                                 A       __ TG  A
GAM180  ZNF236  3'  CACGGGTGGGATTTGGTTTGG 3976    C   CTCTGG   C
                                CAC GGTG     TTGGT TGG
                                ||| ||||     ||||| |||
                                GTG CCAC     AACCA ACC
                                  C   CCTA__    A
GAM180  CARD14  3'  CACTGGTCTCTGTAAACTGGA 3977    C  G   GTTGGT
                                CAC GGT CTCTG     CTGGA
                                ||| ||| |||||     |||||
                                GTG CCA GAGAC     GACCT
                                  A  _    ATTT__
GAM180  DD96    5'  CCGGTGTCTGGGCTCCTGGA  3978      C    TTGG
                                CCGGTG TCTGG   TCTGGA
                                |||||| |||||   ||||||
                                GGCCAC AGACC   GGACCT
                                   _    CGA_
GAM180  DKFZP434B044 3'  CACTGTGGGCTTTTGGTCTGG  3979     CG  CT  GG
                                CAC  GTG  CT  TTGGTCTGG
                                |||  |||  ||  |||||||||
                                GTG  CAC  GA  AACCAGACC
                                  A_  CC  A_
GAM180  EPN2    3'  CACAGGTGCTCTGGGTGG   3980     C       T
                                CAC GGTGCTCTGG TGG
                                ||| ||||||||| |||
                                GTG CCACGAGACC ACC
                                  T       C
GAM180  FLJ14397  3'  GGTCAGGCTGGTCTGGA    3981     GCTCT
                                GGT    GGTTGGTCTGGA
                                |||    ||||||||||||
                                CCA    CCGACCAGACCT
                                  GT___
GAM180  FLJ21290  3'  CCAGTGCTCTGGTTTCTGG   3982          GG
                                CCGGTGCTCTGGTT  TCTGG
                                ||||||||||||  |||||
                                GGTCACGAGACCAA  AGACC
                                      __
GAM180  GPR9    5'  GGTGCTCTGGCTGCTGG    3983          GT
                                GGTGCTCTGGTTG  CTGG
                                ||||||||||||  ||||
                                CCACGAGACCGAC  GACC
                                      __
GAM180  GR6     5'  CCGTGCTCTGGGGCTCTGG   3984     G      TT  _
                                CCG TGCTCTGG  GG TCTGG
                                ||| ||||||||  || |||||
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                                GGC ACGAGACC  CC AGACC
                                  _      __ G
GAM180  HSPC171  3' GTGCTCTGGTGCTGG      3985          TG T
                                GTGCTCTGGT  G CTGG
                                ||||||||||  | ||||
                                CACGAGACCA  C GACC
                                      __ _
GAM180  KIAA0445 5' CGTTGGTCAGGCTGGTCTGGA 3968     G  C  T
                                CG TG TC GGTTGGTCTGGA
                                || || || ||||||||||||
                                GC AC AG CCGACCAGACCT
                                 A  C  T
GAM180  KIAA0557 3' TGCCCAGGTTGGTCTGGA    3986       T
                                TGCTC GGTTGGTCTGGA
                                ||||| ||||||||||||
                                ACGGG CCAACCAGACCT
                                   T
GAM180  KIAA0934 3' GGTCTCTGGTTCTAG       3987      G      TGG
                                GGT CTCTGGT   TCTGG
                                ||| |||||||   |||||
                                CCA GAGACCA   AGATC
                                  _     ____
GAM180  KIAA1028 3' GCGGTCCCGTTGGTCTGG    3988      C   G
                                GTG TCT GTTGGTCTGG
                                ||| ||| ||||||||||
                                CGC AGG CAACCAGACC
                                  C   G
GAM180  KIAA1243 3' CGGTGTTCTGGTTAACAGA   3989       C       TC
                                CGGTG TCTGGTTGG  TGGA
                                ||||| |||||||||  ||||
                                GCCAC AGACCAATT  GTCT
                                   A       __
GAM180  LHPP     3' CAGGGCCTTGGTTGGTCTGG  3990      T  TC
                                CGG GC  TGGTTGGTCTGG
                                ||| ||  ||||||||||||
                                GTC CG  ACCAACCAGACC
                                  C  GA
GAM180  OS4      3' CACTGGATGCTGGTCTGG    3991      C  TGCTCTG
                                CAC GG      GTTGGTCTGG
                                ||| ||      ||||||||||
                                GTG CC      CGACCAGACC
                                  A  TA_____
GAM180  RRN3     3' GGTCTCTGAAGTCCCTGGA   3992      G     TTGG
                                GGT CTCTGG    TCTGGA
                                ||| ||||||    ||||||
                                CCA GAGACT    GGACCT
                                  _     TCAG
GAM180  TUSP     3' GGTGGTCTAGTTTGGTCTGG  3993      C     _
                                GGTG TCTGGTT GGTCTGG
                                |||| ||||||| |||||||
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                                CCAC AGATCAA CCAGACC
                                  C      A
GAM180  U5-116KD  3'  CACTGGGGCTCTGGGTTGG   3994      C  T     _
                                CAC GG GCTCTGG TTGG
                                ||| || ||||||| ||||
                                GTG CC CGAGACC AACC
                                  A C      C
GAM180  LOC146445 3'  GGTCTCTGGGGCTGG      3995      G     TT  T
                                GGT CTCTGG  GG CTGG
                                ||| ||||||  || ||||
                                CCA GAGACC  CC GACC
                                  _     __ _
GAM180  LOC149579 5'  CGTTGGTCAGGCTGGTCTGGA  3968     G  C  T
                                CG TG TC GGTTGGTCTGGA
                                || || || ||||||||||||
                                GC AC AG CCGACCAGACCT
                                 A  C  T
GAM180  LOC257104 5'  CCGGGCTCTGGCCTGCATTGGA 3996      T      TG  C_
                                CCGG GCTCTGGT  GT  TGGA
                                |||| ||||||||  ||  ||||
                                GGCC CGAGACCG  CG  ACCT
                                  _      GA  TA
GAM181  DLEC1     3'  TGAGGAACACAGGTGGG     3999           CATCCA
                                TGAGGAACACGGG     TGGG
                                ||||||||||||      ||||
                                ACTCCTTGTGTCC     ACCC
                                                  _______
GAM181  ESRRB     5'  TGAGGACAGTGCTCCATGGGC  4000       ACA  _  A
                                TGAGGA   CGG GC TCCATGGGC
                                ||||||   ||| || |||||||||
                                ACTCCT   GTC CG AGGTACCCG
                                   ___   A  _
GAM181  KLF4      5'  GGAGCGCGCGCGGCCATGGGC  4001     ACA  G  AT
                                GGA   CG GC  CCATGGGC
                                |||   || ||  ||||||||
                                CCT   GC CG  GGTACCCG
                                  CGC  G  CC
GAM181  NTSR1     3'  TGAGAAACATGGGTTAGGGGG  4002        C   CATCCAT
                                TGAGGAACA GGG      GGG
                                |||||||| |||      |||
                                ACTCTTTGT CCC      CCC
                                     A  AATCC__
GAM181  PLA2G2D   3'  TGAGGAACAGGGTAGAGGG   4003        C   CATCCAT
                                TGAGGAACA GGG      GGG
                                |||||||| |||      |||
                                ACTCCTTGT CCC      CCC
                                     _  ATCT___
GAM181  PPP1R3D   3'  TGAGGAGGCATCCGCTATGGGC 4004       ACACG     ___
                                TGAGGA    GGCATCC   ATGGGC
                                ||||||    |||||||   ||||||
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                                ACTCCT    CCGTAGG   TACCCG
                                  _____      CGA
GAM181  RAG2     3'  TGAGAAACTAACTTGTTCATGG 4005         ACGGGCATC
           GC                    TGAGGAAC       CATGGGC
                                 ||||||||       |||||||
                                 ACTCTTTG       GTACCCG
                                    ATTGAACAA
GAM181  SORCS2   3'  TGAGGAACCATGGGCACTGGG  4006         AC_     CCA
                                 TGAGGAAC   GGGCAT   TGGG
                                 ||||||||   ||||||   ||||
                                 ACTCCTTG   CCCGTG   ACCC
                                    GTA     ___
GAM181  TEM5     3'  TGGGGAACATCCGCCTGTGGGC 4007     A     CGG  ATCCA
                                 TG GGAACA   GC    TGGGC
                                 || ||||||   ||    |||||
                                 AC CCTTGT   CG    ACCCG
                                  C     AGG  GAC__
GAM181  B3GALT1  5'  TGAGGTGGAGATTGTCCATGGG 4008       AACAC  GCA
           C                     TGAGG    GG   TCCATGGGC
                                 |||||    ||   |||||||||
                                 ACTCC    CT   AGGTACCCG
                                    ACCT_  AAC
GAM181  BAT8     3'  TGGGGAACACGGGGGGG     4009     A       CATCCAT
                                 TG GGAACACGGG      GGG
                                 || ||||||||||      |||
                                 AC CCTTGTGCCC      CCC
                                  C         ________
GAM181  DKFZp762P2111 3'  TGGGGAACAGAGCCCCATGGGC 4010     A     C    A
                                 TG GGAACA GGGC TCCATGGGC
                                 || |||||| |||| |||||||||
                                 AC CCTTGT CTCG GGGTACCCG
                                  C     _   _
GAM181  FLJ23816 5'  TGGGGGGCACAGGCAGCGG   4011     A  AA      TCCA
                                 TG GG  CACGGGCA    TGG
                                 || ||  ||||||||    |||
                                 AC CC  GTGTCCGT    GCC
                                  C  CC       C___
GAM181  FLJ31737 3'  TGGGAGAGCACTCCATGGG   4012     A  ACAC    _
                                 TG GGA    GGGCA TCCATGGG
                                 || |||    ||||| |||||||||
                                 AC CCT    CTCGT AGGTACCC
                                  _  _____     G
GAM181  GLTP     3'  TGGGGGACACAGGCCAGGGGC  4013     A  A      ATC  T
                                 TG GG ACACGGGC   CA GGGC
                                 || || ||||||||   || ||||
                                 AC CC TGTGTCCG   GT CCCG
                                  C  C       ___  C
GAM181  KIAA0064 3'  TGGGGGACACAGGCACAGGGC  4014     A  A       CCAT
                                 TG GG ACACGGGCAT    GGGC
                                 || || ||||||||||    ||||
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                                AC CC TGTGTCCGTG    CCCG
                                 C  C        T___
GAM181  KIAA0828  3'  TGAAGAACTGTAGTCTATGGGC 4015         ACG  CA  C
                                TGAGGAAC   GG  TC ATGGGC
                                ||||||||   ||  || ||||||
                                ACTTCTTG   TC  AG TACCCG
                                     ACA  __  A
GAM181  KIAA1822  3'  GGATGCGGGCACCAGGC     4016      ACA       CAT
                                GGA   CGGGCATC   GGGC
                                |||   ||||||||   ||||
                                CCT   GCCCGTGG   TCCG
                                  AC_       ___
GAM181  NOL5A     3'  TGGGAACACGGGCACAGGG    4017     A          CCAT
                                TG GGAACACGGGCAT    GGG
                                || ||||||||||||    |||
                                AC CCTTGTGCCCGTG    CCC
                                 _          T___
GAM181  PLAGL2    3'  TGGGGGACACAGACGGGGTGGG 4018     A  A       ATCCA
                                TG GG ACACGGGC     TGGG
                                || || ||||||||     ||||
                                AC CC TGTGTCTG     ACCC
                                 C  C       CCCC_
GAM181  RASD2     3'  TGAGGAACGCGGTCAGGAGGTG 4019         A   G  TCCA_
           GGC                    TGAGGAAC CGG CA     TGGGC
                                ||||||||| ||| ||     |||||
                                ACTCCTTG GCC GT     ACCCG
                                     C   A  CCTCC
GAM181  LOC145195 3'  TGGGAAGCACCCTCTATGGGC  4020     A   ACACG      ___
                                TG GGA    GGCATCC   ATGGGC
                                || |||    |||||||   ||||||
                                AC CCT    TCGTGGG   TACCCG
                                 _  ______      AGA
GAM181  LOC146223 3'  TGAGGAACGTGGGCCTCC    4021         AC    A
                                TGAGGAAC  GGGC TCC
                                ||||||||  |||| |||
                                ACTCCTTG  CCCG AGG
                                     CA    G
GAM181  LOC152845 3'  TGGGGGACACGGACGGGGTGGG 4022     A  A       ATCCA
                                TG GG ACACGGGC     TGGG
                                || || ||||||||     ||||
                                AC CC TGTGCCTG     ACCC
                                 C  C       CCCC_
GAM181  LOC200205 3'  GAAACATGGGAGATGGGC    4023        C   CATCC
                                GGAACA GGG     ATGGGC
                                ||||||| |||    ||||||
                                CTTTGT CCC     TACCCG
                                   A   TC___
GAM181  LOC204084 5'  TGAGGAAAGTCCCATGGG    4024         CACG  CA
                                TGAGGAA    GG  TCCATGGG
                                |||||||    ||  ||||||||
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                                ACTCCTT   TC  GGGTACCC
                                    _____ A_
GAM181  LOC221632 3'  GGAGAACAGCCATCCATGGG  4025     AC   G
                                GGA  ACGG CATCCATGGG
                                |||  |||| ||||||||||
                                CCT  TGTC GTAGGTACCC
                                  CT   G
GAM181  LOC90768  3'  CGGGAACACGGGCTGTGGG   4026    A        ATCCA
                                TG GGAACACGGGC    TGGG
                                || ||||||||||     ||||
                                GC CCTTGTGCCCG    ACCC
                                 _         AC___
GAM182  CENPE    5'  GCCAGGACCCTCCGCG     4029      A   AGA
                                GCCA GGA   TCCTCCGCG
                                |||| |||   |||||||||
                                CGGT CCT   GGGAGGCGC

                                 _   ___
GAM182  MAF      5'  GCTCGGGAAGATCCTCCGCGA  4030    CAA
                                GC   GGAAGATCCTCCGCGA
                                ||   ||||||||||||||||
                                CG   CCTTCTAGGAGGCGCT
                                 AGC
GAM182  ZNF80    3'  ATGCTGAGGAAGATATTTCC   4031     CA      CC_
                                ATGC  AGGAAGAT   TCC
                                ||||  ||||||||   |||
                                TACG  TCCTTCTA   AGG
                                  AC       TAA
GAM182  AKL3L    3'  TATGCCAAGGGAGCATTTCCCA 4032          A  ATCC   G
                                TATGCCAAGG AG    TCC CG
                                |||||||||| ||    ||| ||
                                ATACGGTTCC TC    AGG GT
                                     C  GTAA  _
GAM182  RAP140   3'  TATGTTAAGGGAGACTCC    4033      CC    A   TC
                                TATG  AAGG AGA  CTCC
                                ||||  |||| |||  ||||
                                ATAC  TTCC TCT  GAGG
                                  AA   C   __
GAM182  U5-100K  3'  TGCCAAAGGAGGTCCCATCCG  4034        A  A   __
                                TGCCAAGG AG TCC  TCCG
                                |||||||| || |||  ||||
                                ACGGTTTC TC AGG  AGGC
                                    C  C   GT
GAM182  LOC150538 5'  CCTGGGGATCCTCCGCG    4035     AA  AA
                                CC  GG  GATCCTCCGCG
                                ||  ||  ||||||||||||
                                GG  CC  CTAGGAGGCGC
                                 AC  __
GAM182  LOC151174 5'  TGCCAAGGAAAGGTCCG     4036          ATCC
                                TGCCAAGGAAG    TCCG
                                ||||||||||    ||||
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                                ACGGTTCCTTT    AGGC
                                      CC__
GAM182  LOC204084 5'  ATGCCAAGGAAGCTGCG     4037           ATCCTCC
                                ATGCCAAGGAAG      GCG
                                ||||||||||||      |||
                                TACGGTTCCTTC      CGC
                                      GA_____
GAM182  LOC220758 3'  CATGCCAGGACCACCTCC     4038         A   AGAT
                                TATGCCA GGA    CCTCC
                                ||||||| |||    |||||
                                GTACGGT CCT    GGAGG
                                    _  GGT_
GAM182  LOC222171 3'  TATGCCACCCTCCTCCGCG    4039         AGGAAGA
                                TATGCCA      TCCTCCGCG
                                |||||||      |||||||||
                                ATACGGT      AGGAGGCGC
                                     GGG____
GAM182  LOC255040 3'  TGCCAGTCCTCCGCG       4040        AGGAA A
                                TGCCA     G TCCTCCGCG
                                |||||     | |||||||||
                                ACGGT     C AGGAGGCGC
                                      _____ _
GAM182  LOC255041 3'  TGCCAGTCCTCCGCG       4040        AGGAA A
                                TGCCA     G TCCTCCGCG
                                |||||     | |||||||||
                                ACGGT     C AGGAGGCGC
                                      _____ _
GAM182  LOC54505  5'  TGTGGCAGAAGATCCTTCGCG  4041     CCAA         C
                                TG    GGAAGATCCT CGCG
                                ||    |||||||||| ||||
                                AC    TCTTCTAGGA GCGC
                                  ACCG         A
GAM183  FANCD2    3'  TGTGGAGATAGGGTCTTGTTA  4044         CA      GA
                                TGTGGAGG  AGGGTTT  TGTTA
                                ||||||||  |||||||  |||||
                                ACACCTCT  TCCCAGA  ACAAT
                                     A_      __
GAM183  SLC22A1LS 5'  GTGGGGGTGGGGGTTTCATG   4045       A  CAA     G
                                GTGG GG   GGGTTT ATG
                                |||| ||   |||||| |||
                                CACC CC   CCCAAA TAC
                                   C  ACC     G
GAM183  ARHGEF2   3'  TGGGGGCAAGGGTTCCAC     4046      A         G
                                TGG GGCAAGGGTTT AT
                                ||| |||||||||| ||
                                ACC CCGTTCCCAAG TG
                                  C          G
GAM183  FLJ12681  3'  TGTGGGGCGAGGGTTTG      4047        A   A
                                TGTGG GGC AGGGTTTG
                                ||||| ||| ||||||||
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                                ACACC CCG TCCCAAAC
                                  _  C
GAM183  FLJ30213  3'  GTGGAGGCAGGGGAGGGGTTG  4048          ____   T
                                GTGGAGGCA   AGGG TTG
                                |||||||||   |||| |||
                                CACCTCCGT   TCCC AAC
                                     CCCC   C
GAM183  HSPC023   3'  TATGGAGGTAGGGGGTGGGATG 4049         CAA_   TT
          TT                    TGTGGAGG   GGGT  GATGTT
                                ||||||||   ||||  ||||||
                                ATACCTCC   CCCA  CTACAA
                                     ATCC   CC
GAM183  KIAA1819  5'  TGTGGGGGAGGGGAGT     4050       A  CA   TTT  T
                                TGTGG GG  AGGG   GA GT
                                ||||| ||  ||||   || ||
                                ACACC CC  TCCC   CT CA
                                  _ C_   ___  _
GAM183  LOC150868 5'  GTGGAGGCGGCTGGTGTT   4051         AAG   T A
                                GTGGAGGC   GGTT G TGTT
                                ||||||||   |||| | ||||
                                CACCTCCG   CCGA C ACAA
                                     ___   _ C
GAM183  LOC153688 3'  TGTGGTGGCCTTGATGTT   4052       A   AAGGG
                                TGTGG GGC    TTTGATGTT
                                |||||  |||   |||||||||
                                ACACC CCG    GAACTACAA
                                   A  _____
GAM183  LOC222066 3'  TGTCGAGGCAGGGTCTCTGTT  4053     G     A     GA
                                TGT GAGGCA GGGTTT  TGTT
                                |||  |||||| ||||||  ||||
                                ACA CTCCGT CCCAGA  ACAA
                                  G     _     G_
GAM183  LOC91464  5'  TGGAGGCAGGGGTCCACCTT   4054         A     G  G
                                TGGAGGCA GGGTTT AT TT
                                |||||||| |||||| || ||
                                ACCTCCGT CCCAGG TG AA
                                     C     _ G
GAM184  BACH1    3'  TCTGGCATTGGTGACCCA    4057     A       CG   G
                                TC TGGCATTGG  GGC TCA
                                || |||||||||  ||| |||
                                AG ACCGTAACC  CTG GGT
                                  _       A_  _
GAM184  HTRA3    5'  CTCAGGCTGGCGGGCGTCAG   4058      T   AT
                                CTCA GGC  TGGCGGGCGTCAG
                                |||| |||  ||||||||||||||
                                GAGT CCG  ACCGCCCGCAGTC
                                  _  __
GAM184  DCOHM    3'  TCTCATGGATTGGTGGGCA   4059         C    C
                                TCTCATGG ATTGG GGGCG
                                ||||||||  |||||  |||||
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                                AGAGTACC TAACC CCCGT
                                    _    A
GAM184  FLJ14816  3'  TCCCATGGCTTGGGGTGT    4060        A   C  GC
                                TCTCATGGC TTGG GG  GT
                                ||||||||| |||| ||  ||
                                AGGGTACCG AACC CC  CA
                                    _   _  A_
GAM184  KIAA0449  3'  TCTCATGGATGTTGGGCTCAG  4061       CAT  GC   G
                                TCTCATGG   TG  GGGC TCAG
                                ||||||||   ||  |||| ||||
                                AGAGTACC   AC  CCCG AGTC
                                    T__  AA   _
GAM184  KIAA0557  3'  TCTCACGGTGTTGCCCAGG   4062       CA   G_
                                TCTCATGG  TTG  CGGG
                                ||||||||  |||  ||||
                                AGAGTGCC  AAC  GTCC
                                    AC   GG
GAM184  KIAA0574  3'  TCTGTGGCGCCAGGCGT    4063     CA   ATT G
                                TCT  TGGC   G CGGGCGT
                                |||  ||||   | |||||||
                                AGA  ACCG   C GTCCGCA
                                  C_   ___ G
GAM184  MDS018    3'  TCTCATGGCATGGTCTGCA   4064         T  CGG
                                TCTCATGGCAT GG   GCG
                                |||||||||| ||   |||
                                AGAGTACCGTA CC   CGT
                                    _  AGA
GAM184  MIR       3'  TCGCATGGCAGATGGGTGT   4065    T     TT GC   C
                                TC CATGGCA  G  GGG GT
                                || |||||||  |  ||| ||
                                AG GTACCGT  C  CCC CA
                                 C      __ TA   A
GAM184  TRIP-Br2  3'  TCACAGTACTGGCGGGTGT   4066       C       C
                                TCATGG ATTGGCGGG GT
                                |||||| ||||||||| ||
                                AGTGTC TGACCGCCC CA
                                   A       A
GAM184  LOC147400 3'  TCATGGTTTGGCAAAGT    4067       CA      C
                                TCATGG  TTGGCGGG GT
                                ||||||  |||||||| ||
                                AGTACC  AACCGTTT CA
                                   A_      _
GAM184  LOC160414 3'  TCGTGGTTTGGCAAAGT    4068    A  CA      C
                                TC TGG  TTGGCGGG GT
                                || |||  |||||||| ||
                                AG ACC  AACCGTTT CA
                                 C  A_      _
GAM184  LOC164375 5'  TCTTCTGGCATTGTGGTCA   4069     CA      GC  GCG
                                TCT  TGGCATTG  GG   TCA
                                |||  ||||||||  ||   |||
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                                AGA  ACCGTAAC  CC   AGT
                                  AG       A_ ___
GAM184  LOC254381 5'  TCTCATGGCTTTGGCAGCCA  4070         A      G
                                TCTCATGGC TTGGCGG CG
                                ||||||||| ||||||| ||
                                AGAGTACCG AACCGTC GT
                                     A      G
GAM184  LOC93082  3'  TCCCATGGCATGGGTGT     4071          TGGC   C
                                TCTCATGGCAT    GGG GT
                                ||||||||||    ||| ||
                                AGGGTACCGTA    CCC CA
                                      ____  A
GAM185  LCE       3'  TGCCTTGGGTTTTGTGTTTGC  4074      ACTA       A  C
                                TGC    GGTTTTGT TT GC
                                |||    |||||||| || ||
                                ACG    CCAAAACA AA CG
                                  GAAC       C  A
GAM186  KCNK5     3'  AAGGGCAGAACCAGCCA     4077      AAC   T_    AA
                                AAGG   GCA  ACCAG  CCG
                                ||||   |||  |||||  |||
                                TTCC   CGT  TGGTC  GGT
                                  ___   CT    __
GAM186  UBE2I     3'  AAAGGAAGTGGCGCAGAACCGA 4078        C__  ATAC
                                AAAGGAA   GC    CAGAACCGA
                                |||||||   ||   |||||||||
                                TTTCCTT   CG    GTCTTGGCT
                                    CAC  C___
GAM186  BTN3A1    3'  AAAAGAACGGCCATAGGGCCG  4079         CATA   GAA__
                                AAAGGAACG    CCA     CCG
                                |||||||||    |||     |||
                                TTTTCTTGC    GGT     GGC
                                     C___   ATCCC
GAM186  FLJ20730  5'  GGAAGAACGCACATCCTAGA   4080    A         _ _
                                A AGGAACGCATA CC AGA
                                | ||||||||||| || |||
                                C TTCTTGCGTGT GG TCT
                                 C          A  A
GAM186  FLJ22555  5'  TGAGGAACGCTTTAGAGCCGAA 4081    A       ATACC   A
                                A AGGAACGC     AGA CCGAA
                                | ||||||||     ||| |||||
                                A TCCTTGCG     TCT GGCTT
                                 C       AAA__   C
GAM186  KIAA0057  3'  AAAGGAACCATAAGCTCG    4082         G    CC  AAC
                                AAAGGAAC CATA  AG   CG
                                |||||||| ||||  ||   ||
                                TTTCCTTG GTAT  TC   GC
                                     _    __  GA_
GAM186  KIAA1030  3'  AAAGGAACAGGAGAGGAACTGA 4083          CATACCA    C
              A                   AAAGGAACG      GAAC GAA
                                  |||||||||      |||| |||
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                                TTTCCTTGT      CTTG CTT
                                     CCTCTC_   A
GAM186  KIAA1388 3'  GGAGGGGCGCTTCCAAAACCG 4084    A  AA  ATA
                                A AGG  CGC   CCAGAACCG
                                | |||  |||   |||||||||
                                C TCC  GCG   GGTTTTGGC
                                 C   CC   AA_
GAM186  MAPK6    3'  AAAGAATGCATACCAGAA    4085       C
                                AAGGAA GCATACCAGAA
                                |||||| ||||||||||
                                TTTCTT CGTATGGTCTT
                                   A
GAM186  MMP28    3'  AAAGGAACTGTACCTTTAGCCG 4086        GCA   AGAA_
           AA                    AAAGGAAC   TACC    CCGAA
                                |||||||||   ||||    |||||
                                TTTCCTTG   ATGG    GGCTT
                                     AC_   AAATC
GAM186  MMP28    3'  AAAGGAACTGTACCTTTAGCCG 4086        GCA   AGAA_
           AA                    AAAGGAAC   TACC    CCGAA
                                |||||||||   ||||    |||||
                                TTTCCTTG   ATGG    GGCTT
                                     AC_   AAATC
GAM186  MRP63    5'  AAGGAGTTCCCTAGAGAACCGA 4087      ACGCATA  ___
           A                     AAGGA      CC   AGAACCGAA
                                |||||      ||   |||||||||
                                TTCCT      GG   TCTTGGCTT
                                   CAAG___  ATC
GAM186  NFAT5    5'  GGAAGAACGCATTTAACTGA   4088    A       ACCAG   C
                                A AGGAACGCAT     AAC GA
                                | ||||||||||     ||| ||
                                C TTCTTGCGTA     TTG CT
                                 C         AA___   A
GAM186  PIK4CA   5'  AAAGGAACACGTGCTCACTGAA 4089          ATACCAGA  C
                                AAAGGAACGC       AC GAA
                                ||||||||||       || |||
                                TTTCCTTGTG       TG CTT
                                     CACGAG__  A
GAM186  RP4-622L5 3'  AAAGGAACCAGACCG       4090        ACGCAT     A
                                AAAGGA     ACCAGA CCG
                                ||||||     |||||| |||
                                TTTCCT     TGGTCT GGC
                                  _______     _
GAM186  SLC16A10  3'  AGGTACCAGAACTGAA      4091      AACGCA       C
                                AGG     TACCAGAAC GAA
                                |||     ||||||||| |||
                                TCC     ATGGTCTTG CTT
                                  _______       A
GAM186  LOC127262 3'  AAGGAAAACACCAGAACTGAA  4092        CGC        C
                                AAGGAA   ATACCAGAAC GAA
                                ||||||   |||||||||| |||
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                                TTCCTT   TGTGGTCTTG CTT
                                   T__         A
GAM186  LOC143158 5'  GGAGGAACACTGAACTGA    4093    A       ATACCA    C
                                A AGGAACGC      GAAC GA
                                | ||||||||      |||| ||
                                C TCCTTGTG      CTTG CT
                                 C       A_____    A
GAM186  LOC170372 3'  AAAGAATGCATACCAGAA    4085        C
                                AAGGAA GCATACCAGAA
                                |||||| ||||||||||
                                TTTCTT CGTATGGTCTT
                                   A
GAM186  LOC255518 3'  AAAGGAACTGGTGCAGGACTGA 4094         GCATAC   A  C
           A                     AAAGGAAC      CAG AC GAA
                                ||||||||      ||| || |||
                                TTTCCTTG      GTC TG CTT
                                     ACCAC_   C  A
GAM186  LOC91300  5'  GGGACACGGAGAAGAACCGAA  4095     A    ATACC
                                GG ACGC     AGAACCGAA
                                || ||||     |||||||||
                                CC TGTG     TCTTGGCTT
                                 C    CCTCT
GAM186  LOC91300  5'  GGGACACGGAGAAGAACCGAA  4095     A    ATACC
                                GG ACGC     AGAACCGAA
                                || ||||     |||||||||
                                CC TGTG     TCTTGGCTT
                                 C    CCTCT
GAM186  LOC92573  5'  AAGGAACGTATCCACCC     4096         C  A   GAA
                                AAGGAACG AT CCA   CC
                                |||||||| || |||   ||
                                TTCCTTGC TA GGT   GG
                                     A  _   G__
GAM187  ABL1      3'  CATGCCGACTGCAGTCCACG   4099         AC   A_  T
                                CATGCCGA  GCA  CT CG
                                ||||||||  |||  || ||
                                GTACGGCT  CGT  GG GC
                                     GA   CA  T
GAM187  ABL1      3'  CATGCCGACTGCAGTCCACG   4099         AC   A_  T
                                CATGCCGA  GCA  CT CG
                                ||||||||  |||  || ||
                                GTACGGCT  CGT  GG GC
                                     GA   CA  T
GAM187  TSN       3'  ATGCCAAATGGCCCCTTGTACA 4100         C_  AA   C
           A                     ATGCCGAA  GC  CTT GTACAA
                                ||||||||  ||  ||| ||||||
                                TACGGTTT  CG  GAA CATGTT
                                     AC  GG   _
GAM187  FLJ22477  5'  CGCCGGAACTTCGTGCA     4101        AACGC       A
                                TGCCG     AACTTCGT CA
                                |||||     |||||||| ||
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                                GCGGC    TTGAAGCA GT
                                  C____      C
GAM187  Nup43    5'  CATGCCGAAAGCGGCCGCA   4102         C  AACT
                                CATGCCGAA GC   TCGTA
                                ||||||||| ||   |||||
                                GTACGGCTT CG   GGCGT
                                     T  CC__
GAM187  LOC204970 3'  CATGCCGAAGCAGCCGTCACA  4103         C   ACT   _
                                CATGCCGAA GCA   TCGT ACA
                                ||||||||| |||   |||| |||
                                GTACGGCTT CGT   GGCA TGT
                                     _  C__   G
GAM187  LOC256510 3'  CATGTCAACATGTACTTCGTAC 4104      C   ACGCA
          A                      CATG CGA    ACTTCGTACA
                                |||| |||    ||||||||||
                                GTAC GTT    TGAAGCATGT
                                  A  GTACA
GAM188  AKR1B1   3'  GCAAAGCAAACTGGAA     4107      _  CAGA
                                GCAA GCA   GACTGGAA
                                |||| |||   ||||||||
                                CGTT CGT   TTGACCTT
                                  T  ____
GAM188  ALOX12B  5'  AGCCAGGCACAGAGTGGA    4108     AA_      AC
                                AGC  GCACAGAG  TGGA
                                |||  ||||||||  ||||
                                TCG  CGTGTCTC  ACCT
                                  GTC      __
GAM188  CCND1    3'  AAGCAAAGTACAGAGATGCCTA 4109       _ C     ___
          G                      AAGCAA G ACAGAGA   CTGG
                                |||||| | |||||||   ||||
                                TTCGTT C TGTCTCT   GATC
                                   T A      ACG
GAM188  CCND2    3'  AAGCAGGAGCAGGCAGAAA   4110      __   __
                                AAGCA  AGCA  CAGAGA
                                |||||  ||||  ||||||
                                TTCGT  TCGT  GTCTTT
                                  CC   CC
GAM188  COL4A5   3'  AAGAAGCACAGGGAAA     4111     C      AGACT
                                AAG AAGCACAG    GGAAA
                                ||| ||||||||    |||||
                                TTC TTCGTGTC    CCTTT
                                  _     _____
GAM188  COL4A5   3'  AAGAAGCACAGGGAAA     4111     C      AGACT
                                AAG AAGCACAG    GGAAA
                                ||| ||||||||    |||||
                                TTC TTCGTGTC    CCTTT
                                  _     _____
GAM188  COL4A5   3'  AAGAAGCACAGGGAAA     4111     C      AGACT
                                AAG AAGCACAG    GGAAA
                                ||| ||||||||    |||||
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                                TTC TTCGTGTC    CCTTT
                                  _     _____
GAM188  CYP27B1  3'  AAGCAAGCAGAGAGACCATGG  4112          C     __
                                AAGCAAGCA AGAGACT  GG
                                ||||||||| |||||||  ||
                                TTCGTTCGT TCTCTGG  CC
                                     C      TA
GAM188  DHCR7    3'  AAGAAAGCACAGAAAAGG    4113     C        CT
                                AAG AAGCACAGAGA  GG
                                ||| ||||||||||  ||
                                TTC TTCGTGTCTTT  CC
                                  T        T_
GAM188  DRP2     3'  GCCAGTGGAAACTGGAAA    4114    A  CACA
                                GC AG   GAGACTGGAAA
                                || ||   ||||||||||
                                CG TC   CTTTGACCTTT
                                 G  AC__
GAM188  EVA1     3'  AAACGGGTCACAACTGGAAAAG 4115      AAG_   GAG
                                AAGC   CACA   ACTGGAAAAG
                                ||||   ||||   ||||||||||
                                TTTG   GTGT   TGACCTTTTC
                                  CCCA   ___
GAM188  FACL2    3'  AACCACAGGGGACTGGAGAAG  4116    G    A_     A
                                AA CACAG  GACTGGA AAG
                                || |||||  ||||||| |||
                                TT GTGTC  CTGACCT TTC
                                 G    CC      C
GAM188  FGF13    5'  AGCAGACACAGAGAGAGA    4117      AG      CT
                                AGCA  CACAGAGA  GGA
                                ||||  ||||||||  |||
                                TCGT  GTGTCTCT  TCT
                                  CT       C_
GAM188  FRAT2    3'  AAGCACAGAAAACAGGAAA   4118          _ T
                                AAGCACAGAGA C GGAAA
                                |||||||||||  | |||||
                                TTCGTGTCTTT G CCTTT
                                       T T
GAM188  GHRHR    3'  AGCAGACACAGAGGGACCACAG 4119      AG    __   __
           AA                    AGCA  CACAGA  GACT  GGAA
                                ||||  ||||||  ||||  ||||
                                TCGT  GTGTCT  CTGG  TCTT
                                  CT     CC    TG
GAM188  GLUL     3'  GCAGGGCAGAAACCCAAAA   4120     A CA      G
                                GCA G  CAGAGACT GAAA
                                ||| |  |||||||| ||||
                                CGT C  GTCTTTGG TTTT
                                  _ CC       G
GAM188  GNAS     3'  AAGCAAGCTGAAGGGAAAA   4121         ACA   ACT
                                AAGCAAGC   GAG   GGAAAA
                                ||||||||   |||   ||||||
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                                TTCGTTCG  TTC  CCTTTT
                                    AC_  ___
GAM188  GNAS    3' AAGCAAGCTGAAGGGAAAA  4121       ACA  ACT
                                AAGCAAGC  GAG  GGAAAA
                                ||||||||  |||  ||||||
                                TTCGTTCG  TTC  CCTTTT
                                    AC_  ___
GAM188  GNAS    3' AAGCAAGCTGAAGGGAAAA  4121       ACA  ACT
                                AAGCAAGC  GAG  GGAAAA
                                ||||||||  |||  ||||||
                                TTCGTTCG  TTC  CCTTTT
                                    AC_  ___
GAM188  GNAS    3' AAGCAAGCTGAAGGGAAAA  4121       ACA  ACT
                                AAGCAAGC  GAG  GGAAAA
                                ||||||||  |||  ||||||
                                TTCGTTCG  TTC  CCTTTT
                                    AC_  ___
GAM188  HOXA7   3' AAGCAAGCAAGAGCAAGAA  4122        C   ACT
                                AAGCAAGCA AGAG  GGAA
                                ||||||||| ||||  ||||
                                TTCGTTCGT TCTC  TCTT
                                     _  GT_
GAM188  IL8RA   3' GGACAAGCACGGAACAGAA  4123   A     A  A T
                                A GCAAGCAC GAG C GGAA
                                | |||||||| ||| | ||||
                                C TGTTCGTG CTT G TCTT
                                 C      C  _ _
GAM188  ITGB4BP 3' AAGCACAGGTGGAAAA     4124       AGAC
                                AAGCACAG   TGGAAAA
                                ||||||||   |||||||
                                TTCGTGTC   ACCTTTT
                                    C___
GAM188  ITPKB   3' AAGGAAGCACAGGAGGA    4125    C     A  CT
                                AAG AAGCACAG GA  GGA
                                ||| |||||||| ||  |||
                                TTC TTCGTGTC CT  CCT
                                  C      _ __
GAM188  ITPR1   5' AAGCAAGCCCAGCGAGGGG  4126       A  A  CT
                                AAGCAAGC CAG GA  GG
                                |||||||| ||| ||  ||
                                TTCGTTCG GTC CT  CC
                                    G  G  CC
GAM188  KIF3C   3' AACAGGCAAAGCTGGAAAA  4127     A  CA  A
                                AGCA GCA  GAG CTGGAAAA
                                |||| |||  ||| ||||||||
                                TTGT CGT  TTC GACCTTTT
                                  C  __  _
GAM188  MLC1    3' AGCAAACACAGGAGGGA    4128         A  CT
                                AGCAAGCACAG GA  GGA
                                |||||||||| ||  |||
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                                TCGTTTGTGTC CT  CCT
                                      _ C_
GAM188  MLC1    3' AGCAAACACAGGAGGGA    4128          A  CT
                                AGCAAGCACAG GA  GGA
                                |||||||||| ||  |||
                                TCGTTTGTGTC CT  CCT
                                      _ C_
GAM188  MYEOV   3' AGGAAGCACAGCAGGGAGGA  4129    C      _ ACT
                                AG AAGCACAG AG   GGA
                                || ||||||| ||   |||
                                TC TTCGTGTC TC   CCT
                                 C       G  CCT
GAM188  MYO10   3' GCAAGCACGTACACTTAAAAG 4130        AGAG   GG
                                GCAAGCAC    ACT  AAAAG
                                ||||||||    |||  |||||
                                CGTTCGTG    TGA  TTTTC
                                     CATG   A_
GAM188  PA2G4   5' AGCAAGCAAGGGAGCGG    4131        C  A  C
                                AGCAAGCA AG GA TGG
                                |||||||| || || |||
                                TCGTTCGT TC CT GCC
                                     _ C  C
GAM188  PRKACG  3' AGAAGCACAGAGGGACCAGGAA 4132    C       __   _
                                AG AAGCACAGA  GACT GGAA
                                || |||||||||  |||| ||||
                                TC TTCGTGTCT  CTGG CCTT
                                 _       CC    T
GAM188  PROX1   5' GCAAGTGATTCTGGAAAAG   4133      CACA  GA
                                GCAAG   GA  CTGGAAAAG
                                |||||   ||  |||||||||
                                CGTTC   CT  GACCTTTTC
                                   A___  AA
GAM188  SACM2L  3' AAGCAAGGGGAAAACTGGAA  4134       CACA
                                AAGCAAG   GAGACTGGAA
                                |||||||   ||||||||||
                                TTCGTTC   TTTTGACCTT
                                     CCC_
GAM188  SACM2L  3' AAGCAAGGGGAAAACTGGAA  4134       CACA
                                AAGCAAG   GAGACTGGAA
                                |||||||   ||||||||||
                                TTCGTTC   TTTTGACCTT
                                     CCC_
GAM188  SLC2A5  3' AGACAGGTATTTCTGGAAAAG 4135    C   AGA___
                                AG ACAG     CTGGAAAAG
                                || ||||     |||||||||
                                TC TGTC     GACCTTTTC
                                 _   CATAAA
GAM188  SMT3H1  3' AAGCAAGCAAGAGATGATGG  4136        C    C__
                                AAGCAAGCA AGAGA   TGG
                                ||||||||| |||||   |||
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                                TTCGTTCGT TCTCT   ACC
                                      _    ACT
GAM188  THBS1    3' GCAAGCACAGAAAAGAA    4137          CT
                                GCAAGCACAGAGA  GGAA
                                ||||||||||||  ||||
                                CGTTCGTGTCTTT  TCTT
                                      __
GAM188  TIMP3    5' AGCAGGCACAGAGGAGAAA   4138     A      ACT
                                AGCA GCACAGAG   GGAAA
                                |||| ||||||||   |||||
                                TCGT CGTGTCTC   TCTTT
                                  C      C__
GAM188  TRPV1    3' AAGCACGGCACAGAGAGGAA  4139      A_      CT
                                AAGCA  GCACAGAGA  GGAA
                                |||||  |||||||||  ||||
                                TTCGT  CGTGTCTCT  CCTT
                                   GC       __
GAM188  TRPV1    3' AAGCACGGCACAGAGAGGAA  4139      A_      CT
                                AAGCA  GCACAGAGA  GGAA
                                |||||  |||||||||  ||||
                                TTCGT  CGTGTCTCT  CCTT
                                   GC       __
GAM188  TRPV1    3' AAGCACGGCACAGAGAGGAA  4139      A_      CT
                                AAGCA  GCACAGAGA  GGAA
                                |||||  |||||||||  ||||
                                TTCGT  CGTGTCTCT  CCTT
                                   GC       __
GAM188  TRPV1    3' AAGCACGGCACAGAGAGGAA  4139      A_      CT
                                AAGCA  GCACAGAGA  GGAA
                                |||||  |||||||||  ||||
                                TTCGT  CGTGTCTCT  CCTT
                                   GC       __
GAM188  TRPV1    3' AAGCACGGCACAGAGAGG    4140      A_      CT
                                AAGCA  GCACAGAGA  GG
                                |||||  |||||||||  ||
                                TTCGT  CGTGTCTCT  CC
                                   GC       __
GAM188  TRPV1    3' AAGCACGGCACAGAGAGG    4140      A_      CT
                                AAGCA  GCACAGAGA  GG
                                |||||  |||||||||  ||
                                TTCGT  CGTGTCTCT  CC
                                   GC       __
GAM188  TRPV1    3' AAGCACGGCACAGAGAGG    4140      A_      CT
                                AAGCA  GCACAGAGA  GG
                                |||||  |||||||||  ||
                                TTCGT  CGTGTCTCT  CC
                                   GC       __
GAM188  TRPV1    3' AAGCACGGCACAGAGAGG    4140      A_      CT
                                AAGCA  GCACAGAGA  GG
                                |||||  |||||||||  ||
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                                TTCGT  CGTGTCTCT  CC
                                  GC       __
GAM188  WNT5A    3'  AAGCTAGCAGCCCTGCTGGGGA 4141      A   CAGAGA   AA
              AG                   AAGC AGCA     CTGG  AAG
                                |||| ||||     ||||  |||
                                TTCG TCGT     GACC  TTC
                                  A   CGGGAC   CC
GAM188  ZNF239   5'  AAGTCAGCAGCACTGGAAAAG  4142     _ _  AG
                                AAG CA CAG  ACTGGAAAAG
                                ||| || |||  ||||||||||
                                TTC GT GTC  TGACCTTTTC
                                  A  C   G_
GAM188  A2BP1    5'  GCTCGCACGGGGACTGGAAA  4143     AA   AGA
                                GC  GCAC   GACTGGAAA
                                ||  ||||   |||||||||
                                CG  CGTG   CTGACCTTT
                                  AG   CCC
GAM188  AFAP     3'  GCAAGCAAGAAAGCTGGGAAAG 4144        C   _   A
                                GCAAGCA AGAGA CTGG AAAG
                                ||||||| ||||| |||| ||||
                                CGTTCGT TCTTT GACC TTTC
                                    _    C   C
GAM188  AP4M1    3'  GCCAGGAGGCTGGAAAAG    4145     A  _  A
                                GC CAG AG CTGGAAAAG
                                || ||| || |||||||||
                                CG GTC TC GACCTTTTC
                                  _  C  C
GAM188  C12orf4  3'  AACACAGAGAAGAAAAA     4146          CT
                                AGCACAGAGA  GGAAAAG
                                ||||||||||  |||||||
                                TTGTGTCTCT  TCTTTTT
                                      __
GAM188  C1orf24  3'  AGAAAGCAGAGACTGG      4147     C    CA
                                AG AAGCA  GAGACTGG
                                || |||||  ||||||||
                                TC TTCGT  CTCTGACC
                                  T    __
GAM188  C20orf110 3'  AGTGAGCACACACTAGAAAAG  4148     CA     GAG
                                AG  AGCACA   ACTGGAAAAG
                                ||  ||||||   ||||||||||
                                TC  TCGTGT   TGATCTTTTC
                                  AC     G__
GAM188  C21orf25  3'  AAACAAAGCAGGTTGGAAAAG  4149       C  _  AC
                                AAGCA AG AG  TGGAAAAG
                                ||||| || ||  ||||||||
                                TTTGT TC TC  ACCTTTTC
                                   T  G  CA
GAM188  CBX6     3'  AAGCAAGCTAGAGAGACAGG   4150         AC_     T
                                AAGCAAGC   AGAGAC GG
                                ||||||||   |||||| ||
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                                TTCGTTCG   TCTCTG CC
                                     ATC     T
GAM188  CGI-127  3'  AAGCAACACAGGACCAAAA   4151       G    A   TG
                                AAGCAA CACAG GAC  GAA
                                |||||| ||||| |||  |||
                                TTCGTT GTGTC CTG  TTT
                                   _    _  GT
GAM188  COE2     3'  AAGCTGGTGCACCTGGAAAAG  4152      AA__   AGAGA
                                AAGC   GCAC    CTGGAAAAG
                                ||||   ||||    |||||||||
                                TTCG   CGTG    GACCTTTTC
                                  ACCA   _____
GAM188  CSMD1    3'  GCATCACATCTTGGAAAAG   4153     AG   GAGAC
                                GCA  CACA    TGGAAAAG
                                |||  ||||    ||||||||
                                CGT  GTGT    ACCTTTTC
                                  A_   AGA__
GAM188  dA141H5.1 5'  AAGCTGTGCAAAGGCTGGAAAA 4154      AAGCA    A
           G                     AAGC    CAGAG CTGGAAAAG
                                ||||    ||||| |||||||||
                                TTCG    GTTTC GACCTTTTC
                                  ACAC_    C
GAM188  DKFZp761A132 3'  AAGGAGCACAGAAAGGAAA   4155     CA       CT
                                AAG  AGCACAGAGA  GGAAA
                                |||  ||||||||||  |||||
                                TTC  TCGTGTCTTT  CCTTT
                                  C_        __
GAM188  FLJ10932  3'  GCAAACACAGAAGAGAAAAG   4156          ACT
                                GCAAGCACAGAG   GGAAAAG
                                ||||||||||||   |||||||
                                CGTTTGTGTCTT   TCTTTTC
                                       C__
GAM188  FLJ13322  3'  ACCCAGAGACTGGGGAAG    4157    A       AA
                                GC CAGAGACTGG  AAG
                                || ||||||||||  |||
                                TG GTCTCTGACC  TTC
                                 G        CC
GAM188  FLJ13448  3'  GCAAACTACTGGAAAAG     4158       ACAGAG
                                GCAAGC     ACTGGAAAAG
                                ||||||     ||||||||||
                                CGTTTG     TGACCTTTTC
                                   A_____
GAM188  FLJ14442  3'  AGAAGCACAGGACAGG      4159    C      A   T
                                AG AAGCACAG GAC GG
                                || |||||||| ||| ||
                                TC TTCGTGTC CTG CC
                                 _       _  T
GAM188  FLJ20275  3'  AAGCAAGCACGGAGGTGG    4160          A   AC
                                AAGCAAGCAC GAG  TGG
                                |||||||||| |||  |||
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                                TTCGTTCGTG CTC  ACC
                                      C   C_
GAM188  FLJ32332  3'  AAGCAAGCAGCAAGTCTGG   4161          CA   A
                                AAGCAAGCA  GAG CTGG
                                |||||||||  ||| ||||
                                TTCGTTCGT  TTC GACC
                                     CG   A
GAM188  GORASP2   3'  AAGCAAACATAGGACGTGAAAA 4162          C  A  _
                                AAGCAAGCA AG GAC TGGAAA
                                ||||||||| || ||| ||||||
                                TTCGTTTGT TC CTG ACTTTT
                                     A  _  C
GAM188  H2AFZ    5'  AAGCAAGCAAGGCAGAGAAAAG 4163          ___     CT
                                AAGCAAGCA   CAGAGA  GG
                                |||||||||   ||||||  ||
                                TTCGTTCGT   GTCTCT  TC
                                     TCC     TT
GAM188  HCA4     3'  AAGCAAGCTAGGACTGAA    4164          AC  A
                                AAGCAAGC  AG GACTGGA
                                ||||||||  || |||||||
                                TTCGTTCG  TC CTGACTT
                                     A_  _
GAM188  HSD-3.1   5'  GCAGTGGAGGACTGGAAAAG   4165      CA_  _
                                GCA   GAG ACTGGAAAAG
                                |||   ||| ||||||||||
                                CGT   CTC TGACCTTTTC
                                  CAC   C
GAM188  IPLA2(GAMMA) 3'  AAGCTAGTGTTAGATCTGGAAA 4166       A  CACAG  _
           AG                     AAGC AG     AGA CTGGAAAAG
                                |||| ||     ||| |||||||||
                                TTCG TC     TCT GACCTTTTC
                                  A  ACAA_   A
GAM188  KIAA0607  3'  AAGCAAGCTCAGGTGGAA    4167          A   AGAC
                                AAGCAAGC CAG    TGGAA
                                |||||||| |||    |||||
                                TTCGTTCG GTC    ACCTT
                                     A   C___
GAM188  KIAA0618  3'  GCAAGAGGAATAGAAAAG    4168       CAC  A  C
                                GCAAG   AG GA TGGAAAAG
                                |||||   || || ||||||||
                                CGTTC   TC CT ATCTTTTC
                                   ___  _  T
GAM188  KIAA0668  3'  AAGCAAGCTCAGGGGCACTGG  4169          A   AG__
                                AAGCAAGC CAG    ACTGG
                                |||||||| |||    |||||
                                TTCGTTCG GTC    TGACC
                                     A   CCCG
GAM188  KIAA0757  5'  AAGCAAGCGAGAGGCGCGG   4170          AC    AC_
                                AAGCAAGC  AGAG   TGG
                                ||||||||  ||||   |||
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                                TTCGTTCG  TCTC   GCC
                                    C_    CGC
GAM188  KIAA1084  3'  AAGCAAGCATGGAAGCTCATGA 4171         CA_   AC__
          AAAAG                   AAGCAAGCA   GAG    TGGAAAAG
                                |||||||||   |||    ||||||||
                                TTCGTTCGT   TTC    ACTTTTTC
                                    ACC   GAGT
GAM188  KIAA1323  3'  AAGTAATCACAGAAAACCGGAA 4172      CAAG      _
                                AAG    CACAGAGA CTGGAA
                                |||    |||||||| ||||||
                                TTC    GTGTCTTT GGCCTT
                                  ATTA       T
GAM188  KIAA1831  3'  AAGGAGCACAGAAAAGAAA   4173     CA        CT
                                AAG  AGCACAGAGA  GGAAA
                                |||  ||||||||||  |||||
                                TTC  TCGTGTCTTT  TCTTT
                                  C_         __
GAM188  KIAA1949  5'  AAGCAGGGCAGAGGGGCTAAG  4174       A CA    ACT  AA
                                AAGCA G  CAGAG   GG  AAG
                                |||||  |  |||||   ||  |||
                                TTCGT C  GTCTC   CC  TTC
                                   _ CC    C__  GA
GAM188  KIAA1949  5'  AAGCAGGGCAGAGGGGCTAAG  4174       A CA    ACT  AA
                                AAGCA G  CAGAG   GG  AAG
                                |||||  |  |||||   ||  |||
                                TTCGT C  GTCTC   CC  TTC
                                   _ CC    C__  GA
GAM188  KIAA1949  5'  AAGCAGGGCAGAGGGGCTAAG  4174       A CA    ACT  AA
                                AAGCA G  CAGAG   GG  AAG
                                |||||  |  |||||   ||  |||
                                TTCGT C  GTCTC   CC  TTC
                                   _ CC    C__  GA
GAM188  KUB3     5'  GCCAGAGCGAGACTGGGAAAG  4175     A  CACA       A
                                GC AG    GAGACTGG AAAG
                                || ||    |||||||| ||||
                                CG TC    CTCTGACC TTTC
                                  G  TCG_       C
GAM188  LIMK2    3'  AGCAAACATGGGAGGTAGAA   4176         CA_   AC
                                AGCAAGCA   GAG  TGGAA
                                |||||||   |||  |||||
                                TCGTTTGT   CTC  ATCTT
                                    ACC   C_
GAM188  LIMK2    3'  AGCAAACATGGGAGGTAGAA   4176         CA_   AC
                                AGCAAGCA   GAG  TGGAA
                                |||||||   |||  |||||
                                TCGTTTGT   CTC  ATCTT
                                    ACC   C_
GAM188  LIPG     3'  AAGCAATCACAGAAACAAGA   4177        G        T
                                AAGCAA CACAGAGAC GGA
                                ||||||  |||||||| |||
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                                TTCGTT GTGTCTTTG TCT
                                   A       T
GAM188  MacGAP   3'  AAGCAAACCTAACTGGGAAAG  4178        ACAGA     A
                                AAGCAAGC    GACTGG AAAG
                                ||||||||    |||||| ||||
                                TTCGTTTG    TTGACC TTTC
                                   GA___     C
GAM188  MDS018   3'  AAGCAGGCAAGAGGCCTGG   4179      A  C   A_
                                AAGCA GCA AGAG  CTGG
                                ||||| ||| ||||  ||||
                                TTCGT CGT TCTC  GACC
                                  C  _   CG
GAM188  MGC16169 5'  GCAAGCACAAAGACAAGG    4180           T_
                                GCAAGCACAGAGAC  GG
                                ||||||||||||||  ||
                                CGTTCGTGTTTCTG  CC
                                      TT
GAM188  MGC22014 3'  CAAGCCGGGGACTGGAAAA   4181       ACAGA
                                CAAGC    GACTGGAAAA
                                |||||    ||||||||||
                                GTTCG    CTGACCTTTT
                                  GCCC_
GAM188  MGC3047  3'  AAGCAACACAGAGGAGCAAGG  4182       G      ACT___
                                AAGCAA CACAGAG     GG
                                |||||| |||||||     ||
                                TTCGTT GTGTCTC     CC
                                   _      CTCGTT
GAM188  MGC5457  5'  AGGACAGAAGACTGGAAA    4183     C    _
                                AG ACAGA GACTGGAAA
                                || ||||| |||||||||
                                TC TGTCT CTGACCTTT
                                 C    T
GAM188  MRVI1    5'  AGCAAGCATGTGAGCCTGGAGA 4184        CA_  A    A
            AG                    AGCAAGCA   GAG CTGGA AAG
                                ||||||||   ||| ||||| |||
                                TCGTTCGT   CTC GACCT TTC
                                     ACA  G    C
GAM188  NOVA2    3'  AGCCAAGCACAGGGAGG     4185     _      A  CT
                                AGC AAGCACAG GA  GG
                                ||| |||||||| ||  ||
                                TCG TTCGTGTC CT  CC
                                  G       C  __
GAM188  NXPH3    3'  AAGCGGGCACAGAAGTATCTGG 4186      AA      A___
                                AAGC  GCACAGAG   CTGG
                                ||||  ||||||||   ||||
                                TTCG  CGTGTCTT   GACC
                                  CC       CATA
GAM188  OR51E2   5'  ACAGGCACAGAGCTAAAA    4187     A       A
                                GCA GCACAGAG CTGGAA
                                ||| |||||||| ||||||
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                                TGT CGTGTCTC GATTTT
                                  C       _
GAM188  PGLYRP   5'  ACAGGCACAGAGAACTGA    4188      A       _
                                GCA GCACAGAGA CTGG
                                ||| ||||||||| ||||
                                TGT CGTGTCTCT GACT
                                  C        T
GAM188  PWP1     3'  AGCAAGCACAAAGACCGG    4189
                                AGCAAGCACAGAGACTGG
                                ||||||||||||||||||
                                TCGTTCGTGTTTCTGGCC

GAM188  RAB10    3'  AAGCAGTCACAGATGAAA    4190       AG     GAC
                                AAGCA  CACAGA   TGGAA
                                |||||  ||||||   |||||
                                TTCGT  GTGTCT   ACTTT
                                   CA     ____
GAM188  RASSF2   3'  GCAGGACAAAATGGAAAAG   4191      A C     AC
                                GCA G ACAGAG  TGGAAAAG
                                ||| | ||||||  ||||||||
                                CGT C TGTTTT  ACCTTTTC
                                  _ C     __
GAM188  SERP1    3'  AAACAAGTACAGAGACTG    4192        C
                                AAGCAAG ACAGAGACTG
                                ||||||| ||||||||||
                                TTTGTTC TGTCTCTGAC
                                    A
GAM188  ST6GalNAcI 3'  AAGAAGCTTTTGGACTGGAA   4193      C    ACAGA
                                AAG AAGC    GACTGGAA
                                ||| ||||    ||||||||
                                TTC TTCG    CTGACCTT
                                  _   AAAAC
GAM188  TINF2    3'  AGCAAGCAAAGAGGATAG    4194        C    AC
                                AGCAAGCA AGAG  TGG
                                |||||||| ||||  |||
                                TCGTTCGT TCTC  ATC
                                     T    CT
GAM188  LOC115574 3'  GCAAGCACAGAGACGGGA    4195             T
                                GCAAGCACAGAGAC GGA
                                |||||||||||||| |||
                                CGTTCGTGTCTCTG CCT
                                          C
GAM188  LOC126526 3'  AAGAAAGCACAGAGGACATGAG 4196      C        _ _ _
          A                      AAG AAGCACAGAG AC TG GA
                                ||| |||||||||| || || ||
                                TTC TTCGTGTCTC TG AC CT
                                  T        C  T  T
GAM188  LOC129642 3'  GCAAGACATTCATTTGGAAAAG 4197       C   GAGAC_
                                GCAAG ACA     TGGAAAAG
                                ||||| |||     ||||||||
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                                CGTTC TGT     ACCTTTTC
                                  _  AAGTAA
GAM188  LOC130589 3'  AGCCAGTCACTGGAAAA     4198      A   AG
                                AGC CAG  ACTGGAAAA
                                ||| |||  |||||||||
                                TCG GTC  TGACCTTTT
                                  _  AG
GAM188  LOC143451 3'  ACAAGCACAGGAGGGA      4199          A  CT
                                GCAAGCACAG GA  GGA
                                |||||||||| ||  |||
                                TGTTCGTGTC CT  CCT
                                      _ C_
GAM188  LOC145125 3'  ACAAGCACAGGAGGGA      4199          A  CT
                                GCAAGCACAG GA  GGA
                                |||||||||| ||  |||
                                TGTTCGTGTC CT  CCT
                                      _ C_
GAM188  LOC146184 5'  AAGAAGCACAGAGGTGG     4200      C        AC
                                AAG AAGCACAGAG  TGG
                                ||| ||||||||||  |||
                                TTC TTCGTGTCTC  ACC
                                  _        C_
GAM188  LOC146958 5'  AGCAGCACAGAATGAAA     4201      A       AC
                                AGCA GCACAGAG  TGGAA
                                |||| ||||||||  |||||
                                TCGT CGTGTCTT  ACTTT
                                  _      __
GAM188  LOC149448 3'  AGCAGGAGCTAAGACTGGA   4202       __  ACA
                                AGCA  AGC   GAGACTGGA
                                ||||  |||   |||||||||
                                TCGT  TCG   TTCTGACCT
                                  CC   A__
GAM188  LOC149711 3'  ACAGTAACAATAGACTGGA   4203      AGC   _
                                GCA   ACAG AGACTGGA
                                |||   |||| ||||||||
                                TGT   TGTT TCTGACCT
                                  CAT    A
GAM188  LOC152275 3'  GCCAGCACAGAGTGACCCAGG  4204     A      __   __
                                GC AGCACAGA  GACT  GG
                                || ||||||||  ||||  ||
                                CG TCGTGTCT  CTGG  CC
                                 G       CA    GT
GAM188  LOC152316 3'  GCAAGCGCAGACTAGAA     4205        A  GA
                                GCAAGC CA  GACTGGAA
                                ||||||  ||  ||||||||
                                CGTTCG GT  CTGATCTT
                                   C  __
GAM188  LOC153277 3'  AAGAAGCACAGGAAGA      4206      C       A  CT
                                AAG AAGCACAG GA  GGA
                                ||| ||||||||  ||  |||
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                                TTC TTCGTGTC CT  TCT
                                  _      _ __
GAM188  LOC158055 3'  AGCAGGGGCAGAGACTTGGA  4207      AGCA      _
                                AGCA   CAGAGACT GGA
                                ||||   |||||||| |||
                                TCGT   GTCTCTGA CCT
                                  CCCC       A
GAM188  LOC158450 5'  AAGCAATATAGAGACTAG    4208       GCAC
                                AAGCAA   AGAGACTGG
                                ||||||   |||||||||
                                TTCGTT   TCTCTGATC
                                   ATA_
GAM188  LOC158504 5'  AAGCAATATAGAGACTAG    4208       GCAC
                                AAGCAA   AGAGACTGG
                                ||||||   |||||||||
                                TTCGTT   TCTCTGATC
                                   ATA_
GAM188  LOC160414 3'  AGCAAGCACTGACACAAGG   4209         A  G  T_
                                AGCAAGCAC GA AC  GG
                                ||||||||| || ||  ||
                                TCGTTCGTG CT TG  CC
                                     A  G  TT
GAM188  LOC196500 3'  AGCTGAGCACAGAATGTGGGAA 4210     A_       ACT_
                                AGC  AGCACAGAG   GGAA
                                |||  |||||||||   ||||
                                TCG  TCGTGTCTT   CCTT
                                  AC        ACAC
GAM188  LOC197114 5'  AAGCACAGCACGGGGACTG   4211       _    AGA
                                AAGCA AGCAC   GACTG
                                ||||| |||||   |||||
                                TTCGT TCGTG   CTGAC
                                   G    CCC
GAM188  LOC197117 3'  AAGCACAGCACGGGGACTG   4211       _    AGA
                                AAGCA AGCAC   GACTG
                                ||||| |||||   |||||
                                TTCGT TCGTG   CTGAC
                                   G    CCC
GAM188  LOC200150 3'  AGCAAGACAGAAAAGG      4212        C      CT
                                AGCAAG ACAGAGA  GG
                                |||||| |||||||  ||
                                TCGTTC TGTCTTT  CC
                                   _      T_
GAM188  LOC222178 5'  AGCAGGCACAGAGTCAGAA   4213      A       ACT
                                AGCA GCACAGAG   GGAA
                                |||| ||||||||   ||||
                                TCGT CGTGTCTC   TCTT
                                  C       AG_
GAM188  LOC253776 3'  GCAGGCCCAGAACAAAAAAAG  4214     A  A    ACT
                                GCA GC CAGAG   GGAAAAG
                                ||| || |||||   |||||||
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                                CGT CG GTCTT   TTTTTTC
                                  C  G    GT_
GAM188  LOC254440 3'  GCAAGCACAGGAGGGA      4215          A  CT
                                GCAAGCACAG GA  GGA
                                |||||||||| ||  |||
                                CGTTCGTGTC CT  CCT
                                      _  C_
GAM188  LOC255104 3'  AGCTGCATATGGAGACTGGGGA 4216     AA   CA__      AA
          AG                    AGC  GCA   GAGACTGG  AAG
                                |||  |||   ||||||||  |||
                                TCG  CGT   CTCTGACC  TTC
                                  A_  ATAC       CC
GAM188  LOC256364 5'  AAGTCAGCACAGAGACCAG   4217     CA         TG
                                AAG  AGCACAGAGAC  G
                                |||  ||||||||||  |
                                TTC  TCGTGTCTCTG  C
                                  AG         GT
GAM188  LOC256733 5'  AAGCAAGCAAGAAAAAGGAA   4218         C    CT
                                AAGCAAGCA AGAGA  GGAA
                                |||||||| |||||  ||||
                                TTCGTTCGT TCTTT  CCTT
                                      _    TT
GAM188  LOC92573  5'  ACAGCAGTGAGGATTGGAAAAG 4219     A   CA   AC_
                                GCA GCA  GAG   TGGAAAAG
                                ||| |||  |||   ||||||||
                                TGT CGT  CTC   ACCTTTTC
                                  _  CA   CTA
GAM189  ACE2     3'  CCATACAAGATCCAACAC    4222         AACCC
                                CCATACAA    TTCGGCGC
                                ||||||||    ||||||||
                                GGTATGTT    AGGTTGTG
                                     CT___
GAM189  CXCR6    3'  TACCTATACAAAAGTCAAGC   4223      C       CCC  C
                                TACC ATACAAAA   TT GGC
                                |||| ||||||||   || |||
                                ATGG TATGTTTT   AG TCG
                                  A       C__  T
GAM189  NCOA2    3'  TACCTTACAAAACTTCGGC    4224      CA       CC
                                TACC  TACAAAAC  TTCGGC
                                ||||  ||||||||  ||||||
                                ATGG  ATGTTTTG  AAGCCG
                                  A_       __
GAM189  LOC158954 3'  CCCATACAAAGCTTTTCAG   4225          ACCC
                                CCCATACAAA    TTCGG
                                ||||||||||    |||||
                                GGGTATGTTT    AAGTC
                                      CGAA
GAM189  LOC256596 5'  CCACACAAAATCCTGC      4226          C   TCG
                                CCATACAAAA CCT   GC
                                |||||||||| |||   ||
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                                GGTGTGTTTT GGA   CG
                                      A  ___
GAM190  DXYS155E  3'  TGCGGTGCCTGCTCGGGG    4229          AAGGACA  A
                                TGTGGTGCCT      TC GGG
                                ||||||||||      || |||
                                ACGCCACGGA      AG CCC
                                      CG_____  C
GAM190  DYT1      3'  TGTGGTGCCTGAAGGCGTC   4230          _   ACA
                                TGTGGTGCCT AAGG   TC
                                |||||||||| ||||   ||
                                ACACCACGGA TTCC   AG
                                      C   GC_
GAM190  FABP3     3'  TGTGGTGCTGAGTCGAGGG   4231         CTA  GACA  _
                                TGTGGTGC   AG    TC AGGG
                                ||||||||   ||    || ||||
                                ACACCACG   TC    AG TCCC
                                     AC_  _____  C
GAM190  IHPK1     3'  TGTGGTGCCCTGAGGGCACC  4232          A_   A
                                TGTGGTGCCT  AGG CATC
                                ||||||||||  ||| ||||
                                ACACCACGGG  TCC GTGG
                                      AC   C
GAM190  SLC13A4   3'  TGTGGTGCTGAGGGCAGGA   4233         CTA   ACAT
                                TGTGGTGC   AGG   CAGGG
                                ||||||||   |||   |||||
                                ACACCACG   TCC   GTCCT
                                     AC_   C___
GAM190  FLJ13479  3'  TGTGGTGCTGGGGGGTCATGGG 4234        CTAA  ACA  _
                                TGTGGTGC    GG   TCA GGG
                                ||||||||    ||   ||| |||
                                ACACCACG    CC   AGT CCC
                                     AC__  CCC   A
GAM190  FLJ14800  3'  TGTGGTGCCTGAGCAGG     4235          A  GACAT
                                TGTGGTGCCT AG     CAGG
                                |||||||||| ||     ||||
                                ACACCACGGA TC     GTCC
                                      C  _____
GAM190  FLJ23519  5'  TGTGGAGCAGACATCAGGG   4236       T  CTAA
                                TGTGG GC    GGACATCAGGG
                                ||||| ||    ||||||||||
                                ACACC CG    TCTGTAGTCCC
                                   T  ____
GAM190  HSA243666 3'  GTGGTGCCTGGGGAGGG     4237         AA   CATCA
                                GTGGTGCCT  GGA    GGG
                                |||||||||  |||    |||
                                CACCACGGA  CCT    CCC
                                      CC  _____
GAM190  ITGB5     3'  TGTGGTGCCTACCTAGGG    4238          AGGACATC
                                TGTGGTGCCTA       AGGG
                                ||||||||||        ||||
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                                ACACCACGGAT       TCCC
                                      GGA_____
GAM190  KIAA0775  3'  GTGGTGCCTGGACCAGGG    4239          AA    AT
                                GTGGTGCCT  GGAC  CAGGG
                                |||||||||  ||||  |||||
                                CACCACGGA  CCTG  GTCCC
                                     __    __
GAM190  PCQAP     3'  TGTGGTGCTCTGAGGACACGGG 4240          _ A      CA
                                TGTGGTGC CT AGGACAT  GGG
                                |||||||| || |||||||  |||
                                ACACCACG GA TCCTGTG  CCC
                                     A  C      __
GAM190  QSCN6     3'  TGTGGTGCTAAGAGGCCAGGGA 4241          C     ACA
                                TGTGGTGC TAAGG   TCAGGGA
                                |||||||| |||||   |||||||
                                ACACCACG ATTCT   GGTCCCT
                                     _    CC_
GAM190  RASSF2    3'  TGTGCTGCTATATCAGGGA    4242       G   C  AGGAC
                                TGTG TGC TA    ATCAGGGA
                                |||| ||| ||    ||||||||
                                ACAC ACG AT    TAGTCCCT
                                  G   _ A____
GAM190  SCAMP5    3'  TGTGTGCCCCTCCTACATCAGG 4243       G    AAGG_
           G                     TGTG TGCCT    ACATCAGGG
                                |||| |||||    |||||||||
                                ACAC ACGGG    TGTAGTCCC
                                  _    GAGGA
GAM190  ZNF304    3'  TGGGGTTCTGGATATCAGGGA  4244     T   GC  AA   C
                                TG GGT  CT  GGA ATCAGGGA
                                || |||  ||  ||| ||||||||
                                AC CCA  GA  CCT TAGTCCCT
                                 C   A_  __   A
GAM190  LOC124930 3'  TGGTGCCCCTGGCATCAGGGA  4245          AA  A
                                TGGTGCCT  GG CATCAGGGA
                                ||||||||  || |||||||||
                                ACCACGGG  CC GTAGTCCCT
                                     GA  _
GAM190  LOC221510 3'  TGTGGTGCTAAGAAGAAGGGA  4246          C     CATC
                                TGTGGTGC TAAGGA    AGGGA
                                |||||||| ||||||    |||||
                                ACACCACG ATTCTT    TCCCT
                                     _     CT__
GAM190  LOC257476 3'  TGTGGTGCCCTGAGGGCACC   4232          A_   A
                                TGTGGTGCCT  AGG CATC
                                ||||||||||  ||| ||||
                                ACACCACGGG  TCC GTGG
                                      AC   C
GAM191  NTSR1     3'  GTCCTGTGGTTGGAGAGG    4249      G      GAAA   CT
                                GTC TGTGGTT    GGA  AGG
                                ||| |||||||    |||  |||
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                                CAG ACACCAA   CCT  TCC
                                  G     _____  C_
GAM191  CDC14B   3'  GTCATGTGGTTGAAGACAGTTT 4250          AA   TA____
            TGGG                  TCGTGTGGTTGA  GGAC    GGG
                                |||||||||||  ||||    |||
                                AGTACACCAACT  TCTG    CCC
                                      __   TCAAAA
GAM191  LOC91614 5'  TGTGGTTGAGACAGG      4251         AAG   T
                                TGTGGTTGA   GAC AGG
                                |||||||||   ||| |||
                                ACACCAACT   CTG TCC
                                     ___  _
GAM191  LOC96597 3'  GTCGTGTGGTTGCAGGGCT   4252          AA   A
                                GTCGTGTGGTTG  AGG CT
                                ||||||||||||  ||| ||
                                CAGCACACCAAC  TCC GA
                                      G_   C
GAM192  CDKN1B   3'  CCTAAAATTTTAGTGTTA    4255    AG
                                TC  GAGTTTTAGTGTTA
                                ||  ||||||||||||||
                                GG  TTTAAAATCACAAT
                                 AT
GAM192  EVA1     3'  TCTCAGAGTTTTATATAAAACT 4256       G     _   TT  C
            GT                    TCTCAG AGTTTTA GTG  AC GT
                                |||||| ||||||| |||  || ||
                                AGAGTC TCAAAAT TAT  TG CA
                                   _     A   TT  A
GAM192  LIFR     3'  TCTTAGAAGTTTTAAAATC   4257     C        T
                                TCT AGGAGTTTTAG GTT
                                ||| ||||||||||| |||
                                AGA TCTTCAAAATT TAG
                                  A         T
GAM192  SLC4A4   3'  AGGAGTATCAGGTACTGT    4258       T    T  T  C
                                AGGAGT TTAG GT AC GT
                                |||||| |||| || || ||
                                TCCTCA AGTC CA TG CA
                                   T   _ _  A
GAM192  KIAA0648 3'  TCTCAAGAGTTTCTGCT     4259           AG
                                TCTCAGGAGTTTT  TGTT
                                ||||||||||||  ||||
                                AGAGTTCTCAAAG  ACGA
                                      __
GAM192  MGC14353 3'  AGGAGTTTTTAGGTATTACCGT 4260         A__
                                AGGAGTTTT   GTGTTACCGT
                                |||||||||   ||||||||||
                                TCCTCAAAA   CATAATGGCA
                                     ATC
GAM192  MGC3020  3'  TCAGGGGCTTTTAGTCACCGT  4261       A    AGT
                                TCAGG GTTTT   GTTACCGT
                                ||||| |||||   ||||||||
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                                AGTCC CGAAA   CAGTGGCA
                                   C     AT_
GAM192  PRO0478  3'  CTCAGGAGTTTGAAGTTGCT   4262          T_  _
                                CTCAGGAGTTT  AGT GTT
                                ||||||||||  ||| |||
                                GAGTCCTCAAA  TCA CGA
                                      CT   A
GAM193  A1BG     3'  TGGGAAAGAACACAGAG     4265       A      A  A
                                TGGGA GAGAACA CA AG
                                ||||| ||||||| || ||
                                ACCCT TTCTTGT GT TC
                                   _      _ C
GAM193  ATF7     3'  TGGGAAGAGAGGGAACTGAGAA 4266          AC_   AA
                                TGGGAAGAGA   AAC  AGAA
                                ||||||||||   |||  ||||
                                ACCCTTCTCT   TTG  TCTT
                                      CCC   AC
GAM193  ATRN     3'  TGGGAGAAACCGTCAAAGAAA  4267       A    ACAA
                                TGGGA GAGA    CAAAGAAA
                                ||||| ||||    ||||||||
                                ACCCT CTTT    GTTTCTTT
                                   _    GGCA
GAM193  BAZ1B    3'  GGGAGGAGCTGTCACAAAGAA  4268       A   AACA_
                                GGGA GAG     ACAAAGAA
                                |||| |||     ||||||||
                                CCCT CTC     TGTTTCTT
                                   C   GACAG
GAM193  BAZ2A    3'  TGGGAGAGGAACACAAAG    4269       A   _   A
                                TGGGA GAG AACA CAAAG
                                ||||| ||| |||| |||||
                                ACCCT CTC TTGT GTTTC
                                   _   C    _
GAM193  BSN      3'  GGGGAGAGAGAAACAAAAGAAA 4270      A    AC     _
             A                   GGG AGAGA  AACAAA GAAAA
                                ||| |||||  |||||| |||||
                                CCC TCTCT  TTGTTT CTTTT
                                  C     CT     T
GAM193  C4orf1   3'  GGGAAAAAAGCAAAGAA     4271          ACAA
                                GGGAAGAGA    CAAAGAA
                                |||||||||    |||||||
                                CCCTTTTTT    GTTTCTT
                                      C___
GAM193  CHAD     3'  TGGGAAGATGGACAGCAAAG   4272         GA_   A
                                TGGGAAGA   ACA CAAAG
                                ||||||||   ||| |||||
                                ACCCTTCT   TGT GTTTC
                                     ACC   C
GAM193  CLN5     3'  TGGGAAGAGGGAGAACTACAGG 4273          ____    A   AA
             AAA                    TGGGAAGA    GAAC ACA  GAAA
                                ||||||||    |||| |||  ||||
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                                ACCCTTCT   CTTG TGT  CTTT
                                    CCCT   A  C_
GAM193  CRTAP   3'  TGGGAAAAGGACAAAGA    4274         AACA
                                TGGGAAGAG   ACAAAGA
                                |||||||||   |||||||
                                ACCCTTTTC   TGTTTCT
                                    C___
GAM193  CTNND2  3'  TGGGAGAAAGTAAAGAAAA   4275      A   ACAAC
                                TGGGA GAGA    AAAGAAAA
                                ||||| ||||    ||||||||
                                ACCCT CTTT    TTTCTTTT
                                  _   CA___
GAM193  CYFIP2  3'  GGGGGGAGAAAAGAAAA     4276     AA    CAACA
                                GGG  GAGAA    AAGAAAA
                                |||  |||||    |||||||
                                CCC  CTCTT    TTCTTTT
                                  CC    _____
GAM193  CYP24   5'  TGGGAAAAGGAAGCAAAGA   4277         AACAA
                                TGGGAAGAG    CAAAGA
                                |||||||||    ||||||
                                ACCCTTTTC    GTTTCT
                                    CTTC_
GAM193  CYP2B6  3'  TGGGAATGAGGACTGGGGAAGA 4278       _  A  AACA_
                                TGGGAA GAG AC    AAGA
                                ||||||| ||| ||    ||||
                                ACCCTT CTC TG    TTCT
                                   A   C  ACCCC
GAM193  EDN3    3'  TGGGAAGAGCGCAGCTGAAA  4279         AA  ACAAA
                                TGGGAAGAG  CA    GAAA
                                |||||||||  ||    ||||
                                ACCCTTCTC  GT    CTTT
                                    GC  CGA__
GAM193  F8      3'  TGGGAAAAGAATGCCAAAA   4280          CAA
                                TGGGAAGAGAA   CAAAG
                                ||||||||||   |||||
                                ACCCTTTTCTT   GTTTT
                                      ACG
GAM193  FLRT2   3'  GGGAAGAGGACAGTAGAA    4281         A   ACAA
                                GGGAAGAG ACA    AGAA
                                |||||||| |||    ||||
                                CCCTTCTC TGT    TCTT
                                    C   CA__
GAM193  GAS7    3'  TGGGAAAAAAATAAAGAA    4282          CAAC
                                TGGGAAGAGAA    AAAGAA
                                ||||||||||    ||||||
                                ACCCTTTTTTT    TTTCTT
                                      A___
GAM193  GAS7    3'  TGGGAAAAAAATAAAGAA    4282          CAAC
                                TGGGAAGAGAA    AAAGAA
                                ||||||||||    ||||||
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                                ACCCTTTTTTT   TTTCTT
                                      A___
GAM193  GDI1     3'  GGGAAGAGACACACACAAGGA  4283         _  _   A
                                GGGAAGAGA ACA ACAA GA
                                ||||||||| ||| |||| ||
                                CCCTTCTCT TGT TGTT CT
                                     G  G   C
GAM193  GRIN2C   3'  TGAGAAGAGGACAGCAAAA   4284         A  A
                                TGGGAAGAG ACA CAAAG
                                ||||||||| ||| |||||
                                ACTCTTCTC TGT GTTTT
                                     C  C
GAM193  GRLF1    3'  TGGGAAGAGACAGACCAACAGG 4285         A____    AA
           AA                     TGGGAAGAGA    CAACA  GAA
                                ||||||||||    |||||  |||
                                ACCCTTCTCT    GTTGT  CTT
                                     GTCTG    C_
GAM193  HSPA9B   3'  TGGGTAAGAGAACAATCA    4286      _       _
                                TGGG AAGAGAACAA CA
                                |||| |||||||||| ||
                                ACCC TTCTCTTGTT GT
                                  A        A
GAM193  KIAA0857 3'  TGGGAGGACAACAAAG      4287       A A  A
                                TGGGA G GA CAACAAAG
                                ||||| | || ||||||||
                                ACCCT C CT GTTGTTTC
                                  _ _  _
GAM193  KMO      3'  GGGACAGGCCAAAGAAAA    4288      AG  AACAA
                                GGGA  AG    CAAAGAAAA
                                ||||  ||    |||||||||
                                CCCT  TC    GTTTCTTTT
                                  G_  CG___
GAM193  KRTHA8   3'  GGGAAGAGCACCCCAGAGA   4289        A  AA  A
                                GGGAAGAG AC  CA AGA
                                |||||||| ||  || |||
                                CCCTTCTC TG  GT TCT
                                     G  GG  C
GAM193  L1CAM    3'  TGGAGCAGAGATGGCAAAGAAA 4290      A_    ACAA
           A                     TGGG  AGAGA   CAAAGAAAA
                                ||||  |||||   |||||||||
                                ACCT  TCTCT   GTTTCTTTT
                                  CG    ACC_
GAM193  L1CAM    3'  TGGAGCAGAGATGGCAAAGAAA 4290      A_    ACAA
           A                     TGGG  AGAGA   CAAAGAAAA
                                ||||  |||||   |||||||||
                                ACCT  TCTCT   GTTTCTTTT
                                  CG    ACC_
GAM193  LASS2    3'  GGGAAGAGGCCAGAGAAA    4291        AA  ACAA
                                GGGAAGAG  CA   AGAAA
                                ||||||||  ||   |||||
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                                CCCTTCTC  GT   TCTTT
                                    CG  C___
GAM193  LCP1    3'  TAGGAAGAGGGGACAGAAAGA  4292        A__  AC
                                TGGGAAGAG  ACA  AAAGA
                                |||||||||  |||  |||||
                                ATCCTTCTC  TGT  TTTCT
                                    CCC  C_
GAM193  LIF     3'  GGGAAGAGAACGAAGA     4293          AACA
                                GGGAAGAGAAC   AAGA
                                ||||||||||   ||||
                                CCCTTCTCTTG   TTCT
                                      C___
GAM193  LYPLA1  3'  GAAGGACAATAAAGAAAA   4294      A  A  C
                                GAAG GA CAA AAAGAAAA
                                |||| || ||| ||||||||
                                CTTC CT GTT TTTCTTTT
                                  _ _  A
GAM193  MAPRE2  3'  TGGAAAGAGACTAAGAAA   4295        ACAACA
                                TGGGAAGAGA    AAGAAA
                                ||||||||||    ||||||
                                ACCTTTCTCT    TTCTTT
                                    GA____
GAM193  MGAT5   5'  TGGGGGTAACTAGACAAAGAA  4296     AAGAG  A__
                                TGGG   AAC  ACAAAGAA
                                ||||   |||  ||||||||
                                ACCC   TTG  TGTTTCTT
                                  CCA__  ATC
GAM193  MHC2TA  3'  TAGGAAGCCACAAAGAAA   4297       AGAACA
                                TGGGAAG    ACAAAGAAA
                                |||||||    |||||||||
                                ATCCTTC    TGTTTCTTT
                                   GG____
GAM193  MMP16   3'  AGAACTGAATGACAAAGAAA  4298     GA  CA
                                GGAA  GAA  ACAAAGAAA
                                ||||  |||  |||||||||
                                TCTT  CTT  TGTTTCTTT
                                  GA  AC
GAM193  MS4A12  3'  TAGGAAGAGACAGTGAAG   4299        A  ACA
                                TGGGAAGAGA CA  AAG
                                |||||||||| ||  |||
                                ATCCTTCTCT GT  TTC
                                    _ CAC
GAM193  MS4A4A  3'  GGAAAGAAAAGCAGGAGAA  4300        _ ACAA
                                GGGAAGAGAA CA   AGAA
                                |||||||||| ||   ||||
                                CCTTTCTTTT GT   TCTT
                                    C  CC__
GAM193  MUC4    5'  TGGGAAGAGGACAAAAGA   4301        A   CA
                                TGGGAAGAG ACAA  AAGA
                                ||||||||| ||||  ||||
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                                ACCCTTCTC TGTT  TTCT
                                     C   __
GAM193  MUC4    5'  TGGGAAGAGGACAAAAGA   4301         A   CA
                                TGGGAAGAG ACAA  AAGA
                                ||||||||| ||||  ||||
                                ACCCTTCTC TGTT  TTCT
                                     C   __
GAM193  NOS1    3'  GGGAAGAGGACGGACAGAG   4302        A  A_  A
                                GGGAAGAG AC  ACA AG
                                |||||||| ||  ||| ||
                                CCCTTCTC TG  TGT TC
                                     C  CC   C
GAM193  ORC1L   5'  TGGAAGGAGAAAAGAAA    4303       A    CAACA
                                TGGGA GAGAA    AAGAAA
                                ||||| |||||    ||||||
                                ACCTT CTCTT    TTCTTT
                                   C   _____
GAM193  PCBD    3'  TGGGAAGTTGCAAAGAAA    4304       AGAACAA
                                TGGGAAG      CAAAGAAA
                                |||||||      ||||||||
                                ACCCTTC      GTTTCTTT
                                     AAC____
GAM193  PCDH11Y 3'  TAGGAAGAGAAGGCATAG   4305          CAA  A
                                TGGGAAGAGAA   CA AG
                                ||||||||||   || ||
                                ATCCTTCTCTT   GT TC
                                      CC_  A
GAM193  PCDHB11 3'  TGGGGGAGAAAAGAAA     4306      AA    CAACA
                                TGGG  GAGAA    AAGAAA
                                ||||  |||||    ||||||
                                ACCC  CTCTT    TTCTTT
                                  C_    _____
GAM193  PCTK3   3'  GGGAAGCACAAAGAA      4307       AGAA  A
                                GGGAAG   CA CAAAGAA
                                ||||||   || |||||||
                                CCCTTC   GT GTTTCTT
                                     ____  _
GAM193  PDYN    3'  TGGGAATGAGAGAGCAAAAGA 4308       _   ACAAC
                                TGGGAA GAGA    AAAGA
                                |||||| ||||    |||||
                                ACCCTT CTCT    TTTCT
                                    A   CTCGT
GAM193  POLR2K  3'  TGGGAAGAGAGCAAATCCAAG 4309         A  CA__
                                TGGGAAGAGA CAA   AAG
                                |||||||||| |||   |||
                                ACCCTTCTCT GTT   TTC
                                      C  TAGG
GAM193  RABL2A  3'  TGGGAGAAAACGTAGGGAAA  4310      A    AACAAA
                                TGGGA GAGAAC    GAAA
                                ||||| ||||||    ||||
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                                ACCCT CTTTTG     CTTT
                                   _     CATCC_
GAM193  RABL2B   3'  TGGGAGAAAACGTAGGGAAA  4310       A     AACAAA
                                TGGGA GAGAAC     GAAA
                                ||||| ||||||     ||||
                                ACCCT CTTTTG     CTTT
                                   _     CATCC_
GAM193  RBBP5    3'  TGAGAGGAAAACAAGGGAAA  4311       A      CAAA
                                TGGGA GAGAACAA   GAAA
                                ||||| ||||||||   ||||
                                ACTCT CTTTTGTT   CTTT
                                   C      CC__
GAM193  SHOC2    3'  GGGAAAAAAAAAAAGAAA    4312          CAAC
                                GGGAAGAGAA   AAAGAAA
                                ||||||||||   |||||||
                                CCCTTTTTTT   TTTCTTT
                                             _____
GAM193  SLC1A4   3'  TAGAAAGAGAACAGCAGGGGAA 4313           A  AA_
           A                     TGGGAAGAGAACA CA   GAAA
                                 ||||||||||||| ||   ||||
                                 ATCTTTCTCTTGT GT   CTTT
                                       C  CCC
GAM193  SLC5A1   3'  GGGAGGAGGACGGACAGGAAAA 4314      A  A  A_  AA
                                GGGA GAG AC  ACA  GAAAA
                                |||| ||| ||  |||  |||||
                                CCCT CTC TG  TGT  CTTTT
                                  C  C  CC   C_
GAM193  SMARCD1  3'  TGGGAAGAGATAGGGTGAAAGA 4315          ACAAC__
           A                     TGGGAAGAGA      AAAGAA
                                 ||||||||||      ||||||
                                 ACCCTTCTCT      TTTCTT
                                       ATCCCAC
GAM193  SMARCD1  3'  TGGGAAGAGATAGGGTGAAAGA 4315          ACAAC__
           A                     TGGGAAGAGA      AAAGAA
                                 ||||||||||      ||||||
                                 ACCCTTCTCT      TTTCTT
                                       ATCCCAC
GAM193  SNX6     5'  TGGGGGAGACACAAAG      4316      AA   A  A
                                TGGG  GAGA CA CAAAG
                                ||||  |||| || |||||
                                ACCC  CTCT GT GTTTC
                                  C_   _ _
GAM193  SORBS1   3'  TGGGAAAAGAATGAACCACAA  4317          ____  A
                                TGGGAAGAGA   AC ACAA
                                ||||||||||   || ||||
                                ACCCTTTTCT   TG TGTT
                                       TACT  G
GAM193  SORCS1   3'  GGAAACAGAACAACAAAG    4318       G
                                GGGAA AGAACAACAAAG
                                ||||| ||||||||||||
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                                CCTTT TCTTGTTGTTTC
                                   G
GAM193  SRGAP2   3'  GGAAAGAACACAGAGA      4319      A      A  A
                                GGA GAGAACA CA AGA
                                ||| ||||||| || |||
                                CCT TTCTTGT GT TCT
                                  _      _ C
GAM193  SURF4    3'  GGGAAGAGGATACATAAAA   4320         AACA   A
                                GGGAAGAG    ACA AGAA
                                ||||||||    ||| ||||
                                CCCTTCTC    TGT TTTT
                                     CTA_   A
GAM193  TBR1     3'  TGAGAGGAGAGAAAGAAA    4321       A    ACAAC
                                TGGGA GAGA     AAAGAAA
                                ||||| ||||     |||||||
                                ACTCT CTCT     TTTCTTT
                                   C    C____
GAM193  TCF1     3'  TGGGAAGAAATACAGGAAAG  4322          _   AC
                                TGGGAAGAGA ACA  AAAG
                                |||||||||| |||  ||||
                                ACCCTTCTTT TGT  TTTC
                                      A   CC
GAM193  TDGF1    3'  TGGGAGAGGGCAGGGCAAAG  4323       A   AA  A__
                                TGGGA GAG  CA   CAAAG
                                ||||| |||  ||   |||||
                                ACCCT CTC  GT   GTTTC
                                   _   CC  CCC
GAM193  TMP21    3'  TGGGAGAAGAAAAGAAA     4324       AG    CAACA
                                TGGGA  AGAA     AAGAAA
                                |||||  ||||     ||||||
                                ACCCT  TCTT     TTCTTT
                                   CT   ______
GAM193  TNFSF5   3'  GGGAAGAGACTGACAAAG    4325          ACA
                                GGGAAGAGA   ACAAAG
                                |||||||||   ||||||
                                CCCTTCTCT   TGTTTC
                                      GAC
GAM193  TPST2    3'  TGAGGAGGAATCAAAGAAA   4326      A  A   CAA
                                TGGG AG GAA   CAAAGAAA
                                |||| || |||   ||||||||
                                ACTC TC CTT   GTTTCTTT
                                   C  _   A__
GAM193  TUFT1    3'  TAGGAAGAGCCCTAAAGAAAA 4327          AACAAC
                                TGGGAAGAG     AAAGAAAA
                                |||||||||     ||||||||
                                ATCCTTCTC     TTTCTTTT
                                      GGGA__
GAM193  WNT2     3'  TGGGAAGACATTGAGAAA    4328         GAA  ACAA
                                TGGGAAGA   CA    AGAAA
                                ||||||||   ||    |||||
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                                ACCCTTCT  GT   TCTTT
                                   ___  AAC_
GAM193  XT3      3'  TGGGAAGAAGGTCAGCAGGGAA 4329         AA_  A  AA
            A                    TGGGAAGAG  CA CA  GAAA
                                 |||||||||  || ||  ||||
                                 ACCCTTCTT  GT GT  CTTT
                                      CCA  C  CC
GAM193  ATP6V1H  3'  TGGGAAAAGCTATATAACAGAG 4330         AAC___   A
                                 TGGGAAGAG     AACA AG
                                 |||||||||     |||| ||
                                 ACCCTTTTC     TTGT TC
                                      GATATA   C
GAM193  CCNB3    3'  TGGGAAAAGACAAAGAAA    4331         ACAA
                                 TGGGAAGAGA    CAAAGAAA
                                 ||||||||||    ||||||||
                                 ACCCTTTTCT    GTTTCTTT
                                      _____
GAM193  CCNB3    3'  TGGGAAAAGACAAAGAAA    4331         ACAA
                                 TGGGAAGAGA    CAAAGAAA
                                 ||||||||||    ||||||||
                                 ACCCTTTTCT    GTTTCTTT
                                      _____
GAM193  CCNI     5'  GGGAGGGGAGAAAAGAAAA   4332      A__    CAACA
                                 GGGA  GAGAA    AAGAAAA
                                 ||||  |||||    |||||||
                                 CCCT  CTCTT    TTCTTTT
                                   CCC   ______
GAM193  CGI-57   3'  TGGGAAGAGAATACCTGGGAGA 4333         __  AACAA
            A                    TGGGAAGAGA  AC    AGAA
                                 ||||||||||  ||    ||||
                                 ACCCTTCTCT  TG    TCTT
                                      TA  GACCC
GAM193  COTL1    3'  GGAAGAGAAATGCCAGGAAAA  4334         CAA_  AA
                                 GGAAGAGAA   CA  GAAAA
                                 |||||||||   ||  |||||
                                 CCTTCTCTT   GT  CTTTT
                                      TACG  C_
GAM193  CRNKL1   3'  TGGGCAGTGAACAAAGAAAA  4335      A  A     CAA
                                 TGGG AG GAACAA   AGAAAA
                                 |||| || ||||||   ||||||
                                 ACCC TC CTTGTT   TCTTTT
                                   G  A     ___
GAM193  DKFZP434I0714 3'  TGCGACAAAGCGACAAAGAAAA 4336     G  _   AACA
                                 TG GA AGAG    ACAAAGAAAA
                                 || || ||||    ||||||||||
                                 AC CT TTTC    TGTTTCTTTT
                                  G  G   GC__
GAM193  DKFZP434J037 3'  GGGAAGAGAACCATTGAAGA   4337          AACA_
                                 GGGAAGAGAAC    AAGA
                                 ||||||||||     ||||
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                                CCCTTCTCTTG    TTCT
                                      GTAAC
GAM193  DKFZP564G202 3'  AGAAGAACAACAAAGAA    4338       GA
                                GGAAGA  ACAACAAAGAA
                                ||||||  ||||||||||
                                TCTTCT  TGTTGTTTCTT
                                  __
GAM193  DKFZp564K142 3'  TGGGAAGAGAAGGTTAAGA   4339          CAACA
                                TGGGAAGAGAA    AAGA
                                ||||||||||    ||||
                                ACCCTTCTCTT    TTCT
                                      CCAA_
GAM193  DKFZP566D193 3'  TGGGGAGAGAACATGAAAG   4340      A       AC
                                TGGG AGAGAACA  AAAG
                                |||| ||||||||  ||||
                                ACCC TCTCTTGT  TTTC
                                  C       AC
GAM193  DKFZP586F1524 3'  GGAAGGGCAGCAAAGAAA   4341       AGAA  A
                                GGAAG   CA CAAAGAAA
                                |||||   || ||||||||
                                CCTTC   GT GTTTCTTT
                                   CC__  C
GAM193  DKFZp586H0623 3'  GGGAAGAGAGACAGGGAAA   4342         ACA   AA
                                GGGAAGAGA   ACA  GAAA
                                |||||||||   |||  ||||
                                CCCTTCTCT   TGT  CTTT
                                      C__   CC
GAM193  DKFZp761O132 5'  TGGAAAGAGACACCGAGAAAA  4343          A  A AA
                                TGGGAAGAGA CA C  AGAAAA
                                |||||||||| || |  ||||||
                                ACCTTTCTCT GT G  TCTTTT
                                      _  _ GC
GAM193  DNAJC5   3'  TGAGAAGAAACAAAGAAA    4344         GAAC
                                TGGGAAGA   AACAAAGAAA
                                ||||||||   ||||||||||
                                ACTCTTCT   TTGTTTCTTT
                                  _____
GAM193  DOCK3    3'  TGGAAAGAGGGGCAGTGGAGAA 4345         AA_  ACAA
                                TGGGAAGAG   CA   AGAA
                                |||||||||   ||   ||||
                                ACCTTTCTC   GT   TCTT
                                      CCC  CACC
GAM193  ERF      3'  GGGAAGAGACAAGAGA     4346         A   CAA
                                GGGAAGAGA CAA   AGA
                                ||||||||| |||   |||
                                CCCTTCTCT GTT   TCT
                                      _  C__
GAM193  FENS-1   3'  TGGGAAGAGAAACAACTGAA  4347          _   AAA
                                TGGGAAGAGAA CAAC   GAA
                                |||||||||| ||||   |||
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                                ACCCTTCTCTT GTTG   CTT
                                      T    A__
GAM193   FLJ10546  5'  TGGGAAGAAAGCTGCAGAAAA  4348          ACAACAA
                                TGGGAAGAGA      AGAAAA
                                ||||||||||      ||||||
                                ACCCTTCTTT      TCTTTT
                                     CGACG__
GAM193   FLJ11274  5'  TGGGAAAAGTCAATGGGGAAAA 4349          AA   CAAA
                                TGGGAAGAG  CAA    GAAAA
                                |||||||||  |||    |||||
                                ACCCTTTTC  GTT    CTTTT
                                     A_   ACCC
GAM193   FLJ13189  3'  TGGGAAGAGAGAAAGA      4350          ACAAC
                                TGGGAAGAGA     AAAGA
                                ||||||||||     |||||
                                ACCCTTCTCT     TTTCT
                                     C_____
GAM193   FLJ13614  3'  TGGGAAGAAACAGAAAG     4351           A  AC
                                TGGGAAGAGA CA  AAAG
                                |||||||||| ||  ||||
                                ACCCTTCTTT GT  TTTC
                                     _  C_
GAM193   FLJ14106  3'  TGGGAGAGAAGACAGGAGA    4352       A    CA   A_
                                TGGGA GAGAA  ACA  AGA
                                ||||| |||||  |||  |||
                                ACCCT CTCTT  TGT  TCT
                                   _    C_   CC
GAM193   FLJ14594  3'  GGGAAGAGAAGAGAAA      4353          CAACAA
                                GGGAAGAGAA     AGAAA
                                ||||||||||     |||||
                                CCCTTCTCTT     TCTTT
                                     C______
GAM193   FLJ14824  3'  GGAAGAGAATGGGACATCAAGG 4354          ______   A   A
           AAAA                    GGAAGAGA    ACA CAA GAAAA
                                |||||||||    ||| ||| |||||
                                CCTTCTCT     TGT GTT CTTTT
                                     TACCC   A   C
GAM193   FLJ22690  3'  TGGAAAGAGAAACAGAG     4355           CA   A
                                TGGGAAGAGAA  ACA AG
                                ||||||||||  ||| ||
                                ACCTTTCTCTT  TGT TC
                                      __   C
GAM193   FRAT1     3'  TGAGAAGAGAGACAGTTGCAAA 4356          _   A___
           GA                     TGGGAAGAGA ACA    CAAAGA
                                |||||||||| |||    ||||||
                                ACTCTTCTCT TGT    GTTTCT
                                     C   CAAC
GAM193   FRSB      3'  TGGGAAGAGAATCACACCACAG 4357          _  _  AA_
           A                       TGGGAAGAGAA CA AC   AGA
                                |||||||||| || ||   |||
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                                ACCCTTCTCTT GT TG   TCT
                                      A  G  GTG
GAM193  GABBR1   3'  TGGAAAGAGATTATGACAGTGG 4358      _____  ACAA    III
            AGAAAAT                AGAGA    ACA   AGAAAA  T
                                |||||    |||   ||||||  |
                                TCTCT    TGT   TCTTTT  A
                                   AATAC  CACC     III
GAM193  GABBR1   3'  TGGAAAGAGATTATGACAGTGG 4358      _____  ACAA    III
            AGAAAAT                AGAGA    ACA   AGAAAA  T
                                |||||    |||   ||||||  |
                                TCTCT    TGT   TCTTTT  A
                                   AATAC  CACC     III
GAM193  GHITM    3'  TGGAAAGAGAGCACTGAGAA  4359         A  ACAA
                                TGGGAAGAGA CA   AGAA
                                ||||||||||  ||   ||||
                                ACCTTTCTCT GT    TCTT
                                      C  GAC_
GAM193  GIT1     3'  GGGAAGAAGAAAGAAA     4360        AACAAC
                                GGGAAGAG     AAAGAAA
                                ||||||||     |||||||
                                CCCTTCTT     TTTCTTT
                                     C_____
GAM193  HMG17L1  3'  TGGAAAGAGAAAAGA      4361          CAACA
                                TGGGAAGAGAA    AAGA
                                ||||||||||    ||||
                                ACCTTTCTCTT    TTCT
                                      _____
GAM193  HTATIP2  3'  GGGAAGTATAAACAAAGAAAA  4362       AGAAC
                                GGGAAG    AACAAAGAAAA
                                ||||||    ||||||||||
                                CCCTTC    TTGTTTCTTTT
                                   ATAT_
GAM193  JIK      3'  GGGAAGAACACGAAGAA     4363        GA   ACA
                                GGGAAGA  ACA   AAGAA
                                |||||||  |||   |||||
                                CCCTTCT  TGT   TTCTT
                                   __  GC_
GAM193  JIK      3'  GGGAAGGGAGATAAAGAAAA  4364       A  ACAAC
                                GGGAAG GA    AAAGAAAA
                                |||||| ||    ||||||||
                                CCCTTC CT    TTTCTTTT
                                   C  CTA__
GAM193  KIAA0280 3'  TGGGAAGGGCAAAAGAAAA   4365       AGAA   CA
                                TGGGAAG   CAA  AAGAAAA
                                |||||||   |||  |||||||
                                ACCCTTC   GTT  TTCTTTT
                                    CC__   __
GAM193  KIAA0286 3'  TGGGAAGAGAAGAATACAAA  4366          CA__
                                TGGGAAGAGAA   ACAAA
                                ||||||||||   |||||
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                                ACCCTTCTCTT   TGTTT
                                      CTTA
GAM193  KIAA0628 3' TGGGAAAAGAACAAAACGGAA 4367            CAAA
                                TGGGAAGAGAACAA   GAA
                                |||||||||||||   |||
                                ACCCTTTTCTTGTT   CTT
                                      TTGC
GAM193  KIAA0776 3' TGGAAAGAGAACAAACCTGAAA 4368            _ AAA
                                TGGGAAGAGAACAA C   GAAA
                                |||||||||||||| |   ||||
                                ACCTTTCTCTTGTT G   CTTT
                                      T GA_
GAM193  KIAA0836 3' GGAAGAGAAACAAGAAA     4369         CA   A
                                GGAAGAGAA  ACAA GAAA
                                |||||||||  |||| ||||
                                CCTTCTCTT  TGTT CTTT
                                     __   _
GAM193  KIAA0853 5' TGGGGAGACGACAAAGA     4370      AA   ACA
                                TGGG  GAGA   ACAAAGA
                                ||||  ||||   |||||||
                                ACCC  CTCT   TGTTTCT
                                   __   GC_
GAM193  KIAA0871 3' TGGGGAGAAAACAATAAGAAAA 4371      A       CA
                                TGGG AGAGAACAA  AAGAAAA
                                |||| |||||||||  |||||||
                                ACCC TCTTTTGTT  TTCTTTT
                                   C       A_
GAM193  KIAA0937 3' TGGAAAGAGAGCAAAG      4372          ACAA
                                TGGGAAGAGA    CAAAG
                                ||||||||||    |||||
                                ACCTTTCTCT    GTTTC
                                      C___
GAM193  KIAA0984 3' TGAGAAGGGGCAAAGAAA    4373        AGAACAA
                                TGGGAAG      CAAAGAAA
                                |||||||      ||||||||
                                ACTCTTC      GTTTCTTT
                                     CCC____
GAM193  KIAA1030 3' TGGGAAGAGGAGAAAAAAA   4374         AACAAC
                                TGGGAAGAG     AAAGAAA
                                |||||||||     |||||||
                                ACCCTTCTC     TTTTTTT
                                      CTC___
GAM193  KIAA1037 3' TGGGAGCGGAGCAACAAAA   4375       AGA  A
                                TGGGA   GA CAACAAAG
                                |||||   || ||||||||
                                ACCCT   CT GTTGTTTT
                                   CGC  C
GAM193  KIAA1045 3' TGGGTAGCCACAAAGAAA    4376      A  AGAACA
                                TGGG AG     ACAAAGAAA
                                |||| ||     |||||||||
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                                ACCC TC     TGTTTCTTT
                                  A  GG____
GAM193  KIAA1155 3' TGAGAAGATTAAAACAAAG   4377        GAAC
                                TGGGAAGA    AACAAAG
                                ||||||||    |||||||
                                ACTCTTCT    TTGTTTC
                                     AATT
GAM193  KIAA1202 3' TGAGAAACTGCTAACAAAGAA 4378        AGAAC
                                TGGGAAG     AACAAAGAA
                                |||||||     |||||||||
                                ACTCTTT     TTGTTTCTT
                                    GACGA
GAM193  KIAA1486 3' TGGTAACAAACAGCAAAGAAA 4379     GAAGA    A
                                TGG     GAACA CAAAGAAA
                                |||     ||||| ||||||||
                                ACC     TTTGT GTTTCTTT
                                  ATTG_     C
GAM193  KIAA1766 3' TGGGAAGAGAAAGACAAGAGAA 4380          CA   _
                                TGGGAAGAGAA  ACAA AGAA
                                ||||||||||  |||| ||||
                                ACCCTTCTCTT  TGTT TCTT
                                      TC    C
GAM193  KIAA1808 3' TGGAAAAATAACAGCAAGGAAA 4381        G    A   A
           A                     TGGGAAGA AACA CAA GAAAA
                                ||||||||| |||| ||| |||||
                                ACCTTTTT TTGT GTT CTTTT
                                     A    C   C
GAM193  KIAA1831 5' TGGGTAGAGAAGGATACGGTGA 4382      A     CA__  A___
           AGAA                    TGGG AGAGAA    AC    AAGAA
                                |||| ||||||    ||    |||||
                                ACCC TCTCTT    TG    TTCTT
                                  A     CCTA  CCAC
GAM193  KIAA1949 5' GGAAAGAGGCAGCAAAG     4383        AA  A
                                GGGAAGAG  CA CAAAG
                                ||||||||  || |||||
                                CCTTTCTC  GT GTTTC
                                     C_  C
GAM193  KIAA1949 5' GGAAAGAGGCAGCAAAG     4383        AA  A
                                GGGAAGAG  CA CAAAG
                                ||||||||  || |||||
                                CCTTTCTC  GT GTTTC
                                     C_  C
GAM193  KIAA1949 5' GGAAAGAGGCAGCAAAG     4383        AA  A
                                GGGAAGAG  CA CAAAG
                                ||||||||  || |||||
                                CCTTTCTC  GT GTTTC
                                     C_  C
GAM193  KRTAP4-10 3' TGGGAAGAGATCCATGGGAAAA 4384          ACAA  AA_
                                TGGGAAGAGA    CA   GAAAA
                                ||||||||||    ||   |||||
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                                ACCCTTCTCT   GT   CTTTT
                                     AG__  ACC
GAM193  MGC11271 3' GGGAGAAAGAAAACAAAG    4385      _     C
                                GGGA AGAGAA AACAAAG
                                |||| |||||| |||||||
                                CCCT TTTCTT TTGTTTC
                                  C     _
GAM193  MGC20255 3' GGGAGAGAGACAGAAAG     4386      _    A  AC
                                GGGA AGAGA CA  AAAG
                                |||| ||||| ||  ||||
                                CCCT TCTCT GT  TTTC
                                  C    _ C_
GAM193  MGC21688 3' TGAGAAGAAAAGCAGAGAA   4387          CAA  A
                                TGGGAAGAGAA   CA AGAA
                                ||||||||||   || ||||
                                ACTCTTCTTTT   GT TCTT
                                      C__  C
GAM193  MGC2603  3' TGGGAAAAGGGTAACAGAG   4388         AAC   A
                                TGGGAAGAG   AACA AG
                                |||||||||   |||| ||
                                ACCCTTTTC   TTGT TC
                                     CCA   C
GAM193  MGC32043 3' GGAAGAGAGTGCATCAGAGA  4389         A__  A  A
                                GGAAGAGA   CA CA AGA
                                ||||||||   || || |||
                                CCTTCTCT   GT GT TCT
                                     CAC  A  C
GAM193  MGC5566  3' TGGGAAGAGGAAACATGGGAA 4390         AAC   AA_
                                TGGGAAGAG   AACA   GAA
                                |||||||||   ||||   |||
                                ACCCTTCTC   TTGT   CTT
                                     CT_   ACC
GAM193  MYOM1    3' GGGAAGAGGACAGACGTGAAAA 4391        A  _  AAA
                                GGGAAGAG ACA AC   GAAAA
                                |||||||| ||| ||   |||||
                                CCCTTCTC TGT TG   CTTTT
                                     C   C  CA_
GAM193  NAPG     3' TGGGAAGATGGTAACTAAAA  4392         GAAC   A
                                TGGGAAGA    AAC AAGA
                                ||||||||    ||| ||||
                                ACCCTTCT    TTG TTTT
                                     ACCA   A
GAM193  NCK1     3' GGGAAAACAGCAAAGAAAA   4393       AGA    A
                                GGGA   GAACA CAAAGAAAA
                                ||||   ||||| |||||||||
                                CCCT   TTTGT GTTTCTTTT
                                  ___    C
GAM193  NCOA2    3' GGGAAGAGTCAGGCTGACAGGG 4394        AA _____   AA
           AA                     GGGAAGAG  CA    ACA  GAA
                                ||||||||  ||    |||  |||
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                                CCCTTCTC  GT    TGT  CTT
                                    A_  CCGAC   CC
GAM193  NFAT5    3'  GGGAAGGAGAAACAAAGAA   4395       _   CA
                                GGGAAG AGAA  ACAAAGAA
                                |||||| ||||  ||||||||
                                CCCTTC TCTT  TGTTTCTT
                                   C   __
GAM193  OAZIN    5'  TGAGAAGAGGCAGAGAA     4396         AACAA  A
                                TGGGAAGAG    CA AGAA
                                |||||||||    || ||||
                                ACTCTTCTC    GT TCTT
                                     C____  C
GAM193  OR7C1    3'  TAGGAAAACAACAAAGA     4397       AGA
                                TGGGA   GAACAACAAAGA
                                |||||   ||||||||||||
                                ATCCT   TTTGTTGTTTCT
                                  ___
GAM193  PCDH10   3'  TGGGACAGACGCAAAGAAAA  4398      AG   ACAA
                                TGGGA  AGA   CAAAGAAAA
                                |||||  |||   |||||||||
                                ACCCT  TCT   GTTTCTTTT
                                   G_  GC__
GAM193  PEPP2    3'  TGGGAAGAAAAAAAAGAAA    4399          CAAC
                                TGGGAAGAGAA   AAAGAAA
                                ||||||||||   |||||||
                                ACCCTTCTTTT   TTTCTTT
                                     ____
GAM193  PRKRIR   3'  TGGAAAAAGACAGAGAAA    4400          ACAA  A
                                TGGGAAGAGA   CA AGAAA
                                ||||||||||   || |||||
                                ACCTTTTTCT   GT TCTTT
                                     ____  C
GAM193  PRO0245  5'  GAACTAGAATAACAAAGAAAA 4401     AG   C
                                GGA  AGAA AACAAAGAAAA
                                |||  |||| ||||||||||
                                CTT  TCTT TTGTTTCTTTT
                                  GA   A
GAM193  RAB6C    3'  TGAGAAGAGCAAGGAGA     4402         AA   CAA
                                TGGGAAGAG  CAA   AGA
                                |||||||||  |||   |||
                                ACTCTTCTC  GTT   TCT
                                     __   CC_
GAM193  RP4-622L5 3'  TGGGAAGAGGCAGCAAGGA   4403         AA  A   A
                                TGGGAAGAG  CA CAA GA
                                |||||||||  || ||| ||
                                ACCCTTCTC  GT GTT CT
                                     C_  C   C
GAM193  SCAMP5   3'  GGGAAGACAAAGAAA       4404        GAACAA
                                GGGAAGA     CAAAGAAA
                                |||||||     ||||||||
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                                CCCTTCT     GTTTCTTT
                                        ______
GAM193  SENP3    3'  TGGGAAGAGGCAAGAGA     4405          AA   CAA
                                TGGGAAGAG  CAA   AGA
                                |||||||||  |||   |||
                                ACCCTTCTC  GTT   TCT
                                     C_   C__
GAM193  SUPT4H1  5'  TGGGAAGAACAACAGGGA    4406         GA     AA
                                TGGGAAGA  ACAACA  GA
                                ||||||||  ||||||  ||
                                ACCCTTCT  TGTTGT  CT
                                     __     CC
GAM193  SV2      3'  GGGGAGGGCACCAAAGAAA   4407      AA   AA  A
                                GGG  GAG  CA CAAAGAAA
                                |||  |||  || ||||||||
                                CCC  CTC  GT GTTTCTTT
                                  __   CC  G
GAM193  TEB4     3'  TGGGAAAAATCTCCAAAGA   4408          AACAA
                                TGGGAAGAG    CAAAGA
                                |||||||||    ||||||
                                ACCCTTTTT    GTTTCT
                                     AGAG_
GAM193  TIEG     3'  TGGAAAGACTAGGAATAATAAA 4409          ____   C  C
           GAA                    TGGGAAGA    GAA AA AAAGAA
                                |||||||||   ||| || ||||||
                                ACCTTTCT    CTT TT TTTCTT
                                     GATC   A  A
GAM193  TNK1     3'  TGGGAAAAAACAAAG       4410          GAAC
                                TGGGAAGA    AACAAAG
                                ||||||||    |||||||
                                ACCCTTTT    TTGTTTC
                                        _____
GAM193  TU12B1-TY 3'  TGAGAAGAGGACAGAAGAAAA  4411          A   ACA
                                TGGGAAGAG ACA   AAGAAAA
                                ||||||||| |||   |||||||
                                ACTCTTCTC TGT   TTCTTTT
                                     C   C__
GAM193  ZD52F10  3'  TGGGAAGAAACAAGGAGA    4412          A   CAA
                                TGGGAAGAGA CAA   AGA
                                |||||||||| |||   |||
                                ACCCTTCTTT GTT   TCT
                                     _   CC_
GAM193  ZDHHC5   5'  TGGGAGGAGGGAAGCAACAGAG 4413       __ A   _    A
           A                    TGGGA  AG GAA CAACA AGA
                                |||||  || ||| ||||| |||
                                ACCCT  TC CTT GTTGT TCT
                                   CC  C   C    C
GAM193  ZNF220   3'  TAGGAAGAGAATGGGCAAA   4414          CAA_
                                TGGGAAGAGAA    CAAA
                                ||||||||||    ||||
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                                ATCCTTCTCTT   GTTT
                                      ACCC
GAM193  ZNF291   3'  TGGGAAGAGTATAAACATGGGA 4415        AAC_   AA_
          AAA                   TGGGAAGAG   AACA  GAAAA
                                |||||||||   ||||  |||||
                                ACCCTTCTC   TTGT  CTTTT
                                     ATAT   ACC
GAM193  LOC113523 3'  TGGAAAGAGACAGGAAAG    4416         A  AC
                                TGGGAAGAGA CA  AAAG
                                |||||||||| ||  ||||
                                ACCTTTCTCT GT  TTTC
                                      _  CC
GAM193  LOC123342 3'  TGGGAAGCATCATCAAAGAAAA 4417        AGAA  A
                                TGGGAAG   CA CAAAGAAAA
                                |||||||   || |||||||||
                                ACCCTTC   GT GTTTCTTTT
                                    GTA_  A
GAM193  LOC128954 5'  TAGGAAGAGGACAGTGAAAG  4418         A  AC_
                                TGGGAAGAG ACA  AAAG
                                ||||||||| |||  ||||
                                ATCCTTCTC TGT  TTTC
                                      C  CAC
GAM193  LOC138241 5'  AGGAGGAGCAAAGAAA     4419      A  AACAA
                                GGGA GAG    CAAAGAAA
                                |||| |||    ||||||||
                                TCCT CTC    GTTTCTTT
                                  C  _____
GAM193  LOC143914 5'  TGGGAGAGAACAGACCAAAA  4420      A     A__
                                TGGGA GAGAACA  CAAAG
                                ||||| |||||||  |||||
                                ACCCT CTCTTGT  GTTTT
                                   _     CTG
GAM193  LOC145371 3'  GGGAAGAGAGAAAAAGCAGAGA 4421         ACAA___  A
          A                     GGGAAGAGA     CA AGAA
                                |||||||||     || ||||
                                CCCTTCTCT     GT TCTT
                                      CTTTTTC  C
GAM193  LOC145609 5'  TGAGAAGACGTGAACAGAGAGA 4422         ___    ACAA
                                TGGGAAGA  GAACA   AGA
                                ||||||||  |||||   |||
                                ACTCTTCT  CTTGT   TCT
                                    GCA   CTC_
GAM193  LOC146287 5'  TGGAAAGCACAAAGA      4423        AGAA  A
                                TGGGAAG   CA CAAAGA
                                |||||||   || ||||||
                                ACCTTTC   GT GTTTCT
                                     ____  _
GAM193  LOC146506 3'  GGGAGAGAGCACAGGCAGGAAA 4424      _   A  ACAAA
                                GGGA AGAG ACA    GAAA
                                |||| |||| |||    ||||
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                                CCCT TCTC TGT     CTTT
                                  C    G   CCGTC
GAM193   LOC146723 3'  GGGAAGGGACCATCTAAAGAAA 4425        A  A  AC_
                                GGGAAG GA CA   AAAGAAA
                                ||||||  ||  ||   |||||||
                                CCCTTC CT GT   TTTCTTT
                                   C  G  AGA
GAM193   LOC147742 5'  TGGAAAGAGAGCAAAG      4372           ACAA
                                TGGGAAGAGA    CAAAG
                                ||||||||||    |||||
                                ACCTTTCTCT    GTTTC
                                      C___
GAM193   LOC149301 5'  GGGAAGAGGACTCCAGAGAAA  4426         A  AA  A
                                GGGAAGAG AC  CA AGAAA
                                ||||||||  ||  ||  |||||
                                CCCTTCTC TG  GT TCTTT
                                     C  AG  C
GAM193   LOC149422 3'  TGGGAAGAGGGCCAGACCTGGA 4427          AA_  _  AAA
            A                    TGGGAAGAG   CA AC   GAA
                                |||||||||   ||  ||   |||
                                ACCCTTCTC   GT TG   CTT
                                     CCG  C  GAC
GAM193   LOC150368 3'  TGGGAAGAGTAGCAAGGAGA   4428         AA_   CAA
                                TGGGAAGAG   CAA   AGA
                                |||||||||   |||   |||
                                ACCCTTCTC   GTT   TCT
                                     ATC   CC_
GAM193   LOC151568 5'  TGGGAGATTTCCAAAGAAA    4429       A  GAACAA
                                TGGGA GA     CAAAGAAA
                                |||||  ||     ||||||||
                                ACCCT CT     GTTTCTTT
                                   _  AAAG__
GAM193   LOC152905 3'  TGGGAAAAGATCAAGAAA     4430          A  ACAA
                                TGGGAAGAGA CA    AGAAA
                                ||||||||||  ||    |||||
                                ACCCTTTTCT GT    TCTTT
                                     A  _____
GAM193   LOC153480 5'  TGAGAAGAGGCGAAAAAGAAA  4431          AACAAC
                                TGGGAAGAG     AAAGAAA
                                |||||||||     |||||||
                                ACTCTTCTC     TTTCTTT
                                     CGCTT_
GAM193   LOC155072 3'  GGGAAGAGACAGAGAA      4432          ACAA  A
                                GGGAAGAGA    CA AGAA
                                |||||||||    ||  ||||
                                CCCTTCTCT    GT TCTT
                                     _____  C
GAM193   LOC158434 5'  TGGGAGAGACAAAGAA      4433        A    ACAA
                                TGGGA GAGA    CAAAGAA
                                |||||  ||||    |||||||
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                                ACCCT CTCT    GTTTCTT
                                  _   ____
GAM193   LOC158819 5'  AGGATGAAGAACAGCAAAGAAA 4434      A_      A
             A                    GGGA  GAGAACA CAAAGAAAA
                                  ||||  ||||||| |||||||||
                                  TCCT  TTCTTGT GTTTCTTTT
                                    AC      C
GAM193   LOC201245 3'  TGGGAAAAAACAAAG       4410         GAAC
                                  TGGGAAGA    AACAAAG
                                  ||||||||    |||||||
                                  ACCCTTTT    TTGTTTC
                                      ____
GAM193   LOC202868 3'  GGGAAGAGACAGAGAA      4432          ACAA  A
                                  GGGAAGAGA    CA AGAA
                                  |||||||||    || ||||
                                  CCCTTCTCT    GT TCTT
                                       ____  C
GAM193   LOC203378 5'  TGGGAAAAGACACGAGGAA    4435          A  ACAAA
                                  TGGGAAGAGA CA     GAA
                                  |||||||||| ||     |||
                                  ACCCTTTTCT GT     CTT
                                        _  GCTC_
GAM193   LOC219848 3'  GGGAAGAGAGCAAACCTCAG   4436          A   _ AA_
                                  GGGAAGAGA CAA C   AG
                                  ||||||||| ||| |   ||
                                  CCCTTCTCT GTT G   TC
                                        C   T GAG
GAM193   LOC221454 5'  GGAAAAGGCAAAGAAA      4437         AACAA
                                  GGAAGAG     CAAAGAAA
                                  |||||||     ||||||||
                                  CCTTTTC     GTTTCTTT
                                      C____
GAM193   LOC221692 3'  GGGAAGAGAATAAAAGA     4438          CAAC
                                  GGGAAGAGAA    AAAGA
                                  ||||||||||    |||||
                                  CCCTTCTCTT    TTTCT
                                        AT__
GAM193   LOC221738 3'  GGAGAGTCGCAAAGAAAA    4439      A   AACAA
                                  GGA GAG     CAAAGAAAA
                                  ||| |||     |||||||||
                                  CCT CTC     GTTTCTTTT
                                    _   AGC__
GAM193   LOC222493 5'  GGGAAGAGGGGACAAGGAAA   4440         AACA    A
                                  GGGAAGAG    ACAA GAAA
                                  ||||||||    |||| ||||
                                  CCCTTCTC    TGTT CTTT
                                       CCC_    C
GAM193   LOC253011 3'  TGGGAAGCAGAGCAAGTAAAG  4441         _   A   C_
                                  TGGGAAG AGA CAA  AAAG
                                  ||||||| ||| |||  ||||
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                                ACCCTTC TCT GTT  TTTC
                                    G   C   CA
GAM193  LOC253150 3'  TGGCAAGAGAGAAAGAAA    4442      G     ACAAC
                                TGG AAGAGA    AAAGAAA
                                ||| ||||||    |||||||
                                ACC TTCTCT    TTTCTTT
                                  G     C____
GAM193  LOC255328 3'  GGAAGAGAACACATTCAAGA   4443          ACA__
                                GGAAGAGAACA    AAGA
                                ||||||||||    ||||
                                CCTTCTCTTGT    TTCT
                                      GTAAG
GAM193  LOC90495  3'  AGGATTTGGAATAACAAAGA   4444      AGA_  C
                                GGGA   GAA AACAAAGA
                                ||||   ||| ||||||||
                                TCCT   CTT TTGTTTCT
                                  AAAC   A
GAM193  LOC90509  5'  TGGAAAGAAATTAAAGAAA    4445         ACAAC
                                TGGGAAGAGA    AAAGAAA
                                ||||||||||    |||||||
                                ACCTTTCTTT    TTTCTTT
                                      AA___
GAM193  LOC90981  3'  TGGGAGAAGAAAAGAAA     4324       AG   CAACA
                                TGGGA  AGAA    AAGAAA
                                |||||  ||||    ||||||
                                ACCCT  TCTT    TTCTTT
                                   CT   ______
GAM193  LOC92399  3'  GGGAAGAGAGAGCCAGGCAGAG 4446         A___  A_  A
          AAAA                    GGGAAGAGA   CA  CA AGAAAA
                                |||||||||   ||  || ||||||
                                CCCTTCTCT   GT  GT TCTTTT
                                      CTCG  CC  C
GAM193  LOC92935  3'  GGAAGGAGGCACAAAGAA    4447       A  ACA
                                GGAAG GA   ACAAAGAA
                                ||||| ||   ||||||||
                                CCTTC CT   TGTTTCTT
                                   _  CCG
GAM194  AHR       3'  TTAGTTCTCTAACTT       4450       TCTT
                                TTAGT    TCTCTAACTT
                                |||||    ||||||||||
                                AATCA    AGAGATTGAA
                                     _____
GAM194  HFE       5'  TTAGTTCTCTCTCTCCTAC    4451            AA
                                TTAGTTCTTTCTCT  CTTAT
                                ||||||||||||||  |||||
                                AATCAAGAGAGAGA  GGATG
                                          __
GAM194  PROCR     3'  TTACTTCTTTCTACCCTATTAT 4452      G      _  AAC
          A                      TTA TTCTTTCT CT   TTATA
                                ||| |||||||| ||   |||||
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                                AAT AAGAAAGA GG   AATAT
                                  G       T  GAT
GAM194  ZAK      3'  TTAGTTCTTTTGCCTCATA   4453          CTCTAA
                                TTAGTTCTTT     CTTATA
                                ||||||||||     ||||||
                                AATCAAGAAA     GAGTAT
                                     ACG___
GAM195  CKTSF1B1  5'  TTCGACGCGTGGCGCTGAGTGC 4456      _     TA  GG
           GG                     TTCG CGCGTG  TG  GAGTGCGG
                                ||||  ||||||  ||  ||||||||
                                AAGC GCGCAC  GC  CTCACGCC
                                  T     C_  GA
GAM195  LOC126299 5'  TTCGCGCGTGCGTGTGCG    4457          ATGGGGA
                                TTCGCGCGTGT      GTGCG
                                ||||||||||       |||||
                                AAGCGCGCACG      CACGC
                                     CA_____
GAM196  BSG      3'  GTGGCGGTGGGTGGGAGGGGG  4460          C  CGC
                                GTGGCGGTGGG GG   GGGGG
                                ||||||||||| ||   |||||
                                CACCGCCACCC CC   CCCCC
                                     A  CT_
GAM196  BSG      3'  GTGGCGGTGGGTGGGAGGGGG  4460          C  CGC
                                GTGGCGGTGGG GG   GGGGG
                                ||||||||||| ||   |||||
                                CACCGCCACCC CC   CCCCC
                                     A  CT_
GAM196  CACNB4   5'  GTGCGGTGGGCGGAGGGGG   4461      G        CGC
                                GTG CGGTGGGCGG   GGGGG
                                ||| ||||||||||   |||||
                                CAC GCCACCCGCC   CCCCC
                                  _        T__
GAM196  FHL2     5'  CGGGCGTGGGGCGCGGGG    4462     T   G   CG
                                CG GGCG TGGG  GCGCGGGG
                                || |||| ||||  ||||||||
                                GC CCGC ACCC  CGCGCCCC
                                  _   _   __
GAM196  G6PD     3'  CGTGGCGGGGGTGGAGG     4463         T   C  CGC
                                CGTGGCGG GGG GG   GGG
                                |||||||| ||| ||   |||
                                GCACCGCC CCC CC   TCC
                                     _   A  ___
GAM196  GNB2     5'  GTGGCGGTGGGACTCTGCGGCG 4464          CG___  _
           GGGG                    GTGGCGGTGGG    GCG CGGGGG
                                ||||||||||     ||| ||||||
                                CACCGCCACCC    CGC GCCCCC
                                     TGAGA   C
GAM196  HPD      3'  CGTGGGGTGGGCGGG       4465       C      GGCGC
                                CGTGG GGTGGGC    GGG
                                ||||| |||||||    |||
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                                GCACC CCACCCG    CCC
                                  _    _____
GAM196  IL6R    5' CGGGGCGGTGGGCGGGCAGG  4466    T        C
                                CG GGCGGTGGGCGG GCGGG
                                || |||||||||||| |||||
                                GC CCGCCACCCGCC CGTCC
                                 C         _
GAM196  JUND    3' GGGGCGGCCGCGCGGGG    4467    C   G G
                                GG GGTGG C GCGCGGGG
                                || ||||| | ||||||||
                                CC CCGCC G CGCGCCCC
                                 _   _ G
GAM196  KLF4    5' CGGGGCGGTGGGCGGGCGG  4468    T        C
                                CG GGCGGTGGGCGG GCGG
                                || |||||||||||| ||||
                                GC CCGCCACCCGCC CGCC
                                 C         _
GAM196  MSX2    3' GGCGGTGGGGGGCGGGGG   4469        C  C
                                GGCGGTGGG GG GCGGGGG
                                ||||||||| || |||||||
                                CCGCCACCC CC CGCCCCC
                                    _ _
GAM196  PAX2    5' CGGGGCGGTGGGCCGGGG   4470    T       GGCG
                                CG GGCGGTGGGC   CGGGG
                                || ||||||||||   |||||
                                GC CCGCCACCCG   GCCCC
                                 C        ____
GAM196  PAX2    5' CGGGGCGGTGGGCCGGGG   4470    T       GGCG
                                CG GGCGGTGGGC   CGGGG
                                || ||||||||||   |||||
                                GC CCGCCACCCG   GCCCC
                                 C        ____
GAM196  RBP1    5' CGGGTGGTGGGCGGCCCGG  4471    T C       G
                                CG GG GGTGGGCGGC CGG
                                || || |||||||||| |||
                                GC CC CCACCCGCCG GCC
                                 _ A       G
GAM196  SIX1    5' TGGCGGTGGGCGGCCAAGG  4472           G
                                TGGCGGTGGGCGGC CGGGG
                                |||||||||||||| |||||
                                ACCGCCACCCGCCG GTTCC
                                      _
GAM196  SMT3H1  5' CGCGGGGAGGCGGCGCGGGGG 4473      C T
                                CGTGG GG GGGCGGCGCGGGGG
                                ||||| || ||||||||||||||
                                GCGCC CC TCCGCCGCGCCCCC
                                   _ _
GAM196  SPG3A   5' TGGCGGTGGGCGGCTCCG   4474          G_
                                TGGCGGTGGGCGGC  CG
                                ||||||||||||||  ||
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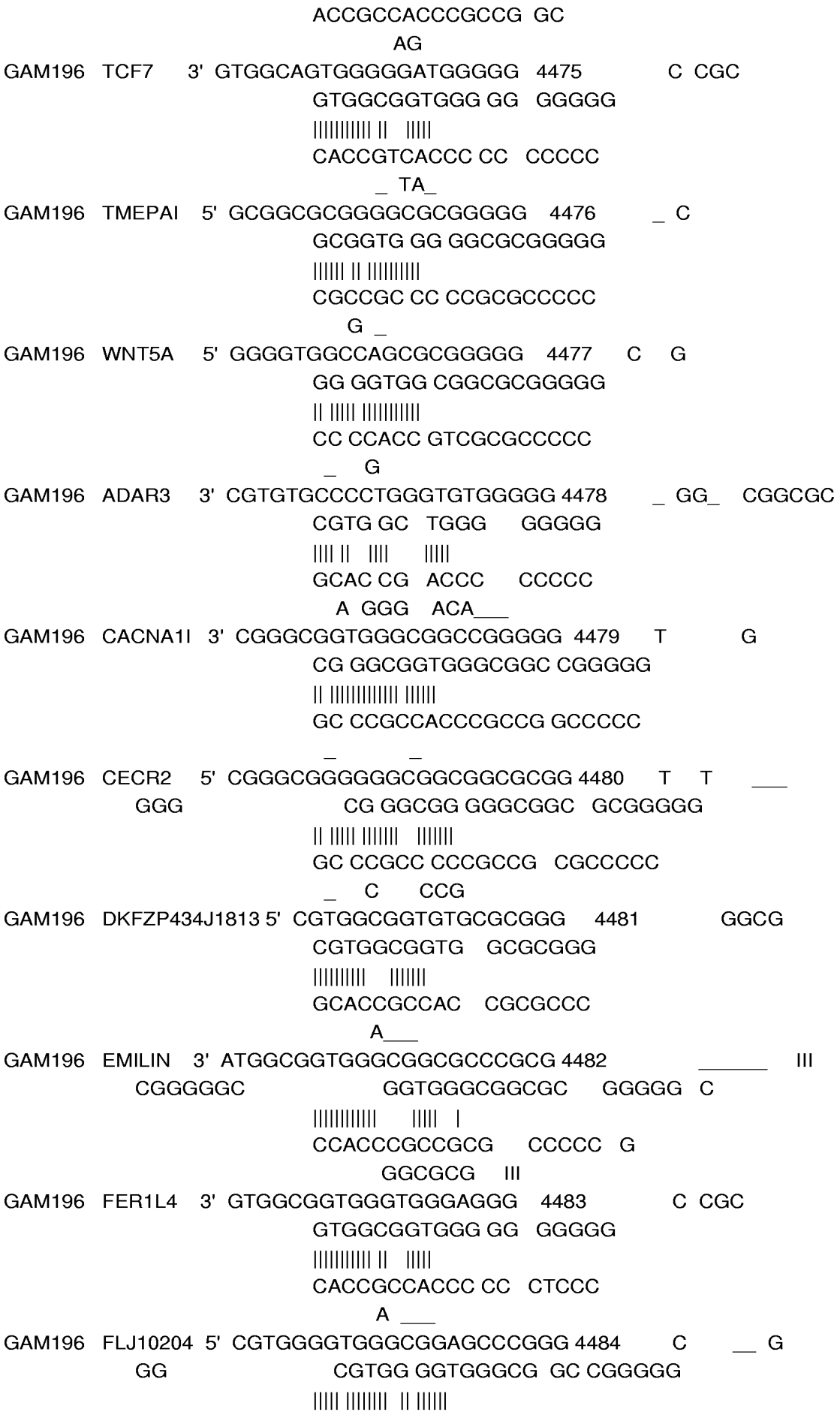
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GAM196 TCF7 3' GTGGCAGTGGGGGATGGGGG 4475 C CGC
GTGGCGGTGGG GG GGGGG
CACCGTCACCC CC CCCCC
_ TA_
GAM196 TMEPAI 5' GCGGCGCGGGGCGCGGGGG 4476 _ C
GCGGTG GG GGCGCGGGGG
CGCCGC CC CCGCGCCCCC
G _
GAM196 WNT5A 5' GGGGTGGCCAGCGCGGGGG 4477 C G
GG GGTGG CGGCGCGGGGG
CC CCACC GTCGCGCCCCC
_ G
GAM196 ADAR3 3' CGTGTGCCCCTGGGTGTGGGGG 4478 _ GG_ CGGCGC
CGTG GC TGGG GGGGG
GCAC CG ACCC CCCCC
A GGG ACA___
GAM196 CACNA1I 3' CGGGCGGTGGGCGGCCGGGGG 4479 T G
CG GGCGGTGGGCGGC CGGGGG
GC CCGCCACCCGCCG GCCCCC
_ _
GAM196 CECR2 5' CGGGCGGGGGGCGGCGGCGCGG 4480 T T ___
GGG CG GGCGG GGGCGGC GCGGGGG
GC CCGCC CCCGCCG CGCCCCC
_ C CCG
GAM196 DKFZP434J1813 5' CGTGGCGGTGTGCGCGGG 4481 GGCG
CGTGGCGGTG GCGCGGG
GCACCGCCAC CGCGCCC
A___
GAM196 EMILIN 3' ATGGCGGTGGGCGGCGCCCGCG 4482 _____ III
CGGGGGC GGTGGGCGGCGC GGGGG C
CCACCCGCCGCG CCCCC G
GGCGCG III
GAM196 FER1L4 3' GTGGCGGTGGGTGGGAGGG 4483 C CGC
GTGGCGGTGGG GG GGGGG
CACCGCCACCC CC CTCCC
A ___
GAM196 FLJ10204 5' CGTGGGGTGGGCGGAGCCCGGG 4484 C __ G
GG CGTGG GGTGGGCG GC CGGGGG

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                                GCACC CCACCCGC  CG GCCCCC
                                  _      CT  G
GAM196  FLJ14827  5'  CGTCGGTGAGGGCGCGGGGG  4485     GG     C
                                CGT  CGGTGGG GGCGCGGGGG
                                |||  ||||||| ||||||||||
                                GCA  GCCACTC CCGCGCCCCC
                                 __     _
GAM196  FLJ21865  3'  CATGGCGGTGGGCTGGGG    4486           GGCGC
                                CGTGGCGGTGGGC    GGGG
                                ||||||||||||    ||||
                                GTACCGCCACCCG    CCCC
                                       A____
GAM196  FLJ22215  3'  GTGGCGGTGGGCGGGTGGGG  4487            CGC
                                GTGGCGGTGGGCGG  GGGG
                                ||||||||||||  ||||
                                CACCGCCACCCGCC  CCCC
                                       CA_
GAM196  FLJ22215  5'  GTGGCGGTGGGCGGGTGGGG  4487            CGC
                                GTGGCGGTGGGCGG  GGGG
                                ||||||||||||  ||||
                                CACCGCCACCCGCC  CCCC
                                       CA_
GAM196  FLJ22693  5'  GTGGCGGCTCGCGGGG     4488         GGGCGG
                                GTGGCGGT    CGCGGGG
                                ||||||||    |||||||
                                CACCGCCG    GCGCCCC
                                   A_____
GAM196  HSRNAFEV  5'  GGCGGTGGGAGATGGGGG    4489         C  CGC
                                GGCGGTGGG GG  GGGGG
                                |||||||||  ||  |||||
                                CCGCCACCC CT  CCCCC
                                     T  A__
GAM196  HSRNAFEV  5'  CGTGGCGGGGGTTGCGGGGG  4490         T  CG  C
                                CGTGGCGG GGG  GCG GGGG
                                |||||||| |||  ||| ||||
                                GCACCGCC CCC  CGC CCCC
                                   _  AA  _
GAM196  KIAA0339  3'  CGGGGCGGTGGCGGCGGGGG  4491    T     G    C
                                CG GGCGGTGG CGGCG GGGG
                                || |||||||| ||||| ||||
                                GC CCGCCACC GCCGC CCCC
                                 C      _    _
GAM196  KIAA1908  5'  CGTGGCGGGGGGCGTGCAGGG  4492        T    GC
                                CGTGGCGG GGGCG  GCGGGG
                                |||||||| |||||  ||||||
                                GCACCGCC CCCGC  CGTCCC
                                   _    A_
GAM196  KIAA1981  5'  GGGGCGCGGGGCGCGGGGG  4493    C   _ C
                                GG GGTG GG GGCGCGGGGG
                                || |||| || ||||||||||
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                                CC CCGC CC CCGCGCCCCC
                                 _   G  _
GAM196  MGC15737  5'  GGCGGGCGGGCGCGGGGG   4494          _
                                GGTGGGCGG CGCGGGGG
                                ||||||||| ||||||||
                                CCGCCCGCC GCGCCCCC
                                    C
GAM196  NRN1      3'  GTGGGTGGGCGCGCGGGGG   4495      CG      G
                                GTGG  GTGGGCG CGCGGGGG
                                ||||  ||||||| ||||||||
                                CACC  CACCCGC GCGCCCCC
                                  __     _
GAM196  PALM      5'  GGGGCTGCGCGGCGCGGGGG  4496     C  _  G
                                GG GG TG GCGGCGCGGGGG
                                || || || ||||||||||||
                                CC CC AC CGCCGCGCCCCC
                                 _ G  G
GAM196  PLAGL2    3'  GGCGGTGGGCTGGAGGGCGGGG 4497          _  C__
              G                  GGCGGTGGGC GG   GCGGGGG
                                 |||||||||| ||   |||||||
                                 CCGCCACCCG CC   CGCCCCC
                                      A  TCC
GAM196  RAB11B    3'  CGTGGCGGGGGGCGGGCGG    4498         T     C
                                CGTGGCGG GGGCGG GCGG
                                |||||||| |||||| ||||
                                GCACCGCC CCCGCC CGCC
                                  _     _
GAM196  SE70-2    5'  CCTGGCGGTGGTACTGGGGG   4499    G       GCG  GC
                                C TGGCGGTGG   GC  GGGGG
                                | |||||||||   ||  |||||
                                G ACCGCCACC   TG  CCCCC
                                 G        A__  A_
GAM196  SEMA4G    5'  GTGGCGGTGGGGGCGGTGGGGG 4500           C    C_
                                GTGGCGGTGGG GGCG  GGGGG
                                |||||||||| ||||  |||||
                                CACCGCCACCC CCGC  CCCCC
                                      _   CA
GAM196  SLC37A1   5'  CGGGCGGTGGGGCGGGG     4501     T       CGGC
                                CG GGCGGTGGG    GCGGGG
                                || |||||||||    ||||||
                                GC CCGCCACCC    CGCCCC
                                  _       _____
GAM196  STAT5A    5'  CGGGCGGCGCCGGGCGTGGGGG 4502     T      GGC    C
                                CG GGCGGTG   GGCG GGGGG
                                || |||||||   |||| |||||
                                GC CCGCCGC   CCGC CCCCC
                                 _      GGC    A
GAM196  ZNF213    5'  TGGCAGAGCGGCGCGGGGG    4503        TG
                                TGGCGG  GGCGGCGCGGGGG
                                ||||||  ||||||||||||
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                                ACCGTC  TCGCCGCGCCCCC
                                  __
GAM196  LOC126823 5'  CGTGGTGACTGCGCGGGGG   4504      CGGTG  G
                                CGTGG    GGC GCGCGGGGG
                                |||||    ||| |||||||||
                                GCACC    CTG CGCGCCCCC
                                  A____  A
GAM196  LOC132241 5'  CGTGGTGGTGGGCGCCGG    4505      C      G G
                                CGTGG GGTGGGCG C CGG
                                ||||| |||||||| | |||
                                GCACC CCACCCGC G GCC
                                  A      _ _
GAM196  LOC138128 5'  CGGGGCGGTGGGACGGGG    4506    T      CGGC
                                CG GGCGGTGGG   GCGGGG
                                || |||||||||   ||||||
                                GC CCGCCACCC   TGCCCC
                                 C       _____
GAM196  LOC144114 5'  GTGGGGAGGGTGCGGGG     4507     C  T  CGGC
                                GTGG GG GGG    GCGGGG
                                |||| || |||    ||||||
                                CACC CC CCC    CGCCCC
                                  _ T  A___
GAM196  LOC145801 5'  GGTGGCGGGCGGCGTGGGGG  4508    C       C
                                GG GGTGGGCGGCG GGGGG
                                || ||||||||||| |||||
                                CC CCGCCCGCCGC CCCCC
                                 A         A
GAM196  LOC149297 5'  CGTGGGGCAGCGCGGGG     4509      CGGTG
                                CGTGG    GGCGGCGCGGGG
                                |||||    ||||||||||||
                                GCACC    CCGTCGCGCCCC
                                  ______
GAM196  LOC158373 5'  GGCGGGGGCGGCGTGGGGG   4510      T      C
                                GGCGG GGGCGGCG GGGGG
                                ||||| ||||||| |||||
                                CCGCC CCCGCCGC CCCCC
                                  _      A
GAM196  LOC158969 3'  GTGGCGGTGGGGATGGGGG   4511          C  CGC
                                GTGGCGGTGGG GG   GGGGG
                                |||||||||| ||   |||||
                                CACCGCCACCC CT   CCCCC
                                     _  A__
GAM196  LOC165104 5'  CGTGGCGATGGGCGGAAAAACG 4512            C___
          G                      CGTGGCGGTGGGCGG   GCGG
                                 ||||||||||||||    ||||
                                 GCACCGCTACCCGCC   TGCC
                                       TTTT
GAM196  LOC197342 5'  CGGGCGGTGGTCTCGGGG    4513    T      GCGGCG
                                CG GGCGGTGG     CGGGG
                                || ||||||||     |||||
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                                GC CCGCCACC     GCCCC
                                 _       AGA___
GAM196  LOC200860 3'  GTGGCGGTAGGGTGGAG     4514          CGGCGC
                                GTGGCGGTGGG     GGGG
                                ||||||||||      ||||
                                CACCGCCATCC     CCTC
                                      CA____
GAM196  LOC201501 5'  GTGGCGGTGGGGGTGGGGG    4515          C  CGC
                                GTGGCGGTGGG GG   GGGGG
                                |||||||||| ||   |||||
                                CACCGCCACCC CC   CCCCC
                                      _ A__
GAM196  LOC202038 5'  GGTGGTGGGCGCCGATGGG    4516     C       G  CG
                                GG GGTGGGCG CG  GGG
                                || |||||||| ||  |||
                                CC CCACCCGC GC  CCC
                                 A       G  TA
GAM196  LOC204515 5'  CGGGGCGGTGGGCGGGCAGGGG 4517     T          C
                                CG GGCGGTGGGCGG GCGGGGG
                                || ||||||||||| |||||||
                                GC CCGCCACCCGCC CGTCCCC
                                 C          _
GAM196  LOC204970 5'  TGGCGGTGGCGTTGGGG     4518          G  GCGC
                                TGGCGGTGG CG    GGGG
                                |||||||| ||    ||||
                                ACCGCCACC GC    CCCC
                                      _ AA__
GAM196  LOC55565  3'  GTGGCAGTGGGCTGGGG     4519          GGCGC
                                GTGGCGGTGGGC    GGGG
                                ||||||||||||    ||||
                                CACCGTCACCCG    CCCC
                                      A____
GAM196  LOC91397  5'  GTGGGGGTGGGCGGTGG     4520       C       CGC
                                GTGG GGTGGGCGG   GG
                                |||| |||||||||   ||
                                CACC CCACCCGCC   CC
                                  C       A__
GAM197  DISC1     3'  GCACTTTGGGAAGTGCTGC    4523     GG       C  T
                                GC  ACTTTGGGG GT TTGC
                                ||  ||||||||| || ||||
                                CG  TGAAACCCT CA GACG
                                 __        T  C
GAM197  KPNA3     3'  TTTGGAGCCTTTTGTTGC     4524          G    CC
                                TTTGGGGC TTTTG  GC
                                |||||||| |||||  ||
                                AAACCTCG AAAAC  CG
                                     G    AA
GAM197  POLG      3'  GAACTTTGGGGCTTCTGC     4525            G
                                GGACTTTGGGGC TTTTGC
                                |||||||||||| ||||||
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                                CTTGAAACCCCG AAGACG
                                          _
GAM197  SLC30A3  3'  GCGGGCTTTGGGGCCCCTGC  4526      A       G
                                GCGG CTTTGGGGC TTTTGC
                                |||| ||||||||| ||||||
                                CGCC GAAACCCCG GGGACG
                                  C       _
GAM197  BHLHB2   3'  GCACTTTGGGGTGCTCGC    4527    GG      C   T
                                GC  ACTTTGGGG GTTT GC
                                ||  ||||||||| |||| ||
                                CG  TGAAACCCC CGAG CG
                                 __       A   _
GAM197  cerk     3'  GGGTTTTGGGGCAGGCCA    4528    AC      TTTT
                                GG  TTTGGGGGCG   GCCG
                                ||  |||||||||   ||||
                                CC  AAACCCCGT   CGGT
                                 CA       C___
GAM197  ICAP-1A  5'  GCGGACTTCGGGGTCC     4529           CGTTTTG
                                GCGGACTTTGGGG     CC
                                ||||||||||||      ||
                                CGCCTGAAGCCCC     GG
                                       A_______
GAM197  NTT73    5'  GCTGGGTTTTGGGGGTCGC   4530    _ AC     C   TT
                                GC GG  TTTGGGG GTT  GC
                                || ||  ||||||| |||  ||
                                CG CC  AAACCCC CAG  CG
                                 A  CA     _  __
GAM197  PODLX2   3'  GCGGGCTTTGAGGCCTGC    4531     A       GTT
                                GCGG CTTTGGGGC   TTGC
                                |||| |||||||||   ||||
                                CGCC GAAACTCCG   GACG
                                  C       ___
GAM197  SARM     3'  GGGCTTTGGGGCCCTCTG    4532    A       G
                                GG CTTTGGGGC TTTTG
                                || ||||||||| |||||
                                CC GAAACCCCG GAGAC
                                 C       G
GAM197  USP20    3'  GGCTTTGGTGCCTTGC      4533    A     GGC
                                GG CTTTGG   GTTTTGC
                                || ||||||   |||||||
                                CC GAAACC   CGGAACG
                                 _     A__
GAM197  LOC155179 3'  GGACAGGCCGTGTTTTGC    4534      TTT   G   __
                                GGAC   GGG CGT  TTTGC
                                ||||   ||| |||  |||||
                                CCTG   TCC GCA  AAACG
                                  ___   G   CA
GAM197  LOC158314 5'  GGATGTTTCATTTTGCTGC   4535     CTT  GGG      C
                                GGA   TG   CGTTTTGC GC
                                |||   ||   |||||||| ||
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                                CCT   AC   GTAAAACG CG
                                  ___  AAA       A
GAM197  LOC158572 3'  GGGCTCTGGGGTGCTGC     4536     A       C  TT
                                GG CTTTGGGG GT  TGC
                                || |||||||| ||  |||
                                CC GAGACCCC CG  ACG
                                 C       A  __
GAM197  LOC90522  3'  GGACCTTGGGGCCTGC      4537            GTT
                                GGACTTTGGGGC   TTGC
                                ||||||||||||   ||||
                                CCTGGAACCCCG   GACG
                                       ___
GAM198  FGF2     5'  CCGCGGACGCCGCCTGGGGAGA 4540             CTC___
              GCC                   CCGTGGACGCCGCC     GAGCC
                                ||||||||||||||      |||||
                                GGCGCCTGCGGCGG     CTCGG
                                      ACCCCT
GAM198  FGF8     5'  CCCGTGGAACGTCGTGC     4541         _  CCGCCC   A
                                CCCGTGGA CG     TCG GC
                                |||||||| ||      ||| ||
                                GGGCACCT GC     AGC CG
                                     T _______  A
GAM198  FGF8     5'  CCCGTGGAACGTCGTGC     4541         _  CCGCCC   A
                                CCCGTGGA CG     TCG GC
                                |||||||| ||      ||| ||
                                GGGCACCT GC     AGC CG
                                     T _______  A
GAM198  FGF8     5'  CCCGTGGAACGTCGTGC     4541         _  CCGCCC   A
                                CCCGTGGA CG     TCG GC
                                |||||||| ||      ||| ||
                                GGGCACCT GC     AGC CG
                                     T _______  A
GAM198  FGF8     5'  CCCGTGGAACGTCGTGC     4541         _  CCGCCC   A
                                CCCGTGGA CG     TCG GC
                                |||||||| ||      ||| ||
                                GGGCACCT GC     AGC CG
                                     T _______  A
GAM198  FGF8     5'  CCCGTGGAACGTCGTGC     4541         _  CCGCCC   A
                                CCCGTGGA CG     TCG GC
                                |||||||| ||      ||| ||
                                GGGCACCT GC     AGC CG
                                     T _______  A
GAM198  PAK1     5'  CCCCGTGGGTGCGCCTAGC   4542          AC  C   CTCG
                                CCCCGTGG  GC GCC    AGC
                                ||||||||  || |||    |||
                                GGGGCACC  CG CGG    TCG
                                     CA  _   A___
GAM198  PPP2R5A  5'  CCCCGGGACGCCGCCGAGC   4543       T        CTC
                                CCCCG GGACGCCGCC   GAGC
                                ||||| ||||||||||   ||||
                                GGGGC CCTGCGGCGG   CTCG
                                      _       ___
GAM198  PTPN14   5'  CCCCGTGGCGCCCCGGAG    4544          ACGC     C
                                CCCCGTGG    CGCCCT GAG
                                ||||||||    |||||| |||
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                                GGGGCACC   GCGGGG CTC
                                    ____     C
GAM198  SORCS2   3'  CCCCGTGGGCCTGGGCGGGC  4545        AC   GCCCT  A
                                CCCCGTGG  GCC    CG GC
                                ||||||||  |||    || ||
                                GGGGCACC  CGG    GC CG
                                    __   ACCC_  C
GAM198  THOP1    3'  CCTTGAGGACGCCGTCTCTAGC 4546    GT__      CC   G
          C                      CC   GGACGCCG  CTC AGCC
                                ||   ||||||||  ||| ||||
                                GG   CCTGCGGC  GAG TCGG
                                 AACT       A_   A
GAM198  APPD     5'  CCCCGCGCCCAGCCCTCGAG   4547        GA  CC
                                CCCCGTG  CG  GCCCTCGAG
                                |||||||  ||  |||||||||
                                GGGGCGC  GT  CGGGAGCTC
                                    GG  __
GAM198  ATPAF2   5'  CCCTTGGACGCCGCCATC    4548     G        C
                                CCC TGGACGCCGCC TC
                                ||| ||||||||||| ||
                                GGG ACCTGCGGCGG AG
                                  A         T
GAM198  DCOHM    3'  CCTGGACACCAAAGTTCTTGGG 4549     G       CCC_  GA__
          C                      CC TGGACGCCG    TC    GC
                                || |||||||||    ||    ||
                                GG ACCTGTGGT    AG    CG
                                 _        TTCA  AACC
GAM198  DKFZP434P0316 3'  CCCGCGTGGGCTCCTCGAGCC  4550      _    ACGCC  _
                                CCC CGTGG     GC CCTCGAGCC
                                ||| |||||     || |||||||||
                                GGG GCACC     CG GGAGCTCGG
                                  C    ______ A
GAM198  DKFZP727G051 5'  CCCCGCGGGCCTACTCG     4551         AC   GCC
                                CCCCGTGG  GCC   CTCG
                                ||||||||  |||   ||||
                                GGGGCGCC  CGG   GAGC
                                    __   AT_
GAM198  FKBP7    5'  CCCCGTGGATGTCCCGCGGCCG 4552         CG__    CC
          AG                      CCCCGTGGA    CCGC  TCGAG
                                |||||||||    ||||  |||||
                                GGGGCACCT    GGCG  GGCTC
                                     ACAG    CC
GAM198  FLJ21438  5'  CCACGTGGATGCTGCCCTCGGA 4553     _     C  C      _
          GC                      CC CGTGGA GC GCCCTCG AGC
                                || |||||| || ||||||| |||
                                GG GCACCT CG CGGGAGC TCG
                                 T     A  A      C
GAM198  FLJ21596  3'  CCTCGGGGACGCCGTGAGGGCC 4554     _  T       CCCTCGA
                                CC CG GGACGCCG       GCC
                                || || ||||||||       |||
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                                GG GC CCTGCGGC      CGG
                                 A  C       ACTCC__
GAM198  KIAA0447  5'  CCCCGCGGGCGCCGCTCC    4555         A     _
                                CCCCGTGG CGCCGC CC
                                |||||||| |||||| ||
                                GGGGCGCC GCGGCG GG
                                     C     A
GAM198  KIAA1079  5'  CCGGGGCCGGCCCTCGAG    4556     T  AC   _
                                CCG GG  GCCG CCCTCGAG
                                ||| ||  |||| ||||||||
                                GGC CC  CGGC GGGAGCTC
                                  _ __   C
GAM198  KIAA1373  5'  CCCCGTGGCTGCCGTGTGGCC  4557         AC   CCCTCGA
                                CCCCGTGG  GCCG      GCC
                                ||||||||  ||||      |||
                                GGGGCACC  CGGC      CGG
                                     GA   ACAC___
GAM198  MGC20258  5'  GTGGAGCCGCCCCAGC      4558       C       CG
                                GTGGA GCCGCCCT  AGC
                                ||||| ||||||||  |||
                                CACCT CGGCGGGG  TCG
                                  _      __
GAM198  MGC4266  5'  CCCGTGGACCTGCCCGCGCC  4559         GCC   TCGA
                                CCCGTGGAC   GCCC   GCC
                                |||||||||   ||||   |||
                                GGGCACCTG   CGGG   CGG
                                     GA_    CG__
GAM198  NEUROG3  3'  CCCCGTGGAGGCCTGGGCC   4560         C   ___
                                CCCCGTGGA GCC   GCC
                                ||||||||| |||   |||
                                GGGGCACCT CGG   CGG
                                     C   ACC
GAM198  NTN1     3'  CGCTCGCCCCGCCCTCGGGCC  4561      GGACG       A
                                CGT     CCGCCCTCG GCC
                                |||     ||||||||| |||
                                GCG     GGCGGGAGC CGG
                                  AGCGG       C
GAM198  OSBPL1A  5'  CCCCGAGGACGCTCGAGC    4562       T     CGCCC
                                CCCCG GGACGC    TCGAGC
                                ||||| ||||||    ||||||
                                GGGGC CCTGCG    AGCTCG
                                   T    _____
GAM198  OSBPL1A  5'  CCCCGAGGACGCTCGAGC    4562       T     CGCCC
                                CCCCG GGACGC    TCGAGC
                                ||||| ||||||    ||||||
                                GGGGC CCTGCG    AGCTCG
                                   T    _____
GAM198  PDE10A   5'  CCCTGGGGACGCCGCGGAG   4563      GT_       CCTC
                                CCC   GGACGCCGC   GAG
                                |||   |||||||||   |||
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                                GGG  CCTGCGGCG   CTC
                                  ACC       C___
GAM198  PP1044   3'  CCCGTGGACCCCGGCTAGGGCC 4564        G  CC  CGA
                                CCCGTGGAC CCG  CT   GCC
                                ||||||||| |||  ||   |||
                                GGGCACCTG GGC  GA   CGG
                                     G   C_  TCC
GAM198  SDC3     5'  CCCCGTGGGCTTCTCAGAG   4565        AC  CGCC  _
                                CCCCGTGG  GC   CTC GAG
                                ||||||||  ||   ||| |||
                                GGGGCACC  CG   GAG CTC
                                     __  AA__   T
GAM198  SEMA3E   5'  CCCGTGGAGGTCCTCTCTTCGG 4566        CG_  GCCC_  A
           GC                     CCCGTGGA   CC    TCG GC
                                ||||||||   ||    ||| ||
                                GGGCACCT   GG    AGC CG
                                     CCA  AGAGA   C
GAM198  LOC115073 5'  CCTCGTGGCGCCGCCCTCG   4567    _    A
                                CC CGTGG CGCCGCCCTCG
                                || ||||| ||||||||||
                                GG GCACC GCGGCGGGAGC
                                 A    _
GAM198  LOC115704 3'  CCCCGTGGGTGCCTGCCCCG   4568        AC  _   T
                                CCCCGTGG  GCC GCCC CG
                                ||||||||  ||| |||| ||
                                GGGGCACC  CGG CGGG GC
                                     CA   A   _
GAM198  LOC144184 5'  CCCGGGGCGCCGCCCGCAGCC  4569      T  A      T G
                                CCCG GG CGCCGCCC C AGCC
                                |||| || |||||||| | ||||
                                GGGC CC GCGGCGGG G TCGG
                                  _ C       C _
GAM198  LOC147160 5'  CCTCATGGACGCCCTGGGCC   4570    _       ____
                                CC CGTGGACGCC   GCC
                                || ||||||||||   |||
                                GG GTACCTGCGG   CGG
                                 A        GACC
GAM198  LOC147929 5'  CCGTTGACGATGCCTCGAGC   4571      G   CC   C
                                CCGT GACG  GCC TCGAGC
                                |||| ||||  ||| ||||||
                                GGCA CTGC  CGG AGCTCG
                                  A   TA   _
GAM198  LOC199993 5'  CCCCGCGGGCGCCGCTCC    4555        A    _
                                CCCCGTGG CGCCGC CC
                                |||||||| |||||| ||
                                GGGGCGCC GCGGCG GG
                                     C     A
GAM198  LOC200931 5'  CCACCGTGGGTGCCGAGC    4572    _    AC   GCCCTC
                                CC CCGTGG  GCC     GAGC
                                || ||||||  |||     ||||
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                                GG GGCACC  CGG     CTCG
                                 T     CA  _______
GAM198  LOC203595 5'  CCGCGTGGACGCTGCCACC   4573     _       C   C
                                CC CGTGGACGC GCC TC
                                || ||||||||| ||| ||
                                GG GCACCTGCG CGG GG
                                 C       A   T
GAM198  LOC253039 5'  CCTCGAGGACGCCGACGAG   4574     _ T      CCCT
                                CC CG GGACGCCG   CGAG
                                || || ||||||||   ||||
                                GG GC CCTGCGGC   GCTC
                                 A  T      T___
GAM198  LOC255070 3'  CCCCGTGGGCTCGCTGGGGAGC 4575         AC  _  CCTC
          C                      CCCCGTGG  GC CGC   GAGCC
                                ||||||||  || |||   |||||
                                GGGGCACC  CG GCG   CTCGG
                                     __  A   ACCC
GAM198  LOC256855 3'  GCGGCACCGCCCTCGGGCC   4576      A        A
                                GTGG CGCCGCCCTCG GCC
                                |||| |||||||||| |||
                                CGCC GTGGCGGGAGC CGG
                                  _        C
GAM199  LOC168512 5'  TAATGTTTCACCTCGTATAT   4579       C
                                TAATGT TTATCTCGTATAT
                                |||||| ||||||||||||
                                ATTACA AGTGGAGCATATA
                                   A
GAM199  LOC200059 3'  ATGTCTTATAACAAAATATAT  4580         CT  T_
                                ATGTCTTAT  CG  ATATAT
                                |||||||||  ||  ||||||
                                TACAGAATA  GT  TATATA
                                     TT  TT
GAM199  LOC81537  3'  TAATGTCTTATTTTTACAT   4581          CTCG
                                TAATGTCTTAT   TATAT
                                ||||||||||   |||||
                                ATTACAGAATA   ATGTA
                                      AAA_
GAM200  BSG       3'  TCCACAAAGGGCAAGGACC   4584       AGTTT       A
                                TCCACA    GAGGGCAAG ACC
                                ||||||    ||||||||| |||
                                AGGTGT    TTCCCGTTC TGG
                                   _____        C
GAM200  BSG       3'  TCCACAAAGGGCAAGGACC   4584       AGTTT       A
                                TCCACA    GAGGGCAAG ACC
                                ||||||    ||||||||| |||
                                AGGTGT    TTCCCGTTC TGG
                                   _____        C
GAM200  C18orf1   3'  CATAAGTTTGAGCCAAAA    4585     C       G G
                                CA AAGTTTGA G CAAGA
                                || |||||||| | |||||
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                                GT TTCAAACT C GTTTT
                                 A       _ G
GAM200  CDH18    3'  TCCACAAGGTTGCAAGAAC   4586          TTTGAGG
                                TCCACAAG      GCAAGAAC
                                ||||||||      ||||||||
                                AGGTGTTC      CGTTCTTG
                                    CAA____
GAM200  CHD4     3'  CAAGCCTGGCAGGAACC     4587         GAG    A
                                CAAGTTT   GGCA GAACC
                                |||||||   |||| |||||
                                GTTCGGA   CCGT CTTGG
                                    ___    C
GAM200  LARGE    3'  TCCACAGTGAAGCAGGCAAGAA 4588         A  TTGA_
            CC                    TCCACA GT     GGGCAAGAACC
                                |||||| ||     ||||||||||
                                AGGTGT CA     TCCGTTCTTGG
                                   _ CTTCG
GAM200  LARGE    3'  TCCACAGTGAAGCAGGCAAGAA 4588         A  TTGA_
            CC                    TCCACA GT     GGGCAAGAACC
                                |||||| ||     ||||||||||
                                AGGTGT CA     TCCGTTCTTGG
                                   _ CTTCG
GAM200  LTB4R    5'  ACAAGCTTTGGCAGGAAC    4589          GAG    A
                                ACAAGTTT   GGCA GAAC
                                ||||||||   |||| ||||
                                TGTTCGAA   CCGT CTTG
                                    A__    C
GAM200  MECP2    3'  CCACTATGGGGGCAGGAGCC  4590       AAGTT  A    A  A
                                CCAC    TG GGGCA GA CC
                                ||||    || ||||| || ||
                                GGTG    AC CCCGT CT GG
                                  AT___  C    C  C
GAM200  NFRKB    5'  TCCATGAGTTTGAGACCA    4591       CA       G
                                TCCA  AGTTTGAGG CA
                                ||||  ||||||||| ||
                                AGGT  TCAAACTCT GT
                                  AC       G
GAM200  PAICS    3'  CAGGAGTTTGAGACGAACC   4592     CA       GCAA
                                CA  AGTTTGAGG   GAACC
                                ||  |||||||||   |||||
                                GT  TCAAACTCT   CTTGG
                                 CC       G___
GAM200  PSCD4    3'  CACAGGCTGACAAGAA      4593       A   TGAG
                                CACA GTT   GGCAAGAA
                                |||| |||   ||||||||
                                GTGT CGA   CTGTTCTT
                                  C  ____
GAM200  WNT3A    3'  CCCGCACCTTGAGGGTGGGAGC 4594      A  AG       CAA  A
            C                     TCC CA  TTTGAGGG   GA CC
                                ||| ||  ||||||||   || ||
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                                GGG GT  GAACTCCC   CT GG
                                  C  G_       ACC  C
GAM200  AMOT     5'  AGCAAGGGCAAGGACC      4595      TT        A
                                AGT  GAGGGCAAG ACC
                                |||  ||||||||| |||
                                TCG  TTCCCGTTC TGG
                                  __        C
GAM200  C6orf37   3'  CACAAGTTGGAGTGAGACC    4596          T   GGCA   A
                                CACAAGTT GAG    AGA CC
                                |||||||| |||    ||| ||
                                GTGTTCAA CTC    TCT GG
                                     C   AC__   _
GAM200  CENTB5    3'  CACACAGGGAGAGGGGCAAGAA 4597       AGTTT_    _
                                CACA      GAGGG CAAGAA
                                ||||      ||||| ||||||
                                GTGT      CTCCC GTTCTT
                                   GTCCCT     C
GAM200  DKFZP434P0111 3'  TCCTTAAGTTTGAAGCA     4598      AC        G
                                TCC  AAGTTTGAGG CA
                                |||  |||||||||| ||
                                AGG  TTCAAACTTC GT
                                  AA         _
GAM200  FLJ10547  3'  TCCACAAATTTGGATTGAGC   4599            A___
                                TCCACAAGTTTG    GGGC
                                ||||||||||||    ||||
                                AGGTGTTTAAAC    CTCG
                                       CTAA
GAM200  FLJ10713  3'  TCCAGGAGTTTGAGACCAA    4600       CA        G
                                TCCA  AGTTTGAGG CAA
                                ||||  ||||||||| |||
                                AGGT  TCAAACTCT GTT
                                   CC        G
GAM200  FLJ14327  3'  CACAGAAACAGGGCAAGGGCC  4601       A TTTG       AA
                                CACA G    AGGGCAAG  CC
                                |||| |    ||||||||  ||
                                GTGT C    TCCCGTTC  GG
                                  _ TTTG       CC
GAM200  FLJ20010  3'  CACAAGCTAAGTGAGGGC     4602          ___
                                CACAAGTT   TGAGGGC
                                ||||||||   |||||||
                                GTGTTCGA   ACTCCCG
                                     TTC
GAM200  FLJ22659  3'  TCCCCTCCATGAGGGCAGGAAC 4603      ACAAGTT       A
           C                     TCC       TGAGGGCA GAACC
                                |||       |||||||| |||||
                                AGG       ACTCCCGT CTTGG
                                  GGAGGT_       C
GAM200  FLJ22814  3'  TCCGCGTGGGGCAAGA      4604      ACAA  T  A
                                TCC    GT TG GGGCAAGA
                                |||    || || ||||||||
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                                AGG   CG AC CCCGTTCT
                                  _____ C  _
GAM200  HIP-55   3' TCCTGTCAGGGGCAAGAC   4605     ACAA  TGA      A
                                TCC   GTT  GGGCAAGA C
                                |||   |||  |||||||| |
                                AGG   CAG  CCCGTTCT G
                                  A___  TC_      C
GAM200  INSM2    3' CCCACAAAATAGCTGAGGGTGA 4606        T___     CA
           GAA                    TCCACAAG   TTGAGGG  AGAA
                                |||||||   |||||||  ||||
                                GGGTGTTT   GACTCCC  TCTT
                                     TATC      AC
GAM200  KIAA0064 5' AGTCTAAAGGGCAAGAGCC   4607        _      A
                                AGTTTGA GGGCAAGA CC
                                ||||||| |||||||| ||
                                TCAGATT CCCGTTCT GG
                                     T       C
GAM200  KIAA0426 3' AAGTTTGAGGAAAGACC     4608          C   A
                                AAGTTTGAGGG AAGA CC
                                |||||||||| |||| ||
                                TTCAAACTCCT TTCT GG
                                        _   _
GAM200  KIAA1076 5' TCCGAGGATGAGGGCGAGGAC 4609     ACA  TT     A  A
                                TCC   AG  TGAGGGC AG AC
                                |||   ||  ||||||| || ||
                                AGG   TC  ACTCCCG TC TG
                                  C__  CT      C  C
GAM200  KIAA1553 3' CCATACAGACAGGGCAAGGACC 4610     CA_  TTTG      A
                                CCA   AG    AGGGCAAG ACC
                                |||   ||    |||||||| |||
                                GGT   TC    TCCCGTTC TGG
                                  ATG  TG__       C
GAM200  KIAA1712 3' CACGAGTTTGAGAACAGA    4611      A         A
                                CAC AGTTTGAGGGCA GA
                                ||| |||||||||||| ||
                                GTG TCAAACTCTTGT CT
                                  C          _
GAM200  KIAA1795 3' TCCAAAGTTTCCAGGCAAGAA  4612      C     GA
                                TCCA AAGTTT  GGGCAAGAA
                                |||| ||||||  |||||||||
                                AGGT TTCAAA  TCCGTTCTT
                                  _     GG
GAM200  LEAP-2   5' TCCATCAGTTTAAGTAGGAAC  4613      CA      GGCAA
                                TCCA  AGTTTGAG    GAAC
                                ||||  ||||||||    ||||
                                AGGT  TCAAATTC    CTTG
                                  AG       ATC__
GAM200  MGC11257 3' TCCACAAGCTCCCACCAGGGGC 4614          GA_____
                                TCCACAAGTTT      GGGC
                                ||||||||||       ||||
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                                AGGTGTTCGAG      CCCG
                                      GGTGGTC
GAM200  NXPH3    3'  TCCTCAGGATGGCAAGAAC   4615      A  AGTTT  G
                                TCC CA    GA GGCAAGAAC
                                ||| ||    || |||||||||
                                AGG GT    CT CCGTTCTTG
                                  A  C____  A
GAM200  RAB3D    3'  GCATGATTGGGCAAGAAC    4616     T  __
                                GT TGA  GGGCAAGAAC
                                || |||  ||||||||||
                                CG ACT  CCCGTTCTTG
                                 T   AA
GAM200  SDC3     3'  TCCGAGAAAGGCAAGGGCC   4617      ACA  TTT       AA
                                TCC   AG   GAGGGCAAG  CC
                                |||   ||   |||||||||  ||
                                AGG   TC   TTTCCGTTC  GG
                                  C__  ___        CC
GAM200  SHANK3   5'  TCGGGCAGCCAGGGCAAGGGCC 4618     CACA    TG      AA
                                TC    AGTT  AGGGCAAG  CC
                                ||    ||||  ||||||||  ||
                                AG    TCGG  TCCCGTTC  GG
                                 CCCG    __       CC
GAM200  SNRK     5'  TCCGCAGGAGCCTGGGCAAGAA 4619      A  __    GA
                                TCC CA  AGTTT  GGGCAAGAA
                                ||| ||  |||||  |||||||||
                                AGG GT  TCGGA  CCCGTTCTT
                                  C  CC    __
GAM200  SPIN     3'  TCCACAAATTTGGCAGA     4620           GAG    A
                                TCCACAAGTTT   GGCA GA
                                ||||||||||   |||| ||
                                AGGTGTTTAAA   CCGT CT
                                      ___   _
GAM200  SPRY4    3'  TCCAGAAGTTTGAGACCA    4621       C        G
                                TCCA AAGTTTGAGG CA
                                |||| |||||||||| ||
                                AGGT TTCAAACTCT GT
                                  C        G
GAM200  SYTL3    5'  TCCAGGTCAGCAGGAAC     4622      CAA   TGAG    A
                                TCCA   GTT    GGCA GAAC
                                ||||   |||    |||| ||||
                                AGGT   CAG    TCGT CTTG
                                  C__   ____    C
GAM200  TRIM35   3'  CCCATGAGTTTGAGGTTACA   4623      CA       __
                                TCCA  AGTTTGAGG  GCA
                                ||||  |||||||||  |||
                                GGGT  TCAAACTCC  TGT
                                  AC        AA
GAM200  LOC124801 3'  TCTACAAAGTTCGCAGCAAGAA 4624     C   _    AG
                                TC ACAA GTTTG  GGCAAGAA
                                || |||| |||||  ||||||||
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                                AG TGTT CAAGC  TCGTTCTT
                                 A   T    G_
GAM200  LOC149684 5'  TCCAGGAGTTTGAGACCA    4625      CA       G
                                TCCA  AGTTTGAGG CA
                                ||||  ||||||||| ||
                                AGGT  TCAAACTCT GT
                                  CC        G
GAM200  LOC150139 3'  ACAGGCAAGGCAAGGGCC    4626     A  TTG      AA
                                ACA GT   AGGGCAAG  CC
                                ||| ||   ||||||||  ||
                                TGT CG   TTCCGTTC  GG
                                 C  ___       CC
GAM200  LOC196955 5'  TCTGCAAGTTTGAGGAGCAAG  4627     CA         _
                                TC  CAAGTTTGAGG GCAAG
                                ||  |||||||||||| |||||
                                AG  GTTCAAACTCC CGTTC
                                 AC          T
GAM200  LOC206426 3'  TCAACATTGCTGGGGCAAG    4628     C   AGT   A
                                TC ACA   TTG GGGCAAG
                                || |||   ||| |||||||
                                AG TGT   GAC CCCGTTC
                                 T   AAC  _
GAM200  LOC220776 3'  TCCATGAGCAGGCAAGGAC    4629      CA   TTGA     A
                                TCCA  AGT    GGGCAAG AC
                                ||||  |||    ||||||| ||
                                AGGT  TCG    TCCGTTC TG
                                  AC  _____      C
GAM200  LOC221362 5'  ACAAGAAAGGCAAGA       4630       TTT
                                ACAAG   GAGGGCAAGA
                                |||||   ||||||||||
                                TGTTC   TTTCCGTTCT
                                   ___
GAM200  LOC256167 5'  TCCGAGAGTTTACAGCCAAGAA 4631      ACA     A  G
                                TCC   AGTTTG GG CAAGAA
                                |||   |||||| || ||||||
                                AGG   TCAAAT TC GTTCTT
                                  CTC     G  G
GAM200  LOC51193  3'  TCCAGGAGTTTGAGACTGGC   4632      CA      ___
                                TCCA  AGTTTGAG   GGC
                                ||||  ||||||||   |||
                                AGGT  TCAAACTC   CCG
                                  CC       TGA
GAM200  LOC92935  3'  CCACAAGCCGGTAAGAAC    4633         TGA  GC
                                CCACAAGTT   GG  AAGAAC
                                |||||||||   ||  ||||||
                                GGTGTTCGG   CC  TTCTTG
                                     ___  A_
GAM201  CLCN4     3'  GCCCAGTGCCCAAATTGGC    4636         GC__
                                GCCCGGTGCC    TTGGC
                                ||||||||||    |||||
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                                CGGGTCACGG   AACCG
                                     GTTT
GAM201  INPP1   5' GCACCGGATCCGAGCTTGGC  4637    _   TG __
                                GC CCGG  CC  GCTTGGC
                                || ||||  ||  |||||||
                                CG GGCC  GG  CGAACCG
                                 T   TA  CT
GAM201  PNUTL1  3' GCCCAGTGCCCCGGGGGC   4638        G  T__
                                GCCCGGTGCC CT   GGC
                                |||||||||| ||   |||
                                CGGGTCACGG GG   CCG
                                      _ CCC
GAM201  SYCP1   5' GCCCGCTGCCACGCTGGC   4639      G    _
                                GCCCG TGCCGC TTGGC
                                ||||| |||||| |||||
                                CGGGC ACGGTG GACCG
                                   G     C
GAM201  TAF6    5' GCTCGGCGCCATCTTGGC   4640    C      _
                                GC CGGTGCCG CTTGGC
                                || |||||||| ||||||
                                CG GCCGCGGT GAACCG
                                 A       A
GAM201  CNNM1   5' GCGCCGGTGCACACGAGC   4641    _     _  TT
                                GC CCGGTGC CGC  GGC
                                || ||||||| |||  |||
                                CG GGCCACG GTG  TCG
                                 C      T  C_
GAM201  FLJ22127 3' GCCCAGTGCCCTGGATGGC  4642        G ____
                                GCCCGGTGCC CT   TGGC
                                |||||||||| ||   ||||
                                CGGGTCACGG GA   ACCG
                                      _ CCT
GAM201  FLJ22415 5' GCTCAGCTGCTGCTTGGCG  4643    C  _  C     III
                                GC CGG TGC GCTTGGC   G
                                || ||| ||| |||||||   |
                                CG GTC ACG CGAACCG   C
                                 A  G  A      III
GAM201  KIAA0280 3' ACCCTGCAGCCGCTTGGC   4644     G  _
                                GCCC GT GCCGCTTGGC
                                |||| || ||||||||||
                                TGGG CG CGGCGAACCG
                                  A  T
GAM201  MGC20481 5' GCCCAGTAAACGCTTGGC   4645       C_
                                GCCCGGTG  CGCTTGGC
                                ||||||||  ||||||||
                                CGGGTCAT  GCGAACCG
                                     TT
GAM201  PCQAP   5' GCCCGTATCCCGCTTGGC   4646      _  G
                                GCCCG GT CCGCTTGGC
                                ||||| || |||||||||
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                                CGGGC TA GGCGAACCG
                                  A  G
GAM201  LOC145622 5'  GCCAGGGGAACCGCTTGGC   4647     C  T__
                                GCC GG   GCCGCTTGGC
                                ||| ||   ||||||||||
                                CGG CC   TGGCGAACCG
                                  T  CCT
GAM201  LOC220538 3'  CCTGGTGCCGCGTGTTTGGC   4648     C      ____
                                CC GGTGCCGC    TTGGC
                                || ||||||||    |||||
                                GG CCACGGCG    AACCG
                                 A       CACA
GAM201  LOC253256 5'  GCCGGGTGCCACCCTGGC    4649     C       _
                                GCC GGTGCCGCT TGGC
                                ||| ||||||||| ||||
                                CGG CCACGGTGG ACCG
                                  C        G
GAM201  LOC256586 5'  ACCCGGTGCTCCACATGGC   4650          __  T
                                GCCCGGTGC  CGC TGGC
                                |||||||||  ||| ||||
                                TGGGCCACG  GTG ACCG
                                     AG   T
GAM201  LOC91252  3'  GCCCGGCAGGCTGCTGTTTGGC 4651        __ C  ___   III
    G                    GCCCGGT  GC GCT   TGGC   G
                                |||||||  || |||   ||||   |
                                CGGGCCG  CG CGA   ACCG   C
                                    TC  A   CAA    III
GAM202  ALDH3B1   3'  TGATTCCATGGTGTGGCCT   4654     GA_       A
                                TGA   CATGGTGTG CCT
                                |||   ||||||||| |||
                                ACT   GTACCACAC GGA
                                  AAG        C
GAM202  FGF5     3'  TGGCGTGGTGGCATGA      4655         AGACA
                                TGGCGTG    TGGTGTGA
                                |||||||    ||||||||
                                ACCGCAC    ACCGTACT
                                    C____
GAM202  FGF5     3'  TGGCGTGGTGGCATGA      4655         AGACA
                                TGGCGTG    TGGTGTGA
                                |||||||    ||||||||
                                ACCGCAC    ACCGTACT
                                    C____
GAM202  FIGF     3'  TGGTGTGAATGGAAGGTTGGTC 4656      C   ___  CA__   G
    TG                    TGG GTGA   GA    TGGT TG
                                ||| ||||   ||    |||| ||
                                ACC CACT   CT    ACCA AC
                                  A    TAC  TCCA    G
GAM202  GPD1     3'  TGGCATGAGGCTGCCAGTGGCT 4657          A____  _   G
    TG                    TGGCGTGAG    CA TGGT TG
                                |||||||||    || |||| ||
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                                ACCGTACTC    GT ACCG AC
                                     CGACG  C    A
GAM202  LNK     3'  TGGTGTGGACACAGCAGACCT  4658     C   A       T
                                TGG GTG GACATGGTG GACCT
                                ||| ||| ||||||||| |||||
                                ACC CAC CTGTGTCGT CTGGA
                                  A  _       _
GAM202  SHOX    3'  TGGTTTGGGAAACGGTGTG   4659     CG  A  C
                                TGG  TG GA ATGGTGTG
                                |||  || || ||||||||
                                ACC  AC CT TGCCACAC
                                  AA  C  T
GAM202  TRPM2   5'  GCGTGAGATGTGTCCCT    4660        CATG   GA
                                GCGTGAGA   GTGT  CCT
                                ||||||||   ||||  |||
                                CGCACTCT   CACA  GGA
                                     A___   G_
GAM202  XPR1    3'  TGGTGTGAAGTGTGGGATTCCT 4661     C   GACAT    A____
                                TGG GTGA    GGTGTG    CCT
                                ||| ||||    ||||||    |||
                                ACC CACT    TCACAC    GGA
                                  A   _____     CCTAA
GAM202  DKFZp761B0514 3'  TGATGTGAGGCAGGAGACCT   4662    GC    A  T  TGT
                                TG  GTGAG CA GG   GACCT
                                ||  ||||| || ||   |||||
                                AC  CACTC GT CC   CTGGA
                                 TA    C  _  T__
GAM202  DKFZP761G1913 3'  TGGTGAGAGACATGGTGGTG   4663     CGT        _
                                TGG   GAGACATGGTG TG
                                |||   |||||||||| ||
                                ACC   CTCTGTACCAC AC
                                  ACT         C
GAM202  ELOVL2  3'  TGGTGTGGAGCATGGCAT    4664     C  _  A
                                TGG GTG AG CATGGTGT
                                ||| ||| || ||||||||
                                ACC CAC TC GTACCGTA
                                  A  C  _
GAM202  FLJ14525  3'  TGGCGTGAGGGTGGA      4665         ACAT   T
                                TGGCGTGAG   GGTG GA
                                |||||||||   |||| ||
                                ACCGCACTC   CCAC CT
                                     ____   _
GAM202  FLJ20190  5'  TGGCCTGGGGCGTCTCTGCCTA 4666      G  AGACAT    GA___
                                TGGC TG     GGTGT    CCTA
                                |||| ||     |||||    ||||
                                ACCG AC     CCGCA    GGAT
                                  G  C_____    GAGAC
GAM202  FLJ22282  3'  TGGTGTGAGGCTGCGCCT    4667     C   GACAT  _   A
                                TGG GTGA    GG TGTG CCT
                                ||| ||||    || |||| |||
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                                ACC CACT    CC ACGC GGA
                                  A  _____ G  _
GAM202  HSPC133  3' TGGTGTGAGTCATTTCTGGTCT 4668    C   A ____  G
          G                      TGG GTGAG CA   TGGT TG
                                 ||| ||||| ||   |||| ||
                                ACC CACTC GT   ACCA AC
                                  A   A AAAG   G
GAM202  KIAA1508 3' TGGAGTGCAGTGGTGTGATCT 4669    C  AGACA     C
                                TGG GTG    TGGTGTGA CT
                                ||| |||    |||||||| ||
                                ACC CAC    ACCACACT GA
                                  T  GTC__      A
GAM202  KIAA1666 3' TGGTGTGAGGGTCTGAACGCT 4670    C   ACAT  G  _ _
                                TGG GTGAG   GGT TGA C CT
                                ||| |||||   ||| ||| | ||
                                ACC CACTC   CCA ACT G GA
                                  A   ____  G  T C
GAM202  MGC10646 3' TGGTTGAGACATGAGGACCT  4671    CG       TGT
                                TGG  TGAGACATGG  GACCT
                                |||  ||||||||||  |||||
                                ACC  ACTCTGTACT  CTGGA
                                  A_       C__
GAM202  MGC2721  5' TGGCGTGAGCTCCTGACCT   4672        ACATGGTG
                                TGGCGTGAG      TGACCT
                                |||||||||      ||||||
                                ACCGCACTC      ACTGGA
                                     GAGG____
GAM202  MSTP028  3' TGGTGTGAGGGTGTCCCT   4673    C   ACAT   GA
                                TGG GTGAG   GGTGT  CCT
                                ||| |||||   |||||  |||
                                ACC CACTC   CCACA  GGA
                                  A   ____    G_
GAM202  RHOBTB1  3' TGGTGGTGAGATGTGAC    4674    C_    CATGG
                                TGG  GTGAGA    TGTGAC
                                |||  ||||||    ||||||
                                ACC  CACTCT    ACACTG
                                  AC    _____
GAM202  LOC126528 3' TGGTGTGAGGAGCAGGGCCTG 4675    C   A__  T  G
                                TGG GTGAG   CA GGT TG
                                ||| |||||   || ||| ||
                                ACC CACTC   GT CCG AC
                                  A    CTC  C   G
GAM202  LOC149386 5' TGGTGTGAAACAGTCTA    4676    C      TG  G
                                TGG GTGAGACA  GT TG
                                ||| ||||||||  || ||
                                ACC CACTTTGT  CA AT
                                  A       __ G
GAM202  LOC150221 3' TGGTGTGAGGGTCTGAACGCT 4670    C   ACAT  G  _ _
                                TGG GTGAG   GGT TGA C CT
                                ||| |||||   ||| ||| | ||
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                                ACC CACTC    CCA ACT G GA
                                  A    ____  G   T C
GAM202  LOC155054 3'  TGGTGTGAGCATGGCTCAC   4677     C    A    GTG
                                TGG GTGAG CATGGT   AC
                                ||| ||||| ||||||   ||
                                ACC CACTC GTACCG   TG
                                  A    _     AG_
GAM202  LOC203392 5'  TGGTGTGAGGGTGCAGCCC   4678     C    ACAT    GA
                                TGG GTGAG    GGTGT  CCT
                                ||| |||||    |||||  |||
                                ACC CACTC    CCACG  GGG
                                  A    _____     TC
GAM202  LOC221463 3'  TGGTGTGTGGTGTGAC      4679     C   AGACA
                                TGG GTG     TGGTGTGAC
                                ||| |||     |||||||||
                                ACC CAC     ACCACACTG
                                  A  ______
GAM202  LOC221463 3'  TGGTGTGACACACCTTGAC   4680     C   G   GGTG
                                TGG GTGA ACAT    TGAC
                                ||| |||| ||||    ||||
                                ACC CACT TGTG    ACTG
                                  A   G   GA__
GAM202  LOC253566 5'  TGGTGTGGACATGGTACG    4681     C  A
                                TGG GTG GACATGGTGTG
                                ||| ||| ||||||||||
                                ACC CAC CTGTACCATGC
                                  A  _
GAM202  LOC90918  5'  TGGAGTGCAATGGTGTGATCT  4682     C   AGAC       C
                                TGG GTG    ATGGTGTGA CT
                                ||| |||    ||||||||| ||
                                ACC CAC    TACCACACT GA
                                  T   GT__       A
GAM203  ABCC1     5'  GCTGCTGGCGCTAGCGCTGGCG 4685     C  _   GAC T
                                GC GC GGCG   G CGCTGGCG
                                || || ||||   | ||||||||
                                CG CG CCGC   C GCGACCGC
                                 A  A   GAT _
GAM203  ABCC1     5'  GCTGCTGGCGCTAGCGCTGGCG 4685     C  _   GAC T
                                GC GC GGCG   G CGCTGGCG
                                || || ||||   | ||||||||
                                CG CG CCGC   C GCGACCGC
                                 A  A   GAT _
GAM203  ABCC1     5'  GCTGCTGGCGCTAGCGCTGGCG 4685     C  _   GAC T
                                GC GC GGCG   G CGCTGGCG
                                || || ||||   | ||||||||
                                CG CG CCGC   C GCGACCGC
                                 A  A   GAT _
GAM203  ACTN1     5'  CCGCCGCGGCGCTGCTGGC   4686      G   A  C
                                CCGC GCGG CGT GCTGGC
                                |||| |||| ||| ||||||
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                                GGCG CGCC GCG CGACCG
                                  G   _  A
GAM203  BAZ1B   5' GCGGCGGCGGTGGGACTGGCG 4687    C     ACGTC
                                GC GCGGCGG   GCTGGCG
                                || |||||||   |||||||
                                CG CGCCGCC   TGACCGC
                                 C     ACCC_
GAM203  BID     5' CAGCCGCGGGGGCGCGGGC  4688        C  AC T  T
                                CAGCCGCGG GG  G CGC GGC
                                ||||||||| ||  | ||| |||
                                GTCGGCGCC CC  C GCG CCG
                                     _ __ _  C
GAM203  CUL3    5' CAGCCGCGGCGGCGG      4689          ACGTCGC
                                CAGCCGCGGCGG     TGG
                                ||||||||||||     |||
                                GTCGGCGCCGCC     GCC
                                         _______
GAM203  CYLN2   3' CAGCCGCGTGGGGCTCTGG  4690       GC  AC  CG
                                CAGCCGCG  GG  GT  CTGG
                                ||||||||  ||  ||  ||||
                                GTCGGCGC  CC  CG  GACC
                                    A_  C_  A_
GAM203  EGR1    5' GCTGCGGCGGCGGATGGCG  4691    C     A  TCGC
                                GC GCGGCGG CG   TGGCG
                                || ||||||| ||   |||||
                                CG CGCCGCC GC   ACCGC
                                 A     _  CT__
GAM203  IL12A   5' GCCGCGGCAGGTGAGGGCG  4692        AC  CGCT
                                GCCGCGGCGG  GT   GGCG
                                ||||||||||  ||   ||||
                                CGGCGCCGTC  CA   CCGC
                                     __  CTC_
GAM203  JAG2    5' CAGCTCCGGCTCGCTGGC   4693     CG   GGACG
                                CAGC  CGGC   TCGCTGGC
                                ||||  ||||   ||||||||
                                GTCG  GCCG   AGCGACCG
                                  AG   _____
GAM203  MAP3K4  5' GCCGCGGCGGGCAGTAAGCTG 4694        A _  C_
                                GCCGCGGCGG C GT  GCTG
                                |||||||||| | ||  ||||
                                CGGCGCCGCC G CA  CGAC
                                     C T  TT
GAM203  MAP3K4  5' GCCGCGGCGGGCAGTAAGCTG 4694        A _  C_
                                GCCGCGGCGG C GT  GCTG
                                |||||||||| | ||  ||||
                                CGGCGCCGCC G CA  CGAC
                                     C T  TT
GAM203  POU4F1  5' CAGCCGCGGCGGTCGCGGC  4695         ACG   T
                                CAGCCGCGGCGG  TCGC GGC
                                ||||||||||||  |||| |||
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                                GTCGGCGCCGCC  AGCG CCG
                                      ____  _
GAM203  PTMS     5'  GCCGCGGCCGGAACCTGGCG  4696        _  CGTCG
                                GCCGCGGC GGA    CTGGCG
                                |||||||| |||    ||||||
                                CGGCGCCG CCT    GACCGC
                                     G  TG___
GAM203  RPS28    5'  CGCGGCGGCGGTCTGGCG   4697        A  TCG
                                CGCGGCGG CG  CTGGCG
                                |||||||| ||  ||||||
                                GCGCCGCC GC  GACCGC
                                     _ CA_
GAM203  SORCS2   3'  CAGCCGCCGGCTTTGCTGG   4698        _  GGACGTC
                                CAGCCGC GGC     GCTGG
                                ||||||| |||     |||||
                                GTCGGCG CCG     CGACC
                                    G  AAA_____
GAM203  ABTB1    5'  CAGCTGGCGAACAGGTCGCTGG 4699      CGC     __
                                CAGC  GGCGGAC  GTCGCTGG
                                ||||  |||||||  ||||||||
                                GTCG  CCGCTTG  CAGCGACC
                                  A__      TC
GAM203  ARGBP2   3'  CAGCAGCGGCGGCTACTCTGCT 4700      C     ACG_ _
          GG                    CAGC GCGGCGG   TC GCTGG
                                |||| |||||||   || |||||
                                GTCG CGCCGCC   AG CGACC
                                  T     GATG  A
GAM203  Cab45    3'  CAGCCGCGGTCGGTCGGCCGG  4701        _  A  TC
                                CAGCCGCGG CGG CG  GCTGG
                                ||||||||| ||| ||  |||||
                                GTCGGCGCC GCC GC  CGGCC
                                     A  A  __
GAM203  CAMK2B   5'  GCCGCGGCGGACGGGCTCGGCG 4702           TC  _
                                GCCGCGGCGGACG  GCT GGCG
                                ||||||||||||  ||| ||||
                                CGGCGCCGCCTGC  CGA CCGC
                                       C_  G
GAM203  DKFZp434J0226 5'  GCTGCAGCGGAGTGAGCTGG  4703    C      C  C_
                                GC GCGGCGGA GT  GCTGG
                                || ||||||| ||  |||||
                                CG CGTCGCCT CA  CGACC
                                 A      _ CT
GAM203  DKFZP434J1813 5'  CAGCCGCGGCGCACGGGATTGG 4704         G  TCGC
                                CAGCCGCGGCG ACG   TGG
                                |||||||||| |||   |||
                                GTCGGCGCCGC TGC   ACC
                                       G  CCTA
GAM203  FLJ12687  3'  CAGCCGCGGCGGGGTGTGG   4705          AC  CGC
                                CAGCCGCGGCGG  GT  TGG
                                |||||||||| ||  |||
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                                GTCGGCGCCGCC CA  ACC
                                      C_ C__
GAM203  FLJ14075 5' CGGCGTGCGGCCGCTGGC   4706      GA _
                                CGGCG CG TCGCTGGC
                                ||||| || ||||||||
                                GCCGC GC GGCGACCG
                                   AC C
GAM203  FLJ14466 5' GCTCCGGCGGCTGCCGCTGG 4707    CG    AC
                                GC CGGCGG GTCGCTGG
                                || |||||| ||||||||
                                CG GCCGCC CGGCGACC
                                 AG    GA
GAM203  FLJ14810 5' CAGCCGTGGCTGGGCCTGG  4708      C  _ AC CG
                                CAGCCG GGC GG GT CTGG
                                |||||| ||| ||  ||  ||||
                                GTCGGC CCG CC CG GACC
                                   A  A __ __
GAM203  HCA4    5' CAGCCGCGGCGGGGATTGC   4709         AC C
                                CAGCCGCGGCGG GT GC
                                |||||||||||  || ||
                                GTCGGCGCCGCC TA CG
                                      CC A
GAM203  KIAA0211 5' GCCGCGGCGGGGGGATTGGCG 4710        ACGTCGC
                                GCCGCGGCGG     TGGCG
                                ||||||||||     |||||
                                CGGCGCCGCC     ACCGC
                                      CCCTA__
GAM203  KIAA1228 5' GCTGCGGCGACACCAGGCG  4711    C    G GT CT
                                GC GCGGCG AC CG GGCG
                                || |||||| ||  ||  ||||
                                CG CGCCGC TG GT CCGC
                                 A    _ TG __
GAM203  KIAA1889 5' GCCGCGGCGATGTTGCT    4712         AC C
                                GCCGCGGCGG GT GCT
                                |||||||||| || |||
                                CGGCGCCGCT CA CGA
                                      A_ A
GAM203  MGC14425 3' GCCGCGGCGCGGTGGC     4713        GACGT C
                                GCCGCGGCG    CG TGGC
                                |||||||||    || ||||
                                CGGCGCCGC    GC ACCG
                                     _____ C
GAM203  MGC4415  3' GCCGCGGCGGGCGCGGGCG  4714         AC T  T
                                GCCGCGGCGG G CGC GGCG
                                |||||||||| | ||| ||||
                                CGGCGCCGCC C GCG CCGC
                                     __ _  C
GAM203  MST4    5' CAGCCGCGCTCCGCTGG    4715        GCGGACG
                                CAGCCGCG     TCGCTGG
                                ||||||||     |||||||
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                                GTCGGCGC      GGCGACC
                                   GA_____
GAM203  PDE10A   5'  GCCGCGGCGGCGAGGGC     4716          A  TCGCT
                                GCCGCGGCGG CG    GGC
                                |||||||||| ||    |||
                                CGGCGCCGCC GC    CCG
                                     _  TC___
GAM203  RLUCL    5'  CAGCCGCGCGCCCGCGCGCTGG 4717         G  GA  _
          CG                      CAGCCGCG CG  CGT CGCTGGCG
                                |||||||| ||  ||| ||||||||
                                GTCGGCGC GC  GCG GCGACCGC
                                   _ GG   C
GAM203  RNF2     5'  CAGCTGCCGCGGACGCCGGCG  4718      C  G     GTC
                                CAGC GC GCGGAC   GCTGGCG
                                |||| || ||||||   |||||||
                                GTCG CG CGCCTG   CGGCCGC
                                  A  G     ___
GAM203  STRAIT11499 5'  GCCGCGCGGACGTTGGAGCG   4719        G      CGCT
                                GCCGCG CGGACGT    GGCG
                                ||||||| |||||||    ||||
                                CGGCGC GCCTGCA    TCGC
                                   _      ACC_
GAM203  UGTREL7   5'  CAGCAGCGGTGGCCTGGC    4720      C    C  ACGTCG
                                CAGC GCGG GG     CTGGC
                                |||| |||| ||     |||||
                                GTCG CGCC CC     GACCG
                                  T   A  G_____
GAM203  LOC124801 5'  CAGCCGCGGCCGGCGG      4721          GGA  TC  T
                                CAGCCGCGGC   CG  GC GG
                                ||||||||||   ||  || ||
                                GTCGGCGCCG   GC  CG CC
                                     ___  __  _
GAM203  LOC145773 5'  GCGGCGGCCGCTGGCG      4722         ACG
                                GCGGCGG   TCGCTGGCG
                                |||||||   |||||||||
                                CGCCGCC   GGCGACCGC
                                     ___
GAM203  LOC221424 5'  GCTGCGGCGGAGGCTGC     4723     C       CGTC    G
                                GC GCGGCGGA    GCTG C
                                || ||||||||    |||| |
                                CG CGCCGCCT    CGAC G
                                 A       C___   _
GAM203  LOC221496 5'  GCCGCGGCGGGCCGGGC     4724          AC    CT
                                GCCGCGGCGG  GTCG  GGC
                                ||||||||||  ||||  |||
                                CGGCGCCGCC  CGGC  CCG
                                     __   __
GAM203  LOC51112  5'  GCCGAGGCCTCGCTGGC     4725       C   GGACG
                                GCCG GGC    TCGCTGGC
                                |||| |||    ||||||||
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                                CGGC CCG    AGCGACCG
                                  T  G____
GAM203  LOC51315  5' AGCCGCGGTGGAGGTGGC   4726       C  C  CGCT
                                AGCCGCGG GGA GT   GGC
                                |||||||| ||| ||   |||
                                TCGGCGCC CCT CA   CCG
                                   A  C  ____
GAM203  LOC51696  5' CAGCCGCGCGGGCGCCGC   4727       G  A
                                CAGCCGCG CGG CGTCGC
                                |||||||| ||| ||||||
                                GTCGGCGC GCC GCGGCG
                                   _  C
GAM203  LOC90850  3' CAGCTCTGGCCACGCTGGC   4728     CGC  GGA  T
                                CAGC  GGC  CG CGCTGGC
                                ||||  |||  || |||||||
                                GTCG  CCG  GT GCGACCG
                                  AGA  ___ _
GAM203  LOC91272  5' GCAGCGGCGGAGGTGGC    4729    C      C  CGCT
                                GC GCGGCGGA GT   GGC
                                || |||||||| ||   |||
                                CG CGCCGCCT CA   CCG
                                 T      C  ____
GAM203  LOC92002  5' GCTCGCGGCGGGCGTGCCG   4730   _     A  C
                                GC CGCGGCGG CGT GCTG
                                || |||||||| ||| ||||
                                CG GCGCCGCC GCA CGGC
                                 A      C  _
GAM204  ADCY7     3' CTGCTGCTCCCCGCCTTCTTGC 4733         _  GC
                                TTGCTGCTCTT GCT  TCTTGC
                                |||||||||||| |||  ||||||
                                GACGACGAGGG CGG  AGAACG
                                      G  A_
GAM204  ANK1      3' CTCCCCGCTTCTTGCTGCTTTT 4734     G   _     C
          G                      CTT CTGCT CTTGCTGCT TTG
                                 ||| ||||| ||||||||| |||
                                 GAG GGCGA GAACGACGA AAC
                                   G   A       A
GAM204  ANK1      3' CTCCCCGCTTCTTGCTGCTTTT 4734     G   _     C
          G                      CTT CTGCT CTTGCTGCT TTG
                                 ||| ||||| ||||||||| |||
                                 GAG GGCGA GAACGACGA AAC
                                   G   A       A
GAM204  ANK1      3' CTCCCCGCTTCTTGCTGCTTTT 4734     G   _     C
          G                      CTT CTGCT CTTGCTGCT TTG
                                 ||| ||||| ||||||||| |||
                                 GAG GGCGA GAACGACGA AAC
                                   G   A       A
GAM204  ANK1      3' CTCCCCGCTTCTTGCTGCTTTT 4734     G   _     C
          G                      CTT CTGCT CTTGCTGCT TTG
                                 ||| ||||| ||||||||| |||
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                                GAG GGCGA GAACGACGA AAC
                                  G    A       A
GAM204  ANK1    3'  CTCCCCGCTTCTTGCTGCTTTT 4734     G   _      C
                G                  CTT CTGCT CTTGCTGCT TTG
                                   ||| ||||| |||||||||| |||
                                   GAG GGCGA GAACGACGA AAC
                                     G    A       A
GAM204  BPGM    3'  TTGCTGCTTATTCTTG     4735        CTTGC  C
                                   TTGCTGCT    TG TCTTG
                                   ||||||||    || |||||
                                   AACGACGA    AT AGAAC
                                       _____ A
GAM204  CXorf6  5'  TCTTCCTGGGCTGCTCTTG   4736     G   CTCTT
                                   TCTT CTG    GCTGCTCTTG
                                   |||| |||    ||||||||||
                                   AGAA GAC    CGACGAGAAC
                                     G  C____
GAM204  KEL     5'  TCTGCTGCTCTTTCGCCTTG   4737     T      GC   T
                                   TCT GCTGCTCTT  TGC CTTG
                                   ||| |||||||||  ||| ||||
                                   AGA CGACGAGAA  GCG GAAC
                                    _       A_  _
GAM204  MLLT4   3'  GCTGCTCTTAAACATTTG    4738         CT  TC
                                   GCTGCTCTTG  GC  TTG
                                   ||||||||||  ||  |||
                                   CGACGAGAAT  TG  AAC
                                         T_  TA
GAM204  SCA2    3'  TCTTGTTACTTCTTTTGC    4739      C   _  GC
                                   TCTTG TGCT CTT  TGC
                                   ||||| |||| |||  |||
                                   AGAAC ATGA GAA  ACG
                                      A   A  A_
GAM204  AKR1B10 5'  TTGCTGTTTTTGAGACAGTCTT 4740       CTC  CT  __
                GC                   TTGCTG  TTG  GC  TCTTGC
                                     ||||||  |||  ||  ||||||
                                     AACGAC  AAC  TG  AGAACG
                                        AAA  TC  TC
GAM204  DICER1  5'  TCTGTGTTGCTCTTGTCTGAAC 4741     _ C      _  CT  T
                TGC                   TCT TG TGCTCTTG CTG  CT GC
                                      ||| || |||||||| |||  || ||
                                      AGA AC ACGAGAAC GAC  GA CG
                                        C  A       A  TT  _
GAM204  EPB41L1 3'  TCTTGCTGCTGTGACTTCTCTT 4742         CTT  G
                GC                    TCTTGCTGCT  GCT CTCTTGC
                                      ||||||||||  ||| |||||||
                                      AGAACGACGA  TGA GAGAACG
                                           CAC  A
GAM204  FLJ10350 3' TCTTGCCGCTCTTGCTCCTGC  4743          TGC
                                      TCTTGCTGCTCT  TGCTCTTGC
                                      ||||||||||||  |||||||||
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                                AGAACGGCGAGA  ACGAGGACG
                                              ____
GAM204  FLJ22418 3'  TCTTTTTGTTTCTTGCTCTTG 4744     GC  C_  TGC
                                TCTT  TG  TCT  TGCTCTTG
                                ||||  ||  |||  ||||||||
                                AGAA  AC  AGA  ACGAGAAC
                                  AA  AA  ___
GAM204  HTEX4    5'  TCTTGCTGCTGTTGTATGC   4745        C  C_
                                TCTTGCTGCT TTG  TGC
                                |||||||||| |||  |||
                                AGAACGACGA AAC  ACG
                                      C  AT
GAM204  HTEX4    5'  TCTTGCTGCTGTTGTATGC   4745        C  C_
                                TCTTGCTGCT TTG  TGC
                                |||||||||| |||  |||
                                AGAACGACGA AAC  ACG
                                      C  AT
GAM204  HTEX4    5'  TCTTGCTGCTGTTGTATGC   4745        C  C_
                                TCTTGCTGCT TTG  TGC
                                |||||||||| |||  |||
                                AGAACGACGA AAC  ACG
                                      C  AT
GAM204  KIAA0317 3'  TCTTACTGTTCTAATCTTTTGC 4746       C  TGCTG  C
                                TCTTGCTG TCT    CT TTGC
                                |||||||| |||    || ||||
                                AGAATGAC AGA    GA AACG
                                     A  TTA__  A
GAM204  KIAA0410 3'  TTCCTGCTCTTGCTGTTCT   4747    G        C
                                TT CTGCTCTTGCTG TCT
                                || ||||||||||| |||
                                AA GACGAGAACGAC AGA
                                 G         A
GAM204  KIAA0446 3'  TTGCTGCTCCTGCTCCCT    4748           G
                                TTGCTGCTCTTGCT CTCT
                                |||||||||||||| ||||
                                AACGACGAGGACGA GGGA
                                              _
GAM204  LIPG     3'  TCTTGCTGCCTTGCTGGC    4749        T    _
                                TCTTGCTGC CTTGCTG C
                                ||||||||| ||||||| |
                                AGAACGACG GAACGAC G
                                      _     C
GAM204  PLAC3    5'  TCTTGCTGTACTTTAGTCCTTG 4750       CT  GCTG T
           C                     TCTTGCTG  CTT   C CTTGC
                                ||||||||  |||   | |||||
                                AGAACGAC  GAA   G GAACG
                                     AT  ATCA _
GAM204  STK22D   3'  TCCTGCTGCTCTTCCTGCTCTT 4751           G
           GC                     TCTTGCTGCTCTT CTGCTCTTGC
                                ||||||||||||| ||||||||||
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                                AGGACGACGAGAA GACGAGAACG
                                      G
GAM204  TCL6     3'  TCTTGCTGCCTTGCACCTG   4752          T    TGCT
                                TCTTGCTGC CTTGC   CTTG
                                ||||||||| |||||   ||||
                                AGAACGACG GAACG   GGAC
                                     _    T___
GAM204  TCL6     3'  TCTTGCTGCCTTGCACCTG   4752          T    TGCT
                                TCTTGCTGC CTTGC   CTTG
                                ||||||||| |||||   ||||
                                AGAACGACG GAACG   GGAC
                                     _    T___
GAM204  LOC115073 5' CTGCAGACTGCTGCTCTTGC  4753       TC_
                                CTGC  TTGCTGCTCTTGC
                                ||||  ||||||||||||
                                GACG  GACGACGAGAACG
                                  TCT
GAM204  LOC115442 3' TCTTGCTTTTCTGCTTTTG   4754        GCTCTTG    C
                                TCTTGCT      CTGCT TTG
                                |||||||      ||||| |||
                                AGAACGA      GACGA AAC
                                    AAA____    A
GAM204  LOC142955 5' TCTTGCCTGCTTCTCTTG    4755        GCTCT   G
                                TCTTGCT    TGCT CTCTTG
                                |||||||    |||| ||||||
                                AGAACGG    ACGA GAGAAC
                                     _____   A
GAM204  LOC146435 5' TCCTGCTGAGCTGTTCTTG   4756         CTCTT   C
                                TCTTGCTG    GCTG TCTTG
                                ||||||||    |||| |||||
                                AGGACGAC    CGAC AGAAC
                                    T____   A
GAM204  LOC148738 3' TCTTCTGCTTTCAGCTCTTGC 4757       G    CTTGCT
                                TCTT CTGCT     GCTCTTGC
                                |||| |||||     ||||||||
                                AGAA GACGA     CGAGAACG
                                  _    AAGT__
GAM204  LOC152343 3' TCTTGCTCTCTTGCCATGTGCA 4758       G     T_______  TCTT
           AGG                    TGCT CTCTTGC       GC   G
                                |||| |||||||       ||   |
                                ACGA GAGAACG       CG   C
                                  _      GTACAIII  TTCT
GAM204  LOC154007 3' TCTTGCTCTTCTTGCCAATGAT 4759        GC      GCTC_
           TGC                    TCTTGCT  TCTTGCT    TTGC
                                |||||||  |||||||    ||||
                                AGAACGA  AGAACGG    AACG
                                    GA      TTACT
GAM204  LOC200010 3' TCTTCCTGCTCCTTTTCTTG  4760       G      GCTGC
                                TCTT CTGCTCTT    TCTTG
                                |||| ||||||||    |||||
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                                AGAA GACGAGGA     AGAAC
                                  G       AA___
GAM204  LOC220980 5'  TCTTGTTCTCTTGCTGTCGTCT 4761       CTG       C__
            TGC                    TCTTG   CTCTTGCTG   TCTTGC
                                |||||   |||||||||   ||||||
                                AGAAC   GAGAACGAC   AGAACG
                                  AA_       AGC
GAM204  LOC222160 3'  TGTTGCTCAGGCTGCTTTTGC  4762     C     TT     C
                                TG TGCTC  GCTGCT TTGC
                                || |||||  |||||| ||||
                                AC ACGAG  CGACGA AACG
                                 A    TC     A
GAM204  LOC253148 5'  TCTTGCTCCTCTTGCCGTG    4763         G        CTCT
                                TCTTGCT CTCTTGCTG    TG
                                |||||||| |||||||||    ||
                                AGAACGA GAGAACGGC    AC
                                   G        _____
GAM204  LOC90495  3'  TCTTTTGCTCACTGCCCTCTTG 4764       GC    _    G
                                TCTT  TGCTC TTGCT CTCTTG
                                ||||  ||||| ||||| ||||||
                                AGAA  ACGAG GACGG GAGAAC
                                  A_    T    _
GAM205  ABCD1    3'  GGCTGCGCTGCTGTGTGGC    4767         C    CAGC
                                GGTTGCGC GCTG    GGC
                                |||||||| ||||    |||
                                CCGACGCG CGAC    CCG
                                     A    ACA_
GAM205  DPYSL3    5'  GGTGGTGGCTGCAGCGGCTGGC 4768      TGCGCC
                                GGT     GCTGCAGCGGCTGGC
                                |||     ||||||||||||||||
                                CCA     CGACGTCGCCGACCG
                                  CCAC__
GAM205  RHBG     5'  GGTTGGGCTGCGATCTCGGCTG 4769       CGCC     AG___
            GC                    GGTTG    GCTGC    CGGCTGGC
                                |||||    |||||    ||||||||
                                CCAAC    CGACG    GCCGACCG
                                  C___     CTAGA
GAM205  ARHGEF16  3'  GGCTGTGCTGCCGCCGGCTGGC 4770       C  C     AG
                                GGTTG GC GCTGC  CGGCTGGC
                                ||||| || |||||  ||||||||
                                CCGAC CG CGGCG  GCCGACCG
                                  A  A    __
GAM205  EPN2     5'  GGTGCGCCGCTGCGGCCACCGG 4771      T        A  G
            C                     GGT GCGCCGCTGC GC GCTGGC
                                ||| ||||||||| || ||||||
                                CCA CGCGGCGACG CG TGGCCG
                                  _        C  G
GAM205  FLJ13441  3'  GGCTGTCATGCAGCGGTTGGC  4772        _  CCGC       C
                                GGTTG CG    TGCAGCGG TGGC
                                ||||| ||    |||||||| ||||
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                                CCGAC GT   ACGTCGCC ACCG
                                  A ____      A
GAM205  KIAA1100 5' GGTCTGCGCGGCAGCCGGCGGC 4773     _    C  T  A_
           TGGC                   GGT TGCGC GC GC  GCGGCTGGC
                                ||| ||||| || ||  |||||||||
                                CCA ACGCG CG CG  CGCCGACCG
                                  G    C  T  GC
GAM205  LGALS4   5' GGCTGCGCTAGTGGCTGG    4774         CGCTGC  C
                                GGTTGCGC     AG GGCTGG
                                ||||||||     || ||||||
                                CCGACGCG     TC CCGACC
                                     A_____  A
GAM206  CD59     3' AAAGACAGAGGAAAAACTC    4777        C  TAT
                                AAAGAC GA   GGAAACTC
                                |||||| ||   ||||||||
                                TTTCTG CT   TTTTTGAG
                                    T  CC_
GAM206  CR1      3' TCAAAGACTTTATGAAGCTCA  4778         CGA     AA
                                TCAAAGAC   TATGGA  CTCA
                                ||||||||   ||||||  ||||
                                AGTTTCTG   ATACTT  GAGT
                                     AA_     C_
GAM206  FGA      3' TCAAAGACTAATATGTCTCA   4779         CG    GAAA
                                TCAAAGAC  ATATG    CTCA
                                ||||||||  |||||    ||||
                                AGTTTCTG  TATAC    GAGT
                                     AT    A___
GAM206  GALR1    3' CCACTTATATGGAAACTCAA   4780      ___
                                CCG   ATATGGAAACTCAA
                                |||   ||||||||||||||
                                GGT   TATACCTTTGAGTT
                                  GAA
GAM206  NOL3     5' AGGCCAACACGGGGAACTC    4781     A       A_
                                AG CCGATATGG  AACTC
                                || |||||||||  |||||
                                TC GGTTGTGCC  TTGAG
                                 C        CC
GAM206  NOX4     5' TCAAAGACTGAGTGGAAGCCC  4782         C  TA    A
                                TCAAAGAC GA  TGGAA CTC
                                |||||||| ||  ||||| |||
                                AGTTTCTG CT  ACCTT GGG
                                     A  C_    C
GAM206  PPP2R5C  3' AAGACCGATGAAAACTCA    4783         TA
                                AAGACCGA  TGGAAACTCA
                                ||||||||  ||||||||||
                                TTCTGGCT  ACTTTTGAGT
                                          __
GAM206  PRDM2    3' TCAAGAGCCAGAAACTCA     4784      A  _  GATAT
                                TCAA GA CC    GGAAACTCA
                                |||| || ||    |||||||||
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                                AGTT CT GG    TCTTTGAGT
                                  _ C _____
GAM206  RFC2    5' CCGAGAAATGGAAACTCA   4785     T__
                                CCGA  ATGGAAACTCA
                                ||||  ||||||||||
                                GGCT  TACCTTTGAGT
                                  CTT
GAM206  SON     3' TCATGGACCAATAGAAATTCA 4786    AA    AT   C
                                TCA GACCGAT GGAAA TCA
                                |||  |||||||  ||||| |||
                                AGT CTGGTTA TCTTT AGT
                                  AC     __    A
GAM206  SON     3' TCATGGACCAATAGAAATTCA 4786    AA    AT   C
                                TCA GACCGAT GGAAA TCA
                                |||  |||||||  ||||| |||
                                AGT CTGGTTA TCTTT AGT
                                  AC     __    A
GAM206  VWF     5' CCAAGGTCCCTGGGAAACTCA 4787    AGA_ GATAT
                                TCAA   CC   GGAAACTCA
                                ||||   ||   |||||||||
                                GGTT   GG   CCTTTGAGT
                                  CCAG AC___
GAM206  VWF     5' CCAAGGTCCCTGGGAAACTCA 4787    AGA_ GATAT
                                TCAA   CC   GGAAACTCA
                                ||||   ||   |||||||||
                                GGTT   GG   CCTTTGAGT
                                  CCAG AC___
GAM206  ZNF80   5' AGACTGCAGGGAAACTCAA   4788    CGA T
                                AGAC  TA GGAAACTCAA
                                ||||  || ||||||||||
                                TCTG  GT CCTTTGAGTT
                                  AC_ C
GAM206  DKFZp762M136 3' TCTAAGGAGAATGGAAACT   4789    A  ACC T
                                TC AAG  GA ATGGAAACT
                                || |||  || |||||||||
                                AG TTC  CT TACCTTTGA
                                 A  CT_ _
GAM206  FLJ10213 3' TCAAAGACTGGGATCTCA   4790      CGATA  AAA
                                TCAAAGAC   TGG  CTCA
                                ||||||||   |||  ||||
                                AGTTTCTG   ACC  GAGT
                                     _____  CTA
GAM206  FLJ11011 3' TCAAAGACTGAATGATCA   4791      C  T   AAAC
                                TCAAAGAC GA ATGG   TCA
                                |||||||| || ||||   |||
                                AGTTTCTG CT TACT   AGT
                                     A _   ____
GAM206  KIAA0061 3' AAGCCATATGTGGAAACT   4792    A  _ A
                                AAG CCG AT TGGAAACT
                                ||| ||| || ||||||||
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                                TTC GGT TA ACCTTTGA
                                  _  A  C
GAM206  KIAA0229  3'  TCAAAGACAGACCCAATTCA  4793        C  ATGGA  C
                                TCAAAGAC GAT    AA TCA
                                |||||||| |||    || |||
                                AGTTTCTG CTG    TT AGT
                                     T  GG___  A
GAM206  KIAA1145  3'  TCAAAGACGATGCTCTCA   4794        C  ATGGAAA
                                TCAAAGAC GAT     CTCA
                                |||||||| |||     ||||
                                AGTTTCTG CTA     GAGT
                                     _  CGA____
GAM206  KIAA1354  3'  TCAAAGATGAAAACTC     4795        CCGATA
                                TCAAAGA    TGGAAACTC
                                |||||||    |||||||||
                                AGTTTCT    ACTTTTGAG
                                  _______
GAM206  KIAA1610  3'  AAAGACATTTCAAGAAACTCA  4796       CGATAT
                                AAAGAC     GGAAACTCA
                                ||||||     |||||||||
                                TTTCTG     TCTTTGAGT
                                   TAAAGT
GAM206  KIAA1673  3'  AAAAACTATATGGAAATTCA  4797       CG       C
                                AAAGAC  ATATGGAAA TCA
                                ||||||  ||||||||| |||
                                TTTTTG  TATACCTTT AGT
                                   A_       A
GAM206  OSRF      3'  TCAAAGACCATTTTACTCA   4798         ATATGGAA
                                TCAAAGACCG      ACTCA
                                ||||||||||      |||||
                                AGTTTCTGGT      TGAGT
                                     AAAA____
GAM206  RBM9      3'  TCAAAGACCAGAAACTCA    4799         GATAT
                                TCAAAGACC    GGAAACTCA
                                |||||||||    |||||||||
                                AGTTTCTGG    TCTTTGAGT
                                  _____
GAM206  RENT2     3'  AGAGACACTGAAACTCA     4800     CC    G
                                AGA  GATAT GAAACTCA
                                |||  ||||| ||||||||
                                TCT  CTGTG CTTTGAGT
                                  __    A
GAM206  RENT2     3'  AGAGACACTGAAACTCA     4800     CC    G
                                AGA  GATAT GAAACTCA
                                |||  ||||| ||||||||
                                TCT  CTGTG CTTTGAGT
                                  __    A
GAM206  STAF65(gamma) 5'  TCAAAGACTGATAATGTGA   4801         C  _ _
                                TCAAAGAC GATA TG GA
                                |||||||| |||| || ||
```

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                                AGTTTCTG CTAT AC CT
                                     A   T  A
GAM206  LOC132949 5'  AAAAACCTAGTGGAATTCA   4802       GATA    AC
                                AAAGACC   TGGAA  TCA
                                |||||||   |||||  |||
                                TTTTTGG   ACCTT  AGT
                                    ATC_    A_
GAM206  LOC146475 5'  TCAAAGACTGAGGCTCTCA   4803        C  TAT  AAA
                                TCAAAGAC GA   GG   CTCA
                                |||||||| ||   ||   ||||
                                AGTTTCTG CT   CC   GAGT
                                     A  ___  GA_
GAM206  LOC148936 3'  TCAAAGACATCTTGGAGTTCA  4804        CGATA   AAC
                                TCAAAGAC    TGGA   TCA
                                ||||||||    ||||  |||
                                AGTTTCTG    ACCT   AGT
                                     TAGA_   CA_
GAM206  LOC148938 3'  TCAAAGACATCTTGGAGTTCA  4804        CGATA   AAC
                                TCAAAGAC    TGGA   TCA
                                ||||||||    ||||  |||
                                AGTTTCTG    ACCT   AGT
                                     TAGA_   CA_
GAM206  LOC152018 5'  GAACAATATGGAAACTCAA   4805     C
                                GA CGATATGGAAACTCAA
                                || ||||||||||||||||
                                CT GTTATACCTTTGAGTT
                                 T
GAM206  LOC152762 5'  TCAAAGACGACCAACAGAGGCT 4806         C  __    AA
                                TCAAAGAC GAT  ATGGA  CT
                                |||||||| |||  |||||  ||
                                AGTTTCTG CTG  TGTCT  GA
                                     _  GT    CC
GAM206  LOC154860 5'  TCAAAGACCTGTCCCAGGCTCA 4807         GATAT__  AAA
                                TCAAAGACC      GG   CTCA
                                |||||||||      ||   ||||
                                AGTTTCTGG      CC   GAGT
                                     ACAGGGT  ___
GAM206  LOC157623 5'  AGAGACAAGGAAACTCA     4808     CC    T
                                AGA  GATA GGAAACTCA
                                |||  |||| |||||||||
                                TCT  CTGT CCTTTGAGT
                                  __    T
GAM206  LOC221303 3'  TCAAAGGTGATGAAACTCA   4809       ACC   ATG
                                TCAAAG   GAT   GAAACTCA
                                ||||||   |||   ||||||||
                                AGTTTC   CTA   CTTTGAGT
                                   CA_   ___
GAM206  LOC51145  3'  TCAAAGAAGAATTGGAAACT   4810        CC   A
                                TCAAAGA  GAT TGGAAACT
                                |||||||  ||| ||||||||
```

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                                AGTTTCT  TTA ACCTTTGA
                                   TC  _
GAM207  ACP5    3' TGCCTGTGAGCAGGGTCCCGG 4813      CA      TACAC
                                TGCC  TGAGCAGG    TTTGG
                                ||||  ||||||||    |||||
                                ACGG  ACTCGTCC    GGGCC
                                  AC      CA___
GAM207  APM1    3' TGCCTGTAATCCCAGCACTTTG 4814      CA  G__  GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC  AGG   ___
GAM207  APM1    3' TGCCTGTAATCCCAGCACTTTG 4814      CA  G__  GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC  AGG   ___
GAM207  ARCN1   3' TGCCTGTAATCCCAACACTTTG 4815      CA  GCAGGT
           G                     TGCC  TGA    ACACTTTGG
                                ||||  |||    |||||||||
                                ACGG  ATT    TGTGAAACC
                                  AC  AGGGT_
GAM207  AXL     3' TGCCTGTAATCTCAGCACTTTG 4816      CA  G__  GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC  AGA   ___
GAM207  AXL     3' TGCCTGTAATCTCAGCACTTTG 4816      CA  G__  GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC  AGA   ___
GAM207  BAZ2B   5' TGCCTGTAATCCCAGCACTTTG 4814      CA  G__  GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC  AGG   ___
GAM207  CBFA2T2  3' TGCCTGTAATCCTGGCACTTTG 4817      CA  GCA_  TA
           G                     TGCC  TGA   GG  CACTTTGG
                                ||||  |||   ||  ||||||||
                                ACGG  ATT   CC  GTGAAACC
                                  AC  AGGA  __
GAM207  CCNF    3' TGCCTGTAATCCCAGCACTTTG 4814      CA  G__  GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC  AGG   ___
GAM207  CLECSF11 5' TGCCTATAATCTCAGCACTTTG 4818      C   G__  GTA
           G                     TGCC ATGA   CAG   CACTTTGG
                                ||||  ||||   |||   ||||||||
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                                ACGG TATT  GTC  GTGAAACC
                                  A  AGA  ___
GAM207  COX15    3' TGCCTGTAATCTCAGCACTTTG 4816     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGA  ___
GAM207  CYP2B6   3' TGCCTGTAATATCAGCACTTTG 4819     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  ATA  ___
GAM207  CYP51    3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  DFFB     3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  DNASE1L1 5' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  DSC3     3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  DSC3     3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  FCAR     3' TGCCTATAATCTCAGCACTTTG 4818     C   G__  GTA
           G                     TGCC ATGA  CAG  CACTTTGG
                                 |||| ||||  |||  ||||||||
                                ACGG TATT  GTC  GTGAAACC
                                  A  AGA  ___
GAM207  FCAR     3' TGCCTATAATCTCAGCACTTTG 4818     C   G__  GTA
           G                     TGCC ATGA  CAG  CACTTTGG
                                 |||| ||||  |||  ||||||||
                                ACGG TATT  GTC  GTGAAACC
                                  A  AGA  ___
GAM207  FCAR     3' TGCCTATAATCTCAGCACTTTG 4818     C   G__  GTA
           G                     TGCC ATGA  CAG  CACTTTGG
                                 |||| ||||  |||  ||||||||
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                                ACGG TATT   GTC   GTGAAACC
                                  A   AGA   ___
GAM207  FCAR    3' TGCCTATAATCTCAGCACTTTG 4818      C   G__   GTA
          G                      TGCC ATGA   CAG   CACTTTGG
                                 |||| ||||   |||   ||||||||
                                ACGG TATT   GTC   GTGAAACC
                                  A   AGA   ___
GAM207  FCAR    3' TGCCTATAATCTCAGCACTTTG 4818      C   G__   GTA
          G                      TGCC ATGA   CAG   CACTTTGG
                                 |||| ||||   |||   ||||||||
                                ACGG TATT   GTC   GTGAAACC
                                  A   AGA   ___
GAM207  HTR1D   3' TGCCTGTAATCCCAGCACTTTG 4814      CA  G__   GTA
          G                      TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  LAMA4   3' TGTCCATTGCAGACACTTTGG  4820    C   GA   GT
                                TG CCAT  GCAG  ACACTTTGG
                                || ||||  ||||  |||||||||
                                AC GGTA  CGTC  TGTGAAACC
                                 A   A_   __
GAM207  MDM2    3' TGCCTGTAATCCCAGCACTTTG 4814      CA  G__   GTA
          G                      TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  MDM2    3' TGCCTGTAATCCCAGCACTTTG 4814      CA  G__   GTA
          G                      TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  MDM2    3' TGCCTGTAATCCCAGCACTTTG 4814      CA  G__   GTA
          G                      TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  MDM2    3' TGCCTGTAATCCCAGCACTTTG 4814      CA  G__   GTA
          G                      TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  MDM2    3' TGCCTGTAATCCCAGCACTTTG 4814      CA  G__   GTA
          G                      TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  MDM2    3' TGCCTGTAATCCCAGCACTTTG 4814      CA  G__   GTA
          G                      TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  MEFV    3' TGCCTGTAATCCCAGCACTTTG 4814      CA  G__   GTA
          G                      TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
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                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  MEFV    3' TGCCTGTAATCCCTGCACTTTG 4821     CA  GCAGGTA
           G                     TGCC TGA    CACTTTGG
                                 |||| |||    ||||||||
                                ACGG ATT    GTGAAACC
                                  AC  AGGGAC_
GAM207  MPL     3' TGCCTGTAATCCTAACACTTTG 4822     CA  GCAGGT
           G                     TGCC TGA    ACACTTTGG
                                 |||| |||    |||||||||
                                ACGG ATT    TGTGAAACC
                                  AC  AGGAT_
GAM207  NAGA    3' GCCGTGAGATTGCACTTTGG  4823     CA  CAGGTA
                                GCC TGAG    CACTTTGG
                                ||| ||||    ||||||||
                                CGG ACTC    GTGAAACC
                                  C_  TAAC__
GAM207  NDRG3   3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  PDE1B   3' TGCTGATGACATCAAACACTTT 4824     CC  G GGT_
           GG                    TGC ATGA CA   ACACTTTGG
                                 ||| |||| ||   |||||||||
                                ACG TACT GT   TGTGAAACC
                                  AC  _ AGTT
GAM207  PIK3CD  3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  PPEF2   3' TGCCTATGAGGCACTTTG   4825     C   CAGGTA
                                TGCC ATGAG    CACTTTG
                                |||| |||||    |||||||
                                ACGG TACTC    GTGAAAC
                                  A   C_____
GAM207  PPEF2   3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  PTGES   3' TGCCTGTCATCCCAGCACTTTG 4826     ___  GAG  GTA
           G                     TGCC  CAT  CAG  CACTTTGG
                                 ||||  |||  |||  ||||||||
                                ACGG  GTA  GTC  GTGAAACC
                                  ACA  GG_  ___
GAM207  PTGIS   3' TGCCTGTAATCCTAGCACTTTG 4827     CA  GCAGGTA
           G                     TGCC TGA    CACTTTGG
                                 |||| |||    ||||||||
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                              ACGG ATT     GTGAAACC
                                AC  AGGATC_
GAM207  RABL2A   3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                   TGCC TGA  CAG  CACTTTGG
                               |||| |||  |||  ||||||||
                              ACGG ATT  GTC  GTGAAACC
                                AC  AGG  ___
GAM207  RABL2B   3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                   TGCC TGA  CAG  CACTTTGG
                               |||| |||  |||  ||||||||
                              ACGG ATT  GTC  GTGAAACC
                                AC  AGG  ___
GAM207  RBBP9    3' TGCCTGTAATCCCAACACTTTG 4815     CA  GCAGGT
           G                   TGCC TGA    ACACTTTGG
                               |||| |||    |||||||||
                              ACGG ATT    TGTGAAACC
                                AC  AGGGT_
GAM207  SCNN1G   3' TGCCTGTAATCCCTGCACTTTG 4821     CA  GCAGGTA
           G                   TGCC TGA    CACTTTGG
                               |||| |||    ||||||||
                              ACGG ATT    GTGAAACC
                                AC  AGGGAC_
GAM207  SEDL     3' TGCCTGTAATCCTAGCACTTTG 4827     CA  GCAGGTA
           G                   TGCC TGA    CACTTTGG
                               |||| |||    ||||||||
                              ACGG ATT    GTGAAACC
                                AC  AGGATC_
GAM207  SERPINB9 3' TGCCTGTAATCCTAGCACTTTG 4827     CA  GCAGGTA
           G                   TGCC TGA    CACTTTGG
                               |||| |||    ||||||||
                              ACGG ATT    GTGAAACC
                                AC  AGGATC_
GAM207  SH3BP2   3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                   TGCC TGA  CAG  CACTTTGG
                               |||| |||  |||  ||||||||
                              ACGG ATT  GTC  GTGAAACC
                                AC  AGG  ___
GAM207  SHOX     3' TGCTTGTAATTCTAACACTTTG 4828     CCA  GCAGGT
           G                   TGC  TGA    ACACTTTGG
                               |||  |||    |||||||||
                              ACG  ATT    TGTGAAACC
                                AAC  AAGAT_
GAM207  SNX15    3' TGCCTGTAATCTCAGCACTTTG 4816     CA  G__  GTA
           G                   TGCC TGA  CAG  CACTTTGG
                               |||| |||  |||  ||||||||
                              ACGG ATT  GTC  GTGAAACC
                                AC  AGA  ___
GAM207  STAT6    3' TGTCCAGAGCAGGTCTGTG   4829    C  T     ACA  T
                              TG CCA GAGCAGGT  CT TG
                              || ||| ||||||||  || ||
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                                AC GGT CTCGTCCA  GA AC
                                 A  _      ___  C
GAM207  TBXA2R   3'  TGCCTGTGATCCCAGCACTTTG 4830     CA  G__  GTA
           G                     TGCC  TGA  CAG  CACTTTGG
                                 ||||  |||  |||  ||||||||
                                 ACGG  ACT  GTC  GTGAAACC
                                   AC  AGG  ___
GAM207  TERF2    3'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC  TGA  CAG  CACTTTGG
                                 ||||  |||  |||  ||||||||
                                 ACGG  ATT  GTC  GTGAAACC
                                   AC  AGG  ___
GAM207  TRAF5    3'  TGCCTGTAATCTCAGCACTTTG 4816     CA  G__  GTA
           G                     TGCC  TGA  CAG  CACTTTGG
                                 ||||  |||  |||  ||||||||
                                 ACGG  ATT  GTC  GTGAAACC
                                   AC  AGA  ___
GAM207  TSG      3'  TGCCTATGTCAGCACTTTG   4831     C  AG  GTA
                                 TGCC ATG  CAG  CACTTTG
                                 ||||  |||  |||  |||||||
                                 ACGG TAC  GTC  GTGAAAC
                                   A  A_  ___
GAM207  VENTX2   3'  TGCCCGTAATCCCAGCACTTTG 4832      A  G__  GTA
           G                     TGCCC TGA  CAG  CACTTTGG
                                 |||||  |||  |||  ||||||||
                                 ACGGG ATT  GTC  GTGAAACC
                                    C  AGG  ___
GAM207  WHSC1    5'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC  TGA  CAG  CACTTTGG
                                 ||||  |||  |||  ||||||||
                                 ACGG  ATT  GTC  GTGAAACC
                                   AC  AGG  ___
GAM207  WHSC1    5'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC  TGA  CAG  CACTTTGG
                                 ||||  |||  |||  ||||||||
                                 ACGG  ATT  GTC  GTGAAACC
                                   AC  AGG  ___
GAM207  WHSC1    5'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC  TGA  CAG  CACTTTGG
                                 ||||  |||  |||  ||||||||
                                 ACGG  ATT  GTC  GTGAAACC
                                   AC  AGG  ___
GAM207  WHSC1    5'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC  TGA  CAG  CACTTTGG
                                 ||||  |||  |||  ||||||||
                                 ACGG  ATT  GTC  GTGAAACC
                                   AC  AGG  ___
GAM207  ARHGAP11A 3'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC  TGA  CAG  CACTTTGG
                                 ||||  |||  |||  ||||||||
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                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  C20orf142 3'  TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  C22orf19  3'  TGCCTATAATCCTAGCACTTTG 4833      C    GCAGGTA
           G                     TGCC ATGA      CACTTTGG
                                |||| ||||      ||||||||
                                ACGG TATT      GTGAAACC
                                  A   AGGATC_
GAM207  C2F     3'  TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  CIP29    3'  TGCCTGTAATCCAGCACTTTGG 4834      CA   G_   GTA
                                TGCC  TGA  CAG   CACTTTGG
                                ||||  |||  |||   ||||||||
                                ACGG  ATT  GTC   GTGAAACC
                                  AC   AG   ___
GAM207  CPSF2    3'  TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  DCOHM    3'  TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  DKFZP434F0318 3'  TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  DKFZp434F1719 3'  TGCCTGTAATCCCAACACTTTG 4815      CA   GCAGGT
           G                     TGCC  TGA     ACACTTTGG
                                ||||  |||     |||||||||
                                ACGG  ATT     TGTGAAACC
                                  AC   AGGGT_
GAM207  FKBP9    3'  TGCCTGTAATCCCAACACTTTG 4815      CA   GCAGGT
           G                     TGCC  TGA     ACACTTTGG
                                ||||  |||     |||||||||
                                ACGG  ATT     TGTGAAACC
                                  AC   AGGGT_
GAM207  FKSG42   3'  CCATGAGCAGCATTTG      4835          GTA  C
                                CCATGAGCAG   CA TTTG
                                ||||||||||   || ||||
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                          GGTACTCGTC  GT AAAC
                                ___  _
GAM207  FLB6421  3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                 TGCC  TGA  CAG  CACTTTGG
                             |||| |||  |||  ||||||||
                             ACGG  ATT  GTC  GTGAAACC
                               AC  AGG  ___
GAM207  FLJ10298 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                 TGCC  TGA  CAG  CACTTTGG
                             |||| |||  |||  ||||||||
                             ACGG  ATT  GTC  GTGAAACC
                               AC  AGG  ___
GAM207  FLJ10535 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                 TGCC  TGA  CAG  CACTTTGG
                             |||| |||  |||  ||||||||
                             ACGG  ATT  GTC  GTGAAACC
                               AC  AGG  ___
GAM207  FLJ10713 3' TGCCCATAGTCCCAGCATTTTG 4836       AGCA_  CAC
           G                 TGCCCATG   GGTA  TTTGG
                             ||||||||   ||||  |||||
                             ACGGGTAT   TCGT  AAACC
                                CAGGG   A__
GAM207  FLJ10847 3' TGCCTATAATCCCAACACTTTG 4837     C  GCAGGT
           G                 TGCC ATGA    ACACTTTGG
                             |||| ||||    |||||||||
                             ACGG TATT    TGTGAAACC
                               A  AGGGT_
GAM207  FLJ11186 3' TGCCTGTAATCCCAACACTTTG 4815     CA  GCAGGT
           G                 TGCC  TGA    ACACTTTGG
                             |||| |||    |||||||||
                             ACGG  ATT    TGTGAAACC
                               AC  AGGGT_
GAM207  FLJ12610 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                 TGCC  TGA  CAG  CACTTTGG
                             |||| |||  |||  ||||||||
                             ACGG  ATT  GTC  GTGAAACC
                               AC  AGG  ___
GAM207  FLJ12700 3' TGCCTGGAGCAGGTCCCATGG  4838     CAT     ACA  T
                          TGCC  GAGCAGGT  CT TGG
                          ||||  ||||||||  || |||
                          ACGG  CTCGTCCA  GG ACC
                            AC_     G__  T
GAM207  FLJ12975 3' TGCCTGTAATCTCAGCACTTTG 4816     CA  G__  GTA
           G                 TGCC  TGA  CAG  CACTTTGG
                             |||| |||  |||  ||||||||
                             ACGG  ATT  GTC  GTGAAACC
                               AC  AGA  ___
GAM207  FLJ13102 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                 TGCC  TGA  CAG  CACTTTGG
                             |||| |||  |||  ||||||||
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                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  FLJ13193 3' TGCCTGTGATCCCAGCACTTTG 4830     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ACT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  FLJ13305 5' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  FLJ14957 3' TGCCTGTAATCTCAGCACTTTG 4816     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGA  ___
GAM207  FLJ20045 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  FLJ20097 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  FLJ20136 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  FLJ20344 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  FLJ20507 3' TGCCTATAATCCCAGCACTTTG 4839     C   G__  GTA
           G                     TGCC ATGA  CAG  CACTTTGG
                                 |||| ||||  |||  ||||||||
                                ACGG TATT  GTC  GTGAAACC
                                  A   AGG  ___
GAM207  FLJ20507 3' TGCCTATAATCCCAGCACTTTG 4839     C   G__  GTA
           G                     TGCC ATGA  CAG  CACTTTGG
                                 |||| ||||  |||  ||||||||
                                ACGG TATT  GTC  GTGAAACC
                                  A   AGG  ___
GAM207  FLJ20671 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
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                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  FLJ21302 3' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  FLJ22316 5' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  FLJ22329 3' TGCCTGTAACCCTAGCACTTTG 4840    CATG  AGGTA
           G                     TGCC  AGC   CACTTTGG
                                 ||||  |||   ||||||||
                                ACGG  TTG   GTGAAACC
                                  ACA_  GGATC
GAM207  FLJ22684 3' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  FLJ23024 3' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  GTPBG3   3' GCCTGTGATCCCAGCACTTTGG 4841    CA  G__  GTA
                                GCC TGA  CAG  CACTTTGG
                                ||| |||  |||  ||||||||
                                CGG ACT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  HRH4     3' TGCCTATAATCCCAGCACTTTG 4839     C   G__  GTA
           G                     TGCC ATGA  CAG  CACTTTGG
                                 |||| ||||  |||  ||||||||
                                ACGG TATT  GTC  GTGAAACC
                                  A  AGG  ___
GAM207  HSMPP8   3' TGCCTGTAATCCAAGCACTTTG 4842    CA  G_  TA
           G                     TGCC TGA CAGG CACTTTGG
                                 |||| ||| |||| ||||||||
                                ACGG ATT GTTC GTGAAACC
                                  AC  AG  __
GAM207  KIAA0090 3' TGCCTGTAATCCCGGCACTTTG 4843    CA  GCA_  TA
           G                     TGCC TGA  GG CACTTTGG
                                 |||| |||  || ||||||||
                                ACGG ATT  CC GTGAAACC
                                  AC  AGGG __
GAM207  KIAA0173 3' TGCTCCTGGGCAGAGGCTTTTG 4844    _ A A   TACAC
           G                     TGC CC TG GCAGG   TTTGG
                                 ||| || || |||||   |||||
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                          ACG GG AC CGTCT    AAACC
                            A _ C    CCGA_
GAM207  KIAA0326 3' GCCTGTGAGCAGGCTTG    4845     CA      ACACT
                          GCC  TGAGCAGGT    TTG
                          |||  |||||||||    |||
                          CGG  ACTCGTCCG    AAC
                            AC       _____
GAM207  KIAA0469 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                 TGCC  TGA   CAG   CACTTTGG
                             ||||  |||   |||   ||||||||
                             ACGG  ATT   GTC   GTGAAACC
                               AC  AGG   ___
GAM207  KIAA0475 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                 TGCC  TGA   CAG   CACTTTGG
                             ||||  |||   |||   ||||||||
                             ACGG  ATT   GTC   GTGAAACC
                               AC  AGG   ___
GAM207  KIAA0562 3' TGCCTGTAATTCCAGCACTTTG 4846     CA  G__  GTA
           G                 TGCC  TGA   CAG   CACTTTGG
                             ||||  |||   |||   ||||||||
                             ACGG  ATT   GTC   GTGAAACC
                               AC  AAG   ___
GAM207  KIAA0737 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                 TGCC  TGA   CAG   CACTTTGG
                             ||||  |||   |||   ||||||||
                             ACGG  ATT   GTC   GTGAAACC
                               AC  AGG   ___
GAM207  KIAA0798 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                 TGCC  TGA   CAG   CACTTTGG
                             ||||  |||   |||   ||||||||
                             ACGG  ATT   GTC   GTGAAACC
                               AC  AGG   ___
GAM207  KIAA0841 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                 TGCC  TGA   CAG   CACTTTGG
                             ||||  |||   |||   ||||||||
                             ACGG  ATT   GTC   GTGAAACC
                               AC  AGG   ___
GAM207  KIAA1143 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                 TGCC  TGA   CAG   CACTTTGG
                             ||||  |||   |||   ||||||||
                             ACGG  ATT   GTC   GTGAAACC
                               AC  AGG   ___
GAM207  KIAA1161 5' TGCCTGTAATCCCAACACTTTG 4815     CA  GCAGGT
           G                 TGCC  TGA    ACACTTTGG
                             ||||  |||    |||||||||
                             ACGG  ATT    TGTGAAACC
                               AC  AGGGT_
GAM207  KIAA1200 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                 TGCC  TGA   CAG   CACTTTGG
                             ||||  |||   |||   ||||||||
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                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  KIAA1349 5' TGCCTATAATCTCAGCACTTTG 4818      C    G__   GTA
            G                    TGCC ATGA   CAG   CACTTTGG
                                ||||  ||||   |||   ||||||||
                                ACGG TATT   GTC   GTGAAACC
                                  A    AGA   ___
GAM207  KIAA1373 3' TGCCTATAATCTCAGCACTTTG 4818      C    G__   GTA
            G                    TGCC ATGA   CAG   CACTTTGG
                                ||||  ||||   |||   ||||||||
                                ACGG TATT   GTC   GTGAAACC
                                  A    AGA   ___
GAM207  KIAA1443 3' TGCCTATAATCCCAGCACTTTG 4839      C    G__   GTA
            G                    TGCC ATGA   CAG   CACTTTGG
                                ||||  ||||   |||   ||||||||
                                ACGG TATT   GTC   GTGAAACC
                                  A    AGG   ___
GAM207  KIAA1530 3' TGCCTGTAATCCCAACACTTTG 4815      CA   GCAGGT
            G                    TGCC  TGA     ACACTTTGG
                                ||||  |||     |||||||||
                                ACGG  ATT     TGTGAAACC
                                  AC   AGGGT_
GAM207  KIAA1576 3' TGCCCATGAGATGTATTTTGG  4847          CAG   CAC
                                TGCCCATGAG   GTA   TTTGG
                                ||||||||||   |||   |||||
                                ACGGGTACTC   CAT   AAACC
                                     TA_   A__
GAM207  KIAA1615 3' TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
            G                    TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  KIAA1615 3' TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
            G                    TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  KIAA1784 3' GCCTGTGATCCCAGCACTTTGG 4841     CA   G__   GTA
                                GCC  TGA   CAG   CACTTTGG
                                |||  |||   |||   ||||||||
                                CGG  ACT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  KIAA1924 3' TGCCTGTGATCCCAGCACTTTG 4830      CA   G__   GTA
            G                    TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ACT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207  KIAA1971 3' TGCCTATAATCCCAACACTTTG 4837      C    GCAGGT
            G                    TGCC ATGA     ACACTTTGG
                                ||||  ||||     |||||||||
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                              ACGG TATT     TGTGAAACC
                                A   AGGGT_
GAM207  KLK7    3'  TGCCTGTAATCCCAGCACTTTG 4814      CA  G__  GTA
          G                    TGCC  TGA   CAG   CACTTTGG
                               ||||  |||   |||   ||||||||
                              ACGG  ATT   GTC   GTGAAACC
                                AC   AGG   ___
GAM207  KLK7    3'  TGCCTGTAATCCCAGCACTTTG 4814      CA  G__  GTA
          G                    TGCC  TGA   CAG   CACTTTGG
                               ||||  |||   |||   ||||||||
                              ACGG  ATT   GTC   GTGAAACC
                                AC   AGG   ___
GAM207  LAMP3   3'  TGCCTGTAATCCCAGCACTTTG 4814      CA  G__  GTA
          G                    TGCC  TGA   CAG   CACTTTGG
                               ||||  |||   |||   ||||||||
                              ACGG  ATT   GTC   GTGAAACC
                                AC   AGG   ___
GAM207  LY75    3'  TGCCTGTAATCCCAGCACTTTG 4814      CA  G__  GTA
          G                    TGCC  TGA   CAG   CACTTTGG
                               ||||  |||   |||   ||||||||
                              ACGG  ATT   GTC   GTGAAACC
                                AC   AGG   ___
GAM207  MCLC    3'  TGCCTGTAATCCCAGCACTTTG 4814      CA  G__  GTA
          G                    TGCC  TGA   CAG   CACTTTGG
                               ||||  |||   |||   ||||||||
                              ACGG  ATT   GTC   GTGAAACC
                                AC   AGG   ___
GAM207  MGC12518 3'  TGCCTGTAATCCCAGCACTTTG 4814      CA  G__  GTA
          G                    TGCC  TGA   CAG   CACTTTGG
                               ||||  |||   |||   ||||||||
                              ACGG  ATT   GTC   GTGAAACC
                                AC   AGG   ___
GAM207  MGC21675 3'  TGCCTGTAATCTCAGCACTTTG 4816      CA  G__  GTA
          G                    TGCC  TGA   CAG   CACTTTGG
                               ||||  |||   |||   ||||||||
                              ACGG  ATT   GTC   GTGAAACC
                                AC   AGA   ___
GAM207  MGC2603  3'  TGCCTGTAATCTCAGCACTTTG 4816      CA  G__  GTA
          G                    TGCC  TGA   CAG   CACTTTGG
                               ||||  |||   |||   ||||||||
                              ACGG  ATT   GTC   GTGAAACC
                                AC   AGA   ___
GAM207  MGC2721  5'  TGCCCATGGCTCAGTTTTG   4848        A  A_   ACAC
                              TGCCCATG GC  GGT   TTTG
                              ||||||||  ||  |||   ||||
                              ACGGGTAC CG  TCA   AAAC
                                   _ AG   _____
GAM207  NFAT5   3'  TGCCTGTAATCCTAGCACTTTG 4827      CA  GCAGGTA
          G                    TGCC  TGA     CACTTTGG
                               ||||  |||     ||||||||
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                                ACGG ATT    GTGAAACC
                                  AC  AGGATC_
GAM207  NICN1    3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                 ACGG ATT  GTC  GTGAAACC
                                   AC  AGG  ___
GAM207  PRO1992  3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                 ACGG ATT  GTC  GTGAAACC
                                   AC  AGG  ___
GAM207  RAB39    3' TGCCTATAATTCCAGCACTTTG 4849     C   G__  GTA
           G                     TGCC ATGA  CAG  CACTTTGG
                                 |||| ||||  |||  ||||||||
                                 ACGG TATT  GTC  GTGAAACC
                                   A   AAG  ___
GAM207  RNF8     3' TGCCTGTAATCTCAGCACTTTG 4816     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                 ACGG ATT  GTC  GTGAAACC
                                   AC  AGA  ___
GAM207  SIRPB1   3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                 ACGG ATT  GTC  GTGAAACC
                                   AC  AGG  ___
GAM207  SLC16A4  3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                 ACGG ATT  GTC  GTGAAACC
                                   AC  AGG  ___
GAM207  SREC     3' TGCCTGTCATCCCAGCACTTTG 4826     ___  GAG  GTA
           G                     TGCC  CAT  CAG  CACTTTGG
                                 ||||  |||  |||  ||||||||
                                 ACGG  GTA  GTC  GTGAAACC
                                   ACA  GG_  ___
GAM207  SYTL4    5' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                 ACGG ATT  GTC  GTGAAACC
                                   AC  AGG  ___
GAM207  TCL6     5' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                 ACGG ATT  GTC  GTGAAACC
                                   AC  AGG  ___
GAM207  TCL6     5' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
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                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  TCL6    5'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  TCL6    5'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  TUCAN   3'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  UBF-fl  3'  TGCCTGTAATTTCAGCACTTTG 4850     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AAA  ___
GAM207  ZNF17   3'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC120114 3'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC145009 3'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC146050 3'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC146108 3'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC146332 3'  TGAACAGGTGGACTTGG    4851        AC   T
                                TGAGCAGGT  ACTT GG
                                |||||||||  ||||  ||
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                                ACTTGTCCA  TGAA CC
                                    CC   _
GAM207  LOC146784 5'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
            G                    TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                 ACGG  ATT   GTC   GTGAAACC
                                   AC   AGG  ___
GAM207  LOC146909 3'  TGCCTGTAATCTCAGCACTTTG 4816     CA  G__  GTA
            G                    TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                 ACGG  ATT   GTC   GTGAAACC
                                   AC   AGA  ___
GAM207  LOC147817 3'  TGCCTATAATCCCAACACTTTG 4837     C   GCAGGT
            G                    TGCC ATGA     ACACTTTGG
                                 ||||  ||||     |||||||||
                                 ACGG TATT     TGTGAAACC
                                   A    AGGGT_
GAM207  LOC149421 3'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
            G                    TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                 ACGG  ATT   GTC   GTGAAACC
                                   AC   AGG  ___
GAM207  LOC149577 3'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
            G                    TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                 ACGG  ATT   GTC   GTGAAACC
                                   AC   AGG  ___
GAM207  LOC149692 3'  TGCCTGTAGTGCCAGCACTTTG 4852     CATGA_ A  TA
            G                    TGCC     GC GG  CACTTTGG
                                 ||||     || ||  ||||||||
                                 ACGG     CG TC  GTGAAACC
                                   ACATCA  G  __
GAM207  LOC150054 5'  TGCCTATAATCCCAGCACTTTG 4839     C   G__  GTA
            G                    TGCC ATGA   CAG   CACTTTGG
                                 ||||  ||||   |||   ||||||||
                                 ACGG TATT   GTC   GTGAAACC
                                   A    AGG  ___
GAM207  LOC150282 5'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
            G                    TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                 ACGG  ATT   GTC   GTGAAACC
                                   AC   AGG  ___
GAM207  LOC150960 3'  TGCCTGTAATTACAGCACTTTG 4853     CA  __   GTA
            G                    TGCC  TGA  GCAG   CACTTTGG
                                 ||||  |||  ||||   ||||||||
                                 ACGG  ATT  TGTC   GTGAAACC
                                   AC   AA  ___
GAM207  LOC151475 5'  TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
            G                    TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
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                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC151826 3' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
            G                    TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC153077 3' TGCCTGTTAACCCAGCACTTTG 4854    CATG  AGGTA
            G                    TGCC  AGC   CACTTTGG
                                ||||  |||   ||||||||
                                ACGG  TTG   GTGAAACC
                                  ACAA  GGTC_
GAM207  LOC153688 3' TGCCTGTAATCCTAGCACTTTG 4827    CA  GCAGGTA
            G                    TGCC TGA    CACTTTGG
                                ||||  |||    ||||||||
                                ACGG ATT    GTGAAACC
                                  AC  AGGATC_
GAM207  LOC154282 5' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
            G                    TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC154726 5' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
            G                    TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC157247 5' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
            G                    TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC157506 3' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
            G                    TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC157507 5' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
            G                    TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC158476 3' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
            G                    TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC169611 3' TGCCTGTAATCCCAACACTTTG 4815    CA  GCAGGT
            G                    TGCC TGA    ACACTTTGG
                                ||||  |||    |||||||||
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                                ACGG  ATT     TGTGAAACC
                                  AC   AGGGT_
GAM207   LOC196264 3'  TGCCTGTAATCCCAACACTTTG 4815      CA   GCAGGT
           G                     TGCC  TGA     ACACTTTGG
                                 ||||  |||     |||||||||
                                ACGG  ATT     TGTGAAACC
                                  AC   AGGGT_
GAM207   LOC199725 5'  TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207   LOC199786 3'  TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207   LOC200169 5'  TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207   LOC200314 3'  TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207   LOC200470 3'  TGTCCATGAGCAGGGACA    4855    C        T
                                TG CCATGAGCAGG ACA
                                || ||||||||||| |||
                                AC GGTACTCGTCC TGT
                                 A         C
GAM207   LOC200845 5'  TGCCTATAATCCCAGCACTTTG 4839      C   G__   GTA
           G                     TGCC ATGA   CAG   CACTTTGG
                                 |||| ||||   |||   ||||||||
                                ACGG TATT   GTC   GTGAAACC
                                  A   AGG   ___
GAM207   LOC203378 3'  TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207   LOC205251 5'  TGCCTGTAATCCCAGCACTTTG 4814      CA   G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                 ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM207   LOC219673 5'  TGCCTGTAATCCTAGCACTTTG 4827      CA   GCAGGTA
           G                     TGCC  TGA     CACTTTGG
                                 ||||  |||     ||||||||
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                                ACGG ATT     GTGAAACC
                                  AC  AGGATC_
GAM207  LOC219700 5' GCCCATGGGATGGGCACTTTGG 4856       AGCA TA
                                GCCCATG   GG CACTTTGG
                                |||||||   || ||||||||
                                CGGGTAC   CC GTGAAACC
                                   CCTA C_
GAM207  LOC219735 3' TGCCTGTAATCCCAACACTTTG 4815     CA  GCAGGT
           G                     TGCC TGA    ACACTTTGG
                                ||||  |||    |||||||||
                                ACGG ATT    TGTGAAACC
                                  AC  AGGGT_
GAM207  LOC220662 3' TGCCTGTAATCCCAACACTTTG 4815     CA  GCAGGT
           G                     TGCC TGA    ACACTTTGG
                                ||||  |||    |||||||||
                                ACGG ATT    TGTGAAACC
                                  AC  AGGGT_
GAM207  LOC221060 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC221271 3' TGCCTGTAATCTCAACACTTTG 4857     CA  GCAGGT
           G                     TGCC TGA    ACACTTTGG
                                ||||  |||    |||||||||
                                ACGG ATT    TGTGAAACC
                                  AC  AGAGT_
GAM207  LOC221663 5' TGCCTGTAATCCCGGCACTTTG 4843     CA  GCA_ TA
           G                     TGCC TGA   GG CACTTTGG
                                ||||  |||   || ||||||||
                                ACGG ATT   CC GTGAAACC
                                  AC  AGGG __
GAM207  LOC222999 5' CCATGAGCACCCTGGGCTTTGG 4858       GGTACA_
                                CCATGAGCA     CTTTGG
                                |||||||||     ||||||
                                GGTACTCGT     GAAACC
                                    GGGACCC
GAM207  LOC254268 3' TGCCTGTAATCCCAACACTTTG 4815     CA  GCAGGT
           G                     TGCC TGA    ACACTTTGG
                                ||||  |||    |||||||||
                                ACGG ATT    TGTGAAACC
                                  AC  AGGGT_
GAM207  LOC256364 5' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
                                ACGG ATT  GTC  GTGAAACC
                                  AC  AGG  ___
GAM207  LOC257465 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                ||||  |||  |||  ||||||||
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                          ACGG ATT  GTC  GTGAAACC
                            AC  AGG  ___
GAM207  LOC51159  5' TGCCTGTAATCCCAACACTTTG 4815    CA  GCAGGT
          G                TGCC TGA    ACACTTTGG
                           |||| |||    |||||||||
                           ACGG ATT    TGTGAAACC
                             AC  AGGGT_
GAM207  LOC51219  5' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
          G                TGCC TGA  CAG  CACTTTGG
                           |||| |||  |||  ||||||||
                           ACGG ATT  GTC  GTGAAACC
                             AC  AGG  ___
GAM207  LOC89932  3' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
          G                TGCC TGA  CAG  CACTTTGG
                           |||| |||  |||  ||||||||
                           ACGG ATT  GTC  GTGAAACC
                             AC  AGG  ___
GAM207  LOC90485  3' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
          G                TGCC TGA  CAG  CACTTTGG
                           |||| |||  |||  ||||||||
                           ACGG ATT  GTC  GTGAAACC
                             AC  AGG  ___
GAM207  LOC90591  3' TGCCTGTCATCCCAGCACTTTG 4826    ___  GAG  GTA
          G                TGCC  CAT  CAG  CACTTTGG
                           |||| |||  |||  ||||||||
                           ACGG  GTA  GTC  GTGAAACC
                             ACA  GG_  ___
GAM207  LOC90591  3' TGCCTGTATGCACAGCACTTTG 4859    C__  A  GTA
          G                TGCC  ATG GCAG  CACTTTGG
                           |||| ||| ||||  ||||||||
                           ACGG  TAC TGTC  GTGAAACC
                             ACA  G  ___
GAM207  LOC90906  3' TGCCCAGAGTAGGTACAC   4860      T  C
                           TGCCCA GAG AGGTACAC
                           |||||| ||| ||||||||
                           ACGGGT CTC TCCATGTG
                              _  A
GAM207  LOC90918  3' TGCCTGTAATCCCGGCACTTTG 4843    CA  GCA_  TA
          G                TGCC TGA  GG  CACTTTGG
                           |||| |||  ||  ||||||||
                           ACGG ATT  CC  GTGAAACC
                             AC  AGGG  __
GAM207  LOC91250  5' TGCCTGTAATCCCAGCACTTTG 4814    CA  G__  GTA
          G                TGCC TGA  CAG  CACTTTGG
                           |||| |||  |||  ||||||||
                           ACGG ATT  GTC  GTGAAACC
                             AC  AGG  ___
GAM207  LOC92267  3' TGCCTGTAAACCTAGCACTTTG 4861    CA   AGGTA
          G                TGCC TGAGC   CACTTTGG
                           |||| |||||   ||||||||
```

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                                ACGG ATTTG   GTGAAACC
                                  AC   GATC_
GAM207  LOC92661 5' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                 ACGG ATT  GTC  GTGAAACC
                                   AC AGG  ___
GAM207  LOC92841 3' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                 ACGG ATT  GTC  GTGAAACC
                                   AC AGG  ___
GAM207  LOC93408 5' TGCCTGTAATCCCAGCACTTTG 4814     CA  G__  GTA
           G                     TGCC TGA  CAG  CACTTTGG
                                 |||| |||  |||  ||||||||
                                 ACGG ATT  GTC  GTGAAACC
                                   AC AGG  ___
GAM208  STARD5   5' CCAGCGCCGGGTCCATT    4864       T  ACGCG
                                 CCAGCGCC GG   CTGTT
                                 |||||||| ||   |||||
                                 GGTCGCGG CC   GGTAA
                                     _ CA___
GAM208  FLJ32449 3' CACCAGCGTCTGGGTGCAC   4865       C   AC
                                 TACCAGCG CTGG  GCGC
                                 |||||||| ||||  ||||
                                 GTGGTCGC GACC  CGTG
                                     A   CA
GAM208  PPAP2B   5' GCGCAGCTTGGGGCGCGCTGTT 4866     C___  A_
           G                     GCGC   TGG  CGCGCTGTTG
                                 ||||   |||  ||||||||||
                                 CGCG   ACC  GCGCGACAAC
                                   TCGA  CC
GAM208  LOC152273 5' CCAGCGCCTGGGCCT      4867         AC  G
                                 CCAGCGCCTGG  GC CT
                                 ||||||||||  || ||
                                 GGTCGCGGACC  CG GA
                                      __ _
GAM208  LOC197358 5' CCAGCGCCTTGGCCCCTTG   4868        GGAC  G  G
                                 CCAGCGCCT   GC CT TTG
                                 |||||||||   || || |||
                                 GGTCGCGGA   CG GG AAC
                                     AC__ _  G
GAM209  ANK1     3' CAGCCACCGGCCTGTCCC    4871       TC  A_
                                 CAGCCGCCG  GCC  TCCC
                                 |||||||||  |||  ||||
                                 GTCGGTGGC  CGG  AGGG
                                     __  AC
GAM209  ANK1     3' CAGCCACCGGCCTGTCCC    4871       TC  A_
                                 CAGCCGCCG  GCC  TCCC
                                 |||||||||  |||  ||||
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                                GTCGGTGGC CGG AGGG
                                    __ AC
GAM209  ATF5    3' CAGTACCCCGCCATCCC    4872    CC  G
                                CAG GCC TCGCCATCCC
                                ||| ||| ||||||||||
                                GTC TGG GGCGGTAGGG
                                 A_ _
GAM209  BSN     5' GCCGCTGCCGCCGCCATC   4873    ___
                                GCC GCCGTCGCCATC
                                ||| ||||||||||||
                                CGG CGGCGGCGGTAG
                                 CGA
GAM209  CAPN10  5' CAGCCGCCGCCGCCTCC    4874        A
                                CAGCCGCCGTCGCC TCC
                                |||||||||||||| |||
                                GTCGGCGGCGGCGG AGG
                                    _
GAM209  CAPN10  5' CAGCCGCCGCCGCCTCC    4874        A
                                CAGCCGCCGTCGCC TCC
                                |||||||||||||| |||
                                GTCGGCGGCGGCGG AGG
                                    _
GAM209  CAPN10  5' CAGCCGCCGCCGCCTCC    4874        A
                                CAGCCGCCGTCGCC TCC
                                |||||||||||||| |||
                                GTCGGCGGCGGCGG AGG
                                    _
GAM209  CAPN10  5' CAGCCGCCGCCGCCTCC    4874        A
                                CAGCCGCCGTCGCC TCC
                                |||||||||||||| |||
                                GTCGGCGGCGGCGG AGG
                                    _
GAM209  CAPN10  5' CAGCCGCCGCCGCCTCC    4874        A
                                CAGCCGCCGTCGCC TCC
                                |||||||||||||| |||
                                GTCGGCGGCGGCGG AGG
                                    _
GAM209  CAPN10  5' CAGCCGCCGCCGCCTCC    4874        A
                                CAGCCGCCGTCGCC TCC
                                |||||||||||||| |||
                                GTCGGCGGCGGCGG AGG
                                    _
GAM209  CAPN10  5' CAGCCGCCGCCGCCTCC    4874        A
                                CAGCCGCCGTCGCC TCC
                                |||||||||||||| |||
                                GTCGGCGGCGGCGG AGG
                                    _
GAM209  CKAP1   5' CAGCCGCCTCACACCC     4875        G   C
                                CAGCCGCC TCGC ATCC
                                |||||||| |||| ||||
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                                GTCGGCGG AGTG TGGG
                                      _  _
GAM209  CYP21A2  5' AGCCCCAGCCATCCC     4876     G  TC
                                AGCC CCG  GCCATCCC
                                |||| |||  ||||||||
                                TCGG GGT  CGGTAGGG
                                   _  __
GAM209  DCLRE1C  5' AGCGCCGCCGATCCC      4877     C     CC
                                AGC GCCGTCG  ATCCC
                                ||| |||||||  |||||
                                TCG CGGCGGC  TAGGG
                                   _    __
GAM209  DGAT1    3' GCCTGCTGTCGCCATCCC    4878     _ C
                                GCC GC GTCGCCATCCC
                                ||| || ||||||||||
                                CGG CG CAGCGGTAGGG
                                  A  A
GAM209  DSCR3    5' CAGCAGCCGCCACTTCC     4879     C      CA
                                CAGC GCCGTCGC  TCC
                                |||| ||||||||  |||
                                GTCG CGGCGGTG  AGG
                                  T       A_
GAM209  DUSP4    5' CAGCCGCCAGGCCTTCC     4880        TC  A
                                CAGCCGCCG  GCC TCC
                                |||||||||  ||| |||
                                GTCGGCGGT  CGG AGG
                                     C_  A
GAM209  DUSP7    5' CAGCCGCCGCCGCCCCC     4881           A
                                CAGCCGCCGTCGCC TCC
                                |||||||||||||| |||
                                GTCGGCGGCGGCGG GGG
                                      _
GAM209  DXYS155E 3' CAGCCGCCGCCGCTCC      4882           CA
                                CAGCCGCCGTCGC  TCC
                                ||||||||||||  |||
                                GTCGGCGGCGGCG  AGG
                                      __
GAM209  EGLN2    5' CAGCTCACCACCATCC      4883     _  GTC
                                CAGC CGCC   GCCATCC
                                |||| ||||   |||||||
                                GTCG GTGG   TGGTAGG
                                  A  ____
GAM209  EN2      5' GCCGCCGCCCGGCCGTCCC   4884        __  A
                                GCCGCCGTC  GCC TCCC
                                |||||||||  ||| ||||
                                CGGCGGCGG  CGG AGGG
                                     GC  C
GAM209  F2R      5' CAGCCGCCGCTCGCAAGCCC  4885        _   CAT
                                CAGCCGCCG TCGC   CCC
                                |||||||||  ||||   |||
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                                GTCGGCGGC AGCG   GGG
                                     G    TTC
GAM209   FBN1     5'  CCGCCGGGGTCCCGCTATCCC  4886        _____    C
                                CCGCCG    TCGC ATCCC
                                ||||||    |||| |||||
                                GGCGGC    GGCG TAGGG
                                   CCCAG    A
GAM209   FBXL7    5'  CCGCCGCCGCCGGGTCCC    4887           A__
                                CCGCCGTCGCC   TCCC
                                ||||||||||   ||||
                                GGCGGCGGCGG   AGGG
                                      CCC
GAM209   FSTL1    3'  CAGCCACCTTCATATCC     4888         G   CC
                                CAGCCGCC TCG  ATCC
                                |||||||| |||  ||||
                                GTCGGTGG AGT  TAGG
                                     A   A_
GAM209   FZD10    5'  CAGCGCCGCCGCTCCC      4889       C       CA
                                CAGC GCCGTCGC  TCCC
                                |||| ||||||||  ||||
                                GTCG CGGCGGCG  AGGG
                                  _       __
GAM209   GPC1     3'  CAGCCACCAGCATCCC      4890          TC  C
                                CAGCCGCCG  GC ATCCC
                                |||||||||  || |||||
                                GTCGGTGGT  CG TAGGG
                                     __  _
GAM209   GPR30    5'  GCCACCGTGCACAGTCCC    4891          _   CA
                                GCCGCCGT CGC  TCCC
                                |||||||| |||  ||||
                                CGGTGGCA GTG  AGGG
                                     C   TC
GAM209   GPR44    3'  GCTTGACCACGCCATCCC    4892     C__    T
                                GC   GCCG CGCCATCCC
                                ||   |||| |||||||||
                                CG   TGGT GCGGTAGGG
                                  AAC    _
GAM209   HSF4     5'  CAGCGCGCCGCCAGCTCC    4893       _       CCA
                                CAGC CGCCGTCG   TCC
                                |||| ||||||||   |||
                                GTCG GCGGCGGT   AGG
                                   C       CG_
GAM209   IDS      5'  CAGCCGCCGCCGCAGCC     4894             CAT
                                CAGCCGCCGTCGC   CC
                                ||||||||||||   ||
                                GTCGGCGGCGGCG   GG
                                       TC_
GAM209   IFNAR1   5'  CAGCCGCCATCGCCCCGTCC  4895              A__
                                CAGCCGCCGTCGCC   TCC
                                ||||||||||||   |||
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                                GTCGGCGGTAGCGG  AGG
                                      GGC
GAM209  IFNAR2   3' AGCCACCGCCACTTGTCC   4896          CA_
                                AGCCGCCGTCGC  TCC
                                ||||||||||||  |||
                                TCGGTGGCGGTG  AGG
                                      AAC
GAM209  MAN2A1   5' CAGCCGCCGGAGGCTCCC   4897        TC_ CA
                                CAGCCGCCG  GC  TCCC
                                |||||||||  ||  ||||
                                GTCGGCGGC  CG  AGGG
                                     CTC  __
GAM209  MAP4K5   5' CAGCCGCTGCACGGCGCGTCC 4899       ____ T  CA
                                CAGCCGC   CG CGC  TCC
                                |||||||   || |||  |||
                                GTCGGCG   GC GCG  AGG
                                    ACGT  C  C_
GAM209  MAP4K5   5' GCCGCCGCACCACGTTCC   4898       T   ___
                                GCCGCCG CGCCA  TCC
                                ||||||| |||||  |||
                                CGGCGGC GTGGT  AGG
                                   _   GCA
GAM209  NMB     5' GCCGCCCTCCCCGCCGTCCC  4900       G ___  A
                                GCCGCC TC  GCC TCCC
                                |||||| ||  ||| ||||
                                CGGCGG AG  CGG AGGG
                                   G  GGG  C
GAM209  NPTX1    3' CAGTGTCCTCAGCCATCCC   4901     CCG  G  _
                                CAG  CC TC GCCATCCC
                                |||  || || ||||||||
                                GTC  GG AG CGGTAGGG
                                  ACA  _  T
GAM209  RAB33A   5' CAGCCGCCGCCGCGCC     4902          CAT
                                CAGCCGCCGTCGC  CC
                                ||||||||||||  ||
                                GTCGGCGGCGGCG  GG
                                      C__
GAM209  RAB6A    5' CAGCTGCCGCCGCCCC     4903     C      AT
                                CAGC GCCGTCGCC  CC
                                |||| |||||||||  ||
                                GTCG CGGCGGCGG  GG
                                  A      __
GAM209  RAB6A    5' CAGCCGCCGCCGCCTCCC   4904          A
                                CAGCCGCCGTCGCC TCCC
                                |||||||||||||| ||||
                                GTCGGCGGCGGCGG AGGG
                                                _
GAM209  RANBP9   5' CAGCCGCCGCTGCAACTCC   4905        C  CA_
                                CAGCCGCCGT GC  TCC
                                |||||||||| ||  |||
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                                GTCGGCGGCG CG   AGG
                                     A  TTG
GAM209  RB1CC1   5'  CAACCGCCGGCGTCCC     4906         T  CCA
                                CAGCCGCCG CG   TCCC
                                ||||||||| ||   ||||
                                GTTGGCGGC GC   AGGG
                                     C  ___
GAM209  RREB1    5'  TGACCGCAGTTGCCATCCC   4907    A    C  C
                                C GCCGC GT GCCATCCC
                                | ||||| || ||||||||
                                A TGGCG CA CGGTAGGG
                                 C    T  A
GAM209  SLC12A4  5'  CAGCCGCCCGCCGCTGTCCC  4908         _    CA
                                CAGCCGCC GTCGC  TCCC
                                |||||||| |||||  ||||
                                GTCGGCGG CGGCG  AGGG
                                     G    AC
GAM209  SLC35A3  5'  CAGCGCCGCCGGCTCCC    4909      C      CCA
                                CAGC GCCGTCG   TCCC
                                |||| |||||||   ||||
                                GTCG CGGCGGC   AGGG
                                  _      CG_
GAM209  SLC6A12  5'  CAGCTCGCCACCATCCC    4910      CGC
                                CAGC   CGTCGCCATCCC
                                ||||   ||||||||||||
                                GTCG   GCGGTGGTAGGG
                                  A__
GAM209  SOX4     3'  CCGCCGCCGCCAGCTCCC    4911           __
                                CCGCCGTCGCCA  TCCC
                                ||||||||||||  ||||
                                GGCGGCGGCGGT  AGGG
                                       CG
GAM209  TBL1X    5'  CCGCCGCCGCCGAGTCCC    4912          A__
                                CCGCCGTCGCC   TCCC
                                ||||||||||   ||||
                                GGCGGCGGCGG   AGGG
                                       CTC
GAM209  TXNRD2   3'  CAGTCCCCTGAGCCATCCC   4913     _  G  GTC
                                CAG CC CC   GCCATCCC
                                ||| || ||   ||||||||
                                GTC GG GG   CGGTAGGG
                                  A  _  ACT
GAM209  UBE2B    5'  CCGCCGCCTCCGGATCCC    4914        G  __
                                CCGCCGTC CC  ATCCC
                                |||||||| ||  |||||
                                GGCGGCGG GG  TAGGG
                                     A  CC
GAM209  ARPP-19  5'  CCGGCCGCCGCCCGTCCC    4915     _      A_
                                CCG CCGTCGCC  TCCC
                                ||| ||||||||  ||||
```

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                                GGC GGCGGCGG  AGGG
                                  C       GC
GAM209  ARTN     5'  CAGCGTCACCAGATCCC     4916      CGCC     __
                                CAGC   GTCGCCA  TCCC
                                ||||   |||||||  ||||
                                GTCG   CAGTGGT  AGGG
                                  ____      CT
GAM209  BC008967 5'  CCGCCGTCCCATACATCCC   4917        G  ____
                                CCGCCGTC CCA   TCCC
                                ||||||||  |||   ||||
                                GGCGGCAG GGT   AGGG
                                    _  ATGT
GAM209  C1QTNF7  3'  CAGCCGCCATGCAACCC     4918         C  C
                                CAGCCGCCGT GC ATCC
                                ||||||||||  ||  ||||
                                GTCGGCGGTA CG TGGG
                                    _  T
GAM209  C20orf60 5'  CAGCCGCCGCGATCCC      4919         T  CC
                                CAGCCGCCG CG  ATCCC
                                |||||||||  ||  |||||
                                GTCGGCGGC GC  TAGGG
                                    _  __
GAM209  C5orf7   5'  CACCCGCGGCCGCCGTTCC   4920     G   C     A_
                                CA CCGC GTCGCC  TCC
                                ||  ||||  ||||||  |||
                                GT GGCG CGGCGG  AGG
                                 G   C     CA
GAM209  CBLN1    5'  CAGCCGCCCCCCCCGTCCC   4921        G  G  A
                                CAGCCGCC TC CC TCCC
                                ||||||||  ||  ||  ||||
                                GTCGGCGG GG GG AGGG
                                    G  G  C
GAM209  CENTA1   5'  GCCGCCGCCCCTGCGCCATCCC 4922         _____       III
           G                     GCCGCCGT    CGCCATCCC   G
                                ||||||||    |||||||||   |
                                CGGCGGCG    GCGGTAGGG   C
                                    GGGAC       III
GAM209  CENTG1   3'  CAGCCACCTCGAATCC      4923        G   CC
                                CAGCCGCC TCG  ATCC
                                ||||||||  |||  ||||
                                GTCGGTGG AGC  TAGG
                                    _   T_
GAM209  COASTER  5'  CCGCCGTCGCCACGAATCCC   4924          ____
                                CCGCCGTCGCCA   TCCC
                                ||||||||||||   ||||
                                GGCGGCAGCGGT   AGGG
                                      GCTT
GAM209  CXYorf1  5'  CAGCTGCCACCCCATCCC    4925      C   GT G
                                CAGC GCC  C CCATCCC
                                ||||  |||  |  |||||||
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                                GTCG CGG  G GGTAGGG
                                  A   TG _
GAM209  DKFZP434J154 5'  CAACCGCCGCCTCATCCC    4926          GC
                                CAGCCGCCGTC  CATCCC
                                ||||||||||  ||||||
                                GTTGGCGGCGG  GTAGGG
                                     A_
GAM209  DKFZP434P1750 3'  CAGGCCAACGCCATCC     4927     CC    T
                                CAG  GCCG CGCCATCC
                                |||  |||| ||||||||
                                GTC  CGGT GCGGTAGG
                                  __   T
GAM209  FASTK    5'  AGCCACCGAGTCCGCCATC   4928        ___
                                AGCCGCCG   TCGCCATC
                                ||||||||   ||||||||
                                TCGGTGGC   GGCGGTAG
                                     TCA
GAM209  FASTK    5'  AGCCACCGAGTCCGCCATC   4928        ___
                                AGCCGCCG   TCGCCATC
                                ||||||||   ||||||||
                                TCGGTGGC   GGCGGTAG
                                     TCA
GAM209  FASTK    5'  AGCCACCGAGTCCGCCATC   4928        ___
                                AGCCGCCG   TCGCCATC
                                ||||||||   ||||||||
                                TCGGTGGC   GGCGGTAG
                                     TCA
GAM209  FLJ10211  5'  CAGCGCCGTCACATGGTCCC   4929      C      CA__
                                CAGC GCCGTCGC    TCCC
                                ||||  ||||||||    ||||
                                GTCG CGGCAGTG    AGGG
                                  _       TACC
GAM209  FLJ13621  5'  CAGCCGCCGTTGCCTCC     4930          C   A
                                CAGCCGCCGT GCC TCC
                                |||||||||| ||| |||
                                GTCGGCGGCA CGG AGG
                                     A   _
GAM209  FLJ20984  3'  CAGCCGCCCTCTGCAGCCC   4932         G  GC  T
                                CAGCCGCC TC  CA CCC
                                |||||||| ||  || |||
                                GTCGGCGG AG  GT GGG
                                     G  AC  C
GAM209  FLJ20984  3'  CAGCCACCCTGTGCCATCC   4931         __ C
                                CAGCCGCC  GT GCCATCC
                                ||||||||  || |||||||
                                GTCGGTGG  CA CGGTAGG
                                     GA  _
GAM209  FLJ22938  5'  CAGCCACCAGCCGTCC     4933          TC   A
                                CAGCCGCCG  GCC TCC
                                |||||||||  ||| |||
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                                GTCGGTGGT  CGG AGG
                                     __  C
GAM209  FLJ23375  5'  CAGCCGCCGCCCAGCACC    4934          GC_
                                CAGCCGCCGTC  CATC
                                ||||||||||  ||||
                                GTCGGCGGCGG  GTGG
                                      GTC
GAM209  GAPCENA  5'  GCCCGCCGCTCGCCGTCCCG  4935     _  _   A   III
                                GCC GCCG TCGCC TCCC  G
                                ||| |||| ||||| ||||  |
                                CGG CGGC AGCGG AGGG  C
                                  G   G    C   III
GAM209  HSPC232  5'  GCTCGCCGCCGTTATCCC    4936     _      CC
                                GC CGCCGTCG  ATCCC
                                || ||||||||  |||||
                                CG GCGGCGGC  TAGGG
                                 A       AA
GAM209  HSSEXGENE 5'  CAGCCGCCGCCGCAGCC     4894           CAT
                                CAGCCGCCGTCGC  CC
                                ||||||||||||  ||
                                GTCGGCGGCGGCG  GG
                                       TC_
GAM209  HUMGT198A 3'  CAGCCACCAGCCCTCATCC   4937        _  GC
                                CAGCCGCC GTC  CATCC
                                ||||||||  |||  |||||
                                GTCGGTGG CGG  GTAGG
                                     T  GA
GAM209  HUMGT198A 3'  CAGCCACCAGCCCTCATCC   4937        _  GC
                                CAGCCGCC GTC  CATCC
                                ||||||||  |||  |||||
                                GTCGGTGG CGG  GTAGG
                                     T  GA
GAM209  KIAA0445  5'  CACCCGCGCGCCATCC     4938     G   C T
                                CA CCGC G CGCCATCC
                                || |||| | ||||||||
                                GT GGCG C GCGGTAGG
                                 G   _ _
GAM209  KIAA0701  5'  CAGCCGCCGCCGAGAACCC   4939          CCAT
                                CAGCCGCCGTCG   CCC
                                ||||||||||||   |||
                                GTCGGCGGCGGC   GGG
                                       TCTT
GAM209  KIAA1028  5'  CCGCCGCCGCTCAGTCCC    4940         _  _
                                CCGCCGTCGC CA TCCC
                                |||||||||| || ||||
                                GGCGGCGGCG GT AGGG
                                      A  C
GAM209  KIAA1666  5'  CAGCTGCCGCCGCTCCC     4941      C      CA
                                CAGC GCCGTCGC  TCCC
                                |||| ||||||||  ||||
```

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                                GTCG CGGCGGCG  AGGG
                                  A      __
GAM209  KIF13B   3'  GCCCGTCCGCCACCATTCC   4942     _ _       _
                                GCC G CCGTCGCCAT CC
                                ||| | |||||||||| ||
                                CGG C GGCGGTGGTA GG
                                  G A        A
GAM209  KIF13B   3'  GCCCGTCCGCCACCATTCC   4942     _ _       _
                                GCC G CCGTCGCCAT CC
                                ||| | |||||||||| ||
                                CGG C GGCGGTGGTA GG
                                  G A        A
GAM209  LANO     5'  CAGTCGCCGTCGCCGCCC    4943     C        AT
                                CAG CGCCGTCGCC  CC
                                ||| ||||||||||  ||
                                GTC GCGGCAGCGG  GG
                                  A        CG
GAM209  LASP1    3'  AGTCCCCATCGCCATCCC    4944     _ G
                                AG CC CCGTCGCCATCCC
                                || || ||||||||||||||
                                TC GG GGTAGCGGTAGGG
                                 A _
GAM209  MAPK8IP3 5'  CAGCCCGTCGCCTCCC     4945      GC      A
                                CAGCC  CGTCGCC TCCC
                                |||||  ||||||| ||||
                                GTCGG  GCAGCGG AGGG
                                   __     _
GAM209  MFN2     3'  CAGCCACCAACGTCCC      4946         T  CCA
                                CAGCCGCCG CG   TCCC
                                |||||||||  ||   ||||
                                GTCGGTGGT GC   AGGG
                                     T  ___
GAM209  MGC4368  5'  CAGTGGCCGAGCCATCCC    4947     CC    TC
                                CAG  GCCG  GCCATCCC
                                |||  ||||  ||||||||
                                GTC  CGGC  CGGTAGGG
                                  AC    T_
GAM209  MGC9753  5'  GCCGCCAGGCCGGCCATCC   4948        __   _
                                GCCGCC  GTCG CCATCC
                                ||||||  |||| ||||||
                                CGGCGG  CGGC GGTAGG
                                   TC    C
GAM209  MGC9753  3'  AGCCCCAGCCATCCC       4876      G   TC
                                AGCC CCG  GCCATCCC
                                |||| |||  ||||||||
                                TCGG GGT  CGGTAGGG
                                  _  __
GAM209  MOST2    5'  CAACCCACGCCATCCC       4949       GC  T
                                CAGCC  CG CGCCATCCC
                                |||||  || |||||||||
```

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                                GTTGG  GT GCGGTAGGG
                                   __ _
GAM209  MPZL1    5'  GCCGCCGCCGCCGCGTCCC   4950          A__
                                GCCGCCGTCGCC  TCCC
                                ||||||||||||  ||||
                                CGGCGGCGGCGG  AGGG
                                      CGC
GAM209  OR2C3    3'  CCGCTGCCACCAGGTCCC    4951      C     __
                                CCGC GTCGCCA  TCCC
                                |||| |||||||  ||||
                                GGCG CGGTGGT  AGGG
                                  A      CC
GAM209  OSBPL5   3'  CAGCCGCCGCGCCTCC     4952         T   A
                                CAGCCGCCG CGCC TCC
                                |||||||| |||| |||
                                GTCGGCGGC GCGG AGG
                                   _   _
GAM209  PCSK7    5'  CAGCTGCCGCCGCCTCCC    4953      C       A
                                CAGC GCCGTCGCC TCCC
                                |||| |||||||||| ||||
                                GTCG CGGCGGCGG AGGG
                                  A       _
GAM209  phospho1 5'  CAGCCGCCGCGTCCC      4954         T  CCA
                                CAGCCGCCG CG   TCCC
                                |||||||| ||   ||||
                                GTCGGCGGC GC   AGGG
                                   _ ___
GAM209  PRDM8    3'  CCGCCGCCGCCAGCGTCC    4955          ___
                                CCGCCGTCGCCA   TCC
                                ||||||||||||   |||
                                GGCGGCGGCGGT   AGG
                                      CGC
GAM209  PRO0971  5'  CAGGCGCCGCCGCTCC     4956     C       CA
                                CAG CGCCGTCGC  TCC
                                ||| |||||||||  |||
                                GTC GCGGCGGCG  AGG
                                  C       __
GAM209  PTR4     5'  CAGCCGCCGCCGCGGCC     4957           CAT
                                CAGCCGCCGTCGC   CC
                                ||||||||||||   ||
                                GTCGGCGGCGGCG   GG
                                      CC_
GAM209  PV1      3'  CCGCCGAGTCGGGCCATCCC  4958       __  __
                                CCGCC  GTC  GCCATCCC
                                |||||  |||  ||||||||
                                GGCGG  CAG  CGGTAGGG
                                   CT   CC
GAM209  RAB3D    5'  CAGCCACCCGGATCCC      4959        GT  CC
                                CAGCCGCC  CG  ATCCC
                                ||||||||  ||  |||||
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                                GTCGGTGG  GC  TAGGG
                                   __  C_
GAM209  RAB3IL1  5'  CAGCGCCGCCGCGTCC      4960       C       CA
                                CAGC GCCGTCGC  TCC
                                |||| ||||||||  |||
                                GTCG CGGCGGCG  AGG
                                  _       C_
GAM209  RAB6C    5'  CAGCCGCCGCCGCCTCCC    4904              A
                                CAGCCGCCGTCGCC TCCC
                                |||||||||||||| ||||
                                GTCGGCGGCGGCGG AGGG
                                          _
GAM209  RASD2    5'  CAGCCGCCGAGCCTCCC     4961          TC   A
                                CAGCCGCCG  GCC TCCC
                                |||||||||  ||| ||||
                                GTCGGCGGC  CGG AGGG
                                     T_  _
GAM209  RBPMS    3'  CAGCCGCCATCACACACC    4962              _
                                CAGCCGCCGTCGC CATC
                                |||||||||||| ||||
                                GTCGGCGGTAGTG GTGG
                                        T
GAM209  SLIT1    5'  CAGCCGCTGACCATCCC     4963         CGTC
                                CAGCCGC    GCCATCCC
                                |||||||    ||||||||
                                GTCGGCG    TGGTAGGG
                                    AC__
GAM209  SPACA1   5'  CAGTCGCCGCCGCGGCTCC   4964      C       CA_
                                CAG CGCCGTCGC   TCC
                                ||| |||||||||   |||
                                GTC GCGGCGGCG   AGG
                                  A        CCG
GAM209  STIM2    5'  GCCGCCGCGGCGCATCCC    4965         C  _
                                GCCGCCGT GC CATCCC
                                |||||||| || ||||||
                                CGGCGGCG CG GTAGGG
                                     C  C
GAM209  TRIM28   5'  CAGCCGCCGCCGAAACCC    4966            CC
                                CAGCCGCCGTCG  ATCC
                                ||||||||||||  ||||
                                GTCGGCGGCGGC  TGGG
                                       TT
GAM209  VILL     5'  AGCCGTCGTCCACCATCC     4967       C   _
                                AGCCG CGTC GCCATCC
                                ||||| |||| |||||||
                                TCGGC GCAG TGGTAGG
                                   A    G
GAM209  LOC112868 3'  CAGCCACCAGGACTGTCCC  4968          TC  CA
                                CAGCCGCCG  GC  TCCC
                                |||||||||  ||  ||||
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                                GTCGGTGGT  TG  AGGG
                                     CC  AC
GAM209  LOC115708 3'  CAGCCGCCCTTCCTGCTGTCCC 4969        G_  __  CA
                                CAGCCGCC  TC  GC  TCCC
                                ||||||||  ||  ||  ||||
                                GTCGGCGG  AG  CG  AGGG
                                     GA  GA  AC
GAM209  LOC115811 5'  CAGTTACCGCCGCGGTCCC   4970     CC      CA
                                CAG  GCCGTCGC  TCCC
                                |||  ||||||||  ||||
                                GTC  TGGCGGCG  AGGG
                                  AA      CC
GAM209  LOC124968 5'  TGACCGCCGTGTAGCCGTTCC  4971    A      C__   A_
                                C GCCGCCGT   GCC  TCC
                                | ||||||||   |||  |||
                                A TGGCGGCA   CGG  AGG
                                 C       CAT   CA
GAM209  LOC126526 3'  CAGCTGCGACGACCATCCC   4972      C  C T  _
                                CAGC GC G CG CCATCCC
                                |||| || | || |||||||
                                GTCG CG C GC GGTAGGG
                                  A  _ T  T
GAM209  LOC130250 5'  AGCCACTGTCACCATCCC    4973       C
                                AGCCGC GTCGCCATCCC
                                |||||| ||||||||||
                                TCGGTG CAGTGGTAGGG
                                   A
GAM209  LOC145990 5'  GCCGCCCCCCGCCGCCATC   4974       _____
                                GCCGCC   GTCGCCATC
                                ||||||   |||||||||
                                CGGCGG   CGGCGGTAG
                                   GGGG
GAM209  LOC146057 5'  GCCGCCGCCGCCTCGTCCC   4975          A__
                                GCCGCCGTCGCC   TCCC
                                ||||||||||||   ||||
                                CGGCGGCGGCGG   AGGG
                                       AGC
GAM209  LOC146108 5'  CAGTCGCGGAGCCATCCC    4976     C   C TC
                                CAG CGC G  GCCATCCC
                                ||| ||| |  ||||||||
                                GTC GCG C  CGGTAGGG
                                  A  _ CT
GAM209  LOC146227 3'  CAGCCACTCACCATCCC     4977        CG
                                CAGCCGC  TCGCCATCCC
                                |||||||  ||||||||||
                                GTCGGTG  AGTGGTAGGG
                                      __
GAM209  LOC146325 5'  CCGCCGCCGCCCGCGTCCC   4978          A___
                                CCGCCGTCGCC   TCCC
                                ||||||||||   ||||
```

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                                GGCGGCGGCGG   AGGG
                                      GCGC
GAM209  LOC148887 3'  CAGCCACCTTCTATCCC     4979        G  GCC
                                CAGCCGCC TC   ATCCC
                                |||||||| ||   |||||
                                GTCGGTGG AG   TAGGG
                                    A  A__
GAM209  LOC149506 3'  CAACCGCCCCATTGTCCC    4980        G   CCA
                                CAGCCGCC TCG   TCCC
                                |||||||| |||   ||||
                                GTTGGCGG GGT   AGGG
                                    _   AAC
GAM209  LOC149579 5'  CACCCGCGCGCCATCC      4938     G    C T
                                CA CCGC G CGCCATCC
                                || |||| | ||||||||
                                GT GGCG C GCGGTAGG
                                 G   _ _
GAM209  LOC150221 5'  CAGCTGCCGCCGCTCCC     4941      C       CA
                                CAGC GCCGTCGC  TCCC
                                |||| ||||||||  ||||
                                GTCG CGGCGGCG  AGGG
                                  A       __
GAM209  LOC151318 5'  CAGCCACCCTCCCATCC     4981        G  G
                                CAGCCGCC TC CCATCC
                                |||||||| || ||||||
                                GTCGGTGG AG GGTAGG
                                    G  _
GAM209  LOC159090 5'  CAGCCGCCGCCGCGGTGCC   4982           CAT_
                                CAGCCGCCGTCGC    CC
                                ||||||||||||    ||
                                GTCGGCGGCGGCG    GG
                                      CCAC
GAM209  LOC196214 3'  CAGCCCGCCGCCTCC       4983       GC      A
                                CAGCC  CGTCGCC TCC
                                |||||  ||||||| |||
                                GTCGG  GCGGCGG AGG
                                   __     _
GAM209  LOC197342 3'  GCTGCCGCCATCCATCCC    4984     C      _
                                GC GCCGTCG CCATCCC
                                || ||||||| |||||||
                                CG CGGCGGT GGTAGGG
                                 A      A
GAM209  LOC201176 3'  CAGCCGCCTACCCTGCCATCC 4985         GTC___
                                CAGCCGCC     GCCATCC
                                ||||||||     |||||||
                                GTCGGCGG     CGGTAGG
                                    ATGGGA
GAM209  LOC202754 3'  CAGCCCTCAAGCCATCCC    4986       GC  TC
                                CAGCC  CG  GCCATCCC
                                |||||  ||  ||||||||
```

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                                GTCGG  GT  CGGTAGGG
                                   GA  T_
GAM209   LOC203069 5'  CAGCCGCCCTCGGCGTCCC   4987        G   CCA
                                CAGCCGCC TCG   TCCC
                                |||||||| |||   ||||
                                GTCGGCGG AGC   AGGG
                                     G   CGC
GAM209   LOC203636 3'  CAGCCACCTCTGCCGTCCC   4988        G _   A
                                CAGCCGCC TC GCC TCCC
                                |||||||| || ||| ||||
                                GTCGGTGG AG CGG AGGG
                                     _ A   C
GAM209   LOC220110 5'  GCCCGCCGTCTAGCGACCC   4989      _     __ C
                                GCC GCCGTC  GC ATCC
                                ||| ||||||  || ||||
                                CGG CGGCAG  CG TGGG
                                  G     AT  C
GAM209   LOC255057 3'  CAGTACCAGCGCCATCC     4990      CC    T
                                CAG  GCCG CGCCATCC
                                |||  |||| ||||||||
                                GTC  TGGT GCGGTAGG
                                  A_   C
GAM209   LOC255870 3'  CAGCACCATCAGCTATCCC   4991       C     _ C
                                CAGC GCCGTC GC ATCCC
                                |||| |||||| || |||||
                                GTCG TGGTAG CG TAGGG
                                   _     T  A
GAM209   LOC256273 3'  CAGCCACCGCGCTCCC      4992         T   CA
                                CAGCCGCCG CGC  TCCC
                                |||||||| |||  ||||
                                GTCGGTGGC GCG  AGGG
                                      _  __
GAM209   LOC256310 3'  CAGCCGCCGCCGCTTGTCC   4993           CA_
                                CAGCCGCCGTCGC   TCC
                                ||||||||||||   |||
                                GTCGGCGGCGGCG   AGG
                                       AAC
GAM209   LOC55908  5'  CAGCCGCCGCCCAGCTATTCC  4994          __ CA_
                                CAGCCGCCGTC  GC   TCC
                                ||||||||||  ||   |||
                                GTCGGCGGCGG  CG   AGG
                                     GT  ATA
GAM209   LOC57107  3'  ACCGCCCTGGCGCCATCCC   4995       GT__
                                GCCGCC    CGCCATCCC
                                ||||||    |||||||||
                                TGGCGG    GCGGTAGGG
                                   GACC
GAM209   LOC84570  5'  CAGGCGTGCACCATCCC     4996      CC  C  _
                                CAG  GC GT CGCCATCCC
                                |||  || || |||||||||
```

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                                GTC  CG CA GTGGTAGGG
                                  __ _ C
GAM209  LOC90268  5' GCCGCCTTCCCGCCGTCCC   4997       G__    A
                                GCCGCC   TCGCC TCCC
                                ||||||   ||||| ||||
                                CGGCGG   GGCGG AGGG
                                   AAG    C
GAM209  LOC91040  5' CAGCTGCCACCCCATCCC    4925      C   GT G
                                CAGC GCC  C CCATCCC
                                |||| |||  | |||||||
                                GTCG CGG  G GGTAGGG
                                  A  TG _
GAM209  LOC91156  5' AGCCGCGTGTAGCCATCCC   4998       C_  C
                                AGCCGC  GT GCCATCCC
                                ||||||  || ||||||||
                                TCGGCG  CA CGGTAGGG
                                   CA  T
GAM209  LOC91266  3' CAGCCACCATCACCTTGTCCC  4999           A__
                                CAGCCGCCGTCGCC   TCCC
                                ||||||||||||||   ||||
                                GTCGGTGGTAGTGG   AGGG
                                      AAC
GAM209  LOC92360  3' CAGCCGACATCACCATCC    5000       C
                                CAGCCG CGTCGCCATCC
                                |||||| ||||||||||
                                GTCGGC GTAGTGGTAGG
                                   T
GAM209  LOC93081  5' CAACCGCCGTCACTCCC     5001           CA
                                CAGCCGCCGTCGC  TCCC
                                ||||||||||||  ||||
                                GTTGGCGGCAGTG  AGGG
                                      __
GAM210  ALDH1A2   3' CTGGGCTTCATCCTCCT     5004       CCC
                                CTGGGC   CGTCCTCTT
                                ||||||   |||||||||
                                GACCCG   GTAGGAGGA
                                   AA_
GAM210  B4GALT3   5' GATCTAGGTTCAAGCTGTCTTC 5005        CCCCC___   C
          TT                    GATCTGGG       GTC TCTT
                                ||||||||       ||| ||||
                                CTAGATCC       CAG AGAA
                                    AAGTTCGA   A
GAM210  CRY2      3' AATCTGGGCCTCGGCCT     5006         CC  T
                                GATCTGGGCC  CG CCT
                                ||||||||||  || |||
                                TTAGACCCGG  GC GGA
                                    A_  C
GAM210  ENG       3' TCTGGGCTGGGCCCTCTT    5007        CCCC
                                TCTGGGC   GTCCTCTT
                                |||||||   ||||||||
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                                AGACCCG   CGGGAGAA
                                   ACC_
GAM210  GNB3    5'  GATCTGGATAATCCTTCTT   5008       CCCCC   _
                                GATCTGGG    GTCCT CTT
                                ||||||||    ||||| |||
                                CTAGACCT    TAGGA GAA
                                    AT___    A
GAM210  HSD17B1  5'  GACCTTCTCCTGTCCTCTT   5009      GGG  CCC
                                GATCT   CC   GTCCTCTT
                                |||||   ||   ||||||||
                                CTGGA   GG   CAGGAGAA
                                  AGA  A__
GAM210  IL18    5'  TCTGAGGTTCCTTTCCTCTT   5010      _  CC  CG
                                TCTG GG  CC  TCCTCTT
                                |||| ||  ||  |||||||
                                AGAC CC  GG  AGGAGAA
                                  T  AA  AA
GAM210  KCNN4    3'  GATCCGGGCCCCTAGTACCCTC 5011          CG___
           TT                    GATCTGGGCCCC    TCCTCTT
                                ||||||||||||    |||||||
                                CTAGGCCCGGGG    GGGAGAA
                                      ATCAT
GAM210  LLGL1    3'  GGGCCCCACCTGTCCTCTT   5012       C___
                                GGGCCCC   GTCCTCTT
                                |||||||   ||||||||
                                CCCGGGG   CAGGAGAA
                                    TGGA
GAM210  LPIN2    3'  TCTGGGCTCCTGACAGTTCTCT 5013       _  CC___  C    III
           TA                    TCTGGGC CC    GT CTCTT   A
                                ||||||| ||    || |||||  |
                                AGACCCG GG    CA GAGAA   T
                                    A  ACTGT  A    III
GAM210  MYO7A    3'  GAGCTAGATTGTCCTCTT    5014    T    CCCCC
                                GA CTGGG    GTCCTCTT
                                || |||||    ||||||||
                                CT GATCT    CAGGAGAA
                                 C    AA___
GAM210  NDST1    5'  GATCTGGGCCCCCAGTCCT   5015          _
                                GATCTGGGCCCCC GTCCT
                                |||||||||||| |||||
                                CTAGACCCGGGGG CAGGA
                                       T
GAM210  PNUTL1   3'  GATCCTGGGAATCCTCTT    5016     _   CCCCC
                                GATC TGGG    GTCCTCTT
                                |||| ||||    ||||||||
                                CTAG ACCC    TAGGAGAA
                                  G   T____
GAM210  SECTM1   5'  GACTTGGGCCCCTGGTCCT   5017    TC      C_
                                GA  TGGGCCCC  GTCCT
                                ||  ||||||||  |||||
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```
                                CT  ACCCGGGG  CAGGA
                                 GA       AC
GAM210  SERPINE1  3'  TGTCCCCCCACTCCGTCCT   5018     GG     _  _
                                TG  CCCCCG TCC TCTT
                                ||  |||||| ||| ||||
                                AC  GGGGGT AGG AGGA
                                 AG     G   C
GAM210  SRRM1     3'  TCTGGGCCCTTCCAGCCT    5019          __  T
                                TCTGGGCCC  CCG CCT
                                |||||||||  ||| |||
                                AGACCCGGG  GGT GGA
                                      AA   C
GAM210  TLL2      5'  GGCGCCCCCTGTCTTCTT    5020     _     _  C
                                GG GCCCCC GTC TCTT
                                || |||||| ||| ||||
                                CC CGGGGG CAG AGAA
                                 G     A   A
GAM210  TNFSF15   3'  GATCTGGGCTCACCGCAACCT  5021          CC_   __
                                GATCTGGGC   CCGT  CCT
                                |||||||||   ||||  |||
                                CTAGACCCG   GGCG  GGA
                                      AGT    TT
GAM210  WDR1      3'  GACTGGGCCCTCCTGCCTCTT  5022     T      _  GT
                                GA CTGGGCCC CC  CCTCTT
                                || |||||||| ||  ||||||
                                CT GACCCGGG GG  GGAGAA
                                 _       A  AC
GAM210  ACAS2     3'  GACCTGGGCCCTGTCCT     5023          CC
                                GATCTGGGCCC  GTCCT
                                ||||||||||   |||||
                                CTGGACCCGGG  CAGGA
                                      A_
GAM210  ACAS2     3'  GACCTGGGCCCTGTCCT     5023          CC
                                GATCTGGGCCC  GTCCT
                                ||||||||||   |||||
                                CTGGACCCGGG  CAGGA
                                      A_
GAM210  BM-002    3'  GATCTGGGCTTCCCCATC    5024          __
                                GATCTGGGC  CCCCGTC
                                |||||||||  |||||||
                                CTAGACCCG  GGGGTAG
                                      AA
GAM210  BNIP2     5'  TGGCCCCCTCGTCCTCTT    5025      G   _
                                TGG CCCC CGTCCTCTT
                                ||| |||| |||||||||
                                ACC GGGG GCAGGAGAA
                                  G   A
GAM210  C1orf34   3'  AAGCCTTCCTGTCCTCTT    5026        __  C
                                GGGCC  CC GTCCTCTT
                                |||||  || ||||||||
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                                TTCGG  GG CAGGAGAA
                                   AA  A
GAM210  CHSY1    5'  GCCTGTCCCCGTCCTCTT    5027    A   GGC
                                G TCTG   CCCCGTCCTCTT
                                | ||||   ||||||||||||
                                C GGAC   GGGGCAGGAGAA
                                _    A__
GAM210  FLJ12768 3'  GATCTGGGCCACCTGTTCTCT  5028          _  C  C
                                GATCTGGGCC CC GT CTCT
                                |||||||||| || || ||||
                                CTAGACCCGG GG CA GAGA
                                      T  A  A
GAM210  KIAA0599 3'  AATCTGGGTCCCTCTGATCTT  5029         C   CGTCC
                                GATCTGGG CCC     TCTT
                                |||||||| |||     ||||
                                TTAGACCC GGG     AGAA
                                     A   AGACT
GAM210  KIAA0781 3'  GACCTGGGTCTGAATGTCTTCT 5030         CCCCC__   C
             T                   GATCTGGG      GTC TCTT
                                 ||||||||      ||| ||||
                                 CTGGACCC      CAG AGAA
                                     AGACTTA   A
GAM210  KIAA1014 3'  GAACTAGAATTGTCCTCTT    5031     T    CCCCC
                                GA CTGGG     GTCCTCTT
                                || |||||    ||||||||
                                CT GATCT     CAGGAGAA
                                 T    TAA__
GAM210  MGC15606 3'  GATCTGGGGCCCTCCT      5032         C   CG
                                GATCTGGG CCC  TCCT
                                |||||||| |||  ||||
                                CTAGACCC GGG  AGGA
                                     C   __
GAM210  NPTXR    3'  AATCTGGGCTCCATCACT    5033         CC    _
                                GATCTGGGC  CCGTC CT
                                |||||||||  ||||| ||
                                TTAGACCCG  GGTAG GA
                                     A_     T
GAM210  NPTXR    3'  AATCTGGGCTCCATCACT    5033         CC    _
                                GATCTGGGC  CCGTC CT
                                |||||||||  ||||| ||
                                TTAGACCCG  GGTAG GA
                                     A_     T
GAM210  OLFM3    5'  GATCTGGGTTTTTGCCCCTCTT 5034         CCCCC   _
                                GATCTGGG     GTCC TCTT
                                ||||||||     |||| ||||
                                CTAGACCC     CGGG AGAA
                                     AAAAA    G
GAM210  PHT2     5'  CTGGGCCCCCCGCGGCTCTT   5035          _  C_
                                CTGGGCCCCC GT  CTCTT
                                |||||||||| ||  |||||
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                                GACCCGGGGG CG  GAGAA
                                      G  CC
GAM210  SCAMP5   3'  GACCTGGGCCCTCCT      5036          CCG
                                GATCTGGGCCC   TCCT
                                ||||||||||   ||||
                                CTGGACCCGGG   AGGA
                                      ___
GAM210  SYNJ2BP  3'  GACTGAACGTCCTCT      5037     T     CCCC
                                GA CTGGGC    GTCCTCT
                                || ||||||    |||||||
                                CT GACTTG    CAGGAGA
                                 _    _____
GAM210  SYT12    3'  GACCTGGGTCTGGGCCTCTT  5038         CCCCC T
                                GATCTGGG     G CCTCTT
                                ||||||||     | ||||||
                                CTGGACCC     C GGAGAA
                                     AGACC _
GAM210  LOC124602 3' GATGTGGGCCCCCTCCT     5039     C        G
                                GAT TGGGCCCCC TCCT
                                ||| |||||||| ||||
                                CTA ACCCGGGGG AGGA
                                  C       _
GAM210  LOC126353 3' GATCTGTGCCACCCTCTT    5040       G   CCCG
                                GATCTG GCC    TCCTCTT
                                |||||| |||    |||||||
                                CTAGAC CGG    GGGAGAA
                                   A   T___
GAM210  LOC135932 5' GATAACTCCTGTCCTCTT    5041     CTG   C  C
                                GAT   GGC CC GTCCTCTT
                                |||   ||| || ||||||||
                                CTA   TTG GG CAGGAGAA
                                  ___   A  A
GAM210  LOC138389 5' TGGCTCCTCCCTGTCCTCTT  5042     G_  _   _
                                TGG  CC CCC GTCCTCTT
                                |||  || ||| ||||||||
                                ACC  GG GGG CAGGAGAA
                                  GA  A   A
GAM210  LOC145801 3' ATCTTCATCCTCCTCGTCTTCT 5043      GGG_  _  _   C
           T                     ATCT    CC CC CGTC TCTT
                                 ||||    || || |||| ||||
                                 TAGA    GG GG GCAG AGAA
                                   AGTA  A  A    A
GAM210  LOC147057 3' TCTGGGCCCTGCCTCTCTT   5044          CC   _
                                TCTGGGCCC  GTC CTCTT
                                |||||||||  ||| |||||
                                AGACCCGGG  CGG GAGAA
                                     A_   A
GAM210  LOC147229 5' GACCTGGGTCCGAGCAGCCT  5045          _  CC_  T
                                GATCTGGG CC   CG CCT
                                |||||||| ||   || |||
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                                CTGGACCC GG   GT GGA
                                    A  CTC  C
GAM210  LOC148137 3'  GACTTGGGCCCCAGGCTCTT  5046     TC       CGTC
                                GA  TGGGCCCC    CTCTT
                                ||  ||||||||    |||||
                                CT  ACCCGGGG    GAGAA
                                 GA       TCC_
GAM210  LOC150696 3'  GATCTGAGGTCTGTCCATCTC  5047         CCCCC   _
                                GATCTGGG     GTCC TCTT
                                ||||||||     |||| ||||
                                CTAGACTC     CAGG AGAG
                                    CAGA_    T
GAM210  LOC151647 3'  AATCTGGGTCAGTCATTCTT   5048         CCCCC   C_
                                GATCTGGG     GTC  TCTT
                                ||||||||     |||  ||||
                                TTAGACCC     CAG  AGAA
                                    AGT__    TA
GAM210  LOC151816 5'  TCTGGGCCTGTCTCTT      5049         CCC   C
                                TCTGGGCC   GTC TCTT
                                ||||||||   ||| ||||
                                AGACCCGG   CAG AGAA
                                    A__    _
GAM210  LOC153505 3'  GAGCTGGGCCACCCTCTT    5050     T      CCCG
                                GA CTGGGCC    TCCTCTT
                                || |||||||    |||||||
                                CT GACCCGG    GGGAGAA
                                 C      T___
GAM210  LOC153516 3'  GATCCGGGCCCTGGTGATTCCT 5051           CCG____
           CTT                    GATCTGGGCCC      TCCTCTT
                                ||||||||||       |||||||
                                CTAGGCCCGGG      AGGAGAA
                                     ACCACTA
GAM210  LOC154760 5'  GATAACTCCTGTCCTCTT    5041      CTG   C  C
                                GAT   GGC CC GTCCTCTT
                                |||   ||| || ||||||||
                                CTA   TTG GG CAGGAGAA
                                  ___   A  A
GAM210  LOC158263 5'  GATCTGGCATCCTCT       5052         GCCCC
                                GATCTGG     CGTCCTCT
                                |||||||     ||||||||
                                CTAGACC     GTAGGAGA
                                   _____
GAM210  LOC196047 5'  GATTGGGGTCCACCCTCTT   5053      C    CCC  GT
                                GAT TGGG   CC  CCTCTT
                                ||| ||||   ||  ||||||
                                CTA ACCC   GG  GGAGAA
                                  _    CA_  TG
GAM210  LOC196993 3'  GATCCGGGTGATGCCTCTT   5054         CCCCC T
                                GATCTGGG     G CCTCTT
                                ||||||||     | ||||||
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                                CTAGGCCC    C GGAGAA
                                    ACTA_ _
GAM210  LOC203274 5'  TGGCTCCTCCCTGTCCTCTT  5042     G_ _  _
                                TGG  CC CCC GTCCTCTT
                                |||  || ||| ||||||||
                                ACC  GG GGG CAGGAGAA
                                  GA  A   A
GAM210  LOC203397 3'  GATGTGGGCCCCCTCCT    5039     C       G
                                GAT TGGGCCCCC TCCT
                                ||| ||||||||| ||||
                                CTA ACCCGGGGG AGGA
                                  C       _
GAM210  LOC221399 5'  GATCTGTGCAATCCTCTT    5055       G  CCCC
                                GATCTG GC    GTCCTCTT
                                |||||| ||    ||||||||
                                CTAGAC CG    TAGGAGAA
                                   A  T___
GAM210  LOC221442 3'  TCTGAGCCAGCTTCCTCTT   5056         CCCG
                                TCTGGGCC    TCCTCTT
                                ||||||||    |||||||
                                AGACTCGG    AGGAGAA
                                    TCGA
GAM210  LOC51233  5'  GATCTGGGTCCTCAGCCCT   5057         C  C _
                                GATCTGGG CC C GTCCT
                                |||||||| || | |||||
                                CTAGACCC GG G CGGGA
                                    A  A T
GAM210  LOC90538  3'  GATCTGGGATCTGCTCCCTCCT 5058        _____ C   G
            CTT                   GATCTGG    GC CCC TCCTCTT
                                |||||||    || ||| |||||||
                                CTAGACC    CG GGG AGGAGAA
                                   CTAGA  A  _
GAM210  LOC91812  5'  GATGCTGGAGTCCTCT     5059     _    CCCCC
                                GAT CTGGG    GTCCTCT
                                ||| |||||    |||||||
                                CTA GACCT    CAGGAGA
                                  C   _____
GAM210  LOC91813  5'  GATGCTGGAGTCCTCT     5059     _    CCCCC
                                GAT CTGGG    GTCCTCT
                                ||| |||||    |||||||
                                CTA GACCT    CAGGAGA
                                  C   _____
GAM211  CUL3     3'  CACTAGTTACTGAAAATGAGTA 5062     A   AT   A
                                CAC AGT  TATT AAAATGAGTA
                                ||| |||  |||| ||||||||||
                                GTG TCA  ATGA TTTTACTCAT
                                  A  __   C
GAM211  C6orf33   3'  ACAAGTATTATTAAGCATCAGT 5063           AA  G
            A                    ACAAGTATTATTAA  AT AGTA
                                ||||||||||||||  || ||||
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                                TGTTCATAATAATT  TA TCAT
                                        CG  G
GAM211  DKFZP564J157 3'  CACAAGTATTATAAG       5064            TAAAAAT
                                CACAAGTATTAT      GAG
                                ||||||||||||      |||
                                GTGTTCATAATA      TTC
                                          _______
GAM211  FLJ11210  3'  CAAATATAAAATGAGT      5065         TATTA
                                CAAGTAT    AAAATGAGT
                                |||||||    |||||||||
                                GTTTATA    TTTTACTCA
                                     _____
GAM211  KIAA1796  3'  ACAAGTATTTTTAAAAATG   5066          A
                                ACAAGTATT TTAAAAATG
                                ||||||||| |||||||||
                                TGTTCATAA AATTTTTAC
                                      A
GAM211  NUCKS    3'  ACAAGGTAAAAAATGAGT    5067       TATTATT
                                ACAAG      AAAAATGAGT
                                |||||      ||||||||||
                                TGTTC      TTTTTACTCA
                                   CAT____
GAM211  LOC152313 3'  GCACAATTAAAAATGGGTA   5068       T        A
                                GTAT ATTAAAAATG GTA
                                |||| |||||||||| |||
                                CGTG TAATTTTTAC CAT
                                   T        C
GAM212  GSPT1    5'  TGTGTGGTGGACAGAGAGC   5071     GA    AG TTGG
                                TG  TGGTG  C    AGAGAGC
                                ||  |||||  |    |||||||
                                AC  ACCAC  G    TCTCTCG
                                 AC     CT ____
GAM212  LZTFL1   3'  TGGAATGGATTTTTGGAGAGAG 5072      _   TGAGC
                                TGGA TGG     TTGGAGAGAG
                                |||| |||     ||||||||||
                                ACCT ACC     AACCTCTCTC
                                   T   TAAA_
GAM212  POU4F1   3'  GGTGGAGGAAAGAGAGC     5073      _ CTT
                                GGTG AG   GGAGAGAGC
                                |||| ||   |||||||||
                                CCAC TC   TTTCTCTCG
                                   C  C__
GAM212  SH3BP2   3'  TGGAAGGTGTGCCAGGGAGAG  5074      T   A   T  A
                                TGGA GGTG GCT GG GAGAG
                                |||| |||| ||| || |||||
                                ACCT CCAC CGG CC CTCTC
                                   T   A   T  _
GAM212  TEM5     3'  GGGTGGGAGTACTTGGGGAG   5075     A   T   __    A
                                GG TGG GAG  CTTGG GAG
                                || ||| |||  ||||| |||
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                                CC ACC CTC  GAACC CTC
                                 C  _  AT    C
GAM212  TNFRSF8  3' TGGGTGGGGCCCACAGAGAGCG 5076     A  TGA    G
                                TGG TGG  GCTTG AGAGAGCG
                                ||| |||  ||||| ||||||||
                                ACC ACC  CGGGT TCTCTCGC
                                  C  C__    G
GAM212  C1orf29  3' TGAATGTGATGTTGGAGAGAG  5077       G  GC
                                TGGATG TGA  TTGGAGAGAG
                                |||||| |||  ||||||||||
                                ACTTAC ACT  AACCTCTCTC
                                    _  AC
GAM212  CENTA1   3' TGGAGGTGGGGGGAGGGC    5078     T   AGCTT  A  A
                                TGGA GGTG    GG GAG GC
                                |||| ||||    || ||| ||
                                ACCT CCAC    CC CTC CG
                                  _   CC___ _  C
GAM212  DCOHM    3' TGGATGGTGAGGTTATAG    5079          C  G
                                TGGATGGTGAG TTG AG
                                |||||||||| ||| ||
                                ACCTACCACTC AAT TC
                                       C  A
GAM212  EMILIN   3' TGGAGGGCCAGTGGAGGGAGCG 5080      T  G  CT    A
                                TGGA GGT AG  TGGAG GAGCG
                                |||| ||| ||  ||||| |||||
                                ACCT CCG TC  ACCTC CTCGC
                                  C  G __    C
GAM212  KIAA0552 3' GGGTGGGAGGAAGAGAG    5081    A  T  CTT
                                GG TGG GAG   GGAGAGAG
                                || ||| |||   ||||||||
                                CC ACC CTC   CTTCTCTC
                                 C  _  ___
GAM212  KIAA1715 3' GGATGGTGAGCAGAGAG    5082          TT
                                GGATGGTGAGC  GGAGAG
                                ||||||||||  ||||||
                                CCTACCACTCG  TCTCTC
                                          __
GAM212  MBLL39   3' TGGATGGTGAGTTTGAAA    5083          C
                                TGGATGGTGAG TTGGAG
                                |||||||||| ||||||
                                ACCTACCACTC AACTTT
                                       A
GAM212  MGC10966 3' TGGGTGTGGGCTTGGGAG    5084     ATG  A    A
                                TGG   GTG GCTTGG GAG
                                |||   ||| |||||| |||
                                ACC   CAC CGAACC CTC
                                  CA_  C    _
GAM212  NAGK     3' TGTCCACTGAGCTTGGAG    5085     GA  G
                                TG  TG TGAGCTTGGAG
                                ||  || ||||||||||
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                                AC  GT ACTCGAACCTC
                                 AG  G
GAM212  PTK9L    3'  GGATGGTGGCAGGGAGC     5086         A  TT  AGA
                                GGATGGTG GC  GG   GAGC
                                |||||||| ||  ||   ||||
                                CCTACCAC CG  CC   CTCG
                                     _  T_  ____
GAM212  VPS4A    3'  TGGATGTGAACCTAGGAG    5087        G       A
                                TGGATG TGAGCTTGG GAG
                                |||||| ||||||||| |||
                                ACCTAC ACTTGGATC CTC
                                   _       _
GAM212  LOC157931 3'  GGATGGTGGCAAGTGGGGGAG  5088         A  T__   A_
                                GGATGGTG GC   TGG  GAG
                                |||||||| ||   |||  |||
                                CCTACCAC CG   ACC  CTC
                                     _ TTC   CC
GAM212  LOC201175 5'  TGGTGGGACTGGGGAGGGC    5089       A_   T  A   A
                                TGGTG  GCT GG GAG GC
                                |||||  ||| || ||| ||
                                ACCAC  TGA CC CTC CG
                                   CC   C  _   C
GAM212  LOC220002 3'  TGCATGGTGAGCTGCAGAG    5090     G        T G
                                TG ATGGTGAGCT G AGAG
                                || ||||||||| | ||||
                                AC TACCACTCGA C TCTC
                                 G         _ G
GAM212  LOC253980 3'  GGATGGTGGGGAGGAGGGGGCG 5091         AGCTT    AGA
                                GGATGGTG    GGAG   GCG
                                ||||||||    ||||  |||
                                CCTACCAC    CCTC   CGC
                                     CCCT_    CCC
GAM212  LOC256158 5'  TGGATGGTGAACTTCCCCTCGG 5092             GGAGAGA
              CG                  TGGATGGTGAGCTT      GCG
                                |||||||||||||       |||
                                ACCTACCACTTGAA      CGC
                                       GGGGAGC
GAM212  LOC256980 3'  TGGAGGGTGGGGGGCGGGAGCG  5093      T   AGCTT  AGA
                                TGGA GGTG    GG   GAGCG
                                |||| ||||    ||   |||||
                                ACCT CCAC    CC   CTCGC
                                  C   CC___  GCC
GAM212  LOC92154  3'  GGATGGTGTGGAGGGGGC    5094        AGCT    AGA
                                GGATGGTG   TGGAG   GC
                                ||||||||   |||||  ||
                                CCTACCAC   ACCTC   CG
                                     _____    CCC
GAM213  HOXC11   3'  TCGCCGAGGTGTGTTTTC    5097      _ T   GGACGC
                                TCGC G GGTG     GTTTTC
                                |||| | ||||     ||||||
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                                AGCG C CCAC     CAAAAG
                                  G T   A_____
GAM213  TNFSF4   3'  TCTGTGGCAAAGAATGTGTTTT 5098    GC   TG _  CGC_
            C                    TC  GTGG  G GA   GTTTTC
                                 ||  ||||  | ||   ||||||
                                 AG  CACC  T CT   CAAAAG
                                  A_   GT T  TACA
GAM213  APCL     3'  CATCCGTGGTGGGGC      5099      G       AC
                                 CATC CGTGGTGGG  GC
                                 |||| |||||||||  ||
                                 GTAG GCACCACCC  CG
                                   _       __
GAM214  GCN5L1   5'  CCATGTCACGTGCCCGCTG   5102    TC       G
                                 CC  GTCACGTGC CGCTG
                                 ||  |||||||||  |||||
                                 GG  CAGTGCACG GCGAC
                                  TA       G
GAM214  P4HB     3'  TCGGAGGCGTGCGCTGCTG   5103    TCAC   C
                                 TCG   GTG GCGCTGCTG
                                 |||   ||| |||||||||
                                 AGC   CGC CGCGACGAC
                                   CTC_   A
GAM214  POLR2E   3'  GACCTCGTCACGTCCACCTG   5104          G   G
                                 GACCTCGTCACGT CGC CTG
                                 |||||||||||||  ||| |||
                                 CTGGAGCAGTGCA GTG GAC
                                        G   _
GAM214  DKFZP434H204 5'  GACCTCGTCGTGGCCACC    5105        AC   CGC  TG
                                 GACCTCGTC  GTG   GC  CT
                                 |||||||||  |||   ||  ||
                                 CTGGAGCAG  CAC   CG  GG
                                      __   ____  GT
GAM214  DRIM     5'  GACTTTCTCACGTGCGGCT   5106     C_  G       C
                                 GAC  TC TCACGTGCG GCT
                                 |||  ||  |||||||||  |||
                                 CTG  AG AGTGCACGC CGA
                                   AA  _       _
GAM214  FLJ20195 3'  GACCCGCAGCGCGCTGCT    5107      T  T  CGT
                                 GACC CG CA   GCGCGCTGCT
                                 |||| ||  ||   ||||||||||
                                 CTGG GC GT   CGCGCGACGA
                                   _  _  ____
GAM214  FLJ31978 3'  GACCTCGCTGTGTGGCTG    5108        CAC   CGC
                                 GACCTCGT   GTG   GCTG
                                 ||||||||   |||   ||||
                                 CTGGAGCG   CAC   CGAC
                                     A__   AC_
GAM214  MGC12760 3'  CCTCGTCATGCTCCTGCTG   5109        CG   GCG
                                 CCTCGTCA  TGC   CTGCTG
                                 ||||||||  |||   ||||||
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                                GGAGCAGT  ACG   GACGAC
                                    __   AG_
GAM214  PHYHIP   3'  CCTTGCCGGCCCGCTGCTG   5110     C  CA  T  G
                                CCT GT  CG GC CGCTGCTG
                                ||| ||  || || ||||||||
                                GGA CG  GC CG GCGACGAC
                                  A  __  _  G
GAM214  SAMHD1   3'  GACCTCACTTGTGCGTTGCTG 5111        TCAC    CGC
                                GACCTCG   GTGCG   TGCTG
                                |||||||   |||||  |||||
                                CTGGAGT   CACGC   ACGAC
                                    GAA_    A__
GAM214  LOC138752 3'  GACCTCGTTGTGGCTCTG    5112        CAC   C  G
                                GACCTCGT   GTG GC CTG
                                ||||||||   ||| || |||
                                CTGGAGCA   CAC CG GAC
                                    A__   _  A
GAM214  LOC149579 3'  CCTCGTCATGCTCCTGCTG   5109        CG   GCG
                                CCTCGTCA  TGC   CTGCTG
                                ||||||||  |||   ||||||
                                GGAGCAGT  ACG   GACGAC
                                    __   AG_
GAM214  LOC153688 3'  CTTCTCACGTGCAGCTG     5113     CG       C
                                CT  TCACGTGCG GCTG
                                ||  ||||||||| ||||
                                GA  AGTGCACGT CGAC
                                  AG       _
GAM214  LOC221035 3'  CCTTGTTATGTCACTGCTG   5114     C  CAC   CG
                                CCT GT   GTG  CGCTGCTG
                                ||| ||   |||  ||||||||
                                GGA CA   TAC  GTGACGAC
                                  A  A__   A_
GAM214  LOC92912  5'  GCCTCGTCGAGCGCTGCT    5115    A      ACGT C
                                G CCTCGTC    G GCGCTGCT
                                | |||||||    | ||||||||
                                C GGAGCAG    C CGCGACGA
                                _      _____ T
GAM215  ABL2     5'  CCTCCTCGGCTCCGGCCTCG   5118     GG TC        C
                                CC  T  CGGCTCCGGCC CG
                                ||  |  |||||||||||| ||
                                GG  G  GCCGAGGCCGG GC
                                 A_ GA         A
GAM215  ARIH1    5'  CAGGCCTGGCTCCGGCCCCG   5119      TT C
                                CGG  C GGCTCCGGCCCCG
                                |||  | ||||||||||||||
                                GTC  G CCGAGGCCGGGGC
                                  CG A
GAM215  ARIH1    5'  GCCCCGGCTCTCGCTCCGGCTC 5120          CG       C
            CG                    GCCCCGGTTC  GCTCCGGC CCG
                                ||||||||||  |||||||| |||
```

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                                CGGGGCCGAG  CGAGGCCG GGC
                                      AG       A
GAM215  COL6A2   5'  CCTGGTCCCGAGGAGGCTCCG  5121     C     _____
                                CC GGTTCC    GGCTCCG
                                || ||||||    |||||||
                                GG CCAGGG    CCGAGGC
                                 A     CTCCT
GAM215  COL6A2   5'  CCTGGTCCCGAGGAGGCTCCG  5121     C     _____
                                CC GGTTCC    GGCTCCG
                                || ||||||    |||||||
                                GG CCAGGG    CCGAGGC
                                 A     CTCCT
GAM215  CTSZ     5'  GGATCCCGCCCCGGCCTCG   5122     T   G       C
                                GG TCC GCTCCGGCC CG
                                || ||| ||||||||| ||
                                CC AGG CGGGGCCGG GC
                                 T   G        A
GAM215  DLG5     3'  CCTGGTTCCGGATCCTTCCCC  5123     C       C   GG
                                CC GGTTCCGG TCC  CCCC
                                || |||||||| |||  ||||
                                GG CCAAGGCC AGG  GGGG
                                 A       T   AA
GAM215  DMN      5'  GCCGCGACGCTCCGGCCC    5124     C   TTCCG       C
                                GCC CGG    GCTCCGGCC C
                                ||| |||    ||||||||| |
                                CGG GCT    CGAGGCCGG G
                                  C   G____        A
GAM215  GCLM     5'  GCTGCGGCTCCGGCTCCG    5125     CC
                                GC  CGGTTCCGGCTCCG
                                ||  ||||||||||||||
                                CG  GCCGAGGCCGAGGC
                                 AC
GAM215  GNA11    5'  GCCGCGGCCCTCCGGCCC    5126     C    CCGG       C
                                GCC CGGTT    CTCCGGCC C
                                ||| |||||    |||||||| |
                                CGG GCCGG    GAGGCCGG G
                                  C    _____        A
GAM215  GOSR2    5'  GCTCCGGCTCTGGCTTCCTCG  5127          C   __ _
                                GTTCCGGCTC GGC  CC CG
                                |||||||||| |||  || ||
                                CGAGGCCGAG CCG  GG GC
                                      A   AA  A
GAM215  GOSR2    5'  GCCACGGCTCCGGCTCTGCGGG 5128     C         _____ GCCC
           GC                     CC CGGTTCCGGCTC    CG    C
                                || ||||||||||||    ||    |
                                GG GCCGAGGCCGAG    GC    G
                                 T          ACIII  CCCG
GAM215  GOSR2    5'  GCCACGGCTCCGGCTCTGCGGG 5128     C         _____ GCCC
           GC                     CC CGGTTCCGGCTC    CG    C
                                || ||||||||||||    ||    |
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                                GG GCCGAGGCCGAG    GC   G
                                 T          ACIII  CCCG
GAM215  GOSR2    5'  GCTCCGGCTCTGGCTTCCTCG  5127          C  __ _
                                GTTCCGGCTC GGC  CC CG
                                |||||||||| |||  || ||
                                CGAGGCCGAG CCG  GG GC
                                      A   AA  A
GAM215  HDAC5    5'  GCTGCGGCTCGAGCTCCGGCTT 5129     CC     C       CC
              CG                  GC  CGGTTC GGCTCCGGC  CG
                                || ||||||  |||||||||  ||
                                CG  GCCGAG TCGAGGCCG  GC
                                 AC     C        AA
GAM215  HDAC5    5'  GCTGCGGCTCGAGCTCCGGCTT 5129     CC     C       CC
              CG                  GC  CGGTTC GGCTCCGGC  CG
                                || ||||||  |||||||||  ||
                                CG  GCCGAG TCGAGGCCG  GC
                                 AC     C        AA
GAM215  IRF1     5'  GCCTCGGTTCGGCGGGGC    5130      C     C   TCC
                                GCC CGGTTC GGC   GGC
                                ||| ||||||  |||   |||
                                CGG GCCAAG CCG   CCG
                                 A      _   CC_
GAM215  KCNK4    5'  GCCCGGGTTCCAGCACGGCCTC 5131       C        TC     C
              G                   GCCC GGTTCCGGC  CGGCC CG
                                |||| |||||||||  ||||| ||
                                CGGG CCAAGGTCG  GCCGG GC
                                  C        T_     A
GAM215  LRP3     5'  CGGCTCCGGCTCCGGTTCCG   5132              CC
                                CGGTTCCGGCTCCGG  CCG
                                ||||||||||||||  |||
                                GCCGAGGCCGAGGCC  GGC
                                         AA
GAM215  LRP3     5'  GCTCCGGTTCCGGCTGCGGCTC 5133     C          C   C
              CG                    GC CCGGTTCCGGCT CGGC CCG
                                || ||||||||||| |||| |||
                                CG GGCCAAGGCCGA GCCG GGC
                                 A          C   A
GAM215  LRP3     5'  GCCCCGCGGCTCCGGCTCCG   5134        GTTC         C
                                GCCCCG    CGGCTCCGGC CCG
                                ||||||    |||||||||| |||
                                CGGGGC    GCCGAGGCCG GGC
                                     ____          A
GAM215  LRP3     5'  GCTCCGGTTCCGGCTGCGGCTC 5133     C          C   C
              CG                    GC CCGGTTCCGGCT CGGC CCG
                                || ||||||||||| |||| |||
                                CG GGCCAAGGCCGA GCCG GGC
                                 A          C   A
GAM215  MAP3K7   5'  GCCGTGTCCGGCTCTGGCTCCG 5135      ____       C
                                GCC    CCGGTTC GGCTCCG
                                |||    ||||||| |||||||
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                                CGG   GGCCGAG CCGAGGC
                                  CACA      A
GAM215  MAPRE1   5'  GCCCGCAACCGGCTCCGGTTCC 5137      _  TT       CC
            G                    GCCC CGG  CCGGCTCCGG  CCG
                                 |||| |||  ||||||||||  |||
                                 CGGG GTT  GGCCGAGGCC  GGC
                                   C  __        AA
GAM215  MAPRE1   5'  GCTCCGGTTCCGTCTTCG    5136    C       G  C
                                 GC CCGGTTCCG CT CG
                                 || |||||||| || ||
                                 CG GGCCAAGGC GA GC
                                  A       A  A
GAM215  MTMR1    5'  GCCCCGGGTTCGGGCCCC    5138        _  C
                                 GCCCCGG TTC GGCTCC
                                 ||||||| ||| ||||||
                                 CGGGGCC AAG CCGGGG
                                     C  C
GAM215  NAGA     5'  GCCTACGGGCGCCTTCGGCCCC 5139     C_  TTC  G  C
            G                    GCC  CGG   CG CT CGGCCCCG
                                 |||  |||   || || ||||||||
                                 CGG  GCC   GC GA GCCGGGGC
                                  AT   C__  G  A
GAM215  NEU1     5'  GCCCCGGTCTGGAGGCCCC   5140         CC  CTCC
                                 GCCCCGGTT  GG   GGCCCC
                                 |||||||||  ||   ||||||
                                 CGGGGCCAG  CC   CCGGGG
                                      A_  T___
GAM215  NFE2L2   5'  GCCCTGTTCCGGCTGCCG    5141      CG       _
                                 GCCC  GTTCCGGCT CCG
                                 ||||  |||||||| |||
                                 CGGG  CAAGGCCGA GGC
                                   A_       C
GAM215  NKX2H    3'  CCAGGCGTTCGGCTCCGGCCC  5142    C   TC_
                                 CC GGT   CGGCTCCGGCCC
                                 || |||   ||||||||||||
                                 GG CCG   GCCGAGGCCGGG
                                  T   CAA
GAM215  NRBP     5'  GCTCGGGTTCCGGGGCCCC   5143    CCC      CTCC
                                 GC   GGTTCCGG   GGCCCC
                                 ||   ||||||||   ||||||
                                 CG   CCAAGGCC   CCGGGG
                                  AGC      ____
GAM215  OLFM1    5'  CGCGCTCCGGCTCTGGCCCCG  5145    _       C
                                 CG GTTCCGGCTC GGCCCCG
                                 || ||||||||| |||||||
                                 GC CGAGGCCGAG CCGGGGC
                                  G        A
GAM215  OLFM1    5'  GCCCCGGCTCCGCTGGCTCCG  5144          ___
                                 GCCCCGGTTCC   GGCTCCG
                                 ||||||||||   |||||||
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                                CGGGGCCGAGG  CCGAGGC
                                      CGA
GAM215  OLFM1   5'  CGCGCTCCGGCTCTGGCCCCG  5145    _       C
                                CG GTTCCGGCTC GGCCCCG
                                || |||||||||| |||||||
                                GC CGAGGCCGAG CCGGGGC
                                 G        A
GAM215  OLFM1   5'  CGCGCTCCGGCTCTGGCCCCG  5145    _       C
                                CG GTTCCGGCTC GGCCCCG
                                || |||||||||| |||||||
                                GC CGAGGCCGAG CCGGGGC
                                 G        A
GAM215  OLFM1   5'  GCCCCGGCTCCGCTGGCTCCG  5144          ___
                                GCCCCGGTTCC  GGCTCCG
                                ||||||||||   |||||||
                                CGGGGCCGAGG  CCGAGGC
                                      CGA
GAM215  OLFM1   5'  GCCCCGGCTCCGCTGGCTCCG  5144          ___
                                GCCCCGGTTCC  GGCTCCG
                                ||||||||||   |||||||
                                CGGGGCCGAGG  CCGAGGC
                                      CGA
GAM215  PDXK    5'  GCTCGGGCTCGGGCTCCGGCCC 5146    CCC    C
          CG                    GC  GGTTC GGCTCCGGCCCCG
                                ||  ||||| ||||||||||||
                                CG  CCGAG CCGAGGCCGGGGC
                                 AGC    C
GAM215  PPP2R5D  5'  GCCCCGCTCCGGCTCCGGC   5147       G
                                GCCCCG TTCCGGCTCCGGC
                                |||||| ||||||||||||
                                CGGGGC GAGGCCGAGGCCG
                                     _
GAM215  PPP4C   5'  ACTCCGGTTCCGGCTCTCCGCG 5148          ________ GCCC
          GGGCCG                CGGTTCCGGCTC     CG   CG
                                ||||||||||||     ||   ||
                                GCCAAGGCCGAG     GC   GC
                                      AGGCIII  CCCG
GAM215  PVRL2   5'  GGCTCCGGCTCCGGCTCC   5149            C
                                GGTTCCGGCTCCGGC CC
                                |||||||||||||| ||
                                CCGAGGCCGAGGCCG GG
                                      A
GAM215  PVRL2   5'  GCCTGTGGGGCTCCGGCTCCG  5150    CC___
                                GCC   GGTTCCGGCTCCG
                                |||   ||||||||||||
                                CGG   CCGAGGCCGAGGC
                                 ACACC
GAM215  RAB2L   5'  CCGTCGGTCTCCGGCCCC   5151    GTTC  _
                                CCG   CGG CTCCGGCCCC
                                |||   ||| ||||||||||
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                                GGC   GCC GAGGCCGGGG
                                 A___  A
GAM215  RASD1   5' GCTTGGGGCTCCGGCTCCG  5152    CCC_
                                GC   GGTTCCGGCTCCG
                                ||   ||||||||||||
                                CG   CCGAGGCCGAGGC
                                 AACC
GAM215  SLC22A2  5' GGTTCCAGTCCACCTCG    5153       C   G  C
                                GGTTCCGG TCCG CC CG
                                |||||||| |||| || ||
                                CCAAGGTC AGGT GG GC
                                    _   _ A
GAM215  TNFRSF11A 3' GCCCTGGCTCCGAGCTTCG   5154     C     _  C
                                GCCC GGTTCCG GCT CG
                                |||| ||||||| ||| ||
                                CGGG CCGAGGC CGA GC
                                  A     T  A
GAM215  TRAM    5' GCCCCGGTTCTGCTCTTCCC  5155        CG   CGG
                                GCCCCGGTTC  GCTC   CCC
                                ||||||||||  ||||   |||
                                CGGGGCCAAG  CGAG   GGG
                                    A_   AA_
GAM215  WT1     5' GCCCCGCGGCTCCTCCGGCCC 5156      __    GGC
                                GCCCC  GGTTCC   TCCGGCCC
                                |||||  ||||||   ||||||||
                                CGGGG  CCGAGG   AGGCCGGG
                                  CG     ___
GAM215  WT1     5' GCCCCGCGGCTCCTCCGGCCC 5156      __    GGC
                                GCCCC  GGTTCC   TCCGGCCC
                                |||||  ||||||   ||||||||
                                CGGGG  CCGAGG   AGGCCGGG
                                  CG     ___
GAM215  WT1     5' GCCCCGCGGCTCCTCCGGCCC 5156      __    GGC
                                GCCCC  GGTTCC   TCCGGCCC
                                |||||  ||||||   ||||||||
                                CGGGG  CCGAGG   AGGCCGGG
                                  CG     ___
GAM215  WT1     5' GCCCCGCGGCTCCTCCGGCCC 5156      __    GGC
                                GCCCC  GGTTCC   TCCGGCCC
                                |||||  ||||||   ||||||||
                                CGGGG  CCGAGG   AGGCCGGG
                                  CG     ___
GAM215  ZNF198   5' CCCGGTTCTGGCTGCGCTCCG 5157       C   C  G C
                                CCCGGTTC GGCT CG C CCG
                                |||||||| |||| || | |||
                                GGGCCAAG CCGA GC G GGC
                                    A   C  _ A
GAM215  C19orf7  3' GGTTCCGGGTCTCTTCGCGGGG 5158       __  ________ GCCC
           CCG                  GTTCCGG  CTC     CG   CG
                                |||||||  |||     ||   ||
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                                CAAGGCC  GAG      GC    GC
                                    CA   AAGCIII  CCCG
GAM215  DKFZP434J1813 5'  GCTCCGGCTCCGGCTCCAACCC 5160     C
                                GC CCGGTTCCGGCTCCGGCCC
                                || ||||||||||||||||||
                                CG GGCCGAGGCCGAGGTTGGG
                                 A
GAM215  DKFZP434J1813 5'  GCGGGATCCGGCTCCGGCTCCG 5159     CCC  T          C
                                GC   GG TCCGGCTCCGGC CCG
                                ||   || |||||||||||| |||
                                CG   CC AGGCCGAGGCCG GGC
                                 C__  T          A
GAM215  DKFZp667O2416 5'  GCCTCGGCTCCGCGCCCC    5161     TC       _
                                GT  CGGCTCCG GCCCC
                                ||  |||||||| |||||
                                CG  GCCGAGGC CGGGG
                                 GA       G
GAM215  ECE2     5'  GCCCCGGTCCCCTGCCCGGCCC 5162           G_  T
              CG                    GCCCCGGTTCC  GC CCGGCCCCG
                                ||||||||||  || |||||||||
                                CGGGGCCAGGG  CG GGCCGGGGC
                                      GA  _
GAM215  FADS3    5'  GCCCGCTGCTCCGGCCCC    5163      CG   CCG
                                GCCC  GTT   GCTCCGGCCCC
                                ||||  |||   ||||||||||
                                CGGG  CGA   CGAGGCCGGGG
                                  __   ___
GAM215  FBXO2    5'  GCCCCGCCTCTGGCCCCG    5164       G   C
                                GCCCCG TTC GGCTCCG
                                |||||| ||| |||||||
                                CGGGGC GAG CCGGGGC
                                   G   A
GAM215  FLJ10211  5'  GGTCCCGGCTCTGGCCC     5165           C    C
                                GGTTCCGGCTC GGCC C
                                |||||||||| |||| |
                                CCAGGGCCGAG CCGG G
                                      A    A
GAM215  FLJ21438  5'  GCTCCGGCTCCGGGTCTGGCTC 5166     C        C  C   C
              CG                    GC CCGGTTCCGG TC GGC CCG
                                || |||||||||| || ||| |||
                                CG GGCCGAGGCC AG CCG GGC
                                 A        C  A   A
GAM215  FLJ21438  5'  GCTCCGGGTCTGGCTCCGGC   5167     C    T  C
                                GC CCGG TC GGCTCCGGC
                                || |||| || |||||||||
                                CG GGCC AG CCGAGGCCG
                                 A   C  A
GAM215  FLJ30663  5'  ACCCCGGGCTCCGGCTCTGCGG 5168       _       _____  GCCC
              GGC                   CCCGG TTCCGGCTC    CG    C
                                ||||| |||||||||    ||    |
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                                GGGCC GAGGCCGAG    GC   G
                                  C       ACIII  CCCG
GAM215  HMP19    3'  CCCAGCTGGTTCTGGCCC    5169       CC  C  C
                                CCCGGTT  GG TC GGCCC
                                |||||||  || || |||||
                                GGGTCGA  CC AG CCGGG
                                   __  A  A
GAM215  HNK-1ST  3'  CCCAGTTCTCAGCGGTCC    5170        _   TCC  _
                                CCCGGTTC CGGC   GG CC
                                |||||||| ||||   || ||
                                GGGTCAAG GTCG   CC GG
                                    A   ___  A
GAM215  KEAP1    5'  GCCATGGCCGCGCTCCGGCTCC 5171     ____  _
            G                    GCC   CCG GTTCCGGCTCCG
                                |||   ||| ||||||||||||
                                CGG   GGC CGAGGCCGAGGC
                                  TACC  G
GAM215  KIAA0073 5'  CCGGTTCCTCCGGGTCCCG   5172       GGC    C_
                                CCGGTTCC   TCCGG  CCCG
                                ||||||||   |||||  ||||
                                GGCCAAGG   AGGCC  GGGC
                                    ___     CA
GAM215  KIAA0415 3'  GCCCCGGCTCAGCGGCCC    5173         C   TCC
                                GCCCCGGTTC GGC   GGCCC
                                |||||||||| |||   |||||
                                CGGGGCCGAG TCG   CCGGG
                                   _  ___
GAM215  KIAA0515 5'  GCTCCAGCTTTCGGCTCTGCGG 5174   C     C_    _____  GCCC
            GGC                   CCGGTT  CGGCTC    CG   C
                                 ||||||  ||||||    ||   |
                                 GGTCGA  GCCGAG    GC   G
                                A     AA     ACIII  CCCG
GAM215  KIAA0544 3'  GCCCTGGTTCCGGTTTCC    5175      C      C_
                                GCCC GGTTCCGG  TCC
                                |||| ||||||||  |||
                                CGGG CCAAGGCC  AGG
                                  A       AA
GAM215  KIAA0682 3'  CCCGGTCCCCAGGGCCCCG   5176         _ CTCC
                                CCCGGTTCC GG   GGCCCCG
                                |||||||| ||   |||||||
                                GGGCCAGGG TC   CCGGGGC
                                    G  ____
GAM215  KIAA1668 5'  GCCCGGCTCCGGCTCTGGCTTC 5177      C        C   CC
            G                    GCCC GGTTCCGGCTC GGC  CG
                                |||| |||||||||| |||  ||
                                CGGG CCGAGGCCGAG CCG  GC
                                  _        A   AA
GAM215  KIAA1813 5'  GCCCGGCCCCGGCTCCGGCTCC 5178      C          C
            G                    GCCC GGTTCCGGCTCCGGC CCG
                                |||| ||||||||||||| |||
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                                CGGG CCGGGGCCGAGGCCG GGC
                                  _          A
GAM215  KIAA1813  5'  GCCCCGGCTCCGGCTCCGGCCC 5179
            CG                    GCCCCGGTTCCGGCTCCGGCCCCG
                                  |||||||||||||||||||||||
                                  CGGGGCCGAGGCCGAGGCCGGGGC

GAM215  KIAA1887  5'  GCCCATGGTTCGGCCGGCCCCG 5180      C_    C   TC
                                  GCCC  GGTTC GGC  CGGCCCCG
                                  ||||  ||||| |||  ||||||||
                                  CGGG  CCAAG CCG  GCCGGGGC
                                    TA    _  __
GAM215  MGC11303  5'  GCTGCAGCTCCGGCTCTGGCTC 5181     CC          C   C
            CG                    GC  CGGTTCCGGCTC GGC CCG
                                  ||  |||||||||||| ||| |||
                                  CG  GTCGAGGCCGAG CCG GGC
                                   AC          A   A
GAM215  MGC15396  5'  CCCGAAGGCCGGCTCCGGCCTC 5182       TT_          C
            G                     CCCGG   CCGGCTCCGGCC CG
                                  |||||   |||||||||||| ||
                                  GGGCT   GGCCGAGGCCGG GC
                                     TCC          A
GAM215  MGC15730  5'  GCGCCCGGCTCGACTCGGCTCC 5183     _      ____
            GGC                     GC CCCGGTTC    CGGCTCCGGC
                                  || ||||||||    ||||||||||
                                  CG GGGCCGAG    GCCGAGGCCG
                                   C       CTGA
GAM215  MGC15875  5'  GCTCAGGTTCGCACTCGGCCCC 5184     CCC     CG    C
            G                     GC   GGTTC  GCTC GGCCCCG
                                  ||   |||||  |||| |||||||
                                  CG   CCAAG  TGAG CCGGGGC
                                   AGT    CG   _
GAM215  MGC20702  5'  GCTCCAGCATTCTGGCCC    5185          __ C    C
                                  GTTCCGGC  TC GGCC C
                                  ||||||||  || |||| |
                                  CGAGGTCG  AG CCGG G
                                       TA  A    A
GAM215  MGC3036   5'  GCCTGGTTCCGATGCCC     5186      CC       CTCCG
                                  GCC  GGTTCCGG    GCCC
                                  |||  ||||||||    ||||
                                  CGG  CCAAGGCT    CGGG
                                    A_       A____
GAM215  MRPL41    5'  GCCCCGGCTCCGGCGCCAACCC 5187              T
                                  GCCCCGGTTCCGGC CCGGCCC
                                  |||||||||||||| |||||||
                                  CGGGGCCGAGGCCG GGTTGGG
                                            C
GAM215  NR6A1     5'  CCCGGTTCCGCGCCGCTCCG   5188          ____
                                  CCCGGTTCCG    GCTCCG
                                  ||||||||||    ||||||
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                                GGGCCAAGGC   CGAGGC
                                     GCGG
GAM215  NR6A1    5'  CCCGGTTCCGCGCCGCTCCG  5188          ____
                                CCCGGTTCCG   GCTCCG
                                ||||||||||   ||||||
                                GGGCCAAGGC   CGAGGC
                                     GCGG
GAM215  PF1      5'  CCCGGCTCCGGGGGGTCAGGCCT 5189          C__ C   C
             CG                   CCCGGTTCCGG  TC GGCC CG
                                ||||||||||   || |||| ||
                                GGGCCGAGGCC  AG CCGG GC
                                      CCC  T   A
GAM215  RAB1B    3'  GCCCTGGATCCCAGGTCC    5190      C _    C
                                GCCC GG TTCCGG TCC
                                |||| || |||||| |||
                                CGGG CC AGGGTC AGG
                                  A  T     C
GAM215  RAB6B    5'  CCCGGTCCCGGCTGCGGC    5191           C
                                CCCGGTTCCGGCT CGGC
                                |||||||||||| ||||
                                GGGCCAGGGCCGA GCCG
                                       C
GAM215  RINZF    5'  GCCCCGGCTCGCGCACGGCCTC 5192          CG  TC    C
             G                   GCCCCGGTTC  GC  CGGCC CG
                                |||||||||  ||  ||||| ||
                                CGGGGCCGAG  CG  GCCGG GC
                                     CG  T_    A
GAM215  RYBP     5'  ACCCCGAGCTGCTCTGG     5193       _  CCG   C
                                GCCCCG GTT   GCTC GG
                                |||||| |||   |||| ||
                                TGGGGC CGA   CGAG CC
                                   T  ___   A
GAM215  SARM     3'  GCCCTGGCTCTGGCCCCG    5194      C    C
                                GCCC GGTTC GGCTCCG
                                |||| ||||| |||||||
                                CGGG CCGAG CCGGGGC
                                  A    A
GAM215  SEC10L1  5'  GCTCGCCAGCTCCGGCTCCG  5195    C__
                                GC   CCGGTTCCGGCTCCG
                                ||   ||||||||||||||
                                CG   GGTCGAGGCCGAGGC
                                 AGC
GAM215  SMARCE1  5'  GCCCGCAGCTCCGGCTTCG   5196      _       C
                                GCCC CGGTTCCGGCT CG
                                |||| |||||||||| ||
                                CGGG GTCGAGGCCGA GC
                                  C         A
GAM215  USP19    5'  CCGGTTCCGGCGCAGGTCGGTT 5197          TC____  CC
             CCG                   CCGGTTCCGGC     CGG  CCG
                                ||||||||||     |||  |||
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                                GGCCAAGGCCG     GCC  GGC
                                      CGTCCA   AA
GAM215  ZDHHC1   5'  GCTCCGGCTCCGGCTCCGGCTC 5198     C            C
             CG                   GC CCGGTTCCGGCTCCGGC CCG
                                  || |||||||||||||||| |||
                                  CG GGCCGAGGCCGAGGCCG GGC
                                   A             A
GAM215  ZDHHC1   5'  GCTCCGGCTCCGGCTCCAG   5199     C
                                  GC CCGGTTCCGGCTCCGG
                                  || ||||||||||||||||
                                  CG GGCCGAGGCCGAGGTC
                                   A
GAM215  ZDHHC1   5'  GGCTCCGGCTCCGGCTCCG   5201             C
                                  GGTTCCGGCTCCGGC CCG
                                  |||||||||||||| |||
                                  CCGAGGCCGAGGCCG GGC
                                        A
GAM215  ZDHHC1   5'  GGCTCTGGCTCCGGCTCCG   5200       C       C
                                  GGTTC GGCTCCGGC CCG
                                  ||||| ||||||||| |||
                                  CCGAG CCGAGGCCG GGC
                                     A        A
GAM215  ZDHHC1   5'  GCTCCGGCTCCGGCTCCGGCTC 5198     C            C
             CG                   GC CCGGTTCCGGCTCCGGC CCG
                                  || |||||||||||||||| |||
                                  CG GGCCGAGGCCGAGGCCG GGC
                                   A             A
GAM215  ZDHHC1   5'  GCTCCGGCTCCGGCTCCGGCTC 5198     C            C
             CG                   GC CCGGTTCCGGCTCCGGC CCG
                                  || |||||||||||||||| |||
                                  CG GGCCGAGGCCGAGGCCG GGC
                                   A             A
GAM215  ZNF145   5'  GCTCCGGTGTCACCGCCGGTCC 5202     C    _ CG  _   C
             CG                   GC CCGGT TC  GCT CCGG CCCG
                                  || ||||| ||  ||| |||| ||||
                                  CG GGCCA AG  TGG GGCC GGGC
                                   A    C __  C   A
GAM215  LOC115704 3'  GCCCCGGTCCCCAGGCTTCG   5203          __   C
                                  GCCCCGGTTCC  GGCT CG
                                  ||||||||||  |||| ||
                                  CGGGGCCAGGG  CCGA GC
                                        GT   A
GAM215  LOC127703 5'  GCTCCGGCGCGTCTGGCTCTGG 5204     C    ___ C    C  C
             CTCCG                   GC CCGGT   TC GGCTC GGC CCG
                                  || |||||   || ||||| ||| |||
                                  CG GGCCG   AG CCGAG CCG GGC
                                   A    CGC A    A  A
GAM215  LOC144699 5'  GCCCCGCCGCTCCGGCCTCG   5205       GTT  G      C
                                  GCCCCG   CCG CTCCGGCC CG
                                  ||||||   ||| |||||||| ||
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                                CGGGGC   GGC GAGGCCGG GC
                                   ___  _      A
GAM215  LOC146562 3'  CCCGGTTCTGGCGGCACAGGCC 5206        ___   TCC
           CCG                   CCCGGTTC   CGGC   GGCCCCG
                                 ||||||||   ||||   |||||||
                                 GGGCCAAG   GCCG   CCGGGGC
                                     ACC    TGT
GAM215  LOC147700 5'  ACCGCGGGCGGCTCCGGCCCCG 5207     C   TTC
                                 GCC CGG   CGGCTCCGGCCCCG
                                 ||| |||   ||||||||||||||
                                 TGG GCC   GCCGAGGCCGGGGC
                                   C   C__
GAM215  LOC148229 5'  GCTCCGGCTTCTCCAGGCTCTG 5208    ___  _    _____  GCCC
           CGGGGCCG                GT   TCC GGCTC    CG    CG
                                 ||   ||| |||||    ||    ||
                                 CG   AGG CCGAG    GC    GC
                                  AAG   T    ACIII  CCCG
GAM215  LOC148764 5'  CCCCGGCCTGGCTCTGGCCC   5209        CC    C
                                 CCCCGGTT  GGCTC GGCCC
                                 ||||||||  ||||| |||||
                                 GGGGCCGG  CCGAG CCGGG
                                     A_    A
GAM215  LOC149478 5'  GCCTCGGGTCCGGAGGGCCTCC 5210     C   T    CTCC   _
                                 GCC CGG TCCGG    GGCC CC
                                 ||| ||| |||||    |||| ||
                                 CGG GCC AGGCC    CCGG GG
                                   A   C    TC__    A
GAM215  LOC149706 3'  GCCCTGGGTTCGGCTCCA    5211      C_    C
                                 GCCC  GGTTC GGCTCCG
                                 ||||  ||||| |||||||
                                 CGGG  CCAAG CCGAGGT
                                   AC    _
GAM215  LOC153684 5'  GCTCCGGGTTTCCAGTGGCCTC 5212     C   __     CTCC    C
           G                      GC CCGG  TTCCGG    GGCC CG
                                 || ||||  ||||||    |||| ||
                                 CG GGCC  AAGGTC    CCGG GC
                                  A   CA     A___    A
GAM215  LOC155382 5'  GCTCCAGGATCCGCTCCGGCTC 5213     _ C  T   G     C
           CG                     GC CC GG TCCG CTCCGGC CCG
                                 || || || |||| ||||||| |||
                                 CG GG CC AGGC GAGGCCG GGC
                                  A  T  T   _      A
GAM215  LOC219540 3'  GTTCTGGCTCCAAGGCCC    5214      C     __   C
                                 GTTC GGCTCC  GGCC C
                                 |||| ||||||  |||| |
                                 CAAG CCGAGG  CCGG G
                                   A     TT    A
GAM215  LOC255251 5'  GCTCAGGTTCGCACTCGGCCCC 5184     CCC    CG   C
           G                      GC   GGTTC  GCTC GGCCCCG
                                 ||   |||||  |||| |||||||
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                                CG   CCAAG  TGAG CCGGGGC
                                 AGT    CG   _
GAM215  LOC256451 5'  GCCTGGGGCTCCGGCCCCG   5215     CC  TTCC
                                GCC  GG   GGCTCCGGCCCCG
                                |||  ||   |||||||||||||
                                CGG  CC   CCGAGGCCGGGGC
                                 A_  ____
GAM215  LOC256740 5'  CGGCTCCGGCTGGGGCCCCG  5217          CC
                                CGGTTCCGGCT  GGCCCCG
                                ||||||||||  |||||||
                                GCCGAGGCCGA  CCGGGGC
                                      CC
GAM215  LOC256740 5'  GCCCCGGATCCAGCTCTGGC  5216        T      C
                                GCCCCGG TCCGGCTC GGC
                                ||||||| |||||||| |||
                                CGGGGCC AGGTCGAG CCG
                                    T       A
GAM216  ADH5    3'  GCTGTGAAGCTCTACGAGG   5220    CA   GAA      A
                                GC  TGA   AGCTCTAC AGG
                                ||  |||   |||||||| |||
                                CG  ACT   TCGAGATG TCC
                                 AC  ___       C
GAM216  ARHGEF12  3'  GCCATGAGGAAGCTGACTGTGA 5221         A    __  ACA
           GG                    GCCATGAG AAGCT  CT   AGG
                                |||||||| |||||  ||   |||
                                CGGTACTC TTCGA  GA   TCC
                                    C     CT  CAC
GAM216  CD5L    3'  ACGTCATGAAAAGGTCTA    5222     C       A C
                                ACG CATGAGAA G TCTA
                                ||| |||||||| | ||||
                                TGC GTACTTTT C AGAT
                                 A       _ C
GAM216  GNA11    5'  GCCATGAGAGAGGGCCCAGG   5223          AA__    TACA
                                GCCATGAGA    GCTC    AGG
                                |||||||||    ||||    |||
                                CGGTACTCT    CGGG    TCC
                                     CTCC   _____
GAM216  GRM6    3'  ACCCATGAGAGAGCTGCACAGG 5224    G       A   C   A
                                AC CCATGAGA AGCT TACA GG
                                || |||||||| |||| |||| ||
                                TG GGTACTCT TCGA GTGT CC
                                 _       C   C   _
GAM216  NF2     3'  ACGCCATGAGAGAAATCTCTAC 5225           _  _      A
           AGGG                   ACGCCATGAGA AAG CTCTACA GG
                                ||||||||||| ||| ||||||| ||
                                TGCGGTACTCT TTT GAGATGT CC
                                      C  A      C
GAM216  OIP2    5'  ACGCCACGGGAAATGCCAAGG  5226         A   _  TCTA
                                ACGCCATG GAAA GC    CAAGG
                                |||||||| |||| ||    |||||
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                                TGCGGTGC CTTT CG   GTTCC
                                    C   A ____
GAM216  SGT     3' CGCCATGAGCGGCTGCAGG   5227        AAA  CTACA
                                CGCCATGAG  GCT   AGG
                                |||||||||  |||   |||
                                GCGGTACTC  CGA   TCC
                                    GC_  CG___
GAM216  SLC6A12  3' GCCATGAGAGACTCGGAGG   5228        AA   TACA
                                GCCATGAGA  GCTC   AGG
                                |||||||||  ||||   |||
                                CGGTACTCT  TGAG   TCC
                                    C_   CC__
GAM216  TNFSF11  3' ACGCGTGTTCTCTACAAG   5229     CA  AGAAAG
                                ACGC  TG    CTCTACAAG
                                ||||  ||    |||||||||
                                TGCG  AC    GAGATGTTC
                                  C_  AA____
GAM216  TNFSF11  3' ACGCGTGTTCTCTACAAG   5229     CA  AGAAAG
                                ACGC  TG    CTCTACAAG
                                ||||  ||    |||||||||
                                TGCG  AC    GAGATGTTC
                                  C_  AA____
GAM216  TP63    3' GCCATGAGGAGGTAAGCCAGTA 5230        A____    CTAC
           AGG                  GCCATGAG    AAGCT   AAGG
                                ||||||||    |||||   ||||
                                CGGTACTC    TTCGG   TTCC
                                    CTCCA    TCA_
GAM216  DKFZp434C0923 3'  GCCATGAAGAAAGCAGGTGAGG 5231        _     TCTACA
                                GCCATGA GAAAGC     AGG
                                ||||||| ||||||     |||
                                CGGTACT CTTTCG     TCC
                                   T     TCCAC_
GAM216  HERC3    3'  CACTGTGAGAAAACATCAGG   5232     CA       TCTACA
                                CGC  TGAGAAAGC     AGG
                                |||  |||||||||     |||
                                GTG  ACTCTTTTG     TCC
                                  AC       TAG___
GAM216  HSA277841 3'  GCCATGAGCAATCCCCGAGG   5233        AAAG   ACA
                                GCCATGAG   CTCT   AGG
                                ||||||||   ||||  |||
                                CGGTACTC   GGGG   TCC
                                    GTTA   C__
GAM216  KIAA0318  3'  GCCATGAGAAGCAAAG     5234          A  TCTAC
                                GCCATGAGAA GC    AAG
                                |||||||||| ||    |||
                                CGGTACTCTT CG    TTC
                                      _  T_____
GAM216  KIAA0481  3'  GCCTCAAATCAGCTCTACAGGG 5235     A   AA       A
                                GCC TGAG  AGCTCTACA GG
                                ||| ||||  ||||||||| ||
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                                CGG GTTT  TCGAGATGT CC
                                  A   AG       C
GAM216  KIAA0819  3'  GCTGTGAGGAGGACCCACACAG 5236    CA   AAA_ T   _
           G                     GC  TGAG   GC CTACA AGG
                                 ||  ||||   || ||||| |||
                                 CG  ACTC   TG GGTGT TCC
                                  AC   CTCC  _    G
GAM216  KIAA1554  3'  GCGTGAGAAAACCAAG     5237    CA       TCTA
                                 GC  TGAGAAAGC   CAAG
                                 ||  |||||||||   ||||
                                 CG  ACTCTTTTG   GTTC
                                  C_       ____
GAM216  MGC10731  3'  GCCATGAATTCTGCAAG     5238        AAAGC   A
                                 GCCATGAG    TCT CAAG
                                 ||||||||    ||| ||||
                                 CGGTACTT    AGA GTTC
                                      A____   C
GAM216  PF1       5'  CGCTTGAGAAAGCTTGTAGG   5239     CA       CTACA
                                 CGC  TGAGAAAGCT    AGG
                                 |||  ||||||||||    |||
                                 GCG  ACTCTTTCGA    TCC
                                   A_        ACA__
GAM216  PFTK1     3'  ATGAGAAAAGTACAAGG     5240         CTC
                                 ATGAGAAAG   TACAAGG
                                 |||||||||   |||||||
                                 TACTCTTTT   ATGTTCC
                                      C__
GAM216  LOC124930 3'  CACCATGAGGGAGTCAG     5241         AA  C  TACA
                                 CGCCATGAG  AG TC    AG
                                 |||||||||  || ||    ||
                                 GTGGTACTC  TC AG    TC
                                      CC  _  ____
GAM216  LOC127703 3'  GCCATGAGGAACACAAG     5242         AA   TCT
                                 GCCATGAG  AGC   ACAAG
                                 ||||||||  |||   |||||
                                 CGGTACTC  TTG   TGTTC
                                      C_   ___
GAM216  LOC152274 3'  GCCATGAGGAAGTCGAAGG   5243         A   C  TAC
                                 GCCATGAG AAG TC   AAGG
                                 ||||||| ||| ||   ||||
                                 CGGTACTC TTC AG   TTCC
                                      C   _  C__
GAM216  LOC200059 3'  GCTGTGAGAAAGCCAGTGAGG  5244     CA       CTACA
                                 GC  TGAGAAAGCT    AGG
                                 ||  ||||||||||    |||
                                 CG  ACTCTTTCGG    TCC
                                  AC        TCAC_
GAM216  LOC253805 3'  GCCATAAGGGAGCAACAGGG   5245         AA   TCT   A
                                 GCCATGAG  AGC   ACA GG
                                 ||||||||  |||   ||| ||
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                                CGGTATTC  TCG   TGT CC
                                    CC   T__   C
GAM216  LOC91373  3'  GCTATGAGAAGGGCCCTAAGG  5246    C     A_    CA
                                GC ATGAGAA  GCTCTA  AGG
                                || |||||||  ||||||  |||
                                CG TACTCTT  CGGGAT  TCC
                                 A      CC    __
GAM217  KIAA0603  3'  GAGGCCGTGCCTCTTCAA    5249          CGCG
                                GAGGCCGTGCT   TTCAA
                                ||||||||||   |||||
                                CTCCGGCACGG   AAGTT
                                      AG__
GAM217  KLK7    3'  CATCTGAGGTCAGGCGTTCAA  5250      _   C  TGCTC
                                CATC GAGG CG    GCGTTCAA
                                |||| |||| ||    ||||||||
                                GTAG CTCC GT    CGCAAGTT
                                  A   A  C____
GAM217  KLK7    3'  CATCTGAGGTCAGGCGTTCAA  5250      _   C  TGCTC
                                CATC GAGG CG    GCGTTCAA
                                |||| |||| ||    ||||||||
                                GTAG CTCC GT    CGCAAGTT
                                  A   A  C____
GAM217  p25     3'  TCGAGGCCGTGCTTGTC     5251           CGC
                                TCGAGGCCGTGCT   GTT
                                ||||||||||||   |||
                                AGCTCCGGCACGA   CAG
                                      A__
GAM217  LOC150115 5'  CCGGGCCGCCGCGTTCAA    5252     A     GCT
                                TCG GGCCGT   CGCGTTCAA
                                ||| ||||||   |||||||||
                                GGC CCGGCG   GCGCAAGTT
                                 _     ___
GAM218  DISC1    3'  TACTAAGCAATTCACTGCCTTA 5255          C  C  C
            C                    TACTGAGCAA TC CT TCTTAC
                                ||||||||||  ||  ||  ||||||
                                ATGATTCGTT AG GA GGAATG
                                      A  T  C
GAM218  GJB5    3'  CTGAATCCTCTCTCTT      5256       CAAC  _
                                CTGAG    TCC CTCTCTT
                                |||||    ||| |||||||
                                GACTT    AGG GAGAGAA
                                   _____  A
GAM218  INMT    3'  TGGCTCTCTCTCTCTTAC    5257     A  AA   C
                                TG GC  CTC CTCTCTTAC
                                || ||  ||| |||||||||
                                AC CG  GAG GAGAGAATG
                                 _ A_   A
GAM218  ZIC1    3'  TGATGCTTCCTCTCTTAC    5258      GCAA  C
                                TGA    CT CCTCTCTTAC
                                |||    || ||||||||||
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                                ACT    GA GGAGAGAATG
                                  AC__  A
GAM218  DKFZp547D155 3'  CTGTTCTCTCTCTCTCTCTTAC 5259      AGCAA_  C
                                CTG     CTC CTCTCTTAC
                                |||     ||| |||||||||
                                GAC     GAG GAGAGAATG
                                  AAGAGA  A
GAM218  FLJ10569  3'  CTGAGTGTCTTCTCCTAC    5260       CAAC  CC
                                CTGAG   TC  TCTCTTAC
                                |||||   ||  ||||||||
                                GACTC   AG  AGAGGATG
                                  AC__  A_
GAM218  FLJ11560  5'  TACTGAGCAGCCCTAGCT    5261         ACT   CT
                                TACTGAGCA   CCCT  CT
                                |||||||||   ||||  ||
                                ATGACTCGT   GGGA  GA
                                     C__    TC
GAM218  FLJ25438  3'  CTTAGCTGACTCTCTCTTA   5262     G   A_   CC
                                CT AGC  ACTC  TCTCTTA
                                || |||  ||||  |||||||
                                GA TCG  TGAG  AGAGAAT
                                 A   AC   __
GAM218  KIAA0972  3'  TACTAAGCAGCTGTGACTTTTA 5263         A  CCCT  C
          C                      TACTGAGCA CT    CT TTAC
                                |||||||||  ||    ||  ||||
                                ATGATTCGT GA    GA AATG
                                     C  CACT  A
GAM218  LOC149827 5'  CTGCTCCCTCTCTTAC      5264      AGCAA
                                CTG     CTCCCTCTCTTAC
                                |||     ||||||||||||||
                                GAC     GAGGGAGAGAATG
                                  _____
GAM218  LOC149839 5'  CTGAGCAAATCTCATTAC    5265         CTCCC   _
                                CTGAGCAA    TCTC TTAC
                                ||||||||    ||||  ||||
                                GACTCGTT    AGAG AATG
                                     T____   T
GAM218  LOC150378 3'  CACTGGGCACTCTCTTA     5266       A   ACTCC
                                TACTG GCA    CTCTCTTA
                                |||||  |||    ||||||||
                                GTGAC CGT    GAGAGAAT
                                  C  _____
GAM218  LOC219513 5'  CTGAAAGTCCCTCTCTTAC   5267       CAAC
                                CTGAG   TCCCTCTCTTAC
                                |||||   ||||||||||||
                                GACTT   AGGGAGAGAATG
                                  TC__
GAM218  LOC255535 5'  TACTGAGCATCTCTT       5268          ACTCCC
                                TACTGAGCA     TCTCTT
                                |||||||||     ||||||
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                                ATGACTCGT    AGAGAA
                                         ______
GAM218  LOC92379  3'  TGAGTGACTCTCTCCTA    5269     CA   CC
                                TGAG  ACTC  TCTCTTA
                                ||||  ||||  |||||||
                                ACTC  TGAG  AGAGGAT
                                  AC   __
GAM219  PSMA1     3'  TAGATTATTGTCATCA     5272          TTCTGA
                                TGGATTATTGT    CATCA
                                ||||||||||    |||||
                                ATCTAATAACA    GTAGT
                                         ______
GAM219  H_GS165L15.1 3'  TGGTATTATTTGGACATCAAT  5273     AT      CT
                                TGG  TATTGTTT  GACATCAAT
                                |||  ||||||||  |||||||||
                                ACC  ATAATAAA  CTGTAGTTA
                                  __      C_
GAM219  LOC122847 3'  TGGATTATTGTTCTTTTCCTG  5274          _____
                                TGGATTATTGT    TTCTG
                                ||||||||||    |||||
                                ACCTAATAACA    AGGAC
                                      AGAAA
GAM219  LOC149296 5'  TGGGTATAGCTGACATCAA   5275     ATTAT   TT
                                TGG    TGT  CTGACATCAA
                                |||    |||  ||||||||||
                                ACC    ATA  GACTGTAGTT
                                  C____   TC
GAM219  LOC151907 3'  TGGGTATATTGAACATCAA   5276     AT_    TTTCT
                                TGG   TATTG    GACATCAA
                                |||   |||||    ||||||||
                                ACC   ATAAC    TTGTAGTT
                                  CAT    _____
GAM219  LOC255545 3'  TGGGTATATTGAACATCAA   5276     AT_    TTTCT
                                TGG   TATTG    GACATCAA
                                |||   |||||    ||||||||
                                ACC   ATAAC    TTGTAGTT
                                  CAT    _____
GAM220  ARHGAP6   3'  CACCTGGACGTGGGGCGTGC   5279          CCGAC   AC
                                TACCTGGACG    GGC  GC
                                ||||||||||    |||  ||
                                GTGGACCTGC    CCG  CG
                                      ACC__   CA
GAM220  CDK6      5'  CCTGGACGCCGCCCGCC     5280           ACGGCA
                                CCTGGACGCCG     CGCC
                                ||||||||||     ||||
                                GGACCTGCGGC     GCGG
                                      GG____
GAM220  SERPINB9  5'  CCTGGACGCCGACCCCCGCGGC 5281          A__________   CACG
            GTGCC                   GGACGCCG        CGG   CC
                                ||||||||        |||   ||
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                                CCTGCGGC        GCC   GG
                                    TGGGGGCIII  GCAC
GAM220  TRIM14   3'  TACCTGGAGGCTGTCACGCCG  5282        C  CGACGG
                                TACCTGGA GC     CACGCCG
                                |||||||| ||     |||||||
                                ATGGACCT CG     GTGCGGC
                                    C  ACA___
GAM220  B3GALT6  3'  CACCTGGACACGGCGCGC    5283         GCCG    A
                                TACCTGGAC   ACGGC CGC
                                |||||||||   ||||| |||
                                GTGGACCTG   TGCCG GCG
                                    ____    C
GAM220  KIAA1068 5'  CCTGGACGTTGCCCACGTGC  5284         ___  G  _
                                CCTGGAC  GCC ACG GC
                                |||||||  ||| ||| ||
                                GGACCTG  CGG TGC CG
                                    CAA  G  A
GAM220  KIAA1265 3'  TACCTGGATGCATGTGCTGCGG 5285      C  CGA_________  CACG
            CGTGCC                  TGGA GC         CGG   CC
                                |||| ||         |||   ||
                                ACCT CG         GCC   GG
                                  A  TACACGACIII  GCAC
GAM220  PPP1R10  3'  TACCTGGAAGCCTCCTTCACGC 5286        C  GACGG
                                TACCTGGA GCC    CACGC
                                |||||||| |||    |||||
                                ATGGACCT CGG    GTGCG
                                    T  AGGAA
GAM220  LOC146220 3'  TACCTGAACGTGTACGCGCCG  5287         CCG  GCA
                                TACCTGGACG  ACG  CGCCG
                                ||||||||||  |||  |||||
                                ATGGACTTGC  TGC  GCGGC
                                    ACA  ___
GAM220  LOC152002 5'  TACCCGGACGCCGGCGGC    5288           A
                                TACCTGGACGCCG CGGC
                                |||||||||||| ||||
                                ATGGGCCTGCGGC GCCG
                                      C
GAM220  LOC169008 5'  CCTGGACGTCGGCGCC      5289        CCGA   AC
                                CCTGGACG   CGGC  GCC
                                ||||||||   ||||  |||
                                GGACCTGC   GCCG  CGG
                                    A___   __
GAM220  LOC253970 5'  CCTGGACGCGGTGAGCGCGC  5290         CGAC  A
                                CCTGGACGC   GGC CGC
                                |||||||||   ||| |||
                                GGACCTGCG   TCG GCG
                                    CCAC  C
GAM220  LOC255242 5'  TACTTGGATGCCAACAAAGC  5291     C   C    __
                                TAC TGGA GCCGAC  GGC
                                ||| |||| ||||||  |||
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                                ATG ACCT CGGTTG  TCG
                                  A   A     TT
GAM221  PGAM1    3'  TGTCTACAGATGTGGTCAGTGT 5294      GA   CGC      C
                                TGTC  GCGG   GTGGTCAG GT
                                |||| ||||   |||||||| ||
                                ACAG  TGTC   CACCAGTC CA
                                  A_   TA_      A
GAM221  CAMP-GEFII 5'  TGAGCGGCGGCGCGCGGT    5295    T_ A
                                TG  CG GCGGCGCGTGGT
                                ||  || ||||||||||||
                                AC  GC CGCCGCGCGCCA
                                 TC  _
GAM221  LOC144483 3'  TGTCTACAGATGTGGTCAGTGT 5294      GA   CGC      C
                                TGTC  GCGG   GTGGTCAG GT
                                |||| ||||   |||||||| ||
                                ACAG  TGTC   CACCAGTC CA
                                  A_   TA_      A
GAM222  ALDH3A2  5'  TGGCCTGGGCGGCCCACG    5298     GC      GTGC
                                TGGC  GGGCGGCC   CGCG
                                ||||  ||||||||   ||||
                                ACCG  CCCGCCGG   GTGC
                                  GA     _____
GAM222  FZD3     5'  CTGCCGCGGGCGGCCGCGC   5299     G
                                CTG CGCGGGCGGCCGTGC
                                ||| ||||||||||||||
                                GAC GCGCCCGCCGGCGCG
                                  G
GAM222  GLTSCR1  3'  CTGGCGCGGGCGGCTGGAACGC 5300          _________  TGCCG
           GGCC                   GCGCGGGCGGC      CG    C
                                ||||||||||       ||    |
                                CGCGCCCGCCG      GC    G
                                      ACCTIIIT  GCCGT
GAM222  KRTHB6   3'  CCGGCGCGGGCGGCGCGT    5301           _
                                CTGGCGCGGGCGGC CGT
                                |||||||||||||| |||
                                GGCCGCGCCCGCCG GCA
                                       C
GAM222  RAP1GDS1  5'  TGGTGCGGGCGGCGCGGC    5302     C       _ T
                                TGG GCGGGCGGC CG GC
                                ||| ||||||||| || ||
                                ACC CGCCCGCCG GC CG
                                  A       C _
GAM222  KIAA1855  3'  CTGGCGGGGCGCCGCG     5303       C    G
                                CTGGCG GGGCG CCGTG
                                |||||| ||||| |||||
                                GACCGC CCCGC GGCGC
                                     _    _
GAM222  REC8     5'  CTGGCTTGGGCGGCCGCG    5304      GC
                                CTGGC  GGGCGGCCGTG
                                |||||  ||||||||||
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                                GACCG  CCCGCCGGCGC
                                  AA
GAM222  LOC133308 5'  GGCGCGGGTGCAGAGCCGCGT  5305        CG  CGT
                                GGCGCGGG  GC   GCCGCGT
                                ||||||||  ||   |||||||
                                CCGCGCCC  CG   CGGCGCA
                                    A_  TCT
GAM222  LOC145870 5'  CTGGCCGGGCGGCGTTGCG   5306      G      C  GCC
                                CTGGC CGGGCGGC GT   GCG
                                ||||| ||||||| ||   |||
                                GACCG GCCCGCCG CA   CGC
                                  _       _ A__
GAM222  LOC147929 5'  CTGGCGCGGGGGGAGACGTG   5307         C  C__
                                CTGGCGCGGG GG   CGTG
                                |||||||||| ||   ||||
                                GACCGCGCCC CC   GCAC
                                    _ TCT
GAM222  LOC51277  5'  GGCGCGGGCGGTTGGGAGCGT  5308         CCGTGCC
                                GGCGCGGGCGG      GCGT
                                ||||||||||       ||||
                                CCGCGCCCGCC      CGCA
                                     AACCCT_
GAM223  ATP11A    3'  TCTCCCGGCCCTCGCA      5311      G      CAACG
                                TCTC CGGCCCTT    GCA
                                |||| ||||||||    |||
                                AGAG GCCGGGAG    CGT
                                  G      ______
GAM223  BLK       3'  TCGCGGCCCGTCTGGGATGGCA 5312         T  AAC___
          C                      TCGCGGCCC TC     GGCAC
                                |||||||||  ||     |||||
                                AGCGCCGGG AG     CCGTG
                                     C  ACCCTA
GAM223  CDX2      5'  CCTCGCGGCTCTTCTGC     5313         C    AACG
                                TCTCGCGGC CTTC    GC
                                |||||||||  ||||    ||
                                GGAGCGCCG GAAG    CG
                                     A    A___
GAM223  DLC1      5'  CCTCGCGGTCCTCAACGCA   5314        C  T    G
                                TCTCGCGG CCT CAACG CA
                                |||||||| ||| ||||| ||
                                GGAGCGCC GGA GTTGC GT
                                     A  _    _
GAM223  FPGS      3'  TCTCGCGGCCCTGCAGC     5315          TCAA
                                TCTCGCGGCCCT    CGGC
                                ||||||||||||    ||||
                                AGAGCGCCGGGA    GTCG
                                     C___
GAM223  NFATC1    3'  TCTCGCAGCCTTCCAGCA    5316         C   AA
                                TCTCGCGGCC TTC  CGGCA
                                |||||||||| |||  |||||
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                                AGAGCGTCGG AAG  GTCGT
                                          _  __
GAM223  SQLE     5'  TCCAACCCTTCTTTGGTGGCAC 5317     G       AAC___
                                TC CGGCCCTTC     GGCAC
                                || |||||||||     |||||
                                AG GTTGGGAAG     CCGTG
                                  _       AAACCA
GAM223  CBX3     5'  TCTCCGGCCCTCCGCGC     5318      G       AACG
                                TCTC CGGCCCTTC    GC
                                |||| |||||||||    ||
                                AGAG GCCGGGAGG    CG
                                  _       CG__
GAM223  DJ159A19.3 3'  CCTCGCGGTCCAGTCGGCAC   5319         C  TTCAA
                                TCTCGCGG CC     CGGCAC
                                |||||||| ||     ||||||
                                GGAGCGCC GG     GCCGTG
                                     A  TCA__
GAM223  DKFZp434G0920 5'  TCTCGCGGCGCAGGGCA     5320          CCTT  AC
                                TCTCGCGGC    CA  GGCA
                                |||||||||    ||  ||||
                                AGAGCGCCG    GT  CCGT
                                     C___  C_
GAM223  DKFZp547I094 3'  TCTCATGGCCCTTCGAGGAC   5321       C       AAC
                                TCTCG GGCCCTTC   GGC
                                ||||| ||||||||   |||
                                AGAGT CCGGGAAG   CTG
                                   A       CTC
GAM223  FLJ22940  5'  TCTCGCAGGCCTTCCGCG    5322         C     AA
                                TCTCGCGG CCTTC  CG
                                |||||||| |||||  ||
                                AGAGCGTC GGAAG  GC
                                     C     GC
GAM223  FOXJ1    5'  TCTCGCGACCCCGGGGGC    5323           TCAAC
                                TCTCGCGGCCCT    GGC
                                ||||||||||||    |||
                                AGAGCGCTGGGG    CCG
                                       CCC__
GAM223  MGC2555  5'  TCTCGCGGCCCCGCGCCGGC  5324           TCAA
                                TCTCGCGGCCCT    CGGC
                                ||||||||||||   ||||
                                AGAGCGCCGGGG   GCCG
                                       CGCG
GAM223  PDCD5    5'  TCTCGCAGCCCCTCGGC     5325           AAC
                                TCTCGCGGCCCTTC   GGC
                                ||||||||||||||  |||
                                AGAGCGTCGGGGAG   CCG
                                          ___
GAM223  TBDN100   3'  TCACCAAGTTCTTCAACGG   5326      __  CC
                                TCGC  GG  CTTCAACGG
                                ||||  ||  |||||||||
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                                AGTG  TC  GAAGTTGCC
                                  GT  AA
GAM223  LOC145694 5'  CCGCGGCCCTTTCAGC      5327          CAA
                                TCGCGGCCCTT   CGGC
                                ||||||||||   ||||
                                GGCGCCGGGAA   GTCG
                                      A__
GAM223  LOC151188 5'  TCTCGCGGTTCCTTAACTGC   5328        C_   C   G
                                TCTCGCGG  CCTT AAC GC
                                ||||||||  |||| ||| ||
                                AGAGCGCC  GGAA TTG CG
                                     AA   _  A
GAM223  LOC253172 3'  TCTCGGCGGCCTTGGC      5329       _    C  CAAC
                                TCTCG CGGCC TT    GGC
                                ||||| ||||| ||    |||
                                AGAGC GCCGG AA    CCG
                                   C    _ ____
GAM223  LOC257041 5'  TCCCGCGGTTCCCGGCA     5330        CCC   AA
                                TCTCGCGG   TTC  CGGCA
                                ||||||||   |||  |||||
                                AGGGCGCC   AAG  GCCGT
                                     ___   G_
GAM223  LOC92162  5'  TCTTGCAGCCCTCCCGG     5331     C        AA
                                TCT GCGGCCCTTC  CGG
                                ||| ||||||||||  |||
                                AGA CGTCGGGAGG  GCC
                                  A         __
GAM224  ALDH3B1   3'  TTCCATGGTGTGGCCTGAGTCA 5334       AAGC  C   _
                                TTCCA    GG GTG TCTGAGTCA
                                |||||    || ||| |||||||||
                                AAGGT    CC CAC GGACTCAGT
                                   A___  A   C
GAM224  BAI2      3'  TTCCAAAGTGGAGTGTGAAAAT 5335         C  C    CT
                                TTCCAAAG GG GTGT  GAGT
                                |||||||| || ||||  ||||
                                AAGGTTTC CC CACA  TTTA
                                     A  T    CT
GAM224  SPAG8     3'  TTCCGGAATGGTGTGTCCA    5336      AA  C  C
                                TTCC  AG GG GTGTCTG
                                ||||  || || |||||||
                                AAGG  TT CC CACAGGT
                                   CC  A  A
GAM224  VAPB      3'  TTCCAAAGCGCTGGGT      5337          GCGTGT   A
                                TTCCAAAGCG     CTG GT
                                ||||||||||     ||| ||
                                AAGGTTTCGC     GAC CA
                                      _______  C
GAM224  FLJ10839  5'  TTCTATAGCATCGATCTGAGTC 5338      CAA    G  T
                                TTC   AGCG CG GTCTGAGTC
                                |||   |||| || |||||||||
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                                AAG   TCGT GC TAGACTCAG
                                  ATA    A  _
GAM224  KIAA1363  3'  TTCCAAAGCAGGTGTAGGAGGT 5339          C    CT   _
            CA                    TTCCAAAGCGG GTGT  GAG TCA
                                  |||||||||||  ||||  |||  |||
                                  AAGGTTTCGTC CACA  CTC AGT
                                        _    TC   C
GAM224  KIAA1486  3'  TCCAAAAAGTGTTTGAGT    5340        CGGC    C
                                  TCCAAAG    GTGT TGAGT
                                  |||||||    ||||  |||||
                                  AGGTTTT    CACA ACTCA
                                      T___    A
GAM224  KIAA1946  3'  TTCCAAATCATTTTGAGTC    5341        GCGG   GTC
                                  TTCCAAA    CGT   TGAGTC
                                  |||||||    |||   ||||||
                                  AAGGTTT    GTA   ACTCAG
                                      A___   AA_
GAM224  KLF12     3'  TTCCAAAGTGTCTGAGTC    5342        GCGGC
                                  TTCCAAA    GTGTCTGAGTC
                                  |||||||    ||||||||||||
                                  AAGGTTT    CACAGACTCAG
                                       _____
GAM224  MRPS18C   3'  TCCAAAGGTTGGTTTGAGTCA  5343        CGGCGT  C
                                  TCCAAAG     GT TGAGTCA
                                  |||||||     || |||||||
                                  AGGTTTC     CA ACTCAGT
                                      CAAC__  A
GAM224  SIAT8D    3'  TTCCCAAGGTCTGAGT     5344      A   CGGCGT
                                  TTCC AAG     GTCTGAGT
                                  ||||  |||     ||||||||
                                  AAGG TTC     CAGACTCA
                                    G  _______
GAM224  LOC155032 3'  TTCCAAAATGTGCTTGAGTCA  5345        CGGC   TC
                                  TTCCAAAG   GTG  TGAGTCA
                                  ||||||||   |||  |||||||
                                  AAGGTTTT   CAC  ACTCAGT
                                      A___   GA
GAM224  LOC91963  5'  TCCCAAAGCGGCTTGAGT    5346          GTGTC
                                  TTCCAAAGCGGC    TGAGT
                                  ||||||||||||    |||||
                                  AGGGTTTCGCCG    ACTCA
                                        A_____
GAM224  LOC93064  3'  TTCCAAAGCGGTGCGTCCA    5347          C
                                  TTCCAAAGCGG GTGTCTG
                                  |||||||||||  |||||||
                                  AAGGTTTCGCC CGCAGGT
                                        A
GAM225  FLII      3'  TGGAGCAGGTGGTGTCACC    5350        CGA  T   CT
                                  TGGAGTAGG   TG TGTC  CC
                                  |||||||||   || ||||  ||
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                                ACCTCGTCC  AC ACAG  GG
                                    ___ C   T_
GAM225  PYCR1    3'  GGAGTGGGTGAAGACCCTCCG  5351      A  C  TGTTG
                                GGAGT GG GA    TCCTCCG
                                ||||| || ||    |||||||
                                CCTCA CC CT    GGGAGGC
                                  C  A  TCT__
GAM225  SPON1    3'  TGGAGTAGGTCAAAGTCTCCG  5352        _  T  TGTC
                                TGGAGTAGG CGA GT   CTCCG
                                ||||||||| ||| ||   |||||
                                ACCTCATCC GTT CA   GAGGC
                                     A  T ____
GAM225  FLJ13868 3'  TGGGGTGGGCAGTCCTCC    5353     A  A   ATGTT
                                TGG GT GGCG    GTCCTCC
                                ||| || ||||    |||||||
                                ACC CA CCGT    CAGGAGG
                                 C  C   _____
GAM225  FLJ23022 5'  TGAGGTAGGAAATGTCCTCCG  5354    GA    CGATGT
                                TG  GTAGG     TGTCCTCCG
                                ||  |||||     |||||||||
                                AC  CATCC     ACAGGAGGC
                                 TC    TTT___
GAM225  SCYA15   3'  TGGAGGTGGGTGGCTGCCCTC  5355      TA  CGAT
                                TGGAG  GG   GTTGTCCTC
                                |||||  ||   |||||||||
                                ACCTC  CC   CGACGGGAG
                                  CA  CAC_
GAM225  LOC122509 3'  GGAGTAGGAGACTTGTCCT   5356       C   G
                                GGAGTAGG GAT TTGTCCT
                                |||||||| ||| |||||||
                                CCTCATCC CTG AACAGGA
                                     T  _
GAM225  LOC200515 3'  TGGGTAGGTCACTGTCCTC   5357     A    _  ATG
                                TGG GTAGG CG   TTGTCCTC
                                ||| ||||| ||   ||||||||
                                ACC CATCC GT   GACAGGAG
                                  _    A  ___
GAM226  KIAA0711  3'  CAAAAGACAAAAGAACG     5360         CCACGC
                                CAAAAGAT     GAAGAACG
                                ||||||||     ||||||||
                                GTTTTCTG     TTTCTTGC
                                     T_____
GAM226  LOC202316 3'  ACAAAAGACCTGAGAGAACGT  5361          CACGC  _
                                ACAAAAGATC    GA AGAACGT
                                ||||||||||    || |||||||
                                TGTTTTCTGG    CT TCTTGCA
                                      A____  C
GAM227  BAZ2B    3'  CATTATGTATGTGCCTTGCA   5364     C   TCCTACAC
                                CAT ATGT      GCCTTGCA
                                ||| ||||      ||||||||
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                                GTA TACA       CGGAACGT
                                  A    TACA____
GAM227  DMRT2    3'  CATCATGTCCTGCTCTGC    5365         T   ACAC  C
                                CATCATGT CCT    GC TTGC
                                |||||||| |||    || ||||
                                GTAGTACA GGA    CG GACG
                                     _   _____  A
GAM227  EPM2A    3'  CATCATGTTTTTAAATTAGCTT 5366          CCTACACGC_
           GCA                    CATCATGTT         CTTGCA
                                |||||||||          ||||||
                                GTAGTACAA         GAACGT
                                     AAATTTAATC
GAM227  ESR1     3'  ATCATGTTCCTACACCC     5367             G
                                ATCATGTTCCTACAC CC
                                |||||||||||||| ||
                                TAGTACAAGGATGTG GG
                                     _
GAM227  ETV5     3'  CATCATGTCCCGTTTTGC    5368          TACAC CC
                                CATCATGTTCC    G  TTGC
                                ||||||||||     |  ||||
                                GTAGTACAGGG    C  AACG
                                     ______ AA
GAM227  MAP3K13  3'  TCATGTTCCTGTTATTGCA   5369          ACACGCC
                                TCATGTTCCT      TTGCA
                                |||||||||       |||||
                                AGTACAAGGA      AACGT
                                     CAAT___
GAM227  PCDHB6   3'  CATCATGTTCTTACATGAGGC  5370           C    CGCCTT
                                CATCATGTTC TACA     GC
                                |||||||||| ||||     ||
                                GTAGTACAAG ATGT     CG
                                     A   ACTC__
GAM227  SKIV2L   3'  CATCATGTTTTTACATGGGGCA 5371          CC    CGCCTT
                                CATCATGTT  TACA     GCA
                                |||||||||  ||||     |||
                                GTAGTACAA  ATGT     CGT
                                     AA    ACCC__
GAM227  CEPT1    3'  CATGATGTTCCTATATACC    5372      C       CAC
                                CAT ATGTTCCTA   GCC
                                ||| |||||||||   |||
                                GTA TACAAGGAT   TGG
                                  C         ATA
GAM227  KIAA0449 3'  TCGTGCAAGAACACGCCTTGCA 5373     A   TCCT
                                TC TGT    ACACGCCTTGCA
                                || |||    ||||||||||||
                                AG ACG    TGTGCGGAACGT
                                 C   TTCT
GAM227  MGC32104 3'  TCATATTCTTTACATTTGCA   5374         C_   CGCC
                                TCATGTTC  TACA    TTGCA
                                ||||||||  ||||    |||||
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                                AGTATAAG  ATGT   AACGT
                                    AA   A___
GAM227  LOC142927 3'  CAGCATGCCACAACATGCCTTG 5375    T    CCT  C
                                CA CATGTT  ACA GCCTTG
                                || ||||||  ||| ||||||
                                GT GTACGG  TGT CGGAAC
                                 C    TGT  A
GAM227  LOC146515 3'  TGTTCCTATTAGCTCTTGCA  5376       CAC  _
                                TGTTCCTA  GC CTTGCA
                                ||||||||  || ||||||
                                ACAAGGAT  CG GAACGT
                                    AAT  A
GAM227  LOC148918 5'  ATCATGTTCTCTTTTGC    5377        _  ACACGCC
                                ATCATGTTC CT     TTGC
                                ||||||||| ||     ||||
                                TAGTACAAG GA     AACG
                                    A  A______
GAM227  LOC149372 3'  CATGTTCCTGCTACTGCA   5378       ACAC  C_
                                CATGTTCCT   GC  TTGCA
                                |||||||||   ||  |||||
                                GTACAAGGA   CG  GACGT
                                    ____  AT
GAM227  LOC149832 3'  ATCATGTTCTTACATTGC   5379        C   CGCC
                                ATCATGTTC TACA   TTGC
                                ||||||||| ||||   ||||
                                TAGTACAAG ATGT   AACG
                                    A   ____
GAM227  LOC219920 5'  CATTCACGTTACGTGCCTTGCA 5380    _   TCC  AC
                                CAT CATGT  TAC  GCCTTGCA
                                ||| |||||  |||  ||||||||
                                GTA GTGCA  ATG  CGGAACGT
                                  A   ___  CA
GAM228  ADCY6   3'  TTGGGGACAGATCATGG    5383     C  A     C
                                TTG GG ACAGGTCG GG
                                ||| || |||||||| ||
                                AAC CC TGTCTAGT CC
                                  _ C      A
GAM228  ADCY6   3'  TTGGGGACAGATCATGG    5383     C  A     C
                                TTG GG ACAGGTCG GG
                                ||| || |||||||| ||
                                AAC CC TGTCTAGT CC
                                  _ C      A
GAM228  ADRA2A   5'  CTGGCGGAACATGAACGCGG  5384    T     _ GT
                                CT GCGGAACA G  CGCGG
                                || |||||||| |  |||||
                                GA CGCCTTGT C  GCGCC
                                 C      A TT
GAM228  ALDH1A3  3'  CTTGCAGAACACACAG     5385          GGT
                                CTTGCGGAACA  CGCGG
                                ||||||||||  |||||
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                              GAACGTCTTGT  GTGTC
                                    ___
GAM228  CDKN2B   3'  CCTGCGGAACCCGCGG     5386        AGG
                              CTTGCGGAAC  TCGCGG
                              ||||||||||  ||||||
                              GGACGCCTTG  GGCGCC
                                    ___
GAM228  CENTD1   5'  CTTGCGCTCGGGTCGCGGA   5387      GAACA
                              CTTGCG    GGTCGCGGA
                              ||||||    |||||||||
                              GAACGC    CCAGCGCCT
                                 GAGC_
GAM228  COL4A3   3'  CCTGCGGAGTGTGCTTGGA   5388       ACAG  C  __
                              CTTGCGGA   GT GC  GGA
                              ||||||||   || ||  |||
                              GGACGCCT   CA CG  CCT
                                   CA__  _  AA
GAM228  COL4A3   3'  CCTGCGGAGTGTGCTTGGA   5388       ACAG  C  __
                              CTTGCGGA   GT GC  GGA
                              ||||||||   || ||  |||
                              GGACGCCT   CA CG  CCT
                                   CA__  _  AA
GAM228  COL4A3   3'  CCTGCGGAGTGTGCTTGGA   5388       ACAG  C  __
                              CTTGCGGA   GT GC  GGA
                              ||||||||   || ||  |||
                              GGACGCCT   CA CG  CCT
                                   CA__  _  AA
GAM228  COL6A2   3'  TTGGGGGACACCACGGA    5389     C  A   GG
                              TTG GG ACA  TCGCGGA
                              ||| || |||  |||||||
                              AAC CC TGT  GGTGCCT
                                C  C  __
GAM228  CYP24    5'  CTTGCTGGAGCCACGG      5390      _  ACAG
                              CTTGC GGA   GTCGCGG
                              ||||| |||   |||||||
                              GAACG CCT   CGGTGCC
                                 A  _____
GAM228  FGF23    3'  CTTGGGAACAGAGTGG      5391      C     _  CGC
                              CTTG GGAACAG GT   GG
                              |||| ||||||| ||   ||
                              GAAC CCTTGTC CA   CC
                                 _      T  ___
GAM228  ISG20    3'  CCTGCGGAACGGGCTGGA    5392        A  CGC
                              CTTGCGGAAC GGT   GGA
                              |||||||||| |||   |||
                              GGACGCCTTG CCG   CCT
                                    C  A__
GAM228  MN1      5'  CTTGCGAGGCCGCGG       5393       GAAC
                              CTTGCG   AGGTCGCGG
                              ||||||   |||||||||
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                                GAACGC   TCCGGCGCC
                                      ____
GAM228  NKX2E   3' CTCGCGGAATGGGCGG     5394        CA  TC
                                CTTGCGGAA  GG  GCGG
                                |||||||||  ||  ||||
                                GAGCGCCTT  CC  CGCC
                                     A_  __
GAM228  NRXN3   3' CCTGCGGAAGTGGTGGA    5395        CA  CGC
                                CTTGCGGAA  GGT  GGA
                                |||||||||  |||  |||
                                GGACGCCTT  CCA  CCT
                                     CA  ___
GAM228  NRXN3   3' CCTGCGGAAGTGGTGGA    5395        CA  CGC
                                CTTGCGGAA  GGT  GGA
                                |||||||||  |||  |||
                                GGACGCCTT  CCA  CCT
                                     CA  ___
GAM228  PATE    3' CTTGTGAACAGGTTCGG    5396     CG     CG
                                CTTG  GAACAGGT  CGG
                                ||||  ||||||||  |||
                                GAAC  CTTGTCCA  GCC
                                  A_      A_
GAM228  RBBP9   3' CTTACGGAACTTAACTGGA  5397         AGGTC  _
                                CTTGCGGAAC    GC GGA
                                ||||||||||    || |||
                                GAATGCCTTG    TG CCT
                                     AAT__  A
GAM228  RNASE1  5' TTGCTGGAGTGGCCACAGA  5398     _  ACA
                                TTGC GGA   GGTCGCGGA
                                ||||  |||   |||||||||
                                AACG CCT   CCGGTGTCT
                                  A  CA_
GAM228  SCA1    3' CTTGCAGAAAAGACCGTGGA 5399        C  GT  C
                                CTTGCGGAA AG  CG GGA
                                |||||||||  ||  || |||
                                GAACGTCTT TC  GC CCT
                                     T  TG  A
GAM228  SLC2A4  5' CCTGCGGAGGCCGCGG     5400        ACA
                                CTTGCGGA   GGTCGCGG
                                ||||||||   ||||||||
                                GGACGCCT   CCGGCGCC
                                     ___
GAM228  BNIP1   3' CTTGCAGAAAAGTGG      5401        C   CGC
                                CTTGCGGAA AGGT   GG
                                |||||||||  ||||   ||
                                GAACGTCTT TTCA   CC
                                     _   ____
GAM228  BNIP1   3' CTTGCAGAAAAGTGG      5401        C   CGC
                                CTTGCGGAA AGGT   GG
                                |||||||||  ||||   ||
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                                GAACGTCTT TTCA   CC
                                      _   ___
GAM228  D21S2056E 3'  CCTGCGGACCCGCGG      5402         A AGG
                                CTTGCGGA C   TCGCGG
                                |||||||| |   ||||||
                                GGACGCCT G   GGCGCC
                                     _ ___
GAM228  DKFZP566G1424 3'  CTTGCAGAACACACAG     5385          GGT
                                CTTGCGGAACA   CGCGG
                                ||||||||||   |||||
                                GAACGTCTTGT   GTGTC
                                     ___
GAM228  DKFZP586G1122 3'  TTGCGGAAGGCGAGGCGG    5403        AC   C__
                                TTGCGGA  AGGT   GCGG
                                |||||||  ||||   ||||
                                AACGCCT  TCCG   CGCC
                                   __   CTC
GAM228  FLJ20079  3'  CTTGTGGGGCATCACGGA    5404      C  AA  GG
                                CTTG GG  CA  TCGCGGA
                                |||| ||  ||  |||||||
                                GAAC CC  GT  AGTGCCT
                                  A  CC  __
GAM228  GABARAPL2 5'  CTCGCGGAGCCGCGG      5405         ACAG
                                CTTGCGGA   GTCGCGG
                                ||||||||   |||||||
                                GAGCGCCT   CGGCGCC
                                     _____
GAM228  GPR64    3'  TTGCGGAACGAGCAAGGA    5406         AG T  C
                                TTGCGGAAC  G CG GGA
                                |||||||||  | || |||
                                AACGCCTTG  C GT CCT
                                     CT _  T
GAM228  HSPC051   5'  CCTGCGGAACAGCAG      5407          GGTC
                                CTTGCGGAACA   GCGG
                                ||||||||||   ||||
                                GGACGCCTTGT   CGTC
                                     _____
GAM228  KCNK13   3'  CTTGCGGAGGCTCCCGG     5408         ACA  _  G
                                CTTGCGGA   GG TC CGG
                                ||||||||   || || |||
                                GAACGCCT   CC AG GCC
                                     ___  G  G
GAM228  KIAA0159  5'  CTTAGCGACGAGTCGCGGA   5409     _   AACA
                                CTT GCGG   GGTCGCGGA
                                ||| ||||   |||||||||
                                GAA CGCT   TCAGCGCCT
                                  T   GC__
GAM228  KIAA0546  3'  CTTGCGGATGAAAGTGGA    5410         AC_   CGC
                                CTTGCGGA   AGGT   GGA
                                ||||||||   ||||   |||
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                                GAACGCCT  TTCA  CCT
                                    ACT   ___
GAM228  KIAA1866  3'  CTTGCAGACAAGTGTGGA   5411       A    CGC
                                CTTGCGGA CAGGT  GGA
                                |||||||| |||||  |||
                                GAACGTCT GTTCA  CCT
                                    _    CA_
GAM228  KIAA1941  3'  CTTGTGAACAGACACCAGGA  5412     CG     T  __
                                CTTG  GAACAGG CGC  GGA
                                ||||  ||||||| |||  |||
                                GAAC  CTTGTCT GTG  CCT
                                  A_      _  GT
GAM228  KIF13B    3'  CTTGCGGAGTGAGCCAGGA   5413       ACA    C
                                CTTGCGGA  GGTCG GGA
                                ||||||||  ||||| |||
                                GAACGCCT  TCGGT CCT
                                    CAC   _
GAM228  KIF13B    5'  CTTGCGGAGTGAGCCAGGA   5413       ACA    C
                                CTTGCGGA  GGTCG GGA
                                ||||||||  ||||| |||
                                GAACGCCT  TCGGT CCT
                                    CAC   _
GAM228  MGC2963   5'  CTCGCGGAACAACGCGGA   5414         GT
                                CTTGCGGAACAG  CGCGGA
                                ||||||||||||  ||||||
                                GAGCGCCTTGTT  GCGCCT
                                              __
GAM228  NKX2C     3'  TCGCGGAGGCCGCGGA     5415       ACA
                                TTGCGGA  GGTCGCGGA
                                |||||||  |||||||||
                                AGCGCCT  CCGGCGCCT
                                             ___
GAM228  PIG7      5'  CTTGCGCGAAGTCGCGG     5416       _ ACA
                                CTTGCG GA  GGTCGCGG
                                |||||| ||  ||||||||
                                GAACGC CT  TCAGCGCC
                                   G  ___
GAM228  TADA3L    3'  TTGAGGGACAGCCACAG     5417     C  A   G
                                TTG GG ACAG TCGCGG
                                ||| || |||| ||||||
                                AAC CC TGTC GGTGTC
                                  T  C   _
GAM228  LOC145482 5'  TCGGGAGCCACAGTCGCGG   5418     C  A_  _
                                TTG GGA  CA GGTCGCGG
                                ||| |||  || ||||||||
                                AGC CCT  GT TCAGCGCC
                                  _  CG  G
GAM228  LOC147791 3'  CCTGCGGAGCCGGGCGGA    5419       ACA  TC
                                CTTGCGGA  GG  GCGGA
                                ||||||||  ||  |||||
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                                GGACGCCT  CC  CGCCT
                                    CGG  __
GAM228  LOC150174 5'  CTTGCAGGATCACGG      5420       AACA
                                CTTGCGG   GGTCGCGG
                                |||||||   ||||||||
                                GAACGTC   CTAGTGCC
                                    ____
GAM228  LOC150213 5'  CTTGCAGGATCACGG      5420       AACA
                                CTTGCGG   GGTCGCGG
                                |||||||   ||||||||
                                GAACGTC   CTAGTGCC
                                    ____
GAM228  LOC150236 5'  CTTGCAGGATCACGG      5420       AACA
                                CTTGCGG   GGTCGCGG
                                |||||||   ||||||||
                                GAACGTC   CTAGTGCC
                                    ____
GAM228  LOC199733 3'  CTGGGACAGGTCATGGA    5421     C  A     C
                                TTG GGA CAGGTCG GGA
                                ||| ||| ||||||| |||
                                GAC CCT GTCCAGT CCT
                                  _  _      A
GAM228  LOC200339 3'  CTTGGGAACAAGCTGGA    5422      C       CGC
                                CTTG GGAACAGGT  GGA
                                |||| |||||||||  |||
                                GAAC CCTTGTTCG  CCT
                                  _       A__
GAM228  LOC205355 5'  CTTGCGGAAGGACGG      5423       AC  TC
                                CTTGCGGA  AGG  GCGG
                                ||||||||  |||  ||||
                                GAACGCCT  TCC  TGCC
                                    __  __
GAM228  LOC221914 3'  TTGCAGAATAAACATGGA   5424       C  T  C
                                TTGCGGAA AGG CG GGA
                                |||||||| ||| || |||
                                AACGTCTT TTT GT CCT
                                    A  _  A
GAM228  LOC222008 5'  CCTGCGGAGCCCAGGCTGGA  5425       A__   CGC
                                CTTGCGGA  CAGGT  GGA
                                ||||||||  |||||  |||
                                GGACGCCT  GTCCG  CCT
                                    CGG   A__
GAM228  LOC254873 5'  CCTGCGGAGGCCGCGG     5400       ACA
                                CTTGCGGA  GGTCGCGG
                                ||||||||  ||||||||
                                GGACGCCT  CCGGCGCC
                                    ___
GAM228  LOC255096 3'  CTTGCGGAACGGCTCCAG   5426        A  CG
                                CTTGCGGAAC GGT  CGG
                                |||||||||| |||  |||
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                                GAACGCCTTG CCG  GTC
                                      _  AG
GAM228  LOC255533 5'  CTTACAACGGTCGCGG     5427       GA  A
                                CTTGCG  AC GGTCGCGG
                                ||||||  || ||||||||
                                GAATGT  TG CCAGCGCC
                                  __  _
GAM228  LOC257222 5'  CTTGAGGCTGGTCGCGGA    5428      C  AACA
                                CTTG GG   GGTCGCGGA
                                |||| ||   |||||||||
                                GAAC CC   CCAGCGCCT
                                  T  GA__
GAM228  LOC51020  5'  CTGGCGGAGCAGGCCGCGG   5429     T    A
                                CT GCGGA CAGGTCGCGG
                                || ||||| ||||||||||
                                GA CGCCT GTCCGGCGCC
                                 C    C
GAM228  LOC91547  5'  CTTGCGGAGAAGCGCAGA    5430        AC   T
                                CTTGCGGA  AGG CGCGGA
                                ||||||||  ||| ||||||
                                GAACGCCT  TTC GCGTCT
                                    C_  _
GAM228  LOC93538  5'  CTCGCGGAGCCCCCGCCGCGGA 5431         ACAG__
                                CTTGCGGA    GTCGCGGA
                                ||||||||    ||||||||
                                GAGCGCCT    CGGCGCCT
                                    CGGGGG
GAM228  LOC96652  5'  CTTGGTGAGGTCGCGGA    5432      CG  ACA
                                CTTG  GA   GGTCGCGGA
                                ||||  ||   |||||||||
                                GAAC  CT   CCAGCGCCT
                                  CA  ___
GAM229  APG5L     3'  GCTGTACTGGCTATTCTTT   5435     C   GCG  G
                                GC GTA   GG TGTTTTTT
                                || |||   || ||||||||
                                CG CAT   CC ATAAGAAA
                                 A  GA_  G
GAM229  KIAA0420  3'  CGCCTGGCTCATTTTTTAA   5436      GTA  GGGGT
                                CGCC   GC    GTTTTTTAA
                                ||||   ||    |||||||||
                                GCGG   CG    TAAAAAATT
                                  AC_  AG___
GAM229  LOC257354 3'  CGCCTGGCTCATTTTTTAA   5436      GTA  GGGGT
                                CGCC   GC    GTTTTTTAA
                                ||||   ||    |||||||||
                                GCGG   CG    TAAAAAATT
                                  AC_  AG___
GAM230  EGR3      3'  CGTGCGTGCGGCGGGCAGCAA  5439     T  AC       C
                                CGT GC  GCGGCGGGTA CGA
                                ||| ||  |||||||||| |||
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                                GCA CG  CGCCGCCCGT GTT
                                  _ CA        C
GAM230  L1CAM    3'  GTTGTGTGGTGGGTACCGAA  5440      CACGC  C
                                GTTG    GG GGGTACCGAA
                                ||||    || ||||||||||
                                CAAC    CC CCCATGGCTT
                                  ACA__  A
GAM230  L1CAM    3'  GTTGTGTGGTGGGTACCGAA  5440      CACGC  C
                                GTTG    GG GGGTACCGAA
                                ||||    || ||||||||||
                                CAAC    CC CCCATGGCTT
                                  ACA__  A
GAM230  ACAS2    5'  TTGCGGTCGCGGCGGGTGCCG  5441      A__       A
                                TTGC   CGCGGCGGGT CCG
                                ||||   |||||||||| |||
                                AACG   GCGCCGCCCA GGC
                                  CCA        C
GAM230  C14orf4  5'  GTTGCGCGGCGGCGGCGGCCCG 5442      A _     GTA_
                                GTTGC CG CGGCGG    CCG
                                ||||| || ||||||    |||
                                CAACG GC GCCGCC    GGC
                                  C  C     GCCG
GAM230  FLJ10700 3'  GTTGCACGTGGAGGGCAGCA  5443        C  C    C
                                GTTGCACG GG GGGTA CG
                                |||||||| || ||||| ||
                                CAACGTGC CC CCCGT GT
                                    A  T    C
GAM230  KIAA0014 3'  CGTTGCACTCGGGAATCC    5444        G   C    A
                                CGTTGCAC CGG GGGT CC
                                |||||||| ||| |||| ||
                                GCAACGTG GCC CTTA GG
                                    A  _   _
GAM230  LOC150299 3'  GTTGTACACAGATACTGGA   5445      C  GCG      C_
                                GTTG AC   GCGGGTAC  GA
                                |||| ||   ||||||||  ||
                                CAAC TG   TGTCTATG  CT
                                  A ____       AC
GAM231  GIPR     3'  GCCTATGCTATCGCTTCC    5448          _   GCG
                                GCCTATGCT TCGC   TC
                                |||||||| ||||   ||
                                CGGATACGA AGCG   GG
                                    T    AA_
GAM231  MAP3K14  3'  GCTATGCTCCTACAGTGTCAC  5449    C       _   C_
                                GC TATGCTTC GCG  GTCAC
                                || |||||||| |||  |||||
                                CG ATACGAGG TGT  CAGTG
                                  _       A   CA
GAM231  CBX6     3'  TCACCTGTGCAATCACTGCGTT 5450       A   T_   _   C
            AC                    TCGCCT TGC  TCGC GCGT AC
                                ||||||| |||  |||| |||| ||
```

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                                AGTGGA ACG  AGTG CGCA TG
                                   C  TT   A   A
GAM231  FLJ13441  3'  CCGCCTGTGCTTCGTGCA   5451       A     C
                                TCGCCT TGCTTCG GCG
                                |||||| ||||||| |||
                                GGCGGA ACGAAGC CGT
                                   C     A
GAM231  GPR64    3'  GCTTATGCTTCTCCAGATGTTG 5452    C     G_  C__  CA
          CC                     GC TATGCTTC  CG   GT  CC
                                || ||||||||  ||   ||  ||
                                CG ATACGAAG  GT   CA  GG
                                 A      AG  CTA  AC
GAM231  NFKBIE   3'  CCGCTTGTGCTTTTCTCACCA  5453     CTA    CGCGCG
                                TCGC   TGCTT     TCACCA
                                ||||   |||||     ||||||
                                GGCG   ACGAA     AGTGGT
                                  AAC    AAG___
GAM231  PHIP     5'  TCGCCTGTATTTTGCATCATCA 5454       A  C  C  _
                                TCGCCT TG TT GCG CGTCA
                                |||||| || || ||| |||||
                                AGCGGA AT AA CGT GTAGT
                                   C  A  A   A
GAM231  LOC149506 3'  TCGTCTAGCTTCAACATCTGCC 5455     C  T     C    A_
          A                     TCG CTA GCTTCG GCGTC  CCA
                                ||| ||| |||||| |||||  |||
                                AGC GAT CGAAGT TGTAG  GGT
                                  A  _     _    AC
GAM232  IGSF3    3'  TCCGTGGCCAACATCCGCTGG  5458     A  A   CC  G
                                TCC TG GCT  AC ATCCGCTGG
                                ||| || |||  || |||||||||
                                AGG AC CGG  TG TAGGCGACC
                                  C  _   T_  _
GAM232  IL21R    3'  TCCATGAGTGCCACGGGGGGTG 5459         CT    ATCCGC
          G                     TCCATGAG  CCACG     TGG
                                ||||||||  |||||     |||
                                AGGTACTC  GGTGC     ACC
                                     AC    CCCCC_
GAM232  TARBP2   3'  TCCATGAGTCCAGCT      5460         C   CGATCC
                                TCCATGAG TCCA     GCT
                                |||||||| ||||     |||
                                AGGTACTC AGGT     CGA
                                     _   _______
GAM232  TARBP2   3'  TCCATGAGTCCAGCT      5460         C   CGATCC
                                TCCATGAG TCCA     GCT
                                |||||||| ||||     |||
                                AGGTACTC AGGT     CGA
                                     _   _______
GAM232  TARBP2   3'  TCCATGAGTCCAGCT      5460         C   CGATCC
                                TCCATGAG TCCA     GCT
                                |||||||| ||||     |||
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                                AGGTACTC AGGT     CGA
                                   _   _______
GAM232  DKFZP434F0318 3'  CCCATGAGGATGATTTGCTGG  5461         CTCCAC   CC
                                TCCATGAG     GAT  GCTGG
                                ||||||||     |||  |||||
                                GGGTACTC     CTA  CGACC
                                     CTA___   AA
GAM232  FLJ23209  5'  TCCATGAGCCTCTGTGCGGGGC 5462          CCACGATCC_
           TGG                    TCCATGAGCT        GCTGG
                                ||||||||||         |||||
                                AGGTACTCGG         CGACC
                                     AGACACGCCC
GAM232  FLJ32334  3'  CATGAGCTTCGCTGGGCTGG   5463         CCA  ATCC
                                CATGAGCT   CG    GCTGG
                                ||||||||   ||    |||||
                                GTACTCGA   GC    CGACC
                                     A__  GACC
GAM232  MGC2654   3'  TCCAGAGCTCCAGCTGCTG   5464      T      CGATCC
                                TCCA GAGCTCCA     GCTG
                                |||| ||||||||      ||||
                                AGGT CTCGAGGT     CGAC
                                  _       CGA___
GAM232  MGC33345  5'  TCCAGAGCTCCATGGCCACGG  5465      T      CGAT    T
                                TCCA GAGCTCCA    CCGC GG
                                |||| ||||||||    |||| ||
                                AGGT CTCGAGGT    GGTG CC
                                  _       ACC_   _
GAM232  MYT1      3'  TCCATGAGCTTCCACT      5466          CCACGA
                                TCCATGAGCT     TCCGCT
                                ||||||||||     ||||||
                                AGGTACTCGA     AGGTGA
                                     _______
GAM232  PAXIP1L   3'  TCCATGAGCTTCCGGAAAGATG 5467          _ AC  TCCGC
           G                     TCCATGAGCT CC  GA     TGG
                                ||||||||||  ||  ||     |||
                                AGGTACTCGA GG  CT     ACC
                                     A  C_  TTCT_
GAM232  TRPM3     5'  TCCAGGAGCTCCACAGCCAGCT 5468       T        AT C
           GG                     TCCA GAGCTCCACG  C GCTGG
                                |||| ||||||||||  | |||||
                                AGGT CTCGAGGTGT  G CGACC
                                  C         CG T
GAM232  LOC131965 3'  TCCTGGGCTCAAGGGATCTGCT 5469      A  A    CAC_    C
           GG                     TCC TG GCTC    GATC GCTGG
                                ||| || ||||    |||| |||||
                                AGG AC CGAG    CTAG CGACC
                                  _ C    TTCC    A
GAM232  LOC148854 3'  TCCATGAGCTCTGTAAGTCCGT 5470           CACGA_    C
           TGG                    TCCATGAGCTC     TCCG TGG
                                ||||||||||      |||| |||
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                                AGGTACTCGAG     AGGC ACC
                                      ACATTC    A
GAM232  LOC150356 3'  TCGATGAGCTCCAGCT     5471     C        CGATCC
                                TC ATGAGCTCCA     GCT
                                || ||||||||||     |||
                                AG TACTCGAGGT     CGA
                                 C        _______
GAM232  LOC254122 3'  TCCATGAGCTCTTGCTG     5472           CACGATCC  _
                                TCCATGAGCTC       GCT G
                                ||||||||||        ||| |
                                AGGTACTCGAG       CGA C
                                      AA_______   A
GAM232  LOC255777 5'  TCTGTGAACTCCTTCACGCTGG 5473     CA       ACGA  _
                                TC  TGAGCTCC    TC CGCTGG
                                ||  ||||||||    || ||||||
                                AG  ACTTGAGG    AG GCGACC
                                 AC       A___  T
GAM233  B3GALT3   3'  AATTTCTTTAGCAAAAACCT   5476           CATTT
                                AATTTCTTTAGCA     CCT
                                ||||||||||||     |||
                                TTAAAGAAATCGT     GGA
                                      TTTT_
GAM233  B3GALT3   3'  AATTTCTTTAGCAAAAACCT   5476           CATTT
                                AATTTCTTTAGCA     CCT
                                ||||||||||||     |||
                                TTAAAGAAATCGT     GGA
                                      TTTT_
GAM233  B3GALT3   3'  AATTTCTTTAGCAAAAACCT   5476           CATTT
                                AATTTCTTTAGCA     CCT
                                ||||||||||||     |||
                                TTAAAGAAATCGT     GGA
                                      TTTT_
GAM233  BCL11B    3'  TTTCTTACATTTCCT      5477        TAGC
                                TTTCTT    ACATTTCCT
                                ||||||    |||||||||
                                AAAGAA    TGTAAAGGA
                                    ____
GAM233  C8orf1    5'  TTTCTTTGGGCATTTCCT    5478         AGCA
                                TTTCTTT    CATTTCCT
                                |||||||    ||||||||
                                AAAGAAA    GTAAAGGA
                                    CCC_
GAM233  CASP2     3'  CAGTTTCTCTTGCATTTCCT   5479     A      A   CA
                                CA TTTCTTT GCA  TTTCCT
                                || ||||||| |||  ||||||
                                GT AAAGAGA CGT  AAAGGA
                                 C      A  __
GAM233  CASP2     3'  CAGTTTCTCTTGCATTTCCT   5479     A      A   CA
                                CA TTTCTTT GCA  TTTCCT
                                || ||||||| |||  ||||||
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                                GT AAAGAGA CGT  AAAGGA
                                 C      A  __
GAM233  LPHH1    3'  AATTTCTTTAGCCATTT     5480           A
                                AATTTCTTTAGC CATTT
                                |||||||||||| |||||
                                TTAAAGAAATCG GTAAA
                                        _
GAM233  MTMR1    5'  AATCTCTGGACACATTTTCT  5481        TTA       C
                                AATTTCT   GCACATTT CT
                                |||||||   |||||||| ||
                                TTAGAGA   TGTGTAAA GA
                                    CC_       A
GAM233  MYH4     3'  ATTTCTTTGGTCACATTTTCT 5482         AG_      C
                                ATTTCTTT   CACATTT CT
                                ||||||||   ||||||| ||
                                TAAAGAAA   GTGTAAA GA
                                     CCA      A
GAM233  PDE4D    3'  CAATTTCTGTGGCTCATCCT  5483         TTA  A  TT
                                CAATTTCT   GC CA  TCCT
                                ||||||||   || ||  ||||
                                GTTAAAGA   CG GT  AGGA
                                     CAC  A  __
GAM233  SMARCA1  3'  TAAATTTCTTATAGACATTTC 5484    C       _  C
                                A AATTTCTT TAG ACATTTC
                                | |||||||| ||| |||||||
                                A TTAAAGAA ATC TGTAAAG
                                 T       T  _
GAM233  SMARCA1  3'  TAAATTTCTTATAGACATTTC 5484    C       _  C
                                A AATTTCTT TAG ACATTTC
                                | |||||||| ||| |||||||
                                A TTAAAGAA ATC TGTAAAG
                                 T       T  _
GAM233  TRHR     3'  CAATTTCTTTGTCATCCATTTT 5485          AG  __    C
          CT                     CAATTTCTTT  CA  CATTT CT
                                ||||||||||  ||  ||||| ||
                                GTTAAAGAAA  GT  GTAAA GA
                                      CA  AG    A
GAM233  ZNF6     5'  CAATTTCTTTTTATTTTTCCT  5486          AGCACA
                                CAATTTCTTT     TTTCCT
                                ||||||||||     ||||||
                                GTTAAAGAAA     AAAGGA
                                      AATAA_
GAM233  ABCC13   3'  TTTCTTTGCATTTCCT     5487        A   CA
                                TTTCTTT GCA  TTTCCT
                                ||||||| |||  ||||||
                                AAAGAAA CGT  AAAGGA
                                       _  __
GAM233  DARS     3'  TGAATTTCTCAAGTTATTTCCT 5488    C       T  CAC
                                A AATTTCTT AG   ATTTCCT
                                | |||||||| ||   |||||||
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                                A TTAAAGAG TC   TAAAGGA
                                 C       T  AA_
GAM233  DKFZp547I224 5'  TAAATTTCTTTGCCTTTCC   5489    C       A  ACA
                                A AATTTCTTT GC   TTTCC
                                | |||||||||| ||   |||||
                                A TTAAAGAAA CG   AAAGG
                                 T       _ G__
GAM233  DKFZP564F013 3'  TACAATTTCTTTCAATTTC   5490           AGCAC
                                TACAATTTCTTT    ATTTC
                                ||||||||||||    |||||
                                ATGTTAAAGAAA    TAAAG
                                       GT___
GAM233  DKFZP762D096 3'  CAATTTCTTTTTTCAAATATTT 5491          AG_  C__
           CCT                   CAATTTCTTT   CA   ATTTCCT
                                ||||||||||   ||   |||||||
                                GTTAAAGAAA   GT   TAAAGGA
                                      AAA  TTA
GAM233  FLJ11457  3'  ATTTCTTTCATTTCC      5492         AGCA
                                ATTTCTTT    CATTTCC
                                ||||||||    |||||||
                                TAAAGAAA    GTAAAGG
                                      _____
GAM233  FLJ13187  3'  TTTCTTTCACATTTCCT     5493         AG
                                TTTCTTT  CACATTTCCT
                                |||||||  ||||||||||
                                AAAGAAA  GTGTAAAGGA
                                      __
GAM233  FLJ25415  5'  TACATTTACTAGCACATTTTCT 5494      A   CT        C
                                TACA TTT  TTAGCACATTT CT
                                |||| |||  |||||||||| ||
                                ATGT AAA  GATCGTGTAAA GA
                                   _  T_         A
GAM233  HSPC019   3'  TACAATTTCCTTATTTCC    5495           GCACA
                                TACAATTTCTTTA    TTTCC
                                ||||||||||||    |||||
                                ATGTTAAAGGAAT    AAAGG
                                      ______
GAM233  NFAT5     3'  TACAACTTTCTCATTTCC    5496         _  TTAGCA
                                TACAATTT CT     CATTTCC
                                ||||||||  ||    |||||||
                                ATGTTGAA GA     GTAAAGG
                                     A  _______
GAM233  NFAT5     3'  ATTTCTTTAGTCTCC      5497          CACA
                                ATTTCTTTAG    TTTCC
                                ||||||||||    |||||
                                TAAAGAAATC    AGAGG
                                      _____
GAM233  SH3BGRL2  3'  CAATTTCTTATAAATTTCCT   5498         TAGCAC
                                CAATTTCTT     ATTTCCT
                                |||||||||     |||||||
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                                GTTAAAGAA     TAAAGGA
                                     TATT__
GAM233  LOC122786 3'  CAATCAGTAAAGCGCATTTCCT 5499       TCTTT   A
                                CAATT     AGC CATTTCCT
                                |||||     ||| ||||||||
                                GTTAG     TCG GTAAAGGA
                                   TCATT   C
GAM233  LOC134492 3'  TTCCCACAGTACATTTCCT    5500       T   C
                                TTTCT TAG ACATTTCCT
                                ||||| ||| |||||||||
                                AAGGG GTC TGTAAAGGA
                                   T   A
GAM233  LOC219899 3'  ATTTCTTTGTCATCTTTCCT   5501         AG  CA
                                ATTTCTTT  CA  TTTCCT
                                ||||||||  ||  ||||||
                                TAAAGAAA  GT  AAAGGA
                                     CA  AG
GAM233  LOC221490 5'  ATTTCTCCAGGTATTTCCT    5502          CAC
                                ATTTCTTTAG   ATTTCCT
                                ||||||||||   |||||||
                                TAAAGAGGTC   TAAAGGA
                                     CA_
GAM233  LOC254393 3'  CAATTTCTTAAGCATCC      5503          T    CATT
                                CAATTTCTT AGCA    TCC
                                ||||||||| ||||    |||
                                GTTAAAGAA TCGT    AGG
                                     T   _____
GAM234  AKAP13    5'  ACAGCTTCTGCCTGGCC      5506          A  TT
                                GCAGCTTCTGC TG  GCC
                                |||||||||||  ||  |||
                                TGTCGAAGACG AC  CGG
                                     G  __
GAM234  AKAP13    3'  ACAGCTTCTGCCTGGCC      5506          A  TT
                                GCAGCTTCTGC TG  GCC
                                |||||||||||  ||  |||
                                TGTCGAAGACG AC  CGG
                                     G  __
GAM234  AP1B1     3'  ACAGCTTCTGTGGCTGC      5507          CAT
                                GCAGCTTCTG   GTTGC
                                |||||||||   |||||
                                TGTCGAAGAC   CGACG
                                     AC_
GAM234  APOC3     3'  AGCAGCTTCTTGTCC       5508          GCA   TGC
                                AGCAGCTTCT   TGT   CC
                                ||||||||||   |||   ||
                                TCGTCGAAGA   ACA   GG
                                     ___   ___
GAM234  B3GALT5   5'  CAGCAGATTCTGCACTCCA   5509        C       GTTGC
                                CAGCAG TTCTGCAT    CCA
                                ||||||  ||||||||     |||
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                                GTCGTC AAGACGTG    GGT
                                   T       A____
GAM234  B3GALT5  5'  CAGCAGATTCTGCACTCCA   5509       C      GTTGC
                                CAGCAG TTCTGCAT    CCA
                                |||||| ||||||||    |||
                                GTCGTC AAGACGTG    GGT
                                   T       A____
GAM234  CBFA2T2  3'  CAGAGTTTTGCTCTGTTGCCCA 5510     C  C  C   A_
          G                     CAG AG TT TGC  TGTTGCCCAG
                                ||| || || |||  ||||||||||
                                GTC TC AA ACG  ACAACGGGTC
                                  _ _  A   AG
GAM234  CCR9     3'  CAGTGCTTCTGTGTCCCC    5511     CA     CA   G
                                CAG  GCTTCTG  TGTT CCC
                                |||  |||||||  |||| |||
                                GTC  CGAAGAC  ACAG GGG
                                  A_      __   _
GAM234  CCR9     3'  CAGTGCTTCTGTGTCCCC    5511     CA     CA   G
                                CAG  GCTTCTG  TGTT CCC
                                |||  |||||||  |||| |||
                                GTC  CGAAGAC  ACAG GGG
                                  A_      __   _
GAM234  CDC2L2   5'  GCTGGCTTCTGCGCACGCGCC  5512     A_      __   T
                                GC  GCTTCTGC  ATGT GCC
                                ||  ||||||||  |||| |||
                                CG  CGAAGACG  TGCG CGG
                                  AC       CG   _
GAM234  CHRNA5   5'  AGCAGCTTCTGGCGGGCT    5513          _ AT
                                AGCAGCTTCTG C  GTT
                                |||||||||||  |  |||
                                TCGTCGAAGAC G  CGA
                                       C CC
GAM234  CHST5    5'  GCTGCTTCTGCTGCAGCCTCAG 5514     A      A   T   _
                                GC GCTTCTGC TGT GCC CAG
                                || |||||||| ||| ||| |||
                                CG CGAAGACG ACG CGG GTC
                                  A       _   T   A
GAM234  CLTCL1   3'  CAGCAACTTCTGGGCCAGCTCA 5515          CAT   _  C
          G                     CAGCAGCTTCTG   GTT GC CAG
                                ||||||||||||   ||| || |||
                                GTCGTTGAAGAC   CGG CG GTC
                                       C__   T  A
GAM234  CPT2     3'  AGCTTTTCATCTGCCCAG    5516       CTG   G
                                AGCTT   CAT TTGCCCAG
                                |||||   ||| ||||||||
                                TCGAA   GTA GACGGGTC
                                  AA_  _
GAM234  DGSI     3'  CAACAGCTTCTGGCCC      5517            CATGTT
                                CAGCAGCTTCTG     GCCC
                                ||||||||||||     ||||
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                                GTTGTCGAAGAC     CGGG
                                          _______
GAM234  EHHADH   3'  CAGGGTTTTGCTATGTTGCCCA 5518     CTTC_  _
              G                  CAG    TGC ATGTTGCCCAG
                                 |||    ||| ||||||||||
                                 GTC    ACG TACAACGGGTC
                                   CCAAA   A
GAM234  GALNT7   3'  CAGCAGCTTCTGATGTT     5519           C
                                 CAGCAGCTTCTG ATGTT
                                 |||||||||||| |||||
                                 GTCGTCGAAGAC TACAA
                                          _
GAM234  GP1BB    3'  GCAGGCCCGTGTTGCCCAG   5520      CT   CA
                                 GCAG  TCTG  TGTTGCCCAG
                                 ||||  ||||  ||||||||||
                                 CGTC  GGGC  ACAACGGGTC
                                   C_   __
GAM234  HS3ST3B1 5'  GCGGCTCTTGACATGTTGCCC  5521    A   TC  _
                                 GC GCT  TG CATGTTGCCC
                                 || |||  || ||||||||||
                                 CG CGA  AC GTACAACGGG
                                  C   GA  T
GAM234  IFRD1    3'  CAGGGTCTCGCTATGTTGCCCA 5522     CT   _  _
              G                  CAG  TCT GC ATGTTGCCCAG
                                 |||  ||| || ||||||||||
                                 GTC  AGA CG TACAACGGGTC
                                   CC   G  A
GAM234  ITCH     3'  CAGGGTCTCCCTATGTTGCCCA 5523     CAG    GC
              G                  CAG   CTTCT  ATGTTGCCCAG
                                 |||   |||||  ||||||||||
                                 GTC   GAGGG  TACAACGGGTC
                                   CCA    A_
GAM234  MAP3K1   3'  ACAGTTTCTGCACTAGTT    5524      C      __
                                 GCAG TTCTGCAT  GTT
                                 |||| ||||||||  |||
                                 TGTC AAGACGTG  CAA
                                   A       AT
GAM234  MECP2    3'  AGCAGCTTCCGCCATCCA    5525           ATGTTGC
                                 AGCAGCTTCTGC      CCA
                                 ||||||||||||      |||
                                 TCGTCGAAGGCG      GGT
                                        GTA_____
GAM234  MOG      3'  AGCAGGCATGTTGCCCA     5526       CTTCT
                                 AGCAG    GCATGTTGCCCA
                                 |||||    ||||||||||||
                                 TCGTC    CGTACAACGGGT
                                          ______
GAM234  OPA3     3'  TCTTGCTCTGTTGCCCAG    5527      _  A_
                                 TCT GC  TGTTGCCCAG
                                 ||| ||  ||||||||||
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                                AGA CG  ACAACGGGTC
                                  A  AG
GAM234  POLL     3'  GCAGCTTCTGTCCCCACCCAG  5528          CATG TG
                                GCAGCTTCTG   T  CCCAG
                                ||||||||||   |  |||||
                                CGTCGAAGAC   G  GGGTC
                                     AGG_ GT
GAM234  PPP1R12B 3'  CAGCAGCTTCAGACCAGCC   5529          T_  ATGTT
                                CAGCAGCTTC  GC   GCC
                                ||||||||||  ||   |||
                                GTCGTCGAAG  TG   CGG
                                     TC  GT___
GAM234  RFX2     5'  CAGCGGCTGCTGCGTGTTG   5530      A  T   A
                                CAGC GCT CTGC TGTTG
                                |||| ||| |||| |||||
                                GTCG CGA GACG ACAAC
                                  C   C   C
GAM234  SLC7A5   3'  CAGTAGCTCTGTTTGCCCA   5531     C   T  CATG
                                CAG AGCT CTG   TTGCCCA
                                ||| |||| |||   |||||||
                                GTC TCGA GAC   AACGGGT
                                  A   _  A___
GAM234  UVRAG    3'  CAGAGCTTCTGCCCC      5532     C       ATGTTG
                                CAG AGCTTCTGC    CCC
                                ||| |||||||||    |||
                                GTC TCGAAGACG    GGG
                                _      _______
GAM234  WNT3A    3'  CAGCAGCTCTGGGCAGCC   5533        T  CAT  T
                                CAGCAGCT CTG  GT GCC
                                |||||||| |||  || |||
                                GTCGTCGA GAC  CG CGG
                                     _  C__  T
GAM234  WW45     3'  GCTTCACCATGTTGCCCAG   5534      TG
                                GCTTC  CATGTTGCCCAG
                                |||||  ||||||||||||
                                CGAAG  GTACAACGGGTC
                                   TG
GAM234  YWHAG    3'  ACAGCTTCTGCACCC      5535          ATGTT
                                GCAGCTTCTGC    GCCC
                                ||||||||||    ||||
                                TGTCGAAGACG    TGGG
                                      _____
GAM234  C20orf106 3'  CAGGGTTTCACCATGTTGCCCA 5536     C__  TG
          G                    CAG  TTC  CATGTTGCCCAG
                               |||  |||  ||||||||||||
                               GTC  AAG  GTACAACGGGTC
                                 CCA  TG
GAM234  C20orf142 3'  CAGGGTCTCACTATGTTGCCCA 5537     CT  _ _
          G                    CAG  TCT GC ATGTTGCCCAG
                               |||  ||| || ||||||||||
```

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                                GTC  AGA TG TACAACGGGTC
                                  CC   G  A
GAM234  CPR2     3'  CAGGGTTTTGCCTGTTGCCCAG 5538      CTTC_  A
                                CAG     TGC TGTTGCCCAG
                                |||     ||| ||||||||||
                                GTC     ACG ACAACGGGTC
                                  CCAAA   G
GAM234  CSNK1G1  3'  CAGCAGCTCTGGGACCTGCTCA 5539         T  CATG   C
           G                     CAGCAGCT CTG    TTGC CAG
                                |||||||| |||    |||| |||
                                GTCGTCGA GAC    GACG GTC
                                     _  CCTG    A
GAM234  CYB5-M   3'  TCTCGCTATGTTGCCCAG    5540      _ _
                                TCT GC ATGTTGCCCAG
                                ||| || ||||||||||
                                AGA CG TACAACGGGTC
                                  G  A
GAM234  CYB5-M   3'  TCTCGCTATGTTGCCCAG    5540      _ _
                                TCT GC ATGTTGCCCAG
                                ||| || ||||||||||
                                AGA CG TACAACGGGTC
                                  G  A
GAM234  DKFZP434A0131 3'  CAGCGTCTTGATAGGTTGCCCA 5541       T  GCAT__
           G                     CAGC TCT     GTTGCCCAG
                                |||| |||     |||||||||
                                GTCG AGA     CAACGGGTC
                                  C   ACTATC
GAM234  DKFZp434E0519 3'  CAGGGTTCCACCATGTTGCCCA 5542      C_  TG _
           G                     CAG  TTC  C ATGTTGCCCAG
                                |||  |||  | ||||||||||
                                GTC  AAG  G TACAACGGGTC
                                  CC   GT G
GAM234  DKFZp434N035 3'  CAGCAGCTCCTGCGTCGC    5543           AT
                                CAGCAGCTTCTGC  GTTGC
                                ||||||||||||  |||||
                                GTCGTCGAGGACG  CAGCG
                                              __
GAM234  DKFZP586D2223 3'  GCAGTCTCGCTATGTTGCCCAG 5544       CT  T  _
                                GCAG  TC GC ATGTTGCCCAG
                                ||||  || || ||||||||||
                                CGTC  AG CG TACAACGGGTC
                                  AG  _  A
GAM234  DKFZP667O116 3'  TCTCGCTATGTTGCCCAG    5540      _ _
                                TCT GC ATGTTGCCCAG
                                ||| || ||||||||||
                                AGA CG TACAACGGGTC
                                  G  A
GAM234  EPS8R3   5'  CAGCAGCTTCTCTGCTA     5545          GCA
                                CAGCAGCTTCT   TGTTG
                                ||||||||||   |||||
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                                GTCGTCGAAGA  ACGAT
                                     G__
GAM234  EPS8R3   5' CAGCAGCTTCTCTGCTA    5545         GCA
                                CAGCAGCTTCT  TGTTG
                                ||||||||||  |||||
                                GTCGTCGAAGA  ACGAT
                                     G__
GAM234  FBXL3B   5' GCAGCTTCTGCTGACTCAG   5546          A  TT  C
                                GCAGCTTCTGC TG  GC CAG
                                |||||||||| ||  || |||
                                CGTCGAAGACG AC  TG GTC
                                     _ __ A
GAM234  FLJ10058 3' CAGAGTCTCACTGTGTTGCCCA 5547     C  _  _  CA
           G                    CAG AG CTT CTG  TGTTGCCCAG
                                ||| || ||| |||  ||||||||||
                                GTC TC GAG GAC  ACAACGGGTC
                                  _ A  T  __
GAM234  FLJ10803 3' CAGGGTTTCACCATGTTGCCCA 5536     C__  TG
           G                    CAG  TTC  CATGTTGCCCAG
                                |||  |||  ||||||||||||
                                GTC  AAG  GTACAACGGGTC
                                  CCA  TG
GAM234  FLJ11149 3' TCTCGCTATGTTGCCCAG    5540     _ _
                                TCT GC ATGTTGCCCAG
                                ||| || ||||||||||
                                AGA CG TACAACGGGTC
                                  G  A
GAM234  FLJ11320 3' CAGCACGCTTCTGGGGTCCAG  5548       _     CAT  TGC
                                CAGCA GCTTCTG  GT  CCAG
                                ||||| |||||||  ||  ||||
                                GTCGT CGAAGAC  CA  GGTC
                                   G     CC_ ____
GAM234  FLJ12592 3' TCTCGCTATGTTGCCCAG    5540     _ _
                                TCT GC ATGTTGCCCAG
                                ||| || ||||||||||
                                AGA CG TACAACGGGTC
                                  G  A
GAM234  FLJ12606 3' CAGGGTTTCACCATGTTGCCCA 5536     C__  TG
           G                    CAG  TTC  CATGTTGCCCAG
                                |||  |||  ||||||||||||
                                GTC  AAG  GTACAACGGGTC
                                  CCA  TG
GAM234  FLJ13102 3' CAGCAGCTCTGCAGCAAGTCC  5549         T    T  TG__
                                CAGCAGCT CTGCA GT   CC
                                |||||||| ||||| ||   ||
                                GTCGTCGA GACGT CG   GG
                                     _    _ TTCA
GAM234  FLJ13769 3' CAGGGTCTCGCTATGTTGCC  5550     CT  _ _
                                CAG  TCT GC ATGTTGCC
                                |||  ||| || ||||||||
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                                GTC  AGA CG TACAACGG
                                  CC   G  A
GAM234  FLJ14356  5' GCCGGCTTCTGCATTGTGCC   5551     A_       GT
                                GC  GCTTCTGCAT  TGCC
                                ||  ||||||||||  ||||
                                CG  CGAAGACGTA  ACGG
                                 GC         AC
GAM234  FLJ20139  3' CAGGGTTTCACCATGTTGCCCA 5536      C__   TG
           G                     CAG   TTC  CATGTTGCCCAG
                                 |||   |||  ||||||||||||
                                 GTC   AAG  GTACAACGGGTC
                                   CCA   TG
GAM234  FLJ20294  3' CAGCAGCTCTTCCACATGTCCA 5552          __ TG    TGC
           G                     CAGCAGCT  TC  CATGT   CCAG
                                 ||||||||  ||  |||||   ||||
                                 GTCGTCGA  AG  GTACA   GGTC
                                     GA  GT    ____
GAM234  FLJ20546  3' AGTTTCGCTCGTTGCCCAG    5553     C   T  A
                                 AG TTC GC TGTTGCCCAG
                                 || ||| || ||||||||||
                                 TC AAG CG GCAACGGGTC
                                  A   _  A
GAM234  FLJ20644  5' CAGCAGCTTCTGCATTTGC    5554              G
                                 CAGCAGCTTCTGCAT TTGC
                                 ||||||||||||||| ||||
                                 GTCGTCGAAGACGTA AACG
                                                 _
GAM234  FLJ21308  5' CAGCAGCTTATGCGTTTTG    5555          C   ATG
                                 CAGCAGCTT TGC   TTG
                                 |||||||||  |||   |||
                                 GTCGTCGAA ACG   AAC
                                      T   CAA
GAM234  FLJ21736  3' CAGCAGCTGCTGGCCC      5556          T   CATGTT
                                 CAGCAGCT CTG     GCCC
                                 ||||||||  |||     ||||
                                 GTCGTCGA GAC     CGGG
                                     C   _______
GAM234  FLJ21919  3' GCAGCTTCTCAAACTCA     5557          G  TGTT  C
                                 GCAGCTTCT CA    GC CA
                                 |||||||||  ||    ||  ||
                                 CGTCGAAGA GT    TG GT
                                      _  T___   A
GAM234  FLJ22009  3' CAGGGTCTCACTATGTTGCC   5558      CT   _  _
                                 CAG  TCT GC ATGTTGCC
                                 |||  |||  ||  ||||||||
                                 GTC  AGA TG TACAACGG
                                   CC   G  A
GAM234  FLJ22965  3' CAGGGTTTCACCATGTTGCCCA 5536      C__   TG
           G                     CAG   TTC  CATGTTGCCCAG
                                 |||   |||  ||||||||||||
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                                GTC  AAG  GTACAACGGGTC
                                  CCA  TG
GAM234  FLJ23042  3'  GCAGCTTCCGTGGTGCCC    5559          CA  T
                                GCAGCTTCTG  TG TGCCC
                                ||||||||||  || |||||
                                CGTCGAAGGC  AC ACGGG
                                      __  C
GAM234  FLJ23191  5'  GCAGCTCCTGGAGGCTCAG   5560          CATGTT  C
                                GCAGCTTCTG     GC CAG
                                ||||||||||     || |||
                                CGTCGAGGAC     CG GTC
                                      CTC___  A
GAM234  FLJ30092  3'  CAGGGTCTCGCCATGTTGCCCA 5561      CT  _  _
           G                     CAG  TCT GC ATGTTGCCCAG
                                |||  ||| || ||||||||||
                                GTC  AGA CG TACAACGGGTC
                                  CC   G  G
GAM234  GOLGA2LY  5'  CAGCAGCTCCTACCCCTTGTCC 5562            ATG   C
           AG                     CAGCAGCTTCTGC   TTG CCAG
                                ||||||||||||   ||| ||||
                                GTCGTCGAGGATG   AAC GGTC
                                      GGG   A
GAM234  GPA33    5'  CAGCAGCTTCTGGCC       5563           CATGTT
                                CAGCAGCTTCTG     GCC
                                ||||||||||||     |||
                                GTCGTCGAAGAC     CGG
                                      _______
GAM234  KIAA0415  3'  CAGCAGCTCTGTGGCCC     5564          CTGCA   T
                                CAGCAGCTT    TGT GCCC
                                |||||||||    ||| ||||
                                GTCGTCGAG    ACA CGGG
                                      ______  C
GAM234  KIAA0415  3'  CAGCAGCTGCTGGTCC      5565          T   CAT  TGC
                                CAGCAGCT CTG   GT   CC
                                |||||||| |||   ||   ||
                                GTCGTCGA GAC   CA   GG
                                     C   ___  ___
GAM234  KIAA0418  3'  CAGGGGCTTAGGGTTGCCCAG  5566      CA    CTGCAT
                                CAG  GCTT     GTTGCCCAG
                                |||  ||||     |||||||||
                                GTC  CGAA     CAACGGGTC
                                  CC    TCC___
GAM234  KIAA0420  3'  CAGGGTCTCACTATGTTGCCCA 5537      CT  _  _
           G                     CAG  TCT GC ATGTTGCCCAG
                                |||  ||| || ||||||||||
                                GTC  AGA TG TACAACGGGTC
                                  CC   G  A
GAM234  KIAA0476  3'  CAGTAGCTCTGCATCTTTCCAG 5567      C    T     G  GC
                                CAG AGCT CTGCAT TT  CCAG
                                ||| |||| |||||| ||  ||||
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                                GTC TCGA GACGTA AA  GGTC
                                  A   _     G  A_
GAM234  KIAA0596 3' CAGAGCTTCATGTTTGCCCAG 5568     C     TGC    _
                                CAG AGCTTC   ATGTT GCCCAG
                                ||| ||||||   ||||| ||||||
                                GTC TCGAAG   TACAA CGGGTC
                                  _     ___    A
GAM234  KIAA0700 5' GCAGCTTCTCGTGGCC      5569          GCA   T
                                GCAGCTTCT   TGT GCC
                                |||||||||   ||| |||
                                CGTCGAAGA   GCA CGG
                                      ___  C
GAM234  KIAA0752 3' AGTTTCGCTCGTTGCCCAG   5553     C   T  A
                                AG TTC GC TGTTGCCCAG
                                || ||| || ||||||||||
                                TC AAG CG GCAACGGGTC
                                 A  _ A
GAM234  KIAA1030 3' GCTTCACTATGTTGCCCAG   5570       T  _
                                GCTTC GC ATGTTGCCCAG
                                ||||| || ||||||||||
                                CGAAG TG TACAACGGGTC
                                   _ A
GAM234  KIAA1183 3' GCCGGCTTCTGCACTGCCCAG 5571     A_        GT
                                GC  GCTTCTGCAT  TGCCCAG
                                ||  ||||||||||  |||||||
                                CG  CGAAGACGTG  ACGGGTC
                                 GC         __
GAM234  KIAA1190 3' CAGCAGCTTCTGGGGACATCTC 5572            C__    GC
           CAG                   CAGCAGCTTCTG   ATGTT  CCAG
                                ||||||||||||  |||||  ||||
                                GTCGTCGAAGAC   TGTAG  GGTC
                                      CCC    A_
GAM234  KIAA1253 3' CAGGGTTTCACCATGTTGCCCA 5536     C__   TG
           G                    CAG   TTC  CATGTTGCCCAG
                                |||   |||  ||||||||||||
                                GTC   AAG  GTACAACGGGTC
                                  CCA   TG
GAM234  KIAA1715 3' CAGCAGTTAGCATGTTGCC   5573       CTTCT
                                CAGCAG    GCATGTTGCC
                                ||||||    ||||||||||
                                GTCGTC    CGTACAACGG
                                   AAT__
GAM234  KIAA1856 5' CAGCGGCTCTGTGATCTTG   5574      A   T   C_  G
                                CAGC GCT CTG  AT TTG
                                |||| ||| |||  || |||
                                GTCG CGA GAC  TA AAC
                                  C   _  AC  G
GAM234  KIAA1922 5' CAGCAGCTGCTGCTCC      5575          TCTGCAT    _
                                CAGCAGCT      GTTGC CC
                                ||||||||      ||||| ||
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                                GTCGTCGA      CGACG GG
                                   _______    A
GAM234  KIAA1948  3'  CAGGGTCTCACCATGTTGCCCA 5576     CT   G__
            G                    CAG  TCT   CATGTTGCCCAG
                                 |||  |||   ||||||||||||
                                 GTC  AGA   GTACAACGGGTC
                                   CC   GTG
GAM234  KIAA1950  3'  CAGAGTCTCACCATGTTGCCCA 5577     C  CT  TG
            G                    CAG AG  TC  CATGTTGCCCAG
                                 ||| ||  ||  ||||||||||||
                                 GTC TC  AG  GTACAACGGGTC
                                   _ AG  TG
GAM234  KIF13B   3'  CAGCAGCTCTGCAATGGCCAG  5578        T    TGT  C
                                 CAGCAGCT CTGCA   TG CCAG
                                 |||||||| |||||   || ||||
                                 GTCGTCGA GACGT   AC GGTC
                                      _    T__  C
GAM234  LSM1     5'  CAGCACTTCTGCCCC      5579       G     ATGTTG
                                 CAGCA CTTCTGC     CCC
                                 ||||| |||||||     |||
                                 GTCGT GAAGACG     GGG
                                   _     _______
GAM234  MGC11115  3'  CAGCAGCTCTGTGGGCCCA   5580        T   CA  TT
                                 CAGCAGCT CTG  TG  GCCCA
                                 |||||||| |||  ||  |||||
                                 GTCGTCGA GAC  AC  CGGGT
                                      _  __  C_
GAM234  MGC11352  3'  CAGTGGCCTCTGCATGGAATCT 5581     CA        TTG___
            CCCAG                   CAG  GCTTCTGCATG     CCCAG
                                 |||  ||||||||||     |||||
                                 GTC  CGGAGACGTAC     GGGTC
                                   AC         CTTAGA
GAM234  MGC4400   3'  AGTCTCGCTATGTTGCCCAG   5582     CT  T  _
                                 AG  TC GC ATGTTGCCCAG
                                 ||  || || ||||||||||
                                 TC  AG CG TACAACGGGTC
                                  AG  _  A
GAM234  MGC4737   3'  GCTTCTGCGTAGCCCAG     5583        AT  T
                                 GCTTCTGC  GT GCCCAG
                                 ||||||||  || ||||||
                                 CGAAGACG  CA CGGGTC
                                      __  T
GAM234  NMT1     3'  CAGCAGCTTCTTTGGTCTCAG  5584          GCAT   GCC
                                 CAGCAGCTTCT    GTT   CAG
                                 ||||||||||    |||   |||
                                 GTCGTCGAAGA    CAG   GTC
                                       AAC_   A__
GAM234  OSBPL7   5'  CAGCAGCTGCTGCAGGAACCAG 5585        T    TGTTGC
                                 CAGCAGCT CTGCA     CCAG
                                 |||||||| |||||     ||||
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                                GTCGTCGA GACGT     GGTC
                                    C    CCTT__
GAM234  p25     3'  GCTTCTGCTCTGCTCAG    5586        ATG   C
                                GCTTCTGC   TTGC CAG
                                ||||||||   |||| |||
                                CGAAGACG   GACG GTC
                                    A__    A
GAM234  PRO0529  3'  CAGCACTTCTGCCTTTG    5587      G     ATG
                                CAGCA CTTCTGC   TTG
                                ||||| |||||||   |||
                                GTCGT GAAGACG   AAC
                                  _     GA_
GAM234  PRO1596  5'  CAGAGTTTTTGCATGTT    5588     C  C  C
                                CAG AG TT TGCATGTT
                                ||| || || ||||||||
                                GTC TC AA ACGTACAA
                                  _ A  A
GAM234  RNPS1    3'  CAGCACTTCTGCAGCC      5589      G      TGTT
                                CAGCA CTTCTGCA   GCC
                                ||||| ||||||||   |||
                                GTCGT GAAGACGT   CGG
                                  _     _____
GAM234  RNPS1    3'  CAGCACTTCTGCAGCC      5589      G      TGTT
                                CAGCA CTTCTGCA   GCC
                                ||||| ||||||||   |||
                                GTCGT GAAGACGT   CGG
                                  _     _____
GAM234  SCMH1    5'  CAGCAGCTTCTTGATATTG   5590          GC
                                CAGCAGCTTCT  ATGTTG
                                ||||||||||  ||||||
                                GTCGTCGAAGA  TATAAC
                                      AC
GAM234  SEMA5A   3'  AGTTTCCCCATGTTGCCCAG  5591    C   G
                                AG TTCT CATGTTGCCCAG
                                || |||| ||||||||||||
                                TC AAGG GTACAACGGGTC
                                 A   G
GAM234  SIAT4A   3'  CAGGAGTCTCACTATGTTGCCC 5592     C  CT  T  _
           AG                    CAG AG  TC GC ATGTTGCCCAG
                                ||| ||  || || ||||||||||
                                GTC TC  AG TG TACAACGGGTC
                                  C  AG  _  A
GAM234  TADA3L   3'  GCAGTTTCACTCTTGTTGCCCA 5593      C   TGCA_
           G                     GCAG TTC    TGTTGCCCAG
                                |||| |||    ||||||||||
                                CGTC AAG    ACAACGGGTC
                                  A  TGAGA
GAM234  TADA3L   3'  GCAGTTTCACTCTTGTTGCCCA 5593      C   TGCA_
           G                     GCAG TTC    TGTTGCCCAG
                                |||| |||    ||||||||||
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                                CGTC AAG    ACAACGGGTC
                                  A  TGAGA
GAM234  TBDN100   3'  CAGCAGCTTCTTTACAGTCTCC 5594          __  T  GC
                                CAGCAGCTTCT  GCA GTT  CC
                                ||||||||||  ||| |||  ||
                                GTCGTCGAAGA  TGT CAG  GG
                                      AA  _  A_
GAM234  LOC144348 5'  CAGCAGCCTTCTGCGCTG    5595       _    AT
                                CAGCAGC TTCTGC  GTTG
                                |||||||  ||||||  ||||
                                GTCGTCG AAGACG  CGAC
                                    G    __
GAM234  LOC145231 3'  AGTTTCATCATGTTGCTCAG  5596    C  TG      C
                                AG TTC  CATGTTGC CAG
                                || |||  |||||||| |||
                                TC AAG  GTACAACG GTC
                                 A  TA       A
GAM234  LOC145566 5'  GCAGCTTCTGCTTCACTCAG  5597          ATG TG C
                                GCAGCTTCTGC   T  C CAG
                                ||||||||||   |  | |||
                                CGTCGAAGACG   A  G GTC
                                      A__ GT A
GAM234  LOC145824 3'  GCTTTCTGTATGTTGCCCAG  5598      _  C
                                GCTT CTG ATGTTGCCCAG
                                |||| ||| ||||||||||
                                CGAA GAC TACAACGGGTC
                                  A  A
GAM234  LOC145945 5'  CAGCAACTTTTGCTATT     5599         C  A
                                CAGCAGCTT TGC TGTT
                                |||||||| ||| ||||
                                GTCGTTGAA ACG ATAA
                                      A  _
GAM234  LOC146839 5'  AGCTTGCTATGTTGCCCAG   5600      TC  _
                                AGCT  TGC ATGTTGCCCAG
                                ||||  ||| ||||||||||
                                TCGA  ACG TACAACGGGTC
                                  __  A
GAM234  LOC147165 5'  CAGCAGCTCTCCCTGCCTG   5601         ___   A
                                CAGCAGCTT   CTGC TG
                                |||||||||   |||| ||
                                GTCGTCGAG   GACG AC
                                      AGG   G
GAM234  LOC147515 3'  CAGCAGCTTCTTACACATCCCA 5602          _    TG
          G                      CAGCAGCTTCT GCATGT  CCCAG
                                ||||||||||| ||||||  |||||
                                GTCGTCGAAGA TGTGTA  GGGTC
                                      A    __
GAM234  LOC148426 5'  CAGCAGCTCCTGCCCC      5603            ATGTTG
                                CAGCAGCTTCTGC     CCC
                                ||||||||||||      |||
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                                GTCGTCGAGGACG     GGG
                                          _______
GAM234   LOC149606 3'  CAGAGTCTCGCTATGTTGCCCA 5604      CT   _ _
                  G                 CAG  TCT GC ATGTTGCCCAG
                                    |||  ||| || ||||||||||
                                    GTC  AGA CG TACAACGGGTC
                                      TC   G  A
GAM234   LOC149995 3'  CAGCAGCTTCTTACACACCCCA 5605           _   TG TG
                  G                 CAGCAGCTTCT GCA  T  CCCAG
                                    |||||||||| |||  |  |||||
                                    GTCGTCGAAGA TGT  G  GGGTC
                                          A   GT __
GAM234   LOC152317 3'  AGTTTCACCATGTTGCCCAG   5606     C   TG
                                    AG TTC  CATGTTGCCCAG
                                    || |||  ||||||||||||
                                    TC AAG  GTACAACGGGTC
                                     A   TG
GAM234   LOC153027 3'  CAGCACTTCTGCAGCC      5589       G       TGTT
                                    CAGCA CTTCTGCA    GCC
                                    ||||| ||||||||    |||
                                    GTCGT GAAGACGT    CGG
                                      _       _____
GAM234   LOC153688 3'  CAGGGTTTCACCACGTTGCCCA 5607      C__   TG
                  G                 CAG   TTC  CATGTTGCCCAG
                                    |||   |||  ||||||||||||
                                    GTC   AAG  GTGCAACGGGTC
                                      CCA   TG
GAM234   LOC154089 3'  CAGGGTTTCACCATGTTGCC   5608     C__   TG
                                    CAG   TTC  CATGTTGCC
                                    |||   |||  |||||||||
                                    GTC   AAG  GTACAACGG
                                      CCA   TG
GAM234   LOC157693 5'  CAGCGGCTTCTGCCTGGAGGCC 5609       A       A  TT_
                                    CAGC GCTTCTGC TG   GCC
                                    |||| |||||||| ||   |||
                                    GTCG CGAAGACG AC   CGG
                                      C       G  CTC
GAM234   LOC158288 5'  CAGGGGCCTCACTATGTTGCCC 5610      CA    T  _
                  AG                CAG  GCTTC GC ATGTTGCCCAG
                                    |||  ||||| || ||||||||||
                                    GTC  CGGAG TG TACAACGGGTC
                                      CC    _  A
GAM234   LOC158382 5'  CAGGGTCTCACTATGTTGCCCA 5537      CT   _ _
                  G                 CAG  TCT GC ATGTTGCCCAG
                                    |||  ||| || ||||||||||
                                    GTC  AGA TG TACAACGGGTC
                                      CC   G  A
GAM234   LOC161823 3'  CAGGGTTTCTCCATGTTGCC   5611      C__    G
                                    CAG   TTCT CATGTTGCC
                                    |||   |||| |||||||||
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                                GTC   AAGA GTACAACGG
                                  CCA    G
GAM234   LOC196418 5'  CAGCAGCCTTCTGCGCTG    5595        _     AT
                                CAGCAGC TTCTGC  GTTG
                                ||||||| ||||||  ||||
                                GTCGTCG AAGACG  CGAC
                                   G     __
GAM234   LOC199883 3'  AGCTTCTGTAAACTGTCCAG   5612         CATG   C
                                AGCTTCTG    TTG CCAG
                                ||||||||    ||| ||||
                                TCGAAGAC    GAC GGTC
                                     ATTT   A
GAM234   LOC200020 3'  AGCTTCTGTAAACTGTCCAG   5612         CATG   C
                                AGCTTCTG    TTG CCAG
                                ||||||||    ||| ||||
                                TCGAAGAC    GAC GGTC
                                     ATTT   A
GAM234   LOC201100 3'  CAGCAGCTTTTGCCCAG     5613         CTGCATG
                                CAGCAGCTT      TTGCCCAG
                                |||||||||      ||||||||
                                GTCGTCGAA      AACGGGTC
                                               _______
GAM234   LOC201931 3'  CAGTGTCTCATTGTTGCCCAG  5614      CT   G   _
                                CAG  TCT CAT GTTGCCCAG
                                |||  ||| ||| |||||||||
                                GTC  AGA GTA CAACGGGTC
                                  AC   _   A
GAM234   LOC219627 3'  CAGAGTTTCGCTTGTTGCCCAG 5615      C  C   T  A
                                CAG AG TTC GC TGTTGCCCAG
                                ||| || ||| || ||||||||||
                                GTC TC AAG CG ACAACGGGTC
                                  _  A   _  A
GAM234   LOC219688 5'  CACCAGCTTCTGCAAGCCTCCC 5616     G         T  TG
            AG                    CA CAGCTTCTGCA GT  CCCAG
                                || ||||||||||| ||  |||||
                                GT GTCGAAGACGT CG  GGGTC
                                 G         T  GA
GAM234   LOC220032 3'  CAGCAGTTTTCCCCTTGCC    5617        C_   GCATG
                                CAGCAG  TTCT     TTGCC
                                ||||||  ||||     |||||
                                GTCGTC  AAGG     AACGG
                                   AA    GG___
GAM234   LOC220906 3'  CAGAGTTTCGCTTGTTGCCCAG 5615      C  C   T  A
                                CAG AG TTC GC TGTTGCCCAG
                                ||| || ||| || ||||||||||
                                GTC TC AAG CG ACAACGGGTC
                                  _  A   _  A
GAM234   LOC253664 3'  CAGAGTCTCACTATGTTGCCCA 5618      C  CT  T  _
            G                     CAG AG  TC GC ATGTTGCCCAG
                                ||| ||  || || ||||||||||
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                                GTC TC  AG TG TACAACGGGTC
                                  _ AG  _ A
GAM234  LOC254082 5'  AGCTTCTGTATCTCCAG     5619         CA   GC
                                AGCTTCTG  TGTT  CCAG
                                ||||||||  ||||  ||||
                                TCGAAGAC  ATAG  GGTC
                                    __    A_
GAM234  LOC254249 5'  CAGGGTTTCACCATGTTGCCCA 5536      C__   TG
          G                      CAG   TTC  CATGTTGCCCAG
                                |||   |||  ||||||||||||
                                GTC   AAG  GTACAACGGGTC
                                  CCA   TG
GAM234  LOC255974 5'  AGCAGCTTCCCTTGTCCA    5620          GCATG   C
                                AGCAGCTTCT    TTG CCA
                                ||||||||||    ||| |||
                                TCGTCGAAGG    AAC GGT
                                     G____   A
GAM234  LOC256073 3'  ACAGTCTCGCTATGTTGCCCAG 5621       CT  T  _
                                GCAG  TC GC ATGTTGCCCAG
                                ||||  || || ||||||||||||
                                TGTC  AG CG TACAACGGGTC
                                  AG  _  A
GAM234  LOC256115 3'  AGCCTCCCTATGTTGCCCAG   5622        GC
                                AGCTTCT  ATGTTGCCCAG
                                |||||||  ||||||||||||
                                TCGGAGG  TACAACGGGTC
                                   GA
GAM234  LOC257354 3'  CAGGGTCTCACTATGTTGCCCA 5537      CT   _  _
          G                      CAG  TCT GC ATGTTGCCCAG
                                |||  ||| ||  ||||||||||||
                                GTC  AGA TG TACAACGGGTC
                                  CC   G  A
GAM234  LOC257431 5'  CAGCAGCTCCTACCCCTTGTCC 5562            ATG   C
          AG                     CAGCAGCTTCTGC   TTG CCAG
                                ||||||||||||||   ||| ||||
                                GTCGTCGAGGATG   AAC GGTC
                                      GGG   A
GAM234  LOC257447 5'  CAGCAGCTCCTCCACCTTGTCC 5623          G   G   C
          AG                     CAGCAGCTTCT CAT TTG CCAG
                                ||||||||||| ||| ||| ||||
                                GTCGTCGAGGA GTG AAC GGTC
                                     G   G   A
GAM234  LOC51759  3'  CAGAGTTTTTTGCTCGTTGCCC 5624      C  CTTC_   A
          AG                     CAG AG    TGC TGTTGCCCAG
                                |||  ||    ||| ||||||||||
                                GTC TC    ACG GCAACGGGTC
                                  _ AAAAA   A
GAM234  LOC93512  5'  CAGCAGCTCTCCCTGCCTG   5601          ___    A
                                CAGCAGCTT   CTGC TG
                                |||||||||   |||| ||
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                                GTCGTCGAG   GACG AC
                                     AGG    G
GAM235  CD63     5'  TGGCTGCGCGTTCCTCTCCCG  5627      G       A   GT
                                TGGC TGCGCGTTCC CTC  CCG
                                |||| |||||||||| |||  |||
                                ACCG ACGCGCAAGG GAG  GGC
                                  _        A  __
GAM235  GTF2F1   5'  TGGCGTGCGCGTCCCTCG    5628           T  A
                                TGGCGTGCGCGT CC CTCG
                                |||||||||||| || ||||
                                ACCGCACGCGCA GG GAGC
                                       _ _
GAM235  LOC125058 3'  TGGCTGCGCGTTCCACT     5629      G
                                TGGC TGCGCGTTCCACT
                                |||| ||||||||||||
                                ACCG ACGCGCAAGGTGA
                                  _
GAM236  EGR3     3'  ACGCAGGCGCGCGTGCGTGCG  5632       AA     A    CA
                                ACGCG  GCGCGC TGCG  CG
                                |||||  |||||| ||||  ||
                                TGCGT  CGCGCG ACGC  GC
                                   C_     C    AC
GAM236  PPP2R5C   3'  CGCTGAGGCGGACGCACGTT   5633     GA  C   CAT
                                CGC  AG GCG   GCGCACGTT
                                |||  || |||   |||||||||
                                GCG  TC CGC   TGCGTGCAA
                                  AC  _   C__
GAM236  SERPINA10 3'  ACGCGAAGTGCTTATGCG    5634         C  GC
                                ACGCGAAG GC  ATGCG
                                |||||||| ||  |||||
                                TGCGCTTC CG  TACGC
                                     A  AA
GAM236  LOC152992 3'  GAAGATGCTGCGCACGTT    5635      CGC  A
                                GAAG   GC TGCGCACGTT
                                ||||   || ||||||||||
                                CTTC   CG ACGCGTGCAA
                                  TA_  _
GAM237  LOC134353 5'  CGGGGTCCGGGGCGGGCGCGTC 5638     AAGC   A  ___
                                TGG    GGT CC   GCGGGCGCGTC
                                |||    ||| ||   ||||||||||||
                                GCC    CCA GG   CGCCCGCGCAG
                                  _____   _ CCC
GAM237  LOC197320 5'  TGGAAGCGGTGCCGGGGGC   5639          A   C
                                TGGAAGCGGT CCG GGGC
                                |||||||||| ||| ||||
                                ACCTTCGCCA GGC CCCG
                                      C   C
GAM238  CR2      3'  TTGTTTATAGCCATGGCCTGGC 5642      C       GTC   A
           TT                    TTG TTATGGCCA   CCT GCTT
                                ||| |||||||||   ||| ||||
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                                AAC AATATCGGT   GGA CGAA
                                  A       ACC   C
GAM238  SORBS1   3'  TTGCTTATGGTTGTCCCC    5643          CCA
                                TTGCTTATGG   GTCCCT
                                ||||||||||   ||||||
                                AACGAATACC   CAGGGG
                                     AA_
GAM238  FLJ10697 3'  TTCCTTATTAGATTCCTAGCTT 5644     G    GGCCA  C
                                TT CTTAT    GT CCTAGCTT
                                || |||||    || ||||||||
                                AA GAATA    TA GGATCGAA
                                 G    ATC__  A
GAM238  ZNF228   3'  TTGCGTTATGAAATGTCCTAG  5645      _    CCA   C
                                TTGC TTATGG   GTCC TAG
                                |||| ||||||   ||||| |||
                                AACG AATACT   CAGG ATC
                                  C     TTA   _
GAM238  LOC158382 3'  TGACACAGTTCCTAGCTT    5646      _   C
                                TGGC CAGT CCTAGCTT
                                |||| |||| ||||||||
                                ACTG GTCA GGATCGAA
                                  T   A
GAM239  ACVR1B   3'  GGGAAAGCGCGGCTCAGAGC   5649    A     TAA  ___
                                GG GAAAGCG   CGG   AGAGC
                                || |||||||   |||   |||||
                                CC CTTTCGC   GCC   TCTCG
                                 _     ___   GAG
GAM239  ANXA5    5'  GGAGAGCGGCGGAGAGC     5650      AA   TAA
                                GGAGA  GCG   CGGAGAGC
                                |||||  |||   ||||||||
                                CCTCT  CGC   GCCTCTCG
                                   __  C__
GAM239  ASK      5'  GGAGAAAGTGTCGCACCGG    5651        ___   A
                                GGAGAAAG   CGTA CGG
                                ||||||||   |||| |||
                                CCTCTTTC   GCGT GCC
                                     ACA   G
GAM239  B3GALT3  5'  GGTGAGTAGTCGGAGAGC    5652    A  AAGC  A_
                                GG GA    GTA  CGGAGAGC
                                || ||    |||  ||||||||
                                CC CT    CAT  GCCTCTCG
                                 A _____  CA
GAM239  B3GALT3  5'  GGTGAGTAGTCGGAGAGC    5652    A  AAGC  A_
                                GG GA    GTA  CGGAGAGC
                                || ||    |||  ||||||||
                                CC CT    CAT  GCCTCTCG
                                 A _____  CA
GAM239  B3GALT3  5'  GGTGAGTAGTCGGAGAGC    5652    A  AAGC  A_
                                GG GA    GTA  CGGAGAGC
                                || ||    |||  ||||||||
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                                CC CT   CAT  GCCTCTCG
                                 A _____  CA
GAM239  C14orf1  3'  GGGAAGGCTGGAAAAGGGAGC  5653    A   A  GT__  C  A
                                GG GAA GC   AA GG GAGC
                                || ||| ||   || || ||||
                                CC CTT CG   TT CC CTCG
                                 _  C  ACCT  T  _
GAM239  CDC5L   5'  GGAGGGGGCGCAGAATAGC   5654     AAA    AC   G
                                GGAG  GCGTA  GGA AGC
                                ||||  |||||  ||| |||
                                CCTC  CGCGT  CTT TCG
                                  CCC    __  A
GAM239  CFL1    5'  GGAGAGGGCACCGAGAGC    5655      AA  GTA  G
                                GGAGA  GC   AC GAGAGC
                                |||||  ||   || ||||||
                                CCTCT  CG   TG CTCTCG
                                   CC  ___  G
GAM239  COL1A1   3'  GGAGAGAGGTCGGAGAGC    5656      A  C  AA
                                GGAGA AG GT  CGGAGAGC
                                ||||| || ||  ||||||||
                                CCTCT TC CA  GCCTCTCG
                                   C  _  __
GAM239  CSPG3    3'  AGAGAAAGTGTAAGCAGAG   5657        C   _
                                GGAGAAAG GTAA CGGAG
                                |||||||| |||| |||||
                                TCTCTTTC CATT GTCTC
                                     A   C
GAM239  CYFIP2   3'  GGAGAAAGGGTGAAACTAGGAG 5658        C  __  __
                                GGAGAAAG GT  AAC  GGAG
                                |||||||| ||  |||  ||||
                                CCTCTTTC CA  TTG  CCTC
                                     C  CT   AT
GAM239  DLX4    5'  GAAGAAAGCGCCGAGGGC    5659          AACG   A
                                GGAGAAAGCGT   GAG GC
                                ||||||||||   ||| ||
                                CTTCTTTCGCG   CTC CG
                                      G___  C
GAM239  DPH2L1   5'  GAAGAACGCGGAGAG      5660       AA   TAA
                                GGAGA  GCG   CGGAGAG
                                |||||  |||   |||||||
                                CTTCT  TGC   GCCTCTC
                                   __  ___
GAM239  EHD2    5'  GGAGAGACGTGCAGATGGAGAG 5661       AA   AAC___
           C                     GGAGA  GCGT    GGAGAGC
                                 |||||  ||||    |||||||
                                 CCTCT  TGCA    CCTCTCG
                                   C_   CGTCTA
GAM239  ELF3    3'  GGAGAAAGGAGCTGGGAGC   5662        C_  AAC  A
                                GGAGAAAG  GT   GG GAGC
                                ||||||||  ||   || ||||
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                                CCTCTTTC  CG   CC CTCG
                                    CT  A__  _
GAM239  ENC1    3'  AGAGATTAACGGAGAG      5663       AAGCG
                                GGAGA    TAACGGAGAG
                                |||||    ||||||||||
                                TCTCT    ATTGCCTCTC
                                  A_____
GAM239  ENG     3'  GAAGGGTAGGCGCGGAGAGC   5664      AAA__   TAA
                                GGAG    GCG   CGGAGAGC
                                ||||    |||   ||||||||
                                CTTC    CGC   GCCTCTCG
                                  CCATC   ___
GAM239  FOXE3   3'  GGAGAAGGATGTAGCAGGAG   5665       AGC_   A   A
                                GGAGAA    GTA CGG GAG
                                ||||||    ||| ||| |||
                                CCTCTT    CAT GTC CTC
                                    CCTA   C   _
GAM239  GPRK7   5'  GGGAAAGCACAAGAGGGC    5666     A       AC    A
                                GG GAAAGCGTA  GGAG GC
                                || |||||||||  |||| ||
                                CC CTTTCGTGT  TCTC CG
                                 _       __    C
GAM239  HR      5'  GGTAGAGCGCGGCGGAGAGC   5667     _   AA    AA
                                GG AGA  GCGT  CGGAGAGC
                                || |||  ||||  ||||||||
                                CC TCT  CGCG  GCCTCTCG
                                 A   __    CC
GAM239  IHPK1   3'  GAAAGAGCAGCAGAGAGC    5668       C   A
                                GAAAG GTA CGGAGAGC
                                ||||| ||| ||||||||
                                CTTTC CGT GTCTCTCG
                                   T   C
GAM239  IHPK1   3'  GGAGAAAGCAGTGGCAGACAG  5669          _  AA    G
                                GGAGAAAGC GT  CGGA AG
                                ||||||||| ||  |||| ||
                                CCTCTTTCG CA  GTCT TC
                                     T  CC    G
GAM239  LDB3    3'  GGAGAAAATGACTTAGAGC    5670         CGTA  GG
                                GGAGAAAG    AC  AGAGC
                                ||||||||    ||  |||||
                                CCTCTTTT    TG  TCTCG
                                    AC__  AA
GAM239  NKX2H   3'  GGAGGCGGACGGAGAGC     5671      AAA   TA
                                GGAG   GCG  ACGGAGAGC
                                ||||   |||  |||||||||
                                CCTC   CGC  TGCCTCTCG
                                  ___   C_
GAM239  NUMA1   3'  GGAGGCAAGGTAGGGAGAGC   5672      A_   C   AC
                                GGAG  AAG GTA  GGAGAGC
                                ||||  ||| |||  |||||||
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                                CCTC  TTC CAT  CCTCTCG
                                  CG  _  C_
GAM239  POU4F1   3'  GGAGAAAACAGGAGAG      5673          TAAC
                                GGAGAAAGCG   GGAGAG
                                ||||||||||   ||||||
                                CCTCTTTTGT   CCTCTC
                                     _____
GAM239  PPP3R1   5'  GGAGAGCGCGGGAGGAGC    5674       AA   AAC   _
                                GGAGA  GCGT  GGAG AGC
                                |||||  ||||  |||| |||
                                CCTCT  CGCG  CCTC TCG
                                   __   C__   C
GAM239  PTGER3   5'  GGGATGGCGTCCAGAGAGC   5675     A  AA   AA
                                GG GA  GCGT  CGGAGAGC
                                || ||  ||||  ||||||||
                                CC CT  CGCA  GTCTCTCG
                                 _ AC   G_
GAM239  RAPSN    3'  GGAGAAAGAGCAGGAG      5676         C   AC
                                GGAGAAAG GTA  GGAG
                                |||||||| |||  ||||
                                CCTCTTTC CGT  CCTC
                                     T  __
GAM239  RARA     3'  AGAGAAAAGCCGGGGCGGAGGG 5677         _ GTAA_    A
          C                      GGAGAAA GC    CGGAG GC
                                |||||||  ||    ||||| ||
                                TCTCTTT CG    GCCTC CG
                                    T  GCCCC    C
GAM239  RARG     3'  GGGACTTATAACGGAGGGC   5678     A  AAGC       A
                                GG GA   GTAACGGAG GC
                                || ||   ||||||||| ||
                                CC CT   TATTGCCTC CG
                                 _ GAA_       C
GAM239  RERE     3'  GGAGAAAGTGCGTTACGG    5679         __   A
                                GGAGAAA  GCGT ACGG
                                |||||||  |||| ||||
                                CCTCTTT  CGCA TGCC
                                    CA   A
GAM239  RORA     5'  GGAGAGCGCAGGGAGAGC    5680       AA    AC
                                GGAGA  GCGTA  GGAGAGC
                                |||||  |||||  |||||||
                                CCTCT  CGCGT  CCTCTCG
                                   __    C_
GAM239  SFN      3'  GAGGAAGCGGGTGCGGAGAGC  5681     A    TAA_
                                GAG AAGCG   CGGAGAGC
                                ||| |||||   ||||||||
                                CTC TTCGC   GCCTCTCG
                                  C   CCAC
GAM239  SHANK2   3'  GGAGAAAGTGCAAATTACAGGA 5682         C  ____   A
          GC                     GGAGAAAG GTA   ACGG GAGC
                                |||||||| |||   |||| ||||
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                                CCTCTTTC CGT   TGTC CTCG
                                    A  TTAA  _
GAM239  SLC25A6  5' GGAGAACGGGCGCGGAGAG  5683      A__  TAA
                                GGAGAA  GCG  CGGAGAG
                                ||||||  |||  |||||||
                                CCTCTT  CGC  GCCTCTC
                                   GCC  ___
GAM239  SQLE   5' AGAGGAGCACGGAGAG    5684     AA  GTA
                                GGAG  AGC  ACGGAGAG
                                ||||  |||  ||||||||
                                TCTC  TCG  TGCCTCTC
                                  C_  ___
GAM239  STAC   3' AGAGAGGAAGCCTGGAGAGC  5685      __  GTAAC
                                GGAGA  AAGC   GGAGAGC
                                |||||  ||||   |||||||
                                TCTCT  TTCG   CCTCTCG
                                   CC   GA___
GAM239  SUFU   3' GGAGGGCAGCAGAGAGC    5686     AAA  TAA
                                GGAG  GCG  CGGAGAGC
                                ||||  |||  ||||||||
                                CCTC  CGT  GTCTCTCG
                                  C__  C__
GAM239  TAX1BP1  5' GGAGAAAGTTACGCAGGC   5687       CGTA  G  A
                                GGAGAAAG   ACG AG GC
                                ||||||||   ||| || ||
                                CCTCTTTC   TGC TC CG
                                    AA__  G  _
GAM239  TEAD2   5' GGAGAAAGTTGCCGGGAGC  5688       CGTAA  A
                                GGAGAAAG   CGG GAGC
                                ||||||||   ||| ||||
                                CCTCTTTC   GCC CTCG
                                    AACG_  _
GAM239  TGFBI   3' AGAGAAATTGGCGGAGAGC  5689       GCGTAA
                                GGAGAAA    CGGAGAGC
                                |||||||    ||||||||
                                TCTCTTT    GCCTCTCG
                                    AACC__
GAM239  THBD   3' AGAGAGAGAGACCGGAGAGC  5690      A  CGTAA
                                GGAGA AG   CGGAGAGC
                                |||||  ||  ||||||||
                                TCTCT TC   GCCTCTCG
                                  C  TCTG_
GAM239  ACTR1A  3' GGAGAAAGAGCCTGGTGGGAG  5691       C  AAC__  A
                                GGAGAAAG GT   GG GAG
                                |||||||| ||   || |||
                                CCTCTTTC CG   CC CTC
                                    T  GACCA  _
GAM239  BPES   3' GGGGAACGCGGAGAGC    5692    A  AA  TAA
                                GG GA  GCG  CGGAGAGC
                                ||  ||  |||  ||||||||
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                                CC CT  TGC   GCCTCTCG
                                 C  __  ____
GAM239  C17orf31  3'  GGAGAAAGGCTGAGAG      5693         C  AACG
                                GGAGAAAG GT    GAGAG
                                |||||||| ||    |||||
                                CCTCTTTC CG    CTCTC
                                    _  A____
GAM239  C20orf150 3'  GGAGAAAGCTCTGGAGGAGC   5694          GTAAC   _
                                GGAGAAAGC     GGAG AGC
                                |||||||||     |||| |||
                                CCTCTTTCG     CCTC TCG
                                     AGA__    C
GAM239  C20orf48  5'  GGGAAAGCGTATAAAG      5695     A       AC
                                GG GAAAGCGTA  GGAG
                                || |||||||||  ||||
                                CC CTTTCGCAT  TTTC
                                 _       A_
GAM239  C4.4A     3'  GGAGAAAGTGAGTAGGAAGC   5696         C__   AC   G
                                GGAGAAAG   GTA  GGA AGC
                                ||||||||   |||  ||| |||
                                CCTCTTTC   CAT  CCT TCG
                                     ACT   __   _
GAM239  CAMKK2    5'  GGAGAAACGAAGACCTGGAGGG 5697        G  TA_  __    A
           C                     GGAGAAA CG   AC  GGAG GC
                                ||||||| ||   ||  |||| ||
                                CCTCTTT GC   TG  CCTC CG
                                    _  TTC  GA    C
GAM239  CXorf12   5'  GGCAGGGAGCTTCAGAGAGC   5698     _  AA   GTAA
                                GG AG  AGC    CGGAGAGC
                                || ||  |||    ||||||||
                                CC TC  TCG    GTCTCTCG
                                 G  CC   AA__
GAM239  DDX31     3'  GGAGAAGGTGGAGGAAAGC    5699        A C  AAC
                                GGAGAA G GT   GGAGAGC
                                |||||| | ||   |||||||
                                CCTCTT C CA   CCTTTCG
                                    _ _  CCT
GAM239  DKFZP434J193 3'  GGAAAAAGTGTAGGAG      5700          C   AC
                                GGAGAAAG GTA  GGAG
                                |||||||| |||  ||||
                                CCTTTTTC CAT  CCTC
                                     A   __
GAM239  DKFZP566G1424 5'  GAAAGGCAACAGAGGGC     5701        C        A
                                GAAAG GTAACGGAG GC
                                ||||| |||||||||  ||
                                CTTTC CGTTGTCTC CG
                                   _        C
GAM239  DKFZP586I2223 3'  GGAGAAAGCCTGAGGGAGGAGC 5702           GTAAC   _
                                GGAGAAAGC     GGAG AGC
                                |||||||||     |||| |||
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                                CCTCTTTCG    CCTC TCG
                                     GACTC   C
GAM239  DKFZP586I2223 3'  GGAGAAAGCCTGAGGGAGGAGC 5702          GTAAC  _
                                GGAGAAAGC    GGAG AGC
                                |||||||||    |||| |||
                                CCTCTTTCG    CCTC TCG
                                     GACTC   C
GAM239  DKFZP586I2223 3'  GGAGAAAGCCTGAGGGAGGAGC 5702          GTAAC  _
                                GGAGAAAGC    GGAG AGC
                                |||||||||    |||| |||
                                CCTCTTTCG    CCTC TCG
                                     GACTC   C
GAM239  DKFZp761B0514 3'  GGGGAAAGTACAGAGAGC    5703    A    CGTA
                                GG GAAAG   ACGGAGAGC
                                || |||||   |||||||||
                                CC CTTTC   TGTCTCTCG
                                 C    A___
GAM239  FLJ10743  3'  AGAGAAGGGCAGGGAGAG    5704       A C   AC
                                GGAGAA G GTA  GGAGAG
                                |||||| | |||  ||||||
                                TCTCTT C CGT  CCTCTC
                                   _ C   C_
GAM239  FLJ10815  3'  GGGAAAGCTAACGGAG     5705    A     G
                                GG GAAAGC TAACGGAG
                                || |||||| ||||||||
                                CC CTTTCG ATTGCCTC
                                 _     _
GAM239  FLJ11743  3'  GGGACGGAAGCGGAGAGC    5706    A AAA   T  _
                                GG G   GCG AA CGGAGAGC
                                || |   ||| || ||||||||
                                CC C   TGC TT GCCTCTCG
                                 _ ____   C  C
GAM239  FLJ13612  3'  GGAGAAAGGTGGCAGGAAGGAG 5707          C  AA _  __
          C                      GGAGAAAG GT  C GGA  GAGC
                                |||||||| ||  | |||  ||||
                                CCTCTTTC CA  G CCT  CTCG
                                     _  CC T   TC
GAM239  FLJ14356  5'  GGATAAGATCTCGGAGAGC   5708    GA   C  AA
                                GGA  AAG GT  CGGAGAGC
                                |||  ||| ||  ||||||||
                                CCT  TTC TA  GCCTCTCG
                                  A_   _  GA
GAM239  FLJ14936  5'  GGAGAAAGGTGGAAGAA     5709        C  AAC
                                GGAGAAAG GT   GGAGAG
                                |||||||| ||   ||||||
                                CCTCTTTC CA   CTTCTT
                                     _ C__
GAM239  FLJ20445  5'  GGAGGCGGCGGAGAGC      5710      AAA   TAA
                                GGAG   GCG   CGGAGAGC
                                ||||   |||   ||||||||
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                                CCTC  CGC  GCCTCTCG
                                  ___  C__
GAM239  FLJ22555  5'  GGAGAAAGAGACTGGAGAGC  5711       CGTA _
                                GGAGAAAG   AC GGAGAGC
                                ||||||||   || |||||||
                                CCTCTTTC   TG CCTCTCG
                                    TC__  A
GAM239  FLJ22671  3'  GGAGAAAGAGGAAGAGAGC   5712       CGTAAC
                                GGAGAAAG    GGAGAGC
                                ||||||||    |||||||
                                CCTCTTTC    TCTCTCG
                                    TCCT__
GAM239  HABP4     3'  GAGAAAGCGGGGAGAGC    5713       TAAC
                                GAGAAAGCG   GGAGAGC
                                |||||||||   |||||||
                                CTCTTTCGC   CCTCTCG
                                    C___
GAM239  HSP105B   5'  GGAGAAAGCGGGGCTCAGC  5714       TAAC  AG_
                                GGAGAAAGCG  GG  AGC
                                ||||||||||  ||  |||
                                CCTCTTTCGC  CC  TCG
                                    C___  GAG
GAM239  KIAA0082  3'  GGAAAGGGTAGTAAGGGAGC  5715     AAGC_  C  A
                                GGAGA   GTAA GG GAGC
                                |||||   |||| || ||||
                                CCTTT   CATT CC CTCG
                                  CCCAT  _ _
GAM239  KIAA0427  5'  GGACGAGGCTCCGGAGAGC  5716     GAA  C  AA
                                GGA  AG GT  CGGAGAGC
                                |||  || ||  ||||||||
                                CCT  TC CG  GCCTCTCG
                                  GC_ _ AG
GAM239  KIAA0515  3'  GGAGAAAGGCGTCCACACAGAG 5717       _  A_  G
          C                      GGAGAAAG CGT  ACG AGAGC
                                |||||||| |||  ||| |||||
                                CCTCTTTC GCA  TGT TCTCG
                                    C  GG  G
GAM239  KIAA0527  5'  GGAGGAGCGCGGAGAGC    5718     AA   TAA
                                GGAG  AGCG  CGGAGAGC
                                ||||  ||||  ||||||||
                                CCTC  TCGC  GCCTCTCG
                                  C_  ___
GAM239  KIAA0552  3'  GGAGGTGAGCACAGAGAGC  5719     AA_  GTA
                                GGAG  AGC  ACGGAGAGC
                                ||||  |||  |||||||||
                                CCTC  TCG  TGTCTCTCG
                                  CAC  ___
GAM239  KIAA0555  5'  GGAGAGCACAGAGAGC     5720      AA  GTA
                                GGAGA  GC  ACGGAGAGC
                                |||||  ||  |||||||||
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                                CCTCT  CG   TGTCTCTCG
                                  __  ___
GAM239  KIAA0848  3'  GGATGAAGTGTCACAAAGAG   5721     GA   C  A
                                GGA  AAG GT ACGGAGAG
                                |||  ||| || ||||||||
                                CCT  TTC CA TGTTTCTC
                                  AC   A  G
GAM239  KIAA1032  3'  GGAGAAAGGGCTGAGGGC    5722        C  AACG   A
                                GGAGAAAG GT    GAG GC
                                |||||||| ||    ||| ||
                                CCTCTTTC CG    CTC CG
                                     C  A___   C
GAM239  KRTAP4-14 3'  GGAGAAAGCAGGAGAG      5723          TAAC
                                GGAGAAAGCG    GGAGAG
                                ||||||||||    ||||||
                                CCTCTTTCGT    CCTCTC
                                    _____
GAM239  LR8       3'  GGAGGAGGGTCTGGAGAGC   5724      AA  C  AAC
                                GGAG  AG GT   GGAGAGC
                                ||||  || ||   |||||||
                                CCTC  TC CA   CCTCTCG
                                  C_  C  GA_
GAM239  LRPPRC    3'  GGGGAAGTGTGCCGAAGAGC  5725     A   A C  AA
                                GG GAA G GT  CGGAGAGC
                                || ||| | ||  ||||||||
                                CC CTT C CA  GCTTCTCG
                                 C   _ A  CG
GAM239  MGC11242  3'  AGAGAAAGTAAAGGGAGC    5726        GC    C  A
                                GGAGAAA  GTAA GG GAGC
                                |||||||  |||| || ||||
                                TCTCTTT  CATT CC CTCG
                                   __    T  _
GAM239  MGC4093   5'  GGAGAAAGCGGCAACCGG    5727          _    _
                                GGAGAAAGCG TAAC GG
                                |||||||||| |||| ||
                                CCTCTTTCGC GTTG CC
                                      C    G
GAM239  NBL1      3'  AGAGAAAGGCCCGGAGAGC   5728         C  AA
                                GGAGAAAG GT  CGGAGAGC
                                |||||||| ||  ||||||||
                                TCTCTTTC CG  GCCTCTCG
                                   _  G_
GAM239  NY-REN-41 3'  GGAGAAAAGTAGAGG       5729         C  AAC    A
                                GGAGAAAG GT   GGAG G
                                |||||||| ||   |||| |
                                CCTCTTTT CA   TCTC C
                                   _  ____    C
GAM239  PIP3-E    3'  GGAGGAAATGGGCAGAGAGC  5730      _   GCGTAA
                                GGAG AAA     CGGAGAGC
                                |||| |||     ||||||||
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                                CCTC TTT     GTCTCTCG
                                  C   ACCC__
GAM239  PRDM8   5'  GGAGAAGCTGTGACAGAGAGC  5731       A  _  A
                                GGAGAA GC GT ACGGAGAGC
                                |||||| || || |||||||||
                                CCTCTT CG CA TGTCTCTCG
                                   _  A  C
GAM239  RAB6B   5'  GGAAAAAGCGAAGGAG      5732          T  C
                                GGAGAAAGCG AA GGAG
                                |||||||||| || ||||
                                CCTTTTTCGC TT CCTC
                                      _  _
GAM239  ROBO4   3'  GGAGAAAGCAGTGGCTAGGAG  5733         _  AAC__
                                GGAGAAAGC GT    GGAG
                                ||||||||| ||    ||||
                                CCTCTTTCG CA    CCTC
                                     T  CCGAT
GAM239  SIRPB1  3'  AGAGAGAGAAGGGAGAGC    5734       A  CGT  C
                                GGAGA AG   AA GGAGAGC
                                ||||| ||   || |||||||
                                TCTCT TC   TT CCTCTCG
                                  C  ___  C
GAM239  STX12   5'  GGAGAAACTGGGAAGAGC    5735        G GTAAC
                                GGAGAAA C    GGAGAGC
                                ||||||| |    |||||||
                                CCTCTTT G    CTTCTCG
                                   _ ACC__
GAM239  TU3A    3'  GGAGAAGCGGGGCCCTGGGGAG 5736       A   TAAC___  A
          C                      GGAGAA GCG      GG GAGC
                                ||||||| |||      || ||||
                                CCTCTT CGC      CC CTCG
                                   _   CCCGGGA  C
GAM239  UPK1A   3'  GGAGGAGGTCAGAGAGC     5737      AA  C  AA
                                GGAG  AG GT  CGGAGAGC
                                ||||  || ||  ||||||||
                                CCTC  TC CA  GTCTCTCG
                                  C_  _  __
GAM239  VPS33A  3'  GGAGAAAGCAGTAAACAG    5738         _   _
                                GGAGAAAGC GTAA CGG
                                ||||||||| |||| |||
                                CCTCTTTCG CATT GTC
                                     T   T
GAM239  YME1L1  3'  GGGAAAGCGTTGTAAAAG    5739     A      AACG
                                GG GAAAGCGT   GAGAG
                                || ||||||||   |||||
                                CC CTTTCGCA   TTTTC
                                 _      ACA_
GAM239  YME1L1  3'  GGGAAAGCGTTGTAAAAG    5739     A      AACG
                                GG GAAAGCGT   GAGAG
                                || ||||||||   |||||
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                                CC CTTTCGCA    TTTTC
                                 _       ACA_
GAM239  ZFP100    5'  GGGAAGCACAAGGGAGC     5740     A  A     C  A
                                GG GAA GCGTAA GG GAGC
                                || ||| |||||| || ||||
                                CC CTT CGTGTT CC CTCG
                                 _  _     _ _
GAM239  ZNF282    3'  GGAGGTAGGCGGAGAGC     5741      AAAGC  A_
                                GGAG    GTA  CGGAGAGC
                                ||||    |||  ||||||||
                                CCTC    CAT  GCCTCTCG
                                  _____  CC
GAM239  LOC119369 3'  GGAAAAGCCAGAGAG       5742       A  GTAA
                                GGAGAA GC    CGGAGAG
                                |||||| ||   |||||||
                                CCTTTT CG    GTCTCTC
                                  _ ____
GAM239  LOC128439 3'  GGGAAAAGCGTAGGGAAGGGGC 5743     AG      AC   A_
                                GG  AAAGCGTA  GGAG  GC
                                ||  ||||||||  ||||  ||
                                CC  TTTCGCAT  CTTC  CG
                                 CT       CC   CC
GAM239  LOC130813 3'  GGAGTGAGGCAGGAGAGAGC   5744      AA  C   AC
                                GGAG  AG GTA  GGAGAGC
                                ||||  || |||  |||||||
                                CCTC  TC CGT  TCTCTCG
                                  AC  _   CC
GAM239  LOC135932 5'  GGAGAAAGTGCACACAGGC   5745        C   A  G  A
                                GGAGAAAG GTA CG AG GC
                                |||||||| ||| || || ||
                                CCTCTTTC CGT GT TC CG
                                    A   _  G  _
GAM239  LOC143187 3'  GGAAAGGCGGCCAGAGAGC   5746       AA   TAA
                                GGAGA  GCG   CGGAGAGC
                                |||||  |||   ||||||||
                                CCTTT  CGC   GTCTCTCG
                                  C_   CG_
GAM239  LOC146880 5'  GAGGCACCGGCGGAGAGC    5747     AAA   AA_
                                GAG   GCGT   CGGAGAGC
                                |||   ||||   ||||||||
                                CTC   CGTG   GCCTCTCG
                                  ___   GCC
GAM239  LOC149401 3'  GGAGAAAGGGCAGGAGAG    5748        C   AC
                                GGAGAAAG GTA  GGAGAG
                                |||||||| |||  ||||||
                                CCTCTTTC CGT  CCTCTC
                                    C   __
GAM239  LOC151188 5'  GGGTAAACCACGGAGAGC    5749     AG   G GTA
                                GG  AAA C   ACGGAGAGC
                                ||  ||| |   |||||||||
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                                CC  TTT G   TGCCTCTCG
                                 CA   G ___
GAM239   LOC151429 3'  GGGAAAGCGTGAAGAAC     5750     A       AAC
                                GG GAAAGCGT   GGAGAGC
                                || ||||||||   |||||||
                                CC CTTTCGCA   CTTCTTG
                                 _      ____
GAM239   LOC151959 5'  GGGAAATGCCAGAGAGC     5751     A   _  GTAA
                                GG GAAA GC    CGGAGAGC
                                || |||| ||    ||||||||
                                CC CTTT CG    GTCTCTCG
                                 _    A  _____
GAM239   LOC154760 5'  GGAGAAAGTGCACACAGGC   5745          C   A  G  A
                                GGAGAAAG GTA CG AG GC
                                |||||||| ||| || || ||
                                CCTCTTTC CGT GT TC CG
                                     A   _  G  _
GAM239   LOC161003 5'  GGAGAAAGTATGAGAGAG    5752          CG AAC
                                GGAGAAAG  T   GGAGAG
                                ||||||||  |   ||||||
                                CCTCTTTC  A   TCTCTC
                                     AT C___
GAM239   LOC170082 3'  GGGAAGACACGGAGAGC     5753     A   AG GTA
                                GG GAA  C   ACGGAGAGC
                                || |||  |   |||||||||
                                CC CTT  G   TGCCTCTCG
                                 _   CT ____
GAM239   LOC200953 5'  GGAGGGGGGCTAACGGAGAGC  5754       AAA_  G
                                GGAG    GC TAACGGAGAGC
                                ||||    || ||||||||||||
                                CCTC    CG ATTGCCTCTCG
                                  CCCC  _
GAM239   LOC201175 5'  GGAGGCACCGGCGGAGAGC    5755       AAA    AA_
                                GGAG   GCGT   CGGAGAGC
                                ||||   ||||   ||||||||
                                CCTC   CGTG   GCCTCTCG
                                  ____   GCC
GAM239   LOC219848 3'  GGAGTCAACGGAGAGC       5756       AAAGCG
                                GGAG     TAACGGAGAGC
                                ||||     ||||||||||||
                                CCTC     GTTGCCTCTCG
                                  A_____
GAM239   LOC221585 5'  GGAGAAAGGTAGAACCAGC    5757          C   AC  AG
                                GGAGAAAG GTA  GG  AGC
                                |||||||| |||  ||  |||
                                CCTCTTTC CAT  TT  TCG
                                     _  C_  GG
GAM239   LOC221876 5'  AGAGAAAGGGGCGGAGAGC    5758          CGTAA
                                GGAGAAAG    CGGAGAGC
                                ||||||||    ||||||||
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                                TCTCTTTC    GCCTCTCG
                                    CCC__
GAM239  LOC253070 3'  GAGAAGCCACCCGCGGAGAGC  5759      A  GTAA__
                                GAGAA GC    CGGAGAGC
                                ||||| ||    ||||||||
                                CTCTT CG    GCCTCTCG
                                  _ GTGGGC
GAM239  LOC253992 3'  GGAAAAAGTCAAGGGGAGC   5760       CG  C  A
                                GGAGAAAG  TAA GG GAGC
                                ||||||||  ||| || ||||
                                CCTTTTTC  GTT CC CTCG
                                    A_  C  _
GAM239  LOC255520 3'  GGAGAAAGAGTGCATGAGC   5761       C  AA  GA
                                GGAGAAAG GT  CG  GAGC
                                |||||||| ||  ||  ||||
                                CCTCTTTC CA  GT  CTCG
                                    T  C_  A_
GAM239  LOC256789 3'  GAGGGGTAACGGAGAGC    5762     AAAGC
                                GAG    GTAACGGAGAGC
                                |||    ||||||||||||
                                CTC    CATTGCCTCTCG
                                 CC____
GAM239  LOC257476 3'  GAAAGAGCAGCAGAGAGC    5668      C  A
                                GAAAG GTA CGGAGAGC
                                ||||| ||| ||||||||
                                CTTTC CGT GTCTCTCG
                                  T  C
GAM239  LOC257476 3'  GGAGAAAGCAGTGGCAGACAG  5669        _ AA   G
                                GGAGAAAGC GT  CGGA AG
                                ||||||||| ||  |||| ||
                                CCTCTTTCG CA  GTCT TC
                                    T  CC   G
GAM239  LOC83690  5'  GGGACCGCAGACGGAGAGC   5763    A  AA   TA
                                GG GA  GCG  ACGGAGAGC
                                || ||  |||  |||||||||
                                CC CT  CGT  TGCCTCTCG
                                 _ GG   C_
GAM239  LOC90120  5'  AGAGAGGCGGAACGGAGGGC  5764      AA  T     A
                                GGAGA  GCG AACGGAG GC
                                |||||  ||| |||||||  ||
                                TCTCT  CGC TTGCCTC CG
                                  C_  C      C
GAM239  LOC91963  5'  GGAGAAAATGTAATTTGAG   5765       C   CG_
                                GGAGAAAG GTAA   GAG
                                |||||||| ||||   |||
                                CCTCTTTT CATT   CTC
                                    A   AAA
GAM240  DLG5      5'  CAGCTCGCGGCTGACAT     5768         G  TAT
                                CAGCTCGCGG TG   GCGT
                                |||||||||| ||   ||||
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                                GTCGAGCGCC AC   TGTA
                                      G ___
GAM240  DSC2     5' CAGGTCGCGGGCCGAGCGT   5769     C      GTAT
                                CAG TCGCGGGT   GCGT
                                ||| ||||||||   ||||
                                GTC AGCGCCCG   CGCA
                                  C       GCT_
GAM240  DSC2     5' CAGGTCGCGGGCCGAGCGT   5769     C      GTAT
                                CAG TCGCGGGT   GCGT
                                ||| ||||||||   ||||
                                GTC AGCGCCCG   CGCA
                                  C       GCT_
GAM240  LPIN1    3' CAACTCGTATATGCG      5770       GCGG
                                CAGCTC   GTGTATGCG
                                ||||||   |||||||||
                                GTTGAG   CATATACGC
                                     _____
GAM240  RU2      5' CAGCTCGCTGCTTCGCGT    5771        GG  GTA
                                CAGCTCGC  GT   TGCGT
                                ||||||||  ||   |||||
                                GTCGAGCG  CG   GCGCA
                                    A_  AA_
GAM240  SHH      5' GCGCGGCGGGTGTGTGCGT   5772     T _     A
                                GC CG CGGGTGT TGCGT
                                || || ||||||| |||||
                                CG GC GCCCACA ACGCA
                                 C  C      C
GAM240  UBE4A    3' AGCACATGGGGTGTATGTGT  5773     T  C_      C
                                AGC CG  GGGTGTATG GT
                                ||| ||  ||||||||| ||
                                TCG GT  CCCACATAC CA
                                  T  AC        A
GAM240  WEE1     5' CAGCACGTGGGCATGCGT    5774      T  C    GT
                                CAGC CG GGGT  ATGCGT
                                |||| || ||||  ||||||
                                GTCG GC CCCG  TACGCA
                                  T  A   __
GAM240  CA5A     5' CAGCTCTGCGGGGTACACGT  5775        _    T
                                CAGCTC GCGGG GTATGCGT
                                |||||| ||||| ||||||||
                                GTCGAG CGCCC CATGTGCA
                                   A    _
GAM240  DKFZP434A0225 5'  GCCCGCGGGAAGCGCTGCGT  5776         T_  A_
                                GCTCGCGGG  GT  TGCGT
                                |||||||||  ||  |||||
                                CGGGCGCCC  CG  ACGCA
                                     TT  CG
GAM240  DKFZP566H073 3'  ACCAGAGGTGTATGTGT    5777     T  C       C
                                GC CG GGGTGTATG GT
                                || || ||||||||| ||
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                                TG GT TCCACATAC CA
                                 _ C       A
GAM240  EKN1     5' CACCTCGCGGACTCCATGCGT 5778    G      G_
                                CA CTCGCGGGT  TATGCGT
                                || |||||||||  |||||||
                                GT GAGCGCCTG  GTACGCA
                                 G       AG
GAM240  FLJ10774 5' GCTCCGCGGCACGCGT     5779     _   GTG
                                GCTC GCGG   TATGCGT
                                |||| ||||   |||||||
                                CGAG CGCC   GTGCGCA
                                  G   ___
GAM240  FLJ20413 3' CAGACGGGTGTATGTGT    5780     CTC       C
                                CAG   GCGGGTGTATG GT
                                |||   ||||||||||| ||
                                GTC   TGCCCACATAC CA
                                 ___         A
GAM240  FLJ21613 5' CAGCGTGCACGCATGCGT   5781     TC   GG
                                CAGC  GCG  TGTATGCGT
                                ||||  |||  |||||||||
                                GTCG  CGT  GCGTACGCA
                                  CA  __
GAM240  GR6      5' ACCGCAGGTGTGTGCGT    5782    T      A
                                GC CGCGGGTGT TGCGT
                                || |||||||| |||||
                                TG GCGTCCACA ACGCA
                                 _       C
GAM240  HSPC156  5' CAGTGCGCGGCACGCGT    5783    CT    GTG
                                CAG  CGCGG   TATGCGT
                                |||  |||||   |||||||
                                GTC  GCGCC   GTGCGCA
                                  AC    ___
GAM240  KIAA1203 3' CAGCTATGCATGCATATGTGT 5784     C_  G     C
                                CAGCT  GCG GTGTATG GT
                                |||||  ||| ||||||| ||
                                GTCGA  CGT CGTATAC CA
                                   TA  A     A
GAM240  KIAA1938 3' CCCGGCTGGGTGTATGTGT  5785     _ _      C
                                CTCG C GGGTGTATG GT
                                |||| | ||||||||| ||
                                GGGC G CCCACATAC CA
                                  C A       A
GAM240  PPFIA1   5' CAGCCCGCGGCCGGCGT    5786         G  TAT
                                CAGCTCGCGG TG   GCGT
                                ||||||||||  ||   ||||
                                GTCGGGCGCC GC   CGCA
                                      G  ___
GAM240  SNAP29   3' GCTCAGAGTGTGTGTGT    5787      C     A  C
                                GCTCG GGGTGT TG GT
                                ||||| |||||| || ||
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                                CGAGT CTCACA AC CA
                                  _     C  A
GAM240  TSLRP    5' AGCATCCAAGTATGCGT     5788      _ G    GT
                                AGC TC CGGGT  ATGCGT
                                ||| || |||||  ||||||
                                TCG AG GTTCA  TACGCA
                                  T _    __
GAM240  LOC127696 5' CAGCTCGCGGTGCCAGC     5789          G   AT
                                CAGCTCGCGG TGT  GC
                                |||||||||| |||  ||
                                GTCGAGCGCC ACG  CG
                                      _  GT
GAM240  LOC129198 3' CAGCTCGCAGGTCATAGGT   5790           G   C
                                CAGCTCGCGGGT TATG GT
                                |||||||||||| |||| ||
                                GTCGAGCGTCCA GTAT CA
                                      _   C
GAM240  LOC144866 5' CAGCTGCACATGCTGTGCGT  5791       C  G   A_
                                CAGCT GCG GTGT  TGCGT
                                ||||| ||| ||||  |||||
                                GTCGA CGT TACG  ACGCA
                                  _  G   AC
GAM240  LOC148872 3' GCTGCGGGCGCGCGT       5792      C       AT
                                GCT GCGGGTGT  GCGT
                                ||| ||||||||  ||||
                                CGA CGCCCGCG  CGCA
                                  _      __
GAM240  LOC151878 5' CACCTCGGAGGAAGTGTGTGT 5793     G   C  T_ A C
                                CA CTCG GGG  GT TG GT
                                || |||| |||  || || ||
                                GT GAGC TCC  CA AC CA
                                 G   C  TT  C  A
GAM240  LOC153346 3' CAGACGTGTGTATGTGT     5794      CTC  G     C
                                CAG   GCG GTGTATG GT
                                |||   ||| |||||||  ||
                                GTC   TGC CACATAC CA
                                  ___  A     A
GAM240  LOC169026 3' AGCTGCCAATGTATGTGT    5795      C  G      C
                                AGCT GC GGTGTATG GT
                                |||| || ||||||||  ||
                                TCGA CG TTACATAC CA
                                  _ G       A
GAM240  LOC197209 5' CAGCTCTGCGGGGTACACGT  5775       _    T
                                CAGCTC GCGGG GTATGCGT
                                |||||| ||||| ||||||||
                                GTCGAG CGCCC CATGTGCA
                                   A    _
GAM240  LOC253946 3' CAGCTCGCTGGTCAGCGT    5796         G  GTAT
                                CAGCTCGC GGT    GCGT
                                |||||||| |||    ||||
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                                GTCGAGCG CCA   CGCA
                                    A  GT__
GAM240  LOC254557 5'  ACTCGCGGACTGCGCGT    5797        _  AT
                                GCTCGCGGG TGT  GCGT
                                ||||||||| |||  ||||
                                TGAGCGCCT ACG  CGCA
                                    G  __
GAM240  LOC91409  3'  CAGCTCGCGGATGAGCAC    5798          TA
                                CAGCTCGCGGGTG  TGC
                                ||||||||||||  |||
                                GTCGAGCGCCTAC  GTG
                                      TC
GAM241  ABCB4    5'  TGCTCCTGATCCTTTCCCC   5801     _   CC  CC
                                TGC CCTGG  TCC  TCCCC
                                ||| |||||  |||  |||||
                                ACG GGACT  AGG  AGGGG
                                  A   __  AA
GAM241  ABCB4    5'  TGCTCCTGATCCTTTCCCC   5801     _   CC  CC
                                TGC CCTGG  TCC  TCCCC
                                ||| |||||  |||  |||||
                                ACG GGACT  AGG  AGGGG
                                  A   __  AA
GAM241  ABCD1    3'  CCCTCTCCCCTCTCCC     5802     GGC     _
                                CCCT   CTCCCCTC CCC
                                ||||   |||||||| |||
                                GGGA   GAGGGGAG GGG
                                  ___      A
GAM241  ACTR1B   3'  GCTCTGTCTCCCCTCCC    5803    C  GC
                                GC CTG  CTCCCCTCCC
                                || |||  ||||||||||
                                CG GAC  GAGGGGAGGG
                                 A  A_
GAM241  ADAM11   3'  TGCCCTGGCCCCAGCACCCCC  5804          CCCT
                                TGCCCTGGCCTC   CCCCC
                                ||||||||||||   |||||
                                ACGGGACCGGGG   GGGGG
                                      TCGT
GAM241  ADAM11   3'  TGCCCTGGCCCCAGCACCCCC  5804          CCCT
                                TGCCCTGGCCTC   CCCCC
                                ||||||||||||   |||||
                                ACGGGACCGGGG   GGGGG
                                      TCGT
GAM241  ADCY6    3'  TGCTACTGACCCCTCCCC    5805    C_  CCT
                                TGC  CTGG   CCCCTCCCC
                                |||  ||||  |||||||||
                                ACG  GACT   GGGGAGGGG
                                  AT   ___
GAM241  ADCY6    3'  TGCTACTGACCCCTCCCC    5805    C_  CCT
                                TGC  CTGG   CCCCTCCCC
                                |||  ||||  |||||||||
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                              ACG  GACT   GGGGAGGGG
                                AT   ___
GAM241  ADORA1   3'  GCCACCTCCCCTCCC      5806     CTG
                              GCC   GCCTCCCCTCCC
                              |||   ||||||||||||
                              CGG   TGGAGGGGAGGG
                                    ___
GAM241  AGPAT2   3'  GCCCTCCAGGCCCCTCCTC   5807      ___     C
                              GCCCT   GGCCTC CCTC
                              |||||   |||||| ||||
                              CGGGA   CCGGGG GGAG
                                 GGT     A
GAM241  AP2A1    5'  GCCCCCTGCCCCTCCCC     5809      TGG  _
                              GCCC   CCT CCCCTCCCC
                              ||||   ||| |||||||||
                              CGGG   GGA GGGGAGGGG
                                ___   C
GAM241  AP2A1    3'  CCCTGGCCCCTCTCCCC     5808        T  C
                              CCCTGGCC CC CTCCCC
                              |||||||| || ||||||
                              GGGACCGG GG GAGGGG
                                   _  A
GAM241  AP2A1    3'  CCCTGGCCCCTCTCCCC     5808        T  C
                              CCCTGGCC CC CTCCCC
                              |||||||| || ||||||
                              GGGACCGG GG GAGGGG
                                   _  A
GAM241  AP2A1    5'  GCCCCCTGCCCCTCCCC     5809      TGG  _
                              GCCC   CCT CCCCTCCCC
                              ||||   ||| |||||||||
                              CGGG   GGA GGGGAGGGG
                                ___   C
GAM241  ARF3     5'  TGCCCTGGCCCACTCCC     5810          CCC
                              TGCCCTGGCCT   CTCCC
                              ||||||||||   |||||
                              ACGGGACCGGG   GAGGG
                                    T__
GAM241  ARHGAP6  3'  GCCCTGGCACTCTGTAAAGCTT 5811     _  CC_________   CCCIII
           CTCCGGG                GC CTC        CTCC     G
                              || |||        ||||     |
                              CG GAG        GAGG     C
                               T   ACATTTCGAA    IIICCC
GAM241  ASCL1    5'  CCTCCTCCCTCCCCTCCTCC   5812     _ GG       _
                              CC CT  CCTCCCCTCC CC
                              || ||  |||||||||| ||
                              GG GG  GGAGGGGAGG GG
                               A  AG        A
GAM241  ASIC4    3'  CCCCCTCCCTCTCCTTCC    5813      TGG     _   __
                              CCC   CCTCCC CTCC  CC
                              |||   |||||| ||||  ||
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                                GGG  GGAGGG GAGG  GG
                                 ___    A   AA
GAM241  ATF5    3'  GCCTTTAGCCTCCCTCCC   5814    C_      C
                                GCC  TGGCCTCCC TCCC
                                |||  ||||||||| ||||
                                CGG  ATCGGAGGG AGGG
                                  AA       _
GAM241  ATP1A1  3'  GCCCTCCCCCCTCCCCC    5815      GGC
                                GCCCT  CTCCCCTCCCCC
                                |||||  ||||||||||||
                                CGGGA  GGGGGGAGGGGG
                                  ___
GAM241  BCL2L2  3'  GCCAAAACATTCCCCTCCCC  5816    CT  C_
                                GCC  GGC  TCCCCTCCCC
                                |||  |||  ||||||||||
                                CGG  TTG  AGGGGAGGGG
                                  TT   TA
GAM241  BLTR2   5'  CTGTTCTCATCCCTCCCCC  5817    GC  __
                                CTG  CTC  CCCTCCCCC
                                |||  |||  |||||||||
                                GAC  GAG  GGGAGGGGG
                                  AA   TA
GAM241  BLTR2   5'  GCTCTGGCCCCAATCCTCC  5818    C     C__
                                GC CTGGCCTC  CCTCC
                                || ||||||||  |||||
                                CG GACCGGGG  GGAGG
                                 A       TTA
GAM241  BTEB1   3'  TGGCCTTACCCCCTCCCCC  5819      ___
                                TGGCCT  CCCCTCCCCC
                                ||||||  ||||||||||
                                ACCGGA  GGGGAGGGGG
                                   ATG
GAM241  CACNA2D2 3' TGCCCCAGAGCCTCTCTCC  5820      __    CC
                                TGCCCT  GGCCTC  CTCC
                                ||||||  ||||||  ||||
                                ACGGGG  TCGGAG  GAGG
                                   TC     A_
GAM241  CACNB1  3'  GCCCCTCGCTCCCTCCCC   5823     G_  CTC
                                GCCCT  GC   CCCTCCCC
                                |||||  ||   ||||||||
                                CGGGG  CG   GGGAGGGG
                                  AG  A__
GAM241  CACNB1  3'  CGCTCCCTCCCCTCCCC    5822    C TGG
                                TGC C   CCTCCCCTCCCC
                                |||  |   ||||||||||||
                                GCG G   GGAGGGGAGGGG
                                 A ___
GAM241  CACNB1  3'  CCCTGGCTCAGAGCCCTTCCTC 5821       C _____   _ _
          C                      CCCTGGC TC    CCCT CC CC
                                |||||||  ||    ||||  ||  ||
```

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                                GGGACCG AG    GGGA GG GG
                                   _ TCTC    A  A
GAM241  CD34     3'  GCCCTGGCCTCCACCGTTTTCC 5824            _ ____
                                GCCCTGGCCTCC CC    TCC
                                |||||||||||| ||    |||
                                CGGGACCGGAGG GG    AGG
                                      T  CAAA
GAM241  CD3Z     3'  GCCCTGGCTGACCCTCCCC    5825         CTC
                                GCCCTGGC   CCCTCCCC
                                ||||||||   ||||||||
                                CGGGACCG   GGGAGGGG
                                     ACT
GAM241  CDC25A   3'  CCCCTCCGTCTCCTCTCCCC   5826       GG _ _ _
                                CCCT  CC TC CC CTCCCC
                                ||||  || || || ||||||
                                GGGG  GG AG GG GAGGGG
                                  A_  C  A  A
GAM241  CDC25A   3'  TGCCCTGGGCTCCAACCT     5827         C   __
                                TGCCCTGG CTCC  CCT
                                |||||||| ||||  |||
                                ACGGGACC GAGG  GGA
                                     C    TT
GAM241  CDS1     5'  TGCCCGGGCCTCCCGCACC    5828        T       CT_
                                TGCCC GGCCTCCC   CC
                                ||||| ||||||||   ||
                                ACGGG CCGGAGGG   GG
                                   C       CGT
GAM241  CEBPA    3'  CCCTGAGCCCCCCTCCTCC    5829        _  T      _
                                CCCTG GCC CCCCTCC CC
                                ||||| ||| ||||||| ||
                                GGGAC CGG GGGGAGG GG
                                   T  _      A
GAM241  CELSR3   3'  CCCTCTATCTCCCTCCCCC    5830       GGCC  _
                                CCCT   TC CCCTCCCCC
                                ||||   || |||||||||
                                GGGA   AG GGGAGGGGG
                                  GAT_  A
GAM241  CENTD2   5'  CCTCACACTCCCCTCCCCC    5831       G  _
                                CCT GC CTCCCCTCCCCC
                                ||| || ||||||||||||
                                GGA TG GAGGGGAGGGGG
                                  G  T
GAM241  CHD4     3'  TGCCCCTCACTCCCTCCCC    5832        GGC    C
                                TGCCCT   CTCCC TCCCC
                                ||||||   ||||| |||||
                                ACGGGG   GAGGG AGGGG
                                   AGT    _
GAM241  CHRNE    3'  CCCTCCCCCCTCCCC       5833       GGC
                                CCCT   CTCCCCTCCCC
                                ||||   ||||||||||
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                                GGGA  GGGGGGAGGGG
                                  ___
GAM241  COL11A2  3' GCCCTGGCCCAGGGCTCCC  5834        CCC_
                                GCCCTGGCCT  CTCCC
                                ||||||||||  |||||
                                CGGGACCGGG  GAGGG
                                     TCCC
GAM241  COL11A2  3' GCCCTGGCCCAGGGCTCCC  5834        CCC_
                                GCCCTGGCCT  CTCCC
                                ||||||||||  |||||
                                CGGGACCGGG  GAGGG
                                     TCCC
GAM241  COL9A2   3' TGCTCTACCTCCCCTTCCCC  5835    C  G     _
                                TGC CTG CCTCCCCT CCCC
                                ||| ||| |||||||| ||||
                                ACG GAT GGAGGGGA GGGG
                                  A  _     A
GAM241  COPG2    3' CCCCTCCCCCCTCCCCC    5836     GG  T
                                CCCT  CC CCCCTCCCCC
                                ||||  || ||||||||||
                                GGGG  GG GGGGAGGGGG
                                  A_ _
GAM241  COPG2    3' ACTCTGGCTTCCCCTCCCCC  5837    C    C
                                GC CTGGC TCCCCTCCCCC
                                || ||||| ||||||||||
                                TG GACCG AGGGGAGGGGG
                                 A    A
GAM241  CPNE6    5' GCCCTGGCCCTGACTCCC    5838        CCC
                                GCCCTGGCCT  CTCCC
                                ||||||||||  |||||
                                CGGGACCGGG  GAGGG
                                     ACT
GAM241  CPNE7    3' TGCCTTGCTGGCCCTCCCCC  5839     ___    TCCC
                                TGCC  CTGGCC  CTCCCCC
                                ||||  ||||||  |||||||
                                ACGG  GACCGG  GAGGGGG
                                  AAC    ____
GAM241  CRHR1    3' TGCCCTGGCTGTCCAGTCCC  5840        C_  CC
                                TGCCCTGGC  TCC  TCCC
                                |||||||||  |||  ||||
                                ACGGGACCG  AGG  AGGG
                                     AC  TC
GAM241  CRYBA2   5' GCTCCCCTCCCTTCCCC    5841    _ TGG    C
                                GC CC  CCTCCC TCCCC
                                || ||  |||||| |||||
                                CG GG  GGAGGG AGGGG
                                 A ___    A
GAM241  CSH2     5' TACCCTGGCCAGTTCTCTCTCC 5842        TCCC__  _
           C                     TGCCCTGGCC    CTC CCC
                                ||||||||||    ||| |||
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                                ATGGGACCGG     GAG GGG
                                     TCAAGA   A
GAM241  CSH2     5'  TACCCTGGCCAGTTCTCTCTCC 5842          TCCC__  _
           C                    TGCCCTGGCC     CTC CCC
                                ||||||||||     ||| |||
                                ATGGGACCGG     GAG GGG
                                     TCAAGA   A
GAM241  CSH2     5'  TACCCTGGCCAGTTCTCTCTCC 5842          TCCC__  _
           C                    TGCCCTGGCC     CTC CCC
                                ||||||||||     ||| |||
                                ATGGGACCGG     GAG GGG
                                     TCAAGA   A
GAM241  CSH2     5'  TACCCTGGCCAGTTCTCTCTCC 5842          TCCC__  _
           C                    TGCCCTGGCC     CTC CCC
                                ||||||||||     ||| |||
                                ATGGGACCGG     GAG GGG
                                     TCAAGA   A
GAM241  CSRP1    3'  GCCCAGCCCTTTCCCCTTCC   5843      T   ___     C
                                GCCC GGCC   TCCCCT CC
                                |||| ||||   |||||| ||
                                CGGG TCGG   AGGGGA GG
                                  _   GAA     A
GAM241  CYP26A1  5'  CCCTGGCTCCTCCCCC      5844        CTCC
                                CCCTGGC    CCTCCCCC
                                |||||||    ||||||||
                                GGGACCG    GGAGGGGG
                                    A___
GAM241  DISC1    3'  GCCCACCTCCCTCCCCC     5845      TG     C
                                GCCC  GCCTCCC TCCCCC
                                ||||  ||||||| ||||||
                                CGGG  TGGAGGG AGGGGG
                                   __     _
GAM241  DSC1     5'  CCCTGGCCAGTCTCCTTCC   5846         __ _ C
                                CCCTGGCC  TC CC TCC
                                ||||||||  || || |||
                                GGGACCGG  AG GG AGG
                                     TC  A  A
GAM241  DSC1     5'  CCCTGGCCAGTCTCCTTCC   5846         __ _ C
                                CCCTGGCC  TC CC TCC
                                ||||||||  || || |||
                                GGGACCGG  AG GG AGG
                                     TC  A  A
GAM241  DSC3     3'  TGCCCTGAGTTCTTTCTCCC  5847         CC  CC_
                                TGCCCTGG  TC   CTCCC
                                ||||||||  ||   |||||
                                ACGGGACT  AG   GAGGG
                                     CA  AAA
GAM241  DSC3     3'  TGCCCTGAGTTCTTTCTCCC  5847         CC  CC_
                                TGCCCTGG  TC   CTCCC
                                ||||||||  ||   |||||
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                                ACGGGACT  AG   GAGGG
                                    CA  AAA
GAM241  DTNB    3'  GCTCTGGCTCCCCTCTCCC   5848    C    C     _
                                GC CTGGC TCCCCTC CCC
                                || ||||| ||||||| |||
                                CG GACCG AGGGGAG GGG
                                 A    _     A
GAM241  DTNB    3'  GCTCTGGCTCCCCTCTCCC   5848    C    C     _
                                GC CTGGC TCCCCTC CCC
                                || ||||| ||||||| |||
                                CG GACCG AGGGGAG GGG
                                 A    _     A
GAM241  DXYS155E 3'  GCCCGGCTCCTCTCCC     5849     T   C   C
                                GCCC GGC TCC CTCCC
                                |||| ||| ||| |||||
                                CGGG CCG AGG GAGGG
                                  _  _  A
GAM241  E2F1    3'  TGCCCTGGGCCTTGTGGGACCC 5850        _  CCCCT__
            CC                    TGCCCTGG CCT      CCCCC
                                |||||||| |||      |||||
                                ACGGGACC GGA      GGGGG
                                    C   ACACCCT
GAM241  ECE1    3'  GCCCCTTCCCCTCCTCC    5851       GGCC      _
                                GCCCT    TCCCCTCC CC
                                |||||    |||||||| ||
                                CGGGG    AGGGGAGG GG
                                   A___       A
GAM241  EDARADD  5'  CCTCCGCCTTCCCCTCCC    5852    _  G  _
                                CC CTG CCT CCCCTCCC
                                || ||| ||| ||||||||
                                GG GGC GGA GGGGAGGG
                                 A  _  A
GAM241  EDN2    3'  GCCCTGGCCACTTCTCTCCTCC 5853         _____  C
                                GCCCTGGCC    TC CCTCC
                                |||||||||    || |||||
                                CGGGACCGG    AG GGAGG
                                     TGAAG  A
GAM241  EGLN2    5'  TGCCCTGACCTCTCTGCCC   5854          CC  C
                                TGCCCTGGCCTC  CT CCC
                                ||||||||||||  || |||
                                ACGGGACTGGAG  GA GGG
                                       A_  C
GAM241  EGR3    3'  GCTCCTTACCCCCTCCCCC   5855    _  GGCC
                                GC CCT    TCCCCTCCCCC
                                || |||    ||||||||||
                                CG GGA    GGGGGAGGGGG
                                 A  AT__
GAM241  EIF4A1   3'  TGGCTCCCTTCCCTCCCCC   5856     _  ___
                                TGGC CTC  CCCTCCCCC
                                |||| |||  |||||||||
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                                ACCG GGG  GGGAGGGGG
                                  A  AA
GAM241  EIF5A   3'  CCCCTCCCCTCTCCTCC    5857    TGG      _ _
                                CC  CCTCCCCTC CC CC
                                ||  ||||||||| || ||
                                GG  GGAGGGGAG GG GG
                                 ___       A  A
GAM241  EMP1    3'  CCCCCTCCCCCCTCCCC    5858     GG  T
                                CCCT  CC CCCCTCCCC
                                ||||  || |||||||||
                                GGGG  GG GGGGAGGGG
                                  GA  _
GAM241  EPB41L2 3'  GCCCCCTCCCCCTCTCCC   5859      GG   C
                                GCCCT  CCTCC CTCCC
                                |||||  ||||| |||||
                                CGGGG  GGGGG GAGGG
                                   GA    A
GAM241  EPB49   5'  TGCCTGGCCCTCTCTCCC   5860     C    CCC
                                TGCC TGGCCT  CTCCC
                                |||| ||||||  |||||
                                ACGG ACCGGG  GAGGG
                                  _    AGA
GAM241  EPHB3   3'  CCTGGAGTCCCCTCCTCC   5861      CC     _
                                CCTGG  TCCCCTCC CC
                                |||||  |||||||| ||
                                GGACC  AGGGGAGG GG
                                   TC      A
GAM241  EXT1    3'  CCCTTCTTGCTTCCCCTCCCCC 5862     G___  C
                                CCCT   GC TCCCCTCCCCC
                                ||||   || ||||||||||
                                GGGA   CG AGGGGAGGGGG
                                  AGAA  A
GAM241  FBXW1B  3'  TGCCCCCTCCCTTCCCCC   5863      TGG    C
                                TGCCC  CCTCCC TCCCCC
                                |||||  |||||| ||||||
                                ACGGG  GGAGGG AGGGGG
                                  ___     A
GAM241  FBXW1B  3'  TGCCCCCTCCCTTCCCCC   5863      TGG    C
                                TGCCC  CCTCCC TCCCCC
                                |||||  |||||| ||||||
                                ACGGG  GGAGGG AGGGGG
                                  ___     A
GAM241  FBXW1B  3'  TGCCCCCTCCCTTCCCCC   5863      TGG    C
                                TGCCC  CCTCCC TCCCCC
                                |||||  |||||| ||||||
                                ACGGG  GGAGGG AGGGGG
                                  ___     A
GAM241  FGF23   5'  GCCTTACTGGCCTTTTCCTTCT 5864    ___    ___  C_
            CC                  GCC  CTGGCC  TCC  CTCC
                                |||  ||||||  |||  ||||
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                                CGG  GACCGG  AGG  GAGG
                                  AAT    AAA  AA
GAM241  FHL2    5'  GCTCTGCTCCCCTCTCC    5865    C  GC     C
                                GC CTG  CTCCCCTC CC
                                || |||  |||||||| ||
                                CG GAC  GAGGGGAG GG
                                 A  __      A
GAM241  FOS     3'  GCCGGCTGCCTCCCCTTCCC  5866    CTG_      C
                                GCC   GCCTCCCCT CCC
                                |||   ||||||||| |||
                                CGG   CGGAGGGGA GGG
                                  CCGA       A
GAM241  FOXO1A  5'  ACCCCCGCCCCTCCCCC    5867     TGG  T
                                GCCC  CC CCCCTCCCCC
                                ||||  || ||||||||||
                                TGGG  GG GGGGAGGGGG
                                  ___  C
GAM241  FRZB    5'  CTGGGAGCTTCTCCTCCCCC  5868    ___  C  C
                                CTG  GC TC CCTCCCCC
                                |||  || || ||||||||
                                GAC  CG AG GGAGGGGG
                                  CCT  A  A
GAM241  FXR2    3'  TGCCACCCCCCTCCCCC    5869     CTG  T
                                TGCC  GCC CCCCTCCCCC
                                ||||  ||| ||||||||||
                                ACGG  TGG GGGGAGGGGG
                                   ___  _
GAM241  FZD5    5'  GCCCCCTCCCTCCCC      5870     TGG    C
                                GCCC  CCTCCC TCCCC
                                ||||  |||||| |||||
                                CGGG  GGAGGG AGGGG
                                   ___    _
GAM241  GAPD    3'  CCCTAGGCCCCTCCCC      5871       CCT
                                CCCTGG  CCCCTCCCC
                                ||||||  |||||||||
                                GGGATC  GGGGAGGGG
                                   C__
GAM241  GCNT2   5'  GCCCAGCCTTCCCTCCTCC  5872     T   C    _
                                GCCC GGCCT CCCTCC CC
                                |||| ||||| |||||| ||
                                CGGG TCGGA GGGAGG GG
                                  _   A    A
GAM241  GCS1    3'  TGGCTCCCCTCCTCTCCC    5873     C     ___
                                TGGC TCCCCTCC  CCC
                                |||| ||||||||  |||
                                ACCG AGGGGAGG  GGG
                                  _      AGA
GAM241  GLDC    5'  CCTGGCCTCGGTCCCCC    5874        CCC
                                CCTGGCCTC  TCCCCC
                                |||||||||  ||||||
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                                GGACCGGAG  AGGGGG
                                     CC_
GAM241  GPC1    3' GCCCAGCTTCCCCTCCTCC   5875     T  C     _
                                GCCC GGC TCCCCTCC CC
                                |||| ||| |||||||| ||
                                CGGG TCG AGGGGAGG GG
                                  _  A      A
GAM241  GPR61   3' TACCCAGGTTCCCTCCCC   5876      T  CCTC
                                TGCCC GG   CCCTCCCC
                                ||||| ||   ||||||||
                                ATGGG CC   GGGAGGGG
                                   T  AA__
GAM241  GRIA3   5' GCTCTTACACCCCCTCCCC   5877    C  G  C
                                GC CT GC TCCCCTCCCC
                                || || || ||||||||||
                                CG GA TG GGGGGAGGGG
                                 A  A  T
GAM241  GRIA3   5' GCTCTTACACCCCCTCCCC   5877    C  G  C
                                GC CT GC TCCCCTCCCC
                                || || || ||||||||||
                                CG GA TG GGGGGAGGGG
                                 A  A  T
GAM241  GRM1    3' TGGCCTGGCCCTTCCCTTCCCC 5878    C     __   C
                                TG CCTGGCC  TCCC TCCCC
                                || |||||||  |||| |||||
                                AC GGACCGG  AGGG AGGGG
                                 C      GA   A
GAM241  GSTM5   3' TGCTCAGCCCCCTTCCCC   5879    CC   T  C
                                TGC  TGGCC CCC TCCCC
                                |||  ||||| ||| |||||
                                ACG  GTCGG GGG AGGGG
                                 A_    _  A
GAM241  H1F0    3' GCCCACTCCCCCTCCCCC   5880     TG  CT
                                GCCC  GC  CCCCTCCCCC
                                ||||  ||  ||||||||||
                                CGGG  TG  GGGGAGGGGG
                                  __ AG
GAM241  HCCS    5' TGCACCTAAGCCCTCCCCC   5881    _   CCTC
                                TGC CCTGG   CCCTCCCCC
                                ||| |||||   |||||||||
                                ACG GGATT   GGGAGGGGG
                                  T   C___
GAM241  HCN4    3' CCCTCCTCCCTCCCC     5882     GG    C
                                CCCT  CCTCCC TCCCC
                                ||||  |||||| |||||
                                GGGA  GGAGGG AGGGG
                                  __    _
GAM241  HIRA    3' TGCCAGTGTCTCCTCCCCC   5883     CT  CC  C
                                TGCC  GG  TC CCTCCCCC
                                ||||  ||  || ||||||||
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                                ACGG  TC  AG GGAGGGGG
                                  __ AC  A
GAM241  HIS1    3'  CCCCTTTGCCCCCTCCCCC   5884      GGCC
                                CCCT   TCCCCTCCCCC
                                ||||   ||||||||||
                                GGGG   GGGGGAGGGGG
                                  AAAC
GAM241  HOXA7   3'  TACTACTGGTCCCCTCCTCC  5885     C_   CC      _
                                TGC  CTGG  TCCCCTCC CC
                                |||  ||||  |||||||| ||
                                ATG  GACC  AGGGGAGG GG
                                  AT   __       A
GAM241  HOXC13  5'  GCTCCTGTTTCCCCTCCCCC  5886    _   GCC
                                GC CCTG   TCCCCTCCCCC
                                || ||||   ||||||||||
                                CG GGAC   AGGGGAGGGGG
                                 A   AA_
GAM241  HYAL2   3'  CCCAGGGACTTCCCCTCCCCC 5887     T_ _ C
                                CCC  GG C TCCCCTCCCCC
                                |||  || | ||||||||||
                                GGG  CC G AGGGGAGGGGG
                                  TC  T A
GAM241  HYAL2   3'  CCCAGGGACTTCCCCTCCCCC 5887     T_ _ C
                                CCC  GG C TCCCCTCCCCC
                                |||  || | ||||||||||
                                GGG  CC G AGGGGAGGGGG
                                  TC  T A
GAM241  ICAM1   3'  TACCTTGGCCCCCTTCCCC   5888     C    T   C
                                TGCC TGGCC CCC TCCCC
                                |||| ||||| ||| |||||
                                ATGG ACCGG GGG AGGGG
                                  A    _   A
GAM241  IFNGR2  5'  CCCCCGCCCCCCTCCCC    5889     G   T
                                CCCT GCC CCCCTCCCC
                                |||| ||| |||||||||
                                GGGG CGG GGGGAGGGG
                                  G   _
GAM241  IGF2R   3'  TGGCCTCCCTCCTCCTCC   5890         __   _
                                TGGCCTCCC  CTCC CC
                                |||||||||  |||| ||
                                ACCGGAGGG  GAGG GG
                                     AG   A
GAM241  IGHMBP2 3'  GCCCTCCGCTCCTCCCCC   5891      GG  TCC
                                GCCCT  CC   CCTCCCCC
                                |||||  ||   ||||||||
                                CGGGA  GG   GGAGGGGG
                                  __ CGA
GAM241  IL18R1  3'  TGCCAGCCCCTCCTCC     5892      CT    C
                                TGCC  GGCCTC CCTCC
                                ||||  |||||| |||||
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                                ACGG  TCGGGG GGAGG
                                  __     A
GAM241  INHBA   5'  GCCCTGCTTTTCCTCCCCC   5893       G CTCC
                                GCCCTG C   CCTCCCCC
                                |||||| |   ||||||||
                                CGGGAC G   GGAGGGGG
                                  _ AAAA
GAM241  ITPKA   3'  GCCCTTTGCCCCCTCCCC   5894      GGCC
                                GCCCT   TCCCCTCCCC
                                |||||   ||||||||||
                                CGGGA   GGGGGAGGGG
                                  AAC_
GAM241  JAG2    5'  TGCCCGGCCCGGCTCCC    5895      T    CCC
                                TGCCC GGCCT   CTCCC
                                ||||| |||||   |||||
                                ACGGG CCGGG   GAGGG
                                  _    CC_
GAM241  JJAZ1   5'  CCTGCCTCCTCCCCC      5896      G    CC
                                CCTG CCTCC  TCCCCC
                                |||| |||||  ||||||
                                GGAC GGAGG  AGGGGG
                                  _    __
GAM241  LETM1   5'  TGCGCTGCCTCCTTCTCC    5897     C  G    C_
                                TGC CTG CCTCC  CTCC
                                ||| ||| |||||  ||||
                                ACG GAC GGAGG  GAGG
                                  C  _    AA
GAM241  LHX4    5'  TGGCCGGCCCCCTCCCCC    5898      __
                                TGGCC  TCCCCTCCCCC
                                |||||  ||||||||||
                                ACCGG  GGGGGAGGGGG
                                  CC
GAM241  LIF     3'  TGCAGCCTCCCTCTCCTCC   5899     CCT      _  _
                                TGC   GGCCTCCC CTCC CC
                                |||   |||||||| |||| ||
                                ACG   TCGGAGGG GAGG GG
                                  ___      A   A
GAM241  LIF     3'  TGCTGCCTCCTTCCCTCCCC  5900     CCTG    ___
                                TGC   GCCTCC   CCTCCCC
                                |||   ||||||   |||||||
                                ACG   CGGAGG   GGAGGGG
                                  A___     AAG
GAM241  LMNB1   3'  CCCTCCACCTCCCTCCCCC   5901      G_     C
                                CCCT  GCCTCCC TCCCCC
                                ||||  ||||||| ||||||
                                GGGA  TGGAGGG AGGGGG
                                  GG     _
GAM241  LMO2    5'  TGCCTGTGCCATCTCCCC    5902      C  _  TCCC
                                TGCC TG GCC   CTCCCC
                                |||| || |||   ||||||
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                                ACGG AC CGG   GAGGGG
                                  _ A  TA__
GAM241  LNK     5'  GCCCTGGGCGCGTCCTCTCCC  5903       _ C__  C
                                GCCCTGG C  TCC CTCCC
                                ||||||| |  ||| |||||
                                CGGGACC G  AGG GAGGG
                                    C CGC  A
GAM241  LYL1    5'  TGCCCTGGCTCTGTCCC    5904        C  CCC
                                TGCCCTGGC TC  TCCC
                                ||||||||| ||  ||||
                                ACGGGACCG AG  AGGG
                                     _ AC_
GAM241  LZTS1   3'  TGCCTGTCTCTCCCCTCC   5905     C  GC_
                                TGCC TG  CTCCCCTCC
                                |||| ||  |||||||||
                                ACGG AC  GAGGGGAGG
                                  _ AGA
GAM241  MAD2L2  3'  TGCCCTAGGCGGGGATCCCCC  5906      _  CTCCCC
                                TGCCCT GGC    TCCCCC
                                |||||| |||    ||||||
                                ACGGGA CCG    AGGGGG
                                   T  CCCCT_
GAM241  MAF     5'  GCCCGCCCTCCCTCCCCC   5907     TG  TC
                                GCCC  GCC  CCCTCCCCC
                                ||||  |||  |||||||||
                                CGGG  CGG  GGGAGGGGG
                                  __  GA
GAM241  MAGEA4  3'  GCCCTGCCCCTTCCCC    5908      GCCT   _
                                GCCCTG   CCCCT CCCC
                                ||||||   ||||| ||||
                                CGGGAC   GGGGA GGGG
                                   ____   A
GAM241  MAML1   3'  GCCTACGGCCTCCTTCCCC  5909    C_     CC
                                GCC  TGGCCTCC  TCCCC
                                |||  ||||||||  |||||
                                CGG  GCCGGAGG  AGGGG
                                  AT      A_
GAM241  MAP3K10 3'  CCCTGCCCACCCTCCCCC   5910     G  TC
                                CCCTG CC  CCCTCCCCC
                                ||||| ||  |||||||||
                                GGGAC GG  GGGAGGGGG
                                  _ GT
GAM241  MAP3K11 3'  CCCTGCACCTCCCCTCCTCC  5911     _       _
                                CCCTG GCCTCCCCTCC CC
                                ||||| |||||||||| ||
                                GGGAC TGGAGGGGAGG GG
                                  G        A
GAM241  MAP3K12 3'  GCCTTAGCCTCCCTCCTCC  5912    C      C  _
                                GCC TGGCCTCCC TCC CC
                                ||| ||||||||| ||| ||
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                                CGG ATCGGAGGG AGG GG
                                  A       _  A
GAM241  MAP3K12  3'  CCCACCGCCCCTCCCCC    5913     TG  T
                                CCC  GCC CCCCTCCCCC
                                |||  ||| ||||||||||
                                GGG  TGG GGGGAGGGGG
                                  __  C
GAM241  MAPK1    3'  TGCCCTAGGTAGTAGCCTTCCC 5914       ________    C
          T                      TGCCCT     GGCCT CCCT
                                 ||||||      ||||| ||||
                                 ACGGGA     TCGGA GGGA
                                    TCCATCA    A
GAM241  MAPK12   5'  TGCGCACGGCCCCTCCCCC   5915     CC_   TCC
                                TGC  TGGCC  CCTCCCCC
                                |||  |||||  ||||||||
                                ACG  GCCGG  GGAGGGGG
                                  CGT   ____
GAM241  MAPK12   5'  GCTCCCGGCCCTTCCCTC    5916    _      C_
                                GC CCTGGCCT  CCCTC
                                || ||||||||  |||||
                                CG GGGCCGGG  GGGAG
                                 A       AA
GAM241  MAPRE3   3'  TGCCCCCCTCCCTTTCCC    5917      GG    C_
                                TGCCCT  CCTCCC  TCCC
                                ||||||  ||||||  ||||
                                ACGGGG  GGAGGG  AGGG
                                   __      AA
GAM241  MASP1    5'  TGCCCGGCCTTGGTCCTCC   5918      T    CC__
                                TGCCC GGCCT   CCTCC
                                |||||  |||||   |||||
                                ACGGG CCGGA   GGAGG
                                   _    ACCA
GAM241  MASP1    5'  TGCCCGGCCTTGGTCCTCC   5918      T    CC__
                                TGCCC GGCCT   CCTCC
                                |||||  |||||   |||||
                                ACGGG CCGGA   GGAGG
                                   _    ACCA
GAM241  MAZ      3'  TACTCCATTCTCCCCTCTCCC  5919     C  GC      _
                                TGC CTG  CTCCCCTC CCC
                                |||  |||  |||||||| |||
                                ATG GGT  GAGGGGAG GGG
                                  A  AA       A
GAM241  MBD1     5'  CGCCCTCCTCCCCTTCC     5920       GG      C
                                TGCCCT  CCTCCCCT CC
                                ||||||  |||||||| ||
                                GCGGGA  GGAGGGGA GG
                                   __       A
GAM241  MBD1     5'  CGCCCTCCTCCCCTTCC     5920       GG      C
                                TGCCCT  CCTCCCCT CC
                                ||||||  |||||||| ||
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                                GCGGGA  GGAGGGGA GG
                                  __       A
GAM241  MBD1    5'  CGCCCTCCTCCCCTTCC     5920        GG      C
                                TGCCCT  CCTCCCCT CC
                                ||||||  |||||||| ||
                                GCGGGA  GGAGGGGA GG
                                  __       A
GAM241  MBD1    5'  CGCCCTCCTCCCCTTCC     5920        GG      C
                                TGCCCT  CCTCCCCT CC
                                ||||||  |||||||| ||
                                GCGGGA  GGAGGGGA GG
                                  __       A
GAM241  MBD1    5'  CGCCCTCCTCCCCTTCC     5920        GG      C
                                TGCCCT  CCTCCCCT CC
                                ||||||  |||||||| ||
                                GCGGGA  GGAGGGGA GG
                                  __       A
GAM241  MBNL    5'  CTGCGCGGCCCCTCCCCC    5921      _ CT
                                CTG GC  CCCCTCCCCC
                                ||| ||  ||||||||||
                                GAC CG  GGGGAGGGGG
                                  G  CC
GAM241  MEN1    5'  CCTGGCCTCGGTCCCCC     5874          CCC
                                CCTGGCCTC   TCCCCC
                                |||||||||   ||||||
                                GGACCGGAG   AGGGGG
                                     CC_
GAM241  MFGE8   3'  TGCCTCTGAACACCCTCCCCTT 5922   _   ____      _   CIII
          CCCCG                   CTGG    CCTCCCCT CCCC    G
                                  ||||    |||||||| ||||    |
                                  GACT    GGAGGGGA GGGG    C
                                A    TGTG       A    IIIC
GAM241  MGAT1   5'  TGCCCTGGGCTTGCCCGGCTCC 5923          C __   __
          C                      TGCCCTGG CT  CCC  CTCCC
                                 ||||||||  ||  |||  |||||
                                 ACGGGACC GA  GGG  GAGGG
                                      C  AC   CC
GAM241  MGAT3   5'  GCCCCGATCCCCTCCCCC    5924         CC
                                GCCCTGG  TCCCCTCCCCC
                                |||||||  ||||||||||
                                CGGGGCT  AGGGGAGGGGG
                                   __
GAM241  MGEA5   5'  CCGGCTCCTTCCCCTCCCCC  5925       _ __
                                CTGGC C  TCCCCTCCCCC
                                |||||  |  ||||||||||
                                GGCCG G  AGGGGAGGGGG
                                   A GA
GAM241  MNT     3'  CCCTGACTCCTCCCCC      5926         CTCC
                                CCCTGGC    CCTCCCCC
                                |||||||    ||||||||
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                                GGGACTG   GGAGGGGG
                                   A___
GAM241  MTA1L1   3' TGCACGCCCCCCTCCCCC   5927     CCTG  T
                                TGC   GCC CCCCTCCCCC
                                |||   ||| ||||||||||
                                ACG   CGG GGGGAGGGGG
                                  TG__  _
GAM241  MYLK2    3' TGGCTTCTCCCCTCCCCC   5928     __
                                TGGC  CTCCCCTCCCCC
                                ||||  ||||||||||||
                                ACCG  GAGGGGAGGGGG
                                  AA
GAM241  MYO10    3' GCGTGGTTCCTCCCCTCC   5929    CC  __
                                GC  TGG  CCTCCCCTCC
                                ||  |||  ||||||||||
                                CG  ACC  GGAGGGGAGG
                                 C_  AA
GAM241  MYOC     3' GCCCTGGCTGGCTGGCTCTCCC 5930        ________  _
           T                     GCCCTGGC      CTC CCCT
                                 ||||||||      ||| ||||
                                 CGGGACCG      GAG GGGA
                                     ACCGACC   A
GAM241  MYOD1    5' TGTCCCCCACCCCTCCCTC   5931    _   G    _
                                TG CCCT GCCTC CCCTC
                                || |||| ||||| |||||
                                AC GGGG TGGGG GGGAG
                                 A   G    A
GAM241  NCOR2    3' CCCCGGCCCCTTCCCC     5932        T  CC
                                CCCTGGCC CC  TCCCC
                                |||||||| ||  |||||
                                GGGGCCGG GG  AGGGG
                                    _  A_
GAM241  NDRG2    3' GCCCCAAATCCCCTCCCC   5933     TG CC
                                GCCC  G  TCCCCTCCCC
                                ||||  |  ||||||||||
                                CGGG  T  AGGGGAGGGG
                                  GT T_
GAM241  NDST1    3' GCCAGGCTCTCCTCCCC    5934    CT  C  C
                                GCC  GGC TC CCTCCCC
                                |||  ||| || |||||||
                                CGG  CCG AG GGAGGGG
                                  T_  _ A
GAM241  NDUFB10  5' TGCCCTGGCCTCTACCTCC   5935          C_
                                TGCCCTGGCCTC  CCTCC
                                ||||||||||||  |||||
                                ACGGGACCGGAG  GGAGG
                                       AT
GAM241  NEURL    3' TGCCTGATACCCCCCTCTCCC  5937     CTG_    _
                                TGCC   GCCTCCC CTCCC
                                ||||   ||||||| |||||
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                                ACGG   TGGGGGG GAGGG
                                  ACTA      A
GAM241  NEURL    3'  TGCGGCCTCCTCTCCTCC    5936     CCT     C   _
                                TGC   GGCCTCC CTCC CC
                                |||   ||||||| |||| ||
                                ACG   CCGGAGG GAGG GG
                                  ___      A   A
GAM241  NIPSNAP1 3'  TGGCCTGGCCTCCTCTCTTCCG 5938    C       C   CC  III
                                TG CCTGGCCTCC CTC  CC   G
                                || ||||||||||| |||  ||   |
                                AC GGACCGGAGG GAG  GG   C
                                 C        A   AA  III
GAM241  NLGN1    5'  TGCACCCCCCCCCTCC     5939     _ TGG
                                TGC CC   CCTCCCCTCC
                                ||| ||   ||||||||||
                                ACG GG   GGGGGGGAGG
                                  T  ___
GAM241  NOTCH3   3'  TGCCCTGGCTCCCATTTCCC   5940         C   C__
                                TGCCCTGGC TCCC   TCCC
                                |||||||| ||||   ||||
                                ACGGGACCG AGGG   AGGG
                                      _   TAA
GAM241  NOTCH3   5'  GCCGCGACCCTCCCCTCCTCC  5941     C   _     _
                                GCC TGGCC TCCCCTCC CC
                                ||| ||||| |||||||| ||
                                CGG GCTGG AGGGGAGG GG
                                  C    G       A
GAM241  NPR1     3'  TGCGCCACCCCTCTTCTCCCC  5942     CCTG  T    _____
                                TGC    GCC CCCCTC    CCCC
                                |||    ||| ||||||    ||||
                                ACG    CGG GGGGAG    GGGG
                                  _____  T     AAGA
GAM241  NRD1     5'  GGCCTGAACCCCTCCCCC    5943       ___
                                GGCCT   CCCCTCCCCC
                                |||||   ||||||||||
                                CCGGA   GGGGAGGGGG
                                   CTT
GAM241  NT5C2    3'  GCCCCCTCCCTCCCC       5870       TGG     C
                                GCCC   CCTCCC TCCCC
                                ||||   |||||| |||||
                                CGGG   GGAGGG AGGGG
                                  ___     _
GAM241  OPHN1    5'  TGCACTGTCCCCTCCCC     5944     C   GCC
                                TGC CTG   TCCCCTCCCC
                                ||| |||   ||||||||||
                                ACG GAC   AGGGGAGGGG
                                  T  ___
GAM241  PAFAH1B1 5'  GCCCGAGCGCTCCCCTCC    5945      T   _
                                GCCC GGC CTCCCCTCC
                                |||| ||| |||||||||
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                                CGGG TCG GAGGGGAGG
                                  C   C
GAM241  PAX5    3'  TGCTCTCCTGCCCCTCCC    5946     C  GG  _
                                TGC CT  CCT CCCCTCCC
                                ||| ||  ||| ||||||||
                                ACG GA  GGA GGGGAGGG
                                  A  __   C
GAM241  PAX8    5'  TGCCCTGGGCCCGGTGTCTCTC 5947    _ ________ C    CCCIII
          CTCCGGG                 GG CC     TC CCTCC    G
                                || ||     || |||||    |
                                CC GG     AG GGAGG    C
                                 C  GCCACAG  A    IIICCC
GAM241  PAX8    5'  TGCCCTGGGCCCGGTGTCTCTC 5947    _ ________ C    CCCIII
          CTCCGGG                 GG CC     TC CCTCC    G
                                || ||     || |||||    |
                                CC GG     AG GGAGG    C
                                 C  GCCACAG  A    IIICCC
GAM241  PAX8    5'  TGCCCTGGGCCCGGTGTCTCTC 5947    _ ________ C    CCCIII
          CTCCGGG                 GG CC     TC CCTCC    G
                                || ||     || |||||    |
                                CC GG     AG GGAGG    C
                                 C  GCCACAG  A    IIICCC
GAM241  PCDH7   5'  CCCCGAGTCCTCTCCCC    5948      CC  C
                                CCCTGG  TCC CTCCCC
                                ||||||  ||| ||||||
                                GGGGCT  AGG GAGGGG
                                   C_  A
GAM241  PCDH7   5'  CCCCGAGTCCTCTCCCC    5948      CC  C
                                CCCTGG  TCC CTCCCC
                                ||||||  ||| ||||||
                                GGGGCT  AGG GAGGGG
                                   C_  A
GAM241  PCDH7   5'  CCCCGAGTCCTCTCCCC    5948      CC  C
                                CCCTGG  TCC CTCCCC
                                ||||||  ||| ||||||
                                GGGGCT  AGG GAGGGG
                                   C_  A
GAM241  PDE7A   3'  CCAACCTTCCCCTCCCCC    5949    TG  _
                                C  GCCT CCCCTCCCCC
                                |  |||| ||||||||||
                                G  TGGA GGGGAGGGGG
                                 GT   A
GAM241  PIG3    5'  TGCCCTGGTCTGCCGCGGACCC 5950        C  _  CCT__
                                TGCCCTGG CT CC    CCC
                                |||||||| || ||    |||
                                ACGGGACC GA GG    GGG
                                    A  C  CGCCT
GAM241  PIN1    3'  TGCCCTGGGTCTGGGAGCCTCC 5951        C_  CC___
                                TGCCCTGG  CT    CCTCC
                                ||||||||  ||    |||||
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                                ACGGGACC  GA    GGAGG
                                    CA  CCCTC
GAM241  PK428   5' CCCCCGCCTTCCCTCTCC   5953      G   C    C
                                CCCT GCCT CCCTC CC
                                |||| |||| ||||| ||
                                GGGG CGGA GGGAG GG
                                  G   A    A
GAM241  PK428   5' CCCTTCCAGCCCTCCCCC   5952      GG  TC
                                CCCT  CC  CCCTCCCCC
                                ||||  ||  |||||||||
                                GGGA  GG  GGGAGGGGG
                                  A_  TC
GAM241  PLA2G2A  5' TGCCCCGGCCGTCGCTCCCC  5954          _ CC
                                TGCCCTGGCC TC  CTCCCC
                                |||||||||| ||  ||||||
                                ACGGGGCCGG AG  GAGGGG
                                      C  C_
GAM241  PNOC    5' GCACAGCCCTCCCCTTCCC   5955    CCT   _    C
                                GC   GGCC TCCCCT CCC
                                ||   |||| |||||| |||
                                CG   TCGG AGGGGA GGG
                                 TG_   G     A
GAM241  PNUTL2   3' TGCCCTGGGTTTTCCACTTCC  5956        CC__  C  C
                                TGCCCTGG    TCC CT CC
                                ||||||||    ||| || ||
                                ACGGGACC    AGG GA GG
                                     CAAA   T  A
GAM241  PNUTL2   3' TGCCCTGGGTTTTCCACTTCC  5956        CC__  C  C
                                TGCCCTGG    TCC CT CC
                                ||||||||    ||| || ||
                                ACGGGACC    AGG GA GG
                                     CAAA   T  A
GAM241  PODXL    3' CCCTGGCCTTCCTTTTCCC   5957         _ CC_
                                CCCTGGCCT CC   TCCC
                                ||||||||| ||   ||||
                                GGGACCGGA GG   AGGG
                                     A  AAA
GAM241  PPP2R5B  3' TGCCCTCCCCCTCCCCC    5958       GGCC
                                TGCCCT   TCCCCTCCCCC
                                ||||||   ||||||||||
                                ACGGGA   GGGGGAGGGGG
                                        ____
GAM241  PPP5C    3' TGCTCCACCTCCTTCCTC    5959     _ TG    __
                                TGC CC  GCCTCC  CCTC
                                ||| ||  ||||||  ||||
                                ACG GG  TGGAGG  GGAG
                                  A __     AA
GAM241  PRELP    5' CCTCTTCCACCCCCTCCC    5960     _ GG  _
                                CC CT  CC TCCCCTCCC
                                || ||  || |||||||||
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                                GG GA  GG GGGGGAGGG
                                 A  A_  T
GAM241  PRX     5'  GCTCCTGTGTCCTCTCCCC   5961     _   GCC   C
                                GC CCTG   TCC CTCCCC
                                || ||||   ||| ||||||
                                CG GGAC   AGG GAGGGG
                                 A    AC_   A
GAM241  PRX     3'  TGTCCCGGCCTCTGACCCC   5962     C       CCCT
                                TG CCTGGCCTC    CCCC
                                || |||||||||    ||||
                                AC GGGCCGGAG    GGGG
                                 A        ACT_
GAM241  PTGIR   3'  TGCAGCAGCCTCCCCTTCC   5963      CC         C
                                TGC  TGGCCTCCCCT CC
                                |||  |||||||||| ||
                                ACG  GTCGGAGGGGA GG
                                  TC          A
GAM241  PTPRN   3'  TGCCCTGGGCTCTGGGATGCCC 5964         C   CCCT___
            C                    TGCCCTGG CTC      CCCC
                                |||||||| |||      ||||
                                ACGGGACC GAG      GGGG
                                     C   ACCCTAC
GAM241  PVR     3'  CCCCTGCATCCCTTCCCCC   5965      G  C    C
                                CCCT GC TCCC TCCCCC
                                |||| || |||| ||||||
                                GGGG CG AGGG AGGGGG
                                  A  T    A
GAM241  RAB1A   5'  CCCTGCTCCCCTCCCC      5966       GC
                                CCCTG  CTCCCCTCCCC
                                |||||  ||||||||||
                                GGGAC  GAGGGGAGGGG
                                   __
GAM241  RBL1    3'  GCCTTGGCCTCCCAAAGTCC   5967      C       C___
                                GCC TGGCCTCCC    TCC
                                ||| |||||||||    |||
                                CGG ACCGGAGGG    AGG
                                  A        TTTC
GAM241  REQ     3'  CTGATCCTTCCCCTCTCCC    5969      _  _    _
                                CTGG CCT CCCCTC CCC
                                |||| ||| |||||| |||
                                GACT GGA GGGGAG GGG
                                  A  A     A
GAM241  REQ     3'  TGGCCTGGCCCCCTGATCCTTC 5968     C        ____  _
            CCC                    TG CCTGGCCTCC    CCT CCCC
                                || ||||||||||    ||| ||||
                                AC GGACCGGGGG    GGA GGGG
                                 C         ACTA   A
GAM241  RUNX3   3'  CCTATCCCCCCTCCCCC     5970       GC
                                CCTG  CTCCCCTCCCCC
                                ||||  ||||||||||||
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                                GGAT  GGGGGGAGGGGG
                                  A_
GAM241  S100A10  5'  GCCCTGTCTCCTCCCCC    5971       GC   CC
                                GCCCTG  CTCC  TCCCCC
                                ||||||  ||||  ||||||
                                CGGGAC  GAGG  AGGGGG
                                   A_   __
GAM241  SDC2     3'  TGCCTACCCTCCTTCCC    5972      C  G    CC
                                TGCC TG CCTCC  TCCC
                                |||| || |||||  ||||
                                ACGG AT GGAGG  AGGG
                                  _ G    A_
GAM241  SDC4     3'  CCCTGGCTTCCCTCCCC    5973        CTC
                                CCCTGGC   CCCTCCCC
                                |||||||   ||||||||
                                GGGACCG   GGGAGGGG
                                    AA_
GAM241  SFRP5    3'  TGCCCTGAGCCCCTCC     5974        CCT
                                TGCCCTGG   CCCCTCC
                                ||||||||   |||||||
                                ACGGGACT   GGGGAGG
                                    C__
GAM241  SIAT4C   3'  TGCCCTGGCCGGGCTCCC   5975          TCCC
                                TGCCCTGGCC   CTCCC
                                ||||||||||   |||||
                                ACGGGACCGG   GAGGG
                                     CCC_
GAM241  SIT      3'  GCCCTTACCCCTCCCCC    5976       GGCCT
                                GCCCT    CCCCTCCCCC
                                |||||    ||||||||||
                                CGGGA    GGGGAGGGGG
                                  AT___
GAM241  SLC14A2  5'  TGCCCCTGGCCCCTCC     5977       _    TCC
                                TGCCC TGGCC   CCTCC
                                ||||| |||||   |||||
                                ACGGG ACCGG   GGAGG
                                  G    ___
GAM241  SLC18A3  5'  GCCGCTGCGCTCCCCTCCCC  5978     _  _ C
                                GCC CTG GC TCCCCTCCCC
                                ||| ||| || ||||||||||
                                CGG GAC CG AGGGGAGGGG
                                  C  G  _
GAM241  SLC19A2  5'  GCCCGGCCCCTTCCTTCTCC  5979      T    __ __
                                GCCC GGCCTC  CC  CTCC
                                |||| ||||||  ||  ||||
                                CGGG CCGGGG  GG  GAGG
                                  _     AA  AA
GAM241  SLC6A8   3'  TGCCCCTCCCCTGCCTCCC   5980       TGGC     _ _
                                TGCCC   CTCCCCT CC CCC
                                |||||   ||||||| || |||
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                                ACGGG   GAGGGGA GG GGG
                                  ____     C  A
GAM241  SMARCC1  3'  TGCCAAACTCCCTCCCC    5981      CT   CTC
                                TGCC  GGC   CCCTCCCC
                                ||||  |||   ||||||||
                                ACGG  TTG   GGGAGGGG
                                  T_   A__
GAM241  SMURF1   3'  CCCCATCCCCCTCCCCC    5982      GC T
                                CCCTG  C CCCCTCCCCC
                                |||||  | ||||||||||
                                GGGGT  G GGGGAGGGGG
                                  A_ _
GAM241  SOX11    3'  CCTACCTCCCCTCCCCC    5983      G
                                CCTG CCTCCCCTCCCCC
                                |||| ||||||||||||
                                GGAT GGAGGGGAGGGGG
                                  _
GAM241  SOX4     3'  CCCTCAACATCTCCTCCTCC  5984      _  __   _
                                CCCT GGC  CTCC CCTCC
                                |||| |||  |||| |||||
                                GGGA TTG  GAGG GGAGG
                                  G   TA   A
GAM241  SPK      5'  GCTCTGGCCTCCGTTCCCC   5986    C       CC
                                GC CTGGCCTCC  TCCCC
                                || |||||||||  |||||
                                CG GACCGGAGG  AGGGG
                                 A        CA
GAM241  SPK      3'  TGTCCCACCCCCTTTCCC    5985    _  TG     CC
                                TG CCC  GCCTCC  TCCC
                                || |||  ||||||  ||||
                                AC GGG  TGGGGG  AGGG
                                 A  __     AA
GAM241  SRC      3'  TGCTTGGCCTCCTTCCCC    5987     CC      CC
                                TGC  TGGCCTCC  TCCCC
                                |||  ||||||||  |||||
                                ACG  ACCGGAGG  AGGGG
                                  A_      A_
GAM241  SRRM2    3'  CTGTATCCTCCCCTCCCCC   5988     G__
                                CTG   CCTCCCCTCCCCC
                                |||   ||||||||||||
                                GAC   GGAGGGGAGGGGG
                                  ATA
GAM241  STK6     3'  GCCCTGGCTCAAGGATTTCTCC 5989       C  CC_______      III
            CCCG                   CTGGC TC       CTCCCCC   G
                                |||||  ||       |||||||   |
                                GACCG AG       GAGGGGG   C
                                  _  TTCCTAAA      III
GAM241  TBL1X    3'  GCCCTGACCCTTCCCC      5990          CCCC
                                GCCCTGGCCT    TCCCC
                                |||||||||    |||||
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                                CGGGACTGGG  AGGGG
                                     A___
GAM241  TCF15   3' GCTCCTGGCCTCCTTCTCC  5991   _      C_
                                GC CCTGGCCTCC  CTCC
                                || ||||||||||  ||||
                                CG GGACCGGAGG  GAGG
                                 A        AA
GAM241  TEM5    3' CCCTCCCTCCCCTTTCCC   5993    GG     CC
                                CCCT  CCTCCCCT  CCC
                                ||||  ||||||||  |||
                                GGGA  GGAGGGGA  GGG
                                  G_      AA
GAM241  TEM5    3' CCCACTCCCCTCCCCC    5992    TGGC
                                CCC   CTCCCCTCCCCC
                                |||   ||||||||||||
                                GGG   GAGGGGAGGGGG
                                 T___
GAM241  TNFRSF6B 5' GCCCTGACCGCCCCCTCTCC  5994       _    C
                                GCCCTGGCC TCCCCTC CC
                                ||||||||| ||||||| ||
                                CGGGACTGG GGGGGAG GG
                                     C      A
GAM241  TNFRSF8  3' GCCTCACGACCTCTCCCTC   5995    C__    _
                                GCC   TGGCCTC CCCTC
                                |||   ||||||| |||||
                                CGG   GCTGGAG GGGAG
                                  AGT      A
GAM241  TNXB    3' ACCCCTCCCCTCCCCC    5996    TGGC
                                GCCC   CTCCCCTCCCCC
                                ||||   ||||||||||||
                                TGGG   GAGGGGAGGGGG
                                  ____
GAM241  TNXB    3' ACCCCTCCCCTCCCCC    5996    TGGC
                                GCCC   CTCCCCTCCCCC
                                ||||   ||||||||||||
                                TGGG   GAGGGGAGGGGG
                                  ____
GAM241  TRPS1   5' CCCCCCCCTTTCCCTCCCCC  5998    GG  C_
                                CCCT  CCT  CCCTCCCCC
                                ||||  |||  |||||||||
                                GGGG  GGA  GGGAGGGGG
                                  GG   AA
GAM241  TRPS1   3' TGCCCTGGACCTTCAATTTCTC 5997       _  _ CC___
          C                      TGCCCTGG CCT C    CTCC
                                ||||||||| ||| |    ||||
                                ACGGGACC GGA G    GAGG
                                     T   A TTAAA
GAM241  USP7    3' CCACTAACCTCTTCTCCCCC  5999    _     CC
                                CC CTGGCCTC  CTCCCCC
                                || ||||||||  |||||||
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                                GG GATTGGAG  GAGGGGG
                                 T       AA
GAM241  YWHAG    3'  TGCCCCCCCCCCTCCCCC     6000       TGGC
                                TGCCC    CTCCCCTCCCCC
                                |||||    ||||||||||||
                                ACGGG    GGGGGGAGGGGG
                                  ____
GAM241  YWHAG    3'  CCCTCCCTTTCCCTCCCCC    6001      GG   C_
                                CCCT  CCT  CCCTCCCCC
                                ||||  |||  |||||||||
                                GGGA  GGA  GGGAGGGGG
                                  G_   AA
GAM241  YY1      5'  GCCCTGGCCGCGCCTCCTCC   6002         TCC    _
                                GCCCTGGCC   CCTCC CC
                                |||||||||   ||||| ||
                                CGGGACCGG   GGAGG GG
                                     CGC    A
GAM241  ZIC1     3'  CCCTCCCCCCTCCCCC      6004      GGC
                                CCCT   CTCCCCTCCCCC
                                ||||   ||||||||||||
                                GGGA   GGGGGGAGGGGG
                                  ___
GAM241  ZIC1     3'  CCCCCTCCCCCTCCCCC     6003      TGG      _
                                CCC   CCTCCCC TCCCCC
                                |||   ||||||| ||||||
                                GGG   GGAGGGG AGGGGG
                                  ___      G
GAM241  ZNF179   3'  CCCTGGCATCACCCTCCCCC   6005        C  _
                                CCCTGGC TC CCCTCCCCC
                                ||||||| || |||||||||
                                GGGACCG AG GGGAGGGGG
                                    T  T
GAM241  ZNF184   5'  TACCCTGAGCTCCCCTCCCCC  6006         GC
                                TGCCCTG  CTCCCCTCCCCC
                                |||||||  ||||||||||||
                                ATGGGAC  GAGGGGAGGGGG
                                    TC
GAM241  ZNF205   3'  CGCCCTCGCCCTCCCCC     6007        G   TCCC
                                TGCCCT GCC    CTCCCCC
                                ||||||| |||    |||||||
                                GCGGGA CGG    GAGGGGG
                                   G   ____
GAM241  ZNF278   5'  TGCCCGCCCCCTCCCTTCCCC  6008       T G   _   _
                                TGCCC G CCTC CCCT CCCC
                                ||||| | |||| |||| ||||
                                ACGGG C GGGG GGGA GGGG
                                  _ G    A    A
GAM241  ZNF278   5'  TGCCCGCCCCCTCCCTTCCCC  6008       T G   _   _
                                TGCCC G CCTC CCCT CCCC
                                ||||| | |||| |||| ||||
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                                ACGGG C GGGG GGGA GGGG
                                  _ G   A   A
GAM241  ZNF278   5'  TGCCCGCCCCCTCCCTTCCCC  6008      T G   _   _
                                TGCCC G CCTC CCCT CCCC
                                ||||| | |||| |||| ||||
                                ACGGG C GGGG GGGA GGGG
                                  _ G   A   A
GAM241  ZNF278   5'  TGCCCGCCCCCTCCCTTCCCC  6008      T G   _   _
                                TGCCC G CCTC CCCT CCCC
                                ||||| | |||| |||| ||||
                                ACGGG C GGGG GGGA GGGG
                                  _ G   A   A
GAM241  ABLIM    3'  TGCTCTGACCTCCACATCCC  6009     C       CC_
                                TGC CTGGCCTCC  TCCC
                                ||| |||||||||  ||||
                                ACG GACTGGAGG  AGGG
                                  A       TGT
GAM241  ABLIM    3'  TGCTCTGACCTCCACATCCC  6009     C       CC_
                                TGC CTGGCCTCC  TCCC
                                ||| |||||||||  ||||
                                ACG GACTGGAGG  AGGG
                                  A       TGT
GAM241  ADMP     5'  TGCAACACTCCCCTCCCCC   6010     CCT  _
                                TGC   GGC CTCCCCTCCCCC
                                |||   ||| ||||||||||||
                                ACG   TTG GAGGGGAGGGGG
                                  ___   T
GAM241  AGS3     5'  TGCCCTGGGCCAGCCTCC    6011        _ TCC
                                TGCCCTGG CC   CCTCC
                                |||||||| ||   |||||
                                ACGGGACC GG   GGAGG
                                     C  TC_
GAM241  AGS3     5'  TGCCCCGGACTTCTCCCC    6012        C  CCC
                                TGCCCTGG CT   CTCCCC
                                |||||||| ||   ||||||
                                ACGGGGCC GA   GAGGGG
                                     T  A__
GAM241  APELIN   5'  TGCAGCCTCCTCTCCC     6013     CCT     C
                                TGC   GGCCTCC CTCCC
                                |||   ||||||| |||||
                                ACG   TCGGAGG GAGGG
                                  ___      A
GAM241  ARHGEF11 5'  GCCCCTCTTCCCCTCCCCC   6014      GGCC
                                GCCCT   TCCCCTCCCCC
                                |||||   ||||||||||
                                CGGGG   AGGGGAGGGGG
                                  AGA_
GAM241  ARHGEF16 3'  TGCCGGGTCCCCTCCC     6015     CT  CC
                                TGCC  GG  TCCCCTCCC
                                ||||  ||  |||||||||
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                                ACGG  CC  AGGGGAGGG
                                  C_ __
GAM241  ATP6V1B2 3'  TGCTTCTGCTCCCTCCCC    6016     C_  GC    C
                                TGC  CTG  CTCCC TCCCC
                                |||  |||  ||||| |||||
                                ACG  GAC  GAGGG AGGGG
                                  AA  __   _
GAM241  BCDO     3'  GCCGAGCTCCCCTCCCC     6017     CT  C
                                GCC  GGC TCCCCTCCCC
                                |||  ||| ||||||||||
                                CGG  TCG AGGGGAGGGG
                                  C_  _
GAM241  BLCAP    3'  TGCCTGGCCCATCTCTCTTTCC 6018      C     CCC_  ___
           CC                     TGCC TGGCCT   CTC   CCCC
                                |||| ||||||   |||   ||||
                                ACGG ACCGGG   GAG   GGGG
                                  _     TAGA   AAA
GAM241  BOLL     5'  TGCCTCGGCGCTCCTCCCCC  6019      C   _   CC
                                TGCC TGGC CTCC  TCCCCC
                                |||| |||| ||||  ||||||
                                ACGG GCCG GAGG  AGGGGG
                                  A   C   __
GAM241  BPES     5'  CGCTGCTCTCCCCTCTCC    6020     CCTG  _      C
                                TGC   GC CTCCCCTC CC
                                |||   || |||||||| ||
                                GCG   CG GAGGGGAG GG
                                  A___  A       A
GAM241  BRD2     3'  TGTCCCTGCATCCCTCCCCC  6021     _    G CTC
                                TG CCCTG C   CCCTCCCCC
                                || ||||| |   |||||||||
                                AC GGGAC G   GGGAGGGGG
                                 A    _ TA_
GAM241  C1orf34  5'  CCCTTGGCCCCCTCTCCC    6022      _     C
                                CCCT GGCCTCC CTCCC
                                |||| ||||||| |||||
                                GGGA CCGGGGG GAGGG
                                  A      A
GAM241  C1QR1    3'  CCCTGGCCTCTCTCGCCC    6023          CC  _
                                CCCTGGCCTC  CTC CCC
                                ||||||||||  ||| |||
                                GGGACCGGAG  GAG GGG
                                     A_  C
GAM241  C1QTNF2  3'  TACCTTGGCCCCTCCCTC    6024      C     _
                                TGCC TGGCCTC CCCTC
                                |||| ||||||| |||||
                                ATGG ACCGGGG GGGAG
                                  A      A
GAM241  C20orf139 3'  TGCCCCAACACCTCTTCCCC  6025       TG  CT  C  _
                                TGCCC  GC  CC CT CCCC
                                |||||  ||  || || ||||
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                                ACGGG  TG  GG GA GGGG
                                   GT  T_  A  A
GAM241  C20orf178 3'  GCCCGCCCCCCTCCCCC     6026      TG   T
                                GCCC  GCC CCCCTCCCCC
                                ||||  ||| ||||||||||
                                CGGG  CGG GGGGAGGGGG
                                  __  _
GAM241  C20orf42  3'  GCCCCACCCCTCCCC       6027       GCCT
                                GCCCTG   CCCCTCCCC
                                ||||||   |||||||||
                                CGGGGT   GGGGAGGGG
                                  _____
GAM241  CAP350    5'  TGCCCGGCCTGGCCTCC     6028       T    CC
                                TGCCC GGCCT  CCTCC
                                ||||| |||||  |||||
                                ACGGG CCGGA  GGAGG
                                   _    CC
GAM241  CENTA1    3'  TGCCTGGCCTCGGAAACCCCC  6029      C     CCCT_
                                TGCC TGGCCTC    CCCCC
                                |||| |||||||    |||||
                                ACGG ACCGGAG    GGGGG
                                   _     CCTTT
GAM241  CENTG2    3'  CCTCGCCTCCCCTCCCCC    6030     G
                                CCT GCCTCCCCTCCCCC
                                ||| ||||||||||||||
                                GGA CGGAGGGGAGGGGG
                                  G
GAM241  CHST3     3'  TGTCCTAGCCCCTCCTCC    6031     C       C
                                TG CCTGGCCTC CCTCC
                                || |||||||| |||||
                                AC GGATCGGGG GGAGG
                                 A       A
GAM241  CX46.6    3'  GCCCCCCAACCCTCCTCTTCCC 6032       GG  TC    _____
                                GCCCT  CC  CCCTCC   CCC
                                |||||  ||  ||||||   |||
                                CGGGG  GG  GGGAGG   GGG
                                   __  TT     AGAA
GAM241  D21S2056E 3'  GCCCTGGCCTTCCCTCTCC   6033         C    C
                                GCCCTGGCCT CCCTC CC
                                |||||||||| ||||| ||
                                CGGGACCGGA GGGAG GG
                                     A    A
GAM241  DDX33     3'  TACCCCTCTCCCCTCCCCC   6034       GGC
                                TGCCCT   CTCCCCTCCCCC
                                ||||||   ||||||||||||
                                ATGGGG   GAGGGGAGGGGG
                                   A__
GAM241  Di-Ras2   3'  CCTGCCCCTCCCCTCCCCC   6035      G  _
                                CCTG CC TCCCCTCCCCC
                                |||| || ||||||||||
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                                GGAC GG AGGGGAGGGGG
                                  G  G
GAM241  DJ726C3.2 5'  TGCCCTGGCCGCTGCCC     6036          TCCC  C
                                TGCCCTGGCC    CT CCC
                                ||||||||||    || |||
                                ACGGGACCGG    GA GGG
                                      C___  C
GAM241  DKFZP434A1319 5'  CCCCGGGCCCCCTTCCCC    6037        C     C
                                CCCTGG CTCCC TCCCC
                                |||||| ||||| |||||
                                GGGGCC GGGGG AGGGG
                                   C     A
GAM241  DKFZp434B217 3'  TGCTCCAGCCTCTCCCCC    6038      C TG     CCC
                                TGC C  GCCTC   TCCCCC
                                ||| |  |||||   ||||||
                                ACG G  CGGAG   AGGGGG
                                  A GT    ____
GAM241  DKFZP434C171 3'  TAGCCTCACCTCTTCCCC    6039        C    __
                                TGGCCTC CCTC  CCCC
                                ||||||| ||||  ||||
                                ATCGGAG GGAG  GGGG
                                     T    AA
GAM241  DKFZp434H2215 3'  TGGCCTGGCCTGAGATGCCTCC 6040     C       CC_____
                                TG CCTGGCCT      CCTCC
                                || ||||||||      |||||
                                AC GGACCGGA      GGAGG
                                 C       CTCTAC
GAM241  DKFZp434H2215 3'  TGTCCTGGGGCCCTCCCCC    6041     C     CCTC
                                TG CCTGG    CCCTCCCCC
                                || |||||    |||||||||
                                AC GGACC    GGGAGGGGG
                                 A     CC__
GAM241  DKFZP434I0714 5'  TACCTTACCCCCTCCTCC     6042       CTG     _
                                TGCC   GCCTCC CCTCC
                                ||||   |||||| |||||
                                ATGG   TGGGGG GGAGG
                                  AA_      A
GAM241  DKFZP434I2117 3'  TGCCCCCTCCCCTCCTCC     6043        TGG         _
                                TGCCC   CCTCCCCTCC CC
                                |||||   |||||||||| ||
                                ACGGG   GGAGGGGAGG GG
                                   ___          A
GAM241  DKFZP434L0117 3'  TGCAGGCTCTCCCCTCCCC    6044      CCT  _
                                TGC   GGC CTCCCCTCCCC
                                |||   ||| ||||||||||
                                ACG   CCG GAGGGGAGGGG
                                  T__   A
GAM241  DKFZp434N035 3'  GCCCTGGCCATCTCCTCC     6045          _  C
                                GCCCTGGCC TC CCTCC
                                ||||||||| || |||||
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                                CGGGACCGG AG GGAGG
                                      T  A
GAM241  DKFZp434O0320 3'  TGCCCAGCCCCTCTCCC     6046       T    T  C
                                TGCCC GGCC CC CTCCC
                                ||||| |||| || |||||
                                ACGGG TCGG GG GAGGG
                                  _   _  A
GAM241  DKFZP434P0111 3'  GCCCACACCCCCTCCCCC    6047      TG  C
                                GCCC  GC TCCCCTCCCCC
                                ||||  || ||||||||||
                                CGGG  TG GGGGGAGGGGG
                                  __ T
GAM241  DKFZp547D155 3'  TGCTCCTCCCCTCCCCC     6048      CCTGG
                                TGC    CCTCCCCTCCCCC
                                |||    ||||||||||||
                                ACG    GGAGGGGAGGGGG
                                 A____
GAM241  DKFZP586C1619 3'  GCCCTGGCCTCGGCAGCCTCC  6049          C____
                                GCCCTGGCCTC    CCTCC
                                ||||||||||    |||||
                                CGGGACCGGAG    GGAGG
                                      CCGTC
GAM241  DKFZP586G1122 3'  CGCCTGCTCCCCTCCCCC    6050      C  GC
                                TGCC TG  CTCCCCTCCCCC
                                |||| ||  ||||||||||||
                                GCGG AC  GAGGGGAGGGGG
                                  _ __
GAM241  DKFZP586M0122 3'  TGCCCTGGATTCCAGTCTCC   6051        CC   C__
                                TGCCCTGG  TCC   CTCC
                                ||||||||  |||   ||||
                                ACGGGACC  AGG   GAGG
                                     TA   TCA
GAM241  DKFZP586N0721 5'  TGCCCTGGTTTCCTCTTGCCC  6052        CC   C  CC
                                TGCCCTGG  TCC CT  CCC
                                ||||||||  ||| ||  |||
                                ACGGGACC  AGG GA  GGG
                                     AA   A  AC
GAM241  DKFZP761C169 5'  TGCCGCTTTTCCCTCCCCC    6053      _  GGCCTC
                                TGCC CT     CCCTCCCCC
                                |||| ||     |||||||||
                                ACGG GA     GGGAGGGGG
                                  C  AAA___
GAM241  DKFZp761F2014 3'  GCCCTGGCCTCAGTTTTCTCC  6054          CC____
                                GCCCTGGCCTC     CTCC
                                ||||||||||     ||||
                                CGGGACCGGAG     GAGG
                                      TCAAAA
GAM241  DKFZP761F241 3'  TGCTCCTAATTCCCTCCCC   6055      _    CCTC
                                TGC CCTGG    CCCTCCCC
                                ||| |||||    ||||||||
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                                ACG GGATT    GGGAGGGG
                                  A     AA__
GAM241   DKFZp761G2113 3'  GCCCCACCCCCCTCCCCC    6056        G  T
                                GCCCTG CC CCCCTCCCCC
                                |||||| || ||||||||||
                                CGGGGT GG GGGGAGGGGG
                                   _ _
GAM241   DOCK3    3'  CTGGCCTCCCATTTCCCC    6057          C__
                                CTGGCCTCCC   TCCCC
                                ||||||||||   |||||
                                GACCGGAGGG   AGGGG
                                     TAA
GAM241   DPP3     3'  GCTCCTGCCCCTCCCCC     6058     _   GCCT
                                GC CCTG    CCCCTCCCCC
                                || ||||    ||||||||||
                                CG GGAC    GGGGAGGGGG
                                 A   _____
GAM241   DRG1     3'  TGCCTCCATCTCCCTCCCC    6059      _  GC    C
                                TGCC CTG  CTCCC TCCCC
                                |||| |||  ||||| |||||
                                ACGG GGT  GAGGG AGGGG
                                  A  A_    _
GAM241   DRIL2    3'  TGCCCTCACAGCCTCTTCCT   6060        ___     C_
                                TGCCCT   GGCCTC  CCT
                                ||||||   ||||||  |||
                                ACGGGA   TCGGAG  GGA
                                   GTG     AA
GAM241   DUSP9    3'  GCCCTCCTGCCCTCCCCTCCC  6061       ___ G
                                GCCCT   G CCTCCCCTCCC
                                |||||   | ||||||||||
                                CGGGA   C GGAGGGGAGGG
                                   GGA G
GAM241   EDR1     5'  CCCTCGCCTCCTCCCC      6062       G     CC
                                CCCT GCCTCC  TCCCC
                                |||| ||||||  |||||
                                GGGA CGGAGG  AGGGG
                                  G     __
GAM241   EIF4B    3'  CCTTCTACCTCCCTCCCC    6063      G__      C
                                CCT   GCCTCCC TCCCC
                                |||   ||||||| |||||
                                GGA   TGGAGGG AGGGG
                                  AGA      _
GAM241   EML2     3'  TGCCCTGACACCTGACTCTTCC 6064          CT  C__   __
           C                     TGCCCTGGC  CC   CTC  CCC
                                |||||||||  ||   |||  |||
                                ACGGGACTG  GG   GAG  GGG
                                     T_  ACT   AA
GAM241   FADS1    3'  TGCCCCAACAGCTCCTTCCC   6065       TG  __    CC
                                TGCCC  GC  CTCC  TCCC
                                |||||  ||  ||||  ||||
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                                ACGGG  TG  GAGG  AGGG
                                  GT  TC    A_
GAM241  FAM3C    5'  TGCTCCGGCCTCCCGCCC    6066     C        CT
                                TGC CTGGCCTCCC  CCC
                                ||| ||||||||||  |||
                                ACG GGCCGGAGGG  GGG
                                  A         C_
GAM241  FAM8A1   5'  TGCTCCGTTTCCCTCCCCC   6067     C   GCCTC
                                TGC CTG    CCCTCCCCC
                                ||| |||    |||||||||
                                ACG GGC    GGGAGGGGG
                                  A   AAA__
GAM241  FLJ00007 3'  TACCCTCACTCCCCTCCTCC   6069       G  C      _
                                TGCCCT GC TCCCCTCC CC
                                |||||| || |||||||| ||
                                ATGGGA TG AGGGGAGG GG
                                   G  _       A
GAM241  FLJ00007 3'  TGGCCTGGCCTTCGTGCCCT   6068     C      _ ____
                                TG CCTGGCCT C   CCCT
                                || |||||||| |   ||||
                                AC GGACCGGA G   GGGA
                                 C       A CAC
GAM241  FLJ00024 3'  TGCTTAGATCTCCCCTCTCCC  6070      CCT GC      _
                                TGC   G  CTCCCCTC CCC
                                |||   |  |||||||| |||
                                ACG   C  GAGGGGAG GGG
                                  AAT TA       A
GAM241  FLJ10211 5'  GCCCGCAAGCTCCCCTCCC    6071      T__   C
                                GCCC   GGC TCCCCTCCC
                                ||||   ||| |||||||||
                                CGGG   TCG AGGGGAGGG
                                  CGT   _
GAM241  FLJ10408 3'  TGCCTGGCCTGGGCTCCC     6072      C     CCC
                                TGCC TGGCCT   CTCCC
                                |||| ||||||   |||||
                                ACGG ACCGGA   GAGGG
                                  _     CCC
GAM241  FLJ10724 3'  TGCCCTGGACCCGTTTCCTC   6073         _  CC__
                                TGCCCTGG CCT    CCTC
                                |||||||| |||    ||||
                                ACGGGACC GGG    GGAG
                                     T   CAAA
GAM241  FLJ10829 3'  TGCCTGATTTTCCTCCCCC    6075      C   CCTCC
                                TGCC TGG    CCTCCCCC
                                |||| |||    ||||||||
                                ACGG ACT    GGAGGGGG
                                  _  AAAA_
GAM241  FLJ10829 3'  GCCGTTGCCTTCCCTCCCC    6074     CTG   C
                                GCC   GCCT CCCTCCCC
                                |||   |||| ||||||||
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                                CGG  CGGA GGGAGGGG
                                  CAA   A
GAM241  FLJ11017  5' GCCCTGAGTTTTCCTTCCCC  6076       CC__  CC
                                GCCCTGG   TCC  TCCCC
                                |||||||   |||  |||||
                                CGGGACT   AGG  AGGGG
                                    CAAA  A_
GAM241  FLJ11939  3' CCCTGGCCTCACTTCTCCTCC  6077         CC__  _
                                CCCTGGCCTC   CTCC CC
                                ||||||||||   |||| ||
                                GGGACCGGAG   GAGG GG
                                     TGAA   A
GAM241  FLJ12541  3' TGCCCTGGCTCAACTGGCTCC  6078        C  CC____
                                TGCCCTGGC TC     CTCC
                                |||||||| ||     ||||
                                ACGGGACCG AG     GAGG
                                     _ TTGACC
GAM241  FLJ12783  3' TGCCCTGGCCCTGCCCCC    6079         CC
                                TGCCCTGGCCT  CCTCC
                                ||||||||||  |||||
                                ACGGGACCGGG  GGGGG
                                      AC
GAM241  FLJ12875  3' GCCCAGCCTTTCCTCCCC    6080      T    CC
                                GCCC GGCCT  CCTCCCC
                                |||| |||||  |||||||
                                CGGG TCGGA  GGAGGGG
                                  _    AA
GAM241  FLJ13063  3' TGCTCAGCCTCCTCCC      6082     CC      CC
                                TGC  TGGCCTCC  TCCC
                                |||  ||||||||  ||||
                                ACG  GTCGGAGG  AGGG
                                  A_      __
GAM241  FLJ13063  3' GCCTTGGCTTCTCGCTCCC   6081     C   __  CC
                                GCC TGGC  CTC  CTCCC
                                ||| ||||  |||  |||||
                                CGG ACCG  GAG  GAGGG
                                  A   AA  C_
GAM241  FLJ13491  3' TGCTCCCTCCCCTCCCC     6083     C TGG
                                TGC C   CCTCCCCTCCCC
                                ||| |   ||||||||||||
                                ACG G   GGAGGGGAGGGG
                                  A ___
GAM241  FLJ13868  3' TGCCCTGGGCTTGGGCCTCC  6084        C  CC__
                                TGCCCTGG CT    CCTCC
                                |||||||| ||    |||||
                                ACGGGACC GA    GGAGG
                                     C  ACCC
GAM241  FLJ13955  5' GCGCTGCCTCCTCTCCTCC   6085    C  G    C   _
                                GC CTG CCTCC CTCC CC
                                || ||| ||||| |||| ||
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                                CG GAC GGAGG GAGG GG
                                 C  _    A   A
GAM241  FLJ14107  3' GCCTTTGGCTCCCTTCCTCC  6086     C_  C  C  _
                                GCC  TGGC TCCC TCC CC
                                |||  |||| |||| ||| ||
                                CGG  ACCG AGGG AGG GG
                                  AA   _   A  A
GAM241  FLJ14146  3' GCCCTGGCTACCCAGCCTCCC  6087        CT  ___
                                GCCCTGGC  CCC  CTCCC
                                ||||||||  |||  |||||
                                CGGGACCG  GGG  GAGGG
                                    AT  TCG
GAM241  FLJ14249  3' TGCCCTGGCGCACGGCTCCTTC 6088        _______  C_
           TCC                    TGCCCTGGC    CTCC  CTCC
                                |||||||||    ||||  ||||
                                ACGGGACCG    GAGG  GAGG
                                    CGTGCC   AA
GAM241  FLJ14249  3' TGCCCTGGCGCACGGCTCCTTC 6088        _______  C_
           TCC                    TGCCCTGGC    CTCC  CTCC
                                |||||||||    ||||  ||||
                                ACGGGACCG    GAGG  GAGG
                                    CGTGCC   AA
GAM241  FLJ14299  5' CGCCGCCTCCCCTCCTCC   6089     CTG       _
                                TGCC  GCCTCCCCTCC CC
                                ||||  |||||||||| ||
                                GCGG  CGGAGGGGAGG GG
                                  ___       A
GAM241  FLJ14596  3' CCTGGCCTCTGCTTCCCCC   6090        CC  _
                                CCTGGCCTC  CT CCCCC
                                |||||||||  || |||||
                                GGACCGGAG  GA GGGGG
                                    AC  A
GAM241  FLJ14840  5' GCTCCGCCCTTCCCTTCCC   6091    C  G  _  C
                                GC CTG CCT CCC TCCC
                                || ||| ||| ||| ||||
                                CG GGC GGA GGG AGGG
                                 A  G  A  A
GAM241  FLJ20004  5' GCCTCGTCCTTCCTTCCTCC  6092    C  G  _ __
                                GCC TG CCT CC  CCTCC
                                ||| || ||| ||  |||||
                                CGG GC GGA GG  GGAGG
                                  A  A  A  AA
GAM241  FLJ20079  3' TGCACACTCCCTCCCC     6093     CCTG  _   C
                                TGC   GC CTCCC TCCCC
                                |||   || ||||| |||||
                                ACG   TG GAGGG AGGGG
                                  _____ T   _
GAM241  FLJ20128  3' GCGGGGCTTCTCCCCTCCTCC  6094    CCT  __      _
                                GC  GGC  CTCCCCTCC CC
                                ||  |||  ||||||||| ||
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                                CG  CCG  GAGGGGAGG GG
                                 CC_  AA       A
GAM241  FLJ20203  3' TGTCCTGGCCTCCTGCTC   6095    C       C_
                                TG CCTGGCCTCC  CTC
                                || ||||||||||  |||
                                AC GGACCGGAGG  GAG
                                 A        AC
GAM241  FLJ20232  3' GCCCACCTCCTCCCC     6096     TG    CC
                                GCCC  GCCTCC  TCCCC
                                ||||  ||||||  |||||
                                CGGG  TGGAGG  AGGGG
                                  __    __
GAM241  FLJ20241  5' CCTCATCCGTCCCCTCCTCC  6097     GG_ _     _
                                CCT   CC TCCCCTCC CC
                                |||   || ||||||||  ||
                                GGA   GG AGGGGAGG GG
                                  GTA  C       A
GAM241  FLJ20374  5' TGCCGCCAGGCCCCTCCCC   6098     _ TG CCT
                                TGCC C  G   CCCCTCCCC
                                |||| |  |   |||||||||
                                ACGG G  C   GGGGAGGGG
                                  C GT C__
GAM241  FLJ20378  3' GCTCTGTCCCCCTCCTCTTCCC 6099    C   G    _   __
          C                      GC CTG CCTCC CCTC  CCCC
                                || ||| ||||| ||||  ||||
                                CG GAC GGGGG GGAG  GGGG
                                 A  A    A   AA
GAM241  FLJ20548  3' TGCCCTGGCACTGCCCTC    6100         _ C
                                TGCCCTGGC CT CCCTC
                                ||||||||| || |||||
                                ACGGGACCG GA GGGAG
                                     T  C
GAM241  FLJ21736  3' TGCCCTGGTCCAGATGCCCTCC 6101        _ TC___
          CC                     TGCCCTGG CC    CCCTCCCC
                                |||||||| ||    ||||||||
                                ACGGGACC GG    GGGAGGGG
                                    A  TCTAC
GAM241  FLJ22004  5' TGCTCTGGCCCCGGCCCC    6102     C      CCCT
                                TGC CTGGCCTC   CCCC
                                ||| ||||||||   ||||
                                ACG GACCGGGG   GGGG
                                  A       CC__
GAM241  FLJ22031  3' TGCCCTGGTGCCAGCCCCT   6103       __  T_
                                TGCCCTG  GCC  CCCCT
                                |||||||  |||  |||||
                                ACGGGAC  CGG  GGGGA
                                   CA   TC
GAM241  FLJ22625  5' GCCCATGGCCTCCTTTCTTCC  6104     _      CC  CC
                                GCCC TGGCCTCC  TC  CC
                                |||| ||||||||  ||  ||
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                                CGGG ACCGGAGG  AG  GG
                                  T       AA  AA
GAM241  FLJ22659  3'  TGCTTATTGCCTCCCTCCCC  6105     CCTG_     C
                                TGC    GCCTCCC TCCCC
                                |||    ||||||| |||||
                                ACG    CGGAGGG AGGGG
                                  AATAA     _
GAM241  FLJ22688  3'  CCCCTCCCTCCCTTTCCCC  6106     GG     C_
                                CCCT  CCTCCC  TCCCC
                                ||||  ||||||  |||||
                                GGGG  GGAGGG  AGGGG
                                  AG     AA
GAM241  FLJ23598  5'  GCCCCATGCTTCCCTTTCCC  6107       _ C    C_
                                GCCCTG GC TCCC  TCCC
                                |||||| || ||||  ||||
                                CGGGGT CG AGGG  AGGG
                                   A  A    AA
GAM241  FLJ23816  3'  GCCCTGGACGCCTCCCTC    6108       ___      C
                                GCCCTG   GCCTCCC TC
                                ||||||   ||||||| ||
                                CGGGAC   CGGAGGG AG
                                   CTG      _
GAM241  FLNC      3'  CCCTGGCCTCGCAGCCCTC   6109         ____
                                CCCTGGCCTC    CCCTC
                                ||||||||||    |||||
                                GGGACCGGAG    GGGAG
                                     CGTC
GAM241  FUT10     3'  CTAGAAACCTCCCCTCCC    6110      ___
                                CTGG   CCTCCCCTCCC
                                ||||   ||||||||||
                                GATC   GGAGGGGAGGG
                                  TTT
GAM241  G4        3'  TGCCCTGGTCTCCTCCACCCC  6111         C   _  T
                                TGCCCTGG CTCC CC CCCC
                                |||||||| |||| || ||||
                                ACGGGACC GAGG GG GGGG
                                     A   A  T
GAM241  GALNT6    3'  TGCCCTGAACCCTCCCCC    6112         CCTC
                                TGCCCTGG    CCCTCCCCC
                                ||||||||    |||||||||
                                ACGGGACT    GGGAGGGGG
                                     T___
GAM241  GDF11     3'  TGCCCCTGCTTCCCCTTTCCC  6113       G  C     CC
                                TGCCCT GC TCCCCT  CCC
                                |||||| || ||||||  |||
                                ACGGGG CG AGGGGA  GGG
                                   A  A     AA
GAM241  GMPPB     5'  TGCCCTTGCACCCTCCCC    6114       G  CTC
                                TGCCCT GC   CCCTCCCC
                                |||||| ||   ||||||||
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                                ACGGGA CG   GGGAGGGG
                                   A  T__
GAM241  GRIN3A   3'  TACCACATCCCCTCCCC     6115      CTG  C
                                TGCC   GC TCCCCTCCCC
                                ||||   || ||||||||||
                                ATGG   TG AGGGGAGGGG
                                  ___  T
GAM241  HEMK     3'  TGCCCTGGCCTGGGCCTC    6116          CC_
                                TGCCCTGGCCT   CCTC
                                ||||||||||   ||||
                                ACGGGACCGGA   GGAG
                                      CCC
GAM241  HIC2     3'  CCATGGGTCTCCTCCCCC    6117     C   CC  C
                                CC TGG  TC CCTCCCCC
                                || |||  || ||||||||
                                GG ACC  AG GGAGGGGG
                                 T   C_  A
GAM241  HIC2     3'  CCCTCCCCCCTCCCC       5833      GGC
                                CCCT   CTCCCCTCCCC
                                ||||   ||||||||||
                                GGGA   GGGGGGAGGGG
                                  ___
GAM241  HIF3A    3'  CTAGTCCCTCCCCTTTCCC   6118      __      CC
                                CTGG  CCTCCCCT  CCC
                                ||||  ||||||||  |||
                                GATC  GGAGGGGA  GGG
                                  AG       AA
GAM241  HSGP25L2G 3'  CCTGCCCATTCCCCTCCCCC   6119      G  __
                                CCTG CC  TCCCCTCCCCC
                                |||| ||  ||||||||||
                                GGAC GG  AGGGGAGGGGG
                                  G  TA
GAM241  HSPB7    3'  TGCCCTGGCTTCCATCTC    6120         C   C_
                                TGCCCTGGC TCC  CTC
                                ||||||||| |||  |||
                                ACGGGACCG AGG  GAG
                                     A   TA
GAM241  HSPC049  3'  TGTCCTATATCTCCTCCCCC   6121     C    GCC  C
                                TG CCTG   TC CCTCCCCC
                                || ||||   || ||||||||
                                AC GGAT   AG GGAGGGGG
                                 A    AT_  A
GAM241  HSPC195  3'  TGGCCTGGTGCTCCCTCCCC   6122     C    C_    C
                                TG CCTGG  CTCCC TCCCC
                                || |||||  ||||| |||||
                                AC GGACC  GAGGG AGGGG
                                 C    AC    _
GAM241  HSSEXGENE 3'  CGCCCTGTCACCCCTCCCCC   6123        GCCT
                                TGCCCTG   CCCCTCCCCC
                                |||||||   ||||||||||
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                                GCGGGAC   GGGGAGGGGG
                                   AGT_
GAM241  ITGA10   5' CCTCTGGCCTCTGTCCCTC   6124    _     ___
                                CC CTGGCCTC   CCCTC
                                || ||||||||   |||||
                                GG GACCGGAG   GGGAG
                                 A       ACA
GAM241  KCNH4    5' CCTGCCTCCTCCCCTCCC    6125     G__
                                CCTG   CCTCCCCTCCC
                                ||||   ||||||||||
                                GGAC   GGAGGGGAGGG
                                  GGA
GAM241  KIAA0097 3' TGCCACAATGACTCCTCCCCC 6126     C___   CTCC
                                TGCC   TGGC   CCTCCCCC
                                ||||   ||||   ||||||||
                                ACGG   ACTG   GGAGGGGG
                                  TGTT   A___
GAM241  KIAA0100 3' TGCCCTGGGCCCATTCCC    6127       CCT   C_
                                TGCCCTGG   CCC  TCCC
                                ||||||||   |||  ||||
                                ACGGGACC   GGG  AGGG
                                     C__   TA
GAM241  KIAA0140 3' TGCCCTGGCCGCCTCC     6128         TCC
                                TGCCCTGGCC   CCTCC
                                ||||||||||   |||||
                                ACGGGACCGG   GGAGG
                                      C__
GAM241  KIAA0174 3' TGCTCTGGCCTCAGTCTCC   6129     C      CC_
                                TGC CTGGCCTC   CTCC
                                ||| ||||||||   ||||
                                ACG GACCGGAG   GAGG
                                  A       TCA
GAM241  KIAA0227 3' CCCTGGCCATCATCTTTCCCTC 6130        _ _______
                                CCCTGGCC TC     CCCTC
                                |||||||| ||     |||||
                                GGGACCGG AG     GGGAG
                                     T  TAGAAA
GAM241  KIAA0258 3' GCCCGCAGCTCCCCTCTCCC  6131      _   C     _
                                GCCC TGGC TCCCCTC CCC
                                |||| |||| ||||||| |||
                                CGGG GTCG AGGGGAG GGG
                                  C   _      A
GAM241  KIAA0296 3' TGCACGCGCTCCCTCCCCC   6132     CCTG  _    C
                                TGC   GC CTCCC TCCCCC
                                |||   || ||||| ||||||
                                ACG   CG GAGGG AGGGGG
                                  TG__  C    _
GAM241  KIAA0391 3' TGCCCTGACTCCTCCCCC    6133         CTCC
                                TGCCCTGGC   CCTCCCCC
                                |||||||||   ||||||||
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                                ACGGGACTG   GGAGGGGG
                                     A___
GAM241  KIAA0445 3' CCTGGTCCCCCTCCTCTTTCCC 6135      _   _   ___
                                CCTGG CCTCC CCTC  CCC
                                ||||| ||||| ||||  |||
                                GGACC GGGGG GGAG  GGG
                                   A    A   AAA
GAM241  KIAA0445 3' TGCCCTGGGCCTGGTCCCCCTC 6134       _  ____
          C                      TGCCCTGG CCT   CCCCTCC
                                ||||||||| |||   |||||||
                                ACGGGACC GGA   GGGGAGG
                                     C  CCAG
GAM241  KIAA0446 5' TGTGCTGGCCTCTCAGAGCTCC 6136    CC      CC____
          CC                     TG  CTGGCCTC    CTCCCC
                                ||  ||||||||     ||||||
                                AC  GACCGGAG     GAGGGG
                                 AC       AGTCTC
GAM241  KIAA0450 3' TGCCCTGGGCCTCCAGAGCC  6137       _    CCTC
                                TGCCCTGG CCTCC   CC
                                ||||||||| |||||   ||
                                ACGGGACC GGAGG   GG
                                     C    TCTC
GAM241  KIAA0513 3' TGGAGTCCTTCCCCTCCTCC  6138    ___  _     _
                                TGG   CCT CCCCTCC CC
                                |||   ||| ||||||| ||
                                ACC   GGA GGGGAGG GG
                                  TCA  A      A
GAM241  KIAA0515 3' ACCCCCCCCCCTCCCCC     6139      TGGC
                                GCCC   CTCCCCTCCCCC
                                ||||   ||||||||||||
                                TGGG   GGGGGGAGGGGG
                                  ____
GAM241  KIAA0545 3' TGCCCTGACTTCATCCCTC   6140        C __
                                TGCCCTGGC TC  CCCTC
                                ||||||||| ||  |||||
                                ACGGGACTG AG  GGGAG
                                     A  TA
GAM241  KIAA0570 5' GCCCCCCCCCCTCCCC      6141      TGGC
                                GCCC   CTCCCCTCCCC
                                ||||   ||||||||||
                                CGGG   GGGGGGAGGGG
                                  ____
GAM241  KIAA0607 3' TACCCTGGAGCCTCCCTC    6142       __     C
                                TGCCCTG  GCCTCCC TC
                                |||||||  ||||||| ||
                                ATGGGAC  CGGAGGG AG
                                    CT     _
GAM241  KIAA0620 3' TGCCCCCCATCCCTCCCC    6143       GG  TC
                                TGCCCT  CC  CCCTCCCC
                                ||||||  ||  ||||||||
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                                ACGGGG  GG  GGGAGGGG
                                  __  TA
GAM241  KIAA0620  3'  GCTGGCGGCCTCCTCTCCCCC  6144    CC_      C
                                GC   TGGCCTCC CTCCCCC
                                ||   |||||||| |||||||
                                CG   GCCGGAGG GAGGGGG
                                 ACC       A
GAM241  KIAA0668  3'  GCTCTAAAAGTCCCCTCCTCC  6146    C   CC_      _
                                GC CTGG   TCCCCTCC CC
                                || ||||   |||||||| ||
                                CG GATT   AGGGGAGG GG
                                 A   TTC      A
GAM241  KIAA0668  3'  TGCCAGCCTCTTCCCC     6145      CT     CCC
                                TGCC  GGCCTC   TCCCC
                                ||||  ||||||   |||||
                                ACGG  TCGGAG   AGGGG
                                  __     A__
GAM241  KIAA0731  3'  CCCCCCTTTCCCTCCCCC    6147      GG   C_
                                CCCT  CCT  CCCTCCCCC
                                ||||  |||  |||||||||
                                GGGG  GGA  GGGAGGGGG
                                  __   AA
GAM241  KIAA0746  3'  TGCCCTGGCCCCAGCTTCC   6148           CC  C
                                TGCCCTGGCCTC  CT CC
                                ||||||||||||  || ||
                                ACGGGACCGGGG  GA GG
                                       TC  A
GAM241  KIAA0757  3'  TGCCCCAAACTCTCCTCTCCC  6149       TG C   C   _
                                TGCCC  G CTC CCTC CCC
                                |||||  | ||| |||| |||
                                ACGGG  T GAG GGAG GGG
                                   GT T   A    A
GAM241  KIAA0767  3'  GCCTCTGCCCCCTCCCCC    6150     _  GCC
                                GCC CTG   TCCCCTCCCCC
                                ||| |||   ||||||||||
                                CGG GAC   GGGGGAGGGGG
                                  A  ___
GAM241  KIAA0843  3'  TGCTCCCCTCCCCCTCCCCC   6151     _  TGG      _
                                TGC CC   CCTCCCC TCCCCC
                                ||| ||   ||||||| ||||||
                                ACG GG   GGAGGGG AGGGGG
                                  A  ___      G
GAM241  KIAA0913  5'  GCCCTCGGCCTTCTCTTCCTC  6152       _    _ C___
                                GCCCT GGCCT C    CCTC
                                ||||| ||||| |    ||||
                                CGGGA CCGGA G    GGAG
                                   G     A AGAA
GAM241  KIAA0939  3'  GCCCTGGCCCATCCCCC     6156          CCCC
                                GCCCTGGCCT    TCCCCC
                                ||||||||||    ||||||
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                                CGGGACCGGG   AGGGGG
                                     T___
GAM241  KIAA0939 3' TGGCCTGGCCTCGGCTACCC  6155    C       CC  C
                                TG CCTGGCCTC  CT CCC
                                || |||||||||  || |||
                                AC GGACCGGAG  GA GGG
                                 C        CC  T
GAM241  KIAA0939 3' GCCCCATGCTCCCTCCCC    6153       GC    C
                                GCCCTG  CTCCC TCCCC
                                ||||||  ||||| |||||
                                CGGGGT  GAGGG AGGGG
                                   AC    _
GAM241  KIAA0939 3' TGCTCTGGCCCCTGCCCC    6154     C     TCC  _
                                TGC CTGGCC   CCT CCCC
                                ||| ||||||   ||| ||||
                                ACG GACCGG   GGA GGGG
                                  A     ___  C
GAM241  KIAA0945 3' TACCCTGGCCTCCCCAGCTCCC 6157             ___
                                TGCCCTGGCCTCCCC   TCCC
                                ||||||||||||||   ||||
                                ATGGGACCGGAGGGG   AGGG
                                         TCG
GAM241  KIAA1045 3' TGACCTGGCCCACCAACTCTCC 6158    C      TC __  C
                                TG CCTGGCC  CC  CTC CC
                                || |||||||  ||  ||| ||
                                AC GGACCGG  GG  GAG GG
                                 T      GT  TT   A
GAM241  KIAA1056 3' GCTCAGCCTCCCTTCCCCC   6159    CC       C
                                GC  TGGCCTCCC TCCCCC
                                ||  ||||||||| ||||||
                                CG  GTCGGAGGG AGGGGG
                                 A_       A
GAM241  KIAA1076 5' CCCTGGCCACTACCTCCTCC  6160        TCC_   _
                                CCCTGGCC    CCTCC CC
                                ||||||||    ||||| ||
                                GGGACCGG    GGAGG GG
                                     TGAT    A
GAM241  KIAA1091 3' GCCTCGCTCCCTCTCCC     6162     C G  C   _
                                GCC T GC TCCC CTCCC
                                ||| | || |||| |||||
                                CGG A CG AGGG GAGGG
                                  _ G  _   A
GAM241  KIAA1091 5' GCCCTGGCCCGGTCCCC     6161         CCCC
                                GCCCTGGCCT   TCCCC
                                ||||||||||   |||||
                                CGGGACCGGG   AGGGG
                                     CC__
GAM241  KIAA1130 3' TGCAACCACCTCCCCTCTTCC  6163     __ TG       CC
                                TGC  CC  GCCTCCCCTC  CC
                                |||  ||  ||||||||||  ||
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                                ACG  GG  TGGAGGGGAG  GG
                                  TT  __        AA
GAM241  KIAA1140  3'  CCCTGCTGCCTCTCCCTC    6164       __    _
                                CCCTG  GCCTC CCCTC
                                |||||  ||||| |||||
                                GGGAC  CGGAG GGGAG
                                   GA     A
GAM241  KIAA1184  3'  CGCCTGATCCCTCCCCTCCCC  6165      C   __
                                TGCC TGG  CCTCCCCTCCCC
                                ||||  |||  ||||||||||||
                                GCGG ACT  GGAGGGGAGGGG
                                  _  AG
GAM241  KIAA1196  3'  CCCTCCCCTCCCCTCCCC    6166      GG
                                CCCT  CCTCCCCTCCCC
                                ||||  ||||||||||||
                                GGGA  GGAGGGGAGGGG
                                  GG
GAM241  KIAA1196  3'  CCCTCCCCTCCCCTCCCC    6166      GG
                                CCCT  CCTCCCCTCCCC
                                ||||  ||||||||||||
                                GGGA  GGAGGGGAGGGG
                                  GG
GAM241  KIAA1196  3'  TGCTCCCCTCCCCTCCCC    6168     _  TGG
                                TGC CC   CCTCCCCTCCCC
                                |||  ||   ||||||||||||
                                ACG GG   GGAGGGGAGGGG
                                  A  ____
GAM241  KIAA1196  3'  TGCCTGCTCCCCTCCCC     6167      C  GC
                                TGCC TG  CTCCCCTCCCC
                                ||||  ||  ||||||||||||
                                ACGG AC  GAGGGGAGGGG
                                  _  __
GAM241  KIAA1205  3'  ACCCATGACCCCCTTTCCC   6169      _      CC
                                GCCC TGGCCTCC  TCCC
                                ||||  ||||||||  ||||
                                TGGG ACTGGGGG  AGGG
                                  T       AA
GAM241  KIAA1328  3'  TGCCTCGGCCTCCCAAAGCC  6170      C       CTCC
                                TGCC TGGCCTCCC    CC
                                ||||  |||||||||    ||
                                ACGG GCCGGAGGG    GG
                                  A        TTTC
GAM241  KIAA1373  5'  TGCCTCCGCCCCCTCCTC    6171      _  G    _
                                TGCC CTG CCTCC CCTC
                                ||||  |||  |||||  ||||
                                ACGG GGC GGGGG GGAG
                                  A  _    A
GAM241  KIAA1465  3'  GCCGCGCCCCCTCCCCTTCCC  6172     C  G  _     C
                                GCC TG CC TCCCCT CCC
                                |||  ||  ||  ||||||  |||
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                                CGG GC GG AGGGGA GGG
                                  C  G  G     A
GAM241  KIAA1580  5'  CCCCGGGTCCCCTTCTCC    6173       CC     _ C
                                CCCTGG  TCCCCT C CC
                                ||||||  |||||| | ||
                                GGGGCC  AGGGGA G GG
                                   C_     A A
GAM241  KIAA1691  3'  TGCTCCGGCCTCGGCTCC    6174     C      CC
                                TGC CTGGCCTC  CTCC
                                ||| ||||||||  ||||
                                ACG GGCCGGAG  GAGG
                                  A       CC
GAM241  KIAA1719  3'  GCCCTGGCCTCTGGGTCCC   6175          CCC_
                                GCCCTGGCCTC   TCCC
                                ||||||||||    ||||
                                CGGGACCGGAG   AGGG
                                      ACCC
GAM241  KIAA1719  3'  GCCCCCAGGCCTCTCTCC    6176       __     CC
                                GCCCT  GGCCTC  CTCC
                                |||||  ||||||  ||||
                                CGGGG  CCGGAG  GAGG
                                   GT     A_
GAM241  KIAA1762  3'  GCCCTGAGGCCCTCCCCTCTCC 6177         ___       _
          C                      GCCCTGG   CCTCCCCTC CCC
                                |||||||   ||||||||| |||
                                CGGGACT   GGAGGGGAG GGG
                                    CCG       A
GAM241  KIAA1811  3'  GCTCCCGTCCCTCCCCC     6178    _   GCCTC
                                GC CCTG    CCCTCCCCC
                                || ||||    |||||||||
                                CG GGGC    GGGAGGGGG
                                 A   A____
GAM241  KIAA1813  5'  ACCCCCTCCCCTCCCC      6179      TGG
                                GCCC   CCTCCCCTCCCC
                                ||||   ||||||||||||
                                TGGG   GGAGGGGAGGGG
                                  ___
GAM241  KIAA1855  3'  TGGCCCACTTTCCCTCCCCC   6180       C____
                                TGGCCT    CCCTCCCCC
                                ||||||    |||||||||
                                ACCGGG    GGGAGGGGG
                                   TGAAA
GAM241  KIAA1867  3'  TGCCCTGACCTCTTCCC     6181          CCC
                                TGCCCTGGCCTC   TCCC
                                ||||||||||||   ||||
                                ACGGGACTGGAG   AGGG
                                      A__
GAM241  KIAA1870  3'  TACCCAAGCTTCCTCCCCC    6182       T   CTCC
                                TGCCC GGC    CCTCCCCC
                                ||||| |||    ||||||||
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                                ATGGG TCG   GGAGGGGG
                                  T  AA__
GAM241  KIAA1904  3'  GCCTGGACCCTTCCCCC    6183     C  CCT  C
                                GCC TGG  CCC TCCCCC
                                ||| |||  ||| ||||||
                                CGG ACC  GGG AGGGGG
                                  _  T__  A
GAM241  KIAA1904  3'  GCCTCCATCTCCCCTCCC    6184     _  GC
                                GCC CTG  CTCCCCTCCC
                                ||| |||  ||||||||||
                                CGG GGT  GAGGGGAGGG
                                  A  A_
GAM241  KIAA1904  3'  TGGCTTCCTTCCTCCCCC    6185     C  __
                                TGGC TCC  CCTCCCCC
                                |||| |||  ||||||||
                                ACCG AGG  GGAGGGGG
                                  A  AA
GAM241  KIAA1908  3'  TGCCCTGGTTCTCAGGCCTCC  6186       C_  C__
                                TGCCCTGG  CTC  CCTCC
                                ||||||||  |||  |||||
                                ACGGGACC  GAG  GGAGG
                                    AA  TCC
GAM241  KIAA1941  3'  TGCCCGGCCTCCTGTATGCCT  6187      T    _______
                                TGCCC GGCCTCC    CCT
                                ||||| |||||||    |||
                                ACGGG CCGGAGG    GGA
                                  _     ACATAC
GAM241  KIAA1944  3'  CTGCCCTCTCCCTCCCCC    6188     G  _
                                CTG CCTC CCCTCCCCC
                                ||| |||| |||||||||
                                GAC GGAG GGGAGGGGG
                                  G  A
GAM241  KIAA1944  5'  TGCTTAGCCCCTCTTCTTCCCC 6189     CC     CCC___
                                TGC  TGGCCTC    TCCCC
                                |||  |||||||    |||||
                                ACG  ATCGGGG    AGGGG
                                  A_     AGAAGA
GAM241  KIAA1957  3'  TGGCCTGGCCTGGCCCCT    6190     C      __
                                TG CCTGGCCT  CCCCT
                                || ||||||||  |||||
                                AC GGACCGGA  GGGGA
                                 C      CC
GAM241  KIAA1981  3'  TGCCTCGGCCTCCGCGGCCTC  6191      C      ____
                                TGCC TGGCCTCC   CCTC
                                |||| ||||||||   ||||
                                ACGG GCCGGAGG   GGAG
                                  A      CGCC
GAM241  KPNA6     3'  TGCTTCCCATCCCCTCCCC    6192     CCTGG  _
                                TGC    CC TCCCCTCCCC
                                |||    || ||||||||||
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                                ACG    GG AGGGGAGGGG
                                  AAG__ T
GAM241  LENG9    3'  CCTCTGCCTCCCCTTCCCC   6193     G_      _
                                CCT  GCCTCCCCT CCCC
                                |||  ||||||||| ||||
                                GGA  CGGAGGGGA GGGG
                                  GA       A
GAM241  LGALS9   3'  TGCCCACTCCTCCCCTCTCCC  6194      TGG      _
                                TGCCC   CCTCCCCTC CCC
                                |||||   ||||||||| |||
                                ACGGG   GGAGGGGAG GGG
                                   TGA       A
GAM241  LGALS9   3'  TGCCCACTCCTCCCCTCTCCC  6194      TGG      _
                                TGCCC   CCTCCCCTC CCC
                                |||||   ||||||||| |||
                                ACGGG   GGAGGGGAG GGG
                                   TGA       A
GAM241  LGI3     5'  GCTGCGGTCCCCTCCCC    6195    CC   CC
                                GC  TGG  TCCCCTCCCC
                                ||  |||  ||||||||||
                                CG  GCC  AGGGGAGGGG
                                 AC  __
GAM241  LGI4     5'  GCCCTGGCTTCTCTCTCC    6196        __  CC
                                GCCCTGGC  CTC  CTCC
                                ||||||||  |||  ||||
                                CGGGACCG  GAG  GAGG
                                     AA   A_
GAM241  LIMK2    5'  TGCCCTGAGCTCACCTCTCCC  6197       GC  _ _
                                TGCCCTG  CTC CC CTCCC
                                |||||||  ||| || |||||
                                ACGGGAC  GAG GG GAGGG
                                     TC   T  A
GAM241  LIMR     3'  TGCCCTGGCCCAGTCCTTTCCC 6198         ___  CC
                                TGCCCTGGCC   TCC  TCCC
                                ||||||||||   |||  ||||
                                ACGGGACCGG   AGG  AGGG
                                      GTC   AA
GAM241  LRRFIP2  3'  TGCCCTGCCCTACCCTCCCCC  6199       G   C
                                TGCCCTG CCT CCCTCCCCC
                                |||||||  ||| |||||||||
                                ACGGGAC GGA GGGAGGGGG
                                     G   T
GAM241  MARKL1   5'  CCCCTCTCTTCCCCTCCCCC   6200     GGCC_
                                CCCT    TCCCCTCCCCC
                                ||||    ||||||||||
                                GGGG    AGGGGAGGGGG
                                  AGAGA
GAM241  MGC10334 5'  GCCCTGGCTTCCCGCCTC    6201        C   __
                                GCCCTGGC TCCC  CTC
                                ||||||||  ||||  |||
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                                CGGGACCG AGGG  GAG
                                    A   CG
GAM241  MGC10871 5' TGCTTCCCTCCCCTTCCCC   6202     CCTGG      _
                                TGC    CCTCCCCT CCCC
                                |||    |||||||| ||||
                                ACG    GGAGGGGA GGGG
                                  AAG__       A
GAM241  MGC10871 5' GCGCTGCTTCCCTCCCC    6203    C   GC  C
                                GC CTG  CT CCCTCCCC
                                || |||  || ||||||||
                                CG GAC  GA GGGAGGGG
                                 C   __ A
GAM241  MGC10902 3' TGCCCATGGCCCTCCCCT   6204       _    _
                                TGCCC TGGCC TCCCCT
                                ||||| ||||| ||||||
                                ACGGG ACCGG AGGGGA
                                   T    G
GAM241  MGC10986 3' CCCCATCTCCTCCCCC     6206      GCC  C
                                CCCTG   TC CCTCCCCC
                                |||||   || ||||||||
                                GGGGT   AG GGAGGGGG
                                   ____ A
GAM241  MGC10986 3' TGCCCTGGTCCCCTACGCC   6205        CC     CC_
                                TGCCCTGG  TCCCCT   CC
                                ||||||||  ||||||   ||
                                ACGGGACC  AGGGGA   GG
                                    __      TGC
GAM241  MGC11271 5' TGTCCTTTGGGCCCCTCCCTC  6207    C  ____     _
                                TG CCT   GGCCTC CCCTC
                                || |||   |||||| |||||
                                AC GGA   CCGGGG GGGAG
                                 A  AAC     A
GAM241  MGC1136  3' TGGCCTGACCTCTCTCCC    6208    C       CC
                                TG CCTGGCCTC  CTCCC
                                || |||||||||  |||||
                                AC GGACTGGAG  GAGGG
                                 C       A_
GAM241  MGC14425 5' TGCCCTGGCCCCCATCCC    6209         T   C
                                TGCCCTGGCC CCC TCCC
                                |||||||||| ||| ||||
                                ACGGGACCGG GGG AGGG
                                      _  T
GAM241  MGC14839 3' GCCTCAGCCCCCTTCCCC    6210     CT   T   C
                                GCC  GGCC CCC TCCCC
                                |||  |||| ||| |||||
                                CGG  TCGG GGG AGGGG
                                  AG   _  A
GAM241  MGC18079 3' TGCCCTGGCCCCATTTCC    6211          CCC
                                TGCCCTGGCCTC   TCC
                                ||||||||||||   |||
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                                ACGGGACCGGGG  AGG
                                      TAA
GAM241  MGC20235 3' TGCCTCTCTCCCCTCC     6212      _ GGC
                                TGCC CT  CTCCCCTCC
                                |||| ||  |||||||||
                                ACGG GA  GAGGGGAGG
                                  A ___
GAM241  MGC20481 3' GCCCAGCCTCTCTCCC     6213     T    CC
                                GCCC GGCCTC  CTCCC
                                |||| ||||||  |||||
                                CGGG TCGGAG  GAGGG
                                  _     A_
GAM241  MGC20496 3' TGCCTCGGCCTCCCAAAGTCC 6214      C       C___
                                TGCC TGGCCTCCC   TCC
                                |||| |||||||||   |||
                                ACGG GCCGGAGGG   AGG
                                  A       TTTC
GAM241  MGC23280 3' GCCCTGGCCTCAGACCCT   6215          ___
                                GCCCTGGCCTC  CCCT
                                ||||||||||  ||||
                                CGGGACCGGAG  GGGA
                                      TCT
GAM241  MGC2555  3' CTGGACTCCTCCCCTCCCCC 6216     ___
                                CTGG  CCTCCCCTCCCCC
                                ||||  |||||||||||||
                                GACC  GGAGGGGAGGGGG
                                  TGA
GAM241  MGC2718  3' TGCCCGACCCCTTCCCC    6217      T   T  CC
                                TGCCC GGCC CC  TCCCC
                                ||||| |||| ||  |||||
                                ACGGG CTGG GG  AGGGG
                                  _   _ A_
GAM241  MGC2941  5' GCCCCCTCCCCTCCTCC    6218      TGG       _
                                GCCC  CCTCCCCTCC CC
                                ||||  |||||||||| ||
                                CGGG  GGAGGGGAGG GG
                                  ___       A
GAM241  MGC3113  3' TGCCCTGGCCTTCCTGCTC  6219          _ C_
                                TGCCCTGGCCT CC  CTC
                                |||||||||| ||  |||
                                ACGGGACCGGA GG  GAG
                                      A  AC
GAM241  MGC33371 5' CCTCCTCCCCCTCCCCC    6220     GG    _
                                CCT  CCTCCCC TCCCCC
                                |||  ||||||| ||||||
                                GGA  GGAGGGG AGGGGG
                                  __     G
GAM241  MGC4655  5' GCCCTGGCCTCCGGGGCTC  6221          C___
                                GCCCTGGCCTCC   CTC
                                ||||||||||||  |||
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                                CGGGACCGGAGG   GAG
                                      CCCC
GAM241  MGC5384  3'  TGCCTGGCCTCATATCCC   6222     C     CCC
                                TGCC TGGCCTC   TCCC
                                |||| |||||||   ||||
                                ACGG ACCGGAG   AGGG
                                  _      TAT
GAM241  MGC5469  3'  GCCCTTCCATTCCCCTCCC   6223      GG __
                                GCCCT  CC  TCCCCTCCC
                                |||||  ||  |||||||||
                                CGGGA  GG  AGGGGAGGG
                                   A_  TA
GAM241  MGC9753  3'  GCATAGCTCCCCTCCC     6224    CC   C
                                GC  TGGC TCCCCTCCC
                                ||  |||| |||||||||
                                CG  ATCG AGGGGAGGG
                                 T_   _
GAM241  MMPL1    3'  GCCCTGGGAGCATCCCCTCCTC 6225       ___ C      _
            C                    GCCCTG   GC TCCCCTCC CC
                                |||||||   || ||||||| ||
                                CGGGAC   CG AGGGGAGG GG
                                    CCT  T       A
GAM241  MRPL24   5'  GCCCTCAGCGTCCCCTCCCCC  6226      _  C
                                GCCCT GGC TCCCCTCCCCC
                                ||||| ||| ||||||||||
                                CGGGA TCG AGGGGAGGGGG
                                   G   C
GAM241  MSI2     5'  CCCTCCTCCCCCTCCTCC    6227     GG     TC _
                                CCCT  CCTCCCC  CC CC
                                ||||  |||||||  || ||
                                GGGA  GGAGGGG  GG GG
                                  __      GA  A
GAM241  N4BP3    3'  TGACCTGGCCACTCCCCC    6228    C     TCCC
                                TG CCTGGCC    CTCCCCC
                                || |||||||    |||||||
                                AC GGACCGG    GAGGGGG
                                 T      T___
GAM241  NBL1     3'  CCCCTCCTCCCCTTCCCC    6229     GG      _
                                CCCT  CCTCCCCT CCCC
                                ||||  |||||||| ||||
                                GGGG  GGAGGGGA GGGG
                                  A_       A
GAM241  NBL1     3'  TGCCCTGTCCCTCCCCC     6230       GCCTC
                                TGCCCTG    CCCTCCCCC
                                |||||||    |||||||||
                                ACGGGAC    GGGAGGGGG
                                    A____
GAM241  NFASC    3'  CCCCTTCTCCCCTCCTCC    6231     GGC      _
                                CCCT   CTCCCCTCC CC
                                ||||   ||||||||| ||
```

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                                GGGG   GAGGGGAGG GG
                                  AA_        A
GAM241  NIP30    3'  TGTCCTGGCCTGCCTCC     6232     C       CC
                                TG CCTGGCCT  CCTCC
                                || ||||||||  |||||
                                AC GGACCGGA  GGAGG
                                 A       C_
GAM241  NLI-IF   3'  TACCCTGACCCTTCCCTC     6233           C_
                                TGCCCTGGCCT  CCCTC
                                ||||||||||  |||||
                                ATGGGACTGGG  GGGAG
                                      AA
GAM241  NRN1     3'  CCCTGGCCTTCTCCTCTCC    6234          _ C    C
                                CCCTGGCCT C CCTC CC
                                ||||||||| | |||| ||
                                GGGACCGGA G GGAG GG
                                     A A    A
GAM241  NSE1     3'  CCCTCAGCCCCTTCCCC      6235       _    T  CC
                                CCCT GGCC CC  TCCCC
                                |||| |||| ||  |||||
                                GGGA TCGG GG  AGGGG
                                  G    _ A_
GAM241  NYD-SP20 5'  GCCCTCAGTTTCCCTCCCCC   6236        _  CCTC
                                GCCCT GG    CCCTCCCCC
                                ||||| ||    |||||||||
                                CGGGA TC    GGGAGGGGG
                                   G  AAA_
GAM241  ORMDL3   3'  TACCCTACCCCTCCCC       6237         GCCT
                                TGCCCTG    CCCCTCCCC
                                |||||||    |||||||||
                                ATGGGAT    GGGGAGGGG
                                     ____
GAM241  OS4      3'  ACCTCTGGCCTCCTCTTCCCTG 6238      _        C  C   CIIIA
                                GCC CTGGCCTCC CT CCC     G
                                ||| ||||||||| || |||    |
                                TGG GACCGGAGG GA GGG     C
                                  A        A  A   AIIIC
GAM241  OSBPL1A  5'  GCCGCTCCTCCCCTTCCCC    6239      CTGG       _
                                GCC    CCTCCCCT CCCC
                                |||    |||||||| ||||
                                CGG    GGAGGGGA GGGG
                                  CGA_       A
GAM241  PADI3    3'  GCCCCTTAGCCCCCTCTCC    6240        __      C
                                GCCCT  GGCCTCC CTCC
                                |||||  ||||||| ||||
                                CGGGG  TCGGGGG GAGG
                                   AA      A
GAM241  PCBP4    5'  TGCCCTGGGCTCCTCCCCC    6241          C    CC
                                TGCCCTGG CTCC  TCCCCC
                                |||||||| ||||  ||||||
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                                ACGGGACC GAGG  AGGGGG
                                    C   __
GAM241  PDE8B    5'  TGCGCCCGTCCCCTCCC     6242     _   GCC
                                TGC CCTG   TCCCCTCCC
                                ||| ||||   |||||||||
                                ACG GGGC   AGGGGAGGG
                                  C   ___
GAM241  PFDN1    3'  TGCCCTGGCTCCCATCTTCCCT 6243          _  _____    C
           CTCC                    TGCCCTGGC CTC    CCCTC CC
                                |||||||||  |||    ||||| ||
                                ACGGGACCG GGG    GGGAG GG
                                     A   TAGAA    A
GAM241  PISD     5'  CCTCTTTCCTCCCCTTCCCC   6244     _  GG       _
                                CC CT  CCTCCCCT CCCC
                                || ||  |||||||| ||||
                                GG GA  GGAGGGGA GGGG
                                 A  AA       A
GAM241  PITPNM   3'  GCCCTCCTCCCTCCCCC     6245       GG     C
                                GCCCT  CCTCCC TCCCCC
                                |||||  ||||||  ||||||
                                CGGGA  GGAGGG AGGGGG
                                   __     _
GAM241  PLP1     3'  TGCTTTGACCCCCTTCTCC    6246      CC       C_
                                TGC  TGGCCTCC  CTCC
                                |||  ||||||||  ||||
                                ACG  ACTGGGGG  GAGG
                                  AA       AA
GAM241  PLSCR4   3'  GCCCTGGCCAGCTCCTTTCC   6247          ___  CC
                                GCCCTGGCC   TCC  TCC
                                |||||||||   |||  |||
                                CGGGACCGG   AGG  AGG
                                     TCG   AA
GAM241  PNMA5    3'  CTTCCTCCTTCTCCTCCCCC   6248     GG    ____
                                CT  CCTCC    CCTCCCCC
                                ||  |||||    ||||||||
                                GA  GGAGG    GGAGGGGG
                                 A_     AAGA
GAM241  PPFIA4   3'  TGCCCTTCTCTCCTTCCCC    6249       GGC    CC
                                TGCCCT   CTCC  TCCCC
                                ||||||   ||||  |||||
                                ACGGGA   GAGG  AGGGG
                                   AGA    A_
GAM241  PPP1R16B 3'  GCTTAGCAGGTCCCCTCCCC   6250     CC    C__
                                GC  TGGC   TCCCCTCCCC
                                ||  ||||   ||||||||||
                                CG  ATCG   AGGGGAGGGG
                                 A_    TCC
GAM241  PPP1R3B  3'  CCCTGGCCTTCCATCTCC     6251          _  C_
                                CCCTGGCCT CC  CTCC
                                |||||||||  ||  ||||
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                                GGGACCGGA GG  GAGG
                                     A  TA
GAM241  PRO2389  3'  TACCCATGCCCCTCCCC     6252       _ GCCT
                                TGCCC TG    CCCCTCCCC
                                ||||| ||    |||||||||
                                ATGGG AC    GGGGAGGGG
                                  T _____
GAM241  PRO2730  5'  CCGCTACCCTCCCCTTTCCC  6253     _  G       CC
                                CC CTG CCTCCCCT  CCC
                                || ||| ||||||||  |||
                                GG GAT GGAGGGGA  GGG
                                 C  G       AA
GAM241  PSK      5'  GCCCCGGCCTCCTCCC      6254            CC
                                GCCCTGGCCTCC  TCCC
                                ||||||||||||  ||||
                                CGGGGCCGGAGG  AGGG
                                              __
GAM241  PSKH1    3'  TGCCTTGGCCCCCAGGTGCCCC 6255       C       CCT__
                                TGCC TGGCCTCC     CCCC
                                |||| ||||||||     ||||
                                ACGG ACCGGGGG     GGGG
                                  A       TCCAC
GAM241  PTPRN2   3'  GCCCTGATCTCCTCTCCC    6256        GC    C
                                GCCCTG  CTCC CTCCC
                                ||||||  |||| |||||
                                CGGGAC  GAGG GAGGG
                                   TA    A
GAM241  PTPRN2   3'  GCCCTGATCTCCTCTCCC    6256        GC    C
                                GCCCTG  CTCC CTCCC
                                ||||||  |||| |||||
                                CGGGAC  GAGG GAGGG
                                   TA    A
GAM241  RAI17    3'  TGCCTCTGCACCTCCCTC     6257      _  _      C
                                TGCC CTG GCCTCCC TC
                                |||| ||| ||||||| ||
                                ACGG GAC TGGAGGG AG
                                  A  G      _
GAM241  RAI17    3'  TGTCCTGGCCCTCTTCCCC    6258     C       CCCC
                                TG CCTGGCCT    TCCCC
                                || ||||||||    |||||
                                AC GGACCGGG    AGGGG
                                 A       AGA_
GAM241  RGPR     3'  GCCCCTGCCCCTCCCCC     6259       GGCCT
                                GCCCT    CCCCTCCCCC
                                |||||    ||||||||||
                                CGGGG    GGGGAGGGGG
                                  AC___
GAM241  RNF34    5'  TGCCGACCTCCTTCCC      6260       CT      CC
                                TGCC  GGCCTCC  TCCC
                                ||||  |||||||  ||||
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                                ACGG  CTGGAGG  AGGG
                                  __      A_
GAM241  RoXaN    3'  TGTCCTGAACACCCTCCCC   6261     C    CCTC
                                TG CCTGG   CCCTCCCC
                                || |||||   ||||||||
                                AC GGACT   GGGAGGGG
                                 A    TGT_
GAM241  RPL39L   5'  GCCCTGGCCTCTGCTTTTTTCC 6262          CC _____
          C                      GCCCTGGCCTC  C    TCCC
                                ||||||||||  |    ||||
                                CGGGACCGGAG  G    AGGG
                                      AC AAAAA
GAM241  SARM     3'  TGCCCTGGCTCTGGCCCC    6263         _ __
                                TGCCCTGGC CT  CCCC
                                |||||||| ||  ||||
                                ACGGGACCG GA  GGGG
                                      A  CC
GAM241  SCYA18   3'  TGCCCTGGCTCAGGCTCC    6264         C  CC_
                                TGCCCTGGC TC   CTCC
                                |||||||| ||   ||||
                                ACGGGACCG AG   GAGG
                                     _ TCC
GAM241  SDC3     3'  TGCCCTGGGCCTTCCGTCC    6265         _  C  C
                                TGCCCTGG CCT CC TCC
                                |||||||| ||| || |||
                                ACGGGACC GGA GG AGG
                                     C   A  C
GAM241  SDF1     3'  GCCTCTGGCCCCTTCCTC     6266     _      C_
                                GCC CTGGCCTC  CCTC
                                ||| ||||||||  ||||
                                CGG GACCGGGG  GGAG
                                  A       AA
GAM241  SEC14L1  3'  TGCTCGGTCCCTCCCCC     6267     CC   CCTC
                                TGC  TGG   CCCTCCCCC
                                |||  |||   |||||||||
                                ACG  GCC   GGGAGGGGG
                                  A_   A___
GAM241  SEMA3B   5'  TGCCCTGGACTCTGCCCC    6268         C   CCCT
                                TGCCCTGG CTC   CCCC
                                |||||||| |||   ||||
                                ACGGGACC GAG   GGGG
                                     T   AC__
GAM241  SEMA4C   3'  GCTCCATCTCCCTCCCCC    6269     _ TGGC    C
                                GC CC   CTCCC TCCCCC
                                || ||   ||||| ||||||
                                CG GG   GAGGG AGGGGG
                                 A  TA__    _
GAM241  SERHL    3'  GCCCGCCCTTCCTTCCTCC    6270      T G  _  __
                                GCCC G CCT CC  CCTCC
                                |||| | ||| ||  |||||
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                                CGGG C GGA GG  GGAGG
                                  _ G   A  AA
GAM241  SEZ6     3'  TGCCCACCCCCTCCCC      6271       TGGCC
                                TGCCC    TCCCCTCCCC
                                |||||    ||||||||||
                                ACGGG    GGGGGAGGGG
                                   T_____
GAM241  SFXN2    3'  TACCCTGGCCTTCAGGCCT   6272          _ C__
                                TGCCCTGGCCT C   CCT
                                |||||||||||| |   |||
                                ATGGGACCGGA G   GGA
                                       A TCC
GAM241  SLC6A14  3'  TACCTTCATGTCCCCTCCCCC 6273      CTGGCC
                                TGCC     TCCCCTCCCCC
                                ||||     ||||||||||
                                ATGG     AGGGGAGGGGG
                                  AAGTAC
GAM241  SMARCA4  5'  CGCCGGCTCCCCTCCCCC    6274      CT   C
                                TGCC  GGC TCCCCTCCCCC
                                ||||  ||| ||||||||||
                                GCGG  CCG AGGGGAGGGGG
                                   __  _
GAM241  SMOC1    3'  TGTCCTGTCCCCTCCCC     6275     C    GCC
                                TG CCTG   TCCCCTCCCC
                                || ||||   ||||||||||
                                AC GGAC   AGGGGAGGGG
                                 A   ____
GAM241  SMOC2    5'  CCCTCCCCCTCTCCTCCCCC  6276      GG_   C
                                CCCT   CCTC CCTCCCCC
                                ||||   |||| ||||||||
                                GGGA   GGAG GGAGGGGG
                                  GGG   A
GAM241  SNPH     3'  GCCCTCGCTCCCTCCCC     6277       G  CTC
                                GCCCT GC   CCCTCCCC
                                ||||| ||   ||||||||
                                CGGGA CG   GGGAGGGG
                                   G  A__
GAM241  SR-A1    3'  CCCTGCAGCAACCCTCCCCC  6278       __ CTC
                                CCCTG  GC   CCCTCCCCC
                                |||||  ||   |||||||||
                                GGGAC  CG   GGGAGGGGG
                                   GT  TT_
GAM241  SRCRB4D  3'  TGCTTTGGCCCCTCCCCC    6279     CC    TCC
                                TGC  TGGCC   CCTCCCCC
                                |||  |||||   ||||||||
                                ACG  ACCGG   GGAGGGGG
                                  AA    ____
GAM241  SRPK1    3'  TGCCATCCCACCCCTCCCC    6280      CTGG  _
                                TGCC    CCT CCCCTCCCC
                                ||||    ||| |||||||||
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                                ACGG   GGG GGGGAGGGG
                                  TA__  T
GAM241  SSBP3   5'  GCTCCCCTCCCTCCCCC    6282    _ TGG    C
                                GC CC  CCTCCC TCCCCC
                                || ||  |||||| ||||||
                                CG GG  GGAGGG AGGGGG
                                 A ____    _
GAM241  SSBP3   5'  CGCCGCGCTCCCCTCCC    6281     CTG _
                                TGCC  GC CTCCCCTCCC
                                ||||  || ||||||||||
                                GCGG  CG GAGGGGAGGG
                                  ___ C
GAM241  STC2    5'  CGCCGCTTCCCCTCCTCC    6284     CTG C     _
                                TGCC  GC TCCCCTCC CC
                                ||||  || |||||||| ||
                                GCGG  CG AGGGGAGG GG
                                  ___ A      A
GAM241  STC2    3'  CCCTGGTTCACCTCCCCC    6283      CC  C
                                CCCTGG  TC CCTCCCCC
                                ||||||  || ||||||||
                                GGGACC  AG GGAGGGGG
                                   A_  T
GAM241  STMN4   3'  TGGCCACCCCCCTCCCCC    6285      __
                                TGGCC  TCCCCTCCCCC
                                |||||  ||||||||||
                                ACCGG  GGGGGAGGGGG
                                   TG
GAM241  SV2B    3'  TGTCCTAAGCTCCTCCCCC   6286    C   C   CC
                                TG CCTGG CTCC  TCCCCC
                                || ||||| ||||  ||||||
                                AC GGATT GAGG  AGGGGG
                                 A   C   __
GAM241  SYNE-2  3'  TGCCCTGGGCTCCAGGGAGCCC 6287        C   CCTC__
                                TGCCCTGG CTCC     CCC
                                |||||||| ||||     |||
                                ACGGGACC GAGG     GGG
                                     C   TCCCTC
GAM241  T2BP    3'  GCTCATGACCTCCCCTTCC   6288    CC_       C
                                GC  TGGCCTCCCCT CC
                                ||  |||||||||| ||
                                CG  ACTGGAGGGGA GG
                                 AGT         A
GAM241  THG-1   3'  TGTCCACACTCCCTCCCC    6289    C TG _    C
                                TG CC  GC CTCCC TCCCC
                                || ||  || ||||| |||||
                                AC GG  TG GAGGG AGGGG
                                 A __  T    _
GAM241  TIAF1   3'  GCACTGCTTCTCCTCCCCC   6290    C   G C  C
                                GC CTG C TC CCTCCCCC
                                || ||| | || ||||||||
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                                CG GAC G AG GGAGGGGG
                                 T  _ A  A
GAM241  TMLHE   5'  GCCCCACGCTCCCCTCCCCC  6291       G _
                                GCCCTG C CTCCCCTCCCCC
                                |||||| | ||||||||||||
                                CGGGGT G GAGGGGAGGGGG
                                   _ C
GAM241  TMPRSS5  3'  CCTACCTCTCTCCTCCCCC   6292      G   C__
                                CCTG CCTC   CCTCCCCC
                                |||| ||||   ||||||||
                                GGAT GGAG   GGAGGGGG
                                  _   AGA
GAM241  TRPV6   3'  TGCCCTGGGAAGGGCTCTCTCC 6293        C_____  CC
           C                     TGCCCTGG     CTC  CTCCC
                                ||||||||     |||  |||||
                                ACGGGACC     GAG  GAGGG
                                     CTTCCC   A_
GAM241  UCK1    3'  GCTCAGCCCCCTTCCCC     6294     CC    T  C
                                GC  TGGCC CCC TCCCC
                                ||  ||||| ||| |||||
                                CG  GTCGG GGG AGGGG
                                 A_    _  A
GAM241  VCY2IP1  3'  TGCCCGGCCTCCCTTCTC    6295       T      __
                                TGCCC GGCCTCCC  CTC
                                ||||| ||||||||  |||
                                ACGGG CCGGAGGG  GAG
                                   _       AA
GAM241  VEGFC   5'  GCCCTCGTCCCCCTCCTCC   6296       GG_    _
                                GCCCT   CCTCC CCTCC
                                |||||   ||||| |||||
                                CGGGA   GGGGG GGAGG
                                   GCA    A
GAM241  VRP     5'  GCTCTGCTCCCCTCTCC     5865     C  GC      C
                                GC CTG  CTCCCCTC CC
                                || |||  |||||||| ||
                                CG GAC  GAGGGGAG GG
                                 A  __       A
GAM241  WBSCR22  3'  GCTTCACCTCCCTCCCCTCC  6297     _____  GG
                                GC   CCT  CCTCCCCTCC
                                ||   |||  ||||||||||
                                CG   GGA  GGAGGGGAGG
                                 AAGT   G_
GAM241  WBSCR23  3'  TGCCTGGCCTCGTGGGACCCT  6298      C      _______
                                TGCC TGGCCTC     CCCT
                                |||| |||||||     ||||
                                ACGG ACCGGAG     GGGA
                                   _      CACCCT
GAM241  ZDHHC7   3'  TGCCTCATGGTCCCCTCCCC   6300      C__   CC
                                TGCC   TGG  TCCCCTCCCC
                                ||||   |||  ||||||||||
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                                ACGG  ACC  AGGGGAGGGG
                                  AGT  __
GAM241  ZDHHC7   3'  GCGGCTCTCTCCCCTCTTCC  6299    CCT  ___      CC
                                GC  GGC  CTCCCCTC  CC
                                ||  |||  ||||||||  ||
                                CG  CCG  GAGGGGAG  GG
                                 ___  AGA       AA
GAM241  ZF       5'  GCCGCCGTCTCCTCCTCC    6301     _  GC   _
                                GCC CTG  CTCC CCTCC
                                ||| |||  |||| |||||
                                CGG GGC  GAGG GGAGG
                                  C  A_   A
GAM241  ZFP106   3'  GCCCTGGGCTCCTCCCCC    6302       C   CC
                                GCCCTGG CTCC  TCCCCC
                                |||||||  ||||  ||||||
                                CGGGACC GAGG  AGGGGG
                                    C  __
GAM241  ZFPL1    3'  TACCCCGCCTCTCCTCC     6303       G   C
                                TGCCCTG CCTC CCTCC
                                |||||||  |||| |||||
                                ATGGGGC GGAG GGAGG
                                   _   A
GAM241  ZNF213   3'  TGCCGTGGCTGGGCCTCCCCC  6304     C   CTCC
                                TGCC TGGC   CCTCCCCC
                                ||||  ||||   ||||||||
                                ACGG ACCG   GGAGGGGG
                                  C   ACCC
GAM241  ZNF237   5'  GCCTCCGCCTCCTCCTCC    6305     _  G   _
                                GCC CTG CCTCC CCTCC
                                ||| ||| ||||| |||||
                                CGG GGC GGAGG GGAGG
                                  A  _    A
GAM241  LOC113251 3'  CCTGGCTACCCCCTCCCC    6306       C_
                                CCTGGC  TCCCCTCCCC
                                ||||||  ||||||||||
                                GGACCG  GGGGGAGGGG
                                   AT
GAM241  LOC115219 5'  ACACCTGGCCTCTCCTTCCC  6307    _       _ C
                                GC CCTGGCCTC CC TCCC
                                || |||||||| || ||||
                                TG GGACCGGAG GG AGGG
                                 T       A  A
GAM241  LOC115708 3'  TGCCCCCCTCCCTCCTCC    6308       GG    C  _
                                TGCCCT  CCTCCC TCC CC
                                ||||||  |||||| ||| ||
                                ACGGGG  GGAGGG AGG GG
                                   __    _  A
GAM241  LOC116113 3'  GCCCGCTTTCTCCCCTCC    6310      TG  ___
                                GCCC  GC   CTCCCCTCC
                                ||||  ||   |||||||||
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                                CGGG  CG   GAGGGGAGG
                                  __  AAA
GAM241   LOC116113 3'  CCCCTCCTTTCTCCTTCCCC   6309      GG  __  _  C
                                CCCT  CC  TC CC TCCCC
                                ||||  ||  || || |||||
                                GGGG  GG  AG GG AGGGG
                                  A_  AA  A  A
GAM241   LOC121457 5'  GCCCAGCCCCTTCCCTCTCCC  6311      T     __    _
                                GCCC GGCCTC  CCCTC CCC
                                |||| ||||||  ||||| |||
                                CGGG TCGGGG  GGGAG GGG
                                  _     AA    A
GAM241   LOC122728 5'  GCCGCCATCTTCTCCCCC    6312     CTG  _  CC
                                GCC   GCC TC  CTCCCCC
                                |||   ||| ||  |||||||
                                CGG   CGG AG  GAGGGGG
                                  ___   T  AA
GAM241   LOC127281 3'  TGACCCCACGCTCCTCTCC   6313    C   G  _   C
                                TG CCT GC CTCC CTCC
                                || ||| || |||| ||||
                                AC GGG TG GAGG GAGG
                                 T   G  C    A
GAM241   LOC128344 3'  TGCCCTGGGGAGTCCTCCTC   6314        CC__   _
                                TGCCCTGG    TCC CCTC
                                ||||||||    ||| ||||
                                ACGGGACC    AGG GGAG
                                     CCTC   A
GAM241   LOC132332 3'  TGCGTAGATTCCCCTCCTCC   6315     CC   CC      _
                                TGC  TGG  TCCCCTCC CC
                                |||  |||  |||||||| ||
                                ACG  ATC  AGGGGAGG GG
                                  C_   TA       A
GAM241   LOC136345 5'  GCCCCAAACCCCTCCCCC    6316      TG CCT
                                GCCC  G   CCCCTCCCCC
                                ||||  |   ||||||||||
                                CGGG  T   GGGGAGGGGG
                                  GT T__
GAM241   LOC137964 3'  CTGGCCTCTTCCCCTCCC    6317       ___
                                CTGGCC   TCCCCTCCC
                                ||||||   |||||||||
                                GACCGG   AGGGGAGGG
                                   AGA
GAM241   LOC138389 3'  TGTCCTGGCCCCTCCCTC    6318     C       _
                                TG CCTGGCCTC CCCTC
                                || |||||||| |||||
                                AC GGACCGGGG GGGAG
                                 A        A
GAM241   LOC139728 5'  TGCCCTGGCCCCTCCTCCTCC  6319           C    _
                                TGCCCTGGCCTC CCTCC CC
                                |||||||||||| ||||| ||
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                                ACGGGACCGGGG GGAGG GG
                                      A     A
GAM241   LOC143243 3'  CCCCTCCCCTCTCCTCC     5857     TGG       _ _
                                CC   CCTCCCCTC CC CC
                                ||   ||||||||| || ||
                                GG   GGAGGGGAG GG GG
                                 ___        A  A
GAM241   LOC144017 5'  CCTTCCTCCCCCTTCCCTCCCC 6320      GG      ______
           C                     CCT  CCTCCCC     TCCCCC
                                 |||  |||||||     ||||||
                                 GGA  GGAGGGG     AGGGGG
                                   A_      GAAGGG
GAM241   LOC144596 3'  GCCTCTGTCCCCTCCC      6321      _   GCC
                                GCC CTG   TCCCCTCCC
                                ||| |||   |||||||||
                                CGG GAC   AGGGGAGGG
                                  A  ___
GAM241   LOC144667 3'  TGCCCTGCCTCTGGCCTCC    6322        G    C__
                                TGCCCTG CCTC   CCTCC
                                ||||||| ||||   |||||
                                ACGGGAC GGAG   GGAGG
                                    _    ACC
GAM241   LOC144678 5'  CCTCTGGCCTCCTGCTCC     6323     _       C_
                                CC CTGGCCTCC  CTCC
                                || |||||||||  ||||
                                GG GACCGGAGG  GAGG
                                  A         AC
GAM241   LOC145127 3'  CCCTGGCCTCTCTGGCCCC    6324          CC  __
                                CCCTGGCCTC  CT  CCCC
                                ||||||||||  ||  ||||
                                GGGACCGGAG  GA  GGGG
                                     A_  CC
GAM241   LOC145384 3'  CCCTCTCCCCTCCCCC      6325      GGC
                                CCCT   CTCCCCTCCCCC
                                ||||   ||||||||||||
                                GGGA   GAGGGGAGGGGG
                                  ___
GAM241   LOC146013 3'  GCTTCTGGCCCTCCCCTCC    6326     C_     _
                                GC  CTGGCC TCCCCTCC
                                ||  |||||| ||||||||
                                CG  GACCGG AGGGGAGG
                                  AA      G
GAM241   LOC146429 5'  TGCGTGGCCTTCCCTCCCC    6327      CC     C
                                TGC  TGGCCT CCCTCCCC
                                |||  |||||| ||||||||
                                ACG  ACCGGA GGGAGGGG
                                  C_     A
GAM241   LOC146488 3'  TGCCCCTCCCTTGCCTCCC    6328        GG   CC
                                TGCCCT  CCT  CCTCCC
                                ||||||  |||  ||||||
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                                ACGGGG  GGA  GGAGGG
                                   AG   AC
GAM241   LOC146714 5'  GCCCTCTGGATCCTCCTCC   6329      __  CC  _
                                GCCCT  GG  TCC CCTCC
                                |||||  ||  ||| |||||
                                CGGGA  CC  AGG GGAGG
                                   GA  T_   A
GAM241   LOC146733 3'  GCCCCGCCCCTCCCC      6330       GCCT
                                GCCCTG   CCCCTCCCC
                                ||||||   |||||||||
                                CGGGGC   GGGGAGGGG
                                     ____
GAM241   LOC146909 3'  CCCCGTCCCCTCCTCC      6331       GCC      _
                                CCCTG   TCCCCTCC CC
                                |||||   |||||||| ||
                                GGGGC   AGGGGAGG GG
                                   ___      A
GAM241   LOC147040 3'  CCCTTCCCATCTCCTCCCCC   6332      GG  _  C
                                CCCT  CC TC CCTCCCCC
                                ||||  || || ||||||||
                                GGGA  GG AG GGAGGGGG
                                  AG  T  A
GAM241   LOC147063 5'  TGCCTTGACCTCCCAGGCTC   6333      C       ___
                                TGCC TGGCCTCCC   CTC
                                |||| |||||||||   |||
                                ACGG ACTGGAGGG   GAG
                                   A        TCC
GAM241   LOC147124 3'  TGCCCGCTCCTCCCCTCTCCC  6334       TGG       _
                                TGCCC   CCTCCCCTC CCC
                                |||||   ||||||||| |||
                                ACGGG   GGAGGGGAG GGG
                                   CGA        A
GAM241   LOC147515 3'  CTAAGCCTCCCCTCTTCC    6335     _        CC
                                CTG GCCTCCCCTC  CC
                                ||| ||||||||||  ||
                                GAT CGGAGGGGAG  GG
                                  T         AA
GAM241   LOC147650 5'  TGACTCTCCATCCTCCCC    6336      _   __
                                TGGC CTCC  CCTCCCC
                                |||| ||||  |||||||
                                ACTG GAGG  GGAGGGG
                                   A   TA
GAM241   LOC147671 3'  TGGTCTCCCCCCCTCTCCC   6337     ___       _
                                TGG   CCTCCCCTC CCC
                                |||   ||||||||| |||
                                ACC   GGGGGGGAG GGG
                                  AGA        A
GAM241   LOC147912 5'  CCCCAGCCTCCTCCCCC    6338     TG     CC
                                CCC  GCCTCC  TCCCCC
                                |||  ||||||  ||||||
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                                GGG  CGGAGG  AGGGGG
                                  GT     __
GAM241   LOC148089 3'  TGCCCTGGCCCATGCCCT    6339          C__
                                TGCCCTGGCCT   CCCT
                                ||||||||||   ||||
                                ACGGGACCGGG   GGGA
                                      TAC
GAM241   LOC148114 5'  ACCCCAGGTCTCCTCTTTCC   6340       _ C    C  CC
                                GCCCT GG CTCC CT  CC
                                ||||| || |||| ||  ||
                                TGGGG CC GAGG GA  GG
                                   T  A    A  AA
GAM241   LOC148529 5'  CCCCCCCCATCCCTCTCCC    6341       GG  _    _
                                CCCT  CC TCCC CTCCC
                                ||||  || |||| |||||
                                GGGG  GG AGGG GAGGG
                                  G_  T    A
GAM241   LOC149086 3'  TGCCCTTCCTCTCCTCC     6342        GG    C
                                TGCCCT  CCTC CCTCC
                                ||||||  |||| |||||
                                ACGGGA  GGAG GGAGG
                                   A_    A
GAM241   LOC149127 3'  ACCTCCCACCTCTCTCCC    6343      _ G     CC
                                GCC CT GCCTC  CTCCC
                                ||| || |||||  |||||
                                TGG GG TGGAG  GAGGG
                                  A  G     A_
GAM241   LOC149276 5'  CCTCTGGCCTCCACCCC     6344     _        CCT
                                CC CTGGCCTCC   CCCC
                                || |||||||||   ||||
                                GG GACCGGAGG   GGGG
                                 A        T__
GAM241   LOC149460 3'  TGACCTCCACCTCTTCCC     6345         _    __
                                TGGCCTCC CCTC  CCC
                                |||||||| ||||  |||
                                ACTGGAGG GGAG  GGG
                                     T    AA
GAM241   LOC149576 3'  CCCGTGACTCCCTCCCCC     6346      _    CTC
                                CCC TGGC   CCCTCCCCC
                                ||| ||||   |||||||||
                                GGG ACTG   GGGAGGGGG
                                  C    A__
GAM241   LOC149722 3'  TGCCCTGGCCTGTAGGTGCCCC 6347           ________
           T                    TGCCCTGGCCT      CCCCT
                                ||||||||||       |||||
                                ACGGGACCGGA      GGGGA
                                      CATCCAC
GAM241   LOC149912 5'  GCCTGGGAACTCCTCTCTTCC  6348      C   C__    C   CC
                                GCC TGG   CTCC CTC  CC
                                ||| |||   |||| |||  ||
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                                CGG ACC   GAGG GAG  GG
                                  _  CTT    A   AA
GAM241   LOC149995 3'  CTAAGCCTCCCCTCTTCC    6335     _        CC
                                CTG GCCTCCCCTC  CC
                                ||| ||||||||||  ||
                                GAT CGGAGGGGAG  GG
                                  T         AA
GAM241   LOC150113 5'  GCGGGGCCTTCCCCTCCTCC   6349     CCT    _     _
                                GC   GGCCT CCCCTCC CC
                                ||   ||||| ||||||| ||
                                CG   CCGGA GGGGAGG GG
                                 CC_    A      A
GAM241   LOC150397 3'  GCCGGCCTCCCTCCC       6350      CT       C
                                GCC  GGCCTCCC TCCC
                                |||  |||||||| ||||
                                CGG  CCGGAGGG AGGG
                                  __      _
GAM241   LOC151174 5'  TGCCCTGGCCCTGTCCCCC    6351           CCCC
                                TGCCCTGGCCT    TCCCCC
                                ||||||||||    ||||||
                                ACGGGACCGGG    AGGGGG
                                      AC__
GAM241   LOC151178 5'  GCTTCCTGCCCCTCCCCC    6352     CCTGG   _
                                GC     CCT CCCCTCCCCC
                                ||     ||| ||||||||||
                                CG     GGA GGGGAGGGGG
                                 AA___   C
GAM241   LOC151878 3'  CTGACCTCCTTCCCTCCTCC   6353          ___     _
                                CTGGCCTCC   CCTCC CC
                                |||||||||   ||||| ||
                                GACTGGAGG   GGAGG GG
                                     AAG     A
GAM241   LOC152179 5'  CCTCCACCTCCTCCCCC     6354      GG  T  _
                                CCT  CC CC CCTCCCCC
                                |||  || || ||||||||
                                GGA  GG GG GGAGGGGG
                                  __  T  A
GAM241   LOC152283 3'  GCCTCCTCCTCCTCTTCCCC   6355     _  GG     C  _
                                GCC CT  CCTCC CT CCCC
                                ||| ||  ||||| || ||||
                                CGG GG  GGAGG GA GGGG
                                  A  A_     A  A
GAM241   LOC152283 3'  CCCCTCCTCCTCTCCTCC    6357      GG     C   _
                                CCCT  CCTCC CTCC CC
                                ||||  ||||| |||| ||
                                GGGG  GGAGG GAGG GG
                                  A_     A    A
GAM241   LOC152283 3'  CCTTCTCCTCCCCTCCTCC    6356      GG_        _
                                CCT   CCTCCCCTCC CC
                                |||   |||||||||| ||
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                                GGA   GGAGGGGAGG GG
                                  AGA         A
GAM241   LOC152633 5'  GCCCTTGGCCCCCTCCC     6358       _   TC
                                GCCCT GGCC  CCCTCCC
                                ||||| ||||  |||||||
                                CGGGA CCGG  GGGAGGG
                                  A   __
GAM241   LOC152698 3'  TGCCTGGCCTGGGCTCCC    6072       C     CCC
                                TGCC TGGCCT   CTCCC
                                |||| ||||||   |||||
                                ACGG ACCGGA   GAGGG
                                  _     CCC
GAM241   LOC152762 3'  CCCGCCCCTCCCCTCCCC    6359       G  _
                                CCTG CC TCCCCTCCCC
                                |||| || ||||||||||
                                GGGC GG AGGGGAGGGG
                                  G  G
GAM241   LOC153146 5'  TGACCAGGCCCCTCCCCC    6360       T__
                                TGGCC   CCCCTCCCCC
                                |||||   ||||||||||
                                ACTGG   GGGGAGGGGG
                                   TCC
GAM241   LOC153196 5'  GCCAGGCTCTCCTCCCC     5934      CT   C  C
                                GCC  GGC TC CCTCCCC
                                |||  ||| || |||||||
                                CGG  CCG AG GGAGGGG
                                  T_  _  A
GAM241   LOC153196 5'  TGCCCTAGGCCAGCCCACCTCT 6361        _   __  _   C
          CC                      TGCCCT GGCC  TCC CCTC CC
                                |||||| ||||  ||| |||| ||
                                ACGGGA CCGG  GGG GGAG GG
                                   T   TC  T   A
GAM241   LOC153396 3'  TAGCCCCTTTCCCTCCCC    6362        ___
                                TGGCCTC   CCCTCCCC
                                |||||||   ||||||||
                                ATCGGGG   GGGAGGGG
                                    AAA
GAM241   LOC154092 3'  TGCCCTGACCTCCCACTC    6363            _
                                TGCCCTGGCCTCCC CTC
                                |||||||||||||| |||
                                ACGGGACTGGAGGG GAG
                                         T
GAM241   LOC154760 3'  GCCTCTGACCCCTCCTCC    6364      _      C
                                GCC CTGGCCTC CCTCC
                                ||| |||||||| |||||
                                CGG GACTGGGG GGAGG
                                  A       A
GAM241   LOC155038 3'  TGCCCCGCCCCTCCCCC     6365        GCCT
                                TGCCCTG   CCCCTCCCCC
                                |||||||   ||||||||||
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                                ACGGGGC   GGGGAGGGGG
                                   ____
GAM241  LOC155434 3'  CGCCCACCCCCCTCCC      6366       TG  T
                                TGCCC  GCC CCCCTCCC
                                |||||  ||| ||||||||
                                GCGGG  TGG GGGGAGGG
                                  __  _
GAM241  LOC157280 3'  TGCCTGGCCTGGGCTCCC    6072      C     CCC
                                TGCC TGGCCT   CTCCC
                                |||| ||||||   |||||
                                ACGG ACCGGA   GAGGG
                                  _     CCC
GAM241  LOC157313 5'  TGCCCGGCAGCCTCCTCC    6367       T  CT  _
                                TGCCC GGC  CC CCTCC
                                ||||| |||  || |||||
                                ACGGG CCG  GG GGAGG
                                  _  TC  A
GAM241  LOC157349 5'  TGCCCCGGCTTCTCAGGAGCCC 6368          __  CCCTC
                                TGCCCTGGC  CTC    CCC
                                |||||||||  |||    |||
                                ACGGGGCCG  GAG    GGG
                                     AA   TCCTC
GAM241  LOC157848 3'  CCCCGCCTCCCCTCTCCC    6369     G        _
                                CCT GCCTCCCCTC CCC
                                ||| |||||||||| |||
                                GGG CGGAGGGGAG GGG
                                  G         A
GAM241  LOC157858 3'  CCCTGCCCTCCCCTCTCC    6371       G       C
                                CCCTG CCTCCCCTC CC
                                ||||| ||||||||| ||
                                GGGAC GGAGGGGAG GG
                                   G        A
GAM241  LOC157858 3'  TGCCCTCCCCTCTCCTTCCC  6370        GG   _  C
                                TGCCCT  CCTC CC TCCC
                                ||||||  |||| || ||||
                                ACGGGA  GGAG GG AGGG
                                    GG    A  A
GAM241  LOC157931 3'  TGCCCTAAGTTCTCTCCTCC  6372         C__  C
                                TGCCCTGG   CTC CCTCC
                                ||||||||   ||| |||||
                                ACGGGATT   GAG GGAGG
                                     CAA   A
GAM241  LOC158572 3'  TGCTGCCCCCCTCCCC      6373      CCTG  T
                                TGC    GCC CCCCTCCCC
                                |||    ||| |||||||||
                                ACG    CGG GGGGAGGGG
                                  A___   _
GAM241  LOC158955 3'  GCCCTGGCTTCCCGCCTC    6201         C   __
                                GCCCTGGC TCCC  CTC
                                |||||||| ||||  |||
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                                CGGGACCG AGGG  GAG
                                     A    CG
GAM241   LOC159053 3'  GCCTTGGCCTCCCAAAGTCC   5967      C        C___
                                GCC TGGCCTCCC    TCC
                                ||| |||||||||    |||
                                CGG ACCGGAGGG    AGG
                                  A        TTTC
GAM241   LOC162417 3'  GCACCCTCCCCTCCCC      6374     CCT G
                                GC   G CCTCCCCTCCCC
                                ||   | ||||||||||||
                                CG   T GGAGGGGAGGGG
                                 ___ G
GAM241   LOC163682 3'  GCCCCTCGCGGTCTTCCCTTCC 6375       _____  C  C    C
           C                     GCCCT    GG CT CCCT CCC
                                |||||    || || |||| |||
                                CGGGG    CC GA GGGA GGG
                                   AGCG  A  A    A
GAM241   LOC163895 5'  CGCTTCGGCTTTCTCCTCCC   6376     CC    C_  C
                                TGC  TGGC  TC CCTCCC
                                |||  ||||  || ||||||
                                GCG  GCCG  AG GGAGGG
                                  AA    AA  A
GAM241   LOC164584 5'  TGCCCTGGACTTCGACCTC    6377          _ C  C_
                                TGCCCTGG C TC  CCTC
                                |||||||| | ||  ||||
                                ACGGGACC G AG  GGAG
                                     T A  CT
GAM241   LOC164714 5'  GCTCCCGGCCTCCTCCC      6378     _         CC
                                GC CCTGGCCTCC  TCCC
                                || ||||||||||  ||||
                                CG GGGCCGGAGG  AGGG
                                 A         __
GAM241   LOC167837 5'  GCTCTGACCTCTCTCCC      6379     C        CC
                                GC CTGGCCTC  CTCCC
                                || ||||||||  |||||
                                CG GACTGGAG  GAGGG
                                 A       A_
GAM241   LOC169981 5'  TGCCTGCAGTAACCTTCCTCC  6380       C_____      CC
                                TGCC     TGGCCT  CCTCC
                                ||||     ||||||  |||||
                                ACGG     ATTGGA  GGAGG
                                   ACGTC      A_
GAM241   LOC170127 3'  TGACCTCCACCTTTCCCC     6381          _  __
                                TGGCCTCC CC  TCCCC
                                |||||||| ||  |||||
                                ACTGGAGG GG  AGGGG
                                     T  AA
GAM241   LOC170370 3'  ACCCTGGTCCTCTCTCCC     6382          _    CC
                                GCCCTGG CCTC  CTCCC
                                ||||||| ||||  |||||
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                                TGGGACC GGAG  GAGGG
                                   A    A_
GAM241   LOC195977 5'  TGCCTGGCCCTTCCCCC     6383      C     CCCC
                                TGCC TGGCCT    TCCCCC
                                |||| ||||||    ||||||
                                ACGG ACCGGG    AGGGGG
                                  _     A___
GAM241   LOC196047 5'  GCCCTGGCCTTCCGGCCT    6384          _ __
                                GCCCTGGCCT CC  CCT
                                |||||||||| ||  |||
                                CGGGACCGGA GG  GGA
                                      A  CC
GAM241   LOC196205 3'  CGTCCCTCTCCCCTCTTCC   6385     _   GGC       CC
                                TG CCCT   CTCCCCTC  CC
                                || ||||   ||||||||  ||
                                GC GGGA   GAGGGGAG  GG
                                 A   ____       AA
GAM241   LOC196540 3'  TGCCTGGCCCAAGCCCCT    6386      C     ___
                                TGCC TGGCCT   CCCCT
                                |||| ||||||   |||||
                                ACGG ACCGGG   GGGGA
                                  _     TTC
GAM241   LOC196955 5'  GCTTGGCCTTTTCCCTCCCC  6387     CC     C__
                                GC  TGGCCT   CCCTCCCC
                                ||  ||||||   ||||||||
                                CG  ACCGGA   GGGAGGGG
                                 A_     AAA
GAM241   LOC197273 5'  GCCCTGCTCCCTCTCCC     6388       GC    _
                                GCCCTG  CTCCC CTCCC
                                ||||||  ||||| |||||
                                CGGGAC  GAGGG GAGGG
                                   __     A
GAM241   LOC199936 3'  GCCTGTGGGCTCCCCTCCCCC 6389      C_   C
                                GCC  TGG CTCCCCTCCCCC
                                |||  ||| ||||||||||||
                                CGG  ACC GAGGGGAGGGGG
                                  AC   C
GAM241   LOC200222 5'  TGCCCTGGTGTGTCCAGTCTTT 6390      CC__   CC____     CIII
            CCCCG                  CTGG    TCC     TCCCC    G
                                ||||   |||     |||||   |
                                GACC    AGG     AGGGG    C
                                  ACAC   TCAGAA    IIIC
GAM241   LOC201181 5'  TGCCCCCCAACCCCCTCCCC   6391       GG  __
                                TGCCCT  CC  TCCCCTCCCC
                                ||||||  ||  ||||||||||
                                ACGGGG  GG  GGGGGAGGGG
                                   __ TT
GAM241   LOC201324 5'  TGCCTGGCGTACCCTCCC    6392      C    CTC
                                TGCC TGGC   CCCTCCC
                                |||| ||||   |||||||
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                                ACGG ACCG   GGGAGGG
                                  _   CAT
GAM241   LOC201382 5'  CGCCGGGTCCCCTCTCCC    6393      CT  CC     _
                                TGCC  GG  TCCCCTC CCC
                                ||||  ||  ||||||| |||
                                GCGG  CC  AGGGGAG GGG
                                  C_ ___      A
GAM241   LOC202025 5'  TGCCTGCACCCTCCCCTCCCC  6394      CT_ G
                                TGCC   G CCTCCCCTCCCC
                                ||||   | ||||||||||||
                                ACGG   T GGAGGGGAGGGG
                                  ACG G
GAM241   LOC203392 5'  GCCTTCTGCGCCCCCTCCCC   6395     CTG_  C
                                GCC    GC TCCCCTCCCC
                                |||    || ||||||||||
                                CGG    CG GGGGGAGGGG
                                  AAGA  C
GAM241   LOC205143 5'  TGCCCTGGTCCGCCAACTCC   6396        _  T  C_
                                TGCCCTGG CC CC  CTCC
                                |||||||| || ||  ||||
                                ACGGGACC GG GG  GAGG
                                     A  C  TT
GAM241   LOC219686 5'  GCCTCGGCCTCCTCCTCC    6397      C       _
                                GCC TGGCCTCC CCTCC
                                ||| |||||||| |||||
                                CGG GCCGGAGG GGAGG
                                  A       A
GAM241   LOC219700 3'  GCCCTGCACCCCCCTCTCCC   6398        _      _
                                GCCCTG GCCTCCC CTCCC
                                |||||| ||||||| |||||
                                CGGGAC TGGGGGG GAGGG
                                   G      A
GAM241   LOC219701 3'  GCCCTGCACCCCCCTCTCCC   6398        _      _
                                GCCCTG GCCTCCC CTCCC
                                |||||| ||||||| |||||
                                CGGGAC TGGGGGG GAGGG
                                   G      A
GAM241   LOC219899 5'  CTGCGCCTCTCCTCCCCC    6399      _    C
                                CTG GCCTC CCTCCCCC
                                ||| ||||| ||||||||
                                GAC CGGAG GGAGGGGG
                                  G    A
GAM241   LOC219920 5'  TGCCCTGGCCCCCAGGCC    6400            CCT
                                TGCCCTGGCCTCC   CC
                                ||||||||||||   ||
                                ACGGGACCGGGGG   GG
                                        TCC
GAM241   LOC219920 3'  GCCCCACCCCTCCCC       6027        GCCT
                                GCCCTG   CCCCTCCCC
                                ||||||   |||||||||
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                                CGGGGT   GGGGAGGGG
                                   ____
GAM241  LOC219920 5'  GCCCAGTGTCCCTTCCCCC   6401     T  CC   C
                                GCCC GG  TCCC TCCCCC
                                |||| ||  |||| ||||||
                                CGGG TC  AGGG AGGGGG
                                  _ AC   A
GAM241  LOC220003 3'  TGCCCTGGGGATGGGCCTCTCC 6402       _______    C
          T                      TGCCCT     GGCCTC CCT
                                 ||||||     |||||| |||
                                 ACGGGA     CCGGAG GGA
                                    CCCCTAC     A
GAM241  LOC220020 5'  TACCCTGGCTCGGCCCC    6403        C  CCCT
                                TGCCCTGGC TC   CCCC
                                ||||||||| ||   ||||
                                ATGGGACCG AG   GGGG
                                     _ CC__
GAM241  LOC220758 5'  CCTGGCCTCGGTCCCCC    5874        CCC
                                CCTGGCCTC  TCCCCC
                                |||||||||  ||||||
                                GGACCGGAG  AGGGGG
                                     CC_
GAM241  LOC221092 3'  TGCTTGAGCACCCTCCCCC   6404    CCT  CTC
                                TGC  GGC  CCCTCCCCC
                                |||  |||  |||||||||
                                ACG  TCG  GGGAGGGGG
                                  AAC  T__
GAM241  LOC221410 3'  TGCTTGGCCTCCAGCCTC    6405    CC     __
                                TGC  TGGCCTCC  CCTC
                                |||  ||||||||  ||||
                                ACG  ACCGGAGG  GGAG
                                  A_      TC
GAM241  LOC221474 5'  TGCCCGGCCCTGCTTCCCTC  6406     T    C____
                                TGCCC GGCCT    CCCTC
                                ||||| |||||    |||||
                                ACGGG CCGGG    GGGAG
                                   _    ACGAA
GAM241  LOC221540 3'  TGCGTACCCCCCTCCCCC    6407    CCTG  T
                                TGC   GCC CCCCTCCCCC
                                |||   ||| ||||||||||
                                ACG   TGG GGGGAGGGGG
                                  CA__  _
GAM241  LOC221683 5'  GCTTAACGATCCCTCCCCC   6408    CC   CTC
                                GC  TGGC   CCCTCCCCC
                                ||  ||||   |||||||||
                                CG  ATTG   GGGAGGGGG
                                 A_   CTA
GAM241  LOC221895 3'  TGCCAGCCCCTCCTCC      5892     CT    C
                                TGCC  GGCCTC CCTCC
                                ||||  |||||| |||||
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                                ACGG  TCGGGG GGAGG
                                  __     A
GAM241   LOC221935 3'  ACCCTCCACTCCCTCTCCC   6409      GGC    _
                                GCCCT   CTCCC CTCCC
                                |||||   ||||| |||||
                                TGGGA   GAGGG GAGGG
                                   GGT    A
GAM241   LOC222255 3'  GCAGCTCTCCCCTCCCC    6410    CCT   _
                                GC   GGC CTCCCCTCCCC
                                ||   ||| ||||||||||
                                CG   TCG GAGGGGAGGGG
                                 ___   A
GAM241   LOC253502 3'  TGCCTTGCTGGCCCTCCCCC   5839     ___     TCCC
                                TGCC   CTGGCC    CTCCCCC
                                ||||   ||||||    |||||||
                                ACGG   GACCGG    GAGGGGG
                                  AAC     ____
GAM241   LOC253681 3'  CCCTTCCCATCTCCTCCCCC   6332     GG  _  C
                                CCCT  CC TC CCTCCCCC
                                ||||  || || ||||||||
                                GGGA  GG AG GGAGGGGG
                                  AG  T  A
GAM241   LOC253891 3'  TGCCCCCGGCCCCTCCCC    6411      _   TCC
                                TGCCCT GGCC   CCTCCCC
                                |||||| ||||   |||||||
                                ACGGGG CCGG   GGAGGGG
                                   G   ___
GAM241   LOC253897 3'  CTGGCCTCTTCCCCTCCC    6317      ___
                                CTGGCC   TCCCCTCCC
                                ||||||   |||||||||
                                GACCGG   AGGGGAGGG
                                   AGA
GAM241   LOC254266 5'  GCCCTGGCAGCTCCCCC    6413       CTCCC
                                GCCCTGGC    CTCCCCC
                                ||||||||    |||||||
                                CGGGACCG    GAGGGGG
                                     TC___
GAM241   LOC254266 5'  TGCCTGGCCTCCTGGCCCC   6412     C      CCT
                                TGCC TGGCCTCC   CCCC
                                |||| ||||||||   ||||
                                ACGG ACCGGAGG   GGGG
                                  _       ACC
GAM241   LOC254532 5'  GCCCTGGCTGGTCCCCCTCCTC 6414        C___      _
           C                     GCCCTGGC    TCCCCTCC CC
                                ||||||||    |||||||| ||
                                CGGGACCG    GGGGGAGG GG
                                     ACCA       A
GAM241   LOC254532 5'  TGGTCCCCCTCCTCCTCC    6415     _    _    _
                                TGG CCTCC CCTCC CC
                                ||| ||||| ||||| ||
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                                ACC GGGGG GGAGG GG
                                  A    A    A
GAM241  LOC254842 5'  TGCCCTGGCCCCTTTCC    6416          T  CC
                                TGCCCTGGCC CC  TCC
                                |||||||||| ||  |||
                                ACGGGACCGG GG  AGG
                                      _  AA
GAM241  LOC254892 5'  GCCCGGCCCCTCCCC      6417      T   TCC
                                GCCC GGCC   CCTCCCC
                                |||| ||||   |||||||
                                CGGG CCGG   GGAGGGG
                                  _   ____
GAM241  LOC255146 3'  GCTCCTTCCCCTCCTCC    6418    _  GGCC      _
                                GC CCT    TCCCCTCC CC
                                || |||    |||||||| ||
                                CG GGA    AGGGGAGG GG
                                 A  _____       A
GAM241  LOC255242 3'  GCCCTTCCATTCCCCTCCC   6223      GG __
                                GCCCT  CC  TCCCCTCCC
                                |||||  ||  |||||||||
                                CGGGA  GG  AGGGGAGGG
                                   A_  TA
GAM241  LOC255448 3'  TGCCTGGCCTGGGCTCCC    6072      C     CCC
                                TGCC TGGCCT   CTCCC
                                |||| ||||||   |||||
                                ACGG ACCGGA   GAGGG
                                   _     CCC
GAM241  LOC255481 3'  TGCCCTGGTCCTGTCACCCC  6419        _  CCCCT
                                TGCCCTGG CCT    CCCC
                                |||||||| |||    ||||
                                ACGGGACC GGA    GGGG
                                     A  CAGT_
GAM241  LOC255486 3'  TGCCCCGGCGCCCCTTCCCC  6420         CT   _
                                TGCCCTGGC  CCCCT CCCC
                                |||||||||  ||||| ||||
                                ACGGGGCCG  GGGGA GGGG
                                     C_    A
GAM241  LOC256273 3'  TGCCCTGGTCTGGACTCCCCC 6421         C  CCC
                                TGCCCTGG CT   CTCCCCC
                                |||||||| ||   |||||||
                                ACGGGACC GA   GAGGGGG
                                     A  CCT
GAM241  LOC256474 5'  TGCGCCTTCTCCCCTCCTCC  6422    _  GGC      _
                                TGC CCT   CTCCCCTCC CC
                                ||| |||   |||||||| ||
                                ACG GGA   GAGGGGAGG GG
                                  C  A__       A
GAM241  LOC256790 5'  TGCCCTGAGCCACTCCC     6423        _  TCCC
                                TGCCCTG GCC    CTCCC
                                ||||||| |||    |||||
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                                ACGGGAC CGG   GAGGG
                                   T  T___
GAM241  LOC256982 5'  CCCCCGCCTTCCTCCTCTCCTC 6424      G  _ _  _ _
            C                   CCCT GCCT CC CCTC CC CC
                                |||| |||| || |||| || ||
                                GGGG CGGA GG GGAG GG GG
                                  G   A A   A A
GAM241  LOC257319 3'  CCTAACAGATCCCCTCCCCC  6425       C__
                                CCTGGC  TCCCCTCCCCC
                                ||||||  ||||||||||
                                GGATTG  AGGGGAGGGGG
                                   TCT
GAM241  LOC257442 5'  TGCCCTGGCCTGAAGTCTCCC  6426          CCC__
                                TGCCCTGGCCT   CTCCC
                                ||||||||||    |||||
                                ACGGGACCGGA   GAGGG
                                      CTTCA
GAM241  LOC257545 3'  TGCGTACCCCCCTCCCCC   6407     CCTG  T
                                TGC   GCC CCCCTCCCCC
                                |||   ||| ||||||||||
                                ACG   TGG GGGGAGGGGG
                                  CA__  _
GAM241  LOC257554 3'  TGCCCTGGTCTCCTCCACCCC  6111        C  _ T
                                TGCCCTGG CTCC CC CCCC
                                |||||||| |||| || ||||
                                ACGGGACC GAGG GG GGGG
                                    A   A T
GAM241  LOC257598 3'  TGCGTACCCCCCTCCCCC   6407     CCTG  T
                                TGC   GCC CCCCTCCCCC
                                |||   ||| ||||||||||
                                ACG   TGG GGGGAGGGGG
                                  CA__  _
GAM241  LOC51087  5'  GCCCCGGCCCCTCCCCC    6427        TCC
                                GCCCTGGCC  CCTCCCCC
                                |||||||||  ||||||||
                                CGGGGCCGG  GGAGGGGG
                                     ___
GAM241  LOC51195  3'  CTCTGCCATCCCCCTCCCCC  6428    G_  __
                                CT  GCC  TCCCCTCCCCC
                                ||  |||  ||||||||||
                                GA  CGG  GGGGGAGGGGG
                                 GA  TA
GAM241  LOC51320  3'  CCCTCCTCCCTCCCC      5882      GG    C
                                CCCT  CCTCCC TCCCC
                                ||||  |||||| |||||
                                GGGA  GGAGGG AGGGG
                                   __    _
GAM241  LOC51667  3'  TGCCCTGGACACCTTCCCC   6429        CCT  CC
                                TGCCCTGG   CC  TCCCC
                                ||||||||   ||  |||||
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                                ACGGGACC   GG  AGGGG
                                    TGT  A_
GAM241  LOC54550  5' GCCCCCCTTCCCTCTCCC    6430      GG   C    _
                                GCCCT  CCT CCCTC CCC
                                |||||  ||| ||||| |||
                                CGGGG  GGA GGGAG GGG
                                   __  A    A
GAM241  LOC56181  3' TGCTCTTTCCCCCTCCTCC   6431     C  GG    _
                                TGC CT  CCTCC CCTCC
                                ||| ||  ||||| |||||
                                ACG GA  GGGGG GGAGG
                                  A  AA    A
GAM241  LOC56961  5' GCTCCCGGCCCCTCTCCC    6433    _     T  C
                                GC CCTGGCC CC CTCCC
                                || ||||||| || |||||
                                CG GGGCCGG GG GAGGG
                                 A      _ A
GAM241  LOC56961  5' CCCCGCCCCTCCCCTCCCCC  6432      G  _
                                CCCTG CC TCCCCTCCCCC
                                ||||| || ||||||||||
                                GGGGC GG AGGGGAGGGGG
                                   G  G
GAM241  LOC57106  3' TGCTCGGCCTCCTCTCCCCC  6434     CC       C
                                TGC  TGGCCTCC CTCCCCC
                                |||  |||||||| |||||||
                                ACG  GCCGGAGG GAGGGGG
                                  A_       A
GAM241  LOC57805  3' TGCCCTGGCTCCCAGGTCTC  6436         C   ____
                                TGCCCTGGC TCCC    CTC
                                ||||||||| ||||    |||
                                ACGGGACCG AGGG    GAG
                                      _   TCCA
GAM241  LOC57805  5' CCTTTGGCCTCCGATCCTCC  6435     C_      ___
                                CC  TGGCCTCC   CCTCC
                                ||  ||||||||   |||||
                                GG  ACCGGAGG   GGAGG
                                 AA       CTA
GAM241  LOC90525  3' TGCCCGAGCCCCTCCCC     6437       T   TCC
                                TGCCC GGCC   CCTCCCC
                                ||||| ||||   |||||||
                                ACGGG TCGG   GGAGGGG
                                   C   ___
GAM241  LOC90589  5' TGTCCTGGCCTCCTCTCC    6438     C        C
                                TG CCTGGCCTCC CTCC
                                || ||||||||| ||||
                                AC GGACCGGAGG GAGG
                                 A         A
GAM241  LOC90777  3' TGCACTGACCTCCTTCTCC   6439      C       C_
                                TGC CTGGCCTCC  CTCC
                                ||| |||||||||  ||||
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                                ACG GACTGGAGG  GAGG
                                  T       AA
GAM241  LOC90829  3' TGCTATCCCTCCCCTCTCCC  6440     CCTGG      _
                                TGC    CCTCCCCTC CCC
                                |||    ||||||||| |||
                                ACG    GGAGGGGAG GGG
                                  ATAG_       A
GAM241  LOC90987  5' TGCCCTGGCCTGAAGTCTCCC  6426          CCC__
                                TGCCCTGGCCT    CTCCC
                                ||||||||||    |||||
                                ACGGGACCGGA    GAGGG
                                      CTTCA
GAM241  LOC91056  3' GCCCAGGCCCGTCTTTCCTCTC 6441      T   _______  C
          C                     GCCC GGCC     TCC CTCC
                                |||| ||||     ||| ||||
                                CGGG CCGG     AGG GAGG
                                  T   GCAGAA   A
GAM241  LOC91409  3' TGCCCTGGTGCTGGCTGTTCCC 6442        C_  CCCC__
          C                     TGCCCTGG  CT     TCCCC
                                ||||||||  ||     |||||
                                ACGGGACC  GA     AGGGG
                                    AC  CCGACA
GAM241  LOC91663  5' GCCCCGCCCCCTCCCC     6443       GCC
                                GCCCTG   TCCCCTCCCC
                                ||||||   ||||||||||
                                CGGGGC   GGGGGAGGGG
                                   ___
GAM241  LOC91960  3' TACCCTGCCCCCCTCTTCC   6444       G  T     CC
                                TGCCCTG CC CCCCTC  CC
                                ||||||| || ||||||  ||
                                ATGGGAC GG GGGGAG  GG
                                   _ _     AA
GAM241  LOC92162  5' CTTTCCTGCCCCTCCCCC    6445     GG  _
                                CT  CCT CCCCTCCCCC
                                ||  ||| ||||||||||
                                GA  GGA GGGGAGGGGG
                                 AA   C
GAM241  LOC92340  3' CCCTGGCCTTGGCTCCCC    6446         CCC
                                CCCTGGCCT   CTCCCC
                                |||||||||   ||||||
                                GGGACCGGA   GAGGGG
                                     ACC
GAM241  LOC92499  3' CCTAATGCTTTCCCTCCCCC   6447      __ CTC
                                CCTG  GC   CCCTCCCCC
                                ||||  ||   |||||||||
                                GGAT  CG   GGGAGGGGG
                                  TA  AAA
GAM241  LOC92568  3' CCCTCCCCCCTCCTCC      6448      GGC       _
                                CCCT   CTCCCCTCC CC
                                ||||   |||||||| ||
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                                GGGA  GGGGGGAGG GG
                                  ___       A
GAM241  LOC96597  3'  TGCCTCTGGTGCCTCTCTC   6449      _  __    CC
                                TGCC CTG  GCCTC  CTC
                                |||| |||  |||||  |||
                                ACGG GAC  CGGAG  GAG
                                  A  CA    A_
GAM242  CAV2      3'  ATCTACTTTCACATTTATTT  6452     _      GTG
                                ATC ACTTTCACG  ATTT
                                ||| |||||||||  ||||
                                TAG TGAAAGTGT  TAAA
                                  A       AAA
GAM242  CENPB     3'  ACTTCCACGGTGGGGGGCCTCT 6453           ATTTA_
                                ACTTTCACGGTG     TTCT
                                ||||||||||||     ||||
                                TGAAGGTGCCAC     GAGA
                                       CCCCCG
GAM242  GPR63     3'  ATCACTTTCCTATTATTTATTC 6454         ACG  G
           T                    ATCACTTTC  GT ATTTATTCT
                                |||||||||  || |||||||||
                                TAGTGAAAG  TA TAAATAAGA
                                     GA_  A
GAM242  HGF       3'  ATCATGACAAGTGATTTATT  6455      CTTT  C
                                ATCA   CA GGTGATTTATT
                                ||||   || ||||||||||
                                TAGT   GT TCACTAAATAA
                                  ACT_  _
GAM242  POLR2E    3'  CTTTCACAGGCACGTTTATT  6456       _   A_
                                CTTTCAC GGTG  TTTATT
                                ||||||| ||||  ||||||
                                GAAAGTG CCGT  AAATAA
                                    T   GC
GAM242  ZNF36     3'  ATCACTTTCGTGGAGCCAATCT 6457         AC  TGAT  T
                                ATCACTTTC  GG   TTA TCT
                                |||||||||  ||   ||| |||
                                TAGTGAAAG  CC   GGT AGA
                                     CA  TC__   T
GAM242  CART      3'  TCACTTAGGGTGATTTATT   6458       TCAC
                                TCACTT   GGTGATTTATT
                                ||||||   ||||||||||||
                                AGTGAA   CCACTAAATAA
                                   TC__
GAM242  FLJ10546  3'  ATCATTTTTGCAGTGATC    6459      C  CA
                                ATCA TTT  CGGTGATT
                                |||| |||  ||||||||
                                TAGT AAA  GTCACTAG
                                  A  AC
GAM242  FLJ12643  3'  ATCACTTTCAGAATGTTC    6460         CG  A
                                ATCACTTTCA  GTG TTT
                                ||||||||||  ||| |||
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                                TAGTGAAAGT  TAC AAG
                                     CT  _
GAM242  FLJ21159  3'  TCACTTTCAATTCTTTTTATTC 6461          CGGTGA
            T                    TCACTTTCA     TTTATTCT
                                 |||||||||     ||||||||
                                 AGTGAAAGT     AAATAAGA
                                     TAAGAA
GAM242  KIAA0863  3'  CTTTCAATGTTTATTC      6462        CG   A
                                 CTTTCA  GTG TTTATTC
                                 |||||||  ||| |||||||
                                 GAAAGT  TAC AAATAAG
                                   __  _
GAM242  MRPL13    3'  ATCACTTCACTGTTATTT    6463         T  G  G
                                 ATCACTT CAC GT ATTT
                                 ||||||| ||| || ||||
                                 TAGTGAA GTG CA TAAA
                                    _  A  A
GAM242  PTD015    3'  CACTTAGTGATTTATTC     6464        TCAC
                                 CACTT   GGTGATTTATTC
                                 |||||   ||||||||||||
                                 GTGAA   TCACTAAATAAG
                                   _____
GAM242  TRIM36    3'  ACCACTTTTATGGTGTTT    6465         CAC   A
                                 ATCACTTT   GGTG TTT
                                 ||||||||   |||| |||
                                 TGGTGAAA   CCAC AAA
                                     ATA   _
GAM242  LOC123016 3'  TTTACACAATGATTTATT    6466     _
                                 TTT CACGGTGATTTATT
                                 ||| ||||||||||||||
                                 AAA GTGTTACTAAATAA
                                   T
GAM242  LOC145790 5'  ATCACTTTTACAGTGACTT   6467          C
                                 ATCACTTT ACGGTGATTT
                                 |||||||| ||||||||||
                                 TAGTGAAA TGTCACTGAA
                                     A
GAM242  LOC152313 3'  ATCACTTTGGTGCTGTTC    6468         CAC   ATTTA
                                 ATCACTTT   GGTG    TTC
                                 ||||||||   ||||    |||
                                 TAGTGAAA   CCAC    AAG
                                     ___    GAC__
GAM242  LOC154850 3'  CACTTTTACAACTTATTC    6469         C  GGT
                                 CACTTT AC   GATTTATTC
                                 |||||| ||   |||||||||
                                 GTGAAA TG   TTGAATAAG
                                    A  ___
GAM242  LOC158434 3'  TCCTTCCCAGTGGTTTATTCT  6470     A    A    A
                                 TC CTTTC CGGTG TTTATTCT
                                 || ||||| ||||| ||||||||
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                                AG GAAGG GTCAC AAATAAGA
                                 _   _    C
GAM242  LOC255654 3'  CACTTATGATTTATTC     6471      TCACG
                                CACTT   GTGATTTATTC
                                |||||   ||||||||||
                                GTGAA   TACTAAATAAG
                                  _____
GAM243  IL1A    3'  GAACTGTCAACACTGC      6474        TC  G
                                GAACTGTC  AAC ACTGC
                                ||||||||  ||| |||||
                                CTTGACAG  TTG TGACG
                                    __  _
GAM243  FLJ22009 3'  CGCTGTTTTGACGACTGCA  6475    AA   CTCA
                                CG  CTGT   ACGACTGCA
                                ||  ||||   |||||||||
                                GC  GACA   TGCTGACGT
                                 __   AAAC
GAM243  KIAA0022 5'  TAACAACTGTCTTGGAACTG  6476     G      CAAC
                                TAAC AACTGTCT   GACTG
                                |||| ||||||||   |||||
                                ATTG TTGACAGA   TTGAC
                                  _      ACC_
GAM243  KIAA0159 5'  CAAATCTCAACGGCTGCA   6477     ACT      A
                                CGA  GTCTCAACG CTGCA
                                |||  ||||||||| |||||
                                GTT  TAGAGTTGC GACGT
                                 ___       C
GAM243  SLIT1   3'  CGACTGTCTCCGCTGC     6478     A     AA  A
                                CGA CTGTCTC  CG CTGC
                                ||| |||||||  || ||||
                                GCT GACAGAG  GC GACG
                                  _     __ _
GAM243  TDPGD   3'  ACAACTGTCTCGACTA     6479    G       AAC
                                AC AACTGTCTC   GACTG
                                || |||||||||   |||||
                                TG TTGACAGAG   CTGAT
                                  _      ___
GAM244  RBBP9   3'  TGTATAAGTTTCTTTTTTA   6482    CT        C
                                TG  TAAGTTTCTTTT TA
                                ||  ||||||||||||| ||
                                AC  ATTCAAAGAAAA AT
                                 AT          A
GAM244  TAC1    5'  GGGTGCTGAGTTTCTCT     6483    A   TA
                                GG TGCT  AGTTTCTTT
                                || ||||  |||||||||
                                CC ACGA  TCAAAGAGA
                                 C   C_
GAM244  TAC1    5'  GGGTGCTGAGTTTCTCT     6483    A   TA
                                GG TGCT  AGTTTCTTT
                                || ||||  |||||||||
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                                CC ACGA  TCAAAGAGA
                                 C   C_
GAM244  TAC1     5'  GGGTGCTGAGTTTCTCT    6483    A   TA
                                GG TGCT  AGTTTCTTT
                                || ||||  |||||||||
                                CC ACGA  TCAAAGAGA
                                 C   C_
GAM244  TAC1     5'  GGGTGCTGAGTTTCTCT    6483    A   TA
                                GG TGCT  AGTTTCTTT
                                || ||||  |||||||||
                                CC ACGA  TCAAAGAGA
                                 C   C_
GAM244  ELAC1    3'  AGGATGCTGGGTTTTTTTTCT 6484        TAA   C
                                AGGATGCT   GTTT TTTTCT
                                ||||||||   |||| ||||||
                                TCCTACGA   CAAA AAAAGA
                                     CC_   A
GAM244  KIAA0090 3'  AGATGCCTGTTTTTTTCT    6485        AA   C
                                GGATGCTT  GTTT TTTTCT
                                ||||||||  |||| ||||||
                                TCTACGGA  CAAA AAAAGA
                                    __   _
GAM244  KIAA0553 3'  AGGATCTTCTTTTCT      6486      GCTTAAG
                                AGGAT     TTTCTTTTCT
                                |||||     ||||||||||
                                TCCTA     GAAGAAAAGA
                                   _______
GAM244  KIAA1223 3'  AGTATGTTTAAGTTTCTTT   6487    G   C
                                AG ATG TTAAGTTTCTTT
                                || ||| ||||||||||||
                                TC TAC AATTCAAAGAAA
                                 A   A
GAM244  KIAA1545 3'  AAGAAGCAAAAGTTTCTTTT  6488      T  TT
                                AGGA GC  AAGTTTCTTTT
                                |||| ||  ||||||||||
                                TTCT CG  TTCAAAGAAAA
                                  T  TT
GAM244  SP192    5'  AGGGTGCTTAAGTAACCT    6489     A       TT
                                AGG TGCTTAAGT  CTT
                                ||| |||||||||  |||
                                TCC ACGAATTCA  GGA
                                  C        TT
GAM244  LOC124997 3'  GGATGCTTAAGTCTTCCTCT  6490            C
                                GGATGCTTAAGTTT TTTTCT
                                |||||||||||||| ||||||
                                CCTACGAATTCAGA AGGAGA
                                    _
GAM244  LOC145815 5'  AGGATGTTAGGTTTCTTT    6491       C   A
                                AGGATG TTA GTTTCTTT
                                |||||| ||| ||||||||
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                                TCCTAC AAT CAAAGAAA
                                   _  C
GAM244  LOC205272 5'  AGGATGTTGGAGAGGTTTTCTA 6492       CTTA  TTTC
           G                    AGGATG   AG   TTTTCTAG
                                ||||||   ||   ||||||||
                                TCCTAC   TC   AAAAGATC
                                   AACC  TCC_
GAM244  LOC255552 5'  AGGATGCTGTACTTTTCT    6493        TAA  TT
                                AGGATGCT   GT  CTTTTCT
                                ||||||||   ||  |||||||
                                TCCTACGA   CA  GAAAAGA
                                     ___   T_
GAM244  LOC91355  5'  AGGATGCTGAGGTGATTCTAG  6494        TAA  TTCTT
                                AGGATGCT   GT    TTCTAG
                                ||||||||   ||    ||||||
                                TCCTACGA   CA    AAGATC
                                     CTC  CT___
GAM244  LOC92270  5'  AGGAGCCTACTTTTTTTTTCTA 6495      T    AG   C
           G                    AGGA GCTTA  TTT TTTTCTAG
                                ||||  |||||  |||  ||||||||
                                TCCT CGGAT  AAA AAAAGATC
                                   _    GA   A
GAM245  SLC17A5   3'  CATAGAACAGGCTGGGCACA   6498     TA       ACAT
                                CAT  AACAGGCTGG   GCGCG
                                |||  ||||||||||   |||||
                                GTA  TTGTCCGACC   CGTGT
                                  TC        _____
GAM245  EML4      3'  CATTAAATAGCTGGAACG    6499        CA     CAT
                                CATTAAA  GGCTGGA   GCG
                                |||||||  |||||||   |||
                                GTAATTT  TCGACCT   TGC
                                   A_      ___
GAM245  FLJ20752  5'  CATTAGCCACAGCGCATGCGCG 6500       AA  _   TGGA
                                CATTA  CA GGC    CATGCGCG
                                |||||  || |||    ||||||||
                                GTAAT  GT TCG    GTACGCGC
                                   CG  G   C___
GAM245  LOC148479 3'  CATTAACAGGCTGGGGAAACCG 6501        A      ACAT  G
                                CATTAA CAGGCTGG    GC CG
                                ||||||| ||||||||   || ||
                                GTAATT GTCCGACC    TG GC
                                   _       CCTT  _
GAM246  ASTN      3'  CAGAACTGGGTATCCCAGAGT  6504        AT   CAG
                                CAGAACT  GTAT   CCTAGAGT
                                |||||||  ||||   ||||||||
                                GTCTTGA  CATA   GGGTCTCA
                                   CC    ____
GAM246  BMP1      3'  CAGAACTTGCCATGCAGCTTGG 6505        A  AT__   CTA
           AGT                    CAGAACT TGT    CAGC   GAGT
                                |||||||  |||    ||||   ||||
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                                GTCTTGA ACG   GTCG  CTCA
                                   _  GTAC   AAC
GAM246  BMP1     3'  CAGAACTTGCCATGCAGCTTGG 6505       A  AT__   CTA
            AGT                   CAGAACT TGT   CAGC  GAGT
                                  ||||||| |||   ||||  ||||
                                  GTCTTGA ACG   GTCG  CTCA
                                     _  GTAC   AAC
GAM246  HMOX2    3'  CAGAAGTGTGGAAGCCTGGAGT 6506      CTA  ATC   A
                                  CAGAA  TGT  AGCCT GAGT
                                  |||||  |||  ||||| ||||
                                  GTCTT  ACA  TCGGA CTCA
                                    C__  CCT   C
GAM246  PRSS16   3'  CAGAATCATGAATCCCTAGAGT 6507      C   T  AG
                                  CAGAA TATG ATC  CCTAGAGT
                                  ||||| |||| |||  ||||||||
                                  GTCTT GTAC TAG  GGATCTCA
                                    A   T  __
GAM246  C11orf15 3'  CAAGACTATGTTTAGTCTTTAG 6508    GA     ATCAGCC_
            AGT                   CA  ACTATGT      TAGAGT
                                  ||  |||||||      ||||||
                                  GT  TGATACA      ATCTCA
                                   TC     AATCAGAA
GAM246  DKFZP566A1524 5'  CAGGACGGTGGCCTCCTAGAGT 6509     A  TA  TATCAG
                                  CAG AC  TG     CCTAGAGT
                                  ||| ||  ||     ||||||||
                                  GTC TG  AC     GGATCTCA
                                    C  CC  CGGA__
GAM246  KIAA1350 3'  CAGGCTATGTATCACCT    6510     AA       G
                                  CAG  CTATGTATCA CCT
                                  |||  |||||||||| |||
                                  GTC  GATACATAGT GGA
                                    C_       _
GAM246  KIAA1497 3'  CAGACTGGAAGCCTAGAG    6511      A  ATGTATC
                                  CAGA CT      AGCCTAGAG
                                  |||| ||      |||||||||
                                  GTCT GA      TCGGATCTC
                                    _ CCT____
GAM246  KIAA1655 3'  GAACTCATGGCCTAGAG    6512       _  TATCA
                                  GAACT ATG    GCCTAGAG
                                  ||||| |||    ||||||||
                                  CTTGA TAC    CGGATCTC
                                     G  _____
GAM246  LOC123036 3'  CAGAACTTCAGTTTAGG    6513       ATGTA   CC  A
                                  CAGAACT    TCAG  TAG G
                                  |||||||    ||||  ||| |
                                  GTCTTGA    AGTC  ATC C
                                       _____   AA  C
GAM246  LOC196411 3'  CAGGACTATATATTGAGC    6514     A       C_
                                  CAG ACTATGTAT  AGC
                                  ||| |||||||||  |||
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                                GTC TGATATATA  TCG
                                  C        AC
GAM246  LOC91907  3'  CAGACTGGAAGCCTAGAG    6511      A  ATGTATC
                                CAGA CT      AGCCTAGAG
                                |||| ||      |||||||||
                                GTCT GA      TCGGATCTC
                                  _  CCT____
GAM247  ANXA4     3'  GTAACCAGATGTATAT      6517     _  TTT
                                GTA CC   GGATGTATAT
                                ||| ||   ||||||||||
                                CAT GG   TCTACATATA
                                  T  ___
GAM247  EGR3      3'  CCATACATAGATGTGTATA    6518       CTT      A
                                CCGTAC   TGGATGT TATA
                                ||||||   ||||||| ||||
                                GGTATG   ATCTACA ATAT
                                    T__      C
GAM247  SIAH1     3'  CCCATCTTGGGTGTATATA    6519       ACC    A
                                CCCGT   TTTGG TGTATATA
                                |||||   ||||| ||||||||
                                GGGTA   GAACC ACATATAT
                                   ___     C
GAM247  FLJ11252  3'  GTAGCTAGGATGTATATA    6520     C  TT
                                GTA CT  GGATGTATATA
                                ||| ||  ||||||||||||
                                CAT GA  CCTACATATAT
                                  C  T_
GAM247  FLJ20288  5'  CCTGTGTCTCTGGATCCACA   6521     C  AC      G
                                CC GT  CTTTGGAT TATA
                                || ||  |||||||| ||||
                                GG CA  GAGACCTA GTGT
                                 A  CA       G
GAM247  KIAA1238  3'  TACTTGTATGTTTAGATATATA 6522      CC   CC
                                TAC  GTA  TTTGGATGTATA
                                |||  |||  ||||||||||||
                                ATG  CAT  AAATCTATATAT
                                  AA   AC
GAM247  KIAA1615  3'  CCCAGTATATAGTGTATATA   6523     _  CCTT   A
                                CCC GTA    TGG TGTATATA
                                ||| |||    ||| ||||||||
                                GGG CAT    ATC ACATATAT
                                  T   AT__   _
GAM247  PRO0641   5'  GTACCAGTGTATATA      6524       TTT  A
                                GTACC   GG TGTATATA
                                |||||   || ||||||||
                                CATGG   TC ACATATAT
                                   ___  _
GAM247  WIRE      5'  GTACCTTTAGGTCATTCATATA 6525          ATG___
                                GTACCTTTGG     TATATA
                                ||||||||||     ||||||
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                                CATGGAAATC     GTATAT
                                     CAGTAA
GAM247  LOC152078 3'  TACCCTAGATGTATATA     6526       T
                                TACCTT GGATGTATATA
                                |||||| ||||||||||
                                ATGGGA TCTACATATAT
                                  _
GAM247  LOC222008 3'  GTATTTCTACATGTATATA   6527     CC   G
                                GTA  TTTG ATGTATATA
                                |||  |||| |||||||||
                                CAT  AGAT TACATATAT
                                  AA   G
GAM247  LOC257319 3'  TACCTATATAGAGATGTATATA 6528      CG  CCTTT
                                TACC  TA    GGATGTATATA
                                ||||  ||    ||||||||||
                                ATGG  AT    TCTACATATAT
                                  AT  ATC__
GAM248  HTR2A    3'  GAACCCCGCTTTTCATTGACA  6531      TG  A_  C
                                GAACT  CC  TT TCATTGACA
                                |||||  ||  || |||||||||
                                CTTGG  GG  AA AGTAACTGT
                                  __  CG  A
GAM248  KMO      3'  TAGAACTCAAGGTTTTCATTGA 6532        GCCATTC
           CA                     TAGAACTT      TCATTGACA
                                |||||||      |||||||||
                                ATCTTGAG      AGTAACTGT
                                    TTCCAAA
GAM248  MMP13    3'  TAAATTATGCTCTCATTGACA  6533      ACT   CAT
                                TAGA   TGC   TCTCATTGACA
                                ||||   |||   ||||||||||
                                ATTT   ACG   AGAGTAACTGT
                                  AAT   ___
GAM248  PEX10    3'  CTGCTGTTCTCACTGCA     6534      CA       A
                                TTGC  TTCTCATTG CA
                                ||||  ||||||||| ||
                                GACG  AAGAGTGAC GT
                                  AC       _
GAM248  PGAM1    3'  TAGAACTGCTATTCTGAC    6535       T  C    CATT
                                TAGAACT GC ATTCT   GAC
                                ||||||| || |||||   |||
                                ATCTTGA CG TAAGA   CTG
                                   _  A    ____
GAM248  FEM-2    3'  CAGAACTTGTGGTTTATTGACA 6536         CCATTCTC
                                TAGAACTTG       ATTGACA
                                |||||||||       |||||||
                                GTCTTGAAC       TAACTGT
                                    ACCAAA__
GAM248  FLJ12716  3'  TAGAATTTACCATTCATCA   6537       C       _
                                TAGAA TTGCCATTC TCA
                                ||||| ||||||||| |||
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                                ATCTT AATGGTAAG AGT
                                  A       T
GAM248  PPP4R2   5'  TAGAACTTACCATTTTTCCTG  6538           CTCA
                                TAGAACTTGCCATT   TTG
                                ||||||||||||||  |||
                                ATCTTGAATGGTAA   GAC
                                      AAAG
GAM248  LOC144483 3'  TAGAACTGCTATTCTGAC    6535       T  C    CATT
                                TAGAACT GC ATTCT   GAC
                                ||||||| || |||||   |||
                                ATCTTGA CG TAAGA   CTG
                                   _ A    ____
GAM248  LOC200854 5'  TAGAACTTACCATTTTTCCTG  6538           CTCA
                                TAGAACTTGCCATT   TTG
                                ||||||||||||||  |||
                                ATCTTGAATGGTAA   GAC
                                      AAAG
GAM248  LOC201617 5'  GAACTATATTCATTGAC     6539      TGCC  TC
                                GAACT   AT  TCATTGAC
                                |||||   ||  ||||||||
                                CTTGA   TA  AGTAACTG
                                  ____  TA
GAM248  LOC255692 5'  CAGAACTTGCGGACCTTGTTGA 6540         CAT   CA
          CA                    TAGAACTTGC   TCT  TTGACA
                                ||||||||||  |||  ||||||
                                GTCTTGAACG   GGA  AACTGT
                                     CCT   AC
GAM248  LOC90355  3'  TAGAGTTTGCCATTCATTCTG  6541      AC       TCA
                                TAGA  TTGCCATTC   TTG
                                ||||  |||||||||  |||
                                ATCT  AACGGTAAG   GAC
                                  CA        TAA
GAM249  KIAA0711  3'  GAGTAGCAATGGTGTGGGGAA  6544     CGT   C  C
                                GAG   CAG GG GTGGGGAA
                                |||   ||| || ||||||||
                                CTC   GTT CC CACCCCTT
                                  ATC   A  A
GAM249  PCBP4    3'  TCTGGGCGTTAGCGGCGTTTGG 6545     GA_   C      G_
          GA                    TC   GCGT AGCGGCGT  GGGA
                                ||   |||| ||||||||  ||||
                                AG   CGCA TCGCCGCA  CCCT
                                 ACC    A       AA
GAM249  PCBP4    3'  TCTGGGCGTTAGCGGCGTTTGG 6545     GA_   C      G_
          GA                    TC   GCGT AGCGGCGT  GGGA
                                ||   |||| ||||||||  ||||
                                AG   CGCA TCGCCGCA  CCCT
                                 ACC    A       AA
GAM249  PCBP4    3'  TCTGGGCGTTAGCGGCGTTTGG 6545     GA_   C      G_
          GA                    TC   GCGT AGCGGCGT  GGGA
                                ||   |||| ||||||||  ||||
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                                AG  CGCA TCGCCGCA  CCCT
                                 ACC   A      AA
GAM249  SEPT6    3' CCAGGCGGCGGTGTGGGGAA  6546     A  TCA   C
                                TCG GCG   GCGG GTGGGGAA
                                ||| |||   |||| ||||||||
                                GGT CGC   CGCC CACCCCTT
                                  C  ___   A
GAM249  LOC152641 5' CTCGGGGCGCGGCGTGGGGA  6547      A_  GTCA
                                TTCG  GC   GCGGCGTGGGGA
                                ||||  ||   ||||||||||||
                                GAGC  CG   CGCCGCACCCCT
                                  CC  ____
GAM249  LOC89944  3' TTCGGGCGTGGGGGGTGGGG  6548      A   CAGC  C
                                TTCG GCGT   GG GTGGGG
                                |||| ||||   || ||||||
                                AAGC CGCA   CC CACCCC
                                  C   CCC_  _
GAM250  ANK1     3' AGCTGCGGGGTCCGCGGGG   6551      _    AC
                                GGTT CGGGG  CCGCGGGG
                                |||| |||||  ||||||||
                                TCGA GCCCC  GGCGCCCC
                                  C    A_
GAM250  ANK1     3' AGCTGCGGGGTCCGCGGGG   6551      _    AC
                                GGTT CGGGG  CCGCGGGG
                                |||| |||||  ||||||||
                                TCGA GCCCC  GGCGCCCC
                                  C    A_
GAM250  DDX3     3' ATGCAGTTTGGGATGGGG    6552        CG   CCCGC
                                ATGCGGTT  GGGA    GGGG
                                ||||||||  ||||    ||||
                                TACGTCAA  CCCT    CCCC
                                    A_   A____
GAM250  IL12RB2   5' CGCGGTCCCGGGCCTGCGGGGA 6553        G  A  C
                                TGCGGTTC GGG CC GCGGGGA
                                ||||||||  ||| || |||||||
                                GCGCCAGG CCC GG CGCCCCT
                                    G  _  A
GAM250  IRS2     5' GTCCGGGGAGGCCCGCGGGG  6554         __
                                GTTCGGGGA  CCCGCGGGG
                                |||||||||  |||||||||
                                CAGGCCCCT  GGGCGCCCC
                                     CC
GAM250  MTA1L1   5' GTCCGGGAGGCTCGCGGGG   6555        ACC_
                                GTTCGGGG   CGCGGGG
                                ||||||||   |||||||
                                CAGGCCCT   GCGCCCC
                                    CCGA
GAM250  PDLIM1   5' GCGGGCGACGACCCGCGGGGA  6556      TT  G
                                GCGG  CGG GACCCGCGGGGA
                                ||||  ||| ||||||||||||
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                                CGCC  GCT CTGGGCGCCCCT
                                  C_  G
GAM250  RUNX3    3'  GCAGCTGGGGGTCCGCGGGG  6557       C   AC
                                GCGGTT GGGG  CCGCGGGG
                                |||||| ||||  ||||||||
                                CGTCGA CCCC  GGCGCCCC
                                   _   CA
GAM250  CALN1    3'  GGTTCGGGGGTCAGGGA     6558         ACCCG
                                GGTTCGGGG    CGGGGA
                                |||||||||    ||||||
                                CCAAGCCCC    GTCCCT
                                     CA___
GAM250  FOXD4    5'  GCGGCCCGGCTCGCGGGG    6559         GGACC
                                GCGGTTCGG    CGCGGGG
                                |||||||||    |||||||
                                CGCCGGGCC    GCGCCCC
                                     GA___
GAM250  LOC146325 3'  GGCCACGGCCCGTGGGG    6560     T  G  A   C
                                GGT CG GG CCCG GGGG
                                ||| || || |||| ||||
                                CCG GT CC GGGC CCCC
                                  _ G _   A
GAM250  LOC146325 5'  ATGCGGCTCCCGTGGG     6561        CGGGGA   C
                                ATGCGGTT     CCCG GGG
                                ||||||||     |||| |||
                                TACGCCGA     GGGC CCC
                                     _______   A
GAM250  LOC199990 3'  CGCGGCGGATCCGCGGGGA   6562       TCGG   C
                                TGCGGT   GGA CCGCGGGGA
                                ||||||   ||| |||||||||
                                GCGCCG   CCT GGCGCCCCT
                                   _____  A
GAM250  LOC254454 5'  TGGGGTCCGCCCGCGGGG    6563    C     GGGA
                                TG GGTTCG    CCCGCGGGG
                                || ||||||    |||||||||
                                AC CCAGGC    GGGCGCCCC
                                 C     _____
GAM251  FMR2     3'  CATGTCAGACGCAAAAAG    6566        ACCCCAA
                                TATGTCA      GCAAAAAG
                                |||||||      ||||||||
                                GTACAGT      CGTTTTTC
                                    CTG_____
GAM251  MEST     3'  TATGTCAACCTTAGTCAGA   6567         CCA  CAAAA
                                TATGTCAACC   AG    AGA
                                ||||||||||   ||    |||
                                ATACAGTTGG   TC    TCT
                                     AA_  AG___
GAM251  MGAT5    5'  TCAACCAGAAAAAGA       6568        CCA  C
                                TCAACC   AG AAAAAGA
                                ||||||   || |||||||
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                                AGTTGG  TC TTTTTCT
                                   ___  _
GAM251  PLIN    3'  TATGTGGCCATCAAAAAGA   6569      CAACC  AG
                                TATGT   CCA  CAAAAAGA
                                |||||    |||  ||||||||
                                ATACA   GGT  GTTTTTCT
                                   CC___  A_
GAM251  VBP1    3'  TATGTCAACCTGTAAGGATAAA 6570         CC_  CAA
          G                      TATGTCAACC  AAG  AAAG
                                ||||||||||  |||  ||||
                                ATACAGTTGG  TTC  TTTC
                                      ACA  CTA
GAM251  CTCF    3'  GCTGACTCCAAGCAAAGGGAG  6571    CA  C      AA
                                GT  AC CCAAGCAAA  GAG
                                ||  || |||||||||  |||
                                CG  TG GGTTCGTTT  CTC
                                 AC  A       CC
GAM251  KIAA1191  3'  TATGTCAAAGCCAAGGTAAAAG 6572        CC   CA
                                TATGTCAA  CCAAG  AAAAG
                                ||||||||  |||||  |||||
                                ATACAGTT  GGTTC  TTTTC
                                     TC   CA
GAM251  MGC35558  3'  AACAAAAGCAAAAAGAG    6573     CCC
                                AAC  AAGCAAAAAGAG
                                |||  ||||||||||||
                                TTG  TTCGTTTTTCTC
                                  TT_
GAM251  LOC112868 5'  TGTTTGACCCCAAGAAACCCAG 6574     CA_     C  AA_
                                TGT  ACCCCAAG AA  AG
                                |||  |||||||| ||  ||
                                ACA  TGGGGTTC TT  TC
                                  AAC      T  GGG
GAM251  LOC132793 5'  ATGTCAACCCCACAAGA    6575         AA  AAA
                                ATGTCAACCCC  GCA  AGA
                                ||||||||||  |||  |||
                                TACAGTTGGGG  TGT  TCT
                                      __  ___
GAM251  LOC148645 3'  TGTTGTCCCCAAGCATGGAG  6576    CAA      AAAA
                                TGT  CCCCAAGCA   GAG
                                |||  |||||||||   |||
                                ACA  GGGGTTCGT   CTC
                                  ACA       AC__
GAM251  LOC221814 3'  TATTTCAACCCCAAGCAATCAG 6577    G         AA
          AG                     TAT TCAACCCCAAGCAA  AGAG
                                ||| ||||||||||||||  ||||
                                ATA AGTTGGGGTTCGTT  TCTC
                                  A          AG
GAM252  ACN     3'  TGGTATGTATGTAGGGATAGG  6580         GCTACTA
                                TGGTATGTGTG     ATAGG
                                ||||||||||      |||||
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                                ACCATACATAC      TATCC
                                      ATCCC__
GAM252  KCNS3    5'  TGGAATGTGTGGTGCACATAGG 6581      T       CTACTA
              C                    TGG ATGTGTGG     ATAGGC
                                   ||| ||||||||     ||||||
                                   ACC TACACACC     TATCCG
                                     T       ACGTG_
GAM252  MNT      3'  TGGAATGTGTGGAGCTGGTGGG 6582      T       CTA  AATA
                                   TGG ATGTGTGG   CT    GG
                                   ||| ||||||||   ||    ||
                                   ACC TACACACC   GA    CC
                                     T       TC_  CCAC
GAM252  PTBP1    3'  TGGGTGTGTGGCTGCAGGAAGG 6583      TA        ACTAAT
              C                    TGG  TGTGTGGCT     AGGC
                                   |||  |||||||||     ||||
                                   ACC  ACACACCGA     TCCG
                                     C_        CGTCCT
GAM252  PTBP1    3'  TGGGTGTGTGGCTGCAGGAAGG 6583      TA        ACTAAT
              C                    TGG  TGTGTGGCT     AGGC
                                   |||  |||||||||     ||||
                                   ACC  ACACACCGA     TCCG
                                     C_        CGTCCT
GAM252  KIAA0227 3'  TGGTATGTGTGGTCACCAGAGG 6584           C     ATA
              GC                     TGGTATGTGTGG TACTA   GGC
                                   ||||||||||||| |||||   |||
                                   ACCATACACACC GTGGT   CCG
                                          A    CTC
GAM252  LOC126906 3'  TGGATGTGTGAGGTAGTAGGC  6585      T       CTAC  A
                                   TGG ATGTGTGG    TA TAGGC
                                   ||| ||||||||    || |||||
                                   ACC TACACACT    AT ATCCG
                                     _       CC__  C
GAM252  LOC143310 3'  TGGTGTGTGGCACACAGTAGGC 6586       AT      _   TAA
                                   TGGT  GTGTGGC TAC   TAGGC
                                   ||||  ||||||| |||   |||||
                                   ACCA  CACACCG GTG   ATCCG
                                     __      T   TC_
GAM252  LOC222166 3'  TGTGTTTTACTAATAGG     6587       GGC
                                   TGTGT   TACTAATAGG
                                   |||||   ||||||||||
                                   ACACA   ATGATTATCC
                                      AA_
GAM253  ANGPT1   3'  TATCATCTGGCTACCATAG   6590          _   A
                                   TATCATCTG CTAT ATAG
                                   ||||||||| |||| ||||
                                   ATAGTAGAC GATG TATC
                                         C   G
GAM253  CPS1     3'  TCTACCATCTGCTGATATAG   6591            ATA
                                   TCTATCATCTGCT   ATAG
                                   ||||||||||||   ||||
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                                AGATGGTAGACGA  TATC
                                       CTA
GAM253  FCGR2B   3'  CTATTATCTGTTAATAACAGT  6592      C    CTA
                                CTAT ATCTG  TAATAGCAGT
                                |||| |||||  ||||||||||
                                GATA TAGAC  ATTATTGTCA
                                  A    A__
GAM253  HRH1     5'  TCTGTTATCTGCCATCTAG   6593     ATC       AA
                                TCT  ATCTGCTAT  TAG
                                |||  |||||||||  |||
                                AGA  TAGACGGTA  ATC
                                  CAA       G_
GAM253  LNK      3'  TCTGTCATCCGCTGTGACAGT  6594     A       ATAATA
                                TCT TCATCTGCT     GCAGT
                                ||| |||||||||     |||||
                                AGA AGTAGGCGA     TGTCA
                                  C       CAC___
GAM253  FIGNL1   5'  TCTATCATCTGCCAGCAG    6595           ATAAT
                                TCTATCATCTGCT    AGCAG
                                ||||||||||||    |||||
                                AGATAGTAGACGG    TCGTC
                                                 _____
GAM253  HSD17B12 3'  TCTGTGATTTGCTATAATAG  6596     ATC  C
                                TCT   AT TGCTATAATAG
                                |||   || ||||||||||
                                AGA   TA ACGATATTATC
                                  CAC  A
GAM253  KIAA0964 3'  TCTCTCATCTGCTCAGCG    6597     A       ATAA   A
                                TCT TCATCTGCT    TAGC G
                                ||| |||||||||    |||| |
                                AGA AGTAGACGA    GTCG C
                                  G        ____    C
GAM253  KIAA1416 3'  ATCTTACATGATAGCAGT    6598      GC   A
                                ATCT  TAT ATAGCAGT
                                ||||  ||| ||||||||
                                TAGA  GTA TATCGTCA
                                  AT   C
GAM253  PCSK7    3'  TCTGCCATCTGCTCTGCAG   6599     AT      ATAATA
                                TCT  CATCTGCT     GCAG
                                |||  ||||||||     ||||
                                AGA  GTAGACGA     CGTC
                                  CG       GA____
GAM254  C20orf12 5'  TCTTATATTTTTTCTTTAGT   6602       AGATA
                                TCTTA    TTTCTTTAGT
                                |||||    ||||||||||
                                AGAAT    AAAGAAATCA
                                   ATAAA
GAM254  DKFZP434A043 3'  TCTGTAGAATATTCTTTAGT   6603     TA   TAT
                                TCT  AGA   TTCTTTAGT
                                |||  |||   |||||||||
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                                AGA  TCT   AAGAAATCA
                                  CA   TAT
GAM254  KIAA1010 3'  ATCTTAAGATTCTTGGTC    6604          ATT   TA
                                ATCTTAAGAT   TCTT  GTC
                                ||||||||||  ||||  |||
                                TAGAATTCTA   AGAA  CAG
                                     ____   C_
GAM254  KIAA1795 3'  TCTTAGTTTTTTCTTTAGT   6605       AGATA
                                TCTTA    TTTCTTTAGT
                                |||||    ||||||||||
                                AGAAT    AAAGAAATCA
                                   CAAA_
GAM254  MGC2541  3'  TACCTTAATTCTTTAGTC    6606         GATAT
                                TATCTTAA    TTCTTTAGTC
                                ||||||||    ||||||||||
                                ATGGAATT    AAGAAATCAG
                                     ______
GAM254  NCOA2    3'  CTTAAAACATCTTTAGT     6607          TT
                                CTTAAGATA  TCTTTAGT
                                |||||||||  ||||||||
                                GAATTTTGT  AGAAATCA
                                     __
GAM254  ST7L     3'  CTTAAGATGTTTTAGTC     6608         ATTTC
                                CTTAAGAT    TTTAGTC
                                ||||||||    |||||||
                                GAATTCTA    AAATCAG
                                     CA___
GAM254  ST7L     3'  CTTAAGATGTTTTAGTC     6608         ATTTC
                                CTTAAGAT    TTTAGTC
                                ||||||||    |||||||
                                GAATTCTA    AAATCAG
                                     CA___
GAM254  ST7L     3'  CTTAAGATGTTTTAGTC     6608         ATTTC
                                CTTAAGAT    TTTAGTC
                                ||||||||    |||||||
                                GAATTCTA    AAATCAG
                                     CA___
GAM254  LOC147299 5'  TCTTAGAAAATCTTTAGT    6609       A  TATT
                                TCTTA GA    TCTTTAGT
                                ||||| ||    ||||||||
                                AGAAT CT    AGAAATCA
                                   _ TTT_
GAM254  LOC91768  5'  TCTTAAAATTCTTTGGTC    6610          ATT    A
                                TCTTAAGAT   TCTTT GTC
                                |||||||||   ||||| |||
                                AGAATTTTA   AGAAA CAG
                                     ____    C
GAM255  AKAP13    3'  AGGGGTGGTATGTGCCCGGGAT 6613     A    __ C        C
            GG                    AG GGGT  TA GTGCCCGGGA GG
                                || ||||  || ||||||||||  ||
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                                TC CCCA  AT CACGGGCCCT CC
                                 _   CC  A        A
GAM255  AKAP13   3'  AGGGGTGGTATGTGCCCGGGAT 6613     A   __ C       C
           GG                     AG GGGT  TA GTGCCCGGGA GG
                                || ||||  || ||||||||||  ||
                                TC CCCA  AT CACGGGCCCT CC
                                 _   CC  A        A
GAM255  AKAP13   3'  AGGGGTGGTATGTGCCCGGGAT 6613     A   __ C       C
           GG                     AG GGGT  TA GTGCCCGGGA GG
                                || ||||  || ||||||||||  ||
                                TC CCCA  AT CACGGGCCCT CC
                                 _   CC  A        A
GAM255  CD3E     3'  AGAGGGCTGCAAAAGGGGACGG 6614         A  TGCCC
                                AGAGGGTT CG    GGGACGG
                                ||||||||  ||    |||||||
                                TCTCCCGA GT    CCCTGCC
                                     C  TTTC_
GAM255  OTOF     3'  AGGGTGTGCCCGGGATGG    6615       TAC        C
                                AGGGT   GTGCCCGGGA GG
                                |||||   ||||||||||  ||
                                TCCCA   CACGGGCCCT CC
                                  ___         A
GAM255  RAB3A    3'  GAGGGGCAGGGCTTGGGGCGG  6616       T  CGT  CC   A
                                GAGGG TA   GC  GGG CGG
                                |||||  ||   ||  |||  |||
                                CTCCC GT   CG  CCC GCC
                                   C  CC_  AA   C
GAM255  SCG3     5'  GAGGGTGGGTGTGGGGCGG   6617       TAC   CCC   A
                                GAGGGT   GTG   GGG CGG
                                ||||||   |||   |||  |||
                                CTCCCA   CAC   CCC GCC
                                   CC_   AC_   _
GAM255  SYBL1    5'  GAGGGCGCGCGGGCTCGGGACG 6618        TA_  T  C
           G                     GAGGGT   CG GC CGGGACGG
                                ||||||   || ||  ||||||||
                                CTCCCG   GC CG GCCCTGCC
                                   CGC  C  A
GAM255  FLJ12387 3'  GGGCGGTGCCCGGGGCGG    6619       TAC        A
                                GGGT   GTGCCCGGG CGG
                                ||||   |||||||||  |||
                                CCCG   CACGGGCCC GCC
                                  C__        C
GAM255  FLJ13940 5'  AGAGGGTTGGTGGGAACG    6620         AC   CCC
                                AGAGGGTT  GTG   GGGACG
                                ||||||||  |||   ||||||
                                TCTCCCAA  CAC   CCTTGC
                                     C_   ___
GAM255  FLJ30663 3'  AAGAAGGTTATGTGTTGACTGG 6621           C   CCCGG  _
                                AAGAGGGTTA GTG    GAC GG
                                ||||||||||  |||     |||  ||
```

```
                                TTCTTCCAAT CAC    CTG CC
                                     A  AA___  A
GAM255  KIAA1908  5'  AGAGGGGCTGAGGCCCGGGACG 6622       TTACGT
          G                   AGAGGG    GCCCGGGACGG
                              ||||||    ||||||||||
                              TCTCCC    CGGGCCCTGCC
                                 CGACTC
GAM255  MGC5457   3'  AGAGGGTTTACACTTGGGGTGG 6623        AC TG CC  AC
                              AGAGGGTT  G  C  GGG  GG
                              ||||||||  |  |  |||  ||
                              TCTCCCAA  T  G  CCC  CC
                                   A_ GT AA  CA
GAM255  PF1       5'  GAGAGGTTACGTGAGG      6624     _       CCC
                              GAG GGTTACGTG   GGG
                              ||| |||||||||   |||
                              CTC CCAATGCAC   TCC
                                T       ___
GAM255  PP1628    5'  AACAGGGTGCCTGGGACG    6625    G    TACGT  C
                              AA AGGGT    GCC GGGACG
                              || |||||    ||| ||||||
                              TT TCCCA    CGG CCCTGC
                               G    _____  A
GAM255  TBX21     5'  AGAGGGTCGCGTGGGCTGGGAT 6626       TA   CCC_   C
          GG                    AGAGGGT  CGTG   GGGA GG
                              |||||||  ||||   |||| ||
                              TCTCCCA  GCAC   CCCT CC
                                   GC   CCGA   A
GAM255  LOC148397 3'  GAGGGGGTCAGGACGG     6627      TTAC  GCC
                              GAGGG   GT   CGGGACGG
                              |||||   ||   ||||||||
                              CTCCC   CA   GTCCTGCC
                                C___  ___
GAM255  LOC196326 5'  AGAGGGTTGTGTAGCGAG    6628       AC   CC_
                              AGAGGGTT  GTG   CGGG
                              ||||||||  |||   ||||
                              TCTCCCAA  CAC   GCTC
                                   __  ATC
GAM255  LOC220980 5'  AGGGGCGTGCTCGGGGCG    6629     TTA    C   A
                              AGGG   CGTGC CGGG CG
                              ||||   ||||| |||| ||
                              TCCC   GCACG GCCC GC
                                C__    A   C
GAM256  ADCY3     3'  CCCTCAGGGGCAAGGACGG    6632     _     CCC
                              CCC CAGGGGT   GACGG
                              ||| |||||||   |||||
                              GGG GTCCCCG   CTGCC
                                A      TTC
GAM256  ADCY9     3'  GCCTCCACTCCCGACGG     6633     _  GGGG
                              GCC CCA   TCCCGACGG
                              ||| |||   |||||||||
```

```
                                CGG GGT    AGGGCTGCC
                                  A   G___
GAM256  AGL      5'  GCCCCAGGTGGGAGCGG     6634          _  TCCC  _
                                GCCCCAGG GG    GA CGG
                                |||||||| ||    || |||
                                CGGGGTCC CC    CT GCC
                                    A  _____  C
GAM256  AGPAT2   5'  GCCCGGCGCCCGACGG      6635       CA  G T
                                GCCC  GG G CCCGACGG
                                ||||  || | ||||||||
                                CGGG  CC C GGGCTGCC
                                  __  G _
GAM256  AGPAT2   5'  GCCCGGCGCCCGACGG      6635       CA  G T
                                GCCC  GG G CCCGACGG
                                ||||  || | ||||||||
                                CGGG  CC C GGGCTGCC
                                  __  G _
GAM256  AGRN     3'  GCCCTGTGGGGTCACCCGG   6636       CA_     _ GA
                                GCCC   GGGGTC CC  CGG
                                ||||   |||||| ||  |||
                                CGGG   CCCCAG GG  GCC
                                  ACA     T  __
GAM256  AHCY     3'  GCCCCAGAGAGTCGATGG     6637          _  CC  C
                                GCCCCAGGG GTC  GA GG
                                ||||||||| |||  || ||
                                CGGGGTCTC CAG  CT CC
                                    T   __  A
GAM256  AMN      3'  GCCCCAAGGTCGACGG       6638          GTCC
                                GCCCCAGGG    CGACGG
                                |||||||||    ||||||
                                CGGGGTTCC    GCTGCC
                                    A___
GAM256  APBB1    5'  GCCCCGGGCCCAGATGACGG   6639       AG     C___
                                GCCCC  GGGTCC    GACGG
                                |||||  ||||||    |||||
                                CGGGG  CCCGGG    CTGCC
                                  __      TCTA
GAM256  APOB     5'  GCCCCGCAGGTCCCGGTGG    6640       AG       AC
                                GCCCC  GGGTCCCG  GG
                                |||||  ||||||||  ||
                                CGGGG  TCCAGGGC  CC
                                  CG       CA
GAM256  B4GALT2  3'  GCCCCGAGGGGGCCACGACGG  6641        _    T _
                                GCCCC AGGGG CC CGACGG
                                ||||| ||||| || ||||||
                                CGGGG TCCCC GG GCTGCC
                                  C    C  T
GAM256  BARHL1   3'  GCCCCGGAGCCGACGG      6642       A    TC
                                GCCCC GGGG  CCGACGG
                                ||||| ||||  |||||||
```

```
                                CGGGG CCTC  GGCTGCC
                                  _   __
GAM256  BDP1    5'  GCCCCGAGCCCCGGCGG    6643      AG      A
                                GCCCC  GGGTCCCG CGG
                                |||||  |||||||| |||
                                CGGGG  CTCGGGGC GCC
                                   __      C
GAM256  CDC25B  3'  GCCCCAGGGTTCACAG     6644        G  CCG
                                GCCCCAGGG TC   ACGG
                                |||||||| ||   ||||
                                CGGGGTCCC AG   TGTC
                                     A ___
GAM256  CDC25B  3'  GCCCCAGGGTTCACAG     6644        G  CCG
                                GCCCCAGGG TC   ACGG
                                |||||||| ||   ||||
                                CGGGGTCCC AG   TGTC
                                     A ___
GAM256  CDK5R2  5'  GCCCCAGCGGGAGCCGCGG  6645       _  TC   A
                                GCCCCAG GGG  CCG CGG
                                ||||||| |||  ||| |||
                                CGGGGTC CCC  GGC GCC
                                    G   TC  _
GAM256  CDKN2D  5'  ACCCCGGCCCTCCCGGCGG  6646      A  GG_    A
                                GCCCC GG   TCCCG CGG
                                ||||| ||   ||||| |||
                                TGGGG CC   AGGGC GCC
                                   _ GGG    C
GAM256  CHI3L1  3'  GCTCAGGGGTCCCAAGG    6647    CC        C
                                GC  CAGGGGTCCCGA GG
                                ||  ||||||||||| ||
                                CG  GTCCCCAGGGTT CC
                                 A_         _
GAM256  CKAP1   5'  GCCATGGAGCCCGACGG    6648    CCA   T
                                GCC   GGGG CCCGACGG
                                |||   |||| ||||||||
                                CGG   CCTC GGGCTGCC
                                  TA_   _
GAM256  COL1A2  5'  GCCCCTGGGTCACCGGCGG  6649      AG    _  A
                                GCCCC  GGGTC CCG CGG
                                |||||  ||||| ||| |||
                                CGGGG  CCCAG GGC GCC
                                   A_    T  C
GAM256  CRAT    5'  GCCCCGGGCGGGCAACGG   6650      AG   CC_
                                GCCCC  GGGT   CGACGG
                                |||||  ||||   ||||||
                                CGGGG  CCCG   GTTGCC
                                   __   CCC
GAM256  CSNK1G2 3'  GCCCCAAGGGGCTGCACGG  6651       _    CC G
                                GCCCCA GGGGT  C ACGG
                                |||||| |||||  | ||||
```

```
                                CGGGGT CCCCG  G TGCC
                                   T    AC _
GAM256  EDNRB   5'  GCTCCAGAAGCGTCCGGTGG  6652    C      C_  AC
                                GC CCAGGGGT  CCG  GG
                                || ||||||||  |||  ||
                                CG GGTCTTCG  GGC  CC
                                 A       CA  CA
GAM256  EMS1    3'  GCCCCAGGCTGCCCGGTGG  6653        G_ T   AC
                                GCCCCAGG  G CCCG  GG
                                ||||||||  | ||||  ||
                                CGGGGTCC  C GGGC  CC
                                     GA _   CA
GAM256  EMS1    3'  GCCCCAGGCTGCCCGGTGG  6653        G_ T   AC
                                GCCCCAGG  G CCCG  GG
                                ||||||||  | ||||  ||
                                CGGGGTCC  C GGGC  CC
                                     GA _   CA
GAM256  EVA1    5'  GCCCCAGAGACCGGACGG   6654        T  C
                                GCCCCAGGGG CC GACGG
                                |||||||||| || |||||
                                CGGGGTCTCT GG CTGCC
                                      _  C
GAM256  EVA1    5'  GCCCCAGAGACCGGACGG   6654        T  C
                                GCCCCAGGGG CC GACGG
                                |||||||||| || |||||
                                CGGGGTCTCT GG CTGCC
                                      _  C
GAM256  FGFR2   5'  GCCCCCGGGGCTCGCGG    6655      A    CC  A
                                GCCCC GGGGT  CG CGG
                                ||||| |||||  || |||
                                CGGGG CCCCG  GC GCC
                                   G    A_  _
GAM256  FGFR2   5'  GCCCCCGGGGCTCGCGG    6655      A    CC  A
                                GCCCC GGGGT  CG CGG
                                ||||| |||||  || |||
                                CGGGG CCCCG  GC GCC
                                   G    A_  _
GAM256  FGFR2   5'  GCCCCCGGGGCTCGCGG    6655      A    CC  A
                                GCCCC GGGGT  CG CGG
                                ||||| |||||  || |||
                                CGGGG CCCCG  GC GCC
                                   G    A_  _
GAM256  FGFR2   5'  GCCCCCGGGGCTCGCGG    6655      A    CC  A
                                GCCCC GGGGT  CG CGG
                                ||||| |||||  || |||
                                CGGGG CCCCG  GC GCC
                                   G    A_  _
GAM256  FGFR2   5'  GCCCCCGGGGCTCGCGG    6655      A    CC  A
                                GCCCC GGGGT  CG CGG
                                ||||| |||||  || |||
```

```
                                CGGGG CCCCG  GC GCC
                                  G    A_ _
GAM256  FGFR2   5' GCCCCCGGGGCTCGCGG    6655      A   CC  A
                                GCCCC GGGGT  CG CGG
                                ||||| |||||  || |||
                                CGGGG CCCCG  GC GCC
                                  G    A_ _
GAM256  FGFR2   5' GCCCCCGGGGCTCGCGG    6655      A   CC  A
                                GCCCC GGGGT  CG CGG
                                ||||| |||||  || |||
                                CGGGG CCCCG  GC GCC
                                  G    A_ _
GAM256  FGFR2   5' GCCCCCGGGGCTCGCGG    6655      A   CC  A
                                GCCCC GGGGT  CG CGG
                                ||||| |||||  || |||
                                CGGGG CCCCG  GC GCC
                                  G    A_ _
GAM256  FGFR2   5' GCCCCCGGGGCTCGCGG    6655      A   CC  A
                                GCCCC GGGGT  CG CGG
                                ||||| |||||  || |||
                                CGGGG CCCCG  GC GCC
                                  G    A_ _
GAM256  FGFR2   5' GCCCCCGGGGCTCGCGG    6655      A   CC  A
                                GCCCC GGGGT  CG CGG
                                ||||| |||||  || |||
                                CGGGG CCCCG  GC GCC
                                  G    A_ _
GAM256  FXYD6   3' CCAGAGGCTTCCACCTGATGGC 6656        _____ C  C  III
                                CCAGGGGT    CC GA GG   C
                                ||||||||    || || ||   |
                                GGTCTCCG    GG CT CC   G
                                     AAGGT  A  A  III
GAM256  GCK     5' GCCGCAGGGGTCACGG     6657     C      CCG
                                GCC CAGGGGTC   ACGG
                                ||| |||||||   ||||
                                CGG GTCCCCAG   TGCC
                                  C      ___
GAM256  GNAO1   3' GCCCCAGGCGGCAGATGG   6658        _  CCC  C
                                GCCCCAGG GGT   GA GG
                                |||||||| |||   || ||
                                CGGGGTCC CCG   CT CC
                                     G   T__  A
GAM256  HNF4G   5' GCCTAGGGGTCCTGAGG    6659     CC      C  C
                                GCC  AGGGGTCC GA GG
                                |||  |||||||| || ||
```

```
                                CGG  TCCCCAGG CT CC
                                  A_       A  _
GAM256  HYOU1    3'  GCCCCAGGGGGTCAGGCCGTCG 6660          _ _______  GAC
                G                  GCCCCAGGGG TC     CC   GG
                                   |||||||||| ||     ||   ||
                                   CGGGGTCCCC AG     GG   CC
                                        C  TCCIII  CAG
GAM256  INHBB    5'  GCCCCGGGGGCCCGAGG     6661       A   T    C
                                   GCCCC GGGG CCCGA GG
                                   ||||| |||| ||||| ||
                                   CGGGG CCCC GGGCT CC
                                     C   _    _
GAM256  ITGB4    3'  CCCCAGGGGTGCAAGG      6662          CC   C
                                   CCCCAGGGGT  CGA GG
                                   ||||||||||  ||| ||
                                   GGGGTCCCCA  GTT CC
                                         C_  _
GAM256  LEF1     5'  GCCCGAATCCCGGCGG      6663       CAG       A
                                   GCCC   GGGTCCCG CGG
                                   ||||   |||||||| |||
                                   CGGG   CTTAGGGC GCC
                                     ___       C
GAM256  LHB      3'  GCTCCAGGAGTCGGGATGG   6664     C        CC  C
                                   GC CCAGGGGTC  GA GG
                                   || |||||||||  || ||
                                   CG GGTCCTCAG  CT CC
                                    A        CC  A
GAM256  LHX5     3'  GCCCCCGGGGGCCGAGCG    6665       A    TC   _
                                   GCCCC GGGG  CCGA CG
                                   ||||| ||||  |||| ||
                                   CGGGG CCCC  GGCT GC
                                     G   C_    C
GAM256  LOXL2    3'  GCCCCAAGGGTCAGGCCGTG  6666           _______  GAC
                                   GCCCCAGGGGTC     CC   G
                                   ||||||||||||     ||   |
                                   CGGGGTTCCCAG     GG   C
                                         TCCIII  CAG
GAM256  LTBR     5'  ACCCCAGGGCCGGGAGCGG   6667         G  CC  _
                                   GCCCCAGGG TC  GA CGG
                                   |||||||| ||  || |||
                                   TGGGGTCCC GG  CT GCC
                                         _ CC  C
GAM256  M11S1    5'  CCCGGAGGAACCCGACGG    6668      A   T_
                                   CCC GGGG  CCCGACGG
                                   ||| ||||  ||||||||
                                   GGG CTCC  GGGCTGCC
                                    C    TT
GAM256  MAP3K10  5'  GCCCCGGCGGCCGGGATGG   6669       A  _   CC  C
                                   GCCCC GG GGTC  GA GG
                                   ||||| || ||||  || ||
```

```
                                CGGGG CC CCGG  CT CC
                                  _ G   CC  A
GAM256  MGAT3   5' GCCCCCGGGGTCCCCGGCGG  6670      A      _ A
                                GCCCC GGGGTCCC G CGG
                                ||||| |||||||| | |||
                                CGGGG CCCCAGGG C GCC
                                  G       G C
GAM256  NDST1   5' GCCCCAGGGCGTCAGGCCGTCG 6671         _  _______  GAC
          G                      GCCCCAGGG GTC     CC   GG
                                ||||||||| |||     ||   ||
                                CGGGGTCCC CAG     GG   CC
                                     G   TCCIII  CAG
GAM256  NONO    3' GCTCCAGGAGCTGCACGG    6672     C       CC G
                                GC CCAGGGGT  C ACGG
                                || ||||||||  | ||||
                                CG GGTCCTCG  G TGCC
                                 A       AC _
GAM256  NRGN    3' GCCCCAGGAGCCCGGCGG    6673          T    A
                                GCCCCAGGGG CCCG CGG
                                |||||||||| |||| |||
                                CGGGGTCCTC GGGC GCC
                                     _   C
GAM256  PARK2   3' CCCCAGGATGTGGCGATGG   6674         _ CC   C
                                CCCCAGGG GT  CGA GG
                                |||||||| ||  ||| ||
                                GGGGTCCT CA  GCT CC
                                     A  CC   A
GAM256  PARK2   3' CCCCAGGATGTGGCGATGG   6674         _ CC   C
                                CCCCAGGG GT  CGA GG
                                |||||||| ||  ||| ||
                                GGGGTCCT CA  GCT CC
                                     A  CC   A
GAM256  PARK2   3' CCCCAGGATGTGGCGATGG   6674         _ CC   C
                                CCCCAGGG GT  CGA GG
                                |||||||| ||  ||| ||
                                GGGGTCCT CA  GCT CC
                                     A  CC   A
GAM256  PGF     5' GCCCCGAGGCCCCGGCCGG   6675       A       A_
                                GCCCC GGGGTCCCG  CGG
                                ||||| |||||||||  |||
                                CGGGG CTCCGGGGC  GCC
                                  _       CG
GAM256  PKHD1   3' GCCTCAGGGATCACAG      6676      C       CCG
                                GCC CAGGGGTC   ACGG
                                ||| ||||||||   ||||
                                CGG GTCCCTAG   TGTC
                                 A       ___
GAM256  PLA2G10 5' GCTCCAGAGGCCGCGG      6677     C      TC   A
                                GC CCAGGGG  CCG CGG
                                || |||||||  ||| |||
```

```
                                CG GGTCTCC  GGC GCC
                                 A      __  _
GAM256  PMX1     5'  GCTTCAAGAGTCCGACGG    6678     CC       C
                                GC  CAGGGGTCC GACGG
                                ||  ||||||||| |||||
                                CG  GTTCTCAGG CTGCC
                                 AA       _
GAM256  PMX1     5'  GCTTCAAGAGTCCGACGG    6678     CC       C
                                GC  CAGGGGTCC GACGG
                                ||  ||||||||| |||||
                                CG  GTTCTCAGG CTGCC
                                 AA       _
GAM256  PPP2R4   3'  GCCCTAGGAGAAACCTCGGCGG 6679      C    T__  _  A
                                GCCC AGGGG   CC CG CGG
                                |||| |||||   || || |||
                                CGGG TCCTC   GG GC GCC
                                  A    TTT  A  C
GAM256  PRex1    3'  GCTCCAGAGGCCGCGG      6677     C      TC   A
                                GC CCAGGGG  CCG CGG
                                || |||||||  ||| |||
                                CG GGTCTCC  GGC GCC
                                 A      __  _
GAM256  PTPRA    5'  GCTCCGAGCCCCGCGG      6680     C  AG       A
                                GC CC  GGGTCCCG CGG
                                || ||  |||||||| |||
                                CG GG  CTCGGGGC GCC
                                 A  __       _
GAM256  REST     5'  GCCCCGGGCCTCGGCGG     6681       AG    C  A
                                GCCCC  GGGTC CG CGG
                                |||||  ||||| || |||
                                CGGGG  CCCGG GC GCC
                                   __     A  C
GAM256  RUNX1    3'  GCCCGGGATCCCGGCGG     6682       CA       A
                                GCCC  GGGGTCCCG CGG
                                ||||  ||||||||| |||
                                CGGG  CCCTAGGGC GCC
                                   __        C
GAM256  RYR2     5'  GCCCCGCGGAGCTCGGCGG   6683       A_    CC  A
                                GCCCC  GGGGT  CG CGG
                                |||||  |||||  || |||
                                CGGGG  CCTCG  GC GCC
                                   CG    A_  C
GAM256  SIAH2    5'  GCCCCGGGGGCGCGCGCGG   6684       A    CC_  A
                                GCCCC GGGGT   CG CGG
                                ||||| |||||   || |||
                                CGGGG CCCCG   GC GCC
                                   C    CGC  _
GAM256  SLC17A5  5'  GCCCCCGGGCCGAGCGG     6685       A  GTC    _
                                GCCCC GGG   CCGA CGG
                                ||||| |||   |||| |||
```

```
                                CGGGG CCC   GGCT GCC
                                  G  ___    C
GAM256  SOX11    3'  GCCTCAAGGGCCCGCGGCGG  6686     C       _ A
                                GCC CAGGGGTCC CG CGG
                                ||| ||||||||| || |||
                                CGG GTTCCCGGG GC GCC
                                  A        C  C
GAM256  SRD5A1   5'  GCCCCAGAGGCCGCGGCGG   6687           C  A
                                GCCCCAGGGGTC CG CGG
                                |||||||||||| || |||
                                CGGGGTCTCCGG GC GCC
                                       C  C
GAM256  TGFA     3'  GCCCCATGGGTCAGATGG    6688       G    CC  C
                                GCCCCA GGGTC  GA GG
                                |||||| |||||  || ||
                                CGGGGT CCCAG  CT CC
                                   A    T_  A
GAM256  TNFRSF6B 5'  CCTCCTGGGGTCCCGGTGG   6689    _ A       AC
                                CC CC GGGGTCCCG  GG
                                || || |||||||||  ||
                                GG GG CCCCAGGGC  CC
                                 A  A        CA
GAM256  TRPS1    3'  CCTCCAAAGTCCCGACGG    6690    _     G
                                CC CCAGGG TCCCGACGG
                                || |||||| |||||||||
                                GG GGTTTC AGGGCTGCC
                                 A     _
GAM256  TRPV1    5'  GCCTCAGAGGTGAGCAG     6691     C      CCC  _
                                GCC CAGGGGT   GA CGG
                                ||| |||||||   || |||
                                CGG GTCTCCA   CT GTC
                                  A      ___  C
GAM256  TXNRD2   3'  GCCTGGGGGGGGGGTGCCCGGCG 6692      CCA___    _   A
           G                     GCC     GGGGT CCCG CGG
                                |||      ||||| |||| |||
                                CGG     CCCCA GGGC GCC
                                  ACCCCC    C   C
GAM256  WBP2     3'  GCCCCAGCACAGCCCCGATGG  6693        G__       C
                                GCCCCAG   GGTCCCGA GG
                                |||||||   |||||||| ||
                                CGGGGTC   TCGGGGCT CC
                                    GTG       A
GAM256  WNT7A    5'  GCCGCCGGGGCCGCGG      6694     _ A   TC   A
                                GCC CC GGGG  CCG CGG
                                ||| || ||||  ||| |||
                                CGG GG CCCC  GGC GCC
                                  C  _   __  _
GAM256  ZNF264   5'  GCCCCGGGCGGCCTGACGG   6695       A  _  T  C
                                GCCCC GG GG CC GACGG
                                ||||| || || || |||||
```

```
                                CGGGG CC CC GG CTGCC
                                  C  G  _  A
GAM256  AD-017   5'  GCTCCGGGGATCCCACCAG   6696    C  A       A
                                GC CC GGGGTCCCG CGG
                                || || ||||||||| |||
                                CG GG CCCTAGGGT GTC
                                 A  C        G
GAM256  ALS2CR12 3'  GCCCCAGGGGACAAAGG    6697          TCC   C
                                GCCCCAGGGG   CGA GG
                                ||||||||||   ||| ||
                                CGGGGTCCCC   GTT CC
                                      T__   T
GAM256  ARFGAP1  3'  GCTCCAGGAGTGCTGCAGACGG 6698    C       CCC___
                                GC CCAGGGGT     GACGG
                                || ||||||||     |||||
                                CG GGTCCTCA     CTGCC
                                 A       CGACGT
GAM256  ASB16    5'  GCCCCAGAGGAAAACTGG    6699          TCCC  _
                                GCCCCAGGGG    GAC GG
                                ||||||||||    ||| ||
                                CGGGGTCTCC    TTG CC
                                      TT__   A
GAM256  ASE-1    5'  GCCCGTCGGGTCCCGATGG   6700      CAG       C
                                GCCC   GGGTCCCGA GG
                                ||||   ||||||||| ||
                                CGGG   CCCAGGGCT CC
                                  CAG        A
GAM256  C11orf11 5'  ACTCCAGGGGCGAACCGCGG  6701     C       C__   A
                                GC CCAGGGGT   CCG CGG
                                || ||||||||   ||| |||
                                TG GGTCCCCG   GGC GCC
                                 A       CTT   _
GAM256  C20orf124 3'  GCCCCAGGCGCAGCGCGG    6702        G  CC  A
                                GCCCCAGG GT  CG CGG
                                |||||||| ||  || |||
                                CGGGGTCC CG  GC GCC
                                     G  TC  _
GAM256  CAMTA2   5'  GCTCCCGGGGTCCCGCGG    6703    _  A       A
                                GC CCC GGGGTCCCG CGG
                                || ||| ||||||||| |||
                                CG GGG CCCCAGGGC GCC
                                 A  _        _
GAM256  CARM1    3'  GCCCCTGAAGCCTCGGCGG   6704      A     C  A
                                GCCCC GGGGTC CG CGG
                                ||||| |||||| || |||
                                CGGGG CTTCGG GC GCC
                                   A     A  C
GAM256  CCNB2    3'  CCCCAGGGCCCACGG       6705         GT   G
                                CCCCAGGG  CCC ACGG
                                ||||||||  ||| ||||
```

```
                                GGGGTCCC  GGG TGCC
                                   __   _
GAM256  CDIPT    5'  GCCCCGAGGTGCGCGG      6706       A    CC  A
                                GCCCC GGGGT  CG CGG
                                ||||| |||||  || |||
                                CGGGG CTCCA  GC GCC
                                   _    C_  _
GAM256  CGB2     3'  GCCCCGGGAGTCGGGATGG   6707       A     CC  C
                                GCCCC GGGGTC  GA GG
                                ||||| ||||||  || ||
                                CGGGG CCTCAG  CT CC
                                   C     CC  A
GAM256  DKFZP434B205 3'  CCTCAAGGGGTCCCGGTGG   6708     C  _       AC
                                CC CA GGGGTCCCG  GG
                                || || |||||||||  ||
                                GG GT CCCCAGGGC  CC
                                 A  T        CA
GAM256  DKFZP564K0322 5'  GCCCCAGGGACGCGG       6709          TCC  A
                                GCCCCAGGGG   CG CGG
                                ||||||||||   || |||
                                CGGGGTCCCT   GC GCC
                                   ____  _
GAM256  DKFZP586M1120 3'  ACTCCAGGGGCTGCAAGG    6710     C       CC   C
                                GC CCAGGGGT  CGA GG
                                || ||||||||  ||| ||
                                TG GGTCCCCG  GTT CC
                                 A       AC  _
GAM256  EIF2S2   5'  GCCCCAGGCCCCGGCGG     6711       GG      A
                                GCCCCA  GGTCCCG CGG
                                ||||||  ||||||| |||
                                CGGGGT  CCGGGGC GCC
                                   __      C
GAM256  FBXO26   5'  GCCCCGGGACCGGCGG      6712       A   TC   A
                                GCCCC GGGG  CCG CGG
                                ||||| ||||  ||| |||
                                CGGGG CCCT  GGC GCC
                                   _   __  C
GAM256  FEM-2    3'  GCCCCAGGGTCCCACG       6713         G   G
                                GCCCCAGGG TCCC ACG
                                ||||||||| |||| |||
                                CGGGGTCCC AGGG TGC
                                   _   _
GAM256  FJX1     5'  GCACCCGGGTCCCGGCGG    6714     _  AG       A
                                GC CCC  GGGTCCCG CGG
                                || |||  |||||||| |||
                                CG GGG  CCCAGGGC GCC
                                 T  __       C
GAM256  FLJ10006 5'  ACCTGGAAGCCCCGGCGG    6715      CCA        A
                                GCC   GGGGTCCCG CGG
                                |||   ||||||||| |||
```

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                                TGG   CTTCGGGGC GCC
                                  AC_       C
GAM256  FLJ11743  3'  GCCCCAAAACGCCGATGG    6716         GTC    C
                                GCCCCAGGG   CCGA GG
                                |||||||||   |||| ||
                                CGGGGTTTT   GGCT CC
                                     GC_    A
GAM256  FLJ14251  3'  ACCCCAGGGCTTCTGATGG   6717          G_  CC  C
                                GCCCCAGGG  TC  GA GG
                                |||||||||  ||  || ||
                                TGGGGTCCC  AG  CT CC
                                     GA  A_  A
GAM256  FLJ14668  3'  GCCTCAGGGGCCATCAGCCGTC 6718     C       _________  GAC
           GG                     GCC CAGGGGTC       CC   GG
                                ||| ||||||||       ||   ||
                                CGG GTCCCCGG       GG   CC
                                  A       TAGTCIII  CAG
GAM256  FLJ20034  3'  GCCCCAGCTCATCCTGATGG   6719        GG_   C  C
                                GCCCCAG   GTCC GA GG
                                |||||||   |||| || ||
                                CGGGGTC   TAGG CT CC
                                    GAG    A  A
GAM256  FLJ20783  3'  GCCCCAGAGGGCAGGACGG    6720         _    CCC
                                GCCCCAG GGGT   GACGG
                                ||||||| ||||   |||||
                                CGGGGTC CCCG   CTGCC
                                    T    TC_
GAM256  FLJ21438  3'  GCCCCAGGGCTCAGATGG     6721         G  CC  C
                                GCCCCAGGG TC  GA GG
                                ||||||||| ||  || ||
                                CGGGGTCCC AG  CT CC
                                     G  T_  A
GAM256  FLJ21736  5'  GCTCATGAAGTCCCCGG      6722     CC  _       GA
                                GC  CA GGGGTCCC  CGG
                                ||  || ||||||||  |||
                                CG  GT CTTCAGGG  GCC
                                 A_  A       __
GAM256  FLJ32919  3'  CCCCAGGGGTCAAGGCCGTCGG 6723           ________  GAC
                                CCCCAGGGGTC      CC   GG
                                ||||||||||       ||   ||
                                GGGGTCCCCAG      GG   CC
                                      TTCCIII  CAG
GAM256  GPS2      5'  ACCCCAGGGGACGCGG      6724          TCC  A
                                GCCCCAGGGG   CG CGG
                                ||||||||||   || |||
                                TGGGGTCCCC   GC GCC
                                     T__  _
GAM256  HPCAL4    3'  CCCTCAAAGATCTTGATGG    6725      _      CC  C
                                CCC CAGGGGTC  GA GG
                                ||| ||||||||  || ||
```

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                                GGG GTTTCTAG  CT CC
                                  A       AA  A
GAM256  HUMNPIIY20 3'  GCCAGGGCCCCGCGG      6726      CCA       A
                                GCC   GGGGTCCCG CGG
                                |||   ||||||||| |||
                                CGG   TCCCGGGGC GCC
                                  ___       _
GAM256  IRAK3    5'  GCCCCGGGGACGAGGCGG    6727       A    TCC  __
                                GCCCC GGGG   CGA  CGG
                                ||||| ||||   |||  |||
                                CGGGG CCCC   GCT  GCC
                                  _   T__   CC
GAM256  KIAA0014  3'  GCCCCGGCCCGAGGCGG     6728       AGG  T    __
                                GCCCC   GG CCCGA  CGG
                                |||||   || |||||  |||
                                CGGGG   CC GGGCT  GCC
                                  ___ _    CC
GAM256  KIAA0140  3'  GCCCCACGGGTGGACGG     6729       G    CCC
                                GCCCCA GGGT   GACGG
                                |||||| ||||   |||||
                                CGGGGT CCCA   CTGCC
                                   G    C__
GAM256  KIAA0152  3'  GCCCCAGGAGTCAGGCCGTG   6730           _______  GAC
                                GCCCCAGGGGTC     CC   G
                                ||||||||||||     ||   |
                                CGGGGTCCTCAG     GG   C
                                      TCCIII  CAG
GAM256  KIAA0194  5'  GCCCCGGGGGTCAAGCCGTCGG 6731       A     _______  GAC
                                GCCCC GGGGTC     CC   GG
                                ||||| ||||||     ||   ||
                                CGGGG CCCCAG     GG   CC
                                   C     TTCIII  CAG
GAM256  KIAA0222  3'  GCCCCAGGGAGGAGTGCGATGG 6732           TCC___   C
                                GCCCCAGGGG     CGA GG
                                ||||||||||     ||| ||
                                CGGGGTCCCT     GCT CC
                                      CCTCAC   A
GAM256  KIAA0285  5'  ACCCCAGGGGTCAGCCGTG   6733           _____  GAC
                                GCCCCAGGGGTC    CC   G
                                ||||||||||||    ||   |
                                TGGGGTCCCCAG    GG   C
                                      TCIII  CAG
GAM256  KIAA0652  3'  GCCCCAGGGATCAGGCCGTG  6734           _______  GAC
                                GCCCCAGGGGTC     CC   G
                                ||||||||||||     ||   |
                                CGGGGTCCCTAG     GG   C
                                      TCCIII  CAG
GAM256  KIAA0939  3'  GCCGCAGGGGTCCTCCGG    6735      C        CGA
                                GCC CAGGGGTCC   CGG
                                ||| |||||||||   |||
```

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                                CGG GTCCCCAGG   GCC
                                  C       AG_
GAM256  KIAA1116 5' GCCCCGAGCCCGGCGG     6736      AG   T   A
                                GCCCC  GGG CCCG CGG
                                |||||  ||| |||| |||
                                CGGGG  CTC GGGC GCC
                                  __  _   C
GAM256  KIAA1130 5' GCCCCAGGTGGGGGACTGG   6737        _ TCCC  _
                                GCCCCAGG GG   GAC GG
                                |||||||| ||   ||| ||
                                CGGGGTCC CC   CTG CC
                                    A  CC__  A
GAM256  KIAA1190 3' GCCCCAGCGGGTGCACGG    6738       _   CCCG
                                GCCCCAG GGGT   ACGG
                                ||||||| ||||   ||||
                                CGGGGTC CCCA   TGCC
                                    G   CG__
GAM256  KIAA1193 3' CCCCGGCTGCCCGACGG     6739      A  G_ T
                                CCCC GG  G CCCGACGG
                                |||| ||  | ||||||||
                                GGGG CC  C GGGCTGCC
                                  _  GA _
GAM256  KIAA1194 5' GCCTCAGCCGCCCCGACGG   6740     C   GG
                                GCC CAG  GTCCCGACGG
                                ||| |||  ||||||||||
                                CGG GTC  CGGGGCTGCC
                                  A   GG
GAM256  KIAA1857 5' GCCCTGGAGAGGCAGCGACGG 6741      C__     CC
                                GCCC   AGGGGT  CGACGG
                                ||||   ||||||  ||||||
                                CGGG   TCTCCG  GCTGCC
                                  ACC     TC
GAM256  KIAA1879 3' GCCCCAGGGCTTCAGGCCGTCG 6742         G_ _______  GAC
          G                   GCCCCAGGG  TC     CC   GG
                              |||||||||  ||     ||   ||
                              CGGGGTCCC  AG     GG   CC
                                   GA  TCCIII  CAG
GAM256  KIAA1904 3' CCCCAGGCTCCCCGACGG    6743       GG
                                CCCCAGG  TCCCGACGG
                                |||||||  |||||||||
                                GGGGTCC  GGGGCTGCC
                                   GA
GAM256  LIMK2    5' GCCCCAGGCGCGAACGG     6744        G  CCC
                                GCCCCAGG GT   GACGG
                                |||||||| ||   |||||
                                CGGGGTCC CG   TTGCC
                                   G  C__
GAM256  LYPLA2   3' ACCCCGGGGCCATGGCCGTCGG 6745       A     ________  GAC
                                GCCCC GGGGTC      CC   GG
                                ||||| ||||||      ||   ||
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                                TGGGG CCCCGG      GG   CC
                                  _     TACCIII  CAG
GAM256  MGC10334  5'  GCTCCGGGGGCCCCACG     6746     C  A       G
                                GC CC GGGGTCCC ACG
                                || || |||||||| |||
                                CG GG CCCCGGGG TGC
                                 A  C       _
GAM256  MGC12904  5'  GCCTCAGGTCCCACGG      6747      C  GG     G
                                GCC CA  GGTCCC ACGG
                                ||| ||  |||||| ||||
                                CGG GT  CCAGGG TGCC
                                  A  __     _
GAM256  MGC15438  3'  GCCGGGGTCCCGGCGG      6748      CCA       A
                                GCC   GGGGTCCCG CGG
                                |||   ||||||||| |||
                                CGG   CCCCAGGGC GCC
                                  ____        C
GAM256  MGC16491  5'  GCCCCCGGGCCCCGACGG    6749       AG
                                GCCCC  GGGTCCCGACGG
                                |||||  ||||||||||||
                                CGGGG  CCCGGGGCTGCC
                                   G_
GAM256  MGC2487   5'  GCCCCAGGAGGGACGG      6750          TCCC
                                GCCCCAGGGG    GACGG
                                ||||||||||    |||||
                                CGGGGTCCTC    CTGCC
                                      C___
GAM256  MGC4701   5'  GCCCCAGGGATCCGCGG     6751            C A
                                GCCCCAGGGGTCC G CGG
                                |||||||||||| | |||
                                CGGGGTCCCTAGG C GCC
                                          _ _
GAM256  MGC5442   3'  GCCCCGAGCCCCGGCGG     6643       AG       A
                                GCCCC  GGGTCCCG CGG
                                |||||  |||||||| |||
                                CGGGG  CTCGGGGC GCC
                                   __       C
GAM256  MGC5442   3'  GCCCCGGCGGTCGCAGGGCGG  6752       A  _    C  A__
                                GCCCC GG GGTC CG   CGG
                                ||||| || |||| ||   |||
                                CGGGG CC CCAG GT   GCC
                                   _ G    C  CCC
GAM256  NCX       5'  GCCTCAGGGGCCCGCGG     6753      C     T    A
                                GCC CAGGGG CCCG CGG
                                ||| |||||| |||| |||
                                CGG GTCCCC GGGC GCC
                                  A     _    _
GAM256  NEIL1     5'  GCCCTAGGGACCCGGTGG     6754       C     T    AC
                                GCCC AGGGG CCCG  GG
                                |||| ||||| ||||  ||
```

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                                CGGG TCCCT GGGC  CC
                                  A    _   CA
GAM256  NFAT5    5' ACCCCAGAGGCCGGCGG    6755         TC   A
                                GCCCCAGGGG  CCG CGG
                                ||||||||||  ||| |||
                                TGGGGTCTCC  GGC GCC
                                      __  C
GAM256  NPTXR    5' GCCCCCGGCAGGCGCGGCGG  6756      A __  CC  A
                                GCCCC GG  GGT  CG CGG
                                ||||| ||  |||  || |||
                                CGGGG CC  CCG  GC GCC
                                   G  GT   C_  C
GAM256  NPTXR    5' GCCCCCGGCAGGCGCGGCGG  6756      A __  CC  A
                                GCCCC GG  GGT  CG CGG
                                ||||| ||  |||  || |||
                                CGGGG CC  CCG  GC GCC
                                   G  GT   C_  C
GAM256  NRBF-2   5' ACCCCGGGGTAAGCGGCGG   6757      A    CC_  A
                                GCCCC GGGGT   CG CGG
                                ||||| |||||   || |||
                                TGGGG CCCCA   GC GCC
                                  _    TTC  C
GAM256  OAZ2     3' GCCCCTGGGGTGACAG     6758       A    CCC
                                GCCCC GGGGT   GACGG
                                ||||| |||||   |||||
                                CGGGG CCCCA   CTGTC
                                  A   ___
GAM256  P114-RHO-GEF 3' CCCAGGGGAGCACTTCCTGATG 6759         _______  C  C  III
           GC                    CCCAGGGG     TCC GA GG   C
                                ||||||||     ||| || ||  |
                                GGGTCCCC     AGG CT CC   G
                                    TCGTGA   A  A  III
GAM256  p25      3' CCTCCAGGGGCCAAGATGG   6760    _       CC  C
                                CC CCAGGGGTC  GA GG
                                || |||||||||  || ||
                                GG GGTCCCCGG  CT CC
                                 A        TT  A
GAM256  PADI3    3' GCCCCAGGGGGACAG      6761          TCCC
                                GCCCCAGGGG   GACGG
                                ||||||||||   |||||
                                CGGGGTCCCC   CTGTC
                                     _____
GAM256  PLEKHA4  5' GCTCTGGGGTCCCAGTGACGG 6762     CCCA      ___
                                GC   GGGGTCCC   GACGG
                                ||   ||||||||   |||||
                                CG   CCCCAGGG   CTGCC
                                 AGA_       TCA
GAM256  PPM1G    5' GCCCCGGGGGTGCGCGCGG   6763      A    CC_  A
                                GCCCC GGGGT   CG CGG
                                ||||| |||||   || |||
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                                CGGGG CCCCA  GC GCC
                                  C    CGC  _
GAM256  PRSS25   5'  GCCCAAGGGGCCGCGG     6764      C    TC   A
                                GCCC AGGGG  CCG CGG
                                |||| |||||  ||| |||
                                CGGG TCCCC  GGC GCC
                                  T    __  _
GAM256  PRSS25   5'  GCCCAAGGGGCCGCGG     6764      C    TC   A
                                GCCC AGGGG  CCG CGG
                                |||| |||||  ||| |||
                                CGGG TCCCC  GGC GCC
                                  T    __  _
GAM256  PSKH1    3'  GCCCCAGGGCTTCAGGCCGTCG 6742         G_ _______ GAC
          G                      GCCCCAGGG  TC    CC   GG
                                |||||||||  ||    ||   ||
                                CGGGGTCCC  AG    GG   CC
                                     GA  TCCIII  CAG
GAM256  R32184_3 3'  GCCCCAGGCGAGACGG     6765        _ TCCC
                                GCCCCAGG GG   GACGG
                                |||||||| ||   |||||
                                CGGGGTCC CT   CTGCC
                                     G ____
GAM256  RAI16    5'  GCCCCAGGAGGCGACGCGG   6766        _  CC  A
                                GCCCCAGG GGT  CG CGG
                                |||||||| |||  || |||
                                CGGGGTCC CCG  GC GCC
                                     T  CT  _
GAM256  RASD2    3'  GCCCCAGGGGCCAAGCCGTG  6767          _______ GAC
                                GCCCCAGGGGTC    CC   G
                                ||||||||||||    ||   |
                                CGGGGTCCCCGG    GG   C
                                       TTCIII  CAG
GAM256  RBM5     5'  CCTCCAACAAGGTTCGGCGG  6768    _   __   CC  A
                                CC CCAG  GGGT  CG CGG
                                || ||||  ||||  || |||
                                GG GGTT  TCCA  GC GCC
                                 A   GT   A_  C
GAM256  RBT1     3'  GCCCCAGTGGTCACAG     6769       G   CCG
                                GCCCCAG GGTC   ACGG
                                ||||||| ||||   ||||
                                CGGGGTC CCAG   TGTC
                                   A   ___
GAM256  SDCCAG28 3'  GCCCCAGGGCTCCGCCGG   6770        G   CGA
                                GCCCCAGGG TCC   CGG
                                ||||||||| |||   |||
                                CGGGGTCCC AGG   GCC
                                     G  CG_
GAM256  SEMA7A   3'  GCCCCAGGGTCGAGATGG   6771        G  CC  C
                                GCCCCAGGG TC  GA GG
                                ||||||||| ||  || ||
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                                CGGGGTCCC AG  CT CC
                                     _ CT  A
GAM256  SLC2A10  5'  GCCCCGAGGCCTGGAGGCGG  6772       A     CC __
                                GCCCC GGGGTC  GA  CGG
                                ||||| ||||||  ||  |||
                                CGGGG CTCCGG  CT  GCC
                                   _     AC  CC
GAM256  SMCR7    5'  GCCCCGGGGGCAGCCGCGG   6773       A    C_  A
                                GCCCC GGGGT  CCG CGG
                                ||||| |||||  ||| |||
                                CGGGG CCCCG  GGC GCC
                                   C     TC  _
GAM256  SP2      3'  GCCCCAGGGCGTCCACAG    6774          _   CG
                                GCCCCAGGG GTCC  ACGG
                                ||||||||| ||||  ||||
                                CGGGGTCCC CAGG  TGTC
                                     G   __
GAM256  SSBP4    5'  GCCCCAGGCGGGCACGG     6775         _  TCC G
                                GCCCCAGG GG   C ACGG
                                |||||||| ||   | ||||
                                CGGGGTCC CC   G TGCC
                                     G  C__ _
GAM256  STAF65(gamma) 5'  CCTCCAGGGGTTTCCTCGG   6776    _       C_  GA
                                CC CCAGGGGT  CC  CGG
                                || ||||||||  ||  |||
                                GG GGTCCCCA  GG  GCC
                                 A       AA  A_
GAM256  STAT5A   5'  CCCAGCAGGCCCTCGGCGG   6777       _     _  A
                                CCCAG GGGTCC CG CGG
                                ||||| |||||| || |||
                                GGGTC TCCGGG GC GCC
                                   G     A  C
GAM256  TADA3L   5'  GCCCCAGGGGCCGCGG      6778          TC   A
                                GCCCCAGGGG  CCG CGG
                                ||||||||||  ||| |||
                                CGGGGTCCCC  GGC GCC
                                     __   _
GAM256  TADA3L   5'  GCCCCAGGGGCCGCGG      6778          TC   A
                                GCCCCAGGGG  CCG CGG
                                ||||||||||  ||| |||
                                CGGGGTCCCC  GGC GCC
                                     __   _
GAM256  TADA3L   5'  GCCCCAGGGGCCGCGG      6778          TC   A
                                GCCCCAGGGG  CCG CGG
                                ||||||||||  ||| |||
                                CGGGGTCCCC  GGC GCC
                                     __   _
GAM256  TRAF3    5'  GCTCCAGAAGCCGACGG     6779     C      TC
                                GC CCAGGGG  CCGACGG
                                || |||||||  |||||||
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                                CG GGTCTTC  GGCTGCC
                                 A      __
GAM256  TRIP-Br2  5'  GCTCCAGGGGCCCGAGGG    6780     C      T    C
                                GC CCAGGGG CCCGA GG
                                || ||||||| ||||| ||
                                CG GGTCCCC GGGCT CC
                                 A      _    C
GAM256  LOC112473 5'  ACCCCAAGGCCCGATGG     6781          GT    C
                                GCCCCAGGG  CCCGA GG
                                |||||||||  ||||| ||
                                TGGGGTTCC  GGGCT CC
                                      __    A
GAM256  LOC119559 3'  ACCCCAGGGGTGTCAGACGG  6782           CC _
                                GCCCCAGGGGT  C GACGG
                                ||||||||||  | |||||
                                TGGGGTCCCCA  G CTGCC
                                       CA T
GAM256  LOC123905 5'  GCCCCAAGGGGCTGGATGG   6783        _    CCC  C
                                GCCCCA GGGGT   GA GG
                                ||||||| |||||   || ||
                                CGGGGT CCCCG   CT CC
                                   T    AC_  A
GAM256  LOC124976 3'  GCCCCAGGGGCCCTGCGG    6784          T   GA
                                GCCCCAGGGG CCC  CGG
                                |||||||||| |||  |||
                                CGGGGTCCCC GGG  GCC
                                      _  AC
GAM256  LOC126133 3'  GCCCCAGAGGTCGAGG      6785          CC  C
                                GCCCCAGGGGTC  GA GG
                                ||||||||||||  || ||
                                CGGGGTCTCCAG  CT CC
                                      __ _
GAM256  LOC132617 3'  CCCCAGGGCTCTGTCGATGG  6786         G  C__   C
                                CCCCAGGG TC   CGA GG
                                |||||||| ||   ||| ||
                                GGGGTCCC AG   GCT CC
                                     G  ACA   A
GAM256  LOC143677 3'  GCCCAAGGGAGGCTCTGATGG 6787      C    ___  CC  C
                                GCCC AGGGG   TC  GA GG
                                |||| |||||   ||  || ||
                                CGGG TCCCT   AG  CT CC
                                  T    CCG  A_  A
GAM256  LOC144587 5'  GCCCCAGGTGGAGGACGG    6788         _  TCCC
                                GCCCCAGG GG    GACGG
                                |||||||| ||    |||||
                                CGGGGTCC CC    CTGCC
                                     A  TC__
GAM256  LOC144810 5'  CCCAGGGGAAACCTGACGG   6789         TC_  _
                                CCCAGGGG   CC GACGG
                                ||||||||   || |||||
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                                GGGTCCCC   GG CTGCC
                                    TTT  A
GAM256  LOC145989 5'  GCCGCTGGGCCCCGACGG    6790      CCAG
                                GCC    GGGTCCCGACGG
                                |||    ||||||||||||
                                CGG    CCCGGGGCTGCC
                                  CGA_
GAM256  LOC146237 3'  GCCCACAGAGGTTCGGTGG    6791       _      CC  AC
                                GCCC CAGGGGT  CG  GG
                                |||| |||||||  ||  ||
                                CGGG GTCTCCA  GC  CC
                                  T      A_  CA
GAM256  LOC147958 3'  GCCCGGGCAGCCTGACGG    6792       CAG    __  C
                                GCCC   GGGT  CC GACGG
                                ||||   ||||  || |||||
                                CGGG   CCCG  GG CTGCC
                                  ___    TC  A
GAM256  LOC148936 3'  ACCCCAGCGGTGACGG      6793        G   CCC
                                GCCCCAG GGT   GACGG
                                |||||||  |||   |||||
                                TGGGGTC CCA   CTGCC
                                   G   ___
GAM256  LOC148938 3'  ACCCCAGCGGTGACGG      6793        G   CCC
                                GCCCCAG GGT   GACGG
                                |||||||  |||   |||||
                                TGGGGTC CCA   CTGCC
                                   G   ___
GAM256  LOC149460 5'  GCCCCAGGGGTCAGCCGTG   6794            _____  GAC
                                GCCCCAGGGGTC    CC   G
                                ||||||||||||    ||   |
                                CGGGGTCCCCAG    GG   C
                                      TCIII  CAG
GAM256  LOC149670 3'  GCCCTGGGGGTCCCCCAG    6795       CA       GA
                                GCCC  GGGGTCCC  CGG
                                ||||  ||||||||  |||
                                CGGG  CCCCAGGG  GTC
                                  AC       G_
GAM256  LOC150421 3'  GCCCCAGGGGGTCGAGG     6796           TCC   C
                                GCCCCAGGGG   CGA GG
                                |||||||||   ||| ||
                                CGGGGTCCCC   GCT CC
                                     CA_   _
GAM256  LOC150481 3'  GCCCCAGGGTCAGTGGCCGTCG 6797          G  _________  GAC
          G                      GCCCCAGGG TC       CC   GG
                                 |||||||||  ||       ||   ||
                                 CGGGGTCCC AG       GG   CC
                                      _  TCACCIII  CAG
GAM256  LOC151188 5'  CCCAGGGGTAAACCACGG    6798          C__  G
                                CCCAGGGGT   CC ACGG
                                |||||||||   || ||||
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                                GGGTCCCCA  GG TGCC
                                     TTT  _
GAM256  LOC152189 5'  CCCCAGGGACCCCGGCGG   6799        GT   A
                                CCCCAGGG  CCCG CGG
                                ||||||||  |||| |||
                                GGGGTCCC  GGGC GCC
                                    TG   C
GAM256  LOC152286 3'  CCCTCAGAGGCCTGACGG   6800    _    T  C
                                CCC CAGGGG CC GACGG
                                ||| |||||| || |||||
                                GGG GTCTCC GG CTGCC
                                  A     _ A
GAM256  LOC152426 3'  GCCCCAGGGAGGTTCTGATGG  6801         ___  CC  C
                                GCCCCAGGGG  TC  GA GG
                                ||||||||||  ||  || ||
                                CGGGGTCCCT  AG  CT CC
                                     CCA  A_  A
GAM256  LOC152641 3'  GCCGCAGATGCCCCGACGG   6802    C   GG
                                GCC CAG  GTCCCGACGG
                                ||| |||  ||||||||||
                                CGG GTC  CGGGGCTGCC
                                  C   TA
GAM256  LOC152992 5'  CCCTCAGGGGCACTGAGGCGG  6803    _     CCC  __
                                CCC CAGGGGT  GA  CGG
                                ||| |||||||  ||  |||
                                GGG GTCCCCG  CT  GCC
                                  A      TGA  CC
GAM256  LOC154789 5'  GCCCCAGGTGCGCCGATGG   6804        G  C   C
                                GCCCCAGG GT CCGA GG
                                |||||||| || |||| ||
                                CGGGGTCC CG GGCT CC
                                     A  C   A
GAM256  LOC154860 5'  GCCCCGGCGGCGCCCGCGG   6805      A  _  _   A
                                GCCCC GG GGT CCCG CGG
                                ||||| || ||| |||| |||
                                CGGGG CC CCG GGGC GCC
                                   _  G   C   _
GAM256  LOC157313 5'  GCCCGAGGTCCCGACGG    6806     CA
                                GCCC  GGGGTCCCGACGG
                                ||||  ||||||||||||||
                                CGGG  CTCCAGGGCTGCC
                                   __
GAM256  LOC158191 3'  GCCCCAGGGTCAGTGGCCGTCG 6797         G  _________  GAC
          G                     GCCCCAGGG TC       CC   GG
                                |||||||||  ||       ||   ||
                                CGGGGTCCC AG       GG   CC
                                     _  TCACCIII  CAG
GAM256  LOC158527 5'  GCCCCAAGCCCAGGCGG    6807        GGT   A_
                                GCCCCAGG   CCCG  CGG
                                ||||||||   ||||  |||
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                                CGGGGTTC   GGGT  GCC
                                    ___    CC
GAM256   LOC158955 3'  GCTCCGGGGGCCCCACG     6746     C  A       G
                                GC CC GGGGTCCC ACG
                                || || |||||||| |||
                                CG GG CCCCGGGG TGC
                                 A  C       _
GAM256   LOC166206 5'  GCCCCAGCGGTCAAAAGCCGTC 6808         G   _________  GAC
           GG                     GCCCCAG GGTC       CC   GG
                                ||||||| ||||       ||   ||
                                CGGGGTC CCAG       GG   CC
                                   G    TTTTCIII  CAG
GAM256   LOC196761 3'  GCCCGGGATCCCCGG       6809       CA       GA
                                GCCC  GGGGTCCC  CGG
                                ||||  ||||||||  |||
                                CGGG  CCCTAGGG  GCC
                                  __      __
GAM256   LOC197202 5'  ACCCCAAGGCCCGATGG     6781          GT     C
                                GCCCCAGGG  CCCGA GG
                                |||||||||  ||||| ||
                                TGGGGTTCC  GGGCT CC
                                    __     A
GAM256   LOC199927 3'  GCCCCAGGGAGTCTTCACG    6810          _   CCG
                                GCCCCAGGG GTC   ACG
                                |||||||||  |||   |||
                                CGGGGTCCC CAG   TGC
                                     T   AAG
GAM256   LOC220758 3'  GCCCCATGGGGCCGCACTGACG 6811         _      C ___
           G                     GCCCCA GGGGTC C   GACGG
                                |||||| |||||| |   |||||
                                CGGGGT CCCCGG G   CTGCC
                                   A     C TGA
GAM256   LOC221865 5'  GCCCCGGGAGCCGCGGCGG    6812        A     C  A
                                GCCCC GGGGTC CG CGG
                                ||||| |||||| || |||
                                CGGGG CCTCGG GC GCC
                                   C     C  C
GAM256   LOC221876 5'  CCCCTAAAAATCCGGCGG     6813       _       C A
                                CCCC AGGGGTCC G CGG
                                |||| |||||||| | |||
                                GGGG TTTTTAGG C GCC
                                   A       _ C
GAM256   LOC221882 5'  GCCCCGAGCCGAGAGACGG    6814       AG     CC__
                                GCCCC  GGGTC    GACGG
                                |||||  |||||    |||||
                                CGGGG  CTCGG    CTGCC
                                   __     CTCT
GAM256   LOC253891 3'  CCCAGAGGGTTCTCGCGG     6815       _    _ C  A
                                CCCAG GGGT C CG CGG
                                ||||| |||| | || |||
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                                GGGTC CCCA G GC GCC
                                  T   A A _
GAM256  LOC254181 3'  GCCCCAAGGGCCCCGACGG   6816
                                GCCCCAGGGGTCCCGACGG
                                ||||||||||||||||||
                                CGGGGTTCCCGGGGCTGCC

GAM256  LOC255452 3'  GCCCCAGCGGCGACCCTCGG  6817       G  __  GA
                                GCCCCAG GGT  CCC  CGG
                                ||||||| |||  |||  |||
                                CGGGGTC CCG  GGG  GCC
                                   G  CT  A_
GAM256  LOC257458 5'  GCCACAGGGGCCCGGCGG   6818     C    T   A
                                GCC CAGGGG CCCG CGG
                                ||| |||||| |||| |||
                                CGG GTCCCC GGGC GCC
                                  T    _   C
GAM256  LOC257463 3'  GCCCCAGAGGTCAAGGCCGTCG 6819          _______ GAC
          G                      GCCCCAGGGGTC     CC  GG
                                ||||||||||||     ||  ||
                                CGGGGTCTCCAG     GG  CC
                                      TTCCIII  CAG
GAM256  LOC51195  3'  CCCCAGAACAGATCTCGATGG  6820       ___   C  C
                                CCCCAG   GGGTC CGA GG
                                ||||||   ||||| ||| ||
                                GGGGTC   TCTAG GCT CC
                                   TTG    A  A
GAM256  LOC54505  5'  GCCCAGGCCCCGACGG     6821      CAG
                                GCCC   GGGTCCCGACGG
                                ||||   ||||||||||||
                                CGGG   TCCGGGGCTGCC
                                  ___
GAM256  LOC58525  5'  GCCCAGGGGGCTGCCCGGTGG  6822      CA   __   AC
                                GCCC  GGGGT  CCCG  GG
                                ||||  |||||  ||||  ||
                                CGGG  CCCCG  GGGC  CC
                                  TC    AC   CA
GAM256  LOC90525  3'  GCCCTCAGCCAGGTGATGG   6823      _  __   CCC  C
                                GCCC CAG  GGGT   GA GG
                                |||| |||  ||||   || ||
                                CGGG GTC  TCCA   CT CC
                                  A  GG   ___ A
GAM256  LOC90639  3'  GCCTGGGCACTCCCGACGG   6824     CCA  G__
                                GCC   GGG   TCCCGACGG
                                |||   |||   |||||||||
                                CGG   CCC   AGGGCTGCC
                                 A__   GTG
GAM256  LOC91272  5'  GCCCCAAGGCGGCAGCGGCGG  6825       _ _  CC  A
                                GCCCCA GG GGT  CG CGG
                                |||||| || |||  || |||
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                                CGGGGT CC CCG  GC GCC
                                   T  G   TC  C
GAM256  LOC93129  5'  GCCCCAGGAGCCGGAGCGG   6826          T  C  _
                                GCCCCAGGGG CC GA CGG
                                |||||||||| || || |||
                                CGGGGTCCTC GG CT GCC
                                     _  C  C
GAM256  LOC96597  3'  CCTCCAGAGGCCTTGATGG   6827    _       CC  C
                                CC CCAGGGGTC  GA GG
                                || |||||||||  || ||
                                GG GGTCTCCGG  CT CC
                                 A        AA  A
GAM257  UNG       3'  TTGCAAAACATCCTTATGC   6830         A   C_
                                TTGCAAAA ATCC  ATGC
                                |||||||| ||||  ||||
                                AACGTTTT TAGG  TACG
                                     G   AA
GAM257  UNG       3'  TTGCAAAACATCCTTATGC   6830         A   C_
                                TTGCAAAA ATCC  ATGC
                                |||||||| ||||  ||||
                                AACGTTTT TAGG  TACG
                                     G   AA
GAM257  DJ434O14.5 3'  TTACAAAACCCATGC      6831         AAT
                                TTGCAAAA   CCCATGC
                                ||||||||   |||||||
                                AATGTTTT   GGGTACG
                                     ___
GAM257  DKFZp434C0328 5'  CTGCAAAAGCTCCCCATG   6832         AA_
                                TTGCAAAA   TCCCATG
                                ||||||||   |||||||
                                GACGTTTT   GGGGTAC
                                     CGA
GAM257  FLJ13154  3'  ACAATTAAAATCCCATGC   6833      __
                                GCAA  AAAATCCCATGC
                                ||||  ||||||||||||
                                TGTT  TTTTAGGGTACG
                                  AA
GAM257  FLJ13456  3'  TGCAAAAAAGCCACCATGC   6834          _ _
                                TGCAAAAAA TC CCATGC
                                ||||||||| || ||||||
                                ACGTTTTTT GG GGTACG
                                     C  T
GAM257  FLJ22814  3'  CTGCAAAAGAACAGAGCCCGTG 6835         _  _____  A  III
          CG                      TTGCAAAA AAT    CCC TGC   G
                                ||||||||| |||    ||| |||   |
                                GACGTTTT TTG    GGG ACG   C
                                     C   TCTC   C   III
GAM257  GP5       3'  TTACCCAAAGTCCCATGC    6836       AA   A
                                TTGC  AAA TCCCATGC
                                ||||  ||| ||||||||
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                                AATG  TTT AGGGTACG
                                  GG   C
GAM257  KIAA1069  3'  TTGCAAAAACCATGC      6837         ATC
                                TTGCAAAAA   CCATGC
                                |||||||||   ||||||
                                AACGTTTTT   GGTACG
                                     ___
GAM257  PKNOX2    3'  TTGCAAAAGTCTCACGC     6838         AA  C
                                TTGCAAAA  TC CATGC
                                ||||||||  || |||||
                                AACGTTTT  AG GTGCG
                                    C_  A
GAM257  TBX21     3'  TGCAAAAAGCTCCTTCATGC  6839         A_  __
                                TGCAAAAA  TCC  CATGC
                                ||||||||  |||  |||||
                                ACGTTTTT  AGG  GTACG
                                    CG   AA
GAM258  AICDA     3'  TAACTCTTTTACAAACTTAT  6842          TCC
                                TAATTCTTTT   AACTTAT
                                ||||||||||   |||||||
                                ATTGAGAAAA   TTGAATA
                                     TGT
GAM258  P2RY2     3'  TAATTCCCCCAACTTATAC   6843        TTT
                                TAATTCT   TCCAACTTATAC
                                |||||||   ||||||||||||
                                ATTAAGG   GGGTTGAATATG
                                     ___
GAM258  LOC154007 3'  CTCTTTCCAGATACTTATA   6844          ___
                                CTTTTTCCA   ACTTATA
                                |||||||||   |||||||
                                GAGAAAGGT   TGAATAT
                                     CTA
GAM258  LOC222161 5'  TCCCCCATCCAATTTATA    6845       TT    C
                                TTCTT  TCCAA TTATA
                                |||||  ||||| |||||
                                AGGGG  AGGTT AATAT
                                  GT    A
GAM259  CMAR      3'  AGTAAAGTATCTCAACAATTCT 6848          A_    C
                                AGTAAAGTA  TTAAC AATTCT
                                |||||||||  ||||| ||||||
                                TCATTTCAT  AGTTG TTAAGA
                                     AG    _
GAM259  COIL      3'  TCACTGAAGTGAAACACCAATT 6849      GTA   AATTA
          CT                    TCA   AAGT    ACCAATTCT
                                |||   ||||    |||||||||
                                AGT   TTCA    TGGTTAAGA
                                  GAC   CTTTG
GAM259  HTR2C     3'  TCAGATTTTTCATTAACCAATT 6850       TAAAGTA
                                TCAG      ATTAACCAATT
                                ||||      ||||||||||
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                                AGTC      TAATTGGTTAA
                                  TAAAAAG
GAM259  IL7     3'  CAGTAAAGCAATGTCAATT   6851           TAAC
                                CAGTAAAGTAAT   CAATT
                                ||||||||||||  |||||
                                GTCATTTCGTTA   GTTAA
                                      CA__
GAM259  MSR1    3'  TCAGAAAGTAATTAAAATCAAC 6852      T       C__
          T                      TCAG AAAGTAATTAA   CAATT
                                |||| ||||||||||  |||||
                                AGTC TTTCATTAATT   GTTGA
                                  _        TTA
GAM259  MSR1    3'  TCAGAAAGTAATTAAAATCAAC 6852      T       C__
          T                      TCAG AAAGTAATTAA   CAATT
                                |||| ||||||||||  |||||
                                AGTC TTTCATTAATT   GTTGA
                                  _        TTA
GAM259  SPG7    3'  AGTAAAGTATCTCAACAATTCT 6848         A_    C
                                AGTAAAGTA  TTAAC AATTCT
                                |||||||||  ||||| ||||||
                                TCATTTCAT  AGTTG TTAAGA
                                     AG    _
GAM259  ZNF264  3'  AGTAAAGATACCAATTC     6853        TAATTA
                                AGTAAAG     ACCAATTC
                                |||||||     ||||||||
                                TCATTTC     TGGTTAAG
                                    TA____
GAM259  CGI-127 3'  TCATTCAAATAATTAGCCAATT 6854     GTA       A
                                TCA   AAGTAATTA CCAATT
                                |||   |||||||| ||||||
                                AGT   TTTATTAAT GGTTAA
                                  AAG       C
GAM259  HYPH    3'  GTAAAGTTAACCAATT      6855        AAT
                                GTAAAGT   TAACCAATT
                                |||||||   |||||||||
                                CATTTCA   ATTGGTTAA
                                     ___
GAM259  KIAA0256 3' TCAGTAAAGAATCTGCCCAATT 6856         T   AA_
          CT                    TCAGTAAAG AATT   CCAATTCT
                                |||||||| ||||   ||||||||
                                AGTCATTTC TTAG   GGTTAAGA
                                     _   ACG
GAM260  NFYA    3'  TAAGTGGTTTCTGTCCTGTAG  6859    T    AGG   C
                                A AGTGG   TTG CCTGTAG
                                | |||||   ||| |||||||
                                A TCACC   GAC GGACATC
                                 T    AAA   A
GAM260  NFYA    3'  TAAGTGGTTTCTGTCCTGTAG  6859    T    AGG   C
                                A AGTGG   TTG CCTGTAG
                                | |||||   ||| |||||||
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                                A TCACC   GAC GGACATC
                                 T    AAA  A
GAM260  FLJ14564  3'  TTAATGGTAGAAGTCCTGT   6860       A      TGC
                                TTAAT GTGGAGGT   CCTGT
                                ||||| ||||||||   |||||
                                AATTA CATCTTCA   GGACA
                                   C      ___
GAM260  LOC166341 3'  GGTGGTTCAGCCCTGTAG    6861     A   __
                                GG GGTT  GCCCTGTAG
                                || ||||  |||||||||
                                CC CCAA  CGGGACATC
                                 A   GT
GAM260  LOC256476 5'  CAGAATAAGGTTGCTTTGTAG  6862     TG_      CC
                                TAG   GAGGTTGC  TGTAG
                                |||   ||||||||  |||||
                                GTC   TTCCAACG  ACATC
                                  TTA       AA
GAM261  ADORA1    3'  TGGATGTGGGCTGGTGGGAGC  6865      AACCCATC
                                TGGA       CTGGTGGGAGC
                                ||||       ||||||||||
                                ACCT       GACCACCCTCG
                                  ACACCC__
GAM261  BMP1      3'  CGGAATTTGAGCTGGTGGGGGC 6866       ACCCATC      A
                                TGGAA      CTGGTGGG GC
                                |||||      |||||||| ||
                                GCCTT      GACCACCC CG
                                   AAACTC_       C
GAM261  BMP1      3'  CGGAATTTGAGCTGGTGGGGGC 6866       ACCCATC      A
                                TGGAA      CTGGTGGG GC
                                |||||      |||||||| ||
                                GCCTT      GACCACCC CG
                                   AAACTC_       C
GAM261  BMP1      3'  CGGAATTTGAGCTGGTGGGGGC 6866       ACCCATC      A
                                TGGAA      CTGGTGGG GC
                                |||||      |||||||| ||
                                GCCTT      GACCACCC CG
                                   AAACTC_       C
GAM261  BMP1      3'  CGGAATTTGAGCTGGTGGGGGC 6866       ACCCATC      A
                                TGGAA      CTGGTGGG GC
                                |||||      |||||||| ||
                                GCCTT      GACCACCC CG
                                   AAACTC_       C
GAM261  HIP12     3'  TGGAAACTCACTCCAGGAG   6867        C  _   TGGT
                                TGGAAAC CA TCC    GGGAG
                                ||||||| || |||    |||||
                                ACCTTTG GT AGG    TCCTC
                                   A  G   ____
GAM261  HOXB5     3'  TGGGAACCGGTCCCCAGCGGG  6868     A    CA_   TG
                                TGG AACC   TCC  GTGGG
                                ||| ||||   |||  |||||
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                                ACC TTGG   GGG  CGCCC
                                  C    CCA   GT
GAM261  INMT     3'  GAAATCAACCATGGTGGGAG   6869      CC  T  _
                                GAAA  CA CC TGGTGGGAG
                                |||| || || |||||||||
                                CTTT  GT GG ACCACCCTC
                                  A_  T  T
GAM261  MTMR8    3'  TGGAAACCTGTACCTTACAGCA 6870        CAT_  GGTGGG
                                TGGAAACC   CCT     AGCA
                                ||||||||   |||     ||||
                                ACCTTTGG   GGA     TCGT
                                    ACAT   ATG___
GAM261  PAX2     3'  TGGAAACTGGTCCTGCGG    6871        CCA    G
                                TGGAAAC   TCCTG TGG
                                |||||||   ||||| |||
                                ACCTTTG   AGGAC GCC
                                    ACC    _
GAM261  PAX2     3'  TGGAAACTGGTCCTGCGG    6871        CCA    G
                                TGGAAAC   TCCTG TGG
                                |||||||   ||||| |||
                                ACCTTTG   AGGAC GCC
                                    ACC    _
GAM261  PHEMX    3'  TGGGTCCACCCTGGGAGCA   6872      AAAC     GGT
                                TGG   CCATCCT   GGGAGCA
                                |||   |||||||   |||||||
                                ACC   GGTGGGA   CCCTCGT
                                  CA__     ___
GAM261  PRPSAP2  3'  GAAATCCATCCCACCGAGCA  6873      C      G GG
                                GAAA CCATCCTG T  GAGCA
                                |||| |||||||| |  |||||
                                CTTT GGTAGGGT G  CTCGT
                                  A      G __
GAM261  PTGFRN   3'  GGAACCTGTTCTAGAAGAGCA 6874      A  CATC   T
                                GGAA CC   CTGG GGGAGCA
                                |||| ||   |||| |||||||
                                CCTT GG   GATC TTCTCGT
                                  _  ACAA   _
GAM261  SLC22A5  3'  TGGGTGCCCATCCAGGAGC   6875     AAA     TGGT
                                TGG   CCCATCC   GGGAGC
                                |||   |||||||   ||||||
                                ACC   GGGTAGG   TCCTCG
                                  CAC     _____
GAM261  UQCRC1   5'  TGGAAACTTACCTGGGAC    6876       CCAT   GGT   G
                                TGGAAAC   CCT   GGGA C
                                |||||||   |||   |||| |
                                ACCTTTG   GGA   CCCT G
                                    AAT_   ___    G
GAM261  BTBD2    3'  TGGGACCCACGGCTCTGGGAGC 6877     AA     CCT   ___
          A                      TGG  ACCCAT   GGT   GGGAGCA
                                |||  ||||||   |||   |||||||
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                                ACC  TGGGTG   CCG   CCCTCGT
                                  C_     ___   AGA
GAM261  CDH22    3'  GGAAACCTGGGGTGGGGGCA  6878        CATCCT     A
                                GGAAACC     GGTGGG GCA
                                |||||||     |||||| |||
                                CCTTTGG     CCACCC CGT
                                    ACC___     C
GAM261  DDX34    3'  TGGGGGCCCATCCTGTGGGGC  6879     AAA       G   A
                                TGG   CCCATCCTG TGGG GC
                                |||   ||||||||| |||| ||
                                ACC   GGGTAGGAC ACCC CG
                                  CCC       _   _
GAM261  DKFZP564A2416 5'  TGGAAACCCGACCAACCCGGGG 6880          AT____    T
                                TGGAAACCC     CCTGG GG
                                |||||||||     ||||| ||
                                ACCTTTGGG     GGGCC CC
                                     CTGGTT    _
GAM261  DKFZP761G1913 3'  TGAAAACTCGTCCTGGGGAG   6881        CCA     TG
                                TGGAAAC   TCCTGG  GGAG
                                |||||||   ||||||  ||||
                                ACTTTTG   AGGACC  CCTC
                                    AGC     __
GAM261  FLJ11539  3'  TGGGGGTCCACCCTGCCCGGAG 6882      AAAC       GTG
           C                     TGG    CCATCCTG   GGAGC
                                |||    ||||||||   |||||
                                ACC    GGTGGGAC   CCTCG
                                  CCCA       GGG
GAM261  FLJ12150  5'  GGAGCCGTCCGGCGAGC     6883      AAC  A   T   GG
                                GGA   CC TCC GGT  GAGC
                                |||   || ||| |||  ||||
                                CCT   GG AGG CCG  CTCG
                                  C__  C   _   __
GAM261  FLJ14640  5'  TGGAAACCCATCTTGATG    6884            C
                                TGGAAACCCATC TGGTG
                                |||||||||||| |||||
                                ACCTTTGGGTAG ACTAC
                                       A
GAM261  FLJ20898  5'  CGGGGCCCATCCCAGGGAGCA  6885      AAA       GGT
                                TGG   CCCATCCT   GGGAGCA
                                |||   ||||||||   |||||||
                                GCC   GGGTAGGG   CCCTCGT
                                  CC_       T__
GAM261  FLJ21276  3'  TGGGACCTCATCCTGGTG    6886      AA  _
                                TGG  ACC CATCCTGGTG
                                |||  ||| ||||||||||
                                ACC  TGG GTAGGACCAC
                                  C_   A
GAM261  HT011    5'  TGGAGGGCCATCCTGTGCACGG 6887       AAC       _   _
                                TGGA   CCATCCTG GTG GG
                                ||||   |||||||| ||| ||
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                                ACCT   GGTAGGAC CGT CC
                                  CCC       A   G
GAM261  HTCD37    3'  TGGAAAACCATTCTTAAAGCA  6888        C    C  GGTGG
                                TGGAAA CCAT CT    GAGCA
                                |||||| |||| ||    |||||
                                ACCTTT GGTA GA    TTCGT
                                   T    A  AT___
GAM261  KIAA0121  3'  TGGAAGCCCAGTACAGTGGGAG 6889       A    TCC
                                TGGAA CCCA   TGGTGGGAG
                                ||||| ||||   |||||||||
                                ACCTT GGGT   GTCACCCTC
                                  C    CAT
GAM261  KIAA0173  3'  TGGAAGCCCATCCTACAATAG  6890       A       __
                                TGGAA CCCATCCTG  GTGG
                                ||||| |||||||||  ||||
                                ACCTT GGGTAGGAT  TATC
                                  C        GT
GAM261  KIAA0864  5'  TGGAGACCCTCTGGTAGGAG   6891      A    ATC
                                TGGA ACCC   CTGGTGGGAG
                                |||| ||||   ||||||||||
                                ACCT TGGG   GACCATCCTC
                                  C    A__
GAM261  KIAA1266  3'  GAAATCCATTTTCCTGGGTG   6892      C  ___     _
                                GAAA CCA   TCCTGG TG
                                |||| |||   |||||| ||
                                CTTT GGT   AGGACC AC
                                  A   AAA     C
GAM261  KIAA1443  5'  GGGGGCCTCCGAGTGGGAG   6893     AAAC  A   T
                                GG    CC TCC GGTGGGAG
                                ||    || ||| ||||||||
                                CC    GG AGG TCACCCTC
                                 CCC_  _   C
GAM261  KIAA1811  3'  TGGAGCCCCATCCCTGCAGGGC 6894      AA       G TG  A
          A                      TGGA  CCCATCCT G  GG GCA
                                ||||  |||||||| |  || |||
                                ACCT  GGGTAGGG C  CC CGT
                                  CG       A GT  _
GAM261  LGP1     3'  GGACTCCATCCTGCTGGG    6895      AAC       G
                                GGA   CCATCCTG TGGG
                                |||   |||||||| ||||
                                CCT   GGTAGGAC ACCC
                                  GA_       G
GAM261  MFN2     3'  TGGAAACATGTCTCTTAAAGGG 6896        CCA  _  GGT   A
          CA                     TGGAAAC   TC CT   GGG GCA
                                |||||||   || ||   ||| |||
                                ACCTTTG   AG GA   TCC CGT
                                    TAC  A  ATT  _
GAM261  MRPS21   5'  TGGAAGTCATCCTAGAAAG   6897       ACC       TG
                                TGGAA   CATCCTGG  GG
                                |||||   ||||||||  ||
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                                ACCTT  GTAGGATC  TC
                                  CA_      TT
GAM261  NPC1L1   3'  TGGGGACCCACTATGGGAGCA  6898     AA    CCTG
                                TGG  ACCCAT   GTGGGAGCA
                                |||  ||||||   |||||||||
                                ACC  TGGGTG   TACCCTCGT
                                  CC     A___
GAM261  PLA2G12  3'  TGGAAACCTTGTCCTTGTAAG  6899       CA_   G
                                TGGAAACC   TCCT GTGGG
                                ||||||||   |||| |||||
                                ACCTTTGG   AGGA CATTC
                                     AAC    A
GAM261  TFIP11   3'  TGGAAATTTATCCCAGAAGAG  6900      CCC   TG T
                                TGGAAA   ATCC  G GGGAG
                                ||||||   ||||  | |||||
                                ACCTTT   TAGG  C TTCTC
                                   AAA    GT _
GAM261  LOC118462 3'  GGAAACCCATTCTGTGCA    6901         C  _
                                GGAAACCCAT CTG GTG
                                |||||||||| ||| |||
                                CCTTTGGGTA GAC CGT
                                     A   A
GAM261  LOC124470 3'  TGGAAACATTGTCCTGAGTG   6902       CCA_   _
                                TGGAAAC    TCCTG GTG
                                |||||||    ||||| |||
                                ACCTTTG    AGGAC CAC
                                    TAAC    T
GAM261  LOC128209 3'  TGGTGGCTCACGAGGTGGGAGC 6903     AAACC   CCT
                                TGG    CAT   GGTGGGAGC
                                |||    |||  |||||||||
                                ACC    GTG   CCACCCTCG
                                  ACCGA   CT_
GAM261  LOC130074 3'  TGGAGGTCCTGTCCTGTCCGGG 6904      AA_  CA    G_
                                TGGA   CC  TCCTG  TGGG
                                ||||   ||  |||||  ||||
                                ACCT   GG  AGGAC  GCCC
                                  CCA  AC    AG
GAM261  LOC133022 3'  GAAACACTGGTGGGAG      6905       CCATC
                                GAAAC    CTGGTGGGAG
                                |||||    ||||||||||
                                CTTTG    GACCACCCTC
                                   T_____
GAM261  LOC145678 3'  TGGAGCCCTATCCTAGTG    6906      AA  C
                                TGGA  CC ATCCTGGTG
                                ||||  || |||||||||
                                ACCT  GG TAGGATCAC
                                  CG  A
GAM261  LOC153910 3'  TGGAAGCACATCTCCTTTGGG  6907       ACC   _  GG
                                TGGAA   CATC CT  TGGG
                                |||||   |||| ||  ||||
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                                ACCTT   GTAG GG  ACCC
                                   CGT    A  AA
GAM261   LOC155435 3'  TGGGAACCTGCTGATGGG    6908      A    CATC
                                TGG AACC    CTGGTGGG
                                ||| ||||    ||||||||
                                ACC TTGG    GACTACCC
                                  C    AC__
GAM261   LOC158668 3'  TGGAGACCATCCTGACCAGCA  6909      AAC        TGGG
                                TGGA   CCATCCTGG    AGCA
                                ||||   |||||||||    ||||
                                ACCT   GGTAGGACT    TCGT
                                  CT_        GG__
GAM261   LOC164584 5'  TGGAAGTCATCTTCTTGTGGG  6910       ACC    __  G
                                TGGAA   CATC  CT GTGGG
                                |||||   ||||  || |||||
                                ACCTT   GTAG  GA CACCC
                                   CA_    AA  A
GAM261   LOC253664 3'  TGGAAGCCTGCGGTTAAGGAG  6911       A  CATCC    __
                                TGGAA CC    TGGT  GGGAG
                                ||||| ||    ||||  |||||
                                ACCTT GG    GCCA  TCCTC
                                   C  AC___    AT
GAM261   LOC253666 3'  TGGAGACTATCCTGGCG     6912       A  CC
                                TGGA AC  ATCCTGGTG
                                |||| ||  |||||||||
                                ACCT TG  TAGGACCGC
                                  C  A_
GAM261   LOC253842 5'  TGGAGACCATCCTGGCTAAC   6913      AAC        GGGA
                                TGGA   CCATCCTGGT    GC
                                ||||   ||||||||||    ||
                                ACCT   GGTAGGACCG    TG
                                  CT_        AT__
GAM261   LOC255452 3'  TGGAGACCCATCCGCTGAGCA  6914      A       TG  GG
                                TGGA ACCCATCC  GT  GAGCA
                                |||| ||||||||  ||  |||||
                                ACCT TGGGTAGG  CG  CTCGT
                                  C       __  A_
GAM261   LOC89932  5'  TGGGGCCCATCCTGTCACAGGC 6915      AAA        GTG_  A
            A                    TGG   CCCATCCTG    GG GCA
                                |||   |||||||||    || |||
                                ACC   GGGTAGGAC    TC CGT
                                  CC_        AGTG  _
GAM261   LOC90362  5'  TGGAAACCTATCACACGGG    6916         C   CTGG
                                TGGAAACC ATC    TGGG
                                |||||||| |||    ||||
                                ACCTTTGG TAG    GCCC
                                     A   TGT_
GAM262   ADAM10    5'  TTCCTCCTTTCCCCGC      6919      G     T  A
                                TTC TCCTTT CC CCGC
                                ||| |||||| || ||||
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                                AAG AGGAAA GG GGCG
                                  G     _ _
GAM262  ADCY7    3'  TTCGTTCCCTCCACCGC     6920       _  TT
                                TTCGT CCT  TCCACCGC
                                ||||| |||  ||||||||
                                AAGCA GGG  AGGTGGCG
                                   A  __
GAM262  ATP11A   3'  TTCTCCTTCCAGGCCGC     6921      G   TT   __
                                TTC TCCT  TCCA  CCGC
                                ||| ||||  ||||  ||||
                                AAG AGGA  AGGT  GGCG
                                  _   __   CC
GAM262  DAXX     5'  TCCTTCCCACTCCCACCGC    6922      G   _
                                TTC TCCT TTTCCACCGC
                                ||| |||| ||||||||||
                                AGG AGGG GAGGGTGGCG
                                  A   T
GAM262  DMN      5'  CTCGTCCTCTCCGCCGC     6923          T  A
                                TTCGTCCTTT CC CCGC
                                |||||||||| || ||||
                                GAGCAGGAGA GG GGCG
                                      _ C
GAM262  FLT1     5'  TCCGTCCTCTCGTTCGCCGC  6924           CCA__
                                TTCGTCCTTTT    CCGC
                                ||||||||||    ||||
                                AGGCAGGAGAG    GGCG
                                      CAAGC
GAM262  HOXC9    3'  TTCGTCTCTCCCCCGC      6925       C     A
                                TTCGTC TTTTCC CCGC
                                |||||| |||||| ||||
                                AAGCAG AGAGGG GGCG
                                   _     _
GAM262  KCNA7    5'  TCCGTCCTTCTGCCGC      6926           CCA
                                TTCGTCCTTTT   CCGC
                                ||||||||||   ||||
                                AGGCAGGAAGA   GGCG
                                      C__
GAM262  MAP3K9   5'  CTCGTCCTCGCCCGCCGC    6927          T   A
                                TTCGTCCTT TCC CCGC
                                ||||||||| ||| ||||
                                GAGCAGGAG GGG GGCG
                                     C   C
GAM262  MLLT7    3'  TTCCTCCCCTCCCCGC      6928      G     T  A
                                TTC TCCTTT CC CCGC
                                ||| |||||| || ||||
                                AAG AGGGGA GG GGCG
                                  G     _ _
GAM262  OVOL1    5'  TCCGTCCCTCCCATCGC     6929           T   C
                                TTCGTCCTTT CCA CGC
                                |||||||||| ||| |||
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                                AGGCAGGGAG GGT GCG
                                      _  A
GAM262  PAPPA    5'  TTCGCCCCTGCACCGC      6930          TTC
                                TTCGTCCTT   CACCGC
                                |||||||||   ||||||
                                AAGCGGGGA   GTGGCG
                                     C__
GAM262  POMC     5'  TTCTTCCCCTCCTTCGCCGC   6931      G       CA__
                                TTC TCCTTTTC    CCGC
                                ||| ||||||||    ||||
                                AAG AGGGGAGG    GGCG
                                  A       AAGC
GAM262  SMURF1   5'  CTCGCCGCTTCCGCCGC     6932      T  T    A
                                TTCG CC TTTCC CCGC
                                |||| || ||||| ||||
                                GAGC GG GAAGG GGCG
                                  _ C    C
GAM262  SREBF1   3'  CTCGGGCCTTCCACCGC     6933      TC    T
                                TTCG  CTTT CCACCGC
                                ||||  |||| |||||||
                                GAGC  GGAA GGTGGCG
                                  CC   _
GAM262  TIMP3    3'  TTCCTCTCCATTCCACTGC    6934      G  _  T     C
                                TTC TC CT TTCCAC GC
                                ||| || || |||||| ||
                                AAG AG GG AAGGTG CG
                                  G  A  T     A
GAM262  TM6SF1   5'  CTCGCCCTTCACCGC       6935          TTC
                                TTCGTCCTT   CACCGC
                                |||||||||   ||||||
                                GAGCGGGAA   GTGGCG
                                      ___
GAM262  VIL2     5'  CTCGTCCTCCTGCCGC      6936          CCA
                                TTCGTCCTTTT   CCGC
                                ||||||||||   ||||
                                GAGCAGGAGGA   GGCG
                                      C__
GAM262  ADAM7    5'  TTCCTCCTCACTTCCACTGCG  6937      G    __     C  III
                                TTC TCCTT  TTCCAC GC   G
                                ||| |||||  |||||| ||   |
                                AAG AGGAG  AAGGTG CG   C
                                  G     TG      A  III
GAM262  AKAP6    3'  TTCCTCCTTGTACCCACTGC   6938      G    T__    C
                                TTC TCCTT   TCCAC GC
                                ||| |||||   ||||| ||
                                AAG AGGAA   GGGTG CG
                                  G     CAT     A
GAM262  DKFZP434L1435 5'  TTCGCCTCCTTCCACTGC    6939        CT      C
                                TTCGTC  TTTCCAC GC
                                ||||||  ||||||| ||
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                                AAGCGG  GAAGGTG CG
                                   AG      A
GAM262  DKFZp762E1511 3'  TTCATCTTCCCACCTGC     6940        CT      _
                                TTCGTC  TTTCCACC GC
                                ||||||  |||||||| ||
                                AAGTAG  AAGGGTGG CG
                                   __       A
GAM262  ESDN     5'  TTCGTCCCTTCCCTCCGC    6941             A
                                TTCGTCCTTTTCC CCGC
                                |||||||||||| ||||
                                AAGCAGGGAAGGG GGCG
                                      A
GAM262  FBP17    3'  TTCCTCCCTTTCACTGC     6942      G      C  C
                                TTC TCCTTTTC AC GC
                                ||| |||||||| || ||
                                AAG AGGGAAAG TG CG
                                  G       _  A
GAM262  FLJ12242 5'  TTCGCCCTTCCCCGC       6943         TT   A
                                TTCGTCCT  TCC CCGC
                                ||||||||  ||| ||||
                                AAGCGGGA  AGG GGCG
                                      __  _
GAM262  FLJ14596 5'  TTCTTCCTCCTCCGTCGC    6944      G        AC
                                TTC TCCTTTTCC  CGC
                                ||| |||||||||  |||
                                AAG AGGAGGAGG  GCG
                                  A        CA
GAM262  KIAA0339 3'  TTCGCCCTCCTCCCGC      6945            AC
                                TTCGTCCTTTTCC  CGC
                                ||||||||||||  |||
                                AAGCGGGAGGAGG  GCG
                                      __
GAM262  KIAA1340 5'  CTCGTCCACCCCGCCGC     6946         TT    A
                                TTCGTCC  TTCC CCGC
                                |||||||  |||| ||||
                                GAGCAGG  GGGG GGCG
                                   T_   C
GAM262  KIAA1814 3'  TCCGTCCTTGCCTCTGCCG   6947          __   CA
                                TTCGTCCTT  TTC  CCG
                                |||||||||  |||  |||
                                AGGCAGGAA  GAG  GGC
                                     CG   AC
GAM262  MGC17347 3'  TTCTCTCTCTCCACTGC     6948      G  C       C
                                TTC TC TTTTCCAC GC
                                ||| ||  ||||||||  ||
                                AAG AG GAGAGGTG CG
                                  _  A       A
GAM262  MGC20647 5'  TTCTCCTTTCCAACCGC     6949      G       C
                                TTC TCCTTTTC ACCGC
                                ||| |||||||| |||||
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                                AAG AGGAAAGG TGGCG
                                  _      T
GAM262  MGC26778  5'  TCCGTCCCTTTCTTCACTGC  6950          __  C
                                TTCGTCCTTTTC  CAC GC
                                ||||||||||||  ||| ||
                                AGGCAGGGAAAG  GTG CG
                                      AA   A
GAM262  MGC2752   5'  TTCGGCCCTTCCCCATCGC   6951     _   TT  C
                                TTCG TCCTT  CCA CGC
                                ||||| |||||  ||| |||
                                AAGC GGGAA  GGT GCG
                                  C    GG   A
GAM262  MGC29667  5'  TCCGTCCCCCCCGCCGC     6952       TT  A
                                TTCGTCCT  TCC CCGC
                                ||||||||  ||| ||||
                                AGGCAGGG  GGG GGCG
                                     __  C
GAM262  N4BP1     5'  TCCGCCCCTTTGCCGC     6953         CCA
                                TTCGTCCTTTT   CCGC
                                ||||||||||   ||||
                                AGGCGGGGAAA   GGCG
                                      C__
GAM262  PARVA     3'  CTCGTCCCCTAGTCACTGC   6954         TC_  C
                                TTCGTCCTTT   CAC GC
                                |||||||||   ||| ||
                                GAGCAGGGGA   GTG CG
                                     TCA   A
GAM262  RC3       5'  TTCGCCTTCCCTCCGC     6955      T    T  A
                                TTCG CCTTT CC CCGC
                                |||| ||||| || ||||
                                AAGC GGAAG GG GGCG
                                  _    _  A
GAM262  SP2       5'  TTCGCCCCCTTCATCGC    6956          CAC
                                TTCGTCCTTTTC   CGC
                                ||||||||||||   |||
                                AAGCGGGGGAAG   GCG
                                      TA_
GAM262  LOC127294 5'  TCCGTGACCTTCCACTGC   6957      CC      C
                                TTCGT  TTTTCCAC GC
                                |||||  |||||||| ||
                                AGGCA  GGAAGGTG CG
                                   CT       A
GAM262  LOC142901 5'  TCCGTCCTCCCTAGCCACCGC 6958          ___
                                TTCGTCCTTTT   CCACCGC
                                ||||||||||   |||||||
                                AGGCAGGAGGG   GGTGGCG
                                      ATC
GAM262  LOC143241 5'  TTCGTCCCTACACACGC    6959         TTC  _
                                TTCGTCCTT   CAC CGC
                                |||||||||   ||| |||
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                                AAGCAGGGA   GTG GCG
                                     T__   T
GAM262   LOC143666 5'  CTCGTCCTTCCCCGC       6960         TT   A
                                TTCGTCCT  TCC CCGC
                                ||||||||  ||| ||||
                                GAGCAGGA  AGG GGCG
                                    __  _
GAM262   LOC147093 5'  TTCTCCTCCTCCACTGC      6961      G         C
                                TTC TCCTTTTCCAC GC
                                ||| ||||||||||| ||
                                AAG AGGAGGAGGTG CG
                                  _         A
GAM262   LOC150319 3'  TCCGTCCCCTTCCTCCAC     6962            A
                                TTCGTCCTTTTCC CCGC
                                |||||||||||| ||||
                                AGGCAGGGGAAGG GGTG
                                        A
GAM262   LOC152829 5'  TTCCTCTCCTCCATCGC      6963      G  C      C
                                TTC TC TTTTCCA CGC
                                ||| || ||||||| |||
                                AAG AG AGGAGGT GCG
                                  G  _      A
GAM262   LOC153711 5'  TTCTTCCTTCCACCGC       6964      G    TT
                                TTC TCCT  TCCACCGC
                                ||| ||||  ||||||||
                                AAG AGGA  AGGTGGCG
                                  A   __
GAM262   LOC158972 3'  CTCGTCCTGCATCCCCGC     6965          TT_   A
                                TTCGTCCT   TCC CCGC
                                ||||||||   ||| ||||
                                GAGCAGGA   AGG GGCG
                                     CGT   _
GAM262   LOC200488 5'  TTCATCCTTTTCCACCTGC    6966              _
                                TTCGTCCTTTTCCACC GC
                                |||||||||||||| ||
                                AAGTAGGAAAAGGTGG CG
                                        A
GAM262   LOC219942 3'  TTCGGCCTCCCACCGC       6967       T    TT
                                TTCG CCTT  CCACCGC
                                |||| ||||  |||||||
                                AAGC GGAG  GGTGGCG
                                  C   __
GAM262   LOC221092 5'  TTCATCCTTCTCATCCCGC    6968            CA_
                                TTCGTCCTTTTC   CCGC
                                ||||||||||||   ||||
                                AAGTAGGAAGAG   GGCG
                                       TAG
GAM262   LOC253258 3'  CTCGTCCTTCCCCGC       6960         TT   A
                                TTCGTCCT  TCC CCGC
                                ||||||||  ||| ||||
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                                GAGCAGGA  AGG GGCG
                                   __  _
GAM262  LOC253573 3'  TTCTCCACCTTCCACTGC    6969     G  _      C
                                TTC TCC TTTTCCAC GC
                                ||| ||| |||||||| ||
                                AAG AGG GGAAGGTG CG
                                  _  T       A
GAM262  LOC254962 3'  TTCTCCTTTTCCATGC      6970     G        CC
                                TTC TCCTTTTCCA  GC
                                ||| ||||||||||  ||
                                AAG AGGAAAAGGT  CG
                                  _        A_
GAM262  LOC255736 5'  TCCAGCCTTTCCACCGC     6971      T    T
                                TTCG CCTTT CCACCGC
                                |||| ||||| |||||||
                                AGGT GGAAA GGTGGCG
                                   C    _
GAM262  LOC256880 5'  TTCTTCCCTCCCGCCGC     6972     G     T  A
                                TTC TCCTTT CC CCGC
                                ||| |||||| || ||||
                                AAG AGGGAG GG GGCG
                                  A     _ C
GAM262  LOC51289  3'  TTCATCCTTTCACCTCTTTACC 6973          _ _____    III
          GCG                     TCGTCCTTTT CC    ACCGC   G
                                ||||||||||  ||    |||||   |
                                AGTAGGAAAG GG    TGGCG   C
                                      T  AGAAA    III
GAM262  LOC51705  3'  TTCTCCTTTTCCACGC      6974     G        C
                                TTC TCCTTTTCCAC GC
                                ||| ||||||||||| ||
                                AAG AGGAAAAGGTG CG
                                  _        _
GAM262  LOC91812  5'  CTCCTCCCTTCACCGC      6975     G     TC
                                TTC TCCTTT  CACCGC
                                ||| ||||||  ||||||
                                GAG AGGGAA  GTGGCG
                                  G     __
GAM262  LOC91813  5'  CTCCTCCCTTCACCGC      6975     G     TC
                                TTC TCCTTT  CACCGC
                                ||| ||||||  ||||||
                                GAG AGGGAA  GTGGCG
                                  G     __
GAM263  GJA5      3'  CTCCTGACCTCGTAC       6978      AAACG
                                CTCC    TGACCTCGTAC
                                ||||    ||||||||||
                                GAGG    ACTGGAGCATG
                                   _____
GAM263  MAP       3'  GTACTCCAGAGTGACACT    6979         AAC    _
                                GTACTCCA   GTGAC CT
                                ||||||||   ||||| ||
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                                CATGAGGT   CACTG GA
                                    CT_    T
GAM264  NPY1R    3'  TGATTTCAACCCCATTCCTTGG 6982      _ TG   A   CC
           GA                     TGAT T  GCT TCA  CCTTGGGA
                                  |||| |  ||| |||  ||||||||
                                  ACTA A  TGG GGT  GGAACCCT
                                    A GT   _   AA
GAM264  TRIM     3'  TGATTTGGTTATCAGTGGG    6983         C    CCCCT
                                  TGATTTGG TATCA    TGGG
                                  |||||||| |||||    ||||
                                  ACTAAACC ATAGT    ACCC
                                      A    C____
GAM264  DKFZP761G1913 3'  TGATTTGGCTTTGCTTTTCTTG 6984           ATCACCC_
           GGA                     TGATTTGGCT       CTTGGGA
                                  ||||||||||       |||||||
                                  ACTAAACCGA       GAACCCT
                                       AACGAAAA
GAM264  RAB35    3'  TGATTTGGCTTCATTTTCTTGA 6985           A   CCC_
                                  TGATTTGGCT TCA    CTTGG
                                  |||||||||| |||    |||||
                                  ACTAAACCGA AGT    GAACT
                                       _   AAAA
GAM264  SSR1     3'  TGTTTTGGAATATATTCCTTGG 6986     A    CTATCACC
           GA                      TG TTTGG       CCTTGGGA
                                  || |||||       ||||||||
                                  AC AAACC       GGAACCCT
                                    A    TTATATAA
GAM264  STATI2   3'  TGATTTGGTTAATTGCATAAAA 6987         C  TCACCCCT___
           TGGGA                      TGATTTGG TA         TGGGA
                                  |||||||| ||         |||||
                                  ACTAAACC AT         ACCCT
                                      A  TAACGTATTTT
GAM264  STATI2   3'  TGATTTGGTTAATTGCATAAAA 6987         C  TCACCCCT___
           TGGGA                      TGATTTGG TA         TGGGA
                                  |||||||| ||         |||||
                                  ACTAAACC AT         ACCCT
                                      A  TAACGTATTTT
GAM264  ZAK      3'  TGGTTTGGCTATAGTCTCATCC 6988         CAC_________  CTTG
           CAAGGG                   TTGGCTAT         CC    GG
                                  ||||||||         ||    ||
                                  AACCGATA         GG    CC
                                      TCAGAGTIIIA  GTTC
GAM264  LOC132617 3'  TTGCCTATTACCCCTTGGG    6989      G    C
                                  TTG CTAT ACCCCTTGGG
                                  ||| |||| ||||||||||
                                  AAC GATA TGGGGAACCC
                                    G    A
GAM264  LOC144473 3'  TGATTTGTTTGCTATTTGGGA  6990         ___     CACCCC
                                  TGATTTG   GCTAT     TTGGGA
                                  |||||||   |||||     ||||||
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                                ACTAAAC   CGATA     AACCCT
                                   AAA    _____
GAM264  LOC149182 5'  TGATTTGGCTGCCACTGGATCC 6991        AT  _________  CTTG
          CAAGGG                 TTGGCT  CAC       CC    GG
                                |||||| |||       ||    ||
                                AACCGA  GTG       GG    CC
                                   CG   ACCTIIIA  GTTC
GAM264  LOC221362 3'  TGATTTGGCATATTACTTATCC 6992       _   C  _______  CTTG
          CAAGGG                 TTGGC TAT AC      CC    GG
                                ||||| ||| ||      ||    ||
                                AACCG ATA TG      GG    CC
                                  T   A  AATIIIA  GTTC
GAM264  LOC221938 3'  TGATCTGGCTGTCACCAGATCC 6993        A   _______  TTG
          CAAGG                  TTTGGCT TCACC      CC   GG
                                ||||||| |||||      ||   ||
                                AGACCGA AGTGG      GG   CC
                                   C    TCTIIIA  GTT
GAM264  LOC91796  3'  TGCTTTGGCTATTTGG      6994     A       CACCCC
                                TG TTTGGCTAT     TTGG
                                || |||||||||     ||||
                                AC AAACCGATA     AACC
                                 G       _____
GAM265  ARHGEF12  3'  CCCCAGAAAACAGAAAGT    6997          TCTCC
                                TCCCAGAAAG    CAGAAAGT
                                ||||||||||    ||||||||
                                GGGGTCTTTT    GTCTTTCA
                                              _____
GAM265  ASH2L     3'  CCCCAGTATTATTCCCAGAAAG 6998        AAAGTC
          TC                     TCCCAG     TCCCAGAAAGTC
                                ||||||     ||||||||||||
                                GGGGTC     AGGGTCTTTCAG
                                   ATAATA
GAM265  B3GALT5   3'  TCCCAGAAAGCTCCCAGAA   6999          T
                                TCCCAGAAAG CTCCCAGAA
                                |||||||||| |||||||||
                                AGGGTCTTTC GAGGGTCTT
                                          _
GAM265  B3GALT5   3'  TCCCAGAAAGCTCCCAGAA   6999          T
                                TCCCAGAAAG CTCCCAGAA
                                |||||||||| |||||||||
                                AGGGTCTTTC GAGGGTCTT
                                          _
GAM265  B3GALT5   3'  TCCCAGAAAGCTCCCAGAA   6999          T
                                TCCCAGAAAG CTCCCAGAA
                                |||||||||| |||||||||
                                AGGGTCTTTC GAGGGTCTT
                                          _
GAM265  B3GALT5   3'  TCCCAGAAAGCTCCCAGAA   6999          T
                                TCCCAGAAAG CTCCCAGAA
                                |||||||||| |||||||||
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                                AGGGTCTTTC GAGGGTCTT
                                       _
GAM265  B3GALT5  3'  TCCCAGAAAGCTCCCAGAA   6999          T
                                TCCCAGAAAG CTCCCAGAA
                                |||||||||| |||||||||
                                AGGGTCTTTC GAGGGTCTT
                                       _
GAM265  CACNG2   3'  GAAGGTCTCCCAGCGGAGGGTC 7000     A       AAA___
                                GAA GTCTCCCAG     GTC
                                ||| |||||||||     |||
                                CTT CAGAGGGTC     CAG
                                  C       GCCTCC
GAM265  CD4      3'  TCCCAGCAAAGCTCGCTTCCAG 7001       _   T  ____
                                TCCCAG AAAG CTC   CCAG
                                |||||| |||| |||   ||||
                                AGGGTC TTTC GAG   GGTC
                                   G   _  CGAA
GAM265  CKTSF1B1 3'  TCCCAGAGTCTGGAGGGT   7002       AA   CCCA  AA
                                TCCCAGA  GTCT   GA  GT
                                |||||||  ||||   ||  ||
                                AGGGTCT  CAGA   CT  CA
                                   __   C___  CC
GAM265  DNAH9    5'  TCCCAGGAAGTTCCCAGA    7003       A   C
                                TCCCAG AAGT TCCCAGA
                                |||||| |||| |||||||
                                AGGGTC TTCA AGGGTCT
                                   C   _
GAM265  GAN      3'  TCCCAGGTAGTTTTTCAACAGT 7004       AA  CTCC  AA
                                TCCCAG  AGT   CAG  AGT
                                ||||||  |||   |||  |||
                                AGGGTC  TCA   GTT  TCA
                                   CA   AAAA  G_
GAM265  GTF2E2   3'  TCCCAGGGAGTAACAGAAGGT  7005       AA  CTCC   A
                                TCCCAG  AGT   CAGAA GT
                                ||||||  |||   ||||| ||
                                AGGGTC  TCA   GTCTT CA
                                   CC   TT__    C
GAM265  HOXD4    3'  TCCATAGACAACCCAGAAAGTC 7006     C_  AAGTCT
                                TCC  AGA     CCCAGAAAGTC
                                |||  |||     ||||||||||
                                AGG  TCT     GGGTCTTTCAG
                                  TA   GTT___
GAM265  MYO7A    3'  TCCCAGTGGTACACAGAAAGTC 7007       AAA  CTCC
                                TCCCAG   GT   CAGAAAGTC
                                ||||||   ||   |||||||||
                                AGGGTC   CA   GTCTTTCAG
                                   AC_  TGT_
GAM265  NGFR     3'  AAGCCATTTCCCAGAAGGTC   7008       ___      A
                                AAGTC   TCCCAGAA GTC
                                |||||   |||||||| |||
```

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                                TTCGG   AGGGTCTT CAG
                                  TAA       C
GAM265  P53AIP1  3'  TCCTATGGCCCATTCCAGAAAG 7009     CAGAAA   C__
            T                    TCC     GTCT   CCAGAAAGT
                                 |||     ||||   |||||||||
                                 AGG     CGGG   GGTCTTTCA
                                   ATAC__    TAA
GAM265  PIGC     3'  CAAGAGGTCCCCAGAAAGT    7010      AAA   T
                                 CAG   GTC CCCAGAAAGT
                                 |||   ||| ||||||||||
                                 GTT   CAG GGGTCTTTCA
                                   CTC   _
GAM265  PLAB     5'  TCCTAGGAACCCCAGAAGGT   7011      C  A  GTC       A
                                 TCC AG AA   TCCCAGAA GT
                                 ||| || ||   |||||||| ||
                                 AGG TC TT   GGGGTCTT CA
                                   A  C  ___       C
GAM265  RNH      5'  CCAGAAGCCCCAGAAAGT    7012        A  CT
                                 CCAGAA GT  CCCAGAAAGT
                                 ||||||  ||  ||||||||||
                                 GGTCTT CG  GGGTCTTTCA
                                    _  __
GAM265  RNH      5'  CCAGAAGCCCCAGAAAGT    7012        A  CT
                                 CCAGAA GT  CCCAGAAAGT
                                 ||||||  ||  ||||||||||
                                 GGTCTT CG  GGGTCTTTCA
                                    _  __
GAM265  TJP1     5'  TCCTGAAAGTCTTGATGGTC   7013      CA       CCCA  AA
                                 TCC  GAAAGTCT    GA  GTC
                                 |||  ||||||||    ||  |||
                                 AGG  CTTTCAGA    CT  CAG
                                   A_       A___  AC
GAM265  ZNF8     3'  TCCTTAGAAAGTCAGAAGT    7014      C_       TCCC    A
                                 TCC  AGAAAGTC    AGAA GT
                                 |||  ||||||||    |||| ||
                                 AGG  TCTTTCAG    TCTT CA
                                   AA       _____   _
GAM265  C11orf23 3'  TCCCAGAGGCTCTCTCCCAGCA 7015         AAG__       AA
            GTC                    TCCCAGA    TCTCCCAG  AGTC
                                   |||||||    ||||||||  ||||
                                   AGGGTCT    AGAGGGTC  TCAG
                                      CCGAG       G_
GAM265  C1QR1    3'  TCCAAGAGTCTCCCAGAA    7016      C   AA
                                 TCC AGA  GTCTCCCAGAA
                                 ||| |||  ||||||||||
                                 AGG TCT  CAGAGGGTCTT
                                   T   __
GAM265  C22orf4  3'  TCCCAGGAAGTCTCCAAAAGC  7017        A       CA
                                 TCCCAG AAGTCTCC  GAAAGT
                                 ||||||  ||||||||  ||||||
```

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                                AGGGTC TTCAGAGG  TTTTCG
                                   C      __
GAM265  C4orf6   5'  CCACAGCCTCCCAGGAAGTC  7018     GAA       A
                                CCA  AGTCTCCCAG AAGTC
                                |||  |||||||||| |||||
                                GGT  TCGGAGGGTC TTCAG
                                  G__       C
GAM265  CLSTN3   3'  TCCCAGAAAGTCCTTCTCCCA  7019          ____
                                TCCCAGAAAGTC   TCCCA
                                ||||||||||||   |||||
                                AGGGTCTTTCAG   AGGGT
                                       GAAG
GAM265  DDX33    3'  CCAGAAAATCTCCCTCAGTC  7020           AGAA
                                CCAGAAAGTCTCCC   AGTC
                                ||||||||||||||   ||||
                                GGTCTTTTAGAGGG   TCAG
                                       AG__
GAM265  DKFZP564K0822 3'  TCCCACAAAATTCCCCAG    7021      G    CT
                                TCCCA AAAGT  CCCAG
                                ||||| |||||  |||||
                                AGGGT TTTTA  GGGTC
                                   G    AG
GAM265  FHR5     3'  CAGAAAGTTTCAAAGT     7022        C  CCAG
                                CAGAAAGT TC   AAAGT
                                |||||||| ||   |||||
                                GTCTTTCA AG   TTTCA
                                     A  ____
GAM265  FLJ10545  3'  TCCCAAAAAGACTAGGGAGT  7023         T  CCC  AA
                                TCCCAGAAAG CT  AG  AGT
                                |||||||||| ||  ||  |||
                                AGGGTTTTTC GA  TC  TCA
                                      T  ___  CC
GAM265  FLJ13150  3'  TCCTTGAGTCCAGAAAGT   7024     CAGAA  CTC
                                TCC    AGT  CCAGAAAGT
                                |||    |||  |||||||||
                                AGG    TCA  GGTCTTTCA
                                  AAC__  ___
GAM265  FLJ21438  5'  CCCCAGAGGGCCTTGGAGAGTC 7025       AA   CCCA  A
                                TCCCAGA  GTCT   GA AGTC
                                |||||||  ||||   || ||||
                                GGGGTCT  CGGA   CT TCAG
                                    CC   AC__  C
GAM265  FLJ22353  3'  TCCCAAAGGGCTACAGGGAGT  7026       AA  CTCC  AA
                                TCCCAGA  GT   CAG  AGT
                                |||||||  ||   |||  |||
                                AGGGTTT  CG   GTC  TCA
                                    CC  AT__  CC
GAM265  FLJ23519  5'  CCAGAAGCCCCAGAAAGT   7012       A  CT
                                CCAGAA GT  CCCAGAAAGT
                                ||||||  ||  ||||||||||
```

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                                GGTCTT CG  GGGTCTTTCA
                                   _  __
GAM265  HA-1     3'  TCCCAGAATGGTTTCTGGAGTC 7027         A_  C  CCAGAA
                                TCCCAGAA  GT TC     AGTC
                                ||||||||  || ||     ||||
                                AGGGTCTT  CA AG     TCAG
                                    AC  A  ACC___
GAM265  KIAA0557 3'  CCATAAAGTCCCAGGAGGTC   7028     G    TC     AAA
                                CCA AAAG  TCCCAG   GTC
                                ||| ||||  ||||||   |||
                                GGT TTTC  AGGGTC   CAG
                                  A   __     CTC
GAM265  KIAA0806 3'  TCCCAGAAGGCTCCAAAGT   7029         A T    CAG
                                TCCCAGAA G CTCC   AAAGT
                                |||||||| | ||||   |||||
                                AGGGTCTT C GAGG   TTTCA
                                    C _   ____
GAM265  KIAA1036 3'  TCCCGGGAAGCTCCCAGA    7030      AGA   T
                                TCCC   AAG CTCCCAGA
                                ||||   ||| ||||||||
                                AGGG   TTC GAGGGTCT
                                  CCC   _
GAM265  KIAA1321 3'  CCCAGAAAGTTTCTTGTGAGT  7031          C  CCAGAA
                                CCCAGAAAGT TC     AGT
                                |||||||||| ||     |||
                                GGGTCTTTCA AG     TCA
                                    A  AACAC_
GAM265  MLL3     3'  TCCCAGAAGCTTTTTCAAAAAG 7032         A  CTCC_
            TC                   TCCCAGAA GT    CAGAAAGTC
                                ||||||||  ||    |||||||||
                                AGGGTCTT CG    GTTTTTCAG
                                    _  AAAAA
GAM265  PADI2    3'  TCCCAAAGGTCTCCCAG     7033         AA
                                TCCCAGA  GTCTCCCAG
                                |||||||  |||||||||
                                AGGGTTT  CAGAGGGTC
                                    C_
GAM265  PRDM10   3'  TCCTAGAAAGTCTTTCTAGA   7034     C       CCC_
                                TCC AGAAAGTCT    AGA
                                |||  |||||||||    |||
                                AGG TCTTTCAGA    TCT
                                  A        AAGA
GAM265  PYY      3'  TCCCAGGAGGCCTCAGGGGTC  7035       AAA    CC  AAA
                                TCCCAG   GTCTC  AG   GTC
                                ||||||   |||||  ||   |||
                                AGGGTC   CGGAG  TC   CAG
                                   CTC     __  CC_
GAM265  RAB17    5'  TCCCAGAAGGTTTCAGGGCAAA 7036         A  C  CCAG_
            GTC                    TCCCAGAA GT TC     AAAGTC
                                ||||||||  || ||     ||||||
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                                AGGGTCTT CA AG    TTTCAG
                                    C  A  TCCCG
GAM265  RoXaN    3'  CCAGAAAGCCTCAAAGT    7037          CCAG
                                CCAGAAAGTCTC   AAAGT
                                ||||||||||||  |||||
                                GGTCTTTCGGAG   TTTCA
                                      ____
GAM265  ZID      3'  GAAAGTCTCAAGGAAAGT    7038         CCA
                                GAAAGTCTC  GAAAGT
                                |||||||||  ||||||
                                CTTTCAGAG  CTTTCA
                                     TTC
GAM265  LOC121232 5'  TCCTGAGTCTACTTCAGAAAGT 7039     CAGAA    CC__
                                TCC    AGTCT   CAGAAAGT
                                |||    |||||   ||||||||
                                AGG    TCAGA   GTCTTTCA
                                  AC___    TGAA
GAM265  LOC124602 3'  TCCCAGAGAGTCCTTCAG    7040        A    CC
                                TCCCAGA AGTCT  CAG
                                |||||||  |||||  |||
                                AGGGTCT TCAGG  GTC
                                    C    AA
GAM265  LOC144165 5'  CCAGAGCCCAGAAAGT     7041       AAGTCT
                                CCAGA     CCCAGAAAGT
                                |||||     ||||||||||
                                GGTCT     GGGTCTTTCA
                                  C_____
GAM265  LOC145387 5'  TCCCAGAAATTTCCGACTAAGT 7042         GTC   CAGA
          C                      TCCCAGAAA   TCC    AAGTC
                                |||||||||   |||    |||||
                                AGGGTCTTT   AGG    TTCAG
                                     AA_   CTGA
GAM265  LOC145694 3'  CCAGAAAGCTCTCCAAGGGTC  7043         _    C  AAA
                                CCAGAAAG TCTCC AG   GTC
                                ||||||||  ||||| ||   |||
                                GGTCTTTC AGAGG TC   CAG
                                     G    T  C__
GAM265  LOC146138 3'  CCCTAGGCCACACCCAGAAAGT 7044      _ AAA   T__
          C                      CCC AG   GTC   CCCAGAAAGTC
                                |||  ||   |||   ||||||||||||
                                GGG TC   CGG   GGGTCTTTCAG
                                  A  ___   TGT
GAM265  LOC149372 3'  CCAAAAGGTAATACAGAAAGT  7045        A  CTCC
                                CCAGAA GT    CAGAAAGT
                                ||||||  ||    ||||||||
                                GGTTTT CA    GTCTTTCA
                                   C  TTAT
GAM265  LOC150311 5'  TCCAAGAGTACAGAAAGT    7046      C   AA  CTCC
                                TCC AGA  GT    CAGAAAGT
                                |||  |||  ||    ||||||||
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                                AGG TCT  CA    GTCTTTCA
                                  T   __  T___
GAM265  LOC152765 3'  TCCCGGGAATCTCCCAAAA   7047      AGAA
                                TCCC    AGTCTCCCAGAA
                                ||||    ||||||||||||
                                AGGG    TTAGAGGGTTTT
                                  CCC_
GAM265  LOC157753 5'  CCCCAGCAGCTTCCGGAAAGTC 7048       AA  TC   CA
                                TCCCAG  AG  TCC  GAAAGTC
                                ||||||  ||  |||  |||||||
                                GGGGTC  TC  AGG  CTTTCAG
                                   G_  GA   C_
GAM265  LOC159176 5'  TCCCAGCTACTCAGAAAGT   7049       AAAGT   CC
                                TCCCAG    CTC  AGAAAGT
                                ||||||    |||  |||||||
                                AGGGTC    GAG  TCTTTCA
                                   GAT__   __
GAM265  LOC197131 3'  TCCCAGCCCTCAGAAAGT    7050       AAAGTC  _
                                TCCCAG     TCC CAGAAAGT
                                ||||||     ||| ||||||||
                                AGGGTC     GGG GTCTTTCA
                                   _______  A
GAM265  LOC201252 3'  CCATCTGTTTCTCAGAAAGT   7051     GAAA  C  C
                                CCA    GT TC CAGAAAGT
                                |||    || || ||||||||
                                GGT    CA AG GTCTTTCA
                                  AGA_  A  A
GAM265  LOC203397 3'  TCCCAGAGAGTCCTTCAG    7040        A    CC
                                TCCCAGA AGTCT  CAG
                                ||||||| |||||  |||
                                AGGGTCT TCAGG  GTC
                                   C    AA
GAM265  LOC254242 5'  TCCCAGAAGAGTTCCCAGGAAG 7052         _  C     A
           TC                     TCCCAGAA AGT TCCCAG AAGTC
                                ||||||||| ||| |||||| |||||
                                AGGGTCTT TCA AGGGTC TTCAG
                                   C  _     C
GAM265  LOC255811 3'  CCCCAGTATTATTCCCAGAAAG 6998        AAAGTC
           TC                     TCCCAG     TCCCAGAAAGTC
                                ||||||     ||||||||||||
                                GGGGTC     AGGGTCTTTCAG
                                   ATAATA
GAM265  LOC91689  3'  TCTCAGGGAGCCTCCCAGA   7053     C   AA
                                TC CAG  AGTCTCCCAGA
                                || |||  ||||||||||
                                AG GTC  TCGGAGGGTCT
                                 A  CC
GAM266  BHLHB3    3'  TCTGTACAGATAGATATCTA   7056          TAACT
                                TCTGTACGG    GATATCTA
                                |||||||||    ||||||||
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                                AGACATGTC    CTATAGAT
                                     TAT__
GAM266  FLRT2    3'  TCTGTACAGTGACATTTAC   7057         AACT    C
                                TCTGTACGGT   GATAT TAC
                                ||||||||||   ||||| |||
                                AGACATGTCA   CTGTA ATG
                                     _____    A
GAM266  RCN1     3'  TCTGTACAGGTTGTGTCTGCC  7058       _  AAC  ATA   A
                                TCTGTAC GGT   TG   TCT CC
                                ||||||| |||   ||   ||| ||
                                AGACATG CCA   AC   AGA GG
                                    T  ___  AC_   C
GAM266  RCN1     3'  TCTGTACAGGTTGTGTCTGCC  7058       _  AAC  ATA   A
                                TCTGTAC GGT   TG   TCT CC
                                ||||||| |||   ||   ||| ||
                                AGACATG CCA   AC   AGA GG
                                    T  ___  AC_   C
GAM266  IMAGE:4907098 3'  TGCACGGTGAAGATTTCTACC  7059        AACT   A
                                TGTACGGT    GAT TCTACC
                                ||||||||    ||| ||||||
                                ACGTGCCA    CTA AGATGG
                                     CTT_   A
GAM266  KIAA1754  3'  TGTGGGGTAACTGGGCACC   7060     AC      A_
                                TGT  GGTAACTG  TATC
                                |||  ||||||||  ||||
                                ACA  CCATTGAC  GTGG
                                  CC       CC
GAM266  LAT1-3TM  5'  TCTGTACAGTACATCT     7061          AACTG
                                TCTGTACGGT    ATATCT
                                ||||||||||    ||||||
                                AGACATGTCA    TGTAGA
                                     ______
GAM266  NCOA2    3'  TCTGTCGTGATATCT      7062       A  GTAAC
                                TCTGT CG    TGATATCT
                                |||||  ||    ||||||||
                                AGACA GC    ACTATAGA
                                     _  _____
GAM266  SLC26A9  3'  TGCAGAATAACTGGTATCTA  7063      CG     A
                                TGTA  GTAACTG TATCTA
                                ||||  ||||||| ||||||
                                ACGT  TATTGAC ATAGAT
                                  CT      C
GAM266  SLC26A9  3'  TGCAGAATAACTGGTATCTA  7063      CG     A
                                TGTA  GTAACTG TATCTA
                                ||||  ||||||| ||||||
                                ACGT  TATTGAC ATAGAT
                                  CT      C
GAM267  AP1G1    3'  TTTTTTTTTTTTTAACCG    7066          GC
                                TTTTTTTTTT  TGGCCG
                                ||||||||||  ||||||
```

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                                AAAAAAAAAA  ATTGGC
                                      AA
GAM267  C1R      3'  TGTTTTTTTTTTTCCACAC   7067          GCTGG
                                TGTTTTTTTTTT    CCGCGC
                                ||||||||||||    ||||||
                                ACAAAAAAAAAA    GGTGTG
                                      A_____
GAM267  CDH11    3'  TGTTTTTTTTTTCTAGC    7068          G
                                TGTTTTTTTTTT CTGGC
                                |||||||||||| |||||
                                ACAAAAAAAAAA GATCG
                                      _
GAM267  CDK5R2   3'  TTTTTTTTTTGCTGGGGC   7069            CC
                                TTTTTTTTTTGCTGG  GC
                                ||||||||||||||  ||
                                AAAAAAAAAACGACC  CG
                                      C_
GAM267  COX15    3'  TTTTTTTTTTGCTGAAGAC   7070            CC
                                TTTTTTTTTTGCTGG  GC
                                ||||||||||||||  ||
                                AAAAAAAAAACGACT  TG
                                      TC
GAM267  CRYPTIC  3'  TTTTTTTTTTTTGGCGC    7071          GC   C
                                TTTTTTTTTT  TGGC GC
                                ||||||||||  |||| ||
                                AAAAAAAAAA  ACCG CG
                                      A_   _
GAM267  CST3     3'  TTTTTTTTTTGCCGATGC   7072            CC
                                TTTTTTTTTTGCTGG  GC
                                ||||||||||||||  ||
                                AAAAAAAAAACGGCT  CG
                                      A_
GAM267  HCN2     3'  TTTTTTTTTTTTGGCGC    7071          GC   C
                                TTTTTTTTTT  TGGC GC
                                ||||||||||  |||| ||
                                AAAAAAAAAA  ACCG CG
                                      A_   _
GAM267  HOXC9    3'  TGTTTTTCCCTTGGCTGTGC  7073            _  _
                                TGTTTTTTTTTTG CTG GC
                                |||||||||||| ||| ||
                                ACAAAAAGGGAAC GAC CG
                                      C   A
GAM267  ING1     3'  TTTTTTTTTTGTGTTCCGC   7074          C  G_
                                TTTTTTTTTTG TG  CCGC
                                |||||||||| ||  ||||
                                AAAAAAAAAAC AC  GGCG
                                      _ AA
GAM267  KIP2     3'  GTTTTTTTTTTGCTGAAAGGGC 7075            CC__
                                GTTTTTTTTTTGCTGG   GC
                                ||||||||||||||||   ||
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                                CAAAAAAAAAACGACT   CG
                                      TTCC
GAM267  MPP6    3'  TTTTTTTTTTGCTTCAACGC  7076          GGCC
                                TTTTTTTTTTGCT   GCGC
                                |||||||||||||   ||||
                                AAAAAAAAAACGA   TGCG
                                      AGT_
GAM267  NCOA1   3'  TTTTTTTTTTGCTCCA     7077          GG
                                TTTTTTTTTTGCT  CCG
                                |||||||||||||  |||
                                AAAAAAAAAACGA  GGT
                                      __
GAM267  NCOA6IP  3'  TTTTTTTTTTGCTTTCATTGC  7078          GGCC__
                                TTTTTTTTTTGCT     GC
                                |||||||||||||     ||
                                AAAAAAAAAACGA     CG
                                      AAGTAA
GAM267  PDGFB   5'  TTTTTTTTTTCCTTTTTGCGC  7079         G  GGCC
                                TTTTTTTTTT CT   GCGC
                                |||||||||| ||   ||||
                                AAAAAAAAAA GA   CGCG
                                     G  AAAA
GAM267  PITX3   3'  TTTTTTTTTTGACAGTCCGCGC 7080          C  _
                                TTTTTTTTTTG TGG CCGCGC
                                |||||||||||| ||| ||||||
                                AAAAAAAAAAC GTC GGCGCG
                                      T   A
GAM267  PLA2G2A  3'  TTTTTTTTTTGCTAATTGC   7081           CC
                                TTTTTTTTTTGCTGG  GC
                                ||||||||||||||  ||
                                AAAAAAAAAACGATT  CG
                                      AA
GAM267  PRAME   3'  TTTTTTTTTTGCTTCACATTGC 7082          G_  C__
                                TTTTTTTTTTGCT  GC   GC
                                ||||||||||||  ||   ||
                                AAAAAAAAAACGA  TG   CG
                                      AG  TAA
GAM267  PTPRN   3'  TTTTTTTTTTGCAGCTGC    7083          T   C
                                TTTTTTTTTTGC GGC GC
                                |||||||||||| ||| ||
                                AAAAAAAAAACG TCG CG
                                     _   A
GAM267  SORBS1   3'  TTTTTTTTTTTTGCCACG    7084         GCTG
                                TTTTTTTTTT   GCCGCG
                                ||||||||||   ||||||
                                AAAAAAAAAA   CGGTGC
                                     AA__
GAM267  TRIM8   3'  TTTTTTTTTTGGGACTGCGC  7085          CT   C
                                TTTTTTTTTTG  GGC GCGC
                                ||||||||||  ||| ||||
```

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                                AAAAAAAAAAC  CTG CGCG
                                      C_  A
GAM267  BIK     3'  TTTTTTTTTTGCTGGAAAC   7086          CC
                                TTTTTTTTTTGCTGG  GC
                                ||||||||||||||  ||
                                AAAAAAAAAACGACC  TG
                                      TT
GAM267  BTBD2   3'  TTTTTTTTTTGCAGGTGC    7087          T  CC
                                TTTTTTTTTTGC GG  GC
                                ||||||||||| ||  ||
                                AAAAAAAAAACG CC  CG
                                      T  A_
GAM267  CNNM1   3'  TGTTTGTTTTTTGCTTTGATTT 7088      T       GGCC___
          GC                      TGTTT TTTTTTGCT      GC
                                |||||  |||||||||      ||
                                ACAAA AAAAAACGA      CG
                                   C        AACTAAA
GAM267  FASTK   3'  TTTTTTTTTTGCTCCCCG    7089          GG
                                TTTTTTTTTTGCT  CCG
                                ||||||||||||  |||
                                AAAAAAAAAACGA  GGC
                                      GG
GAM267  FASTK   3'  TTTTTTTTTTGCTCCCCG    7089          GG
                                TTTTTTTTTTGCT  CCG
                                ||||||||||||  |||
                                AAAAAAAAAACGA  GGC
                                      GG
GAM267  FBH1    3'  TTTTTTTTTTGCCAGTGC    7090          TG CC
                                TTTTTTTTTTGC  G  GC
                                ||||||||||||  |  ||
                                AAAAAAAAAACG  C  CG
                                      GT A_
GAM267  FLJ10743 3' TTTTTTTTTTGCCCATTGC   7091            GGCC
                                TTTTTTTTTTGCT   GC
                                ||||||||||||    ||
                                AAAAAAAAAACGG   CG
                                      GTAA
GAM267  FLJ12598 3' TTTTTTTTTTGCATGTGC    7092          _ _
                                TTTTTTTTTTGC TG GC
                                ||||||||||| || ||
                                AAAAAAAAAACG AC CG
                                      T  A
GAM267  FLJ12687 3' TTTTTTTTTTGAGATGGC    7093          C__
                                TTTTTTTTTTG   TGGC
                                ||||||||||   ||||
                                AAAAAAAAAAC   ACCG
                                      TCT
GAM267  FLJ13057 3' TTTTTTTTTTTCCAAATGCGC 7094          G TG CC
                                TTTTTTTTTT C  G  GCGC
                                ||||||||||  |  |  ||||
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                                AAAAAAAAAA G  T  CGCG
                                     A GT TA
GAM267  FLJ21120  3'  TTTTTTTTTTGTGGCTGC    7095          C   C
                                TTTTTTTTTTG TGGC GC
                                |||||||||| |||| ||
                                AAAAAAAAAAC ACCG CG
                                     _   A
GAM267  FLJ21135  3'  TTTTTTTTTTGTGCACGC    7096          CTG _
                                TTTTTTTTTTG  GC CGC
                                |||||||||||  || |||
                                AAAAAAAAAAC  CG GCG
                                     A__  T
GAM267  FLJ22269  3'  TTTTTTTTTTGCAGGTGC    7087          T  CC
                                TTTTTTTTTTGC GG  GC
                                |||||||||||| ||  ||
                                AAAAAAAAAACG CC  CG
                                      T  A_
GAM267  FLJ22531  3'  TTTTTTTTTTGGTGAGCGC   7097          C  GC
                                TTTTTTTTTTG TG  CGC
                                |||||||||| ||  |||
                                AAAAAAAAAAC AC  GCG
                                     C  TC
GAM267  FLJ32416  3'  TTTTTTTTTTTTGCCGC     7098          GCTG
                                TTTTTTTTTT   GCCGC
                                |||||||||   |||||
                                AAAAAAAAAA   CGGCG
                                     AA__
GAM267  GAS2L1    3'  TTTTTTTTTTGCTGGAGC    7099            CC
                                TTTTTTTTTTGCTGG  GC
                                ||||||||||||||  ||
                                AAAAAAAAAACGACC  CG
                                      T_
GAM267  HAIK1     3'  TTTTTTTTTTGCTAGTGC    7100            CC
                                TTTTTTTTTTGCTGG  GC
                                ||||||||||||||  ||
                                AAAAAAAAAACGATC  CG
                                      A_
GAM267  HCA112    3'  TTTTTTTTTTGCTGGGAAC   7101            CC
                                TTTTTTTTTTGCTGG  GC
                                ||||||||||||||  ||
                                AAAAAAAAAACGACC  TG
                                      CT
GAM267  humNRDR   3'  TTTTTTTTTTTCAAAGCCGCGC 7102          GCT_
                                TTTTTTTTTT   GGCCGCGC
                                |||||||||   ||||||||
                                AAAAAAAAAA   TCGGCGCG
                                     AGTT
GAM267  KIAA0020  5'  TGTTTTTTTCTTGTGCTG    7103          __
                                TGTTTTTTTTT  TGCTG
                                ||||||||||  |||||
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                                ACAAAAAAAGA  ACGAC
                                      AC
GAM267  KIAA0596 3'  TTTTTTTTTTGAGATGGC    7093          C__
                                TTTTTTTTTTG   TGGC
                                ||||||||||   ||||
                                AAAAAAAAAAC   ACCG
                                      TCT
GAM267  KIAA1554 3'  TTTTTTTTTTGCCTCTGC    7104          GGCC
                                TTTTTTTTTTGCT   GC
                                ||||||||||||   ||
                                AAAAAAAAAACGG   CG
                                      AGA_
GAM267  MGC2963  3'  TTTTTTTTTTGTCTCACGC   7105          _ G  C
                                TTTTTTTTTTG CT GC GC
                                |||||||||| || || ||
                                AAAAAAAAAAC GA TG CG
                                      A  G  _
GAM267  MIP-T3   3'  TTTTTTTTTTGTTTGGAAGCGC 7106          C_   CC
                                TTTTTTTTTTG  TGG  GCGC
                                ||||||||||  |||  ||||
                                AAAAAAAAAAC  ACC  CGCG
                                      AA   TT
GAM267  NMT1     3'  TTTTTTTTTTGTTCAGCTGC  7107          CT_   C
                                TTTTTTTTTTG   GGC GC
                                ||||||||||   ||| ||
                                AAAAAAAAAAC   TCG CG
                                      AAG   A
GAM267  PAPA-1   3'  TTTTTTTTTTGCACCG     7108          TG
                                TTTTTTTTTTGC  GCCG
                                ||||||||||||  ||||
                                AAAAAAAAAACG  TGGC
                                       __
GAM267  PMFBP1   3'  TTTTTTTTTTGCTCATGC    7109          GGCC
                                TTTTTTTTTTGCT   GC
                                ||||||||||||   ||
                                AAAAAAAAAACGA   CG
                                      GTA_
GAM267  R32184_3 3'  TTTTTTTTTTTTGCCGC     7098          GCTG
                                TTTTTTTTTT   GCCGC
                                ||||||||||   |||||
                                AAAAAAAAAA   CGGCG
                                      AA__
GAM267  RAI      3'  TGTTTTTTTTTTTTCTGTGC  7110          G_  _
                                TGTTTTTTTTTT  CTG GC
                                ||||||||||||  ||| ||
                                ACAAAAAAAAAA  GAC CG
                                      AA   A
GAM267  RPH3A    3'  TGTTTTTGTTTTGCTAGGAAGC 7111         T       CC_
                                TGTTTTT TTTTGCTGG   GC
                                ||||||| |||||||||   ||
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```
                                ACAAAAA AAAACGATC   CG
                                   C       CTT
GAM267  RTBDN    3' TTTTTTTTTTGCTCTAGC    7112          __
                                TTTTTTTTTTGCT  GGC
                                |||||||||||||  |||
                                AAAAAAAAAACGA  TCG
                                    GA
GAM267  SCAND1   3' TTTTTTTTTTTTGGCGC     7071         GC   C
                                TTTTTTTTTT  TGGC GC
                                ||||||||||  |||| ||
                                AAAAAAAAAA  ACCG CG
                                    A_   _
GAM267  SCAND1   3' TTTTTTTTTTTTGGCGC     7071         GC   C
                                TTTTTTTTTT  TGGC GC
                                ||||||||||  |||| ||
                                AAAAAAAAAA  ACCG CG
                                    A_   _
GAM267  SDOS     3' TTTTTTTTTTGCAGCTGC    7083          T  C
                                TTTTTTTTTTGC GGC GC
                                |||||||||||| ||| ||
                                AAAAAAAAAACG TCG CG
                                    _  A
GAM267  SEPT1    3' TTTTTTTTTTTTGCCGC     7098         GCTG
                                TTTTTTTTTT   GCCGC
                                |||||||||   |||||
                                AAAAAAAAAA   CGGCG
                                    AA__
GAM267  SMBP     3' TGTTTGTTTTTGCTGTGC    7113       TT      _
                                TGTTT  TTTTTGCTG GC
                                |||||  ||||||||| ||
                                ACAAA  AAAAACGAC CG
                                   C_       A
GAM267  SPRY4    3' TGTTTTTTTTTGAGACAGCG  7114          TGCT  C
                                TGTTTTTTTTT   GGC GCG
                                ||||||||||   ||| |||
                                ACAAAAAAAAA   CTG CGC
                                    CT__  T
GAM267  TUBA1    3' TTTTTTTTTTTTTAACCGTGC 7115         GC    C
                                TTTTTTTTTT  TGGCCG GC
                                ||||||||||  |||||| ||
                                AAAAAAAAAA  ATTGGC CG
                                    AA    A
GAM267  LOC115950 3' TTTTTTTTTGCTTTCTCGC  7116          GGC_
                                TTTTTTTTTGCT   CGC
                                ||||||||||||   |||
                                AAAAAAAAAACGA   GCG
                                    AAGA
GAM267  LOC124145 3' TGTTTTTTTTTTTTAGC    7117          GC
                                TGTTTTTTTTT  TGGC
                                ||||||||||| ||||
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                                ACAAAAAAAAAA  ATCG
                                      A_
GAM267  LOC145608 3'  TGTTTTTTTTTTTTACAGC   7118          GCTG  C
                                TGTTTTTTTTTT   GC GC
                                ||||||||||||   || ||
                                ACAAAAAAAAAA   TG CG
                                      AA__  T
GAM267  LOC151871 3'  TTTTTTTTTTGCCAATTGC   7119          TG CC
                                TTTTTTTTTTGC  G  GC
                                ||||||||||||  |  ||
                                AAAAAAAAAACG  T  CG
                                      GT AA
GAM267  LOC164173 3'  TGTTTTTTTCTCTTCTGCGC  7120           G_  GC
                                TGTTTTTTTTTT  CTG  CGC
                                ||||||||||||  |||  |||
                                ACAAAAAAAGAG  GAC  GCG
                                      AA  __
GAM267  LOC165140 5'  TGTTTTTTCTTTGCTTGC    7121           G
                                TGTTTTTTTTTTGCT GC
                                ||||||||||||||| ||
                                ACAAAAAAGAAACGA CG
                                       A
GAM267  LOC196027 3'  TGTTTTTTTTTTTTTTGGC   7122          GC_
                                TGTTTTTTTTTT   TGGC
                                ||||||||||||   ||||
                                ACAAAAAAAAAA   ACCG
                                      AAA
GAM267  LOC220477 5'  TGTCTTTTTTTTGTGTGC    7123          C  _
                                TGTTTTTTTTTTG TG GC
                                ||||||||||||| || ||
                                ACAGAAAAAAAAC AC CG
                                      _  A
GAM267  LOC221662 3'  TGTTTTTTTTTTTAAAGCTG  7124          ____
                                TGTTTTTTTTTT   GCTG
                                ||||||||||||   ||||
                                ACAAAAAAAAAA   CGAC
                                      ATTT
GAM267  LOC255995 5'  TTTTTTTTTTGCTCCA      7077          GG
                                TTTTTTTTTTGCT  CCG
                                ||||||||||||  |||
                                AAAAAAAAAACGA  GGT
                                      __
GAM267  LOC90355  3'  TTTTCTTTGCAGTTGCG     7125          T  CC
                                TTTTTTTTGC GG  GCG
                                |||||||||| ||  |||
                                AAAAGAAACG TC  CGC
                                      _  AA
GAM267  LOC91561  3'  TGTTTTTTTTTTCAC       7126          GCTGGC
                                TGTTTTTTTTTT     CGC
                                ||||||||||||     |||
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                                ACAAAAAAAAAA     GTG
                                             _______
GAM268  ADCY9    3'  GCGGTGCTCGGGAAAGTGC   7129        AAAA    T
                                GCGGTGCT    AAAGT GT
                                ||||||||    ||||| ||
                                CGCCACGA    TTTCA CG
                                    GCCC    _
GAM268  DTNA     3'  GGTGCTAAGGAAAAAGCTGAG  7130        AA   TT
                                GGTGCTAA  AAAG  GTTGAG
                                ||||||||  ||||  ||||||
                                CCACGATT  TTTT  CGACTC
                                    CC    T_
GAM268  DTNA     3'  GGTGCTAAGGAAAAAGCTGAG  7130        AA   TT
                                GGTGCTAA  AAAG  GTTGAG
                                ||||||||  ||||  ||||||
                                CCACGATT  TTTT  CGACTC
                                    CC    T_
GAM268  DTNA     3'  GGTGCTAAGGAAAAAGCTGAG  7130        AA   TT
                                GGTGCTAA  AAAG  GTTGAG
                                ||||||||  ||||  ||||||
                                CCACGATT  TTTT  CGACTC
                                    CC    T_
GAM268  DTNA     3'  GGTGCTAAGGAAAAAGCTGAG  7130        AA   TT
                                GGTGCTAA  AAAG  GTTGAG
                                ||||||||  ||||  ||||||
                                CCACGATT  TTTT  CGACTC
                                    CC    T_
GAM268  FGFR3    3'  GCGGTGCCAGAAAAAGCCCTG  7131         A      G
                                GCGGTGCTA AAAAAGTT TTG
                                ||||||||| |||||||| |||
                                CGCCACGGT TTTTTCGG GAC
                                     C      _
GAM268  GALNT1   3'  GGTATTAAAAAAAATCAGAG   7132      C        GTT
                                GGTG TAAAAAAAGTT   GAG
                                ||||  ||||||||||   |||
                                CCAT ATTTTTTTTAG   CTC
                                  A         T__
GAM268  PML      3'  GGGCAAAAAAGTTGTTGAG    7133     T  TA
                                GG GC  AAAAAAGTTGTTGAG
                                || ||  ||||||||||||||||
                                CC CG  TTTTTTCAACAACTC
                                 _ __
GAM268  PML      3'  GGGCAAAAAAGTTGTTGAG    7133     T  TA
                                GG GC  AAAAAAGTTGTTGAG
                                || ||  ||||||||||||||||
                                CC CG  TTTTTTCAACAACTC
                                 _ __
GAM268  RAI3     3'  GGTGCTGGGGAGCTGCTGAG   7134        AAAAAA
                                GGTGCT     AGTTGTTGAG
                                ||||||     ||||||||||
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                                CCACGA     TCGACGACTC
                                   CCCC__
GAM268  SIRT2    5'  GCGGTGCTGAAGCCCTTGA   7135        AAAAA    G
                                GCGGTGCT    AAGTT TTGA
                                ||||||||    ||||| ||||
                                CGCCACGA    TTCGG AACT
                                     C____    G
GAM268  SIRT2    5'  GCGGTGCTGAAGCCCTTGA   7135        AAAAA    G
                                GCGGTGCT    AAGTT TTGA
                                ||||||||    ||||| ||||
                                CGCCACGA    TTCGG AACT
                                     C____    G
GAM268  FLJ11996 3'  GGCACCTAAAGAGTTGTTG   7136    TG  A   AA
                                GG  CT AAA  AGTTGTTG
                                ||  || |||  ||||||||
                                CC  GG TTT  TCAACAAC
                                 GT  A   C_
GAM268  HSRTSBETA 3'  CAGAAAGAAAAAAGTTGTTG   7137     TGCTA
                                CGG    AAAAAAGTTGTTG
                                |||    ||||||||||||||
                                GTC    TTTTTTCAACAAC
                                  TTTC_
GAM268  KIAA1879  3'  GCTGTGCTGGAGGTGTCTGTTG 7138     G    AAAAAAAG
           AG                    GC GTGCT       TTGTTGAG
                                || |||||       ||||||||
                                CG CACGA       GACAACTC
                                 A    CCTCCACA
GAM268  KIAA1884  3'  GCGGTGCTCGGAGCCACCCTTG 7139        AAAAAA   TG ___
           AG                    GCGGTGCT     AGT  T   TGAG
                                ||||||||     |||  |   ||||
                                CGCCACGA     TCG  G   ACTC
                                     GCC___   GT GGA
GAM268  LOC148171 5'  TGAGTCCAAAGAGGTTGTTGAG 7140    C   G    AAAA
                                G GGT CTAAA    GTTGTTGAG
                                | ||| |||||    |||||||||
                                A TCA GGTTT    CAACAACTC
                                 C   _     CTC_
GAM268  LOC149124 5'  TGAGTCCAAAGAGGTTGTTGAG 7140    C   G    AAAA
                                G GGT CTAAA    GTTGTTGAG
                                | ||| |||||    |||||||||
                                A TCA GGTTT    CAACAACTC
                                 C   _     CTC_
GAM268  LOC51186  5'  GCGCTGCTGAAGGAAGCTG    7141     G    A  AA
                                GCG TGCT AA  AAGTTG
                                ||| |||| ||  ||||||
                                CGC ACGA TT  TTCGAC
                                  G    C  CC
GAM269  SRR      3'  CAGAGAGATTCTGTCTTACCGG 7144     AT       AG___
           T                     CA  AGAGATTC    TACCGGT
                                ||  ||||||||    |||||||
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                                GT  TCTCTAAG    ATGGCCA
                                 C_      ACAGA
GAM269  DUSP14   3'  ATCCAGTAGAGACTGAAGCTGG 7145      A      C_  ACC
             T                   ATCCA TAGAGATT  AGT   GGT
                                 ||||| ||||||||  |||   |||
                                 TAGGT ATCTCTGA  TCG   CCA
                                   C       CT   A__
GAM269  MGC13251 3'  TCCAATAGGCCAGGTACCGGT  7146        AGAT   _
                                 TCCAATAG    TCAG TACCGGT
                                 ||||||||    |||| |||||||
                                 AGGTTATC    GGTC ATGGCCA
                                      C___    C
GAM269  MGC4737  5'  TCCGATCTCAGTACTGG     7147     AATA  GA      C
                                 TCC    GA  TTCAGTAC GG
                                 |||    ||  |||||||| ||
                                 AGG    CT  GAGTCATG CC
                                  _____  A_      A
GAM269  ZIC4     5'  CAATAGAGATTCAGGGCCG   7148            TA
                                 CAATAGAGATTCAG  CCG
                                 ||||||||||||||  |||
                                 GTTATCTCTAAGTC  GGC
                                         CC
GAM269  LOC157603 5'  TCCAATAGGGAGATCAGTGCTG 7149        A  T_    ACC
             GT                    TCCAATAG GA  TCAGT   GGT
                                 ||||||||  ||  |||||   |||
                                 AGGTTATC CT  AGTCA   CCA
                                      C  CT    CGA
GAM269  LOC90843  3'  ATCCAATGAGATGCTG      7150        A    TCA  ACC
                                 ATCCAAT GAGAT   GT   G
                                 |||||||  |||||   ||   |
                                 TAGGTTA CTCTA   CG   C
                                    _    ____  A__
GAM269  LOC92002  3'  ATCCGTAGGGATTCAGT     7151      AA   A
                                 ATCC  TAG GATTCAGT
                                 ||||  |||  ||||||||
                                 TAGG  ATC CTAAGTCA
                                   C_   C
GAM270  EGFR     3'  CTGTGGCTTGGTCCTGG     7154     GATC    CC
                                 CTG    TGGT  TGGTCCTGG
                                 |||    ||||  |||||||||
                                 GAC    ACCG  ACCAGGACC
                                  _____    A_
GAM270  FGF13    3'  CTGAATTTGGTTGATTTGGAT  7155       C    CC    CC
                                 CTGGAT TGGT  TGGT  TGGAT
                                 ||||||  ||||  ||||  |||||
                                 GACTTA ACCA  ACTA  ACCTA
                                    A    __    A_
GAM270  NLGN2    5'  CTGGATCTGGTCCAGGAGCCCA 7156            T  T_
                                 CTGGATCTGGTCC GG  CCTG
                                 ||||||||||||| ||  ||||
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                                GACCTAGACCAGG CC  GGGT
                                       T  TC
GAM270  SLC22A2  3'  GGATCTGGTCCCATGG     7157          GTCC
                                GGATCTGGTCCTG   TGG
                                ||||||||||||   |||
                                CCTAGACCAGGGT   ACC
                                      ____
GAM270  TMPRSS3  3'  TGGGTTTGGTTCTGGTCCC   7158     ATC   C
                                TGG   TGGT CTGGTCCT
                                |||   |||| ||||||||
                                ACC   ACCA GACCAGGG
                                  CAA   A
GAM270  TMPRSS3  3'  TGGGTTTGGTTCTGGTCCC   7158     ATC   C
                                TGG   TGGT CTGGTCCT
                                |||   |||| ||||||||
                                ACC   ACCA GACCAGGG
                                  CAA   A
GAM270  TMPRSS3  3'  TGGGTTTGGTTCTGGTCCC   7158     ATC   C
                                TGG   TGGT CTGGTCCT
                                |||   |||| ||||||||
                                ACC   ACCA GACCAGGG
                                  CAA   A
GAM270  FLJ10761 3'  TGGATCTGGTTTGGAGAAGG   7159         CC   TCCT
                                TGGATCTGGT  TGG   GG
                                ||||||||||  |||   ||
                                ACCTAGACCA  ACC   CC
                                      A_   TCTT
GAM270  FLJ13215 3'  CTAGGGGAGTCTTGGTCCTGGA 7160      ATCT   C
           T                    CTGG   GGTC TGGTCCTGGAT
                                ||||   |||| ||||||||||||
                                GATC   TCAG ACCAGGACCTA
                                  CCC_   A
GAM270  FLJ13693 3'  CTGGGTTTGGGAAGTCCTGG   7161      ATC   TCCT
                                CTGG   TGG   GGTCCTGG
                                ||||   |||   ||||||||
                                GACC   ACC   TCAGGACC
                                  CAA   CT__
GAM270  FLJ20249 3'  CTGAGTTCATGGTCCTGG    7162      _  _ C
                                CTG GT C TGGTCCTGG
                                ||| || | |||||||||
                                GAC CA G ACCAGGACC
                                  T  A T
GAM270  FLJ21438 3'  TGGGGTTTGGCCAGTCCTGG   7163     ATC_    CT
                                TGG   TGGTC  GGTCCTGG
                                |||   |||||  ||||||||
                                ACC   ACCGG  TCAGGACC
                                  CCAA    __
GAM270  LOC139221 5'  TGGGTCTGGTCCTGTGG     7164     A        GTCC
                                TGG TCTGGTCCTG   TGG
                                ||| ||||||||||   |||
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                                ACC AGACCAGGAC   ACC
                                  C       ____
GAM270  LOC51631  3'  CTGGATCTGGTGTCTGGA    7165          CCTG  C
                                CTGGATCTGGT   GTC TGGA
                                ||||||||||   ||| ||||
                                GACCTAGACCA   CAG ACCT
                                      ____  _
GAM271  ABCD2     5'  TCTGCTGGCGAACAAAACCGG  7168       CAC   AAC
                                TCTGC  CGAG  CGAAACCGG
                                |||||  ||||  |||||||||
                                AGACG  GCTT  GTTTTGGCC
                                  ACC  ___
GAM271  CACNG1    3'  CACCGAGAAAGAGACAGG    7169        CC  A  C
                                CACCGAGAA  GA AC GG
                                |||||||||  || || ||
                                GTGGCTCTT  CT TG CC
                                     T_  C  T
GAM271  CUTL1     3'  TCTGCCACCAGGGCTAGAGGCC 7170       AGAA_________  AAAC
           GGTTTCG                CACCG         CCG   CG
                                |||||          |||   ||
                                GTGGT          GGC   GC
                                  CCCGATCTCCIII  CAAA
GAM271  GFRA2     3'  TCTGCCACCGAGAAAGAA     7171           CC
                                TCTGCCACCGAGAA  GAA
                                ||||||||||||||  |||
                                AGACGGTGGCTCTT  CTT
                                       T_
GAM271  RET       3'  TCTGCCACCTGGGAACTGAACA 7172        GA_   C  AC
           CGG                   TCTGCCACC   GAAC GAA  CGG
                                |||||||||   |||| |||  |||
                                AGACGGTGG   CTTG CTT  GCC
                                     ACC    A   GT
GAM271  RET       3'  TCTGCCACCTGGGAACTGAACA 7172        GA_   C  AC
           CGG                   TCTGCCACC   GAAC GAA  CGG
                                |||||||||   |||| |||  |||
                                AGACGGTGG   CTTG CTT  GCC
                                     ACC    A   GT
GAM271  STAM      3'  TCTGCCACCAAGAGGAACACCG 7173           ACC  _
           G                    TCTGCCACCGAGA   GAA ACCGG
                                |||||||||||||   ||| |||||
                                AGACGGTGGTTCT   CTT TGGCC
                                       C__   G
GAM271  FLJ10520  3'  TCTGCCACTGAAACTAGGCCGG 7174       C   AC_______  AAAC
           TTC                    TGCCAC GAGA       CG   C
                                |||||| ||||       ||   |
                                ACGGTG CTTT       GC   G
                                   A   GATCCIIIG  CAAA
GAM271  FLJ23074  3'  TCTGCCACTTGGAATCTCCGG  7175        CGA   CCGAAA
                                TCTGCCAC   GAA     CCGG
                                ||||||||   |||     ||||
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                                AGACGGTG  CTT    GGCC
                                    AAC  AGA___
GAM271  HAN11    3'  TCTGCCACAGAGGGCGATGGCC 7176     C  AA__________  AAAC
           GGTTTCG                CAC GAG        CCG   CG
                                |||  |||        |||   ||
                                GTG CTC        GGC   GC
                                  T  CCGCTACCIII  CAAA
GAM271  PINK1    3'  TCTGCCACTGACAGCCAGTGCC 7177        C  GAA  AAA
                                TCTGCCAC GA  CCG  CC
                                ||||||||  ||  |||  ||
                                AGACGGTG CT  GGT  GG
                                    A  GTC  CAC
GAM271  SYNPO2   5'  TCTGCCACTGGAGATCTGGCCG 7178     C_   A________  AAAC
           GTTTCG                 CCAC  GAGA      CCG   CG
                                ||||  ||||      |||   ||
                                GGTG  CTCT      GGC   GC
                                  AC   AGACCIII  CAAA
GAM271  LOC164397 5'  TCTCCACCGAGGCACTGGCCGG 7179   G      AA_________  AAAC
           TTC                   CCACCGAG       CCG   C
                                 ||||||||       |||   |
                                 GGTGGCTC       GGC   G
                                _      CGTGACCIII  CAAA
GAM271  LOC221143 3'  TCTGCCACGAGAGCTAGGCCGG 7180      C   AC_________  AAAC
           TTC                   GCCAC GAGA       CG   C
                                |||||  ||||       ||   |
                                CGGTG CTCT       GC   G
                                   _   CGATCCIIIG  CAAA
GAM272  DKK1     3'  TCAGAAAATAAGCTAGTATTTT 7183        _    TAA
                                TCAGAAAG AGGTT  TATTTT
                                |||||||| |||||  ||||||
                                AGTCTTTT TTCGA  ATAAAA
                                    A    TC_
GAM272  KERA     3'  AGAAAGCATTCAATATTTT   7184       AG
                                AGAAAG  GTTTAATATTTT
                                ||||||  ||||||||||||
                                TCTTTC  TAAGTTATAAAA
                                   G_
GAM272  PPP1R12A  3'  CCAGAAAGATGTAGTATTTT  7185        G  TTAA
                                TCAGAAAGA GT   TATTTT
                                |||||||| ||   ||||||
                                GGTCTTTCT CA   ATAAAA
                                    A  TC__
GAM272  S100B    3'  GAAAGAGGTTTTCAATTTT   7186          AAT
                                GAAAGAGGTTT  ATTTT
                                ||||||||||  |||||
                                CTTTCTCCAAA  TAAAA
                                    AGT
GAM272  DKFZP564I0422 3'  ATCAGAAGAATGCAATATTTT  7187       A  GTT
                                ATCAGAA GAG  TAATATTTT
                                |||||||  |||  |||||||||
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                                TAGTCTT CTT   GTTATAAAA
                                    _  AC_
GAM272  EML4     3'  AGAAAGAGGAAACATTTT    7188         TTT
                                AGAAAGAGG   AATATTTT
                                |||||||||   ||||||||
                                TCTTTCTCC   TTGTAAAA
                                    T__
GAM272  FLJ21657  3'  ATCAGGCAGAGTAAAATATTTT 7189       AA   GTTT
                                ATCAG  AGAG   AATATTTT
                                |||||  ||||   ||||||||
                                TAGTC  TCTC   TTATAAAA
                                   CG   ATT_
GAM272  KIAA1054  3'  GAAAGAGGTACCATTTT     7190         TTAA
                                GAAAGAGGT   TATTTT
                                |||||||||   ||||||
                                CTTTCTCCA   GTAAAA
                                    TG__
GAM272  SEMA3E    5'  TCAGGAAGAAGCTGTATTTT   7191      A      TAA
                                TCAG AAGAGGTT   TATTTT
                                |||| ||||||||   ||||||
                                AGTC TTCTTCGA   ATAAAA
                                  C       C__
GAM272  LOC130507 3'  CAGAAAGTTATCTTAATATTTT 7192       AGG_
                                CAGAAAG   TTTAATATTTT
                                |||||||   ||||||||||
                                GTCTTTC   GAATTATAAAA
                                    AATA
GAM272  LOC148145 5'  ATCAGGTCCAGGTTTAATATTT 7193      AAAG
           T                     ATCAG   AGGTTTAATATTTT
                                |||||   ||||||||||||||
                                TAGTC   TCCAAATTATAAAA
                                   CAGG
GAM273  DSC3     3'  TAAGTCTAAAACACATAGATTT 7196       AGT      A
           TA                    TAAGTT   AATACATA ATTTTA
                                |||||||  |||||||| ||||||
                                ATTCAG   TTGTGTAT TAAAAT
                                    ATT      C
GAM273  DSC3     3'  TAAGTCTAAAACACATAGATTT 7196       AGT      A
           TA                    TAAGTT   AATACATA ATTTTA
                                |||||||  |||||||| ||||||
                                ATTCAG   TTGTGTAT TAAAAT
                                    ATT      C
GAM273  FLJ20366  3'  TAAGTTAGTACATGTAAACTT  7197         ATACA
                                TAAGTTAGTA    TAAATTT
                                ||||||||||    |||||||
                                ATTCAATCAT    ATTTGAA
                                     GTAC_
GAM274  CD38     3'  TAAGACTTTGGGGAAAAA    7200         A_
                                TAAGATTTT  GGAAAAA
                                |||||||||  |||||||
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                                ATTCTGAAA  CCTTTTT
                                     CC
GAM274  EGR2     3'  TAAGTTTTAGGAAGAACC    7201       A        A
                                TAAG TTTTAGGAA AATT
                                |||| ||||||||| ||||
                                ATTC AAAATCCTT TTGG
                                  _        C
GAM274  GALNT1   3'  TAAGATTTAGGAAAAGAAATG  7202          T      ATT
                                TAAGATTT AGGAAAA   ATG
                                |||||||| |||||||   |||
                                ATTCTAAA TCCTTTT   TAC
                                     _      CTT
GAM274  PAPPA    3'  TAGAATTTTAGGAGGCTCTGGG 7203     AG        AAAATTA
                                TA  ATTTTAGGA      TGGG
                                ||  |||||||||      ||||
                                AT  TAAAATCCT      ACCC
                                 CT        CCGAG__
GAM274  SH3BP4   3'  CTCTGGGAGAAATTATGGG   7204       A   A
                                TTTT GGA AAATTATGGG
                                |||| ||| ||||||||||
                                GAGA CCT TTTAATACCC
                                  C   C
GAM274  SPAG8    3'  AATCCCAAGGAAAGGTTATGGG 7205          _    AA
                                GATTTTA GGAAA  TTATGGG
                                ||||||| |||||  |||||||
                                TTAGGGT CCTTT  AATACCC
                                    T    CC
GAM274  COQ7     3'  AAGTTTTAGGAGAAAATGGG   7206      A       A   TT
                                AAG TTTTAGGA AAA  ATGGG
                                ||| |||||||| |||  |||||
                                TTC AAAATCCT TTT  TACCC
                                  _       C   __
GAM274  DKFZp434A2417 3'  GAATGCCCAAGAAAGATTATGG 7207     T__        A
           G                     GA   TTTAGGAAA ATTATGGG
                                ||   ||||||||| ||||||||
                                CT   GGGTTCTTT TAATACCC
                                 TAC        C
GAM274  DKFZp434C0328 5'  TAAGGCTTTAGGGGGTTTCGTG 7208       AT     AAAAA TA
           GG                    TAAG  TTTAGG    T  TGGG
                                ||||  ||||||    |  ||||
                                ATTC  AAATCC    A  ACCC
                                  CG      CCCAA GC
GAM274  DKFZp761O0113 5'  TAAGACTTTAGGGAAGATAAGG 7209            A  A  TAT
                                TAAGATTTTAGG AA AT   GG
                                |||||||||||| || ||   ||
                                ATTCTGAAATCC TT TA   CC
                                       C  C  TT_
GAM274  FLJ31547  3'  GATTGCGGGAGAAATTATGGG  7210       TTA   A
                                GATT   GGA AAATTATGGG
                                ||||   ||| ||||||||||
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                                CTAA   CCT TTTAATACCC
                                  CGC   C
GAM274  KIAA0769  3'  TAAGATTCTTAGGAGGGATGG  7211          _   AAAATT
                                TAAGATTTT AGGA     ATGG
                                ||||||||| ||||     ||||
                                ATTCTAAGA TCCT     TACC
                                     A   CCC___
GAM274  MacGAP    3'  GATTTTAGGAGAAAAGAATGGG 7212          _   TT
                                GATTTTAGGA AAAA  ATGGG
                                |||||||||| ||||  |||||
                                CTAAAATCCT TTTT  TACCC
                                     C   CT
GAM274  MDS031    3'  AGATTCTAGGAGAAAACC    7213          _
                                AGATTTTAGGA AAAATT
                                |||||||||| ||||||
                                TCTAAGATCCT TTTTGG
                                     C
GAM274  POPX1     3'  AGATTTTAGTCCTCTGTTATGG 7214         GAAAAA_
          G                      AGATTTTAG      TTATGGG
                                 |||||||||      |||||||
                                 TCTAAAATC      AATACCC
                                      AGGAGAC
GAM274  ZNF183    3'  AAATTTAAGAATTATGG     7215    T     AAA
                                GA TTTAGGA   ATTATGG
                                || |||||||   |||||||
                                TT AAATTCT   TAATACC
                                 T     ____
GAM274  LOC148697 3'  GAGCAGGAAAAGTTGTGGG   7216    TTT      A  A
                                GA   TAGGAAAA TT TGGG
                                ||   |||||||| || ||||
                                CT   GTCCTTTT AA ACCC
                                 C__       C  C
GAM274  LOC158819 5'  AGATTTTAGGAAGACACGTGG  7217          AAAT   _
                                AGATTTTAGGAA    TATG GG
                                ||||||||||||    |||| ||
                                TCTAAAATCCTT    GTGC CC
                                      CT__    A
GAM274  LOC219700 5'  TAAGATTTTAGAGGAAAA    7218          __
                                TAAGATTTT  AGGAAAA
                                |||||||||  |||||||
                                ATTCTAAAA  TCCTTTT
                                     TC
GAM275  ARGBP2    5'  TGAGTTGGTGATCTTTTATCTT 7221    T      CAGTC___   C
          GTAGG                    TG GTTGGTGA       CTTG AGG
                                   || ||||||||       |||| |||
                                   AC CAACCACT       GAAC TCC
                                    T       AGAAAATA    A
GAM275  BDG-29    5'  GCGAGTGGTAGTCCTTGCGGG  7222    T    AC       A
                                GT GGTG  AGTCCTTGC GG
                                || ||||  ||||||||| ||
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                                CG TCAC  TCAGGAACG CC
                                 C   CA       C
GAM275  KIAA1243  3'  TGTGTTAGGTCCATTTTGCAGG 7223         TGACA   ___
                                TGTGTTGG    GTCC   TTGCAGG
                                ||||||||    ||||  |||||||
                                ACACAATC    CAGG   AACGTCC
                                     _____   TAA
GAM275  MGC26778  3'  TGTGTTGGAGACAGTTTAGCCT 7224       T    T_______  TTGCA
           GCAG                   GTTGG GACAG       CC    G
                                |||||  |||||       ||    |
                                CAACC CTGTC       GG    C
                                   T    AAATCIII  ACGTT
GAM275  MGC4832  3'  TGTTTTGGTGACAGTTTTCTGC 7225         T_________  TTGCA
           CTGCAAGG                 GGTGACAG        CC    GG
                                ||||||||        ||    ||
                                CCACTGTC        GG    CC
                                     AAAAGACIII  ACGTT
GAM275  SEMA6C   5'  TGGGTTGGTGACTCCT     7226     T       AG
                                TG GTTGGTGAC  TCCT
                                || |||||||||  ||||
                                AC CAACCACTG  AGGA
                                 C       __
GAM275  LOC138399 5'  TGTCTTAAGTTTTTGCAG    7227      G   GTGAC   CC
                                TGT TTG    AGT  TTGCAG
                                ||| |||    |||  ||||||
                                ACA AAT    TCA  AACGTC
                                  G  _____  AA
GAM275  LOC92293  3'  TGTGTGGTGACAGTTGAAG   7228       T       CCT  C
                                TGTGT GGTGACAGT   TG AG
                                ||||| |||||||||   || ||
                                ACACA CCACTGTCA   AC TC
                                   _       ___  T
GAM276  LYZ      3'  CAAGATTAAGTCTGGGTTATTT 7231        C  _  CAAC
           C                     CAAGAT AA TC    GGTTGTTTC
                                ||||||  || ||   |||||||||
                                GTTCTA TT AG    CCAATAAAG
                                    A  C  AC__
GAM276  BAG5     3'  CAAGGTCAATCTGATCATTTC  7232      A     CAAC   TG
                                CAAG TCAATC    GGT  TTTC
                                ||||  ||||||    |||  ||||
                                GTTC AGTTAG    CTA  AAAG
                                   C     A___   GT
GAM276  CDH26    3'  GATCAGTACAGCTGTTC     7233       ATCCA
                                GATCA    ACGGTTGTTT
                                |||||    ||||||||||
                                CTAGT    TGTCGACAAG
                                   CA___
GAM276  FLJ10895  3'  AGGGTCAATCCAATGAAAGT   7234     A_       C  TT
                                AG  TCAATCCAA GG  GT
                                ||  |||||||| ||  ||
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                                TC  AGTTAGGTT CT  CA
                                 CC        A  TT
GAM276  FLJ11608  3'  CAAGATCAGTCCTCATTTGTTT 7235          A   AACGG
              C                   CAAGATCA TCC     TTGTTTC
                                  |||||||| |||     |||||||
                                  GTTCTAGT AGG     AACAAAG
                                      C   AGTA_
GAM276  FLJ23356  3'  CAAGATTAAGTCTGGGTTATTT 7231        C  _  CAAC
              C                   CAAGAT AA TC    GGTTGTTTC
                                  |||||| || ||    |||||||||
                                  GTTCTA TT AG    CCAATAAAG
                                     A  C  AC__
GAM276  KIAA0493  5'  AAGATCAATATACTGGTT    7236          CCA  _
                                  AAGATCAAT   AC GGTT
                                  |||||||||   || ||||
                                  TTCTAGTTA   TG CCAA
                                       TA_  A
GAM276  KIAA1183  5'  CAGGATTATCCAACTCCTCTGT 7237     A   CA      GG__
              TTC                   CA GAT  ATCCAAC    TTGTTTC
                                  || |||  |||||||    |||||||
                                  GT CTA  TAGGTTG    GACAAAG
                                   C   A_      AGGA
GAM276  KIAA1915  3'  CAAGAGTAGTCCAACGATT    7238       TCAA
                                  CAAGA    TCCAACGGTT
                                  |||||    ||||||||||
                                  GTTCT    AGGTTGCTAA
                                     CATC
GAM276  NKIR      3'  CAAGATCAGTTTCAATGGGCT  7239         ATC_  C_
                                  CAAGATCA    CAA  GGTT
                                  ||||||||    |||  ||||
                                  GTTCTAGT    GTT  CCGA
                                       CAAA   AC
GAM276  PISD      3'  TGAGATCATTCCAGCCTGC    7240     A      A    ACGG
                                  C AGATCA TCCA    TTGT
                                  | |||||| ||||    ||||
                                  A TCTAGT AGGT    GACG
                                   C      A    CG__
GAM276  PTPNS1    3'  CAAGATCACGTTGCTGTTGTTT 7241          ATCCAACG
                                  CAAGATCA       GTTGTTT
                                  ||||||||       |||||||
                                  GTTCTAGT       CAACAAA
                                       GCAACGA_
GAM276  LOC145355 5'  TGAGATGAATCTGGTTGCTT   7242     A    C    CAAC
                                  C AGAT AATC    GGTTGTTT
                                  | |||| ||||    ||||||||
                                  A TCTA TTAG    CCAACGAA
                                   C    C    A___
GAM276  LOC157567 3'  AAGATCAAATCAATTATCT    7243          TCCAA
                                  AAGATCAA     CGGTTGTTT
                                  ||||||||     |||||||||
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                                TTCTAGTT    GTTAATAGA
                                    TA___
GAM276  LOC196478 5'  AAGGCCAATCCAATGGTC    7244      AT       C
                                AAG  CAATCCAA GGTT
                                |||  |||||||| ||||
                                TTC  GTTAGGTT CCAG
                                  CG       A
GAM276  LOC219397 3'  GATGTCCGCGGTTGTTT     7245      CAA   AA
                                GAT   TCC  CGGTTGTTT
                                |||   |||  |||||||||
                                CTA   AGG  GCCAACAAA
                                  C__   C_
GAM276  LOC90643  3'  TGAGATCAGTCAAAGTTGCTT  7246    A     A  CAAC
                                C AGATCA TC    GGTTGTTT
                                | |||||| ||    ||||||||
                                A TCTAGT AG    TCAACGAA
                                 C     C  TT__
GAM277  FANCC     3'  TAGCATTGCCACATACCAAAA  7249      ATCAT
                                TAG    TTATATACCAAAA
                                |||    ||||||||||||
                                ATC    GGTGTATGGTTTT
                                  GTAAC
GAM277  PPAT      3'  AGACTATATACCAAA       7250       CATT
                                AGAT    TATATACCAAA
                                ||||    ||||||||||
                                TCTG    ATATATGGTTT
                                    ____
GAM277  PRKG1     3'  CTAGTCATTTACTTCCA     7251       A       ATA
                                CTAG TCATTTAT   CCA
                                |||| ||||||||   |||
                                GATC AGTAAATG   GGT
                                  _       AA_
GAM277  SSRP1     3'  TAAATCATTTTCACAGACCA   7252          __     T
                                TAGATCAT  TTATA ACCA
                                ||||||||  ||||| ||||
                                ATTTAGTA  AGTGT TGGT
                                     AA    C
GAM277  FLJ13194  3'  GAAAACCATTTATATATCAAA  7253    T           C
                                C AGATCATTTATATA CAAA
                                | ||||||||||||| ||||
                                C TTTGGTAAATATAT GTTT
                                 T           A
GAM277  HCGIV.9   3'  TAGACACATTTATATGTCAA   7254       _       AC
                                TAGAT CATTTATAT  CAA
                                ||||| |||||||||  |||
                                ATCTG GTAAATATA  GTT
                                   T       CA
GAM277  KIAA0256  3'  TACTAAATCATCAACCAA    7255            TATAT
                                TACTAGATCATT    ACCAA
                                ||||||||||||    |||||
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                                ATGATTTAGTAG    TGGTT
                                       T____
GAM277  MGC9912  3'  TAGATCATTTCATACCA    7256          A
                                TAGATCATTT TATACCA
                                |||||||||| |||||||
                                ATCTAGTAAA GTATGGT
                                       _
GAM277  PROL2    3'  CTGGAATGGATATATACCAAAA 7257    A  TCATT
                                CT GA    TATATACCAAAA
                                || ||    ||||||||||||
                                GA CT    ATATATGGTTTT
                                 C  TACCT
GAM277  PSPH     3'  TACAGATCATTTGTACCAA   7258     T       ATA
                                TAC AGATCATTT   TACCAA
                                ||| |||||||||   ||||||
                                ATG TCTAGTAAA   ATGGTT
                                  _       C__
GAM277  RNP24    3'  CTGGATCATCCCCATACCAAAA 7259    A      TA
                                CT GATCATT  TATACCAAAA
                                || |||||||  ||||||||||
                                GA CTAGTAG  GTATGGTTTT
                                 C      GG
GAM277  SCDGF-B  3'  TACCTGGTTATATATACCAAAA 7260      AGATCATT
                                TACT       TATATACCAAAA
                                ||||       ||||||||||||
                                ATGG       ATATATGGTTTT
                                  ACCAAT__
GAM277  SCDGF-B  3'  TACCTGGTTATATATACCAAAA 7260      AGATCATT
                                TACT       TATATACCAAAA
                                ||||       ||||||||||||
                                ATGG       ATATATGGTTTT
                                  ACCAAT__
GAM277  SCYA11   3'  TACTGATCATCTTTGCCA    7261      A      ATATA
                                TACT GATCATTT    CCA
                                |||| ||||||||    |||
                                ATGA CTAGTAGA    GGT
                                  _       AAC__
GAM277  SE70-2   5'  TACTGGATCACTTCCATGATCA 7262      A      A  AC_
           AAA                    TACT GATCATTT TAT   CAAAA
                                |||| |||||||| |||   |||||
                                ATGA CTAGTGAA GTA   GTTTT
                                  C       G   CTA
GAM277  LOC202460 5'  CACTAGATCATTTTTGTTCCA  7263           ATATA
                                TACTAGATCATTT    CCA
                                ||||||||||||    |||
                                GTGATCTAGTAAA    GGT
                                       AACAA
GAM277  LOC221814 3'  CTAGAGTACCTATATACTAAAA 7264       TC        C
                                CTAGA  ATTTATATAC AAAA
                                |||||  |||||||||| ||||
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                                GATCT  TGGATATATG TTTT
                                   CA        A
GAM278  ARHGAP6  3'  TGGTTTGGGTTCTGTTTGTTT  7267      CA     GTTTAG
                                TGGTT  GGTTTTG     GTTT
                                |||||  |||||||     ||||
                                ACCAA  CCAAGAC     CAAA
                                   AC      AAA___
GAM278  ARHGAP6  3'  TGGTTTGGGTTCTGTTTGTTT  7267      CA     GTTTAG
                                TGGTT  GGTTTTG     GTTT
                                |||||  |||||||     ||||
                                ACCAA  CCAAGAC     CAAA
                                   AC      AAA___
GAM278  ATP2C1   3'  TGGTTCAGGTTTTGCCTT    7268            G
                                TGGTTCAGGTTTTG TTT
                                |||||||||||||| |||
                                ACCAAGTCCAAAAC GAA
                                         G
GAM278  KIAA1635  3'  TGGTTTAGGTTCTTGGTTT   7269       C     _
                                TGGTT AGGTTTT GGTTT
                                ||||| ||||||| |||||
                                ACCAA TCCAAGA CCAAA
                                   A      A
GAM278  PRO0132   5'  AGTTCAGGGTTTAGGTT     7270         TTTTG
                                GGTTCAGG    GTTTAGGTT
                                ||||||||    |||||||||
                                TCAAGTCC    CAAATCCAA
                                      _____
GAM278  LOC149722 5'  TGGTTCAGGTTTGTCCCGGTTT 7271           TG   TA
                                TGGTTCAGGTTT  GTT  GGTTT
                                ||||||||||||  |||  |||||
                                ACCAAGTCCAAA  CAG  CCAAA
                                      __  GG
GAM278  LOC152756 3'  TGGTTTAGTTTTGGCTTA    7272       CA
                                TGGTT  GGTTTTGGTTTA
                                |||||  ||||||||||||
                                ACCAA  TCAAAACCGAAT
                                   A_
GAM278  LOC152816 3'  TGCTTCAGTATGTTTGGGTTT  7273     G    GTTTTG   A
                                TG TTCAG     GTTT GGTTT
                                || |||||     |||| |||||
                                AC AAGTC     CAAA CCAAA
                                 G    ATA___    C
GAM279  D12S2489E 3'  TTGGTCCTACCTTTAGAA    7276        CAT   CAC
                                TTGGTCC   CCTT   AGGA
                                |||||||   ||||   ||||
                                AACCAGG   GGAA   TCTT
                                    AT_    A__
GAM279  DKFZP434I092 3'  TTGATTCCATCCTTTCCAGA   7277       C       CA
                                TTGGT CCATCCTT  CAGG
                                ||||| ||||||||  ||||
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                                AACTA GGTAGGAA  GTCT
                                  A       AG
GAM279  FLJ12439  3'  TTGCTCCTATTTTTCACAGA   7278      G   C  CC
                                TTG TCC AT  TTCACAGG
                                ||| ||| ||  ||||||||
                                AAC AGG TA  AAGTGTCT
                                  G   A  AA
GAM279  MGC2865   3'  CTGGTCAAGCCCTTTACAGGAT 7279        CCA    C
           TT                    TTGGTC   TCCTT ACAGGATTT
                                ||||||   ||||| |||||||||
                                GACCAG   GGGAA TGTCCTAAA
                                   TTC    A
GAM280  MAPK4     3'  TCAGTTGAGGCTAGTTGGG    7282      G      GG  GC
                                TCAG TTGAGGC  AG  TTGGG
                                |||| |||||||  ||  |||||
                                AGTC AACTCCG  TC  AACCC
                                  _      A_  __
GAM280  NAP1L3    5'  GGCAGTGGAGGCTTGGGC    7283      TGA  C
                                GGT   GG GGAGGCTTGGGC
                                |||   || ||||||||||||
                                CCG   TC CCTCCGAACCCG
                                  ___  A
GAM280  PLA2G4C   5'  TCCGGTGCGGAGGCTTGGG    7284     A   TGAG
                                TC GGT    GCGGAGGCTTGGG
                                || |||    ||||||||||||
                                AG CCA    CGCCTCCGAACCC
                                 G  _____
GAM280  PLA2G4C   5'  TCCGGTGCGGAGGCTTGGG    7284     A   TGAG
                                TC GGT    GCGGAGGCTTGGG
                                || |||    ||||||||||||
                                AG CCA    CGCCTCCGAACCC
                                 G  _____
GAM280  SLC7A6    3'  CCAGGTTGGGATTGCTTGGG   7285         A  CGGAG
                                TCAGGTTG GG     GCTTGGG
                                |||||||| ||     |||||||
                                GGTCCAAC CC     CGAACCC
                                     _  TAA__
GAM280  DKFZp434J1015 3'  TCAGGTGGAGGCGGGTGGGGGG 7286        T      A_  CTT
                                TCAGGT GAGGCGG  GG   GGG
                                |||||| |||||||  ||   |||
                                AGTCCA CTCCGCC  CC   CCC
                                   C      CA  C__
GAM280  DKFZp547M072 3'  TCAGGTTGGGCCGGGAAGGAGG 7287         A  __    CTT
           GC                    TCAGGTTG GGC  GGAGG   GGGC
                                |||||||| |||  |||||   ||||
                                AGTCCAAC CCG  CCTTC   CCCG
                                     _  GC    CT_
GAM280  FLJ11939  3'  AGGTTGGGGGGACACCTGGGC  7288        A  C   G
                                AGGTTG GG GGA GCTTGGGC
                                |||||| || ||| ||||||||
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                                TCCAAC CC CCT TGGACCCG
                                   C _  G
GAM280  KIAA0255  3'  TCAGGTGTGGGGTGGAGGGGA  7289       _ A  C    CTT
                                TCAGGT TG GG GGAGG  GGG
                                |||||| || || |||||  |||
                                AGTCCA AC CC CCTCC  CCT
                                   C  C  A   ____
GAM280  KIAA0295  3'  TCAGGTGGGGTGGGATGACGG  7290       T A  C  A  CT_
                                TCAGGT G GG GG GG  TGG
                                |||||| | || || ||  |||
                                AGTCCA C CC CC CT  GCC
                                   _ C  A  _  ACT
GAM280  TUBAL2   3'  TCAGGCTGGGGCGGGGAGAG  7291        A    A  CTT
                                TCAGGTTG GGCGG GG  GGG
                                |||||||| ||||| ||  |||
                                AGTCCGAC CCGCC CC  CTC
                                    C    _ T__
GAM280  LOC145082 5'  AGGTTAGGTGGATCGCCTGGGC 7292      G  C  G_
                                AGGTT AGG GGA  GCTTGGGC
                                ||||| ||| |||  ||||||||
                                TCCAA TCC CCT  CGGACCCG
                                   _  A  AG
GAM280  LOC146957 3'  AGCTCAGCCTGGAGGCTTGGG  7293     GA  __
                                GGTT  GGC  GGAGGCTTGGG
                                ||||  |||  ||||||||||
                                TCGA  TCG  CCTCCGAACCC
                                  G_  GA
GAM280  LOC148708 3'  GGTTGAGGCGGGCCCAGGC   7294         AG  TG
                                GGTTGAGGCGG  GCT  GGC
                                ||||||||||  |||  |||
                                CCAACTCCGCC  CGG  CCG
                                      __  GT
GAM280  LOC152762 3'  CCAGGTTGGGGTGGGGGC    7295       A  C  A
                                TCAGGTTG GG GG GGC
                                |||||||| || || |||
                                GGTCCAAC CC CC CCG
                                    C  A  C
GAM280  LOC155061 3'  CCAGGTTGGGGTGGGCGGC   7296       A  C  A_
                                TCAGGTTG GG GG  GGC
                                |||||||| || ||  |||
                                GGTCCAAC CC CC  CCG
                                    C  A  CG
GAM281  DKK1     3'  TCAGAAAATAAGCTAGTATTTT 7183         _   TAA
                                TCAGAAAG AGGTT  TATTTT
                                |||||||| |||||  ||||||
                                AGTCTTTT TTCGA  ATAAAA
                                    A    TC_
GAM281  KERA     3'  AGAAAGCATTCAATATTTT   7184       AG
                                AGAAAG  GTTTAATATTTT
                                ||||||  ||||||||||||
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                                TCTTTC  TAAGTTATAAAA
                                   G_
GAM281  PPP1R12A  3'  CCAGAAAGATGTAGTATTTT  7185        G  TTAA
                                TCAGAAAGA GT   TATTTT
                                ||||||||| ||   ||||||
                                GGTCTTTCT CA   ATAAAA
                                     A  TC__
GAM281  S100B   3'  GAAAGAGGTTTTCAATTTT   7186         AAT
                                GAAAGAGGTTT  ATTTT
                                ||||||||||  |||||
                                CTTTCTCCAAA  TAAAA
                                      AGT
GAM281  DKFZP564I0422 3'  ATCAGAAGAATGCAATATTTT  7187       A  GTT
                                ATCAGAA GAG  TAATATTTT
                                ||||||| |||  |||||||||
                                TAGTCTT CTT  GTTATAAAA
                                   _  AC_
GAM281  EML4    3'  AGAAAGAGGAAACATTTT   7188        TTT
                                AGAAAGAGG  AATATTTT
                                |||||||||  ||||||||
                                TCTTTCTCC  TTGTAAAA
                                     T__
GAM281  FLJ21657  3'  ATCAGGCAGAGTAAAATATTTT 7189      AA   GTTT
                                ATCAG  AGAG   AATATTTT
                                |||||  ||||   ||||||||
                                TAGTC  TCTC   TTATAAAA
                                  CG   ATT_
GAM281  KIAA1054  3'  GAAAGAGGTACCATTTT    7190        TTAA
                                GAAAGAGGT   TATTTT
                                |||||||||   ||||||
                                CTTTCTCCA   GTAAAA
                                     TG__
GAM281  SEMA3E   5'  TCAGGAAGAAGCTGTATTTT  7191     A      TAA
                                TCAG AAGAGGTT  TATTTT
                                |||| ||||||||  ||||||
                                AGTC TTCTTCGA  ATAAAA
                                  C      C__
GAM281  LOC130507 3'  CAGAAAGTTATCTTAATATTTT 7192       AGG_
                                CAGAAAG   TTTAATATTTT
                                |||||||   ||||||||||
                                GTCTTTC   GAATTATAAAA
                                     AATA
GAM281  LOC148145 5'  ATCAGGTCCAGGTTTAATATTT 7193      AAAG
           T                     ATCAG   AGGTTTAATATTTT
                                |||||   ||||||||||||||
                                TAGTC   TCCAAATTATAAAA
                                  CAGG
GAM282  DTNA    3'  TGAAAAGCTAAGACTGGTTTGA 7300      A     TTCACA
                                TGAA GAGCTAA    GTTTGA
                                |||| |||||||    ||||||
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                                ACTT TTCGATT     CAAACT
                                  _      CTGAC_
GAM282  DTNA    3'  TGAAAAGCTAAGACTGGTTTGA 7300      A     TTCACA
                                TGAA GAGCTAA     GTTTGA
                                |||| |||||||     ||||||
                                ACTT TTCGATT     CAAACT
                                  _      CTGAC_
GAM282  DTNA    3'  TGAAAAGCTAAGACTGGTTTGA 7300      A     TTCACA
                                TGAA GAGCTAA     GTTTGA
                                |||| |||||||     ||||||
                                ACTT TTCGATT     CAAACT
                                  _      CTGAC_
GAM282  DTNA    3'  TGAAAAGCTAAGACTGGTTTGA 7300      A     TTCACA
                                TGAA GAGCTAA     GTTTGA
                                |||| |||||||     ||||||
                                ACTT TTCGATT     CAAACT
                                  _      CTGAC_
GAM282  F8      3'  TAAAAGAGCTAGTTCCA     7301           A   A
                                TGAAAGAGCTA TTC CA
                                |||||||||||| ||| ||
                                ATTTTCTCGAT AAG GT
                                       C   _
GAM282  GYS1    3'  TGAAGGCAGGGCACAGTTTG   7302      A A  TAATT
                                TGAA G GC    CACAGTTTG
                                |||| | ||    |||||||||
                                ACTT C CG    GTGTCAAAC
                                  _ _  TCCC_
GAM282  SVIL    3'  TGGCAGAGCTAATTCAACAG   7303     AA         _
                                TG  AGAGCTAATTCA CAG
                                ||  ||||||||||||| |||
                                AC  TCTCGATTAAGT GTC
                                 CG          T
GAM282  SVIL    3'  TGGCAGAGCTAATTCAACAG   7303     AA         _
                                TG  AGAGCTAATTCA CAG
                                ||  ||||||||||||| |||
                                AC  TCTCGATTAAGT GTC
                                 CG          T
GAM282  TPM4    3'  TGAAAAAGCTGGTGCCATTTGA 7304          AATTCACA
                                TGAAAGAGCT       GTTTGA
                                ||||||||||       ||||||
                                ACTTTTTCGA       TAAACT
                                      CCACGG__
GAM282  FLJ20573 3'  TGAAGAGGGCTGAGACAGTTTG 7305      _  A   AATTC
          A                    TGAA AG GCT    ACAGTTTGA
                               |||| || |||    |||||||||
                               ACTT TC CGA    TGTCAAACT
                                 C  C   CTC__
GAM282  FLJ32389 3'  TGGGAGAGTCTGTACAGTTTG  7306     AA   _  AATTC
                                TG  AGAG CT    ACAGTTTG
                                ||  |||| ||    ||||||||
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                                AC  TCTC GA    TGTCAAAC
                                 CC    A  CA___
GAM282  KIAA0379  3'  TGAAAAAGCACAGTTT     7307         TAATTC
                                TGAAAGAGC     ACAGTTT
                                |||||||||     |||||||
                                ACTTTTTCG     TGTCAAA
                                          _______
GAM282  MGC10940  3'  TGAAAGAGCTAATTTTACTGCT 7308             C_  A
           TGA                    TGAAAGAGCTAATT  AC GTTTGA
                                |||||||||||||  || ||||||
                                ACTTTCTCGATTAA  TG CGAACT
                                        AA  A
GAM282  MGC5466   5'  TGAAGCAGTCTTCAAACAGTTT 7309    A    TAA_  __
           GA                     A GAGC    TTC  ACAGTTTGA
                                | ||||    |||  |||||||||
                                A TTCG    AAG  TGTCAAACT
                                 C    TCAG   TT
GAM282  LOC115219 3'  TGGGAGGCTGAGGCAGCAGTTT 7310     AA  A   AATT  _
           GA                     TG  AG GCT    CA CAGTTTGA
                                ||  || |||    || ||||||||
                                AC  TC CGA    GT GTCAAACT
                                 CC  _   CTCC  C
GAM282  LOC130612 3'  TGGCAGAGGCCACACAGTTTG  7311     AA   _   ATT
                                TG  AGAG CTA   CACAGTTTG
                                ||  |||| |||   |||||||||
                                AC  TCTC GGT   GTGTCAAAC
                                 CG    C  ___
GAM282  LOC89932  3'  TGAAAGAGCTAATGTATTCCAG 7312             _____  A
                                TGAAAGAGCTAAT    TC CAG
                                ||||||||||||    || |||
                                ACTTTCTCGATTA    AG GTC
                                        CATA  _
GAM283  HYAL2     3'  GGGTGCGAGCTGGTATGGAT   7315      A       TTGAGT
                                GGG GCGAGCTG     TGGAT
                                ||| ||||||||     |||||
                                CCC CGCTCGAC     ACCTA
                                  A       CAT___
GAM283  HYAL2     3'  GGGTGCGAGCTGGTATGGAT   7315      A       TTGAGT
                                GGG GCGAGCTG     TGGAT
                                ||| ||||||||     |||||
                                CCC CGCTCGAC     ACCTA
                                  A       CAT___
GAM283  MPDZ      3'  AGGAGGTGAGCTAGGGGTTGG  7316       C_     TTGA
                                GGGAG  GAGCTG   GTTGG
                                |||||  ||||||   |||||
                                TCCTC  CTCGAT   CAACC
                                   CA     CCC_
GAM283  SLC35A2   3'  GGGGGCTGAGCTGAGGTGG   7317      A  _    GTT   T
                                GGG GC GAGCT   GAG TGG
                                ||| || |||||   ||| |||
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                                CCC CG CTCGA   CTC ACC
                                  C  A    ___   C
GAM283  TMEM4    5'  AGGGAGCAGGGCTGTCCGGGAT 7318        A_     GAGTT
                                AGGGAGCG  GCTGTT    GGAT
                                ||||||||  ||||||    ||||
                                TCCCTCGT  CGACAG    CCTA
                                    CC     GC___
GAM283  BCoR     5'  AAGGAGCGGGGGGGCGGTTGG   7319        AGCT  T A
                                AGGGAGCG    GT G GTTGG
                                ||||||||    || | |||||
                                TTCCTCGC    CG C CAACC
                                    CCCC  _ _
GAM283  BCoR     5'  AAGGAGCGGGGGGGCGGTTGG   7319        AGCT  T A
                                AGGGAGCG    GT G GTTGG
                                ||||||||    || | |||||
                                TTCCTCGC    CG C CAACC
                                    CCCC  _ _
GAM283  C14orf4  3'  GGGAGGGAGGGTCGAGTTGG   7320      C   CT
                                GGGAG GAG  GTTGAGTTGG
                                ||||| |||  ||||||||||
                                CCCTC CTC  CAGCTCAACC
                                  C   C_
GAM283  FLJ20695 3'  GGGAGCGAGCTGTAGCTGTGAT 7321           TG    _
                                GGGAGCGAGCTGT  AGTTG GAT
                                ||||||||||||  ||||| |||
                                CCCTCGCTCGACA  TCGAC CTA
                                       __    A
GAM283  FLJ21438 5'  GGAGCGAGCTGGCTTTGG    7322          TTGAG
                                GGAGCGAGCTG    TTGG
                                ||||||||||    ||||
                                CCTCGCTCGAC    AACC
                                     CGA__
GAM283  KIAA0298 3'  AGGAGTGAGCTGGTTGTGG   7323      C    _   AGT
                                GGGAG GAGCTG TTG   TGG
                                ||||| |||||| |||   |||
                                TCCTC CTCGAC AAC   ACC
                                  A     C   ___
GAM283  KIAA0514 5'  AGGGAGTGGAGTTGAGTTGG   7324       CGAGCT
                                AGGGAG     GTTGAGTTGG
                                ||||||     ||||||||||
                                TCCCTC     CAACTCAACC
                                   ACCT__
GAM283  KIAA1030 3'  AGGGAGCGAGCTTCGG      7325          GTTGAG
                                AGGGAGCGAGCT     TTGG
                                ||||||||||||     ||||
                                TCCCTCGCTCGA     AGCC
                                         _______
GAM283  KIAA1987 3'  AGGGAGTGGCTGCCAATGG   7326       CGA    TG GT
                                AGGGAG   GCTGT  A  TGG
                                ||||||   |||||  |  |||
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                                TCCCTC  CGACG  T  ACC
                                   AC_    GT __
GAM283  LMOD1    5' GGGGTGAGCTGATCTGGAT   7327     AGC    TTGAG
                                GGG  GAGCTG    TTGGAT
                                |||  ||||||    ||||||
                                CCC  CTCGAC    GACCTA
                                  CA_    TA___
GAM283  TIP120B  3' GGGGGCCTTTGAGTTGG    7328     AGCGA  G
                                GGG    GCT TTGAGTTGG
                                |||    ||| |||||||||
                                CCC    CGG AACTCAACC
                                  C____  A
GAM283  LOC145662 3' AGGGAGCAGTTGTGG      7329        AGCT   AGT
                                AGGGAGCG   GTTG  TGG
                                ||||||||   ||||  |||
                                TCCCTCGT   CAAC  ACC
                                     _____  ___
GAM283  LOC158376 3' AGGGAGCAGGCCTCGAGGTTGG 7330        A  G   _
                                AGGGAGCG GCT TTGAG TTGG
                                |||||||| ||| ||||| ||||
                                TCCCTCGT CGG AGCTC AACC
                                     C  _   C
GAM283  LOC220776 5' GGGAGCCAGAAAGTTGG    7331       G  CTGTT
                                GGGAGC AG    GAGTTGG
                                |||||| ||    |||||||
                                CCCTCG TC    TTCAACC
                                   G  T____
GAM283  LOC253664 3' AAGGAGTGAGCTGAGTCACTGG 7332       C     TTGA
                                AGGGAG GAGCTG   GTTGG
                                |||||| ||||||   |||||
                                TTCCTC CTCGAC   TGACC
                                   A    TCAG
GAM284  MME     3' TATTTCTGTAACTTTTTTT   7335         AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA
                                     __
GAM284  MME     3' TATTTCTGTAACTTTTTTT   7335         AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA
                                     __
GAM284  MME     3' TATTTCTGTAACTTTTTTT   7335         AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA
                                     __
GAM284  MME     3' TATTTCTGTAACTTTTTTT   7335         AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA
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                                ATAAAGACAT  TGAAAAAAA
                                    __
GAM284  DKFZP434C212 3'  AATATTTCTGTGTACTTTTT  7336          AAA
                                AATATTTTTGT  ACTTTTT
                                ||||||||||  |||||||
                                TTATAAAGACA  TGAAAAA
                                     CA_
GAM284  FLJ11275  3'  AATATTTTTATAAATCCCATTT 7337           A  TT
           TA                    AATATTTTTGTAAA CT  TTTTA
                                ||||||||||||| ||  |||||
                                TTATAAAAATATTT GG  AAAAT
                                      A  GT
GAM284  GOLPH3   3'  AATATGGCAGTAAAACTTTTTT 7338      TTTT
           TA                    AATAT   GTAAAACTTTTTTTA
                                |||||   ||||||||||||||
                                TTATA   CATTTTGAAAAAAAT
                                   CCGT
GAM284  KIAA0563  5'  ATACTTTTGCTCCTTTTTTTA  7339         AAAA
                                ATATTTTTGT   CTTTTTTTA
                                ||||||||||   |||||||||
                                TATGAAAACG   GAAAAAAAT
                                     AG__
GAM284  TAF2     3'  TATTTTTGTCAAACTTTCT   7340         A
                                TATTTTTGT AAACTTTTT
                                ||||||||| |||||||||
                                ATAAAAACA TTTGAAAGA
                                     G
GAM284  LOC147071 5'  ATACTTTTGCTCCTTTTTTTA  7339         AAAA
                                ATATTTTTGT   CTTTTTTTA
                                ||||||||||   |||||||||
                                TATGAAAACG   GAAAAAAAT
                                     AG__
GAM284  LOC147639 5'  AATATTTTTGCAGCACTTTT  7341          AA
                                AATATTTTTGTA  ACTTTT
                                ||||||||||||  ||||||
                                TTATAAAAACGT  TGAAAA
                                      CG
GAM284  LOC201173 5'  ATACTTTTGCTCCTTTTTTTA  7339         AAAA
                                ATATTTTTGT   CTTTTTTTA
                                ||||||||||   |||||||||
                                TATGAAAACG   GAAAAAAAT
                                     AG__
GAM284  LOC201220 5'  ATACTTTTGCTCCTTTTTTTA  7339         AAAA
                                ATATTTTTGT   CTTTTTTTA
                                ||||||||||   |||||||||
                                TATGAAAACG   GAAAAAAAT
                                     AG__
GAM285  ACCN2    3'  GAGGAGAGAGGGGCAGCC   7344          AGAAATAA  _
                                GAGGAGAGAG       GCA CC
                                ||||||||||       ||| ||
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                                CTCCTCTCTC       CGT GG
                                     CC_______   C
GAM285  APBA1    3'  AGAGAGAGAGAAGCAGACAGTA 7345           A  AG ___
             CCT                    GGAGAGAGAGAA TA  C   ACCT
                                    |||||||||||| ||  |  ||||
                                    TCTCTCTCTCTT GT  G   TGGA
                                          C  CT TCA
GAM285  BARX2    3'  AGGGAGAGAGCTAAGCAC    7346      A      AAA
                                    AGG GAGAGAG   TAAGCAC
                                    ||| |||||||   |||||||
                                    TCC CTCTCTC   ATTCGTG
                                      _      G__
GAM285  CELSR2   3'  GGAGAAAGAGGAACAGGACCT  7347          A    A C
                                    GGAGAGAGAG AATA G ACCT
                                    |||||||||| |||| | ||||
                                    CCTCTTTCTC TTGT C TGGA
                                          C    _ C
GAM285  CLCN3    3'  GAGAGAGAGAGAGAAATAAAGG 7348     _           __
             C                      GAG GAGAGAGAGAAATAA  GC
                                    ||| ||||||||||||||  ||
                                    CTC CTCTCTCTCTTTATT  CG
                                      T            TC
GAM285  CREBL2   3'  GAGAAGAGAGAGTGGTAAG   7350           AAA
                                    GAGGAGAGAGAG   TAAG
                                    ||||||||||||   ||||
                                    CTCTTCTCTCTC   ATTC
                                          ACC
GAM285  CREBL2   3'  GAGAAGAGGGAAAGTACC    7349         A  GAAAT   C
                                    GAGGAGAG GA     AAG ACC
                                    |||||||| ||     ||| |||
                                    CTCTTCTC CT     TTC TGG
                                         C  _____   A
GAM285  ELL      3'  GAGGAGAGGGAGGCAC      7351         A   AAATAA
                                    GAGGAGAG GAG      GCAC
                                    |||||||| |||      ||||
                                    CTCCTCTC CTC      CGTG
                                         C  _______
GAM285  EPHB2    3'  GAGGTGGGAGAGAAATCACACA 7352       AGA        AA_
             C                      GAGG   GAGAGAAAT   GCAC
                                    ||||   |||||||||   ||||
                                    CTCC   CTCTCTTTA   TGTG
                                      ACC        GTG
GAM285  EXTL2    3'  GAGGAGAAGGAGGAATAAG   7353         A   A
                                    GAGGAGAG GAG AATAAG
                                    |||||||| ||| ||||||
                                    CTCCTCTT CTC TTATTC
                                         C   C
GAM285  FMR2     3'  GGAGAGAGAGAGAGACC     7354           AATA  C
                                    GGAGAGAGAGA    AG ACC
                                    ||||||||||    || |||
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                                CCTCTCTCTCT   TC TGG
                                      C___  _
GAM285  FOLH1   5'  GAGCGAGAGAGAGAGGCAACAT 7355     _       AATA   C
            CT                   GAG GAGAGAGAGA   AGCA CT
                                 ||| ||||||||||   |||| ||
                                 CTC CTCTCTCTCT   TTGT GA
                                   G        CCG_   A
GAM285  FOSB    3'  GAGGAGAGAGAGAGAGGC    7356           AATAA
                                 GAGGAGAGAGAGA    GC
                                 ||||||||||||    ||
                                 CTCCTCTCTCTCT    CG
                                       CTC__
GAM285  G1P3    5'  GAGGAGAGAAGAGAAGCA    7357         _   AATA
                                 GAGGAGAGA GAGA   AGCA
                                 |||||||| ||||   ||||
                                 CTCCTCTCT CTCT   TCGT
                                      T  _____
GAM285  G1P3    5'  GAGGAGAGAAGAGAAGCA    7357         _   AATA
                                 GAGGAGAGA GAGA   AGCA
                                 |||||||| ||||   ||||
                                 CTCCTCTCT CTCT   TCGT
                                      T  _____
GAM285  G1P3    5'  GAGGAGAGAAGAGAAGCA    7357         _   AATA
                                 GAGGAGAGA GAGA   AGCA
                                 |||||||| ||||   ||||
                                 CTCCTCTCT CTCT   TCGT
                                      T  _____
GAM285  GAS7    3'  GAGGAGAGCAGAGGAATGCCC  7358        _   A  AA  A
                                 GAGGAGAG AGAG AAT  GC CC
                                 |||||||| |||| |||  || ||
                                 CTCCTCTC TCTC TTA  CG GG
                                     G   C  __ _
GAM285  HDAC5   3'  GAGGAGAGTGAAATTAAGGCA  7359        A   AATAA
                                 GAGGAGAG GAGA    GCA
                                 |||||||| ||||    |||
                                 CTCCTCTC CTTT    CGT
                                     A   AATTC
GAM285  HMG20A  3'  GAGGAGAGAGGAGGTGGCAC   7360         A  AATAA
                                 GAGGAGAGAG GA    GCAC
                                 |||||||||| ||    ||||
                                 CTCCTCTCTC CT    CGTG
                                      _  CCAC_
GAM285  HOXC13  3'  GAGGAGAGAGGAGCCCT     7361         A  AATAA  A
                                 GAGGAGAGAG GA    GC CCT
                                 |||||||||| ||    || |||
                                 CTCCTCTCTC CT    CG GGA
                                      _  ______  _
GAM285  HS2ST1  3'  GAAGAGAGAAAGTAGTGAGCAT 7362          AAATA   C
            CT                   GAGGAGAGAGAG    AGCA CT
                                 ||||||||||||    |||| ||
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                                CTTCTCTCTTTC    TCGT GA
                                      ATCAC   A
GAM285  IMPDH1   3'  GAGGAGAAGGGAGGAATGGTTC 7363       ___  A  ATAAG
           ACCT                  GAGGAGA  GAG GAA    CACCT
                                |||||||  ||| |||    |||||
                                CTCCTCT  CTC CTT    GTGGA
                                   TCC  _  ACCAA
GAM285  INSR    3'  AAGGAGAGAGGGGGATGAGC  7364         AGAA  A
                                GAGGAGAGAG   AT AGC
                                ||||||||||   || |||
                                TTCCTCTCTC   TA TCG
                                      CCCC  C
GAM285  LRP1    3'  GAGGGGATGGAGAAATAATAC  7365      A  GA       GC
                                GAGG GA  GAGAAATAA  AC
                                |||| ||  |||||||||  ||
                                CTCC CT  CTCTTTATT  TG
                                  C  AC       A_
GAM285  MPL     3'  GAGGAGAGAGGAAGTAAA    7366         A  A
                                GAGGAGAGAG GAA TAAG
                                |||||||||| ||| ||||
                                CTCCTCTCTC CTT ATTT
                                      _  C
GAM285  MXI1    3'  GAGGAAGAGAGAGACTGC    7367       _      AATAA
                                GAGGA GAGAGAGA    GC
                                ||||| ||||||||    ||
                                CTCCT CTCTCTCT    CG
                                   T       GA___
GAM285  MXI1    3'  GAGGAAGAGAGAGACTGC    7367       _      AATAA
                                GAGGA GAGAGAGA    GC
                                ||||| ||||||||    ||
                                CTCCT CTCTCTCT    CG
                                   T       GA___
GAM285  MYD88   3'  GAGAGAGGGAGAGAACAGC   7368     _  A     ATA
                                GAG GAG GAGAGAA   AGC
                                ||| ||| |||||||   |||
                                CTC CTC CTCTCTT   TCG
                                  T  C      G__
GAM285  PEA15   3'  AAGGAGAGAGGGAAGGTTGC  7369         A  ATAA
                                GAGGAGAGAG GAA   GC
                                |||||||||| |||   ||
                                TTCCTCTCTC CTT   CG
                                      C  CCAA
GAM285  POU2AF1  3'  GAGGTGAGAGAGAAATGGC   7370      A        AA
                                GAGG GAGAGAGAAAT  GC
                                |||| ||||||||||  ||
                                CTCC CTCTCTCTTTA  CG
                                  A         C_
GAM285  PPP2R5D  3'  GGAGAGAGAGGAGGGGAGATAC 7371         AAATA_  C_
           CT                   GGAGAGAGAG     AG  ACCT
                                |||||||||     ||  ||||
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                                CCTCTCTCTC     TC  TGGA
                                     CTCCCC  TA
GAM285  PRPSAP2  3'  GGAGAGGGAGGAACAAGCA   7372        A   A
                                GGAGAG GAG AATAAGCA
                                |||||| ||| ||||||||
                                CCTCTC CTC TTGTTCGT
                                   C   C
GAM285  PRSS16   3'  GAGGAGAGACAGAAATAGAGC  7373          G     _
                                GAGGAGAGA AGAAATA AGC
                                ||||||||| ||||||| |||
                                CTCCTCTCT TCTTTAT TCG
                                     G      C
GAM285  PSEN1    3'  GAGGACAGAGGAGGCAC     7374       G   A  AATAA   C
                                GAGGA AGAG GA     GCA C
                                ||||| |||| ||     ||| |
                                CTCCT TCTC CT     CGT G
                                   G    _ C____   A
GAM285  PSEN1    3'  GAGGACAGAGGAGGCAC     7374       G   A  AATAA   C
                                GAGGA AGAG GA     GCA C
                                ||||| |||| ||     ||| |
                                CTCCT TCTC CT     CGT G
                                   G    _ C____   A
GAM285  PSMD9    3'  AGGGAGGAAGAATAAGCA    7375      A   AG    A
                                AGG GAG  AGAA TAAGCA
                                ||| |||  |||| ||||||
                                TCC CTC  TCTT ATTCGT
                                  _   CT    _
GAM285  PYGM     5'  GAGGGGAGGGAGAGGTGAGCTC 7376      A   A    AATA   A
          C                      GAGG GAG GAGA    AGC CC
                                |||| ||| ||||    ||| ||
                                CTCC CTC CTCT    TCG GG
                                  C   C    CCAC   A
GAM285  SIX3     3'  AAGGAGAGGGAGGAGGGCGGCC 7377         A   AAATAA  A_
          T                      GAGGAGAG GAG      GC  CCT
                                |||||||| |||      ||  |||
                                TTCCTCTC CTC      CG  GGA
                                     C   CTCC__  CC
GAM285  SLA2     3'  GGAGAGAGGGCTTAGCACCT   7378         AGAAATA
                                GGAGAGAG       AGCACCT
                                ||||||||       |||||||
                                CCTCTCTC       TCGTGGA
                                     CCGAA__
GAM285  SPS2     5'  GAGGAGAAGAGGGCCCT     7379         G   AAATAA  A
                                GAGGAGA AGAG      GC CCT
                                ||||||| ||||      || |||
                                CTCCTCT TCTC      CG GGA
                                     _    C_____  _
GAM285  SPTA1    5'  GAGAGAGAGAGAGAAATAA   7380      _
                                GAG GAGAGAGAGAAATAA
                                ||| ||||||||||||||
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                                CTC CTCTCTCTCTTTATT
                                  T
GAM285  SSX2     3'  GGAGAGAGGAGGGTAATGC   7381        A  AA_  _
                                GGAGAGAG GA   TAA GC
                                |||||||| ||   ||| ||
                                CCTCTCTC CT   ATT CG
                                     _ CCC   A
GAM285  TMC2     3'  GAGGAAAGAGGGGAGAGAACCT 7382          A_  AATA  C
                                GAGGAGAGAG  GA    AG ACCT
                                ||||||||||  ||    || ||||
                                CTCCTTTCTC  CT    TC TGGA
                                      CC  C___  T
GAM285  TWIST    5'  GAGGAGAAGAGCGGGGCGCCT  7383       G    AAATAA  A
                                GAGGAGA AGAG     GC CCT
                                ||||||| ||||     || |||
                                CTCCTCT TCTC     CG GGA
                                    _   GCCC__  C
GAM285  UGDH     3'  GGAGAGAAAGAAATGC      7384            AA
                                GGAGAGAGAGAAAT  GC
                                ||||||||||||||  ||
                                CCTCTCTTTCTTTA  CG
                                          __
GAM285  XPNPEP2  5'  GGAGAGAGGGAGGGCTCCT   7385        A  AATAA  A
                                GGAGAGAG GA    GC CCT
                                |||||||| ||    || |||
                                CCTCTCTC CT    CG GGA
                                     C  CC___  A
GAM285  AP1GBP1  3'  AGGAGAGAGAGAATGACCCACC 7386           ATAAG
           T                     AGGAGAGAGAGAA    CACCT
                                ||||||||||||     |||||
                                TCCTCTCTCTCTT    GTGGA
                                       ACTGG
GAM285  ARHGEF11 3'  GAGGGGAGGAAGAAAGTGCA  7387     A  AG    TAA
                                GAGG GAG  AGAAA   GCA
                                |||| |||  |||||   |||
                                CTCC CTC  TCTTT   CGT
                                  C   CT    CA_
GAM285  BET1     5'  GAGGAGAGAGAGAAAAGGC   7388           TAA
                                GAGGAGAGAGAGAAA   GC
                                ||||||||||||||   ||
                                CTCCTCTCTCTCTTT   CG
                                       TC_
GAM285  BLOV1    3'  GAGAGAGAGAGAGAGACA    7389     _       A
                                GAG GAGAGAGAGA ATA
                                ||| |||||||||| |||
                                CTC CTCTCTCTCT TGT
                                  T        C
GAM285  BTN2A2   3'  GAGGAGAGAAGAATTTGC    7390         G   ATAA
                                GAGGAGAGA AGAA   GC
                                |||||||| ||||   ||
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                                CTCCTCTCT TCTT    CG
                                      _    AAA_
GAM285  C5orf6    3'  GAGGAGAGAGAGAGATAGAGCC 7391            A  _  A
            CCT                    GAGGAGAGAGAGA ATA AGC CCT
                                   |||||||||||| ||| ||| |||
                                   CTCCTCTCTCTCT TAT TCG GGA
                                         C   C   G
GAM285  CLSTN2    3'  GAGAGAGAGAGAGAATGTGTGT 7392      _         ATAAGC_
            ACCT                    GAG GAGAGAGAGAA      ACCT
                                   ||| ||||||||||       ||||
                                   CTC CTCTCTCTCTT      TGGA
                                     T         ACACACA
GAM285  DKFZP564O0823 3'  GAGGAGAGGGAGGAAAAC    7393         A   AAAT
                                   GAGGAGAG GAG    AAGC
                                   |||||||| |||    ||||
                                   CTCCTCTC CTC    TTTG
                                        C   CT__
GAM285  FLJ10251  3'  GAGGGGAAGAGAGAAATGC    7394      A_        AA
                                   GAGG  GAGAGAGAAAT  GC
                                   ||||  ||||||||||  ||
                                   CTCC  TTCTCTCTTTA  CG
                                     CC         __
GAM285  FLJ11539  5'  GGAGAGAGGAGAAGCA      7395         A  AAT
                                   GGAGAGAG GA   AAGCA
                                   |||||||| ||   |||||
                                   CCTCTCTC CT   TTCGT
                                        _  C__
GAM285  FLJ11608  3'  GAGGAGAGAGAGGTCACC    7396           AAATAAG
                                   GAGGAGAGAGAG      CACC
                                   ||||||||||||      ||||
                                   CTCCTCTCTCTC      GTGG
                                          CA_____
GAM285  FLJ13110  3'  AAGGGGAGAGAGAAAAGGC    7397      A        TAA
                                   GAGG GAGAGAGAAA   GC
                                   |||| ||||||||||   ||
                                   TTCC CTCTCTCTTT   CG
                                     C         TC_
GAM285  FRSB      3'  GAGGAGAAAGGGACAC      7398          A AAATAA
                                   GAGGAGAGAG G      GCAC
                                   |||||||||| |      ||||
                                   CTCCTCTTTC C      TGTG
                                         C _______
GAM285  GEMIN7    3'  GAGGAGGGAGTGAAGTTGCACC 7399        A   A   ATAA
            C                       GAGGAG GAG GAA    GCACCT
                                   |||||| ||| |||    ||||||
                                   CTCCTC CTC CTT    CGTGGG
                                      C   A   CAA_
GAM285  HMGN4     5'  GAGTGAGGAATAAGCACC    7400      A   A
                                   GAG GAG AATAAGCACC
                                   ||| ||| ||||||||||
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                                CTC CTC TTATTCGTGG
                                  A   C
GAM285  HZFW1    3'  GAGGAGAGAGGGGAAATAGCAC 7401          A_     A
              C                   GAGGAGAGAG  GAAATA GCACC
                                  ||||||||||  |||||| |||||
                                  CTCCTCTCTC  CTTTAT CGTGG
                                        CC     _
GAM285  IGSF9    3'  GAGAGAGAGAGAGAGGCAGACC 7402      _        AATA  C
              T                   GAG GAGAGAGAGA    AG ACCT
                                  ||| ||||||||||    || ||||
                                  CTC CTCTCTCTCT    TC TGGA
                                    T         CCG_ _
GAM285  KIAA0258 3'  GAGGAAAGAGAGGACACC    7403            AAATAA
                                  GAGGAGAGAGAG     GCACC
                                  ||||||||||||     |||||
                                  CTCCTTTCTCTC     TGTGG
                                          C_____
GAM285  KIAA0552 5'  GGAGGGAGAGAAATACACCC   7404       A        AA
                                  GGAG GAGAGAAAT  GCACCT
                                  |||| |||||||||  ||||||
                                  CCTC CTCTCTTTA  TGTGGG
                                    C        __
GAM285  KIAA0662 3'  AGAGAGAGAGAACAGC      7405            ATA
                                  GGAGAGAGAGAA   AGC
                                  ||||||||||||   |||
                                  TCTCTCTCTCTT   TCG
                                          G__
GAM285  KIAA0843 3'  GAGGAGAAGAGAGGTTAAGC   7406         _    AAA
                                  GAGGAGA GAGAG   TAAGC
                                  ||||||| |||||   |||||
                                  CTCCTCT CTCTC   ATTCG
                                       T    CA_
GAM285  KIAA0940 3'  GGAGGATTCTAAAATAAGCA   7407       A  GA__
                                  GGAG GA    GAAATAAGCA
                                  |||| ||    ||||||||||
                                  CCTC CT    TTTTATTCGT
                                    _  AAGA
GAM285  KIAA1028 3'  GGTGAGGGTGCAATAAGCATCT 7408     A   AGAGA       C
                                  GG GAG     AATAAGCA CT
                                  || |||     |||||||| ||
                                  CC CTC     TTATTCGT GA
                                   A   CCACG       A
GAM285  KIAA1189 3'  GGAGAGAGAGATGGTAGCA    7409           AATA
                                  GGAGAGAGAGA    AGCA
                                  ||||||||||||   ||||
                                  CCTCTCTCTCT    TCGT
                                          ACCA
GAM285  KIAA1274 3'  GAGGACAGAGAGATCCACA    7410        G      AATAA
                                  GAGGA AGAGAGA     GCA
                                  ||||| |||||||     |||
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                                CTCCT TCTCTCT    TGT
                                  G      AGG__
GAM285  KIAA1384  5'  GGAGAGAGAGAGGGAGCA    7411          AATA
                                GGAGAGAGAGA   AGCA
                                ||||||||||   ||||
                                CCTCTCTCTCT   TCGT
                                     CCC_
GAM285  KIAA1437  5'  GAGGAGAGAGTACATGGCATCT 7412          AGAAATAA  C
                                GAGGAGAGAG      GCA CT
                                |||||||||       ||| ||
                                CTCCTCTCTC      CGT GA
                                     ATGTAC__   A
GAM285  KIAA1494  3'  GAGGAGAGGGGAAAATGCA   7413        AGA   TAA
                                GAGGAGAG  GAAA  GCA
                                ||||||||  ||||  |||
                                CTCCTCTC  CTTT  CGT
                                    CC_   TA_
GAM285  KIAA1602  3'  GGCAGAGAGAGAAGGCAACT  7414    _       ATAA  C
                                GG AGAGAGAGAA   GCA CT
                                || ||||||||||   ||| ||
                                CC TCTCTCTCTT   CGT GA
                                 G        C___   T
GAM285  KIAA1674  3'  AGGAGAGAGGCAAGTGCC    7415        AGAAA   CA
                                AGGAGAGAG    TAAG  CC
                                |||||||||    ||||  ||
                                TCCTCTCTC    GTTC  GG
                                     C_____   AC
GAM285  KLK14     3'  GAGTAGAGAGAGGAGGGCC   7416     G      AAATA  CA
                                GAG AGAGAGAG    AG  CC
                                ||| ||||||||    ||  ||
                                CTC TCTCTCTC    TC  GG
                                  A       C_____  CC
GAM285  NFAT5     3'  GAGGGAGGGAGGAATAAG    7417      A  A  A
                                GAGG GAG GAG AATAAG
                                |||| ||| ||| ||||||
                                CTCC CTC CTC TTATTC
                                  _  C  C
GAM285  NTT73     5'  AAGGAGAGACTCGTGAGCGCCT 7418         GAGAAATA  A
                                GAGGAGAGA       AGC CCT
                                |||||||||       ||| |||
                                TTCCTCTCT       TCG GGA
                                     GAGCAC__   C
GAM285  PELI1     5'  GAGAGAGAGAGAGAACACTGCA 7419     _       ATAA
                                GAG GAGAGAGAGAA   GCA
                                ||| ||||||||||   |||
                                CTC CTCTCTCTCTT   CGT
                                  T         GTGA
GAM285  PFTK1     3'  GAGAGAGAGAGAGACACCAAAC 7420     _       AA_
                                GAG GAGAGAGAGA   TAAGC
                                ||| ||||||||||   |||||
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                                CTC CTCTCTCTCT   GTTTG
                                  T         GTG
GAM285  SNFT     3'  AAGGGAGAGACAATAAGCATCT 7421       A     GA       C
                                GAGG GAGAGA  AATAAGCA CT
                                |||| ||||||  |||||||| ||
                                TTCC CTCTCT  TTATTCGT GA
                                  _     G_       A
GAM285  SSH2     3'  GAGGAGAGAGAGAGAGGC     7356             AATAA
                                GAGGAGAGAGAGA     GC
                                ||||||||||||     ||
                                CTCCTCTCTCTCT     CG
                                       CTC__
GAM285  STAF65(gamma) 3'  GAGGAGAGATGGAGTAAG     7422          GA  AA
                                GAGGAGAGA  GA  TAAG
                                |||||||||  ||  ||||
                                CTCCTCTCT  CT  ATTC
                                     AC  C_
GAM285  THG-1    3'  GAGGAGAGGAGGCAC       7423          A   AAATAA
                                GAGGAGAG GAG      GCAC
                                |||||||| |||      ||||
                                CTCCTCTC CTC      CGTG
                                   _  _______
GAM285  TNKS1BP1  3'  GAGGAGAGGAAGGGACAAAACC 7424          AG  AA    C
          T                      GAGGAGAG  AG  ATAAG ACCT
                                 |||||||  ||  ||||| ||||
                                 CTCCTCTC  TC  TGTTT TGGA
                                      CT  CC    _
GAM285  LOC129285 3'  GAGAGAGAGAGAGAAATA     7425      _
                                GAG GAGAGAGAGAAATA
                                ||| ||||||||||||||
                                CTC CTCTCTCTCTTTAT
                                  T
GAM285  LOC130813 5'  GAGAGAGAGAGAGACCTGTGC  7426      _        AATAA
                                GAG GAGAGAGAGA     GC
                                ||| ||||||||||     ||
                                CTC CTCTCTCTCT     CG
                                  T         GGACA
GAM285  LOC130813 5'  GAGAGAGAGAGAGAGAGACCT  7427      _        AATA  C
                                GAG GAGAGAGAGA    AG ACCT
                                ||| ||||||||||    || ||||
                                CTC CTCTCTCTCT    TC TGGA
                                  T         C___  _
GAM285  LOC138639 5'  GAGGAGAGGGAGGTGCACC    7428          A   AAATAA
                                GAGGAGAG GAG      GCACC
                                |||||||| |||      |||||
                                CTCCTCTC CTC      CGTGG
                                     C   CA____
GAM285  LOC143879 3'  GAGGAGAGAGAGAGAGAGAGC  7429             AATA_
                                GAGGAGAGAGAGA     AGC
                                ||||||||||||     |||
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                                CTCCTCTCTCTCT     TCG
                                      CTCTC
GAM285   LOC144266 3'  GAGAGAGAGAGAGATACA     7430      _        A
                                GAG GAGAGAGAGA ATA
                                ||| |||||||||| |||
                                CTC CTCTCTCTCT TGT
                                  T         A
GAM285   LOC146667 5'  GAGGAGAGAAGAGAGGCAGAGC 7431          _    AA  _
                                GAGGAGAGA GAGA  TA AGC
                                ||||||||| ||||  || |||
                                CTCCTCTCT CTCT  GT TCG
                                      T    CC  C
GAM285   LOC147699 3'  GAGAAGAAGAAATAAGCA     7432        AG
                                GAGAG  AGAAATAAGCA
                                |||||  ||||||||||
                                CTCTT  TCTTTATTCGT
                                   CT
GAM285   LOC148894 3'  GGTGAGAGAGACCAGAGCACCT 7433     A       AATA
                                GG GAGAGAGA    AGCACCT
                                || ||||||||    |||||||
                                CC CTCTCTCT    TCGTGGA
                                 A       GGTC
GAM285   LOC151009 5'  GGGAGAGAGCCAAGCACC     7434     A      AAA
                                GG GAGAGAG   TAAGCACC
                                || |||||||   ||||||||
                                CC CTCTCTC   GTTCGTGG
                                 _      G__
GAM285   LOC154761 3'  GAGGGAGAGAGAATCAACC    7435      A       A  AGC
                                GAGG GAGAGAGAA TA   ACC
                                |||| ||||||||| ||   |||
                                CTCC CTCTCTCTT GT   TGG
                                  _       A  ___
GAM285   LOC157627 3'  GAGGAAAGGGAGGCTCC      7436         A   AAATAA  A
                                GAGGAGAG GAG     GC CC
                                |||||||| |||     || ||
                                CTCCTTTC CTC     CG GG
                                     C  _______  A
GAM285   LOC158257 3'  GAGGTGAGGGAGAAGTTCCCT  7437      A   A    ATAAGCA
                                GAGG GAG GAGAA      CCT
                                |||| ||| |||||      |||
                                CTCC CTC CTCTT      GGA
                                  A  C    CAAG___
GAM285   LOC158722 5'  AGAAGAGGGAAGTGAGCAC    7438        A   AAATA
                                AGGAGAG GAG     AGCAC
                                ||||||| |||     |||||
                                TCTTCTC CTT     TCGTG
                                     C   CAC__
GAM285   LOC160414 3'  GAGGAGAAAGGGTGGGAGCATC 7439          AGAAATA    C
            T                    GAGGAGAGAG      AGCA CT
                                ||||||||||      |||| ||
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                                CTCCTCTTTC      TCGT GA
                                     CCACCC_    A
GAM285  LOC166968 3'  GAGGAAGAGAGAAGCAGAGC   7440       G       A  _
                                GAGGA AGAGAGAA TA AGC
                                ||||| |||||||| || |||
                                CTCCT TCTCTCTT GT TCG
                                   _       C  C
GAM285  LOC196264 3'  GAGAGAGAGAATAGCACC     7441            ATA
                                GAGAGAGAGAA   AGCACC
                                ||||||||||   ||||||
                                CTCTCTCTCTT   TCGTGG
                                      A__
GAM285  LOC199745 5'  GGGAGAGAGCTGAGAGCGCCT  7442     A      AAATA   A
                                GG GAGAGAG     AGC CCT
                                || |||||||     ||| |||
                                CC CTCTCTC     TCG GGA
                                 _      GACTC   C
GAM285  LOC200597 5'  GAGGAGAGGAGACAGGGGTACC 7443          A    AATAAGC
          T                      GAGGAGAG GAGA       ACCT
                                |||||||| ||||       ||||
                                CTCCTCTC CTCT       TGGA
                                     _   GTCCCCA
GAM285  LOC203508 3'  AAGGGAGAGAGAGATAGACATC 7444       A       A   AG  _
          CT                      GAGG GAGAGAGA ATA  CA CCT
                                |||| |||||||| |||  || |||
                                TTCC CTCTCTCT TAT  GT GGA
                                   _       C   CT  A
GAM285  LOC257122 5'  GAGGAGAGACAGCAGCACC    7445          G  AAATA
                                GAGGAGAGA AG     AGCACC
                                |||||||||  ||     ||||||
                                CTCCTCTCT TC     TCGTGG
                                      G  G____
GAM285  LOC257453 3'  GGAGAGAGGAGGGTAATGC    7381          A  AA_  _
                                GGAGAGAG GA   TAA GC
                                |||||||| ||   ||| ||
                                CCTCTCTC CT   ATT CG
                                     _ CCC   A
GAM285  LOC51200  3'  GAGGAGGGAGGGAGAGACCT   7446        A   A  AATA  C
                                GAGGAG GAG GA    AG ACCT
                                |||||| ||| ||    || ||||
                                CTCCTC CTC CT    TC TGGA
                                    C   C  C___  _
GAM285  LOC51336  5'  GAGGAGAGAGGGATATAAGGAC 7447          A  A    C
                                GAGGAGAGAG GA ATAAG AC
                                |||||||||| || ||||| ||
                                CTCCTCTCTC CT TATTC TG
                                      C  A    C
GAM285  LOC55580  5'  GAGGGCAGAGAAAAGGCATCT  7448       AG       ATAA   C
                                GAGG  AGAGAGAA    GCA CT
                                ||||  ||||||||    ||| ||
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                                CTCC  TCTCTTTT   CGT GA
                                  CG      C___   A
GAM285  LOC81558  3'  GAGGAGAGGGAAGGAAAT   7449        A __
                                GAGGAGAG GA  GAAAT
                                ||||||||  ||  |||||
                                CTCCTCTC CT  CTTTA
                                    C  TC
GAM285  LOC90643  3'  GAGGAGAGAGAAAAGC     7450           AATA
                                GAGGAGAGAGAGA   AGC
                                ||||||||||||||   |||
                                CTCCTCTCTCTTT   TCG
                                          ____
GAM286  ATP2B3    3'  TGCATGTGTGCGTGTGACT   7453      TATGG  AAA
                                TGCAT    GT   GTGTGACT
                                |||||    ||   ||||||||
                                ACGTA    CA   CACACTGA
                                   CA___  CG_
GAM286  NR3C2     3'  ATTACCTTCAAAGTGTGGCT  7454      GGG       A
                                ATTAT   TAAAGTGTG CT
                                |||||   |||||||||  ||
                                TAATG   GTTTCACAC GA
                                   GAA       C
GAM286  PAX5      3'  TGCATCATGGGTGGAGCAGT  7455          AA  _
                                TGCATTATGGGT  AGT GT
                                ||||||||||||  |||  ||
                                ACGTAGTACCCA  TCG CA
                                      CC   T
GAM286  PML       3'  TGCAGTATGGGTACACAGACT 7456      T      AAGTGT
                                TGCA TATGGGTA     GACT
                                ||||  ||||||||     ||||
                                ACGT ATACCCAT     CTGA
                                  C       GTGT__
GAM286  RFX5      3'  TGTGTTATGGGTCATAGGTACT 7457    CA       AA_  T   A
            C                    TG  TTATGGGT   AG GTG CTC
                                ||  ||||||||   || ||| |||
                                AC  AATACCCA   TC CAT GAG
                                 AC       GTA  _   _
GAM286  TACSTD2   5'  TCATTGCAAAGTGTGGCT   7458      GG        A
                                TTAT  GTAAAGTGTG CT
                                ||||  ||||||||||  ||
                                AGTA  CGTTTCACAC GA
                                  A_        C
GAM286  C21orf91  3'  TTATGGGTAGGTGCGACT   7459         AA
                                TTATGGGTA  GTGTGACT
                                |||||||||  ||||||||
                                AATACCCAT  CACGCTGA
                                     C_
GAM286  PPP1R10   3'  TGCATGTAGTGTGAC      7460       TATGG  AA
                                TGCAT    GT  AGTGTGAC
                                |||||    ||  ||||||||
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                                ACGTA    CA  TCACACTG
                                  _____  __
GAM286  RPF-1    3'  TGATTATGGGTGGGCAT     7461     C       AAA
                                TG ATTATGGGT   GTGT
                                || |||||||||   ||||
                                AC TAATACCCA   CGTA
                                 _       CC_
GAM286  SNAP29   3'  TGCATTATGGGATGGGA     7462          TAAA   T
                                TGCATTATGGG    GTG GA
                                ||||||||||    ||| ||
                                ACGTAATACCC    TAC CT
                                      ____  C
GAM286  LOC112448 5'  TGTATTGTGAGGTATGACT   7463     C   A    TAAA
                                TG ATT TGGG    GTGTGACT
                                || ||| ||||    ||||||||
                                AC TAA ACTC    CATACTGA
                                 A   C   ____
GAM286  LOC144571 3'  TGCTTATGGGTAATGA      7464      A       AAGT
                                TGC TTATGGGTA    GTGA
                                ||| |||||||||    ||||
                                ACG AATACCCAT    TACT
                                 _       ____
GAM286  LOC144715 3'  ATTGTGGGTAGCTATGACTC   7465      A     AAG
                                ATT TGGGTA   TGTGACTC
                                ||| ||||||   ||||||||
                                TAA ACCCAT   ATACTGAG
                                  C     CG_
GAM287  CAPN2    3'  TGGTGAAGTTCATAAAGTTTT  7468     A     _    AAA
                                TG TGGAGT CGTAA   AGTTTT
                                || |||||| |||||   ||||||
                                AC ACTTCA GTATT   TCAAAA
                                 C     A    ___
GAM287  DAAM2    3'  TGATGGAGTTTTAGAAAAATTT 7469          CG  A
           T                     TGATGGAGT  TA AAAAGTTTT
                                |||||||||  || |||||||||
                                ACTACCTCA  AT TTTTTAAAA
                                      AA  C
GAM287  SELE     3'  TAATGGAAGTGTAGGAGAGTTT 7470        _  C   AAAA
           T                     TGATGGA GT GTA    AGTTTT
                                ||||||| || |||    ||||||
                                ATTACCT CA CAT    TCAAAA
                                    T  _   CCTC
GAM287  KIAA0475  3'  TGATGGAATGCAAGGTTTT   7471          C    AAAA
                                TGATGGAGT GTAA    GTTTT
                                ||||||||| ||||    |||||
                                ACTACCTTA CGTT    CAAAA
                                      _   C___
GAM287  LOC222671 5'  TGGCGGAGTCGTAGAAGC    7472     A        AAA
                                TG TGGAGTCGTA   AAGT
                                || ||||||||||   ||||
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                                AC GCCTCAGCAT   TTCG
                                 C         C__
GAM287  LOC254901 5'  TGGTGGAGTCAGTGAAGAAATT 7473     A      _ A  A
                                TG TGGAGTC GT AA AAGTT
                                || ||||||| || || |||||
                                AC ACCTCAG CA TT TTTAA
                                 C      T  C  C
GAM287  LOC257615 5'  TGGCGGAGTCGTAGAAGC    7472     A        AAA
                                TG TGGAGTCGTA   AAGT
                                || ||||||||||   ||||
                                AC GCCTCAGCAT   TTCG
                                 C         C__
GAM288  DGCR2     3'  CCCCAGGGACCGGTGTT     7476        AACTCTA
                                TCCCAG      GACCGGTGTT
                                ||||||      ||||||||||
                                GGGGTC      CTGGCCACAA
                                   C_______
GAM288  APOARGC   3'  TCCCAGAATCTGGATTCC     7477         C   A __
                                TCCCAGAA TCT GA  CC
                                |||||||| ||| ||  ||
                                AGGGTCTT AGA CT  GG
                                     _  C  AA
GAM288  FLJ10486  3'  TCCCAGAACTTCAGACCAGGTT 7478           C       T
                                TCCCAGAACT TAGACCGG GTT
                                |||||||||| |||||||| |||
                                AGGGTCTTGA GTCTGGTC CAA
                                      A       _
GAM288  FLJ14981  5'  CCCGGAGCTCTAGACTCCGGC  7479      A  A      __
                                CCC GA CTCTAGA  CCGGT
                                ||| || |||||||  |||||
                                GGG CT GAGATCT  GGCCG
                                  C  C       GA
GAM288  KIAA0426  5'  AGAACTACCGGTGTT       7480        CTAG
                                AGAACT    ACCGGTGTT
                                ||||||    |||||||||
                                TCTTGA    TGGCCACAA
                                     ____
GAM288  KIAA1284  3'  CAGCAATTCTGACAGTGTTT   7481      _ C   A   C
                                CAG AA TCT GAC GGTGTTT
                                ||| || ||| ||| |||||||
                                GTC TT AGA CTG TCACAAA
                                  G  A  _  _
GAM288  MGC4266   5'  TCCCAGCGCTCTGGATCCGGC  7482        AA   A _
                                TCCCAG  CTCT GA CCGGT
                                ||||||  |||| || |||||
                                AGGGTC  GAGA CT GGCCG
                                   GC    C  A
GAM288  SLC38A4   3'  AGATGCTCTAGACTGGTGTTT  7483      A_       C
                                AGA  CTCTAGAC GGTGTTT
                                |||  |||||||| |||||||
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                                TCT  GAGATCTG CCACAAA
                                  AC       A
GAM288  LOC146184 5'  TCTCAGAACTCTAATGCT    7484     C        GACCG
                                TC CAGAACTCTA    GTGTT
                                || ||||||||||    |||||
                                AG GTCTTGAGAT    TACGA
                                 A       _____
GAM288  LOC147463 5'  TCCCGGGGCTCTCGGCGTT   7485      AGAA   AGAC
                                TCCC   CTCT   CGGTGTT
                                ||||   ||||   |||||||
                                AGGG   GAGA   GCCGCAA
                                  CCCC   ____
GAM288  LOC257302 5'  GAACTCTAGGGCTGTTT     7486          ACC  _
                                GAACTCTAG   GG TGTTT
                                |||||||||   || |||||
                                CTTGAGATC   CC ACAAA
                                     ___  G
GAM289  CAPN2    3'  TGGTGAAGTTCATAAAGTTTT  7468     A    _    AAA
                                TG TGGAGT CGTAA   AGTTTT
                                || |||||| |||||   ||||||
                                AC ACTTCA GTATT   TCAAAA
                                 C     A    ___
GAM289  DAAM2    3'  TGATGGAGTTTTAGAAAAATTT 7469          CG  A
           T                     TGATGGAGT  TA AAAAGTTTT
                                 |||||||||  || |||||||||
                                 ACTACCTCA  AT TTTTTAAAA
                                       AA  C
GAM289  SELE     3'  TAATGGAAGTGTAGGAGAGTTT 7470        _  C   AAAA
           T                     TGATGGA GT GTA    AGTTTT
                                 |||||||  || |||    ||||||
                                 ATTACCT CA CAT    TCAAAA
                                     T  _   CCTC
GAM289  KIAA0475  3'  TGATGGAATGCAAGGTTTT   7471          C    AAAA
                                TGATGGAGT GTAA    GTTTT
                                |||||||||  ||||    |||||
                                ACTACCTTA CGTT    CAAAA
                                      _    C___
GAM289  LOC222671 5'  TGGCGGAGTCGTAGAAGC    7472     A        AAA
                                TG TGGAGTCGTA   AAGT
                                || ||||||||||   ||||
                                AC GCCTCAGCAT   TTCG
                                 C         C__
GAM289  LOC254901 5'  TGGTGGAGTCAGTGAAGAAATT 7473     A      _  A  A
                                TG TGGAGTC GT AA AAGTT
                                || |||||||  || ||  |||||
                                AC ACCTCAG CA TT TTTAA
                                 C       T  C  C
GAM289  LOC257615 5'  TGGCGGAGTCGTAGAAGC    7472     A        AAA
                                TG TGGAGTCGTA   AAGT
                                || ||||||||||   ||||
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                                AC GCCTCAGCAT   TTCG
                                 C        C__
GAM290  FGF2     3'  AAAAAGCAGCCACAAAAATAT  7490        T_
                                AAAAAGT  TTACAAAAATAT
                                |||||||  ||||||||||||
                                TTTTTTCG  GGTGTTTTTATA
                                    TC
GAM290  MPHOSPH1  3'  AAAAAAGCCTTATAAAAATAT  7491            C
                                AAAAAAGTTTTA AAAAATAT
                                |||||||||||| ||||||||
                                TTTTTTTCGGAAT TTTTTATA
                                       A
GAM290  FLJ11274  3'  TAAAAAAAGCTACTACAAAGAT 7492           _      A
           AT                    TAAAAAAAGTT TTACAAA ATAT
                                |||||||||||| ||||||| ||||
                                ATTTTTTTTCGA GATGTTT TATA
                                       T      C
GAM290  FLJ31101  3'  ACAAATACATTTTACAAAAATA 7493       AAAA
           T                     ATAAA    GTTTTACAAAAATAT
                                |||||    ||||||||||||||||
                                TGTTT    TAAAATGTTTTTATA
                                   ATG_
GAM290  GPT2     3'  AAAAAAGCAATTGTTACAAAAA 7494         T____
           TAT                     AAAAAAGT     TTACAAAAATAT
                                |||||||||    ||||||||||||
                                TTTTTTTCG    AATGTTTTTATA
                                     TTAAC
GAM290  RMP      3'  GAAAAAAAAGTTTTACAAAA   7495    T
                                A AAAAAAAGTTTTACAAAA
                                | ||||||||||||||||||
                                C TTTTTTTCAAAATGTTTT
                                 T
GAM290  RMP      3'  GAAAAAAAAGTTTTACAAAA   7495    T
                                A AAAAAAAGTTTTACAAAA
                                | ||||||||||||||||||
                                C TTTTTTTCAAAATGTTTT
                                 T
GAM290  SOX6     3'  AAAAAAAGTAAGACAAAAATAT 7496          TTT
                                AAAAAAAGT   ACAAAAATAT
                                |||||||||   ||||||||||
                                TTTTTTTCA   TGTTTTTATA
                                     TTC
GAM290  LOC136288 3'  ACAAAAAAAGCCTCAGAAATAT 7497              CAA
                                ATAAAAAAAGTTTTA   AAATAT
                                ||||||||||||||   ||||||
                                TGTTTTTTTCGGAGT   TTTATA
                                       C__
GAM291  ABCA3    5'  AAGCCTCCTTGACTCAC     7500          CATTCG
                                AAGCCTCC     GATTCAC
                                ||||||||     |||||||
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                                TTCGGAGG     CTGAGTG
                                    AA____
GAM291  AKAP2   3'  AGTCCTCCCATTTCAC      7501     _       CGGAT
                                AG CCTCCCATT     TCAC
                                || |||||||||     ||||
                                TC GGAGGGTAA     AGTG
                                 A       _____
GAM291  ANKH    3'  AGCCTTACATTCAAATGCA   7502       CC        T
                                AGCCT  CATTCGGAT CA
                                |||||  ||||||||| ||
                                TCGGA  GTAAGTTTA GT
                                   AT        C
GAM291  ATRN    3'  CTCTCCAAATTCACA       7503      CCA
                                CTC   TTCGGATTCACA
                                |||   ||||||||||||
                                GAG   AGGTTTAAGTGT
                                  ___
GAM291  CABC1   5'  AGCCTCCCGTTGGCCC      7504         A  C  A
                                AGCCTCCC TT GG TTC
                                |||||||| || || |||
                                TCGGAGGG AA CC GGG
                                    C  _  _
GAM291  CDH8    5'  AAGCCTCCAGGTTCAC      7505         CATTC  A
                                AAGCCTCC     GG TTCAC
                                ||||||||     || |||||
                                TTCGGAGG     CC AAGTG
                                    T_____  _
GAM291  CDKN2A  3'  AGCTTCCCTAGTTCACA     7506     C    ATTC  A
                                AGC TCCC    GG TTCACA
                                ||| ||||    || ||||||
                                TCG AGGG    TC AAGTGT
                                  A    A___  _
GAM291  CDKN2A  3'  AGCTTCCCTAGTTCACA     7506     C    ATTC  A
                                AGC TCCC    GG TTCACA
                                ||| ||||    || ||||||
                                TCG AGGG    TC AAGTGT
                                  A    A___  _
GAM291  CDKN2A  3'  AGCTTCCCTAGTTCACA     7506     C    ATTC  A
                                AGC TCCC    GG TTCACA
                                ||| ||||    || ||||||
                                TCG AGGG    TC AAGTGT
                                  A    A___  _
GAM291  CDKN2A  3'  AGCTTCCCTAGTTCACA     7506     C    ATTC  A
                                AGC TCCC    GG TTCACA
                                ||| ||||    || ||||||
                                TCG AGGG    TC AAGTGT
                                  A    A___  _
GAM291  CLCA2   5'  AAGCCTCCAGTTCACTCACA  7507         CA   GG
                                AAGCCTCC  TTC  ATTCACA
                                ||||||||  |||  |||||||
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                                TTCGGAGG  AAG  TGAGTGT
                                    TC  __
GAM291  EPS8    5'  AAGCCCCCCAATCTGATTC   7508        T  G
                                AAGCCTCCCA TC GATTC
                                |||||||||| || |||||
                                TTCGGGGGGT AG CTAAG
                                     T  A
GAM291  ETS2    3'  GCTTCCCACTCAGTCCAC    7509    C       A
                                GC TCCCATTCGG TTCAC
                                || |||||||||| |||||
                                CG AGGGTGAGTC AGGTG
                                 A       _
GAM291  FGFR2   5'  AAGCCTCCCGGGCTTCAC    7510        ATTC  A
                                AAGCCTCCC   GG TTCAC
                                |||||||||   || |||||
                                TTCGGAGGG   CC AAGTG
                                     C___  G
GAM291  FGFR2   5'  AAGCCTCCCGGGCTTCAC    7510        ATTC  A
                                AAGCCTCCC   GG TTCAC
                                |||||||||   || |||||
                                TTCGGAGGG   CC AAGTG
                                     C___  G
GAM291  FGFR2   5'  AAGCCTCCCGGGCTTCAC    7510        ATTC  A
                                AAGCCTCCC   GG TTCAC
                                |||||||||   || |||||
                                TTCGGAGGG   CC AAGTG
                                     C___  G
GAM291  FGFR2   5'  AAGCCTCCCGGGCTTCAC    7510        ATTC  A
                                AAGCCTCCC   GG TTCAC
                                |||||||||   || |||||
                                TTCGGAGGG   CC AAGTG
                                     C___  G
GAM291  FOXD2   5'  AACTCTCCCATTCCAC      7511    _       GGATT
                                AGC CTCCCATTC    CAC
                                ||| |||||||||    |||
                                TTG GAGGGTAAG    GTG
                                  A       _____
GAM291  GNPI    3'  AAGCCTCCTCTTTGGCCCCA  7512        CA  C  A
                                AAGCCTCC  TT GG TTCA
                                ||||||||  || || ||||
                                TTCGGAGG  AA CC GGGT
                                     AG  A  G
GAM291  HCK     3'  AAGTTTCCCTTCCAAATCACA  7513      CC   A  G  T
                                AAG  TCCC TTC GA TCACA
                                |||  |||| ||| || |||||
                                TTC  AGGG AAG TT AGTGT
                                  AA   _  G  T
GAM291  HK2     5'  GGACCTCTCCGATTCACA    7514    A    CCAT  G
                                A GCCTC    TC GATTCACA
                                | |||||    || ||||||||
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                                C TGGAG    AG CTAAGTGT
                                 C    _____ G
GAM291  HNRPH1   3'  AACCCTCCCATTCCGTTCAC  7515     G        GGA
                                AA CCTCCCATTC   TTCAC
                                || ||||||||||   |||||
                                TT GGAGGGTAAG   AAGTG
                                  G         GC_
GAM291  HSF2BP   5'  AAACCTCCCAGAATT       7516          TTC
                                AAGCCTCCCA   GGATT
                                ||||||||||   |||||
                                TTTGGAGGGT   CTTAA
                                           ___
GAM291  LMO4     3'  AGTCTCCCATTAGCCCAGGTTC 7517     C      _____    A
           A                     AG CTCCCAT    TCGG TTCA
                                || |||||||    |||| ||||
                                TC GAGGGTA    GGTC AAGT
                                 A       ATCG    C
GAM291  MBNL     5'  CTCCCACTAGAAATTCACA   7518         C_
                                CTCCCATT  GGATTCACA
                                ||||||||  |||||||||
                                GAGGGTGA  TTTAAGTGT
                                     TC
GAM291  MYC      5'  AAGCCCCCTATTCGCTCC    7519         C    GA
                                AAGCCTCC ATTCG  TTC
                                ||||||||  |||||  |||
                                TTCGGGGG TAAGC  AGG
                                     A    G_
GAM291  NCSTN    5'  AAGCCCCCGTTCGGCTCC    7520       T  A    A
                                AAGCC CCC TTCGG TTC
                                |||||  |||  |||||  |||
                                TTCGG GGG AAGCC AGG
                                   _  C    G
GAM291  PLAUR    3'  AGCTCTCCCATTGCCCAC    7521      _       CGGA
                                AGC CTCCCATT    TTCAC
                                |||  ||||||||    |||||
                                TCG GAGGGTAA    GGGTG
                                  A       C___
GAM291  PRKAR1A  3'  AAACCTCTTCCCCAGATT    7522         CCA
                                AAGCCTC   TTCGGATT
                                |||||||   ||||||||
                                TTTGGAG   GGGTCTAA
                                    AAG
GAM291  PSMB2    3'  AGCCTCCCAAGTAGTTGGGTTT 7523          TTC____  A  C
           ACA                    AGCCTCCCA      GG TT ACA
                                |||||||||      || || |||
                                TCGGAGGGT      CC AA TGT
                                     TCATCAA  C  A
GAM291  RBL2     3'  AAGCCTCCTATGCTCAC     7524         C  TCGGA
                                AAGCCTCC AT    TTCAC
                                ||||||||  ||    |||||
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                                TTCGGAGG TA    GAGTG
                                   A  C____
GAM291  SFRP1   3'  AGCCTCCCTTTTGGTTC    7525        A  C  A
                                AGCCTCCC TT GG TTC
                                |||||||| || || |||
                                TCGGAGGG AA CC AAG
                                   A  A  _
GAM291  SIAH2   3'  GCCTCCCATTCCTAACACA   7526          GGATT
                                GCCTCCCATTC    CACA
                                ||||||||||     ||||
                                CGGAGGGTAAG    GTGT
                                      GATT_
GAM291  SRD5A2  5'  AAGCCACCCAGGTTCA     7527       T   TTC  A
                                AAGCC CCCA   GG TTCA
                                ||||| ||||   || ||||
                                TTCGG GGGT   CC AAGT
                                  T   ___  _
GAM291  TJP1    5'  GCCTCCCGCAGCTTTCGCA   7528       ATT  A_  A
                                GCCTCCC   CGG  TTC CA
                                |||||||   |||  ||| ||
                                CGGAGGG   GTC  AAG GT
                                   C__   GA   C
GAM291  TLL1    3'  AAGACTCCCATTTCAC     7529     C      CGGAT
                                AAG CTCCCATT    TCAC
                                ||| ||||||||    ||||
                                TTC GAGGGTAA    AGTG
                                  T     _____
GAM291  WHSC1   3'  AAGCTGCCCATTCGGACACA  7530     CT       TT
                                AAGC  CCCATTCGGA  CACA
                                ||||  ||||||||||  ||||
                                TTCG  GGGTAAGCCT  GTGT
                                  AC        __
GAM291  WHSC1   3'  AAGCTGCCCATTCGGACACA  7530     CT       TT
                                AAGC  CCCATTCGGA  CACA
                                ||||  ||||||||||  ||||
                                TTCG  GGGTAAGCCT  GTGT
                                  AC        __
GAM291  WHSC1   3'  AAGCTGCCCATTCGGACACA  7530     CT       TT
                                AAGC  CCCATTCGGA  CACA
                                ||||  ||||||||||  ||||
                                TTCG  GGGTAAGCCT  GTGT
                                  AC        __
GAM291  BCAA    3'  AAGCCTCCATTTGCCAC     7531        C   CGGAT
                                AAGCCTCC ATT    TCAC
                                |||||||| |||    ||||
                                TTCGGAGG TAA    GGTG
                                   _  AC___
GAM291  CABP5   3'  GCTTCCTATTTCCATCCACA  7532    C   C   CGG
                                GC TCC ATT   ATTCACA
                                || ||| |||   |||||||
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                                CG AGG TAA   TAGGTGT
                                 A  A  AGG
GAM291  CLDN6    3' AGCCCCCATTCCCCTCCAC   7533      T     GGA
                                AGCC CCCATTC   TTCAC
                                |||| |||||||   |||||
                                TCGG GGGTAAG   AGGTG
                                  _     GGG
GAM291  CYorf15B 3' AGCTTACATCCAGATTTACA  7534     C CC       C
                                AGC T  CATTCGGATT ACA
                                ||| |  |||||||||| |||
                                TCG A  GTAGGTCTAA TGT
                                  _ AT        A
GAM291  ESM1     3' GCCTTCCACACACATTCACA  7535     C   T  G
                                GCCT CCAT CG ATTCACA
                                |||| |||| || |||||||
                                CGGA GGTG GT TAAGTGT
                                  A   T  G
GAM291  FLJ10420 3' AAGCCTCCCGCTGAACT    7536        A  C
                                AAGCCTCCC TT GGATT
                                ||||||||| || |||||
                                TTCGGAGGG GA CTTGA
                                     C  _
GAM291  FLJ12476 3' AAGCCTTTATTCAAACC    7537       CCC
                                AAGCCT   ATTCGGATT
                                ||||||   |||||||||
                                TTCGGA   TAAGTTTGG
                                   AA_
GAM291  FLJ12581 3' AAGCCTCCCAATCCCAAAC  7538         __
                                AAGCCTCCCA  TTCGGAT
                                ||||||||||  |||||||
                                TTCGGAGGGT  GGGTTTG
                                      TA
GAM291  FLJ20337 3' AGCCTCCCGTTCTACCCCTCAC 7539        A  GGA__
           A                     AGCCTCCC TTC    TTCACA
                                |||||||| |||    ||||||
                                TCGGAGGG AAG    GAGTGT
                                     C  ATGGG
GAM291  FLJ21369 3' AGCCTCCCAAAGTGCTGGGTTT 7540         TTC____  A  C
           ACA                    AGCCTCCCA     GG TT ACA
                                |||||||||      || || |||
                                TCGGAGGGT     CC AA TGT
                                     TTCACGA  C  A
GAM291  FLJ22059 5' GCCTTTCCAAATTCAC     7541      CCCA
                                GCCT   TTCGGATTCAC
                                ||||   ||||||||||
                                CGGA   AGGTTTAAGTG
                                  A___
GAM291  GPS2     3' AGACTCCTCTGGGATTCACA  7542    C   CATTC
                                AG CTCC    GGATTCACA
                                || ||||    |||||||||
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                                TC GAGG    CCTAAGTGT
                                 T   AGAC_
GAM291  JAM1     3' AGCTCCCATTTTCCAC     7543     C     CGGA
                                AGC TCCCATT   TTCAC
                                ||| |||||||   |||||
                                TCG AGGGTAA   AGGTG
                                  _     A___
GAM291  JAM1     3' AGCTCCCATTTTCCAC     7543     C     CGGA
                                AGC TCCCATT   TTCAC
                                ||| |||||||   |||||
                                TCG AGGGTAA   AGGTG
                                  _     A___
GAM291  JAM1     3' AGCTCCCATTTTCCAC     7543     C     CGGA
                                AGC TCCCATT   TTCAC
                                ||| |||||||   |||||
                                TCG AGGGTAA   AGGTG
                                  _     A___
GAM291  JAM1     3' AGCTCCCATTTTCCAC     7543     C     CGGA
                                AGC TCCCATT   TTCAC
                                ||| |||||||   |||||
                                TCG AGGGTAA   AGGTG
                                  _     A___
GAM291  JAM1     3' AGCTCCCATTTTCCAC     7543     C     CGGA
                                AGC TCCCATT   TTCAC
                                ||| |||||||   |||||
                                TCG AGGGTAA   AGGTG
                                  _     A___
GAM291  KIAA0089 3' AAGCTTCATCAAAGATTCACA 7544     CTCC   C_
                                AAGC   CATT  GGATTCACA
                                ||||   ||||  |||||||||
                                TTCG   GTAG  TCTAAGTGT
                                  AA__   TT
GAM291  KIAA0391 3' CTCCCATTTGGCCTCCCA    7545       C  A  A
                                CTCCCATT GG TTC CA
                                |||||||| || ||| ||
                                GAGGGTAA CC GAG GT
                                     A  G  G
GAM291  KIAA1069 3' AAGTCCCCCAGACTTTTGGATT 7546    C     _____  C
                                AAG CTCCCA   TT GGATT
                                ||| ||||||   || |||||
                                TTC GGGGGT   AA CCTAA
                                  A     CTGA  A
GAM291  KIAA1143 3' AGCCTCCCATAAAGATTTAC  7547         TC    C
                                AGCCTCCCAT  GGATT AC
                                ||||||||||  ||||| ||
                                TCGGAGGGTA  TCTAA TG
                                      TT    A
GAM291  KIAA1948 3' GCCTCCCAAAGTGCTGGATTTA 7548        TTC_____    C
           CA                   GCCTCCCA     GGATT ACA
                                ||||||||     ||||| |||
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                                CGGAGGGT      CCTAA TGT
                                    TTCACGA    A
GAM291  MGC22014  3'  AAGCCCCCCATTCACCACA   7549            GAT
                                AAGCCTCCCATTCG   TCACA
                                ||||||||||||||  |||||
                                TTCGGGGGGGTAAGT   GGTGT
                                          ____
GAM291  MGC4643   3'  GCCTTCCATCCATGATTCACA  7550      C     _
                                GCCT CCATTCG GATTCACA
                                |||| ||||||| ||||||||
                                CGGA GGTAGGT CTAAGTGT
                                  A      A
GAM291  PGR1      3'  AGCTCTTCTCCAGATTCAC   7551     C  CCA
                                AGC TC   TTCGGATTCAC
                                ||| ||   ||||||||||
                                TCG AG   AGGTCTAAGTG
                                  _ AAG
GAM291  PISD      3'  AAGTCTCCCACTTTTCA     7552      C      CGGA
                                AAG CTCCCATT    TTCA
                                ||| ||||||||    ||||
                                TTC GAGGGTGA    AAGT
                                  A       A___
GAM291  SDF1      3'  AGCCTCCCATGTGGCCCTCCA  7553          TC  A_   A
                                AGCCTCCCAT  GG  TTC CA
                                ||||||||||  ||  ||| ||
                                TCGGAGGGTA  CC  GAG GT
                                     CA  GG  _
GAM291  SERP1     3'  AAGCCCCCTGTGAGGTTCAC   7554         CATTC  A
                                AAGCCTCC     GG TTCAC
                                ||||||||     || |||||
                                TTCGGGGGG    CC AAGTG
                                    ACACT  _
GAM291  SSH2      3'  AAGCCTCCTCACATTGGTTCA  7555          _   TC_  A
                                AAGCCTCC CAT   GG TTCA
                                |||||||| |||   || ||||
                                TTCGGAGG GTG   CC AAGT
                                    A   TAA  _
GAM291  ZFP100    5'  AAGCCTCCCTTCCACCCA    7556          A   GG
                                AAGCCTCCC TTC  ATTCA
                                ||||||||| |||  |||||
                                TTCGGAGGG AAG  TGGGT
                                     _  G_
GAM291  ZNF185    3'  AGCTTTTCCTGGATTCACA   7557      C__   CATTC
                                AGC   TCC    GGATTCACA
                                |||   |||    |||||||||
                                TCG   AGG    CCTAAGTGT
                                  AAA  A_____
GAM291  LOC124976 3'  CCCCCATTGGCCACA       7558          C  AT
                                CTCCCATT GG  TCACA
                                |||||||| ||  |||||
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                                GGGGGTAA CC  GGTGT
                                   _  __
GAM291   LOC144512 5'  GCCTCCCATCCATCAC      7559          GAT
                                GCCTCCCATTCG   TCAC
                                ||||||||||||  ||||
                                CGGAGGGTAGGT   AGTG
                                   ____
GAM291   LOC144747 5'  CCCCCATCATGGTATTTACA   7561        C_ _  C
                                CTCCCATT  GG ATT ACA
                                ||||||||  || ||| |||
                                GGGGGTAG  CC TAA TGT
                                     TA  A   A
GAM291   LOC144747 5'  AGCCCCCATTTCCCAC      7560      T     CGGA
                                AGCC CCCATT    TTCAC
                                |||| ||||||    |||||
                                TCGG GGGTAA    GGGTG
                                  _     A___
GAM291   LOC144840 3'  ACCTCCCATGGGTGTTCAC    7562         TC  A_
                                GCCTCCCAT  GG  TTCAC
                                |||||||||  ||  |||||
                                TGGAGGGTA  CC  AAGTG
                                     C_  AC
GAM291   LOC145757 3'  GCCCCCATTCATTCAC      7563      T     GG
                                GCC CCCATTC  ATTCAC
                                ||| |||||||  ||||||
                                CGG GGGTAAG  TAAGTG
                                  _     __
GAM291   LOC147639 5'  CTCCCTTCCCGATTCACA    7564       A   G
                                CTCCC TTC GATTCACA
                                ||||| ||| ||||||||
                                GAGGG AGG CTAAGTGT
                                   A   G
GAM291   LOC148254 3'  AAGCCTACTGTCCAATTCACA  7565       CCCAT  G
                                AAGCCT    TC GATTCACA
                                ||||||    || ||||||||
                                TTCGGA    AG TTAAGTGT
                                   TGAC_  G
GAM291   LOC148947 3'  ACCTCCCATGGGTGTTCA    7566         TC  A_
                                GCCTCCCAT  GG  TTCA
                                |||||||||  ||  ||||
                                TGGAGGGTA  CC  AAGT
                                     C_  AC
GAM291   LOC149132 5'  AGTCTCTCTTCCTGGATTCACA 7567     C   CCA  _
                                AG CTC   TTC GGATTCACA
                                || |||   ||| |||||||||
                                TC GAG   AGG CCTAAGTGT
                                 A  AGA   A
GAM291   LOC149620 5'  AAGCCTCCCATACTTCAG    7568          ___
                                AAGCCTCCCAT   TCGG
                                ||||||||||   ||||
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                                TTCGGAGGGTA  AGTC
                                      TGA
GAM291  LOC150115 5' AACTCTCCCATTAAAAACACA 7569     _      C  TT
                                AGC CTCCCATT GGA  CACA
                                ||| |||||||| |||  ||||
                                TTG GAGGGTAA TTT  GTGT
                                  A       _  TT
GAM291  LOC150319 3' AAGCCTCCCATCCTCCCA    7570           GGAT
                                AAGCCTCCCATTC    TCA
                                ||||||||||||    |||
                                TTCGGAGGGTAGG    GGT
                                      AG__
GAM291  LOC151475 3' AACCTCCCCCACATTTACA   7571         AT  G  C
                                AGCCTCCC  TCG ATT ACA
                                ||||||||  ||| ||| |||
                                TTGGAGGG  GGT TAA TGT
                                    __  G  A
GAM291  LOC151571 5' AGCTCCCCATTCGAGGCCTTCA 7572     CT     __ A_
          CA                      AGC  CCCATTC  GG  TTCACA
                                ||| |||||||  ||  ||||||
                                TCG  GGGTAAG  CC  AAGTGT
                                  AG      CT  GG
GAM291  LOC151658 5' GCCTCCATTCAAACACA     7573       C      TT
                                GCCTCC ATTCGGA  CACA
                                |||||| |||||||  ||||
                                CGGAGG TAAGTTT  GTGT
                                   _     __
GAM291  LOC158401 5' AACTTCCTCAAATTCAC     7574     C  CAT
                                AGC TCC   TCGGATTCAC
                                ||| |||   ||||||||||
                                TTG AGG   AGTTTAAGTG
                                  A  ____
GAM291  LOC158402 3' AGCTCTCCTAAGATTCACA   7575     _   CATTC
                                AGC CTCC    GGATTCACA
                                ||| ||||    |||||||||
                                TCG GAGG    TCTAAGTGT
                                  A   AT____
GAM291  LOC158674 3' ACCTCCCATGGGTGTTCAC   7562         TC  A_
                                GCCTCCCAT  GG  TTCAC
                                |||||||||  ||  |||||
                                TGGAGGGTA  CC  AAGTG
                                    C_  AC
GAM291  LOC163882 3' AAGCCCTTTAAGATTCACA   7576       CCCA  C
                                AAGCCT    TT GGATTCACA
                                ||||||    || |||||||||
                                TTCGGG    AA TCTAAGTGT
                                   A____  T
GAM291  LOC200982 5' AAGCCTCCAATGGCTCGCA   7577         C  TC  A  A
                                AAGCCTCC AT  GG TTC CA
                                |||||||| ||  || ||| ||
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                                TTCGGAGG TA  CC GAG GT
                                    T __ _   C
GAM291  LOC221092 5'  AAGCCTCCTCTCGGAATTCA  7578        CA    _
                                AAGCCTCC  TTCGGA TTCA
                                ||||||||  |||||| ||||
                                TTCGGAGG  GAGCCT AAGT
                                   A_     T
GAM291  LOC221395 5'  GCATCCCATTCAATCACA    7579    C       AT
                                GC TCCCATTCGG  TCACA
                                || ||||||||||  |||||
                                CG AGGGTAAGTT  AGTGT
                                 T        __
GAM291  LOC221474 5'  AGTCTCTTGTCCAGTCCACA  7580    C  CCA    A
                                AG CTC   TTCGG TTCACA
                                || |||   ||||| ||||||
                                TC GAG   AGGTC AGGTGT
                                 A  AAC    _
GAM291  LOC221683 5'  GCCTCTCCCGTTCACA     7581      _ ATT  GA
                                GCCTC CC   CG  TTCACA
                                ||||| ||   ||  ||||||
                                CGGAG GG   GC  AAGTGT
                                  A  ____ __
GAM291  LOC245757 3'  ACCTCCCATGGGTGTTCAC   7562        TC  A_
                                GCCTCCCAT  GG  TTCAC
                                |||||||||  ||  |||||
                                TGGAGGGTA  CC  AAGTG
                                    C_  AC
GAM291  LOC254143 5'  GCCTCCCATCCATCAC     7559          GAT
                                GCCTCCCATTCG   TCAC
                                ||||||||||||   ||||
                                CGGAGGGTAGGT   AGTG
                                       ____
GAM291  LOC255520 3'  AAGCCTCCCCACACCTGTTCA  7582        AT__  GGA
                                AAGCCTCCC    TC   TTCA
                                |||||||||    ||   ||||
                                TTCGGAGGG    GG   AAGT
                                     GTGT  AC_
GAM291  LOC90249  3'  CTCCCATTGCATATTCACA   7583        _  G
                                CTCCCATT CG ATTCACA
                                |||||||| || |||||||
                                GAGGGTAA GT TAAGTGT
                                    C  A
GAM292  DMD     5'  TAGTGGTCAGTCCAGGAGCTAG 7586        C __   A   A
          GT                    TAGTGGTC GT  GGGA GCTA GT
                                |||||||| ||  |||| |||| ||
                                ATCACCAG CA  TCCT CGAT CA
                                    T  GG   _   C
GAM292  DMD     5'  TAGTGGTCAGTCCAGGAGCTAG 7586        C __   A   A
          GT                    TAGTGGTC GT  GGGA GCTA GT
                                |||||||| ||  |||| |||| ||
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                                ATCACCAG CA  TCCT CGAT CA
                                    T  GG   _   C
GAM292  DMD      5'  TAGTGGTCAGTCCAGGAGCTAG 7586         C __   A   A
           GT                    TAGTGGTC GT  GGGA GCTA GT
                                ||||||||  ||  |||| |||| ||
                                ATCACCAG CA  TCCT CGAT CA
                                    T  GG   _   C
GAM292  SCAMP3   3'  TTAGGGACGGGAGCTAAG    7587      T  TCCG    A
                                TTAG GG   TGGGA GCTAAG
                                |||| ||   ||||| ||||||
                                AATC CC   GCCCT CGATTC
                                  _ T___   _
GAM292  SCAMP3   3'  TTAGGGACGGGAGCTAAG    7587      T  TCCG    A
                                TTAG GG   TGGGA GCTAAG
                                |||| ||   ||||| ||||||
                                AATC CC   GCCCT CGATTC
                                  _ T___   _
GAM292  DKFZP761G1913 3'  GTGGTGTGGGAAGTTGAGT   7588       CC       CTA
                                GTGGT  GTGGGAAG   AGT
                                |||||  ||||||||   |||
                                CACCA  CACCCTTC   TCA
                                   __       AAC
GAM292  SHAPY    5'  TGGCAACGTGGGAAGCTGAGT  7589      C_        A
                                TGGT  CGTGGGAAGCT AGT
                                ||||  |||||||||| |||
                                ACCG  GCACCCTTCGA TCA
                                  TT         C
GAM292  LOC255017 3'  TTAGGGACGGGAGCTAAG    7587      T  TCCG    A
                                TTAG GG   TGGGA GCTAAG
                                |||| ||   ||||| ||||||
                                AATC CC   GCCCT CGATTC
                                  _ T___   _
GAM293  EPM2A    3'  TAAAAAAACACTTCTCTTTCT  7592         TT  A
                                TAAAAAAG  TT TCTCTTTCT
                                ||||||||  || |||||||||
                                ATTTTTTT  GA AGAGAAAGA
                                     GT  _
GAM293  PPP2R2B  3'  GTCGAAAGTGCTCTCTTTCT  7593     AAA    TTTA
                                GT  AAAGT   TCTCTTTCT
                                ||  |||||   |||||||||
                                CA  TTTCA   AGAGAAAGA
                                 GC_    CG__
GAM293  TEM8     3'  GTAGGCAAAGTTTTCCTCTTTC 7594      AA_      A
           T                     GTA  AAAGTTTT TCTCTTTCT
                                |||  |||||||| |||||||||
                                CAT  TTTCAAAA GGAGAAAGA
                                  CCG       _
GAM293  BET3     3'  GTAAAATGGTTTGAGCTCTTTC 7595       AA   TAT
           T                     GTAAAA  GTTT   CTCTTTCT
                                ||||||  ||||   ||||||||
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                                CATTTT  CAAA   GAGAAAGA
                                   AC    CTC
GAM293  FLJ14957  3'  GCAAGGAGAATGTCTCTTTCT  7596      AAA  TTTTA
                                GTAA   AG    TCTCTTTCT
                                ||||   ||    |||||||||
                                CGTT   TC    AGAGAAAGA
                                  CC_  TTAC_
GAM293  GTF2A2    3'  GTAAAAAAGTCATATTTTTTCT 7597          T   CTC
                                GTAAAAAAGTT TAT   TTTCT
                                |||||||||||| |||   |||||
                                CATTTTTTCAG ATA   AAAGA
                                       T   AA_
GAM293  RBM9      3'  ATAAAAAAGTATTCTTTC    7598          TTTATC
                                GTAAAAAAGT     TCTTTC
                                ||||||||||     ||||||
                                TATTTTTTCA     AGAAAG
                                       TA____
GAM293  SLC26A7   3'  TAAAAAAGAAAGATCTCTTTCT 7599         TTTT
                                TAAAAAAG    ATCTCTTTCT
                                ||||||||    ||||||||||
                                ATTTTTTC    TAGAGAAAGA
                                     TTTC
GAM293  LOC221509 3'  GTAAAATTTATCTCTTT     7600        AAGT
                                GTAAAA    TTTATCTCTTT
                                ||||||    ||||||||||
                                CATTTT    AAATAGAGAAA
                                          ____
GAM293  LOC254700 5'  GTCGAAAAGCTCATTTTCTTTC 7601     AA       TATC
           T                     GT  AAAAGTTT    TCTTTCT
                                 ||  ||||||||    |||||||
                                 CA  TTTTCGAG    AGAAAGA
                                  GC       TAAA
GAM293  LOC254700 5'  GTAAGAAAGCTCTCCTT     7602       A     TTTA
                                GTAA AAAGT    TCTCTTT
                                |||| |||||    |||||||
                                CATT TTTCG    AGAGGAA
                                  C    _____
GAM293  LOC51219  5'  GTGAAAACCAGGCATCTCTTTC 7603     A    AGTTT
           T                     GT AAAA     TATCTCTTTCT
                                 || ||||     ||||||||||
                                 CA TTTT     GTAGAGAAAGA
                                  C    GGTCC
GAM293  LOC51644  3'  ATAGAAAAGAATTCTCTTTCT  7604      A     TTTTA
                                GTA AAAAG     TCTCTTTCT
                                ||| |||||     |||||||||
                                TAT TTTTC     AGAGAAAGA
                                  C    TTA__
GAM294  SCA1      3'  TTTCCCATCTTAGTGT      7607           CGC
                                TTTCCTATCTT   GGTGT
                                ||||||||||   |||||
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                                AAAGGGTAGAA   TCACA
                                    ___
GAM294  TMEPAI   3'  TAACTTTCCTATTTTGCTTGT  7608    C       C  C  GG
                                A ACTTTCCTAT TT GC  TGT
                                | ||||||||||  || ||  |||
                                A TGAAAGGATA AA CG  ACA
                                 T        A  _  A_
GAM294  CDC42BPB 3'  CACTTTCCTGTCTTCAAAAT   7609         A     CG
                                CACTTTCCT TCTTCG  GT
                                |||||||||  ||||||  ||
                                GTGAAAGGA AGAAGT  TA
                                      C     TT
GAM294  GAB3     3'  CTTTTCTATCTCCAATCTGGTG 7610      C       C___
           T                     CTTT CTATCTTCG    GGTGT
                                ||||  |||||||||    |||||
                                GAAA GATAGAGGT    CCACA
                                  A        TAGA
GAM294  KIAA0831  5'  TAACTTTCCTATCTTCCA    7611    C          G
                                A ACTTTCCTATCTTC CG
                                | ||||||||||||||  ||
                                A TGAAAGGATAGAAG GT
                                 T          _
GAM294  RPH3A    3'  TACACTTTTTTTGCTGTTGTTT 7612   CTATCTTC_______     III
           TTGCGGTGTAC                          GCGGTGT   AC
                                      |||||||   ||
                                      CGCCACA   TG
                                AAACGACAACAAAAA      III
GAM294  YWHAQ    3'  TACATTTTCTTATTTTCACAGT 7613      C   C   C
                                TACA TTTC TAT TTCGCGGT
                                ||||  ||||  |||  ||||||||
                                ATGT AAAG ATA AAGTGTCA
                                  A   A   A
GAM294  LOC146506 3'  TACACTTTTCAATTTTGAGCCA 7614        _ CTATCTTC  G
           TGT                    TACACTTT C       GC GTGT
                                ||||||||  |       ||  ||||
                                ATGTGAAA G       CG TACA
                                     A TTAAAACT  G
GAM294  LOC91351  3'  TACACTTTTTTTCTTTCCAGT  7615         CCTA    CG
                                TACACTTT    TCTT  CGGT
                                ||||||||    ||||  ||||
                                ATGTGAAA    AGAA  GTCA
                                     AAA_    AG
GAM294  LOC91650  5'  TACATTCCTATCAGTGGTGT   7616      CT       TTCGC
                                TACA  TTCCTATC    GGTGT
                                ||||  ||||||||    |||||
                                ATGT  AAGGATAG    CCACA
                                  __       TCA__
GAM295  AICDA    3'  AAATATTGTTCTCTTTCT    7619         TTTA
                                AAATATT    TTCTCTTTCT
                                |||||||    ||||||||||
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                                TTTATAA   AAGAGAAAGA
                                   C___
GAM295  AS3      3'  TAAAATACTTTAAATCTTTCT  7620          TATTC
                                TAAAATATTTT    TCTTTCT
                                ||||||||||    |||||||
                                ATTTTATGAAA    AGAAAGA
                                     TTT__
GAM295  EPM2A    3'  AAAACACTTCTCTTTCT     7621        TTTTA
                                AAAATAT    TTCTCTTTCT
                                |||||||    ||||||||||
                                TTTTGTG    AAGAGAAAGA
                                    _____
GAM295  HRH1     3'  AAAATATTTCATTTCTCTTTCT 7622          TA
                                AAAATATTTT  TTCTCTTTCT
                                ||||||||||  ||||||||||
                                TTTTATAAAG  AAGAGAAAGA
                                     TA
GAM295  MAPK14   3'  TAAAATAATTTGCCCTTTCTC  7623        T   TATT
                                TAAAATA TTT   CTCTTTCTC
                                ||||||| |||   |||||||||
                                ATTTTAT AAA   GGGAAAGAG
                                   T  C___
GAM295  MAPK14   3'  TAAAATAATTTGCCCTTTCTC  7623        T   TATT
                                TAAAATA TTT   CTCTTTCTC
                                ||||||| |||   |||||||||
                                ATTTTAT AAA   GGGAAAGAG
                                   T  C___
GAM295  MAPK14   3'  TAAAATAATTTGCCCTTTCTC  7623        T   TATT
                                TAAAATA TTT   CTCTTTCTC
                                ||||||| |||   |||||||||
                                ATTTTAT AAA   GGGAAAGAG
                                   T  C___
GAM295  NOTCH2   3'  TAAAATATTTTAATTCTC    7624          T
                                TAAAATATTTT ATTCTC
                                |||||||||| ||||||
                                ATTTTATAAAA TAAGAG
                                     T
GAM295  SIM1     3'  TATCTCTCTCTTTCTC      7625        TAT
                                TATTTT   TCTCTTTCTC
                                ||||||   ||||||||||
                                ATAGAG   AGAGAAAGAG
                                   ___
GAM295  C11orf25 3'  TAAAATATTTTTCTCTTT    7626          TAT
                                TAAAATATTTT   TCTCTTT
                                ||||||||||   |||||||
                                ATTTTATAAAA   AGAGAAA
                                    ___
GAM295  DKFZP564D116 3'  TAAAATATTTTTATTGCTTTTC 7627             _  C
                                TAAAATATTTTTATT CT TTTC
                                |||||||||||||| || ||||
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                                ATTTTATAAAAATAA GA AAAG
                                        C _
GAM295  DSCR6    3'  TGACATAGACCTTCTCTTTCTC 7628    A    TTTTA
                                A ATAT     TTCTCTTTCTC
                                | ||||     ||||||||||
                                A TGTA     AAGAGAAAGAG
                                 C    TCTGG
GAM295  FLJ10006 3'  TAAAATATCTTCTTTCTC     7629           A
                                TAAAATATTTTT TTCTC
                                |||||||||||| |||||
                                ATTTTATAGAAG AAGAG
                                        A
GAM295  HTPAP    3'  TAAAATCTTTTTATTCTC     7630        A
                                TAAAAT TTTTTATTCTC
                                |||||| ||||||||||
                                ATTTTA AAAAATAAGAG
                                    G
GAM295  KIAA0979 3'  TAAAATACTTTAAATCTTTCT  7620          TATTC
                                TAAAATATTTT     TCTTTCT
                                ||||||||||     |||||||
                                ATTTTATGAAA     AGAAAGA
                                        TTT__
GAM295  KIAA1634 3'  TAAAATAGTTTTATTCTC     7631         T
                                TAAAATA TTTTATTCTC
                                ||||||| ||||||||||
                                ATTTTAT AAAATAAGAG
                                    C
GAM295  PTD012   3'  ATATTTTTGTTCCCAATCTC   7632          A    TT
                                ATATTTTT TTCTC  TCTC
                                |||||||| |||||  ||||
                                TATAAAAA AAGGG  AGAG
                                    C     TT
GAM295  SAMHD1   3'  ATATTTCTTTCTCTTTCT     7633          A
                                ATATTTTT TTCTCTTTCT
                                |||||||| ||||||||||
                                TATAAAGA AAGAGAAAGA
                                        _
GAM295  LOC196758 3'  AAAATATTTCACCTGCTCTTTC 7634          TATT_
          TC                    AAAATATTTT     CTCTTTCTC
                                ||||||||||     |||||||||
                                TTTTATAAAG     GAGAAAGAG
                                    TGGAC
GAM295  LOC219790 3'  TAAATTATTTTTATTCTC     7635       A
                                TAAA TATTTTTATTCTC
                                |||| ||||||||||||
                                ATTT ATAAAAATAAGAG
                                  A
GAM296  ACOX3    3'  TCCCTTCGTTTCATTAGA     7638          CCC   CG_
                                TCCCTTTGT   TTC   AGA
                                |||||||||   |||   |||
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                                AGGGAAGCA  AAG  TCT
                                     ___  TAA
GAM296  ADAR    3'  CCTCTTTGCCCTCTGAG    7639    _   T   CC
                                CC CTTTG CCCTT  GAG
                                || ||||| |||||  |||
                                GG GAAAC GGGAG  CTC
                                 A   _   A_
GAM296  ADAR    3'  CCTCTTTGCCCTCTGAG    7639    _   T   CC
                                CC CTTTG CCCTT  GAG
                                || ||||| |||||  |||
                                GG GAAAC GGGAG  CTC
                                 A   _   A_
GAM296  ADAR    3'  CCTCTTTGCCCTCTGAG    7639    _   T   CC
                                CC CTTTG CCCTT  GAG
                                || ||||| |||||  |||
                                GG GAAAC GGGAG  CTC
                                 A   _   A_
GAM296  ANK3    3'  TCCTTCTGTCCCTTCTGA   7640    C       C
                                TCC TTTGTCCCTTC GA
                                ||| |||||||||| ||
                                AGG AGACAGGGAAG CT
                                  A       A
GAM296  AQP6    3'  CCTTTCTCCCCCAAGA     7641      G   TT
                                CCTTT TCCC  CCGAGA
                                ||||| ||||  ||||||
                                GGAAA AGGG  GGTTCT
                                   G   __
GAM296  AQP6    3'  CCTTTCTCCCCCAAGA     7641      G   TT
                                CCTTT TCCC  CCGAGA
                                ||||| ||||  ||||||
                                GGAAA AGGG  GGTTCT
                                   G   __
GAM296  BIN1    3'  TCCCTTTGCTCTTCAAAAGA  7642        CC   C_
                                TCCCTTTGT  CTTC  GAGA
                                |||||||||  ||||  ||||
                                AGGGAAACG  GAAG  TTCT
                                     A_   TT
GAM296  BIN1    3'  TCCCTTTGCTCTTCAAAAGA  7642        CC   C_
                                TCCCTTTGT  CTTC  GAGA
                                |||||||||  ||||  ||||
                                AGGGAAACG  GAAG  TTCT
                                     A_   TT
GAM296  CLCA2   3'  TCCCTTTGCCTTTAAAGA   7643        TC   CC
                                TCCCTTTG  CCTT  GAGA
                                ||||||||  ||||  ||||
                                AGGGAAAC  GGAA  TTCT
                                     __   AT
GAM296  CMAR    3'  TCCCCTTAGCATTCCGAG   7644        TCCC
                                TCCCTTTG   TTCCGAG
                                ||||||||   |||||||
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                                AGGGGAAT   AAGGCTC
                                     CGT_
GAM296  CRMP1   3'  CCCCTGCCATTCCGAGA    7645       T  C
                                CCTTTG CC TTCCGAGA
                                ||||||| || ||||||||
                                GGGGAC GG AAGGCTCT
                                   _  T
GAM296  CXCL1   3'  CCCCTTTGTTCTAAGCCAGA  7646         _ CCTT  G
                                TCCCTTTGT C   CC AGA
                                ||||||||| |   || |||
                                GGGGAAACA G   GG TCT
                                     A ATTC  _
GAM296  EXO1    5'  TCCCTCTGTCTCGCGGA    7647          CCT  _  A
                                TCCCTTTGTC   TC CG GA
                                ||||||||||   || || ||
                                AGGGAGACAG   AG GC CT
                                     ____  C  _
GAM296  EXO1    5'  TCCCTCTGTCTCGCGGA    7647          CCT  _  A
                                TCCCTTTGTC   TC CG GA
                                ||||||||||   || || ||
                                AGGGAGACAG   AG GC CT
                                     ____  C  _
GAM296  EXO1    5'  TCCCTCTGTCTCGCGGA    7647          CCT  _  A
                                TCCCTTTGTC   TC CG GA
                                ||||||||||   || || ||
                                AGGGAGACAG   AG GC CT
                                     ____  C  _
GAM296  FCGR2A  3'  TCCCTTCGTCTTCCCCAAG  7648          CC
                                TCCCTTTGTC  TTCCGAG
                                ||||||||||  |||||||
                                AGGGAAGCAG  GGGGTTC
                                     AA
GAM296  IFNGR2  5'  CCCCCTCCCCTTTTTTTTGAGA 7649       G     CC____
                                CCCTTT TCCCTT     GAGA
                                |||||| ||||||     ||||
                                GGGGGA GGGGAA     CTCT
                                   _     AAAAAA
GAM296  LAIR1   3'  TCTCTCTGTCCTTCTCAG    7650     C      C   CG
                                TC CTTTGTCC TTC  AG
                                || ||||||| |||  ||
                                AG GAGACAGG AAG  TC
                                 A       _   AG
GAM296  MEN1    5'  TCCCTTTGGTTCTCGGA     7651         TCCC  _  A
                                TCCCTTTG   TTC CG GA
                                ||||||||   ||| || ||
                                AGGGAAAC   AAG GC CT
                                     C___   A  _
GAM296  MLH3    3'  TCCCTTTGTTCCTTTTAGA   7652          C   CCG
                                TCCCTTTGT CCTT   AGA
                                ||||||||| ||||   |||
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                                AGGGAAACA GGAA   TCT
                                     A    AA_
GAM296  MLLT2    3'  TCCCTTTGTATATCAGAGA   7653         CCCT  C
                                TCCCTTTGT    TC GAGA
                                |||||||||    || ||||
                                AGGGAAACA    AG CTCT
                                     TAT_  T
GAM296  PAX5     3'  CCTCTGTCCCCCAGA      7654          TT  G
                                CCTTTGTCCC  CC AGA
                                ||||||||||  || |||
                                GGAGACAGGG  GG TCT
                                      __  _
GAM296  PCDHB7   3'  TCTCCTTAACTTCCGAGA    7655     _    TGTCC
                                TC CCTT     CTTCCGAGA
                                || ||||     |||||||||
                                AG GGAA     GAAGGCTCT
                                 A    TT___
GAM296  PSMB2    3'  TCCCTCCATATCCTTTCTGAG  7656        __     C   C
                                TCCCTT  TGTCC TTC GAG
                                ||||||  ||||| ||| |||
                                AGGGAG  ATAGG AAG CTC
                                   GT     A   A
GAM296  QDPR     3'  TCCACCCCCTTCTGAGA     7657     _ TTGT     C
                                TCC CT    CCCTTC GAGA
                                ||| ||    |||||| ||||
                                AGG GG    GGGAAG CTCT
                                  T _____      A
GAM296  REN      3'  TCTCTTTGTCCTCAAAG     7658     C       CT  C
                                TC CTTTGTCC  TC GAG
                                || ||||||||  || |||
                                AG GAAACAGG  AG TTC
                                 A       __  T
GAM296  SFRP5    3'  CCCCTGCCTACTTTCTGAGA  7659         CC__   C
                                CCTTTGTC    TTC GAGA
                                ||||||||    ||| ||||
                                GGGGACGG    AAG CTCT
                                     ATGA   A
GAM296  SPG7     3'  TCCCCTTAGCATTCCGAG    7644         TCCC
                                TCCCTTTG    TTCCGAG
                                ||||||||    |||||||
                                AGGGGAAT    AAGGCTC
                                     CGT_
GAM296  STK18    5'  TCCCTGACACCTTCCGAG    7660       TT TC
                                TCCCT  G  CCTTCCGAG
                                |||||  |  |||||||||
                                AGGGA  T  GGAAGGCTC
                                   C_ GT
GAM296  T        5'  CCGCCGCCCTTCCGAGA     7661     T   T
                                CC TTG CCCTTCCGAGA
                                || ||| ||||||||||
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                                GG GGC GGGAAGGCTCT
                                 C  _
GAM296  TNFRSF1B  3'  CCCAGCCAGCCTTCCGAGA   7662     TTT  __
                                CCC  GTC  CCTTCCGAGA
                                |||  |||  ||||||||||
                                GGG  CGG  GGAAGGCTCT
                                  T__  TC
GAM296  TSPY    3'  CCCCTTTGTTCCCCAAAGA   7663         _   TCC
                                TCCCTTTGT CCCT  GAGA
                                |||||||||  ||||  ||||
                                GGGGAAACA GGGG  TTCT
                                     A   T__
GAM296  ARL5    3'  TCCCTTTGTACTTACCATAG  7664         CC  _  _
                                TCCCTTTGT  CTT CCG AG
                                |||||||||  ||| ||| ||
                                AGGGAAACA  GAA GGT TC
                                     T_  T  A
GAM296  BHLHB2  3'  TCTCTTTATTCTTCCGAG   7665    C    CC
                                TC CTTTGT  CTTCCGAG
                                || ||||||  ||||||||
                                AG GAAATA  GAAGGCTC
                                 A     A_
GAM296  DKFZp761D221 3'  TCCTTTTGCTTCTCCAAGA   7666     C    CC  T
                                TCC TTTGT  CT CCGAGA
                                ||| |||||  || ||||||
                                AGG AAACG  GA GGTTCT
                                  A    AA  _
GAM296  EFS2    3'  CCCTCCGGTCTTTCCGAGA   7667        _ CC
                                CCCTTTG TC  TTCCGAGA
                                |||||||  ||  ||||||||
                                GGGAGGC AG  AAGGCTCT
                                    C  A_
GAM296  FACTP140  5'  TCTCCTCGGGTTCCGAGA   7668    C    TCCC
                                TC CTTTG   TTCCGAGA
                                || |||||   ||||||||
                                AG GGAGC   AAGGCTCT
                                 A    CC__
GAM296  FBP17   5'  TCCCTTTGCCCCCCGAGA   7669          TT
                                TCCCTTTGTCCC  CCGAGA
                                ||||||||||||  ||||||
                                AGGGAAACGGGG  GGCTCT
                                              __
GAM296  FLJ10829  3'  CCTCTTTGTCTTCAAAGA   7670    _     CC  C
                                CC CTTTGTC  TTC GAGA
                                || |||||||  ||| ||||
                                GG GAAACAG  AAG TTCT
                                 A      __  T
GAM296  FLJ11712  5'  TCGTTTCGTTTCCGAGA    7671    CC    CCC
                                TC  TTTGT   TTCCGAGA
                                ||  |||||   ||||||||
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                                AG  AAGCA   AAGGCTCT
                                 CA    ___
GAM296  FLJ12691  3'  CCTCTGTCCTCCCTGAGA    7672         C   _
                                CCTTTGTCC TTCC GAGA
                                ||||||||| |||| ||||
                                GGAGACAGG AGGG CTCT
                                     _   A
GAM296  FLJ14054  3'  TCTCTTTCTTCCCCCGAG    7673    C   G_   TT
                                TC CTTT  TCCC  CCGAG
                                || ||||  ||||  |||||
                                AG GAAA  AGGG  GGCTC
                                 A   GA   __
GAM296  FLJ20419  3'  TCCCTTTGGCCTGAGA      7674        TC   TCC
                                TCCCTTTG  CCT   GAGA
                                ||||||||  |||   ||||
                                AGGGAAAC  GGA   CTCT
                                     C_   ___
GAM296  FLJ20811  3'  TCCCATTGTGTTCGAGA     7675      T   CCC   C
                                TCCC TTGT   TTC GAGA
                                |||| ||||   ||| ||||
                                AGGG AACA   AAG CTCT
                                  T   C__   _
GAM296  FLJ21144  3'  TCCCTTGTCTCTTTGAGA    7676       T   C   CC
                                TCCCTT GTC CTT  GAGA
                                |||||| ||| |||  ||||
                                AGGGAA CAG GAA  CTCT
                                    _   A   A_
GAM296  FLJ21977  5'  TCCCTTTGTGCCATCCGAG   7677         C  T
                                TCCCTTTGT CC TCCGAG
                                ||||||||| || ||||||
                                AGGGAAACA GG AGGCTC
                                     C  T
GAM296  FLJ30681  3'  TCCCTTTGCCACCCAGAG    7678          _   TCC
                                TCCCTTTGTC CCT   GAG
                                |||||||||| |||   |||
                                AGGGAAACGG GGG   CTC
                                      T   T__
GAM296  GTPBP2    5'  TCCCTTTGGCCCCCCGAGA   7679         T   T
                                TCCCTTTG CCCT CCGAGA
                                |||||||| |||| ||||||
                                AGGGAAAC GGGG GGCTCT
                                     C   _
GAM296  KCNK16    3'  CCTTTGTACCCCAAAAGA    7680         _   TCC
                                CCTTTGT CCCT   GAGA
                                ||||||| ||||   ||||
                                GGAAACA GGGG   TTCT
                                    T   TT_
GAM296  KCNN1     5'  TCCTGTCCCTTTGAGA      7681      CTT       CC
                                TCC   TGTCCCTT  GAGA
                                |||   ||||||||  ||||
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                                AGG   ACAGGGAA  CTCT
                                 ___       A_
GAM296  KIAA0285 3' TCCCCCTCCCAGTTTCTTCTGA 7682        G _____   C
             G                   TCCCTTT TCC    CTTC GAG
                                 ||||||| |||    |||| |||
                                 AGGGGGA GGG    GAAG CTC
                                    _  TCAAA   A
GAM296  KIAA0365 3' CCCTTCCCCTTCCGAG     7683       GT
                                 CCCTTT  CCCTTCCGAG
                                 ||||||  ||||||||||
                                 GGGAAG  GGGAAGGCTC
                                   __
GAM296  KIAA0427 3' CTTTTTCAGCCTTCCGAG    7685      G __
                                 CTTT TC  CCTTCCGAG
                                 |||| ||  |||||||||
                                 GAAA AG  GGAAGGCTC
                                   A  TC
GAM296  KIAA0427 3' CCTTTGTCCTCCCGGA     7684         C    A
                                 CCTTTGTCC TTCCG GA
                                 ||||||||| ||||| ||
                                 GGAAACAGG AGGGC CT
                                     _    _
GAM296  KIAA0546 3' TCTCTTTGTCCCTTTAGA    7686    C        CC
                                 TC CTTTGTCCCTT  GA
                                 || ||||||||||  ||
                                 AG GAAACAGGGAA  CT
                                  A         AT
GAM296  KIAA0557 3' CCCTACGACTTCCGAGA     7687      T  TCC
                                 CCCT TG   CTTCCGAGA
                                 |||| ||   |||||||||
                                 GGGA GC   GAAGGCTCT
                                   T  T__
GAM296  KIAA0976 3' CCTTTATCTCTCCAGAGA    7688        C   C
                                 CCTTTGTC CTTC GAGA
                                 |||||||| |||| ||||
                                 GGAAATAG GAGG CTCT
                                     A   T
GAM296  KIAA1253 5' CTTTCTCGCCTTTCCGAGA   7689      G _   _
                                 CTTT TC CCTT CCGAGA
                                 |||| || |||| ||||||
                                 GAAA AG GGAA GGCTCT
                                   G C   A
GAM296  KIAA1443 3' TCCCTCTGTCCCTAAGA     7690           TCC
                                 TCCCTTTGTCCCT   GAGA
                                 ||||||||||||   ||||
                                 AGGGAGACAGGGA   TTCT
                                      ___
GAM296  KIAA1576 3' TCCCTCTGTTTCTCGA      7691         CCC  _
                                 TCCCTTTGT   TTC CGA
                                 |||||||||   ||| |||
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                                AGGGAGACA   AAG GCT
                                    ___   A
GAM296  KIAA1750  3'  TCCCTCTCATTTCTTTTTGAGA 7692        _  CC   CC_
                                TCCCTTT GT  CTT   GAGA
                                ||||||| ||  |||   ||||
                                AGGGAGA TA  GAA   CTCT
                                    G  AA   AAA
GAM296  KIAA1950  3'  TCCCTTTGCATTTTCCGGGA   7693         CCC    A
                                TCCCTTTGT   TTCCG GA
                                |||||||||   ||||| ||
                                AGGGAAACG   AAGGC CT
                                     TAA    C
GAM296  LBP-9     3'  CCCCTTTTATTCCGAGA     7694        GTCCC
                                TCCCTTT    TTCCGAGA
                                |||||||    ||||||||
                                GGGGAAA    AAGGCTCT
                                    AT___
GAM296  LIG-1     3'  TCCTTTCTGTCCCCCAAG    7695     C_      TT
                                TCC  TTTGTCCC  CCGAG
                                |||  ||||||||  |||||
                                AGG  AGACAGGG  GGTTC
                                  AA      __
GAM296  MGC2776   5'  TCCCTTTGCTTCTTTCCTTGA  7696         CC  _  GA
                                TCCCTTTGT  CTT CC  GA
                                |||||||||  ||| ||  ||
                                AGGGAAACG  GAA GG  CT
                                     AA   A  AA
GAM296  MGC4796   3'  TCCCTATTGTGGCCCGGGA   7697      _   CCCT   A
                                TCCCT TTGT   TCCG GA
                                ||||| ||||   |||| ||
                                AGGGA AACA   GGGC CT
                                   T   CC__   C
GAM296  MOST2     5'  TCCCTTTTCTGCCAAAA     7698        GTCC  T
                                TCCCTTT    CT CCGAGA
                                |||||||    || ||||||
                                AGGGAAA    GA GGTTTT
                                    A___  C
GAM296  NUDT13    3'  CCCTTTGCTCTGCCCTTCTGAG 7699         ____     C
                                CCCTTTGT    CCCTTC GAG
                                ||||||||    |||||| |||
                                GGGAAACG    GGGAAG CTC
                                     AGAC     A
GAM296  PEX16     3'  TCCCCACACCCTCCTTCCGGGA 7700       T GT  __     A
                                TCCCT T  CC  CTTCCG GA
                                ||||| |  ||  |||||| ||
                                AGGGG G  GG  GAAGGC CT
                                   T TG  AG     C
GAM296  PSK       5'  TCCCTTCTCTCTTCCGAGA   7701        G  C
                                TCCCTTT TC CTTCCGAGA
                                ||||||| || |||||||||
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                                AGGGAAG AG GAAGGCTCT
                                    _ A
GAM296  PTK9    3'  TCTTTCTGTCCCACAAGA   7702    CC      TTC
                                TC  TTTGTCCC   CGAGA
                                ||  ||||||||   |||||
                                AG  AGACAGGG   GTTCT
                                 AA       T__
GAM296  RELB    3'  TCCCTTTTCCTCTCCGGA   7703        G   C    A
                                TCCCTTT TCC TTCCG GA
                                ||||||| ||| ||||| ||
                                AGGGAAA AGG GAGGC CT
                                    _  A    _
GAM296  SDC3    3'  TCCCTTTGGCTCCAAGA    7704        TCCC
                                TCCCTTTG   TTCCGAGA
                                ||||||||   ||||||||
                                AGGGAAAC   GAGGTTCT
                                     C___
GAM296  SLC5A6  5'  TCCCTTTGTGCTTCCTGAGA  7705        CC   _
                                TCCCTTTGT  CTTCC GAGA
                                |||||||||  ||||| ||||
                                AGGGAAACA  GAAGG CTCT
                                     C_    A
GAM296  TED     3'  TCCCTTTTCCCCTTCTGAG   7706        GT    C
                                TCCCTTT  CCCTTC GAG
                                |||||||  |||||| |||
                                AGGGAAA  GGGAAG CTC
                                    AG     A
GAM296  TNRC5   5'  TCCCCTCGCCGCTTCCGGGA  7707         C    A
                                TCCCTTTGTC CTTCCG GA
                                |||||||||| |||||| ||
                                AGGGGAGCGG GAAGGC CT
                                      C     C
GAM296  WNT16   3'  TCTCTTTGTCCATTCTGA   7708    C      C  C
                                TC CTTTGTCC TTC GA
                                || |||||||| ||| ||
                                AG GAAACAGG AAG CT
                                 A       T  A
GAM296  WNT16   3'  TCTCTTTGTCCATTCTGA   7708    C      C  C
                                TC CTTTGTCC TTC GA
                                || |||||||| ||| ||
                                AG GAAACAGG AAG CT
                                 A       T  A
GAM296  ZFP106  3'  TCCCTTTATTTCTTAATAGA  7709        CC  CCG
                                TCCCTTTGT  CTT   AGA
                                |||||||||  |||   |||
                                AGGGAAATA  GAA   TCT
                                     AA  TTA
GAM296  ZNF212  3'  TCCTCTTGGTCCTTTTGAGA  7710    C   TC   CC
                                TCC TTTG  CCTT  GAGA
                                ||| ||||  ||||  ||||
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                                AGG GAAC  GGAA  CTCT
                                  A   CA   AA
GAM296  ZNF221   5'  TCCCTTTGCTTTCCGA     7711         CCC
                                TCCCTTTGT  TTCCGA
                                |||||||||  ||||||
                                AGGGAAACG  AAGGCT
                                     A__
GAM296  ZNF304   3'  CCTTTGGTCCCCTCTGAG    7712       _     C
                                CCTTTG TCCCTTC GAG
                                |||||| ||||||| |||
                                GGAAAC AGGGGAG CTC
                                   C      A
GAM296  LOC122553 3'  TCCCTTTGTTTCTACTAAGAGA 7713         CC  TCC__
                                TCCCTTTGT  CT    GAGA
                                |||||||||  ||    ||||
                                AGGGAAACA  GA    CTCT
                                     AA  TGATT
GAM296  LOC123096 3'  CCTCTGTCCCTAACACAGA   7714          TC  _
                                CCTTTGTCCCT  CG AGA
                                ||||||||||  || |||
                                GGAGACAGGGA  GT TCT
                                      TT  G
GAM296  LOC126549 5'  TCCCTTTGCCCACGTAGA    7715          CTTC  _
                                TCCCTTTGTCC    CG AGA
                                ||||||||||    || |||
                                AGGGAAACGGG    GC TCT
                                      T___  A
GAM296  LOC144755 5'  CCCCTCACAGGCTTCCGAGA  7716       TGTCC
                                TCCCTT    CTTCCGAGA
                                ||||||    |||||||||
                                GGGGAG    GAAGGCTCT
                                   TGTCC
GAM296  LOC146923 3'  TCCAGCACATCTTTCCGAGA  7717     CTT_   CC
                                TCC   TGTC  TTCCGAGA
                                |||   ||||  ||||||||
                                AGG   GTAG  AAGGCTCT
                                  TCGT   A_
GAM296  LOC146952 5'  TCCCTTTGCCTCACAGA     7718        TC   TC G
                                TCCCTTTG  CCT  C AGA
                                ||||||||  |||  | |||
                                AGGGAAAC  GGA  G TCT
                                     __   GT _
GAM296  LOC147515 3'  CCTTTTGTCCCTTAAG      7719     C       CC
                                CC TTTGTCCCTT  GAG
                                || ||||||||||  |||
                                GG AAACAGGGAA  TTC
                                 A        __
GAM296  LOC148413 3'  TCCCTATGTCCCCCAGA     7720       T     TT  G
                                TCCCT TGTCCC  CC AGA
                                ||||| ||||||  || |||
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                                AGGGA ACAGGG  GG TCT
                                  T     __ _
GAM296  LOC148513 3'  TCCCTCTGTCTCCTCCAGA   7721          C    G
                                TCCCTTTGTC CTTCC AGA
                                |||||||||| ||||| |||
                                AGGGAGACAG GGAGG TCT
                                     A    _
GAM296  LOC149319 5'  CCTAGTGTCCCTTCCGGGA   7722     T_        A
                                CCT  TGTCCCTTCCG GA
                                |||  |||||||||| ||
                                GGA  ACAGGGAAGGC CT
                                  TC         C
GAM296  LOC149995 3'  CCTTTTGTCCCTTAAG      7719     C        CC
                                CC TTTGTCCCTT  GAG
                                || ||||||||||  |||
                                GG AAACAGGGAA  TTC
                                 A        __
GAM296  LOC151176 5'  TCCATTTGCCCCTGAGA     7723     C        TCC
                                TCC TTTGTCCCT   GAGA
                                ||| |||||||||   ||||
                                AGG AAACGGGGA   CTCT
                                  T       ____
GAM296  LOC152317 3'  TCTCTCTGTCCCTCCTCA    7724     C          _
                                TC CTTTGTCCCTTC CG
                                || ||||||||||| ||
                                AG GAGACAGGGAGG GT
                                 A          A
GAM296  LOC152404 5'  CTTTATCCATTCATCTGAGA   7725         C   C___
                                CTTTGTCC TTC    GAGA
                                |||||||| |||    ||||
                                GAAATAGG AAG    CTCT
                                     T   TAGA
GAM296  LOC152453 5'  TCTCCTTGTCCTCCTCTGAG   7726     C       _   C
                                TC CTTTGTCC CTTC GAG
                                || |||||||| |||| |||
                                AG GGAACAGG GGAG CTC
                                 A       A    A
GAM296  LOC157681 3'  TCCCTTTTTCTTCCAAG     7727         GTCC
                                TCCCTTT    CTTCCGAG
                                |||||||    ||||||||
                                AGGGAAA    GAAGGTTC
                                    AA__
GAM296  LOC158088 3'  TCACTTTGCGTGTCTTCTGAG  7728     C     CC__    C
                                TC CTTTGT    CTTC GAG
                                || ||||||    |||| |||
                                AG GAAACG    GAAG CTC
                                 T     CACA    A
GAM296  LOC158969 3'  TCCCTTTGTCATTCTTAGA    7729          CC   CG
                                TCCCTTTGTC  TTC  AGA
                                ||||||||||  |||  |||
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                                AGGGAAACAG  AAG  TCT
                                     T_   AA
GAM296  LOC159121 3'  TCCCTCTGTCTCTGTAAAAGA  7730          C  TCC_
                                TCCCTTTGTC CT    GAGA
                                |||||||||| ||    ||||
                                AGGGAGACAG GA    TTCT
                                     A  CATT
GAM296  LOC163682 3'  TCCCTCTGTCTCCAG       7731          CCT   G
                                TCCCTTTGTC   TCC AG
                                |||||||||   ||| ||
                                AGGGAGACAG   AGG TC
                                    ___   _
GAM296  LOC196205 3'  CCCTTTGTTCTCCAGA      7732         CCC    G
                                CCCTTTGT   TTCC AGA
                                ||||||||   |||| |||
                                GGGAAACA   GAGG TCT
                                     A__    _
GAM296  LOC199720 5'  TCCCCTTGAAATACTCCGAG   7733         TCCC_
                                TCCCTTTG    TTCCGAG
                                ||||||||    |||||||
                                AGGGGAAC    GAGGCTC
                                     TTTAT
GAM296  LOC200301 3'  CCTCTGTCTCTTTCTGAG    7734         C   _ C
                                CCTTTGTC CTT C GAG
                                ||||||| ||| | |||
                                GGAGACAG GAA G CTC
                                     A   A A
GAM296  LOC201911 3'  TCCCTCTGTGACCCGGGA    7735          CCCT    A
                                TCCCTTTGT    TCCG GA
                                |||||||||    |||| ||
                                AGGGAGACA    GGGC CT
                                     CT__    C
GAM296  LOC219654 3'  CCTTTGTCCCCTCCACTGAGA  7736              ___
                                CCTTTGTCCCTTCC   GAGA
                                ||||||||||||||   ||||
                                GGAAACAGGGGAGG   CTCT
                                       TGA
GAM296  LOC220038 5'  CCTTTGTCCATCAGAGA     7737         CT  C
                                CCTTTGTCC  TC GAGA
                                |||||||||  || ||||
                                GGAAACAGG  AG CTCT
                                     T_  T
GAM296  LOC220587 3'  CCCTTGTCTACCCCTGAG    7738         CC    _
                                CCTTTGTC  TTCC GAG
                                ||||||||  |||| |||
                                GGGAACAG  GGGG CTC
                                     AT    A
GAM296  LOC221552 5'  TCCCTTCTGAATCTCCGAGA   7739         GTCCC
                                TCCCTTT    TTCCGAGA
                                |||||||    ||||||||
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                                AGGGAAG    GAGGCTCT
                                   ACTTA
GAM296  LOC222112 5'  CCTCTGCCGCTTTTGAGA    7740        C   CC
                                CCTTTGTC CTT  GAGA
                                |||||||| |||  ||||
                                GGAGACGG GAA  CTCT
                                   C   AA
GAM296  LOC222183 3'  TCCCCTCCCTTCTGAG     7741       TTG     C
                                TCCCT   TCCCTTC GAG
                                |||||   ||||||| |||
                                AGGGG   AGGGAAG CTC
                                   ___      A
GAM296  LOC255809 3'  CCTCTGTCCAATTCCCTGAGA  7742         C__   _
                                CCTTTGTCC   TTCC GAGA
                                |||||||||   |||| ||||
                                GGAGACAGG   AGGG CTCT
                                    TTA    A
GAM296  LOC256789 5'  TCTCCTTGGGCTTTCCGAGA   7743    C    TCCC
                                TC CTTTG    TTCCGAGA
                                || |||||    ||||||||
                                AG GGAAC    AAGGCTCT
                                 A    CCGA
GAM296  LOC257493 5'  TCCCTTCTGAATCTCCGAGA   7739       GTCCC
                                TCCCTTT    TTCCGAGA
                                |||||||    ||||||||
                                AGGGAAG    GAGGCTCT
                                   ACTTA
GAM296  LOC257609 5'  TCCCTTCTGAATCTCCGAGA   7739       GTCCC
                                TCCCTTT    TTCCGAGA
                                |||||||    ||||||||
                                AGGGAAG    GAGGCTCT
                                   ACTTA
GAM296  LOC56920  3'  TCCCTTCGTTTTCTAGA     7744        CCC   CG
                                TCCCTTTGT   TTC  AGA
                                |||||||||   |||  |||
                                AGGGAAGCA   AAG  TCT
                                    A__   A_
GAM296  LOC89932  3'  TCCCTTTGCCAGCCAGAGA   7745         CCTT  _
                                TCCCTTTGTC    CC GAGA
                                ||||||||||    || ||||
                                AGGGAAACGG    GG CTCT
                                    TC__  T
GAM296  LOC90538  3'  TCCTCTTGCCCCTGAG      7746     C       TCC
                                TCC TTTGTCCCT   GAG
                                ||| |||||||||   |||
                                AGG GAACGGGGA   CTC
                                  A       ___
GAM296  LOC92340  3'  CCTTTGTCCCCTGCAGA     7747          C G
                                CCTTTGTCCCTT C AGA
                                |||||||||||| | |||
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                                GGAAACAGGGGA G TCT
                                      C _
GAM296  LOC93613  5'  TCTTTTTGTCCCCAAGTTCCGA 7748    CC      ____
            G                  TC  TTTGTCCCT   TCCGAG
                               ||  |||||||||   ||||||
                               AG  AAACAGGGG   AGGCTC
                                AA       TTCA
GAM297  LMCD1    3'  TGTGTCTTTAGTTGGTTGT   7751    _  C__
                               TG GTT   AGTTGGTTGT
                               || |||   ||||||||||
                               AC CAG   TCAACCAACA
                                A  AAA
GAM297  PCDHGA11 5'  CTCGAGCTGGTTGGTTGT   7752    AT   CA
                               CT  GGTT  GTTGGTTGT
                               ||  ||||  |||||||||
                               GA  TCGA  CAACCAACA
                                GC   C_
GAM297  PCDHGA11 5'  CTCGAGCTGGTTGGTTGT   7752    AT   CA
                               CT  GGTT  GTTGGTTGT
                               ||  ||||  |||||||||
                               GA  TCGA  CAACCAACA
                                GC   C_
GAM297  PCDHGA11 5'  CTCGAGCTGGTTGGTTGT   7752    AT   CA
                               CT  GGTT  GTTGGTTGT
                               ||  ||||  |||||||||
                               GA  TCGA  CAACCAACA
                                GC   C_
GAM297  DCTN3    3'  CATCTCTATGGTTTATTG    7753     C      CA
                               TATC CTATGGTT  GTTG
                               ||||  ||||||||  ||||
                               GTAG GATACCAA  TAAC
                                 A      A_
GAM297  DCTN3    3'  CATCTCTATGGTTTATTG    7753     C      CA
                               TATC CTATGGTT  GTTG
                               ||||  ||||||||  ||||
                               GTAG GATACCAA  TAAC
                                 A      A_
GAM297  SLC26A7  3'  CCATGTAAATTGGTTGT    7754      GTTC
                               CTATG   AGTTGGTTGT
                               |||||   ||||||||||
                               GGTAC   TTAACCAACA
                                  AT__
GAM297  LOC146333 5'  TCCCATGGCTCTGGTTGT   7755     T     AGT
                               TCCC ATGGTTC   TGGTTGT
                               ||||  |||||||  |||||||
                               AGGG TACCGAG   ACCAACA
                                 _     ___
GAM298  ITGB7    5'  GTGGGGCAAGTCAGACTTTCTC 7758    AAAA_    TTAT
            T                  GT    AAGTT   CTTTCTCT
                               ||    |||||   ||||||||
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                                CA    TTCAG   GAAAGAGA
                                 CCCCG    TCT_
GAM298  RPP30    3'  CGCAGAACAGTTGTCTTTCTCT 7759      A  A   TTA
                                CGTA AA AGTT   TCTTTCTCT
                                |||| || ||||   |||||||||
                                GCGT TT TCAA   AGAAAGAGA
                                  C  G   C__
GAM298  TAF1C    3'  TGAAAAAAGACCTTTCTC    7760    T     TTTT
                                G AAAAAAG    ATCTTTCTC
                                | |||||||    |||||||||
                                A TTTTTTC    TGGAAAGAG
                                C      _____
GAM298  FLJ13263 3'  AAAAGCTAAAATCTTTCTCT   7761        TT_
                                AAAAGTT   ATCTTTCTCT
                                |||||||   ||||||||||
                                TTTTCGA   TAGAAAGAGA
                                    TTT
GAM298  FLJ23074 5'  AAACCCTTGTCTTTCTCT    7762     G   A
                                AAA TTTT TCTTTCTCT
                                ||| |||| |||||||||
                                TTT GGAA AGAAAGAGA
                                  G   C
GAM298  GTF2A2   3'  GTAAAAAAGTCATATTTTTTCT 7597          T  C_
                                GTAAAAAAGTT TAT  TTTCT
                                |||||||||| |||  |||||
                                CATTTTTTCAG ATA  AAAGA
                                      T  AA
GAM298  IMP-2    3'  TAGAAAAGCCTGCTTTCTCT   7763    A      TAT
                                TA AAAAGTTT   CTTTCTCT
                                || ||||||||   ||||||||
                                AT TTTTCGGA   GAAAGAGA
                                 C       C__
GAM298  KIAA0212 3'  GTAAAAAGATTTACCTTTCT   7764        A T
                                GTAAAAA G TTTATCTTTCT
                                ||||||| | ||||||||||
                                CATTTTT C AAATGGAAAGA
                                    _ T
GAM298  OSBPL2   5'  GTAAGGAATTTTACAAACTTTC 7765      AAA     ___
          TCT                   GTAA   AGTTTTAT   CTTTCTCT
                                ||||   ||||||||   ||||||||
                                CATT   TTAAAATG   GAAAGAGA
                                  CC_      TTT
GAM298  OSBPL2   5'  GTAAGGAATTTTACAAACTTTC 7765      AAA     ___
          TCT                   GTAA   AGTTTTAT   CTTTCTCT
                                ||||   ||||||||   ||||||||
                                CATT   TTAAAATG   GAAAGAGA
                                  CC_      TTT
GAM298  RBM9     3'  ATAAAAAAGTATTCTTTCT   7766          TTTA
                                GTAAAAAAGT    TCTTTCT
                                ||||||||||    |||||||
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                                TATTTTTTCA   AGAAAGA
                                     TA__
GAM298  RNF8     3'  GTAGGAAGTTTCTTTCTC    7767     AAA    TTA
                                GTA  AAGTT  TCTTTCTC
                                |||  |||||  ||||||||
                                CAT  TTCAA  AGAAAGAG
                                  CC_   ___
GAM298  LOC254826 3'  AAAAAGCAAGACTTTCTCT   7768       TTTAT
                                AAAAAGT    CTTTCTCT
                                |||||||    ||||||||
                                TTTTTCG    GAAAGAGA
                                    TTCT_
GAM299  CBFA2T2   3'  CTGTTGTAATGGCTCTGTGA  7771     CA    T_
                                TTG  GTGAT  CTCTGTGA
                                |||  |||||  ||||||||
                                GAC  CATTA  GAGACACT
                                  AA    CC
GAM299  GNAO1     3'  GGTTTGCAGTGGCCTGTG    7772     A      ATTC
                                GGT TTGCAGTG   TCTGTG
                                ||| ||||||||   ||||||
                                CCA AACGTCAC   GGACAC
                                  _      C___
GAM299  IL15RA    3'  GGTATGTCACTTTTCTCTGTGA 7773      TG  G GA
                                GGTAT  CA T  TTCTCTGTGA
                                |||||  || |  ||||||||||
                                CCATA  GT G  AAGAGACACT
                                   CA  _ AA
GAM299  TRIP15    3'  AGTTATTGCAGGTTATTTGTGA 7774     G      TG_   CTC
                                AG TATTGCAG   ATT   TGTGA
                                || ||||||||   |||   |||||
                                TC ATAACGTC   TAA   ACACT
                                 A       CAA   ___
GAM299  ARHGAP8   3'  GGTTTACATTCTCTGTG     7775     A    GTGA
                                GGT TTGCA    TTCTCTGTG
                                ||| |||||    |||||||||
                                CCA AATGT    AAGAGACAC
                                  _    _____
GAM299  G2        5'  GGAGGCATGATTCTCTGTG   7776     TATT   G
                                GG    GCA TGATTCTCTGTG
                                ||    ||| ||||||||||||
                                CC    CGT ACTAAGAGACAC
                                 TC__   _
GAM299  KIAA0978  3'  AGGTATTGCTGTGACAGGTG   7777         A    TCTCT
                                AGGTATTGC GTGAT    GTG
                                ||||||||| |||||    |||
                                TCCATAACG CACTG    CAC
                                     A    TC___
GAM299  LOC115110 3'  GGTGTTGCAGTGGTTTCC    7778     A      A_
                                GGT TTGCAGTG  TTCT
                                ||| ||||||||  ||||
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                                CCA AACGTCAC  AAGG
                                  C       CA
GAM299  LOC115399 3'  AGGTATTCTGTGCTCTGTG   7779        GCA   ATT
                                AGGTATT   GTG   CTCTGTG
                                |||||||   |||   |||||||
                                TCCATAA   CAC   GAGACAC
                                   GA_   ___
GAM299  LOC220692 5'  AGGTACTGCTTTTCTGTG    7780        AGTGA  C
                                AGGTATTGC    TT TCTGTG
                                |||||||||    || ||||||
                                TCCATGACG    AA AGACAC
                                     _____ A
GAM300  CAPN2     3'  TGGTGAAGTTCATAAAGTTTT  7468     A     _    AAA
                                TG TGGAGT CGTAA   AGTTTT
                                || |||||| |||||   ||||||
                                AC ACTTCA GTATT   TCAAAA
                                 C     A    ___
GAM300  DAAM2     3'  TGATGGAGTTTTAGAAAAATTT 7469         CG  A
           T                     TGATGGAGT  TA AAAAGTTTT
                                 |||||||||  || |||||||||
                                 ACTACCTCA  AT TTTTTAAAA
                                      AA  C
GAM300  SELE      3'  TAATGGAAGTGTAGGAGAGTTT 7470        _  C   AAAA
           T                     TGATGGA GT GTA    AGTTTT
                                 |||||||  || |||    ||||||
                                 ATTACCT CA CAT    TCAAAA
                                    T  _   CCTC
GAM300  KIAA0475  3'  TGATGGAATGCAAGGTTTT   7471         C    AAAA
                                TGATGGAGT GTAA    GTTTT
                                |||||||||  ||||    |||||
                                ACTACCTTA CGTT    CAAAA
                                      _    C___
GAM300  LOC222671 5'  TGGCGGAGTCGTAGAAGC    7472     A        AAA
                                TG TGGAGTCGTA   AAGT
                                || ||||||||||   ||||
                                AC GCCTCAGCAT   TTCG
                                 C         C__
GAM300  LOC254901 5'  TGGTGGAGTCAGTGAAGAAATT 7473     A      _  A  A
                                TG TGGAGTC GT AA AAGTT
                                || ||||||| || || |||||
                                AC ACCTCAG CA TT TTTAA
                                 C      T  C  C
GAM300  LOC257615 5'  TGGCGGAGTCGTAGAAGC    7472     A        AAA
                                TG TGGAGTCGTA   AAGT
                                || ||||||||||   ||||
                                AC GCCTCAGCAT   TTCG
                                 C         C__
GAM301  ASGR1     5'  CAGTGCTGTGCAGATGCC    7784          _    _
                                CAGTGCTGTG AGAT CT
                                |||||||||| |||| ||
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                                GTCACGACAC TCTA GG
                                     G   C
GAM301  GOLGA4   5' CAGTTTAGTTTCATCTTGTGCA 7785     GCT  GAG
                                CAGT  GT  ATCTTGTGCA
                                ||||  ||  ||||||||||
                                GTCA  CA  TAGAACACGT
                                  AAT  AAG
GAM301  MRC1     3' GTGCTGTGGTGCTGTGCA   7786       AGATC
                                GTGCTGTG   TTGTGCA
                                ||||||||   |||||||
                                CACGACAC   GACACGT
                                    CAC__
GAM301  RANBP2L1 5' CAGTTCTGTCTGACTTGTGCA 7787     G   GA  T
                                CAGT CTGT  GA CTTGTGCA
                                |||| ||||  || ||||||||
                                GTCA GACA  CT GAACACGT
                                  A   GA  _
GAM301  SCRT1    5' TCCGGCGCTGTGGGCCTGCG  7788    A     AGAT
                                TCC GTGCTGTG   CTTGTG
                                ||| ||||||||   ||||||
                                AGG CGCGACAC   GGACGC
                                  C      CC__
GAM301  TRIM9    3' TCTGGTGCTATGGCCAGAATGT 7789    CA     ___  TCT
           GTG                   TC  GTGCTGTG  AGA  TGTG
                                ||  ||||||||  |||  ||||
                                AG  CACGATAC  TCT  ACAC
                                 AC      CGG  TAC
GAM301  DKFZp434M0331 5' TCCAGGGTTGTGAGTCCTGTA  7790      TGC    A
                                TCCAG  TGTGAG TCTTGTG
                                |||||  |||||| |||||||
                                AGGTC  ACACTC AGGACAT
                                   CCA    _
GAM301  DKFZP547L112 5' TCCAGTGCTGGAATCCAGTGCA 7791         T  A  T
                                TCCAGTGCTG GAG TCT GTGCA
                                |||||||||| ||| ||| |||||
                                AGGTCACGAC CTT AGG CACGT
                                      _  _  T
GAM301  DKFZP586P0123 5' CCTGGTGCTGTGAGATGGC   7792    A_       TCT  T
                                CC  GTGCTGTGAGA  TG GC
                                ||  ||||||||||  || ||
                                GG  CACGACACTCT  AC CG
                                 AC        ___  _
GAM301  KIAA0077 3' TCCAGTCTGTGGGAAGTGC   7793      G    A  TCTT
                                TCCAGT CTGTG GA   GTGC
                                |||||| ||||| ||   ||||
                                AGGTCA GACAC CT   CACG
                                   _    C  T___
GAM301  KIAA0872 3' AGGCTGCTTGTCTTGTGCA   7794    T    GAGA
                                AG GCTGT   TCTTGTGCA
                                || |||||   |||||||||
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                                TC CGACG    AGAACACGT
                                 _    AAC_
GAM301  KIAA1644  3'  CCCAGTGCTGTGGGGGCCAAGC 7795          AGAT  TGT
            A                    TCCAGTGCTGTG    CT   GCA
                                 ||||||||||||    ||   |||
                                 GGGTCACGACAC    GG   CGT
                                       CCCC  TT_
GAM301  MGC3248   3'  GTGCTGTGGGGCCACACTGTG  7796        AG___  C
                                 GTGCTGTG     AT TTGTG
                                 ||||||||     || |||||
                                 CACGACAC     TG GACAC
                                      CCCGG  T
GAM301  TIGD5     3'  TCCAGTGCATGTGACTGGTGCA 7797          _    GAT  T
                                 TCCAGTGC TGTGA   CT GTGCA
                                 |||||||| |||||   || |||||
                                 AGGTCACG ACACT   GA CACGT
                                      T    ____ C
GAM301  LOC169369 5'  TCCATGCTGTGAGATTGTA    7798      G         CT
                                 TCCA TGCTGTGAGAT  TGTG
                                 |||| ||||||||||  ||||
                                 AGGT ACGACACTCTA  ACAT
                                   _         __
GAM301  LOC254826 3'  TCCAGTCTTATCTTGTG     7799        G  GTGAG
                                 TCCAGT CT    ATCTTGTG
                                 |||||| ||    ||||||||
                                 AGGTCA GA     TAGAACAC
                                    _ A_____
GAM301  LOC90231  3'  CAGTGCTGGGTGTCTTGTGCA  7800         TGAGA
                                 CAGTGCTG    TCTTGTGCA
                                 ||||||||    |||||||||
                                 GTCACGAC    AGAACACGT
                                      CCAC_
GAM302  BAIAP3    3'  CTCTGTGTCCTGCCTCGGCG   7803      A  CA      CA
                                 CTCT TG  CTGCTTCG  GCG
                                 |||| ||  ||||||||  |||
                                 GAGA AC  GACGGAGC  CGC
                                   C  AG       __
GAM302  SLC16A1   5'  TATGCGCGGATCGCAGCG    7804       AC  CT
                                 TATGC  TG  TCGCAGCG
                                 |||||  ||  ||||||||
                                 ATACG  GC  AGCGTCGC
                                    C_  CT
GAM302  BIKE      3'  ACTCTATGCTGCTGTGGC    7805         AC    TC_
                                 ACTCTATGC  TGCT   GC
                                 |||||||||  ||||   ||
                                 TGAGATACG  ACGA   CG
                                       __    CAC
GAM302  CDC42BPB  3'  CCCAGTGGCTGCTTCGTGGCG  7806      TA  CA      CA
                                 CTC  TG  CTGCTTCG  GCG
                                 |||  ||  ||||||||  |||
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                                GGG  AC  GACGAAGC  CGC
                                  TC  C_      AC
GAM302  FLJ20507  3'  CACTCTGGCATCACAGCA    7807       AT   CTGCT
                                CACTCT  GCA    TCGCAGCG
                                ||||||  |||    ||||||||
                                GTGAGA  CGT    AGTGTCGT
                                   C_  _____
GAM302  FLJ20507  3'  CACTCTGGCATCACAGCA    7807       AT   CTGCT
                                CACTCT  GCA    TCGCAGCG
                                ||||||  |||    ||||||||
                                GTGAGA  CGT    AGTGTCGT
                                   C_  _____
GAM302  KIAA0992  5'  CACTCTGTGTCTGCTTTCAG   7808       A  CA    CG
                                CACTCT TG  CTGCTT  CAG
                                |||||| ||  ||||||  |||
                                GTGAGA AC  GACGAA  GTC
                                   C  A_     A_
GAM303  AHR       5'  GCCTGGGTCGCTCACGGTG    7811      AGAGA   T
                                GCTT    GTC CTCACGGTG
                                ||||    ||| |||||||||
                                CGGA    CAG GAGTGCCAC
                                  CC___   C
GAM303  TMPRSS3   5'  GCCTGGAGAGTCTTTACAG    7812      A      CTC
                                GCTT GAGAGTCT   ACGG
                                |||| ||||||||   ||||
                                CGGA CTCTCAGA   TGTC
                                  C       AA_
GAM303  ZNF137    3'  TAACTTAGGGGCCGGGCGCGGT 7813         AGA   TCTCA
          G                      TAGCTTAG   GTC    CGGTG
                                |||||||||  |||    |||||
                                ATTGAATC   CGG    GCCAC
                                    CC_   CCCGC
GAM303  SBBI31    3'  GCTGAGAAAATCTCACGGTG   7814     TA    TC
                                GCT  GAGAG  TCTCACGGTG
                                |||  |||||  ||||||||||
                                CGA  CTCTT  AGAGTGCCAC
                                  __     TT
GAM304  ASTN      3'  CAGCAGCTCCCTGGCCTTATG  7817        GCA  GGC
                                CAGCAGC   TC   GCCTTATG
                                |||||||   ||   ||||||||
                                GTCGTCG   GG   CGGAATAC
                                   AG_  AC_
GAM304  ANAPC11   3'  CAGCAGCCATCGGCGCCAGCAT 7818         G       T_
          GA                     CAGCAGC CATCGGCGCC  TATGA
                                ||||||| ||||||||||  |||||
                                GTCGTCG GTAGCCGCGG  GTACT
                                   _        TC
GAM304  LOC129401 5'  AACGGCGTGCTACCTTATG   7819      CAT  _  _
                                AGCG   CG GC GCCTTATG
                                ||||   || || ||||||||
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                                TTGC   GC CG TGGAATAC
                                  C__  A  A
GAM304  LOC132617 5'  CAGCAGCGTGGCGGCGACG   7820        CAT    CCTT
                                CAGCAGCG   CGGCG    ATG
                                ||||||||   |||||    |||
                                GTCGTCGC   GCCGC    TGC
                                    ACC    ____
GAM304  LOC255792 5'  CAGCAGCGTAGTGCCTTGTGA  7821        CATC  C    A
                                CAGCAGCG    GG GCCTT TGA
                                ||||||||    || ||||| |||
                                GTCGTCGC    TC CGGAA ACT
                                    A___  A    C
GAM305  BHLHB3   3'  TCCCTGACTTAGTTCTGACGAT 7824     A    ATCAACC
          G                      TC CCTGG      CTGACGATG
                                || |||||      |||||||||
                                AG GGACT      GACTGCTAC
                                 _    GAATCAA
GAM305  MEFV     3'  TCACCCGGATTGACTAACA   7825          CAACC
                                TCACCTGGAT    CTGACG
                                ||||||||||    ||||||
                                AGTGGGCCTA    GATTGT
                                    ACT__
GAM305  MEPE     3'  TCACCTGGTCAGCTGTCA    7826         A   ACC   A
                                TCACCTGG TCA   CTG CG
                                |||||||| |||   ||| ||
                                AGTGGACC AGT   GAC GT
                                    _   C__   A
GAM305  FKSG42   5'  TCACCTGGGCAGCCCTTCAC   7827         AT  A    G_
                                TCACCTGG  CA CCCT  AC
                                ||||||||  || ||||  ||
                                AGTGGACC  GT GGGA  TG
                                    C_  C    AG
GAM305  FLJ10895 3'  CCATCTGGATCAGTCCATCAC  7828      C       AC  TG_
                                TCA CTGGATCA  CC   AC
                                ||| ||||||||  ||   ||
                                GGT GACCTAGT  GG   TG
                                  A       CA  TAG
GAM305  KIAA0987 3'  CCTGGATCGACCTGTGATG   7829         AAC    AC
                                CCTGGATC   CCTG  GATG
                                ||||||||   ||||  ||||
                                GGACCTAG   GGAC  CTAC
                                    CT_    A_
GAM305  PRO0899  3'  TCACCTGGTCAGCCCTATCCA  7830         A  A    A_
                                TCACCTGG TCA CCCTG  CG
                                |||||||| ||| |||||  ||
                                AGTGGACC AGT GGGAT  GT
                                    _  C    AG
GAM305  TCL6     3'  TCACTTGAATCAATTTACA   7831       C       CCCTG
                                TCAC TGGATCAA     ACG
                                |||| ||||||||     |||
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                                AGTG ACTTAGTT    TGT
                                  A       AAA__
GAM305  TCL6     3'  TCACTTGAATCAATTTACA   7831      C      CCCTG
                                TCAC TGGATCAA    ACG
                                |||| ||||||||    |||
                                AGTG ACTTAGTT    TGT
                                  A       AAA__
GAM305  TREX1    5'  TCACCTGGTCAAACTGA    7832        A   CC
                                TCACCTGG TCAA  CTGA
                                |||||||| ||||  ||||
                                AGTGGACC AGTT  GACT
                                     _    T_
GAM305  TREX1    5'  TCACCTGGTCAAACTGA    7832        A   CC
                                TCACCTGG TCAA  CTGA
                                |||||||| ||||  ||||
                                AGTGGACC AGTT  GACT
                                     _    T_
GAM305  LOC149603 5'  CCGCCTGGATCCTAGCG    7833    A     CAAC   A
                                TC CCTGGAT    CCTG CG
                                || |||||||    |||| ||
                                GG GGACCTA    GGAT GC
                                 C      _____    C
GAM306  RASA1    3'  CAGAATCTTGGATTTTGT    7836       C
                                TAGAATC TGGATTTTGT
                                ||||||| ||||||||||
                                GTCTTAG ACCTAAAACA
                                    A
GAM306  C11orf25  3'  GAATCTTAGATTTTTGGTT   7837      C      GTAG
                                GAATC TGGATTTT    GGTT
                                ||||| ||||||||    ||||
                                CTTAG ATCTAAAA    CCAA
                                   A       A___
GAM306  CDA02    3'  TAGAATCTTGGATAAATGGTT  7838       C    TTTGTAG
                                TAGAATC TGGAT      GGTT
                                ||||||| |||||      ||||
                                ATCTTAG ACCTA      CCAA
                                    A    TTTA___
GAM306  IL14     5'  AATTTTGGATTTTGTGGGT   7839     CC       A
                                AAT  TGGATTTTGT GGGT
                                |||  |||||||||| ||||
                                TTA  ACCTAAAACA CCCA
                                  AA         _
GAM306  NIFU     5'  TAGAATCCTGGTTCGGT     7840          A   T
                                TAGAATCCTGG TTT GT
                                |||||||||| ||| ||
                                ATCTTAGGACC AAG CA
                                       _  C
GAM306  PRO0628  3'  TAGAATTATGGATTTTCTA   7841       CC      G
                                TAGAAT  TGGATTTT TA
                                ||||||  |||||||| ||
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                                ATCTTA  ACCTAAAA AT
                                   AT       G
GAM306  LOC124460 5'  GAATTTGGATGCAGGGT     7842      CC    TTT
                                GAAT  TGGA   TGTAGGGT
                                ||||  ||||   ||||||||
                                CTTA  ACCT   ACGTCCCA
                                  A_   ____
GAM306  LOC144486 3'  AAATTTTGGTAAATAGGGTT   7843      CC   ATTTT
                                GAAT  TGG    GTAGGGTT
                                ||||  |||    ||||||||
                                TTTA  ACC    TATCCCAA
                                  AA   ATT__
GAM306  LOC51145  3'  TAGAATTCTGTGGTTTTGCA   7844       C   GA_
                                TAGAAT CTG   TTTTGTA
                                ||||||| |||   |||||||
                                ATCTTA GAC   AAAACGT
                                   A   ACC
GAM307  CAPN2     3'  TGGTGAAGTTCATAAAGTTTT  7468     A     _    AAA
                                TG TGGAGT CGTAA   AGTTTT
                                || ||||||| |||||   ||||||
                                AC ACTTCA GTATT   TCAAAA
                                 C     A    ____
GAM307  DAAM2     3'  TGATGGAGTTTTAGAAAAATTT 7469          CG  A
           T                     TGATGGAGT  TA AAAAGTTTT
                                 |||||||||  || |||||||||
                                 ACTACCTCA  AT TTTTTAAAA
                                       AA  C
GAM307  SELE      3'  TAATGGAAGTGTAGGAGAGTTT 7470         _  C   AAAA
           T                     TGATGGA GT GTA    AGTTTT
                                 |||||||| || |||    ||||||
                                 ATTACCT CA CAT    TCAAAA
                                     T  _   CCTC
GAM307  KIAA0475  3'  TGATGGAATGCAAGGTTTT    7471          C    AAAA
                                 TGATGGAGT GTAA    GTTTT
                                 |||||||||| ||||    |||||
                                 ACTACCTTA CGTT    CAAAA
                                       _    C____
GAM307  LOC222671 5'  TGGCGGAGTCGTAGAAGC     7472     A        AAA
                                 TG TGGAGTCGTA   AAGT
                                 || ||||||||||   ||||
                                 AC GCCTCAGCAT   TTCG
                                  C         C__
GAM307  LOC254901 5'  TGGTGGAGTCAGTGAAGAAATT 7473     A      _  A  A
                                 TG TGGAGTC GT AA AAGTT
                                 || ||||||| || || |||||
                                 AC ACCTCAG CA TT TTTAA
                                  C      T  C  C
GAM307  LOC257615 5'  TGGCGGAGTCGTAGAAGC     7472     A        AAA
                                 TG TGGAGTCGTA   AAGT
                                 || ||||||||||   ||||
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                                AC GCCTCAGCAT   TTCG
                                 C        C__
GAM308  ID3     3'  GGAGATACTCACCTGGAGG   7848     AA       GC  A
                                GGA  GTACTCGCC  TG AGG
                                |||  |||||||||  || |||
                                CCT  TATGAGTGG  AC TCC
                                  C_        __  C
GAM308  BAG2    5'  GGAGGACTCGCCGACACCGCG  7849     AA T      _ TGAAG
                                GGA  G ACTCGCCG C    GCG
                                |||  | ||||||| |    |||
                                CCT  C TGAGCGGC G    CGC
                                  __ C       T TGG__
GAM308  C20orf102 3'  GGAAGGACTCGCCAGGAGG   7850      A T      CT  A
                                GGAA G ACTCGCCG  GA GG
                                ||||  | ||||||||  || ||
                                CCTT C TGAGCGGT  CT CC
                                  _ C       C_  _
GAM308  FLJ10193  3'  GGAAGGGAGCAAGAGCTGAAGG 7851      ___   CTCGCC
            CG                    GGAA   AGTA     GCTGAAGGCG
                                ||||   ||||     ||||||||||
                                CCTT   TCGT     CGACTTCCGC
                                  CCC    TCT___
GAM308  FLJ14251  5'  GAAGTACTTGCCGAAGGCG   7852     A    CGCC
                                GAA GTACT    GCTGAAGGCG
                                ||| |||||    ||||||||||
                                CTT CATGA    CGGCTTCCGC
                                  _    A___
GAM308  FLJ22174  3'  GGAAGTGTTCGCCGCTA     7853      A  AC
                                GGAA GT  TCGCCGCTG
                                ||||  ||  |||||||||
                                CCTT CA  AGCGGCGAT
                                  _  CA
GAM308  KIAA1145  3'  GGAAAGTATCATCTGGGCTGAA 7854        C__  GCC
            GGCG                    GGAAAGTA   TC   GCTGAAGGCG
                                ||||||||   ||   ||||||||||
                                CCTTTCAT   AG   CGACTTCCGC
                                     AGT  ACC
GAM308  LOC221751 3'  GGAAGTGTTCGCCGCTA     7853      A  AC
                                GGAA GT  TCGCCGCTG
                                ||||  ||  |||||||||
                                CCTT CA  AGCGGCGAT
                                  _  CA
GAM309  BAI3    3'  CTTCCCAAGTCTTAAGTG    7857        ACAC   GTTT
                                CTTCCCAA    TCT    GGTG
                                ||||||||    |||    ||||
                                GAAGGGTT    AGA    TCAC
                                     C___   AT__
GAM309  BDKRB2   3'  CTTCCCAAAGGCTTCTGAGTGT 7858         CA  _   TTT
                                CTTCCCAAA  CT CTG   GGTGT
                                |||||||||  || |||   |||||
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                                GAAGGGTTT  GA GAC   TCACA
                                     CC  A  ___
GAM309  DDEF1    3'  TTCCTCATGCTCTGTTTGGTGT 7859      _  AACA
                                TTCC CA   CTCTGTTTGGTGT
                                |||| ||   ||||||||||||
                                AAGG GT   GAGACAAACCACA
                                  A  AC__
GAM309  DDIT3    5'  CTTCTTGAACACTCTCTCC   7860      CCA      G
                                CTTC  AACACTCT TTT
                                ||||  |||||||| |||
                                GAAG  TTGTGAGA AGG
                                  AAC       G
GAM309  GLRX     3'  TTCACAGATACACTCTTGGTGT 7861     C  A__     GTT
                                TTC CA  ACACTCT  TGGTGT
                                ||| ||  |||||||  ||||||
                                AAG GT  TGTGAGA  ACCACA
                                  T  CTA     ___
GAM309  GUCY2F   5'  TTCCCGACACAGACGGTGGTGT 7862      AA   TCTGTT
                                TTCCC  ACAC     TGGTGT
                                |||||  ||||     ||||||
                                AAGGG  TGTG     ACCACA
                                   C_   TCTGCC
GAM309  HDGF     3'  CTTCCCAAGCATCCTATTTG  7863        A  CT
                                CTTCCCAA CA  CTGTTTG
                                |||||||| ||  |||||||
                                GAAGGGTT GT  GATAAAC
                                     C  AG
GAM309  MCL1     3'  TTCCCAAACCACTTGGGGTGT  7864        ACT  GTTT
                                TTCCCAAAC  CT   GGTGT
                                |||||||||  ||   |||||
                                AAGGGTTTG  GA   CCACA
                                     GT_  ACC_
GAM309  MYO15A   3'  TTCCCAAACTTCTCCCTTG   7865        A_   G
                                TTCCCAAAC  CTCT TTTG
                                |||||||||  |||| ||||
                                AAGGGTTTG  GAGG GAAC
                                     AA   _
GAM309  PER2     3'  CTTCCAAGCACCACCTGGTGT  7866      C  A   CT TT
                                CTTCC AA CACT  G  TGGTGT
                                ||||| || ||||  |  ||||||
                                GAAGG TT GTGG  T  ACCACA
                                   _ C   __ GG
GAM309  PTER     3'  CTTCCCAAGAGTTATGCATGGT 7867        ACACTC   T
           GT                    CTTCCCAA     TGT TGGTGT
                                ||||||||     ||| ||||||
                                GAAGGGTT     ACG ACCACA
                                     CTCAAT   T
GAM309  RNF17    3'  CTTCTCCAGTACTTTGGCG   7868      _  AAC   CTGT
                                CTTC CCA   ACT    TTGGTG
                                |||| |||   |||   ||||||
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                                GAAG GGT   TGA    AACCGC
                                  A  CA_  ____
GAM309  SMCY     3'  TTCCCAAACATACTCATTG   7869          CT  GT
                                TTCCCAAACA  CT  TTG
                                ||||||||||  ||  |||
                                AAGGGTTTGT  GA  AAC
                                      AT  GT
GAM309  SOCS5    3'  TTCTCAAACACTTTGGT     7870      C       CTGT
                                TTC CAAACACT    TTGGT
                                ||| ||||||||    |||||
                                AAG GTTTGTGA    AACCA
                                  A       ____
GAM309  SORCS1   3'  TTCCAACACTTTGTCT      7871       CA     C
                                TTCC  AACACT TGTTT
                                ||||  |||||| |||||
                                AAGG  TTGTGA ACAGA
                                  __      A
GAM309  USP9Y    5'  CCTCCTAAATATCTGGTG    7872       C   CACTC
                                CTTCC AAA     TGTTTGGTG
                                ||||| |||     |||||||||
                                GGAGG TTT     ATAGACCAC
                                  A  _____
GAM309  ZNF135   3'  TTCTGGAACACTCTGCCATACT 7873      CCA         _  G
           GT                     TTC   AACACTCTGTT TG TGT
                                |||   |||||||||||| || |||
                                AAG   TTGTGAGACGG AT ACA
                                  ACC          T  G
GAM309  CHSY1    3'  TCCCCAACGTTTTGATTAGGGT 7874         ACACTCT   T_
           GT                     TTCCCAA      GTT  GGTGT
                                |||||||      |||  |||||
                                AGGGGTT      TAA  CCACA
                                    GCAAAAC   TC
GAM309  CLIPR-59 3'  CTTCCAGGACTGTTTTGGTGT  7875       CAAACACT     _
                                CTTCC       CTGTTT GGTGT
                                |||||       |||||| |||||
                                GAAGG       GACAAA CCACA
                                   TCCT____     A
GAM309  DKFZP761D0211 3'  CTTCCCAGGACGTTTAGTG   7876         AACACTC
                                CTTCCCA      TGTTTGGTG
                                |||||||      |||||||||
                                GAAGGGT      GCAAATCAC
                                    CCT____
GAM309  FLJ10847  3'  TTCCCAACTGTTTTTCAGTGT  7877         ACACT     ___
                                TTCCCAA    CTGTTT   GGTGT
                                |||||||    ||||||   |||||
                                AAGGGTT    GACAAA   TCACA
                                    _____     AAG
GAM309  FLJ12606  5'  CTTCCCGGGTGTCCTGGCG   7878        AAACACTC   _
                                CTTCCC       TGTT TGGTG
                                ||||||       |||| |||||
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                                GAAGGG       ACAG ACCGC
                                   CCC_____   G
GAM309  FLJ13352  3' TTCCTGAAACTTTTGGTG    7879      CA  C   CTG
                                TTCC  AA ACT   TTTGGTG
                                ||||  || |||   |||||||
                                AAGG  TT TGA   AAACCAC
                                  AC  _  ___
GAM309  FLJ13725  5' CTTCCCGGGGACCCAGTGGTGT 7880       AAAC    TGTT
                                CTTCCC    ACTC    TGGTGT
                                ||||||    ||||    ||||||
                                GAAGGG    TGGG    ACCACA
                                   CCCC    TC__
GAM309  FLJ14213  3' TTCCCAGGAGCTCTGCTTG   7881       AACA
                                TTCCCA    CTCTGTTTG
                                ||||||    |||||||||
                                AAGGGT    GAGACGAAC
                                   CCTC
GAM309  FLJ20073  3' TTCCCAGACATTCTAATGT    7882       A   C    TTTG
                                TTCCCA ACA TCTG    GTGT
                                |||||| ||| ||||    ||||
                                AAGGGT TGT AGAT    TACA
                                   C   A   _____
GAM309  FLJ20558  3' TTCCAACACTGTTGGTG     7883      CA     CTGT
                                TTCC  AACACT    TTGGTG
                                ||||  ||||||    ||||||
                                AAGG  TTGTGA    AACCAC
                                  __      C___
GAM309  FLJ22031  3' TTCATGAACACTCTGAAAGT   7884     CCA       TTT
                                TTC   AACACTCTG   GGT
                                |||   |||||||||   |||
                                AAG   TTGTGAGAC   TCA
                                  TAC       TT_
GAM309  FLJ23588  5' CTTTTCAAACTCTCTTGGTGT  7885     CC    A   GTT
                                CTT  CAAAC CTCT   TGGTGT
                                |||  ||||| ||||   ||||||
                                GAA  GTTTG GAGA   ACCACA
                                  AA    A   ___
GAM309  FOXP1    5' CTTCTGGGACACTCTGGCTG   7886      CCAA      T
                                CTTC    ACACTCTG TTG
                                ||||    |||||||| |||
                                GAAG    TGTGAGAC GAC
                                  ACCC       C
GAM309  KIAA0319  3' TTCTCTGGCACTCCTGCCCTGG 7887     CCAAA    _   _
           TGT                    TTC     CACTC TGTT TGGTGT
                                |||     ||||| |||| ||||||
                                AAG     GTGAG ACGG ACCACA
                                  AGACC    G   G
GAM309  KIAA1045  3' CTTCCCAGGCAGTTTAATGC   7888        AA  CTCT
                                CTTCCCA  CA   GTTTGGTGT
                                |||||||  ||   |||||||||
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                                GAAGGGT GT   CAAATTACG
                                   CC ____
GAM309  KIAA1246 3' CTTTCCAAACACTCAGGGCTCA 7889     C       T__  TG
          GT                    CTT CCAAACACTC  GTT GT
                                ||| ||||||||||  ||| ||
                                GAA GGTTTGTGAG  CGA CA
                                  A       TCC  GT
GAM309  KIAA1915 3' CTTCTCAAACTTCTGTT    7890     C    AC
                                CTTC CAAAC TCTGTT
                                |||| |||||  ||||||
                                GAAG GTTTG AGACAA
                                  A   A_
GAM309  LOXL4   3' CTTCTCAAGCACTCCGTAACTG 7891     C  A      TTGG
          T                     CTTC CAA CACTCTGT   TGT
                                |||| ||| ||||||||   |||
                                GAAG GTT GTGAGGCA   ACA
                                  A  C      TTG_
GAM309  MGC5566  3' CTTCCTGGCACTCTTAGTTTG 7892      CAAA    __
                                CTTCC   CACTCT GTTTG
                                |||||   ||||||  |||||
                                GAAGG   GTGAGA CAAAC
                                   ACC_    AT
GAM309  NDRG4   3' CTGCCCAAACATTCTGTT   7893    T     C
                                CT CCCAAACA TCTGTT
                                || |||||||| ||||||
                                GA GGGTTTGT AGACAA
                                 C      A
GAM309  NDRG4   3' CTGCCCAAACATTCTGTT   7893    T     C
                                CT CCCAAACA TCTGTT
                                || |||||||| ||||||
                                GA GGGTTTGT AGACAA
                                 C      A
GAM309  NR5A1   3' CTTCCCAAACACACAGTG   7894         TCTGTTT
                                CTTCCCAAACAC     GGTG
                                ||||||||||||     ||||
                                GAAGGGTTTGTG     TCAC
                                      TG_____
GAM309  SC65    3' CTTCCCAAGCTTGAGCGGTGT 7895       ACA C TT
                                CTTCCCAA  CT TG  TGGTGT
                                ||||||||  || ||  ||||||
                                GAAGGGTT  GA AC  GCCACA
                                    C__  _  TC
GAM309  SLC37A1  3' CTTCCCAAACCTCTGCT    7896         A
                                CTTCCCAAAC CTCTGTT
                                |||||||||| |||||||
                                GAAGGGTTTG GAGACGA
                                          _
GAM309  UXS1    5' CTTCCTGATGCTCTCCACAGTG 7897      CAAACA   GTT
          T                     CTTCC    CTCT  TGGTGT
                                |||||    ||||  ||||||
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                                GAAGG     GAGA   GTCACA
                                   ACTAC_    GGT
GAM309   LOC126669 3'  CTTTTCAAACACTTCTGTATAG 7898      CC       _    T
            T                    CTT  CAAACACT CTGT TGGT
                                 |||  |||||||| |||| ||||
                                 GAA  GTTTGTGA GACA ATCA
                                   AA       A    T
GAM309   LOC144305 3'  CTTCCCAGGTTCCTGGTG    7899        AACAC   GTT
                                 CTTCCCA    TCT   TGGTG
                                 |||||||    |||  |||||
                                 GAAGGGT    AGG   ACCAC
                                     CCA__   ___
GAM309   LOC146733 5'  CTTCCCCAGCCGTTTGGTG   7900        AAACACT
                                 CTTCCC      CTGTTTGGTG
                                 ||||||      ||||||||||
                                 GAAGGG      GGCAAACCAC
                                     GTC____
GAM309   LOC146952 5'  TTCCCAAACACTTTGGTG    7901           CTGT
                                 TTCCCAAACACT    TTGGTG
                                 ||||||||||||    ||||||
                                 AAGGGTTTGTGA    AACCAC
                                                 _____
GAM309   LOC149302 5'  TTCCTAAACACTTGGT      7902       C      CTGTT
                                 TTCC AAACACT     TGGT
                                 |||| |||||||     ||||
                                 AAGG TTTGTGA     ACCA
                                   A      ______
GAM309   LOC153630 5'  CTTCCCAAGTCTCTGCCT    7903         ACA
                                 CTTCCCAA   CTCTGTTT
                                 ||||||||   ||||||||
                                 GAAGGGTT   GAGACGGA
                                     CA_
GAM309   LOC153937 5'  TTCTCAATATTCTCTGCTGTGT 7904      C   ACA_      TG
                                 TTC CAA    CTCTGTT  GTGT
                                 ||| |||    |||||||  ||||
                                 AAG GTT    GAGACGA  CACA
                                   A   ATAA      __
GAM309   LOC157860 3'  TTCCCAATGCTTCCATGGTGT  7905        ACAC    TT
                                 TTCCCAA    TCTG  TGGTGT
                                 |||||||    ||||  ||||||
                                 AAGGGTT    AGGT  ACCACA
                                     ACGA    __
GAM309   LOC158954 3'  TTCTGGAACACTCTGCCATATT 7906      CCA         TGG_
            GT                     TTC   AACACTCTGTT    TGT
                                   |||   ||||||||||    |||
                                   AAG   TTGTGAGACGG    ACA
                                     ACC          TATA
GAM309   LOC165568 5'  CTTCCCAAGCATGTTTACTGT  7907         A  CTC     G
                                 CTTCCCAA CA   TGTTTG TGT
                                 |||||||| ||   |||||| |||
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                                GAAGGGTT GT   ACAAAT ACA
                                    C ___     G
GAM309  LOC169436 5'  CTTCCCAGGGACTCTGTCCTGG 7908        AAC      _
          T                      CTTCCCA   ACTCTGTT TGGT
                                 |||||||   |||||||| ||||
                                 GAAGGGT   TGAGACAG ACCA
                                    CCC       G
GAM309  LOC200627 5'  TTCCCAATATTCCTTCCTTGGT 7909        ACAC   G_
          GT                     TTCCCAA    TCT  TTTGGTGT
                                 |||||||    |||  ||||||||
                                 AAGGGTT    GGA  GAACCACA
                                    ATAA   AG
GAM309  LOC203042 5'  TTCCCAACTGCTTTGGT     7910        ACACT     _
                                 TTCCCAA    CTGTTT GGT
                                 |||||||    |||||| |||
                                 AAGGGTT    GACGAA CCA
                                    _____     A
GAM309  LOC220567 3'  CTTCCCAGACGTCTGGT     7911        A  ACTCT
                                 CTTCCCA AC    GTTTGGT
                                 ||||||| ||    |||||||
                                 GAAGGGT TG    CAGACCA
                                    C _____
GAM309  LOC221400 3'  TTCTCAAATACTCTGTTGGT   7912     C   C      T
                                 TTC CAAA ACTCTGTT GGT
                                 ||| |||| |||||||| |||
                                 AAG GTTT TGAGACAA CCA
                                   A   A      _
GAM309  LOC221718 3'  TTCCCAAACGTTTCCCAAATGT 7913        AC_   GTTT
                                 TTCCCAAAC   TCT   GGTGT
                                 |||||||||   |||   |||||
                                 AAGGGTTTG   AGG   TTACA
                                      CAA   GT__
GAM309  LOC90092  5'  TTCTGAACCATCCACCTGGTGT 7914     CCA   AC  TG
                                 TTC   AAC  TC  TTTGGTGT
                                 |||   |||  ||  ||||||||
                                 AAG   TTG  AG  GGACCACA
                                   AC_   GT  GT
GAM309  LOC90309  3'  CTCCCAAATGTTTGT       7915        CACTC     G
                                 TTCCCAAA    TGTTTG T
                                 ||||||||    |||||| |
                                 GAGGGTTT    ACAAAC A
                                    _____     _
GAM309  LOC90334  3'  TTCCCAAGTCCTCTGTTCTGT  7916        ACA       G
                                 TTCCCAA   CTCTGTTT GT
                                 |||||||   |||||||| ||
                                 AAGGGTT   GAGACAAG CA
                                    CAG       A
GAM309  LOC90906  3'  TTCCGGAACTCTGAGGCTGGT  7917      CAAAC     T__
                                 TTCC    ACTCTG   TTGGT
                                 ||||    ||||||   |||||
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                                AAGG    TGAGAC   GACCA
                                  CCT__     TCC
GAM309  LOC91445  3'  AAACACTGAACTCTGGTGT   7918        CTG_
                                AAACACT    TTTGGTGT
                                |||||||    ||||||||
                                TTTGTGA    AGACCACA
                                    CTTG
GAM310  CHAC      3'  GCTTTAAAAATTCTCCTTTGAT 7921        TCTCT       C
                                GTTTTA     TTCTCCTT GAT
                                ||||||     |||||||| |||
                                CGAAAT     AAGAGGAA CTA
                                   TTTT_       A
GAM310  CHD1      5'  GTTTTCTGGGACTCTCCTTTGA 7922        ATCTCT       C
           T                     GTTTT      TTCTCCTT GAT
                                 |||||      |||||||| |||
                                 CAAAA      GAGAGGAA CTA
                                   GACCCT       A
GAM310  CYFIP1    3'  AGTTTTATTTCTATAACCTTTC 7923         C   TTCT   _
           GAT                    AGTTTTAT TCT    CCTT CGAT
                                  |||||||| |||    |||| ||||
                                  TCAAAATA AGA    GGAA GCTA
                                      A   TATT    A
GAM310  ABCA5     5'  AGTGGTACTTTTTCTCCTT    7924      TT  T  C
                                  AGT  TA CT TTTCTCCTT
                                  |||  || || |||||||||
                                  TCA  AT GA AAAGAGGAA
                                    CC  _  A
GAM310  LOC152579 3'  AGTTTTATCTCTTTATTACCAA 7925             CTCCT
           C                      AGTTTTATCTCTTT     TCGAT
                                  ||||||||||||||     |||||
                                  TCAAAATAGAGAAA     GGTTG
                                          TAAT_
GAM310  LOC55893  3'  GTTTCCGTTCTTTCTCTTTCG  7926       ATC       C
                                  GTTTT   TCTTTCTC TTCG
                                  |||||   |||||||| ||||
                                  CAAAG   AGAAAGAG AAGC
                                     GCA       A
GAM311  ABP1      3'  GATCACAGTGTCTCTG      7929      G     AT
                                  GA CGCGG  TGTCTCTG
                                  || |||||  ||||||||
                                  CT GTGTC  ACAGAGAC
                                   A    __
GAM311  ACADM     5'  GAACGCGGGACTCCTCTG    7930         _   G
                                  GAGCGCGG ATT TCTCTG
                                  |||||||| ||| ||||||
                                  CTTGCGCC TGA GGAGAC
                                       C   _
GAM311  AK2       3'  AAGCTGCCTTGTCTCTG     7931       _  GGA
                                  GAGC GC   TTGTCTCTG
                                  |||| ||   |||||||||
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                                TTCG CG   AACAGAGAC
                                  A  G__
GAM311  BCL10    5'  GAGCCCGCCCTGTCTCTG    7932      G  GA
                                GAGC CG  TTGTCTCTG
                                |||| ||  |||||||||
                                CTCG GC  GACAGAGAC
                                  G  GG
GAM311  CCND3    5'  GAGCGCGGGGCGCGGGTCTG  7933        AT   C__
                                GAGCGCGG  TGT   TCTG
                                ||||||||  |||   ||||
                                CTCGCGCC  GCG   AGAC
                                     CC   CCC
GAM311  CHAC     5'  GAGCGCGGTGCAGACCTG    7934        AT   C__
                                GAGCGCGG  TGT   TCTG
                                ||||||||  |||   ||||
                                CTCGCGCC  ACG   GGAC
                                     __   TCT
GAM311  CHAC     5'  GAGCGCGGTGCAGACCTG    7934        AT   C__
                                GAGCGCGG  TGT   TCTG
                                ||||||||  |||   ||||
                                CTCGCGCC  ACG   GGAC
                                     __   TCT
GAM311  COL4A2   5'  GAGCGCGGAGCCCTG      7935         TT   T
                                GAGCGCGGA  GTC CTG
                                |||||||||  ||| |||
                                CTCGCGCCT  CGG GAC
                                     __   _
GAM311  DMRT2    3'  GAACGCGGACCTCTCTG     7936          G
                                GAGCGCGGATT TCTCTG
                                |||||||||||| ||||||
                                CTTGCGCCTGG AGAGAC
                                     _
GAM311  FBXL7    3'  GAGGCATCTGTCTCTG      7937      C   GA
                                GAG GCG  TTGTCTCTG
                                ||| |||  |||||||||
                                CTC CGT  GACAGAGAC
                                  _  A_
GAM311  HIP1     3'  GAGCACGGGTCTCACTCTG   7938         A  GT_
                                GAGCGCGG TT   CTCTG
                                ||||||||  ||   |||||
                                CTCGTGCC AG   GAGAC
                                     C  AGT
GAM311  HR       5'  GAGCGCAGCACGACCTCTG   7939         _  TG
                                GAGCGCGG AT  TCTCTG
                                ||||||||  ||  ||||||
                                CTCGCGTC TG  GGAGAC
                                     G  CT
GAM311  IKBKG    5'  GAACAGAATATGTCTCTG    7940       C   _
                                GAGCG GGAT TGTCTCTG
                                ||||| |||| ||||||||
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                                CTTGT CTTA ACAGAGAC
                                  _   T
GAM311  ITGA4   5' GAGCGCGGGATGGCTCTG   7941       AT  T
                                GAGCGCGG  TG CTCTG
                                ||||||||  || |||||
                                CTCGCGCC  AC GAGAC
                                    CT  C
GAM311  JTB     5' GAGGCGGCACTTACTCTG   7942     C   _  GT
                                GAG GCGG ATT  CTCTG
                                ||| |||| |||  |||||
                                CTC CGCC TGA  GAGAC
                                  _   G  AT
GAM311  MAPK4   3' AAGCGAGTGTCTCTG      7943      C  AT
                                GAGCG GG  TGTCTCTG
                                ||||| ||  ||||||||
                                TTCGC TC  ACAGAGAC

                                  _ __
GAM311  MEOX2   3' GCACATACTGATTGTCTCTG  7944      ____
                                GCGCG   GATTGTCTCTG
                                |||||   ||||||||||
                                CGTGT   CTAACAGAGAC
                                   ATGA
GAM311  MSX1    5' GAGCGCGGCCGGCCTCTG   7945       ATT
                                GAGCGCGG  GTCTCTG
                                ||||||||  |||||||
                                CTCGCGCC  CGGAGAC
                                    GGC
GAM311  NEBL    5' GAGATGCTGACGTCTCTG   7946    C_  G  T
                                GAG  GC GAT GTCTCTG
                                |||  || ||| |||||||
                                CTC  CG CTG CAGAGAC
                                  TA  A  _
GAM311  PTPRF   5' GAGCCGCCGCCTCTG      7947     G  GA
                                GAGC CG  TTGTCTCTG
                                |||| ||  |||||||||
                                CTCG GC  GGCGGAGAC

                                  _ __
GAM311  PTPRF   5' GAGCCGCCGCCTCTG      7947     G  GA
                                GAGC CG  TTGTCTCTG
                                |||| ||  |||||||||
                                CTCG GC  GGCGGAGAC

                                  _ __
GAM311  TMEPAI  3' AAGCGCGGAGTGTTCTG    7948       T  C
                                GAGCGCGGA TGT TCTG
                                ||||||||| ||| ||||
                                TTCGCGCCT ACA AGAC
                                    C  _
GAM311  VDR     3' GAGGTGCAGGTGTCTCTG   7949    C_   AT
                                GAG  GCGG  TGTCTCTG
                                |||  ||||  ||||||||
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                                CTC  CGTC  ACAGAGAC
                                  CA   C_
GAM311  VIM      5' GAGCGCGGCTGCGTCTCTG   7950        AT_
                                GAGCGCGG  TGTCTCTG
                                ||||||||  ||||||||
                                CTCGCGCC  GCAGAGAC
                                    GAC
GAM311  ZNF36    3' GAGCACACATCTCTG      7951        GAT
                                GAGCGCG  TGTCTCTG
                                |||||||  ||||||||
                                CTCGTGT  GTAGAGAC
                                   ___
GAM311  DIM1     3' GAGCACACATCTCTG      7951        GAT
                                GAGCGCG  TGTCTCTG
                                |||||||  ||||||||
                                CTCGTGT  GTAGAGAC
                                   ___
GAM311  FLJ10898 3' AAGTAACATTTGTCTCTG   7952     C_  GA
                                GAG  GCG  TTGTCTCTG
                                |||  |||  |||||||||
                                TTC  TGT  AACAGAGAC
                                  AT   A_
GAM311  FLJ13902 3' GAGCACGGATGGTGTCTG   7953          T  C
                                GAGCGCGGAT GT TCTG
                                |||||||||| || ||||
                                CTCGTGCCTA CA AGAC
                                     C  C
GAM311  FLJ14100 3' GAACGCGAGTCTCTG      7954        ATT
                                GAGCGCGG  GTCTCTG
                                ||||||||  |||||||
                                CTTGCGCT  CAGAGAC
                                   ___
GAM311  FLJ20896 3' GAGACGCGCGTCTCTG     7955     _  GAT
                                GAG CGCG  TGTCTCTG
                                ||| ||||  ||||||||
                                CTC GCGC  GCAGAGAC
                                  T  ___
GAM311  FLJ22087 3' GAACGGATTGTTTCTG     7956    GC      C
                                GA  GCGGATTGT TCTG
                                ||  ||||||||| ||||
                                CT  TGCCTAACA AGAC
                                __       A
GAM311  FLJ22283 5' GAGCAGCGGCTCGTCTCTG  7957     _  A
                                GAGC GCGG TTGTCTCTG
                                |||| |||| |||||||||
                                CTCG CGCC AGCAGAGAC
                                  T   G
GAM311  FLJ31300 3' GAGCTGCATGTCTCTG     7958     _  GAT
                                GAGC GCG  TGTCTCTG
                                |||| |||  ||||||||
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                                CTCG CGT   ACAGAGAC
                                  A  ___
GAM311  FYCO1    3'  GAGGCAGAGTGTCTCTG     7959     C    T
                                GAG GCGGA TGTCTCTG
                                ||| ||||| ||||||||
                                CTC CGTCT ACAGAGAC
                                  _    C
GAM311  HSA250303 5'  GAGCGCAGGCCCTTCTG     7960        ATT  __
                                GAGCGCGG  GTC  TCTG
                                ||||||||  |||  ||||
                                CTCGCGTC  CGG  AGAC
                                    ___  GA
GAM311  HSJ001348 5'  GAGCACGGGCTCACCTCTG   7961        A_ TG
                                GAGCGCGG  T  TCTCTG
                                ||||||||  |  ||||||
                                CTCGTGCC  A  GGAGAC
                                    CG GT
GAM311  KIAA1371  3'  AAGTCAAACTTGTCTCTG    7962     CG    _
                                GAG  CGGATT GTCTCTG
                                |||  |||||| |||||||
                                TTC  GTTTGA CAGAGAC
                                  A_     A
GAM311  KIAA1449  3'  GAGGGAACCCTGTCTCTG    7963     CGC  ___
                                GAG  GGA  TTGTCTCTG
                                |||  |||  |||||||||
                                CTC  CCT  GACAGAGAC
                                  ___  TGG
GAM311  KIAA1522  3'  GAGCGCAGGATGACTCTG    7964        AT  T
                                GAGCGCGG  TG CTCTG
                                ||||||||  || |||||
                                CTCGCGTC  AC GAGAC
                                    CT  T
GAM311  KIAA1877  3'  GAGCACAAAGTTCTCTG     7965        TTG
                                GAGCGCGGA  TCTCTG
                                |||||||||  ||||||
                                CTCGTGTTT  AGAGAC
                                    CA_
GAM311  MGC15854  5'  GAGGCGCCGTCTCTG       7966     C  GA
                                GAG GCG  TTGTCTCTG
                                ||| |||  |||||||||
                                CTC CGC  GGCAGAGAC
                                  _  __
GAM311  MGC2647   3'  GAGCGGGGACATCCCTG     7967      C   T
                                GAGCG GGAT GTCTCTG
                                ||||| |||| |||||||
                                CTCGC CCTG TAGGGAC
                                  C   _
GAM311  RAB3GAP   3'  GAGGCAGCACTGTCTCTG    7968     C   _
                                GAG GCGG ATTGTCTCTG
                                ||| |||| ||||||||||
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                                CTC CGTC TGACAGAGAC
                                  _   G
GAM311  SCYA28   3'  GAGGAATTGTCTCTG      7969     CGC
                                GAG  GGATTGTCTCTG
                                |||  ||||||||||||
                                CTC  CTTAACAGAGAC
                                 ___
GAM311  SIAT4A   5'  GAGGGAAACTGTCTCTG    7970     CGC
                                GAG  GGATTGTCTCTG
                                |||  ||||||||||||
                                CTC  TTTGACAGAGAC
                                  CC_
GAM311  SLC16A5  5'  GAGCGCGGCGTCCTG      7971       AT   T
                                GAGCGCGG  TGTC CTG
                                ||||||||  |||| |||
                                CTCGCGCC  GCAG GAC
                                    __   _
GAM311  SMOC1    5'  GAGCGCGAGCGTGTGCTCTG  7972       _ AT  _
                                GAGCGCG G  TGT CTCTG
                                |||||||  |  ||| |||||
                                CTCGCGC C  ACA GAGAC
                                    T GC   C
GAM311  SPINT1   5'  GAGCGCGGGCCTCTG      7973       ATT
                                GAGCGCGG   GTCTCTG
                                ||||||||   |||||||
                                CTCGCGCC   CGGAGAC
                                    ___
GAM311  TIP-1    3'  GAACGCGGAGCCCACCTG    7974       TT   __
                                GAGCGCGGA  GTCT  CTG
                                |||||||||  ||||  |||
                                CTTGCGCCT  CGGG  GAC
                                    __   TG
GAM311  ZNF297B  3'  AAGTGCAGGTGTCTCTG     7975     C   AT
                                GAG GCGG  TGTCTCTG
                                ||| ||||  ||||||||
                                TTC CGTC  ACAGAGAC
                                  A   C_
GAM311  ZNF297B  3'  AAGTGCAGGTGTCTCTG     7975     C   AT
                                GAG GCGG  TGTCTCTG
                                ||| ||||  ||||||||
                                TTC CGTC  ACAGAGAC
                                  A   C_
GAM311  LOC116236 3' GAGCTGGAGCTCCCTCTG    7976      GC  _ G
                                GAGC  GGA TT TCTCTG
                                ||||  ||| || ||||||
                                CTCG  CCT GA GGAGAC
                                  A_  C  G
GAM311  LOC138199 3' AGCGGGATCCTGTCTCTG    7977      C   __
                                AGCG GGAT  TGTCTCTG
                                |||| ||||  ||||||||
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                                TCGC CCTA  ACAGAGAC
                                  _   GG
GAM311   LOC147276 5'  GAGCGCAGCTGTTCTG     7978        A   C
                                GAGCGCGG TTGT TCTG
                                |||||||| |||| ||||
                                CTCGCGTC GACA AGAC
                                  _   _
GAM311   LOC150759 3'  GAAGTCAAACTGTCTCTG    7979     CG
                                GAG  CGGATTGTCTCTG
                                |||  ||||||||||||
                                CTT  GTTTGACAGAGAC
                                  CA
GAM311   LOC154739 5'  GAGCACTTTTGTCTCTG     7980       GGA
                                GAGCGC   TTGTCTCTG
                                ||||||   |||||||||
                                CTCGTG   AACAGAGAC
                                   AA_
GAM311   LOC157858 5'  GAGCTGGATGTCTCTG      7981      GC   T
                                GAGC  GGAT GTCTCTG
                                ||||  |||| |||||||
                                CTCG  CCTA CAGAGAC
                                  A_   _
GAM311   LOC165741 3'  GAGTCGGGACGCCTCTG     7982     _ C   T
                                GAG CG GGAT GTCTCTG
                                ||| || |||| |||||||
                                CTC GC CCTG CGGAGAC
                                  A _   _
GAM311   LOC203276 3'  GAGCACTTTTGTCTCTG     7980       GGA
                                GAGCGC   TTGTCTCTG
                                ||||||   |||||||||
                                CTCGTG   AACAGAGAC
                                   AA_
GAM311   LOC203305 3'  GAGCACTTTTGTCTCTG     7980       GGA
                                GAGCGC   TTGTCTCTG
                                ||||||   |||||||||
                                CTCGTG   AACAGAGAC
                                   AA_
GAM311   LOC254243 3'  GAGCACTTTTGTCTCTG     7980       GGA
                                GAGCGC   TTGTCTCTG
                                ||||||   |||||||||
                                CTCGTG   AACAGAGAC
                                   AA_
GAM311   LOC254617 5'  GAACGGGCTGTCTCTG      7983      C  A
                                GAGCG GG TTGTCTCTG
                                ||||| || |||||||||
                                CTTGC CC GACAGAGAC
                                  _ _
GAM311   LOC254896 5'  GAGCGCAGCGCCTCTG      7984        AT
                                GAGCGCGG  TGTCTCTG
                                ||||||||  ||||||||
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                                CTCGCGTC  GCGGAGAC
                                          __
GAM311  LOC254962 5'  GAGCGCAGCGTTCTG      7985        AT   C
                                GAGCGCGG  TGT TCTG
                                ||||||||  ||| ||||
                                CTCGCGTC  GCA AGAC
                                          __  _
GAM311  LOC255518 3'  AAGCCCATTGTCTCTG      7986      G GG
                                GAGC C  ATTGTCTCTG
                                ||||  |  ||||||||||
                                TTCG G  TAACAGAGAC
                                  G __
GAM311  LOC256586 5'  GAGCGCGATGCCCTG       7987        AT    T
                                GAGCGCGG  TGTC CTG
                                ||||||||  ||||  |||
                                CTCGCGCT  ACGG GAC
                                          __   _
GAM311  LOC256856 5'  GAGCGCGAGGCCGGCCTCTG  7988        ATT__
                                GAGCGCGG    GTCTCTG
                                ||||||||    |||||||
                                CTCGCGCT    CGGAGAC
                                     CCGGC
GAM311  LOC51195  5'  GAGGCGGCGCTGTCTCTG    7989     C    A_
                                GAG GCGG  TTGTCTCTG
                                |||  ||||  |||||||||
                                CTC CGCC  GACAGAGAC
                                  _   GC
GAM311  LOC91263  3'  GACCACAATGTCTCTG      7990     G    AT
                                GA CGCGG  TGTCTCTG
                                ||  |||||  ||||||||
                                CT GTGTT  ACAGAGAC
                                 G    __
GAM311  LOC91748  3'  GAGCGCAGGTGGCTCTG     7991         AT  T
                                GAGCGCGG  TG CTCTG
                                ||||||||  ||  |||||
                                CTCGCGTC  AC GAGAC
                                     C_  C
GAM311  LOC92659  3'  GAGCTGCCCGCCTCTG      7992       _  GGA
                                GAGC GC   TTGTCTCTG
                                ||||  ||   |||||||||
                                CTCG CG   GGCGGAGAC
                                  A ____
GAM312  DSC3      3'  TAAGTCTAAAACACATAGATTT 7196        AGT       A
          TA                    TAAGTT   AATACATA ATTTTA
                                ||||||   |||||||| ||||||
                                ATTCAG   TTGTGTAT TAAAAT
                                   ATT       C
GAM312  DSC3      3'  TAAGTCTAAAACACATAGATTT 7196        AGT       A
          TA                    TAAGTT   AATACATA ATTTTA
                                ||||||   |||||||| ||||||
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                                ATTCAG   TTGTGTAT TAAAAT
                                   ATT       C
GAM312  FLJ20366  3'  TAAGTTAGTACATGTAAACTT  7197          ATACA
                                TAAGTTAGTA    TAAATTT
                                ||||||||||    |||||||
                                ATTCAATCAT    ATTTGAA
                                     GTAC_
GAM313  ARSD      3'  TCTCTCACAGTCCTGG      7996          A   GCG
                                TCTCTCACA TCT   TGG
                                ||||||||| |||   |||
                                AGAGAGTGT AGG   ACC
                                     C  ___
GAM313  C18orf2   3'  TCTCCCACAGTCTCACAG    7997          A   G  TG
                                TCTCTCACA TCT CG  G
                                ||||||||| ||| ||  |
                                AGAGGGTGT AGA GT  C
                                     C  _  GT
GAM313  DLG5      5'  TCTTCACCTGCGTGG       7998      C    AAT
                                TCT TCAC   CTGCGTGG
                                ||| ||||   ||||||||
                                AGA AGTG   GACGCACC
                                  _   ___
GAM313  EPHB6     3'  TCTCTCACAGAGGCTGTTGG   7999          AT__   CG
                                TCTCTCACA    CTG  TGG
                                |||||||||    |||  |||
                                AGAGAGTGT    GAC  ACC
                                     CTCC   A_
GAM313  FGF2      3'  TCTCTCACACTATCCACTGG   8000          __   TG G
                                TCTCTCACA  ATC  C TGG
                                |||||||||  |||  | |||
                                AGAGAGTGT  TAG  G ACC
                                     GA   GT _
GAM313  GPR48     3'  CTCTCACAGTTCTAGCTGG    8001          A_   _  G
                                CTCTCACA  TCT GC TGG
                                ||||||||  ||| || |||
                                GAGAGTGT  AGA CG ACC
                                     CA   T  _
GAM313  GYPC      3'  TCTCCCACCTCCGTGG       8002          AAT  G
                                TCTCTCAC   CT CGTGG
                                ||||||||   || |||||
                                AGAGGGTG   GA GCACC
                                     ___  G
GAM313  GYPC      3'  TCTCCCACCTCCGTGG       8002          AAT  G
                                TCTCTCAC   CT CGTGG
                                ||||||||   || |||||
                                AGAGGGTG   GA GCACC
                                     ___  G
GAM313  LAMA5     3'  TCTCTCACAATTAAAAATGG   8003          CTGC_
                                TCTCTCACAAT    GTGG
                                ||||||||||    ||||
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                                AGAGAGTGTTA    TACC
                                     ATTTT
GAM313  MN1     3'  TCTCCCACAGCCCATGG    8004        AT TG
                                TCTCTCACA  C  CGTGG
                                |||||||||  |  |||||
                                AGAGGGTGT  G  GTACC
                                     CG __
GAM313  OXTR    3'  TCTCTCACAGCCTCCAGG    8005        AT  G  T
                                TCTCTCACA  CT CG GG
                                |||||||||  || || ||
                                AGAGAGTGT  GA GT CC
                                     CG  G  _
GAM313  PPP2R5C  3'  TCTCTCACAAACATA      8006         TCT
                                TCTCTCACAA   GCGTG
                                ||||||||||   |||||
                                AGAGAGTGTT   TGTAT
                                          ____
GAM313  RPA3    5'  TCTTGCCAGTTCTGCGTGG   8007     C_  CAA
                                TCT  TCA   TCTGCGTGG
                                |||  |||   |||||||||
                                AGA  GGT   AGACGCACC
                                  AC   CA_
GAM313  SIM1    3'  TCTCTAACAATCTGTGG     8008       C      GC
                                TCTCT ACAATCT  GTGG
                                |||||  |||||||  ||||
                                AGAGA TGTTAGA  CACC
                                   T      __
GAM313  SLC6A1   3'  CCCCTCTCTGCGTGG      8009       ACAA
                                TCTCTC    TCTGCGTGG
                                ||||||    |||||||||
                                GGGGAG    AGACGCACC
                                          _____
GAM313  SLC9A6   3'  TCTTCACAATCACATG     8010     C       T
                                TCT TCACAATC GCGTG
                                |||  ||||||||  |||||
                                AGA AGTGTTAG TGTAC
                                          _       _
GAM313  TPI1    3'  TCCCTCACATGGGTGG      8011         ATC  C
                                TCTCTCACA   TG GTGG
                                |||||||||   ||  ||||
                                AGGGAGTGT   AC CACC
                                      ___  C
GAM313  UCP3    3'  TCTCCCACTCCATTGTGG    8012         AA   GC_
                                TCTCTCAC  TCT   GTGG
                                ||||||||  |||   ||||
                                AGAGGGTG  AGG   CACC
                                     __   TAA
GAM313  VIL2    3'  TCTCTGCCAGCTGCGTGG    8013       CA  AT
                                TCTCT  CA  CTGCGTGG
                                |||||  ||  ||||||||
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                                AGAGA  GT  GACGCACC
                                   CG  C_
GAM313  ADPRH    5'  TCCCTCACAATTGCTGG     8014          C   G
                                TCTCTCACAAT TGC TGG
                                |||||||||| ||| |||
                                AGGGAGTGTTA ACG ACC
                                        _  _
GAM313  APOF     3'  CCTCTCACAGTGCTGG      8015         ATC   G
                                TCTCTCACA   TGC TGG
                                |||||||||   ||| |||
                                GGAGAGTGT   ACG ACC
                                     C__   _
GAM313  CLSTN3   3'  TCCCCCTCTGCGTGG       8016       ACAA
                                TCTCTC    TCTGCGTGG
                                ||||||    |||||||||
                                AGGGGG    AGACGCACC
                                    _____
GAM313  CST11    3'  TCTCTCACATGCAGTGG      8017         ATC  _
                                TCTCTCACA   TGC GTGG
                                |||||||||   ||| ||||
                                AGAGAGTGT   ACG CACC
                                     ___   T
GAM313  CST11    3'  TCTCTCACATGCAGTGG      8017         ATC  _
                                TCTCTCACA   TGC GTGG
                                |||||||||   ||| ||||
                                AGAGAGTGT   ACG CACC
                                     ___   T
GAM313  DDX21    5'  TCTTCTCAACCGCGTGG      8018     _   CAAT
                                TCT CTCA    CTGCGTGG
                                |||  ||||    ||||||||
                                AGA GAGT    GGCGCACC
                                  A   T___
GAM313  DECR2    3'  CCTCAGACACCTGCGTGG     8019       CA_
                                TCTCA   ATCTGCGTGG
                                |||||   ||||||||||
                                GGAGT   TGGACGCACC
                                   CTG
GAM313  DKFZP434P211 3'  CCTCTCACACAGCACGTGG    8020          ATC
                                TCTCTCACA   TGCGTGG
                                |||||||||   |||||||
                                GGAGAGTGT   GTGCACC
                                     GTC
GAM313  DKFZP564D172 3'  CTCTCACAATTAGCTGG      8021          CT  G
                                CTCTCACAAT  GC TGG
                                ||||||||||  || |||
                                GAGAGTGTTA  CG ACC
                                     AT  _
GAM313  FLJ10040  5'  CTACTCACAGTCTGCGTGG    8022     _     A
                                CT CTCACA TCTGCGTGG
                                ||  |||||| |||||||||
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                                GA GAGTGT AGACGCACC
                                 T     C
GAM313  FLJ13385  3'  TCCCTCACAACGTTGG      8023          ATCT   _
                                TCTCTCACA   GCGT GG
                                |||||||||   |||| ||
                                AGGGAGTGT   TGCA CC
                                     ____   A
GAM313  FLJ14346  3'  CTCTCACAGGACCCTGG     8024          __   GCG
                                CTCTCACA  ATCT   TGG
                                ||||||||  ||||   |||
                                GAGAGTGT  TGGG   ACC
                                    CC    ___
GAM313  FLJ14957  3'  TCTCTCACAACACCCCAGTGG  8025          _  G _
                                TCTCTCACAAT CT C GTGG
                                |||||||||||  || | ||||
                                AGAGAGTGTTG GG G CACC
                                      T  G T
GAM313  FLJ21016  3'  TCTTCACAACCGATGG      8026     C     T   C
                                TCT TCACAA CTG GTGG
                                |||  ||||||  ||| ||||
                                AGA AGTGTT GGC TACC
                                 _     _   _
GAM313  FLJ31951  3'  TCTCCCACAATGTCAGG     8027          CTG  T
                                TCTCTCACAAT   CG GG
                                ||||||||||   || ||
                                AGAGGGTGTTA   GT CC
                                      CA_  _
GAM313  H-plk     5'  TCTCTCACATCACATG      8028          A  T
                                TCTCTCACA TC GCGTG
                                |||||||||  || |||||
                                AGAGAGTGT AG TGTAC
                                      _  _
GAM313  HAVCR-1   5'  TCACTCACAATGCTGG      8029     T      TC   G
                                TC CTCACAA  TGC TGG
                                ||  |||||||  |||  |||
                                AG GAGTGTT  ACG ACC
                                 T      __   _
GAM313  ICAM4     3'  TCTGTCGACCCGCGTGG      8030      C  ACA
                                TCT TC   ATCTGCGTGG
                                |||  ||   ||||||||||
                                AGA AG   TGGGCGCACC
                                  C  C__
GAM313  IF2       5'  TCTCTCACAGACCCACTG     8031          _   TG G
                                TCTCTCACA ATC  C TG
                                |||||||||  |||  |  ||
                                AGAGAGTGT TGG  G AC
                                      C   GT _
GAM313  KIAA0174  3'  CCTCTCACACTCCTGTGG     8032          A   GC
                                TCTCTCACA TCT  GTGG
                                |||||||||  |||  ||||
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                                GGAGAGTGT AGG  CACC
                                    G   A_
GAM313  KIAA0226 3' CCTCTCACGCTGGTGG     8033        AAT   C
                                TCTCTCAC   CTG GTGG
                                ||||||||   ||| ||||
                                GGAGAGTG   GAC CACC
                                    C__   _
GAM313  KIAA0404 3' CCTCTCACAGCAGATTGG    8034         ATCT  ___
                                TCTCTCACA    GCG   TGG
                                |||||||||    |||   |||
                                GGAGAGTGT    CGT   ACC
                                     ____  CTA
GAM313  KIAA0940 3' TCTTTCACAATCCTGG      8035     C       GCG
                                TCT TCACAATCT   TGG
                                ||| |||||||||   |||
                                AGA AGTGTTAGG   ACC
                                  A       ___
GAM313  KIAA1045 3' CCTCTCACAAACTTGG      8036         TCT  G
                                TCTCTCACAA   GC TGG
                                ||||||||||   || |||
                                GGAGAGTGTT   TG ACC
                                     ___  A
GAM313  KIAA1183 5' TCTCTCACAGCCAGCAGG    8037         AT T   T
                                TCTCTCACA  C GCG GG
                                |||||||||  | ||| ||
                                AGAGAGTGT  G CGT CC
                                     CG T  _
GAM313  KIAA1218 5' TCTCCCACAGACTGTCGTGG  8038         AT   _
                                TCTCTCACA  CTG CGTGG
                                |||||||||  ||| |||||
                                AGAGGGTGT  GAC GCACC
                                     CT   A
GAM313  KIAA1724 3' TCTCTACACAACAAATGG    8039       _     CTGC
                                TCTCT CACAAT    GTGG
                                ||||| ||||||    ||||
                                AGAGA GTGTTG    TACC
                                   T     TT__
GAM313  KIAA1878 3' TCCCTCACAAGCACTGG     8040         TCT   _
                                TCTCTCACAA   GCG TGG
                                ||||||||||   ||| |||
                                AGGGAGTGTT   CGT ACC
                                     ____  G
GAM313  KLK12    3' TCTCTCACCCCGCTCGTGG   8041         AA    __
                                TCTCTCAC  TCTGC  GTGG
                                ||||||||  |||||  ||||
                                AGAGAGTG  GGGCG  CACC
                                     __    AG
GAM313  MGC15563 3' TCTTCCACAATCCATTTGG   8042      CT       CG
                                TCT  CACAATCTG  TGG
                                |||  |||||||||  |||
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                                AGA  GTGTTAGGT  ACC
                                  AG        AA
GAM313  MGC22014  3'  TCTCCCACAATTACATG     8043           C
                                TCTCTCACAAT TGCGTG
                                |||||||||||  ||||||
                                AGAGGGTGTTA ATGTAC
                                          _
GAM313  MGC4614   5'  CCTCTCACAGTCTCATAG    8044          A  G
                                TCTCTCACA TCT CGTGG
                                |||||||||  |||  |||||
                                GGAGAGTGT AGA GTATC
                                      C  _
GAM313  MRPL45    3'  TCTCTCACAGTCCCTGCTGTGG 8045          A__   _
                                TCTCTCACA   TCTGC GTGG
                                |||||||||   |||||  ||||
                                AGAGAGTGT   GGACG CACC
                                      CAG    A
GAM313  MYOZ2     3'  TCTCTCACAAACATG       8046          TCT
                                TCTCTCACAA   GCGTG
                                ||||||||||   |||||
                                AGAGAGTGTT   TGTAC
                                          ____
GAM313  NFASC     3'  TCTCCCACACTGGTGG      8047          AT  C
                                TCTCTCACA  CTG GTGG
                                |||||||||  |||  ||||
                                AGAGGGTGT  GAC CACC
                                          __  _
GAM313  PRDM15    3'  CCTTTCACAATCCAATGG    8048      C       C
                                TCT TCACAATCTG GTGG
                                |||  ||||||||||  ||||
                                GGA AGTGTTAGGT TACC
                                  A        _
GAM313  RRP40     3'  TCTCCCACAAAAGCGTGG    8049          TCT
                                TCTCTCACAA   GCGTGG
                                ||||||||||   ||||||
                                AGAGGGTGTT   CGCACC
                                      TT_
GAM313  SARM      3'  TCTCTCACAGGATGCTGG    8050          ATC  G
                                TCTCTCACA   TGC TGG
                                |||||||||   |||  |||
                                AGAGAGTGT   ACG ACC
                                      CCT  _
GAM313  SEC6      5'  TCCCTCACAATCTCAGG     8051           G  T
                                TCTCTCACAATCT CG GG
                                ||||||||||||  ||  ||
                                AGGGAGTGTTAGA GT CC
                                          _  _
GAM313  SES2      3'  CCTCTCACACACTGTGG     8052          AT  GC
                                TCTCTCACA  CT  GTGG
                                |||||||||  ||  ||||
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                                GGAGAGTGT  GA  CACC
                                    GT  __
GAM313  TRIM38    3'  TCTCTCACACTTTGCTTGG   8053        ATC   G
                                TCTCTCACA   TGC TGG
                                |||||||||   ||| |||
                                AGAGAGTGT   ACG ACC
                                    GAA   A
GAM313  TUSP      3'  TCTCTACACAAAGGCAATGG  8054      _    TCT  _
                                TCTCT CACAA   GCG TGG
                                |||||  |||||   ||| |||
                                AGAGA GTGTT   CGT ACC
                                   T    TC_   T
GAM313  LOC115761 3'  TCTCCCACAGTGCTGG     8055        ATC   G
                                TCTCTCACA   TGC TGG
                                |||||||||   ||| |||
                                AGAGGGTGT   ACG ACC
                                    C__   _
GAM313  LOC118611 5'  TCTCACACAACCCAGTGTGG  8056     T      GC_
                                TCTC CACAATCT   GTGG
                                ||||  ||||||||   ||||
                                AGAG GTGTTGGG   CACC
                                  T       TCA
GAM313  LOC131308 5'  TCTCTCACATGTCCAAAGG   8057        A_   CGT
                                TCTCTCACA  TCTG   GG
                                |||||||||  ||||   ||
                                AGAGAGTGT  AGGT   CC
                                    AC    TT_
GAM313  LOC150174 3'  CCTCTCACACAGCACGTGG   8020        ATC
                                TCTCTCACA   TGCGTGG
                                |||||||||   |||||||
                                GGAGAGTGT   GTGCACC
                                    GTC
GAM313  LOC150213 3'  CCTCTCACACAGCACGTGG   8020        ATC
                                TCTCTCACA   TGCGTGG
                                |||||||||   |||||||
                                GGAGAGTGT   GTGCACC
                                    GTC
GAM313  LOC150236 3'  CCTCTCACACAGCACGTGG   8020        ATC
                                TCTCTCACA   TGCGTGG
                                |||||||||   |||||||
                                GGAGAGTGT   GTGCACC
                                    GTC
GAM313  LOC152190 5'  TCTCTACATACTCCTCGTGG  8058      _ CAA   G
                                TCTCT CA   TCT CGTGG
                                |||||  ||   |||  |||||
                                AGAGA GT   AGG GCACC
                                   T  ATG   A
GAM313  LOC152345 3'  TCTCCCACATTCTCTGTGTGG 8060        A__   C
                                TCTCTCACA   TCTG GTGG
                                |||||||||   ||||  ||||
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                                AGAGGGTGT   AGAC CACC
                                     AAG    A
GAM313  LOC152345 5'  TCTCCCGGCTCTGCGTGG    8059       ACAA
                                TCTCTC   TCTGCGTGG
                                ||||||   |||||||||
                                AGAGGG   AGACGCACC
                                   CCG_
GAM313  LOC155004 5'  TCTCTCACCGAGCGCTATGCGT 8061       AATC_____     III
          GGC                    CTCTCAC       TGCGTGG   C
                                |||||||       |||||||  |
                                GAGAGTG       ACGCACC   G
                                   GCTCGCGAT      III
GAM313  LOC162952 3'  TCCCTCACAGTGATGG     8062         ATC  C
                                TCTCTCACA   TG GTGG
                                |||||||||   || ||||
                                AGGGAGTGT   AC TACC
                                     C__  _
GAM313  LOC203042 3'  TCCCTCAGCTGCGTGG     8063       CAAT
                                TCTCTCA    CTGCGTGG
                                |||||||    ||||||||
                                AGGGAGT    GACGCACC
                                   C___
GAM313  LOC255536 3'  TCTCCCACGCTCTGGTG    8064        AA    C
                                TCTCTCAC  TCTG GTG
                                ||||||||  |||| |||
                                AGAGGGTG  AGAC CAC
                                     CG   _
GAM313  LOC57105  3'  TCTCTCACTGTCCTTACTTGG  8065       AA   __  G
                                TCTCTCAC  TCT  GC TGG
                                ||||||||  |||  || |||
                                AGAGAGTG  AGG  TG ACC
                                     AC   AA  A
GAM313  LOC90625  3'  CCTCTCACAATCTTTGG    8066          GCG
                                TCTCTCACAATCT   TGG
                                ||||||||||||   |||
                                GGAGAGTGTTAGA   ACC
                                       A__
GAM313  LOC91694  3'  TCTCTCACAGACATAA     8067         ATCT
                                TCTCTCACA    GCGTGG
                                |||||||||    ||||||
                                AGAGAGTGT    TGTATT
                                     C___
GAM313  LOC92285  5'  TCTCCCACAGTCACTG     8068         A  T  G
                                TCTCTCACA TC GC TG
                                ||||||||| || || ||
                                AGAGGGTGT AG TG AC
                                     C  _  _
GAM314  AP1M1     3'  AAGGGGCTTCTGAGACGAG   8071      A   G      CAT
                                AAGG GCT TCTGAGAC   GAG
                                |||| ||| ||||||||   |||
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                                TTCC CGA AGACTCTG   CTC
                                  C  _      ____
GAM314  CD79B    3'  AAGGGGTTGGGCCATGAG    8072      AGCT  C  AGA
                                AAGG   GT TG   CCATGAG
                                ||||   || ||   |||||||
                                TTCC   CA AC   GGTACTC
                                  C___  _  CC_
GAM314  CD79B    3'  AAGGGGTTGGGCCATGAG    8072      AGCT  C  AGA
                                AAGG   GT TG   CCATGAG
                                ||||   || ||   |||||||
                                TTCC   CA AC   GGTACTC
                                  C___  _  CC_
GAM314  CIT      5'  GGAGAGCTGTAGCTCTGTGAGC 8073    A      CTG  ACCA_
                                A GGAGCTGT   AG    TGAGC
                                | ||||||||  ||    |||||
                                C TCTCGACA   TC    ACTCG
                                 C       ____ GAGAC
GAM314  CLC      3'  AAGAAGCAGGAGGCCATGAGC  8074       TGTCT   A
                                AAGGAGC    GAG CCATGAGC
                                |||||||    ||| ||||||||
                                TTCTTCG    CTC GGTACTCG
                                    TC___   C
GAM314  EHF      3'  AAGTGGTTAGAGACCATGAG   8075     CT  CT
                                GAG  GT  GAGACCATGAG
                                |||  ||  ||||||||||
                                TTC  CA  CTCTGGTACTC
                                  AC  AT
GAM314  GRLF1    3'  AAGGGCTGTCTGGCATGGGGC  8076      A      AGAC   A_
                                AAGG GCTGTCTG    CATG  GC
                                |||| ||||||||    ||||  ||
                                TTCC CGACAGAC    GTAC  CG
                                  _       C___    CC
GAM314  ITPR3    3'  GGAGCTGCACAGCCATGGGC   8077       CTG  A    A
                                GGAGCTGT   AG CCATG GC
                                ||||||||   || ||||| ||
                                CCTCGACG   TC GGTAC CG
                                    TG_  _    C
GAM314  KCNC3    3'  GGAGCTGTCTGGACAAAAG   8078         A  CAT
                                GGAGCTGTCTG GAC   GAG
                                ||||||||||| |||   |||
                                CCTCGACAGAC CTG   TTC
                                      _  TT_
GAM314  MAPRE1   3'  AAGGAACTGAATAGGCTGTGGG 8079        TCTG  ACCA  A
            C                   AAGGAGCTG    AG    TG GC
                                |||||||||    ||    || ||
                                TTCCTTGAC    TC    AC CG
                                    TTA_  CGAC  C
GAM314  PPP1R8   5'  AAGGGGCTGCCTAAGTGAG   8080      A       ACCA
                                AAGG GCTGTCTGAG    TGAG
                                |||| ||||||||||    ||||
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                                TTCC CGACGGATTC   ACTC
                                  C       ____
GAM314  PPP1R8   5'  AAGGGGCTGCCTAAGTGAG   8080      A        ACCA
                                AAGG GCTGTCTGAG   TGAG
                                |||| ||||||||||   ||||
                                TTCC CGACGGATTC   ACTC
                                  C       ____
GAM314  RHCE     3'  AAGGAGCTTTGCTGTCATGAGC 8081        GT_  AGAC
                                AAGGAGCT  CTG   CATGAGC
                                ||||||||  |||   |||||||
                                TTCCTCGA  GAC   GTACTCG
                                    AAC   A___
GAM314  SLC9A1   5'  AGGAGCTGGGACTCTGGGC   8082        TCTGA  CA  A
                                AGGAGCTG    GAC  TG GC
                                ||||||||    |||  || ||
                                TCCTCGAC    CTG  AC CG
                                    C____   AG  C
GAM314  SMURF1   3'  AAAGAGCTCAGGGCTGTGAGC  8083        GT___  AGACCA
                                AAGGAGCT    CTG    TGAGC
                                ||||||||    |||    |||||
                                TTTCTCGA    GAC    ACTCG
                                    GTCCC  _______
GAM314  TNFSF8   3'  GGGGCTGTCCGAGCCTG    8084    A       A  A
                                GG GCTGTCTGAG CC TG
                                || |||||||||| || ||
                                CC CGACAGGCTC GG AC
                                 C       _  _
GAM314  AKAP11   3'  AAAGAGCTGTTTGACTATAGAG 8085         C  GACCAT
          C                      AAGGAGCTGT TGA     GAGC
                                ||||||||||| |||     ||||
                                TTTCTCGACA ACT     CTCG
                                     A  GATAT_
GAM314  ASB16    3'  AGGGACTGTCTGAGGCAGTGAG 8086     AG       AC  _
                                AGG  CTGTCTGAG  CA TGAG
                                |||  |||||||||  || ||||
                                TCC  GACAGACTC  GT ACTC
                                  CT       C_  C
GAM314  FLJ12190 3'  AAGGATTTGACAGCCATGAGC  8087      GC  TCTG  A
                                AAGGA  TG   AG CCATGAGC
                                |||||  ||   || ||||||||
                                TTCCT  AC   TC GGTACTCG
                                   AA  TG__  _
GAM314  FLJ13710 3'  AAGGAGCTAGTATCTGTGAG   8088        ___   AGACCA
                                AAGGAGCT   GTCTG    TGAG
                                ||||||||   |||||    ||||
                                TTCCTCGA   TAGAC    ACTC
                                    TCA   _______
GAM314  FLJ20085 3'  AGGGGCTGTGGCACCATGAGC  8089     A    CT AG
                                AGG GCTGT  G  ACCATGAGC
                                ||| |||||  |  |||||||||
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                                TCC CGACA  C  TGGTACTCG
                                  C    __ CG
GAM314  FLJ22056  5'  AAGGAGTTGTTTGAGAACC   8090       C  C   _
                                AAGGAG TGT TGAGA CC
                                |||||| ||| ||||| ||
                                TTCCTC ACA ACTCT GG
                                   A  A    T
GAM314  FLJ31890  3'  AAGGAGCTTCTCATTTGTGAGC 8091        G  GAGACCA
                                AAGGAGCT TCT      TGAGC
                                |||||||| |||      |||||
                                TTCCTCGA AGA      ACTCG
                                    _  GTAAAC_
GAM314  HARS2     3'  AGAGCTGTCTGCTGTGAATGAG 8092          AGACC_
          C                      GGAGCTGTCTG     ATGAGC
                                ||||||||||      ||||||
                                TCTCGACAGAC     TACTCG
                                      GACACT
GAM314  IL18BP    3'  GGAGCTGTCTGGGAAAAGC   8093          A  CCAT
                                GGAGCTGTCTG GA    GAGC
                                |||||||||| ||    ||||
                                CCTCGACAGAC CT    TTCG
                                      C  T___
GAM314  ILF3      3'  GGAGCTGTAGTTCGACTGTGAG 8094        CTGA_  CA
          C                      GGAGCTGT    GAC  TGAGC
                                ||||||||    |||  |||||
                                CCTCGACA    CTG  ACTCG
                                    TCAAG   AC
GAM314  KIAA0757  3'  AGGAGCCGTCTCTCTGATGGGC 8095          GAGACC  A
                                AGGAGCTGTCT     ATG GC
                                ||||||||||      ||| ||
                                TCCTCGGCAGA     TAC CG
                                      GAGAC_   C
GAM314  KIAA0876  3'  CGAGAGCGAGGCCGTGAG    8096    A    TGTCT  A  A
                                A GGAGC    GAG CC TGAG
                                | |||||    ||| || ||||
                                G TCTCG    CTC GG ACTC
                                 C    ______  C  C
GAM314  KIAA1280  5'  GGAGGTGCGGGCCATGAGC   8097      C  CTGAGA
                                GGAG TGT     CCATGAGC
                                |||| |||     ||||||||
                                CCTC ACG     GGTACTCG
                                  C  CCC___
GAM314  MGC5442   3'  AAGGAGCTGTCAGGGATTGGAG 8098          TGA  CCAT
                                AAGGAGCTGTC  GA   GAG
                                ||||||||||  ||   |||
                                TTCCTCGACAG  CT   CTC
                                      TCC  AAC_
GAM314  OSBPL2    3'  AGGGGCTGTCTGTGCAG     8099      A      AGACCA  _
                                AGG GCTGTCTG     TG AG
                                ||| ||||||||     || ||
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                                TCC CGACAGAC     AC TC
                                  C      _______ G
GAM314  OSBPL2   3'  AGGGGCTGTCTGTGCAG     8099      A       AGACCA _
                                AGG GCTGTCTG     TG AG
                                ||| ||||||||     || ||
                                TCC CGACAGAC     AC TC
                                  C      _______ G
GAM314  SARM     3'  AGGAGCTATTTGGGACAGGAG  8100          C  A   CAT
                                AGGAGCTGT TG GAC   GAG
                                |||||||||| || |||   |||
                                TCCTCGATA AC CTG   CTC
                                     A  C   TC_
GAM314  TU3A     3'  GGAGTTCTCTGAGACCTAGGAG 8101       CTG       AT_
           C                     GGAG   TCTGAGACC   GAGC
                                ||||   |||||||||   ||||
                                CCTC   AGACTCTGG   CTCG
                                  AAG        ATC
GAM314  WBSCR16  3'  AGGCGGCCAGGAAGGGCCATGA 8102      A_   TCT   A_
           GC                    AGG  GCTG   GAG  CCATGAGC
                                |||  ||||   |||  ||||||||
                                TCC  CGGT   TTC  GGTACTCG
                                  GC    CC_   CC
GAM314  LOC149832 5'  AAGCAGTCCAGACTGTGG     8103       T   G    CA  A
                                GAGC GTCT AGAC  TG G
                                |||| |||| ||||  || |
                                TTCG CAGG TCTG  AC C
                                  T    _    AC  C
GAM314  LOC151584 3'  AAGGAGCTATTTGGGAAAG    8104          C  A  CCAT
                                AAGGAGCTGT TG GA    GAG
                                |||||||||| || ||    |||
                                TTCCTCGATA AC CT    TTC
                                     A  C  _____
GAM314  LOC157349 3'  AAGGAGTTGCCTGGGGTTCGAG 8105        C      AGACCA
                                AAGGAG TGTCTG      TGAG
                                ||||||  ||||||      ||||
                                TTCCTC ACGGAC      GCTC
                                   A     CCCAA_
GAM314  LOC196202 5'  AAGGAGCTTTTGGCCAATG    8106         GTC  AGA   _
                                AAGGAGCT   TG   CCA TG
                                ||||||||   ||   ||| ||
                                TTCCTCGA   AC   GGT AC
                                     AA_  C__   T
GAM314  LOC204720 5'  AAGAGCTGACTGTGACTATGGG 8107          T   A   C   A
           C                     AGGAGCTG CTG GAC ATG GC
                                |||||||| ||| ||| ||| ||
                                TTCTCGAC GAC CTG TAC CG
                                     T   A   A   C
GAM314  LOC221504 3'  AGGGGCTGTCTATCATA     8108      A       AGAC
                                AGG GCTGTCTG    CATG
                                ||| ||||||||    ||||
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                                TCC CGACAGAT    GTAT
                                  C       A___
GAM314  LOC222223 5'  AAGGAGCTGTCAGAATGAGAGC 8109          T   ACCAT
                                AAGGAGCTGTC GAG     GAGC
                                |||||||||| |||     ||||
                                TTCCTCGACAG CTT     CTCG
                                      T   ACT__
GAM314  LOC253181 5'  GGCGGCTGTGGGGCCATGAGC  8110     A_    CTGAGA
                                GG  GCTGT     CCATGAGC
                                ||  |||||     ||||||||
                                CC  CGACA     GGTACTCG
                                 GC    CCCC__
GAM315  DLG5     5'  CTGGTGCTGCAGCTGGATG    8113     A        CATTCTA
                                CT GTGCTGCGGC      ATG
                                || ||||||||||      |||
                                GA CACGACGTCG      TAC
                                 C         ACC____
GAM315  ARTS-1    3'  TAGTGCTGTAGTCTGAGATTCT 8114         CG CC____    A
            GATGG                   TAGTGCTG  G     ATTCT ATGG
                                |||||||| |     ||||| ||||
                                ATCACGAC  C     TAAGA TACC
                                     AT AGACTC     C
GAM315  DPYSL4    3'  GTGCTGCACCAAGTTCTGATGG 8115         G  __   A
                                GTGCTGCG CCA  TTCT ATGG
                                |||||||| |||  |||| ||||
                                CACGACGT GGT  AAGA TACC
                                     _  TC    C
GAM315  FLJ14775  3'  CTAATGCTGCTTTTAATG    8116          GGCCATTC
                                CTAGTGCTGC       TAATG
                                ||||||||||       |||||
                                GATTACGACG       ATTAC
                                      AAA_____
GAM315  KIAA1093  3'  TAGTGCTGCTGCTGTTCC    8117          G  CA
                                TAGTGCTGC GC  TTCT
                                ||||||||| ||  ||||
                                ATCACGACG CG  AAGG
                                      A  AC
GAM315  LOC157292 3'  GTTTACAGTCATTCTAATGG   8118     GC    C
                                GT  TGCGG CATTCTAATGG
                                ||  ||||| ||||||||||
                                CA  ATGTC GTAAGATTACC
                                 A_    A
GAM315  LOC160484 3'  GTGCTGCGGTTATTATCTGG   8119         CC   CTAA
                                GTGCTGCGG  ATT    TGG
                                |||||||||  |||   |||
                                CACGACGCC  TAA    ACC
                                     AA   TAG_
GAM315  LOC56270  3'  CTGGTGTCTGCCTCATTCTAAT 8120     A  _   GGC
            GG                    CT GTG CTGC   CATTCTAATGG
                                || ||| ||||   ||||||||||
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                                GA CAC GACG   GTAAGATTACC
                                 C   A    GA_
GAM316  B4GALT3   5'  TCATGGGGGCTCCAGGGGG   8123          AC    AGTGC
                                TCATGGGGG  CCAG    GGG
                                |||||||||  ||||    |||
                                AGTACCCCC  GGTC    CCC
                                     GA    C____
GAM316  FSTL3     3'  TGGGGGACCAAGGAGCCCTGGG 8124          CA_   GC_
                                TGGGGGACC   GAGT   GGG
                                |||||||||   ||||   |||
                                ACCCCCTGG   CTCG   CCC
                                     TTC    GGA
GAM316  ODF2      5'  TCAGGGGGACCCAGAGGGG   8125      T          TGC
                                TCA GGGGGACCCAGAG   GGG
                                ||| ||||||||||||   |||
                                AGT CCCCCTGGGTCTC   CCC
                                  _          ___
GAM316  PLA2G2D   3'  CCACAGGCCCAGAGTGTGGG   8126        GGA       C
                                TCATGGG   CCCAGAGTG GGG
                                |||||||   ||||||||| |||
                                GGTGTCC   GGGTCTCAC CCC
                                   ___        A
GAM316  PLCD1     3'  TCAGGGGGGACCCCACTGGG   8127      T       AGAGTGC
                                TCA GGGGGACCC      GGG
                                ||| |||||||||      |||
                                AGT CCCCCTGGG      CCC
                                  C        GTGA___
GAM316  RHCG      3'  TCTGGGGGACCCAGGGAGC    8128     A         AGT
                                TC TGGGGGACCCAG   GC
                                || ||||||||||||   ||
                                AG ACCCCCTGGGTC   CG
                                  _          CCT
GAM316  TCN2      3'  TCATGGGAGACCTGCAGGG    8129           CAGAG   _
                                TCATGGGGGACC    TGC GGG
                                ||||||||||||    ||| |||
                                AGTACCCTCTGG    ACG CCC
                                       _____   T
GAM316  AMAC      5'  GACCTCATTGGAGTGCGGG    8130       _ ___
                                GACC CA   GAGTGCGGG
                                |||| ||   |||||||||
                                CTGG GT   CTCACGCCC
                                  A  AAC
GAM316  FLJ12294  3'  TCTGGGGGACTTGGCTGAGTGG 8131     A       CCA___   GC
          GC                    TC TGGGGGAC     GAGT  GGGC
                                || ||||||||     ||||  ||||
                                AG ACCCCCTG     CTCA  CCCG
                                  _       AACCGA   __
GAM316  GAL3ST2   5'  TCATGGGGGATCCTGCGG    8132           C  AGAG
                                TCATGGGGGA CC    TGCGG
                                |||||||||| ||    |||||
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                                AGTACCCCCT GG    ACGCC
                                      A _____
GAM316  PLAGL2   3'  TCATGGGGGACACAGACGGGG  8133          C   G  C
                                TCATGGGGGAC CAGA TG GGG
                                |||||||||||  |||| || |||
                                AGTACCCCCTG GTCT GC CCC
                                      T   _ _
GAM316  SDC3     3'  GGGGGACCCAATATGGGC    8135          GA  C
                                GGGGGACCCA  GTG GGGC
                                ||||||||||  ||| ||||
                                CCCCCTGGGT  TAT CCCG
                                      __  A
GAM316  SDC3     3'  TGTGGTGCCAGAGTGTGGG   8134     G  GAC      C
                                TG GG   CCAGAGTG GGG
                                || ||   |||||||| |||
                                AC CC   GGTCTCAC CCC
                                 A  AC_       A
GAM316  LOC132671 5' TCTGGGGGGCTCAGAGCGCGG  8136     A     ACC
                                TC TGGGGG   CAGAGTGCGG
                                || ||||||   ||||||||||
                                AG ACCCCC   GTCTCGCGCC
                                 _     CGA
GAM316  LOC149672 5' CCGTGGGGGACCTGGATGTGGC 8137     A       CA  GTGCG
                                TC TGGGGGACC  GA    GGC
                                || |||||||||  ||    |||
                                GG ACCCCCTGG  CT    CCG
                                 C        AC  ACA__
GAM316  LOC152845 3' TCATGGGGGACACGGAC     8138          CCAGAGT
                                TCATGGGGGAC      GCGGGC
                                ||||||||||       ||||||
                                AGTACCCCCTG      TGCCTG
                                      ________
GAM316  LOC154452 3' TCATGGTGGACACGGGTGTGGG 8139       G   CCAGA   C
          C                      TCATGG GGAC    GTG GGGC
                                ||||||  ||||    ||| ||||
                                AGTACC CCTG    CAC CCCG
                                   A   TGCC_   A
GAM316  LOC255974 5' TGGGGGACCCTGCTCCGGC   8140          AGAG   G__
                                TGGGGGACCC   TGC   GGC
                                ||||||||||   |||   |||
                                ACCCCCTGGG   ACG   CCG
                                      _____  AGG
GAM316  LOC256310 5' TCGTGGGAGACTCAGGGG    8141     A      C   AGTGC
                                TC TGGGGGAC CAG    GGG
                                || ||||||||  |||    |||
                                AG ACCCTCTG GTC    CCC
                                 C       A  ______
GAM316  LOC257492 3' TCATGGTGGACACGGGTGTGGG 8139       G   CCAGA   C
          C                      TCATGG GGAC    GTG GGGC
                                ||||||  ||||    ||| ||||
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                                AGTACC CCTG    CAC CCCG
                                   A   TGCC_  A
GAM316  LOC257606 3'  TCATGGTGGACACGGGTGTGGG 8139       G   CCAGA  C
            C                   TCATGG GGAC    GTG GGGC
                                |||||| ||||    ||| ||||
                                AGTACC CCTG    CAC CCCG
                                   A   TGCC_  A
GAM317  CHAC    3'  TTTAAGGAGCCTGAGAAGAATT 8144              TC__
            TCAC                TTTGAGGAGCCTGAGAGGG   CAC
                                |||||||||||||||||||   |||
                                AAATTCCTCGGACTCTTCT   GTG
                                      TAAA
GAM317  CYBB    3'  TTTGAGGATTCTGAGGCAGC  8145       GC    AG
                                TTTGAGGA  CTGAG  GGT
                                ||||||||  |||||  |||
                                AAACTCCT  GACTC  TCG
                                    AA    CG
GAM317  GRIN2A   3'  TTTGAGGAGTTTGGGGT    8146        CC  AGA
                                TTTGAGGAG  TG   GGGT
                                |||||||||  ||   ||||
                                AAACTCCTC  AC   CCCA
                                    AA  ___
GAM317  NGB     3'  CTTGGGGAGCCTGGGC     8147     A     GAGA
                                TTTG GGAGCCT   GGGT
                                |||| |||||||   ||||
                                GAAC CCTCGGA   CCCG
                                  C     ____
GAM317  S100P   3'  TTTGGGAAGCCTGGGACCA  8148     A     GAGA  T
                                TTTG GGAGCCT   GGG CCA
                                |||| |||||||   ||| |||
                                AAAC CTTCGGA   CCC GGT
                                  C     ____  T
GAM317  5T4     3'  TTTGAAGAGCCTGCTAACGTC  8149          AG  G
                                TTTGAGGAGCCTG  AG GTC
                                ||||||||||||  || |||
                                AAACTTCTCGGAC  TT CAG
                                      GA  G
GAM317  ANKRD6   3'  TTTGAGAAAGAGGGT      8150        GCCTG
                                TTTGAGGA    AGAGGGT
                                ||||||||    |||||||
                                AAACTCTT    TCTCCCA
                                     _____
GAM317  APEG1   3'  CTTGGGGAGGGAGGGTCCA   8151     A   CCTGA
                                TTTG GGAG    GAGGGTCCA
                                |||| ||||    |||||||||
                                GAAC CCTC    CTCCCAGGT
                                  C   C____
GAM317  ARHGEF10  3'  TTTGAGAAGCTTGGGAAGAAAT 8152         C  A    TC_
            CAC                 TTTGAGGAGC TG GAGGG   CAC
                                |||||||||| || |||||   |||
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                                AAACTCTTCG AC CTTCT   GTG
                                     A  C    TTA
GAM317  ARPP-21  3'  TTTGGGGAGCTGAGAGG    8153      A    C
                                TTTG GGAGC TGAGAGG
                                |||| ||||| |||||||
                                AAAC CCTCG ACTCTCC
                                  C    _
GAM317  ERN1     3'  TTTGGGAAGCCTGGTCTCCC  8154      A      AGAGGG
                                TTTG GGAGCCTG    TCC
                                |||| ||||||||     |||
                                AAAC CTTCGGAC    GGG
                                  C      CAGA__
GAM317  FLJ31812 3'  TTTGAGGACCTTGGTC     8155        G  GAGAG
                                TTTGAGGA CCT    GGTC
                                |||||||| |||    ||||
                                AAACTCCT GGA    CCAG
                                     _  A____
GAM317  KIAA0953 3'  TTTGAGGGCCCTGGGGT    8156       A   GAGA
                                TTTGAGG GCCT   GGGT
                                ||||||| ||||   ||||
                                AAACTCC CGGG   CCCA
                                    _   AC__
GAM317  KIAA1089 3'  CTTGAGGAGGGGAAGGGTC  8157        CCTGA
                                TTTGAGGAG   GAGGGTC
                                |||||||||   |||||||
                                GAACTCCTC   TTCCCAG
                                     CCC__
GAM317  MGC2656  3'  TTTGGTGAGTTTGAGGCCAGGT 8158     AG  CC   A__
                                TTTG  GAG  TGAG  GGGT
                                ||||  |||  ||||  ||||
                                AAAC  CTC  ACTC  TCCA
                                  CA  AA   CGG
GAM317  SRF      3'  TCTGGGGAGCCTGAGGG    8159      A       A
                                TTTG GGAGCCTGAG GG
                                |||| |||||||||| ||
                                AGAC CCTCGGACTC CC
                                  C       _
GAM317  ZNF323   3'  AGGGGTCTGAGGGTCCAC   8160     AGC   GA
                                AGG  CTGA  GGGTCCAC
                                |||  ||||  ||||||||
                                TCC  GACT  CCCAGGTG
                                  CCA   __
GAM317  LOC144108 3'  TTTGAGGACCTTGGGC    8161        G  GAGA
                                TTTGAGGA CCT   GGGT
                                |||||||| |||   ||||
                                AAACTCCT GGA   CCCG
                                     _  A___
GAM317  LOC146268 3'  TCTGGGGAGCCTGAGGA    8162      A       A
                                TTTG GGAGCCTGAG GG
                                |||| |||||||||| ||
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                                AGAC CCTCGGACTC CT
                                  C       _
GAM317  LOC151171 5'  TTTGATGAGCCTGATCC    8163      G      GAGGG
                                TTTGA GAGCCTGA    TCC
                                ||||| ||||||||    |||
                                AAACT CTCGGACT    AGG
                                  A      _____
GAM317  LOC92579  3'  TTTGGGGGCTTGAGAGGA    8164      A  A  C
                                TTTG GG GC TGAGAGGG
                                |||| || || ||||||||
                                AAAC CC CG ACTCTCCT
                                  _  C  A
GAM318  DEDD      3'  AGGGGTGTGATTGGTTGG    8167     TATTT   C  C
                                AGG    GTGT GA TGGTTGG
                                |||    |||| || |||||||
                                TCC    CACA CT ACCAACC
                                  C____   _  A
GAM318  DSP       5'  GGTGTTGGTGTTGGTCGG    8168     A  T   CGAC
                                GGT TT GTGT   TGGTTGG
                                ||| || ||||   |||||||
                                CCA AA CACA   ACCAGCC
                                  C  C   ____
GAM318  NUP54     5'  AGTATTTATCAGCTGGTTGGA  8169       TG    A
                                GGTATT  TGTCG CTGGTTGGA
                                ||||||  ||||| |||||||||
                                TCATAA  ATAGT GACCAACCT
                                   __    C
GAM318  LOC123036 3'  AGCTATTTGTGTTGATCTGA   8170    G      C  _
                                AG TATTTGTGT GA CTGG
                                || |||||||| || ||||
                                TC ATAAACACA CT GACT
                                 G       A  A
GAM318  LOC146280 5'  GGTGTTTGTGTCTGCTACCTGG 8171     A      GA   G
                                GGT TTTGTGTC  CTG TTGG
                                ||| ||||||||  ||| ||||
                                CCA AAACACAG  GAT GACC
                                  C       AC   G
GAM319  BTEB1     5'  GGTGGCGAGGGCCCCGCCGA   8174    _   A  TCCT
                                GG GGC GA    CCCCGCCGA
                                || ||| ||    |||||||||
                                CC CCG CT    GGGGCGGCT
                                 A   _  CCC_
GAM319  CAPON     3'  AGGGGCAGGTCCTCCAGC    8175       A     CC
                                AGGGGCAG TCCTCC  GC
                                |||||||| ||||||  ||
                                TCCCCGTC AGGAGG  CG
                                     C     T_
GAM319  CST1      3'  AGGGCAGAGCGCCCTGCTGA  8176       TCCT   C  C
                                GGGGCAGA    CCC GC GA
                                ||||||||    ||| || ||
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                                TCCCGTCT   GGG CG CT
                                    CGC_   A  A
GAM319  CST2    3'  AGGGCAGAGTCCCCTGCTGA  8177        TCC    _ C
                                GGGGCAGA   TCCCC GC GA
                                ||||||||   ||||| || ||
                                TCCCGTCT   AGGGG CG CT
                                    C__    A  A
GAM319  CST3    3'  AGGGCAGAGCCCCTTGCTGA  8178        T   CCC  C
                                GGGGCAGA CCTC   GC GA
                                |||||||| ||||   || ||
                                TCCCGTCT GGGG   CG CT
                                    C   AA_  A
GAM319  CST4    3'  AGGGCAGAGCGCCCTGCTGA  8176        TCCT   C  C
                                GGGGCAGA   CCC GC GA
                                ||||||||   ||| || ||
                                TCCCGTCT   GGG CG CT
                                    CGC_   A  A
GAM319  GNB3    3'  AGGGGCAGGTTGTCCTTGCTCA 8179        ATCC   CC  _
                                AGGGGCAG   TCC  GC CG
                                ||||||||   |||  || ||
                                TCCCCGTC   AGG  CG GT
                                    CAAC   AA  A
GAM319  GPR17   3'  AAGGGCAGATGCCTCTTGC   8180         _   CCC
                                AGGGGCAGAT CCTC   GC
                                |||||||||| ||||   ||
                                TTCCCGTCTA GGAG   CG
                                    C   AA_
GAM319  HYAL2   3'  AGGGTCAGGTCCTCCCCAGC  8181      G  A      _
                                AGGG CAG TCCTCCCC GC
                                |||| ||| |||||||| ||
                                TCCC GTC AGGAGGGG CG
                                  A  C       T
GAM319  HYAL2   3'  AGGGTCAGGTCCTCCCCAGC  8181      G  A      _
                                AGGG CAG TCCTCCCC GC
                                |||| ||| |||||||| ||
                                TCCC GTC AGGAGGGG CG
                                  A  C       T
GAM319  ID3     3'  AGGAGCAGTCAGTTTCCGCCGA 8182        A  CTCC_
                                AGGGGCAG TC    CCGCCGA
                                |||||||| ||    |||||||
                                TCCTCGTC AG    GGCGGCT
                                    _  TCAAA
GAM319  MHC2TA  3'  AGGAGCTGTCCCCGCTGA   8183       AGATCC     C
                                AGGGGC     TCCCCGC GA
                                ||||||     ||||||| ||
                                TCCTCG     AGGGGCG CT
                                   AC____      A
GAM319  PITX2   5'  AGGGGACGCAACCCCCGCCGA  8184      CAGATCC
                                AGGGG      TCCCCGCCGA
                                |||||      ||||||||||
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                                TCCCC      GGGGGCGGCT
                                   TGCGTT_
GAM319  RALBP1   3'  GGGCAGCCTCCTCCCCGC    8185        A_
                                GGGCAG  TCCTCCCCGC
                                ||||||  ||||||||||
                                CCCGTC  AGGAGGGGCG
                                   GG
GAM319  SMARCD2  3'  GGGGCAGAGGAGGCATCTGCTG 8186         TCC____  CCC  C
           AAC                    GGGGCAGA      TC   GC GAAC
                                ||||||||      ||   || ||||
                                CCCCGTCT      AG   CG CTTG
                                     CCTCCGT  A__  A
GAM319  SORCS2   3'  GGGGCAGAACCTGCCTGA    8187         T  CCCC  _
                                GGGGCAGA CCT    GCC GA
                                |||||||| |||    ||| ||
                                CCCCGTCT GGA    CGG CT
                                     T  _____   A
GAM319  WWP2     3'  GGCCAGTCTCCTCGCCGAAC  8188     G  ATC   C
                                GG CAG   CTCC CGCCGAAC
                                || |||   |||| ||||||||
                                CC GTC   GAGG GCGGCTTG
                                 G  A__    A
GAM319  DKFZp434M0331 3'  AGGGGCAGAGCCTCCAGC    8189         T    CC
                                AGGGGCAGA CCTCC  GC
                                ||||||||| |||||  ||
                                TCCCCGTCT GGAGG  CG
                                     C    T_
GAM319  FLJ11099  3'  AGGGGCAGGCCCTACTGA    8190         AT   CCCC  C
                                AGGGGCAG  CCT    GC GA
                                ||||||||  |||    || ||
                                TCCCCGTC  GGA    TG CT
                                     CG   _____  A
GAM319  FLJ13593  3'  AGGGGCAGAACCTCCTCCA    8191         T    _
                                AGGGGCAGA CCTCC CCG
                                ||||||||| ||||| |||
                                TCCCCGTCT GGAGG GGT
                                     T    A
GAM319  FLJ20986  5'  GAGGCAGATCTTCCTAGC    8192         C   CC
                                GGGGCAGATC TCC  GC
                                |||||||||| |||  ||
                                CTCCGTCTAG AGG  CG
                                      A   AT
GAM319  GIOT-3    5'  GAGGCAGATCCTCCTGGGGC   8193           CC__
                                GGGGCAGATCCTCC    GC
                                ||||||||||||||    ||
                                CTCCGTCTAGGAGG    CG
                                        ACCC
GAM319  HCRTR1    3'  AGGGGCAGATCCCCCGAGC    8194           CC
                                AGGGGCAGATCCTCC  GC
                                ||||||||||||||  ||
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                                TCCCCGTCTAGGGGG CG
                                        CT
GAM319  HSU79303 3' AGGGGCAGGTCATCCACCG  8195        A CTCC
                                AGGGGCAG TC   CCGCCG
                                |||||||| ||   ||||||
                                TCCCCGTC AG   GGTGGC
                                    C TA__
GAM319  KIAA0064 3' AGGGGCAATCCTCTGTGC   8196       A   CCC
                                AGGGGCAG TCCTC  GC
                                |||||||| |||||  ||
                                TCCCCGTT AGGAG  CG
                                    _   ACA
GAM319  KIAA0379 3' GGGGCAGACTCTCACAGA   8197       TC  CCC C
                                GGGGCAGA CTC  GC GA
                                |||||||| |||  || ||
                                CCCCGTCT GAG  TG CT
                                    GA ___ T
GAM319  KIAA1196 3' GGGCAGACCCTGCTGA     8198         CCCC C
                                GGGCAGATCCT   GC GA
                                ||||||||||   || ||
                                CCCGTCTGGGA   CG CT
                                     ____ A
GAM319  KIAA1655 5' GGGGCAGATCCCTCCGGCTGA 8199         TC C C
                                GGGGCAGATCC CC GC GA
                                |||||||||| || || ||
                                CCCCGTCTAGG GG CG CT
                                     GA C A
GAM319  MAD4    3' AGGGACAGGTCCCTGAGACGC 8200        A  CCC__
                                AGGGGCAG TCCT   CGC
                                |||||||| ||||   |||
                                TCCCTGTC AGGG   GCG
                                    C  ACTCT
GAM319  PMF1    3' AGGGGCAGAGCTGACCTGAAC 8201        TC CC GCC
                                AGGGGCAGA CT CC  GAAC
                                ||||||||| || ||  ||||
                                TCCCCGTCT GA GG  CTTG
                                    C_ CT A__
GAM319  SAE1    3' AGGGGCAGGCTCCTCCCTCC  8202        A_    CG
                                AGGGGCAG TCCTCCC CC
                                |||||||| |||||| ||
                                TCCCCGTC AGGAGGG GG
                                    CG     A_
GAM319  TESK2   3' GAGGCAGACCTCCTTGC     8203        T   CC
                                GGGGCAGA CCTCC GC
                                |||||||| ||||| ||
                                CTCCGTCT GGAGG CG
                                    _   AA
GAM319  TSC22   3' GAGGCAGATTCTCCCTAGC   8204        C   C_
                                GGGGCAGAT CTCCC GC
                                ||||||||| ||||| ||
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                                CTCCGTCTA GAGGG  CG
                                     A    AT
GAM319  LOC127435 3'  AGGGGCAGACCCTTCCCTGC  8205          _  C
                                AGGGGCAGATCCT CCC GC
                                |||||||||||| ||| ||
                                TCCCCGTCTGGGA GGG CG
                                      A  A
GAM319  LOC145384 3'  AGGGGCAGTATTTTCCAGAC  8206       _ CC  CC
                                AGGGGCAG AT  TCC  GC
                                |||||||| ||  |||  ||
                                TCCCCGTC TA  AGG  TG
                                    A  AA  TC
GAM319  LOC146268 3'  AGACATCCTCCCTGTTGAA   8207      GA     CGCC
                                GGGCA  TCCTCCC   GAA
                                |||||  |||||||   |||
                                TCTGT  AGGAGGG   CTT
                                  __     ACAA
GAM319  LOC153277 3'  AGGGGTATGGTCCTCTCATGAA 8208      CAGA_   CC  CC
                                AGGGG   TCCTC  CG  GAA
                                |||||   |||||  ||  |||
                                TCCCC   AGGAG  GT  CTT
                                  ATACC   A_  A_
GAM319  LOC157638 5'  AGGGGCATGTCTTTCCCCCGC  8209       GA  C__
                                AGGGGCA  TC   TCCCCGC
                                |||||||  ||   |||||||
                                TCCCCGT  AG   GGGGGCG
                                    AC  AAA
GAM319  LOC158382 5'  GAGGCAGATCCTTCACCAA   8210         CCC
                                GGGGCAGATCCT   CGCCGA
                                ||||||||||||   ||||||
                                CTCCGTCTAGGA   GTGGTT
                                      A__
GAM319  LOC200982 3'  AGGAGCAGAGGGCCCTGTTGAA 8211        TCCTC   GCC_
          C                    AGGGGCAGA    CCC    GAAC
                               |||||||||    |||    ||||
                               TCCTCGTCT    GGG    CTTG
                                    CCC__   ACAA
GAM319  LOC222962 3'  GGGGCGGTCCTCCCCCTGGAA  8212      AGA      GCC
                                GGGGC   TCCTCCCC   GAA
                                |||||   ||||||||   |||
                                CCCCG   AGGAGGGG   CTT
                                  CC_      GAC
GAM319  LOC254263 3'  GGGGCTGCCCCCCTGCTGA   8213      AGAT    C  C
                                GGGGC   CCTCCC GC GA
                                |||||   |||||| || ||
                                CCCCG   GGGGGG CG CT
                                  AC__     A  A
GAM319  LOC90799  5'  AGAGGCAGGTCGCCGCCG    8214        A  CTCC
                                AGGGGCAG TC   CCGCCG
                                |||||||| ||   ||||||
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                                TCTCCGTC AG   GGCGGC
                                    C  C___
GAM320  ACK1    5'  CAGCAGCCTCCGCGGGC    8217          AAC
                                CAGCAGCCTCCGC  GC
                                ||||||||||||  ||
                                GTCGTCGGAGGCG  CG
                                     CC_
GAM320  AQP2    3'  GCAGCCTCCTCCCCGCCTGCT  8218        GCAA   C
                                GCAGCCTCC   CGCC TGCT
                                |||||||||   |||| ||||
                                CGTCGGAGG   GCGG ACGA
                                    AGGG   _
GAM320  BTRC    3'  CAGGAGTCTCAAAGCCCTGCT  8219     C  C   CGC  C
                                CAG AG CTC   AA GCCCTGCT
                                ||| || |||   || ||||||||
                                GTC TC GAG   TT CGGGACGA
                                  C  A   ___  T
GAM320  BTRC    3'  CAGGAGTCTCAAAGCCCTGCT  8219     C  C   CGC  C
                                CAG AG CTC   AA GCCCTGCT
                                ||| || |||   || ||||||||
                                GTC TC GAG   TT CGGGACGA
                                  C  A   ___  T
GAM320  CCND1   3'  CAGGTGGCCTTTCCCGACCCTG 8220    CA_   ___   CAAC
          CT                    AG   GCCT   CCG   GCCCTGCT
                                ||   ||||   |||   ||||||||
                                TC   CGGA   GGC   TGGGACGA
                                 CAC   AAG   ____
GAM320  DPH2L1  5'  CAGGGCCGTCTCGGCGCCCTGC 8221     CA   _  _  CAA
          T                     CAG  GCC TC CG   CGCCCTGCT
                                |||  ||| || ||   |||||||||
                                GTC  CGG AG GC   GCGGGACGA
                                  C_   C  A  C__
GAM320  DRD2    3'  CAGCAGCCTCTTAGCCGTGGGC 8222         CGCAAC   CT__
          T                     CAGCAGCCTC     GCC    GCT
                                ||||||||||     |||   |||
                                GTCGTCGGAG     CGG    CGA
                                     AAT___   CACC
GAM320  DYRK3   5'  GCTGCCTCCGCGGCGCGACGCT 8223     A      AA   CC
                                GC GCCTCCGC  CGC  TGCT
                                || ||||||||  |||  ||||
                                CG CGGAGGCG  GCG  GCGA
                                 A       CC   CT
GAM320  FAT2    3'  CAGCAGCCCTGTGGGCAAGGC  8224         CC___   C
                                CAGCAGCCT    GCAA GC
                                |||||||||    |||| ||
                                GTCGTCGGG    CGTT CG
                                     ACACC    C
GAM320  FSTL3   3'  GCCGGACACAGTGCCCTGCT   8225     TC_   AC
                                GCC   CGCA  GCCCTGCT
                                |||   ||||  ||||||||
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                                CGG  GTGT  CGGGACGA
                                  CCT   CA
GAM320  HMX1    5'  GCGGCCTCCGCGCCGGGCT   8226    A     AAC  CT
                                GC GCCTCCGC  GCC  GCT
                                || ||||||||  |||  |||
                                CG CGGAGGCG  CGG  CGA
                                 C      ___  CC
GAM320  HS3ST3A1  5'  CAGCGGCCCCCGCCACTCTGCT 8227     A     AA  C
                                CAGC GCCTCCGC  CGC CTGCT
                                |||| ||||||||  ||| |||||
                                GTCG CGGGGGCG  GTG GACGA
                                  C      __  A
GAM320  HYOU1   3'  CAGCAGCCCTAGCTCCTGC   8228        CC  AACGC
                                CAGCAGCCT  GC   CCTGC
                                |||||||||  ||   |||||
                                GTCGTCGGG  CG   GGACG
                                     AT  A____
GAM320  IL17BR  3'  CAGCAGCCATCGTGGCAGGCT  8229        TC  CAAC  CCT
                                CAGCAGCC  CG   GC   GCT
                                ||||||||  ||   ||   |||
                                GTCGTCGG  GC   CG   CGA
                                    TA  AC__  TC_
GAM320  IRF2    3'  CAGCACCTCCACTGCCCT    8230      G     AAC
                                CAGCA CCTCCGC   GCCCT
                                ||||| |||||||   |||||
                                GTCGT GGAGGTG   CGGGA
                                  _      A__
GAM320  LMO2    5'  GCCCCGGGTCGCGGCGCCCTGC 8231      _____  AA
          T                      GCCTC   CGC  CGCCCTGCT
                                |||||   |||  |||||||||
                                CGGGG   GCG  GCGGGACGA
                                   CCCA   CC
GAM320  POLR2C  5'  CACCAGCCTCCGCGTCTGC   8232    G       AACGCC
                                CA CAGCCTCCGC     CTGC
                                || ||||||||||     ||||
                                GT GTCGGAGGCG     GACG
                                 G        CA____
GAM320  PPP1R12B  3'  GCAGCTTCCACCCTGC     8233      C  GCAAC
                                GCAGC TCC    GCCCTGC
                                ||||| |||    |||||||
                                CGTCG AGG    TGGGACG
                                  A  _____
GAM320  RUNX1   3'  CAGCAGTCCAGCTGCCCTGCT  8234       CC  _  AAC
                                CAGCAG  TCC GC   GCCCTGCT
                                ||||||  ||| ||   ||||||||
                                GTCGTC  AGG CG   CGGGACGA
                                   __   T  A__
GAM320  SCAMP3  5'  GCGGCCTCCGCGGCCCT    8235    A     AAC
                                GC GCCTCCGC   GCCCT
                                || ||||||||   |||||
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                                CG CGGAGGCG   CGGGA
                                 C       C__
GAM320  SCAMP3   5'  GCGGCCTCCGCGGCCCT     8235     A       AAC
                                GC GCCTCCGC   GCCCT
                                || ||||||||   |||||
                                CG CGGAGGCG   CGGGA
                                 C       C__
GAM320  SFTPC    3'  GCTTCCACTGACCCTGCT    8236     C     AAC
                                GC TCCGC   GCCCTGCT
                                || |||||   ||||||||
                                CG AGGTG   TGGGACGA
                                 A    AC_
GAM320  TYRO3    3'  CAGGAGCCTCCACACCTTGCT  8237      C        AAC   C
                                CAG AGCCTCCGC   GCC TGCT
                                ||| |||||||||   ||| ||||
                                GTC TCGGAGGTG   TGG ACGA
                                  C        ___   A
GAM320  C20orf27 5'  CAGCAGCCTCCCATG       8238            G  ACGCCC
                                CAGCAGCCTCC CA     TG
                                |||||||||| ||     ||
                                GTCGTCGGAGG GT     AC
                                          _ _______
GAM320  CDC14B   3'  GCGGCCTCCGCTGCTGAGAGGC 8239     A       AAC  CCT___
           T                     GC GCCTCCGC   GC      GCT
                                || ||||||||   ||      |||
                                CG CGGAGGCG   CG      CGA
                                 C       A__  ACTCTC
GAM320  cerk     3'  CAGCAGCCTTCCCGGCGC     8240          __   CAA
                                CAGCAGCCT  CCG   CGC
                                |||||||||  |||   |||
                                GTCGTCGGA  GGC   GCG
                                      AG   C__
GAM320  CRYGN    5'  ACACCGGGCAGCGCCCTGCT   8241      G  TCC   A
                                GCA CC   GCA CGCCCTGCT
                                ||| ||   ||| ||||||||||
                                TGT GG   CGT GCGGGACGA
                                  _  CC_   C
GAM320  DEPP     3'  GGACAGCTGGACAGTGCCCTGC 8242    A    CTCC   AC
           T                     C GCAGC    GCA  GCCCTGCT
                                | |||||    |||  ||||||||
                                C TGTCG    TGT  CGGGACGA
                                 C     ACC_   CA
GAM320  DKFZP434L1123 5'  GCAGCCTCTGCAGCAGTCT    8243         C   A  CC
                                GCAGCCTC GCA CG  CT
                                |||||||| ||| ||  ||
                                CGTCGGAG CGT GT  GA
                                      A   C  CA
GAM320  DKFZP586M1120 3'  GCAATCTTGCGTTTGCCCTGCT 8244      GC  CC  AAC_
                                GCA  CT  GC    GCCCTGCT
                                |||  ||  ||    ||||||||
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                                CGT  GA  CG   CGGGACGA
                                  TA  A_  CAAA
GAM320  FLJ00001  3'  GCAGCCCCCTCCCTGC      8245          GCAACG
                                GCAGCCTCC     CCCTGC
                                |||||||||     ||||||
                                CGTCGGGGGG     GGGACG
                                     A_____
GAM320  FLJ00058  5'  CAGCAGCCTCCGTTCCCTGCT  8246           CAACG
                                CAGCAGCCTCCG    CCCTGCT
                                ||||||||||||    |||||||
                                GTCGTCGGAGGC    GGGACGA
                                      AA___
GAM320  FLJ12355  3'  CAGCAGCCTCTGTGTGACAAC  8247          C_____
                                CAGCAGCCTC     GCAAC
                                ||||||||||     |||||
                                GTCGTCGGAG     TGTTG
                                     ACACAC
GAM320  FLJ13491  5'  CAGCAGCCTCTGCTAACAGCTG 8248          C _   CC
           CT                    CAGCAGCCTC GC AACG  CTGCT
                                ||||||||||| || ||||  |||||
                                GTCGTCGGAG CG TTGT  GACGA
                                     A  A   C_
GAM320  FLJ13868  3'  CAACCTCAATGCCCTGCT    8249        CGC  C
                                CAGCCTC   AA GCCCTGCT
                                |||||||   || ||||||||
                                GTTGGAG   TT CGGGACGA
                                    ___  A
GAM320  FLJ20200  5'  CAGCAGCCCCTGCAACAC    8250          C
                                CAGCAGCCTC GCAACGC
                                |||||||||| |||||||
                                GTCGTCGGGG CGTTGTG
                                     A
GAM320  FLJ20298  3'  CAGCAGCCTCTGAACCCCT   8251          CGC   G
                                CAGCAGCCTC   AAC CCCT
                                ||||||||||   ||| ||||
                                GTCGTCGGAG   TTG GGGA
                                     AC_  _
GAM320  FLJ20330  5'  GCCAGCCTCCTCATTCTGCT  8252     _     G  ACGCC
                                GC AGCCTCC CA    CTGCT
                                || ||||||| ||    |||||
                                CG TCGGAGG GT    GACGA
                                  G      A  AA___
GAM320  GOLGA2LY  5'  ACAGCCTCTCATCCTGC     8253        CG  ACGC
                                GCAGCCTC  CA   CCTGC
                                ||||||||  ||   |||||
                                TGTCGGAG  GT   GGACG
                                     A_  A___
GAM320  IL-17RE   3'  CAGCAGCAGCACAGTGCCCTGC 8254        CTC   AC
           T                     CAGCAGC   CGCA  GCCCTGCT
                                |||||||   ||||  ||||||||
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                                GTCGTCG  GTGT  CGGGACGA
                                   TC_   CA
GAM320  KIAA1184  3'  CAGCAGCCCCCATGTCCTTGCT 8255          CAACG  C
                                CAGCAGCCTCCG    CC TGCT
                                ||||||||||||    || ||||
                                GTCGTCGGGGGT    GG ACGA
                                      ACA__  A
GAM320  KIAA1505  5'  CAACAGCCTCTGTGATGCAAC  8256         C_____
                                CAGCAGCCTC     GCAAC
                                ||||||||||     |||||
                                GTTGTCGGAG     CGTTG
                                     ACACTA
GAM320  KIAA1906  3'  CAGTTTCCAGCCCTGCT     8257     CC   CAAC
                                CAG  TCCG   GCCCTGCT
                                |||  ||||   ||||||||
                                GTC  AGGT   CGGGACGA
                                  AA   _____
GAM320  LRP15     5'  GCGGCCGCTGCAGACCCTGCT  8258     A  TCC  AC
                                GC GCC   GCA  GCCCTGCT
                                || |||   |||  ||||||||
                                CG CGG   CGT  TGGGACGA
                                 C  CGA  C_
GAM320  MGC10966  5'  CAGCAGCCACTGCCTCT     8259        TCC  AAC  _
                                CAGCAGCC   GC   GCC CT
                                ||||||||   ||   ||| ||
                                GTCGTCGG   TG   CGG GA
                                     ___  A__   A
GAM320  MGC5469   5'  CAGCAGCCTCCACGGCGC    8260          AA
                                CAGCAGCCTCCGC  CGC
                                ||||||||||||  |||
                                GTCGTCGGAGGTG  GCG
                                       CC
GAM320  MKNK1     3'  GCAGCCTCTGTCAACTGATGCT 8261        CG_   GCCC
                                GCAGCCTC   CAAC    TGCT
                                ||||||||   ||||    ||||
                                CGTCGGAG   GTTG    ACGA
                                     ACA    ACT_
GAM320  NASP      3'  ACCTCCACTGCAGTGCCCTGCT 8262       ___   AC
                                GCCTCC   GCA  GCCCTGCT
                                ||||||   |||  ||||||||
                                TGGAGG   CGT  CGGGACGA
                                   TGA   CA
GAM320  NEIL2     5'  CAGCACCTCCGCAGGCGGC    8263      G      AC  CCT
                                CAGCA CCTCCGCA  GC   GC
                                ||||| ||||||||  ||   ||
                                GTCGT GGAGGCGT  CG   CG
                                   _      C_  C__
GAM320  NMU       5'  GCTCCACCTGGTGCCCTGCT   8264     C    AAC__
                                GC TCCGC    GCCCTGCT
                                || |||||    ||||||||
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                                CG AGGTG    CGGGACGA
                                 _    GACCA
GAM320  PEX16    5'  ACAGGCTGCGGCGCCCTGCT  8265     C  C  CAA
                                GCAG CT CG   CGCCCTGCT
                                |||| || ||   |||||||||
                                TGTC GA GC   GCGGGACGA
                                  C  C  C__
GAM320  PEX16    5'  ACAGGCTGCGGCGCCCTGCT  8265     C  C  CAA
                                GCAG CT CG   CGCCCTGCT
                                |||| || ||   |||||||||
                                TGTC GA GC   GCGGGACGA
                                  C  C  C__
GAM320  SLC11A1  5'  GCCAGCCCACGCCCTG     8266    _    CCGCA
                                GC AGCCT    ACGCCCTG
                                || |||||    ||||||||
                                CG TCGGG    TGCGGGAC
                                 G    ______
GAM320  SLC22A6  5'  CAGCAGCCTCCTTGGCTGC  8267         GCAACGCC
                                CAGCAGCCTCC      CTGC
                                ||||||||||       ||||
                                GTCGTCGGAGG      GACG
                                      AACC_____
GAM320  SLC26A9  3'  CAGCGGGCTCTGCAACCCT  8268     AGC  C  AC
                                CAGC  CTC GCA  GCCCT
                                ||||  ||| |||  |||||
                                GTCG  GAG CGT  TGGGA
                                  CCC  A  __
GAM320  SLC26A9  3'  CAGCGGGCTCTGCAACCCT  8268     AGC  C  AC
                                CAGC  CTC GCA  GCCCT
                                ||||  ||| |||  |||||
                                GTCG  GAG CGT  TGGGA
                                  CCC  A  __
GAM320  TCL6     3'  CAGCAGCCTCTTTCCAGCCCTG 8269        CGCAAC
                                CAGCAGCCTC    GCCCTG
                                ||||||||||    ||||||
                                GTCGTCGGAG    CGGGAC
                                      AAAGGT
GAM320  TCL6     3'  CAGCAGCCTCTTTCCAGCCCTG 8269        CGCAAC
                                CAGCAGCCTC    GCCCTG
                                ||||||||||    ||||||
                                GTCGTCGGAG    CGGGAC
                                      AAAGGT
GAM320  TUB      3'  CAGCAGCCCTGCAGTGTGC   8270        CC  ACGCCC
                                CAGCAGCCT  GCA    TGC
                                |||||||||  |||    |||
                                GTCGTCGGG  CGT    ACG
                                     A_  CAC___
GAM320  LOC124944 3'  CAGCAGCCTTTCAGCCCT   8271        CCG  AC
                                CAGCAGCCT  CA  GCCCT
                                |||||||||  ||  |||||
```

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                                GTCGTCGGA   GT  CGGGA
                                     AA_  __
GAM320  LOC129228 5'  GCAGCCTCCCTGTCCTTGCT   8272         GCAACG  C
                                GCAGCCTCC     CC TGCT
                                |||||||||     || ||||
                                CGTCGGAGG     GG ACGA
                                     GACA__  A
GAM320  LOC147791 3'  GCAGTCTCAGGCCCTGCT    8273      C   CGCAAC
                                GCAG CTC     GCCCTGCT
                                |||| |||     ||||||||
                                CGTC GAG     CGGGACGA
                                  A  TC____
GAM320  LOC148137 3'  GCAGCCTCTGGGCGAGGGGCTC 8274         C__  AAC__  C
           TGCT                    GCAGCCTC   GC    GC CTGCT
                                |||||||   ||    || |||||
                                CGTCGGAG   CG    CG GACGA
                                     ACC  CTCCC  A
GAM320  LOC149127 3'  CAGCAGCCTCCTAACCGATCTC 8275          GCAA  CC__
           TGCT                    CAGCAGCCTCC    CG    CTGCT
                                ||||||||||    ||    |||||
                                GTCGTCGGAGG    GC    GACGA
                                     ATTG  TAGA
GAM320  LOC149372 5'  CAGCAGCCTCCTTGACAC    8276          GCA
                                CAGCAGCCTCC   ACGC
                                ||||||||||   ||||
                                GTCGTCGGAGG   TGTG
                                     AAC
GAM320  LOC150378 5'  GCTGTCTTCGAAACCCTGCT   8277     AGC  C  C  C
                                GC   CT CG AA GCCCTGCT
                                ||   || || || ||||||||
                                CG   GA GC TT TGGGACGA
                                 ACA  A  _  _
GAM320  LOC152286 3'  CAGCGCTTTTCCCCTGCCCTGC 8278      A  _____   GCAAC
           T                     AGC GC    CTCC    GCCCTGCT
                                |||  ||    ||||    ||||||||
                                TCG CG    GGGG    CGGGACGA
                                  _  AAAA    A_____
GAM320  LOC168544 3'  CAGCAGCCCAGGTCGCCTTGCT 8279         CCGCAA    C
                                CAGCAGCCT     CGCC TGCT
                                |||||||||     |||| ||||
                                GTCGTCGGG     GCGG ACGA
                                     TCCA__    A
GAM320  LOC196955 3'  CAGCAGCCTCTTTGGCTGC    8280          CGCAAC  CC
                                CAGCAGCCTC     GC  TGC
                                ||||||||||     ||  |||
                                GTCGTCGGAG     CG  ACG
                                     AAAC__  __
GAM320  LOC196955 5'  CAGAGGCCTCTGAGGCCTTGCT 8281      CA    CGCAAC   C
                                CAG  GCCTC     GCC TGCT
                                |||  |||||     ||| ||||
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                                GTC  CGGAG     CGG ACGA
                                  TC    ACTC__   A
GAM320  LOC202347 3'  AGCAGCCTCTGGCCCTG     8282          CGCAAC
                                AGCAGCCTC     GCCCTG
                                |||||||||     ||||||
                                TCGTCGGAG     CGGGAC
                                     AC_____
GAM320  LOC220793 5'  GCAGTCTCCGCAAGCGGCT    8283       C       C  CCT
                                GCAG CTCCGCAA GC   GCT
                                |||| |||||||| ||   |||
                                CGTC GAGGCGTT CG   CGA
                                  A       _  C__
GAM320  LOC255017 5'  GCGGCCTCCGCGGCCCT     8235     A       AAC
                                GC GCCTCCGC   GCCCT
                                || ||||||||   |||||
                                CG CGGAGGCG   CGGGA
                                 C       C__
GAM320  LOC255952 5'  CAGCAGCCCTGCTTCCTTG    8284          CC  AACG  C
                                CAGCAGCCT  GC    CC TG
                                |||||||||  ||    || ||
                                GTCGTCGGG  CG    GG AC
                                     A_  AA__  A
GAM320  LOC256158 5'  CAGGAGCCGGTAGGCGCCCTGC 8285      C    TCCGCAA
          T                      CAG AGCC      CGCCCTGCT
                                |||| ||||      |||||||||
                                GTC TCGG      GCGGGACGA
                                  C    CCATCC_
GAM320  LOC257431 5'  ACAGCCTCTCATCCTGC     8253         CG  ACGC
                                GCAGCCTC  CA    CCTGC
                                ||||||||  ||    |||||
                                TGTCGGAG  GT    GGACG
                                     A_  A___
GAM320  LOC257447 5'  ACAGCCTCTCATCCTGC     8253         CG  ACGC
                                GCAGCCTC  CA    CCTGC
                                ||||||||  ||    |||||
                                TGTCGGAG  GT    GGACG
                                     A_  A___
GAM320  LOC51063  5'  CAGCAGCCTCCCAGCAGC    8286          G  AC  CCT
                                CAGCAGCCTCC CA  GC   GC
                                |||||||||||  ||  ||   ||
                                GTCGTCGGAGG GT  CG   CG
                                       _  __  T__
GAM320  LOC51604  3'  CAGCAGCCACCGACCACTTTTG 8287         T   CAA   CC_
          CT                     CAGCAGCC CCG   CGC   TGCT
                                |||||||| |||   |||   ||||
                                GTCGTCGG GGC   GTG   ACGA
                                     T   TG_   AAA
GAM320  LOC90170  5'  CAGCAGCCTTCTAACCCTATTG 8288         CCGCAAC    ___
          CT                     CAGCAGCCT     GCCCT   GCT
                                |||||||||      |||||   |||
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                                GTCGTCGGA      TGGGA   CGA
                                     AGAT___     TAA
GAM320  LOC90231  5' CAGCAGCCGCCACCCCTGC   8289        T   AACG
                                CAGCAGCC CCGC    CCCTGC
                                |||||||| ||||    ||||||
                                GTCGTCGG GGTG    GGGACG
                                    C   _____
GAM320  LOC90917  3' GCAGCCTCCCTAGCAATGGC  8290         ___   C_
                                GCAGCCTCC   GCAA  GC
                                |||||||||   ||||  ||
                                CGTCGGAGG   CGTT  CG
                                     GAT    AC
GAM320  LOC92710  3' GCAGCTTGCATGGGCCCTGCT  8291       CTCC   AC_
                                GCAGC    GCA   GCCCTGCT
                                |||||    |||   ||||||||
                                CGTCG    CGT   CGGGACGA
                                   AA__   ACC
GAM321  CSNK1G2   3' GAGGACTAGACACAGGTGTAGA 8294     AATA   CG    A
           A                     GAG    TAG  ACAG TGTAGAA
                                |||    |||  |||| |||||||
                                CTC    ATC  TGTC ACATCTT
                                  CTG_   TG    C
GAM321  MTAP     3' GAGAAATTGCTAGATGTAGA   8295       TATA  GAC
                                GAGAA    GC   AGATGTAGA
                                |||||    ||   |||||||||
                                CTCTT    CG   TCTACATCT
                                   TAA_  A__
GAM321  RAB27A   3' GAATATAGCGGGGAGACAGA   8296         _____
                                GAATATAGC     GACAGA
                                |||||||||     ||||||
                                CTTATATCG     CTGTCT
                                     CCCCT
GAM321  STATH    3' GAGAATATGGATGTAGA     8297         AGCGACA
                                GAGAATAT      GATGTAGA
                                ||||||||      ||||||||
                                CTCTTATA      CTACATCT
                                     C_______
GAM321  AKAP3    3' GAGGATATAGAGGGGGAGATGT 8298      A     CGAC__     A
           GGAA                    GAG ATATAG      AGATGT GAA
                                ||| ||||||      |||||| |||
                                CTC TATATC      TCTACA CTT
                                  C     TCCCCC     C
GAM321  DKFZp434G179 3'  GAGAGTATGTTGACAGTCTGTC 8299       A   AGC    A_  __
           TAGAA                   GAGA TAT   GACAG  TGT  AGAA
                                |||| |||   |||||  |||  ||||
                                CTCT ATA   CTGTC  ACA  TCTT
                                  C   CAA    AG   GA
GAM321  ELKS     3'  AGAGTAAGATGGCAGATGTAGA 8300      A  TAGCGA
           A                     AGA TA     CAGATGTAGAA
                                ||| ||     ||||||||||
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                                TCT AT     GTCTACATCTT
                                  C  TCTACC
GAM321  SLC25A21  3'  GAGATATAAAGTAGATGTAG  8301      A    CGAC
                                GAGA TATAG    AGATGTAG
                                |||| |||||    ||||||||
                                CTCT ATATT    TCTACATC
                                  _    TCA_
GAM321  WBSCR20A  5'  GAGATATCCCACAGATGTGGA  8302      A   AG G      A
                                GAGA TAT  C ACAGATGT GA
                                |||| |||  | |||||||| ||
                                CTCT ATA  G TGTCTACA CT
                                  _  GG _      C
GAM321  ZNF287    3'  GAAACCTGCATAGATGTAG   8303      ATATA   AC
                                GAGA    GCG  AGATGTAG
                                ||||    |||  ||||||||
                                CTTT    CGT  TCTACATC
                                  GGA__   A_
GAM322  CLCA1     5'  GAGAATGATAACAATATCT   8306       ATA  CTT
                                GAGAAT   GA   GCAATATCT
                                ||||||   ||   |||||||||
                                CTCTTA   CT   TGTTATAGA
                                   ___  AT_
GAM322  IL17      3'  GAGAGTTAGACTTGCTGTATCT 8307      ATA       AA
            C                    GAGA   TAGACTTGC  TATCTT
                                ||||   |||||||||  ||||||
                                CTCT   ATCTGAACG  ATAGAG
                                  CA_       AC
GAM322  JJAZ1     3'  AAGAATATGAAAATGCAATATC 8308         AG CT
            TT                    GAGAATAT  A  TGCAATATCTT
                                |||||||| |  ||||||||||
                                TTCTTATA  T  ACGTTATAGAA
                                    CT TT
GAM322  SLC4A4    3'  GATAATATAGACTCATCA    8309     G         _
                                GA AATATAGACTTG CA
                                || ||||||||||| ||
                                CT TTATATCTGAGT GT
                                 A          A
GAM322  KIAA1084  3'  GAGAATATAGGCTTTTGC    8310          A  __
                                GAGAATATAG CT  TGC
                                |||||||||| ||  |||
                                CTCTTATATC GA  ACG
                                     C  AA
GAM322  KIAA1726  3'  GAAAATATACAATATC      8311         AGACTT
                                GAGAATAT     GCAATATC
                                ||||||||     ||||||||
                                CTTTTATA     TGTTATAG
                                   _______
GAM322  KIAA1751  3'  GAGTGTAAACTTGCACAACC   8312      AATA        AT
                                GAG   TAGACTTGCA  ATC
                                |||   ||||||||||  |||
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                                CTC   ATTTGAACGT  TGG
                                  AC__        GT
GAM323  WBSCR1   3' GCTCTGAACTGAAGG      8315    G    ATC
                                GC TCTGGG   CTGAAGG
                                || ||||||   |||||||
                                CG AGACTT   GACTTCC
                                 _    ____
GAM323  WBSCR1   3' GCTCTGAACTGAAGG      8315    G    ATC
                                GC TCTGGG   CTGAAGG
                                || ||||||   |||||||
                                CG AGACTT   GACTTCC
                                 _    ____
GAM323  DKFZp434G171 5' GCTCTGGGATCCGCCAGGG   8316    G       TGA
                                GC TCTGGGATCC   AGGG
                                || ||||||||||   ||||
                                CG AGACCCTAGG   TCCC
                                 _        CGG
GAM323  SLC31A2  3' TAGTGTCTGGAAGAGGG    8317    C      TCCT  A
                                TAG GTCTGGGA    GA GG
                                ||| ||||||||    || ||
                                ATC CAGACCTT    CT CC
                                  A       _____  C
GAM323  LOC51185 3' TTCAGTGTCTGGGATCGTGGG  8318      C       CTGAA
                                TTTAG GTCTGGGATC    GGG
                                ||||| ||||||||||    |||
                                AAGTC CAGACCCTAG    CCC
                                   A        CA___
GAM324  HIS1     3' TCCAGTATTTCTTACCTCT   8321        CTACG   C
                                TCTAGTAT    TCT ACCTCT
                                ||||||||    ||| ||||||
                                AGGTCATA    AGA TGGAGA
                                     A_____  A
GAM324  TLR4     3' TCTAGCATTTATTCCCTCT   8322        C  CGTC  A
                                TCTAGTAT TA    TC CCTCT
                                |||||||| ||    || |||||
                                AGATCGTA AT    AG GGAGA
                                     A  A___  _
GAM324  TLR4     3' TCTAGCATTTATTCCCTCT   8322        C  CGTC  A
                                TCTAGTAT TA    TC CCTCT
                                |||||||| ||    || |||||
                                AGATCGTA AT    AG GGAGA
                                     A  A___  _
GAM324  TLR4     3' TCTAGCATTTATTCCCTCT   8322        C  CGTC  A
                                TCTAGTAT TA    TC CCTCT
                                |||||||| ||    || |||||
                                AGATCGTA AT    AG GGAGA
                                     A  A___  _
GAM324  TLR4     3' TCTAGCATTTATTCCCTCT   8322        C  CGTC  A
                                TCTAGTAT TA    TC CCTCT
                                |||||||| ||    || |||||
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                                AGATCGTA AT    AG GGAGA
                                    A  A___  _
GAM324  TNFSF8   3'  TCTGGTTCTATACCACACCTCT 8323      A  A    CG  T
           G                     TCT GT TCTA  TC CACCTCTG
                                 ||| || ||||  || ||||||||
                                 AGA CA AGAT  GG GTGGAGAC
                                   C  _    AT  T
GAM324  CRIPT    3'  TCTATTATCTCCTTCTCAC    8324       G    ACG
                                 TCTA TATCT   TCTCAC
                                 |||| |||||   ||||||
                                 AGAT ATAGA   AGAGTG
                                   A    GGA
GAM324  DKFZp564K142 3'  TCCAGTGTCTATATATCTC    8325        A   C__
                                 TCTAGT TCTA   GTCTC
                                 |||||| ||||   |||||
                                 AGGTCA AGAT   TAGAG
                                    C   ATA
GAM324  FLJ31890  3'  TCTATATCTACCAGTGTCT    8326       G     _____
                                 TCTA TATCTAC    GTCT
                                 |||| |||||||    ||||
                                 AGAT ATAGATG    CAGA
                                   _      GTCA
GAM324  KIAA0332  3'  CTAGTATCTGCACAATTTTCTG 8327          A  TCTCACC
                                 CTAGTATCT CG      TCTG
                                 |||||||||  ||      ||||
                                 GATCATAGA GT      AGAC
                                      C  GTTAAA_
GAM324  MGC2941   3'  TCTAGTACTCCACCT       8328         CTACG  T
                                 TCTAGTAT    TC CACCT
                                 ||||||||    || |||||
                                 AGATCATG    AG GTGGA
                                      _____  _
GAM324  MKP-7     3'  TCTAGCATCTGCCCTTCC     8329          AC   CA
                                 TCTAGTATCT  GTCT  CC
                                 ||||||||||  ||||  ||
                                 AGATCGTAGA  CGGG  GG
                                      __    AA
GAM324  TU12B1-TY 3'  TCCAGTATTTAGCCCAGTCTCT 8330         C  C   CAC
           G                     TCTAGTAT TA GTCT   CTCTG
                                 |||||||| || ||||   |||||
                                 AGGTCATA AT CGGG   GAGAC
                                    A  _    TCA
GAM325  CGTHBA    5'  GGGGCCAGAGGAGGACGGAGCC 8333      AT CT_     A
                                 GGG  C   GGAGGAC GAGCC
                                 |||  |   ||||||| |||||
                                 CCC  G   CCTCCTG CTCGG
                                   CG TCT      C
GAM325  ITGA3     3'  TGGGGGAGGGGCAGAGCCAG   8334      ATCCT    A_
                                 TGGG    GGAGG  CAGAGCCAG
                                 ||||    |||||  |||||||||
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                                ACCC    CCTCC  GTCTCGGTC
                                  _____    CC
GAM325  ITGA3    3'  TGGGGGAGGGGCAGAGCCAG  8334      ATCCT    A_
                                TGGG    GGAGG  CAGAGCCAG
                                ||||    |||||  |||||||||
                                ACCC    CCTCC  GTCTCGGTC
                                  _____    CC
GAM325  PEX14    3'  TGGGGGGAAGGACAGAGC    8335      ATCCT
                                TGGG    GGAGGACAGAGC
                                ||||    ||||||||||||
                                ACCC    CTTCCTGTCTCG
                                  CC___
GAM325  RELA     3'  GGATCCTGGAGAGAGCCA    8336          GAC
                                GGATCCTGGAG   AGAGCCA
                                ||||||||||   |||||||
                                CCTAGGACCTC   TCTCGGT
                                      ___
GAM325  SCA1     3'  TGGTATTCTGGAGGACAG    8337     G  C
                                TGG AT CTGGAGGACAG
                                ||| || ||||||||||||
                                ACC TA GACCTCCTGTC
                                  A  A
GAM325  SCD      3'  GGGACAGACAGGGTAGAGCCAG 8338       CCTGG   AC
                                GGGAT    AGG  AGAGCCAG
                                |||||    |||  ||||||||
                                CCCTG    TCC  TCTCGGTC
                                   TCTG_   CA
GAM325  SIGLEC11 3'  GGCCTGGAGGACAGAGTCAG   8339     AT          C
                                GG  CCTGGAGGACAGAG CAG
                                ||  ||||||||||||| |||
                                CC  GGACCTCCTGTCTC GTC
                                  __          A
GAM325  SOX13    3'  TGGGAACCGACTGGCAGAGCCA 8340       TC    A_  A
           G                     TGGGA  CTGG  GG CAGAGCCAG
                                |||||  ||||  || |||||||||
                                ACCCT  GGCT  CC GTCTCGGTC
                                   T_    GA  _
GAM325  STAC     3'  TGGGATCCTGGGGGACAG    8341          A
                                TGGGATCCTGG GGACAG
                                |||||||||| ||||||
                                ACCCTAGGACC CCTGTC
                                       C
GAM325  SURF6    3'  TGGAGATCCTGGGACAGAGCCA 8342     _      AG
           G                     TGG GATCCTGG  GACAGAGCCAG
                                ||| ||||||||  ||||||||||
                                ACC CTAGGACC  CTGTCTCGGTC
                                  T       __
GAM325  SYNGR1   3'  GGGATACCGGACAGAG      8343       _ TGGA
                                GGGAT CC    GGACAGAG
                                ||||| ||    ||||||||
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                                CCCTA GG   CCTGTCTC
                                  T ____
GAM325  WBSCR14  3'  GGGAAGGGCAGAGCC      8344      TCCT  A  A
                                GGGA   GG GG CAGAGCC
                                ||||   || || |||||||
                                CCCT   TC CC GTCTCGG
                                  ____ _ _
GAM325  WBSCR14  3'  GGGAAGGGCAGAGCC      8344      TCCT  A  A
                                GGGA   GG GG CAGAGCC
                                ||||   || || |||||||
                                CCCT   TC CC GTCTCGG
                                  ____ _ _
GAM325  CYP4F11  5'  TGGGATCCTGAGGCCCAG   8345         G  A_
                                TGGGATCCTG AGG  CAG
                                |||||||||| |||  |||
                                ACCCTAGGAC TCC  GTC
                                     _  GG
GAM325  DKFZP434J193 3'  TGGGGTTGAGGCAGAGCCAG  8346     ATCCTG   A
                                TGGG     GAGG CAGAGCCAG
                                ||||     |||| |||||||||
                                ACCC     CTCC GTCTCGGTC
                                  CAA___   _
GAM325  FAM3A    3'  AGGAATGGAGGACAGGGC    8347      TCC       A
                                GGGA   TGGAGGACAG GC
                                ||||   |||||||||| ||
                                TCCT   ACCTCCTGTC CG
                                  T__        C
GAM325  FLJ00001  3'  TGGGGCCTGGAGACGGAG    8348      AT     G  A
                                TGGG  CCTGGAG AC GAG
                                ||||  ||||||| || |||
                                ACCC  GGACCTC TG CTC
                                  C_      _ C
GAM325  FLJ10656  3'  TGGGACCTGGAAAGAG      8349      T     GAC
                                TGGGA CCTGGAG   AGAG
                                ||||| |||||||   ||||
                                ACCCT GGACCTT   TCTC
                                  _     ____
GAM325  FLJ12783  3'  TGGGGTCCTCGTCAGAGCCAG  8350     A   GGAGGA
                                TGGG TCCT     CAGAGCCAG
                                |||| ||||     |||||||||
                                ACCC AGGA     GTCTCGGTC
                                  C   GCA___
GAM325  FLJ13055  3'  TGGGGCCCTGGAGGAGACACAG 8351      AT       __  G
          C                      TGGG  CCTGGAGGA  CA AGC
                                ||||  |||||||||  || |||
                                ACCC  GGACCTCCT  GT TCG
                                  CG       CT  G
GAM325  FLJ14326  3'  GGGATCCTGCAAGGGCCA    8352         _   ACAGA
                                GGGATCCTG GAGG    GCCA
                                ||||||||| ||||    ||||
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                                CCCTAGGAC TTCC    CGGT
                                     G  _____
GAM325  FTCD     3'  GGGAACTGAGGACAGGGCCAG  8353      TC  G     A
                                GGGA  CTG AGGACAG GCCAG
                                ||||  ||| ||||||| |||||
                                CCCT  GAC TCCTGTC CGGTC
                                  T_  _     C
GAM325  HNOEL-iso 3'  AGGAAGAGAGGACAGAGC    8354      TCCT
                                GGGA   GGAGGACAGAGC
                                ||||   ||||||||||||
                                TCCT   TCTCCTGTCTCG
                                  TC__
GAM325  ITPK1    3'  GGGGTCAGACGGCAGAGCCAG  8355     A  CT GA  A
                                GGG TC  G  GG CAGAGCCAG
                                ||| ||  |  || |||||||||
                                CCC AG  C  CC GTCTCGGTC
                                  C  T_ TG  _
GAM325  KIAA0194  5'  TGGGGTCCTGAAGGGCAA    8356      A       A
                                TGGG TCCTGGAGG CAG
                                |||| ||||||||| |||
                                ACCC AGGACTTCC GTT
                                  C       C
GAM325  KIAA0748  3'  TGGGGGTTTGGAGGACCAAG  8357      ATCC      A
                                TGGG   TGGAGGAC GAG
                                ||||   |||||||| |||
                                ACCC   ACCTCCTG TTC
                                  CCAA      G
GAM325  KIAA0773  3'  TGAGGTCCTGGGACATGGAGTC 8358      A    AG   __  C
           AG                     TGGG TCCTGG  GACA  GAG CAG
                                |||| ||||||  ||||  ||| |||
                                ACTC AGGACC  CTGT  CTC GTC
                                  C     __    AC   A
GAM325  KIAA0892  3'  TGGGTAGCAAAGGACAGGGCCA 8359      ATCC GG     A
           G                      TGGG   T  AGGACAG GCCAG
                                ||||   |  ||||||| |||||
                                ACCC   G  TCCTGTC CGGTC
                                  ATC_ TT     C
GAM325  KIAA1228  3'  TGGGATCCTGGAGTGCTGAG  8360           GACA
                                TGGGATCCTGGAG   GAG
                                ||||||||||||   |||
                                ACCCTAGGACCTC   CTC
                                       ACGA
GAM325  MEIS3    3'  TGGGATCCTGAAGCCAG    8361           GA
                                TGGGATCCTGGAG  CAG
                                ||||||||||||  |||
                                ACCCTAGGACTTC  GTC
                                       G_
GAM325  MGC13064  3'  TAGGCTCTGGAGGACAGAGC  8362      ATC
                                TGGG  CTGGAGGACAGAGC
                                ||||  ||||||||||||||
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                                ATCC   GACCTCCTGTCTCG
                                  GA_
GAM325  MGC20576 3'  TAGGAGAGCCAGGGCAGAGC   8363      TC_ TG A  A
                                TGGGA   C  G GG CAGAGC
                                |||||   |  | || ||||||
                                ATCCT   G  C CC GTCTCG
                                   CTC GT _  _
GAM325  MGC4604  3'  GGGGTATGGGGCAGAGCCAG   8364     ATCC   A  A
                                GGG    TGG GG CAGAGCCAG
                                |||    ||| || |||||||||
                                CCC    ACC CC GTCTCGGTC
                                  CAT_  _  _
GAM325  MGC4737  3'  GGGATCCTGGGACCTGGGC    8365         AG   AGA_
                                GGGATCCTGG  GAC    GC
                                ||||||||||  |||    ||
                                CCCTAGGACC  CTG    CG
                                      __   GACC
GAM325  NRM      3'  TGGGGCCTGGAGGGACAG    8366      AT      _
                                TGGG  CCTGGAGG ACAG
                                ||||  |||||||| ||||
                                ACCC  GGACCTCC TGTC
                                   C_       C
GAM325  NRM      3'  TGGGGCCTGGAGGGACAG    8366      AT      _
                                TGGG  CCTGGAGG ACAG
                                ||||  |||||||| ||||
                                ACCC  GGACCTCC TGTC
                                   C_       C
GAM325  NRM      3'  TGGGGCCTGGAGGGACAG    8366      AT      _
                                TGGG  CCTGGAGG ACAG
                                ||||  |||||||| ||||
                                ACCC  GGACCTCC TGTC
                                   C_       C
GAM325  PV1      3'  TGGGATCCTGTGGGTACC    8367          GA  ACAGA
                                TGGGATCCTG  GG    GCC
                                ||||||||||  ||    |||
                                ACCCTAGGAC  CC    TGG
                                      AC  A____
GAM325  SLC38A5  5'  AGGTGGGGGACAGAGCCAG   8368     ATCC   A
                                GGG    TGG GGACAGAGCCAG
                                |||    ||| ||||||||||||
                                TCC    ACC CCTGTCTCGGTC
                                  ____   C
GAM325  LOC124739 3'  TGGGATCCTGAGGGCAG     8369         GA  A
                                TGGGATCCTG  GG CAG
                                ||||||||||  || |||
                                ACCCTAGGAC  CC GTC
                                      TC  _
GAM325  LOC124997 3'  GGACCCAGAGGGCAGAGC    8370        T    A
                                GGATCC GGAGG CAGAGC
                                |||||| ||||| ||||||
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                                CCTGGG TCTCC GTCTCG
                                   _    C
GAM325  LOC149668 5'  TGGGATCCTGGGAGGTCTGTGC 8371          _  ACAGA
                C                  TGGGATCCTGG AGG    GCC
                                   |||||||||| |||    |||
                                   ACCCTAGGACC TCC    CGG
                                         C  AGACA
GAM325  LOC151816 5'  TGGGGACCTGGGACAGTCA  8372      AT   AG   AGC
                                   TGGG  CCTGG  GACAG  CA
                                   ||||  |||||  |||||  ||
                                   ACCC  GGACC  CTGTC  GT
                                     CT    __    A__
GAM325  LOC159121 5'  TGGGTATCTTCCCACCAGAGCC 8373      _  CTGGAGGA
                AG                   TGGG ATC       CAGAGCCAG
                                   |||| |||       |||||||||
                                   ACCC TAG       GTCTCGGTC
                                     A  AAGGGTG_
GAM325  LOC168540 5'  TGGGGGTTTGGGGGAAAGCCAG 8374      ATCC  A  CA
                                   TGGG   TGG GGA  GAGCCAG
                                   ||||   ||| |||  |||||||
                                   ACCC   ACC CCT  TTCGGTC
                                     CCAA  C  __
GAM325  LOC170221 3'  TGGGACCCTCAATGGAGCCAG  8375        G  GGACA
                                   TGGGATCCT GA    GAGCCAG
                                   |||||||| ||    |||||||
                                   ACCCTGGGA TT    CTCGGTC
                                         G  AC___
GAM325  LOC199800 5'  TGGGACCCTGGAACCTCGGGGG 8376           GACAGA__
                CCAG                  TGGGATCCTGGAG      GCCAG
                                   ||||||||||||       |||||
                                   ACCCTGGGACCTT      CGGTC
                                         GGAGCCCC
GAM325  LOC254504 5'  TGGGATTACTGAGAGCCA   8377       C_  GAGGAC
                                   TGGGAT  CTG    AGAGCCA
                                   ||||||  |||    |||||||
                                   ACCCTA  GAC    TCTCGGT
                                      AT  _______
GAM325  LOC90520  5'  TGGGATTACTGAGAGCCA   8377       C_  GAGGAC
                                   TGGGAT  CTG    AGAGCCA
                                   ||||||  |||    |||||||
                                   ACCCTA  GAC    TCTCGGT
                                      AT  _______
GAM325  LOC96652  3'  TGGGACCCTGGGAGGCCAG  8378          _  A
                                   TGGGATCCTGG AGG CAG
                                   |||||||||| ||| |||
                                   ACCCTGGGACC TCC GTC
                                         C  G
GAM326  CARPX     3'  TGCAAGTGCTTGTGTGTGTG  8381        A  CG_  A
                                   TGCAAGT CT   GTG GTG
                                   ||||||| ||   ||| |||
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                                ACGTTCA GA   CAC CAC
                                    C  ACA   A
GAM326  WNT1     3'  GTACTCGGGTGGGCGAAT    8382        _  AGT
                                GTACTCGG TG   GCGAAT
                                |||||||| ||   ||||||
                                CATGAGCC AC   CGCTTA
                                    C  C__
GAM326  FLJ10508 5'  TGCATAGTGCTTGGTGAGGCA 8383      _  A  C     T
                                TGCA AGT CT GGTGAG GCG
                                |||| ||| || |||||| |||
                                ACGT TCA GA CCACTC CGT
                                  A   C  A     _
GAM326  FLJ20033 3'  TGCAAGTAGTCGTGTGAGT   8384        C   _
                                TGCAAGTA TCG GTGAGT
                                |||||||| ||| ||||||
                                ACGTTCAT AGC CACTCA
                                    C   A
GAM326  PRO1635  3'  AAGTAGTGAGTGTGAA      8385      ACTC       C
                                AAGT    GGTGAGTG GAA
                                ||||    |||||||| |||
                                TTCA    TCACTCAC CTT
                                  ____       A
GAM326  LOC152426 3'  GTATAAAATGGGTGCGAAT   8386     CTC    A
                                GTA   GGTG GTGCGAAT
                                |||   |||| ||||||||
                                CAT   TTAC CACGCTTA
                                  ATT    C
GAM326  LOC196500 3'  TGCAAGGCTTTCATGTGAGT  8387       TAC_   _
                                TGCAAG    TCG GTGAGT
                                ||||||    ||| ||||||
                                ACGTTC    AGT CACTCA
                                   CGAA   A
GAM326  LOC255328 3'  TGCAAGACTTCTGTGAAT    8388       T   _ G
                                TGCAAG ACT C GTGAGT
                                |||||| ||| | ||||||
                                ACGTTC TGA G CACTTA
                                   _   A A
GAM326  LOC90075  5'  TGTGAGTACTCTGATGC     8389     CA      GG   G
                                TG  AGTACTC  TGA TGC
                                ||  |||||||  ||| |||
                                AC  TCATGAG  ACT ACG
                                 AC      __   _
GAM326  LOC93333  5'  GTACTCGGTGCTATAAAT    8390          AG  CG
                                GTACTCGGTG  TG  AAT
                                ||||||||||  ||  |||
                                CATGAGCCAC  AT  TTA
                                      G_  AT
GAM327  ELK1     3'  TGTCTTGTCTTGGGGAAAAAAG 8393          GA___
            T                    TGTCTTGTCT    AAGAAAGT
                                ||||||||||    ||||||||
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                                ACAGAACAGA    TTTTTTCA
                                      ACCCC
GAM327  RP42    3'  TGTTTGTCTGAAAGAGCAGT  8394     C         A_
                                TGT TTGTCTGAAAGA  AGT
                                ||| ||||||||||||  |||
                                ACA AACAGACTTTCT  TCA
                                  _         CG
GAM327  FLJ13385  3'  TCTTGTTTCGGTGGAAAGTCTA 8395       CTGAAA_
           T                     TCTTGT      GAAAGTCTAT
                                ||||||      ||||||||||
                                AGAACA      CTTTCAGATA
                                   AAGCCAC
GAM327  KIAA0036  3'  GTCTTGTCTGGAGGAGAACCT  8396          AAA  A GT
                                GTCTTGTCTG   GA A  CT
                                ||||||||||   || |  ||
                                CAGAACAGAC   CT T  GA
                                      CTC  C TG
GAM327  KIAA1775  3'  TGTCCTGTTTGGGAGAAAA   8397         C  AA
                                TGTCTTGT TG  AGAAAG
                                |||||||| ||  ||||||
                                ACAGGACA AC  TCTTTT
                                     A  CC
GAM327  MGC1136   3'  TGTGCTTGGAGTGGAAAGTCT  8398     _   TCTGAAA
                                TGT CTTG      GAAAGTCT
                                ||| ||||      ||||||||
                                ACA GAAC      CTTTCAGA
                                  C   CTCAC__
GAM327  TPC2    3'  TTGTCTGAAAGGTCC       8399           AAA
                                TTGTCTGAAAG   GTCT
                                ||||||||||   ||||
                                AACAGACTTTC   CAGG
                                      ___
GAM327  LOC253981 3'  TGTTTTCTAGAGAAAGTCT   8400     CTTG   AA
                                TGT   TCTG  AGAAAGTCT
                                |||   ||||  |||||||||
                                ACA   AGAT  TCTTTCAGA
                                  AA__   C_
GAM327  LOC51285  3'  TGCTTGTCTGCTAAGAGTCT   8401    T      AAA  A
                                TG CTTGTCTG   GA AGTCT
                                || ||||||||   || |||||
                                AC GAACAGAC   TT TCAGA
                                  _       GA_  C
GAM327  LOC91263  5'  TGTCTGTCTGAAGATGTCTAT  8402       T      A  AA
                                TGTCT GTCTGAA GA  GTCTAT
                                ||||| ||||||| ||  ||||||
                                ACAGA CAGACTT CT  CAGATA
                                   _      _ A_
GAM328  CUGBP1   3'  TCAAAGGTGAGAGTTCAAGCAT 8405          A     ATGAC
                                TTAAAGGT AGAGTT    GCAT
                                |||||||| ||||||    ||||
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                                AGTTTCCA TCTCAA    CGTA
                                    C     GTT__
GAM328  PCK1     3'  TAAAGGTAAGGAACAATG    8406          _ TT
                                TAAAGGTAAG AG  ATG
                                |||||||||| ||  |||
                                ATTTCCATTC TT  TAC
                                    C  GT
GAM328  KIAA1872 3'  GGGGAGGGTTTATGACGCAT   8407     TA  A  _
                                GG  AG GTT ATGACGCAT
                                ||  || ||| |||||||||
                                CC  TC CAA TACTGCGTA
                                 CC  C   A
GAM328  LOC124602 3'  AGGTGGGGAATGTGACGCAT   8408      AA_   TA
                                AGGT   GAGT  TGACGCAT
                                ||||   ||||  ||||||||
                                TCCA   CTTA  ACTGCGTA
                                  CCC    C_
GAM328  LOC149628 3'  TTAAAGGTGAAAGAAATATG   8409         __    T
                                TTAAAGGT  AAGAG TATG
                                ||||||||  ||||| ||||
                                AATTTCCA  TTCTT ATAC
                                    CT    T
GAM328  LOC203397 3'  AGGTGGGGAATGTGACGCAT   8408      AA_   TA
                                AGGT   GAGT  TGACGCAT
                                ||||   ||||  ||||||||
                                TCCA   CTTA  ACTGCGTA
                                  CCC    C_
GAM329  SLC7A8   3'  TTGGCATCTCACCAACTATGGG 8412       CACGGTTT       A
                                TTGGT       CCAACTAT GG
                                |||||       |||||||| ||
                                AACCG       GGTTGATA CC
                                   TAGAGT__       C
GAM329  SRp25    3'  TTGGTTACGATTTCCTCTAGG  8413       C        AACTA
                                TTGGT ACGGTTTCC    TAGG
                                ||||| |||||||||    ||||
                                AACCA TGCTAAAGG    ATCC
                                   A        AG___
GAM329  LOC164832 3'  GGTTGTTTTCCAACTATGGG   8414     CACGG          A
                                GGT    TTTCCAACTAT GG
                                |||    |||||||||| ||
                                CCA    AAAGGTTGATA CC
                                  ACA__          C
GAM330  DMD      3'  TATAATAAGTCCTGTGTA    8417         A  G
                                TATAATAA TC TGTGTA
                                |||||||| || ||||||
                                ATATTATT AG ACACAT
                                    C  G
GAM330  DMD      3'  TATAATAAGTCCTGTGTA    8417         A  G
                                TATAATAA TC TGTGTA
                                |||||||| || ||||||
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                              ATATTATT AG ACACAT
                                   C  G
GAM330  DMD    3' TATAATAAGTCCTGTGTA   8417      A  G
                              TATAATAA TC TGTGTA
                              |||||||| || ||||||
                              ATATTATT AG ACACAT
                                   C  G
GAM330  DMD    3' TATAATAAGTCCTGTGTA   8417      A  G
                              TATAATAA TC TGTGTA
                              |||||||| || ||||||
                              ATATTATT AG ACACAT
                                   C  G
GAM330  DMD    3' TATAATAAGTCCTGTGTA   8417      A  G
                              TATAATAA TC TGTGTA
                              |||||||| || ||||||
                              ATATTATT AG ACACAT
                                   C  G
GAM330  DMD    3' TATAATAAGTCCTGTGTA   8417      A  G
                              TATAATAA TC TGTGTA
                              |||||||| || ||||||
                              ATATTATT AG ACACAT
                                   C  G
GAM330  DMD    3' TATAATAAGTCCTGTGTA   8417      A  G
                              TATAATAA TC TGTGTA
                              |||||||| || ||||||
                              ATATTATT AG ACACAT
                                   C  G
GAM330  DMD    3' TATAATAAGTCCTGTGTA   8417      A  G
                              TATAATAA TC TGTGTA
                              |||||||| || ||||||
                              ATATTATT AG ACACAT
                                   C  G
GAM330  DMD    3' TATAATAAGTCCTGTGTA   8417      A  G
                              TATAATAA TC TGTGTA
                              |||||||| || ||||||
                              ATATTATT AG ACACAT
                                   C  G
GAM330  DMD    3' TATAATAAGTCCTGTGTA   8417      A  G
                              TATAATAA TC TGTGTA
                              |||||||| || ||||||
                              ATATTATT AG ACACAT
                                   C  G
GAM330  DMD    3' TATAATAAGTCCTGTGTA   8417      A  G
                              TATAATAA TC TGTGTA
                              |||||||| || ||||||
                              ATATTATT AG ACACAT
                                   C  G
GAM330  DMD    3' TATAATAAGTCCTGTGTA   8417      A  G
                              TATAATAA TC TGTGTA
                              |||||||| || ||||||
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                                ATATTATT AG ACACAT
                                    C  G
GAM330  DMD      3'  TATAATAAGTCCTGTGTA    8417        A  G
                                TATAATAA TC TGTGTA
                                |||||||| || ||||||
                                ATATTATT AG ACACAT
                                    C  G
GAM330  PRO0246  5'  TATAATAAAATCTACACATCTC 8418         _  G  TG
          A                      TATAATAAA TC TG  TATCTCA
                                 |||||||||| || ||  |||||||
                                 ATATTATTT AG AT  GTAGAGT
                                      T  _  GT
GAM330  PTP4A1   3'  TATAACAAATTAGGCCCTATCT 8419          CGT  G_
          CAA                     TATAATAAAT   GT  TATCTCAA
                                  |||||||||||   ||  ||||||||
                                  ATATTGTTTA   CG  ATAGAGTT
                                       ATC  GG
GAM330  UNC93B1  3'  TAAAAAATCGTGGCTCTC    8420     T      T  A
                                TAA AAATCGTG GT TCTC
                                ||| |||||||| || ||||
                                ATT TTTAGCAC CG AGAG
                                  T      _  _
GAM330  LOC151778 3'  TAAAAAATCGTGGCTCTC    8420     T      T  A
                                TAA AAATCGTG GT TCTC
                                ||| |||||||| || ||||
                                ATT TTTAGCAC CG AGAG
                                  T      _  _
GAM330  LOC152915 3'  TAAAAAATCGTGGCTCTC    8420     T      T  A
                                TAA AAATCGTG GT TCTC
                                ||| |||||||| || ||||
                                ATT TTTAGCAC CG AGAG
                                  T      _  _
GAM330  LOC153883 3'  TATAATAAATCATGATCT    8421           TGT
                                TATAATAAATCGTG   ATCT
                                ||||||||||||||   ||||
                                ATATTATTTAGTAC   TAGA
                                                 ____
GAM330  LOC155340 3'  TAAAAAATCGTGGCTCTC    8420     T      T  A
                                TAA AAATCGTG GT TCTC
                                ||| |||||||| || ||||
                                ATT TTTAGCAC CG AGAG
                                  T      _  _
GAM330  LOC255620 3'  TAAAAAATCGTGGCTCTC    8420     T      T  A
                                TAA AAATCGTG GT TCTC
                                ||| |||||||| || ||||
                                ATT TTTAGCAC CG AGAG
                                  T      _  _
GAM330  LOC256598 3'  TAAAAAATCGTGGCTCTC    8420     T      T  A
                                TAA AAATCGTG GT TCTC
                                ||| |||||||| || ||||
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                                ATT TTTAGCAC CG AGAG
                                  T      _ _
GAM331  PSG5    5'  TCTCTGCGCCTGCGTGTTC   8424        G _ C
                                TCTCTGCG CT CG GTTC
                                |||||||| || || ||||
                                AGAGACGC GA GC CAAG
                                     G  C  A
GAM331  ADMP    5'  TCTGCAGCTCGTTCGCAGTTC  8425          GC    _
                                TCTGCGGCTC  GTTCGC GTTC
                                ||||||||||  |||||| ||||
                                AGACGTCGAG  CAAGCG CAAG
                                      __     T
GAM332  BAZ2A   3'  TGAAAACTGGGGGGGTGGGAGG  8428          AGC_
                                TGAAAACTGGG   GGGGGG
                                ||||||||||    ||||||
                                ACTTTTGACCC   CCCTCC
                                      CCCA
GAM332  CPNE7   3'  GAGGACTGGGAGTGGGGC    8429    AA      CGG
                                GA  ACTGGGAG   GGGGC
                                ||  ||||||||   |||||
                                CT  TGACCCTC   CCCCG
                                 CC       A__
GAM332  CXorf6  5'  TGGAAACTGGAAGTGGTCGG   8430    A       C _____
                                TG AAACTGGGAG GG    GG
                                || ||||||||| ||    ||
                                AC TTTGACCTTC CC    CC
                                 C        A  AGIII
GAM332  HD      3'  TGAAGATGGGGGGCGAGGGG   8431     AAC   A
                                TGAA   TGGG GCGGGGGG
                                ||||   |||| ||||||||
                                ACTT   ACCC CGCTCCCC
                                  CT_   C
GAM332  IMMP2L  5'  TGAGGACTGGGAGAGGGCGC  8432    AA      CGG
                                TGA  ACTGGGAG   GGGGCGC
                                |||  ||||||||   |||||||
                                ACT  TGACCCTC   TCCCGCG
                                  CC       ___
GAM332  ODF2    5'  TGAAAACTTGGGAGGCGC    8433        GGGAGC
                                TGAAAACT     GGGGGGCGC
                                ||||||||     |||||||||
                                ACTTTTGA     CCCTCCGCG
                                     A_____
GAM332  PTGFRN  3'  TGAAAACAGGGGGTGGGG    8434       T  AGC _
                                TGAAAAC GGG   GG GGGG
                                ||||||| |||   || ||||
                                ACTTTTG CCC   CC CCCC
                                     T  ___  A
GAM332  RNPEPL1 3'  GAGAGCTGGGAGTGGGGAGGCC 8435    AAA     C    C
                                GA   CTGGGAG GGGGGG GCC
                                ||   ||||||| |||||| |||
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                                CT   GACCCTC CCCCTC CGG
                                 CTC      A     _
GAM332  SEZ6L    5'  TGAGGAACTGGGGGGCGC    8436    T     _
                                C GGGAGC GGGGGGCGC
                                | |||||| |||||||||
                                A TCCTTG CCCCCCGCG
                                 C      A
GAM332  TEM5     3'  TGAAGACTGGGAGGGAAC    8437       A      GCG
                                TGAA ACTGGGA   GGGGGC
                                |||| |||||||   ||||||
                                ACTT TGACCCT   CCCTTG
                                  C      ____
GAM332  TNFSF4   3'  TGAGGGGTGGGGGCGGGAGGGC 8438      AAAC    A       C
             C                   TGA    TGGG GCGGGGGGG GCC
                                |||    |||| |||||||| |||
                                ACT    ACCC CGCCCTCC CGG
                                  CCCC    C       _
GAM332  WNT11    3'  TGGAAACTGGAGAGCTCC     8439         _      G
                                TGGGAGC GGGGGGC CC
                                ||||||| ||||||| ||
                                ACCTTTG CCTCTCG GG
                                    A      A
GAM332  CAMK1G   3'  TGGAAGCTGGTGGGCACC     8440         G  _
                                TGGGAGC GG GGGCGCC
                                ||||||| || |||||||
                                ACCTTCG CC CCCGTGG
                                    A  A
GAM332  CAPN13   3'  TGAGACTGGGTGGGGCGC     8441      AA     AGCGG
                                TGA  ACTGGG     GGGGCGC
                                |||  ||||||     |||||||
                                ACT  TGACCC     CCCCGCG
                                  C_     A_____
GAM332  FLJ00024 3'  TGAGGGCCTGGGAGGGGCGCC  8442      AAA_     GCGG
                                TGA    CTGGGA    GGGGCGCC
                                |||    ||||||    ||||||||
                                ACT    GACCCT    CCCCGCGG
                                  CCCG     _____
GAM332  FLJ10743 3'  TGAGAACTGGGAGTGGCCGG   8443      A       C  ______
                                TGA AACTGGGAG GG     GG
                                ||| ||||||||| ||     ||
                                ACT TTGACCCTC CC     CC
                                  C        A  GGIII
GAM332  FLJ20105 3'  ACTATGGAGTGGGGGGCG     8444       _   C
                                ACTG GGAG GGGGGGCG
                                |||| |||| ||||||||
                                TGAT CCTC CCCCCCGC
                                  A   A
GAM332  FLJ21742 3'  TGAAGGCTGGGAGCAGAACGGC 8445       AA          _
                                TGAA  CTGGGAGCGGGG GGC
                                ||||  |||||||||||| |||
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                                ACTT  GACCCTCGTCTT CCG
                                  CC          G
GAM332  FLJ23306  5'  TGATGACTGGGAGGCGTCGG  8446     AA      _ _____
                                TGA  ACTGGGAG CG    GG
                                |||  |||||||| ||    ||
                                ACT  TGACCCTC GC    CC
                                  AC       C  AGIII
GAM332  HSPC189  5'  GAAGGTTGGGGCGGGGCGCC  8447     AAC   A  GG
                                GAA   TGGG GC  GGGGCGCC
                                |||   |||| ||  ||||||||
                                CTT   ACCC CG  CCCCGCGG
                                  CCA   _ __
GAM332  KIAA0125  5'  TGGAAACTGAGGAGTGGTCGGC 8448   A    _   C _____  GGCG
            GCC                    AAACTG GGAG GG    GG   C
                                |||||| |||| ||    ||   |
                                TTTGAC CCTC CC    CC   G
                                C     T    A  AGIII  GCGG
GAM332  KIAA1036  3'  TGAAAGCTGGGATGGGA    8449      A     GC
                                TGAAA CTGGGA  GGGG
                                |||||| ||||||  ||||
                                ACTTT GACCCT  CCCT
                                   C     A_
GAM332  KIAA1465  3'  TGAAGGTTGGGGACGGGGGAC  8450     AAC   AG
                                TGAA   TGGG  CGGGGGGC
                                ||||   ||||  ||||||||
                                ACTT   ACCC  GCCCCCTG
                                  CCA    CT
GAM332  KIAA1630  3'  GAAGCTGGGATCACAGGTGCC  8451     AA    G  G   GC
                                GAA  CTGGGA CG GGG  GCC
                                |||  |||||| || |||  |||
                                CTT  GACCCT GT TCC  CGG
                                  C_     A  G   A_
GAM332  LASP1    3'  TGAAGACAGATGGGGGCGC   8452     AACT  G  CG
                                TGAA    GG AG  GGGGGCGC
                                ||||    || ||  ||||||||
                                ACTT    CT TC  CCCCCGCG
                                  _____  G  TA
GAM332  PPP1R10  3'  TGGGAGCAGGGAGTGAGC    8453          C__
                                TGGGAGCGGGGGG   GC
                                ||||||||||||   ||
                                ACCCTCGTCCCTC   CG
                                       ACT
GAM332  RAB3IL1  3'  TGGGGACTGGGGAGGGGGCGC  8454    AAA    AGC
                                TG   ACTGGG   GGGGGGCGC
                                ||   ||||||   |||||||||
                                AC   TGACCC   TCCCCCGCG
                                  CCC     C__
GAM332  STMN3    3'  TGAAGCTGGGGGCGGGGG    8455     AA    A
                                TGAA  CTGGG GCGGGGG
                                ||||  ||||| |||||||
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                                ACTT  GACCC CGCCCCC
                                  C_    C
GAM332  TCF-3    3'  TGAAAGCTGGGGCTGGCGAG  8456       A    A _  G
                                TGAAA CTGGG GC GG GGG
                                ||||| ||||| || || |||
                                ACTTT GACCC CG CC CTC
                                   C    _ A  G
GAM332  TNFRSF13B 3'  TGGGAACTGGGACTCAGAGTGC 8457     AA       G GG    C
          C                      TG  AACTGGGA C  GGGG GCC
                                ||  |||||||| |  |||| |||
                                AC  TTGACCCT G  TCTC CGG
                                 CC       _ AG    A
GAM332  WBSCR17   3'  ACTGGGAGATGGGACAGCC   8458         CGG    _
                                ACTGGGAG   GGGGC GCC
                                ||||||||   ||||| |||
                                TGACCCTC   CCCTG CGG
                                     TA_    T
GAM332  LOC116113 3'  ACTGGGAGGGCAGGTGC     8459         C  G   C
                                ACTGGGAG GG GGG GC
                                |||||||| || ||| ||
                                TGACCCTC CC TCC CG
                                     _ G   A
GAM332  LOC145481 5'  CGAGGCTGGGAGCGCGGAGCGC 8460      AAA       G
          C                      TGA   CTGGGAGCG GGGGCGCC
                                |||   ||||||||| ||||||||
                                GCT   GACCCTCGC CCTCGCGG
                                  CC_        G
GAM332  LOC146562 3'  TGGGGGCTGGGAGGCAGC    8461       A _      _
                                TGGG GC GGGGGGC GC
                                |||| || ||||||| ||
                                ACCC CG CCCTCCG CG
                                  C A      T
GAM332  LOC149692 3'  TGAAAACTGGTAGTGTAGG   8462          G  CGG
                                TGAAAACTGG AG   GGG
                                |||||||||| ||   |||
                                ACTTTTGACC TC   TCC
                                      A  ACA
GAM332  LOC196415 3'  TGAAAACTGGGATTGGCA    8463           GCGGGG
                                TGAAAACTGGGA     GGCG
                                ||||||||||||     ||||
                                ACTTTTGACCCT     CCGT
                                       AA____
GAM332  LOC201484 5'  TGAAACTGGGAGCCG       8464       A      GGGGGG
                                TGAAA CTGGGAGC     CG
                                ||||| ||||||||     ||
                                ACTTT GACCCTCG     GC
                                   _      _______
GAM332  LOC253502 3'  GAGGACTGGGAGTGGGGC    8429     AA       CGG
                                GA  ACTGGGAG   GGGGC
                                ||  ||||||||   |||||
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                                CT  TGACCCTC   CCCCG
                                 CC       A__
GAM332  LOC255718 5'  TGGAAACTGGGATGGGG     8465     A       GC
                                TG AAACTGGGA  GGGG
                                || |||||||||  ||||
                                AC TTTGACCCT  CCCC
                                 C        A_
GAM333  PLN      3'  CTTGAGATAATATATTTTTCTG 8468      A      GC_
                                CTT AGATAGTA   TTTTCTG
                                ||| ||||||||   |||||||
                                GAA TCTATTAT   AAAAGAC
                                  C       ATA
GAM333  SERPINI1  3'  TATCTTAAGATATACT      8469            GTA
                                TATCTTAAGATA   GCT
                                ||||||||||||   |||
                                ATAGAATTCTAT   TGA
                                       A__
GAM333  SURF6    3'  TATCTTAAGACTTCTTTTCTG  8470           AGTAG
                                TATCTTAAGAT    CTTTTCTG
                                ||||||||||     ||||||||
                                ATAGAATTCTG    GAAAAGAC
                                       AA___
GAM333  TTID     3'  TATTTTAAGATAGTCTTCT    8471      C        AGCT
                                TAT TTAAGATAGT    TTTCT
                                ||| ||||||||||    |||||
                                ATA AATTCTATCA    GAAGA
                                  A         _____
GAM333  DKFZP564D206 3'  TATCTGAGAAGCCCTTTTCTG  8472       TA   T   AG
                                TATCT  AGA AGT  CTTTTCTG
                                |||||  ||| |||  ||||||||
                                ATAGA  TCT TCG  GAAAAGAC
                                   C_   _   G_
GAM333  LOC57105  3'  ATCTTAGGATGTGCTTCTTTTC 8473       A   A_  AG
            TG                    ATCTTA GAT  GT  CTTTTCTG
                                ||||||| |||  ||  ||||||||
                                TAGAAT CTA  CG  GAAAAGAC
                                   C   CA  AA
GAM333  LOC91156  5'  TATCTCTAGAGGCTTTTCT    8474       AAGA   TA
                                TATCTT    TAG  GCTTTTCT
                                ||||||    |||  ||||||||
                                ATAGAG    ATC  CGAAAAGA
                                   _____   TC
GAM334  ARAF1    5'  TGGGCTGAGGTGGGGCTGGGCA 8477        ACA     _____
            GGTG                  GGGCTGA   GTGGGG    GCAGGTG
                                |||||||   |||||||   |||||||
                                CCCGACT   CACCCC    CGTCCAC
                                   C__      GACC
GAM334  CDA      3'  TAGGCTGGGGCCACTGGGCAGG 8478        AACAGTGG
            TG                    TGGGCTG       GGGCAGGTG
                                |||||||       |||||||||
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                                ATCCGAC      CCCGTCCAC
                                    CCCGGTGA
GAM334  DAG1    3'  TGGGCTGGAAGTGGGGA    8479       AAC
                                TGGGCTG  AGTGGGGG
                                |||||||  ||||||||
                                ACCCGAC  TCACCCCT
                                    CT_
GAM334  FUT1    3'  TGGGCTGGGAAGAGCAGGT   8480       AACAGT
                                TGGGCTG    GGGGGCAGGT
                                |||||||    ||||||||||
                                ACCCGAC    TTCTCGTCCA
                                    CC____
GAM334  HCK     3'  GGCTGAAGCGAGGGTGGGTG  8481       AC      CA
                                GGCTGA  AGTGGGGG  GGTG
                                ||||||  ||||||||  ||||
                                CCGACT  TCGCTCCC  CCAC
                                    __      AC
GAM334  LEP     3'  GGGCTGAGCATGAAGCAGGTG  8482       A  GTG
                                GGGCTGA CA   GGGGCAGGTG
                                ||||||| ||   ||||||||||
                                CCCGACT GT   CTTCGTCCAC
                                    C  A__
GAM334  LFG     3'  TGGGCTGAGTGAGTGGCCAGTG 8483        ACA   _  A
                                TGGGCTGA   GTGGG GGC GGTG
                                ||||||||   ||||| ||| ||||
                                ACCCGACT   CACTC CCG TCAC
                                    ___    A  G
GAM334  MATN1   5'  TGGGCTGAATGGAGGTGT    8484       ACA     CAG
                                TGGGCTGA   GTGGGGG  GT
                                ||||||||   |||||||  ||
                                ACCCGACT   TACCTCC  CA
                                    ___     A__
GAM334  MOCS1   3'  TGGGTGAGAAGGGCAGGT    8485     C  ACAGT
                                TGGG TGA    GGGGGCAGGT
                                |||| |||    ||||||||||
                                ACCC ACT    TTCCCGTCCA
                                  _  C____
GAM334  MX1     5'  TGAGCTGGGTGAGCAGGT    8486       AACAGT  _
                                TGGGCTG     GG GGGCAGGT
                                |||||||     || ||||||||
                                ACTCGAC     CC CTCGTCCA
                                    _______  A
GAM334  PSD     5'  TGGGCCGGGCCGTGGGGCAGGT 8487       AACA    G
          G                      TGGGCTG   GTGGGG CAGGTG
                                |||||||   |||||| ||||||
                                ACCCGGC   CACCCC GTCCAC
                                    CCGG    _
GAM334  SPTB    3'  TGGGCTGAGCTAGTAGGGG   8488       AC_
                                TGGGCTGA   AGTGGGGG
                                ||||||||   ||||||||
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                                ACCCGACT   TCATCCCC
                                     CGA
GAM334  SUV39H1  3'  GAGCAGGTGGGGGGCAGGTG   8489      TGAACA
                                GGGC     GTGGGGGGCAGGTG
                                ||||     |||||||||||||
                                CTCG     CACCCCCGTCCAC
                                  TC____
GAM334  VAX2     3'  TGAGCTGGGGGGGCAGG     8490        AACAGT
                                TGGGCTG     GGGGGGCAGG
                                |||||||     |||||||||
                                ACTCGAC     CCCCCGTCC
                                            _______
GAM334  DKFZp434I099 3'  TGGGCTGGCAGTGAGGCCAGGT 8491        AA       G
           G                     TGGGCTG  CAGTGGGG CAGGTG
                                |||||||  |||||||| ||||||
                                ACCCGAC  GTCACTCC GTCCAC
                                     C_       G
GAM334  FJX1     3'  TGGGATTGAAAGAAAGGGGCAG 8492      C_    C  T_
           GTG                     TGGG  TGAA AG  GGGGGCAGGTG
                                |||| |||| ||  ||||||||||
                                ACCC  ACTT TC  TCCCCGTCCAC
                                  TA   _  TT
GAM334  FLJ00007  3'  TGGGCAGGTGGGGCAGGT    8493       TGAAC  TG
                                TGGGC    AG  GGGGCAGGT
                                |||||    ||  |||||||||
                                ACCCG    TC  CCCCGTCCA
                                  _____  CA
GAM334  FLJ11000  3'  TGGGTTGGGAAGTGGAGGGTG  8494      C  AAC      CAG
                                TGGG TG   AGTGGGGG   GTG
                                |||| ||   ||||||||   |||
                                ACCC AC   TCACCTCC   CAC
                                  A  CCT      ___
GAM334  FLJ21865  3'  TGGGCTGGCGCGGGGGGCAGGT 8495        AACA     _
           G                     TGGGCTG   GTGGGGG CAGGTG
                                |||||||    ||||||| ||||||
                                ACCCGAC    CGCCCCC GTCCAC
                                     CG__      C
GAM334  FLJ32865  3'  GGCTGGGGAGGGCAGGT     8496       AACAGT
                                GGCTG     GGGGGCAGGT
                                |||||     ||||||||||
                                CCGAC     CTCCCGTCCA
                                  CC____
GAM334  FYCO1    3'  TGGGCTGAGCAGTGGGAAGTG  8497         A      GCA
                                TGGGCTGA CAGTGGGG   GGTG
                                |||||||| ||||||||   ||||
                                ACCCGACT GTCACCCT   TCAC
                                     C       ___
GAM334  KIAA0731  3'  TGGGCTGGGGAGTAAAGGGTG  8498        AAC      CAG
                                TGGGCTG   AGTGGGGG   GTG
                                |||||||   ||||||||   |||
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                                ACCCGAC  TCATTTCC  CAC
                                   CCC     ___
GAM334  KIAA1453  5'  GGGCTGAGTTTGGTTGGGCAGG 8499       ACAG  __
           TG                    GGGCTGA   TGG  GGGCAGGTG
                                |||||||   |||  |||||||||
                                CCCGACT   ACC  CCCGTCCAC
                                   CAA_   AA
GAM334  LHPP     3'  TGGTCTGGGCACTGGGGCAGGT 8500     G  AA  G   G
           G                     TGG CTG  CA TGGGG CAGGTG
                                ||| |||  || ||||| ||||||
                                ACC GAC  GT ACCCC GTCCAC
                                  A  CC  G   _
GAM334  MFN2     3'  TGGGCTGCAAGGAGGGCAGGTG 8501       AAC  T
                                TGGGCTG   AG GGGGGCAGGTG
                                |||||||   || ||||||||||
                                ACCCGAC   TC CTCCCGTCCAC
                                   GT_  _
GAM334  MGC23918  3'  TGGGCGAGTGGTGGGGCAG   8502      TGAAC   __
                                TGGGC    AGTGG  GGGCAG
                                |||||    |||||  ||||||
                                ACCCG    TCACC  CCCGTC
                                  C____    AC
GAM334  NXPH3    3'  TGGGCTGAGGGGTTAGG    8503        ACAGT   GC
                                TGGGCTGA    GGGG  AGG
                                ||||||||    ||||  |||
                                ACCCGACT    CCCC  TCC
                                     _____   AA
GAM334  SEF      3'  TGGGCTGAATGCTGAGAAAACG 8504        CAGT__ GG  A
           GGTG                    TGGGCTGAA     G  GGC GGTG
                                |||||||||     |  ||| ||||
                                ACCCGACTT     C  TTG CCAC
                                     ACGACT TT   C
GAM334  TRAF3    3'  TGGGCTGAGAAGTAGATTTGGG 8505        AC     GGCA
           TG                    TGGGCTGA  AGTGGG   GGTG
                                ||||||||  ||||||   ||||
                                ACCCGACT  TCATCT   CCAC
                                   CT     AAAC
GAM334  VCY2IP1  3'  TGGGCTGAGTGGGGGGCGT   8506       ACA     CAG
                                TGGGCTGA   GTGGGGG   GT
                                ||||||||   |||||||   ||
                                ACCCGACT   CACCCCC   CA
                                     ___      CG_
GAM334  LOC115861 5'  TGGGTTGGGTGCTGGGGACAG  8507      C  AACAG
                                TGGG TG    TGGGGGCAG
                                |||| ||    |||||||||
                                ACCC AC    ACCCCTGTC
                                  A  CCACG
GAM334  LOC124402 3'  TGGGCTGGGCTGGGCAGGTG   8508       AACA  GG
                                TGGGCTG   GT  GGGCAGGTG
                                |||||||   ||  |||||||||
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                                ACCCGAC   CG  CCCGTCCAC
                                    C___  A_
GAM334  LOC147040 5'  TGGGTTGGAGGCACAGGT    8509      C  AACAGT   G
                                TGGG TG     GGG GCAGGT
                                |||| ||     ||| ||||||
                                ACCC AC     TCC TGTCCA
                                  A  C_____  G
GAM334  LOC148870 3'  GGACGCATGGTGGGGGCGGGTG 8510      T AACA      A
                                GGGC G   GTGGGGGC GGTG
                                |||| |   |||||||| ||||
                                CCTG C   CACCCCCG CCAC
                                  _ GTAC      C
GAM334  LOC149577 3'  GGCTGGGAGGGCAGGT     8511       AACAGT
                                GGCTG     GGGGGCAGGT
                                |||||     ||||||||||
                                CCGAC     CTCCCGTCCA
                                  C_____
GAM334  LOC150684 3'  TGGCCTGAGCAGTGGGAGC   8512     G   A
                                TGG CTGA CAGTGGGGGC
                                ||| |||| ||||||||||
                                ACC GACT GTCACCCTCG
                                  G   C
GAM334  LOC151701 5'  TGAGCTGGGCAGTGGGGAC   8513        AA
                                TGGGCTG  CAGTGGGGGC
                                |||||||  ||||||||||
                                ACTCGAC  GTCACCCCTG
                                    CC
GAM334  LOC152845 5'  TGGGCTGAGTGGGTGGCCATGT 8514         ACA   _  AG_
          G                      TGGGCTGA  GTGGG GGC  GTG
                                ||||||||  ||||| |||  |||
                                ACCCGACT  CACCC CCG  CAC
                                    ___    A  GTA
GAM334  LOC158678 3'  TGGCCTGAGCAGTGGGAGC   8512     G   A
                                TGG CTGA CAGTGGGGGC
                                ||| |||| ||||||||||
                                ACC GACT GTCACCCTCG
                                  G   C
GAM334  LOC162333 5'  GCTGAGCTGGGGGCAGGTG   8515      ACAG
                                GCTGA   TGGGGGCAGGTG
                                |||||   ||||||||||||
                                CGACT   ACCCCCGTCCAC
                                  CG__
GAM334  LOC197419 5'  TGGGCTGAATGGGGG      8516        ACA
                                TGGGCTGA  GTGGGGG
                                ||||||||  |||||||
                                ACCCGACT  TACCCCC
                                    ___
GAM334  LOC221466 3'  TGGGCTGAGATGGTGATTATGT 8517         ACA   _  GCAG
          G                      TGGGCTGA  GTGG GG   GTG
                                ||||||||  |||| ||   |||
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                                ACCCGACT   TACC CT    CAC
                                    C__    A  AATA
GAM334   LOC245757 3'  TGGCCTGAGCAGTGGGAGC    8512      G    A
                                TGG CTGA CAGTGGGGGC
                                ||| |||| ||||||||||
                                ACC GACT GTCACCCTCG
                                  G    C
GAM334   LOC253216 3'  GGGCTGGGTCTCGGGGGCAGGT 8518        AACAG
           G                     GGGCTG    TGGGGGCAGGTG
                                ||||||    ||||||||||||
                                CCCGAC    GCCCCCGTCCAC
                                   CCAGA
GAM334   LOC253681 5'  TGGGTTGGAGGCACAGGT    8509      C  AACAGT   G
                                TGGG TG     GGG GCAGGT
                                |||| ||     ||| ||||||
                                ACCC AC     TCC TGTCCA
                                  A  C_____   G
GAM334   LOC257016 3'  TGGGCTGGAAAAGCAGGT    8519        AACAGT
                                TGGGCTG     GGGGGCAGGT
                                |||||||     ||||||||||
                                ACCCGAC     TTTTCGTCCA
                                    C_____
GAM334   LOC257397 5'  TGGGCTGAATAGGTTCTGGTG  8520         ACA    GGCA
                                TGGGCTGA   GTGGG   GGTG
                                ||||||||   |||||   ||||
                                ACCCGACT   TATCC   CCAC
                                    ___    AAGA
GAM334   LOC95702  5'  GGGCTGGGTCTCGGGGGCAGGT 8518       AACAG
           G                     GGGCTG    TGGGGGCAGGTG
                                ||||||    ||||||||||||
                                CCCGAC    GCCCCCGTCCAC
                                   CCAGA
GAM335   FUT7     3'  GGGCCGGATGCCTGGTGG    8523       TCA       C
                                GGGTC   GATGCCTGG GG
                                |||||   ||||||||| ||
                                CCCGG   CTACGGACC CC
                                   C__        A
GAM335   DKFZP564M182 3'  GGGTCTCAGATGCTGGC     8524            C
                                GGGTCTCAGATGC TGGC
                                |||||||||||| ||||
                                CCCAGAGTCTACG ACCG
                                              _
GAM335   LOC140380 5'  TACGGGTCTCGGAATGAGTGTG 8525          A_   CC__
           GC                    TATGGGTCTC  GATG   TGGC
                                ||||||||||  ||||   ||||
                                ATGCCCAGAG  TTAC   ACCG
                                     CC    TCAC
GAM335   LOC162333 5'  CATGGGTCTTGGACGTGG    8526         CA   CC
                                TATGGGTCT  GATG  TGG
                                |||||||||  ||||  |||
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                                GTACCCAGA  CTGC  ACC
                                     AC   __
GAM335  LOC169696 5'  CGGAACCCGGTGCCTGGCGGC  8527     GT   AGA
                                TGG  CTC   TGCCTGGCGGC
                                |||  |||   ||||||||||
                                GCC  GGG   ACGGACCGCCG
                                  TT   CC_
GAM335  LOC221583 5'  TATGGGTCTCGGGCTGTAGC   8528         AGAT  C_
                                TATGGGTCTC    GC  TGGC
                                ||||||||||    ||  ||||
                                ATACCCAGAG    CG  ATCG
                                     CC__  AC
GAM336  ARF3     3'  CAGTGTCCTGGCTGCAAGCCCT 8531         __ C    A
          G                      CAGTGTCT  GT GCAA CCCTG
                                ||||||||  || |||| |||||
                                GTCACAGG  CG CGTT GGGAC
                                     AC  A    C
GAM336  ARNT2    3'  TCAGTGCCCCACAGACCCTG   8532         GT    A
                                TCAGTGTCT  CGCA ACCCTG
                                |||||||||  |||| ||||||
                                AGTCACGGG  GTGT TGGGAC
                                     __    C
GAM336  COL4A1   3'  AGTGTTTAAAACCCTG      8533       C  TCGC
                                AGTGT TG    AAACCCTG
                                ||||| ||    ||||||||
                                TCACA AT    TTTGGGAC
                                  A  _____
GAM336  DUSP5    3'  ATCATGTCCCTACAAACCCTG  8534      G    GTC
                                ATCA TGTCT   GCAAACCCTG
                                |||| |||||   ||||||||||
                                TAGT ACAGG   TGTTTGGGAC
                                  _    GA_
GAM336  GNPI     3'  CAGTGTCTGTTGCCCC      8535          C  AAA
                                CAGTGTCTGT GC   CCC
                                ||||||||||  ||   |||
                                GTCACAGACA CG   GGG
                                     A  ____
GAM336  LFG      3'  GTGTCTGTCCCATCCTG     8536         G  AAC
                                GTGTCTGTC CA   CCTG
                                |||||||||  ||   ||||
                                CACAGACAG GT   GGAC
                                     G  A__
GAM336  TGFBR2   5'  AATCAGTATTCACAAACCCTG  8537         CTG
                                AATCAGTGT   TCGCAAACCCTG
                                |||||||||   ||||||||||||
                                TTAGTCATA   AGTGTTTGGGAC
                                     ____
GAM336  FLJ12587  3'  GCGTCAGTGGGCAAACCCT   8538       T  C_
                                GTGTC GT  GCAAACCCT
                                ||||| ||  |||||||||
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                                CGCAG CA  CGTTTGGGA
                                   T  CC
GAM336  FLJ23598  5'  AGCATCCAGTCGCAAACCCTG  8539        _
                                AGTGTCT GTCGCAAACCCTG
                                ||||||| ||||||||||||
                                TCGTAGG CAGCGTTTGGGAC
                                    T
GAM336  HLA-DOA  3'  GTGTCCAACAAACCCTG     8540        TC
                                GTGTCTG  GCAAACCCTG
                                |||||||  ||||||||||
                                CACAGGT  TGTTTGGGAC
                                   __
GAM336  MFN1     3'  ATCAGTGTATGTAGTTTATCCT 8541         C   CGCAAAC
           G                     ATCAGTGT TGT      CCTG
                                ||||||||| |||      ||||
                                TAGTCACA ACA      GGAC
                                    T   TCAAATA
GAM336  NCKX3    3'  AACCAGTGTCTGTAACTCCTG  8542           CGCA  _
                                AATCAGTGTCTGT    AAC CCTG
                                ||||||||||||    ||| ||||
                                TTGGTCACAGACA    TTG GGAC
                                      ____  A
GAM336  P311     3'  ATCAGTGTCTCAGGTCCT    8543          GTCG  AAC
                                ATCAGTGTCT    CA   CCT
                                ||||||||||    ||   |||
                                TAGTCACAGA    GT   GGA
                                      ____ CCA
GAM336  PRO2176  3'  AGTGTCTGTAAAACCCTG    8544         CGC
                                AGTGTCTGT   AAACCCTG
                                |||||||||   ||||||||
                                TCACAGACA   TTTGGGAC
                                    T__
GAM336  STX18    3'  TCAGTGTCTTCCTTTGAACCCT 8545         GT GCA_
           G                     TCAGTGTCT  C    AACCCTG
                                |||||||||  |   |||||||
                                AGTCACAGA  G    TTGGGAC
                                    AG AAAC
GAM336  LOC145842 5'  CAGTGTCTAAGCTGACTCTG  8546         TC  AA  C
                                CAGTGTCTG  GC  AC CTG
                                |||||||||  ||  || |||
                                GTCACAGAT  CG  TG GAC
                                    T_  AC  A
GAM336  LOC158236 3'  CAGTGTCTCGGCTAAACC    8547         GTC  _
                                CAGTGTCT   GC AAACC
                                ||||||||   || |||||
                                GTCACAGA   CG TTTGG
                                    GC_  A
GAM336  LOC196385 3'  AATCAGTGTCAGTCCCCCT   8548           T   GCAAA
                                AATCAGTGTC GTC    CCCT
                                |||||||||| |||    ||||
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                                TTAGTCACAG CAG    GGGA
                                     T  G____
GAM336  LOC90092  5'  CAGTGTCTGCCATCCT     8549          CAAAC
                                CAGTGTCTGTCG    CCT
                                ||||||||||||    |||
                                GTCACAGACGGT    GGA
                                      A____
GAM337  ADAM19   3'  CCCACCAGACCCTGGACTTTGG 8552     _      C  _ AGGC
          GCC                    CCC CCAGACCC GG C   GGCC
                                ||| |||||||| || |   ||||
                                GGG GGTCTGGG CC G   CCGG
                                  T      A  T AAAC
GAM337  ADRA2A   5'  CCCCCAGACGCTGCGG     8553         CCCG  AG
                                CCCCCAGAC   GC  GCGG
                                |||||||||   ||  ||||
                                GGGGGTCTG   CG  CGCC
                                     ____  A_
GAM337  AP2S1    5'  CCGTCCAGACCCCAGCGGC   8554    CC         A
                                CC  CCAGACCCCGGC GGC
                                ||  ||||||||||||| |||
                                GG  GGTCTGGGGTCG CCG
                                 CA         _
GAM337  BSN      3'  CCCCAGACCTCGCCCTGGGG  8555         C  GCA_  C
                                CCCCAGACC CG   GG GG
                                |||||||||  ||   ||  ||
                                GGGGTCTGG GC   CC CC
                                     A  GGGA  _
GAM337  DLG5     5'  CCCCCAGCTGCTCCAGGCGGC  8556        ACCCCGG
                                CCCCCAG      CAGGCGGC
                                |||||||      |||||||||
                                GGGGGTC      GTCCGCCG
                                    GACGAG_
GAM337  DPH2L1   3'  CCTCCAGGCCCCTGCAGAC   8557    C   A   G
                                CC CCAG CCCC GCAGGC
                                ||  |||| |||| ||||||
                                GG GGTC GGGG CGTCTG
                                 A   C   A
GAM337  DTX1     5'  CCCAGACCCTGCGCCCGGC   8558         CG  AGG
                                CCCAGACCC  GC   CGGC
                                |||||||||  ||   ||||
                                GGGTCTGGG  CG   GCCG
                                     A_  CGG
GAM337  EIF4G1   3'  CCCCCTGCAGTCCAGGCGGC  8559       __  A  CCGGC
                                CCCCC  CAG CC    AGGCGGC
                                |||||  ||| ||    |||||||
                                GGGGG  GTC GG    TCCGCCG
                                  AC   A  _____
GAM337  FBXL7    5'  CCCCCCAAGCTCCGGGGC    8560         ACC   CAGGC
                                CCCCCCAG   CCGG    GGC
                                ||||||||   ||||    |||
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                                GGGGGGTT  GGCC    CCG
                                    CGA   _____
GAM337  FKRP    3'  CCCCCCAGGCCCACCTGGC   8561        A_  _  _
                                CCCCCCAG  CC CC GGC
                                ||||||||  || || |||
                                GGGGGGTC  GG GG CCG
                                    CG  T  A
GAM337  FZD3    5'  CCTCAGACCCCGGCGCCTGGC  8562    C       AG  __
                                CC CAGACCCCGGC  GC  GGC
                                || ||||||||||  ||  |||
                                GG GTCTGGGGCCG  CG  CCG
                                 A         __ GA
GAM337  GCK     3'  CCCCAGCGGTATGGCAGGCGGC 8563       ACCCC_
          C                      CCCCAG     GGCAGGCGGCC
                                 ||||||     ||||||||||
                                 GGGGTC     CCGTCCGCCGG
                                    GCCATA
GAM337  GCK     3'  CCCCAGCGGTATGGCAGGCGGC 8563       ACCCC_
          C                      CCCCAG     GGCAGGCGGCC
                                 ||||||     ||||||||||
                                 GGGGTC     CCGTCCGCCGG
                                    GCCATA
GAM337  GCK     3'  CCCCAGCGGTATGGCAGGCGGC 8563       ACCCC_
          C                      CCCCAG     GGCAGGCGGCC
                                 ||||||     ||||||||||
                                 GGGGTC     CCGTCCGCCGG
                                    GCCATA
GAM337  GCN1L1  3'  CCCCAGACTTGGGAACTGCC  8564        CCC  CA  G
                                CCCCAGAC  GG  GGC GCC
                                ||||||||  ||  ||| |||
                                GGGGTCTG  CC  TTG CGG
                                    AA_  C_  A
GAM337  LASS1   3'  CCCCCCGGACCCCGACAG    8565       A
                                CCCCCC GACCCCGGCAG
                                |||||| ||||||||||
                                GGGGGG CTGGGGCTGTC
                                    C
GAM337  MAOB    3'  CCCCCAGATACCAGTGGC    8566        CC   CA
                                CCCCCAGA  CCGG  GGC
                                ||||||||  ||||  |||
                                GGGGGTCT  GGTC  CCG
                                    AT   A_
GAM337  MTMR6   5'  CCCCAAACCCCGCGGC     8567          GGCAG
                                CCCCAGACCCC    GCGGC
                                ||||||||||    |||||
                                GGGGTTTGGGG    CGCCG
                                              _____
GAM337  NCOR2   3'  CCCCCCAGGCCGCACCTGGCC  8568        A  CCG   GGC
                                CCCCCCAG CC   GCA   GGCC
                                |||||||| ||   |||   ||||
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                                GGGGGGTC GG  CGT  CCGG
                                    C ___  GGA
GAM337  OTP     5' CCCCCCAAATTTTAGCGGC  8569        CCCCGGCA
                                CCCCCCAGA     GGCGGC
                                |||||||||     ||||||
                                GGGGGGTTT     TCGCCG
                                    AAAA____
GAM337  OXTR    3' CCTCCAGGCCCTGGCAAACG  8570    C   A  C
                                CC CCAG CCC GGCAGGCG
                                || |||| ||| ||||||||
                                GG GGTC GGG CCGTTTGC
                                 A   C  A
GAM337  POLR2E  3' CCCCTGCACCCCGGCTCAGC  8571     CAG      AGG
                                CCCC  ACCCCGGC  CGGC
                                ||||  ||||||||  ||||
                                GGGG  TGGGGCCG  GTCG
                                  ACG      A__
GAM337  PTP4A2  5' CCCCCCAGCCTCGGCGC    8572       A  C   AG
                                CCCCCCAG CC CGGC  GC
                                |||||||| || ||||  ||
                                GGGGGGTC GG GCCG  CG
                                    _ A   __
GAM337  PTP4A2  5' CCCCCCAGCCTCGGCGC    8572       A  C   AG
                                CCCCCCAG CC CGGC  GC
                                |||||||| || ||||  ||
                                GGGGGGTC GG GCCG  CG
                                    _ A   __
GAM337  S100A10 5' CCCCCGACCCCGGGCGCGCGGC 8573      A      _ AG
          C                      CCCCC GACCCCGG C  GCGGCC
                                |||||  |||||||| |  ||||||
                                GGGGG CTGGGGCC G  CGCCGG
                                  _      C CG
GAM337  SECTM1  3' CCCCCAGACCCTACCTCGGCC  8574         CG  AGG
                                CCCCCAGACCC  GC  CGGCC
                                ||||||||||  ||  |||||
                                GGGGGTCTGGG  TG  GCCGG
                                     A_  GA_
GAM337  SF3B3   5' CCTCCAGGCCTTGGTTACACC  8575    C   A  CC  CAG  G
                                CC CCAG CC  GG  GCG CC
                                || |||| ||  ||  ||| ||
                                GG GGTC GG  CC  TGT GG
                                 A   C  AA  AA_  _
GAM337  SLC19A1 3' CCCCATTGCTAAGGCAGGCGGC 8576      GACCCC_
          C                     CCCCA     GGCAGGCGGCC
                                |||||     ||||||||||
                                GGGGT     CCGTCCGCCGG
                                  AACGATT
GAM337  SLC7A5  3' CCCCCCAACCCTGGGGC    8577       A  C  CA
                                CCCCCCAG CCC GG  GGC
                                |||||||| ||| ||  |||
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                                GGGGGGTT GGG CC  CCG
                                    _  A  __
GAM337  TBXAS1   5'  CCTCTGAGACCCCAGAGTGGTG 8578    CCCC      CA_  C
          G                      CC   AGACCCCGG  GG GG
                                 ||   |||||||||  || ||
                                 GG   TCTGGGGTC  CC CC
                                  AGAC       TCA  A
GAM337  TBXAS1   5'  CCTCTGAGACCCCAGAGTGGTG 8578    CCCC      CA_  C
          G                      CC   AGACCCCGG  GG GG
                                 ||   |||||||||  || ||
                                 GG   TCTGGGGTC  CC CC
                                  AGAC       TCA  A
GAM337  24432    5'  CCCCAGACTCCGGGGGCG    8579        C   CA
                                 CCCCAGAC CCGG  GGCG
                                 |||||||| ||||  ||||
                                 GGGGTCTG GGCC  CCGC
                                     A   C_
GAM337  C14orf4  5'  CCCCCCAGGCCGTTGGGCAG  8580        ACC  GCA
                                 CCCCCCAG  CCG  GGCGG
                                 ||||||||  |||  |||||
                                 GGGGGGTC  GGC  CCGTC
                                     C__  AAC
GAM337  C20orf180 5'  CCCCCCAACCCTGACAGTGGGC 8581        A  C   ___
          GGCC                    CCCCCCAG CCC GGCA  GGCGGCC
                                 |||||||| ||| ||||  |||||||
                                 GGGGGGTT GGG CTGT  CCGCCGG
                                     _  A   CAC
GAM337  C20orf27  3'  CCCAGACCCTGGTGGGAG    8582         C  CA  C
                                 CCCAGACCC GG  GG GG
                                 |||||||| ||  || ||
                                 GGGTCTGGG CC  CC TC
                                     A  A_  C
GAM337  CLSTN1   5'  CCCCCCAGAACCTCGGGG    8583         C  _  CA
                                 CCCCCCAGA CC CGG  GG
                                 |||||||| || |||  ||
                                 GGGGGGTCT GG GCC  CC
                                     T  A  __
GAM337  DKFZp434A171 5'  CCTCCCCGACCCCGGCCGACC  8584    _   A      AGG
                                 CC CCCC GACCCCGGC  CGGCC
                                 || |||| |||||||||  |||||
                                 GG GGGG CTGGGGCCG  GCTGG
                                  A  _       ____
GAM337  DKFZP434C171 3'  CCCCCCCAACCCCTACTCTGGCC 8585        A   G  AGGC
                                 CCCCCCAG CCCC GC   GGCC
                                 |||||||| |||| ||   ||||
                                 GGGGGGTT GGGG TG   CCGG
                                     _   A  AGA_
GAM337  DKFZP434K1172 5'  CCCTCAGAGGGGGCAGGCGGCC 8586     C   CCCC
                                 CCC CAGA   GGCAGGCGGCC
                                 ||| ||||   ||||||||||
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                                GGG GTCT   CCGTCCGCCGG
                                  A   CCC_
GAM337  DKFZP434O047 5'  CCCCCCAGACCCCGAGGC   8587            GC
                                CCCCCCAGACCCCG  AGGC
                                |||||||||||||  ||||
                                GGGGGGTCTGGGGC  TCCG
                                      __
GAM337  DKFZP564K247 5'  CCTCTCACACCCCAACCGGC  8588    CCC  G      A
                                CC   CA ACCCCGGC GGC
                                ||   || ||||||||| |||
                                GG   GT TGGGGTTG CCG
                                 AGA  G       G
GAM337  DKFZP586G1122 3'  CCCCCCCGGACCCCGACCATGGC 8589       A       AGGC
                                CCCCCC GACCCCGGC   GGC
                                |||||| |||||||||   |||
                                GGGGGG CTGGGGCTG   CCG
                                   C        GTA_
GAM337  DUSP9    3'  CCCCCCAGCACCCTGCTCAGGC 8590        AC   GG__
                                CCCCCCAG  CCC   CAGGC
                                ||||||||  |||   |||||
                                GGGGGGTC  GGG   GTCCG
                                    GT   ACGA
GAM337  EPB41L1   3'  CCCCAAACCCTGGTGGC    8591          CGGCA  C
                                CCCCAGACCC    GG GGC
                                ||||||||||    || |||
                                GGGGTTTGGG    CC CCG
                                     A_____  A
GAM337  EPI64    3'  CCCCCCAGGCCCTAGCTTCTGC 8592        A   CG  AGGCG
          C                      CCCCCCAG CCC  GC    GCC
                                ||||||||| |||  ||    |||
                                GGGGGGTC GGG  CG    CGG
                                    C   AT  AAGA_
GAM337  FBXO6    5'  CCCCTCCAGGCGGCGGGCGGC  8593     _   ACCC   A
                                CCCC CCAG   CGGC GGCGGC
                                |||| ||||   |||| ||||||
                                GGGG GGTC   GCCG CCGCCG
                                  A   C___   C
GAM337  FLJ10101  3'  CCCCCAGACCCAGGCGGGGCAG 8594          C   A_
          CC                     CCCCCAGACCC GGC  GGCGGCC
                                ||||||||||| |||  |||||||
                                GGGGGTCTGGG CCG  CCGTCGG
                                      T   CC
GAM337  FLJ10101  3'  CCCCCAGACCCAGGCGGGGCAG 8594          C   A_
          CC                     CCCCCAGACCC GGC  GGCGGCC
                                ||||||||||| |||  |||||||
                                GGGGGTCTGGG CCG  CCGTCGG
                                      T   CC
GAM337  FLJ10101  3'  CCCCCAGACCCAGGCGGGGCAG 8594          C   A_
          CC                     CCCCCAGACCC GGC  GGCGGCC
                                ||||||||||| |||  |||||||
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                                GGGGGTCTGGG CCG  CCGTCGG
                                      T  CC
GAM337  FLJ10618  5' CCGCCCGCTACGGCAGGCGGC 8595    _  AGACCC
                                CC CCC     CGGCAGGCGGC
                                || |||     ||||||||||
                                GG GGG     GCCGTCCGCCG
                                 C  CGAT__
GAM337  FLJ13441  3' CCCTGACGGCAGGCGGC     8596     A  CCC
                                CCC GAC  GGCAGGCGGC
                                ||| |||  ||||||||||
                                GGG CTG  CCGTCCGCCG
                                 A  ___
GAM337  FLJ14124  3' CCCCTGACCCCGGGCGC     8597      A      CAG  G
                                CCCC GACCCCGG  GCG C
                                |||| ||||||||  ||| |
                                GGGG CTGGGGCC  CGC G
                                  A      ___  _
GAM337  FLJ14124  3' CCCCTGTGTGGCGGCAGGCGGC 8598      CAGACCC
          C                      CCCC      CGGCAGGCGGCC
                                ||||      ||||||||||||
                                GGGG      GCCGTCCGCCGG
                                  ACACACC
GAM337  FLJ14249  3' CCACCCAGACCCTGCAGGC   8599    _       CG
                                CC CCCAGACCC  GCAGGC
                                || |||||||||  ||||||
                                GG GGGTCTGGG  CGTCCG
                                 T       A_
GAM337  FLJ14249  3' CCACCCAGACCCTGCAGGC   8599    _       CG
                                CC CCCAGACCC  GCAGGC
                                || |||||||||  ||||||
                                GG GGGTCTGGG  CGTCCG
                                 T       A_
GAM337  FLJ14346  5' CCCTTCAGACCCCGCAGGC   8600     CC       G
                                CCC  CAGACCCCG CAGGC
                                |||  ||||||||| |||||
                                GGG  GTCTGGGGC GTCCG
                                  AA       _
GAM337  FLJ20254  5' CCTCCAGGCTGCGGAAGCGGCC 8601    C   ACCC  C
                                CC CCAG   CGG AGGCGGCC
                                || ||||   ||| ||||||||
                                GG GGTC   GCC TTCGCCGG
                                 A   CGAC  _
GAM337  FLJ20288  5' CCCTCCCGGCGGAGGCGGC   8602     AGAC    __
                                CCC   CCCGGC  AGGCGGC
                                |||   ||||||  |||||||
                                GGG   GGGCCG  TCCGCCG
                                  A___     CC
GAM337  FLJ20551  3' CCTCAGGCCCGGCAGGCAGC  8603    C  AC
                                CC CAG  CCCGGCAGGCGGC
                                || |||  ||||||||||||
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                                GG GTC  GGGCCGTCCGTCG
                                 A  C_
GAM337  FLJ20584  5'  CCCTGCAGACCCCGGCCCAG  8604     CC        A_
                                CCC  CAGACCCCGGC  GG
                                |||  ||||||||||  ||
                                GGG  GTCTGGGGCCG  TC
                                  AC         GG
GAM337  FLJ20625  3'  CCAGACCCTGGTCACAAACC  8605        C  _  GGC
                                CCAGACCC GG CA   GGCC
                                |||||||| || ||   ||||
                                GGTCTGGG CC GT   TTGG
                                     A  A  GT_
GAM337  FLJ21125  3'  CCCCCAGAATCAAAGTGGCC  8606        CCC   C  GC
                                CCCCCAGA   CGG AG  GGCC
                                ||||||||   ||| ||  ||||
                                GGGGGTCT   GTT TC  CCGG
                                     TA_   _  A_
GAM337  FLJ21839  5'  CCTTGGGCCCCGGCACCCGGGC 8607    CCAGA      GG  _
          C                      CC    CCCCGGCA  CGG CC
                                ||    ||||||||  ||| ||
                                GG    GGGGCCGT  GCC GG
                                 AACCC       GG   C
GAM337  FLJ22127  3'  CCTCAGACTCCGGCAGGAAC  8608    C    C      C
                                CC CAGAC CCGGCAGG GGC
                                || ||||| |||||||| |||
                                GG GTCTG GGCCGTCC TTG
                                 A    A      _
GAM337  HAND2     5'  CCCCCCAGCCCCCGGGCGC   8609        A    CAG   G
                                CCCCCCAG CCCCGG   GCG C
                                |||||||| ||||||   ||| |
                                GGGGGGTC GGGGCC   CGC G
                                     G     ___   _
GAM337  KIAA0293  5'  CCCCCCAGCCCCGGGG     8610         A    CAGGC
                                CCCCCCAG CCCCGG    GG
                                |||||||| ||||||    ||
                                GGGGGGTC GGGGCC    CC
                                     _    _____
GAM337  KIAA0542  3'  CCTCAGCAGCCAGGCGGCC   8611    C  ACCC   _
                                CC CAG    CGGC AGGCGGCC
                                || |||    |||| ||||||||
                                GG GTC    GTCG TCCGCCGG
                                 A  _____   G
GAM337  KIAA0542  5'  CCGCCCAGACCCCGGGGC    8612    _        CA
                                CC CCCAGACCCCGG  GGC
                                || ||||||||||||  |||
                                GG GGGTCTGGGGCC  CCG
                                 C          __
GAM337  KIAA0662  3'  CCTCCCAGACCCCAAGATGTGG 8613    _        CAGGC
          C                      CC CCCAGACCCCGG    GGC
                                || ||||||||||||    |||
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                                GG GGGTCTGGGGTT    CCG
                                 A         CTACA
GAM337  KIAA0767  3'  CCCTTCAGCCCAGCGCAGGCGG 8614     CC   A  CG_
            CC                   CCC  CAG CCC   GCAGGCGGCC
                                 |||  ||| |||   ||||||||||
                                 GGG  GTC GGG   CGTCCGCCGG
                                  AA   _   TCG
GAM337  KIAA1036  3'  CCCCAAACCCTGGCCCTAGGC  8615          C  ___
                                 CCCCAGACCC GGC   AGGC
                                 |||||||||| |||   ||||
                                 GGGGTTTGGG CCG   TCCG
                                       A   GGA
GAM337  KIAA1553  3'  CCCCCCAAGGCAGGGGGTGGCC 8616         ACCCC     C___
                                 CCCCCCAG    GGCAGG    GGCC
                                 ||||||||    ||||||    ||||
                                 GGGGGGTT    CCGTCC    CCGG
                                     _____     CCCA
GAM337  KIAA1656  3'  CCTCCCATGGCCGCAGGCGGCC 8617     _   GACC   G
                                 CC CCCA    CCG CAGGCGGCC
                                 || ||||    ||| |||||||||
                                 GG GGGT    GGC GTCCGCCGG
                                  A    ACC_   _
GAM337  LSFR2     3'  CCCCCCAGGGTCCTGGTTGAGG 8618         AC_  C  C__   C
            GGC                    CCCCCCAG   CC GG   AGG GGC
                                 |||||||   || ||   ||| |||
                                 GGGGGGTC   GG CC   TCC CCG
                                      CCA  A  AAC   _
GAM337  MG61      3'  CCCTCTAGGCCCCAGCAGGCAC 8619      CCC  A         G
            C                     CCC   AG CCCCGGCAGGCG CC
                                 |||   || ||||||||||||| ||
                                 GGG   TC GGGGTCGTCCGT GG
                                   AGA  C         _
GAM337  MGC13064  3'  CCCCCAGACCCCAGAGAGCC   8620            C  GC
                                 CCCCCAGACCCCGG AG  GGCC
                                 |||||||||||||| ||  ||||
                                 GGGGGTCTGGGGTC TC  TCGG
                                              _ __
GAM337  MGC15416  5'  CCCCAGACTTGGCCAGC     8621         CCC   AGG
                                 CCCCAGAC   GGC   CGGC
                                 ||||||||   |||   ||||
                                 GGGGTCTG   CCG   GTCG
                                      AA_   ___
GAM337  MGC3077   3'  CCCCCAGATCCCTGTTCGGCCG 8622        _   C________   AGGCG
            CCG                    CCCAGA CCC       GGC    G
                                 ||||||  |||       |||    |
                                 GGGTCT GGG       CCG    C
                                    A   ACAAGIII   GCGGA
GAM337  MGC3103   3'  CCCAGGCCAGGCGGCGGCC   8623       A  CC   A
                                 CCCAG CC  GGC GGCGGCC
                                 |||||  ||  |||  |||||||
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                                GGGTC GG  CCG CCGCCGG
                                  C  T_  _
GAM337  OBTP     5'  CCTCCCCCGGCAGGTGGCC   8624     AGA        C
                                CC   CCCCGGCAGG GGCC
                                ||   |||||||||| ||||
                                GG   GGGGCCGTCC CCGG
                                 AG_        A
GAM337  PACSIN2  5'  CCCAGACCCCTGCGGC      8625          GGCAG
                                CCCAGACCCC    GCGGC
                                ||||||||||    |||||
                                GGGTCTGGGG    CGCCG
                                     A____
GAM337  PADI1    3'  CCCCCAGGCCCCGTTCGGCCGC 8626        A    ________ AGGCG
           CG                     CCCCAG CCCCG      GC    G
                                ||||||| |||||      ||    |
                                GGGGTC GGGGC      CG    C
                                   C    AAGIIIC  GCGGA
GAM337  PP1044   3'  CCCGTGGACCCCGGCTAGGGCC 4564     CCA       A  C
                                CCC   GACCCCGGC GG GGCC
                                |||   ||||||||| || ||||
                                GGG   CTGGGGCCG TC CCGG
                                  CAC       A  _
GAM337  PTPRT    3'  CCTTCCAGACCCCAGCTGC   8627     CC         AG
                                CC  CCAGACCCCGGC  GC
                                ||  ||||||||||||  ||
                                GG  GGTCTGGGGTCG  CG
                                 AA          A_
GAM337  RIS1     5'  CCCTCCAGACCCGGTTGCG   8628     _      C  CAG
                                CCC CCAGACCC GG   GCG
                                ||| |||||||| ||   |||
                                GGG GGTCTGGG CC   CGC
                                  A       _ AA_
GAM337  SLC1A7   5'  CCCCTCAGCAGGCAGGTGG   8629      _  ACCCC     C
                                CCCC CAG    GGCAGG GG
                                |||| |||    |||||| ||
                                GGGG GTC    CCGTCC CC
                                  A  GT___     A
GAM337  STC2     3'  CCCCTGAGACCCCACGGC    8630      CC      GGCAG
                                CCCC  AGACCCC    GCGGC
                                ||||  |||||||    |||||
                                GGGG  TCTGGGG    TGCCG
                                  AC     _____
GAM337  T1A-2    5'  CCCAGACCCTAGGCAGCC    8631          CGGC
                                CCCAGACCC   AGGCGGCC
                                |||||||||   ||||||||
                                GGGTCTGGG   TCCGTCGG
                                     A___
GAM337  TXI1     5'  CCCCCCAGATGCCTGGCGAC  8632         CC  GGCA
                                CCCCCCAGA  CC   GGCGGC
                                |||||||||  ||   ||||||
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                                GGGGGGTCT GG   CCGCTG
                                     AC A___
GAM337  UBN1     3' CCCCCAGACCCCGAGGC    8633          GC
                                CCCCCAGACCCCG AGGC
                                |||||||||||| ||||
                                GGGGGTCTGGGGC TCCG
                                       __
GAM337  WBSCR18  3' CCTTCGGATCCCAGCAAAGG 8634    CCCA C      C
                                CC   GA CCCGGCAGG GG
                                ||   || ||||||||| ||
                                GG   CT GGGTCGTTT CC
                                 AAGC A       _
GAM337  LOC130535 5' CCCGCCAGACCCTCGGCGCGGC 8635     _      _   AG
          C                      CCC CCAGACCC CGGC  GCGGCC
                                ||| |||||||| ||||  ||||||
                                GGG GGTCTGGG GCCG  CGCCGG
                                  C       A   __
GAM337  LOC130813 5' CCTCCTAACCCCGGGAGAGCC  8636    C  A      C  GC
                                CC CC GACCCCGG AG  GGCC
                                || || |||||||| ||  ||||
                                GG GG TTGGGGCC TC  TCGG
                                 A  A       C  __
GAM337  LOC134266 3' CCCTAGACTTTAGACAGCC   8637     C   CCCGGC
                                CCC AGAC     AGGCGGCC
                                ||| ||||     ||||||||
                                GGG TCTG     TCTGTCGG
                                  A   AAA___
GAM337  LOC145317 3' CCAGGACCCCAGCACGGCC   8638      _      AG
                                CCAG ACCCCGGC  GCGGCC
                                |||| ||||||||  ||||||
                                GGTC TGGGGTCG  TGCCGG
                                  C      __
GAM337  LOC146725 5' CCCCCCAACCCAGGTGGTGG  8639        A  C  CA  C
                                CCCCCCAG CCC GG  GG GG
                                |||||||| ||| ||  || ||
                                GGGGGGTT GGG CC  CC CC
                                     _  T  A_  A
GAM337  LOC147136 5' CCCCCAGATCCTTCCGGGCGG  8640        _ __   CAG
                                CCCCCAGA CC  CCGG   GCGG
                                |||||||| ||  ||||   ||||
                                GGGGGTCT GG  GGCC   CGCC
                                     A  AA   ___
GAM337  LOC147791 3' CCCCAGCATCCCGGCGGC    8641       AC_     A
                                CCCCAG   CCCGGC GGC
                                ||||||   |||||| |||
                                GGGGTC   GGGCCG CCG
                                   GTA     _
GAM337  LOC148046 5' CCCCCCAGGACGGGGCGGC   8642        ACCC   CA
                                CCCCCCAG   CGG  GGCGGC
                                ||||||||   |||  ||||||
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                                GGGGGGTC   GCC  CCGCCG
                                    CT__  __
GAM337  LOC148195 3'  CCAGGCCAAGGCAGGCGGC   8643      A  CC
                                CCAG CC  GGCAGGCGGC
                                |||| ||  ||||||||||
                                GGTC GG  CCGTCCGCCG
                                  C  TT
GAM337  LOC148397 3'  CCCCAGACTCCCAGCTTGG   8644        _    A_
                                CCCCAGAC CCCGGC  GG
                                |||||||| ||||||  ||
                                GGGGTCTG GGGTCG  CC
                                    A     AA
GAM337  LOC149668 5'  CCCCCCAGCCCTGCGG     8645        A  CGGCAG
                                CCCCCCAG CCC     GCGG
                                |||||||| |||     ||||
                                GGGGGGTC GGG     CGCC
                                    _  A_____
GAM337  LOC150482 5'  CCCCCGACCCCGGCCGACC   8646      A       AGG
                                CCCCC GACCCCGGC   CGGCC
                                ||||| |||||||||   |||||
                                GGGGG CTGGGGCCG   GCTGG
                                  _       ___
GAM337  LOC151534 5'  CCACCCGGACCCCGGGG     8647    _  A      CA
                                CC CCC GACCCCGG  GG
                                || ||| ||||||||  ||
                                GG GGG CTGGGGCC  CC
                                 T  C       __
GAM337  LOC152274 5'  CCTCCTAGACCCCGAGGC    8648    _ C      GC
                                CC CC AGACCCCG  AGGC
                                || || ||||||||  ||||
                                GG GG TCTGGGGC  TCCG
                                 A  A       __
GAM337  LOC152283 5'  CCTCCGGACCCCGGCCAG    8649    C  A      A
                                CC CC GACCCCGGC GG
                                || || |||||||||  ||
                                GG GG CTGGGGCCG TC
                                 A  C       G
GAM337  LOC154790 5'  CCTTGCAGAGGGCAGGCGGC  8650    CCC   CCCC
                                CC   CAGA   GGCAGGCGGC
                                ||   ||||   ||||||||||
                                GG   GTCT   CCGTCCGCCG
                                 AAC   C___
GAM337  LOC157918 5'  CCCCTAGCGGAGGCGGC     8651      C  ACCC   C
                                CCCC AG   CGG AGGCGGC
                                |||| ||   ||| |||||||
                                GGGG TC   GCC TCCGCCG
                                  A  ____  _
GAM337  LOC162461 3'  CCTCCCAGACCTCCCAGGTGGC 8652    _      _ GG   C
                                CC CCCAGACC CC  CAGG GGC
                                || |||||||| ||  |||| |||
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                                GG GGGTCTGG GG  GTCC CCG
                                 A       A __    A
GAM337   LOC170396 5'  CCCTCCAGACCCTCGCGG    8653     _      CGGCAG
                                CCC CCAGACCC     GCGG
                                ||| ||||||||     ||||
                                GGG GGTCTGGG     CGCC
                                  A       AG____
GAM337   LOC200132 5'  CCTCCCAGACCTCCGGCA    8654     _      _
                                CC CCCAGACC CCGGCA
                                || |||||||| ||||||
                                GG GGGTCTGG GGCCGT
                                 A       A
GAM337   LOC201911 5'  CCTCCAGGTTCCAGACAGCC   8655     C    ACCCCGG
                                CC CCAG      CAGGCGGCC
                                || ||||      |||||||||
                                GG GGTC      GTCTGTCGG
                                 A   CAAG___
GAM337   LOC203396 5'  CCCCCCAACCCAGGTGGTGG   8639         A   C  CA  C
                                CCCCCCAG CCC GG  GG GG
                                |||||||| ||| ||  || ||
                                GGGGGGTT GGG CC  CC CC
                                     _  T  A_  A
GAM337   LOC220758 5'  CCCCCAGCCAGGCGGCGGCC   8656         A  CC   A
                                CCCCCAG CC  GGC GGCGGCC
                                ||||||| ||  ||| |||||||
                                GGGGGTC GG  CCG CCGCCGG
                                    _  T_  _
GAM337   LOC253955 5'  CCCCCCAACCCTGGCGGGACC  8657         A   C   A  C
                                CCCCCCAG CCC GGC GG GGCC
                                |||||||| ||| ||| || ||||
                                GGGGGGTT GGG CCG CC CTGG
                                     _   A   _ _
GAM337   LOC254115 5'  CCCTGCAGACCCCGCAGGGCC  8658      CC        G    CG
                                CCC  CAGACCCCG CAGG  GCC
                                |||  ||||||||| ||||  |||
                                GGG  GTCTGGGGC GTCC  CGG
                                  AC        _   ___
GAM337   LOC254617 5'  CCCTCCAGACCCGGCGAGGC   8659      _       C   _
                                CCC CCAGACCC GGC AGGC
                                ||| |||||||| ||| ||||
                                GGG GGTCTGGG CCG TCCG
                                  A       _   C
GAM337   LOC255761 5'  CCAGACCCTGAGCAGGGTACC  8660         C _    CG
                                CCAGACCC G GCAGG  GCC
                                |||||||| | |||||  |||
                                GGTCTGGG C CGTCC  TGG
                                     A T     CA
GAM337   LOC256277 5'  CCAGACCCGCCGAACTGGCGGC 8661          __   _ A
              C                  CCAGACCC  CGG C GGCGGCC
                                ||||||||  ||| | |||||||
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                                GGTCTGGG  GCT G CCGCCGG
                                    CG   T A
GAM337  LOC51308  3'  CCCCCCAGATCCCCGTTCGGCC 8662       _   ________ AGGCG
            GCCG                  CCCAGA CCCCG      GC    G
                                |||||| |||||      ||    |
                                GGGTCT GGGGC      CG    C
                                   A    AAGIIIC  GCGGA
GAM337  LOC63929  3'  CCAGGTCCCAGGCAACC    8663      AC   GGC
                                CCAG  CCC   AGGCGGCC
                                ||||  |||   ||||||||
                                GGTC  GGG   TCCGTTGG
                                  CA  ___
GAM337  LOC83693  5'  CCCGCCAGACCCGCGCGGC   8664     _      CG  AG
                                CCC CCAGACCC  GC  GCGGC
                                ||| ||||||||  ||  |||||
                                GGG GGTCTGGG  CG  CGCCG
                                  C       __  __
GAM337  LOC90507  5'  CCTCCAAGACCCCAGCTCGG   8665    _ C        AGG
                                CC CC AGACCCCGGC   CGG
                                || || ||||||||||   |||
                                GG GG TCTGGGGTCG   GCC
                                 A  T        A__
GAM337  LOC93550  5'  CCCCAGACCCACCGGC      8666          CG  AGG
                                CCCCAGACCC  GC   CGGC
                                ||||||||||  ||   ||||
                                GGGGTCTGGG  TG   GCCG
                                            __  ____
GAM337  LOC93622  3'  CCAGACCCGCGCGGC       8667         CG  AG
                                CCAGACCC  GC  GCGGC
                                ||||||||  ||  |||||
                                GGTCTGGG  CG  CGCCG
                                            __  __
GAM338  VCL       3'  TGGAAAAAATAAGGTTTCAT   8670         T    C   G
                                TGGAAAAA TAAGG TTT CGT
                                |||||||| ||||| ||| |||
                                ACCTTTTT ATTCC AAA GTA
                                     T    _  _
GAM338  VCL       3'  TGGAAAAAATAAGGTTTCAT   8670         T    C   G
                                TGGAAAAA TAAGG TTT CGT
                                |||||||| ||||| ||| |||
                                ACCTTTTT ATTCC AAA GTA
                                     T    _  _
GAM338  LOC144473 3'  TGGAAAGAGTAAGGCTCT    8671        AAT
                                TGGAAA   TAAGGCTTT
                                ||||||   |||||||||
                                ACCTTT   ATTCCGAGA
                                   CTC
GAM338  LOC145231 5'  TGGAAAAATGAAGGTGGGGC   8672          T   CTTT
                                TGGAAAAAT AAGG   GC
                                ||||||||| ||||   ||
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                                ACCTTTTTA TTCC    CG
                                     C    ACCC
GAM338  LOC221398 3'  GGAAAGTTAAGGCCTGCAT   8673       AA       T
                                GGAAA  TTAAGGCTT GCGT
                                |||||  ||||||||| ||||
                                CCTTT  AATTCCGGA CGTA
                                   C_       _
GAM338  LOC90594  3'  TGGAACAATTAAGGCTTTA   8674       A
                                TGGAA AATTAAGGCTTTG
                                ||||| ||||||||||||
                                ACCTT TTAATTCCGAAAT
                                   G
GAM339  EGFL5     3'  AAGAGTTCAAAGATTT      8677         TATCT
                                AAGAGTTT    AAAGATTT
                                ||||||||    ||||||||
                                TTCTCAAG    TTTCTAAA
                                            _____
GAM339  MYT1      3'  GAGTTATATCAAGATTTTT   8678       T   TA
                                GAGTT TATC  AAGATTTTT
                                ||||| ||||  |||||||||
                                CTCAA ATAG  TTCTAAAAA
                                   T   __
GAM339  LOC256940 3'  AGAGTTCAAAGATTTT     8679         TATCT
                                AGAGTTT    AAAGATTTT
                                |||||||    |||||||||
                                TCTCAAG    TTTCTAAAA
                                           _____
GAM340  C20orf98  5'  CAAGTGCTTCCACCTTTCTG  8682       AC  GGA GT
                                CAAGT  CT   C  CTTTCTG
                                |||||  ||   |  |||||||
                                GTTCA  GA   G  GAAAGAC
                                   C_  AG_ TG
GAM340  CMG1      5'  GTGCCTTGACTTCTTTCTG   8683     A   G   G
                                GT CCT GAC TCTTTCTG
                                || ||| ||| ||||||||
                                CA GGA CTG AGAAAGAC
                                 C   A   A
GAM340  ERO1-L(BETA) 3'  GTCAGATTAGTGTCTTTCT   8684       AG ACC   AC
                                GTCA  T   TGG  GTCTTTCT
                                ||||  |   |||  ||||||||
                                CAGT  A   ATC  CAGAAAGA
                                   CT ___   A_
GAM340  KIAA0146  5'  GTTAAGTGCCTGCATCTCTTCT 8685     C    A    GA     _
          G                      GT AAGT CCTG  CGTCTTT CTG
                                || |||| ||||  ||||||| |||
                                CA TTCA GGAC  GTAGAGA GAC
                                 A   C   __      A
GAM340  LANCL2    3'  GTCCAGTTGAGTGTCTTTCTG  8686     A   ACC   AC
                                GTC AGT   TGG  GTCTTTCTG
                                ||| |||   |||  |||||||||
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                                CAG TCA   ACT  CAGAAAGAC
                                  G  ___   CA
GAM340  PRO1600  5'  GTCAAGTATCTGATTCTTCTTT 8687         C    ACG_    _
              TCTG                  GTCAAGTA CTGG    TCTTT CTG
                                |||||||| ||||    ||||| |||
                                CAGTTCAT GACT    AGAAA GAC
                                    A    AAGA     A
GAM340  LOC157848 3'  CAAGTGCTTGGTCCCTTCTG   8688       ACC   ACG
                                CAAGT   TGG   TCTTTCTG
                                |||||   |||   ||||||||
                                GTTCA   ACC   GGGAAGAC
                                   CGA   A__
GAM340  LOC203427 3'  GTCATGGTATAAACTGTCTTTC 8689       A_   CC     _
              TG                    GTCA  GTA  TGGAC GTCTTTCTG
                                |||| |||  ||||| |||||||||
                                CAGT  CAT  ATTTG CAGAAAGAC
                                  AC  __    A
GAM340  LOC91252  3'  GCTGAGTACCTGGGCGTC    8690     CA       A
                                GT  AGTACCTGG CGTC
                                ||  ||||||||| ||||
                                CG  TCATGGACC GCAG
                                 AC        C
GAM341  CASP4    5'  TCTTCAGTTTTAGCATC     8693          CCCTAC
                                TCTTTAGTT     AGCATC
                                |||||||||     ||||||
                                AGAAGTCAA     TCGTAG
                                     AA_____
GAM341  CASP4    5'  TCTTCAGTTTTAGCATC     8693          CCCTAC
                                TCTTTAGTT     AGCATC
                                |||||||||     ||||||
                                AGAAGTCAA     TCGTAG
                                     AA_____
GAM341  CTBP2    3'  TCTTCAGTTTTCTAGCTC    8694          CC  AC   A
                                TCTTTAGTT  CT  AGC TC
                                |||||||||  ||  ||| ||
                                AGAAGTCAA  GA  TCG AG
                                     AA  __   _
GAM341  CTBP2    3'  TCTTCAGTTTTCTAGCTC    8694          CC  AC   A
                                TCTTTAGTT  CT  AGC TC
                                |||||||||  ||  ||| ||
                                AGAAGTCAA  GA  TCG AG
                                     AA  __   _
GAM341  CUL3     3'  TTCAGTGCAGCATCAC      8695        TCCCTA
                                TTTAGT     CAGCATCAC
                                ||||||     |||||||||
                                AAGTCA     GTCGTAGTG
                                   C_____
GAM341  PTPN1    3'  TCTTCAGTTCCCTTTGCA    8696             ACA
                                TCTTTAGTTCCCT   GCA
                                ||||||||||||   |||
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                                AGAAGTCAAGGGA  CGT
                                      AA_
GAM341  SORCS2   3'  TCTTTGTTAAAAGCATCAC   8697      A  CCCTAC
                                TCTTT GTT     AGCATCAC
                                ||||| |||     ||||||||
                                AGAAA CAA     TCGTAGTG
                                  _  TTT___
GAM341  STK24    3'  TCTTTAGTTGCCTTATCAT   8698        C  ACAG
                                TCTTTAGTT CCT   CAT
                                ||||||||| |||   |||
                                AGAAATCAA GGA   GTA
                                     C  ATA_
GAM341  ZNF138   5'  TCTGTAGTTCTCTAACATCACA 8699     T    C  CA
                                TCT TAGTTC CTA  GCATCACA
                                ||| |||||| |||  ||||||||
                                AGA ATCAAG GAT  TGTAGTGT
                                  C     A  __
GAM341  ZNF239   5'  TCTGTAGTTGCCCAGCATCACA 8700     T   _  TAC
                                TCT TAGTT CCC   AGCATCACA
                                ||| ||||| |||   |||||||||
                                AGA ATCAA GGG   TCGTAGTGT
                                  C    C  ___
GAM341  BIRC2    5'  TCCATTTCCTGCAGCATCA   8701     TTAG   CTA
                                TCT   TTCC   CAGCATCA
                                |||   ||||  ||||||||
                                AGG   AAGG   GTCGTAGT
                                  TA__   AC_
GAM341  C1orf34  3'  TCTTTAGTTCCTTCCAAGC   8702          __  C
                                TCTTTAGTTCC  CTA AGC
                                ||||||||||  ||| |||
                                AGAAATCAAGG  GGT TCG
                                      AA  _
GAM341  C20orf13 3'  TCTTCAGTTCTGACATATCACA 8703         CCT  GC
                                TCTTTAGTTC   ACA  ATCACA
                                ||||||||||   |||  ||||||
                                AGAAGTCAAG   TGT  TAGTGT
                                      AC_  A_
GAM341  DKFZp434G179 3'  CCTTTAGTTCTTTGCTACA   8704         C___
                                TCTTTAGTTC   CTACA
                                ||||||||||   |||||
                                GGAAATCAAG   GATGT
                                      AAAC
GAM341  EHM2     3'  TTTAGTTCTTCTACTCACA   8705        C_  AGCA
                                TTTAGTTC  CTAC   TCACA
                                ||||||||  ||||   |||||
                                AAATCAAG  GATG   AGTGT
                                     AA   ____
GAM341  FLJ11186 3'  TCTTCAGTTCCAAATTATCACA 8706          CTACAGC
                                TCTTTAGTTCC     ATCACA
                                ||||||||||     ||||||
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                                AGAAGTCAAGG      TAGTGT
                                      TTTAA__
GAM341  FLJ14297  5'  TCTGTAGTTCTCCAACATCACA 8707     T     CCTA
                                TCT TAGTTC    CAGCATCACA
                                ||| ||||||    ||||||||||
                                AGA ATCAAG    GTTGTAGTGT
                                  C     AG__
GAM341  FYCO1     3'  TCCTTGGTTCTAAGCATCAC   8708       A    CCTAC
                                TCTTT GTTC    AGCATCAC
                                ||||| ||||    ||||||||
                                AGGAA CAAG    TCGTAGTG
                                   C    AT___
GAM341  H-plk     5'  TCTGTAGTTCTCTCACATCACA 8709     T     C  A  G
                                TCT TAGTTC CT CA CATCACA
                                ||| |||||| || || |||||||
                                AGA ATCAAG GA GT GTAGTGT
                                  C     A  _  _
GAM341  KIAA0332  3'  TTTAGTCTAGCATCAC      8710         CCCTAC
                                TTTAGTT     AGCATCAC
                                |||||||     ||||||||
                                AAATCAG     TCGTAGTG
                                    A_____
GAM341  KR19      5'  TCTGTAGTTCTCTAACATCACA 8699     T     C   CA
                                TCT TAGTTC CTA  GCATCACA
                                ||| |||||| |||  ||||||||
                                AGA ATCAAG GAT  TGTAGTGT
                                  C     A  __
GAM341  NLI-IF    3'  TCTTTAGTTCTCATCA      8711           CCTACAG
                                TCTTTAGTTC      CATCA
                                ||||||||||      |||||
                                AGAAATCAAG      GTAGT
                                      A_______
GAM341  TBDN100   3'  TCTTTAGCTCTTTGTCAGACAT 8712          CCTA_  _
                                TCTTTAGTTC    CAG CAT
                                ||||||||||    ||| |||
                                AGAAATCGAG    GTC GTA
                                      AAACA   T
GAM341  ZNF90     5'  TCTGTAGTTCTCTAACATCACA 8699     T     C   CA
                                TCT TAGTTC CTA  GCATCACA
                                ||| |||||| |||  ||||||||
                                AGA ATCAAG GAT  TGTAGTGT
                                  C     A  __
GAM341  LOC120448 5'  TCAGCTTCTCCCTGTGGCGTCA 8713       ___    ACA  A
            C                    TTAGT   TCCCT   GC TCAC
                                |||||   |||||   || ||||
                                AGTCG   AGGGA   CG AGTG
                                   AAG    CAC  C
GAM341  LOC144558 3'  TCTTTAGTTTCTGCAGCAT   8714          CC  A
                                TCTTTAGTT  CT CAGCAT
                                |||||||||  || ||||||
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                                AGAAATCAA  GA GTCGTA
                                     A_  C
GAM341  LOC148530 5'  TCTTTAATTCTCTGGCAT    8715          C  ACA
                                TCTTTAGTTC CT   GCAT
                                |||||||||| ||   ||||
                                AGAAATTAAG GA   CGTA
                                      A  C__
GAM341  LOC151556 5'  TCTTTATTTTTCCCACCATC   8716       G__    T  AG
                                TCTTTA   TTCCC AC  CATC
                                ||||||   ||||| ||  ||||
                                AGAAAT   AAGGG TG  GTAG
                                   AAA    _ __
GAM341  LOC151623 5'  TCTTTAGTTTCTGTAGCAT   8717         CC  AC
                                TCTTTAGTT  CT  AGCAT
                                |||||||||  ||  |||||
                                AGAAATCAA  GA  TCGTA
                                     A_  CA
GAM341  LOC152373 5'  TCTCTATATGATTATAGCATCA 8718       GTTCCC  C
          CA                      TCTTTA     TA AGCATCACA
                                |||||||     || |||||||||
                                AGAGAT      AT TCGTAGTGT
                                   ATACTA  A
GAM341  LOC152582 5'  TCTTTAGTTTCCTCTGCTTGTC 8719         C   ACA  A__
          ACA                     TCTTTAGTT CCT   GC   TCACA
                                |||||||||| |||   ||   |||||
                                AGAAATCAA GGA   CG   AGTGT
                                     A   GA_  AAC
GAM341  LOC153146 5'  TCTTTAGTTTTCTTTTTTTCAC 8720         CC  ACAGCA
          A                       TCTTTAGTT  CT     TCACA
                                |||||||||  ||     |||||
                                AGAAATCAA  GA     AGTGT
                                     AA  AAAAA_
GAM341  LOC154813 3'  TCTCTTAGGAACAGCATCA   8721       _  TTCCCT
                                TCTTT AG     ACAGCATCA
                                ||||| ||     |||||||||
                                AGAGA TC     TGTCGTAGT
                                   A  CT____
GAM341  LOC157278 3'  TCTTTAGTTTCTGCAGCAT   8714         CC  A
                                TCTTTAGTT  CT CAGCAT
                                |||||||||  || ||||||
                                AGAAATCAA  GA GTCGTA
                                     A_  C
GAM341  LOC157922 3'  CCTTTAGTTCCCTATTTACA   8722            CA_
                                TCTTTAGTTCCCTA   GCA
                                ||||||||||||||   |||
                                GGAAATCAAGGGAT   TGT
                                         AAA
GAM341  LOC202759 5'  TCTGTAGTTCTCTAACATCACA 8699      T     C   CA
                                TCT TAGTTC CTA  GCATCACA
                                ||| |||||| |||  ||||||||
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                                AGA ATCAAG GAT  TGTAGTGT
                                  C     A  __
GAM341  LOC221962 3'  TCTTTAGTTTCTGTAGCAT   8717         CC  AC
                                TCTTTAGTT  CT  AGCAT
                                |||||||||  ||  |||||
                                AGAAATCAA  GA  TCGTA
                                     A_  CA
GAM341  LOC255461 5'  TCTTTAGTTTCTGCAGCAT   8714         CC  A
                                TCTTTAGTT  CT CAGCAT
                                |||||||||  || ||||||
                                AGAAATCAA  GA GTCGTA
                                     A_  C
GAM341  LOC255516 5'  TCTTTAGTTTCTGCAGCAT   8714         CC  A
                                TCTTTAGTT  CT CAGCAT
                                |||||||||  || ||||||
                                AGAAATCAA  GA GTCGTA
                                     A_  C
GAM341  LOC51133  5'  TCTTAGTTAAGGCATCAC    8723      T   CCCTACA
                                TCTT AGTT      GCATCAC
                                |||| ||||      |||||||
                                AGAA TCAA      CGTAGTG
                                  _   TTC_____
GAM342  ADM       3'  CCCTGGTGGGGTGACACGCC   8726      C       _ A
                                CCC GGTGGGGTG CA GTC
                                ||| ||||||||| || |||
                                GGG CCACCCCAC GT CGG
                                  A       T  G
GAM342  CAV3      3'  CCCCTGTGAAGAAGTCCCCCG  8727      G     TGC
                                CCCC GTGGGG   AAGTCCCCCG
                                |||| ||||||   ||||||||||
                                GGGG CACTTC   TTCAGGGGGC
                                  A     ____
GAM342  COL18A1   3'  CCACGGTGGGGGCTTCCTCCG  8728     _      T  AAG   C
                                CC CGGTGGGG GC   TCC CCG
                                || |||||||| ||   ||| |||
                                GG GCCACCCC CG   AGG GGC
                                 T       _ A__   A
GAM342  COL18A1   3'  CCACGGTGGGGGCTTCCTCCG  8728     _      T  AAG   C
                                CC CGGTGGGG GC   TCC CCG
                                || |||||||| ||   ||| |||
                                GG GCCACCCC CG   AGG GGC
                                 T       _ A__   A
GAM342  COL18A1   3'  CCACGGTGGGGGCTTCCTCCG  8728     _      T  AAG   C
                                CC CGGTGGGG GC   TCC CCG
                                || |||||||| ||   ||| |||
                                GG GCCACCCC CG   AGG GGC
                                 T       _ A__   A
GAM342  E48       3'  CCTCTGTGGGGTGGCTTCATCC 8729     CCG      _ AA_
                                CC   GTGGGGTG C   GTCC
                                ||   |||||||| |   ||||
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                                GG  CACCCCAC G  TAGG
                                 AGA      C AAG
GAM342  FBXW1B   3' CCTTGGGTGCCAAAGTCCCC  8730    GGTG    __
                                CC  GGGTGC  AAGTCCCC
                                ||  ||||||  ||||||||
                                GG  CCCACG  TTCAGGGG
                                 AA__    GT
GAM342  FBXW1B   3' CCTTGGGTGCCAAAGTCCCC  8730    GGTG    __
                                CC  GGGTGC  AAGTCCCC
                                ||  ||||||  ||||||||
                                GG  CCCACG  TTCAGGGG
                                 AA__    GT
GAM342  FBXW1B   3' CCTTGGGTGCCAAAGTCCCC  8730    GGTG    __
                                CC  GGGTGC  AAGTCCCC
                                ||  ||||||  ||||||||
                                GG  CCCACG  TTCAGGGG
                                 AA__    GT
GAM342  PRSS8    3' CCGGTGGGGGCTCAGTCCTCCG 8731        T A_   C
                                CCGGTGGGG GC  AGTCC CCG
                                |||||||| ||  ||||| |||
                                GGCCACCCC CG  TCAGG GGC
                                     _ AG   A
GAM342  SLC6A3   3' CCAGTGGGGTCCCTTCC    8732        TGCAAG  __
                                CCGGTGGGG    TCCC  CC
                                |||||||||    ||||  ||
                                GGTCACCCC    AGGG  GG
                                     _______   AA
GAM342  AP3D1    3' CCCAGGTGGGGGGAGTCCC    8733    C     TGCA
                                CCC GGTGGGG   AGTCCC
                                ||| |||||||   ||||||
                                GGG CCACCCC   TCAGGG
                                  T     C___
GAM342  AP3D1    5' CCCAGGTGGGGGGAGTCCC    8733    C     TGCA
                                CCC GGTGGGG   AGTCCC
                                ||| |||||||   ||||||
                                GGG CCACCCC   TCAGGG
                                  T     C___
GAM342  C11orf11 5' CCTTGGGGGACAGGGTCCCCCG 8734    GG    TG  A_
                                CC  TGGGG  CA  GTCCCCCG
                                ||  |||||  ||  ||||||||
                                GG  ACCCC  GT  CAGGGGGC
                                 A_    CT  CC
GAM342  C20orf98 3' CCCTGGTGGGGGGCCGCC    8735    C     T  AA
                                CCC GGTGGGG GC  GTC
                                ||| ||||||| ||  |||
                                GGG CCACCCC CG  CGG
                                  A     _ G_
GAM342  DKFZP761D0211 3' CCCTGGTGGGGTGCAGAGT   8736    C       _
                                CCC GGTGGGGTGCA AGT
                                ||| |||||||||| |||
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                                GGG CCACCCCACGT TCA
                                  A         C
GAM342  FLJ20174  5'  CCGGCTTCTAAGTCCCCCG   8737      GGGGTGC
                                CCGGT      AAGTCCCCCG
                                |||||      ||||||||||
                                GGCCG      TTCAGGGGGC
                                  AAGA___
GAM342  FLJ22202  3'  CCAGTGGGAGTCCCC       8738        GTGCA
                                CCGGTGGG    AGTCCCC
                                ||||||||    |||||||
                                GGTCACCC    TCAGGGG
                                      _____
GAM342  KIAA1908  5'  GGGGGCCGCAGTCCCCCG    8739    T  G   A
                                GG GGG TGCA GTCCCCCG
                                || ||| |||| ||||||||
                                CC CCC GCGT CAGGGGGC
                                 _  G   _
GAM342  MGC4638   3'  CCCAGTGGGTCCTGTCCCC   8740        GTGCAA
                                CCCGGTGGG     GTCCCC
                                |||||||||     ||||||
                                GGGTCACCC     CAGGGG
                                    AGGA__
GAM342  MGC5302   5'  CCCAGGTGAGGGTCCCC     8741     C      TGCAA
                                CCC GGTGGGG    GTCCCC
                                ||| |||||||    ||||||
                                GGG CCACTCC    CAGGGG
                                  T     _____
GAM342  NY-REN-25 5'  CCCCGGCGGGGTCTCCC     8742          GCAAG
                                CCCCGGTGGGGT    TCCC
                                ||||||||||||    ||||
                                GGGGCCGCCCCA    AGGG
                                      G____
GAM342  SLC12A5   3'  CCTCGGTGGGGCGCGGGCC   8743    _        AA
                                CC CGGTGGGGTGC  GTC
                                || ||||||||||  |||
                                GG GCCACCCCGCG  CGG
                                 A          CC
GAM342  SMARCF1   5'  CCCCGGGGCCCAGTCCCCC   8744     GGT    G  A
                                CCCC   GGGGT CA GTCCCCC
                                ||||   ||||| || |||||||
                                GGGG   CCCCG GT CAGGGGG
                                  ___     G  _
GAM342  SMARCF1   5'  CCCCGGGGCCCAGTCCCCC   8744     GGT    G  A
                                CCCC   GGGGT CA GTCCCCC
                                ||||   ||||| || |||||||
                                GGGG   CCCCG GT CAGGGGG
                                  ___     G  _
GAM342  SMARCF1   5'  CCCCGGGGCCCAGTCCCCC   8744     GGT    G  A
                                CCCC   GGGGT CA GTCCCCC
                                ||||   ||||| || |||||||
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                                GGGG  CCCCG GT CAGGGGG
                                  ___    G  _
GAM342  TETRAN   5' CCTGGGTGGGGTGCGGCGGGTC 8745    CC       AA___
                                CC  GGTGGGGTGC    GTC
                                ||  ||||||||||    |||
                                GG  CCACCCCACG    CAG
                                 AC        CCGCC
GAM342  TOLLIP   3' CCCCACTGTGTGGGTCCCTCG  8746      G  GG   CAA    C
                                CCCCG TG  GTG   GTCCC CG
                                |||||  ||  |||   ||||| ||
                                GGGGT AC  CAC   CAGGG GC
                                   G  A_   C__    A
GAM342  LOC126353 5' CCCGTGGGGTGGAGACC    8747      G      CA  T
                                CCCG TGGGGTG  AG CC
                                ||||  |||||||  || ||
                                GGGC ACCCCAC  TC GG
                                  _      C_  T
GAM342  LOC130471 5' CCCGGTAGGGCTCCCCC    8748          GCAAG
                                CCCGGTGGGGT    TCCCCC
                                ||||||||||    ||||||
                                GGGCCATCCCG    AGGGGG
                                              _____
GAM342  LOC143666 3' GATGGTAGTGGTCCCCCG    8749       _   CAA
                                GGTGG GGTG   GTCCCCCG
                                |||||  ||||   ||||||||
                                CTACC TCAC   CAGGGGGC
                                   A   ___
GAM342  LOC148479 5' CCCCGGTGTGTGGAGGCGGGTC 8750         ___   T  AA
                                CCCCGGTG   GGG GC  GTC
                                ||||||||   ||| ||  |||
                                GGGGCCAC   CCT CG  CAG
                                     ACA   C  CC
GAM342  LOC163682 3' GGTGGGGGTGTGAGCACCACCG  8751         CA  TC  _
                                GGTGGGGGTG  AG  CC CCG
                                |||||||||  ||  || |||
                                CCACCCCAC  TC  GG GGC
                                      AC  GT  T
GAM342  LOC253258 3' GATGGTAGTGGTCCCCCG    8749       _   CAA
                                GGTGG GGTG   GTCCCCCG
                                |||||  ||||   ||||||||
                                CTACC TCAC   CAGGGGGC
                                   A   ___
GAM343  ADM      3' CCCTGGTGGGGGTGACACGCC   8726      C       _  A
                                CCC GGTGGGGGTG CA GTC
                                |||  |||||||||  || |||
                                GGG CCACCCCAC GT CGG
                                  A        T  G
GAM343  CAV3     3' CCCCTGTGAAGAAGTCCCCCG  8727       G     TGC
                                CCCC GTGGGG   AAGTCCCCCG
                                ||||  ||||||   ||||||||||
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                                GGGG CACTTC   TTCAGGGGGC
                                  A     ___
GAM343  COL18A1  3'  CCACGGTGGGGGCTTCCTCCG  8728     _      T  AAG   C
                                CC CGGTGGGG GC   TCC CCG
                                || |||||||| ||   ||| |||
                                GG GCCACCCC CG   AGG GGC
                                 T      _ A__   A
GAM343  COL18A1  3'  CCACGGTGGGGGCTTCCTCCG  8728     _      T  AAG   C
                                CC CGGTGGGG GC   TCC CCG
                                || |||||||| ||   ||| |||
                                GG GCCACCCC CG   AGG GGC
                                 T      _ A__   A
GAM343  COL18A1  3'  CCACGGTGGGGGCTTCCTCCG  8728     _      T  AAG   C
                                CC CGGTGGGG GC   TCC CCG
                                || |||||||| ||   ||| |||
                                GG GCCACCCC CG   AGG GGC
                                 T      _ A__   A
GAM343  E48      3'  CCTCTGTGGGGTGGCTTCATCC 8729     CCG      _ AA_
                                CC   GTGGGGTG C   GTCC
                                ||   |||||||| |   ||||
                                GG   CACCCCAC G   TAGG
                                 AGA       C AAG
GAM343  FBXW1B   3'  CCTTGGGTGCCAAAGTCCCC   8730     GGTG     __
                                CC    GGGTGC  AAGTCCCC
                                ||    ||||||  ||||||||
                                GG    CCCACG  TTCAGGGG
                                 AA__     GT
GAM343  FBXW1B   3'  CCTTGGGTGCCAAAGTCCCC   8730     GGTG     __
                                CC    GGGTGC  AAGTCCCC
                                ||    ||||||  ||||||||
                                GG    CCCACG  TTCAGGGG
                                 AA__     GT
GAM343  FBXW1B   3'  CCTTGGGTGCCAAAGTCCCC   8730     GGTG     __
                                CC    GGGTGC  AAGTCCCC
                                ||    ||||||  ||||||||
                                GG    CCCACG  TTCAGGGG
                                 AA__     GT
GAM343  PRSS8    3'  CCGGTGGGGGCTCAGTCCTCCG 8731          T  A_    C
                                CCGGTGGGG GC  AGTCC CCG
                                |||||||| ||  ||||| |||
                                GGCCACCCC CG  TCAGG GGC
                                      _ AG    A
GAM343  SLC6A3   3'  CCAGTGGGGTCCCTTCC     8732          TGCAAG   __
                                CCGGTGGGG     TCCC  CC
                                |||||||||     ||||  ||
                                GGTCACCCC     AGGG  GG
                                      _______   AA
GAM343  AP3D1    3'  CCCAGGTGGGGGAGTCCC    8733      C      TGCA
                                CCC GGTGGGG    AGTCCC
                                ||| |||||||    ||||||
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                                GGG CCACCCC   TCAGGG
                                  T     C___
GAM343  AP3D1    5'  CCCAGGTGGGGGAGTCCC   8733    C     TGCA
                                CCC GGTGGGG   AGTCCC
                                ||| |||||||   ||||||
                                GGG CCACCCC   TCAGGG
                                  T     C___
GAM343  C11orf11  5'  CCTTGGGGGACAGGGTCCCCCG 8734    GG    TG  A_
                                CC  TGGGG  CA  GTCCCCCG
                                ||  |||||  ||  ||||||||
                                GG  ACCCC  GT  CAGGGGGC
                                 A_    CT  CC
GAM343  C20orf98  3'  CCCTGGTGGGGGCCGCC    8735    C     T  AA
                                CCC GGTGGGG GC  GTC
                                ||| ||||||| ||  |||
                                GGG CCACCCC CG  CGG
                                  A     _ G_
GAM343  DKFZP761D0211 3'  CCCTGGTGGGGTGCAGAGT   8736    C       _
                                CCC GGTGGGGTGCA AGT
                                ||| |||||||||| |||
                                GGG CCACCCCACGT TCA
                                  A         C
GAM343  FLJ20174  5'  CCGGCTTCTAAGTCCCCCG   8737     GGGGTGC
                                CCGGT     AAGTCCCCCG
                                |||||     ||||||||||
                                GGCCG     TTCAGGGGGC
                                   AAGA___
GAM343  FLJ22202  3'  CCAGTGGGAGTCCCC      8738       GTGCA
                                CCGGTGGG    AGTCCCC
                                ||||||||    |||||||
                                GGTCACCC    TCAGGGG
                                          _____
GAM343  KIAA1908  5'  GGGGGCCGCAGTCCCCCG   8739    T  G   A
                                GG GGG TGCA GTCCCCCG
                                || ||| |||| ||||||||
                                CC CCC GCGT CAGGGGGC
                                 _  G   _
GAM343  MGC4638   3'  CCCAGTGGGTCCTGTCCCC   8740       GTGCAA
                                CCCGGTGGG     GTCCCC
                                |||||||||     ||||||
                                GGGTCACCC     CAGGGG
                                     AGGA__
GAM343  MGC5302   5'  CCCAGGTGAGGGTCCCC    8741    C     TGCAA
                                CCC GGTGGGG    GTCCCC
                                ||| |||||||    ||||||
                                GGG CCACTCC    CAGGGG
                                  T     _____
GAM343  NY-REN-25 5'  CCCCGGCGGGGTCTCCC    8742         GCAAG
                                CCCCGGTGGGGT    TCCC
                                ||||||||||||    ||||
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                                GGGGCCGCCCCA    AGGG
                                      G____
GAM343  SLC12A5   3'  CCTCGGTGGGGCGCGGGCC   8743    _       AA
                                CC CGGTGGGGTGC  GTC
                                || ||||||||||  |||
                                GG GCCACCCCGCG  CGG
                                 A         CC
GAM343  SMARCF1   5'  CCCCGGGGCCCAGTCCCCC   8744     GGT    G  A
                                CCCC   GGGGT CA GTCCCCC
                                ||||   ||||| || |||||||
                                GGGG   CCCCG GT CAGGGGG
                                  ___    G  _
GAM343  SMARCF1   5'  CCCCGGGGCCCAGTCCCCC   8744     GGT    G  A
                                CCCC   GGGGT CA GTCCCCC
                                ||||   ||||| || |||||||
                                GGGG   CCCCG GT CAGGGGG
                                  ___    G  _
GAM343  SMARCF1   5'  CCCCGGGGCCCAGTCCCCC   8744     GGT    G  A
                                CCCC   GGGGT CA GTCCCCC
                                ||||   ||||| || |||||||
                                GGGG   CCCCG GT CAGGGGG
                                  ___    G  _
GAM343  TETRAN    5'  CCTGGGTGGGGTGCGGCGGGTC 8745    CC       AA___
                                CC  GGTGGGGTGC    GTC
                                ||  ||||||||||    |||
                                GG  CCACCCCACG    CAG
                                 AC        CCGCC
GAM343  TOLLIP    3'  CCCCACTGTGTGGGTCCCTCG  8746     G  GG   CAA    C
                                CCCCG TG  GTG   GTCCC CG
                                |||||  ||  |||   ||||| ||
                                GGGGT AC  CAC   CAGGG GC
                                  G  A_   C__     A
GAM343  LOC126353 5'  CCCGTGGGGTGGAGACC    8747     G      CA  T
                                CCCG TGGGGTG  AG CC
                                ||||  |||||||  || ||
                                GGGC ACCCCAC  TC GG
                                  _      C_  T
GAM343  LOC130471 5'  CCCGGTAGGGCTCCCCC    8748          GCAAG
                                CCCGGTGGGGT    TCCCCC
                                ||||||||||    ||||||
                                GGGCCATCCCG    AGGGGG
                                      _____
GAM343  LOC143666 3'  GATGGTAGTGGTCCCCCG    8749      _   CAA
                                GGTGG GGTG   GTCCCCCG
                                |||||  ||||   ||||||||
                                CTACC TCAC   CAGGGGGC
                                  A   ___
GAM343  LOC148479 5'  CCCCGGTGTGTGGAGGCGGGTC 8750         ___   T  AA
                                CCCCGGTG   GGG GC  GTC
                                ||||||||   ||| ||  |||
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                                GGGGCCAC   CCT CG  CAG
                                    ACA   C  CC
GAM343  LOC163682 3'  GGTGGGGTGTGAGCACCACCG  8751          CA  TC  _
                                GGTGGGGTG  AG  CC CCG
                                |||||||||  ||  || |||
                                CCACCCCAC  TC  GG GGC
                                     AC  GT  T
GAM343  LOC253258 3'  GATGGTAGTGGTCCCCCG    8749       _   CAA
                                GGTGG GGTG   GTCCCCCG
                                ||||| ||||   ||||||||
                                CTACC TCAC   CAGGGGGC
                                  A   ___
GAM344  ATP6V0A4  3'  AGTCCTTCCTCTGACGTGG   8755    G   GACGCAC
                                AG CCTT      CTGACGTGG
                                || ||||      |||||||||
                                TC GGAA      GACTGCACC
                                 A   GGA____
GAM344  ATP6V0A4  3'  AGTCCTTCCTCTGACGTGG   8755    G   GACGCAC
                                AG CCTT      CTGACGTGG
                                || ||||      |||||||||
                                TC GGAA      GACTGCACC
                                 A   GGA____
GAM344  ATP6V0A4  3'  AGTCCTTCCTCTGACGTGG   8755    G   GACGCAC
                                AG CCTT      CTGACGTGG
                                || ||||      |||||||||
                                TC GGAA      GACTGCACC
                                 A   GGA____
GAM344  MAPK3     3'  AGGCCTTGGCCTGCCTGAAGC  8756        AC  A__    C
                                AGGCCTTG  GC   CCTGA GT
                                ||||||||  ||   ||||| ||
                                TCCGGAAC  CG   GGACT CG
                                    __  GAC    T
GAM344  PIAS3     3'  AGGCCTTGGCGAGCCTGA    8757         A  CA
                                AGGCCTTG CG  CCTGA
                                |||||||| ||  |||||
                                TCCGGAAC GC  GGACT
                                    C  TC
GAM344  TEM6      3'  AGGCCTTATTCTGATGTGG   8758         ACGCAC   C
                                AGGCCTTG     CTGA GTGG
                                ||||||||     |||| ||||
                                TCCGGAAT     GACT CACC
                                    AA____   A
GAM344  C22orf23  3'  GCCACCACCTGACGTGG     8759      TTG  G
                                GCC   AC CACCTGACGTGG
                                |||   || ||||||||||||
                                CGG   TG GTGGACTGCACC
                                  ___  _
GAM344  C5orf4    3'  AGGCCTTGGTCTGCTTGAACAT 8760         AC__  ACCT
          GG                    AGGCCTTG   GC   GACGTGG
                                ||||||||   ||   |||||||
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                                TCCGGAAC   CG   TTGTACC
                                    CAGA  AAC_
GAM344  DKFZP566G1424 5' AGGCCTTGGGCACTGGAGG   8761        AC   C  ACGT
                                AGGCCTTG  GCAC TG   GG
                                ||||||||  |||| ||   ||
                                TCCGGAAC  CGTG AC   CC
                                    C_   _ CT__
GAM344  FLJ10565  5' AGGCCTCGGTGCACTTGG    8762        AC   CTGACG
                                AGGCCTTG  GCAC    TGG
                                ||||||||  ||||    |||
                                TCCGGAGC  CGTG    ACC
                                    CA   A_____
GAM344  FLJ14001  5' AGGCCTTCGCGGACGTGG    8763        GA   ACCT
                                AGGCCTT  CGC   GACGTGG
                                |||||||  |||   |||||||
                                TCCGGAA  GCG   CTGCACC
                                   __  C___
GAM344  FLJ14154  3' AGGCCTTGGAGCAGCAGCTTGT 8764        AC   CCTGAC_
           GGC                    AGGCCTTG  GCA     GTGGC
                                |||||||  |||     |||||
                                TCCGGAAC  CGT     CACCG
                                    CT   CGTCGAA
GAM344  FLJ20306  5' GGCCGGCTGCGCCTGACGTGGC 8765      TTGAC  A
                                GGCC    GC CCTGACGTGGC
                                ||||    || ||||||||||
                                CCGG    CG GGACTGCACCG
                                  CCGA_  C
GAM344  HCA4     3'  AGGCCTTGATGTGGCCTCTGAT 8766        C___  AC   C
           GT                    AGGCCTTGA   GC  CTGA GT
                                |||||||||   ||  |||| ||
                                TCCGGAACT   CG  GACT CA
                                    ACAC  GA   A
GAM344  KCNT1    3'  AGGCCTTGGCGTCTTCATAGC  8767        AC  AC  GA
                                AGGCCTTG  GC  CT  CGTGGC
                                |||||||  ||  ||  ||||||
                                TCCGGAAC  CG  GA  GTATCG
                                    __  CA  A_
GAM344  KIAA0682  3'  GACCTTGATGCATTTCACAGGG 8768        C   CCTG   T
           C                     GGCCTTGA GCA    ACG GGC
                                |||||||| |||    ||| |||
                                CTGGAACT CGT    TGT CCG
                                    A   AAAG   C
GAM344  MGC15416  3'  AGGCCTTGGCCCGCCCTCACCG 8769        A__   A   G  G
           GC                    AGGCCTTG   CGC CCT AC TGGC
                                ||||||||   ||| ||| || ||||
                                TCCGGAAC   GCG GGA TG GCCG
                                    CGG   _   G  _
GAM344  MR       5'  GGTCTTGACGCAGTCGATGG   8770     C       CC   CG
                                GG CTTGACGCA  TGA  TGG
                                ||  |||||||||  |||  |||
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                                CC GAACTGCGT  GCT  ACC
                                 A       CA  __
GAM344  PP1628   5'  GGCCTTGATGGACTTGATGGAT 8771        CGC  C   C__
          GGC                    GGCCTTGA   AC TGA   GTGGC
                                |||||||||   || |||   |||||
                                CCGGAACT   TG ACT   TACCG
                                    ACC  A   ACC
GAM344  RCD-8    3'  AGCTTTTGGCGCACCTGGG   8772     C_  A      ACGT
                                GGC  TTG CGCACCTG    GG
                                |||  ||| |||||||||    ||
                                TCG  AAC GCGTGGAC    CC
                                 AA  C       _____
GAM344  LOC129198 5'  AGGCCTTGGGTGGTCCGTGTGG 8773         ACGCAC   AC
          C                     AGGCCTTG     CTG  GTGGC
                                |||||||||     |||  |||||
                                TCCGGAAC     GGC  CACCG
                                    CCACCA   A_
GAM344  LOC148345 5'  AGGCCCTGTCTGGCGTGG    8774         ACGCAC   A
                                AGGCCTTG     CTG CGTGG
                                |||||||||     ||| |||||
                                TCCGGGAC     GAC GCACC
                                    A_____   C
GAM344  LOC148753 3'  GGCTCTGGGGGACTTGACGTGG 8775      C   ACGC  C
                                GGC TTG    AC TGACGTGG
                                ||| |||    || ||||||||
                                CCG GAC    TG ACTGCACC
                                  A   CCCC  A
GAM344  LOC150538 3'  AGGCCTTGATGACTTG      8776          CGCACC    G
                                AGGCCTTGA     TGAC TG
                                |||||||||      |||| ||
                                TCCGGAACT     ACTG AC
                                    _______    A
GAM344  LOC153338 5'  AGGCCTTGGCACATGGATGG   8777         AC    C  AC
                                AGGCCTTG  GCAC TG  GTGG
                                ||||||||  |||| ||  ||||
                                TCCGGAAC  CGTG AC  TACC
                                    __    T  C_
GAM344  LOC163682 3'  GGCCTTGATTCACTGCATGG   8778         CG   C  A
                                GGCCTTGA  CAC TG CGTGG
                                ||||||||  ||| || |||||
                                CCGGAACT  GTG AC GTACC
                                    AA  _  _
GAM344  LOC200301 3'  GGCCTGACGTCCCTCGTGG    8779       T    CA   GA
                                GGCCT GACG  CCT  CGTGG
                                |||||  ||||  |||  |||||
                                CCGGA CTGC  GGA  GCACC
                                   _    AG   __
GAM344  LOC222962 3'  AGGTCCTGACGTGCCCAGCTGG 8780      C      CA    ACG
          C                     AGG CTTGACG  CCTG   TGGC
                                |||  |||||||  ||||   ||||
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                                TCC GGACTGC  GGGT   ACCG
                                  A      AC    CG_
GAM344  LOC255645 3'  AGGCCTTGGGTGAAGAGTGGC  8781         ACGCACCT  C
                                AGGCCTTG       GA GTGGC
                                ||||||||       || |||||
                                TCCGGAAC       CT CACCG
                                    CCACTT__  _
GAM344  LOC90485  3'  AGGCCTTGGCGCACTG      8782          A    CTGACG
                                AGGCCTTG CGCAC     TG
                                |||||||| |||||     ||
                                TCCGGAAC GCGTG     AC
                                    C    _______
GAM344  LOC90485  3'  AGGCCTTGCCGCACTCGGGGC  8783         A    CTGA  T
                                AGGCCTTG CGCAC    CG GGC
                                |||||||| |||||    || |||
                                TCCGGAAC GCGTG    GC CCG
                                    G    A___  C
GAM344  LOC90485  3'  AGGCCTTGGCGCACTG      8782          A    CTGACG
                                AGGCCTTG CGCAC     TG
                                |||||||| |||||     ||
                                TCCGGAAC GCGTG     AC
                                    C    _______
GAM345  CPNE3     3'  AATAATGTAGAATTCAGGAC   8786       __   T_
                                AATAA  TAG  TTCAGGAC
                                |||||  |||  ||||||||
                                TTATT  ATC  AAGTCCTG
                                   AC   TT
GAM345  DAAM2     3'  TCACAACAATGGCCAGG     8787          A  TT
                                TCACAATAAT GT  CAGG
                                |||||||||| ||  ||||
                                AGTGTTGTTA CG  GTCC
                                     C  __
GAM345  DAZ       3'  TCACAATATAAAATGAGGAC   8788         A   TTTC
                                TCACAATA TAG    AGGAC
                                |||||||| |||    |||||
                                AGTGTTAT ATT    TCCTG
                                    _   TTAC
GAM345  FRK       3'  TCATAATAACAGCCTGATGGGA 8789      C         CA__
                                TCA AATAATAGTTT    GGA
                                ||| ||||||||||    |||
                                AGT TTATTGTCGGA    CCT
                                  A          CTAC
GAM345  FTSJ2     3'  TCACAATATAGCGGA       8790         A    TTCA
                                TCACAATA TAGT    GGA
                                |||||||| ||||    |||
                                AGTGTTAT ATCG    CCT
                                    _   _____
GAM345  GUCY1B2   5'  TCCAAAGAGTTTCAGGA     8791     A   TAAT
                                TC CAA    AGTTTCAGGA
                                || |||    ||||||||||
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                                AG GTT    TCAAAGTCCT
                                 _  TC__
GAM345  MAGEB4   3'  TCACAAAAATTATTTCAGGA  8792       T  A
                                TCACAA AAT GTTTCAGGA
                                |||||| ||| |||||||||
                                AGTGTT TTA TAAAGTCCT
                                   T  A
GAM345  PHKA2    3'  ACATACATCAGTTTCAGG    8793     _  A
                                ACA ATA TAGTTTCAGG
                                ||| ||| ||||||||||
                                TGT TGT GTCAAAGTCC
                                  A  A
GAM345  PMCHL1   3'  TCACAATATGCATTAGGAC   8794        ATA  TTC
                                TCACAATA  GT  AGGAC
                                ||||||||  ||  |||||
                                AGTGTTAT  CG  TCCTG
                                    A__  TAA
GAM345  PPP1R12B 3'  CACAATAATAGAAAGCTGGAC 8795          TTTCA_
                                CACAATAATAG    GGAC
                                ||||||||||     ||||
                                GTGTTATTATC    CCTG
                                      TTTCGA
GAM345  PRDX3    3'  TCAAGATGAAAATTTCAGGAC 8796     CA  AAT
                                TCA  AT  AGTTTCAGGAC
                                |||  ||  ||||||||||
                                AGT  TA  TTAAAGTCCTG
                                  TC  CTT
GAM345  RAB6A    3'  TCACAATAACTAGTAAAGA   8797         _  TTC
                                TCACAATAAT AGT  AGGA
                                |||||||||| |||  ||||
                                AGTGTTATTG TCA  TTCT
                                      A  T__
GAM345  RGS5     3'  ATAATAGCATCATAGGAC    8798        T  __
                                ATAATAGT TCA  GGAC
                                |||||||| |||  ||||
                                TATTATCG AGT  CCTG
                                     T  AT
GAM345  SNAP23   3'  TCATAACACTTTTCAGGA    8799     C   ATAG
                                TCA AATA   TTTCAGGA
                                ||| ||||   ||||||||
                                AGT TTGT   AAAGTCCT
                                  A  GA__
GAM345  SNAP23   3'  TCATAACACTTTTCAGGA    8799     C   ATAG
                                TCA AATA   TTTCAGGA
                                ||| ||||   ||||||||
                                AGT TTGT   AAAGTCCT
                                  A  GA__
GAM345  TRIP12   3'  TCACAACAACGTTTTAGG    8800         A   C
                                TCACAATAAT GTTT AGG
                                |||||||||| |||| |||
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                                AGTGTTGTTG CAAA TCC
                                      _   A
GAM345  TRIP15   3'  TCCAATAATTTTCAGGAC    8801     A      AG
                                TC CAATAAT  TTTCAGGAC
                                || |||||||  |||||||||
                                AG GTTATTA  AAAGTCCTG
                                  _     __
GAM345  TSN      3'  ACATAATAGTCAGGA       8802      A     TT
                                ACA TAATAG  TCAGGA
                                ||| ||||||  ||||||
                                TGT ATTATC  AGTCCT
                                  _     __
GAM345  WW45     3'  TCACAATAAGGTTCCAAA    8803          TA
                                TCACAATAA  GTTTCAGG
                                |||||||||  ||||||||
                                AGTGTTATT  CAAGGTTT
                                     C_
GAM345  ZNF264   3'  CCACAATCATGTTCAGGAC   8804         AATAGT
                                TCACAAT     TTCAGGAC
                                |||||||     ||||||||
                                GGTGTTA     AAGTCCTG
                                   GTAC__
GAM345  BANK     3'  TCAAATAATAATGTTTTCAGG  8805      C       ___
                                TCA AATAATAGT   TTCAGG
                                ||| |||||||||   ||||||
                                AGT TTATTATTA   AAGTCC
                                  _       CAA
GAM345  C20orf16 3'  ACAATAACAAGGCAGGAC    8806          TTT
                                ACAATAATAG   CAGGAC
                                ||||||||||   ||||||
                                TGTTATTGTT   GTCCTG
                                     CC_
GAM345  CCT6B    3'  CACAATAGTAGTCAGA      8807         A   TT
                                CACAATA TAG  TCAGG
                                ||||||| |||  |||||
                                GTGTTAT ATC  AGTCT
                                   C  __
GAM345  CHL1     3'  TCACAATTAAAATCAGG     8808         AA   TT
                                TCACAAT  TAG  TCAGG
                                |||||||  |||  |||||
                                AGTGTTA  ATT  AGTCC
                                   __   TT
GAM345  COE2     3'  TCCAATCCATTTCAGGAC    8809     A    AATA
                                TC CAAT    GTTTCAGGAC
                                || ||||    ||||||||||
                                AG GTTA    TAAAGTCCTG
                                  _   GG__
GAM345  CTRP5    3'  TCACAATATTCCAGG       8810         AATA
                                TCACAAT    GTTTCAGG
                                |||||||    ||||||||
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                                AGTGTTA    TAAGGTC
                                       ____
GAM345  ERG-1    5'  CACAATAAGCCAGCTCAGGA  8811         __    T
                                CACAATAA  TAGTT CAGGA
                                ||||||||  ||||| |||||
                                GTGTTATT  GTCGA GTCCT
                                     CG    _
GAM345  FKBP3    5'  TAATAGTTGAACATCAGGAC  8812         _____
                                TAATAGTT    TCAGGAC
                                ||||||||    |||||||
                                ATTATCAA    AGTCCTG
                                     CTTGT
GAM345  FLJ21802 3'  ACAATAACAAACAGGA     8813          TTT
                                ACAATAATAG   CAGGA
                                ||||||||||   |||||
                                TGTTATTGTT   GTCCT
                                      T__
GAM345  FLJ30567 3'  TCACAATATCACAGGA     8814        AATA   T
                                TCACAAT    GTT CAGGA
                                |||||||    ||| |||||
                                AGTGTTA    TAG GTCCT
                                     ____  T
GAM345  GGA2     3'  CCACAGCCACTTTCAGGAC   8815       ATAA  G
                                TCACA    TA TTTCAGGAC
                                |||||    || |||||||||
                                GGTGT    GT AAAGTCCTG
                                   CG__  G
GAM345  GGA2     3'  CCACAGCCACTTTCAGGAC   8815       ATAA  G
                                TCACA    TA TTTCAGGAC
                                |||||    || |||||||||
                                GGTGT    GT AAAGTCCTG
                                   CG__  G
GAM345  HBXAP    3'  TCACAGAAAGACTTCAGGA   8816       ATAAT  _
                                TCACA     AG TTTCAGGA
                                |||||     || ||||||||
                                AGTGT     TC GAAGTCCT
                                   CTT__  T
GAM345  HIC      3'  CAAAATAGTGTATTCAGGA   8817     T    ___
                                CAA AATAGT   TTCAGGA
                                ||| ||||||   |||||||
                                GTT TTATCA   AAGTCCT
                                  _     CAT
GAM345  HMGN4    3'  TCACAAAAATCAGTTCAGGAC 8818       T  _   T
                                TCACAA AAT AGTT CAGGAC
                                |||||| ||| |||| ||||||
                                AGTGTT TTA TCAA GTCCTG
                                   T  G   _
GAM345  KIAA1041 5'  TCACAATATCCAGGA      8819        ATAGT
                                TCACAATA    TTCAGGA
                                ||||||||    |||||||
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                                AGTGTTAT    AGGTCCT
                                        _____
GAM345  KIAA1136  3'  CAGATAATAGTTTTAGGA    8820    _       C
                                CA ATAATAGTTT AGGA
                                || |||||||||| ||||
                                GT TATTATCAAA TCCT
                                  C         A
GAM345  MGC27382  5'  TCAGAATAATAGTCTTTGG   8821     C        CA
                                TCA AATAATAGTTT  GG
                                ||| ||||||||||  ||
                                AGT TTATTATCAGA  CC
                                  C         AA
GAM345  MGC2817   3'  TCACAATTAAGACCTCAGG   8822       AAT  _
                                TCACAAT   AG TTTCAGG
                                |||||||   || |||||||
                                AGTGTTA   TC GGAGTCC
                                     AT_  T
GAM345  MGC5509   3'  CCACAATAATCAGGA      8823        TAGTT
                                TCACAATAA    TCAGGA
                                |||||||||    ||||||
                                GGTGTTATT    AGTCCT
                                        _____
GAM345  NDP52     3'  TCAAGATAACTGCCAGGAC   8824     CA    A  TT
                                TCA  ATAAT GT  CAGGAC
                                |||  ||||| ||  ||||||
                                AGT  TATTG CG  GTCCTG
                                  TC    A  __
GAM345  OMD       3'  CACAATAACATTGTTTAGGA  8825         __   C
                                CACAATAATA  GTTT AGGA
                                ||||||||||  |||| ||||
                                GTGTTATTGT  CAAA TCCT
                                      AA   _
GAM345  PRO2133   3'  TCACAATATGGCCCAGG     8826        ATA   T
                                TCACAATA   GTT CAGG
                                ||||||||   ||| ||||
                                AGTGTTAT   CGG GTCC
                                     AC_  _
GAM345  PRO2730   5'  TCACAATACTGGCCCACAGG  8827        ATA   _
                                TCACAATA   GTTT CAGG
                                ||||||||   |||| ||||
                                AGTGTTAT   CGGG GTCC
                                     GAC    T
GAM345  RAB6C     3'  TCACAATAACTAGTAAAGA   8797         _  TTC
                                TCACAATAAT AGT   AGGA
                                |||||||||| |||   ||||
                                AGTGTTATTG TCA   TTCT
                                      A   T__
GAM345  SPRY4     3'  CACAAAGTTTCAGGAC      8828       TAAT
                                CACAA    AGTTTCAGGAC
                                |||||    ||||||||||
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                                GTGTT   TCAAAGTCCTG
                                  ____
GAM345  TRIM15   3'  TCACAGGGAGGCTCAGGAC   8829      ATAAT  T
                                TCACA    AG TTCAGGAC
                                ||||||    || ||||||||
                                AGTGT    TC GAGTCCTG
                                   CCC__  C
GAM345  TTY7     3'  ACAATCCAACTTCAGGAC    8830      AA  GT
                                ACAAT  TA  TTCAGGAC
                                ||||||  ||  ||||||||
                                TGTTA  GT  AAGTCCTG
                                   G_  TG
GAM345  LOC135307 5'  TCACAACAGTAGGAACCTAGGA 8831        A   TT_ _
            C                    TCACAATA TAG   TC AGGAC
                                ||||||||| |||   || |||||
                                AGTGTTGT ATC   GG TCCTG
                                     C   CTT  A
GAM345  LOC154215 3'  CCACAATAATACAGGA     8832          GTTT
                                TCACAATAATA    CAGGA
                                ||||||||||    |||||
                                GGTGTTATTAT    GTCCT
                                  ____
GAM345  LOC220515 5'  TCACAACAATACAGAAAGGAC  8833          GTTTC
                                TCACAATAATA     AGGAC
                                ||||||||||     |||||
                                AGTGTTGTTAT    TCCTG
                                      GTCTT
GAM345  LOC221178 3'  TCACAGAATGTTCCAAG     8834       AT   A
                                TCACA  AAT GTTTCAGG
                                |||||  ||| ||||||||
                                AGTGT  TTA CAAGGTTC
                                   C_   _
GAM345  LOC254672 3'  TCACAATATGCATTAGGAC   8794        ATA  TTC
                                TCACAATA   GT   AGGAC
                                ||||||||   ||   |||||
                                AGTGTTAT   CG   TCCTG
                                     A__  TAA
GAM345  LOC51020  3'  ACAATAAAGGTCTCAAGA    8835        TA
                                ACAATAA  GTTTCAGGA
                                |||||||  |||||||||
                                TGTTATT  CAGAGTTCT
                                     TC
GAM345  LOC90841  3'  ACATAATTTTCAGGA      8836      A   AG
                                ACA TAAT  TTTCAGGA
                                ||| ||||  ||||||||
                                TGT ATTA  AAAGTCCT
                                  _   __
GAM346  CAPON    5'  GCCGAGGGCCGAGCGGCAGCG  8839     AA       _  A  A
                                GC  GAGGGTCGA CG CA CG
                                ||  ||||||||| || || ||
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                                CG  CTCCCGGCT GC GT GC
                                 G_       C  C  C
GAM346  CSE1L    5'  CGGCAAAATGGCGCGACAGCGA 8840         G  T  A    A
                                CGGCAAGA GG CG CGACA CGA
                                |||||||| || || ||||| |||
                                GCCGTTTT CC GC GCTGT GCT
                                     A  _  _    C
GAM346  HTR2C    5'  CGACGACTCCGACGACAACGA  8841       AA  GGG
                                CGGC  GA   TCGACGACAACGA
                                ||||  ||   ||||||||||||||
                                GCTG  CT   GGCTGCTGTTGCT
                                  __  GA_
GAM346  KAI1     3'  GGCAAGAGGGTCTTCGCA    8842           GA  A
                                GGCAAGAGGGTC  CG CA
                                ||||||||||||  || ||
                                CCGTTCTCCCAG  GC GT
                                       AA  _
GAM346  RPL8     5'  CGGAAGAGGATGGCGGCG    8843      C       __  A
                                CGG AAGAGGGT  CG CG
                                ||| ||||||||  || ||
                                GCC TTCTCCTA  GC GC
                                  _       CC  C
GAM346  SLC3A2   5'  GGCGCGGAATCGACACGACG   8844      AAGA       G  A
                                GGC    GGGTCGAC AC ACG
                                |||    |||||||| || |||
                                CCG    CTTAGCTG TG TGC
                                  CGC_        _  C
GAM346  SPG4     5'  CGACGGGAACCAAGCGACGGCG 8845       AAGA GG    _    AA
                                CGGC    G  TCGA CGAC  CG
                                ||||    |  |||| ||||  ||
                                GCTG    C  GGTT GCTG  GC
                                  CC__ TT    C    CC
GAM346  BRD2     5'  CAGCAAGAAAATGGCGGCG    8846          ___  T  A
                                CGGCAAGAG   GG CG CG
                                |||||||||   || || ||
                                GTCGTTCTT   CC GC GC
                                      TTA  _  C
GAM346  C5orf5   5'  CGGCAAGAGGGCGAGAAC    8847           T   C
                                CGGCAAGAGGG CGA GAC
                                |||||||||||  ||| |||
                                GCCGTTCTCCC GCT TTG
                                       _   C
GAM346  CNOT8    3'  GGCAAGAGGGTTGGACACGA   8848           CGAC    A
                                GGCAAGAGGGT    GACA CGA
                                ||||||||||    ||||  |||
                                CCGTTCTCCCA    CTGT GCT
                                       AC__    _
GAM346  ERN1     5'  CGGGGGCGCCGCGACGACAGCG 8849     CAAGA    ____       A
            A                    GG    GGGT    CGACGACA CGA
                                ||    ||||    |||||||| |||
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                                CC    CCCG   GCTGCTGT GCT
                                 _____  CGGC      C
GAM346  ERp44    5'  CGGGAGCCGACGGCAGCG   8850     CAAGA      A  A
                                CGG    GGGTCGACG CA CG
                                |||    ||||||||| || ||
                                GCC    CTCGGCTGC GT GC
                                 _____      C  C
GAM346  FLJ13153  5'  CGGCCAGAGCCGAGTGGCAACG 8851      AAG      CGA_
                                CGGC   AGGGTCGA   CAACG
                                ||||   ||||||||   |||||
                                GCCG   TCTCGGCT   GTTGC
                                  G__      CACC
GAM346  KIAA0140  3'  GGCAAGAGGGTATGGCAACGA  8852          CGACGA
                                GGCAAGAGGGT    CAACGA
                                ||||||||||    ||||||
                                CCGTTCTCCCA    GTTGCT
                                      TACC__
GAM346  KIAA1305  5'  CGGTAGGAGGTTCGGTAGATAA 8853     CAA   G   AC_  C_
           ACG                   CGG   GAGG TCG   GA  AACG
                                |||   |||| |||   ||  ||||
                                GCC   CTCC AGC   CT  TTGC
                                 ATC    A   CAT  AT
GAM346  NUDE1    5'  CGGCGAGGCCAACGCGGCG   8854      AAGA      ACAA
                                CGGC   GGGTCGACG   CG
                                ||||   |||||||||   ||
                                GCCG   TCCGGTTGC   GC
                                  C___       GCC_
GAM346  PDP      5'  CGACGAGGAGGGGGCGACAACG 8855      AA_    TCGA
           A                    CGGC   GAGGG   CGACAACGA
                                ||||   |||||   |||||||||
                                GCTG   CTCCC   GCTGTTGCT
                                  CTC    CC__
GAM346  PPP1R1B   5'  CGGGAGGAGGGTCGGCGCCCG  8856     CAA      A  ACAA
                                CGG   GAGGGTCG CG   CG
                                |||   |||||||| ||   ||
                                GCC   CTCCCAGC GC   GC
                                 CTC      C  GG__
GAM346  TPARL    5'  GCAAGAGGAAGTGCCGGCGAC  8857         ____   A
                                GCAAGAGG   GTCG CGAC
                                ||||||||   |||| ||||
                                CGTTCTCC   CGGC GCTG
                                     TTCA   C
GAM346  LOC146745 5'  CAGCGACGGCGACAAC     8858      AA  G  T
                                CGGC  GA GG CGACGAC
                                ||||  || || |||||||
                                GTCG  CT CC GCTGTTG
                                  __ G  _
GAM346  LOC146774 3'  CGGGGGCGCCGCGACGACAGCG 8849     CAAGA  ____      A
           A                    GG    GGGT   CGACGACA CGA
                                ||    ||||   |||||||| |||
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                                CC    CCCG   GCTGCTGT GCT
                                 _____   CGGC      C
GAM346  LOC153684 5'  CGGGAAGAGAGCCTGGCAGCGA 8859     C       GACGA  A
                                CGG AAGAGGGTC    CA CGA
                                ||| |||||||||    || |||
                                GCC TTCTCTCGG    GT GCT
                                  C       ACC__  C
GAM346  LOC200627 5'  CGGGAGAGGGCCGGGCAACG  8860     CA       ACGA
                                CGG  AGAGGGTCG   CAACG
                                |||  |||||||||   |||||
                                GCC  TCTCCCGGC   GTTGC
                                  C_       CC__
GAM346  LOC201243 5'  CAGCGACGGCGACAAC     8858      AA  G  T
                                CGGC  GA GG CGACGAC
                                ||||  || || |||||||
                                GTCG  CT CC GCTGTTG
                                  __  G  _
GAM347  ABCF1    3'  TGGTTGCCAGGTCAGCTGCAGG 8863    A   G      AA_
                                TG TTGC AGGTCAGC   AGG
                                || |||| ||||||||   |||
                                AC AACG TCCAGTCG   TCC
                                 C   G       ACG
GAM347  ATP1A2   3'  TGATTGCAAGGTCTGAAGGGGA 8864           AGCA   A
                                TGATTGCGAGGTC   AAGG GA
                                ||||||||||||   |||| ||
                                ACTAACGTTCCAG   TTCC CT
                                       AC__   C
GAM347  GPR86    3'  TGATTGTGGGTCAGCAA    8865       CGA
                                TGATTG   GGTCAGCAA
                                ||||||   |||||||||
                                ACTAAC   CCAGTCGTT
                                   AC_
GAM347  MRPL49   3'  TGATTGCAGGTCAGAAGG    8866       G     CA
                                TGATTGC AGGTCAG  AAGG
                                ||||||| |||||||  ||||
                                ACTAACG TCCAGTC  TTCC
                                   _     ___
GAM347  PTPRG    5'  TGTTTGCGAGAGGGGAAGGGGA 8867    A      TCAGCA   A
                                TG TTGCGAGG     AAGG GA
                                || ||||||||     |||| ||
                                AC AACGCTCT     TTCC CT
                                 A       CCCC__   C
GAM347  APCL     3'  TGGCTGCGAGGTCCTAGGAG  8868    AT       AGCAA
                                TG  TGCGAGGTC    AGGAG
                                ||  |||||||||    |||||
                                AC  ACGCTCCAG    TCCTC
                                 CG       GA___
GAM347  ARHGEF10 3'  TGATGCGTTCTGCAGAGGAG  8869      T   AGG  A   A
                                TGAT GCG   TC GCA AGGAG
                                |||| |||   || ||| |||||
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                                ACTA CGC   AG CGT TCCTC
                                  _  A__  A   C
GAM347  CUGBP2    3'  TGATGTGAGGTCAGAAAGA   8870      T C      C
                                TGAT G GAGGTCAG AAAGG
                                |||| | |||||||| |||||
                                ACTA C CTCCAGTC TTTCT
                                  _ A      _
GAM347  FLJ20499  3'  ATTGCGAGGTCGCAAGGGAGA  8871          A   A
                                ATTGCGAGGTC GCAA GGAGA
                                |||||||||||| |||| |||||
                                TAACGCTCCAG CGTT CCTCT
                                       _   C
GAM347  FLJ21069  3'  TAATTGCGCTTGCAAAGGAG   8872        AGGTCA
                                TGATTGCG    GCAAAGGAG
                                ||||||||    |||||||||
                                ATTAACGC    CGTTTCCTC
                                     GAA___
GAM347  FLJ21432  3'  GATTGCAAGGGCGAGGGAG   8873         TCA  AAA
                                GATTGCGAGG  GC  GGAG
                                ||||||||||  ||  ||||
                                CTAACGTTCC  CG  CCTC
                                      ___ CTC
GAM347  KIAA1030  3'  TGACTGCGGGGGCAGGGGGAG  8874        A  T  CAAA
                                TGATTGCG GG CAG   GGAG
                                |||||||| || |||   ||||
                                ACTGACGC CC GTC   CCTC
                                     C  C  CC__
GAM347  RES4-22   3'  GATTGTGGAGAACAAAGGAG   8875      CGA  TC
                                GATTG  GG  AGCAAAGGAG
                                |||||  ||  ||||||||||
                                CTAAC  CC  TTGTTTCCTC
                                   A__  TC
GAM347  LOC122553 3'  TGCATTGCTTAGCAAAGGGGA  8876      AG  C_      A
                                TGCG  GT  AGCAAAGG GA
                                ||||  ||  |||||||| ||
                                ACGT  CG  TCGTTTCC CT
                                  AA  AA       C
GAM347  LOC149657 3'  GCAGGTCAGCAAGGGAG    8877     G        A
                                GC AGGTCAGCAA GGAG
                                || |||||||||| ||||
                                CG TCCAGTCGTT CCTC
                                 _         C
GAM347  LOC149657 3'  GCAGGTCAGCAAGGGAG    8877     G        A
                                GC AGGTCAGCAA GGAG
                                || |||||||||| ||||
                                CG TCCAGTCGTT CCTC
                                 _         C
GAM347  LOC149657 3'  GCAGGTCAGCAAGGGAG    8877     G        A
                                GC AGGTCAGCAA GGAG
                                || |||||||||| ||||
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                                CG TCCAGTCGTT CCTC
                                 _       C
GAM347  LOC149657 3'  GCAGGTCAGCAAGGGAG    8877    G       A
                                GC AGGTCAGCAA GGAG
                                || |||||||||| ||||
                                CG TCCAGTCGTT CCTC
                                 _       C
GAM347  LOC149657 3'  GCAGGTCAGCAAGGGAG    8877    G       A
                                GC AGGTCAGCAA GGAG
                                || |||||||||| ||||
                                CG TCCAGTCGTT CCTC
                                 _       C
GAM347  LOC51281  3'  ATTGCGAGGTCGCAAGGGAGA  8871          A   A
                                ATTGCGAGGTC GCAA GGAGA
                                |||||||||||| |||| |||||
                                TAACGCTCCAG CGTT CCTCT
                                      _   C
GAM347  LOC56961  5'  TAATTGCGGGCAGGGGGAG   8878        A  T   CAAA
                                TGATTGCG GG CAG   GGAG
                                |||||||| || |||   ||||
                                ATTAACGC CC GTC   CCTC
                                    _ _  CC__
GAM348  AP1M1    3'  TGGCCTGGCGAGGCTGGC    8881      GC  _
                                TGGTC  GG GAGGCTGGC
                                |||||  || |||||||||
                                ACCGG  CC CTCCGACCG
                                   A_  G
GAM348  CHAD     3'  GCAGGTGGGGGCTGGC     8882     T   CGC   A
                                GCA GGT   GGG GGCTGGC
                                ||| |||   ||| |||||||
                                CGT CCA   CCC CCGACCG
                                 _  ___  _
GAM348  DES      5'  GGCGCGGGCGAGGCTGGC    8883     T    __
                                GG CGCGGG  AGGCTGGC
                                || ||||||  ||||||||
                                CC GCGCCC  TCCGACCG
                                 _     GC
GAM348  EGR4     5'  GGTGGCGGGGAGGCTGGC    8884     C    _
                                GGT GCGGG AGGCTGGC
                                ||| ||||| ||||||||
                                CCA CGCCC TCCGACCG
                                  C    C
GAM348  FZD5     5'  TGGCGCCGGGGCTGGCA     8885     T  G  A
                                TGG CGC GG GGCTGGCA
                                ||| ||| || ||||||||
                                ACC GCG CC CCGACCGT
                                  _  G  _
GAM348  GATA2    5'  CAGCACGTCCGGAGGCTGGC   8886       G  G   G
                                CAGCATG TC CGG AGGCTGGC
                                ||||||| || ||| ||||||||
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                                GTCGTGC AG GCC TCCGACCG
                                      _ _  _
GAM348  GNAL    3'  CATGGCATGGGGCTGGCA    8887       CGCG  A
                                CATGGT   GG GGCTGGCA
                                ||||||   || ||||||||
                                GTACCG   CC CCGACCGT
                                   TA__  _
GAM348  KCNF1   5'  GGCGGGGCTCGGGGCTGGCA  8888     C__  G_  A
                                GGT  GC  GG GGCTGGCA
                                |||  ||  || ||||||||
                                CCG  CG  CC CCGACCGT
                                  CCC  AG  _
GAM348  MAP3K14 3'  AGCCGGGGGGCTGGCA     8889       C   A
                                GGTCG GGG GGCTGGCA
                                ||||| ||| ||||||||
                                TCGGC CCC CCGACCGT
                                      _  _
GAM348  MFNG    5'  GCAGGCATCAGGGGCTGGCA  8890     T   CG   A
                                GCA GGT  CGGG GGCTGGCA
                                ||| |||  |||| ||||||||
                                CGT CCG  GTCC CCGACCGT
                                  _  TA   _
GAM348  MGAM    3'  TGGTCAAGAGGGGCTGGCA   8891       C   A
                                TGGTCG GGG GGCTGGCA
                                |||||| ||| ||||||||
                                ACCAGT CTC CCGACCGT
                                   T  C
GAM348  MUC4    3'  ACTCGGGCGGGAGGCTGGC   8892    A  TC
                                GC TGG  GCGGGAGGCTGGC
                                || |||  ||||||||||||
                                TG GCC  CGCCCTCCGACCG
                                 A  __
GAM348  RNH     3'  AGCATGGCAGGGGCTGG     8893        CGC   A
                                AGCATGGT   GGG GGCTGG
                                ||||||||   ||| ||||||
                                TCGTACCG   TCC CCGACC
                                      ___  _
GAM348  RNH     3'  AGCATGGCAGGGGCTGG     8893        CGC   A
                                AGCATGGT   GGG GGCTGG
                                ||||||||   ||| ||||||
                                TCGTACCG   TCC CCGACC
                                      ___  _
GAM348  STAT6   3'  CAGCATGCTCCTGAGGCTGGCA 8894       G  GCGG
                                CAGCATG TC    GAGGCTGGCA
                                ||||||| ||    ||||||||||
                                GTCGTAC AG    CTCCGACCGT
                                   G  GA__
GAM348  VIL2    3'  AGCGTGGCGGGGCTGGC     8895     A   CGCG  A
                                AGC TGGT    GG GGCTGGC
                                ||| ||||    || |||||||
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                                TCG ACCG    CC CCGACCG
                                  C   ____ _
GAM348  WNT1     5'  CAGCATGGCTCGCGGTCCCGGC 8896         _     GA__
              TGG                   CAGCATGG TCGCGG    GGCTGG
                                    |||||||| ||||||    ||||||
                                    GTCGTACC AGCGCC    CCGACC
                                       G     AGGG
GAM348  XK       3'  TAGTCAGTGGGAGGCTGG    8897        C_
                                    TGGTCG  GGGAGGCTGG
                                    ||||||  ||||||||||
                                    ATCAGT  CCCTCCGACC
                                       CA
GAM348  ZNF76    3'  CAGCATGGTGTGGGACC     8898          CGCG  A
                                    CAGCATGGT    GG GGCT
                                    |||||||||    || ||||
                                    GTCGTACCA    CC CTGG
                                         CA__  _
GAM348  AIP      3'  CAGCACGGGCAGGGGGGCTGGC 8899          T  C   A
              A                      CAGCATGG CG GGG GGCTGGCA
                                     |||||||| || ||| ||||||||
                                     GTCGTGCC GT CCC CCGACCGT
                                          C  C   _
GAM348  BAIAP1   3'  ACATGGTGCGAGAGGCTGG    8900         C
                                    GCATGGT GCGGGAGGCTGG
                                    ||||||| ||||||||||||
                                    TGTACCA CGCTCTCCGACC
                                                _
GAM348  CCR5     3'  CAGTCTGAAATACGGAGGCTGG 8901      CA   TC_   G
                                    CAG  TGG   GCGG AGGCTGG
                                    |||  |||   |||| |||||||
                                    GTC  ACT   TGCC TCCGACC
                                      AG   TTA   _
GAM348  DXS9928E 3'  GCATGGTCGCAGGGGAGC    8902            A  CT
                                    GCATGGTCGCGGG GG  GGC
                                    |||||||||||| ||  |||
                                    CGTACCAGCGTCC CC  TCG
                                                 _  __
GAM348  FKBP8    3'  GCGGGGTGGGGGGCTGGCA    8903     AT   CGC   A
                                    GC  GGT   GGG GGCTGGCA
                                    ||  |||   ||| ||||||||
                                    CG  CCA   CCC CCGACCGT
                                      CC   C__   _
GAM348  FLJ12425 3'  TGGTATGTTAAAAGGCTGGCA  8904       CGC__
                                    TGGT    GGGAGGCTGGCA
                                    ||||    ||||||||||||
                                    ACCA    TTTTCCGACCGT
                                       TACAA
GAM348  FLJ13940 3'  CACCACAGTGGGAGGCTGG    8905     G     CGC
                                    CA CATGGT   GGGAGGCTGG
                                    || ||||||   ||||||||||
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                                GT GTGTCA  CCCTCCGACC
                                 G    ___
GAM348  FLJ22056 3' AGCAGGTGGGAGGCTGGCA  8906     T  CGC
                                AGCA GGT  GGGAGGCTGGCA
                                |||| |||  ||||||||||||
                                TCGT CCA  CCCTCCGACCGT
                                  _  ___
GAM348  FLJ22479 3' CAGCAGGTGTCGGGCTGGC  8907     T  CG  GAG
                                CAGCA GGT  CGG  GCTGGC
                                ||||| |||  |||  ||||||
                                GTCGT CCA  GCC  CGACCG
                                   _  CA  ___
GAM348  FLJ23519 3' AGCATGGCAGGGGCTGG    8893       CGC  A
                                AGCATGGT  GGG GGCTGG
                                ||||||||  ||| ||||||
                                TCGTACCG  TCC CCGACC
                                    ___  _
GAM348  FRAT1    3' ACATGGTCGCGGGGCTG    8908          AG
                                GCATGGTCGCGGG  GCTG
                                ||||||||||||  ||||
                                TGTACCAGCGCCC  CGAC
                                      __
GAM348  HSPB7    3' GCGTGGGGCTTGGAGGCTGG  8909    A  TC  G_
                                GC TGG  GC  GGAGGCTGG
                                || |||  ||  |||||||||
                                CG ACC  CG  CCTCCGACC
                                 C  C_  AA
GAM348  KCNJ9    3' GCCATATGTGGGGAGGCTGGCA 8910    ATG  CGC
                                GC  GT  GGGAGGCTGGCA
                                ||  ||  ||||||||||||
                                CG  TA  CCCTCCGACCGT
                                 GTA  CAC
GAM348  KIAA0775 3' GCATGGGCCTGGGAGGCTGGCA 8911      _  GC
                                GCATGG TC  GGGAGGCTGGCA
                                |||||| ||  ||||||||||||
                                CGTACC GG  CCCTCCGACCGT
                                   C  A_
GAM348  KIAA1497 5' CAGCACTGTGGGAGGCTGGCA  8912      G  CGC
                                CAGCAT GT  GGGAGGCTGGCA
                                |||||| ||  ||||||||||||
                                GTCGTG CA  CCCTCCGACCGT
                                   A  ___
GAM348  KIAA1576 3' CAGCATGGTTACGGGAGAAACA 8913        CG     CT
                                CAGCATGGT  CGGGAGG  GGCA
                                |||||||||  |||||||  ||||
                                GTCGTACCA  GCCCTCT  TTGT
                                     AT     __
GAM348  KIAA1853 3' CAGGTGGTTGGGGGAGGCTGGC 8914    CA   CGC
           A                     CAG  TGGT  GGGAGGCTGGCA
                                |||  ||||  ||||||||||||
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                                GTC  ACCA   CCCTCCGACCGT
                                  C_    ACC
GAM348  MGC14128  5'  TGGTGCTGGGGGAGGCTGGCA  8915      C  ___
                                TGGT GC   GGGAGGCTGGCA
                                |||| ||   ||||||||||||
                                ACCA CG   CCCTCCGACCGT
                                  _  ACC
GAM348  MGC4342  3'  CAGCCTGGGAAGGGGCTGGCA  8916      A   TCGC   A
                                CAGC TGG    GGG GGCTGGCA
                                |||| |||    ||| |||||||||
                                GTCG ACC    TCC CCGACCGT
                                  G   CT__   _
GAM348  MGC9753  5'  ACATGGGGGAGGAGGCTGGCA  8917       TCGC
                                GCATGG    GGGAGGCTGGCA
                                ||||||    ||||||||||||
                                TGTACC    TCCTCCGACCGT
                                   CCC_
GAM348  PEG10    3'  ACTGTGGTACCGGAGGCTGGC  8918     A_    C  G
                                GC  TGGT GC GGAGGCTGGC
                                ||  |||| || ||||||||||
                                TG  ACCA TG CCTCCGACCG
                                 AC    _  G
GAM348  RAB3D    3'  GCAGGGTCGTGGGTGATG    8919      T    C   A  C
                                GCA GGTCG GGG GG TG
                                ||| ||||| ||| || ||
                                CGT CCAGC CCC CT AC
                                  C    A   A  _
GAM348  SHANK3   5'  CAGCAGGTCGCGGCCGGC    8920       T     GGGA
                                CAGCA GGTCGC    GGCTGGC
                                |||||| ||||||    |||||||
                                GTCGT CCAGCG    CCGGCCG
                                   _     _____
GAM348  TU3A     3'  CAGTGTGGTCACACTGG     8921      CA      GGGAG
                                CAG  TGGTCGC    GCTGG
                                |||  |||||||    |||||
                                GTC  ACCAGTG    TGACC
                                  AC      ______
GAM348  ZFP106   3'  CAGTGGGAGAGATGGAGGCTGG 8922      CAT  TCGCG_
           CA                   CAG   GG     GGAGGCTGGCA
                                |||   ||     ||||||||||
                                GTC   CC     CCTCCGACCGT
                                  AC_  TCTCTA
GAM348  LOC144501 3'  GCAGTGGGAGGCTGG       8923      TG  CGC
                                GCA  GT   GGGAGGCTGG
                                |||  ||   ||||||||||
                                CGT  CA   CCCTCCGACC
                                   __  ____
GAM348  LOC150356 3'  GCACTGGGCCTGGAGGCTGG   8924       __    GCG
                                GCAT  GGTC   GGAGGCTGG
                                ||||  ||||   |||||||||
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                                CGTG  CCGG   CCTCCGACC
                                  AC   A__
GAM348  LOC151484 3'  ACAGGTGGGAGGCTGGC     8925      T   CGC
                                GCA GGT   GGGAGGCTGGC
                                ||| |||   ||||||||||
                                TGT CCA   CCCTCCGACCG
                                 _  ___
GAM348  LOC204285 3'  CAGCTGTGGGGAGGGAGGCTGG 8926      A_   TCGC
          C                      CAGC  TGG   GGGAGGCTGGC
                                ||||  |||   ||||||||||
                                GTCG  ACC   CCCTCCGACCG
                                  AC  CCT_
GAM348  LOC255187 3'  AGCTCAGGGAGGCTGG      8927      ATGG   C
                                AGC   TCG GGGAGGCTGG
                                |||   ||| ||||||||||
                                TCG   AGT CCCTCCGACC
                                 _____  _
GAM348  LOC54557  5'  CAGCACTGGTCGCGGCGGC    8928       _       GA
                                CAGCA TGGTCGCGG  GGC
                                ||||| |||||||||  |||
                                GTCGT ACCAGCGCC  CCG
                                   G       G_
GAM348  LOC90630  5'  CAGATGTGGGGGCTGG      8929      C   GTCGC   A
                                CAG ATG    GGG GGCTGG
                                ||| |||    ||| ||||||
                                GTC TAC    CCC CCGACC
                                  _  A____  _
GAM348  LOC91208  5'  CAGATGTGGGGGCTGG      8929      C   GTCGC   A
                                CAG ATG    GGG GGCTGG
                                ||| |||    ||| ||||||
                                GTC TAC    CCC CCGACC
                                  _  A____  _
GAM349  CASP3     3'  TACACAGTCTTAAGTGGGGGGA 8932          CG  CC  AA
                                TGCACAGTCT  GG  TG  GGGA
                                ||||||||||  ||  ||  ||||
                                ATGTGTCAGA  TC  AC  CCCT
                                      AT  __  CC
GAM349  CASP3     3'  TACACAGTCTTAAGTGGGGGGA 8932          CG  CC  AA
                                TGCACAGTCT  GG  TG  GGGA
                                ||||||||||  ||  ||  ||||
                                ATGTGTCAGA  TC  AC  CCCT
                                      AT  __  CC
GAM349  MAP3K14   3'  CAGTGCTGGGCCTGAAGGG   8933      _ C
                                CAGT CT GGGCCTGAAGGG
                                |||| || ||||||||||||
                                GTCA GA CCCGGACTTCCC
                                  C  _
GAM349  RBP5      3'  GCACAATCTGGGCTTGAAGGG  8934          C   C
                                GCACAGTCT GGGC TGAAGGG
                                ||||||||| |||| |||||||
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                                CGTGTTAGA CCCG ACTTCCC
                                     _   A
GAM349  RDS      3'  CAGCGGGCCTGAAGGG     8935     TCT
                                CAG   CGGGCCTGAAGGG
                                |||   ||||||||||||
                                GTC   GCCCGGACTTCCC
                                 ____
GAM349  TRPM2    3'  CACAGACATAGGCCTGAGGGG  8936       TCTC       A
                                CACAG    GGGCCTGA GGG
                                |||||    |||||||| |||
                                GTGTC    TCCGGACT CCC
                                   TGTA       C
GAM349  ZNF144   3'  TGCCTAAAGCTTTGGGTCTGAA 8937      AC__   CTC   C
           GGG                     TGC    AGT   GGG CTGAAGGG
                                |||    |||   ||| ||||||||
                                ACG    TCG   CCC GACTTCCC
                                  GATT   AAA   A
GAM349  C(27)-3BETA-HSD 5'  TGCCCAGACTGGCCTGGAGGG  8938      A   T  CG     A
                                TGC CAG CT  GGCCTG AGGG
                                ||| ||| ||  |||||| ||||
                                ACG GTC GA  CCGGAC TCCC
                                  G   T __     C
GAM349  FASTK    3'  GCACAGCAGGAAGTCTGGAGGG 8939        CTC   C   A
                                GCACAGT   GGG CTG AGGG
                                |||||||   ||| ||| ||||
                                CGTGTCG   TTC GAC TCCC
                                     TCC   A   C
GAM349  FLJ00007 3'  TGCACAGTCTCAGGCTGGGGG  8940             C  AA
                                TGCACAGTCTCGGGC TG  GGG
                                |||||||||||||| ||  |||
                                ACGTGTCAGAGTCCG AC  CCC
                                         _ C_
GAM349  FLJ10932 3'  GTCCGGGGGCCTGAAGGG    8941      C_
                                GTCT  GGGCCTGAAGGG
                                ||||  ||||||||||||
                                CAGG  CCCGGACTTCCC
                                  CC
GAM349  FLJ11273 5'  TGCGCAGTCCCGGGCTGCTTCG 8942      A         C  AA__
           G                     TGC CAGTCTCGGGC TG    GG
                                ||| ||||||||||| ||    ||
                                ACG GTCAGGGCCCG AC    CC
                                  C          _ GAAG
GAM349  FREQ     3'  AGCGCTCAAGGGTCTGGGGGGA 8943      _  __  C   AA
                                AGT CTC  GGG CTG  GGGA
                                ||| |||  ||| |||  ||||
                                TCG GAG  CCC GAC  CCCT
                                  C   TT   A   CC
GAM349  GABARAPL1 3'  TGCATGTGAGCCTGAAGGGA   8944      CA  CTC
                                TGCA  GT   GGGCCTGAAGGGA
                                ||||  ||   ||||||||||||
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                                ACGT  CA   CTCGGACTTCCCT
                                  A_ ___
GAM349  GDBR1    3' TGCCCGGTCTCGGGCCGCACCA 8945     ACA       TGA__
           GGG                   TGC   GTCTCGGGCC    AGGG
                                |||   ||||||||||    ||||
                                ACG   CAGAGCCCGG    TCCC
                                  GGC        CGTGG
GAM349  KIAA0063 3' TGCACTGTCAGATCTGAAGGG  8946       A   TC  GC
                                TGCAC GTC  GG  CTGAAGGG
                                ||||| |||  ||  ||||||||
                                ACGTG CAG  TC  GACTTCCC
                                  A   __ TA
GAM349  KIAA1029 5' TGCATGGCCTGGGAGGCTTGAA 8947      CA   C__   C
           GGGA                   TGCA  GTCT   GGGC TGAAGGGA
                                |||| ||||  |||| ||||||||
                                ACGT  CGGA   TCCG ACTTCCCT
                                  AC   CCC   A
GAM349  KIAA1679 3' GCAGCAGGACGGGCCTGAGGGG 8948     _  TCT       A
           A                    GCA CAG   CGGGCCTGA GGGA
                                ||| |||   ||||||||| ||||
                                CGT GTC   GCCCGGACT CCCT
                                  C   CT_       C
GAM349  KIAA1862 5' GCACAGTCTCCGGGGGGG     8949          _  CCTGAA
                                GCACAGTCTC GGG     GGG
                                |||||||||| |||     |||
                                CGTGTCAGAG CCC     CCC
                                      G  _______
GAM349  KIAA1909 5' TGACGGTCTCGGGTCCCTGGGA 8950     C  A      _  GAA
                                TG AC GTCTCGGG CCT   GGGA
                                || || |||||||| |||   ||||
                                AC TG CAGAGCCC GGG   CCCT
                                 _ C       A  A__
GAM349  MGC2628  5' TGCCGGTCTCGGGCGCCGGG   8951     ACA       _ GAA
                                TGC   GTCTCGGGC CT   GGG
                                |||   ||||||||| ||   |||
                                ACG   CAGAGCCCG GG   CCC
                                  GC_       C  ___
GAM349  N4BP3    3' GTCAGAAGCCTGAAGGGA    8952     TC
                                GTC  GGGCCTGAAGGGA
                                |||  ||||||||||||
                                CAG  TTCGGACTTCCCT
                                  TC
GAM349  NPC1L1   3' TGCAGGTGCGCCCTGGAGGGA  8953      CA  CT  GG   A
                                TGCA  GT  CG  CCTG AGGGA
                                ||||  ||  ||  |||| |||||
                                ACGT  CA  GC  GGAC TCCCT
                                  C_  C_  G_   C
GAM349  SLC2A4RG 3' CAGCCCCGGGCCTGGAGGG   8954            A
                                CAGTCTCGGGCCTG AGGG
                                |||||||||||||| ||||
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                                GTCGGGGCCCGGAC TCCC
                                       C
GAM349  LOC129052 5'  TGCGCAGCTCGGGCCGCCCGG  8955     A  T      TGAA
                                TGC CAG CTCGGGCC    GG
                                ||| ||| ||||||||    ||
                                ACG GTC GAGCCCGG    CC
                                  C  _       CGGG
GAM349  LOC136345 3'  AGCTGGGCCTGAGGGG      8956     T  C      A
                                AG CT GGGCCTGA GGG
                                || || |||||||| |||
                                TC GA CCCGGACT CCC
                                 _ _       C
GAM349  LOC155032 5'  AGCTGGGCCTGAGGGG      8956     T  C      A
                                AG CT GGGCCTGA GGG
                                || || |||||||| |||
                                TC GA CCCGGACT CCC
                                 _ _       C
GAM349  LOC256113 5'  GCACAGTCTTGGGTGTGTACAG 8957          C   CC  A__
           GGA                    GCACAGTCT GGG  TG   AGGGA
                                |||||||| |||  ||   |||||
                                CGTGTCAGA CCC  AC   TCCCT
                                     A   AC  ATG
GAM350  ABL1     3'  CCTGGGTGGGGGGCTTTGCTC   8960     _       G__
                                CC GGGTGGGGGGC   GCTC
                                || ||||||||||   ||||
                                GG CCCACCCCCG   CGAG
                                 A         AAA
GAM350  ABL1     3'  CCTGGGTGGGGGGCTTTGCTC   8960     _       G__
                                CC GGGTGGGGGGC   GCTC
                                || ||||||||||   ||||
                                GG CCCACCCCCG   CGAG
                                 A         AAA
GAM350  CLDN5    3'  TCCGGTGGGGGGCCCCGGGCTC  8961       G      GG    _
                                TCCGG TGGGGGC  CTCGG CTC
                                ||||| |||||||  ||||| |||
                                AGGCC ACCCCCG  GGGCC GAG
                                   _      __     C
GAM350  COL5A1   3'  CTCCAGGTGGGGGGCGCGGCTC  8962             GCT
                                CTCCGGGTGGGGGGCG   CGGCTC
                                ||||||||||||||   ||||||
                                GAGGTCCACCCCCGC   GCCGAG
                                                 ___
GAM350  DNMT3A   5'  GGGTGGGGGGCTTCGATGGCTC  8963          GGCTC_
                                GGGTGGGGGGC     GGCTC
                                ||||||||||      |||||
                                CCCACCCCCG      CCGAG
                                      AAGCTA
GAM350  ILVBL    5'  CCGGGTGGCCCACTTGGCTC   8964         GGGCG   C
                                CCGGGTGG    GCT GGCTC
                                ||||||||    ||| |||||
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                                GGCCCACC    TGA CCGAG
                                    GGG__   A
GAM350  IRF1    5'  CTCCGGGTGGCCTCGGTTC   8965        GGG  C
                                CTCCGGGTGG  CGG TC
                                ||||||||||  ||| ||
                                GAGGCCCACC  GCC AG
                                    GGA   A
GAM350  NTSR1   3'  CCCGGGTGGGGGGCTGCTC   8966          G
                                TCCGGGTGGGGGGC GCTC
                                |||||||||||| ||||
                                GGGCCCACCCCCG CGAG
                                       A
GAM350  PDXK    5'  CGGGCTCCGGCTCGGCT    8967      GGGGG
                                CGGGT   CGGCTCGGCT
                                |||||   ||||||||||
                                GCCCG   GCCGAGCCGA
                                  AG___
GAM350  TLL1    3'  CTACGGGTGGGTTGGCTC   8968    C     GGC
                                CT CGGGTGGG  GGCTC
                                || ||||||||  |||||
                                GA GCCCACCC  CCGAG
                                 T      AA_
GAM350  BRI3    5'  CTCCGGCCCGGCTCGGCT   8969      GTGGGGG
                                CTCCGG     CGGCTCGGCT
                                ||||||     ||||||||||
                                GAGGCC     GCCGAGCCGA
                                   GG_____
GAM350  C20orf178 5'  CTCCGGCTCGGCTCGGCT   8970      GTGGGGG
                                CTCCGG     CGGCTCGGCT
                                ||||||     ||||||||||
                                GAGGCC     GCCGAGCCGA
                                   GA_____
GAM350  CDIPT   3'  CTCTGGCTGGGGGCGGAGG   8971    C G      CTC
                                CTC GG TGGGGGCGG  GG
                                ||| || |||||||||  ||
                                GAG CC ACCCCCGCC  CC
                                  A G       T__
GAM350  DDX39   3'  CTCCGGGTGGGCGGCTC    8972       GG
                                CTCCGGGT  GGGCGGCTC
                                ||||||||  |||||||||
                                GAGGCCCA  CCCGCCGAG
                                      __
GAM350  DDX39   3'  CTCCGGGTGGGCGGCTC    8972       GG
                                CTCCGGGT  GGGCGGCTC
                                ||||||||  |||||||||
                                GAGGCCCA  CCCGCCGAG
                                      __
GAM350  DKFZP434B0335 5'  CTCTGGTGGGGCACTCGGCTC  8973    CG     G  G
                                CTC  GGTGGGG CG CTCGGCTC
                                |||  ||||||| || ||||||||
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                                GAG  CCACCCC GT GAGCCGAG
                                  A_     _ _
GAM350  GRWD     3'  CTCTGGGTGGGAGTGGTCT   8974     C       C _
                                CTC GGGTGGGGG GG CT
                                ||| ||||||||| || ||
                                GAG CCCACCCTC CC GA
                                  A        A A
GAM350  HN1L     3'  CTCCGGGTGGAGCAGTGGCT  8975          G   CTC
                                CTCCGGGTGGGG CGG   GGCT
                                |||||||||||| |||   ||||
                                GAGGCCCACCTC GTC   CCGA
                                       _  A__
GAM350  HRK      3'  CTCCGGCTGGGTCTCGGCTC  8976       G   GG_
                                CTCCGG TGGG   CGGCTC
                                |||||| ||||   ||||||
                                GAGGCC ACCC   GCCGAG
                                   G   AGA
GAM350  HSA275986 5'  CTCTGGTGGGGGCGGAGTC   8977     CG        C_
                                CTC  GGTGGGGGCGG  TC
                                |||  ||||||||||  ||
                                GAG  CCACCCCCGCC  AG
                                  A_         TC
GAM350  KIAA0247  5'  CTCCGGGATGGGGGCGCTC   8978        _      G
                                CTCCGGG TGGGGGCG CTC
                                ||||||| |||||||| |||
                                GAGGCCC ACCCCCGC GAG
                                    T      _
GAM350  KIAA0939  3'  CTCCGGGTGGGGGGGGTAGGC  8979          C  CTC
                                CTCCGGGTGGGGG GG   GGC
                                |||||||||||| ||   |||
                                GAGGCCCACCCCC CC   CCG
                                       _  AT_
GAM350  KIAA1691  3'  CTCTGGGTGGGGGAAGGGGG  8980     C       C  CTC
                                CTC GGGTGGGGG GG   GG
                                ||| ||||||||| ||   ||
                                GAG CCCACCCCC TC   CC
                                  A        T  CC_
GAM350  MCF2L    3'  CTCTGGGTGGGGGCGGTGAGG  8981     C         CTC
                                CTC GGGTGGGGGCGG   GG
                                ||| ||||||||||||   ||
                                GAG CCCACCCCCGCC   CC
                                  A          ACT
GAM350  MGC21688  3'  CTCCAGGTGGGGGGTGATTC   8982          C GC
                                CTCCGGGTGGGGG G  TC
                                |||||||||||| |  ||
                                GAGGTCCACCCCC C  AG
                                       A TA
GAM350  PP1628   5'  GGGTGGGGGGTGTAGGGGGCT  8983         C___  CTC
                                GGGTGGGGG   GG   GGCT
                                |||||||||   ||   ||||
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                                CCCACCCCC   CC  CCGA
                                     ACAT  C__
GAM350  PPP1R12C  3'  CTCGGGTGGCCCCCTCGGCTC  8984     C     GGGCGG
                                CTC GGGTGG     CTCGGCTC
                                ||| ||||||     ||||||||
                                GAG CCCACC     GAGCCGAG
                                  _     GGGG__
GAM350  SCYA17    3'  CTCAGGGTGGGGGCGGTGAAC  8985     C          CTC
                                CTC GGGTGGGGGCGG   GGC
                                ||| ||||||||||||   |||
                                GAG CCCACCCCCGCC   TTG
                                  T          AC_
GAM350  LOC200197 3'  CTCTGGCATGTGGCTTGGCT   8986     CG   GGGGC   C
                                CTC  GGTG    GGCT GGCT
                                |||  ||||    |||| ||||
                                GAG  CCGT    CCGA CCGA
                                  A_   ACA__   A
GAM350  LOC200597 5'  GGGTGGGGCTCGGCT       8987        GGCG
                                GGGTGGG    GCTCGGCT
                                |||||||    ||||||||
                                CCCACCC    CGAGCCGA
                                     _____
GAM350  LOC219654 3'  TCTGGGTGGGGGCAGGCGGC   8988     C          CT
                                TC GGGTGGGGGCGG  CGGC
                                || ||||||||||||  ||||
                                AG CCCACCCCCGTC  GCCG
                                 A          C_
GAM351  BAZ2A     3'  ATACCAAGGGAAAATTGCCAGG 8991        T    TTAAATA
            G                    ATACCA GGGA      CCAGGG
                                ||||||| ||||      ||||||
                                TATGGT CCCT      GGTCCC
                                   T   TTTAAC_
GAM351  CNTFR     3'  ATACTGTGGGATAGGAGCAGGG 8992      CA     TAAATAC
                                ATAC  TGGGAT      CAGGG
                                ||||  ||||||      |||||
                                TATG  ACCCTA      GTCCC
                                  AC     TCCTC__
GAM351  IFI35     5'  CCTCGGAATACCAGGG      8993     A    TTAAA
                                CC TGGGA    TACCAGGG
                                || |||||    ||||||||
                                GG GCCTT    ATGGTCCC
                                 A    ______
GAM351  INHA      3'  CCATGGGATTAAGAAGG     8994           ATACC
                                CCATGGGATTAA    AGG
                                ||||||||||||    |||
                                GGTACCCTAATT    TCC
                                       CT___
GAM351  SLC21A2   3'  CCATGGGAAAGACCAGGG    8995         TTAAAT
                                CCATGGGA     ACCAGGG
                                ||||||||     |||||||
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                                GGTACCCT     TGGTCCC
                                    TTC___
GAM351  TRPC6    3'  CACCAAAAAAATTAGATACTAG 8996       T_     A   C
           GG                     TACCA  GGGATTA ATAC AGGG
                                  |||||  ||||||| |||| ||||
                                  GTGGT  TTTTAAT TATG TCCC
                                     TT      C    A
GAM351  CLST11240 3'  TACCAGGGATTGAGTTAGGG   8997       T     AAATACC
                                  TACCA GGGATT      AGGG
                                  ||||| ||||||      ||||
                                  ATGGT CCCTAA      TCCC
                                     _     CTCAA__
GAM351  DKFZP434L1435 5'  CACCATGGAGCCACGGATATCA 8998         GA   A__   C
           GGG                     TACCATGG  TTA   ATA CAGGG
                                  ||||||||  |||   ||| |||||
                                  GTGGTACC  GGT   TAT GTCCC
                                       TC   GCC   A
GAM351  DNAJA4   5'  ATACCATGAGACAGTGCCAGGG 8999            TAAATA
                                  ATACCATGGGAT     CCAGGG
                                  ||||||||||||     ||||||
                                  TATGGTACTCTG     GGTCCC
                                        TCAC__
GAM351  FLJ20045  3'  ATACAGTGGGATTAGATA    9000       CA       A
                                  ATAC  TGGGATTA ATA
                                  ||||  |||||||| |||
                                  TATG  ACCCTAAT TAT
                                    TC       C
GAM351  KIAA0418  3'  ATACCAGGGATACCTGG     9001        T    TTAAA    A
                                  ATACCA GGGA     TACC GG
                                  |||||| ||||     |||| ||
                                  TATGGT CCCT     ATGG CC
                                     _   ______    A
GAM351  KIAA1229  3'  CACTGTGGGAGACACCAGGG   9002      CA     TTAA
                                  TAC  TGGGA    ATACCAGGG
                                  |||  |||||    |||||||||
                                  GTG  ACCCT    TGTGGTCCC
                                    AC    C___
GAM351  LOC149837 5'  CATGGGATTCTTCCAGGG    9003          AAATA
                                  CATGGGATT     CCAGGG
                                  |||||||||     ||||||
                                  GTACCCTAA     GGTCCC
                                       GAA__
GAM351  LOC221431 3'  TGAGGCAAATACCAGGG     9004       AT
                                  TGGG  TAAATACCAGGG
                                  ||||  ||||||||||||
                                  ACTC  GTTTATGGTCCC
                                    C_
GAM351  LOC255458 3'  CATAGTTATTAAATGCCAGGG  9005       G_      A
                                  CATGG  ATTAAAT CCAGGG
                                  |||||  ||||||| ||||||
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                                GTATC  TAATTTA GGTCCC
                                  AA      C
GAM352  APP     3'  GATGTGTGGATTAATTCAA   9008       A___
                                GATGT   ATTAATTCAA
                                |||||   ||||||||||
                                CTACA   TAATTAAGTT
                                  CACC
GAM352  SIM2    3'  CGGGGTCCAATTCAAA     9009      AT  AA
                                CGGG  GT  TTAATTCAAA
                                ||||  ||  ||||||||||
                                GCCC  CA  GGTTAAGTTT
                                  __  __
GAM352  TDG     3'  GAATGATAATTAATTCAAA   9010       _
                                GGATG TAATTAATTCAAA
                                ||||| ||||||||||||
                                CTTAC ATTAATTAAGTTT
                                  T
GAM352  OAZ     3'  GGATGTAATGTTCAAA     9011         TAA
                                GGATGTAAT   TTCAAA
                                |||||||||   ||||||
                                CCTACATTA   AAGTTT
                                     C__
GAM352  PDE3A   3'  CAGGATGTATCAGAATTCAAA  9012         ATT_
                                CGGGATGTA   AATTCAAA
                                |||||||||   ||||||||
                                GTCCTACAT   TTAAGTTT
                                     AGTC
GAM353  AIM1    3'  AGGTTCGAGATCAGCCTGGGC  9015     ACCAAA  T      A
                                AGG     AG TTAGCCTG GC
                                |||     || |||||||| ||
                                TCC     TC AGTCGGAC CG
                                  AAGC__  T      C
GAM353  CLCN4   3'  AAGGAGTAAAAGTTTCTTGAG  9016      CC      AGCC
                                AAGGA  AAAAGTTT   TGAG
                                |||||  ||||||||   ||||
                                TTCCT  TTTTCAAA   ACTC
                                  CA      GA__
GAM353  CST     5'  AGGATTGCTTGAGCCTGAG   9017      CCAAAA   _
                                AGGA     GTTT AGCCTGAG
                                ||||     |||| ||||||||
                                TCCT     CGAA TCGGACTC
                                  AA____    C
GAM353  EIF5A2  3'  AACGATCAAAACTTGGCCTGAG 9018     G  C    G   A
          C                      AA GA CAAAA TTT GCCTGAGC
                                 || || ||||| ||| ||||||||
                                 TT CT GTTTT GAA CGGACTCG
                                  G  A    _   C
GAM353  FABP2   3'  AGGGGTTCAAGACCAGCCTGGG 9019      ACCAA   T      A
          C                      AGG     AAG TTAGCCTG GC
                                 |||     ||| |||||||| ||
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                                TCC    TTC GGTCGGAC CG
                                  CCAAG  T      C
GAM353  FMO5    3'  GACTAAAAGAGTACCTGAGC  9020     C    TTTA
                                GAC AAAAG   GCCTGAGC
                                ||| |||||   ||||||||
                                CTG TTTTC   TGGACTCG
                                  A    TCA_
GAM353  GGT1    3'  AAGGCCAGGAGGCCACCTGAGC 9021      A  AA  TTTA
                                AAGG CCA  AG   GCCTGAGC
                                |||| |||  ||   ||||||||
                                TTCC GGT  TC   TGGACTCG
                                  _  CC  CGG_
GAM353  GPRC5C  3'  AGGAGCAAGATCCAGGCCTGAG 9022     C  AA    _
          C                      AGGA CAA  GTTTAG CCTGAGC
                                |||| |||  |||||| |||||||
                                TCCT GTT  TAGGTC GGACTCG
                                  C  C_    C
GAM353  GPRC5C  3'  AGGAGCAAGATCCAGGCCTGAG 9022     C  AA    _
          C                      AGGA CAA  GTTTAG CCTGAGC
                                |||| |||  |||||| |||||||
                                TCCT GTT  TAGGTC GGACTCG
                                  C  C_    C
GAM353  LAMC1   3'  AGGATCAAAAGTTGAGAAGC  9023     C      T  CCT
                                AGGA CAAAAGTT AG   GAGC
                                |||| |||||||| ||   ||||
                                TCCT GTTTTCAA TC   TTCG
                                  A      C  ___
GAM353  LENG4   3'  AAGGGGCAGCTAGGCGGCCTGA 9024     ACCAAA   TA___
          GC                     AAGG    AGTT    GCCTGAGC
                                ||||    ||||    ||||||||
                                TTCC    TCGA    CGGACTCG
                                  CCG___   TCCGC
GAM353  MAPK8IP1 3'  AGGTGGCTGGGCTCAGCCTGAG 9025     ACCAAAA
          C                      AGG     GTTTAGCCTGAGC
                                |||     ||||||||||||
                                TCC     CGAGTCGGACTCG
                                  ACCGACC
GAM353  MPP2    3'  AAGGACCAGGGCTTTGGAG   9026       AAA   AGCCT
                                AAGGACCA  GTTT   GAG
                                ||||||||  ||||   |||
                                TTCCTGGT  CGAA   CTC
                                    CC_   AC___
GAM353  NFE2L1  5'  AAGGACCAGAATGTTTATGC  9027       A  _   _
                                AAGGACCA AA GTTTA GC
                                |||||||| || ||||| ||
                                TTCCTGGT TT CAAAT CG
                                    C  A    A
GAM353  NPR2L   3'  AAGACCAGACCAGCCTGG   9028       AAAGT     A
                                AGGACCA   TTAGCCTG G
                                |||||||   |||||||| |
```

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                                TTCTGGT    GGTCGGAC C
                                   CT___      C
GAM353  RAB11A   3'  AAGACCAATAGGTCTGAG    9029        AAGTT  C_
                                AGGACCAA    TAG  CTGAG
                                ||||||||    |||  |||||
                                TTCTGGTT    ATC  GACTC
                                    _____  CA
GAM353  ROCK2    5'  AGGCTGAAGCCCAGGCCTGGGC 9030     ACCAA      _   A
                                AGG    AAGTTTAG CCTG GC
                                |||    |||||||| |||| ||
                                TCC    TTCGGGTC GGAC CG
                                  GAC__      C   C
GAM353  SIRT1    3'  AAGAATCAAAAGTTTAGC    9031       C
                                AAGGA CAAAAGTTTAGC
                                ||||| ||||||||||||
                                TTCTT GTTTTCAAATCG
                                   A
GAM353  SLC7A5   3'  GGAGACCAAAAGCTGCTCCTGG 9032    A         TAG   A
           GC                     A GGACCAAAAGTT   CCTG GC
                                | ||||||||||||   |||| ||
                                C TCTGGTTTTCGA   GGAC CG
                                 C          CGA   C
GAM353  TGFA     3'  AGGGCAGGGGTCTCCTGAGC   9033     AC  AAA   AG
                                AGG  CA   GTTT  CCTGAGC
                                |||  ||   ||||  |||||||
                                TCC  GT   CAGA  GGACTCG
                                  C_  CCC   __
GAM353  TK1      3'  GGCCAGCTCCAGCCTGGGC   9034     A   AAAG       A
                                GG CCA    TTTAGCCTG GC
                                || |||    ||||||||| ||
                                CC GGT    AGGTCGGAC CG
                                 _  CG__       C
GAM353  DKFZP434C131 3'  AGGACCAAGGAACCCTCCTGAG 9035         AAGT  AG
                                AGGACCAA    TT  CCTGAG
                                ||||||||    ||  ||||||
                                TCCTGGTT    GG  GGACTC
                                     CCTT  GA
GAM353  DKFZP434O047 5'  AAGGGCAGCTGGAGCCTGAGC  9036      ACCAAA   T_
                                AAGG     AGTT  AGCCTGAGC
                                ||||     ||||  |||||||||
                                TTCC     TCGA  TCGGACTCG
                                  CG_____    CC
GAM353  FLJ10607  3'  AGGAGTTAAGAGACCAGCCTGG 9037      CC_  A  T      A
           GC                     AGGA   AA AG TTAGCCTG GC
                                ||||   || || |||||||| ||
                                TCCT   TT TC GGTCGGAC CG
                                  CAA  C  T       C
GAM353  FLJ10726  3'  AAGACCGAAAGTCTGA      9038        A    TTAGC
                                AGGACC AAAGT    CTGA
                                |||||| |||||    ||||
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                                TTCTGG TTTCA     GACT
                                   C    _____
GAM353  FLJ11036  3'  AAGCGACCCTTAGCCTGAG   9039     _   AAAAG
                                AAG GACC    TTTAGCCTGAG
                                ||| ||||    ||||||||||
                                TTC CTGG    GAATCGGACTC
                                  G   _____
GAM353  FLJ13057  3'  AGGGTAAAAAGTCCTGAG    9040     ACC     TTAG
                                AGG   AAAAGT   CCTGAG
                                |||   ||||||   ||||||
                                TCC   TTTTCA   GGACTC
                                  CAT    ____
GAM353  FLJ22969  3'  AGGAGGTTGAGACCAGCCTGGG 9041      CCAAA  T      A
            C                    AGGA    AG TTAGCCTG GC
                                ||||    || |||||||| ||
                                TCCT    TC GGTCGGAC CG
                                  CCAAC  T       C
GAM353  HSNOV1    3'  GGAGGTCAAGACCAGCCTGGGC 9042     CCAA   T      A
                                GGA    AAG TTAGCCTG GC
                                |||    ||| |||||||| ||
                                CCT    TTC GGTCGGAC CG
                                  CCAG   T       C
GAM353  KIAA0061  3'  AAGGACCAAGGCTATGAG    9043          AA   TAGCC
                                AAGGACCAA  GTT    TGAG
                                |||||||||  |||    ||||
                                TTCCTGGTT  CGA    ACTC
                                     C_   T____
GAM353  KIAA0494  3'  AAGGACCAAGAAGCAGTGCTTT 9044          _    TTA  C_
            GAG                    AAGGACCAA AAGT   GC  TGAG
                                ||||||||| ||||   ||  ||||
                                TTCCTGGTT TTCG   CG  ACTC
                                     C    TCA  AA
GAM353  KIAA1018  3'  AGGCCCAGATCAGCCTG     9045      A  AAA  T
                                AGG CC   AG TTAGCCTG
                                ||| ||   || ||||||||
                                TCC GG   TC AGTCGGAC
                                  _  G__  T
GAM353  KIAA1492  3'  AAGGACCAAGAGTTTTGAAAAA 9046          A    AGCCT_
            AGC                    AAGGACCAA AGTTT     GAGC
                                |||||||| |||||     ||||
                                TTCCTGGTT TCAAA     TTCG
                                     C    ACTTTT
GAM353  KIAA1853  3'  GGAGACTGAAGTCCAGTCTG   9047    A   CAA      C
                                A GGAC   AAGTTTAG CTG
                                | ||||   |||||||| |||
                                C TCTG   TTCAGGTC GAC
                                 C   AC_       A
GAM353  MGC12972  3'  GGCCGACTCCAGGCCTGAGC   9048     A  AAAAG    _
                                GG CC    TTTAG CCTGAGC
                                || ||    ||||| |||||||
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                                CC GG    AGGTC GGACTCG
                                 _ CTG__    C
GAM353  MGC29654  3'  GGATGAAGGCCTGGCCTGAGC  9049     CCAAAA   A
                                GGA     GTTT GCCTGAGC
                                |||     |||| ||||||||
                                CCT     CGGA CGGACTCG
                                  ACTTC_   C
GAM353  MGC3113   3'  AGACCAGCCTGGGCCTGGGC   9050      AAA   A_   A
                                GGACCA   GTTT  GCCTG GC
                                ||||||   ||||  ||||| ||
                                TCTGGT   CGGA  CGGAC CG
                                   ___   CC    C
GAM353  NK4       5'  GGCCAAAAGTTCAAGGAGC   9051    A        CCT
                                GG CCAAAAGTTTAG   GAGC
                                || ||||||||||||   ||||
                                CC GGTTTTCAAGTT   CTCG
                                 _         C__
GAM353  PPIL2     3'  AGGCCTGAGGCACCAGCCTG   9052     A  AAAA  _
                                AGG CC    GT TTAGCCTG
                                ||| ||    || ||||||||
                                TCC GG    CG GGTCGGAC
                                  _ ACTC  T
GAM353  PPP1R15B  5'  AGGGTTGAAAAGCCCCTGAGC  9053     ACC_     TAG
                                AGG    AAAAGTT   CCTGAGC
                                |||    |||||||   |||||||
                                TCC    TTTTCGG   GGACTCG
                                  CAAC      ___
GAM353  PRO0899   5'  AGGAGATTGAGACCAGCCTGGG 9054      CCAAA  T      A
            C                    AGGA     AG TTAGCCTG GC
                                ||||     || |||||||| ||
                                TCCT     TC GGTCGGAC CG
                                  CTAAC  T       C
GAM353  SDCBP     3'  GGAGTCAAAAGTTTATCCTG   9055     C_       G
                                GGA  CAAAAGTTTA CCTG
                                |||  |||||||||| ||||
                                CCT  GTTTTCAAAT GGAC
                                  CA         A
GAM353  SNAPC3    3'  AAGGATCAAAATTTAGC     9056       CCA
                                AAGGA   AAAGTTTAGC
                                |||||   ||||||||||
                                TTCCT   TTTTAAATCG
                                   AG_
GAM353  SP192     3'  AAGGGCTAAAGTTACCCGAGC  9057      ACCA     TA
                                AAGG    AAAGTT  GCCTGAGC
                                ||||    ||||||  ||||||||
                                TTCC    TTTCAA  TGGGCTCG
                                  CGA_     ___
GAM353  TSPAN-3   3'  AAGACCAAAAAGCTCAGGCTTG 9058          _     _ C
            AG                    AGGACCAAAA GTTTAG C TGAG
                                ||||||||| |||||| | ||||
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                                TTCTGGTTTT CGAGTC G ACTC
                                      T     C A
GAM353  UST      3'  AGGAGTCAAATGCCTGAG    9059      CCAA   TTA
                                AGGA   AAGT   GCCTGAG
                                ||||   ||||  |||||||
                                TCCT   TTTA  CGGACTC
                                  CAG_  ___
GAM353  YAP1     3'  AGGATAAAATCCACCTGAGC  9060      CCA      G
                                AGGA  AAAGTTTA CCTGAGC
                                ||||  |||||||| |||||||
                                TCCT  TTTTAGGT GGACTCG
                                  A__       _
GAM353  ZER6     3'  AGGACCAAGAGTTCACTGGC  9061        A     GC  A
                                AGGACCAA AGTTTA  CTG GC
                                |||||||| ||||||  ||| ||
                                TCCTGGTT TCAAGT  GAC CG
                                     C     __  _
GAM353  LOC134266 3'  AGGAGTTGGAGGTCAGCCTGGG 9062      CCAAA  T      A
              C                   AGGA    AG TTAGCCTG GC
                                ||||    || |||||||| ||
                                TCCT    TC AGTCGGAC CG
                                  CAACC  C       C
GAM353  LOC147219 3'  AAGGACCAATAAAATACCTGAG 9063        A  TT  G
                                AAGGACCAA AG  TA CCTGAG
                                ||||||||| ||  || ||||||
                                TTCCTGGTT TT  AT GGACTC
                                     A  TT  _
GAM353  LOC148894 3'  AGACCAGAGCACCTGCCTGAGC 9064       AA   TTA_
                                GGACCA  AGT    GCCTGAGC
                                ||||||  |||    ||||||||
                                TCTGGT  TCG    CGGACTCG
                                   C_   TGGA
GAM353  LOC149706 5'  GGACCAAAGGCAGCCTG     9065        A  TT
                                GGACCAAA GT  AGCCTG
                                |||||||| ||  ||||||
                                CCTGGTTT CG  TCGGAC
                                     C  __
GAM353  LOC151512 5'  AAGGGGCAAGCAGGGCCTGAGC 9066      ACCAA    TTA
                                AAGG    AAGT   GCCTGAGC
                                ||||    ||||   ||||||||
                                TTCC    TTCG   CGGACTCG
                                  CCG__    TCC
GAM353  LOC152220 3'  AGGAGTTGGAGACCAGCCTGGG 9067      CCAAA  T      A
              C                   AGGA    AG TTAGCCTG GC
                                ||||    || |||||||| ||
                                TCCT    TC GGTCGGAC CG
                                  CAACC  T       C
GAM353  LOC154043 3'  AGGAGCCAGGCAGGTGGCCTGA 9068      _  AA_  TTTA
              GC                  AGGA CCA   AG    GCCTGAGC
                                |||| |||   ||    ||||||||
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                                TCCT GGT   TC    CGGACTCG
                                  C   CCG  CAC_
GAM353   LOC221272 3'  AGGAACCAAGAGTTTAGC    9069      _   A
                                AGGA CCAA AGTTTAGC
                                |||| |||| ||||||||
                                TCCT GGTT TCAAATCG
                                  T   C
GAM353   LOC254100 3'  AGGAGTTGGAGACCAGCCTGGG 9067      CCAAA  T      A
           C                     AGGA    AG TTAGCCTG GC
                                ||||    || |||||||| ||
                                TCCT    TC GGTCGGAC CG
                                  CAACC  T      C
GAM353   LOC254359 3'  AAGGGGCAGCTAGGCGGCCTGA 9024      ACCAAA   TA___
           GC                    AAGG    AGTT    GCCTGAGC
                                ||||    ||||    ||||||||
                                TTCC    TCGA    CGGACTCG
                                  CCG___   TCCGC
GAM353   LOC255196 5'  AGGAGTTGGAGACCAGCCTGGG 9067      CCAAA  T      A
           C                     AGGA    AG TTAGCCTG GC
                                ||||    || |||||||| ||
                                TCCT    TC GGTCGGAC CG
                                  CAACC  T      C
GAM353   LOC255360 3'  AAGGACCAGTAGTGGTGAG   9070       AA   TTAGCC
                                AAGGACCA  AGT     TGAG
                                ||||||||  |||     ||||
                                TTCCTGGT  TCA     ACTC
                                    CA   CC____
GAM353   LOC256360 5'  AGGAGTTGGAGTTCAGCCTGGG 9071      CCAAA        A
           C                     AGGA    AGTTTAGCCTG GC
                                ||||    |||||||||||| ||
                                TCCT    TCAAGTCGGAC CG
                                  CAACC         C
GAM353   LOC257445 3'  AGGACCAAGGAACCCTCCTGAG 9035        AAGT  AG
                                AGGACCAA   TT  CCTGAG
                                ||||||||   ||  ||||||
                                TCCTGGTT   GG  GGACTC
                                    CCTT  GA
GAM353   LOC91355  3'  AAGACCAAGAAGGCCTTGGGC  9072        _  TTTA   GA_
                                AGGACCAA AAG   GCCT   GC
                                |||||||| |||   ||||  ||
                                TTCTGGTT TTC   CGGA   CG
                                    C  ____   ACC
GAM353   LOC91373  3'  AGAGCCAGGCAGCCTGAG   9073    GA   AAA  TT
                                AG  CCA   GT  AGCCTGAG
                                ||  |||   ||  ||||||||
                                TC  GGT   CG  TCGGACTC
                                 TC   C__  __
GAM354   ATRX      3'  TGAGAAGAGTGTATACAAAG   9076      T    ACAC
                                TGAG AGAGT    ATGCGGAG
                                |||| |||||    ||||||||
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                                ACTC TCTCA    TATGTTTC
                                  T    CA__
GAM354  ATRX     3'  TGAGAAGAGTGTATACAAAG  9076      T    ACAC
                                TGAG AGAGT    ATGCGGAG
                                |||| |||||    ||||||||
                                ACTC TCTCA    TATGTTTC
                                  T    CA__
GAM354  BMP1     3'  TGAGCAGAGTAGCCATTGG   9077          CA   GC
                                TGAGTAGAGTA  CAT  GG
                                ||||||||||  |||  ||
                                ACTCGTCTCAT  GTA  CC
                                      CG   A_
GAM354  DBH      3'  GAGTAGAGTGCACAGTGTGCTC 9078         A   A_______   GGA
          G                      GAGTAGAGT CAC      TGC   G
                                |||||||| |||      |||  |
                                CTCATCTCA GTG      ACG   C
                                     C   TCACIII   AGG
GAM354  DYRK2    3'  TGAGTAGAGTTATTGAGC    9079         ACACA  CG
                                TGAGTAGAGT    TG  GAGC
                                ||||||||||    ||  ||||
                                ACTCATCTCA    AT  CTCG
                                      ______  AA
GAM354  DYRK2    3'  TGAGTAGAGTTATTGAGC    9079         ACACA  CG
                                TGAGTAGAGT    TG  GAGC
                                ||||||||||    ||  ||||
                                ACTCATCTCA    AT  CTCG
                                      ______  AA
GAM354  EIF2C1   3'  TGAGTAGAGTAAGGGAGAGCA  9080          CACATGC
                                TGAGTAGAGTA      GGAGCA
                                ||||||||||       ||||||
                                ACTCATCTCAT      TCTCGT
                                      TCCC___
GAM354  PTPRCAP  3'  TGAGCGGGGTACACATGGA   9081       AGA       C
                                TGAGT   GTACACATG GG
                                |||||   ||||||||| ||
                                ACTCG   CATGTGTAC CT
                                   CCC       _
GAM354  THPO     5'  TGGGCAGAGTAGGGTGGGGCA  9082     A      CACA  C  A
                                TG GTAGAGTA    TG GG GCA
                                || ||||||||    || || |||
                                AC CGTCTCAT    AC CC CGT
                                 C       CCC_  _  _
GAM354  VAT1     3'  TGGTGGGGTACACAAAAGC    9083     A  AGA      TGC
                                TG GT   GTACACA   GGAGC
                                || ||   |||||||   |||||
                                AC CA   CATGTGT   TTTCG
                                 _  CCC      ____
GAM354  FLJ21709 3'  TGGGTGGAGTGCAGAGC     9084     A  A   ACACAT
                                TG GT GAGT     GCGGAGC
                                || || ||||     |||||||
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                                AC CA CTCA     CGTCTCG
                                 C  C   _______
GAM354  HPCAL4   3'  GTAGAGTATGTGAGAAGGCA  9085        CACA  C   _
                                GTAGAGTA   TG GGAG CA
                                ||||||||   || |||| ||
                                CATCTCAT   AC CTTC GT
                                     AC__  T   C
GAM354  KLK7     3'  TGGGTAGGGTCACATACA   9086    A   A  A
                                TG GTAG GT CACATGCG
                                || |||| || ||||||||
                                AC CATC CA GTGTATGT
                                 C   C  _
GAM354  KLK7     3'  TGGGTAGGGTCACATACA   9086    A   A  A
                                TG GTAG GT CACATGCG
                                || |||| || ||||||||
                                AC CATC CA GTGTATGT
                                 C   C  _
GAM354  MRPS23   3'  TGAGTAGAGTGTGAATGCCAGC 9087         ACAC   GG
            A                    TGAGTAGAGT   ATGC  AGCA
                                ||||||||||   ||||  ||||
                                ACTCATCTCA   TACG  TCGT
                                      CACT   G_
GAM354  SV2      3'  GAGTAGGGTGGGATGGGGCA  9088       A  ACAC   C  A
                                GAGTAG GT   ATG GG GCA
                                |||||| ||   ||| || |||
                                CTCATC CA   TAC CC CGT
                                   C  CCC_  _ _
GAM354  ZFP106   3'  TGAGTAGAGACGTATGC    9089         T  AC
                                TGAGTAGAG AC  ATGC
                                ||||||||| ||  ||||
                                ACTCATCTC TG  TACG
                                      _ CA
GAM354  LOC115219 3'  TGAGTAGAGGCACCAGAG   9090         TA   ATG
                                TGAGTAGAG  CAC   CGGAG
                                |||||||||  |||   |||||
                                ACTCATCTC  GTG   GTCTC
                                     C_   ___
GAM354  LOC143914 5'  GAGGAGCGCATGCGGAG    9091     TA   ACA
                                GAG  GAGT   CATGCGGAG
                                |||  ||||   |||||||||
                                CTC  CTCG   GTACGCCTC
                                  __    C__
GAM354  LOC153810 5'  TGGGTAGGGATACAGAGC    9092     A   AGTACAC
                                TG GTAG      ATGCGGAGC
                                || ||||      |||||||||
                                AC CATC      TATGTCTCG
                                 C   CC_____
GAM354  LOC256714 3'  TGAGTAGAGACACATACA    9093         T
                                TGAGTAGAG ACACATGCG
                                ||||||||| |||||||||
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                                ACTCATCTC TGTGTATGT
                                          _
GAM355  CYP1B1   3'  TGTTATAAAAATAAGAACA   9096          A
                                TGTTATAAAAA TAAGAATA
                                |||||||||| ||||||||
                                ACAATATTTTT ATTCTTGT
                                          _
GAM355  MME      3'  TGTTAGGAAAAATAAGAAT   9097       TA
                                TGTTA  AAAAATAAGAAT
                                |||||  ||||||||||||
                                ACAAT  TTTTTATTCTTA
                                   CC
GAM355  MME      3'  TGTTAGGAAAAATAAGAAT   9097       TA
                                TGTTA  AAAAATAAGAAT
                                |||||  ||||||||||||
                                ACAAT  TTTTTATTCTTA
                                   CC
GAM355  MME      3'  TGTTAGGAAAAATAAGAAT   9097       TA
                                TGTTA  AAAAATAAGAAT
                                |||||  ||||||||||||
                                ACAAT  TTTTTATTCTTA
                                   CC
GAM355  MME      3'  TGTTAGGAAAAATAAGAAT   9097       TA
                                TGTTA  AAAAATAAGAAT
                                |||||  ||||||||||||
                                ACAAT  TTTTTATTCTTA
                                   CC
GAM355  C1QTNF3  3'  TGTTATAAAGAATAATGAAC  9098         A    _
                                TGTTATAAA AATAA GAAT
                                ||||||||| ||||| ||||
                                ACAATATTT TTATT CTTG
                                      C    A
GAM355  FHOD2    3'  TTATAAAAAATAAGAAAAAAT  9099             T
                                TTATAAAAAATAAGAA AAGAT
                                |||||||||||||||| |||||
                                AATATTTTTTATTCTT TTTTA
                                          _
GAM355  FLJ21087 3'  TGTTATAAAAATATATAATAAG 9100          ATAAG
          AT                    TGTTATAAAAA    AATAAGAT
                                ||||||||||    ||||||||
                                ACAATATTTTT    TTATTCTA
                                      ATATA
GAM355  KIAA0438 3'  TATTATAAGAAATAAGAA    9101         A
                                TGTTATAA AAATAAGAA
                                |||||||| |||||||||
                                ATAATATT TTTATTCTT
                                      C
GAM356  ACP2     3'  CGTGGAGGAGGCAAATCCTGT  9104     C      G____
                                CG GGAGGAGG    CCTGT
                                || ||||||||    |||||
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                                GC CCTCCTCC    GGACA
                                 A      GTTTA
GAM356  ATRX    5' TCGTGGAGGAGAACTTGT   9105     C       C
                                TCG GGAGGAGGGC TGT
                                ||| |||||||||| |||
                                AGC CCTCCTCTTG ACA
                                  A        A
GAM356  DTX1    5' CCGCCAGACAGGGCCTGT   9106     _  GG
                                TCGC GGA  AGGGCCTGT
                                |||| |||  |||||||||
                                GGCG TCT  TCCCGGACA
                                  G  G_
GAM356  DVL1    3' TCCAGACAGGGGGCCTGT   9107    G  __ A
                                TC CGGA  GG GGGCCTGT
                                || ||||  || ||||||||
                                AG GTCT  CC CCCGGACA
                                 _   GT  _
GAM356  EHD2    5' CCGCGGAGCGGCCTGT     9108       GAG
                                TCGCGGAG  GGCCTGT
                                ||||||||  |||||||
                                GGCGCCTC  CCGGACA
                                    G__
GAM356  GM2A    3' CGTGGTGGCAGGGCCTGT   9109    C  A  _
                                CG GG GG AGGGCCTGT
                                || || || |||||||||
                                GC CC CC TCCCGGACA
                                 A  A  G
GAM356  OSCAR   5' TCGAGGTGGGGGCCTGT    9110    C  A  A
                                TCG GG GG GGGCCTGT
                                ||| || || ||||||||
                                AGC CC CC CCCGGACA
                                  T  A  _
GAM356  OSCAR   5' TCGAGGTGGGGGCCTGT    9110    C  A  A
                                TCG GG GG GGGCCTGT
                                ||| || || ||||||||
                                AGC CC CC CCCGGACA
                                  T  A  _
GAM356  OSCAR   5' TCGAGGTGGGGGCCTGT    9110    C  A  A
                                TCG GG GG GGGCCTGT
                                ||| || || ||||||||
                                AGC CC CC CCCGGACA
                                  T  A  _
GAM356  PIG3    5' TCGCGGAGCAGCCAGCCT   9111       G  __
                                TCGCGGAG AG  GGCCT
                                |||||||| ||  |||||
                                AGCGCCTC TC  TCGGA
                                    G  GG
GAM356  PIK3CD  3' TCGGGAGGAGAACAGT    9112    C       CT
                                TCG GGAGGAGGGC  GT
                                ||| ||||||||||  ||
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                                AGC CCTCCTCTTG  CA
                                  _       T_
GAM356  PROS1    5'  CCGCGGAGCTGCGAGCCTGT  9113        GA__
                                TCGCGGAG   GGGCCTGT
                                ||||||||   ||||||||
                                GGCGCCTC   CTCGGACA
                                    GACG
GAM356  SIL      5'  CCGCGGAGCTGAGGTCTGT   9114        __   GC
                                TCGCGGAG  GAGG  CTGT
                                ||||||||  ||||  ||||
                                GGCGCCTC  CTCC  GACA
                                    GA   A_
GAM356  CAPN13   3'  TCCCAGTAAGGGCCTGT    9115    G   AG
                                TC CGG  GAGGGCCTGT
                                || |||  ||||||||||
                                AG GTC  TTCCCGGACA
                                 G   A_
GAM356  CDH24    3'  TCACTCAGAGGGCCTGT    9116     GGA
                                TCGC   GGAGGGCCTGT
                                ||||   ||||||||||
                                AGTG   TCTCCCGGACA
                                  AG_
GAM356  CHST8    5'  TCCCGGAGAAGCTGCTTGT   9117    G      G_  C
                                TC CGGAGGAG  GC TGT
                                || ||||||||  || |||
                                AG GCCTCTTC  CG ACA
                                 G       GA  A
GAM356  DKFZp434I099 5'  GCGGAAGAACCGCTCTGT   9118         G_  _
                                GCGGAGGAG  GC CTGT
                                |||||||||  || ||||
                                CGCCTTCTT  CG GACA
                                     GG  A
GAM356  DKFZP434N178 3'  CCGTGGAGGAGGCAACCTGT  9119     C      __
                                TCG GGAGGAGG  GCCTGT
                                ||| ||||||||  ||||||
                                GGC CCTCCTCC  TGGACA
                                  A       GT
GAM356  DKFZP434P1750 5'  TCCCAGAGGGGCCTGT     9120     G     AG
                                TC CGGAGG  GGCCTGT
                                || ||||||  |||||||
                                AG GTCTCC  CCGGACA
                                 G    __
GAM356  DKFZP564B147 5'  CGCGGAGGGAGGGCGCCTGT  9121         _    __
                                CGCGGAGG AGGGC  CTGT
                                |||||||| |||||  ||||
                                GCGCCTCC TCCCG  GACA
                                     C    CG
GAM356  DLAT     5'  TCCAGAGGGGCCTGT      9122     G     AG
                                TC CGGAGG  GGCCTGT
                                || ||||||  |||||||
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                                AG GTCTCC  CCGGACA
                                 _    __
GAM356  FLJ10996  5'  TCCGGAGGAAGCTGT      9123    G       GC
                                TC CGGAGGAGG  CTGT
                                || |||||||||  ||||
                                AG GCCTCCTTC  GACA
                                 _       __
GAM356  FLJ14564  3'  TCGGGGAGGAGGCCTGGGCCTG 9124     C     _____      III
              TA                  TCG GGAGGA    GGGCCTGT   A
                                ||| ||||||    ||||||||   |
                                AGC CCTCCT    CCCGGACA   T
                                  C     CCGGA       III
GAM356  HSU84971  5'  CCGCGGAGGGGCTGC      9125         AG   C
                                TCGCGGAGG  GGC TGT
                                |||||||||  ||| |||
                                GGCGCCTCC  CCG ACG
                                     __  _
GAM356  KCNT1     3'  TCGCGGAAGAACTTGCTGT   9126          GGC_
                                TCGCGGAGGAG   CTGT
                                ||||||||||    ||||
                                AGCGCCTTCTT   GACA
                                    GAAC
GAM356  KIAA1040  3'  TCTGGAGGAAAATCCTGT    9127     GC       _
                                TC  GGAGGAGGG CCTGT
                                ||  ||||||||| |||||
                                AG  CCTCCTTTT GGACA
                                 A_       A
GAM356  KIAA1432  3'  GCAGAGGAGCAAGCCCTGT   9128         ___ G
                                GCGGAGGAG   G CCTGT
                                |||||||||   | |||||
                                CGTCTCCTC   C GGACA
                                    GTT G
GAM356  MGC26733  3'  CCGCGGAGGGGCCAGT      9129         AG   T
                                TCGCGGAGG  GGCC GT
                                |||||||||  |||| ||
                                GGCGCCTCC  CCGG CA
                                     __   T
GAM356  NSE1      3'  TCGCGGGGAAGGCCATGT    9130       A      _
                                TCGCGG GGAGGGCC TGT
                                |||||| |||||||| |||
                                AGCGCC CCTTCCGG ACA
                                    _       T
GAM356  RAI17     3'  TCGGGAGCAGACCTGT      9131     C   GA
                                TCG GGAG  GGGCCTGT
                                ||| ||||  ||||||||
                                AGC CCTC  TCTGGACA
                                  _   G_
GAM356  SEC14L1   3'  TCGGGAGGAAACCCTGT     9132     C      G
                                TCG GGAGGAGG CCTGT
                                ||| |||||||| |||||
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                                AGC CCTCCTTT GGACA
                                  _      G
GAM356  TOB2     5'  TCGCGGAGCAGCTCCTGT    9133        G  GG
                                TCGCGGAG AG  CCTGT
                                |||||||| ||  |||||
                                AGCGCCTC TC  GGACA
                                     G  GA
GAM356  LOC112473 5'  CGCGGGGCACAGGCCTGT    9134       A  A__
                                CGCGG GG   GGGCCTGT
                                ||||| ||   ||||||||
                                GCGCC CC   TCCGGACA
                                   _ GTG
GAM356  LOC125268 3'  GCAGGCAGGAGGGCCTGT    9135     _ _
                                GC GG AGGAGGGCCTGT
                                || || ||||||||||||
                                CG CC TCCTCCCGGACA
                                 T  G
GAM356  LOC126248 3'  TCACTCAAAGGGGCCTGT    9136      G_   A
                                TCGC  GAGG GGGCCTGT
                                ||||  |||| ||||||||
                                AGTG  TTTC CCCGGACA
                                  AG   _
GAM356  LOC144110 3'  TCCCAACTAGGGGCCTGT    9137     G  A_  A
                                TC CGG  GG GGGCCTGT
                                || |||  || ||||||||
                                AG GTT  TC CCCGGACA
                                 G   GA  _
GAM356  LOC147054 5'  TCTGGGGACAGACCTGT     9138     GC  A  _
                                TC  GG GGA GGGCCTGT
                                ||  || ||| ||||||||
                                AG  CC CCT TCTGGACA
                                 A_  _   G
GAM356  LOC197202 5'  CGCGGGGCACAGGCCTGT    9134       A  A__
                                CGCGG GG   GGGCCTGT
                                ||||| ||   ||||||||
                                GCGCC CC   TCCGGACA
                                   _ GTG
GAM356  LOC219920 5'  TCCCGGAGAAACTGGTCTGT  9139     G       __  C
                                TC CGGAGGAG  GG CTGT
                                || ||||||||  || ||||
                                AG GCCTCTTT  CC GACA
                                 G       GA  A
GAM356  LOC255374 5'  CCGCGGAGGTAGCTGT      9140         AG   C
                                TCGCGGAGG  GGC TGT
                                |||||||||  ||| |||
                                GGCGCCTCC  TCG ACA
                                     A_   _
GAM356  LOC51608  3'  CCGCGGTAAGGCCTGT      9141        AGG
                                TCGCGG   AGGGCCTGT
                                ||||||   |||||||||
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                                GGCGCC   TTCCGGACA
                                   A__
GAM356  LOC90249  3'  CCGGGAGGGGGCCTGT     9142     C    A
                                TCG GGAGG GGGCCTGT
                                ||| ||||| ||||||||
                                GGC CCTCC CCCGGACA
                                 _    _
GAM357  APOL1    3'  GGCCATGGCCCACCACCTG   9145      __
                                GGCCA  GCTCGCCACCTG
                                |||||  ||||||||||||
                                CCGGT  CGGGTGGTGGAC
                                   AC
GAM357  BRF1     3'  GCTGTGGGACAGGTGCCACCTG 9146    CAC_  C   CTC
                                GC    GG CAG   GCCACCTG
                                ||    || |||   ||||||||
                                CG    CC GTC   CGGTGGAC
                                 ACAC  T   CA_
GAM357  CARPX    5'  GCGGCGGCAGCAGCCACCTG   9147    CA   C   TC
                                GC  CGGC AGC  GCCACCTG
                                ||  |||| |||  ||||||||
                                CG  GCCG TCG  CGGTGGAC
                                 CC    _   T_
GAM357  CSF2     3'  GCTTGGCCAGCCTCATCTG   9148    CAC     T GC  C
                                GC   GGCCAGC C  CA CTG
                                ||   ||||||| |  || |||
                                CG   CCGGTCG G  GT GAC
                                 AA_      _ A_  A
GAM357  EP300    5'  GCCACGGCCGGCCCCT     9149         AGCTC   A
                                GCCACGGCC    GCC CCT
                                |||||||||    ||| |||
                                CGGTGCCGG    CGG GGA
                                     C_____   _
GAM357  HCCS     5'  GCCGCGGCCAGCCTGCCCTTCT 9150     A      TC   AC_
           G                     GCC CGGCCAGC  GCC   CTG
                                ||| ||||||||  |||   |||
                                CGG GCCGGTCG  CGG   GAC
                                  C       GA   GAA
GAM357  LEP      3'  AGTCCTGGTCCTGCCACCTG   9151    _ AC  _  AGCTC
                                AG CC  GG CC    GCCACCTG
                                || ||  || ||    ||||||||
                                TC GG  CC GG    CGGTGGAC
                                 A  A_  A  A_____
GAM357  MMP14    3'  CAGCGTGGCCAGCCAGGCC   9152      CAC      C_
                                CAGC   GGCCAGCT  GCC
                                ||||   ||||||||  |||
                                GTCG   CCGGTCGG  CGG
                                  CA_       TC
GAM357  MMP15    3'  CAGCCACGGCCTCTTGC     9153          AG  C
                                CAGCCACGGCC  CT GC
                                ||||||||||  || ||
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                                GTCGGTGCCGG  GA CG
                                      A_  A
GAM357  MYCL2    5'  GCTCACGCAGCTTGCCACCTG  9154     _   GC    C
                                GC CACG  CAGCT GCCACCTG
                                || ||||  ||||| ||||||||
                                CG GTGC  GTCGA CGGTGGAC
                                 A   __    A
GAM357  MYO7A    5'  CAGCCTGGTACAGCTGCCACCT 9155       AC  C_    C
           G                     CAGCC  GG  CAGCT GCCACCTG
                                ||||||  ||  ||||| ||||||||
                                GTCGG  CC  GTCGA CGGTGGAC
                                  A_  AT    _
GAM357  PRX      3'  GCGGCGGCCAGCCGGGCTGCCT 9156     CA       C_  CA
           G                     GC  CGGCCAGCT  GC  CCTG
                                ||  |||||||||  ||  ||||
                                CG  GCCGGTCGG  CG  GGAC
                                 CC       CC  AC
GAM357  SEPN1    3'  CAGCCATGGTGGCATGCACCTG 9157       C  CCA  TC  C
                                CAGCCA GG   GC  GC ACCTG
                                |||||| ||   ||  || |||||
                                GTCGGT CC   CG  CG TGGAC
                                   A  AC_  TA  _
GAM357  SIGLEC11 3'  CAGCTGTGGTGGCTCACGTCTG 9158      CAC  CCA     CAC
                                CAGC   GG   GCTCGC   CTG
                                ||||   ||   ||||||   |||
                                GTCG   CC   CGAGTG   GAC
                                  ACA  AC_     CA_
GAM357  SLC22A11 3'  GCCACGGCTGCCTGGCCTCTG  9159        CA   C_   AC
                                GCCACGGC  GCT  GCC  CTG
                                ||||||||  |||  |||  |||
                                CGGTGCCG  CGG  CGG  GAC
                                    A_   AC   A_
GAM357  STARD5   5'  GCCACAGCCTCGCTCATCTG   9160         AGC   _  C
                                GCCACGGCC   TCGC CA CTG
                                |||||||||   |||| || |||
                                CGGTGTCGG   AGCG GT GAC
                                     ___    A  A
GAM357  TMPRSS2  3'  CAGCCGCTGCAGGTGCCACCTG 9161       ACG  C  CTC
                                CAGCC   GC AG   GCCACCTG
                                |||||   || ||   ||||||||
                                GTCGG   CG TC   CGGTGGAC
                                  CGA  _  CA_
GAM357  TOP1     5'  ACCACGGCGGCGACGCTGCCTG 9162         CA  T_   CA
                                GCCACGGC  GC  CGC  CCTG
                                ||||||||  ||  |||  ||||
                                TGGTGCCG  CG  GCG  GGAC
                                    C_   CT   AC
GAM357  AGTRL2   5'  CAGCCTGGCCAAATGCCA    9163       AC     CTC
                                CAGCC  GGCCAG   GCCA
                                |||||  ||||||   ||||
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                                GTCGG  CCGGTT   CGGT
                                  A_     TA_
GAM357  AP3D1    3'  CAGCCTGGCTGGCGCGTGGCCT 9164       AC   CA  T  CCA
          G                      CAGCC  GGC  GC CG   CCTG
                                 |||||  |||  || ||   ||||
                                 GTCGG  CCG  CG GC   GGAC
                                   A_   AC  C  ACC
GAM357  APOL2    3'  GGCCATGGCCTACCACCTG   9165       __  CG
                                 GGCCA  GCT  CCACCTG
                                 |||||  |||  |||||||
                                 CCGGT  CGG  GGTGGAC
                                   AC   AT
GAM357  CLDN15   3'  GCCGTGGCCAGCCCCTACTG  9166     AC      T G  AC
                                 GCC  GGCCAGC C CC  CTG
                                 |||  |||||||  | ||  |||
                                 CGG  CCGGTCG G GG  GAC
                                   CA      _ _  AT
GAM357  CNNM3    3'  CACGGCCACACAGCACCTG   9167         G T  C
                                 CACGGCCA C CG CACCTG
                                 ||||||||  | || ||||||
                                 GTGCCGGT G GT GTGGAC
                                     _ T  C
GAM357  DKFZP434C128 3'  CAGCCATGGACCACACCT   9168        C  _  GCTCGC
                                 CAGCCA GG CCA     CACCT
                                 ||||||  || |||     |||||
                                 GTCGGT CC GGT     GTGGA
                                   A  T  _______
GAM357  FLJ10298 3'  CAGCTGTGGTGGCTCATGCCTG 9169      CAC  CCA    CCA
                                 CAGC   GG   GCTCG   CCTG
                                 ||||   ||   |||||   ||||
                                 GTCG   CC   CGAGT   GGAC
                                   ACA  AC_    AC_
GAM357  FLJ12541  5'  CAGCCCACGGCCAGCTCCGCAC 9170      _         _  CA__
          TGCCTG                  AGCC ACGGCCAGCTC GC    CCTG
                                 |||| ||||||||||  ||    ||||
                                 TCGG TGCCGGTCGAG CG    GGAC
                                   G          G  TGAC
GAM357  FLJ13153  5'  CAGCCAATGGCCCAGCACTGCC 9171        C_   _  TC_
                                 CAGCCA  GGCC AGC   GCC
                                 ||||||  |||| |||   |||
                                 GTCGGT  CCGG TCG   CGG
                                    TA    G   TGA
GAM357  FLJ20150  3'  AGCCACAGGCTTCTCTGCC   9172        _  CAG  _
                                 AGCCAC GGC   CTC GCC
                                 ||||||  |||   ||| |||
                                 TCGGTG CCG   GAG CGG
                                    T   AA_   A
GAM357  FLJ20154  3'  CAGCCTGCGGCCAGCCAGAGCC 9173       A_       C__
                                 CAGCC  CGGCCAGCT   GCC
                                 |||||  |||||||||   |||
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                                GTCGG  GCCGGTCGG   CGG
                                  AC        TCT
GAM357  FLJ21162  3'  CAGCCACGCTCCCTCGTTGCCT 9174         G_  AG    CCA
          G                     CAGCCACG  CC  CTCG   CCTG
                                ||||||||  ||  ||||   ||||
                                GTCGGTGC  GG  GAGC   GGAC
                                    GA  __    AAC
GAM357  FLJ22202  5'  GCCTGGCCAGCTGCCCCT    9175     AC       C   A
                                GCC  GGCCAGCT GCC CCT
                                |||  |||||||| ||| |||
                                CGG  CCGGTCGA CGG GGA
                                 A_       _  _
GAM357  FYCO1     3'  AGCCAGGGCTACCACCT     9176       C  CCA   C
                                AGCCA GG   GCT GCCACCT
                                ||||| ||   ||| |||||||
                                TCGGT CC   CGA TGGTGGA
                                  _ ___   _
GAM357  HERC3     5'  AGCCACAGGTCACACAC     9177         CCAGC   _
                                AGCCACGG    TCGC CAC
                                ||||||||    |||| |||
                                TCGGTGTC    AGTG GTG
                                    C____    T
GAM357  IMAGE:4215339 3'  GCCCTGGCCAGCTCAGCTCTG  9178      AC       _  CAC
                                GCC  GGCCAGCTC GC   CTG
                                |||  ||||||||| ||   |||
                                CGG  CCGGTCGAG CG   GAC
                                 GA       T  A__
GAM357  KIAA0788  3'  CAGCCCTGGCTGGCCAGACCTG 9179       AC   CA   CGCC
                                CAGCC  GGC  GCT   ACCTG
                                |||||  |||  |||   |||||
                                GTCGG  CCG  CGG   TGGAC
                                  GA   AC   TC__
GAM357  KIAA0821  3'  CAGCCACTGCCTCCATCT    9180         G   AGCTCG   C
                                CAGCCAC GCC     CCA CT
                                ||||||| |||     ||| ||
                                GTCGGTG CGG     GGT GA
                                    A   A_____   A
GAM357  KIAA1023  3'  ACCTGTGGCTCACCAGCCACCT 9181      AC_   CA   C
          G                     GCC   GGC  GCT GCCACCTG
                                |||   |||  ||| ||||||||
                                TGG   CCG  TGG CGGTGGAC
                                 ACA   AG   T
GAM357  LEFTB     3'  CAGTCATCGCCAGCTCTCC    9182      C  CG       G
                                CAG CA  GCCAGCTC CC
                                ||| ||  |||||||| ||
                                GTC GT  CGGTCGAG GG
                                 A  AG       A
GAM357  MGC10981  3'  AGCCCAGAACTGGTTTGCCACC 9183       A   CC    C____
          TG                    AGCC CGG  AGCT    GCCACCTG
                                |||| |||  ||||    ||||||||
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                                TCGG GTC  TTGA    CGGTGGAC
                                  _  __   CCAAA
GAM357  MGC4400  5' CAGTCCATACACTTGCCACCTG 9184     _  CG  CA  C
                                CAG CCA  GC  GCT GCCACCTG
                                ||| |||  ||  ||| ||||||||
                                GTC GGT  TG  TGA CGGTGGAC
                                  A  A_ __  A
GAM357  MGC861   3' CAGCCACGGCGGGCTGAGCC  9185         CA  C_
                                CAGCCACGGC  GCT  GCC
                                ||||||||||  |||  |||
                                GTCGGTGCCG  CGA  CGG
                                      CC  CT
GAM357  OVCOV1   3' GCTTGGCCCCACCACCT    9186    CAC   AGC
                                GC  GGCC  TCGCCACCT
                                ||  ||||  |||||||||
                                CG  CCGG  GGTGGTGGA
                                 AA_  ___
GAM357  PLSCR4   3' GCCCTGGCCAGCTCCTTTCCTG 9187     AC       GCCA
                                GCC  GGCCAGCTC   CCTG
                                |||  |||||||||   ||||
                                CGG  CCGGTCGAG   GGAC
                                  GA       GAAA
GAM357  PPFIA1   5' CAGCCCGCGGCCGGCGTCCGCC 9188       A_    A  TCG  A
           TG                     CAGCC  CGGCC GC   CC CCTG
                                |||||  ||||| ||   || ||||
                                GTCGG  GCCGG CG   GG GGAC
                                   GC    C  CA_  C
GAM357  RAB21    5' CAGCCACGGCCGGCTCAGCC  9189          A   _
                                CAGCCACGGCC GCTC GCC
                                |||||||||| |||| |||
                                GTCGGTGCCGG CGAG CGG
                                      C   T
GAM357  RLUCL    3' GCCGCGGTGCGGTCGTCACCTG 9190     A  CCA  __  C
                                GCC CGG   GC  TCG CACCTG
                                ||| |||   ||  ||| ||||||
                                CGG GCC   CG  AGC GTGGAC
                                  C  A__  CC  A
GAM357  RNF38    5' CAGCCCGCGGCCAGCTCGCCA  9191       A_
                                CAGCC  CGGCCAGCTCGCCA
                                |||||  ||||||||||||||
                                GTCGG  GCCGGTCGAGCGGT
                                   GC
GAM357  SCYA22   3' AGCCTGGCCCAACCACCT    9192      AC   AGCTC
                                AGCC  GGCC    GCCACCT
                                ||||  ||||    |||||||
                                TCGG  CCGG    TGGTGGA
                                  A_   GT___
GAM357  SLC16A3  3' AGCAGTGGCCGCAGGCCACCTG 9193     CAC   A  TC
                                AGC   GGCC GC  GCCACCTG
                                |||   |||| ||  ||||||||
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                                TCG   CCGG CG  CGGTGGAC
                                  TCA   _  TC
GAM357  TRIM28   5'  CACGGCCAACTGCTGCCTG   9194          C  CA
                                CACGGCCAGCT GC  CCTG
                                |||||||||| ||  ||||
                                GTGCCGGTTGA CG  GGAC
                                      _  AC
GAM357  TUBB4    3'  GCCCCGGCCGCCACCT     9195     A    AGCTC
                                GCC CGGCC    GCCACCT
                                ||| |||||    |||||||
                                CGG GCCGG    CGGTGGA
                                  G   _____
GAM357  ZDHHC8   3'  GCCACAGCTGGCTGGCTGGCCG 9196         CA____  C   AC
           TCTG                   GCCACGGC     GCT GCC  CTG
                                |||||||     ||| |||  |||
                                CGGTGTCG     CGA CGG  GAC
                                     ACCGAC   C   CA
GAM357  LOC112817 3'  CAGCCATGGACCCTGCC     9197       C  CCA   _
                                CAGCCA GG   GCTC GCC
                                |||||| ||   |||| |||
                                GTCGGT CC   TGGG CGG
                                   A ___    A
GAM357  LOC112868 5'  CAGCACGAACCAGCTCGCCACC 9198      C   _
           TG                     CAGC ACGG CCAGCTCGCCACCTG
                                |||| |||| ||||||||||||||||
                                GTCG TGCT GGTCGAGCGGTGGAC
                                  _   T
GAM357  LOC126661 5'  GCCGCAGCGCCACCTG      9199     A   CAGCTC
                                GCC CGGC     GCCACCTG
                                ||| ||||     ||||||||
                                CGG GTCG     CGGTGGAC
                                  C   _______
GAM357  LOC131118 5'  GCCGCGGCCAACACCT      9200     A      TCGCC
                                GCC CGGCCAGC    ACCT
                                ||| ||||||||    ||||
                                CGG GCCGGTTG    TGGA
                                  C      _____
GAM357  LOC138050 5'  CAGCGCGGCCAGCGCC      9201      CA      TC
                                CAGC  CGGCCAGC  GCC
                                ||||  ||||||||  |||
                                GTCG  GCCGGTCG  CGG
                                  C_      __
GAM357  LOC148089 3'  AGCCACGGACGCCCGCC     9202         CCA
                                AGCCACGG   GCTCGCC
                                ||||||||   |||||||
                                TCGGTGCC   CGGGCGG
                                     TG_
GAM357  LOC151648 5'  CAGCCACGGCTAGCCCCGCGCA 9203          C    _ _
           C                     CAGCCACGGC AGCTC GC CAC
                                |||||||||| ||||| || |||
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                                GTCGGTGCCG TCGGG CG GTG
                                     A    G  C
GAM357  LOC155179 3'  ACCTGTGGCTCACCAGCCACCT 9181     AC_  CA  C
          G                    GCC  GGC  GCT GCCACCTG
                               |||  |||  ||| ||||||||
                               TGG  CCG  TGG CGGTGGAC
                                 ACA  AG  T
GAM357  LOC162137 5'  CAGCTGCTGCTCTCCACCT   9204     CACG  CA   G
                               CAGC   GC  GCTC CCACCT
                               ||||   ||  |||| ||||||
                               GTCG   CG  CGAG GGTGGA
                                 A___  A_   A
GAM357  LOC201931 5'  CAGCCCGGCCTCTCCACCT   9205      A    AGC  G
                               CAGCC CGGCC   TC CCACCT
                               ||||| |||||   || ||||||
                               GTCGG GCCGG   AG GGTGGA
                                 _    ___  A
GAM357  LOC222021 5'  GCCACCGGCGGCCACCT    9206      _  CAGCTC
                               GCCAC GGC     GCCACCT
                               ||||| |||     |||||||
                               CGGTG CCG     CGGTGGA
                                 G  C_____
GAM357  LOC253069 3'  CAGTCACAGCCACACC     9207     C      GCTCGC
                               CAG CACGGCCA     CACC
                               ||| ||||||||     ||||
                               GTC GTGTCGGT     GTGG
                                 A      _______
GAM357  LOC254610 5'  GCTATGGCGACGGCCACCTG  9208    CAC   CA  TC
                               GC   GGC  GC  GCCACCTG
                               ||   |||  ||  ||||||||
                               CG   CCG  TG  CGGTGGAC
                                ATA   C_  C_
GAM357  LOC255397 5'  CAGCCCTGGCCAGCTGGCC   9209      AC      C
                               CAGCC  GGCCAGCT GCC
                               |||||  |||||||| |||
                               GTCGG  CCGGTCGA CGG
                                  GA      C
GAM357  LOC51161  5'  CAGCCTGTGGTTCCTGCCACCT 9210      AC_  CCAG TC
          G                    CAGCC   GG   C  GCCACCTG
                               |||||   ||   |  ||||||||
                               GTCGG   CC   G  CGGTGGAC
                                  ACA  AA__ GA
GAM357  LOC51701  3'  CAGCCACGATCAGCTCAC    9211        GC
                               CAGCCACG  CAGCTCGC
                               ||||||||  ||||||||
                               GTCGGTGC  GTCGAGTG
                                    TA
GAM357  LOC81558  3'  CATGGCCAGCTTGCTCTG    9212     C      C  CAC
                               CA GGCCAGCT GC   CTG
                               || |||||||| ||   |||
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                                GT CCGGTCGA CG   GAC
                                 A       A  A__
GAM357  LOC91301  5'  GCCCGGCCAGCCGGGTCTACCT 9213      A       T  CC___
              G                   GCC CGGCCAGC CG     ACCTG
                                  ||| |||||||| ||     |||||
                                  CGG GCCGGTCG GC     TGGAC
                                   _       _  CCAGA
GAM357  LOC96597  3'  CAGCTGGGCGTGTGCCACCTG  9214      CAC   CAGCTC
                                  CAGC   GGC     GCCACCTG
                                  ||||   |||     ||||||||
                                  GTCG   CCG     CGGTGGAC
                                    AC_   CACA__
GAM358  ASGR2     5'  CTGTGAAAGGTGTGGAGA    9217      GTC    AGGC
                                  CTG   GGGGT    GTGGAGA
                                  |||   |||||    |||||||
                                  GAC   TTCCA    CACCTCT
                                    ACT    _____
GAM358  ASGR2     5'  CTGTGAAAGGTGTGGAGA    9217      GTC    AGGC
                                  CTG   GGGGT    GTGGAGA
                                  |||   |||||    |||||||
                                  GAC   TTCCA    CACCTCT
                                    ACT    _____
GAM358  POLG      5'  ACTGGCTGGAAGACGTGGAGAG 9218        C   GT
                                  ACTGGT GGG  AGGCGTGGAGAG
                                  |||||| |||  ||||||||||||
                                  TGACCG CCT  TCTGCACCTCTC
                                     A   __
GAM358  RTN4R     3'  CTGGCTTGGCGGCGTGGAGAG  9219       CGG   A
                                  CTGGT   GGT GGCGTGGAGAG
                                  |||||   ||| ||||||||||
                                  GACCG   CCG CCGCACCTCTC
                                     AA_   _
GAM358  SYNGR1    3'  GGGGCTGGGTGTGGAGAG    9220       A_  C
                                  GGGGT  GG GTGGAGAG
                                  |||||  || ||||||||
                                  CCCCG  CC CACCTCTC
                                     AC  A
GAM358  BCoR      5'  GGTTGGGTGGGTGGAGA     9221      CG    A  C
                                  GGT  GGGT GG GTGGAGA
                                  |||  |||| || |||||||
                                  CCA  CCCA CC CACCTCT
                                    A_    _ _
GAM358  BCoR      5'  GGTTGGGTGGGTGGAGA     9221      CG    A  C
                                  GGT  GGGT GG GTGGAGA
                                  |||  |||| || |||||||
                                  CCA  CCCA CC CACCTCT
                                    A_    _ _
GAM358  DKFZp762A227 5'  CGGTTGGGGTAGAGGAG     9222       C       CGT
                                  TGGT GGGGTAGG   GGAG
                                  ||||  ||||||||   ||||
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                                GCCA CCCCATCT   CCTC
                                  A      ___
GAM358  GRID1     3'  CTGGTCGGGTGGGTGGGAG   9223         GTA  C    A
                                CTGGTCGGG   GG GTGG GAG
                                |||||||||   || |||| |||
                                GACCAGCCC   CC CACC CTC
                                    A__  _   _
GAM358  MSE55     3'  CTGGTGGGGGTGGCATGGAG  9224       C     A
                                CTGGT GGGGT GGCGTGGAG
                                ||||| ||||| |||||||||
                                GACCA CCCCA CCGTACCTC
                                  C    _
GAM358  NY-REN-60 3'  TGGTCGGGGTAGGTCCCCATTG 9225            CG_____
          G                      TGGTCGGGGTAGG      TGG
                                ||||||||||||       |||
                                ACCAGCCCCATCC      ACC
                                       AGGGGTA
GAM358  SCYA28    3'  TGGTCAGGGTAAGGGAG     9226           CGT
                                TGGTCGGGGTAGG   GGAG
                                ||||||||||||   ||||
                                ACCAGTCCCATTC   CCTC
                                          ___
GAM358  SMOC2     5'  CTGGGCGGGCGCGTGGAG    9227      T    GTAG
                                CTGG CGGG    GCGTGGAG
                                |||| ||||    ||||||||
                                GACC GCCC    CGCACCTC
                                  C    G___
GAM358  LOC148181 5'  CTAGCTGGGCGTGGAGA     9228       C  GGTAG
                                CTGGT GG     GCGTGGAGA
                                ||||| ||     |||||||||
                                GATCG CC     CGCACCTCT
                                  A  _____
GAM358  LOC154990 5'  CTAGCTGGGCGTGGAGA     9228       C  GGTAG
                                CTGGT GG     GCGTGGAGA
                                ||||| ||     |||||||||
                                GATCG CC     CGCACCTCT
                                  A  _____
GAM358  LOC203427 5'  CTGGTCGGGGGTGGGGCGCGA  9229          TA__
                                CTGGTCGGGG    GGCGTGG
                                ||||||||||    |||||||
                                GACCAGCCCC    CCGCGCT
                                      CACC
GAM358  LOC222057 3'  CTAGCTGGGCGTGGAGA     9228       C  GGTAG
                                CTGGT GG     GCGTGGAGA
                                ||||| ||     |||||||||
                                GATCG CC     CGCACCTCT
                                  A  _____
GAM358  LOC255975 3'  CTAGCTGGGCGTGGAGA     9228       C  GGTAG
                                CTGGT GG     GCGTGGAGA
                                ||||| ||     |||||||||
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                                GATCG CC    CGCACCTCT
                                  A _____
GAM358  LOC256019 3'  CTAGCTGGGCGTGGAGA    9228      C  GGTAG
                                CTGGT GG    GCGTGGAGA
                                ||||| ||    |||||||||
                                GATCG CC    CGCACCTCT
                                  A _____
GAM358  LOC256019 5'  CTAGCTGGGCGTGGAGA    9228      C  GGTAG
                                CTGGT GG    GCGTGGAGA
                                ||||| ||    |||||||||
                                GATCG CC    CGCACCTCT
                                  A _____
GAM358  LOC257069 5'  CTAGCTGGGCGTGGAGA    9228      C  GGTAG
                                CTGGT GG    GCGTGGAGA
                                ||||| ||    |||||||||
                                GATCG CC    CGCACCTCT
                                  A _____
GAM358  LOC257069 3'  CTAGCTGGGCGTGGAGA    9228      C  GGTAG
                                CTGGT GG    GCGTGGAGA
                                ||||| ||    |||||||||
                                GATCG CC    CGCACCTCT
                                  A _____
GAM358  LOC51277  5'  GGTTGGGAGCGTGGGGA    9230    C  GTA     A
                                GGT GGG   GGCGTGG GA
                                ||| |||   ||||||| ||
                                CCA CCC   TCGCACC CT
                                  A ___      C
GAM358  LOC91301  5'  CTGGCCGGGGTGGGGCGGAG  9231          A  C
                                CTGGTCGGGGT GG GTGGAG
                                |||||||||||| || ||||||
                                GACCGGCCCCA CC CGCCTC
                                      C _
GAM358  LOC92405  5'  TGGTCGGGGGGGGCGGG     9232         TA   T
                                TGGTCGGGG  GGCG GG
                                |||||||||  |||| ||
                                ACCAGCCCC  CCGC CC
                                     C_   _
GAM359  AXUD1     3'  CTCAGGGTGGCAGAAGCCA   9235         AT   GA
                                CTCAGGGTG  GGG  CCA
                                |||||||||  |||  |||
                                GAGTCCCAC  TCT  GGT
                                     CG   TC
GAM359  BARX1     3'  GAGCTCAGGGTAGAGAC     9236    A      GAT
                                GA CTCAGGGT   GGGGAC
                                || ||||||||   ||||||
                                CT GAGTCCCA   TCTCTG
                                 C       ___
GAM359  BGN       3'  GAACATGTGATGGGGGCC    9237      TCAGG       A
                                GAAC    GTGATGGGG CC
                                ||||    ||||||||| ||
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                                CTTG    CACTACCCC GG
                                  TA___       C
GAM359  GCDH    3'  GAACTCAGTGTGAGGGGG    9238        G   T
                                GAACTCAG GTGA GGGG
                                |||||||| |||| ||||
                                CTTGAGTC CACT CCCC
                                    A   C
GAM359  GCDH    3'  GAACTCAGTGTGAGGGGG    9238        G   T
                                GAACTCAG GTGA GGGG
                                |||||||| |||| ||||
                                CTTGAGTC CACT CCCC
                                    A   C
GAM359  HSPG2   3'  ACGAGCTGGTGGGGATGGGGAC 9239      A  CA_  T
          C                      ACGA CT   GGG GATGGGGACC
                                |||| ||   ||| ||||||||||
                                TGCT GA   CCC CTACCCCTGG
                                  C  CCA  _
GAM359  ITGA4   5'  ACAAACTCGGGGAGTGGGAC   9240        A  T  TG
                                ACGAACTC GGG GA  GGGAC
                                |||||||| ||| ||  |||||
                                TGTTTGAG CCC CT  CCCTG
                                    _  _  CA
GAM359  ITGB3   3'  GAACTCAGGGTAGAGCC     9241          GAT   A
                                GAACTCAGGGT   GGGG CC
                                ||||||||||   |||| ||
                                CTTGAGTCCCA   TCTC GG
                                      ___   _
GAM359  LBX1    5'  CGGCTCGGGCGCGGGGACCA  9242     AA  A    A
                                CG  CTC GGGTG TGGGGACCA
                                ||  ||| ||||| |||||||||
                                GC  GAG CCCGC GCCCCTGGT
                                 C_  _   _
GAM359  MAPK8IP1 3'  GAGCTCAGGGCTCTTCGGTGGG 9243     A      GA_____
          G                      GA CTCAGGGT      TGGGG
                                || ||||||||      |||||
                                CT GAGTCCCG      ACCCC
                                 C       AGAAGCC
GAM359  PRKCABP  3'  CCGAGGTGTGATGGGGAC    9244     C  _
                                CT AGG GTGATGGGGAC
                                || ||| ||||||||||
                                GG TCC CACTACCCCTG
                                 C  A
GAM359  SLC13A3  3'  ACGAGTCAGGGCCCCTGGG   9245      AC     GA_
                                ACGA  TCAGGGT   TGGG
                                ||||  |||||||   ||||
                                TGCT  AGTCCCG   ACCC
                                  C_      GGG
GAM359  STK9    3'  GATTCAGGGCATTGGGACCA  9246     AC      ATG
                                GA  TCAGGGTG   GGGACCA
                                ||  ||||||||   |||||||
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                                CT  AGTCCCGT   CCCTGGT
                                 A_       AA_
GAM359  TERT     3'  CGAATCTGGGGATGGA      9247       C  A   T
                                CGAA TC GGG GATGGG
                                |||| || ||| ||||||
                                GCTT AG CCC CTACCT
                                  _  A   _
GAM359  TNFRSF10B 3'  CTCAGGGTGACAGATAACCA  9248              _
                                CTCAGGGTGATGGG GACCA
                                |||||||||||||| |||||
                                GAGTCCCACTGTCT TTGGT
                                        A
GAM359  VDAC1    3'  GAACTGGGGTGGGAAC      9249        CA    GAT
                                GAACT  GGGT   GGGGAC
                                |||||  ||||   ||||||
                                CTTGA  CCCA   CCCTTG
                                   C_   ____
GAM359  XRCC3    3'  CCAGCTCAGCAGTGGGGACCA  9250       ____  GA
                                TCAG   GGT  TGGGGACCA
                                ||||   |||  |||||||||
                                GGTC   TCG  ACCCCTGGT
                                  GAG   TC
GAM359  APCL     3'  CGCGCTCAGGGCTGGGCC     9251     AA       GATG   A
                                CG  CTCAGGGT    GGG CC
                                ||  ||||||||    ||| ||
                                GC  GAGTCCCG    CCC GG
                                 GC       A___  _
GAM359  C20orf141 5'  GAGCTCAGAGTGGGGAA     9252     A        AT
                                GA CTCAGGGTG  GGGGA
                                || |||||||||  |||||
                                CT GAGTCTCAC  CCCTT
                                 C        __
GAM359  DKFZP434F1735 3'  ACTCAAGGTGATCCCCA     9253            GGGGA
                                ACTCAGGGTGAT    CCA
                                ||||||||||||    |||
                                TGAGTTCCACTA    GGT
                                       GG___
GAM359  DKFZp586H0623 3'  AACTCAGGGGCTCAAGGACCA  9254          TGA
                                AACTCAGGG   TGGGGACCA
                                |||||||||   |||||||||
                                TTGAGTCCC   GTTCCTGGT
                                     CGA
GAM359  DKFZP586M1120 3'  ACCAACTTAGGGTGAATCCTGT 9255    C     A__________   GGA
          GGTCCCCA                T AGGGTG        TGG   CCA
                                | ||||||        |||   |||
                                A TCCCAC        ACC   GGT
                                 A     TTAGGACIII   AGG
GAM359  DZIP1    5'  ACAAACTTGGGTCGGGG     9256        CA    GA
                                ACGAACT  GGGT  TGGGG
                                |||||||  ||||  |||||
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                                TGTTTGA  CCCA  GCCCC
                                   A_   __
GAM359  FLJ00024  5'  CTCAGGGCCAGGGCC      9257        GA    A
                                CTCAGGGT  TGGGG CC
                                ||||||||  ||||| ||
                                GAGTCCCG  GTCCC GG
                                   __    _
GAM359  FLJ20507  3'  GAGCTCAGGGTTTGAAG    9258    A      GA
                                GA CTCAGGGT  TGGGG
                                || ||||||||  |||||
                                CT GAGTCCCA  ACTTC
                                 C       A_
GAM359  FLJ20507  3'  GAGCTCAGGGTTTGAAG    9258    A      GA
                                GA CTCAGGGT  TGGGG
                                || ||||||||  |||||
                                CT GAGTCCCA  ACTTC
                                 C       A_
GAM359  KIAA0323  3'  ACCAACTCAGGGTGCCTCTGGA 9259    G        ATGG_   C
          TCA                    AC AACTCAGGGTG    GGA CA
                                || ||||||||||     ||| ||
                                TG TTGAGTCCCAC    CCT GT
                                 G         GGAGA   A
GAM359  KIAA0427  3'  TCAGGGCCAGGGACCA     9260        GA
                                TCAGGGT  TGGGGACCA
                                |||||||  |||||||||
                                AGTCCCG  GTCCCTGGT
                                   __
GAM359  KIAA0544  3'  CGAACTCATGGTGGGACC    9261        G   GATG
                                CGAACTCA GGT    GGGACC
                                |||||||| |||    ||||||
                                GCTTGAGT CCA    CCCTGG
                                   A   _____
GAM359  KIAA0669  5'  CGAACCCAGGGGCGGGCC    9262          TGATG   A
                                CGAACTCAGGG    GGG CC
                                ||||||||||     ||| ||
                                GCTTGGGTCCC    CCC GG
                                     CG___   _
GAM359  KIAA1554  3'  ACTCAGGGGTGAAGTTATGGTC 9263       _ A_________   GGA
          CCCA                   TCAGGG TG       TGG   CCA
                                |||||| ||       |||   |||
                                AGTCCC AC       ACC   GGT
                                   C  TTCAATIII   AGG
GAM359  MGC14258  3'  GACCTCAGAATGGGGGCCA   9264    A       AT    A
                                GA CTCAGGGTG  GGGG CCA
                                || |||||||||  |||| |||
                                CT GAGTCTTAC  CCCC GGT
                                 G       __    _
GAM359  PLPL      5'  GAGCCAGGGTGATGTTCCC   9265    A T        GGGA
                                GA C CAGGGTGATG    CC
                                || | ||||||||||    ||
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                                CT G GTCCCACTAC    GG
                                 C _         AAG_
GAM359  RBM5     3'  CGAATTCGGGAGATGGACCA   9266      C  A   T   GG
                                CGAA TC GGG GAT  GGACCA
                                |||| || ||| |||  ||||||
                                GCTT AG CCC CTA  CCTGGT
                                  A _   T   __
GAM359  SCYA25   3'  ACCAACTCAGGTGCAGGGA   9267     G      G  A
                                AC AACTCAGG TG TGGGGA
                                || |||||||| || ||||||
                                TG TTGAGTCC AC GTCCCT
                                 G       _ _
GAM359  SLC16A3  3'  GAGCCCAGGGTAGGACGGG   9268     A       __
                                GA CTCAGGGT  GATGGG
                                || ||||||||  ||||||
                                CT GGGTCCCA  CTGCCC
                                 C       TC
GAM359  THEA     3'  AACTCAGGGTTAAATGGA    9269           __
                                AACTCAGGGT  GATGGG
                                ||||||||||  ||||||
                                TTGAGTCCCA  TTACCT
                                      AT
GAM359  TNKS2    5'  ACGCGCTCAGGGCCCGGGCC  9270      AA      GA   GA
                                ACG  CTCAGGGT  TGGG  CC
                                |||  ||||||||  ||||  ||
                                TGC  GAGTCCCG  GCCC  GG
                                  GC       G_   __
GAM359  LOC144308 3'  ACTCAGGGTGACGTGGACC   9271            G
                                ACTCAGGGTGATG GGACC
                                |||||||||||| |||||
                                TGAGTCCCACTGC CCTGG
                                       A
GAM359  LOC148397 3'  CGGGCTCAGGGTGGGGG     9272     AA       AT
                                CG  CTCAGGGTG  GGGG
                                ||  |||||||||  ||||
                                GC  GAGTCCCAC  CCCC
                                 CC        __
GAM359  LOC148397 3'  CGGCTCCACTGTGGGGGCCA  9273     AA  AGG_  AT   A
                                CG  CTC    GTG  GGGG CCA
                                ||  |||    |||  |||| |||
                                GC  GAG    CAC  CCCC GGT
                                 C_   GTGA  __   _
GAM359  LOC149401 5'  ACAAACTCAGGGTTTGGGGCCA 9274            GA    A
                                ACGAACTCAGGGT  TGGGG CCA
                                ||||||||||||  ||||| |||
                                TGTTTGAGTCCCA  ACCCC GGT
                                       A_    _
GAM359  LOC151701 5'  GAGCTGGGCAGTGGGGACC   9275     A  CA   GA
                                GA CT  GGGT  TGGGGACC
                                || ||  ||||  ||||||||
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                                CT GA  CCCG  ACCCCTGG
                                 C  __    TC
GAM359  LOC201245 5'  GAGCTCAGGGTAGGCCC     9276     A       GAT   GA
                                GA CTCAGGGT   GGG  CC
                                || ||||||||   |||  ||
                                CT GAGTCCCA   TCC  GG
                                 C       ____   G_
GAM359  LOC219920 5'  ACGAGCCATCCCCTATGGGGAC 9277       A T  GGGTG_
          CA                     ACGA C CA     ATGGGGACCA
                                |||| | ||     ||||||||||
                                TGCT G GT     TACCCCTGGT
                                  C _  AGGGGA
GAM359  LOC221399 5'  GATTCAGTATGGGGATCA    9278     AC    GGTG      C
                                GA  TCAG    ATGGGGA CA
                                ||  ||||    ||||||| ||
                                CT  AGTC    TACCCCT GT
                                 A_    A___      A
GAM359  LOC221543 5'  AAGCTTAGGGTGGGGCGGCCA  9279     A  C     AT  _  A
                                GA CT AGGGTG  GG GG CCA
                                || || ||||||  || || |||
                                TT GA TCCCAC  CC CC GGT
                                 C  A     C_  G  _
GAM359  LOC222484 3'  GACCCATGATGGGGACC     9280     A    GGG
                                GA CTCA   TGATGGGGACC
                                || ||||   ||||||||||
                                CT GGGT   ACTACCCCTGG
                                 _   ____
GAM359  LOC257463 3'  ACTTTGGGTGATAATGGA    9281      CA        _
                                ACT  GGGTGATGG GGA
                                |||  ||||||||| |||
                                TGA  CCCACTATT CCT
                                  AA        A
GAM359  LOC257464 5'  GAACGCCAGTGTGGGGG     9282       _    G   AT
                                GAAC TCAG GTG  GGGG
                                |||| |||| |||  ||||
                                CTTG GGTC CAC  CCCC
                                  C    A   __
GAM359  LOC257596 5'  AAGCTTAGGGTGGGGCGGCCA  9279     A  C     AT  _  A
                                GA CT AGGGTG  GG GG CCA
                                || || ||||||  || || |||
                                TT GA TCCCAC  CC CC GGT
                                 C  A     C_  G  _
GAM359  LOC51696  3'  CAAGCTTGGGGTATTAAGG   9283      A  CA    A
                                CGA CT  GGGTG TGGGG
                                ||| ||  ||||| |||||
                                GTT GA  CCCAT ATTCC
                                  C  AC     A
GAM360  DSC3      3'  AGGGAATCTCTGCTGGAG    9286      ACAC         A
                                AGG    AATCTCTGCT GAG
                                |||    |||||||||| |||
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                                TCC    TTAGAGACGA CTC
                                  C___         C
GAM360  DSC3     3'  AGGGAATCTCTGCTGGAG    9286      ACAC         A
                                AGG    AATCTCTGCT GAG
                                |||    |||||||||| |||
                                TCC    TTAGAGACGA CTC
                                  C___         C
GAM360  HLF      3'  TCCAAGACGCAGTTTTTGGCTC 9287      A  AT__________   TGCTA
             TAGCAGA                  GAC CA         CTC     GA
                                ||| ||          |||     ||
                                CTG GT          GAG     CT
                                  C  CAAAAACCIII   ATCGT
GAM360  TRPC5    3'  TCTAGGACTCAGACCTAGA   9288     C     A  AT TCTG
                                TC AGGAC CA  C    CTAGA
                                || ||||| ||  |    |||||
                                AG TCCTG GT  G    GATCT
                                  A     A  CT _____
GAM360  DKFZp727G131 5'  TCCAGGGACACCTCTGCT    9289        _    AAT
                                TCCAGG ACAC   CTCTGCT
                                |||||| ||||   |||||||
                                AGGTCC TGTG   GAGACGA
                                    C    ___
GAM360  FKBP4    3'  GGACACAACCTGGCCGAG    9290           CT   A
                                GGACACAATCT  GCT GAG
                                ||||||||||  ||| |||
                                CCTGTGTTGGA  CGG CTC
                                      C_  _
GAM360  FLJ11053  5'  TCCGGGACACAACTTCCG    9291      A       TC
                                TCC GGACACAA  TCTG
                                ||| ||||||||  ||||
                                AGG CCTGTGTT  AGGC
                                  C       GA
GAM360  FOXH1    5'  CCCAGGACATGATCAGGTGGAG 9292          CA   TCTGCTA
                                TCCAGGACA  ATC      GAG
                                |||||||||  |||      |||
                                GGGTCCTGT  TAG      CTC
                                      AC   TCCAC__
GAM360  KIAA0317  3'  TCCAGGATCAGTCTCTG     9293         CA  A
                                TCCAGGA  CA TCTCTG
                                |||||||  || ||||||
                                AGGTCCT  GT AGAGAC
                                    A_  C
GAM360  MGC13090  3'  GGACACAAGGTTGCTGGAG   9294         TCTC    A
                                GGACACAA    TGCT GAG
                                ||||||||    |||| |||
                                CCTGTGTT    ACGA CTC
                                      CCA_    C
GAM360  MGC20576  5'  TCCAGGAACAGTCCCCACCTGG 9295         C   A    TG  A_
             AG                    TCCAGGA ACA TCTC  CT  GAG
                                ||||||| ||| ||||  ||  |||
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                                AGGTCCT TGT AGGG  GG  CTC
                                   _  C    GT  AC
GAM360  PDGFC    3'  CCCAGGACATGGAGCTTTAGAG 9296         CAATCT  GC
                                TCCAGGACA     CT  TAGAG
                                |||||||||     ||  |||||
                                GGGTCCTGT     GA  ATCTC
                                     ACCTC_  A_
GAM360  RAB14    3'  TCTGGGACACAATTTTCTG   9297     CA       C_
                                TC  GGACACAAT  TCTG
                                ||  |||||||||  ||||
                                AG  CCTGTGTTA  AGAC
                                 AC        AA
GAM360  RAB40A   5'  TCTAGGACATGGATTTTGCTAG 9298     C     CAATCTC
            AG                    TC AGGACA      TGCTAGAG
                                || ||||||      ||||||||
                                AG TCCTGT      ACGATCTC
                                 A     ACCTAAA
GAM360  LOC150372 3'  TCCATGGGCCCTCTGCTAG    9299      _  ACACAA
                                TCCA GG     TCTCTGCTAG
                                |||| ||     ||||||||||
                                AGGT CC     GGAGACGATC
                                  A  CG_____
GAM360  LOC152317 3'  TCCAGGACTCAGTTTTTCTATC 9300         A  ATC__    C
            AG                    TCCAGGAC CA     TCTG TAG
                                |||||||| ||     |||| |||
                                AGGTCCTG GT     AGAT GTC
                                     A  CAAAA    A
GAM360  LOC153727 5'  TCCAGGACAAAATCAACAGAG  9301          C    TCT  T
                                TCCAGGACA AATC   GC AGAG
                                ||||||||| ||||   || ||||
                                AGGTCCTGT TTAG   TG TCTC
                                     T    T__  _
GAM360  LOC196047 5'  TCCAGGACACAGTGAGGGCTCT 9302         AT_________   TGCTA
            AGCG                    AGGACACA        CTC    G
                                ||||||||        |||    |
                                TCCTGTGT        GAG    C
                                     CACTCCCIII   ATCGT
GAM360  LOC220739 3'  TCCGAGGGTCTCTGCTGGAG   9303     _  ACACAA       A
                                TCC AGG     TCTCTGCT GAG
                                ||| |||     |||||||| |||
                                AGG TCC     AGAGACGA CTC
                                  C   C_____       C
GAM360  LOC253142 3'  CAGGGCACAATCTACAG     9304       A       CT  T
                                CAGG CACAATCT  GC AG
                                |||| ||||||||  || ||
                                GTCC GTGTTAGA  TG TC
                                  C       __  _
GAM360  LOC254532 3'  TCCAGAACGCAGTCTGGA    9305          A  ATC    CTA
                                TCCAGGAC CA   TCTG   GA
                                |||||||| ||   ||||   ||
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                                AGGTCTTG GT   AGAC   CT
                                    C  C__   ___
GAM360  LOC90019  5'  CCCAGGACGCACCACAGCT   9306        A  A  TCT
                                TCCAGGAC CA TC   GCT
                                |||||||| || ||   |||
                                GGGTCCTG GT GG   CGA
                                    C  _  TGT
GAM360  LOC93512  3'  CCCAGGACGCGCCCGCGCT   9307        ACAAT  _
                                TCCAGGAC    CTC TGCT
                                ||||||||    ||| ||||
                                GGGTCCTG    GGG GCGA
                                    CGC__   C
GAM361  APLP1     5'  TGCGCCCTCACGTCCCCTG   9310         G    T
                                TGCGCCCTCA GTCCC CTG
                                |||||||||| ||||| |||
                                ACGCGGGAGT CAGGG GAC
                                     G    _
GAM361  ATP10C    3'  TGTGCTCTGCCCTCTGCCA   9311     C  C  CAG T
                                TG GC CT   G CCCTCTGCCA
                                || || ||   | ||||||||||
                                AC CG GA   C GGGAGACGGT
                                 A  A  ___ _
GAM361  B4GALT6   5'  CTGCGCTCTCAGGCCGGACTC  9312       C      C__
                                CTGCGC CTCAGGTC   CTC
                                |||||| ||||||||   |||
                                GACGCG GAGTCCGG   GAG
                                   A       CCT
GAM361  BCL7C     5'  CCGCGCTCTCGGCCTGCC    9313       C   A   CCCT
                                CTGCGC CTC GGT    CTGCC
                                |||||| ||| |||    |||||
                                GGCGCG GAG CCG    GACGG
                                   A   _   _____
GAM361  CARD15    3'  TGCTCCCTCCTCTGCCA     9314     G    CAGGTC
                                TGC CCCT     CCTCTGCCA
                                ||| ||||     |||||||||
                                ACG GGGA     GGAGACGGT
                                  A   _______
GAM361  DDB2      3'  CTGCTTGATCCCTCTGC     9315      GCCCTCA
                                CTGC      GGTCCCTCTGC
                                ||||      ||||||||||
                                GACG      CTAGGGAGACG
                                  AA_____
GAM361  EFNB1     5'  CGCCTCGCCTTCCTCTGCC   9316      C  AG   __
                                CGCC TC  GTC  CCTCTGCC
                                |||| ||  |||  ||||||||
                                GCGG AG  CGG  GGAGACGG
                                  _  __   AA
GAM361  FBXL11    3'  TGGCCCAGTCCTCTGCC     9317     C    TCA    C
                                TG GCCC   GGTCC TCTGCC
                                || ||||   ||||| ||||||
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                                AC CGGG   TCAGG AGACGG
                                 _  ___    _
GAM361  GAN     5'  GCGCCCGCTCCTCTGCC    9318       TCAG TC
                                GCGCCC   G  CCTCTGCC
                                ||||||   |  ||||||||
                                CGCGGG   C  GGAGACGG
                                   ____ GA
GAM361  HAO1    3'  CTGCACAGTGTCTCTTTGTCA  9319       CCTC _  C  C  C
                                CTGCGC   AG GTC CT TG CA
                                ||||||   || ||| || || ||
                                GACGTG   TC CAG GA AC GT
                                   ____ A  A  A  A
GAM361  HMGCL   3'  CTGGGCAGGAGGTCCTTCTGCC 9320     C  CCTC    C
          A                      CTG GC   AGGTCC TCTGCCA
                                ||| ||   |||||| |||||||
                                GAC CG   TCCAGG AGACGGT
                                  C  TCC_    A
GAM361  HYAL1   5'  GCCTCTCAGACCAGGCCTCTGC 9321     _   GT ___
          CA                     GCC CTCAG  C   CCTCTGCCA
                                ||| |||||  |  |||||||||
                                CGG GAGTC  G   GGAGACGGT
                                  A    TG TCC
GAM361  IL10RA  3'  CTGCCCTTCTCAGCTCTGCCA  9322     G __   GTCC
                                CTGC CC  CTCAG   CTCTGCCA
                                |||| ||  |||||   ||||||||
                                GACG GG  GAGTC   GAGACGGT
                                  _ AA   _____
GAM361  ISG20   5'  CTGCGCCCTCAGCTCACGTCTG 9323          G  CC_
                                CTGCGCCCTCAG TC   TCTG
                                ||||||||||||| ||   ||||
                                GACGCGGGAGTC AG   AGAC
                                       G  TGC
GAM361  KRT16   5'  TGTGCCTCAGGTCCTC     9324    C  C      C
                                TG GCC TCAGGTCC TC
                                || ||| ||||||||| ||
                                AC CGG AGTCCAGG AG
                                 A  _      _
GAM361  LMO2    5'  CTGTGCCATCTCCCCTCTCTGC 9325     C  C  AGG  _
          CA                     CTG GCC TC   TCC CTCTGCCA
                                ||| ||| ||   ||| ||||||||
                                GAC CGG AG   GGG GAGACGGT
                                  A  T  AG_  A
GAM361  PAX5    3'  GCCCTGGCTCTCTGCCA    9326      CA  CC
                                GCCCT  GGT  CTCTGCCA
                                |||||  |||  ||||||||
                                CGGGA  CCG  GAGACGGT
                                   __  A_
GAM361  PLXNB3  3'  CTGTGCCCCCAGGCTCTGCCA  9327     C       TCC
                                CTG GCCCTCAGG   CTCTGCCA
                                ||| |||||||||   ||||||||
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                                GAC CGGGGGTCC   GAGACGGT
                                  A       ___
GAM361  PRX      5'  CTGTGTCCTCTCCCCTTTCTGC 9328      CGC    AGG    ___
                                CTG   CCTC   TCCC   TCTGC
                                |||   ||||   ||||   |||||
                                GAC   GGAG   AGGG   AGACG
                                  ACA    ___    GAA
GAM361  PTGS1    3'  CTGTCCTCTCTCTCTGC     9329      CGC    AGG  C
                                CTG   CCTC   TC CTCTGC
                                |||   ||||   || ||||||
                                GAC   GGAG   AG GAGACG
                                  A__    ___  A
GAM361  PTGS1    3'  CTGTCCTCTCTCTCTGC     9329      CGC    AGG  C
                                CTG   CCTC   TC CTCTGC
                                |||   ||||   || ||||||
                                GAC   GGAG   AG GAGACG
                                  A__    ___  A
GAM361  PTK2B    3'  CTGTGCCCCAGGTCCTCCCT   9330      C    T      _
                                CTG GCCC CAGGTCC CTCT
                                ||| |||| ||||||| ||||
                                GAC CGGG GTCCAGG GGGA
                                  A   _      A
GAM361  PTPRF    5'  CTGCTCCCACTCCTCTGCC    9331      G   TCAG TC
                                CTGC CCC    G  CCTCTGCC
                                |||| |||    |  ||||||||
                                GACG GGG    T  GGAGACGG
                                  A  _____ GA
GAM361  PTPRF    5'  CTGCTCCCACTCCTCTGCC    9331      G   TCAG TC
                                CTGC CCC    G  CCTCTGCC
                                |||| |||    |  ||||||||
                                GACG GGG    T  GGAGACGG
                                  A  _____ GA
GAM361  RAB13    3'  CTGCTCACTCCCTCTGCC     9332      GCCC   GG
                                CTGC    TCA  TCCCTCTGCC
                                ||||    |||  ||||||||||
                                GACG    AGT  AGGGAGACGG
                                  _____  G_
GAM361  RARA     3'  CTGTCCCACCCCCTCTGC     9333      CG   TCAGG      C
                                CTG  CCC    TCCCTCTG C
                                |||  |||    |||||||| |
                                GAC  GGG    GGGGAGAC G
                                  A_   TG___       A
GAM361  RNPEPL1  3'  CTGTGTCCTTGTTCCTCTGCCA 9334      CGC   CAG  C
                                CTG   CCT   GT CCTCTGCCA
                                |||   |||   || |||||||||
                                GAC   GGA   CA GGAGACGGT
                                  ACA   A__  A
GAM361  RPS6KA2  3'  CTGCGCCCTCGCACTGCC    9336          AG  CCCT
                                CTGCGCCCTC  GT    CTGCC
                                ||||||||||  ||    |||||
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                                GACGCGGGAG  CG    GACGG
                                      __  T___
GAM361  RPS6KA2  3'  CTGCCCCTCAGTCTGC      9335       G      GTCCC
                                CTGC CCCTCAG    TCTGC
                                |||| |||||||    |||||
                                GACG GGGAGTC    AGACG
                                  _     _____
GAM361  SEPN1    3'  GCCTTCCTTCTTCCTCTGCCA  9337      C  AGG  __
                                GCC TC   TC  CCTCTGCCA
                                ||| ||   ||  |||||||||
                                CGG AG   AG  GGAGACGGT
                                  A  GA_  AA
GAM361  SLC18A3  5'  CTGTGCCTCAGGTGGGCC    9338      C   C     CCCTCT
                                CTG GCC TCAGGT     GCC
                                ||| ||| ||||||     |||
                                GAC CGG AGTCCA     CGG
                                  A  _     CC____
GAM361  SLC2A2   3'  TGCATCCTCAGGTTTCTA    9339       C       CCC
                                TGCG CCTCAGGT   TCTG
                                |||| ||||||||   ||||
                                ACGT GGAGTCCA   AGAT
                                  A       A__
GAM361  SLC6A6   3'  CTGTGGCCTCCTGTGCCTCTGC 9340      CGC    AG  C
           CA                     CTG   CCTC  GT CCTCTGCCA
                                |||   ||||  || |||||||||
                                GAC   GGAG  CA GGAGACGGT
                                  ACC    GA  C
GAM361  SPO11    5'  CTGCGCCCTTGGGGCGTGGCTG 9341          CA_  CCCT
                                CTGCGCCCT   GGT    CTG
                                |||||||||   |||    |||
                                GACGCGGGA   CCG    GAC
                                     ACC   CACC
GAM361  STAT6    5'  GCCTCGGCAACCCCTCTGC   9342      C  A   ___
                                GCC TC GGT   CCCTCTGC
                                ||| || |||   ||||||||
                                CGG AG CCG   GGGAGACG
                                  _  _   TTG
GAM361  TERF2    3'  TGTGCCTGTCATCTCTGCCA  9343     C   CTCAG   C_
                                TG GCC    GTC  CTCTGCCA
                                || |||    |||  ||||||||
                                AC CGG    CAG  GAGACGGT
                                 A  A____   TA
GAM361  VIPR1    3'  GCCCTCAGGTCACACCA     9344           CCTC
                                GCCCTCAGGTC    TGCCA
                                ||||||||||    |||||
                                CGGGAGTCCAG    GTGGT
                                      T___
GAM361  AAMP     3'  CTGTGCCCTACTGCCTCTGC  9345      C    CAGGTC
                                CTG GCCCT     CCTCTGC
                                ||| |||||     |||||||
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                                GAC CGGGA     GGAGACG
                                  A    TGAC__
GAM361  ARFRP1   3'  CTGCGCCCTGTGGAAAGGCTGC 9346          CA  TCCCT
            C                    CTGCGCCCT  GG    CTGCC
                                 |||||||||  ||    |||||
                                 GACGCGGGA  CC    GACGG
                                      CA  TTTCC
GAM361  C11orf9  3'  CTGGCTCTCAGGTTCCCTCTG  9347      C  C      _
                                 CTG GC CTCAGGT CCCTCTG
                                 ||| || ||||||| |||||||
                                 GAC CG GAGTCCA GGGAGAC
                                   _ A      A
GAM361  CAMK1G   3'  GCCTTCCTCCCTCTGCC     9348      C  AGG
                                 GCC TC   TCCCTCTGCC
                                 ||| ||   ||||||||||
                                 CGG AG   AGGGAGACGG
                                   A  G__
GAM361  CHST3    3'  CTGTCCTCTCCCTCTGCC    9349      CGC    AGG
                                 CTG   CCTC   TCCCTCTGCC
                                 |||   ||||   ||||||||||
                                 GAC   GGAG   AGGGAGACGG
                                   A__    ____
GAM361  CTSO     5'  GCGCCCGGCTCCTCTGCC    9350        TCA  TC
                                 GCGCCC   GG  CCTCTGCC
                                 ||||||   ||  ||||||||
                                 CGCGGG   CC  GGAGACGG
                                     ____  GA
GAM361  DGKD     3'  CTGGCTTATTTCTCCCTCTGCC 9351      C  CCTCAGG
            A                    CTG GC      TCCCTCTGCCA
                                 ||| ||      ||||||||||||
                                 GAC CG      AGGGAGACGGT
                                   _  AATAAAG
GAM361  DGS-A    3'  CTGCCCCTCAGGTCCTC     9352       G         C
                                 CTGC CCCTCAGGTCC TC
                                 |||| ||||||||||| ||
                                 GACG GGGAGTCCAGG AG
                                    _         _
GAM361  DKFZP434H204 5'  GCCTCTGCACACCTCTGCC   9353      _  _  G TC
                                 GCC CT CA G  CCTCTGCC
                                 ||| || || |  ||||||||
                                 CGG GA GT T  GGAGACGG
                                   A  C  G __
GAM361  DKFZp434N2435 5'  CTGCGCCCCTTGGGGACTGCCA 9354          CA  TCCCT
                                 CTGCGCCCT  GG    CTGCCA
                                 |||||||||  ||    ||||||
                                 GACGCGGGG  CC    GACGGT
                                      AA  CCT__
GAM361  DNAJC6   5'  CTGCTTCCTCCCTCTGC     9355       GC  TCAGG
                                 CTGC  CC    TCCCTCTGC
                                 ||||  ||    |||||||||
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                                GACG  GG    AGGGAGACG
                                  AA  _____
GAM361  FLJ00001  3'  CTGGCCCTGCCTCTGC      9356      C     CAGGTC
                                CTG GCCCT     CCTCTGC
                                ||| |||||     |||||||
                                GAC CGGGA     GGAGACG
                                  _    C_____
GAM361  FLJ12783  3'  GCCTCCGAAGCCCTCTGC    9357      _ C   T
                                GCC CT AGG CCCTCTGC
                                ||| || ||| ||||||||
                                CGG GG TTC GGGAGACG
                                  A  C   _
GAM361  FLJ14621  3'  CTGCTGCCTGATCCCTCCCTCT 9358      _   C__  AGG
           GC                   CTGC GCC   TC   TCCCTCTGC
                                |||| |||   ||   |||||||||
                                GACG CGG   AG   AGGGAGACG
                                  A   ACT  GG_
GAM361  FLJ21511  5'  CTGCGCCCCCAGGTTCCC    9359            _
                                CTGCGCCCTCAGGT CCC
                                |||||||||||||| |||
                                GACGCGGGGGTCCA GGG
                                       A
GAM361  FLJ32384  5'  CTGCTCCTCGGGTCCCTCACCA 9360      GC    A       T
                                CTGC  CCTC GGTCCCTC GCCA
                                ||||  |||| |||||||| ||||
                                GACG  GGAG CCAGGGAG TGGT
                                  A_   C       _
GAM361  HSJ1      3'  GCCCTCGAAGCTCTCTGCCA   9361       _   CC
                                GCCCTC AGGT  CTCTGCCA
                                |||||| ||||  ||||||||
                                CGGGAG TTCG  GAGACGGT
                                   C   A_
GAM361  KIAA0275  3'  CTGCTGCCCTCCTCCTCTGCC  9362      _     AGGTC
                                CTGC GCCCTC    CCTCTGCC
                                |||| ||||||    ||||||||
                                GACG CGGGAG    GGAGACGG
                                  A     GA___
GAM361  KIAA0367  3'  CTATGCCCTCAGGTTTGCACCA 9363     C        CCCTCT
                                CTG GCCCTCAGGT     GCCA
                                ||| ||||||||||     ||||
                                GAT CGGGAGTCCA     TGGT
                                  A         AACG__
GAM361  KIAA0800  3'  TGTCCCCTCTTCTCTCTGCCA  9364     CG    AGG  C
                                TG  CCCTC   TC CTCTGCCA
                                ||  |||||   || ||||||||
                                AC  GGGAG   AG GAGACGGT
                                 AG    A__  A
GAM361  KIAA0806  3'  GCCCCGTATCTTCCCTCTGCC  9365       CAGG__
                                GCCCT     TCCCTCTGCC
                                |||||     ||||||||||
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                              CGGGG     AGGGAGACGG
                                 CATAGA
GAM361  KIAA1037 3' GCCCCACCCTCTGCC      9366      T  GGT
                              GCCC CA   CCCTCTGCC
                              |||| ||   |||||||||
                              CGGG GT   GGGAGACGG
                                 _ ___
GAM361  KIAA1193 3' CTGTGCCCTCAGCTTCTCCT  9367     C      G_ _
                              CTG GCCCTCAG  TC CCT
                              ||| ||||||||  || |||
                              GAC CGGGAGTC  AG GGA
                                A       GA  A
GAM361  KIAA1204 5' CTGCCCCTCCGTCTCTGCC   9368      G    AG   CC
                              CTGC CCCTC  GTC  TCTGCC
                              |||| |||||  |||  ||||||
                              GACG GGGAG  CAG  AGACGG
                                 _    G_  __
GAM361  KIAA1276 5' CTGGCCTTGGTCTCTGCC    9369     C   CTCA   CC
                              CTG GCC    GGTC  TCTGCC
                              ||| |||    ||||  ||||||
                              GAC CGG    CCAG  AGACGG
                                 _  AA__   __
GAM361  KIAA1364 3' CTGCCCCTCGGGTTTGC     9371      G    A  CCCTC
                              CTGC CCCTC GGT    TGC
                              |||| ||||| |||    |||
                              GACG GGGAG CCA    ACG
                                 _    C  A____
GAM361  KIAA1364 3' TGTGCCCGTCCTTCCCTCTGC  9370     C   _ AGG
                              TG GCCC TC   TCCCTCTGC
                              || |||| ||   |||||||||
                              AC CGGG AG   AGGGAGACG
                               A   C  GA_
GAM361  KIAA1573 3' CTGCCCCTCCCCATCTCTGTCA 9372      G    AGG  __    C
                              CTGC CCCTC   TCC  CTCTG CA
                              |||| |||||   |||  ||||| ||
                              GACG GGGAG   GGG  GAGAC GT
                                 _    ___  TA    A
GAM361  KIAA1735 3' TGAGCTCCTTCTCTCTGCCA  9373     C _  CAGG  C
                              TG GC CCT    TC CTCTGCCA
                              || || |||    || ||||||||
                              AC CG GGA    AG GAGACGGT
                               T  A  _____ A
GAM361  KIAA1814 3' CTGTGGCCGTCTTCTCTGCCA 9374     C_  CTCAG  C_
                              CTG  GCC    GTC  CTCTGCCA
                              |||  |||    |||  ||||||||
                              GAC  CGG    CAG  GAGACGGT
                                AC  ______  AA
GAM361  KIAA1922 5' TGGCCCGGCTCTCTGCC     9375    C   TCA  CC
                              TG GCCC   GGT  CTCTGCC
                              || ||||   |||  |||||||
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                                AC CGGG  CCG  GAGACGG
                                 _   ___   A_
GAM361  KIF13B   3' CTGCCCCCTGTCCCCTCTGC  9376     G   CAGG
                                CTGC CCCT   TCCCTCTGC
                                |||| ||||   |||||||||
                                GACG GGGA   GGGGAGACG
                                  G   CA__
GAM361  KIF13B   3' CTGCCCCCTGTCCCCTCTGC  9376     G   CAGG
                                CTGC CCCT   TCCCTCTGC
                                |||| ||||   |||||||||
                                GACG GGGA   GGGGAGACG
                                  G   CA__
GAM361  LHX6     3' GCCCTCAGTCAGCTGTCA    9377       G  CCT  C
                                GCCCTCAG TC  CTG CA
                                |||||||| ||  ||| ||
                                CGGGAGTC AG  GAC GT
                                    _ TC_  A
GAM361  LIECG3   3' CTGCGCCCCGGGCTCTG    9378        CA  TCC
                                CTGCGCCCT  GG  CTCTG
                                |||||||||  ||  |||||
                                GACGCGGGG  CC  GAGAC
                                     __ C__
GAM361  MESDC2   3' CTGCTGCCTCTCCCTCTGCCA 9379     GC   AGG
                                CTGC  CCTC  TCCCTCTGCCA
                                ||||  ||||  ||||||||||
                                GACG  GGAG  AGGGAGACGGT
                                  AC   ___
GAM361  MGC2488  5' CTGTTCTCAGCCTCTGCCA   9380    CGCC   GTC
                                CTG   CTCAG  CCTCTGCCA
                                |||   |||||  |||||||||
                                GAC   GAGTC  GGAGACGGT
                                 AA__   ___
GAM361  MGC29761 5' CTGTGCTTCCAGGTCTTTCC  9381    C  CC     CC
                                CTG GC  TCAGGTC  TCT
                                ||| ||  |||||||  |||
                                GAC CG  GGTCCAG  AGG
                                  A  AA     AA
GAM361  ORMDL3   5' CTGCTGCCCCTCTCTGC    9382     _   CAGGTCC
                                CTGC GCCCT     CTCTGC
                                |||| |||||     ||||||
                                GACG CGGGG     GAGACG
                                  A    A_______
GAM361  PTPRU    3' CTGAGCCTTTGTCACTCTGCCA 9383    C  CTCAG  C
                                CTG GCC    GTC CTCTGCCA
                                ||| |||    ||| ||||||||
                                GAC CGG    CAG GAGACGGT
                                 T  AAA__  T
GAM361  PTPRU    3' CTGAGCCTTTGTCACTCTGCCA 9383    C  CTCAG  C
                                CTG GCC    GTC CTCTGCCA
                                ||| |||    ||| ||||||||
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                                GAC CGG    CAG GAGACGGT
                                  T  AAA__  T
GAM361  PTPRU    3'  CTGAGCCTTTGTCACTCTGCCA 9383     C  CTCAG  C
                                CTG GCC    GTC CTCTGCCA
                                ||| |||    ||| ||||||||
                                GAC CGG    CAG GAGACGGT
                                  T  AAA__  T
GAM361  SDCCAG28  5'  TGGGCCCTCAGGTTTGC    9384    C       CCCTC
                                TG GCCCTCAGGT    TGC
                                || ||||||||||    |||
                                AC CGGGAGTCCA    ACG
                                 C        A____
GAM361  TIGD5    3'  CTGTGCCCCCAGGGTGCC    9385     C       TCCCTC
                                CTG GCCCTCAGG     TGCC
                                ||| |||||||||     ||||
                                GAC CGGGGGTCC     ACGG
                                  A       C_____
GAM361  UBN1     3'  CTGCCCCACCCTCTGC     9386      G  TCAGGT
                                CTGC CCC     CCCTCTGC
                                |||| |||     ||||||||
                                GACG GGG     GGGAGACG
                                  _  T_____
GAM361  ZDHHC2   5'  CTGCGCCCTCGGGCGGGCTCTG 9387          A  CC_
                                CTGCGCCCTC GGT  CTCTG
                                |||||||||| |||  |||||
                                GACGCGGGAG CCG  GAGAC
                                      C  CCC
GAM361  LOC120425 3'  CTGTCCAGTCTCTCTGCC    9388     CG  CTCA   C
                                CTG  CC   GGTC CTCTGCC
                                |||  ||   |||| |||||||
                                GAC  GG   TCAG GAGACGG
                                  A_ ____   A
GAM361  LOC134265 5'  CTGCGCTCTCAGGCCAGCC   9389       C      CCTCT
                                CTGCGC CTCAGGTC    GCC
                                |||||| ||||||||    |||
                                GACGCG GAGTCCGG    CGG
                                   A      T____
GAM361  LOC145195 3'  CTGTGTCCCCACTGGCTCTGCC 9390     CG_   CA_  TCC
          A                     CTG  CCCT  GG  CTCTGCCA
                                |||  ||||  ||  ||||||||
                                GAC  GGGG  CC  GAGACGGT
                                  ACA   TGA  ___
GAM361  LOC146378 3'  CGCGCCCTCGGGCCCTGCCA  9391         A   CTC
                                TGCGCCCTC GGTCC  TGCCA
                                ||||||||| |||||  |||||
                                GCGCGGGAG CCGGG  ACGGT
                                      C   ___
GAM361  LOC148029 3'  GCCCTGCCCTCTGCC      9392       CAG T
                                GCCCT  G CCCTCTGCC
                                |||||  | |||||||||
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                                CGGGA  C GGGAGACGG
                                  ___ _
GAM361  LOC148132 5' CTGCCCCTCCGGCCTCTTTGCC 9393     G   A  C C
          A                    CTGC CCCTC GGTC CT TGCCA
                               |||| ||||| |||| || |||||
                               GACG GGGAG CCGG GA ACGGT
                                 _   G   A A
GAM361  LOC150095 5' CTGCTCTTCTTCCCCTCTGC  9394     GCCC AGG
                               CTGC   TC  TCCCTCTGC
                               ||||   ||  |||||||||
                               GACG   AG  GGGGAGACG
                                 AGA_ AA_
GAM361  LOC150142 5' CTGCGCCCTCGGGCTGCTCCA 9395         A  CC
                               CTGCGCCCTC GGT CTCTG
                               |||||||||| |||  |||||
                               GACGCGGGAG CCG  GAGGT
                                     C  AC
GAM361  LOC151742 3' CTGCCAGGTCCCTTTGC    9396     GCCCT      C
                               CTGC    CAGGTCCCT TGC
                               ||||    ||||||||| |||
                               GACG    GTCCAGGGA ACG
                                 _____       A
GAM361  LOC153196 5' CTGTCCTCAGACCCTTTGC  9397     CGC     T  C
                               CTG  CCTCAGG CCCT TGC
                               |||  ||||||| |||| |||
                               GAC  GGAGTCT GGGA ACG
                                 A__     _  A
GAM361  LOC157273 5' CTGCCCTCTCAGGTCACC   9398     G _     _
                               CTGC CC CTCAGGTC CC
                               |||| || |||||||| ||
                               GACG GG GAGTCCAG GG
                                 _ A      T
GAM361  LOC164944 5' GCCCAAGTCCCTCTGC     9399     TC
                               GCCC  AGGTCCCTCTGC
                               ||||  ||||||||||||
                               CGGG  TTCAGGGAGACG
                                 __
GAM361  LOC165246 5' CTGGTCCTCAGGTCTTCTG  9400     CGC      CC
                               CTG  CCTCAGGTC  TCTG
                               |||  |||||||||  ||||
                               GAC  GGAGTCCAG  AGAC
                                 CA_      A_
GAM361  LOC165741 3' GCCCTCTGAGCCCCTCTGC  9401       A_
                               GCCCTC  GGTCCCTCTGC
                               ||||||  ||||||||||||
                               CGGGAG  TCGGGGAGACG
                                  AC
GAM361  LOC196707 3' CTGGCCCTCAGGCCTGCC   9402     C       CCCT
                               CTG GCCCTCAGGT   CTGCC
                               ||| ||||||||||   |||||
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                                GAC CGGGAGTCCG    GACGG
                                  _       ____
GAM361   LOC196707 3'  CTGGCCCCCACCTTTCTCTGCC 9403      C      GGTCC
                                CTG GCCCTCA    CTCTGCC
                                ||| |||||||    |||||||
                                GAC CGGGGGT    GAGACGG
                                  _     GGAAA
GAM361   LOC201139 3'  TGTGCCTCAGGTCCTC      9324     C  C      C
                                TG GCC TCAGGTCC TC
                                || ||| |||||||| ||
                                AC CGG AGTCCAGG AG
                                 A  _      _
GAM361   LOC204084 5'  GCCCTCAGCCACTGCC      9404         GTC  T
                                GCCCTCAG   CC CTGCC
                                ||||||||   || |||||
                                CGGGAGTC   GG GACGG
                                    ___  T
GAM361   LOC222112 5'  CTGTCCCTTCGGTGGCCTCTGC 9405     CG   CA   C_
           C                     CTG  CCCT  GGT  CCTCTGCC
                                ||| ||||  |||  ||||||||
                                GAC  GGGA  CCA  GGAGACGG
                                  A_   AG   CC
GAM361   LOC222968 5'  TGGCCGGCCCTCTGC      9406     C  CTCA  T
                                TG GCC    GG CCCTCTGC
                                || |||    || ||||||||
                                AC CGG    CC GGGAGACG
                                 _  _____  _
GAM361   LOC253216 5'  GCCTCTGCACACCTCTGCCA  9407     _  _  G TC
                                GCC CT CA G  CCTCTGCCA
                                ||| || || |  |||||||||
                                CGG GA GT T  GGAGACGGT
                                  A  C  G __
GAM361   LOC255193 5'  CTGCGCCCCTCTCTGC      9408         CAGGTCC
                                CTGCGCCCT      CTCTGC
                                |||||||||      ||||||
                                GACGCGGGG      GAGACG
                                     A_______
GAM361   LOC256310 3'  TGGCCTTCTCCTCTGCC     9409     C  C  AGGTC
                                TG GCC TC     CCTCTGCC
                                || ||| ||     ||||||||
                                AC CGG AG     GGAGACGG
                                 _  A  A_____
GAM361   LOC51195  3'  GCGCCTTTACAGTCTCTGCCA 9410       CTCA_   CC
                                GCGCC    GGTC  TCTGCCA
                                |||||    ||||  |||||||
                                CGCGG    TCAG  AGACGGT
                                   AAATG   __
GAM361   LOC51608  3'  CTGGGCTCTCAGGTCCGAGGGC 9411     C  C       CTCT
           CA                    CTG GC CTCAGGTCC    GCCA
                                ||| || |||||||||    ||||
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                                GAC CG GAGTCCAGG    CGGT
                                  C  A        CTCC
GAM361  LOC54466  3'  CTGTATTCTCACTCCCTCTGTC 9412     CGCC    GG       C
              A                    CTG    CTCA  TCCCTCTG CA
                                  |||    ||||  |||||||| ||
                                  GAC    GAGT  AGGGAGAC GT
                                    ATAA   G_       A
GAM361  LOC56996  3'  TGTGCTGGGGTCCCTCTGCCA  9413     C  CCTCA
                                  TG GC    GGTCCCTCTGCCA
                                  || ||    ||||||||||||
                                  AC CG    CCAGGGAGACGGT
                                   A  ACC__
GAM361  LOC90979  3'  CCGCGCCCAGCCTCCT      9414         TCA   _
                                  CTGCGCCC   GGTC CCT
                                  ||||||||   |||| |||
                                  GGCGCGGG   TCGG GGA
                                       ___    A
GAM362  ACADS     3'  CCCCAGGGAGCCCCCGCCG   9417       TCCCT
                                  CCCCAG    GGCCCCCGCCG
                                  ||||||    ||||||||||
                                  GGGGTC    TCGGGGGCGGC
                                     CC___
GAM362  ADARB1    3'  TCCACCAGTCCCTGGAACCCG  9418     C         CC
                                  TCC CCAGTCCCTGG  CCCG
                                  ||| ||||||||||  ||||
                                  AGG GGTCAGGGACC  GGGC
                                    T         TT
GAM362  AKT1      3'  TCCCCCATCCCTGGTCCC    9419         G     _
                                  TCCCCCA TCCCTGG CCC
                                  ||||||| ||||||| |||
                                  AGGGGGT AGGGACC GGG
                                       _      A
GAM362  ALDH3B1   3'  TCCCACAGAAGCCCCCGC    9420      C   TCCCT
                                  TCCC CAG    GGCCCCCGC
                                  |||| |||    |||||||||
                                  AGGG GTC    TCGGGGGCG
                                    T   T_____
GAM362  ANK1      3'  TCTCCTGGCCCTGGGGGCGCCC 9421     C  CA T   ___   C
              GCCG                   TC CC  G CCCT   GGC CCCGCCG
                                  || ||  | ||||   ||| |||||||
                                  AG GG  C GGGA   CCG GGGCGGC
                                   A  AC _    CCC   C
GAM362  ANK1      3'  TCTCCTGGCCCTGGGGGCGCCC 9421     C  CA T   ___   C
              GCCG                   TC CC  G CCCT   GGC CCCGCCG
                                  || ||  | ||||   ||| |||||||
                                  AG GG  C GGGA   CCG GGGCGGC
                                   A  AC _    CCC   C
GAM362  BLTR2     5'  TCCCCCAGCTCTGGCCCC    9422          CC
                                  TCCCCCAGT  CTGGCCCC
                                  |||||||||  ||||||||
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                                AGGGGGTCG  GACCGGGG
                                     A_
GAM362  BYSL     5'  TCTCCTGTCCCGCGACCCCGCC 9423     C  CA    _      C
              G                   TC CC  GTCCC TGGCCCC GCCG
                                  || ||  ||||| ||||||| ||||
                                  AG GG  CAGGG GCTGGGG CGGC
                                   A  A_    C      _
GAM362  EP300    5'  CCACTGTTCTGGCCCCTGCCG  9424      __ CC       C
                                  CCA  GT  CTGGCCCC GCCG
                                  |||  ||  |||||||| ||||
                                  GGT  CA  GACCGGGG CGGC
                                    GA  A_       A
GAM362  EPHA8    3'  TCCTCTGGTCCCTGATCCTAGG 9425     CCCA      GC  CC_
              CC                    TCC    GTCCCTG  CC   GCC
                                  |||    |||||||  ||   |||
                                  AGG    CAGGGAC  GG   CGG
                                    AGAC      TA  ATC
GAM362  GNL1     5'  CCCCCCGGGGCAGCCCCCGCCG 9426       AGTCCCT
                                  CCCCC      GGCCCCCGCCG
                                  |||||      ||||||||||
                                  GGGGG      TCGGGGGCGGC
                                     GCCCCG_
GAM362  GNL1     5'  CCCCCCGGGGCAGCCCCCGCCG 9426       AGTCCCT
                                  CCCCC      GGCCCCCGCCG
                                  |||||      ||||||||||
                                  GGGGG      TCGGGGGCGGC
                                     GCCCCG_
GAM362  HR       3'  TCCCCTAGCGCCATCCCCTGC  9427       C   C  TGG    C
                                  TCCCC AGT CC   CCCC GC
                                  ||||| ||| ||   |||| ||
                                  AGGGG TCG GG   GGGG CG
                                     A   C  TA_    A
GAM362  HR       3'  TCCCCTAGCGCCATCCCCTGC  9427       C   C  TGG    C
                                  TCCCC AGT CC   CCCC GC
                                  ||||| ||| ||   |||| ||
                                  AGGGG TCG GG   GGGG CG
                                     A   C  TA_    A
GAM362  JUN      5'  GTCTCCGGTCCTCCCCGCCG   9428      C    _  __
                                  GTC CTGG CC  CCCGCCG
                                  ||| |||| ||  |||||||
                                  CAG GGCC GG  GGGCGGC
                                    A    A  AG
GAM362  JUNB     5'  TCCCCCAGCTCCCAGCTCCCTG 9429         TC  TG  _   C
              C                    TCCCCCAG  CC  GC CCC GC
                                  ||||||||  ||  || ||| ||
                                  AGGGGGTC  GG  CG GGG CG
                                       GA  GT  A   A
GAM362  MAN2B1   5'  CCCCGGCCCTGGAAAGGCCG   9430       A T     CCCCC
                                  CCCC G CCCTGG     GCCG
                                  |||| | ||||||     ||||
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                                GGGG C GGGACC    CGGC
                                  C _     TTTC_
GAM362  MPDU1    3'  CCTCCCAGTCCCTCCACTCTGC 9431    _       GG  CCC__
            CG                    CC CCCAGTCCCT  CC    GCCG
                                  || ||||||||||  ||    ||||
                                  GG GGGTCAGGGA  GG    CGGC
                                   A        __  TGAGA
GAM362  MPP6     5'  CCCGGTCGCTCCCCGCCG    9432     A   CCTG  _
                                  CCC GTC    GC CCCCGCCG
                                  ||| |||    || ||||||||
                                  GGG CAG    CG GGGGCGGC
                                    C   ____  A
GAM362  PAPOLA   5'  TCTCCCGCACCGCTCCCGCCG  9433    C   A TC  TG  C
                                  TC CCC G  CC  GC CCCGCCG
                                  || ||| |  ||  || |||||||
                                  AG GGG C  GG  CG GGGCGGC
                                   A  _ GT  __  A
GAM362  ROM1     3'  CCCCAGTCCAGCTCGC      9434          CT   CCC
                                  CCCCAGTCC  GGC   CGC
                                  |||||||||  |||   |||
                                  GGGGTCAGG  TCG   GCG
                                       __   A__
GAM362  TGFB1    5'  CCCCCGGCCGGGGCCCTCGC   9435       A   CCT    C
                                  CCCCC GTC   GGCCC CGC
                                  ||||| |||   ||||| |||
                                  GGGGG CGG   CCGGG GCG
                                     C   CC_    A
GAM362  AGS3     5'  TCCCCCGGCTCCTGGGGCTCGC 9436       A TC    CCCC
            CG                    TCCCCC G  CCTGG    CGCCG
                                  ||||||  |  |||||    |||||
                                  AGGGGG C  GGACC    GCGGC
                                     C GA     CCGA
GAM362  C20orf178 5'  CCCAGTCCCGCCGCTCCCTGCC 9437          TG_  _   C
            G                     CCCAGTCCC   GC CCC GCCG
                                  |||||||||   || ||| ||||
                                  GGGTCAGGG   CG GGG CGGC
                                       CGG  A   A
GAM362  CBCIP2   3'  TCCCCCAGGCTGTCCCCTCGC  9438        TCC   G   _
                                  TCCCCCAG   CTG CCCC CGC
                                  ||||||||   ||| |||| |||
                                  AGGGGGTC   GAC GGGG GCG
                                       C__   A   A
GAM362  DKFZP434H0820 3'  TCTCCCGGTCCTGGCCC     9439     C   A   C
                                  TC CCC GTCC TGGCCC
                                  || ||| |||| ||||||
                                  AG GGG CAGG ACCGGG
                                   A  C   _
GAM362  DKFZP564O0423 3'  TCCCCCAGCCTGCTGGCTGC   9440          C_    CCCC
                                  TCCCCCAGTC  CTGGC    GC
                                  |||||||||  |||||    ||
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                                AGGGGGTCGG  GACCG    CG
                                      AC     A___
GAM362  DKFZP762D096 5'  CCCCGGTCCTGGCCCACCCCGC 9441       A    C     ___
          CG                      CCCC GTCC TGGCCC   CCGCCG
                                  |||| |||| ||||||   ||||||
                                  GGGG CAGG ACCGGG   GGCGGC
                                    C    _      TGG
GAM362  DKFZp762K222 5'  CCCAGCCCCTCCTCGTCG    9442           GGC  C  C
                                  CCCAGTCCCT   CC CG CG
                                  ||||||||||   || || ||
                                  GGGTCGGGGA   GG GC GC
                                        ___  A  A
GAM362  FLJ11618  3'  CCCCAGGTCCTGCCCCC     9443        TC    G
                                  CCCCAG  CCTG CCCCC
                                  ||||||  |||| |||||
                                  GGGGTC  GGAC GGGGG
                                     CA    _
GAM362  HNK-1ST   5'  TCCCCTGGCCCTGGGGGCGCCG 9444       CA T     CCCC
                                  TCCCC  G CCCTGG    CGCCG
                                  |||||  | ||||||    |||||
                                  AGGGG  C GGGACC    GCGGC
                                     AC _     CCC_
GAM362  KIAA0296  3'  TCCCTTGTTCCCTGGCACCCG  9445      CCAG       C
                                  TCCC    TCCCTGGC CCCG
                                  ||||    |||||||| ||||
                                  AGGG    AGGGACCG GGGC
                                    AACA       T
GAM362  KIAA0861  3'  CCCAGTCTGCGGCCCCCGCCG  9446         CC
                                  CCCAGTC  TGGCCCCCGCCG
                                  |||||||  ||||||||||||
                                  GGGTCAG  GCCGGGGGCGGC
                                      AC
GAM362  KIAA0930  3'  CCCATCGCCGGCCCCTGC    9447       G  C       C
                                  CCCA TC CTGGCCCC GC
                                  |||| || |||||||| ||
                                  GGGT AG GGCCGGGG CG
                                    _  C       A
GAM362  KIAA1229  5'  TCTCCACATAAGGCCCCCGCCG 9448     C  _  GTCCCT
                                  TC CC CA     GGCCCCCGCCG
                                  || || ||     ||||||||||||
                                  AG GG GT     CCGGGGGCGGC
                                   A  T  ATT___
GAM362  KIAA1464  5'  CCCCCAGCGCCCCCGCC     9449         CCCTG
                                  CCCCCAGT    GCCCCCGCC
                                  ||||||||    |||||||||
                                  GGGGGTCG    CGGGGGCGG
                                              _____
GAM362  KIAA1754  5'  CCCCGGTCCCGGTCCCCGCCG  9450       A     T  C
                                  CCCC GTCCC GG CCCCGCCG
                                  |||| ||||| || ||||||||
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                                GGGG CAGGG CC GGGGCGGC
                                  C    _ A
GAM362  KIAA1904  3'  TCTCCTGGGCCTTGGCCCCCG  9451    C  CAGT  C
                                TC CC   CC TGGCCCCCG
                                || ||   || |||||||||
                                AG GG   GG ACCGGGGGC
                                 A  ACCC  A
GAM362  LYPLA2   5'  CCCCTCGGCCGCCCCCGCC   9452     AGTC  TG
                                CCCC   CC  GCCCCCGCC
                                ||||   ||  |||||||||
                                GGGG   GG  CGGGGGCGG
                                  AGCC  __
GAM362  MAST205   3'  CCCCCTGGTTCTTGGCCCCTCC 9453      AG__  CC     CG
                                CCCCC   TC  TGGCCCC  CC
                                |||||   ||  |||||||  ||
                                GGGGG   AG  ACCGGGG  GG
                                   ACCA  A_     A_
GAM362  MGC13102  3'  TCCCCTGGTCCTGGCCCC    9454      CA   C
                                TCCCC  GTCC TGGCCCC
                                |||||  ||||  |||||||
                                AGGGG  CAGG ACCGGGG
                                   AC   _
GAM362  MGC2452   5'  CCCAGTCCCGCTCCTGCCG   9455        TG  C  C
                                CCCAGTCCC  GC CC GCCG
                                |||||||||  || || ||||
                                GGGTCAGGG  CG GG CGGC
                                     __  A  A
GAM362  PACSIN2   3'  TCCCCCACGTTCCCCCCACCCC 9456       _ __   G
          CGCCG                   TCCCCCA GT  CCCT GCCCCCGCCG
                                |||||||  ||  ||||  ||||||||||
                                AGGGGGT CA  GGGG TGGGGGCGGC
                                    G  AG   G
GAM362  PDCD4    5'  ATCCCTCGGGCCCCCGCC    9457       __
                                GTCCCT  GGCCCCCGCC
                                ||||||  ||||||||||
                                TAGGGA  CCGGGGGCGG
                                   GC
GAM362  SRF      3'  TCCCCTGCTCTCTGGCCCC   9458      CAG  C
                                TCCCC   TC CTGGCCCC
                                |||||   || ||||||||
                                AGGGG   AG GACCGGGG
                                   ACG  A
GAM362  STIM2    5'  TCCTCCGGCCGCCCCCGCCG  9459     C  A   CCTG
                                TCC CC GTC   GCCCCCGCCG
                                ||| || |||   ||||||||||
                                AGG GG CGG   CGGGGGCGGC
                                  A  C  _____
GAM362  TGOLN2   5'  CCAGTCCCGCCCCTGC     9460        TG    C
                                CCAGTCCC  GCCCC GC
                                ||||||||  ||||| ||
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                                GGTCAGGG  CGGGG CG
                                   __     A
GAM362   LOC121536 5'  TCCCCCAGTCCCGTAGCCCTCG 9461            _     C  C
           TCG                    TCCCCCAGTCCC TGGCCC CG CG
                                  |||||||||||| |||||| || ||
                                  AGGGGGTCAGGG ATCGGG GC GC
                                        C     A  A
GAM362   LOC124801 3'  TCCCCCGGCCTGCCTCCGC   9462        AGTC    G  C
                                  TCCCCC    CCTG CC CCGC
                                  ||||||    |||| || ||||
                                  AGGGGG    GGAC GG GGCG
                                     CC__    _  A
GAM362   LOC126066 5'  CCCAGTCCTCCCTACGGCTCCT 9463          _ _____  C  C
           GC                     CCCAGTCC CT    GGC CC GC
                                  |||||||| ||    ||| || ||
                                  GGGTCAGG GG    CCG GG CG
                                       A  GATG   A  A
GAM362   LOC145601 3'  TCCCCCAGGCCTTGGCAGGTCC 9464          T  C    C___  C
           TGCCG                    TCCCCCAG CC TGGC    CC GCCG
                                  |||||||| || ||||    || ||||
                                  AGGGGGTC GG ACCG    GG CGGC
                                       C  A    TCCA  A
GAM362   LOC148029 5'  TCACCCTAGTCCTAGCCCTGCC 9465     _  C     C     CC
           G                       TC CCC AGTCC TGGCCC  GCCG
                                  || ||| ||||| ||||||  ||||
                                  AG GGG TCAGG ATCGGG  CGGC
                                   T   A    _     A_
GAM362   LOC149077 5'  AGTCCCTACCCTGCCG      9466          G   CC
                                  AGTCCCTG CCC  GCCG
                                  ||||||||| |||  ||||
                                  TCAGGGAT GGG  CGGC
                                       _   A_
GAM362   LOC149319 3'  CCCTAGCCCTGGCTCTTGCC   9467      C  T      CCCC
                                  CCC AG CCCTGGC    GCC
                                  ||| || |||||||    |||
                                  GGG TC GGGACCG    CGG
                                    A  _      AGAA
GAM362   LOC158062 3'  CCTCTGTGGCTCTCCCCGCCG  9468     AG  CC    ___
                                  CC  TC  TGGC   CCCCGCCG
                                  ||  ||  ||||   ||||||||
                                  GG  AG  ACCG   GGGGCGGC
                                   __  AC    AGA
GAM362   LOC201507 3'  CCCCCGGCGGCCCTTGCC    9469       A  CCCT    CC
                                  CCCCC GT    GGCCC  GCC
                                  ||||| ||    |||||  |||
                                  GGGGG CG    CCGGG  CGG
                                     C  _____     AA
GAM362   LOC220514 3'  TCCCCCACGTTCCCCCCACCCC 9456          _ __    G
           CGCCG                    TCCCCCA GT  CCCT GCCCCCGCCG
                                  ||||||| ||  |||| ||||||||||
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                                AGGGGGT CA  GGGG TGGGGGCGGC
                                    G  AG    G
GAM362  LOC257541 5'  CCCCCCGGGGCAGCCCCCGCCG 9426       AGTCCCT
                                CCCCC      GGCCCCCGCCG
                                |||||      ||||||||||
                                GGGGG      TCGGGGGCGGC
                                   GCCCCG_
GAM362  LOC56961  5'  CCCCCAGTCCCGCGGCCCCCGC 9470          _
           CG                     CCCCCAGTCCC TGGCCCCCGCCG
                                  |||||||||| ||||||||||
                                  GGGGGTCAGGG GCCGGGGGCGGC
                                        C
GAM363  DVL1     3'  GCGGGCCATGGTCCCTCC    9473            G
                                  GCGGGCCATGGTC CCTTC
                                  |||||||||||| |||||
                                  CGCCCGGTACCAG GGAGG
                                                _
GAM363  POLR2J   3'  GCGGGCCATGGCTGGGACC   9474           CGCCTTC
                                  GCGGGCCATGGT      GACC
                                  ||||||||||||      ||||
                                  CGCCCGGTACCG      CTGG
                                        ACC_____
GAM363  CHODL    5'  GCGCGCATCGCCTTCGGCC   9475      G  CATG        A
                                  GCG GC    GTCGCCTTCG CC
                                  ||| ||    |||||||||| ||
                                  CGC CG    TAGCGGAAGC GG
                                    G  _____         C
GAM363  KIAA1084 3'  GCAGGCCATGCCTTTTGGCCA  9476          GGTC    CGA_
                                  GCGGGCCAT    GCCTT    CCA
                                  |||||||||    |||||    |||
                                  CGTCCGGTA    CGGAA    GGT
                                        _____     AACC
GAM363  MARK2    5'  GCTGGGCTGTGCCGCCTTTCGG 9477     _    CATG       _  A
           CC                       GC GGGC    GTCGCCTT CG CC
                                    || ||||    |||||||| || ||
                                    CG CCCG    CGGCGGAA GC GG
                                     A    ACA_       A  C
GAM364  LAMP2    3'  TCTAAATTTTAAAAAGCTT    9480          A
                                  TCTAAATTT AAAAAGTTT
                                  |||||||||  |||||||||
                                  AGATTTAAA TTTTTCGAA
                                        A
GAM364  FLJ11220 3'  TCAAAATTTAAAAAAGTT     9481      T
                                  TC AAATTTAAAAAAGTT
                                  || ||||||||||||||
                                  AG TTTAAATTTTTTCAA
                                   T
GAM364  FLJ14600 3'  TAAATTTAAAAAGTTTATA    9482            A
                                  TAAATTTAAAAA GTTTATA
                                  ||||||||||||  |||||||
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                                ATTTAAATTTTT CAAATAT
                                          _
GAM364  PIP3-E   3'  TCTAAATTTAAGAGCTCAT   9483          AAA
                                TCTAAATTTAA  AGTTTAT
                                ||||||||||  |||||||
                                AGATTTAAATT  TCGAGTA
                                      C__
GAM364  SGP28    3'  TAAATCACAAAGTTTATATA  9484       TAAA
                                TAAATT   AAAGTTTATATA
                                ||||||   ||||||||||||
                                ATTTAG   TTTCAAATATAT
                                   TG__
GAM364  SRF      3'  TCTTAATTTAAAAAAGTT    9485     A
                                TCT AATTTAAAAAAGTT
                                ||| ||||||||||||||
                                AGA TTAAATTTTTTCAA
                                  A
GAM364  TRIM2    3'  TCTAAATTTTAAGAAGTCCTAT 9486         A  A    _
           ATA                   TCTAAATTT AA AAGTT TATATA
                                ||||||||| || ||||| |||||||
                                AGATTTAAA TT TTCAG ATATAT
                                     A  C    G
GAM364  LOC149103 3'  TCCAAATTTGAAAAAAATTTAT 9487          _
           A                     TCTAAATTT AAAAAAGTTTATA
                                ||||||||| ||||||||||||||
                                AGGTTTAAA TTTTTTTAAATAT
                                     C
GAM365  PTPN22   3'  GAAGATTTACAAGGTATAC   9490          TATCT
                                GAAGATTTAT   GTATAC
                                ||||||||||   ||||||
                                CTTCTAAATG   CATATG
                                     TTC__
GAM365  KIAA0820 3'  TTAGAAAATTTTGTAT     9491          ATTATC
                                TTAGAAGATTT    TGTAT
                                ||||||||||    |||||
                                AATCTTTTAAA    ACATA
                                          _______
GAM365  KIAA0831 3'  TTAAAAGATTTATTGCAGTA  9492            ATCT
                                TTAGAAGATTTATT   GTA
                                ||||||||||||||   |||
                                AATTTTCTAAATAA   CAT
                                       CGT_
GAM365  KIAA1726 3'  TTAGAAGCATTTACTGTATAC 9493        _   TTAT
                                TTAGAAG ATTTA   CTGTATAC
                                ||||||| |||||   ||||||||
                                AATCTTC TAAAT   GACATATG
                                   G   _____
GAM365  MESDC2   3'  TTAGAAATGACATCTGTATA  9494        ATTTAT
                                TTAGAAG    TATCTGTATA
                                |||||||    ||||||||||
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                                AATCTTT     GTAGACATAT
                                   ACT___
GAM365  RPS27L   3'  TAGGAGATTACTGCTGTATAC  9495      A    T   AT
                                TAG AGATT ATT  CTGTATAC
                                ||| ||||| |||  ||||||||
                                ATC TCTAA TGA  GACATATG
                                  C    _  C_
GAM365  LOC146987 3'  TTAGAGATTTATTCCACTG   9496       A       AT_
                                TTAGA GATTTATT   CTG
                                ||||| ||||||||   |||
                                AATCT CTAAATAA   GAC
                                   _       GGT
GAM366  CHES1    3'  TGACAATTCCAGTGGCTTTC   9499           ATAC
                                TGACAATTCCGG    CTTTT
                                ||||||||||||    |||||
                                ACTGTTAAGGTC    GAAAG
                                      ACC_
GAM366  CUL4B    3'  TATGACAATTCATTTCTCTTTT 9500          CGGATAC
              C                  TATGACAATTC      CTTTTC
                                ||||||||||       ||||||
                                ATACTGTTAAG      GAAAAG
                                      TAAAGA_
GAM366  DTNA     3'  ATGACAATTCGTTCCCTTTTC  9501          C GATA
                                ATGACAATTC G    CCTTTTC
                                ||||||||| |    |||||||
                                TACTGTTAAG C    GGAAAAG
                                   _ AAG_
GAM366  DTNA     3'  ATGACAATTCGTTCCCTTTTC  9501          C GATA
                                ATGACAATTC G    CCTTTTC
                                ||||||||| |    |||||||
                                TACTGTTAAG C    GGAAAAG
                                   _ AAG_
GAM366  DTNA     3'  ATGACAATTCGTTCCCTTTTC  9501          C GATA
                                ATGACAATTC G    CCTTTTC
                                ||||||||| |    |||||||
                                TACTGTTAAG C    GGAAAAG
                                   _ AAG_
GAM366  DTNA     3'  ATGACAATTCGTTCCCTTTTC  9501          C GATA
                                ATGACAATTC G    CCTTTTC
                                ||||||||| |    |||||||
                                TACTGTTAAG C    GGAAAAG
                                   _ AAG_
GAM366  HNRPDL   3'  CATAACCAAGATACCTTTTC   9502       AATTCC
                                TATGAC     GGATACCTTTTC
                                ||||||     ||||||||||||
                                GTATTG     TCTATGGAAAAG
                                   GT_____
GAM366  RFPL1    5'  TGACAAGTGACAACCTTTTC   9503       TTCCG   _
                                TGACAA     GATA CCTTTTC
                                ||||||     |||| |||||||
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                                ACTGTT    CTGT GGAAAAG
                                   CA___   T
GAM366  RFPL2    5'  TGACAAGTGACAACCTTTTC  9503      TTCCG  _
                                TGACAA    GATA CCTTTTC
                                ||||||    |||| |||||||
                                ACTGTT    CTGT GGAAAAG
                                   CA___   T
GAM366  RFPL3    5'  TGACAAGTGACAACCTTTTC  9503      TTCCG  _
                                TGACAA    GATA CCTTTTC
                                ||||||    |||| |||||||
                                ACTGTT    CTGT GGAAAAG
                                   CA___   T
GAM366  FLJ10900 3'  TGACAACTTCGATTCTTTTC  9504       C  ATAC
                                TGACAATT CGG   CTTTTC
                                |||||||| |||   ||||||
                                ACTGTTGA GCT   GAAAAG
                                    A  AA__
GAM366  FLJ10900 3'  TGACAACTTCGATTCTTTTC  9504       C  ATAC
                                TGACAATT CGG   CTTTTC
                                |||||||| |||   ||||||
                                ACTGTTGA GCT   GAAAAG
                                    A  AA__
GAM366  KIAA0182 3'  GACAGTTCTTACCTTTT    9505     A  CGGA
                                GACA TTC   TACCTTTT
                                |||| |||   ||||||||
                                CTGT AAG   ATGGAAAA
                                  C  A___
GAM366  SYNJ2    3'  CAATTCCAATTGTCCTTTT   9506       ATA_
                                CAATTCCGG   CCTTTT
                                |||||||||   ||||||
                                GTTAAGGTT   GGAAAA
                                     AACA
GAM366  TNK1     3'  ATGGCAGTTCCGGATGGCTGTT 9507    A  A     AC  T
           C                     ATG CA TTCCGGAT  CT TTC
                                ||| || ||||||||  || |||
                                TAC GT AAGGCCTA  GA AAG
                                  C  C      CC  C
GAM366  LOC147658 3'  TGCAATTCGATCACCTTTT   9508    A    C  A
                                TG CAATTC GG TACCTTTT
                                || |||||| || ||||||||
                                AC GTTAAG CT GTGGAAAA
                                 _    _  A
GAM366  LOC51301 3'  TATGGAATTTTGGACACCTTTT 9509     AC   CC
                                TATG  AATT  GGATACCTTTT
                                ||||  ||||  ||||||||||||
                                ATAC  TTAA  CCTGTGGAAAA
                                  C_   AA
GAM367  GLRB     3'  TGCCATTCAAAATTAAGGTGCC 9512      _   GATC
                                TGCTAT CGGGA   AAGGTGCC
                                |||||| |||||   ||||||||
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                                ACGGTA GTTTT   TTCCACGG
                                   A    AA__
GAM367  IL1A     3'  TGCTATTGTGGAGGATGC    9513       CG_   ATCAA
                                TGCTAT   GGAG    GGTGC
                                ||||||   ||||    |||||
                                ACGATA   CCTC    CTACG
                                   ACA   _____
GAM367  IQGAP1   3'  TGTATCAGATTGAGGTGC    9514    C   GGG   CA
                                TG TATC   AGAT  AGGTGC
                                || ||||   ||||  ||||||
                                AC ATAG   TCTA  TCCACG
                                 _   ___    AC
GAM367  EIF4B    3'  TGCAAACCAAGATCAAGGTG  9515     T_   GG
                                TGC  ATC  GAGATCAAGGTG
                                |||  |||  ||||||||||||
                                ACG  TGG  TTCTAGTTCCAC
                                  TT  __
GAM367  FLJ22059 5'  TGCTATGGTCTCCAAGGTGC  9516       C  GAGA
                                TGCTAT GG    TCAAGGTGC
                                |||||| ||    |||||||||
                                ACGATA CC    GGTTCCACG
                                   _ AGA_
GAM367  KIAA0186 3'  TGCAATCTCAATCAAGGTGCC  9517     T   GGGA
                                TGC ATC    GATCAAGGTGCC
                                ||| |||    ||||||||||||
                                ACG TAG    TTAGTTCCACGG
                                  T   AG__
GAM367  P114-RHO-GEF 5'  TGCCATCGGACAGGAGGGTGCC 9518          AGATCAA
                                TGCTATCGGG      GGTGCC
                                ||||||||||      ||||||
                                ACGGTAGCCT      CCACGG
                                     GTCCTC_
GAM367  SCGB1D2  3'  TGCAGTGAAGATCAGGGTG   9519     TATCG      A
                                TGC    GGAGATCA GGTG
                                |||    |||||||| ||||
                                ACG    CTTCTAGT CCAC
                                  TCA__       C
GAM367  ZNFN1A2  5'  CTGTCGGGAGATCTCAGC    9520     A        AA
                                CT TCGGGAGATC  GGT
                                || ||||||||||  |||
                                GA AGCCCTCTAG  TCG
                                 C         AG
GAM367  LOC147054 5'  TCAGTCCAAGATCAAGGTG   9521      ___
                                TCGG   GAGATCAAGGTG
                                ||||   ||||||||||||
                                AGTC   TTCTAGTTCCAC
                                  AGG
GAM367  LOC169426 5'  TGCTGTCAGGAGAGGC      9522       A       TCAA
                                TGCT TCGGGAGA    GGT
                                |||| ||||||||    |||
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                                ACGA AGTCCTCT    CCG
                                  C      ____
GAM367  LOC221683 3'  GCTAGAGATCAGGGTGC     9523      ATCG       A
                                GCT    GGAGATCA GGTGC
                                |||    |||||||| |||||
                                CGA    TCTCTAGT CCACG
                                 ____       C
GAM368  CBFA2T2   3'  TACATTATTGGCTTTCTTTTGT 9526           CCGAG__  C
          GAGC                    TATATTATTGGC      TG GAGC
                                |||||||||||       || ||||
                                ATGTAATAACCG      AC CTCG
                                      AAAGAAA  A
GAM368  CHRNA3    3'  TATGTCATTGGCATCTAGTG   9527      A       CCG_
                                TAT TTATTGGC    AGTG
                                ||| ||||||||    ||||
                                ATA AGTAACCG    TCAC
                                  C       TAGA
GAM368  NEBL      3'  TATTATTGGCTGCATTACAGAG 9528          CCGAG  _
                                TATTATTGGC     TGC GAG
                                ||||||||||     ||| |||
                                ATAATAACCG     ATG CTC
                                      ACGTA   T
GAM368  FLJ00024  3'  TAATTATTAGGCTGAGTG    9529    T     _  CC
                                A ATTATT GGC  GAGTG
                                | |||||| |||  |||||
                                A TAATAA CCG  CTCAC
                                 T     T   A_
GAM368  ZWINT     3'  CATGTTATTGGCTTCTGAGT   9530      A       CC__
                                TAT TTATTGGC    GAGT
                                ||| ||||||||    ||||
                                GTA AATAACCG    CTCA
                                  C       AAGA
GAM368  ZWINT     3'  CATGTTATTGGCTTCTGAGT   9530      A       CC__
                                TAT TTATTGGC    GAGT
                                ||| ||||||||    ||||
                                GTA AATAACCG    CTCA
                                  C       AAGA
GAM369  CDC25B    5'  GGCAGAAGGCTGGCTGGA    9533          C   CGGTC
                                GGCAGAAGGC GGC     GGA
                                |||||||||| |||     |||
                                CCGTCTTCCG CCG     CCT
                                      A   A_____
GAM369  CDC25B    5'  GGCAGAAGGCTGGCTGGA    9533          C   CGGTC
                                GGCAGAAGGC GGC     GGA
                                |||||||||| |||     |||
                                CCGTCTTCCG CCG     CCT
                                      A   A_____
GAM369  DGCR2     3'  TGGCAGAAGGCGGGCTGTGG  9534          C   CG  C
                                TGGCAGAAGGC GGC  GT GG
                                |||||||||| |||  || ||
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                                ACCGTCTTCCG CCG  CA CC
                                      C   A_ _
GAM369  FACL5    5'  GGCAGAAGGCCGGCCCAGAG  9535            GGT
                                GGCAGAAGGCCGGCC  CGGAG
                                |||||||||||||||  |||||
                                CCGTCTTCCGGCCGG  GTCTC
                                                 ___
GAM369  KCNK4    5'  TGGCAGAGGAGCCGGAGAG  9536       A  CC    TC
                                TGGCAGA GG  GGCCGG  GGAG
                                |||||||  ||  ||||||  ||||
                                ACCGTCT CC  TCGGCC  TCTC
                                    _ __    __
GAM369  LIMK1    3'  TGGCAGGTGGCCGGCCAG    9537       AA
                                TGGCAG  GGCCGGCCGG
                                ||||||  ||||||||||
                                ACCGTC  CCGGCCGGTC
                                   CA
GAM369  LMO1     5'  TGGCGGGGCGGCCGGTC    9538      AGAA  C
                                TGGC   GGC GGCCGGTC
                                ||||   ||| ||||||||
                                ACCG   CCG CCGGCCAG
                                  CC__  _
GAM369  PGM1     5'  TGGCGGAGGGGCGGCCGG    9539      A  A  C
                                TGGC GA GG CGGCCGG
                                |||| || || |||||||
                                ACCG CT CC GCCGGCC
                                  C  C  C
GAM369  PPP4C    3'  TGGTGCGAGGGCCAGAAGGGTT 9540     CA_  A    CC_  C
           GGAG                    TGG  GA GGCCGG  GGT GGAG
                                |||  || ||||||  ||| ||||
                                ACC  CT CCGGTC  CCA CCTC
                                  ACG  C    TTC  A
GAM369  C22orf23  3'  TGGCAGAAGGCTGGTAGCTCCG 9541        C G_________  GGTC
           ACCGG                   CAGAAGGC G       CC   GG
                                |||||||| |       ||   ||
                                GTCTTCCG C       GG   CC
                                   A CATCIIIGA  CTGG
GAM369  DKFZP761F241 3'  TGGCAGAAGCTTGGCCGTGTGA 9542         GCC   GTCG
           G                    TGGCAGAAG  GGCCG   GAG
                                |||||||||  |||||   |||
                                ACCGTCTTC  CCGGC   CTC
                                     GAA    ACA_
GAM369  EPN2     3'  TGGCAGAAGGTGGCTGG    9543          CC  C
                                TGGCAGAAGG  GGC GG
                                ||||||||||  ||| ||
                                ACCGTCTTCC  CCG CC
                                     A_  A
GAM369  FBXO9    5'  TAGCAGAGTTCTCGGTCGGAG  9544        A GCCGGC
                                TGGCAGA G    CGGTCGGAG
                                |||||||  |    |||||||||
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                                ATCGTCT C     GCCAGCCTC
                                   _ AAGA__
GAM369  FLJ20195  3'  TGGTGGAAGGTAGGCTGGGGCG 9545     CA    CC   C  T_
           G                     TGG  GAAGG  GGC GG  CGG
                                 |||  |||||  ||| ||  |||
                                 ACC  CTTCC  CCG CC  GCC
                                   AC    AT   A  CC
GAM369  FLJ22021  3'  TGGTGGGGGGGCCAGCCCCCAAG 9546     CAGAA      GG  G
                                 TGG    GGCCGGCC  TC GAG
                                 |||    ||||||||  || |||
                                 ACC    CCGGTCGG  GG TTC
                                   ACCCC       __  G
GAM369  HUMAGCGB  5'  TGGTGGAAGAGCCGGTCCTCGA 9547     CA   _    _ GG
                                 TGG  GAAG GCCGG CC  TCGG
                                 |||  |||| ||||| ||  ||||
                                 ACC  CTTC CGGCC GG  AGCT
                                   AC   T    A __
GAM369  KIAA0562  5'  TGGAGAGGGCGGCTAGGTCGGA 9548     C   A   C   C_
           G                     TGG AGA GGC GGC  GGTCGGAG
                                 ||| ||| ||| |||  ||||||||
                                 ACC TCT CCG CCG  CCAGCCTC
                                   _  C   _  AT
GAM369  KIAA0652  3'  GGCAGGAGGCCGGCAGCAGGAG 9549       A      C   C
                                 GGCAG AGGCCGGC GGT GGAG
                                 ||||| |||||||| ||| ||||
                                 CCGTC TCCGGCCG TCG CCTC
                                    C       _  T
GAM369  KIAA0677  3'  TGGCAGAAGCTGGTCCAG    9550          G C  _
                                 TGGCAGAAG C GG CCGG
                                 ||||||||| | || ||||
                                 ACCGTCTTC G CC GGTC
                                       _ A  A
GAM369  KIAA1196  3'  TGCCAGAAGGCTGAACACTGGA 9551     G       C GC  GTC
           G                     TG CAGAAGGC G  CG   GGAG
                                 || ||||||||  |  ||   ||||
                                 AC GTCTTCCG C  GT   CCTC
                                  G       A TT  GA_
GAM369  KIAA1881  3'  TGGCAGGAGAGCTGGGCGGGAG 9552       A  _  C  C   TCG
                                 TGGCAG AG GC GG CGG   GAG
                                 |||||| || || || |||   |||
                                 ACCGTC TC CG CC GCC   CTC
                                    C  T  A  C  ___
GAM369  MAD3     5'  TGGCGGCGGGCCGGCCTAGG   9553      AGAA  C      __
                                 TGGC   GGC GGCCGGTC  GG
                                 ||||   ||| ||||||||  ||
                                 ACCG   CCG CCGGCCGG  CC
                                   ____  C       AT
GAM369  SPRY4    5'  GCAGACGCCGGTCGGA      9554       AGGCCG
                                 GCAGA     GCCGGTCGGA
                                 |||||     ||||||||||
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                                CGTCT     CGGCCAGCCT
                                  G_____
GAM369  LOC145255 3'  TGGCAGAAGGCTGTGG      9555          CGGCCG  C
                                TGGCAGAAGGC     GT GG
                                ||||||||||     || ||
                                ACCGTCTTCCG     CA CC
                                      A_____  _
GAM369  LOC152586 5'  GCGGGAGGCCGGCGGGTGGAG  9556     AGA       C   C
                                GC   AGGCCGGC GGT GGAG
                                ||   |||||||| ||| ||||
                                CG   TCCGGCCG CCA CCTC
                                 CCC       C  _
GAM369  LOC157349 3'  TGGCAGGAGGGCTGGTCAGAG  9557        A   CCG  C
                                TGGCAG AGG   GC GGTCGGAG
                                |||||| |||   || ||||||||
                                ACCGTC TCC   CG CCAGTCTC
                                   C   ___  A
GAM369  LOC199745 3'  TGGCAGAAGCCTGGTACCCAGG 9558          G  _  ___    TC
          GG                      TGGCAGAAG CC GG   CCGG  GG
                                |||||||| || ||   ||||  ||
                                ACCGTCTTC GG CC   GGTC  CC
                                      _  A  ATG    C_
GAM369  LOC200213 5'  GGCAGGAGGCTGGCCGGCCCGG 9559       A    C       _
                                GGCAG AGGC GGCCGGTC GG
                                ||||| |||| |||||||| ||
                                CCGTC TCCG CCGGCCGG CC
                                   C    A       G
GAM369  LOC51185  3'  TGTAGAAGGCCGGCCTATCAG  9560     GC          G
                                TG  AGAAGGCCGGCC GTCGG
                                ||  ||||||||||| |||||
                                AC  TCTTCCGGCCGG TAGTC
                                 A_          A
GAM370  ALOX12B   5'  GGAGCCCAGCTGGTGGTGAGTG 9563      C     ____      CA
          AGCA                     GGA CCCGGC    GGTGAG  AGCA
                                ||| ||||||    ||||||  ||||
                                CCT GGGTCG    CCACTC  TCGT
                                  C      ACCA     AC
GAM370  CLTCL1    5'  GGGACCTCGGCGGCGGC     9564    A    C       A
                                G GGACC CGGCGGTG GC
                                | ||||| |||||||| ||
                                C CCTGG GCCGCCGC CG
                                _     A       _
GAM370  COL6A1    3'  GAGGACCCTGCACAAAGCAGGC 9565          CG   GT    A
          A                      GAGGACCC  GCG  GAGCA GCA
                                ||||||||  |||  ||||| |||
                                CTCCTGGG  CGT  TTCGT CGT
                                     A_   GT    C
GAM370  CRYBA2    5'  GAGGGCATTCACCGGGTGGGTG 9566       ACC_____    C__
          AGC                      GAGG      CCGG   GGTGAGC
                                ||||      ||||   |||||||
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                                CTCC      GGCC   CCACTCG
                                  CGTAAGT    CAC
GAM370  DLX2    3'  GGCCCCGGGAGTGAGCA     9567     A     C
                                GG CCCCGG GGTGAGCA
                                || |||||| ||||||||
                                CC GGGGCC TCACTCGT
                                 _     C
GAM370  DLX2    3'  GAACCCCGGCTCGGGGTAAGCA 9568          ____
                                GGACCCCGGC    GGTGAGCA
                                ||||||||||    ||||||||
                                CTTGGGGCCG    CCATTCGT
                                      AGCC
GAM370  EIF4G1  3'  AAGGACCCCAGGGGCAGGC   9569          C   GA
                                GAGGACCCCGG GGT  GC
                                |||||||||| |||  ||
                                TTCCTGGGGTC CCG  CG
                                       C   TC
GAM370  ESPN    3'  AAGGGTCCCGGCAGCGAG    9570      AC
                                GAGG  CCCGGCGGTGAG
                                ||||  ||||||||||||
                                TTCC  GGGCCGTCGCTC
                                  CA
GAM370  EXTL1   5'  GAGGCCTCTGCCAGCAAGC   9571      A  CCGGCG  G
                                GAGG CC     GT AGCAAGC
                                |||| ||     || |||||||
                                CTCC GG     CG TCGTTCG
                                  _  AGA___  G
GAM370  FDX1    5'  GAGGGCCGCGGCGAGGGGC   9572      A  CCG      CAA
                                GAGG CC   GCGGTGAG   GC
                                |||| ||   ||||||||   ||
                                CTCC GG   CGCCGCTC   CG
                                  C ___       CC_
GAM370  FUT3    3'  GAGGTTCCCGGCAGCCCAGGCA 9573      AC       GAG  A
                                GAGG  CCCGGCGGT   CA GCA
                                ||||  |||||||||   || |||
                                CTCC  GGGCCGTCG   GT CGT
                                  AA        G__  C
GAM370  GFRA2   3'  GGGTCCCCAGAGTGGGCA    9574    A  A     C    A
                                G GG CCCCGG GGTG GCA
                                | || |||||| |||| |||
                                C CC GGGGTC TCAC CGT
                                 _ A     _    C
GAM370  GNA11   5'  GGACCCGGCGGCTCGCCAGGC  9575       C     GA  AA_
                                GGACCC GGCGGT  GC   GC
                                |||||| ||||||  ||   ||
                                CCTGGG CCGCCG  CG   CG
                                    _     AG  GTC
GAM370  HPN     3'  GAGGACCCTGGAGGGAG     9576         C  C  T
                                GAGGACCC GG GG GAG
                                |||||||| || || |||
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                                CTCCTGGG CC CC CTC
                                     A  T  _
GAM370  HTR6    5'  GAGGGCCCCGGCGAAGC     9577       A       GT
                                GAGG CCCCGGCG  GAGC
                                |||| ||||||||  ||||
                                CTCC GGGGCCGC  TTCG
                                  C       __
GAM370  ITGA3   5'  GGGGTCCCGGCGAGAGC     9578    A  AC       T
                                G GG  CCCGGCGG GAGC
                                | ||  |||||||| ||||
                                C CC  GGGCCGCT CTCG
                                 _  CA       _
GAM370  ITGA3   5'  GGGGTCCCGGCGAGAGC     9578    A  AC       T
                                G GG  CCCGGCGG GAGC
                                | ||  |||||||| ||||
                                C CC  GGGCCGCT CTCG
                                 _  CA       _
GAM370  JAM2    5'  GAGGGTCCCGGCGGCAGGAGC  9579       AC       __
                                GAGG  CCCGGCGGT  GAGC
                                ||||  |||||||||  ||||
                                CTCC  GGGCCGCCG  CTCG
                                  CA        TC
GAM370  JJAZ1   5'  GGCCCCGGAGAGCAAGC     9580     A     CGGT
                                GG CCCCGG    GAGCAAGC
                                || ||||||    ||||||||
                                CC GGGGCC    CTCGTTCG
                                 _     T____
GAM370  JPH3    3'  GGGACCCACAGTGAGTGGGCA  9581    A     CG       CAA
                                G GGACCC  GCGGTGAG   GCA
                                | ||||||  ||||||||   |||
                                C CCTGGG  TGTCACTC   CGT
                                 _     __       ACC
GAM370  MCM7    3'  GAGGACCCCAGGGTTGCAAGCA 9582           C   GA
                                GAGGACCCCGG GGT  GCAAGCA
                                |||||||||||  |||  |||||||
                                CTCCTGGGGTC CCA  CGTTCGT
                                       _  A_
GAM370  NF2     5'  GAGGACCCTGCCTGAGC     9583         CG  GG
                                GAGGACCC  GC  TGAGC
                                ||||||||  ||  |||||
                                CTCCTGGG  CG  ACTCG
                                     A_  G_
GAM370  RAB3B   3'  GAGAACCCCAGGGGCAGGCA  9584           C   GA
                                GAGGACCCCGG GGT  GCA
                                |||||||||||  |||  |||
                                CTCTTGGGGTC CCG  CGT
                                       C   TC
GAM370  SLC19A2 3'  AGGACTTTGGTGATAAGCA   9585       CCC  C
                                AGGAC   GG GGTGAGCA
                                |||||   || ||||||||
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                                TCCTG   CC CTATTCGT
                                   AAA  A
GAM370  SLC25A1  3'  GAGGACCCAGGCCACACGGGCA 9586         C   G __  A
                                GAGGACCC GGC G  TG GCA
                                |||||||| ||| |  || |||
                                CTCCTGGG CCG T  GC CGT
                                    T   G GT  C
GAM370  SSRP1    5'  GAGGGCCCCGGCGCGAGAGGTG 9587      A      G   CAA___
           GGC                    GAGG CCCCGGCG TGAG     GC
                                |||| |||||||| ||||     ||
                                CTCC GGGGCCGC GCTC     CG
                                  C       _    TCCACC
GAM370  TBX1     5'  GAGGACCCTGAGCCCTGGTGGG 9588         C _  ___   A
           C                     GAGGACCC G GC   GGTG GC
                                |||||||| | ||   |||| ||
                                CTCCTGGG C CG   CCAC CG
                                    A T  GGA   C
GAM370  TBX1     5'  GAGGACCCTGAGCCCTGGTGGG 9588         C _  ___   A
           C                     GAGGACCC G GC   GGTG GC
                                |||||||| | ||   |||| ||
                                CTCCTGGG C CG   CCAC CG
                                    A T  GGA   C
GAM370  TBX1     5'  GAGGACCCTGAGCCCTGGTGGG 9588         C _  ___   A
           C                     GAGGACCC G GC   GGTG GC
                                |||||||| | ||   |||| ||
                                CTCCTGGG C CG   CCAC CG
                                    A T  GGA   C
GAM370  TRPC6    3'  GGATCCACAGAGCAGGC     9589     C  CG   GT    A
                                GGA CC  GCG  GAGCA GC
                                ||| ||  |||  ||||| ||
                                CCT GG  TGT  CTCGT CG
                                  A __  __    C
GAM370  VEGF     3'  GAGGACCCTGGCCCCACCAAG  9590         C   GG  AG
                                GAGGACCC GGC  TG  CAAG
                                |||||||| |||  ||  ||||
                                CTCCTGGG CCG  GT  GTTC
                                    A   GG  G_
GAM370  WNT6     5'  GAGGGATCCGGCGGCGGC    9591      ACC       A
                                GAGG   CCGGCGGTG GC
                                ||||   |||||||||| ||
                                CTCC   GGCCGCCGC CG
                                  CTA       _
GAM370  ADPRTL3  3'  AGGACCCCGGGGGGACAGGGCGG 9592          C  T  ____  AA
           GCA                    AGGACCCCGG GG GA   GC  GCA
                                |||||||||| || ||   ||  |||
                                TCCTGGGGCC CC CT   CG  CGT
                                    _ _  GTCC  CC
GAM370  CDH22    3'  GGGGCCCCGGCGTGTGCTGGGC 9593    A  A      _   AGCAA
                                G GG CCCCGGCG GTG    GC
                                | || |||||||| |||    ||
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                                C CC GGGGCCGC CAC    CG
                                 C _      A  GACC_
GAM370  CRF      3' GGACCCCGGCGGGTGAGGGAC 9594          _   CAA
                                GGACCCCGGCGG TGAG  GC
                                |||||||||||| ||||  ||
                                CCTGGGGCCGCC ACTC  TG
                                      C   CC_
GAM370  DJ1042K10.2 3' AAGGACCCTGGTGGGGCA   9595       C  C  TGA
                                GAGGACCC GG GG  GCA
                                |||||||| || ||  |||
                                TTCCTGGG CC CC  CGT
                                    A  A  C__
GAM370  EFS2     5' GGGGCGGGTGAGCAGGC    9596    ACCCC   _    A
                                GG    GGCGG TGAGCA GC
                                ||    ||||| |||||| ||
                                CC    CCGCC ACTCGT CG
                                 _____    C    C
GAM370  ELOVL2   3' GAGGTCCTCGGAGGTGAGCA  9597     A  C  C
                                GAGG CC CGG GGTGAGCA
                                |||| || ||| ||||||||
                                CTCC GG GCC CCACTCGT
                                  A  A  T
GAM370  FLJ12442 5' AGGGCCCCAGTGAGCAAG   9598    A   GGC
                                AGG CCCC  GGTGAGCAAG
                                ||| ||||  ||||||||||
                                TCC GGGG  TCACTCGTTC
                                 C   ___
GAM370  FLJ13057 3' GAGGAATCATAATGAGCA   9599     CCC  GC
                                GAGGA  CG  GGTGAGCA
                                |||||  ||  ||||||||
                                CTCCT  GT  TTACTCGT
                                   TA_  A_
GAM370  FLJ13057 3' GAGGAATCACAATGAGCA   9600     CCCCG
                                GAGGA   GCGGTGAGCA
                                |||||   ||||||||||
                                CTCCT   TGTTACTCGT
                                   TAG__
GAM370  FLJ14549 3' GAGGACCCCGGGTAGGTG   9601         C__
                                GAGGACCCCGG  GGTG
                                ||||||||||  ||||
                                CTCCTGGGGCC  CCAC
                                      CAT
GAM370  FLJ14594 3' AAGGACTGGAGAGTGAGCA  9602      CCC  C _
                                GAGGAC  GG G GTGAGCA
                                ||||||  || | |||||||
                                TTCCTG  CC C CACTCGT
                                   A__  T T
GAM370  FLJ22405 5' GAGGACCCCGCCGAGGCA   9603        G  TGA
                                GAGGACCCCG CGG  GCA
                                |||||||||| |||  |||
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                                CTCCTGGGGC GCT   CGT
                                      G  C__
GAM370  KIAA0140 3' AGGACCCCATGAGCAGGC    9604        GGCG      A
                                AGGACCCC   GTGAGCA GC
                                ||||||||   ||||||| ||
                                TCCTGGGG   TACTCGT CG
                                    _____      C
GAM370  KIAA0415 3' GAGGACCCCGCGGTTCGGCTCG 9605          G   GA_  AA__
          GGCA                    GAGGACCCCG CGGT   GC   GCA
                                ||||||||||| ||||  ||   |||
                                CTCCTGGGGC GCCA   CG   CGT
                                      _   AGC  AGCC
GAM370  KIAA0513 3' GGACCCCAGGCGGCCTAGCA  9606        _     G_
                                GGACCCC GGCGGT  AGCA
                                |||||||  ||||||  ||||
                                CCTGGGG CCGCCG  TCGT
                                     T     GA
GAM370  KIAA0544 3' GGCCGCGGCGAGAGCA     9607     A  C     T
                                GG CC CGGCGG GAGCA
                                || || |||||| |||||
                                CC GG GCCGCT CTCGT
                                 _ C     _
GAM370  KIAA0603 5' GAGGCTCCGGCGGCGGGCA   9608      ACC       A
                                GAGG   CCGGCGGTG GCA
                                ||||   ||||||||| |||
                                CTCC   GGCCGCCGC CGT
                                  GA_       C
GAM370  KIAA1026 5' AGACCCCGGCGGGCGGGC    9609           _ A
                                GGACCCCGGCGG TG GC
                                ||||||||||| || ||
                                TCTGGGGCCGCC GC CG
                                       C  C
GAM370  KIAA1237 3' GGGTTCTGGGGGTGAGCAGGCA 9610     ACCCC  C       A
                                GG    GG GGTGAGCA GCA
                                ||    || |||||||| |||
                                CC    CC CCACTCGT CGT
                                 CAAGA  C       C
GAM370  KIAA1246 5' GGCTCCGGCGAATGCAGGCA  9611     ACC      TGA   A
                                GG   CCGGCGG   GCA GCA
                                ||   |||||||   ||| |||
                                CC   GGCCGCT   CGT CGT
                                 GA_      TA_   C
GAM370  KIAA1322 5' GAGGACGCCGGGCACGCGGTAG 9612        C  _____     A
          GCA                    GAGGAC CCG    GCGGTG GCA
                                ||||||| |||    |||||| |||
                                CTCCTG GGC     CGCCAT CGT
                                   C   CCGTG     C
GAM370  KIAA1399 3' AGGGTCCCCAGAGCGAGCA   9613      A_     C
                                AGG  CCCCGG GGTGAGCA
                                |||  |||||| ||||||||
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                                TCC  GGGGTC TCGCTCGT
                                  CA     _
GAM370  KIAA1831 5'  GGCCCCAGCGAGGGCAGGCA  9614     A       TGA   A
                                GG CCCCGGCGG   GCA GCA
                                || |||||||||   ||| |||
                                CC GGGGTCGCT   CGT CGT
                                 _       CC_   C
GAM370  KLK6     3'  GGACACCGACAGTAAGCA    9615      C
                                GGAC CCGGCGGTGAGCA
                                |||| ||||||||||||
                                CCTG GGCTGTCATTCGT
                                  T
GAM370  KRTHB5   3'  GAAGATTCTGGAAGCAAGC   9616      CCCC  CGGT
                                GAGGA   GG   GAGCAAGC
                                |||||   ||   ||||||||
                                CTTCT   CC   TTCGTTCG
                                   AAGA  ____
GAM370  MGC1127  3'  GAGGAGCCTGGCAGTGAGCA  9617      C  C
                                GAGGA CC GGCGGTGAGCA
                                ||||| || ||||||||||
                                CTCCT GG CCGTCACTCGT
                                   C  A
GAM370  MGC15438 3'  GGGGTCCCGGCGGCGGAGC   9618    A  AC       _
                                G GG  CCCGGCGGTG AGC
                                | ||  |||||||||| |||
                                C CC  GGGCCGCCGC TCG
                                _ CA         C
GAM370  MRPL9    5'  GAGGACCCCGGCGTCGGC    9619           G  A
                                GAGGACCCCGGCG TG GC
                                |||||||||||| || ||
                                CTCCTGGGGCCGC GC CG
                                        A  _
GAM370  NAC1     5'  GGGTCCCGGCGGGCTCCGCAGC 9620     AC      _ GA_   A
                                GG  CCCGGCGG T   GCA GC
                                ||  |||||||| |   ||| ||
                                CC  GGGCCGCC G   CGT CG
                                 CA       C AGG  _
GAM370  NXPH3    3'  GAGAACCCCGGTCTGACAGGTG 9621          C_______
                                GAGGACCCCGG      GGTG
                                ||||||||||       ||||
                                CTCTTGGGGCC      CCAC
                                      AGACTGT
GAM370  PALM     3'  AGGACCCTGGTCCAAGC     9622        CGGC   GAG
                                AGGACCC    GGT   CAAGC
                                |||||||    |||   |||||
                                TCCTGGG    CCA   GTTCG
                                   A___    G__
GAM370  PRKWNK2  3'  GAGGGACTTGAGCAAG      9623      ACCCC   GG
                                GAGG    GGC  TGAGCAAG
                                ||||    |||  ||||||||
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                                CTCC    CTG  ACTCGTTC
                                  _____  A_
GAM370  PTK6    5'  GGAACCCACTGGGCAAGC    9624     C   GC  TGA
                                GGA CCCG  GG   GCAAGC
                                ||| ||||  ||   ||||||
                                CCT GGGT  CC   CGTTCG
                                  T   GA  ___
GAM370  TLN2    5'  GAGGGTCCTGGCAGCTCTGAGC 9625      AC  C    ___
          A                      GAGG  CC GGCGGT   GAGCA
                                ||||  || ||||||   |||||
                                CTCC  GG CCGTCG   CTCGT
                                  CA  A     AGA
GAM370  LOC115219 5'  GAGCACTTTGCAGGTGAGCA   9626     G  CCCG  _
                                GAG AC    GC GGTGAGCA
                                ||| ||    || ||||||||
                                CTC TG    CG CCACTCGT
                                  G  AAA_  T
GAM370  LOC116236 5'  GAGAGCCCCGGCGGGCAGCGGG 9627     GA       TG   AA
          C                      GAG  CCCCGGCGG  AGC  GC
                                |||  |||||||||  |||  ||
                                CTC  GGGGCCGCC  TCG  CG
                                  TC       CG   CC
GAM370  LOC131583 5'  GGCGCCCCGGCGCAGCTGGGC  9628    A_      GTG   AA_
                                GG  CCCCGGCG   AGC   GC
                                ||  ||||||||   |||   ||
                                CC  GGGGCCGC   TCG   CG
                                 GC       G__   ACC
GAM370  LOC144455 5'  GGACCCCGCGGCGTCCGGGCA  9629         G    AGCAA
                                GGACCCCG CGGTG    GCA
                                |||||||| |||||    |||
                                CCTGGGGC GCCGC    CGT
                                     _    AGGCC
GAM370  LOC148872 3'  GGCCCCGGGGTTGCGGGC    9630    A     C   GA  AA
                                GG CCCCGG GGT  GC  GC
                                || |||||| |||  ||  ||
                                CC GGGGCC CCA  CG  CG
                                 _     _  A_  CC
GAM370  LOC148894 3'  GAGCACCTGCCTGAGCAAG   9631     G   CCG  GG
                                GAG ACC   GC  TGAGCAAG
                                ||| |||   ||  ||||||||
                                CTC TGG   CG  ACTCGTTC
                                  G   A__  G_
GAM370  LOC153469 3'  GGACCTTCGGAGTGAGCA    9632       C_   C
                                GGACC  CGG GGTGAGCA
                                |||||  ||| ||||||||
                                CCTGG  GCC TCACTCGT
                                   AA   _
GAM370  LOC163412 5'  GGGGCCGTGCGGTGAGCA    9633     ACC   _
                                GG   CCG GCGGTGAGCA
                                ||   ||| ||||||||||
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                                CC   GGC CGCCACTCGT
                                 CC_   A
GAM370   LOC163911 5'  GAGGACCCGAAGGTGAGCA   9634          C  C
                                GAGGACCC GG GGTGAGCA
                                |||||||| || ||||||||
                                CTCCTGGG CT CCACTCGT
                                     _  T
GAM370   LOC168574 5'  GAGGACCCGCTCCACTGAGCAG 9635          CGG_  G     A
           GCA                    GAGGACCC    CG TGAGCA GCA
                                |||||||||    || |||||| |||
                                CTCCTGGG    GT ACTCGT CGT
                                     CGAG  G     C
GAM370   LOC204515 5'  AGCCGGGGCGGTGGGCGGGCA  9636     A  CC      A  AA
                                GG CC  GGCGGTG GC  GCA
                                || ||  ||||||| ||  |||
                                TC GG  CCGCCAC CG  CGT
                                 _ CC      C  CC
GAM370   LOC220549 5'  GGCTCCCGGCGGTGGCA     9637     AC        A
                                GG  CCCGGCGGTG GCA
                                ||  |||||||||| |||
                                CC  GGGCCGCCAC CGT
                                 GA        _
GAM370   LOC220932 3'  GAGGACCCCGGGGCTGGGGC   9638           C   GA__
                                GAGGACCCCGG GGT    GC
                                |||||||||| |||    ||
                                CTCCTGGGGCC CCG    CG
                                      _  ACCC
GAM370   LOC254387 5'  GAGGTTAGCTTTGGTGAGCAAG 9639      ACCCC   ___
           CA                    GAGG    GGC   GGTGAGCAAGCA
                                ||||    |||   ||||||||||||
                                CTCC    TCG   CCACTCGTTCGT
                                  AA___   AAA
GAM370   LOC255070 3'  AGGGCCCGGCGGTGGGCGGGC  9640      AC        A  AA
                                AGG  CCCGGCGGTG GC  GC
                                |||  |||||||||| ||  ||
                                TCC  GGGCCGCCAC CG  CG
                                  C_        C  CC
GAM371   ABCA2    3'  GGGGGCCAAGCTGGGTGGG   9643        G   G
                                GGGGGT GGG CTGGGTGGG
                                |||||| ||| |||||||||
                                CCCCCG TTC GACCCACCC
                                   G  _
GAM371   ABCA2    3'  GGGGGCCAAGCTGGGTGGG   9643        G   G
                                GGGGGT GGG CTGGGTGGG
                                |||||| ||| |||||||||
                                CCCCCG TTC GACCCACCC
                                   G  _
GAM371   ABL1     3'  CGGGGGACCTGGGTGG      9644         TGGG G
                                CGGGGG    G CTGGGTGG
                                ||||||    | ||||||||
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                                GCCCCC   T GACCCACC
                                   ____ G
GAM371  ABL1    3'  CGGGGGACCTGGGTGG     9644       TGGG G
                                CGGGGG   G CTGGGTGG
                                ||||||   | ||||||||
                                GCCCCC   T GACCCACC
                                   ____ G
GAM371  AEGL1   3'  AGGCGGGGGTGGGAGTTG   9645    A         C
                                AG CGGGGGTGGGGG TG
                                || ||||||||||| ||
                                TC GCCCCCACCCTC AC
                                 C          A
GAM371  AGRN    3'  GATGGGGGTGGGGAAGGG   9647    C        CT
                                GA GGGGGTGGGGG  GGG
                                || ||||||||||  |||
                                CT CCCCCACCCCT  CCC
                                 A         T_
GAM371  AGRN    3'  GGGGATGGGATGGGGGTGGG  9646         GCT
                                GGGGGTGGGG  GGGTGGG
                                ||||||||||  |||||||
                                CCCCTACCCT  CCCACCC
                                      ACC
GAM371  ALX3    3'  AGGCGGGGGTGGGCTGGG    9648    A     GG
                                AG CGGGGGT  GGGCTGGG
                                || |||||||  ||||||||
                                TC GCCCCCA  CCCGACCC
                                 C      __
GAM371  AR      5'  GGGCGGGGGGGGCGGGTGG    9649     _ T    T
                                GGG GG GGGGGC GGGTGG
                                ||| || |||||| ||||||
                                CCC CC CCCCCG CCCACC
                                  G _    _
GAM371  ATP1A2  3'  GATGGGAGTGGGCAGGGTGGG 9650    C       GGCT
                                GA GGGGGTGGG   GGGTGGG
                                || |||||||||   |||||||
                                CT CCCTCACCC   CCCACCC
                                 A       GT__
GAM371  ATRN    3'  ACGGGGGTGGGGGGCAGGG    9651           T
                                ACGGGGGTGGGGGGC GGG
                                ||||||||||||| |||
                                TGCCCCCACCCCCG CCC
                                        T
GAM371  AXIN1   3'  GGGTGGGGTGGCATGGTGG   9653        __ TG
                                GGGTGGGG  GC  GGTGG
                                ||||||||  ||  |||||
                                CCCACCCC  CG  CCACC
                                     AC  TA
GAM371  AXIN1   3'  GGGTTGGGAGCTGGGTGG    9652     GG
                                GGG  TGGGGGCTGGGTGG
                                |||  ||||||||||||||
```

```
                                CCC  ACCCTCGACCCACC
                                  A_
GAM371  AXL     3'  AGGCGTGGGGTGGGAAAGTGGG 9654     A  _        CTG
                                AG CG GGGGTGGGGG   GGTGGG
                                || || ||||||||||   ||||||
                                TC GC CCCCACCCTT   TCACCC
                                 C  A        ____
GAM371  AXL     3'  AGGCGTGGGGTGGGAAAGTGGG 9654     A  _        CTG
                                AG CG GGGGTGGGGG   GGTGGG
                                || || ||||||||||   ||||||
                                TC GC CCCCACCCTT   TCACCC
                                 C  A        ____
GAM371  BARX1   3'  AGACGGGGTGGGGGTGCG    9655         G     CTGG TG
                                AGACGGGG TGGGGG    G  G
                                |||||||| ||||||    |  |
                                TCTGCCCC ACCCCC    C  C
                                      _     A____ GT
GAM371  BCL3    3'  AGATGGGGGGGGGGGGG     9656      C     T     CT
                                AGA GGGGG GGGGG  GGG
                                ||| ||||| |||||  |||
                                TCT CCCCC CCCCC  CCC
                                  A    _    ___
GAM371  BCL7A   3'  GGGCGAGGGGTGCAGGGTGGG  9658      _  T    _  T
                                GGG GG GGGG GC GGGTGGG
                                ||| || |||| || |||||||
                                CCC CT CCCC CG CCCACCC
                                  G  _    A  T
GAM371  BCL7A   3'  GATGGGGGTGGTGGTGGTGGG  9657     C       G  CTG
                                GA GGGGGTGG GG   GGTGGG
                                || ||||||||  ||   ||||||
                                CT CCCCCACC CC   CCACCC
                                 A       A  A__
GAM371  BIG1    5'  AGAGGGGGTGGAGGTGGG    9659      C         C
                                AGA GGGGGTGGGGG TGGG
                                ||| ||||||||||| ||||
                                TCT CCCCCACCTCC ACCC
                                  _         _
GAM371  BSN     3'  GGGGTGGGGAGGGGTGGG    9660          CT
                                GGGGTGGGGG  GGGTGGG
                                ||||||||||  |||||||
                                CCCCACCCCT  CCCACCC
                                      C_
GAM371  C1QG    3'  GGGGGTGGGTCAGGGTGGG   9661          GGCT
                                GGGGGTGGG   GGGTGGG
                                |||||||||   |||||||
                                CCCCCACCC   CCCACCC
                                     AGT_
GAM371  CALM3   3'  GGGGTGGGGAGGTGGTGGG   9663          CTG
                                GGGGTGGGGG  GGTGGG
                                ||||||||||  ||||||
```

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                                CCCCACCCCT  CCACCC
                                     CCA
GAM371  CALM3   3'  GGGTGGGGGGGTGGGGTGG   9662        CT_
                                GGGTGGGGGG  GGGTGG
                                |||||||||  ||||||
                                CCCACCCCCC  CCCACC
                                     CAC
GAM371  CLC     3'  GGGTGGGGCTGGGGGGG     9664        G   T
                                GGGTGGGG CTGGG GGG
                                |||||||| ||||| |||
                                CCCACCCC GACCC CCC
                                   _    _
GAM371  COPE    3'  AGATGGGGGGTGCTGGGGGGTGGG 9665     C     GG  CT
                                AGA GGGGGGTG  GG  GGGTGGG
                                ||| |||||||  ||  |||||||
                                TCT CCCCCAC  CC  CCCACCC
                                  A      GA  __
GAM371  CSPG3   3'  GGGGTGGGGCAGGAGTGGG   9666        G T  _
                                GGGGTGGGG C GG GTGGG
                                ||||||||| | || |||||
                                CCCCACCCC G CC CACCC
                                     _ T  T
GAM371  CYP26A1  5'  AGGCGGCGGTGGGGGAGGG   9667    A  G      CT
                                AG CGG GGTGGGGG  GGG
                                || ||| ||||||||  |||
                                TC GCC CCACCCCC  CCC
                                 C   G       T_
GAM371  DBH     3'  CGGGGGCGGGGGGCGTTCCCGG  9668          TGGG_
                                CGGGGGTGGGGGGC    TGG
                                ||||||||||||     |||
                                GCCCCCGCCCCCG    GCC
                                       CAAGG
GAM371  DCTN1   5'  AGGGGTGGGGGGCAGTGATGGG  9669          TG_
                                GGGGGTGGGGGC  GGTGGG
                                ||||||||||||  ||||||
                                TCCCCACCCCCG  CTACCC
                                       TCA
GAM371  DIA1    3'  AGGCGGGAGTGGGGGGTGACAGG 9670    A        CTG  TG
                                AG CGGGGGTGGGGG  GG  GG
                                || ||||||||||||  ||  ||
                                TC GCCCTCACCCCC  CT  CC
                                 C         A__  GT
GAM371  DMPK    5'  GGGGGTTGGGGGCTGGGTGGG  9671       G
                                GGGGGT GGGGCTGGGTGGG
                                |||||| ||||||||||||
                                CCCCCA CCCCGACCCACCC
                                   A
GAM371  DMPK    3'  CGGGGGTGGGGGGTCCTAGGTGG 9672          __
            G                    CGGGGGTGGGGG  CTGGGTGGG
                                ||||||||||||  |||||||||
```

```
                                GCCCCCACCCCC  GATCCACCC
                                      AG
GAM371  DRIL1   5'  CGGGGGCGGGGGCCGCCGGG  9673           GG
                                CGGGGGTGGGGGCTG  TGGG
                                |||||||||||||||  ||||
                                GCCCCCGCCCCCGGC  GCCC
                                       G_
GAM371  EMX2    5'  GGGGTGGGGGTGGGGGTGG   9674         CT_
                                GGGGTGGGGG  GGGTGG
                                ||||||||||  ||||||
                                CCCCACCCCC  CCCACC
                                      ACC
GAM371  FZD7    3'  GGGGTGGGAAAGGTGGG    9675          CT
                                GGGGTGGGGG  GGGTGGG
                                ||||||||||  |||||||
                                CCCCACCCTT  TCCACCC

                                     __
GAM371  GLI4    3'  GACGGGGTGGAGGGTGGG   9676        G    C
                                GACGGGG TGGGGG TGGG
                                ||||||| |||||| ||||
                                CTGCCCC ACCTCC ACCC
                                   _    C
GAM371  HCFC1   3'  GACGGGGTGGGAGGGGTGGG  9677       G    CT
                                GACGGGG TGGGGG  GGGTGGG
                                ||||||| ||||||  |||||||
                                CTGCCCC ACCCTC  CCCACCC

                                   _    __
GAM371  HIP2    3'  AGGCGGGGGTGGGGGGGG   9678    A        CT
                                AG CGGGGGTGGGGG  GGG
                                || ||||||||||||  |||
                                TC GCCCCCACCCCC  CCC
                                 C         __
GAM371  HOXC13  3'  GATGGGGGTGGAGGCTGGG  9679    C
                                GA GGGGGTGGGGGCTGGG
                                || ||||||||||||||||
                                CT CCCCCACCTCCGACCC
                                 A
GAM371  HSF4    5'  GGGGTGGAGTGGGGTGGG   9680        GCT
                                GGGGTGGGG  GGGTGGG
                                |||||||||  |||||||
                                CCCCACCTC  CCCACCC
                                     AC_
GAM371  HSF4    5'  GGGGTGGGGTGGAGTGGG   9681        GCT
                                GGGGTGGGG  GGGTGGG
                                |||||||||  |||||||
                                CCCCACCCC  CTCACCC
                                     AC_
GAM371  HYOU1   3'  GGGGGTGGGGTGAGGGGTGGG 9682         GCT_
                                GGGGGTGGGG  GGGTGGG
                                ||||||||||  |||||||
```

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                                CCCCCACCCC   CCCACCC
                                     ACTC
GAM371  IL1F5   3' GAAGGGGGTGGGGCTGGG   9683    C       G
                                GA GGGGGTGGGG CTGGG
                                || |||||||||| |||||
                                CT CCCCCACCCC GACCC
                                 T       _
GAM371  JAM2    5' GGGGGTGGGGGGGATTGGG   9684          CT GG
                                GGGGGTGGGGG  G  TGGG
                                |||||||||||  |  ||||
                                CCCCCACCCCC  C  ACCC
                                      __ TA
GAM371  KCNE1L  3' GGGGGTGGAAGGTGG      9685         GGCT
                                GGGGGTGGG   GGGTGG
                                |||||||||   ||||||
                                CCCCCACCT   TCCACC

                                    _____
GAM371  KPNB1   5' GATGGGGGTTGGGGGTCGGGTG 9686    C    _   C
           GG                     GA GGGGGT GGGGG TGGGTGGG
                                || |||||| ||||| ||||||||
                                CT CCCCCA CCCCC GCCCACCC
                                 A    A    A
GAM371  LAG3    5' GGGGGCGGGGGGTGTCCCAGGG  9687          C  GGT__
                                GGGGGTGGGGG TG    GGG
                                |||||||||| ||    |||
                                CCCCCGCCCCC AC    CCC
                                      _ AGGGT
GAM371  LMO6    3' CGGGGCGTGGGGGTGAGGG   9688      _     C   T
                                CGGGG GTGGGGG TGGG GG
                                ||||| ||||||| |||| ||
                                GCCCC CACCCCC ACTC CC
                                   G     _   _
GAM371  LY6E    3' GGAGGTGCAGGGGGTGGG    9689       G   CT
                                GGGGGTG GGG  GGGTGGG
                                ||||||| |||  |||||||
                                CCTCCAC TCC  CCCACCC
                                    G  __
GAM371  MAPRE3  3' GGGCAGGGGGCCTTGGGTGGG  9690      _     __
                                GGGT GGGGGCT  GGGTGGG
                                |||| |||||||  |||||||
                                CCCG CCCCCGG  CCCACCC
                                   T      AA
GAM371  MAPRE3  3' GGGGGTGGGGAGGGCAGGTGGG 9691          ___  T
                                GGGGGTGGGG   GC GGGTGGG
                                ||||||||||   || |||||||
                                CCCCCACCCC   CG TCCACCC
                                      TCC  _
GAM371  MEOX1   3' GATTGGGGTGGGGGTAGTTGGG 9692    CG       C   G
                                GA  GGGGTGGGGG TGG TGGG
                                ||  |||||||||| ||| ||||
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                                CT  CCCCACCCCC ATC ACCC
                                 AA         _  A
GAM371  MEOX1    3'  GATTGGGGTGGGGGGTAGTTGGG 9692     CG        C  G
                                GA  GGGGTGGGGG TGG TGGG
                                ||  |||||||||| ||| ||||
                                CT  CCCCACCCCC ATC ACCC
                                 AA         _  A
GAM371  MPP3     5'  AGAAGGGGGTGGAGGTGGG   9693      C         C
                                AGA GGGGGTGGGGG TGGG
                                |||  |||||||||||  ||||
                                TCT CCCCCACCTCC ACCC
                                  T         _
GAM371  MUS81    3'  AGACGGGGGCTGGGGGCTG   9694           _
                                AGACGGGGG TGGGGGCTG
                                |||||||||  |||||||||
                                TCTGCCCCC ACCCCCGAC
                                      G
GAM371  NGFR     3'  GGGGGTGCGGGCTCCACAGG   9695         G     GG TG
                                GGGGGTG GGGCT  G  GG
                                |||||||  |||||  |  ||
                                CCCCCAC CCCGA  T  CC
                                    G     GG GT
GAM371  PAX2     3'  AGGCGGGGCTGGGGGCGGTGGG 9696     A     G      TG
                                AG CGGGG TGGGGGC  GGTGGG
                                ||  |||||  |||||||  ||||||
                                TC GCCCC ACCCCCG  CCACCC
                                 C     G      __
GAM371  PAX2     3'  AGGCGGGGCTGGGGGCGGTGGG 9696     A     G      TG
                                AG CGGGG TGGGGGC  GGTGGG
                                ||  |||||  |||||||  ||||||
                                TC GCCCC ACCCCCG  CCACCC
                                 C     G      __
GAM371  PBX2     3'  CGGGGGTGGGGATGCATGGG   9697            C  G
                                CGGGGGTGGGGG TG GTGGG
                                ||||||||||||  ||  |||||
                                GCCCCCACCCCT AC TACCC
                                       _  G
GAM371  PES1     3'  CAGTAGGTAGGGGGCTGGGTGG 9698      _   _
                G                CGG GGGT GGGGGCTGGGTGGG
                                 |||  ||||  ||||||||||||||
                                 GTC TCCA CCCCCGACCCACCC
                                   A    T
GAM371  PFKFB4   3'  GGGGTGGGGGCTCTGGG     9699            GGG
                                GGGGTGGGGGCT   TGGG
                                ||||||||||||   ||||
                                CCCCACCCCCGA   ACCC
                                       G__
GAM371  PLXNB3   3'  GGGGGGAAGGTGGGTGGG    9700       T     C
                                GGGGG GGGGG TGGGTGGG
                                |||||  |||||  ||||||||
```

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                                CCCCC CTTCC ACCCACCC
                                  _   _
GAM371  PRKACA   3' GGGATGGGGGTGTGGGTGG  9702        C_
                                GGGGTGGGGG TGGGTGG
                                |||||||||| |||||||
                                CCCTACCCCC ACCCACC
                                     AC
GAM371  PRKACA   3' GGGGCCTGTGGTTGGGTGGG 9701      GGG_ C
                                GGGGT  GG TGGGTGGG
                                |||||  || ||||||||
                                CCCCG  CC ACCCACCC
                                   GACA A
GAM371  RAB3A    3' AGGCGGGGGGGGGGGTTCAGG 9703    A   T   CT_
                                AG CGGGGG GGGGG  GGG
                                || |||||| |||||  |||
                                TC GCCCCC CCCCC  TCC
                                 C   _   AAG
GAM371  RAD54L   5' GGGGTGGGATTGGGGGTGGG 9704       GCT_
                                GGGGTGGGG  GGGTGGG
                                |||||||||  |||||||
                                CCCCACCCT  CCCACCC
                                     AACC
GAM371  RARA     3' CGGGGGTGGGGGCAGCTCGGG 9705         TGGG
                                CGGGGGTGGGGGC  TGGG
                                ||||||||||||  ||||
                                GCCCCCACCCCCG  GCCC
                                      TCGA
GAM371  RTN4R    3' AGATGGGGGTGGCGGGCGG  9706    C     _  T
                                AGA GGGGGTGG GGGC GG
                                ||| |||||||| |||| ||
                                TCT CCCCCACC CCCG CC
                                  A     G  _
GAM371  RYR1     3' GGGGGTGGAGGGCCAGCTGGG 9707       _  TG G
                                GGGGGTGG GGGC  G TGGG
                                |||||||| ||||  | ||||
                                CCCCCACC CCCG  C ACCC
                                     T  GT G
GAM371  S100A1   3' GGGGTGGGGGTGGGGTGG  9709        CT
                                GGGGTGGGGG  GGGTGG
                                ||||||||||  ||||||
                                CCCCACCCCC  CCCACC
                                     AC
GAM371  S100A1   3' GGGTGGGGTGGGCAAGGGTGGG 9708   _ T _  T_
                                GGG GG GG GGGC  GGGTGGG
                                ||| || || ||||  |||||||
                                CCC CC CC CCCG  CCCACCC
                                  A _ A  TT
GAM371  SEPN1    3' GGGGTGAGGGGGTGG     9710        CTG
                                GGGGTGGGGG  GGTGG
                                ||||||||||  |||||
```

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                                CCCCACTCCC  CCACC
                                    ___
GAM371  SOX13   3' GAGGGGCAGGGCTGGGTGGG 9711      TG
                                GGGGG GGGGCTGGGTGGG
                                ||||| |||||||||||||
                                CTCCC TCCCGACCCACCC
                                  CG
GAM371  SPTBN4  3' GGGTGGGGGGTGGTGAGTGG  9712       C__
                                GGGTGGGGG  TGGGTGG
                                |||||||||  |||||||
                                CCCACCCCC  ACTCACC
                                     ACC
GAM371  TCF2    5' AGAAGGGGGTGAGGGGGTGGG 9713    C       CTG
                                AGA GGGGGGTGGGGG  GGTGGG
                                ||| ||||||||||  ||||||
                                TCT CCCCCACTCCC  CCACCC
                                  T       ___
GAM371  TCF2    5' AGAAGGGGGTGAGGGGGTGGG 9713    C       CTG
                                AGA GGGGGGTGGGGG  GGTGGG
                                ||| ||||||||||  ||||||
                                TCT CCCCCACTCCC  CCACCC
                                  T       ___
GAM371  TFAP4   3' AGGTGGGGGGCTGGGGGG    9714          T
                                GGGTGGGGGGCTGGG GGG
                                |||||||||||||| |||
                                TCCACCCCCGACCC CCC
                                        _
GAM371  THY1    3' GGGTGGGGGGCTGGGGGTTGGG 9715          ___
                                GGGTGGGGGGCTGGG  TGGG
                                ||||||||||||||  ||||
                                CCCACCCCCGACCC  ACCC
                                      CCA
GAM371  TJP1    5' GAGGGTGGGGAGGACCTGGG  9716          ____
                                GGGGGTGGGGG   CTGGG
                                ||||||||||   |||||
                                CTCCCACCCCT   GACCC
                                     CCTG
GAM371  TNNI3   3' GGGGGTGGCGGGTACTGAGTGG 9717       _  __
          G                      GGGGGTGG GGG  CTGGGTGGG
                                ||||||||  |||  |||||||||
                                CCCCCACC CCC  GACTCACCC
                                    G  AT
GAM371  TP53    3' AGATGGGGGTGGGAGGCTGTCA 9718    C      _   __
          GTGGG                   AGA GGGGGTGGG GGCTG  GGTGGG
                                ||| |||||||| |||||  ||||||
                                TCT CCCCCACCC CCGAC  TCACCC
                                  A       T    AG
GAM371  VDR     3' GGGGTGGGAGCTGTGGG    9719          GG
                                GGGGTGGGGGCT  GTGGG
                                ||||||||||  |||||
```

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                                CCCCACCCTCGA  CACCC
                                          __
GAM371  ZAP70    3'  GGGTGGGGCTGAGGGTGG    9720        G __
                                GGGTGGGG CT  GGGTGG
                                |||||||| ||  ||||||
                                CCCACCCC GA  CCCACC
                                     _ CT
GAM371  ZFP36L1  3'  GGGGGTGGGGGGGGCGG     9721          CTG
                                GGGGGTGGGGG  GGTGG
                                ||||||||||  |||||
                                CCCCCACCCCC  CCGCC
                                          ___
GAM371  ZFP36L1  3'  CAGGGGTGGGGGGGGTGGG   9722           CT
                                CGGGGGTGGGGG  GGGTGGG
                                ||||||||||| |||||||
                                GTCCCCACCCCC  CCCACCC
                                          __
GAM371  ACTR1A   3'  GGGGTGGGGGTGAGGGTGG   9723          CT_
                                GGGGTGGGGG  GGGTGG
                                ||||||||||  ||||||
                                CCCCACCCCC  CCCACC
                                      ACT
GAM371  AGPAT1   3'  GGGCTGCAGGGGGCTGGGTGGG 9724     G_ _
                                GGG  GT GGGGGCTGGGTGGG
                                |||  || ||||||||||||||
                                CCC  CG CCCCCGACCCACCC
                                  GA  T
GAM371  AGPAT1   3'  GGGCTGCAGGGGGCTGGGTGGG 9724     G_ _
                                GGG  GT GGGGGCTGGGTGGG
                                |||  || ||||||||||||||
                                CCC  CG CCCCCGACCCACCC
                                  GA  T
GAM371  APELIN   3'  GATGGGGTGTGGGGGCAGG   9725     C  _      T
                                GA GGGG GTGGGGGC GG
                                || |||| |||||||| ||
                                CT CCCC CACCCCCG CC
                                 A   A       T
GAM371  ATP6V0A1 3'  GGATGGGAGTGCAGGGTGG   9726        _ _ T
                                GGGTGGG G GC GGGTGG
                                ||||||| | || ||||||
                                CCTACCC C CG CCCACC
                                    T A  T
GAM371  BCoR     5'  GGAGCGGGGGGCGGTTGGGTGG 9727          _ ___
          G                      GGGGTGGGGG C   TGGGTGGG
                                 |||||||||| |   ||||||||
                                 CCTCGCCCCC G   ACCCACCC
                                       C CCA
GAM371  BCoR     5'  GGAGCGGGGGGCGGTTGGGTGG 9727          _ ___
          G                      GGGGTGGGGG C   TGGGTGGG
                                 |||||||||| |   ||||||||
```

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                                CCTCGCCCCC G   ACCCACCC
                                      C CCA
GAM371  C20orf149 3'  GGGGGTGGGAGGTGGG      9728          GGCT
                                GGGGGTGGG   GGGTGGG
                                |||||||||   |||||||
                                CCCCCACCC   TCCACCC
                                     ____
GAM371  C8orf13   3'  AGATGTGGGTGGGGGCTGAG  9729      CGG
                                AGA  GGGTGGGGGCTGGG
                                |||  ||||||||||||||
                                TCT  CCCACCCCCGACTC
                                  ACA
GAM371  CDK5RAP3  5'  GGGGGTGCGGGGGTGGG     9730        G  CTG
                                GGGGGTG GGG  GGTGGG
                                ||||||| |||  ||||||
                                CCCCCAC CCC  CCACCC
                                    G  ___
GAM371  CHRNA6    3'  AGATGGGGGACTTGGGTGGG  9731          _ _
                                GGGTGGGGG CT GGGTGGG
                                ||||||||| || |||||||
                                TCTACCCCC GA CCCACCC
                                      T  A
GAM371  CLSTN1    3'  GGGCGGGGCTGGGCGGG     9732         G
                                GGGTGGGG CTGGGTGGG
                                |||||||| |||||||||
                                CCCGCCCC GACCCGCCC
                                     _
GAM371  CPLX1     3'  GACGGGGGTGGGGGCTGGG   9733
                                GACGGGGGTGGGGGCTGGG
                                |||||||||||||||||||
                                CTGCCCCCACCCCCGACCC

GAM371  CXYorf1   3'  GGTGGTGGGGGCGGTGGG    9734     G       TG
                                GG GGTGGGGGC  GGTGGG
                                || |||||||||  ||||||
                                CC CCACCCCCG  CCACCC
                                 A       __
GAM371  CXYorf1   3'  GGGAGTGGGGGTGCACTGG   9735          C  G _
                                GGGGGTGGGGG TG G TGG
                                |||||||||| || | |||
                                CCCTCACCCCC AC T ACC
                                      _  G G
GAM371  DDX8      3'  AGACGGGGTGGGAAGTGG    9736         G    GCTG
                                AGACGGGG TGGGG   GGTGG
                                |||||||| |||||   |||||
                                TCTGCCCC ACCCT   TCACC
                                     _   _____
GAM371  DKFZp434P0531 3'  GGAGTGGGGGTGGGGTGG   9737          CT
                                GGGGTGGGGG  GGGTGG
                                ||||||||||  ||||||
```

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                                CCTCACCCCC  CCCACC
                                      AC
GAM371  DKFZP564G202 3'  AGATGGGTGTGGGGTCATTTGG 9738      C   G     GCTGGG
           G                      AGA GGG GTGGGG      TGGG
                                  ||| ||| ||||||      ||||
                                  TCT CCC CACCCC      ACCC
                                    A   A     AGTAA_
GAM371  DKFZp586I021 3'  GGGTGGGGATGGAGGGTGG   9740          CT__
                                  GGGTGGGGGG    GGGTGG
                                  |||||||||    ||||||
                                  CCCACCCCT    CCCACC
                                        ACCT
GAM371  DKFZp586I021 3'  GATGGAGGGTGGGGATGGAGGG 9739     C  _       CT__
           TGGG                     GA GG GGGTGGGGG    GGGTGGG
                                  || || |||||||||    |||||||
                                  CT CC CCCACCCCT    CCCACCC
                                    A  T        ACCT
GAM371  DKFZp761H079 3'  GAGGGGGTGGGGGTGG      9741     C         C
                                  GA GGGGGTGGGGG TGG
                                  || ||||||||||| |||
                                  CT CCCCCACCCCC ACC
                                   _         _
GAM371  DKFZp762K222 5'  GGGTGGATGGCTGGGTGG     9742          _
                                  GGGTGGG GGCTGGGTGG
                                  ||||||| ||||||||||
                                  CCCACCT CCGACCCACC
                                       A
GAM371  DRIL2    3'  GGGGGTGGGGGTGTGG      9743           CTGG
                                  GGGGGTGGGGG    GTGG
                                  ||||||||||    ||||
                                  CCCCCACCCCC    CACC
                                         A___
GAM371  EFNA5    3'  GGGGGTGGGGCGGGGTGGG    9744           G T
                                  GGGGGTGGGG C GGGTGGG
                                  |||||||||| | |||||||
                                  CCCCCACCCC G CCCACCC
                                         _ C
GAM371  FLJ10748  3'  AGATGGGGGTGGGGGGGAGGTGG 9745      C         CT
           G                      AGA GGGGGTGGGGG  GGGTGGG
                                  ||| ||||||||||  |||||||
                                  TCT CCCCCACCCCC  TCCACCC
                                    A          C_
GAM371  FLJ10898  3'  GGGTGGGGGTGGGCAGTGGTGGG 9746      _  T  _    TG_
                                  GGG GG GG GGGC   GGTGGG
                                  ||| || || ||||   ||||||
                                  CCC CC CC CCCG   CCACCC
                                    A  _  A    TCA
GAM371  FLJ12529  3'  GATGGGGTTGGGGGACAGGG   9747     C    G     _ T
                                  GA GGGG TGGGGG C GGG
                                  || |||| |||||| | |||
```

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                                CT CCCC ACCCCC G CCC
                                 A   A     T T
GAM371  FLJ14280  3'  AGGCGGGGGTAGGGGAGCGGTG 9748     A          CTG
          GG                     AG CGGGGGTGGGGG   GGTGGG
                                || ||||||||||||   ||||||
                                TC GCCCCCATCCCC   CCACCC
                                 C          TCG
GAM371  FLJ14299  3'  CGGTGGGGAAGGGTTGGGTGGG 9749      _   TG    C
                                CGG GGG  GGGG TGGGTGGG
                                ||| |||  |||| ||||||||
                                GCC CCC  TCCC ACCCACCC
                                  A  CT   A
GAM371  FLJ14594  3'  GGGCGGGGTGGGCAGGTGG   9750      _ T _   T
                                GGG GG GG GGGC GGGTGG
                                ||| || || |||| ||||||
                                CCC CC CC CCCG TCCACC
                                  G _ A   _
GAM371  FLJ14950  3'  GGGGTGGGGGTGGGTGG     9751          C     _
                                GGGGTGGGGG TGGGTG G
                                |||||||||| |||||| |
                                CCCCACCCCC ACCCAC C
                                      _     A
GAM371  FLJ20005  5'  GGGCTGGCTTGGGGTTGGGTGG 9752      __   G_    C
          G                      GGG  GGT  GGGG TGGGTGGG
                                |||  |||  |||| ||||||||
                                CCC  CCG  CCCC ACCCACCC
                                  GA  AA   A
GAM371  FLJ20359  3'  GGGGTGGGGGTGAGGGTGG   9723          CT_
                                GGGGTGGGGG   GGGTGG
                                ||||||||||   ||||||
                                CCCCACCCCC   CCCACC
                                      ACT
GAM371  FLJ22471  5'  CGGCGGTGGGGGCCCGTGG   9753      G         GG
                                CGG GGTGGGGGCT  GTGG
                                ||| ||||||||||  ||||
                                GCC CCACCCCCGG  CACC
                                  G         G_
GAM371  FTSJ3     3'  GATGGGGGTGGGGAGGG     9754     C         CT
                                GA GGGGGTGGGGG  GGG
                                || ||||||||||  |||
                                CT CCCCCACCCCT  CCC
                                 A         __
GAM371  GMPPB     3'  AGGGTGGGGGCCTGGGTGG   9755           _
                                GGGGTGGGGGC TGGGTGG
                                |||||||||| |||||||
                                TCCCACCCCCG ACCCACC
                                      G
GAM371  GTPBP1    3'  GGGGGTGGGGGCAATGCGG   9756           TGG
                                GGGGGTGGGGGC   GTGG
                                ||||||||||||   ||||
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                                CCCCCACCCCCG  CGCC
                                      TTA
GAM371  HES6     3'  GGGCTGGTGAAGGCTGGGTGGG 9757     __
                                GGG  GGTGGGGGCTGGGTGGG
                                |||  ||||||||||||||||
                                CCC  CCACTTCCGACCCACCC
                                  GA
GAM371  ILF3     3'  GATGGGGGCGGGGGCCTGG   9758    C        _
                                GA GGGGGTGGGGGC TGG
                                || ||||||||||| |||
                                CT CCCCCGCCCCCG ACC
                                 A         G
GAM371  ILF3     3'  GATGGGGGCGGGGGCCTGG   9758    C        _
                                GA GGGGGTGGGGGC TGG
                                || ||||||||||| |||
                                CT CCCCCGCCCCCG ACC
                                 A         G
GAM371  KIAA0125 3'  GATGGAGGTGAGGGTGGG    9759    C        C
                                GA GGGGGTGGGGG TGGG
                                || ||||||||||| ||||
                                CT CCTCCACTCCC ACCC
                                 A        _
GAM371  KIAA0284 3'  AGGCAGGGGTGGGGGTGGCCAT 9760    A        C  __
          GGG                    AG CGGGGGTGGGGG TGG  GTGGG
                                || ||||||||||| |||  |||||
                                TC GTCCCCACCCCC ACC  TACCC
                                 C         _  GG
GAM371  KIAA0451 3'  GGGGATGGGGAGGGTGGG    9761          CT
                                GGGGGTGGGGG  GGGTGGG
                                ||||||||||  |||||||
                                CCCCTACCCCT  CCCACCC
                                      __
GAM371  KIAA0545 3'  GGGGGTGGGGGACGGGTGGG  9762          C
                                GGGGGTGGGGG TGGGTGGG
                                |||||||||| ||||||||
                                CCCCCACCCCC GCCCACCC
                                      T
GAM371  KIAA0664 3'  ACGGGGGTGGGGTGGG     9763          GC
                                ACGGGGGTGGGG  TGGG
                                ||||||||||  ||||
                                TGCCCCCACCCC  ACCC
                                      __
GAM371  KIAA0748 3'  AGGCAGGGGTGGGGGTCACAAG 9764    A        CTGGGT
          G                     AG CGGGGGTGGGGG    GG
                                || ||||||||||     ||
                                TC GTCCCCACCCCC    CC
                                 C         AGTGTT
GAM371  KIAA1171 3'  GACGGGGGTGGGGGCAGG    9765           T
                                GACGGGGGTGGGGGC GG
                                ||||||||||||||| ||
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                                CTGCCCCCACCCCCG CC
                                          T
GAM371  KIAA1196 3' AGGCGGGGGTGGGGGATGG   9766    A        C
                                AG CGGGGGTGGGGG TGG
                                || |||||||||||| |||
                                TC GCCCCCACCCCC ACC
                                 C          T
GAM371  KIAA1441 3' CGGGGGCGGGGGGCGGGGGTGGG 9767           T_
                                CGGGGGTGGGGGC  GGGTGGG
                                ||||||||||||  |||||||
                                GCCCCCGCCCCCG  CCCACCC
                                       CC
GAM371  KIAA1462 3' GGGTGGGGTGGCAGGGTGG   9768       __ T
                                GGGTGGGG  GC GGGTGG
                                ||||||||  || ||||||
                                CCCACCCC  CG CCCACC
                                     AC  T
GAM371  KIAA1464 3' GATGGGGATGGGGGTTCTGG  9769    C       __
                                GA GGGGGTGGGGG  CTGG
                                || ||||||||||  ||||
                                CT CCCCTACCCCC  GACC
                                 A         AA
GAM371  KIAA1866 3' GGGGATGGGAGTGGTGGG    9770         CTG
                                GGGGGTGGGGG  GGTGGG
                                ||||||||||  ||||||
                                CCCCTACCCTC  CCACCC
                                       A__
GAM371  KIAA1878 3' GGGGGTGGGGAAGCCTGTGGG 9771         __  GG
                                GGGGGTGGGG  GCT  GTGGG
                                |||||||||  |||  |||||
                                CCCCCACCCC  CGG  CACCC
                                      TT  A_
GAM371  KIAA1910 3' GGGGGTGGGGTAGAGGGTGGG 9772         GCT_
                                GGGGGTGGGG   GGGTGGG
                                ||||||||||   |||||||
                                CCCCCACCCC   CCCACCC
                                      ATCT
GAM371  KIAA1938 3' GGGGGTGGTGGGGCTGGG    9773       __
                                GGGGGTGG  GGGCTGGG
                                ||||||||  ||||||||
                                CCCCCACC  CCCGACCC
                                     AC
GAM371  KRTAP4-13 5' GGGTGGAGGTTCTGGGTGG  9774        __
                                GGGTGGGGG  CTGGGTGG
                                |||||||||  ||||||||
                                CCCACCTCC  GACCCACC
                                      AA
GAM371  KRTAP4-4  5' GGGTGGAGGTTCTGGGTGG  9774        __
                                GGGTGGGGG  CTGGGTGG
                                |||||||||  ||||||||
```

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                                CCCACCTCC  GACCCACC
                                     AA
GAM371  LASP1    3'  AGACTGGGGGTGGGCGTGGG  9775      _       GGC
                                AGAC GGGGGTGGG   TGGG
                                |||| |||||||||   ||||
                                TCTG CCCCCACCC   ACCC
                                  A        GC_
GAM371  LHPP     3'  AGGCAGGGGTGGAGGAGGTGGG 9776     A          CT
                                AG CGGGGGTGGGGG  GGGTGGG
                                || ||||||||||||  |||||||
                                TC GTCCCCACCTCC  TCCACCC
                                 C          __
GAM371  LW-1     5'  AGACGGGGTGTGGGTGGG    9777          _    GGC
                                AGACGGGG GTGGG   TGGG
                                |||||||| |||||   ||||
                                TCTGCCCC CACCC   ACCC
                                     A    ____
GAM371  MARCKS   5'  GAGGGGGGTGGGGGTGG     9778     C         C
                                GA GGGGGTGGGGG TGG
                                || ||||||||||| |||
                                CT CCCCCACCCCC ACC
                                 C         _
GAM371  MGC10485 3'  AGATGGGGGTGCTGGGTGGG   9779      C     GGGG
                                AGA GGGGGT    GCTGGGTGGG
                                ||| ||||||    ||||||||||
                                TCT CCCCCA    CGACCCACCC
                                  A     _____
GAM371  MGC10924 3'  GGGGTGGGGGGTGGGGGTGG    9674           CT_
                                GGGGTGGGGG   GGGTGG
                                ||||||||||   ||||||
                                CCCCACCCCC   CCCACC
                                      ACC
GAM371  MGC13186 5'  CGGGGGTAGGGGTTGCGG    9780            CTGG
                                CGGGGGTGGGGG    GTGG
                                ||||||||||||    ||||
                                GCCCCCATCCCC    CGCC
                                      AA__
GAM371  MGC20255 3'  GATGGGGATGGGGCAGGCGGTG 9781     C         ___  TG
           GG                     GA GGGGGTGGGG   GC  GGTGGG
                                || ||||||||||   ||  ||||||
                                CT CCCCTACCCC   CG  CCACCC
                                 A         GTC  __
GAM371  MGC35521 3'  AGGTGGGGACCTGGGTGG    9782           _
                                GGGTGGGGGC TGGGTGG
                                |||||||||| |||||||
                                TCCACCCCTG ACCCACC
                                      G
GAM371  MGC4796  3'  GGGAGTGGCGCTGAGGGTGGG  9783         G G  __
                                GGGGGTG G GCT  GGGTGGG
                                ||||||| | |||  |||||||
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                                CCCTCAC C CGA  CCCACCC
                                   _ G   CT
GAM371  NAPA    3'  AGACGGGCACTGGGGGGCTGGG 9784        G T__
          TGGG                   AGACGGG G   GGGGGCTGGGTGGG
                                 ||||||| |   |||||||||||||
                                 TCTGCCC T   CCCCCGACCCACCC
                                    G GAC
GAM371  NET-6   5'  AGACGTGGGTGGGGGGCCGGG  9785       G       _
                                 AGACG GGGTGGGGG CTGGG
                                 ||||| ||||||||| |||||
                                 TCTGC CCCACCCCC GGCCC
                                   A       C
GAM371  NKX2B   5'  CGGGGGAGGGGGGGAGTGGG   9786       T    CT
                                 CGGGGG GGGGG  GGGTGGG
                                 |||||| |||||  |||||||
                                 GCCCCC CCCCC  CTCACCC
                                    T    __
GAM371  NOPAR   5'  GATGGGGGTGGGGGTGGG    9787    C        C
                                 GA GGGGGTGGGGG TGGG
                                 || ||||||||||| ||||
                                 CT CCCCCACCCCC ACCC
                                  A         _
GAM371  NPTXR   3'  GGGAGGTGGGGGTCTGGG    9788    _      _
                                 GGG GGTGGGGG CTGGG
                                 ||| |||||||| |||||
                                 CCC CCACCCCC GACCC
                                   T       A
GAM371  NPTXR   3'  GGGAGGTGGGGGTCTGGG    9788    _      _
                                 GGG GGTGGGGG CTGGG
                                 ||| |||||||| |||||
                                 CCC CCACCCCC GACCC
                                   T       A
GAM371  ODC-p   3'  CGGGGGTGGCAGGGTGGG    9789        G GCT
                                 CGGGGGTGG G   GGGTGGG
                                 ||||||||| |   |||||||
                                 GCCCCCACC T   CCCACCC
                                      G ___
GAM371  OLFM2   3'  GGGGGTGGGAGTGAGGG     9790         C   T
                                 GGGGGTGGGGG TGGG GG
                                 |||||||||| |||| ||
                                 CCCCCACCCTC ACTC CC
                                        _   _
GAM371  OLFM2   3'  GGGGTGGGGGTGGGGGTGG   9674         CT_
                                 GGGGTGGGGG  GGGTGG
                                 ||||||||||  ||||||
                                 CCCCACCCCC  CCCACC
                                      ACC
GAM371  P66     3'  GGGGGTAGGGGGTGTGG     9792          CTGG
                                 GGGGGTGGGGG  GTGG
                                 ||||||||||  ||||
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                                CCCCCATCCCC   CACC
                                      CA__
GAM371  P66     3'  GACGGGGGTGGGGGTAGGG   9791           CT
                                GACGGGGGTGGGGG  GGG
                                |||||||||||||  |||
                                CTGCCCCCACCCCC  CCC
                                      AT
GAM371  PADI1   3'  GATGGCGGGTGGGGGCAGG   9793    C _       T
                                GA GG GGGTGGGGGC GG
                                || || ||||||||| ||
                                CT CC CCCACCCCCG CC
                                 A  G        T
GAM371  PDGFC   5'  GGGGGTGGGGGTGAAGG    9794          C   T
                                GGGGGTGGGGG TGGG GG
                                |||||||||| |||| ||
                                CCCCCACCCCC ACTT CC

                                      _   _
GAM371  PIB5PA  3'  AGATGGGGGCCTGGGTGG    9795          _
                                GGGTGGGGGC TGGGTGG
                                |||||||||| |||||||
                                TCTACCCCCG ACCCACC
                                      G
GAM371  PLAGL2  3'  AGGCGGGGGTGGGGGCACAGG  9796    A          _
                                AG CGGGGGTGGGGGC TGGG
                                || ||||||||||||| ||||
                                TC GCCCCCACCCCCG GTCC
                                 C           T
GAM371  PRIC285 3'  GGGGTGGGGCGGGGTGGG    9797          G T
                                GGGGTGGGG C GGGTGGG
                                ||||||||| | |||||||
                                CCCCACCCC G CCCACCC
                                      _ C
GAM371  PTPN9   3'  AGGCAGGGACAGGTTGGGTGGG 9798    A     TG  GGC
                                AG CGGGGG  GG   TGGGTGGG
                                || ||||||  ||   ||||||||
                                TC GTCCCT  CC   ACCCACCC
                                 C     GT  A__
GAM371  R3HDM   5'  CGACGGCGGGGCTGGGTGGG   9799     G      G
                                CGG GGTGGGG CTGGGTGGG
                                ||| ||||||| |||||||||
                                GCT CCGCCCC GACCCACCC
                                  G     _
GAM371  RIN3    3'  GGGTGTGGGGGACTCATGGG   9800     G     _ GG
                                GGG GTGGGGG CT  GTGGG
                                ||| ||||||| ||  |||||
                                CCC CACCCCC GA  TACCC
                                  A      T  G_
GAM371  RTBDN   3'  GACGAGGGGGTGGGGTTCTGGG  9801      _       G_
                                GACG GGGGTGGGG  CTGGG
                                |||| |||||||||  |||||
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                                CTGC CCCCACCCC  GACCC
                                  T       AA
GAM371  SCAM-1   3'  GATGGGGGTGGGGGACTTGGG  9802    C       _ _
                                GA GGGGGTGGGGG CT GGG
                                || |||||||||| || |||
                                CT CCCCCACCCCC GA CCC
                                 A         T  A
GAM371  SEMA5A   3'  GAGGGTGAATGGACTGGGTGGG 9803        __
                                GGGGGTGG  GGGCTGGGTGGG
                                ||||||||  ||||||||||||
                                CTCCCACT  CCTGACCCACCC
                                     TA
GAM371  SEMA6A   5'  GGGCGGGGGGCGGGGTGG    9804        _ T
                                GGGTGGGGG C GGGTGG
                                ||||||||| | ||||||
                                CCCGCCCCC G CCCACC
                                      C C
GAM371  SHAPY    3'  GGGTGGGGGTCGGGGTGA    9805        CT_
                                GGGTGGGGG   GGGTGG
                                |||||||||   ||||||
                                CCCACCCCC   CCCACT
                                      AGC
GAM371  SP2      3'  GATCGGGGTGGGGGGTAGG   9806    CG       C
                                GA  GGGGTGGGGG TGGG
                                ||  |||||||||| ||||
                                CT  CCCCACCCCC ATCC
                                 AG         C
GAM371  STIM2    3'  AGGTGGGGAGTGGAGGGTGGG  9807        CT___
                                GGGTGGGGG    GGGTGGG
                                |||||||||    |||||||
                                TCCACCCCT    CCCACCC
                                      CACCT
GAM371  THG-1    3'  AGATGGGGGTGGGGTGTCTGCC 9808    C       _____
           GGG                    AGA GGGGGTGGGG    GCTGGG
                                ||| ||||||||||    ||||||
                                TCT CCCCCACCCC    CGGCCC
                                  A         ACAGA
GAM371  TOLLIP   3'  AGGCGGGGGCGGGGGAGGGTGG 9809    A        CT
           G                     AG CGGGGGTGGGGG  GGGTGGG
                                || ||||||||||||  |||||||
                                TC GCCCCCGCCCCC  CCCACCC
                                 C          T_
GAM371  UBP1     3'  GGGGGTGGGGGGGTTAGGGTGGG 9810          CT__
                                GGGGGTGGGGG   GGGTGGG
                                ||||||||||    |||||||
                                CCCCCACCCCC   CCCACCC
                                      CAAT
GAM371  VCY2IP1  3'  AGACCGGGGACTTGGGTGG   9811     G      _
                                GGG TGGGGGCT GGGTGG
                                ||| |||||||| ||||||
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                                TCT GCCCCTGA CCCACC
                                  G       A
GAM371  VEGFC    5'  CAGGGGTGGGGGGCGCGGG    9812           TGG
                                CGGGGGTGGGGGGC   GTGGG
                                ||||||||||||   |||||
                                GTCCCCACCCCCG   CGCCC
                                          ___
GAM371  ZNF145   5'  CGTGGCGGGGCTGGGTGG    9813     GG      G
                                CG  GGTGGGG CTGGGTGG
                                ||  ||||||| ||||||||
                                GC  CCGCCCC GACCCACC
                                 A_      _
GAM371  ZNF238   3'  GGGTGGAGGGTGGTGGTGG   9815          C  __
                                GGGTGGGGGG TGG  GTGG
                                |||||||||| |||  ||||
                                CCCACCTCC ACC  CACC
                                      C   AC
GAM371  ZNF238   3'  GGGTGGTGGTGGGGGGGG     9814     _    _  CT   T
                                GGG GGTGG GGG  GGG G
                                ||| ||||| |||  ||| |
                                CCC CCACC CCC  CCC C
                                  A    A  __  _
GAM371  ZWINT    3'  AGACAGGGGTTAGCTCTGGGTG 9816          G  GG
           GG                    AGACGGGGGT GG  CTGGGTGGG
                                ||||||||||  ||  |||||||||
                                TCTGTCCCCA TC  GACCCACCC
                                      A  GA
GAM371  LOC115207 3'  GGGGTGGGGGGTTCCTCTGGG   9817          _____
                                GGGGGTGGGGG     CTGGG
                                ||||||||||     |||||
                                CCCCACCCCC     GACCC
                                      AAGGA
GAM371  LOC116113 3'  AAACGGGGGGTGGGGGTGG    9818              C
                                AGACGGGGGGTGGGGG TGG
                                |||||||||||||||  |||
                                TTTGCCCCCCACCCCC ACC
                                          _
GAM371  LOC123591 5'  GGGGTGGGGAGGACTGGG    9819          ___
                                GGGGGTGGGG   GCTGGG
                                |||||||||   ||||||
                                CCCCACCCC   TGACCC
                                      TCC
GAM371  LOC124930 3'  GACGGGTGTGGGGGGCTGGGGG  9820        G          T
                                GACGGG GTGGGGGCTGGG GG
                                ||||||  ||||||||||||  ||
                                CTGCCC CACCCCCGACCC CC
                                   A          _
GAM371  LOC129198 5'  GGAGTCTGGGGGTTGGGTGG   9821        G_   C
                                GGGGGT  GGGG TGGGTGG
                                |||||  ||||  |||||||
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                                CCTCA  CCCC ACCCACC
                                   GA    A
GAM371   LOC145608 5'  CGGGGGTGGGGGGGAGGTGGG  9822           CT
                                CGGGGGTGGGGGG  GGGTGGG
                                |||||||||||  |||||||
                                GCCCCCACCCCC  TCCACCC
                                      C_
GAM371   LOC145693 5'  GGTGGGCGTGGGGTACATGGG  9823     _    _   C  G
                                GG GGGTG GGGG TG GTGGG
                                || ||||| |||| || |||||
                                CC CCCGC CCCC AT TACCC
                                 A    A   _ G
GAM371   LOC147054 5'  GGACTGGGTGGTTGGGTGG   9824     G   _ C
                                GGG TGGG GG TGGGTGG
                                ||| |||| || |||||||
                                CCT ACCC CC ACCCACC
                                  G   A  A
GAM371   LOC147071 5'  GGGGTGGGGGGCGCGG      9825          TGG
                                GGGGTGGGGGC   GTGG
                                ||||||||||   ||||
                                CCCCACCCCCG   CGCC
                                      ___
GAM371   LOC147791 3'  GGGCGGGGAGACTGGGTGG   9826     _ T
                                GGG GG GGGGGCTGGGTGG
                                ||| || ||||||||||||
                                CCC CC CCTCTGACCCACC
                                  G  _
GAM371   LOC148223 3'  GACGGAGCCAGCTGGGTGGG  9827        G GGG
                                GACGGGG T   GGCTGGGTGGG
                                ||||||| |   ||||||||||
                                CTGCCTC G   TCGACCCACCC
                                    G ___
GAM371   LOC151361 3'  GGTGGTGGGGAGATGGGGTGGG 9828     G      CT__
                                GG GGTGGGGG    GGGTGGG
                                || ||||||||    |||||||
                                CC CCACCCCT    CCCACCC
                                 A       CTAC
GAM371   LOC152762 3'  GGGGTGGGGGCTGTGG      9829          GG
                                GGGGTGGGGGCT  GTGG
                                ||||||||||  ||||
                                CCCCACCCCCGA  CACC
                                      __
GAM371   LOC152793 3'  GATGGGGTGTGGATTGCAGGGT 9830     C   _    G_  T
           GGG                    GA GGGG GTGGG  GC GGGTGGG
                                || |||| |||||  || |||||||
                                CT CCCC CACCT  CG CCCACCC
                                 A   A    AA  T
GAM371   LOC153525 5'  GGGGTGGGGGGTGGGGGTGG   9674          CT_
                                GGGGTGGGGG   GGGTGG
                                ||||||||||   ||||||
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                                CCCCACCCCC  CCCACC
                                     ACC
GAM371  LOC155006 3'  GGGGGTGAAGATGGTGGG   9831          CTG
                                GGGGGTGGGGG  GGTGGG
                                ||||||||||  ||||||
                                CCCCCACTTCT  CCACCC
                                     A__
GAM371  LOC159090 5'  GACGGGGGCGGGGGCTGGGGG  9832              T
                                GACGGGGGTGGGGGCTGGG GG
                                |||||||||||||||||| ||
                                CTGCCCCCGCCCCCGACCC CC
                                                 _
GAM371  LOC162333 5'  GATGGGGGTGGCAGAGTGGG  9833    C      G  CTG
                                GA GGGGGTGG GG  GGTGGG
                                || ||||||| ||  ||||||
                                CT CCCCCACC TC  TCACCC
                                  A      G  ___
GAM371  LOC163682 3'  GGGTGTGGGGGCCTGTGGG   9834     G       GG
                                GGG GTGGGGGCT  GTGGG
                                ||| |||||||||  |||||
                                CCC CACCCCCGG  CACCC
                                  A       A_
GAM371  LOC164537 5'  CGGGGGTGGGGGCCCGAGGG  9835           G  T
                                CGGGGGTGGGGGCT GG GGG
                                |||||||||||||| || |||
                                GCCCCCACCCCCGG CT CCC
                                       G  _
GAM371  LOC197419 3'  GGGGTGGGGGGCTCTGGG   9836          ___
                                GGGGTGGGGG  CTGGG
                                ||||||||||  |||||
                                CCCCACCCCC  GACCC
                                     CGA
GAM371  LOC200093 3'  GGGAGTGGGGGTGCACTGG   9735          C  G _
                                GGGGGTGGGGG TG G TGG
                                |||||||||||| || | |||
                                CCCTCACCCCC AC T ACC
                                      _  G G
GAM371  LOC200093 3'  GGTGGTGGGGGCGGTGGG   9734    G       TG
                                GG GGTGGGGGC  GGTGGG
                                || |||||||||  ||||||
                                CC CCACCCCCG  CCACCC
                                  A       __
GAM371  LOC200251 5'  GGGCGTGGGGGCGCGG     9837     G      TGG
                                GGG GTGGGGGC  GTGG
                                ||| ||||||||  ||||
                                CCC CACCCCCG  CGCC
                                  G      ____
GAM371  LOC200812 5'  GGGGGTGGGGAGGTGGG    9838          GCT
                                GGGGGTGGGG  GGGTGGG
                                |||||||||  |||||||
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                                CCCCCACCCC  TCCACCC
                                     ___
GAM371  LOC201173 5'  GGGGTGGGGGCGCGG      9825         TGG
                                GGGGTGGGGGC  GTGG
                                ||||||||||  ||||
                                CCCCACCCCCG  CGCC
                                     ___
GAM371  LOC202347 3'  CGGGGGGGGGGGGCGCGG    9839      T    TGG
                                CGGGGG GGGGGC  GTGG
                                |||||| ||||||  ||||
                                GCCCCC CCCCCG  CGCC
                                   C    ___
GAM371  LOC202518 5'  AGGCGGGGGGTAGGGGGCGG  9840    A    _    T
                                AG CGGGGGT GGGGGC GG
                                || ||||||| |||||| ||
                                TC GCCCCCA CCCCCG CC
                                 C     T    _
GAM371  LOC205095 3'  GGGGTTGGGGAGCCTGGG    9841     G   _ _
                                GGGG TGGGG GC TGGG
                                |||| ||||| || ||||
                                CCCC ACCCC CG ACCC
                                  A    T G
GAM371  LOC205418 3'  GGGTGGGCACGGGGGTGGG   9842       G T_
                                GGGTGGG GC  GGGTGGG
                                |||||||  ||  |||||||
                                CCCACCC TG  CCCACCC
                                     G CC
GAM371  LOC221415 5'  GAGGGGTGTGGGGGTGGG    9843    C   _    C
                                GA GGGG GTGGGGG TGGG
                                || |||| ||||||| ||||
                                CT CCCC CACCCCC ACCC
                                 _   A     _
GAM371  LOC221915 3'  AGGGGTGGGAGGTGG       9844        GGCT
                                GGGGGTGGG   GGGTGG
                                |||||||||   ||||||
                                TCCCCACCC   TCCACC
                                     ____
GAM371  LOC255299 5'  GGTGGGCGGTGGGGCTGGG   9845    _    __
                                GG GGGTGG  GGGCTGGG
                                || ||||||  ||||||||
                                CC CCCGCC  CCCGACCC
                                 A     AC
GAM371  LOC257200 3'  GGGTGGGAGGTGGGGGG     9846        C   T
                                GGGTGGGGG TGGG GGG
                                ||||||||| |||| |||
                                CCCACCCTC ACCC CCC
                                     C   _
GAM371  LOC257200 3'  GGGGGTGGGAGGTGGG      9728        GGCT
                                GGGGGTGGG   GGGTGGG
                                |||||||||   |||||||
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                                CCCCCACCC   TCCACCC
                                     _____
GAM371  LOC257619 5' AGGCGGGGGTAGGGGGCGG   9840    A     _    T
                                AG CGGGGGT GGGGGC GG
                                || ||||||| |||||| ||
                                TC GCCCCCA CCCCCG CC
                                 C      T     _
GAM371  LOC90630  5' AGATGGGGTGGGGGCTGG    9847    CG
                                AGA  GGGGTGGGGGCTGG
                                |||  ||||||||||||||
                                TCT  CCCCACCCCCGACC
                                  A_
GAM371  LOC91040  3' GGTGGTGGGGGGCGGTGGG    9734    G       TG
                                GG GGTGGGGGC  GGTGGG
                                || |||||||||  ||||||
                                CC CCACCCCCG  CCACCC
                                 A       __
GAM371  LOC91040  3' GGGAGTGGGGGGTGCACTGG   9735          C  G _
                                GGGGGTGGGGG TG G TGG
                                |||||||||| || | |||
                                CCCTCACCCCC AC T ACC
                                       _  G G
GAM371  LOC91208  5' AGATGGGGTGGGGGCTGG    9847    CG
                                AGA  GGGGTGGGGGCTGG
                                |||  ||||||||||||||
                                TCT  CCCCACCCCCGACC
                                  A_
GAM371  LOC91397  5' AAGGTGGGGGTGCAGGGTGGG  9848         CT__
                                GGGGGTGGGGG   GGGTGGG
                                ||||||||||   |||||||
                                TTCCACCCCC   CCCACCC
                                      ACGT
GAM371  LOC91522  3' CGGTGGCTTTGGGGCTGGGTGG 9849    G   G__
           G                     CGG GGT   GGGGCTGGGTGGG
                                ||| |||   ||||||||||||
                                GCC CCG   CCCCGACCCACCC
                                  A   AAA
GAM371  LOC91813  5' GGGGTGGGGGTGGGGGTGG   9674         CT_
                                GGGGTGGGGG   GGGTGG
                                |||||||||   ||||||
                                CCCCACCCCC   CCCACC
                                      ACC
GAM371  LOC92162  3' AGGCAGGGGTGGGGGCAGGG  9850    A         T
                                AG CGGGGGTGGGGGC GGG
                                || ||||||||||||| |||
                                TC GTCCCCACCCCCG CCC
                                 C          T
GAM371  LOC92689  3' GATGGGGGTGGGGGATGG    9851    C        C
                                GA GGGGGTGGGGG TGG
                                || |||||||||| |||
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                                CT CCCCCACCCCC ACC
                                 A         T
GAM371  LOC92906  5'  GGGTGGGGGTGGCGGTGG    9852          C  __
                                GGGTGGGGG TGG  GTGG
                                ||||||||| |||  ||||
                                CCCACCCCC ACC  CACC
                                     _  GC
GAM371  LOC95633  3'  GAGGGGGTGGGGGGCCAAGGTGG 9853     C          _
          G                      GA GGGGGTGGGGGCTG GGTGGG
                                || |||||||||||||| ||||||
                                CT CCCCCACCCCCGGT CCACCC
                                 _          T
GAM372  BDP1     5'  AGGCAGCCTCACGGCCGC    9856          __
                                AGGCAGCC  GCGGCCGC
                                ||||||||  ||||||||
                                TCCGTCGG  TGCCGGCG
                                     AG
GAM372  CACNA1B  5'  AGCAGCCACGGAGCCGCC    9857           __
                                GGCAGCCGCG  GCCGCC
                                ||||||||||  ||||||
                                TCGTCGGTGC  CGGCGG
                                      CT
GAM372  CDKN2C   5'  GGCAGCCAGTCCGGTCGCC   9858          ___  C
                                GGCAGCCG   CGG CGCC
                                ||||||||   ||| ||||
                                CCGTCGGT   GCC GCGG
                                     CAG   A
GAM372  COL18A1  3'  AGACAGCCAATGACTGCC    9859          C_  C
                                AGGCAGCCG  GGC GCC
                                |||||||||  ||| |||
                                TCTGTCGGT  CTG CGG
                                      TA   A
GAM372  COL18A1  3'  AGACAGCCAATGACTGCC    9859          C_  C
                                AGGCAGCCG  GGC GCC
                                |||||||||  ||| |||
                                TCTGTCGGT  CTG CGG
                                      TA   A
GAM372  COL18A1  3'  AGACAGCCAATGACTGCC    9859          C_  C
                                AGGCAGCCG  GGC GCC
                                |||||||||  ||| |||
                                TCTGTCGGT  CTG CGG
                                      TA   A
GAM372  FKBP2    5'  AGCAGCCAGGGACCCGCC    9860          C  __
                                GGCAGCCG GG  CCGCC
                                |||||||| ||  |||||
                                TCGTCGGT CC  GGCGG
                                     C  TG
GAM372  ING1L    5'  GCACCGGCCGCGGCCGCC    9861      ____
                                GCA   GCCGCGGCCGCC
                                |||   ||||||||||||
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                                CGT  CGGCGCCGGCGG
                                  GGC
GAM372  LEF1    5'  GGCAGCCGGAGCAGCTGCC   9862        ___    C
                                GGCAGCC  GCGGC GCC
                                |||||||  ||||| |||
                                CCGTCGG  CGTCG CGG
                                    CCT    A
GAM372  MAG     3'  GGTCAGCCACGCAGGCTGCC  9863    _    ___  C
                                GG CAGCCGC  GGC GCC
                                || |||||||  ||| |||
                                CC GTCGGTG  CCG CGG
                                 A      CGT  A
GAM372  MAG     3'  GGTCAGCCACGCAGGCTGCC  9863    _    ___  C
                                GG CAGCCGC  GGC GCC
                                || |||||||  ||| |||
                                CC GTCGGTG  CCG CGG
                                 A      CGT  A
GAM372  NDRG1   3'  GGCAGCCGCACTGGCCGCC   9864        ___
                                GGCAGCCGC  GGCCGCC
                                |||||||||  |||||||
                                CCGTCGGCG  CCGGCGG
                                     TGA
GAM372  PIK3R2  5'  AGGCGACCACAGGGGCCGC   9865     A   ___
                                AGGC GCCGC  GGCCGC
                                ||||  |||||  ||||||
                                TCCG TGGTG  CCGGCG
                                  C    TCC
GAM372  PTBP1   3'  GCAGCCGCGGCCGCCG     9866          III
                                GCAGCCGCGGCCGCC  G
                                ||||||||||||||  |
                                CGTCGGCGCCGGCGG  C
                                        III
GAM372  PTBP1   3'  GCAGCCGCGGCCGCCG     9866          III
                                GCAGCCGCGGCCGCC  G
                                ||||||||||||||  |
                                CGTCGGCGCCGGCGG  C
                                        III
GAM372  PTEN    5'  AGCCGCCGCGGCCGCCG    9867     A       III
                                GGC GCCGCGGCCGCC  G
                                |||  ||||||||||||  |
                                TCG CGGCGCCGGCGG  C
                                  G         III
GAM372  SLC19A1 3'  AGGCAGCCCCCCCCAAGGCTGCC 9868       GC_____  C  III
          G                      AGGCAGCC     GGC GCC  G
                                 ||||||||     ||| |||  |
                                 TCCGTCGG     CCG CGG  C
                                     GGGGGTT  A  III
GAM372  SLC9A5  5'  GGCACCGCAGCGGCCGCC   9869     __  C
                                GGCA  GC GCGGCCGCC
                                ||||  ||  |||||||||
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                                CCGT  CG CGCCGGCGG
                                  GG  T
GAM372  TCIRG1   5' AGGAAGCCGCGGCAGGCC    9870     C       C_
                                AGG AGCCGCGGC  GCC
                                ||| |||||||||  |||
                                TCC TCGGCGCCG  CGG
                                  T       TC
GAM372  FLJ10375 3' AGGAGCCACGATGCTGCC    9871     C     __ C
                                AGG AGCCGCG  GC GCC
                                ||| |||||||  || |||
                                TCC TCGGTGC  CG CGG
                                  _     TA  A
GAM372  FLJ10493 5' ACAGCCGCGGCCGCCG      9872            III
                                GCAGCCGCGGCCGCC  G
                                ||||||||||||||  |
                                TGTCGGCGCCGGCGG  C
                                        III
GAM372  FLJ20151 3' AGGCAACCAAGAGGGGCTGCC 9873         C____  C
                                AGGCAGCCG    GGC GCC
                                |||||||||    ||| |||
                                TCCGTTGGT    CCG CGG
                                     TCTCC   A
GAM372  FLJ20255 5' AGCCAGCTCGCAAGCCGCC   9874     G  _  _
                                AG CAGC CGCG GCCGCC
                                || |||| |||| ||||||
                                TC GTCG GCGT CGGCGG
                                 G   A   T
GAM372  FLJ20359 3' AGCAGCCACCACAGCCGCC   9875        ___
                                GGCAGCCGC  GGCCGCC
                                |||||||||  |||||||
                                TCGTCGGTG  TCGGCGG
                                     GTG
GAM372  FLJ20666 5' AGCCAGCACAGCAGCCGCC   9876     G  _ _
                                AG CAGC C GCGGCCGCC
                                || |||| | |||||||||
                                TC GTCG G CGTCGGCGG
                                 G   T T
GAM372  HSPC048  5' AGACAGCCCCGCACCGCC    9877        G _
                                AGGCAGCC CG GCCGCC
                                |||||||| || ||||||
                                TCTGTCGG GC TGGCGG
                                    G  G
GAM372  KIAA0652 3' AGGCAGCCACCAGGGCTGC   9878         ___  C
                                AGGCAGCCGC  GGC GC
                                ||||||||||  ||| ||
                                TCCGTCGGTG  CCG CG
                                      GTC   A
GAM372  KIAA1300 3' AGCAGCCACCATCTGGCTGCC 9879         _____  C
                                GGCAGCCGC    GGC GCC
                                |||||||||    ||| |||
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                                TCGTCGGTG    CCG CGG
                                     GTAGA   A
GAM372  MGC11303  5'  GGCAGCCGCGCAGCCGCC    9880          __
                                GGCAGCCGCG  GCCGCC
                                ||||||||||  ||||||
                                CCGTCGGCGC  CGGCGG
                                     GT
GAM372  MGC4796   5'  GCAGCCACCCGAGCCGCC    9881         ___
                                GCAGCCGC   GGCCGCC
                                ||||||||   |||||||
                                CGTCGGTG   TCGGCGG
                                     GGC
GAM372  MOT8      5'  GGGAGCCGCGGCTTCGCC    9882     C       __
                                GG AGCCGCGGC  CGCC
                                || |||||||||  ||||
                                CC TCGGCGCCG  GCGG
                                 C        AA
GAM372  RAP2B     3'  GGCCGGCGCGCGGTGGCCGCC 9883      A_ _  ___
                                GGC  GC CGC   GGCCGCC
                                |||  || |||   |||||||
                                CCG  CG GCG   CCGGCGG
                                  GC  C   CCA
GAM372  TMLHE     5'  AGGCAGCCTTTCACCCGCC   9884         G__  G
                                AGGCAGCC   CG CCGCC
                                ||||||||   || |||||
                                TCCGTCGG   GT GGCGG
                                     AAA  G
GAM372  TPC2      3'  GGCTGGCCACAGCATGGCCGCC 9885     A_    ______      III
          G                      GGC  GCCGC    GGCCGCC   G
                                |||  |||||    |||||||  |
                                CCG  CGGTG    CCGGCGG   C
                                  AC    TCGTA      III
GAM372  LOC122830 5'  GGCAGCCTCCACAGCCGCC   9886         ___
                                GGCAGCC   GCGGCCGCC
                                |||||||   |||||||||
                                CCGTCGG   TGTCGGCGG
                                     AGG
GAM372  LOC149506 3'  AGGCAGCCCCCAACCGCC    9887         _ G
                                AGGCAGC C CGGCCGCC
                                ||||||| | ||||||||
                                TCCGTCG G GTTGGCGG
                                     G G
GAM372  LOC163597 5'  AGGCAGCCGGCACCCTTGC   9888          _  G  __
                                AGGCAGCCG CG CC  GC
                                |||||||||  || ||  ||
                                TCCGTCGGC GT GG  CG
                                     C  G  AA
GAM372  LOC164714 5'  GGCTCAACCACCGGCTGCCG  9889      __     _  C   III
                                GGC  AGCCGC GGC GCC   G
                                |||  |||||| ||| |||   |
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                                CCG  TTGGTG CCG CGG   C
                                  AG     G   A   III
GAM372   LOC219392 5'  AGGCAGCCAAAGACTGCC    9890          C_   C
                                AGGCAGCCG  GGC GCC
                                |||||||||  ||| |||
                                TCCGTCGGT  CTG CGG
                                     TT   A
GAM372   LOC219686 5'  AGCAGCCGCGGCCGCCG     9891               III
                                GGCAGCCGCGGCCGCC   G
                                ||||||||||||||||   |
                                TCGTCGGCGCCGGCGG   C
                                          III
GAM372   LOC219790 5'  AGGAGCCGCAGAGGACGCC    9892      C       C___
                                AGG AGCCGCGG    CGCC
                                ||| ||||||||    ||||
                                TCC TCGGCGTC    GCGG
                                  _       TCCT
GAM372   LOC220954 3'  AGCAGCCACACAACTGCC     9893           __  C
                                GGCAGCCGCG  GC GCC
                                ||||||||||  || |||
                                TCGTCGGTGT  TG CGG
                                      GT  A
GAM372   LOC253489 5'  AGCAGAAGACAGCGGCCGCC   9894        ____ C
                                GGCAG    C GCGGCCGCC
                                |||||    | |||||||||
                                TCGTC    G CGCCGGCGG
                                   TTCT T
GAM372   LOC90268  5'  GGCTGCCCGCTGGCCGCC    9895      A  _ _
                                GGC GCC GC GGCCGCC
                                ||| ||| || |||||||
                                CCG CGG CG CCGGCGG
                                  A   G  A
GAM372   LOC90362  5'  AGCGGCCGCAGCAGCGCC    9896      A       __
                                GGC GCCGCGGC  CGCC
                                ||| ||||||||  ||||
                                TCG CGGCGTCG  GCGG
                                  C       TC
GAM372   LOC91661  3'  AAGCAGCCCAGATCCTGC    9897         G  __ _
                                AGGCAGCC CGG  CC GC
                                ||||||||  |||  || ||
                                TTCGTCGG GTC  GG CG
                                     _   TA  A
GAM372   LOC92305  5'  GGCCGCCGCCCGGCCGCC    9898      A    __
                                GGC GCCGC  GGCCGCC
                                ||| |||||  |||||||
                                CCG CGGCG  CCGGCGG
                                  G    GG
GAM373   ATF6      5'  TAACGCTGACGAGACGGTGGCC 9901          TT_  AAC
                                TGACGCTGAC   AC   GGCC
                                ||||||||||   ||   ||||
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                                ATTGCGACTG  TG  CCGG
                                     CTC  CCA
GAM373  BSG     3'  TGGCACTGACTCCGGC     9902    A      ACAA
                                TG CGCTGACTT   CGGC
                                || |||||||||   ||||
                                AC GTGACTGAG   GCCG
                                 C       ____
GAM373  BSG     3'  TGGCACTGACTCCGGC     9902    A      ACAA
                                TG CGCTGACTT   CGGC
                                || |||||||||   ||||
                                AC GTGACTGAG   GCCG
                                 C       ____
GAM373  CKTSF1B1 3'  TGAGCAGATTGCAACGGCC   9903    C  T  C  A
                                TGA GC GA TT CAACGGCC
                                ||| || || || ||||||||
                                ACT CG CT AA GTTGCCGG
                                  _  T  _  C
GAM373  FBXL11   3'  TGACGCTGGCCTCAGAGCC   9904       A   A  AC
                                TGACGCTG CTT CA  GGCC
                                |||||||| ||| ||  ||||
                                ACTGCGAC GGA GT  TCGG
                                     C   _  C_
GAM373  IL10RA   3'  TGAGCTGACTTCAGCC     9905    C      ACAA
                                TGA GCTGACTT   CGGCC
                                ||| ||||||||   |||||
                                ACT CGACTGAA   GTCGG
                                  _      ____
GAM373  LPIN2    3'  TGACGCTGCTTCCACGGGCC  9906       A   ACA   _
                                TGACGCTG CTT   ACGG CC
                                |||||||| |||   |||| ||
                                ACTGCGAC GAA   TGCC GG
                                     _  GG_   C
GAM373  PFKFB4   3'  TGACATGGATACAACGGCC   9907     C  ACT
                                TGACG TG   TACAACGGCC
                                ||||| ||   ||||||||||
                                ACTGT AC   ATGTTGCCGG
                                   _ CT_
GAM373  SLC7A5   3'  TGACGCTGGACCACTTGGC   9908       _  T  AAC
                                TGACGCTG ACT AC   GGC
                                |||||||| ||| ||   |||
                                ACTGCGAC TGG TG   CCG
                                     C   _  AA_
GAM373  WHSC1    3'  TGAGCTGGGCTCAGACGG    9909    C   A_   CA
                                TGA GCTG  CTTA  ACGG
                                ||| ||||  ||||  ||||
                                ACT CGAC  GAGT  TGCC
                                  _   CC   C_
GAM373  WHSC1    3'  TGAGCTGGGCTCAGACGG    9909    C   A_   CA
                                TGA GCTG  CTTA  ACGG
                                ||| ||||  ||||  ||||
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                                ACT CGAC  GAGT  TGCC
                                  _   CC   C_
GAM373  WHSC1    3'  TGAGCTGGGCTCAGACGG   9909     C   A_   CA
                                TGA GCTG  CTTA  ACGG
                                ||| ||||  ||||  ||||
                                ACT CGAC  GAGT  TGCC
                                  _   CC   C_
GAM373  WHSC1    3'  TGAGCTGGGCTCAGACGG   9909     C   A_   CA
                                TGA GCTG  CTTA  ACGG
                                ||| ||||  ||||  ||||
                                ACT CGAC  GAGT  TGCC
                                  _   CC   C_
GAM373  CBX1     5'  TGACGCTGCTTGTGCGGCC   9910        A  ACAA
                                TGACGCTG CTT   CGGCC
                                |||||||| |||   |||||
                                ACTGCGAC GAA   GCCGG
                                     _  CAC_
GAM373  DKFZP434C171 3'  TGACGCTGGCTTAGGGCC   9911        A   CAAC
                                TGACGCTG CTTA   GGCC
                                |||||||| ||||   ||||
                                ACTGCGAC GAAT   CCGG
                                     C   C___
GAM373  DKFZP434P211 3'  TGACTTGACTTAGACAGGCC  9912      GC     CA _
                                TGAC  TGACTTA  AC GGCC
                                ||||  |||||||  || ||||
                                ACTG  ACTGAAT  TG CCGG
                                  A_     C_  T
GAM373  EPS8R3   5'  TGACGCTGCTGAGGACGGC   9913        A  TACA
                                TGACGCTG CT   ACGGC
                                |||||||| ||   |||||
                                ACTGCGAC GA   TGCCG
                                     _ CTCC
GAM373  EPS8R3   5'  TGACGCTGCTGAGGACGGC   9913        A  TACA
                                TGACGCTG CT   ACGGC
                                |||||||| ||   |||||
                                ACTGCGAC GA   TGCCG
                                     _ CTCC
GAM373  FLJ10932 3'  TGACACTGGCTTACGGGACC  9914        A   AAC
                                TGACGCTG CTTAC  GGCC
                                |||||||| |||||  ||||
                                ACTGTGAC GAATG  CTGG
                                     C   CC_
GAM373  KIAA0527 3'  TGACGCTGATGCTACTGG   9915        C_  AAC
                                TGACGCTGA  TTAC  GG
                                |||||||||  ||||  ||
                                ACTGCGACT  GATG  CC
                                     AC   A__
GAM373  KIAA1183 3'  TGACGCTGGCAAAACGCGGCC 9916        ACTT_  AA
                                TGACGCTG   AC  CGGCC
                                ||||||||   ||  |||||
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                                ACTGCGAC    TG  GCCGG
                                    CGTTT  C_
GAM373  PINK1    3'  TGACGCTGATTTAGGC     9917         C   CAAC
                                TGACGCTGA TTA    GGC
                                ||||||||| |||    |||
                                ACTGCGACT AAT    CCG
                                    A  _____
GAM373  SKD3     3'  TGAGGCTGACTCCATGGCC   9918      C       ACAAC
                                TGA GCTGACTT    GGCC
                                ||| ||||||||    ||||
                                ACT CGACTGAG    CCGG
                                  C       GTA__
GAM373  TCBAP0758 3'  TGACGCTGGGCTGCAGGCC   9919         AC  A  AC
                                TGACGCTG  TT CA  GGCC
                                ||||||||  || ||  ||||
                                ACTGCGAC  GA GT  CCGG
                                    CC  C  __
GAM373  LOC145842 5'  AACGCTGCAGCCAACGGCC   9920        ACTTA
                                GACGCTG    CAACGGCC
                                |||||||    ||||||||
                                TTGCGAC    GTTGCCGG
                                    GTCG_
GAM373  LOC150174 3'  TGACTTGACTTAGACAGGCC  9912      GC      CA  _
                                TGAC  TGACTTA  AC GGCC
                                ||||  |||||||  || ||||
                                ACTG  ACTGAAT  TG CCGG
                                  A_      C_  T
GAM373  LOC150213 3'  TGACTTGACTTAGACAGGCC  9912      GC      CA  _
                                TGAC  TGACTTA  AC GGCC
                                ||||  |||||||  || ||||
                                ACTG  ACTGAAT  TG CCGG
                                  A_      C_  T
GAM373  LOC150236 3'  TGACTTGACTTAGACAGGCC  9912      GC      CA  _
                                TGAC  TGACTTA  AC GGCC
                                ||||  |||||||  || ||||
                                ACTG  ACTGAAT  TG CCGG
                                  A_      C_  T
GAM373  LOC166983 5'  CGGCGCTGACCCACTGGCC   9921     A         AAC
                                TG CGCTGACTTAC   GGCC
                                || ||||||||||   ||||
                                GC GCGACTGGGTG   CCGG
                                 C         A__
GAM373  LOC255777 5'  GATGCTGACTTAAAGCC     9922     C       CAAC
                                GA GCTGACTTA    GGCC
                                || |||||||||    ||||
                                CT CGACTGAAT    TCGG
                                 A        T___
GAM373  LOC257096 5'  GCTGCCGGGTACAACGGC    9923      A  ___
                                GCTG CT   TACAACGGC
                                |||| ||   |||||||||
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                                CGAC GG   ATGTTGCCG
                                  _ CCC
GAM373  LOC91301  5'  GCTGCCCACAGCAACGGCC   9924      A    ___
                                GCTG CTTACA   ACGGCC
                                |||| ||||||   ||||||
                                CGAC GGGTGT   TGCCGG
                                  _     CGT
GAM374  KYNU      3'  AGTTACATGTGGTCAATGGT  9927     _   C      C
                                AGT ACGT GTGGTCAA GGT
                                ||| |||| |||||||| |||
                                TCA TGTA CACCAGTT CCA
                                  A   _      A
GAM374  P17.3     5'  TCCAGTTGTCGTGGCTTCG   9928       AC      CAA
                                TCCAGT  GTCGTGGT   CG
                                ||||||  ||||||||   ||
                                AGGTCA  CAGCACCG   GC
                                   A_      AA_
GAM375  ADRBK1    3'  CAGCCAAGCCCCGCAGTG    9931      CCCT    _
                                TAGCC    GGCCC GCAGTG
                                |||||    ||||| ||||||
                                GTCGG    TCGGG CGTCAC
                                   T___    G
GAM375  BCAR1     3'  ACCCAACCCGGGCCCGTGGTGC 9932      __    _   CA
                                GCCC  CCTGG CCCG  GTGC
                                ||||  ||||| ||||  ||||
                                TGGG  GGGCC GGGC  CACG
                                  TT    C    AC
GAM375  BCAT1     5'  TAGCCCCTGGCCGTG      9933       C    CGCA
                                TAGCCCC TGGCC    GTG
                                ||||||| |||||    |||
                                ATCGGGG ACCGG    CAC
                                   _    ____
GAM375  BLTR2     5'  CAGCCCACCTTCTGCAGTG   9934       _  GGCCC
                                TAGCCC CCT    GCAGTG
                                |||||| |||    ||||||
                                GTCGGG GGA    CGTCAC
                                   T   AGA__
GAM375  CDH7      5'  CAGCCCACTCCGCGGTGC    9935       C  GGC   A
                                TAGCCC CT   CCGC GTGC
                                |||||| ||   |||| ||||
                                GTCGGG GA   GGCG CACG
                                   T ___    C
GAM375  CDX2      5'  GCGCCCCAGCCCCGCGGTGC   9936    C   TG    A
                                GC CCC  GCCCGC GTGC
                                || |||  |||||| ||||
                                CG GGG  CGGGCG CACG
                                 C  GT     C
GAM375  CHRNA3    3'  CAGCCCAAAATGTCCGTAGTGC 9937       CC__  GC   C
                                TAGCCC    TG  CCG AGTGC
                                ||||||    ||  ||| |||||
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                                GTCGGG   AC  GGC TCACG
                                   TTTT  A_   A
GAM375  CREBL2   3'  GCCCACTAGCTGCGGTGC    9938      C    CC  A
                                GCCC CTGGC  GC GTGC
                                |||| |||||  || ||||
                                CGGG GATCG  CG CACG
                                  T    A_  C
GAM375  CRSP6    5'  AGCCCGCAGCCGCGGTGC    9939       CCT   C  A
                                AGCCC   GGCC GC GTGC
                                |||||   |||| || ||||
                                TCGGG   TCGG CG CACG
                                   CG_   _  C
GAM375  ELAC2    3'  CAGCCTCCTGGCCCGCGGC   9940       C        A
                                TAGCC CCTGGCCCGC GT
                                ||||| |||||||||| ||
                                GTCGG GGACCGGGCG CG
                                   A         C
GAM375  GNB2     3'  CAGCCCCGCAGCCCTGGCCTGT 9941        C     __ ____
            AGTG                   TAGCCCC TGGCCC  GC   AGTG
                                ||||||| ||||||  ||   ||||
                                GTCGGGG GTCGGG  CG   TCAC
                                   C     AC  GACA
GAM375  GNL1     5'  GCCCTCTGGCCCGAGAGC    9942      C       C  T
                                GCCC CTGGCCCG AG GC
                                |||| |||||||| || ||
                                CGGG GACCGGGC TC CG
                                  A       _  T
GAM375  GNL1     5'  GCCCTCTGGCCCGAGAGC    9942      C       C  T
                                GCCC CTGGCCCG AG GC
                                |||| |||||||| || ||
                                CGGG GACCGGGC TC CG
                                  A       _  T
GAM375  HOXD3    3'  AGTCCCTTGGTCCGCAGT    9943     C  C   C
                                AG CCC TGG CCGCAGT
                                || ||| ||| |||||||
                                TC GGG ACC GGCGTCA
                                 A  A   A
GAM375  JUND     3'  AGCCCCCTTGCGGCGCGGTG  9944         G  C_   A
                                AGCCCCCT GC  CGC GTG
                                |||||||| ||  ||| |||
                                TCGGGGGA CG  GCG CAC
                                    A  CC   C
GAM375  KCNK5    3'  CAGCTCCCTGGCCACCAGC   9945      C       CG
                                TAGC CCCTGGCC  CAGT
                                |||| ||||||||  ||||
                                GTCG GGGACCGG  GTCG
                                  A       TG
GAM375  KCNK5    5'  AGCTCCGCATGCGCAGTGC   9946     C  CTG  C__
                                AGC CC   GC   CGCAGTGC
                                ||| ||   ||   ||||||||
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                                TCG GG   CG   GCGTCACG
                                  A ___  TAC
GAM375  LARS2   3' AGCCCTCTGGGGCGTGC    9947      C   CCC  A
                                AGCCC CTGG   GC GTGC
                                ||||| ||||   || ||||
                                TCGGG GACC   CG CACG
                                  A   C__  _
GAM375  MATK    5' CAGCCCCCTGCAGCCTGGTG  9948         __  CGCA
                                TAGCCCCCTG  GCC   GTG
                                ||||||||||  |||   |||
                                GTCGGGGGAC  CGG   CAC
                                      GT   AC__
GAM375  NCOR2   3' GCCGCCCTGGCCGCCTG    9949     _      C  AG
                                GCC CCCTGGCC GC  TG
                                ||| |||||||| ||  ||
                                CGG GGGACCGG CG  AC
                                  C       _ G_
GAM375  NOLA2   3' TAGCTTCCAGCGGCAGGTGC  9950     CC  T   CC   _
                                TAGC  CC GGC  GCAG TGC
                                ||||  || |||  |||| |||
                                ATCG  GG TCG  CGTC ACG
                                  AA  _   C_   C
GAM375  NTSR1   3' AGCCCCCTCCCATGTG     9951        GG   CA
                                AGCCCCCT  CCCG  GTG
                                ||||||||  ||||  |||
                                TCGGGGGA  GGGT  CAC
                                    __    A_
GAM375  OPHN1   3' GCTCCCTGGCCTCCAGGC   9952    C      CG   T
                                GC CCCTGGCC  CAG GC
                                || ||||||||  ||| ||
                                CG GGGACCGG  GTC CG
                                 A       AG  _
GAM375  PBX2    3' TAGCCCCCCGGCCCATGC   9953          GCA
                                TAGCCCCCTGGCCC   GTGC
                                ||||||||||||||   ||||
                                ATCGGGGGGCCGGG   TACG
                                      ____
GAM375  RAD52   3' CAGCCCTCTTCAGCTGCAGTG 9954      C  __  CC
                                TAGCCC CT  GGC  GCAGTG
                                ||||||  ||  |||  ||||||
                                GTCGGG GA  TCG  CGTCAC
                                   A  AG   A_
GAM375  RAD52   3' CAGCCCTCTTCAGCTGCAGTG 9954      C  __  CC
                                TAGCCC CT  GGC  GCAGTG
                                ||||||  ||  |||  ||||||
                                GTCGGG GA  TCG  CGTCAC
                                   A  AG   A_
GAM375  RAD52   3' CAGCCCTCTTCAGCTGCAGTG 9954      C  __  CC
                                TAGCCC CT  GGC  GCAGTG
                                ||||||  ||  |||  ||||||
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                                GTCGGG GA  TCG  CGTCAC
                                   A  AG   A_
GAM375  RAD52    3'  CAGCCCTCTTCAGCTGCAGTG  9954       C  __   CC
                                TAGCCC CT  GGC  GCAGTG
                                |||||| ||  |||  ||||||
                                GTCGGG GA  TCG  CGTCAC
                                   A  AG   A_
GAM375  SMARCC1  5'  GCCCACCCCGGCCCTCGCGGTG 9955      __      __ A
                                GCCC  CCTGGCCC  GC GTG
                                ||||  ||||||||  || |||
                                CGGG  GGGCCGGG  CG CAC
                                  TG       AG  C
GAM375  SREBF1   3'  GCTCGGCCCCTGCAGTGC    9956    CCCC    __
                                GC   TGGCCC  GCAGTGC
                                ||   ||||||  |||||||
                                CG   GCCGGG  CGTCACG
                                 A___     GA
GAM375  TNFSF9   3'  TAGCCCCCTAGCCTGGGC    9957           C__
                                TAGCCCCCTGGCC   GC
                                ||||||||||||   ||
                                ATCGGGGGATCGG   CG
                                       ACC
GAM375  VRK2     5'  GCGTCGGCCTCGCAGTGC    9958    CCCC    _
                                GC   TGGCC CGCAGTGC
                                ||   ||||| ||||||||
                                CG   GCCGG GCGTCACG
                                 CA__    A
GAM375  AFAP     3'  GCCCTCCTGGTGGGCGTGC   9959     _   CCC  A
                                GCCC CCTGG   GC GTGC
                                |||| |||||   || ||||
                                CGGG GGACC   CG CACG
                                  A    ACC  _
GAM375  C20orf100 3'  GCCCTCTGGCCCATGC     9960     C     GCA
                                GCCC CTGGCCC   GTGC
                                |||| |||||||   ||||
                                CGGG GACCGGG   TACG
                                  A     ___
GAM375  CBX6     3'  GCCCTCTCCACAGTGC     9961     C  GGC
                                GCCC CT   CCGCAGTGC
                                |||| ||   |||||||||
                                CGGG GA   GGTGTCACG
                                  A ___
GAM375  DKFZP434K028 3'  TAGTGCCCTGGCCCGGGGC   9962     CC       CA
                                TAG  CCCTGGCCCG  GT
                                |||  ||||||||||  ||
                                ATC  GGGACCGGGC  CG
                                  AC        CC
GAM375  DKFZp547H236 5'  CAGCCCCTGACGGCCCGCGGTG 9963        C__      A
                                TAGCCCC   TGGCCCGC GTG
                                |||||||   |||||||| |||
```

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                                GTCGGGG  GCCGGGCG CAC
                                   ACT      C
GAM375  DKFZP566J091 3'  TAACCCCCTGGCTCTAAGC   9964          CCGC
                                TAGCCCCCTGGC   AGT
                                ||||||||||||  |||
                                ATTGGGGGACCG   TCG
                                     AGAT
GAM375  DNAJC5   3'  CAGCCCCTTCTGGAGGTGGTGC 9965       __   CCCGCA
                                TAGCCCC  CTGG    GTGC
                                |||||||  ||||    ||||
                                GTCGGGG  GACC    CACG
                                   AA   TCCAC_
GAM375  DSCR1L1  3'  TAGCCCTTTTGTCCGAGAGGC  9966      CC_ GC  C  T_
                                TAGCCC  TG  CCG AG  GC
                                ||||||  ||  ||| ||  ||
                                ATCGGG  AC  GGC TC  CG
                                   AAA  A_  _  TC
GAM375  EFNA5    3'  TAGCCCGCTGACACAGTGC   9967      C    CC
                                TAGCCC CTGGC  GCAGTGC
                                |||||| |||||  |||||||
                                ATCGGG GACTG  TGTCACG
                                   C    __
GAM375  FLJ13902  3'  GCTCCCAGCACAGTGC     9968    C  T  CC
                                GC CCC GGC  GCAGTGC
                                || ||| |||  |||||||
                                CG GGG TCG  TGTCACG
                                 A  _  __
GAM375  FLJ14957  3'  AGTCCTCTGGCCCACAGGC   9969    C  C       T
                                AG CC CTGGCCCGCAG GC
                                || || ||||||||||| ||
                                TC GG GACCGGGTGTC CG
                                 A  A        _
GAM375  FLJ20234  3'  TAGCCCGCTGGTCCCTGGTG  9970      C   _  GCA
                                TAGCCC CTGG CCC   GTG
                                |||||| |||| |||   |||
                                ATCGGG GACC GGG   CAC
                                   C   A  AC_
GAM375  FLJ22349  3'  GCCCCCTGAGCCCTGAGC    9971        _   GC
                                GCCCCCTG GCCC  AGT
                                |||||||| ||||  |||
                                CGGGGGAC CGGG  TCG
                                     T   AC
GAM375  FLJ23375  5'  GCCCGCCAGGCCGTAGTGC   9972     _ T   C C
                                GCCC CC GGCC G AGTGC
                                |||| || |||| | |||||
                                CGGG GG CCGG C TCACG
                                  C  T   _ A
GAM375  GP5      3'  CAGCCCCCCGGCAGTG     9973          CCGC
                                TAGCCCCCTGGC   AGTG
                                ||||||||||||  ||||
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                                GTCGGGGGGCCG   TCAC
                                      _____
GAM375  KCNJ14   5' GCCAGGCCCCCGCAGTGC   9974     CCCT   __
                                GCC   GGCCC  GCAGTGC
                                |||   |||||  |||||||
                                CGG   CCGGG  CGTCACG
                                  T___    GG
GAM375  KIAA0087 3' TAGCCCACTGTGTGCTAGTG  9975       C  GCCC  _
                                TAGCCC CTG   GC AGTG
                                |||||| |||   || ||||
                                ATCGGG GAC   CG TCAC
                                   T  ACA_  A
GAM375  KIAA0089 5' GCTTCCCTGGCCGGCTGC   9976    C_      C  AG
                                GC  CCCTGGCC GC  TGC
                                ||  |||||||| ||  |||
                                CG  GGGACCGG CG  ACG
                                 AA       C __
GAM375  KIAA0789 3' TAGCCCCCTGGGCTCTTGC   9977          CCC  AG_
                                TAGCCCCCTGG   GC   TGC
                                ||||||||||   ||   |||
                                ATCGGGGGACC   CG   ACG
                                      ___  AGA
GAM375  KIAA1579 5' CAGCCTGCTCCGCAGTGC   9978       CCCTG  _
                                TAGCC    GC CCGCAGTGC
                                |||||    || |||||||||
                                GTCGG    CG GGCGTCACG
                                   A_____  A
GAM375  KIAA1828 5' CAGCCCCCAGCATCTGTGGTGC 9979         T   CCGCA__
                                TAGCCCCC GGC      GTGC
                                |||||||| |||      ||||
                                GTCGGGGG TCG      CACG
                                     _  TAGACAC
GAM375  KIAA1867 3' GCCCGTCCCCACCCGCGGTG  9980      __  G     A
                                GCCC  CCT GCCCGC GTG
                                ||||  ||| |||||| |||
                                CGGG  GGG TGGGCG CAC
                                  CA  G     C
GAM375  KIAA1879 5' CAGCCCCCTGGCCTGCACAGC  9981           __
                                TAGCCCCCTGGCC  CGCAGT
                                ||||||||||||  ||||||
                                GTCGGGGGACCGG  GTGTCG
                                      AC
GAM375  MGC16186 3' TAGCCCCCATGGCCGGGTG   9982         _    CGCA
                                TAGCCCCC TGGCC   GTG
                                |||||||| |||||   |||
                                ATCGGGGG ACCGG   CAC
                                     T    CC__
GAM375  MGC16491 3' GCCCAACCCTGCAGTGC     9983      CCT    _
                                GCCC   GGCCC GCAGTGC
                                ||||   ||||| |||||||
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                                CGGG  TTGGG CGTCACG
                                  ___   A
GAM375  MGC19556  5'  CAGCCCCCTGGCCTGGGAGT  9984          CGC_
                                TAGCCCCCTGGCC  AGT
                                ||||||||||||  |||
                                GTCGGGGGACCGG  TCA
                                      ACCC
GAM375  MUF1    3'  TAACCTCCTGGCCCAGGGT  9985     C      CA
                                TAGCC CCTGGCCCG  GT
                                ||||| |||||||||  ||
                                ATTGG GGACCGGGT  CA
                                  A       CC
GAM375  ODZ2    3'  CAGCCCAGCCGCAGTG     9986      CCT   C
                                TAGCCC  GGCC GCAGTG
                                ||||||  |||| ||||||
                                GTCGGG  TCGG CGTCAC
                                  ___   _
GAM375  P2RXL1  3'  TAGCCCACCTGGTAGCTGC  9987      _   CCC  AG
                                TAGCCC CCTGG  GC  TGC
                                ||||||| |||||  ||  |||
                                ATCGGG GGACC  CG  ACG
                                   T   AT_ __
GAM375  PMX2B   3'  CAGCCCCCTGAGAGTG     9988         CCCGC
                                TAGCCCCCTGG   AGTG
                                ||||||||||    ||||
                                GTCGGGGGACT   TCAC
                                      C____
GAM375  SEMA5A  3'  GCTCCCCTGGCCTGGAGGC  9989    _      CGC  T
                                GC CCCCTGGCC  AG GC
                                || |||||||||  || ||
                                CG GGGGACCGG  TC CG
                                 A       ACC  _
GAM375  SLC12A5 3'  GCCTCGCCTCCCCGCAGTGC  9990    C__  GG
                                GCC  CCT  CCCGCAGTGC
                                |||  |||  ||||||||||
                                CGG  GGA  GGGCGTCACG
                                  AGC  G_
GAM375  LOC122618 3'  GCTCCTGGCGCAGTGC    9991    CC    CC
                                GC  CCTGGC  GCAGTGC
                                ||  ||||||  |||||||
                                CG  GGACCG  CGTCACG
                                 A_    __
GAM375  LOC123435 5'  TAGTCCCCTGACAGTG    9992    C    GCCC
                                TAG CCCCTG   GCAGTG
                                ||| ||||||   ||||||
                                ATC GGGGAC   TGTCAC
                                  A    ____
GAM375  LOC124976 3'  CAGCCCCCTGGCCCTTCGT  9993          GCA
                                TAGCCCCCTGGCCC  GT
                                ||||||||||||||  ||
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                                GTCGGGGGACCGGG  CA
                                      AAG
GAM375  LOC125268 3'  GCTCCCCTGGCTTCGGTG   9994    _     C_ CA
                                GC CCCCTGGC  CG  GTG
                                || ||||||||  ||  |||
                                CG GGGGACCG  GC  CAC
                                 A       AA  __
GAM375  LOC138128 5'  TAGCCGCAACCCGCAGTGC   9995      CCC
                                TAGCC   TGGCCCGCAGTGC
                                |||||   ||||||||||||||
                                ATCGG   GTTGGGCGTCACG
                                   C__
GAM375  LOC143666 3'  TAACCCCCTCCCTGTGGTGC  9996        GG   GCA_
                                TAGCCCCCT  CCC    GTGC
                                |||||||||  |||    ||||
                                ATTGGGGGA  GGG    CACG
                                     __   ACAC
GAM375  LOC147807 3'  GCCCCCTGGCTCAGGC     9997         CCG   T
                                GCCCCCTGGC   CAG GC
                                ||||||||||   ||| ||
                                CGGGGGACCG   GTC CG
                                     A__   _
GAM375  LOC149194 5'  TAGGTCCCTGGCCCGTGC    9998     CC       GCA
                                TAG  CCCTGGCCC   GTGC
                                |||  |||||||||   ||||
                                ATC  GGGACCGGG   CACG
                                  CA        ____
GAM375  LOC152441 5'  TAGCCCCCTGGTCCCATTTTG  9999          _   CAG
                                TAGCCCCCTGG CCCG   TG
                                ||||||||||| ||||   ||
                                ATCGGGGGACC GGGT   AC
                                      A    AAA
GAM375  LOC152586 5'  AGCCCCCTCCCCGCGGTGC   10000        GG    A
                                AGCCCCCT  CCCGC GTGC
                                ||||||||  ||||| ||||
                                TCGGGGGA  GGGCG CACG
                                    G_    C
GAM375  LOC153546 5'  ACCCCCTGGCGCGGCTGGTGC  10001         C  _ A_
                                GCCCCCTGGC CG C  GTGC
                                |||||||||| || |  ||||
                                TGGGGGACCG GC G  CACG
                                     C  C AC
GAM375  LOC197342 3'  GCCCTGGGCCTGCAGTGC    10002     CCT   C
                                GCCC   GGCC GCAGTGC
                                ||||   |||| |||||||
                                CGGG   CCGG CGTCACG
                                  AC_    A
GAM375  LOC219654 3'  GCTCCCTGGCCACGGACGTGC  10003    C      _  CA_
                                GC CCCTGGCC CG   GTGC
                                || ||||||| ||   ||||
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                                CG GGGACCGG GC   CACG
                                 A       T  CTG
GAM375  LOC221960 3'  ACCCCTTGGCCCACTGC     10004      C       AG
                                GCCCC TGGCCCGC  TGC
                                ||||| ||||||||  |||
                                TGGGG ACCGGGTG  ACG
                                  A       __
GAM375  LOC253258 3'  TAACCCCCTCCCTGTGGTGC   9996         GG   GCA_
                                TAGCCCCCT  CCC    GTGC
                                |||||||||  |||    ||||
                                ATTGGGGGGA  GGG    CACG
                                     __   ACAC
GAM375  LOC255645 3'  TAGATCCCTGGCGGTGACAGTG 10005     CC      CC__
                                TAG  CCCTGGC    GCAGTG
                                |||  |||||||    ||||||
                                ATC  GGGACCG    TGTCAC
                                  TA      CCAC
GAM375  LOC257478 5'  CAGCCCTGGTCGCAGTGC    10006       CC   CC
                                TAGCCC  TGG  CGCAGTGC
                                ||||||  |||  ||||||||
                                GTCGGG  ACC  GCGTCACG
                                   __   A_
GAM375  LOC257541 5'  GCCCTCTGGCCCGAGAGC    9942       C       C  T
                                GCCC CTGGCCCG AG GC
                                |||| |||||||| || ||
                                CGGG GACCGGGC TC CG
                                  A       _  T
GAM375  LOC51622  3'  ACCCCTTGGCCCACTGC     10004      C       AG
                                GCCCC TGGCCCGC  TGC
                                ||||| ||||||||  |||
                                TGGGG ACCGGGTG  ACG
                                  A       __
GAM375  LOC55833  3'  GCCCACTGGGCAGTGC      10007      C    CCC
                                GCCC CTGG   GCAGTGC
                                |||| ||||   |||||||
                                CGGG GACC   CGTCACG
                                  T   ____
GAM375  LOC91040  5'  GCTCCTGGCCCATGTGC     10008    CC       CA
                                GC  CCTGGCCCG  GTGC
                                ||  |||||||||  ||||
                                CG  GGACCGGGT  CACG
                                 A_       A_
GAM375  LOC91355  5'  TAGCCCCCTGCGCCCAGGC   10009          _   __
                                TAGCCCCCTG GCCC  GC
                                |||||||||| ||||  ||
                                ATCGGGGGAC CGGG  CG
                                      G   TC
GAM375  LOC96597  3'  CAGCCCCCTCCACAGTG     10010         GGC
                                TAGCCCCCT   CCGCAGTG
                                |||||||||   ||||||||
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                                GTCGGGGGA  GGTGTCAC
                                    ___
GAM376  FMO5     3'  AATTTGATAAACAACAAACATT 10013            TT
                                AATTTGATAAATAAC  AGATATT
                                |||||||||||||||  |||||||
                                TTAAACTATTTGTTG  TTTGTAA
                                    __
GAM376  SERPINB5 3'  AATTTGACAAATAATGAATAAA 10014           CT__
           TATT                   AATTTGATAAATAA   TAGATATT
                                |||||||||||||||   ||||||||
                                TTAAACTGTTTATT   ATTTATAA
                                      ACTT
GAM376  LOC85415 3'  ATTTGACAACAGATAGATATT  10015        ATAACT
                                ATTTGATAA     TAGATATT
                                |||||||||     ||||||||
                                TAAACTGTT     ATCTATAA
                                     GTCT__
GAM377  ADAM10   5'  TCCTCCTTTCCCCGCTTTCCTT 10018        _   TTCCCC
                                TTCTCCTT CCCC     TCCTT
                                |||||||| ||||     |||||
                                AGGAGGAA GGGG     AGGAA
                                    A   CGAA__
GAM377  AGL      5'  TCTCTTTCTCCTTCCCCT    10019     C  C
                                TCTC TTC CCTTCCCCT
                                |||| ||| |||||||||
                                AGAG AAG GGAAGGGGA
                                  A  A
GAM377  AOAH     5'  CTCTCCTTCTCTTCCTCACTCT 10020        CC    C__  _
           CTT                    TTCTCCTTC  CTTCC   CTC CTT
                                |||||||||  |||||   ||| |||
                                GAGAGGAAG  GAAGG   GAG GAA
                                    A_    AGT   A
GAM377  ATP5J    5'  CCCGTTCTTTTTCCCCTCCTT  10021    _  CCC
                                TCC TTC   TTCCCCTCCTT
                                ||| |||   ||||||||||
                                GGG AAG   AAGGGGAGGAA
                                  C   AAA
GAM377  BARX2    3'  TTCTCTCTTTTCCCTTCTCC   10022      _  C_    C
                                TTCTC CTT  CCCTTC CC
                                ||||| |||  |||||| ||
                                AAGAG GAA  GGGAAG GG
                                   A   AA     A
GAM377  BMP4     5'  CTCCTCTTTCCCTCCCTCGCTT 10023      C    CTTC   _
                                CTTCTC TTCCC    CCCTC CTT
                                |||||| |||||    ||||| |||
                                GAGGAG AAGGG    GGGAG GAA
                                   A    A___    C
GAM377  BMP4     5'  CTCCTCTTTCCCTCCCTCGCTT 10023      C    CTTC   _
                                CTTCTC TTCCC    CCCTC CTT
                                |||||| |||||    ||||| |||
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                                GAGGAG AAGGG   GGGAG GAA
                                   A    A___    C
GAM377  CACNA1C  5' CTTCTGCTCTTCCCTCCT   10024     C  TCCC    C
                                CTTCT CT   CTTCCC TCCT
                                |||||| ||   |||||| ||||
                                GAAGA GA   GAAGGG AGGA
                                  C ____    _
GAM377  CDC2L1   5' TTCTCCTCTTGTTCCTTCCTT  10025       CCCC   CC
                                TTCTCCTT   TTCC  TCCTT
                                ||||||||   ||||  |||||
                                AAGAGGAG   AAGG  AGGAA
                                     AAC_   A_
GAM377  CDC2L1   5' TTCTCCTCTTGTTCCTTCCTT  10025       CCCC   CC
                                TTCTCCTT   TTCC  TCCTT
                                ||||||||   ||||  |||||
                                AAGAGGAG   AAGG  AGGAA
                                     AAC_   A_
GAM377  CDC2L2   5' TTCTCCTCTTGTTCCTTCCTT  10025       CCCC   CC
                                TTCTCCTT   TTCC  TCCTT
                                ||||||||   ||||  |||||
                                AAGAGGAG   AAGG  AGGAA
                                     AAC_   A_
GAM377  CDH12    5' CTTCTGTTTCCCCTTTCC    10026      CC      C
                                CTTCT  TTCCCCTT CC
                                |||||  |||||||| ||
                                GAAGA  AAGGGGAA GG
                                   CA       A
GAM377  CDKN2C   5' TTCTTTTTCCCCTTTCCTT   10027     CC      CCCC
                                TTCT  TTCCCCTT   TCCTT
                                ||||  ||||||||   |||||
                                AAGA  AAGGGGAA   AGGAA
                                  AA       ____
GAM377  CDX2     5' TCCTTCTTTCCTCCCACCTCCT 10028       C__     _
           T                     TCCTTC   CCTTCC CCTCCTT
                                 ||||||   |||||| |||||||
                                 AGGAAG   GGAGGG GGAGGAA
                                    AAA     T
GAM377  CNTNAP2  5' CTCCTCCCGCTTCCTCTTCTT  10029       C    C  C
                                CTCCTTCC CTTCC CT CTT
                                |||||||| ||||| || |||
                                GAGGAGGG GAAGG GA GAA
                                     C    A  A
GAM377  COL17A1  3' CTTCTCCCTTTATTCCTTCCTT 10030       CCCC   CC
                                CTTCTCCTT   TTCC  TCCTT
                                |||||||||   ||||  |||||
                                GAAGAGGGA   AAGG  AGGAA
                                     AAT_   A_
GAM377  COL17A1  3' CTTCTCCCTTTATTCCTTCCTT 10030       CCCC   CC
                                CTTCTCCTT   TTCC  TCCTT
                                |||||||||   ||||  |||||
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                                GAAGAGGGA   AAGG  AGGAA
                                     AAT_   A_
GAM377  CPLX2    5'  TTCTCCCTCCCCCTCTTCCTT  10031           CCC
                                TTCTCCTTCCCCTTC   TCCTT
                                |||||||||||||||  |||||
                                AAGAGGGAGGGGGAG   AGGAA
                                       A__
GAM377  CSF1R    5'  CCTCTTCTTCCCCTTTTAGCCT 10032      C       CCCCT
                                CTTCT CTTCCCCTT    CCT
                                ||||| |||||||||    |||
                                GGAGA GAAGGGGAA    GGA
                                   A       AATC_
GAM377  CSNK2A1  3'  CTTTCCTTCCTTCCTTTC    10034    C     CC   CC
                                CTT TCCTTCC  TTCC  TC
                                ||| |||||||  ||||  ||
                                GAA AGGAAGG  AAGG  AG
                                  _     __   AA
GAM377  CSNK2A1  3'  CCTTCCTTCTTTCCTTCCT   10033      C_   C  C
                                CCTTCC  CTT CC TCCT
                                ||||||  ||| || ||||
                                GGAAGG  GAA GG AGGA
                                   AA   A  A
GAM377  DCT      5'  TTCTCCTTATCTTCTACTC   10035       CCC   CC
                                TTCTCCTT   CTTC  CTC
                                ||||||||   ||||  |||
                                AAGAGGAA   GAAG  GAG
                                     TA_   AT
GAM377  DDX11    3'  CTTCTCCTCCTCAGCTCCTT   10036       TCC   CCC
                                CTTCTCCT   CCTT   CTCCTT
                                ||||||||   ||||   ||||||
                                GAAGAGGA   GGAG   GAGGAA
                                     ____   TC_
GAM377  DDX11    3'  CTTCTCCTGCCTCCTCCTC   10037       TCC    C
                                CTTCTCCT   CCTTC CCTC
                                ||||||||   ||||| ||||
                                GAAGAGGA   GGAGG GGAG
                                     C__     A
GAM377  DDX6     3'  CTTCTCTTCTTTCTTTTCCTT  10038      C   CCC   CCC
                                CTTCTC TTC   TTC   TCCTT
                                ||||||  |||   |||   |||||
                                GAAGAG AAG   AAG   AGGAA
                                   _   A__   AAA
GAM377  DDX6     3'  CTTTTCCTTCCTTGTCCCCT   10039     C      CCT
                                CTT TCCTTCC   TCCCCT
                                ||| |||||||   ||||||
                                GAA AGGAAGG   AGGGGA
                                  A      AAC
GAM377  DDX6     3'  CTTCTCTTCTTTCTTTTCCTTC 10040      C   CC_   CC   _
           CTT                   CTTCTC TTC   CTT  CCT CCTT
                                ||||||  |||   |||  |||  ||||
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                                GAAGAG AAG   GAA  GGA GGAA
                                   _  AAA   AA   A
GAM377  DLEC1    3'  CTCCTTCTTCCCTTCCT     10041        CCC    C
                                CTCCTTC   TTCCC TCCT
                                |||||||   ||||| ||||
                                GAGGAAG   AAGGG AGGA
                                   ___    A
GAM377  DOC1     5'  TTCTCCTTTTCTTGCTCCTT   10042        CCC   CCC
                                TTCTCCTT   CTT   CTCCTT
                                ||||||||   |||   ||||||
                                AAGAGGAA   GAA   GAGGAA
                                    AA_   C__
GAM377  DTR      3'  CTCTCCTTCTTCTTCTTCT    10043         CC    CC
                                TTCTCCTTC  CTTC  CT
                                |||||||||  ||||  ||
                                GAGAGGAAG  GAAG  GA
                                     AA    AA
GAM377  EDARADD  5'  CTTCCCCTCCCTTCTTCTTCTC 10044        C____    C      III
            CTCCTTA                CCTTCC    CTTC CCTCCTT   A
                                ||||||    |||| |||||||  |
                                GGAGGG    GAAG GGAGGAA   T
                                   AAGAA    A      III
GAM377  EGR1     3'  CTTTCTTTCCCCTTTCCCT    10045     C  C      C
                                CTT TC TTCCCCTT CCCT
                                ||| || |||||||| ||||
                                GAA AG AAGGGGAA GGGA
                                  _ A       A
GAM377  EGR1     3'  TTCCCTTTCTTTCCCCT     10046      C   CCC
                                TTCTC TTC   TTCCCCT
                                ||||| |||   |||||||
                                AAGGG AAG   AAGGGGA
                                   A   A__
GAM377  ELAVL3   3'  CTTCCCCTCCCACCCCCCT    10047          _
                                CTTCCCCTTCC CCTCCTT
                                |||||||||| |||||||
                                GAAGGGGAGGG GGGGGGA
                                      T
GAM377  EMX2     3'  TTCTCTCTCTCCCTCCCTC    10048      _ TC    TC
                                TTCTC CT  CCCT  CCCTC
                                ||||| ||  ||||  |||||
                                AAGAG GA  GGGA  GGGAG
                                   A  GA   __
GAM377  ERBB3    3'  TCCTCCCTTTCCTCTTCT     10049     T   C    C  C
                                TCCT CCC TTCC CT CT
                                |||| ||| |||| || ||
                                AGGA GGG AAGG GA GA
                                   _  A    A  A
GAM377  FZD10    3'  CTTCTCCCTCTTCCCCCCTCCT 10050          CCC
            T                   CTTCTCCTTC   TTCCCCTCCTT
                                ||||||||||   ||||||||||
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                                GAAGAGGGAG  GGGGGGAGGAA
                                     AA_
GAM377  GAP43   5'  CTCTCCTTTCCTTCTCTCTCTT 10051       CC    CC  _
                                TTCTCCTT  CCTTC  CTC CTT
                                ||||||||  |||||  ||| |||
                                GAGAGGAA  GGAAG  GAG GAA
                                     A_    A_  A
GAM377  GDF2    3'  TCTCCTTTTCATCACCTCCTT  10052       CCCCT  C
                                TCTCCTT    TC CCTCCTT
                                |||||||    || |||||||
                                AGAGGAA    AG GGAGGAA
                                     AAGT_  T
GAM377  GPR4    3'  TTCTCCTTCCACTTTCCCC   10053         C  _
                                TTCTCCTTCC CTT CCCC
                                |||||||||| ||| ||||
                                AAGAGGAAGG GAA GGGG
                                      T  A
GAM377  GRAF    3'  CTCCTGGAGTCTTCCTCTTCTT 10054      TCCC_    C  C
                                CTCCT    CTTCC CT CTT
                                |||||    ||||| || |||
                                GAGGA    GAAGG GA GAA
                                   CCTCA    A  A
GAM377  GRIA3   5'  CTCCTCTTCTTCCTCTTC    10055       __    C
                                CTTCTC  CTTCC CTTC
                                ||||||  ||||| ||||
                                GAGGAG  GAAGG GAAG
                                    AA    A
GAM377  HNMT    5'  CTTCTCTTCCCAGTTCCCTC  10056       C    CTTC
                                CTTCTC TTCCC   CCCTC
                                |||||| |||||   |||||
                                GAAGAG AAGGG   GGGAG
                                   _    TCAA
GAM377  HOXB7   3'  TTCTCCTTTCTCCCTCCTT   10057       CCCCT  _
                                TTCTCCTT    TC CCCTCCTT
                                ||||||||    || ||||||||
                                AAGAGGAA    AG GGGAGGAA
                                     _____  A
GAM377  IGF1    3'  TTCTCCTTTTTCTTTTCCTTTC 10058       CCCC__   C__  _
           TCTCTT                TCTCCTT    TTCC  CTC CTT
                                |||||||     ||||  ||| |||
                                AGAGGAA     AAGG  GAG GAA
                                    AAAGAA   AAA  A
GAM377  IL13RA1 3'  CTTTTCCCTCCCTTTTCCC   10059    C      C_
                                CTT TCCTTCCC  TTCCC
                                ||| ||||||||  |||||
                                GAA AGGGAGGG  AAGGG
                                  A       AA
GAM377  IL2RA   3'  CTTCTCCCTCTTCACTTCC   10060         CC__
                                CTTCTCCTTC   CTTCC
                                ||||||||||   |||||
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                                GAAGAGGGAG   GAAGG
                                     AAGT
GAM377  IL2RA   3'  CTCTTCACTTCCTTCTTTCTTT 10061    TC _    C_  CCCC
            CCTT                  CT  TC CTTCC  CTT   TCCTT
                                  ||  || |||||  |||   |||||
                                  GA  AG GAAGG  GAA   AGGAA
                                   GA  T    AA   AGAA
GAM377  LASS2   3'  TCTCCTCTCACTTTCTCCTT  10062       CCC   CCC
                                  TCTCCTT   CTT   CTCCTT
                                  |||||||   |||   ||||||
                                  AGAGGAG   GAA   GAGGAA
                                      AGT   A__
GAM377  LRP1    5'  TCCTCCTTTCCCCCTCCTCCT  10063        _      _
                                  TTCTCCTT CCCCTTCC CCT
                                  |||||||| |||||||| |||
                                  AGGAGGAA GGGGGAGG GGA
                                       A       A
GAM377  MAP1B   3'  TCTCCTTCTCTTGCATTCCTT  10064       CC   CCCC
                                  TCTCCTTC  CTT   TCCTT
                                  ||||||||  |||   |||||
                                  AGAGGAAG  GAA   AGGAA
                                       A_   CGTA
GAM377  MAP1B   3'  TCTCCTTCTCTTGCATTCCTT  10064       CC   CCCC
                                  TCTCCTTC  CTT   TCCTT
                                  ||||||||  |||   |||||
                                  AGAGGAAG  GAA   AGGAA
                                       A_   CGTA
GAM377  MDFI    3'  TCCTTTCCCCTTCCAGTC    10067      _      CC
                                  TCCTT CCCCTTCC  TC
                                  ||||| ||||||||  ||
                                  AGGAA GGGGAAGG  AG
                                     A       TC
GAM377  MDFI    3'  CTCCCTCCCTTCCCTTCCTT   10066        C    C
                                  CTCCTTCCC TTCCC TCCTT
                                  ||||||||| ||||| |||||
                                  GAGGGAGGG AAGGG AGGAA
                                       _    A
GAM377  MDFI    3'  CTTCCCTTCCTTTCCCCT    10065     T    CC
                                  CTTC CCTTCC  TTCCCCT
                                  |||| ||||||  |||||||
                                  GAAG GGAAGG  AAGGGGA
                                    _     A_
GAM377  MYO5A   3'  CTCCTCCTTTCCTTCCTCCCTT 10068      _ C_    C    III
            CCTTA                 CTCCTT CC  CTTCCC TCCTT   A
                                  ||||||  ||  ||||||  |||||   |
                                  GAGGAA GG  GGAGGG AGGAA   T
                                     A  AA     A    III
GAM377  NOTCH2  3'  TCCTCCTTTTCCAACCTTC   10069       __   __
                                  TTCTCCT  TCC  CCTTC
                                  |||||||  |||  |||||
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                                AGGAGGA  AGG  GGAAG
                                   AA   TT
GAM377  PIGR     3'  TTCTCTTCTCCCTCCTCCTCCT 10070      C   C     _
              T                    TTCTC TTC CCTTCC CCTCCTT
                                   |||||| ||| |||||| |||||||
                                   AAGAG AAG GGGAGG GGAGGAA
                                     _  A     A
GAM377  PK428    5'  TTCTCCTCCCGAGGTCCTTC   10071          _____
                                   TTCTCCTTCC    CCTTC
                                   ||||||||||    |||||
                                   AAGAGGAGGG    GGAAG
                                         CTCCA
GAM377  PLXNA2   3'  CTTCTCCTCTTTCTCTC     10072         CCCC   CC
                                   CTTCTCCTT    TTC  CTC
                                   |||||||||    |||  |||
                                   GAAGAGGAG    AAG  GAG
                                        A___   A_
GAM377  PMX1     5'  CTTCTCTCTCTCCCCCTCTTCT 10073       _ _      CC
                                   CTTCTC CT TCCCCTTC  CT
                                   |||||| || ||||||||  ||
                                   GAAGAG GA AGGGGGAG  GA
                                      A  G       AA
GAM377  PMX1     5'  CTTCTCTCTCTCCCCCTCTTCT 10073       _ _      CC
                                   CTTCTC CT TCCCCTTC  CT
                                   |||||| || ||||||||  ||
                                   GAAGAG GA AGGGGGAG  GA
                                      A  G       AA
GAM377  PRKCABP  3'  CTTTTCCTTCCTGCCCTCCCTC 10074     C      __      _
              TCCTT                    CTT TCCTTCC  CCTTCCC CTCCTT
                                   ||| |||||||  ||||||| ||||||
                                   GAA AGGAAGG  GGGAGGG GAGGAA
                                     A      AC      A
GAM377  RAB13    3'  CCTCTCTCTTCCTTTTTTTCCT 10077       _    CCTTCCCC
              T                     CTTCTC CTTCC       TCCTT
                                   |||||| |||||       |||||
                                   GGAGAG GAAGG       AGGAA
                                      A    AAAAAA__
GAM377  RAB13    3'  TTCTCCTTTTTCTCCTC     10076         CCCC   C
                                   TTCTCCTT    TTC CCTC
                                   ||||||||    ||| ||||
                                   AAGAGGAA    AAG GGAG
                                        A___   A
GAM377  RAB13    3'  CTTCTCCCTTCCTCTCTCTT   10075     _      C   _
                                   CTTC CCCTTCC CTC CTT
                                   |||| ||||||| ||| |||
                                   GAAG GGGAAGG GAG GAA
                                     A      A  A
GAM377  RARG     3'  CTTCTCCTTTGTCCCCTT    10078         ___
                                   CTTCTCCT   TCCCCTT
                                   ||||||||   |||||||
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                                GAAGAGGA  AGGGGAA
                                    AAC
GAM377  SDC2    5'  CTCCTCCTTCTCCTCCTC    10080      TCC    C
                                CTCCT  CCTTC CCTCCTT
                                |||||  ||||| |||||||
                                GAGGA  GGAAG GGAGGAG
                                   ___    A
GAM377  SDC2    5'  CTTCTCCTCCTCTTCTTTTCCT 10079        T  C   CCC
                                CTTCTCCT CC CTTC  TCCT
                                |||||||| || ||||  ||||
                                GAAGAGGA GG GAAG  AGGA
                                    _ A   AAA
GAM377  SEZ6L   5'  CTTCTCCTTTCTCCCTCCCTCC 10081   ____  _     C    III
          CTTCCTTA                CT   TCC CCTTCCC TCCTT  A
                                ||   ||| ||||||| |||||  |
                                GA   GGG GGGAGGG AGGAA  T
                                 AAGA  A     A    III
GAM377  SFRS2IP  5'  CTTCTTTTCTTCCCCTTC    10082      C__
                                CTTCT  CTTCCCCTTC
                                |||||  ||||||||||
                                GAAGA  GAAGGGGAAG
                                   AAA
GAM377  SIX6    3'  CTCTCATCTTCTTCCCCTC   10083      CT  CC
                                TTCTC  TC  CTTCCCCTC
                                |||||  ||  |||||||||
                                GAGAG  AG  GAAGGGGAG
                                   T_  AA
GAM377  SLC39A1  3'  TTCCCTTCCCCTTTCCTTCCT  10084    T       C  C
                                TTC CCTTCCCCTT CC TCCT
                                ||| |||||||||| || ||||
                                AAG GGAAGGGGAA GG AGGA
                                  _       A  A
GAM377  SOX11   3'  TTCCTCTTCCCCTTCCCCC   10085    TC
                                TTC  CTTCCCCTTCCCCT
                                |||  ||||||||||||||
                                AAG  GAAGGGGAAGGGGG
                                  GA
GAM377  STC1    5'  TCCTGCCCCCCTTTCCTC    10086     _     CC
                                TCCT TCCCCTT  CCTC
                                |||| |||||||  ||||
                                AGGA GGGGGGA  GGAG
                                   C      AA
GAM377  TAF1    3'  TTCTTTCATAATTTCCCCTCCT 10087     CCTTCCCC
            T                    TTCT      TTCCCCTCCTT
                                ||||      ||||||||||
                                AAGA      AAGGGGAGGAA
                                  AAGTATTA
GAM377  TAF1    3'  TTCTTTCATAATTTCCCCTCCT 10087     CCTTCCCC
            T                    TTCT      TTCCCCTCCTT
                                ||||      ||||||||||
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                                AAGA       AAGGGGAGGAA
                                  AAGTATTA
GAM377  TBX5    3'  CTCTCTTTCTCCTCTCTCTCTC 10088      C   C    CCC  _
             TC                    TTCTC TTC CCTT   CTC CTT
                                |||||| ||| ||||   ||| |||
                                GAGAG AAG GGAG   GAG GAG
                                  A   A    AGA   A
GAM377  TBX5    3'  CTCTCTTTCTCCTCTCTCTCTC 10088      C   C    CCC  _
             TC                    TTCTC TTC CCTT   CTC CTT
                                |||||| ||| ||||   ||| |||
                                GAGAG AAG GGAG   GAG GAG
                                  A   A    AGA   A
GAM377  THRA    3'  CTTCTCCTTCCCCATCGGCCT  10089           T  C_
                                CTTCTCCTTCCCC TC  CCT
                                |||||||||||| ||  |||
                                GAAGAGGAAGGGG AG  GGA
                                       T  CC
GAM377  TRHDE   5'  CTTCTTCTTCCTCTTTTTCTTC 10091      C    C   CCC  C
             TT                    CTTCT CTTCC CTT   CT CTT
                                ||||| ||||| |||   || |||
                                GAAGA GAAGG GAA   GA GAA
                                  A    A   AAA  A
GAM377  TRHDE   5'  CTCCTCCTCCTCCTTCTTCTTC 10092         C    CC  C
             TT                    CTTCTCCTTC CCTTC  CT CTT
                                |||||||||| |||||  || |||
                                GAGGAGGAGG GGAAG  GA GAA
                                     A    AA  A
GAM377  TRHDE   5'  CTCCTCCTTCTTCTTCTTCCTC 10090         CC   C_
                                CTTCTCCTTC  CTTC  CCTC
                                ||||||||||  ||||  ||||
                                GAGGAGGAAG  GAAG  GGAG
                                     AA   AA
GAM377  VEGF    5'  CTCCTCTTCCTTCTCTTCT   10093       CC    CC  C
                                CTCCTT  CCTTC  CT CT
                                ||||||  |||||  || ||
                                GAGGAG  GGAAG  GA GA
                                   AA    A_  A
GAM377  AP3M2   3'  CTCCTTTACTTCTTTTTCCTC  10095       CCC   CCC_
                                CTCCTT   CTTC   TCCTT
                                ||||||   ||||   |||||
                                GAGGAA   GAAG   AGGAG
                                   AT_   AAAA
GAM377  AP3M2   3'  CTTTCCTTCCCATCCCTCCTT  10094    C      CTTC
                                CTT TCCTTCCC   CCCTCCTT
                                ||| ||||||||   ||||||||
                                GAA AGGAAGGG   GGGAGGAA
                                  _      TA__
GAM377  APELIN  3'  CTTTTCTTCCCTCCTTCC    10097    C  C   _
                                CTT TC TTCC CCTTCC
                                ||| || |||| ||||||
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                                GAA AG AGGG GGAAGG
                                  A A   A
GAM377  APELIN   3'  CTCCTTCCTTCTGCCCTTCCCT 10096      _   __      C
          TCCTT                   CTTCT CCTTC  CCCTTCCC TCCTT
                                |||||| |||||  |||||||| |||||
                                GAGGA GGAAG  GGGAAGGG AGGAA
                                   A    AC       A
GAM377  ARG99    3'  TTCTCCTTCCCTCTCAGACCTT 10098          _  CC_  C
          CTT                     TTCTCCTTCCC CTT   CCT CTT
                                |||||||||||| |||   ||| |||
                                AAGAGGAAGGG GAG   GGA GAA
                                      A  TCT  A
GAM377  ASB10    5'  CTTCTCCTTTCACTCAAGCCCT 10099         CCC  C__
                                CTTCTCCTT   CTT   CCCT
                                |||||||||   |||   ||||
                                GAAGAGGAA   GAG   GGGA
                                     AGT   TTC
GAM377  BPES     5'  CCTCTCCTTCCCCTTCCCCT   10100
                                CTTCTCCTTCCCCTTCCCCT
                                ||||||||||||||||||||
                                GGAGAGGAAGGGGAAGGGGA

GAM377  C5orf4   3'  TTCTCCTTATCTCCTACCCTTC 10101       __ C  T  C _
          TCTT                    TTCTCCT  TC CCT CCC TC CTT
                                |||||||  || ||| ||| || |||
                                AAGAGGA  AG GGA GGG AG GAA
                                    AT  A   T   A  A
GAM377  C5orf4   3'  TTCTCCTTATCTCCTACCCTTC 10101       __ C  T  C _
          TCTT                    TTCTCCT  TC CCT CCC TC CTT
                                |||||||  || ||| ||| || |||
                                AAGAGGA  AG GGA GGG AG GAA
                                    AT  A   T   A  A
GAM377  CNOT8    3'  TCCTCCTTCTTCTCGTTTGCCT 10102         CC  CCCCT
          T                      TTCTCCTTC  CTT    CCTT
                                |||||||||  |||    ||||
                                AGGAGGAAG  GAG    GGAA
                                     AA   CAAAC
GAM377  DDM36    3'  TCTCACTCCCCTTCTCTTCCTT 10103     C       CCC
                                TCTC TTCCCCTTC   TCCTT
                                |||| |||||||||   |||||
                                AGAG GAGGGGAAG   AGGAA
                                   T        AGA
GAM377  DKFZP564K0822 3'  CTTCTCCTGTCTTTTCCC    10104        _ CCC
                                CTTCTCCT TC   TTCCC
                                |||||||| ||   |||||
                                GAAGAGGA AG   AAGGG
                                     C  AA_
GAM377  DKFZp762E1312 5'  CTCTCCTTTGTTTCTTTCCTT  10105        CCCC  CCC
                                TTCTCCTT    TTC   TCCTT
                                ||||||||    |||   |||||
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                                GAGAGGAA   AAG  AGGAA
                                    ACA_  AA_
GAM377  DKK2    5' CCTCTCTTTTCCTATCCT   10106      C  CCCC   CC
                                CTTCTC TT   TTCC  TCCT
                                |||||| ||   ||||  ||||
                                GGAGAG AA   AAGG  AGGA
                                   _ _____   AT
GAM377  DUSP9   3' CTTCTTCTTCCCCTCCCCCT  10107      C
                                CTTCT CTTCCCCTTCCCCT
                                ||||| ||||||||||||||
                                GAAGA GAAGGGGAGGGGGA
                                   A
GAM377  ELKS    3' TTCTCTTCCCTTCCCCCCTT  10108      C    C     T
                                TTCTC TTCCC TTCCCC CCTT
                                ||||| ||||| |||||| ||||
                                AAGAG AAGGG AAGGGG GGAA
                                   _    _     _
GAM377  FLJ10116 5' CTTCGGGCTTTTTTTCCCCTC  10109     TC_  CCCC
                                CTTC   CTT   TTCCCCTC
                                ||||   |||   ||||||||
                                GAAG   GAA   AAGGGGAG
                                  CCC   AAA_
GAM377  FLJ10508 3' CTCCTCCTTCCTCTCTTAACTC 10110          C   CCC_
           CTT                  CTTCTCCTTCC CTT   CTCCTT
                                |||||||||| |||   ||||||
                                GAGGAGGAAGG GAG   GAGGAA
                                     A   AATT
GAM377  FLJ10898 5' CTGCTCTTTTTTCCCTCCTT  10111    T   C  CCCC  C
                                CT CTC TT   TT CCCTCCTT
                                || ||| ||   || ||||||||
                                GA GAG AA   AA GGGAGGAA
                                 C   A  ____  A
GAM377  FLJ11850 5' CCTCTTTTTTTTGTTCTTTCCT 10112      CCTTCCCC   C__
           CCTT                  CTTCT      TTC   CCTCCTT
                                 |||||      |||   |||||||
                                 GGAGA      AAG   GGAGGAA
                                   AAAAAAAC   AAA
GAM377  FLJ13189 3' CTTCTCCTATCCCTTTCCC   10113        _   C
                                CTTCTCCT TCCC TTCCC
                                |||||||| |||| |||||
                                GAAGAGGA AGGG AAGGG
                                     T   A
GAM377  FLJ13848 3' TTCTCCTTCCCCTGCTCC    10114           TCCC
                                TTCTCCTTCCCCT   CTCC
                                ||||||||||||   ||||
                                AAGAGGAAGGGGA   GAGG
                                       C___
GAM377  FLJ14124 3' TTCTCCTTTCCCCTTCCCCACG 10115        _       TC_
           CTT                  TTCTCCTT CCCCTTCCCC   CTT
                                |||||||| ||||||||||   |||
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                                AAGAGGAA GGGGAAGGGG  GAA
                                   A        TGC
GAM377  FLJ14146  3' CTTCTCCTCTACCCCTTCC   10116        __
                                CTTCTCCTT  CCCCTTCC
                                |||||||||  ||||||||
                                GAAGAGGAG  GGGGAAGG
                                   AT
GAM377  FLJ14351  3' CCTCTCCTTTTCACAGCCTCCT 10117        CCCCTTCC
          T                     CTTCTCCTT      CCTCCTT
                                |||||||||      |||||||
                                GGAGAGGAA      GGAGGAA
                                   AAGTGTC_
GAM377  FLJ14399  3' CCTCCCTTCCTTCCTT     10118    TC     CC
                                CCT  CCCTTCC  TCCTT
                                |||  |||||||  |||||
                                GGA  GGGAAGG  AGGAA
                                  __     A_
GAM377  FLJ14524  3' TCCTTTTCTTCCCCTTCT    10119     CCC      C
                                TCCTT   CTTCCCCT CT
                                |||||   |||||||| ||
                                AGGAA   GAAGGGGA GA
                                   AA_      A
GAM377  FLJ14524  3' CTTCCCCTTCTTCCTT     10120        CCC
                                CTTCCCCTTC   TCCTT
                                ||||||||||   |||||
                                GAAGGGGAAG   AGGAA
                                   A__
GAM377  FLJ20257  3' TTCCTCTTCCCCCAGGTCCTT  10121    TC      TCCCC
                                TTC  CTTCCCCT    TCCTT
                                |||  ||||||||    |||||
                                AAG  GAAGGGGG    AGGAA
                                  GA       TCC__
GAM377  FLJ22795  3' CTTTCCCTTCCAGCCCCTC   10122    CT     CCTT
                                CTT  CCTTCC   CCCCTC
                                |||  ||||||   ||||||
                                GAA  GGAAGG   GGGGAG
                                  AG     TC__
GAM377  FLJ23129  3' TTCTTTTCCTTTTCCCCTCCTT 10124     CC   CC
                                TTCT  TTCC  TTCCCCTCCTT
                                ||||  ||||  ||||||||||
                                AAGA  AAGG  AAGGGGAGGAA
                                   A_   AA
GAM377  FLJ23129  3' CTTTTCCTTTTCCCCTCCTT  10123    C    CCCC
                                CTT TCCTT   TTCCCCTCCTT
                                ||| |||||   ||||||||||
                                GAA AGGAA   AAGGGGAGGAA
                                  A    _____
GAM377  FLJ23306  3' CCTTTTTCTTTGAAACCCTCCT 10125     CCC  C____
          T                     CCTT  CTT    CCCTCCTT
                                ||||  |||    ||||||||
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                                GGAA  GAA    GGGAGGAA
                                  AAA  ACTTT
GAM377  FLJ23469  3'  TCTTCTTCCCCTCCCCT    10126    C      T
                                TCT CTTCCCCT CCCCT
                                ||| |||||||| |||||
                                AGA GAAGGGGA GGGGA
                                  A      _
GAM377  FLJ30567  3'  TTCTCCTTTACCCTCCTCTCCT 10127       CC     C
           T                     TTCTCCTT  CCTTCC CTCCTT
                                ||||||||  |||||| ||||||
                                AAGAGGAA  GGGAGG GAGGAA
                                    AT     A
GAM377  FLJ32421  5'  CTTCTCCCTCGGCCTTCC    10128         C_
                                CTTCTCCTTC  CCTTCC
                                ||||||||||  ||||||
                                GAAGAGGGAG  GGAAGG
                                     CC
GAM377  FLN29     3'  TCCAAAATCTTCCCCTCCTT   10129     TTCCC
                                TCC    CTTCCCCTCCTT
                                |||    ||||||||||||
                                AGG    GAAGGGGAGGAA
                                  TTTTA
GAM377  GT650     3'  TTCTCCTTTTTTTCCCTTTTCC 10130        CCCC    C__
           TT                    TTCTCCTT   TTCCC  TCCTT
                                ||||||||   |||||  |||||
                                AAGAGGAA   AAGGG  AGGAA
                                    AAA_    AAA
GAM377  ITGA10    3'  CTTTTCCTCCTCCCTCCTT   10131    CC    _
                                CTT  CCTTC CCCTCCTT
                                |||  ||||| ||||||||
                                GAA  GGAGG GGGAGGAA
                                  AA    A
GAM377  jdp2      3'  CTTTTCCTTCTCCTCTTCC   10132    C    _ _
                                CTT TCCTTC CC CTTCC
                                ||| |||||| || |||||
                                GAA AGGAAG GG GAAGG
                                  A     A  A
GAM377  KCNS1     5'  CCTCTCCTTCCTTCTTCC    10133         C_
                                CTTCTCCTTCC  CTTCC
                                ||||||||||  |||||
                                GGAGAGGAAGG  GAAGG
                                     AA
GAM377  KIAA0193  3'  TTCTTCCTTTTCTTTCCCTCCT 10134     _   CCC  C
           T                     TTCT CCTT   CTT CCCTCCTT
                                |||| ||||   ||| ||||||||
                                AAGA GGAA   GAA GGGAGGAA
                                  A   AA_   A
GAM377  KIAA0537  3'  CTTCCCCTTCCCTTTCCC    10135         C
                                CTTCTCCTTCCC TTCCC
                                |||||||||||| |||||
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                                GAAGGGGAAGGG AAGGG
                                      A
GAM377  KIAA0552 3' CTCCTCCTATTCCCTCCT    10136      T  CC    C
                                CTCCT CC  TTCCC TCCT
                                ||||| ||  ||||| ||||
                                GAGGA GG  AAGGG AGGA
                                  _ AT    _
GAM377  KIAA0855 3' CTTTTCCTTCCCACCATTTCTT 10137     C      _ TCCCC_
           CCTT                   CTT TCCTTCCC CT     TCCTT
                                ||| |||||||| ||     |||||
                                GAA AGGAAGGG GG     AGGAA
                                  A       T  TAAAGA
GAM377  KIAA0871 5' CTTCTCCCAGCTTCCTCTCCTT 10138        TCCC    C
                                CTTCTCCT   CTTCC CTCCTT
                                ||||||||   ||||| ||||||
                                GAAGAGGG   GAAGG GAGGAA
                                     TC__    A
GAM377  KIAA1056 3' CCTTTCTCCTCCCCTCCTT   10139     CCC
                                CCTT   CTTCCCCTCCTT
                                ||||   ||||||||||||
                                GGAA   GGAGGGGAGGAA
                                  AGA
GAM377  KIAA1076 5' CTTCTTCCTCCTCTTCCC    10140      C    C
                                CTTCT CTTCC CTTCCC
                                ||||| ||||| ||||||
                                GAAGA GGAGG GAAGGG
                                   A    A
GAM377  KIAA1076 5' CTCCTCCTCCTCCTCTTC    10141         _ _
                                CTTCTCCTTC CC CTTC
                                |||||||||| || ||||
                                GAGGAGGAGG GG GAAG
                                      A  A
GAM377  KIAA1136 3' TCCCTCCTTTTCCTCTTCTT  10142       CC   C  C
                                TCCTTCC  TTCC CT CTT
                                |||||||  |||| || |||
                                AGGGAGG  AAGG GA GAA
                                     AA   A  A
GAM377  KIAA1287 3' TTCTCCTTTCCCTTTACCCT  10143       C    C_
                                TTCTCCTT CCCTT  CCCT
                                |||||||| |||||  ||||
                                AAGAGGAA GGGAA  GGGA
                                     A    AT
GAM377  KIAA1303 3' CTCCTTCTTCCTCTCTCT    10144       CCC   C  _
                                CTCCTTC   TTCC CTC CT
                                |||||||   |||| ||| ||
                                GAGGAAG   AAGG GAG GA
                                     ___   A  A
GAM377  KIAA1434 3' CTTCATCCTTTCTTCTGTCTCC 10145     _    CCC   CC_
           TT                    CTTC TCCTT   CTTC   CTCCTT
                                |||| |||||   ||||  ||||||
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                                GAAG AGGAA   GAAG   GAGGAA
                                  T    A__    ACA
GAM377  KIAA1453  3'  TTCTCCTCTTCTCTCTCT    10146       TCCC    CC  _
                                TTCTCCT    CTTC  CTC CT
                                |||||||    ||||  ||| ||
                                AAGAGGA    GAAG  GAG GA
                                   _____    A_   A
GAM377  KIAA1573  3'  CTTCTCCTGTGTTTCCTTTCCT 10147        TCCCC    CC
           T                     CTTCTCCT    TTCC  TCCTT
                                |||||||||    ||||  |||||
                                GAAGAGGA    AAGG  AGGAA
                                     CACA_    AA
GAM377  KIAA1649  3'  TCTTAATGCCCCTTCCTCTCCT 10148     CCTT_       C
           T                     TCT    CCCCTTCC CTCCTT
                                |||    |||||||| ||||||
                                AGA    GGGGAAGG GAGGAA
                                  ATTAC       A
GAM377  KIAA1649  3'  TCTTAATGCCCCTTCCTCTCCT 10148     CCTT_       C
           T                     TCT    CCCCTTCC CTCCTT
                                |||    |||||||| ||||||
                                AGA    GGGGAAGG GAGGAA
                                  ATTAC       A
GAM377  KIAA1719  3'  CTCCCAGGCCTTCTTTCTCTTC 10149      TCC    CCC____
           CTT                    CTCCT   CCTTC      TCCTT
                                |||||   |||||      |||||
                                GAGGG   GGAAG      AGGAA
                                   TCC    AAAGAGA
GAM377  KIAA1854  3'  CTCCTTCTTCTTCTTCTAAGAG 10150       CC    CC _____
           CCTT                    CTCCTTC  CTTC  CT    CCTT
                                |||||||  ||||  ||    ||||
                                GAGGAAG  GAAG  GA    GGAA
                                    AA    AA  TTCTC
GAM377  KIAA1854  3'  TTCTCCCTTTCTCCTTCTTCTT 10151       __  C    CC  C
           CTT                    TTCTCCT  TC CCTTC  CT CTT
                                |||||||  ||  |||||  ||  |||
                                AAGAGGG  AG GGAAG  GA GAA
                                    AA  A    AA  A
GAM377  KIAA1910  5'  CTTTTCCTTTCCTCCCCT    10154    C    CCC
                                CTT TCCTT   CTTCCCCT
                                |||  |||||   ||||||||
                                GAA AGGAA   GGAGGGGA
                                  A    A__
GAM377  KIAA1910  5'  CTTCTCTTTCTTCTGCTC    10153      C  CCC   CC
                                CTTCTC TTC   TTC  CTC
                                ||||||  |||   |||  |||
                                GAAGAG AAG   AAG  GAG
                                   A   ___   AC
GAM377  KIAA1910  5'  TTCTCCTTCTCTTTCTTCTGCT 10152        CC___    CC
           C                     TTCTCCTTC    CTTC  CTC
                                |||||||||    ||||  |||
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                                AAGAGGAAG    GAAG  GAG
                                     AGAAA   AC
GAM377  KIAA1944  5'  CCTCTTCTTCCCCTTCTACT  10155      C       CC
                                CTTCT CTTCCCCTTC  CT
                                ||||| ||||||||||  ||
                                GGAGA GAAGGGGAAG  GA
                                   A        AT
GAM377  LENG9     3'  CTTTTCCTTCCTTCCTTCCTTT 10156  C     __    CC    III
           CCTTA                  TCCTTCC  CCTTCC  TCCTT   A
                                  |||||||  ||||||  |||||  |
                                  AGGAAGG  GGAAGG  AGGAA   T
                                A      AA     AA    III
GAM377  LENG9     3'  CTCCTCTCCCCTCCTTTTCCTT 10157      TC     ____  _
           CCTT                   CTCCT  CCCTTCC    CCT CCTT
                                ||||| |||||||   ||| ||||
                                GAGGA  GGGGAGG    GGA GGAA
                                   GA      AAAA   A
GAM377  MESDC2    3'  TTCTCCTCTCCTCCTC      10158        CCCCT  _
                                TTCTCCTT     TCC CCTC
                                ||||||||     ||| ||||
                                AAGAGGAG     AGG GGAG
                                     _____   A
GAM377  MGC20647  5'  CCTCTTCTTCCCCCTCTCCT   10159      C       C
                                CTTCT CTTCCCCTTC CCT
                                ||||| |||||||||| |||
                                GGAGA GAAGGGGGAG GGA
                                   A        A
GAM377  MGC4415   5'  CCTCTCTTCCTCTCCTCCT    10160      C    CCT  C
                                CTTCTC TTCC   TC CCTCCT
                                |||||| ||||   || ||||||
                                GGAGAG AAGG   AG GGAGGA
                                   _   ___  A
GAM377  MGC5139   5'  CTCCTCCTTCCTCCACATCCTC 10161          _  TTCC
                                CTTCTCCTTCC CC    CCTC
                                |||||||||| ||    ||||
                                GAGGAGGAAGG GG    GGAG
                                      A  TGTA
GAM377  MOV10     3'  TTCTTCCTTCCCCTTCCCCC   10162     _
                                TTCT CCTTCCCCTTCCCCT
                                |||| ||||||||||||||
                                AAGA GGAAGGGGAAGGGGG
                                  A
GAM377  MSTP032   3'  CTTCTCCCCTTTCTTCCC    10163        CCC
                                CTTCTCCTT   CTTCCC
                                |||||||||   ||||||
                                GAAGAGGGG   GAAGGG
                                     AAA
GAM377  NRN1      3'  CTTCTCCTCTCCTCGCCT    10164        TC  CT  C
                                CTTCTCCT  CC  TC CCT
                                ||||||||  ||  || |||
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                                GAAGAGGA  GG  AG GGA
                                    GA  __  C
GAM377  NXPH3    5'  CTTCCCCTTCCTGCTCCT    10165          C_
                                CTTCCCCTTCC  CTCCT
                                ||||||||||  |||||
                                GAAGGGGAAGG  GAGGA
                                      AC
GAM377  OR2C3    3'  CCTCCCTTTTCCCCTCCT    10166       CC
                                CCTTCC  TTCCCCTCCT
                                ||||||  ||||||||||
                                GGAGGG  AAGGGGAGGA
                                   AA
GAM377  PCDH17   3'  CTCTCCTTTTTCTTCTCTC   10167        CCC   CC
                                TTCTCCTT   CTTC  CTC
                                ||||||||   ||||  |||
                                GAGAGGAA   GAAG  GAG
                                     AAA   A_
GAM377  PRO1489  5'  CTTCCCTTCCCCGTTCCCTCT  10168     T     _   _
                                CTTC CCTTCCCC TTCCC CT
                                |||| |||||||| ||||| ||
                                GAAG GGAAGGGG AAGGG GA
                                  _      C    A
GAM377  PRO1496  3'  TTCTCCCTCTCTCTCTC     10169        CC   CCC
                                TTCTCCTTC  CTT   CTC
                                |||||||||  |||   |||
                                AAGAGGGAG  GAG   GAG
                                     A_   A__
GAM377  PRO2435  5'  TCCATCCCTTTTCCCTCCTT   10170    T   C  C
                                TCC TCCC TT CCCTCCTT
                                ||| |||| || ||||||||
                                AGG AGGG AA GGGAGGAA
                                  T   A  A
GAM377  PRO2893  5'  CTTCCCTTTTCTCCCACCCTC  10171       C_  _  _
                                CTTCCC  TTC CCC TCCTT
                                ||||||  ||| ||| |||||
                                GAAGGG  AAG GGG GGGAG
                                   AA   A   T
GAM377  PTRF     3'  CTTCTCCTATTTTCCTTTTTTT 10172        TCC__   CCCC_
           TCCTT                 CTTCTCCT    CCTT    TCCTT
                                ||||||||    ||||    |||||
                                GAAGAGGA    GGAA    AGGAA
                                     TAAAA   AAAAA
GAM377  RAB10    3'  CTCCTCCTTCCTGCTTTTCCT  10173          C_  CC
                                CTTCTCCTTCC  CTT  CCT
                                ||||||||||  |||  |||
                                GAGGAGGAAGG  GAA  GGA
                                      AC   AA
GAM377  RENT2    3'  TCTCCTTCACGCTCTCCTT   10174        CC_  TCCC
                                TCTCCTTC   CT   CTCCTT
                                ||||||||   ||   ||||||
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                                AGAGGAAG  GA   GAGGAA
                                    TGC  ____
GAM377  RENT2   3'  TCTCCTTCACGCTCTCCTT   10174       CC_  TCCC
                                TCTCCTTC  CT   CTCCTT
                                ||||||||  ||   ||||||
                                AGAGGAAG  GA   GAGGAA
                                    TGC  ____
GAM377  RHOBTB2  3'  CTTCTCCTTCCCCTTATCCC  10175          __
                                CTTCTCCTTCCCCT  TCCC
                                ||||||||||||||  ||||
                                GAAGAGGAAGGGGA  AGGG
                                       AT
GAM377  RYBP    5'  TTCTCCTTCTTCTCCT     10176        CCC  C
                                TTCTCCTTC  TTC CCT
                                |||||||||  ||| |||
                                AAGAGGAAG  AAG GGA
                                    ___  A
GAM377  RYBP    5'  TTCTCCTTCTTCTCCT     10176        CCC  C
                                TTCTCCTTC  TTC CCT
                                |||||||||  ||| |||
                                AAGAGGAAG  AAG GGA
                                    ___  A
GAM377  S164    5'  TCCTCCTTCTTTTCCTTCTTCT 10177        C___   CC  C
          TCTT                  TTCTCCTTC   CCTTC  CT CTT
                                |||||||||   |||||  || |||
                                AGGAGGAAG   GGAAG  GA GAA
                                    AAAA    AA  A
GAM377  SAMHD1   3'  CCCTCCTTCCTTCCTTCCTTTC 10179         __    CC
                                TTCTCCTTCC  CCTTCC  TC
                                ||||||||||  ||||||  ||
                                GGGAGGAAGG  GGAAGG  AG
                                     AA     AA
GAM377  SAMHD1   3'  TCCTTCCTTCCTTCCCTCCTT  10178       __     C
                                TCCTTCC  CCTTCCC TCCTT
                                |||||||  ||||||| |||||
                                AGGAAGG  GGAAGGG AGGAA
                                    AA     _
GAM377  SLC38A5  3'  CTCCTCCTCCTCCTCTTC    10141         _ _
                                CTTCTCCTTC CC CTTC
                                |||||||||| || ||||
                                GAGGAGGAGG GG GAAG
                                     A  A
GAM377  SPEC1   3'  CTTCTCTCTCCCCTTTCCC   10180       C      C
                                CTTCTC TTCCCCTT CCC
                                |||||| |||||||| |||
                                GAAGAG GAGGGGAA GGG
                                   A       A
GAM377  SRPUL   5'  CTCCTCTTTCTCCTTCCTCTC  10181       C  C    C
                                CTTCTC TTC CCTTCC CTC
                                |||||| ||| |||||| |||
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                                GAGGAG AAG GGAAGG GAG
                                   A  A    A
GAM377  TINF2    3'  CTGCTCCTTCCCACTCACCTTT 10182    T      _ TC  C_
           CCTT                   CT CTCCTTCCC CT  CC  TCCTT
                                || |||||||| ||  ||  |||||
                                GA GAGGAAGGG GA  GG  AGGAA
                                 C       T  GT  AA
GAM377  TNFRSF13B 3'  CTCTCCTTCTCTGCCTGTCTCT 10183        CC  T  CC  _
           T                    TTCTCCTTC  CT CC  TC CTT
                                |||||||||  || ||  || |||
                                GAGAGGAAG  GA GG  AG GAA
                                     A_  C  AC  A
GAM377  ZFP106   3'  CTTTTCCTCCTTGACCCCCTCC 10184    C     CCCT
           TT                    CTT TCCTTC    TCCCCTCCTT
                                ||| ||||||    ||||||||||
                                GAA AGGAGG    GGGGGAGGAA
                                  A     AACT
GAM377  ZNFN1A2  5'  CTTCTCTCTTTCCCTCCC    10185      _  C
                                CTTCTC CTT CCCTTCC
                                ||||||| ||| |||||||
                                GAAGAG GAA GGGAGGG
                                   A  A
GAM377  LOC123876 3'  TCCTCCTTCCCTTGCTTCCTCT 10186      ____    C__     III
           CTCCTTA                 CTTCCC   CTTCC   CTCCTT   A
                                ||||||   |||||   ||||||   |
                                GAAGGG   GAAGG   GAGGAA   T
                                   AAC    AGA     III
GAM377  LOC123876 3'  TTCTCCCTCTCTTTCTCCCTCT 10187        CCC  _    _
           CTT                    TTCTCCTTC   TTC CCCTC CTT
                                |||||||||   ||| ||||| |||
                                AAGAGGGAG   AAG GGGAG GAA
                                     AGA   A    A
GAM377  LOC123876 3'  CTCCTCTTTCCTTTCTTCCTCC 10188      C   CC   C_
           TT                    CTTCTC TTCC  TTC  CCTCCTT
                                |||||| ||||  |||  |||||||
                                GAGGAG AAGG  AAG  GGAGGAA
                                   A   A_   AA
GAM377  LOC124222 3'  CTCGGGGCTCCTTCCCCTCCTT 10189    CTTCC_
                                CTC     CCTTCCCCTCCTT
                                |||     ||||||||||||
                                GAG     GGAAGGGGAGGAA
                                  CCCCGA
GAM377  LOC125488 5'  CTTCTCCTCCAGCGTTCTCTCC 10190        CCC_  CC
           TT                    CTTCTCCTTC    TTC  CTCCTT
                                ||||||||||    |||  ||||||
                                GAAGAGGAGG    AAG  GAGGAA
                                     TCGC   A_
GAM377  LOC126917 3'  CCCTTCCTTCCACCTTTCTCTC 10191    TC      _   CCC
           CTT                    CT  TCCTTCC CCTT   CTCCTT
                                ||  ||||||| ||||   ||||||
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                                GG  AGGAAGG GGAA   GAGGAA
                                 GA      T    AGA
GAM377   LOC127435 3'  CTCCTCCTTTTCCTTCCCC    10192         CC
                                CTTCTCCTT  CCTTCCCC
                                |||||||||  ||||||||
                                GAGGAGGAA  GGAAGGGG
                                     AA
GAM377   LOC129676 3'  TTCTCTCTCTCTGCTCCT     10194      _   CCCCT  CC
                                TTCTC CTT     TC  CTCCT
                                ||||| |||     ||  |||||
                                AAGAG GAG     AG  GAGGA
                                   A  _____  AC
GAM377   LOC129676 3'  TCCCCCTTCCCTTTTCCTC    10193          C__
                                TTCCCCTTCCC   TCCTT
                                ||||||||||   |||||
                                AGGGGGAAGGG   AGGAG
                                      AAA
GAM377   LOC132617 5'  CTCCTCCTTCCCCACATCCTT  10195           TTCCCC
                                CTTCTCCTTCCCC     TCCTT
                                ||||||||||||      |||||
                                GAGGAGGAAGGGG     AGGAA
                                      TGT___
GAM377   LOC133383 5'  CTTCGTCCTTCCCCTTTCC    10196      _        C
                                CTTC TCCTTCCCCTT CC
                                |||| |||||||||| ||
                                GAAG AGGAAGGGGAA GG
                                   C          A
GAM377   LOC136319 5'  CTTCCTCTTCCTCTTCTCCTCC 10197      TC     C    C
                                CTTC  CTTCC CTTC CCTCC
                                ||||  ||||| |||| |||||
                                GAAG  GAAGG GAAG GGAGG
                                   GA     A    A
GAM377   LOC139673 3'  CTTTTCCTTCTCCCTCCC     10198     C     C
                                CTT TCCTTC CCTTCCC
                                ||| |||||| |||||||
                                GAA AGGAAG GGGAGGG
                                   A      A
GAM377   LOC143279 5'  TTCTTGTCGCCCCCTCCTTTTC 10199      CC  _      CC_
            CTT                    TTCT  TT CCCCTTCC   TCCTT
                                ||||  || ||||||||   |||||
                                AAGA  AG GGGGGAGG   AGGAA
                                   AC  C       AAA
GAM377   LOC143308 5'  CTTCCTCCCTCCCTCCCTT    10200      _     CT
                                CTTCC CCTTCCC  CCTT
                                ||||| |||||||  ||||
                                GAAGG GGGAGGG  GGAA
                                   A      AG
GAM377   LOC145693 5'  TTCTCCTTCCCTGTTCTCC    10201          CTTCCC
                                TTCTCCTTCCC     CTCC
                                ||||||||||      ||||
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                                AAGAGGAAGGG     GAGG
                                      ACAA__
GAM377  LOC145717 3'  CTTTCCCTTCCAGCCCCTC    10122     CT     CCTT
                                CTT  CCTTCC    CCCCTC
                                |||  ||||||    ||||||
                                GAA  GGAAGG    GGGGAG
                                  AG     TC__
GAM377  LOC145748 3'  CCTCTCCTTTTTCATTCCT    10202         CCCC   CCC
                                CTTCTCCTT    TTC   TCCT
                                |||||||||    |||   ||||
                                GGAGAGGAA    AAG   AGGA
                                      A___   TA_
GAM377  LOC146794 5'  CTTCTCCCTCGGTCATTTCTTC 10203          CCCTTCCCC_
           CTT                    CTTCTCCTTC         TCCTT
                                ||||||||||         |||||
                                GAAGAGGGAG         AGGAA
                                      CCAGTAAAGA
GAM377  LOC146953 5'  CTTCTTTCTCCCCGTCCCCTCC 10204       CC     T
           TT                     CTTCT  TTCCCC TCCCCTCCTT
                                |||||  |||||| ||||||||||
                                GAAGA  GAGGGG AGGGGAGGAA
                                   AA     C
GAM377  LOC147229 5'  TTCTCATTTCGGAACCCTCCTT 10205       C_   CCCTTC
                                TTCTC  TTC     CCCTCCTT
                                |||||  |||     ||||||||
                                AAGAG  AAG     GGGAGGAA
                                   TA   CCTT__
GAM377  LOC147299 3'  CTTCCCTCCTTCCTTCCT     10206      T   TCC     CC
                                CTTC CCT   CCTTCC  TCCT
                                ||||  |||   ||||||  ||||
                                GAAG GGA   GGAAGG  AGGA
                                  _   ____      A_
GAM377  LOC148137 3'  CTTCCCTTCTTAGCAGCCTCCT 10207      T    CCCTTCC
           T                      CTTC CCTTC      CCTCCTT
                                ||||  |||||      |||||||
                                GAAG GGAAG      GGAGGAA
                                  _     AATCGTC
GAM377  LOC148758 5'  CTCCTTCCTTCCCCTCCCCTCC 10208       _       T
           TT                     CTTCT CCTTCCCCT CCCCTCCTT
                                |||||  |||||||||  |||||||||
                                GAGGA GGAAGGGGA GGGGAGGAA
                                   A       _
GAM377  LOC148932 3'  TTCTCCCTCTTCTTCTCCT    10209         CC    C
                                TTCTCCTTC  CTTC CCT
                                |||||||||  ||||  |||
                                AAGAGGGAG  GAAG GGA
                                      AA    A
GAM377  LOC149086 5'  TTCTCCCTTCTATCTCTCTT   10210     _     CC_   _
                                TTC CCCTTC   CTC CTT
                                |||  ||||||   |||  |||
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                                AAG GGGAAG   GAG GAA
                                  A     ATA   A
GAM377   LOC149506 3'  CTTCTCTTTGCCTTCCCCT   10211       C  CC
                                CTTCTC TT  CCTTCCCCT
                                |||||| ||  |||||||||
                                GAAGAG AA  GGAAGGGGA
                                   _  AC
GAM377   LOC149711 3'  CCTCTCCTTTCTTCATCCT   10212         CCC   CCC
                                CTTCTCCTT   CTTC   TCCT
                                |||||||||   ||||   ||||
                                GGAGAGGAA   GAAG   AGGA
                                     A__    T__
GAM377   LOC149844 5'  CTTTCCTTTCCCTTCCC     10213     C     C
                                CTT TCCTT CCCTTCCC
                                ||| ||||| ||||||||
                                GAA AGGAA GGGAAGGG
                                  _     A
GAM377   LOC150311 5'  CTTCCCCTTTCTCCTCCT     10214         _ C
                                CTTCCCCTT C CCTCCT
                                ||||||||| | ||||||
                                GAAGGGGAA G GGAGGA
                                     A A
GAM377   LOC151094 3'  CTTTTCCTTTCTCCCCATCTT  10215     C    CCCC     TC
                                CTT TCCTT    TTCCCC  CTT
                                ||| |||||    ||||||  |||
                                GAA AGGAA    GAGGGG  GAA
                                  A    A___      TA
GAM377   LOC152190 5'  CTTCTCCGTTTTCTCCCCTT   10216       _____
                                CTTCTCC    TTCCCCTT
                                |||||||    ||||||||
                                GAAGAGG    GAGGGGAA
                                    CAAAA
GAM377   LOC154789 5'  CTTCCCTTCCCTTCCC      10217      T      C
                                CTTC CCTTCCC TTCCC
                                |||| ||||||| |||||
                                GAAG GGAAGGG AAGGG
                                   _     _
GAM377   LOC157489 3'  CTTCCCCTTTCTTCTTTCTC   10218         CCC    CC_
                                CTTCTCCTT   CTTC   CTC
                                |||||||||   ||||   |||
                                GAAGGGGAA   GAAG   GAG
                                     A__    AAA
GAM377   LOC157556 5'  CCTCTCCTTTCCTCCTTCC    10219         _ _
                                CTTCTCCTT CC CCTTCC
                                ||||||||| || ||||||
                                GGAGAGGAA GG GGAAGG
                                     A  A
GAM377   LOC157848 3'  CCTGTCCCCTTTCCCTCCT    10220     _      C
                                CCT TCCCCTT CCCTCCT
                                ||| ||||||| |||||||
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                                GGA AGGGGAA GGGAGGA
                                  C      A
GAM377  LOC158947 5'  TTCTCCTCTCCTTCCTTTC   10221        CC     CC
                                TTCTCCTT  CCTTCC  TC
                                ||||||||  ||||||  ||
                                AAGAGGAG  GGAAGG  AG
                                    A_     AA
GAM377  LOC159036 3'  CTTCTTCTTCCTTTTTCCCCC  10225      C    CC_
                                CTTCT CTTCC   TTCCCCT
                                ||||| |||||   |||||||
                                GAAGA GAAGG   AAGGGGG
                                   A     AAA
GAM377  LOC159036 3'  TTCTACTTCCTCCTGTCTTCCT 10228     C    _  _ CCC
           T                     TTCT CTTCC CCT TC   TCCTT
                                ||||| ||||| ||| ||   |||||
                                AAGA GAAGG GGA AG   AGGAA
                                   T    A   C  A__
GAM377  LOC159036 3'  TCCTTCTTCCTCCTCCCTCCTT 10223       C_    _
                                TCCTTC  CCTTC CCCTCCTT
                                ||||||  ||||| ||||||||
                                AGGAAG  GGAGG GGGAGGAA
                                   AA     A
GAM377  LOC159036 3'  CTTCCTTTTTCCTCCTTACTTC 10222      CC_   _   CCCC
           CTT                    CTTCT   TTCC CCTT    TCCTT
                                |||||   |||| ||||    |||||
                                GAAGG   AAGG GGAA    AGGAA
                                   AAA    A    TGA_
GAM377  LOC159036 3'  CTTCCTCCTTTCTACTGCCTT  10224      _   _ CC  _
                                CTTCC CCTT C  CT CCTT
                                ||||| |||| |  || ||||
                                GAAGG GGAA G  GA GGAA
                                   A    A AT  C
GAM377  LOC159036 3'  CTCCTCCTTCGTCTTCTTCT   10229         CC    CC
                                CTTCTCCTTC  CTTC  CT
                                ||||||||||  ||||  ||
                                GAGGAGGAAG  GAAG  GA
                                      CA    AA
GAM377  LOC159036 3'  TCCTCCTTCATTCTTCCTTTTT 10226     CC_    _____      III
           CCTCCTTA                TTC   CTTCC    CCTCCTT   A
                                |||   |||||    |||||||  |
                                AAG   GAAGG    GGAGGAA   T
                                  TAA     AAAAA      III
GAM377  LOC159036 3'  CTCCTTCCTACTTCCTTCTTCT 10227        C_    C_  C
           T                     CTCCTTCC  CTTCC  CT CTT
                                ||||||||  |||||  || |||
                                GAGGAAGG  GAAGG  GA GAA
                                     AT     AA  A
GAM377  LOC162952 3'  CTTCTCCTCTCTCTTCTTCCTT 10230         CCC    CCC
                                CTTCTCCTT   CTTC   TCCTT
                                |||||||||   ||||   |||||
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                                GAAGAGGAG  GAAG  AGGAA
                                    AGA   A__
GAM377  LOC163231 5'  CCTCTCCTTCCCTTTCCCC  10231          C
                                CTTCTCCTTCCC TTCCCC
                                |||||||||||| ||||||
                                GGAGAGGAAGGG AAGGGG
                                   A
GAM377  LOC163682 5'  TTCTCCTTCCTGGTGGTCCTCC 10232        CCTTCC_
          TT                    TTCTCCTTCC     CCTCCTT
                                ||||||||||     |||||||
                                AAGAGGAAGG     GGAGGAA
                                    ACCACCA
GAM377  LOC163682 5'  TTCTCCTTCCTGGTGGTCCTCC 10232        CCTTCC_
          TT                    TTCTCCTTCC     CCTCCTT
                                ||||||||||     |||||||
                                AAGAGGAAGG     GGAGGAA
                                    ACCACCA
GAM377  LOC163682 5'  TTCTCCTTCCTGGTGGTCCTCC 10232        CCTTCC_
          TT                    TTCTCCTTCC     CCTCCTT
                                ||||||||||     |||||||
                                AAGAGGAAGG     GGAGGAA
                                    ACCACCA
GAM377  LOC164382 3'  CTTCATCCTTTTTTTCCCCTC  10233    _   CCCC
                                CTTC TCCTT   TTCCCCTC
                                |||| |||||   ||||||||
                                GAAG AGGAA   AAGGGGAG
                                  T   AAA_
GAM377  LOC167147 5'  CTTCCCCTTTGGCTTCCTCT  10234       CCC   C
                                CTTCTCCTT  CTTCC CT
                                |||||||||  ||||| ||
                                GAAGGGGAA  GAAGG GA
                                    ACC   A
GAM377  LOC169026 5'  TTCTTTTTCTCTCCCTCCTCCT 10235    CC  CC   _
          T                     TTCT  TTC  CTTCC CCTCCTT
                                ||||  |||  ||||| |||||||
                                AAGA  AAG  GAGGG GGAGGAA
                                  AA  A_   A
GAM377  LOC196205 3'  CCTCTTCTTCATCGCTCCTCCT 10236    C   CCCTTCC
          T                     CTTCT CTTC     CCTCCTT
                                |||||  ||||     |||||||
                                GGAGA GAAG     GGAGGAA
                                  A   TAGCGA_
GAM377  LOC196205 3'  CTTCGCCTACATCCTTTCCCTC 10237    T  TCC_  C
          CTT                     CTTC CCT   CCTT CCCTCCTT
                                ||||  |||   |||| ||||||||
                                GAAG GGA   GGAA GGGAGGAA
                                  C  TGTA   A
GAM377  LOC196759 3'  TCTCCTTCTCTCTTCTCTTCTT 10238       CC_  CC  C
                                TCTCCTTC  CTTC  CT CTT
                                ||||||||  ||||  || |||
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                                AGAGGAAG   GAAG  GA GAA
                                    AGA    A_  A
GAM377  LOC196759 3'  TTCTCTCTTCTCTTCTTCT    10239      _   CC    CC
                                TTCTC CTTC  CTTC  CT
                                ||||| ||||  ||||  ||
                                AAGAG GAAG  GAAG  GA
                                   A    A_    AA
GAM377  LOC197407 3'  TTCTTCCTCCCCTTTCTTCCCT 10240  _     ___     C    III
          TCCTTA                  CCTTCCC   CTTCCC TCCTT   A
                                 |||||||   |||||| |||||   |
                                 GGAGGGG   GAAGGG AGGAA   T
                                A      AAA     A    III
GAM377  LOC197408 5'  TTCTTCCTCCCCTTTCTTCCCT 10240  _     ___     C    III
          TCCTTA                  CCTTCCC   CTTCCC TCCTT   A
                                 |||||||   |||||| |||||   |
                                 GGAGGGG   GAAGGG AGGAA   T
                                A      AAA     A    III
GAM377  LOC199864 3'  CTCTCCTTCTCTCTTCTCTTCT 10241        CC_   CC  C
          T                      TTCTCCTTC   CTTC  CT CTT
                                 |||||||||   ||||  || |||
                                 GAGAGGAAG   GAAG  GA GAA
                                      AGA    A_  A
GAM377  LOC199864 3'  TTCTCTCTTCTCTTCTTCT    10239      _   CC    CC
                                TTCTC CTTC  CTTC  CT
                                ||||| ||||  ||||  ||
                                AAGAG GAAG  GAAG  GA
                                   A    A_    AA
GAM377  LOC200030 3'  CTTCTTTTCTTCCCCTTCCCCT 10242    C__          C   III
          TCTTA                    CT   CTTCCCCTTCCCCT CTT   A
                                 ||   |||||||||||||| |||   |
                                 GA   GAAGGGGAAGGGGA GAA   T
                                  AAA           A   III
GAM377  LOC200030 3'  CTTCCCCTTCTTTTCTTCCCCT 10243       CC__       C   III
          TCTTA                    CTCCTTC    CTTCCCCT CTT   A
                                 |||||||    |||||||| |||   |
                                 GGGGAAG    GAAGGGGA GAA   T
                                      AAAA       A   III
GAM377  LOC200030 3'  CTTCTTTTCTTCCCCTTCCCCT 10242    C__          C   III
          TCTTA                    CT   CTTCCCCTTCCCCT CTT   A
                                 ||   |||||||||||||| |||   |
                                 GA   GAAGGGGAAGGGGA GAA   T
                                  AAA           A   III
GAM377  LOC200030 3'  CTTCCCCTTCTTTTCTTCCCCT 10243       CC__       C   III
          TCTTA                    CTCCTTC    CTTCCCCT CTT   A
                                 |||||||    |||||||| |||   |
                                 GGGGAAG    GAAGGGGA GAA   T
                                      AAAA       A   III
GAM377  LOC200933 3'  TTCTCCTTTACCCTCAATATCC 10244        CC    CCC_
          TT                      TTCTCCTT  CCTTC    TCCTT
                                 ||||||||  |||||    |||||
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                                AAGAGGAA  GGGAG    AGGAA
                                    AT    TTAT
GAM377  LOC201158 3'  CTCCTCTCTCCCGTCTCTTTCT 10245      C    ____  CCC
          CTCCTT                 TTCTC TTCCC   CTT  CTCCTT
                                |||||  |||||   |||  ||||||
                                AGGAG GAGGG   GAA  GAGGAA
                                   A    CAGA   AGA
GAM377  LOC202025 3'  CTTCCCTTCTCAGCTTTCCTT  10246     T    CC__  CCCC
                                CTTC CCTTC    CTT   TCCTT
                                ||||  |||||   |||   |||||
                                GAAG GGAAG    GAA   AGGAA
                                  _    AGTC   ____
GAM377  LOC219680 5'  CTCCTCTTTCACTTTTTCCTC  10247       C  CC  CC_
                                CTTCTC TTC  CTT   CCTC
                                ||||||  |||  |||   ||||
                                GAGGAG AAG  GAA   GGAG
                                   A  T_   AAA
GAM377  LOC220070 3'  TCTCCCTCAATTTTTCTTTCCT 10248        CCC__  CCC
          T                     TCTCCTTC    TTC   TCCTT
                                ||||||||    |||   |||||
                                AGAGGGAG    AAG   AGGAA
                                    TTAAA   AA_
GAM377  LOC220537 3'  CTTTCCCTTCCAGCCCCTC   10122    CT    CCTT
                                CTT  CCTTCC    CCCCTC
                                |||  ||||||    ||||||
                                GAA  GGAAGG    GGGGAG
                                  AG     TC__
GAM377  LOC220549 5'  CCTCCTCCTTCTCCTCCT    10249     _    C
                                CTTCC CCTTC CCTCCT
                                |||||  |||||  ||||||
                                GGAGG GGAAG GGAGGA
                                   A    A
GAM377  LOC221395 3'  TCCCTCCCTTCTTTCCTTCCTT 10251        __  C  C
                                TCCTTCCC  CTT CC TCCTT
                                ||||||||  ||| || |||||
                                AGGGAGGG  GAA GG AGGAA
                                    AA   A  A
GAM377  LOC221395 3'  CTTTCCTTCCTTTCTTCC    10252    C     C__
                                CTT TCCTTCC   CTTCC
                                |||  |||||||   |||||
                                GAA AGGAAGG   GAAGG
                                  _     AAA
GAM377  LOC221395 3'  TCCTTTCTTCCTTCCTTCCTT  10250     _ C_    CC
                                TCCTT C  CCTTCC  TCCTT
                                |||||  |  ||||||  |||||
                                AGGAA G  GGAAGG  AGGAA
                                   A AA     A_
GAM377  LOC221876 3'  CTCCTCCTTATTCCTTTCCTT  10253        CCCC   CC
                                CTTCTCCTT    TTCC  TCCTT
                                |||||||||    ||||  |||||
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                                GAGGAGGAA   AAGG  AGGAA
                                     T___   AA
GAM377  LOC222171 3'  CTTCTTCCTCCCCCACTCCTT  10254      _      TTCCC
                                CTTCT CCTTCCCC    CTCCTT
                                ||||| ||||||||    ||||||
                                GAAGA GGAGGGGG    GAGGAA
                                   A      T____
GAM377  LOC222933 5'  CTCCTCTGCAAACCCTTCCTTT 10255      CTTC__     CC
            C                    CTTCTC    CCCTTCC  TC
                                ||||||    |||||||  ||
                                GAGGAG    GGGAAGG  AG
                                   ACGTTT     AA
GAM377  LOC253670 5'  TTCTCCTCTTCAAACTCCTT   10256      TCCC   CC_
                                TTCTCCT   CTTC   CTCCTT
                                |||||||   ||||   ||||||
                                AAGAGGA   GAAG   GAGGAA
                                   ____   TTT
GAM377  LOC254659 3'  CTTCTCCTTCTCCTTCTTCT   10258        C    CC
                                CTTCTCCTTC CCTTC  CT
                                |||||||||| |||||  ||
                                GAAGAGGAAG GGAAG  GA
                                     A    AA
GAM377  LOC254659 3'  TCTCCTTCTCCTTCTCCTTCTT 10257       C    C   C
                                TCTCCTTC CCTTC CCT CTT
                                |||||||| ||||| ||| |||
                                AGAGGAAG GGAAG GGA GAA
                                     A    A   A
GAM377  LOC255101 5'  CTCCTCCTTCTCCTCTATCTCC 10259         _ _ _  C
            TCCTT                   CTTCTCCTTC CC CT TC CCTCCTT
                                |||||||||| || || || |||||||
                                GAGGAGGAAG GG GA AG GGAGGAA
                                     A  A  T  A
GAM377  LOC255106 3'  CTTCTCCTTTTCCTTACTC   10260        CC   CCC
                                CTTCTCCTT  CCTT   CTC
                                |||||||||  ||||   |||
                                GAAGAGGAA  GGAA   GAG
                                     AA    T__
GAM377  LOC255130 5'  TTCCCCTTTCCATTTTCCTT   10261       _  CC__
                                TTCCCCTT CC    TCCTT
                                |||||||| ||    |||||
                                AAGGGGAA GG    AGGAA
                                     A  TAAA
GAM377  LOC255849 5'  TTCTCTCCCTTCCCTTTTCCTT 10263      CTTC      C__
                                TTCTC   CCCTTCCC   TCCTT
                                |||||   ||||||||   |||||
                                AAGAG   GGGAAGGG   AGGAA
                                   A___       AAA
GAM377  LOC255849 5'  CTTCCCTTTTCCTTTTCCTC   10262     T   CC   CC
                                CTTC CCTT  CCTT  CCTC
                                |||| ||||  ||||  ||||
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                                GAAG GGAA  GGAA  GGAG
                                  _   AA    AA
GAM377  LOC256337 3'  TTCTCCTTTCCTTCTTCTC   10264       CC    CC
                                TTCTCCTT  CCTTC  CTC
                                ||||||||  |||||  |||
                                AAGAGGAA  GGAAG  GAG
                                    A_    AA
GAM377  LOC257418 5'  CTTCTCTCTCCTCTATCC    10265      C   C  _
                                CTTCTC TTCC CT TCC
                                |||||| |||| || |||
                                GAAGAG GAGG GA AGG
                                   A   A  T
GAM377  LOC257464 5'  CTCCACCCCCTTTTTTTCCTT  10267     T     CCCC
                                CTCC TCCCCTT   TCCTT
                                |||| |||||||   |||||
                                GAGG GGGGGAA   AGGAA
                                  T     AAAA
GAM377  LOC257464 3'  CTTCCTTTCTTCCTTTCCTT   10266     C__   CC
                                CTTCC  CTTCC  TCCTT
                                |||||  |||||  |||||
                                GAAGG  GAAGG  AGGAA
                                   AAA    AA
GAM377  LOC51194  3'  TTCTCCTTTTCCCCT      10268       CCCC
                                TTCTCCTT   TTCCCCT
                                ||||||||   |||||||
                                AAGAGGAA   AAGGGGA
                                           ____
GAM377  LOC51289  3'  CTTCATCCTTTCACCTC    10269    _   CCCCT  C
                                CTTC TCCTT    TC CCTC
                                |||| |||||    || ||||
                                GAAG AGGAA    AG GGAG
                                  T    _____  T
GAM377  LOC55862  5'  TCTCCTTTCCTTTCTCC    10270      CC   CCC
                                TCTCCTT  CCTT  CTCC
                                |||||||  ||||  ||||
                                AGAGGAA  GGAA  GAGG
                                   A_   A__
GAM377  LOC85479  5'  TTCTCCCTTGTTCTTTCCTT  10271       CCCC  CCC
                                TTCTCCTT   TTC  TCCTT
                                ||||||||   |||  |||||
                                AAGAGGGA   AAG  AGGAA
                                    AC__   AA_
GAM377  LOC90342  5'  CTCTTCCTTCCCCAACTCCTT  10272   TC      TTCCC
                                CT  TCCTTCCCC   CTCCTT
                                ||  |||||||||   ||||||
                                GA  AGGAAGGGG   GAGGAA
                                 GA       TT___
GAM377  LOC90371  3'  TCCTGAACCTTTCCCTCCTT  10273    TCC   C
                                TCCT  CCTT CCCTCCTT
                                ||||  |||| ||||||||
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                                AGGA   GGAA GGGAGGAA
                                  CTT    A
GAM377  LOC91156  5' CTTCTCTTTCCTCCTCCAACCT 10274       C    C    CCT
                                CTTCTC TTCC CTTCC   CCT
                                |||||| |||| |||||   |||
                                GAAGAG AAGG GGAGG   GGA
                                   A    A    TT_
GAM377  LOC91170  5' CTTCTCCTGCTCTGCCTTC    10275        __ C_
                                CTTCTCCT  TC  CCTTC
                                ||||||||  ||  |||||
                                GAAGAGGA  AG  GGAAG
                                     CG  AC
GAM377  LOC91796  5' CTCCTTTCCTTCCTTTCCTT   10278       CC     CC
                                CTCCTT  CCTTCC  TCCTT
                                ||||||  ||||||  |||||
                                GAGGAA  GGAAGG  AGGAA
                                   A_     AA
GAM377  LOC91796  5' CTTTCCTTCCTTTCCTTTCCTT 10280     C      CC    CC
                                CTT TCCTTCC  TTCC  TCCTT
                                ||| |||||||  ||||  |||||
                                GAA AGGAAGG  AAGG  AGGAA
                                  _     A_   AA
GAM377  LOC91796  5' CTTTCCTTTCCTTTCCC     10276     C    C  C
                                CTT TCCTT CC TTCCC
                                ||| ||||| || |||||
                                GAA AGGAA GG AAGGG
                                  _    A  A
GAM377  LOC91796  5' CCTTTCCCTCCCTCCCTTCCTT 10277     C       CT    C
                                CTT TCCTTCCC  TCCC TCCTT
                                ||| ||||||||  |||| |||||
                                GGA AGGGAGGG  AGGG AGGAA
                                  A       __    A
GAM377  LOC91796  5' CTCCCTCCCTCCTTTCCTTCCT 10279         _  CC  _   III
          TA                    CTCCTTCCC CTT  CCT CCTT   A
                                ||||||||| |||  ||| ||||  |
                                GAGGGAGGG GGA  GGA GGAA   T
                                     A   AA   A    III
GAM377  LOC92710  3' TTCTCCTTTCTCTCTGATCCTT 10281        CCC   CCCC
                                TTCTCCTT   CTT    TCCTT
                                ||||||||   |||    |||||
                                AAGAGGAA   GAG    AGGAA
                                     AGA   ACT_
GAM377  LOC93132  5' CTTCCCCTTCCCCTTCGCCT   10282             C
                                CTTCTCCTTCCCCTTC CCT
                                |||||||||||||||| |||
                                GAAGGGGAAGGGGAAG GGA
                                          C
GAM377  LOC96610  5' TCTCCTTCAATTTTCTCTTCTT 10283        CCC_   CC  C
                                TCTCCTTC    TTC  CT CTT
                                ||||||||    |||  || |||
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                                AGAGGAAG    AAG  GA GAA
                                    TTAA   A_  A
GAM378  ABCA2    5'  TCGCCCGCGCGGGGGCGGGGCG 10286      G _   CC
              C                   TCGCC CG GCGG  GGCGGGGCGC
                                  ||||| || ||||  ||||||||||
                                  AGCGG GC CGCC  CCGCCCCGCG
                                    _ G   C_
GAM378  ABCC4    5'  GCCGGGCGGGGCGGGCG     10287     C    CC     G
                                  GCCG GGCGG  GGCGGG CG
                                  |||| |||||  |||||| ||
                                  CGGC CCGCC  CCGCCC GC
                                    _    __    _
GAM378  AMMECR1  5'  CGCCAGAGGCTGGCGGGGCGC  10288      C  C   C
                                  CGCCG GG GGC GGCGGGGCGC
                                  ||||| || ||| ||||||||||
                                  GCGGT CT CCG CCGCCCCGCG
                                    _ _  A
GAM378  ANKRD3   5'  CGCCGCGGCGGCTGCCCAGGTG 10289          CGG_   _
              C                   CGCCGCGGCGGC   CGGG GC
                                  ||||||||||||   |||| ||
                                  GCGGCGCCGCCG   GTCC CG
                                        ACGG   A
GAM378  BCR      5'  TCGGCGCGCGGGGCGGGGCGC  10290    C   G   CC
                                  TCG CGCG CGG  GGCGGGGCGC
                                  ||| |||| |||  ||||||||||
                                  AGC GCGC GCC  CCGCCCCGCG
                                    C   _  __
GAM378  BCR      5'  TCGGCGCGCGGGGCGGGGCGC  10290    C   G   CC
                                  TCG CGCG CGG  GGCGGGGCGC
                                  ||| |||| |||  ||||||||||
                                  AGC GCGC GCC  CCGCCCCGCG
                                    C   _  __
GAM378  BTAF1    5'  TCCCCGCGGCGGCCGGTAAGC  10291    G          CG
                                  TC CCGCGGCGGCCGG  GGGC
                                  || ||||||||||||  ||||
                                  AG GGCGCCGCCGGCC  TTCG
                                    G          A_
GAM378  CDKN2C   5'  CGCCGCGGTGGCTGGATGC   10292        C   C  CGGG
                                  CGCCGCGG GGC GG    GC
                                  |||||||| ||| ||    ||
                                  GCGGCGCC CCG CC    CG
                                      A   A  TA__
GAM378  CSDA     5'  CGCGGCGGCCGGGGC       10293          GGC
                                  CGCGGCGGCC   GGGGC
                                  ||||||||||   |||||
                                  GCGCCGCCGG   CCCCG
                                       ____
GAM378  DGKG     5'  GCGCGGTGGCCCGGGGCGC   10294    C   C   GG
                                  GC GCGG GGCC  CGGGGCGC
                                  || |||| ||||  ||||||||
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                                CG CGCC CCGG  GCCCCGCG
                                 _   A   __
GAM378  EP300    5'  TCGCGCGGCGGCCGGCGGAGGC 10295     C          _
              GC                   TCGC GCGGCGGCCGGCGG GGCGC
                                   |||| |||||||||||||| |||||
                                   AGCG CGCCGCCGGCCGCC CCGCG
                                     _          T
GAM378  GALGT    5'  CCGGGGGCGGTTGGCGGGGCGC 10296    C_    CC
                                   CCG  GGCGG  GGCGGGGCGC
                                   |||  |||||  ||||||||||
                                   GGC  CCGCC  CCGCCCCGCG
                                     CC    AA
GAM378  HNRPDL   5'  CCGCTGCGGCGGCCGCTGCGCG 10297   C       ________  GGG
              CCCCG                  C GCGGCGGCCG      GCG   CG
                                   | ||||||||||      |||   ||
                                   G CGCCGCCGGC      CGC   GC
                                    A         GACGIII   GGG
GAM378  HR       5'  CGTCGTGGCCGGCACCGGGCGC 10298    _ GC      __
                                   CG CG  GGCCGGCG  GGGCGC
                                   || ||  ||||||||  ||||||
                                   GC GC  CCGGCCGT  CCCGCG
                                    A  A_       GG
GAM378  KCNS2    5'  TCGCGGCGGTGGCCGCTGCGCG 10299   C   C   ________  GGG
              CCCCG                  C GCGG GGCCG      GCG   CG
                                   | |||| |||||      |||   ||
                                   G CGCC CCGGC      CGC   GC
                                    C   A    GACGIII   GGG
GAM378  MEL      3'  GCCGCGGCGTGGGCGGGGCG   10300         GCC
                                   GCCGCGGCG   GGCGGGGCG
                                   |||||||||   |||||||||
                                   CGGCGCCGC   CCGCCCCGC
                                         AC_
GAM378  MFRP     3'  TCGCCCGGCGGCCGGCCAAA   10301       G         G
                                   TCGCC CGGCGGCCGGC GGG
                                   ||||| |||||||||| |||
                                   AGCGG GCCGCCGGCCG TTT
                                     _          G
GAM378  NUP50    5'  GCGGCGAAACCCGGGGCGC    10302       __  GG
                                   GCGGCG  GCC  CGGGGCGC
                                   ||||||  |||  ||||||||
                                   CGCCGC  TGG  GCCCCGCG
                                      TT   __
GAM378  PABPC4   5'  CGCTGCGGCGGCGGGCG     10303     C       CGGCG
                                   CGC GCGGCGGC    GGGCG
                                   ||| ||||||||    |||||
                                   GCG CGCCGCCG    CCCGC
                                     A       ______
GAM378  PITPN    5'  TCGCCGCGGTCGCCGCGC    10304         CG   _
                                   TCGCCGCGG  GCCG GC
                                   |||||||||  |||| ||
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                                AGCGGCGCC CGGC CG
                                    AG  G
GAM378  PTPRS   3' TCGCTGGGGCGGCCGGGGC  10305    CGC    GGC
                                TCGC  GGCGGCC  GGGGC
                                ||||  |||||||  |||||
                                AGCG  CCGCCGG  CCCCG
                                  ACC    ___
GAM378  PTPRS   3' TCGCTGGGGCGGCCGGGGC  10305    CGC    GGC
                                TCGC  GGCGGCC  GGGGC
                                ||||  |||||||  |||||
                                AGCG  CCGCCGG  CCCCG
                                  ACC    ___
GAM378  PTPRS   3' TCGCTGGGGCGGCCGGGGC  10305    CGC    GGC
                                TCGC  GGCGGCC  GGGGC
                                ||||  |||||||  |||||
                                AGCG  CCGCCGG  CCCCG
                                  ACC    ___
GAM378  PTPRS   3' TCGCTGGGGCGGCCGGGGC  10305    CGC    GGC
                                TCGC  GGCGGCC  GGGGC
                                ||||  |||||||  |||||
                                AGCG  CCGCCGG  CCCCG
                                  ACC    ___
GAM378  AF9Q34  5' CGCGGCGGCGGCGGCGGCGC  10306       C   _
                                CGCGGCGGC GGCGG GGCGC
                                ||||||||| ||||| |||||
                                GCGCCGCCG CCGCC CCGCG
                                    _   G
GAM378  ARNTL2  5' GCCGCGGCGGCCGCCACCGC  10307         G  GG
                                GCCGCGGCGGCCG CG  GC
                                |||||||||||| ||  ||
                                CGGCGCCGCCGGC GT  CG
                                      G  GG
GAM378  CHDH    5' CGCCGCGGCGGCCCGTGC   10308         GG  GG
                                CGCCGCGGCGGCC  CG  GC
                                ||||||||||||  ||  ||
                                GCGGCGCCGCCGG  GC  CG
                                    __  A_
GAM378  CRMP5   5' TCGCCGCGGCGCCGGAGC   10309        G   CGG
                                TCGCCGCGGCG CCGG  GGC
                                |||||||||| ||||  |||
                                AGCGGCGCCGC GGCC  TCG
                                    _   ___
GAM378  DIM1    5' TCGCCGCCGCCCAAGGCGGGGC 10310      G  GG  __
          GC                    TCGCCGC GC  CC  GGCGGGGCGC
                                ||||||| ||  ||  ||||||||||
                                AGCGGCG CG  GG  CCGCCCCGCG
                                   G  __  TT
GAM378  ETAA16  5' CCGCCATTTTGGTCGGTGGGGC 10311      CGGC  C   C
          GC                    TCGCCG   GG CGG GGGGCGC
                                ||||||   || ||| |||||||
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                                GGCGGT   CC GCC CCCCGCG
                                   AAAA  A   A
GAM378  FLJ14440  5'  TCGCTGGGGTGGCTGGCATCGC 10312     CGC  C   C   GG
                                TCGC   GG GGC GGCG  GC
                                ||||   || ||| ||||  ||
                                AGCG   CC CCG CCGT  CG
                                  ACC  A   A   AG
GAM378  KIAA0469  3'  TCCCGCGGCGGCCGGGG    10313    G         C
                                TC CCGCGGCGGCCGG GG
                                || ||||||||||||| ||
                                AG GGCGCCGCCGGCC CC
                                 _         _
GAM378  KIAA1545  5'  CGCGGCGGCGGCGGCGC    10314        C    G
                                CGCGGCGGC GGCGG GC
                                ||||||||| ||||| ||
                                GCGCCGCCG CCGCC CG
                                     _    G
GAM378  LRP15    5'  GCTGCGGCGGCCGCTGCGCGCC 10315   C        _______   GGG
            CCG                   C GCGGCGGCCG      GCG   CG
                                | ||||||||||      |||   ||
                                G CGCCGCCGGC      CGC   GC
                                 A        GACGIII   GGG
GAM378  MGC2601   5'  CCGCTGCCCCGGCGGGGCG   10316     G  GG
                                CCGC GC  CCGGCGGGGCG
                                |||| ||  ||||||||||
                                GGCG CG  GGCCGCCCCGC
                                  A  G_
GAM378  MOT8     5'  CGCCGTGGAGCGCGGGGCG   10317      C  C   CG
                                CGCCG GG GGC  GCGGGGCG
                                ||||| || |||  ||||||||
                                GCGGC CC TCG  CGCCCCGC
                                   A  _  __
GAM378  OSBPL8   5'  TCGCCGCGGCGCCGGGG    10318         G   C
                                TCGCCGCGGCG CCGG GG
                                |||||||||| |||| ||
                                AGCGGCGCCGC GGCC CC
                                        _   _
GAM378  P114-RHO-GEF 3'  TCGCGCGGCGGCTGTGGAGCG  10319     C      CGGC
                                TCGC GCGGCGGC    GGGGCG
                                |||| ||||||||    ||||||
                                AGCG CGCCGCCG    CCTCGC
                                  _       ACA_
GAM378  TOB2     5'  TCTCCGCGGCGGCGGGGCG   10320    G       CGGC
                                TC CCGCGGCGGC    GGGGCG
                                || ||||||||||    ||||||
                                AG GGCGCCGCCG    CCCCGC
                                 A        _____
GAM378  UBE2E1   5'  CCGCCGCGGCGGCTGCTGC    10321          CG  GGG
                                TCGCCGCGGCGGC  GC   GC
                                ||||||||||||  ||   ||
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                                GGCGGCGCCGCCG  CG   CG
                                      A_  A__
GAM378  UBE4B    3'  TCGCTGCGGCCGCTGCTTCTGC 10322     C    G  CG  GGG_
                                TCGC GCGGC GC  GC    GC
                                |||| ||||| ||  ||    ||
                                AGCG CGCCG CG  CG    CG
                                  A    G  A_  AAGA
GAM378  LOC123099 5'  CGCGGCGGCCGCGGCGC     10323          G   G
                                CGCGGCGGCCG CGG GC
                                |||||||||||| ||| ||
                                GCGCCGCCGGC GCC CG
                                      _  G
GAM378  LOC126282 5'  GCCGCGGCGGTGGGAGCAGCGC 10324          CC__    G
                                GCCGCGGCGG   GGCGG GC
                                |||||||||    ||||| ||
                                CGGCGCCGCC   TCGTC CG
                                     ACCC    G
GAM378  LOC153572 3'  GCGGCCACCGCGGGGCGC    10325      G   G
                                GCGGC GCCG CGGGGCGC
                                ||||| |||| ||||||||
                                CGCCG TGGC GCCCCGCG
                                  G   _
GAM378  LOC200213 5'  GCTTGCGGCGGCCCTCGGCGC  10326    C_       GG   G
                                GC  GCGGCGGCC  CGG GC
                                ||  |||||||||  ||| ||
                                CG  CGCCGCCGG  GCC CG
                                 AA        GA   G
GAM378  LOC202781 5'  TCGCCGCGGAGGCCACCAGTGC 10327         C    G   G
                                TCGCCGCGG GGCCG CGG GC
                                ||||||||| ||||| ||| ||
                                AGCGGCGCC CCGGT GTC CG
                                     T    G   A
GAM378  LOC221749 5'  GCCGCAGCGGCCCCTGCGC   10328          GGCGGG
                                GCCGCGGCGGCC     GCGC
                                ||||||||||||     ||||
                                CGGCGTCGCCGG     CGCG
                                      GGA___
GAM378  LOC253219 5'  CGCTCAAGCTGGCGGGGCGC   10329     GGC   C
                                CGC   GGC GGCGGGGCGC
                                |||   ||| ||||||||||
                                GCG   TCG CCGCCCCGCG
                                  AGT   A
GAM378  LOC90120  5'  TCTCCGCGGCGGCGCCGGCG   10331    G        __
                                TC CCGCGGCGGC  CGGCG
                                || ||||||||||  |||||
                                AG GGCGCCGCCG  GCCGC
                                 A         CG
GAM378  LOC90120  5'  TCGCAGTGGCGGCGGCGG    10330      CGC     C
                                TCGC   GGCGGC GGCGG
                                ||||   |||||| |||||
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                                AGCG   CCGCCG CCGCC
                                  TCA     _
GAM379  BMP2     5'  TGCCGGCCGCGCAGTCTCTCTT 10334    G       C_     C
             TTC                   TG CGGCCGCGT  TCTCTC TTTC
                                || |||||||||  |||||| ||||
                                AC GCCGGCGCG  AGAGAG AAAG
                                 G        TC     A
GAM379  DOC1     5'  TGGTGACCCTTTTCTCCTTT   10335     C    GCGTCTC
                                TGG GGCC      TCTCCTTT
                                ||| ||||      ||||||||
                                ACC CTGG      AGAGGAAA
                                  A   GAAA___
GAM379  KCNN3    3'  AGCTCGGTCTCTCTTCTTTC   10336     _ C       C
                                GGC CG GTCTCTCT CTTTC
                                ||| || |||||||| |||||
                                TCG GC CAGAGAGA GAAAG
                                  A _       A
GAM379  LY64     3'  TGGGGGCTGATGATCTCCTTTC 10337     C   CGCGTCTC
                                TGG GGC       TCTCCTTTC
                                ||| |||       |||||||||
                                ACC CCG       AGAGGAAAG
                                  C   ACTACT__
GAM379  PRex1    3'  TGGAGGCCCCGTCTCTCCTTTC 10338     C    G     TC
                                TGG GGCC CGTCTC  TCCTTTC
                                ||| |||| ||||||  |||||||
                                ACC CCGG GCAGAG  AGGAAAG
                                  T   G     __
GAM379  SERPINB13 3'  TGGAGAAACTTTCTCTCCTTTC 10339     C  CC  GTC
                                TGG GG  GC   TCTCTCCTTTC
                                ||| ||  ||   ||||||||||
                                ACC TC  TG   AGAGAGGAAAG
                                  _  TT  AA_
GAM379  FLJ21596 3'  TGGTGGCTACTTCTCCTTTC   10340     C   CG GTCTC
                                TGG GGC  C    TCTCCTTTC
                                ||| |||  |    |||||||||
                                ACC CCG  G    AGAGGAAAG
                                  A   AT A_____
GAM379  FLJ30567 3'  TGACTTTCGTCTCTCTCTTTT  10341      GGCCG        C
                                TGGC    CGTCTCTCTC TTT
                                ||||    |||||||||| |||
                                ACTG    GCAGAGAGAG AAA
                                   AAA__         A
GAM379  FYCO1    3'  TGATGGCTGTGTACCTCCTTT  10342    GC   CGC  CTC
                                TG  GGC   GT   TCTCCTTT
                                ||  |||   ||   ||||||||
                                AC  CCG   CA   GGAGGAAA
                                 TA   A__  CAT
GAM379  MGC22793 5'  TGGCTGCCGCCTCCTT      10343      G    GTCTCT
                                TGGC GCCGC     CTCCTT
                                |||| |||||     ||||||
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                                ACCG CGGCG     GAGGAA
                                  A    _______
GAM379  MKRN2    3'  TGGCTGGCTGTTACCTCCTTT  10344     _  CGC  CT T
                                TGGC GGC   GT  C CTCCTTT
                                |||| |||   ||  | |||||||
                                ACCG CCG   CA  G GAGGAAA
                                  A  A__  AT _
GAM379  NUCKS    3'  TGGCAGCCCCTGCTTT     10345        GCGTCTC   C
                                TGGCGGCC      TCT CTTT
                                ||||||||      ||| ||||
                                ACCGTCGG      GGA GAAA
                                    ________  C
GAM379  POLA2    3'  TGGCTGGCTCCTCTCTCCTTTC 10346     _  CGCG
                                TGGC GGC    TCTCTCTCCTTTC
                                |||| |||    ||||||||||||
                                ACCG CCG    GGAGAGAGGAAAG
                                  A  A___
GAM379  LOC148166 5'  TGGTTGGAATCTCTCTTTCTTT 10347     C_  CCGC      C_
                                TGG  GG    GTCTCTCT  CTTT
                                |||  ||    ||||||||  ||||
                                ACC  CC    TAGAGAGA  GAAA
                                  AA  T___       AA
GAM379  LOC157556 5'  TGGAGGCCCCTCTCCTTT    10348     C    GCGTC
                                TGG GGCC     TCTCTCCTTT
                                ||| ||||     ||||||||||
                                ACC CCGG     GGAGAGGAAA
                                  T   ______
GAM379  LOC92080  5'  TGGCGATTCCTCTCCTTT    10349       CCGCG  T
                                TGGCGG     TC CTCTCCTTT
                                ||||||     || |||||||||
                                ACCGCT     AG GAGAGGAAA
                                   A_____  _
GAM380  CARD4    3'  TTGCTCACAGCTTTATTCCTC  10352        C  CGGGG
                                TTGCTCAC GC     TCCTC
                                |||||||| ||     |||||
                                AACGAGTG CG     AGGAG
                                     T  AAATA
GAM380  FAAH     3'  GCCTGCTCACTGGCTTCTC   10353         CGCC  GG  C
                                GCTTGCTCAC    GG  TC TC
                                ||||||||||    ||  || ||
                                CGGACGAGTG    CC  AG AG
                                     A___  GA  _
GAM380  FGF18    5'  GCTCGCTCACTGCTGGCCGG   10354         C  C  _____
                                GCTTGCTCAC GC GG     GG
                                |||||||||| || ||     ||
                                CGAGCGAGTG CG CC     CC
                                     A  A  GGIII
GAM380  FGF18    5'  GCTCGCTCACTGCTGGCCGG   10354         C  C  _____
                                GCTTGCTCAC GC GG     GG
                                |||||||||| || ||     ||
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                                CGAGCGAGTG CG CC    CC
                                     A  A  GGIII
GAM380  FGF18    3'  TTCCTCATTCAAGTCCTCC   10355    G   CCGCCG
                                TT CTCA     GGGTCCTCC
                                || ||||     |||||||||
                                AA GAGT     TTCAGGAGG
                                 G   AAG___
GAM380  FGF18    3'  TTCCTCATTCAAGTCCTCC   10355    G   CCGCCG
                                TT CTCA     GGGTCCTCC
                                || ||||     |||||||||
                                AA GAGT     TTCAGGAGG
                                 G   AAG___
GAM380  LMO4     5'  GCTTGCTCGCTCCGGGAT    10356        ACCG
                                GCTTGCTC    CCGGGGT
                                ||||||||    |||||||
                                CGAACGAG    GGCCCTA
                                     CGA_
GAM380  P2RX3    3'  CTTGCTCAGGCAGGGTCCTC   10357        CC  C
                                CTTGCTCA  GC GGGGTCCTC
                                ||||||||  || |||||||||
                                GAACGAGT  CG TCCCAGGAG
                                     C_  _
GAM380  PDGFB    5'  GCCTGCTCGCCGCTCTGGGCGT 10358        A   C__  _
           CCTC                      GCTTGCTC CCGC   GGG GTCCTC
                                ||||||||| ||||   ||| ||||||
                                CGGACGAG GGCG   CCC CAGGAG
                                     C    AGA   G
GAM380  PPP3CB   3'  CTTGCTCACTGCTCTCCGGAGG 10359        C  C________  GTCC
           AC                       TTGCTCAC GC       GGG    T
                                |||||||| ||       |||   |
                                AACGAGTG CG       CCT    G
                                     A  AGAGGIII   CCTG
GAM380  REQ      3'  GCTTGCTCGCTCCCAGCTCC   10360        ACCG  G  G
                                GCTTGCTC    CC GG TCC
                                ||||||||    || || |||
                                CGAACGAG    GG TC AGG
                                     CGA_  G  G
GAM380  RHCG     3'  GCTTGCTCACTCTTGCATCC   10361         C___  CGGG
                                GCTTGCTCAC    GC    GTCC
                                ||||||||||    ||    ||||
                                CGAACGAGTG    CG    TAGG
                                      AGAA  _____
GAM380  C20orf97 3'  TTGCTCACTGCTGTACTCC    10362        C  CGGG  C
                                TTGCTCAC GC    GT CTCC
                                |||||||| ||    || ||||
                                AACGAGTG CG    CA GAGG
                                     A  A___  T
GAM380  CSRP2BP  3'  GCTGCTCACTGCTCATTTCGGA 10363       C  _ G________  TCC
           GGACC                     GCTCAC GC C       GGG   TC
                                |||||| || |       |||   ||
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                                CGAGTG CG G       CCT   GG
                                   A  A TAAAGIII   CCT
GAM380  DCNP1    3'  GCTTGCTTGCCTCCGCACCTC  10364       CA  G   GGGT
                                GCTTGCT  CC CCG    CCTC
                                |||||||  || |||    ||||
                                CGAACGA  GG GGC    GGAG
                                   AC  A   GT__
GAM380  DEFCAP   3'  GCTTGCTCTTGTAGATCTTCC  10365       ACCGCCG    C
                                GCTTGCTC      GGGTC TCC
                                ||||||||      ||||| |||
                                CGAACGAG      TCTAG AGG
                                   AACA___     A
GAM380  DEFCAP   3'  GCTTGCTCTTGTAGATCTTCC  10365       ACCGCCG    C
                                GCTTGCTC      GGGTC TCC
                                ||||||||      ||||| |||
                                CGAACGAG      TCTAG AGG
                                   AACA___     A
GAM380  DEFCAP   3'  GCTTGCTCTTGTAGATCTTCC  10365       ACCGCCG    C
                                GCTTGCTC      GGGTC TCC
                                ||||||||      ||||| |||
                                CGAACGAG      TCTAG AGG
                                   AACA___     A
GAM380  FLJ22418 3'  TTGCTCACTCCAGACTTC    10366        CG    G_
                                TTGCTCAC  CCGGG  TC
                                |||||||  |||||  ||
                                AACGAGTG  GGTCT  AG
                                   A_    GA
GAM380  FLJ32934 3'  GCCTGCTCAGGGTCCT      10367        CCGCCG
                                GCTTGCTCA     GGGTCCT
                                |||||||||     |||||||
                                CGGACGAGT     CCCAGGA
                                              _______
GAM380  GR6      5'  GCTTGCCCACTGCCGTGCTCTG 10368     C  __________  TCC
           GAGGACCC                TCAC GCCG       GGG   TCC
                                |||| ||||       |||   |||
                                GGTG CGGC       CCT   GGG
                                  A   ACGAGAIII   CCT
GAM380  KIAA0701 5'  TTGCTCACTGCCTCCTC     10369        C   GGGG
                                TTGCTCAC GCC    TCCTC
                                |||||||| |||    |||||
                                AACGAGTG CGG    AGGAG
                                   A  ____
GAM380  KIAA1077 3'  GCTTGCTCACATGCTCACTAGC 10370         C_  _  G_
                                GCTTGCTCAC  GC CG  GGT
                                ||||||||||  || ||  |||
                                CGAACGAGTG  CG GT  TCG
                                      TA  A  GA
GAM380  KIAA1086 3'  GCTTGCTGTACTGCTGGCCGGA 10371      C_  C  C  _____  TCCT
           GGC                    TTGCT  AC GC GG    GG    C
                                |||||  || || ||    ||   |
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                                AACGA  TG CG CC    CC   G
                                  CA  A  A  GGIII  TCCT
GAM380  KIAA1932  5'  GCTTTTTCACTGCCAGGATCCT 10372     GC   C
                                GCTT  TCAC GCCGGGGTCCT
                                ||||  |||| ||||||||||
                                CGAA  AGTG CGGTCCTAGGA
                                  AA   A
GAM380  MESDC2   3'  GCTCACACCTGCTGGGGTCCTC 10373    TG TC  _  C
                                GCT  C  ACC GC GGGGTCCTC
                                |||  |  ||| || |||||||||
                                CGA  G  TGG CG CCCCAGGAG
                                  GT __  A  A
GAM380  MGC10940  3'  GCTTGCTCACGTTGACTGGACT 10374          C___  C  G
           CC                     GCTTGCTCAC   GC GGG TCC
                                |||||||||   || ||| |||
                                CGAACGAGTG   TG CCT AGG
                                     CAAC  A  G
GAM380  PSK      5'  GCTTCCGCCTGGGGTCCTC   10375    CA   _
                                GCT  CCGCC GGGGTCCTC
                                |||  ||||| |||||||||
                                CGA  GGCGG CCCCAGGAG
                                  A_    A
GAM380  SAE1     3'  GCTTGCTCATTCCTGGCAGGCA 10376        __ __  C  G  C
           TCTCC                   CTTGCTCA  CC  GC GG GTC TCC
                                |||||||  ||  || || ||| |||
                                GAACGAGT  GG  CG CC TAG AGG
                                     AA  AC  T  G  _
GAM380  Sfmbt    3'  GCTTCCTCACTGTGAGTCCTCC 10377     G    CGCCG
                                GCTT CTCAC    GGGTCCTCC
                                |||| |||||    |||||||||
                                CGAA GAGTG    CTCAGGAGG
                                  G    ACA__
GAM380  TAO1     5'  GCTTCCGCCTGGGGTCCTC   10375    CA   _
                                GCT  CCGCC GGGGTCCTC
                                |||  ||||| |||||||||
                                CGA  GGCGG CCCCAGGAG
                                  A_    A
GAM380  LOC112724 5'  GCTTCCTCACCGCCGATGAGAC 10378     G       __  T
           CTCC                    GCTT CTCACCGCCG  GGG CCTCC
                                |||| ||||||||||  ||| |||||
                                CGAA GAGTGGCGGC  CTC GGAGG
                                  G        TA   T
GAM380  LOC148398 5'  GCTGCCGTCTCGGGGTCCTC   10379    CA  C__
                                GCT  CCG   CGGGGTCCTC
                                |||  |||   ||||||||||
                                CGA  GGC   GCCCCAGGAG
                                  C_   AGA
GAM380  LOC151196 5'  GCTGCTCACCAGTGTCCTC   10380    T      CCGGG
                                GCT GCTCACCG    GTCCTC
                                ||| ||||||||    ||||||
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                                CGA CGAGTGGT    CAGGAG
                                  _      CA___
GAM380  LOC220021 3'  GCTTGCTCCTGGCTCCTC    10381       ACCGCCG  G
                                GCTTGCTC      GG TCCTC
                                ||||||||      || |||||
                                CGAACGAG      CC AGGAG
                                    GA_____  G
GAM380  LOC254173 3'  GCTTGTCCACGGGAGGTCCTCC 10382      CT   CGCC
                                GCTTG  CAC   GGGGTCCTCC
                                |||||  |||   ||||||||||
                                CGAAC  GTG   CTCCAGGAGG
                                  AG   CC__
GAM380  LOC51145  3'  GCTTGCTCCTGCGCCTTTGGAG 10383     AC_   C_________  GGTC
           GACCCC                GCTC   CGC       GG    CT
                                ||||   |||       ||    ||
                                CGAG   GCG       TC    GG
                                  GAC   GAAAIIICC  CTGG
GAM380  LOC90906  3'  GCTTGCTGTTGCTGGGATCC   10384       CACC  C
                                GCTTGCT    GC GGGGTCC
                                |||||||    || |||||||
                                CGAACGA    CG CCCTAGG
                                    CAA_  A
GAM381  ACTB     3'  GGGGAAGGGGGGGGCACGAAGGC 10387        AGAA    C___
                                GGGGAAGG    GGCGC    GC
                                ||||||||    |||||    ||
                                CCCCTTCC    CCGTG    CG
                                    CCC_     CTTC
GAM381  ALMS1    5'  AGGGGAAGGGGAGAGCCC    10388        A  AG  G
                                AGGGGAAGG GA  GC CC
                                ||||||||| ||  || ||
                                TCCCCTTCC CT  CG GG
                                    C  CT  _
GAM381  ARL4     3'  GGGGTAGGGAGAAGAGACCAC  10389      AA_      C
                                GGGG   GGAGAAGG GCCGC
                                ||||   |||||||| |||||
                                CCCC   CCTCTTCT TGGTG
                                  ATC       C
GAM381  ATP7A    3'  GGGAGGGAGAAGGAGGCATGC  10390      A      C_  C_
                                GGGA GGAGAAGG  GC  GC
                                |||| ||||||||  ||  ||
                                CCCT CCTCTTCC  CG  CG
                                  C       TC  TA
GAM381  BACE     3'  AGGGGTGAGGAGGGGGCTTAAC 10391      A_    AA  ___  C
           TGC                    AGGGG  AGGAG  GGC   GC GC
                                |||||  |||||  |||   || ||
                                TCCCC  TCCTC  CCG   TG CG
                                  AC    CC   AAT  A
GAM381  BACE     3'  AGGGGTGAGGAGGGGGCTTAAC 10391      A_    AA  ___  C
           TGC                    AGGGG  AGGAG  GGC   GC GC
                                |||||  |||||  |||   || ||
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                                TCCCC  TCCTC  CCG   TG CG
                                  AC    CC   AAT  A
GAM381  BLAME    3'  AGGGAAGGGGGAGGTGTGAAAC 10392        A_ _______    CC
            GTGC                  GGGGAAGG  GA     AGGCG  GC
                                |||||||| ||     ||||| ||
                                TCCCTTCC  CT     TTTGC  CG
                                    CC  CCACAC    A_
GAM381  BMP1     3'  AGGGGAGGAGAAGTTGCCTGTG 10393       A      GC  ___
            C                    AGGGGA GGAGAAG  GCC   GC
                                |||||| |||||||  |||   ||
                                TCCCCT CCTCTTC  CGG   CG
                                   _      AA   ACA
GAM381  CADPS    5'  AGGGGAAGGGAGAGGTGC    10394         _  A  C
                                AGGGGAAGG AGA GG GC
                                ||||||||| ||| || ||
                                TCCCCTTCC TCT CC CG
                                     C   _  A
GAM381  CDC42    3'  GGGGAAGGGGGGGGGCCATACC  10395        AGAA  C    C
                                GGGGAAGG    GG GCCG ACT
                                ||||||||    || |||| |||
                                CCCCTTCC    CC CGGT TGG
                                     CCC_ _    A
GAM381  CLTC     5'  AGGAGAAGGGGAGGGGGGAGGC 10396         A  _______
                                AGGGGAAGG GA     AGGC
                                ||||||||| ||     ||||
                                TCCTCTTCC CT     TCCG
                                     C  CCCCCC
GAM381  DRIL1    5'  GGGGAGGGGGCCCGGCCGCACT 10397      A  AGAA  ___
                                GGGGA GG    GGC   GCCGCACT
                                ||||| ||    |||   ||||||||
                                CCCCT CC    CCG   CGGCGTGA
                                   C  ____   GGC
GAM381  EIF2C1   3'  AGGGGAAGGAAAAAGATGCACT 10398             CGCC
                                AGGGGAAGGAGAAGG    GCACT
                                ||||||||||||||    |||||
                                TCCCCTTCCTTTTTC    CGTGA
                                        TA__
GAM381  FOSL1    3'  GGGGAAGGGGAGGAGACA    10399         A  __
                                GGGGAAGG GA  AGGCG
                                |||||||| ||  |||||
                                CCCCTTCC CT  TCTGT
                                     C  CC
GAM381  GLI2     5'  GGGGAAGGTGAAGGCTGGGC   10400         A     GCC
                                GGGGAAGG GAAGGC   GC
                                |||||||| ||||||   ||
                                CCCCTTCC CTTCCG   CG
                                     A     ACC
GAM381  GRB2     5'  AAGGGAGGGAGGAGGGC     10401        A   A   C
                                AGGGGA GGAG AGG GC
                                |||||| |||| ||| ||
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                                TTCCCT CCTC TCC CG
                                   C   C  _
GAM381  GRM6    5'  GGGGAAGGAGAGCGCGGGC   10402          AG   C_
                                GGGGAAGGAGA  GCGC  GC
                                ||||||||||  ||||  ||
                                CCCCTTCCTCT  CGCG  CG
                                      __   CC
GAM381  HMGA2   5'  GAGGAGAGGAGGAGGCGC    10403      _    A
                                GGGGA AGGAG AGGCGC
                                ||||| ||||| ||||||
                                CTCCT TCCTC TCCGCG
                                   C    C
GAM381  HOXC10  3'  AGGGAGGAGGAGAGGCCGCGCT 10404      A   A  C    A
                                GGGGA GGAG AGG GCCGC CT
                                ||||| |||| ||| ||||| ||
                                TCCCT CCTC TCT CGGCG GA
                                   _   C  C    C
GAM381  IGHMBP2 3'  AGGGGAAGGGACGTGCA    10405        AGAA   CC
                                AGGGGAAGG   GGCG  GCA
                                |||||||||   ||||  |||
                                TCCCCTTCC   CTGC  CGT
                                      ____   A_
GAM381  LBX1    5'  GGTGGAAGGAGGCCGCAC    10406   _      AAGGC
                                GG GGAAGGAG    GCCGCAC
                                || ||||||||    |||||||
                                CC CCTTCCTC    CGGCGTG
                                 A      _____
GAM381  LGALS3BP 3'  AGGGGAAGGAGGAGGTGC    10407         A  C
                                AGGGGAAGGAG AGG GC
                                |||||||||||  ||| ||
                                TCCCCTTCCTC TCC CG
                                      C  A
GAM381  MADH4   5'  AGGGGAGTGGGAAGGCGC    10408       A_  A
                                AGGGGA  GG GAAGGCGC
                                ||||||  ||  ||||||||
                                TCCCCT  CC CTTCCGCG
                                   CA  _
GAM381  MKI67   5'  AGGAGGAGCCGGCGCCGCGCT  10409     A   AA      A
                                GGGA GGAG  GGCGCCGC CT
                                ||||  ||||  ||||||||  ||
                                TCCT CCTC  CCGCGGCG GA
                                  _   GG       C
GAM381  MLC1    5'  AGGGGAAGGAGAGCTGC     10410          AGGC  C
                                AGGGGAAGGAGA    GC GC
                                ||||||||||||    ||  ||
                                TCCCCTTCCTCT    CG CG
                                      _____  A
GAM381  MNT     3'  AGGGGAAGCAGGAGCGGCACT  10411        G  AA   CC
                                AGGGGAAG AG  GGCG  GCACT
                                ||||||||  ||  ||||  |||||
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                                TCCCCTTC TC  TCGC  CGTGA
                                    G  C_   __
GAM381  PAFAH1B1  5'  AGGGGGGAGGATGGCGCGC   10412      AA   AA_    C
                                AGGGG  GGAG   GGCGC GC
                                |||||  ||||   ||||| ||
                                TCCCC  CCTC   CCGCG CG
                                  __    CTA    _
GAM381  PDGFB     3'  AGGGGTGGGGGAAGCACCA   10413      AA A   G
                                AGGGG  GG GAAG CGCCG
                                |||||  || |||| |||||
                                TCCCC  CC CTTC GTGGT
                                  AC  C   _
GAM381  PML       3'  AGGGAGGAGGAGGAAGGGGC  10414      __   _   C
                                GGGGA  AGGAG AAGG GC
                                |||||  ||||| |||| ||
                                TCCCT  TCCTC TTCC CG
                                  CC    C   C
GAM381  PPFIA3    3'  AGGAGAAGGGGAAGCGCCA   10415        A   G
                                AGGGGAAGG GAAG CGCCG
                                |||||||||  |||| |||||
                                TCCTCTTCC CTTC GCGGT
                                    C   _
GAM381  SNX15     3'  GGGGAGAGGAGAAGGGGC    10416      _      C
                                GGGGA AGGAGAAGG GC
                                |||||  ||||||||| ||
                                CCCCT TCCTCTTCC CG
                                  C       C
GAM381  SOLH      3'  AGGGGAAGGAGGGGGGCG    10417        AA_
                                AGGGGAAGGAG   GGCG
                                ||||||||||   ||||
                                TCCCCTTCCTC   CCGC
                                     CCC
GAM381  TULP3     3'  AGGGGAAGGGGAGGCCAC    10418        A  AG C
                                AGGGGAAGG GA  G GCCGC
                                |||||||||  ||  |  |||||
                                TCCCCTTCC CT  C CGGTG
                                    C  __ _
GAM381  UBE2V1    3'  GGGGAAGGGGAAGGGCC     10419       A    C
                                GGGGAAGG GAAGG GCC
                                ||||||||  ||||| |||
                                CCCCTTCC CTTCC CGG
                                    C   _
GAM381  UBE2V1    3'  GGGGAAGGGGAAGGGCC     10419       A    C
                                GGGGAAGG GAAGG GCC
                                ||||||||  ||||| |||
                                CCCCTTCC CTTCC CGG
                                    C   _
GAM381  UBE2V1    3'  GGGGAAGGGGAAGGGCC     10419       A    C
                                GGGGAAGG GAAGG GCC
                                ||||||||  ||||| |||
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                                CCCCTTCC CTTCC CGG
                                    C    _
GAM381  APR-3    5'  AGGAGAAGGGGGAGCCGC    10420        AGAA  C
                                AGGGGAAGG   GG GCCGC
                                |||||||||   || |||||
                                TCCTCTTCC   CC CGGCG
                                    C___  T
GAM381  ARHGEF11 3'  AGGGGAGGAAGAAAGTGC    10421       A      C
                                AGGGGA GGAGAAGG GC
                                |||||| |||||||| ||
                                TCCCCT CTTCTTTC CG
                                   C       A
GAM381  CSEN     3'  AGGGGAGGGAGAAGATCCC   10422       A      CG
                                AGGGGA GGAGAAGG  CC
                                |||||| ||||||||  ||
                                TCCCCT CCTCTTCT  GG
                                   C       AG
GAM381  DKFZp434K1210 3'  AGGGGAAGGGGAGGCCC     10423         A  A   G
                                AGGGGAAGG GA GGC CC
                                ||||||||| || ||| ||
                                TCCCCTTCC CT CCG GG
                                    C  _   _
GAM381  DKFZP434O125 3'  AGGGGAAGGAGAGAGAAGC    10424           _  C
                                AGGGGAAGGAGA AGG GC
                                |||||||||||| ||| ||
                                TCCCCTTCCTCT TCT CG
                                      C   T
GAM381  DKFZP586G1122 3'  AGGGGAAGGGCGGGGGCGAGGC 10425         AGAA_   CC
                                AGGGGAAGG    GGCG  GC
                                |||||||||    ||||  ||
                                TCCCCTTCC    CCGC  CG
                                    CGCCC    TC
GAM381  E1B-AP5  5'  GGGGAAAGGGGGGGGGCCCACT 10426        AGAA  C   G
                                GGGGAAGG    GG GCC CACT
                                ||||||||    || ||| ||||
                                CCCCTTTC    CC CGG GTGA
                                    CCCC  C   _
GAM381  FKSG43   3'  GGGGAAGGGAGGGCAGGC    10427        A  A   CC
                                GGGGAAGG GA GGCG  GC
                                |||||||| || ||||  ||
                                CCCCTTCC CT CCGT  CG
                                    _  C    C_
GAM381  FLJ10330 5'  AGGGGGGGGAGGGGGCCA    10428      AA   AA  C
                                AGGGG  GGAG  GG GCCG
                                |||||  ||||  || ||||
                                TCCCC  CCTC  CC CGGT
                                   CC    C_  _
GAM381  FLJ11320 3'  AGGGGGGAGAAGACCCGC    10429      AA       G
                                AGGGG  GGAGAAGGC CCGC
                                |||||  ||||||||| ||||
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                                TCCCC  CCTCTTCTG GGCG
                                  __      _
GAM381  FLJ12998 3' AGGGGAAGAGGGGAGGCTGGC  10430        AGA_   GCC
                                AGGGGAAGG   AGGC   GC
                                |||||||||   ||||  ||
                                TCCCCTTCT   TCCG   CG
                                    CCCC   AC_
GAM381  FLJ13855 3' AGGGGAGGGGAGAAAGGTGC   10431      A_    _ C
                                AGGGGA  GGAGAA GG GC
                                ||||||  |||||| || ||
                                TCCCCT  CCTCTT CC CG
                                   CC     T  A
GAM381  FLJ14249 3' AGGGGAAGGGGAGGATACCGGT 10432        A  A GC   __
           CACT                 AGGGGAAGG GA G  GCCG  CACT
                                |||||||||  || |  ||||  ||||
                                TCCCCTTCC CT C  TGGC  GTGA
                                     C  C TA    CA
GAM381  FLJ14249 3' AGGGGAAGGGGAGGATACCGGT 10432        A  A GC   __
           CACT                 AGGGGAAGG GA G  GCCG  CACT
                                |||||||||  || |  ||||  ||||
                                TCCCCTTCC CT C  TGGC  GTGA
                                     C  C TA    CA
GAM381  FLJ14800 3' AGGGGAGGGAGGGGCCACGCT  10433      A    AA  C    A
                                AGGGGA GGAG  GG GCCGC CT
                                |||||| ||||  || ||||| ||
                                TCCCCT CCTC  CC CGGTG GA
                                   C    __  _    C
GAM381  FLJ20507 3' AGGGAAGGGAGGCTGCA     10434        A  A   GCC
                                GGGGAAGG GA GGC   GCA
                                ||||||||  || |||   |||
                                TCCCTTCC CT CCG   CGT
                                     _  _   A__
GAM381  FLJ20507 3' AGGGAAGGGAGGCTGCA     10434        A  A   GCC
                                GGGGAAGG GA GGC   GCA
                                ||||||||  || |||   |||
                                TCCCTTCC CT CCG   CGT
                                     _  _   A__
GAM381  FLJ22055 3' AGGGGTGGGAGAAGGAAGTGTG 10435      AA      CGCC__
           C                     AGGGG  GGAGAAGG     GC
                                |||||  ||||||||     ||
                                TCCCC  CCTCTTCC     CG
                                   AC       TTCACA
GAM381  FLJ22558 3' AGGGAGAAGGGGGAGAAATGTAC 10436     _  __     GC_
                                AGGG GAA  GGAGAAG   GC
                                ||||  |||  |||||||   ||
                                TCCC CTT  CCTCTTT   TG
                                  T   CC      ACA
GAM381  FLJ22679 3' AGGGGAAGAGGGGGCAGAGGCA  10437        G  AA   CC_
                                AGGGGAAG AG  GGCG   GCA
                                ||||||||  ||  ||||   |||
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                                TCCCCTTC TC  CCGT   CGT
                                     _ C_    CTC
GAM381  FLJ22679  3'  AGGGGAAGAGGGGCAGAGGCA  10437        G  AA    CC_
                                AGGGGAAG AG  GGCG   GCA
                                |||||||| ||  ||||   |||
                                TCCCCTTC TC  CCGT   CGT
                                     _ C_    CTC
GAM381  FLJ31709  5'  AGGGAAGGAGGGGAATAGACA  10438         A_____
                                GGGGAAGGAG     AGGCG
                                ||||||||||     |||||
                                TCCCTTCCTC     TCTGT
                                      CCCTTA
GAM381  FLJ31951  3'  GGGGTGGAGGAGAGGGCTGGTT 10439      A__     A   GCC__
           GC                     GGGG   AGGAGA GGC     GC
                                ||||   |||||| |||     ||
                                CCCC   TCCTCT CCG     CG
                                  ACC     C   ACCAA
GAM381  FLJ32818  5'  GGGGAAAGAGAACCGCAC    10440          AGGC
                                GGGGAAGGAGA    GCCGCAC
                                ||||||||||    |||||||
                                CCCCTTTCTCT    TGGCGTG
                                      ____
GAM381  FLJ32942  3'  GGGGGAGGAAAAAAGTGTGC   10441      A        CGCC
                                GGGG AGGAGAAGG    GC
                                |||| |||||||||    ||
                                CCCC TCCTTTTTT    CG
                                  C        CACA
GAM381  GAL3ST-4  3'  AGGGGAAGGGGAGGTCAGGCC  10442         A  A  _ ___
                                AGGGGAAGG GA GG C  GCC
                                ||||||||| || || |  |||
                                TCCCCTTCC CT CC G  CGG
                                     C  _  A TC
GAM381  ITM3      3'  GGGGAAGGAGGAGGGCC     10443          A   C
                                GGGGAAGGAG AGG GCC
                                |||||||||| ||| |||
                                CCCCTTCCTC TCC CGG
                                     C   _
GAM381  KIAA0152  3'  AGGGGAAGGAAGGGCATAC    10444          AA    CC
                                AGGGGAAGGAG  GGCG  GC
                                ||||||||||  ||||  ||
                                TCCCCTTCCTT  CCGT  TG
                                      C_    A_
GAM381  KIAA0218  3'  AGGGAAGGGAGGAGGACGAC   10445       A    A   C  C
                                AGGGGA GGAG AGG GC GC
                                |||||| |||| ||| || ||
                                TCCCTT CCTC TCC TG TG
                                   C    C   _  C
GAM381  KIAA0226  3'  GGGGAAGGGGGAGGCAGCA   10446         AGA    CC
                                GGGGAAGG   AGGCG  GCA
                                ||||||||   |||||  |||
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                                CCCCTTCC  TCCGT  CGT
                                    CCC   __
GAM381  KIAA0227  3'  GGGGAAGGAGGCAGGGGC   10447        A_  C
                                GGGGAAGGAG  AGG GC
                                ||||||||||  ||| ||
                                CCCCTTCCTC  TCC CG
                                     CG  C
GAM381  KIAA0427  5'  AGGGGAAGGGAGGGACGAGGC  10448       A  A  _  CC
                                AGGGGAAGG GA GG CG  GC
                                ||||||||| || || ||  ||
                                TCCCCTTCC CT CC GC  CG
                                     _  C  T  TC
GAM381  KIAA0945  3'  AGGGCAAGGGGAGCCACAGCAC 10449    G   A  A G   C
          T                      AGGG AAGG GA G CGC GCACT
                                ||||  ||||  ||  |  |||  |||||
                                TCCC TTCC CT C GTG CGTGA
                                  G   C  _ G   T
GAM381  KIAA1673  3'  AGGGGAAAGGAGAGGGTTCC  10450       _    A  CG
                                AGGGGAA GGAGA GG  CC
                                |||||||  |||||  ||  ||
                                TCCCCTT CCTCT CC  GG
                                    T    C  AA
GAM381  KIAA1831  5'  AGGAGAAGGAGATGCAC    10451          AG
                                AGGGGAAGGAGA  GCGC
                                ||||||||||||  ||||
                                TCCTCTTCCTCT  CGTG
                                      A_
GAM381  LOH12CR1  5'  GGAGAAGGAGAGGCCC     10452         A  G
                                GGGGAAGGAGA GGC CC
                                ||||||||||| ||| ||
                                CCTCTTCCTCT CCG GG
                                      _  _
GAM381  MGC2668   3'  AGGGGAGGAGGGGCAAAGCACT 10453      A   AA   CC
                                AGGGGA GGAG  GGCG  GCACT
                                ||||||  ||||  ||||  |||||
                                TCCCCT CCTC  CCGT  CGTGA
                                   _   C_   TT
GAM381  MRPS34    3'  GGGGAAAGGGAGCGAGCGC   10454      __   AA
                                GGGGAA  GGAG  GGCGC
                                ||||||  ||||  |||||
                                CCCCTT  CCTC  TCGCG
                                   TC   GC
GAM381  NYD-SP25  3'  AAGGGAAGGGGGTCCTTGCACT 10455       AGAA  CG  __
                                AGGGGAAGG   GG  CC  GCACT
                                |||||||||   ||  ||  |||||
                                TTCCCTTCC   CC  GG  CGTGA
                                     ____  CA  AA
GAM381  ORMDL3    3'  AGGGGAAGGGGCTGCA     10456        AGAA  GCC
                                AGGGGAAGG   GGC  GCA
                                |||||||||   |||  |||
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                                TCCCCTTCC   CCG  CGT
                                    ____  A__
GAM381  PHYHIP   3' GGGGAAGGAAAGGGCC     10457         A  C
                                GGGGAAGGAGA GG GCC
                                |||||||||| || |||
                                CCCCTTCCTTT CC CGG
                                    _ _
GAM381  RALGPS1A 3' AGGGGAAGAGGGAAGAGAAGAT 10458       _______    GC
          AC                  AGGGGAAG    GAGAAG  GC
                              ||||||||    ||||||  ||
                              TCCCCTTC    CTCTTC  TG
                                  TCCCTT    TA
GAM381  RHO6     3' AGGGGAAGGGAAGGGC     10459        A    C
                              AGGGGAAGG GAAGG GC
                              ||||||||| ||||| ||
                              TCCCCTTCC CTTCC CG
                                    _   _
GAM381  SENP3    3' GGGGAAGGGGGAGGATGACTGC 10460       AGA  C__  C
                              GGGGAAGG  AGG  GC GC
                              ||||||||  |||  || ||
                              CCCCTTCC  TCC  TG CG
                                  CCC  TAC  A
GAM381  SH3BGRL3 3' AGGGAGGAGAAGTGGCCTGCA  10461     A     GC  _
                              GGGGA GGAGAAG  GCC GCA
                              ||||| |||||||  ||| |||
                              TCCCT CCTCTTC  CGG CGT
                                 _     AC  A
GAM381  SLC25A18 3' AGGGGAAGAAGGCTGTGC    10462      AGG     GCC
                              AGGGGA  AGAAGGC  GC
                              ||||||  |||||||  ||
                              TCCCCT  TCTTCCG  CG
                                  ___     ACA
GAM381  SLC2A4RG 3' GGGGAGGGAGAAGGTGGTAGC  10463     A      CGCC_
                              GGGGA GGAGAAGG    GC
                              ||||| ||||||||    ||
                              CCCCT CCTCTTCC    CG
                                 C      ACCAT
GAM381  SPRY4    3' AGGGAGGGAGAAGGAGGGGC   10464     A      CGCC
                              GGGGA GGAGAAGG   GC
                              ||||| ||||||||   ||
                              TCCCT CCTCTTCC   CG
                                 C      TCCC
GAM381  UBAP     3' AGGGGAAGGGGGGAAGCACC   10465       AGA
                              AGGGGAAGG  AGGCGCC
                              |||||||||  |||||||
                              TCCCCTTCC  TTCGTGG
                                    CCC
GAM381  VPS4A    3' GGGGGAGGCAGAAGGAGC    10466     A  _    C
                              GGGG AGG AGAAGG GC
                              |||| ||| |||||| ||
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                                CCCC TCC TCTTCC CG
                                  C  G    T
GAM381  LOC132740 5'  AGGGGAGGAGAAGGGC     10467      A      C
                                AGGGGA GGAGAAGG GC
                                |||||| |||||||| ||
                                TCCCCT CCTCTTCC CG
                                  _      _
GAM381  LOC133584 3'  GGGGAAGGGGGCCGCA     10468       AGAA  C
                                GGGGAAGG   GG GCCGCA
                                ||||||||   || ||||||
                                CCCCTTCC   CC CGGCGT
                                   ____ _
GAM381  LOC142955 3'  AGGGGAGGAGAGCGAGCGC   10469      A    A_ _
                                AGGGGA GGAGA  G GCGC
                                |||||| |||||  | ||||
                                TCCCCT CCTCT  C CGCG
                                  _    CG T
GAM381  LOC146159 5'  AGGGGAAGGGGATGGTCAGCA 10470       A  A  _  CC
                                AGGGGAAGG GA GG CG  GCA
                                ||||||||| || || ||  |||
                                TCCCCTTCC CT CC GT  CGT
                                    C  A  A  __
GAM381  LOC146378 3'  GGGGAAGGAGGTGGCTGC    10471        AA  _
                                GGGGAAGGAG  GGC GC
                                |||||||||  ||| ||
                                CCCCTTCCTC  CCG CG
                                     CA   A
GAM381  LOC148137 3'  AGGGGAAGGAGTGGCTTCGC  10472        AA   GC
                                AGGGGAAGGAG  GGC  CGC
                                ||||||||||  |||  |||
                                TCCCCTTCCTC  CCG  GCG
                                     A_   AA
GAM381  LOC149271 3'  AGGAGGAGGAGAGGGAGGC   10473     A     ___
                                AGGGG AGGAGA   AGGC
                                ||||| ||||||   ||||
                                TCCTC TCCTCT   TCCG
                                  C     CCC
GAM381  LOC149684 3'  AGAGGAGGGAGAAGGAAC    10474      A      C
                                AGGGGA GGAGAAGG GC
                                |||||| |||||||| ||
                                TCTCCT CCTCTTCC TG
                                   C       T
GAM381  LOC151429 5'  GGGGAAGGGGCGAGACCAC   10475       AGAA   ___
                                GGGGAAGG   GGCG   CCGC
                                ||||||||   ||||   ||||
                                CCCCTTCC   CCGC   GGTG
                                     _____   TCT
GAM381  LOC152220 3'  AGGGGAGGGGAGAAGGGAGGGC 10476      A_      CGCC
          ACT                   AGGGGA  GGAGAAGG   GCACT
                                ||||||  ||||||||   |||||
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                                TCCCCT  CCTCTTCC   CGTGA
                                   CC       CTCC
GAM381   LOC163682 3'  AGGTGAAGGAGAAGGCCC    10477     G         G
                                AGG GAAGGAGAAGGC CC
                                ||| |||||||||||| ||
                                TCC CTTCCTCTTCCG GG
                                  A          _
GAM381   LOC199886 3'  GGGGAAGGTGAGGGCTGAC    10478        A  A   GCC
                                GGGGAAGG GA GGC   GC
                                |||||||| || |||   ||
                                CCCCTTCC CT CCG   TG
                                     A  C   AC_
GAM381   LOC200078 3'  AGGGGAAGGAAGAGGCAGC    10479         GA    CC
                                AGGGGAAGGA  AGGCG  GC
                                ||||||||||  |||||  ||
                                TCCCCTTCCT  TCCGT  CG
                                      TC    __
GAM381   LOC219333 3'  GGGGAAGGGAAGGAAGGAC    10480        A    CGCC
                                GGGGAAGG GAAGG    GC
                                |||||||| |||||    ||
                                CCCCTTCC CTTCC    TG
                                     _    TTCC
GAM381   LOC220587 3'  AGGGAAGGGGGGAGGAACCAGGC 10481         AGA   C  __
   ACT                             GGGGAAGG   AGG GCC  GCACT
                                |||||||   ||| |||  |||||
                                TCCCTTCC   TCC TGG  CGTGA
                                     CCC   T   TC
GAM381   LOC221495 3'  AGGGAAGGAGGGGGCC      10482          AA  C
                                GGGGAAGGAG  GG GCC
                                ||||||||||  || |||
                                TCCCTTCCTC  CC CGG
                                      C_  _
GAM381   LOC221683 5'  GGGAAGGAGAGACGGCAC    10483          A    CC
                                GGGAAGGAGA GGCG  GCAC
                                |||||||||| ||||  ||||
                                CCCTTCCTCT CTGC  CGTG
                                      _   __
GAM381   LOC221935 3'  AGGGGAAGGAGGTGGCAC    10484          AA
                                AGGGGAAGGAG  GGCGC
                                ||||||||||  |||||
                                TCCCCTTCCTC  CCGTG
                                      CA
GAM381   LOC253430 5'  AGGGCGAGGGAGGGGGCGCC   10485     _  A    AA
                                AGGG GA GGAG  GGCGCC
                                |||| || ||||  ||||||
                                TCCC CT CCTC  CCGCGG
                                  G  C    CC
GAM381   LOC256940 5'  GGAGAAGGAGGGGGTGCC    10486          AA  C
                                GGGGAAGGAG  GG GCC
                                ||||||||||  || |||
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                                CCTCTTCCTC  CC CGG
                                      CC  A
GAM381  LOC257095 5'  AGAGGAGGGAGGAACTGTGC   10487       A    AA   GCC
                                AGGGGA GGAG  GGC   GC
                                |||||| ||||  |||   ||
                                TCTCCT CCTC  TTG   CG
                                   C    C_   ACA
GAM381  LOC257364 3'  AGGGGAAGGAGGGGGCCC    10488          AA   G
                                AGGGGAAGGAG  GGC CC
                                ||||||||||  ||| ||
                                TCCCCTTCCTC  CCG GG
                                      CC   _
GAM381  LOC91308  3'  AGGGAAGGGGAGAGTAAGTGC  10489       A_    __   C
                                AGGGGA  GGAGA  AGG GC
                                ||||||  |||||  ||| ||
                                TCCCTT  CCTCT  TTC CG
                                   CC    CA   A
GAM381  LOC91948  3'  AGGGGAAGGGTGGGGGAGAAAC 10490        ________      G
          G                      AGGGGAA      GGAGAAG CG
                                |||||||      ||||||| ||
                                TCCCCTT      CCTCTTT GC
                                   CCCACCC      _
GAM382  BAP1     3'  GGCTGGACAGAGGCTCTTC   10493     ACC    CT    C
                                GGC   GCGG  GGGC CTTC
                                |||   ||||  |||| ||||
                                CCG   TGTC  TCCG GAAG
                                  ACC   __    A
GAM382  CACNA1A  3'  AGGGTTCGTGCAGGCCCTTC   10494     CACCG  _  T
                                AGG    CG GC GGGCCCTTC
                                |||    || || |||||||||
                                TCC    GC CG TCCGGGAAG
                                  CAA__  A  _
GAM382  CD7      3'  GGCACGGCTGGGCCCTTC    10495     ACC
                                GGC   GCGGCTGGGCCCTTC
                                |||   ||||||||||||||
                                CCG   TGCCGACCCGGGAAG
                                   ___
GAM382  CTBP1    3'  GGCACCGCCCAAGCTTTTC    10496        GG TG   CC
                                GGCACCGC  C  GGC  TTC
                                ||||||||  |  |||  |||
                                CCGTGGCG  G  TCG  AAG
                                    __ GT   AA
GAM382  FRAT2    3'  TAAAGCACCAACAGGGCTCTTC 10497         CG  T    C
                                TAAGGCACCG  GC GGGC CTTC
                                ||||||||||  || |||| ||||
                                ATTTCGTGGT  TG CCCG GAAG
                                    __  T    A
GAM382  OAS2     3'  AGGCACCGTGGCCGCTTTCGAA 10498       C    _________  CCCT
          GGGCC                   CACCG GGCTG       GG    TC
                                |||||  |||||       ||    ||
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                                GTGGC CCGGC      CT   GG
                                  A   GAAAGIII  TCCC
GAM382  PCDHA9   3' TAAGGTGTTCACAGCCCTT   10499     CAC_  GGCTG
                                TAAGG   CGC    GGCCCTT
                                |||||   |||    |||||||
                                ATTCC   GTG    TCGGGAA
                                  ACAA  _____
GAM382  RAD9     3' TAAGACACTGCCTGGCAGCTCT 10500       C __  TG  C
           TC                    TAAGGCAC GC  GGC  GGC CTTC
                                 |||||||| ||  |||  ||| ||||
                                 ATTCTGTG CG  CCG  TCG GAAG
                                     A  GA  __  A
GAM382  BC002942 3' TAAGGCACAGTGGCTGGGTCCT 10501       CGC     C
                                 TAAGGCAC   GGCTGGG CCT
                                 ||||||||   ||||||| |||
                                 ATTCCGTG   CCGACCC GGA
                                     TCA      A
GAM382  C5orf4   3' AAGGATAGGGCTGGGCCCTTC  10502     CACCGC
                                 AAGG     GGCTGGGCCCTTC
                                 ||||     ||||||||||||
                                 TTCC     CCGACCCGGGAAG
                                   TATC__
GAM382  C5orf4   3' AAGGATAGGGCTGGGCCCTTC  10502     CACCGC
                                 AAGG     GGCTGGGCCCTTC
                                 ||||     ||||||||||||
                                 TTCC     CCGACCCGGGAAG
                                   TATC__
GAM382  FLJ20548 3' GGGGTGCTGAGGCTTGGTCCTT 10503    CACC ___   G  C
           C                     GG   GC   GGCT GG CCTTC
                                 ||   ||   |||| || |||||
                                 CC   CG   CCGA CC GGAAG
                                  CCA_  ACT   A  A
GAM382  FLJ22529 5' TGAGCACCCTGGGTCCTT    10504   A    GCGG    C
                                 A GGCACC    CTGGG CCTT
                                 | ||||||    ||||| ||||
                                 A TCGTGG    GACCC GGAA
                                 C     _____     A
GAM382  FLJ25473 5' TAAGGCACGTGCGGCTGGA   10505       C_
                                 TAAGGCAC  GCGGCTGGG
                                 ||||||||  |||||||||
                                 ATTCCGTG  CGCCGACCT
                                     CA
GAM382  KIAA0280 3' AGGGGTGCTGGACCTGGGCTCT 10506    CACC _ __    C
           TC                    AGG   GC GG  CTGGGC CTTC
                                 |||   || ||  |||||| ||||
                                 TCC   CG CC  GACCCG GAAG
                                   CCA_  A  TG    A
GAM382  MGC13114 3' TGAGCAGGCTGGGCCCTT    10507   A   CCGC
                                 A GGCA   GGCTGGGCCCTT
                                 | ||||   ||||||||||||
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                                A TCGT   CCGACCCGGGAA
                                 C  ____
GAM382  MGC19556  3'  GGGGCACGGCTGGATGGCCCTT 10508    CAC      ___
            C                    GG  CGCGGCTGG  GCCCTTC
                                 ||  |||||||||  |||||||
                                 CC  GTGCCGACC  CGGGAAG
                                  CC_       TAC
GAM382  NR6A1    3'  AAGGTGCCGTGGGCCCTT    10509     CA  CGGC
                                 AAGG  CCG   TGGGCCCTT
                                 ||||  |||   |||||||||
                                 TTCC  GGC   ACCCGGGAA
                                   AC  ____
GAM382  NR6A1    3'  AAGGTGCCGTGGGCCCTT    10509     CA  CGGC
                                 AAGG  CCG   TGGGCCCTT
                                 ||||  |||   |||||||||
                                 TTCC  GGC   ACCCGGGAA
                                   AC  ____
GAM382  NR6A1    3'  AAGGTGCCGTGGGCCCTT    10509     CA  CGGC
                                 AAGG  CCG   TGGGCCCTT
                                 ||||  |||   |||||||||
                                 TTCC  GGC   ACCCGGGAA
                                   AC  ____
GAM382  SMA3     3'  TGAGCACTGCGGCTGGTCC   10510   A   C      GC
                                 A GGCAC GCGGCTGG  CC
                                 | ||||| ||||||||  ||
                                 A TCGTG CGCCGACC  GG
                                  C    A      A_
GAM382  LOC124302 3'  AGGCTTGTAGGCAGCCCTTC  10511     ACCGC  TG
                                 AGGC    GGC  GGCCCTTC
                                 ||||    |||  ||||||||
                                 TCCG    CCG  TCGGGAAG
                                   AACAT  __
GAM382  LOC127435 3'  AGGTGCAGCTGGGTCCTT    10512     CACC       C
                                 AGG   GCGGCTGGG CCTT
                                 |||   ||||||||| ||||
                                 TCC   CGTCGACCC GGAA
                                   A___       A
GAM382  LOC138649 5'  TGAGCCGCCGCGGCTCCTCGTG 10513  _      ____ _   C  III
            GCCTTTCG                 CCGCGGCT   G GGCC TTC  G
                                  ||||||||   | |||| |||  |
                                  GGCGCCGA   C CCGG AAG  C
                                 C       GGAG A   A  III
GAM382  LOC145719 5'  AGGTGAGGCTGGGCCCTT    10514     CACCGC
                                 AGG     GGCTGGGCCCTT
                                 |||     ||||||||||||
                                 TCC     CCGACCCGGGAA
                                   ACT___
GAM382  LOC145720 5'  AGGTGAGGCTGGGCCCTT    10514     CACCGC
                                 AGG     GGCTGGGCCCTT
                                 |||     ||||||||||||
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                                TCC     CCGACCCGGGAA
                                  ACT___
GAM382  LOC148710 3'  AGGCATCCTGGGCTCTTC    10515      _ GCGGC    C
                                AGGCA CC    TGGGC CTTC
                                ||||| ||    ||||| ||||
                                TCCGT GG    ACCCG GAAG
                                  A _____    A
GAM382  LOC152453 5'  GGTCACCAGGGCCCTTC     10516   _    CGGCT
                                GG CACCG    GGGCCCTTC
                                || |||||    |||||||||
                                CC GTGGT    CCCGGGAAG
                                 A    _____
GAM382  LOC152485 3'  GGCTGGACACAGGCCCTTC   10517    ACCGC  _
                                GGC    GGC TGGGCCCTTC
                                |||    ||| ||||||||||
                                CCG    CTG GTCCGGGAAG
                                  AC___   T
GAM382  LOC197114 5'  AGGTGAGGCTGGGCCCTT    10514    CACCGC
                                AGG     GGCTGGGCCCTT
                                |||     ||||||||||||
                                TCC     CCGACCCGGGAA
                                  ACT___
GAM382  LOC197117 5'  AGGTGAGGCTGGGCCCTT    10514    CACCGC
                                AGG     GGCTGGGCCCTT
                                |||     ||||||||||||
                                TCC     CCGACCCGGGAA
                                  ACT___
GAM382  LOC201549 5'  TAAGGCACGGCGTCCCTT    10518      ACC    T GG
                                TAAGGC   GCGGC G  CCCTT
                                ||||||   ||||| |  |||||
                                ATTCCG   TGCCG C  GGGAA
                                   ___    _ A_
GAM382  LOC254024 5'  TAAGGCACTGGTAACATCCTTC 10519        CGC  CTGGGC
                                TAAGGCAC   GG     CCTTC
                                ||||||||   ||     |||||
                                ATTCCGTG   CC     GGAAG
                                     A__  ATTGTA
GAM382  LOC255452 3'  AGACACCGTGGCTGCCTT    10520       C    GGC
                                AGGCACCG GGCTG   CCTT
                                |||||||| |||||   ||||
                                TCTGTGGC CCGAC   GGAA
                                     A    ___
GAM382  LOC93259  5'  AGGGCCGTGCTGGGCCCTTC   10521    CA   CG
                                AGG  CCG  GCTGGGCCCTTC
                                |||  |||  ||||||||||||
                                TCC  GGC  CGACCCGGGAAG
                                  C_   A_
GAM383  AK1       3'  GAGGTGGGGGTGAGGGGGACA  10524    A  A       CT  GT
                                GAG TG GGGTGGGGGG  GG  G
                                ||| || |||||||||  ||  |
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                                CTC AC CCCACTCCC  CC  T
                                  C  C        __  TG
GAM383  ALPI     3'  GAGGCAGGGTGGGGGGTTGGGTG 10525     ATG        C     III
              C                   GAG   AGGGTGGGGG TGGGTG   C
                                  |||   |||||||||| ||||||   |
                                  CTC   TCCCACCCCC ACCCAC   G
                                    CG_         A     III
GAM383  ALPL     5'  GAGGGGGTGGGCTGGCAGTG   10526       T  _      __
                                  GAGGG GG GGGCTGG  GTG
                                  ||||| || |||||||  |||
                                  CTCCC CC CCCGACC  CAC
                                     _ A      GT
GAM383  ARHGEF1  3'  TGGGGGTGGGGGGTGGAGGGGTG 10527    A       CT___
                                  TG GGGTGGGGGG     GGGTG
                                  || |||||||||     |||||
                                  AC CCCACCCCC     CCCAC
                                   C        ACCTC
GAM383  CACNA2D2 3'  GAGGTGGGAGTGGAGGTG    10528     A  A       C
                                  GAG TG GGGTGGGGG TG
                                  ||| || |||||||||  ||
                                  CTC AC CTCACCTCC AC
                                    C  C       _
GAM383  CALR     3'  GAGGGGGTGGGGGGAGAGTG    10529     ATGA       CT
                                  GAG    GGGTGGGGG  GGGTG
                                  |||    |||||||||  |||||
                                  CTC    CCCACCCCC  CTCAC
                                    C___         T_
GAM383  CDKN1A   3'  GAGCTGGGGGGTGGGGGGTG    10530     A  A       C
                                  GAG TG GGGTGGGGG TG
                                  ||| || |||||||||  ||
                                  CTC AC CCCACCCCC AC
                                    G  C       _
GAM383  COL1A1   3'  CGGGCTGAGGGTGGGGGGCCACT 10531    AGA          _____
                TGGGTG                  G   TGAGGGTGGGGGCT    GGGTG
                                  |   ||||||||||||||    |||||
                                  C   ACTCCCACCCCCGG    CCCAC
                                   CCG            TGAA
GAM383  COPE     3'  AGATGGGGGGTGCTGGGGGGTG   10532       A    GG  CT
                                  AGATG GGGTG  GG  GGGTG
                                  ||||| |||||  ||  |||||
                                  TCTAC CCCAC  CC  CCCAC
                                     C    GA  __
GAM383  DES      3'  GAGGGGAGGACTGAGGCTGGGT 10533     AT    TG
                G                   GAG  GAGGG  GGGGCTGGGTG
                                  |||  |||||  ||||||||||
                                  CTC  CTCCT  CTCCGACCCAC
                                    CC    GA
GAM383  DMPK     5'  TGGGGGTTGGGGCTGGGT    10534    A   G
                                  TG GGGT GGGGCTGGGT
                                  || |||| ||||||||||
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                                AC CCCA CCCCGACCCA
                                 C   A
GAM383  EFNA1   3'  CGAGGTGAAGGTGGGGATG   10535     A         C
                                CGAG TGAGGGTGGGGG TG
                                |||| |||||||||||| ||
                                GCTC ACTTCCACCCCT AC
                                  C         _
GAM383  EGR3    3'  GAGGTAGGGTGGGGAGAAGGTG 10536    ATG       CT
                                GAG  AGGGTGGGGG GGGTG
                                |||  |||||||||| |||||
                                CTC  TCCCACCCCT TCCAC
                                 CA_       CT
GAM383  EMX2    5'  TGGGGTGGGGGTGGGGGT   10537   A      CT_
                                TG GGGTGGGGG  GGGT
                                || |||||||||  ||||
                                AC CCCACCCCC  CCCA
                                 _       ACC
GAM383  EPB49   3'  GAGTATGGGAGGGCTGGGTG  10538    ATGAG  T
                                GAG   GG GGGGGCTGGGTG
                                |||   || ||||||||||||
                                CTC   CC CTCCCGACCCAC
                                 ATA__  _
GAM383  FASN    3'  TGGGGTGGGGTGGGGATG   10539   A      GCT
                                TG GGGTGGGG  GGGTG
                                || ||||||||  |||||
                                AC CCCACCCC  CCTAC
                                 _       ACC
GAM383  HEPH    5'  GAGGGAGGGGGAAGGGCTGGGT 10540    AT    T __
          G                      GAG  GAGGG GG  GGGCTGGGTG
                                ||| |||||  ||  ||||||||||
                                CTC  CTCCC CC  CCCGACCCAC
                                 C_    _  TT
GAM383  HOXC4   3'  GAGGGGAGGGTGGGGGGCATGGG 10541    AT        T__
          GTG                     GAG  GAGGGTGGGGGGC  GGGTG
                                |||  ||||||||||||  |||||
                                CTC  CTCCCACCCCCG  CCCAC
                                  CC         TAC
GAM383  IGFBP5  3'  TGGGGGTGGGAGGGGGTG   10542   A      CT
                                TG GGGTGGGGGG  GGGTG
                                || |||||||||  |||||
                                AC CCCACCCTC  CCCAC
                                 C       C_
GAM383  JAM2    5'  TGGGGGTGGGGGGGATTGGGTG  10543   A      C__
                                TG GGGTGGGGGG  TGGGTG
                                || |||||||||  ||||||
                                AC CCCACCCCC  ACCCAC
                                 C       CTA
GAM383  KCNC3   3'  CGGGGGGTGGGGGGGCGGTG   10544   A      CTG
                                TG GGGTGGGGGG  GGTG
                                || |||||||||  ||||
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                                GC CCCACCCCC  CCAC
                                 C       CG_
GAM383  KRT5     3'  GATTGGGGTGGGGATTCTG   10545    GA      __
                                GAT  GGGTGGGGG  CTG
                                |||  |||||||||  |||
                                CTA  CCCACCCCT  GAC
                                  AC       AA
GAM383  MAP3K7IP1 3'  CGAGGTGAGGGAGGTGATGGTG 10546     A    T  GGCTG
                                CGAG TGAGGG GGG    GGTG
                                |||| |||||| |||    ||||
                                GCTC ACTCCC TCC    CCAC
                                  C    _  ACTA_
GAM383  MEOX1    3'  GATTGGGGTGGGGGTAG    10547    GA      C
                                GAT  GGGTGGGGG TGG
                                |||  ||||||||| |||
                                CTA  CCCACCCCC ATC
                                  AC       _
GAM383  MEOX1    3'  GATTGGGGTGGGGGTAG    10547    GA      C
                                GAT  GGGTGGGGG TGG
                                |||  ||||||||| |||
                                CTA  CCCACCCCC ATC
                                  AC       _
GAM383  PER2     3'  GATGTGGGCTTGGCTGGGTG  10548     A  GGG
                                GATG GGGT  GGCTGGGTG
                                ||||  ||||  |||||||||
                                CTAC CCCG  CCGACCCAC
                                  A   AA_
GAM383  PRKACA   3'  TGGGATGGGGGGTGTGGGT   10549   A      C_
                                TG GGGTGGGGG  TGGGT
                                ||  |||||||||  |||||
                                AC CCTACCCCC  ACCCA
                                 _       AC
GAM383  PTPN7    3'  GAGATGGGGTTGGGGGGACAGT 10550      A  _   CTG
          G                      GAGATG GGGT GGGGG  GGTG
                                |||||| |||| |||||  ||||
                                CTCTAC CCCA CCCCC  TCAC
                                   _   A    CTG
GAM383  PTPN7    3'  GAGATGGGGTTGGGGGGACAGT 10550      A  _   CTG
          G                      GAGATG GGGT GGGGG  GGTG
                                |||||| |||| |||||  ||||
                                CTCTAC CCCA CCCCC  TCAC
                                   _   A    CTG
GAM383  PTPN7    3'  GAGATGGGGTTGGGGGGACAGT 10550      A  _   CTG
          G                      GAGATG GGGT GGGGG  GGTG
                                |||||| |||| |||||  ||||
                                CTCTAC CCCA CCCCC  TCAC
                                   _   A    CTG
GAM383  RABL2B   3'  GAGGGGGTGGGGAAGGTG   10551    ATGA     CT
                                GAG   GGGTGGGGG  GGGTG
                                |||   |||||||||  |||||
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                                CTC   CCCACCCCT  TCCAC
                                  C___       __
GAM383  RANBP3   3'  TGGGGTGGGGGGCGGGTG    10552   A       T
                                TG GGGTGGGGGC GGGTG
                                || |||||||||| |||||
                                AC CCCACCCCCG CCCAC
                                 _       _
GAM383  RANBP3   3'  TGGGGTGGGGGGCGGGTG    10552   A       T
                                TG GGGTGGGGGC GGGTG
                                || |||||||||| |||||
                                AC CCCACCCCCG CCCAC
                                 _       _
GAM383  RANBP3   3'  TGGGGTGGGGGGCGGGTG    10552   A       T
                                TG GGGTGGGGGC GGGTG
                                || |||||||||| |||||
                                AC CCCACCCCCG CCCAC
                                 _       _
GAM383  REST     5'  GAGGGTGGTAAAGTTGGGTG  10553       __  C
                                GAGGGTGG  GGG TGGGTG
                                ||||||||  ||| ||||||
                                CTCCCACC  TTC ACCCAC
                                     AT   A
GAM383  RYR1     3'  GAGGTGGGGGTGGAGGGCCAG  10554    A  A   _   TG
                                GAG TG GGGTGG GGGC  G
                                ||| || |||||| ||||  |
                                CTC AC CCCACC CCCG  C
                                  C  C     T   GT
GAM383  S100A1   3'  TGGGGGTGGGGGTGGGGT   10555   A      CT
                                TG GGGTGGGGGG  GGGT
                                || |||||||||  ||||
                                AC CCCACCCCC  CCCA
                                  C       AC
GAM383  SOX13    3'  AGGTGAGGGGCAGGGCTGGGTG 10556   A    TG
                                AG TGAGGG  GGGGCTGGGTG
                                || ||||||  ||||||||||
                                TC ACTCCC  TCCCGACCCAC
                                  C     CG
GAM383  SPTBN4   3'  TGGGGTGGGGGGTGGTGAGT   10557   A      C__
                                TG GGGTGGGGGG   TGGGT
                                || |||||||||   |||||
                                AC CCCACCCCC   ACTCA
                                  _       ACC
GAM383  TJP1     5'  AGGTGAGGGTGGGGAGGACCTG 10558   A        ____
                                AG TGAGGGTGGGGG    CTG
                                || ||||||||||||    |||
                                TC ACTCCCACCCCT    GAC
                                  C          CCTG
GAM383  TLR9     3'  GAGGTGAGTGTGGAGGTG    10559    A   G     C
                                GAG TGAG GTGGGGG TG
                                ||| |||| ||||||| ||
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                                CTC ACTC CACCTCC AC
                                  C   A     _
GAM383  TNC     5'  TGGAGGTGGGTTTGGCTGGGTG 10560   AG    ___
                                TG  GGTGGG  GGCTGGGTG
                                ||  ||||||  |||||||||
                                AC  CCACCC  CCGACCCAC
                                 CT     AAA
GAM383  TNNI3   3'  GGGGTGGGGGTGGCGGGTA   10561   A      C__
                                G GGGTGGGGG  TGGGTG
                                | |||||||||  ||||||
                                C CCCACCCCC  GCCCAT
                                _       ACC
GAM383  TRAF1   3'  AGGATGTGGGGGCTGGGT    10562    __
                                AGG  GTGGGGGCTGGGT
                                |||  ||||||||||||
                                TCC  CACCCCCGACCCA
                                  TA
GAM383  TRIM14  3'  TGAGGGTGCGGAGGTCTG    10563       _ _ _
                                TGAGGGTG GG GG CTG
                                |||||||| || || |||
                                ACTCCCAC CC CC GAC
                                     G  T  A
GAM383  TRIM14  3'  CCAGATGAGATCTGGCTGGGTG 10564   G      GTGGG
                                C AGATGAGG    GGCTGGGTG
                                | ||||||||    |||||||||
                                G TCTACTCT    CCGACCCAC
                                 G       AGA__
GAM383  UNC13   3'  GATGAGGAGTGGAGAGGTG   10565       _    GCT
                                GATGAGG GTGGGG  GGGTG
                                ||||||| ||||||  |||||
                                CTACTCC CACCTC  TCCAC
                                    T    ___
GAM383  VARS2   3'  TGAGGGGTGAAGCTGGGTG   10566      TG
                                TGAGGG  GGGGCTGGGTG
                                ||||||  ||||||||||
                                ACTCCC  CTTCGACCCAC
                                   CA
GAM383  YWHAH   3'  GATGATGGGGGTGGTGGGTG  10567     G  T  _  C
                                GATGA GG GGG GG TGGGTG
                                ||||| || ||| || ||||||
                                CTACT CC CCC CC ACCCAC
                                   A  _  A  _
GAM383  ACTR1A  3'  TGGGGGTGGGGGTGAGGGT   10568   A      CT_
                                TG GGGTGGGGG  GGGT
                                || |||||||||  ||||
                                AC CCCACCCCC  CCCA
                                 C       ACT
GAM383  CXYorf1 3'  GAGTGAGGGTGGTTGGT    10569    A      GGGCTG
                                GAG TGAGGGTGG    GGT
                                ||| |||||||||    |||
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                                CTC ACTCCCACC     CCA
                                  _       AA____
GAM383  DDX34    3'  TGGGGTGGGGGGGACAGGGT   10570    A       CT__
                                TG GGGTGGGGGG   GGGT
                                || |||||||||   ||||
                                AC CCCACCCCC    CCCA
                                  _       CTGT
GAM383  DKFZp434P0531 3'  TGGGAGTGGGGGTGGGGT    10571    A       CT
                                TG GGGTGGGGGG  GGGT
                                || |||||||||  ||||
                                AC CTCACCCCC  CCCA
                                 C       AC
GAM383  FLJ10305  3'  TGGGGTGGGGGGTGGGGT     10572    A       CT
                                TG GGGTGGGGGG  GGGT
                                || |||||||||  ||||
                                AC CCCACCCCC  CCCA
                                  _       AC
GAM383  FLJ10748  3'  GAGGGGGTGGCAAAAGGTG    10574      T  G   T__
                                GAGGG GG GGC   GGGTG
                                ||||| || |||   |||||
                                CTCCC CC CCG   TCCAC
                                   _ A   TTT
GAM383  FLJ10748  3'  GAGATGGGGGGTGGGGGGGAGGTG 10573       A       CT
                                GAGATG GGGTGGGGGG  GGGTG
                                |||||| |||||||||  |||||
                                CTCTAC CCCACCCCC  TCCAC
                                    C       C_
GAM383  FLJ14950  3'  TGGGGTGGGGGGTGGGT      10575    A       C
                                TG GGGTGGGGGG TGGGT
                                || |||||||||| |||||
                                AC CCCACCCCC ACCCA
                                  _       _
GAM383  FLJ20359  3'  TGGGGGTGGGGGGTGAGGGT   10568    A       CT_
                                TG GGGTGGGGGG   GGGT
                                || |||||||||   ||||
                                AC CCCACCCCC   CCCA
                                 C       ACT
GAM383  FLJ23059  3'  GAGATGGGGGGTGGTGGGC    10576       A    _
                                GAGATG GGGTGG GGGC
                                |||||| |||||| ||||
                                CTCTAC CCCACC CCCG
                                    C     A
GAM383  ILF3     3'  CGGGATGGGGGGCGGGGGCC    10577    A   A
                                CG GATG GGGTGGGGGGCT
                                || |||| ||||||||||
                                GC CTAC CCCGCCCCCGG
                                 C   C
GAM383  ILF3     3'  CGGGATGGGGGGCGGGGGCC    10577    A   A
                                CG GATG GGGTGGGGGGCT
                                || |||| ||||||||||
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                                GC CTAC CCCGCCCCCGG
                                 C   C
GAM383  JM4      3' AGGTAATGGGGGCTGGGTG   10578    __
                                AGG  GTGGGGGCTGGGTG
                                |||  |||||||||||||
                                TCC  TACCCCCGACCCAC
                                  AT
GAM383  KIAA0125 3' TGGGATGGAGGTGAGGGT    10579    A       CT_
                                TG GGGTGGGGG   GGGT
                                || |||||||||   ||||
                                AC CCTACCTCC   CCCA
                                 _       ACT
GAM383  KIAA0446 3' TGAGGGTGGGGGGAACTG    10580          ___
                                TGAGGGTGGGGG   CTG
                                ||||||||||||   |||
                                ACTCCCACCCCC   GAC
                                       CTT
GAM383  KIAA0545 3' TGGGGGTGGGGGGACGGGTG   10581    A       C
                                TG GGGTGGGGG TGGGTG
                                || ||||||||| ||||||
                                AC CCCACCCCC GCCCAC
                                 C       T
GAM383  KIAA0802 5' TGAGGTAGGAATGCTGGGT   10582      GT   _
                                TGAGG  GGGG GCTGGGT
                                |||||  |||| |||||||
                                ACTCC  CCTT CGACCCA
                                   AT   A
GAM383  KIAA1111 3' TGAGGTTGGAGTGGGTG     10583      GTG   C
                                TGAGG   GGGG TGGGTG
                                |||||   |||| ||||||
                                ACTCC   CCTC ACCCAC
                                   AA_   _
GAM383  KIAA1602 5' AGGGTGTCGGGGCTGGGT    10584       __
                                AGGGTG  GGGGCTGGGT
                                ||||||  ||||||||||
                                TCCCAC  CCCCGACCCA
                                   AG
GAM383  KIAA1855 3' TGGGGTGGGGTGGACAGGT   10586    A      GC__
                                TG GGGTGGGG    TGGGT
                                || ||||||||    |||||
                                AC CCCACCCC    GTCCA
                                 _       ACCT
GAM383  KIAA1855 3' CGGGGTGAGGGTGGGGGACCG  10585    AGA         _
                                CG   TGAGGGTGGGGG CTG
                                ||   |||||||||||| |||
                                GC   ACTCCCACCCCC GGC
                                 CCC          T
GAM383  KIAA1862 3' GAGAGGGTGGCCTGGG      10587    T      GGG
                                GA GAGGGTGG   CTGGG
                                || ||||||||   |||||
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                                CT CTCCCACC   GACCC
                                 _      G__
GAM383  KIAA1910 3' GAAGGTGGGGGGTGGGGTA    10588          CT
                                GAGGGTGGGGG  GGGTG
                                ||||||||||  |||||
                                CTTCCACCCCC  CCCAT
                                      AC
GAM383  KIAA1949 5' GGGTGAGGGGAACCTGGGTG   10589         ____
                                GGGTGGGGG   CTGGGTG
                                |||||||||   |||||||
                                CCCACTCCC   GACCCAC
                                     CTTG
GAM383  KIAA1949 5' GAGGTGAGGGTAGGGAGCACTG 10590     A        ___
                                GAG TGAGGGTGGGG   GCTG
                                ||| ||||||||||   ||||
                                CTC ACTCCCATCCC   TGAC
                                  C         TCG
GAM383  KIAA1949 5' GGGTGAGGGGAACCTGGGTG   10589         ____
                                GGGTGGGGG   CTGGGTG
                                |||||||||   |||||||
                                CCCACTCCC   GACCCAC
                                     CTTG
GAM383  KIAA1949 5' GAGGTGAGGGTAGGGAGCACTG 10590     A        ___
                                GAG TGAGGGTGGGG   GCTG
                                ||| ||||||||||   ||||
                                CTC ACTCCCATCCC   TGAC
                                  C         TCG
GAM383  KIAA1949 5' GGGTGAGGGGAACCTGGGTG   10589         ____
                                GGGTGGGGG   CTGGGTG
                                |||||||||   |||||||
                                CCCACTCCC   GACCCAC
                                     CTTG
GAM383  KIAA1949 5' GAGGTGAGGGTAGGGAGCACTG 10590     A        ___
                                GAG TGAGGGTGGGG   GCTG
                                ||| ||||||||||   ||||
                                CTC ACTCCCATCCC   TGAC
                                  C         TCG
GAM383  KPNA6    3' GAGGTGGGGGGTGGGGCAGACTG 10591     A  A      ___
                                GAG TG GGGTGGGG   GCTG
                                ||| || ||||||||   ||||
                                CTC AC CCCACCCC   TGAC
                                  C  C       GTC
GAM383  MGC10924 3' TGGGGGTGGGGGGTGGGGGT    10592    A       CT_
                                TG GGGTGGGGG   GGGT
                                || |||||||||   ||||
                                AC CCCACCCCC   CCCA
                                  C        ACC
GAM383  MGC11271 3' TGCGGACATGGGGGCTGGGTG  10593    A  __
                                TG GG  GTGGGGGGCTGGGTG
                                || ||  ||||||||||||||
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                                AC CC  TACCCCCGACCCAC
                                 G  TG
GAM383  MGC2780  5' GAGGTGGGGGGGGGGGGT    10594     A A   T    CT
                                GAG TG GGG GGGGG  GGGT
                                ||| || ||| |||||  ||||
                                CTC AC CCC CCCCC  CCCA
                                  C  _  _    __
GAM383  MGC3329  3' TGGAGGTGGGGGGTATGGGT   10595    AG      C_
                                TG  GGTGGGGG  TGGGT
                                ||  ||||||||  |||||
                                AC  CCACCCCC  ACCCA
                                 CT       AT
GAM383  MIG      3' GAGTGGGATGTGGTTGGGTG   10596     A A    GG  C
                                GAG TG GGGTG  GG TGGGTG
                                ||| || |||||  || ||||||
                                CTC AC CCTAC  CC ACCCAC
                                  _ _    A_  A
GAM383  MRPS21   3' GATGAGGGTTTCGCACTGGGTG 10597         GGGG_
                                GATGAGGGT    GCTGGGTG
                                |||||||||    ||||||||
                                CTACTCCCA    TGACCCAC
                                     AAGCG
GAM383  MRPS21   3' GATGAGGGTTTCGCACTGGGTG 10597         GGGG_
                                GATGAGGGT    GCTGGGTG
                                |||||||||    ||||||||
                                CTACTCCCA    TGACCCAC
                                     AAGCG
GAM383  OLFM2    3' TGGGGGTGGGGGTGGGGGT    10592    A       CT_
                                TG GGGTGGGGG   GGGT
                                || |||||||||   ||||
                                AC CCCACCCCC   CCCA
                                 C        ACC
GAM383  P450RAI-2 3' GAGGGAGGGTGGGAACCG    10598     AT
                                GAG  GAGGGTGGGGGCTG
                                |||  ||||||||||||||
                                CTC  CTCCCACCCTTGGC
                                  C_
GAM383  PLSCR3   5' CGAGATGATGGTGTCTGGGTG  10599         G   GGGG
                                CGAGATGA GGTG   CTGGGTG
                                |||||||| ||||   |||||||
                                GCTCTACT CCAC   GACCCAC
                                     A   A___
GAM383  PRIC285  3' TGGGGTGGGGCGGGGTG     10600    A      G T
                                TG GGGTGGGG C GGGTG
                                || |||||||| | |||||
                                AC CCCACCCC G CCCAC
                                 _       _ C
GAM383  R3HDM    5' CGACGGCGGGGCTGGGTG     10601     G      G
                                TGA GGTGGGG CTGGGTG
                                ||| ||||||| |||||||
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                                GCT CCGCCCC GACCCAC
                                  G     _
GAM383  SCAMP-4   3'  TGGGGTGGGGGGTTGGGC    10602    A       C
                                TG GGGTGGGGG TGGGT
                                || ||||||||| |||||
                                AC CCCACCCCC ACCCG
                                  _       A
GAM383  SEMA4G    3'  TGGAGGTGGGAGAGGTTGGGTG 10603    AG      C___
                                TG  GGTGGGGG   TGGGTG
                                ||  ||||||||   ||||||
                                AC  CCACCCTC   ACCCAC
                                  CT      TCCA
GAM383  SEMA4G    3'  TGGAGGTGGGAGAGGTTGGGTG 10603    AG      C___
                                TG  GGTGGGGG   TGGGTG
                                ||  ||||||||   ||||||
                                AC  CCACCCTC   ACCCAC
                                  CT      TCCA
GAM383  SEMA5A    3'  GAGGTGAGGGTGAATGGACTGG 10604    A       __
              GTG                  GAG TGAGGGTGG  GGGCTGGGTG
                                ||| |||||||||  ||||||||||
                                CTC ACTCCCACT  CCTGACCCAC
                                  C       TA
GAM383  SERF2     5'  AGGGTGGGGGGTGGAGGGGTG   10605         CT___
                                AGGGTGGGGG    GGGTG
                                ||||||||||    |||||
                                TCCCACCCCC    CCCAC
                                      ACCTC
GAM383  STX1B2    3'  CAAGGTGGGGGTGGAGGGGGTG 10606     A  A       CT
                                CGAG TG GGGTGGGGG  GGGTG
                                |||| || |||||||||  |||||
                                GTTC AC CCCACCTCC  CCCAC
                                  C  C       __
GAM383  ZDHHC8    3'  TGGGGAGGGGGGCTCTGGGT   10607    A  T     __
                                TG GGG GGGGGGCT  GGGT
                                || ||| |||||||  ||||
                                AC CCC CCCCCGA  CCCA
                                  _  T      GA
GAM383  ZNF238    3'  GAGTTGGGGGGTGGAGGGTG   10608    A  A       C
                                GAG TG GGGTGGGGG TG
                                ||| || ||||||||| ||
                                CTC AC CCCACCTCC AC
                                  A  C        C
GAM383  LOC123242 5'  TGAGGGCCTCCTGCTGGGTG   10609        GGGG_
                                TGAGGGT    GCTGGGTG
                                |||||||    ||||||||
                                ACTCCCG    CGACCCAC
                                     GAGGA
GAM383  LOC131034 5'  GATGGGGGTGGGGGAAGAGGGT 10610      A       CT__
              G                   GATG GGGTGGGGG    GGGTG
                                |||| |||||||||    |||||
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                                CTAC CCCACCCCC   CCCAC
                                  C       TTCT
GAM383  LOC144231 5'  GAGATGGGGTGGGGATGAGGTG 10611       A       CT
                                GAGATG GGGTGGGGG  GGGTG
                                |||||| |||||||||  |||||
                                CTCTAC CCCACCCCT  TCCAC
                                   _       AC
GAM383  LOC144519 5'  AGGGTGAGGGTGGGGGTG    10612    A_         C
                                AG  TGAGGGTGGGGG TG
                                ||  |||||||||||| ||
                                TC  ACTCCCACCCCC AC
                                 CC          _
GAM383  LOC145693 5'  TGGGGTGGAGGTGGGC      10613    A       C
                                TG GGGTGGGGG TGGGT
                                || ||||||||| |||||
                                AC CCCACCTCC ACCCG

                                _       _
GAM383  LOC147111 3'  TGGGGTGAGGTGGCACTGGTG  10614    A    _ _   TG_
                                TG GGGTG GG GGC   GGTG
                                || ||||| || |||   ||||
                                AC CCCAC CC CCG   CCAC
                                 _    T  A   TGA
GAM383  LOC147965 3'  GAGATGGGGGGCTTGGGT    10615       AGGGT      _
                                GAGATG     GGGGGCT GGGT
                                ||||||     ||||||| ||||
                                CTCTAC     CCCCCGA CCCA
                                   _____       A
GAM383  LOC148887 3'  CGAGCTGGGGGTGGGGAAGCTG 10616      A  A       __
                                CGAG TG GGGTGGGG  GCTG
                                |||| || ||||||||  ||||
                                GCTC AC CCCACCCC  CGAC
                                  G  C       TT
GAM383  LOC149606 3'  GATGGTGAGGGTGGCGTGGGTG 10617      AG  T   _  _
                                GATG  GG GGG GGC TGGGTG
                                ||||  || ||| ||| ||||||
                                CTAC  CT CCC CCG ACCCAC
                                  CA  _   A   C
GAM383  LOC153525 5'  TGGGGGTGGGGGTGGGGGT   10592    A       CT_
                                TG GGGTGGGGG   GGGT
                                || |||||||||   ||||
                                AC CCCACCCCC   CCCA
                                 C        ACC
GAM383  LOC155006 3'  GAGGTGGGGGGTGAAGATGG    10618    A  A       C
                                GAG TG GGGTGGGGG TGG
                                ||| || ||||||||| |||
                                CTC AC CCCACTTCT ACC
                                  C  C       _
GAM383  LOC157860 3'  GAGAGGGACACAGCTGGGTG   10619    T    TGGG
                                GA GAGGG    GGCTGGGTG
                                || |||||    |||||||||
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                                CT CTCCC    TCGACCCAC
                                 _     TGTG
GAM383  LOC200093 3'  GAGTGAGGGTGGTTGGT     10569     A       GGGCTG
                                GAG TGAGGGTGG     GGT
                                ||| |||||||||     |||
                                CTC ACTCCCACC     CCA
                                  _       AA_____
GAM383  LOC219920 5'  GATGAGGGCATAATCTGGGTG  10620          GGGG
                                GATGAGGGTG    CTGGGTG
                                ||||||||||    |||||||
                                CTACTCCCGT    GACCCAC
                                      ATTA
GAM383  LOC253001 5'  TGAGGGCCTCCTGCTGGGTG   10609        GGGG_
                                TGAGGGT     GCTGGGTG
                                |||||||     ||||||||
                                ACTCCCG     CGACCCAC
                                    GAGGA
GAM383  LOC91040  3'  GAGTGAGGGTGGTTGGT     10569     A       GGGCTG
                                GAG TGAGGGTGG     GGT
                                ||| |||||||||     |||
                                CTC ACTCCCACC     CCA
                                  _       AA_____
GAM383  LOC91363  3'  GAGATGGGGGTGGTGGGC     10576       A     _
                                GAGATG GGGTGG GGGC
                                |||||| |||||| ||||
                                CTCTAC CCCACC CCCG
                                   C     A
GAM383  LOC92689  3'  CGGGATGGGGGGTGGGGGATG   10621    A   A       C
                                CG GATG GGGTGGGGGG TG
                                || |||| ||||||||| ||
                                GC CTAC CCCACCCCC AC
                                 C   C        T
GAM383  LOC93259  5'  TGGGGTGACGGGCTGGGT     10622     A     _
                                TG GGGTGG GGGCTGGGT
                                || |||||| |||||||||
                                AC CCCACT CCCGACCCA
                                 _     G
GAM384  ARRB2     5'  CCGCCGCCCGCTCGGTTAGCCG 10625       A_  C________   TAGC
          CTAGG                    CCGCCC  TC       GCC    GG
                                |||||| ||       |||   ||
                                GGCGGG  AG       CGG    CC
                                   CG  CCAAIIIT   CGAT
GAM384  CDKN2A    5'  CCGCCGCCCGCTGCCTGC     10626        ATCC    A
                                CCGCCGCCC    GCCT GC
                                |||||||||    |||| ||
                                GGCGGCGGG    CGGA CG
                                     CGA_    _
GAM384  CDKN2A    5'  CCGCCGCCCGCTGCCTGC     10626        ATCC    A
                                CCGCCGCCC    GCCT GC
                                |||||||||    |||| ||
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                                GGCGGCGGG   CGGA CG
                                     CGA_   _
GAM384  CEBPD    5'  CCGCCGCCTTTTCTAGCCCCGG 10627       CA_ C_   AG
            CT                    CCGCCGCC  TC  GCCT  CGGCT
                                  ||||||||  ||  ||||  |||||
                                  GGCGGCGG  AG  CGGG  GCCGA
                                      AAA  AT   __
GAM384  CLCN7    3'  GCCGCCTGCCCGCCCAGC    10628      CA
                                  GCCGCC  TCCGCCTAGC
                                  ||||||  |||||||||
                                  CGGCGG  GGGCGGGTCG
                                     AC
GAM384  FBN1     5'  CCGCCGCCCGTCCCCCGGGCCG 10629        A  G  TA  __
            GGCT                   CCGCCGCCC TCC CC  GC  GGCT
                                  |||||||||  |||  ||  ||  ||||
                                  GGCGGCGGG AGG GG  CG  CCGA
                                       C   G  CC  GC
GAM384  FOXD2    5'  CCCTCCCGCCTAGCGGCT    10630    AT
                                  CCC  CCGCCTAGCGGCT
                                  |||  |||||||||||||
                                  GGG  GGCGGATCGCCGA
                                    AG
GAM384  FUS1     5'  CCGCCGCCTTCCGCAGGC    10631       CA    CTAGC
                                  CCGCCGCC  TCCGC    GGC
                                  ||||||||  |||||    |||
                                  GGCGGCGG  AGGCG    CCG
                                       A_    T____
GAM384  HRB      5'  CCGCCGCCCTCCGTCTGC    10632       A   C  A
                                  CCGCCGCCC TCCG CT GC
                                  |||||||||  |||| || ||
                                  GGCGGCGGG AGGC GA CG
                                       _   A  _
GAM384  IVD      5'  CGCCGCCCACCAAACCGGCT   10633         C_   TAGC
                                  CGCCGCCCATC  GCC   GGCT
                                  ||||||||||  |||   ||||
                                  GCGGCGGGTGG  TGG   CCGA
                                        TT   ____
GAM384  MAP3K1   5'  CCGCCGCCAGTCCGCCCGC   10634       CA     A
                                  CCGCCGCC  TCCGCCT GC
                                  ||||||||  ||||||| ||
                                  GGCGGCGG  AGGCGGG CG
                                       TC     _
GAM384  PHLDA1   5'  CGCCGCCCACTTGCTTCCGCGC 10635        CC  CTA_   G
            T                     CGCCGCCCAT  GC   GCG CT
                                  ||||||||||  ||   ||| ||
                                  GCGGCGGGTG  CG   CGC GA
                                       AA  AAGG   _
GAM384  PRX      3'  CCTTGCCCATTTTAGCGGCT   10636    GCC    CCGCC
                                  CC   GCCCAT    TAGCGGCT
                                  ||   ||||||    ||||||||
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                                GG  CGGGTA   ATCGCCGA
                                 AA_    AA___
GAM384  PTPRA   5'  CCGCCGCCCGGCCCGCGGC  10637       ATCC   A
                                CCGCCGCCC   GCCT GCGGC
                                |||||||||   |||| |||||
                                GGCGGCGGG   CGGG CGCCG
                                    C___   _
GAM384  RB1CC1  5'  CCGCCGCCTAGTCCTCGGCAGC 10638       CA_  GCC_
          GG                  CCGCCGCC  TCC   TAGCGG
                              ||||||||  |||   ||||||
                              GGCGGCGG  AGG   GTCGCC
                                  ATC  AGCC
GAM384  SH3BP4  5'  CCGCTCGTCGGCCAGCGGCT  10639    _ CCCA  C   T
                              CCGC CG   TC GCC AGCGGCT
                              |||| ||   || ||| |||||||
                              GGCG GC   AG CGG TCGCCGA
                                A  ____  C  _
GAM384  SLC25A15 5'  CCGCCGCCCGCTCTCGGC   10640       ATCC  C AG
                              CCGCCGCCC   GC T  CGGC
                              |||||||||   || |  ||||
                              GGCGGCGGG   CG A  GCCG
                                   ____  _ GA
GAM384  TIAL1   3'  GCCACCCATTTGCCATATACT  10641       CC   TAGCG
                              GCCGCCCAT  GCC   GCT
                              |||||||||  |||   |||
                              CGGTGGGTA  CGG   TGA
                                   AA  TATA_
GAM384  TIMP3   5'  GCTGCCCGCTCTGCGCCGCT  10642   C   A_  C  CTA  G
                              GC GCCC  TC GC  GC GCT
                              || ||||  || ||  || |||
                              CG CGGG  AG CG  CG CGA
                               A   CG  A  ___  G
GAM384  TIMP3   5'  CCGCCGCCTGCCTGCTGCC   10643       CATCC   A  G
                              CCGCCGCC    GCCT GC GCT
                              ||||||||    |||| || |||
                              GGCGGCGG    CGGA CG CGG
                                   A____   _ A
GAM384  TPD52L2 3'  GCTCATCCGCCCTGGCT    10644   C       AGC
                              GC CATCCGCCT  GGCT
                              || |||||||||  ||||
                              CG GTAGGCGGG  CCGA
                               A       A__
GAM384  ACTR2   5'  CCGCCGCCCGGCCGTTTTAGCC 10645     AT __________  TAGC
          GCTAGG                CGCCC  CC       GCC   GG
                              |||||  ||       |||   ||
                              GCGGG  GG       CGG   CC
                                CC  CAAAAIIIT  CGAT
GAM384  ARPP-19 5'  CCGCCGCCCGTCCCAGC    10646       ATCCG
                              CCGCCGCCC   CCTAGC
                              |||||||||   ||||||
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                                GGCGGCGGG    GGGTCG
                                     CA___
GAM384  BIKE     5'  CCGCCGCCCGCTCCGCGGC   10647        A_    CTAGC
                                CCGCCGCCC  TCCGC    GGC
                                |||||||||  |||||    |||
                                GGCGGCGGG  AGGCG    CCG
                                     CG    _____
GAM384  BLCAP    5'  CGCCGTCTGCCGCAGCC     10648      CCCA  C   TA
                                CGCCG   TC GCC  GCGGCT
                                |||||   || |||  ||||||
                                GCGGC   AG CGG  CGTCGG
                                   _____ A   __
GAM384  DKFZP434H0820 5'  CCGCCGCCCGGCTGCGGC    10649         ATCC  CTA
                                CCGCCGCCC   GC   GCGGC
                                |||||||||   ||   |||||
                                GGCGGCGGG   CG   CGCCG
                                     C___  A__
GAM384  DKFZp761G2113 3'  GCCGTCCATTTGCCAGGCT   10650     C    CC   TAGC
                                GCCG CCAT  GCC    GGCT
                                |||| ||||  |||    ||||
                                CGGC GGTA  CGG    CCGA
                                  A   AA   T___
GAM384  DRAP1    5'  CGCCGCCCGCCCGTCGCGG   10651        AT   CCTA
                                CGCCGCCC  CCG   GCGG
                                ||||||||  |||   ||||
                                GCGGCGGG  GGC   CGCC
                                     CG   AG__
GAM384  FLJ10199  3'  CCGCCGCCATCCAAATGGC   10652        C    CCTAGC
                                CCGCCGCC ATCCG     GGC
                                |||||||| |||||     |||
                                GGCGGCGG TAGGT     CCG
                                     _    TTA___
GAM384  FLJ10700  5'  CCGCCGCCCGCCGCCACCACT  10653         AT    TA  G
                                CCGCCGCCC  CCGCC  GC GCT
                                |||||||||  |||||  || |||
                                GGCGGCGGG  GGCGG  TG TGA
                                     C_    __  G
GAM384  FLJ20539  5'  CCGCCGCCCGCCCCGCGGC   10654         ATCC   A
                                CCGCCGCCC   GCCT GCGGC
                                |||||||||   |||| |||||
                                GGCGGCGGG   CGGG CGCCG
                                     _____   G
GAM384  FLJ20758  5'  CCGCCGACCCGTCAGCGGC   10655      C    CC
                                CCGCC ATCCG  TAGCGGC
                                |||||  |||||  |||||||
                                GGCGG TGGGC  GTCGCCG
                                   C    A_
GAM384  FLJ22362  5'  CCGCCGCCTTCTGCAGCGC   10656        CA  C  CT   G
                                CCGCCGCC  TC GC  AGCG C
                                ||||||||  || ||  |||| |
```

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                                GGCGGCGG  AG CG  TCGC G
                                    A_  A  __   _
GAM384  FOXO3A   5'  CGCCGCCCGCCCGCCCGCGGCT 10657        AT     A
                                CGCCGCCC  CCGCCT GCGGCT
                                ||||||||  |||||| ||||||
                                GCGGCGGG  GGCGGG CGCCGA
                                    CG     _
GAM384  GIOT-3   5'  CCGCCGCCCCTTCGCCTCCGC  10658        ATC    A_
                                CCGCCGCCC   CGCCT  GC
                                |||||||||   |||||  ||
                                GGCGGCGGG   GCGGA  CG
                                     GAA    GG
GAM384  GKAP42   5'  CCGCCGCCTCTCCCGCGGC   10659        CA   GCCTA
                                CCGCCGCC  TCC    GCGGC
                                ||||||||  |||    |||||
                                GGCGGCGG  AGG    CGCCG
                                    AG   G____
GAM384  GPA33    3'  CCGCCGCCCTCTGCTGC     10660        A  C  CTA
                                CCGCCGCCC TC GC   GC
                                ||||||||| || ||   ||
                                GGCGGCGGG AG CG   CG
                                     _  A  A__
GAM384  HA-1     3'  CCGCCCCCATCCACGG      10661       G      GCCTA
                                CCGCC CCCATCC    GCGG
                                |||||  |||||||    ||||
                                GGCGG GGGTAGG    TGCC
                                  _      _____
GAM384  KIAA0084 5'  CCGCCGCGCGTCCGCCGGC   10662        CCA     TAGC
                                CCGCCGC   TCCGCC   GGC
                                |||||||   ||||||   |||
                                GGCGGCG   AGGCGG   CCG
                                    CGC     ____
GAM384  KIAA1194 5'  CCGCCGCTCCTCTGCCGCCT   10663        _  AT__
                                CCGCCGC CC    CCGCCT
                                |||||||  ||    ||||||
                                GGCGGCG GG    GGCGGA
                                    A  AGAC
GAM384  KIF13B   3'  CGCTGCCCGTCCGCCACCA   10664     C    A     T G
                                CGC GCCC TCCGCC A CG
                                ||| |||| |||||| | ||
                                GCG CGGG AGGCGG T GT
                                  A   C     _ G
GAM384  KIF13B   3'  CGCTGCCCGTCCGCCACCA   10664     C    A     T G
                                CGC GCCC TCCGCC A CG
                                ||| |||| |||||| | ||
                                GCG CGGG AGGCGG T GT
                                  A   C     _ G
GAM384  LGI4     5'  CCGCCCTCCATCCGCCTGC   10665      GC        A
                                CCGCC  CCATCCGCCT GC
                                |||||  |||||||||| ||
```

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                                GGCGG  GGTAGGCGGA CG
                                  GA       _
GAM384  MGC2647  5'  CCGCCGCCCGCTGTCCTAGCCG 10666      A___  _____  TAGC
          CTAGG                   CCGCCC   TCC    GCC   GG
                                  ||||||   |||    |||   ||
                                  GGCGGG   AGG    CGG   CC
                                     CGAC   AIIIT   CGAT
GAM384  MGC4172  5'  CGCCGCCCGTCCGCCTCGC   10667       A     A
                                  CGCCGCCC TCCGCCT GC
                                  |||||||| ||||||| ||
                                  GCGGCGGG AGGCGGA CG
                                       C      G
GAM384  NIFU     5'  CCGCCGCCATCTTGCCGGC   10668       C   C_   TAGC
                                  CCGCCGCC ATC  GCC   GGC
                                  |||||||| |||  |||   |||
                                  GGCGGCGG TAG  CGG   CCG
                                       _   AA   ____
GAM384  PCCX2    5'  CCGCCGCCCGCCCGGAGCAGGC 10669        AT   CCT   _
          T                        CCGCCGCCC  CCG   AGC GGCT
                                   |||||||||  |||   ||| ||||
                                   GGCGGCGGG  GGC   TCG CCGA
                                        CG   C__   T
GAM384  PF1      5'  CCGCCGCCGTCTGCGTCCCGGC 10670       CA  C  CTAG
          T                        CCGCCGCC  TC GC    CGGCT
                                   ||||||||  || ||    |||||
                                   GGCGGCGG  AG CG    GCCGA
                                        C_  A  CAGG
GAM384  QKI      5'  CCGCCGCCTGTGCCGCGGGCT  10671       CATCC   TA   _
                                   CCGCCGCC    GCC  GCGG CT
                                   ||||||||    |||  |||| ||
                                   GGCGGCGG    CGG  CGCC GA
                                        ACA__   __    C
GAM384  RGS17    5'  GCTGCCATCCGCCCAAC    10672    C   C
                                   GC GCC ATCCGCCTAGC
                                   || ||| ||||||||||
                                   CG CGG TAGGCGGGTTG
                                    A   _
GAM384  RGS7     5'  CCGCCGCCCGTGCACAGGCGGC 10673        ATC   CTA
          T                        CCGCCGCCC   CGC   GCGGCT
                                   |||||||||   |||   ||||||
                                   GGCGGCGGG   GTG   CGCCGA
                                        CAC   TC_
GAM384  LOC115110 5'  CCGCCGCCTGCTCCGCCC    10674       CA_
                                   CCGCCGCC   TCCGCCT
                                   ||||||||   |||||||
                                   GGCGGCGG   AGGCGGG
                                        ACG
GAM384  LOC126917 5'  CCGCCGCCCGTGCGCCGCACCT 10675         ATC    TA   G
                                   CCGCCGCCC   CGCC  GCG CT
                                   |||||||||   ||||  ||| ||
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                                GGCGGCGGG  GCGG  CGT GA
                                     CAC   __  G
GAM384  LOC146223 5'  CCGCCGCCCGGCTGCGGC   10649       ATCC  CTA
                                CCGCCGCCC   GC  GCGGC
                                |||||||||   ||  |||||
                                GGCGGCGGG   CG  CGCCG
                                     C___  A__
GAM384  LOC146243 3'  CCATTTAGCACTGCCTAGCGGC 10676    CCGCC  CC
          T                      CCG    CAT  GCCTAGCGGCT
                                 |||    |||  ||||||||||
                                 GGT    GTG  CGGATCGCCGA
                                   AAATC  A_
GAM384  LOC150383 5'  CCGCCCTCGTCCCACGGC    10677      A  CG   G
                                CCGCCC TC  CCTA CGGC
                                |||||| ||  |||| ||||
                                GGCGGG AG  GGGT GCCG
                                   _ CA   _
GAM384  LOC167517 5'  CGCGGCCCGTTTCCCGCGGCT  10678    C   ATCCG  A
                                CGC GCCC    CCT GCGGCT
                                ||| ||||    ||| ||||||
                                GCG CGGG    GGG CGCCGA
                                  C   CAAA_  _
GAM384  LOC201780 5'  CGCCGCCCGTCGTTCTAGCCGC 10679      A  C_________  TAGC
          TAGG                   CCGCCC TC       GCC   GG
                                 |||||| ||       |||   ||
                                 GGCGGG AG       CGG   CC
                                    C  CAAGAIIIT  CGAT
GAM384  LOC205095 5'  CCGCCGCCCCATCTGTTGCCC  10680        _  C___
                                CCGCCGCCC ATC   GCCT
                                ||||||||| |||   ||||
                                GGCGGCGGG TAG   CGGG
                                     G  ACAA
GAM384  LOC221154 5'  CCGCCGCCTACCGCTTGGGAAC 10681       CAT   CTAGC
          T                     CCGCCGCC  CCGC   GGCT
                                ||||||||  ||||   ||||
                                GGCGGCGG  GGCG   TTGA
                                     AT_   AACCC
GAM384  LOC254636 5'  CCCCGCCCACCCTGGTGGC   10682   G       GCCTAGC
                                CC CCGCCCATCC      GGC
                                || ||||||||||      |||
                                GG GGCGGGTGGG      CCG
                                  _        ACCA___
GAM384  LOC255426 5'  CCGCCGCCCGACCGCCCGGCT  10683       AT    TAG
                                CCGCCGCCC  CCGCC  CGGCT
                                |||||||||  |||||  |||||
                                GGCGGCGGG  GGCGG  GCCGA
                                     CT    ___
GAM384  LOC256160 5'  CGCCGCCCGTCGTTCTAGCCGC 10679      A  C_________  TAGC
          TAGG                   CCGCCC TC       GCC   GG
                                 |||||| ||       |||   ||
```

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                                GGCGGG AG       CGG   CC
                                   C  CAAGAIIIT  CGAT
GAM384  LOC91409  3'  CCGCCCCCATCTGCCTGC    10684      G    C   A
                                CCGCC CCCATC GCCT GC
                                ||||| |||||| |||| ||
                                GGCGG GGGTAG CGGA CG
                                   _     A   _
GAM385  C12orf6   5'  TTGGATTTTTTTTTTTCCCGCG 10687          GC___  G
           GG                     TTGGATTTTTT    CC CGCGGG
                                ||||||||||     || ||||||
                                AACCTAAAAAA    GG GCGCCC
                                      AAAAA  _
GAM385  C20orf46  3'  CAGTGGGCTGCTTGCCCGTGTG 10688    T   AT T      CGC
           GG                     CA TGG  T TTTGCCCG   GGG
                                || |||  | ||||||||   |||
                                GT ACC  A GAACGGGC   CCC
                                 C   CG C       ACA
GAM385  EMILIN    3'  TGGGCGGCGCCCGCGCGGG    10689     ATTTTT
                                TGG     TGCCCGCGCGGG
                                |||     ||||||||||||
                                ACC     GCGGGCGCGCCC
                                  CGCC__
GAM385  LOC151826 3'  CATTGGAATTTTTGTTCCCTAG 10690        T     __   GCGC
           G                     CATTGGA TTTTTG  CCC    GG
                                ||||||| ||||||  |||    ||
                                GTAACCT AAAAAC  GGG    CC
                                    T     AA   AT__
GAM386  ACO1      3'  GCTTCCTCCCTGGGCGCACGA  10693     G  C   C  C
                                GCT CC CCC GG GCGCGCGA
                                ||| || ||| || ||||||||
                                CGA GG GGG CC CGCGTGCT
                                  A  A   A  _
GAM386  ADRA2A    5'  CAGCTGCCTTCCGGCCCG    10694        CCC    G
                                CAGCTGCC   CCGGC CG
                                ||||||||   ||||| ||
                                GTCGACGG   GGCCG GC
                                     AA_    G
GAM386  ANKTM1    5'  CAGCTGCTCACCACGCGCGCG  10695       CCCC   G
                                CAGCTGC    CCG CGCGCGCG
                                |||||||    ||| ||||||||
                                GTCGACG    GGT GCGCGCGC
                                    AGT_   _
GAM386  BID       5'  CAGCGTCTCCCAGGCGCGCG   10696     TGCCCC    C
                                CAGC     CCCGG GCGCGCG
                                ||||     ||||| |||||||
                                GTCG     GGGTC CGCGCGC
                                  CAGA__    _
GAM386  CHRNA5    5'  CAGCCGCCTCTCGACCGCCGCG 10697        CCC___   G
           CG                     CAGCTGCC     CCG CGCGCG
                                ||||||||     ||| ||||||
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                                GTCGGCGG     GGC GCGCGC
                                     AGAGCT   G
GAM386  DIO3    3'  CAGCTGCGCTCAGGGCGCGCG  10698       CCCCCC
                                CAGCTGC     GGCGCGCG
                                |||||||     ||||||||
                                GTCGACG     CCGCGCGC
                                    CGAGTC
GAM386  FBXL7   5'  GCTGCCCCTGCGCGCCCGCG   10699        CC  G   G
                                GCTGCCCC  CG CGC CGCG
                                ||||||||  || ||| ||||
                                CGACGGGG  GC GCG GCGC
                                     AC  _   G
GAM386  FKBP6   5'  AGCTGCCCTCCCTGTGGCG    10700        _   C__
                                AGCTGCCC CCC   GGCG
                                |||||||| |||   ||||
                                TCGACGGG GGG   CCGC
                                     A   ACA
GAM386  GPC1    5'  AGCCAAGGTCCCGGCGCGCGCG 10701      GCCCC
                                AGCT    CCCGGCGCGCGCG
                                ||||    |||||||||||||
                                TCGG    GGGCCGCGCGCGC
                                  TTCCA
GAM386  LASS2   5'  GCTGCCCCTTCGCCCCGGCGCG 10702        _____
                                GCTGCCCC    CCCGGCGCG
                                ||||||||    |||||||||
                                CGACGGGG    GGGCCGCGC
                                     AAGCG
GAM386  MADD    5'  CAGTCGCTCCCCAGCGCG    10703     C   CC
                                CAG TGC  CCCCGGCGCG
                                ||| |||  ||||||||||
                                GTC GCG  GGGGTCGCGC
                                  A   A_
GAM386  MADD    5'  CAGTCGCTCCCCAGCGCG    10703     C   CC
                                CAG TGC  CCCCGGCGCG
                                ||| |||  ||||||||||
                                GTC GCG  GGGGTCGCGC
                                  A   A_
GAM386  MADH7   5'  GCTGCCCCACCCCGCGCG    10704        _   G
                                GCTGCCCC CCC GCGCG
                                |||||||| ||| |||||
                                CGACGGGG GGG CGCGC
                                     T   G
GAM386  MAPT    5'  TGACTGCGAGGGCGCGCGCG   10705   A    CCCCCC
                                C GCTGC     GGCGCGCGCG
                                | |||||     ||||||||||
                                A TGACG     CCGCGCGCGC
                                 C    CTC___
GAM386  MAPT    5'  TGACTGCGAGGGCGCGCGCG   10705   A    CCCCCC
                                C GCTGC     GGCGCGCGCG
                                | |||||     ||||||||||
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                              A TGACG     CCGCGCGCGC
                               C    CTC___
GAM386  MAPT    5'  TGACTGCGAGGGCGCGCGCG  10705   A    CCCCCC
                              C GCTGC     GGCGCGCGCG
                              | |||||     ||||||||||
                              A TGACG     CCGCGCGCGC
                               C    CTC___
GAM386  MAPT    5'  TGACTGCGAGGGCGCGCGCG  10705   A    CCCCCC
                              C GCTGC     GGCGCGCGCG
                              | |||||     ||||||||||
                              A TGACG     CCGCGCGCGC
                               C    CTC___
GAM386  N33     5'  CAGTGTCTCCTCCACGCGCG  10706    C  CCCCC  GG
                              CAG TG    CC  CGCGCGCG
                              ||| ||    ||  ||||||||
                              GTC AC    GG  GTGCGCGC
                                _  AGA__  AG
GAM386  NAGLU   5'  CAGCTGCCGCCTCCGGCCACG  10707        _  C    G
                              CAGCTGCC CC CCGGC CGCG
                              |||||||| || ||||| ||||
                              GTCGACGG GG GGCCG GTGC
                                   C  A    _
GAM386  PAX2    5'  ACTGCCTTCCCCGTGGTCGCGC 10708     C_    _________  GCGC
           GCGC                  TGCC  CCCCG      GC   GC
                              ||||  |||||       ||   ||
                              ACGG  GGGGC       CG   CG
                                AA    ACCIIIAG  CGCG
GAM386  PAX2    5'  ACTGCCTTCCCCGTGGTCGCGC 10708     C_    _________  GCGC
           GCGC                  TGCC  CCCCG      GC   GC
                              ||||  |||||       ||   ||
                              ACGG  GGGGC       CG   CG
                                AA    ACCIIIAG  CGCG
GAM386  PDGFB   5'  GCTGCTCCGCGCGCGCG     10709      C  CCCG
                              GCTGC CC   GCGCGCGCG
                              ||||| ||   |||||||||
                              CGACG GG   CGCGCGCGC
                                A  _____
GAM386  PTGER3  5'  GCTGCCCCCCCATGGTGCG    10710         C_  C
                              GCTGCCCCCCC  GG GCG
                              ||||||||||  || |||
                              CGACGGGGGGG  CC CGC
                                    TA  A
GAM386  PTPN11  5'  CAGCTGCCCCCCCGGCCCG    10711          C   G
                              CAGCTGCCCCCC GGC CG
                              |||||||||||| ||| ||
                              GTCGACGGGGGG CCG GC
                                     _  G
GAM386  PTPN11  5'  CAGCTGCCCCCCCGGCCCG    10711          C   G
                              CAGCTGCCCCCC GGC CG
                              |||||||||||| ||| ||
```

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                                GTCGACGGGGGG CCG GC
                                      _  G
GAM386  RAPSN   5'  CAGCTGCCCCCCGAAACG   10712          C  C
                                CAGCTGCCCCCC GG GCG
                                |||||||||||| || |||
                                GTCGACGGGGGG CT TGC
                                      _  T
GAM386  SGT     3'  CAGCTGCCTTCCCTGTGCCCG  10713        CC   GGC  G
                                CAGCTGCC  CCC   GC CG
                                ||||||||  |||   || ||
                                GTCGACGG  GGG   CG GC
                                     AA   ACA  G
GAM386  SLC9A5  5'  CAGCCGCCCTCCCGGCACCGCA 10714         C      _ _
           GCG                     CAGCTGCCC CCCGGCGC GC GCG
                                |||||||||  ||||||||  || |||
                                GTCGGCGGG GGGCCGTG CG CGC
                                     A       G  T
GAM386  SORBS1  3'  TGTCCCCCCCAGCAGCCA    10715   C       C  G
                                TG CCCCCCGGCG GC CG
                                || ||||||||||  || ||
                                AC GGGGGGTCGT CG GT
                                 A        _ _
GAM386  ACAS2   3'  CAGCTGCCTCCCTGCTTCA   10716        C   CG  GCG
                                CAGCTGCC CCC  GC   CG
                                ||||||||  |||  ||   ||
                                GTCGACGG GGG  CG   GT
                                     A   A_  AA_
GAM386  ACAS2   3'  CAGCTGCCTCCCTGCTTCA   10716        C   CG  GCG
                                CAGCTGCC CCC  GC   CG
                                ||||||||  |||  ||   ||
                                GTCGACGG GGG  CG   GT
                                     A   A_  AA_
GAM386  ALTE    3'  CAGCTGCCCTTCTGCCGATCGC 10717      CC___  _______  GCGC
           GCGCGC                  TGCCC    CCG     GC   GC
                                |||||    |||     ||   ||
                                ACGGG    GGC     CG   CG
                                   AAGAC   TIIIAG  CGCG
GAM386  CBX4    5'  CAGCTGCCGCCCCGGCCG    10718        C      G
                                CAGCTGCC CCCCGGC CG
                                |||||||| |||||||  ||
                                GTCGACGG GGGGCCG GC
                                     C      _
GAM386  cerk    3'  CAGCAGCCTTCCCGGCGCTGGC 10719      T   CC       GC
           G                     CAGC GCC  CCCGGCGC  GCG
                                ||||  |||  ||||||||  |||
                                GTCG CGG  GGGCCGCG  CGC
                                  T  AA       AC
GAM386  CHSY1   5'  GCTCCTCCCGCTCGCGCGCG  10720    G  CC   G_
                                GCT CC  CCCG  CGCGCGCG
                                ||| ||  ||||  ||||||||
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                                CGA GG  GGGC  GCGCGCGC
                                  _ A_   GA
GAM386  DKFZp547C176 5'  CAGCAGCTCCCGGCGCGCG   10721     T  CCC
                                CAGC GC   CCCGGCGCGCG
                                |||| ||   ||||||||||
                                GTCG CG   GGGCCGCGCGC
                                  T  A__
GAM386  DKFZP727M111 5'  CAGCTGCCTCCCCAGTACG   10722        C     CG
                                CAGCTGCC CCCCGG  CG
                                |||||||| ||||||  ||
                                GTCGACGG GGGGTC  GC
                                     A     AT
GAM386  FBXO9    5'  AGCTGCCCCCTCAGCTGCG   10723          C   GC
                                AGCTGCCCCC CGGC  GCG
                                |||||||||| ||||  |||
                                TCGACGGGGG GTCG  CGC
                                      A   A_
GAM386  FLJ21195  3'  CAGCGGCCGGGCGCGCGCG   10724     T   CCCCC
                                CAGC GCC    GGCGCGCGCG
                                |||| |||    ||||||||||
                                GTCG CGG    CCGCGCGCGC
                                  C   C____
GAM386  FLJ22415  5'  GCGCCTCGGGGTGCGCGCGA   10725    T   CCCCC  C
                                GC GCC    GG GCGCGCGA
                                || |||    || ||||||||
                                CG CGG    CC CGCGCGCT
                                 _  AGCC_  A
GAM386  FLJ31564  5'  GCCGCCCCCTCCCCGCTGCGA  10726         _  GG   GC
                                GCTGCCCCC CC  CGC  GCGA
                                ||||||||| ||  |||  ||||
                                CGGCGGGGG GG  GCG  CGCT
                                      A  G_   A_
GAM386  FLJ32468  5'  CAGCTGCCTCCTGGTAGCG   10727        C  CC  CGC
                                CAGCTGCC CC  GG   GCG
                                |||||||| ||  ||   |||
                                GTCGACGG GG  CC   CGC
                                     A  A_  AT_
GAM386  GMPPB    5'  CAGCTGCCTCCCTGGTGATCGC 10728       C   C  ________  CGCG
           GCC                    GCTGCC CCC GG      CG    C
                                |||||| ||| ||      ||    |
                                CGACGG GGG CC      GC    G
                                   A   A  ACTIIIA  GCGC
GAM386  HSPC157   5'  CAGCTGCCACCTCGGAGGACG  10729        C  C   CGC
                                CAGCTGCC CC CGG   GCG
                                |||||||| || |||   |||
                                GTCGACGG GG GCC   TGC
                                     T  A   TCC
GAM386  KIAA0444  5'  GCTGCCGGACCGGCGCGCGCG  10730       CCC
                                GCTGCC   CCGGCGCGCGCG
                                ||||||   ||||||||||||
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                                CGACGG  GGCCGCGCGCGC
                                   CCT
GAM386  KIAA0450  5'  CAGCTGCCTTCCACGTGATCGC 10731     CC  _ _________  GCGC
            GCGCGC                  TGCC  CC CG       GC   GC
                                ||||  || ||       ||   ||
                                ACGG  GG GC       CG   CG
                                  AA  T  ACTIIIAG  CGCG
GAM386  KIAA1373  5'  GCTGCCCCCGTGGCTGCCG   10732        CC   GC  G
                                GCTGCCCCC  GGC  GC CG
                                |||||||||  |||  || ||
                                CGACGGGGG  CCG  CG GC
                                     CA   A_  _
GAM386  KIAA1705  5'  GCTGTCCGGCGGCGCGCG   10733     CCCCC     _
                                GCTG    CCGGCG CGCGCG
                                ||||    |||||| ||||||
                                CGAC    GGCCGC GCGCGC
                                  A____     C
GAM386  KIAA1904  3'  CAGCTGCCTCCCGGGGACG   10734        C   C  C
                                CAGCTGCC CCC GG GCG
                                |||||||| ||| || |||
                                GTCGACGG GGG CC TGC
                                     A   C  C
GAM386  KIAA1940  5'  CAGCTTCTCCAGCGCGCG    10735      GCCCCC
                                CAGCT     CCGGCGCGCG
                                |||||     ||||||||||
                                GTCGA     GGTCGCGCGC
                                  AGA___
GAM386  KIAA1957  3'  CAGCTGCCTCCTGGGCTCCGA  10736        C  CC  C  GCG
                                CAGCTGCC CC  GG GC   CGA
                                |||||||| ||  || ||   |||
                                GTCGACGG GG  CC CG   GCT
                                     A  A_  _  AG_
GAM386  LSM10    5'  CAGCTGCCTGCTTGCACGCG   10737        CCCCCG
                                CAGCTGCC     GCGCGCG
                                ||||||||     |||||||
                                GTCGACGG     CGTGCGC
                                     ACGAA_
GAM386  MGC5139  5'  CAGCTCCTTTGGCGCGCA    10738      G  CCCCC
                                CAGCT CC    GGCGCGCG
                                |||||  ||    ||||||||
                                GTCGA GG    CCGCGCGT
                                  _  AAA__
GAM386  MIR      5'  CAGCCGCCTTCTCTTTGGTGTG 10739        CCCCC___  CGC
            CGCG                   CAGCTGCC       GG   GCGCG
                                ||||||||       ||   |||||
                                GTCGGCGG       CC   CGCGC
                                     AAGAGAAA  ACA
GAM386  MYT1     5'  CAGCTGCCTCCCGTACAGCG   10740        CC   GC   C
                                CAGCTGCC  CCCG  GCG GCG
                                ||||||||  ||||  ||| |||
```

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                                GTCGACGG  GGGC  TGT CGC
                                    A_   A_  _
GAM386  RGC32    5'  CAGCTGGGCCCGGCGCGCG   10741      CCCC
                                CAGCTG   CCCGGCGCGCG
                                ||||||   ||||||||||
                                GTCGAC   GGGCCGCGCGC
                                   CC__
GAM386  STAG1    5'  CAGCTGCCCATCCGGCGCCGC  10742        CC     G
                                CAGCTGCCC  CCGGCGC CGC
                                |||||||||  ||||||| |||
                                GTCGACGGG  GGCCGCG GCG
                                     TA     _
GAM386  TRIM28   5'  GCTGCCCGCCGCGCGCG     10743       CCCC G
                                GCTGCCC   G CGCGCGCG
                                |||||||   | ||||||||
                                CGACGGG   C GCGCGCGC
                                   ____ G
GAM386  LOC124930 3'  CAGCTGCCCCCCAGGAGTGATC 10744       C _________  CGCG
           GCGCGCG                 GCCCCCC GG       CG   CG
                                ||||||| ||       ||   ||
                                CGGGGGG CC       GC   GC
                                    T  TCACTIIIA  GCGC
GAM386  LOC124987 5'  CAGCTGCCCCTTGGCAGCTGA  10745        CCC   C  GC
                                CAGCTGCCCC   GGCG GC  GA
                                ||||||||||   |||| ||  ||
                                GTCGACGGGG   CCGT CG  CT
                                     AA_   _  A_
GAM386  LOC128977 5'  GCTGCGGCGCGCGCG      10746      CCCCCC
                                GCTGC     GGCGCGCGCG
                                |||||     ||||||||||
                                CGACG     CCGCGCGCGC
                                  _______
GAM386  LOC132166 3'  CAGTGGCCCCCTCGGGCGC   10747     CT     C   C
                                CAG  GCCCCC CGG GCGC
                                |||  |||||| ||| ||||
                                GTC  CGGGGG GCC CGCG
                                  AC     A  _
GAM386  LOC143666 5'  CAGGTGCTCCCGCCGCGCGCG  10748     C   CCC   G
                                CAG TGC   CCCG CGCGCGCG
                                ||| |||   |||| ||||||||
                                GTC ACG   GGGC GCGCGCGC
                                  C   A__    G
GAM386  LOC145481 5'  CAGCGGCCGGCCGGCGCGCGCG 10749      T   CCC
                                CAGC GCC   CCGGCGCGCGCG
                                |||| |||   ||||||||||||
                                GTCG CGG   GGCCGCGCGCGC
                                  C   CC_
GAM386  LOC147990 5'  CAGCCGTCCTCACGCGCG    10750       CCCCC  GG
                                CAGCTG    CC  CGCGCGCG
                                ||||||    ||  ||||||||
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                                GTCGGC    GG  GTGCGCGC
                                  A____  A_
GAM386  LOC148646 5'  CAGTGGCTCCAGACAGCGCGCG 10751    CT  C  CCC  _
          A                     CAG  GC CC   GGC GCGCGCGA
                                |||  || ||   ||| ||||||||
                                GTC  CG GG   CTG CGCGCGCT
                                  AC  A  T__   T
GAM386  LOC196205 5'  GCTGCTCCTCCGACACGCG   10752      C  C
                                GCTGC CC CCGGCGCGCG
                                ||||| || ||||||||||
                                CGACG GG GGCTGTGCGC
                                  A  A
GAM386  LOC197342 3'  CAGCTGCCCACCCGGGTGATCG 10753      C   _________  CGCG
          CGCGCG                  TGCCC CCCGG       CG   CG
                                |||||  |||||       ||   ||
                                ACGGG GGGCC       GC   GC
                                  T    CACTIIIA  GCGC
GAM386  LOC201175 5'  ACTTGCCCCGGCAGGCGCGCG  10754    GCCC     __
                                GCT   CCCCGGC  GCGCGCG
                                |||   |||||||  |||||||
                                TGA   GGGGCCG  CGCGCGC
                                  AC__      TC
GAM386  LOC203429 3'  CAGCTGCCATCTCGGGCACG   10755       CCCC   C
                                CAGCTGCC   CGG GCGCG
                                ||||||||   ||| |||||
                                GTCGACGG   GCC CGTGC
                                     TAGA  _
GAM386  LOC221922 5'  CAGCTGCCCCCATGGTCCACG  10756         CC  CG
                                CAGCTGCCCCC  GG  CGCG
                                ||||||||||  ||  ||||
                                GTCGACGGGGG  CC  GTGC
                                      TA  AG
GAM386  LOC253172 3'  GCGGCCTTGGCGCGCGCG    10757    T  CCCCC
                                GC GCC    GGCGCGCGCG
                                || |||    ||||||||||
                                CG CGG    CCGCGCGCGC
                                 C  AA___
GAM386  LOC253258 5'  CAGGTGCTCCCGCCGCGCGCG  10748    C  CCC   G
                                CAG TGC   CCCG CGCGCGCG
                                ||| |||   |||| ||||||||
                                GTC ACG   GGGC GCGCGCGC
                                  C  A__   G
GAM386  LOC255031 5'  CAGCTCTTCCGGCGCGTGCGCG 10758      GCCCCC     __
          A                     CAGCT     CCGGCGC  GCGCGA
                                |||||     |||||||  ||||||
                                GTCGA     GGCCGCG  CGCGCT
                                  GAA___      CA
GAM386  LOC255394 5'  CAGTGTCCCCCCCCAACGCG   10759    C  _
                                CAG TG CCCCCCCCGGCGCG
                                ||| || ||||||||||||
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                                GTC AC GGGGGGGTTGCGC
                                  _ A
GAM386  LOC257448 5'  AGCTGCCCTCCCTGTGGCG   10700        _  C__
                                AGCTGCCC CCC   GGCG
                                |||||||| |||   ||||
                                TCGACGGG GGG   CCGC
                                    A   ACA
GAM387  AKAP13   5'  CTTGGAGGGGCTATGTGG    10762    A  GAG     _
                                CTT GA   GGGGTTA GTGG
                                ||| ||   ||||||| ||||
                                GAA CT   CCCCGAT CACC
                                  C ___      A
GAM387  APOC3    3'  TGCCTGGAGGGGGGCCAG    10763      TA   A
                                TGCCT  GAG GGGGGTTAG
                                |||||  ||| |||||||||
                                ACGGA  CTC CCCCCGGTC
                                   C_  _
GAM387  ESRRA    3'  TGCTTTGAAGAGGGGGTAG   10764    C  AG       T
                                TGC TT  AGAGGGGGT AG
                                ||| ||  |||||||||| ||
                                ACG AA  TCTCCCCCA TC
                                  A  CT       _
GAM387  LOXL3    3'  TGCCATTAGGGGCCAGTGG   10765     TTAGAGA
                                TGCC      GGGGGGTTAGTGG
                                ||||      ||||||||||||
                                ACGG      TCCCCGGTCACC
                                  TAA_____
GAM387  MLLT3    3'  CCTTGGAGAGAAGAGTGG    10766     A      GTT
                                CCTT GAGAGGGG   AGTGG
                                |||| ||||||||   |||||
                                GGAA CTCTCTTC   TCACC
                                  C      ____
GAM387  P4HB     3'  TGCTGTAGAGAGGCCAGTGG  10767    CT     GGG
                                TGC  TAGAGA   GGTTAGTGG
                                |||  ||||||   |||||||||
                                ACG  ATCTCT   CCGGTCACC
                                  AC     ____
GAM387  RYR1     3'  TGCCTTAGGGGGAGGGGCTT  10768        A__     G
                                TGCCTTAG   GAGGGG TT
                                ||||||||   |||||| ||
                                ACGGAATC   CTCCCC AA
                                     CCC     G
GAM387  STAT6    3'  TGCCTTGAGAGGGAGAATGG  10769       A       TT
                                TGCCTT GAGAGGGGG  AGTGG
                                ||||||| |||||||||  |||||
                                ACGGAA CTCTCCCTC  TTACC
                                   _      __
GAM387  AF9Q34   3'  TGTCTTGGAGAGGGAGCAAG  10770    C  A       T
                                TG CTT GAGAGGGGGT AG
                                || ||| |||||||||| ||
```

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                                AC GAA CTCTCCCTCG TC
                                 A  C        T
GAM387  DKFZP564O0423 3' CCTTTGGGGAGGGGGCTGTGG 10771     AGA_       A
                                CCTT   GAGGGGGTT GTGG
                                ||||   ||||||||| ||||
                                GGAA   CTCCCCCGA CACC
                                  ACCC       _
GAM387  FLJ22757  3' TGCCCTTGGAGGGACAGAGGTG 10772      AGA     GTTA_
           G                     TGCCTT   GAGGGG    GTGG
                                ||||||   ||||||    ||||
                                ACGGGA   CTCCCT    CACC
                                   AC_     GTCTC
GAM387  FLJ23263  5' TGTCTTGGAGGAGGGGGC    10773    C   A   _
                                TG CTT GAG AGGGGGT
                                || ||| ||| |||||||
                                AC GAA CTC TCCCCCG
                                 A  C   C
GAM387  KIAA0092  3' TGCTTTGGAAAGGGGAAGTGG  10774     C  A       TT
                                TGC TT GAGAGGGGG  AGTGG
                                ||| || |||||||||  |||||
                                ACG AA CTTTCCCCT  TCACC
                                 A  C       __
GAM387  KIAA0237  3' TTAGAGAGGTGGAATAGTGG   10775         _ GT
                                TTAGAGAGG GG  TAGTGG
                                |||||||| ||  ||||||
                                AATCTCTCC CC  ATCACC
                                     A  TT
GAM387  KIAA0349  3' TACCTTGGAGAGGAATGTGG   10776       A      GTTA
                                TGCCTT GAGAGGGG   GTGG
                                |||||| ||||||||   ||||
                                ATGGAA CTCTCCTT    CACC
                                   C       A___
GAM387  KIAA0930  3' TGTCTTAAAGGGGGTTTG    10777    C   GA       AG
                                TG CTTA  GAGGGGGTT  TG
                                || ||||  |||||||||  ||
                                AC GAAT  TTCCCCCAA  AC
                                 A   __       __
GAM387  KIAA1904  3' TGTCTTAGAAGGGGCACCCAGG 10778    C     GA     TAGT_
                                TG CTTAGA  GGGGGT    GG
                                || ||||||  ||||||    ||
                                AC GAATCT  TCCCCG    CC
                                 A     __     TGGGT
GAM387  MIDORI    3' TGCCTGGGAGAGGGGGACCTTG 10779      TA       TTAG
                                TGCCT  GAGAGGGGG   TG
                                |||||  |||||||||   ||
                                ACGGA  CTCTCCCCC   AC
                                   CC       TGGA
GAM387  TNRC4     3' CCTTAGAGGGGGCCCTTGG   10780     AG       AG
                                CCTT  AGAGGGGGTT  TGG
                                ||||  ||||||||||  |||
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                                GGAA  TCTCCCCCGG  ACC
                                  __         GA
GAM387   LOC126661 3'  GCCTTGGAGGGGAGGGTGG    10781      A  A    TTA
                                GCCTT GAG GGGGG   GTGG
                                ||||| ||| |||||   ||||
                                CGGAA CTC CCCTC   CACC
                                   C   _    C__
GAM387   LOC135293 3'  TGCTTTAGGAGGCTGAGGTGG  10782     C   A   __  TTA
                                TGC TTAG GAGG  GGG   GTGG
                                ||| |||| ||||  |||   ||||
                                ACG AATC CTCC  CTC   CACC
                                  A   _   GA  ___
GAM387   LOC142927 3'  CTAGGGGAGGGGTCAACCTGG  10783      AGA       __
                                TTAG   GGGGGTTAG  TGG
                                ||||   |||||||||  |||
                                GATC   TCCCCAGTT  ACC
                                   CCC        GG
GAM387   LOC142941 5'  TGCCTTAGGAGGAAGGTG    10784        A      TTA
                                TGCCTTAG GAGGGGG   GTG
                                |||||||| |||||||   |||
                                ACGGAATC CTCCTTC   CAC
                                      _     ___
GAM387   LOC150170 5'  TGTCTTGGAGAGGAGGTAAAAG 10785    C   A        T__
      TGG                       TG CTT GAGAGGGGGT   AGTGG
                                || ||| ||||||||||   |||||
                                AC GAA CTCTCCTCCA   TCACC
                                 A   C         TTT
GAM387   LOC150175 5'  TGTCTTGGAGAGGAGGTAAAAG 10785    C   A        T__
      TGG                       TG CTT GAGAGGGGGT   AGTGG
                                || ||| ||||||||||   |||||
                                AC GAA CTCTCCTCCA   TCACC
                                 A   C         TTT
GAM387   LOC150215 5'  TGTCTTGGAGAGGAGGTAAAAG 10785    C   A        T__
      TGG                       TG CTT GAGAGGGGGT   AGTGG
                                || ||| ||||||||||   |||||
                                AC GAA CTCTCCTCCA   TCACC
                                 A   C         TTT
GAM387   LOC206426 3'  TGCTGTGGAGAGGATGGAGTGG 10786     CTTA      _  TT
                                TGC    GAGAGGG GG  AGTGG
                                |||    ||||||| ||  |||||
                                ACG    CTCTCCT CC  TCACC
                                  ACAC       A  __
GAM387   LOC253609 3'  GCCTTGGAGGGGGCACTGG    10787       AGA       T G
                                GCCTT   GAGGGGGT A TGG
                                |||||   |||||||| | |||
                                CGGAA   CTCCCCCG T ACC
                                   C__        _ G
GAM387   LOC256337 3'  TTAGAAGGTTTGCTGTGG    10788       G   GG_   A
                                TTAGA AGG   GTT GTGG
                                ||||| |||   ||| ||||
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                                AATCT TCC   CGA CACC
                                  _  AAA  _
GAM388  BCL11A   3'  TATTTCTTTTGGTGCCAGTATT 10791       CCCAACACC
                                TATTTCT       CCAGTATT
                                |||||||       ||||||||
                                ATAAAGA       GGTCATAA
                                   AAACCAC__
GAM388  KCNJ3    3'  TATTTCTCCCCAGTACT    10792       CCCAACA
                                TATTTCT     CCCCAGTATT
                                |||||||     ||||||||||
                                ATAAAGA     GGGGTCATGA
                                  _______
GAM388  PPP1R12B 3'  TTTCTCTTGGCACCCCAAT   10793      CCAA
                                TTTCTC   CACCCCAGT
                                ||||||   |||||||||
                                AAAGAG   GTGGGGTTA
                                   AACC
GAM388  PPP1R12B 3'  TTTCTCTTGGCACCCCAAT   10793      CCAA
                                TTTCTC   CACCCCAGT
                                ||||||   |||||||||
                                AAAGAG   GTGGGGTTA
                                   AACC
GAM388  PPP1R12B 3'  TTTCTCTTGGCACCCCAAT   10793      CCAA
                                TTTCTC   CACCCCAGT
                                ||||||   |||||||||
                                AAAGAG   GTGGGGTTA
                                   AACC
GAM388  RANBP9   3'  ATTTCTCCTAACACTAAGT   10794       C    CCC
                                ATTTCTCC AACAC   AGT
                                |||||||| |||||   |||
                                TAAAGAGG TTGTG   TCA
                                   A    AT_
GAM388  AQP9     5'  TTTCTACCAATACCTACCTGT  10795     C   C   __  A
                                TTTCT CCAA ACC  CC GT
                                ||||| |||| |||  || ||
                                AAAGA GGTT TGG  GG CA
                                  T   A   AT  A
GAM388  FLJ20772 3'  CTTCTCCCAAACAGGTATT   10796       C  CCCA
                                TTTCTCCCAA AC   GTATT
                                |||||||||| ||   |||||
                                GAAGAGGGTT TG   CATAA
                                   _ TC__
GAM388  FLJ21817 3'  TTTCTCCCAAAAGTGCCAGT  10797       CACC_
                                TTTCTCCCAA    CCAGT
                                ||||||||||    |||||
                                AAAGAGGGTT    GGTCA
                                   TTCAC
GAM388  KIAA1321 3'  TATTTCCCCAACACCCCA    10798      T
                                TATTTC CCCAACACCCCA
                                |||||| ||||||||||||
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                                ATAAAG GGGTTGTGGGGT
                                      _
GAM388  LIMK2    3'  TATCTCTCTCAGCATCTCAGC  10799        C  A  CCC
                                TATTTCTC CA CA   CAGT
                                |||||||| || ||   ||||
                                ATAGAGAG GT GT   GTCG
                                     A  C  AGA
GAM388  LIMK2    3'  TATCTCTCTCAGCATCTCAGC  10799        C  A  CCC
                                TATTTCTC CA CA   CAGT
                                |||||||| || ||   ||||
                                ATAGAGAG GT GT   GTCG
                                     A  C  AGA
GAM388  NALP2    3'  TATTTCTCTCAATATACCC    10800        C   C__
                                TATTTCTC CAA   ACCC
                                |||||||| |||   ||||
                                ATAAAGAG GTT   TGGG
                                     A   ATA
GAM388  LOC255249 5'  TACTTCTCCCAGCATCCACA   10801          A  C  _
                                TATTTCTCCCA CA CC CA
                                |||||||||||| || || ||
                                ATGAAGAGGGT GT GG GT
                                       C  A  T
GAM388  LOC95244  5'  TACTTCTCCCAGCATCCACA   10801          A  C  _
                                TATTTCTCCCA CA CC CA
                                |||||||||||| || || ||
                                ATGAAGAGGGT GT GG GT
                                       C  A  T
GAM389  ADCY8     5'  CGGGCCGGGGGGTGGCGGAGGG  10804     A  CACAT  C
                                CGG CC     GG GGCGGAGGG
                                ||| ||     || |||||||||
                                GCC GG     CC CCGCCTCCC
                                  C  CCC__  A
GAM389  AQP6      5'  ACGGGGCTGCATGGCGGCTCCA 10805      ACCCA       GG_
            AG                    ACGG    CATGGCGGC   AGG
                                ||||    |||||||||   |||
                                TGCC    GTACCGCCG   TTC
                                  CCGAC        AGG
GAM389  ARHC      5'  CGGCCCGTGTCCGGGGGG    10806     A  ACA  G_  C  A
                                CGG CCC   TG  CGG GG GG
                                ||| |||   ||  ||| || ||
                                GCC GGG   AC  GCC CC CC
                                  _  C__  AG   _ _
GAM389  CGTHBA    5'  ACGGAGCCGGAGGCGGAGG    10807      C  ACAT  C
                                ACGGA CC    GG GGCGGAGG
                                ||||| ||    || ||||||||
                                TGCCT GG    CC CCGCCTCC
                                  C  _____  T
GAM389  ECH1      5'  ACGTGCCCGTTAGCGGAGG    10808     GA   ACAT GC
                                ACG  CCC    G  GGCGGAGG
                                |||  |||    |  ||||||||
```

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                                TGC  GGG   C  TCGCCTCC
                                  AC  ____ AA
GAM389  EGLN2   5'  ACGGCGTCCACATGGGCCATGA 10809     AC_      CGGCG
            GGG                   ACGG  CCACATGG    GAGGG
                                ||||  ||||||||   |||||
                                TGCC  GGTGTACC    CTCCC
                                  GCA      CGGTA
GAM389  FABP5   5'  CGGGCTGGCGTGCAGAGAG   10810    ACCCACA   _
                                CGG     TGGCG GCGGAGGG
                                |||     ||||| ||||||||
                                GCC     ACCGC CGTCTCTC
                                  CG_____    A
GAM389  G6PD    5'  CGGCCTCGCGCGCTCGCGGAGG 10811    A  CACA  _  G_
            G                    CGG CC   TG GC  GCGGAGGG
                                ||| ||   || ||  ||||||||
                                GCC GG   GC CG  CGCCTCCC
                                  _ AGC_  G  AG
GAM389  GAS41   5'  CGGGCCCAGGCGGAGG     10812    A   CATGGC
                                CGG CCCA    GGCGGAGG
                                ||| ||||    ||||||||
                                GCC GGGT    CCGCCTCC
                                  C  _______
GAM389  HK2     5'  CGCCCGGCTGGCGGAGGG    10813   GA  ACAT  _
                                CG  CCC   GGC GGCGGAGGG
                                ||  |||   ||| |||||||||
                                GC  GGG   CCG CCGCCTCCC
                                  __  _____  A
GAM389  HMX1    3'  GGACCCACAGGTCCAGGG    10814        T  CGG  A
                                GGACCCACA GG  CGG GG
                                ||||||||| ||  ||| ||
                                CCTGGGTGT CC  GTC CC
                                     _ AG_  _
GAM389  MAPK1   5'  CGGGCCGGCGGGCGGGCGGAGG 10815    A  CACAT   _
            G                    CGG CC    GGCGG CGGAGGG
                                ||| ||    ||||| |||||||
                                GCC GG    CCGCC GCCTCCC
                                  C  CCGC_    C
GAM389  MAPK1   5'  CGGGCCGGCGGGCGGGCGGAGG 10815    A  CACAT   _
            G                    CGG CC    GGCGG CGGAGGG
                                ||| ||    ||||| |||||||
                                GCC GG    CCGCC GCCTCCC
                                  C  CCGC_    C
GAM389  MAPRE3  5'  CGGCTCCGGGGCGGAGG    10816    AC  ACAT  C
                                CGG  CC   GG GGCGGAGG
                                |||  ||   || ||||||||
                                GCC  GG   CC CCGCCTCC
                                  GA  ____  _
GAM389  NF1     5'  CGGCCGGGGGGCGGCGGAGGG  10817    A  CACAT
                                CGG CC    GGCGGCGGAGGG
                                ||| ||    ||||||||||||
```

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                                GCC GG    CCGCCGCCTCCC
                                  _ CCCC_
GAM389  PGM1    5'  CGGACTTGGCTGGCGGAGGG  10818      CCACA   _
                                CGGAC    TGGC GGCGGAGGG
                                |||||    |||| |||||||||
                                GCCTG    ACCG CCGCCTCCC
                                   A____   A
GAM389  PLXNA1  3'  CGGCCCGCAGGTCGGGGGGG  10819    A  A  T  _  C  A
                                CGG CCC CA GG CGG GG GG
                                ||| ||| || || ||| || ||
                                GCC GGG GT CC GCC CC CC
                                  _  C  _  A  _ _
GAM389  SIX2    3'  ACTGACCCACATGGGCGAGGG  10820   G        CG  G
                                AC GACCCACATGG  GCG AGGG
                                || ||||||||||  ||| ||||
                                TG CTGGGTGTACC  CGC TCCC
                                 A         __  _
GAM389  SOX12   5'  CGGGCCCAACGGACGGCGGGGG 10821    A   C   _    A
                                CGG CCCA ATGG CGGCGG GGG
                                ||| |||| |||| |||||| |||
                                GCC GGGT TGCC GCCGCC CCC
                                  C   _   T    _
GAM389  TARBP2  5'  GGACATGCGTACTAGCGGAGGG 10822     CCACATG  _
                                GGAC      GC GGCGGAGGG
                                ||||      || |||||||||
                                CCTG      TG TCGCCTCCC
                                   TACGCA_  A
GAM389  TARBP2  5'  GGACATGCGTACTAGCGGAGGG 10822     CCACATG  _
                                GGAC      GC GGCGGAGGG
                                ||||      || |||||||||
                                CCTG      TG TCGCCTCCC
                                   TACGCA_  A
GAM389  TLL1    5'  GGCCCACGGGTGGGCGGAGGG  10823    A    AT  C_
                                GG CCCAC  GG  GGCGGAGGG
                                || |||||  ||  |||||||||
                                CC GGGTG  CC  CCGCCTCCC
                                 _    C_  AC
GAM389  WEE1    5'  CGAGCCTGGGGCGGCGGGGG  10824   GA  CACAT      A
                                CG  CC    GGCGGCGG GGG
                                ||  ||    |||||||| |||
                                GC  GG    CCGCCGCC CCC
                                 TC  ACC__       _
GAM389  WNT1    3'  GACCCCATGGCGGAGG      10825      A     GGC
                                GACCC CATGGC   GGAGG
                                ||||| ||||||   |||||
                                CTGGG GTACCG   CCTCC
                                   _     ____
GAM389  WNT6    5'  GGATCCGGCGGCGGCGGGGG  10826     C  ACA       A
                                GGA CC   TGGCGGCGG GGG
                                ||| ||   ||||||||| |||
```

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                                CCT GG   GCCGCCGCC CCC
                                  A  CC_       _
GAM389  ZRF1     5'  CGGCTCACGTCCCGGGCGGAGG 10827     ACC   ATGGC_
              G                   CGG   CAC     GGCGGAGGG
                                  |||   |||     |||||||||
                                  GCC   GTG     CCGCCTCCC
                                    GA_   CAGGGC
GAM389  DDX28    5'  GGACCATGAGGGCGGAGGG   10828      CAC    C
                                  GGACC   ATGG GGCGGAGGG
                                  |||||   |||| |||||||||
                                  CCTGG   TACT CCGCCTCCC
                                     ___    C
GAM389  FLJ12768 5'  GGACCGCAGGGCGGAGGG    10829      CACA   C
                                  GGACC    TGG GGCGGAGGG
                                  |||||    ||| |||||||||
                                  CCTGG    GTC CCGCCTCCC
                                     C___   _
GAM389  FLJ20623 5'  GGACCCGAGGGGCGGAGG    10830       ACAT  C
                                  GGACCC    GG GGCGGAGG
                                  ||||||    || ||||||||
                                  CCTGGG    CC CCGCCTCC
                                     CT__  _
GAM389  FLJ22378 3'  CGGATCCACAAGGCGTTCAGG  10831      C    T    GCGG
                                  CGGA CCACA GGCG    AGG
                                  |||| ||||| ||||    |||
                                  GCCT GGTGT CCGC    TCC
                                    A    T    AAG_
GAM389  KIAA0527 5'  CGGGTACAGCGGGGCGGAGGG  10832     ACCC   _   C
                                  CGG    ACA TGG GGCGGAGGG
                                  |||    ||| ||| |||||||||
                                  GCC    TGT GCC CCGCCTCCC
                                    CA__   C   _
GAM389  KIAA1140 5'  GGCCCGGGCGGCGGAGGG    10833    A   ACAT
                                  GG CCC    GGCGGCGGAGGG
                                  || |||    ||||||||||||
                                  CC GGG    CCGCCGCCTCCC
                                   _   C___
GAM389  KIAA1522 3'  GGACCCACAGGGGCCAATGGG  10834         T  C   G  _
                                  GGACCCACA GG GGC GA GGG
                                  ||||||||| || ||| || |||
                                  CCTGGGTGT CC CCG TT CCC
                                        _ _   G  A
GAM389  MACMARCKS 5'  CGGCCCGGCCGGCGGAGGG   10835     A   ACAT   _
                                  CGG CCC    GGC GGCGGAGGG
                                  ||| |||    ||| |||||||||
                                  GCC GGG    CCG CCGCCTCCC
                                    _   _____   G
GAM389  MARKL1   5'  CGGCCCAAGCGGCGGCGGAGGG 10836     A    CA
                                  CGG CCCA  TGGCGGCGGAGGG
                                  ||| ||||  ||||||||||||
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                                GCC GGGT  GCCGCCGCCTCCC
                                  _   TC
GAM389  MGC2817   5'  CGGGCTCAGAGGCGCGCGGAGG 10837    ACC  CAT   _
           G                     CGG   CA   GGCG GCGGAGGG
                                 |||   ||   |||| ||||||||
                                 GCC   GT   CCGC CGCCTCCC
                                   CGA  CT_   G
GAM389  NFAT5    5'  ACGGACCCCAGAGGCCGGCGGC 10838       ACA____
           GGAGGG                  CGGACCC      TGGCGGCGGAGGG
                                 |||||||      ||||||||||||
                                 GCCTGGG      GCCGCCGCCTCCC
                                     GTCTCCG
GAM389  PRP4     5'  CGGCTCCCGGACGGTGGAGGG  10839    A_  ACAT    C
                                 CGG  CCC    GGCGG GGAGGG
                                 |||  |||    ||||| ||||||
                                 GCC  GGG    CTGCC CCTCCC
                                   GA   C___    A
GAM389  Rab11-FIP2 5'  ACGGACCCGGGCGGAGG     10840        ACATGGC
                                 ACGGACCC      GGCGGAGG
                                 ||||||||      ||||||||
                                 TGCCTGGG      CCGCCTCC
                                     C_______
GAM389  LOC125268 3'  GGCCACGTCGTGGCGGAGGG   10841    AC    A_  GC
                                 GG  CCAC  TG  GGCGGAGGG
                                 ||  ||||  ||  |||||||||
                                 CC  GGTG  GC  CCGCCTCCC
                                   __    CA  A_
GAM389  LOC146443 5'  GGACTGTCACAGAGCGGAGGG  10842     CCA    C
                                 GGAC   CATGG GGCGGAGGG
                                 ||||   ||||| |||||||||
                                 CCTG   GTGTC TCGCCTCCC
                                    ACA    _
GAM389  LOC148343 5'  GGGCCCGGGGGGCGGAGGG   10843    A   ACAT  C
                                 GG CCC    GG GGCGGAGGG
                                 || |||    || |||||||||
                                 CC GGG    CC CCGCCTCCC
                                  C   CC__  _
GAM389  LOC152283 5'  GGGCTCACACGGCCAGGG    10844    ACC      GG   A
                                 GG   CACATGGC  CGG GG
                                 ||   ||||||||  ||| ||
                                 CC   GTGTGCCG  GTC CC
                                   CGA       __   _
GAM389  LOC221060 5'  ACGGGCTCACTGGGACAGGG   10845     ACC   A   C    A
                                 ACGG   CAC TGG GGCGG GG
                                 ||||   ||| ||| ||||| ||
                                 TGCC   GTG ACC CTGTC CC
                                    CGA   _   _    _
GAM389  LOC90525  3'  ACGGACCCAGTGGGGAGAGGG  10846         CA   C  C
                                 ACGGACCCA  TGG GG GGAGGG
                                 |||||||||  ||| || ||||||
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                                TGCCTGGGT  ACC CC TCTCCC
                                     C_  _ _
GAM390  CACNA1C  5'  TCAATGGTTTGTGGCCCTT   10849       G
                                TCAATGG TTTGTGGCCTTT
                                ||||||| ||||||||||||
                                AGTTACC AAACACCGGGAA
                                    _
GAM390  FABP6    3'  TGGGTTTGTAGCTCCCTG    10850        _
                                TGGGTTTGTGGC CTTTG
                                |||||||||||| |||||
                                ACCCAAACATCG GGGAC
                                       A
GAM390  ITSN1    3'  GGGCCTGTCTTTGCCA      10851        GGC
                                GGGTTTGT   CTTTGCCA
                                ||||||||   ||||||||
                                CCCGGACA   GAAACGGT
                                    ___
GAM390  MGEA5    3'  TCAATTGTAGGCTTTTGCC    10852      GGGTT  _  C
                                TCAAT    TGT GGC TTTGCC
                                |||||    ||| ||| ||||||
                                AGTTA    ACA CCG AAACGG
                                   _____  T  A
GAM390  PTER     3'  AATTAAATTGTGGCCTTTG    10853     GGGT
                                AAT    TTGTGGCCTTTG
                                |||    ||||||||||||
                                TTA    AACACCGGAAAC
                                  ATTT
GAM390  UNG      3'  TCAAAGGGTAGCCTTTG      10854     T    TTGT
                                TCAA GGGT    GGCCTTTG
                                |||| ||||    ||||||||
                                AGTT CCCA    TCGGAAAC
                                  T   ____
GAM390  UNG      3'  TCAAAGGGTAGCCTTTG      10854     T    TTGT
                                TCAA GGGT    GGCCTTTG
                                |||| ||||    ||||||||
                                AGTT CCCA    TCGGAAAC
                                  T   ____
GAM390  FLJ22104 3'  TGGGTTTCTGTTTGCCA      10855       G  GCC
                                TGGGTTT TG   TTTGCCA
                                ||||||| ||   |||||||
                                ACCCAAA AC   AAACGGT
                                    G  ___
GAM390  INPP5E   3'  ATAGGTCAGCCTTTGC       10856       TGT
                                ATGGGTT   GGCCTTTGC
                                |||||||   |||||||||
                                TATCCAG   TCGGAAACG
                                    ___
GAM390  KIAA0284 3'  TCAATGGGTTTGGCAACTG    10857         TG   CT
                                TCAATGGGTT  TGGC  TTG
                                ||||||||||  ||||  |||
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                                AGTTACCCAA  ACCG  GAC
                                      __    TT
GAM390  MGC5139   5' TCAGAGGGTTTGTGGAGTCTG 10858    AT       CC
                                TCA  GGGTTTGTGG  TTTG
                                |||  ||||||||||  ||||
                                AGT  CCCAAACACC  AGAC
                                  CT        TC
GAM390  YWHAQ     3' AATGGGTTTCTTTGC      10859       GTGGC
                                AATGGGTTT    CTTTGC
                                |||||||||    ||||||
                                TTACCCAAA    GAAACG
                                      _____
GAM390  LOC219513 5' TCGCTGGGTTTGTTTGCC    10860    AA       GGCCT
                                TC  TGGGTTTGT    TTGCC
                                ||  |||||||||    |||||
                                AG  ACCCAAACA    AACGG
                                 CG       _____
GAM390  LOC219690 5' TGGGTTGGCCTTTGC      10861      TTG
                                TGGGT   TGGCCTTTGC
                                |||||   ||||||||||
                                ACCCA   ACCGGAAACG
                                     ___
GAM391  CD28      3' ATAGTTGAAGAACCATCATCT  10864     AA_
                                ATGG   GGGGATCATCATCT
                                ||||   |||||||||||||
                                TATC   TTCTTGGTAGTAGA
                                  AAC
GAM391  GRPR      3' TATAATGGTGATCCATCAT    10865       AAGGG   _
                                TATAATGG    GATC ATCAT
                                ||||||||    |||| |||||
                                ATATTACC    CTAG TAGTA
                                     A____   G
GAM391  LRP4      3' TGATAGGGGACCCAGTTATCT  10866    A      ATC__
                                TGG AGGGGATC    ATCT
                                ||| ||||||||    ||||
                                ACT TCCCCTGG    TAGA
                                  A       GTCAA
GAM391  HAPIP     3' TGAAATGGAATCATCATC    10867      G
                                TGGAA GGGATCATCATC
                                ||||| ||||||||||||
                                ACTTT CCTTAGTAGTAG
                                   A
GAM391  KIAA0555  3' TAAATGGAGGGGATCGTC    10868   T    A     A
                                A AATGGA GGGGATC TC
                                | |||||| ||||||| ||
                                A TTACCT CCCCTAG AG
                                 T     _      C
GAM391  KIAA0939  3' TAAATGGAAGGGGGCTGGCTCT 10869   T        ATCATCA
                                A AATGGAAGGGG      TCT
                                | ||||||||||      |||
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                                A TTACCTTCCCC      AGA
                                 T         CGACCG_
GAM391  MDS028   3'  TAAATGGAAGAAAATCATC   10870   T      GG
                                A AATGGAAG  GATCATC
                                | ||||||||  |||||||
                                A TTACCTTC  TTAGTAG
                                 T       TT
GAM391  LOC170281 5'  ATAGTGGAAGGGGATGGCAC   10871     A         CAT
                                ATA TGGAAGGGGAT   CAT
                                ||| ||||||||||   |||
                                TAT ACCTTCCCCTA   GTG
                                  C         CC_
GAM391  LOC201595 3'  TGTAAAGGAACCATCATC    10872    G
                                TG AAGGGGATCATCATC
                                || ||||||||||||||
                                AC TTTCCTTGGTAGTAG
                                 A
GAM392  C8orf17   5'  TGGTGTTCAGTGAGTGGCA   10875    T   __   A
                                TG TGTT  GTGA TGGCA
                                || ||||  |||| |||||
                                AC ACAA  CACT ACCGT
                                 C   GT   C
GAM392  FLJ14641  3'  CAGTATGTTGTATGACTTGGCA 10876    A      T   A_
                                CA TATGTTGT GTGA  TGGCA
                                || |||||||| ||||  |||||
                                GT ATACAACA TACT  ACCGT
                                 C       _   GA
GAM392  FLJ22601  3'  CAACATGTTTTAAGATGGCA   10877        GTTGT  A
                                CAATATGTT    GA TGGCA
                                |||||||||    || |||||
                                GTTGTACAA    CT ACCGT
                                     AATT_  _
GAM392  SCAMP-4   3'  CCCAACCGTTGTGAATGG    10878      ATGT
                                TCCAAT   TGTTGTGAATGG
                                ||||||   ||||||||||||
                                GGGTTG   GCAACACTTACC
                                  ____
GAM392  LOC202309 5'  TATGTTCCCAGAGAATGGCA   10879      G  GT_
                                TATGTT TT   GAATGGCA
                                |||||| ||   ||||||||
                                ATACAA GG   CTTACCGT
                                   G  TCT
GAM392  LOC90170  5'  TCCGAGAATCGCTGTGGATGG  10880     AATAT       A
                                TCC    GTTGTTGTG ATGG
                                |||    ||||||||| ||||
                                AGG    TAGCGACAC TACC
                                  CTCT_       C
GAM393  MYO1C    3'  CATCCACTGTGTCCTTGGGTG  10883     A  GG  GG
                                CATC CA  TG  GTCCTTGGGTG
                                |||| ||  ||  ||||||||||
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                                GTAG GT  AC  CAGGAACCCAC
                                  _ G_  A_
GAM393  OAS2     3'  GGCAGACATCCTTGGGTG    10884    TG _
                                GG  GG GTCCTTGGGTG
                                ||  || ||||||||||
                                CC  CT TAGGAACCCAC
                                 GT  G
GAM393  XDH      5'  TCACAGGTTGGGGTCCCCG    10885        _
                                TCACAGGT GGGGTCCTTG
                                |||||||| ||||||||||
                                AGTGTCCA CCCCAGGGGC
                                     A
GAM393  ACTR1A   3'  TCACAGGTGAGGGTGCCGGTG  10886         _   _ TTG
                                TCACAGGTG GGGT CC   GGTG
                                ||||||||| |||| ||   ||||
                                AGTGTCCAC CCCA GG   CCAC
                                      T   C ___
GAM393  AKAP11   3'  ATCTGGGTGGGGCGGGGT    10887     ACA      CCTT
                                ATC   GGTGGGGT   GGGT
                                |||   ||||||||   ||||
                                TAG   CCACCCCG   CCCA
                                  AC_      C___
GAM393  BCL2L1   5'  ATCACAGGTCGGGAGAGGAGGT 10888         G   TCCTT
           G                     ATCACAGGT GGG    GGGTG
                                ||||||||| |||    |||||
                                TAGTGTCCA CCC    TCCAC
                                     G   TCTCC
GAM393  FLJ10898 5'  TCACAGGGGCCTCTTCTTGGGT 10889        T  GG __
           G                     TCACAGG GG  TC  CTTGGGTG
                                ||||||| ||  ||  ||||||||
                                AGTGTCC CC  AG  GAACCCAC
                                    _ GG  AA
GAM393  KIAA0748 3'  AGGTGGGGCCTGGTG       10890        T   TG
                                AGGTGGGG CCT  GGTG
                                |||||||| |||  ||||
                                TCCACCCC GGA  CCAC
                                    _  __
GAM393  MIG      3'  AGTGGGATGTGGTTGGGTG   10891         CC__
                                GGTGGGGT   TTGGGTG
                                ||||||||   |||||||
                                TCACCCTA   AACCCAC
                                     CACC
GAM393  SE70-2   5'  ACAGGTGGGAGACTGGGTG   10892          TC  T
                                ACAGGTGGGG  CT GGGTG
                                ||||||||||  || |||||
                                TGTCCACCCT  GA CCCAC
                                      CT  _
GAM393  LOC124216 3'  CACGCGGGTGGGGTGTGGGGGT 10893     A__       CCTT
           G                     CAC   GGTGGGGT   GGGTG
                                |||   ||||||||   |||||
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                                GTG  CCACCCCA   CCCAC
                                  CGC      CACC
GAM393  LOC149322 3'  CATCCTGGGTATAAGTCTTGGG 10894     ACA  _   C
          TG                      CATC  GGTG GGGTC TTGGGTG
                                  |||| |||| ||||| |||||||
                                  GTAG  CCAT TTCAG AACCCAC
                                    GAC   A   _
GAM393  LOC150951 5'  ACAGGTGGGGCAGGT      10895          CCTT
                                  ACAGGTGGGGT   GGGT
                                  ||||||||||   ||||
                                  TGTCCACCCCG   TCCA
                                        ____
GAM393  LOC151234 3'  TCATGGTGGGGTTGAGT    10896    CA      CCT
                                  TCA GGTGGGGT  TGGGT
                                  |||  ||||||||  |||||
                                  AGT  CCACCCCA  ACTCA
                                    A_      ___
GAM393  LOC220635 3'  CATCCTGGGTATAAGTCTTGGG 10894     ACA  _   C
          TG                      CATC  GGTG GGGTC TTGGGTG
                                  |||| |||| ||||| |||||||
                                  GTAG  CCAT TTCAG AACCCAC
                                    GAC   A   _
GAM393  LOC255397 5'  CATCTGGGGGTCTCCTTGGGTG 10897     ACA  T  G_
                                  CATC  GG GGG  TCCTTGGGTG
                                  ||||  || |||  ||||||||||
                                  GTAG  CC CCC  AGGAACCCAC
                                    A__ _  AG
GAM393  LOC86651  3'  CATCCTGGGTATAAGTCTTGGG 10894     ACA  _   C
          TG                      CATC  GGTG GGGTC TTGGGTG
                                  |||| |||| ||||| |||||||
                                  GTAG  CCAT TTCAG AACCCAC
                                    GAC   A   _
GAM394  ABCC8    5'  CCGCCGCCCGGCCCGGCC    10900     G   CC
                                  CCGC CGCCC  GCCCGGCC
                                  |||| |||||  ||||||||
                                  GGCG GCGGG  CGGGCCGG
                                    _   C_
GAM394  ADARB1   5'  CCGCACGCGCGCCCCACGCTTC 10901     _      _  C_
          GGCCG                     CCGC CGCGCGCCCC CGC  CGGCCG
                                  |||| |||||||||| |||  ||||||
                                  GGCG GCGCGCGGGG GCG  GCCGGC
                                    T       T  AA
GAM394  ADARB1   5'  CCGCACGCGCGCCCCACGCTTC 10901     _      _  C_
          GGCCG                     CCGC CGCGCGCCCC CGC  CGGCCG
                                  |||| |||||||||| |||  ||||||
                                  GGCG GCGCGCGGGG GCG  GCCGGC
                                    T       T  AA
GAM394  ADORA1   5'  CCGCCGCAGCGCTCCCAGCCCG 10902       _  _  C
                                  CCGCCGC GCGC CCC GCCCG
                                  ||||||| |||| ||| |||||
```

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                                GGCGGCG CGCG GGG CGGGC
                                    T   A  T
GAM394  ADRBK1   3' GCTGCCCGCCCACCTGGCCG  10903   C G   CC  C
                                GC GC CGCCC  GCC GGCCG
                                || || |||||  ||| |||||
                                CG CG GCGGG  TGG CCGGC
                                 A G   __  A
GAM394  AHR     5' CCGCCGCGCGCACCGGC    10904         CCCCGC
                                CCGCCGCGCGC    CCGGC
                                ||||||||||     |||||
                                GGCGGCGCGCG    GGCCG
                                      T_____
GAM394  ALX4    5' CCACCGCGCGCCTTGGC    10905         CCCGCCC
                                CCGCCGCGCGCC     GGC
                                ||||||||||||     |||
                                GGTGGCGCGCGG     CCG
                                      AA_____
GAM394  APP     5' CCTCCGCGTGCTCTCGCCTACC 10906   G   C CCC   CG
          G                      CC CCGCG GC  CGCC  GCCG
                                || ||||| ||  ||||  ||||
                                GG GGCGC CG  GCGG  TGGC
                                 A   A AGA   A_
GAM394  ATRN    5' CCGGCTCCGCTTCGCCTGGCCG 10907   C G  CC__   C
                                CCG GC CC   CGCC GGCCG
                                ||| || ||   |||| |||||
                                GGC CG GG   GCGG CCGGC
                                  _ A CGAA   A
GAM394  ATRN    5' CCGGCTCCGCTTCGCCTGGCCG 10907   C G  CC__   C
                                CCG GC CC   CGCC GGCCG
                                ||| || ||   |||| |||||
                                GGC CG GG   GCGG CCGGC
                                  _ A CGAA   A
GAM394  ATRN    5' CCGGCTCCGCTTCGCCTGGCCG 10907   C G  CC__   C
                                CCG GC CC   CGCC GGCCG
                                ||| || ||   |||| |||||
                                GGC CG GG   GCGG CCGGC
                                  _ A CGAA   A
GAM394  BCL7B   5' CCGCCGCAGCGTCACAGCGGCC 10908      _  CCCC  C_
          G                      CCGCCGC GCG   CGC  CGGCCG
                                ||||||| |||   |||  ||||||
                                GGCGGCG CGC   GTG  GCCGGC
                                    T  A___   TC
GAM394  BIN1    5' GCCGCGCGTCCAGACCGGC   10909       C  CCGC
                                GCCGCGCG CC   CCGGC
                                |||||||| ||   |||||
                                CGGCGCGC GG   GGCCG
                                    A  TCT_
GAM394  BIN1    5' GCCGCGCGTCCAGACCGGC   10909       C  CCGC
                                GCCGCGCG CC   CCGGC
                                |||||||| ||   |||||
```

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                                CGGCGCGC GG   GGCCG
                                    A  TCT_
GAM394  BRF1    5'  CGCCGCGCGCGCCCGGGCCG  10910        C   CCC
                                CGCCGCGCGC CCCG  GGCCG
                                |||||||||| ||||  |||||
                                GCGGCGCGCG GGGC  CCGGC
                                    C   ___
GAM394  CALM3   5'  CCGCCGCGCGTCCGCGCC   10911        C  C
                                CCGCCGCGCG CC CGCC
                                |||||||||| || ||||
                                GGCGGCGCGC GG GCGG
                                    A  C
GAM394  CAPN10  3'  GCTGCCCCCCCGCCGTCTGGCCG 10912   _  G      C___
                                GC GC CCCCCGCC   GGCCG
                                || || ||||||||   |||||
                                CG CG GGGGGCGG   CCGGC
                                 A  _      CAGA
GAM394  CDK2AP1 5'  CCGCGCGCGTCCGGGCGGC  10913       CC  CC
                                CCGCGCGC  CCG  CGGC
                                ||||||||  |||  ||||
                                GGCGCGCG  GGC  GCCG
                                    CA  CC
GAM394  CDK9    5'  CCGCCGCCGCCCCCAGTCG   10914       G      CC
                                CCGCCGC CGCCCCCG  CG
                                ||||||| ||||||||  ||
                                GGCGGCG GCGGGGGT  GC
                                   _      CA
GAM394  CHN2    5'  CCGCCGCTGCCCTCGCCCGGCC 10915       GC   C
          G                      CCGCCGC  GCCC CGCCCGGCCG
                                |||||||  |||| ||||||||||
                                GGCGGCG  CGGG GCGGGCCGGC
                                   A_   A
GAM394  CHN2    5'  CCGCGCGCCCCTCGCGTCG   10916         _  C_
                                CCGCGCGCCCC CGC  CG
                                |||||||||| |||  ||
                                GGCGCGCGGGG GCG  GC
                                    A  CA
GAM394  CRK     5'  CCGCCGCGCGCGCCCCTCCG  10917         _   GC
                                CCGCCGCGCGC CCCC  CCG
                                |||||||||| ||||  |||
                                GGCGGCGCGCG GGGG  GGC
                                    C   A_
GAM394  CRMP1   5'  CCGCCGCCGCTCCGGC     10918       GCGCCCC  _
                                CCGCCGC     CGC CCGGC
                                |||||||     ||| |||||
                                GGCGGCG     GCG GGCCG
                                   _______  A
GAM394  DUSP7   5'  CCGCCGCCGCCCCCGAAGTCG  10919       G      CCC  C
                                CCGCCGC CGCCCCCG   GG CG
                                ||||||| ||||||||   || ||
```

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                                GGCGGCG GCGGGGGC   TC GC
                                   _       T__  A
GAM394  DUSP7    5'  CCGCCGCGCGCCTCCAGCTCCT 10920          _ C _ GG
          CC                     CCGCCGCGCGCC CC GC CC  CC
                                 |||||||||||| || || ||  ||
                                 GGCGGCGCGCGG GG CG GG  GG
                                       A  T  A  A_
GAM394  DYRK2    5'  CCGCCGCCGCCGCCTCCCGGCC 10921        G   C  G
          G                      CCGCCGC CGCC CC CCCGGCCG
                                 ||||||| |||| || ||||||||
                                 GGCGGCG GCGG GG GGGCCGGC
                                    _   C  A
GAM394  DYRK2    5'  CCGCCGCCGCCGCCTCCCGGCC 10921        G   C  G
          G                      CCGCCGC CGCC CC CCCGGCCG
                                 ||||||| |||| || ||||||||
                                 GGCGGCG GCGG GG GGGCCGGC
                                    _   C  A
GAM394  EHD3     5'  CCGCCGCTCGCCCCCGGCACG  10922        G      _ C
                                 CCGCCGC CGCCCCCG C CG
                                 ||||||| |||||||| | ||
                                 GGCGGCG GCGGGGGC G GC
                                    A       C T
GAM394  EN2      5'  GCCGCCGCCGCCGCCCGGCCG  10923      G   C
                                 GCCGC CGCC CCGCCCGGCCG
                                 ||||| |||| ||||||||||
                                 CGGCG GCGG GGCGGGCCGGC
                                    _   C
GAM394  EN2      5'  CCGCCCGCGCTCCCCGGCCG   10924      G   _    C
                                 CCGCC CGCGC CCCCG CCG
                                 ||||| ||||| ||||| |||
                                 GGCGG GCGCG GGGGC GGC
                                    _    A    C
GAM394  ENPP1    5'  CCGCCGCGGCTCCCGCCCCCCG 10925        C  C      GG
                                 CCGCCGCG GC CCCGCCC  CCG
                                 |||||||| || |||||||  |||
                                 GGCGGCGC CG GGGCGGG  GGC
                                      _ A      G_
GAM394  ESR2     5'  CCGGCGCGCGCCCCGCC     10926     C        C
                                 CCG CGCGCGCCCC GCC
                                 ||| |||||||||| |||
                                 GGC GCGCGCGGGG CGG
                                   C        _
GAM394  GNA11    5'  CCGCCGCGGCCCTCCGGCC    10927        C   CCGC
                                 CCGCCGCG GCCC   CCGGCC
                                 |||||||| ||||   ||||||
                                 GGCGGCGC CGGG   GGCCGG
                                    _   A___
GAM394  GNAI2    5'  CCGCCGTCCGCCGGCCCGGCCG 10928       CG   CCC
                                 CCGCCG  CGCC   GCCCGGCCG
                                 ||||||  ||||  |||||||||
```

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                                GGCGGC  GCGG   CGGGCCGGC
                                   AG    C__
GAM394  H3F3B    5'  CCGCCGCGCCGCTTCCGC    10929         _  CC
                                CCGCCGCGC GC  CCGC
                                ||||||||| ||  ||||
                                GGCGGCGCG CG  GGCG
                                    G  AA
GAM394  HERC2    5'  ACGCGCAGGGCCCGGCCG    10930       CCCC
                                GCGCGC   GCCCGGCCG
                                ||||||   |||||||||
                                TGCGCG   CGGGCCGGC
                                   TCC_
GAM394  HRB      5'  CCGCCCGCGCCGGACCCGGCCG 10931       G     CCC
                                CCGCC CGCGCC   GCCCGGCCG
                                ||||| ||||||   |||||||||
                                GGCGG GCGCGG   TGGGCCGGC
                                  _     CC_
GAM394  ID4      5'  CCGCCGCGCTCCCCTAGCCCG  10932         G    C_
                                CCGCCGCGC CCCC  GCCCG
                                ||||||||| ||||  |||||
                                GGCGGCGCG GGGG  CGGGC
                                    A    AT
GAM394  IFNGR2   5'  CCGCCCGCGCCCCCGCCCCCG  10933       G          GG
                                CCGCC CGCGCCCCCGCCC  CCG
                                ||||| ||||||||||||  |||
                                GGCGG GCGCGGGGGCGGG  GGC
                                  _          __
GAM394  ING1     5'  GCCCGCGCCCCCCCG      10934     G       GC
                                GCC CGCGCCCCC  CCG
                                ||| |||||||||  |||
                                CGG GCGCGGGGG  GGC
                                  _       __
GAM394  KCNF1    5'  CCGCGCGCGCCCTCGCAGCC   10935     C       C   CC
                                CCGC GCGCGCCC CGC  GGCC
                                |||| |||||||| |||  ||||
                                GGCG CGCGCGGG GCG  TCGG
                                  _       A   __
GAM394  KCNF1    5'  CCGCCCCGCGCCCCCTGCAGCC 10936       G       GCC
          G                      CCGCC CGCGCCCCC   CGGCCG
                                ||||| |||||||||   ||||||
                                GGCGG GCGCGGGGG   GTCGGC
                                  G        AC_
GAM394  KCNK1    5'  CCGCCGCCCGCTCCCCCG    10937       G   CC  G
                                CCGCCGC CGC  CC CCCG
                                ||||||| |||  || ||||
                                GGCGGCG GCG  GG GGGC
                                    G   A_  _
GAM394  KIFC3    5'  CCGCTCGCGCCCCTCCCG    10938      CG       CG
                                CCGC  CGCGCCCC  CCCG
                                ||||  ||||||||  ||||
```

```
                                GGCG  GCGCGGGG  GGGC
                                  A_      A_
GAM394  KLHL2    5'  CCGCGGCCATGGCCCGCTCGGC 10939      C  ____    C
              CG                  CCGCG GCC   CCCGC CGGCCG
                                  ||||| |||   ||||| ||||||
                                  GGCGC CGG   GGGCG GCCGGC
                                    _  TACC    A
GAM394  LAD1     5'  CCCCCGCGCGCCCCGGCC    10940    G       CGCCC
                                  CC CCGCGCGCCCC    GGCC
                                  || ||||||||||    ||||
                                  GG GGCGCGCGGGG    CCGG
                                   G       _____
GAM394  LAD1     5'  CCGCCCGCGCCCCGCCGGCCG  10941      G      C  C
                                  CCGCC CGCGCCCC GCC GGCCG
                                  ||||| |||||||| ||| |||||
                                  GGCGG GCGCGGGG CGG CCGGC
                                    _      _  _
GAM394  LEF1     5'  CCGCCGCGCTTTCCCGCTTCG  10942        GCC    C_
                                  CCGCCGCGC   CCCGC  CG
                                  |||||||||   |||||  ||
                                  GGCGGCGCG   GGGCG  GC
                                       AAA    AA
GAM394  LENG4    3'  CCGTCCGTGCTCCCAGCC    10943    _  C  GCCCCCG
                                  CCG CCG GC      CCCGGCC
                                  ||| ||| ||      |||||||
                                  GGC GGC CG      GGGTCGG
                                    A  A  A_______
GAM394  LMO4     5'  CCGCCCGCGCTCCTCCCG    10944      G    CC  G
                                  CCGCC CGCGC  CC CCCG
                                  ||||| |||||  || ||||
                                  GGCGG GCGCG  GG GGGC
                                    _    A_  A
GAM394  LNK      5'  CGTCGCGCGCCCCCGGGCC   10945    C        CCC
                                  CG CGCGCGCCCCCG   GGCC
                                  || ||||||||||||   ||||
                                  GC GCGCGCGGGGGC   CCGG
                                   A          ____
GAM394  LRP8     5'  GCCGCTGCCCCCGCCGCCG   10946      GC       CG
                                  GCCGC  GCCCCCGCC  GCCG
                                  |||||  |||||||||  ||||
                                  CGGCG  CGGGGGCGG  CGGC
                                    A_       __
GAM394  LRP8     5'  GCCGCTGCCCCCGCCGCCG   10946      GC       CG
                                  GCCGC  GCCCCCGCC  GCCG
                                  |||||  |||||||||  ||||
                                  CGGCG  CGGGGGCGG  CGGC
                                    A_       __
GAM394  LRP8     5'  GCCGCTGCCCCCGCCGCCG   10946      GC       CG
                                  GCCGC  GCCCCCGCC  GCCG
                                  |||||  |||||||||  ||||
```

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                                CGGCG  CGGGGGCGG  CGGC
                                  A_       __
GAM394  MAPK12   5'  CGGCGCGCGCCTCGGGCC    10947    C      CC  CCC
                                CG CGCGCGCC  CG   GGCC
                                || ||||||||  ||   ||||
                                GC GCGCGCGG  GC   CCGG
                                 C       A_  ___
GAM394  MGAT1    5'  CCGCCGCGCCCCGCCCCCCGGC 10948         G  _  G
           CG                    CCGCCGCGC CCC CC CCCGGCCG
                                ||||||||| ||| || ||||||||
                                GGCGGCGCG GGG GG GGGCCGGC
                                     _  C  G
GAM394  MLLT1    5'  CCGCCGCCGCCGATCCCGGCCG 10949        G   CCCG
                                CCGCCGC CGCC   CCCGGCCG
                                ||||||| ||||   ||||||||
                                GGCGGCG GCGG   GGGCCGGC
                                   _   CTA_
GAM394  MVK      5'  CCGCCGCCGCCTCCCCGGCCG  10950        G   CCCG
                                CCGCCGC CGCC   CCCGGCCG
                                ||||||| ||||   ||||||||
                                GGCGGCG GCGG   GGGCCGGC
                                   _   AG__
GAM394  MYO1C    5'  CCGGTAGCGCATCCTGCCCGGC 10951     CC_    C  CC
           CG                    CCG   GCGCG CC  GCCCGGCCG
                                |||   ||||| ||  |||||||||
                                GGC   CGCGT GG  CGGGCCGGC
                                  CAT    A  A_
GAM394  NFIA     5'  CCCGCGCCGGCCCGGCC     10952    G     CCC
                                CC CGCGCC   GCCCGGCC
                                || ||||||   ||||||||
                                GG GCGCGG   CGGGCCGG
                                 _     C__
GAM394  NOS1     5'  CCGCTGCTCGCTGCCCGGCCG  10953      C  G   CCCC
                                CCGC GC CGC    GCCCGGCCG
                                |||| || |||    |||||||||
                                GGCG CG GCG    CGGGCCGGC
                                  A  A   A___
GAM394  OPRD1    5'  CCGCCGCGTCCCTCTCCACCGG 10955         CG  ___    C
           C                     CCGCCGCG  CCC   CCGCC GGC
                                ||||||||  |||   ||||| |||
                                GGCGGCGC  GGG   GGTGG CCG
                                   A_   AGA    _
GAM394  OPRD1    5'  CCGCCGCGTGCCGCGCCCCGGC 10954         C   CC    _
           CG                    CCGCCGCG GCC  CGCCC GGCCG
                                ||||||||| |||  ||||| |||||
                                GGCGGCGC CGG  GCGGG CCGGC
                                   A  C_    G
GAM394  PKIA     5'  CCGCCGCGGAGCTCCGGC    10956         CGCCCCC  _
                                CCGCCGCG      GC CCGGC
                                ||||||||      || |||||
```

```
                                GGCGGCGC      CG GGCCG
                                    CT_____  A
GAM394  PPP3CA   5'  CCGCCGCGCTGCAAACCGCTCG 10957         _ CC_   C
            GC                    CCGCCGCGC GC   CCGC CGGC
                                  ||||||||| ||   |||| ||||
                                  GGCGGCGCG CG   GGCG GCCG
                                     A  TTT    A
GAM394  PTP4A2   5'  CCTCGCGCCGTGCCCGGCC   10958    G     CCC
                                  CC CGCGCC   GCCCGGCC
                                  || ||||||   ||||||||
                                  GG GCGCGG   CGGGCCGG
                                   A     CA_
GAM394  PTP4A2   5'  CCTCGCGCCGTGCCCGGCC   10958    G     CCC
                                  CC CGCGCC   GCCCGGCC
                                  || ||||||   ||||||||
                                  GG GCGCGG   CGGGCCGG
                                   A     CA_
GAM394  RAD23B   5'  CCGCCGCGCAGCTCGGC     10959         CCCCC  C
                                  CCGCCGCGCG    GC CGGC
                                  ||||||||||    || ||||
                                  GGCGGCGCGT    CG GCCG
                                        _____  A
GAM394  RASD1    3'  CCGCGCGCGCTCCCGGCC    10960     C     CCCCG
                                  CCGC GCGCGC    CCCGGCC
                                  |||| ||||||    |||||||
                                  GGCG CGCGCG    GGGCCGG
                                    _     A____
GAM394  RBP4     5'  CCGCGCGCAAGCCTGGCC    10961        CCCC   C
                                  CCGCGCGC    GCC GGCC
                                  ||||||||    ||| ||||
                                  GGCGCGCG    CGG CCGG
                                      TT__   A
GAM394  RELN     5'  CCGCCGCGCGCCCTACGCGCCG 10962           C_  _
                                  CCGCCGCGCGCCC  CGC CCG
                                  |||||||||||||  ||| |||
                                  GGCGGCGCGCGGG  GCG GGC
                                         AT   C
GAM394  RET      5'  GCTGCGCGCCCTGCTTCGGTCG 10963    C      CC  C_  C
                                  GC GCGCGCCC  GC  CGG CG
                                  || ||||||||  ||  ||| ||
                                  CG CGCGCGGG  CG  GCC GC
                                   A       A_  AA   A
GAM394  RET      5'  GCTGCGCGCCCTGCTTCGGTCG 10963    C      CC  C_  C
                                  GC GCGCGCCC  GC  CGG CG
                                  || ||||||||  ||  ||| ||
                                  CG CGCGCGGG  CG  GCC GC
                                   A       A_  AA   A
GAM394  RET      5'  GCTGCGCGCCCTGCTTCGGTCG 10963    C      CC  C_  C
                                  GC GCGCGCCC  GC  CGG CG
                                  || ||||||||  ||  ||| ||
```

```
                                CG CGCGCGGG  CG  GCC GC
                                 A       A_  AA   A
GAM394  RET     5'  GCTGCGCGCCCTGCTTCGGTCG 10963    C      CC  C_   C
                                GC GCGCGCCC  GC  CGG CG
                                || ||||||||  ||  ||| ||
                                CG CGCGCGGG  CG  GCC GC
                                 A       A_  AA   A
GAM394  SCN4A   3'  GCTGCACGCCCCAGGGTCG   10964    C       CGCCC  C
                                GC GCGCGCCCC    GG CG
                                || |||||||||    || ||
                                CG CGTGCGGGG    CC GC
                                 A       TC___  A
GAM394  SFRP5   5'  CCGGCGTGCGCCCCCGGCCC   10965    C  C       _
                                CCG CG GCGCCCCCG CCC
                                ||| || ||||||||| |||
                                GGC GC CGCGGGGGC GGG
                                  C  A       C
GAM394  SIX2    5'  CCGCGCGCGCCCTCACC     10966     C      C
                                CCGC GCGCGCCC CGCC
                                |||| |||||||| ||||
                                GGCG CGCGCGGG GTGG
                                  _       A
GAM394  SLC12A4  5'  CCGCCGCTGTCCCCGCCC    10967       GCGC
                                CCGCCGC   CCCCGCCC
                                |||||||   ||||||||
                                GGCGGCG   GGGGCGGG
                                    ACA_
GAM394  SLC25A4  5'  CCGCCGCGCAGTCCCCGACCC  10968         C_   _
                                CCGCCGCGCG  CCCCG CCC
                                ||||||||||  ||||| |||
                                GGCGGCGCGT  GGGGC GGG
                                      CA    T
GAM394  SNX3    5'  CCGCCGCGGGCTCCCTCCTCG  10969        C  C   G  _
                                CCGCCGCG GC CCC CC CG
                                |||||||| || ||| || ||
                                GGCGGCGC CG GGG GG GC
                                    C  A   A  A
GAM394  SRR     5'  CCTCCGCGCGCCTCCCCGGCCG 10970    G       CCCG
                                CC CCGCGCGCC   CCCGGCCG
                                || |||||||||   ||||||||
                                GG GGCGCGCGG   GGGCCGGC
                                 A       AG__
GAM394  STIP1   5'  CCGCTCCGCGTTCCCAACC   10971     CG   CCCCCG
                                CCGC  CGCG    CCCGGCC
                                ||||  ||||    |||||||
                                GGCG  GCGC    GGGTTGG
                                  AG   AA____
GAM394  TBL1X   5'  CGCCGCGCGCCCGGC      10972          CCGCCC
                                CGCCGCGCGCCC    GGC
                                ||||||||||||    |||
```

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                                GCGGCGCGCGGG    CCG
                                        ______
GAM394  TERF2    5'  CGCCGCGCGCCCTCCCCG    10973          CCG
                                GCCGCGCGCCC  CCCG
                                ||||||||||||  ||||
                                GCGGCGCGCGGG  GGGC
                                      AG_
GAM394  TESK1    5'  CCGCCGCGCCGGCTGGC     10974        GCCC C  CC
                                CCGCCGCGC   C GC  GGC
                                |||||||||   | ||  |||
                                GGCGGCGCG   G CG  CCG
                                     ____ C  A_
GAM394  TPX1     5'  GCTGCGCGCCCCTCTCACC   10975    C       ___
                                GC GCGCGCCCC  CGCC
                                || |||||||||  ||||
                                CG CGCGCGGGG  GTGG
                                 A        AGA
GAM394  TRPC1    5'  CCGCCGGCGCCCCGGC      10976       C      CGCCC
                                CCGCCG GCGCCCC    GGC
                                |||||| |||||||    |||
                                GGCGGC CGCGGGG    CCG
                                     _     _____
GAM394  UGCG     5'  CCGCCCGCGCGCTCTCGCC   10977      _     CCC
                                CCGCC GCGCGC  CGCC
                                ||||| ||||||  ||||
                                GGCGG CGCGCG  GCGG
                                   G     AGA
GAM394  XYLB     5'  CCGCCCCTAGCTCCGCCCGGCC 10978      GCGC  CC
           G                     CCGCC   GC  CCGCCCGGCCG
                                |||||   ||  ||||||||||
                                GGCGG   CG  GGCGGGCCGGC
                                   GGAT  A_
GAM394  ARF6     5'  CCGCCGCGGTTCCCGCTCCTCC 10979        CGCC    _ GG
           G                     CCGCCGCG   CCCGC CC  CCG
                                |||||||   ||||| ||  |||
                                GGCGGCGC   GGGCG GG  GGC
                                     CAA_    A  A_
GAM394  ARNTL2   5'  CCGCCCCGCAGCCCGGCC    10980      G   CCCCC
                                CCGCC CGCG    GCCCGGCC
                                ||||| ||||    ||||||||
                                GGCGG GCGT    CGGGCCGG
                                   G   _____
GAM394  C20orf177 5'  CCGCGCGGGGACGCCCGGC   10981       CCCC
                                CCGCGCG   CGCCCGGC
                                |||||||   ||||||||
                                GGCGCGC   GCGGGCCG
                                    CCCT
GAM394  C20orf39  5'  CCGCCTGCGCCCCCGGC     10982      GC      GCCC
                                CCGCC  GCGCCCCC   GGC
                                |||||  ||||||||   |||
```

```
                                GGCGG  CGCGGGGG   CCG
                                  A_      _____
GAM394  C2orf7   5'  CCGCCGCGCGTCGCTCG     10983         CCCC  C
                                CCGCCGCGCG   CGC CG
                                ||||||||||   ||| ||
                                GGCGGCGCGC   GCG GC
                                     A___   A
GAM394  CASKIN1  3'  GCAGGGCCCTGCCCGGCCG   10984    C_   CC
                                GCG  GCCC  GCCCGGCCG
                                |||  ||||  |||||||||
                                CGT  CGGG  CGGGCCGGC
                                  CC   A_
GAM394  CBX4     5'  CCGCCGCTCGCCCCGCACAGCC 10985       G    _ ____
           CGGCCG                  CGCCGC CGCCCC C   GCCCGGCCG
                                |||||| |||||| |   |||||||||
                                GCGGCG GCGGGG G   CGGGCCGGC
                                   A     C TGT
GAM394  CDH22    5'  CCGCCCGCGCCCCCGTCGCCG  10986      G        CCCG
                                CCGCC CGCGCCCCCG    GCCG
                                |||||| ||||||||||    ||||
                                GGCGG GCGCGGGGGC    CGGC
                                  _        AG__
GAM394  CENTG2   5'  CCGCCGCGCGCCGCCCGCC    10987           _
                                CCGCCGCGCGCC CCCGCC
                                |||||||||||| ||||||
                                GGCGGCGCGCGG GGGCGG
                                     C
GAM394  CHSY1    5'  CCCCGCGCGCCCTCAGCCCG   10988    G        C _
                                CC CCGCGCGCCC C GCCCG
                                || |||||||||| | |||||
                                GG GGCGCGCGGG G CGGGC
                                  _        A T
GAM394  CTHRC1   5'  CCGCCGCGCTCCGAGGCC    10989         GCCC   CCC
                                CCGCCGCGC    CCG   GGCC
                                |||||||||    |||   ||||
                                GGCGGCGCG    GGC   CCGG
                                     A___   T__
GAM394  DKFZP434H0820 5'  CCGCCGCTCCCGCCGCCCGGC  10990        GCG  _
                                CCGCCGC   CCC CCGCCCGGC
                                |||||||   ||| |||||||||
                                GGCGGCG   GGG GGCGGGCCG
                                   A__   C
GAM394  DKFZp434N035 3'  CCGCTGCGCGCGCTCCCGCGCC 10991      __      C    _
           G                     CCGC  CGCGCGC CCCGC CCG
                                ||||  ||||||| ||||| |||
                                GGCG  GCGCGCG GGGCG GGC
                                  AC      A    C
GAM394  DKFZp434N2435 5'  CCGCGCACACCCGCTCGGC    10992         C    C
                                CCGCGCGC CCCGC CGGC
                                |||||||| ||||| ||||
```

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                                GGCGCGTG GGGCG GCCG
                                    T    A
GAM394  DKFZP586F1524 5'  CCGCCCGAGCGCCCGCCCGGC  10993      G  C  C
                                CCGCC CG GC CCCGCCCGGC
                                ||||| || || ||||||||||
                                GGCGG GC CG GGGCGGGCCG
                                  _ T  C
GAM394  DKFZp761B0514 5'  CCGCCCGCGTCCCTTCAGGTGC 10994      G   _  CCGCCCG
          CG                    CCGCC CGCG CCC      GCCG
                                ||||| |||| |||      ||||
                                GGCGG GCGC GGG      CGGC
                                  _   A  AAGTCCA
GAM394  DKFZP761D0211 5'  CCGCCGCGGCCTCTCACCCG  10995       C  CC_
                                CCGCCGCG GCC  CGCCCG
                                |||||||| |||  ||||||
                                GGCGGCGC CGG  GTGGGC
                                    _  AGA
GAM394  DNAJL1   5'  CCGCCGCGCAGCTCCGTTGGCC 10996        _ CC  CCC
          G                     CCGCCGCGC GC  CCG  GGCCG
                                |||||||| ||  |||  |||||
                                GGCGGCGCG CG  GGC  CCGGC
                                    T  A_  AA_
GAM394  ECE2    5'  CCGCCGCGCAGCACCCCCGCTC 10997        ___      C
          GGCCG                 CCGCCGCGC  GCCCCCGC CGGCCG
                                |||||||||  |||||||| ||||||
                                GGCGGCGCG  TGGGGGCG GCCGGC
                                    TCG      A
GAM394  EHM2    5'  CCGCCGCGCGCTCTCCGGGCCG 10998         CCCCG  C
                                CCGCCGCGCGC    CC GGCCG
                                ||||||||||    || |||||
                                GGCGGCGCGCG    GG CCGGC
                                    AGA__  C
GAM394  ESDN    5'  CCCCGCGCGCCTCTGGCC    10999    G      CCCGCCC
                                CC CCGCGCGCC      GGCC
                                || |||||||||      ||||
                                GG GGCGCGCGG      CCGG
                                 _       AGA_____
GAM394  FEM1B   5'  GCCGTGCGCCCCCGGAGGCCG  11000     C       CCC
                                GCCG GCGCCCCCG  GGCCG
                                |||| |||||||||  |||||
                                CGGC CGCGGGGGC  CCGGC
                                  A       CT_
GAM394  FLJ10081  5'  GCCGCGCGCTCGGCCACGGCCG 11001        CCCC  _
                                GCCGCGCGC   GCC CGGCCG
                                |||||||||   ||| ||||||
                                CGGCGCGCG   CGG GCCGGC
                                    AGC_  T
GAM394  FLJ10579  5'  CCGCCGCGGCCCCCGAAGGC  11002       C     CCC
                                CCGCCGCG GCCCCCG  GGC
                                |||||||| |||||||  |||
```

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                                GGCGGCGC CGGGGGC  CCG
                                   _     TT_
GAM394  FLJ12132  5' CCGCCCCGCCCGCGTCCGGCCG 11003     GCG   C C
                                CCGCC  CGCCC CG CCGGCCG
                                ||||||  |||||| || |||||||
                                GGCGG  GCGGG GC GGCCGGC
                                  G__   C  A
GAM394  FLJ12587  5' CCGCCGCGGCTCCCGTCGGCCG 11004       C C   CC
                                CCGCCGCG GC CCCG  CGGCCG
                                |||||||| || ||||  ||||||
                                GGCGGCGC CG GGGC  GCCGGC
                                   _ A   A_
GAM394  FLJ13057  5' CCGCCCGCAGCGTCCGGC    11005     G   CCCC  C   C
                                CCGCC CGCG   CG CCGG C
                                ||||| ||||   || |||| |
                                GGCGG GCGT   GC GGCC G
                                  _   C___  A   A
GAM394  FLJ14117  5' CCGCCGCGGCTTAGCCGGCCG  11006       C  CCCC   C
                                CCGCCGCG GC   GCC GGCCG
                                |||||||| ||   ||| |||||
                                GGCGGCGC CG   CGG CCGGC
                                   _ AAT_  _
GAM394  FLJ14594  3' CCCCTTCCCCTGCCCGGCC   11007   G  GCGCG   C
                                CC CC    CCCC GCCCGGCC
                                || ||    |||| ||||||||
                                GG GG    GGGG CGGGCCGG
                                 _ AA___   A
GAM394  FLJ21511  5' CCGCCGCGTCCTCCCGGGCC   11008       CG  _   CCC
                                CCGCCGCG  CC CCCG   GGCC
                                ||||||||  || ||||   ||||
                                GGCGGCGC  GG GGGC   CCGG
                                   A_ A   ___
GAM394  FLJ21511  5' CCGCCGCCGCGTCCTCCCG   11009       G   CC  G
                                CCGCCGC CGC  CC CCCG
                                ||||||| |||  || ||||
                                GGCGGCG GCG  GG GGGC
                                   _  CA  A
GAM394  FLJ23471  5' GCCGCGACCGCCCGGCCG    11010      CGCCC
                                GCCGCG    CCGCCCGGCCG
                                ||||||    ||||||||||
                                CGGCGC    GGCGGGCCGGC
                                  T_____
GAM394  FLJ32743  5' CCGCCGCGTTTCCCCCAACCG  11011       CG_    C
                                CCGCCGCG   CCCCCG CCG
                                ||||||||   |||||| |||
                                GGCGGCGC   GGGGGT GGC
                                   AAA     T
GAM394  FLJ32818  5' GCCGCCCAGGCCTCCCGCCTGG 11012     G __  _    C
          C                     GCCGC C  GCC CCCGCC GGC
                                ||||| |  ||| |||||| |||
```

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                                CGGCG G  CGG GGGCGG CCG
                                   G TC   A     A
GAM394  FN5     5'  CCGCCGCCGCCCCCGCCACCA  11013        G        CG
                                CCGCCGC CGCCCCCGCC  GCCG
                                ||||||| ||||||||||  ||||
                                GGCGGCG GCGGGGGCGG  TGGT
                                          _        __
GAM394  GDF10   5'  CCACTGCGCGCCCGGCCCGGC  11014      C       CC
                                CCGC GCGCGCCC  GCCCGGC
                                |||| ||||||||  |||||||
                                GGTG CGCGCGGG  CGGGCCG
                                  A       C_
GAM394  GIOT-3  5'  CCGCCGTCGTCACCGCCCGGCC 11015       _ _    CCC
           G                     CCGCCG CG CGCC   GCCCGGCCG
                                ||||||| || ||||   |||||||||
                                GGCGGC GC GTGG   CGGGCCGGC
                                   A  A   ___
GAM394  GKAP42  5'  CCGCCGCCGCCTCTCCCG    11016        G   CCCG
                                CCGCCGC CGCC    CCCG
                                ||||||| ||||    ||||
                                GGCGGCG GCGG    GGGC
                                   _   AGA_
GAM394  GMPPB   5'  GCCGCGCACTCCCAACGCCG   11017          _  C  _
                                GCCGCGCGC CCC GC CCG
                                ||||||||| ||| || |||
                                CGGCGCGTG GGG TG GGC
                                     A   T  C
GAM394  GMPPB   5'  GCCGCGCACTCCCAACGCCG   11017          _  C  _
                                GCCGCGCGC CCC GC CCG
                                ||||||||| ||| || |||
                                CGGCGCGTG GGG TG GGC
                                     A   T  C
GAM394  GTPBP1  5'  CCGCCGCGGCCCTGGC      11018        C   CCGCCC
                                CCGCCGCG GCCC     GGC
                                |||||||| ||||     |||
                                GGCGGCGC CGGG     CCG
                                   _   A_____
GAM394  H2AV    5'  GCCGCGCGCCCTCCCG      11019          CCG
                                GCCGCGCGCCC   CCCG
                                ||||||||||   ||||
                                CGGCGCGCGGG   GGGC
                                      A__
GAM394  H2AV    5'  GCCGCGCGCCCTCCCG      11019          CCG
                                GCCGCGCGCCC   CCCG
                                ||||||||||   ||||
                                CGGCGCGCGGG   GGGC
                                      A__
GAM394  HES6    5'  CCGTCCGCGCTCCCCTCG    11020     _     G   _
                                CCG CCGCGC CCCC CG
                                ||| |||||| |||| ||
```

```
                                GGC GGCGCG GGGG GC
                                  A     A   A
GAM394  HSA250839 5'  GCCGCTGCTACATGCCCGGCCG 11021      _  GCCCCC
                                GCCGC GC     GCCCGGCCG
                                ||||| ||     |||||||||
                                CGGCG CG     CGGGCCGGC
                                   A  ATGTA_
GAM394  HSJ001348 5'  CCTCCGCGCGCCTCTCCCCG   11022    G       CCCG
                                CC CCGCGCGCC    CCCG
                                || |||||||||    ||||
                                GG GGCGCGCGG    GGGC
                                 A        AGAG
GAM394  HSPC195   5'  CCGCCGCGCGCCCGCCCG    11023           CC
                                CCGCCGCGCGCCC  GCCCG
                                ||||||||||||  |||||
                                GGCGGCGCGCGGG  CGGGC
                                                __
GAM394  HUMNPIIY20 3'  CCGCCGCGAGTTCCCGGGGC   11024        CGCC   CCC
                                CCGCCGCG   CCCG   GGC
                                ||||||||   ||||   |||
                                GGCGGCGC   GGGC   CCG
                                     TCAA   C__
GAM394  ING5      3'  CCGCCCGCACGCCCGGCC    11025      G    CCCC
                                CCGCC CGCGC    GCCCGGCC
                                ||||| |||||    ||||||||
                                GGCGG GCGTG    CGGGCCGG
                                  _    _____
GAM394  KATII     5'  CGCCGCGCCCCCTCCCG     11026       GC     G
                                CGCCGC  GCCCCC CCCG
                                ||||||  |||||| ||||
                                GCGGCG  CGGGGG GGGC
                                   __      A
GAM394  KIAA0014  3'  CCGCGTGCCCCCGCCGGTCG   11027      C       C  C
                                CCGCG GCCCCCGCC GG CG
                                ||||| ||||||||| || ||
                                GGCGC CGGGGGCGG CC GC
                                   A        _  A
GAM394  KIAA0084  5'  CCGCCGCGCGTCCGCC      11028          CCC
                                CCGCCGCGCG   CCGCC
                                ||||||||||   |||||
                                GGCGGCGCGC   GGCGG
                                      A__
GAM394  KIAA0172  5'  CCGCCGCGCTCCCCGCCAGCC  11029         GC      C
                                CCGCCGCGC  CCCCGCC GGCC
                                |||||||||  ||||||| ||||
                                GGCGGCGCG  GGGGCGG TCGG
                                      A_      _
GAM394  KIAA0211  5'  CCGCGCGCGTCCCCAGCGCCGG 11030      C    _    C  _
              C                    CCGC GCGCG CCCC GC CCGGC
                                ||||| ||||| |||| || |||||
```

```
                                GGCG CGCGC GGGG CG GGCCG
                                  _    A   T  C
GAM394  KIAA0431  3' CCGCTGCTGCTTCCCTAGCCG  11031     C  GC  CCCCG  _
                                CCGC GC  GC    CCC GGCCG
                                |||| ||  ||    ||| |||||
                                GGCG CG  CG    GGG TCGGC
                                  A  A_  AA___   A
GAM394  KIAA0435  3' CCAGCCTCCCCGCCCGGCC   11032    C  GC
                                CCG GC  CCCCGCCCGGCC
                                ||| ||  ||||||||||||
                                GGT CG  GGGGCGGGCCGG
                                  _ GA
GAM394  KIAA0534  5' CCGCCGTCGCCTCCGCTCG   11033      CG   C   C
                                CCGCCG  CGCC CCGC CG
                                ||||||  |||| |||| ||
                                GGCGGC  GCGG GGCG GC
                                   A_   A   A
GAM394  KIAA0672  5' CCGCCGCGCCGCCTCCTGCC   11034       _  _ C
                                CCGCCGCGC GCC CC GCC
                                ||||||||| ||| || |||
                                GGCGGCGCG CGG GG CGG
                                     G   A A
GAM394  KIAA0757  5' GCCGCCGAGGACGGCCCGGCCG 11035     G  CCCCC_
                                GCCGC CG     GCCCGGCCG
                                ||||| ||     |||||||||
                                CGGCG GC     CGGGCCGGC
                                  _ TCCTGC
GAM394  KIAA0863  5' CCGCCCGCGCCTCCGCCC    11036     G     C
                                CCGCC CGCGCC CCGCCC
                                ||||| |||||| ||||||
                                GGCGG GCGCGG GGCGGG
                                  _     A
GAM394  KIAA0995  5' CCGCCGCCGTCCCCGCCC    11037      G  C
                                CCGCCGC CG CCCCGCCC
                                ||||||| || ||||||||
                                GGCGGCG GC GGGGCGGG
                                   _ A
GAM394  KIAA1061  5' CCGCCCCGCGTCCTTCGGC   11038     G   CCC  GCC
                                CCGCC CGCG   CC   CGGC
                                ||||| ||||   ||   ||||
                                GGCGG GCGC   GG   GCCG
                                  G   A__  AA_
GAM394  KIAA1183  3' CGCTGGCGCCCCCGGCC     11039    CGC      GCCC
                                CGC   GCGCCCCC   GGCC
                                |||   ||||||||   ||||
                                GCG   CGCGGGGG   CCGG
                                 AC_      _____
GAM394  KIAA1297  3' CCGCCGCGGGCCTCCCAGGCCG 11040       C  _   CCC
                                CCGCCGCG GCC CCCG   GGCCG
                                |||||||| ||| ||||   |||||
```

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                                GGCGGCGC CGG GGGT  CCGGC
                                    C  A   ___
GAM394  KIAA1691  5'  CCGTCGACCCCCGCCTGGCCG  11041    _ C      C
                                CCG CG GCCCCCGCC GGCCG
                                ||| || ||||||||| |||||
                                GGC GC TGGGGGCGG CCGGC
                                  A _      A
GAM394  KIAA1940  5'  GCCGCGCAGTCTCCAGTTCGGC 11042       CCC_  CC_
          CG                    GCCGCGCG   CCG  CGGCCG
                                ||||||||   |||  ||||||
                                CGGCGCGT   GGT  GCCGGC
                                    CAGA  CAA
GAM394  LANO     5'  CCGTCGCCGCCCCCGCCGCCG  11043    C  G      CG
                                CCG CGC CGCCCCCGCC  GCCG
                                ||| ||| ||||||||||  ||||
                                GGC GCG GCGGGGGCGG  CGGC
                                  A  _       __
GAM394  MAP2K7   5'  CCGCCGCCGCGCACCGCCCGGC 11044       _   CC
          CG                    CCGCCGC GCGC  CCGCCCGGCCG
                                ||||||| ||||  ||||||||||
                                GGCGGCG CGCG  GGCGGGCCGGC
                                   G   T_
GAM394  MARK2    5'  CCGCCGCATGGGCCCCGGCCG  11045       C__    CGCCC
                                CCGCCGCG  GCCCC   GGCCG
                                ||||||||  |||||   |||||
                                GGCGGCGT  CGGGG   CCGGC
                                    ACC   _____
GAM394  MGC11115 5'  CCGCCGCGCGTCCGCCC    11046        CCC
                                CCGCCGCGCG  CCGCCC
                                ||||||||||  ||||||
                                GGCGGCGCGC  GGCGGG
                                     A__
GAM394  MGC12679 3'  GCTGCGCCGCCCGGCC     11047   _    CCC
                                GC GCGCC  GCCCGGCC
                                || |||||  ||||||||
                                CG CGCGG  CGGGCCGG
                                 A   ___
GAM394  MGC14386 5'  CCGCCGCGCCGCTGGC     11048        GCCCC  CC
                                CCGCCGCGC   CGC  GGC
                                |||||||||   |||  |||
                                GGCGGCGCG   GCG  CCG
                                    _____  A_
GAM394  MGC14439 5'  GCCGGCCCGCCCGGCC     11049     C  GCCC
                                GCCG GC   CCGCCCGGCC
                                |||| ||   ||||||||||
                                CGGC CG   GGCGGGCCGG
                                  _ _____
GAM394  MGC20806 3'  CCGCCGCGCGCAGGCGGCC   11050          CCCCGCC
                                CCGCCGCGCGC     CGGCC
                                ||||||||||      |||||
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                                GGCGGCGCGCG      GCCGG
                                      TCC____
GAM394  MGC33371  5'  CCGCCGCCGCCCGGGC      11051        G    CCGCCC
                                CCGCCGC CGCCC     GGC
                                ||||||| |||||      |||
                                GGCGGCG GCGGG     CCG
                                   _    C_____
GAM394  MGC4342   3'  GCCCCCACACCCTGCCTGGC   11052    _ G     CC   C
                                GC C CGCGCCC  GCC GGC
                                || | |||||||  ||| |||
                                CG G GTGTGGG  CGG CCG
                                 G G      A_  A
GAM394  MGC5528   5'  CCGCCGCGCCCGGGTGGC    11053         GCCC   CCC
                                CCGCCGCGC    CCG   GGC
                                |||||||||    |||   |||
                                GGCGGCGCG    GGC   CCG
                                     ____   CCA
GAM394  MIP-T3    5'  CCGCCCGCGCCCCTCAGCC    11054      G      CGCC
                                CCGCC CGCGCCCC    CGGCC
                                ||||| ||||||||    |||||
                                GGCGG GCGCGGGG    GTCGG
                                   _       A___
GAM394  MY014     5'  CCGCCGCCGTTCCCGGC      11055        G  CCCCCG
                                CCGCCGC CG     CCCGGC
                                ||||||| ||     ||||||
                                GGCGGCG GC     GGGCCG
                                   _ AA____
GAM394  N4BP1     5'  CCGCCCGCGCCCCGCC      11056      G      C
                                CCGCC CGCGCCCC GCC
                                ||||| |||||||| |||
                                GGCGG GCGCGGGG CGG
                                   _      _
GAM394  N4BP1     5'  CCGCCGCCCGCCCTCAGGCCCG 11057        G    CC__
                                CCGCCGC CGCCC    GCCCG
                                ||||||| |||||    |||||
                                GGCGGCG GCGGG    CGGGC
                                    G    AGTC
GAM394  NCK1      5'  CCGCCGCGTAGCTCTTGGCCTC 11058        C_  CCCC_  _
          G                      CCGCCGCG  GC     GCC CG
                                 ||||||||  ||     ||| ||
                                 GGCGGCGC  CG     CGG GC
                                     AT  AGAAC   A
GAM394  NR6A1     5'  CCGCTCCGCGCCCCTCCG    11059      CG      CGC
                                CCGC  CGCGCCCC   CCG
                                ||||  ||||||||   |||
                                GGCG  GCGCGGGG   GGC
                                  AG       A__
GAM394  NR6A1     5'  CCGCTCCGCGCCCCTCCG    11059      CG      CGC
                                CCGC  CGCGCCCC   CCG
                                ||||  ||||||||   |||
```

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                                GGCG  GCGCGGGG   GGC
                                  AG       A__
GAM394  PKMYT1   5'  CCGCGCGCGTTCACGGGCC   11060        CCC   CC
                                CCGCGCGC   CGC  GGCC
                                ||||||||   |||  ||||
                                GGCGCGCG   GTG  CCGG
                                    CAA   C_
GAM394  PLCL2    5'  CCGCCGCCGCCTCGGGCC    11061       G   CC  CCC
                                CCGCCGC CGCC  CG   GGCC
                                |||||||  ||||  ||   ||||
                                GGCGGCG GCGG  GC   CCGG
                                    _   A_  ___
GAM394  PPP1R13B 5'  CCGCCGTGCTCTCCGGCCCGGC 11062       C  GCC  C
           CG                     CCGCCG GC   CC GCCCGGCCG
                                ||||||  ||   ||  |||||||||
                                GGCGGC CG   GG CGGGCCGGC
                                   A  AGA  C
GAM394  PRDM13   5'  CCGACGTGCGTCCTCCGCCCG  11063     C  C   _  C
                                CCG CG GCG CC CCGCCCG
                                |||  ||  |||  ||  |||||||
                                GGC GC CGC GG GGCGGGC
                                  T  A   A  A
GAM394  QKI      5'  CCGCCGCCGCTCTCGGCC    11065        G   CCCCGCC
                                CCGCCGC CGC      CGGCC
                                |||||||  |||      |||||
                                GGCGGCG GCG      GCCGG
                                    _   AGA_____
GAM394  QKI      5'  CCGCCGCGGCGCCTCTGCC    11064         _   CCC
                                CCGCCGCG CGCC   GCC
                                ||||||||  ||||   |||
                                GGCGGCGC GCGG   CGG
                                    C    AGA
GAM394  RAB22A   5'  CCGCCGCGGCCTTCCGGGAGCC 11066        C   C_   CCC
           G                     CCGCCGCG GCC  CCG   GGCCG
                                ||||||||  |||  |||   |||||
                                GGCGGCGC CGG  GGC   TCGGC
                                    _   AA   CC_
GAM394  RAB32    5'  CCGCCGCGCCCCCGGCGGCCG  11067       GC      CC
                                CCGCCGC  GCCCCCG  CGGCCG
                                |||||||  |||||||  ||||||
                                GGCGGCG  CGGGGGC  GCCGGC
                                    __      C_
GAM394  RAB3IL1  5'  CCGCCGCGTCCTCCCAGCGCCG 11068        CG  _   _  _
                                CCGCCGCG  CC CCC GC CCG
                                ||||||||  ||  |||  ||  |||
                                GGCGGCGC  GG GGG CG GGC
                                    A_  A   T  C
GAM394  RHOBTB3  5'  CCGCCGCGCCTCCTCGGC    11069         GCCCCCG  _
                                CCGCCGCGC      CC CGGC
                                |||||||||      ||  ||||
```

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                                GGCGGCGCG      GG GCCG
                                     GA_____  A
GAM394  RHOBTB3  5' CCTCGCGCGCCTCCACC     11070    GC      C
                                CC  CGCGCGCC CCGCC
                                ||  |||||||| |||||
                                GG  GCGCGCGG GGTGG
                                 A_       A
GAM394  RIP5     5' CCGTCGCGCCGCCCGGGCC   11071    _     CCC     _
                                CCG CGCGCC   GCCCGG CC
                                ||| ||||||   |||||| ||
                                GGC GCGCGG   CGGGCC GG
                                 A     ___      C
GAM394  RNASE6PL 5' CCGCCGCGCTCCCTCCGC    11072         G  _
                                CCGCCGCGC CCC CCGC
                                ||||||||| ||| ||||
                                GGCGGCGCG GGG GGCG
                                     A  A
GAM394  RNPC1    5' CCGCCGTGCGCGCCGAGC    11073       C   CCCC  C
                                CCGCCG GCGC    GCC GGC
                                |||||| ||||    ||| |||
                                GGCGGC CGCG    CGG TCG
                                   A    _____  C
GAM394  SEC24D   5' CCGCCGCGCCTCTTCCCCGGCC 11074         GCCCCCG
           G                     CCGCCGCGC      CCCGGCCG
                                 |||||||||      ||||||||
                                 GGCGGCGCG      GGGCCGGC
                                      GAGAAG_
GAM394  SERF1B   5' CCTCGTGGGCCCTCCGCCCGGC 11075    G  C__   _
                                CC CG   GCCC CCGCCCGGC
                                || ||   |||| |||||||||
                                GG GC   CGGG GGCGGGCCG
                                 A  ACC    A
GAM394  SIAT8C   5' CGCCGTGCGTCCCCGGCCG   11076      C  C    C
                                CGCCG GCG CCCCG CCG
                                ||||| ||| ||||| |||
                                GCGGC CGC GGGGC GGC
                                   A  A    C
GAM394  SLC21A11 5' CGTCGCCGCCCGAGCCGTTGGC 11077    C  G    CC  C__
                                CG CGC CGCCC  GCC   GGC
                                || ||| |||||  |||   |||
                                GC GCG GCGGG  CGG   CCG
                                 A  _    CT   CAA
GAM394  SLC39A3  5' CCGCTGCACGCCCAACGGCCG  11078     C      CCGCC
                                CCGC GCGCGCCC    CGGCCG
                                |||| ||||||||    ||||||
                                GGCG CGTGCGGG    GCCGGC
                                  A       TT___
GAM394  SSB-3    5' CCGCTGCGCGCTCCGCCAGCC  11079     C     CC    C
                                CCGC GCGCGC  CCGCC GGCC
                                |||| ||||||  ||||| ||||
```

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                                GGCG CGCGCG  GGCGG TCGG
                                  A     A_    _
GAM394  STARD7   5'  CCGCCCCGCGTCCCCGCC    11080      G    C
                                CCGCC CGCG CCCCGCC
                                ||||| |||| |||||||
                                GGCGG GCGC GGGGCGG
                                  G    A
GAM394  STARD7   5'  CCGCCCCGCGTCCCCGCC    11080      G    C
                                CCGCC CGCG CCCCGCC
                                ||||| |||| |||||||
                                GGCGG GCGC GGGGCGG
                                  G    A
GAM394  TAF5L    5'  CCGCCGCCGCCTCCGGGATCG  11081       G    C   CCC GC
                                CCGCCGC CGCC CCG   G  CG
                                ||||||| |||| |||   |  ||
                                GGCGGCG GCGG GGC   C  GC
                                   _    A   C__ TA
GAM394  TRAF3    5'  CCGCCGCGGCTGCCGCCGGC   11082        C  CC     C
                                CCGCCGCG GC  CCGCC GGC
                                |||||||| ||  ||||| |||
                                GGCGGCGC CG  GGCGG CCG
                                   _ AC    _
GAM394  TRIM28   5'  CCGCCACGCGCCTCCTGGGCCG 11083           C  GCCC
                                CCGCCGCGCGCC CC    GGCCG
                                |||||||||||| ||    |||||
                                GGCGGTGCGCGG GG    CCGGC
                                     A  AC__
GAM394  ZDHHC2   5'  CCGCCGTTCCCCGCCGCCCGGC 11084       CGCG  _
           CG                    CCGCCG    CCC CCGCCCGGCCG
                                ||||||    ||| ||||||||||
                                GGCGGC    GGG GGCGGGCCGGC
                                   AAG_  C
GAM394  ZDHHC5   5'  GCCGCGCGCTCCCGCCAGGC   11085        C     C
                                GCCGCGCGC CCCGCC GGC
                                ||||||||| |||||| |||
                                CGGCGCGCG GGGCGG CCG
                                     A     T
GAM394  LOC115708 3'  CCCCGACACACTTGCCTGG    11086    G  _    CCCC   C
                                CC CCG CGCGC    GCC GG
                                || ||| |||||    ||| ||
                                GG GGC GTGTG    CGG CC
                                 _  T    AA__   A
GAM394  LOC121536 5'  GCTGCCGCCCCCGCCGCCG    11087    C  G        CG
                                GC GC CGCCCCCGCC  GCCG
                                || || ||||||||||  ||||
                                CG CG GCGGGGGCGG  CGGC
                                 A  _         __
GAM394  LOC125150 5'  CCGCCGCGACGCTCCAGC     11088         _  C  C
                                CCGCCGCG CGC CC GC
                                |||||||| ||| || ||
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                                GGCGGCGC GCG GG CG
                                     T  A  T
GAM394  LOC138128 5'  CCTGCGCAGCTGCCCGGCCG  11089    _   _ CCCC
                                CC GCGC GC    GCCCGGCCG
                                || |||| ||    |||||||||
                                GG CGCG CG    CGGGCCGGC
                                 A    T  A___
GAM394  LOC145990 5'  CCGCCGCCGCCCCCGCC     11090        G
                                CCGCCGC CGCCCCCGCC
                                ||||||| ||||||||||
                                GGCGGCG GCGGGGGCGG
                                      _
GAM394  LOC146223 5'  CCGCCGCCGCCTCTCGCCCG  11091        G   CC_
                                CCGCCGC CGCC   CGCCCG
                                ||||||| ||||   ||||||
                                GGCGGCG GCGG   GCGGGC
                                    _   AGA
GAM394  LOC147165 3'  GCTCGCTCACCCGCCCGGC   11092   _  G    CC
                                GC CGC CGCCC  GCCCGGC
                                || ||| |||||  |||||||
                                CG GCG GTGGG  CGGGCCG
                                 A  A    __
GAM394  LOC150465 5'  CGCCGCGCGCCCGGGCC     11093          CCGCCC
                                CGCCGCGCGCCC     GGCC
                                ||||||||||||     ||||
                                GCGGCGCGCGGG     CCGG
                                      C_____
GAM394  LOC151009 5'  GCCTGCGCCCCCGACACC    11094    GC       _ _
                                GCC  GCGCCCCCG C CC
                                |||  ||||||||| | ||
                                CGG  CGCGGGGGC G GG
                                  A_       T T
GAM394  LOC152048 3'  CCGCCGCGGCTCCCGGGGC   11095        C  C   CCC
                                CCGCCGCG GC CCCG   GGC
                                |||||||| || ||||   |||
                                GGCGGCGC CG GGGC   CCG
                                    _ A   C__
GAM394  LOC152559 5'  CCGCTGGCGCCCCCGCCC    11096     CGC
                                CCGC   GCGCCCCCGCCC
                                ||||   ||||||||||||
                                GGCG   CGCGGGGGCGGG
                                  AC_
GAM394  LOC154428 5'  CCGCCTGCGCTCCCGGAAGGCC 11097      GC   C   CCC
          G                      CCGCC  GCGC CCCG   GGCCG
                                |||||  |||| ||||   |||||
                                GGCGG  CGCG GGGC   CCGGC
                                  A_   A   CTT
GAM394  LOC155382 5'  CCGCCCGCGCCCCCAGCTCGGC 11098      G       _ C
                                CCGCC CGCGCCCCC GC CGGC
                                ||||| ||||||||| || ||||
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                                GGCGG GCGCGGGGG CG GCCG
                                  _       T  A
GAM394  LOC159201 5'  GCCGCGCGCCACAGCGGCCG  11099          CCC  C_
                                GCCGCGCGCC  GC  CGGCCG
                                ||||||||||  ||  ||||||
                                CGGCGCGCGG  TG  GCCGGC
                                     ____  TC
GAM394  LOC165253 5'  CCGCCGCGGGCCTGCGGTCCCG 11100        C  CC  __
          GCCG                    CCGCCGCG GCC  CG  CCCGGCCG
                                ||||||||| |||  ||  ||||||||
                                GGCGGCGC CGG  GC  GGGCCGGC
                                    C  AC  CA
GAM394  LOC200862 5'  CCGTGTGCGCCCCCTGGCCCG  11101     C__       __
                                CCG  GCGCCCCC  GCCCG
                                |||  ||||||||  |||||
                                GGC  CGCGGGGG  CGGGC
                                  ACA       AC
GAM394  LOC201780 5'  CCGCCGCGTGCCTCTCGCC   11102        C  CC_
                                CCGCCGCG GCC  CGCC
                                |||||||| |||  ||||
                                GGCGGCGC CGG  GCGG
                                    A  AGA
GAM394  LOC203197 5'  CCCGCCCCCCCGCCCGGCC    11103    G  G
                                CC CGC CCCCCGCCCGGCC
                                || ||| ||||||||||||
                                GG GCG GGGGGCGGGCCGG
                                 _  _
GAM394  LOC203197 5'  CCGCCCGGCCGGCCCCGCTCGG 11104      __ G  C     C  C
          TCG                     CCGCC  GC CG CCCCGC CGG CG
                                |||||  || || |||||| ||| ||
                                GGCGG  CG GC GGGGCG GCC GC
                                  GC  _  C     A  A
GAM394  LOC221184 5'  GCCCGCGCTCCGAGCC     11106     G    CC  CCC
                                GCC CGCGC  CCG  GGCC
                                ||| |||||  |||  ||||
                                CGG GCGCG  GGC  TCGG
                                  _    A_  ____
GAM394  LOC221184 5'  CGCGTGCGCTCCCAGCC     11105     C C   CCCCG
                                CGC G GCGC    CCCGGCC
                                ||| | ||||    |||||||
                                GCG C CGCG    GGGTCGG
                                  _ A   A_____
GAM394  LOC254573 5'  CCGCCGCGCGCCCTCCCG    11107          CCG
                                CCGCCGCGCGCCC  CCCG
                                ||||||||||||  ||||
                                GGCGGCGCGCGGG  GGGC
                                       A__
GAM394  LOC255082 5'  CGTCGCGCGCCTCCAGTCG   11108    C      C  CC
                                CG CGCGCGCC CCG  CG
                                || |||||||| |||  ||
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                                GC GCGCGCGG GGT  GC
                                 A       A   CA
GAM394   LOC255854 5'  CCTGCGCGCCCCGGCC      11109    _       CGCCC
                                CC GCGCGCCCC    GGCC
                                || |||||||||    ||||
                                GG CGCGCGGGG    CCGG
                                 A       _____
GAM394   LOC256160 5'  CCGCCGCGTGCCTCTCGCC    11102        C   CC_
                                CCGCCGCG GCC   CGCC
                                |||||||| |||   ||||
                                GGCGGCGC CGG   GCGG
                                     A   AGA
GAM394   LOC256329 3'  CCGCCCGCGCCCTCCC      11110      G      CCG
                                CCGCC CGCGCCC   CCC
                                ||||| |||||||   |||
                                GGCGG GCGCGGG   GGG
                                   _      A__
GAM394   LOC256949 5'  CCGCCGCTGCCTCCTCCG    11111        GC   C  GC
                                CCGCCGC  GCC CC  CCG
                                |||||||  ||| ||  |||
                                GGCGGCG  CGG GG  GGC
                                    A_   A  A_
GAM394   LOC256973 3'  CCGCCGCGCCCCTCCCGGAGGC 11112          G  _   CCC
            CG                    CCGCCGCGC CC CCCG   GGCCG
                                |||||||||| || ||||   |||||
                                GGCGGCGCG GG GGGC   CCGGC
                                     G  A    CT_
GAM394   LOC56961  5'  CCGCCGCGTCCCCCGCCC    11113        CG
                                CCGCCGCG  CCCCCGCCC
                                ||||||||  |||||||||
                                GGCGGCGC  GGGGGCGGG
                                    A_
GAM394   LOC92299  5'  CCGCCGCGGCCTCCAACCACCG 11114         C   _  C   __
            GCCG                    CCGCCGCG GCC CC GCC  CGGCCG
                                |||||||| ||| || |||  ||||||
                                GGCGGCGC CGG GG TGG  GCCGGC
                                    _  A  T   TG
GAM394   LOC92305  5'  GCGGCGGCCGCCGCCCGGCCG  11115    C   C   C
                                GC GCG GCC CCGCCCGGCCG
                                || ||| ||| ||||||||||
                                CG CGC CGG GGCGGGCCGGC
                                 C   _   C
GAM394   LOC92340  3'  CCACCGCAACTTCTCCTGCCTG 11116         _ GCC_  C   C
            GC                    CCGCCGCG C    CC GCC GGC
                                |||||||| |    || ||| |||
                                GGTGGCGT G    GG CGG CCG
                                     T AAGA  A   A
GAM394   LOC93512  3'  GCTCGCTCACCCGCCCGGC    11092    _  G    CC
                                GC CGC CGCCC  GCCCGGC
                                || ||| |||||  |||||||
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                                CG GCG GTGGG  CGGGCCG
                                 A  A    __
GAM395  CNOT4    5'  TAAAATGTAGGACTTTGAC   11119      ATG    TTT
                                TAAAAT  AGGAT  TTTGAC
                                ||||||  |||||  ||||||
                                ATTTTA  TCCTG  AAACTG
                                   CA_   ___
GAM395  PAPSS2   3'  TAAAATATCAGGAAGAATCTTG 11120       G   TTT_
           A                     TAAAATAT AGGA   TTTTGA
                                ||||||||| ||||   ||||||
                                ATTTTATA TCCT   AGAACT
                                     G   TCTT
GAM395  ZDHHC3   3'  TAAAATGTGGGGACTTTTTT  11121      A  A
                                TAAAAT TG GGATTTTTTT
                                |||||| || ||||||||||
                                ATTTTA AC CCTGAAAAAA
                                   C  C
GAM396  ABCC11   5'  GCCTGCTCTTTCCTCTCC   11124    GC  C   C
                                GC  GC CTT TCCTCTCC
                                ||  || ||| ||||||||
                                CG  CG GAA AGGAGAGG
                                 GA  A  _
GAM396  ABCD1    3'  GTGCGTCCCTCTCCCCTC   11125   C   CCCT  T
                                G GCG   TC CCTCTCCCCTC
                                | |||   || ||||||||||
                                C CGC   AG GGAGAGGGGAG
                                 A  _____ _
GAM396  ADAMTS8  3'  GCCGCCCCATACCCTCTCCTCT 11126    G     TC_      C
                                GC CGCCCT   TCCTCTCC CT
                                || ||||||   |||||||| ||
                                CG GCGGGG   GGGAGAGG GA
                                  _     TAT       A
GAM396  AES      3'  GCCTCTGTCTCCCCTC     11127    CT   CC
                                GCC  TCT  TCTCCCCTC
                                |||  |||  |||||||||
                                CGG  AGA  AGAGGGGAG
                                  __   C_
GAM396  AQP6     5'  CGCTCTCCACCTCTCCTCC   11128    C   T     _
                                CGC CTTC CCTCTCC CC
                                ||| |||| ||||||| ||
                                GCG GAGG GGAGAGG GG
                                  A   T      A
GAM396  ARSD     3'  GCGGCTCTTCCTCTCCTCTC  11129    C  C  TC      C
                                GCG GC CT  TCCTCTCC CTC
                                ||| || ||  |||||||| |||
                                CGC CG GA  AGGAGAGG GAG
                                  _ A __       A
GAM396  ATP8A2   3'  GCTCGCCCTTCTTTTCTGCTCC 11130    G       CC   CCC
                                GC CGCCCTTCT  TCT   CTCC
                                || |||||||||  |||   ||||
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                                CG GCGGGAAGA  AGA   GAGG
                                 A        AA   C__
GAM396  B4GALT4   3'  CGTCGCCTTTTCTCCCCTC   11131    _   C  CTCC
                                CG CGCC TT    TCTCCCCTC
                                || |||| ||    |||||||||
                                GC GCGG AA    AGAGGGGAG
                                 A    A  ____
GAM396  CD34      5'  ACGCGCTCTTCCCGCCCCCTCC 11132       C    T  T T
                                GCGCGC CTTC CC C CCCCTCC
                                |||||| |||| || | |||||||
                                TGCGCG GAAG GG G GGGGAGG
                                   A    _ C _
GAM396  CDKN1A    3'  GCCCTTCTTCTTGTGTGTCCCT 11133       C  C_____    C   III
            TCCG                   CCTTCT CT     TCCC TCC   G
                                |||||| ||     |||| |||   |
                                GGAAGA GA     AGGG AGG   C
                                   A  ACACAC    A   III
GAM396  CNP       3'  GCACGTTTCCCTCTCCCCT    11134       CCC   T
                                GCGCG   TTC CCTCTCCCCT
                                ||||||   ||| ||||||||||
                                CGTGC   AAG GGAGAGGGGA
                                  A__   _
GAM396  COL1A1    3'  GCCCTTCCTGACTCTCCTCC   11135         CCT   C
                                GCCCTTCT   CTC CCTCC
                                ||||||||   ||| |||||
                                CGGGAAGG   GAG GGAGG
                                     ACT   A
GAM396  CRTL1     5'  GCGCTCTTTCTCCTCACC     11136      C  _     T
                                GCGC CTT CTCCTC CC
                                |||| ||| |||||| ||
                                CGCG GAA GAGGAG GG
                                  A  A     T
GAM396  DES       3'  GCCTCTCTCCTCTCCTCTC    11137     C         C
                                GCC TTCTCCTCTCC CTC
                                ||| |||||||||| |||
                                CGG GAGAGGAGAGG GAG
                                  A         A
GAM396  DLX4      5'  GCCCCCCCATGACTTTCCCCTC 11138         C___  C
            C                    GCCCTTCT    CT TCCCCTCC
                                |||||||    || ||||||||
                                CGGGGGGG    GA AGGGGAGG
                                     TACT  A
GAM396  DXYS155E  3'  GCGCTCCTTCTCCTCCTCC    11139      _        TC
                                GCGC CCTTCTCCTC  CC
                                |||| ||||||||||  ||
                                CGCG GGAAGAGGAG  GG
                                  A         GA
GAM396  EGR3      3'  GCGCTCCTTACCCCCTCC     11140      _   CT
                                GCGC CCTT  CCTCTCC
                                |||| ||||  |||||||
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                                CGCG GGAA  GGGGAGG
                                  A    TG
GAM396  EPHB2    3'  GCGGCCCCTGTCTCTCCCCT   11142     C     CTC
                                GCG GCCCTT   CTCTCCCCT
                                ||| ||||||   |||||||||
                                CGC CGGGGA   GAGAGGGGA
                                  _     CA_
GAM396  EPHB2    3'  GCCCCTGTCTCTCCCCT     11141       CTC
                                GCCCTT   CTCTCCCCT
                                ||||||   |||||||||
                                CGGGGA   GAGAGGGGA
                                   CA_
GAM396  FKBP6    3'  GCTGCGCTTTCCCCTCCCTTC  11143    _   CCTTC       C
                                GC GCGC    TCCTCTCCC TC
                                || ||||    ||||||||| ||
                                CG CGCG    AGGGGAGGG AG
                                 A   AA___       A
GAM396  GNA15    3'  GCGTTCCTTCTCCTGTCC    11144     C_       C
                                GCG  CCTTCTCCT TCC
                                |||  ||||||||| |||
                                CGC  GGAAGAGGA AGG
                                  AA        C
GAM396  HCFC1    3'  GCGCGCTCCTCTCTCTGCTTTC 11145       C     _ _  CC
          C                      GCGCGC CTTCTC CT CT  CC
                                |||||| |||||| || ||  ||
                                CGCGCG GGAGAG GA GA  GG
                                   A     A  C  AA
GAM396  HEXB     3'  GCTGTGGCCTTTTTCCCCTCC  11146    GC__   C  C
                                GC    GCC TT TCCTCTCC
                                ||    ||| || ||||||||
                                CG    CGG AA AGGGGAGG
                                 ACAC   A  A
GAM396  HOXB6    3'  CGCGTCCTCCCTCCC       11147      CCC     T
                                CGCG   TTCTCC CTCCC
                                ||||   |||||| |||||
                                GCGC   AGGAGG GAGGG
                                  ____     _
GAM396  HOXD13   5'  GCGCGCCTCCTCCCTCCTCTCC 11148        C     T    C
                                GCGCGCC TTCTCC CTCC CTCC
                                ||||||| |||||| |||| ||||
                                CGCGCGG AGGAGG GAGG GAGG
                                   _     _    A
GAM396  ITPR1    5'  GCGGCTTTCTCTCTCC      11149     C  CC     C
                                GCG GC  TTCTC TCTCC
                                ||| ||  ||||| |||||
                                CGC CG  AAGAG AGAGG
                                  _ A_    _
GAM396  KCNA4    5'  GCACGCCCCATGCTCTCTCT   11150          T__   _
                                GCGCGCCCT   CTC CTCT
                                |||||||||   ||| ||||
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                                CGTGCGGGG  GAG GAGA
                                     TAC  A
GAM396  KPNB1   5' GCTCCCCTTCCTCTCCTCT  11151   G   C     C
                                GC CCCTT TCCTCTCC CT
                                || ||||| |||||||| ||
                                CG GGGGA AGGAGAGG GA
                                 A   _     A
GAM396  LZTS1   3' GCTGCCTGTCTCTCCCCTC  11152   GC  CTTCTC
                                GC  GCC    CTCTCCCCTC
                                ||  |||    ||||||||||
                                CG  CGG    GAGAGGGGAG
                                 A_  ACA___
GAM396  MYLK2   3' CCCTTGGCTTCTCCCCTCC  11153     CTCC
                                CCCTT   TCTCCCCTCC
                                |||||   ||||||||||
                                GGGAA   AGAGGGGAGG
                                   CCGA
GAM396  NNMT    5' GCCCTCCTTCTCTTTCCTC  11154       C   CC
                                GCCCTTCT CTCT  CCTC
                                |||||||| ||||  ||||
                                CGGGAGGA GAGA  GGAG
                                     A   AA
GAM396  NR2F6   5' GCGCCCCCACCGCGCTCTTCCC 11155      TC ___   C
          TCC                     GCGCCCT  TC   CTCT CCCTCC
                                |||||||  ||   |||| ||||||
                                CGCGGGG  GG   GAGA GGGAGG
                                    GT  CGC   A
GAM396  OGG1    5' GCTCGCCTTTCCCCCTCC   11156   G   C    T
                                GC CGCC TTCTCC CTCC
                                || |||| |||||| ||||
                                CG GCGG AAGGGG GAGG
                                 A   A    _
GAM396  OGG1    5' GCTCGCCTTTCCCCCTCC   11156   G   C    T
                                GC CGCC TTCTCC CTCC
                                || |||| |||||| ||||
                                CG GCGG AAGGGG GAGG
                                 A   A    _
GAM396  OGG1    5' GCTCGCCTTTCCCCCTCC   11156   G   C    T
                                GC CGCC TTCTCC CTCC
                                || |||| |||||| ||||
                                CG GCGG AAGGGG GAGG
                                 A   A    _
GAM396  OSCAR   5' CGCACCCTCTCCCCTCC    11157       T
                                CGCGCCCT CTCCTCTCC
                                |||||||| |||||||||
                                GCGTGGGA GAGGGGAGG
                                      _
GAM396  OSCAR   5' CGCACCCTCTCCCCTCC    11157       T
                                CGCGCCCT CTCCTCTCC
                                |||||||| |||||||||
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                                GCGTGGGA GAGGGGAGG
                                        _
GAM396  OSCAR    5'  CGCACCCTCTCCCCTCC     11157        T
                                CGCGCCCT CTCCTCTCC
                                |||||||| |||||||||
                                GCGTGGGA GAGGGGAGG
                                        _
GAM396  PAWR     5'  GCCGCTGCCTCCTCTTCCTTCC 11158    _ _      C  C
                                GCC CT TCTCCTCT CC TCC
                                ||| || |||||||| || |||
                                CGG GA GGAGGAGA GG AGG
                                  C  C       A  A
GAM396  PIK3CG   5'  CGTGCCCTCCCTTTTCCTCC   11159    C       CCTCTCC
                                CG GCCCTTCT      CCTCC
                                || ||||||||      |||||
                                GC CGGGAGGG      GGAGG
                                 A       AAAA___
GAM396  POMC     5'  GCGGCTCTTCTTCCCCTC    11160     C  C    CCTC
                                GCG GC CTTCT    TCCCCTC
                                ||| || |||||    |||||||
                                CGC CG GAAGA    AGGGGAG
                                  _ A    _____
GAM396  POU3F1   3'  GCGGCTCTCGCGACCTCCCCTC 11161     C  C   CTCC
          C                      GCG GC CTT    TCTCCCCTCC
                                ||| || |||    ||||||||||
                                CGC CG GAG    GGAGGGGAGG
                                  _ A   CGCT
GAM396  POU3F2   5'  GCTCGCTCTTTCTGTCTCCTCT 11162    G   C ______
          C                      GC CGC CT     TCTCCTCTC
                                || ||| ||     |||||||||
                                CG GCG GA     AGAGGAGAG
                                 A   A  AAGAC
GAM396  PPP1R11  3'  CGTCCTCCTCTTCCTCTTCCCT 11163    _ _    _    C
          C                      CG CC CTTCT CCTCT CCCTC
                                || || ||||| ||||| |||||
                                GC GG GGAGA GGAGA GGGAG
                                 A A    A    A
GAM396  PPP1R11  3'  CGTCCTCCTCTTCCTCTTCCCT 11163    _ _    _    C
          C                      CG CC CTTCT CCTCT CCCTC
                                || || ||||| ||||| |||||
                                GC GG GGAGA GGAGA GGGAG
                                 A A    A    A
GAM396  RFC2     5'  CGCGCCTCCTCTTCCCTC    11164       CTTC     C
                                CGCGCC    TCCTCT CCCTC
                                ||||||    |||||| |||||
                                GCGCGG    AGGAGA GGGAG
                                    _____     A
GAM396  SGCE     5'  CCGTCCTCGATTCTCCCCTCC  11165    C    C__
                                CC TTCTC   TCTCCCCTCC
                                || |||||   ||||||||||
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                                GG AGGAG   AGAGGGGAGG
                                 C    CTA
GAM396  SLC22A7  3'  GCCTGCCCTTCTGCTCTCC   11166   GC      C
                                GC  GCCCTTCT CTCTCC
                                ||  |||||||| ||||||
                                CG  CGGGAAGA GAGAGG
                                 GA       C
GAM396  SLC22A7  3'  GCCTGCCCTTCTGCTCTCC   11166   GC      C
                                GC  GCCCTTCT CTCTCC
                                ||  |||||||| ||||||
                                CG  CGGGAAGA GAGAGG
                                 GA       C
GAM396  SLC25A6  3'  GCGCCCCTTTTCTAGAGCCTTC 11167     G    C  CTCTC  C
           C                     GCGC CCCTT TC    CC TCC
                                |||| ||||| ||    || |||
                                CGCG GGGAA AG    GG AGG
                                  _    A  ATCTC  A
GAM396  SLC6A8   5'  GCGCGCCTCGCCCTCTCC    11168       C  C
                                GCGCGCC TT TCCTCTCC
                                ||||||| || ||||||||
                                CGCGCGG AG GGGAGAGG
                                   _ C
GAM396  SOX11    3'  GCGGGTCCTACCTCCCCTCC   11170    CG_  CT
                                GCG   CC  TCTCCTCTCC
                                |||   ||  ||||||||||
                                CGC   GG  GGAGGGGAGG
                                  CCA  AT
GAM396  SOX11    3'  GCATCTTCTTCTCTCCCCTCC  11169    CC    C
                                GCG  CTTCT CTCTCCCCTCC
                                |||  ||||| ||||||||||
                                CGT  GAAGA GAGAGGGGAGG
                                  A_    A
GAM396  SOX4     3'  GCGCTGGGTTCTCCCCTCC   11171     GCCC
                                GCGC    TTCTCCTCTCC
                                ||||    ||||||||||
                                CGCG    AAGAGGGGAGG
                                   ACCC
GAM396  T        5'  GCGCGCCTCCCTCCCCTC    11172        CTTC   T
                                GCGCGCC    TCC CTCCCCTC
                                |||||||    ||| ||||||||
                                CGCGCGG    AGG GAGGGGAG
                                     ____  _
GAM396  TEAD3    3'  CGCTGAGCCCTCCTCTCCTCTC 11173     ___    TTC      C
                                CGC   GCCC   TCCTCTCC CTC
                                |||   ||||   |||||||| |||
                                GCG   CGGG   AGGAGAGG GAG
                                  ACT    ___       A
GAM396  TRHDE    5'  GCTGCTCTTCTCGGCCCCCTCC 11174    GC  C     CTC
                                GC  GC CTTCTC   TCCCCTCC
                                ||  || ||||||   ||||||||
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                                CG  CG GAAGAG   GGGGGAGG
                                 A_  A     CC_
GAM396  TRIM34   5'  GCTTCCTCCTCTTCCTTC    11175    CC       C  C
                                GC  TTCTCCTCT CC TC
                                ||  |||||||||| || ||
                                CG  AGGAGGAGA GG AG
                                 A_       A  A
GAM396  VEGF     5'  GCCCCCTCTCCTCTTCCTTC   11176    G        C  C
                                GC CCCTTCTCCTCT CC TC
                                || ||||||||||||| || ||
                                CG GGGGAGAGGAGA GG AG
                                 _         A  A
GAM396  VEGFB    3'  GCTGCCTCCCAGTCTCCTCT   11177    _ G_   T_
                                GC GC  CCC  TCTCCTCT
                                || ||  |||  ||||||||
                                CG CG  GGG  AGAGGAGA
                                 A  GA   TC
GAM396  ZNF278   5'  GCGCCACTCTCTCCTCTCC    11178      _ _
                                GCGCC CT TCTCCTCTCC
                                ||||| || ||||||||||
                                CGCGG GA AGAGGAGAGG
                                   T  G
GAM396  ZNF278   5'  GCGCCACTCTCTCCTCTCC    11178      _ _
                                GCGCC CT TCTCCTCTCC
                                ||||| || ||||||||||
                                CGCGG GA AGAGGAGAGG
                                   T  G
GAM396  ZNF278   5'  GCGCCACTCTCTCCTCTCC    11178      _ _
                                GCGCC CT TCTCCTCTCC
                                ||||| || ||||||||||
                                CGCGG GA AGAGGAGAGG
                                   T  G
GAM396  ZNF278   5'  GCGCCACTCTCTCCTCTCC    11178      _ _
                                GCGCC CT TCTCCTCTCC
                                ||||| || ||||||||||
                                CGCGG GA AGAGGAGAGG
                                   T  G
GAM396  20D7-FC4 3'  GCTCTCCCCTCCCCTCC     11179    CCT
                                GC   TCTCCTCTCCCCTCC
                                ||   ||||||||||||||
                                CG   AGAGGGGAGGGGAGG
                                     ___
GAM396  AAMP     3'  GCCCCACCCTCCTCTTCCCTC  11180    G  _       C
                                GC CCC TTCTCCTCT CCCTC
                                || ||| ||||||||| |||||
                                CG GGG GGGAGGAGA GGGAG
                                 _  T       A
GAM396  AP3D1    3'  GCGGCCCTTCCTTCCCCTC    11181     C    TC   C
                                GCG GCCCT  TCCT TCCCCTC
                                ||| |||||  |||| |||||||
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                                CGC CGGGA  AGGA AGGGGAG
                                  _   __   _
GAM396  AP3D1    5' GCGGCCCTTCCTTCCCCTC   11181    C    TC   C
                                GCG GCCCT  TCCT TCCCCTC
                                ||| |||||  |||| |||||||
                                CGC CGGGA  AGGA AGGGGAG
                                  _   __   _
GAM396  AQP10    3' GCCGCCCTCCTTCCCTCC    11182    G       C
                                GC CGCCCTTCT CTCTCC
                                || |||||||| ||||||
                                CG GCGGGAGGA GGGAGG
                                  _       A
GAM396  CARD9    3' GCGCGTCCTTCTCCTGCAGGCC 11183      C       CTCC_
                                GCGCG CCTTCTCCT    CC
                                ||||| |||||||||    ||
                                CGCGC GGAAGAGGA    GG
                                   A       CGTCC
GAM396  CCT7     5' GCGGCCCTCCACTCTCCCCTC  11184    C      TC
                                GCG GCCCTTC  CTCTCCCCTC
                                ||| |||||||  ||||||||||
                                CGC CGGGAGG  GAGAGGGGAG
                                  _      T_
GAM396  CDH24    3' GCCGCCTCCCCCTTTCCTTTCC 11185    G   C     C   CC
                                GC CGCC TTCTCCT TCC  TCC
                                || |||| ||||||| |||  |||
                                CG GCGG AGGGGGA AGG  AGG
                                  _   _      A   AA
GAM396  D123     5' GCTGCCTTTCCCTCTCC     11186    GC   C   T
                                GC  GCC TTC CCTCTCC
                                ||  ||| ||| |||||||
                                CG  CGG AAG GGAGAGG
                                 A_   A   _
GAM396  DAPK2    3' GCGTGTCCTAACCTCCCCT    11187    CCC    CC
                                GCG   TTCT  TCTCCCCT
                                |||   ||||  ||||||||
                                CGC   AGGA  GGAGGGGA
                                  AC_    TT
GAM396  DKFZP434E2318 5' GCGCCCTTTCTCCGCCTC    11188        CTCC    _
                                GCGCCCTT    TCTCC CCTC
                                ||||||||    ||||| ||||
                                CGCGGGAA    AGAGG GGAG
                                     _____     C
GAM396  DKFZp434K114 5' CCCTTCCGGATTCCCCTCC    11189       CCTC
                                CCCTTCT    TCCCCTCC
                                |||||||    ||||||||
                                GGGAAGG    AGGGGAGG
                                    CCTA
GAM396  DKFZp434N0650 3' GCGGCCCTTTCCCCTCC     11190     C     C
                                GCG GCCCTT TCCTCTCC
                                ||| |||||| ||||||||
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                                CGC CGGGAA AGGGGAGG
                                  _     _
GAM396  DKFZp586I021 3'  CGCCCTCCCTTTTCCTCTCTCC 11191        ____      C
            TCC                    CGCCCTTC    TCCTCTC CCTCC
                                   ||||||||    ||||||| |||||
                                   GCGGGAGG    AGGAGAG GGAGG
                                       GAAA      A
GAM396  DKK2     5'  GCTTTTCTCTCCTCTCTTTTCC 11192    GCCC        CCC
                                   GC    TTCTCCTCTC   TCC
                                   ||    ||||||||||   |||
                                   CG    GAGAGGAGAG   AGG
                                    AAAA         AAA
GAM396  FLJ10300 5'  GCGTCTCTTCTCCTCTCC    11193     CC_
                                   GCG   CTTCTCCTCTCC
                                   |||   ||||||||||||
                                   CGC   GAAGAGGAGAGG
                                     AGA
GAM396  FLJ10648 5'  GCCGCCCTCTCCTCTCC     11194    G     T
                                   GC CGCCCT CTCCTCTCC
                                   || |||||| |||||||||
                                   CG GCGGGA GAGGAGAGG
                                    _     _
GAM396  FLJ14566 3'  GCTTCCTCCTCTCCTCT     11195    CC         C
                                   GC  TTCTCCTCTCC CT
                                   ||  ||||||||||| ||
                                   CG  AGGAGGAGAGG GA
                                    A_          A
GAM396  FLJ14966 5'  GCCCTCCCTCTTCTTCCTTCC  11196        TC  _  C  C
                                   GCCCTTC  CT CT CC TCC
                                   |||||||  || || || |||
                                   CGGGAGG  GA GA GG AGG
                                       GA  A  A  A
GAM396  G0S2     3'  GCGCGCCCCCTCTGTCTCTCCC 11197          T  ___      C
              TTCC                    GCGCGCCCT CTC   CTCTCCC TCC
                                      ||||||||| |||   ||||||| |||
                                      CGCGCGGGG GAG   GAGAGGG AGG
                                           _  ACA      A
GAM396  H2AFY    5'  GCTCGCGCCTTTTCTCTCC    11198    G  _   CTC
                                   GC CGC CCTT   CTCTCC
                                   || ||| ||||   ||||||
                                   CG GCG GGAA   GAGAGG
                                    A  C    AA_
GAM396  H2AFY    5'  GCTCGCGCCTTTTCTCTCC    11198    G  _   CTC
                                   GC CGC CCTT   CTCTCC
                                   || ||| ||||   ||||||
                                   CG GCG GGAA   GAGAGG
                                    A  C    AA_
GAM396  HAND1    3'  GCTGCCTTCCTCTCCTCC     11199    GC   CTTC       _
                                   GC  GCC    TCCTCTCC CC
                                   ||  |||    |||||||| ||
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                                CG  CGG    AGGAGAGG GG
                                 A_   A___       A
GAM396  HSGP25L2G 3'  GCCTCCAGCCCCTCTCCCTTCC 11200     _  T_        C
                                GCC CT  CTCCTCTCCC TCC
                                ||| ||  |||||||||| |||
                                CGG GG  GGGGAGAGGG AGG
                                  A  TC         A
GAM396  KIAA0215 5'  GCTCGCTTTCTTCTCTTCCCTC 11201    G   CC    C    C
              C                  GC CGC  TTCT CTCT CCCTCC
                                || |||  |||| |||| ||||||
                                CG GCG  AAGA GAGA GGGAGG
                                 A  A_   A    A
GAM396  KIAA0247 3'  GCCTCTCGGCCTCCCCTCC    11202     CT    C_
                                GCC  TCTC  TCTCCCCTCC
                                |||  ||||  ||||||||||
                                CGG  AGAG  GGAGGGGAGG
                                  __    CC
GAM396  KIAA0316 3'  GCCTCTCCCCTCTCCTCT     11203     C         C
                                GCC TTCTCCTCTCC CT
                                ||| |||||||||| ||
                                CGG GAGGGGAGAGG GA
                                  A          A
GAM396  KIAA0542 3'  CGCCTTCTTTCTCCTCC      11204      C    CC     _
                                CGCC TTCT  TCTCC CC
                                |||| ||||  ||||| ||
                                GCGG AAGA  AGAGG GG
                                  _    A_    A
GAM396  KIAA0556 3'  ACAGCCTTTTTTTCCCCTCC   11205     C    CTCCTC
                                GCG CCTT     TCCCCTCC
                                ||| ||||     ||||||||
                                TGT GGAA     AGGGGAGG
                                  C    AAAA__
GAM396  KIAA0795 3'  GCAGCTTTCCTCTCCCCTCC   11206     C  CCTTC
                                GCG GC    TCCTCTCCCCTCC
                                ||| ||    ||||||||||||
                                CGT CG    AGGAGAGGGGAGG
                                  _  AA___
GAM396  KIAA1043 3'  GTGCTCCCTTTCCTCTCC     11207    C  G    C
                                G GC CCCTT TCCTCTCC
                                | || ||||| ||||||||
                                C CG GGGAA AGGAGAGG
                                 A  A    _
GAM396  KIAA1203 3'  GCAACTTCTTTCCTCTCC     11208     CC    __
                                GCG  CTTC  TCCTCTCC
                                |||  ||||  ||||||||
                                CGT  GAAG  AGGAGAGG
                                  T_    AA
GAM396  KIAA1211 5'  GCGGCTTCTTTCCTCTCC     11209     C  C_   C
                                GCG GC  CTT TCCTCTCC
                                ||| ||  ||| ||||||||
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                                CGC CG  GAA AGGAGAGG
                                  _ AA  _
GAM396  KIAA1237  3'  GCAGCTGGCCTCTCCCTTCC  11210    C  CCTTCT      C
                                GCG GC     CCTCTCCC TCC
                                ||| ||     |||||||| |||
                                CGT CG     GGAGAGGG AGG
                                  _ ACC___      A
GAM396  KIAA1280  5'  GCGTGCCCTCCTCTCCAACCTC 11211    C       C  CC
                                GCG GCCCTTCTC TCT  CCTC
                                ||| ||||||||| |||  ||||
                                CGC CGGGAGGAG AGG  GGAG
                                  A       _  TT
GAM396  KIAA1465  3'  GCGCCCCTCCCCTTCCCTC   11212          CTC
                                GCGCCCTTCTCCT  CCCTC
                                ||||||||||||  |||||
                                CGCGGGGAGGGGA  GGGAG
                                       A__
GAM396  KIAA1655  3'  GCTCGCCCTTCGGGTCTCTCC  11214   G      TC__
                                GC CGCCCTTC   CTCTCC
                                || ||||||||   ||||||
                                CG GCGGGAAG   GAGAGG
                                 A      CCCA
GAM396  KIAA1655  5'  ACGCCCTCCTCTCTCCTCC   11213         C   _
                                GCGCCCTTCTC TCTCC CC
                                |||||||||| ||||| ||
                                TGCGGGAGGAG AGAGG GG
                                      _   A
GAM396  KIAA1755  3'  GCCTGCCTCTCTCCCCT    11215    CT  C
                                GCC  TCTC TCTCCCCT
                                |||  |||| ||||||||
                                CGG  GGAG AGAGGGGA
                                  AC  _
GAM396  KIAA1904  3'  CCTTTCCTCTCCTTTCC    11216    C     CC
                                CCTT TCCTCTCC  TCC
                                |||| ||||||||  |||
                                GGAA AGGAGAGG  AGG
                                  _      AA
GAM396  MAFB    3'  GCGCGCCCTTCCTCCCTC   11217         TC
                                GCGCGCCCTTC  CTCTC
                                ||||||||||  |||||
                                CGCGCGGGAAG  GGGAG
                                       GA
GAM396  MAP3K6   3'  GCTGCCTTTGTCCTCTCC   11218   GC  C  C
                                GC  GCC TT TCCTCTCC
                                ||  ||| || ||||||||
                                CG  CGG AA AGGAGAGG
                                 A_  A  C
GAM396  MGC10871  5'  GCGCGCTGCTTCCCTCCCCT  11219     C_   CCT
                                GCGCGC  CTTCT  CTCCCCT
                                ||||||  |||||  |||||||
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                                CGCGCG  GAAGG   GAGGGGA
                                   AC    ___
GAM396  MGC4663  3'  CGTGCTGCTTTCCCCTCC    11220    C  C_  C
                                CG GC  CTT TCCTCTCC
                                || ||  ||| ||||||||
                                GC CG  GAA AGGGGAGG
                                 A  AC  _
GAM396  MO25     5'  GCGTTCCCTTCTCTGCCTCC  11221     CG      C_
                                GCG  CCCTTCTC  TCTCC
                                |||  ||||||||  |||||
                                CGC  GGGAAGAG  GGAGG
                                  AA       AC
GAM396  PASK     5'  GCGCCCTCTTCTCTGCCTC   11222       T  C   CC
                                GCGCCCT CT CTCT  CCTC
                                ||||||| || ||||  ||||
                                CGCGGGA GA GAGA  GGAG
                                    _  A   C_
GAM396  PHT2     5'  CGGCTCTTCTCTCCTCTCC   11223    C  C  __
                                CG GC CT  TCTCCTCTCC
                                || || ||  ||||||||||
                                GC CG GA  AGAGGAGAGG
                                 _  A  AG
GAM396  PHT2     5'  GCTCTTCTCTCCTCTCCTCTCC 11224    GCCC        C
                                GC    TTCTCCTCTCC CTCC
                                ||    |||||||||||| ||||
                                CG    GAGAGGAGAGG GAGG
                                 AGAA          A
GAM396  PPAP2B   5'  GCGCGCCTCTGCTTTCCTCT   11225       _  T __
                                GCGCGCC CT C  TCCTCT
                                ||||||| || |  ||||||
                                CGCGCGG GA G  AGGAGA
                                    A  C AA
GAM396  PRDM7    3'  GCCCTTCTGGACTCTTCCTTCC 11226        C__   C  C
                                GCCCTTCT   CTCT CC TCC
                                ||||||||   |||| || |||
                                CGGGAAGA   GAGA GG AGG
                                     CCT    A  A
GAM396  PRO1257  5'  GCGCCCCCTTCCTTCCTTC   11227       TC    C   CC
                                GCGCCCT  TCCT TCC  TC
                                |||||||  |||| |||  ||
                                CGCGGGG  AGGA AGG  AG
                                    GA   _   A_
GAM396  PSK      5'  CGCGCCCTCTCTGCCTCTCCTC 11228        _  _     C
          T                      CGCGCCCT TCT CCTCTCC CT
                                 |||||||| ||| ||||||| ||
                                 GCGCGGGA AGA GGAGAGG GA
                                     G   C      A
GAM396  RAB40C   3'  GCACCTCCTTTCTCCCCTC   11229      C    CC
                                GCGCC TTCT  TCTCCCCTC
                                ||||| ||||  |||||||||
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                                CGTGG AGGA  AGAGGGGAG
                                  _   A_
GAM396  SERHL    3'  GCCCGCCCTTCCTTCCTCC   6270     G       CC
                                GC CGCCCTTCT  TCTCC
                                || |||||||||  |||||
                                CG GCGGGAAGG  GGAGG
                                 G        AA
GAM396  SGK2     3'  GCGCCCTTTGCTCTTCTCCCCT 11230         __   C
                                GCGCCCTT  CTC TCTCCCCT
                                ||||||||  ||| ||||||||
                                CGCGGGAA  GAG AGAGGGGA
                                     AC   A
GAM396  SIAT8A   5'  GCGTCCCCTTGTCCCCTCC   11231     CG    C
                                GCG  CCCTT TCCTCTCC
                                |||  ||||| ||||||||
                                CGC  GGGAA AGGGGAGG
                                  AG    C
GAM396  SIAT8C   5'  GCCTGCCTTCCTCTCCCCT   11232     CT   _
                                GCC  TCT CCTCTCCCCT
                                |||  ||| ||||||||||
                                CGG  GGA GGAGAGGGGA
                                  AC   A
GAM396  SLC12A5  3'  GCCCCAGCTCCTCTCCTTTCC  11233      T_       CC
                                GCCCT  CTCCTCTCC  TCC
                                |||||  |||||||||  |||
                                CGGGG  GAGGAGAGG  AGG
                                   TC        AA
GAM396  STAG3    3'  GCTGCCCTTCTCCACTCC    11234    GC        T
                                GC  GCCCTTCTCC CTCC
                                ||  |||||||||| ||||
                                CG  CGGGAAGAGG GAGG
                                 A_        T
GAM396  STOML1   3'  GCTGCCTTCCCTTCCCTC    11235    GC    T   CTC
                                GC  CCTTC CCT   CCCTC
                                ||  ||||| |||   |||||
                                CG  GGAAG GGA   GGGAG
                                 AC     _   A__
GAM396  TED      3'  CACATTTCTCCTCTCCTCTCC  11236     CC         C
                                CGC  TTCTCCTCTCC CTCC
                                |||  |||||||||| ||||
                                GTG  AAGAGGAGAGG GAGG
                                  TA          A
GAM396  TIP47    3'  GCCCGCTGAGTCCTCTCCTCTC 11237    G   C____
           C                     GC CGC     CTTCTCCTCTCC
                                || |||     ||||||||||||
                                CG GCG     GGAGAGGAGAGG
                                 G   ACTCA
GAM396  TLOC1    5'  GCGGTGCCTTCTCTCCCCTC   11238     CGC      CTC
                                GCG   CCTTCTC   TCCCCTC
                                |||   |||||||   |||||||
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                                CGC  GGAAGAG  AGGGGAG
                                  CAC     ___
GAM396  TRIM11   3'  GCTCGCCCTTCTCCTTCC   11239   G        C
                                GC CGCCCTTCTCCT TCC
                                || ||||||||||| |||
                                CG GCGGGAAGAGGA AGG
                                 A         _
GAM396  U5-116KD 3'  GCCCAAGCTCCTCTCTTTTCC 11240     TT_     CCC
                                GCCC  CTCCTCTC  TCC
                                ||||  ||||||||  |||
                                CGGG  GAGGAGAG  AGG
                                  TTC      AAA
GAM396  VRHO     3'  GCTGCTTTTCCCTCCCCTCC  11241   GCC  C  T
                                GC  CTT TCC CTCCCCTCC
                                ||  ||| ||| |||||||||
                                CG  GAA AGG GAGGGGAGG
                                 AC_  A  _
GAM396  WDR13    5'  GCCGCCCTCCGCCTTCCCTTC 11242   G     T  C   C
                                GC CGCCCTTC CCT TCCC TC
                                || |||||||| ||| |||| ||
                                CG GCGGGAGG GGA AGGG AG
                                 _      C  _   A
GAM396  LOC116113 3'  GCCCGCTTTCTCCCCTCC   6310    G  CC
                                GC CGC  TTCTCCTCTCC
                                || |||  ||||||||||
                                CG GCG  AAGAGGGGAGG
                                 G  A_
GAM396  LOC120227 5'  CGTGCTGCTTTCCCCTCC   11220   C  C_  C
                                CG GC  CTT TCCTCTCC
                                || ||  ||| ||||||||
                                GC CG  GAA AGGGGAGG
                                 A  AC  _
GAM396  LOC127702 3'  CCCCTCTTCTCCCTTC     11243      CC    C
                                CCCTTCT  TCTCCC TC
                                |||||||  |||||| ||
                                GGGGAGA  AGAGGG AG
                                    __     A
GAM396  LOC130595 5'  GCCGCTCTGTCTCCCCTC   11244   C   CC
                                GCC TTCT  TCTCCCCTC
                                ||| ||||  |||||||||
                                CGG GAGA  AGAGGGGAG
                                  C   C_
GAM396  LOC145725 3'  CGCCCATCTCTCCCCTC    11245     TTCTC
                                CGCCC    CTCTCCCCTC
                                |||||    ||||||||||
                                GCGGG    GAGAGGGGAG
                                   TA___
GAM396  LOC145732 3'  CGCCCATCTCTCCCCTC    11245     TTCTC
                                CGCCC    CTCTCCCCTC
                                |||||    ||||||||||
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                                GCGGG    GAGAGGGGAG
                                  TA___
GAM396  LOC146429 5'  GCGTGGCCTTCCCTCCCCT   11246    C_  CTTC  T
                                GCG  GCC   TCC CTCCCCT
                                |||  |||   ||| |||||||
                                CGC  CGG   AGG GAGGGGA
                                 AC   A___  _
GAM396  LOC147922 3'  GCTGCCCTTCTCCTGTC    11247    GC       C
                                GC  GCCCTTCTCCT TC
                                ||  ||||||||||| ||
                                CG  CGGGAAGAGGA AG
                                 A_         C
GAM396  LOC148426 5'  CGCTGCCCTTCTTCTTTCCTTT 11248    _      C  C   CC
          C                      CGC GCCCTTCT CT TCC  TC
                                |||  |||||||| || |||  ||
                                GCG CGGGAAGA GA AGG  AG
                                 A       A  A   AA
GAM396  LOC148645 3'  GCTTCCTCTCCTTTCTCCTCC  11249    GCC      C  C
                                GC   CTTCTCCT TC CCTCC
                                ||   |||||||| || |||||
                                CG   GGAGAGGA AG GGAGG
                                 AA_       A  A
GAM396  LOC149706 5'  GCGTCTCCATCTCCCCT     11250    CCCT    _
                                GCG    TCTCC TCTCCCCT
                                |||    ||||| ||||||||
                                CGC    AGAGG AGAGGGGA
                                  _____    T
GAM396  LOC149844 5'  GCGTGATCCCCCCCTTTCCTTT 11251    CG__   TT    C   CC
          CC                      GCG    CCC  CTCCT TCC  TCC
                                |||    |||  ||||| |||  |||
                                CGC    GGG  GGGGA AGG  AGG
                                  ACTA   __     A   AA
GAM396  LOC149950 5'  GCCGCCCTTCTCCGCCCTTC   11252    G        TCT   C
                                GC CGCCCTTCTCC   CCC TC
                                || ||||||||||   ||| ||
                                CG GCGGGAAGAGG   GGG AG
                                 _         C__   A
GAM396  LOC158056 5'  CACACACCTTCTCCCCTCC    11253      _
                                CGCGC CCTTCTCCTCTCC
                                |||||| ||||||||||||
                                GTGTG GGAAGAGGGGAGG
                                   T
GAM396  LOC162333 5'  GCCCGCTCCTCTCTTTCCT    11254      TT       C__
                                GCCC  CTCCTCTC   CCT
                                ||||  ||||||||   |||
                                CGGG  GAGGAGAG   GGA
                                  C_       AAA
GAM396  LOC162952 3'  GCCTCCTCCTCTTCTCCTCTC  11255    GC      C    C
                                GC  CCTTCTC TCTCC CTC
                                ||  ||||||| ||||| |||
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                                CG  GGAGGAG AGAGG GAG
                                 GA      A    A
GAM396  LOC196957 3'  GCCGCCCATCTCTCCCCTC   11256   G    TTCTC
                                GC CGCCC    CTCTCCCCTC
                                || |||||    ||||||||||
                                CG GCGGG    GAGAGGGGAG
                                 _    TA___
GAM396  LOC196961 3'  GCCGCCCATCTCTCCCCTC   11256   G    TTCTC
                                GC CGCCC    CTCTCCCCTC
                                || |||||    ||||||||||
                                CG GCGGG    GAGAGGGGAG
                                 _    TA___
GAM396  LOC197138 3'  GCCGCCCATCTCTCCCCTC   11256   G    TTCTC
                                GC CGCCC    CTCTCCCCTC
                                || |||||    ||||||||||
                                CG GCGGG    GAGAGGGGAG
                                 _    TA___
GAM396  LOC219654 3'  GCTTGCCTTTGTCCCCTCC   11257   GC   C  C
                                GC  GCC TT TCCTCTCC
                                ||  ||| || ||||||||
                                CG  CGG AA AGGGGAGG
                                 AA   A  C
GAM396  LOC219940 3'  GCGCCCCCTTCTGGGCCCTC  11258     G     CCTCTC
                                GCGC CCCTTCT     CCCTC
                                |||| |||||||     |||||
                                CGCG GGGAAGA     GGGAG
                                  G      CCC___
GAM396  LOC220776 3'  GCGGCCCTTCCCCACCTCCCTT 11259    C       _    C
           C                     GCG GCCCTTCTCC TCTCCC TC
                                ||| |||||||||| |||||| ||
                                CGC CGGGAAGGGG GGAGGG AG
                                 _        T     A
GAM396  LOC222193 5'  GCCTTCTTCTCCTCAGTCC   11260    __       __
                                GCC  CTTCTCCTC  TCC
                                |||  |||||||||  |||
                                CGG  GAAGAGGAG  AGG
                                  AA        TC
GAM396  LOC245727 3'  GCCGCCCATCTCTCCCCTC   11256   G    TTCTC
                                GC CGCCC    CTCTCCCCTC
                                || |||||    ||||||||||
                                CG GCGGG    GAGAGGGGAG
                                 _    TA___
GAM396  LOC253219 5'  GCCCGCCCTTCTCTGCGGGTCT 11261   G       C_____
           CC                     GC CGCCCTTCTC     TCTCC
                                || ||||||||||     |||||
                                CG GCGGGAAGAG     AGAGG
                                 G         ACGCCC
GAM396  LOC253219 3'  GCCCGCCCTTCTCTGCGGGTCT 11261   G       C_____
           CC                     GC CGCCCTTCTC     TCTCC
                                || ||||||||||     |||||
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                                CG GCGGGAAGAG     AGAGG
                                 G         ACGCCC
GAM396  LOC253289 3'  GCTGCTCTTCCCCTTCCCCTC  11262    GC  C       C
                                GC  GC CTTCTCCT TCCCCTC
                                ||  || |||||||| |||||||
                                CG  CG GAAGGGGA AGGGGAG
                                 A_  A       _
GAM396  LOC255104 3'  GCGTGTTCTCTCCTCCAAATTC 11263     CCC_      _____
            CCCT                   GCG    TTCTCCTC    TCCCCT
                                |||    ||||||||    ||||||
                                CGC    GAGAGGAG    AGGGGA
                                  ACAA       GTTTA
GAM396  LOC256880 5'  GCGGTGCCCTTCTTCTCCC    11264     C_       CC
                                GCG  GCCCTTCT  TCTCCC
                                |||  ||||||||  ||||||
                                CGC  CGGGAAGA  AGAGGG
                                  CA       __
GAM396  LOC257104 5'  GCCCCCACCGTCTCCCCTC    11265       CT  _
                                GCCCTT  CC TCTCCCCTC
                                ||||||  || |||||||||
                                CGGGGG  GG AGAGGGGAG
                                    T_  C
GAM396  LOC51281  5'  GCTTCCTCCTCTTCCTTC    11175    CC       C  C
                                GC  TTCTCCTCT CC TC
                                ||  ||||||||| || ||
                                CG  AGGAGGAGA GG AG
                                 A_       A  A
GAM396  LOC51700  5'  GCCGCCCTGCTCCTCTCC    11266    G     T
                                GC CGCCCT CTCCTCTCC
                                || |||||| |||||||||
                                CG GCGGGA GAGGAGAGG
                                 _     C
GAM396  LOC90183  3'  GCGCGCCCTTCCTCCCTC    11217          TC
                                GCGCGCCCTTC  CTCTC
                                ||||||||||  |||||
                                CGCGCGGGAAG  GGGAG
                                       GA
GAM396  LOC90230  5'  GCTGCTCTGTCTCTCCCCTC   11267    GC  C  TCTC
                                GC  GC CT    CTCTCCCCTC
                                ||  || ||    ||||||||||
                                CG  CG GA    GAGAGGGGAG
                                 A_  A  CA__
GAM396  LOC91409  3'  GCCTGTCCCTTTCTCCCCTC   11268     CT    C_
                                GCC  TCTC  TCTCCCCTC
                                |||  ||||  |||||||||
                                CGG  AGGG  AGAGGGGAG
                                  AC    AA
GAM396  LOC92080  5'  GGCGATTCCTCTCCTTTCC    11269    C   CC_      C
                                G GCG   CTTCTCCT TCC
                                | |||   |||||||| |||
```

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                                C CGC   GGAGAGGA AGG
                                 _  TAA       A
GAM397  ABCC3   3'  CACCACGGCCACCAGTGCCCC  11272     T   G  ___
                                CACC CGGC GCC   GCCCC
                                |||| |||| |||   |||||
                                GTGG GCCG TGG   CGGGG
                                  T   G   TCA
GAM397  ARF4L   5'  CACCGCAGCCGCCCC      11273     TCG
                                CACC   GCGGCCGCCCC
                                ||||   ||||||||||
                                GTGG   CGTCGGCGGGG
                                  ___
GAM397  BAX     3'  CAGCCCAACAGCCGCTCC    11274    C         _
                                CA CTCGGCGGCCGC CC
                                || |||||||||| ||
                                GT GGGTTGTCGGCG GG
                                 C          A
GAM397  CDK9    3'  CACTCAGCGGGCTGCTCC    11275    C     _ C _
                                CAC TCGGCGG C GC CC
                                ||| ||||||| | || ||
                                GTG AGTCGCC G CG GG
                                 _      C A  A
GAM397  CDS1    5'  CACCTCGCAGCCGCGCCC    11276       G     _
                                CACCTCG CGGCCGC CCC
                                ||||||| ||||||| |||
                                GTGGAGC GTCGGCG GGG
                                    _      C
GAM397  CLCN4   5'  CCTCGCGCTGGCCGCCCC    11277      _ _
                                CCTCG GC GGCCGCCCC
                                ||||| || |||||||||
                                GGAGC CG CCGGCGGGG
                                   G  A
GAM397  DYRK2   5'  CGCCTCCCGGCCGCCCC     11278   A   GG
                                C CCTC  CGGCCGCCCC
                                | ||||  ||||||||||
                                G GGAG  GCCGGCGGGG
                                 C   G_
GAM397  DYRK2   5'  CGCCTCCCGGCCGCCCC     11278   A   GG
                                C CCTC  CGGCCGCCCC
                                | ||||  ||||||||||
                                G GGAG  GCCGGCGGGG
                                 C   G_
GAM397  ELK1    5'  CACCTAGAAGCCGCCCC     11279      C  C
                                CACCT GG GGCCGCCCC
                                ||||| || |||||||||
                                GTGGA TC TCGGCGGGG
                                   _ T
GAM397  EN2     5'  CACCCGGCGACAGCCCC     11281     T     C
                                CACC CGGCGGC GCCCC
                                |||| ||||||| |||||
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```
                                GTGG GCCGCTG CGGGG
                                  _      T
GAM397  EN2     5'  CACCACGAGCCGCCCC      11280      T  GC
                                CACC CG  GGCCGCCCC
                                |||| ||  |||||||||
                                GTGG GC  TCGGCGGGG
                                  T  __
GAM397  EN2     5'  CCTCGCGGCCGCCGCCCC    11282      __  G
                                CCTC  GGC GCCGCCCC
                                ||||  ||| ||||||||
                                GGAG  CCG CGGCGGGG
                                  CG   G
GAM397  FZD10   5'  CCTCAGCGCCGCCGCTCC    11283        __    _
                                CCTCGGCG  GCCGC CC
                                ||||||||  ||||| ||
                                GGAGTCGC  CGGCG GG
                                     GG    A
GAM397  GATA6   5'  CAGCTCGACAGGTTGCCCC   11284    C      CC_
                                CA CTCGGCGG   GCCCC
                                || |||||||   |||||
                                GT GAGCTGTC   CGGGG
                                 C       CAA
GAM397  GMDS    3'  ACCTCGGCGGGGCGGCCCC   11285        __  C
                                ACCTCGGC  GGC GCCCC
                                ||||||||  ||| |||||
                                TGGAGCCG  CCG CGGGG
                                     CC   C
GAM397  HOXB5   3'  CACCTCAACTGCTGCCCC    11286        G  C
                                CACCTCGGC GC GCCCC
                                ||||||||| || |||||
                                GTGGAGTTG CG CGGGG
                                     A  A
GAM397  HR      5'  CACCCCAAAGCCGTTCC     11287        C    CC
                                CACCTCGG GGCCG  CC
                                |||||||| |||||  ||
                                GTGGGGTT TCGGC  GG
                                     _    AA
GAM397  KCNC1   5'  CCCCTGGCGGCCGCTCCG    11288     _      _ CIII
                                CCTC GGCGGCCGC CC   G
                                |||| |||||||| ||   |
                                GGGG CCGCCGGCG GG   C
                                  A       A  IIIC
GAM397  LHX3    5'  CACCCCGCAATAGCCCC     11289       G  CC
                                CACCTCG CGG  GCCCC
                                ||||||| |||  |||||
                                GTGGGGC GTT  CGGGG
                                     _  AT
GAM397  LIF     3'  CACCCTTGGACAGGCCCC    11290      C__    CC
                                CACCT   GGCGG  GCCCC
                                |||||   |||||  |||||
```

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                                GTGGG  CTGTC  CGGGG
                                  AAC    __
GAM397  MAP3K5   5' CCCGGCGGCGGCTCGCTCC   11291    __     _  _
                                CCT  CGGCGGC CGC CC
                                |||  ||||||| ||| ||
                                GGG  GCCGCCG GCG GG
                                  CC      A   A
GAM397  MDFI     3' CACCCCAGCCCTGCCCC    11292        GG  _
                                CACCTCGGC  CC GCCCC
                                |||||||||  || |||||
                                GTGGGGTCG  GG CGGGG
                                     __ A
GAM397  MGAM     5' ACCTCTTGCAGCCGCTCC   11293      G_      _
                                ACCTC  GCGGCCGC CC
                                |||||  |||||||| ||
                                TGGAG  CGTCGGCG GG
                                  AA       A
GAM397  MOCS1    3' CACCCCGGTGGGGCCCC    11294       C  CC
                                CACCTCGG GG  GCCCC
                                |||||||| ||  |||||
                                GTGGGGCC CC  CGGGG
                                    A  C_
GAM397  MUCDHL   5' ACCTCAGCGACCTTCGCCCC  11295          ___
                                ACCTCGGCGGCC   GCCCC
                                ||||||||||||   |||||
                                TGGAGTCGCTGG   CGGGG
                                     AAG
GAM397  MUCDHL   5' ACCTCAGCGACCTTCGCCCC  11295          ___
                                ACCTCGGCGGCC   GCCCC
                                ||||||||||||   |||||
                                TGGAGTCGCTGG   CGGGG
                                     AAG
GAM397  NDUFA8   5' CCTCAGCCGCGTCGCCCC   11296       G  __
                                CCTCGGC GC  CGCCCC
                                |||||||  ||  ||||||
                                GGAGTCG CG  GCGGGG
                                    G  CA
GAM397  NLGN2    3' CCTCGGCAGGGTCCGCCCC   11297         ___
                                CCTCGGCGG   CCGCCCC
                                |||||||||   |||||||
                                GGAGCCGTC   GGCGGGG
                                     CCA
GAM397  NTRK2    5' CACCTCGAGGCCGGGCTCC   11298       C   __ _
                                CACCTCGG GGCC  GC CC
                                ||||||||  ||||  || ||
                                GTGGAGCT CCGG  CG GG
                                    _   CC  A
GAM397  PLA2G10  5' CACCCCGGCTGTCACGCCCC  11299         GGC__
                                CACCTCGGC    CGCCCC
                                |||||||||    ||||||
```

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                                GTGGGGCCG    GCGGGG
                                     ACAGT
GAM397  REST    5'  CCTCGGCGGCGCTCGCTCC   11300        ___  _
                                CCTCGGCGGC   CGC CC
                                ||||||||||   ||| ||
                                GGAGCCGCCG   GCG GG
                                     CGA   A
GAM397  SLC4A2  5'  CACCCCGGGGCGCGCCCC    11301       C  _
                                CACCTCGG GGC CGCCCC
                                |||||||| ||| ||||||
                                GTGGGGCC CCG GCGGGG
                                     _  C
GAM397  STIM1   5'  CACCCGCGAGCCTGCCCC    11302      CG  _  _
                                CACCT  GCG GCC GCCCC
                                |||||  ||| ||| |||||
                                GTGGG  CGC CGG CGGGG
                                   __  T   A
GAM397  TFRC    5'  CACCGGAGCGGCCGCTCC    11303     TC      _
                                CACC  GGCGGCCGC CC
                                ||||  |||||||||| ||
                                GTGG  TCGCCGGCG GG
                                  CC        A
GAM397  TRRAP   5'  ACCTCGGCGGCCCGGCTCC   11304          __ _
                                ACCTCGGCGGCC  GC CC
                                ||||||||||||  || ||
                                TGGAGCCGCCGG  CG GG
                                     GC  A
GAM397  UROS    5'  CACCCGCGCTGGGCCCC     11305     T _ _ CC
                                CACC CG GC GG  GCCCC
                                |||| || || ||  |||||
                                GTGG GC CG CC  CGGGG
                                  _ G  A __
GAM397  VDR     3'  CACCCGAGACTGCCCC      11306     T  C  C
                                CACC CGG GGC GCCCC
                                |||| ||| ||| |||||
                                GTGG GCT CTG CGGGG
                                  _  _  A
GAM397  WBSCR5  5'  CCTCACCACGGCCGCCCC    11307      __
                                CCTCG  GCGGCCGCCCC
                                |||||  ||||||||||
                                GGAGT  TGCCGGCGGGG
                                   GG
GAM397  WBSCR5  5'  CCTCAACACGGCCGCCCC    11308      __
                                CCTCG  GCGGCCGCCCC
                                |||||  ||||||||||
                                GGAGT  TGCCGGCGGGG
                                   TG
GAM397  WBSCR5  5'  CCTCACCACGGCCGCCCC    11307      __
                                CCTCG  GCGGCCGCCCC
                                |||||  ||||||||||
```

```
                                GGAGT TGCCGGCGGGG
                                  GG
GAM397  WHSC1    3' CCTCTTGGCGACCAGGCCCC  11309     __     __
                                CCTC GGCGGCC GCCCC
                                |||| ||||||| |||||
                                GGAG CCGCTGG CGGGG
                                  AA     TC
GAM397  WHSC1    3' CCTCTTGGCGACCAGGCCCC  11309     __     __
                                CCTC GGCGGCC GCCCC
                                |||| ||||||| |||||
                                GGAG CCGCTGG CGGGG
                                  AA     TC
GAM397  WHSC1    3' CCTCTTGGCGACCAGGCCCC  11309     __     __
                                CCTC GGCGGCC GCCCC
                                |||| ||||||| |||||
                                GGAG CCGCTGG CGGGG
                                  AA     TC
GAM397  AGS3     5' CACCCGCCGACTGCCCC     11310     T G    C
                                CACC CG CGGC GCCCC
                                |||| || |||| |||||
                                GTGG GC GCTG CGGGG
                                  _ G    A
GAM397  BRD4     3' CACCTCCACCACCGCCCC    11311      G G
                                CACCTC GC GCCGCCCC
                                |||||| || ||||||||
                                GTGGAG TG TGGCGGGG
                                   G G
GAM397  C11orf11 3' CACCTCGGCAGGGGCACCCC  11312          C__
                                CACCTCGGCGG  CGCCCC
                                ||||||||||  ||||||
                                GTGGAGCCGTC  GTGGGG
                                      CCC
GAM397  C11orf11 5' CACCTCAGCAGGCCCC      11313          CC
                                CACCTCGGCGG GCCCC
                                ||||||||||  |||||
                                GTGGAGTCGTC CGGGG
                                          __
GAM397  C6orf37  5' CCTGGAGGCGGCCGCCCC    11314     C__
                                CCT  GGCGGCCGCCCC
                                |||  ||||||||||||
                                GGA  CCGCCGGCGGGG
                                  CCT
GAM397  Cab45    3' CACCCGCGAGGCCGCCCC    11315      _  C
                                CACCT CGG GGCCGCCCC
                                ||||| ||| |||||||||
                                GTGGG GCT CCGGCGGGG
                                  C  _
GAM397  DKFZp434K1815 5' CACCCCGGCGTGTGGCGTCGCC 11316          ____  __
            C                    CACCTCGGC   GGC  CGCCC
                                |||||||||   |||  |||||
```

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                                GTGGGGCCG   CCG  GCGGG
                                     CACA   CA
GAM397  FABP7    5'  CACCTCAGCAAGCAGCTCC   11317        _ C _
                                CACCTCGGCG GC GC CC
                                |||||||||| || || ||
                                GTGGAGTCGT CG CG GG
                                      T  T  A
GAM397  FAM3A    3'  CACCCCGGGCCAGCCTGCTCC 11318       __   _ _
                                CACCTCGG  CGGCC GC CC
                                ||||||||  ||||| || ||
                                GTGGGGCC  GTCGG CG GG
                                     CG    A  A
GAM397  FER1L4   3'  CACCTCGGCCCGGCCCC    11319        GG  _
                                CACCTCGGC  CCG CCCC
                                |||||||||  ||| ||||
                                GTGGAGCCG  GGC GGGG
                                     __  C
GAM397  FLJ10038 5'  CACCATGTCTGCCCGCCCC   11320     ___ G  GG
                                CACC   TC GC  CCGCCCC
                                ||||   || ||  |||||||
                                GTGG   AG CG  GGCGGGG
                                  TAC  A  __
GAM397  FLJ10350 5'  CACCCCAGCAGCGCCCC    11321          C
                                CACCTCGGCGGC GCCCC
                                |||||||||||| |||||
                                GTGGGGTCGTCG CGGGG
                                          _
GAM397  FLJ10874 5'  CACCTGAGACCGCCCC     11322      C  C
                                CACCT GG GGCCGCCCC
                                ||||| || |||||||||
                                GTGGA CT CTGGCGGGG
                                  _  _
GAM397  FLJ11136 5'  CACCCCGGCAGCAGGGCCCC  11323          C__
                                CACCTCGGCGGC   GCCCC
                                ||||||||||||   |||||
                                GTGGGGCCGTCG   CGGGG
                                       TCC
GAM397  FLJ13063 5'  CACTCGGCGGGGACCGCC    11324     C     ___
                                CAC TCGGCGG   CCGCC
                                ||| |||||||   |||||
                                GTG AGCCGCC   GGCGG
                                  _     CCT
GAM397  FLJ13852 3'  CACCTGGTGCCACCCC      11325      C  CG
                                CACCT GG  GCCGCCCC
                                ||||| ||  ||||||||
                                GTGGA CC  CGGTGGGG
                                  _ A_
GAM397  FLJ14356 5'  CACACTTCAGCCGCCCC     11326     _ CGG
                                CAC CT   CGGCCGCCCC
                                ||| ||   ||||||||||
```

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                                GTG GA   GTCGGCGGGG
                                  T  A__
GAM397  FLJ20040  3'  CACCCGGCCGCCGTGCTCC   11327     T   G  __ _
                                CACC CGGC GCC  GC CC
                                |||| |||| |||  || ||
                                GTGG GCCG CGG  CG GG
                                  _   G   CA  A
GAM397  FLJ20257  5'  CACCGTGGGGCCGCCCC     11328     TC  C
                                CACC  GG GGCCGCCCC
                                ||||  || |||||||||
                                GTGG  CC CCGGCGGGG
                                  CA  _
GAM397  FLJ20401  5'  CACCTCGGGGACCCC       11329       C  CC
                                CACCTCGG GG  GCCCC
                                |||||||| ||  |||||
                                GTGGAGCC CC  TGGGG
                                   _  __
GAM397  FLJ20421  5'  CACCAACGCCGCCCC       11330     TC   G
                                CACC  GGCG CCGCCCC
                                ||||  |||| |||||||
                                GTGG  TTGC GGCGGGG
                                   __   _
GAM397  FLJ21613  5'  CGCCTCGGCCGCCGCCGCC   11331   A     G    _
                                C CCTCGGC GCCGCC CC
                                | ||||||| |||||| ||
                                G GGAGCCG CGGCGG GG
                                 C      G     C
GAM397  FLJ22555  5'  CCTTCGGCAACCCGCCCC    11332    _      _
                                CCT CGGCGGCC GCCCC
                                ||| |||||||| |||||
                                GGA GCCGTTGG CGGGG
                                  A       G
GAM397  FLJ22814  3'  CACCCTGCCCACCGCCCC    11333      CG  G_
                                CACCT  GC  GCCGCCCC
                                |||||  ||  ||||||||
                                GTGGG  CG  TGGCGGGG
                                   A_  GG
GAM397  FLJ30927  5'  CACCGCGGCCGCGCCCC     11334     T   G  C
                                CACC CGGC GC GCCCC
                                |||| |||| || |||||
                                GTGG GCCG CG CGGGG
                                  C   G  _
GAM397  FLJ32416  5'  CCCGGGCCAGGCCGCCCC    11335     C  __
                                CCT GGC  GGCCGCCCC
                                ||| |||  |||||||||
                                GGG CCG  CCGGCGGGG
                                  C  GT
GAM397  FLVCR     5'  CACCTCGCTCCCCCGCCCC   11336       G GG__
                                CACCTCG C    CCGCCCC
                                |||||||  |   |||||||
```

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                                GTGGAGC G   GGCGGGG
                                   _ AGGG
GAM397  Gsh-1    5' CCCCGGCGCGCGGTCGCCCC  11337       _ ___
                                CCTCGGCG GC  CGCCCC
                                |||||||| ||  ||||||
                                GGGGCCGC CG  GCGGGG
                                   G  CCA
GAM397  GTPBP1   5' CCGCGGCCCTGGCCGCCCC   11338   T   ___
                                CC CGGC  GGCCGCCCC
                                || ||||  |||||||||
                                GG GCCG  CCGGCGGGG
                                 C   GGA
GAM397  HSPC121  5' CACCTCGAGATACCCC     11339       C  CC
                                CACCTCGG GG  GCCCC
                                |||||||| ||  |||||
                                GTGGAGCT CT  TGGGG
                                   _  A_
GAM397  KIAA0014 3' CCTCCGGCCGCCCGCCCC   11340    _  G  _
                                CCTC GGC GCC GCCCC
                                |||| ||| ||| |||||
                                GGAG CCG CGG CGGGG
                                  G  G  G
GAM397  KIAA0211 3' CACTTCGGCACCACCCC    11341    C    G
                                CAC TCGGCG CCGCCCC
                                ||| |||||| |||||||
                                GTG AGCCGT GGTGGGG
                                  A    _
GAM397  KIAA0258 3' CACCTCTGCACCGCCCC    11342      G  G
                                CACCTC GCG CCGCCCC
                                |||||| ||| |||||||
                                GTGGAG CGT GGCGGGG
                                   A  _
GAM397  KIAA0284 3' CACCTGCCACCCCCGCCCC  11343     CG  G  ___
                                CACCT  GC GCC  GCCCC
                                |||||  || |||  |||||
                                GTGGA  CG TGG  CGGGG
                                   __  G  GGG
GAM397  KIAA0545 3' CACCGGCATGGCCGCCCC   11344    TC  __
                                CACC  GGC  GGCCGCCCC
                                ||||  |||  |||||||||
                                GTGG  CCG  CCGGCGGGG
                                   __  TA
GAM397  KIAA0720 3' CACCCCGACTCTCGCCCC   11345       GGC
                                CACCTCGGC  CGCCCC
                                |||||||||  ||||||
                                GTGGGGCTG  GCGGGG
                                     AGA
GAM397  KIAA1094 5' CATCTTGGCACCGCCCC    11346   C  C   G
                                CA CT GGCG CCGCCCC
                                || || |||| |||||||
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                                GT GA CCGT GGCGGGG
                                 A  A   _
GAM397  KIAA1196  3'  CACTTCTGGCAGTAGCCCC   11347    C  _    CC
                                CAC TC GGCGG  GCCCC
                                ||| || |||||  |||||
                                GTG AG CCGTC  CGGGG
                                  A  A    AT
GAM397  KIAA1354  5'  CACCTCAGCGAACGGCCC    11348         GC  _
                                CACCTCGGCG  CG CCC
                                ||||||||||  || |||
                                GTGGAGTCGC  GC GGG
                                      TT  C
GAM397  KIAA1857  3'  CACCTCGGGCCGCACCC     11349        CG    _
                                CACCTCGG  GCCGC CCC
                                ||||||||  ||||| |||
                                GTGGAGCC  CGGCG GGG
                                    __    T
GAM397  KIAA1924  3'  CCTGGCATCAGCCGCCCC    11350    C  ___
                                CCT GGC   GGCCGCCCC
                                ||| |||   |||||||||
                                GGA CCG   TCGGCGGGG
                                  _  TAG
GAM397  LANCL2    3'  CACCCCAGCACGCCCC      11351         GC
                                CACCTCGGCG  CGCCCC
                                ||||||||||  ||||||
                                GTGGGGTCGT  GCGGGG
                                            __
GAM397  MGC:5244  5'  CACCCCGGCCCGCGCCCC    11352         GGC
                                CACCTCGGC   CGCCCC
                                |||||||||   ||||||
                                GTGGGGCCG   GCGGGG
                                     GGC
GAM397  MGC15396  5'  CCTCCCGCGGGCCGCCCC    11353      G_   _
                                CCTC  GCGG CCGCCCC
                                ||||  |||| |||||||
                                GGAG  CGCC GGCGGGG
                                  GG    C
GAM397  MGC15438  3'  ACCTCAGCTGCGGCTGCTCC   11354         ___   C  _
                                ACCTCGGC   GGC GC CC
                                ||||||||   ||| || ||
                                TGGAGTCG   CCG CG GG
                                    ACG   A  A
GAM397  MGC15523  5'  CCTCAGGGCCATGCGTCCC    11355       C   __ __
                                CCTCGG GGCC  GC  CCC
                                |||||| ||||  ||  |||
                                GGAGTC CCGG  CG  GGG
                                   _   TA  CA
GAM397  MGC20486  5'  CGCCCCTACGCCGCCCC     11356    A   G   G
                                C CCTC GCG CCGCCCC
                                | |||| ||| |||||||
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```
                                G GGGG TGC GGCGGGG
                                 C   A  _
GAM397  MGC23280  3'  CACCTCGATACCAGCTGCCC  11357       ___   C
                                CACCTCGG  CGGC GCCC
                                ||||||||  |||| ||||
                                GTGGAGCT  GTCG CGGG
                                    ATG   A
GAM397  MGC26655  5'  CACCCCGCACGCCCC     11358      G  GC
                                CACCTCG CG  CGCCCC
                                |||||||  ||  ||||||
                                GTGGGGC GT  GCGGGG
                                  _  __
GAM397  MGC3079   3'  CACTTCGGAGACCGCCCC   11359    C   C
                                CAC TCGG GGCCGCCCC
                                |||  |||| |||||||||
                                GTG AGCC CTGGCGGGG
                                  A   T
GAM397  MGC4415   3'  CACCTCGGCGGATGGGCCCC  11360        CC__
                                CACCTCGGCGG   GCCCC
                                ||||||||||   |||||
                                GTGGAGCCGCC   CGGGG
                                     TACC
GAM397  MLL3      5'  CCTCGGCCACCTCGCCCC   11361      G  __
                                CCTCGGC GCC  GCCCC
                                |||||||  |||  |||||
                                GGAGCCG TGG  CGGGG
                                   G   AG
GAM397  p25       3'  CCTGGGCCTGGCCGCCCC   11362    C  __
                                CCT GGC  GGCCGCCCC
                                |||  |||  |||||||||
                                GGA CCG  CCGGCGGGG
                                  C   GA
GAM397  PADI3     3'  CACCTCGAGAACCGGGCCCC  11363       CG  __
                                CACCTCGG  GCC  GCCCC
                                ||||||||  |||  |||||
                                GTGGAGCT  TGG  CGGGG
                                     CT   CC
GAM397  PCTAIRE2BP 5'  CACCTCAAGCCCCCGCCCC  11364       _  GG
                                CACCTCG GC  CCGCCCC
                                |||||||  ||  |||||||
                                GTGGAGT CG  GGCGGGG
                                   T  GG
GAM397  PCTAIRE2BP 5'  CACCGGAGCCGCCCC     11365     TC  C
                                CACC  GG GGCCGCCCC
                                ||||  ||  |||||||||
                                GTGG  CC TCGGCGGGG
                                  __  _
GAM397  PF1       5'  CACCCGCGCAGGCGCCCC   11366     T  _   C
                                CACC CG GCGG CGCCCC
                                ||||  ||  ||||  ||||||
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```
                                GTGG GC CGTC GCGGGG
                                  _ G   C
GAM397  PMVK     3'  CACCTCAGCAGGCCCC     11313          CC
                                CACCTCGGCGG  GCCCC
                                ||||||||||  |||||
                                GTGGAGTCGTC  CGGGG
                                          __
GAM397  PMVK     3'  CACCTCAGCAGGCCCC     11313          CC
                                CACCTCGGCGG  GCCCC
                                ||||||||||  |||||
                                GTGGAGTCGTC  CGGGG
                                          __
GAM397  PPP1R13B 3'  CACCTCAGTGAAGCGCCC   11367        C  C_
                                CACCTCGG GG  CGCCC
                                ||||||||  ||  |||||
                                GTGGAGTC CT  GCGGG
                                     A  TC
GAM397  RAB24    5'  CACTTCGGCAGCGCCCC    11368    C      C
                                CAC TCGGCGGC GCCCC
                                |||  ||||||||  |||||
                                GTG AGCCGTCG CGGGG
                                  A       _
GAM397  SLC11A2  5'  CACCTGACACGCCGCCCC   11369      C   _
                                CACCT GGCG GCCGCCCC
                                |||||  ||||  ||||||||
                                GTGGA CTGT CGGCGGGG
                                   _   G
GAM397  SLC2A10  5'  CGCCCCCGGCCGCCCC     11370   A   GG
                                C CCTC  CGGCCGCCCC
                                |  ||||  ||||||||||
                                G GGGG  GCCGGCGGGG
                                 C   __
GAM397  SMARCA4  5'  CGCCTCGGCCACCGCCCC   11371   A     G
                                C CCTCGGC GCCGCCCC
                                |  |||||||  ||||||||
                                G GGAGCCG TGGCGGGG
                                 C      G
GAM397  SOUL     5'  CACCCCGGGCCGCCCC      11372        CG
                                CACCTCGG  GCCGCCCC
                                ||||||||  ||||||||
                                GTGGGGCC  CGGCGGGG
                                          __
GAM397  SRPUL    3'  CACCTCAGAGTCCTGTCCC   11373        C  _  GC_
                                CACCTCGG GG CC   CCC
                                ||||||||  ||  ||   |||
                                GTGGAGTC TC GG   GGG
                                     _  A  ACA
GAM397  TLN1     5'  CCGCCGGCCCGCCGCCCC    11374    _    G_
                                CC TCGGC  GCCGCCCC
                                ||  |||||  ||||||||
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                                GG GGCCG  CGGCGGGG
                                 C    GG
GAM397   LOC113201 5'  CCCGGCGGACACGGCCCC    11375        _ _ _
                                CTCGGCGG C CG CCCC
                                |||||||| | || ||||
                                GGGCCGCC G GC GGGG
                                     T T  C
GAM397   LOC121504 3'  CACCCCCACCCCGCCCC     11376       G  GG
                                CACCTC GC  CCGCCCC
                                |||||| ||  |||||||
                                GTGGGG TG  GGCGGGG
                                   G  G_
GAM397   LOC124044 3'  CACCCGGCAGAGCCCC      11377      T     CC
                                CACC CGGCGG  GCCCC
                                |||| ||||||  |||||
                                GTGG GCCGTC  CGGGG
                                  _     T_
GAM397   LOC125704 5'  CACCCGGCAGGGCCCC      11378      T     CC
                                CACC CGGCGG  GCCCC
                                |||| ||||||  |||||
                                GTGG GCCGTC  CGGGG
                                  _     C_
GAM397   LOC126031 5'  CCCCAGCGCTGGCCGCTCC    11379        ____     _
                                CCTCGGC   GGCCGC CC
                                |||||||   |||||| ||
                                GGGGTCG   CCGGCG GG
                                    CGA     A
GAM397   LOC130814 5'  CACCCGGCCAGGGCCCGCCCC  11380      T   ____   _
                                CACC CGGC   GGCC GCCCC
                                |||| ||||   |||| |||||
                                GTGG GCCG   CCGG CGGGG
                                  _   GTC   G
GAM397   LOC144266 5'  CACCCTTGGCACCACCCC     11381       C_   G
                                CACCT  GGCG CCGCCCC
                                |||||  |||| |||||||
                                GTGGG  CCGT GGTGGGG
                                   AA   _
GAM397   LOC144347 3'  CACCCCGGGCCGGCCCC      11382         CG   _
                                CACCTCGG  GCCG CCCC
                                ||||||||  |||| ||||
                                GTGGGGCC  CGGC GGGG
                                    __   C
GAM397   LOC146243 5'  CACCCGGCAGGCCCC       11383      T     CC
                                CACC CGGCGG  GCCCC
                                |||| ||||||  |||||
                                GTGG GCCGTC  CGGGG
                                  _     __
GAM397   LOC148898 5'  CACCCCGCCCCCGCCCC      11384        G GG
                                CACCTCG C  CCGCCCC
                                |||||||  |  |||||||
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                                GTGGGGC G  GGCGGGG
                                    _ GG
GAM397   LOC149297 5'  CACCCCGGGCCGGAGCCCC   11385        __   CC
                                CACCTCGG  CGG  GCCCC
                                ||||||||  |||  |||||
                                GTGGGGCC  GCC  CGGGG
                                    CG   T_
GAM397   LOC149478 5'  CACCTCAGCCACCGGCCGCTCC 11386         ____     _  CIII
           G                     CACCTCGGC    GGCCGC CC    G
                                |||||||||    |||||| ||    |
                                GTGGAGTCG    CCGGCG GG    C
                                     GTGG     A  IIIC
GAM397   LOC150225 3'  CACTTTGGCAGCCAAGCCCC   11387     CTC      __
                                CAC   GGCGGCC  GCCCC
                                |||   |||||||  |||||
                                GTG   CCGTCGG  CGGGG
                                  AAA      TT
GAM397   LOC150577 3'  CAGCTCGACAGGCCCC      11388    C       CC
                                CA CTCGGCGG  GCCCC
                                || ||||||||  |||||
                                GT GAGCTGTC  CGGGG
                                 C       __
GAM397   LOC150630 5'  CATCTCACAGCCGCCCC     11389    C    G
                                CA CTCG CGGCCGCCCC
                                || |||| ||||||||||
                                GT GAGT GTCGGCGGGG
                                 A   _
GAM397   LOC152359 3'  CACCTCGGCTGCATGCACCC   11390         G  ___
                                CACCTCGGC GC   CGCCC
                                |||||||||  ||   |||||
                                GTGGAGCCG CG   GTGGG
                                     A  TAC
GAM397   LOC159201 3'  CACCCGGGGCCGCCCC      11391      T   C
                                CACC CGG GGCCGCCCC
                                |||| ||| |||||||||
                                GTGG GCC CCGGCGGGG
                                   _  _
GAM397   LOC163915 5'  CACCTCGGTCAGTGCGTCCC   11392         _   C_  _
                                CACCTCGG CGG  CG CCC
                                |||||||| |||  ||  |||
                                GTGGAGCC GTC  GC GGG
                                     A   AC  A
GAM397   LOC197273 5'  CACCCCGGGCCGCCGCCC     11393         _ G
                                CACCTCGG C GCCGCCC
                                |||||||| | |||||||
                                GTGGGGCC G CGGCGGG
                                     C G
GAM397   LOC197414 3'  CACTGTCAGGGCTGCCCC     11394     C_   C   C
                                CAC  TCGG GGC GCCCC
                                |||  |||| ||| |||||
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                                GTG  AGTC CCG CGGGG
                                  AC   _  A
GAM397   LOC199964 5'  CACCCCGGCGCCCGCCCC   11395         G
                                CACCTCGGCG CCGCCCC
                                |||||||||| |||||||
                                GTGGGGCCGC GGCGGGG
                                     G
GAM397   LOC199994 5'  CCTCGGCGGCGGCTCGCTCC  11396          ____  _
                                CCTCGGCGGC   CGC CC
                                ||||||||||   ||| ||
                                GGAGCCGCCG   GCG GG
                                     CCGA  A
GAM397   LOC202347 3'  CACCTCGATGAGACCGCC   11397        C__
                                CACCTCGG  GGCCGCC
                                ||||||||  |||||||
                                GTGGAGCT  CTGGCGG
                                    ACT
GAM397   LOC202775 5'  ACCTCGGCGGCACCCGCCCC  11398          ___
                                ACCTCGGCGGC  CGCCCC
                                ||||||||||  ||||||
                                TGGAGCCGCCG  GCGGGG
                                     TGG
GAM397   LOC202915 3'  CACACTCACTCTCCGCCCC   11399    _   G GG_
                                CAC CTCG C  CCGCCCC
                                ||| |||| |  |||||||
                                GTG GAGT G  GGCGGGG
                                  T   _ AGA
GAM397   LOC205418 5'  CACCCCCAGGCCGGCTGTCCC  11400      __  _  CG_
                                CACCTC  GGC GGC  CCC
                                ||||||  ||| |||  |||
                                GTGGGG  CCG CCG  GGG
                                   GT  G  ACA
GAM397   LOC220581 5'  CACCCCGGTAGCTGATGCCCC  11401       CG  C___
                                CACCTCGG  GC   GCCCC
                                ||||||||  ||   |||||
                                GTGGGGCC  CG   CGGGG
                                    AT  ACTA
GAM397   LOC220635 5'  CCTCGGCCACCTCGCCCC   11361       G  __
                                CCTCGGC GCC  GCCCC
                                ||||||| |||  |||||
                                GGAGCCG TGG  CGGGG
                                    G  AG
GAM397   LOC220758 5'  CCAGGCGGCGGCCGCCCC   11402    T__
                                CC  CGGCGGCCGCCCC
                                ||  ||||||||||||
                                GG  GCCGCCGGCGGGG
                                 TCC
GAM397   LOC220776 3'  CACCTCAGCTCCCGTTGCTCC  11403        GG  ___  _
                                CACCTCGGC  CC  GC CC
                                |||||||||  ||  || ||
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                                GTGGAGTCG  GG   CG GG
                                     AG  CAA  A
GAM397   LOC245744 3'  CACCCCGGGACCCGCGCCCC   11404        C   ___
                                CACCTCGG GGCC   GCCCC
                                |||||||| ||||   |||||
                                GTGGGGCC CTGG   CGGGG
                                     _   GCG
GAM397   LOC254531 5'  CACCTGCGGCCACTTGCC    11405      CG      ___
                                CACCT  GCGGCCGC   CC
                                |||||  ||||||||   ||
                                GTGGA  CGCCGGTG   GG
                                   __       AAC
GAM397   LOC255167 5'  CCCCGGCCGCGCCGCCCC    11406        _ _
                                CCTCGGC G GCCGCCCC
                                ||||||| | ||||||||
                                GGGGCCG C CGGCGGGG
                                     G G
GAM397   LOC255196 5'  CACCCCGGCACTGCTGCCC   11407          __ C
                                CACCTCGGCG  GC GCCC
                                ||||||||||  || ||||
                                GTGGGGCCGT  CG CGGG
                                      GA  A
GAM397   LOC256158 5'  CACCCCAGTCATGCTGCCCC   11408        _ _ C
                                CACCTCGG CG GC GCCCC
                                |||||||| || || |||||
                                GTGGGGTC GT CG CGGGG
                                     A  A  A
GAM397   LOC256310 3'  CGCCTTCCGCAGCCGCTCC   11409   A  _ G      _
                                C CCT C GCGGCCGC CC
                                | ||| | |||||||| ||
                                G GGA G CGTCGGCG GG
                                 C   A G       A
GAM397   LOC51093  5'  CACCCACGCCGCCCC      11410      CG   G
                                CACCT  GCG CCGCCCC
                                |||||  ||| |||||||
                                GTGGG  TGC GGCGGGG
                                   __  _
GAM397   LOC57109  5'  ACCTCAGCACGCACGCTCC   11411          _ _  _
                                ACCTCGGCG GC CGC CC
                                ||||||||| || ||| ||
                                TGGAGTCGT CG GCG GG
                                      G  T   A
GAM397   LOC89941  3'  CACCCCAGCTGTGCTGCCCC   11412         G__ C
                                CACCTCGGC   GC GCCCC
                                |||||||||   || |||||
                                GTGGGGTCG   CG CGGGG
                                      ACA  A
GAM397   LOC91632  5'  CACCCCGGCCCGCGCCCC    11352         GGC
                                CACCTCGGC   CGCCCC
                                |||||||||   ||||||
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                                GTGGGGCCG   GCGGGG
                                     GGC
GAM398  ACADM    3'  AACCTATGTAGTTTTCTAGGT  11415      CG ATCCTTT
                                AACC  T      TTTTCTAGGT
                                ||||  |      ||||||||||
                                TTGG  A      AAAAGATCCA
                                  AT CATC___
GAM398  EDNRA    3'  CGATCTTTTTCTCTTAGGT    11416    T   C       _
                                CG ATC TTTTTTTCT AGGT
                                || ||| ||||||||| ||||
                                GC TAG AAAAAGAGA TCCA
                                  _  _       A
GAM398  MBD1     3'  ACCAGCAAGTTTTTTCTGGGT  11417     C   TCCT      A
                                ACC GTA    TTTTTTCT GGT
                                ||| |||    |||||||| |||
                                TGG CGT    AAAAAAGA CCA
                                  T   TC__       C
GAM398  MBD1     3'  ACCAGCAAGTTTTTTCTGGGT  11417     C   TCCT      A
                                ACC GTA    TTTTTTCT GGT
                                ||| |||    |||||||| |||
                                TGG CGT    AAAAAAGA CCA
                                  T   TC__       C
GAM398  MBD1     3'  ACCAGCAAGTTTTTTCTGGGT  11417     C   TCCT      A
                                ACC GTA    TTTTTTCT GGT
                                ||| |||    |||||||| |||
                                TGG CGT    AAAAAAGA CCA
                                  T   TC__       C
GAM398  MBD1     3'  ACCAGCAAGTTTTTTCTGGGT  11417     C   TCCT      A
                                ACC GTA    TTTTTTCT GGT
                                ||| |||    |||||||| |||
                                TGG CGT    AAAAAAGA CCA
                                  T   TC__       C
GAM398  OTOR     3'  AACCTACAGACTTTTTTTTTC 11418      CG  TC     ___   A
           TGGGT                    AACC  TA  CTTTTTT   TCT GGT
                                ||||  ||  |||||||   ||| |||
                                TTGG  GT  GAAAAAA   AGA CCA
                                  AT  CT      AAA   C
GAM398  POLQ     3'  ATCTCTGTTCTTTCCAGG    11419     _  _
                                ATC CT TTTTTTCTAGG
                                ||| || ||||||||||
                                TAG GA AAGAAAGGTCC
                                  A  C
GAM398  FLJ13220 5'  CCCGTTTTTTTTCGAAGGT   11420      ATCC      T_
                                CCCGT   TTTTTTTC  AGGT
                                |||||   ||||||||  ||||
                                GGGCA   AAAAAAAG  TCCA
                                   _____      CT
GAM398  PPFIA4   3'  ACCTGTATCCCTCAGCTTGG  11421     C       TTTT  A
                                ACC GTATCCTTT   CT GG
                                ||| |||||||||   || ||
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                                TGG CATAGGGAG    GA CC
                                  A        TC__  A
GAM398  LOC144742 5'  ACCCTGTTTGCCTCTAGG    11422      GTATCC   T
                                ACCC      TTT TTTCTAGG
                                ||||      ||| ||||||||
                                TGGG      AAA GGAGATCC
                                  AC_____   C
GAM398  LOC145826 3'  GTATCTTGCCCTAGGT      11423       CTT  T
                                GTATC   TT TTCTAGGT
                                ||||||   || ||||||||
                                CATAG   AA GGGATCCA
                                   ___  C
GAM398  LOC221336 3'  AACCCATATTTTTTTTCAG    11424          CC       T
                                AACCCGTAT  TTTTTTTC AG
                                |||||||||  |||||||| ||
                                TTGGGTATA  AAAAAAAG TC
                                     __       _
GAM398  LOC257364 3'  CCCTGTCTTTTTTCCTCTTAGGT 11425     GTA  C       _
                                CCC   TC TTTTTTTCT AGGT
                                |||   || |||||||||| ||||
                                GGG   AG AAAAGGAGA TCCA
                                  AC_  A        A
GAM398  LOC90906  5'  GTATCCCTGTTTTGGGT     11426         T    CTA
                                GTATCCTT TTTT   GGT
                                |||||||| ||||   |||
                                CATAGGGA AAAA   CCA
                                     C    C__
GAM398  LOC92126  5'  AACCCATATTTTTTTCCAGG    11427          CCTT
                                AACCCGTAT    TTTTTCTAGG
                                |||||||||    ||||||||||
                                TTGGGTATA    AAAAAGGTCC
                                     ____
GAM399  ARHGEF1   3'  AGCGAAGGCACTTGGGGGTGG  11430        AAA  __  A  A
                                AGCGGA   AC  GG GG TGG
                                ||||||   ||  || || |||
                                TCGCTT   TG  CC CC ACC
                                   CCG  AA  _  C
GAM399  ASIC4     5'  AAGCGGGAAGAGGACAG     11431       AAAAAC
                                AAGCGG     GGAGGATGG
                                ||||||     |||||||||
                                TTCGCC     TCTCCTGTC
                                   CT____
GAM399  AXUD1     3'  AAGGGGGAAGATGGAA      11432     C  AAAAAC
                                AAG GG     GGAGGATGGAA
                                ||| ||     ||||||||||
                                TTC CC     CCTTCTACCTT
                                  _ _______
GAM399  B4GALT6   5'  AGCGGACGGAATGAATGG    11434       AAAA   __
                                AGCGGA   CGGA  GGATGG
                                ||||||   ||||  ||||||
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                                TCGCCT   GCCT  CTTACC
                                   ____   TA
GAM399  B4GALT6  5' AGCGGAAAAGAGGAAATGG   11433       AAC    __
                                AGCGGAAA   GGAGGA  TGG
                                ||||||||   ||||||  |||
                                TCGCCTTT   TCTCCT  ACC
                                   ___     TT
GAM399  BASP1    3' AGAGGAAGAATGGAGGATTGG  11435    C   A  C    _
                                AG GGAA AA GGAGGAT GG
                                || |||| || ||||||| ||
                                TC CCTT TT CCTCCTA CC
                                 T   C  A     A
GAM399  BGN      3' AGAGGAAGGACGGGGAAAG   11436    C   AA   A  T
                                AG GGAA  ACGG GGA GG
                                || ||||  |||| ||| ||
                                TC CCTT  TGCC CCT TC
                                 T   CC   _  T
GAM399  CALM2    3' AAGGGAAGAAAACATGGAGG   11437    C   __   __
                                AAG GGAA  AAAC  GGAGG
                                ||| ||||  ||||  |||||
                                TTC CCTT  TTTG  CCTCC
                                  _   CT   TA
GAM399  CCND2    3' AGGGGAAAGACGGAGGGG    11438   C   A     AT
                                AG GGAAA ACGGAGG  GG
                                || ||||| |||||||  ||
                                TC CCTTT TGCCTCC  CC
                                 C   C     __
GAM399  COG2     5' AAGCGAGAAAACGCAGGAGG   11439     GA    G   T
                                AAGCG  AAAACG AGGA GG
                                |||||  |||||| |||| ||
                                TTCGC  TTTTGC TCCT CC
                                   TC    G   _
GAM399  CRY1     5' AGTGGAAAGATGAATGGA    11440   C   AAAC  _
                                AG GGAA   GGA GGATGGA
                                || ||||   ||| |||||||
                                TC CCTT   TCT CTTACCT
                                 A   ____  A
GAM399  DYSF     3' GGAGAAGGAAATGATGGAAG   11441    AAAAC   __
                                GGA   GGAG  GATGGAAG
                                |||   ||||  ||||||||
                                CCT   CCTT  CTACCTTC
                                  CTT__   TA
GAM399  FCAR     3' AAGCGGAAAGTGTGGTGGGG   11442       AAC_  A  AT
                                AAGCGGAAA   GG GG  GG
                                |||||||||   || ||  ||
                                TTCGCCTTT   CC CC  CC
                                     CACA  A  __
GAM399  FCAR     3' AAGCGGAAAGTGTGGTGGGG   11442       AAC_  A  AT
                                AAGCGGAAA   GG GG  GG
                                |||||||||   || ||  ||
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                                TTCGCCTTT   CC CC  CC
                                     CACA  A  __
GAM399  FGF2    3'  AGGGAGAAAGGATGGAA    11443   C   AAAAC
                                AG GGA    GGAGGATGGAA
                                || |||    ||||||||||
                                TC CCT    TTTCCTACCTT
                                 _  C____
GAM399  FOXD2   5'  GCAGAAAAAAATGGAA     11444        CGGAG
                                GCGGAAAAA    GATGGAA
                                |||||||||    |||||||
                                CGTCTTTTT    TTACCTT
                                     _____
GAM399  GDI1    3'  AGCAGAAGAATTAGGGGTGG  11445       A  C__  A  A
                                AGCGGAA AA   GG GG TGG
                                ||||||| ||   || || |||
                                TCGTCTT TT   CC CC ACC
                                    C  AAT  _  _
GAM399  GPRK6   3'  GCTGAGGGACGGAGGACACTGG 11446    G  AAA     ___
                                GC GA   ACGGAGGA   TGG
                                || ||   ||||||||   |||
                                CG CT   TGCCTCCT   ACC
                                 A  CCC       GTG
GAM399  GRF2    3'  AAGAGGGGAGAGATGGAA    11447    C  AAAAAC   _
                                AAG GG     GGAG GATGGAA
                                ||| ||     |||| |||||||
                                TTC CC     CCTC CTACCTT
                                  T _______   T
GAM399  ID1     5'  AAGCGAAAAAAATGAGGTGGAA 11448          CG   A
          G                      AAGCGGAAAAA  GAGG TGGAAG
                                ||||||||||  |||| ||||||
                                TTCGCTTTTTT  CTCC ACCTTC
                                      TA   _
GAM399  KLF8    5'  GCTGGAAAATGAGGAGG     11449   _    ACG    T
                                GC GGAAAA   GAGGA GG
                                || ||||||   ||||| ||
                                CG CCTTTT   CTCCT CC
                                 A     A__    _
GAM399  LAMC2   3'  GGAAAGATGGATGGAAG     11450     AAAC  _
                                GGAA   GGA GGATGGAAG
                                ||||   ||| |||||||||
                                CCTT   TCT CCTACCTTC
                                   ____  A
GAM399  MAPRE2  3'  AAGCGGAAAGTGGGGTGG    11451        AAC  A  A
                                AAGCGGAAA   GG GG TGG
                                |||||||||   || || |||
                                TTCGCCTTT   CC CC ACC
                                     CA_  _  _
GAM399  MMP19   3'  AGGGAGGGAGAACATGGGA   11452   C   AAAAC     ___
                                AG GGA    GGAGGAT   GGA
                                || |||    |||||||   |||
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                                TC CCT    CCTCTTG   CCT
                                 _  C____      TAC
GAM399  MMP19    3'  AGGGAGGGAGAACATGGGA   11452    C   AAAAC     ___
                                AG GGA    GGAGGAT   GGA
                                || |||    |||||||   |||
                                TC CCT    CCTCTTG   CCT
                                 _  C____      TAC
GAM399  NF2      5'  AGCGGAAAGGGGAGTTGG    11453        AAC   GA
                                AGCGGAAA   GGAG  TGG
                                ||||||||   ||||  |||
                                TCGCCTTT   CCTC  ACC
                                     CC_   A_
GAM399  NPR3     3'  GCAGAAAAAAAAAAGTGG    11454         CG    A
                                GCGGAAAAA  GAGG TGG
                                |||||||||  |||| |||
                                CGTCTTTTT  TTTC ACC
                                      TT   _
GAM399  PDE4A    3'  GGACAGAGGGATGGAAG     11455     AAAA     _
                                GGA   CGGAGG ATGGAAG
                                |||   |||||| |||||||
                                CCT   GTCTCC TACCTTC
                                 ____     C
GAM399  PDGFB    3'  AAGAGGAAAATGCAGGGTGGA  11456     C     A_   A  A
                                AAG GGAAAA  CGG GG TGGA
                                ||| ||||||  ||| || ||||
                                TTC CCTTTT  GTC CC ACCT
                                  T     AC   _ _
GAM399  PIK4CB   3'  AAGCGGGTGAGAGAACATGGAA 11457       AAAAAC    G
          G                      AAGCGG     GGAG ATGGAAG
                                ||||||     |||| |||||||
                                TTCGCC     TCTT TACCTTC
                                   CACTC_    G
GAM399  PKM2     3'  AGTGGGGGAAAATGGAA     11458    C  AAAAAC
                                AG GG     GGAGGATGGAA
                                || ||     ||||||||||
                                TC CC     CCTTTTACCTT
                                 A  C_____
GAM399  POU2AF1  3'  AGGGGAAGAATGGAAGGATGG  11459    C    A  C   _
                                AG GGAA AA GGA GGATGG
                                || |||| || ||| ||||||
                                TC CCTT TT CCT CCTACC
                                 C    C  A   T
GAM399  PPP2R2B  3'  GGAAAAAAAAATGGTGGA    11460        CG  _  A
                                GGAAAAA  GA GG TGGA
                                |||||||  || || ||||
                                CCTTTTT  TT CC ACCT
                                     TT  A  _
GAM399  PPP2R4   3'  AAGGGAAAAGCAATGGAA    11461     C     AAC  AG
                                AAG GGAAA   GG  GATGGAA
                                ||| |||||   ||  |||||||
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                                TTC CCTTT   TC  TTACCTT
                                  _    ___  G_
GAM399  RABL2A   3'  AAGAGGAAAAAAGATGG     11462     C    AACG
                                AAG GGAAA    GAGGATGG
                                ||| |||||    ||||||||
                                TTC CCTTT    TTTCTACC
                                  T    ____
GAM399  RABL2B   3'  AAGAGGAAAAAAGATGG     11462     C    AACG
                                AAG GGAAA    GAGGATGG
                                ||| |||||    ||||||||
                                TTC CCTTT    TTTCTACC
                                  T    ____
GAM399  RAD52    3'  AAGTGGGAAAACGGCAGACAG  11463     C  A      A
                                AAG GG AAAACGG GGATGG
                                ||| || ||||||| ||||||
                                TTC CC TTTTGCC TCTGTC
                                  A  C      G
GAM399  RAP1GDS1 3'  AAGCGGAAGAAGCCGCTGGATG 11464         AAA__  GA
           GA                     AAGCGGAA    CG  GGATGGA
                                ||||||||    ||  |||||||
                                TTCGCCTT    GC  CCTACCT
                                    CTTCG  GA
GAM399  RELA     3'  AAGCTGGAGGATGGGGATGG   11465      _  AAAAC  A
                                AAGC GGA    GG GGATGG
                                |||| |||    || ||||||
                                TTCG CCT    CC CCTACC
                                  A  CCTA_ _
GAM399  RNF26    5'  AAGTGGGTAAGACGGAAGTGGA 11466     C  AAAA_     A
                                AAG GG    ACGGAGG TGGA
                                ||| ||    ||||||| ||||
                                TTC CC    TGCCTTC ACCT
                                  A  CATTC     _
GAM399  SCNN1B   5'  AGCGGGGACACGGAGGATG   11467      AAAA
                                AGCGG   ACGGAGGATG
                                |||||   ||||||||||
                                TCGCC   TGCCTCCTAC
                                   CCTG
GAM399  SEPN1    5'  AAGCGAAAGAGCGGGGCGG   11468        AAA  A  A
                                AAGCGGAA   CGG GG TGG
                                ||||||||   ||| || |||
                                TTCGCTTT   GCC CC GCC
                                    CTC  _ _
GAM399  SFTPA2   3'  AAGGGGAAAGTGGAGCCGG   11469     C    AAC   GA
                                AAG GGAAA   GGAG  TGG
                                ||| |||||   ||||  |||
                                TTC CCTTT   CCTC  GCC
                                  C    CA_   G_
GAM399  SLC9A1   5'  AAGGGGGAGGACGGA      11470     C  AAAAAC
                                AAG GG    GGAGGATGGA
                                ||| ||    ||||||||||
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                                TTC CC     CCTCCTGCCT
                                  _ ______
GAM399  TBL1X    3'  AGTGGAAAGACAGGGGGAGGG  11471    C    A   A_  T
                                AG GGAAA ACGG  GGA GG
                                || ||||| ||||  ||| ||
                                TC CCTTT TGTC  CCT CC
                                 A    C   CC  C
GAM399  TIMELESS 5'  AAGTGGAGAAACAGGAGACAG  11472     C  A     AG
                                AAG GGA AAACGG  GATGG
                                ||| ||| ||||||  |||||
                                TTC CCT TTTGTC  CTGTC
                                  A  C     CT
GAM399  TNFRSF10B 3'  GGAAGTGGGAGAGGATGGAAG  11473      AAAC_
                                GGAA    GGAGGATGGAAG
                                ||||    ||||||||||||
                                CCTT    TCTCCTACCTTC
                                  CACCC
GAM399  VARS2    5'  AAGTGGAAAAACTGGAGG    11474    C      _
                                AAG GGAAAAAC GGAGG
                                ||| |||||||| |||||
                                TTC CCTTTTTG CCTCC
                                  A       A
GAM399  ZNF144   3'  AAGTGGAAGGAGTGGA      11475    C   AAAC   GA
                                AAG GGAA   GGAG  TGGA
                                ||| ||||   ||||  ||||
                                TTC CCTT   CCTC  ACCT
                                  A  _____   __
GAM399  BCL2L12  5'  AGCGGGAAAGAGGATGG     11476      A  AAC
                                AGCGG AA   GGAGGATGG
                                ||||| ||   |||||||||
                                TCGCC TT   TCTCCTACC
                                   C ___
GAM399  C1orf2   5'  AAGCGGGAAGGATGGAAA    11477      AAAAAC
                                AAGCGG     GGAGGATGGAAG
                                ||||||     ||||||||||||
                                TTCGCC     CTTCCTACCTTT
                                  _______
GAM399  C1orf2   5'  AAGCGGGAAGGATGGAAA    11477      AAAAAC
                                AAGCGG     GGAGGATGGAAG
                                ||||||     ||||||||||||
                                TTCGCC     CTTCCTACCTTT
                                  _______
GAM399  C20orf98 3'  AAGGGAAGGTGGGATGGAA   11478    C   AAAC  A_
                                AAG GGAA   GG  GGATGGAA
                                ||| ||||   ||  ||||||||
                                TTC CCTT   CC  CCTACCTT
                                  _  _____ AC
GAM399  CDK5RAP3 3'  AAGCGGAGAAGATGG       11479       AAAACG
                                AAGCGGA     GAGGATGG
                                |||||||     ||||||||
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                                TTCGCCT     CTTCTACC
                                        ______
GAM399  CYYR1    5' AGGGAATGGGGAGGATGGA   11480    C    AAAC
                                AG GGAA    GGAGGATGGA
                                || ||||    ||||||||||
                                TC CCTT    CCTCCTACCT
                                 _   ACC_
GAM399  DGKD     3' AGCGGGAGGAGAGAGGATGGA 11482      AAAAAC
                                AGCGG     GGAGGATGGA
                                |||||     ||||||||||
                                TCGCC     TCTCCTACCT
                                   CTCCTC
GAM399  DGKD     3' GCAGGGAACAGGATGGA     11481     AAA   GG
                                GCGG   AAC  AGGATGGA
                                ||||   |||  ||||||||
                                CGTC   TTG  TCCTACCT
                                  CC_  ___
GAM399  E1B-AP5  3' GGAAGAACAGGAGGTGGAAG  11483     A  _    A
                                GGAA AAC GGAGG TGGAAG
                                |||| ||| ||||| ||||||
                                CCTT TTG CCTCC ACCTTC
                                  C   T    _
GAM399  E1B-AP5  3' GGAAGAACAGGAGGTGGAAG  11483     A  _    A
                                GGAA AAC GGAGG TGGAAG
                                |||| ||| ||||| ||||||
                                CCTT TTG CCTCC ACCTTC
                                  C   T    _
GAM399  FAM3A    5' AAGCGGAAGGACAGGTTTGGGT 11484        AA   A___  A
           GG                    AAGCGGAA  ACGG   GG TGG
                                ||||||||  ||||   || |||
                                TTCGCCTT  TGTC   CC ACC
                                    CC    CAAA  C
GAM399  FLJ10482 3' GGAGAAATGGGGCCATGGAAG 11485    A  C  A  __
                                GGA AAA GG GG  ATGGAAG
                                ||| ||| || ||  |||||||
                                CCT TTT CC CC  TACCTTC
                                  C   A  _  GG
GAM399  FLJ11539 3' AGGGAAGGTGGACAGAAA    11486   C    AAAC  A
                                AG GGAA    GG GGATGGAAG
                                || ||||    || |||||||||
                                TC CCTT    CC CCTGTCTTT
                                 _   _____  A
GAM399  FLJ20010 3' AAGTGAAGGGGGAGATGGAAG 11487    C   AAAAC  AG
                                AAG GGA    GG  GATGGAAG
                                ||| |||    ||  ||||||||
                                TTC CTT    CC  CTACCTTC
                                  A   CC___  CT
GAM399  FLJ20254 3' GGAAGAACTGAGGTGGA     11488     A  G   A
                                GGAA AAC GAGG TGGA
                                |||| ||| |||| ||||
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                                CCTT TTG CTCC ACCT
                                  C   A   _
GAM399  FLJ21240  3'  AACGGAAGAAAAACAATGGAAG 11489       A  C   G
                                AGCGGAA AA GGA GATGGAAG
                                ||||||| || ||| ||||||||
                                TTGCCTT TT TTT TTACCTTC
                                    C  _   G
GAM399  GAL3ST-4  3'  AACAAAATGAGTGGAGGGTGGA 11490       AAAC_    A
                                AGCGGAA    GGAGG TGGA
                                |||||||    ||||| ||||
                                TTGTTTT    CCTCC ACCT
                                    ACTCA    C
GAM399  GMPPB    5'  AAGCAGGGAGACGGA      11491       AAAAAC    G
                                AAGCGG     GGAG ATGGA
                                ||||||     |||| |||||
                                TTCGTC     CCTC TGCCT
                                  _______   _
GAM399  IL-17RC   3'  GGAGTCCCCGGGGGATGGAAG  11492     AAAA_  A
                                GGA    CGG GGATGGAAG
                                |||    ||| |||||||||
                                CCT    GCC CCTACCTTC
                                  CAGGG   C
GAM399  KCNH8    5'  AGGGGAAGTGGAAGGATGGA   11493    C    AAAC
                                AG GGAA    GGAGGATGGA
                                || ||||    ||||||||||
                                TC CCTT    CTTCCTACCT
                                 C    CAC_
GAM399  KIAA0354  3'  AGTGAAGAAATGGAGAACAG   11494    C   A   C
                                AG GGA AAA GGAGGATGG
                                || ||| ||| |||||||||
                                TC CTT TTT CCTCTTGTC
                                 A   C   A
GAM399  KIAA0894  3'  AAGGGAGAAAGAATGGAA    11495     C   AAAAC
                                AAG GGA    GGAGGATGGAA
                                ||| |||    ||||||||||
                                TTC CCT    TTTCTTACCTT
                                  _   C____
GAM399  KIAA0995  5'  AGCGGCGGGGCGGAGGACGG   11496      AAAAA
                                AGCGG    CGGAGGATGG
                                |||||    ||||||||||
                                TCGCC    GCCTCCTGCC
                                   GCCCC
GAM399  KIAA1317  5'  AAGCAGAAAGATGGA      11497       AAACGGA
                                AAGCGGAA     GGATGGA
                                ||||||||     |||||||
                                TTCGTCTT     TCTACCT
                                             _______
GAM399  KIAA1430  5'  AGCGGAAAGGGAAAGGAGG   11498       AAC     T
                                AGCGGAAA   GGAGGA GG
                                ||||||||   |||||| ||
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                                TCGCCTTT   TTTCCT CC
                                    CCC    _
GAM399  KIAA1434  3'  AAGTGGAAAAATGGCAGCAG  11499    C     C  A  A
                                AAG GGAAAAA GG GG TGG
                                ||| ||||||| || || |||
                                TTC CCTTTTT CC TC GTC
                                  A     A  G  _
GAM399  KIAA1915  3'  AAGCAGGGAAAATGATGGAGG  11500    __    AC__
                                AAGC  GGAAAA   GGAGG
                                ||||  ||||||   |||||
                                TTCG  CCTTTT   CCTCC
                                   TC     ACTA
GAM399  KIAA1924  3'  AAGCCGGAAGGTGGATAAAAA  11501    _   AAAC  A
                                AAGC GGAA   GG GGATGGAAG
                                |||| ||||   || |||||||||
                                TTCG CCTT   CC CCTATTTTT
                                  G   ____  A
GAM399  MGC14799  5'  AAGCGGGAAGACAGAGGA   11502      A  A
                                AAGCGG AA ACGGAGGA
                                |||||| || ||||||||
                                TTCGCC TT TGTCTCCT
                                   C  C
GAM399  MGC15429  3'  AAGTGGAAGAACAGGAGAA   11503    C   A  _
                                AAG GGAA AAC GGAGGA
                                ||| |||| ||| ||||||
                                TTC CCTT TTG CCTCTT
                                  A   C   T
GAM399  MGC16824  5'  GGAGGAGGAGGACGTGGAAG  11504    AAAAC    __
                                GGA    GGAGGA  TGGAAG
                                |||    ||||||  ||||||
                                CCT    CCTCCT  ACCTTC
                                  CCT__     GC
GAM399  NMT1    3'  AGCAGGCCAAGGGGATGGAAG  11505     AAA  C  A
                                AGCGG   AA GG GGATGGAAG
                                |||||   || || |||||||||
                                TCGTC   TT CC CCTACCTTC
                                   CGG  _  _
GAM399  OS-9    5'  AAGCGAAGAGCGGACGAAAA   11506      AAAAC  A
                                AAGCGGA    GG GGATGGAAG
                                |||||||    || |||||||||
                                TTCGCTT    TC CCTGCTTTT
                                    C____  G
GAM399  OSBPL3   3'  GCAGAGGTATGGATGGAAG   11507     AAAAC  A__
                                GCGGA    GG   GGATGGAAG
                                |||||    ||   |||||||||
                                CGTCT    CC   CCTACCTTC
                                   _____  ATA
GAM399  PI4KII   3'  AGGGGAAAAGACACATGGAAG  11508    C    _  GAGG
                                AG GGAAAA ACG    ATGGAAG
                                || |||||| |||    |||||||
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                                TC CCTTTT TGT    TACCTTC
                                 C     C  G___
GAM399  PMX2B    5'  AAGTGGAAAAATGAAATAAAAG 11509     C      CG   G
                                AAG GGAAAAA  GAG ATGGAAG
                                ||| |||||||  ||| |||||||
                                TTC CCTTTTT  CTT TATTTTC
                                  A      A_  _
GAM399  RAN      5'  GCTGGAAAGATGGCGGAAG   11510    _    AAAC   _ A
                                GC GGAA    GGA GG TGGAAG
                                || ||||    ||| || ||||||
                                CG CCTT    TCT CC GCCTTC
                                 A   _____  A  _
GAM399  RBAF600  3'  AGGGAGAACAGAGGGTGGAAG  11511    C   AA       A
                                AG GGA  AACGGAGG TGGAAG
                                || |||  |||||||| ||||||
                                TC CCT  TTGTCTCC ACCTTC
                                 _   C_       C
GAM399  RNF8     3'  GCAGAAGAATGGAAATGAA    11512       A  C    G
                                GCGGAA AA GGAG ATGGA
                                |||||| || |||| |||||
                                CGTCTT TT CCTT TACTT
                                    C  A    _
GAM399  SAE1     3'  GCAGAGGGGTGCTTGGAAG    11513      AAAAC  A  A___
                                GCGGA    GG GG    TGGAAG
                                |||||    || ||    ||||||
                                CGTCT    CC CC    ACCTTC
                                   ______ _  ACGA
GAM399  SIAT4A   5'  AGAGGAGAAAAATGGAA     11514    C   AAAAC
                                AG GGA     GGAGGATGGAA
                                || |||     ||||||||||
                                TC CCT     CTTTTTACCTT
                                 T  ______
GAM399  SIAT8C   5'  AAGCAGGGAGGATGG       11515       AAAAAC
                                AAGCGG     GGAGGATGG
                                ||||||     |||||||||
                                TTCGTC     CCTCCTACC
                                           _______
GAM399  STX12    3'  AGCGGGAGAACGATCGGAGG   11516      AAA    A_   T
                                AGCGG   AACGG  GGA GG
                                |||||   |||||  ||| ||
                                TCGCC   TTGCT  CCT CC
                                   CTC     AG   _
GAM399  LOC113230 5'  GCGGAAAACGCAGGTGG     11517        A  G   A
                                GCGGAAAA CG AGG TGG
                                |||||||| || ||| |||
                                CGCCTTTT GC TCC ACC
                                     _ G   _
GAM399  LOC124222 3'  GCAGAAAGATGGAGATCAGGAA 11518        AAC    AT_
           G                     GCGGAAA   GGAGG   GGAAG
                                |||||||   |||||   |||||
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                                CGTCTTT   CCTCT   CCTTC
                                    CTA     AGT
GAM399   LOC124987 5'  AGGGAGAGGTGGAGGACGAA   11519    C   AAAAC
                                AG GGA     GGAGGATGGA
                                || |||     ||||||||||
                                TC CCT     CCTCCTGCTT
                                 _   CTCCA
GAM399   LOC131000 5'  GGAAAAACCGAGGCTTCCAAAG 11520         G    ATG__
                                GGAAAAAC GAGG     GAAG
                                |||||||| ||||     ||||
                                CCTTTTTG CTCC     TTTC
                                     G    GAAGG
GAM399   LOC133688 3'  GGAAGAATTTGAAATGGAAG   11521      A  CG_   G
                                GGAA AA   GAG ATGGAAG
                                |||| ||   ||| |||||||
                                CCTT TT   CTT TACCTTC
                                  C  AAA   _
GAM399   LOC138389 5'  AGGGAGGGTAGAACAGATGGAA 11522     C   AAAAC   __
           G                     AG GGA     GGA  GGATGGAAG
                                || |||     |||  |||||||||
                                TC CCT     TCT  TCTACCTTC
                                 _   CCCA_   TG
GAM399   LOC144970 3'  AAGGGAAAAACGGGGCCTGG   11523     C         A  A_
                                AAG GGAAAAACGG GG  TGG
                                ||| ||||||||| ||  |||
                                TTC CCTTTTTGCC CC  ACC
                                  _         _  GG
GAM399   LOC145871 5'  GGAAAATGCCGGCGGAGGGTGG 11524        A_____     A
                                GGAAAA      CGGAGG TGG
                                ||||||      |||||| |||
                                CCTTTT      GCCTCC ACC
                                    ACGGCC      C
GAM399   LOC148171 3'  AAGGGAAAAACGGGGCCTGG   11523     C         A  A_
                                AAG GGAAAAACGG GG  TGG
                                ||| ||||||||| ||  |||
                                TTC CCTTTTTGCC CC  ACC
                                  _         _  GG
GAM399   LOC148172 3'  AAGGGAAAAACGGGGCCTGG   11523     C         A  A_
                                AAG GGAAAAACGG GG  TGG
                                ||| ||||||||| ||  |||
                                TTC CCTTTTTGCC CC  ACC
                                  _         _  GG
GAM399   LOC151701 5'  ACGGAAGGAAAAGTGGA     11525       AAAC     _
                                GCGGAA    GGAGGA TGGA
                                ||||||    |||||| ||||
                                TGCCTT    CCTTTT ACCT
                                    ____      C
GAM399   LOC152317 5'  AAGGGGAAGGATGGA       11526     C  AAAAAC
                                AAG GG     GGAGGATGGA
                                ||| ||     ||||||||||
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                                TTC CC     CTTCCTACCT
                                  _ ______
GAM399  LOC153914 5'  GCGAGAAGGATGAATGGA    11527     _  AAAC  _
                                GCG GAA    GGA GGATGGA
                                ||| |||    ||| |||||||
                                CGC CTT    CCT CTTACCT
                                  T  _____  A
GAM399  LOC154877 3'  AGAGGAAGGAGGATGG      11528    C   AAAC
                                AG GGAA    GGAGGATGG
                                || ||||    |||||||||
                                TC CCTT    CCTCCTACC
                                 T  _____
GAM399  LOC155064 3'  AGGGAGGGAGGATGGAA     11529    C  AAAAC
                                AG GGA     GGAGGATGGAA
                                || |||     ||||||||||
                                TC CCT     CCTCCTACCTT
                                 _  C_____
GAM399  LOC159090 5'  GGGAAAACAAGGATGGA     11530    A     G
                                GG AAAACG AGGATGGA
                                || |||||| ||||||||
                                CC TTTTGT TCCTACCT
                                 C     _
GAM399  LOC159121 5'  AGGTGAGAGACGCCAGAATGGA 11531    CG  AAA   G_
                                AG  GA   ACG  AGGATGGA
                                ||  ||   |||  ||||||||
                                TC  CT   TGC  TCTTACCT
                                 CA  CTC   GG
GAM399  LOC170396 3'  AGCTGGGAAAATGGAGGCCAAG 11532     __     AC     AT_
                                AGC  GGAAAA  GGAGG   GG
                                |||  ||||||  |||||   ||
                                TCG  CCTTTT  CCTCC   TC
                                  AC     A_    GGT
GAM399  LOC196500 3'  AGTGGAAGGAAGGAGGGA    11533    C   AAAC     T
                                AG GGAA    GGAGGA GGA
                                || ||||    |||||| |||
                                TC CCTT    CTTCCT CCT
                                 A   C___     C
GAM399  LOC197114 5'  AAGGGGAGGAAGATGGA     11534     C   AAAAC
                                AAG GGA     GGAGGATGGA
                                ||| |||     ||||||||||
                                TTC CCT     CCTTCTACCT
                                  C  _____
GAM399  LOC199692 3'  AAGCAGGAAAATGGGATGGAAG 11535      _     ACGGA
                                AAGC GGAAAA     GGATGGAAG
                                |||| ||||||     |||||||||
                                TTCG CCTTTT     CCTACCTTC
                                  T     AC___
GAM399  LOC199747 3'  GCGGGAAGGTTGATGAAAG    11536      A  AAC  AG
                                GCGG AA   GG  GATGGAAG
                                |||| ||   ||  ||||||||
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                                CGCC TT   CC  CTACTTTC
                                  C ___  AA
GAM399   LOC219404 5'  GCGCGGAGGACGGAAG      11537     GAAAAA
                                GCG     CGGAGGATGGAAG
                                |||     ||||||||||||
                                CGC     GCCTCCTGCCTTC
                                 _______
GAM399   LOC220954 3'  GGAAGGAAAAATGGAAG     11538      AAAC
                                GGAA    GGAGGATGGAAG
                                ||||    ||||||||||||
                                CCTT    CTTTTTACCTTC
                                  C___
GAM399   LOC221466 5'  AAGGGGACAAGGGATGGAA    11539     C   AAAAC  A
                                AAG GGA     GG GGATGGAA
                                ||| |||     || ||||||||
                                TTC CCT     TC CCTACCTT
                                  C   GT___  _
GAM399   LOC221692 3'  GGGAAAACGGATGGAAG      11540    A       GGA
                                GG AAAACGGA   TGGAAG
                                || ||||||||   ||||||
                                CC TTTTGCCT   ACCTTC
                                 C       ___
GAM399   LOC222057 3'  AAGGGAAAAACGGGGCCTGGGA 11541      C         A  AT__
           AG                     AAG GGAAAAACGG GG    GGAAG
                                ||| |||||||||| ||    |||||
                                TTC CCTTTTTGCC CC    CCTTC
                                  _         _  GGAC
GAM399   LOC253866 5'  GCGAGAAAGACGATGCTTGGA  11542      _    A    AGGA
                                GCG GAAA ACGG    TGGA
                                ||| |||| ||||    ||||
                                CGC CTTT TGCT    ACCT
                                  T    C    ACGA
GAM399   LOC254842 5'  GGGGAAACGGAGGCCTCAAAAG 11543     AA        AT__
                                GG  AAACGGAGG    GGAAG
                                ||  |||||||||    |||||
                                CC  TTTGCCTCC    TTTTC
                                 CC        GGAG
GAM399   LOC256019 3'  AAGGGAAAAACGGGGCCTGGGA 11541      C         A  AT__
           AG                     AAG GGAAAAACGG GG    GGAAG
                                ||| |||||||||| ||    |||||
                                TTC CCTTTTTGCC CC    CCTTC
                                  _         _  GGAC
GAM399   LOC256942 3'  AAGCAGGAAAATGGATGGA    11544      _     ACGGA
                                AAGC GGAAAA     GGATGGA
                                |||| ||||||     |||||||
                                TTCG CCTTTT     CCTACCT
                                  T     A____
GAM399   LOC257069 3'  AAGGGAAAAACGGGGCCTGGGA 11541      C         A  AT__
           AG                     AAG GGAAAAACGG GG    GGAAG
                                ||| |||||||||| ||    |||||
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                                TTC CCTTTTTGCC CC   CCTTC
                                  _       _ GGAC
GAM399  LOC51000  5' GCGAAAAACGGGCGAGG    11545    G      AG  T
                                GCG AAAAACGG  GA GG
                                ||| ||||||||  || ||
                                CGC TTTTTGCC  CT CC
                                  _       CG  _
GAM399  LOC90784  5' GGACGGAAGTGGGGTGGA   11546   A    AAAC  A  A
                                A GCGGAA    GG GG TGGA
                                | ||||||    || || ||||
                                C TGCCTT    CC CC ACCT
                                 C     CA__ _ _
GAM400  ABL2     5' CCCGCGCCCCCGCCGACCCCTG 11549    A   T     _ ATTA
          G                      CCC CGCC CCCGCCG C    GG
                                ||| |||| ||||||| |    ||
                                GGG GCGG GGGCGGC G    CC
                                  C    _      T GGGA
GAM400  AKAP13   3' CCCACGCCTCCCCTGCGC    11550          GC_
                                CCCACGCCTCCC   CGC
                                ||||||||||||   |||
                                GGGTGCGGAGGG   GCG
                                       GAC
GAM400  ALDH3B1  3' CCCATGCCTCCCACCTCGG   11551     C        GCATTA
                                CCCA GCCTCCCGCC     GG
                                |||| ||||||||||     ||
                                GGGT CGGAGGGTGG     CC
                                  A        AG_____
GAM400  CDS1     5' CCCGGGCCTCCCGCACCAGG   11552    AC      GCC
                                CCC  GCCTCCC   GCATTAGG
                                |||  |||||||   ||||||||
                                GGG  CGGAGGG   CGTGGTCC
                                  CC      ____
GAM400  DRD1     5' CCCGCGCCTCCCCGCAGG    11553    A      GC    TTA
                                CCC CGCCTCCC  CGCA   GG
                                ||| ||||||||  ||||   ||
                                GGG GCGGAGGG  GCGT   CC
                                  C       __    ____
GAM400  DSCR3    5' CCCACGCCTTCCTCCTTCCGGC 11554         C  G  GCATTA
                                CCCACGCCT CC CC     GGC
                                |||||||| || ||     |||
                                GGGTGCGGA GG GG     CCG
                                     A  A  AAGG__
GAM400  DVL1     3' CCCTGCCTCCCGTCCTGGC    11555     AC      _ __
                                CCC  GCCTCCCG CC  GC
                                |||  |||||||| ||  ||
                                GGG  CGGAGGGC GG  CG
                                  A_       A  AC
GAM400  HDAC1    5' CGCCCTCCCGCCCGCGG     11556      _      _ ATTA
                                CGCC TCCCGCC GC    GG
                                |||| ||||||| ||    ||
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                                GCGG AGGGCGG CG   CC
                                  G     G ____
GAM400  HDAC4   5' CCCGCGCCCCCGCCCCGG   11557    A   T    GCATTA
                                CCC CGCC CCCGCC    GG
                                ||| |||| ||||||    ||
                                GGG GCGG GGGCGG    CC
                                  C   _    GG____
GAM400  HIRA    5' CCCGCGCCACCCGCCCTCCGGC 11558    A   T    GCATTA
                                CCC CGCC CCCGCC    GGC
                                ||| |||| ||||||    |||
                                GGG GCGG GGGCGG    CCG
                                  C   T    GAGG__
GAM400  KCNF1   5' CCCACGCCGTCCGCGAGG   11559       TCCCG   ATT
                                CCCACGCC   CCGC  AGG
                                ||||||||   ||||  |||
                                GGGTGCGG   GGCG  TCC
                                     CA___   C__
GAM400  MAD2L2  5' CGCCTCCCGCTCAACCCGGGC  11560        _ CA TA
                                CGCCTCCCGC CG  T  GGC
                                |||||||||| ||  |  |||
                                GCGGAGGGCG GT  G  CCG
                                      A  TG GC
GAM400  MADH6   3' CCCGCCCCTCCCGCCGGGG   11561    ACG       CATTA
                                CCC  CCTCCCGCCG   GG
                                |||  ||||||||||   ||
                                GGG  GGAGGGCGGC   CC
                                  CGG       C____
GAM400  MAFK    5' CCCGCGCCGCCCGCCGCCACCG 11562    A   T     ATTAG
          C                      CCC CGCC CCCGCCGC   GC
                                ||| |||| ||||||||   ||
                                GGG GCGG GGGCGGCG   CG
                                  C   C      GTGG_
GAM400  MYO1D   5' CCGCTCCTCCCGCCGCGG   11563   ACG       ATTA
                                CC  CCTCCCGCCGC   GG
                                ||  ||||||||||   ||
                                GG  GGAGGGCGGCG   CC
                                 CGA       ____
GAM400  NMB     5' CCCACCCTCCCGCTAG     11564      G      CGCAT
                                CCCAC CCTCCCGC    TAG
                                ||||| ||||||||    |||
                                GGGTG GGAGGGCG    ATC
                                  _     _____
GAM400  PSCD3   3' CCACGCCTTCCGCGGAGGGGC  11565       C   CGCATTA
                                CCACGCCT CCGC      GGC
                                |||||||| ||||      |||
                                GGTGCGGA GGCG      CCG
                                     A   CCTCC__
GAM400  SLC6A8  5' CCCGCGCCCCCCCGCCCCGG   11566    A       GCATTA
                                CCC CGCCTCCCGCC    GG
                                ||| ||||||||||    ||
```

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                                GGG GCGGGGGGCGG     CC
                                  C         GG____
GAM400  SMURF1   3'  CGCCTCCCGCGGGTTAGGC   11567          C CA
                                CGCCTCCCGC G  TTAGGC
                                |||||||||| |  ||||||
                                GCGGAGGGCG C  AATCCG
                                      _ CC
GAM400  TNFRSF7  3'  CCCGCCCTCCTGCAGCGCAGGC 11568    A   _   C  C  AT
                                CC CGCC TCC GC GC  TAGGC
                                || |||| ||| || ||  |||||
                                GG GCGG AGG CG CG  GTCCG
                                 _   G   A  T  C_
GAM400  APCL     3'  CCCGTCTCCCGCCAAGG     11569    A  C       CATT
                                CC CG CTCCCGCCG    AGG
                                || || |||||||||    |||
                                GG GC GAGGGCGGT    TCC
                                 _ A        _____
GAM400  C20orf28 3'  CCTGCCTCCCGTCTCAGGC    11570    AC       CCGCA
                                CC  GCCTCCCG    TTAGGC
                                ||  ||||||||    ||||||
                                GG  CGGAGGGC    AGTCCG
                                 A_       AG___
GAM400  C20orf39 5'  CCCACGCCTCTCCCCGCCCTGC 11571          _ G    ATTAG
                                CCCACGCCTC CC CCGC    GC
                                |||||||||| || ||||    ||
                                GGGTGCGGAG GG GGCG    CG
                                      A  _    GGA__
GAM400  C6orf33  5'  CCCGCGCTCCCGCCTCGGGG   11572     A  C     GCATTA
                                CCC CGC TCCCGCC     GG
                                ||| ||| |||||||     ||
                                GGG GCG AGGGCGG     CC
                                  C  _      AGCC__
GAM400  CBCIP2   3'  CCCCGCCTCCTGCTGCCACAGC 11573     A     C  C  ATTA
                                CCC CGCCTCC GC GC   GGC
                                ||| ||||||| || ||   |||
                                GGG GCGGAGG CG CG   TCG
                                  _      A  A  GTG_
GAM400  CBX6     3'  CCCGGCCTCCCGCAAGAGG   11574     AC       CGCATT
                                CCC  GCCTCCCGC     AGG
                                |||  |||||||||     |||
                                GGG  CGGAGGGCG     TCC
                                  C_        TTC___
GAM400  DKFZP564O0423 3'  CATGCCTCCCACAGCAGGC   11575    C       C   TTA
                                CA GCCTCCCGC GCA   GGC
                                || |||||||| |||   |||
                                GT CGGAGGGTG CGT   CCG
                                 A        T   ___
GAM400  DTX2     3'  CCCAGCCTCTCGGGCTGGG   11576     C    C  CC  ATTA
                                CCCA GCCTC CG  GC   GG
                                |||| ||||| ||  ||   ||
```

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                                GGGT CGGAG GC  CG    CC
                                  _    A  C_  AC__
GAM400  FLJ10350  3'  CCTCCGCCTCCCGCTCCGCCCG 11577    CA        __   A TA
            GGC                   CC  CGCCTCCCGC  CGC T  GGC
                                  ||  ||||||||||  ||| |  |||
                                  GG  GCGGAGGGCG  GCG G  CCG
                                   AG         AG   _ GC
GAM400  FLJ10936  5'  CCCGCGCCTCCCGGCGCCCCCG 11578     A       C   ATTAG
            C                     CCC CGCCTCCCG CGC    GC
                                  ||| |||||||||  |||    ||
                                  GGG GCGGAGGGC GCG    CG
                                    C        C   GGGG_
GAM400  FLJ11467  5'  CCCGTGCCTCCCACCTGCCCGG 11579     AC        _  ATTA
            C                     CCC  GCCTCCCGCC GC    GGC
                                  |||  ||||||||||  ||    |||
                                  GGG  CGGAGGGTGG CG    CCG
                                    CA         A  GG__
GAM400  FLJ12526  3'  CCCTCGCCTCCCGTGGAGG    11580     A       CCGCATT
                                  CCC CGCCTCCCG      AGG
                                  ||| |||||||||      |||
                                  GGG GCGGAGGGC      TCC
                                    A        ACC____
GAM400  FLJ20374  5'  CCGCGCCTCCCCGCGGG     11581    A      GC   ATTA
                                  CC CGCCTCCC  CGC    GG
                                  ||  ||||||||  |||    ||
                                  GG GCGGAGGG  GCG    CC
                                   C       __   C___
GAM400  FLJ22795  3'  CCTACGCCTTCCCCTTCCCGGC 11582    C     C  G  GCATTA
                                  CC ACGCCT CC CC      GGC
                                  ||  ||||||  ||  ||      |||
                                  GG TGCGGA GG GG      CCG
                                   A     A  _  AAGGG_
GAM400  FLJ32818  5'  CCCAGGCCTCCCGCCTGGC    11583      C         __
                                  CCCA GCCTCCCGCC  GC
                                  ||||  ||||||||||  ||
                                  GGGT CGGAGGGCGG  CG
                                    C         AC
GAM400  GS3955    3'  CCCACGCCTCTTGCCCCCATGC 11584          ____  G  __
                                  CCCACGCCTC   CC CC  GC
                                  ||||||||||   ||  ||  ||
                                  GGGTGCGGAG   GG GG  CG
                                        AAC  G  TA
GAM400  HCGIX     5'  CCTTCGCCTCCCGTTCCCAGG  11585    CA       CCGCA
                                  CC  CGCCTCCCG    TTAGG
                                  ||  |||||||||    |||||
                                  GG  GCGGAGGGC    GGTCC
                                   AA        AAG__
GAM400  KIAA0211  5'  CCCGCCTCCCGCCCGAGGC    11586    A        GCATT
                                  CC CGCCTCCCGCC    AGGC
                                  ||  ||||||||||    ||||
```

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                                GG GCGGAGGGCGG    TCCG
                                 _        GC___
GAM400  KIAA1042  3'  CCACACTTCCTCCATTAGGC  11587      C  CG  GC
                                CCACGC TCC  CC  ATTAGGC
                                ||||||| |||  ||  |||||||
                                GGTGTG AGG  GG  TAATCCG
                                   A  A_  __
GAM400  LCHN      5'  CCCAGCCTCCCGCCTGCGG   11588     C       _  ATTA
                                CCCA GCCTCCCGCC GC   GG
                                |||| |||||||||| ||   ||
                                GGGT CGGAGGGCGG CG   CC
                                  _       A  ____
GAM400  NUDE1     3'  CCCAGCTTCCCCTGCTATTGGG 11589     C  C   GCC  _  A
                                CCCA GC TCCC   GC ATT GG
                                |||| || ||||   || ||| ||
                                GGGT CG AGGG   CG TAA CC
                                  _ A   GA_  A  C
GAM400  PCYT2     3'  CACCTCCCGCCACAGCTGGG  11590          _  A
                                CGCCTCCCGCCGCA TT GG
                                |||||||||||||| || ||
                                GTGGAGGGCGGTGT GA CC
                                       C  C
GAM400  PLCL2     5'  CCCGCGTCCCCGCCGCCGC   11591     A  _   _
                                CCC CG CCTC CCGCCGC
                                ||| || |||| |||||||
                                GGG GC GGGG GGCGGCG
                                  C  A   C
GAM400  SAD1      5'  CACCTCCCGCTCAGG      11592          CGCA
                                CGCCTCCCGC   TTAGG
                                ||||||||||   |||||
                                GTGGAGGGCG   AGTCC
                                       _____
GAM400  SEMA4C    3'  CCCACGCTTCCCGCCGACGCGG 11593       C       CATTA
                                CCCACGC TCCCGCCG    GG
                                ||||||| ||||||||    ||
                                GGGTGCG AGGGCGGC    CC
                                   A       TGCG_
GAM400  STARD7    5'  CCCGCGTCCCCGCCAGCCAGGC 11594     A  C T     _  AT
                                CCC CG C CCCGCC GC  TAGGC
                                ||| || | |||||| ||  |||||
                                GGG GC G GGGCGG CG  GTCCG
                                  C  A _     T __
GAM400  STARD7    5'  CCCGCGTCCCCGCCAGCCAGGC 11594     A  C T     _  AT
                                CCC CG C CCCGCC GC  TAGGC
                                ||| || | |||||| ||  |||||
                                GGG GC G GGGCGG CG  GTCCG
                                  C  A _     T __
GAM400  TOLLIP    5'  CCTGCGCCCCCGCCGGAG    11595    CA   T     CATTA
                                CC  CGCC CCCGCCG    GG
                                ||  |||| |||||||    ||
```

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                                GG  GCGG GGGCGGC    TC
                                 AC   _     C____
GAM400  LOC115219 3'  CACGCCTCTCCCACATGGC   11597       CCG    TA
                                CACGCCTC  CCGCAT  GGC
                                ||||||||  ||||||  |||
                                GTGCGGAG  GGTGTA  CCG
                                    AG_    __
GAM400  LOC115219 5'  CCCGCGTCCCCGCCGAGG    11596    A  C T     CATT
                                CCC CG C CCCGCCG   AGG
                                ||| || | |||||||   |||
                                GGG GC G GGGCGGC   TCC
                                 C  A _     ____
GAM400  LOC124446 5'  CCCCGCCTCCCGTCCGGC    11598    A       _  _
                                CCC CGCCTCCCG CCG C
                                ||| ||||||||| ||| |
                                GGG GCGGAGGGC GGC G
                                 _       A  C
GAM400  LOC145717 3'  CCTACGCCTTCCCCTTCCCGGC 11582    C    C  G  GCATTA
                                CC ACGCCT CC CC     GGC
                                || |||||| || ||     |||
                                GG TGCGGA GG GG     CCG
                                 A     A  _  AAGGG_
GAM400  LOC146174 5'  CACGCCTCCCGCCCCATGGGC  11599          G   TA
                                CACGCCTCCCGCC CAT  GGC
                                |||||||||||| |||  |||
                                GTGCGGAGGGCGG GTA  CCG
                                      G   C_
GAM400  LOC146336 3'  CCACGCCCCTGCTGCGG     11600       T  C  C  ATTA
                                CCACGCC CC GC GC   GG
                                ||||||| || || ||   ||
                                GGTGCGG GG CG CG   CC
                                   _  A  A  ____
GAM400  LOC150095 5'  CCCATGCCCCCCGCCGGGG   11601     C        CATTA
                                CCCA GCCTCCCGCCG    GG
                                |||| ||||||||||    ||
                                GGGT CGGGGGGCGGC    CC
                                  A         C____
GAM400  LOC150150 3'  CGCCTCCCCCGCCTGGC     11602       G   ATTA
                                CGCCTCCC CCGC   GGC
                                |||||||| ||||   |||
                                GCGGAGGG GGCG   CCG
                                   _   GA__
GAM400  LOC196485 3'  CGCCTCCCGCCACAGGGC    11603          TTA
                                CGCCTCCCGCCGCA  GGC
                                ||||||||||||||  |||
                                GCGGAGGGCGGTGT  CCG
                                      C__
GAM400  LOC200953 5'  CCCAGGCCTCCCGCTGTGTGAT 11604     C       CGCATTA__
           GGGC                  CCCA GCCTCCCGC       GGC
                                ||||| |||||||||       |||
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                                GGGT CGGAGGGCG        CCG
                                  C        ACACACTAC
GAM400  LOC201514 5'  CCCGCGCCTCCCCTCGCTCGGC 11605     A       GC   ATTA
                                CCC CGCCTCCC  CGC    GGC
                                ||| ||||||||  |||    |||
                                GGG GCGGAGGG  GCG    CCG
                                  C       GA   AG__
GAM400  LOC202559 5'  CCTGCGACTCCCGCCGTCGGGC 11606    CA  C        CA TA
                                CC  CG CTCCCGCCG  T  GGC
                                ||  || |||||||||  |  |||
                                GG  GC GAGGGCGGC  A  CCG
                                 AC  T        __ GC
GAM400  LOC202986 3'  CGCCTCCCGCCACAGGGC     11603             TTA
                                CGCCTCCCGCCGCA   GGC
                                ||||||||||||||   |||
                                GCGGAGGGCGGTGT   CCG
                                         C__
GAM400  LOC220537 3'  CCTACGCCTTCCCCTTCCCGGC 11582    C     C  G  GCATTA
                                CC ACGCCT CC CC      GGC
                                || |||||| || ||      |||
                                GG TGCGGA GG GG      CCG
                                 A     A  _  AAGGG_
GAM400  LOC222166 5'  CCCGCCCTCCCGCTCCTAGGC  11607    A   _     CGCA
                                CC CGCC TCCCGC    TTAGGC
                                || |||| ||||||    ||||||
                                GG GCGG AGGGCG    GATCCG
                                  _   G     AG__
GAM400  LOC255057 3'  CGCTCCTCCCGCTGCCTCGGC  11608     __      C  ATTA
                                CGC  CTCCCGC GC    GGC
                                |||  ||||||| ||    |||
                                GCG  GAGGGCG CG    CCG
                                  AG      A  GAG_
GAM400  LOC257054 3'  CCCACGCCCCCTGCTGCCCACG 11609          C  C  A   G
              C                   CCCACGCCTCC GC GC TTA GC
                                ||||||||||| || || ||| ||
                                GGGTGCGGGGG CG CG GGT CG
                                       A  A  _   G
GAM400  LOC57801  5'  CCCGCGCCTCCCCGTGCCG    11610     A       ___
                                CCC CGCCTCCC   GCCG
                                |||  |||||||   ||||
                                GGG GCGGAGGG   CGGC
                                  C       GCA
GAM400  LOC63928  5'  CCACGCCTCCCCCGGGG     11611           G   CATTA
                                CCACGCCTCCC CCG     GG
                                |||||||||| |||     ||
                                GGTGCGGAGGG GGC     CC
                                       _   C_____
GAM400  LOC90835  5'  CCCCGCTTCCCGCCGCA     11612     A   C
                                CCC CGC TCCCGCCGCA
                                ||| ||| ||||||||||
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                                GGG GCG AGGGCGGCGT
                                  _  A
GAM400  LOC93070  5'  CCCGCGCCTCCCGGCGCCCCCG 11578    A      C  ATTAG
          C                      CCC CGCCTCCCG CGC    GC
                                 ||| ||||||||| |||    ||
                                 GGG GCGGAGGGC GCG    CG
                                   C       C  GGGG_
GAM401  PP      3'  TGAGTATATTGGATTAGTCACA 11615        CA ____
                                 TGAGTATAT  GA   TCATA
                                 |||||||||  ||   |||||
                                 ACTCATATA  CT   AGTGT
                                       AC  AATC
GAM401  SLC21A3  5'  GAGTGTGCATGTCATATTATAA 11616     ATAT  GA
                                 GAGT   CA  TCATATTATAA
                                 ||||   ||  ||||||||||
                                 CTCA   GT  AGTATAATATT
                                   CAC_  AC
GAM401  DKFZP761E1824 3'  AGTATATCAACTAATTATA   11617        ATCAT
                                 AGTATATCAG    ATTATA
                                 ||||||||||    ||||||
                                 TCATATAGTT    TAATAT
                                       GAT__
GAM401  KIAA1309  3'  TGAGTATACAGAATACATAT   11618       T   T__
                                 TGAGTATA CAGA   CATAT
                                 |||||||| ||||   |||||
                                 ACTCATAT GTCT   GTATA
                                      _   TAT
GAM401  KIAA1371  3'  TGAGCATTCATATTAT     11619       ATCAGA
                                 TGAGTAT     TCATATTAT
                                 |||||||     |||||||||
                                 ACTCGTA     AGTATAATA
                                      _______
GAM402  CUGBP1    3'  TCAAAGGTGAGAGTTCAAGCAT 8405        A     ATGAC
                                 TTAAAGGT AGAGTT    GCAT
                                 |||||||| ||||||    ||||
                                 AGTTTCCA TCTCAA    CGTA
                                      C     GTT__
GAM402  PCK1     3'  TAAAGGTAAGGAACAATG    8406          _  TT
                                 TAAAGGTAAG AG  ATG
                                 |||||||||| ||  |||
                                 ATTTCCATTC TT  TAC
                                       C  GT
GAM402  KIAA1872  3'  GGGGAGGGTTTATGACGCAT   8407     TA  A  _
                                 GG  AG GTT ATGACGCAT
                                 ||  || ||| |||||||||
                                 CC  TC CAA TACTGCGTA
                                  CC  C   A
GAM402  LOC124602 3'  AGGTGGGGAATGTGACGCAT   8408      AA_   TA
                                 AGGT   GAGT  TGACGCAT
                                 ||||   ||||  ||||||||
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                                TCCA  CTTA  ACTGCGTA
                                  CCC   C_
GAM402  LOC149628 3'  TTAAAGGTGAAAGAAATATG  8409        __   T
                                TTAAAGGT  AAGAG TATG
                                ||||||||  ||||| ||||
                                AATTTCCA  TTCTT ATAC
                                    CT    T
GAM402  LOC203397 3'  AGGTGGGGAATGTGACGCAT  8408     AA_   TA
                                AGGT  GAGT  TGACGCAT
                                ||||  ||||  ||||||||
                                TCCA  CTTA  ACTGCGTA
                                  CCC   C_
GAM403  FGF2    3'  ACACAAATCAAAATACCA   11623          G
                                GCACAAATCAAAA TATTA
                                |||||||||||| |||||
                                TGTGTTTAGTTTT ATGGT
                                          _
GAM403  IL13RA1  3'  AGCACAAACCAAAGACAC   11624          AG
                                AGCACAAATCAAA  TAT
                                |||||||||||  |||
                                TCGTGTTTGGTTT  GTG
                                      CT
GAM403  IMPA1   3'  CAGCACAATCAAATCAGTA   11625       A   __
                                CAGCACAA TCAAA  AGTA
                                |||||||| |||||  ||||
                                GTCGTGTT AGTTT  TCAT
                                    _    AG
GAM403  KIAA0442  3'  AGCACATTTTAAGAAGTATTAA 11626      AATCAA_
          T                      AGCACA     AAGTATTAAT
                                ||||||     ||||||||||
                                TCGTGT     TTCATAATTA
                                   AAAATTC
GAM403  KLHL3   3'  CAGCACAAACTAGAAAATA   11627        CA_
                                CAGCACAAAT   AAAGTA
                                ||||||||||   ||||||
                                GTCGTGTTTG   TTTTAT
                                      ATC
GAM403  MMP10   3'  CAGTGCAATTCAAAAGCA   11628    CA  A
                                CAG  CAA TCAAAAGTA
                                |||  ||| |||||||||
                                GTC  GTT AGTTTTCGT
                                  AC   A
GAM403  SDHC    3'  CAGCACAAATCAAAGCCCAATA 11629          A  A
                                CAGCACAAATCAAA GT TTAATA
                                |||||||||||||| || ||||||
                                GTCGTGTTTAGTTT CG GGTTAT
                                          _ _
GAM403  SLC14A2  5'  CAGTAAAATCAAAAGCA    11630    CAC
                                CAG   AAATCAAAAGTA
                                |||   ||||||||||||
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                                GTC   TTTAGTTTTCGT
                                  AT_
GAM403   AFAP      3'  CAGCACAAATAATTAATTAATA 11631          CAAAAGT
                                CAGCACAAAT      ATTAATA
                                ||||||||||      |||||||
                                GTCGTGTTTA      TAATTAT
                                     TTAAT__
GAM403   DKFZp434C0923 3'  CAGGCAAATCAAAACCACCA   11632     CA        G
                                CAG  CAAATCAAAA TATTA
                                |||  |||||||||| |||||
                                GTC  GTTTAGTTTT GTGGT
                                  C_         G
GAM403   FLJ12619  3'  CAGCACAAATGGGAAGACCA   11633          CAA   T
                                CAGCACAAAT   AAG ATTA
                                ||||||||||   ||| ||||
                                GTCGTGTTTA   TTC TGGT
                                     CCC   _
GAM403   HSPC228   3'  CAGCACAAATGCAGGTAGTA   11634          _  AA_
                                CAGCACAAAT CA   AGTA
                                |||||||||| ||   ||||
                                GTCGTGTTTA GT   TCAT
                                     C  CCA
GAM403   KIAA0820  3'  AACACAAATCAAGTAGTA    11635           A_
                                AGCACAAATCAA  AGTA
                                ||||||||||||  ||||
                                TTGTGTTTAGTT  TCAT
                                   CA
GAM403   KIAA1054  3'  CAGCACAAATGCAATAAT    11636          _  A
                                CAGCACAAAT CAA AGT
                                |||||||||| ||| |||
                                GTCGTGTTTA GTT TTA
                                     C   A
GAM403   MDN1      3'  AGCACAGCATCAACTAGTA   11637        A_    A_
                                AGCACA  ATCAA  AGTA
                                ||||||  |||||  ||||
                                TCGTGT  TAGTT  TCAT
                                   CG    GA
GAM403   RINZF     3'  CAGCACAAAATCGAGAAATAAT 11638         TCAAA  TAT
            A                    CAGCACAAA    AG   TAATA
                                 |||||||||    ||   |||||
                                 GTCGTGTTT    TC   ATTAT
                                      TAGC_  TTT
GAM403   RNAH      3'  ACACAAATTAAAAGATTA    11639        C    T
                                GCACAAAT AAAAG ATTA
                                |||||||| ||||| ||||
                                TGTGTTTA TTTTC TAAT
                                     A    _
GAM403   LOC139065 3'  GCCACAAATCAAAAGGATTA   11640    _          T
                                GC ACAAATCAAAAG ATTA
                                || ||||||||||| ||||
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                                CG TGTTTAGTTTTC TAAT
                                 G          C
GAM404  BIN3    3'  GAATTCTTGTGGGACAGTTC  11643     C  C    _  TT
                                GAAT TC TGTGG AC  GGTTC
                                |||| || ||||| ||  |||||
                                CTTA AG ACACC TG  TCAAG
                                  _ A    C __
GAM404  EFNA1   5'  CGGGTCTCCTATGGGTCTGGGT 11644    AA       A_  T
          TC                     CG  TCTCCTGTGG  CT GGTTC
                                || ||||||||||  || |||||
                                GC  AGAGGATACC  GA CCAAG
                                 CC        CA  C
GAM404  HCS     3'  GAATCTTGCTTGGTT      11645       CC  TGGA
                                GAATCT  TG   CTTGGTT
                                ||||||  ||   |||||||
                                CTTAGA  AC   GAACCAA
                                  __ _____
GAM404  Nrap    3'  ATCTCCTGGGTTCAGTTC    11646        T  AC TG
                                ATCTCCTG GG  T  GTTC
                                |||||||| ||  |  ||||
                                TAGAGGAC CC  A  CAAG
                                    _  A_ GT
GAM404  Nrap    3'  ATCTCCTGGGTTCAGTTC    11646        T  AC TG
                                ATCTCCTG GG  T  GTTC
                                |||||||| ||  |  ||||
                                TAGAGGAC CC  A  CAAG
                                    _  A_ GT
GAM404  RELN    3'  CTTTTATAGCTTGGTTC    11647    CC    A
                                CT  TGTGG CTTGGTTC
                                ||  ||||| ||||||||
                                GA  ATATC GAACCAAG
                                 AA    _
GAM404  RREB1   5'  CGAGTCTCCTGGGGACGTG   11648    A     T   T
                                CGA TCTCCTG GGAC TG
                                ||| ||||||| |||| ||
                                GCT AGAGGAC CCTG AC
                                  C      C   C
GAM404  SNCAIP  3'  GAATGTCCTGTGGGTAGGGT  11649     C      ACTT
                                GAAT TCCTGTGG   GGT
                                |||| ||||||||   |||
                                CTTA AGGACACC   CCA
                                  C       CATC
GAM404  TBDN100 5'  ACGGGTCTCCGTCGGCGGTTC 11650    AA    TG  ACT
                                ACG  TCTCC  TGG   TGGTTC
                                |||  |||||  |||   ||||||
                                TGC  AGAGG  GCC   GCCAAG
                                  CC    CA  ___
GAM404  LOC138654 5'  GAACTCCTGTGGGCGGGT   11651    T       ACTT
                                GAA CTCCTGTGG   GGT
                                ||| |||||||||   |||
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                                CTT GAGGACACC   CCA
                                  _       CGC_
GAM404  LOC157317 3'  GAATCTTGCTTGGTT      11645       CC  TGGA
                                GAATCT  TG   CTTGGTT
                                ||||||  ||   |||||||
                                CTTAGA  AC   GAACCAA
                                  __  _____
GAM404  LOC164390 5'  GAGCTCCTGTGGGGCT     11652    AT       ACTT
                                GA  CTCCTGTGG   GGTT
                                ||  |||||||||   ||||
                                CT  GAGGACACC   CCGA
                                 C_       _____
GAM404  LOC203392 5'  CGGGTTTCCTGTGACCGTTC  11653    AATC     G   TG
                                CG   TCCTGTG ACT  GTTC
                                ||   ||||||| |||  ||||
                                GC   AGGACAC TGG  CAAG
                                 CCAA      _  __
GAM404  LOC219843 5'  GAACTTCCTCATAGAATTTGGT 11654     TC   _    C_
            T                    GAA  TCCT GTGGA  TTGGTT
                                |||  |||| |||||  ||||||
                                CTT  AGGA TATCT  AACCAA
                                  GA   G    TA
GAM405  EPB49    5'  AGCCACCCAGAGTCCTGCTCGT 11657          ATAG_  TT
                                AGCCGCCCAGA    GT  TCGT
                                ||||||||||    ||  ||||
                                TCGGTGGGTCT    CG  AGCA
                                      CAGGA  __
GAM405  FHL1     3'  AAGCTTCCAGAAGTATTCG   11658     CGC    ATA   T
                                AAGC   CCAGA   GGT TTCG
                                ||||   |||||   ||| ||||
                                TTCG   GGTCT   TCA AAGC
                                  AA_    ____   T
GAM405  NPEPPS   3'  AAACCAGAACAGGGTAGGTTTT 11659       CC_   AA      C
            TGT                    AAGCCG   CAG  TAGGTTTT GT
                                ||||||   |||  |||||||| ||
                                TTTGGT   GTC  ATCCAAAA CA
                                   CTT   CC       A
GAM405  BIK      5'  AAGCCACCCGGGAGGCTTCGT  11660         AGAAT     T
                                AAGCCGCCC    AGGTTT CGT
                                |||||||||    |||||| |||
                                TTCGGTGGG    TCCGAA GCA
                                     CCC__     _
GAM405  CPR2     3'  AAGCCTCCCAGGATGGCT    11661      G    A  A
                                AAGCC CCCAG AT GGTT
                                ||||| ||||| || ||||
                                TTCGG GGGTC TA CCGA
                                  A    C  _
GAM405  CXYorf1   3'  AGCCCCCTAGGATTCCCA    11662     G   AGAA   _  TT
                                AGCC CCC    TAGG TT  CG
                                |||| |||    |||| ||  ||
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                                TCGG GGG   ATCC AA  GT
                                  _  ____   T  GG
GAM405  KIAA1100 3'  AAGCCCCTCAGGATACGT   11663      G  _  A  G
                                AAGCC CC CAG ATA GT
                                ||||| || ||| ||| ||
                                TTCGG GG GTC TAT CA
                                  _ A  C  G
GAM405  KIAA1545 3'  AGCCGCCCAGGAGTGCT    11664         AAT  _
                                AGCCGCCCAG  AG GTT
                                ||||||||||  || |||
                                TCGGCGGGTC  TC CGA
                                     C__  A
GAM405  MISS     3'  AGCTGCCTCAGGTTTTTGT   11665    C  CAGAA      C
                                AGC GCC    TAGGTTTT GT
                                ||| |||    |||||||| ||
                                TCG CGG    GTCCAAAA CA
                                  A  A____      A
GAM405  SYT12    3'  AGCCCCCAGGGTGCCCCTCGT  11666    G    AATA  ___
                                AGCC CCCAG   GGT  TTTCGT
                                |||| |||||   |||  ||||||
                                TCGG GGGTC   CCA  GGAGCA
                                  _   ____  CGG
GAM405  TOR2A    3'  AAGCCGCCCGGGAGGGGGCT  11667        A_  ATA
                                AAGCCGCCC  GA  GGTT
                                |||||||||  ||  ||||
                                TTCGGCGGG  CT  CCGA
                                     CC  CCC
GAM405  LOC163682 5'  GCCTCCAGAATGCTCGTTTCGT 11668    GC     AGGT_
                                GCC  CCAGAAT    TTTCGT
                                |||  |||||||    ||||||
                                CGG  GGTCTTA    AAAGCA
                                  A_     CGAGC
GAM405  LOC255177 3'  AAGCCTCCTGGAATGGGACC  11669     G  CA   A  TT
                                AAGCC CC  GAAT GG  TT
                                ||||| ||  |||| ||  ||
                                TTCGG GG  CTTA CC  GG
                                   A  AC   _  CT
GAM406  ALDOC    3'  GTATGGTATGTACTCAAGGC  11672      _   _ A_
                                GTGTG TGTG GC  AAGGC
                                ||||| |||| ||  |||||
                                CATAC ATAC TG  TTCCG
                                   C   A  AG
GAM406  B4GALT1  3'  GCACAGTAGGTGCAGAGGC   11673       T  TG CAA
                                GCACAGTG GTG  G  AGGC
                                |||||||| |||  |  ||||
                                CGTGTCAT CAC  C  TCCG
                                     C  GT ___
GAM406  CACNA2D2 3'  CCCCATAGTGTGTGTGTTTGTG 11674  C       _________  AAAG
            CCTTTGC                AGTGTGTGTG      GC   GC
                                |||||||||      ||   ||
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```
                                TCACACACAC      CG   CG
                               A        AAACAIII  GAAA
GAM406  CALM1    3'  GTGTGTGTGGACAGAAGG    11675          _ _
                               GTGTGTGTGG CA AAGG
                               |||||||||| || ||||
                               CACACACACC GT TTCC
                                     T  C
GAM406  DIA1     3'  CCTTATAGTGTGTGTGGGGGG  11676    GCAC        CAAA
                               CC   AGTGTGTGTGG   GG
                               ||   ||||||||||   ||
                               GG   TCACACACACC   CC
                                AATA        CC__
GAM406  DRD2     3'  GCGTCAGAGTGTGGCAGAGGC  11677    A_  TGT      A
                               GC  CAG   GTGTGGCA AGGC
                               ||  |||   |||||||| ||||
                               CG  GTC   CACACCGT TCCG
                                CA  T__      C
GAM406  FGFR3    3'  CCGTGGTGCAAAGGCAGAGGC  11678    CACA    TGT   A
                               CCG   GTGTG   GGCA AGGC
                               |||   |||||   |||| ||||
                               GGC   CACGT   CCGT TCCG
                                 AC__    TT_   C
GAM406  FGFRL1   3'  CCGTGTGTGTGTGTGTGTCCAG 11680    CACA       GCAA_
          GC                    CCG   GTGTGTGTG    AGGC
                               |||   |||||||||    ||||
                               GGC   CACACACAC    TCCG
                                 ACA_       ACAGG
GAM406  FGFRL1   3'  CCGTGCATGTGTGTGTCAAGGC 11679    CACA       GCA
                               CCG   GTGTGTGTG   AAGGC
                               |||   |||||||||  |||||
                               GGC   TACACACAC   TTCCG
                                 ACG_       AG_
GAM406  GFRA2    3'  GCAAGGTGTGTGTGTGTGCCTT 11681    CA       _______  AAAG
          G                     GCA  GTGTGTGTG     GC   G
                               |||  |||||||||     ||   |
                               CGT  CACACACAC     CG   C
                                 TC       ACAIII  GAAA
GAM406  GNA11    3'  CCACACGTGGCAAGGG      11682       AGTGTGT      A
                               CCGCAC      GTGGCAA GG
                               ||||||      ||||||| ||
                               GGTGTG      CACCGTT CC
                                  ________      C
GAM406  GOT2     3'  CACAGTGTGAGATGAGAGGC   11683         T_   CAA
                               CACAGTGTG  GTGG   AGGC
                               |||||||||  ||||   ||||
                               GTGTCACAC  TACT   TCCG
                                     TC   C__
GAM406  HAGH     5'  CCGCACAGTGGATCCCTGGAGG 11684          TG G__   CAA
          C                     CCGCACAGTG  T   TGG   AGGC
                               ||||||||||  |   |||   ||||
```

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                                GGCGTGTCAC  A   ACC   TCCG
                                      CT GGG  ___
GAM406  PLXNB2   3'  GCTGGTGCGTGGGCGGAGGC  11685    ACA     T   AA
                                GC   GTGTGTG GGC  AGGC
                                ||   ||||||| |||  ||||
                                CG   CACGCAC CCG  TCCG
                                 AC_      _  CC
GAM406  PTER     3'  GCATGGTGTGCCTATCTGAAGG 11686     CA     G  GCA_
                                GCA  GTGTGT TG    AAGG
                                |||  |||||| ||    ||||
                                CGT  CACACG AT    TTCC
                                  AC     G  AGAC
GAM406  RAB36    3'  CCGTGTGTGTGCAGGGAGCGGA 11687    CACA      ____  AA
           GGC                    CG    GTGTGTGT    GGC  AGGC
                                ||   ||||||||   |||  ||||
                                GC   CACACACG    TCG  TCCG
                                 A___       TCCC   CC
GAM406  RABIF    3'  GTATAATGTGGCAAAGGC    11688      _
                                GTGTG TGTGGCAAAGGC
                                ||||| ||||||||||||
                                CATAT ACACCGTTTCCG
                                   T
GAM406  VAPB     3'  GTATGTGTGTGCAGGGAGG   11689         _  A__
                                GTGTGTGTG GCA   AGG
                                ||||||||| |||   |||
                                CATACACAC CGT   TCC
                                      A   CCC
GAM406  VDAC2    3'  GCACAGTTTTCATAAAGG    11690       GTG   GCA
                                GCACAGT   TGTG   AAGG
                                |||||||   ||||   ||||
                                CGTGTCA   GTAT   TTCC
                                    AAA   ___
GAM406  WDR4     3'  GCAGTGTGTGCCAAGG      11691     CAGT      G   A
                                GCA    GTGTGTG CAA GG
                                |||    ||||||| ||| ||
                                CGT    CACACAC GTT CC
                                  ____       G   _
GAM406  WDR4     3'  GCAGTGTGTGCCAAGG      11691     CAGT      G   A
                                GCA    GTGTGTG CAA GG
                                |||    ||||||| ||| ||
                                CGT    CACACAC GTT CC
                                  ____       G   _
GAM406  BTN1A1   3'  GCACAGTGTGGAAACGGAGGC  11692         TGT   AA
                                GCACAGTGTG   GGC  AGGC
                                ||||||||||   |||  ||||
                                CGTGTCACAC   TTG  TCCG
                                      CT_   CC
GAM406  C1orf21  5'  CCCCACAGTGTGTCCGGGG   11693    G        G   CAAA
                                CC CACAGTGTGT TGG    GG
                                || |||||||||| |||    ||
```

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                                GG GTGTCACACA GCC    CC
                                 G         G  _____
GAM406  C20orf150 3'  GCACGCTGTGAACAAAAG    11694      A  G    T
                                GCAC GT TGTG GGCAAAGG
                                |||| || |||| ||||||||
                                CGTG CG ACAC TTGTTTTC
                                  _ _    _
GAM406  C22orf5   3'  GCACGGTGTGTGGGGGAGC    11695      A      T  CAAA
                                GCAC GTGTGTG GG    GGC
                                |||| ||||||| ||    |||
                                CGTG CACACAC CC    TCG
                                  C       _  CC__
GAM406  CBX6      3'  GCAAGTGTGTGGGAGGC      11696     C       T  CAA
                                GCA AGTGTGTG GG   AGGC
                                ||| |||||||| ||   ||||
                                CGT TCACACAC CC   TCCG
                                  _       _ ____
GAM406  DKFZp434E1822 3'  GTGAGGGGATGTGGCAAAGG   11697     T_____
                                GTG     GTGTGGCAAAGG
                                |||     ||||||||||||
                                CAC     TACACCGTTTCC
                                  TCCCC
GAM406  DKFZP434I216 3'  GCACATGTAGGTTGGAGG     11698      G    TG_   CAA
                                GCACA TGTG   TGG   AGG
                                ||||| ||||   |||   |||
                                CGTGT ACAT   ACC   TCC
                                   _    CCA   ____
GAM406  DKFZP564O0423 5'  GCAGCAGTGTGTAGAAGGC    11699     _       T__
                                GCA CAGTGTGTG   GGC
                                ||| |||||||||   |||
                                CGT GTCACACAT   CCG
                                  C        CTT
GAM406  FLJ10704  3'  GCACAGTGCTGCAGGGGGGC   11700         G  TG CAAA
                                GCACAGTGT TG  G    GGC
                                |||||||||  ||  |    |||
                                CGTGTCACG AC  C    CCG
                                      _  GT CCC_
GAM406  FLJ20043  3'  GCACACTGTGTGTGTGTGCCTT 11701       G       _______  AAAG
             G                   GCACA TGTGTGTG      GC    G
                                |||||  ||||||||      ||    |
                                CGTGT ACACACAC      CG    C
                                   G       ACAIII  GAAA
GAM406  FLJ21615  3'  GCGTATGTAGCACTGGGGGGC   11702           AA___
                                GTGTGTGTGGCA     GGC
                                ||||||||||||     |||
                                CGCATACATCGT     CCG
                                       GACCC
GAM406  FLJ21777  3'  CACATAGCTGACCTGTGGCAGA 11703      C  _  _ G      A
             GG                    CGCA AG TG T TGTGGCA AGG
                                |||| || || | ||||||| |||
```

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                                GTGT TC AC G ACACCGT TCC
                                  A  G  T G      C
GAM406  FLJ23447  5'  CACAGTGTCGACTCGGGGGC  11704        _ TG_   CAAA
                                CACAGTGT G   TGG    GGC
                                |||||||| |   |||    |||
                                GTGTCACA C   GCC    CCG
                                     G TGA   C___
GAM406  FLNC      3'  CGCAGTGTGTAAAAAAGGC   11705      CAGT       C
                                CGCA    GTGTGTGG AAAGGC
                                ||||    |||||||| ||||||
                                GCGT    CACACATT TTTCCG
                                  _____        T
GAM406  GRM5      3'  GTGTGTGTGAACACGGGGGGC  11706          _ AA___
                                GTGTGTGTGG CA     GGC
                                |||||||||| ||     |||
                                CACACACACT GT     CCG
                                      T  GCCCC
GAM406  HABP4     3'  GCACAGTGTGTGTTCCCGGGC  11707            GGCAAA
                                GCACAGTGTGTGT     GGC
                                ||||||||||||      |||
                                CGTGTCACACACA     CCG
                                       AGGGC_
GAM406  HES6      3'  CCGCACAGGGCTGGTGAAGGC  11708         T  GTG   CA
                                CCGCACAG GT   TGG  AAGGC
                                |||||||| ||   |||  |||||
                                GGCGTGTC CG   ACC  TTCCG
                                     C  ___   AC
GAM406  HH114     3'  CAGCATGGCAGGGTGGCGGGGG 11709        T_____     AAA
              C                  CAGTGTG    GTGGC   GGC
                                 |||||||    |||||   |||
                                 GTCGTAC    CACCG   CCG
                                    CGTCC    CCC
GAM406  IL22R     3'  CGCAGAGTGTGTGGCATGGGC  11710      CA T         AA
                                CGCA  G GTGTGTGGCA  GGC
                                ||||  | ||||||||||  |||
                                GCGT  C CACACACCGT  CCG
                                  __ T         AC
GAM406  KIAA0321  3'  CAGCGTGGTGTTCAAAGG    11711        T   G_
                                CAGTGTG GTG  CAAAGG
                                ||||||| |||  ||||||
                                GTCGCAC CAC  GTTTCC
                                   _   AA
GAM406  KIAA0329  3'  GCGCCGTGTGTGGGCAGTGAGG 11712    ACA      T    A__
                                GC   GTGTGTG GGCA   AGG
                                ||   ||||||| ||||   |||
                                CG   CACACAC CCGT   TCC
                                 CGG       _    CAC
GAM406  KIAA1210  3'  GCACAGTGTAACAGAGG     11713          TGTG   A
                                GCACAGTGTG    GCA AGG
                                ||||||||||    ||| |||
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                                CGTGTCACAT    TGT TCC
                                      ____  C
GAM406  KIAA1550  3'  GCATGTGTGTGTGTATGTGCCT 11714   CA       _________ AAAG
            TG                   A  GTGTGTGTG       GC    G
                                 |  |||||||||       ||    |
                                 T  CACACACAC       CG    C
                                  A_       ATACAIII  GAAA
GAM406  KIAA1813  5'  GCACAATGGCCATGGTGGCAGA 11715        T  ____     A
            GGC                    GCACAGTG GT    GTGGCA AGGC
                                 ||||||||| ||    |||||| ||||
                                 CGTGTTAC CG    CACCGT TCCG
                                      _ GTAC     C
GAM406  LANCL2    3'  CCTACAGTGTGGCCATCAAAGG 11716    GC       T  GG_
            C                     CC  ACAGTGTG GT   CAAAGGC
                                 ||  |||||||| ||   |||||||
                                 GG  TGTCACAC CG   GTTTCCG
                                  A_       _ GTA
GAM406  MGC3113   3'  CACGTGGCTGGCAGGGG     11717     A   T  G    AA
                                 CAC GTG GT TGGCA  GG
                                 ||| ||| || |||||  ||
                                 GTG CAC CG ACCGT  CC
                                   _  _ _    CC
GAM406  MGC4400   3'  CACAGTGTAATCACAAGGG    11718         T  G    A
                                 CACAGTGTG GT GCAA GG
                                 |||||||||  || ||||  ||
                                 GTGTCACAT TA TGTT CC
                                       _ G    C
GAM406  NT5C1B    5'  GTATTGTGTGGCAGGGGC     11719      _       AA
                                 GTGT GTGTGGCA  GGC
                                 ||||  ||||||||  |||
                                 CATA CACACCGT  CCG
                                   A       CC
GAM406  PRO1728   5'  GCAGATGAGCTGGCAAAGG    11720     CA   T  G
                                 GCA  GTG GT TGGCAAAGG
                                 |||  ||| ||  |||||||||
                                 CGT  TAC CG ACCGTTTCC
                                   C_   T  _
GAM406  PRO1880   3'  CCATGGTGCACGAGCAGGGGC  11721     CACA   TG  T    AA
                                 CCG    GTG  TG GGCA  GGC
                                 |||    |||  || ||||  |||
                                 GGT    CAC  GC TCGT  CCG
                                   AC__   GT  _    CC
GAM406  SEMA4G    5'  GCCCCAGGTGTGGCAGGGGC   11722    A_   TGT       AA
                                 GC  CAG   GTGTGGCA  GGC
                                 ||  |||   ||||||||  |||
                                 CG  GTC   CACACCGT  CCG
                                  GG   ____       CC
GAM406  SPRY4     3'  CCGTCACAACTGTGGCAAGGG  11723     _    TGTG       A
                                 CCG CACAG    TGTGGCAA GG
                                 ||| |||||    |||||||| ||
```

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                                GGC GTGTT   ACACCGTT CC
                                  A    G___      C
GAM406  SSR1    3'  GCTTAGTGTGTGGACCAAGGC  11724   AC      T  A
                                GC  AGTGTGTG GGC AAGGC
                                ||  |||||||| ||| |||||
                                CG  TCACACAC CTG TTCCG
                                 AA       _  G
GAM406  TCEA3   3'  GCACGTGTGACTCGGAGG   11725    A   TG_  CAA
                                GCAC GTGTG  TGG  AGG
                                |||| |||||  |||  |||
                                CGTG CACAC  GCC  TCC
                                  _    TGA  ____
GAM406  TCL6    5'  CAGGTGTGTAGCTGGAAGG   11726    T      A__
                                CAG GTGTGTGGC  AAGG
                                ||| |||||||||  ||||
                                GTC CACACATCG  TTCC
                                  _       ACC
GAM406  TCL6    5'  CAGGTGTGTAGCTGGAAGG   11726    T      A__
                                CAG GTGTGTGGC  AAGG
                                ||| |||||||||  ||||
                                GTC CACACATCG  TTCC
                                  _       ACC
GAM406  TCL6    5'  CAGGTGTGTAGCTGGAAGG   11726    T      A__
                                CAG GTGTGTGGC  AAGG
                                ||| |||||||||  ||||
                                GTC CACACATCG  TTCC
                                  _       ACC
GAM406  TCL6    5'  CAGGTGTGTAGCTGGAAGG   11726    T      A__
                                CAG GTGTGTGGC  AAGG
                                ||| |||||||||  ||||
                                GTC CACACATCG  TTCC
                                  _       ACC
GAM406  TRAF2   3'  CCACACAGTGGTCTGAGCAGAG 11727         T  G  _  A
          GC                      CCGCACAGTG GT TG GCA AGGC
                                ||||||||||  || ||  ||| ||||
                                GGTGTGTCAC CA AC CGT TCCG
                                      _  G  T  C
GAM406  URG4    3'  GCGTGAAGTGTGTGGCAGAGG  11728   ACAGT       A
                                GC    GTGTGTGGCA AGG
                                ||    |||||||||| |||
                                CG    CACACACCGT TCC
                                 CACTT        C
GAM406  LOC112868 5'  AGGCTGTGTGGCAAGGGC   11729   TG       A
                                AG  TGTGTGGCAA GGC
                                ||  |||||||||| |||
                                TC  ACACACCGTT CCG
                                 CG        C
GAM406  LOC113444 3'  GTGTGGTGTGGGAAGGGC   11730      _   C  A
                                GTGTG TGTGG AA GGC
                                ||||| ||||| || |||
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                                CACAC ACACC TT CCG
                                  C    C  C
GAM406  LOC115110 3'  CCGTGCAGTGTGTGTCCACGG  11731    CA       GGCAAA
                                CCG  CAGTGTGTGT     GG
                                |||  ||||||||||     ||
                                GGC  GTCACACACA     CC
                                  AC        GGTG__
GAM406  LOC123096 3'  ACAGTGTGGGCATGAGG     11732        TGT    A_
                                ACAGTGTG   GGCA  AGG
                                ||||||||   ||||  |||
                                TGTCACAC   CCGT  TCC
                                     ___    AC
GAM406  LOC126528 3'  CCGTCAGTGGCCCGTGAGGGC  11733    CA    ___    T_
                                CCG  CAGTG   TGTG  GGC
                                |||  |||||   ||||  |||
                                GGC  GTCAC   GCAC  CCG
                                  A_    CGG    TC
GAM406  LOC127435 3'  GTGTGTGCCAGGGCAGGGGC   11734         ___    AA
                                GTGTGTGT   GGCA  GGC
                                ||||||||   ||||  |||
                                CACACACG   CCGT  CCG
                                    GTC    CC
GAM406  LOC137964 3'  CCGCACAGCGTGCAAAGG    11735          GTGTG
                                CCGCACAGTGT    GCAAAGG
                                ||||||||||    |||||||
                                GGCGTGTCGCA    CGTTTCC
                                       _____
GAM406  LOC144347 3'  GCATGTGTGCGAAAAGG     11736     CAG       C
                                GCA   TGTGTGTGG AAAGG
                                |||   |||||||| |||||
                                CGT   ACACACGCT TTTCC
                                  ___       _
GAM406  LOC151031 5'  CCGAGCGGTGTGCAGGGG    11737     CAC    T    G  AA
                                CCG   AGTG GTGTG CA  GG
                                |||   |||| ||||| ||  ||
                                GGC   TCGC CACAC GT  CC
                                  ___   _    _ CC
GAM406  LOC151643 3'  GCACAGTTGGCAAAGG      11738       GTGTG
                                GCACAGT    TGGCAAAGG
                                |||||||    |||||||||
                                CGTGTCA    ACCGTTTCC
                                       _____
GAM406  LOC151701 5'  CCGTGAGTGTGTGTGTGGTGCC 11739   CAC        _______  AAAG
          TTG                     AGTGTGTGTG      GC    G
                                  ||||||||||      ||    |
                                  TCACACACAC      CG    C
                                AC_         ACCAIII  GAAA
GAM406  LOC153579 3'  ACAGTGTGATGTGAAGCGCCTT 11740        _   _______  AAAG
          TGC                     CAGTGTG TGTG      GC    GC
                                |||||||  ||||      ||    ||
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                                GTCACAC ACAC      CG   CG
                                    T   TTCGIII  GAAA
GAM406  LOC155060 5'  CCGACGGTGGCTGGCGGGGG  11741    C  A   T  G   AAA
                                CCG AC GTG GT TGGC   GG
                                ||| || ||| || ||||   ||
                                GGC TG CAC CG ACCG   CC
                                  _  C   _  _    CCC
GAM406  LOC157651 3'  GCACAGCGGCCGGGCAGAGG  11742       TG  T   A
                                GCACAGTG  TG GGCA AGG
                                ||||||||  || |||| |||
                                CGTGTCGC  GC CCGT TCC
                                     CG  _   C
GAM406  LOC157695 3'  GCACAGTGTAACTGGAGG    11743         TG   CAA
                                GCACAGTGTG  TGG   AGG
                                ||||||||||  |||   |||
                                CGTGTCACAT  ACC   TCC
                                      TG  ___
GAM406  LOC160414 3'  CAGCTTGTGTGGCAGAGG    11744     G       A
                                CAGT TGTGTGGCA AGG
                                |||| |||||||| |||
                                GTCG ACACACCGT TCC
                                  A       C
GAM406  LOC162239 5'  CAGTTTTGGGCAAAGGC     11745     GTG  T
                                CAGT   TG GGCAAAGGC
                                ||||   || |||||||||
                                GTCA   AC CCGTTTCCG
                                  AA_  _
GAM406  LOC196337 5'  CCCACAGATTGGCAAGGG    11746    G    TGTGTG     A
                                CC CACAG     TGGCAA GG
                                || |||||     |||||| ||
                                GG GTGTC     ACCGTT CC
                                 _    TA____     C
GAM406  LOC196500 3'  CCGGGTGGTGTGCAAGGGG   11747     CACA   T    G   A_
                                CCG    GTG GTGTG CAA  GG
                                |||    ||| ||||| |||  ||
                                GGC    CAC CACAC GTT  CC
                                 C___  _    _   CC
GAM406  LOC200081 3'  GCACATGTGGGGGTGGGGGC  11748      G   T__   CAAA
                                GCACA TGTG   GTGG    GGC
                                ||||| ||||   ||||    |||
                                CGTGT ACAC   CACC    CCG
                                  _    CCC    C___
GAM406  LOC201249 3'  GCACAGTGTCTGTCTCTGGC   11749        G   ____
                                GCACAGTGT TGT    GGC
                                ||||||||| |||    |||
                                CGTGTCACA ACA    CCG
                                      G   GAGA
GAM406  LOC201522 3'  CGCACGTGAGCTTGGTGGAGGC 11750      A   T  G   CAA
                                CGCAC GTG GT TGG   AGGC
                                ||||| ||| || |||   ||||
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                                GCGTG CAC CG ACC   TCCG
                                  _  T A   ACC
GAM406  LOC220827 3'  GCACGGGTGCTGGCAGGGGC  11751     AGT   G    AA
                                GCAC   GTGT TGGCA  GGC
                                ||||   |||| |||||  |||
                                CGTG   CACG ACCGT  CCG
                                  CC_   _    CC
GAM406  LOC220954 3'  CAGGTATCTGGCAAAGGC    11752     T   G
                                CAG GTGT TGGCAAAGGC
                                ||| |||| ||||||||||
                                GTC CATA ACCGTTTCCG
                                  _   G
GAM406  LOC253897 3'  CCGCACAGCGTGCAAAGG    11735          GTGTG
                                CCGCACAGTGT    GCAAAGG
                                ||||||||||    |||||||
                                GGCGTGTCGCA    CGTTTCC
                                       _____
GAM406  LOC255974 3'  GTGCAGTGTAGCAACTGAAGGC 11753     _       ____
                                GTGT GTGTGGCAA    AGGC
                                |||| |||||||||    ||||
                                CACG CACATCGTT    TCCG
                                  T        GACT
GAM406  LOC256310 3'  GCACTGTGTGCAGAAAGG    11754     AG     TG C
                                GCAC  TGTGTG  G AAAGG
                                ||||  ||||||  | |||||
                                CGTG  ACACAC  C TTTCC
                                  __     GT _
GAM406  LOC257472 3'  GCACATGTAGGTTGGAGG    11698      G   TG_  CAA
                                GCACA TGTG   TGG   AGG
                                ||||| ||||   |||   |||
                                CGTGT ACAT   ACC   TCC
                                  _   CCA  ___
GAM406  LOC257486 3'  GCACAGTGTAACAGAGG     11713         TGTG  A
                                GCACAGTGTG    GCA AGG
                                ||||||||||    ||| |||
                                CGTGTCACAT    TGT TCC
                                      _____  C
GAM406  LOC51308  3'  GCACAGTGTGGAGCAGGGGC  11755         TGT   AA
                                GCACAGTGTG   GGCA  GGC
                                ||||||||||   ||||  |||
                                CGTGTCACAC   TCGT  CCG
                                     C__    CC
GAM406  LOC57801  3'  GCTACAGTCTCGGCAAAGGC  11756   _    GTGTG
                                GC ACAGT    TGGCAAAGGC
                                || |||||    ||||||||||
                                CG TGTCA    GCCGTTTCCG
                                 A    GA___
GAM406  LOC90313  3'  CCGCGCGCGGTCCACGTGGCAG 11757     ACA    _____      A
           AGG                    CGC   GTGTG    TGTGGCA AGG
                                |||   |||||    ||||||| |||
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                                GCG  CGCGC    GCACCGT TCC
                                  ___    CAGGT      C
GAM406  LOC91812  5' CAGTACAGTGTGGCAGAAGGC  11758     GT_      _
                                CAGT  GTGTGGCA AAGGC
                                ||||  |||||||| |||||
                                GTCA  CACACCGT TTCCG
                                  TGT      C
GAM406  LOC91813  5' CAGTACAGTGTGGCAGAAGGC  11758     GT_      _
                                CAGT  GTGTGGCA AAGGC
                                ||||  |||||||| |||||
                                GTCA  CACACCGT TTCCG
                                  TGT      C
GAM406  LOC92231  3' CCTTACAGTGTGAACCAGG   11759   GC      TGT  AA
                                CC  ACAGTGTG  GGC  AGG
                                ||  ||||||||  |||  |||
                                GG  TGTCACAC  TTG  TCC
                                 AA       ___  G_
GAM406  LOC92231  3' CCTTACAGTGTGAACCAGG   11759   GC      TGT  AA
                                CC  ACAGTGTG  GGC  AGG
                                ||  ||||||||  |||  |||
                                GG  TGTCACAC  TTG  TCC
                                 AA       ___  G_
GAM406  LOC93626  3' CCACACGTGGCAAGGG     11682      AGTGTGT     A
                                CCGCAC     GTGGCAA GG
                                ||||||     ||||||| ||
                                GGTGTG     CACCGTT CC
                                  _______     C
GAM407  MHC2TA   3' ACGTGCACACACGTGCA     11762     T  T    A
                                ACGT GC CGCAC TGCG
                                |||| || ||||| ||||
                                TGCA CG GTGTG ACGT
                                  _ T    C
GAM407  CHIC1    3' TATGTATATGCACACACGCA  11763     CCACGT  TC
                                TATG     TGC  GCACATGCG
                                ||||     |||  |||||||||
                                ATAC     ACG  TGTGTGCGT
                                  ATAT__  __
GAM407  KIAA1303  3' TGCCATCTGCACATGC      11764      CGTTG  C
                                TGCCA    CT GCACATGC
                                |||||    || ||||||||
                                ACGGT    GA CGTGTACG
                                  A_____ _
GAM408  ARNT2    3' AGCAGGAGCCTCACTCT     11767         C  GC
                                AGCAGGAGCC CAC  CT
                                |||||||||| |||  ||
                                TCGTCCTCGG GTG  GA
                                     A  A_
GAM408  CDA      5' AAACAGGAGCTCCGGCCAGCC  11768         C  AC   TC
                                AAGCAGGAGC CC  GCC  CC
                                |||||||||| ||  |||  ||
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                                TTTGTCCTCG GG  CGG  GG
                                      A  C_   TC
GAM408  COL9A2   3'  GCAGGGCCCGGGCCTCCCGA  11769      A    CAC
                                GCAGG GCCC   GCCTCCCGA
                                ||||| ||||   |||||||||
                                CGTCC CGGG   CGGAGGGCT
                                   _    CC_
GAM408  DRD1     5'  AGCAGGGCCCCGCGCCTCCC   11770       A    A
                                AGCAGG GCCCC CGCCTCCC
                                |||||| ||||| ||||||||
                                TCGTCC CGGGG GCGGAGGG
                                   _    C
GAM408  DUSP4    5'  AGCCAGGAACTGCCTCCCG   11771     _     CCCAC
                                AGC AGGAGC    GCCTCCCG
                                ||| ||||||    ||||||||
                                TCG TCCTTG    CGGAGGGC
                                  G     A____
GAM408  EGFL4    5'  GCAGCAGCCCCCCGACCCG   11772      G     A  CCT
                                GCAG AGCCCC CG   CCCG
                                |||| |||||| ||   ||||
                                CGTC TCGGGG GC   GGGC
                                  G     G  T__
GAM408  EMP1     5'  GAAGGACCCGCCTCCCG     11773      CC  A
                                GGAG  CC CGCCTCCCG
                                ||||  || |||||||||
                                CTTC  GG GCGGAGGGC
                                  CT  _
GAM408  FOLH1    5'  AGCAGAGCCGGCCTCCCG    11774      G    CCAC
                                AGCAG AGCC    GCCTCCCG
                                ||||| ||||    ||||||||
                                TCGTC TCGG    CGGAGGGC
                                   _    C___
GAM408  HMGCL    3'  AGCAAGGGCCCCACGGCC    11775       A      _
                                AGCAGG GCCCCACG CC
                                |||||| |||||||| ||
                                TCGTTC CGGGGTGC GG
                                   C       C
GAM408  IL2RB    3'  AAGTGGGAGCCTCCCAA     11776     CA     CCACGCC
                                AAG  GGAGCC      TCCCGA
                                |||  ||||||      ||||||
                                TTC  CCTCGG      AGGGTT
                                  AC     ________
GAM408  IRTA2    3'  AAGCAGGAGTTCCCCCTTAC   11777         __    AC_
                                AAGCAGGAG  CCCC   GC
                                |||||||||  ||||   ||
                                TTCGTCCTC  GGGG   TG
                                     AA    GAA
GAM408  KIF3C    3'  GCAGGAGCTCCTCCTCC     11778         C  ACG
                                GCAGGAGC CC   CCTCC
                                |||||||| ||   |||||
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                                CGTCCTCG GG   GGAGG
                                    A  A__
GAM408  MAPK8IP1  3'  GCAGGAGCCACAGCGCCCGA  11779        C  C  CT
                                GCAGGAGCC CA GC  CCCGA
                                ||||||||| || ||  |||||
                                CGTCCTCGG GT CG  GGGCT
                                     T  _  C_
GAM408  MCM4    5'  GCCGGGCCCGCCTCCCG    11780    A  A    CAC
                                GC GG GCCC   GCCTCCCG
                                || || ||||   ||||||||
                                CG CC CGGG   CGGAGGGC
                                 G  _   ___
GAM408  MNT     3'  AAGCAGCAGCCCTAGCTCT   11781       G    CAC  _
                                AAGCAG AGCCC   GC CT
                                |||||| |||||   || ||
                                TTCGTC TCGGG   CG GA
                                   G    AT_  A
GAM408  NFATC4   5'  GCAGGAGCCCCCAGGTCCCG   11782          A  CC
                                GCAGGAGCCCC CG  TCCCG
                                |||||||||||  ||  |||||
                                CGTCCTCGGGG GT  AGGGC
                                      _  CC
GAM408  PCTK3    3'  AAGCAGGAGCCACCTC      11783          CCAC
                                AAGCAGGAGCC    GCCTC
                                ||||||||||    |||||
                                TTCGTCCTCGG    TGGAG
                                      ____
GAM408  POU3F2   3'  AGGGGGAGCCCCGCGCTCT   11784    CA      A  _
                                AG  GGAGCCCC CGC CT
                                ||  |||||||| ||| ||
                                TC  CCTCGGGG GCG GA
                                 CC       C   A
GAM408  RDBP     5'  AACCGGGGGCCCCACGGTCTCC 11785     A_  A      C_
                                AGC  GG GCCCCACG  CTCC
                                |||  || ||||||||  ||||
                                TTG  CC CGGGGTGC  GAGG
                                  GC  C       CA
GAM408  SDC1     3'  GCGGCGGCCCCACGGCAGCCT  11786    A  A_     _____
                                GC GG  GCCCCAC    GCCT
                                || ||  |||||||    ||||
                                CG CC  CGGGGTG    CGGA
                                 _  GC      CCGT
GAM408  SLC2A8   3'  GCAGTGAGCCTCCTAGCCCC   11787     _    _  AC
                                GCAG GAGCC CC  GCCTC
                                |||| ||||| ||  |||||
                                CGTC CTCGG GG  CGGGG
                                  A    A  AT
GAM408  TCIRG1   5'  GCAGGAGGCCTCCCG       11788        CCCCAC
                                GCAGGAG     GCCTCCCG
                                |||||||     ||||||||
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                                CGTCCTC     CGGAGGGC
                                        _______
GAM408  TMEPAI   3'  AAGCAGGAGCCCTTGGTGGACC 11789          CACGCCT_
              C                  AAGCAGGAGCCC       CCC
                                 ||||||||||||       |||
                                 TTCGTCCTCGGG       GGG
                                       AACCACCT
GAM408  YES1     3'  AAGCAGGAGCCTCACTGTCC   11790          C   GCC
                                 AAGCAGGAGCC CAC   TCC
                                 |||||||||||| |||   |||
                                 TTCGTCCTCGG GTG   AGG
                                       A   AC_
GAM408  AEBP1    3'  AGCAGGAGCCTCTACACAGCCT 11791          C___   _
              C                  AGCAGGAGCC    CAC GCCTC
                                 ||||||||||    ||| |||||
                                 TCGTCCTCGG    GTG CGGAG
                                       AGAT   T
GAM408  BPESC1   3'  GGAGCCACCACCTCCCG     11792       CCA
                                 GGAGCC   CGCCTCCCG
                                 ||||||   |||||||||
                                 CCTCGG   GTGGAGGGC
                                    TG_
GAM408  CNNM4    3'  AGGAGGAGCCCTCCTCTCC    11793    C      CACG   _
                                 AG AGGAGCCC    CCTC CC
                                 || ||||||||    |||| ||
                                 TC TCCTCGGG    GGAG GG
                                  C       A___    A
GAM408  DKFZp434C0923 3'  GCAGGAGCGCCCCCGCCT    11794        _   A
                                 GCAGGAGC CCC CGCCT
                                 |||||||| ||| |||||
                                 CGTCCTCG GGG GCGGA
                                      C   G
GAM408  DKFZP564C196 3'  AAGCAGGATCCCCACTGC    11795        G     _
                                 AAGCAGGA CCCCAC GC
                                 |||||||| |||||| ||
                                 TTCGTCCT GGGGTG CG
                                      A     A
GAM408  DNAJA3   3'  GCAGGAGCCCTCCATGCCT   11796          __  C
                                 GCAGGAGCCC  CA GCCT
                                 ||||||||||  || ||||
                                 CGTCCTCGGG  GT CGGA
                                       AG  A
GAM408  EHM2     3'  AAGCAGGAAGCCCAGAGCCTCC 11797         _   CAC
                                 AAGCAGGA GCCC   GCCTCC
                                 |||||||| ||||   ||||||
                                 TTCGTCCT CGGG   CGGAGG
                                      T    TCT
GAM408  FAM3D    3'  GCAGGAGCTTCTTCAGGCCCC  11798        CC___  C
                                 GCAGGAGC    CA GCCTC
                                 ||||||||    || |||||
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                                CGTCCTCG    GT CGGGG
                                     AAGAA  C
GAM408  FLJ10743  3'  AAGCAGGAAGCCTCAGGCACTC 11799        _  C  C  _
                                AAGCAGGA GCC CA GC CTC
                                |||||||| ||| || || |||
                                TTCGTCCT CGG GT CG GAG
                                     T   A  C  T
GAM408  FLJ10751  3'  AAGCAAGAGCCCCAGGCCCTCT 11800           C  _ _
          CC                     AAGCAGGAGCCCCA GCC TC CC
                                |||||||||||||| ||| || ||
                                TTCGTTCTCGGGGGT CGG AG GG
                                       C   G  A
GAM408  FLJ10751  3'  AAGCAAGAGCCCCAGGCCCTCT 11800           C  _ _
          CC                     AAGCAGGAGCCCCA GCC TC CC
                                |||||||||||||| ||| || ||
                                TTCGTTCTCGGGGGT CGG AG GG
                                       C   G  A
GAM408  FLJ10936  5'  AGGAGCAAAGCCCGCGCCTCCC 11801       _____  A
          G                      AGGAGC    CCC CGCCTCCCG
                                ||||||    ||| |||||||||
                                TCCTCG    GGG GCGGAGGGC
                                   TTTC   C
GAM408  FLJ11004  3'  GCAGGAGCGCTTTCCCG     11802        CCCAC  C_
                                GCAGGAGC    GC  TCCCG
                                ||||||||    ||  |||||
                                CGTCCTCG    CG  AGGGC
                                     ______ AA
GAM408  FLJ12122  5'  AGTCAGGAGCCCCCGACCCG   11803    _       A  CCT
                                AG CAGGAGCCCC CG   CCCG
                                || ||||||||||  ||   ||||
                                TC GTCCTCGGGG GC   GGGC
                                 A         _  T__
GAM408  FLJ12700  5'  GCAGGGCCCGCCTCCCG     11804      A    CAC
                                GCAGG GCCC   GCCTCCCG
                                ||||| ||||   ||||||||
                                CGTCC CGGG   CGGAGGGC
                                     _    ____
GAM408  FLJ14129  3'  GGACAGGAGCCTCCCCCG    11805   A       CCACGC
                                A GCAGGAGCC     CTCCCG
                                | |||||||||     ||||||
                                C TGTCCTCGG     GGGGGC
                                 C        A_____
GAM408  FLJ20452  3'  AACCAGGGCTGCCTCCCG    11806    G   A  CCCAC
                                AA CAGG GC    GCCTCCCG
                                || |||| ||    ||||||||
                                TT GTCC CG    CGGAGGGC
                                 G    _  A____
GAM408  FLJ22843  5'  GCAGCGGCCGCCTCCCG     11807     GA   CCAC
                                GCAG  GCC    GCCTCCCG
                                ||||  |||    ||||||||
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                                CGTC  CGG   CGGAGGGC
                                  GC  _____
GAM408  HSJ001348 5'  AGGGGGAGCCCCGCCCGCCCCG 11808    CA      AC   __
                                AG  GGAGCCCC  GCCT  CCCG
                                ||  ||||||||  ||||  ||||
                                TC  CCTCGGGG  CGGG  GGGC
                                 CC       __   CG
GAM408  KCNH8    3'  AGCAGGAGCTGTGCACTCCTGA 11809         CCCAC  _   C
                                AGCAGGAGC    GC CTCC GA
                                |||||||||    || |||| ||
                                TCGTCCTCG    CG GAGG CT
                                      ACA__  T   A
GAM408  KIAA0008  5'  AAGCAGGAACCCTCACAACCCG 11810           _   CCT
          A                      AAGCAGGAGCCC CACG   CCCGA
                                ||||||||||| ||||   |||||
                                TTCGTCCTTGGG GTGT   GGGCT
                                       A   T__
GAM408  KIAA0415  3'  GCGGTGGCCCCACGAGTGCCT  11811    A  A_     _____
                                GC GG  GCCCCAC    GCCT
                                || ||  |||||||    ||||
                                CG CC  CGGGGTG    CGGA
                                 _ AC      CTCA
GAM408  KIAA0429  5'  AAGAGGAGCCCCACTCT     11812     C         GC
                                AAG AGGAGCCCCAC  CT
                                ||| ||||||||||  ||
                                TTC TCCTCGGGGTG  GA
                                  _         A_
GAM408  KIAA1157  3'  AGGAGGGGCTCCAGGCCTTTTC 11813    C   A  C   C    CC_
          GA                     AG AGG GC CCA GCCT   CGA
                                || ||| || ||| ||||   |||
                                TC TCC CG GGT CGGA   GCT
                                 C   C  A   C    AAA
GAM408  KIAA1533  5'  GCAGGAGCTGCAGCCGTTTCCG 11814         CC  C   TC__
                                GCAGGAGC  CA GCC    CCG
                                ||||||||  || |||    |||
                                CGTCCTCG  GT CGG    GGC
                                     AC  _   CAAA
GAM408  KIAA1641  3'  AGCAGCAGTCCCCAGCCT    11815      G  _    C
                                AGCAG AG CCCCA GCCT
                                ||||| || ||||| ||||
                                TCGTC TC GGGGT CGGA
                                   G  A    _
GAM408  KIAA1789  5'  AAGCAGGAGTCCTGGTTTCCTC 11816          _  CCACG_
                                AAGCAGGAG CC      CCTC
                                ||||||||| ||      ||||
                                TTCGTCCTC GG      GGAG
                                     A  ACCAAA
GAM408  LANO     5'  AGCGGGAGCCCCTGCCCC    11817     A       AC
                                AGC GGAGCCCC  GCCTC
                                ||| ||||||||  |||||
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                                TCG CCTCGGGG  CGGGG
                                  C       A_
GAM408  MAPKAP1  5' GGCTCCCCCACGCCTCCCG   11818    AG_
                                GG   CCCCACGCCTCCCG
                                ||   ||||||||||||||
                                CC   GGGGTGCGGAGGGC
                                 GAG
GAM408  MFN2     3' GCAGGAGCCACACGTGCCCC   11819         C    CC
                                GCAGGAGCC CACG  TCCC
                                |||||||||  ||||  ||||
                                CGTCCTCGG GTGC  GGGG
                                      T   AC
GAM408  PPFIA4   3' AGCAGGAGCTCCACCCG     11820         C   CGCCT
                                AGCAGGAGC CCA    CCCG
                                |||||||||  |||    ||||
                                TCGTCCTCG GGT    GGGC
                                     A  _____
GAM408  PRSS25   3' AGCAGGAGCCTCATACTCT   11821         C  CG _
                                AGCAGGAGCC CA  C CT
                                ||||||||||  ||  | ||
                                TCGTCCTCGG GT  G GA
                                      A  AT A
GAM408  PRSS25   3' AGCAGGAGCCTCATACTCT   11821         C  CG _
                                AGCAGGAGCC CA  C CT
                                ||||||||||  ||  | ||
                                TCGTCCTCGG GT  G GA
                                      A  AT A
GAM408  RAB40C   3' AGGAGGGGCCTAGCCTCCCGA  11822    C   A   CCAC
                                AG AGG GCC    GCCTCCCGA
                                || ||| |||    |||||||||
                                TC TCC CGG    CGGAGGGCT
                                 C   C   AT__
GAM408  SIAT4B   3' GCCGGAGCCCCGGTGCCCGA   11823    A       ACGCCT
                                GC GGAGCCCC     CCCGA
                                || ||||||||     |||||
                                CG CCTCGGGG     GGGCT
                                 G       CCAC__
GAM408  SLC37A1  5' GCGGGGGGTCCCCGCCTCCCG  11824    A  AGC_   A
                                GC GG    CCC CGCCTCCCG
                                || ||    ||| |||||||||
                                CG CC    GGG GCGGAGGGC
                                 C  CCCA  _
GAM408  SLI      5' AGCAGGAGGCCCTGAGCCT    11825         _   CAC
                                AGCAGGAG CCC   GCCT
                                ||||||||  |||   ||||
                                TCGTCCTC GGG   CGGA
                                     C   ACT
GAM408  STX6     5' AGGGCGCCCGTGCCTCCCG    11826     A_    CAC
                                AGG  GCCC   GCCTCCCG
                                |||  ||||   ||||||||
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                                TCC  CGGG   CGGAGGGC
                                  CG    CA_
GAM408  TNKS2     5'  AGCAGGAGCCCCGGCCCCGCGA 11827          AC     C
                                AGCAGGAGCCCC  GCCTC CGA
                                ||||||||||||  ||||| |||
                                TCGTCCTCGGGG  CGGGG GCT
                                      C_     C
GAM408  TSPEAR    3'  AAGCAGGAGCACCGTTCCT    11828         C  ACG
                                AAGCAGGAGC CC   CCT
                                |||||||||| ||   |||
                                TTCGTCCTCG GG   GGA
                                      T  CAA
GAM408  LOC115219 5'  GGACAGGGTGCCCACGCCT    11829    A     AGC
                                A GCAGG   CCCACGCCT
                                | |||||   |||||||||
                                C TGTCC   GGGTGCGGA
                                 C     CAC
GAM408  LOC132617 5'  AGCAGAAGGAGCTTCCCG     11830        CCCCAC  C
                                AGCAGGAG     GC TCCCG
                                ||||||||     || |||||
                                TCGTCTTC     CG AGGGC
                                     CT_____  A
GAM408  LOC136319 5'  GCAGGAACCTTTACACTTCC   11831         CC_    C
                                GCAGGAGCC   ACGC TCC
                                |||||||||   |||| |||
                                CGTCCTTGG   TGTG AGG
                                      AAA    A
GAM408  LOC139709 5'  AGCAAGGAGTCCTCCCG     11832      _   CCCCACG
                                AGCA GGAG      CCTCCCG
                                |||| ||||      |||||||
                                TCGT CCTC      GGAGGGC
                                  T    A_______
GAM408  LOC143451 3'  GCGGGAGCCCCGCCCTCCCA   11833    A       ACG
                                GC GGAGCCCC   CCTCCCG
                                || ||||||||   |||||||
                                CG CCTCGGGG   GGAGGGT
                                 C       CG_
GAM408  LOC145125 3'  GCAGGAGCCCCGCCCTCCCA   11834          ACG
                                GCAGGAGCCCC   CCTCCCG
                                ||||||||||   |||||||
                                CGTCCTCGGGG   GGAGGGT
                                      CG_
GAM408  LOC145693 5'  AGCAGGAGCTCAGAGAGCCT   11835         CC  C___
                                AGCAGGAGC  CA    GCCT
                                |||||||||  ||    ||||
                                TCGTCCTCG  GT    CGGA
                                     A_  CTCT
GAM408  LOC151124 5'  AGCAGGAGCCACCATCCTC    11836          _  CG
                                AGCAGGAGCC CCA  CCTC
                                |||||||||| |||  ||||
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                                TCGTCCTCGG GGT  GGAG
                                      T   A_
GAM408  LOC151963 3'  AAGCAGGACCCCACAACT    11837        G      C
                                AAGCAGGA CCCCACG CT
                                |||||||| ||||||| ||
                                TTCGTCCT GGGGTGT GA
                                     _      T
GAM408  LOC153505 3'  AGTAGGGGCTGGGCCGCCTCCC 11838    C   A  CCCA_
          G                      AG AGG GC     CGCCTCCCG
                                 || ||| ||     |||||||||
                                 TC TCC CG     GCGGAGGGC
                                  A   C  ACCCG
GAM408  LOC196872 3'  AAGCAGGAGGCCTAACA     11839         CCCCAC    CC
                                AAGCAGGAG     GCCT  CG
                                |||||||||     ||||  ||
                                TTCGTCCTC     CGGA  GT
                                      _______   TT
GAM408  LOC197414 3'  AGCAGGAGCACCTGGCCCC    11840         C  AC
                                AGCAGGAGC CC  GCCTC
                                ||||||||| ||  |||||
                                TCGTCCTCG GG  CGGGG
                                      T  AC
GAM408  LOC204285 3'  AGCTAGGAGCCCTGTCCCC    11841     _       CACG
                                AGC AGGAGCCC    CCTC
                                ||| ||||||||    ||||
                                TCG TCCTCGGG    GGGG
                                  A       ACA_
GAM408  LOC205095 3'  GCGGGAGCCCCGCGATTTCCTC 11842    A       A  CC_  _
          G                      GC GGAGCCCC CG   TCC CG
                                 || |||||||| ||   ||| ||
                                 CG CCTCGGGG GC   AGG GC
                                  C       C  TAA   A
GAM408  LOC221914 5'  AAGCAGAGCCTCCCAA      11843        AGCCCCAC
                                AAGCAGG       GCCTCCCGA
                                |||||||       |||||||||
                                TTCGTCT       CGGAGGGTT
                                      _________
GAM408  LOC221955 3'  AAGCGTGAGTCCATCGTTCC   11844     AG   CC   _  CC
                                AAGC  GAG  CCA CG  TCC
                                ||||  |||  ||| ||  |||
                                TTCG  CTC  GGT GC  AGG
                                  CA   A_   A  A_
GAM408  LOC254440 3'  GCAGGAGCCCCGCCCTCCCA   11834          ACG
                                GCAGGAGCCCC   CCTCCCG
                                ||||||||||   |||||||
                                CGTCCTCGGGG   GGAGGGT
                                      CG_
GAM408  LOC51205  5'  AGCAGGGACCGCTGTGCCTCCC 11845       AG  CCAC_
          G                      AGCAGG  CC    GCCTCCCG
                                 ||||||  ||    ||||||||
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                                TCGTCC  GG    CGGAGGGC
                                   CT  CGACA
GAM408  LOC51759  3'  GCAGGAGCCACCACGCCC    11846        _
                                GCAGGAGCC CCACGCCT
                                ||||||||| ||||||||
                                CGTCCTCGG GGTGCGGG
                                     T
GAM408  LOC90639  3'  AAGCAGGAGCTCAATACACCT  11847         CCC__
                                AAGCAGGAGC    ACGCCT
                                ||||||||||    ||||||
                                TTCGTCCTCG    TGTGGA
                                      AGTTA
GAM408  LOC92703  3'  AACAGGAGCCCTAGAACCT   11848         CAC_
                                AGCAGGAGCCC    GCCT
                                ||||||||||    ||||
                                TTGTCCTCGGG    TGGA
                                      ATCT
GAM408  LOC93017  5'  GCAGGAGCCCCGGCTTC     11849         AC  C
                                GCAGGAGCCCC  GC TC
                                ||||||||||  || ||
                                CGTCCTCGGGG  CG AG
                                      C_  A
GAM408  LOC93070  5'  AGGAGCAAAGCCCGCGCCTCCC 11801       ____  A
          G                      AGGAGC    CCC CGCCTCCCG
                                ||||||   ||| |||||||||
                                TCCTCG    GGG GCGGAGGGC
                                   TTTC   C
GAM409  FBXL11    3'  GGGAAGATCGGTTTCCTGTTG  11852        ATG  G_
                                GGGAAGATCG   TT  GTTG
                                ||||||||||   ||  ||||
                                CCCTTCTAGC   AG  CAAC
                                      CAA  GA
GAM409  MUC4      3'  TAAGGGAAGTTCTAGGTT    11853        A  GATGTT
                                TAAGGGAAG TC     GGTT
                                ||||||||| ||     ||||
                                ATTCCCTTC AG     CCAA
                                     A  AT____
GAM409  TRPM1     5'  AGGGGGGATATGCTGGTTG   11854     AA   CG
                                AGGG  GAT  ATGTTGGTTG
                                ||||  |||  ||||||||||
                                TCCC  CTA  TACGACCAAC
                                  CC  __
GAM409  FLJ21616  3'  AGGGAAGTTTGGTTGGTTG   11855       ATCGAT
                                AGGGAAG     GTTGGTTG
                                |||||||     ||||||||
                                TCCCTTC     CAACCAAC
                                    AAAC__
GAM409  KIAA0478  3'  AGGTGAGACTGTGTTGGTTG  11856    GA   CGA
                                AGG  AGAT   TGTTGGTTG
                                |||  ||||   |||||||||
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                                TCC  TCTG   ACAACCAAC
                                  AC    AC_
GAM409  SEMA6B   3'  AGGGGGAGGGCGAGCTGGTTG  11857     A_  AT   T
                                AGGG  AG  CGA GTTGGTTG
                                ||||  ||  ||| ||||||||
                                TCCC  TC  GCT CGACCAAC
                                  CC  CC  _
GAM409  STARD7   5'  AGGGGAGAGTCGGTCA      11858      A   TCGAT
                                AGGG AGA    GTTGGTTG
                                |||| |||    ||||||||
                                TCCC TCT    CAGCCAGT
                                  C  _____
GAM409  LOC256248 5'  AAGGGGCTCTATGTTGGTTG   11859      AAGA  G
                                AAGGG    TC ATGTTGGTTG
                                |||||    || ||||||||||
                                TTCCC    AG TACAACCAAC
                                   CG__  A
GAM409  LOC91828  5'  TAACGGAAGGGTTGGTT     11860     G    ATCGAT
                                TAA GGAAG     GTTGGTT
                                ||| |||||     |||||||
                                ATT CCTTC     CAACCAA
                                  G    C_____
GAM410  ELF3     3'  TCAGTGTTCTGAGTTCATGTCC 11863         CA   G_
           T                     TCGGTGTTC  GAG  CATGTCCT
                                |||||||||  |||  ||||||||
                                AGTCACAAG  CTC  GTACAGGA
                                     A_   AA
GAM410  PTP4A2   5'  TCGGTGTCCAGGAGTCT     11864        T   A  CAT   C
                                TCGGTGT CCAG GG   GTC T
                                ||||||| |||| ||   ||| |
                                AGCCACA GGTC CT   CAG A
                                   _   _ ___   A
GAM410  PTP4A2   5'  TCGGTGTCCAGGAGTCT     11864        T   A  CAT   C
                                TCGGTGT CCAG GG   GTC T
                                ||||||| |||| ||   ||| |
                                AGCCACA GGTC CT   CAG A
                                   _   _ ___   A
GAM410  CXorf12   3'  TCGGTTTTCAGCAGGTTCT   11865      G  CAGA   T  C
                                TCGGT TTC    GGCA GT CT
                                ||||| |||    |||| || ||
                                AGCCA AAG    TCGT CA GA
                                   A  _____   C  A
GAM410  DKFZp547D155 3'  GGTGGGAGGCATGTCCTC    11866      TTCCA
                                GGTG    GAGGCATGTCCTC
                                ||||    ||||||||||||||
                                CCAC    CTCCGTACAGGAG
                                  C_____
GAM410  DKFZP566F2124 5'  TCGTTGAGATCAGGCATGTCCT 11867     G  TTCCAG
                                TCG TG     AGGCATGTCCT
                                ||| ||     ||||||||||
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                                AGC AC     TCCGTACAGGA
                                  A  TCTAG_
GAM410  ETAA16   5'  GGTGTTTCATACCTTTCCTC  11868       C  GAG  ATG
                                GGTGTT CA   GC   TCCTC
                                |||||| ||   ||   |||||
                                CCACAA GT   TG   AGGAG
                                   A  A__  GAA
GAM410  KIAA1735 5'  TGTTCCAACAGCTGTTCT    11869        A   A   C
                                TGTTCCAG GGC TGT CT
                                |||||||| ||| ||| ||
                                ACAAGGTT TCG ACA GA
                                     G   _   A
GAM410  MAEA     3'  TCGGTGTTTAGGTCAGTC    11870        CCAG   _  T
                                TCGGTGTT    AGG CA GTC
                                ||||||||    ||| || |||
                                AGCCACAA    TCC GT CAG
                                     A___   A  _
GAM410  LOC144321 3'  TCAGTGTTTTTCCTGTCATGTC 11871        ___   AGAGG
                                TCGGTGT   TCC    CATGTC
                                |||||||   |||    ||||||
                                AGTCACA   AGG    GTACAG
                                    AAA   ACA__
GAM410  LOC157638 5'  CGGGCAGACTAGGGGCATGTC  11872     T  TCC__  A
                                CGG GT     AG GGCATGTC
                                ||| ||     || ||||||||
                                GCC CG     TC CCGTACAG
                                  _  TCTGA  C
GAM410  LOC200010 5'  TCAGTGTTTCAGGGACTGTCTT 11873        C   A   A   C
            C                    TCGGTGTT CAG GGC TGTC TC
                                |||||||| ||| ||| |||| ||
                                AGTCACAA GTC CTG ACAG AG
                                     A   C   _   A
GAM411  LOC161580 5'  CCTTTAGTCTGTGTACA     11876        CA   C
                                CCTTTGGTC  TGT GCG
                                |||||||||  ||| |||
                                GGAAATCAG  ACA TGT
                                     AC   _
GAM412  GNAS     3'  CTCCACGGGGGGCACCAGG    11879      _    AGGAG
                                TTCC CGGGG     GGCACCAGG
                                |||| |||||     |||||||||
                                GAGG GCCCC     CCGTGGTCC
                                  T    ______
GAM412  KRTHB6   5'  GGGGAAGAGAGGAGGT      11880          CACC
                                GGGGAGGAGGG    AGGT
                                ||||||||||    ||||
                                CCCCTTCTCTC    TCCA
                                      C___
GAM412  PSD      5'  TTCCCGGGGGGAGGACCAGGT  11881         A    GC
                                TTCCCGGGG GGAGG  ACCAGGT
                                ||||||||| |||||  |||||||
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                                AAGGGCCCC CCTCC  TGGTCCA
                                      _   __
GAM412  C8orf13   5' TTCTCGGGAAGGGCAG     11882     C   GAG      CCA
                                TTC CGGG   GAGGGCA   G
                                ||| ||||   |||||||   |
                                AAG GCCC   TTCCCGT   C
                                  A   ___     ___
GAM412  FLJ10874  3' TTCCTCGGGGACACCAGG    11883     _    AGGAGG
                                TTCC CGGGG     GCACCAGG
                                |||| |||||     ||||||||
                                AAGG GCCCC     TGTGGTCC
                                  A   _______
GAM412  FLJ12389  3' TTCCTGGTGAGGAGGGTCC    11884     C  G      CA
                                TTCC GG GAGGAGGG  CC
                                |||| || ||||||||  ||
                                AAGG CC CTCCTCCC  GG
                                  A A       A_
GAM412  NLI-IF    3' TTCCTGGGAGGAGGTGTGGGT  11885     CG       GCACCA
                                TTCC  GGGAGGAGG     GGT
                                ||||  |||||||||     |||
                                AAGG  CCCTCCTCC     CCA
                                  A_       ACAC__
GAM412  PIP5K1C   3' TCCCCGGGGGGGTGCCTGCTGGG 11886         A  AGG  ACCA__
           T                     TTCCCGGGG GG   GC     GGT
                                |||||||| ||   ||     |||
                                AGGGGCCCC CC   CG     CCA
                                      _ A__  GACGAC
GAM412  PRO0159   5' TTCTGGGAGAGCAATACATCAG 11887     CC     G  G   C
           GT                     TTC  GGGGAG AG GCA CAGGT
                                |||  |||||| || ||| |||||
                                AAG  CCTCTC TT TGT GTCCA
                                  AC     G  A   A
GAM412  SLC38A5   3' TCCCTGGGGAGGAGGGAAG   11888     _        CACC
                                TCCC GGGGAGGAGGG    AGG
                                |||| ||||||||||    |||
                                AGGG CCCCTCCTCCC    TTC
                                  A         _____
GAM412  LOC153592 3' TTCCTGGGGAGGAGGAGGCACC 11889      C         __     A
           GGGT                    TTCC GGGGAGGAGG  GCACC GGT
                                |||| ||||||||||  ||||| |||
                                AAGG CCCCTCCTCC  CGTGG CCA
                                  A         TC    C
GAM412  LOC253868 3' CCAGAAAGAGGGGTGCCAGGT  11890     GG  GA   CA
                                CCGG  AG  GGG  CCAGGT
                                ||||  ||  |||  ||||||
                                GGTC  TC  CCC  GGTCCA
                                  TT  TC   AC
GAM413  GGT1      5' TGTTGGCCACGAAAGACAGG   11893          TGTG_
                                TGTTGGCCGCG    TAGG
                                ||||||||||     ||||
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                                ACAACCGGTGC    GTCC
                                      TTTCT
GAM413  GGT1    5'  TGTTGGCCACGAAAGACAGG  11893         TGTG_
                                TGTTGGCCGCG    TAGG
                                ||||||||||    ||||
                                ACAACCGGTGC    GTCC
                                      TTTCT
GAM413  GGT1    5'  TGTTGGCCACGAAAGACAGG  11893         TGTG_
                                TGTTGGCCGCG    TAGG
                                ||||||||||    ||||
                                ACAACCGGTGC    GTCC
                                      TTTCT
GAM413  GGT2    5'  TGTTGGCCACGAAAGACAGG  11893         TGTG_
                                TGTTGGCCGCG    TAGG
                                ||||||||||    ||||
                                ACAACCGGTGC    GTCC
                                      TTTCT
GAM413  PMP2    3'  TAAAATGTTGGCTGGAGTAGAG 11894          CGCGT   T
          G                      TAAAATGTTGGC    GTG AGG
                                ||||||||||||    ||| |||
                                ATTTTACAACCG    CAT TCC
                                      ACCT_   C
GAM413  SLC21A9 3'  AAATCTTGGCAATGTGTAGG  11895     G    CGC
                                AAAT TTGGC   GTGTGTAGG
                                |||| |||||   |||||||||
                                TTTA AACCG   TACACATCC
                                  G    T__
GAM413  WISP2   3'  ATATAGGCTGTGTGTGTAGG  11896     T   CGC
                                ATGT GGC   GTGTGTAGG
                                |||| |||   |||||||||
                                TATA CCG   CACACATCC
                                  T   ACA
GAM413  ZNF36   3'  ATGTTGGCCAAAGTAGG     11897         CGTGT
                                ATGTTGGCCG    GTAGG
                                ||||||||||    |||||
                                TACAACCGGT    CATCC
                                      TT____
GAM413  ESM1    3'  TAAAATGTTGGCTGTGTG    11898          CGC
                                TAAAATGTTGGC   GTGTG
                                ||||||||||||   |||||
                                ATTTTACAACCG   CACAC
                                      A__
GAM413  FLJ10687 3'  AAAATGTTCATTGGGTGTGTGT 11899       _____  CCGC     A
          GGG                    AAAATGT    TGG    GTGTGT GG
                                |||||||    |||    |||||| ||
                                TTTTACA    ACC    CACACA CC
                                    AGTA   CA__     C
GAM413  SOX7    3'  TAAAATGTGGGCTGCA      11900         T   CGCGTG
                                TAAAATGT GGC     TGTA
                                |||||||| |||     ||||
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                                ATTTTACA CCG     ACGT
                                    C  _______
GAM413  LOC144747 5'  GTTGGTTCATGTGTAGG     11901      CCG
                                GTTGG  CGTGTGTAGG
                                |||||  ||||||||||
                                CAACC  GTACACATCC
                                  AA_
GAM413  LOC145134 5'  AAATGTTGCCGTGTCCTGCAGG 11902        G  C  G_
                                AAATGTTG CCG GT  TGTAGG
                                |||||||| ||| ||  ||||||
                                TTTACAAC GGC CA  ACGTCC
                                    _  A  GG
GAM413  LOC220522 5'  TGTTGGCCACGAAAGACAGG   11893          TGTG_
                                TGTTGGCCGCG    TAGG
                                ||||||||||     ||||
                                ACAACCGGTGC    GTCC
                                      TTTCT
GAM413  LOC257422 5'  AATGTTGGCCGCTTTGAGG    11903          GTG  T
                                AATGTTGGCCGC   TG AGG
                                ||||||||||||   || |||
                                TTACAACCGGCG   AC TCC
                                      AA_  _
GAM414  AQP2     5'  CGGGGCTGGCCCAGCTG     11906    CA    C TATA
                                CG  GCTG G    CCCAGCTG
                                ||  |||| |    ||||||||
                                GC  CGAC C    GGGTCGAC
                                 CC    _ _____
GAM414  CENTD2    5'  GCGGGCTGCGTATGCCCA    11907    A_       A
                                GC  GCTGCGTAT CCCA
                                ||  |||||||| ||||
                                CG  CGACGCATA GGGT
                                 CC        C
GAM414  GPR30     3'  CGCAGTTGTCCCCAGCTGT    11908      C  CGTATA
                                CGCAG TG     CCCAGCTGT
                                ||||| ||     |||||||||
                                GCGTC AC     GGGTCGACA
                                   A  AG_____
GAM414  IL2RA     3'  ACGCAGACAATGTCCAGTTGT  11909       CT   TATAC    C
                                ACGCAG  GCG    CCAG TGT
                                ||||||  |||    |||| |||
                                TGCGTC  TGT    GGTC ACA
                                   __   TACA_    A
GAM414  STAT5B    5'  CGCGGCTGCTCCGGCCCAGCTG 11910     A    GTATA
           T                     CGC GCTGC    CCCAGCTGT
                                ||| |||||    |||||||||
                                GCG CGACG    GGGTCGACA
                                  C    AGGCC
GAM414  C(27)-3BETA-HSD 3'  GCACCTGTGGTCCCAGCTGT   11911     G   CGTATA
                                GCA CTG     CCCAGCTGT
                                ||| |||     |||||||||
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                                CGT GAC     GGGTCGACA
                                  G  ACCA__
GAM414  C20orf130 5'  GCAGCTGGCTGCCCAGCTGT  11912       C  ATA
                                GCAGCTG GT  CCCAGCTGT
                                ||||||| ||  |||||||||
                                CGTCGAC CG  GGGTCGACA
                                   _ AC_
GAM414  FLJ11280  5'  GCCAGCTGCCTTCCAGCTGT  11913   _    GTATAC
                                GC AGCTGC    CCAGCTGT
                                || ||||||    ||||||||
                                CG TCGACG    GGTCGACA
                                 G    GAA___
GAM414  FLJ23093  3'  GCTGCACTCACCCAGCTGT  11914      TA
                                GCTGCG  TACCCAGCTGT
                                ||||||  ||||||||||
                                CGACGT  GTGGGTCGACA
                                   GA
GAM414  FZD9    3'  GCAGCTGCTAGTCAGCTGT  11915       GTATACC
                                GCAGCTGC     CAGCTGT
                                ||||||||     |||||||
                                CGTCGACG     GTCGACA
                                    ATCA___
GAM414  KIAA0945  3'  GCAGCCCCTGCCCAGCTGT  11916      GCGTATA
                                GCAGCT     CCCAGCTGT
                                ||||||     |||||||||
                                CGTCGG     GGGTCGACA
                                   GGAC___
GAM414  KIAA1679  3'  ACCAGTTGCCAAGGACCCAGCT 11917   G  C  GTAT_
          GT                    AC CAG TGC    ACCCAGCTGT
                                || ||| |||    ||||||||||
                                TG GTC ACG    TGGGTCGACA
                                 _  A  GTTCC
GAM414  KLK15   3'  CGGGGCTGCTGGCCAGCTGT  11918   CA   GTATAC
                                CG  GCTGC    CCAGCTGT
                                ||  |||||    ||||||||
                                GC  CGACG    GGTCGACA
                                 CC    ACC___
GAM414  KLK15   3'  CGGGGCTGCTGGCCAGCTGT  11918   CA   GTATAC
                                CG  GCTGC    CCAGCTGT
                                ||  |||||    ||||||||
                                GC  CGACG    GGTCGACA
                                 CC    ACC___
GAM414  KLK15   3'  CGGGGCTGCTGGCCAGCTGT  11918   CA   GTATAC
                                CG  GCTGC    CCAGCTGT
                                ||  |||||    ||||||||
                                GC  CGACG    GGTCGACA
                                 CC    ACC___
GAM414  KLK15   3'  CGGGGCTGCTGGCCAGCTGT  11918   CA   GTATAC
                                CG  GCTGC    CCAGCTGT
                                ||  |||||    ||||||||
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                                GC  CGACG     GGTCGACA
                                 CC     ACC___
GAM414  LHX6     3'  ACGCAGCTGTGTCTGACCTCTG 11919         C  AT_   CAG
              T                   ACGCAGCTG GT   ACC   CTGT
                                  ||||||||| ||   |||   ||||
                                  TGCGTCGAC CA   TGG   GACA
                                       A  GAC   A__
GAM414  SS18L1   3'  GCTGCATGTGTGTCCAGCTGT  11920        ATAC__
                                  GCTGCGT     CCAGCTGT
                                  |||||||     ||||||||
                                  CGACGTA     GGTCGACA
                                      CACACA
GAM414  LOC147229 5'  GCAGCTGCGTATGCCCAG    11921           A
                                  GCAGCTGCGTAT CCCAG
                                  |||||||||||| |||||
                                  CGTCGACGCATA GGGTC
                                         C
GAM414  LOC165552 3'  GCAGCTGCGCCAGCTGT     11922         TATAC
                                  GCAGCTGCG    CCAGCTGT
                                  |||||||||    ||||||||
                                  CGTCGACGC    GGTCGACA
                                       _____
GAM414  LOC221448 5'  CGCAGTGACCGTTCCAGCTGT  11923       C  __   ATAC
                                  CGCAG TG  CGT    CCAGCTGT
                                  ||||| ||  |||    ||||||||
                                  GCGTC AC  GCA    GGTCGACA
                                     _  TG   A___
GAM414  LOC221486 3'  ACATGGCATGCCCAGCTG    11924     GC  C    A
                                  GCA  TG GTAT CCCAGCTG
                                  |||  || |||| ||||||||
                                  TGT  AC CGTA GGGTCGAC
                                    __  _    C
GAM414  LOC222488 3'  CACAGCTGTCCCAGTTG     11925         CGTATA    C
                                  CGCAGCTG     CCCAG TG
                                  ||||||||     ||||| ||
                                  GTGTCGAC     GGGTC AC
                                       A_____     A
GAM414  LOC92223  3'  ACGCAGCTGCTGTTAAATGCTG 11926          GTATACCCA
              T                   ACGCAGCTGC        GCTGT
                                  ||||||||||        |||||
                                  TGCGTCGACG        CGACA
                                        ACAATTTA_
GAM415  ARHGAP6   5'  TGGGTTCCCAGCTCCAGCC    11929     TA       GAGGTT
                                  TGG  TTCCCAGCT     GCC
                                  |||  |||||||||     |||
                                  ACC  AAGGGTCGA     CGG
                                    C_        GGT___
GAM415  ARHGAP6   5'  TGGGTTCCCAGCTCCAGCC    11929     TA       GAGGTT
                                  TGG  TTCCCAGCT     GCC
                                  |||  |||||||||     |||
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                                ACC  AAGGGTCGA     CGG
                                  C_       GGT___
GAM415  CIT     3'  TGGTTTTTCTGGCTGAGAT   11930     A_   CCA
                                TGGT  TTC   GCTGAGGT
                                ||||  |||   ||||||||
                                ACCA  AAG   CGACTCTA
                                  AA   AC_
GAM415  LDHB    5'  TGGGTTCCTTTTTGGTTGCCT  11931     TA    CAGCTGA
                                TGG  TTCC      GGTTGCCT
                                |||  ||||      ||||||||
                                ACC  AAGG      CCAACGGA
                                  C_   AAAAA__
GAM415  POU2AF1  3'  TGGTACTTCTGGCTGAGGCT   11932       CCCA
                                TGGTATT    GCTGAGGTT
                                |||||||    |||||||||
                                ACCATGA    CGACTCCGA
                                    AGAC
GAM415  PPP1R2   3'  TGGTATTCCTAGCTGAAAT   11933        C
                                TGGTATTCC AGCTGAGGT
                                ||||||||| |||||||||
                                ACCATAAGG TCGACTTTA
                                     A
GAM415  SLC25A19 3'  TGGTGTCCCAGCTGGGT    11934      AT       A
                                TGGT  TCCCAGCTG GGT
                                ||||  ||||||||| |||
                                ACCA  AGGGTCGAC CCA
                                  C_       _
GAM415  SNRPN    5'  TGGTGTCTCAGCTAAGAATGCC 11935     AT  C      GT
          T                      TGGT  TC CAGCTGAG  TGCCT
                                 ||||  || ||||||||  |||||
                                 ACCA  AG GTCGATTC  ACGGA
                                   C_ A       TT
GAM415  SNRPN    5'  TGGTGTCTCAGCTAAGAATGCC 11935     AT  C      GT
          T                      TGGT  TC CAGCTGAG  TGCCT
                                 ||||  || ||||||||  |||||
                                 ACCA  AG GTCGATTC  ACGGA
                                   C_ A       TT
GAM415  SNRPN    5'  TGGTGTCTCAGCTAAGAATGCC 11935     AT  C      GT
          T                      TGGT  TC CAGCTGAG  TGCCT
                                 ||||  || ||||||||  |||||
                                 ACCA  AG GTCGATTC  ACGGA
                                   C_ A       TT
GAM415  SNRPN    5'  TGGTGTCTCAGCTAAGAATGCC 11935     AT  C      GT
          T                      TGGT  TC CAGCTGAG  TGCCT
                                 ||||  || ||||||||  |||||
                                 ACCA  AG GTCGATTC  ACGGA
                                   C_ A       TT
GAM415  TRPM8    3'  TGGTAATCGCTAGAGGTTGCCT 11936      T  CCA  _
                                TGGTA TC   GCT GAGGTTGCCT
                                ||||| ||   ||| ||||||||||
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                                ACCAT AG   CGA CTCCAACGGA
                                  T ___  T
GAM415  TSG      3'  GGTATTCCTAAAAAGTTGC   11937        CAGCT
                                GGTATTCC    GAGGTTGC
                                ||||||||    ||||||||
                                CCATAAGG    TTTCAACG
                                    ATT__
GAM415  BY55     5'  TGGTATCCTTGGCTTCAGTC  11938        CCA  GA
                                TGGTATTC  GCT  GGTT
                                ||||||||  |||  ||||
                                ACCATAGG  CGA  TCAG
                                    AAC  AG
GAM415  FLJ10697 3'  TGATATTCTTAGCTGTGTT   11939        CC    AG
                                TGGTATTC  AGCTG  GTT
                                ||||||||  |||||  |||
                                ACTATAAG  TCGAC  CAA
                                    AA    A_
GAM415  FLJ10997 3'  TGGTTTTCTGACTAGTTGCCT  11940     A  CCA  GA
                                TGGT TTC  GCT  GGTTGCCT
                                |||| |||  |||  ||||||||
                                ACCA AAG  TGA  TCAACGGA
                                  A  AC_  __
GAM415  FLJ20038 3'  TGGTATTTCCACATCATGCCT  11941       C  G TGAGGT
                                TGGTATT CCA C     TGCCT
                                ||||||| ||| |     |||||
                                ACCATAA GGT G     ACGGA
                                    A  _ TAGT__
GAM415  FLJ20079 3'  GGTATTCTCTTATGGTTGTCT  11942       CCAG  GA_    C
                                GGTATTC   CT   GGTTG CT
                                |||||||   ||  ||||| ||
                                CCATAAG   GA   CCAAC GA
                                    A___  ATA    A
GAM415  KIAA0040 5'  TGGGTTCCTTTTTGGTTGCCT  11931    TA   CAGCTGA
                                TGG  TTCC     GGTTGCCT
                                |||  ||||     ||||||||
                                ACC  AAGG     CCAACGGA
                                  C_   AAAAA__
GAM415  RFX3     3'  GTATTCCCAGCCCTTTGC    11943         GAGG
                                GTATTCCCAGCT   TTGC
                                ||||||||||||   ||||
                                CATAAGGGTCGG   AACG
                                      GA__
GAM415  LOC144563 5'  TGGACTCATTGGCTGAGGTTGC 11944    T   CCA_
                                TGG ATTC   GCTGAGGTTGC
                                ||| ||||   ||||||||||||
                                ACC TGAG   CGACTCCAACG
                                  _   TAAC
GAM415  LOC145598 5'  TAGTATTCCCGGTTG      11945         AGCTGA
                                TGGTATTCCC     GGTTG
                                ||||||||||     |||||
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                                ATCATAAGGG     CCAAC
                                          _______
GAM415  LOC151632 5'  TGGACTCATTGGCTGAGGTTGC 11944     T    CCA_
                                TGG ATTC    GCTGAGGTTGC
                                ||| ||||    ||||||||||
                                ACC TGAG    CGACTCCAACG
                                  _    TAAC
GAM415  LOC152503 5'  GGTATTGGTCTGAGGTTGC    11946       CCCAG
                                GGTATT     CTGAGGTTGC
                                ||||||     ||||||||||
                                CCATAA     GACTCCAACG
                                   CCA__
GAM415  LOC153469 3'  GTATTCCCAGCTTCAAGGCC   11947           __
                                GTATTCCCAGCT  GAGGTT
                                ||||||||||||  ||||||
                                CATAAGGGTCGA  TTCCGG
                                       AG
GAM415  LOC159053 3'  TGGTCTTCCAGAGGTTGC     11948      A    CAGCT
                                TGGT TTCC     GAGGTTGC
                                |||| ||||     ||||||||
                                ACCA AAGG     CTCCAACG
                                  G    T____
GAM415  LOC200904 5'  TGGACTCATTGGCTGAGGTTGC 11944     T    CCA_
                                TGG ATTC    GCTGAGGTTGC
                                ||| ||||    ||||||||||
                                ACC TGAG    CGACTCCAACG
                                  _    TAAC
GAM415  LOC219919 5'  TGGACTCACTGGCTGAGGTTGC 11949     T    CCA_
                                TGG ATTC    GCTGAGGTTGC
                                ||| ||||    ||||||||||
                                ACC TGAG    CGACTCCAACG
                                  _    TGAC
GAM415  LOC221795 5'  TGGACTCATTGGCTGAGGTTGC 11944     T    CCA_
                                TGG ATTC    GCTGAGGTTGC
                                ||| ||||    ||||||||||
                                ACC TGAG    CGACTCCAACG
                                  _    TAAC
GAM415  LOC256515 5'  TGGACTCATTGGCTGAGGTTGC 11944     T    CCA_
                                TGG ATTC    GCTGAGGTTGC
                                ||| ||||    ||||||||||
                                ACC TGAG    CGACTCCAACG
                                  _    TAAC
GAM415  LOC256594 5'  TGGACTCATTGGCTGAGGTTGC 11944     T    CCA_
                                TGG ATTC    GCTGAGGTTGC
                                ||| ||||    ||||||||||
                                ACC TGAG    CGACTCCAACG
                                  _    TAAC
GAM416  AGTR1     5'  GAGGGCCGGCTGCGCTG     11952     T  G  C
                                GAG GC CG GCTGCGCTG
                                ||| || || |||||||||
```

```
                                CTC CG GC CGACGCGAC
                                  C _ _
GAM416  AGTR1    5' GAGGGCCGGCTGCGCTG     11952     T  G  C
                                GAG GC CG GCTGCGCTG
                                ||| || || |||||||||
                                CTC CG GC CGACGCGAC
                                  C _ _
GAM416  AGTR1    5' GAGGGCCGGCTGCGCTG     11952     T  G  C
                                GAG GC CG GCTGCGCTG
                                ||| || || |||||||||
                                CTC CG GC CGACGCGAC
                                  C _ _
GAM416  AGTR1    5' GAGGGCCGGCTGCGCTG     11952     T  G  C
                                GAG GC CG GCTGCGCTG
                                ||| || || |||||||||
                                CTC CG GC CGACGCGAC
                                  C _ _
GAM416  APP      5' GAGTGCGCTGCTGTGCGA    11953        GC   C  T
                                GAGTGCGC  GCTG GC GA
                                ||||||||  |||| || ||
                                CTCACGCG  CGAC CG CT
                                    A_   A _
GAM416  CHRM1    5' GAGCTGCGCCCTGTGCTG    11954      GC   G  C
                                GAGT  GCGC CTG GCTG
                                ||||  |||| ||| ||||
                                CTCG  CGCG GAC CGAC
                                  A_   G  A
GAM416  CML66    5' GAGGCGGCCCGCGCTG      11955     T  C  G
                                GAG GCG GC CTGCGCTG
                                ||| ||| || ||||||||
                                CTC CGC CG GGCGCGAC
                                 _  _ _
GAM416  ETF1     3' GTAGGCTGCTGCGCTGAC    11956     C  GC
                                GTG GC  GCTGCGCTGAC
                                ||| ||  ||||||||||
                                CAT CG  CGACGCGACTG
                                  C  A_
GAM416  EXTL1    3' GAGTGCGGCGCGACGCTGAC  11957        C   T
                                GAGTGCG GCGC GCGCTGAC
                                ||||||| |||| ||||||||
                                CTCACGC CGCG TGCGACTG
                                   _   C
GAM416  EXTL3    3' ATGTGCACGCTGCTGA      11958     C       GC
                                GTG GCGCGCTGC  TGA
                                ||| |||||||||  |||
                                TAC CGTGCGACG  ACT
                                  A       __
GAM416  GSPT1    5' GAGTGGGCAACGCTGA      11959      C   CGCT
                                GAGTG GCG   GCGCTGA
                                ||||| |||   |||||||
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                                CTCAC CGT    TGCGACT
                                  C  _____
GAM416  HMX1     5'  GAGTGCGCGCCGACAGCTGA  11960          GCT  _
                                GAGTGCGCGC   GC GCTGA
                                ||||||||||   || |||||
                                CTCACGCGCG   TG CGACT
                                     GC_  T
GAM416  HNRPDL   5'  GACTGCGCCCGGCGCTG     11961    G    G  CT
                                GA TGCGC CG  GCGCTG
                                || ||||| ||  ||||||
                                CT ACGCG GC  CGCGAC
                                 G    G  __
GAM416  KCNF1    5'  GTGCCACCCGTGCGCTGA     11962     _  G  C
                                GTGC GC CG TGCGCTGA
                                |||| || || ||||||||
                                CACG TG GC ACGCGACT
                                  G  G  _
GAM416  LAMP1    5'  AGTGCGCGCGAGACGGCGCTG  11963          ___ T
                                AGTGCGCGCG   C GCGCTG
                                ||||||||||   | ||||||
                                TCACGCGCGC   G CGCGAC
                                     TCT C
GAM416  LMNA     5'  GAGTGCGCCGGCCGGCTG     11964        GC   C
                                GAGTGCGC  GCTG GCTG
                                ||||||||  |||| ||||
                                CTCACGCG  CGGC CGAC
                                    GC   _
GAM416  MOX2     5'  GAGGCGCGCGCGAGGTGGC    11965     T      ____  C
                                GAG GCGCGCGC    TG GC
                                ||| ||||||||    || ||
                                CTC CGCGCGCG    AC CG
                                  _       CTCC  _
GAM416  PFKL     3'  GAGCCCTGGCGCTGCGCTG    11966      GCGC
                                GAGT    GCGCTGCGCTG
                                ||||    ||||||||||
                                CTCG    CGCGACGCGAC
                                  GGAC
GAM416  PPFIA3   3'  GCGCGCGCACTCCCGCTG     11967          G_
                                GTGCGCGCGCT  CGCTG
                                ||||||||||  |||||
                                CGCGCGCGTGA  GCGAC
                                     GG
GAM416  SCNN1B   5'  GGTGCGCGCCAAGCTGGC     11968   A      ___   C
                                G GTGCGCGC   GCTG GC
                                | ||||||||   |||| ||
                                C CACGCGCG   CGAC CG
                                 _       GTT   _
GAM416  SIAH2    5'  GCGCGCGCGGACGTGAC      11969         CT   C
                                GTGCGCGCG  GCG TGAC
                                |||||||||  ||| ||||
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                                CGCGCGCGC  TGC ACTG
                                     C_  _
GAM416  SOX12    3'  GCGTGCGCGCCCCGCTGAC   11970    C     G
                                GTG GCGCGCT CGCTGAC
                                ||| ||||||| |||||||
                                CGC CGCGCGG GCGACTG
                                  A      G
GAM416  VEGF     5'  GAGCGCGCGCGCTGGAGC    11971           C_
                                GAGTGCGCGCGCTG  GC
                                ||||||||||||||  ||
                                CTCGCGCGCGCGAC  CG
                                         CT
GAM416  DKFZp434K1815 5'  GAGGCGCAGCCCGCGCTGAC   11972    T   _  G
                                GAG GCGC GC CTGCGCTGAC
                                ||| |||| || ||||||||||
                                CTC CGCG CG GGCGCGACTG
                                  _   T  _
GAM416  DKFZP761C169 5'  GTGCCGCCGCGCCTGA     11973     GCG      _
                                GTGC   CGCTGCGC TGA
                                ||||   |||||||| |||
                                CACG   GCGGCGCG ACT
                                  ____      G
GAM416  FLJ14251  5'  ATGCTGACGTGCGCTGAC    11974     GC   C
                                GTGC  GCG TGCGCTGAC
                                ||||  ||| |||||||||
                                TACG  TGC ACGCGACTG
                                  AC  _
GAM416  FLJ23277  3'  GTGGCGCTGCAGCTGAC     11975     CGC      _
                                GTG   GCGCTGC GCTGAC
                                |||   ||||||| ||||||
                                CAC   CGCGACG CGACTG
                                  ____      T
GAM416  KIAA0527  5'  GAGTGCGCGGGCCAGCGGAC   11976         C    C  T
                                GAGTGCGCG GCTG GC GAC
                                ||||||||| |||| || |||
                                CTCACGCGC CGGT CG CTG
                                     C    _  C
GAM416  MGC20576  5'  GACTGCAGGTCTGCGCTGA   11977    G   CGCG
                                GA TGCG    CTGCGCTGA
                                || ||||    |||||||||
                                CT ACGT    GACGCGACT
                                 G   CCA_
GAM416  MGC5139   5'  GAGGGCAGACTGCGCTGA    11978     TGC   C
                                GAG   GCG GCTGCGCTGA
                                |||   ||| ||||||||||
                                CTC   CGT TGACGCGACT
                                  C__   C
GAM416  PP3501    3'  GTGGCCGCGCCGTGCTGA    11979     _ G      C
                                GTG C CGCGCTG GCTGA
                                ||| | ||||||| |||||
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                                CAC G GCGCGGC CGACT
                                  C _      A
GAM416  RAB6B    5'  TGCGCGCGTCCCTGAC      11980        _ GCG
                                TGCGCGCG CT   CTGAC
                                |||||||| ||   |||||
                                ACGCGCGC GG   GACTG
                                    A ___
GAM416  SIAT8C   5'  GAGCGCGCGCGCGTGTGGC   11981          _ C_
                                GAGTGCGCGCGC TG  GC
                                |||||||||||| ||  ||
                                CTCGCGCGCGCG AC  CG
                                      C  AC
GAM416  SPIB     3'  GAGGGCGCGCGCCAGCTTCTG  11982     T       _ G_
                                GAG GCGCGCGCT GC  CTG
                                ||| ||||||||| ||  |||
                                CTC CGCGCGCGG CG  GAC
                                  C        T  AA
GAM416  LOC143381 3'  AAGTCGCAGCTGCGCTG     11983     G   C
                                GAGT CGCG GCTGCGCTG
                                |||| |||| |||||||||
                                TTCA GCGT CGACGCGAC
                                  _   _
GAM416  LOC145553 5'  GAGTGCGCTCAGCCCTGGC   11984        ___ G  C
                                GAGTGCGC   GC CTG GC
                                ||||||||   || ||| ||
                                CTCACGCG   CG GAC CG
                                    AGT  G  _
GAM416  LOC147057 5'  GAGGCGCGGGCCGCGCTG    11985     T    C
                                GAG GCGCG GCTGCGCTG
                                ||| ||||| |||||||||
                                CTC CGCGC CGGCGCGAC
                                  _    C
GAM416  LOC151278 5'  GAGGCTCACTGCGCTG      11986     TGC  G
                                GAG   GC CGCTGCGCTG
                                |||   || ||||||||||
                                CTC   CG GTGACGCGAC
                                  ___  A
GAM416  LOC200382 5'  GAGTGGCGCGCTGTCGTG    11987      C      _ C
                                GAGTG GCGCGCTG CG TG
                                ||||| |||||||| || ||
                                CTCAC CGCGCGAC GC AC
                                  _       A _
GAM416  LOC204285 3'  GAGTGCGCTGAGGACAGCTGGC 11988        _____ _   C
                                GAGTGCGC    GC GCTG GC
                                ||||||||    || |||| ||
                                CTCACGCG    TG CGAC CG
                                    ACTCC  T   _
GAM417  KIAA0435  3'  TGGTTTGGGATTCTGGACAAGT 11991     A  A  TGCTG
                                TGG TT GG    CTGGACAAGT
                                ||| || ||    ||||||||||
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                                ACC AA CC    GACCTGTTCA
                                  A  C  TAA__
GAM417  KIAA1404  3'  TGGGATAGGTGCTGCTGG    11992    AT
                                TGG  TAGGTGCTGCTGG
                                |||  ||||||||||||||
                                ACC  ATCCACGACGACC
                                  CT
GAM417  LOC145333 5'  TGGAGAACCTGTTGCTGGACAA 11993     TTAGG  C
          GT                    TGGA    TG TGCTGGACAAGT
                                ||||    || ||||||||||||
                                ACCT    AC ACGACCTGTTCA
                                  CTTGG  A
GAM417  LOC50999  3'  TGGATTAGGTTTTCTCAAG   11994        GCTG  GGA
                                TGGATTAGGT   CT   CAAG
                                ||||||||||   ||   ||||
                                ACCTAATCCA   GA   GTTC
                                     AAA_  ____
GAM417  LOC54466  3'  GGTTTCTGCTGGACAAGT    11995    G_
                                GGT  CTGCTGGACAAGT
                                |||  ||||||||||||||
                                CCA  GACGACCTGTTCA
                                  AA
GAM418  ARIH1     5'  TCAGTCAGACGCGGC       11998        A  AG
                                TTAGTCAGAT GC  GGC
                                |||||||||| ||  |||
                                AGTCAGTCTG CG  CCG
                                       _  __
GAM418  BHMT2     3'  AGCTGGAGATAGCAGGGC    11999    C__
                                AGT   AGATAGCAGGGC
                                |||   ||||||||||||
                                TCG   TCTATCGTCCCG
                                  ACC
GAM418  FGF5      3'  TTAATCAGATAATTGGC     12000         CAG
                                TTAGTCAGATAG   GGC
                                ||||||||||||   |||
                                AATTAGTCTATT   CCG
                                     AA_
GAM418  FGF5      3'  TTAATCAGATAATTGGC     12000         CAG
                                TTAGTCAGATAG   GGC
                                ||||||||||||   |||
                                AATTAGTCTATT   CCG
                                     AA_
GAM418  FPGS      3'  TAGTCAAACTGGCAGGGC    12001        A_
                                TAGTCAGAT  GCAGGGC
                                |||||||||  |||||||
                                ATCAGTTTG  CGTCCCG
                                    AC
GAM418  GALNT7    5'  TCAGTCAAGCAGGGC       12002       GAT
                                TTAGTCA   AGCAGGGC
                                |||||||   ||||||||
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                              AGTCAGT  TCGTCCCG
                                   ___
GAM418  IRAK1   3' CTAGAACAGCAGGGC      12003     TCA
                              TTAG  GATAGCAGGGC
                              ||||  ||||||||||
                              GATC  TTGTCGTCCCG
                                  ___
GAM418  LRPAP1  3' TCAGTCAGAGCTGGGC     12004       TA A
                              TTAGTCAGA GC GGGC
                              |||||||||  || ||||
                              AGTCAGTCT CG CCCG
                                   __ A
GAM418  MAK     3' TTAGTCAAATAAGAAC     12005        GC
                              TTAGTCAGATA AGGGC
                              ||||||||||  |||||
                              AATCAGTTTAT TCTTG
                                   __
GAM418  MAP4K2  3' TCAGCCCCAGCAGGGC     12006      AGA
                              TTAGTC  TAGCAGGGC
                              ||||||  |||||||||
                              AGTCGG  GTCGTCCCG
                                 G__
GAM418  MOG     3' TTAGCCAGAGAGGGC      12007       TA C
                              TTAGTCAGA G AGGGC
                              |||||||||  | |||||
                              AATCGGTCT C TCCCG
                                   __ _
GAM418  MSN     3' GTCAAACAGAGGCAGGGC   12008        ___
                              GTCAGATA  GCAGGGC
                              ||||||||  |||||||
                              CAGTTTGT  CGTCCCG
                                   CTC
GAM418  PLCB2   3' TCAGCCAAGCAGGGC      12009       GAT
                              TTAGTCA  AGCAGGGC
                              |||||||  ||||||||
                              AGTCGGT  TCGTCCCG
                                   ___
GAM418  RGS5    3' TTAATTAATAACAGGGC    12010      CA
                              TTAGT  GATAGCAGGGC
                              |||||  ||||||||||
                              AATTA  TTATTGTCCCG
                                 A_
GAM418  TUBG1   3' TCAGTCAGGCAGGGC      12011       ATA
                              TTAGTCAG  GCAGGGC
                              ||||||||  |||||||
                              AGTCAGTC  CGTCCCG
                                   ___
GAM418  UPF3B   3' TTAGATCGGAACAAGGC    12012      _ A TA
                              TTAG TC GA  GCAGGGC
                              |||| || ||  |||||||
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```
                                AATC AG CT  TGTTCCG
                                  T  C  __
GAM418  UPF3B    3'  TTAGATCGGAACAAGGC     12012      _  A  TA
                                TTAG TC GA  GCAGGGC
                                |||| || ||  |||||||
                                AATC AG CT  TGTTCCG
                                  T  C  __
GAM418  FLJ12057 3'  TCAGTCAGAAAGTGGGC     12013         T  CA
                                TTAGTCAGA AG  GGGC
                                |||||||||  ||  ||||
                                AGTCAGTCT TC  CCCG
                                     T  A_
GAM418  FLJ13055 3'  TTAGCCAGGCAATGGC      12014         ATA   _
                                TTAGTCAG   GCAG GGC
                                ||||||||   |||| |||
                                AATCGGTC   CGTT CCG
                                   ___   A
GAM418  FLJ21841 3'  CTAGCCAGGCAGGGC       12015         ATA
                                TTAGTCAG   GCAGGGC
                                ||||||||   |||||||
                                GATCGGTC   CGTCCCG
                                   ___
GAM418  HSA250839 3'  TTAGTAGCCAGCAGGGC     12016       C  A
                                TTAGT AG TAGCAGGGC
                                ||||| || |||||||||
                                AATCA TC GTCGTCCCG
                                  _  G
GAM418  KCNJ14   5'  CTAGCAAAAGCAGGGC      12017      T    T
                                TTAG CAGA AGCAGGGC
                                |||| |||| ||||||||
                                GATC GTTT TCGTCCCG
                                  _   _
GAM418  KIAA0237 3'  TTAGCAGATAACATGC       12018      T        GG
                                TTAG CAGATAGCA  GC
                                |||| |||||||||  ||
                                AATC GTCTATTGT  CG
                                  _       A_
GAM418  KIAA0513 5'  TCAAGCAGTAGCAGGGC      12019      T   A
                                TTAG CAG TAGCAGGGC
                                |||| ||| |||||||||
                                AGTT GTC ATCGTCCCG
                                  C  _
GAM418  KIAA1866 3'  TCAGTCAGAGAGCACGGGGC   12020         T   __
                                TTAGTCAGA AGCA  GGGC
                                |||||||||  ||||  ||||
                                AGTCAGTCT TCGT  CCCG
                                     C   GC
GAM418  KLHL8    3'  TTAGTCAATGAACTTTAGGGC  12021         AT  ___
                                TTAGTCAG  AGC   AGGGC
                                ||||||||  |||   |||||
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                                AATCAGTT TTG  TCCCG
                                    AC  AAA
GAM418  MGC11115 3' TTAGTCAACGGGCAGGGC   12022       ATA
                                TTAGTCAG  GCAGGGC
                                ||||||||  |||||||
                                AATCAGTT  CGTCCCG
                                    GCC
GAM418  MGC15875 3' TTAGGCAGAGCAGGGC    12023    T  TA
                                TTAG CAGA  GCAGGGC
                                |||| ||||  |||||||
                                AATC GTCT  CGTCCCG
                                  C  __
GAM418  NPAS3    3' TTAGTCAAACAGGGC      12024       ATA
                                TTAGTCAG  GCAGGGC
                                ||||||||  |||||||
                                AATCAGTT  TGTCCCG

                                   ___
GAM418  PRO2859  3' TTAATCAGATAAATAGC    12025         CAG
                                TTAGTCAGATAG  GGC
                                ||||||||||||  |||
                                AATTAGTCTATT  TCG
                                      TA_
GAM418  RAB4B    3' CTAGCAACAGCAGGGC     12026     CA
                                TTAGT  GATAGCAGGGC
                                |||||  ||||||||||
                                GATCG  TTGTCGTCCCG

                                   __
GAM418  RBMS2    3' TTAGTCCTTAGCAGGGC    12027     AGA
                                TTAGTC  TAGCAGGGC
                                ||||||  |||||||||
                                AATCAG  ATCGTCCCG
                                   GA_
GAM418  SARM     3' TTAGTCAGGCTAGCTAAGGGC 12028       A_  __
                                TTAGTCAG  TAGC  AGGGC
                                ||||||||  ||||  |||||
                                AATCAGTC  ATCG  TCCCG
                                     CG   AT
GAM418  SCYA1    3' CTAGCAAAAGCAGGGC     12017    T  T
                                TTAG CAGA AGCAGGGC
                                |||| |||| ||||||||
                                GATC GTTT TCGTCCCG

                                  _  _
GAM418  TADA3L   3' CTAGCCCAGCAGGGC      12029     AGA
                                TTAGTC  TAGCAGGGC
                                ||||||  |||||||||
                                GATCGG  GTCGTCCCG

                                   ___
GAM418  TCL6     3' TTAGTCAATAGCTGGC     12030       A  AG
                                TTAGTCAG TAGC  GGC
                                |||||||| ||||  |||
```

```
                                AATCAGTT ATCG  CCG
                                   _   A_
GAM418  TCL6     3'  TTAGTCAATAGCTGGC      12030        A   AG
                                TTAGTCAG TAGC  GGC
                                |||||||| ||||  |||
                                AATCAGTT ATCG  CCG
                                   _   A_
GAM418  LOC132617 3'  TCAGCACCAGCAGGGC      12031      T  GA
                                TTAG CA  TAGCAGGGC
                                |||| ||  |||||||||
                                AGTC GT  GTCGTCCCG
                                  _ G_
GAM418  LOC135932 3'  TTAGTCAAATGAACGAGG    12032          _  AG
                                TTAGTCAGAT AGC  GG
                                |||||||||| |||  ||
                                AATCAGTTTA TTG  CC
                                      C   CT
GAM418  LOC143425 3'  TTAGCAGAAAACAGGGC     12033      T   T
                                TTAG CAGA AGCAGGGC
                                |||| |||| ||||||||
                                AATC GTCT TTGTCCCG
                                  _   T
GAM418  LOC144571 3'  TCAGTCAGTTAACCTGGG    12034        A   A_
                                TTAGTCAG TAGC  GGG
                                |||||||| ||||  |||
                                AGTCAGTC ATTG  CCC
                                     A   GA
GAM418  LOC146733 3'  TTAGTCAGCAGGGGGC      12035        A  CA
                                TTAGTCAG TAG  GGGC
                                |||||||| |||  ||||
                                AATCAGTC GTC  CCCG
                                     _   C_
GAM418  LOC202301 5'  CTAGCAGAGCAGGGC       12036      T   TA
                                TTAG CAGA  GCAGGGC
                                |||| ||||  |||||||
                                GATC GTCT  CGTCCCG
                                  _   __
GAM418  LOC256273 3'  TTAGCCAGACTGCGGC      12037          A  AG
                                TTAGTCAGAT GC  GGC
                                |||||||||| ||  |||
                                AATCGGTCTG CG  CCG
                                     A  __
GAM418  LOC91115  3'  TTAGTCAGAGTCCAGGGC    12038         TAG
                                TTAGTCAGA   CAGGGC
                                |||||||||   ||||||
                                AATCAGTCT   GTCCCG
                                     CAG
GAM419  ANXA9    5'  CCGGAATCTCTAGGTCA     12041    A   _  AC
                                CC GGGA CT  CTAGGTCA
                                || |||| ||  ||||||||
```

```
                                GG CCTT GA  GATCCAGT
                                 _   A  __
GAM419  BFSP2    3'  CAGCAGGGACTGGAGCTCA   12042    C      ACCT  G
                                CA CAGGGACT   AG TCA
                                || ||||||||   || |||
                                GT GTCCCTGA   TC AGT
                                 C      CC__  G
GAM419  CD5L     3'  CCAGGGGGGCCAGGTCAA    12043       ACTAC
                                CCAGGG    CTAGGTCAA
                                ||||||    |||||||||
                                GGTCCC    GGTCCAGTT
                                   CCC__
GAM419  CEACAM6  3'  CACCAGGGAGTATGACTACTAG 12044          _______   C
                                CACCAGGGA     CTAC TAG
                                |||||||||     |||| |||
                                GTGGTCCCT     GATG ATC
                                     CATACT   _
GAM419  CHAD     3'  CACCAGGACTGGCTGGGTCA   12045       G   AC  A
                                CACCAGG ACT  CT GGTCA
                                ||||||| |||  || |||||
                                GTGGTCC TGA  GA CCAGT
                                   _  CC  C
GAM419  CHI3L1   3'  CACCAGGGCTGAGCTCA     12046        A  ACCT  G
                                CACCAGGG CT    AG TCA
                                |||||||| ||    || |||
                                GTGGTCCC GA    TC AGT
                                     _  C___  G
GAM419  CUTL1    3'  CACCAGGGCTAGAGGTCA     12047        A   CCT
                                CACCAGGG CTA   AGGTCA
                                |||||||| |||   ||||||
                                GTGGTCCC GAT   TCCAGT
                                   _   C__
GAM419  DIO1     3'  AGGGACACAGGTCAA       12048       T  CT
                                AGGGAC AC  AGGTCAA
                                |||||| ||  |||||||
                                TCCCTG TG  TCCAGTT
                                  _  __
GAM419  EIF1A    3'  ACCAGGAACTATATCA       12049          CCTAG
                                ACCAGGGACTA    GTCA
                                ||||||||||     ||||
                                TGGTCCTTGAT    TAGT
                                     A_____
GAM419  EIF5A    3'  CACCAGGGCTGTAGTGT     12050        A  ACC  _
                                CACCAGGG CT   TAG GT
                                |||||||| ||   ||| ||
                                GTGGTCCC GA   ATC CA
                                   _  C__   A
GAM419  GABRE    3'  CACCAAGGCCTAGTGCCTGGGT 12051        A  ___  A
             CA                   CACCAGGG CTA   CCT GGTCA
                                |||||||| |||   ||| |||||
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                                GTGGTTCC GAT   GGA CCAGT
                                    G   CAC   C
GAM419  GABRE    3'  CACCAAGGCCTAGTGCCTGGGT 12051        A  ___   A
            CA                   CACCAGGG CTA   CCT GGTCA
                                 |||||||| |||   ||| |||||
                                 GTGGTTCC GAT   GGA CCAGT
                                    G   CAC   C
GAM419  HDGF     3'  CACTGAGGGGGCCAGGTCA   12052    C_   ACTAC
                                 CAC  AGGG    CTAGGTCA
                                 |||  ||||    ||||||||
                                 GTG  TCCC    GGTCCAGT
                                   AC   CC___
GAM419  HK1      3'  CACGTGGGGGACCAGGTCAA   12053    CA__    ACCT
                                 CAC   GGGACT   AGGTCAA
                                 |||   ||||||   |||||||
                                 GTG   CCCTGG   TCCAGTT
                                   CACC    _____
GAM419  HK1      3'  CACGTGGGGGACCAGGTCAA   12053    CA__    ACCT
                                 CAC   GGGACT   AGGTCAA
                                 |||   ||||||   |||||||
                                 GTG   CCCTGG   TCCAGTT
                                   CACC    _____
GAM419  HK1      3'  CACGTGGGGGACCAGGTCAA   12053    CA__    ACCT
                                 CAC   GGGACT   AGGTCAA
                                 |||   ||||||   |||||||
                                 GTG   CCCTGG   TCCAGTT
                                   CACC    _____
GAM419  HK1      3'  CACGTGGGGGACCAGGTCAA   12053    CA__    ACCT
                                 CAC   GGGACT   AGGTCAA
                                 |||   ||||||   |||||||
                                 GTG   CCCTGG   TCCAGTT
                                   CACC    _____
GAM419  HK1      3'  CACGTGGGGGACCAGGTCAA   12053    CA__    ACCT
                                 CAC   GGGACT   AGGTCAA
                                 |||   ||||||   |||||||
                                 GTG   CCCTGG   TCCAGTT
                                   CACC    _____
GAM419  IRTA2    5'  CACCAAGGGCTGAGATCAA    12054       A  ACCT
                                 CACCAGGG CT    AGGTCAA
                                 |||||||| ||    |||||||
                                 GTGGTTCC GA    TCTAGTT
                                    C  C___
GAM419  KCNA6    3'  ACCAGTGAGAGCAGGTCAA    12055     G  CTACC
                                 ACCAG GA     TAGGTCAA
                                 ||||| ||     ||||||||
                                 TGGTC CT     GTCCAGTT
                                   A  CTC__
GAM419  LPHH1    3'  CACCAGAGAACCACAGGTCAA  12056        CT  _
                                 CACCAGGGA  ACC TAGGTCAA
                                 |||||||||  ||| ||||||||
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                                GTGGTCTCT  TGG GTCCAGTT
                                    __  T
GAM419  MBD3    3'  CACCAGGGACTGGCC      12057          ACCTA
                                CACCAGGGACT    GGTC
                                ||||||||||    ||||
                                GTGGTCCCTGA    CCGG
                                    _____
GAM419  MFNG    3'  CCAGGGACTGCCTATCACAA  12058        A   GGT
                                CCAGGGACT CCTA  CAA
                                ||||||||| ||||  |||
                                GGTCCCTGA GGAT  GTT
                                    C   AGT
GAM419  MKPX    3'  CACCAAGGGCTATTTCCCAA  12059        A  ___
                                CACCAGGG CTA  CCTAG
                                |||||||| |||  |||||
                                GTGGTTCC GAT  GGGTT
                                    C  AAA
GAM419  MYCL2   3'  CAGTGGATCACCTAGGTCA   12060    _  C
                                CAG GGA TACCTAGGTCA
                                ||| ||| ||||||||||
                                GTC CCT GTGGATCCAGT
                                  A  A
GAM419  NTSR1   3'  CACCAGGGGCCGGCTCA    12061       A  ACCTA  _
                                CACCAGGG CT    GG TCA
                                |||||||| ||    || |||
                                GTGGTCCC GG    CC AGT
                                    C  _____  G
GAM419  PRX     3'  CAACAGGGGCCAGGTCA    12062   C   ACTAC
                                CA CAGGG    CTAGGTCA
                                || |||||    ||||||||
                                GT GTCCC    GGTCCAGT
                                 T    C____
GAM419  RDS     3'  CACCAGGGCTTGGGAAGTCA  12063       A  ACCT
                                CACCAGGG CT   AGGTCA
                                |||||||| ||   ||||||
                                GTGGTCCC GA   TTCAGT
                                    _  ACCC
GAM419  SFRP5   3'  CCCAGGACCCCTGGGTCAA  12064   A    A  A
                                CC GGGACT CCT GGTCAA
                                || |||||| ||| ||||||
                                GG TCCTGG GGA CCAGTT
                                 G     _  C
GAM419  SH2D2A  3'  CACCAAGGACTGAGCCA    12065         ACCTA
                                CACCAGGGACT    GGTCA
                                ||||||||||    |||||
                                GTGGTTCCTGA    TCGGT
                                    C____
GAM419  SMARCC1 3'  ACCAGGGACACCTGGT     12066        T   A
                                ACCAGGGAC ACCT GGT
                                ||||||||| |||| |||
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                                TGGTCCCTG TGGA CCA
                                      _   _
GAM419  T       3'  CACTGGGTACCTAGTAGGTCAA 12067     CA   AC    ___
                                CAC  GGG  TACCT   AGGTCAA
                                |||  |||  |||||   |||||||
                                GTG  CCC  ATGGA   TCCAGTT
                                  A_   __    TCA
GAM419  WW45    5'  CAGGGACTGCCGCATGTTCA   12068        A  _  GG_
                                CAGGGACT CC TA   TCA
                                |||||||| || ||   |||
                                GTCCCTGA GG GT   AGT
                                     C  C  ACA
GAM419  BPES    3'  CACAAGACCGCCTAGGTC    12069     CA    TA
                                CAC  GGGAC  CCTAGGTC
                                |||  |||||  ||||||||
                                GTG  TTCTG  GGATCCAG
                                  __    GC
GAM419  C20orf26  3'  CACCAGGGGCTGGCTTCGCTGT 12070        A  AC  AG___
            CAA                   CACCAGGG CT  CT    GTCAA
                                |||||||| ||  ||    |||||
                                GTGGTCCC GA  GA    CAGTT
                                     C  CC  AGCGA
GAM419  C5orf4   3'  CACCAGGAACTGTATTCAA   12071          ACCTAGG
                                CACCAGGGACT      TCAA
                                ||||||||||       ||||
                                GTGGTCCTTGA      AGTT
                                      CATA___
GAM419  C5orf4   3'  CACCAGGAACTGTATTCAA   12071          ACCTAGG
                                CACCAGGGACT      TCAA
                                ||||||||||       ||||
                                GTGGTCCTTGA      AGTT
                                      CATA___
GAM419  CACNG4   3'  ACCAGGACTACAGGC       12072       G    CT
                                ACCAGG ACTAC  AGGT
                                ||||||  |||||  ||||
                                TGGTCC TGATG  TCCG
                                      _    __
GAM419  CECR7    5'  CACCAGGGCTGCCTGGGTCA   12073        A  A   A
                                CACCAGGG CT CCT GGTCA
                                |||||||| || ||| |||||
                                GTGGTCCC GA GGA CCAGT
                                     _ C   C
GAM419  CYorf14  3'  CACTGGGACTATAGGT      12074     CA      CC
                                CAC  GGGACTA  TAGGT
                                |||  |||||||  |||||
                                GTG  CCCTGAT  ATCCA
                                  A_      __
GAM419  DKFZP564K0822 3'  CACCAGGAGCTGTCTCACTCCA 12075        GA  _____  _
            G                     CACCAGG  CT    AC CTAG
                                |||||||  ||    || ||||
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                                GTGGTCC  GA    TG GGTC
                                    TC  CAGAG  A
GAM419  DKFZp761O132 5' CAGGGACTGGGTAAGTCAA   12076       ACC
                                CAGGGACT   TAGGTCAA
                                ||||||||   ||||||||
                                GTCCCTGA   ATTCAGTT
                                    CCC
GAM419  FLJ11362  3' CACCAGGGAATAGCTTTGTCA  12077        C  C  AG
                                CACCAGGGA TA CT  GTCA
                                ||||||||| || ||  ||||
                                GTGGTCCCT AT GA  CAGT
                                     T  C  AA
GAM419  FLJ11726  3' CACCAGGGCCTGCCA      12078       ACTA   AG
                                CACCAGGG    CCT  GTCA
                                ||||||||    |||  ||||
                                GTGGTCCC    GGA  CGGT
                                     _____  __
GAM419  FLJ11773  5' CCAGACCACCTGGGTC     12079     GG      A
                                CCA  GACTACCT GGTC
                                |||  |||||||| ||||
                                GGT  CTGGTGGA CCAG
                                  __       C
GAM419  FLJ12592  3' CACCAGGGATCAGAGCCAGGTC 12080         C  C__
          AA                      CACCAGGGA TA   CTAGGTCAA
                                ||||||||| ||   |||||||||
                                GTGGTCCCT GT   GGTCCAGTT
                                     A  CTC
GAM419  FLJ20123  3' CCAGGGACAGGGAGGTCAA   12081       TACCT
                                CCAGGGAC    AGGTCAA
                                ||||||||    |||||||
                                GGTCCCTG    TCCAGTT
                                    TCCC_
GAM419  FLJ20580  3' CACCAGGAGACAAGGGTCAA  12082       _   TACCTA
                                CACCAGG GAC     GGTCAA
                                ||||||| |||     ||||||
                                GTGGTCC CTG     CCAGTT
                                    T   TTC___
GAM419  FLJ20972  3' CACCAGGAACTGACTTGG    12083         AC  A
                                CACCAGGGACT  CT GG
                                ||||||||||  || ||
                                GTGGTCCTTGA  GA CC
                                      CT  A
GAM419  FLJ23537  3' CACCGGGGACCACAGCTC    12084     A      CT  G
                                CACC GGGACTAC  AG TC
                                |||| ||||||||  || ||
                                GTGG CCCTGGTG  TC AG
                                  C       __ G
GAM419  GREB1     3' AAGGCTAATTTTAGGTCAA   12085     A   CC__
                                AGGG CTA    TAGGTCAA
                                |||| |||    ||||||||
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                                TTCC GAT   ATCCAGTT
                                  _  TAAA
GAM419  H2AV     3' CACCAGGAACTGTGCTAA   12086        AC_
                                CACCAGGGACT  CTAG
                                ||||||||||  ||||
                                GTGGTCCTTGA  GATT
                                     CAC
GAM419  KIAA0010 3' CACCAGGGACTGTCCCGTC  12087        A_  AG
                                CACCAGGGACT  CCT  GTC
                                ||||||||||  |||  |||
                                GTGGTCCCTGA  GGG  CAG
                                     CA  __
GAM419  KIAA0237 3' CCAGGGACTGTAGGTAGGTCA 12088       ACC__
                                CCAGGGACT    TAGGTCA
                                |||||||||    |||||||
                                GGTCCCTGA    ATCCAGT
                                     CATCC
GAM419  KIAA0352 3' CACCAGGGGCAGTGCCA    12089       ACTACC  _
                                CACCAGGG     TAG GTCA
                                ||||||||     ||| ||||
                                GTGGTCCC     GTC CGGT
                                     C_____  A
GAM419  KIAA0418 3' ACCAGGGATACCTGGGGT   12090       C    A_
                                ACCAGGGA TACCT  GGT
                                |||||||| |||||  |||
                                TGGTCCCT ATGGA  CCA
                                     _    CC
GAM419  KIAA0514 3' CCACTGCCTAGCCTAGGTCA  12091    GGGA  _
                                CCA   CTA CCTAGGTCA
                                |||   ||| |||||||||
                                GGT   GAT GGATCCAGT
                                  GACG  C
GAM419  KIAA0783 3' CACTAGGACTAATAAGTCAA  12092    CA     CC
                                CAC  GGGACTA  TAGGTCAA
                                |||  |||||||  ||||||||
                                GTG  TCCTGAT  ATTCAGTT
                                  A_     T_
GAM419  KIAA1029 3' CACCAGGCACTAGCTAGGTCA 12093      G   C
                                CACCAGG ACTA CTAGGTCA
                                ||||||| |||| ||||||||
                                GTGGTCC TGAT GATCCAGT
                                     G   C
GAM419  KIAA1196 3' CACCAGGGATTATCTGTGG   12094       C  C  A_
                                CACCAGGGA TA CT  GG
                                ||||||||| || ||  ||
                                GTGGTCCCT AT GA  CC
                                     A  A  CA
GAM419  LY117    5' CAGGGACTGGCCTGGAGGTCA 12095       A_  __
                                CAGGGACT  CCT  AGGTCA
                                ||||||||  |||  ||||||
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                                GTCCCTGA GGA TCCAGT
                                    CC  CC
GAM419  LY117    5' CAGGGACTGGCCTGGAGGTCA 12095      A_  __
                                CAGGGACT CCT AGGTCA
                                |||||||| ||| ||||||
                                GTCCCTGA GGA TCCAGT
                                    CC  CC
GAM419  LY117    5' CAGGGACTGGCCTGGAGGTCA 12095      A_  __
                                CAGGGACT CCT AGGTCA
                                |||||||| ||| ||||||
                                GTCCCTGA GGA TCCAGT
                                    CC  CC
GAM419  MGC12981 5' CACCAAGGCCTCTGGGTCA  12096      A AC A
                                CACCAGGG CT CT GGTCA
                                |||||||| ||  || |||||
                                GTGGTTCC GG GA CCAGT
                                    _ A_ C
GAM419  MGC15416 3' CACCACTCGTCTAGGTCAA  12097    AGGG AC_
                                CACC  ACT  CTAGGTCAA
                                ||||  |||  |||||||||
                                GTGG  TGA  GATCCAGTT
                                  ____ GCA
GAM419  MGC15416 3' CACCACTCGTCTAGGTCAA  12097    AGGG AC_
                                CACC  ACT  CTAGGTCAA
                                ||||  |||  |||||||||
                                GTGG  TGA  GATCCAGTT
                                  ____ GCA
GAM419  MGC2747  3' CACCAGGAACTAGCTCA    12098      ACCT G
                                CACCAGGGACT  AG TCA
                                ||||||||||   || |||
                                GTGGTCCTTGA  TC AGT
                                     ____ G
GAM419  MGC3035  5' CACCAGGGGCCACAGCAG   12099      A  C_
                                CACCAGGG CTAC  TAG
                                |||||||| ||||  |||
                                GTGGTCCC GGTG  GTC
                                    C   TC
GAM419  OAZIN    3' ACAAGGGTTACATTAGGTCAA 12100  C  AC  C_
                                AC AGGG  TAC  TAGGTCAA
                                || ||||  |||  ||||||||
                                TG TCCC  ATG  ATCCAGTT
                                 T   A_  TA
GAM419  OSBPL1A  5' CACCAGAGACTGCTCTAA   12101      AC_
                                CACCAGGGACT  CTAG
                                ||||||||||  ||||
                                GTGGTCTCTGA  GATT
                                      CGA
GAM419  P101-PI3K 3' CAGGGACTTCAGAGGTCAA  12102      ACCT
                                CAGGGACT  AGGTCAA
                                ||||||||  |||||||
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                                GTCCCTGA   TCCAGTT
                                     AGTC
GAM419  RGS19    5'  CAGCAGGGACTCAAGTCA    12103    C      ACC
                                CA CAGGGACT   TAGGTCA
                                || ||||||||   |||||||
                                GT GTCCCTGA   GTTCAGT
                                 C      ___
GAM419  SERHL    3'  CAGGGACTCCTTGTCA      12104       A   AG
                                CAGGGACT CCT  GTCA
                                |||||||| |||  ||||
                                GTCCCTGA GGA  CAGT
                                     _   A_
GAM419  LOC139904 5'  CACCAGGGACGGCGCA      12105         TACCTA  _
                                CACCAGGGAC     GGT CA
                                ||||||||||     ||| ||
                                GTGGTCCCTG     CCG GT
                                      _______  C
GAM419  LOC143101 5'  CACCAGGAGGCTACAGCTCA  12106       _ A   CT  G
                                CACCAGG G CTAC  AG TCA
                                ||||||| | ||||  || |||
                                GTGGTCC C GATG  TC AGT
                                     T C    __  G
GAM419  LOC143243 3'  CACCAGGGCTGTAGTGT     12050       A  ACC  _
                                CACCAGGG CT   TAG GT
                                |||||||| ||   ||| ||
                                GTGGTCCC GA   ATC CA
                                     _ C__   A
GAM419  LOC145623 5'  ACACAGGGACTAGTCTTGG   12107   _      C_  A
                                AC CAGGGACTA  CT GG
                                || |||||||||  || ||
                                TG GTCCCTGAT  GA CC
                                 T       CA  A
GAM419  LOC145858 5'  CAGGAACTGAGTCTGGGTCA  12108       AC__  A
                                CAGGGACT    CT GGTCA
                                ||||||||    || |||||
                                GTCCTTGA    GA CCAGT
                                     CTCA  C
GAM419  LOC147040 3'  CCAGGGACCTATACATCA    12109       ACC  G
                                CCAGGGACT   TA GTCA
                                |||||||||   || ||||
                                GGTCCCTGG   AT TAGT
                                     AT_  G
GAM419  LOC149773 5'  CACCAGAGTCCCAGTGCC    12110       ACTA   _
                                CACCAGGG    CCTAG GTC
                                ||||||||    ||||| |||
                                GTGGTCTC    GGGTC CGG
                                     A___     A
GAM419  LOC151178 5'  CACCAGGGACTGGCTGTGCCA 12111         AC  AG
                                CACCAGGGACT  CT  GTCA
                                ||||||||||  ||  ||||
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                                GTGGTCCCTGA  GA  CGGT
                                      CC  CA
GAM419  LOC157273 3'  CCAGAGACTGACAATGGGTCAA 12112         _  CTA_
                                CCAGGGACT AC    GGTCAA
                                ||||||||| ||    ||||||
                                GGTCTCTGA TG    CCAGTT
                                     C  TTAC
GAM419  LOC164832 3'  CACCTGGGACTACAACAG    12113      A       C_
                                CACC GGGACTAC  TAG
                                |||| ||||||||  |||
                                GTGG CCCTGATG  GTC
                                  A       TT
GAM419  LOC165127 5'  CACCAGGGACATGGAGGTCA   12114          TACCT
                                CACCAGGGAC     AGGTCA
                                ||||||||||     ||||||
                                GTGGTCCCTG     TCCAGT
                                      TACC_
GAM419  LOC199786 3'  CACCAAGGGTCTTGGTCAA    12115        ACTAC  A
                                CACCAGGG     CT GGTCAA
                                ||||||||     || ||||||
                                GTGGTTCC     GA CCAGTT
                                     CA___  A
GAM419  LOC202460 5'  CACCAGGGACTGCCTTCA     12116          A   AGG
                                CACCAGGGACT CCT   TCA
                                |||||||||| |||   |||
                                GTGGTCCCTGA GGA   AGT
                                      C  ___
GAM419  LOC253681 3'  CCAGGGACCTATACATCA     12109        ACC  G
                                CCAGGGACT   TA GTCA
                                |||||||||   || ||||
                                GGTCCCTGG   AT TAGT
                                     AT_  G
GAM419  LOC91010  3'  CACCAGGGACCTACAGACCTAG 12117           _____
                                CACCAGGGACT     ACCTAG
                                ||||||||||     ||||||
                                GTGGTCCCTGG     TGGATC
                                      ATGTC
GAM419  LOC92539  5'  ACCAACTAAATCTAGGTCAA   12118     GGG   C__
                                ACCA   ACTA   CTAGGTCAA
                                ||||   ||||   |||||||||
                                TGGT   TGAT   GATCCAGTT
                                  ___    TTA
GAM419  LOC93259  5'  CCCAGGACTGGCCTAGGTCA   12119    A     A_
                                CC GGGACT  CCTAGGTCA
                                || ||||||  |||||||||
                                GG TCCTGA  GGATCCAGT
                                 G     CC
GAM420  BCL10     3'  AAGTAGTATAATTAGTAAGG   12122          C  CT
                                AGGTAGTATAAT AG  AGG
                                |||||||||||| ||  |||
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                                TTCATCATATTA TC  TCC
                                      A  AT
GAM420  CLTCL1   3' AGTGCAATCAGCTGGGTCT   12123    A       A  C
                                AGT TAATCAGCT GG CT
                                ||| ||||||||| || ||
                                TCA GTTAGTCGA CC GA
                                  C       C  A
GAM420  RDX      3' AGGTAGTATTGTTGTCCCCTC  12124        AATCAG  AGG
                                AGGTAGTAT     CT   CCTC
                                |||||||||     ||   ||||
                                TCCATCATA     GG   GGAG
                                     ACAACA  ___
GAM420  C1orf25  3' AGGTAGTATATTTAAACCT   12125         ATCAGC
                                AGGTAGTATA     TAGGCCT
                                ||||||||||     |||||||
                                TCCATCATAT     ATTTGGA
                                     AA____
GAM420  FLJ10948 3' AGGTGGTAGGATCAGCACCT  12126     A   TA     TAG
                                AGGT GTA  ATCAGC   GCCT
                                |||| |||  ||||||   ||||
                                TCCA CAT  TAGTCG   TGGA
                                  C   CC     ___
GAM420  FLJ14775 3' AGGTAGTATGGCAGTTAA    12127         AAT   C
                                AGGTAGTAT   CAG TAG
                                |||||||||   ||| |||
                                TCCATCATA   GTC ATT
                                     CC_   A
GAM420  KLHL8    3' AGTTAGCCCAGCTAGGTCT   12128    G   ATAA       C
                                AG TAGT    TCAGCTAGG CT
                                || ||||    |||||||||| ||
                                TC ATCG    GGTCGATCC GA
                                 A   _____        A
GAM420  MGC20702 3' AGGTAGTATGTTCAGAGTCT  12129         AA   CT  GC
                                AGGTAGTAT  TCAG  AG  CT
                                |||||||||  ||||  ||  ||
                                TCCATCATA  AGTC  TC  GA
                                     CA   __  A_
GAM420  PRO0365  3' AGGTAGCATGAATTCAGGCCTC 12130         AATCAGC
                                AGGTAGTAT      TAGGCCTC
                                |||||||||      ||||||||
                                TCCATCGTA      GTCCGGAG
                                     CTTAA__
GAM420  ZNF84    5' GGAGTGAGGTCTCAGCTAGGTC 12131    T   ATAA__       C
          T                      GG AGT     TCAGCTAGG CT
                                 || |||     |||||||||| ||
                                 CC TCA     AGTCGATCC GA
                                  _  CTCCAG        A
GAM420  LOC131368 3' AGTAGTATGGTCAGTTAA    12132         AA   C
                                GGTAGTAT  TCAG TAG
                                ||||||||  |||| |||
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                                TCATCATA  AGTC ATT
                                    CC    A
GAM420  LOC169693 3'  GGTAGTATGGTCAGCTGG    12133        AA     A
                                GGTAGTAT  TCAGCT GG
                                ||||||||  ||||||  ||
                                CCATCATA  AGTCGA CC
                                    CC     _
GAM420  LOC51142  5'  AGGTACGCGACGGCTAGGCCTC 12134      _  ATAATCA
                                AGGTA GT      GCTAGGCCTC
                                |||||  ||      ||||||||||
                                TCCAT CG      CGATCCGGAG
                                   G  CTGC___
GAM421  AOC3     3'  TGTGTCAGGCATCACAGG    12137     A   CC
                                TGTG TAG  CATCACAGG
                                ||||  |||  |||||||||
                                ACAC GTC  GTAGTGTCC
                                  A   C_
GAM421  ATP6V1G2  3'  GTAATAGTATCACAGG      12138       CCC
                                GTGATAG   ATCACAGG
                                |||||||   ||||||||
                                CATTATC   TAGTGTCC
                                    A__
GAM421  ATP6V1G2  3'  GTAATAGTATCACAGG      12138       CCC
                                GTGATAG   ATCACAGG
                                |||||||   ||||||||
                                CATTATC   TAGTGTCC
                                    A__
GAM421  DLG5     5'  GTGAGGTCCTCATCACAGG    12139     TAG  _
                                GTGA   CC CATCACAGG
                                ||||   ||  |||||||||
                                CACT   GG GTAGTGTCC
                                  CCA  A
GAM421  DRD3     3'  GTGGTATAGATCACAGG     12140     __    CCC
                                GTG  ATAG   ATCACAGG
                                |||  ||||   ||||||||
                                CAC  TATC   TAGTGTCC
                                  CA   ____
GAM421  DRD3     3'  GTGGTATAGATCACAGG     12140     __    CCC
                                GTG  ATAG   ATCACAGG
                                |||  ||||   ||||||||
                                CAC  TATC   TAGTGTCC
                                  CA   ____
GAM421  GIF      3'  TATGGTAGCATCACAGG     12141      A    CC
                                TGTG TAGC  ATCACAGG
                                ||||  ||||  ||||||||
                                ATAC ATCG  TAGTGTCC
                                  C    __
GAM421  IPP      3'  TGTATAGCCCATTACAA     12142      A       C
                                TGTG TAGCCCAT ACAG
                                ||||  ||||||||  ||||
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                                ACAT ATCGGGTA TGTT
                                  _      A
GAM421  KCND3    3'  TGAGATGCAGTATCACAGG   12143    T   A  CC_
                                TG GAT GC   ATCACAGG
                                || ||| ||   ||||||||
                                AC CTA CG   TAGTGTCC
                                 T   _  TCA
GAM421  KCNJ12   3'  TGTGATAGCCTCTGAGG     12144         CA  AC
                                TGTGATAGCC  TC  AGG
                                ||||||||||  ||  |||
                                ACACTATCGG  AG  TCC
                                      __  AC
GAM421  MEN1     5'  TGTGATAACCACCCTCACAGG  12145         CA__
                                TGTGATAGCC    TCACAGG
                                ||||||||||    |||||||
                                ACACTATTGG    AGTGTCC
                                      TGGG
GAM421  NOV      3'  TGTAATAAAACCACAGG      12146        CCC
                                TGTGATAG   ATCACAGG
                                ||||||||   ||||||||
                                ACATTATT   TGGTGTCC
                                     T__
GAM421  RFC1     3'  TGTGGAAGCCATCACAGG     12147      AT    C
                                TGTG  AGCC ATCACAGG
                                ||||  |||| ||||||||
                                ACAC  TCGG TAGTGTCC
                                  CT    _
GAM421  RGS5     3'  TATGATAATAGCATCATAGG   12148        CC_    C
                                TGTGATAG   CATCA AGG
                                ||||||||   ||||| |||
                                ATACTATT   GTAGT TCC
                                     ATC     A
GAM421  SHANK2   3'  TGGATGCAAACCACAGG      12149    T   A  CC
                                TG GAT GC  ATCACAGG
                                || ||| ||  ||||||||
                                AC CTA CG  TGGTGTCC
                                 _   _  TT
GAM421  SORCS3   3'  TGTGACAGACAACAGG       12150        CC  TC
                                TGTGATAG  CA  ACAGG
                                ||||||||  ||  |||||
                                ACACTGTC  GT  TGTCC
                                     T_  __
GAM421  TEGT     3'  TGTGGCAGCCCACAGG       12151      A     ATC
                                TGTG TAGCCC   ACAGG
                                |||| ||||||   |||||
                                ACAC GTCGGG   TGTCC
                                  C     ____
GAM421  C20orf130 5'  TGTGACAGCTCCTGGCGCAGG  12152          _  ATCA_
                                TGTGATAGC CC    CAGG
                                |||||||| ||    ||||
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                                ACACTGTCG GG    GTCC
                                    A  ACCGC
GAM421  DKFZp434B0417 3'  TGTCACTACATATCACAGG   12153    G  A  CC
                                TGT AT GC  ATCACAGG
                                ||| || ||  ||||||||
                                ACA TG TG  TAGTGTCC
                                  G  A  TA
GAM421  DKFZp566H0824 5'  TGTGAAGTACCACAGG     12154      T  CCC
                                TGTGA AG   ATCACAGG
                                ||||| ||   ||||||||
                                ACACT TC   TGGTGTCC
                                   _  A__
GAM421  FLJ12875  3'  TGTGACAGCCTTGCAAGG    12155         CAT  C
                                TGTGATAGCC   CA AGG
                                ||||||||||   || |||
                                ACACTGTCGG   GT TCC
                                     AAC  _
GAM421  FLJ13204  3'  GTGGCCCAATCACAGG     12156     ATA    _
                                GTG   GCCCA TCACAGG
                                |||   ||||| |||||||
                                CAC   CGGGT AGTGTCC
                                  ___    T
GAM421  FLJ22002  3'  TATGATAGCTCAAAGG     12157        CCA   C
                                TGTGATAGC   TCA AGG
                                |||||||||   ||| |||
                                ATACTATCG   AGT TCC
                                     ___   T
GAM421  FLJ23119  3'  TGTGACAGTCATTCCACAGG   12158       CC   __
                                TGTGATAG  CAT  CACAGG
                                ||||||||  |||  ||||||
                                ACACTGTC  GTA  GTGTCC
                                    A_   AG
GAM421  FLJ30567  3'  TGTGGATAAATCACAGG     12159     _   CCC
                                TGTG ATAG   ATCACAGG
                                |||| ||||   ||||||||
                                ACAC TATT   TAGTGTCC
                                  C   ___
GAM421  KIAA0447  3'  TGTGACAGTTCAACAAG     12160       CC  TC
                                TGTGATAG  CA  ACAGG
                                ||||||||  ||  |||||
                                ACACTGTC  GT  TGTTC
                                    AA  __
GAM421  KIAA1233  3'  TGTGACAGCCTATCCAG     12161         C   A
                                TGTGATAGCC ATC CAG
                                |||||||||| ||| |||
                                ACACTGTCGG TAG GTC
                                     A  _
GAM421  KIAA1908  3'  ATGAACCCATCATAGG      12162      TA      C
                                GTGA  GCCCATCA AGG
                                ||||  |||||||| |||
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                                TACT  TGGGTAGT TCC
                                  __      A
GAM421  LIPG     3'  GTCCCAGCCATCACAGG     12163    GA    C
                                GT  TAGCC ATCACAGG
                                ||  ||||| ||||||||
                                CA  GTCGG TAGTGTCC
                                 GG    _
GAM421  PACSIN2  3'  TATGATAGGCCAACAGG     12164        C   TC
                                TGTGATAG CCA  ACAGG
                                |||||||| |||  |||||
                                ATACTATC GGT  TGTCC
                                     C  __
GAM421  POPX1    3'  CGAGACACATCACAGG      12165    T   GCC
                                TG GATA   CATCACAGG
                                || ||||   |||||||||
                                GC CTGT   GTAGTGTCC
                                 T   ____
GAM421  SLC5A6   3'  TGTGACAGCTTCTCCTGCAGG  12166        CCA  A__
                                TGTGATAGC   TC   CAGG
                                |||||||||   ||   ||||
                                ACACTGTCG   AG   GTCC
                                     AAG  GAC
GAM421  TRIM11   3'  TGTAATAGCTCCCCAGG     12167         _  AT A
                                TGTGATAGC CC  C CAGG
                                ||||||||| ||  | ||||
                                ACATTATCG GG  G GTCC
                                     A  __ _
GAM421  LOC112970 3'  TGTGATAGCCCAAGTAGG    12168          TCAC
                                TGTGATAGCCCA    AGG
                                ||||||||||||    |||
                                ACACTATCGGGT    TCC
                                       TCA_
GAM421  LOC145813 5'  TGTGACAGCTCACAG       12169         CCA
                                TGTGATAGC   TCACAG
                                |||||||||   ||||||
                                ACACTGTCG   AGTGTC
                                            ____
GAM421  LOC149386 5'  TGGATAGCCCCTCCAGG     12170    T      A  A
                                TG GATAGCCC TC CAGG
                                || |||||||| || ||||
                                AC CTATCGGG AG GTCC
                                  _       G  _
GAM421  LOC150407 3'  TGTGACAGAGACCACAGG    12171        CCC
                                TGTGATAG   ATCACAGG
                                ||||||||   ||||||||
                                ACACTGTC   TGGTGTCC
                                     TC_
GAM421  LOC157349 5'  TGTGGAGACCCATCACAGG   12172      ATA
                                TGTG   GCCCATCACAGG
                                ||||   ||||||||||||
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                                ACAC   TGGGTAGTGTCC
                                  CTC
GAM421   LOC158156 3'  TGTTGTAGCCCACCCTAGG   12173    GA       AC
                                TGT  TAGCCCATC  AGG
                                |||  |||||||||  |||
                                ACA  ATCGGGTGG  TCC
                                  AC        GA
GAM421   LOC158267 3'  TGTGGTGCCTATCACAAG    12174     ATA   C
                                TGTG   GCC ATCACAGG
                                ||||   ||| ||||||||
                                ACAC   CGG TAGTGTTC
                                  CA_   A
GAM421   LOC158848 3'  TGTGATAATCCTCCAGG     12175       GC  A  A
                                TGTGATA  CC TC CAGG
                                |||||||  || || ||||
                                ACACTAT  GG AG GTCC
                                    TA  _  _
GAM421   LOC158852 3'  TGTGATAATCCTCCAGG     12175       GC  A  A
                                TGTGATA  CC TC CAGG
                                |||||||  || || ||||
                                ACACTAT  GG AG GTCC
                                    TA  _  _
GAM421   LOC199733 3'  ATGACCCCATCACGGG      12176      AG       A
                                GTGAT  CCCATCAC GG
                                |||||  |||||||| ||
                                TACTG  GGGTAGTG CC
                                  __       C
GAM421   LOC203339 5'  TGGGACCCCCATCACAGG    12177    T   AG
                                TG GAT  CCCATCACAGG
                                || |||  ||||||||||
                                AC CTG  GGGTAGTGTCC
                                 C  G_
GAM421   LOC253786 5'  TGTGATAGATCACAGG      12178        CCC
                                TGTGATAG   ATCACAGG
                                ||||||||   ||||||||
                                ACACTATC   TAGTGTCC
                                    ___
GAM421   LOC255772 3'  TATGTTACCTCATCACAGG    12179     ATA   _
                                TGTG   GCC CATCACAGG
                                ||||   ||| |||||||||
                                ATAC   TGG GTAGTGTCC
                                  AA_   A
GAM421   LOC256940 3'  TGTGATAGCAGTGTCCGCAGG  12180         CCA__  A
                                TGTGATAGC     TC CAGG
                                |||||||||     || ||||
                                ACACTATCG     GG GTCC
                                     TCACA  C
GAM421   LOC257103 5'  TGTGACAGCTTTACAGCAGG   12181         CCAT  _
                                TGTGATAGC    CA CAGG
                                |||||||||    || ||||
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                                ACACTGTCG   GT GTCC
                                     AAAT  C
GAM421  LOC257122 3'  TGTGATAATCCTCCAGG     12175       GC  A  A
                                TGTGATA  CC TC CAGG
                                |||||||  || || ||||
                                ACACTAT  GG AG GTCC
                                    TA  _  _
GAM421  LOC92841  5'  TGTGACAGAATCTCACAGG   12182       CCCA
                                TGTGATAG   TCACAGG
                                ||||||||   |||||||
                                ACACTGTC   AGTGTCC
                                     TTAG
GAM422  JUP      3'  TTGGATTTTGGGGGTTTGGG   12185     ___    A
                                TTGG   TTGGG GTTTGGG
                                ||||   ||||| |||||||
                                AACC   AACCC CAAACCC
                                  TAA    C
GAM422  KIAA0685  3'  TATTGGGAGTTGGGGGTTTGGG 12186      CGTT     A
                                TGTTG   GGTTGGG GTTTGGG
                                |||||   ||||||| |||||||
                                ATAAC   TCAACCC CAAACCC
                                  CC__     C
GAM423  INMT     3'  TTGAGCCCGTGGCTTCCA    12189     GA       CGCGA
                                TTG  CCCGTGGCT    CCA
                                |||  |||||||||    |||
                                AAC  GGGCACCGA    GGT
                                  TC       A____
GAM423  PIK3R2   3'  TTGGTCCGTGGCTCCCG     12190     AC       G
                                TTGG  CCGTGGCTC CG
                                ||||  ||||||||| ||
                                AACC  GGCACCGAG GC
                                  A_       G
GAM423  RANBP9   5'  TTGGATGCGTGGCTCGAAC   12191      CC       C
                                TTGGA  CGTGGCTCG GAC
                                |||||  ||||||||| |||
                                AACCT  GCACCGAGC TTG
                                  AC       _
GAM423  SECTM1   3'  TTGGACCCTGGCTCCG      12192       G     G
                                TTGGACCC TGGCTC CG
                                |||||||| |||||| ||
                                AACCTGGG ACCGAG GC
                                     _     _
GAM423  SLC7A5   3'  CTGGACCCGGGGCCGTGGC   12193        T   C__
                                TTGGACCCG GGCT   GC
                                ||||||||| ||||   ||
                                GACCTGGGC CCGG   CG
                                     C   CAC
GAM423  D15Wsu75e 5'  GGACCCGTGGCGACGGCGGCCA 12194          TC__   A
          C                     GGACCCGTGGC   GCG CCAC
                                ||||||||||    ||| ||||
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                                CCTGGGCACCG   CGC GGTG
                                      CTGC  C
GAM423  FLJ21977  3'  TTGGACCCTGGCTCCCAA   12195       G    G
                                TTGGACCC TGGCTC CGA
                                |||||||| |||||| |||
                                AACCTGGG ACCGAG GTT
                                     _    G
GAM423  KIAA1924  3'  TTGGCCCCGTGGCACC     12196     A      TCGCG
                                TTGG CCCGTGGC    ACC
                                |||| ||||||||    |||
                                AACC GGGCACCG    TGG
                                  G      _____
GAM423  MGC2718   3'  TTGCACCCGTGGCTCCTGC   12197    G        __
                                TTG ACCCGTGGCTC  GC
                                ||| ||||||||||  ||
                                AAC TGGGCACCGAG  CG
                                  G         GA
GAM423  LOC146880 3'  TTGGACCCATGGACAGAACC  12198          CT  C
                                TTGGACCCGTGG  CG GACC
                                ||||||||||||  || ||||
                                AACCTGGGTACC  GT TTGG
                                       T_  C
GAM423  LOC152217 3'  TCGGTCCGTGGCTCTCCG    12199     AC       G_
                                TTGG  CCGTGGCTC  CG
                                ||||  |||||||||  ||
                                AGCC  GGCACCGAG  GC
                                  A_       AG
GAM423  LOC152316 3'  TGGGGCATGGCTCGTGGCCAC  12200    ACC       CGA
                                TGG   CGTGGCTCG   CCAC
                                |||   |||||||||   ||||
                                ACC   GTACCGAGC   GGTG
                                  CC_       ACC
GAM423  LOC256115 5'  TTGGGTCCGTGGCTCTGGGGC  12201     AC       ____
                                TTGG  CCGTGGCTC   GC
                                ||||  |||||||||   ||
                                AACC  GGCACCGAG   CG
                                  CA        ACCC
GAM423  LOC91748  3'  TTGGACTCGTGGCTCCG     12202       C      G
                                TTGGAC CGTGGCTC CG
                                |||||| |||||||| ||
                                AACCTG GCACCGAG GC
                                   A      _
GAM424  GSTT1     3'  AGAGGCTCAGGCTGAGCCCA   12205      GC      _
                                AGAGG  CAGGCTGA CCCA
                                |||||  |||||||| ||||
                                TCTCC  GTCCGACT GGGT
                                  GA       C
GAM424  LANCL1    3'  AGAGAGCCACATGACTCA    12206        GGC   C
                                AGAGGGCCA   TGAC CA
                                |||||||||   |||| ||
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                                TCTCTCGGT   ACTG GT
                                     GT_    A
GAM424  SERPINH2  3'  AGAGGGCTGGCTGACCC     12207        CA
                                AGAGGGC  GGCTGACCC
                                |||||||  |||||||||
                                TCTCCCG  CCGACTGGG
                                   A_
GAM424  SLC7A5    3'  GGTGTCAAGTTGACCCAAAATT 12208    GC_    C
                                GG   CAGG TGACCCAAAATT
                                ||   |||| ||||||||||||
                                CC   GTTC ACTGGGTTTTAA
                                 ACA    A
GAM424  TERF2     3'  AGGAGGTTGCCCAAAA      12209     CC   C  A
                                GGG  AGG TG CCCAAAA
                                |||  ||| || |||||||
                                TCC  TCC AC GGGTTTT
                                  __   A  _
GAM424  XT3       3'  GAGGGCCAGATCCTCCA     12210          _  GAC
                                GAGGGCCAGG CT   CCA
                                |||||||||| ||   |||
                                CTCCCGGTCT GG   GGT
                                     A  A__
GAM424  FLJ12934  3'  AGGCAGCTGATCCAAAATT   12211      CA     C
                                GGGC  GGCTGA CCAAAATT
                                ||||  |||||| ||||||||
                                TCCG  TCGACT GGTTTTAA
                                  __      A
GAM424  MRPL4     3'  AGGGGGCCAGGTGACACC    12212    A      C   _
                                AG GGGCCAGG TGAC CC
                                || |||||||| |||| ||
                                TC CCCGGTCC ACTG GG
                                 C       _    T
GAM424  MY014     3'  AGGGAGGCTGATTTACCCAAAA 12213      CC      ____
           TT                     AGGG  AGGCTGA    CCCAAAATT
                                ||||  |||||||   |||||||||
                                TCCC  TCCGACT    GGGTTTTAA
                                  __      AAAT
GAM424  SERPINH1  3'  AGAGGGCTGGCTGACCC     12207        CA
                                AGAGGGC  GGCTGACCC
                                |||||||  |||||||||
                                TCTCCCG  CCGACTGGG
                                   A_
GAM424  SKIP      3'  AGGGGGCCAGGCTGGGCCC   12214    A        A_
                                AG GGGCCAGGCTG  CCC
                                || ||||||||||  |||
                                TC CCCGGTCCGAC  GGG
                                 C         CC
GAM424  SKIP      3'  AGGGGGCCAGGCTGGGCCC   12214    A        A_
                                AG GGGCCAGGCTG  CCC
                                || ||||||||||  |||
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                                TC CCCGGTCCGAC  GGG
                                 C         CC
GAM424  SNPH     3'  AGAGGGGCCGGGTTGGCCC   12215      _  A  C  A
                                AGAGGG CC GG TG CCC
                                |||||| || || || |||
                                TCTCCC GG CC AC GGG
                                   C  C  A  C
GAM424  LOC139673 3'  AGGGTGGCCCCCAAAACT    12216     CCA   GA
                                AGGG   GGCT  CCCAAAATT
                                ||||   ||||  |||||||||
                                TCCC   CCGG  GGGTTTTGA
                                  A__    __
GAM424  LOC145739 3'  AAGGGCCAGGTACAAAAT    12217        C  ACC
                                GAGGGCCAGG TG   CAAAAT
                                |||||||||| ||   ||||||
                                TTCCCGGTCC AT   GTTTTA
                                          _  ____
GAM424  LOC152445 3'  AGAGGTTGCAGTGACCCAA   12218      GC_   GC
                                AGAGG   CAG  TGACCCAA
                                |||||   |||  ||||||||
                                TCTCC   GTC  ACTGGGTT
                                   AAC   __
GAM424  LOC152502 3'  GGCCAAGGTCTCCAAAATT   12219       CTGAC
                                GGCCAGG    CCAAAATT
                                |||||||    ||||||||
                                CCGGTTC    GGTTTTAA
                                    CAGA_
GAM424  LOC201252 3'  AGAAGGCCAGGGCCCCA     12220         CTGA
                                AGAGGGCCAGG    CCCA
                                ||||||||||    ||||
                                TCTTCCGGTCC    GGGT
                                      CG__
GAM425  BCL10    5'  CGGGCCGATCCTGTTCCCGCC  12223      A      GAGATG
                                CGGGC GATCCTGT     CGCC
                                ||||| ||||||||     ||||
                                GCCCG CTAGGACA     GCGG
                                   G       AGG___
GAM425  BMP1     3'  CGGGTGTGACAGAGATGCGCC  12224     CA_   CCTGT
                                CGGG   GAT    GAGATGCGCC
                                ||||   |||    ||||||||||
                                GCCC   CTG    CTCTACGCGG
                                  ACA   T_____
GAM425  KRT12    3'  GGGCAGATCTTGTGAAAT    12225        C
                                GGGCAGATC TGTGAGAT
                                ||||||||| ||||||||
                                CCCGTCTAG ACACTTTA
                                     A
GAM425  SNL      3'  CGGGCAGACCCTGTGGCC    12226           AGATGC
                                CGGGCAGATCCTGTG     GCC
                                ||||||||||||||     |||
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                                GCCCGTCTGGGACAC     CGG
                                        _______
GAM425  BCL2L1    3'  GGACAGATTTTGTGGAAAT    12227        CC   _
                                GGGCAGAT  TGTG AGAT
                                ||||||||  |||| ||||
                                CCTGTCTA  ACAC TTTA
                                     AA    C
GAM425  DKFZP434D1335 3'  GGACAGATCCTGTGATATGC   12228             G
                                GGGCAGATCCTGTGA ATGC
                                |||||||||||||| ||||
                                CCTGTCTAGGACACT TACG
                                          A
GAM425  DKFZp547I094 3'  GGGCGATCTGTGATGTGC    12229      A   C    GA
                                GGGC GATC TGTGA  TGC
                                |||| |||| |||||  |||
                                CCCG CTAG ACACT  ACG
                                  _   _     AC
GAM425  KIAA0182  3'  GGGCAGACCTCTCATGGTGTGC 12230          _ _  AGA  C
              C                   GGGCAGATC CT GTG   TG GCC
                                |||||||||| || |||   || |||
                                CCCGTCTGG GA TAC   AC CGG
                                     A  G   C__  A
GAM425  KIAA0478  3'  GGCAATGTGAGATGTGC     12231       ATCC       C
                                GGCAG    TGTGAGATG GC
                                |||||    ||||||||| ||
                                CCGTT    ACACTCTAC CG
                                  _____        A
GAM425  UBN1      3'  CAGGCAGATTCACCCACAGGTG 12232          ___  TG G  A  C
              TGCC                    CGGGCAGAT   CC  T AG TG GCC
                                |||||||||   ||  | || || |||
                                GTCCGTCTA   GG  G TC AC CGG
                                     AGT  GT _  C  A
GAM425  LOC145989 3'  CGGGCAGACCCTGTGGCC    12226              AGATGC
                                CGGGCAGATCCTGTG     GCC
                                ||||||||||||||     |||
                                GCCCGTCTGGGACAC     CGG
                                        _______
GAM425  LOC147958 5'  GGGCAGATCCGGGGTTTGTGCC 12233          TGTGAGA  C
                                GGGCAGATCC      TG GCC
                                ||||||||||      || |||
                                CCCGTCTAGG      AC CGG
                                     CCCCAA_  A
GAM425  LOC221712 3'  AGGCAGATTTTATTAGATG    12234        CC   G
                                GGGCAGAT  TGT AGATG
                                ||||||||  ||| |||||
                                TCCGTCTA  ATA TCTAC
                                     AA   A
GAM425  LOC90750  3'  GGGGGATCCTGTGATGAC    12235     CA        _
                                GGG  GATCCTGTGA GAT
                                |||  |||||||||| |||
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                                CCC  CTAGGACACT CTG
                                  C_         A
GAM426  CNTNAP2   3'  GTCATGGTTATGGAGGCTGC   12238     T     _____
                                GTC ATGGTT     GGCTGC
                                ||| ||||||     ||||||
                                CAG TACCAA     CCGACG
                                  _     TACCT
GAM426  COL17A1   3'  GCTAGGTTGGCTGTGCTG    12239   T   T       C
                                G CTA GGTTGGCTG GCTG
                                | ||| |||||||| ||||
                                C GAT CCAACCGAC CGAC
                                 _  _        A
GAM426  ICA1      3'  GTCTTTGGTTGGCCAGAGC    12240      A        C_
                                GTCT TGGTTGGCTG  GC
                                |||| ||||||||||  ||
                                CAGA ACCAACCGGT  CG
                                   A         CT
GAM426  MBP       3'  GTCCATGGTACTTGCTG     12241         TG   GC
                                GTCTATGGT  GCT  GCTG
                                |||||||||  |||  ||||
                                CAGGTACCA  TGA  CGAC
                                     __   A_
GAM426  NGFR      5'  CTGATGGGGCTGCGCTGC    12242    _   TT
                                CT ATGG  GGCTGCGCTGC
                                || ||||  ||||||||||||
                                GA TACC  CCGACGCGACG
                                 C   __
GAM426  NR2E1     5'  GTCAGTCGCGCGCTGCGCTGC  12243     TAT    ___
                                GTC   GGTTG   GCTGCGCTGC
                                |||   |||||   ||||||||||
                                CAG   TCAGC   CGACGCGACG
                                  ___     GCG
GAM426  DKFZp434N074 5'  GTCCATGACGTGCGTTGC    12244        GTTG _   C
                                GTCTATG    GC TGCG TGC
                                |||||||    || |||| |||
                                CAGGTAC    TG ACGC ACG
                                     ____ C    A
GAM426  DKFZP564D0764 5'  GTCTTGGACTGCGCTG      12245      A   TTG
                                GTCT TGG   GCTGCGCTG
                                |||| |||   |||||||||
                                CAGA ACC   TGACGCGAC
                                  _  ___
GAM426  FGD3      5'  GTCTGGGGTTGGCCGGC     12246      AT       C
                                GTCT  GGTTGGCTG GC
                                ||||  ||||||||| ||
                                CAGA  CCAACCGGC CG
                                  CC       _
GAM426  FLJ20558  3'  GTGTATGGCTGAGTGCTGC   12247    C      ___
                                GT TATGGTTG   GCTGC
                                || ||||||||   |||||
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                                CA ATACCGAC   CGACG
                                 C       TCA
GAM426  KIAA0555  5'  GTCTCTGGTTGGCGATGGTGC  12248      A       _____
                                GTCT TGGTTGGC     TGC
                                |||| ||||||||     |||
                                CAGA ACCAACCG     ACG
                                  G       CTACC
GAM426  PHYHIP    3'  TCTGTGGTTGGCCCTG      12249     A       GCG
                                TCT TGGTTGGCT   CTG
                                ||| |||||||||   |||
                                AGA ACCAACCGG   GAC
                                  C       ___
GAM426  PLCE1     3'  GTCTATGGCTGCTTTTGC    12250          G  GC_
                                GTCTATGGTTG CT   GC
                                |||||||||| ||   ||
                                CAGATACCGAC GA   CG
                                       _  AAA
GAM426  SCYB14    5'  GTCTGTGGCCGTGCGCTGC   12251     A     GC
                                GTCT TGGTTG  TGCGCTGC
                                |||| ||||||  ||||||||
                                CAGA ACCGGC  ACGCGACG
                                  C     __
GAM426  WWP1      5'  TCTATGGTTGGAGATGAGCTGC 12252          C__  C
                                TCTATGGTTGG   TG GCTGC
                                ||||||||||   || |||||
                                AGATACCAACC   AC CGACG
                                       TCT  T
GAM426  LOC120448 5'  TCCTGTGGCTGCGCTGC     12253     A  GT
                                TCT TG  TGGCTGCGCTGC
                                ||| ||  ||||||||||||
                                AGG AC  ACCGACGCGACG
                                  _ __
GAM426  LOC147299 3'  GCCTGTTGCTGCGCTG      12254      ATG   G
                                GTCT   GTTG CTGCGCTG
                                ||||   |||| ||||||||
                                CGGA   CAAC GACGCGAC
                                  ___   _
GAM426  LOC158972 3'  GCCTGCATGGCGCTGCGCTGC  12255      __    TG
                                GTCT  ATGGT  GCTGCGCTGC
                                ||||  |||||  ||||||||||
                                CGGA  TACCG  CGACGCGACG
                                  CG    __
GAM426  LOC163682 5'  GTCTAGGCTGGGTGCTGC    12256      T     CTGC
                                GTCTA GGTTGG    GCTGC
                                ||||| ||||||    |||||
                                CAGAT CCGACC    CGACG
                                   _     CA__
GAM426  LOC219731 5'  GTTTATGGTGGCTGAGGC    12257    C     T    C_
                                GT TATGGT GGCTG  GC
                                || |||||| |||||  ||
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                                CA ATACCA CCGAC  CG
                                 A     _    TC
GAM426  LOC222681 5'  GTCTATAGTTTTGGAGTTGC   12258        __   C__
                                GTCTATGGT  TGG   TGC
                                |||||||||  |||   |||
                                CAGATATCA  ACC   ACG
                                     AA   TCA
GAM426  LOC253714 3'  GTCTATGGATGAAGTATCTGC  12259        T   CTGCG
                                GTCTATGG TGG    CTGC
                                |||||||| |||    ||||
                                CAGATACC ACT    GACG
                                    T   TCATA
GAM426  LOC257507 5'  GTCTATAGTTTTGGAGTTGC   12258        __   C__
                                GTCTATGGT  TGG   TGC
                                |||||||||  |||   |||
                                CAGATATCA  ACC   ACG
                                     AA   TCA
GAM426  LOC257625 5'  GTCTATAGTTTTGGAGTTGC   12258        __   C__
                                GTCTATGGT  TGG   TGC
                                |||||||||  |||   |||
                                CAGATATCA  ACC   ACG
                                     AA   TCA
GAM426  LOC59346  5'  GTCAGTGGACTCCGCGCTGC   12260     TA   TTGG
                                GTC  TGG    CTGCGCTGC
                                |||  |||    |||||||||
                                CAG  ACC    GGCGCGACG
                                  TC   TGA_
GAM426  LOC88523  5'  GTCTGCTGGTTGCACTGC    12261      ATG    C
                                GTCT   GTTGG TGCGCTGC
                                ||||   ||||| ||||||||
                                CAGA   CGACC ACGTGACG
                                   ___     A
GAM426  LOC91409  3'  GTCCTGCTGGTTGCGCTGC    12262      ATG    C
                                GTCT   GTTGG TGCGCTGC
                                ||||   ||||| ||||||||
                                CAGG   CGACC ACGCGACG
                                   A__     A
GAM427  CYP4F3    3'  TCTGTGGAGTTTGCAGGG     12265          GTTT G
                                TCTGTGGAGTTTG    C AGGG
                                ||||||||||||    | ||||
                                AGACACCTCAAAC    G TCCC
                                          _____ _
GAM427  DLG5      5'  TCTGGGAGGTTTTGGGGG     12266      T   __    TTTCGA
                                TCTG GGAG  TTTGG     GGG
                                |||| ||||  |||||     |||
                                AGAC CCTC  AAACC     CCC
                                   _   CA    _______
GAM427  SECTM1    3'  TCTGTGGGTTTGATGAGGG    12267       A      TTC
                                TCTGTGG GTTTGGT   GAGGG
                                |||||||  |||||||   |||||
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                                AGACACC CAAACTA   CTCCC
                                      _     ___
GAM427  DDX34     3'  TGGAGGGTTTCGAGGG      12268       TTT
                                TGGAG   GGTTTCGAGGG
                                |||||   ||||||||||
                                ACCTC   CCAAAGCTCCC
                                   ___
GAM427  DKFZP667O116 3'  TCTGTTGGGTTTGGTTTTCCAG 12269       _ A        _ G
                                TCTGT GG GTTTGGTTT C AG
                                ||||| || ||||||||| | ||
                                AGACA CC CAAACCAAA G TC
                                   A _        A G
GAM427  FLJ20972  3'  TCTGTGGTGTTTGGTTATGGC  12270        A       TCGAG
                                TCTGTGG GTTTGGTT     GGC
                                ||||||| ||||||||     |||
                                AGACACC CAAACCAA     CCG
                                    A       TA___
GAM427  PRDX2     3'  CTGTGGAGTTTGGAGGGG     12271            TTTCGA
                                CTGTGGAGTTTGG      GGG
                                ||||||||||||      |||
                                GACACCTCAAACC      CCC
                                       TC____
GAM427  LOC127540 5'  TGTCGAGTTTGGCCAGGGC    12272     G         TCG
                                TGT GAGTTTGGTT   AGGGC
                                ||| ||||||||||   |||||
                                ACA CTCAAACCGG   TCCCG
                                  G        ___
GAM427  LOC139420 3'  TGTTGAGCCACATTTTGAGGG  12273     G    TG    C
                                TGT GAGTT  GTTT GAGGG
                                ||| |||||  |||| |||||
                                ACA CTCGG  TAAA CTCCC
                                  A    TG    A
GAM427  LOC149566 5'  TCTGTGGAGTTTGTGTCTCG   12274            _
                                TCTGTGGAGTTTG GTTTCG
                                |||||||||||| ||||||
                                AGACACCTCAAAC CAGAGC
                                       A
GAM428  KIAA1303  3'  TGGTCACTCTCTGCTCTTAGC  12277     A     GCCC
                                TGG TCGCTC    GCTCTTAGC
                                ||| ||||||    |||||||||
                                ACC AGTGAG    CGAGAATCG
                                  _     AGA_
GAM429  MAPK4     3'  TAAGGCGTGTGGTGTGAG     12280         AC   C    AC
                                TAAGGTGT  GTG GTGT  GAG
                                ||||||||  ||| ||||  |||
                                ATTCCGCA  CAC CACA  CTC
                                      __  _   __
GAM429  NPR1      5'  AGTGTGCGTGCGTGTTAGAGA  12281       A         AC
                                GGTGT CGTGCGTGT  GAGA
                                ||||| |||||||||  ||||
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                                TCACA GCACGCACA  CTCT
                                  C       AT
GAM429  SH3GL1   3'  AAGGAGTGCGTGTGTGAG    12282     TGTAC      AC
                                AAGG    GTGCGTGT  GAG
                                ||||    ||||||||  |||
                                TTCC    CACGCACA  CTC
                                  T____       CA
GAM429  UBE2G2   3'  GGTGTGTGCGCGCCTGTGCGAG 12283      A__    G   A
                                GGTGT   CGTGC TGT CGAG
                                |||||   ||||| ||| ||||
                                CCACA   GCGCG ACA GCTC
                                  CAC    G   C
GAM429  HH114    3'  TAAAGTGTGTGTGTGTGT    12284       AC   C
                                TAAGGTGT  GTG GTGT
                                ||||||||  ||| ||||
                                ATTTCACA  CAC CACA
                                     CA   A
GAM429  KIAA0446 3'  TAAAACTGCGTGTGTGTACGAG 12285     GG GTA    C
           A                     TAA  T   CGTG GTGTACGAGA
                                |||  |   |||| ||||||||||
                                ATT  G   GCAC CACATGCTCT
                                  TT AC_   A
GAM429  MGC3040  3'  AGGTGTGCGTATGAG      12286      ACGT     AC
                                AGGTGT   GCGTGT  GAG
                                ||||||   ||||||  |||
                                TCCACA   CGCATA  CTC
                                   ____    __
GAM429  NINJ2    5'  TGAGTGTATGTGTGTGCA    12287    A     C   C
                                A GGTGTA GTG GTGTA
                                | ||||||| ||| |||||
                                A TCACAT CAC CACGT
                                 C     A   A
GAM429  TRABID   3'  TAAGGTGTGTGTGGTCCA    12288       AC   C  G
                                TAAGGTGT  GTG GT TA
                                ||||||||  ||| || ||
                                ATTCCACA  CAC CA GT
                                     CA   _  G
GAM429  LOC126299 5'  AAGGGTTCGCGCGTGCGTGTGC 12289      ___  TA       A
           G                     AAGG   TG  CGTGCGTGT CG
                                ||||   ||  |||||||||  ||
                                TTCC   GC  GCACGCACA GC
                                  CAA  GC       C
GAM429  LOC152765 5'  CAAGGTGTGTGTGTGTGT    12290       AC   C
                                TAAGGTGT  GTG GTGT
                                ||||||||  ||| ||||
                                GTTCCACA  CAC CACA
                                     CA   A
GAM430  DNAH9    5'  GACCTTTTTCTCAACTTC    12293         CC    C
                                GACTTTTTTC  CAAC TC
                                ||||||||||  ||||  ||
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                                CTGGAAAAAG  GTTG AG
                                     A_   A
GAM430  FIGF     5' AAACTTTTTTGCACAACCT   12294        CCC
                                AGACTTTTTT   CAACCT
                                ||||||||||   ||||||
                                TTTGAAAAAA   GTTGGA
                                     CGT
GAM430  FMR2     3' TCAAAGATATTTTCCAACCTC  12295       CT   TCC
                                TTAAAGA  TTTT   CCAACCTC
                                |||||||  ||||   ||||||||
                                AGTTTCT  AAAA   GGTTGGAG
                                   AT   ___
GAM430  UBE2V1   3' TCAGAGGCTCTTTCCAACCT   12296    A  A    TCC
                                TTA AG CTTTTT   CCAACCT
                                ||| || ||||||   |||||||
                                AGT TC GAGAAA   GGTTGGA
                                  C  C    ___
GAM430  UBE2V1   3' TCAGAGGCTCTTTCCAACCT   12296    A  A    TCC
                                TTA AG CTTTTT   CCAACCT
                                ||| || ||||||   |||||||
                                AGT TC GAGAAA   GGTTGGA
                                  C  C    ___
GAM430  UBE2V1   3' TCAGAGGCTCTTTCCAACCT   12296    A  A    TCC
                                TTA AG CTTTTT   CCAACCT
                                ||| || ||||||   |||||||
                                AGT TC GAGAAA   GGTTGGA
                                  C  C    ___
GAM430  DC11     3' TTAAAGCTTCTTCCTAACCT   12297      A     CCC
                                TTAAAG CTTTTTTC   AACCT
                                ||||||| ||||||||   |||||
                                AATTTC GAAGAAGG   TTGGA
                                   _      A__
GAM430  FLJ23132 3' AAGAAATTTTTCCCCAATCT   12298     CT       C
                                AAGA  TTTTTCCCCAA CT
                                ||||  |||||||||||| ||
                                TTCT  AAAAAGGGGTT GA
                                  TT         A
GAM430  KIAA0280 3' CTAAAGACTTTTTTCCCC    12299
                                TTAAAGACTTTTTTCCCC
                                ||||||||||||||||||
                                GATTTCTGAAAAAAGGGG

GAM430  KIAA0323 3' GACTTTTTCTCCAACCTC    12300        CC
                                GACTTTTTT  CCAACCTC
                                |||||||||  ||||||||
                                CTGAAAAAG  GGTTGGAG
                                     A_
GAM430  KIAA1855 3' TTAAAGCCCCCTCCAACT    12301      ACTTT TT  _    C
                                TTAAAG    T  CC CCAAC T
                                ||||||    |  || ||||| |
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                                AATTTC    G  GG GGTTG A
                                   _____ GG  A    A
GAM430  MGC10924  3'  TTAAAGACTTATTTTTGACCAC 12302          __    CC  _
          ACCT                    TTAAAGACTT  TTTT  CCA ACCT
                                  ||||||||||  ||||  ||| ||||
                                  AATTTCTGAA  AAAA  GGT TGGA
                                     TA   CT   G
GAM430  MGC11061  3'  TTAAAGGTCTCTTTCCCCAAC  12303       AC
                                  TTAAAG  TTTTTTCCCCAAC
                                  ||||||  ||||||||||||
                                  AATTTC  GAGAAAGGGGTTG
                                     CA
GAM430  MGC3251   5'  GAGCCTTTTTCCAACCTC    12304    _       CC
                                  GA CTTTTTTCC  AACCTC
                                  || |||||||||  ||||||
                                  CT GGAAAAAGG  TTGGAG
                                   C        __
GAM430  NASP      3'  TCAGAGACTTCTGATCCAGCCT 12305     A       TTCC   A
          C                        TTA AGACTTTT    CCA CCTC
                                  ||| ||||||||    ||| ||||
                                  AGT TCTGAAGA    GGT GGAG
                                    C       CTA_   C
GAM430  SENP8     5'  AGAGGTTTCGTCCCCAACCT   12306     CT   _
                                  AGA  TTTT TCCCCAACCT
                                  |||  |||| ||||||||||
                                  TCT  AAAG AGGGGTTGGA
                                    CC    C
GAM430  LOC124460 5'  TTAGAGACTTTTCTCTCC    12307     A         C
                                  TTA AGACTTTTTTC CC
                                  ||| ||||||||||| ||
                                  AAT TCTGAAAAGAG GG
                                    C         A
GAM430  LOC138649 3'  TTAAAGACTTTTGCACCT    12308           TTCCCCA
                                  TTAAAGACTTTT      ACCT
                                  ||||||||||||      ||||
                                  AATTTCTGAAAA      TGGA
                                         CG_____
GAM430  LOC149944 3'  TTAAAGACGAGTTCCTTAGCCT 12309         TTTT    CCAA
          C                        TTAAAGAC    TTCC    CCTC
                                  ||||||||    ||||    ||||
                                  AATTTCTG    AAGG    GGAG
                                       CTC_    AATC
GAM430  LOC221300 3'  AAACTACCCTTCCCAGCCTC   12310      _      CAA
                                  AGACT TTTTTCCC   CCTC
                                  ||||| ||||||||   ||||
                                  TTTGA GGGAAGGG   GGAG
                                     T       TC_
GAM430  LOC55974  3'  CTAAAGATTGCACCCCAACCTC 12311        CTTTTTT
                                  TTAAAGA      CCCCAACCTC
                                  |||||||      ||||||||||
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                                GATTTCT     GGGGTTGGAG
                                    AACGT__
GAM430  LOC91768  3'  TTAAAAGTTTTCCCCCAACTTC 12312      ACT        C
                                TTAAAG   TTTTTCCCCAAC TC
                                ||||||   |||||||||||| ||
                                AATTTT   AAAAGGGGGTTG AG
                                   C__         A
GAM430  LOC93613  5'  AGACTCTCTTTCCAGCCTC   12313        CC   A
                                AGACTTTTTT  CCA CCTC
                                ||||||||||  ||| ||||
                                TCTGAGAGAA  GGT GGAG
                                     A_  C
GAM431  ADAM11    3'  GTCTTTGCCTGTCCAG     12316        CCT  C
                                GTCTTTGCC   TG TCCAG
                                |||||||||   || |||||
                                CAGAAACGG   AC AGGTC
                                    ___ _
GAM431  CHRNE     3'  GTCCTTGCTTTCTGTCAGT   12317       CCC   CTC
                                GTCTTTGC   TTG   CAGT
                                ||||||||   |||   ||||
                                CAGGAACG   GAC   GTCA
                                    AAA   A__
GAM431  DAAM1     3'  GTTTTTCCAACAACTCCAGT   12318    C   G  CCTT
                                GT TTT CC    GCTCCAGT
                                || ||| ||    ||||||||
                                CA AAA GG    TGAGGTCA
                                 A  _  TTGT
GAM431  MAPK14    3'  GCCTCCTTCCTTCTTGCTCCAG 12319      GC  __
           T                     GTCTTT  CC  CTTGCTCCAGT
                                 ||||||  ||  ||||||||||
                                 CGGAGG  GG  GAACGAGGTCA
                                    AA  AA
GAM431  MAPK14    3'  GCCTCCTTCCTTCTTGCTCCAG 12319      GC  __
           T                     GTCTTT  CC  CTTGCTCCAGT
                                 ||||||  ||  ||||||||||
                                 CGGAGG  GG  GAACGAGGTCA
                                    AA  AA
GAM431  MAPK14    3'  GCCTCCTTCCTTCTTGCTCCAG 12319      GC  __
           T                     GTCTTT  CC  CTTGCTCCAGT
                                 ||||||  ||  ||||||||||
                                 CGGAGG  GG  GAACGAGGTCA
                                    AA  AA
GAM431  NAV2      3'  GTGTTTCCGACTTTGCTCCAGT 12320    C   G  C_  _
                                GT TTT CC  CTT GCTCCAGT
                                || ||| ||  ||| ||||||||
                                CA AAA GG  GAA CGAGGTCA
                                 C  _  CT   A
GAM431  PMP22     3'  GTTTTTGCAAGGGCTCCAGT   12321    C    CCCTT
                                GT TTTGC    GCTCCAGT
                                || |||||    ||||||||
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                                CA AAACG    CGAGGTCA
                                 A    TTCC_
GAM431  PTPRF    5'  GTCTTTGCTTCTTCACCCCGGT 12322       CC  _   A
                                GTCTTTGC  CTT GCTCC GT
                                ||||||||  ||| ||||| ||
                                CAGAAACG  GAA TGGGG CA
                                     AA  G    C
GAM431  PTPRF    5'  GTCTTTGCTTCTTCACCCCGGT 12322       CC  _   A
                                GTCTTTGC  CTT GCTCC GT
                                ||||||||  ||| ||||| ||
                                CAGAAACG  GAA TGGGG CA
                                     AA  G    C
GAM431  PVR      3'  CACGTCCTTGCCAGCTCCAGT  12323         CCTT
                                CACGTCTTTGCC   GCTCCAGT
                                ||||||||||||   ||||||||
                                GTGCAGGAACGG   CGAGGTCA
                                       T___
GAM431  SPTA1    3'  ACTCTTTGCCCCCCA      12324    G       TTGCT
                                AC TCTTTGCCCC    CCA
                                || ||||||||||    |||
                                TG AGAAACGGGG    GGT
                                 _       _____
GAM431  TACSTD2  5'  CACTCCCTCTCTTCTTTGTTCC 12325    GT   GCCC   GC_
           AGT                   CAC  CTTT   CTT   TCCAGT
                                |||  ||||   |||   ||||||
                                GTG  GGAG   GAA   AGGTCA
                                  AG   AGAA   ACA
GAM431  C1orf2   3'  GCCTTTGCCCTGACCA     12326         CT  CT
                                GTCTTTGCCC  TG  CCA
                                ||||||||||  ||  |||
                                CGGAAACGGG  AC  GGT
                                     __  T_
GAM431  C1orf2   3'  GCCTTTGCCCTGACCA     12326         CT  CT
                                GTCTTTGCCC  TG  CCA
                                ||||||||||  ||  |||
                                CGGAAACGGG  AC  GGT
                                     __  T_
GAM431  FLJ11000 3'  GTCTCTGCCTCTGTTTTCAGT  12327        C  TGCTC
                                GTCTTTGCC CT    CAGT
                                |||||||| ||    ||||
                                CAGAGACGG GA    GTCA
                                     A  CAAAA
GAM431  KIAA0057 3'  ACGTCTTTTCTCCTGCTC    12328        GCCC
                                ACGTCTTT   CTTGCTC
                                ||||||||   |||||||
                                TGCAGAAA   GGACGAG
                                     AGA_
GAM431  KIAA1855 3'  CGTCTCTGCCAGCTCCAGT   12329         CCTT
                                CGTCTTTGCC   GCTCCAGT
                                ||||||||||   ||||||||
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                                GCAGAGACGG   CGAGGTCA
                                     T___
GAM431  KIAA1950  3'  CATCTTTGCTTCTCTGAAGT  12330       CC  GCTCC
                                CGTCTTTGC  CTT    AGT
                                |||||||||  |||    |||
                                GTAGAAACG  GAG    TCA
                                     AA  ACT__
GAM431  NFAT5     3'  ATCTCTACAATTTTGCTCTAGT 12331       CCC_    C
                                GTCTTTGC   TTGCTC AGT
                                ||||||||   |||||| |||
                                TAGAGATG   AACGAG TCA
                                     TTAA    A
GAM431  SH120     3'  GTCTTGCCCCAGAGTTCCAGT  12332     T   TTGC_
                                GTCTT GCCCC    TCCAGT
                                ||||| |||||    ||||||
                                CAGAA CGGGG    AGGTCA
                                  _    TCTCA
GAM431  SMUG1     3'  CACAGAAGGACCTTTTGCTCCA 12333     TCTTT  CC
           GT                     CACG    GCC  TTGCTCCAGT
                                ||||    |||  ||||||||||
                                GTGT    TGG  AACGAGGTCA
                                  CTTCC   AA
GAM431  LOC146795 3'  ACGGTCTTTGTTCTTGCTCAGT 12334    _    CCC     C
                                ACG TCTTTG   CTTGCTC AGT
                                ||| ||||||   ||||||| |||
                                TGC AGAAAC   GAACGAG TCA
                                  C     AA_     _
GAM431  LOC165693 3'  GTCTTCGCCCCCAGCCAGT   12335          TGCT
                                GTCTTTGCCCCT   CCAGT
                                ||||||||||||   |||||
                                CAGAAGCGGGGG   GGTCA
                                       TC__
GAM431  LOC203260 3'  GTCTCTGTGCTCCAG      12336       CCCCT
                                GTCTTTG    TGCTCCAG
                                |||||||    ||||||||
                                CAGAGAC    ACGAGGTC
                                     _____
GAM431  LOC253539 3'  CATGCTTTGCCCTTGTCCTCAG 12337    _      C  _ TC
           T                     CGT CTTTGCCC TTG C  CAGT
                                ||| ||||||| ||| |  ||||
                                GTA GAAACGGG AAC G  GTCA
                                  C       _  A GA
GAM431  LOC255177 3'  CACTGTGGGGCCCTTGCTCCAG 12338    GTCTTT   C
           T                     CAC     GCCC TTGCTCCAGT
                                |||     |||| ||||||||||
                                GTG     CGGG AACGAGGTCA
                                  ACACCC   _
GAM431  LOC255299 5'  GTCTTTGCCCCAGAACAGT   12339          TTGCTC
                                GTCTTTGCCCC     CAGT
                                ||||||||||     ||||
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                                CAGAAACGGGG     GTCA
                                      TCTT__
GAM431  LOC255631 5'  ACGTCTTTGCCTCCAAGGCCTA 12340          _ TT_  CC
          GT                    ACGTCTTTGCC CC   GCT  AGT
                                ||||||||||| ||   |||  |||
                                TGCAGAAACGG GG   CGG  TCA
                                      A  TTC   A_
GAM431  LOC90141  3'  TTGCTGTTCTTGCTCCAGT   12341     CC__
                                TTGC    CTTGCTCCAGT
                                ||||    ||||||||||
                                AACG    GAACGAGGTCA
                                  ACAA
GAM432  ABL2     5'  CGGCTGGGCCACCGGCG     12344        G  G
                                CGGTTGGGC CGT GGCG
                                ||||||||| ||| ||||
                                GCCGACCCG GTG CCGC
                                      _  G
GAM432  ATP2A3   3'  CGGTGGGCAAGTGGGCGA    12345     T    C
                                CGGT GGGCG GTGGGCGA
                                |||| ||||| ||||||||
                                GCCA CCCGT CACCCGCT
                                  _    T
GAM432  C1orf6   5'  CGGTCGGGCGGGCCGA      12346         CGT  G
                                CGGTTGGGCG   GG CGA
                                ||||||||||   || |||
                                GCCAGCCCGC   CC GCT
                                      ____  G
GAM432  CACNA1C  3'  GGTTGGGCGGAGCCGGCG    12347        C_  G
                                GGTTGGGCG  GT GGCG
                                |||||||||  || ||||
                                CCAACCCGC  CG CCGC
                                      CT  G
GAM432  DECR1    5'  CGGTTGGGCGCAGGGGGCG   12348          T_
                                CGGTTGGGCGCG  GGGCG
                                ||||||||||||  |||||
                                GCCAACCCGCGT  CCCGC
                                       CC
GAM432  DPYS     5'  GGTTGGGCGGGCCGGGCG    12349        C  _
                                GGTTGGGCG GT GGGCG
                                ||||||||| || |||||
                                CCAACCCGC CG CCCGC
                                      C  G
GAM432  DUSP6    5'  CGGTTGGGGCAGACGA      12350        C  GT
                                CGGTTGGG GC  GGGCGA
                                |||||||| ||  ||||||
                                GCCAACCC CG  TCTGCT
                                      _ __
GAM432  FOS      5'  CGGTTAGGCAAAGCCGGGCGA  12351          ___  G
                                CGGTTGGGC   GC TGGGCGA
                                |||||||||   || |||||||
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                                GCCAATCCG   CG GCCCGCT
                                     TTT  _
GAM432  HAX1     3'  GGTGGGCAATGGGTGA      12352     T    C    C
                                GGT GGGCG GTGGG GA
                                ||| ||||| ||||| ||
                                CCA CCCGT TACCC CT
                                  _    _    A
GAM432  HK1      5'  CGGTCGGGGTCGCGGGGCG   12353          __   T
                                CGGTTGGG  CGCG GGGCG
                                ||||||||  |||| |||||
                                GCCAGCCC  GCGC CCCGC
                                     CA   _
GAM432  IL12RB2  5'  CGGTGGCCGCAGGGCG      12354      T  G   T
                                CGGT GG CGCG GGGCG
                                |||| || |||| |||||
                                GCCA CC GCGT CCCGC
                                  _ G   _
GAM432  KCNS3    5'  CGCGGACGCGTGGGCG      12355    GT
                                CG  TGGGCGCGTGGGCG
                                ||  ||||||||||||||
                                GC  GCCTGCGCACCCGC
                                 __
GAM432  MAN1A1   5'  CGGCTCAGGTGGGCGA      12356      G  CGC
                                CGGTT GG   GTGGGCGA
                                ||||| ||   ||||||||
                                GCCGA TC   CACCCGCT
                                   G  ___
GAM432  MCM5     3'  GGCGAGGCGTGGGCGA      12357     T   C
                                GGT GGG GCGTGGGCGA
                                ||| ||| ||||||||||
                                CCG CTC CGCACCCGCT
                                  _  _
GAM432  NEUROD1  5'  CGTGCCTCCTGCGTGGGCGA  12358    _   GGGC
                                CG GTT    GCGTGGGCGA
                                || |||    ||||||||||
                                GC CGG    CGCACCCGCT
                                 A   AGGA
GAM432  NFKB1    5'  CGGTGGCCGCGGGCG       12359      TG   G
                                CGGT  GGC CGTGGGCG
                                ||||  ||| ||||||||
                                GCCA  CCG GCGCCCGC
                                   __  _
GAM432  NKX2E    3'  CGGGTGGGTGCGTGGGCG    12360     T    C
                                CGG TGGG GCGTGGGCG
                                ||| |||| |||||||||
                                GCC ACCC CGCACCCGC
                                  C    A
GAM432  NRXN3    5'  GGGTGGGCGAAATCAGCGA   12361    T     C_  G
                                GG TGGGCG  GT GGCGA
                                || ||||||  || |||||
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                                CC ACCCGC  TA TCGCT
                                 C     TT  G
GAM432  SLC22A1LS 5'  CAGTTGGAGGCCGGGCG     12362        C  G
                                CGGTTGGG GC TGGGCG
                                |||||||| || ||||||
                                GTCAACCT CG GCCCGC
                                     C  _
GAM432  VAPB      5'  CGGTCGGGGCACGGGCG     12363        C
                                CGGTTGGG GCGTGGGCG
                                |||||||| |||||||||
                                GCCAGCCC CGTGCCCGC
                                    _
GAM432  ZNF278    5'  CGGCTGGAGCGGGCG       12364        CGC
                                CGGTTGGG  GTGGGCG
                                ||||||||  |||||||
                                GCCGACCT  CGCCCGC
                                    ___
GAM432  ZNF278    5'  CGGCTGGAGCGGGCG       12364        CGC
                                CGGTTGGG  GTGGGCG
                                ||||||||  |||||||
                                GCCGACCT  CGCCCGC
                                    ___
GAM432  ZNF278    5'  CGGCTGGAGCGGGCG       12364        CGC
                                CGGTTGGG  GTGGGCG
                                ||||||||  |||||||
                                GCCGACCT  CGCCCGC
                                    ___
GAM432  ZNF278    5'  CGGCTGGAGCGGGCG       12364        CGC
                                CGGTTGGG  GTGGGCG
                                ||||||||  |||||||
                                GCCGACCT  CGCCCGC
                                    ___
GAM432  ABHD3     5'  CGGCTGGCGAGCGGGCGA    12365        G  C
                                CGGTTGG CG GTGGGCGA
                                ||||||| || ||||||||
                                GCCGACC GC CGCCCGCT
                                    _  T
GAM432  CHPT1     5'  CGGTCGGGCCCGCACGGCG   12366         G   _
                                CGGTTGGGC CGTG GGCG
                                ||||||||| |||| ||||
                                GCCAGCCCG GCGT CCGC
                                     G   G
GAM432  CPLX1     3'  CAGCAGCCGCGTGGGCG     12367      T  G
                                CGGT GG CGCGTGGGCG
                                |||| || ||||||||||
                                GTCG TC GCGCACCCGC
                                  _  G
GAM432  CRF       3'  CGGGTGGGCGAGGGGCGA    12368     T     CGT
                                CGG TGGGCG   GGGCGA
                                ||| ||||||   ||||||
```

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                                GCC ACCCGC   CCCGCT
                                  C     TC_
GAM432  DKFZp547I094 3'  CAGACAAACGTGTGGGCGA   12369     T GG   C
                                CGG T  GCG GTGGGCGA
                                ||| |  ||| ||||||||
                                GTC G  TGC CACCCGCT
                                  T TT   A
GAM432  DKFZp547M072 3'  CGGCTGGGGCGGGGCG      12370        C   T
                                CGGTTGGG GCG GGGCG
                                |||||||| ||| |||||
                                GCCGACCC CGC CCCGC

                                    _   _
GAM432  DKFZP566B183 5'  CGGTTGGAGGCCCGGGGCG   12371        __  G  T
                                CGGTTGG  GC CG GGGCG
                                |||||||  || || |||||
                                GCCAACC  CG GC CCCGC
                                    TC  G  _
GAM432  EFS2     5'  CGGTTGGGCTGGACGA      12372         GCG
                                CGGTTGGGC   TGGGCGA
                                |||||||||   |||||||
                                GCCAACCCG   ACCTGCT

                                    ____
GAM432  EPN3     3'  CGGTATGGGACGGGGCG     12373      _   C   T
                                CGGT TGGG GCG GGGCG
                                |||| |||| ||| |||||
                                GCCA ACCC TGC CCCGC
                                  T   _  _
GAM432  ERMAP    3'  GGTTGGGCCAGGCGA       12374         G GT
                                GGTTGGGC C  GGGCGA
                                |||||||| |  ||||||
                                CCAACCCG G  TCCGCT

                                    _ __
GAM432  FLJ12697  3'  CGGTCGGGGTGCGGGGCGA   12375         C_  T
                                CGGTTGGG  GCG GGGCGA
                                ||||||||  ||| ||||||
                                GCCAGCCC  CGC CCCGCT
                                    CA  _
GAM432  FLJ20509  5'  GGTTAGGGGCAAGGGCGA    12376        C   T
                                GGTTGGG GCG GGGCGA
                                ||||||| ||| ||||||
                                CCAATCC CGT CCCGCT
                                    C   T
GAM432  FLJ22004  5'  CGGTGGCGCGTGGGTGA     12377      TG         C
                                CGGT  GGCGCGTGGG GA
                                ||||  |||||||||| ||
                                GCCA  CCGCGCACCC CT
                                  __         A
GAM432  FRAT1     5'  CGGTGGGCCGCGGCG       12378      T   G    G
                                CGGT GGGC CGTGG CG
                                |||| |||| ||||| ||
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                                GCCA CCCG GCGCC GC
                                  _   _   _
GAM432  FREQ     5'  CGGCTGGGCCGGGCG      12379        GCG
                                CGGTTGGGC  TGGGCG
                                |||||||||  ||||||
                                GCCGACCCG  GCCCGC
                                   ___
GAM432  ISL2     3'  CGGGGGTCCGCGTGGGCGA   12380    TT  __
                                CGG  GGG  CGCGTGGGCGA
                                |||  |||  ||||||||||
                                GCC  CCC  GCGCACCCGCT
                                  __  AG
GAM432  KIAA1076 3'  GGCTGGGAGCAAGGTGA    12381       C  T  C
                                GGTTGGG GCG GGG GA
                                ||||||| ||| ||| ||
                                CCGACCC CGT TCC CT
                                    T  _  A
GAM432  KIAA1862 3'  CAGTTGGGACAAAGGGCGA   12382       C  T_
                                CGGTTGGG GCG  GGGCGA
                                |||||||| |||  ||||||
                                GTCAACCC TGT  CCCGCT
                                    _  TT
GAM432  KIAA1870 5'  GGTTGAGCGGCCGCAGGGCGA 12383        __  _
                                GGTTGGGCG  CGT GGGCGA
                                |||||||||  ||| ||||||
                                CCAACTCGC  GCG CCCGCT
                                     CG  T
GAM432  MAN1C1   5'  CGGCTGGGCCCGGGCGA    12384        G GT
                                CGGTTGGGC C  GGGCGA
                                ||||||||| |  ||||||
                                GCCGACCCG G  CCCGCT
                                     G __
GAM432  MGC10992 5'  CGGTCGGGCTCAGGGGCG   12385        G  T
                                CGGTTGGGC CG GGGCG
                                ||||||||| ||  |||||
                                GCCAGCCCG GT CCCGC
                                     A  C
GAM432  MGC3101  3'  CGGCTGGAGCCTCGTGGGCG  12386       _  G_
                                CGGTTGG GC  CGTGGGCG
                                ||||||| ||  ||||||||
                                GCCGACC CG  GCACCCGC
                                    T  GA
GAM432  MMP28    5'  CGAGCGGACGCGTGGGCG   12387    GT
                                CG  TGGGCGCGTGGGCG
                                ||  ||||||||||||||
                                GC  GCCTGCGCACCCGC
                                 TC
GAM432  NECL1    5'  GGCTGGGCGCTGGCGA     12388         GTG
                                GGTTGGGCGC  GGCGA
                                ||||||||||  |||||
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                                CCGACCCGCG  CCGCT
                                     A__
GAM432  NIR3     3'  CGGCTGGGCAGGCAGGCG    12389         C TG
                                CGGTTGGGCG G  GGCG
                                |||||||||| |  ||||
                                GCCGACCCGT C  CCGC
                                     C GT
GAM432  PP3501   3'  CAGCGCGTGGGTGCGTGGG   12390     ___   C
                                CGGT  TGGG GCGTGGG
                                ||||  |||| |||||||
                                GTCG  ACCC CGCACCC
                                  CGC   A
GAM432  PRO0899  5'  CAGTTGGGTGCAGACG      12391        C  GT
                                CGGTTGGG GC  GGGCG
                                |||||||| ||  |||||
                                GTCAACCC CG  TCTGC
                                     A  __
GAM432  RAI1     3'  CGGTTGGGGCTCTGTTGCG    12392        C  G_  G_
                                CGGTTGGG GC  TG  GCG
                                |||||||| ||  ||  |||
                                GCCAACCC CG  AC  CGC
                                     _  AG  AA
GAM432  SCAMP-4  3'  GGTTGGGCCTGCCAGGTGA    12393         __ G   C
                                GGTTGGGC  GC TGGG GA
                                ||||||||  || |||| ||
                                CCAACCCG  CG GTCC CT
                                     GA  _   A
GAM432  SLC21A12 3'  CGGGTGGGCGCGGGCG      12394     T      GT
                                CGG TGGGCGC  GGGCG
                                ||| |||||||  |||||
                                GCC ACCCGCG  CCCGC
                                  C      __
GAM432  VAV3     5'  CGGCTGGGCCGGGGCG       12395         G  T
                                CGGTTGGGC CG GGGCG
                                ||||||||| || |||||
                                GCCGACCCG GC CCCGC
                                     _  _
GAM432  LOC118987 5'  CGGCTGGGTCGGGGCGA     12396         CG  T
                                CGGTTGGG  CG GGGCGA
                                ||||||||  || ||||||
                                GCCGACCC  GC CCCGCT
                                     A_  _
GAM432  LOC125268 3'  CGGTGTGGGTGCACGTGGGCG  12397      _  __
                                CGGT TGG  GCGCGTGGGCG
                                |||| |||  ||||||||||
                                GCCA ACC  CGTGCACCCGC
                                  C   CA
GAM432  LOC139046 5'  CGGCTGGGCACGGGCG       12398          GT
                                CGGTTGGGCGC  GGGCG
                                ||||||||||  |||||
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                                GCCGACCCGTG  CCCGC
                                   __
GAM432  LOC147160 5'  CGGTTGGGTCAGGGTGA    12399       CG  T   C
                                CGGTTGGG  CG GGG GA
                                ||||||||  || ||| ||
                                GCCAACCC  GT CCC CT
                                    A_ _  A
GAM432  LOC149073 5'  GGCTGGAAAGTGGGCGA    12400       CGC
                                GGTTGGG  GTGGGCGA
                                |||||||  ||||||||
                                CCGACCT  CACCCGCT
                                   TT_
GAM432  LOC149422 3'  CGGTTGAGGCTGGGCG     12401       C  G
                                CGGTTGGG GC TGGGCG
                                |||||||| || ||||||
                                GCCAACTC CG ACCCGC
                                   _ _
GAM432  LOC149566 5'  CGGTTAGGACATTGGTGA   12402       C   G  C
                                CGGTTGGG GCGT GG GA
                                |||||||| |||| || ||
                                GCCAATCC TGTA CC CT
                                   _   A  A
GAM432  LOC157280 3'  GGCTGGCCGCTGGGTGA    12403      G   G   C
                                GGTTGG CGC TGGG GA
                                |||||| ||| |||| ||
                                CCGACC GCG ACCC CT
                                   G  _   A
GAM432  LOC159199 5'  CGGAGCACGCGTGGGCGA   12404     TTGG
                                CGG   GCGCGTGGGCGA
                                |||   ||||||||||||
                                GCC   TGCGCACCCGCT
                                  TCG_
GAM432  LOC162828 5'  CGGTTGGGGCAGACGGCG   12405       C  TG_
                                CGGTTGGG GCG  GGCG
                                |||||||| |||  ||||
                                GCCAACCC CGT  CCGC
                                   _  CTG
GAM432  LOC200576 5'  CGGTTGCGGCAGGAAGCGA  12406       _  CGT
                                CGGTTG GGCG  GGGCGA
                                |||||| ||||  ||||||
                                GCCAAC CCGT  TTCGCT
                                   G   CC_
GAM432  LOC201242 5'  CGGTTGGGGGCATAACG    12407       C    G
                                CGGTTGGG GCGTGG CG
                                |||||||| |||||| ||
                                GCCAACCC CGTATT GC
                                    C    _
GAM432  LOC204970 3'  CGGTCTGGGCGCACCTGA   12408     _     __
                                CGGT TGGGCGCG  TGG
                                |||| ||||||||  |||
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                                GCCA ACCCGCGT  ACT
                                  G       GG
GAM432  LOC219731 5'  CGGCTGGGCATGGTGA      12409         GC    GC
                                CGGTTGGGC  GTGG  GA
                                |||||||||  ||||  ||
                                GCCGACCCG  TACC  CT
                                     __    A_
GAM432  LOC219920 5'  CAGTTGGGTCTCAGGGTGA    12410        CG_  T   C
                                CGGTTGGG   CG GGG GA
                                ||||||||   || ||| ||
                                GTCAACCC   GT CCC CT
                                    AGA  _   A
GAM432  LOC221876 5'  CGGCTGGGCGCGCTGCG     12411           GG
                                CGGTTGGGCGCGT  GCG
                                ||||||||||||  |||
                                GCCGACCCGCGCG  CGC
                                      A_
GAM432  LOC255448 3'  GGCTGGCCGCTGGGTGA     12403       G   G    C
                                GGTTGG CGC TGGG GA
                                ||||||| ||| |||| ||
                                CCGACC GCG ACCC CT
                                   G   _    A
GAM432  LOC256812 5'  CGGCACAGCGTGGGCG      12412      TGG  _
                                CGGT   GC GCGTGGGCG
                                ||||   || |||||||||
                                GCCG   TG CGCACCCGC
                                  ____  T
GAM432  LOC257160 3'  GGTTGGACAGTGGGTGA     12413         C     C
                                GGTTGGGCG GTGGG GA
                                ||||||||| ||||| ||
                                CCAACCTGT CACCC CT
                                     _     A
GAM432  LOC51754  5'  CGGTTGGGCAGTGTCCA     12414         C   GG
                                CGGTTGGGCG GTG  CG
                                |||||||||| |||  ||
                                GCCAACCCGT CAC  GT
                                     _   AG
GAM432  LOC90133  5'  GGTTAGCCAATGGGCGA     12415       G  C
                                GGTTGG CG GTGGGCGA
                                |||||| || ||||||||
                                CCAATC GT TACCCGCT
                                   G  _
GAM432  LOC92906  5'  CGGTGGGGCGCGCGCCTCG    12416      T       GG_
                                CGGT GGGCGCGTG   CG
                                |||| |||||||||   ||
                                GCCA CCCGCGCGC   GC
                                  C        GGA
GAM433  CEACAM7   3'  TTAAATAAACTGATTGGTTAAT 12419       TTT  T
            TT                   TTAAAT   TT ATTGGTTAATTT
                                ||||||   || ||||||||||||
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                                AATTTA   GA TAACCAATTAAA
                                   TTT  C
GAM433   LOC254556 3'  TTAAATCTTTTTATCAATTTAA 12420           TG  _
             TTT                  TTAAATTTTTTTAT  GTT AATTT
                                  ||||||||||||||  ||| |||||
                                  AATTTAGAAAAATA  TAA TTAAA
                                        GT   A
GAM434   ARHC     3'  TTGGGCTGTGAGAGGAGTAA   12423     T  GA
                                  TTG GT  TGTGAGAGGAGTAA
                                  ||| ||  ||||||||||||||
                                  AAC CG  ACACTCTCCTCATT
                                    C  __
GAM434   COX10    3'  TGCTGTGTAGCAGAGGAGT    12424         AT  G
                                  TGTTGTGTG  GT AGAGGAGT
                                  |||||||||  || ||||||||
                                  ACGACACAT  CG TCTCCTCA
                                             __  _
GAM434   EHD2     3'  TGTGTGTGATGTGCCTAAGT   12425     T        AGAG
                                  TGT GTGTGATGTG    GAGT
                                  ||| ||||||||||    ||||
                                  ACA CACACTACAC    TTCA
                                    _         GGA_
GAM434   MS4A1    3'  TGTTGTGTGATTGTCGTGA    12426           _____
                                  TGTTGTGTGAT    GTGA
                                  ||||||||||    ||||
                                  ACAACACACTA    CACT
                                         ACAG
GAM434   RAB5B    3'  GTTGTGTGTCGAGGGGTA     12427        ATG   A  A
                                  GTTGTGTG   TGAG GG GTA
                                  ||||||||   |||| || |||
                                  CAACACAC   GCTC CC CAT
                                       A__    _ _
GAM434   KRTAP9-8 3'  TGTTGTGTGAGTATGGTGG    12428          _   AGA
                                  TGTTGTGTGA TGTG   GG
                                  |||||||||| ||||   ||
                                  ACAACACACT ATAC   CC
                                         C    CA_
GAM434   PPIB     3'  TGTGGAATGTGAGGGGAGT    12429      TG      A
                                  TGTG  ATGTGAG GGAGT
                                  ||||  ||||||| |||||
                                  ACAC  TACACTC CCTCA
                                     CT      C
GAM434   LOC126964 3'  TGGTGTGTGATGGGGGT     12430    T       TGAGA  A
                                  TG TGTGTGATG     GG GT
                                  || |||||||||     || ||
                                  AC ACACACTAC     CC CA
                                   C         ______  C
GAM434   LOC151009 3'  TGTTGTGTGATGGACATGG    12431           T  GA_
                                  TGTTGTGTGATG GA   GG
                                  ||||||||||||| ||   ||
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                                ACAACACACTAC CT   CC
                                       _ GTA
GAM434  LOC199858 5'  TGTTGGGCGATGAGAGGGGT  12432      T     T  A  A
                                TGTTG GTGATG GAG GG GT
                                ||||| |||||| ||| || ||
                                ACAAC CGCTAC CTC CC CA
                                   C     T  _ _
GAM434  LOC257200 3'  TGTTGTGTAGTGTGGTGG    12433         A    AGA
                                TGTTGTGTG TGTG   GG
                                ||||||||| ||||   ||
                                ACAACACAT ACAC   CC
                                      C    CA_
GAM435  DMD     5'  AAAAGTTCTTCAAACTT     12436      C   GA
                                GAAAG TCT  TCAAACTT
                                ||||| |||  ||||||||
                                TTTTC AGA  AGTTTGAA
                                   A  __
GAM435  PEA15   3'  AAAAGCTCCTAACTTGAACTT  12437        _   CA_
                                GAAAGCTC TGAT   AACTT
                                |||||||| ||||   |||||
                                TTTTCGAG ATTG   TTGAA
                                     G    AAC
GAM435  PODXL   3'  AAAAGCTCATCCAAAACTT    12438        TGA    _
                                GAAAGCTC   TCAAA CTT
                                ||||||||   ||||| |||
                                TTTTCGAG   GGTTT GAA
                                      TA_    T
GAM435  PTPRA   3'  GAGAGCTCTGAGAACTT     12439    A      TCA
                                GA AGCTCTGA   AACTT
                                || ||||||||   |||||
                                CT TCGAGACT   TTGAA
                                 C       C__
GAM435  PTPRA   3'  GAGAGCTCTGAGAACTT     12439    A      TCA
                                GA AGCTCTGA   AACTT
                                || ||||||||   |||||
                                CT TCGAGACT   TTGAA
                                 C       C__
GAM435  PTPRA   3'  GAGAGCTCTGAGAACTT     12439    A      TCA
                                GA AGCTCTGA   AACTT
                                || ||||||||   |||||
                                CT TCGAGACT   TTGAA
                                 C       C__
GAM435  TEM8    3'  GAAAACAGGATAAACTTCAT   12440       TCT   C
                                GAAAGC   GAT AAACTTCAT
                                ||||||   ||| |||||||||
                                CTTTTG   CTA TTTGAAGTA
                                    TC_  _
GAM435  ARG99   3'  TAGAAGCTCTGCCTTC      12441      A     ATCAAA
                                TAGAA GCTCTG     CTTC
                                ||||| ||||||     ||||
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                                ATCTT CGAGAC     GAAG
                                  _     G_____
GAM435  CREG     3'  TAGGAAGCTCCATCTGAGTTTC 12442     A      G   AAAC_
              AT                   TAG AAGCTCT ATC     TTCAT
                                   ||| ||||||| |||     |||||
                                   ATC TTCGAGG TAG     AAGTA
                                     C      _   ACTCA
GAM435  FLJ23878 3'  TAGAAACAGGATAAACTTCAT  12443       G TCT   C
                                   TAGAAA C   GAT AAACTTCAT
                                   |||||| |   ||| |||||||||
                                   ATCTTT G   CTA TTTGAAGTA
                                      _ TC_  _
GAM435  KIAA1497 5'  TAGCAAGCTCTGAATTCA    12444     A       __
                                   TAG AAGCTCTGA  TCA
                                   ||| |||||||||  |||
                                   ATC TTCGAGACT  AGT
                                     G        TA
GAM435  KIAA1622 3'  GAGAAGCTCTCCAACTTCAT   12445    _     GA    A
                                   GA AAGCTCT  TCAA CTTCAT
                                   || |||||||  |||| ||||||
                                   CT TTCGAGA  GGTT GAAGTA
                                    C      __   _
GAM435  MARCKS   3'  GAAAGTTGCAAACTTCAT    12446      CTC  AT
                                   GAAAG   TG  CAAACTTCAT
                                   |||||   ||  ||||||||||
                                   CTTTC   AC  GTTTGAAGTA
                                     A__  __
GAM435  LOC132617 3'  TAGAAAGCCTGGGCATCCCT   12447        T   AT  AA
                                   TAGAAAGC CTG  CA  CTT
                                   |||||||| |||  ||  |||
                                   ATCTTTCG GAC  GT  GGA
                                        _   CC  AG
GAM435  LOC138693 5'  GAGAGCTCTGATTTCA      12448    A       CAAAC
                                   GA AGCTCTGAT    TTCA
                                   || |||||||||    ||||
                                   CT TCGAGACTA    AAGT
                                    C       ______
GAM435  LOC202459 3'  GACAGCCTTTAAACTTCAT   12449    A   T  GATC
                                   GA AGC CT    AAACTTCAT
                                   || ||| ||    |||||||||
                                   CT TCG GA    TTTGAAGTA
                                    G   _  AA__
GAM435  LOC253587 3'  TAGAAAGCATTGAAATTCA   12450        TC   TCAAAC
                                   TAGAAAGC  TGA     TTCA
                                   ||||||||  |||     ||||
                                   ATCTTTCG  ACT     AAGT
                                        TA   TT_____
GAM435  LOC256021 3'  TAAAAAGCTCTGAACTCA    12451           __
                                   TAGAAAGCTCTGA  TCA
                                   ||||||||||||  |||
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                                ATTTTTCGAGACT  AGT
                                       TG
GAM435  LOC92080  5'  TAGAAAGCTTTTATTACGATCA 12452         C_______
                                TAGAAAGCT      TGATCA
                                |||||||||      ||||||
                                ATCTTTCGA      GCTAGT
                                     AAATAAT
GAM436  BMPR1B    3'  CTTGTACTGTGGATGCTTATTT 12455          A  T  ATC
          GA                      CTTGTGCTGTG AT CT   TTGA
                                ||||||||||| || ||   ||||
                                GAACATGACAC TA GA   AACT
                                      C  C  ATA
GAM436  CGTHBA    3'  CTTGGCCTGGATTTTATCTTGA 12456     T   G  A   C
                                CTTG GCT TG ATT TATCTTGA
                                |||| ||| || ||| ||||||||
                                GAAC CGG AC TAA ATAGAACT
                                  _  _ C   A
GAM436  ZFP93     3'  TTCTGCTGTGTTACATCTTGA  12457    G      AATTC
                                TT TGCTGTG     TATCTTGA
                                || |||||||     ||||||||
                                AA ACGACAC     GTAGAACT
                                 G      AAT__
GAM436  TRIM22    5'  CTTGGCTTCCTTCTGTCTTGA  12458     T   GTGAA    A
                                CTTG GCT     TTCT TCTTGA
                                |||| |||     |||| ||||||
                                GAAC CGA     AAGA AGAACT
                                  _   AGG__    C
GAM436  LOC169693 3'  TTGTGTTTGAACCATCTTGA   12459      CTG    TT
                                TTGTG   TGAA  CTATCTTGA
                                |||||   ||||  |||||||||
                                AACAC   ACTT  GGTAGAACT
                                   AA_   __
GAM436  LOC256987 3'  TGTGCCCCAAATTCTGTTTTG  12460       G       ATC
                                TGTGCT TGAATTCT   TTG
                                |||||| ||||||||   |||
                                ACACGG GTTTAAGA   AAC
                                    G       CAA
GAM437  CASQ1     5'  CATGGAGGTAGTGGGA      12463       ATTA
                                TATGGA    GTAGTGGGA
                                ||||||    |||||||||
                                GTACCT    CATCACCCT
                                   C___
GAM437  KCNK7     5'  TGGGTGGCTGGGACCCGG    12464     AATTA  A _
                                TGG     GT G TGGGACCCGG
                                |||     || | ||||||||||
                                ACC     CA C ACCCTGGGCC
                                  ______  C G
GAM437  KCNK7     5'  TGGGTGGCTGGGACCCGG    12464     AATTA  A _
                                TGG     GT G TGGGACCCGG
                                |||     || | ||||||||||
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                                ACC    CA C ACCCTGGGCC
                                  _____  C G
GAM437  KCNK7    5'  TGGGTGGCTGGGACCCGG   12464    AATTA  A _
                                TGG    GT G TGGGACCCGG
                                |||    || | ||||||||||
                                ACC    CA C ACCCTGGGCC
                                  _____  C G
GAM437  KCNK7    5'  TGGGTGGCTGGGACCCGG   12464    AATTA  A _
                                TGG    GT G TGGGACCCGG
                                |||    || | ||||||||||
                                ACC    CA C ACCCTGGGCC
                                  _____  C G
GAM437  CSMD1    3'  TGGAACTTGAGCAGGACTTGG  12465       AGT  TG   CC
                                TGGAATT   AG  GGAC  GG
                                |||||||   ||  ||||  ||
                                ACCTTGA   TC  CCTG  CC
                                    AC_  GT   AA
GAM437  DNAJC6   3'  TGGGGAGGTGGGACCTGG    12466    AATT  TA      C
                                TGG   AG  GTGGGACC GG
                                |||   ||  |||||||| ||
                                ACC   TC  CACCCTGG CC
                                  CC__ __      A
GAM437  FLJ21195 3'  GGCACAGGTGGGACCCGG    12467    AAT   TA
                                GG   TAG  GTGGGACCCGG
                                ||   |||  ||||||||||
                                CC   GTC  CACCCTGGGCC
                                 GT_  __
GAM437  KIAA0769 3'  ATGTCAGGGTAGTGGGACCTGG 12468     GAATTA         C
                                ATG     GTAGTGGGACC GG
                                |||     |||||||||| ||
                                TAC     CATCACCCTGG CC
                                  AGTCC_         A
GAM438  ABR      3'  GAAGTGGAGATTCCCAAACGG  12471        AACC    TC
                                GAAGTGGA   CTCAG  ACGG
                                ||||||||   |||||  ||||
                                CTTCACCT   GGGTT  TGCC
                                    CTAA    __
GAM438  ABR      3'  GAAGTGGAGATTCCCAAACGG  12471        AACC    TC
                                GAAGTGGA   CTCAG  ACGG
                                ||||||||   |||||  ||||
                                CTTCACCT   GGGTT  TGCC
                                    CTAA    __
GAM438  CDH10    3'  GAAGTGGAGACAGCATGG    12472        AACCCT   T  C
                                GAAGTGGA     CAG CA GG
                                ||||||||     ||| || ||
                                CTTCACCT     GTC GT CC
                                    CT_____   _  A
GAM438  DCTN1    3'  GTGAAGTCCTCAATCAAGGG   12473      AAC       C
                                GTGGA   CCTCAGTCA GGG
                                |||||   ||||||||| |||
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                                CACTT   GGAGTTAGT CCC
                                   CA_        T
GAM438  DCTN1    3'  GTGAAGTCCTCAATCAAGGG   12473       AAC        C
                                GTGGA   CCTCAGTCA GGG
                                |||||   ||||||||| |||
                                CACTT   GGAGTTAGT CCC
                                   CA_        T
GAM438  DLG5     5'  GAGGTGAGGTCCTCATCACAGG 12474    A    AAAC    G
                                GA GTGG    CCTCA TCACGGG
                                || ||||    ||||| |||||||
                                CT CACT    GGAGT AGTGTCC
                                 C    CCA_    _
GAM438  GNL1     5'  GAAGGGAAACCCAAGCGG    12475      T       TC  TCA
                                GAAG GGAAACCC  AG   CGG
                                |||| ||||||||  ||   |||
                                CTTC CCTTTGGG  TC   GCC
                                   _       T_ ___
GAM438  GNL1     5'  GAAGGGAAACCCAAGCGG    12475      T       TC  TCA
                                GAAG GGAAACCC  AG   CGG
                                |||| ||||||||  ||   |||
                                CTTC CCTTTGGG  TC   GCC
                                   _       T_ ___
GAM438  LDLR     3'  GAAGTGGAAGCACTAGG     12476         AACCCTC  T   _
                                GAAGTGGA      AG CAC GGG
                                ||||||||      || ||| |||
                                CTTCACCT      TC GTG TCC
                                      ________ _   A
GAM438  RP1      3'  GAAGTGGAAAATTCTTAGAGG  12477          CC_  C  TCAC
                                GAAGTGGAAA   CT AG    GGG
                                ||||||||||   || ||    |||
                                CTTCACCTTT   GA TC    TCC
                                      TAA  A _____
GAM438  CHST4    5'  GAAGTGGAAGACCTTGCAAGAC 12478         AC   __   TC
           GGG                    GAAGTGGAA  CCT  CAG  ACGGG
                                |||||||||  |||  |||  |||||
                                CTTCACCTT  GGA  GTT  TGCCC
                                      CT   AC   C_
GAM438  DKFZp434G118 3'  GAAATGGAAGCCTTTCCACG   12479         AC   CAG
                                GAAGTGGAA  CCT   TCACG
                                |||||||||  |||   |||||
                                CTTTACCTT  GGA   GGTGC
                                      C_   AA_
GAM438  FLJ21438  5'  GAAGTGGAAGCGCTCGGCCCAG 12480         ACC   A   A
                                GAAGTGGAA   CTC GTC CGG
                                |||||||||   ||| ||| |||
                                CTTCACCTT   GAG CGG GTC
                                      CGC   C   _
GAM438  HPCAL4   3'  GAAGTGAAAATCCTCACCTCCA 12481          C    G__   C
           TGGG                    GAAGTGGAAA CCTCA   TCA GGG
                                |||||||||| |||||   ||| |||
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                                CTTCACTTTT GGAGT   GGT CCC
                                     A    GGA   A
GAM438  KIAA0286 3'  GAGATGGAAACTATATTTCATG 12482    AG     CCTCAG   C
           GG                    GA  TGGAAAC     TCA GGG
                                ||  |||||||     ||| |||
                                CT  ACCTTTG     AGT CCC
                                 CT      ATATAA   A
GAM438  KIAA0447 3'  GAAGTGGGCACCCCCAGCATGG 12483       AA      T  C
           G                     GAAGTGG  ACCCTCAG CA GGG
                                |||||||  |||||||| || |||
                                CTTCACC  TGGGGGTC GT CCC
                                    CG       _ A
GAM438  RNF2     3'  AAGTGGAAACACACTTTGTGGG 12484         C__  CA  CAC
                                AAGTGGAAAC   CT  GT   GGG
                                ||||||||||   ||  ||   |||
                                TTCACCTTTG   GA  CA   CCC
                                     TGT  AA  ___
GAM438  SMCR8    5'  GAAGTGAAGCCCTTACG     12485        AA    CAGTC
                                GAAGTGGA  CCCT    ACG
                                ||||||||  ||||    |||
                                CTTCACTT  GGGA    TGC
                                    C_    A____
GAM438  TUCAN    3'  GAAGTGGAAATTTGCAGAACG  12486         CCCT   TC
                                GAAGTGGAAA    CAG  ACG
                                ||||||||||    |||  |||
                                CTTCACCTTT    GTC  TGC
                                     AAAC   T_
GAM438  UBXD1    3'  ATGGGGGCTCTGCCACGGG    12487     AAACC   A
                                GTGG    CTC GTCACGGG
                                ||||    ||| ||||||||
                                TACC    GAG CGGTGCCC
                                  CCC__   A
GAM438  LOC151057 3'  GAAGTGGAGGTTCTCCAAAGG  12488        AACC   AGT  C
                                GAAGTGGA    CTC   CA GGG
                                ||||||||    |||   || |||
                                CTTCACCT    GAG   GT TCC
                                     CCAA   ___  T
GAM438  LOC158314 3'  GAGCTGGGAACCCACCACGGG  12489    AG   A    TCAG
                                GA  TGG AACCC    TCACGGG
                                ||  ||| |||||    |||||||
                                CT  ACC TTGGG    GGTGCCC
                                 CG   C    T___
GAM438  LOC207089 3'  GAAATGGAGACTCTCTGG    12490        A  C   AGTCAC
                                GAAGTGGA AC CTC     GG
                                |||||||| || |||     ||
                                CTTTACCT TG GAG     CC
                                     C  A   A_____
GAM438  LOC221749 3'  AGTGAAGACCCTCAGAACACAG 12491       A       T_
           G                     AGTGGA ACCCTCAG  CACGGG
                                ||||||  ||||||||  ||||||
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                                TCACTT TGGGAGTC  GTGTCC
                                   C       TT
GAM438  LOC255189 5'  AGCGGGGGTCCTCAGCCTTGG  12492      AAAC      AC
                                AGTGG   CCTCAGTC  GG
                                |||||   ||||||||  ||
                                TCGCC   GGAGTCGG  CC
                                   CCCA       AA
GAM438  LOC257541 5'  GAAGGGAAACCCAAGCGG    12475     T      TC  TCA
                                GAAG GGAAACCC  AG   CGG
                                |||| ||||||||  ||   |||
                                CTTC CCTTTGGG  TC   GCC
                                  _      T_ ___
GAM439  GAC1     5'  TAAGGGTCAGCAACCCTG    12495      AC  A
                                TGAGG  CA CAACCCTG
                                |||||  || ||||||||
                                ATTCC  GT GTTGGGAC
                                   CA  C
GAM439  LZTS1    3'  TGGGGCCAGGCTCTGTGCTTG  12496    A  A   ACAACC
                                TG GG CCA     CTGTGCTTG
                                || || |||     |||||||||
                                AC CC GGT     GACACGAAC
                                 C  _   CCGA__
GAM439  SUOX     5'  TGAGGACCACAGCTCTGTGC   12497        A  ACC
                                TGAGGACCA CA   CTGTGC
                                |||||||| ||   ||||||
                                ACTCCTGGT GT   GACACG
                                     _  CGA
GAM439  FLJ20297 3'  TGAGGACCAGCACCCATCT   12498        ACA   TGTG
                                TGAGGACCA   ACCC   CT
                                |||||||||   ||||   ||
                                ACTCCTGGT   TGGG   GA
                                     CG_   TA__
GAM439  FLJ20297 3'  TGAGGACCAGCACCCATCT   12498        ACA   TGTG
                                TGAGGACCA   ACCC   CT
                                |||||||||   ||||   ||
                                ACTCCTGGT   TGGG   GA
                                     CG_   TA__
GAM439  FLJ22160 3'  ACCTGCATGGCCTTGTGCTTG  12499    AA  A__  C
                                ACC  CA   CC TGTGCTTG
                                |||  ||   || ||||||||
                                TGG  GT   GG ACACGAAC
                                  AC  ACC  A
GAM439  HSN44A4A 3'  TGAGGCTCAGCAGTGCACTTG  12500      AC  A  ACCC  TG
                                TGAGG  CA CA   TG  CTTG
                                |||||  || ||   ||  ||||
                                ACTCC  GT GT   AC  GAAC
                                   GA  C  C___  GT
GAM439  KIAA1867 3'  TGGGGACCCAGATTTGTGCTTG 12501    A    AACAACCC
                                TG GGACC       TGTGCTTG
                                || |||||       ||||||||
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                                AC CCTGG       ACACGAAC
                                 C     GTCTAA__
GAM439  KIAA1940  5'  TGAGGCCAGCAGCTCTAC    12502      A   A  ACC  G
                                TGAGG CCA CA   CT TGC
                                ||||| ||| ||   || |||
                                ACTCC GGT GT   GA ATG
                                   _   C  C__  G
GAM439  PPIL2     3'  TGTAGGGCAGGCCTTGTGCTTG 12503    _   AC  ACAA  C
                                TG AGG  CA    CC TGTGCTTG
                                || |||  ||    || ||||||||
                                AC TCC  GT    GG ACACGAAC
                                 A   C_  CC__  A
GAM439  PRDM10    3'  TGAGGACCAGCATCTGTG    12504         A  ACC
                                TGAGGACCA CA   CTGTG
                                ||||||||| ||   |||||
                                ACTCCTGGT GT   GACAC
                                      C  A__
GAM439  TOPBP1    5'  TGAGGACCAACAATTCTG    12505           CC
                                TGAGGACCAACAA  CTG
                                ||||||||||||  |||
                                ACTCCTGGTTGTT  GAC
                                       AA
GAM439  LOC132617 3'  TGGGGGCCAAGTGGGTGCGCCT 12506    A  A    CAACCC
           G                     TG GG CCAA     TGTGCTTG
                                || || ||||     ||||||||
                                AC CC GGTT     ACGCGGAC
                                 C  C    CACCC_
GAM439  LOC144248 3'  TGAGCATCTACTTTGTGCTTG  12507     GAC  ACA  CC
                                TGAG   CA   AC  TGTGCTTG
                                ||||   ||   ||  ||||||||
                                ACTC   GT   TG  ACACGAAC
                                   ___  AGA  AA
GAM439  LOC150776 3'  TGAGGACCAGCACCCATCT    12498         ACA    TGTG
                                TGAGGACCA   ACCC    CT
                                |||||||||   ||||    ||
                                ACTCCTGGT   TGGG    GA
                                      CG_    TA__
GAM439  LOC152274 3'  TGAGGAGGGCCCTGTGCTTG   12508       CCAACAA
                                TGAGGA      CCCTGTGCTTG
                                ||||||      ||||||||||
                                ACTCCT      GGGACACGAAC
                                   CCC_____
GAM439  LOC199837 5'  TGATGACTGTGCTTTCTGTGCT 12509     G   CAACAACC
           TG                     TGA GAC       CTGTGCTTG
                                ||| |||       |||||||||
                                ACT CTG       GACACGAAC
                                  A   ACACGAAA
GAM439  LOC201305 3'  TGGGGACCAACGGGAGGCTTG  12510    A       AACCCTGT
                                TG GGACCAAC       GCTTG
                                || ||||||||       |||||
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                                AC CCTGGTTG       CGAAC
                                 C       CCCTC___
GAM439  LOC253943 3'  TGAGGAACAACATATGCTT   12511       C    ACCC
                                TGAGGA CAACA    TGTGCTT
                                |||||| |||||    |||||||
                                ACTCCT GTTGT    ATACGAA
                                   T    _____
GAM439  LOC255104 3'  TGGGACTCTAACCTGTGCTTG  12512    A    CAACAAC
                                TG GGAC      CCTGTGCTTG
                                || ||||      ||||||||||
                                AC CCTG      GGACACGAAC
                                 _   AGATT__
GAM440  DPYSL3   3'  CCTAGTCAATGAGGTATATGCT 12515     AT    _ C_
           T                     CCTA  TCGAT AG  ATATGCTT
                                ||||  ||||| ||  ||||||||
                                GGAT  AGTTA TC  TATACGAA
                                  C_    C  CA
GAM440  FZD3     3'  ACCCTTGTTTAAATATGCT    12516      AA  CG TAGC
                                ACCCT  TT  A    ATATGCT
                                |||||  ||  |   |||||||
                                TGGGA  AA  T    TATACGA
                                   AC  AT _____
GAM440  RAI2     5'  CCTAATTCTCAGCTTATATG   12517        GA   __
                                CCTAATTC  TAGC  ATATG
                                ||||||||  ||||  |||||
                                GGATTAAG  GTCG  TATAC
                                     A_   AA
GAM440  CKLFH1   3'  CCCTAATTTTATGGTCACAT   12518        CG  AG_
                                CCCTAATT  AT   CATAT
                                ||||||||  ||   |||||
                                GGGATTAA  TA   GTGTA
                                     AA  CCA
GAM440  LOC220930 3'  CAATTCATAACATATATGCTT  12519       G      __
                                TAATTC ATAGCATA  TGCTT
                                |||||| ||||||||  |||||
                                GTTAAG TATTGTAT  ACGAA
                                   _       AT
GAM441  MGC2718  3'  TCTGGCGGGGACACATCGTCT  12522    GCA   TT_  G
                                TC   GCG   GC ACATCGTCT
                                ||   |||   || ||||||||||
                                AG   CGC   TG TGTAGCAGA
                                 AC_   CCC  _
GAM441  LOC121536 5'  TCGGCTCCGACATCGTCTC    12523     CAGC   G
                                TCG    GTT CGACATCGTCTC
                                |||    ||| ||||||||||||
                                AGC    CGA GCTGTAGCAGAG
                                  _____   G
GAM442  EDAR     3'  TGGGGTGTTTTCTAAATGTT   12526     C         _
                                TGG GTGTTTTCTGAG GTT
                                ||| |||||||||||| |||
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                                ACC CACAAAAGATTT CAA
                                  C         A
GAM442  ETV5    3'  TGGTGGTTTTCTGCCCCTCCC  12527    CGT      AGGTTA
                                TGG  GTTTTCTG    TCCC
                                |||  ||||||||    ||||
                                ACC  CAAAAGAC    AGGG
                                  AC_      GGGG__
GAM442  FUT9    3'  GTGTTTTCTATATATCCC    12528        AGGT
                                GTGTTTTCTG   TATCCC
                                ||||||||||   ||||||
                                CACAAAAGAT   ATAGGG
                                      AT__
GAM442  HPSE    3'  TGGGTGTTTTCTAAAATTTATC 12529    C          _
            C                    TGG GTGTTTTCTGAGGTT ATCC
                                ||| ||||||||||||||| ||||
                                ACC CACAAAAGATTTTAA TAGG
                                  _          A
GAM442  BTN3A1  3'  TGGGTACGGTGAGGTTAT    12530    C   TTTTC
                                TGG GTG    TGAGGTTAT
                                ||| |||    |||||||||
                                ACC CAT    ACTCCAATA
                                  _  GCC__
GAM442  FLJ25416 3'  TGGCATGTTTTTTAGCCT    12531         CTG  G
                                TGGCGTGTTTT  AG TT
                                ||||||||||  || ||
                                ACCGTACAAAA  TC GA
                                      AA_  G
GAM442  HT002   3'  TGGTGGTTTTCTGGCAGTCC  12532    CGT     GA  TA
                                TGG  GTTTTCT  GGT  TCC
                                |||  |||||||  |||  |||
                                ACC  CAAAAGA  CCG  AGG
                                  AC_      __  TC
GAM442  HTCD37  3'  TGGGTGTTTTCTTGATT    12533    C       GA
                                TGG GTGTTTTCT  GGTT
                                ||| |||||||||  ||||
                                ACC CACAAAAGA  CTAA
                                  _       A_
GAM442  KIAA1817 3'  TGGCTGTTTTCTGCAGACATC  12534     G       A  T
                                TGGC TGTTTTCTG GG TATC
                                |||| ||||||||| || ||||
                                ACCG ACAAAAGAC TC GTAG
                                  _       G  T
GAM442  PRO0529  3'  TGGGTGGTGGTGGGGTTGTCC  12535    C   TTTTC  A   A
                                TGG GTG    TG GGTT TCC
                                ||| |||    || |||| |||
                                ACC CAC    AC CCAA AGG
                                  _  CACC_  C   C
GAM442  PRO0971  3'  TGGAGTGTTTTCTATC     12536    C       GAGGTT
                                TGG GTGTTTTCT     ATC
                                ||| |||||||||     |||
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                                ACC CACAAAAGA     TAG
                                 T       _______
GAM442  LOC157278 3'  GCTCTGGTTTTGGGGTTATCC  12537    G_  T   C  A
                                GC  TG TTT TG GGTTATCC
                                ||  || ||| || ||||||||
                                CG  AC AAA AC CCAATAGG
                                 AG  C   _  C
GAM442  LOC196074 3'  TGAGCGCCCTCTGGGGTTATC  12538     C        A
                                TGG GTGTTTTCTG GGTTATC
                                ||| |||||||||| |||||||
                                ACT CGCGGGAGAC CCAATAG
                                  _        C
GAM442  LOC219621 3'  TGGTATGTTTTCACAGTGTTCC 12539     CG      TGA   TA
                                TGG  TGTTTTC   GGT  TCC
                                |||  |||||||   |||  |||
                                ACC  ACAAAAG   TCA  AGG
                                  AT      TG_   CA
GAM442  LOC256987 3'  TGGCATGTTTTTCTATTCC    12540          _  AGGTTA
                                TGGCGTGTTTT CTG     TCC
                                |||||||||||| |||     |||
                                ACCGTACAAAA GAT     AGG
                                       A  A_____
GAM442  LOC92346  3'  TGGCTTGGCGAGGTTAT     12541      G  TTTTC
                                TGGC TG     TGAGGTTAT
                                |||| ||     |||||||||
                                ACCG AC     GCTCCAATA
                                  A  C____
GAM443  LOC147694 5'  CGTTCCGTCACTTCGGT     12544     C  A  GG
                                CG TC TG  TACTTCGGT
                                || || ||  |||||||||
                                GC AG GC  GTGAAGCCA
                                 A  _  A_
GAM443  LOC159199 5'  TCTATGCTCATGGGTAAGTACC 12545   TAC       T________  TTCG
           GAG                      GCTCATGGG       AC    G
                                  |||||||||       ||    |
                                  CGAGTACCC       TG    C
                                TA_       ATTCAIII  GCTT
GAM444  RASD1    3'  GTCCATGTTGACACC       12548          TCAGGT
                                GTCCATGTTGA     CATC
                                ||||||||||      ||||
                                CAGGTACAACT     GTGG
                                        _______
GAM444  KIAA1404  3'  CGCCATGTTGGTCAGGC     12549     T      A
                                CG CCATGTTG TCAGGT
                                || |||||||| ||||||
                                GC GGTACAAC AGTCCG
                                  _       C
GAM444  ZNF347    3'  CGCCATGTTGGTCAGGC     12549     T      A
                                CG CCATGTTG TCAGGT
                                || |||||||| ||||||
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                                GC GGTACAAC AGTCCG
                                 _      C
GAM444  LOC130535 3'  CGCCATGTTGGTCATGC     12550    T      A   G
                                CG CCATGTTG TCA GT
                                || |||||||| ||| ||
                                GC GGTACAAC AGT CG
                                 _      C   A
GAM444  LOC145082 5'  GCCATGTTGGTCAGTC      12551    T      A    G
                                G CCATGTTG TCAG TC
                                | |||||||| |||| ||
                                C GGTACAAC AGTC AG
                                 _      C   _
GAM444  LOC149073 3'  CGCCATGTTGGTCAGGC     12549    T      A
                                CG CCATGTTG TCAGGT
                                || |||||||| ||||||
                                GC GGTACAAC AGTCCG
                                 _      C
GAM445  RAI14    3'  TGCCGACAACTCTGGATCT    12554      TAACCT   _ _
                                TGCC     GATA C CTGGATCT
                                ||||     |||| | ||||||||
                                ACGG     CTGT G GACCTAGA
                                  _______   T A
GAM445  TRIM14   3'  CCTTGGCAACATCTGGATCTA  12555     AACCT    C
                                CCT    GATA CTGGATCTA
                                |||    |||| |||||||||
                                GGA    TTGT GACCTAGAT
                                  ACCG_   A
GAM445  BY55     3'  TGCCAAGTCAATCACTGGATCT 12556     TAACCT   AC
                                TGCC     GAT  CTGGATCT
                                ||||     |||  ||||||||
                                ACGG     TTA  GACCTAGA
                                  TTCAG_   GT
GAM445  C21orf108 3'  CCTGAGTCCAGCTTGGATCTA  12557      TA ____
                                CCTGA  CC    TGGATCTA
                                |||||  ||    ||||||||
                                GGACT  GG    ACCTAGAT
                                   CA  TCGA
GAM445  DJ434O14.3 5'  CCTGGAATAGATGCCTGGATCT 12558     AACCT_   A
                                CCT     GAT CCTGGATCT
                                |||     ||| |||||||||
                                GGA     CTA GGACCTAGA
                                  CCTTAT   C
GAM445  FLJ13158  3'  CCTTGACACTCTGGATCT    12559     _    _
                                CCT GATAC CTGGATCT
                                ||| ||||| ||||||||
                                GGA CTGTG GACCTAGA
                                  A    A
GAM445  FLJ22625  5'  TGCCTAACCTGTGCTCCCCTA  12560          ATA___
                                TGCCTAACCTG     CCTG
                                ||||||||||     ||||
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                                ACGGATTGGAC     GGAT
                                      ACGAGG
GAM445  KIAA1511  3'  GCCTGACCTGATACTACCTG   12561      A     ___
                                GCCT ACCTGA   TACCTG
                                |||| ||||||   ||||||
                                CGGA TGGACT   ATGGAC
                                  C     ATG
GAM445  KIAA1814  3'  TGCCCAGCTTGGTGCTGACATC 12562       AC_______     C
           TG                     TGCCTA       CTGATA CTG
                                |||||||       |||||| |||
                                ACGGGT       GACTGT GAC
                                   CGAACCAC     A
GAM445  MGC15854  5'  TGCTGAGCTGAGGGCCTGGATC 12563     CTAAC    TA_
           T                      TGC    CTGA   CCTGGATCT
                                |||    ||||  |||||||||
                                ACG    GACT   GGACCTAGA
                                  ACTC_   CCC
GAM445  moblak    3'  TGCCGGACCTGGTGGTTTCT   12564     TA    ATACC   A_
                                TGCC  ACCTG    TGG  TCT
                                ||||  |||||    |||  |||
                                ACGG  TGGAC    ACC  AGA
                                  CC    C____   AA
GAM445  SHAPY     3'  TGCCTAACCTGGGTC       12565          ATACCT  A
                                TGCCTAACCTG     GG TC
                                ||||||||||     || ||
                                ACGGATTGGAC     CC AG
                                       _______  _
GAM445  LOC127262 3'  TGCTGGCCTGATACGGTTCC   12566     CTAA      CT  A
                                TGC    CCTGATAC  GG TCT
                                |||    ||||||||  || |||
                                ACG    GGACTATG  CC AGG
                                  ACC_       __  A
GAM445  LOC51631  3'  GCCTAGCTGGATCTGGTGTCTG 12567      AC  _  AC_____
           GATCT                    CCTA  CTG AT      CTGGATCT
                                ||||  ||| ||      ||||||||
                                GGAT  GAC TA      GACCTAGA
                                  C_   C  GACCACA
GAM446  ACR       3'  TATGTTTATTTATTTATT    12570          T
                                TATGTTTATTT TTTATT
                                |||||||||| ||||||
                                ATACAAATAAA AAATAA
                                       T
GAM446  KIAA1798  3'  TTTATGTTTATATATTTTATT  12571          TT_
                                TTTATGTTTAT   TTTTATT
                                ||||||||||   |||||||
                                AAATACAAATA   AAAATAA
                                       TAT
GAM447  ZNF333    3'  ATTAAATCTATCCTAAATATTT 12574           ATTT
           T                      ATTAAATTTATC    AATATTTT
                                ||||||||||||    ||||||||
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                                TAATTTAGATAG   TTATAAAA
                                      GAT_
GAM448  ATP7B    5'  TCGGCGCGGCGCGGCTCGG   12577      GAC  A   TAG
                                TCGGCGC   GG CGCG   CGG
                                |||||||   || ||||   |||
                                AGCCGCG   CC GCGC   GCC
                                   ___ _   CGA
GAM448  CLTCL1   5'  TCGGCGGCGGCGGCGGCAGCGG 12578      _ A   A  C
          C                      TCGGCG CG CGG CG GTAGCGGC
                                |||||| || ||| || ||||||||
                                AGCCGC GC GCC GC CGTCGCCG
                                   C  C   _ _
GAM448  DDEF2    5'  TCGGCGCGAGGGCGCTGGC   12579       C  A   GTA
                                TCGGCGCGA GG CGC   GC
                                ||||||||| || |||   ||
                                AGCCGCGCT CC GCG   CG
                                      C  _   AC_
GAM448  JUP      5'  TCGGCGCGGTCGGGCGGCGGC  12580       A_   AC   TA
                                TCGGCGCG  CGG  GCG  GCGGC
                                ||||||||  |||  |||  |||||
                                AGCCGCGC  GCC  CGC  CGCCG
                                     CA   __   __
GAM448  MECP2    5'  TCGGCGCGGCGGCGGCGG    12581       A   A  CGTA
                                TCGGCGCG CGG CG    GCGG
                                |||||||| ||| ||    ||||
                                AGCCGCGC GCC GC    CGCC
                                     C   _ _____
GAM448  RNTRE    5'  CGGCGCGGCGGCGGCGG     12582       A   A  CGTA
                                CGGCGCG CGG CG    GCGG
                                ||||||| ||| ||    ||||
                                GCCGCGC GCC GC    CGCC
                                     C   _ _____
GAM448  C20orf124 3'  TCGGAGTGACGGACAATGGC   12583     CGC      C  A
                                TCGG   GACGGACG GT GC
                                ||||   |||||||| || ||
                                AGCC   CTGCCTGT TA CG
                                   TCA       _  C
GAM448  DUSP14   5'  TCGGCGCGGCGCGGCGCGG   12584       GAC  A   TA
                                TCGGCGC   GG CGCG  GCGG
                                |||||||   || ||||  ||||
                                AGCCGCG   CC GCGC  CGCC
                                   ___ _   CG
GAM448  GABBR1   5'  TCGGCGCGCGGGCCCG      12585       A   AC  GTAG
                                TCGGCGCG CGG  GC   CG
                                |||||||| |||  ||   ||
                                AGCCGCGC GCC  CG   GC
                                   _  __  G___
GAM448  HGRG8    5'  TCAGCGCGGCGGCGGCGG    12586       A   A  CGTA
                                TCGGCGCG CGG CG    GCGG
                                |||||||| ||| ||    ||||
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                                AGTCGCGC GCC GC    CGCC
                                     C   _ _____
GAM448  ITGB8    5'  TCGGCACGGCGGGTCCCGCGG  12587        A   ACGCGTA
                                TCGGCGCG CGG      GCGG
                                |||||||| |||      ||||
                                AGCCGTGC GCC      CGCC
                                     C   CAGGG__
GAM448  KIAA1813 5'  TCGACGCGGCGGCGGCGG    12588        A   A  CGTA
                                TCGGCGCG CGG CG    GCGG
                                |||||||| ||| ||    ||||
                                AGCTGCGC GCC GC    CGCC
                                     C   _ _____
GAM448  ZDHHC2   5'  CCGGCGCGGCGGACTCCCGGC  12589        A    GCGTAG
                                TCGGCGCG CGGAC     CGGC
                                |||||||| |||||      ||||
                                GGCCGCGC GCCTG     GCCG
                                     C    AGG___
GAM448  LOC134265 5'  CCGGCGCGGCTGGTAGCGGC   12590        ACGGAC __
                                TCGGCGCG     GC  GTAGCGGC
                                ||||||||     ||  ||||||||
                                GGCCGCGC     CG  CATCGCCG
                                     _______  AC
GAM448  LOC93166  5'  TCGGCGGCGACGGCAGCGG    12591       _     ACGCG
                                TCGGCG CGACGG     TAGCGG
                                |||||| ||||||     ||||||
                                AGCCGC GCTGCC     GTCGCC
                                   C     ______
GAM449  ACK1     5'  TCGGGCTGCTGCAGCAGCC    12594    A    A  __
                                TC GGCT GC  CGGCAGCC
                                || |||| ||  ||||||||
                                AG CCGA CG  GTCGTCGG
                                 C    _  AC
GAM449  ACP1     5'  GCTCAGGCTCGCGGCTCC     12595    T       A  C   AG
                                G CTCAGGCT GC GGC  CC
                                | |||||||| || |||  ||
                                C GAGTCCGA CG CCG  GG
                                _       G  _   A_
GAM449  ACP1     5'  GCTCAGGCTCGCGGCTCC     12595    T       A  C   AG
                                G CTCAGGCT GC GGC  CC
                                | |||||||| || |||  ||
                                C GAGTCCGA CG CCG  GG
                                _       G  _   A_
GAM449  ACTR1B   3'  AGCTCAGGGAGGCAGCCC    12596    T     CTAGCC
                                AG CTCAGG     GGCAGCCC
                                || ||||||     ||||||||
                                TC GAGTCC     CCGTCGGG
                                 _     CT_____
GAM449  ADAMTS13 3'  GTTCCGGGCGAGGCAGCCCC   12597    CT A   TAGCC
                                GT  C GGC     GGCAGCCCC
                                ||  | |||     |||||||||
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                                CA  G CCG    CCGTCGGGG
                                 AG C   CT___
GAM449  AIRE    5'  GTCCCGGGACACTGGCAGCCCC 12598      A  CTA  C
                                GTCTC GG   GC GGCAGCCCC
                                ||||| ||   || |||||||||
                                CAGGG CC   TG CCGTCGGGG
                                   C  TG_  A
GAM449  ALPI    3'  AGTCCCAGGCTCAGCC      12599          AGCCGG   _
                                AGTCTCAGGCT     CAGC C
                                ||||||||||      |||| |
                                TCAGGGTCCGA     GTCG G
                                      _______   A
GAM449  AQP2    3'  AGGCTCAGGCTCCTCCGGCAGC 12600    T      AG_
          C                      AG CTCAGGCT   CCGGCAGCC
                                || ||||||||   |||||||||
                                TC GAGTCCGA   GGCCGTCGG
                                 C       GGA
GAM449  BMP8    5'  GCCTCAGGCGCGGTCC      12601         TA  C  CAG
                                GTCTCAGGC  GC GG   CC
                                |||||||||  || ||   ||
                                CGGAGTCCG  CG CC   GG
                                     __ _  A__
GAM449  CBFA2T2  3'  AGCTCAGGCTGGCTGCC     12602    T      AGCC   A
                                AG CTCAGGCT    GGC GCC
                                || ||||||||    ||| |||
                                TC GAGTCCGA    CCG CGG
                                 _      _____   A
GAM449  CD97    3'  AGCCTCAGGCAGTGGCCCC   12603         T  CC   AG
                                AGTCTCAGGC AG  GGC  CCC
                                |||||||||| ||  |||  |||
                                TCGGAGTCCG TC  CCG  GGG
                                     _ A_  __
GAM449  CD97    3'  AGCCTCAGGCAGTGGCCCC   12603         T  CC   AG
                                AGTCTCAGGC AG  GGC  CCC
                                |||||||||| ||  |||  |||
                                TCGGAGTCCG TC  CCG  GGG
                                     _ A_  __
GAM449  ENAM    3'  AGTCTCAGAGCGGCAG      12604        GCT   C
                                AGTCTCAG   AGC GGCAG
                                ||||||||   ||| |||||
                                TCAGAGTC   TCG CCGTC
                                     ___  _
GAM449  FASN    3'  AGTCTCCAAGTCGGCAGC    12605       AGGCT  C
                                AGTCTC    AG CGGCAGC
                                ||||||    || |||||||
                                TCAGAG    TC GCCGTCG
                                   GT___  A
GAM449  GAS7    3'  GCTCAGGCTTCCTGGCCC    12606   T      AG  GGCA
                                G CTCAGGCT  CC    GCCC
                                | ||||||||  ||    ||||
```

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                                C GAGTCCGA  GG    CGGG
                                _       A_  AC__
GAM449  HD      3'  GCCTCAGGCTCAGCC       12607          AGCCGG
                                GTCTCAGGCT     CAGCC
                                ||||||||||     |||||
                                CGGAGTCCGA     GTCGG
                                        _______
GAM449  HIP12    5'  AGCCTCACGGTCCGGCAGCCCC 12608        _ CTAG
                                AGTCTCA GG    CCGGCAGCCCC
                                ||||||| ||    ||||||||||
                                TCGGAGT CC    GGCCGTCGGGG
                                   G  A___
GAM449  IL6R    5'  GCTCAGGCCCCGGGGGCAGCCC 12609    T      AGCC_
            C                    G CTCAGGCT    GGCAGCCCC
                                | ||||||||    |||||||||
                                C GAGTCCGG    CCGTCGGGG
                                _       GGCCC
GAM449  JRK     3'  AGCTCAAGCCTGGCAGCTCC   12610    T      AGCC     _
                                AG CTCAGGCT    GGCAGC CC
                                || ||||||||    |||||| ||
                                TC GAGTTCGG    CCGTCG GG
                                 _       A___     A
GAM449  KRT13    3'  AGCCTTGGGTCCAGCAGCCCC  12611      CA  CTAG
                                AGTCT  GG    CCGGCAGCCCC
                                |||||  ||    ||||||||||
                                TCGGA  CC    GGTCGTCGGGG
                                  A_  CA__
GAM449  LIF     3'  AGTCCCAGGCGTCTGCAGCC   12612          TAGCCG
                                AGTCTCAGGC     GCAGCC
                                ||||||||||     ||||||
                                TCAGGGTCCG     CGTCGG
                                     CAGA__
GAM449  LRP8    5'  GCTCAGGCTGGGCGCGCGGCCC 12613    T      AGC  _  A
            C                    G CTCAGGCT   CG GC GCCCC
                                | ||||||||   || || |||||
                                C GAGTCCGA   GC CG CGGGG
                                _       CCC  G  C
GAM449  LRP8    5'  GCTCAGGCTGGGCGCGCGGCCC 12613    T      AGC  _  A
            C                    G CTCAGGCT   CG GC GCCCC
                                | ||||||||   || || |||||
                                C GAGTCCGA   GC CG CGGGG
                                _       CCC  G  C
GAM449  LRP8    5'  GCTCAGGCTGGGCGCGCGGCCC 12613    T      AGC  _  A
            C                    G CTCAGGCT   CG GC GCCCC
                                | ||||||||   || || |||||
                                C GAGTCCGA   GC CG CGGGG
                                _       CCC  G  C
GAM449  LY64    3'  AGACTCCGGGGCCGGCAGTCCC 12614    T  A  CTA      _
                                AG CTC GG   GCCGGCAG CCC
                                || ||| ||   |||||||| |||
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                                TC GAG CC   CGGCCGTC GGG
                                 T  G  C__      A
GAM449  MECP2    3'  AGCCTCAGGCCCCACTGGCAGC 12616         A_  C
                                AGTCTCAGGCT  GC GGCAGC
                                ||||||||||  || ||||||
                                TCGGAGTCCGG  TG CCGTCG
                                      GG  A
GAM449  MECP2    3'  TCCAGGCTGGAGCCAGCTCC  12615   T    __     AG
                                TC CAGGCT  AGCCGGC  CC
                                || ||||||  |||||||  ||
                                AG GTCCGA  TCGGTCG  GG
                                 _     CC      A_
GAM449  MRPL49   3'  GTCTCAGGCCTTTGGCCCC   12617        AGCC  AG
                                GTCTCAGGCT   GGC  CCC
                                ||||||||||   |||  |||
                                CAGAGTCCGG   CCG  GGG
                                      AAA_  __
GAM449  NFRKB    5'  GTCCAGGCGGGCAGTCCC    12618    T   TAGCC   _
                                GTC CAGGC    GGCAG CCC
                                ||| |||||    ||||| |||
                                CAG GTCCG    CCGTC GGG
                                  _    C____    A
GAM449  NPAS1    3'  GTCCGGCGCCGGCAGC     12619     CA  TA
                                GTCT  GGC  GCCGGCAGC
                                ||||  |||  |||||||||
                                CAGG  CCG  CGGCCGTCG
                                       __  __
GAM449  NR4A1    5'  AGTCTCAGCCTGGTCCCTGGTC 12620       G  AG_  GGCAG
           CC                    AGTCTCAG CT   CC    CCC
                                ||||||||  ||   ||    |||
                                TCAGAGTC GA   GG    GGG
                                    G  CCA  GACCA
GAM449  OXTR     3'  AGCCTCAGGCTGCAGCCC    12621         AGCCG
                                AGTCTCAGGCT    GCAGCCC
                                ||||||||||    |||||||
                                TCGGAGTCCGA    CGTCGGG
                                              _____
GAM449  PCDHGA1  3'  GTCTGGGGTTCTCTGGCAGCCC 12622     CA  CTAGCC
           C                   GTCT  GG     GGCAGCCCC
                               ||||  ||     |||||||||
                               CAGA  CC     CCGTCGGGG
                                 CC  AAGAGA
GAM449  PCDHGA10 3'  GTCTGGGGTTCTCTGGCAGCCC 12622     CA  CTAGCC
           C                   GTCT  GG     GGCAGCCCC
                               ||||  ||     |||||||||
                               CAGA  CC     CCGTCGGGG
                                 CC  AAGAGA
GAM449  PCDHGA11 3'  GTCTGGGGTTCTCTGGCAGCCC 12622     CA  CTAGCC
           C                   GTCT  GG     GGCAGCCCC
                               ||||  ||     |||||||||
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                              CAGA CC    CCGTCGGGG
                                CC AAGAGA
GAM449  PCDHGA11 3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                   GTCT GG    GGCAGCCCC
                              |||| ||    |||||||||
                              CAGA CC    CCGTCGGGG
                                CC AAGAGA
GAM449  PCDHGA12 3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                   GTCT GG    GGCAGCCCC
                              |||| ||    |||||||||
                              CAGA CC    CCGTCGGGG
                                CC AAGAGA
GAM449  PCDHGA2  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                   GTCT GG    GGCAGCCCC
                              |||| ||    |||||||||
                              CAGA CC    CCGTCGGGG
                                CC AAGAGA
GAM449  PCDHGA3  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                   GTCT GG    GGCAGCCCC
                              |||| ||    |||||||||
                              CAGA CC    CCGTCGGGG
                                CC AAGAGA
GAM449  PCDHGA4  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                   GTCT GG    GGCAGCCCC
                              |||| ||    |||||||||
                              CAGA CC    CCGTCGGGG
                                CC AAGAGA
GAM449  PCDHGA5  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                   GTCT GG    GGCAGCCCC
                              |||| ||    |||||||||
                              CAGA CC    CCGTCGGGG
                                CC AAGAGA
GAM449  PCDHGA6  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                   GTCT GG    GGCAGCCCC
                              |||| ||    |||||||||
                              CAGA CC    CCGTCGGGG
                                CC AAGAGA
GAM449  PCDHGA7  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                   GTCT GG    GGCAGCCCC
                              |||| ||    |||||||||
                              CAGA CC    CCGTCGGGG
                                CC AAGAGA
GAM449  PCDHGA8  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                   GTCT GG    GGCAGCCCC
                              |||| ||    |||||||||
                              CAGA CC    CCGTCGGGG
                                CC AAGAGA
GAM449  PCDHGA9  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                   GTCT GG    GGCAGCCCC
                              |||| ||    |||||||||
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                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM449  PCDHGB1  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM449  PCDHGB2  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM449  PCDHGB3  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM449  PCDHGB4  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM449  PCDHGB5  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM449  PCDHGB6  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM449  PCDHGB7  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM449  PCDHGC3  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM449  PCDHGC3  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM449  PCDHGC4  3' GTCTGGGGTTCTCTGGCAGCCC 12622    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
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                              CAGA  CC     CCGTCGGGG
                                CC  AAGAGA
GAM449  PCDHGC5  3'  GTCTGGGGTTCTCTGGCAGCCC 12622      CA  CTAGCC
          C                    GTCT  GG     GGCAGCCCC
                               ||||  ||     |||||||||
                              CAGA  CC     CCGTCGGGG
                                CC  AAGAGA
GAM449  PEX10    3'  GCTCGGGCGCCCCTGGCAGCCC 12623   T   A   TA  ___
          C                    G CTC GGC  GCC   GGCAGCCCC
                               | ||| |||  |||   |||||||||
                              C GAG CCG  CGG   CCGTCGGGG
                               _  C  __  GGA
GAM449  PSEN2    5'  GTCTCAGGTTCCTTCAGCTCC  12624        CTAG  GG   _
                              GTCTCAGG   CC  CAGC CC
                              ||||||||   ||  |||| ||
                              CAGAGTCC   GG  GTCG GG
                                   AA__  AA   A
GAM449  PSEN2    5'  GTCTCAGGTTCCTTCAGCTCC  12624        CTAG  GG   _
                              GTCTCAGG   CC  CAGC CC
                              ||||||||   ||  |||| ||
                              CAGAGTCC   GG  GTCG GG
                                   AA__  AA   A
GAM449  RAB3A    5'  GCTCAGGCCCCTGCAGTCC   12625   T      AG  G   _
                              G CTCAGGCT  CC GCAG CC
                              | ||||||||  || |||| ||
                              C GAGTCCGG  GG CGTC GG
                               _      __ A   A
GAM449  REV3L    5'  GTCCCAGGCTGCAGC      12626          AGCCG
                              GTCTCAGGCT    GCAGC
                              ||||||||||    |||||
                              CAGGGTCCGA    CGTCG
                                    _____
GAM449  RNPEPL1  3'  AGTCCCAGGCTGGAGGCCC   12627          AGCC  CA
                              AGTCTCAGGCT   GG  GCCC
                              ||||||||||    ||  ||||
                              TCAGGGTCCGA   CC  CGGG
                                    ____ TC
GAM449  SLC22A12 3'  ATCTCAGGCTGGCCCTGGACCC 12628          A  __  CA
          C                    GTCTCAGGCT GCC  GG  GCCCC
                               |||||||||| |||  ||  |||||
                              TAGAGTCCGA CGG  CC  TGGGG
                                   C   GA  __
GAM449  SOX12    5'  GTCTCAGGCGGGCTCGGCGCGC 12629        TA  _   A_
          CCC                    GTCTCAGGC  GC CGGC  GCCCC
                               |||||||||  || ||||  |||||
                              CAGAGTCCG  CG GCCG  CGGGG
                                   CC  A   CG
GAM449  SUFU     3'  AGTCCCAGGCTGGCTGCAGCCC 12630          A  CG
          C                    AGTCTCAGGCT GC  GCAGCCCC
                               |||||||||| ||  ||||||||
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                                TCAGGGTCCGA CG  CGTCGGGG
                                      C  A_
GAM449  TIMP3    3'  AGTCTCAGTTACTAGTTCC   12631        __    __
                                AGTCTCAG  GCTAG  CC
                                ||||||||  |||||  ||
                                TCAGAGTC  TGATC  GG
                                    AA    AA
GAM449  TNFAIP1  3'  GTCTCAGGCTGACGCATTCC  12632         AG CG   GC
                                GTCTCAGGCT  C  GCA  CC
                                ||||||||||  |  |||  ||
                                CAGAGTCCGA  G  CGT  GG
                                      CT __   AA
GAM449  TRPM1    5'  AGCTCAGGCTCTTTCAGCC   12633    T      AGCCGG
                                AG CTCAGGCT     CAGCC
                                || ||||||||     |||||
                                TC GAGTCCGA     GTCGG
                                 _       GAAA__
GAM449  WEE1     5'  AGTCTCAGGTTCGGGCTCC   12634         CTAGC   CA  _
                                AGTCTCAGG    CGG  GC CC
                                |||||||||    |||  || ||
                                TCAGAGTCC    GCC  CG GG
                                     AA___   __  A
GAM449  APPD     3'  AGCTCAGGCTGCAGTCC     12635    T      AGCCG   _
                                AG CTCAGGCT    GCAG CC
                                || ||||||||    |||| ||
                                TC GAGTCCGA    CGTC GG
                                 _      _____   A
GAM449  C7orf13  3'  AGTCTCAGCTCTGCCAGTTCC  12636         G_  A    CAG
                                AGTCTCAG  CT GCCGG   CC
                                ||||||||  || |||||   ||
                                TCAGAGTC  GA CGGTC   GG
                                     GA  _    AA_
GAM449  CBCIP2   3'  GTCTTGAACTACCCGGCAGCC  12637     CA    G
                                GTCT  GGCTA CCGGCAGCC
                                ||||  ||||| |||||||||
                                CAGA  TTGAT GGCCGTCGG
                                  AC    G
GAM449  CHAF1B   3'  GTCTCAGGCACCTCCAGC    12638         TA   GG
                                GTCTCAGGC  GCC  CAGC
                                |||||||||  |||  ||||
                                CAGAGTCCG  TGG  GTCG
                                     __  AG
GAM449  CHDH     3'  ATCTCAGGCTGAATGCTGGC   12639          A___  C
                                GTCTCAGGCT   GC GGC
                                ||||||||||   || |||
                                TAGAGTCCGA   CG CCG
                                      CTTA  A
GAM449  COPS7B   3'  CAAGCATTAGCCGGCAGTTCC  12640       __         CC
                                CAGGC  TAGCCGGCAG  CC
                                |||||  ||||||||||  ||
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                                GTTCG  ATCGGCCGTC  GG
                                   TA        AA
GAM449  DKFZP434P0111 3'  GTCTCTGGTAGTGGCAGCCC   12641      A  C   CC
                                GTCTC GG TAG  GGCAGCCC
                                ||||| || |||  ||||||||
                                CAGAG CC ATC  CCGTCGGG
                                   A  _  A_
GAM449  DKFZP564K1964 5'  GCCTCAGGCTGTGGCTCC    12642         AGCC   AG
                                GTCTCAGGCT   GGC  CC
                                ||||||||||   |||  ||
                                CGGAGTCCGA   CCG  GG
                                      CA__   A_
GAM449  DKFZP564M182 3'  GTCTCAGACTCTGCAGC     12643         AGCCG
                                GTCTCAGGCT    GCAGC
                                ||||||||||    |||||
                                CAGAGTCTGA    CGTCG
                                      GA___
GAM449  DKFZP566G1424 5'  AGTCTCAGGTGTCCTGGCCC   12644        CTAG  GGCA
                                AGTCTCAGG   CC   GCCC
                                |||||||||   ||   ||||
                                TCAGAGTCC   GG   CGGG
                                      ACA_  AC__
GAM449  DKFZP586P0123 3'  GTTTCAGGACTGTGACAGCCC  12645    C    _  AGCC
                                GT TCAGG CT   GGCAGCCC
                                || ||||| ||   ||||||||
                                CA AGTCC GA   CTGTCGGG
                                 A    T  CA__
GAM449  DRIL2    3'  CTCTTGGCTCCTGGCAGCCCC  12646    A_   AG  _
                                CTC  GGCT  CC GGCAGCCCC
                                |||  ||||  || |||||||||
                                GAG  CCGA  GG CCGTCGGGG
                                  AA   __  A
GAM449  FASTK    3'  GTCCCAGGCTGGCCC      12647         AGCC   AG
                                GTCTCAGGCT   GGC  CC
                                ||||||||||   |||  ||
                                CAGGGTCCGA   CCG  GG
                                     _____   __
GAM449  FLJ00007  3'  AGTCTCAGGCTGGGGGCC    12648          AGCC  CA
                                AGTCTCAGGCT   GG  GCC
                                ||||||||||   ||  |||
                                TCAGAGTCCGA   CC  CGG
                                      _____  CC
GAM449  FLJ12409  3'  AGTCTCAGCTAATGGGC     12649        G   CC
                                AGTCTCAG CTAG  GGC
                                |||||||| ||||  |||
                                TCAGAGTC GATT  CCG
                                     _   AC
GAM449  FLJ13782  3'  GCTCAGGCTTCGGCTCC     12650   T      AGC   AG
                                G CTCAGGCT   CGGC  CC
                                | ||||||||   ||||  ||
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                                C GAGTCCGA  GCCG  GG
                                _      A__   A_
GAM449  FLJ20584  3' GTCTCAGGCAGCTGGTTCC   12651        T  C  CAG
                                GTCTCAGGC AGC GG  CC
                                ||||||||| ||| ||  ||
                                CAGAGTCCG TCG CC  GG
                                      _  A  AA_
GAM449  FLJ21195  5' GTCCCAGGCTGGCTGCTCC   12652         AGCC  A _
                                GTCTCAGGCT   GGC GC CC
                                ||||||||||   ||| || ||
                                CAGGGTCCGA   CCG CG GG
                                      ____  A  A
GAM449  FLJ22477  5' AGCTCGGGCGGCAGCC     12653    T  A  TAGCC    _
                                AG CTC GGC    GGCAGC C
                                || ||| |||    |||||| |
                                TC GAG CCG    CCGTCG G
                                 _  C  _____     A
GAM449  FLJ22494  5' GTCTCGGGCTCACAGTGCAGCC 12654      A   A  CG_
           CC                    GTCTC GGCT GC  GCAGCCCC
                                ||||| |||| ||  ||||||||
                                CAGAG CCGA TG  CGTCGGGG
                                   C   G  TCA
GAM449  FLJ22746  5' AGCTCGGGTTCAGCAGCC    12655    T  A  CTAGC
                                AG CTC GG    CGGCAGCC
                                || ||| ||    ||||||||
                                TC GAG CC    GTCGTCGG
                                 _  C  AA___
GAM449  FLJ23045  3' GTCCCAGGCTGGCTGGGC    12656         A  C_
                                GTCTCAGGCT GC  GGC
                                |||||||||| ||  |||
                                CAGGGTCCGA CG  CCG
                                      C  AC
GAM449  FLJ23590  5' GTCTCAGGCGGCCGCCAGCCCC 12657         TA   G
                                GTCTCAGGC  GCCG CAGCCCC
                                |||||||||  |||| |||||||
                                CAGAGTCCG  CGGC GTCGGGG
                                      C_   G
GAM449  FXYD5    5' GTCCTAAGCCGGCAGCC     12658     CAGGCT
                                GTCT     AGCCGGCAGCC
                                ||||     ||||||||||
                                CAGG     TCGGCCGTCGG
                                  AT_____
GAM449  FXYD5    3' AGACTCGGACCGGCAGCCC   12659    T  A  CTA
                                AG CTC GG   GCCGGCAGCCC
                                || ||| ||   ||||||||||
                                TC GAG CC   TGGCCGTCGGG
                                 T  _ ____
GAM449  GIPC3    3' GTCTCAGAGCTGGCCTGGGC   12660       _  A  __
                                GTCTCAG GCT GCC  GGC
                                ||||||| ||| |||  |||
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                                CAGAGTC CGA CGG  CCG
                                    T  C  AC
GAM449  GMPPB    5' AGCCTTTGGCTGGCAGC    12661     CA   AGCC
                                AGTCT  GGCT   GGCAGC
                                ||||| ||||   ||||||
                                TCGGA  CCGA   CCGTCG
                                  AA   _____
GAM449  HNK-1ST  3' AGGCTCAGGCTGGCACTCATCC 12662   T      A  CGG  G
          C                      AG CTCAGGCT GC   CA CCC
                                || |||||||| ||   || |||
                                TC GAGTCCGA CG   GT GGG
                                 C       C  TGA  A
GAM449  HSJ001348 5' GCCTCGCGGCCGCTGGCGGCCC 12663     A_   A  C   A
                                GTCTC  GGCT GC GGC GCCC
                                |||||  |||| || ||| ||||
                                CGGAG  CCGG CG CCG CGGG
                                   CG   _  A   C
GAM449  KIAA0544 3' GTCTCAGGCTGGAGTGGGC   12664         __ CC
                                GTCTCAGGCT  AG  GGC
                                ||||||||||  ||  |||
                                CAGAGTCCGA  TC  CCG
                                      CC  AC
GAM449  KIAA0563 5' GCCTCAGATCCTGGTGGTCCC  12665        CTAG  _  CAG_
                                GTCTCAGG    CC GG    CCC
                                ||||||||    || ||    |||
                                CGGAGTCT    GG CC    GGG
                                     A___  A  ACCA
GAM449  KIAA0664 3' GTCTCAGGGTGGCCACATCC   12666        CTA    G  G
                                GTCTCAGG   GCCG CA CC
                                ||||||||   |||| || ||
                                CAGAGTCC   CGGT GT GG
                                     CAC    _  A
GAM449  KIAA0978 3' AGCTCAGGCTGGCTGGC     12667    T      A  C
                                AG CTCAGGCT GC GGC
                                || |||||||| || |||
                                TC GAGTCCGA CG CCG
                                 _       C  A
GAM449  KIAA1259 3' AGCTCAGGCTGGCCGGGC    12668    T      A    CA
                                AG CTCAGGCT GCCGG  GC
                                || |||||||| |||||  ||
                                TC GAGTCCGA CGGCC  CG
                                 _       C    __
GAM449  KIAA1271 3' GTCTCAGGCTGGGCTGCC    12669         AGCC   A
                                GTCTCAGGCT    GGC GCC
                                ||||||||||    ||| |||
                                CAGAGTCCGA    CCG CGG
                                      C___   A
GAM449  KIAA1615 5' GCCTCAGGCTCCCGGCTCC   12670         AG    AG
                                GTCTCAGGCT  CCGGC  CC
                                ||||||||||  |||||  ||
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                                CGGAGTCCGA GGCCG GG
                                     G_    A_
GAM449  KIAA1656 3' GCTTCAGGCGCCGCAGCC   12671  TC    TA   G
                                G TCAGGC GCCG CAGCC
                                | |||||| |||| |||||
                                C AGTCCG CGGC GTCGG
                                 GA    __   _
GAM449  KIAA1678 3' TCTCCGGGCTGGCAGCCCC  12672    A_   AGCC
                                TCTC GGCT  GGCAGCCCC
                                |||| ||||  |||||||||
                                AGAG CCGA  CCGTCGGGG
                                  GC  _____
GAM449  KIAA1784 3' GTCTCAGGCTGGCGGTGGC  12673       A C__
                                GTCTCAGGCT GC  GGC
                                |||||||||| ||  |||
                                CAGAGTCCGA CG  CCG
                                     C CCA
GAM449  MCFP    5' AGCTGCAGGGCCGGCAGTCC  12674   CT   CTA     _
                                AGT CAGG  GCCGGCAG CC
                                ||| ||||  |||||||| ||
                                TCG GTCC  CGGCCGTC GG
                                  AC  ___     A
GAM449  MGC3113  3' AGTCTCAGGTCGTCCAGTCC  12675       CTAG   CAG
                                AGTCTCAGG  CCGG  CC
                                |||||||||  ||||  ||
                                TCAGAGTCC  GGTC  GG
                                     AGCA  A__
GAM449  NAF1    3' AGCTTCAGGCTGGCGCCC   12676   TC    AGCC  A
                                AG TCAGGCT  GGC GCCC
                                || |||||||  ||| ||||
                                TC AGTCCGA  CCG CGGG
                                 GA    _____  _
GAM449  P450RAI-2 3' AGCTTCAGCTGCGGCAGCC  12677   TC   G A C
                                AG TCAG CT GC GGCAGCC
                                || |||| || || |||||||
                                TC AGTC GA CG CCGTCGG
                                 GA  _ _ _
GAM449  PEG10   3' AGTCCCAGGTTAGCACAAAGC 12678       C   _  C
                                AGTCTCAGG TAGC CGG AGC
                                ||||||||| |||| ||| |||
                                TCAGGGTCC ATCG GTT TCG
                                     A  T  _
GAM449  PNMA5   5' GTCCCAGGTTTCACACAGCC  12679       CTA_ CG
                                GTCTCAGG  GC  GCAGCC
                                ||||||||  ||  ||||||
                                CAGGGTCC  TG  TGTCGG
                                     AAAG __
GAM449  SSH2    3' AGTTTCTGGGCAGCAGCC   12680    C A_  TAGCC
                                AGT TC  GGC   GGCAGCC
                                ||| ||  |||   |||||||
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                                TCA AG  CCG    TCGTCGG
                                  A  AC  _____
GAM449  STK23    3'  GTCTCAGGCAGAACACGC    12681        T  CC   _
                                GTCTCAGGC AG  GGCA GC
                                ||||||||| ||  |||| ||
                                CAGAGTCCG TC  TTGT CG
                                     _ __   G
GAM449  TADA3L   3'  GCCTCAGGCTAGCCCAGCAG   12682           _
                                GTCTCAGGCTAGCC GGCAG
                                |||||||||||||| |||||
                                CGGAGTCCGATCGG TCGTC
                                       G
GAM449  WBSCR21  5'  AGTCTCAGGCATGGCTCC    12683         TAGCC  AG
                                AGTCTCAGGC    GGC  CC
                                ||||||||||    |||  ||
                                TCAGAGTCCG    CCG  GG
                                     TA___   A_
GAM449  LOC116437 3'  AGTCTCAGGCTGGCACC     12684         AGCC   G
                                AGTCTCAGGCT   GGCA CC
                                ||||||||||   ||||  ||
                                TCAGAGTCCGA   CCGT GG
                                      ____   _
GAM449  LOC121274 3'  TCAGGAGAACGGCAGCCC    12685      CT  C
                                TCAGG  AGC GGCAGCCC
                                |||||  ||| ||||||||
                                AGTCC  TTG CCGTCGGG
                                   TC  _
GAM449  LOC123887 5'  AGTTTCAGATGCAAAGCAGCCC 12686    C    CTA  C_
          C                     AGT TCAGG   GC  GGCAGCCCC
                                ||| |||||   ||  |||||||||
                                TCA AGTCT   CG  TCGTCGGGG
                                  A    A__  TT
GAM449  LOC125988 3'  AGTCTTCAGGTCAGTGGCAGCC 12687      _   C  CC
          C                     AGTCT CAGG TAG  GGCAGCCC
                                ||||| |||| |||  ||||||||
                                TCAGA GTCC GTC  CCGTCGGG
                                   A   A  A_
GAM449  LOC128844 5'  AGGCTCGGGCTCCGGTCCC   12688   T  A   AG   CAG
                                AG CTC GGCT  CCGG   CCC
                                || ||| ||||  ||||   |||
                                TC GAG CCGA  GGCC   GGG
                                 C  C   __   A__
GAM449  LOC145623 3'  AATCTCAGGCTATGTAGC    12689         GCC
                                AGTCTCAGGCTA   GGC
                                ||||||||||||   |||
                                TTAGAGTCCGAT   TCG
                                       ACA
GAM449  LOC147071 5'  GCCTCAGACCCTGGTGGTCCC  12690        AGCC  CAG_
                                GTCTCAGGCT   GG   CCC
                                ||||||||||   ||   |||
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                                CGGAGTCTGG   CC   GGG
                                     GA__  ACCA
GAM449  LOC148018 5'  AGCCTCAGGCTCTGGACGGCCC 12691          AGCC  A
                      AGTCTCAGGCT   GGC GCCC
                      ||||||||||   ||| ||||
                      TCGGAGTCCGA   CTG CGGG
                            GAC_  C
GAM449  LOC148479 3'  AGTTGCCAGGGCCGGCAGTTCC 12692    C_   CTA     CC
                      AGT  TCAGG  GCCGGCAG  CC
                      |||  |||||  ||||||||  ||
                      TCA  GGTCC  CGGCCGTC  GG
                        AC    ___      AA
GAM449  LOC148824 3'  AGTCTGGGTTACCACAGCCCC  12693     CA  CTA   G
                      AGTCT  GG   GCCG CAGCCCC
                      |||||  ||   |||| |||||||
                      TCAGA  CC   TGGT GTCGGGG
                         __  CAA   _
GAM449  LOC149460 5'  AGCCTCAGGGGCAGCC      12694        CTAGCC
                      AGTCTCAGG     GGCAGCC
                      |||||||||     |||||||
                      TCGGAGTCC     CCGTCGG
                                    _______
GAM449  LOC150319 3'  GTCCCAGGCTGGCTGGAGGCC  12695         A  C  CA
                      GTCTCAGGCT GC GG  GCC
                      |||||||||| || ||  |||
                      CAGGGTCCGA CG CC  CGG
                            C  A  TC
GAM449  LOC151031 5'  CTCCGGACTTAGCCGGCGGCTC 12696    A  _  _     A  _
          C                    CTC GG CT AGCCGGC GC CC
                               ||| || || ||||||| || ||
                               GAG CC GA TCGGCCG CG GG
                                 G  T  A      C  A
GAM449  LOC151568 5'  AGCCTCAGGCTGGCTGAC    12697          A  C
                      AGTCTCAGGCT GC GGC
                      |||||||||||  || |||
                      TCGGAGTCCGA CG CTG
                            C  A
GAM449  LOC155435 3'  TCTGCGCCGGCCGGCAGCTCC  12698    CAG  TA       _
                      TCT   GC  GCCGGCAGC CC
                      |||   ||  |||||||| ||
                      AGA   CG  CGGCCGTCG GG
                        CG_  GC        A
GAM449  LOC158969 5'  AATCTCAGGCTTACAGCC    12699          AGCCG
                      AGTCTCAGGCT    GCAGCC
                      ||||||||||     ||||||
                      TTAGAGTCCGA    TGTCGG
                            A____
GAM449  LOC196707 3'  AGTCTCGGCTGAGAGAGCC   12700       A   _  CC  C
                      AGTCTC GGCT AG  GG AGCC
                      |||||| |||| ||  || ||||
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                                TCAGAG CCGA TC  TC TCGG
                                  _   C  __ _
GAM449  LOC200471 5' AGCCTCAGGCTCCCGGC    12701         AG
                                AGTCTCAGGCT  CCGGC
                                ||||||||||  |||||
                                TCGGAGTCCGA  GGCCG
                                     G_
GAM449  LOC201173 5' GCCTCAGACCCTGGTGGTCCC  12690        AGCC  CAG_
                                GTCTCAGGCT   GG   CCC
                                |||||||||   ||   |||
                                CGGAGTCTGG   CC   GGG
                                     GA__  ACCA
GAM449  LOC201220 5' GCCTCAGACCCTGGTGGTCCC  12690        AGCC  CAG_
                                GTCTCAGGCT   GG   CCC
                                |||||||||   ||   |||
                                CGGAGTCTGG   CC   GGG
                                     GA__  ACCA
GAM449  LOC201689 3' ATCTCAGGCTGAATGCTGGC   12639        A___  C
                                GTCTCAGGCT   GC GGC
                                |||||||||   || |||
                                TAGAGTCCGA   CG CCG
                                     CTTA  A
GAM449  LOC202788 3' AGTCCCAGGCTGGTCTCC    12702        AGCC  CAG
                                AGTCTCAGGCT   GG  CC
                                ||||||||||   ||  ||
                                TCAGGGTCCGA   CC  GG
                                     ____  AGA
GAM449  LOC204970 3' GTCACGGAGAAGCCGGCAGCTC 12703    TCA  CT_      _
          C                      GTC  GG  AGCCGGCAGC CC
                                |||  ||  |||||||||| ||
                                CAG  CC  TCGGCCGTCG GG
                                  TG_  TCT       A
GAM449  LOC205418 3' AGTCTCTGGAGATGGCAGCCCC 12704      A  CT  CC
                                AGTCTC GG  AG  GGCAGCCCC
                                |||||| ||  ||  |||||||||
                                TCAGAG CC  TC  CCGTCGGGG
                                   A  __  TA
GAM449  LOC219920 5' AATCTCAGGCAGAAGGCGGCC  12705        T  CC   A
                                AGTCTCAGGC AG  GGC GCC
                                |||||||||| ||  ||| |||
                                TTAGAGTCCG TC  CCG CGG
                                     _  TT   C
GAM449  LOC221466 3' GTCTCAGGGCTGGTGCAGCCCC 12706       _  AGCCG
                                GTCTCAGG CT    GCAGCCCC
                                ||||||||  ||    ||||||||
                                CAGAGTCC GA    CGTCGGGG
                                     C  CCA__
GAM449  LOC254100 3' AGCCTCAGGCTAGGTGC     12707         CCG
                                AGTCTCAGGCTAG   GC
                                ||||||||||||   ||
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                                TCGGAGTCCGATC   CG
                                       CA_
GAM449  LOC254431 5'  GCTCGGGCGCCCCTGGCAGCCC 12623   T   A   TA  ___
           C                    G CTC GGC  GCC   GGCAGCCCC
                                | ||| |||  |||   |||||||||
                                C GAG CCG  CGG   CCGTCGGGG
                                _  C   __   GGA
GAM449  LOC257054 3'  GTCTTCCCAGCTGGCAGCCC   12708     CAGG    C
                                GTCT    CTAGC GGCAGCCC
                                ||||    ||||| ||||||||
                                CAGA    GGTCG CCGTCGGG
                                  AG__    A
GAM449  LOC257355 3'  AGTCTGGTTCGTTGGCAGCCCC 12709      CA  CTAGCC
                                AGTCT  GG     GGCAGCCCC
                                |||||  ||     |||||||||
                                TCAGA  CC     CCGTCGGGG
                                   __  AAGCAA
GAM449  LOC51172  3'  AGTCTGGTTCGTTGGCAGCCCC 12709      CA  CTAGCC
                                AGTCT  GG     GGCAGCCCC
                                |||||  ||     |||||||||
                                TCAGA  CC     CCGTCGGGG
                                   __  AAGCAA
GAM449  LOC51337  3'  AGCCTCAGGCTGGGACCAGCCC 12710          AGCC  __
           C                    AGTCTCAGGCT    GG  CAGCCCC
                                ||||||||||    ||  |||||||
                                TCGGAGTCCGA    CC  GTCGGGG
                                      C___  TG
GAM449  LOC90050  5'  CTCTGCTGGTGGCCGGCAGCTC 12711     AG   A___       _
           C                    CTC  GCT    GCCGGCAGC CC
                                |||  |||    ||||||||| ||
                                GAG  CGA    CGGCCGTCG GG
                                  A_   CCAC        A
GAM449  LOC91373  3'  AGCTCAGGCTGGGCTGTAGCCC 12712    T      AGCC  ___
           C                    AG CTCAGGCT    GGC   AGCCCC
                                || ||||||||    |||   ||||||
                                TC GAGTCCGA    CCG   TCGGGG
                                 _       C___   ACA
GAM450  FLJ11305  3'  TAATATATAAAAATAGATG    12715    T        TA
                                A ATGTATGAAA  ATAGATG
                                | ||||||||||  |||||||
                                A TATATATTTT  TATCTAC
                                 T        __
GAM450  KRTAP4-14 3'  TAATATGTTTGAAATGGAGATA 12716         A     AAT
                                TAATATGT TGAAAT   AGATG
                                |||||||| ||||||   |||||
                                ATTATACA ACTTTA   TCTAT
                                     A     CC_
GAM450  LOC221968 3'  TAATATGTATCATCATGAGATG 12717          GAAATAAT
           T                    TAATATGTAT       AGATGT
                                ||||||||||       ||||||
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                                ATTATACATA       TCTACA
                                      GTAGTAC_
GAM451  CLECSF5  3' AGACTATCCAAAATTTTAAAAA 12720       CAGT
           TA                   AGATTA    AGATTTTAAAAATA
                                ||||||    ||||||||||||||
                                TCTGAT    TTTAAAATTTTTAT
                                   AGGT
GAM451  IFNA10   3' ATTACATAAATTTTAAAAATA  12721       G
                                ATTACA TAGATTTTAAAAATA
                                |||||| ||||||||||||||
                                TAATGT ATTTAAAATTTTTAT
                                   _
GAM451  IL13RA1  3' AGGTCACAGTGAAGGTAAAAAT 12722    A      A  TTT
           A                    AG TTACAGT GA   TAAAAATA
                                || ||||||| ||   ||||||||
                                TC AGTGTCA CT   ATTTTTAT
                                 C      _  TCC
GAM451  RUNX1    3' GAATACAGTAGTTAAAAAT    12723    T      ATT
                                GA TACAGTAG   TTAAAAAT
                                || ||||||||   ||||||||
                                CT ATGTCATC   AATTTTTA
                                 T      ____
GAM451  TEAD3    3' ACAGCTGGATTTTAAAAAT    12724      A_
                                ACAGT  GATTTTAAAAAT
                                |||||  ||||||||||||
                                TGTCG  CTAAAATTTTTA
                                   AC
GAM451  DKFZP434J193 3'  GATTACAGCAGGCTCCAA    12725          AT
                                GATTACAGTAG  TTTAA
                                ||||||||||  |||||
                                CTAATGTCGTC  AGGTT
                                      CG
GAM451  FLJ00026  3' AGGTCACAGTCATATTAAAAAT 12726    A      AGATT
           A                    AG TTACAGT     TTAAAAATA
                                || |||||||    |||||||||
                                TC AGTGTCA     AATTTTTAT
                                 C      GTAT_
GAM451  FLJ10971  3' GATTCAGTTGATTTTTAAAAAT 12727      A   A     _
                                GATT CAGT GATTTT AAAAAT
                                |||| |||| |||||| ||||||
                                CTAA GTCA CTAAAA TTTTTA
                                   _   A     A
GAM451  FLJ11040  3' AATTACAGTAAAATGTTTTAAA 12728           ____
           AAT                    GATTACAGTAGA   TTTTAAAAAT
                                  ||||||||||||   ||||||||||
                                  TTAATGTCATTT   AAAATTTTTA
                                         TAC
GAM451  FLJ12806  3' GATTACACTAGTTTAAAAATA  12729       G   AT
                                GATTACA TAG  TTTAAAAATA
                                ||||||| |||  ||||||||||
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                                CTAATGT ATC  AAATTTTTAT
                                   G  __
GAM451  MGC4677   5'  AGATACAGTAGCACACAAAATA 12730     T      ATTTTA
                                AGAT ACAGTAG     AAAATA
                                |||| |||||||     ||||||
                                TCTA TGTCATC     TTTTAT
                                  _      GTGTG_
GAM451  LOC150468 3'  GATTAAAGTAGATCAATAAA   12731      C       T_
                                GATTA AGTAGATT  TAAA
                                ||||| ||||||||  ||||
                                CTAAT TCATCTAG  ATTT
                                   T       TT
GAM451  LOC221935 3'  AGATAAAAAGATTTTAAAAATA 12732     TACAGT
                                AGAT     AGATTTTAAAAATA
                                ||||     ||||||||||||||
                                TCTA     TCTAAAATTTTTAT
                                  TTTT__
GAM451  LOC256453 3'  GATTACAGTAGGGTTAAA    12733          ATT
                                GATTACAGTAG   TTAAA
                                ||||||||||   |||||
                                CTAATGTCATC   AATTT
                                      CC_
GAM452  EFEMP1    3'  ATCTTTATTGACCTTTTCCATT 12736     CC_    AAGA
          T                      ATCT   TTGAT    TTTCCATTT
                                ||||   |||||   |||||||||
                                TAGA   AACTG    AAAGGTAAA
                                  AAT    GA__
GAM452  EFEMP1    3'  ATCTTTATTGACCTTTTCCATT 12736     CC_    AAGA
          T                      ATCT   TTGAT    TTTCCATTT
                                ||||   |||||   |||||||||
                                TAGA   AACTG    AAAGGTAAA
                                  AAT    GA__
GAM452  MN1       3'  TCTCCAGGATTTCCATT     12737       TTGATAA
                                TCTCC      GATTTCCATT
                                |||||      ||||||||||
                                AGAGG      CTAAAGGTAA
                                   TC_____
GAM452  RAD52     3'  ATCCTCTTGATAAGGTTC    12738     TC       A
                                ATC  CTTGATAAG TTT
                                |||  ||||||||| |||
                                TAG  GAACTATTC AAG
                                  GA       C
GAM452  RAD52     3'  ATCCTCTTGATAAGGTTC    12738     TC       A
                                ATC  CTTGATAAG TTT
                                |||  ||||||||| |||
                                TAG  GAACTATTC AAG
                                  GA       C
GAM452  RAD52     3'  ATCCTCTTGATAAGGTTC    12738     TC       A
                                ATC  CTTGATAAG TTT
                                |||  ||||||||| |||
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                                TAG  GAACTATTC AAG
                                  GA        C
GAM452  RAD52    3'  ATCCTCTTGATAAGGTTC    12738     TC        A
                                ATC  CTTGATAAG TTT
                                |||  ||||||||| |||
                                TAG  GAACTATTC AAG
                                  GA        C
GAM452  TCP10    3'  ATCTTCTGATAAGATTT     12739     CC
                                ATCT  TTGATAAGATTT
                                ||||  ||||||||||||
                                TAGA  GACTATTCTAAA
                                  A_
GAM452  TEM5     3'  TCCCTCGGTTTCCATT      12740     T    ATAAGA
                                TC CCTTG     TTTCCATT
                                || |||||     ||||||||
                                AG GGAGC     AAAGGTAA
                                 _    C_____
GAM452  ARPP-21  3'  TCTTTTGAATTCCTTTCCATTT 12741     CC    TAAGA
                                TCT  TTGA    TTTCCATTT
                                |||  ||||    |||||||||
                                AGA  AACT    AAAGGTAAA
                                  A_   TAAGG
GAM452  FLJ14146 3'  TCCTCTTGCCTCATTTCCATTT 12742    TC    ATAAG
                                TC  CTTG    ATTTCCATTT
                                ||  ||||    ||||||||||
                                AG  GAAC    TAAAGGTAAA
                                 GA   GGAG_
GAM452  FLJ25416 3'  CTCCTTGTTTTTTCCATTT    12743       ATAAGA
                                CTCCTTG     TTTCCATTT
                                |||||||     |||||||||
                                GAGGAAC     AAAGGTAAA
                                    AAA___
GAM452  KIAA0240 3'  CCTCTTAACTGGTTTCCATTT  12744     C    AAGA
                                TCTC TTGAT    TTTCCATTT
                                |||| |||||   |||||||||
                                GGAG AATTG    AAAGGTAAA
                                  _    ACC_
GAM452  KIAA1350 3'  ATCTCCCTGATTTTCTATT    12745         AAGA   C
                                ATCTCCTTGAT    TTTC ATT
                                ||||||||||    |||| |||
                                TAGAGGGACTA    AAAG TAA
                                      ____    A
GAM452  PELI2    3'  TCTCCTTAATGGAGCCCATC   12746        AA  TT
                                TCTCCTTGAT  GA  TCCATT
                                ||||||||||  ||  ||||||
                                AGAGGAATTA  CT  GGGTAG
                                      C_  C_
GAM452  PRO0149  5'  ATCTCCTTGTGAGATTT     12747        ATA
                                ATCTCCTTG   AGATTT
                                |||||||||   ||||||
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                                TAGAGGAAC   TCTAAA
                                     AC_
GAM452  LOC145942 5'  CTTGAGATTTCCATT      12748      TAA
                                CTTGA   GATTTCCATT
                                |||||   ||||||||||
                                GAACT   CTAAAGGTAA
                                  ___
GAM452  LOC158062 3'  ATCTCCTTGAGAAACCATT   12749         TAA  TTT
                                ATCTCCTTGA   GA   CCATT
                                ||||||||||   ||   |||||
                                TAGAGGAACT   CT   GGTAA
                                     ___  TT_
GAM452  LOC221017 3'  TCTCCTTTAATTTCCATTT   12750       GATAA
                                TCTCCTT    GATTTCCATTT
                                |||||||    ||||||||||||
                                AGAGGAA    TTAAAGGTAAA
                                   A____
GAM453  PSG7     3'  CATGTTTTATTCTGCTAGAA   12753      ATT      C
                                TATGT   TTTATTC GCTAGAA
                                |||||   ||||||| |||||||
                                GTACA   AAATAAG CGATCTT
                                  ___      A
GAM453  DKFZP434D146 3'  TATGTGTTTTTTATTGCCAGAA 12754      A_       CC
           C                     TATGT  TTTTTATT  GCTAGAAC
                                |||||  ||||||||  ||||||||
                                ATACA  AAAAATAA  CGGTCTTG
                                  CA       __
GAM453  DKFZP566F2124 3'  TATGTATTTTTTATTTCCCT   12755          A__    G
                                TATGTATTTTT   TTCC CT
                                ||||||||||   |||| ||
                                ATACATAAAAA   AAGG GA
                                      ATA   _
GAM453  FBXO4    3'  TATGTATTTATATTCTAC    12756         T    CG
                                TATGTATTT TATTC  C
                                |||||||| |||||  |
                                ATACATAAA ATAAG  G
                                     T    AT
GAM453  HCC-4    3'  TATGTAATTTTCACTAGAA    12757       T   ATTC
                                TATGTA TTTT    CGCTAGAA
                                |||||| ||||   ||||||||
                                ATACAT AAAA    GTGATCTT
                                   T   ____
GAM453  KIAA0073  3'  TGTATTTTTATTTGCAAG    12758          CC  T
                                TGTATTTTTATT  GC AG
                                ||||||||||||  || ||
                                ACATAAAAATAA  CG TC
                                      A_  T
GAM453  KIAA1712  3'  TGTATCTTTTAACGGTGGCTAG 12759         ATTCC___
           AA                    TGTATTTTT       GCTAGAA
                                |||||||||       |||||||
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                                ACATAGAAA       CGATCTT
                                      ATTGCCAC
GAM453  KIAA1727  3'  TATGTATTTTTTTCCTGGGA  12760          A   GCTA
                                TATGTATTTTT TTCC   GA
                                |||||||||| ||||   ||
                                ATACATAAAAA AAGG   CT
                                      _   ACC_
GAM453  MGC2780   5'  TGTACTTCTTCCTGCTGGAA  12761        TA  _  A
                                TGTATTTT  TTCC GCT GAA
                                ||||||||  |||| ||| |||
                                ACATGAAG  AAGG CGA CTT
                                     __   A  C
GAM453  ZTL1      3'  TATGCATTTTTATTTACCTTAG 12762          __ GC
                                TATGTATTTTTATT  CC  TAG
                                ||||||||||||||  ||  |||
                                ATACGTAAAAATAA  GG  ATC
                                        AT  A_
GAM453  LOC145945 3'  TATGTTTTTTATTCGGC     12763      A       C
                                TATGT TTTTTATTC GC
                                ||||| ||||||||| ||
                                ATACA AAAAATAAG CG
                                   _       C
GAM453  LOC257249 3'  ATGTATTTTTATTTTCTAG   12764          CCG
                                ATGTATTTTTATT   CTAG
                                ||||||||||||   ||||
                                TACATAAAAATAA   GATC
                                        AA_
GAM454  ABCD4     3'  CAAGCATATGGAGGCTCT    12767        T  A
                                TAAGTGTAT GGA GCTCT
                                ||||||||| ||| |||||
                                GTTCGTATA CCT CGAGA
                                      _  C
GAM454  ABCD4     3'  CAAGCATATGGAGGCTCT    12767        T  A
                                TAAGTGTAT GGA GCTCT
                                ||||||||| ||| |||||
                                GTTCGTATA CCT CGAGA
                                      _  C
GAM454  ABCD4     3'  CAAGCATATGGAGGCTCT    12767        T  A
                                TAAGTGTAT GGA GCTCT
                                ||||||||| ||| |||||
                                GTTCGTATA CCT CGAGA
                                      _  C
GAM454  ABCD4     3'  CAAGCATATGGAGGCTCT    12767        T  A
                                TAAGTGTAT GGA GCTCT
                                ||||||||| ||| |||||
                                GTTCGTATA CCT CGAGA
                                      _  C
GAM454  ADAM19    3'  AAGCCACAGGAAGCTCT     12768      G  T
                                AAGT TAT GGAAGCTCT
                                |||| ||| |||||||||
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                              TTCG GTG CCTTCGAGA
                                _  T
GAM454  ADAM19   3'  AAGCAATGGGAAGCTCT    12769     T  T
                              AAGTG AT GGAAGCTCT
                              ||||| || |||||||||
                              TTCGT TA CCTTCGAGA
                                _ C
GAM454  CLASP1   5'  TAACTGTAGAAGCTCT     12770    G   ATT
                              TAA TGT   GGAAGCTCT
                              ||| |||   |||||||||
                              ATT ACA   TCTTCGAGA
                               G  ___
GAM454  FBXL11   3'  AAGTGCAAAAAGCTCT     12771       TT
                              AAGTGTA  GGAAGCTCT
                              |||||||  |||||||||
                              TTCACGT  TTTTCGAGA

                                __
GAM454  IL1RN    3'  CAAGTGCCAGAAGCTCT     12772       AT
                              TAAGTGT  TGGAAGCTCT
                              |||||||  ||||||||||
                              GTTCACG  GTCTTCGAGA

                                __
GAM454  IRAK4    3'  TAAGTGTATGTCCAAAGCT   12773        __ G
                              TAAGTGTA  TT GAAGCT
                              ||||||||  || ||||||
                              ATTCACAT  AG TTTCGA
                                   AC  G
GAM454  MAML1    3'  AAATATACAGTTGGAAGCTCT  12774        ___
                              AAGTGTAT   TGGAAGCTCT
                              ||||||||   ||||||||||
                              TTTATATG   ACCTTCGAGA
                                   TCA
GAM454  NDUFA7   3'  AAGTGATACCTGAGCTCT    12775     _  TG  A
                              AAGTG TAT  GA GCTCT
                              ||||| |||  || |||||
                              TTCAC ATG  CT CGAGA
                                 T  GA  _
GAM454  RAB27A   3'  TAAATGCTCATGAGCTCT    12776       A   GA
                              TAAGTGT TTG  AGCTCT
                              ||||||| |||  ||||||
                              ATTTACG AGT  TCGAGA
                                 _  AC
GAM454  TSN      3'  CAAGTGTATATGGCTGGTTCT  12777        _  AAGC_
                              TAAGTGTAT TGG    TCT
                              ||||||||| |||    |||
                              GTTCACATA ACC    AGA
                                   T  GACCA
GAM454  DIO2     3'  TAAGCTCCCTGGAGCTCT    12778      GTA    A
                              TAAGT   TTGGA GCTCT
                              |||||   ||||| |||||
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                                ATTCG   GACCT CGAGA
                                  AGG    _
GAM454  DIO2     3'  TAAGCTCCCTGGAGCTCT    12778      GTA    A
                                TAAGT   TTGGA GCTCT
                                |||||   ||||| |||||
                                ATTCG   GACCT CGAGA
                                  AGG    _
GAM454  DKFZP434J214 3'  TAAGTGTGTGGAAGCCCT    12779       AT
                                TAAGTGT  TGGAAGCTCT
                                |||||||  ||||||||||
                                ATTCACA  ACCTTCGGGA
                                   C_
GAM454  FLJ20281  5'  AGGTATTGGAGCTTGCTCT   12780    T      A___
                                AG GTATTGGA    GCTCT
                                || ||||||||    |||||
                                TC CATAACCT    CGAGA
                                 _       CGAA
GAM454  FLJ32468  3'  ATGCTCTCTGGAAGCTCT    12781     A__
                                GTGT   TTGGAAGCTCT
                                ||||   ||||||||||
                                TACG   GACCTTCGAGA
                                  AGA
GAM454  HSC3     3'  AAGTGTTGAAAAGCTCT     12782       ATT
                                AAGTGT   GGAAGCTCT
                                ||||||   |||||||||
                                TTCACA   TTTTCGAGA
                                   AC_
GAM454  KIAA1724  3'  TAAATGTATTAGCTCT      12783         GGA
                                TAAGTGTATT   AGCTCT
                                ||||||||||   ||||||
                                ATTTACATAA   TCGAGA
                                      ___
GAM454  LCE      3'  TAAGTGTATGGGGGCCCT    12784         T  AA
                                TAAGTGTAT GG  GCTCT
                                ||||||||| ||  |||||
                                ATTCACATA CC  CGGGA
                                     _ CC
GAM454  My015    3'  TAAGTGCTTAAAAAGCTCT   12785       ATT
                                TAAGTGT   GGAAGCTCT
                                |||||||   |||||||||
                                ATTCACG   TTTTCGAGA
                                   AAT
GAM454  OLFM3    3'  TAAGTATTATTAAAGCTCT   12786       ATTG
                                TAAGTGT    GAAGCTCT
                                |||||||    ||||||||
                                ATTCATA    TTTCGAGA
                                   ATAA
GAM454  OS4      3'  TAAGCTGTCCTAAAGCTCT   12787      _  ATTG
                                TAAG TGT    GAAGCTCT
                                ||||  |||    ||||||||
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                                ATTC ACA    TTTCGAGA
                                  G   GGA_
GAM454   RoXaN     3'  AAGTGCTGCAAAGCTCT     12788       AT  _
                                AAGTGT  TG GAAGCTCT
                                ||||||  || ||||||||
                                TTCACG  AC TTTCGAGA
                                   __  G
GAM454   SRPK1     3'  TAAATGGGAAAGCTCT      12789       TATT
                                TAAGTG    GGAAGCTCT
                                ||||||    |||||||||
                                ATTTAC    CTTTCGAGA
                                   C___
GAM454   STAG2     3'  AAGTATAGAGAAGCTCT     12790       TT
                                AAGTGTA  GGAAGCTCT
                                |||||||  |||||||||
                                TTCATAT  TCTTCGAGA
                                    C_
GAM454   STAT2     3'  TAAGGCAGAAAGCTCT      12791     T   TT
                                TAAG GTA  GGAAGCTCT
                                |||| |||  |||||||||
                                ATTC CGT  CTTTCGAGA
                                  _   __
GAM454   LOC126364 5'  AAGGTCACTGGAAGCTCT    12792     TG
                                AAG  TATTGGAAGCTCT
                                |||  ||||||||||||
                                TTC  GTGACCTTCGAGA
                                  CA
GAM454   LOC145826 5'  TAAATGTAGTACCAGCTCT    12793        T  GA
                                TAAGTGTA TG  AGCTCT
                                ||||||||  ||  ||||||
                                ATTTACAT AT  TCGAGA
                                     C  GG
GAM454   LOC200035 3'  AAGTTGTAGTGAAGCTCT    12794     _   TTG
                                AAGT GTA   GAAGCTCT
                                ||||  |||   ||||||||
                                TTCA CAT   CTTCGAGA
                                  A   CA_
GAM454   LOC202309 5'  AAATGAGTTTGGAAGCTCT    12795      TA_
                                AAGTG   TTGGAAGCTCT
                                |||||   ||||||||||
                                TTTAC   AACCTTCGAGA
                                   TCA
GAM454   LOC51313  3'  TAAATGTATGGTCAGCTCT    12796        T  A_
                                TAAGTGTAT GG  AGCTCT
                                |||||||||  ||  ||||||
                                ATTTACATA CC  TCGAGA
                                      _  AG
GAM455   SNX7      3'  TTCAAGTTGTTGGTTTTCCAGA 12799        TTC  CGG  A
            TG                    TTCAAGTT   GG   TT AGATG
                                ||||||||   ||   || |||||
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                                AAGTTCAA  CC  AG TCTAC
                                     CAA  AAA  G
GAM456  LCHN     3'  AGTTAAAACTGCAGT      12802       ATGAG
                                AGTTGA    GACTGCAGT
                                ||||||    |||||||||
                                TCAATT    TTGACGTCA
                                  _____
GAM456  MGC5338  3'  GTTGGAAGAACAGTATT     12803     AAT    CT
                                GTTG  GAGGA  GCAGTATT
                                ||||  |||||  ||||||||
                                CAAC  CTTCT  TGTCATAA
                                  ___   __
GAM456  LOC200261 3'  AGTGAGTGAGGACTGGGC    12804     T  A       CA
                                AGT GA TGAGGACTG  GT
                                ||| || |||||||||  ||
                                TCA CT ACTCCTGAC  CG
                                  _  C       C_
GAM456  LOC203297 5'  AGGTGGATGAGGGCTGCAGC  12805    T  A     A
                                AG TG ATGAGG CTGCAGT
                                || || |||||| |||||||
                                TC AC TACTCC GACGTCG
                                 C  C     C
GAM457  CBFA2T3   3'  TGTAGTTTTTTTGTTTTT    12808          GATG
                                TGTAGTTTTT    GTTTTT
                                ||||||||||    ||||||
                                ACATCAAAAA    CAAAAA
                                      AA__
GAM457  CENTD1    3'  TCCTGCAGTTTTGTGCTTTTT  12809           T A  G
                                TCCTGTAGTTTT G TG TTTTT
                                |||||||||||| | || |||||
                                AGGACGTCAAAA C AC AAAAA
                                      _ _  G
GAM457  CENTD1    3'  TCCTGCAGTTTTGTGCTTTTT  12809           T A  G
                                TCCTGTAGTTTT G TG TTTTT
                                |||||||||||| | || |||||
                                AGGACGTCAAAA C AC AAAAA
                                      _ _  G
GAM457  NT5E     3'  CCTGTAAAGATGGTTTT     12810        TTTTT
                                CCTGTAG    GATGGTTTT
                                |||||||    |||||||||
                                GGACATT    CTACCAAAA
                                    T____
GAM457  PCDH11X  3'  TGAGATTTTGATGGTTTTT   12811    T  T
                                TG AG TTTTGATGGTTTTT
                                || || ||||||||||||||
                                AC TC AAAACTACCAAAAA
                                 _  T
GAM457  PCDH11X  3'  TGAGATTTTGATGGTTTTT   12811    T  T
                                TG AG TTTTGATGGTTTTT
                                || || ||||||||||||||
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                                AC TC AAAACTACCAAAAA
                                 _ T
GAM457  PCDH11Y  3'  TGAGATTTTGATGGTTTTT   12811    T  T
                                TG AG TTTTGATGGTTTTT
                                || || |||||||||||||
                                AC TC AAAACTACCAAAAA
                                 _ T
GAM457  TRPC5    5'  ATCCTGAGCCAAGTGGTTTTT  12812       T    TTTGA
                                ATCCTG AGTT    TGGTTTTT
                                |||||| ||||    ||||||||
                                TAGGAC TCGG    ACCAAAAA
                                   _   TTC__
GAM457  DKFZP564O1863 3'  CTGTATCTGGTGGTTTTT    12813      GTT    A
                                CTGTA   TTTG TGGTTTTT
                                |||||   |||| ||||||||
                                GACAT   AGAC ACCAAAAA
                                   ___   C
GAM457  KIAA1473  3'  CCTGTAGTTTTTGAATAAATGT 12814            TG____
            TTTT                  CCTGTAGTTTTTGA     GTTTTT
                                |||||||||||||     ||||||
                                GGACATCAAAAACT     CAAAAA
                                      TATTTA
GAM457  PCDH19   3'  CTGTAGTTTTATTATTTTT   12815         TGATG
                                CTGTAGTTTT    GTTTTT
                                |||||||||    ||||||
                                GACATCAAAA    TAAAAA
                                     TAA__
GAM457  SEPT3    3'  TCCTGTAGTTTTGTGATTTT   12816          T A
                                TCCTGTAGTTTT G TGGTTTT
                                |||||||||||| | |||||||
                                AGGACATCAAAA C ACTAAAA
                                      _ _
GAM457  ZNF294   3'  CTGTAATTTAGGGGTTTTT   12817        TTGAT
                                CTGTAGTTT    GGTTTTT
                                |||||||||    |||||||
                                GACATTAAA    CCAAAAA
                                     TCC__
GAM457  LOC126731 3'  CCGTTTCTTTTGATGGTTTTT  12818     AG
                                CTGT  TTTTTGATGGTTTTT
                                ||||  |||||||||||||||
                                GGCA  GAAAACTACCAAAAA
                                  AA
GAM457  LOC148198 3'  CCTGTAGTTTTTGAATAAATGT 12814            TG____
            TTTT                  CCTGTAGTTTTTGA     GTTTTT
                                |||||||||||||     ||||||
                                GGACATCAAAAACT     CAAAAA
                                      TATTTA
GAM457  LOC150421 3'  CTGTGTTTTTGGCTTTT    12819     A    TGA
                                CTGT GTTTT   TGGTTTTT
                                |||| |||||   ||||||||
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                                GACA CAAAA   ACCGAAAA
                                  _    ___
GAM457  LOC245806 3'  CTGTAGTTGTGGTTTTT     12820        TTT  A
                                CTGTAGT   TG TGGTTTTT
                                |||||||   || ||||||||
                                GACATCA   AC ACCAAAAA
                                   ___  _
GAM457  LOC255056 5'  CTGTAGTTTGTGGCC       12821         TT  A
                                CTGTAGTT  TG TGGTT
                                ||||||||  || |||||
                                GACATCAA  AC ACCGG
                                   __  _
GAM458  ATP7A     3'  TGAGTTCAAAAGCATGAATATC 12824        A   A   A
          T                      TGAGTT AAAA TAT GAATATCT
                                ||||||| |||| ||| ||||||||
                                ACTCAA TTTT GTA CTTATAGA
                                   G   C  _
GAM458  BCRP2     3'  TGAGTTAAATGAATATAG     12825         A_
                                TGAGTTAAA  AATATAG
                                |||||||||  |||||||
                                ACTCAATTT  TTATATC
                                     AC
GAM458  MEIS2     3'  TGAGGTAAACACATAGAATATC 12826      T   AA
          T                      TGAG TAAA  ATATAGAATATCT
                                |||| ||||  ||||||||||||||
                                ACTC ATTT  TGTATCTTATAGA
                                  C   G_
GAM458  DKFZp761H079 3'  TGAGTTAAAAAATGTGAAT   12827           ATA
                                TGAGTTAAAAAAT   GAAT
                                ||||||||||||   ||||
                                ACTCAATTTTTTA   CTTA
                                       CA_
GAM458  KR18      3'  TGAGTTAAAAATATATAA     12828          _
                                TGAGTTAAAAA ATATAG
                                |||||||||| ||||||
                                ACTCAATTTTT TATATT
                                     A
GAM458  LOC220074 3'  TGAGTTAGAGAACATC      12829        AAAAATAT
                                TGAGTTA       AGAATATC
                                |||||||       ||||||||
                                ACTCAAT       TCTTGTAG
                                   C________
GAM459  DMRT1     5'  GAGGGATGAACCCGACGGAC   12832         _   TCCA
                                GAGGGATGG CTCG    AC
                                ||||||||| ||||    ||
                                CTCCCTACT GGGC    TG
                                     T   TGCC
GAM459  PPP2R2B   5'  TGGGGAGATGCCCAACA     12833    A   T  CTC
                                TG GGGA GG   GTCCAACA
                                || |||| ||   ||||||||
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                                AC CCCT CT   CGGGTTGT
                                 _   _ A__
GAM459  ZNF215   3' GAGGGATATCTGACAAA     12834       GGCTC   CA
                                GAGGGAT    GTC  ACAAA
                                |||||||    |||  |||||
                                CTCCCTA    TAG  TGTTT
                                    _____  AC
GAM459  ABCC13   3' TGGGGATGGTTCTAATTACAA  12835    A      C  GTCCA
                                TG GGGATGG TC    ACAA
                                || ||||||| ||    ||||
                                AC CCCTACC AG    TGTT
                                 _     A  ATTAA
GAM459  C20orf21 3' TGAGGGACGAGTGGCTGTTCA  12836        ____    C  C
                                TGAGGGA   TGGCT GT CA
                                |||||||   ||||| || ||
                                ACTCCCT   ACCGA CA GT
                                    GCTC    _ A
GAM459  KIAA0397 3' TGGGGATGGCCGAGCAA     12837    A      T  TC
                                TG GGGATGGC CG  CAA
                                || ||||||| ||  |||
                                AC CCCTACCG GC  GTT
                                 _      _ TC
GAM459  KIAA0993 3' TGAGGGATGTCAGACAAA    12838        GGCTC   CA
                                TGAGGGAT    GTC  ACAAA
                                ||||||||    |||  |||||
                                ACTCCCTA    CAG  TGTTT
                                    _____  TC
GAM459  MRPS11   3' TGAAGGATCTCCAACAA     12839       TGGC  G
                                TGAGGGA   TC TCCAACAA
                                |||||||   || ||||||||
                                ACTTCCT   AG AGGTTGTT
                                    ____ _
GAM459  MRPS11   3' TGAAGGATCTCCAACAA     12839       TGGC  G
                                TGAGGGA   TC TCCAACAA
                                |||||||   || ||||||||
                                ACTTCCT   AG AGGTTGTT
                                    ____ _
GAM459  POLA2    5' AAGGGGTGGCTCCCAA      12840      A    GT
                                GAGGG TGGCTC  CCAA
                                ||||| ||||||  ||||
                                TTCCC ACCGAG  GGTT
                                  C     __
GAM459  STX3A    3' TGAGGGATGTTCTCAGGACAA  12841        G_   TCCA
                                TGAGGGATG  CTCG   ACAA
                                |||||||||  ||||   ||||
                                ACTCCCTAC  GAGT   TGTT
                                     AA   CC__
GAM459  LOC152316 3' TGGGGCATGGCTCGTGGCCACA 12842    A  _       __  A
            A                    TG GGG ATGGCTCGT  CCA CAA
                                || ||| |||||||||  ||| |||
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                                AC CCC TACCGAGCA  GGT GTT
                                 _  G       CC  _
GAM459  LOC158427 3'  GGGTGTGGCTGTTCAATAAAC  12843     A_    C  C   C
                                GGG  TGGCT GT CAA AAAC
                                |||  ||||| || ||| ||||
                                CCC  ACCGA CA GTT TTTG
                                  AC    _ A   A
GAM459  LOC204285 3'  TGAGGGATGGCTCGAACC    12844            T_
                                TGAGGGATGGCTCG  CC
                                ||||||||||||||  ||
                                ACTCCCTACCGAGC  GG
                                        TT
GAM460  ITGA11   3'  ACGACAGTAAAGGTC       12847       A CAA
                                ACGATA G   TAAAGGTC
                                ||||||  |   ||||||||
                                TGCTGT C   ATTTCCAG

                                  _ ___
GAM460  RNAHP    3'  TAAACGATAAACAAAAATCAT  12848           TAA
                                TAAACGATAAGCAA   AGGTCAT
                                ||||||||||||||   |||||||
                                ATTTGCTATTTGTT   TTTAGTA

                                       ___
GAM460  LOC122553 3'  TAAATTATAAGCAATAAAA   12849     CG
                                TAAA  ATAAGCAATAAAG
                                ||||  ||||||||||||
                                ATTT  TATTCGTTATTTT
                                  AA
GAM461  DNMT2    3'  GCTTATTTCACTTCGCATAAT  12852     CAGC    AA
                                GCT   TCGCT  TGCATAAT
                                |||   |||||  ||||||||
                                CGA   AGTGA  GCGTATTA
                                  ATAA    A_
GAM461  SLC12A6  3'  GCTCAGCTTGTTAATTCTAAT  12853        CGC    GCA
                                GCTCAGCT   TAAT   TAAT
                                ||||||||   ||||   ||||
                                CGAGTCGA   ATTA   ATTA
                                     ACA    AG_
GAM461  ADAM9    3'  TAGCTCAGTTCCCTGAAGACAT 12854        C  G  _  T
                                TAGCTCAG TC CT AA GCAT
                                |||||||| || || || ||||
                                ATCGAGTC AG GA TT TGTA
                                     A  G  C  C
GAM461  DICER1   3'  CTCAACGTCTAATGCATAAT   12855       TCG
                                CTCAGC   CTAATGCATAAT
                                ||||||   ||||||||||||
                                GAGTTG   GATTACGTATTA
                                   CA_
GAM461  DKFZP434D0127 5'  TAGTCTAGCTGAGAAATGCATA 12856     _  C    CGCT
           AT                    TAG CT AGCT    AATGCATAAT
                                ||| || ||||    ||||||||||
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                                ATC GA TCGA    TTACGTATTA
                                  A _    CTCT
GAM462  ADAM19   3'  ATGCACTTCCTTGCTC      12859       TATT
                                ATGTA    CTTCCTTGCTC
                                |||||    ||||||||||
                                TACGT    GAAGGAACGAG
                                  _____
GAM462  ALDH8A1  3'  CTATGTACTCTTCTTGTTCC   12860         AT    C   C
                                TTATGTAT  TCTTC TTG TCC
                                ||||||||  ||||| ||| |||
                                GATACATG  AGAAG AAC AGG
                                    __    _  A
GAM462  CDKN1B   3'  TCATGTATATCTTCCTTGCT   12861          T
                                TTATGTATAT CTTCCTTGCT
                                |||||||||| ||||||||||
                                AGTACATATA GAAGGAACGA
                                    _
GAM462  DNMT3B   3'  TTATCTAAGCTCCTTGCT    12862      G  TATTC
                                TTAT TA    TTCCTTGCT
                                |||| ||    |||||||||
                                AATA AT    GAGGAACGA
                                  G  TC___
GAM462  FZD10    3'  TTATGTATTTCTCTTTTGCT   12863         A    CC
                                TTATGTAT TTCTT  TTGCT
                                |||||||| |||||  |||||
                                AATACATA AAGAG  AACGA
                                    _    AA
GAM462  HMG20A   3'  ATGAGAATTCTTCCTTGCT    12864     TAT
                                ATG   ATTCTTCCTTGCT
                                |||   ||||||||||||
                                TAC   TAAGAAGGAACGA
                                  TCT
GAM462  MEF2C    5'  TTATGTATTTTTTCCTTCCTT  12865        A___
                                TTATGTAT    TTCTTCCTT
                                ||||||||    |||||||||
                                AATACATA    AGGAAGGAA
                                    AAAA
GAM462  CAMP-GEFII 3'  TTATGCATATTGTGCTC     12866          CTTCCT
                                TTATGTATATT     TGCTC
                                ||||||||||      |||||
                                AATACGTATAA     ACGAG
                                    C_____
GAM462  CARD6    3'  TCATGTATATCTTTCTTTG   12867          TC   C
                                TTATGTATAT  TTC TTG
                                ||||||||||  ||| |||
                                AGTACATATA  AAG AAC
                                    GA   A
GAM462  FLJ10120 3'  TGTAATTCTTCCGGGCT     12868      T       TT
                                TGTA ATTCTTCC  GCT
                                |||| ||||||||  |||
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                                ACAT TAAGAAGG  CGA
                                  _      CC
GAM462  FLJ10781  3'  GTACGTCTTCCTTGTTC     12869      AT       C
                                GTAT  TCTTCCTTG TC
                                ||||  ||||||||| ||
                                CATG  AGAAGGAAC AG
                                  C_       A
GAM462  FLJ22341  3'  TGTGTCTCCCCCCTTGTTC    12870     ATA       C
                                TGT   TTCTTCCTTG TC
                                |||   |||||||||| ||
                                ACA   AGGGGGGAAC AG
                                  CAG        A
GAM462  KIAA1349  3'  TGTATATTCTTCCATACC     12871           T
                                TGTATATTCTTCC TGCT
                                |||||||||||| ||||
                                ACATATAAGAAGG ATGG
                                         T
GAM462  KIAA1918  3'  TTATTTATATTCTTATGTGCT  12872      G       CCT
                                TTAT TATATTCTT   TGCT
                                |||| |||||||||   ||||
                                AATA ATATAAGAA   ACGA
                                  A        TAC
GAM462  NYD-SP27  5'  CTATGGTGATTCTTCCTTG    12873      TAT
                                TTATG   ATTCTTCCTTG
                                |||||   ||||||||||
                                GATAC   TAAGAAGGAAC
                                   CAC
GAM462  p25       3'  GTCCATTTTTCCTTGCTC     12874    A   C
                                GT TATT TTCCTTGCTC
                                || |||| ||||||||||
                                CA GTAA AAGGAACGAG
                                 G   A
GAM462  PRO1596   3'  TTATGTGGGTGCTTTTGCTCC  12875       ATATT   CC
                                TTATGT    CTT  TTGCTCC
                                ||||||    |||  |||||||
                                AATACA    GAA  AACGAGG
                                   CCCAC   __
GAM462  LOC135138 3'  TTATGTATTGGAAAGCCTTGCT 12876        ATTCTT_
          C                      TTATGTAT      CCTTGCTC
                                 ||||||||      ||||||||
                                 AATACATA      GGAACGAG
                                     ACCTTTC
GAM462  LOC149146 3'  ATGTTAATTTCCTTGCT     12877      A  TTC
                                ATGT TA   TTCCTTGCT
                                |||| ||   |||||||||
                                TACA AT   AAGGAACGA
                                  _ TA_
GAM462  LOC157306 3'  TGTAACACATTCCTTGCTCC   12878      _   TC
                                TGTA TAT  TTCCTTGCTCC
                                |||| |||  ||||||||||
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                                ACAT GTG  AAGGAACGAGG
                                  T  T_
GAM462  LOC221017 5'  TGTATATTCTAGTTGCT     12879          TCC
                                TGTATATTCT  TTGCT
                                ||||||||||  |||||
                                ACATATAAGA  AACGA
                                     TC_
GAM463  FABP3    3'  TGAGTCGAGGGGTAGCCGATTG 12882         CA__   ACA  C
          G                      TGAGTCGAG   GGCC  GA TGG
                                |||||||||   ||||  || |||
                                ACTCAGCTC   TCGG  CT ACC
                                     CCCA   ___  A
GAM463  HDAC4    3'  TGAGTCGAGTGGTTTACACAG  12883         CA  C___
                                TGAGTCGAG  GG   CACAG
                                |||||||||  ||   |||||
                                ACTCAGCTC  CC   GTGTC
                                     A_  AAAT
GAM463  LZTR1    3'  GAGCAGGGTTGCAGACTGG   12884        CCA_
                                GAGCAGG   CAGACTGG
                                |||||||   ||||||||
                                CTCGTCC   GTCTGACC
                                    CAAC
GAM463  FLJ11896  3'  TGAGTCAGTCGCAACAGACTGG 12885       G  CAG  C
                                TGAGTC AG  GC ACAGACTGG
                                |||||| ||  || |||||||||
                                ACTCAG TC  CG TGTCTGACC
                                   _  AG_  T
GAM463  GPS2     5'  TGAGCGACGACGGCTGCAGACT 12886     T  GCA_  CA
          GG                     TGAG CGA   GGC  CAGACTGG
                                |||| |||   |||  ||||||||
                                ACTC GCT   CCG  GTCTGACC
                                  _  GCTG  AC
GAM463  SFXN5    3'  TGAGATGCTGAGGCCACAGGCT 12887     TCGA __       A
          GG                     TGAG   GC  AGGCCACAG CTGG
                                ||||   ||  ||||||||| ||||
                                ACTC   CG  TCCGGTGTC GACC
                                  TA__  AC       C
GAM463  LOC123591 3'  AAGCTGGGCCACAGGCTGG   12888     A_      A
                                GAGC  GGCCACAG CTGG
                                ||||  |||||||| ||||
                                TTCG  CCGGTGTC GACC
                                  AC       C
GAM463  LOC91759  3'  TGAGTTGGCCAGGCCACTCTG  12889      CGAG      AGA
                                TGAGT   CAGGCCAC   CTG
                                |||||   ||||||||  |||
                                ACTCA   GTCCGGTG   GAC
                                  ACCG      A__
GAM464  ALPPL2   3'  GTGCTGGAATGGACCTTAG   12892       G   _  A
                                GTGCTGG AGTGG CTT AG
                                ||||||| ||||| ||| ||
```

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                                CACGACC TTACC GGA TC
                                    _    T  A
GAM464  ATP1A2   3' AGGCTGGGGTGATCTGAGAG  12893   T    A  GC  A
                                AG GCTGGG GTG  TT AGAG
                                || |||||| |||  || ||||
                                TC CGACCC CAC  GA TCTC
                                 _    _  TA  C
GAM464  COL10A1  5' GTGCTGGGAGTTCCTGGAG   12894        GG  AA
                                GTGCTGGGAGT  CTT  GAG
                                ||||||||||  |||  |||
                                CACGACCCTCA  GGA  CTC
                                      A_  C_
GAM464  KIR2DL1  3' TAAGTGCTGCGTTAAG     12895       GGGAGTG  _
                                TAAGTGCT     GC TTAAG
                                ||||||||     || |||||
                                ATTCACGA     CG AATTC
                                   ________ C
GAM464  KIR2DL2  3' TAAGTGCTGCGTTAAG     12895       GGGAGTG  _
                                TAAGTGCT     GC TTAAG
                                ||||||||     || |||||
                                ATTCACGA     CG AATTC
                                   ________ C
GAM464  LOXL3    5' TAAGGGCTGGGAGAAG     12896    T      TGGCTT
                                TAAG GCTGGGAG     AAG
                                |||| ||||||||     |||
                                ATTC CGACCCTC     TTC
                                  C       _______
GAM464  PSMC4    3' GTGCTGGGGGTGCGAGAG    12897       A  G TTA
                                GTGCTGGG GTG C   AGAG
                                |||||||| ||| |   ||||
                                CACGACCC CAC G   TCTC
                                    C   _ C__
GAM464  SORCS3   3' GTGCTGGGGGAAGCGGAGAG  12898       ___    CTTA
                                GTGCTGGG   AGTGG    AGAG
                                ||||||||   |||||    ||||
                                CACGACCC   TCGCC    TCTC
                                    CCT    ____
GAM464  VAMP1    3' AGGGCTGGGAGAGCCAAGAG  12899    T      T   T
                                AG GCTGGGAG GGCT AAGAG
                                || |||||||| |||| |||||
                                TC CGACCCTC TCGG TTCTC
                                 C      _   _
GAM464  AMOTL1   3' AGGGCTGGGGGTGGGTGAGGAG 12900    T    A   CTTAA
                                AG GCTGGG GTGG    GAG
                                || |||||| ||||    |||
                                TC CGACCC CACC    CTC
                                 C    C   CACTC
GAM464  BRPF3    3' AAGTGTTGGGGGGAAGA    12901      C   AGT  CTT
                                AAGTG TGGG   GG   AAGA
                                ||||| ||||   ||   ||||
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                                TTCAC ACCC   CC   TTCT
                                  A    C__  ___
GAM464  C20orf150 3'  GTGCTGGGGGTGCTGGCAGGAG 12902        A  ___   TTAA
                                GTGCTGGG GT   GGC    GAG
                                |||||||| ||   |||    |||
                                CACGACCC CA   CCG    CTC
                                    C  CGA   TC__
GAM464  CCR1     3'  AGTGTCTCCCATGGCTTAGGAG 12903     _  GGGA       A
                                AGTG CT    GTGGCTTA GAG
                                |||| ||    |||||||| |||
                                TCAC GA    TACCGAAT CTC
                                  A  GGG_       C
GAM464  CREG     3'  GTGGAGAGTGGTTTGGGA    12904     CT       C  AA
                                GTG  GGGAGTGG TT  GA
                                |||  |||||||| ||  ||
                                CAC  CTCTCACC AA  CT
                                 __       A  CC
GAM464  CRMP5    3'  AGTGCTGGGAGTGATCA     12905            C
                                AGTGCTGGGAGTGG TTA
                                |||||||||||||| |||
                                TCACGACCCTCACT AGT
                                                _
GAM464  FLJ11320 3'  GTGCTGGGAGACCAGAG     12906          TG   TA
                                GTGCTGGGAG  GCT  AGAG
                                |||||||||  |||  ||||
                                CACGACCCTC  TGG  TCTC
                                          __   __
GAM464  FLJ20489 3'  GTGCTGGGATGGGGGTTTAAGA 12907         GT__  C
           G                     GTGCTGGGA    GG TTAAGAG
                                |||||||||    || |||||||
                                CACGACCCT    CC AATTCTC
                                     ACCC  A
GAM464  KIAA0830 3'  AAGTTATTAGTGGCTTGGGAG  12908      GCTGGG       AA
                                AAGT     AGTGGCTT  GAG
                                ||||     ||||||||  |||
                                TTCA     TCACCGAA  CTC
                                  ATAA__       CC
GAM464  KIAA1727 3'  AAGTGCTGGGAGCACACAAAGA 12909            _  TT
           G                     AAGTGCTGGGAGTG GC  AAGAG
                                |||||||||||||| ||  |||||
                                TTCACGACCCTCGT TG  TTCTC
                                       G  T_
GAM464  PLAGL2   3'  GTGCTGAGGACACTGAGAG   12910        AGT   TTA_
                                GTGCTGGG   GGC    AGAG
                                ||||||||   |||    ||||
                                CACGACTC   CTG    TCTC
                                    ___   TGAC
GAM464  PRDM14   5'  AGGGCTGAGCCAGGCTTAAGAG 12911    T     AGT
                                AG GCTGGG   GGCTTAAGAG
                                || ||||||   ||||||||||
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                                TC CGACTC   CCGAATTCTC
                                 C     GGT
GAM464  SEPT3    3'  TAAGTGCTGGGATTCATAGAG  12912          GTGGCTTA
                                TAAGTGCTGGGA       AGAG
                                ||||||||||||       ||||
                                ATTCACGACCCT       TCTC
                                      AAGTA___
GAM464  LOC146272 5'  CAAGCCAAGGGGTGGCTTA    12913      GCT   A
                                TAAGT   GGG GTGGCTTA
                                |||||   ||| ||||||||
                                GTTCG   CCC CACCGAAT
                                   GTT   _
GAM464  LOC151414 3'  GTGCCTGGCTTAAGA       12914      GGGAG
                                GTGCT    TGGCTTAAGA
                                |||||    ||||||||||
                                CACGG    ACCGAATTCT
                                  _____
GAM464  LOC153894 5'  GTGCTGGGGGTCCTGGAG    12915        AGT  _   AA
                                GTGCTGGG   GG CTT  GAG
                                ||||||||   || |||  |||
                                CACGACCC   CC GGA  CTC
                                    ___  A   C_
GAM464  LOC255040 3'  TGCTGGGGGCTCGGGAG     12916       AGT    AA
                                TGCTGGG   GGCTT  GAG
                                |||||||   |||||  |||
                                ACGACCC   CCGAG  CTC
                                   ___    CC
GAM464  LOC255041 3'  TGCTGGGGGCTCGGGAG     12916       AGT    AA
                                TGCTGGG   GGCTT  GAG
                                |||||||   |||||  |||
                                ACGACCC   CCGAG  CTC
                                   ___    CC
GAM465  BARX2    5'  CCGGCCCGAGCGCGGCTGCGA  12919    A  G    __   CCACC
                                CC GC CGAGC  GGTT    GCGA
                                || || |||||  ||||    ||||
                                GG CG GCTCG  CCGA    CGCT
                                 C  G    CG   _____
GAM465  CACNA1A  3'  GCGGCGGCCCCGCCGCG     12920     A      A
                                GCG GCGGTTCC CCGCG
                                ||| |||||||| |||||
                                CGC CGCCGGGG GGCGC
                                  _       C
GAM465  CDC34    5'  CCGCGCGACCACCGC       12921     A     GCGGTT
                                CC GCGCGA     CCACCGC
                                || ||||||     |||||||
                                GG CGCGCT     GGTGGCG
                                  _    _______
GAM465  CLCN4    5'  CAGCGCGACGGCTGC       12922         G    CCACC
                                CAGCGCGA CGGTT    GC
                                |||||||| |||||    ||
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                                GTCGCGCT GCCGA    CG
                                  _   _____
GAM465  CUL3    5'  GCGCGGCGGCTCCGCG      12923      A      ACC
                                GCGCG GCGGTTCC   GCG
                                ||||| ||||||||   |||
                                CGCGC CGCCGAGG   CGC
                                  _     ___
GAM465  HAGH    5'  CCAGCGCGGCGAGGCTGCG   12924       A   TTCCACC
                                CCAGCGCG GCGG     GCG
                                |||||||| ||||     |||
                                GGTCGCGC CGCT     CGC
                                   _   CCGA___
GAM465  ITPKA   3'  CAGGTGAGCGGCCCGCG    12925    CGC     TCCA
                                CAG   GAGCGGT   CCGCG
                                |||   |||||||   |||||
                                GTC   CTCGCCG   GGCGC
                                  CA_     ____
GAM465  MAP4K2  5'  CCGGCGCGGGGCGGCGCG   12926   A   A_   TTCCAC
                                CC GCGCG  GCGG    CGCG
                                || |||||  ||||    ||||
                                GG CGCGC  CGCC    GCGC
                                 C    CC   _______
GAM465  MFI2    3'  CAGCGCGAGAGGCCGCCGCG  12927       C  TT  A
                                CAGCGCGAG GG  CC CCGCG
                                ||||||||| ||  || |||||
                                GTCGCGCTC CC  GG GGCGC
                                     T  __  C
GAM465  MYO5A   5'  GCCGCGAGCAGCCGCG     12928   _      TTCCA
                                GC GCGAGCGG    CCGCG
                                || ||||||||    |||||
                                CG CGCTCGTC    GGCGC
                                 G      _____
GAM465  NCK2    3'  CCGGGCGGGCAGCTCCACCG  12929   AGC   A
                                CC   GCG GCGGTTCCACCG
                                ||   ||| ||||||||||||
                                GG   CGC CGTCGAGGTGGC
                                 CC_   C
GAM465  PCNA    5'  CAGAGCGAGCGGGCGAACGTCG 12930    C      TTCC __
          CGA                     CAG GCGAGCGG    AC  CGCGA
                                ||| ||||||||   ||  |||||
                                GTC CGCTCGCC    TG  GCGCT
                                  T       CGCT  CA
GAM465  PITX1   3'  CCAGCGCGGCGGGGGGCGCG   12931       A   TTCCAC
                                CCAGCGCG GCGG     CGCG
                                |||||||| ||||     ||||
                                GGTCGCGC CGCC     GCGC
                                   _   CCC___
GAM465  POU4F1  5'  GCGGCGGCCCCCGCCGCG    12920    A      A
                                GCG GCGGTTCC CCGCG
                                ||| |||||||| |||||
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                                CGC CGCCGGGG GGCGC
                                  _      C
GAM465  VEGF     5'  CAGCGCGACTGGTCAGCTGCG  12932        GC   CCACC
                                CAGCGCGA  GGTT    GCG
                                ||||||||  ||||    |||
                                GTCGCGCT  CCAG    CGC
                                    GA    TCGA_
GAM465  ARF6     5'  CCGCGCGAGCGCCGCCGCG   12933    A       GTT  A
                                CC GCGCGAGCG   CC CCGCG
                                || |||||||||   || |||||
                                GG CGCGCTCGC   GG GGCGC
                                  _       ___ C
GAM465  ARHU     5'  AGCGCGGGCTTGCGGTCGCG   12934       A____    TCCAC
                                AGCGCG    GCGGT    CGCG
                                ||||||    |||||    ||||
                                TCGCGC    CGCCA    GCGC
                                   CCGAA    _____
GAM465  CAC-1    5'  CAGCGCGGCTCCCGAGGCTGCG 12935     GCGA      ACC____
                                CAGC   GCGGTTCC      GCG
                                ||||   ||||||||      |||
                                GTCG   CGCCGAGG      CGC
                                  ____       GCTCCGA
GAM465  CTNNBIP1 5'  CAGCCCGAGCAGCCGC      12936     G     TTCCA
                                CAGC CGAGCGG    CCGC
                                |||| |||||||    ||||
                                GTCG GCTCGTC    GGCG
                                  G     _____
GAM465  DKFZP434B205 3'  CCAGCACGGGCCCTGCCG    12937        AGC    CA
                                CCAGCGCG   GGTTC  CCG
                                ||||||||   |||||  |||
                                GGTCGTGC   CCGGG  GGC
                                    ___    AC
GAM465  DKFZP564I1171 5'  CCAGCGCGTGCGGCGGTGCG   12938        A    TCCACC
                                CCAGCGCG GCGGT     GCG
                                |||||||| |||||     |||
                                GGTCGCGC CGCCG     CGC
                                    A    CCA___
GAM465  FLJ10853  5'  GCGGTGCGGTGACTCCACCGCG 12939     CGA    ___
                                GCG   GCGGT   TCCACCGCG
                                |||   |||||   |||||||||
                                CGC   CGCCA   AGGTGGCGC
                                  CA_    CTG
GAM465  KIAA1615  5'  CAGCGCGGGGCCACCTCACCGC 12940       A_  G  TC
           GA                    CAGCGCG  GC GT  CACCGCGA
                                ||||||||  || ||  ||||||||
                                GTCGCGC  CG TG  GTGGCGCT
                                    CC  G  GA
GAM465  MDS025   5'  CCAGCGCAGGCGCCACCG    12941        A   GTT
                                CCAGCGCG GCG   CCACCG
                                |||||||| |||   ||||||
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                                GGTCGCGT CGC   GGTGGC
                                     C  ___
GAM465  MGC14386 5' CCGGCGCGCAGCACCGCG    12942    A   GA   TTC
                                CC GCGC  GCGG   CACCGCG
                                || ||||  ||||   |||||||
                                GG CGCG  CGTC   GTGGCGC
                                 C   __   ___
GAM465  MGC14801 5' CCAGTGCGGCGAGCGCCGCGA  12943     C   A   _  TCCA
                                CCAG GCG GCG GT    CCGCGA
                                |||| ||| ||| ||    ||||||
                                GGTC CGC CGC CG    GGCGCT
                                  A   _   T  C___
GAM465  MGC15730 5' GCGCGCGGTGCCCACCGCG   12944     GA    _
                                GCGC  GCGGT TCCACCGCG
                                ||||  ||||| |||||||||
                                CGCG  CGCCA GGGTGGCGC
                                  __    C
GAM465  NIN      5' CCGGCTCGGGCGGCCGCG    12945    A  G  A    TTCCA
                                CC GC CG GCGG    CCGCG
                                || || || ||||    |||||
                                GG CG GC CGCC    GGCGC
                                 C  A  C   ______
GAM465  RHOBTB3   5' CGCGCGCCTCCACCGCG     12946     GA   G
                                CGC  GCG TTCCACCGCG
                                |||  ||| ||||||||||
                                GCG  CGC GAGGTGGCGC
                                  __   G
GAM465  LOC124512 5' GCGCGAGCGGGAAGCCGCG   12947          TTCCA
                                GCGCGAGCGG    CCGCG
                                ||||||||||    |||||
                                CGCGCTCGCC    GGCGC
                                      CTTC_
GAM465  LOC147837 5' CCAGTGCGGGTCCCAC      12948      C   AGC
                                CCAG GCG   GGTTCCAC
                                |||| |||   ||||||||
                                GGTC CGC   CCAGGGTG
                                  A   ___
GAM465  LOC153474 5' CCAGCGCGTGCGGCGGTGCG   12938         A    TCCACC
                                CCAGCGCG GCGGT     GCG
                                |||||||| |||||     |||
                                GGTCGCGC CGCCG     CGC
                                     A    CCA___
GAM465  LOC220081 5' CCGCGCGTGCATCCACCGCGA  12949    A    A   GT
                                CC GCGCG GCG  TCCACCGCGA
                                || ||||| |||  ||||||||||
                                GG CGCGC CGT  AGGTGGCGCT
                                 _    A   __
GAM465  LOC221069 5' GCGAGCAGATTTTCCGCCGTGA 12950         ___    A   C
                                GCGAGCGG   TTCC CCG GA
                                ||||||||   |||| ||| ||
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                                CGCTCGTC  AAGG GGC CT
                                    TAA   C  A
GAM465  LOC255426 5'  CCGGTGCGAGCCTCGGCGCCGC 12951   AGC    ___  TCCA
          G                      CC  GCGAGC  GGT   CCGCG
                                 ||  ||||||  |||   |||||
                                 GG  CGCTCG  CCG   GGCGC
                                  CCA    GAG  C___
GAM466  LAPTM5   3'  TGACTGAACTAACCTGTGGG  12954    _ GG __
                                 TGAC G  TT  CCTGTGGG
                                 |||| |  ||  ||||||||
                                 ACTG C  GA  GGACACCC
                                   A TT  TT
GAM466  PPT2     3'  ACCCCTGTGGTGGGCAGGGGGT 12955     AA  AC   TCCT_
          GGG                     ACCCC  TG  GGGT   GTGGG
                                 |||||  ||  ||||    |||||
                                 TGGGG  AC  CCCG    CACCC
                                    AC  CA   TCCCC
GAM466  PPT2     3'  ACCCCTGTGGTGGGCAGGGGGT 12955     AA  AC   TCCT_
          GGG                     ACCCC  TG  GGGT   GTGGG
                                 |||||  ||  ||||    |||||
                                 TGGGG  AC  CCCG    CACCC
                                    AC  CA   TCCCC
GAM466  SBF1     5'  ACCCCAATGATGAAGGGCGTGG 12956       C___   TCCT
          G                      ACCCCAATGA   GGGT   GTGGG
                                 ||||||||||   ||||   |||||
                                 TGGGGTTACT   CCCG   CACCC
                                      ACTT   _____
GAM466  SYNGR1   3'  CCCCCAGTGTCCTGTGG    12957    AATGA   GT
                                 CCCC    CGG  TCCTGTGG
                                 ||||    |||  ||||||||
                                 GGGG    GTC  AGGACACC
                                   _____   AC
GAM466  TYRO3    3'  CCCCGATGCCCTCTGCCTGTGG 12958    A   ACGGGTT
          G                      CCCC ATG     CCTGTGGG
                                 |||| |||     ||||||||
                                 GGGG TAC     GGACACCC
                                   C   GGGAGAC
GAM466  ARP5     3'  CCACAGTGGGAAGTTCTGTGGG 12959   C  A  AC    C
                                 CC CA TG  GGGTTC TGTGGG
                                 || || ||  |||||| ||||||
                                 GG GT AC  TTCAAG ACACCC
                                  T  C  CC    _
GAM466  BCL2L1   3'  ACCCTGTGATGGGCAGGTGGG  12960    CAA  C   TCCT
                                 ACCC   TGA GGGT   GTGGG
                                 ||||   ||| ||||   |||||
                                 TGGG   ACT CCCG   CACCC
                                   AC_   A   TC__
GAM466  CD36L1   3'  CCCCTGTGGTCAGGCCTGTGGG 12961    AA  A_   TT
                                 CCCC  TG  CGGG  CCTGTGGG
                                 ||||  ||  ||||  ||||||||
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                                GGGG  AC  GTCC  GGACACCC
                                  AC  CA   __
GAM466  ENDO180  3' CCTACCTCTGGTTCCTGTGGG  12962    A  GACG
                                CC AT   GGTTCCTGTGGG
                                || ||   ||||||||||||
                                GG TG   CCAAGGACACCC
                                 A  GAGA
GAM466  FLJ10350 3' ACTCCACTGAGGCTCCTGTGGG 12963    C   A   CG
                                AC CCA TGA  GGTTCCTGTGGG
                                || ||| |||  ||||||||||||
                                TG GGT ACT  CCGAGGACACCC
                                 A  G  __
GAM466  FLJ11743 3' CCTCGAGGGTCCCTGTGG    12964    AA   C
                                CC  TGA GGGTTCCTGTGG
                                ||  ||| ||||||||||||
                                GG  GCT CCCAGGGACACC
                                 A_  _
GAM466  FLJ12700 3' ACCTCAGAGTTCCTGTGG    12965    C  ATGAC
                                ACC CA    GGGTTCCTGTGG
                                ||| ||    ||||||||||||
                                TGG GT    CTCAAGGACACC
                                 A _____
GAM466  HPCAL4   3' CCCTGTGACAGGCCTGTGGG   12966    AA     TT
                                CCC  TGACGGG  CCTGTGGG
                                |||  |||||||  ||||||||
                                GGG  ACTGTCC  GGACACCC
                                  AC     __
GAM466  KIAA0125 3' CCCCATGGTGGCAGGGGTGGG  12967     A  ACG   TCCT
                                CCCCA TG   GGT   GTGGG
                                ||||| ||   |||   |||||
                                GGGGT AC   CCG   CACCC
                                   _ CA_   TCCC
GAM466  KIAA0775 3' ACCCCAAAGGCAGCCTGTGGG  12968       TGAC   T_
                                ACCCCAA   GGGT  CCTGTGGG
                                |||||||   ||||  ||||||||
                                TGGGGTT   TCCG  GGACACCC
                                    _____   TC
GAM466  KIAA0978 3' CCAAATGATCCTGTGG     12969    C    CGGGT
                                CC AATGA    TCCTGTGG
                                || |||||    ||||||||
                                GG TTACT    AGGACACC
                                 T   _____
GAM466  MGC10902 3' CCCTGAGGGGGCCTGTGG    12970    AA   C   TT
                                CCC  TGA GGG  CCTGTGG
                                |||  ||| |||  |||||||
                                GGG  ACT CCC  GGACACC
                                  __  _  CC
GAM466  PRKWNK4  3' CCATGGTGGGCCCTGGTGTGGG 12971    A  AC     C__
                                CCA TG  GGGTTC   TGTGGG
                                ||| ||  ||||||   ||||||
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                                GGT AC  CCCGGG   ACACCC
                                  _ CA     ACC
GAM466  LOC144817 3'  ACCCTGTGATGGGTTTATG   12972     CAA   C    CC
                                ACCC   TGA GGGTT  TGTG
                                ||||   ||| |||||  ||||
                                TGGG   ACT CCCAA  ATAC
                                  AC_   A    __
GAM466  LOC146333 5'  CCCATGGCTCTGGTTGTGGG   12973     ATGACG    C___
                                CCCA     GGTTC    TGTGGG
                                ||||     |||||    ||||||
                                GGGT     CCGAG    ACACCC
                                  A_____     ACCA
GAM466  LOC158310 5'  ACCCTGAGACGGGTTTGG    12974     CAAT      CCTG
                                ACCC    GACGGGTT    TGG
                                ||||    ||||||||    |||
                                TGGG    CTGCCCAA    ACC
                                  ACT_       _____
GAM466  LOC203246 3'  CCCTGTGAAAAGTCCTGTGGG  12975     AA   CG   T
                                CCC  TGA  GGT CCTGTGGG
                                |||  |||  ||| ||||||||
                                GGG  ACT  TCA GGACACCC
                                  AC   TT   _
GAM466  LOC256117 3'  ACCCCAATCATGTTTGTGG    12976       GACGG   CC
                                ACCCCAAT    GTT  TGTGG
                                ||||||||    |||  |||||
                                TGGGGTTA    CAA  ACACC
                                    GTA__   __
GAM466  LOC56926  5'  CCCTGAGGTCCTGTG      12977     AA   CG   T
                                CCC  TGA  GGT CCTGTG
                                |||  |||  ||| ||||||
                                GGG  ACT  CCA GGACAC
                                  __   __   _
GAM466  LOC91250  5'  ACTCCAATGACGGCTGG     12978    C       GTTC   T
                                AC CCAATGACGG    CTG G
                                || ||||||||||    ||| |
                                TG GGTTACTGCC    GAC C
                                 A        _____   _
GAM466  LOC91661  3'  CCCCACTGGTGGGTCCCTGGG  12979      A  AC       T
                                CCCCA TG  GGGTTCCTG GG
                                |||||  ||  |||||||||  ||
                                GGGGT AC  CCCAGGGAC CC
                                   G  CA       _
GAM466  LOC91963  5'  CCAGTGAGGCCTGTGG      12980     A   C  GTT
                                CCA TGA GG   CCTGTGG
                                ||| ||| ||   |||||||
                                GGT ACT CC   GGACACC
                                  C   _  ____
GAM467  BLP1      3'  GTGTGTTCCACGTCGCTG    12983     C      GTCC   C
                                GTG GTTCCACG    TTGC TG
                                ||| ||||||||    |||| ||
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                                CAC CAAGGTGC    AGCG AC
                                  A      ____   _
GAM467  CNOT8    5'  GTGCGTGTTCGCTCTGCCTGT  12984      TCCA  G  CT
                                GTGCGT    CG TC  TGCCTGT
                                ||||||    || ||  |||||||
                                CACGCA    GC AG  ACGGACA
                                   CAA_  G  __
GAM467  KIAA0179 3'  GTGCCTTCCGCCCGTGTTTGT  12985     G    ACG    T  CC
                                GTGC TTCC   GTCC TG  TGT
                                |||| ||||   |||| ||  |||
                                CACG AAGG   CGGG AC  ACA
                                  G    ___    C  AA
GAM467  LOC146176 5'  GTGCGTTCATTTCTGCTTG   12986       CACGG  CT   C
                                GTGCGTTC     TC  TGC TG
                                ||||||||     ||  ||| ||
                                CACGCAAG     AG  ACG AC
                                     TAA__  __   A
GAM468  CHST6    3'  CACCTTTGGAAGCCTAAAAC   12989       A    ACCTCCT
                                CACCTTTG AAGC      AAC
                                |||||||| ||||      |||
                                GTGGAAAC TTCG      TTG
                                     C    GATT___
GAM468  FLJ21459  3'  CACCTTTGAAGGACTCACCC   12990         AG___
                                CACCTTTGAA     CACCT
                                ||||||||||     |||||
                                GTGGAAACTT     GTGGG
                                      CCTGA
GAM468  FLJ21870  3'  CACCTTTGAAAGCCTCC     12991           AC
                                CACCTTTGAAAGC  CTCC
                                ||||||||||||  ||||
                                GTGGAAACTTTCG  GAGG
                                              __
GAM468  FLJ32783  3'  CCCTTGAAGGGCTTCTTCTAA  12992        A_  AC  C
                                CCTTTGAA  GC  CT CTAA
                                ||||||||  ||  || ||||
                                GGGAACTT  CG  GA GATT
                                     CC  AA  A
GAM468  PRO1489   3'  ACCGACAAGGCACCTCCT    12993     TT   AA
                                ACC  TGA  GCACCTCCT
                                |||  |||  |||||||||
                                TGG  GTT  CGTGGAGGA
                                  CT   C_
GAM468  LOC145757 5'  CAACTTTCTAACACTTCCTAAC 12994    C    GAA    C
          G                      CA CTTT   AGCAC TCCTAACG
                                 || ||||   ||||| ||||||||
                                 GT GAAA   TTGTG AGGATTGC
                                  T   GA_    A
GAM468  LOC254944 3'  CTTTGAAAATGTCCTAA     12995         CACC
                                CTTTGAAAG    TCCTAA
                                |||||||||    ||||||
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                                GAAACTTTT   AGGATT
                                    AC__
GAM468  LOC256865 5'  CACCTTGAAATCCTA      12996      T   GCACC   A
                                CACCTT GAAA    TCCT A
                                |||||| ||||    |||| |
                                GTGGAA CTTT    AGGA T
                                  _   _____   C
GAM468  LOC57862  3'  CTTGAAAACTCAACTTCCT   12997        ___  C
                                TTTGAAAGC   AC TCCT
                                |||||||||   || ||||
                                GAACTTTTG   TG AGGA
                                    AGT  A
GAM469  CRY2      3'  GATGGTGGAGAAGTAG     13000     A   AC  C
                                GAT GTG  GA GAAGTAG
                                ||| |||  || |||||||
                                CTA CAC  CT CTTCATC
                                  C  __ _
GAM469  GABRR1    3'  GATAGTGAAAACATGGGTGGG  13001       C   AA_  A
                                GATAGTGA GACG   GT GG
                                |||||||| ||||   || ||
                                CTATCACT TTGT   CA CC
                                    T   ACC  C
GAM469  KIAA1887  5'  GACGAAGTGATGAGGAGTGGG  13002      T    C  C  A  A
                                GACGA AGTGA GA GA GT GG
                                ||||| ||||| || || || ||
                                CTGCT TCACT CT CT CA CC
                                  _    A  C  _  C
GAM469  MGC3265   3'  GATATGGTGACGACTATTCAGG 13003     __      GAAG
                                GATA  GTGACGAC    TAGG
                                ||||  ||||||||    ||||
                                CTAT  CACTGCTG    GTCC
                                  AC       ATAA
GAM469  ZNF213    3'  GACGTTAGTGACAATGGAGTGG 13004      A       CGA   A
          G                      GACG TAGTGACGA   AGT GG
                                |||| |||||||||   ||| ||
                                CTGC ATCACTGTT   TCA CC
                                  A       ACC   C
GAM469  LOC123036 3'  GATGATAATGATGTTTCAGAGT 13005    C       CGA__  A
          AGG                    GA GATAGTGA     CG AGTAGG
                                || ||||||||     || ||||||
                                CT CTATTACT     GT TCATCC
                                 A       ACAAA  C
GAM470  AKAP1     5'  TAATTACACCTTGCTG      13008     C       TA
                                TGA TACACCTT  GCTG
                                ||| ||||||||  ||||
                                ATT ATGTGGAA  CGAC
                                  A       __
GAM470  EGFL5     5'  TGATACATCAGCTAAAGCTGAA 13009     C   C___  TT
                                TGA TACA    CT  AGCTGAA
                                ||| ||||    ||  |||||||
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                                ACT ATGT   GA  TCGACTT
                                  _   AGTC  TT
GAM470  KCNJ6    3'  TGACACACCTTTTTGA     13010     T      AGC
                                TGAC ACACCTTT   TGA
                                |||| ||||||||   |||
                                ACTG TGTGGAAA   ACT
                                  _      A__
GAM470  MAN1A1   3'  TACACCTTCATGAAAT      13011         GC
                                TACACCTTTA  TGAAAT
                                ||||||||||  ||||||
                                ATGTGGAAGT  ACTTTA
                                           __
GAM470  MRC1     3'  TGACTACATTTTTATGCCA    13012        CC   _
                                TGACTACA  TTTA GCTG
                                ||||||||  |||| ||||
                                ACTGATGT  AAAT CGGT
                                     AA    A
GAM470  C1orf17  3'  TGACTACATATTTGCTGA    13013        CC   A
                                TGACTACA  TTT GCTGA
                                ||||||||  ||| |||||
                                ACTGATGT  AAA CGACT
                                     AT   _
GAM470  DKFZp434E2220 5'  TGATGGTACCTTTAGTGAA    13014     CTAC      C
                                TGA   ACCTTTAG TGAA
                                |||   |||||||| ||||
                                ACT   TGGAAATC ACTT
                                  ACCA       _
GAM470  DKFZP564D172 3'  TGGCCACATCTTAGCTG     13015    A    CC
                                TG CTACA  TTTAGCTG
                                || |||||  ||||||||
                                AC GGTGT  GAATCGAC
                                 C    A_
GAM470  EFA6R    3'  TGACTCACTGCTGAAA      13016      A   CTTTA
                                TGACT CAC    GCTGAAA
                                ||||| |||    |||||||
                                ACTGA GTG    CGACTTT
                                   _  A____
GAM470  FLJ10774 3'  TGACTCTGCCTTTAGCCA    13017      ACA
                                TGACT   CCTTTAGCTG
                                |||||   ||||||||||
                                ACTGA   GGAAATCGGT
                                   GAC
GAM470  FLJ13154 3'  TGGCTACACCTCCTGCCA    13018    A       TA
                                TG CTACACCTT  GCTG
                                || |||||||||  ||||
                                AC GATGTGGAG  CGGT
                                 C        GA
GAM470  FLJ20055 3'  ACTGCACCTTTAAGCATAA   13019     A      _ _
                                ACT CACCTTTA GC TGA
                                ||| |||||||| || |||
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                                TGA GTGGAAAT CG ATT
                                  C       T  T
GAM470  FLJ32894  3'  ACTGCAGGCCTTAGCTGA    13020     A  C_
                                ACT CA  CTTTAGCTGA
                                ||| ||  ||||||||||
                                TGA GT  GGAATCGACT
                                  C  CC
GAM470  KIAA0266  3'  TGACTACATCCTCAGGAA    13021        C     CT
                                TGACTACA CTTTAG  GAA
                                |||||||| ||||||  |||
                                ACTGATGT GGAGTC  CTT
                                     A     __
GAM470  KIAA0433  5'  ACTACACCTCAGGAA       13022          T  CT
                                ACTACACCTT AG  GAA
                                |||||||||| ||  |||
                                TGATGTGGAG TC  CTT
                                      _  __
GAM470  KIAA0779  3'  TGTACTACAATCAGCTGA    13023    _     CCT
                                TG ACTACA   TTAGCTGA
                                || ||||||   ||||||||
                                AC TGATGT   AGTCGACT
                                 A     T__
GAM470  KIAA1198  3'  TGACTACACCTATTAGAGGGA  13024          _   CT_
                                TGACTACACCT TTAG   GA
                                |||||||||| ||||   ||
                                ACTGATGTGGA AATC   CT
                                       T    TCC
GAM470  KIAA1238  3'  TAACTACATTTTTCCTGA    13025        CC   AG
                                TGACTACA  TTT  CTGA
                                ||||||||  |||  ||||
                                ATTGATGT  AAA  GACT
                                     AA   G_
GAM470  KIAA1432  5'  TAACTACACTCCTGA       13026         C  TAG
                                TGACTACAC TT   CTGA
                                ||||||||| ||   ||||
                                ATTGATGTG AG   GACT
                                      _  ___
GAM470  KIAA1656  3'  TGACTCACCTTTACAGA     13027      A       G T
                                TGACT CACCTTTA C GA
                                ||||| |||||||| | ||
                                ACTGA GTGGAAAT G CT
                                   _       _ T
GAM470  KPNB3     3'  CTACAAAATTGGCTGAAAT    13028      CCT  A
                                CTACA   TT GCTGAAAT
                                |||||   || ||||||||
                                GATGT   AA CGACTTTA
                                   TTT  C
GAM470  MGC16386  3'  TGGCCACACCCTGAAA      13029    A      TTTAG
                                TG CTACACC    CTGAAA
                                || |||||||    ||||||
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                                AC GGTGTGG    GACTTT
                                 C     _____
GAM470  NESHBP   3'  GACTCCATTTTTAGCTGAAAT  13030     A  CC
                                GACT CA  TTTAGCTGAAAT
                                |||| ||  ||||||||||||
                                CTGA GT  AAATCGACTTTA
                                  G  AA
GAM470  NOVA2    3'  GACTACACCAAGCTGA      13031        TTT
                                GACTACACC   AGCTGA
                                |||||||||   ||||||
                                CTGATGTGG   TCGACT
                                      T__
GAM470  OBTP     3'  TGGCTACACCCCTGGCTGA   13032    A       A
                                TG CTACACCTTT GCTGA
                                || |||||||||| |||||
                                AC GATGTGGGGA CGACT
                                 C         C
GAM470  OSBPL8   3'  TGACCACACTTTTTTCAGC   13033        C___
                                TGACTACAC    TTTAGC
                                |||||||||    ||||||
                                ACTGGTGTG    AAGTCG
                                      AAAA
GAM470  LOC149773 5'  TGACTCACTCAGATGA     13034      A  CT   C
                                TGACT CAC  TTAG TGA
                                ||||| |||  |||| |||
                                ACTGA GTG  AGTC ACT
                                  _  __    T
GAM470  LOC154849 5'  TGACTACACCATTTATTG    13035         _   GC
                                TGACTACACC TTTA  TG
                                |||||||||| ||||  ||
                                ACTGATGTGG AAAT  AC
                                      T   A_
GAM470  LOC154877 3'  CTGCACACAGCTGAAAT     13036    A  CTT
                                CT CAC   TAGCTGAAAT
                                || |||   ||||||||||
                                GA GTG   GTCGACTTTA
                                 C  T__
GAM470  LOC158062 3'  TGACCACACTGCTGAA      13037        CTTTA
                                TGACTACAC    GCTGAA
                                |||||||||    ||||||
                                ACTGGTGTG    CGACTT
                                      A____
GAM470  LOC158709 5'  TGCTACACCTTTGCTG      13038    A       A
                                TG CTACACCTTT GCTG
                                || |||||||||| ||||
                                AC GATGTGGAAA CGAC
                                 _       _
GAM470  LOC203350 3'  TGACTACCTGGGCAGCTGAAAT 13039       ACCTT
                                TGACTAC    TAGCTGAAAT
                                |||||||    ||||||||||
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                                ACTGATG    GTCGACTTTA
                                   GACCC
GAM470  LOC257358 3'  TGACTCCACTTTGCTGAAAT  13040      A  C  A
                                TGACT CAC TTT GCTGAAAT
                                ||||| ||| ||| ||||||||
                                ACTGA GTG AAA CGACTTTA
                                  G  _  _
GAM471  KPNA1    3'  TAAGGATTAATGCAAATCTG  13043    A        AG
                                TGA GATTAATGCGG  GTCTG
                                ||| ||||||||||  |||||
                                ATT CTAATTACGTT  TAGAC
                                 C        __
GAM471  MGAM     3'  ATGAAGATTAATGTGGTC    13044          CGGA
                                ATGAAGATTAATG   GGTC
                                ||||||||||||   ||||
                                TACTTCTAATTAC   CCAG
                                       A___
GAM471  BICD2    3'  ATGAAGATGCCCAGGTCTG   13045      TTAA  GG
                                ATGAAGA   TGC  AGGTCTG
                                |||||||   |||  |||||||
                                TACTTCT   ACG  TCCAGAC
                                    _____  GG
GAM471  HML2     5'  TGGAGCTGTGGGAGGTCTG   13046    A  ATTAA  C
                                TG AG    TG GGAGGTCTG
                                || ||    || |||||||||
                                AC TC    AC CCTCCAGAC
                                 C  GAC__  _
GAM471  HSPC048  3'  ATGAAGGTTAATGCAGCAGG  13047      A      _
                                ATGAAG TTAATGCGG AGG
                                |||||| ||||||||| |||
                                TACTTC AATTACGTC TCC
                                   C       G
GAM471  TAO1     3'  ATGAGATGAGGAGGTCTG    13048    A  TTAA  C
                                ATG AGA   TG GGAGGTCTG
                                ||| |||   || |||||||||
                                TAC TCT   AC CCTCCAGAC
                                  _  _____  T
GAM471  LOC200563 3'  AAGGGAATGTGGAGGTCTG  13049    ATT   C
                                AAG   AATG GGAGGTCTG
                                |||   |||| |||||||||
                                TTC   TTAC CCTCCAGAC
                                  CC_   A
GAM471  LOC221336 5'  ATGAAGATGATGCTATTCTG  13050       TA   GGAGG
                                ATGAAGAT  ATGC    TCTG
                                ||||||||  ||||    ||||
                                TACTTCTA  TACG    AGAC
                                    C_   ATA__
GAM472  CEP2     5'  TACCTTCCTACTTTTGCTAAGG 13053       _   ___  TT
           AT                    TACCTTC TACTT   CTA  GAT
                                |||||||  |||||   |||  |||
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                                ATGGAAG ATGAA   GAT  CTA
                                    G    AAC   TC
GAM472  CTNNA2   3'  CCTTCTATTTCTAGCAAAATC  13054       C    TT  T
                                CCTTCTA TTCTA  GA AATC
                                ||||||| |||||  || ||||
                                GGAAGAT AAGAT  TT TTAG
                                    A    CG  _
GAM472  ERBB4    3'  TACCTTCTACTTCATATAAATA 13055          _  T
                                TACCTTCTACTTC TAT GATA
                                |||||||||||| ||| ||||
                                ATGGAAGATGAAG ATA TTAT
                                       T  T
GAM472  KLHL1    3'  CTTCTACTCTTGGCAATC    13056        CTA  A
                                CTTCTACTT   TTG TAATC
                                |||||||||   ||| |||||
                                GAAGATGAG   AAC GTTAG
                                    ___  C
GAM472  USP26    5'  CTCCGATTATTGATAATC    13057     ___
                                CTTC   TATTGATAATC
                                ||||   ||||||||||
                                GAGG   ATAACTATTAG
                                  CTA
GAM472  FLJ10688 5'  TACTTTCTACTTCTGCTG    13058     C        A
                                TAC TTCTACTTCT TTG
                                ||| |||||||||| |||
                                ATG AAGATGAAGA GAC
                                  A        C
GAM472  FLJ21126 3'  CTTCTACTTCTAAAAGAT    13059          TT_
                                CTTCTACTTCTA   GAT
                                ||||||||||||   |||
                                GAAGATGAAGAT   CTA
                                       TTT
GAM472  KIAA0470 3'  TACCTTCTACTTCCATGTGGAT 13060           _ ___
           ATAATC                ACCTTCTACTTCTAT TG   ATAATC
                                ||||||||||||||| ||   ||||||
                                TGGAAGATGAAGGTA AC   TATTAG
                                       C  CTA
GAM472  KIAA1287 3'  TACTTTCTACATTGATAAT   13061     C     TTCT
                                TAC TTCTAC    ATTGATAAT
                                ||| ||||||    |||||||||
                                ATG AAGATG    TAACTATTA
                                  A    ____
GAM472  PRO2325  5'  CCTTTCATTTCTATTGGTAATC 13062     C  C       A
                                CCTT TA TTCTATTG TAATC
                                |||| || |||||||| |||||
                                GGAA GT AAGATAAC ATTAG
                                  A A       C
GAM472  LOC123628 5'  CTTCTACTTCTTGTACAA    13063          ATTG
                                CTTCTACTTCT    ATAA
                                ||||||||||    ||||
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                                GAAGATGAAGA   TGTT
                                      ACA_
GAM472  LOC220766 3'  TACCTTCTACTTCCATGTGGAT 13060          _ ___
            ATAATC                 ACCTTCTACTTCTAT TG   ATAATC
                                   |||||||||||||| ||   ||||||
                                   TGGAAGATGAAGGTA AC   TATTAG
                                         C  CTA
GAM472  LOC221362 3'  TACCTTCCATTTCTGTGA    13064        C    AT
                                   TACCTTCTA TTCT  TGA
                                   ||||||||| ||||  |||
                                   ATGGAAGGT AAGA  ACT
                                       A   C_
GAM472  LOC256809 3'  CTTCTACTTCTTTAAAATC   13065         A   T
                                   CTTCTACTTCT TTGA AATC
                                   |||||||||| |||| ||||
                                   GAAGATGAAGA AATT TTAG
                                       _   _
GAM472  LOC90593  3'  TACCTTTTCTTCCACTTGAT  13066      CTA     _
                                   TACCTT   CTTCTATT GAT
                                   ||||||   |||||||| |||
                                   ATGGAA   GAAGGTGA CTA
                                      AA_      A
GAM472  LOC92691  3'  TACCTTCTGCTACACTG     13067       A  TC
                                   TACCTTCT CT  TATTG
                                   |||||||| ||  |||||
                                   ATGGAAGA GA  GTGAC
                                       C  T_
GAM473  FLJ11608  3'  TTCATGGGTGCTATCTTGTCT  13070        GAG   CC
                                   TTTATGGGTG   GTCT  TGTCT
                                   ||||||||||   ||||  |||||
                                   AAGTACCCAC   TAGA  ACAGA
                                        GA_   ___
GAM473  KIAA1463  3'  TAGCCAGAGGTCTTCTGTCT   13071    G       C
                                   TGG TGGAGGTCT CTGTCT
                                   ||| ||||||||| ||||||
                                   ATC GTCTCCAGA GACAGA
                                     G       A
GAM473  LOC152179 5'  TTTATGGGTGGAATCACTTGT  13072          G  TCC
                                   TTTATGGGTGGAG TC   TGT
                                   |||||||||||| ||   |||
                                   AAATACCCACCTT AG   ACA
                                         _  TGA
GAM474  GNRH1    5'  ACTAAAATAGTCTATACTTTT  13075        ACCA
                                   ACTAAAATA    TTTATACTTTT
                                   |||||||||    ||||||||||
                                   TGATTTTAT    AGATATGAAAA
                                        C___
GAM474  SRRM1    3'  TAAAATATTCATTTATACTTTT 13076       AC
                                   TAAAATA  CATTTATACTTTT
                                   |||||||  ||||||||||||
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                                ATTTTAT  GTAAATATGAAAA
                                    AA
GAM474  ARFD1    3'  ACTTAAATAACAAATATACTTT 13077     A      C TT
            T                    ACT AAATAAC A  TATACTTTT
                                 ||| ||||||| |  |||||||||
                                 TGA TTTATTG T  ATATGAAAA
                                   A      _ TT
GAM474  BCAA     3'  TAAAATAACCACCATCCTTTT  13078           TATA
                                 TAAAATAACCATT    CTTTT
                                 ||||||||||||    |||||
                                 ATTTTATTGGTGG    GAAAA
                                        TAG_
GAM474  FLJ13576 3'  ACTAAAATTGCCAATATGAATA 13079        AA   TTT___
            CTTTT                   ACTAAAAT  CCA     ATACTTTT
                                 ||||||||  |||     ||||||||
                                 TGATTTTA  GGT     TATGAAAA
                                     AC   TATACT
GAM474  KIAA0534 3'  TAAAATAACCATTTCGGCTCTT 13080            ATA
                                 TAAAATAACCATTT   CTTTT
                                 ||||||||||||||   |||||
                                 ATTTTATTGGTAAA   GAGAA
                                        GCC
GAM474  KRTAP3-2 3'  CTAAATAACCATAAAAAATACT 13081       A      TT___
            TTT                   CTAAA TAACCAT     ATACTTTT
                                 ||||| |||||||     ||||||||
                                 GATTT ATTGGTA     TATGAAAA
                                    _      TTTTT
GAM474  SFRS12   3'  TAAAATGACCATCTATACTTT  13082       A
                                 TAAAAT ACCATTTATACTTT
                                 |||||| ||||||||||||||
                                 ATTTTA TGGTAGATATGAAA
                                     C
GAM475  APOL3    5'  GAGAGACTTTCCATGGAGCT   13085    AAA       CGA
                                 GA   ACTTTTTAT   GAGCT
                                 ||   |||||||||   |||||
                                 CT   TGAAAGGTA   CTCGA
                                   CTC       C__
GAM475  KIAA0316 3'  GAAAAACTTTTGGTGAGCT   13086          TATCGA
                                 GAAAAACTTTT     GAGCT
                                 ||||||||||      |||||
                                 CTTTTTGAAAA     CTCGA
                                        CCA___
GAM475  KIAA1043 3'  AAAAAACTTTTTGAG       13087           ATCGA
                                 GAAAAACTTTTT    GAG
                                 ||||||||||||    |||
                                 TTTTTTGAAAAA    CTC
                                                 _____
GAM475  KIAA1668 3'  GAGGAAACTCCTCGAGAG    13088    A_      TTA
                                 GA  AAACTTT   TCGAGAG
                                 ||  |||||||   |||||||
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                                CT  TTTGAGG   AGCTCTC
                                 CC      ___
GAM475  KIAA1900  3'  GAAAAACTTTTATTAGAACT   13089          TATCG
                                GAAAAACTTTT    AGAGCT
                                ||||||||||    ||||||
                                CTTTTTGAAAA    TCTTGA
                                     TAA__
GAM475  NYD-SP29  5'  GAAAAGCTCCTTCGAGAGCT   13090      A    TA
                                GAAAA CTTTT  TCGAGAGCT
                                ||||| |||||  |||||||||
                                CTTTT GAGGA  AGCTCTCGA
                                   C    __
GAM475  SFRS10    3'  TAGAAAAACCTTTTAAATGAA  13091            TC_
                                TAGAAAAACTTTTTA   GAG
                                ||||||||||||||   |||
                                ATCTTTTTGGAAAAT   CTT
                                         TTA
GAM475  SNRPG     3'  TAGAAAAAACTGGAATGAGAGC 13092        _  TTTT  C
           T                     TAGAAAAA CT    AT GAGAGCT
                                ||||||||  ||    ||  |||||||
                                ATCTTTTT GA    TA CTCTCGA
                                     T  CCT_  _
GAM475  LOC151146 5'  GAAAATCTTTTATCGAG     13093       A    T
                                GAAAA CTTTT ATCGAG
                                ||||| ||||| ||||||
                                CTTTT GAAAA TAGCTC
                                   A    _
GAM475  LOC221448 3'  GAAAAACTTTTGAGTCAGAGCT 13094          TA_  G
                                GAAAAACTTTT   TC AGAGCT
                                ||||||||||   || ||||||
                                CTTTTTGAAAA   AG TCTCGA
                                      CTC  _
GAM476  DIAPH2    3'  TCTAAATTGTCTACTACAGTAG 13097      CACCA   TTTG
           T                     TCTA    TCT   ACAGTAGT
                                ||||    |||   ||||||||
                                AGAT    AGA   TGTCATCA
                                  TTAAC   TGA_
GAM476  EN1       5'  TCTAGCCATCTTCCTAGGCAGT 13098      CA       GA__
           AGT                    TCTA  CCATCTTTT    CAGTAGT
                                ||||  |||||||||    |||||||
                                AGAT  GGTAGAAGG    GTCATCA
                                  C_       ATCC
GAM476  HDAC5     3'  CATCTTAAAGACAGTAGT    13099       TT_
                                CATCTT   GACAGTAGT
                                ||||||   |||||||||
                                GTAGAA   CTGTCATCA
                                   TTT
GAM476  CARD6     3'  CATGCTAATGACAGTAGT    13100     _  TT
                                CAT CT  TGACAGTAGT
                                ||| ||  ||||||||||
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                                GTA GA  ACTGTCATCA
                                  C  TT
GAM476  CDA02    5'  CCATCTTTAGAAGTAGT     13101        T  C
                                CCATCTTT GA AGTAGT
                                |||||||| || ||||||
                                GGTAGAAA CT TCATCA
                                     T  _
GAM476  DKFZP434A0225 5'  TCTGCAACATCTTTCACA    13102     A  C       G
                                TCT CA CATCTTTT ACA
                                ||| || |||||||| |||
                                AGA GT GTAGAAAG TGT
                                  C  T       _
GAM476  FLJ12618  3'  CATCATTTTAACAATGCAGT   13103      _       __
                                CATC TTTTGACA  GTAGT
                                |||| ||||||||  |||||
                                GTAG AAAATTGT  CGTCA
                                   T       TA
GAM476  FLJ22833  3'  ACCATCACTACAACAGTAGT   13104       TTT_
                                ACCATC    TGACAGTAGT
                                ||||||    ||||||||||
                                TGGTAG    GTTGTCATCA
                                    TGAT
GAM476  HERC3     3'  TCTGCACATCTTTTAAAAG   13105     A   C       C
                                TCT CAC ATCTTTTGA AG
                                ||| ||| |||||||| ||
                                AGA GTG TAGAAAATT TC
                                  C  _       T
GAM476  KIAA0534  3'  TACACAATCTTTTGAACA    13106      C       _
                                TACAC ATCTTTTGA CA
                                ||||| |||||||| ||
                                ATGTG TAGAAAACT GT
                                   T       T
GAM476  KIAA1233  3'  TACACCTTAACAGTG       13107       ATCTT       A
                                TACACC     TTGACAGT G
                                ||||||     |||||||| |
                                ATGTGG     AATTGTCA C
                                    _____       C
GAM476  KIAA1718  3'  TCTACCCATCTTTCCAC     13108      A       G
                                TCTAC CCATCTTTT AC
                                ||||| |||||||| ||
                                AGATG GGTAGAAAG TG
                                   _       G
GAM476  PISD      3'  TCTGCACCTCTGGAACAG    13109     A   A   TTT
                                TCT CACC TCT   GACAG
                                ||| |||| |||   |||||
                                AGA GTGG AGA   TTGTC
                                  C    _  CC_
GAM476  PRC1      3'  TACACTATGTTGACAGTAGT   13110      C  CTT
                                TACAC AT   TTGACAGTAGT
                                ||||| ||   ||||||||||
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                                ATGTG TA   AACTGTCATCA
                                  A  C__
GAM476  PRO0899   3'  TCTACACCATGTTTGTCA    13111          CT    A
                                TCTACACCAT  TTTG CA
                                ||||||||||  |||| ||
                                AGATGTGGTA  AAAC GT
                                     C_    A
GAM476  SE70-2    5'  TCTACACCGTTTCTTTGGCA   13112        A__    T A
                                TCTACACC   TCTTT G CA
                                ||||||||   ||||| | ||
                                AGATGTGG   AGAAA C GT
                                    CAA    _ C
GAM476  LOC143098 5'  CACATTGGGTTTTGACAGTAGT 13113      CCATC
                                TACA    TTTTGACAGTAGT
                                ||||    ||||||||||||
                                GTGT    AAAACTGTCATCA
                                  AACCC
GAM476  LOC253502 5'  TCTGCACCTCCTCGAAGTAGT  13114     A   A    T  C
                                TCT CACC TCTTT GA AGTAGT
                                ||| |||| ||||| || ||||||
                                AGA GTGG AGGAG CT TCATCA
                                  C   _    _ _
GAM476  LOC257017 5'  TCTGTATCATCTCTTGCAGT   13115     ACAC       A
                                TCT    CATCTTTTG CAGT
                                |||    |||||||| ||||
                                AGA    GTAGAGAAC GTCA
                                  CATA       _
GAM476  LOC89919  5'  TCTACACCCTCTTTTAAAGAGT 13116         A      C  T
                                TCTACACC TCTTTTGA AG AGT
                                |||||||| |||||||| || |||
                                AGATGTGG AGAAAATT TC TCA
                                    G       _ _
GAM476  LOC90161  3'  CTATGCCATCTTTTCAGT    13117     CA       GA
                                CTA  CCATCTTTT  CAGT
                                |||  |||||||||  ||||
                                GAT  GGTAGAAAA  GTCA
                                  AC        __
GAM476  LOC92231  3'  TCTTCACCATCCAGTA      13118     A      TTTTGA
                                TCT CACCATC     CAGTA
                                ||| |||||||     |||||
                                AGA GTGGTAG     GTCAT
                                  A     _______
GAM476  LOC92597  3'  TCAATACTATCCTACAGTAGT  13119    TAC  C    TTG
                                TC   AC ATCTT   ACAGTAGT
                                ||   || |||||   ||||||||
                                AG   TG TAGGA   TGTCATCA
                                 TTA  A    ___
GAM477  DKFZp547M236 3'  ACTTTTTCATTGAGTTACTAGT 13122          C   A_   CG
          T                      ACTTTTTTAT GAG  GCT  AGTT
                                ||||||||||  |||  |||  ||||
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                                TGAAAAAGTA CTC  TGA  TCAA
                                      A   AA  __
GAM478  DKFZp547M236 3'  ACTTTTTCATTGAGTTACTAGT 13122          C   A_  CG
           T                   ACTTTTTTAT GAG  GCT  AGTT
                               |||||||||| |||  |||  ||||
                               TGAAAAAGTA CTC  TGA  TCAA
                                      A   AA  __
GAM479  DAG1     3'  AATAAAAAAGTCCCCAAAGTCT 13126          T TT    A
           C                    GATAAAAAAGT T  CGAA TCTC
                               |||||||||||  |  |||| ||||
                               TTATTTTTTCA G  GTTT AGAG
                                      _ GG    C
GAM479  RPL39    3'  GAGGAAAACACGTCGAAATCTC 13127    TA    AGTTTT
                               GA  AAAA     TCGAAATCTC
                               ||  ||||     ||||||||||
                               CT  TTTT     AGCTTTAGAG
                                CC    GTGC__
GAM479  LOC164684 3'  GATAAAAATGTTTTCTCATCTC 13128        A     CGAA
                               GATAAAAA GTTTTT    ATCTC
                               ||||||||  ||||||    |||||
                               CTATTTTT CAAAAG    TAGAG
                                    A     AG__
GAM479  LOC221288 3'  AAAAAGTTTTTTGGAAATC    13129          C_
                               AAAAAGTTTTT  GAAATC
                               ||||||||||  ||||||
                               TTTTTCAAAAA  CTTTAG
                                     AC
GAM480  COL4A6   3'  AGCTTTCCGATCAAGAC     13132          AA  TC
                               AGCTTTTCGA  TC  GAT
                               ||||||||||  ||  |||
                               TCGAAAGGCT  AG  CTG
                                     __  TT
GAM480  COL4A6   3'  AGCTTTCCGATCAAGAC     13132          AA  TC
                               AGCTTTTCGA  TC  GAT
                               ||||||||||  ||  |||
                               TCGAAAGGCT  AG  CTG
                                     __  TT
GAM480  IGFBP3   3'  AAGGTTTTCCTATTCTCGATAA 13133     C     GAAA
           A                    AAG TTTTC    TCTCGATAAA
                               |||  |||||    ||||||||||
                               TTC AAAAG    AGAGCTATTT
                                 C    GATA
GAM480  FLJ12921  3'  AACTTTTTGAAATCCTGA    13134        C     TC
                               AGCTTTT GAAATC  GA
                               |||||||  ||||||  ||
                               TTGAAAA CTTTAG  CT
                                    A     GA
GAM480  MLL3     3'  AAGCTTTTTCAAAAAGTCATAA 13135          _    TC  G
           AA                     AAGCTTTT CGAAA  TC ATAAAA
                               ||||||||  |||||  ||  ||||||
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                                TTCGAAAA GTTTT  AG TATTTT
                                    A    TC  _
GAM480  MST4    3'  AAGCTTTTTGAAGCTTGATAA  13136       C   AT  C
                                AAGCTTTT GAA  CT GATAA
                                |||||||| |||  || |||||
                                TTCGAAAA CTT  GA CTATT
                                    A   C_  A
GAM480  VRP     5'  GCTTCTCGGAATTTCTCG    13137       A  __
                                GCTTTTCG AA  TCTCG
                                |||||||| ||  |||||
                                CGAAGAGC TT  AGAGC
                                    C  AA
GAM481  DAG1    3'  AATAAAAAAGTCCCCAAAGTCT 13126        C  TT   A
            C                    GATAAAAAAG TT  CGAA TCTC
                                |||||||||| ||  |||| ||||
                                TTATTTTTTC AG  GTTT AGAG
                                     _  GG   C
GAM481  KDELR1  3'  GATGGGAAAGCTCTTCATCT  13140    AAA       GAA
                                GAT   AAAGCTTTTC   ATCT
                                |||   ||||||||||   ||||
                                CTA   TTTCGAGAAG   TAGA
                                  CCC       ___
GAM481  KIAA0335 3'  GATGAAAGAGCTCTCCATCTC  13141    A  A      GAA
                                GAT AAA AGCTTTTC   ATCTC
                                ||| ||| ||||||||   |||||
                                CTA TTT TCGAGAGG   TAGAG
                                  C   C      ___
GAM481  RPL39   3'  AAAACACGTCGAAATCTC    13142      TTT
                                AAAGC   TCGAAATCTC
                                |||||   ||||||||||
                                TTTTG   AGCTTTAGAG
                                   TGC
GAM481  STRBP   3'  GATAAAAAGGCTTTTTCT    13143       A    CGAAA
                                GATAAAAA GCTTTT    TCT
                                |||||||| ||||||    |||
                                CTATTTTT CGAAAA    AGA
                                    C    _____
GAM481  LOC157657 3'  GATTGGAAAGCTCCCAAAATCT 13144    AAA    T TT
            C                    GAT   AAAGC T  CGAAATCTC
                                |||   ||||| |  |||||||||
                                CTA   TTTCG A  GTTTTAGAG
                                  ACC    _ GG
GAM481  LOC91650  5'  ATAAAGAAGCTTTTAACATCT  13145      A      CGAA
                                ATAAA AAGCTTTT    ATCT
                                ||||| ||||||||    ||||
                                TATTT TTCGAAAA    TAGA
                                   C      TTG_
GAM482  CASP8   3'  TAACTTTAGCTCTTATAAAAAA 13148      CG     CG
            G                    TAACT  AGCTCT  ATAAAAAAG
                                |||||  ||||||  |||||||||
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                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM482  CASP8    3'  TAACTTTAGCTCTTATAAAAAA 13148      CG     CG
           G                     TAACT  AGCTCT  ATAAAAAAG
                                 |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM482  CASP8    3'  TAACTTTAGCTCTTATAAAAAA 13148      CG     CG
           G                     TAACT  AGCTCT  ATAAAAAAG
                                 |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM482  CASP8    3'  TAACTTTAGCTCTTATAAAAAA 13148      CG     CG
           G                     TAACT  AGCTCT  ATAAAAAAG
                                 |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM482  SUOX     5'  ACTTAAACAGGGATAAAAAAG  13149     CG   TCTC
                                ACT  AGC   GATAAAAAAG
                                |||  |||   ||||||||||
                                TGA  TTG   CTATTTTTTC
                                 AT   TCC_
GAM482  FLJ22477 3'  CTCGGGCTCTTGGTAAAAAAG  13150      A    CGA
                                CTCG GCTCT   TAAAAAAG
                                |||| |||||  ||||||||
                                GAGC CGAGA   ATTTTTTC
                                  C    ACC
GAM482  SFRS6    3'  TAACTCAAGCTTTATAAAAA   13151          CTCG
                                TAACTCGAGCT   ATAAAAA
                                ||||||||||   |||||||
                                ATTGAGTTCGA   TATTTTT
                                      AA__
GAM483  CASP8    3'  TAACTTTAGCTCTTATAAAAAA 13148      CG     CG
           G                     TAACT  AGCTCT  ATAAAAAAG
                                 |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM483  CASP8    3'  TAACTTTAGCTCTTATAAAAAA 13148      CG     CG
           G                     TAACT  AGCTCT  ATAAAAAAG
                                 |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM483  CASP8    3'  TAACTTTAGCTCTTATAAAAAA 13148      CG     CG
           G                     TAACT  AGCTCT  ATAAAAAAG
                                 |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM483  CASP8    3'  TAACTTTAGCTCTTATAAAAAA 13148      CG     CG
           G                     TAACT  AGCTCT  ATAAAAAAG
                                 |||||  ||||||  |||||||||
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                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM483  SUOX     5'  ACTTAAACAGGGATAAAAAAG  13149     CG   TCTC
                                ACT  AGC   GATAAAAAAG
                                |||  |||   ||||||||||
                                TGA  TTG   CTATTTTTTC
                                  AT   TCC_
GAM483  FLJ22477 3'  CTCGGGCTCTTGGTAAAAAAG  13150      A    CGA
                                CTCG GCTCT   TAAAAAAG
                                |||| |||||   ||||||||
                                GAGC CGAGA   ATTTTTTC
                                  C    ACC
GAM483  SFRS6    3'  TAACTCAAGCTTTATAAAAA   13151          CTCG
                                TAACTCGAGCT   ATAAAAA
                                ||||||||||    |||||||
                                ATTGAGTTCGA   TATTTTT
                                      AA__
GAM484  DIO3     3'  GGAGATTGTTCATGTGGCTGAG 13155         GAACC
          G                      GGGGATTGT    GTGGCTGAGG
                                |||||||||    ||||||||||
                                CCTCTAACA    CACCGACTCC
                                     AGTA_
GAM484  GMDS     3'  GGGGATTGTAGCCGGA      13156          AA   TGGCT
                                GGGGATTGTG  CCG    GA
                                |||||||||  |||    ||
                                CCCCTAACAT  GGC    CT
                                      C_  ______
GAM484  MBNL     3'  GGATGTCTTGTGGCTGAGG   13157      T  GAACC
                                GGAT GT    GTGGCTGAGG
                                ||||  ||    ||||||||||
                                CCTA CA    CACCGACTCC
                                  _  GAA__
GAM484  RARA     3'  GGGGGTGCTGGTGGCTGAG   13158      ATT   AACC
                                GGGG   GTG   GTGGCTGAG
                                ||||   |||   |||||||||
                                CCCC   CAC   CACCGACTC
                                  ___   GAC_
GAM484  CREB-H   3'  GGTGATTGTGGGCCGTGG    13159    G      AA
                                GG GATTGTG  CCGTGG
                                ||  |||||||  ||||||
                                CC CTAACAC  GGCACC
                                 A      CC
GAM484  KIAA1500 3'  GGGAGTTCTCTGTGGCTGAGG  13160      TT  GAACC
                                GGGA  GT    GTGGCTGAGG
                                ||||  ||    ||||||||||
                                CCCT  CA    CACCGACTCC
                                  __  AGAGA
GAM484  KIAA1932 5'  GGGGATTTGAGGGCTGAG    13161        G   ACCGT
                                GGGGATT TGA    GGCTGAG
                                |||||||  |||    |||||||
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                                CCCCTAA ACT    CCGACTC
                                   _  C____
GAM484  MGC10334  5'  GGGGGAGCCGTGGCTGAGG   13162     ATTGT  A
                                GGGG    GA CCGTGGCTGAGG
                                ||||    || ||||||||||||
                                CCCC    CT GGCACCGACTCC
                                  _____ C
GAM484  TOLLIP    3'  GGGGTTGTGAACCAGCTAA   13163     A       GT
                                GGGG TTGTGAACC  GGCTGA
                                |||| |||||||||  ||||||
                                CCCC AACACTTGG  TCGATT
                                  _       __
GAM484  TPRA40    3'  GGGGATTGGGAGCCCCAGGGAG 13164       T  A  G   CT
           G                     GGGGATTG GA CC TGG  GAGG
                                ||||||||  || || |||  ||||
                                CCCCTAAC CT GG GTC  CTCC
                                    C  C  G   C_
GAM484  LOC146506 3'  GGGGCTGTGAACTGA      13165     A    ACCGTG
                                GGGG TTGTGA     GCTGA
                                |||| ||||||     |||||
                                CCCC GACACT     TGACT
                                  _     _______
GAM484  LOC221755 5'  GGGGATTGGGACTGGCCTGGG  13166       T  ACCG    GA
                                GGGGATTG GA    TGGCT  GG
                                |||||||| ||    |||||  ||
                                CCCCTAAC CT    ACCGG  CC
                                    C  G___     AC
GAM484  LOC91373  3'  GGGGACTGTGGGTTTCGAG   13167        AACC  GGC
                                GGGGATTGTG    GT   TGAG
                                ||||||||||    ||   ||||
                                CCCCTGACAC    CA   GCTC
                                     C___  AA_
GAM485  NEUROD1   3'  TTTGCACTTTGCAGCAGTAGTA 13170     A   CTA_
                                TTTG CGC    CAGCAGTAGTA
                                |||| |||    ||||||||||||
                                AAAC GTG    GTCGTCATCAT
                                  _   AAAC
GAM485  ABT1      3'  TCTTTGAAGCCTACAGGGC    13171       C       CA
                                TCTTTGA GCCTACAG  GT
                                |||||||  ||||||||  ||
                                AGAAACT CGGATGTC  CG
                                    T       C_
GAM485  FLJ14824  3'  TCTTTGACCCTAATTCTTAGT  13172        G   CAGCAG
                                TCTTTGAC CCTA     TAGT
                                |||||||| ||||     ||||
                                AGAAACTG GGAT     ATCA
                                    _    TAAGA_
GAM485  GFR       3'  TCTTTGACAGCTTATGGACAGT 13173        _  C  CA_
           A                     TCTTTGAC GC TA   GCAGTA
                                |||||||| || ||   ||||||
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                                AGAAACTG CG AT   TGTCAT
                                     T  A  ACC
GAM485  KIAA1244  3'  TCTCTGAGACAGTAGTAGT   13174       CGCCT   C
                                TCTTTGA    ACAG AGTAGT
                                |||||||    |||| ||||||
                                AGAGACT    TGTC TCATCA
                                    C____   A
GAM485  KIAA1416  3'  TCCTTGACTAGAAGCAGTAGT  13175       GCCTAC
                                TCTTTGAC    AGCAGTAGT
                                ||||||||    |||||||||
                                AGGAACTG    TCGTCATCA
                                     ATCT__
GAM485  ZID       3'  TCTGTACCGACTGCAGTAGT   13176     AC  T  A
                                TTTG  GCC AC GCAGTAGT
                                ||||  ||| || ||||||||
                                AGAC  TGG TG CGTCATCA
                                  A_  C  A
GAM485  LOC160404 5'  TCTTTGACTCCTGTGGAAGCAG 13177       G   AC___
              T                  TCTTTGAC CCT    AGCAGT
                                |||||||| |||    ||||||
                                AGAAACTG GGA    TCGTCA
                                     A   CACCT
GAM486  NCAM2     3'  TTAATGGTGAACCTATAACAGT 13180      TTTAAC    C
                                TTAATG     GCCTA AACAGT
                                ||||||     ||||| ||||||
                                AATTAC     TGGAT TTGTCA
                                    CACT__    A
GAM486  LOC157378 3'  AATGTTTACTGCATAACAGT   13181       AC  CTAC
                                AATGTTTA  GC   AACAGT
                                ||||||||  ||   ||||||
                                TTACAAAT  CG   TTGTCA
                                     GA  TA__
GAM487  ARL4      3'  TCCCACAACTGTGTTCT     13184       A  GAC
                                TCCCGCGG TG   GTTCT
                                |||||||| ||   |||||
                                AGGGTGTT AC   CAAGA
                                     G  A__
GAM487  CHC1      3'  TCCCATGGACACCTGTTCT   13185      C    GAC
                                TCCCG GGATG   GTTCT
                                ||||| |||||   |||||
                                AGGGT CCTGT   CAAGA
                                   A    GGA
GAM487  DUSP4     5'  TCCCGCGGGAGAGCCTCT    13186       AT   CG
                                TCCCGCGG  GGA  TTCT
                                ||||||||  |||  ||||
                                AGGGCGCC  TCT  GAGA
                                     C_   CG
GAM487  MASP1     3'  TCCTGCGGGGTGGATTCT    13187     C   A_   CG
                                TCC GCGG  TGGA  TTCT
                                ||| ||||  ||||  ||||
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                                AGG CGCC  ACCT  AAGA
                                  A   CC   __
GAM487  NFATC1   3'  TCTCCATCAGCGACGTTCT   13188   _  _  ATG
                                TC CCG CGG   GACGTTCT
                                || ||| |||   ||||||||
                                AG GGT GTC   CTGCAAGA
                                 A  A  G__
GAM487  PDE4D    5'  TCCCGCAGATGTGCCATT    13189         GA_
                                TCCCGCGGATG   CGTT
                                ||||||||||   ||||
                                AGGGCGTCTAC   GTAA
                                      ACG
GAM487  PRKY     3'  CCTTAAAGTGGACGTTCT    13190    GC  _
                                CC  GGA TGGACGTTCT
                                ||  ||| ||||||||||
                                GG  TTT ACCTGCAAGA
                                 AA   C
GAM487  USP11    5'  CCCGCAGTGGACGTTCT     13191       A
                                CCCGCGG TGGACGTTCT
                                ||||||| ||||||||||
                                GGGCGTC ACCTGCAAGA
                                   _
GAM487  WNT11    3'  TCCCGCAGAACATTCT      13192        TGG
                                TCCCGCGGA   ACGTTCT
                                |||||||||   |||||||
                                AGGGCGTCT   TGTAAGA
                                    ___
GAM487  CDK5RAP1 5'  TCCCGCAGCGTAAGTTCT    13193        A  GAC
                                TCCCGCGG TG   GTTCT
                                |||||||| ||   |||||
                                AGGGCGTC GC   CAAGA
                                     _ ATT
GAM487  DKFZp547I224 5'  TCTCCTGGATGACATCCT    13194    _ GC    G
                                TC CC  GGATG ACGTTCT
                                || ||  ||||| |||||||
                                AG GG  CCTAC TGTAGGA
                                 A  A_   _
GAM487  FLJ10512 5'  TCCTTCACTAGACGTTCT    13195     CG  GA
                                TCC  CG  TGGACGTTCT
                                |||  ||  ||||||||||
                                AGG  GT  ATCTGCAAGA
                                  AA  G_
GAM487  FLJ10540 5'  TCCCGCGGACGCGATCT     13196         GA  T
                                TCCCGCGGATG  CG TCT
                                ||||||||||  || |||
                                AGGGCGCCTGC  GC AGA
                                      __ T
GAM487  FLJ13204 3'  TCCCGCTGATCATTCT      13197       G   GGA
                                TCCCGC GAT   CGTTCT
                                |||||| |||   ||||||
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                                AGGGCG CTA   GTAAGA
                                   A  ___
GAM487  FLJ20574  5'  TCCCGCGGTTGCGCGCATCT  13198       A  GA  _
                                TCCCGCGG TG  CGT TCT
                                |||||||| ||  ||| |||
                                AGGGCGCC AC  GCG AGA
                                     A  GC   T
GAM487  FLJ20574  3'  TCCCGCGGTTGCGCGCATCT  13198       A  GA  _
                                TCCCGCGG TG  CGT TCT
                                |||||||| ||  ||| |||
                                AGGGCGCC AC  GCG AGA
                                     A  GC   T
GAM487  HCA66     5'  CCCCGCGGGTAGCTTCT     13199       A   ACG
                                TCCCGCGG TGG   TTCT
                                |||||||| |||   ||||
                                GGGGCGCC ATC   AAGA
                                     C   G__
GAM487  KIAA0544  3'  TCCTGCAGGACATTCT      13200     C   GAT
                                TCC GCG   GGACGTTCT
                                ||| |||   |||||||||
                                AGG CGT   CCTGTAAGA
                                  A  ___
GAM487  MGC21854  3'  TCCTGCGAATGGAGCACT    13201     C       C  T
                                TCC GCGGATGGA GT CT
                                ||| ||||||||| || ||
                                AGG CGCTTACCT CG GA
                                  A       _  T
GAM487  MGC4796   3'  TCCCGCAGGAGACTTTCT    13202       AT   G
                                TCCCGCGG  GGAC TTCT
                                ||||||||  |||| ||||
                                AGGGCGTC  TCTG AAGA
                                     C_   A
GAM487  PR48      3'  CCCCGCGGCGGCGTTCT     13203       A   A
                                TCCCGCGG TGG CGTTCT
                                |||||||| ||| ||||||
                                GGGGCGCC GCC GCAAGA
                                     _  _
GAM487  SEMA5A    3'  TCCAGTGGAAAACATTCT    13204     CGC   T
                                TCC   GGA GGACGTTCT
                                |||   ||| |||||||||
                                AGG   CCT TTTGTAAGA
                                  TCA  _
GAM487  STMN3     3'  TCCCGCAGGATGGAAGTT    13205       _     C
                                TCCCGC GGATGGA GTT
                                |||||| ||||||| |||
                                AGGGCG CCTACCT CAA
                                   T      T
GAM487  SZF1      5'  TCCCGCGGGGCCCACATC    13206       AT  ___
                                TCCCGCGG  GG   ACGTT
                                ||||||||  ||   |||||
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                                AGGGCGCC  CC   TGTAG
                                    __  GGG
GAM487  VRP      5'  TCCCGCAGGATGTACCTCT   13207       _    G  G
                                TCCCGC GGATG AC TTCT
                                |||||| ||||| || ||||
                                AGGGCG CCTAC TG GAGA
                                   T    A  _
GAM487  LOC146774 3'  TCCCGCAGGTGGGCGGCCT   13208        A   A  TT
                                TCCCGCGG TGG CG  CT
                                |||||||| ||| ||  ||
                                AGGGCGTC ACC GC  GA
                                     C   C  CG
GAM487  LOC168489 5'  TCCTGCAGATGAGGGTTCT   13209     C       AC
                                TCC GCGGATGG  GTTCT
                                ||| ||||||||  |||||
                                AGG CGTCTACT  CAAGA
                                  A       CC
GAM487  LOC199991 5'  TCCTCGGGAGAGACGTTCT   13210     _ C   T
                                TCC CG GGA GGACGTTCT
                                ||| || ||| |||||||||
                                AGG GC CCT TCTGCAAGA
                                  A  _   C
GAM487  LOC200317 3'  TCCCACGGGGATCATTCT    13211        AT   _
                                TCCCGCGG  GGA CGTTCT
                                ||||||||  ||| ||||||
                                AGGGTGCC  CCT GTAAGA
                                    __   A
GAM487  LOC219842 3'  TCCCGCTGGACATTCT      13212       GGA
                                TCCCGC   TGGACGTTCT
                                ||||||   ||||||||||
                                AGGGCG   ACCTGTAAGA
                                   ___
GAM487  LOC220064 3'  TCCCGCGGGGGTCACTTCT   13213        AT  A  _
                                TCCCGCGG  GG CG TTCT
                                ||||||||  || || ||||
                                AGGGCGCC  CC GT AAGA
                                     C_  A  G
GAM487  LOC253219 5'  CCCCGCGGATGGAGCGACT   13214           _  TT
                                TCCCGCGGATGGA CG  CT
                                |||||||||||| ||  ||
                                GGGGCGCCTACCT GC  GA
                                       C  T_
GAM487  LOC253219 3'  CCCCGCGGATGGAGCGACT   13214           _  TT
                                TCCCGCGGATGGA CG  CT
                                |||||||||||| ||  ||
                                GGGGCGCCTACCT GC  GA
                                       C  T_
GAM487  LOC253430 5'  TCCCGCGGCTGGTGCCCT    13215        A   AC
                                TCCCGCGG TGG  GTTCT
                                |||||||| |||  |||||
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                                AGGGCGCC ACC  CGGGA
                                     G   A_
GAM487  LOC256365 5'  TCCCACAGCCACGTTCT     13216        ATGG
                                TCCCGCGG    ACGTTCT
                                ||||||||    |||||||
                                AGGGTGTC    TGCAAGA
                                     GG__
GAM487  LOC257103 5'  TCCCGCAGGACTTTCT      13217        GAT    G
                                TCCCGCG   GGAC TTCT
                                |||||||   |||| ||||
                                AGGGCGT   CCTG AAGA
                                    ___    A
GAM487  LOC84528  5'  TCGCCGCCTGCAACGTTCT    13218    _    GGA  _
                                TC CCGC   TG GACGTTCT
                                || ||||   || ||||||||
                                AG GGCG   AC TTGCAAGA
                                 C   G__  G
GAM487  LOC91263  3'  TCCTGCAGAAAACATTCT    13219     C     T
                                TCC GCGGA GGACGTTCT
                                ||| ||||| |||||||||
                                AGG CGTCT TTTGTAAGA
                                  A    _
GAM488  LAMC1     3'  AGCAGTATAATAATCCCTGTGT 13222        G         AA
                                AGCAGTA TAATAATTTT  TGT
                                ||||||| ||||||||||  |||
                                TCGTCAT ATTATTAGGG  ACA
                                    _        AC
GAM488  NOVA1     3'  AACAGTAGTTAATTTAGTGT   13223        AA     TAA
                                AGCAGTAGT  TAATTT   TGT
                                |||||||||  ||||||   |||
                                TTGTCATCA  ATTAAA   ACA
                                     __     TC_
GAM488  NOVA1     3'  AACAGTAGTTAATTTAGTGT   13223        AA     TAA
                                AGCAGTAGT  TAATTT   TGT
                                |||||||||  ||||||   |||
                                TTGTCATCA  ATTAAA   ACA
                                     __     TC_
GAM488  TRIM      3'  TAGTAATGCATTTTAATG     13224        A_
                                TAGTAAT  ATTTTAATG
                                |||||||  |||||||||
                                ATCATTA  TAAAATTAC
                                    CG
GAM488  CUGBP2    3'  CAGCAGTAGTAAACACATG    13225           TAATTTTA
                                CAGCAGTAGTAA       ATG
                                ||||||||||||       |||
                                GTCGTCATCATT       TAC
                                      TGTG____
GAM488  DKFZP434E2318 3'  AGCAGTAGAAACATCTTAGTGT 13226         T    A    A
                                AGCAGTAG AATA TTTTA TGT
                                |||||||| |||| ||||| |||
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                                TCGTCATC TTGT AGAAT ACA
                                     T   _    C
GAM488  HSPC177  3'  ACAGTAGTGATAATTCCA    13227        A
                                GCAGTAGT ATAATTTTA
                                |||||||| |||||||||
                                TGTCATCA TATTAAGGT
                                     C
GAM488  SAC2     3'  CAGCAGAGTATTTTTAATG   13228      T   ATAA
                                CAGCAG AGTA   TTTTAATG
                                |||||| ||||   ||||||||
                                GTCGTC TCAT   AAAATTAC
                                   _   A___
GAM488  TUSP     3'  GTAGTCAACTGAATTTTAATGT 13229      _  __
                                GTAGT AAT  AATTTTAATGT
                                ||||| |||  ||||||||||
                                CATCA TTG  TTAAAATTACA
                                   G   AC
GAM488  WIT-1    5'  CAGTAGTAGTAACAAAAACTGT 13230    C        TTTTAA
                                CAG AGTAGTAATAA     TGT
                                ||| ||||||||||     |||
                                GTC TCATCATTGTT     ACA
                                  A         TTTG__
GAM488  LOC154743 3'  CAGTATGAGGTAATTTTAATGT 13231      GTAA_
                                CAGTA     TAATTTTAATGT
                                |||||     ||||||||||||
                                GTCAT     ATTAAAATTACA
                                   ACTCC
GAM488  LOC219381 3'  CAGCAGTTAGTGATAACTT   13232       _  A
                                CAGCAGT AGT ATAATTT
                                ||||||| ||| |||||||
                                GTCGTCA TCA TATTGAA
                                     A   C
GAM489  LAMC1    3'  AGCAGTATAATAATCCCTGTGT 13222       G        AA
                                AGCAGTA TAATAATTTT  TGT
                                ||||||| ||||||||||  |||
                                TCGTCAT ATTATTAGGG  ACA
                                   _         AC
GAM489  NOVA1    3'  AACAGTAGTTAATTTAGTGT   13223        AA     TAA
                                AGCAGTAGT  TAATTT   TGT
                                |||||||||  ||||||   |||
                                TTGTCATCA  ATTAAA   ACA
                                     __      TC_
GAM489  NOVA1    3'  AACAGTAGTTAATTTAGTGT   13223        AA     TAA
                                AGCAGTAGT  TAATTT   TGT
                                |||||||||  ||||||   |||
                                TTGTCATCA  ATTAAA   ACA
                                     __      TC_
GAM489  TRIM     3'  TAGTAATGCATTTTAATG    13224        A_
                                TAGTAAT  ATTTTAATG
                                |||||||  |||||||||
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                                ATCATTA  TAAAATTAC
                                    CG
GAM489  CUGBP2   3'  CAGCAGTAGTAAACACATG   13225          TAATTTTA
                                CAGCAGTAGTAA      ATG
                                ||||||||||||      |||
                                GTCGTCATCATT      TAC
                                      TGTG____
GAM489  DKFZP434E2318 3'  AGCAGTAGAAACATCTTAGTGT 13226        T   A   A
                                AGCAGTAG AATA TTTTA TGT
                                |||||||| |||| ||||| |||
                                TCGTCATC TTGT AGAAT ACA
                                     T   _    C
GAM489  HSPC177  3'  ACAGTAGTGATAATTCCA    13227        A
                                GCAGTAGT ATAATTTTA
                                |||||||| |||||||||
                                TGTCATCA TATTAAGGT
                                     C
GAM489  SAC2     3'  CAGCAGAGTATTTTTAATG   13228      T   ATAA
                                CAGCAG AGTA   TTTTAATG
                                |||||| ||||   ||||||||
                                GTCGTC TCAT   AAAATTAC
                                   _   A___
GAM489  TUSP     3'  GTAGTCAACTGAATTTTAATGT 13229      _  __
                                GTAGT AAT  AATTTTAATGT
                                ||||| |||  ||||||||||
                                CATCA TTG  TTAAAATTACA
                                  G   AC
GAM489  WIT-1    5'  CAGTAGTAGTAACAAAAACTGT 13230    C        TTTTAA
                                CAG AGTAGTAATAA     TGT
                                ||| ||||||||||     |||
                                GTC TCATCATTGTT     ACA
                                  A         TTTG__
GAM489  LOC154743 3'  CAGTATGAGGTAATTTTAATGT 13231      GTAA_
                                CAGTA    TAATTTTAATGT
                                |||||    ||||||||||||
                                GTCAT    ATTAAAATTACA
                                   ACTCC
GAM489  LOC219381 3'  CAGCAGTTAGTGATAACTT   13232       _  A
                                CAGCAGT AGT ATAATTT
                                ||||||| ||| |||||||
                                GTCGTCA TCA TATTGAA
                                     A  C
GAM490  ADAMTS5  3'  TGCTTTCCAGTTGGGAAAAA  13236        C___
                                TGCTTTCCGG   GAAAAA
                                ||||||||||   ||||||
                                ACGAAAGGTC   CTTTTT
                                      AACC
GAM490  BMPR1A   3'  ATGCTTTCCGTGACAAAAA   13237         __
                                ATGCTTTCCG  GCGAAAA
                                ||||||||||  |||||||
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                                TACGAAAGGC  TGTTTTT
                                      AC
GAM490  FMN2     5'  AAATGCTTTCTGAAAA      13238          CGGC
                                AAATGCTTTC    GAAAA
                                ||||||||||    |||||
                                TTTACGAAAG    CTTTT
                                      A___
GAM490  MPP1     3'  AAAACGCTTTCTCCAAAA    13239            CGG
                                AAAATGCTTTC   CGAAA
                                ||||||||||   |||||
                                TTTTGCGAAAG   GTTTT
                                      AG_
GAM490  TCF20    3'  CTTTCCAGACTAAAAATA    13240         _ GA
                                CTTTCCGG C  AAAAATA
                                |||||||| |  |||||||
                                GAAAGGTC G  TTTTTAT
                                     T A_
GAM490  VHL      3'  AAAATGCTTCCTACAAAAA   13241         T  G
                                AAAATGCTT CC GCGAAAA
                                ||||||||| || |||||||
                                TTTTACGAA GG TGTTTTT
                                      _  A
GAM490  DKFZP564J0863 3'  AAATGCTTCCAAGAGAAA    13242          C  C
                                AAATGCTTTC GG GAAA
                                |||||||||| || ||||
                                TTTACGAAGG TC CTTT
                                      T  T
GAM490  FLJ21269  3'  AAAACGCTTGGGGGAAAA    13243          TCC  C
                                AAAATGCTT   GG GAAAA
                                |||||||||   || |||||
                                TTTTGCGAA   CC CTTTT
                                      CC_  _
GAM490  KIAA0268  3'  AAATGCTTTCAGGCTGAA    13244          C  _
                                AAATGCTTTC GGC GAA
                                |||||||||| ||| |||
                                TTTACGAAAG CCG CTT
                                      T   A
GAM490  KIAA0469  3'  AAATACTTTTATTGCAAAAA  13245          CCG_
                                AAATGCTTT    GCGAAAA
                                |||||||||    |||||||
                                TTTATGAAA    CGTTTTT
                                      ATAA
GAM490  KIAA1239  3'  TGCTTTCCAAGAGGAAATA   13246          C  AA
                                TGCTTTCCGG GA  AAATA
                                |||||||||| ||  |||||
                                ACGAAAGGTT CT  TTTAT
                                      _  CC
GAM490  USP24     3'  AAAATGCTTTCCTTGAGAAA  13247           GGC_
                                AAAATGCTTTCC    GAAA
                                ||||||||||||    ||||
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                                TTTTACGAAAGG   CTTT
                                     AACT
GAM490  LOC124152 3'  AAAATGCTGTTCTTAACACAAA 13248       _  C_   A
          AATA                   AAAATGCT TTC  GGCG AAAAATA
                                |||||||| |||  |||| |||||||
                                TTTTACGA AAG  TTGT TTTTTAT
                                    C   AA   G
GAM490  LOC130813 3'  AAAATGCTTTACCCTAGAA   13249         _ GGC
                                AAAATGCTTT CC   GAA
                                |||||||||| ||   |||
                                TTTTACGAAA GG   CTT
                                     T  GAT
GAM490  LOC153606 5'  AAAATGCTTTCCCTATGAAAA  13250          GGC_
                                AAAATGCTTTCC   GAAAA
                                ||||||||||||   |||||
                                TTTTACGAAAGG   CTTTT
                                     GATA
GAM490  LOC161742 3'  AAATGCTTTCTTAAAAAAA   13251         CGGC
                                AAATGCTTTC   GAAAAAA
                                ||||||||||   |||||||
                                TTTACGAAAG   TTTTTTT
                                     AA__
GAM490  LOC253613 3'  AAAATGCTTCCATAAAA     13252        T  GC
                                AAAATGCTT CCG  GAAA
                                ||||||||| |||  ||||
                                TTTTACGAA GGT  TTTT
                                     _  A_
GAM490  LOC253832 3'  GCTTTCCGTTTTAAAAAATA  13253       GCG_
                                GCTTTCCG   AAAAAATA
                                ||||||||   ||||||||
                                CGAAAGGC   TTTTTTAT
                                    AAAA
GAM490  LOC253868 5'  AAAATGCTCTCCTCTTAGGGA  13254          _____ C
                                AAAATGCTTTCC    GG GA
                                ||||||||||||    || ||
                                TTTTACGAGAGG    CC CT
                                     AGAAT  _
GAM490  LOC254393 3'  AAAATGCTTTATTGCTAAAAAA 13255         CCG  _
          AT                    AAAATGCTTT  GC GAAAAAAT
                                ||||||||||  || ||||||||
                                TTTTACGAAA  CG TTTTTTTA
                                     TAA  A
GAM490  LOC51146  5'  TGCTTTCCTCACCAAAAA    13256       G_  G
                                TGCTTTCC  GC AAAAA
                                ||||||||  || |||||
                                ACGAAAGG  TG TTTTT
                                    AG  G
GAM491  DKFZP434D1335 3'  TACTTGTTAAGTCCCAC     13259      A        G
                                TACT TGTTAAGTCC TGC
                                |||| |||||||||| |||
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                                ATGA ACAATTCAGG GTG
                                  _       _
GAM491  NAV3    3'  TACTATGTTAACTGGTGTTGC  13260          GTCC  C_
                                TACTATGTTAA   GTG  GC
                                ||||||||||    |||  ||
                                ATGATACAATT   CAC  CG
                                      GAC_   AA
GAM492  ABCE1   3'  AGGGGTTTTTTGCGGGGAATGG 13263    TA      ATATC
                                AG  GTTTTTTG    GAATGG
                                ||  ||||||||    ||||||
                                TC  CAAAAAAC    CTTACC
                                 CC       GCCC_
GAM492  OCA2    3'  GTAGTTTTATGACTAATGG   13264        T   ATCG
                                GTAGTTTT TGAT    AATGG
                                |||||||| ||||    |||||
                                CATCAAAA ACTG    TTACC
                                     T    A___
GAM492  KIAA1735 3' AGTAGTTTGTTGAAATG     13265        T   TATCG
                                AGTAGTTT TTGA     AATG
                                |||||||| ||||     ||||
                                TCATCAAA AACT     TTAC
                                     C    _____
GAM492  MADP-1   3'  AAGTAGTTTCTTCTAGGGAATG 13266          GA  TC
          G                      AAGTAGTTTTTT  TA  GAATGG
                                 ||||||||||||  ||  ||||||
                                 TTCATCAAAGAA  AT  CTTACC
                                       G_  CC
GAM492  LOC170281 5' AGAGTTTTTTGATAGCTTTGG  13267    T         TCGAA
                                AG AGTTTTTTGATA     TGG
                                || ||||||||||||     |||
                                TC TCAAAAAACTAT     ACC
                                 _          CGAA_
GAM493  LBR     5'  CGTTACACACCGAAACA     13270       A  G TT
                                CGTTA CA G  TCGAAACA
                                ||||| || |  ||||||||
                                GCAAT GT T  GGCTTTGT
                                   _  G __
GAM493  MYCN    3'  TACATTAACAGGAAGAAACA   13271           TTTC
                                TACGTTAACAGG    GAAACA
                                ||||||||||||    ||||||
                                ATGTAATTGTCC    CTTTGT
                                       TT__
GAM493  RRM2B   3'  GTTAACAGGTAAAAAACA    13272          TTC
                                GTTAACAGGT   GAAACA
                                ||||||||||   ||||||
                                CAATTGTCCA   TTTTGT
                                      TT_
GAM493  CDC10   3'  TACGTTAACTGGTGGTCAA   13273         A   T_
                                TACGTTAAC GGT  TCGA
                                ||||||||| |||  ||||
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                                ATGCAATTG CCA  AGTT
                                     A   CC
GAM493  KIAA1414  3'  GTTAACAAAAGAGAAACA    13274        TTTC
                                GTTAACAGG   GAAACA
                                |||||||||   ||||||
                                CAATTGTTT   CTTTGT
                                     TCT_
GAM493  TP53INP1  3'  TACTTAACAGGTCAAC     13275    G       TCGA
                                TAC TTAACAGGTT   AAC
                                ||| ||||||||||   |||
                                ATG AATTGTCCAG   TTG
                                  _       _____
GAM493  TP53INP1  3'  TACTTAACAGGTCAAC     13275    G       TCGA
                                TAC TTAACAGGTT   AAC
                                ||| ||||||||||   |||
                                ATG AATTGTCCAG   TTG
                                  _       _____
GAM493  LOC123047 5'  GTTGGCAAGGTCGAAACA   13276    AA   TT
                                GTT  CAGG  TCGAAACA
                                |||  ||||  ||||||||
                                CAA  GTTC  AGCTTTGT
                                  CC   C_
GAM493  LOC197285 3'  CGTTAACAAGGGAAACA    13277        TTTC
                                CGTTAACAGG   GAAACA
                                ||||||||||   ||||||
                                GCAATTGTTC   CTTTGT
                                     C___
GAM493  LOC90979  3'  GTAAACAGGTTTAAAACA   13278    T       C
                                GT AACAGGTTT GAAACA
                                || |||||||| ||||||
                                CA TTGTCCAAA TTTTGT
                                 T       _
GAM493  LOC91917  3'  CGTTAACAAGGGAAACA    13277        TTTC
                                CGTTAACAGG   GAAACA
                                ||||||||||   ||||||
                                GCAATTGTTC   CTTTGT
                                     C___
GAM494  BACE    3'  TAAGAAAAGAAGAATAC    13281     TTTTC
                                TAAG    AAGAAGAATAC
                                ||||    ||||||||||
                                ATTC    TTCTTCTTATG
                                  TT___
GAM494  BACE    3'  TAAGAAAAGAAGAATAC    13281     TTTTC
                                TAAG    AAGAAGAATAC
                                ||||    ||||||||||
                                ATTC    TTCTTCTTATG
                                  TT___
GAM494  SRR     3'  TACAAGTTTTCAAGAACC    13282           AGAAT
                                TATAAGTTTTCAAGA    ACC
                                ||||||||||||||    |||
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                                ATGTTCAAAAGTTCT    TGG
                                      _____
GAM494  ZNF36    3'  TATAAGTTTCTCAAGGGAA   13283       _    AA
                                TATAAGTT TTCAAG  GAA
                                |||||||| ||||||  |||
                                ATATTCAA GAGTTC  CTT
                                     A     C_
GAM494  CECR6    3'  CCTTCAAGGGGAGTACCT    13284       AA  A
                                TTTTCAAG  GA TACCT
                                |||||||||  || |||||
                                GGAAGTTC  CT ATGGA
                                     CC  C
GAM494  FLJ10656 3'  TGAAGTCTTCCTTTTAGGAAGA 13285   T      AA_____
              AT                  A AAGTTTTC      GAAGAAT
                                | ||||||||      |||||||
                                A TTCAGAAG      CTTCTTA
                                 C       GAAAATC
GAM494  FLJ12604 3'  TAAAGTTTTCTTTTAATACCT  13286   T      AAGAAG
                                A AAGTTTTC     AATACCT
                                | ||||||||     |||||||
                                A TTCAAAAG     TTATGGA
                                 T       AAAA__
GAM494  FLJ23360 3'  GTTTTTGAGGAAAATACCT   13287      CA  A
                                GTTTT  AG AGAATACCT
                                |||||  || |||||||||
                                CAAAA  TC TTTTATGGA
                                   AC  C
GAM494  KIAA1209 3'  TATAAGCTATGAGAAGAATAC  13288       TTCA
                                TATAAGTT   AGAAGAATAC
                                ||||||||   ||||||||||
                                ATATTCGA   TCTTCTTATG
                                     TAC_
GAM494  KIAA1254 3'  CATAAGTTTTCAATTATATGCC 13289          GAAGAATA
              T                  TATAAGTTTTCAA       CCT
                                ||||||||||||       |||
                                GTATTCAAAAGTT       GGA
                                       AATATAC_
GAM494  KIAA1431 3'  TATAAGTTTTACAAGAGGA   13290        _    A
                                TATAAGTTTT CAAGA GA
                                |||||||||| ||||| ||
                                ATATTCAAAA GTTCT CT
                                      T    C
GAM494  KIAA1462 3'  AGTTGTCAGGAATACCT     13291     T  AGAA
                                AGTT TCA   GAATACCT
                                |||| |||   ||||||||
                                TCAA AGT   CTTATGGA
                                  C  C___
GAM494  LOC203257 3'  TATAAATTTTTAAGAAGAA   13292         C
                                TATAAGTTTT AAGAAGAA
                                |||||||||| ||||||||
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                                ATATTTAAAA TTCTTCTT
                                      A
GAM495  DKFZp761D112 3'  TATTTGACAAACTAAGTTTATG 13295        C  G   CC
                                TATTTGGCG GA TAAG  TATG
                                ||||||||| || ||||  ||||
                                ATAAACTGT TT ATTC  ATAC
                                     _ G   AA
GAM495  LOC145725 5'  TATTTGGCACCCAGGTCTATG  13296        GAGTA  C_
                                TATTTGGCGC    AG  CTATG
                                ||||||||||    ||  |||||
                                ATAAACCGTG    TC  GATAC
                                      GG___  CA
GAM495  LOC145732 5'  TATTTGGCACCCAGGTCTATG  13296        GAGTA  C_
                                TATTTGGCGC    AG  CTATG
                                ||||||||||    ||  |||||
                                ATAAACCGTG    TC  GATAC
                                      GG___  CA
GAM495  LOC196957 5'  TATTTGGCACCCAGGTCTATG  13296        GAGTA  C_
                                TATTTGGCGC    AG  CTATG
                                ||||||||||    ||  |||||
                                ATAAACCGTG    TC  GATAC
                                      GG___  CA
GAM495  LOC196961 5'  TATTTGGCACCCAGGTCTATG  13296        GAGTA  C_
                                TATTTGGCGC    AG  CTATG
                                ||||||||||    ||  |||||
                                ATAAACCGTG    TC  GATAC
                                      GG___  CA
GAM495  LOC197138 5'  TATTTGGCACCCAGGTCTATG  13296        GAGTA  C_
                                TATTTGGCGC    AG  CTATG
                                ||||||||||    ||  |||||
                                ATAAACCGTG    TC  GATAC
                                      GG___  CA
GAM496  CAPON    5'  TACCCGCGGCGGACCCGC    13299    G    T TTCAA
                                TG CTGC G    CGGACCCGC
                                || |||| |    |||||||||
                                AT GGCG C    GCCTGGGCG
                                  G   C _____
GAM496  DAZL     5'  GGCTGCTGTGAGGTCCGC    13300         TCAAC  AC
                                GGCTGCTGT    GG  CCGC
                                |||||||||    ||  ||||
                                CCGACGACA    CC  GGCG
                                     CT___  A_
GAM496  FOXO1A   3'  TGGTGGCTGTTCAATGAA    13301     CT       C
                                TGG  GCTGTTCAA GGA
                                |||  ||||||||| |||
                                ACC  CGACAAGTT CTT
                                  AC        A
GAM496  G6PD     5'  TGGGCTGAGCGGACCCGC    13302     CT    TTCAA
                                TGG  GCTG    CGGACCCGC
                                |||  ||||    |||||||||
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                                ACC  CGAC    GCCTGGGCG
                                  __   TC___
GAM496  HNRPH1   3'  TAGCTGCTGTTCACTGCTGGCG 13303        A_________  GACC
            GGTCCG                TGCTGTTCA       CG   CG
                                |||||||||       ||   ||
                                ACGACAAGT       GC   GC
                                    GACGAIIICC  CCAG
GAM496  PIG3     5'  TGGTCTGCCGCGGACCCGC   13304    _    TTCAA
                                TGG CTGCTG    CGGACCCGC
                                ||| ||||||    |||||||||
                                ACC GACGGC    GCCTGGGCG
                                  A    _____
GAM496  PTPN11   5'  GGCTCCGCGACGGACCCGC   13305    G   TCA
                                GGCT CTGT   ACGGACCCGC
                                |||| ||||   ||||||||||
                                CCGA GGCG   TGCCTGGGCG
                                  _   C__
GAM496  PTPN11   5'  GGCTCCGCGACGGACCCGC   13305    G   TCA
                                GGCT CTGT   ACGGACCCGC
                                |||| ||||   ||||||||||
                                CCGA GGCG   TGCCTGGGCG
                                  _   C__
GAM496  STAU     5'  TGGCTGCTGCTCCGGACTCG   13306        AA   C
                                TGGCTGCTGTTC  CGGAC CG
                                ||||||||||||  ||||| ||
                                ACCGACGACGAG  GCCTG GC
                                      __    A
GAM496  STAU     5'  TGGCTGCTGCTCCGGACTCG   13306        AA   C
                                TGGCTGCTGTTC  CGGAC CG
                                ||||||||||||  ||||| ||
                                ACCGACGACGAG  GCCTG GC
                                      __    A
GAM496  STAU     5'  TGGCTGCTGCTCCGGACTCG   13306        AA   C
                                TGGCTGCTGTTC  CGGAC CG
                                ||||||||||||  ||||| ||
                                ACCGACGACGAG  GCCTG GC
                                      __    A
GAM496  STAU     5'  TGGCTGCTGCTCCGGACTCG   13306        AA   C
                                TGGCTGCTGTTC  CGGAC CG
                                ||||||||||||  ||||| ||
                                ACCGACGACGAG  GCCTG GC
                                      __    A
GAM496  FLJ20154 3'  TGGCTGCTTTCACCTCCTGCC  13307       G   ACGGA  C
                                TGGCTGCT TTCA    CC GCC
                                |||||||| ||||    || |||
                                ACCGACGA AAGT    GG CGG
                                    _   GGA__  A
GAM496  FLJ21988 3'  TGGCTGCTGCTTCGTACTTGGC 13308        _ A_  __  ACCC
            TTGCC                GGCTGCTGTT C  AC  GG   GCC
                                |||||||||| |  ||  ||   |||
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                                CCGACGACGA G  TG  CC   CGG
                                     A CA  AA  GAA_
GAM496  HNOEL-iso 3'  GCCTGCTCCCTGGGCCTGCC  13309   TG    AAC  A  C
                                GC  CTGTTC   GG CC GCC
                                ||  ||||||   || || |||
                                CG  GACGAG   CC GG CGG
                                 __     GGA  C  A
GAM496  KIAA1172  5'  GGCTGCTCCGGGCCCGC    13310      GTTCAA   A
                                GGCTGCT     CGG CCCGC
                                |||||||     ||| |||||
                                CCGACGA     GCC GGGCG
                                    G_____   C
GAM496  MGC20460  5'  TGGCTGCTGTCCTTGCTGGCGG 13311        AA_________  GACC
           GTCCG                   CTGCTGTTC        CG   CG
                                |||||||||        ||   ||
                                GACGACAGG        GC   GC
                                     AACGAIIICC  CCAG
GAM496  MGC3048   3'  TGGTTGCTGTTCTGAACC    13312    C      AAC
                                TGG TGCTGTTC   GGACC
                                ||| ||||||||   |||||
                                ACC ACGACAAG   CTTGG
                                  A       A__
GAM496  PPM1A    3'  TGGCTGCTGCTCTCCC      13313          AACGGA
                                TGGCTGCTGTTC     CCC
                                ||||||||||||     |||
                                ACCGACGACGAG     GGG
                                      A_____
GAM496  RIN      5'  TGGCTGCTGGTCCTCCGC    13314         T  AACGGAC
                                TGGCTGCTG TC      CCGC
                                ||||||||| ||      ||||
                                ACCGACGAC AG      GGCG
                                     C  GA_____
GAM496  SLC37A1   3'  GGTTGCTGGGCTTGGACCCGCC 13315    C    TTCAAC
                                GG TGCTG     GGACCCGCC
                                || |||||     |||||||||
                                CC ACGAC     CCTGGGCGG
                                 A    CCGAA_
GAM496  SQRDL    3'  TGGTTGCTGTTCAAAGGTAC   13316    C       C  _
                                TGG TGCTGTTCAA GG AC
                                ||| |||||||||| || ||
                                ACC ACGACAAGTT CC TG
                                  A        T  A
GAM496  TBC1D2   3'  TGCCTGACCTCCAGTGGGTCTG 13317    G  _  G   AC  ACCC
             CC                    TG CTG CT TTCA  GG   GCC
                                || ||| || ||||  ||   |||
                                AC GAC GG AGGT  CC   CGG
                                 G   T  _   CA  CAGA
GAM496  LOC144681 5'  TGCCTGTCCGCGTGGACCCGC  13318    G  _   TCAAC
                                TG CTG CTGT    GGACCCGC
                                || ||| ||||    ||||||||
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                                AC GAC GGCG    CCTGGGCG
                                 G   A   CA___
GAM496  LOC148195 5'  TGGGTGCTGTTTGGCATGGCC  13319    C     CAAC  ACCC
                                TGG TGCTGTT   GG   GCC
                                ||| |||||||   ||   |||
                                ACC ACGACAA   CC   CGG
                                  C     A___  GTAC
GAM496  LOC151457 5'  TGGTTGCTGTTCAAGTGAATGC 13320    C       CG  CCC
            C                    TGG TGCTGTTCAA  GA   GCC
                                ||| ||||||||||  ||   |||
                                ACC ACGACAAGTT  CT   CGG
                                  A        CA  TA_
GAM496  LOC151458 5'  TGGTTGCTGTTCAAGTGAATGC 13320    C       CG  CCC
            C                    TGG TGCTGTTCAA  GA   GCC
                                ||| ||||||||||  ||   |||
                                ACC ACGACAAGTT  CT   CGG
                                  A        CA  TA_
GAM496  LOC199986 5'  GGCTGCTGAAGGCTGGACCTGC 13321       TTCAAC    C
            C                    GGCTGCTG     GGACC GCC
                                ||||||||     ||||| |||
                                CCGACGAC     CCTGG CGG
                                     TTCCGA    A
GAM496  LOC222128 5'  TGGCAGCCTCAACGGAC    13322     T   GT
                                TGGC GCT  TCAACGGAC
                                |||| |||  |||||||||
                                ACCG CGG  AGTTGCCTG
                                  T   __
GAM496  LOC222242 5'  TGGCAGCCTCAACGGAC    13322     T   GT
                                TGGC GCT  TCAACGGAC
                                |||| |||  |||||||||
                                ACCG CGG  AGTTGCCTG
                                  T   __
GAM496  LOC253044 3'  TGGCTGCTGTCTGACTGC    13323         CAACG   CC
                                TGGCTGCTGTT    GAC  GC
                                ||||||||||    |||  ||
                                ACCGACGACAG    CTG  CG
                                      A____   A_
GAM496  LOC255718 5'  GGCTGCTGGCGGGGCCCG    13324       TTCAA   A_
                                GGCTGCTG    CGG  CCCG
                                ||||||||    |||  ||||
                                CCGACGAC    GCC  GGGC
                                     C____   CC
GAM496  LOC256950 3'  GCTGCTGTTTGGAGGCTCCCGC 13325       CAAC  A_
                                GCTGCTGTT   GG  CCCGC
                                |||||||||   ||  |||||
                                CGACGACAA   CC  GGGCG
                                      ACCT  GA
GAM496  LOC91516  5'  TGGCTGCCTGTTCAGTGGGA  13326       _     AC_
                                TGGCTGC TGTTCA   GGA
                                ||||||| ||||||   |||
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                                ACCGACG ACAAGT   CCT
                                    G     CAC
GAM497  CAPZA1   3'  TAACAGAAAATTACAAGGCAG  13329          GCTCTT
                                TAACAGGAAAT     AGGCAG
                                ||||||||||      ||||||
                                ATTGTCTTTTA     TCCGTC
                                      ATGT__
GAM497  CDK10    3'  AACAGGAAGTGCAGCA      13330        A   TCTTA
                                AACAGGAA TGC    GGCA
                                |||||||| |||    ||||
                                TTGTCCTT ACG    TCGT
                                    C  _____
GAM497  CHRNA10  3'  ACAGGAAATGCAGCA       13331          TCTTA
                                ACAGGAAATGC    GGCA
                                ||||||||||     ||||
                                TGTCCTTTACG    TCGT
                                       _____
GAM497  DKK1     3'  TAACAAGAGGAAAAATAGGCAG 13332        AATGCTCT
                                TAACAGGA       TAGGCAG
                                ||||||||       |||||||
                                ATTGTTCT       ATCCGTC
                                    CCTTTTT_
GAM497  ESR1     3'  AGGAAATGAGCTGGCAG     13333        CT  TA
                                AGGAAATG  CT  GGCAG
                                ||||||||  ||  |||||
                                TCCTTTAC  GA  CCGTC
                                    TC  __
GAM497  GRLF1    3'  CAACAGGAAGTGTTCTCTTCAG 13334         A  C    AGG
                                TAACAGGAA TG TCTT   CAG
                                ||||||||| || ||||   |||
                                GTTGTCCTT AC AGAG   GTC
                                    C  A   AA_
GAM497  KRTHA4   3'  AACAGGAAATGCAGTAG     13335          TCT
                                AACAGGAAATGC   TAG
                                ||||||||||||   |||
                                TTGTCCTTTACG   ATC
                                      TC_
GAM497  MECP2    3'  AGGAAGTGCTAGACAG      13336      A   CTT
                                AGGAA TGCT   AGGCAG
                                |||||  ||||   ||||||
                                TCCTT ACGA   TCTGTC
                                  C   ___
GAM497  PCSK1    3'  TAACAGAAGATGCGGGTAG   13337        A   TCT
                                TAACAGGA ATGC   TAG
                                |||||||| ||||   |||
                                ATTGTCTT TACG   ATC
                                    C   CCC
GAM497  PIGR     3'  AGGAAAAACCTAGGCAG     13338       TGCT
                                AGGAAA   CTTAGGCAG
                                ||||||   |||||||||
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                                TCCTTT   GGATCCGTC
                                   TT__
GAM497  PPIF    3'  CAGGAAATGCTTCCCTCCGG  13339          ___  A
                                CAGGAAATGCT  CTT GG
                                ||||||||||  ||| ||
                                GTCCTTTACGA  GAG CC
                                      AGG  G
GAM497  TCTA    3'  CAACAGGAAGGAAGTAGGCAG  13340        ATGCTCT
                                TAACAGGAA     TAGGCAG
                                |||||||||     |||||||
                                GTTGTCCTT     ATCCGTC
                                     CCTTC__
GAM497  TGIF    3'  TAACAGGAAGCTGTTTTAG   13341        AT  C__
                                TAACAGGAA  GCT  TTAG
                                |||||||||  |||  ||||
                                ATTGTCCTT  CGA  AATC
                                     __  CAA
GAM497  AKR7A2  3'  ACAGAAAAGCCTTGGGCAG   13342        T  T  A
                                ACAGGAAA GC CTT GGCAG
                                |||||||| || ||| |||||
                                TGTCTTTT CG GAA CCGTC
                                     _ _  C
GAM497  C20orf59  5'  TAACAGAAATGCCACTGTGG  13343      G     _  TA
                                TAACAG AAATGCT CT  GG
                                |||||| ||||||| ||  ||
                                ATTGTC TTTACGG GA  CC
                                   _     T  CA
GAM497  DKFZP434H132 3'  ACAGGGTATGTATCAGGCAG  13344     AA  CTC
                                ACAGG  ATG  TTAGGCAG
                                |||||  |||  ||||||||
                                TGTCC  TAC  AGTCCGTC
                                   CA  AT_
GAM497  DKFZP434H132 3'  ACAGGGTATGTATCAGGCAG  13344     AA  CTC
                                ACAGG  ATG  TTAGGCAG
                                |||||  |||  ||||||||
                                TGTCC  TAC  AGTCCGTC
                                   CA  AT_
GAM497  DKFZP761E1824 3'  TAACAGAAATGCTTTTA    13345      G     C
                                TAACAG AAATGCT TTA
                                |||||| ||||||| |||
                                ATTGTC TTTACGA AAT
                                   _     A
GAM497  FLJ10511  3'  TAACAAGAAATGTTTTCAG   13346         CTC
                                TAACAGGAAATG  TTAG
                                ||||||||||||  ||||
                                ATTGTTCTTTAC  AGTC
                                      AAA
GAM497  FLJ12806  3'  ACAGACCTTCTTAGGCAG   13347      AAATGC
                                ACAGG    TCTTAGGCAG
                                |||||    ||||||||||
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                                TGTCT     AGAATCCGTC
                                  GGA___
GAM497  FLJ13291  3'  TAACAGGATGTCAGCAGGGCAG 13348        AAT__  TCTTA
                                TAACAGGA    GC    GGCAG
                                ||||||||    ||    |||||
                                ATTGTCCT    CG    CCGTC
                                     ACAGT  TC___
GAM497  FLJ23360  3'  TAACAGGAAGGGCTCCCAG   13349        AT
                                TAACAGGAA  GCTCTTAG
                                |||||||||  ||||||||
                                ATTGTCCTT  CGAGGGTC
                                     CC
GAM497  GTPBP5    3'  CAGGAAATACGGAGGGCAG   13350        TCTTA
                                CAGGAAATGC    GGCAG
                                ||||||||||    |||||
                                GTCCTTTATG    CCGTC
                                      CCTC_
GAM497  HNRNPG-T  3'  TAACAGGAAATTCTTAAA    13351         GC
                                TAACAGGAAAT  TCTTAGG
                                ||||||||||  |||||||
                                ATTGTCCTTTA  AGAATTT
                                          __
GAM497  KIAA0057  3'  AGAGTGCTTTTAGGCAG     13352     AA   C
                                GGA  TGCT TTAGGCAG
                                |||  |||| ||||||||
                                TCT  ACGA AATCCGTC
                                  C_   A
GAM497  KIAA0257  3'  TAACGGGAAAGGTTCTCAG   13353      A    TGC
                                TAAC GGAAA   TCTTAG
                                |||| |||||   ||||||
                                ATTG CCTTT   AGAGTC
                                   C    CCA
GAM497  KIAA0937  3'  CAGGAAATTGCCCTGTGG    13354        _    TA
                                CAGGAAAT GCTCT  GG
                                |||||||| |||||  ||
                                GTCCTTTA CGGGA  CC
                                     A    CA
GAM497  KIAA1238  3'  CAGGAAATGTTAGAC       13355        CTC
                                CAGGAAATG   TTAGGC
                                |||||||||   ||||||
                                GTCCTTTAC   AATCTG
                                          ___
GAM497  MGC5601   5'  CAGGTAATGAGCCAGGCAG   13356     A   CTC
                                CAGG AATG   TTAGGCAG
                                |||| ||||   ||||||||
                                GTCC TTAC   GGTCCGTC
                                  A   TC_
GAM497  N-PAC     3'  TAAAAGGAAATGGAGATAGG  13357     C      CTCT
                                TAA AGGAAATG    TAGG
                                ||| ||||||||    ||||
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                                ATT TCCTTTAC    ATCC
                                  T       CTCT
GAM497  PCANAP7   5'  CAGGAGATGCTCTCTGCA    13358       A       AG
                                CAGGA ATGCTCTT  GCA
                                ||||| ||||||||  |||
                                GTCCT TACGAGAG  CGT
                                   C       A_
GAM497  SNPH      3'  CAACGGGAGGAGGTATTAGGCA 13359      A   AATGCTC
          G                      TAAC GGA      TTAGGCAG
                                ||||| |||      ||||||||
                                GTTG CCT      AATCCGTC
                                  C   CCTCCAT
GAM497  TCF-3     3'  TAACAGGAAATGTCACAATGGC 13360          C  TTA__
          AG                     TAACAGGAAATG TC     GGCAG
                                ||||||||||||| ||     |||||
                                ATTGTCCTTTAC AG     CCGTC
                                       _  TGTTA
GAM497  LOC126917 3'  TAACAAGAGATGCTGAC      13361        A    CTTA
                                TAACAGGA ATGCT    GGC
                                |||||||| |||||    |||
                                ATTGTTCT TACGA    CTG
                                     C    _____
GAM497  LOC134111 3'  TAACAGGAAGTTTACACCACAG 13362         A__   T  TAG
                                TAACAGGAA   TGC CT   GCAG
                                |||||||||   ||| ||   ||||
                                ATTGTCCTT   ATG GG   TGTC
                                      CAA   T  ___
GAM497  LOC143381 3'  CAGGAAATGCCACGGGCAG    13363          CTTA
                                CAGGAAATGCT    GGCAG
                                ||||||||||    |||||
                                GTCCTTTACGG    CCGTC
                                       TGC_
GAM497  LOC145891 3'  TAACAGGAAAGCATGGTAG    13364          T  TCT_
                                TAACAGGAAA GC    TAG
                                |||||||||| ||    |||
                                ATTGTCCTTT CG    ATC
                                       _  TACC
GAM497  LOC148413 3'  GGAAATGCTCCCACATCAG    13365          GG_
                                GGAAATGCTCTTA   CAG
                                ||||||||||||   |||
                                CCTTTACGAGGGT   GTC
                                        GTA
GAM497  LOC152426 3'  ACAGGAGGTCCCAGGCAG     13366       AATGC
                                ACAGGA    TCTTAGGCAG
                                ||||||    ||||||||||
                                TGTCCT    AGGGTCCGTC
                                   CC___
GAM497  LOC157285 3'  ACAGGAAAGGGTTAGGCAG    13367        TGCTC
                                ACAGGAAA    TTAGGCAG
                                ||||||||    ||||||||
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                                TGTCCTTT    AATCCGTC
                                    CCC__
GAM497  LOC199923 3'  AGGAAACACTGCTCTTAGGCAG 13368      ___
                                AGGAAA  TGCTCTTAGGCAG
                                ||||||  ||||||||||||||
                                TCCTTT  ACGAGAATCCGTC
                                   GTG
GAM497  LOC219848 3'  CAGGAAATGTTGAGTCCCAG  13369       C____
                                CAGGAAATG   TCTTAG
                                |||||||||   ||||||
                                GTCCTTTAC   AGGGTC
                                     AACTC
GAM497  LOC222112 5'  CAACAGGAAATGCAGTGGCAG 13370          TCTTA
                                TAACAGGAAATGC   GGCAG
                                ||||||||||||    |||||
                                GTTGTCCTTTACG   CCGTC
                                        TCA__
GAM497  LOC222166 3'  TAACATGAAATGCTCATGG   13371     G      TTA
                                TAACA GAAATGCTC  GG
                                ||||| |||||||||  ||
                                ATTGT CTTTACGAG  CC
                                   A       TA_
GAM497  LOC57151  3'  TAACATGAAGTGGAGGCA    13372     G  A  CTCTT
                                TAACA GAA TG    AGGCA
                                ||||| ||| ||    |||||
                                ATTGT CTT AC    TCCGT
                                   A  C  C____
GAM498  MGC12992  5'  GCGCAGCGCGGTTTGGGTG   13375        ACC  CAA
                                GCGCGGCGCGG  TTT  GTG
                                ||||||||||  |||  |||
                                CGCGTCGCGCC  AAA  CAC
                                       ___  CC_
GAM499  ARHGAP6   3'  TCCTATGTAAAAATATGGCTTC 13378     TTACCGCTC
           T                    TCCT       ATATGGCTTCT
                                ||||       ||||||||||
                                AGGA       TATACCGAAGA
                                  TACATTTT_
GAM499  ARHGAP6   3'  TCCTATGTAAAAATATGGCTTC 13378     TTACCGCTC
           T                    TCCT       ATATGGCTTCT
                                ||||       ||||||||||
                                AGGA       TATACCGAAGA
                                  TACATTTT_
GAM499  CDC2L2    5'  CTTTTAACTGTGCTGGCTTCT  13379     ACC  CATA
                                CTTT  GCT   TGGCTTCT
                                ||||  |||   ||||||||
                                GAAA  TGA   ACCGAAGA
                                  AT_  CACG
GAM499  LFG       3'  TCCTTTACAGCTTGTGACACCT 13380       C  CATA  T
                                TCCTTTAC GCT   TGGC TCT
                                |||||||| |||   |||| |||
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                                AGGAAATG CGA   ACTG GGA
                                    T  AC__   T
GAM499  MAPK10   5' CCACAGCTTGTATGGTTTCT  13381    C  CA   C
                                TTAC GCT  TATGG TTCT
                                |||| |||  ||||| ||||
                                GGTG CGA  ATACC AAGA
                                  T  AC    A
GAM499  PDGFRB   5' TCCTTGCTGCTGATGGCTTCT 13382     TACC  CAT
                                TCCTT   GCT  ATGGCTTCT
                                |||||   |||  |||||||||
                                AGGAA   CGA  TACCGAAGA
                                  CGA_  C__
GAM499  FLJ12619 3' TCCTCTACCTATCATGGTTTCT 13383       GCTCA   C
                                TCCTTTACC    TATGG TTCT
                                |||||||||    ||||| ||||
                                AGGAGATGG    GTACC AAGA
                                     ATA__    A
GAM499  FLJ20249 3' TCCTTTAGCTGCCTGGCTTCT 13384      CC  CATA
                                TCCTTTA GCT   TGGCTTCT
                                |||||||  |||   ||||||||
                                AGGAAAT  CGA   ACCGAAGA
                                   __  CGG_
GAM499  FLJ23120 3' TCCTTTGTGACTGGCTTC   13385      ACC  CATAT
                                TCCTTT  GCT   GGCTTC
                                ||||||  |||   ||||||
                                AGGAAA  TGA   CCGAAG
                                   CAC  _____
GAM499  GIOT-2   3' CTTACATTTATATGGCTTCT  13386     CGCTC
                                TTTAC    ATATGGCTTCT
                                |||||    ||||||||||
                                GAATG    TATACCGAAGA
                                  TAAA_
GAM499  HSZFP36  3' TCCTTACACTCATATGGCTTCT 13388     TAC
                                TCCTT  CGCTCATATGGCTTCT
                                |||||  ||||||||||||||||
                                AGGAA  GTGAGTATACCGAAGA
                                  T__
GAM499  HSZFP36  3' TCCTTACATTCATATGGCTTCT 13387     T  CGC
                                TCCTT AC  TCATATGGCTTCT
                                ||||| ||  ||||||||||||
                                AGGAA TG  AGTATACCGAAGA
                                  _ TA_
GAM499  KIAA0193 3' TCCTTTCTGGCTATGGCTTCT  13389     ACC  CAT
                                TCCTTT  GCT  ATGGCTTCT
                                ||||||  |||  |||||||||
                                AGGAAA  CGA  TACCGAAGA
                                   GAC  ___
GAM499  KIAA1737 3' TCCATTTGCTGATCTGGCTTCT 13390    TTTACC  C  A
                                TCC    GCT AT TGGCTTCT
                                |||    ||| || ||||||||
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                                AGG     CGA TA ACCGAAGA
                                  TAAA__   C  G
GAM499  KIAA1871  3'  CTTTACATTCATATGGTTTCT  13391      CGC       C
                                CTTTAC   TCATATGG TTCT
                                ||||||   |||||||| ||||
                                GAAATG   AGTATACC AAGA
                                   TA_       A
GAM499  MGC13071  5'  TCCTTACATTCATGTGGCTTCT 13392      T  CGC    A
                                TCCTT AC   TCAT TGGCTTCT
                                ||||| ||   |||| ||||||||
                                AGGAA TG   AGTA ACCGAAGA
                                   _ TA_   C
GAM499  MGC2488   3'  CTTTAACTGGTCATGGCTTCT  13393      CC   CA_
                                CTTTA  GCT   TATGGCTTCT
                                |||||  |||   ||||||||||
                                GAAAT  TGA   GTACCGAAGA
                                   __   CCA
GAM499  PCDH10    3'  CTTTACCAGTTCAGATGTTTCT 13394       C_   T   GC
                                CTTTACCG  TCA ATG  TTCT
                                ||||||||  ||| |||  ||||
                                GAAATGGT  AGT TAC  AAGA
                                     CA   C   A_
GAM499  RBAK      3'  TCCATTAGAAATATGGCTT    13395     T   CCGCTC
                                TCC TTA      ATATGGCTT
                                ||| |||      |||||||||
                                AGG AAT      TATACCGAA
                                  T   CTT____
GAM499  LOC126133 3'  TCCTTTACTGCATATGGATTCT 13396       C  TC     C
                                TCCTTTAC GC  ATATGG TTCT
                                ||||||||  ||  |||||| ||||
                                AGGAAATG CG  TATACC AAGA
                                     A  __      T
GAM499  LOC149113 3'  TCCTTTGCCTTTTCCAGCTTCT 13397       A  GCTCATA
                                TCCTTT CC       TGGCTTCT
                                ||||||  ||      ||||||||
                                AGGAAA GG       GTCGAAGA
                                   C  AAAAG__
GAM499  LOC154403 3'  TCCTTTGCCTTTTCCAGCTTCT 13397       A  GCTCATA
                                TCCTTT CC       TGGCTTCT
                                ||||||  ||      ||||||||
                                AGGAAA GG       GTCGAAGA
                                   C  AAAAG__
GAM499  LOC154992 3'  TCCTTTGCCTTTTCTAGCTTCT 13398       A  GCTCATA
                                TCCTTT CC       TGGCTTCT
                                ||||||  ||      ||||||||
                                AGGAAA GG       ATCGAAGA
                                   C  AAAAG__
GAM499  LOC158428 3'  TTCACCAGTATGGCTTCT     13399       CTCA
                                TTTACCG    TATGGCTTCT
                                |||||||    ||||||||||
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                                AAGTGGT   ATACCGAAGA
                                   C___
GAM499  LOC163081 3'  TCATTACATTCATATGGTTTCT 13400   CT   CGC      C
                                TC  TTAC   TCATATGG TTCT
                                ||  ||||   |||||||| ||||
                                AG  AATG   AGTATACC AAGA
                                 T_   TA_      A
GAM499  LOC163255 3'  TCCTTACATTCATATGGTTTCT 13401     T  CGC      C
                                TCCTT AC   TCATATGG TTCT
                                ||||| ||   |||||||| ||||
                                AGGAA TG   AGTATACC AAGA
                                   _ TA_      A
GAM499  LOC201868 3'  TCCTTTGCCTTTCCCAGCTTCT 13402      A  GC  ATAT
                                TCCTTT CC  TC   GGCTTCT
                                |||||| ||  ||   |||||||
                                AGGAAA GG  AG   TCGAAGA
                                   C  AA  GG__
GAM499  LOC221069 3'  CTCTTTGTTACACATGGCTTCT 13403     ACCGCT
                                CTTT     CATATGGCTTCT
                                ||||     ||||||||||||
                                GAGA     GTGTACCGAAGA
                                  AACAAT
GAM499  LOC255285 3'  CCCTTTACTGCTTGTGTCTT   13404       C   CATA  G
                                TCCTTTAC GCT   TG CTT
                                |||||||| |||   || |||
                                GGGAAATG CGA   AC GAA
                                     A   AC__  A
GAM499  LOC57149  5'  TCCTTTGCTGGCTTCT     13405      ACC   CATAT
                                TCCTTT   GCT   GGCTTCT
                                ||||||   |||   |||||||
                                AGGAAA   CGA   CCGAAGA
                                   ___   ______
GAM500  KAL1     3'  TGATTAGCAGCTTATTTCA   13408     AC       CG
                                TGA  AGCAGCTTGT  CG
                                |||  ||||||||||  ||
                                ACT  TCGTCGAATA  GT
                                  AA        AA
GAM500  PROC     3'  GAACAGCAGGCCGGTGTGCT   13409       CTT   C___
                                GAACAGCAG   GTCG   GCT
                                |||||||||   ||||   |||
                                CTTGTCGTC   CGGC   CGA
                                     ___    CACA
GAM500  C11orf21  3'  TAAACAGCAGGTGCTTAT    13410        ___
                                TGAACAGCA   GCTTGT
                                |||||||||   ||||||
                                ATTTGTCGT   CGAATA
                                     CCA
GAM500  FLJ14154  3'  GAGCAGCAGCTTGTGGCAGC   13411    A        C  _
                                GA CAGCAGCTTGT GC GC
                                || ||||||||||| || ||
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                                CT GTCGTCGAACA CG CG
                                 C         C  T
GAM500  SYT6     3'  TAAACAGCAGCTTGATACTTCA 13412           TC  GC
           T                    TGAACAGCAGCTTG  GC  TCAT
                                |||||||||||||  ||  ||||
                                ATTTGTCGTCGAAC  TG  AGTA
                                       TA  A_
GAM500  LOC221472 5'  TGAGCAGCAGCTCGTAACG   13413     A        C
                                TGA CAGCAGCTTGT GCG
                                ||| ||||||||||| |||
                                ACT GTCGTCGAGCA TGC
                                  C         T
GAM501  GJB3     5'  GTGCCTTGTTTCTGTGCTGCTG 13416          AT__   C
           T                    GTGCCTTGTTTT   CTGC GT
                                ||||||||||||   |||| ||
                                CACGGAACAAAG   GACG CA
                                       ACAC   A
GAM501  DKFZP727G051 5'  GTGCCTGTTTCTGTGT     13417      T  TTA   CC
                                GTGCCT GTT   TCTG  GT
                                |||||| |||   ||||  ||
                                CACGGA CAA   AGAC  CA
                                   _  ___    A_
GAM501  FLJ10546  3'  CCTTGTTTTATTTGGGCTGT  13418         CT__  C
                                CCTTGTTTTAT   GC GT
                                ||||||||||   || ||
                                GGAACAAAATA   CG CA
                                       AACC  A
GAM501  LOC91695  5'  GTGCCTTGTTGAATGCCGT   13419        TTATC
                                GTGCCTTGTT    TGCCGT
                                ||||||||||    ||||||
                                CACGGAACAA    ACGGCA
                                      CTT__
GAM502  CSK      3'  ACGTCTGCCTCGGGCGCAT   13422     A__
                                GCGT   CCTCGGGCGCGT
                                ||||   ||||||||||||
                                TGCA   GGAGCCCGCGTA
                                  GAC
GAM502  MAPK12    5'  CGCGCGCCTCGGGCCGGC    13423     TA      GCGT
                                CGCG  CCTCGGGC   TGGC
                                ||||  ||||||||   ||||
                                GCGC  GGAGCCCG   GCCG
                                  GC      ____
GAM502  Rabip4R   5'  CGCGGTCTCGGGCGGAGGCT   13424     TAC      CGTT
                                CGCG   CTCGGGCG   GGCT
                                ||||   ||||||||   ||||
                                GCGC   GAGCCCGC   CCGA
                                  CA_      CT__
GAM502  RAI17    3'  GCTACCTGGCGTTGGC     13425    G    CGGGC
                                GC TACCT    GCGTTGGC
                                || |||||    ||||||||
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                                CG ATGGA    CGCAACCG
                                 _    C____
GAM502  LOC150946 3'  GCGTTCTCGGGCAAAGAAGCT  13426     AC      CGTT
                                GCGT  CTCGGGCG   GGCT
                                ||||  ||||||||   ||||
                                CGCA  GAGCCCGT   TCGA
                                  A_      TTCT
GAM502  LOC153572 3'  CGCGGCCTCGGGCGGGGGGCT  13427     TA      CGTT
                                CGCG  CCTCGGGCG   GGCT
                                ||||  |||||||||   ||||
                                GCGC  GGAGCCCGC   CCGA
                                  C_      CCC_
GAM502  LOC219855 5'  CGCGTGTCCCGGGCTGGACTGG 13428      AC      GCG_
          CT                    CGCGT  CTCGGGC   TTGGCT
                                |||||  |||||||   ||||||
                                GCGCA  GGGCCCG   GACCGA
                                  CA      ACCT
GAM502  LOC256158 5'  ACGTGATCTTGGGCGCTGGCT  13429     AC_  C     GT
                                GCGT   CT GGGCGC  TGGCT
                                ||||   || ||||||  |||||
                                TGCA   GA CCCGCG  ACCGA
                                  CTA  A     __
GAM503  ACP1    3'  TACTGTCAATCCACAAAAGGCC 13432     GCAC      T   A
                                TAC    CAATCCACG AGAG CC
                                |||    ||||||||| |||| ||
                                ATG    GTTAGGTGT TTTC GG
                                  ACA_        _    C
GAM503  ACP1    3'  TACTGTCAATCCACAAAAGGCC 13432     GCAC      T   A
                                TAC    CAATCCACG AGAG CC
                                |||    ||||||||| |||| ||
                                ATG    GTTAGGTGT TTTC GG
                                  ACA_        _    C
GAM503  EMS1    3'  CGTCCCAATCCAGAGAC     13433    CA      CGTA
                                CG  CCAATCCA    GAGAC
                                ||  ||||||||    |||||
                                GC  GGTTAGGT    CTCTG
                                 AG       _____
GAM503  EMS1    3'  CGTCCCAATCCAGAGAC     13433    CA      CGTA
                                CG  CCAATCCA    GAGAC
                                ||  ||||||||    |||||
                                GC  GGTTAGGT    CTCTG
                                 AG       _____
GAM503  NKX3A   3'  GCCACCAACAGTAGAGAC    13434    _     CCAC
                                GC ACCAAT    GTAGAGAC
                                || ||||||    ||||||||
                                CG TGGTTG    CATCTCTG
                                 G     T___
GAM503  TPM1    3'  GCACCAATCCACACCTGA    13435           TA_
                                GCACCAATCCACG   GA
                                ||||||||||||   ||
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                                CGTGGTTAGGTGT  CT
                                      GGA
GAM503  WASF3    3'  TACCACTATTTGGGTGTAGAGA 13436    G  CAATCCAC_
           CC                   TAC CAC       GTAGAGACC
                                ||| |||       |||||||||
                                ATG GTG       CATCTCTGG
                                  _  ATAAACCCA
GAM503  RASSF2   3'  TACGCACCAGCGAGA      13437        ATCCAC  A
                                TACGCACCA     GT GAGA
                                |||||||||     || ||||
                                ATGCGTGGT     CG CTCT
                                       _______ _
GAM503  LOC147922 3'  TACTGCCAATCCATAATGACC  13438    GCA      CG  A
                                TAC  CCAATCCA  TAG GACC
                                |||  ||||||||  ||| ||||
                                ATG  GGTTAGGT  ATT CTGG
                                  AC_      __  A
GAM504  ABCC3    3'  GGCCAGGAGGAAATCTCAG   13441        C   C
                                GGCCAGGAGG AATC CAG
                                |||||||||| |||| |||
                                CCGGTCCTCC TTAG GTC
                                      T   A
GAM504  ABCC3    3'  GGCCAGGAGGAAATCTCAG   13441        C   C
                                GGCCAGGAGG AATC CAG
                                |||||||||| |||| |||
                                CCGGTCCTCC TTAG GTC
                                      T   A
GAM504  ABCC3    3'  GGCCAGGAGGAAATCTCAG   13441        C   C
                                GGCCAGGAGG AATC CAG
                                |||||||||| |||| |||
                                CCGGTCCTCC TTAG GTC
                                      T   A
GAM504  ABCF1    3'  GGCCAGAGGCAGTCTTCAGAGG 13442      G    A  C_
           AG                   GGCCAG AGGCA TC  CAGAGGAG
                                |||||| ||||| ||  ||||||||
                                CCGGTC TCCGT AG  GTCTCCTC
                                  _    C  AA
GAM504  ADCY8    5'  GGCCAGAAGCATCCCTCCCGGA 13443      G    A___   A
           GG                   GGCCAG AGGCA   TCCC GAGG
                                |||||| |||||   |||| ||||
                                CCGGTC TTCGT   AGGG CTCC
                                  _    AGGG   C
GAM504  AKT1     3'  GGCCAGGAGGCGTGGAGG    13444         AATCCCA
                                GGCCAGGAGGC     GAGG
                                ||||||||||      ||||
                                CCGGTCCTCCG     CTCC
                                      CAC____
GAM504  ALDH3A1  3'  GGTCAGCAGGTCAGCAGAGGAG 13445   C  G  _  ATCC
                                GG CAG AGG CA   CAGAGGAG
                                || ||| ||| ||   ||||||||
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                                CC GTC TCC GT    GTCTCCTC
                                 A  G  A  C___
GAM504  BLAME    3'  GGCTGGAGGCAATTCCTTGG  13446    CA       C  AGA
                                GGC  GGAGGCAAT CC   GG
                                |||  |||||||||| ||   ||
                                CCG  CCTCCGTTA GG   CC
                                  A_       A  AA_
GAM504  CHRNB4   3'  GGGAAGGCCTCTCAGAGGAG  13447    CCA     AA  C
                                GG   GGAGGC  TC CAGAGGAG
                                ||   ||||||  || ||||||||
                                CC   CTTCCG  AG GTCTCCTC
                                 ___     G_  A
GAM504  DLEC1    3'  GGCCTGGGGACCAGAGGA    13448      A  A  CAATC
                                GGCC GG GG    CCAGAGGA
                                |||| || ||    ||||||||
                                CCGG CC CC    GGTCTCCT
                                  A  _  T____
GAM504  DLEC1    3'  GGCCTGGGGACCAGAGGA    13448      A  A  CAATC
                                GGCC GG GG    CCAGAGGA
                                |||| || ||    ||||||||
                                CCGG CC CC    GGTCTCCT
                                  A  _  T____
GAM504  EFNB1    3'  GGCCAGGAGGCAGTGTGGA   13449          ATCCCAGA
                                GGCCAGGAGGCA       GGA
                                ||||||||||||       |||
                                CCGGTCCTCCGT       CCT
                                       CACA____
GAM504  GAMT     3'  GGCCAGGAAGGCACGGAGGAG  13450        _   ATCCCA
                                GGCCAGGA GGCA     GAGGAG
                                |||||||| ||||     ||||||
                                CCGGTCCT CCGT     CTCCTC
                                    T   GC____
GAM504  IL6R     3'  GGCCAGGAGCATGGCGGCTGGA 13451       ____  AATCCCA
           GGAG                  GCCAGGA   GGC      GAGGAG
                                |||||||   |||      ||||||
                                CGGTCCT   CCG      CTCCTC
                                   CGTA   CCGAC__
GAM504  KCNH3    3'  GACCGGGAGGTCAGAGGA    13452      A    CAATCC
                                GGCC GGAGG     CAGAGGA
                                |||| |||||     |||||||
                                CTGG CCTCC     GTCTCCT
                                  C    A_____
GAM504  KHK      3'  GGCTGGTGGGCAGGGCAGAGGA 13453     CA  A_   ATCC
           G                    GGC  GG  GGCA   CAGAGGAG
                                |||  ||  ||||   ||||||||
                                CCG  CC  CCGT   GTCTCCTC
                                  A_  AC   CCC_
GAM504  KHK      3'  GGCTGGTGGGCAGGGCAGAGGA 13453     CA  A_   ATCC
           G                    GGC  GG  GGCA   CAGAGGAG
                                |||  ||  ||||   ||||||||
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                                CCG  CC  CCGT   GTCTCCTC
                                  A_  AC   CCC_
GAM504  MEN1    3'  GGCAGGAGGCGGCAGGGGA  13454    C     AATCC  A
                                GGC AGGAGGC    CAG GGA
                                ||| |||||||    ||| |||
                                CCG TCCTCCG    GTC CCT
                                  _      CC___   C
GAM504  MLLT7   5'  GGCCAGGAGGCACATTCC    13455          A__
                                GGCCAGGAGGCA   TCC
                                ||||||||||||   |||
                                CCGGTCCTCCGT   AGG
                                       GTA
GAM504  MUC5B   3'  GGCCGGGGGGGCTCCGCAGAGGA 13456     A  A   AA   _
          G                     GGCC GG GGC  TCC CAGAGGAG
                                |||| || |||  ||| ||||||||
                                CCGG CC CCG  AGG GTCTCCTC
                                  C  C   __   C
GAM504  NPTX1   3'  GGCCAGGAGGCTGCAGGG    13457          AATCC   A
                                GGCCAGGAGGC    CAG GG
                                ||||||||||     ||| ||
                                CCGGTCCTCCG    GTC CC
                                       AC___   _
GAM504  NUCB1   3'  GGCCAAGAGGTCCAGGAGGAG  13458         CAA   CA
                                GGCCAGGAGG   TCC  GAGGAG
                                |||||||||   |||  ||||||
                                CCGGTTCTCC   AGG  CTCCTC
                                      ___   TC
GAM504  ODF2    5'  GCTCAGGGGGACCCAGAGG   13459    _   A  CAAT
                                GC CAGG GG    CCCAGAGG
                                || |||| ||    ||||||||
                                CG GTCC CC    GGGTCTCC
                                  A    _  CT__
GAM504  OVOL1   3'  AGCTGGGAGGCAATCCTGG   13460     CA        CAGA
                                GGC  GGAGGCAATCC    GG
                                |||  ||||||||||    ||
                                TCG  CCTCCGTTAGG    CC
                                  AC         A___
GAM504  PHKG2   3'  GGCCAGAGCCCAGAGG      13461       G  GCAAT
                                GGCCAG AG    CCCAGAGG
                                ||||||  ||    ||||||||
                                CCGGTC TC    GGGTCTCC
                                       _  ______
GAM504  PPP2R5B 3'  GGCCAGGAGCAGAGG       13462         GCAATCC
                                GGCCAGGAG      CAGAGG
                                |||||||||      ||||||
                                CCGGTCCTC      GTCTCC
                                       ________
GAM504  PSMB8   3'  GGCCAAGACCTCCCAGAGGAG  13463         GGCAA
                                GGCCAGGA    TCCCAGAGGAG
                                ||||||||    ||||||||||
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                                CCGGTTCT    AGGGTCTCCTC
                                    GG___
GAM504  PSMB8   3'  GGCCAAGACCTCCCAGAGGAG  13463       GGCAA
                                GGCCAGGA    TCCCAGAGGAG
                                ||||||||    ||||||||||
                                CCGGTTCT    AGGGTCTCCTC
                                    GG___
GAM504  PSMB8   3'  GGCCAAGACCTCCCAGAGGAG  13463       GGCAA
                                GGCCAGGA    TCCCAGAGGAG
                                ||||||||    ||||||||||
                                CCGGTTCT    AGGGTCTCCTC
                                    GG___
GAM504  PTPRN   3'  GGCTGGTGGGGCAGTGAGGAG  13464    CA__  A   ATCCCA
                                GGC   GG GGCA     GAGGAG
                                |||   || ||||     ||||||
                                CCG   CC CCGT     CTCCTC
                                  ACCA  _   CA____
GAM504  SHC1    3'  GGCCAGGAGGCACTGAGCAAGG 13465          ATCC_  A
            GAG                   GGCCAGGAGGCA    CAG GGAG
                                ||||||||||||    ||| ||||
                                CCGGTCCTCCGT    GTT CCTC
                                      GACTC   C
GAM504  SLC29A1 3'  GGCAGGAGGCAGACAGGGAG  13466    C      ATCC   A
                                GGC AGGAGGCA    CAG GGAG
                                ||| ||||||||    ||| ||||
                                CCG TCCTCCGT    GTC CCTC
                                  _       CT__   _
GAM504  SLC6A3  3'  GGCCAGAAGGCGATGGGGCTCC 13467       AA__________  CAGA
            TCTGGG                  AGGAGGC         TCC    GG
                                |||||||         |||    ||
                                TCTTCCG         AGG    CC
                                    CTACCCCIIIG   AGAC
GAM504  TCF20   3'  GGACAGGGGGCCCCAGAGGAG  13468    C    A   AAT
                                GG CAGG GGC   CCCAGAGGAG
                                || |||| |||   ||||||||||
                                CC GTCC CCG   GGGTCTCCTC
                                 T    C   ____
GAM504  TFAP2C  3'  GGCCAGGAGGGGTTCCCAG    13469         CAA
                                GGCCAGGAGG   TCCCAG
                                ||||||||||   ||||||
                                CCGGTCCTCC   AGGGTC
                                      CCA
GAM504  TLX1    3'  GGCCAGGAGGGTGGGGAGGAG  13470         CAATCCCA
                                GGCCAGGAGG       GAGGAG
                                ||||||||||       ||||||
                                CCGGTCCTCC       CTCCTC
                                      CACCC___
GAM504  VAMP1   3'  GGCAAGGAGGAGCCCAGAGGAG 13471     C      CAAT
                                GGC AGGAGG    CCCAGAGGAG
                                ||| ||||||    ||||||||||
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                                CCG TCCTCC    GGGTCTCCTC
                                  T     TC__
GAM504  ARF4     3'  GGCCAGGAGTCAATGTAGG    13472         G    CCCAG
                                GGCCAGGAG CAAT     AGG
                                ||||||||| ||||     |||
                                CCGGTCCTC GTTA     TCC
                                     A    CA___
GAM504  C8orf13  3'  CAGGCACAAAATCTCAGAGGAG 13473      AG   __   C
                                CAGG  GCA  ATC CAGAGGAG
                                ||||  |||  ||| ||||||||
                                GTCC  TGT  TAG GTCTCCTC
                                  G_   TT   A
GAM504  CASKIN1  3'  GGCCAGGCACACCCTCAGAGGA 13474        AG   A   _
           G                     GGCCAGG  GCA TCC CAGAGGAG
                                |||||||  ||| ||| ||||||||
                                CCGGTCC  TGT GGG GTCTCCTC
                                    G_   _   A
GAM504  CNOT8    3'  GGCAGGAGGCAACCAGAGAGGA 13475     C         CC
           G                     GGC AGGAGGCAATC  AGAGGAG
                                ||| ||||||||||  |||||||
                                CCG TCCTCCGTTGG  TCTCCTC
                                  _         TC
GAM504  DKFZP434A0131 3'  GGCAGGCTTCCCAGAGGA    13476     CAGG    AA
                                GGC    AGGC  TCCCAGAGGA
                                |||    ||||  ||||||||||
                                CCG    TCCG  AGGGTCTCCT
                                  _____    A_
GAM504  DKFZP434P1750 3'  GGCCAGGAAGTGGGGGAGCTCC 13477       CAA__________  CAGA
           TCTGGG                  AGGAGG          TCC    GG
                                ||||||          |||    ||
                                TCCTTC          AGG    CC
                                   ACCCCCTCIIIG   AGAC
GAM504  FLJ10932  3'  AGCCAGGAGTCAGGGGA     13478         GCAATCC   A
                                GGCCAGGAG      CAG GGA
                                |||||||||      ||| |||
                                TCGGTCCTC      GTC CCT
                                     A_______   C
GAM504  FLJ13154  3'  GGCAGGAGGCAGCAGG      13479     C       ATCCCA _
                                GGC AGGAGGCA     G AGG
                                ||| ||||||||     | |||
                                CCG TCCTCCGT     C TCC
                                  _       _______ G
GAM504  FLJ14957  3'  GGCCAGGAGGGAGTCCCTGG   13480          CAA    AGA
                                GGCCAGGAGG   TCCC   GG
                                ||||||||||   ||||   ||
                                CCGGTCCTCC   AGGG   CC
                                     CTC    A__
GAM504  FLJ20552  3'  GGCTGGGGACGCCCCAGAGG   13481     CA_   G  AAT
                                GGC   GGA GC   CCCAGAGG
                                |||   ||| ||   ||||||||
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                                CCG  CCT CG  GGGTCTCC
                                  ACC  G ___
GAM504  FLJ21736  3'  GGCAGGGAAGGCTTCCTGGGGG 13482    CA  _  AA  CAGA
          AG                      GGC  GGA GGC  TCC   GGAG
                                |||  ||| |||  |||   ||||
                                CCG  CCT CCG  AGG   CCTC
                                  TC  T  A_  ACCC
GAM504  FLJ21977  3'  GGCCAGAAACTCCAGAGG   13483      G   AATC
                                GGCCAG AGGC   CCAGAGG
                                ||||||| ||||   |||||||
                                CCGGTC TTTG   GGTCTCC
                                   _   A___
GAM504  FLJ22169  3'  GGCCAGGGAACACTCAGAGGAG 13484      AG  ATCC
                                GGCCAGG  GCA   CAGAGGAG
                                |||||||  |||   ||||||||
                                CCGGTCC  TGT   GTCTCCTC
                                    CT  GA__
GAM504  FLJ31978  3'  GGTCAGAAGGCAGGCGGGAGGA 13485   C       ATCCCA
          G                      GG CAGGAGGCA    GAGGAG
                                || |||||||||     ||||||
                                CC GTCTTCCGT     CTCCTC
                                 A       CCGCC_
GAM504  FLJ32356  3'  GGCCAGGAGGTGTCCCAG   13486        CAA
                                GGCCAGGAGG  TCCCAG
                                ||||||||||  ||||||
                                CCGGTCCTCC  AGGGTC
                                      AC_
GAM504  HCA4    3'  GACCAGGAGGCAGGAAGGA   13487         ATCCCA
                                GGCCAGGAGGCA    GAGGA
                                ||||||||||||    |||||
                                CTGGTCCTCCGT    TTCCT
                                      CC_____
GAM504  HT002   3'  AGCCAGGAGGCAGCTGAGG   13488         ATCCCA
                                GGCCAGGAGGCA    GAGG
                                ||||||||||||    ||||
                                TCGGTCCTCCGT    CTCC
                                      CGA___
GAM504  HYPC    5'  GGCCAGGAGGCACAGGTGG   13489         ATCC  A_
                                GGCCAGGAGGCA  CAG  GG
                                ||||||||||||  |||  ||
                                CCGGTCCTCCGT  GTC  CC
                                      _____  CA
GAM504  KIAA0237  5'  GGCAGGCTCCCAGAGGA    13490    CAGG   AA
                                GGC   AGGC  TCCCAGAGGA
                                |||   ||||  ||||||||||
                                CCG   TCCG  AGGGTCTCCT
                                  _____   __
GAM504  KIAA0323  3'  GGCCAGAAGGTGATCCCACAG  13491        CA    G
                                GGCCAGGAGG  ATCCCA AG
                                ||||||||||  |||||| ||
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                                CCGGTCTTCC  TAGGGT TC
                                      AC     G
GAM504  KIAA0599  3'  GGCAGGAATCCAGAGGA     13492     C    GCAATC
                                GGC AGGAG     CCAGAGGA
                                ||| |||||     ||||||||
                                CCG TCCTT     GGTCTCCT
                                  _    A_____
GAM504  KIAA0652  3'  GGCCAGGAGGAATGG       13493          C   CCCAGA
                                GGCCAGGAGG AAT     GG
                                |||||||||| |||     ||
                                CCGGTCCTCC TTA     CC
                                      _  _______
GAM504  KIAA1862  3'  GCCCAGGAGGTTCTGCCGGGGG 13494   G       CAATC  AGA
           AG                    G CCAGGAGG    CC   GGAG
                                | ||||||||    ||   ||||
                                C GGTCCTCC    GG   CCTC
                                 G       AAGAC  CCC
GAM504  KREMEN2   3'  CCAGGACCACCCCCAGAGG   13495       GG  AT
                                CCAGGA  CA  CCCAGAGG
                                ||||||  ||  ||||||||
                                GGTCCT  GT  GGGTCTCC
                                   G_  GG
GAM504  KRTHB4    3'  GGCCAGGCAGAATAATCGGGGG 13496        _  C_   CCAGA
           AG                    GGCCAGG AGG  AATC    GGAG
                                ||||||| |||  ||||    ||||
                                CCGGTCC TCT  TTAG    CCTC
                                    G   TA   CCC__
GAM504  LGI4      3'  GGCCAGGAGCCAGCCAAGGG   13497         G  ATC   A
                                GGCCAGGAG CA   CCAG GG
                                ||||||||| ||   |||| ||
                                CCGGTCCTC GT   GGTT CC
                                      G  C__    C
GAM504  LIMR      3'  GGCCAGAGGCAAGGG       13498       G    ATCCC  A
                                GGCCAG AGGCA    AG GG
                                |||||| |||||    || ||
                                CCGGTC TCCGT    TC CC
                                     _    _____  _
GAM504  LYPLA3    3'  GGCCAGGAGCCGATCCCTGG   13499         GCA    AGA
                                GGCCAGGAG   ATCCC   GG
                                |||||||||   |||||   ||
                                CCGGTCCTC   TAGGG   CC
                                      GGC    A__
GAM504  MGC15429  5'  GGTGGCAGTCCCAGAGGAG   13500    A   A
                                GG GGCA TCCCAGAGGAG
                                || |||| ||||||||||
                                CC CCGT AGGGTCTCCTC
                                 A   C
GAM504  MGC2452   5'  GCCAGGAGGTGGGAGAGGAG  13501         CAATCCC
                                GCCAGGAGG      AGAGGAG
                                |||||||||      |||||||
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                                CGGTCCTCC      TCTCCTC
                                     ACCC___
GAM504  MGC2656  3' GGCCAGAGGACCCTTAGAGG  13502       G  CAAT  __
                                GGCCAG AGG   CCC  AGAGG
                                |||||| |||   |||  |||||
                                CCGGTC TCC   GGG  TCTCC
                                   _  T___   AA
GAM504  MGC2749  3' GGCTGGGGTGAACTCAGAGGAG 13503     CA  A  CAATCC
                                GGC  GG GG     CAGAGGAG
                                |||  || ||     ||||||||
                                CCG  CC CC     GTCTCCTC
                                  A_  _  ACTTGA
GAM504  NDRG4    3' GGCCAGGAGGTGGCAGAG    13504         CAATCC
                                GGCCAGGAGG     CAGAG
                                ||||||||||     |||||
                                CCGGTCCTCC     GTCTC
                                     ACC___
GAM504  NDRG4    3' GGCCAGGAGGTGGCAGAG    13504         CAATCC
                                GGCCAGGAGG     CAGAG
                                ||||||||||     |||||
                                CCGGTCCTCC     GTCTC
                                     ACC___
GAM504  NETO1    5' GGCCAGAAGGTAAAAAGGA   13505         C  TCCC
                                GGCCAGGAGG AA   AGAGGA
                                |||||||||| ||   ||||||
                                CCGGTCTTCC TT   TTTCCT
                                     A _____
GAM504  OR51E2   5' GGCTGAGGAGGCTTTAGATTCC 13506       A____ C   A   III
           AGGGGAGC                GGAGGC    AT CCAG GGAG  C
                                |||||     || |||| ||||  |
                                CCTCCG    TA GGTC CCTC  G
                                   AAATC  A   C   III
GAM504  PP1201   3' AGCCAGGAGCAAGCCCAGGGGA 13507         G  T   A
           G                     GGCCAGGAG CAA CCCAG GGAG
                                ||||||||| ||| ||||| ||||
                                TCGGTCCTC GTT GGGTC CCTC
                                     _  C   C
GAM504  PPP2R2A  3' CCAGGAGGCCAGAAGAGGAG  13508        AATCCC
                                CCAGGAGGC     AGAGGAG
                                |||||||||     |||||||
                                GGTCCTCCG     TCTCCTC
                                     GTCT__
GAM504  PRIC285  3' GGCCAGGAGGCAGGCTGGCTCC 13509        A__________  CAGA
           TCTGGG                AGGAGGCA        TCC   GG
                                ||||||||        |||   ||
                                TCCTCCGT        AGG   CC
                                   CCGACCIIIG   AGAC
GAM504  PRO1942  5' GGTTAGGAAGCAATTCCCATAG 13510    CC        _   G
                                GG  AGGAGGCAAT CCCA AG
                                ||  |||||||||| |||| ||
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                                CC  TCCTTCGTTA GGGT TC
                                 AA         A   A
GAM504  PV1      3'  GGCCAGGAAGCTGGAGGA    13511          AATCCCA
                                GGCCAGGAGGC      GAGGA
                                ||||||||||       |||||
                                CCGGTCCTTCG      CTCCT
                                      AC_____
GAM504  RODH-4   3'  GGCCAGGAGTAATGAAGGA   13512         GC   CCCA
                                GGCCAGGAG  AAT   GAGGA
                                |||||||||  |||   |||||
                                CCGGTCCTC  TTA   TTCCT
                                     A_   C___
GAM504  SCAMP5   3'  GGCCAGAGGCAAGAGG      13513       G    ATCCC
                                GGCCAG AGGCA    AGAGG
                                |||||| |||||    |||||
                                CCGGTC TCCGT    TCTCC
                                  _    _____
GAM504  SCGF     3'  GGGAAGGGCGATTCCGGAGGAG 13514    CC   A   A  C  A
                                GG  AGG GGC AT CC GAGGAG
                                ||  ||| ||| || || ||||||
                                CC  TTC CCG TA GG CTCCTC
                                 C_  _   C  A  C
GAM504  SMC1L1   3'  GGCCAGGAGGTAGGGGGCTCCT 13515        CAA_________  CAGA
           CTGGG                  CAGGAGG         TCC   GG
                                  |||||||         |||   ||
                                  GTCCTCC         AGG   CC
                                     ATCCCCCIIIG   AGAC
GAM504  TESK2    5'  GGCCAGGAGGACGATCCGACCA 13516         _ A   ___
           G                      GGCCAGGAGG C ATCC   CAG
                                  |||||||||| | ||||   |||
                                  CCGGTCCTCC G TAGG   GTC
                                       T C    CTG
GAM504  URKL1    3'  GGTCAGGAGGCAGGAGGA    13517    C       ATCCCA
                                GG CAGGAGGCA     GAGGA
                                || |||||||||     |||||
                                CC GTCCTCCGT     CTCCT
                                 A        C_____
GAM504  LOC112476 3'  GGCCAAGAGGCCGGAGG     13518          AATCCCA
                                GGCCAGGAGGC      GAGG
                                ||||||||||       ||||
                                CCGGTTCTCCG      CTCC
                                      GC_____
GAM504  LOC122618 3'  GGCCAGGAGTCAGGGAAGG    13519         G  ATCCCA
                                GGCCAGGAG CA     GAGG
                                |||||||||  ||     ||||
                                CCGGTCCTC GT     TTCC
                                     A  CCC___
GAM504  LOC138429 3'  GGCCAGGAGCAGGGGGCCGGGA 13520          G  ATC__  AGA
           G                      GGCCAGGAG CA    CC   GGAG
                                  |||||||||  ||    ||   ||||
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                                CCGGTCCTC GT    GG   CCTC
                                     _ CCCCC  C__
GAM504   LOC142901 5'  GGCATGAAAAGTCCCAGAGGAG 13521    CAG    CAA
                                GGC   GAGG   TCCCAGAGGAG
                                |||   ||||   ||||||||||
                                CCG   CTTT   AGGGTCTCCTC
                                  TA_    TC_
GAM504   LOC144667 3'  AGCCAGGGTCTCCCAGAGG    13522       AGGCAA
                                GGCCAGG     TCCCAGAGG
                                |||||||     |||||||||
                                TCGGTCC     AGGGTCTCC
                                    CAG___
GAM504   LOC144698 5'  AGCCGGGGGCACATCAGAGGAG 13523     A  A    ATCC
                                GGCC GG GGCA    CAGAGGAG
                                |||| || ||||    ||||||||
                                TCGG CC CCGT    GTCTCCTC
                                  C  _    GTA_
GAM504   LOC145333 3'  GGCCAGGAGGGGTGGGGCTCCT 13524       CAA_________   CAGA
           CTGGG                   CAGGAGG         TCC    GG
                                |||||||         |||    ||
                                GTCCTCC         AGG    CC
                                    CCACCCCIIIG   AGAC
GAM504   LOC148014 3'  GGCCGGGGAGATGTCAGAGGAG 13525     A_    CAATCC
                                GGCC  GGAGG     CAGAGGAG
                                ||||  |||||     ||||||||
                                CCGG  CCTCT     GTCTCCTC
                                  CC    ACA___
GAM504   LOC150527 5'  GGCAGGAGGATTGGCCAGAGGA 13526     C     CAATC
           G                     GGC AGGAGG    CCAGAGGAG
                                |||  ||||||    |||||||||
                                CCG TCCTCC    GGTCTCCTC
                                  _     TAACC
GAM504   LOC155434 3'  AGCCAGGAGGTGGAGGGAGAGG 13527         CAATCCC
           AG                    GGCCAGGAGG      AGAGGAG
                                ||||||||||      |||||||
                                TCGGTCCTCC      TCTCCTC
                                     ACCTCCC
GAM504   LOC158056 5'  GGTCAGGAGACGGGGCAGGGAG 13528    C       AATCC   A
                                GG CAGGAGGC     CAG GGAG
                                || ||||||||     ||| ||||
                                CC GTCCTCTG     GTC CCTC
                                 A       CCCC_   _
GAM504   LOC158263 5'  GACCAGGGAGCCCAGAGGA    13529       AG  AATC
                                GGCCAGG  GC    CCAGAGGA
                                |||||||  ||    ||||||||
                                CTGGTCC  CG    GGTCTCCT
                                    CT  _____
GAM504   LOC158490 3'  GGCCAGGAGGTGCTCCAGGG   13530         CAATC    A
                                GGCCAGGAGG     CCAG GG
                                ||||||||||     |||| ||
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                                CCGGTCCTCC    GGTC CC
                                      ACGA_   _
GAM504   LOC165257 3'  GGCCAGGAGCGGGGCAGGGAG  13531         G AATCC   A
                                GGCCAGGAG C    CAG GGAG
                                ||||||||| |    ||| ||||
                                CCGGTCCTC G    GTC CCTC
                                     _ CCCC_   _
GAM504   LOC166879 5'  GGCGGGAGGCAAGGTTGGGGAG 13532     CA       TCCCAGA
                                GGC  GGAGGCAA      GGAG
                                |||  ||||||||      ||||
                                CCG  CCTCCGTT      CCTC
                                  C_       CCAACC_
GAM504   LOC196214 5'  GGCCAGGAGGCGGAGG      13533          AATCCCA
                                GGCCAGGAGGC      GAGG
                                ||||||||||      ||||
                                CCGGTCCTCCG      CTCC
                                      C_______
GAM504   LOC199796 5'  GGCCAGGAGTCCAGGGG     13534         GCAATC    A
                                GGCCAGGAG     CCAG GG
                                |||||||||     |||| ||
                                CCGGTCCTC     GGTC CC
                                     A_____    C
GAM504   LOC199883 3'  GACCGGGAGGACCTCCAGAGGA 13535     A    CA   _
           G                     GGCC GGAGG  ATC CCAGAGGAG
                                |||| |||||  ||| |||||||||
                                CTGG CCTCC  TGG GGTCTCCTC
                                  C    __   A
GAM504   LOC200020 3'  GACCGGGAGGACCTCCAGAGGA 13535     A    CA   _
           G                     GGCC GGAGG  ATC CCAGAGGAG
                                |||| |||||  ||| |||||||||
                                CTGG CCTCC  TGG GGTCTCCTC
                                  C    __   A
GAM504   LOC200953 5'  AGCCAGGAGGCAGGGGGGCTCC 13536        A__________  CAGA
           TCTGGG                AGGAGGCA        TCC    GG
                                ||||||||        |||    ||
                                TCCTCCGT        AGG    CC
                                     CCCCCCIIIG   AGAC
GAM504   LOC202404 5'  GGCCAGAGGAGCCAGGGGA   13537       G   CAATC    A
                                GGCCAG AGG     CCAG GGA
                                |||||| |||     |||| |||
                                CCGGTC TCC     GGTC CCT
                                   _   TC___    C
GAM504   LOC206426 5'  GGCGTGAAAAGTCCCAGAGGAG 13538     CAG    CAA
                                GGC   GAGG   TCCCAGAGGAG
                                |||   ||||   ||||||||||
                                CCG   CTTT   AGGGTCTCCTC
                                  CA_    TC_
GAM504   LOC221584 5'  GCCAGGAGGCGAGAGGA     13539          AATCCC
                                GCCAGGAGGC     AGAGGA
                                ||||||||||     ||||||
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                                CGGTCCTCCG     TCTCCT
                                      C_____
GAM504  LOC221683 5'  GGCCAGAAGGCAGGGATGGGAG 13540          ATCCCAGA
                                GGCCAGGAGGCA       GGAG
                                ||||||||||||       ||||
                                CCGGTCTTCCGT       CCTC
                                      CCCTAC__
GAM504  LOC222031 3'  GGCCAGGAGGGGTCTCCTTGGA 13541         CAA_  CA_
          GG                    GGCCAGGAGG   TCC  GAGG
                                ||||||||||   |||  ||||
                                CCGGTCCTCC   AGG  CTCC
                                      CCAG  AAC
GAM504  LOC222962 3'  GGCCAGGAAGGCAATGGGA   13542        _    CCCAGA
                                GGCCAGGA GGCAAT     GGA
                                ||||||||| ||||||     |||
                                CCGGTCCT CCGTTA     CCT
                                     T     C_____
GAM504  LOC253805 5'  GGCTGCGGAGGCAGAGGA    13543    CA_     ATCCCA
                                GGC  GGAGGCA     GAGGA
                                |||  |||||||     |||||
                                CCG  CCTCCGT     CTCCT
                                  ACG     _______
GAM504  LOC254848 5'  AGCCGCAGGCGATCCTGGAGGA 13544     AGG   A   CA
          G                     GGCC  AGGC ATCC  GAGGAG
                                ||||  |||| ||||  ||||||
                                TCGG  TCCG TAGG  CTCCTC
                                  CG_   C   AC
GAM504  LOC57795  3'  GGAGGGCACAGAGGAG      13545      _ ATCC
                                GGAGG CA   CAGAGGAG
                                ||||| ||   ||||||||
                                CCTCC GT   GTCTCCTC
                                   C  ____
GAM504  LOC90917  3'  GGCCAGGAGGAGTTCTTGCTCC 13546      CAA__________  CAGA
          TCTGGG                  AGGAGG         TCC   GG
                                ||||||         |||   ||
                                TCCTCC         AGG   CC
                                   TCAAGAACIIIG  AGAC
GAM505  CD86    3'  GGCATACGGAGCAGAGCTGGAG 13549    C____
                                GGT   GAGCAGAGCTGGAG
                                |||   ||||||||||||||
                                CCG   CTCGTCTCGACCTC
                                  TATGC
GAM505  ELL     3'  TCTGGGGGCACCAGCTGGA   13550    AA   CGA  AG
                                TCT  GGGT  GC  AGCTGGA
                                |||  ||||  ||  |||||||
                                AGA  CCCG  TG  TCGACCT
                                  CC   ___  G_
GAM505  KCNA6   3'  TCTAGGGCTTTAAGCTGGA   13551     A   CGAGCA
                                TCTA GGGT     GAGCTGGA
                                |||| ||||     ||||||||
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                                AGAT CCCG     TTCGACCT
                                  _   AAA___
GAM505  LASS1    3'  CCTAGAGGAGCAGAGTTGGAG  13552     A  TC      C
                                TCTA GGG  GAGCAGAG TGGAG
                                |||| |||  |||||||| |||||
                                GGAT CTC  CTCGTCTC ACCTC
                                  _  __       A
GAM505  LMO4     5'  GGGCTGGCGGAGCTGGAG    13553     CGA  A
                                GGGT   GC GAGCTGGAG
                                ||||   || |||||||||
                                CCCG   CG CTCGACCTC
                                  AC_  C
GAM505  MMP15    3'  CCTGGGGGCACAGGGAGCTGGA 13554     AA   CG  CA
           G                     TCT  GGGT  AG  GAGCTGGAG
                                ||| ||||  ||  |||||||||
                                GGA  CCCG  TC  CTCGACCTC
                                  CC   TG  C_
GAM505  NPC2     3'  AAGCAGCAGAGCTGGAG     13555     CG
                                GGGT  AGCAGAGCTGGAG
                                ||||  ||||||||||||||
                                TTCG  TCGTCTCGACCTC
                                  __
GAM505  SDC4     3'  CAAAGGTAATCAGAGCTGGAG  13556       CGAG
                                TAAGGGT    CAGAGCTGGAG
                                |||||||    ||||||||||
                                GTTTCCA    GTCTCGACCTC
                                    TTA_
GAM505  SIAT1    3'  AGGCCAGGCAGAGCTGGAG   13557       A
                                GGGTCG GCAGAGCTGGAG
                                |||||| ||||||||||||
                                TCCGGT CGTCTCGACCTC
                                   C
GAM505  DKFZP566G1424 5'  CTGAGGGCCAGAGCTGGA    13558    A    CGAG
                                CT AGGGT    CAGAGCTGGA
                                || |||||    ||||||||||
                                GA TCCCG    GTCTCGACCT
                                 C    _____
GAM505  DKFZP566M1046 5'  TCTGAGGATTTGCCAGCTGGAG 13559     A    CGA  AG
                                TCT AGGGT   GC  AGCTGGAG
                                ||| |||||   ||  ||||||||
                                AGA TCCTA   CG  TCGACCTC
                                  C    AA_  G_
GAM505  E2F6     3'  GGGAGCAGAGCTGGA      13560     TCG
                                GGG   AGCAGAGCTGGA
                                |||   ||||||||||||
                                CCC   TCGTCTCGACCT
                                  ____
GAM505  FLJ10761  3'  AGGACATAAAGTAGAGCTGGAG 13561      TC__   C
                                AGGG    GAG AGAGCTGGAG
                                ||||    ||| ||||||||||
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                                TCCT    TTC TCTCGACCTC
                                  GTAT   A
GAM505  FLJ10815  5' GGCTTCAGCAGAGCTGGAG   13562    G_ G
                                GG  TC AGCAGAGCTGGAG
                                ||  || ||||||||||||||
                                CC  AG TCGTCTCGACCTC
                                 GA  _
GAM505  FLJ10900  3' TCTAAGGGCCGGGTAAGGGG   13563          AGCA   CT
                                TCTAAGGGTCG    GAG  GG
                                ||||||||||    |||  ||
                                AGATTCCCGGC    TTC  CC
                                      CCA_   C_
GAM505  FLJ22215  3' TCTCGGGATTGCAGAGCTGGAG 13564     AA   TCGA
                                TCT  GGG    GCAGAGCTGGAG
                                |||  |||    ||||||||||||
                                AGA  CCC    CGTCTCGACCTC
                                 G_   TAA_
GAM505  FLJ23022  5' TCTAAGGGCTGATGTTTGGAG  13565        C  GCAGAGC
                                TCTAAGGGT GA      TGGAG
                                |||||||| ||      |||||
                                AGATTCCCG CT      ACCTC
                                     A  ACAA___
GAM505  FLJ32934  3' CTGAGGGTTCTGAAGCTGGAG  13566    A    _ GAGCA
                                CT AGGGT C     GAGCTGGAG
                                || ||||| |     |||||||||
                                GA TCCCA G     TTCGACCTC
                                 C     A AC___
GAM505  GKAP42    5' CAAGTGTCGGCAGAGCTGG    13567     G    A
                                TAAG GTCG GCAGAGCTGG
                                |||| |||| ||||||||||
                                GTTC CAGC CGTCTCGACC
                                  A   _
GAM505  KIAA0125  3' GGCACCTGGGCAGAGCTGGAG  13568     __ GA_
                                GGT  C   GCAGAGCTGGAG
                                |||  |   ||||||||||||
                                CCG  G   CGTCTCGACCTC
                                  TG ACC
GAM505  KIAA1323  3' TAAGGAAAGTAGAGCTGGAG   13569       TC   C
                                TAAGGG  GAG AGAGCTGGAG
                                ||||||  ||| ||||||||||
                                ATTCCT  TTC TCTCGACCTC
                                   __   A
GAM505  PRO1728   5' TAAGAGTCCCAGTTGGA     13570        GAG   AGC
                                TAAGGGTC   CAG   TGGA
                                ||||||||   |||   ||||
                                ATTCTCAG   GTC   ACCT
                                     G__   A__
GAM505  SPRY2     5' TCCGGGGTTCGGAGCTGGA   13571     AA   _  AGCA
                                TCT  GGGT CG    GAGCTGGA
                                |||  |||| ||    ||||||||
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                                AGG  CCCA GC    CTCGACCT
                                  C_    A  ____
GAM505  URG4      3'  GGGGACACAGAGCTGGAG    13572     TCGA
                                GGG    GCAGAGCTGGAG
                                |||    ||||||||||||
                                CCC    TGTCTCGACCTC
                                  CTG_
GAM505  LOC124245 3'  CTAGGGACCCAGAGCTGG    13573     A  GT GAG
                                CTA GG  C   CAGAGCTGG
                                ||| ||  |   |||||||||
                                GAT CC  G   GTCTCGACC
                                  C  TG ___
GAM505  LOC144079 5'  TCTGGGGTTGGGAGCTGGA   13574     AA    CGAGCA
                                TCT  GGGT     GAGCTGGA
                                |||  ||||     ||||||||
                                AGA  CCCA     CTCGACCT
                                  C_    ACC___
GAM505  LOC144893 3'  TCTGGGAGTCCTAGCTGGA   13575     AA    GAGCAG
                                TCT  GGGTC     AGCTGGA
                                |||  |||||     |||||||
                                AGA  CTCAG     TCGACCT
                                  CC     GA____
GAM505  LOC145468 3'  AGGGGCAGGAGCTGGA      13576      TCGA   _
                                AGGG    GCAG AGCTGGA
                                ||||    |||| |||||||
                                TCCC    CGTC TCGACCT
                                  _____    C
GAM505  LOC150155 3'  AGGGGCAGGAGCTGGA      13576      TCGA   _
                                AGGG    GCAG AGCTGGA
                                ||||    |||| |||||||
                                TCCC    CGTC TCGACCT
                                  _____    C
GAM505  LOC155382 3'  CCTAAGAGGCGGGGCTGG    13577        TCGA  AGA
                                TCTAAGGG    GC   GCTGG
                                ||||||||    ||   |||||
                                GGATTCTC    CG   CGACC
                                     _____  CCC
GAM505  LOC157556 5'  TCTAAGGCAGAGCTGGA     13578       GGTCGA
                                TCTAAG      GCAGAGCTGGA
                                ||||||      ||||||||||||
                                AGATTC      CGTCTCGACCT
                                  _______
GAM505  LOC162417 3'  TCCTCTGGGCAGAGCTGG    13579     AAG  TCGA
                                TCT   GG    GCAGAGCTGG
                                |||   ||    ||||||||||
                                AGG   CC    CGTCTCGACC
                                  AGA  _____
GAM505  LOC200982 3'  TAAGAGGCAGAGCTGG      13580       TCGA
                                TAAGGG    GCAGAGCTGG
                                ||||||    ||||||||||
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                                ATTCTC   CGTCTCGACC
                                   ____
GAM505  LOC221576 3'  AGGAGTCATGCAGCTGGAG   13581    _   A  GA
                                AGG GTCG GCA  GCTGGAG
                                ||| |||| |||  |||||||
                                TCC CAGT CGT  CGACCTC
                                  T   A  __
GAM505  LOC254826 5'  AGGCGCAGAGCTGGA      13582     CGA
                                GGGT   GCAGAGCTGGA
                                ||||   ||||||||||
                                TCCG   CGTCTCGACCT
                                   ___
GAM505  LOC257515 3'  AGGAGTCATGCAGCTGGAG   13581    _   A  GA
                                AGG GTCG GCA  GCTGGAG
                                ||| |||| |||  |||||||
                                TCC CAGT CGT  CGACCTC
                                  T   A  __
GAM505  LOC257572 3'  AGGAGTCATGCAGCTGGAG   13581    _   A  GA
                                AGG GTCG GCA  GCTGGAG
                                ||| |||| |||  |||||||
                                TCC CAGT CGT  CGACCTC
                                  T   A  __
GAM506  CR1     3'  TCGAAAGCGGCCAGGCGCGGTG 13585       TA   A T   C
                                TCGAAAGC  GCCA G CGCG TG
                                ||||||||  |||| | |||| ||
                                AGCTTTCG  CGGT C GCGC AC
                                     C_   C _   C
GAM506  PODXL   5'  CCGGGGCTCCCGAGTCGCGCTG 13586    AAA  AG  A
                                TCG   GCT  CC AGTCGCGCTG
                                |||   |||  || ||||||||||
                                GGC   CGA  GG TCAGCGCGAC
                                  CC_   G_  C
GAM506  13CDNA73  5'  TCGGAGGCGGCGGCCGCGCTG  13587    AAA  TA  CAA
                                TCG   GC  GC   GTCGCGCTG
                                |||   ||  ||   |||||||||
                                AGC   CG  CG   CGGCGCGAC
                                  CTC  C_  C__
GAM506  FLJ23022  5'  GCTAGCCAGGCAGCCCTG    13588       A  C  G
                                GCTAGCCA GT GC CTG
                                |||||||| || || |||
                                CGATCGGT CG CG GAC
                                     C  T  G
GAM506  SLI     3'  TCGAAAGCTTGGCCCACGGTGC 13589       A_   AAGT  C_
           TG                     TCGAAAGCT  GCC    CG  GCTG
                                |||||||||  |||    ||  ||||
                                AGCTTTCGA  CGG    GC  CGAC
                                     AC   GT__  CA
GAM506  ZNF-U69274 3'  GAAAGTCAGCCACACAGCTG   13590      C     AGT   _
                                GAAAG TAGCCA   CGC GCTG
                                ||||| ||||||   ||| ||||
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                                CTTTC GTCGGT   GTG CGAC
                                  A     ___   T
GAM506  LOC196374 5'  GAGGGCCAGCTCCCCACGCTG  13591    AA     CAAG
                                GA  GCTAGC    TCGCGCTG
                                ||  ||||||    ||||||||
                                CT  CGGTCG    GGTGCGAC
                                 CC     AGG_
GAM507  ENC1     3'  GAAGACAGCTGTAGGCATTGTT 13594          A  TC  __
          T                      GAAGGCAGCT TA  GCG  GTTT
                                ||||||||||  ||  |||  ||||
                                CTTCTGTCGA AT  CGT  CAAA
                                      C  C_   AA
GAM507  SDHB     5'  AGGCGGCTTCCGGTTT      13595      A   ATA  G
                                AGGC GCT   TC CGGTTT
                                ||||  |||   ||  ||||||
                                TCCG CGA   AG GCCAAA
                                  C   ___  _
GAM507  TSC      5'  GCGGAGGGCGGCGCGCCGCGGT 13596     AA_   A  TATA
          TT                     GCG   GGC GC    TCGCGGTTT
                                |||   |||  ||    |||||||||
                                CGC   CCG CG    GGCGCCAAA
                                 CTC   C  CGC_
GAM507  FLJ32334  3'  GAGGGCAGTTCTGCTGGTTT   13597    A    CTATA  _  _
                                GA GGCAG     TC GC GGTTT
                                ||  |||||     ||  ||  |||||
                                CT CCGTC     AG CG CCAAA
                                 C    A____   A  A
GAM508  EPHB2    3'  CTCGCCCTTGGTGTATTGCCTA 13600        _       C  AAT
          AG                     CTCGCC TTGGTGTAT GC   GG
                                ||||||  |||||||||  ||   ||
                                GAGCGG AACCACATA CG   TC
                                   G        A  GAT
GAM508  LIF      3'  CTCCTCTTGGGAGCAATGG   13601     GC    TGTATC
                                CTC  CTTGG     GCAATGG
                                |||  |||||     |||||||
                                GAG  GAACC     CGTTACC
                                  GA    CT____
GAM508  NUP62    3'  GCCTTGGTGGTTAGCATGG   13602         TATC   A
                                GCCTTGGTG    GCA TGG
                                |||||||||    |||  |||
                                CGGAACCAC    CGT ACC
                                     CAAT   _
GAM508  CLDN15   3'  CTCTCCTTGGGGCAGTGG    13603     G     TGTATC  A
                                CTC CCTTGG     GCA TGG
                                |||  ||||||     |||  |||
                                GAG GGAACC     CGT ACC
                                  A     C_____   C
GAM508  FLJ23548  5'  GCCTTGGTGTATATGG      13604           CGCA
                                GCCTTGGTGTAT    ATGG
                                ||||||||||||    ||||
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                                CGGAACCACATA   TACC
                                      ____
GAM508  HTATIP   3'  CGTCTTGGCACTGCAGTGGG  13605   C    TG ATC  A
                                CG CTTGG  T   GCA TGGG
                                || |||||  |   ||| ||||
                                GC GAACC  G   CGT ACCC
                                 A    GT A__   C
GAM508  HTATIP   3'  CTCGCCTTGGTGCTGGGCAAGT 13606          ATC   _
           GGG                    CTCGCCTTGGTGT   GCAA TGGG
                                ||||||||||||   |||| ||||
                                GAGCGGAACCACG   CGTT ACCC
                                       ACC   C
GAM508  MGC22014 3'  CTCCCTTGGTGTGCCCTTGGG  13607    G       ATC  AA_
                                CTC CCTTGGTGT   GC   TGGG
                                ||| |||||||||   ||   ||||
                                GAG GGAACCACA   CG   ACCC
                                 _       ___  GGA
GAM508  SPBPBP   3'  TCGTCTTTGCTGCAATGG   13608    C   GG   ATC
                                TCG CTT  TGT   GCAATGG
                                ||| |||  |||   |||||||
                                AGC GAA  ACG   CGTTACC
                                  A   __   A__
GAM508  LOC221466 3'  ACCTTGGTGGCGGGGTGGG   13609        TAT  CAA
                                GCCTTGGTG   CG   TGGG
                                |||||||||   ||   ||||
                                TGGAACCAC   GC   ACCC
                                     C__  CCC
GAM508  LOC254110 3'  TCGCCCTGGTGAGATGG    13610          TATCGCA
                                TCGCCTTGGTG      ATGG
                                ||||||||||       ||||
                                AGCGGGACCAC      TACC
                                      TC_____
GAM509  ADCY8    5'  CCCCAGGGTCCCAGCCTGATCT 13613         ATTAACA_
           AT                    CCCCAGGGTC       ATCTAT
                                ||||||||||       ||||||
                                GGGGTCCCAG       TAGATA
                                      GGTCGGAC
GAM509  BBS4     3'  GGGTCATTCATTCTAT      13614        AA  A
                                GGGTCATT  CA TCTAT
                                ||||||||  || |||||
                                CCCAGTAA  GT AGATA
                                     __  A
GAM509  DLEC1    3'  TCCCCAGGTCCCCAAGTCT   13615        G  ATTAA  _
                                TCCCCAGG TC    CAA TCT
                                |||||||| ||    ||| |||
                                AGGGGTCC AG    GTT AGA
                                     _ GG___   C
GAM509  DLEC1    3'  TCCCCAGGTCCCCAAGTCT   13615        G  ATTAA  _
                                TCCCCAGG TC    CAA TCT
                                |||||||| ||    ||| |||
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                                AGGGGTCC AG    GTT AGA
                                     _ GG___   C
GAM509  IL17     3'  TCCTCAGGGCCATTATCT    13616    C        ACAA
                                TCC CAGGGTCATTA   TCT
                                ||| ||||||||||    |||
                                AGG GTCCCGGTAAT   AGA
                                  A        ____
GAM509  MAFF     3'  CCCAGGGTCATTCGGTCCCA  13617          AACAA
                                CCCAGGGTCATT    TCTA
                                ||||||||||||    ||||
                                GGGTCCCAGTAA    GGGT
                                       GCCA_
GAM509  NEK4     3'  TCCTTAAGGTTATTAACAAT  13618    CC    C
                                TCC  AGGGT ATTAACAAT
                                |||  ||||| |||||||||
                                AGG  TTCCA TAATTGTTA
                                  AA    A
GAM509  DKFZP564O0463 3'  TCCCCAGGTCATTGAACA    13619        G    _
                                TCCCCAGG TCATT AACA
                                |||||||| ||||| ||||
                                AGGGGTCC AGTAA TTGT
                                     _    C
GAM509  FLJ10702  3'  AAGGCCATGGCAGTCTAT    13620        TAA  A
                                AGGGTCAT   CA TCTAT
                                ||||||||   || |||||
                                TTCCGGTA   GT AGATA
                                     CC_  C
GAM509  KIAA1432  3'  CCCCAGGGTAGCAATCTAT   13621         CATTAA
                                CCCCAGGGT     CAATCTAT
                                |||||||||     ||||||||
                                GGGGTCCCA     GTTAGATA
                                      TC_____
GAM509  LOC145622 5'  CCTCCGGGGTCACCATCTA   13623    _  A      AACA
                                CC CC GGGTCATT    ATCTA
                                || || ||||||||    |||||
                                GG GG CCCAGTGG    TAGAT
                                 A  C       _____
GAM509  LOC145622 5'  CAGGGTCACCATCTA       13622          AACA
                                CAGGGTCATT    ATCTA
                                ||||||||||    |||||
                                GTCCCAGTGG    TAGAT
                                              _____
GAM510  ADARB1   3'  CCTGCACCCCCCATCATGTCTG 13626    _  G   A   ACCC___
          CC                    CC GCG TCC CCAT      GCC
                                || ||| ||| ||||      |||
                                GG CGT GGG GGTA      CGG
                                 A  G   _    GTACAGA
GAM510  ADARB1   3'  CCTGCACCCCCCATCATGTCTG 13626    _  G   A   ACCC___
          CC                    CC GCG TCC CCAT      GCC
                                || ||| ||| ||||      |||
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                                GG CGT GGG GGTA      CGG
                                 A  G  _   GTACAGA
GAM510  BARX1    5'  TCCGCGGCCCACTCGTGCGCC  13627          CATACC
                                TCCGCGGTCCAC     CGCC
                                ||||||||||||     ||||
                                AGGCGCCGGGTG     GCGG
                                      AGCAC_
GAM510  CABC1    5'  TCCGCGGTCACCTTCTAGCCGC 13628        C  A__  C
              C                  TCCGCGGTC ACC  TA CCGCC
                                |||||||||  |||  ||  |||||
                                AGGCGCCAG TGG  AT GGCGG
                                      _  AAG  C
GAM510  G6PD     5'  CCGGCTGCCTGCCATACCCGC  13629     _ G  CA
                                CCG C GTC  CCATACCCGC
                                |||  |  |||  ||||||||||
                                GGC G CGG  GGTATGGGCG
                                  C A  AC
GAM510  GPC5     5'  TCCTGGTCCCCTTTACCCGCC  13630     GC    A  A_
                                TCC  GGTCC CC  TACCCGCC
                                |||  |||||  ||  ||||||||
                                AGG  CCAGG GG  ATGGGCGG
                                  A_     _  AA
GAM510  HYAL3    5'  GCGCGTCACAACACCCGCC   13631     _  C  C
                                GCG GTC AC ATACCCGCC
                                |||  |||  ||  |||||||||
                                CGC CAG TG TGTGGGCGG
                                  G  _  T
GAM510  LHX2     3'  TCCTCGGTCCACACCGC     13632     G      CATAC
                                TCC CGGTCCAC     CCGC
                                |||  ||||||||     ||||
                                AGG GCCAGGTG     GGCG
                                  A       T_____
GAM510  RAB4A    5'  CCCGCGGTCCGCCGGCGC    13633          A  ATACC
                                TCCGCGGTCC CC     CGC
                                ||||||||||  ||     |||
                                GGGCGCCAGG GG     GCG
                                      C  CC___
GAM510  ADAM9    3'  ACGATCCATACCATATCTGCC  13634        __     CCC
                                GCGGTCC  ACCATA   GCC
                                |||||||  ||||||   |||
                                TGCTAGG  TGGTAT   CGG
                                    TA     AGA
GAM510  C11orf11 5'  TCCGCGGCCCAGGTCTCGCC   13635          CCATACC
                                TCCGCGGTCCA      CGCC
                                ||||||||||||     ||||
                                AGGCGCCGGGT      GCGG
                                      CCAGA__
GAM510  CAPN13   3'  GCTAGGTACCATACCTGC    13636    __  CC       C
                                GC  GGT  ACCATACC GC
                                ||  |||  |||||||| ||
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                                CG  CCA  TGGTATGG CG
                                 AT   __       A
GAM510  DED      5'  TCCCGGTCCACTCCGC      13637     G       CATAC
                                TCC CGGTCCAC     CCGC
                                ||| ||||||||     ||||
                                AGG GCCAGGTG     GGCG
                                  _       A_____
GAM510  DKFZP434A0225 5'  TCCGCAGTTCCGCCTCCGCC   13638         _ A  ATAC
                                TCCGCGGT CC CC    CCGCC
                                |||||||| || ||    |||||
                                AGGCGTCA GG GG    GGCGG
                                     A  C  A___
GAM510  DKFZP434N093 5'  CCGCGAGCCTGCCGTACCCGCC 13639       _   CA  A
                                CCGCG GTC  CC TACCCGCC
                                ||||| |||  || ||||||||
                                GGCGC CGG  GG ATGGGCGG
                                   T   AC  C
GAM510  EIF5     5'  TCCGCGGTCCACACCCG     13640           CAT
                                TCCGCGGTCCAC   ACCCG
                                ||||||||||||   |||||
                                AGGCGCCAGGTG   TGGGC
                                               ___
GAM510  FLJ20019  3'  GCGTGAGCCACCATACCCG   13641     GT__
                                GCG    CCACCATACCCG
                                |||    ||||||||||||
                                CGC    GGTGGTATGGGC
                                  ACTC
GAM510  FLJ23360  5'  TCCGCGGCCGCCCCGCGCC    13642        T  A  ATA  _
                                TCCGCGG CC CC   CC CGCC
                                ||||||| || ||   || ||||
                                AGGCGCC GG GG   GG GCGG
                                     _  C  ___  C
GAM510  HNRPA3    3'  TCCACCACCACCATACCCGCCG 13643       G T           III
                                TCCGC G CCACCATACCCGCC   G
                                ||||| | ||||||||||||||   |
                                AGGTG T GGTGGTATGGGCGG   C
                                   G _            III
GAM510  HSP105B   5'  CGCGGTCCGCCTCCGCC     13644         A  ATAC
                                CGCGGTCC CC    CCGCC
                                |||||||| ||    |||||
                                GCGCCAGG GG    GGCGG
                                     C  A___
GAM510  KIAA0057  3'  TCCTTGGTCCACCAGCGCC    13645     GC        TACC
                                TCC  GGTCCACCA    CGCC
                                |||  |||||||||    ||||
                                AGG  CCAGGTGGT    GCGG
                                  AA        C___
GAM510  KIAA0603  5'  TCCGCGCTTCAGCAGCCCTGCC 13646       GTC  C  TA  C
                                TCCGCG   CA CA  CC GCC
                                ||||||   || ||  || |||
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                                AGGCGC  GT GT  GG CGG
                                   GAA  C  CG  A
GAM510  KIAA0907  3'  CGCCCACCACCATGCCCGC   13647    GGT     A
                                CGC  CCACCAT CCCGC
                                |||  ||||||| |||||
                                GCG  GGTGGTA GGGCG
                                  GGT     C
GAM510  MACMARCKS 5'  TCCGCGGCCGACCCGC     13648       CACCAT
                                TCCGCGGTC    ACCCGC
                                |||||||||    ||||||
                                AGGCGCCGG    TGGGCG
                                     C_____
GAM510  MGC4504   3'  TCCAGCCACCCACCATATCTGC 13649    _ G       CCC
                                TCC GC GTCCACCATA  GC
                                ||| || ||||||||||  ||
                                AGG CG TGGGTGGTAT  CG
                                  T  G       AGA
GAM510  SCOP     5'  TCCGCGGTCACCCCGC     13650       C  ATAC
                                TCCGCGGTC ACC   CCGC
                                ||||||||| |||   ||||
                                AGGCGCCAG TGG   GGCG
                                     _  _____
GAM510  SEMA4B    5'  CCCGCGGTCCGCCCCCG    13651        A  ATA
                                TCCGCGGTCC CC  CCCG
                                |||||||||| ||  ||||
                                GGGCGCCAGG GG  GGGC
                                     C  ___
GAM510  LOC131583 5'  TCCACGGTCTGCTGCCCGCC  13652       CACCATA
                                TCCGCGGTC     CCCGCC
                                |||||||||     ||||||
                                AGGTGCCAG     GGGCGG
                                     ACGAC__
GAM510  LOC134121 5'  CCGCGGTCCGTCCCGCCCGCC 13653        A_  ATA
                                CCGCGGTCC  CC  CCCGCC
                                |||||||||  ||  ||||||
                                GGCGCCAGG  GG  GGGCGG
                                     CA  GC_
GAM510  LOC197387 5'  TCCGCGGCCGTTAACCCGCC  13654       CACCAT
                                TCCGCGGTC    ACCCGCC
                                |||||||||    |||||||
                                AGGCGCCGG    TGGGCGG
                                     CAAT__
GAM510  LOC200269 5'  CCCGCGGTCCTAGCCTGCC   13655       ACCATA  C
                                TCCGCGGTCC     CC GCC
                                ||||||||||     || |||
                                GGGCGCCAGG     GG CGG
                                     ATC___  A
GAM510  LOC221751 5'  TCCACGGTCCTCTCCTGCC   13656       ACCATA  C
                                TCCGCGGTCC     CC GCC
                                ||||||||||     || |||
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                                AGGTGCCAGG     GG CGG
                                     AGA___  A
GAM511  CKTSF1B1  3'  ACATGCTGGGTGCACCTGGA  13659         CC   G
                                ACATGCTGGG  TACC TGGA
                                ||||||||||  |||| ||||
                                TGTACGACCC  GTGG ACCT
                                     AC   _
GAM511  CML66    5'  CATGCTGGGCTATGTAG     13660         C  CC
                                CATGCTGGGC TA  GTGG
                                |||||||||| ||  ||||
                                GTACGACCCG AT  CATC
                                     _  A_
GAM511  EGFR     3'  ACAGTTGGGCCTGGATGAACTC 13661     TGC      ACC
                                ACA   TGGGCCT   GTGGACTC
                                |||   |||||||   ||||||||
                                TGT   ACCCGGA   TACTTGAG
                                  CA_     CC_
GAM511  EN2      3'  ACATGTTTCAGAACTGTGGACT 13662      C__   GC  ACC
            C                    ACATG   TGG  CT   GTGGACTC
                                |||||   |||  ||   ||||||||
                                TGTAC   GTC  GA   CACCTGAG
                                   AAA   TT  ___
GAM511  FXYD7    3'  TGCTGGGCCGGGATGGACTC   13663         TACC
                                TGCTGGGCC    GTGGACTC
                                |||||||||    ||||||||
                                ACGACCCGG    TACCTGAG
                                     CCC_
GAM511  IL17E    5'  ACATGCTGGGCACTGCACACTC 13664          CT  C   G
                                ACATGCTGGGC  AC GTG ACTC
                                ||||||||||  ||  ||| ||||
                                TGTACGACCCG  TG CGT TGAG
                                     __  A   G
GAM511  MAP3K14  3'  TGCTGGGCCTGAAGGGGCTC   13665         ACCGT  A
                                TGCTGGGCCT    GG CTC
                                ||||||||||    ||  |||
                                ACGACCCGGA    CC GAG
                                     CTTCC  _
GAM511  NEU3     5'  GCTGGGCCTGGTGGCT      13666         ACC    A
                                GCTGGGCCT   GTGG CT
                                |||||||||   ||||  ||
                                CGACCCGGA   CACC GA
                                     C__    _
GAM511  VCY      3'  CAGCTGGGCCTAAAC       13667    T       CCGTG
                                CA GCTGGGCCTA    GAC
                                ||  ||||||||||    |||
                                GT CGACCCGGAT    TTG
                                  _       ______
GAM511  VCY      3'  CAGCTGGGCCTAAAC       13667    T       CCGTG
                                CA GCTGGGCCTA    GAC
                                ||  ||||||||||    |||
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                                GT CGACCCGGAT    TTG
                                 _      _____
GAM511  WBP2     3'  ACGCTGGGCAGCACTGTGGGCT 13668        C_  C   A
              C                   ATGCTGGGC  TAC GTGG CTC
                                  |||||||||  ||| |||| |||
                                  TGCGACCCG  GTG CACC GAG
                                       TC   A   C
GAM511  CBCIP2   3'  CATGCCGGGTCTGAGACT    13669        C  ACCGT
                                  CATGCTGGG CT    GGACT
                                  |||||||||  ||    |||||
                                  GTACGGCCC GA    TCTGA
                                       A  C____
GAM511  CHST3    3'  ATGCTGGGCCGCAGAACTC   13670         TAC  T
                                  ATGCTGGGCC   CG GGACTC
                                  ||||||||||   ||  ||||||
                                  TACGACCCGG   GT CTTGAG
                                       C__  _
GAM511  DKFZp547H025 3'  GCTGGGCCTGGTGGCTC     13671         ACC   A
                                  GCTGGGCCT   GTGG CTC
                                  |||||||||   |||| |||
                                  CGACCCGGA   CACC GAG
                                       C__   _
GAM511  DKFZp762E1511 3'  CATGCTGGGCAGAGGGGCTC   13672         CTACCGT  A
                                  CATGCTGGGC      GG CTC
                                  ||||||||||      || |||
                                  GTACGACCCG      CC GAG
                                       TCTCC__  _
GAM511  ITGB5    3'  ATGCTGGTTTTACAGACTC   13673       GCC   CGT
                                  ATGCTGG   TAC   GGACTC
                                  |||||||   |||   ||||||
                                  TACGACC   ATG   TCTGAG
                                     AAA   ___
GAM511  KIAA0296 3'  CAGCTGGGCCTGGAC      13674    T       ACCGT
                                  CA GCTGGGCCT    GGAC
                                  ||  |||||||||    ||||
                                  GT CGACCCGGA    CCTG
                                   _      _____
GAM511  KIAA0449 3'  GCTGGGCCTGACAAGGCTC   13675         AC  T  A
                                  GCTGGGCCT  CG GG CTC
                                  |||||||||  ||  ||  |||
                                  CGACCCGGA  GT CC GAG
                                       CT  T  _
GAM511  KIAA1922 5'  ACAAGCTGGGCCTGCCGC    13676    T       A
                                  ACA GCTGGGCCT CCGT
                                  |||  |||||||||  ||||
                                  TGT CGACCCGGA GGCG
                                    T       C
GAM511  KLHL6    3'  ATGCTGGGCCTGCTCTAACT   13677          ACCGTG
                                  ATGCTGGGCCT     GACT
                                  ||||||||||      ||||
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                                TACGACCCGGA     TTGA
                                      CGAGA_
GAM511  MGC4643   3'  CATGCTGGTCTTGTCCAAGTAG 13678        GC  A__ __    A
            CTC                   CATGCTGG  CT   CC  GTGG CTC
                                  |||||||| ||   ||  |||| |||
                                  GTACGACC  GA   GG  CATC GAG
                                      A_  ACA  TT   _
GAM511  N4BP3    3'  ACATCTGGGCCTGGC      13679      G      ACCGT  A
                                  ACAT CTGGGCCT    GG C
                                  |||| ||||||||    || |
                                  TGTA GACCCGGA    CC G
                                    _      ______ _
GAM511  OBSCN    3'  ACAGGCTGCCCACCGTGGGCTC 13680     T   GG         A
                                  ACA GCT  GCCTACCGTGG CTC
                                  ||| |||  |||||||||||| |||
                                  TGT CGA  CGGGTGGCACC GAG
                                    C  __         C
GAM511  SOX6     3'  CAGCTGCACACGCCGTGGACT  13681    T   G  CTA
                                  CA GCTG GC   CCGTGGACT
                                  || |||| ||   |||||||||
                                  GT CGAC TG   GGCACCTGA
                                   _   G  TGC
GAM511  TUB      3'  CATGCTGAGCCTGTGTCT    13682          ACC   GA
                                  CATGCTGGGCCT   GTG  CT
                                  ||||||||||||   |||  ||
                                  GTACGACTCGGA   CAC  GA
                                        ____   A_
GAM511  LOC145608 5'  ACCTGCTGGGCCTGAACT    13683    A        ACCGT
                                  AC TGCTGGGCCT    GGACT
                                  || ||||||||||    |||||
                                  TG ACGACCCGGA    CTTGA
                                   G        ______
GAM511  LOC145694 5'  TGCTGGGCATTGGTTAGATGGG 13684        CTACC____    A
            CTC                     TGCTGGGC       GTGG CTC
                                    ||||||||       |||| |||
                                    ACGACCCG       TACC GAG
                                        TAACCAATC    C
GAM511  LOC146714 5'  ACATGCTAGGGCTGGAT     13685        _   CTACCG   C
                                  ACATGCT GGGC     TGGA T
                                  ||||||| ||||     |||| |
                                  TGTACGA CCCG     ACCT A
                                      T   _______    A
GAM511  LOC149711 5'  CATGCTGGGCTTGGTGCCT   13686         CTACC   GA
                                  CATGCTGGGC    GTG  CT
                                  ||||||||||    |||  ||
                                  GTACGACCCG    CAC  GA
                                        AAC__   G_
GAM511  LOC150935 3'  TGCTGGGCCCACGGGCT     13687          C T  A
                                  TGCTGGGCCTAC G GG CT
                                  |||||||||||| | || ||
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                                ACGACCCGGGTG C CC GA
                                          _ _ _
GAM511  LOC159199 5'  TGCTGGGCCTGTGCGA      13688          ACC  _
                                TGCTGGGCCT   GTG GA
                                ||||||||||   ||| ||
                                ACGACCCGGA   CAC CT
                                     ____  G
GAM511  LOC164397 5'  TGCTGGGCCTGTGGCT      13689          ACC   A
                                TGCTGGGCCT   GTGG CT
                                ||||||||||   |||| ||
                                ACGACCCGGA   CACC GA
                                     ____  _
GAM511  LOC199936 3'  TGCAGGCCTGTGGGCTC     13690     T    ACC   A
                                TGC GGGCCT   GTGG CTC
                                |||  ||||||  |||| |||
                                ACG TCCGGA   CACC GAG
                                  _    ___   C
GAM511  LOC206389 5'  GCCGTGGCTCTGTCGTGGACTC 13691     _  _ AC
                                GCTG GGC CT  CGTGGACTC
                                ||||  |||  ||  |||||||||
                                CGGC CCG GA  GCACCTGAG
                                  A  A  CA
GAM511  LOC219920 5'  ATGCTGGGCCCTGGGCT     13692          ACCG  A
                                ATGCTGGGCCT    TGG CT
                                ||||||||||    ||| ||
                                TACGACCCGGG    ACC GA
                                     _____  C
GAM511  LOC220097 5'  ACATGCTGGGCCACGT      13693          TAC
                                ACATGCTGGGCC   CGT
                                ||||||||||||   |||
                                TGTACGACCCGG   GCA
                                       T__
GAM511  LOC253954 3'  CTGGGCCTCCGGGGCTC     13694        A  T  A
                                CTGGGCCT CCG GG CTC
                                ||||||||  ||| || |||
                                GACCCGGA GGC CC GAG
                                     _  _  C
GAM511  LOC254842 5'  TGCTGGGCCTGTGTGGGACTC  13695          ACC   _
                                TGCTGGGCCT   GTGG ACTC
                                ||||||||||   |||| ||||
                                ACGACCCGGA   CACC TGAG
                                     CA_    C
GAM511  LOC90249  3'  GCTGGGCCTGGCCCAGGCTC   13696         A_  GT  A
                                GCTGGGCCT  CC  GG CTC
                                |||||||||  ||  || |||
                                CGACCCGGA  GG  CC GAG
                                     CC  GT  _
GAM511  LOC91012  5'  TGCTGGGCCTAAAACT      13697          CCGT
                                TGCTGGGCCTA    GGACT
                                ||||||||||    |||||
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                                ACGACCCGGAT    TTTGA
                                       ____
GAM511  LOC91308  5'  ACAGCTGGGTTTAGCAAACTC  13698     T     CCTACC TG
                                ACA GCTGGG     G  GACTC
                                ||| ||||||     |  |||||
                                TGT CGACCC     C  TTGAG
                                  _     AAAT__ GT
GAM511  LOC96597  5'  GGATGCTGGGTCCTGGGCT   13699   C       _  ACCGT  A
                                A ATGCTGGG CCT    GG CT
                                | |||||||| |||    || ||
                                C TACGACCC GGA    CC GA
                                 C       A  _____  C
GAM512  HXCP2     5'  TAGATCTCTGAGCTCCTGGG   13702        C  A_  GA  C
                                TAGATCTC GG  TC  TG GG
                                |||||||| ||  ||  || ||
                                ATCTAGAG CT  AG  AC CC
                                     A  CG  G_  _
GAM512  MANBAL    3'  TAGATCTCTGCGGTCATAGGGC 13703        __   A   AT__
            G                    TAGATCTC  CGG TCG    GCG
                                ||||||||  ||| |||    |||
                                ATCTAGAG  GCC AGT    CGC
                                     AC   _   ATCC
GAM512  LOC151996 5'  TAGATTTCCAGATCACAG    13704      C       GAT
                                TAGAT TCCGGATC   GCGG
                                ||||| ||||||||   ||||
                                ATCTA AGGTCTAG   TGTC
                                   A       ___
GAM513  ATF5      5'  GGTGAGCGCGGAGACGGGC    13707    _  TT    A
                                GG GGG  CGCG AGACGGGC
                                || |||  |||| ||||||||
                                CC CTC  GCGC TCTGCCCG
                                 A   __    C
GAM513  CA3       5'  TGACGGGGGCGGAGGTGGG    13708        GTTC   A  AC
                                TGACGGGG    GCG AG  GGG
                                ||||||||    ||| ||  |||
                                ACTGCCCC    CGC TC  CCC
                                     _____   C  CA
GAM513  PPP2R5E   5'  GGAGGGGCGGGAGACGGG    13709      TTC   A_
                                GGGGG   GCG  AGACGGG
                                |||||   |||  |||||||
                                CCTCC   CGC  TCTGCCC
                                   C__   CC
GAM513  TRC8      5'  CGGGGGCTAAGGCGGG      13710        CGCG   A
                                CGGGGGTT    AAG CGGG
                                ||||||||    ||| ||||
                                GCCCCCGA    TTC GCCC
                                     _____   C
GAM513  APEG1     5'  GGGGGTTCGCGGCCAGG     13711          AAGA
                                GGGGGTTCGCG    CGGG
                                ||||||||||    ||||
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                                CCCCCAAGCGC   GTCC
                                      CG__
GAM513  C19orf7  3' GGTGGGCCAGGGAGACGGGC  13712   _   CGC  A
                                GG GGGTT  GA GACGGGC
                                || |||||  || |||||||
                                CC CCCGG  CT CTGCCCG
                                 A   TCC  _
GAM513  C20orf46 3' TGGCAGGGGTCAGGTGGG   13713   A     CGCGA  AC
                                TG CGGGGGTT   AG  GGG
                                || ||||||||   ||  |||
                                AC GTCCCCAG   TC  CCC
                                 C      _____ CA
GAM513  CAPN13   5' TGATGGAGGAGGGGAGACGGGC 13714   C   TTCGC  A
                                TGA GGGGG   GA GACGGGC
                                ||| |||||   || |||||||
                                ACT CCTCC   CT CTGCCCG
                                  A   TCCC_ _
GAM513  FHX      3' GACGGGGGGAAGGGACGGGC  13715      TTCGC  __
                                GACGGGGG   GAA  GACGGGC
                                ||||||||   |||  |||||||
                                CTGCCCCC   CTT  CTGCCCG
                                     _____  CC
GAM513  FLJ14708 3' GACGGGGGCCCATGGGGGTGGG 13716         CGAAGAC
                                GACGGGGGTTCG     GGG
                                ||||||||||||     |||
                                CTGCCCCCGGGT     CCC
                                       ACCCCCA
GAM513  HSRNAFEV 5' TGGCGGGGGTTGCGGGGGGG  13717   A     C  AAGAC
                                TG CGGGGGTT GCG   GGG
                                || |||||||| |||   |||
                                AC GCCCCCAA CGC   CCC
                                 C      _  CCC__
GAM513  LHX6     3' GACGGGGGTGGATGCGGAGGTG 13718       TC__  A  AC
           GG                   GACGGGGGT  GCG AG  GGG
                                |||||||||  ||| ||  |||
                                CTGCCCCCA  CGC TC  CCC
                                     CCTA  C  CA
GAM513  NAPA     3' GGGACAGCGAAGACGGGC   13719    TTC
                                GGG  GCGAAGACGGGC
                                |||  ||||||||||||
                                CCC  CGCTTCTGCCCG
                                  TGT
GAM513  PALM     5' TGGCGGGGGCCGGGGCGGG   13720   A     T  CGAAGA
                                TG CGGGGGT CG    CGGG
                                || ||||||| ||    ||||
                                AC GCCCCCG GC    GCCC
                                 C      _ CCC___
GAM513  PCANAP7  5' TGCGGGGGTCCTGGGGCGGG  13721   A      GCGAAGA
                                TG CGGGGGTTC     CGGG
                                || |||||||||     ||||
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                                AC GCCCCCAGG      GCCC
                                 _       ACCCC__
GAM513  WIT-1    5'  TGACAGGGGTAAGAAGGTGGG  13722          TCGC    AC
                                TGACGGGGGT   GAAG  GGG
                                ||||||||||   ||||  |||
                                ACTGTCCCCA   CTTC  CCC
                                      TT__   CA
GAM513  LOC146733 3'  TGCGGGGGCTGGGGAAGGTGGG 13723    A       CGC    AC
          C                      TG CGGGGGTT   GAAG  GGGC
                                || ||||||||   ||||  ||||
                                AC GCCCCCGA   CTTC  CCCG
                                 _      CCC   CA
GAM513  LOC203232 3'  TGACGGGGGTCACGG       13724          CGCGAAG
                                TGACGGGGGTT      ACGG
                                ||||||||||       ||||
                                ACTGCCCCCAG      TGCC
                                          ________
GAM513  LOC205095 3'  TGAGGGGGGCCCGGGAGGTGGG 13725     C        C  A AC
                                TGA GGGGGTTCG GA G  GGG
                                ||| ||||||||| || |  |||
                                ACT CCCCCGGGC CT C  CCC
                                  C        C  _ CA
GAM513  LOC221466 5'  TGGCGGGGGTCACTCATGGGC  13726    A      T   GAAGAC
                                TG CGGGGGT CGC     GGGC
                                || ||||||| |||     ||||
                                AC GCCCCCA GTG     CCCG
                                 C       _   AGTA__
GAM513  LOC91663  5'  GGGCGGCGGCTGTGGAGGCGGG 13727     _   TC  GA___  A
          C                      GGG GGT  GC     AG CGGGC
                                ||| |||  ||     || |||||
                                CCC CCG  CG     TC GCCCG
                                  G   C_  ACACC  C
GAM514  E2F2     5'  CCGAGCAGAGAGCAGCGCTTA  13730    TTTTGA
                                CC      AGAGCAGCGCTTA
                                ||      ||||||||||||
                                GG      TCTCGTCGCGAAT
                                 CTCGTC
GAM514  ZNF200    3'  TACCTTTTTAGGCAGC      13731         GA  A
                                TACCTTTT  AG GCAGC
                                ||||||||  || |||||
                                ATGGAAAA  TC CGTCG
                                     A_  _
GAM514  AMOT     3'  CCTTTTAAGACATATGCTTA   13732         A  G  GC_
                                CCTTTTGA GA CA   GCTTA
                                ||||||||  || ||   |||||
                                GGAAAATT CT GT   CGAAT
                                     _  _  ATA
GAM514  KIAA0275  3'  TACCTTTTGAGGGGACCAG   13733          A__  G
                                TACCTTTTGA   GA CAG
                                ||||||||||   || |||
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                                ATGGAAAACT   CT GTC
                                     CCC  G
GAM514  TUSP     3'  CACCTTTTGGGGAGTAACA   13734        AA  C
                                TACCTTTTG  GAG AGCG
                                |||||||||  ||| ||||
                                GTGGAAAAC  CTC TTGT
                                     CC   A
GAM514  LOC114987 3'  TTTTGAAGAGTAGTCCTAA   13735         C  CG
                                TTTTGAAGAG AG  CTTAA
                                |||||||||| ||  |||||
                                AAAACTTCTC TC  GGATT
                                     A  A_
GAM514  LOC157931 5'  TACCTTTTGAGAGCACTTCTT  13736         A    GCG
                                TACCTTTTGA GAGCA   CTT
                                |||||||||| |||||   |||
                                ATGGAAAACT CTCGT   GAA
                                     _    GAA
GAM515  CNTN2    3'  AAGGGCACTGTTTAAAGTAGG  13739        TCTAC   TGA
                                AAGGGCACT    TGA   TAGG
                                |||||||||    |||   ||||
                                TTCCCGTGA    ATT   ATCC
                                     CAA__   TC_
GAM515  CYP3A43   3'  AAGTGCACTTTTAGAACAATAG 13740     G     C  CT  TG
          G                      AAG GCACTT TA  GA  ATAGG
                                 ||| |||||| ||  ||  |||||
                                 TTC CGTGAA AT  TT  TATCC
                                   A     A  C_  GT
GAM515  B7-H1    3'  AAGGGCACTTCTGCAGGAACTG 13741          _______
                                AAGGGCACTTCT      ACTG
                                ||||||||||||     ||||
                                TTCCCGTGAAGA     TGAC
                                      CGTCCT
GAM515  FLJ10539  3'  AAGGGCACTTGGGAATGATGGG 13742         CTACT     A
                                AAGGGCACTT    GATGAT GG
                                ||||||||||    |||||| ||
                                TTCCCGTGAA    TTACTA CC
                                     CCC__     C
GAM515  FLJ23189  3'  AAAGGCAGCTGATGATG     13743       CTTCTA       A
                                AAGGGCA     CTGATGAT G
                                |||||||     |||||||| |
                                TTTCCGT     GACTACTA C
                                    C_____       C
GAM515  KIAA0599  3'  AGGGCAGTTTCTGTTGGTCTAG 13744       C_   AC  ATGA
          G                      AGGGCA  TTCT  TG   TAGG
                                 ||||||  ||||  ||   ||||
                                 TCCCGT  AAGA  AC   ATCC
                                    CA   CA  CAG_
GAM515  PRO1598   5'  AAGGGCACTTCACTGATG    13745          T
                                AAGGGCACTTC ACTGATG
                                |||||||||| |||||||
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                                TTCCCGTGAAG TGACTAC
                                           _
GAM515  STAB1    3'  AGGGCACCTTTATTGTCTG   13746        C  C  A_
                                AGGGCACTT TA TG  TG
                                ||||||||| || ||  ||
                                TCCCGTGGA AT AC  AC
                                     A  A  AG
GAM515  LOC145945 3'  AAGGGCACTTCTGTCCTAATG  13747          A__
                                AAGGGCACTTCT   CTGATG
                                ||||||||||||   ||||||
                                TTCCCGTGAAGA   GATTAC
                                      CAG
GAM516  DLEC1    3'  TTTGCCATAGTAGACA      13750       CAG
                                TTTGTCA   TAGTAGACA
                                |||||||   |||||||||
                                AAACGGT   ATCATCTGT
                                          ___
GAM516  PLEK     3'  TTTGTCACAGAAGTGGACA   13751         T  A
                                TTTGTCACAG AGT GACA
                                |||||||||| ||| ||||
                                AAACAGTGTC TCA CTGT
                                      T  C
GAM516  TPS1     3'  GTCCAAGTAGTAGGTGACACG  13752     AC      ACA
                                GTC  AGTAGTAG   ACACG
                                |||  ||||||||   |||||
                                CAG  TCATCATC   TGTGC
                                  GT       CAC
GAM516  FLJ14437  3'  TTTGCCACAGGTCCAGCAG   13753         ___
                                TTTGTCACAG   TAGTAG
                                ||||||||||   ||||||
                                AAACGGTGTC   GTCGTC
                                      CAG
GAM516  LOC158427 3'  TCAGGTAAGTGGTAGACAAC   13754     C___   A
                                TCA    AGT GTAGACAAC
                                |||    ||| |||||||||
                                AGT    TCA CATCTGTTG
                                  CCAT   C
GAM516  LOC203197 3'  GTACTGGTAGACAACACG    13755     ___
                                GTA   GTAGACAACACG
                                |||   ||||||||||||
                                CAT   CATCTGTTGTGC
                                  GAC
GAM517  PAFAH1B1  3'  CGAGAGCAATATTATATACAT  13758            CTAG
                                CGAGAGCAATGTTATG    ACAT
                                ||||||||||||||||   ||||
                                GCTCTCGTTATAATAT    TGTA
                                          A___
GAM517  UBQLN1   3'  GAGACAATGTTACATTA     13759      G       GC
                                GAGA CAATGTTAT  TA
                                |||| |||||||||  ||
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                                CTCT GTTACAATG  AT
                                  _       TA
GAM517  CGGBP1   3'  CGAGAGCACTACTCTAGGCAT  13760        ATG   G   A
                                CGAGAGCA   TTAT CTAG CAT
                                ||||||||   |||| |||| |||
                                GCTCTCGT   GATG GATC GTA
                                    ___    A   C
GAM517  CHRFAM7A  3'  GAGTAGTTCCCATGCTAGACAT 13761    _ CAATG
                                GAG AG    TTATGCTAGACAT
                                ||| ||    ||||||||||||
                                CTC TC    GGTACGATCTGTA
                                  A  AAG__
GAM517  HSPC063   3'  GAGAGCATTAGTGCTAGAC   13762       ATG  _
                                GAGAGCA   TTA TGCTAGAC
                                |||||||   ||| ||||||||
                                CTCTCGT   AAT ACGATCTG
                                    ___   C
GAM517  KIAA0767  3'  GCCATGTGCCAGACAT     13763    A   TAT
                                GC ATGT   GCTAGACAT
                                || ||||   |||||||||
                                CG TACA   CGGTCTGTA
                                 G   ___
GAM518  APOD     3'  TCGTGGTTGATTGGTTT     13766    GT   CG
                                TCG  TGG  TGATTGGTTT
                                |||  |||  ||||||||||
                                AGC  ACC  ACTAACCAAA
                                  __   A_
GAM518  CASKIN1   3'  TCAGTTGGTAAATGGTTT    13767        CG   T
                                TCGGTTGG  TGA TGGTTT
                                ||||||||  ||| ||||||
                                AGTCAACC  ATT ACCAAA
                                    __   T
GAM518  DKFZP434B195 5'  TCGGTTGGCATGGGGAGCTT   13768          ATT
                                TCGGTTGGCGTG   GGTTT
                                ||||||||||||   |||||
                                AGCCAACCGTAC   TCGAA
                                      CCC
GAM518  FLJ10159  3'  GGATGGCGTGACATGGTTT   13769    T       _
                                GG TGGCGTGAT TGGTTT
                                || |||||||| ||||||
                                CC ACCGCACTG ACCAAA
                                 T       T
GAM518  FLJ10352  3'  CGGTTTTGTCATTGGTTT    13770      GGC  G
                                CGGTT   GT ATTGGTTT
                                |||||   || ||||||||
                                GCCAA   CA TAACCAAA
                                   AA_  G
GAM518  FLJ20055  3'  GATGAAGCTGATTGGTTT    13771     T_   G
                                GGT  GGC TGATTGGTTT
                                |||  ||| ||||||||||
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                                CTA  TCG ACTAACCAAA
                                  CT  _
GAM518  GRP3     3'  GGTTGGCACAAGTTGGTTT   13772        TG _
                                GGTTGGCG  A TTGGTTT
                                ||||||||  | |||||||
                                CCAACCGT  T AACCAAA
                                     GT C
GAM518  IMP-2    3'  GGTTGATTGGTTGGTTT     13773       CG  A
                                GGTTGG  TG TTGGTTT
                                ||||||  || |||||||
                                CCAACT  AC AACCAAA
                                   A_  C
GAM518  KIAA0182 3'  TCAGTTTGTGAATTGGTTT   13774       GGC   _
                                TCGGTT   GTGA TTGGTTT
                                ||||||   |||| |||||||
                                AGTCAA   CACT AACCAAA
                                   A__    T
GAM518  KIAA1328 3'  GTAAACATTGATTGGTTT    13775    TG   _
                                GT  GCGT GATTGGTTT
                                ||  |||| |||||||||
                                CA  TGTA CTAACCAAA
                                 TT    A
GAM518  PRO0529  3'  GGTTCCCAGATTGGTTT     13776     GG  T
                                GGTT  CG GATTGGTTT
                                ||||  || |||||||||
                                CCAA  GT CTAACCAAA
                                  GG  _
GAM518  RSP3     3'  TTGGCTGTTGATTGGTTT     13777      _ _
                                TTGGC GT GATTGGTTT
                                |||||| || |||||||||
                                AACCG CA CTAACCAAA
                                   A  A
GAM518  LOC144266 5'  GGAACTGATTGGTTT       13778    TT   G
                                GG  GGC TGATTGGTTT
                                ||  ||| ||||||||||
                                CC  TTG ACTAACCAAA
                                 __  _
GAM518  LOC145981 3'  TCGGTTGGTTTGACTACTT   13779        CG     G
                                TCGGTTGG  TGATTG TT
                                ||||||||  |||||| ||
                                AGCCAACC  ACTGAT AA
                                     AA     G
GAM518  LOC149483 3'  GGTTGGAACTGGTTT       13780       CGT
                                GGTTGG   GATTGGTTT
                                ||||||   |||||||||
                                CCAACC   TTGACCAAA
                                  ___
GAM519  DNAJB9   3'  TGAGGTATCAGTCAATCTCTAG 13783     AA   CGAT  _
           A                     TGA  TATC    TCA TCTCTAGA
                                |||  ||||    ||| ||||||||
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                                ACT  ATAG    AGT AGAGATCT
                                  CC    TC__   T
GAM519  MAN1A1   3'  TGAAATACCCTCTCTTTAG   13784          GATTCA   C
                                TGAAATATCC     TCT TAG
                                ||||||||||     ||| |||
                                ACTTTATGGG     AGA ATC
                                      AG_____   A
GAM519  RBBP2    3'  TGAAGGCCATTCATCTTTAGA  13785     ATAT  G      C
                                TGAA    CC ATTCATCT TAGA
                                ||||    || ||||||||| ||||
                                ACTT    GG TAAGTAGA ATCT
                                  CC__ _       A
GAM519  C1QTNF7  3'  TGAAAACGAAATTCATCTCTAG 13786      TATCC
                                TGAAA    GATTCATCTCTAG
                                |||||    ||||||||||||||
                                ACTTT    TTAAGTAGAGATC
                                   TGCT_
GAM519  SFRS12   3'  TGAAATATCCATCTA       13787          ATTCATC
                                TGAAATATCCG      TCTA
                                ||||||||||      ||||
                                ACTTTATAGGT      AGAT
                                                 ________
GAM519  ZAK      3'  TGAGCTATGACCATCTCTGGA  13788     AA   CC   T      A
                                TGA  TAT  GAT CATCTCT GA
                                |||  |||  ||| ||||||| ||
                                ACT  ATA  CTG GTAGAGA CT
                                  CG   __  _      C
GAM520  BIN3     3'  CCAGAAGGTGGGCCAGGGCCGG 13791          AT   TT
                                CTAGAAGGTG  GTT  GGCCGG
                                ||||||||||  |||  ||||||
                                GGTCTTCCAC  CGG  CCGGCC
                                      C_   TC
GAM520  CAPS     3'  GGTTGATGTTTTACAGA     13792     _       GC
                                GGT GATGTTTTG  CGGA
                                ||| |||||||||  ||||
                                CCA CTACAAAAT  GTCT
                                  A       __
GAM520  CDK2     3'  CTAGAAGGTGAGTGTTTAAGG  13793           _    T_
                                CTAGAAGGTGA TGTTT  GG
                                ||||||||||| |||||  ||
                                GATCTTCCACT ACAAA  CC
                                      C     TT
GAM520  CGB      5'  CCAGGAGGTGATAGGATGCTGG 13794      A       TTTTG  C
                                CTAG AGGTGATG    GC GG
                                |||| ||||||||    || ||
                                GGTC TCCACTAT    CG CC
                                  C       CCTA_  A
GAM520  EMP1     3'  CTGGAATGTGATGTTTTGCTTT 13795    A  G         GCC_
            GG                    CT GAA GTGATGTTTTG   GG
                                || ||| ||||||||||    ||
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                                GA CTT CACTACAAAAC   CC
                                 C  A         GAAA
GAM520  F9      3'  TAAACATTGATGTTTTGGTTGG 13796     AGG        CC
             A                   TAGA  TGATGTTTTGG  GGA
                                 ||||  ||||||||||  |||
                                 ATTT  ACTACAAAACC  CCT
                                   GTA         AA
GAM520  IL6R    3'  GGAGGAGGCTTTGGCTGGA   13797    T_ T      C
                                 GG  GA GTTTTGGC GGA
                                 ||  || ||||||| |||
                                 CC  CT CGAAACCG CCT
                                  TC  C       A
GAM520  PTMS    5'  GAGGGTGGCCGCGGCCGGA   13798    A   AT  TT
                                 GA GGTG  GT  TGGCCGGA
                                 || ||||  ||  ||||||||
                                 CT CCAC  CG  GCCGGCCT
                                  C   __  GC
GAM520  SOX10   5'  AGGTGACGCTGGTGGGCTGG  13799         TT__   C
                                 AGGTGATGTT   GGC GG
                                 ||||||||||   ||| ||
                                 TCCACTGCGA   CCG CC
                                       CCAC   A
GAM520  SUFU    3'  CTAGAAGATGAGGCG       13800          TGTTTT   C
                                 CTAGAAGGTGA     GGC G
                                 ||||||||||     ||| |
                                 GATCTTCTACT     CCG C
                                        _______  A
GAM520  C20orf177 5'  CTGGAAGATGATGACAGCTGG  13801    A        TTTT   C
                                 CT GAAGGTGATG    GGC GG
                                 || ||||||||||    ||| ||
                                 GA CTTCTACTAC    TCG CC
                                  C         TG__   A
GAM520  C6orf31  3'  GAGGGTCCGGCGTTTGGCCGG  13802    A   GAT  _
                                 GA GGT   GT TTTGGCCGG
                                 || |||   || |||||||||
                                 CT CCA   CG AAACCGGCC
                                  C   GGC  C
GAM520  DDR1    3'  TAGAGGTGATGGGCTGTCGG   13803     A     TT   GC
                                 TAGA GGTGATG  TTG  CGG
                                 |||| |||||||  |||  |||
                                 ATCT CCACTAC  GAC  GCC
                                   _      CC   A_
GAM520  DDR1    3'  TAGAGGTGATGGGCTGTCGG   13803     A     TT   GC
                                 TAGA GGTGATG  TTG  CGG
                                 |||| |||||||  |||  |||
                                 ATCT CCACTAC  GAC  GCC
                                   _      CC   A_
GAM520  DDR1    3'  TAGAGGTGATGGGCTGTCGG   13803     A     TT   GC
                                 TAGA GGTGATG  TTG  CGG
                                 |||| |||||||  |||  |||
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                                ATCT CCACTAC  GAC  GCC
                                  _      CC   A_
GAM520  DKFZP434L1123 3'  TAGGAGGTGGGGTCTTTGG   13804     A    AT    _
                                TAG AGGTG  GTTTT GG
                                ||| |||||  ||||| ||
                                ATC TCCAC  CAGAA CC
                                  C    CC    A
GAM520  FLJ11320  3'  TAGGAGGTGGGGCCTTTGGA  13805     A    ATGTTTT   ___
                                TAG AGGTG      GGCC   GGA
                                ||| |||||      ||||   |||
                                ATC TCCAC      CCGG   CCT
                                  C    C_______    AAA
GAM520  FLJ20151  3'  CTAGATGGTTGATTTGGCTGGA 13806      A   GA  T     C
                                CTAGA GGT  TG TTTGGC GGA
                                ||||| |||  || |||||| |||
                                GATCT CCA  AC AAACCG CCT
                                   A   __ T     A
GAM520  FLJ20507  3'  TAAAAGGTGAAGGGCTGG    13807         TGTTTT   C
                                TAGAAGGTGA     GGC GG
                                ||||||||||     ||| ||
                                ATTTTCCACT     CCG CC
                                      TC_____   A
GAM520  FLJ20507  3'  TAAAAGGTGAAGGGCTGG    13807         TGTTTT   C
                                TAGAAGGTGA     GGC GG
                                ||||||||||     ||| ||
                                ATTTTCCACT     CCG CC
                                      TC_____   A
GAM520  GIT1      3'  CTAGAAGGCGAGGGGCTGG    13808         TGTTTT   C
                                CTAGAAGGTGA     GGC GG
                                ||||||||||     ||| ||
                                GATCTTCCGCT     CCG CC
                                      CC_____   A
GAM520  KIAA0261  3'  TAAAAGGTGATGGGTAGGGGTT 13809          TTTT  CC__
            GG                    TAGAAGGTGATG   GG   GG
                                ||||||||||||   ||   ||
                                ATTTTCCACTAC   CC   CC
                                      CCAT  CCAA
GAM520  KIAA0515  3'  GAGGGTGACAGCACGGCTGGA  13810    A    _ TT   C
                                GA GGTGAT GT  TGGC GGA
                                || |||||| ||  |||| |||
                                CT CCACTG CG  GCCG CCT
                                  C     T  T_   A
GAM520  KIAA1026  3'  CTGGAAGGTAATGTGTGG    13811    A        TT
                                CT GAAGGTGATGT  TGG
                                || ||||||||||  |||
                                GA CTTCCATTACA  ACC
                                  C         C_
GAM520  MAPK8IP3  3'  CTGGAGGGTGGGGGCAGCCCGG 13812    A  A   AT_  TTT   _
            A                     CT GA GGTG   GT   GGCC GGA
                                || || ||||   ||   |||| |||
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                                GA CT CCAC   CG   TCGG CCT
                                 C  C    CCC  ___    G
GAM520   MGC14141  3'  CTAGGGTGTGGGGAGGGTCGG  13813      AA    A  TTTT_  C
                                CTAG  GGTG TG     GG CGG
                                ||||  |||| ||     || |||
                                GATC  CCAC AC     CC GCC
                                  __    _ CCCTC  A
GAM520   MGC3101   3'  CAGGAGGTGACGGCTGG     13814     A      GTTTT   C
                                TAG AGGTGAT     GGC GG
                                ||| |||||||     ||| ||
                                GTC TCCACTG     CCG CC
                                  C       _____  A
GAM520   ZNF338    5'  CTAGAGGGCGCTGGCCGG    13815      A    ATGTT
                                CTAGA GGTG     TTGGCCGG
                                ||||| ||||     ||||||||
                                GATCT CCGC     GACCGGCC
                                   C   _____
GAM520   LOC116071 3'  CAGAGGGTGGTGTTTCGG    13816      A    A
                                TAGA GGTG TGTTTTGG
                                |||| |||| ||||||||
                                GTCT CCAC ACAAAGCC
                                  C    C
GAM520   LOC126282 3'  CTAGGGGAGTTTGGCCGG    13817      AA  T  T    T
                                CTAG  GG GA GTTT GGCCGG
                                ||||  || || |||| ||||||
                                GATC  CC CT CAAA CCGGCC
                                   __  _  _   _
GAM520   LOC146958 5'  CAGGAGGTGATGTTCAGAGTGG 13818     A         T  CC
                                TAG AGGTGATGTTT GG  GG
                                ||| ||||||||||| ||  ||
                                GTC TCCACTACAAG CT  CC
                                  C          T  CA
GAM520   LOC151056 3'  CTGGAAAGTGATGATCTGG    13819    A        T
                                CT GAAGGTGATG TTTGG
                                || |||||||||| |||||
                                GA CTTTCACTAC AGACC
                                 C         T
GAM520   LOC157651 3'  TAGAAGGTTGCACAGCGGCCGG 13820         GA   TT__
                                TAGAAGGT  TGT    TGGCCGG
                                ||||||||  |||    |||||||
                                ATCTTCCA  ACG    GCCGGCC
                                    __   TGTC
GAM520   LOC158236 5'  CTGGAAGATGATGTTTTCC    13821    A          GG
                                CT GAAGGTGATGTTTT  CC
                                || ||||||||||||||  ||
                                GA CTTCTACTACAAAA  GG
                                 C           __
GAM520   LOC201507 3'  CTAGAAGGTGGGGACGGTCTCG 13822          ATGTTT   C__
            GA                   CTAGAAGGTG     TGG   CGGA
                                ||||||||||     |||   ||||
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                                GATCTTCCAC     GCC   GCCT
                                     CCCT__   AGA
GAM520   LOC219942 3'  TAGAAGGTGGTGTGACTTGG   13823        A   __
                                TAGAAGGTG TGT  TTTGG
                                ||||||||| |||  |||||
                                ATCTTCCAC ACA  GAACC
                                     C   CT
GAM520   LOC222631 5'  CTGGAAGGAGATGGGTCTGG   13824    A    T    T_
                                CT GAAGG GATG  TTTGG
                                || ||||| ||||  |||||
                                GA CTTCC CTAC  AGACC
                                 C    T   CC
GAM520   LOC253815 5'  GAAGGTGATGGGGTCCCGG    13825         TTTT  __
                                GAAGGTGATG    GG  CCGG
                                ||||||||||    ||  ||||
                                CTTCCACTAC    CC  GGCC
                                     C___  AG
GAM520   LOC255927 3'  AAAAGCAGGGTTTTGGCCGG   13826       AT
                                GAAGGTG  GTTTTGGCCGG
                                |||||||  ||||||||||
                                TTTTCGT  CAAAACCGGCC
                                    CC
GAM521   ASTN     3'  TTCCAGATGAGGAGCCCTGGT  13829        CAAA    ____
                                TTCCAGAT    GAGGG    TGGT
                                ||||||||    |||||    ||||
                                AAGGTCTA    CTCCT    ACCA
                                     ____     CGGG
GAM521   CAMK4    3'  TTCCAGATCTGAAGGAAGC    13830         AAA    T
                                TTCCAGATC   GAGGG GGT
                                |||||||||   ||||| |||
                                AAGGTCTAG   CTTCC TCG
                                     A__     T
GAM521   COL4A6   3'  TTCCGATCAAGACGGT      13831      A     A  G
                                TTCC GATCAA GA GGT
                                |||| |||||| || |||
                                AAGG CTAGTT CT CCA
                                  _     _  G
GAM521   COL4A6   3'  TTCCGATCAAGACGGT      13831      A     A  G
                                TTCC GATCAA GA GGT
                                |||| |||||| || |||
                                AAGG CTAGTT CT CCA
                                  _     _  G
GAM521   CYP1B1   3'  TTCCATGTCAAAAATAGGTGGT 13832      GA     _
                                TTCCA  TCAAAGA GGGTGGT
                                |||||  ||||||| |||||||
                                AAGGT  AGTTTTT TCCACCA
                                   AC      A
GAM521   DMXL1    3'  TTCTGAATCAGAAAAGGT    13833     CA    A
                                TTC  GATCA AGAGGGT
                                |||  ||||| |||||||
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                                AAG  TTAGT TTTTCCA
                                  AC    C
GAM521  GOSR1    3'  TTCCAGACCAGGGTG      13834        AAGA
                                TTCCAGATCA   GGGTG
                                ||||||||||   |||||
                                AAGGTCTGGT   CCCAC
                                           _____
GAM521  IGF1     3'  TTCCAGATAGGAATTGGT    13835       CAAAG   __
                                TTCCAGAT    AGGG  TGGT
                                ||||||||    ||||  ||||
                                AAGGTCTA    TCCT  ACCA
                                     ______   TA
GAM521  JPH3     3'  TTCTAGACAGAGAAAGCAGT  13836    C   T  A    TG
                                TTC AGA CA AGAGGG  GT
                                ||| ||| || ||||||  ||
                                AAG TCT GT TCTTTC  CA
                                  A  _ C     GT
GAM521  PDE6A    3'  TCCCAGGAAAGGGTGGT     13837      ATCAA
                                TTCCAG    AGAGGGTGGT
                                ||||||    ||||||||||
                                AGGGTC    TTTCCCACCA
                                   C_____
GAM521  PPP1R12A 3'  TTCTAGATAAGAGGGCA    13838    C   CA
                                TTC AGAT  AAGAGGGTG
                                ||| ||||  |||||||||
                                AAG TCTA  TTCTCCCGT
                                  A   __
GAM521  RET      3'  TTCCAAATCGAGGGT       13839        AAA
                                TTCCAGATC   GAGGGT
                                |||||||||   ||||||
                                AAGGTTTAG   CTCCCA
                                           ___
GAM521  SEL1L    3'  TTCTAATCAAAGAGAAT     13840     CA
                                TTC  GATCAAAGAGGGT
                                |||  |||||||||||||
                                AAG  TTAGTTTCTCTTA
                                  A_
GAM521  SOX12    3'  TCCCGGATCAAAGGAT      13841     A    AA
                                TTCC GATCA  GAGGGT
                                ||||  |||||  ||||||
                                AGGG CTAGT  TTCCTA
                                  C    __
GAM521  TRRAP    3'  TTCCAGACCGGAGAAT      13842        AAA
                                TTCCAGATC   GAGGGT
                                |||||||||   ||||||
                                AAGGTCTGG   CTCTTA
                                      C__
GAM521  ZNF146   3'  CTCCAGATCTATGGTGGT    13843        AAAGAG
                                TTCCAGATC     GGTGGT
                                |||||||||     ||||||
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                                GAGGTCTAG     CCACCA
                                     ATA___
GAM521  ACTR2    3'  TTCCAGTCAAAGGGC       13844       A   AA
                                TTCCAG TCA  GAGGGT
                                |||||| |||  ||||||
                                AAGGTC AGT  TTCCCG
                                  _   __
GAM521  APMCF1   3'  TTCCAGAACAAAGAAATG    13845       T       G
                                TTCCAGA CAAAGAGG TG
                                ||||||| |||||||| ||
                                AAGGTCT GTTTCTTT AC
                                    T       _
GAM521  BRD2     5'  CTCCAGGGAAAGAGGGTGGT   13846       ATC
                                TTCCAG   AAAGAGGGTGGT
                                ||||||   ||||||||||||
                                GAGGTC   TTTCTCCCACCA
                                   CC_
GAM521  C21orf25 3'  TTCCAGATCAAGAGCCGT    13847         AAG    G
                                TTCCAGATCA   AGGGT GT
                                ||||||||||   ||||| ||
                                AAGGTCTAGT   TCTCG CA
                                      ___     G
GAM521  CAPN13   5'  TCTCAGGTTAGAGAGTGGT   13848    _  ATCAA
                                TC CAG    AGAGGGTGGT
                                || |||    ||||||||||
                                AG GTC    TCTCTCACCA
                                 A  CAA__
GAM521  CLDN7    5'  TTCCAGACAAAATTGGTGGT   13849       T    AG
                                TTCCAGA CAAAG  GGTGGT
                                ||||||| |||||  ||||||
                                AAGGTCT GTTTT  CCACCA
                                   _    AA
GAM521  CLDN7    5'  TTCCAGACAAAATTGGTGGT   13849       T    AG
                                TTCCAGA CAAAG  GGTGGT
                                ||||||| |||||  ||||||
                                AAGGTCT GTTTT  CCACCA
                                   _    AA
GAM521  FLJ10853 3'  TTCCAGATTAAAAAAATGGT   13850        CA
                                TTCCAGAT  AAGAGGGTGGT
                                ||||||||  ||||||||||||
                                AAGGTCTA  TTTTTTTACCA
                                   A_
GAM521  FLJ14642 3'  TTCCAGATATGAAGTGGT    13851        CAAA   G
                                TTCCAGAT   GAGG TGGT
                                ||||||||   |||| ||||
                                AAGGTCTA   CTTC ACCA
                                   TA__   _
GAM521  FLJ14768 3'  CTCCAGATCAAGGTG       13852         AAGA   G
                                TTCCAGATCA   GGGT G
                                ||||||||||   |||| |
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                                GAGGTCTAGT   TCCA C
                                     ____   G
GAM521  FLJ20605  3'  TTCCAGGGTAAAGATAGT   13853      ATCAAA
                                TTCCAG    GAGGGTGGT
                                ||||||    |||||||||
                                AAGGTC    TTTCTATCA
                                   CCA___
GAM521  FLJ22615  3'  TCCCAGATTAGGATGG     13854       CAAAG
                                TTCCAGAT   AGGGTGG
                                ||||||||   |||||||
                                AGGGTCTA   TCCTACC
                                    A____
GAM521  FLJ22969  3'  TTCCAGATCAGAGCAGGGGT  13855        A A  T
                                TTCCAGATCA AG GGG GGT
                                |||||||||| || ||| |||
                                AAGGTCTAGT TC TCC CCA
                                      C  G  _
GAM521  FLJ23191  5'  TTCCAGGCCAAAGTGACCGTGG 13856      AT   A __
          T                      TTCCAG  CAAAG GG  GTGGT
                                ||||||  ||||| ||  |||||
                                AAGGTC  GTTTC CT  CACCA
                                   CG    A  GG
GAM521  FLJ23469  3'  TCCGGGTGACAGGAGGGTGGT  13857    A___  CAAA
                                TCC   GAT   GAGGGTGGT
                                |||   |||   |||||||||
                                AGG   CTG   CTCCCACCA
                                  CCCA  TC__
GAM521  GP5       5'  TTCCACAGGAAGAGGGTGGT  13858     GATCA
                                TTCCA   AAGAGGGTGGT
                                |||||   ||||||||||
                                AAGGT   TTCTCCCACCA
                                   GTCC_
GAM521  GPS2      5'  CTCCAGGAACTCGAGGGTGGT  13859     ATCAAA
                                TTCCAG    GAGGGTGGT
                                ||||||    |||||||||
                                GAGGTC    CTCCCACCA
                                   CTTGAG
GAM521  HCA4      3'  TTCCAGATCATAGTCAAGT   13860       A A_
                                TTCCAGATCA AG  GGGT
                                |||||||||| ||  ||||
                                AAGGTCTAGT TC  TTCA
                                      A  AG
GAM521  HCA4      3'  TTCCAGATCATAGTCAAGT   13860       A A_
                                TTCCAGATCA AG  GGGT
                                |||||||||| ||  ||||
                                AAGGTCTAGT TC  TTCA
                                      A  AG
GAM521  HSA250839 3'  TTCCAGTTCAAAGGCAAGC   13861      A    A_
                                TTCCAG TCAAAG  GGGT
                                |||||| ||||||  ||||
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                                AAGGTC AGTTTC  TTCG
                                   A     CG
GAM521  HSMPP8   3' TCCCAGAGAGGGTGGT     13862       TCAAA
                                TTCCAGA    GAGGGTGGT
                                |||||||    |||||||||
                                AGGGTCT    CTCCCACCA
                                   _____
GAM521  KIAA0152 3' TTCCAGATAAGGAAGCA     13863       CA  AG
                                TTCCAGAT  AAG  GGTG
                                ||||||||  |||  ||||
                                AAGGTCTA  TTC  TCGT
                                    __   CT
GAM521  KIAA0326 3' TTCCAGACTCAGTTGTGGT   13864       CAA  AGG
                                TTCCAGAT   AG   GTGGT
                                ||||||||   ||   |||||
                                AAGGTCTG   TC   CACCA
                                    AG_  AA_
GAM521  KIAA0461 3' TTCTGGATAATTAAAGGTGGT 13865    CA   CAAA
                                TTC  GAT   GAGGGTGGT
                                |||  |||   |||||||||
                                AAG  CTA   TTTCCACCA
                                  AC   TTAA
GAM521  KIAA1143 3' TTCCAGATAGAATAAAGGT   13866       CA  _
                                TTCCAGAT  AA GAGGGT
                                ||||||||  ||  ||||||
                                AAGGTCTA  TT TTTCCA
                                    TC  A
GAM521  KIAA1204 3' TTCCAGATGAATCACGGT    13867       CAAA  GG_
                                TTCCAGAT   GAG   TGGT
                                ||||||||   |||   ||||
                                AAGGTCTA   CTT   GCCA
                                    _____  AGT
GAM521  KIAA1866 3' TTCCAGATCTACAATGGT    13868       AAAGAG
                                TTCCAGATC     GGTGGT
                                |||||||||     ||||||
                                AAGGTCTAG     TTACCA
                                    ATG___
GAM521  KIAA1879 5' TCCCAGCAGGAGGGTGGT    13869      ATCAAA
                                TTCCAG     GAGGGTGGT
                                ||||||     |||||||||
                                AGGGTC     CTCCCACCA
                                   GTC___
GAM521  KIAA1958 3' TTCCAATCAAAGGAGC      13870      A     A
                                TTCCAG TCAAAG GGGT
                                |||||| |||||| ||||
                                AAGGTT AGTTTC CTCG
                                   _     _
GAM521  LGALS8   5' TTCAGGACCAGGGTGGT     13871     CA    AAGA
                                TTC  GATCA   GGGTGGT
                                |||  |||||   |||||||
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                                AAG  CTGGT    CCCACCA
                                  TC    _____
GAM521  MGC10334 5'  TTCCGGACCGAGAGGGT     13872      A    AA
                                TTCC GATC  AGAGGGT
                                |||| ||||  |||||||
                                AAGG CTGG  TCTCCCA
                                  C    C_
GAM521  MGC3020   5'  CAGACCAAGGAGGCAGCTGGT  13873         A    G___
                                CAGATCAA GAGG    TGGT
                                |||||||| ||||    ||||
                                GTCTGGTT CTCC    ACCA
                                     C    GTCG
GAM521  ORCTL3    3'  CTCCAGATTGAGGAGA      13874         CAAA     T
                                TTCCAGAT    GAGGG GG
                                ||||||||    ||||| ||
                                GAGGTCTA    CTCCT CT
                                     A___    _
GAM521  PCBP4     3'  TTCCAGTCAAAAGGGT      13875       A    A
                                TTCCAG TCAA GAGGGT
                                |||||| |||| ||||||
                                AAGGTC AGTT TTCCCA
                                   _    _
GAM521  PCBP4     3'  TTCCAGTCAAAAGGGT      13875       A    A
                                TTCCAG TCAA GAGGGT
                                |||||| |||| ||||||
                                AAGGTC AGTT TTCCCA
                                   _    _
GAM521  PCBP4     3'  TTCCAGTCAAAAGGGT      13875       A    A
                                TTCCAG TCAA GAGGGT
                                |||||| |||| ||||||
                                AAGGTC AGTT TTCCCA
                                   _    _
GAM521  PIPPIN    3'  CTCTAGAAGGGAGGGTGGT   13876     C   TCAAA
                                TTC AGA     GAGGGTGGT
                                ||| |||     |||||||||
                                GAG TCT     CTCCCACCA
                                  A   TCC__
GAM521  PRO0800   5'  TTCCAGACCAGACTGG      13877         AAGA  G
                                TTCCAGATCA    GG TGG
                                ||||||||||    || |||
                                AAGGTCTGGT    CT ACC
                                      _____ G
GAM521  PTPRN2    3'  TTCCAGATAGAGAGAAGT    13878         CAA     T
                                TTCCAGAT   AGAGGG GGT
                                ||||||||   |||||| |||
                                AAGGTCTA   TCTCTC TCA
                                     ___      T
GAM521  PTPRN2    3'  TTCCAGATAGAGAGAAGT    13878         CAA     T
                                TTCCAGAT   AGAGGG GGT
                                ||||||||   |||||| |||
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                                AAGGTCTA   TCTCTC TCA
                                    ___      T
GAM521  Rab11-FIP2 3'  CAAATCAAGAAATTGGT     13879        A    G
                                CAGATCAA GAGG TGGT
                                |||||||| |||| ||||
                                GTTTAGTT CTTT ACCA
                                    _    A
GAM521  RAB22A   3'  TTCCAGATGGGATCTGGT     13880        CAAAGA  ___
                                TTCCAGAT     GGG   TGGT
                                ||||||||     |||   ||||
                                AAGGTCTA     CCC   ACCA
                                    _______  TAG
GAM521  STK17B   5'  TTCCAGACAAGGGCCGACGGT  13881        CAAA     ____
                                TTCCAGAT   GAGGGT   GGT
                                ||||||||   ||||||   |||
                                AAGGTCTG   TTCCCG   CCA
                                    _____    GCTG
GAM521  SZF1     3'  TTCCAGACACATTAGGGTGGT  13882        _ AAG
                                TTCCAGAT CA   AGGGTGGT
                                |||||||| ||   ||||||||
                                AAGGTCTG GT   TCCCACCA
                                     T  AA_
GAM521  TGFB1I1  5'  CTCCAGGTCAGAGAGC      13883       A   AA
                                TTCCAG TCA  GAGGGT
                                |||||| |||  ||||||
                                GAGGTC AGT  CTCTCG
                                   C   __
GAM521  ZNF313   3'  TTCCAGCATCAGATGG       13884       _   AAGAG
                                TTCCAG ATCA    GGTGG
                                |||||| ||||    |||||
                                AAGGTC TAGT    CTACC
                                   G   _____
GAM521  ZNF323   3'  TTCCAGATAAGATTTGGT     13885        CA   GGG
                                TTCCAGAT  AAGA   TGGT
                                ||||||||  ||||   ||||
                                AAGGTCTA  TTCT   ACCA
                                    __    AA_
GAM521  LOC115294 3'  TTCCAGATAAAAACATGTGGT  13886        C    AGG
                                TTCCAGAT AAAG   GTGGT
                                |||||||| ||||   |||||
                                AAGGTCTA TTTT   CACCA
                                     T    GTA
GAM521  LOC139795 3'  TTCCAGATTAAGAATA      13887        CAAA
                                TTCCAGAT   GAGGGTG
                                ||||||||   |||||||
                                AAGGTCTA   TTCTTAT
                                     A___
GAM521  LOC143338 3'  TCCAGATCAAGGACAAC     13888         AAG   TG
                                TCCAGATCA   AGGG  GT
                                |||||||||  ||||  ||
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                                AGGTCTAGT   TCCT  TG
                                     ___    GT
GAM521   LOC148114 5'  CTCTAGTCTGAGGGTGGT    13889     C  A  AAA
                                TTC AG TC   GAGGGTGGT
                                ||| || ||   |||||||||
                                GAG TC AG   CTCCCACCA
                                  A  _  A__
GAM521   LOC151996 5'  TTCCAGATCACAGGTG      13890          AAGA
                                TTCCAGATCA    GGGTG
                                ||||||||||    |||||
                                AAGGTCTAGT    TCCAC
                                     G___
GAM521   LOC152674 3'  TTCCAATCAAAGAAAAT     13891       A
                                TTCCAG TCAAAGAGGGT
                                |||||| ||||||||||
                                AAGGTT AGTTTCTTTTA
                                  _
GAM521   LOC153205 3'  TTCCAGATGAGGCTTGGT    13892        CAAA    G_
                                TTCCAGAT    GAGG  TGGT
                                ||||||||    ||||  ||||
                                AAGGTCTA    CTCC  ACCA
                                     _____   GA
GAM521   LOC164714 5'  TCCCTGGAAAGAGGGTGGT   13893     AGATC
                                TCC     AAAGAGGGTGGT
                                |||     ||||||||||||
                                AGG     TTTCTCCCACCA
                                  GACC_
GAM521   LOC164832 3'  TTCCAGATAAAAACGTGGT   13894        CA    G
                                TTCCAGAT  AAGAG GTGGT
                                ||||||||  ||||| |||||
                                AAGGTCTA  TTTTT CACCA
                                     __    G
GAM521   LOC200261 3'  CCCCAGGGAGAGGGTGGT    13895       ATCAA
                                TTCCAG     AGAGGGTGGT
                                ||||||     ||||||||||
                                GGGGTC     TCTCCCACCA
                                   CC___
GAM521   LOC200314 5'  TTCCAGATGTGGAAACTCATGG 13896        CAAA   ___
           T                     TTCCAGAT    GAGG   GTGGT
                                ||||||||    ||||   |||||
                                AAGGTCTA    CTTT   TACCA
                                     CAC_    GAG
GAM521   LOC200382 3'  TTCTAATCAAAAGGGT      13897     CA     A
                                TTC  GATCAA GAGGGT
                                |||  |||||| ||||||
                                AAG  TTAGTT TTCCCA
                                  A_     _
GAM521   LOC201702 5'  CTCCAGACAGGGTGG       13898        CAAAG
                                TTCCAGAT    AGGGTGG
                                ||||||||    |||||||
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                                GAGGTCTG    TCCCACC
                                        _____
GAM521  LOC202460 5'  TTCCATGGACAGGGTGGT    13899      __  CAAAG
                                TTCCA  GAT    AGGGTGGT
                                |||||  |||    ||||||||
                                AAGGT  CTG    TCCCACCA
                                   AC  _____
GAM521  LOC203569 3'  TTCCAGATTAAGAATA      13887        CAAA
                                TTCCAGAT   GAGGGTG
                                ||||||||   |||||||
                                AAGGTCTA   TTCTTAT
                                    A___
GAM521  LOC220766 5'  TTCCAGATGAAGATG       13900        CAAA
                                TTCCAGAT   GAGGGTG
                                ||||||||   |||||||
                                AAGGTCTA   CTTCTAC
                                        ____
GAM521  LOC253866 5'  TCCAGGTTCCCAGAGGGTGGT  13901      A_  AA
                                TCCAG  TC  AGAGGGTGGT
                                |||||  ||  ||||||||||
                                AGGTC  AG  TCTCCCACCA
                                   CA  GG
GAM521  LOC255057 3'  CTCTGGATCAGGGAGGGTGG   13902     CA    AA
                                TTC  GATCA  GAGGGTGG
                                |||  |||||  ||||||||
                                GAG  CTAGT  CTCCCACC
                                  AC    CC
GAM521  LOC256950 3'  TTCGGCGATGCAGAGGGTGGT  13903     CA_   CAA
                                TTC   GAT   AGAGGGTGGT
                                |||   |||   ||||||||||
                                AAG   CTA   TCTCCCACCA
                                  CCG   CG_
GAM521  LOC257258 5'  TTCCAGTTTGAGGGTGGT    13904       ATCAAA
                                TTCCAG     GAGGGTGGT
                                ||||||     |||||||||
                                AAGGTC     CTCCCACCA
                                   AAA___
GAM521  LOC51123  3'  TTCCAAATCAGAGTCAACTG   13905         A  A_  G
                                TTCCAGATCA AG  GG TG
                                |||||||||| ||  || ||
                                AAGGTTTAGT TC  TT AC
                                      C  AG  G
GAM521  LOC51195  3'  TCCGACCCAGAGGGTGGT    13906     A    AA
                                TCC GATC  AGAGGGTGGT
                                ||| ||||  ||||||||||
                                AGG CTGG  TCTCCCACCA
                                  _   G_
GAM521  LOC89985  3'  TTCCAATCAAAGGAAT      13907       A     A
                                TTCCAG TCAAAG GGGT
                                |||||| |||||| ||||
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                              AAGGTT AGTTTC CTTA
                                 _    _
GAM521  LOC90288 3' TTCCAGTCAGAGTAG      13908      A  AAGA
                              TTCCAG TCA   GGGTGG
                              |||||| |||   ||||||
                              AAGGTC AGT   CTCATC
                                 _  ____
GAM521  LOC90625 5' TCCCAGATGGAGGGGTGGT   13909       CAA  A
                              TTCCAGAT  AG GGGTGGT
                              ||||||||  || |||||||
                              AGGGTCTA  TC CCCACCA
                                   CC_ _
GAM521  LOC90670 3' TTCCAGATGAGATTTGGGTGGT 13910       CAA  ___
                              TTCCAGAT  AGA  GGGTGGT
                              ||||||||  |||  |||||||
                              AAGGTCTA  TCT  CCCACCA
                                   C__  AAA
GAM521  LOC90777 3' TCCCAGGTCAGAGGGC     13911      A  AA
                              TTCCAG TCA  GAGGGT
                              |||||| |||  ||||||
                              AGGGTC AGT  CTCCCG
                                 C  __
GAM522  CCND1   5' GGGGCTCTTCCTGGGCAGCT  13914   AA  C    _
                              GG  CTCT CCTGGG GGCT
                              ||  |||| |||||| ||||
                              CC  GAGA GGACCC TCGA
                               CC   A    G
GAM522  GALGT   5' GGAACTCCCGGGGCTTTT   13915       CCTG
                              GGAACTCTC   GGGGCTTTT
                              |||||||||   |||||||||
                              CCTTGAGGG   CCCCGAAAA
                                   ____
GAM522  OGG1    3' GGAACCCTTTCTGCGCTTT   13916       CC  GGG
                              GGAACTCT  CTG  GCTTT
                              ||||||||  |||  |||||
                              CCTTGGGA  GAC  CGAAA
                                   AA  G__
GAM522  PDE5A   5' TCGGAGGCTCTCTGGTACTGCT 13917     ACT  C   GG__
          TTT                 TCGGA  CTC CTGG   GCTTTT
                              |||||  ||| ||||   ||||||
                              AGCCT  GAG GACC   CGAAAA
                                CC_  A   ATGA
GAM522  PDE5A   5' TCGGAGGCTCTCTGGTACTGCT 13917     ACT  C   GG__
          TTT                 TCGGA  CTC CTGG   GCTTTT
                              |||||  ||| ||||   ||||||
                              AGCCT  GAG GACC   CGAAAA
                                CC_  A   ATGA
GAM522  PRKACA  3' GGGGCTCCCCCTCTGTCTTTT 13918   AA     GGGGG
                              GG  CTCTCCCT   CTTTT
                              ||  ||||||||   |||||
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                                CC  GAGGGGGA    GAAAA
                                 CC       GACA_
GAM522  SLC38A2  3'  GGAATTTTCCCTAGGCACTT   13919      CTC       G
                                GGAA   TCCCTGGG GCTT
                                ||||   |||||||| ||||
                                CCTT   AGGGATCC TGAA
                                  AAA       G
GAM522  FLJ20154  3'  CTCCTTCCTTGGGGGCTTTT   13920     __   C
                                CTC  TCC TGGGGGCTTTT
                                |||  ||| ||||||||||
                                GAG  AGG ACCCCCGAAAA
                                 GA   A
GAM522  PEG10    3'  GAACTTTCTCCCACTGGGGTTT 13921      __      TG_   C
           TT                    GAAC  TCTCCC   GGGG TTTT
                                ||||  ||||||   |||| ||||
                                CTTG  AGAGGG   CCCC AAAA
                                  AA     TGA    A
GAM522  LOC115073 5'  TCGGACCCCGCTGGGGGCTTTT 13922       ACT   _
                                TCGGA   CTCC CTGGGGGCTTTT
                                |||||   |||| ||||||||||||
                                AGCCT   GGGG GACCCCCGAAAA
                                   ___    C
GAM523  BAIAP3   3'  TCGGCTCTTTGCGGCTGCTGG  13925    A  C        ACC
                                TC GC TTTTGCGGTT   GCTGG
                                || || ||||||||||   |||||
                                AG CG GAAACGCCGA   CGACC
                                 C  A         ___
GAM523  MIR16    3'  TCAGCTTTCTGAATTGCTG    13926      C    C   ACC
                                TCAGC TTTTG GGTT   GCTG
                                ||||| ||||| ||||   ||||
                                AGTCG AAGAC TTAA   CGAC
                                   A    _   ___
GAM523  PROX1    3'  GCCTTTTGGGGTACTTTGG    13927        C  T   CGC
                                GCCTTTTG GG TAC   TGG
                                |||||||| || |||   |||
                                CGGAAAAC CC ATG   ACC
                                     _ C   AA_
GAM523  RXRA     3'  CTTTTGCACTCCCACCGCTGG  13928        G __
                                CTTTTGCG TT  ACCGCTGG
                                |||||||| ||  ||||||||
                                GAAAACGT AG  TGGCGACC
                                     G  GG
GAM523  ZNF268   5'  TCAGTTTTGTGTGCCTCGCTGG 13929     CC    CG_   AC
                                TCAG  TTTTG   GTT  CGCTGG
                                ||||  |||||   |||  ||||||
                                AGTC  AAAAC   CGG  GCGACC
                                   __    ACA  A_
GAM523  LOC145333 5'  CAGCCTTTCTGCTGCTG     13930        GCG   ACC
                                CAGCCTTTT   GTT   GCTG
                                |||||||||   |||   ||||
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                                GTCGGAAAG  CGA  CGAC
                                     A__  ___
GAM523  LOC147136 3'  CAGCCTTTTAGGGCTGCTGG  13931        C   ACC
                                CAGCCTTTTG GGTT  GCTGG
                                |||||||||| ||||  |||||
                                GTCGGAAAAT CCGA  CGACC
                                     C  ___
GAM523  LOC51667  3'  CAGTGAGGACGGTTACTGCTGG 13932    CCTTTT      C
                                CAG    GCGGTTAC GCTGG
                                |||    |||||||| |||||
                                GTC    TGCCAATG CGACC
                                  ACTCC_      A
GAM523  LOC85439  5'  TCAGCCTCTCTTGCCGTTG   13933        GCG TTA  C
                                TCAGCCTTTT  G  CCG TG
                                ||||||||||  |  ||| ||
                                AGTCGGAGAG  C  GGC AC
                                     AA_ ___  A
GAM524  CHRNA3   3'  TGAGAAGTTTCTGTTGTTT   13936         AAACGA
                                TGAGAGGTTTC    TTGTTT
                                ||||||||||     ||||||
                                ACTCTTCAAAG    AACAAA
                                     AC____
GAM524  FBXW1B   3'  TGGAGGTTTATTGTT     13937    A     CAAACG
                                TG GAGGTTT    ATTGTT
                                || |||||||    ||||||
                                AC CTCCAAA    TAACAA
                                 _    _______
GAM524  FBXW1B   3'  TGGAGGTTTATTGTT     13937    A     CAAACG
                                TG GAGGTTT    ATTGTT
                                || |||||||    ||||||
                                AC CTCCAAA    TAACAA
                                 _    _______
GAM524  FBXW1B   3'  TGGAGGTTTATTGTT     13937    A     CAAACG
                                TG GAGGTTT    ATTGTT
                                || |||||||    ||||||
                                AC CTCCAAA    TAACAA
                                 _    _______
GAM524  LFNG     3'  TGGGAGGTTCCAGATGCT   13938    A      AAC  T
                                TG GAGGTTTCA  GAT GTT
                                || |||||||||  ||| |||
                                AC CTCCAAGGT  CTA CGA
                                  C       ___  _
GAM524  NSF      3'  TGAGAGGTTTGTAAATTACTT  13939        CAAAC
                                TGAGAGGTTT    GATTGTTT
                                ||||||||||    ||||||||
                                ACTCTCCAAA    TTAATGAA
                                     CAT__
GAM524  DKFZP566G1424 3'  TGAGAGGTTTTTGTT      13940        CAAACGA
                                TGAGAGGTTT     TTGTT
                                ||||||||||     |||||
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                                ACTCTCCAAA      AACAA
                                          _______
GAM524  FLJ10701  3'  GAAGTAAAAAACGATTGTTT  13941      TTC
                                GAGGT  AAACGATTGTTT
                                |||||  ||||||||||||
                                CTTCA  TTTGCTAACAAA
                                   TTT
GAM524  FLJ11996  3'  TGAGAGGTTCAAGTGACTCTC  13942        T  AC   G
                                TGAGAGGTT CAA  GATT TT
                                ||||||||| |||  |||| ||
                                ACTCTCCAA GTT  CTGA AG
                                      _  CA   G
GAM524  IRAK3     3'  TGGTAGGTTTTGATTGTTT   13943    AG    CAAAC
                                TG  AGGTTT    GATTGTTT
                                ||  ||||||    ||||||||
                                AC  TCCAAA    CTAACAAA
                                 CA     A____
GAM524  MOST2     5'  GAGAGGTTTTGAATGCT     13944        CAAAC  T
                                GAGAGGTTT    GA TGTT
                                |||||||||    || ||||
                                CTCTCCAAA    CT ACGA
                                      A____  T
GAM524  NYD-SP11  3'  GAGGTTTCAGGGAGGATTTA  13945        AAC  TT
                                GAGGTTTCA   GA  GTTTA
                                |||||||||   ||  |||||
                                CTCCAAAGT   CT  TAAAT
                                      CC_  CC
GAM524  RPH3A     3'  TGAGAGGTTATTAAATGATCA  13946        TC_  C
                                TGAGAGGTT   AAA GATTG
                                |||||||||   ||| |||||
                                ACTCTCCAA   TTT CTAGT
                                      TAA   A
GAM524  ZNF33A    3'  TGAGAGGTTTTAACATGAATG  13947         C  AC_  T
                                TGAGAGGTTT AA   GA TG
                                |||||||||| ||   || ||
                                ACTCTCCAAA TT   CT AC
                                      A  GTA  T
GAM524  LOC143153 5'  TGAGAGGTTCAGGGAGGAGTTT 13948         T  AAC  TT_
                                TGAGAGGTT CA   GA   GTTT
                                ||||||||| ||   ||   ||||
                                ACTCTCCAA GT   CT   CAAA
                                      _  CC_  CCT
GAM524  LOC149566 5'  TGAGAGGTTACAAATTGT    13949        T  AAC
                                TGAGAGGTT CA   GATTGT
                                ||||||||| ||   ||||||
                                ACTCTCCAA GT   TTAACA
                                      T  ___
GAM524  LOC152343 3'  TGAGAGATCTGGTTGTTT    13950         CAAACGA
                                TGAGAGGTTT      TTGTTT
                                ||||||||||      ||||||
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                                ACTCTCTAGA      AACAAA
                                      CC_____
GAM525  ITK      3'  TCTCCTAGCTCAGTACATA   13953    C       __
                                TC CCTGGTTTG  ACATA
                                || |||||||||  |||||
                                AG GGATCGAGT  TGTAT
                                 A        CA
GAM525  NPTX1    3'  CCTCCTGGTCCCCAACAT    13954    _      __
                                CC CCTGGTTT  GACAT
                                || ||||||||  |||||
                                GG GGACCAGG  TTGTA
                                 A       GG
GAM525  UCP2     5'  TCCCCTTGGTTTTCCATA    13955       _    GA
                                TCCCCT GGTTT  CATA
                                |||||| |||||  ||||
                                AGGGGA CCAAA  GTAT
                                    A     AG
GAM525  C21orf41 3'  CCCTCTGTTGGTCTGACAT   13956    _ ___
                                CCC CT   GGTTTGACAT
                                ||| ||   ||||||||||
                                GGG GA   CCAGACTGTA
                                  A  CAA
GAM525  MGC22014 3'  TCCTTTAGTCCGAACATA    13957     CC       _
                                TCC  TGGTTTGA CATA
                                |||  |||||||| ||||
                                AGG  ATCAGGCT GTAT
                                  AA       T
GAM526  RANBP2L1 3'  TTCCAGTTGGTATGGTACC   13960          CCCGATAAC
                                TTCCAGTTGG       GTACT
                                ||||||||||       |||||
                                AAGGTCAACC       CATGG
                                      ATAC_____
GAM526  KIAA0336 3'  TTCCAGTTGGTATGGTACC   13960          CCCGATAAC
                                TTCCAGTTGG       GTACT
                                ||||||||||       |||||
                                AAGGTCAACC       CATGG
                                      ATAC_____
GAM526  LOC220692 3' TTCCAGTTGGTATGGTACC   13960          CCCGATAAC
                                TTCCAGTTGG       GTACT
                                ||||||||||       |||||
                                AAGGTCAACC       CATGG
                                      ATAC_____
GAM526  LOC221078 3' CAGTTGGCCTGACAACAC    13961          C
                                CAGTTGGCC GATAACGT
                                ||||||||| ||||||||
                                GTCAACCGG CTGTTGTG
                                      A
GAM527  DPYSL3   3'  GAATGGAAAGGTGGAACCAGG  13964     AT     A    A  T
                                GAA  GAAAGG TGGAA CA GG
                                |||  |||||| ||||| || ||
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                                CTT  CTTTCC ACCTT GT CC
                                  AC     _    G  _
GAM527  PABPN1   3'  TGAAGGGGGCAGGGAAACATGG 13965     A__  AT_
                                TGAA   GG   GGAAACATGG
                                ||||   ||   ||||||||||
                                ACTT   CC   CCTTTGTACC
                                  CCC  GTC
GAM527  PCDH9    5'  TGACAGGAGATGGAAACATGG  13966     A   __
                                TGA AGGA  TGGAAACATGG
                                ||| ||||  ||||||||||
                                ACT TCCT  ACCTTTGTACC
                                  G   CT
GAM527  PMP22    3'  TGAAAGGGAAGGGGCGACATGG 13967       AT___  AA
                                TGAAAGG    GG  ACATGG
                                |||||||    ||  ||||||
                                ACTTTCC    CC  TGTACC
                                    CTTCC  GC
GAM527  POLR2F   3'  TGAGAATGAAAATTGGGCATGG 13968     _      GA   AAA
                                TGA AATGAAAG  TGG   CATGG
                                ||| ||||||||  |||   |||||
                                ACT TTACTTTT  ACC   GTACC
                                  C       A_   C__
GAM527  SLC38A2  3'  TGAAATGGAAGGGTTGACATG  13969       A   ATG  AA
                                TGAAATG AAGG   GA  CATG
                                ||||||| ||||   ||  ||||
                                ACTTTAC TTCC   CT  GTAC
                                    C   CAA  __
GAM527  SLC7A6   3'  TGAAAGGAGGATGACATG    13970        T   A_
                                TGAAAGGA GGA  ACATG
                                |||||||| |||  |||||
                                ACTTTCCT CCT  TGTAC
                                     _   AC
GAM527  SPN      3'  TGCCGGGTGGAAACATGG    13971    AAA  A
                                TG   GG TGGAAACATGG
                                ||   || ||||||||||
                                AC   CC ACCTTTGTACC
                                 GG_  C
GAM527  STATH    3'  ATGAAAGATGAGAATATGG    13972        G   GA  C
                                ATGAAAG ATG  AA ATGG
                                ||||||| |||  || ||||
                                TACTTTC TAC  TT TACC
                                    _   TC  A
GAM527  ZNF261   3'  TGATGTGAAAGATGGATATGG  13973     AA     G    AAC
                                TGA  TGAAAG ATGGA   ATGG
                                |||  |||||| |||||   ||||
                                ACT  ACTTTC TACCT   TACC
                                  AC     _    A__
GAM527  COE2     3'  GAAAAAAATTAGGGATGGGAAT 13974     T   A___     A  C
            ATGG                    GAAA GAA    GGATGG AA ATGG
                                |||| |||    |||||| || ||||
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                                CTTT TTT    CCTACC TT TACC
                                  T   AATC     C  A
GAM527  FBXO26    3'  TGAAATAAAGGGATGGGTCTGG 13975         A     AAACA
                                TGAAATGAA GGATGG     TGG
                                ||||||||| ||||||     |||
                                ACTTTATTT CCTACC     ACC
                                     C     CAG__
GAM527  FLJ21324  5'  TGCAATGAAAGGCAGGAACGTG 13976    A       AT    ACA
          G                      TG AATGAAAGG  GGAA   TGG
                                || |||||||||  ||||   |||
                                AC TTACTTTCC  CCTT   ACC
                                 G       GT    GC_
GAM527  FLJ30681  3'  GAAATGGGAAAGGACATG    13977       AAA   T_   AA
                                GAAATG   GGA  GGA  CATG
                                ||||||   |||  |||  ||||
                                CTTTAC   CCT  CCT  GTAC
                                   ___   TT   __
GAM527  GABARAPL3 3'  TGAGAATGAAGGGACAGCAGCA 13978     _     A     AAA
          TGG                    TGA AATGAA GGATGG   CATGG
                                ||| |||||| ||||||   |||||
                                ACT TTACTT CCTGTC   GTACC
                                  C     C     GTC
GAM527  GAL3ST2   3'  TGAAAAGAAAGGGCTCTCATGG 13979      T     ATGGAAA
                                TGAAA GAAAGG      CATGG
                                ||||| ||||||      |||||
                                ACTTT CTTTCC      GTACC
                                   T     CGAGA__
GAM527  KIAA0674  5'  TGGAAGGATGGGCAGCATGG   13980    A      AAA_
                                TG AAGGATGG    CATGG
                                || ||||||||    |||||
                                AC TTCCTACC    GTACC
                                 C       CGTC
GAM527  KIAA1754  3'  TGAAGAGGGGGAAAGGCATGG  13981     _  AT    __
                                TGAA AGG  GGAAA  CATGG
                                |||| |||  |||||  |||||
                                ACTT TCC  CCTTT  GTACC
                                  C  C_    CC
GAM527  KIAA1939  3'  TGAAGTGAAAAGATAACTACGT 13982      A        AA  A
          GG                     TGAA TGAAAGGATGG  AC TGG
                                |||| ||||||||||  || |||
                                ACTT ACTTTTCTATT  TG ACC
                                  C         GA  C
GAM527  LAMP3     3'  TAAAGTGAACAATAGGAAATAT 13983      A   AGGAT    C
          GG                     TGAA TGAA     GGAAA ATGG
                                |||| ||||     ||||| ||||
                                ATTT ACTT     CCTTT TACC
                                  C   GTTAT     A
GAM527  MGC11115  3'  TGCAATGAAAGGGTCCGTCATG 13984    A       ATGGAAA
          G                      TG AATGAAAGG      CATGG
                                || |||||||||      |||||
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                                AC TTACTTTCC      GTACC
                                 G        CAGGCA_
GAM527  MIP-T3   3'  TGGAAGGAGGTAAGAAAACATG 13985    A    T____
           G                     TG AAGGA    GGAAACATGG
                                 || |||||    ||||||||||
                                 AC TTCCT    CTTTTGTACC
                                  C    CCATT
GAM527  PMX2B    5'  TGAAATAAAAGATGGATATGG  13986         G    AAC
                                 TGAAATGAAAG ATGGA   ATGG
                                 |||||||||||| |||||   ||||
                                 ACTTTATTTTC TACCT   TACC
                                        _    A__
GAM527  RAB14    3'  TGAAATGGAAGGGAGTAACATG 13987       A   AT  A
           G                     TGAAATG AAGG  GG AACATGG
                                 ||||||| ||||  || |||||||
                                 ACTTTAC TTCC  TC TTGTACC
                                     C   C_  A
GAM527  STAT2    3'  TGAAAAGAACAGAGGAAATGTG 13988      T   A   T    CA
           G                     TGAAA GAA GGA GGAAA  TGG
                                 ||||| ||| ||| |||||  |||
                                 ACTTT CTT TCT CCTTT  ACC
                                    T   G   _    AC
GAM527  UBP1     3'  ATGAAGGACGGAGATATGG    13989      A      AAC
                                 ATGAA GGATGGA   ATGG
                                 ||||| |||||||   ||||
                                 TACTT CCTGCCT   TACC
                                    _      CTA
GAM527  LOC151742 3'  TGAAAATGGAAGGAATCATGG  13990      TGAAA   T    A
                                 TGAAA     GGA GGAA CATGG
                                 |||||     ||| |||| |||||
                                 ACTTT     CCT CCTT GTACC
                                    TA___   T    A
GAM527  LOC201617 5'  TGAAATGATAGGCAGCATG    13991       A   A   AAA
                                 TGAAATGA AGG TGG   CATG
                                 |||||||| ||| |||   ||||
                                 ACTTTACT TCC GTC   GTAC
                                      A   _   ___
GAM527  LOC221405 3'  TGAAATGGATAAAAATGTG    13992       _       CA
                                 TGAAA GGATGGAAA  TG
                                 ||||| |||||||||  ||
                                 ACTTT CCTATTTTT  AC
                                    A        AC
GAM527  LOC221935 3'  TGACGTGAGGGGCTGGAGGCAT 13993     AA   AA  A    AA
           GG                      TGA  TGA  GG TGGA  CATGG
                                 |||  |||  || ||||  |||||
                                 ACT  ACT  CC ACCT  GTACC
                                   GC   CC  G    CC
GAM527  LOC253187 5'  AATGAAAGGAAGAAAGGATG   13994          T    AC
                                 AATGAAAGGA GGAA  ATG
                                 |||||||||| ||||  |||
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                                TTACTTTCCT CTTT  TAC
                                      T   CC
GAM527  LOC81691  3'  GAAATGGCACATGGAAACATGG 13995       AAAGG
                                GAAATG    ATGGAAACATGG
                                ||||||    ||||||||||||
                                CTTTAC    TACCTTTGTACC
                                   CGTG_
GAM527  LOC90408  3'  TGAAAGAAGAGAAATATG    13996        T    C
                                TGAAAGGA GGAAA ATG
                                |||||||| ||||| |||
                                ACTTTCTT TCTTT TAC
                                     C    A
GAM528  ABCB10    3'  CATAGTCTCTGAGTTTTTTTTC 13999         AT__
           T                     CATAGTCTT   TTTTTTTTCT
                                |||||||||   ||||||||||
                                GTATCAGAG   AAAAAAAAGA
                                      ACTC
GAM528  ADH4      3'  TACCAGGTCTTATTCATTCT   14000       TA       T
                                TACCA  GTCTTATTT TTTT
                                |||||  ||||||||| ||||
                                ATGGT  CAGAATAAG AAGA
                                   C_       T
GAM528  C11orf8   3'  CCTGTTTCTTATTTTTTTTTCT 14001    ATAG
                                CC   TCTTATTTTTTTTTCT
                                ||   ||||||||||||||||
                                GG   AGAATAAAAAAAAAGA
                                 ACAA
GAM528  FOG2      3'  ACAGCTTATTTTTTTTTCT    14002      T
                                ATAG CTTATTTTTTTTTCT
                                |||| ||||||||||||||
                                TGTC GAATAAAAAAAAAGA
                                  _
GAM528  ITGB2     3'  AGTTTTATTTTTTTTTCT     14003     C
                                AGT TTATTTTTTTTTCT
                                ||| ||||||||||||
                                TCA AATAAAAAAAAAGA
                                  A
GAM528  RGS5      3'  CATAGTCTTGTCTTATATTTCT 14004         A   TT_
                                CATAGTCTT TTTT   TTTCT
                                ||||||||| ||||   |||||
                                GTATCAGAA AGAA   AAAGA
                                     C   TAT
GAM528  SERPINE2  3'  TACCATAAAACATTTTTTTTC 14005        TCT
           T                     TACCATAG   TATTTTTTTTTCT
                                ||||||||   ||||||||||||
                                ATGGTATT   GTAAAAAAAAAGA
                                     TT_
GAM528  SLC4A10   3'  CATAGTCTTATTCATTTTT    14006          T
                                CATAGTCTTATTT TTTTT
                                |||||||||||| |||||
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                                GTATCAGAATAAG AAAAA
                                       T
GAM528  SMT3H1   3'  TACTTAGTCTTACTTTTTT   14007    CA
                                TAC  TAGTCTTATTTTTTT
                                |||  |||||||||||||||
                                ATG  ATCAGAATGAAAAAA
                                  A_
GAM528  VDR      3'  ACCATGCCCGGCTATTTTTTTT 14008      A   ___
          T                      ACCAT GTCT   TATTTTTTTTT
                                 ||||| ||||   ||||||||||
                                 TGGTA CGGG   ATAAAAAAAAA
                                    _   CCG
GAM528  WIF1     3'  TACCACAGTGTAATTTTTTTTT 14009        CTT
                                 TACCATAGT   ATTTTTTTTT
                                 |||||||||   |||||||||
                                 ATGGTGTCA   TAAAAAAAA
                                       CAT
GAM528  ZNF85    3'  CCATAGTCTTCACATTTTT   14010         ATTT
                                 CCATAGTCTT   TTTTT
                                 ||||||||||   |||||
                                 GGTATCAGAA   AAAAA
                                       GTGT
GAM528  CNOT4    3'  GCCCTTTGATTTTTTTTTCT   14011     ___
                                 GTCTT   ATTTTTTTTTCT
                                 |||||   ||||||||||||
                                 CGGGA   TAAAAAAAAAGA
                                    AAC
GAM528  DKFZP434B044 3'  ATAGTCTTGTTTCCATTTTCT  14012        A   _
                                 ATAGTCTT TTTTT TTTTCT
                                 ||||||||| ||||| ||||||
                                 TATCAGAA AAAGG AAAAGA
                                       C    T
GAM528  DKFZP564D0764 3'  CATAGTCTTTTTTTTTTT    14013         A
                                 CATAGTCTT TTTTTTTT
                                 ||||||||| ||||||||
                                 GTATCAGAA AAAAAAAA
                                       A
GAM528  FLJ10103  3'  TACCATGGCTTTATTTTTCT   14014       A TC
                                 TACCAT G  TTATTTTTTT
                                 ||||||  |  ||||||||||
                                 ATGGTA C  AATAAAAAGA
                                    C GA
GAM528  FLJ13409  3'  CCATAGTTATATTTTTTCT   14015       CT
                                 CCATAGT  TATTTTTTTT
                                 |||||||  ||||||||||
                                 GGTATCA  ATAAAAAAGA
                                    AT
GAM528  FLJ20004  3'  CCACGTCCTTGTTTTTTTTT  14016     A    A_
                                 CCAT GTCTT  TTTTTTTTT
                                 ||||  |||||  |||||||||
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                                GGTG CAGGA  AAAAAAAAA
                                  _    AC
GAM528  FLJ30681  3'  ACCACTATTTTTTTTTC     14017      AGTCT
                                ACCAT    TATTTTTTTTTC
                                |||||    ||||||||||||
                                TGGTG    ATAAAAAAAAAG
                                  ______
GAM528  HIC2      3'  AGCTTATTTTTTTTTCT     14018    T
                                AG CTTATTTTTTTTTCT
                                || ||||||||||||||
                                TC GAATAAAAAAAAAGA
                                 _
GAM528  HSPC121   3'  CATAGTCTTGCTTTTTTT    14019        A
                                CATAGTCTT TTTTTTTT
                                ||||||||| ||||||||
                                GTATCAGAA GAAAAAAA
                                      C
GAM528  KIAA0884  5'  CCAAGGTCATATTTTTTTT   14020     TA   T
                                CCA  GTC TATTTTTTTT
                                |||  ||| ||||||||||
                                GGT  CAG ATAAAAAAAA
                                  TC   T
GAM528  KIAA1409  3'  CACCAGTCTATTTTTTTTTCT  14021      TA    T
                                TACCA  GTCT ATTTTTTTTTCT
                                |||||  |||| ||||||||||||
                                GTGGT  CAGA TAAAAAAAAAGA
                                  __   _
GAM528  KUB3      3'  CCATAGTTACTTTTTCT     14022       CT
                                CCATAGT  TATTTTTTTT
                                |||||||  ||||||||||
                                GGTATCA  ATGAAAAAGA
                                   __
GAM528  POF1B     3'  GTCTTATTTATACTTTCT    14023        TT_
                                GTCTTATTT   TTTTCT
                                |||||||||   ||||||
                                CAGAATAAA   GAAAGA
                                      TAT
GAM528  PRO1048   3'  CCATAGTAATTTTTTTTT    14024       CTT
                                CCATAGT   ATTTTTTTTT
                                |||||||   ||||||||||
                                GGTATCA   TAAAAAAAAA
                                    T__
GAM528  RGS20     3'  CCATATCCCTTTATTTTTTTT 14025      G_   _
                                CCATA  TCTT ATTTTTTTTT
                                |||||  |||| ||||||||||
                                GGTAT  GGAA TAAAAAAAAA
                                   AG    A
GAM528  ZNF297B   3'  TACCATAGTTTATTTTT     14026        C
                                TACCATAGT TTATTTTT
                                ||||||||| ||||||||
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                                ATGGTATCA AATAAAAA
                                        _
GAM528  ZNF297B  3'  TACCATAGTTTATTTTT     14026         C
                                TACCATAGT TTATTTTT
                                ||||||||| ||||||||
                                ATGGTATCA AATAAAAA
                                        _
GAM528  ZNF347   3'  CCACAGTCATTGCATTTTTTTT 14027        T___
           T                     CCATAGTC   TATTTTTTTTT
                                 ||||||||   ||||||||||
                                 GGTGTCAG   GTAAAAAAAAA
                                      TAAC
GAM528  LOC114932 5'  ATCTTTATTTTTTTTTCT    14028      _
                                 GTCTT ATTTTTTTTTCT
                                 ||||| ||||||||||||
                                 TAGAA TAAAAAAAAAGA
                                    A
GAM528  LOC115123 3'  CACCATATTTTTTTTTCT    14029       GTCTTA
                                 TACCATA     TTTTTTTTTCT
                                 |||||||     ||||||||||
                                 GTGGTAT     AAAAAAAAAGA
                                        _______
GAM528  LOC144558 5'  CCATAGTACTGCTTTTTTTTT  14030       _ TA
                                 CCATAGT CT  TTTTTTTTT
                                 ||||||| ||  |||||||||
                                 GGTATCA GA  AAAAAAAAA
                                      T  CG
GAM528  LOC144997 3'  CCATGAAGTGATTTTTTTTTCT 14031     __  CTT
                                 CCAT  AGT   ATTTTTTTTTCT
                                 ||||  |||   ||||||||||||
                                 GGTA  TCA   TAAAAAAAAAGA
                                   CT   C__
GAM528  LOC145786 3'  CATAGTCCTATACACTTCT   14032          TTTTT
                                 CATAGTCTTAT    TTTCT
                                 ||||||||||    |||||
                                 GTATCAGGATA    GAAGA
                                        TGT__
GAM528  LOC151623 5'  CCATAGTACTGCTTTTTTTTT  14030       _ TA
                                 CCATAGT CT  TTTTTTTTT
                                 ||||||| ||  |||||||||
                                 GGTATCA GA  AAAAAAAAA
                                      T  CG
GAM528  LOC253927 5'  TACCATGGCTTTATTTTTCT   14014       A TC
                                 TACCAT G  TTATTTTTTT
                                 |||||| |  ||||||||||
                                 ATGGTA C  AATAAAAAGA
                                    C GA
GAM529  AMACR    3'  CAATACAGGTGAAACTT     14035      TAG   A
                                 CAAT   GCA GTGAAACTT
                                 ||||   ||| |||||||||
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                                GTTA   TGT CACTTTGAA
                                  ___   C
GAM529  RDX      3'  TATCCAATAAGGTAATTAAA  14036        T   C  G
                                TATCCAAT AGG AA TGAA
                                |||||||| ||| || ||||
                                ATAGGTTA TCC TT ATTT
                                     T   A  A
GAM529  CORTBP2  3'  TATCCACTTAGGTACAAAACTT 14037       A     CAA TG
                                TATCCA TTAGG   G  AAACTT
                                |||||| |||||   |  |||||||
                                ATAGGT AATCC   T  TTTGAA
                                   G    A__ GT
GAM529  FLJ12707 3'  AATTTAGCCCAGGTGAAACTT  14038     A   AA__
                                AATT GGC    GTGAAACTT
                                |||| |||    |||||||||
                                TTAA TCG    CACTTTGAA
                                  A   GGTC
GAM529  KIAA1018 3'  CATCCAATTGGGTGATGA    14039         A  CAA
                                TATCCAATT GG   GTGA
                                ||||||||| ||   ||||
                                GTAGGTTAA CC   TACT
                                     C  AC_
GAM529  KIAA1915 5'  TCCAATTAGCTTTGAAA     14040         G AAG
                                TCCAATTAG C   TGAAA
                                ||||||||| |   |||||
                                AGGTTAATC G   ACTTT
                                     _ AA_
GAM529  LOC120526 3'  TATCGGTTAGACCAGAAACTT  14041     CAA     AAGT
                                TATC   TTAGGC    GAAACTT
                                ||||   ||||||   |||||||
                                ATAG   AATCTG    CTTTGAA
                                  CC_     GT__
GAM529  LOC146212 3'  TCCAATTAAAATGAGACTT    14042        GGC     A
                                TCCAATTA   AAGTGA ACTT
                                ||||||||   |||||| ||||
                                AGGTTAAT   TTTACT TGAA
                                     ___      C
GAM529  LOC153387 5'  TATCCAACTTAACATGAAACTT 14043         AG   AG
                                TATCCAATT  GCA  TGAAACTT
                                |||||||||  |||  ||||||||
                                ATAGGTTGA  TGT  ACTTTGAA
                                     AT   __
GAM529  LOC154089 3'  TATCCAATTAGATTTCTAAGT  14044          C____
                                TATCCAATTAGG     AAGT
                                ||||||||||||     ||||
                                ATAGGTTAATCT     TTCA
                                       AAAGA
GAM529  LOC219686 3'  TCCAATTACAAATGAAA     14045        AG
                                TCCAATT  GCAAGTGAAA
                                |||||||  ||||||||||
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                                AGGTTAA  TGTTTACTTT
                                   __
GAM529  LOC256352 3'  TCCAATTAAAATGAGACTT   14042        GGC     A
                                TCCAATTA   AAGTGA ACTT
                                ||||||||   |||||| ||||
                                AGGTTAAT   TTTACT TGAA
                                   ____     C
GAM530  AVP      5'  GAGGACAGGGGCTGCACCA   14048        TATCC
                                GAGGACG    CTGCACCA
                                |||||||    ||||||||
                                CTCCTGT    GACGTGGT
                                    CCCC_
GAM530  FE65L2   3'  TCGAGGGGTTGCCCCTGCACC  14049       ACGTA
                                TCGAGG    TCCCTGCACC
                                ||||||    ||||||||||
                                AGCTCC    GGGGACGTGG
                                   CCAAC
GAM530  FE65L2   3'  TCGAGGGGTTGCCCCTGCACC  14049       ACGTA
                                TCGAGG    TCCCTGCACC
                                ||||||    ||||||||||
                                AGCTCC    GGGGACGTGG
                                   CCAAC
GAM530  MCM6     5'  TGCCGAGGATTCGCCTGCGCCA 14050         CGTA _    A
                                TGTCGAGGA   TC CCTGC CCA
                                |||||||||   || ||||| |||
                                ACGGCTCCT   AG GGACG GGT
                                     A___  C    C
GAM530  KIAA1280 5'  TGTCTAGGGCTTCCTGCAC   14051     G   AC  ATC
                                TGTC AGG  GT   CCTGCAC
                                ||||  |||  ||   |||||||
                                ACAG TCC  CG   GGACGTG
                                  A   __  AA_
GAM530  KIAA1804 3'  TCGGGTAGCCATTTCTGCACCA 14052     A  AC  ATCC_
                                TCG GG  GT    CTGCACCA
                                |||  ||  ||    ||||||||
                                AGC CC  CG    GACGTGGT
                                  _  AT  GTAAA
GAM530  MGC3207  3'  TGTCTGAGCTCCCTGCAC    14053     _  GACGTA
                                TGTC GAG     TCCCTGCAC
                                ||||  |||    |||||||||
                                ACAG CTC     AGGGACGTG
                                  A   G_____
GAM530  LOC155064 3'  TGTTGAGAGAATTCTCCTCTGT 14054     C  _  CGTA  _  CA
           GCCA                    TGT GAG GA    TCC CTG  CCA
                                |||  ||| ||    |||  |||  |||
                                ACA CTC CT    AGG GAC  GGT
                                  A   T  TAAG   A   AC
GAM530  LOC253239 5'  TGCCGAGGAGCCTGTGCC    14055         C TATC    CA
                                TGTCGAGGA G    CCTG  CC
                                |||||||||  |    ||||  ||
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                                ACGGCTCCT C    GGAC  GG
                                      _ _____    AC
GAM530  LOC90342  5'  TGTCAGTTAGTCCCTGCATCA  14056      G  GACGTA       C
                                TGTC AG      TCCCTGCA CA
                                |||| ||      |||||||| ||
                                ACAG TC      AGGGACGT GT
                                  _  AATC__        A
GAM530  LOC93426  5'  TGTGAGGACGTGTCCTGC    14057     C       ATC
                                TGT GAGGACGT   CCTGC
                                ||| ||||||||   |||||
                                ACA CTCCTGCA   GGACG
                                  _      CA_
GAM531  FLJ12598  3'  CTATGAGGGCAGAGAATTT   14060     CTC_
                                CTA    GGCAGAGAATTT
                                |||    ||||||||||||
                                GAT    CCGTCTCTTAAA
                                  ACTC
GAM531  TIAM2     3'  TATACAGCTTGGCAGAGAA   14061       TA  C
                                TATAC  CT GGCAGAGAA
                                |||||  || |||||||||
                                ATATG  GA CCGTCTCTT
                                   TC  A
GAM531  LOC152559 3'  TATACTAGCATGGGGAATTTAT 14062        ACTC    GA__
                                TATACT    GGCA    GAATTTAT
                                ||||||    ||||    ||||||||
                                ATATGA    TCGT    CTTAAATA
                                    _____   ACCC
GAM531  LOC221830 3'  TATACCACTAGCAGAATTTAT  14063         C     GA
                                TATACTACT GGCAGA  ATTTAT
                                ||||||||| ||||||  ||||||
                                ATATGGTGA TCGTCT  TAAATA
                                      _     __
GAM532  ADCY2     3'  TTCTTCAAGGCCTTCTGTC    14066     C       _ _
                                TTC TTAAGGCCT C GTC
                                ||| ||||||||| | |||
                                AAG AGTTCCGGA G CAG
                                  A        A A
GAM532  C20orf140 3'  TTCCCTAAGGTCTGGAGAGTCT 14067          CC  GTCC  A
                                TTCCTTAAGG  TC    GA TCT
                                ||||||||||  ||    || |||
                                AAGGGATTCC  AG    CT AGA
                                      __  ACCT  C
GAM532  FLJ13273  3'  TTCCTTAAGATTCTGAGTC    14068         C_  C_
                                TTCCTTAAGG  CT  GTC
                                ||||||||||  ||  |||
                                AAGGAATTCT  GA  CAG
                                      AA  CT
GAM532  SEMA4F    3'  TTAAGGCCTTGAAAATCT     14069         CGTCC
                                TTAAGGCCT     GAATCT
                                |||||||||     ||||||
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                                AATTCCGGA     TTTAGA
                                     ACT__
GAM532  LOC118786 5'  TTCCTAAGGCCTTGTGTATCT  14070       T      C  CCGA
                                TTCCT AAGGCCT GT    ATCT
                                ||||| ||||||| ||    ||||
                                AAGGA TTCCGGA CA    TAGA
                                   _      A  CA__
GAM532  LOC145858 3'  TTCCTAGGGCCTCGTCGATCCT 14071       TAA        C  A
                                TTCCT   GGCCTCGTC GA TCT
                                |||||   ||||||||| || |||
                                AAGGA   CCGGAGCAG CT GGA
                                   TC_        _  A
GAM532  LOC201283 3'  TTCCTTAAAGGCTTCCTTCCA  14072         _   C  G_
                                TTCCTTAA GGC TC  TCCG
                                |||||||| ||| ||  ||||
                                AAGGAATT CCG AG  AGGT
                                     T   A  GA
GAM533  ANKH     3'  AGGTGATTTTATTCTTCCATT  14075         A      AG
                                AGGTGATT TATTTT  TATT
                                |||||||| ||||||  ||||
                                TCCACTAA ATAAGA  GTAA
                                     A      AG
GAM533  PCSK2    3'  AGCGAGACATATTTTAGTATTA 14076       T_
                                GGTGA  TATATTTTAGTATTA
                                |||||  ||||||||||||||
                                TCGCT  GTATAAAATCATAAT
                                   CT
GAM533  C13orf1  3'  TAAGGTGTTATATATGTATTA  14077         A      TTTA
                                TAAGGTG TTATAT    GTATTA
                                ||||||| ||||||    ||||||
                                ATTCCAC AATATA    CATAAT
                                     _      TA__
GAM533  LOC221395 3'  TGAGTGATTATATTAGATCATT 14078    A          TTAG
           A                     A GGTGATTATATT    TATTA
                                | ||||||||||||    |||||
                                A TCACTAATATAA    GTAAT
                                 C           TCTA
GAM534  EMP3     3'  CAGCCGAGCGAGGCGGG     14081     C   T  ACAA
                                CA CCG AG    CGAGGCGGG
                                || ||| ||    |||||||||
                                GT GGC TC    GCTCCGCCC
                                 C   _  _____
GAM534  MASP1    3'  CACCCGTAGTGGAAAGGGG    14082         ACAAC    C
                                CACCCGTAG     GAGG GG
                                |||||||||     |||| ||
                                GTGGGCATC     TTCC CC
                                     ACCT_    _
GAM534  PPFIA3   3'  CCCGCAGATGACCCGGGGGAC  14083         CA  GA  C
                                CCCGTAGA  AC  GG GGGAC
                                ||||||||  ||  || |||||
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                                GGGCGTCT  TG  CC CCCTG
                                    AC  GG  _
GAM534  SNX9     3'  CACCTGTGGGAGACGGGA    14084      C  AGACAAC
                                CACC GT      GAGGCGGGA
                                |||| ||      |||||||||
                                GTGG CA      CTCTGCCCT
                                  A  CC_____
GAM534  ST5      3'  CACCCGTAGATGGGAAGGAGGG 14085          CAAC    C
           A                     CACCCGTAGA    GAGG GGGA
                                ||||||||||    |||| ||||
                                GTGGGCATCT    TTCC CCCT
                                      ACCC    T
GAM534  ST5      3'  CACCCGTAGATGGGAAGGAGGG 14085          CAAC    C
           A                     CACCCGTAGA    GAGG GGGA
                                ||||||||||    |||| ||||
                                GTGGGCATCT    TTCC CCCT
                                      ACCC    T
GAM534  TLL1     5'  CACCCGGAGGCTCCTCGGCGGG 14086       T  ACAACGA
           AC                     CACCCG AG      GGCGGGAC
                                ||||||| ||      |||||||||
                                GTGGGC TC      CCGCCCTG
                                   C  CGAGGAG
GAM534  ZNF26    5'  CCCGAAGACAGGTGCGGGAC   14087      T    ACGAG
                                CCCG AGACA    GCGGGAC
                                |||| |||||    |||||||
                                GGGC TCTGT    CGCCCTG
                                  T    CCA__
GAM534  C11orf11 5'  CACCCGTAGGCAGCCAGGGC   14088         A  A_  A
                                CACCCGTAG CA  CG GGC
                                ||||||||| ||  || |||
                                GTGGGCATC GT  GT CCG
                                      C  CG  C
GAM534  FLJ20552 3'  CCCTGGAACAGGCGGGA     14089     GTA  CA  G
                                CCC   GA  AC AGGCGGGA
                                |||   ||  || ||||||||
                                GGG   CT  TG TCCGCCCT
                                  AC_  __  _
GAM534  FLJ22184 3'  CACTGCACACGGGGCGGGAC   14090     CC  AG   A  A
                                CAC  GT  ACA CG GGCGGGAC
                                |||  ||  ||| || ||||||||
                                GTG  CG  TGT GC CCGCCCTG
                                  A_  __  _  C
GAM534  HTF9C    5'  CGCCCCAGGCGGGGCGGGAC   14091    A   G   ACAA  A
                                C CCC TAG    CG GGCGGGAC
                                | ||| |||    || ||||||||
                                G GGG GTC    GC CCGCCCTG
                                 C   _   C___  C
GAM534  KIAA0100 3'  CCTCGTGGATAACGGGAAG    14092     _   A  C    A  C
                                CC CGT GA AACG GG GG
                                || ||| || |||| || ||
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                                GG GCA CT TTGC CC TC
                                 A  C A   _ T
GAM534  KIAA1735  3'  CCCCTACAGAGGCGGGA    14093    GTAG  AC
                                CCC   ACA  GAGGCGGGA
                                |||   |||  |||||||||
                                GGG   TGT  CTCCGCCCT
                                  GA__  __
GAM534  KIAA1924  3'  CACTCTTAGGCTAGGCGGGAC  14094    CCG  ACAACG
                                CAC  TAG    AGGCGGGAC
                                |||  |||    |||||||||
                                GTG  ATC    TCCGCCCTG
                                  AGA  CGA___
GAM534  LGI3    3'  CACTCGTGCATGAGACAGG   14095    C  AGA  AC
                                CAC CGT  CA  GAGGCGGG
                                ||| |||  ||  ||||||||
                                GTG GCA  GT  CTCTGTCC
                                  A  C__  A_
GAM534  MGC20253  3'  CACCTGTAGGAGGCGGG    14096    C   ACAAC
                                CACC GTAG   GAGGCGGG
                                |||| ||||   ||||||||
                                GTGG CATC   CTCCGCCC
                                  A  _____
GAM534  PLCL2    5'  CCCGTGGACGAGGCGA     14097     A  AAC
                                CCCGT GAC  GAGGCGG
                                ||||| |||  |||||||
                                GGGCA CTG  CTCCGCT
                                  C  ___
GAM534  LOC138389 5'  CCGTAGACAATGGCAG     14098        CGA
                                CCGTAGACAA  GGCGG
                                ||||||||||  |||||
                                GGCATCTGTT  CCGTC
                                     A__
GAM534  LOC145989 3'  CCCAGAGCGAGGCGGG     14099     T  ACAA
                                CCCG AG   CGAGGCGGG
                                |||| ||   |||||||||
                                GGGT TC   GCTCCGCCC
                                  C  ____
GAM534  LOC148193 5'  CACCCGCGCCGGGAGGCGGG  14100       AGACAAC
                                CACCCGT     GAGGCGGG
                                |||||||     ||||||||
                                GTGGGCG     CTCCGCCC
                                   CGGCC__
GAM534  LOC154007 3'  CCCTTAGAAGACGGGCGGG   14101    G   CA  A
                                CCC TAGA  ACG GGCGGG
                                ||| ||||  ||| ||||||
                                GGG ATCT  TGC CCGCCC
                                  A   TC  _
GAM534  LOC164684 5'  CCCGTAGATGGAAAGGGGCGGG 14102       CAACGA__
           AC                   CCCGTAGA      GGCGGGAC
                                ||||||||      ||||||||
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                                GGGCATCT       CCGCCCTG
                                     ACCTTTCC
GAM534  LOC199800 5'  CACCCGCAGGTAGCTAAGCAGC 14103          ACAACGA___
            GGGA                   CACCCGTAG         GGCGGGA
                                |||||||||         |||||||
                                GTGGGCGTC         TCGCCCT
                                     CATCGATTCG
GAM534  LOC220739 5'  CACCTGTGGACAAAGCAGA   14104      C  A    CGA
                                CACC GT GACAA   GGCGGG
                                |||| || |||||   ||||||
                                GTGG CA CTGTT   TCGTCT
                                  A  C    ___
GAM535  COG4      3'  TCAGATCTCCCCCAAGCCA   14107          ACA    A
                                TCAGATTTTT   CCCAA CCA
                                ||||||||||   ||||| |||
                                AGTCTAGAGG   GGGTT GGT
                                     ___    C
GAM535  DUSP6     3'  TATCAGATTTTTTTTTCCAAAC 14108           ACAC
                                TATCAGATTTTT    CCAAAC
                                ||||||||||||    ||||||
                                ATAGTCTAAAAA    GGTTTG
                                      AAAA
GAM535  NOS1      3'  TAGCAGACACCCAAAC      14109    T    TTTTTA
                                TA CAGA     CACCCAAAC
                                || ||||     |||||||||
                                AT GTCT     GTGGGTTTG
                                 C   _______
GAM535  SIRT1     3'  CAGATTTTGAGTACTTCAAACC 14110         ___   ACC
            A                    CAGATTTT   TAC   CAAACCA
                                ||||||||   |||   |||||||
                                GTCTAAAA   ATG   GTTTGGT
                                     CTC   AA_
GAM535  ARHGEF9   3'  TATCAGACTTGGACCCTGTCCA 14111          TTAC    AAA
                                TATCAGATTT    ACCC   CCA
                                ||||||||||    ||||   |||
                                ATAGTCTGAA    TGGG   GGT
                                      CC__    ACA
GAM535  EFA6R     3'  TCAGATTTTATACATGGGCCA  14112         _   C___
                                TCAGATTTT TACA    CCA
                                |||||||| ||||    |||
                                AGTCTAAAA ATGT    GGT
                                      T    ACCC
GAM535  FLJ14594  3'  TCAGCCACACCCAAGCC     14113      ATTT        A
                                TCAG    TTACACCCAA CC
                                ||||    |||||||||| ||
                                AGTC    GGTGTGGGTT GG
                                  _____         C
GAM535  MGC16142  3'  TCAGGCCCCACCCAAACCA   14114      ATTTTTA
                                TCAG      CACCCAAACCA
                                ||||      ||||||||||
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                                AGTC      GTGGGTTTGGT
                                  CGGG___
GAM535  SLC37A1   5'  TCGGAAAACATCCAAACCA   14115    A  TTTTT   C
                                TC GA     ACA CCAAACCA
                                || ||     ||| ||||||||
                                AG CT     TGT GGTTTGGT
                                 C  TT___   A
GAM535  LOC130813 3'  TCACATGCTCCACCCAAACCA  14116     G  T   A
                                TCA AT TTT CACCCAAACCA
                                ||| || ||| ||||||||||
                                AGT TA GAG GTGGGTTTGGT
                                  G  C   _
GAM535  LOC146452 3'  AGATTTTTGCACCTTTCCA   14117        A    CAAA
                                AGATTTTT CACC    CCA
                                |||||||| ||||    |||
                                TCTAAAAA GTGG    GGT
                                     C    AAA_
GAM535  LOC159110 3'  TCAGATTTTCATGCCAAATCA  14118          CAC    C
                                TCAGATTTTTA   CCAAA CA
                                ||||||||||   ||||| ||
                                AGTCTAAAAGT   GGTTT GT
                                      AC_    A
GAM535  LOC159116 3'  TCAGATTTTCATGCCAAATCA  14118          CAC    C
                                TCAGATTTTTA   CCAAA CA
                                ||||||||||   ||||| ||
                                AGTCTAAAAGT   GGTTT GT
                                      AC_    A
GAM535  LOC200314 3'  TATCAGATTTTTGAACAGACA  14119           __   CC
                                TATCAGATTTTT  ACA  CA
                                ||||||||||||  |||  ||
                                ATAGTCTAAAAA  TGT  GT
                                       CT   CT
GAM535  LOC203536 3'  TACCAATATGCCCAAACCA    14120       ATTTT  CA
                                TATCAG    TA  CCCAAACCA
                                ||||||    ||  |||||||||
                                ATGGTT    AT  GGGTTTGGT
                                   _____  AC
GAM535  LOC253115 5'  ATCAGACCTACTTGCACCCAAA 14121         TTA__
              C                  ATCAGATTT    CACCCAAAC
                                 |||||||||    |||||||||
                                 TAGTCTGGA    GTGGGTTTG
                                      TGAAC
GAM535  LOC254528 3'  TCAGACTCACCCAGACC     14122        TTTA     A
                                TCAGATT    CACCCA ACC
                                |||||||    |||||| |||
                                AGTCTGA    GTGGGT TGG
                                   _____     C
GAM535  LOC257556 5'  ATCAGACCTACTTGCACCCAAA 14121         TTA__
              C                  ATCAGATTT    CACCCAAAC
                                 |||||||||    |||||||||
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                                TAGTCTGGA    GTGGGTTTG
                                     TGAAC
GAM535  LOC257617 5'  ATCAGACCTACTTGCACCCAAA 14121        TTA__
          C                    ATCAGATTT    CACCCAAAC
                               |||||||||    |||||||||
                               TAGTCTGGA    GTGGGTTTG
                                     TGAAC
GAM536  KIAA0644  3'  TTTGTAATGGTAATAAGTTCCT 14125        AC    C
          T                    TTTGTAGTG  GGTGG GTTCCTT
                               |||||||||  ||||| |||||||
                               AAACATTAC  TTATT CAAGGAA
                                     CA    _
GAM536  PROL3    3'  TTTGTGGTGGTGGTGGCACCT  14126      A  AC     TT
                               TTTGT GTG  GGTGGCG  CCT
                               ||||| |||  |||||||  |||
                               AAACA CAC  CCACCGT  GGA
                                  C  CA     __
GAM536  LOC145644 5'  TTTGCAGTGGTGGGCCTTC    14127       GAC    _ G
                               TTTGTAGT   GGTGG C TTC
                               ||||||||   ||||| | |||
                               AAACGTCA   CCACC G AAG
                                    ___     C G
GAM536  LOC149153 3'  TTTGTAGTAAACATGTGTTCCT 14128        CG   GC
          T                    TTTGTAGTGA  GTG  GTTCCTT
                               ||||||||||  |||  |||||||
                               AAACATCATT  TAC  CAAGGAA
                                     TG   A_
GAM536  LOC203078 3'  TTTGTAGTGGTGGTGTT     14129       GAC    C
                               TTTGTAGT   GGTGG GTT
                               ||||||||   ||||| |||
                               AAACATCA   CCACC CAA
                                    ___     A
GAM537  A2BP1    5'  GAGCCCGGCTGCGGTCACGTT  14132     ATGGG    A
                               GGGC    GGCT CGGTCACGTT
                               ||||    |||| ||||||||||
                               CTCG    CCGA GCCAGTGCAA
                                  GG___    C
GAM537  LOC146237 3'  GGGTGTGGGGGCCACGGT    14133     CA
                               GGG  TGGGGGCTACGGT
                               |||  ||||||||||||
                               CCC  ACCCCCGGTGCCA
                                 AC
GAM537  LOC147160 5'  GGGTGTGGGGGCTCTGGACC   14134     CA      AC  _
                               GGG  TGGGGGCT  GG TC
                               |||  ||||||||  || ||
                               CCC  ACCCCCGA  CC GG
                                 AC       GA  T
GAM538  ENO2     5'  TCGGGACTGCAGACTCAGACGG 14137    A   C       T  __
          TG                   TC GGAC TGCAGACTC GA  GTG
                               || |||| |||||||| ||  |||
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                                AG CCTG ACGTCTGAG CT  CAC
                                 C   _       T  GC
GAM538  LIG3     3'  GGCCAGCAGCTGAGTGA     14138    A  T    ACT
                                GG CC GCAG   CTGAGTGA
                                || || ||||   ||||||||
                                CC GG CGTC   GACTCACT
                                 _  T   ____
GAM538  LUM      5'  GGCTGCCAGATTCTGAGTGA   14139    AC   _  C
                                GG  CTGC AGA TCTGAGTGA
                                ||  |||| ||| |||||||||
                                CC  GACG TCT AGACTCACT
                                 __   G   A
GAM538  NRBP     3'  TCAGGGCCTGGCCCGAGTG    14140      A    CAGAC
                                TCAGG CCTG    TCTGAGTG
                                ||||| ||||    ||||||||
                                AGTCC GGAC    GGGCTCAC
                                   C    C____
GAM538  TCF1     3'  TCAGGACCTCAGACTCCTCAGG 14141         G       GA___
            GTG                    TCAGGACCT CAGACTCT    GTG
                                |||||||||| ||||||||    |||
                                AGTCCTGGA GTCTGAGG    CAC
                                      _       AGTCC
GAM538  TRIM14   3'  TCAGGACCTCAGACTCC     14142         G
                                TCAGGACCT CAGACTCT
                                ||||||||| ||||||||
                                AGTCCTGGA GTCTGAGG
                                      _
GAM538  ZNF278   3'  CAGGATCTAGATCTGAGTG   14143      C  GC   C
                                CAGGA CT  AGA TCTGAGTG
                                ||||| ||  ||| ||||||||
                                GTCCT GA  TCT AGACTCAC
                                   A  __   _
GAM538  C20orf110 3'  TCAGGGCCTGCAGAAGGGTG  14144      A       CTCTGA
                                TCAGG CCTGCAGA     GTG
                                ||||| ||||||||     |||
                                AGTCC GGACGTCT     CAC
                                   C       TCC___
GAM538  C21orf93  3'  CCAGGACCTGCAGAGGTG    14145           CTCTGA
                                TCAGGACCTGCAGA     GTG
                                ||||||||||||||     |||
                                GGTCCTGGACGTCT     CAC
                                         C_____
GAM538  DKFZP762D096 3'  CCAGGACCTGCAGGGGGGTG  14146           ACTCTGA
                                TCAGGACCTGCAG      GTG
                                ||||||||||||       |||
                                GGTCCTGGACGTC      CAC
                                         CCCC___
GAM538  FLJ10922  3'  TCAGGGCCTGCAGATGCGC   14147      A       CTC  A
                                TCAGG CCTGCAGA   TG GT
                                ||||| ||||||||   || ||
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                                AGTCC GGACGTCT   AC CG
                                  C       ___  G
GAM538  FLJ14936  3'  TCGGGACCTGCTGCGGTG    14148    A      AGACTC  A
                                TC GGACCTGC     TG GTG
                                || ||||||||     || |||
                                AG CCTGGACG     GC CAC
                                 C       AC____  _
GAM538  FLJ20296  5'  CAGGACCTCAGCCAGGCTCTGG 14149        __ _ A    A
          GTG                     CAGGACCT  GC AG CTCTG GTG
                                |||||||| || || ||||| |||
                                GTCCTGGA  CG TC GAGAC CAC
                                     GT  G  C    C
GAM538  KIAA0275  3'  GGACCCTCTCTGAGTG      14150       GCAGA
                                GGACCT    CTCTGAGTG
                                ||||||    |||||||||
                                CCTGGG    GAGACTCAC
                                   A____
GAM538  KIAA1855  3'  TCAGGACCTGGAGGCCTGGTG  14151         C  A T   A
                                TCAGGACCTG AG C CTG GTG
                                |||||||||| || | ||| |||
                                AGTCCTGGAC TC G GAC CAC
                                      C  C _  _
GAM538  MGC34923  5'  TCAGGACCTTCAGTGAGTG   14152         G   ACTC
                                TCAGGACCT CAG    TGAGTG
                                ||||||||| |||    ||||||
                                AGTCCTGGA GTC    ACTCAC
                                      A  _____
GAM538  SERF2     5'  CAGGACTGGGGACTCTGAGTGA 14153       C  CA
                                CAGGAC TG  GACTCTGAGTGA
                                |||||| ||  ||||||||||||
                                GTCCTG AC  CTGAGACTCACT
                                   _  CC
GAM538  SNX11     5'  CAGGCCCGGGCTCTGAGTG   14154      A   CAGA
                                CAGG CCTG    CTCTGAGTG
                                |||| ||||    |||||||||
                                GTCC GGGC    GAGACTCAC
                                  _    CC__
GAM538  LOC135932 3'  TCAGGACCGGCGGCTGGGGTGA 14155        T  AGACT   A_
                                TCAGGACC GC     CTG  GTGA
                                |||||||| ||     |||  ||||
                                AGTCCTGG CG     GAC  CACT
                                     C  CC___   CC
GAM538  LOC142826 3'  TCAGGACAAACCTCTGAGTGA  14156       CT  AGA
                                TCAGGAC  GC   CTCTGAGTGA
                                |||||||  ||   ||||||||||
                                AGTCCTG  TG   GAGACTCACT
                                     TT  ___
GAM538  LOC143188 3'  GGGCCTGCAGAGAGTG      14157    A      CTCT
                                GG CCTGCAGA    GAGTG
                                || ||||||||    |||||
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                                CC GGACGTCT    CTCAC
                                 C      ____
GAM538  LOC143308 5'  TCAGGGCCTGCAAACTCAAAG  14158      A         T
                                TCAGG CCTGCAGACTC GAG
                                ||||| |||||||||||| |||
                                AGTCC GGACGTTTGAG TTC
                                   C          T
GAM538  LOC145387 5'  TCAGAGCCTGCTCTGAGTG   14159     GA    AGAC
                                TCAG  CCTGC    TCTGAGTG
                                ||||  |||||    ||||||||
                                AGTC  GGACG    AGACTCAC
                                  TC    _____
GAM538  LOC153592 3'  TCAGGACCTGGGACGGTGTGA  14160          CA   TCTGA
                                TCAGGACCTG  GAC     GTGA
                                ||||||||||  |||     ||||
                                AGTCCTGGAC  CTG     CACT
                                      C_   CCA__
GAM538  LOC166206 3'  CCAGGAGGAGACTCTGGGTG   14161       CCTGC       A
                                TCAGGA     AGACTCTG GTG
                                ||||||     |||||||| |||
                                GGTCCT     TCTGAGAC CAC
                                   CC___       C
GAM538  LOC203504 3'  TCAGGACCTGGGTCCAGTG    14162          CAGAC   G
                                TCAGGACCTG     TCT AGTG
                                ||||||||||     ||| ||||
                                AGTCCTGGAC     AGG TCAC
                                      CC___   _
GAM538  LOC254268 3'  CCAGGACCTGCAGCGGTG     14163           ACTC  A
                                TCAGGACCTGCAG    TG GTG
                                ||||||||||||||    || |||
                                GGTCCTGGACGTC    GC CAC
                                          _____ _
GAM538  LOC256741 3'  AGCGACTTGCCTGAGTG      14164     _   C   AGACT
                                AG GAC TGC     CTGAGTG
                                || ||| |||     |||||||
                                TC CTG ACG     GACTCAC
                                 G   A  ______
GAM538  LOC83690  5'  AGACCTGCAGTTGGGGTG     14165          ACTC  A_
                                GGACCTGCAG    TG  GTG
                                ||||||||||    ||  |||
                                TCTGGACGTC    AC  CAC
                                      A___  CC
GAM538  LOC89919  3'  GGATTTGGAGCTTCTGAGTG   14166     CC  C  AC
                                GGA  TG AG  TCTGAGTG
                                |||  || ||  ||||||||
                                CCT  AC TC  AGACTCAC
                                  AA  C  GA
GAM538  LOC91445  3'  TCAGGACCTGCAGAACTG     14167            CT
                                TCAGGACCTGCAGA  CTG
                                ||||||||||||||  |||
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                                AGTCCTGGACGTCT  GAC
                                      T_
GAM538  LOC91522  3'  TGAGACCCAGACTCTGAGTG  14168   A    TG
                                C GGACC  CAGACTCTGAGTG
                                | |||||  ||||||||||||||
                                A TCTGG  GTCTGAGACTCAC
                                 C    __
GAM538  LOC92080  3'  CCAGGACCCTCTGGGT     14169       TGCAGA    A
                                TCAGGACC     CTCTG GT
                                ||||||||     ||||| ||
                                GGTCCTGG     GAGAC CA
                                     _______    C
GAM539  MMP19     3'  TGCAAATGGGGAATCTGAG   14172       AGTATTT
                                TGTAAATGG     ATCTGAG
                                |||||||||     |||||||
                                ACGTTTACC     TAGACTC
                                     CCT____
GAM539  MMP19     3'  TGCAAATGGGGAATCTGAG   14172       AGTATTT
                                TGTAAATGG     ATCTGAG
                                |||||||||     |||||||
                                ACGTTTACC     TAGACTC
                                     CCT____
GAM539  MMP19     3'  TGCAAATGGGGAATCTGAG   14172       AGTATTT
                                TGTAAATGG     ATCTGAG
                                |||||||||     |||||||
                                ACGTTTACC     TAGACTC
                                     CCT____
GAM539  MMP19     3'  TGCAAATGGGGAATCTGAG   14172       AGTATTT
                                TGTAAATGG     ATCTGAG
                                |||||||||     |||||||
                                ACGTTTACC     TAGACTC
                                     CCT____
GAM539  SLC21A2   3'  TGTAAATGGAGGGAGGTGAG  14173        TATTTATC
                                TGTAAATGGAG      TGAG
                                ||||||||||       ||||
                                ACATTTACCTC      ACTC
                                      CCTCC___
GAM539  TOB1      3'  TGTAAGAGGCCATATCTGAGA  14174     AT  AGTATT
                                TGTAA  GG     TATCTGAGA
                                |||||  ||     |||||||||
                                ACATT  CC     ATAGACTCT
                                   CT  GGT___
GAM539  WNT5A     3'  TGCAAATGGAATATTTGAG   14175          TATC
                                TGTAAATGGAGTATT   TGAG
                                ||||||||||||||   ||||
                                ACGTTTACCTTATAA   ACTC
                                                 ____
GAM539  C13orf1   3'  TATAAATGGGAATCTGAG    14176       AGTATTT
                                TGTAAATGG     ATCTGAG
                                |||||||||     |||||||
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                                ATATTTACC      TAGACTC
                                     CT_____
GAM539  CLIC4    3'  GTAAATGGGGTGAAATGAGA  14177        A  ATTTATC
                                GTAAATGG GT      TGAGA
                                |||||||| ||      |||||
                                CATTTACC CA      ACTCT
                                     C  CTTT___
GAM539  DKFZP564D206 3'  GTAGATGGAGGGTATCTGAGA  14178     A     TATT
                                GTA ATGGAG    TATCTGAGA
                                ||| ||||||    |||||||||
                                CAT TACCTC    ATAGACTCT
                                  C     CC__
GAM539  KIAA0515  3'  GTAGATGGGCATCTGAG     14179     A    A  ATTT
                                GTA ATGG GT    ATCTGAG
                                ||| |||| ||    |||||||
                                CAT TACC CG    TAGACTC
                                  C   _ _____
GAM539  KIAA0972  3'  TGAAATGGAGTATTGGCCAGA  14180    T         TA  T
                                TG AAATGGAGTATT  TC GA
                                || ||||||||||||  || ||
                                AC TTTACCTCATAA  GG CT
                                 _          CC  T
GAM539  KIAA1223  3'  TGTAAATGTACTGTATTTGAGA 14181        GA__    TATC
                                TGTAAATG    GTATT    TGAGA
                                ||||||||    |||||    |||||
                                ACATTTAC    CATAA    ACTCT
                                     ATGA    _____
GAM539  KIAA1641  5'  TGTAATGGAGCTCAGTTTTGAG 14182      A     ATTTATC
                                TGTAA TGGAGT      TGAG
                                ||||| ||||||      ||||
                                ACATT ACCTCG      ACTC
                                   _     AGTCAAA
GAM539  PRO0618   3'  TGTAAATAGATTATCTG     14183          GTAT
                                TGTAAATGGA    TTATCTG
                                ||||||||||    |||||||
                                ACATTTATCT    AATAGAC
                                              _____
GAM539  LOC167410 3'  TGTAAATGGAATGTGTGGAGA  14184           ATTTATCT
                                TGTAAATGGAGT       GAGA
                                ||||||||||||       ||||
                                ACATTTACCTTA       CTCT
                                       CACAC___
GAM539  LOC257446 5'  TGTAATGGAGCTCAGTTTTGAG 14182      A     ATTTATC
                                TGTAA TGGAGT      TGAG
                                ||||| ||||||      ||||
                                ACATT ACCTCG      ACTC
                                   _     AGTCAAA
GAM540  DHFR     3'  AATTAATTCTTCCATCTCA    14187           GATAG
                                AATTAATTCTTCT    CTCA
                                ||||||||||||     ||||
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                                TTAATTAAGAAGG    GAGT
                                      TA___
GAM540  FMR2     3'  TGAATAATTCTTTAACATCTCA 14188      T     C    G
                                TGAAT AATTCTT TGATA CTCA
                                ||||| ||||||| ||||| ||||
                                ACTTA TTAAGAA ATTGT GAGT
                                  _     _    A
GAM540  SLA      3'  TGAGTTAATTCTTTAGAC    14189     A       CT
                                TGA TTAATTCTT  GAT
                                ||| |||||||||  |||
                                ACT AATTAAGAA  CTG
                                  C       AT
GAM540  ZNF141   3'  GAATGATTCTTCTACTCTCA   14190     TA       ATAG
                                GAAT  ATTCTTCTG   CTCA
                                ||||  |||||||||   ||||
                                CTTA  TAAGAAGAT   GAGT
                                  C_       GA__
GAM540  CASKIN1  3'  TAAATTAATACTCTTGATAGCT 14191        T  TC
                                TGAATTAAT CT  TGATAGCT
                                ||||||||| ||  ||||||||
                                ATTTAATTA GA  ACTATCGA
                                     T  GA
GAM540  ESDN     3'  TGCATTAATTCTTCACTC    14192    A       TGATA
                                TG ATTAATTCTTC    GCTC
                                || ||||||||||    ||||
                                AC TAATTAAGAAG    TGAG
                                 G        _____
GAM540  KIAA1613 3'  TTAATTCTATGATAGCT     14193       TC
                                TTAATTCT  TGATAGCT
                                ||||||||  ||||||||
                                AATTAAGA  ACTATCGA
                                     T_
GAM540  PNPASE   3'  TGAAGTGATTCTTCTGCCTCA  14194     TTA       ATAG
                                TGAA   ATTCTTCTG   CTCA
                                ||||   |||||||||   ||||
                                ACTT   TAAGAAGAC   GAGT
                                  CAC       G___
GAM540  POPX1    3'  TGAATGAATGAATCTGATAG   14195     T   TCT
                                TGAAT AAT   TCTGATAG
                                ||||| |||   ||||||||
                                ACTTA TTA   AGACTATC
                                   C   CTT
GAM540  LOC91010 5'  TGAATAATTCTTCAAAC     14196     T      T
                                TGAAT AATTCTTC GAT
                                ||||| |||||||| |||
                                ACTTA TTAAGAAG TTG
                                  _       T
GAM541  B4GALT7  3'  TAAGAATCCAGCATTCTA    14199       AT  _
                                TAAGAATT  CAG ATTCTA
                                ||||||||  ||| ||||||
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                                ATTCTTAG  GTC TAAGAT
                                    __  G
GAM541  BIA2     3'  TAAGAATTGCCATGTCTAA   14200       AT  GAT
                                TAAGAATT  CA   TCTAA
                                ||||||||  ||   |||||
                                ATTCTTAA  GT   AGATT
                                    CG  AC_
GAM541  FAM10A6  3'  TATAAGAATTAACAGACCCT  14201         T
                                TATAAGAATTA CAGATTCT
                                |||||||||||| ||||||||
                                ATATTCTTAAT GTCTGGGA
                                       T
GAM541  FAM10A7  3'  TATAAGAATTAACAGACCCT  14201         T
                                TATAAGAATTA CAGATTCT
                                |||||||||||| ||||||||
                                ATATTCTTAAT GTCTGGGA
                                       T
GAM541  FLJ14442 3'  TATAGGAGTTAGCAGATTCT  14202     A  A   T
                                TATA GA TTA CAGATTCT
                                |||| || ||| ||||||||
                                ATAT CT AAT GTCTAAGA
                                  C  C   C
GAM541  MIL1     3'  CATAAGAATTATGATCTAACT  14203          CA   T
                                TATAAGAATTAT  GAT CTAACT
                                ||||||||||||  ||| ||||||
                                GTATTCTTAATA  CTA GATTGA
                                       __  _
GAM541  PDE10A   3'  TAAAGAATTATGTTTAGTCTAA 14204   T       CAGAT_
           CT                    A AAGAATTAT     TCTAACT
                                | |||||||||     |||||||
                                A TTCTTAATA     AGATTGA
                                 T       CAAATC
GAM541  ST13     3'  TATAAGAATTAACAGGCCCT  14205         T   AT
                                TATAAGAATTA CAG  TCT
                                |||||||||||| |||  |||
                                ATATTCTTAAT GTC  GGA
                                       T   CG
GAM541  ZNF317   3'  CATAGGAATTATCAGCACTAA  14206     A        ATT
                                TATA GAATTATCAG   CTAA
                                |||| ||||||||||   ||||
                                GTAT CTTAATAGTC   GATT
                                  C        GT_
GAM541  LOC149052 3'  TATAAGAATTAACAGACCCT  14201         T
                                TATAAGAATTA CAGATTCT
                                |||||||||||| ||||||||
                                ATATTCTTAAT GTCTGGGA
                                       T
GAM541  LOC158886 3'  TATAAGAATTAACAGACCCT  14201         T
                                TATAAGAATTA CAGATTCT
                                |||||||||||| ||||||||
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                                ATATTCTTAAT GTCTGGGA
                                       T
GAM541  LOC245718 3'  TATAAGAATTAACAGATCCT   14207          T
                                TATAAGAATTA CAGATTCT
                                |||||||||| ||||||||
                                ATATTCTTAAT GTCTAGGA
                                       T
GAM542  CLN5    3'  ACATATTAAACGTGAATTG   14210          TGCA
                                ACATATTAAAC   GGATTG
                                ||||||||||   ||||||
                                TGTATAATTTG   CTTAAC
                                       CA__
GAM542  GAN     3'  ACATATTAAACATGATTG    14211          TGCAG
                                ACATATTAAAC    GATTG
                                ||||||||||    |||||
                                TGTATAATTTG    CTAAC
                                       TA___
GAM542  UBE4A   3'  TCAGCATATTAAGCTGCACAAT 14212    A      A    G
          TG                     TCA CATATTAA CTGCA GATTG
                                ||| |||||||| ||||| |||||
                                AGT GTATAATT GACGT TTAAC
                                  C       C    G
GAM542  KIAA1493 3'  TAATAAACTATGCAGGATTG   14213   T    __
                                TA TAAACT  GCAGGATTG
                                || ||||||  |||||||||
                                AT ATTTGA  CGTCCTAAC
                                 T     TA
GAM542  LOC57147 3'  ACATTTAGAGAACAGGATTG   14214     A   AACT
                                ACAT TTA   GCAGGATTG
                                |||| |||   |||||||||
                                TGTA AAT   TGTCCTAAC
                                  _  CTCT
GAM543  COL4A6   3'  TGCTAGATTTTTATGAG     14217        C    A
                                TGCTAGAT TTTTA TGAG
                                |||||||| ||||| ||||
                                ACGATCTA AAAAT ACTC
                                     _    _
GAM543  COL4A6   3'  TGCTAGATTTTTATGAG     14217        C    A
                                TGCTAGAT TTTTA TGAG
                                |||||||| ||||| ||||
                                ACGATCTA AAAAT ACTC
                                     _    _
GAM543  FGFR2    3'  GCTGGATCTTTTGGTGAG    14218     A      AA
                                GCT GATCTTTT  TGAG
                                ||| ||||||||  ||||
                                CGA CTAGAAAA  ACTC
                                  C       CC
GAM543  FGFR2    3'  GCTGGATCTTTTGGTGAG    14218     A      AA
                                GCT GATCTTTT  TGAG
                                ||| ||||||||  ||||
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                                CGA CTAGAAAA  ACTC
                                  C       CC
GAM543  FGFR2    3'  GCTGGATCTTTTGGTGAG    14218     A       AA
                                GCT GATCTTTT  TGAG
                                ||| ||||||||  ||||
                                CGA CTAGAAAA  ACTC
                                  C       CC
GAM543  FGFR2    3'  GCTGGATCTTTTGGTGAG    14218     A       AA
                                GCT GATCTTTT  TGAG
                                ||| ||||||||  ||||
                                CGA CTAGAAAA  ACTC
                                  C       CC
GAM543  FGFR2    3'  GCTGGATCTTTTGGTGAG    14218     A       AA
                                GCT GATCTTTT  TGAG
                                ||| ||||||||  ||||
                                CGA CTAGAAAA  ACTC
                                  C       CC
GAM543  FGFR2    3'  GCTGGATCTTTTGGTGAG    14218     A       AA
                                GCT GATCTTTT  TGAG
                                ||| ||||||||  ||||
                                CGA CTAGAAAA  ACTC
                                  C       CC
GAM543  PLAG1    3'  TGCTAAATTTTTTAATGAG    14219         C
                                TGCTAGAT TTTTAATGAG
                                |||||||| ||||||||||
                                ACGATTTA AAAATTACTC
                                     A
GAM543  SLA2     3'  TGCTAGACTTAAGAG       14220         CTT    T
                                TGCTAGAT   TTAA GAG
                                ||||||||   |||| |||
                                ACGATCTG   AATT CTC
                                     ___   _
GAM543  FLJ23462 3'  GCTTTTTAATGAGATATT    14221     AGATC
                                GCT    TTTTAATGAGATATT
                                |||    ||||||||||||||||
                                CGA    AAAATTACTCTATAA
                                     _____
GAM543  LOC158263 3'  CTAGATCTTGGAGGATAT    14222         TTAAT   _
                                CTAGATCTT    GAG ATAT
                                |||||||||    ||| ||||
                                GATCTAGAA    CTC TATA
                                     C____   C
GAM544  DVS27    3'  TTCCTCGTGTAAGAATGCCT   14225         GCGAACC   A
                                TTCCTCGTG      GAT CCT
                                |||||||||      ||| |||
                                AAGGAGCAC      TTA GGA
                                     ATTC___   C
GAM544  KIAA0923 3'  TTCTTCAGTGGTAAATACCTC  14226     C _    CG ACCG
                                TTC TC GTGG  A    ATACCTC
                                ||| || ||||  |    |||||||
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                                AAG AG CACC  T    TATGGAG
                                  A  T    AT ____
GAM544  LOC201245 5'  TTCATCATGACCGATACCT   14227     C     GCGA
                                TTC TCGTG    ACCGATACCT
                                ||| |||||    ||||||||||
                                AAG AGTAC    TGGCTATGGA
                                  T    _____
GAM544  LOC90161  3'  CCTCATAAACTGATACCTC    14228       GGC    C
                                CCTCGT   GAAC GATACCTC
                                ||||||   |||| ||||||||
                                GGAGTA   TTTG CTATGGAG
                                   ___    A
GAM545  CD28      3'  GAGCTCTGAGCCCTAAACCA   14231         CAAA  _
                                GAGTTCTGA    TC AAACCA
                                |||||||||    || ||||||
                                CTCGAGACT    GG TTTGGT
                                     CG__  A
GAM545  CDKN2C    5'  TTAGGGTCCTGACGATCA     14232      A       AA
                                TTAG GTTCTGAC  ATCA
                                |||| ||||||||  ||||
                                AATC CAGGACTG  TAGT
                                  C       C_
GAM545  COL15A1   3'  TTAGAGTCTGATAGCATCA    14233        T    CAA_
                                TTAGAGT CTGA    ATCA
                                ||||||| ||||    ||||
                                AATCTCA GACT    TAGT
                                   _    ATCG
GAM545  TBP       3'  TTAAAGTTTTCTCCCTCAAACC 14234         CTGACAAA
            A                    TTAGAGTT       TCAAACCA
                                ||||||||       ||||||||
                                AATTTCAA       AGTTTGGT
                                     AAGAGGG_
GAM545  DKFZP434F0318 3'  GAGCCGAGATCAAACCA     14235     TT    CAA
                                GAG  CTGA   ATCAAACCA
                                |||  ||||   |||||||||
                                CTC  GGCT   TAGTTTGGT
                                  __    C__
GAM545  DKFZP564D206 3'  TTAAAGTTTTGAAACAAATCA  14236         CT__
                                TTAGAGTT    GACAAATCA
                                ||||||||    |||||||||
                                AATTTCAA    TTGTTTAGT
                                     AACT
GAM545  KIAA0391  3'  CAGTGAACTGAGATCAAACCA  14237     AGTT    CAA
                                TAG    CTGA   ATCAAACCA
                                |||    ||||   |||||||||
                                GTC    GACT   TAGTTTGGT
                                  ACTT    C__
GAM545  KIAA1712  3'  TTAAAGTTCTGATGACCA     14238           CAA
                                TTAGAGTTCTGA   ATCA
                                ||||||||||||   ||||
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                                AATTTCAAGACT   TGGT
                                      AC_
GAM545  KIAA1900  3'  TTAGGTTCTGACCCAA     14239     A      AAA
                                TTAG GTTCTGAC   TCAA
                                |||| ||||||||   ||||
                                AATC CAAGACTG   GGTT
                                  _      ___
GAM545  POMT2     3'  TTAGAGTTTATGACACTCA   14240       C_    AA
                                TTAGAGTT  TGACA  TCA
                                ||||||||  |||||  |||
                                AATCTCAA  ACTGT  AGT
                                     AT    G_
GAM545  TRIM2     3'  GAGCAGGTCTGAATCAAAC   14241     ___    CAA
                                GAGT   TCTGA   ATCAAAC
                                ||||   |||||   |||||||
                                CTCG   AGACT   TAGTTTG
                                  TCC    ___
GAM545  ZNF338    3'  TTAGAGTTGGAAAATCAA    14242       CT  C
                                TTAGAGTT  GA AAATCAA
                                ||||||||  || |||||||
                                AATCTCAA  CT TTTAGTT
                                     C_  _
GAM545  LOC129138 3'  TTAGAGTTCTAAAATCA     14243         CA
                                TTAGAGTTCTGA  AATCA
                                ||||||||||||  |||||
                                AATCTCAAGATT  TTAGT
                                        __
GAM545  LOC130507 3'  TTAAAGTTCTACTATTAGACCA 14244         ACAAATCAA
                                TTAGAGTTCTG       ACCA
                                ||||||||||        ||||
                                AATTTCAAGAT       TGGT
                                      GATAATC__
GAM545  LOC153205 3'  GAGTTCTGAGCCAAAGTCA   14245        __   _
                                GAGTTCTGA  CAAA TCA
                                |||||||||  |||| |||
                                CTCAAGACT  GTTT AGT
                                     CG    C
GAM545  LOC155054 3'  TAGAGTTCTGCAGACCA     14246        A  A
                                TAGAGTTCTG CA ATCA
                                |||||||||| || ||||
                                ATCTCAAGAC GT TGGT
                                      _  C
GAM545  LOC203378 3'  TTAGAGTCTCCTTAAATCA   14247       _  GAC
                                TTAGAGT TCT   AAATCA
                                ||||||| |||   ||||||
                                AATCTCA AGG   TTTAGT
                                    G   AA_
GAM545  LOC253981 3'  TTAGAGCTCTTCAAGTCAA   14248         GA   A
                                TTAGAGTTCT  CAA TCAA
                                ||||||||||  ||| ||||
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                                AATCTCGAGA  GTT AGTT
                                      A_  C
GAM545  LOC256586 3'  TTAGAGTTATGCCCCCAAATCA 14249        ___  GA
                                TTAGAGTT  CT  CAAATCA
                                ||||||||  ||  |||||||
                                AATCTCAA  GG  GTTTAGT
                                     TAC  GG
GAM545  LOC90355  3'  AGCAACAAATTAAACC      14250     TCT      C
                                AGT  GACAAAT AAACC
                                |||  ||||||| |||||
                                TCG  TTGTTTA TTTGG
                                  ___      A
GAM546  ABCC12    5'  TGAGAACTGTTTTCACCAA    14253    A        A  _
                                C AGAACTGTT TC CCGA
                                | |||||||||| || ||||
                                A TCTTGACAA AG GGTT
                                 C        A  T
GAM546  CD34      3'  CAAGAACAGCCTCTGAGG     14254        T   A  CC
                                CAAGAAC GTT TC  GAGG
                                ||||||| ||| ||  ||||
                                GTTCTTG CGG AG  CTCC
                                    T   _ A_
GAM546  FGF2      3'  AAGAATTGTTATCCATAG     14255       C       CG
                                AAGAA TGTTATCC  AG
                                ||||| ||||||||  ||
                                TTCTT ACAATAGG  TC
                                   A       TA
GAM546  PRDM2     3'  CAAGAACTGAGAGGCCG      14256         TTATCCC     A
                                CAAGAACTG      GAGGC CG
                                |||||||||      ||||| ||
                                GTTCTTGAC      CTCCG GC
                                     T_______    _
GAM546  FLJ10849  3'  TGAGAAATGTTATCCTTTCTAC 14257    A   C       CGAG_
            A                    C AGAA TGTTATCC     GCA
                                | |||| ||||||||     |||
                                A TCTT ACAATAGG     TGT
                                 C   T       AAAGA
GAM546  KIAA0478  3'  AGAACTCTAGCCCGAGGCA    14258       G   T
                                AGAACT TTA CCCGAGGCA
                                |||||| ||| |||||||||
                                TCTTGA GAT GGGCTCCGT
                                   _  C
GAM546  KIAA1301  3'  CAAGAACTGTTGATTGAAAGAC 14259          ATCCC_
                                CAAGAACTGTT     GAGGC
                                ||||||||||      |||||
                                GTTCTTGACAA     TTCTG
                                      CTAACT
GAM546  KIAA1571  3'  CAGGAACTGTTCTCTCTGCA   14260    A       A  CCGAG
                                CA GAACTGTT TC     GCA
                                || |||||||| ||     |||
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                                GT CTTGACAA AG    CGT
                                 C       G  AGA__
GAM546  SDCBP    5'  CGAGGACCGCCCCCGAGGCGCG 14261   A  A    TA       A
                                C AG ACTGT  TCCCGAGGC CG
                                | || |||||  ||||||||| ||
                                G TC TGGCG  GGGGCTCCG GC
                                 C  C     __        C
GAM546  LOC112937 5'  AGAAATCCGTCCCGAGGCGCG  14262     CTG TA       A
                                AGAA   T  TCCCGAGGC CG
                                ||||   |  ||||||||| ||
                                TCTT   G  AGGGCTCCG GC
                                  TA_ GC       C
GAM547  ZNF317   3'  TTGCACCCAGTAAGGTGCG   14265        CCGAC
                                TTGCACCC    GAGGTGCG
                                ||||||||    ||||||||
                                AACGTGGG    TTCCACGC
                                     TCA__
GAM548  CLECSF12  5'  CCCCTGAATAGATATAG     14268     AGTT
                                CCTC    AATAGATATAG
                                ||||    ||||||||||
                                GGGG    TTATCTATATC
                                  AC__
GAM548  ELOVL4   3'  TACCTAGTTAATAAATA     14269      C
                                TACCT AGTTAATAGATA
                                ||||| ||||||||||
                                ATGGA TCAATTATTTAT
                                      _
GAM548  NRAS     3'  CTCAAATAGATATAG       14270     GTT
                                CTCA   AATAGATATAG
                                ||||   ||||||||||
                                GAGT   TTATCTATATC
                                       ___
GAM548  RPE65    3'  CCTCAGTTGATTAAACATAG   14271        AA_
                                CCTCAGTT   TAGATATAG
                                ||||||||   |||||||||
                                GGAGTCAA   ATTTGTATC
                                     CTA
GAM548  SYT1     3'  CTCAGTCAATTTACATAG    14272         AG
                                CTCAGTTAAT  ATATAG
                                ||||||||||  ||||||
                                GAGTCAGTTA  TGTATC
                                      AA
GAM548  FLJ11117  3'  CCTCAGCTGAGGTATAG     14273        AAT  A
                                CCTCAGTT   AG TATAG
                                ||||||||   || |||||
                                GGAGTCGA   TC ATATC
                                     C__  C
GAM548  KIAA1219  3'  TACCCAACAGATATA       14274      CAGTT
                                TACCT    AATAGATATA
                                |||||    ||||||||||
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                                ATGGG    TTGTCTATAT
                                  _____
GAM548  LOC222160 5'  CTAGCATAATAGATATAG    14275    C  _
                                CT AGT TAATAGATATAG
                                || ||| ||||||||||||
                                GA TCG ATTATCTATATC
                                 _  T
GAM548  LOC90167  3'  CTCTTTTACTAGATATAG    14276    AG  A
                                CTC  TTA TAGATATAG
                                |||  ||| |||||||||
                                GAG  AAT ATCTATATC
                                  AA  G
GAM548  LOC91012  5'  TACCTTGGTAATAGATAT    14277     CA  T
                                TACCT  GT AATAGATAT
                                |||||  || |||||||||
                                ATGGA  CA TTATCTATA
                                   AC  _
GAM549  ABP1    3'  GGCCGTTGTCCCGAGGCCAC  14280     ACA__  ACATG
                                GGCC    CCC    GAGGCCAC
                                ||||    |||    ||||||||
                                CCGG    GGG    CTCCGGTG
                                  CAACA  _____
GAM549  APTX    5'  GGCCACACCCGGTGCCA     14281        ACAT  AG
                                GGCCACACCC   GG  GCCA
                                ||||||||||   ||  ||||
                                CCGGTGTGGG   CC  CGGT
                                     _____  A_
GAM549  ARF3    3'  GGCCACACTTGCATGGAG    14282       CCA
                                GGCCACAC   CATGGAG
                                ||||||||   |||||||
                                CCGGTGTG   GTACCTC
                                    AAC
GAM549  B3GAT1   3'  AGGCTGCAGTCCACCAGGG   14283     CA  C_   A  A
                                AGGC  CA  CCAC TGG GG
                                ||||  ||  |||| ||| ||
                                TCCG  GT  GGTG GTC CC
                                  AC  CA   _  _
GAM549  B3GAT1   3'  AGGCTGCAGTCCACCAGGG   14283     CA  C_   A  A
                                AGGC  CA  CCAC TGG GG
                                ||||  ||  |||| ||| ||
                                TCCG  GT  GGTG GTC CC
                                  AC  CA   _  _
GAM549  B4GALT1  3'  AGGCCAGTTCACACAGAGTCAC 14284       CACC       GC
                                AGGCCA   CACATGGAG  CAC
                                ||||||   |||||||||  |||
                                TCCGGT   GTGTGTCTC  GTG
                                   CAA_       A_
GAM549  B4GALT2  3'  GGCCACGACGGAGGCC     14285      ACCCAC
                                GGCCAC     ATGGAGGCC
                                ||||||     |||||||||
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                                CCGGTG     TGCCTCCGG
                                  C_____
GAM549  BIN1     3'  GGCCCCACCCACAGCAGCTGC  14286      A       _   AG
                                GGCC CACCCACA TGG  GC
                                |||| |||||||| |||  ||
                                CCGG GTGGGTGT GTC  CG
                                  G       C   GA
GAM549  BIN1     3'  GGCCCCACCCACAGCAGCTGC  14286      A       _   AG
                                GGCC CACCCACA TGG  GC
                                |||| ||||||||| |||  ||
                                CCGG GTGGGTGT GTC  CG
                                  G       C   GA
GAM549  CENTD2   5'  AGATCACACCCACCCGGGGC   14287     GC       A   A
                                AG  CACACCCAC TGG GGC
                                ||  ||||||||| ||| |||
                                TC  GTGTGGGTG GCC CCG
                                 TA       G   _
GAM549  CYLN2    3'  AGCCACACCCGGGCGGCCAC   14288          ACAT  A
                                GGCCACACCC    GG GGCCAC
                                ||||||||||    || ||||||
                                TCGGTGTGGG    CC CCGGTG
                                      C___  G
GAM549  CYP8B1   3'  AGCTGCACAGTTCGGAGGCCA  14289     CA   CCACA
                                GGC  CAC     TGGAGGCCA
                                |||  |||     |||||||||
                                TCG  GTG     GCCTCCGGT
                                  AC   TCAA_
GAM549  DAAM2    3'  AGGCCTCACCCACAACCTCCCA 14290       A       TGGAGG
                                AGGCC CACCCACA     CCA
                                ||||| ||||||||     |||
                                TCCGG GTGGGTGT     GGT
                                   A       TGGAG_
GAM549  DBH      3'  AGGCCACACCCAGTGAGGC    14291           CATG
                                AGGCCACACCCA    GAGGC
                                ||||||||||||    |||||
                                TCCGGTGTGGGT    CTCCG
                                      CA__
GAM549  FUT5     3'  AGGTCACACCCACAGTGATGC  14292     C        TG  G
                                AGG CACACCCACA  GA GC
                                ||| ||||||||||  || ||
                                TCC GTGTGGGTGT  CT CG
                                  A         CA  A
GAM549  GGT2     5'  AGGCCAGCCTGGGGGCCA     14293       CA  CACA   A
                                AGGCCA  CC    TGG GGCCA
                                ||||||  ||    ||| |||||
                                TCCGGT  GG    ACC CCGGT
                                   C_  _____   C
GAM549  GYPE     3'  AGGCCACATCCTCATGCC     14294         C  A   GGAG
                                AGGCCACA CC CAT    GCC
                                |||||||| || |||    |||
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                                TCCGGTGT GG GTA   CGG
                                    A  A  _____
GAM549  GYS1    3'  GGCCACACCCAGTGCAGA    14295          CA  G
                                GGCCACACCCA  TG AGG
                                ||||||||||  || |||
                                CCGGTGTGGGT  AC TCT
                                      C_  G
GAM549  ICMT    3'  GGCCACGGTCACACAAAGCCAC 14296       ACC   TG   G
                                GGCCAC   CACA  GAG CCAC
                                ||||||   ||||  ||| ||||
                                CCGGTG   GTGT  TTC GGTG
                                   CCA   GT  _
GAM549  IGFBP4  3'  AGGGCACACCCATGCTCA    14297    C      CATGGAG  _
                                AGG CACACCCA      GC CA
                                ||| ||||||||      || ||
                                TCC GTGTGGGT      CG GT
                                  C       A_______  A
GAM549  IRAK4   3'  AGGTCTCATCTCCTAGAGGCCA 14298    CCA  CCCACA
              C                  AGG   CA     TGGAGGCCAC
                                |||   ||     ||||||||||
                                TCC   GT     ATCTCCGGTG
                                  AGA  AGAGG_
GAM549  JAG2    3'  GGCCACACCAACACAGCCA   14300        C   GGA
                                GGCCACACC ACAT   GGCCA
                                |||||||| ||||   |||||
                                CCGGTGTGG TGTG   TCGGT
                                      T   ___
GAM549  JAG2    3'  AGGCCACACCATCAGCCA    14299         CACATGGA
                                AGGCCACACC       GGCCA
                                ||||||||||       |||||
                                TCCGGTGTGG       TCGGT
                                     TAG_____
GAM549  KIP2    3'  AGGCCACACCCATGTGACTGC  14301          CA   AG
                                AGGCCACACCCA  TGG  GC
                                ||||||||||||  |||  ||
                                TCCGGTGTGGGT  ACT  CG
                                      AC   GA
GAM549  KNS2    3'  GGCCACACTCGGCAGTCCCA   14302       CCACA  _  G_
                                GGCCACAC    TGG AG  CCA
                                ||||||||    ||| ||  |||
                                CCGGTGTG    GCC TC  GGT
                                    A____   G  AG
GAM549  KRT3    3'  AGGCCACACCTGGACAATCAC  14303         CACA   GGC_
                                AGGCCACACC   TGGA   CAC
                                ||||||||||   ||||   |||
                                TCCGGTGTGG   ACCT   GTG
                                     _____   GTTA
GAM549  LDLR    3'  AGCCACACCTGGGTGCAGGCCA 14304         CACA  G
              C                  GGCCACACC   TG AGGCCAC
                                |||||||||   || |||||||
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                                TCGGTGTGG   AC TCCGGTG
                                     ACCC  G
GAM549  MCM4    3'  AGACCACACCCATGTGGC    14305          CA  GA
                                AGGCCACACCCA  TG  GGC
                                ||||||||||||  ||  |||
                                TCTGGTGTGGGT  AC  CCG
                                      __  A_
GAM549  MGAT5   5'  AGGCCCCACCCACACCCA    14306      A       GGAGG
                                AGGCC CACCCACAT    CCA
                                |||||| |||||||||    |||
                                TCCGG GTGGGTGTG    GGT
                                  G       ______
GAM549  MYOM2   3'  GCCACACCCATGTGCCCAC   14307         CA  GAGG
                                GCCACACCCA  TG   CCAC
                                ||||||||||  ||   ||||
                                CGGTGTGGGT  AC   GGTG
                                      __  ACG_
GAM549  NID     3'  AGGCTGAGCTCATAAGGCCAC  14308     CACACCCA   G
                                AGGC       CATG AGGCCAC
                                ||||       |||| |||||||
                                TCCG       GTAT TCCGGTG
                                  ACTCGA__   _
GAM549  NUP62   3'  AAGCCACACCCATGAGGC    14309          CATG
                                AGGCCACACCCA   GAGGC
                                ||||||||||||   |||||
                                TTCGGTGTGGGT   CTCCG
                                      A___
GAM549  OCA2    3'  AGGACACACAGAGGAGGTCA  14310    C    CCACAT    C
                                AGG CACAC     GGAGG CA
                                ||| |||||     ||||| ||
                                TCC GTGTG     CCTCC GT
                                  T    TCT___    A
GAM549  OTOF    3'  GGCCGGCCAGGAGGCCA    14311     ACAC   CAT
                                GGCC   CCA   GGAGGCCA
                                ||||   |||   ||||||||
                                CCGG   GGT   CCTCCGGT
                                  CC__   ___
GAM549  P53AIP1 3'  GGCCCACACCCATGAATTCAC  14312     _     CA   GGC
                                GGCC ACACCCA  TGGA   CAC
                                |||| |||||||  ||||   |||
                                CCGG TGTGGGT  ACTT   GTG
                                  G      __    AA_
GAM549  PML     3'  GGTCACTACCCACGAGGCCAC  14313    C  _    ATG
                                GG CAC ACCCAC   GAGGCCAC
                                || ||| ||||||   ||||||||
                                CC GTG TGGGTG   CTCCGGTG
                                 A  A     ____
GAM549  PML     3'  GGTCACTACCCACGAGGCCAC  14313    C  _    ATG
                                GG CAC ACCCAC   GAGGCCAC
                                || ||| ||||||   ||||||||
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                                CC GTG TGGGTG   CTCCGGTG
                                 A  A    ___
GAM549  POLR2E   3'  AGGCCAGTGCCCTGGGCCA   14314      CA_  ACA  AG
                                AGGCCA  CCC   TGG  GCCA
                                ||||||  |||   |||  ||||
                                TCCGGT  GGG   ACC  CGGT
                                   CAC  ___   __
GAM549  PPOX     5'  GGCCACACCCTCGCTATGTGGC 14315       ACA_________  AGG
           CTCC                  CCACACCC        TGG  CC
                                ||||||||         |||  ||
                                GGTGTGGG         ACC  GG
                                    AGCGATAIIIC  GGA
GAM549  PYGO2    3'  GGCCACACCCCATGCCTGC   14316        A   GAG
                                GGCCACACCC CATG   GC
                                |||||||||| ||||   ||
                                CCGGTGTGGG GTAC   CG
                                      _   GGA
GAM549  RPH3AL   3'  GGCCACACGCAGCTTCGGAGGC 14317       C  CA__
           C                    GGCCACAC CA   TGGAGGCC
                                |||||||| ||   ||||||||
                                CCGGTGTG GT   GCCTCCGG
                                    C  CGAA
GAM549  SERPINA3 3'  GGCCACACATGCCATGGCCAC  14318       CCA_  GGA
                                GGCCACAC   CAT   GGCCAC
                                |||||||   |||   ||||||
                                CCGGTGTG   GTA   CCGGTG
                                    TACG   ___
GAM549  SHMT1    3'  AGGCCATTTCTACACCATGTGG 14319    _______    CACA__  AGG
           CCTCC                 CC     ACACC     TGG  CC
                                ||     |||||     |||  ||
                                GG     TGTGG     ACC  GG
                                 TAAAGA    TAIIIC  GGA
GAM549  SHOX     3'  GGCTGAACTCGTGAAGCCAC   14320     CACACCC  A  _
                                GGC      AC TG GAGGCCAC
                                |||      || || ||||||||
                                CCG      TG GC CTTCGGTG
                                  ACT_____  A  A
GAM549  SLC13A3  3'  AGCCACAGAGGCCTATGGGGGC 14321       C___  AC   A
           CAC                   GGCCACA   CC  ATGG GGCCAC
                                |||||||   ||  |||| ||||||
                                TCGGTGT   GG  TACC CCGGTG
                                    CTCC  A_   C
GAM549  STIM1    3'  GGCCACACGCTGGCGGTCAC   14322       CCACA  A  C
                                GGCCACAC    TGG GG CAC
                                ||||||||    ||| || |||
                                CCGGTGTG    ACC CC GTG
                                    CG___   G  A
GAM549  UBE2G2   3'  GGCCTGCACCCACAGACC    14323     A_      TGGA
                                GGCC  CACCCACA   GGCC
                                ||||  ||||||||   ||||
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                                CCGG  GTGGGTGT   CTGG
                                  AC      ____
GAM549  WDR4    5'  GGCCACACCCGTGTGGC     14324         ACA  GA
                                GGCCACACCC   TG  GGC
                                ||||||||||   ||  |||
                                CCGGTGTGGG   AC  CCG
                                     C__   A_
GAM549  WHSC1   3'  AGCCACACCCACGGC       14325         ATGGA  C
                                GGCCACACCCAC    GG C
                                ||||||||||||    || |
                                TCGGTGTGGGTG    CC G
                                      _____  A
GAM549  WHSC1   3'  AGCCACACCCACGGC       14325         ATGGA  C
                                GGCCACACCCAC    GG C
                                ||||||||||||    || |
                                TCGGTGTGGGTG    CC G
                                      _____  A
GAM549  WHSC1   3'  AGCCACACCCACGGC       14325         ATGGA  C
                                GGCCACACCCAC    GG C
                                ||||||||||||    || |
                                TCGGTGTGGGTG    CC G
                                      _____  A
GAM549  WWP2    3'  GGCCACATCCACGGGGGC    14326       C   AT  A
                                GGCCACA CCAC  GG GGC
                                |||||||  ||||  ||  |||
                                CCGGTGT GGTG  CC CCG
                                    A   C_  _
GAM549  ZNF138  5'  AGGCCAGACCTGCAGCACC   14327       C   CACA  G  _
                                AGGCCA ACC    TG AG GCC
                                ||||||  |||    ||  ||  |||
                                TCCGGT TGG    AC TC TGG
                                   C   ____  G  G
GAM549  AGMAT   3'  GGTTGCCCTGCATGAAGCCAC  14328    CCACA   A_   G
                                GG    CCC  CATG AGGCCAC
                                ||    |||  ||||  |||||||
                                CC    GGG  GTAC TTCGGTG
                                 AAC__   AC   _
GAM549  APOL4   3'  GGCCACACCCAAGGAGGCCA   14329          CAT
                                GGCCACACCCA   GGAGGCCA
                                ||||||||||   ||||||||
                                CCGGTGTGGGT   CCTCCGGT
                                      T__
GAM549  ASB13   3'  GGCCACACCCACAACTGTGTGG 14330        A__________   AGG
            CCTCCA                ACACCCAC        TGG   CCA
                                ||||||||        |||   |||
                                TGTGGGTG        ACC   GGT
                                    TTGACAIIIC   GGA
GAM549  BC008967 5' AGGTCGCCCCACATGGAAG   14331     CCACA
                                AGG    CCCACATGGAGG
                                |||    ||||||||||||
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                                TCC    GGGTGTACCTTC
                                  AGCG_
GAM549  BRD1     3'  GGACACACCCACCGGCGGTCAC 14332    C       A  A  C
                                GG CACACCCAC TGG GG CAC
                                || ||||||||| ||| || |||
                                CC GTGTGGGTG GCC CC GTG
                                 T       _  G  A
GAM549  C11orf23  3'  AGGTCCATACCACAGAGGCCAC 14334     _  CAC    TG
                                AGG CCA   CCACA  GAGGCCAC
                                ||| |||   |||||  ||||||||
                                TCC GGT   GGTGT  CTCCGGTG
                                  A  AT_    __
GAM549  C11orf23  3'  AGGTCCATACCACGGAGGCCAC 14333     _  C   CAC
                                AGG CCA ACC   ATGGAGGCCAC
                                ||| ||| |||   ||||||||||
                                TCC GGT TGG   TGCCTCCGGTG
                                  A  A  ___
GAM549  C16orf5   3'  AGGTCATACCCACACGCAG   14335    C  C       G
                                AGG CA ACCCACATG AG
                                ||| || ||||||||| ||
                                TCC GT TGGGTGTGC TC
                                  A  A       G
GAM549  C1orf19   3'  AAGCCACGCCCGTATTGTGTGG 14336     A  ACA_________  AGG
           CCTCC                  CCAC CCC         TGG   CC
                                |||| |||         |||   ||
                                GGTG GGG         ACC   GG
                                  C   CATAACAIIIC   GGA
GAM549  CDC14A    3'  AGATCATACTTACATGAAAGGG 14337    GC  C  CC     __
           C                     AG  CA AC  ACATGGA  GGC
                                ||  || ||  |||||||  |||
                                TC  GT TG  TGTACTT  CCG
                                 TA  A  AA      TC
GAM549  CPLX1     3'  AGGCCACACACGCGCCGGC   14338         CC  A  GA
                                AGGCCACAC  AC TG  GGC
                                |||||||||  || ||  |||
                                TCCGGTGTG  TG GC  CCG
                                     __  C  GG
GAM549  DKFZP434P0111 3'  AGGCCCACACTGGAGGCC    14339      A   CC  A
                                AGGCC CAC  AC TGGAGGCC
                                ||||| |||  || ||||||||
                                TCCGG GTG  TG ACCTCCGG
                                   _   __  _
GAM549  DKFZP564P1916 5'  AGGCCACACCAGGCTGGAGGC  14340          CACA
                                AGGCCACACC    TGGAGGC
                                ||||||||||    |||||||
                                TCCGGTGTGG    ACCTCCG
                                      TCCG
GAM549  DKFZP586M1120 3'  AGGCGTGCCCATGAAGGCTAC  14341      CACAC  A       C
                                AGGC    CC CATGGAGGC AC
                                ||||    || ||||||||| ||
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                                TCCG    GG GTACTTCCG TG
                                  CAC__ _       A
GAM549  DRF1    3'  AGGCCACAGCCTGCACTCTGC  14342       _ CA  GGAG
                                AGGCCACA CC  CAT   GC
                                |||||||| ||  |||   ||
                                TCCGGTGT GG  GTG   CG
                                    C  AC   AGA_
GAM549  ELOVL1  3'  AGGCCACATCCCTGGAG    14343       _  ACA
                                AGGCCACA CCC   TGGAG
                                |||||||| |||   |||||
                                TCCGGTGT GGG   ACCTC
                                    A  ___
GAM549  FKBP4   3'  CCTAGCACCCACATGGAGGCCA 14344   A__
          C                      CC   CACCCACATGGAGGCCAC
                                ||   ||||||||||||||||||
                                GG   GTGGGTGTACCTCCGGTG
                                 ATC
GAM549  FLJ00007 3' AGGCTGCCCCCTGAGAGGCCAC 14345    CACA  ACAT
                                AGGC   CCC   GGAGGCCAC
                                ||||   |||   |||||||||
                                TCCG   GGG   TCTCCGGTG
                                  ACG_  GAC_
GAM549  FLJ12436 5' GGCACACCCACGATGTGCTGC  14346    C      _  GAG_
                                GGC ACACCCAC ATG   GC
                                ||| |||||||| |||   ||
                                CCG TGTGGGTG TAC   CG
                                  _      C   ACGA
GAM549  FLJ20294 3' AAGCCGCCCATGGAGGCCA   14347     ACAC  A
                                AGGCC   CC CATGGAGGCCA
                                |||||   || ||||||||||
                                TTCGG   GG GTACCTCCGGT
                                  C___  _
GAM549  FLJ20297 3' AGGCCAGGCCCAGGTGGC    14348     CA   CAT  A
                                AGGCCA  CCCA   GG GGC
                                ||||||  ||||   || |||
                                TCCGGT  GGGT   CC CCG
                                   CC   ___  A
GAM549  FLJ20297 3' AGGCCAGGCCCAGGTGGC    14348     CA   CAT  A
                                AGGCCA  CCCA   GG GGC
                                ||||||  ||||   || |||
                                TCCGGT  GGGT   CC CCG
                                   CC   ___  A
GAM549  FLJ20509 3' AGGCTCCATCCACATGGA    14349     CA  C
                                AGGC  CA CCACATGGA
                                ||||  || |||||||||
                                TCCG  GT GGTGTACCT
                                  AG  A
GAM549  FLJ22313 5' GGCTCCGGACTGTGGAGGCC  14350    CACA  C_  A_
                                GGC   CC  AC  TGGAGGCC
                                |||   ||  ||  ||||||||
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                                CCG   GG  TG  ACCTCCGG
                                  A___  CC  AC
GAM549  FLJ22584  3'  GACCCACACATGGAGG     14351     A   CC
                                GGCC CAC  ACATGGAGG
                                |||| |||  |||||||||
                                CTGG GTG  TGTACCTCC
                                  _   __
GAM549  GENX-3414 5'  AGGTCACGCACACAGAGCCAC  14352     C   ACC       G
                                AGG CAC   CACATGGAG CCAC
                                ||| |||   ||||||||| ||||
                                TCC GTG   GTGTGTCTC GGTG
                                  A  C__       _
GAM549  GNG4      3'  AGACCGCACCCACAGGTCTGCC 14353      A       T  AG_
           AC                     AGGCC CACCCACA GG   GCCAC
                                |||||| |||||||| ||   |||||
                                TCTGG GTGGGTGT CC   CGGTG
                                  C       _ AGA
GAM549  GPS2      5'  AGGTCACACCCATAATTGTTGC 14354     C       CA__  GAG
                                AGG CACACCCA    TG   GC
                                ||| ||||||||    ||   ||
                                TCC GTGTGGGT    AC   CG
                                  A       ATTA  AA_
GAM549  GPT2      3'  GGCTCACACCCACGCC      14355     _       ATGGAG
                                GGC CACACCCAC     GCC
                                ||| |||||||||     |||
                                CCG GTGTGGGTG     CGG
                                  A       _______
GAM549  GRWD      3'  AGGCCACACCAGGCC       14356          CACATGG
                                AGGCCACACC      AGGCC
                                ||||||||||      |||||
                                TCCGGTGTGG      TCCGG
                                        ________
GAM549  HPCAL4    3'  AGGCCAGCCAGAGAGGTCA    14357       CAC   CAT    C
                                AGGCCA   CCA   GGAGG CA
                                ||||||   |||   ||||| ||
                                TCCGGT   GGT   TCTCC GT
                                   C__   C__     A
GAM549  KIAA0193  3'  AGGCATGCACTCACGGGAGGCC 14358      CA_   C   AT
           AC                     AGGC   CAC CAC  GGAGGCCAC
                                ||||   ||| |||  |||||||||
                                TCCG   GTG GTG  CCTCCGGTG
                                  TAC   A   C_
GAM549  KIAA0415  3'  AGGCCGCAGCCTGCATAGGCCA 14359       A  _  CA   GG
                                AGGCC CA CC  CAT  AGGCCA
                                ||||| || ||  |||  ||||||
                                TCCGG GT GG  GTA  TCCGGT
                                  C  C  AC   __
GAM549  KIAA0449  3'  AGGCTGAATCCAGGGTGAGGCC 14360      CACAC   CATG
           AC                     AGGC    CCA    GAGGCCAC
                                ||||    |||    ||||||||
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                                TCCG    GGT   CTCCGGTG
                                  ACTTA  CCCA
GAM549  KIAA0481  3' AGGCCACACCCACCTGGCC   14361          ATGGA
                                AGGCCACACCCAC   GGCC
                                ||||||||||||    ||||
                                TCCGGTGTGGGTG   CCGG
                                      GA___
GAM549  KIAA0819  3' AGGCCACACTCCTTCCAAGCCA 14362        _ ACATGG
          C                    AGGCCACAC CC    AGGCCAC
                               |||||||| ||    |||||||
                               TCCGGTGTG GG    TTCGGTG
                                    A  AAGG__
GAM549  KIAA0844  3' AGCCATATCCACAGAAGC   14363     CAC   TG
                               GGCCA  CCACA  GAGGC
                               |||||  |||||  |||||
                               TCGGT  GGTGT  CTTCG
                                  ATA   __
GAM549  KIAA0945  3' GGCCACACCCATGACTGTGTGG 14364      CA_________  AGG
          CCTCCA               ACACCCA        TGG  CCA
                               |||||||        |||  |||
                               TGTGGGT        ACC  GGT
                                  ACTGACAIIIC  GGA
GAM549  KIAA1117  3' AGGCCACATTCAGACATTTGC  14365      CC  C  GAG
                               AGGCCACA  CA ATG  GC
                               ||||||||  || |||  ||
                               TCCGGTGT  GT TGT  CG
                                    AA  C  AAA
GAM549  KIAA1183  3' AGGTCACACCCAAACC     14366    C     CATGGA
                               AGG CACACCCA     GGCC
                               ||| ||||||||     ||||
                               TCC GTGTGGGT     TTGG
                                 A      _______
GAM549  KIAA1322  3' GGCTACGTCTGGAGGCCAC   14367    C  ACCCACA
                               GGC AC      TGGAGGCCAC
                               ||| ||      ||||||||||
                               CCG TG      ACCTCCGGTG
                                 A  CAG____
GAM549  KIAA1775  3' AGCTGCACCCACAGAACTGGGC 14368    CA      T  ___
                               GGC  CACCCACA GGA  GGC
                               |||  |||||||| |||  |||
                               TCG  GTGGGTGT CTT  CCG
                                 AC       _  GAC
GAM549  KIAA1949  3' AAGCCACACCTTCAGGTCAC  14369       CA  T  AG
                               AGGCCACACC  CA GG  GC
                               ||||||||||  || ||  ||
                               TTCGGTGTGG  GT CC  TG
                                    AA  _  AG
GAM549  KIAA1949  3' AAGCCACACCTTCAGGTCAC  14369       CA  T  AG
                               AGGCCACACC  CA GG  GC
                               ||||||||||  || ||  ||
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                                TTCGGTGTGG  GT CC  TG
                                     AA  _  AG
GAM549  KIAA1949  3'  AAGCCACACCTTCAGGTCAC   14369         CA  T  AG
                                AGGCCACACC  CA GG  GC
                                ||||||||||  || ||  ||
                                TTCGGTGTGG  GT CC  TG
                                     AA  _  AG
GAM549  MGC16202  5'  AGGCCACGATCCGGGCGGGCC  14370       AC_  ACAT  A_
                                AGGCCAC   CC   GG  GGCC
                                |||||||   ||   ||  ||||
                                TCCGGTG   GG   CC  CCGG
                                   CTA  C___  GC
GAM549  MGC21738  3'  AGGTTACACCCACTGAGC    14371     CC       A  GA
                                AGG  ACACCCAC TG  GGC
                                |||  |||||||| ||  |||
                                TCC  TGTGGGTG AC  TCG
                                  AA       _  __
GAM549  MGC2941   3'  AGGCTGCACTCAATCATGGGCC 14372     CA   C  __    AG
                                AGGC  CAC CA  CATGG  GCC
                                ||||  ||| ||  |||||  |||
                                TCCG  GTG GT  GTACC  CGG
                                  AC   A  TA    __
GAM549  MGC5601   5'  AGGCCACATCAGCAAGGGGG   14373        CC  _  T  A
                                AGGCCACA  CA CA GG GG
                                ||||||||  || || || ||
                                TCCGGTGT  GT GT CC CC
                                     A_  C  T  C
GAM549  MIC2L1    3'  AGGCCACACCCAGCC       14374          CATGGAG
                                AGGCCACACCCA      GCC
                                ||||||||||||      |||
                                TCCGGTGTGGGT      CGG
                                          ________
GAM549  MSC       3'  AGCCACACCCGCCAC       14375         ACATGGAG
                                GGCCACACCC       GCCAC
                                ||||||||||       |||||
                                TCGGTGTGGG       CGGTG
                                          _________
GAM549  MVD       3'  AGCCACACCCAGGCC       14376          CATGGA
                                GGCCACACCCA      GGCC
                                ||||||||||      ||||
                                TCGGTGTGGGT     CCGG
                                          _______
GAM549  PIP5K1C   3'  GGCCACACCTGCTGCTCCGAGT 14377         CACA  ____  GC
             CAC                   GGCCACACC   TG   GAG  CAC
                                |||||||||   ||   |||  |||
                                CCGGTGTGG   AC   CTC  GTG
                                     ACG_  GAGG  A_
GAM549  RNAH      3'  AGGCAACATTTGTTAAAAGGCC 14378     C  CCCACAT
             AC                    AGGC ACA      GGAGGCCAC
                                ||||  |||      |||||||||
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                                TCCG TGT      TTTCCGGTG
                                  T   AAACAAT
GAM549  SH120    5'  AGGCCACAGCACGCTGGGGCCA 14379        CC   A_   A
            C                    AGGCCACA  CAC  TGG GGCCAC
                                 ||||||||  |||  ||| ||||||
                                 TCCGGTGT  GTG  ACC CCGGTG
                                     C_   CG   _
GAM549  SMOC1    3'  AGGTCACACCCAATCTGCGTGG 14380   C      CA_________  AGG
            CCTCC                 CACACCCA        TGG   CC
                                  ||||||||        |||   ||
                                  GTGTGGGT        ACC   GG
                                 A       TAGACGIIIC   GGA
GAM549  SPRY4    3'  AAGCCACACTCATGACCA    14381        CCA    GAG
                                 AGGCCACAC   CATG   GCCA
                                 |||||||||   ||||   ||||
                                 TTCGGTGTG   GTAC   TGGT
                                     A__    ____
GAM549  TPC2     3'  AGTCACACTCATACAAGCCA   14382    C    CCA    G
                                 GG CACAC   CATG AGGCCA
                                 || |||||   |||| ||||||
                                 TC GTGTG   GTAT TTCGGT
                                  A    A__    G
GAM549  TTTY2    5'  AGGACACAAATGTGGAGGCCAC 14383     C    CCCACA
                                 AGG CACA     TGGAGGCCAC
                                 ||| ||||     ||||||||||
                                 TCC GTGT     ACCTCCGGTG
                                   T    TTAC__
GAM549  U5-116KD 3'  AGGCCACGTCATATGAGG    14384        ACCCA   _
                                 AGGCCAC     CATG GAGG
                                 |||||||     |||| ||||
                                 TCCGGTG     GTAT CTCC
                                     CA___    A
GAM549  WDR18    3'  GGCCACACCCGCGGGCC     14385         ACAT GA
                                 GGCCACACCC    G  GGCC
                                 ||||||||||    |  ||||
                                 CCGGTGTGGG    C  CCGG
                                       _____ GC
GAM549  ZNF297B  3'  AGACCCCACTGTATGGAGGCTA 14386      A   CCAC       C
            C                    AGGCC CAC    ATGGAGGC AC
                                 ||||| |||    |||||||| ||
                                 TCTGG GTG    TACCTCCG TG
                                    G   ACA_       A
GAM549  ZNF297B  3'  AGACCCCACTGTATGGAGGCTA 14386      A   CCAC       C
            C                    AGGCC CAC    ATGGAGGC AC
                                 ||||| |||    |||||||| ||
                                 TCTGG GTG    TACCTCCG TG
                                    G   ACA_       A
GAM549  LOC124044 3'  GGCTGCACCCACAGGGAA    14387     CA       T
                                 GGC  CACCCACA GGAG
                                 |||  |||||||| ||||
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                                CCG  GTGGGTGT CCTT
                                  AC       C
GAM549   LOC124842 5'  AGGCCACATCCACGGTGGC   14388        C    AT  A
                                AGGCCACA CCAC  GG GGC
                                |||||||| ||||  || |||
                                TCCGGTGT GGTG  CC CCG
                                    A   __  A
GAM549   LOC145813 3'  AGGTCACACCCGTGGGTAC   14389     C      ACA   AG
                                AGG CACACCC   TGG  GC
                                ||| |||||||   |||  ||
                                TCC GTGTGGG   ACC  TG
                                  A      C__   CA
GAM549   LOC146712 5'  AGCCACACCCACGACC      14390           ATGGA
                                GGCCACACCCAC    GGCC
                                ||||||||||||    ||||
                                TCGGTGTGGGTG    CTGG
                                                _____
GAM549   LOC147622 3'  GGCCACATCCACATGAAGA   14391        C
                                GGCCACA CCACATGGAGG
                                ||||||| ||||||||||
                                CCGGTGT GGTGTACTTCT
                                    A
GAM549   LOC148753 3'  GACTGCATCCACACAAGCTAC  14392     CA  C     GG    C
                                GGC  CA CCACAT  AGGC AC
                                |||  || ||||||  |||| ||
                                CTG  GT GGTGTG  TTCG TG
                                  AC  A     __    A
GAM549   LOC148887 3'  GGCCACACTCACTCGGCCAC   14393        C   ATGGA
                                GGCCACAC CAC    GGCCAC
                                |||||||| |||    ||||||
                                CCGGTGTG GTG    CCGGTG
                                    A   AG___
GAM549   LOC148930 3'  AGGCCACACCTGGGCC      14394          CACA   AG
                                AGGCCACACC    TGG  GCC
                                ||||||||||    |||  |||
                                TCCGGTGTGG    ACC  CGG
                                              ____   __
GAM549   LOC149319 5'  GGCTGCACCCACAGACATACCA 14395     CA       T  AG_
           C                     GGC  CACCCACA GG   GCCAC
                                |||  |||||||| ||   |||||
                                CCG  GTGGGTGT CT   TGGTG
                                  AC       _  GTA
GAM549   LOC150142 5'  GGCCACACTCCAGCCCA     14396         _   CATGGA G
                                GGCCACAC CCA      G CCA
                                |||||||| |||      | |||
                                CCGGTGTG GGT      C GGT
                                    A   _______ G
GAM549   LOC150348 3'  GGCCACACCTGATGGAAG    14397          CAC
                                GGCCACACC   ATGGAGG
                                |||||||||   |||||||
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                                CCGGTGTGG  TACCTTC
                                     AC_
GAM549  LOC150504 5' AGGCCTACCCGCACGAGTCGC 14398     AC   A   AG_
                                AGGCC ACCC CATGG  GC
                                ||||| |||| |||||  ||
                                TCCGG TGGG GTGCT  CG
                                   A_   C    CAG
GAM549  LOC151146 5' AAGTTACACCCACTGCTGC   14399    CC      A GAG
                                AGG ACACCCAC TG  GC
                                |||  |||||||| ||  ||
                                TTC TGTGGGTG AC  CG
                                  AA      _ GA_
GAM549  LOC151171 5' GGCCACACCGTGCATGGCC   14400       CA_  GGA
                                GGCCACACC  CAT  GGCC
                                |||||||||  |||  ||||
                                CCGGTGTGG  GTA  CCGG
                                     CAC  ___
GAM549  LOC151429 3' GGCCGCAGTCCATGGAAGGC  14401    A CCCA    _
                                GGCC CA   CATGGA GGC
                                |||| ||   |||||| |||
                                CCGG GT   GTACCT CCG
                                  C CAG_    T
GAM549  LOC153320 3' AGGCCACATCCATCATCTTTCC 14402       C  _  GGAGG
          CA                    AGGCCACA CCA CAT    CCA
                                |||||||| ||| |||    |||
                                TCCGGTGT GGT GTA    GGT
                                    A  A  GAAAG
GAM549  LOC154215 3' AGGCCAACCCGCTGGGCTGC  14403     C   ACA  AG_
                                AGGCCA ACCC  TGG  GC
                                |||||| ||||  |||  ||
                                TCCGGT TGGG  ACC  CG
                                   _  CG_  CGA
GAM549  LOC154834 3' AGGACACACCCAGGCGGAGGCC 14404    C      CA
          AC                    AGG CACACCCA  TGGAGGCCAC
                                ||| ||||||||  ||||||||||
                                TCC GTGTGGGT  GCCTCCGGTG
                                  T      CC
GAM549  LOC157254 5' AGCCACACCTGCAGCCC     14405       CACA  G  G
                                GGCCACACC   TG AG CC
                                |||||||||   || || ||
                                TCGGTGTGG   AC TC GG
                                    ____  G  G
GAM549  LOC158056 5' AGGGTGCACCTCCAGAGGCC  14406    CCA   CA  TG
                                AGG  CACC  CA  GAGGCC
                                |||  ||||  ||  ||||||
                                TCC  GTGG  GT  CTCCGG
                                  CAC   AG  __
GAM549  LOC158308 5' AGGCTCATGCTGGAGGCCA   14407     _ CACCCACA
                                AGGC CA      TGGAGGCCA
                                |||| ||      |||||||||
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                                TCCG GT       ACCTCCGGT
                                  A  ACG_____
GAM549   LOC158427 3'  AGGCCACTCCCAGGGCCA    14409        A    CATG A
                                AGGCCAC CCCA    G GGCCA
                                ||||||| ||||    | |||||
                                TCCGGTG GGGT    C CCGGT
                                   A    ____ _
GAM549   LOC158427 3'  AGGCCACATCTTTAAGGCCAC  14408        CCCACATG
                                AGGCCACA       GAGGCCAC
                                ||||||||       ||||||||
                                TCCGGTGT       TTCCGGTG
                                    AGAAA___
GAM549   LOC158450 3'  AGGCCATGCGTAGAGGGCCA   14410       CACCCACA     _
                                AGGCCA       TGGAGG CCA
                                ||||||       |||||| |||
                                TCCGGT       ATCTCC GGT
                                   ACGC____      C
GAM549   LOC158504 3'  AGGCCATGCGTAGAGGGCCA   14410       CACCCACA     _
                                AGGCCA       TGGAGG CCA
                                ||||||       |||||| |||
                                TCCGGT       ATCTCC GGT
                                   ACGC____      C
GAM549   LOC159148 5'  AGGACACAAATGTGGAGGCCAC 14383     C    CCCACA
                                AGG CACA     TGGAGGCCAC
                                ||| ||||     ||||||||||
                                TCC GTGT     ACCTCCGGTG
                                  T    TTAC__
GAM549   LOC197136 3'  GGCTGCACCCACAGGGAA     14387     CA       T
                                GGC  CACCCACA GGAG
                                |||  |||||||| ||||
                                CCG  GTGGGTGT CCTT
                                  AC       C
GAM549   LOC200225 5'  AGCCACACCCATGAACTGC    14411          CA    G_
                                GGCCACACCCA  TGGA  GC
                                ||||||||||  ||||  ||
                                TCGGTGTGGGT  ACTT  CG
                                      __    GA
GAM549   LOC204823 5'  AGCCACATCCTTGAAGGTCAC  14412        C  ACA     C
                                GGCCACA CC   TGGAGG CAC
                                ||||||| ||   |||||| |||
                                TCGGTGT GG   ACTTCC GTG
                                   A  A__      A
GAM549   LOC219347 5'  AGGCCCTGGGATGGAGGCCA   14413       ACACCCAC
                                AGGCC        ATGGAGGCCA
                                |||||        ||||||||||
                                TCCGG        TACCTCCGGT
                                  GACCC___
GAM549   LOC219700 5'  AGGCAGCATCCACATGGAGGC  14414      CA  C
                                AGGC  CA CCACATGGAGGC
                                ||||  || ||||||||||||
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                                TCCG  GT GGTGTACCTCCG
                                  TC  A
GAM549  LOC219731 5'  GGCCGGGTAAGCAGGAGGCCAC 14415     ACACCCA  T
                                GGCC      CA GGAGGCCAC
                                ||||      || |||||||||
                                CCGG      GT CCTCCGGTG
                                  CCCATTC  _
GAM549  LOC220114 5'  GGCTCCACTCACGCAGTCAC   14416    CA   CCA    G  GC
                                GGC  CAC   CATG AG  CAC
                                |||  |||   |||| ||  |||
                                CCG  GTG   GTGC TC  GTG
                                  AG   A__    G  A_
GAM549  LOC221486 5'  GCCACACCTGCAGGCC      14417        CACA  G
                                GCCACACC    TG AGGCC
                                ||||||||    || |||||
                                CGGTGTGG    AC TCCGG
                                     _____  G
GAM549  LOC222008 3'  GGGTGCACCCACATGCTTTGAG 14418    CCA        _____
                                GG   CACCCACATG    GAG
                                ||   ||||||||||    |||
                                CC   GTGGGTGTAC    CTC
                                 CAC         GAAA
GAM549  LOC222057 3'  AGGCCGGGCCTGTAGAGGCC   14419      ACA  CACA
                                AGGCC   CC    TGGAGGCC
                                |||||   ||    ||||||||
                                TCCGG   GG    ATCTCCGG
                                   CCC  AC__
GAM549  LOC222255 3'  GGCCACACACTGGGC       14420        CC  A   AG
                                GGCCACAC  AC TGG  GC
                                ||||||||  || |||  ||
                                CCGGTGTG  TG ACC  CG
                                     __  _  __
GAM549  LOC253001 3'  GGTAGCACCCAGGCCGAGGCCA 14421    CCA     CATG
            C                    GG   CACCCA    GAGGCCAC
                                ||   ||||||    ||||||||
                                CC   GTGGGT    CTCCGGTG
                                 ATC     CCGG
GAM549  LOC254105 3'  GGCCACACCTGCAGGC      14422         CACA  G
                                GGCCACACC    TG AGGC
                                |||||||||    || ||||
                                CCGGTGTGG    AC TCCG
                                     _____  G
GAM549  LOC254848 3'  GGCCAGACCCACACGCTGC    14423      C       GAG
                                GGCCA ACCCACATG   GC
                                ||||| |||||||||   ||
                                CCGGT TGGGTGTGC   CG
                                   C       GA_
GAM549  LOC257095 5'  AGGCCACAGGGGGATGGAGGC  14424        CCCAC
                                AGGCCACA    ATGGAGGC
                                ||||||||    ||||||||
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                                TCCGGTGT    TACCTCCG
                                    CCCCC
GAM549  LOC257451 3'  GGCCACACCCCATGCCTGC   14316         A   GAG
                                GGCCACACCC CATG   GC
                                |||||||||| ||||   ||
                                CCGGTGTGGG GTAC   CG
                                     _   GGA
GAM549  LOC51063  3'  AGGCTGCACTGGAGGCCA    14425     CA   CCACA
                                AGGC  CAC    TGGAGGCCA
                                ||||  |||    |||||||||
                                TCCG  GTG    ACCTCCGGT
                                  AC  _____
GAM549  LOC90050  3'  AGGCCACACTGTGGCCCAGCCA 14426        CCACA   A__
          C                      AGGCCACAC    TGG   GGCCAC
                                |||||||||    |||   ||||||
                                TCCGGTGTG    ACC   TCGGTG
                                     AC___   GGG
GAM549  LOC90637  5'  AGGCACACCCACACCC      14427      C        GGAGG
                                AGGC ACACCCACAT    CC
                                |||| ||||||||||    ||
                                TCCG TGTGGGTGTG    GG
                                  _        _____
GAM549  LOC91149  3'  AAGCCACATTCACAGTTACGTG 14428    CC   A__________   AGG
          GCCTCCA                 ACA  CAC        TGG   CCA
                                |||  |||        |||   |||
                                TGT  GTG        ACC   GGT
                                  AA   TCAATGIIIC   GGA
GAM549  LOC91663  5'  AAGCCACACTTGGAACAGGC   14429        CCACA   ___
                                AGGCCACAC    TGGA   GGC
                                |||||||||    ||||   |||
                                TTCGGTGTG    ACCT   CCG
                                     A____    TGT
GAM549  LOC92391  3'  AGGCCACACCCTGGCAGTCAC  14430         ACA   A  C
                                AGGCCACACCC   TGG GG CAC
                                ||||||||||   ||| || |||
                                TCCGGTGTGGG   ACC TC GTG
                                     ___   G  A
GAM550  ADAM22    3'  ACAATTGTCCTTGTATGCTAA  14433         C  CTC
                                ACAATTGTTC TG   GTTAA
                                ||||||||| ||   |||||
                                TGTTAACAGG AC   CGATT
                                     A  ATA
GAM550  ADAM22    3'  ACAATTGTCCTTGTATGCTAA  14433         C  CTC
                                ACAATTGTTC TG   GTTAA
                                ||||||||| ||   |||||
                                TGTTAACAGG AC   CGATT
                                     A  ATA
GAM550  STK38L    3'  CAATTCTTCCCCATTA      14434       G    GCT
                                CAATT TTCCT   CGTTA
                                ||||| |||||   |||||
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                                GTTAA AAGGG   GTAAT
                                  G    ___
GAM550  LOC151098 5'  ATTGTTCCAACGGTTAA     14435        T  TC
                                ATTGTTCC GC  GTTAA
                                |||||||| ||  |||||
                                TAACAAGG TG  CAATT
                                    T  C_
GAM550  LOC203221 5'  AATTGTTCCTCTGGTGTTA   14436         G  C__
                                AATTGTTCCT CT   GTTA
                                |||||||||| ||   ||||
                                TTAACAAGGA GA   CAAT
                                     _  CCA
GAM551  HOXD4    3'  TTGGAGCTTTTCCACACCT    14439        CC   CTAA
                                TTGGAGCT  TCC    ATGCCT
                                ||||||||  |||    ||||||
                                AACCTCGA  AGG    TGTGGA
                                    AA  _____
GAM551  C20orf42  3'  TTGGAGCTTTTGCCTTATCCTT 14440        CCTC   AAATG
                                TTGGAGCT    CCT    CCTT
                                ||||||||    |||    ||||
                                AACCTCGA    GGA    GGAA
                                    AAAC   ATA__
GAM551  KIAA0555 3'  TTGGAGCTGTTCTTGAGCCTT  14441        CC  CCTAAAT
                                TTGGAGCT  TC     GCCTT
                                ||||||||  ||     |||||
                                AACCTCGA  AG     CGGAA
                                    CA  AACT___
GAM551  NUDT11   3'  AGCCTCTTTCCTAAATGCCTT  14442     TC  C_
                                AGC  CT  CCTAAATGCCTT
                                |||  ||  ||||||||||||
                                TCG  GA  GGATTTACGGAA
                                  GA  AA
GAM551  SYNPO2   3'  TTGGAGCTGTCATAAATGC    14443        CC  CC
                                TTGGAGCT  TC  TAAATGC
                                ||||||||  ||  |||||||
                                AACCTCGA  AG  ATTTACG
                                    C_  T_
GAM551  LOC115509 3'  CTGGGGCTCCTCCTTCCC     14444      A       CTAAATG
                                TTGG GCTCCTCC      CCT
                                |||| ||||||||      |||
                                GACC CGAGGAGG      GGG
                                  C       AA_____
GAM551  LOC124222 3'  TCGGGGCTCCTTCCCCTCCTT  14445      A     _   AAATG
                                TTGG GCTCCT CCCT    CCTT
                                |||| |||||| ||||    ||||
                                AGCC CGAGGA GGGG    GGAA
                                  C     A   A____
GAM551  LOC148760 3'  TTGGGGCTTCTCCCTCAGC    14446      A  C     AAAT
                                TTGG GCT CTCCCT    GC
                                |||| ||| ||||||    ||
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                                AACC CGA GAGGGA    CG
                                  C   A     GT__
GAM551  LOC149773 5'  TTGTGGCTCCTGAATGCCT   14447     GA     CCCTA
                                TTG  GCTCCT    AATGCCT
                                |||  ||||||    |||||||
                                AAC  CGAGGA    TTACGGA
                                  AC     C____
GAM551  LOC165741 5'  TTGGAGCTCCCCTTGGCCT   14448          CCTAAAT
                                TTGGAGCTCCTC      GCCT
                                ||||||||||||      ||||
                                AACCTCGAGGGG      CGGA
                                       AAC____
GAM551  LOC199986 5'  CTGGAGCTTCGGGTAAAATGCC 14449        CCTCCCT
              TT                  TTGGAGCT      AAATGCCTT
                                ||||||||      |||||||||
                                GACCTCGA      TTTACGGAA
                                     AGCCCAT
GAM552  IGF1     3'  TGGTGTGCTTCTTGACGACTTG 14452    A  GA        TC__
              CT                  TG TG  CTTCTTGGCG    GCT
                                || ||  ||||||||||    |||
                                AC AC  GAAGAACTGC    CGA
                                 C  AC         TGAA
GAM552  KIP2     3'  TGGTGGACTTCTAGGCCCCTAC 14453    A       T   G  G
                                TG TGGACTTCT GGC TC CTAC
                                || ||||||||| ||| || ||||
                                AC ACCTGAAGA CCG GG GATG
                                 C        T   _  _
GAM552  NXF2     5'  TGATGGACTTCCTGAGACACC  14454            CGT
                                TGATGGACTTCTTGG   CGCT
                                ||||||||||||||   ||||
                                ACTACCTGAAGGACT   GTGG
                                         CT_
GAM552  TRIM9    3'  TGGTGAATTTCTTGGCTCAC   14455    A   C       G
                                TG TGGA TTCTTGGC TCGC
                                || |||| |||||||| ||||
                                AC ACTT AAGAACCG AGTG
                                 C    A       _
GAM552  CXorf12   3'  TGAGGGGCTTCTTGGTGT    14456     T  A       C
                                TGA GG CTTCTTGG GT
                                ||| || |||||||| ||
                                ACT CC GAAGAACC CA
                                  C  C       A
GAM552  DHRS2    5'  TGATGGGTTCTTGGCCTCAC   14457       AC       G
                                TGATGG  TTCTTGGC TCGC
                                ||||||  |||||||| ||||
                                ACTACC  AAGAACCG AGTG
                                    C_       G
GAM552  DKFZP434F0318 3'  TAATGGGCTTTTAGTGTTAC   14458       A   C    C  CG
                                TGATGG CTT TTGG GT  C
                                |||||| ||| |||| ||  |
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                                ATTACC GAA AATC CA  G
                                   C   _    A  AT
GAM552  FLJ23441  5'  GATGGACTTTTTATCAGCTGC  14459        C   GC_  C
                                GATGGACTT TTG   GT GC
                                ||||||||| |||   || ||
                                CTACCTGAA AAT   CG CG
                                     A   AGT  A
GAM552  PRO0618   3'  TGATGGACTACTTGGCCTA    14460        T     GTCG
                                TGATGGACT CTTGGC    CTA
                                ||||||||| ||||||    |||
                                ACTACCTGA GAACCG    GAT
                                     T     _____
GAM552  STX1B2    3'  TGATGGACTGCTGTGTTAC    14461        T  T GC  CG
                                TGATGGACT CT G  GT  C
                                ||||||||| || |  ||  |
                                ACTACCTGA GA C  CA  G
                                     C  _ A_  AT
GAM552  LOC152283 3'  TGATGGGCTTCTTGGTGATGC  14462       A       CGTC
                                TGATGG CTTCTTGG    GC
                                |||||| ||||||||    ||
                                ACTACC GAAGAACC    CG
                                   C       ACTA
GAM552  LOC221895 3'  TGAGGATTTCTTGGCACA    14463     T   C       T
                                TGA GGA TTCTTGGCG CG
                                ||| ||| ||||||||| ||
                                ACT CCT AAGAACCGT GT
                                  _   A       _
GAM553  ABCC1     5'  CCGGTTGCTGGCGCGGGCGGC  14466       CCTCCA    A
                                CCGGTTGT     CGGGC GC
                                ||||||||     ||||| ||
                                GGCCAACG     GCCCG CG
                                     ACCGC_    C
GAM553  ABCC1     5'  CCGGTTGCTGGCGCGGGCGGC  14466       CCTCCA    A
                                CCGGTTGT     CGGGC GC
                                ||||||||     ||||| ||
                                GGCCAACG     GCCCG CG
                                     ACCGC_    C
GAM553  ABCC1     5'  CCGGTTGCTGGCGCGGGCGGC  14466       CCTCCA    A
                                CCGGTTGT     CGGGC GC
                                ||||||||     ||||| ||
                                GGCCAACG     GCCCG CG
                                     ACCGC_    C
GAM553  ARHGEF6   3'  AACTGAAAGGCCTCTACGGGCA 14467     C  TTGT    C
          GC                    AGC GG    CCTC ACGGGCAGC
                                ||| ||    |||| |||||||||
                                TTG CT    GGAG TGCCCGTCG
                                  A  TTCC    A
GAM553  COL18A1   3'  AGCCAGCCTGTCCATGGGCAG  14468       GTCC    C
                                AGCCGGTT    TCCA GGGCAG
                                ||||||||    |||| ||||||
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                                TCGGTCGG   AGGT CCCGTC
                                    AC__   A
GAM553  COL18A1  3'  AGCCAGCCTGTCCATGGGCAG  14468       GTCC   C
                                AGCCGGTT   TCCA GGGCAG
                                ||||||||   |||| ||||||
                                TCGGTCGG   AGGT CCCGTC
                                    AC__   A
GAM553  COL18A1  3'  AGCCAGCCTGTCCATGGGCAG  14468       GTCC   C
                                AGCCGGTT   TCCA GGGCAG
                                ||||||||   |||| ||||||
                                TCGGTCGG   AGGT CCCGTC
                                    AC__   A
GAM553  DDX3     5'  GCCCTCGCTCTTCCGCGGGTAG 14469    GG  TC _ A   C
          C                      GCC  TTG  CT CC CGGG AGC
                                |||  |||  || || |||| |||
                                CGG  AGC  GA GG GCCC TCG
                                  G_   GA  A  C   A
GAM553  DDX3     5'  GCCCTCGCTCTTCCGCGGGTAG 14469    GG  TC _ A   C
          C                      GCC  TTG  CT CC CGGG AGC
                                |||  |||  || || |||| |||
                                CGG  AGC  GA GG GCCC TCG
                                  G_   GA  A  C   A
GAM553  FOXF2    3'  AGCGGTTGTCCTTCTTCCAGC  14470     C       CCACGGG
                                AGC GGTTGTCCT      CAGC
                                ||| |||||||||      ||||
                                TCG CCAACAGGA      GTCG
                                  _       AGAAG__
GAM553  IGF1R    3'  AGCTGTCTCCCGCGGGCAG   14471       CT  A
                                GGTTGTC  CC CGGGCAG
                                |||||||  || |||||||
                                TCGACAG  GG GCCCGTC
                                    AG  C
GAM553  PACE4    3'  GCCTGCCCTCTGTGGGCAGC   14472    GGT     CAC
                                GCC   TGTCCTC   GGGCAGC
                                |||   |||||||   |||||||
                                CGG   ACGGGAG   CCCGTCG
                                  ___      ACA
GAM553  PACE4    3'  GCCTGCCCTCTGTGGGCAGC   14472    GGT     CAC
                                GCC   TGTCCTC   GGGCAGC
                                |||   |||||||   |||||||
                                CGG   ACGGGAG   CCCGTCG
                                  ___      ACA
GAM553  PRM1     5'  AGCAGGTGGAACTCTGTGGGCA 14473    C   TGTC   CAC
          GC                     AGC GGT   CTC   GGGCAGC
                                |||  |||   |||   |||||||
                                TCG CCA   GAG   CCCGTCG
                                  T   CCTT   ACA
GAM553  B3GAT3   3'  GCTGCTTGTCCCCAGCCTGTGG 14474    CGG    T   C_____
          GCAG                     GC   TTGTCC CCA     GGGCAG
                                ||   |||||| |||     ||||||
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                                CG   AACAGG GGT     CCCGTC
                                 ACG     _  CGGACA
GAM553  CARD9    3'  AGCTGGGTGTCCTCCAGG    14475     C  T       C
                                AGC GG TGTCCTCCA GG
                                ||| || |||||||||| ||
                                TCG CC ACAGGAGGT CC
                                  A  C       _
GAM553  DJ37E16.5 3'  AGCCGGTTGTGCTTAACATGGC 14476          C  CC  _
                                AGCCGGTTGT CT  ACG GGC
                                |||||||||| ||  ||| |||
                                TCGGCCAACA GA  TGT CCG
                                      C  AT   A
GAM553  FLJ22390  5'  AGCTGGTTATCCACTGGGCGGC 14477     C       TCCAC    A
                                AGC GGTTGTCC    GGGC GC
                                ||| ||||||||    |||| ||
                                TCG CCAATAGG    CCCG CG
                                  A       TGA__    C
GAM553  FLJ23056  3'  GCTGCCCTAGCTTCATGGGCAG 14478        C____  C
                                GTTGTCCT    CA GGGCAG
                                ||||||||    || ||||||
                                CGACGGGA    GT CCCGTC
                                     TCGAA  A
GAM553  HS6ST    5'  GCCAGGTTGTACGGGCAG    14479    _     CCTCC
                                GCC GGTTGT    ACGGGCAG
                                ||| ||||||    ||||||||
                                CGG CCAACA    TGCCCGTC
                                  T    ______
GAM553  KCNT1    3'  GCCCGAGCCGTTCTCCGTGGGC 14480     __     C    AC
            AG                    GCC  GGTTGT CTCC  GGGCAG
                                ||| ||||||| ||||  ||||||
                                CGG  TCGGCA GAGG  CCCGTC
                                  GC     A    CA
GAM553  KIAA0769  3'  AGCTGGTTTCCTCCACGAGC   14481     C    G
                                AGC GGTT TCCTCCACGGGC
                                ||| |||| ||||||||||||
                                TCG CCAA AGGAGGTGCTCG
                                  A   _
GAM553  KIAA1000  3'  AGCTGTTGTCCTTTCAAAGC   14482     CG       CCAC
                                AGC  GTTGTCCT    GGGC
                                |||  ||||||||    ||||
                                TCG  CAACAGGA    TTCG
                                  A_       AAGT
GAM553  KIAA1828  5'  AGCCAGGACTCCGTGGGCAGC  14483       TTGTC    AC
                                AGCCGG    CTCC  GGGCAGC
                                ||||||    ||||  |||||||
                                TCGGTC    GAGG  CCCGTCG
                                   CT____    CA
GAM553  MGC3130   3'  GGTTGTCCTGCGTTGGGGCAG  14484        CCAC__
                                GGTTGTCCT     GGGCAG
                                |||||||||     ||||||
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                                CCAACAGGA     CCCGTC
                                     CGCAAC
GAM553  PLA2G6   3'  AGTCAGTTGTCCTTGACAG   14485    C        CC
                                AG CGGTTGTCCT  ACGG
                                || ||||||||||  ||||
                                TC GTCAACAGGA  TGTC
                                 A         AC
GAM553  PP5395   5'  CAGTCGGTGATCACGGGCAGC  14486       TCCTC
                                CGGTTG    CACGGGCAGC
                                ||||||    ||||||||||
                                GTCAGC    GTGCCCGTCG
                                   CACTA
GAM553  RHOBTB2  3'  AGCCGCTTGTCCTCCAGC    14487      G        CGG
                                AGCCG TTGTCCTCCA   GC
                                ||||| ||||||||||   ||
                                TCGGC AACAGGAGGT   CG
                                   G        ___
GAM553  SAST     5'  GGCCATCTCTACGGGCAG    14488     TG  C  C
                                GGT  TC TC ACGGGCAG
                                |||  || || ||||||||
                                CCG  AG AG TGCCCGTC
                                  GT  _  A
GAM553  LOC115051 5'  GCCAGGTTGTACGGGCAG    14479     _     CCTCC
                                GCC GGTTGT    ACGGGCAG
                                ||| ||||||    ||||||||
                                CGG CCAACA    TGCCCGTC
                                  T     ______
GAM553  LOC143458 3'  AGCCGGTGCACGGGCA      14489        T TCCTC
                                AGCCGGT G    CACGGGCA
                                ||||||| |    ||||||||
                                TCGGCCA C    GTGCCCGT
                                   _ ______
GAM553  LOC145134 5'  ACCTGGTATCTCACGGGCAG   14490     _   T   CTC
                                GCC GGT GTC   CACGGGCAG
                                ||| ||| |||   |||||||||
                                TGG CCA TAG   GTGCCCGTC
                                  A   _   A__
GAM553  LOC145501 3'  AGCCGGCTGTCCTCGTCATAGC 14491             CACG_
                                AGCCGGTTGTCCTC    GGC
                                ||||||||||||||    |||
                                TCGGCCGACAGGAG    TCG
                                      CAGTA
GAM553  LOC147341 3'  AGCCGGCTGTTAAAGGGGCAGC 14492          CCTCCAC
                                AGCCGGTTGT      GGGCAGC
                                ||||||||||      |||||||
                                TCGGCCGACA      CCCGTCG
                                      ATTTC__
GAM553  LOC147645 5'  GCCCGGTCCGACCGCGGGCAGC 14493     GGTT   T_  A
                                GCC    GTCC  CC CGGGCAGC
                                |||    ||||  || ||||||||
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                                CGG   CAGG  GG GCCCGTCG
                                  GC__   CT  C
GAM553  LOC155179 5'  GGTCTGGGAATCCGCGGGCAGC 14494     GTCC__  A
                                GGTT     TCC CGGGCAGC
                                ||||     ||| ||||||||
                                CCAG     AGG GCCCGTCG
                                  ACCCTT   C
GAM553  LOC90050  5'  GGCTGATCTCAGGCTGCGGGCA 14495     TC   CA____
           GC                   GGTTG  CTC     CGGGCAGC
                                |||||  |||     ||||||||
                                CCGAC  GAG     GCCCGTCG
                                  TA   TCCGAC
GAM553  LOC93624  5'  AGCCTGTTGTCCTCTGGC    14496     G       CACG
                                AGCC GTTGTCCTC    GGC
                                |||| |||||||||    |||
                                TCGG CAACAGGAG    CCG
                                  A       A___
GAM554  PSEN1     3'  TCTCCACTGGCTGTTGCTGAGG 14499     GTTGCC   C
           CT                    TCTC     CTG TGCTGAGGCT
                                ||||     ||| ||||||||||
                                AGAG     GAC ACGACTCCGA
                                  GTGACC   A
GAM554  SLA2      3'  TCTCGTTGACTCTAGGG     14500       CCCT   G   A
                                TCTCGTTG    GCT CTG GG
                                ||||||||    ||| ||| ||
                                AGAGCAAC    TGA GAT CC
                                     _____   _   C
GAM554  TCF8      3'  TCGTTGCCTTCCAGAGGCT    14501       CTG  GCT
                                TCGTTGCC   CT   GAGGCT
                                ||||||||   ||   ||||||
                                AGCAACGG   GG   CTCCGA
                                    AA_  T__
GAM554  TNC       5'  GCTGGGTGCTGCTGGGGCT    14502     CCC       A
                                GTTG   TGCTGCTG GGCT
                                ||||   |||||||| ||||
                                CGAC   ACGACGAC CCGA
                                  CC_       C
GAM554  AP3D1     3'  TCTCCTTGCCCTGCCTGGTGGG 14503     G       GC_  A_
           GGCT                   TCTC TTGCCCTGCT   TG  GGCT
                                ||||  ||||||||||   ||  ||||
                                AGAG AACGGGACGG   AC  CCGA
                                  G        ACC  CC
GAM554  BCDO2     3'  ATTGTGTGCTGCTGAGG     14504     CCC
                                GTTG   TGCTGCTGAGG
                                ||||   ||||||||||
                                TAAC   ACGACGACTCC
                                  AC_
GAM554  FLJ14596  5'  TCGTTGCTCTTGCTGCTGGGGC 14505       C  _      A
           T                     TCGTTGC CT GCTGCTG GGCT
                                |||||||  ||  |||||||  ||||
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                                AGCAACG GA CGACGAC CCGA
                                    A A     C
GAM554  HRMT1L3  3'  TCTCGTTGCTCTCTGCAGC   14506       C  G   TGA
                                TCTCGTTGC CT CTGC   GGC
                                ||||||||| || ||||   |||
                                AGAGCAACG GA GACG   TCG
                                    A  _   ____
GAM554  RAI17    3'  CCTCGTTTTTGCTGAGG    14507       GCCCTGC
                                TCTCGTT     TGCTGAGG
                                |||||||     ||||||||
                                GGAGCAA     ACGACTCC
                                   AA_____
GAM554  LOC158235 3'  TCCTTGCCTCTAAACTGAGGCT 14508   G    _   CT
                                TC TTGCC CTG  GCTGAGGCT
                                || ||||| |||  |||||||||
                                AG AACGG GAT  TGACTCCGA
                                 G    A  T_
GAM554  LOC253258 3'  TCTCTTGCCCTGCTCCTTAG   14509     G       G  G
                                TCTC TTGCCCTGCT CT AG
                                |||| |||||||||| || ||
                                AGAG AACGGGACGA GA TC
                                  _       G  A
GAM555  ACK1     5'  CTGCACCCCGGGCAGCCAAT   14512        CT_  A
                                CTGCACCTC   CA CCAAT
                                |||||||||   || |||||
                                GACGTGGGG   GT GGTTA
                                     CCC  C
GAM555  ANKRD3   3'  CTGCACCTCTTCCCCAA     14513        C  AA
                                CTGCACCTC TC  CCAA
                                ||||||||| ||  ||||
                                GACGTGGAG AG  GGTT
                                     A  G_
GAM555  CLC      3'  TACTGTACCTCCTCCCCA    14514      C      AA
                                TACTG ACCTCCTC  CCA
                                ||||| ||||||||  |||
                                ATGAC TGGAGGAG  GGT
                                   A      G_
GAM555  DYRK1A   3'  CTGTGACCTTCAACCAAT    14515    C_   CC
                                CTG  ACCT  TCAACCAAT
                                |||  ||||  |||||||||
                                GAC  TGGA  AGTTGGTTA
                                  AC   __
GAM555  DYRK1A   3'  CTGTGACCTTCAACCAAT    14515    C_   CC
                                CTG  ACCT  TCAACCAAT
                                |||  ||||  |||||||||
                                GAC  TGGA  AGTTGGTTA
                                  AC   __
GAM555  DYRK1A   3'  CTGTGACCTTCAACCAAT    14515    C_   CC
                                CTG  ACCT  TCAACCAAT
                                |||  ||||  |||||||||
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                              GAC  TGGA  AGTTGGTTA
                                AC   __
GAM555  FANCC    3'  CACTGCACCCAGCCAGGCCAAT 14516         CC   A_
                              TACTGCACCT  TCA  CCAAT
                              ||||||||||  |||  |||||
                              GTGACGTGGG  GGT  GGTTA
                                    TC   CC
GAM555  MEN1     5'  TACTGAAGAGCCTCAACCAAT  14517      CACCT
                              TACTG    CCTCAACCAAT
                              |||||    ||||||||||
                              ATGAC    GGAGTTGGTTA
                                 TTCTC
GAM555  TEM8     3'  TACTGGCATTGCCAACCAAT   14518      _  CCTCC
                              TACTG CA    TCAACCAAT
                              ||||| ||    |||||||||
                              ATGAC GT    GGTTGGTTA
                                 C  AAC__
GAM555  EFA6R    3'  CTGCAGCTCCTCAAGGGCC   14519      C       ___
                              CTGCA CTCCTCAA   CC
                              ||||| ||||||||   ||
                              GACGT GAGGAGTT   GG
                                 C       CCC
GAM555  FLJ10375 5'  TACTGCACTTTCCCCTCAA   14520        ___
                              TACTGCAC   CTCCTCAA
                              ||||||||   ||||||||
                              ATGACGTG   GGGGAGTT
                                   AAA
GAM555  FLJ20303 3'  TACTGCACCTTAAGACCAAT   14521         CCTCA
                              TACTGCACCT    ACCAAT
                              ||||||||||    ||||||
                              ATGACGTGGA    TGGTTA
                                    ATTC_
GAM555  KIAA0982 3'  TACTGCACCTGCACCTACC   14522         ___  CA
                              TACTGCACCT   CCT  ACC
                              ||||||||||   |||  |||
                              ATGACGTGGA   GGA  TGG
                                    CGT   __
GAM555  KIAA1979 3'  TACTGAACACAGCCAACCAAT  14523      C  CTCC
                              TACTG AC    TCAACCAAT
                              ||||| ||    |||||||||
                              ATGAC TG    GGTTGGTTA
                                 T  TGTC
GAM555  MGC12217 5'  TACTGCACTTTCCCCTCAA   14520        ___
                              TACTGCAC   CTCCTCAA
                              ||||||||   ||||||||
                              ATGACGTG   GGGGAGTT
                                   AAA
GAM555  RI58     3'  ACTGCACCCCATGCCAAT    14524         T  TCAA
                              ACTGCACC CC    CCAAT
                              |||||||| ||    |||||
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                                TGACGTGG GG    GGTTA
                                    _  TAC_
GAM555  LOC116068 3'  TACTGACTTCCCAACCA     14525       C  C   T
                                TACTG AC TCC CAACCA
                                ||||| || ||| ||||||
                                ATGAC TG AGG GTTGGT
                                   _  A   _
GAM555  LOC150225 3'  CACTGCACCTCTTCCCC     14526           C  AA
                                TACTGCACCTC TC  CC
                                |||||||||||| ||  ||
                                GTGACGTGGAG AG  GG
                                      A  G_
GAM556  LENG4    5'  CACGGTTATTAGGGCAGTGGT  14529      _         TAACA
                                CACG TTATTAGGGC     GGT
                                |||| ||||||||||     |||
                                GTGC AATAATCCCG     CCA
                                  C         TCA__
GAM556  SLC12A4   3'  CAGGCAAGCAGGGCTGGCAGGT 14530    C  TAT      AA
                                CA GT   TAGGGCT  CAGGT
                                || ||   |||||||  |||||
                                GT CG   GTCCCGA  GTCCA
                                 C  TTC       CC
GAM556  DKFZP434N093 3'  ACACTTATTAAAAACAGG     14531      G       GCT
                                ACAC TTATTAGG   AACAGG
                                |||| ||||||||   ||||||
                                TGTG AATAATTT   TTGTCC
                                   _      ____
GAM556  FLJ21415  3'  ACACGTCAGGATATGGCTAACA 14532         TTAG__
           GGT                    ACACGTTA     GGCTAACAGGT
                                |||||||||     ||||||||||
                                TGTGCAGT     CCGATTGTCCA
                                     CCTATA
GAM556  KIAA0057  3'  CAGTTATTAGGCAAGG      14533    C       G TAAC
                                CA GTTATTAGG C    AGG
                                || |||||||| |    |||
                                GT CAATAATCC G    TCC
                                 _        _ T____
GAM556  KIAA0544  3'  CGGGCCCCAGGGCTGGCAGGT  14534    TTA_       AA
                                CG    TTAGGGCT  CAGGT
                                ||    ||||||||  |||||
                                GC    GGTCCCGA  GTCCA
                                 CCGG       CC
GAM556  LOC120856 3'  GTTATATTAGCTAACAGGT    14535      TAG
                                GTTAT   GGCTAACAGGT
                                |||||   ||||||||||
                                CAATA   TCGATTGTCCA
                                   TAA
GAM557  ADARB1    3'  CGGAGAAAAGAGACCTAAG    14538         TAC   C
                                CGGAGAAAA   GCC AAG
                                |||||||||   ||| |||
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                                GCCTCTTTT  TGG TTC
                                     CTC  A
GAM557  ADARB1   3'  CGGAGAAAAGAGACCTAAG   14538       TAC  C
                                CGGAGAAAA  GCC AAG
                                |||||||||  ||| |||
                                GCCTCTTTT  TGG TTC
                                     CTC  A
GAM557  ATP1A2   5'  CACCAGGAGGATCCCAAGC   14539    _  AAAATACG
                                CACC GGAG      CCCAAGC
                                |||| ||||      |||||||
                                GTGG CCTC      GGGTTCG
                                  T   CTA_____
GAM557  CHS1     5'  CCGGAGAACCCCGAGC     14540      AAAT  G  A
                                CCGGAGA   AC CCC AGC
                                |||||||   || ||| |||
                                GGCCTCT   TG GGG TCG
                                    ____ _  C
GAM557  CIAS1    3'  CACCGGAAGGATCACAGAGC  14541      AAA  A  CCA
                                CACCGGAG  AT CGC  AGC
                                ||||||||  || |||  |||
                                GTGGCCTT  TA GTG  TCG
                                     CC_ _  TC_
GAM557  GDI1     3'  CAACGGGGCCATGCCCAAGCC  14542   C  AGAAAA  C
                                CA CGG     TA GCCCAAGCC
                                || |||     || |||||||||
                                GT GCC     GT CGGGTTCGG
                                 T  CCG___  A
GAM557  IGFBP5   5'  CCGGAGAAACCCTCAAGCC   14543      AAT  G  _
                                CCGGAGAA  AC CC CAAGCC
                                ||||||||  || || ||||||
                                GGCCTCTT  TG GG GTTCGG
                                    ___ _ A
GAM557  LZTS1    3'  CCTGGGGCACTGCCCAAGC   14544   _  AGAAAA  _
                                CC GG     TAC GCCCAAGC
                                || ||     ||| ||||||||
                                GG CC     GTG CGGGTTCG
                                 A  CC____  A
GAM557  PLA2G10  5'  CACCGGAGGCACCAAG     14545      AAAATAC  _
                                CACCGGAG      GC CCAAG
                                ||||||||      || |||||
                                GTGGCCTC      CG GGTTC
                                    ________ T
GAM557  PPP3CB   3'  CACTGGAAATTGCCCCAAGCC  14546    C    AAATACG
                                CAC GGAGA     CCCAAGCC
                                ||| |||||     ||||||||
                                GTG CCTTT     GGGTTCGG
                                  A    AACG___
GAM557  STK6     3'  CACCAGAGAAAAAATACAAG   14547         TACGCC
                                CACCGGAGAAAA     CAAG
                                ||||||||||||     ||||
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                                GTGGTCTCTTTT     GTTC
                                      TTAT__
GAM557  TEM8     3' GGAGACCATAGCCCAAGCC   14548      AA  C
                                GGAGA  ATA GCCCAAGCC
                                |||||  ||| |||||||||
                                CCTCT  TAT CGGGTTCGG
                                   GG  _
GAM557  VWF      5' GGAGATAAAGCCCAAGC     14549      A  TAC
                                GGAGA AA   GCCCAAGC
                                ||||| ||   ||||||||
                                CCTCT TT   CGGGTTCG
                                   A  T__
GAM557  C21orf69  3' CGGAGAAAGTGTGGGCAGAAGC 14550        ATAC__  CC
           C                     CGGAGAAA     GC  AAGCC
                                ||||||||     ||  |||||
                                GCCTCTTT     CG  TTCGG
                                     CACACC  TC
GAM557  FACTP140 3' GGAGAAAATAACCGAGCC    14551         C   CA
                                GGAGAAAATA GCC  AGCC
                                |||||||||| |||  ||||
                                CCTCTTTTAT TGG  TCGG
                                      _  C_
GAM557  FLJ00007  3' CCGGAGGGAGGGGCCCAAGCC  14552       AAAATAC
                                CCGGAG      GCCCAAGCC
                                ||||||      |||||||||
                                GGCCTC      CGGGTTCGG
                                   CCTCCC_
GAM557  FLJ11939  5' CCGGAGAAAGCCCGGGC     14553        ATAC   AA
                                CCGGAGAAA   GCCC  GC
                                |||||||||   ||||  ||
                                GGCCTCTTT   CGGG  CG
                                     ____   CC
GAM557  FLJ12806  5' CCGAGGAGCCGCCCAAGCC   14554     GA  AAATA
                                CCG  GA    CGCCCAAGCC
                                |||  ||    ||||||||||
                                GGC  CT    GCGGGTTCGG
                                  TC  CG___
GAM557  FLJ13491  5' CGGAGAAAGATGCTCCTGGGCC 14555        ATAC  _  AA_
                                CGGAGAAA   GC CC   GCC
                                ||||||||   || ||   |||
                                GCCTCTTT   CG GG   CGG
                                     CTA_  A  ACC
GAM557  FLJ20147  3' CACTGGAGAAAAAAATATAATC 14556     C       TACGCC___
           AAGCC                  CAC GGAGAAAA       CAAGCC
                                ||| ||||||||       ||||||
                                GTG CCTCTTTT       GTTCGG
                                  A       TTTATATTA
GAM557  FLJ20898  5' CCGGAGAAAGCCAAG       14557         ATAC  C
                                CCGGAGAAA   GCC AAG
                                |||||||||   ||| |||
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                                GGCCTCTTT   CGG TTC
                                     _____  _
GAM557  FLJ32894  3'  CACCGGAAAGTAGACCTGGGCC 14558        AAA  C   CAA
                                CACCGGAGA   TA GCC   GCC
                                |||||||||   || |||   |||
                                GTGGCCTTT   AT TGG   CGG
                                     C__  C   ACC
GAM557  FREQ     3'  CACCGAAGGGGTCCACATGCTT 14559        AAAA_  __ CC
          AAGCC                    CACCGGAG    TAC  GC  AAGCC
                                |||||||||    |||  ||  |||||
                                GTGGCTTC    GTG  CG  TTCGG
                                     CCCAG   TA  AA
GAM557  KCNH8    3'  CACTGGGAAAGGACACACCCA  14560     C_    AA
                                CAC  GGAGA  ATACGCCCA
                                |||  |||||  |||||||||
                                GTG  CCTTT  TGTGTGGGT
                                  AC    CC
GAM557  MGC14839  3'  CACTGAGGAAATGGCCCAAGCC 14561     CG   A    AC
                                CAC  GAG AAAT  GCCCAAGCC
                                |||  ||| ||||  |||||||||
                                GTG  CTC TTTA  CGGGTTCGG
                                  A_   C    C_
GAM557  MIL1     3'  GGAAAAAATATACTAGCC     14562          CG CCA
                                GGAGAAAATA  C   AGCC
                                ||||||||||  |   ||||
                                CCTTTTTTAT  G   TCGG
                                     AT A__
GAM557  MSP      3'  CACCGAAGACGGTCCAGGC    14563         AAATA  C_   A
                                CACCGGAGA    CG  CCA GC
                                |||||||||    ||  ||| ||
                                GTGGCTTCT    GC  GGT CG
                                     _____  CA   C
GAM557  SNAP29   3'  GAGAAAATAATAATGCCGAGC  14564         C____   CA
                                GAGAAAATA    GCC  AGC
                                |||||||||    |||  |||
                                CTCTTTTAT    CGG  TCG
                                     TATTA   C_
GAM557  LOC144667 5'  CCGGAGAAGGCCAACC      14565         AATAC   CA
                                CCGGAGAA    GCC  AGCC
                                ||||||||    |||  ||||
                                GGCCTCTT    CGG  TTGG
                                     C____   __
GAM557  LOC149506 3'  CGGAGAAGCCCAAGC       14566         AATAC
                                CGGAGAA    GCCCAAGC
                                |||||||    ||||||||
                                GCCTCTT    CGGGTTCG
                                     _____
GAM557  LOC149773 5'  CACCAGAGTCCCAGTGCC    12110         AAAATACG   A_
                                CACCGGAG      CCCA  GCC
                                ||||||||      ||||  |||
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                                GTGGTCTC       GGGT  CGG
                                    A_______    CA
GAM557  LOC150271 5'  CACCAGAGGAAATTCGGGGAGC 14567        A    A  CCCA
            C                    CACCGGAG AAAT CG    AGCC
                                 |||||||| |||| ||    ||||
                                 GTGGTCTC TTTA GC    TCGG
                                     C    A  CCC_
GAM557  LOC164397 5'  CACCGGAGAGTTTCCAAGC    14568         AAATACGC
                                 CACCGGAGA       CCAAGC
                                 |||||||||       ||||||
                                 GTGGCCTCT       GGTTCG
                                     CAAA____
GAM557  LOC221491 3'  CCTGGGGATTTGTGCCCAAGCC 14569    _  A  AAATAC
                                 CC GG GA     GCCCAAGCC
                                 || || ||     |||||||||
                                 GG CC CT     CGGGTTCGG
                                  A  C  AAACA_
GAM557  LOC90371  3'  AAAGAAAATATGTTCAAGCC   14570         CGCC
                                 GGAGAAAATA    CAAGCC
                                 ||||||||||    ||||||
                                 TTTCTTTTAT    GTTCGG
                                     ACAA
GAM557  LOC91012  5'  GGAGAAAACCCACGGGCC    14571        ATAC    A__
                                 GGAGAAA    GCCCA   GCC
                                 |||||||    |||||   |||
                                 CCTCTTT    TGGGT   CGG
                                     _____    GCC
GAM558  RABIF     3'  TAGTACATAAGCATCTTTTGT  14574         C  AATT    C
                                 TAGTACATA AG    TCTTT GT
                                 ||||||||| ||    ||||| ||
                                 ATCATGTAT TC    AGAAA CA
                                     _ GT__     A
GAM558  TEC       3'  TGATACAGTTTCTTTC      14575   C     AA
                                 A ATACAG  TTTCTTTC
                                 | ||||||  ||||||||
                                 A TATGTC  AAAGAAAG
                                  C     __
GAM559  APOL1     3'  TCCTGGCCTTCTCATTGCTGG  14578        GGCG       C
                                 TCTTGGTC    TCTCATTGC GG
                                 ||||||||    ||||||||| ||
                                 AGGACCGG    AGAGTAACG CC
                                     A___        A
GAM559  KCNQ1     3'  TCCTGGGCTTTTATTGCCG    14579       TCG  GTCTC
                                 TCTTGG   GC    ATTGCCG
                                 ||||||   ||    |||||||
                                 AGGACC   CG    TAACGGC
                                     ___  AAAA_
GAM559  APOL2     3'  TCCTGGCCTTCTCATTGCTGG  14578        GGCG       C
                                 TCTTGGTC    TCTCATTGC GG
                                 ||||||||    ||||||||| ||
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                                AGGACCGG    AGAGTAACG CC
                                   A___        A
GAM559  APOL3    3'  TCCTGGCCTTCTCATTGCTGG  14578        GGCG       C
                                TCTTGGTC    TCTCATTGC GG
                                ||||||||    ||||||||| ||
                                AGGACCGG    AGAGTAACG CC
                                   A___        A
GAM559  C20orf38  3'  TCTTGGTTTGGATCCATTGCCG 14580        C_  C   T
           G                     TCTTGGT  GG GTC CATTGCCGG
                                 |||||||  || ||| |||||||||
                                 AGAACCA  CC TAG GTAACGGCC
                                    AA  _  _
GAM559  KIAA0285 5'  TCTTGGTAGGTGTGATGCTGG  14581        C  C  CTCAT   C
                                TCTTGGT GG GT     TGC GG
                                ||||||| || ||     ||| ||
                                AGAACCA CC CA     ACG CC
                                   T  A  CT___   A
GAM560  ARNT2    3'  CACAGTTCACATCCATAAGAA  14584      CC   G  G
                                CACA  TCG CG TCCATAAGAA
                                ||||  ||| || ||||||||||
                                GTGT  AGT GT AGGTATTCTT
                                  CA  _  _
GAM560  CD164    3'  TCAACAGCCATAAGAAA      14585        T
                                TCGGCGG CCATAAGAAA
                                ||||||| ||||||||||
                                AGTTGTC GGTATTCTTT
                                        _
GAM560  GALNT3   3'  CTCATTTTTTGTGCCATAAGAA 14586      GCG___  _
           A                     CTCG      GT CCATAAGAAA
                                 ||||      || ||||||||||
                                 GAGT      CA GGTATTCTTT
                                   AAAAAA  C
GAM560  GJA1     3'  CACACCACAAAAATCCATGAGA 14587        T   CG     A
           AA                    CACACC CGG  GTCCAT AGAAA
                                 |||||| |||  |||||| |||||
                                 GTGTGG GTT  TAGGTA TCTTT
                                    T   TT     C
GAM560  IRS1     5'  CATCTCGGCGGGTGGAGAAA   14588    C       TCCATA
                                CA CTCGGCGG      AGAAA
                                || ||||||||      |||||
                                GT GAGCCGCC      TCTTT
                                 A       CACC__
GAM560  LOH11CR2A 5'  CCCGAGCGGTCCATGAGAAA   14589     C         A
                                CCT GGCGGTCCAT AGAAA
                                ||| |||||||||| |||||
                                GGG TCGCCAGGTA TCTTT
                                  C         C
GAM560  PSMD9    3'  ACCTCAGCGGTTTACAAA     14590           CC
                                ACCTCGGCGGT  ATAAG
                                ||||||||||  |||||
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                                TGGAGTCGCCA  TGTTT
                                      AA
GAM560  SYT4     3'  ACCTATTTCCTATAAGAAA   14591     CGGCGG  _
                                ACCT     TCC ATAAGAAA
                                ||||     ||| ||||||||
                                TGGA     AGG TATTCTTT
                                  TAA___   A
GAM560  WHSC1    5'  CATATCATTTCATCCATAAGAA 14592    CC   GCG_
                                CA  TCG    GTCCATAAGAA
                                ||  |||    ||||||||||
                                GT  AGT    TAGGTATTCTT
                                 AT   AAAG
GAM560  DKFZP566D1346 3'  CACCTTGGAATAAATAAGAAA  14593      C  C   CC
                                CACCT GG GGT  ATAAGAAA
                                ||||| || |||  ||||||||
                                GTGGA CC TTA  TATTCTTT
                                   A  _   TT
GAM560  FLJ11710  3'  ACACCCCAGCCCATAAG     14594          GGT
                                ACACCTCGGC   CCATAAG
                                ||||||||||   |||||||
                                TGTGGGGTCG   GGTATTC
                                      ___
GAM560  HSPC133   5'  CACCTCGGCCGGTGCCGGAAG  14595          _  _ AT
                                CACCTCGGC GGT CC  AAG
                                |||||||||| ||| ||  |||
                                GTGGAGCCG CCA GG  TTC
                                     G   C  CC
GAM560  KIAA0232  3'  CACACCTCTGCGGTTCCTACTG 14596         G    _ _ AA
           GAAA                    CACACCTC GCGGT CC AT  GAAA
                                ||||||||| ||||| || ||  ||||
                                GTGTGGAG CGCCA GG TG  CTTT
                                     A    A  A  AC
GAM560  KIAA1001  5'  CTCTTTGGCCACTAAGAAA   14597     GGC  T   _
                                CTC   GG CCAT AAGAAA
                                |||   || |||| ||||||
                                GAG   CC GGTG TTCTTT
                                  AAA  _    A
GAM560  KIAA1349  3'  CACCTCCAGGTTTATAAGAAA  14598       GGC   CC
                                CACCTC   GGT  ATAAGAAA
                                ||||||   |||  ||||||||
                                GTGGAG   CCA  TATTCTTT
                                   GT_   AA
GAM560  NDUFC2    3'  TCAACTGTCATAAGAAA     14599      G   C
                                TCGGC GTC ATAAGAAA
                                ||||| ||| ||||||||
                                AGTTG CAG TATTCTTT
                                   A  _
GAM560  PRO2949   3'  ACACCTCGGTGCCAGACATAAG 14600         CG  ___
                                ACACCTCGG  GTC   CATAAG
                                |||||||||  |||   ||||||
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                                TGTGGAGCC  CGG   GTATTC
                                     A_   TCT
GAM560  SEF      3'  CATCTCTTGGCCTCAATAAGAA 14601    C   GGC   _ _
             A                    CA CTC   GGTC CA TAAGAAA
                                  || |||   |||| || |||||||
                                  GT GAG   CCGG GT ATTCTTT
                                   A   AA_   A  T
GAM560  LOC129676 5'  CCTTTGCAATCCATGGGAA   14602     CG       AA
                                  CCT  GCGGTCCAT  GAA
                                  |||  |||||||||  |||
                                  GGA  CGTTAGGTA  CTT
                                    AA        CC
GAM560  LOC157562 5'  ACCTCGACCGTTGTGAGAAA   14603        G  CCATA
                                  ACCTCGGC GT    AGAAA
                                  |||||||| ||    |||||
                                  TGGAGCTG CA    TCTTT
                                       G  ACAC_
GAM561  MYH11    3'  ATGCAATTATAGCTCAT     14606     A        A
                                  ATG AATTATAGCT CGT
                                  ||| ||||||||| |||
                                  TAC TTAATATCGA GTA
                                    G         _
GAM561  MYH11    3'  ATGCAATTATAGCTCAT     14606     A        A
                                  ATG AATTATAGCT CGT
                                  ||| ||||||||| |||
                                  TAC TTAATATCGA GTA
                                    G         _
GAM561  KIAA1024  3'  TGATATTTAGCACGTCTAT   14607     A  A    T
                                  TGA ATT TAGC ACGTCTAT
                                  ||| ||| |||| ||||||||
                                  ACT TAA ATCG TGCAGATA
                                    A  _   _
GAM561  LOC148936 3'  TAACTATAATAGCTATGTCTAT 14608     AATT_      C
                                  TGA     ATAGCTA GTCTAT
                                  |||     ||||||| ||||||
                                  ATT     TATCGAT CAGATA
                                    GATAT      A
GAM561  LOC148938 3'  TAACTATAATAGCTATGTCTAT 14608     AATT_      C
                                  TGA     ATAGCTA GTCTAT
                                  |||     ||||||| ||||||
                                  ATT     TATCGAT CAGATA
                                    GATAT      A
GAM562  BAT4     5'  CCGCGCGCCCAGGTGGC     14611    A     A   TC
                                  TC CGCGCC AGGT  GGC
                                  || |||||| ||||  |||
                                  GG GCGCGG TCCA  CCG
                                   C     G   __
GAM562  CLC      3'  TCACACGCCCAGCCGG      14612          AA   T
                                  TCACGCGCC  GGT CGG
                                  |||||||||  ||| |||
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                                AGTGTGCGG  TCG GCC
                                     G_  _
GAM562  DRD1     5'  CGCGCAGCAGGGGTTCGGC   14613      __  A_
                                CGCGC  CA  GGTTCGGC
                                |||||  ||  ||||||||
                                GCGCG  GT  CCAAGCCG
                                   TC  CC
GAM562  DXYS155E 3'  CCACGCGCCGCAGCTCGGC   14614         AA
                                TCACGCGCC  GGTTCGGC
                                |||||||||  ||||||||
                                GGTGCGCGG  TCGAGCCG
                                     CG
GAM562  GAS7     3'  CCACGCGCCAAAAGGC     14615          TTC
                                TCACGCGCCAAGG  GGC
                                ||||||||||||   |||
                                GGTGCGCGGTTTT  CCG
                                      ___
GAM562  HPS4     5'  TCACGCGCCGCCCCGC     14616         AAG   G
                                TCACGCGCC  GTTC GC
                                |||||||||  ||||  ||
                                AGTGCGCGG  CGGG CG
                                     ___   G
GAM562  KNS2     5'  CCACGCGCTGTCCCCTTGGC  14617        CAAG  ____
                                TCACGCGC   GTTC   GGC
                                ||||||||   ||||   |||
                                GGTGCGCG   CAGG   CCG
                                    A___   GGAA
GAM562  MBP      3'  TCACCGCCAAAGAAGC     14618     G     TTC
                                TCAC CGCCAAGG  GGC
                                ||||  ||||||||  |||
                                AGTG GCGGTTTC  TCG
                                  _      T__
GAM562  NDRG1    3'  TCACGTTCCAGCCCAGC     14619     CG  AG
                                TCACG  CCA  GTTCGGC
                                |||||  |||  |||||||
                                AGTGC  GGT  CGGGTCG
                                   AA  __
GAM562  NFIA     5'  TCCCGCGCCGGCCCGGC     14620    A    AA
                                TC CGCGCC  GGTTCGGC
                                || ||||||  ||||||||
                                AG GCGCGG  CCGGGCCG
                                 G    __
GAM562  PLDN     5'  TCACGCGCTCGAGAGTTGGC  14621        CA_ _  C
                                TCACGCGC   AG GTT GGC
                                ||||||||   || ||| |||
                                AGTGCGCG   TC CAA CCG
                                     AGC  T  _
GAM562  SDC2     5'  TCCCGTGCCGAGGTTCAG    14622    A  C  A
                                TC CG GCC AGGTTCGG
                                || || ||| ||||||||
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                                AG GC CGG TCCAAGTC
                                 G A   C
GAM562  SGT      3'  TCACCGCCATGAGCGGC     14623      G    A  TT
                                TCAC CGCCA GG  CGGC
                                |||| ||||| ||  ||||
                                AGTG GCGGT CT  GCCG
                                  _    A  C_
GAM562  AD-003   3'  TCACCGCTGGTTCAGC      14624      G   CAA
                                TCAC CGC   GGTTCGGC
                                |||| |||   ||||||||
                                AGTG GCG   CCAAGTCG
                                  _  A__
GAM562  ANKRD5   5'  TCAGCGCTGGCCCAGC      14625      C    CAA
                                TCA GCGC   GGTTCGGC
                                ||| ||||   ||||||||
                                AGT CGCG   CCGGGTCG
                                  _   A__
GAM562  B1       3'  TCACACAGGTTCGGC       14626       GCCA
                                TCACGC    AGGTTCGGC
                                ||||||    |||||||||
                                AGTGTG    TCCAAGCCG
                                    _____
GAM562  CBX6     3'  TCATGCACCAAGGCTGGC    14627      C         C
                                TCA GCGCCAAGGTT GGC
                                ||| ||||||||||| |||
                                AGT CGTGGTTCCGA CCG
                                  A         _
GAM562  CDC42BPB 5'  TCACCGCCGGCTCGGC      14628      G    AA
                                TCAC CGCC  GGTTCGGC
                                |||| ||||  ||||||||
                                AGTG GCGG  CCGAGCCG
                                  _   __
GAM562  CNNM1    3'  TCACGCGCCAACATGGC      14629           G  TC
                                TCACGCGCCAA GT  GGC
                                |||||||||| ||  |||
                                AGTGCGCGGTT TA  CCG
                                      G  __
GAM562  DKFZP434J1813 5'  TCACGCGCCGGTCTCCACGGC  14630         AA   _____
                                TCACGCGCC  GGTT    CGGC
                                |||||||||  ||||    ||||
                                AGTGCGCGG  CCAG    GCCG
                                     __    AGGT
GAM562  ELF4     5'  TCACGGGCCCAGCTCGG      14631      C   AA
                                TCACG GCC  GGTTCGG
                                ||||| |||  |||||||
                                AGTGC CGG  TCGAGCC
                                  C   G_
GAM562  FLJ20419 5'  TCACGCACCGGCCGGGC      14632         AA   TC
                                TCACGCGCC  GGT  GGC
                                |||||||||  |||  |||
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                                AGTGCGTGG  CCG  CCG
                                    __  GC
GAM562  HMGN4     3'  TCCGTGCCAAAGTGGC     14633    A  C      TC
                                TC CG GCCAAGGT  GGC
                                || || ||||||||  |||
                                AG GC CGGTTTCA  CCG
                                 _ A      __
GAM562  KIAA1465  5'  TCACGCGCCTGTCCCGC     14634        AAG   G
                                TCACGCGCC   GTTC GC
                                |||||||||   |||| ||
                                AGTGCGCGG   CAGG CG
                                     A__    G
GAM562  LIV-1     5'  CCACGCGCGCAGGTTTGG    14635        _ A   C
                                TCACGCGC CA GGTT GG
                                |||||||| || |||| ||
                                GGTGCGCG GT CCAA CC
                                     C _    A
GAM562  LIV-1     5'  TCTCGTGCCGAATTCGGC    14636    A  C   AA
                                TC CG GCC  GGTTCGGC
                                || || |||  ||||||||
                                AG GC CGG  TTAAGCCG
                                 A  A   C_
GAM562  NTKL      5'  CCACGCGCCGCGGGTTCGGC  14637        AA_
                                TCACGCGCC   GGTTCGGC
                                |||||||||   ||||||||
                                GGTGCGCGG   CCAAGCCG
                                     CGC
GAM562  PMI       5'  TCTCGCGCCAAGGCGGC     14638    A       TT
                                TC CGCGCCAAGG  CGGC
                                || ||||||||||  ||||
                                AG GCGCGGTTCC  GCCG
                                 A        __
GAM562  PTPRR     5'  TCCGCGCCAGCCCAGC      14639    A     AG
                                TC CGCGCCA  GTTCGGC
                                || |||||||  |||||||
                                AG GCGCGGT  CGGGTCG
                                 _     __
GAM562  RAB6C     5'  TCACGCGCGGCGCTTCGGC   14640        CAA  ___
                                TCACGCGC   GGT   TCGGC
                                ||||||||   |||   |||||
                                AGTGCGCG   CCG   AGCCG
                                     ___   CGA
GAM562  LOC124801 5'  TCACACGCCGGGGCGTGGC   14641        AA   TC
                                TCACGCGCC  GGT  GGC
                                |||||||||  |||  |||
                                AGTGTGCGG  CCG  CCG
                                     CC   CA
GAM562  LOC145725 3'  CCACGCGCTGAAGGAGGC    14642        C_   TTC
                                TCACGCGC  AAGG   GGC
                                ||||||||  ||||   |||
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                                GGTGCGCG  TTCC   CCG
                                    AC    T__
GAM562   LOC145732 3'  CCACGCGCTGAAGGAGGC    14642        C_   TTC
                                TCACGCGC  AAGG   GGC
                                ||||||||  ||||   |||
                                GGTGCGCG  TTCC   CCG
                                    AC    T__
GAM562   LOC146433 5'  TCACGTGCCAAGACTCGG    14643      C     GT
                                TCACG GCCAAG  TCGG
                                ||||| ||||||  ||||
                                AGTGC CGGTTC  AGCC
                                   A      TG
GAM562   LOC148775 5'  TCACTGCGGGATTCGGC     14644     _   CCAA
                                TCAC GCG    GGTTCGGC
                                |||| |||    ||||||||
                                AGTG CGC    CTAAGCCG
                                  A  C___
GAM562   LOC149706 3'  TCACAGCCCTGGGTTCGGC   14645      C   AA_
                                TCACG GCC   GGTTCGGC
                                ||||| |||   ||||||||
                                AGTGT CGG   CCAAGCCG
                                   _   GAC
GAM562   LOC155066 5'  TCACGCGCCGCGCCGGC     14646         AAG  T
                                TCACGCGCC   GT CGGC
                                |||||||||   || ||||
                                AGTGCGCGG   CG GCCG
                                     CG_  _
GAM562   LOC196957 3'  CCACGCGCTGAAGGAGGC    14642        C_   TTC
                                TCACGCGC  AAGG   GGC
                                ||||||||  ||||   |||
                                GGTGCGCG  TTCC   CCG
                                    AC    T__
GAM562   LOC196961 3'  CCACGCGCTGAAGGAGGC    14642        C_   TTC
                                TCACGCGC  AAGG   GGC
                                ||||||||  ||||   |||
                                GGTGCGCG  TTCC   CCG
                                    AC    T__
GAM562   LOC197138 3'  CCACGCGCTGAAGGAGGC    14642        C_   TTC
                                TCACGCGC  AAGG   GGC
                                ||||||||  ||||   |||
                                GGTGCGCG  TTCC   CCG
                                    AC    T__
GAM562   LOC197342 3'  TCTCGTCGCGGTTCGGC     14647    A  _   CAA
                                TC CG CGC   GGTTCGGC
                                || || |||   ||||||||
                                AG GC GCG   CCAAGCCG
                                 A  A  ___
GAM562   LOC245726 5'  TCACGCGCGGCCCGGC      14648         CAA
                                TCACGCGC   GGTTCGGC
                                ||||||||   ||||||||
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                                AGTGCGCG  CCGGGCCG
                                    ___
GAM562  LOC245727 3'  CCACGCGCTGAAGGAGGC   14642       C_   TTC
                                TCACGCGC  AAGG  GGC
                                ||||||||  ||||  |||
                                GGTGCGCG  TTCC  CCG
                                    AC   T__
GAM562  LOC255215 3'  TCACGCGCCAGCTCCAGGC   14649        A G  _
                                TCACGCGCCA G TTC GGC
                                |||||||||| | ||| |||
                                AGTGCGCGGT C AGG CCG
                                     _ G  T
GAM562  LOC256208 5'  TCACGCGCCTAGGTGG     14650        A   TC
                                TCACGCGCC AGGT  GG
                                |||||||| ||||  ||
                                AGTGCGCGG TCCA  CC
                                    A   __
GAM562  LOC51608  3'  CACGCGCCGGCATGCGGC   14651       AA  T__
                                CACGCGCC  GGT  CGGC
                                ||||||||  |||  ||||
                                GTGCGCGG  CCG  GCCG
                                    __  TAC
GAM563  EHD3    3'  GCAAGTGAATTGCCTCAGG   14654       CGCA
                                GCAGGTGA   CCTCAGG
                                ||||||||   |||||||
                                CGTTCACT   GGAGTCC
                                    TAAC
GAM563  GNL1    5'  AGCAGGTGACGTCAG      14655         CACC
                                AGCAGGTGACG   TCAG
                                ||||||||||   ||||
                                TCGTCCACTGC   AGTC
                                    ____
GAM563  GNL1    5'  AGCAGGTGACGTCAG      14655         CACC
                                AGCAGGTGACG   TCAG
                                ||||||||||   ||||
                                TCGTCCACTGC   AGTC
                                    ____
GAM563  HD      3'  ACCAGCAGGTGACTATCAGG  14656         GCACC
                                ACCAGCAGGTGAC   TCAGG
                                ||||||||||||   |||||
                                TGGTCGTCCACTG   AGTCC
                                     AT___
GAM563  HIP12   3'  CCAACAGAACACTTCAG    14657       TGAC  C
                                CCAGCAGG   GCAC TCAG
                                ||||||||   |||| ||||
                                GGTTGTCT   TGTG AGTC
                                    ____  A
GAM563  MBD3    3'  CCAGTGGGCACCAACCTCAGG 14658    CA  GA  C
                                CCAG  GGT  CG ACCTCAGG
                                ||||  |||  || ||||||||
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                                GGTC  CCG  GT TGGAGTCC
                                  AC   TG  _
GAM563  MDK      3'  ACTGGTGGGTCACATCTCGGG  14659    A    A__    C   A
                                GC GGTG   CGCA CTC GG
                                || ||||   |||| ||| ||
                                TG CCAC   GTGT GAG CC
                                 A    CCA    A   C
GAM563  SLC4A4   3'  CACTAGGTAAACCTCAGG    14660    GC     CGC
                                CA  AGGTGA   ACCTCAGG
                                ||  ||||||   ||||||||
                                GT  TCCATT   TGGAGTCC
                                 GA     ___
GAM563  ASPSCR1  3'  GCTGGCGGAGTGGGCACCTCAG 14661    A    AC____
           G                     GC GGTG     GCACCTCAGG
                                || ||||     ||||||||||
                                CG CCGC     CGTGGAGTCC
                                 A   CTCACC
GAM563  DKFZP434K046 3'  CCAGCAGGCACTTGTCTCAGG  14662         G  GCAC
                                CCAGCAGGT AC    CTCAGG
                                |||||||||  ||    ||||||
                                GGTCGTCCG TG    GAGTCC
                                      _  AACA
GAM563  FLJ11996  3'  AGTAACACAGCACTTCAGG    14663       ___    C
                                GGTGAC   GCAC TCAGG
                                ||||||   |||| |||||
                                TCATTG   CGTG AGTCC
                                   TGT    A
GAM563  FLJ12568  5'  CCAGCAAATGCATTTCGGG    14664         GAC   CC  A
                                CCAGCAGGT   GCA  TC GG
                                |||||||||   |||  || ||
                                GGTCGTTTA   CGT  AG CC
                                      ___   AA  C
GAM563  FLJ20156  3'  CAGCAAATACTACGTGCTTTGG 14665          AC  AC_  CA
                                CAGCAGGTG  GC   CT  GG
                                |||||||||  ||   ||  ||
                                GTCGTTTAT  TG   GA  CC
                                      GA  CAC  AA
GAM563  FLJ22477  3'  CCAGCAGGTGCGCCTCGGG    14666          A   AC   A
                                CCAGCAGGTG CGC  CTC GG
                                |||||||||| |||  ||| ||
                                GGTCGTCCAC GCG  GAG CC
                                      _   __   C
GAM563  HBP1     3'  CAGCAGGTGGCTCTTAG     14667         AC  AC  C
                                CAGCAGGTG  GC  CT AG
                                |||||||||  ||  || ||
                                GTCGTCCAC  CG  GA TC
                                      __  A_  A
GAM563  KIAA0125  5'  CACCAGCAGGCTTGCAGTCTTG 14668           GAC   C_  CA
           GG                     TACCAGCAGGT   GCA  CT  GG
                                ||||||||||   |||  ||  ||
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                                GTGGTCGTCCG  CGT  GA  CC
                                      AA_   CA  AC
GAM563  KIAA0430  3'  CAGCGGACACCTCAG      14669      A  TGAC
                                CAGC GG    GCACCTCAG
                                |||| ||    |||||||||
                                GTCG CC    TGTGGAGTC
                                  _ _____
GAM563  KIAA0515  5'  CCAGCAGGTGGGGCTCCTC   14670          AC  A
                                CCAGCAGGTG  GC CCTC
                                ||||||||||  || ||||
                                GGTCGTCCAC  CG GGAG
                                      CC  A
GAM563  KIAA0982  3'  GCTAGCATGAGACCTCAG    14671    _ _   CGC
                                GC AG GTGA   ACCTCAG
                                || || ||||   |||||||
                                CG TC TACT   TGGAGTC
                                 A  G   C__
GAM563  KIAA1244  3'  TACCAGCAGATATTGCCTTAGG 14672           ACGCA   C
                                TACCAGCAGGTG    CCT AGG
                                ||||||||||||    ||| |||
                                ATGGTCGTCTAT    GGA TCC
                                      AAC__   A
GAM563  KIAA1297  5'  CACCAGCAGGTTCTCA      14673          GACGCAC
                                TACCAGCAGGT      CTCA
                                ||||||||||       ||||
                                GTGGTCGTCCA      GAGT
                                      A_______
GAM563  MYO3B     5'  ACCAGCAGAACACTTCAG    14674         TGAC   C
                                ACCAGCAGG   GCAC TCAG
                                |||||||||   |||| ||||
                                TGGTCGTCT   TGTG AGTC
                                     _____   A
GAM563  SAST      5'  CCAGCAGGTGGTAGAACTCCTC 14675          AC___  A   A
           GGG                    CCAGCAGGTG    GC CCTC GG
                                ||||||||||    || |||| ||
                                GGTCGTCCAC    TG GGAG CC
                                      CATCT  A   C
GAM563  LOC126549 5'  CCAAGATCTGACGCACCTTGGG 14676      CAGG        CA
                                CCAG   TGACGCACCT  GG
                                ||||   ||||||||||  ||
                                GGTT   ACTGCGTGGA  CC
                                  CTAG         AC
GAM563  LOC128272 3'  CCAGCAGGAGCAGCTTGGG   14677        TGAC   C  CA
                                CCAGCAGG   GCA CT  GG
                                ||||||||   ||| ||  ||
                                GGTCGTCC   CGT GA  CC
                                     T___   C  AC
GAM563  LOC150622 3'  AGCAGGTGACATCAGA      14678          CACC
                                AGCAGGTGACG   TCAGG
                                ||||||||||   |||||
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                                TCGTCCACTGT   AGTCT
                                      ____
GAM563  LOC197131 3'  CAGCAGGTGGCACATTAGG   14679       AC   CTC
                                CAGCAGGTG GCAC  AGG
                                ||||||||| ||||  |||
                                GTCGTCCAC CGTG  TCC
                                     __   TAA
GAM563  LOC257541 5'  AGCAGGTGACGTCAG     14655        CACC
                                AGCAGGTGACG   TCAG
                                ||||||||||   ||||
                                TCGTCCACTGC   AGTC
                                      ____
GAM564  CELSR1   3'  CATGGATCTCTCGGGATA   14682         GC
                                CATGGATCTCTC GGGGTG
                                |||||||||||  ||||||
                                GTACCTAGAGAG CCCTAT
                                      __
GAM564  GPD1     3'  GGATCTCCAGGTGCGT     14683       CGCG
                                GGATCTCT   GGGTGCGT
                                ||||||||   ||||||||
                                CCTAGAGG   TCCACGCA
                                      ____
GAM564  ZRF1     5'  ATGGATCTTTCGTGGTGTG   14684       C  C  G
                                ATGGATCT TCG GG GTG
                                |||||||| ||| || |||
                                TACCTAGA AGC CC CAC
                                     A  A  A
GAM564  ARF6     5'  CATGGATCCTCGCGGGA     14685       T
                                CATGGATC CTCGCGGGG
                                |||||||| |||||||||
                                GTACCTAG GAGCGCCCT
                                      _
GAM564  FLJ12985  3'  ATGGATTCTCTGATGTGT   14686      _   CGCGG   C
                                ATGGAT CTCT   GGTG GT
                                |||||| ||||   |||| ||
                                TACCTA GAGA   CTAC CA
                                   A  _____  A
GAM564  KIAA0513  3'  GGTTCCTGGGGTGCGT     14687   A  T  CGC
                                GG TC CT  GGGGTGCGT
                                || || ||  |||||||||
                                CC AG GA  CCCCACGCA
                                 A  _  ___
GAM564  PLCE1    3'  CATGGATCTCACATGTG     14688        TC  GG
                                CATGGATCTC  GCG  GTG
                                ||||||||||  |||  |||
                                GTACCTAGAG  TGT  CAC
                                     __  A_
GAM564  LOC203595 5'  TGGATGAACGGGGTGCGTA   14689     CTCTC
                                TGGAT   GCGGGGTGCGTA
                                |||||   ||||||||||||
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                                ACCTA    TGCCCCACGCAT
                                  CT___
GAM564  LOC255624 3'  ATGGATTCTCTGATGTGT   14686      _   CGCGG   C
                                ATGGAT CTCT    GGTG GT
                                |||||| ||||    |||| ||
                                TACCTA GAGA    CTAC CA
                                   A   _____   A
GAM564  LOC256416 3'  GGATCTCTTGCTCCACGT   14690       C  GGGG
                                GGATCTCT GC   TGCGT
                                |||||||| ||   |||||
                                CCTAGAGA CG   GTGCA
                                     A  AG__
GAM564  LOC51673  3'  GGATCTCTTGCTCCACGT   14690       C  GGGG
                                GGATCTCT GC   TGCGT
                                |||||||| ||   |||||
                                CCTAGAGA CG   GTGCA
                                     A  AG__
GAM565  CHRNB4    5'  TGGGGTCACAGGGCACCC   14693   A      _
                                TG GGTCGTAGG CACCC
                                || ||||||||| |||||
                                AC CCAGTGTCC GTGGG
                                 C        C
GAM565  COG6      5'  TGAGGCCGTTGGCAGCCC   14694       A   _
                                TGAGGTCGT GGCA CCC
                                ||||||||| |||| |||
                                ACTCCGGCA CCGT GGG
                                     A    C
GAM565  GRLF1     3'  TGGGTCGCAGCAGGTGCCC   14695   A      G  ____
                                TG GGTCGTAG CA    CCC
                                || |||||||| ||    |||
                                AC CCAGCGTC GT    GGG
                                 _       _  CCAC
GAM565  LZTS1     5'  TGAGGTCATAGCAAAGCCC   14696        G  ___
                                TGAGGTCGTAG CA   CCC
                                |||||||||| ||   |||
                                ACTCCAGTATC GT   GGG
                                      _  TTC
GAM565  CAM-KIIN  5'  TGAAGTCATGCAGCATCC   14697       A_   _
                                TGAGGTCGT  GGCA CC
                                |||||||||  |||| ||
                                ACTTCAGTA  TCGT GG
                                     CG    A
GAM565  DKFZp586H0623 3'  TGAGGTCAGAGGCAGGCAC   14698       ____
                                TGAGGTC    GTAGGCAC
                                |||||||    ||||||||
                                ACTCCAG    CGTCCGTG
                                    TCTC
GAM565  FLJ21865  3'  TGGGGTCACAGAGCATCC   14699   A      _  _
                                TG GGTCGTAG GCA CC
                                || |||||||| ||| ||
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                                AC CCAGTGTC CGT GG
                                 C       T   A
GAM565  POFUT1   3'  TAAGGTCACTTTAGGTACC   14700        ___   C
                                TGAGGTCG   TAGG ACC
                                ||||||||   |||| |||
                                ATTCCAGT   ATCC TGG
                                     GAA    A
GAM565  XPO5     3'  TGAGATTGTGGAAGGCACC   14701       C ___
                                TGAGGT GT   AGGCACC
                                ||||||| ||   |||||||
                                ACTCTA CA   TCCGTGG
                                   A  CCT
GAM565  LOC151904 5'  GAGGTCATGAAAAGGCGCCC   14702        ____   A
                                GAGGTCGT    AGGC CCC
                                ||||||||    |||| |||
                                CTCCAGTA    TCCG GGG
                                     CTTT    C
GAM565  LOC200597 3'  TGAGGTCAGCAGGTCATCC   14703       _    _ _
                                TGAGGTC GTAGG CA CC
                                ||||||| ||||| || ||
                                ACTCCAG CGTCC GT GG
                                     T    A  A
GAM565  LOC220164 3'  TGAGGTCAGTGAGAGGTGCCC  14704       _ ___   CA
                                TGAGGTC GT   AGG  CCC
                                ||||||| ||   |||  |||
                                ACTCCAG CA   TCC  GGG
                                     T  CTC   AC
GAM565  LOC93132  5'  TGAGATCGCACCACTGCCC   14705         G_  A_
                                TGAGGTCGTA  GC  CCC
                                ||||||||||  ||  |||
                                ACTCTAGCGT  TG  GGG
                                      GG  AC
GAM566  ADAM19   3'  TGGGAGGAGCTCAGAGGCGGC  14708       _  G_  _
                                TGGGAGG GC  AG GGCGGC
                                ||||||| ||  || ||||||
                                ACCCTCC CG  TC CCGCCG
                                     T  AG  T
GAM566  ALX4     5'  TGGGGAGGCGAGGAGGC     14709      AG      C
                                TGGG  GGCGAGGG GGC
                                ||||  |||||||| |||
                                ACCC  CCGCTCCT CCG
                                  CT       _
GAM566  ARHC     5'  TGGGAGGGGGTGCGGC      14710        CGA  _
                                TGGGAGGG   GG GCGGC
                                ||||||||   || |||||
                                ACCCTCCC   CC CGCCG
                                     ___  A
GAM566  ARNT2    3'  TGGGAGGGACACAAGGGC    14711         ___
                                TGGGAGGG   CGAGGGC
                                ||||||||   |||||||
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                                ACCCTCCC  GTTCCCG
                                    TGT
GAM566  ATP1A1   5' GGGAGGGTGGGAGGGCGGC  14713      C__
                                GGGAGGG  GAGGGCGGC
                                |||||||  |||||||||
                                CCCTCCC  CTCCCGCCG
                                   ACC
GAM566  ATP1A1   5' TGGGAGGGCGGCCGGCGGC  14712       AG_
                                TGGGAGGGCG  GGCGGC
                                ||||||||||  ||||||
                                ACCCTCCCGC  CCGCCG
                                     CGG
GAM566  ATP5G2   3' TGGGAGGTGGAGACGGC    14714      GC  G
                                TGGGAGG  GAGG CGGC
                                |||||||  |||| ||||
                                ACCCTCC  CTCT GCCG
                                   AC  _
GAM566  ATP7A    3' TGGGAGGGAGAAGGAGGC   14715      C   C
                                TGGGAGGG GAGGG GGC
                                |||||||| ||||| |||
                                ACCCTCCC CTTCC CCG
                                   T   T
GAM566  BARX2    3' TGGGAGGGAGGGAGAC     14716      CG  C
                                TGGGAGGG  AGGG GGC
                                ||||||||  |||| |||
                                ACCCTCCC  TCCC CTG
                                  __   T
GAM566  BCL2L2   3' TGGGAGAGGAGGGTGGC    14717      C   C
                                TGGGAGGG GAGGG GGC
                                |||||||| ||||| |||
                                ACCCTCTC CTCCC CCG
                                  _   A
GAM566  BMP1     3' GGGAGGAGGCAGGGTGGC   14718      __ G  C
                                GGGAGG  GC AGGG GGC
                                ||||||  || |||| |||
                                CCCTCC  CG TCCC CCG
                                   TC  _   A
GAM566  C21orf2  3' TGGGAGAACAGCGGC      14719      GAG
                                TGGGAGGGC  GGCGGC
                                |||||||||  ||||||
                                ACCCTCTTG  TCGCCG
                                  ____
GAM566  CYLN2    5' TGGGAAGGCGGGAGGC     14720       A  C
                                TGGGAGGGCG GGG GGC
                                |||||||||| ||| |||
                                ACCCTTCCGC CCT CCG
                                  _  _
GAM566  CYLN2    5' TGGGGGGCGAGGATGC     14721     A      CG
                                TGGG GGGCGAGGG  GC
                                |||| |||||||||  ||
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                                ACCC CCCGCTCCT  CG
                                  _       A_
GAM566  CYP11B1  3'  TGGGAGAGAAGAGGGGTGGC  14722        C_    C_
                                TGGGAGGG  GAGGG  GGC
                                ||||||||  |||||  |||
                                ACCCTCTC  CTCCC  CCG
                                     TT    CA
GAM566  DPYSL3   3'  TGGAAGGGGAAACAGGTGG   14723        C ___  C
                                TGGGAGGG GA   GGG GG
                                |||||||| ||   ||| ||
                                ACCTTCCC CT   TCC CC
                                     _ TTG   A
GAM566  EDNRA    5'  TGGGTGGCGCGGAGGGTGGC  14724      A _  _   C
                                TGGG GG GCG AGGG GGC
                                |||| || ||| |||| |||
                                ACCC CC CGC TCCC CCG
                                  A G   C    A
GAM566  EGR3     3'  TGGGAGGGCAGGGGGC      14725         G    C
                                TGGGAGGGC AGGG GGC
                                |||||||||  |||| |||
                                ACCCTCCCG TCCC CCG
                                     _    _
GAM566  EHD2     3'  TGGGAGGGGGGCCCGGC     14726        CGA   __
                                TGGGAGGG   GGGC  GGC
                                ||||||||   ||||  |||
                                ACCCTCCC   CCCG  CCG
                                     ___    GG
GAM566  ELK1     3'  TGGGAGGGAGGGAAC       14727        CG    C
                                TGGGAGGG  AGGG GGC
                                ||||||||  |||| |||
                                ACCCTCCC  TCCC TTG
                                     __   _
GAM566  FAAH     5'  GGAGGGCGAGAAGGAGGCGGCG 14728          _____     III
                                GGAGGGCGAG    GGCGGC  G
                                ||||||||||    ||||||  |
                                CCTCCCGCTC    CCGCCG  C
                                      TTCCT     III
GAM566  FBXL7    3'  TGCGAGGGAAAGGGCGGC    14729    G    C
                                TG GAGGG GAGGGCGGC
                                || ||||| |||||||||
                                AC CTCCC TTCCCGCCG
                                 G    T
GAM566  FGFR1    3'  TGGGAGGGGATGAAGTGGC   14730        C__   GC
                                TGGGAGGG   GAGG  GGC
                                ||||||||   ||||  |||
                                ACCCTCCC   CTTC  CCG
                                     CTA   A_
GAM566  FGFR1    3'  TGGGAGGGGATGAAGTGGC   14730        C__   GC
                                TGGGAGGG   GAGG  GGC
                                ||||||||   ||||  |||
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                                ACCCTCCC  CTTC  CCG
                                    CTA   A_
GAM566  FGFR1   3'  TGGGAGGGGATGAAGTGGC   14730       C__   GC
                                TGGGAGGG  GAGG  GGC
                                ||||||||  ||||  |||
                                ACCCTCCC  CTTC  CCG
                                    CTA   A_
GAM566  FGFR1   3'  GGGAGGGCGTGTGGGTGGC   14731       A__   C
                                GGGAGGGCG  GGG GGC
                                |||||||||  ||| |||
                                CCCTCCCGC  CCC CCG
                                    ACA   A
GAM566  FGFR1   3'  GGGAGGGCGTGTGGGTGGC   14731       A__   C
                                GGGAGGGCG  GGG GGC
                                |||||||||  ||| |||
                                CCCTCCCGC  CCC CCG
                                    ACA   A
GAM566  FGFR1   3'  GGGAGGGCGTGTGGGTGGC   14731       A__   C
                                GGGAGGGCG  GGG GGC
                                |||||||||  ||| |||
                                CCCTCCCGC  CCC CCG
                                    ACA   A
GAM566  FKBP1B  3'  TGGGAGGGATGACACCGGGGTG 14732      _______ A  C  III
          GCG                   GGAGGG     CG GGG GGC  G
                                ||||||     || ||| |||  |
                                CCTCCC     GC CCC CCG  C
                                  TACTGTG _  A  III
GAM566  FOLR1   5'  TGGGAGAGGAGGTGGC    14733       C   GC
                                TGGGAGGG GAGG  GGC
                                |||||||| ||||  |||
                                ACCCTCTC CTCC  CCG
                                    _   A_
GAM566  FOLR1   5'  TGGGAGAGGAGGTGGC    14733       C   GC
                                TGGGAGGG GAGG  GGC
                                |||||||| ||||  |||
                                ACCCTCTC CTCC  CCG
                                    _   A_
GAM566  FOXD2   5'  TGGGAGAGGTGAGATTGCGGC  14734     _ C   __
                                TGGGAG GG GAGG  GCGGC
                                |||||| || ||||  |||||
                                ACCCTC CC CTCT  CGCCG
                                  T  A   AA
GAM566  GATA3   5'  TGGGAGGTCGGGGGGC    14735       G  A  C
                                TGGGAGG CG GGG GGC
                                ||||||| || ||| |||
                                ACCCTCC GC CCC CCG
                                  A  _  _
GAM566  GFRA1   5'  TGGCGAGGGCGGGAGGCGG   14736    _     A_
                                TGG GAGGGCG  GGGCGG
                                ||| |||||||  ||||||
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                                ACC CTCCCGC  TCCGCC
                                  G      CC
GAM566  GPC1     3'  TGGGAGGAGCGAACAGC     14737        _    GG
                                TGGGAGG GCGA  GCGGC
                                ||||||| ||||  |||||
                                ACCCTCC CGCT  TGTCG
                                    T   __
GAM566  GRB14    5'  GGGAGGGCGCGAGAGCGGC   14738         __
                                GGGAGGGC  GAGGGCGGC
                                ||||||||  |||||||||
                                CCCTCCCG  CTCTCGCCG
                                     CG
GAM566  HIC1     5'  TGGAAGGGCAGCGGC       14739          GAG
                                TGGGAGGGC   GGCGGC
                                |||||||||   ||||||
                                ACCTTCCCG   TCGCCG

                                    ___
GAM566  HPCAL1   3'  TGGGAGGATCATCACGGC    14740         _ AGG
                                TGGGAGGG CG   GCGGC
                                |||||||| ||   |||||
                                ACCCTCCT GT   TGCCG
                                     A  AG_
GAM566  HPCAL1   3'  TGGGAGGATCATCACGGC    14740         _ AGG
                                TGGGAGGG CG   GCGGC
                                |||||||| ||   |||||
                                ACCCTCCT GT   TGCCG
                                     A  AG_
GAM566  KCNK4    5'  TGGGAGGCCGAAAGAGAGC   14741         G     C _
                                TGGGAGG CGAGGG G GC
                                ||||||| |||||| | ||
                                ACCCTCC GCTTTC C CG
                                     G     T T
GAM566  LBX1     3'  TAGGAGCCCAGGGCGGC     14742        GG G
                                TGGGAG  C AGGGCGGC
                                ||||||  | ||||||||
                                ATCCTC  G TCCCGCCG
                                    GG _
GAM566  LEP      3'  TGGGAAGGGCATCCTGGTGGC  14743       _    AG__  C
                                TGGGA GGGCG    GG GGC
                                ||||| |||||    || |||
                                ACCCT CCCGT    CC CCG
                                   T    AGGA  A
GAM566  M11S1    5'  TGAGGGGGCAAGGGTGGC     14744      A        C
                                TGGG GGGCGAGGG GGC
                                |||| ||||||||| |||
                                ACTC CCCGTTCCC CCG
                                  C        A
GAM566  MADH3    5'  GGGAGGGCGTGCGGGCGGC    14745          A__
                                GGGAGGGCG   GGGCGGC
                                |||||||||   |||||||
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                                CCCTCCCGC  CCCGCCG
                                     ACG
GAM566  MATN1   5' TGAGAGGGCGGGAGAGC    14746        A  C
                                TGGGAGGGCG GGG GGC
                                |||||||||| ||| |||
                                ACTCTCCCGC CCT TCG
                                      _  C
GAM566  MEF2B   5' TGAGGAGGGCGGGGGTGG   14747   _     A  C
                                TG GGAGGGCG GGG GG
                                || |||||||| ||| ||
                                AC CCTCCCGC CCC CC
                                 T      C  A
GAM566  MEOX1   3' TAGGAGGAGGCATGGGTGGC  14748       __  A  C
                                TGGGAGG  GCG GGG GGC
                                |||||||  ||| ||| |||
                                ATCCTCC  CGT CCC CCG
                                    TC  A  A
GAM566  MEOX1   3' TAGGAGGAGGCATGGGTGGC  14748       __  A  C
                                TGGGAGG  GCG GGG GGC
                                |||||||  ||| ||| |||
                                ATCCTCC  CGT CCC CCG
                                    TC  A  A
GAM566  MLC1    3' TGGGAGAGCAGCGGC      14749       GAG
                                TGGGAGGGC  GGCGGC
                                |||||||||  ||||||
                                ACCCTCTCG  TCGCCG
                                      ___
GAM566  MLC1    3' TGGGAGAGCAGCGGC      14749       GAG
                                TGGGAGGGC  GGCGGC
                                |||||||||  ||||||
                                ACCCTCTCG  TCGCCG
                                      ___
GAM566  MMP14   3' TGGGGGAGCGAGAGGGC    14750    A      C
                                TGGG GGGCGAGGG GGC
                                |||| ||||||||| |||
                                ACCC CTCGCTCTC CCG
                                  C       _
GAM566  MMP25   5' TGGAGAGGGCGGGGGGC    14751    _     A  C
                                TGG GAGGGCG GGG GGC
                                ||| ||||||| ||| |||
                                ACC CTCCCGC CCC CCG
                                  T      _  _
GAM566  NEK4    5' AGGGGGCAGTGGGGGCGGC   14752    A    A___
                                GGG GGGCG   GGGCGGC
                                ||| |||||   |||||||
                                TCC CCCGT   CCCGCCG
                                  _    CACC
GAM566  NLGN3   3' TGGGAGGGAGGGAGC      14753       CG   C
                                TGGGAGGG  AGGG GGC
                                ||||||||  |||| |||
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                                ACCCTCCC  TCCC TCG
                                   __   _
GAM566  NPAS2    5'  TGGGAGACGAGGCGGC      14754        G    G
                                TGGGAGG CGAGG CGGC
                                ||||||| ||||| ||||
                                ACCCTCT GCTCC GCCG
                                   _    _
GAM566  NR2F2    5'  GGGAGGGCGCCCCGGGTGGC  14755         A___  C
                                GGGAGGGCG   GGG GGC
                                |||||||||   ||| |||
                                CCCTCCCGC   CCC CCG
                                     GGGG  A
GAM566  OTP      3'  TGGGAAGGGAAGAGGGGCGGC 14756         C__   _
                                TGGGAGGG  GAGGG CGGC
                                ||||||||  ||||| ||||
                                ACCCTTCC  CTCCC GCCG
                                     CTT    C
GAM566  P4HA1    5'  TGGGACGAGAGGGCGGC     14757       G  C
                                TGGGA GG GAGGGCGGC
                                ||||| || |||||||||
                                ACCCT CT CTCCCGCCG
                                   G  _
GAM566  PACSIN1  3'  TGGGAGGGGAGGGGCGGC   14758         C    _
                                TGGGAGGG GAGGG CGGC
                                |||||||| ||||| ||||
                                ACCCTCCC CTCCC GCCG
                                   _    C
GAM566  PEX14    3'  TGGGAGGACGACGGGGC     14759          G  C
                                TGGGAGGGCGA GG GGC
                                |||||||||| || |||
                                ACCCTCCTGCT CC CCG
                                     G  _
GAM566  PTBP1    3'  GGGACAGGACGCGGGGGCGG  14760      __    A__
                                GGGA  GGGCG  GGGCGG
                                ||||  |||||  ||||||
                                CCCT  CCTGC  CCCGCC
                                  GT    GCC
GAM566  PTBP1    3'  GGGACAGGACGCGGGGGCGG  14760      __    A__
                                GGGA  GGGCG  GGGCGG
                                ||||  |||||  ||||||
                                CCCT  CCTGC  CCCGCC
                                  GT    GCC
GAM566  PTMS     3'  GGGAGAAAGAAGAGGGTGGC  14761       C___   C
                                GGGAGGG   GAGGG GGC
                                |||||||   ||||| |||
                                CCCTCTT   CTCCC CCG
                                    TCTT   A
GAM566  PTN      5'  TGGGAGGGATGAGAGGAGC   14762       C_   C
                                TGGGAGGG  GAGGG GGC
                                ||||||||  ||||| |||
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                                ACCCTCCC  CTCTC TCG
                                    TA    C
GAM566  PTPRA   5'  TGGCGAGGGGAAGCGGC    14763    _   C   G
                                TGG GAGGG GAGG CGGC
                                ||| ||||| |||| ||||
                                ACC CTCCC CTTC GCCG
                                  G   _   _
GAM566  RAB6A   5'  TGGGAAGGGAAGGAGGGCGG  14764       C___
                                TGGGAGGG   GAGGGCGG
                                ||||||||   ||||||||
                                ACCCTTCC   CTCCCGCC
                                    CTTC
GAM566  RFX1    3'  TGGGAGGGGGGCGGC      14765       CGA
                                TGGGAGGG  GGGCGGC
                                ||||||||  |||||||
                                ACCCTCCC  CCCGCCG
                                    ___
GAM566  S100A5  3'  TGGGAGGGAGAGGAGGGC   14766       C   C
                                TGGGAGGG GAGGG GGC
                                |||||||| ||||| |||
                                ACCCTCCC CTCCT CCG
                                    T   C
GAM566  SAG     5'  TGGGAAGGGCCGGGTGGC   14767     _  GA  C
                                TGGGA GGGC  GGG GGC
                                ||||| ||||  ||| |||
                                ACCCT CCCG  CCC CCG
                                  T   G_  A
GAM566  SEPN1   3'  TGAGGGGCAAGAGGGGCGGC  14768    A   ___
                                TGGG GGGCGA  GGGCGGC
                                |||| ||||||  |||||||
                                ACTC CCCGTT  CCCGCCG
                                  _    CTC
GAM566  SF1     5'  GGGCGGGCCGGGGGCGGC   14769    A  _ A
                                GGG GGGC G GGGCGGC
                                ||| |||| | |||||||
                                CCC CCCG C CCCGCCG
                                  G   G C
GAM566  SLC2A4  3'  TGGGAGGAGTCCAAGGTGG  14770       ___   GC
                                TGGGAGGG  CGAGG  GG
                                ||||||||  |||||  ||
                                ACCCTCCT  GTTCC  CC
                                    CAG   A_
GAM566  SLC39A4 5'  GGGCTGGCTGAGGGCGGC   14771    AG  _
                                GGG  GGC GAGGGCGGC
                                |||  ||| |||||||||
                                CCC  CCG CTCCCGCCG
                                  GA  A
GAM566  SNRPN   5'  GGGAAGACAGGGGGCGGC   14772       A_
                                GGGAGGGCG  GGGCGGC
                                |||||||||  |||||||
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                                CCCTTCTGT  CCCGCCG
                                     CC
GAM566  SNX9    5'  GGCAAGGGCGAGGGCGGC    14773    _
                                GG GAGGGCGAGGGCGGC
                                || ||||||||||||||
                                CC TTCCCGCTCCCGCCG
                                 G
GAM566  STX1A   3'  TGGGAGGGCAGCCCAGC     14774        G  GG
                                TGGGAGGGC AG  CGGC
                                ||||||||| ||  ||||
                                ACCCTCCCG TC  GTCG
                                     _ GG
GAM566  SYN3    3'  TGTGAGGCGAGGGTGGC     14775    G   G     C
                                TG GAGG CGAGGG GGC
                                || |||| |||||| |||
                                AC CTCC GCTCCC CCG
                                 A   _     A
GAM566  TCF12   5'  TGGGAGGGGGAGGCGGC     14776        C   G
                                TGGGAGGG GAGG CGGC
                                |||||||| |||| ||||
                                ACCCTCCC CTCC GCCG
                                     C   _
GAM566  THRA    5'  TGGGAGGGCTGGGGGC      14777        GA  C
                                TGGGAGGGC  GGG GGC
                                |||||||||  ||| |||
                                ACCCTCCCG  CCC CCG
                                     A_  _
GAM566  TRPV1   5'  TGGGAGGGTGGACAGGC     14778        CGA   _
                                TGGGAGGG   GGGC GGC
                                ||||||||   |||| |||
                                ACCCTCCC   CCTG CCG
                                     A__    T
GAM566  USP14   5'  TGGGCCTGACGAGGGCGGC   14779     AG_
                                TGGG   GGCGAGGGCGGC
                                ||||   ||||||||||||
                                ACCC   CTGCTCCCGCCG
                                  GGA
GAM566  WT1     5'  TGGGGGAGCGGACAGGC     14780     A   GA   _
                                TGGG GGGC  GGGC GGC
                                |||| ||||  |||| |||
                                ACCC CTCG  CCTG CCG
                                  C   __   T
GAM566  WT1     5'  TGGGGGAGCGGACAGGC     14780     A   GA   _
                                TGGG GGGC  GGGC GGC
                                |||| ||||  |||| |||
                                ACCC CTCG  CCTG CCG
                                  C   __   T
GAM566  WT1     5'  TGGGGGAGCGGACAGGC     14780     A   GA   _
                                TGGG GGGC  GGGC GGC
                                |||| ||||  |||| |||
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                                ACCC CTCG  CCTG CCG
                                  C   __   T
GAM566  WT1      5'  TGGGGGAGCGGACAGGC    14780     A   GA   _
                                TGGG GGGC  GGGC GGC
                                |||| ||||  |||| |||
                                ACCC CTCG  CCTG CCG
                                  C   __   T
GAM566  ADAR3    5'  GGGAGGGCGGGGAAGGGC    14781        A  C__
                                GGGAGGGCG GGG  GGC
                                |||||||||  |||  |||
                                CCCTCCCGC CCC  CCG
                                     _  TTC
GAM566  APXL2    5'  TGGGAGGGCGACTACGGC    14782         GG
                                TGGGAGGGCGA  GCGGC
                                ||||||||||  |||||
                                ACCCTCCCGCT  TGCCG
                                      GA
GAM566  BCAA     5'  TGGGGAAGAAGGGCGGC     14783     AG  C
                                TGGG  GG GAGGGCGGC
                                ||||  || |||||||||
                                ACCC  TC TTCCCGCCG
                                  CT  _
GAM566  C20orf18 5'  TGGGAGAGGCGGGAGAC     14784       _   A  C
                                TGGGAG GGCG GGG GGC
                                |||||| |||| ||| |||
                                ACCCTC CCGC CCT CTG
                                   T   _  _
GAM566  C20orf18 5'  TGGGAGAGGCGGGAGAC     14784       _   A  C
                                TGGGAG GGCG GGG GGC
                                |||||| |||| ||| |||
                                ACCCTC CCGC CCT CTG
                                   T   _  _
GAM566  C22orf4  3'  TGGGAGAGGACACGGC      14785        C  GG
                                TGGGAGGG GA  GCGGC
                                |||||||| ||  |||||
                                ACCCTCTC CT  TGCCG
                                     _ G_
GAM566  CACNA1H  3'  TGGTGAGGGCGTGACAGGC   14786     _      AG  _
                                TGG GAGGGCG  GGC GGC
                                ||| |||||||  ||| |||
                                ACC CTCCCGC  CTG CCG
                                  A      A_   T
GAM566  CALN1    3'  TGGGAGGGAGGACAAGC     14787        CG    _
                                TGGGAGGG  AGGGCG GC
                                ||||||||  |||||| ||
                                ACCCTCCC  TCCTGT CG
                                     __      T
GAM566  CARD11   5'  GGGAGGGGGCTGCGGGCGGC  14788      __   GA_
                                GGGA  GGGC   GGGCGGC
                                ||||  ||||   |||||||
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                                CCCT  CCCG   CCCGCCG
                                  CC    ACG
GAM566  CCR7     3'  TGGGAGGGCGACGCGGC     14789          GG
                                TGGGAGGGCGA  GCGGC
                                ||||||||||  |||||
                                ACCCTCCCGCT  CGCCG
                                      G_
GAM566  CHST3    5'  TGGAAGGGAAGCGGC       14790        CGA
                                TGGGAGGG   GGGCGGC
                                ||||||||   |||||||
                                ACCTTCCC   TTCGCCG
                                    ___
GAM566  CIDEB    3'  TGGGAGGCTAGAAAGGTGGC   14791        GC__     C
                                TGGGAGG    GAGGG GGC
                                |||||||    ||||| |||
                                ACCCTCC    TTTCC CCG
                                    GATC     A
GAM566  CLPTM1   3'  TGGCAGGGCGAGATGGC     14792     G        GC
                                TGG AGGGCGAGG  GGC
                                ||| |||||||||  |||
                                ACC TCCCGCTCT  CCG
                                  G        A_
GAM566  CNNM2    3'  TGGGAGGGCCAAGGAAGGC    14793         G    C_
                                TGGGAGGGC AGGG  GGC
                                ||||||||| ||||  |||
                                ACCCTCCCG TTCC  CCG
                                      G    TT
GAM566  CORO1B   3'  TGGGAAGGGGGCGGC       14794        CGA
                                TGGGAGGG   GGGCGGC
                                ||||||||   |||||||
                                ACCCTTCC   CCCGCCG
                                    ___
GAM566  CRF      3'  TGGGAGGGCCTAGCTGTGGC   14795         GAG  ___
                                TGGGAGGGC   GGC   GGC
                                |||||||||   |||   |||
                                ACCCTCCCG   TCG   CCG
                                      GA_   ACA
GAM566  dJ309H15.1 3'  TGGGGAGAGAAAGCGGC     14796      A   C
                                TGGG GGG GAGGGCGGC
                                |||| ||| |||||||||
                                ACCC CTC CTTTCGCCG
                                  _   T
GAM566  DKFZP434C131 3'  TGGCAGGGCGAGGGCAAGC    14797     G          _
                                TGG AGGGCGAGGGCG GC
                                ||| ||||||||||| ||
                                ACC TCCCGCTCCCGT CG
                                  G          T
GAM566  DKFZP564C196 5'  TAGGAGGAAGGGGCGGC     14798         CGA
                                TGGGAGGG   GGGCGGC
                                ||||||||   |||||||
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                                ATCCTCCT  CCCGCCG
                                   TC_
GAM566  DKFZP564D0478 3'  GGGGGGCGAGGCGGGCGGC   14799    A    ___
                                GGG GGGCGA  GGGCGGC
                                ||| ||||||  |||||||
                                CCC CCCGCT  CCCGCCG
                                  _    CCG
GAM566  DKFZp761J139 5'  TGGGAGAGCCAAGCGGC    14800        GA
                                TGGGAGGGC  GGGCGGC
                                |||||||||  |||||||
                                ACCCTCTCG  TTCGCCG
                                   G_
GAM566  DNAJC5   3'  TGGGAGGGGGGAGACTGGC   14801       CGA   _
                                TGGGAGGG  GGGC GGC
                                ||||||||  |||| |||
                                ACCCTCCC  TCTG CCG
                                   CCC   A
GAM566  EFNA5    3'  TGGGAGGGGTGAGAGAAGC   14802       C_   C
                                TGGGAGGG  GAGGG GGC
                                ||||||||  ||||| |||
                                ACCCTCCC  CTCTC TCG
                                   CA    T
GAM566  EPN2     3'  GGGACTGGAGAGGGCGGC    14803     G_  C
                                GGGA  GG GAGGGCGGC
                                ||||  || |||||||||
                                CCCT  CC CTCCCGCCG
                                  GA  T
GAM566  F23149_1  5'  TGGGCGGGCGAGAAGAGC    14804     A      C
                                TGGG GGGCGAGGG GGC
                                |||| ||||||||| |||
                                ACCC CCCGCTCTT TCG
                                  G       C
GAM566  FASTK    3'  GGGAGAGGAGAGGGCGGC    14805     _  C
                                GGGAG GG GAGGGCGGC
                                ||||| || |||||||||
                                CCCTC CC CTCCCGCCG
                                  T  T
GAM566  FLJ00001  3'  TGGGAGGGAGGGCTGGC     14806       CG    _
                                TGGGAGGG  AGGGC GGC
                                ||||||||  ||||| |||
                                ACCCTCCC  TCCCG CCG
                                   __    A
GAM566  FLJ10342  5'  TGAGAGCGGGAGGGGCGG    14807      _  C    _
                                TGGGAG GG GAGGG CGG
                                |||||| || ||||| |||
                                ACTCTC CC CTCCC GCC
                                   G  _    C
GAM566  FLJ10709  3'  TGGGGGGCAGAACGGC     14808     A   G
                                TGGG GGGC AGGGCGGC
                                |||| |||| ||||||||
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                                ACCC CCCG TCTTGCCG
                                  _   _
GAM566  FLJ10925  5' TGGGGCGGCGAGGACGGC   14809     AG
                                TGGG  GGCGAGGGCGGC
                                ||||  ||||||||||||
                                ACCC  CCGCTCCTGCCG
                                  CG
GAM566  FLJ12443  3' TGGGAGAACACGGGGCGGC   14810        A_
                                TGGGAGGGCG  GGGCGGC
                                ||||||||||  |||||||
                                ACCCTCTTGT  CCCGCCG
                                      GC
GAM566  FLJ13102  3' TGGGAGGGTGAGGCCGGC   14811       C   G
                                TGGGAGGG GAGG CGGC
                                |||||||| |||| ||||
                                ACCCTCCC CTCC GCCG
                                     A   G
GAM566  FLJ14936  3' TGGGAGAGCGACGGGGC    14812         G  C
                                TGGGAGGGCGA GG GGC
                                |||||||||| || |||
                                ACCCTCTCGCT CC CCG
                                      G  _
GAM566  FLJ20257  5' TGAGAGGGGCTGTGGGCGGC  14814       _ GA_
                                TGGGAGGG C   GGGCGGC
                                |||||||| |   |||||||
                                ACTCTCCC G   CCCGCCG
                                     C ACA
GAM566  FLJ20257  5' TGGGCGGCACGGGGTGGC   14813     A  _   A   C
                                TGGG GG GCG GGG GGC
                                |||| || ||| ||| |||
                                ACCC CC TGC CCC CCG
                                  G  G   _   A
GAM566  FLJ20397  5' TGGGAGGGCTGCAGACAGGC  14815       GA_   _
                                TGGGAGGGC   GGGC GGC
                                |||||||||   |||| |||
                                ACCCTCCCG   TCTG CCG
                                     ACG   T
GAM566  FLJ22625  5' TGGGAGCGCGGGCGCGGC   14816      G  A  _
                                TGGGAG GCG GG GCGGC
                                ||||||| ||| || |||||
                                ACCCTC CGC CC CGCCG
                                    G   _  G
GAM566  FLJ22693  5' GGGAGCCTCGAGGGCGGC   14817      GG_
                                GGGAG   CGAGGGCGGC
                                |||||   ||||||||||
                                CCCTC   GCTCCCGCCG
                                   GGA
GAM566  GAL3ST2   3' TGGGAAGGAGAGGGTGGC   14818       C    C
                                TGGGAGGG GAGGG GGC
                                |||||||| ||||| |||
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                                ACCCTTCC CTCCC CCG
                                    T    A
GAM566  GMPPB    3'  TGGGAAGGGGAGGTGGC    14819       C   GC
                                TGGGAGGG GAGG  GGC
                                |||||||| ||||  |||
                                ACCCTTCC CTCC  CCG
                                    C   A_
GAM566  GTF3C1   3'  TGGGAGGGAGGGGAC      14820       CG   C
                                TGGGAGGG  AGGG GGC
                                |||||||  |||| |||
                                ACCCTCCC  TCCC CTG
                                   __   _
GAM566  GTSE1    3'  TGGCAGCGAGGAGGGTGGC   14821    G _ C    C
                                TGG AG GG GAGGG GGC
                                ||| || || ||||| |||
                                ACC TC CT CTCCC CCG
                                  G G C    A
GAM566  HCGIV.9  5'  TGGCGAGGGCGGGGCTCGG   14822    _     A   __
                                TGG GAGGGCG GGGC  GG
                                ||| ||||||| ||||  ||
                                ACC CTCCCGC CCCG  CC
                                  G      _   AG
GAM566  IL14     5'  TGGGAAGGGAGCGGC      14823       CGA
                                TGGGAGGG   GGGCGGC
                                ||||||||   |||||||
                                ACCCTTCC   CTCGCCG
                                   ____
GAM566  KCND1    5'  TAGGAGAGAAGGTGGC     14824       C   GC
                                TGGGAGGG GAGG  GGC
                                |||||||| ||||  |||
                                ATCCTCTC TTCC  CCG
                                    _   A_
GAM566  KCNN1    5'  TGGGAGAGAGGGTGGC     14825       GC   C
                                TGGGAGG  GAGGG GGC
                                |||||||  ||||| |||
                                ACCCTCT  CTCCC CCG
                                    __    A
GAM566  KIAA0014 3'  TGGATCAAGGAGGGCGGC   14826     A_  C
                                TGGG  GGG GAGGGCGGC
                                ||||  ||| |||||||||
                                ACCT  TTC CTCCCGCCG
                                  AG  _
GAM566  KIAA0415 3'  TGGGCAGGGCAGCAGAGGGGCG 14827    _   ____   _   III
          GCG                    GGG AGGGC   GAGGG CGGC  G
                                ||| |||||   ||||| ||||  |
                                CCC TCCCG   CTCCC GCCG  C
                                  G   TCGT   C   III
GAM566  KIAA0537 5'  GGGAGGGGAGAGGGTGGC   14828       C_   C
                                GGGAGGG  GAGGG GGC
                                |||||||  ||||| |||
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                                CCCTCCC  CTCCC CCG
                                   CT    A
GAM566  KIAA0537  5'  AGACGGGGCGGGGGCGGC   14829    __    A
                                GGA  GGGCG GGGCGGC
                                |||  ||||| |||||||
                                TCT  CCCGC CCCGCCG
                                  GC    C
GAM566  KIAA0757  3'  TAGGAAGGGGGCGGC      14830       CGA
                                TGGGAGGG   GGGCGGC
                                ||||||||   |||||||
                                ATCCTTCC   CCCGCCG
                                    ___
GAM566  KIAA0819  3'  TGGGAGGGTGAGAGTGGC   14831       C    C
                                TGGGAGGG GAGGG GGC
                                |||||||| ||||| |||
                                ACCCTCCC CTCTC CCG
                                    A    A
GAM566  KIAA0821  5'  TGGCGGGACGAGGGCGGC   14832    GA
                                TGG  GGGCGAGGGCGGC
                                |||  ||||||||||||
                                ACC  CCTGCTCCCGCCG
                                  GC
GAM566  KIAA0892  3'  TGGGAGGGCAGGGACTGGC   14833        A   _
                                TGGGAGGGCG GGGC GGC
                                |||||||||| |||| |||
                                ACCCTCCCGT CCTG CCG
                                     C   A
GAM566  KIAA0967  3'  TGGGAGAGTGGAAGGGGC   14834       C_    C
                                TGGGAGGG  GAGGG GGC
                                ||||||||  ||||| |||
                                ACCCTCTC  CTTCC CCG
                                    AC    _
GAM566  KIAA1193  3'  TGGAAGGGACTAGGTGGC   14835       _ GA   C
                                TGGGAGGG C  GGG GGC
                                |||||||| |  ||| |||
                                ACCTTCCC G  TCC CCG
                                    T A_   A
GAM566  KIAA1287  5'  TGAGAGGAAGGGTGGC     14836       GC    C
                                TGGGAGG  GAGGG GGC
                                |||||||  ||||| |||
                                ACTCTCC  TTCCC CCG
                                   __    A
GAM566  KIAA1464  3'  TGGGAAGGCGCTAGGTGGC   14837        A_   C
                                TGGGAGGGCG  GGG GGC
                                ||||||||||  ||| |||
                                ACCCTTCCGC  TCC CCG
                                     GA   A
GAM566  KIAA1548  5'  TGAGAAAGGGGCGGC      14838       CGA
                                TGGGAGGG   GGGCGGC
                                ||||||||   |||||||
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                                ACTCTTTC  CCCGCCG
                                   ___
GAM566  KIAA1831  5'  TGGGGGGGCGAGGTAGTGGC  14839     A      GC__
                                TGGG GGGCGAGG   GGC
                                |||| ||||||||   |||
                                ACCC CCCGCTCC   CCG
                                  C       ATCA
GAM566  KIAA1938  3'  TGGGAAGGAAAAGGGGGCGGC  14840       C ___
                                TGGGAGGG GA  GGGCGGC
                                |||||||| ||  |||||||
                                ACCCTTCC TT  CCCGCCG
                                     T  TCC
GAM566  KIAA1952  5'  TGGGAGAGCATCAGTTGGC   14841        A_ GC
                                TGGGAGGGCG  GG  GGC
                                ||||||||||  ||  |||
                                ACCCTCTCGT  TC  CCG
                                      AG  AA
GAM566  MAP2K1IP1 5'  TGCGAGGGCGCGTCCGGCGGC  14842   G     AG___
                                TG GAGGGCG    GGCGGC
                                || |||||||    ||||||
                                AC CTCCCGC    CCGCCG
                                 G      GCAGG
GAM566  MAPKAPK2  3'  GGGCAGGGTGAGGGCGGC    14843    _   C
                                GGG AGGG GAGGGCGGC
                                ||| |||| |||||||||
                                CCC TCCC CTCCCGCCG
                                  G   A
GAM566  MASA    5'  GGGAGGGCGGAGGGCGGC    14844        _
                                GGGAGGGCG AGGGCGGC
                                ||||||||| ||||||||
                                CCCTCCCGC TCCCGCCG
                                     C
GAM566  MGC11242  5'  TGGGAGGGTGAGACTCGGC   14845       C   G_
                                TGGGAGGG GAGG  CGGC
                                |||||||| ||||  ||||
                                ACCCTCCC CTCT  GCCG
                                     A   GA
GAM566  MGC12921  3'  GGGAAGATGAGGTGGGGGTGGC 14846      GC _____  C  III
          G                      GGGAGG  GA    GGG GGC  G
                                ||||||  ||    ||| |||  |
                                CCCTTC  CT    CCC CCG  C
                                   TA  CCACC   A  III
GAM566  MGC24976  5'  TGGGAGGAGGACCCGGC    14847       GCG   __
                                TGGGAGG   AGGGC  GGC
                                |||||||   |||||  |||
                                ACCCTCC   TCCTG  CCG
                                   ___    GG
GAM566  MGC31963  3'  TGGGGGAGTGAAGGGGC    14848     A  C   C
                                TGGG GGG GAGGG GGC
                                |||| ||| ||||| |||
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                                ACCC CTC CTTCC CCG
                                  C  A   _
GAM566  MGC3262  3' TAGGAGGGAAAGCAGGTGGC  14849       C  __ C
                                TGGGAGGG GAG  GG GGC
                                |||||||| |||  || |||
                                ATCCTCCC TTC  CC CCG
                                     T  GT  A
GAM566  MGC4771  3' TGGGAGGGAGGGAAC      14727       CG   C
                                TGGGAGGG  AGGG GGC
                                ||||||||  |||| |||
                                ACCCTCCC  TCCC TTG
                                      __   _
GAM566  MYO3B    3' TGGGAGGATGGAGAAGAG    14850       C_   C
                                TGGGAGGG  GAGGG GG
                                ||||||||  ||||| ||
                                ACCCTCCT  CTCTT TC
                                     AC    C
GAM566  NAP1L2   5' TGGGTGCAGAGGGCGGC    14851     AGG  _
                                TGGG  GC GAGGGCGGC
                                ||||  || |||||||||
                                ACCC  CG CTCCCGCCG
                                  A__  T
GAM566  NBL1     3' TGGGAGGGAGGAGGC      14852       CG   C
                                TGGGAGGG  AGGG GGC
                                ||||||||  |||| |||
                                ACCCTCCC  TCCT CCG
                                      __   _
GAM566  NFASC    3' TGGGAGGGGGCTTGTGGGTGGC 14853     __   GA__  C
                                TGGGA  GGGC   GGG GGC
                                |||||  ||||   ||| |||
                                ACCCT  CCCG   CCC CCG
                                   CC   AACA  A
GAM566  NMT1     3' TGGGAGGACTGGGTGGC    14854       GA  C
                                TGGGAGGGC  GGG GGC
                                |||||||||  ||| |||
                                ACCCTCCTG  CCC CCG
                                     A_  A
GAM566  PALM     3' TAGGAGGCCCAGAGGGTGGC  14855      GC__   C
                                TGGGAGG   GAGGG GGC
                                |||||||   ||||| |||
                                ATCCTCC   CTCCC CCG
                                    GGGT   A
GAM566  PDK2     3' TGGGAGGGCTCAGGAGGTGGC 14856       ____   GC
                                TGGGAGGGC   GAGG  GGC
                                |||||||||   ||||  |||
                                ACCCTCCCG   CTCC  CCG
                                     AGTC   A_
GAM566  PLAGL2   3' TGGGAGGGGGACAGC      14857       CGA
                                TGGGAGGG  GGGCGGC
                                ||||||||  |||||||
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                                ACCCTCCC  CCTGTCG
                                   ___
GAM566  PPP1R12C  3'  GGGAGGGGTGACGGGGTGGC  14858      ____ A  C
                                GGGAGGG   CG GGG GGC
                                |||||||   || ||| |||
                                CCCTCCC   GC CCC CCG
                                   CACT  _  A
GAM566  PTDSS2   5'  TGGGAAGGGGTCGCGGC    14859      CGA __
                                TGGGAGGG  GG  GCGGC
                                ||||||||  ||  |||||
                                ACCCTTCC  CC  CGCCG
                                   ___ AG
GAM566  RAB11B   3'  TGGGAGGGCTGGAACGAGC   14860      GA  _
                                TGGGAGGGC  GGGCG GC
                                |||||||||  ||||| ||
                                ACCCTCCCG  CTTGC CG
                                     AC    T
GAM566  RAB14    5'  GGGAGAGGGGGCGGGGGCGG  14861    ____  A
                                GGGA   GGGCG GGGCGG
                                ||||   ||||| ||||||
                                CCCT   CCCGC CCCGCC
                                  CTCC    C
GAM566  RAB6B    5'  TAGGAGGGCGAGGGGAGGCGGC 14862         ____
                                TGGGAGGGCGAGG   GCGGC
                                ||||||||||||   |||||
                                ATCCTCCCGCTCC   CGCCG
                                     CCTC
GAM566  RAB6C    5'  TGGGAAGGGAAGGAGGGCGG  14764      C___
                                TGGGAGGG   GAGGGCGG
                                ||||||||   ||||||||
                                ACCCTTCC   CTCCCGCC
                                   CTTC
GAM566  RCD-8    3'  TGGGAGAGCGGGCAGGGTGGC  14863       ___  C
                                TGGGAGGGCG  AGGG GGC
                                ||||||||||  |||| |||
                                ACCCTCTCGC  TCCC CCG
                                     CCG   A
GAM566  RODH-4   3'  TGGGAGGGTGTAGACTGGC   14864      CGA  _
                                TGGGAGGG  GGGC GGC
                                ||||||||  |||| |||
                                ACCCTCCC  TCTG CCG
                                   ACA   A
GAM566  SCAMP-4  3'  TGGGAGGACGGGAGGGCGGC  14865       __
                                TGGGAGGGC  GAGGGCGGC
                                |||||||||  |||||||||
                                ACCCTCCTG  CTCCCGCCG
                                     CC
GAM566  SLC16A10  5'  GGCCGAGGCGAGGGCGGC   14866   GA _
                                GG  G GGCGAGGGCGGC
                                ||  | ||||||||||||
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                                CC  C CCGCTCCCGCCG
                                 GG T
GAM566  SLK      5'  TGGGAGAGAAGAAGCGGC     14867        C    G
                                TGGGAGGG GAGG CGGC
                                |||||||| |||| ||||
                                ACCCTCTC CTTC GCCG
                                     T   _
GAM566  SLK      5'  GGGAGAAGGCGGGGCGGC     14868       __    A
                                GGGAG  GGCG GGGCGGC
                                |||||  |||| |||||||
                                CCCTC  CCGC CCCGCCG
                                   TT   _
GAM566  SSAT2    5'  TGAGAGAGCGGGGTGGC      14869         A   C
                                TGGGAGGGCG GGG GGC
                                |||||||||| ||| |||
                                ACTCTCTCGC CCC CCG
                                      _  A
GAM566  STX5A    3'  GGGAGGACAGGGTGGCG      14870        G    C   III
                                GGGAGGGC AGGG GGC   G
                                |||||||| |||| |||   |
                                CCCTCCTG TCCC CCG   C
                                     _   A   III
GAM566  TNK1     3'  TGGGAGGGAGGAGAC        14871         CG    C
                                TGGGAGGG  AGGG GGC
                                ||||||||  |||| |||
                                ACCCTCCC  TCCT CTG
                                      __   _
GAM566  LOC115207 3'  TGGGAGGGCAGCAGC       14872         GAG
                                TGGGAGGGC   GGCGGC
                                |||||||||   ||||||
                                ACCCTCCCG   TCGTCG
                                       ___
GAM566  LOC120224 5'  TGGGAGGGCGAGGCAGGC    14873           GC
                                TGGGAGGGCGAGG  GGC
                                ||||||||||||  |||
                                ACCCTCCCGCTCC  CCG
                                       GT
GAM566  LOC121457 5'  TAGGAGAGGTGGGCGGC     14874         CGA
                                TGGGAGGG   GGGCGGC
                                ||||||||   |||||||
                                ATCCTCTC   CCCGCCG
                                     CA_
GAM566  LOC124045 3'  TGGAGAAGGGGGCGGC      14875     _    CGA
                                TGG GAGGG   GGGCGGC
                                ||| |||||   |||||||
                                ACC CTTCC   CCCGCCG
                                  T    ___
GAM566  LOC126526 3'  TGGGAGTAGAGGGCGGC     14876       GGC
                                TGGGAG   GAGGGCGGC
                                ||||||   |||||||||
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                                ACCCTC   CTCCCGCCG
                                   AT_
GAM566   LOC129198 5'  TGGCAGCGAGGAGGGTGGC   14821     G _ C    C
                                TGG AG GG GAGGG GGC
                                ||| || || ||||| |||
                                ACC TC CT CTCCC CCG
                                  G  G  C    A
GAM566   LOC130497 3'  TGGGAGAGGCGCCGCTGCGGC  14877       _   AGG__
                                TGGGAG GGCG    GCGGC
                                |||||| ||||    |||||
                                ACCCTC CCGC    CGCCG
                                   T   GGCGA
GAM566   LOC143187 3'  TGAGAGGAAAGGCGGC      14878       GC
                                TGGGAGG  GAGGGCGGC
                                |||||||  |||||||||
                                ACTCTCC  TTTCCGCCG
                                   __
GAM566   LOC143282 5'  TGGGAGAGGCGCCAAAGC    14879       _   __
                                TGGGAG GGCG  AGGGC
                                |||||| ||||  |||||
                                ACCCTC CCGC  TTTCG
                                   T   GG
GAM566   LOC145501 3'  TGGGAGGGAGCACAGC      14880       CG  G
                                TGGGAGGG  AG GCGGC
                                ||||||||  || |||||
                                ACCCTCCC  TC TGTCG
                                   __  G
GAM566   LOC147160 5'  GGGAGGGTCGGGCAGGGTGGC  14881       _ ___   C
                                GGGAGGG CG   AGGG GGC
                                ||||||| ||   |||| |||
                                CCCTCCC GC   TCCC CCG
                                   A  CCG   A
GAM566   LOC148753 3'  TGGGGAGTAGGGCGGC      14882     A   CG
                                TGGG GGG  AGGGCGGC
                                |||| |||  ||||||||
                                ACCC CTC  TCCCGCCG
                                  _  A_
GAM566   LOC149483 3'  TGGGAGGCGCCAGCGGC     14883       G  AG
                                TGGGAGG CG  GGCGGC
                                ||||||| ||  ||||||
                                ACCCTCC GC  TCGCCG
                                   _ GG
GAM566   LOC149773 5'  TGGGAGGGAGGGGGGC      14884       CG   C
                                TGGGAGGG  AGGG GGC
                                ||||||||  |||| |||
                                ACCCTCCC  TCCC CCG
                                   __   C
GAM566   LOC150166 5'  TGGGAGAGGCGATGGGGC    14885       _   __
                                TGGGAG GGCGA  GGGC
                                |||||| |||||  ||||
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                                ACCCTC CCGCT  CCCG
                                   T    AC
GAM566  LOC154197 3'  TGGGGACCCGAGGGTGGC    14886     A  G_    C
                                TGGG GG  CGAGGG GGC
                                |||| ||  |||||| |||
                                ACCC CT  GCTCCC CCG
                                  _ GG     A
GAM566  LOC155060 3'  TGGGAGGGTCCCAAACTGGC   14887       CGA_   _
                                TGGGAGGG    GGGC GGC
                                ||||||||    |||| |||
                                ACCCTCCC    TTTG CCG
                                     AGGG    A
GAM566  LOC157226 5'  GGAAAGGCGGGGGCGGCG    14888        A      III
                                GGGAGGGCG GGGCGGC   G
                                ||||||||| |||||||   |
                                CCTTTCCGC CCCGCCG   C
                                      C       III
GAM566  LOC158301 3'  TGGAAGGGGAGCTGGGTGGC   14889       C  ___   C
                                TGGGAGGG GA   GGG GGC
                                |||||||| ||   ||| |||
                                ACCTTCCC CT   CCC CCG
                                     _ CGA   A
GAM566  LOC158431 3'  TGGGAGGGTTGAATTACGG    14890       C_   G_
                                TGGGAGGG  GAG  GCGG
                                ||||||||  |||  ||||
                                ACCCTCCC  CTT  TGCC
                                     AA   AA
GAM566  LOC161482 3'  TGGGAGGGAGGACTCGC     14891       CG    G_
                                TGGGAGGG  AGGGC  GC
                                ||||||||  |||||  ||
                                ACCCTCCC  TCCTG  CG
                                     __    AG
GAM566  LOC164121 5'  TAGGAAAGCGAAGGGTGGC    14892         _  C
                                TGGGAGGGCGA GGG GGC
                                |||||||||| ||| |||
                                ATCCTTTCGCT CCC CCG
                                      T   A
GAM566  LOC165253 5'  TGGGAGGGAGGGGGC       14893       CG    C
                                TGGGAGGG  AGGG GGC
                                ||||||||  |||| |||
                                ACCCTCCC  TCCC CCG
                                     __   _
GAM566  LOC165568 5'  TGGAAGGGTGAACAGC      14894       CGA
                                TGGGAGGG   GGGCGGC
                                ||||||||   |||||||
                                ACCTTCCC   CTTGTCG
                                     A__
GAM566  LOC201245 3'  TGGGAGGGAGGAGAC       14871       CG    C
                                TGGGAGGG  AGGG GGC
                                ||||||||  |||| |||
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                                ACCCTCCC  TCCT CTG
                                   __   _
GAM566   LOC201294 3'  TGAGAAAGGGGCGGC       14838        CGA
                                TGGGAGGG   GGGCGGC
                                ||||||||   |||||||
                                ACTCTTTC   CCCGCCG
                                   ____
GAM566   LOC203076 3'  GGGAGGGGATGGGGTGGC    14895       C __  C
                                GGGAGGG GA  GGG GGC
                                ||||||| ||  ||| |||
                                CCCTCCC CT  CCC CCG
                                   _ AC   A
GAM566   LOC219513 5'  GGGAGGGCCTGGAGGCGGC   14896        GA__
                                GGGAGGGC    GGGCGGC
                                ||||||||    |||||||
                                CCCTCCCG    TCCGCCG
                                    GACC
GAM566   LOC220776 3'  TGGGAGGCAGGGCGGC      14897       G G
                                TGGGAGG C AGGGCGGC
                                ||||||| | ||||||||
                                ACCCTCC G TCCCGCCG
                                   _ _
GAM566   LOC221486 3'  TGGGAGGGAGGACCAGGC    14898        CG   __
                                TGGGAGGG  AGGGC  GGC
                                ||||||||  |||||  |||
                                ACCCTCCC  TCCTG  CCG
                                   __    GT
GAM566   LOC222171 5'  TGGAAGGGCCAAAGCGGC    14899        G
                                TGGGAGGGC AGGGCGGC
                                ||||||||| ||||||||
                                ACCTTCCCG TTTCGCCG
                                    G
GAM566   LOC253747 5'  TGGGAGGATGCACAGAGC    14900       __  _
                                TGGGAGG  GCG AGGGC
                                |||||||  ||| |||||
                                ACCCTCC  CGT TCTCG
                                   TA   G
GAM566   LOC254220 5'  TGGCAGGGACAGGGCGGC    14901    G   CG
                                TGG AGGG  AGGGCGGC
                                ||| ||||  ||||||||
                                ACC TCCC  TCCCGCCG
                                  G   TG
GAM566   LOC254873 3'  TGGGAGGAGTCCAAGGTGG   14770        ___    GC
                                TGGGAGGG   CGAGG  GG
                                ||||||||   |||||  ||
                                ACCCTCCT   GTTCC  CC
                                    CAG    A_
GAM566   LOC255028 5'  TGGGCAGGGCAGCTCCGCGGC  14902     _    AGG__
                                TGGG AGGGCG    GCGGC
                                |||| ||||||    |||||
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                                ACCC TCCCGT    CGCCG
                                  G     CGAGG
GAM566  LOC255270 3'  TGGGAGGGAGAGGAGGGC   14766       C    C
                                TGGGAGGG GAGGG GGC
                                |||||||| ||||| |||
                                ACCCTCCC CTCCT CCG
                                     T    C
GAM566  LOC256107 5'  TGGAAAGAAGAAGGGTGGC   14903       C_   C
                                TGGGAGGG  GAGGG GGC
                                |||||||| ||||| |||
                                ACCTTTCT  TTCCC CCG
                                     TC    A
GAM566  LOC256158 5'  TGGGAGAGCGGGAGGGGC   14904        A  C
                                TGGGAGGGCG GGG GGC
                                |||||||||| ||| |||
                                ACCCTCTCGC CTC CCG
                                      C  C
GAM566  LOC256536 3'  TGGGAGGAACGCGCGGC    14905       _ AGG
                                TGGGAGGG CG   GCGGC
                                |||||||| ||   |||||
                                ACCCTCCT GC   CGCCG
                                     T  G__
GAM566  LOC56930  5'  TGGGAGGGCCAGCCCGGC   14906       G  GG
                                TGGGAGGGC AG  CGGC
                                ||||||||| ||  ||||
                                ACCCTCCCG TC  GCCG
                                      G  GG
GAM566  LOC90139  3'  TGGGAGGGCAAGGACTGGC   14907           _
                                TGGGAGGGCGAGGGC GGC
                                |||||||||||||| |||
                                ACCCTCCCGTTCCTG CCG
                                         A
GAM566  LOC91040  5'  TGGGAGGGCCAGGATGGC   14908       G   GC
                                TGGGAGGGC AGG  GGC
                                ||||||||| |||  |||
                                ACCCTCCCG TCC  CCG
                                      G   TA
GAM566  LOC92231  3'  TGGCGAGGGCTAAAAGGC   14909    _    __
                                TGG GAGGGC  GAGGGC
                                ||| ||||||  ||||||
                                ACC CTCCCG  TTTCCG
                                  G     AT
GAM566  LOC92558  3'  TGGGAGGGAGAGCAGTGGC   14910       C  _ C
                                TGGGAGGG GAG GG GGC
                                |||||||| ||| || |||
                                ACCCTCCC CTC TC CCG
                                     T  G  A
GAM566  LOC92568  3'  TGGGAGGGAGACAGAGC    14911       C  G  C
                                TGGGAGGG GA GG GGC
                                |||||||| || || |||
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                                ACCCTCCC CT TC TCG
                                     T  G  _
GAM567  CD74    3'  TGTCAGGAACGGGGA       14914          CACCT
                                TGTCAGGGACGG    GGA
                                ||||||||||||    |||
                                ACAGTCCTTGCC    CCT
                                      _____
GAM567  CDH7    5'  TGTAGTAAGTACCTGGGGCCT  14915    C  GGAC  C     AA
                                TGT AG   GG ACCTGG  CCT
                                ||| ||   || ||||||  |||
                                ACA TC   TC TGGACC  GGA
                                  _  AT__  A     CC
GAM567  FCRH1   5'  GTCAGGGATGGTACCTAGAGAT 14916        C  C      A___
           GCCT                   GTCAGGGA GG ACCTGGA    CCT
                                ||||||||| || |||||||    |||
                                CAGTCCCT CC TGGATCT    GGA
                                     A  A      CTAC
GAM567  GUCY1B3  3'  TGTTAGGAGAAAACTGGAACCT 14917    C  _  CG  ACC
                                TGT AGG GA  GC   TGGAACCT
                                ||| ||| ||  ||   ||||||||
                                ACA TCC CT  TG   ACCTTGGA
                                  A   T  TT  ____
GAM567  PTPN7   3'  TGTCAGGGGCGGCGTGCCT   14918        A   A__
                                TGTCAGGG CGGC   CCT
                                ||||||||| ||||   |||
                                ACAGTCCC GCCG   GGA
                                     C    CAC
GAM567  PTPN7   3'  TGTCAGGGGCGGCGTGCCT   14918        A   A__
                                TGTCAGGG CGGC   CCT
                                ||||||||| ||||   |||
                                ACAGTCCC GCCG   GGA
                                     C    CAC
GAM567  PTPN7   3'  TGTCAGGGGCGGCGTGCCT   14918        A   A__
                                TGTCAGGG CGGC   CCT
                                ||||||||| ||||   |||
                                ACAGTCCC GCCG   GGA
                                     C    CAC
GAM567  TRPC5   3'  GCAAAGTGGCACCTGG      14919   T    AC
                                G CAGGG  GGCACCTGG
                                | |||||  |||||||||
                                C GTTTC  CCGTGGACC
                                 _    A_
GAM567  TTC3    5'  AGAAAAATACTTGGAACCT   14920      CG C  C
                                GGGA  G AC TGGAACCT
                                ||||  | || ||||||||
                                TCTT  T TG ACCTTGGA
                                   TT A  A
GAM567  A2BP1   5'  TGTCAGGGGCAGCGGCTG    14921        A   AC
                                TGTCAGGG CGGC  CTG
                                ||||||||| ||||  |||
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                                ACAGTCCC GTCG  GAC
                                    C    CC
GAM567  C20orf4   3'  TGTCAGGGTGGCAGGGCC    14922        AC    CCT  AA
                                TGTCAGGG  GGCA   GG  CC
                                ||||||||  ||||   ||  ||
                                ACAGTCCC  CCGT   CC  GG
                                    A_    ____  C_
GAM567  FLJ12891  3'  GTAAGAAATGGTACCTGGAACC 14923    C  GG C  C
           T                     GT AG  A GG ACCTGGAACCT
                                 || ||  | || ||||||||||
                                 CA TC  T CC TGGACCTTGGA
                                  T  TT A  A
GAM567  FLJ14810  3'  TGTCAGGGATGGCCCGGCCCCT 14924         C   A  T  AA
                                TGTCAGGGA GGC CC GG  CCT
                                ||||||||| ||| || ||  |||
                                ACAGTCCCT CCG GG CC  GGA
                                     A  _  _  GG
GAM567  GMEB2     3'  TGTTGGAGACGGCAGGAGGCCT 14925     CA       CCT   A_
                                TGT  GGGACGGCA   GGA  CCT
                                |||  |||||||||   |||  |||
                                ACA  CTCTGCCGT   CCT  GGA
                                  AC        ____   CC
GAM567  KIAA0711  3'  TGACAGGGAGCACCTGG     14926    T     CG
                                TG CAGGGA  GCACCTGG
                                || ||||||  ||||||||
                                AC GTCCCT  CGTGGACC
                                 T     __
GAM567  KIAA1032  3'  AGGGTATGGCACCTGGAACCT  14927      AC_
                                AGGG   GGCACCTGGAACCT
                                ||||   ||||||||||||||
                                TCCC   CCGTGGACCTTGGA
                                  ATA
GAM567  MGC3101   3'  TGTCAGGAGGTGACGGCTGGAG 14928        ____      ACC    A
           CCT                    GTCAGG    GACGGC   TGGA CCT
                                  ||||||    ||||||   |||| |||
                                  CAGTCC    CTGCCG   ACCT GGA
                                     TCCA      ___    C
GAM567  PIR       5'  TGCGGTAGCGGCACCTGGAGCC 14929     CAG  A         A
           T                      TGT   GG CGGCACCTGGA CCT
                                  |||   || |||||||||| |||
                                  ACG   TC GCCGTGGACCT GGA
                                    CCA  _          C
GAM567  PPFIA4    3'  TGCCAGGGCCTGGAA       14930         ACGGCA
                                TGTCAGGG     CCTGGAA
                                ||||||||     |||||||
                                ACGGTCCC     GGACCTT
                                             _______
GAM567  PRMT6     3'  TGTCAGGGATGTGCATGGACCC 14931         CG_   CC    A
           T                      TGTCAGGGA   GCA  TGGA CCT
                                  |||||||||   |||  |||| |||
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                                ACAGTCCCT  CGT  ACCT GGA
                                     ACA  __   G
GAM567  PRO1331  3'  TGCCAGTTACTACTTGGAACCT 14932      GG  G  ACC
                                TGTCAG  AC GC  TGGAACCT
                                ||||||  || ||  ||||||||
                                ACGGTC  TG TG  ACCTTGGA
                                   AA  A  A__
GAM567  SKIP     3'  TGTCAGGATCTGGAAC     14933        ACGGCAC
                                TGTCAGGG     CTGGAAC
                                ||||||||     |||||||
                                ACAGTCCT     GACCTTG
                                     A_____
GAM567  SKIP     3'  TGTCAGGATCTGGAAC     14933        ACGGCAC
                                TGTCAGGG     CTGGAAC
                                ||||||||     |||||||
                                ACAGTCCT     GACCTTG
                                     A_____
GAM567  LOC115110 5'  TGTCAGGGGCAGGCACTTGA  14934        A _    C
                                TGTCAGGG C GGCAC TGG
                                |||||||| | ||||| |||
                                ACAGTCCC G CCGTG ACT
                                     C T    A
GAM567  LOC145739 3'  TGTCAGGGAGAGGAA       14935        C  CACCT
                                TGTCAGGGA GG    GGAA
                                |||||||| ||    ||||
                                ACAGTCCCT CT    CCTT
                                     _ _____
GAM567  LOC149566 3'  TGTCAGGGATGGGGAGCC    14936        C  CACCT   A
                                TGTCAGGGA GG    GGA CC
                                |||||||| ||    ||| ||
                                ACAGTCCCT CC    CCT GG
                                     A _____  C
GAM567  LOC197319 3'  TGTCTGGGGCTCATGGAACCT  14937     A   ACG  ACC
                                TGTC GGG   GC   TGGAACCT
                                |||| |||   ||   ||||||||
                                ACAG CCC   CG   ACCTTGGA
                                  A  ___  AGT
GAM567  LOC222493 5'  TGTCAGGGACTGGTGCTGG   14938         _  CAC
                                TGTCAGGGAC GG   CTGG
                                |||||||||| ||   ||||
                                ACAGTCCCTG CC   GACC
                                     A  AC_
GAM567  LOC92305  3'  TGTCAGGGCTGTGCCCTGGGGC 14939        ACG_ A    AA
           CT                    TGTCAGGG   GC CCTGG  CCT
                                ||||||||   || |||||  |||
                                ACAGTCCC    CG GGACC  GGA
                                     GACA  _    CC
GAM568  ARHGAP6  3'  TGAGGTCGTGGGCGCCGCA   14942        A  A  ____
                                TGAGGTCGT GGC CC    CA
                                ||||||||| ||| ||    ||
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                                ACTCCAGCA CCG GG    GT
                                      C   C  CIII
GAM568  FSTL3    3'  GAGGCAGCAGGCACCTAGT    14943      C       C
                                GAGGT GTAGGCACC AGT
                                ||||| ||||||||| |||
                                CTCCG CGTCCGTGG TCA
                                   T       A
GAM568  KCNE1L   3'  TGGGGTGATACACCCAGTAATG 14944    A   CGTAG
                                TG GGT    GCACCCAGTAATG
                                || |||    ||||||||||||
                                AC CCA    TGTGGGTCATTAC
                                 C   CTA__
GAM568  XRCC2    3'  GGGTATATACCCAGTAATG   14945    TC   GGC
                                GG  GTA   ACCCAGTAATG
                                ||  |||   ||||||||||
                                CC  CAT   TGGGTCATTAC
                                 __   ATA
GAM568  KIAA1229 3'  GGGTATATACCCAGTAATG   14945    TC   GGC
                                GG  GTA   ACCCAGTAATG
                                ||  |||   ||||||||||
                                CC  CAT   TGGGTCATTAC
                                 __   ATA
GAM568  KIAA1643 3'  TGAGGTCGTGGCTGCCGTGCAT 14946       A   A_ _______ GTAA
           TAT                   GGTCGT GGC  CC     CA    T
                                |||||| |||  ||     ||    |
                                CCAGCA CCG  GG     GT    A
                                   _   AC  CACIII  AATG
GAM568  MGC32104 3'  AGGTATACACCCAGTAATG   14947     CGTAG
                                AGGT    GCACCCAGTAATG
                                ||||    ||||||||||||
                                TCCA    TGTGGGTCATTAC
                                  TA___
GAM568  LOC144766 3'  TGGGTACATACCCAGTAATG   14948    A   _   AGGC
                                TG GGT CGT    ACCCAGTAATG
                                || ||| |||    ||||||||||
                                AC CCA GTA    TGGGTCATTAC
                                 _   T   _____
GAM568  LOC145384 3'  GGGTATATACCCAGTAATG   14945    TC   GGC
                                GG  GTA   ACCCAGTAATG
                                ||  |||   ||||||||||
                                CC  CAT   TGGGTCATTAC
                                 __   ATA
GAM568  LOC207043 3'  TGGGTCGTAGGCACAGGAGT   14949    A         CC_
                                TG GGTCGTAGGCAC   AGT
                                || ||||||||||||   |||
                                AC CCAGCATCCGTG   TCA
                                 _          TCC
GAM568  LOC222252 3'  GGGTATATACCCAGTAATG   14945    TC   GGC
                                GG  GTA   ACCCAGTAATG
                                ||  |||   ||||||||||
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                                CC  CAT   TGGGTCATTAC
                                 __   ATA
GAM568  LOC257017 5'  AAATACGTGGGTACTCAGTAAT 14950      _  A  C  C
            G                    AGGT CGT GG AC CAGTAATG
                                 |||| ||| || || ||||||||
                                 TTTA GCA CC TG GTCATTAC
                                   T   C  A  A
GAM569  GATA1    3'  GTTGTCCAGAATTCTGGC    14953        GC       A
                                 GTTGTCC  GGGATTCT GC
                                 |||||||  |||||||| ||
                                 CAACAGG  TCTTAAGA CG
                                     __       C
GAM569  GNAI1    3'  GTTGCTGCAAGACTCTAG    14954       CC
                                 GTTGT  GCGGGATTCTAG
                                 |||||  ||||||||||||
                                 CAACG  CGTTCTGAGATC
                                    A_
GAM569  RAB5A    3'  TACATTGTTTATTATGGTTCTA 14955         CCGCG__  A
            GCC                     TACGTTGT      GG TTCTAGCC
                                 ||||||||      || ||||||||
                                 ATGTAACA      CC AAGATCGG
                                      AATAATA  _
GAM569  APMCF1   3'  TTGTTCCACAGCATTCTAGCC  14956      _     G
                                 TTGT CCGCGG ATTCTAGCC
                                 |||| |||||| |||||||||
                                 AACA GGTGTC TAAGATCGG
                                   A     G
GAM569  TSGA14   5'  CACGTTCGGGGTTCTAGC    14957       GTCCG    A
                                 TACGTT    CGGG TTCTAGC
                                 ||||||    |||| |||||||
                                 GTGCAA    GCCC AAGATCG
                                     ______   C
GAM570  APBA1    3'  TTCAGCTTGTCTCACTG     14960      ACTT  _
                                 TTCA    GCT GTCTCACTG
                                 ||||    ||| |||||||||
                                 AAGT    CGA CAGAGTGAC
                                   _____  A
GAM570  CYP11A   3'  TTCAACCTGCTGAGCAGGCTG  14961           TCTCA_
                                 TTCAACTTGCTG     CTG
                                 ||||||||||||     |||
                                 AAGTTGGACGAC     GAC
                                        TCGTCC
GAM570  HGD      5'  TTCACTGCGCTTCACTG     14962      AC    T TC
                                 TTCA  TTGC G  TCACTG
                                 ||||  |||| |  ||||||
                                 AAGT  GACG C  AGTGAC
                                   __   _ GA
GAM570  HNRPK    3'  CTCAACTTGTAGTACTG     14963         CT  CTC
                                 TTCAACTTG  GT   ACTG
                                 |||||||||  ||   ||||
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                                GAGTTGAAC  CA   TGAC
                                     AT  ___
GAM570  HNRPK    3'  CTCAACTTGTAGTACTG    14963       CT  CTC
                                TTCAACTTG  GT   ACTG
                                |||||||||  ||   ||||
                                GAGTTGAAC  CA   TGAC
                                     AT  ___
GAM570  HOXB5    3'  CTCAGCTTGACCCCACTG    14964     A    CTG
                                TTCA CTTG   TCTCACTG
                                |||| ||||   ||||||||
                                GAGT GAAC   GGGGTGAC
                                  C   T__
GAM570  JAG1     3'  CTCAACTTGTTCCCTTACTG  14965       CTG   __
                                TTCAACTTG   TCTC  ACTG
                                |||||||||   ||||  ||||
                                GAGTTGAAC   AGGG  TGAC
                                     A__    AA
GAM570  KIF3B    3'  TTCACTTTTCAACCTCACTG  14966     A  GCTG_
                                TTCA CTT    TCTCACTG
                                |||| |||    ||||||||
                                AAGT GAA    GGAGTGAC
                                  _  AAGTT
GAM570  RGL      3'  TTCAACCTGCATGAGGGCTG  14967        _  TCTCA
                                TTCAACTTGC TG    CTG
                                |||||||||| ||    |||
                                AAGTTGGACG AC    GAC
                                     T  TCCC_
GAM570  SCA1     3'  TTCTGTTGCTCTCACTG     14968     AAC   TG
                                TTC   TTGC  TCTCACTG
                                |||   ||||  ||||||||
                                AAG   AACG  AGAGTGAC
                                  AC_   __
GAM570  AFAP     3'  TTCACCTGCCAGCTCGCTG   14969     A     T  A
                                TTCA CTTGCTG CTC CTG
                                |||| ||||||| ||| |||
                                AAGT GGACGGT GAG GAC
                                  _     C  C
GAM570  AP3M2    5'  TTCAACTCTGGCCTTGCTG   14970       GCT   CA
                                TTCAACTT   GTCT  CTG
                                ||||||||   ||||  |||
                                AAGTTGAG   CGGA  GAC
                                     AC_   AC
GAM570  C22orf20 3'  TTCTACTAACATCTCACTG   14971    A  T  T
                                TTC ACT GC GTCTCACTG
                                ||| ||| || |||||||||
                                AAG TGA TG TAGAGTGAC
                                  A  T  _
GAM570  CDCA4    3'  TTCACCCAGGTCTCACTG    14972     A  GCT
                                TTCA CTT   GTCTCACTG
                                |||| |||   |||||||||
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                                AAGT GGG   CAGAGTGAC
                                  _  TC_
GAM570  FKBP5    3'  TTCAATCTTGGCCTCACTG   14973      _   CT
                                TTCAA CTTG  GTCTCACTG
                                ||||| ||||  |||||||||
                                AAGTT GAAC  CGGAGTGAC
                                  A   __
GAM570  FLJ11700 3'  CTCAGCTGCCACCTCTCACTG  14974     A  T   __
                                TTCA CT GCTG  TCTCACTG
                                |||| || ||||  ||||||||
                                GAGT GA CGGT  AGAGTGAC
                                  C  _   GG
GAM570  FLJ13611 3'  CTCAACTTTCTCACT       14975         GCTG
                                TTCAACTT    TCTCACT
                                ||||||||    |||||||
                                GAGTTGAA    AGAGTGA

                                   ____
GAM570  FLJ20073 3'  CTTAACTGAATCTCACTG    14976     _  __
                                CTTG CTG  TCTCACTG
                                |||| |||  ||||||||
                                GAAT GAC  AGAGTGAC
                                  T   TT
GAM570  FLJ20257 5'  TCCGACTTGCTGGAAGTCCTG  14977     A       TC__  A
                                TTC ACTTGCTG    TC CTG
                                ||| ||||||||    || |||
                                AGG TGAACGAC    AG GAC
                                  C       CTTC  _
GAM570  HCC8     3'  TCAGTTACCCCTCACTG     14978     AC     G
                                TCA  TTGCT TCTCACTG
                                |||  ||||| ||||||||
                                AGT  AATGG GGAGTGAC
                                  C_    _
GAM570  KIAA0152 3'  TCAGTTATATCTCACTG     14979     AC   C
                                TCA  TTG TGTCTCACTG
                                |||  ||| ||||||||||
                                AGT  AAT ATAGAGTGAC
                                  C_  _
GAM570  KIAA0711 5'  TCCAACTTGCTGAACTTCTG   14980           TCTCA
                                TTCAACTTGCTG    CTG
                                ||||||||||||    |||
                                AGGTTGAACGAC    GAC
                                       TTGAA
GAM570  KIAA0937 3'  TTCAGTCTGGCTCCCACTG   14981     A_  T  TG
                                TTCA  CT GC  TCTCACTG
                                ||||  || ||  ||||||||
                                AAGT  GA CG  AGGGTGAC
                                  CA  C  __
GAM570  KIAA1026 3'  TTCAATTTACTCCCACACTG   14982      C    G  T
                                TTCAA TTGCT TC CACTG
                                ||||| ||||| || |||||
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                                AAGTT AATGA GG GTGAC
                                  A    G  T
GAM570  KIAA1715  3'  TTCATTGCATTCTCACTG   14983     AC   TG
                                TTCA  TTGC  TCTCACTG
                                ||||  ||||  ||||||||
                                AAGT  AACG  AGAGTGAC
                                  __   TA
GAM570  KPNB3     3'  TTCAACTTTTGGGTCTACTG  14984       GCT_   C
                                TTCAACTT   GTCT ACTG
                                ||||||||   |||| ||||
                                AAGTTGAA   CAGA TGAC
                                    AACC   _
GAM570  MGC12992  3'  TTCAAATGCACCCTCACTG   14985     CT   TG
                                TTCAA  TGC  TCTCACTG
                                |||||  |||  ||||||||
                                AAGTT  ACG  GGAGTGAC
                                  T_   TG
GAM570  N4BP1     5'  CTCAGCTTGCTGCCGCTG    14986     A       TCA
                                TTCA CTTGCTGTC   CTG
                                |||| |||||||||   |||
                                GAGT GAACGACGG   GAC
                                  C       C__
GAM570  OS4       3'  TTCAGCTTCTCCCCCACTG   14987     A   G  G
                                TTCA CTT CT TCTCACTG
                                |||| ||| || ||||||||
                                AAGT GAA GA GGGGTGAC
                                  C   _  G
GAM570  P450RAI-2 3'  TTCAGCTCTCTTCTCACTG   14988     A  TG  G
                                TTCA CT  CT TCTCACTG
                                |||| ||  || ||||||||
                                AAGT GA  GA AGAGTGAC
                                  C  GA  _
GAM570  ZNF17     3'  TTCACTTACCACTCACTG    14989     A     T
                                TTCA CTTGCTG CTCACTG
                                |||| ||||||| |||||||
                                AAGT GAATGGT GAGTGAC
                                  _     _
GAM570  LOC134266 3'  TTCATTCATACTCTCACTG   14990     ACT_   TG
                                TTCA    TGC  TCTCACTG
                                ||||    |||  ||||||||
                                AAGT    ATG  AGAGTGAC
                                  AAGT   __
GAM570  LOC144308 3'  TTCAACCTCCCACCTTGCTG  14991       G TG   CA
                                TTCAACTT C  TCT  CTG
                                |||||||| |  |||  |||
                                AAGTTGGA G  GGA  GAC
                                    G GT   AC
GAM570  LOC145693 3'  TCACCTGCTGTCTCACTG    14992     A
                                TCA CTTGCTGTCTCACTG
                                ||| ||||||||||||||
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                                AGT GGACGACAGAGTGAC
                                  _
GAM570  LOC145951 3'  TCCGGCTTGCTGTCATCATCTG 14993     AA       _  _
                                TTC  CTTGCTGTC TCA CTG
                                |||  ||||||||| ||| |||
                                AGG  GAACGACAG AGT GAC
                                  CC        T   A
GAM570  LOC146136 5'  TCAAAGCCATGTCTCACTG    14994     CTT  __
                                TCAA   GCT  GTCTCACTG
                                ||||   |||  |||||||||
                                AGTT   CGG  CAGAGTGAC
                                  T__   TA
GAM570  LOC146517 3'  TTCAACATGCCTGCTTGCTG   14995       T   GT  CA
                                TTCAAC TGCT  CT  CTG
                                ||||||| ||||  ||  |||
                                AAGTTG ACGG  GA  GAC
                                    T    AC  AC
GAM570  LOC152345 3'  TTCACCTCCACCTCACTG    14996     A   G TG
                                TTCA CTT C  TCTCACTG
                                |||| ||| |  ||||||||
                                AAGT GGA G  GGAGTGAC
                                  _  _ GT
GAM570  LOC153651 5'  TCAATGATCTCACTG       14997     CT  CT
                                TCAA  TG  GTCTCACTG
                                ||||  ||  |||||||||
                                AGTT  AC  TAGAGTGAC
                                  __  __
GAM570  LOC154007 3'  CAACTTGCTATTTTCACTG    14998          C_
                                CAACTTGCTGT  TCACTG
                                ||||||||||  ||||||
                                GTTGAACGATA  AGTGAC
                                      AA
GAM570  LOC157247 5'  TCAATCCTGTTGTCTCACTG   14999     _   C
                                TCAA CTTG TGTCTCACTG
                                |||| |||| ||||||||||
                                AGTT GGAC ACAGAGTGAC
                                  A    A
GAM570  LOC158293 3'  TCCATAGCAGCTCTCACTG    15000     ACTT  T _
                                TTCA    GC G TCTCACTG
                                ||||    || | ||||||||
                                AGGT    CG C AGAGTGAC
                                  AT__  T G
GAM570  LOC163231 3'  TCAACTTGTACCCACTG      15001       C  T
                                TCAACTTG TG CTCACTG
                                |||||||| || |||||||
                                AGTTGAAC AT GGGTGAC
                                    _ _
GAM570  LOC167693 5'  TTCAGCTTTGCTGCTACTG    15002     A  _   T  C
                                TTCA CTT GCTG CT ACTG
                                |||| ||| |||| || ||||
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                                AAGT GAA CGAC GA TGAC
                                  C   A   _ _
GAM570  LOC219988 5'  TTCAATCACCATCTTACTG   15003      C TG     C
                                TTCAA T  CTGTCT ACTG
                                ||||| |  |||||| ||||
                                AAGTT A  GGTAGA TGAC
                                  _ GT     A
GAM570  LOC220565 3'  TCAAAGCCATGTCTCACTG   14994     CTT   __
                                TCAA   GCT  GTCTCACTG
                                ||||   |||  |||||||||
                                AGTT   CGG  CAGAGTGAC
                                  T__   TA
GAM570  LOC222008 5'  TCCGGCTTGCGTGATCACTG  15004     AA    _ TC
                                TTC  CTTGC TG  TCACTG
                                |||  ||||| ||  ||||||
                                AGG  GAACG AC  AGTGAC
                                  CC    C  T_
GAM570  LOC256055 5'  TCCAACTTGAACTGGTTACTG  15005         __   TCTC
                                TTCAACTTG  CTG    ACTG
                                |||||||||  |||    ||||
                                AGGTTGAAC  GAC    TGAC
                                     TT   CAA_
GAM570  LOC51131  3'  TTCAACTGCTGCCACCT     15006        T     TCA
                                TTCAACT GCTGTC   CT
                                ||||||| ||||||   ||
                                AAGTTGA CGACGG   GA
                                   _     TG_
GAM570  LOC56964  5'  CTCAGCTTGCTGCTCCCACTG  15007      A     _
                                TTCA CTTGCTG TCTCACTG
                                |||| ||||||| ||||||||
                                GAGT GAACGAC AGGGTGAC
                                  C      G
GAM570  LOC90246  5'  CAACTTGTCCCACTG       15008       TGC
                                CAACT   TGTCTCACTG
                                |||||   ||||||||||
                                GTTGA   ACAGGGTGAC
                                   ___
GAM570  LOC91796  5'  TTCATACTGTCTTTACTG    15009      ACT      C_
                                TTCA   TGCTGTCT  ACTG
                                ||||   ||||||||  ||||
                                AAGT   ATGACAGA  TGAC
                                   ___       AA
GAM571  EPB41L2   3'  CTGGAATAGTGGTGTGGCATTA 15012          ATCTACAA
                                CTGGAATAGT       CATTA
                                ||||||||||       |||||
                                GACCTTATCA       GTAAT
                                     CCACACC_
GAM571  EXT2      5'  TCTGAGTAGCTCTATAACATTA 15013       AA   A   C
                                TCTGG  TAGT TCTA AACATTA
                                |||||  |||| |||| |||||||
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                                AGACT  ATCG AGAT TTGTAAT
                                  C_   _   A
GAM571  SLC14A2  3'  TCTGGAATGGTGACTACA    15014        A  AT
                                TCTGGAAT GT  CTACA
                                |||||||| ||  |||||
                                AGACCTTA CA  GATGT
                                     C  CT
GAM571  ARF6     3'  CTGGAACATATTACAATATTA  15015        G  C    C
                                CTGGAATA TAT TACAA ATTA
                                |||||||| ||| ||||| ||||
                                GACCTTGT ATA ATGTT TAAT
                                     _  _    A
GAM571  KIAA0970 3'  TGGAACAGTATCCAAACAGACA 15016          __  _
          TTA                    TGGAATAGTATCT  ACA ACATTA
                                |||||||||||||  ||| ||||||
                                ACCTTGTCATAGG  TGT TGTAAT
                                       TT   C
GAM571  PRO0386  3'  TCTGGAATAGCATCTACA    15017
                                TCTGGAATAGTATCTACA
                                ||||||||||||||||||
                                AGACCTTATCGTAGATGT

GAM571  TTTY12   3'  TCTAGAATGCAAGTGACATTA  15018        A  TCTACA
                                TCTGGAAT GTA     ACATTA
                                |||||||| |||     ||||||
                                AGATCTTA CGT     TGTAAT
                                     _  TCAC__
GAM571  LOC196411 3'  TCTGGGGTACTCCACTTGACAT 15019      AATA  _    A__
          TA                     TCTGG   GTA TCTAC   ACATTA
                                |||||   ||| |||||  ||||||
                                AGACC   CAT AGGTG   TGTAAT
                                  C___   G    AAC
GAM572  DUSP4    3'  TAAGTTGGAGTGTTCTGT    15022     A    TCT
                                TAA TTGGA   TGTTCTGT
                                ||| |||||  ||||||||
                                ATT AACCT   ACAAGACA
                                  C    C__
GAM572  DUSP4    3'  TAAGTTGGAGTGTTCTGT    15022     A    TCT
                                TAA TTGGA   TGTTCTGT
                                ||| |||||  ||||||||
                                ATT AACCT   ACAAGACA
                                  C    C__
GAM572  RANBP2L1  3'  TAAATTGGAAACCAATGTTCTG 15023        T_ __
          T                     TAAATTGGA  CT  TGTTCTGT
                                |||||||||  ||  ||||||||
                                ATTTAACCT  GG  ACAAGACA
                                     TT  TT
GAM572  RIMS1    3'  TAGATTGCCTTGTTCTGT    15024      ___
                                TGGAT   CTTGTTCTGT
                                |||||  ||||||||||
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                                ATCTA  GAACAAGACA
                                  ACG
GAM572  UC28    5' TAAATTGAATTGTAGCTCTGT 15025        CTT_
                                TAAATTGGAT  GTTCTGT
                                ||||||||||  |||||||
                                ATTTAACTTA  CGAGACA
                                     ACAT
GAM572  C1orf29  5' TAAATTGAGGATTAACTGTTCT 15026      __  C__
           GT                    TAAATT GGAT  TTGTTCTGT
                                ||||||| ||||  |||||||||
                                ATTTAA CCTA  GACAAGACA
                                   CT  ATT
GAM572  CALN1    3' TAAATTACCTGTTCTGT    15027       GAT
                                TAAATTG  CTTGTTCTGT
                                |||||||  ||||||||||
                                ATTTAAT  GGACAAGACA
                                   ___
GAM572  CASPR3   3' TAAATTGAAAAGATGTTCTGT 15028        TCT_
                                TAAATTGGA  TGTTCTGT
                                |||||||||  ||||||||
                                ATTTAACTT  ACAAGACA
                                     TTCT
GAM572  FLJ13215 3' TTGATATGCTTGTTCTGT   15029     _ _
                                TTGG AT CTTGTTCTGT
                                |||| || ||||||||||
                                AACT TA GAACAAGACA
                                  A  C
GAM572  FLJ22800 3' AAATTGGGCCATTCTGT    15030       AT TT
                                AAATTGG  C  GTTCTGT
                                |||||||  |  |||||||
                                TTTAACC  G  TAAGACA
                                   CG __
GAM572  KIAA0336 3' AATTGGAAACCAATGTTCTGT 15031       T_ __
                                AATTGGA  CT  TGTTCTGT
                                |||||||  ||  ||||||||
                                TTAACCT  GG  ACAAGACA
                                   TT  TT
GAM572  KIAA0555 3' AAATTGAGGTTGTTCTGT   15032       ATC
                                AAATTGG  TTGTTCTGT
                                |||||||  |||||||||
                                TTTAACT  AACAAGACA
                                   CC_
GAM572  KIAA1036 5' TTGGAGGCCTTGTTCTGT   15033     __
                                TTGGA  TCTTGTTCTGT
                                |||||  ||||||||||
                                AACCT  GGAACAAGACA
                                  CC
GAM572  KIAA1493 3' AATCTAATTTTGTTCTGT   15034     G  C
                                AATT GAT TTGTTCTGT
                                |||| ||| |||||||||
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                                TTAG TTA AACAAGACA
                                  A  A
GAM572  MGC20253  3'  AATTGAGTCGTATTCTGT    15035      GA  T
                                AATTG  TC TGTTCTGT
                                |||||  || ||||||||
                                TTAAC  AG ATAAGACA
                                   TC  C
GAM572  NMT2      3'  AAATGGATCTTTTGTTCTGT   15036    T     __
                                AA TGGATCT  TGTTCTGT
                                || |||||||  ||||||||
                                TT ACCTAGA  ACAAGACA
                                 T      AA
GAM572  PC326     5'  TAAATTGGCATTGTCTGT    15037       ATC   T
                                TAAATTGG   TTGT CTGT
                                ||||||||   |||| ||||
                                ATTTAACC   AACA GACA
                                     GT_   _
GAM572  SEC8      3'  TAAATTAGAGGTTCTGT     15038       TCTT
                                TAAATTGGA    GTTCTGT
                                |||||||||    |||||||
                                ATTTAATCT    CAAGACA
                                     C___
GAM572  TRIM36    3'  TAAATTAGATATCCTGT     15039        CTT
                                TAAATTGGAT   GTTCTGT
                                ||||||||||   |||||||
                                ATTTAATCTA   TAGGACA
                                       ___
GAM572  USP24     3'  TAAATTGGATATTCCTGT    15040        CTTG
                                TAAATTGGAT    TTCTGT
                                ||||||||||    ||||||
                                ATTTAACCTA    AGGACA
                                      TA__
GAM572  LOC151248 5'  AATTGAGCTGTTCTGT      15041      ATC
                                AATTGG   TTGTTCTGT
                                ||||||   |||||||||
                                TTAACT   GACAAGACA
                                   C__
GAM572  LOC220692 3'  TAAATTGGAAACCAATGTTCTG 15023        T_ __
           T                    TAAATTGGA  CT  TGTTCTGT
                                |||||||||  ||  ||||||||
                                ATTTAACCT  GG  ACAAGACA
                                     TT  TT
GAM572  LOC255742 5'  TAAGTTGGACCTTCCCGT    15042    A      TG
                                TAA TTGGATCT  TTCTGT
                                |||  ||||||||  ||||||
                                ATT AACCTGGA  AGGGCA
                                  C       __
GAM573  ARG2      3'  AATGTGTAAATGTTCTCATT   15045      A  TAGTT
                                AATGT TA    TGTTCTCATT
                                |||||  ||    ||||||||||
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                                TTACA AT    ACAAGAGTAA
                                  C  TT___
GAM573  CCRL1    3'  TGTATATAGTTCTGTGTCATT  15046          GTTC
                                TGTATATAGTTT   TCATT
                                ||||||||||||  |||||
                                ACATATATCAAG   AGTAA
                                      ACAC
GAM573  IL1RAP   3'  TGAGACATGGTTTGTTCT    15047    T_   A
                                TG  ATAT GTTTGTTCT
                                ||  ||||| |||||||||
                                AC  TGTA CAAACAAGA
                                 TC    C
GAM573  MASP1    3'  TAATATATATATATATATGTTC 15048          GTT___
           TCATT                   TAATGTATATA     TGTTCTCATT
                                ||||||||||||     ||||||||||
                                ATTATATATAT     ACAAGAGTAA
                                      ATATAT
GAM573  NPAT     3'  TAATTATAATTTCTGTTCTCAT 15049      G    TAG
           T                     TAAT TATA   TTTGTTCTCATT
                                ||||| ||||  ||||||||||||
                                ATTA ATAT   AGACAAGAGTAA
                                  _   TAA
GAM573  NPEPPS   3'  TAATGTATATCAGTTTCTCT   15050          _    G
                                TAATGTATAT AGTTT TTCT
                                |||||||||| ||||| ||||
                                ATTACATATA TCAAA GAGA
                                      G    _
GAM573  USP9Y    3'  GTATATATACCTTTCTCATT   15051        GTTTG
                                GTATATA    TTCTCATT
                                |||||||    ||||||||
                                CATATAT    AAGAGTAA
                                    ATGGA
GAM573  WHSC1L1  3'  TAATGTATACAGTTTGGGCT   15052              TT
                                TAATGTATATAGTTTG  CT
                                ||||||||||||||||  ||
                                ATTACATATGTCAAAC  GA
                                          CC
GAM573  AKAP11   3'  TAATGTGTAAGTGCCCTCATT  15053       A  T   TT
                                TAATGT TA AGT  GTTCTCATT
                                ||||||  ||  |||  |||||||||
                                ATTACA AT TCA  CGGGAGTAA
                                   C  _  __
GAM573  CHRNA9   3'  TAATATATATATGACTATTTCA 15054          GT_    C
           TT                    TAATGTATATA   TTGTT TCATT
                                ||||||||||||  ||||| |||||
                                ATTATATATAT   GATAA AGTAA
                                      ACT    _
GAM573  GT650    3'  TAATATATATAAAGTTCTCATT 15055          TTT
                                TAATGTATATAG   GTTCTCATT
                                ||||||||||||  |||||||||
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                                ATTATATATATT  CAAGAGTAA
                                      T__
GAM573  LOC150157 3'  ATGTTGTGTCTTTGTTCTCATT 15056     ATATAG
                                ATGT     TTTGTTCTCATT
                                ||||     ||||||||||||
                                TACA     AAACAAGAGTAA
                                  ACACAG
GAM573  LOC157292 5'  CAATGTGATACTTTTGTTCT   15057      _   AG
                                TAATGT ATAT  TTTGTTCT
                                |||||| ||||  ||||||||
                                GTTACA TATG  AAACAAGA
                                   C   A_
GAM573  LOC196890 3'  ATGTTGTGTCTTTGTTCTCATT 15056     ATATAG
                                ATGT     TTTGTTCTCATT
                                ||||     ||||||||||||
                                TACA     AAACAAGAGTAA
                                  ACACAG
GAM573  LOC257085 3'  ATGTATATATCACATTTTCATT 15058       GTT   C
                                ATGTATATA   TGTT TCATT
                                |||||||||   |||| |||||
                                TACATATAT   GTAA AGTAA
                                     AGT   A
GAM574  CYB561    3'  CAGCCCCAGGGGGCTCTAGCCA 15061       AAA   GTTT
          C                      CAGCCCTAG   GCTT   TCAC
                                |||||||||   ||||   ||||
                                GTCGGGGTC   CGAG   GGTG
                                     CCC   ATC_
GAM574  DBCCR1    3'  CAGTTGCTAGAACGTTTTCA   15062    CC_    AGCT
                                CAG   CTAGAA   TGTTTTCA
                                |||   ||||||   ||||||||
                                GTC   GATCTT   GCAAAAGT
                                  AAC    ____
GAM574  GRM3      3'  CAGCCTAGAAAGTTCTAGCAC  15063     C     C  GTTTT
                                CAGCC TAGAAAG TT    CAC
                                ||||| ||||||| ||    |||
                                GTCGG ATCTTTC AG    GTG
                                   _     A  ATC__
GAM574  MYCL2     3'  CAAGTCTCTGAGCTTGTTTTCA 15064    CC  AGAA
          C                      CAG  CT   AGCTTGTTTTCAC
                                |||  ||   ||||||||||||
                                GTT  GA   TCGAACAAAAGTG
                                  CA  GAC_
GAM574  PAFAH1B1  3'  GCACTGGAATGTCTGTTTTCAC 15065   C  A   AGC
                                GC CT GAA   TTGTTTTCAC
                                || || |||   ||||||||||
                                CG GA CTT   GACAAAAGTG
                                 T  C   ACA
GAM574  PRKCN     3'  CAGCCTTATAAACTGTTTC    15066     C  GA    T
                                CAGCC TA  AAGCT GTTTT
                                ||||| ||  ||||| |||||
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                                GTCGG AT  TTTGA CAAAG
                                  A A_    _
GAM574  PTGS1    3'  AACTTTAGAAAGCGAATTTT  15067     CC       TT
                                AGC  TAGAAAGC  GTTTT
                                |||  ||||||||  |||||
                                TTG  ATCTTTCG  TAAAA
                                  AA       CT
GAM574  PTGS1    3'  AACTTTAGAAAGCGAATTTT  15067     CC       TT
                                AGC  TAGAAAGC  GTTTT
                                |||  ||||||||  |||||
                                TTG  ATCTTTCG  TAAAA
                                  AA       CT
GAM574  PTTG1IP  3'  CCTGGAAGGCTGGCAGGTTCAC 15068     A   A   T  T__
                                CCT GAA GCT GT   TTCAC
                                ||| ||| ||| ||   |||||
                                GGA CTT CGA CG   AAGTG
                                  C   C   C  TCC
GAM574  RP42     3'  CAGCCCTAGTAAAAGTTTT   15069         _    CTT
                                CAGCCCTAG AAAG   GTTTT
                                |||||||||  ||||   |||||
                                GTCGGGATC TTTT   CAAAA
                                     A   ___
GAM574  SLC24A1  5'  CAGCTCTGGAAACTTGT     15070      C  A    G
                                CAGC CT GAAA CTTGT
                                ||||  ||  ||||  |||||
                                GTCG GA CTTT GAACA
                                  A  C   _
GAM574  SMARCD1  3'  CAGCCCTAGGCGCTTTCA    15071         AAA  TT
                                CAGCCCTAG   GC  GTTTTCA
                                |||||||||   ||  |||||||
                                GTCGGGATC   CG  CGAAAGT
                                     ___  __
GAM574  SMARCD1  3'  CAGCCCTAGGCGCTTTCA    15071         AAA  TT
                                CAGCCCTAG   GC  GTTTTCA
                                |||||||||   ||  |||||||
                                GTCGGGATC   CG  CGAAAGT
                                     ___  __
GAM574  SOST     3'  CAGTCCTGCAGGCTTTCA    15072     C   AGAAA  TT
                                CAG CCT     GC  GTTTTCA
                                |||  |||     ||  |||||||
                                GTC GGA     CG  CGAAAGT
                                  A  _____  TC
GAM574  TCF2     3'  AGCTCTAGTCCTTGTTTTC    15073     C    AAAG
                                AGC CTAG    CTTGTTTTC
                                |||  ||||   |||||||||
                                TCG GATC    GAACAAAAG
                                  A   AG__
GAM574  TFRC     5'  AGTTCTAGAAGCCCGCACTCAC 15074     CC     A     T
                                AG  CTAGAA GCTTGT TTCAC
                                ||  |||||| |||||| |||||
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                                TC  GATCTT CGGGCG GAGTG
                                 AA     _     T
GAM574  USP6     5'  CCGGAGAGTCGTCCTCAC    15075   TA  A  C
                                C  GA AG TTGTTTTCAC
                                |  || || ||||||||||
                                G  CT TC AGCAGGAGTG
                                 GC  C  _
GAM574  USP9Y    3'  TAGATCTGACTTGTTTTCA   15076     AA__
                                TAGA   GCTTGTTTTCA
                                ||||   ||||||||||
                                ATCT   TGAACAAAAGT
                                  AGAC
GAM574  ABCA10   5'  AGCCCTAGAAACAATGTT    15077          GCT
                                AGCCCTAGAAA   TGTT
                                ||||||||||   ||||
                                TCGGGATCTTT   ACAA
                                      GTT
GAM574  ARHGEF4  3'  GCTCCTGGAGAGCTGACCAC   15078    _  A  A   TGTTT
                                GC CCT GA AGCT    TCAC
                                || ||| || ||||    ||||
                                CG GGA CT TCGA    GGTG
                                 A   C  C   CT___
GAM574  B3GALT1  5'  GCACTAGTTTGTTTTCA    15079    C   AAAGC
                                GC CTAG    TTGTTTTCA
                                || ||||    |||||||||
                                CG GATC    AACAAAAGT
                                 T   A____
GAM574  C6orf25  3'  GCCTCTGGGGCTCGGTTTTCAC 15080    _ AGAAA    _
                                GCC CT    GCTTG TTTTCAC
                                ||| ||    ||||| |||||||
                                CGG GA    CGAGC AAAAGTG
                                  A  CCC__    C
GAM574  CL683    3'  CAGCCCTATGAGGTAATCA   15081       GAA  CTT  TT
                                CAGCCCTA   AG   GT  TCA
                                ||||||||   ||   ||  |||
                                GTCGGGAT   TC   CA  AGT
                                     AC_  ___  TT
GAM574  DKFZP434B205 3'  GCCCTGCCTGCGTTTGTTTTCA 15082      AGAAA __
           C                     GCCCT    GC  TTGTTTTCAC
                                |||||    ||  ||||||||||
                                CGGGA    CG  AACAAAAGTG
                                   CGGA_  CA
GAM574  DKFZP762N2316 3'  CAGTCCTAAAAAGCAGCTTT   15083    C       TT
                                CAG CCTAGAAAGC  GTTTT
                                ||| ||||||||||  |||||
                                GTC GGATTTTTCG  CGAAA
                                  A        T_
GAM574  FLJ13848  3'  ACCCTTAGAGAGCTATCAGCAC 15084      _  A   T   TT
                                GCCCT AGA AGCT GTT  CAC
                                ||||| ||| |||| |||  |||
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                                TGGGA TCT TCGA TAG  GTG
                                  A  C   _  TC
GAM574  FLJ20337  3'  TAAAAAGCTACCCCTCAC    15085        TG
                                TAGAAAGCT  TTTTCAC
                                |||||||||  |||||||
                                ATTTTTCGA  GGGAGTG
                                     TG
GAM574  HCAP-G    5'  CAGCCCCAGGGAGTATTT    15086        AA  CT
                                CAGCCCTAG  AG  TGTTT
                                |||||||||  ||  |||||
                                GTCGGGGTC  TC  ATAAA
                                     CC  __
GAM574  KIAA0317  3'  CAGCTCAGGAGGGCTTGTTCCT 15087     CCTA  AA      _
          CA                      CAGC   GA  GCTTGTTT TCA
                                ||||   ||  |||||||| |||
                                GTCG   CT  CGAACAAG AGT
                                  AGTC  CC       G
GAM574  KIAA0445  5'  TGACCCTGGGCCTCCGTTTTCA 15088   A    AGAAA  __
          C                      C GCCCT    GCT  TGTTTTCAC
                                | |||||    |||  |||||||||
                                A TGGGA    CGG  GCAAAAGTG
                                 C    CC___   AG
GAM574  KIAA0914  3'  AGTCCTGAGCTTGTTTT    15089    C   A  AA
                                AG CCT GA  GCTTGTTTT
                                || ||| ||  |||||||||
                                TC GGA CT  CGAACAAAA
                                 A  _  __
GAM574  KIAA0931  3'  GCCCTTAGGAAGCTGTCT    15090      _ A    T
                                GCCCT AG AAGCT GTTT
                                ||||| || ||||| ||||
                                CGGGA TC TTCGA CAGA
                                  A  C    _
GAM574  KIAA1034  3'  GCCCTGATTGTTTTCA      15091      A  AAGC
                                GCCCT GA   TTGTTTTCA
                                ||||| ||   |||||||||
                                CGGGA CT   AACAAAAGT
                                     _  _____
GAM574  KIAA1243  3'  CAGCTCAGAAAGATATTTC   15092     CC     CT
                                CAGC  TAGAAAG  TGTTTT
                                ||||  |||||||  ||||||
                                GTCG  GTCTTTC  ATAAAG
                                  A_      T_
GAM574  KIAA1387  3'  GAATTGAGCTTGTTTTCA    15093    ___
                                GAA   AGCTTGTTTTCA
                                |||   ||||||||||||
                                CTT   TCGAACAAAAGT
                                  AAC
GAM574  KIAA1893  3'  CAGCCCTAGAGGCTGC      15094        AA   T
                                CAGCCCTAGA  GCT GT
                                ||||||||||  ||| ||
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                                GTCGGGATCT  CGA CG
                                      C_  _
GAM574  MAL2     3'  CAGCCTCCCCTTGTTTT     15095      _ AGAAAG
                                CAGCC CT     CTTGTTTT
                                ||||| ||     ||||||||
                                GTCGG GG     GAACAAAA
                                   A  G_____
GAM574  MGC13071 5'  AGTCCTAAAAGCTTCCCCAC   15096    C      A   TG  TT
                                AG CCTAGAA GCT  TT  CAC
                                || ||||||| |||  ||  |||
                                TC GGATTTT CGA  AG  GTG
                                 A      _  __  GG
GAM574  MGC9912  3'  CAGCTATAGAAACTAGTTTTTC 15097     CC     G  TG_
           A                     CAGC  TAGAAA CT   TTTTCA
                                ||||  |||||| ||   ||||||
                                GTCG  ATCTTT GA   AAAAGT
                                   AT     _  TCA
GAM574  MRPL45   3'  ACCCTAGAAGTCATTTT     15098         A C TG
                                GCCCTAGAA G T  TTTT
                                ||||||||| | |  ||||
                                TGGGATCTT C A  AAAA
                                     _ _ GT
GAM574  NDRG4    3'  CAGCCCTGCATGTTTTCA     15099        AGAAA  T
                                CAGCCCT    GC TGTTTTCA
                                |||||||    || ||||||||
                                GTCGGGA    CG ACAAAAGT
                                     _____  T
GAM574  NDRG4    3'  CAGCCCTGCATGTTTTCA     15099        AGAAA  T
                                CAGCCCT    GC TGTTTTCA
                                |||||||    || ||||||||
                                GTCGGGA    CG ACAAAAGT
                                     _____  T
GAM574  PLAGL2   3'  CAGCTCTGAAAGCTCAGCT    15100      C  A      _
                                CAGC CT GAAAGCTT GTT
                                |||| || |||||||| |||
                                GTCG GA CTTTCGAG CGA
                                   A  _       T
GAM574  RoXaN    3'  CAGCCCAGAAAGCTGCT     15101       T      T
                                CAGCCC AGAAAGCT GTT
                                |||||| |||||||| |||
                                GTCGGG TCTTTCGA CGA
                                     _       _
GAM574  ZNF33A   3'  ACCCTAGAGAGTACTTTCAC   15102         A  CT
                                GCCCTAGA AG  TGTTTTCAC
                                |||||||| ||  |||||||||
                                TGGGATCT TC  ATGAAAGTG
                                     C  __
GAM574  LOC126917 3'  CAGGCCTAGAAAGCTCAC    15103     C         TG
                                CAG CCTAGAAAGCT  T
                                ||| ||||||||||  |
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                                GTC GGATCTTTCGA  G
                                  C         GT
GAM574   LOC131368 3'  CAACTACAGCTTGTTTTCA   15104     CCTAGAA
                                CAGC      AGCTTGTTTTCA
                                ||||      ||||||||||||
                                GTTG      TCGAACAAAAGT
                                  ATG____
GAM574   LOC134266 3'  CAGTCCTAAAAAGACTAGATTT 15105    C       _  T_
           TCA                    CAG CCTAGAAAG CT  GTTTTCA
                                ||| |||||||| ||  |||||||
                                GTC GGATTTTTC GA  TAAAAGT
                                  A       T  TC
GAM574   LOC145652 3'  AACCCAGCTTGTTTT      15106      TAGAA
                                AGCCC    AGCTTGTTTT
                                |||||    ||||||||||
                                TTGGG    TCGAACAAAA
                                  _____
GAM574   LOC145980 3'  CAGTCCAGAAAGCTGCC    15107    CC        T
                                CAG  CTAGAAAGCT GTT
                                |||  |||||||||| |||
                                GTC  GGTCTTTCGA CGG
                                  A_        _
GAM574   LOC147077 3'  CAGCCCTGGGGGGGATTGTCCTC 15108       AGAAAGC
           A                     CAGCCCT      TTGTTTTCA
                                |||||||      |||||||||
                                GTCGGGA      AACAGGAGT
                                    CCCCCCT
GAM574   LOC149566 3'  GCCCTAGAAACTGCATCTT   15109         G  _
                                GCCCTAGAAA CT TGTTTT
                                |||||||||| || ||||||
                                CGGGATCTTT GA GTAGAA
                                      _  C
GAM574   LOC149579 5'  TGACCCTGGGCCTCCGTTTTCA 15088   A    AGAAA  __
           C                     C GCCCT    GCT  TGTTTTCAC
                                | |||||    |||  |||||||||
                                A TGGGA    CGG  GCAAAAGTG
                                 C    CC___   AG
GAM574   LOC158402 3'  AGCCTTAGAAAGCTAAGC    15110     C       T_
                                AGCC TAGAAAGCT  GT
                                |||| |||||||||  ||
                                TCGG ATCTTTCGA  CG
                                  A       TT
GAM574   LOC158677 5'  CAGCCCTAACGTTTT      15111         AAAGCT
                                CAGCCCTAG     TGTTTT
                                |||||||||     ||||||
                                GTCGGGATT     GCAAAA
                                   ______
GAM574   LOC196549 3'  CAGCTTCATTAAGTTTGTTTTC 15112     CC  GA   C
                                CAGC  TA  AAG TTGTTTTC
                                ||||  ||  ||| ||||||||
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                                GTCG  GT  TTC AACAAAAG
                                  AA  AA   A
GAM574   LOC200583 5'  CAGCCCTTAGAACCATTTTCA  15113        _    AGC TG
                                CAGCCCT AGAA   T  TTTTCA
                                ||||||| ||||   |  ||||||
                                GTCGGGA TCTT   G  AAAAGT
                                   A   ___ GT
GAM574   LOC201952 3'  GCTCAGAGAGCTATCCCCAC   15114    CC    A    T   TT
                                GC  TAGA AGCT GTT  CAC
                                ||  |||| |||| |||  |||
                                CG  GTCT TCGA TAG  GTG
                                 A_   C    _   GG
GAM574   LOC203052 3'  CAGCCCTTGAAATGGGTTTTCA 15115        A    GCTT
           C                     CAGCCCT GAAA    GTTTTCAC
                                ||||||| ||||    ||||||||
                                GTCGGGA CTTT    CAAAAGTG
                                   A    ACC_
GAM574   LOC221511 3'  CAGCCACTGGAGTAGTTTTCAC 15116       _  A  AAGCTT
                                CAGCC CT GA     GTTTTCAC
                                ||||| || ||     ||||||||
                                GTCGG GA CT     CAAAAGTG
                                  T  C  CAT___
GAM574   LOC222614 5'  CAGCTCCTGGAGCATTTTCA   15117      _   A  AA  TT
                                CAGC CCT GA  GC  GTTTTCA
                                |||| ||| ||  ||  |||||||
                                GTCG GGA CT  CG  TAAAAGT
                                  A  C  __  __
GAM574   LOC255043 5'  CAGCTCAGAAGGCTCTCA    15118      CC    A    GTTT
                                CAGC  TAGAA GCTT    TCA
                                ||||  ||||| ||||    |||
                                GTCG  GTCTT CGAG    AGT
                                  A_    C    ____
GAM574   LOC255454 5'  CAGCCTCCTTGTTTTC      15119       _ TAGAAAG
                                CAGCC C      CTTGTTTTC
                                ||||| |      |||||||||
                                GTCGG G      GAACAAAAG
                                  A ________
GAM574   LOC256021 3'  CAGTTCTAAAAAGCTCTGAACT 15120     CC         _  TT
           CA                     CAG  CTAGAAAGCT TG  TTCA
                                |||  |||||||||| ||  ||||
                                GTC  GATTTTTCGA AC  GAGT
                                  AA         G  TT
GAM574   LOC257569 3'  CAGCCACTGGAGTAGTTTTCAC 15116       _  A  AAGCTT
                                CAGCC CT GA     GTTTTCAC
                                ||||| || ||     ||||||||
                                GTCGG GA CT     CAAAAGTG
                                  T  C  CAT___
GAM574   LOC51030  3'  GCCCTAATTGTTTTCA      15121        AAAGC
                                GCCCTAG    TTGTTTTCA
                                |||||||    |||||||||
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                                CGGGATT    AACAAAAGT
                                       _____
GAM574  LOC90643  3'  ACTTTAGAAAGCTTCTCTT   15122   CC       G
                                GC  TAGAAAGCTT TTTT
                                ||  |||||||||| ||||
                                TG  ATCTTTCGAA AGAA
                                 AA        G
GAM575  DDX6      5'  AAAATGAAGAGATAAATATAAG 15125         AATTG
                                AAAGTGAAGA    AAGTATAAG
                                ||||||||||    |||||||||
                                TTTTACTTCT    TTTATATTC
                                      CTA__
GAM575  PRKACB    3'  AAAGGAAGAAATGGATGTA   15126    T      T  A
                                AAAG GAAGAAAT GA GTA
                                |||| |||||||| || |||
                                TTTC CTTCTTTA CT CAT
                                  _      C  A
GAM575  C21orf109 3'  AAATGAAGAAGTTGAGT    15127         A   A
                                AAGTGAAGAA TTGA GT
                                |||||||||| ||||| ||
                                TTTACTTCTT AACT CA
                                      C   _
GAM575  CDC14A    3'  ATGAAGAAATTGTGTCTAAG  15128          AA  A
                                GTGAAGAAATTG  GT TAAG
                                ||||||||||||  || ||||
                                TACTTCTTTAAC  CA ATTC
                                       A_  G
GAM575  DKFZP566K1924 3'  AAGTGAAGAAGACTGTAG    15129         _   A
                                AAGTGAAGAA ATTG AG
                                |||||||||| ||||| ||
                                TTCACTTCTT TGAC TC
                                      C   A
GAM575  FLJ21313  3'  GGAGGAAGGAAGTATA     15130   A  T   AAATT
                                A AG GAAG    GAAGTATA
                                | || ||||    ||||||||
                                C TC CTTC    CTTCATAT
                                 C  _   _____
GAM575  FLJ22004  3'  AAAATGAAGAAAACAGGTAT  15131          TTGAA
                                AAAGTGAAGAAA    GTAT
                                ||||||||||||    ||||
                                TTTTACTTCTTT    CATA
                                       TGTC_
GAM575  HSPC054   3'  AAAGTTAAATCTGAAGTATA  15132     GAA  A
                                AAAGT   GAA TTGAAGTATA
                                |||||   ||| ||||||||||
                                TTTCA   TTT GACTTCATAT
                                   A__   A
GAM575  KIAA0563  3'  GTGAGGAAATTGAGTCACA   15133     A      AG
                                GTGA GAAATTGA  TATA
                                |||| ||||||||  ||||
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                                CACT CTTTAACT  GTGT
                                  C       CA
GAM575  KIAA0603  3'  AAGTGAAGAGTTGAAAT     15134         AA
                                AAGTGAAGA  TTGAAGT
                                |||||||||  |||||||
                                TTCACTTCT  AACTTTA
                                     C_
GAM575  KIAA1505  3'  AGTGAAAAAGAAAATATAAG   15135         ATT
                                AGTGAAGAA   GAAGTATAAG
                                |||||||||   ||||||||||
                                TCACTTTTT   TTTTATATTC
                                     C__
GAM575  KIAA1949  5'  AAAGTGAAGAGAAGT       15136         AATT
                                AAAGTGAAGA    GAAGT
                                ||||||||||    |||||
                                TTTCACTTCT    CTTCA
                                      _____
GAM575  KIAA1949  5'  AAAGTGAAGAGAAGT       15136         AATT
                                AAAGTGAAGA    GAAGT
                                ||||||||||    |||||
                                TTTCACTTCT    CTTCA
                                      _____
GAM575  KIAA1949  5'  AAAGTGAAGAGAAGT       15136         AATT
                                AAAGTGAAGA    GAAGT
                                ||||||||||    |||||
                                TTTCACTTCT    CTTCA
                                      _____
GAM575  SLC31A2   3'  AAAGTGAAGAGGTTCAACTAT  15137          AA  G  G
                                AAAGTGAAGA  TT AA TAT
                                ||||||||||  || || |||
                                TTTCACTTCT  AA TT ATA
                                      CC  G  G
GAM575  TOR1B     3'  AAAGTGAGAGATTGACCCAAG  15138        A  A    AGTA
                                AAAGTGA GA ATTGA    TAAG
                                ||||||| || |||||    ||||
                                TTTCACT CT TAACT    GTTC
                                    _ C     GG__
GAM575  LOC143902 3'  AAAGTGAAGGTATAA       15139         AAATTGAA
                                AAAGTGAAG       GTATAA
                                |||||||||       ||||||
                                TTTCACTTC       CATATT
                                      _________
GAM575  LOC145231 5'  AAAATGAAGAAACTGAAGTGTA 15140                A
          AG                      AAAGTGAAGAAATTGAAGT TAAG
                                ||||||||||||||||||| ||||
                                TTTTACTTCTTTGACTTCA ATTC
                                              C
GAM575  LOC147071 3'  GTGAGGAAATTGAGTCACA    15133      A       AG
                                GTGA GAAATTGA  TATA
                                ||||  ||||||||  ||||
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                                CACT CTTTAACT  GTGT
                                  C       CA
GAM575  LOC201173 3'  GTGAGGAAATTGAGTCACA   15133      A       AG
                                GTGA GAAATTGA  TATA
                                |||| ||||||||  ||||
                                CACT CTTTAACT  GTGT
                                  C       CA
GAM575  LOC201220 3'  GTGAGGAAATTGAGTCACA   15133      A       AG
                                GTGA GAAATTGA  TATA
                                |||| ||||||||  ||||
                                CACT CTTTAACT  GTGT
                                  C       CA
GAM575  LOC221688 3'  AAAGTTAAGAAATTGGGTTATA 15141       G        AAG
          AG                     AAAGT AAGAAATTG   TATAAG
                                ||||| |||||||||   ||||||
                                TTTCA TTCTTTAAC   ATATTC
                                   A        CCA
GAM575  LOC221964 3'  AAAGATGAGGAAATTGAGACAC 15142      _  A       AG
          A                      AAAG TGA GAAATTGA  TATA
                                |||| ||| ||||||||  ||||
                                TTTC ACT CTTTAACT  GTGT
                                  T  C       CT
GAM576  ACP1    3'  AGAGGTAGACTCGATTATCTAA 15145      C   CTAA  GC_
                                AGAGG AGAC   GG   TCTAA
                                ||||| ||||   ||  |||||
                                TCTCC TCTG   CT   AGATT
                                   A   AG__  AAT
GAM576  ACP1    3'  AGAGGTAGACTCGATTATCTAA 15145      C   CTAA  GC_
                                AGAGG AGAC   GG   TCTAA
                                ||||| ||||   ||  |||||
                                TCTCC TCTG   CT   AGATT
                                   A   AG__  AAT
GAM576  ADAR    3'  AGAGGCAGGCTCAGCTCC    15146       AC  AAG
                                AGAGGCAG  CT   GGCTCT
                                ||||||||  ||  ||||||
                                TCTCCGTC  GA   TCGAGG
                                    C_  G__
GAM576  ADAR    3'  AGAGGCAGGCTCAGCTCC    15146       AC  AAG
                                AGAGGCAG  CT   GGCTCT
                                ||||||||  ||  ||||||
                                TCTCCGTC  GA   TCGAGG
                                    C_  G__
GAM576  ADAR    3'  AGAGGCAGGCTCAGCTCC    15146       AC  AAG
                                AGAGGCAG  CT   GGCTCT
                                ||||||||  ||  ||||||
                                TCTCCGTC  GA   TCGAGG
                                    C_  G__
GAM576  ATP10C  3'  AGAGGCAGACTCAGGAC     15147        CTA
                                AGAGGCAGAC   AGGGC
                                ||||||||||   |||||
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                                TCTCCGTCTG  TCCTG
                                     AG_
GAM576  BCL2    3'  GAGGGCAGGAGGGCTCT    15148    _  ACCTA
                                GAGG CAG    AGGGCTCT
                                |||| |||    ||||||||
                                CTCC GTC    TCCCGAGA
                                  C  C____
GAM576  CASP10  3'  AGAGGCAATCTAAGCTC    15149      AC  AG
                                AGAGGCAG  CTA  GGCTC
                                ||||||||  |||  |||||
                                TCTCCGTT  GAT  TCGAG
                                     A_  __
GAM576  CASP10  3'  AGAGGCAATCTAAGCTC    15149      AC  AG
                                AGAGGCAG  CTA  GGCTC
                                ||||||||  |||  |||||
                                TCTCCGTT  GAT  TCGAG
                                     A_  __
GAM576  CEP2    3'  AGAGGCAAGCCCTCAGCTCT  15150      GA  AAG
                                AGAGGCA  CCT   GGCTCT
                                |||||||  |||  ||||||
                                TCTCCGT  GGG  TCGAGA
                                    TC  AG_
GAM576  CIT     3'  GAGGCGGGCCTAAGAGTC    15151      AGA      C
                                GAGGC  CCTAAGGG TC
                                |||||  |||||||| ||
                                CTCCG  GGATTCTC AG
                                   CCC      _
GAM576  D12S2489E 3'  AGAGGCAGCCTTGGGGATATCT 15152        A  AA  C__
                                AGAGGCAG CCT  GGG  TCT
                                |||||||| |||  |||  |||
                                TCTCCGTC GGA  CCC  AGA
                                     _  AC  TAT
GAM576  FLOT2   3'  AGATGGCACAAGGGCTCT    15153    _  GACC
                                AGA GGCA   TAAGGGCTCT
                                ||| ||||   ||||||||||
                                TCT CCGT   GTTCCCGAGA
                                  A  _____
GAM576  FN14    3'  GAGGCAGAGACTGGCTCTA   15154      CCTAAG
                                GAGGCAGA    GGCTCTA
                                ||||||||    |||||||
                                CTCCGTCT    CCGAGAT
                                    CTGA__
GAM576  FPGS    3'  GATGCGGACCCACCGGGCTCT  15155   G  A    A_
                                GA GC GACCTA  GGGCTCT
                                || || ||||||  |||||||
                                CT CG CTGGGT  CCCGAGA
                                 A  C    GG
GAM576  GPRK6   3'  AGAGGCAGACCTATCTGGG   15156         A__
                                AGAGGCAGACCTA  GGG
                                ||||||||||||  |||
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                                TCTCCGTCTGGAT  CCC
                                       AGA
GAM576  HHIP    5'  AGGGCCAGCGCTGGGCTCTA  15157   A  _ AC  AA
                                AG GGC AG  CT  GGGCTCTA
                                || ||| ||  ||  ||||||||
                                TC CCG TC  GA  CCCGAGAT
                                 _  G  GC  __
GAM576  IL21R   3'  GAGGCAGACGCTGGAGGGCT  15158       _ A_
                                GAGGCAGAC CT  AGGGCT
                                ||||||||| ||  ||||||
                                CTCCGTCTG GA  TCCCGA
                                     C  CC
GAM576  ITGB1   3'  AAAGGCAGATTTAGGATC   15159       CCTA   C
                                AGAGGCAGA   AGGG TC
                                |||||||||   |||| ||
                                TTTCCGTCT   TCCT AG
                                     AAA_   _
GAM576  ITPR3   3'  AGAGGCAGGTCCTGGGAGC   15160      A_  AA
                                AGAGGCAG  CCT  GGGC
                                ||||||||  |||  ||||
                                TCTCCGTC  GGA  CTCG
                                    CA   CC
GAM576  KLHL1   5'  AGAGGCAGGACTGGGACGCCAA 15161       AC  AA   T
          A                      AGAGGCAG  CT  GGGC CTAAA
                                 ||||||||  ||  |||| |||||
                                 TCTCCGTC  GA  CCTG GGTTT
                                     CT  C_   C
GAM576  MAPK3   3'  GAGGCAGGTCCAGGCCCCA   15162      A_ TAA
                                GAGGCAG  CC   GGGCTCTA
                                |||||||  ||   ||||||||
                                CTCCGTC  GG   TCCGGGGT
                                    CA  ____
GAM576  MEN1    3'  GGCAGAGCCCTGGGTTCT    15163      _  AA  C
                                GGCAGA CCT  GGG TCT
                                |||||| |||  ||| |||
                                CCGTCT GGG  CCC AGA
                                   C  A_  A
GAM576  MEN1    3'  GGCAGAGCCCTGGGTTCT    15163      _  AA  C
                                GGCAGA CCT  GGG TCT
                                |||||| |||  ||| |||
                                CCGTCT GGG  CCC AGA
                                   C  A_  A
GAM576  MEN1    3'  GGCAGAGCCCTGGGTTCT    15163      _  AA  C
                                GGCAGA CCT  GGG TCT
                                |||||| |||  ||| |||
                                CCGTCT GGG  CCC AGA
                                   C  A_  A
GAM576  MEN1    3'  GGCAGAGCCCTGGGTTCT    15163      _  AA  C
                                GGCAGA CCT  GGG TCT
                                |||||| |||  ||| |||
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                                CCGTCT GGG  CCC AGA
                                   C   A_   A
GAM576  MEN1    3'  GGCAGAGCCCTGGGTTCT    15163       _  AA   C
                                GGCAGA CCT  GGG TCT
                                |||||| |||  ||| |||
                                CCGTCT GGG  CCC AGA
                                   C   A_   A
GAM576  MEN1    3'  GGCAGAGCCCTGGGTTCT    15163       _  AA   C
                                GGCAGA CCT  GGG TCT
                                |||||| |||  ||| |||
                                CCGTCT GGG  CCC AGA
                                   C   A_   A
GAM576  MEN1    3'  GGCAGAGCCCTGGGTTCT    15163       _  AA   C
                                GGCAGA CCT  GGG TCT
                                |||||| |||  ||| |||
                                CCGTCT GGG  CCC AGA
                                   C   A_   A
GAM576  NELL2   3'  AGAGGCAGACTTGAGGTCTAA  15164         CTAA   C
                                AGAGGCAGAC    GGG TCTAA
                                ||||||||||    ||| |||||
                                TCTCCGTCTG    TCC AGATT
                                     AAC_  _
GAM576  OAS3    3'  AGACGGCAGAGAACAGGTTCTA 15165     _     CCTA   GC
                                AGA GGCAGA    AGG  TCTA
                                ||| ||||||    |||  ||||
                                TCT CCGTCT    TCC  AGAT
                                  G     CTTG   A_
GAM576  PPP1R11 3'  AGAGGAGACAGTCGGCTCTAA  15166      C    CTAAG
                                AGAGG AGAC     GGCTCTAA
                                ||||| ||||     ||||||||
                                TCTCC TCTG     CCGAGATT
                                   _    TCAG_
GAM576  PPT2    3'  AGGGGCAGGCCAAGAAC     15167    A    A  T
                                AG GGCAG CC AAGGGC
                                || ||||| || ||||||
                                TC CCGTC GG TTCTTG
                                 C    C  _
GAM576  PSCD4   3'  AGAGGCAGAGCTGGGACT    15168         C  AA
                                AGAGGCAGA CT  GGGCT
                                ||||||||| ||  |||||
                                TCTCCGTCT GA  CCTGA
                                     C  C_
GAM576  PTPRN   3'  AGAGGCAGGCCCGGGGCT    15169         A   AA
                                AGAGGCAG CCT  GGGCT
                                |||||||| |||  |||||
                                TCTCCGTC GGG  CCCGA
                                     C   C_
GAM576  SEMA3F  5'  GAAGCAGGCTCCACTCTCTA  15170         AC_   AGGG
                                GAGGCAG   CTA    CTCTA
                                |||||||   |||    |||||
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                                CTTCGTC  GGT   GAGAT
                                   CGA  GA__
GAM576  SKIV2L   5'  AGGGGCAGACCTGGACC    15171   A      AA
                                AG GGCAGACCT  GGGCT
                                || |||||||||  |||||
                                TC CCGTCTGGA  CCTGG
                                 C       __
GAM576  TCP11    3'  AAGGTACCAGGGCTCT     15172    CAG   TA
                                GAGG   ACC  AGGGCTCT
                                ||||   |||  ||||||||
                                TTCC   TGG  TCCCGAGA
                                  A__   __
GAM576  TMEM1    3'  GAGGGAGGCCAGGGCTCT   15173    C  A  TA
                                GAGG AG CC  AGGGCTCT
                                |||| || ||  ||||||||
                                CTCC TC GG  TCCCGAGA
                                  C  C  __
GAM576  VHL      3'  AGAGGCAGAACCTCTA     15174        CCTAAG G
                                AGAGGCAGA     G CTCTA
                                |||||||||     | |||||
                                TCTCCGTCT     T GAGAT
                                      _______ G
GAM576  ARHGEF4  5'  AGAGGCAGACTCACTAGG   15175        ___   A
                                AGAGGCAGAC   CTA GG
                                ||||||||||   ||| ||
                                TCTCCGTCTG   GAT CC
                                     AGT  _
GAM576  BRD4     3'  GACAGGCCCAGGGCTCT    15176     A   A
                                GGCAG CCTA GGGCTCT
                                ||||| |||| |||||||
                                CTGTC GGGT CCCGAGA
                                  C   _
GAM576  C20orf43 3'  AGAGGCAGACCAGCT      15177         TAAG
                                AGAGGCAGACC    GGCT
                                ||||||||||    ||||
                                TCTCCGTCTGG    TCGA
                                      ____
GAM576  CABIN1   3'  AGGGGTGAGCCTGGCCCTAAA  15178   A  CA  _   AAG
                                AG GG  GA CCT   GGCTCTAAA
                                || ||  || |||   |||||||||
                                TC CC  CT GGA   CCGGGATTT
                                 _  CA  C   ___
GAM576  CYLD     3'  GAGGCAGGGCTAGCCCTAAA   15179       AC  AAG
                                GAGGCAG  CT   GGCTCTAAA
                                |||||||  ||   |||||||||
                                CTCCGTC  GA   TCGGGATTT
                                    CC  ___
GAM576  DCTD     3'  AGAGACAGGCTGTCTCCTCTA  15180        AC  AAGGG
                                AGAGGCAG  CT    CTCTA
                                ||||||||  ||    |||||
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                                TCTCTGTC  GA    GAGAT
                                    C_  CAGAG
GAM576  DKFZp434F142 3'  AGAGGCCGACTTGAGGAAGTTC 15181       A  CTA   C__
            T                    AGAGGC GAC   AGGG   TCT
                                 |||||| |||   ||||   |||
                                 TCTCCG CTG   TCCT   AGA
                                    G   AAC    TCA
GAM576  FLJ12121  5'  AGGGGCAAACCTAAGGGTTCTA 15182    A          C
                                 AG GGCAGACCTAAGGG TCTA
                                 || |||||||||||||| ||||
                                 TC CCGTTTGGATTCCC AGAT
                                  C           A
GAM576  FLJ14681  5'  GAGGCAGGGCTTAGGGCTCT   15183       AC  A
                                 GAGGCAG  CT AGGGCTCT
                                 |||||||  || ||||||||
                                 CTCCGTC  GA TCCCGAGA
                                     CC  A
GAM576  FLJ20200  3'  GAGGCAGAGGGCTCT      15184        CCTAA
                                 GAGGCAGA    GGGCTCT
                                 ||||||||    |||||||
                                 CTCCGTCT    CCCGAGA
                                             _____
GAM576  GGA2      3'  AGAGGTAGGAGCTGGGCTCTAA 15185      C  ACCTAA
                                 AGAGG AG     GGGCTCTAA
                                 ||||| ||     |||||||||
                                 TCTCC TC     CCCGAGATT
                                    A  CTCGA_
GAM576  GGA2      3'  AGAGGTAGGAGCTGGGCTCTAA 15185      C  ACCTAA
                                 AGAGG AG     GGGCTCTAA
                                 ||||| ||     |||||||||
                                 TCTCC TC     CCCGAGATT
                                    A  CTCGA_
GAM576  GOLGA2LY  5'  AGAGGGCCCTGCTGGGGGCTCT 15186      CAGA  AA___
                                 AGAGG   CCT    GGGCTCT
                                 |||||   |||    |||||||
                                 TCTCC   GGA    CCCGAGA
                                    CG__   CGACC
GAM576  GTF3C2    3'  GAGGCAGGCCTAAAGGTCCA   15187       A      C
                                 GAGGCAG CCTAAGGG TCTA
                                 ||||||| |||||||| ||||
                                 CTCCGTC GGATTTCC AGGT
                                     C       _
GAM576  IL17D     3'  AGAGACAGACTTTCAATCTAAA 15188         CTAAGGGC
                                 AGAGGCAGAC       TCTAAA
                                 ||||||||||       ||||||
                                 TCTCTGTCTG       AGATTT
                                       AAAGTT__
GAM576  KIAA0285  3'  AGAGGCAGACACTGGTGCT   15189         _  AA  _
                                 AGAGGCAGAC CT  GG GCT
                                 |||||||||| ||  || |||
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                                TCTCCGTCTG GA  CC CGA
                                      T __ A
GAM576  KIAA0418 3' AGAAGCAGGCTTGAGCTC    15190        AC  AA
                                AGAGGCAG  CT  GGGCTC
                                ||||||||  ||  ||||||
                                TCTTCGTC  GA  CTCGAG
                                    C_  A_
GAM576  KIAA0446 5' AGAGGCAGATATGAGCC     15191        CC  A
                                AGAGGCAGA  TA GGGCT
                                |||||||||  || |||||
                                TCTCCGTCT  AT CTCGG
                                      __ A
GAM576  KIAA1029 3' AGAGGCCAGACCCTTTGGG   15192       _     AA_
                                AGAGGC AGACCT   GGG
                                |||||| ||||||   |||
                                TCTCCG TCTGGG   CCC
                                   G     AAA
GAM576  KIAA1030 3' AGAGCCGCAGGGGGCTCTA   15193     __   ACCTAA
                                AGAG  GCAG     GGGCTCTA
                                ||||  ||||     ||||||||
                                TCTC  CGTC     CCCGAGAT
                                  GG   C_____
GAM576  KIAA1130 3' GAGGAAGCCCAGAGGGCTCT  15194     C  A   _
                                GAGG AG CCTA AGGGCTCT
                                |||| || |||| ||||||||
                                CTCC TC GGGT TCCCGAGA
                                  T _   C
GAM576  KIAA1644 5' AGAAGCAGAGGCTCT       15195         CCTAAG
                                AGAGGCAGA     GGCTCT
                                |||||||||     ||||||
                                TCTTCGTCT     CCGAGA
                                      _______
GAM576  LAP1B    5' AGAGGCAGTGCCTGAGCT    15196        A_  AA
                                AGAGGCAG  CCT  GGGCT
                                ||||||||  |||  |||||
                                TCTCCGTC  GGA  CTCGA
                                    AC  __
GAM576  MGC16142 3' AAAGGCAGGCTTCCAA      15197       GACCTAAG   _
                                AGAGGCA       GGCT CTAA
                                |||||||       |||| ||||
                                TTTCCGT       CCGA GGTT
                                   _________   A
GAM576  MGC2628  3' GAGGCAAAAAGAGGCT      15198        CCT  _
                                GAGGCAGA   AAG GGCT
                                ||||||||   ||| ||||
                                CTCCGTTT   TTC CCGA
                                    ___   T
GAM576  MGC2656  5' GAGTCAGAGGTCAGGGCTCT  15199     G   CCTA
                                GAG CAGA    AGGGCTCT
                                ||| ||||    ||||||||
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                                CTC GTCT   TCCCGAGA
                                  A   CCAG
GAM576  MGC2776  3' AGAGGCAGGAGGCTCT     15200       ACCTAA
                                AGAGGCAG    GGGCTCT
                                ||||||||    |||||||
                                TCTCCGTC    TCCGAGA
                                    C_____
GAM576  MIG     3' AGAGGCAGGACTTGAACT    15201       AC  AA
                                AGAGGCAG  CT  GGGCT
                                ||||||||  ||  |||||
                                TCTCCGTC  GA  CTTGA
                                    CT  A_
GAM576  NRM     3' AGAGGCAGGGCCTAAGGA    15202       A_
                                AGAGGCAG  CCTAAGGG
                                ||||||||  ||||||||
                                TCTCCGTC  GGATTCCT
                                    CC
GAM576  NRM     3' AGAGGCAGGGCCTAAGGA    15202       A_
                                AGAGGCAG  CCTAAGGG
                                ||||||||  ||||||||
                                TCTCCGTC  GGATTCCT
                                    CC
GAM576  NRM     3' AGAGGCAGGGCCTAAGGA    15202       A_
                                AGAGGCAG  CCTAAGGG
                                ||||||||  ||||||||
                                TCTCCGTC  GGATTCCT
                                    CC
GAM576  PHRET1   3' AGAGGTGGATCAGGCCCCA   15203     CA  CCTAA
                                AGAGG  GA    GGGCTCTA
                                |||||  ||    ||||||||
                                TCTCC  CT    TCCGGGGT
                                   AC  AG___
GAM576  PRDM12   3' GAGGGGCCCTCGGGGGCTCTAA 15204     CAGA   AA_
                                GAGG   CCT   GGGCTCTAA
                                ||||   |||   |||||||||
                                CTCC   GGA   CCCGAGATT
                                  CCG_  GCC
GAM576  RAI17    3' AGCAGACCTGTAGCTCT     15205       AAG
                                GGCAGACCT   GGCTCT
                                |||||||||   ||||||
                                TCGTCTGGA   TCGAGA
                                    CA_
GAM576  STARD7   3' AGAGCAATAAGGGCTCT     15206     G   ACC
                                AGAG CAG   TAAGGGCTCT
                                |||| |||   ||||||||||
                                TCTC GTT   ATTCCCGAGA
                                  _  ___
GAM576  STARD7   3' AGAGCAATAAGGGCTCT     15206     G   ACC
                                AGAG CAG   TAAGGGCTCT
                                |||| |||   ||||||||||
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                                TCTC GTT   ATTCCCGAGA
                                  _  ___
GAM576  TUBB5    3'  GAGGGAAAGCGGGGCTCTA   15207     C   CCTAA
                                GAGG AGA    GGGCTCTA
                                |||| |||    ||||||||
                                CTCC TTT    CCCGAGAT
                                  C   CGC__
GAM576  TXN2     3'  AGGGCTGGAGCCTGGGCTCTAA 15208    A  A_ _  AA
                                AG GGC  GA CCT  GGGCTCTAA
                                || |||  || |||  |||||||||
                                TC CCG  CT GGA  CCCGAGATT
                                 _  AC  C  __
GAM576  UBAP     3'  AGAGCAGGGGCTCTA      15209     G   ACCTAA
                                AGAG CAG     GGGCTCTA
                                |||| |||     ||||||||
                                TCTC GTC     CCCGAGAT
                                  _  _______
GAM576  UBN1     3'  AGAGATGAAGGGCTCT      15210      CA  CCTA
                                AGAGG  GA   AGGGCTCT
                                |||||  ||   ||||||||
                                TCTCT  CT   TCCCGAGA
                                  A_  ____
GAM576  LOC130940 5' AGGGGTACATCTAAGGGCTC   15211     CAG  __
                                AGG   AC  CTAAGGGCTC
                                |||   ||  ||||||||||
                                TCC   TG  GATTCCCGAG
                                 CCA  TA
GAM576  LOC150138 5' AGAGGCAGACTCACACCCT    15212         C  AGG
                                AGAGGCAGAC TA   GCTCT
                                |||||||||| ||   |||||
                                TCTCCGTCTG GT   TGGGA
                                     A  G__
GAM576  LOC150372 5' GAGGCAGTGAGCAGGGCTCT   15213        ACCTA
                                GAGGCAG    AGGGCTCT
                                |||||||    ||||||||
                                CTCCGTC    TCCCGAGA
                                    ACTCG
GAM576  LOC151657 3' AGAGGCAGACCACAGCCTAA   15214          TAAG   T
                                AGAGGCAGACC    GGC CTAA
                                ||||||||||    ||| ||||
                                TCTCCGTCTGG    TCG GATT
                                      TG__   _
GAM576  LOC151996 5' AGGAATACCTAAGGGTTCT    15215     CAG       C
                                AGG   ACCTAAGGG TCT
                                |||   ||||||||| |||
                                TCC   TGGATTCCC AGA
                                 TTA       A
GAM576  LOC152275 5' AGGGGCAGATCTCAGACT     15216    A     C  AA
                                AG GGCAGA CT  GGGCT
                                || |||||| ||  |||||
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                                TC CCGTCT GA  TCTGA
                                 C     A  G_
GAM576  LOC153469 3'  AGCAGGTGGACGAGGCTCT   15217    _  CA   CTAA
                                AG AGG  GAC    GGGCTCT
                                || |||  |||    |||||||
                                TC TCC  CTG    TCCGAGA
                                 G   AC   C___
GAM576  LOC157247 5'  AAAGGCAGTGGGCTCT      15218        ACCTAA
                                AGAGGCAG     GGGCTCT
                                ||||||||     |||||||
                                TTTCCGTC     CCCGAGA
                                     A_____
GAM576  LOC157506 3'  GAGGCAGACCTGGATAATCTCT 15219          AA  ____
                                GAGGCAGACCT  GGG    CTCT
                                ||||||||||  |||    ||||
                                CTCCGTCTGGA  CCT    GAGA
                                      __   ATTA
GAM576  LOC158230 5'  AGAGGCAGACTGGTCACTAAA  15220         CTAA  GCT
                                AGAGGCAGAC    GG   CTAAA
                                ||||||||||    ||   |||||
                                TCTCCGTCTG    CC   GATTT
                                      A___  AGT
GAM576  LOC200010 3'  AGAGGCAGAATTTAAATAGTGC 15221         CC_  __  _
          T                    AGAGGCAGA   TAA  GG GCT
                               |||||||||   |||  || |||
                               TCTCCGTCT   ATT  TC CGA
                                     TAA   TA  A
GAM576  LOC200982 3'  AGAGGCAGAGCTGGGGCT    15222         C  AA
                                AGAGGCAGA CT  GGGCT
                                ||||||||| ||  |||||
                                TCTCCGTCT GA  CCCGA
                                     C  C_
GAM576  LOC203350 3'  AGAGGCAGACCTGGGGTTC   15223          AA   C
                                AGAGGCAGACCT  GGG TC
                                ||||||||||||  ||| ||
                                TCTCCGTCTGGA  CCC AG
                                      C_   A
GAM576  LOC204254 5'  AAGGTGGACTCCAGCTCT    15224      CA   _  AAG
                                GAGG  GAC CT   GGCTCT
                                ||||  ||| ||   ||||||
                                TTCC  CTG GG   TCGAGA
                                  AC   A  ___
GAM576  LOC220001 5'  AGAGGCAGACGTGGGGGCCC   15225          CTAA
                                AGAGGCAGAC    GGGCTC
                                ||||||||||    ||||||
                                TCTCCGTCTG    CCCGGG
                                      CACC
GAM576  LOC253675 3'  AAGGCAGCAGGGCTCT      15226        ACCTA
                                GAGGCAG    AGGGCTCT
                                |||||||    ||||||||
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                                TTCCGTC    TCCCGAGA
                                   G____
GAM576  LOC254106 5'  GAGACAGAAGACCTGGCTTTAA 15227      ___    AAG   C
                                GAGGCA  GACCT  GGCT TAA
                                ||||||  |||||  |||| |||
                                CTCTGT  CTGGA  CCGA ATT
                                   CTT    ___   A
GAM576  LOC255452 3'  AGAGGCAGACTCACTAGG    15175        ___  A
                                AGAGGCAGAC  CTA GG
                                ||||||||||  ||| ||
                                TCTCCGTCTG  GAT CC
                                      AGT  _
GAM576  LOC255650 3'  AGAGACAGACCTGGCCCT    15228         AAG
                                AGAGGCAGACCT  GGCTCT
                                ||||||||||||  ||||||
                                TCTCTGTCTGGA  CCGGGA
                                          ___
GAM576  LOC256496 5'  AGAGGCAGACCTATGACC    15229         AG
                                AGAGGCAGACCTA  GGCT
                                ||||||||||||  ||||
                                TCTCCGTCTGGAT  CTGG
                                      A_
GAM576  LOC257431 5'  AGAGGGCCCTGCTGGGGGCTCT 15186      CAGA  AA___
                                AGAGG   CCT    GGGCTCT
                                |||||   |||    |||||||
                                TCTCC   GGA    CCCGAGA
                                  CG__  CGACC
GAM576  LOC90148  5'  AGGGCAGACCTGGGTTC    15230    A      AA  C
                                AG GGCAGACCT  GGG TC
                                || |||||||||  ||| ||
                                TC CCGTCTGGA  CCC AG
                                _      __  A
GAM576  LOC92568  3'  GAGTCAGACCTAAATGGG    15231    G      __
                                GAG CAGACCTAA  GGG
                                ||| |||||||||  |||
                                CTC GTCTGGATT  CCC
                                  A       TA
GAM577  MYO1B     3'  TTTAATCTGTAAGTATT     15234         AA
                                TTTAATCTGTG  AGTATT
                                ||||||||||  ||||||
                                AAATTAGACAT  TCATAA
                                      __
GAM577  FLJ13305  3'  TTTATTCTGTGAAATGCACT  15235    A      _
                                TTTA TCTGTGAAA GTATT
                                ||||  |||||||| |||||
                                AAAT AGACACTTT CGTGA
                                  A       A
GAM577  MORF4     5'  TGTATAAAGTATTTCACT    15236    _
                                TGTG AAAGTATTTCACT
                                ||||  ||||||||||||
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                                ACAT TTTCATAAAGTGA
                                  A
GAM577  SLC31A2  3'  TCTAATCTGTGAGGTATT    15237          AA
                                TTTAATCTGTGA  GTATT
                                ||||||||||||  |||||
                                AGATTAGACACT  CATAA
                                      C_
GAM577  TXNL2    3'  CTTAATTTGTGAAAGCCACACC 15238       C       ATTT
                                TTTAAT TGTGAAAGT    CACT
                                |||||| |||||||||    ||||
                                GAATTA ACACTTTCG    GTGG
                                   A        GT__
GAM577  LOC121536 3'  TTAAGTCTGTGAAAGACATTT  15239     _       _
                                TTAA TCTGTGAAAG TATTT
                                |||| |||||||||| |||||
                                AATT AGACACTTTC GTAAA
                                  C         T
GAM577  LOC221895 3'  TTCAGGGAAAAAAGTATTTCAC 15240     ATCTGT
          T                      TTTA      GAAAGTATTTCACT
                                ||||      ||||||||||||||
                                AAGT      TTTTCATAAAGTGA
                                  CCCTT_
GAM578  WHSC1    3'  ACTGAGTGTGTACGATGAT    15243      ATGT    C
                                ACTGA    TGTGT CGATGAT
                                |||||    ||||| |||||||
                                TGACT    ACACA GCTACTA
                                  C___     T
GAM578  WHSC1    3'  ACTGAGTGTGTACGATGAT    15243      ATGT    C
                                ACTGA    TGTGT CGATGAT
                                |||||    ||||| |||||||
                                TGACT    ACACA GCTACTA
                                  C___     T
GAM578  WHSC1    3'  ACTGAGTGTGTACGATGAT    15243      ATGT    C
                                ACTGA    TGTGT CGATGAT
                                |||||    ||||| |||||||
                                TGACT    ACACA GCTACTA
                                  C___     T
GAM578  KIAA1644  3'  TGACTGAATCTTTCTGATGAT  15244        G  GTG  C
                                TGACTGAAT TT   TC GATGAT
                                ||||||||| ||   || ||||||
                                ACTGACTTA AA   AG CTACTA
                                     G  ___  A
GAM578  LOC51652  3'  TGAGTGAATGTTGGTTATGAT  15245     C       T  CCG
                                TGA TGAATGTTG GT   ATGAT
                                ||| ||||||||| ||   |||||
                                ACT ACTTACAAC CA   TACTA
                                  C        _  A__
GAM579  HLCS     3'  AGAAGAGTGGTTTTTTTTGTGT 15248        _____
          TTT                    GGAAGAGT    TTTTTTGTGTTTT
                                ||||||||    ||||||||||||
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                                TCTTCTCA   AAAAAACACAAAA
                                    CCAA
GAM579  WIF1     3'  AGGTAAGAGCTGTGTTT    15249    _    TTTTT
                                AGG AAGAGT    TGTGTTT
                                ||| ||||||    |||||||
                                TCC TTCTCG    ACACAAA
                                  A    _____
GAM579  C22orf19 3'  GGAAGAGTTTTGCTT      15250         TTTTG
                                GGAAGAGTTT    TGTTT
                                ||||||||||    |||||
                                CCTTCTCAAA    ACGAA
                                      _____
GAM579  FLJ21240 3'  AGGGAGAGTTTTGCTCT    15251    A     TTTTG
                                AGG AGAGTTT    TGTTTT
                                ||| |||||||    ||||||
                                TCC TCTCAAA    ACGAGA
                                  C     _____
GAM579  FUSIP1   3'  TAAGGTGAGTTTTTGTGTTTT 15252     AA     TT
                                TAAGG  GAGTTTT  TGTGTTTT
                                |||||  |||||||  ||||||||
                                ATTCC  CTCAAAA  ACACAAAA
                                  A_     __
GAM579  LHFPL2   3'  GGAAAAATTTTGTGTTTT    15253        TTT
                                GGAAGAGTTT   TGTGTTTT
                                ||||||||||   ||||||||
                                CCTTTTTAAA   ACACAAAA
                                      ___
GAM579  LRRFIP2  3'  GGAGAAGGCACTTGTGTTTT   15254    AG  TTTT
                                GGA  AG    TTTGTGTTTT
                                |||  ||    ||||||||||
                                CCT  TC    GAACACAAAA
                                  CT  CGT_
GAM579  UBXD2    3'  AGGGGAAAGTTTTTTTAT    15255    A_
                                AGG  AGAGTTTTTTTGT
                                |||  |||||||||||||
                                TCC  TTTCAAAAAAATA
                                  CC
GAM579  LOC151040 3'  AGGAAGAGTTTATTGAATC   15256         TT   T
                                AGGAAGAGTTT  TTG GTT
                                ||||||||||  ||| |||
                                TCCTTCTCAAA  AAC TAG
                                      T_   T
GAM579  LOC200488 5'  GGAAGAGTTTTCAGACTGTTTT 15257          TTG_
                                GGAAGAGTTTTT   TGTTTT
                                ||||||||||||   ||||||
                                CCTTCTCAAAAG   ACAAAA
                                       TCTG
GAM579  LOC254945 5'  AGGAAGGATCTGGCTGTGTTTT 15258       AG   TT
                                AGGAAG  TTT  TTGTGTTTT
                                ||||||  |||  |||||||||
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                                TCCTTC  AGA  GACACAAAA
                                   CT   CC
GAM579  LOC257457 3'  GGAAGGGTTTTGTGTT      15259       A    TTT
                                GGAAG GTTT   TGTGTT
                                ||||| ||||   ||||||
                                CCTTC CAAA   ACACAA
                                  C   ___
GAM579  LOC90355  3'  TAAGGAGAGTTTTTTCA     15260       A
                                TAAGGA GAGTTTTTTTG
                                |||||| ||||||||||
                                ATTCCT CTCAAAAAAGT
                                  _
GAM580  APM1      3'  TGAGTGCGTATGTTATTT     15263        AAATAGG
                                TGAGTGC      ATGTTATTT
                                |||||||      |||||||||
                                ACTCACG      TACAATAAA
                                   CA_____
GAM580  OPHN1     3'  GAGTGCAAGTAGGAAAGCTCTT 15264         A    T_   A
           TC                     GAGTGCAA TAGGA  GTT TTTC
                                |||||||| |||||  ||| ||||
                                CTCACGTT ATCCT  CGA AAAG
                                   C    TT   G
GAM580  TTC3      3'  TGAGTGTGGTAGCCGTCATTT  15265       CAAA   GA
                                TGAGTG   TAG  TGTTATTT
                                ||||||   |||  ||||||||
                                ACTCAC   ATC  GCAGTAAA
                                   ACC_  G_
GAM580  DKFZP434A043 3'  TAAGTGTGAAAGTGTTATTTC  15266       CAAAT   A
                                TGAGTG    AGG TGTTATTTC
                                ||||||    ||| |||||||||
                                ATTCAC    TTC ACAATAAAG
                                   ACT__  _
GAM580  FLJ10546  5'  TGGGTGCAATAGGATCTT    15267    A    A    G
                                TG GTGCAA TAGGAT TT
                                || |||||| |||||| ||
                                AC CACGTT ATCCTA AA
                                 C    _    G
GAM580  HSC3      5'  TGACTGCAAATAGGTACACT   15268    G       _ TG
                                TGA TGCAAATAGG A  TT
                                ||| |||||||||| |  ||
                                ACT ACGTTTATCC T  GA
                                  G        A GT
GAM580  KIAA0143  3'  TAAGTGCAAATGAATATATATT 15269          A    _
           T                     TGAGTGCAAAT GGATGT TATTT
                                |||||||||| |||||| ||||||
                                ATTCACGTTTA CTTATA ATAAA
                                       _    T
GAM580  KIAA0555  5'  GTGGATGGGATGTTATTT    15270    CAA  A
                                GTG   AT GGATGTTATTT
                                |||   || ||||||||||
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                                CAC   TA CCTACAATAAA
                                  C__  C
GAM580  LZ16    3'  TGGTGCAATCGTGTTATTT   15271    A    ATAGGA
                                TG GTGCAA     TGTTATTT
                                || ||||||     ||||||||
                                AC CACGTT     ACAATAAA
                                  _     AGC___
GAM580  PRO2955  3'  TGAGTGTAAAGGAACATTT   15272      CAAAT   TGT
                                TGAGTG    AGGA   TATTT
                                ||||||    ||||   |||||
                                ACTCAC    TCCT   GTAAA
                                   ATT__    T__
GAM580  PSTPIP2  3'  TGAGTGTAAAGGAACATTT   15272      CAAAT   TGT
                                TGAGTG    AGGA   TATTT
                                ||||||    ||||   |||||
                                ACTCAC    TCCT   GTAAA
                                   ATT__    T__
GAM581  ADCY9    3'  GGGGTGGCGGAGCTGT     15275    A    CTCA
                                GG GTGGT    GGAGCTGT
                                || |||||    ||||||||
                                CC CACCG    CCTCGACA
                                 C    _____
GAM581  BAT1     3'  CATGGGGTGGGGGCTG      15276      A   TCTCA  A
                                TATGG GTGG    GG GCTG
                                ||||| ||||    || ||||
                                GTACC CACC    CC CGAC
                                   C   ______  _
GAM581  BAT1     3'  CATGGGGTGGGGGCTG      15276      A   TCTCA  A
                                TATGG GTGG    GG GCTG
                                ||||| ||||    || ||||
                                GTACC CACC    CC CGAC
                                   C   ______  _
GAM581  CNGA3    3'  ATGGAGGATAGGGGCTGT    15277      T   CTC   A
                                ATGGAG GGT   AGG GCTGT
                                |||||| |||   ||| |||||
                                TACCTC CTA   TCC CGACA
                                   _   ___   C
GAM581  FOXP2    3'  TGGAGTGGTTATGAAGGTC   15278        CTCA   CT
                                TGGAGTGGT   GGAG  GTC
                                |||||||||   ||||  |||
                                ACCTCACCA   CTTC  CAG
                                     ATA_   __
GAM581  OSM      3'  TGGGGACCCGGGAGCTGTC   15279    AGT  T   A
                                TGG   GG CTC GGAGCTGTC
                                |||   || ||| |||||||||
                                ACC   CC GGG CCTCGACAG
                                  ___  T   C
GAM581  STC1     3'  GGGGTGGTCTCAGGGGAGC   15280    A       __
                                GG GTGGTCTCA  GGAGC
                                || |||||||||  |||||
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                                CC CACCAGAGT  CCTCG
                                 C        CC
GAM581  C20orf162 5'  GGAGAGATGGGAGCTGT     15281      T   CTCA
                                GGAG GGT    GGAGCTGT
                                |||| |||    ||||||||
                                CCTC CTA    CCTCGACA
                                  T  C___
GAM581  FBXO21    3'  TATGAAGTGGTCTCAGGTGGCT 15282              A_
                                TATGGAGTGGTCTCAGG  GCT
                                ||||||||||||||||  |||
                                ATACTTCACCAGAGTCC  CGA
                                           AC
GAM581  FLJ12671  3'  TGGAGCTGGTGGAGCTGTC    15283      _   CTCA
                                TGGAG TGGT    GGAGCTGTC
                                ||||| ||||    |||||||||
                                ACCTC ACCA    CCTCGACAG
                                   G   ____
GAM581  FLJ20618  3'  TGGAGTGGAGGGCTGT      15284        TCTC   A
                                TGGAGTGG    AGG GCTGT
                                ||||||||    ||| |||||
                                ACCTCACC    TCC CGACA
                                      ____  _
GAM581  FLJ20628  3'  TATGGAGTGGTTTACAGGAA   15285          CT_
                                TATGGAGTGGT   CAGGAG
                                ||||||||||   ||||||
                                ATACCTCACCA   GTCCTT
                                      AAT
GAM581  SARM      3'  GGAGACTGGTTTCAGGAGCTGT 15286      __   C
                                GGAG  TGGT TCAGGAGCTGT
                                ||||  |||| ||||||||||
                                CCTC  ACCA AGTCCTCGACA
                                  TG    A
GAM582  PIP5K1C   3'  TGGAAGTTTCCGCCTTGTCAG  15289          _    ATA
                                TGGAAGTTTC GCCTT   CGG
                                |||||||||| |||||   |||
                                ACCTTCAAAG CGGAA   GTC
                                      G    CA_
GAM582  LOC154881 3'  GGAAGTTTTGTCTTCCTACG   15290        CGC   A_
                                GGAAGTTT   CTT  TACG
                                ||||||||   |||  ||||
                                CCTTCAAA   GAA  ATGC
                                     ACA   GG
GAM583  KIAA0089  3'  GGTGGCGCTAAAACTGC     15293        GTTT
                                GGTGGCGT    AAACTGC
                                ||||||||    |||||||
                                CCACCGCG    TTTGACG
                                     AT__
GAM583  KIAA0532  3'  GGTGGTGTAGTCCCAGCTGC   15294      C  _   AAA
                                GGTGG GT GTTT   CTGC
                                ||||| || ||||   ||||
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                                CCACC CA CAGG   GACG
                                   A  T   GTC
GAM583  LOC149386 5'  GTGTTGTCTTAAACTGC     15295     GC  G
                                GTG  GT TTTAAACTGC
                                |||  || ||||||||||
                                CAC  CA GAATTTGACG
                                 AA  _
GAM583  LOC81501  3'  GGTAGAGATTTAAACTG     15296      CGT
                                GGTGG   GTTTAAACTG
                                |||||   ||||||||||
                                CCATC   TAAATTTGAC
                                   TC_
GAM584  RAG1      3'  ACAGTGCCACCAATAGA     15299      ATA  T
                                ACAGT   TC TCAATAGA
                                |||||   || ||||||||
                                TGTCA   GG GGTTATCT
                                   C__  T
GAM584  TRIM      3'  CTTAGAAGCCATCTTCAATAG  15300     AC   A
                                TTTA  AGT TATCTTCAATAG
                                ||||  ||| ||||||||||||
                                GAAT  TCG GTAGAAGTTATC
                                  CT   _
GAM584  FLJ10287  3'  TTTAATGATATATCTTCA    15301      CA
                                TTTAA  GTATATCTTCA
                                |||||  ||||||||||
                                AAATT  TATATAGAAGT
                                   AC
GAM584  KIAA0276  3'  AACAGTAACCCCCAATAGAA   15302       T
                                AACAGTA ATCTTCAATAGAA
                                ||||||| ||||||||||||
                                TTGTCAT TGGGGGTTATCTT
                                      _
GAM584  LAP1B     3'  TTTAACAGAGCTCTCAATGGAA 15303       TATA   T    A
                                TTTAACAG    TCT CAAT GAA
                                ||||||||    ||| |||| |||
                                AAATTGTC    AGA GTTA CTT
                                     TCG_   _    C
GAM584  LGALS8    3'  TTTAACAATATAAACAATAGAA 15304         TCTT
                                TTTAACAGTATA    CAATAGAA
                                ||||||||||||    ||||||||
                                AAATTGTTATAT    GTTATCTT
                                       TT__
GAM584  LOC122210 5'  TTTAACAGTATGACCAAAGAA  15305         ATCT    T
                                TTTAACAGTAT    TCAA AGAA
                                ||||||||||||    |||| ||||
                                AAATTGTCATA    GGTT TCTT
                                       CT__    _
GAM584  LOC132617 3'  TTTAACAGTCACAATAGA     15306        ATATCTT
                                TTTAACAGT      CAATAGA
                                |||||||||      |||||||
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                                AAATTGTCA      GTTATCT
                                     GT_____
GAM584  LOC143872 3'  TTTATCAGTATATTTTCA    15307      A       C
                                TTTA CAGTATAT TTCA
                                |||| |||||||| ||||
                                AAAT GTCATATA AAGT
                                  A       A
GAM584  LOC158156 3'  CAGATGTCTTCAATAGA     15308     T  A
                                CAG AT TCTTCAATAGA
                                ||| || ||||||||||
                                GTC TA AGAAGTTATCT
                                  _  C
GAM585  GRIN2A   3'  TCTCTTGCACATGTTCAAAT   15311     GTC   G  C
                                TCTC   GTA CA GTTCAAAT
                                ||||   ||| || ||||||||
                                AGAG   CGT GT CAAGTTTA
                                  AA_   _  A
GAM585  RABIF    3'  ACCCTCTGCATGTTCAAA    15312       GTCGTA   C
                                ACTCTC     GCA GTTCAAA
                                |||||||     ||| |||||||
                                TGGGAG     CGT CAAGTTT
                                   A_____   A
GAM585  KIAA0164  3'  CTACGATGTAGTGTGTTCAAAT 15313    _  TC    CAC
                                CT CG  GTAG   GTTCAAAT
                                || ||  ||||   ||||||||
                                GA GC  CATC   CAAGTTTA
                                 T  TA    ACA
GAM585  LOC126964 3'  TCTCGCTAGTGTTCAAA     15314       CG   CAC
                                TCTCGT  TAG   GTTCAAA
                                ||||||  |||   |||||||
                                AGAGCG  ATC   CAAGTTT
                                   __   A__
GAM585  LOC158130 3'  ACTCTTTCCAAACGTTCAA   15315      CG   TAGC
                                ACTCT  TCG    ACGTTCAA
                                |||||  |||    ||||||||
                                TGAGA  GGT    TGCAAGTT
                                   AA   T___
GAM586  KIAA0857  3'  TTTATCCTGGGATCCT      15318        CAGGAGC
                                TTTGTCC      GGGGTCCT
                                |||||||      ||||||||
                                AAATAGG      CCCTAGGA
                                   A_______
GAM586  PLA2R1    5'  CTTGTCCCGGGAGCCCCT    15319         A    GGGG
                                TTTGTCCC GGAGC    TCCT
                                |||||||| |||||    ||||
                                GAACAGGG CCTCG    GGGA
                                     C     _____
GAM586  PSCD4     3'  TCTGTCCCGGGGTCCT      15320         AGGAGC
                                TTTGTCCC     GGGGTCCT
                                ||||||||     ||||||||
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                                AGACAGGG     CCCCAGGA
                                        _______
GAM586  TERF1    3'  TTTGTCCCATGGGTAATACTAT 15321        GGAGC   GTC__
                                TTTGTCCCA    GGG    CTAT
                                |||||||||    |||    ||||
                                AAACAGGGT    CCC    GATA
                                     A____   ATTAT
GAM586  FLJ20689  5'  TTTGCTTAGGAAAGTCCTA   15322      CCC    CGG
                                TTTGT   AGGAG   GGTCCTA
                                |||||   |||||   |||||||
                                AAACG   TCCTT   TCAGGAT
                                  AA_    ___
GAM586  KIAA1396  3'  TTTGTCCCAGGGAGATGAGGGT 15323          _  C__
                                TTTGTCCCAGG AG   GGGGT
                                ||||||||||| ||   |||||
                                AAACAGGGTCC TC   TCCCA
                                      C  TAC
GAM586  LIPG     3'  TTTGTGTTTAGGCTCGGGTCCT 15324      CCC_   AG    G
           AT                    TTTGT    AGG  CGGG TCCTAT
                                |||||    |||  |||| ||||||
                                AAACA    TCC  GCCC AGGATA
                                  CAAA   GA   _
GAM586  LOC145786 5'  TTTGTCCCAGGGAGACCT    15325          AGCG   T
                                TTTGTCCCAGG    GGG CCT
                                ||||||||||    ||| |||
                                AAACAGGGTCC    CTC GGA
                                       ____   T
GAM586  LOC152620 3'  TTTGTCCCATGGGTAATACTAT 15321        GGAGC   GTC__
                                TTTGTCCCA    GGG    CTAT
                                |||||||||    |||    ||||
                                AAACAGGGT    CCC    GATA
                                     A____   ATTAT
GAM586  LOC158668 3'  TTTGTCCCATGGGTAATACTAT 15321        GGAGC   GTC__
                                TTTGTCCCA    GGG    CTAT
                                |||||||||    |||    ||||
                                AAACAGGGT    CCC    GATA
                                     A____   ATTAT
GAM587  AICDA    3'  CCCAGTAGGGGACAAT      15328        TTACTT
                                CCCGGTAG     GGACAAT
                                ||||||||     |||||||
                                GGGTCATC     CCTGTTA
                                     C_____
GAM587  FUT9     3'  CCTCAATACTTGGATGATATC  15329    GG   T     CA
                                CC  TAGT ACTTGGA  ATATC
                                ||  |||| |||||||  |||||
                                GG  GTTA TGAACCT  TATAG
                                 A_   _      AC
GAM587  PRO2435   3'  GATAAACTTGGACAGTAT    15330      TT       A
                                GGTAG  ACTTGGACA TAT
                                |||||  ||||||||| |||
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                                CTATT  TGAACCTGT ATA
                                  __       C
GAM587  LOC203246 3'  GTCTCACTTGGGCAGTAT    15331    AG       A  A
                                GT  TTACTTGG CA TAT
                                ||  |||||||| || |||
                                CA  AGTGAACC GT ATA
                                 G_       C  C
GAM587  LOC254413 5'  CCAGGTAGTTACTTTTGCCA   15332    C         GGA_
                                CC GGTAGTTACTT    CA
                                || ||||||||||||   ||
                                GG CCATCAATGAA    GT
                                 T          AACG
GAM588  ADAMTS3   3'  TAGCACATTATTGCAG      15335        CGTT    A
                                TAGCACAT    TATTG CAG
                                ||||||||    ||||| |||
                                ATCGTGTA    ATAAC GTC
                                    _____    _
GAM588  AGM1      3'  GCCATTATTATTGACAGT    15336    A   CGT
                                GC CAT   TTATTGACAGT
                                || |||   ||||||||||||
                                CG GTA   AATAACTGTCA
                                 _   AT_
GAM588  AKAP13    3'  GCACATCGTTCTGCAG      15337          AT  A
                                GCACATCGTTT  TG CAG
                                ||||||||||||  || |||
                                CGTGTAGCAAG  AC GTC
                                     __  _
GAM588  APPBP2    3'  GCATGTGTTCACTGCAGT    15338     CATC       A
                                GCA    GTTTATTG CAGT
                                |||    |||||||| ||||
                                CGT    CAAGTGAC GTCA
                                  ACA_       _
GAM588  B4GALT6   3'  GCTGTCAATTATTGACAGT   15339    ACA   T
                                GC   TCG TTATTGACAGT
                                ||   ||| ||||||||||||
                                CG   AGT AATAACTGTCA
                                 AC_   T
GAM588  BAZ2B     3'  TAGCACATCAGTGTAAACAGT  15340          TTTATT
                                TAGCACATCG     GACAGT
                                ||||||||||     ||||||
                                ATCGTGTAGT     TTGTCA
                                      CACAT_
GAM588  HSPA6     3'  TAGCATAGCCCTGACAG     15341      CATC   TA
                                TAGCA    GTT  TTGACAG
                                |||||    |||  |||||||
                                ATCGT    CGG  GACTGTC
                                   AT__   __
GAM588  LUM       3'  GCACATCATTTGACAGT     15342          TAT
                                GCACATCGTT   TGACAGT
                                ||||||||||   |||||||
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                                CGTGTAGTAA  ACTGTCA
                                    ___
GAM588  SIM2     3'  GCAGTCCATTGACAGT     15343    CATC
                                GCA   GTTTATTGACAGT
                                |||   ||||||||||||
                                CGT   CAGGTAACTGTCA
                                 _____
GAM588  DKFZp761D081 3'  TAGCAACAGTAGGTTGACAGT  15344      C  C  TTA
                                TAGCA AT GT   TTGACAGT
                                ||||| || ||   ||||||||
                                ATCGT TG CA   AACTGTCA
                                   _ T  TCC
GAM588  KIAA1344  3'  CAGCATATTTGGTTGACAGT   15345      CATC   A_
                                TAGCA   GTTT  TTGACAGT
                                |||||   ||||  ||||||||
                                GTCGT   TAAA  AACTGTCA
                                   A___   CC
GAM588  LRRN3    5'  CATCGTTCACCCGATCAGT   15346          _ _
                                CATCGTTTATT GA CAGT
                                |||||||||||  || ||||
                                GTAGCAAGTGG CT GTCA
                                      G  A
GAM588  SE70-2   3'  TAGCAATTGTTTACTGAAGT   15347      C  C       C
                                TAGCA AT GTTTATTGA AGT
                                ||||| || |||||||||  |||
                                ATCGT TA CAAATGACT TCA
                                   _ A       _
GAM588  LOC127702 3'  TAACACATCAGATGATAGT   15348          TTTAT   C
                                TAGCACATCG    TGA AGT
                                ||||||||||    ||| |||
                                ATTGTGTAGT    ACT TCA
                                      CT___   A
GAM588  LOC150225 3'  CAGCACATCACAGGTGACAGT  15349          TTTAT
                                TAGCACATCG    TGACAGT
                                ||||||||||    |||||||
                                GTCGTGTAGT    ACTGTCA
                                      GTCC_
GAM588  LOC221583 3'  TAGCATATCATCTACAG     15350      C     ATTG
                                TAGCA ATCGTTT   ACAG
                                ||||| |||||||   ||||
                                ATCGT TAGTAGA   TGTC
                                   A     _____
GAM589  DVL3     5'  ACCGGGTCCCAGCGCCG     15353    A    T
                                ACC GGTCC CAGCGCCG
                                ||| ||||| ||||||||
                                TGG CCAGG GTCGCGGC
                                  C    _
GAM589  GNB5     3'  CACCAGTCCTCAGTCCA     15354       G      CG
                                CACCAG TCCTCAG  CCG
                                ||||||  |||||||  |||
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                                GTGGTC AGGAGTC  GGT
                                  _      A_
GAM589  GNB5     3'  CACCAGTCCTCAGTCCA     15354       G      CG
                                CACCAG TCCTCAG  CCG
                                |||||| |||||||  |||
                                GTGGTC AGGAGTC  GGT
                                  _      A_
GAM589  NDUFV3   5'  CACCAGGCTTTCAGTGGGCT   15355        CC   CGCC
                                CACCAGGT  TCAG   GCT
                                ||||||||  ||||   |||
                                GTGGTCCG  AGTC   CGA
                                    AA   ACC_
GAM589  ODF2     3'  CACCAGGCTTCTCAGCTATGGC 15356        C_     GCC_
          TT                     CACCAGGT  CTCAGC   GCTT
                                ||||||||  ||||||   ||||
                                GTGGTCCG  GAGTCG   CGAA
                                    AA     ATAC
GAM589  RHCG     3'  CACCAGGTCCCAGCCCCACTT  15357         T   G
                                CACCAGGTCC CAGC CCGCTT
                                |||||||||| |||| ||||||
                                GTGGTCCAGG GTCG GGTGAA
                                  _   G
GAM589  TAF7L    3'  CAGGTCCTAGTGCTTA      15358        C  CGCC
                                CAGGTCCT AG   GCTTA
                                |||||||| ||   |||||
                                GTCCAGGA TC   CGAAT
                                  _ A___
GAM589  XRCC5    5'  CCGGTCCTCAGGCGCTT     15359    A       C  C
                                CC GGTCCTCAG GC GCTT
                                || |||||||| || ||||
                                GG CCAGGAGTC CG CGAA
                                 _       _ _
GAM589  KIAA1940 5'  CACCAGGTCCTGCTT       15360          CAGCGCC
                                CACCAGGTCCT      GCTT
                                ||||||||||       ||||
                                GTGGTCCAGGA      CGAA
                                        _______
GAM589  MGC2541  5'  CCAGGTCCTTAAGCTTA     15361         C  CGCC
                                CCAGGTCCT AG   GCTTA
                                ||||||||| ||   |||||
                                GGTCCAGGA TT   CGAAT
                                   A ____
GAM589  MIC2L1   3'  CAGGCCTCAGCATCATCTT   15362      T      C  _
                                CAGG CCTCAGCG CG CTT
                                |||| |||||||| || |||
                                GTCC GGAGTCGT GT GAA
                                  _      A  A
GAM589  LOC123242 3' CACCAGGTCCTTGGGCCCA   15363          CA_  G
                                CACCAGGTCCT   GC CCG
                                ||||||||||   || |||
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                                GTGGTCCAGGA   CG GGT
                                      ACC  _
GAM589  LOC146332 3'  CACCAGGCACTCTGCTGCTT   15364       TC   AGC  C
                                CACCAGG  CTC   GC GCTT
                                |||||||  |||   || ||||
                                GTGGTCC  GAG   CG CGAA
                                    GT   A__  A
GAM589  LOC168574 5'  CACCACGGTCTTCAGTGC    15365      _   C   C
                                CACCA GGTC TCAG GC
                                ||||| |||| |||| ||
                                GTGGT CCAG AGTC CG
                                   G   A   A
GAM589  LOC197387 5'  CCAGGTCCGCGGCCGTTAA   15366       TCA  _  C
                                CCAGGTCC   GCG CCG TTAA
                                ||||||||   ||| ||| ||||
                                GGTCCAGG   CGC GGC AATT
                                     ___   C  _
GAM589  LOC253001 3'  CACCAGGTCCTTGGGCCCA   15363         CA_  G
                                CACCAGGTCCT   GC CCG
                                ||||||||||   || |||
                                GTGGTCCAGGA   CG GGT
                                      ACC  _
GAM589  LOC254182 3'  CACTGGGTCCCCAGCACAGTCT 15367    CA         CG_
           T                     CAC  GGTCCTCAGCGC   CTT
                                 |||  ||||||||||||   |||
                                 GTG  CCAGGGGTCGTG   GAA
                                   AC          TCA
GAM589  LOC257455 5'  CACCAGGTGCCTTGGCTGCCCT 15368        _  CA  _  G
           T                     CACCAGGT CCT  GC GCC CTT
                                 ||||||||  |||  ||  ||| |||
                                 GTGGTCCA GGA  CG CGG GAA
                                     C   AC  A  _
GAM589  LOC56834  5'  CCAGGTCCTCAGGCCGCT    15369          C
                                CCAGGTCCTCAG GCCGCT
                                ||||||||||| ||||||
                                GGTCCAGGAGTC CGGCGA
                                      _
GAM590  C21orf18  3'  GCCGCTCTGCAGAATCGCT   15372        A  TCC
                                GCCGTTCT GC   GTCGCT
                                |||||||  ||   ||||||
                                CGGCGAGA CG   TAGCGA
                                     _  TCT
GAM590  FLJ23556  3'  TAGTTGCTCTAGCTCAGGGGCT 15373    CC        CGTC
                                TAG  GTTCTAGCTC    GCT
                                |||  ||||||||||    |||
                                ATC  CGAGATCGAG    CGA
                                  AA         TCCC
GAM590  MGC16063  3'  TAGCTGTTCTGCCTCACC    15374     C    A   CCG
                                TAGC GTTCT GCT   TCGCT
                                |||| ||||| |||   |||||
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                                ATCG CAAGA CGG   AGTGG
                                  A    _  ___
GAM591  CLCN4    3'  TGAAAAAGAAATAGCAACGGGA 15377   A     T   TG A_
                                A AAAAAGA ATAG  A  GGA
                                | ||||||| ||||  |  |||
                                A TTTTTCT TATC  T  CCT
                                 C      T   GT GC
GAM591  COL15A1  3'  TAAAAGGAGGATATAACTGTCT 15378     AAAA     _____
           GAAGGA                 GAAA   GATATAG    TGAAGGA
                                ||||   |||||||   |||||||
                                TTTT   CTATATT    ACTTCCT
                                  CCTC     GACAG
GAM591  DACH     5'  TGAAAAGGAGGAGGTTTGAAGG 15379      AA  ATATAG
           AC                    TGAAAA  AG     TGAAGGAC
                                ||||||  ||     ||||||||
                                ACTTTT  TC     ACTTCCTG
                                   CC  CTCCAA
GAM591  FKBP1A   3'  GAGCAAAGGCAGTGAAGG    15380    AAA   ATA
                                GA   AAAG   TAGTGAAGG
                                ||   ||||   |||||||||
                                CT   TTTC   GTCACTTCC
                                 CG_    C__
GAM591  GAS7     3'  TGGGAAAAAAATAAAGAAGGA  15381    AA       TAGT
                                TG  AAAAAGATA    GAAGGA
                                ||  |||||||||    ||||||
                                AC  TTTTTTTAT    CTTCCT
                                 CC        TT__
GAM591  GAS7     3'  TGGGAAAAAAATAAAGAAGGA  15381    AA       TAGT
                                TG  AAAAAGATA    GAAGGA
                                ||  |||||||||    ||||||
                                AC  TTTTTTTAT    CTTCCT
                                 CC        TT__
GAM591  HOXD4    3'  AAAAAAGAAGAGAAGG      15382         TAT  T
                                AAAAAAGA   AG GAAGG
                                ||||||||   || |||||
                                TTTTTTCT   TC CTTCC
                                     ___  T
GAM591  KLHL3    3'  TGAAAAAGGATACATGAGGA   15383        AA     G   A
                                TGAAAAA  GATATA TGA GGA
                                |||||||  |||||| ||| |||
                                ACTTTTT  CTATGT ACT CCT
                                   C_     _  _
GAM591  KRT15    3'  TGAAATAAAAGACCGAGGGAC  15384       _      ATAG   A
                                TGAAA AAAAGAT    TGA GGAC
                                |||||| |||||||    ||| ||||
                                ACTTT TTTTCTG    GCT CCTG
                                   A       _____   C
GAM591  LHCGR    3'  TGAAAAAAAGATATGCAAAA   15385             A TG
                                TGAAAAAAAGATAT G  AAG
                                |||||||||||||| |  |||
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                                ACTTTTTTTCTATA C  TTT
                                       _ GT
GAM591  MT1L    3'  GAAAAAAAGATGTAGCAAA   15386         A  TG
                                GAAAAAAAGAT TAG  AA
                                |||||||||| |||  ||
                                CTTTTTTTCTA ATC  TT
                                      C  GT
GAM591  NBS1    3'  TGAAAAAAAGATGCAATGA   15387          A
                                TGAAAAAAAGAT TAGTGA
                                |||||||||||| ||||||
                                ACTTTTTTTCTA GTTACT
                                       C
GAM591  NOTCH2  3'  TGAAAGAAAGATTGGTGAGCAG 15388      A    ATA   __
          G                     TGAAA AAAGAT  GTGA  AGG
                                ||||| ||||||  ||||  |||
                                ACTTT TTTCTA  CACT  TCC
                                   C    AC_   CG
GAM591  PIGN    3'  TGAAAAAAAAAAAAGTGAAGGA  15389         TAT
                                TGAAAAAAAGA  AGTGAAGGA
                                ||||||||||  |||||||||
                                ACTTTTTTTTT  TCACTTCCT
                                       T__
GAM591  PKHD1   3'  TGAAAGAAAGCATGTGCAGG  15390     A  A  A  A
                                TGAAA AAAG TAT GTG AGG
                                ||||| |||| ||| ||| |||
                                ACTTT TTTC GTA CAC TCC
                                   C  _  _  G
GAM591  POLA    3'  GAAAAAAATAGCAAGCGAGGG  15391       GATAT   A
                                GAAAAAAA    AGTGA GG
                                ||||||||    ||||| ||
                                CTTTTTTT    TCGCT CC
                                     ATCGT    C
GAM591  PRSS16  3'  AAAAGATGGTGAGTGAAGG   15392       AT__
                                AAAAGAT   AGTGAAGG
                                |||||||   ||||||||
                                TTTTCTA   TCACTTCC
                                    CCAC
GAM591  SLC16A2 3'  TGGCAAAAAGATGATGAAAG  15393   AA     ATA
                                TG  AAAAAGAT  GTGAAGG
                                ||  ||||||||  |||||||
                                AC  TTTTTCTA  TACTTTC
                                 CG       C__
GAM591  ST7     3'  TAAAAGAAAGACGGTGGAGGA  15394     A    ATA  A
                                TGAAA AAAGAT  GTG AGGA
                                ||||| ||||||  ||| ||||
                                ATTTT TTTCTG  CAC TCCT
                                   C    C__  C
GAM591  TPM1    3'  TGAACAAAAGACCACAGGGGGA 15395     A     _   TGAA
          C                     TGAA AAAAGAT ATAG   GGAC
                                |||| ||||||| ||||   ||||
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                                ACTT TTTTCTG TGTC   CCTG
                                  G     G   CC__
GAM591  UBE2B   3'  AAAAAAATACAAACAGGA    15396          TGA
                                AAAAAGATATAG  AGGA
                                ||||||||||||  ||||
                                TTTTTTTATGTT  TCCT
                                      TG_
GAM591  WT1     3'  AAAAAAAGAAGGGAAGG     15397        TAT  T
                                AAAAAAAGA  AG GAAGG
                                |||||||||  || |||||
                                TTTTTTTCT  TC CTTCC
                                     ___ C
GAM591  WT1     3'  AAAAAAAGAAGGGAAGG     15397        TAT  T
                                AAAAAAAGA  AG GAAGG
                                |||||||||  || |||||
                                TTTTTTTCT  TC CTTCC
                                     ___ C
GAM591  WT1     3'  AAAAAAAGAAGGGAAGG     15397        TAT  T
                                AAAAAAAGA  AG GAAGG
                                |||||||||  || |||||
                                TTTTTTTCT  TC CTTCC
                                     ___ C
GAM591  WT1     3'  AAAAAAAGAAGGGAAGG     15397        TAT  T
                                AAAAAAAGA  AG GAAGG
                                |||||||||  || |||||
                                TTTTTTTCT  TC CTTCC
                                     ___ C
GAM591  ADPRTL3  3'  TGAAAAAAAGGAGTGATATAGG 15398         ATAT   ___
                                TGAAAAAAAG   AGTGA  AGG
                                ||||||||||   |||||  |||
                                ACTTTTTTTC   TCACT  TCC
                                     C___    ATA
GAM591  FLJ11342 3'  TGAAAAAAAATCAAGG     15399        GATATA  G
                                TGAAAAAAA    GT AAGG
                                |||||||||    || ||||
                                ACTTTTTTT    TA TTCC
                                     _______ G
GAM591  FLJ12644 3'  TGGAAAAAAGATTAGTGAA   15400    A       A
                                TG AAAAAAGAT TAGTGAA
                                || ||||||||| |||||||
                                AC TTTTTTCTA ATCACTT
                                 C       _
GAM591  FLJ21477 3'  AAAAAATGGGTGAAGGA    15401       ATA
                                AAAAGAT  GTGAAGGA
                                |||||||  ||||||||
                                TTTTTTA  CACTTCCT
                                    CC_
GAM591  GGA2    3'  AAGGCACAGTGGTGAAGGAC  15402    A    ___
                                AAG TATAGT  GAAGGAC
                                ||| ||||||  |||||||
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                                TTC GTGTCA   CTTCCTG
                                  C     CCA
GAM591  GGA2     3'  AAGGCACAGTGGTGAAGGAC   15402     A     ___
                                AAG TATAGT   GAAGGAC
                                ||| ||||||   |||||||
                                TTC GTGTCA   CTTCCTG
                                  C     CCA
GAM591  KIAA0872 3'  TGAAAAAAGTACAAGAAGG    15403        A A     T
                                TGAAAAAA G TATAG GAAGG
                                |||||||| | ||||| |||||
                                ACTTTTTT C ATGTT CTTCC
                                     _ _    _
GAM591  KIAA1157 3'  GAAAAAAAGAGAAGG        15404          TATAGT
                                GAAAAAAAGA     GAAGG
                                ||||||||||     |||||
                                CTTTTTTTCT     CTTCC
                                     _______
GAM591  KIAA1323 3'  AAAAAAGGATATCCTTAAAGGA 15405       A     AG_
          C                      AAAAAA GATAT   TGAAGGAC
                                ||||||| |||||   ||||||||
                                TTTTTT CTATA   ATTTCCTG
                                   C    GGA
GAM591  KIAA1364 3'  GAAAAAAAGATGCCTGGGGGAC 15406          ATAG  AA
                                GAAAAAAAGAT    TG  GGAC
                                ||||||||||    ||  ||||
                                CTTTTTTTCTA    AC  CCTG
                                      CGG_  CC
GAM591  KIAA1500 3'  TGAAGGCAAGATATAAAAGG   15407     AAA      GT
                                TGAA   AAGATATA  GAAGG
                                ||||   ||||||||  |||||
                                ACTT   TTCTATAT  TTTCC
                                  CCG      __
GAM591  KIAA1701 3'  AAAAAGATACAAAGGA      15408          AGT
                                AAAAAGATAT   GAAGGA
                                ||||||||||   ||||||
                                TTTTTCTATG   TTTCCT
                                     ___
GAM591  LY6G6C   3'  GAAAAAGGAGAGTGAAGG    15409       AA  TAT
                                GAAAAA  GA   AGTGAAGG
                                ||||||  ||   ||||||||
                                CTTTTT  CT   TCACTTCC
                                   C_  C__
GAM591  MGC16153 3'  TGAAAAGGGAGTCAGCGAAGG  15410       AAA  TA
                                TGAAAA   GA  TAGTGAAGG
                                ||||||   ||  |||||||||
                                ACTTTT   CT  GTCGCTTCC
                                   CC_  CA
GAM591  NAP1L2   3'  TGACAAAAAGACTTCAGAAGGA 15411     A       ATAGT
                                TGA AAAAAGAT    GAAGGA
                                ||| ||||||||    ||||||
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                                ACT TTTTTCTG    CTTCCT
                                  G       AAGT_
GAM591  NCUBE1    3'  AAAAAAAGGAATGAAGG     15412        ATAT
                                AAAAAAAG    AGTGAAGG
                                ||||||||    ||||||||
                                TTTTTTTC    TTACTTCC
                                    C___
GAM591  PEG10     3'  TGAGGGCAGAGATCCTGAAGGA 15413     AAAAA   T  AG
          C                      TGA     AGA AT  TGAAGGAC
                                |||     ||| ||  ||||||||
                                ACT     TCT TA  ACTTCCTG
                                  CCCG_   C  GG
GAM591  PRO1905   3'  TGAGAGTGAAGATCTCGAAGGA 15414     AAAA_    ATAG
                                TGA     AAGAT    TGAAGGA
                                |||     |||||    |||||||
                                ACT     TTCTA    GCTTCCT
                                  CTCAC    GA__
GAM591  SS18L1    3'  TGAAAAAAAAATAACCGATAAG 15415          TAGTG_
          GA                     TGAAAAAAAGATA     AAGGA
                                ||||||||||||      |||||
                                ACTTTTTTTTTAT     TTCCT
                                      TGGCTA
GAM591  UST       3'  GAAAGAAGACATACCTTAGGAC 15416      AA      GTGA
                                GAAA  AAGATATA    AGGAC
                                ||||  ||||||||    |||||
                                CTTT  TTCTGTAT    TCCTG
                                  C_      GGAA
GAM591  LOC163590 3'  TGAAGTAAAGATATAGCCAA   15417      AA        G
                                TGAA  AAAGATATAGT AA
                                ||||  |||||||||| ||
                                ACTT  TTTCTATATCG TT
                                  CA        G
GAM591  LOC200420 5'  GAAAAAGGGATGTGAAGGAC   15418       AA   ATA
                                GAAAAA  GAT   GTGAAGGAC
                                ||||||  |||   |||||||||
                                CTTTTT  CTA   CACTTCCTG
                                   CC  ____
GAM591  LOC220370 3'  TGAAAGCAAAGATATATAACTG 15419       A_       GTGAA
          G                      TGAAA  AAAGATATA    GG
                                |||||  |||||||||    ||
                                ACTTT  TTTCTATAT    CC
                                  CG       ATTGA
GAM591  LOC221490 5'  TGAGAAATATGTGAAGGA    15420    A   T   _
                                A AGA ATA GTGAAGGA
                                | ||| ||| ||||||||
                                A TCT TAT CACTTCCT
                                 C   T   A
GAM591  LOC221573 3'  TGAATAAGAAGGTAAAGGA    15421      AAA    TATA
                                TGAA   AAGA    GTGAAGGA
                                ||||   ||||    ||||||||
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                                ACTT   TTCT    CATTTCCT
                                  A__    TC__
GAM591   LOC253842 3'  AAAAAAGATACACACCAGG    15422          GTGA
                                AAAAAAGATATA    AGG
                                ||||||||||||    |||
                                TTTTTTCTATGT    TCC
                                      GTGG
GAM591   LOC254413 5'  AAGATGCCAGTGAAGGAC     15423      A_
                                AAGAT  TAGTGAAGGAC
                                |||||  ||||||||||
                                TTCTA  GTCACTTCCTG
                                  CG
GAM591   LOC257522 3'  TGAATAAGAAGGTAAAGGA    15421     AAA    TATA
                                TGAA   AAGA    GTGAAGGA
                                ||||   ||||    ||||||||
                                ACTT   TTCT    CATTTCCT
                                  A__    TC__
GAM591   LOC257573 3'  TGAATAAGAAGGTAAAGGA    15421     AAA    TATA
                                TGAA   AAGA    GTGAAGGA
                                ||||   ||||    ||||||||
                                ACTT   TTCT    CATTTCCT
                                  A__    TC__
GAM591   LOC51580  3'  AAAAAAAGGTATGGTGAAAA   15424        A   A
                                AAAAAAAG TAT GTGAAGG
                                |||||||| ||| |||||||
                                TTTTTTTC ATA CACTTTT
                                     C   C
GAM591   LOC51644  3'  TGAAAAAGAATAGGAAGG    15425    A      T    T
                                A AAAAAGA ATAG GAAGG
                                | ||||||| |||| |||||
                                A TTTTTCT TATC CTTCC
                                 C      _   _
GAM591   LOC92017  5'  GAAAAAAAGATGTGAAAGA    15426          ATA
                                GAAAAAAAGAT   GTGAAGGA
                                ||||||||||   ||||||||
                                CTTTTTTTCTA   CACTTTCT
                                        ___
GAM592   ANGPT2    3'  TAGGTGTTCTGTCTAATC     15429     A  _
                                TAG TGT TTGTCTAATT
                                ||| ||| ||||||||||
                                ATC ACA GACAGATTAG
                                  C   A
GAM592   TRIM9     5'  GATGTTTGTACTTTTAGTA    15430         _  AA
                                GATGTTTGT CT  TTTAGTA
                                |||||||| ||  |||||||
                                CTACAAACA GA  AAATCAT
                                      T  __
GAM592   CACNA2D1  3'  AATGTTTGTCTGATTTTATA   15431          A   A
                                GATGTTTGTCT ATTT GTA
                                |||||||||| |||| |||
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                                TTACAAACAGA TAAA TAT
                                      C    A
GAM592  KIAA1041  3'  AGATGTTTGTTTAGTTCAAGTA 15432          C  A   _
                                AGATGTTTGT TA TTTA GTA
                                |||||||||| || |||| |||
                                TCTACAAACA AT AAGT CAT
                                      A  C    T
GAM592  MOST2     5'  AATGTTTGTGTTTTTAGTA   15433         CTAA
                                GATGTTTGT   TTTAGTA
                                |||||||||   |||||||
                                TTACAAACA   AAATCAT
                                      CAA_
GAM592  PRO2730   3'  TAAATGTTTGTTTAGGAACTTA 15434          CT___
              GTAAA                 TAGATGTTTGT    AATTTAGTAAA
                                |||||||||||    ||||||||||
                                ATTTACAAACA    TTGAATCATTT
                                      AATCC
GAM592  STK17A    3'  TAGATGTCTGTTTAGACTAA   15435          C  AT
                                TAGATGTTTGT TA  TTAG
                                |||||||||| ||  ||||
                                ATCTACAGACA AT  GATT
                                      A  CT
GAM592  TACTILE   3'  TAGAAGTTCAGAAATTTAGTAA 15436      T    TCT
              A                  TAGA GTTTG   AATTTAGTAAA
                                |||| |||||  ||||||||||
                                ATCT CAAGT   TTAAATCATTT
                                  T    CT_
GAM592  LOC144481 3'  AATGTTTGCATTTTTAGTA   15437         CTAA
                                GATGTTTGT   TTTAGTA
                                |||||||||   |||||||
                                TTACAAACG   AAATCAT
                                      TAA_
GAM592  LOC149113 3'  AATGTTTGTATTTTTAGTA   15438         CTAA
                                GATGTTTGT   TTTAGTA
                                |||||||||   |||||||
                                TTACAAACA   AAATCAT
                                      TAA_
GAM592  LOC154403 3'  AATGTTTGTATTTTTAGTA   15438         CTAA
                                GATGTTTGT   TTTAGTA
                                |||||||||   |||||||
                                TTACAAACA   AAATCAT
                                      TAA_
GAM592  LOC154992 3'  AATGTTTGTATTTTTAGTA   15438         CTAA
                                GATGTTTGT   TTTAGTA
                                |||||||||   |||||||
                                TTACAAACA   AAATCAT
                                      TAA_
GAM592  LOC157697 5'  GATTTTGTCCATTCTAGTA   15439      G       A
                                GAT TTTGTCTA TTTAGTA
                                ||| |||||||| |||||||
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                                CTA AAACAGGT AGATCAT
                                  _      A
GAM592  LOC201868 3'  AATGTTTGTATTTTTAGTA   15438        CTAA
                                GATGTTTGT   TTTAGTA
                                |||||||||   |||||||
                                TTACAAACA   AAATCAT
                                     TAA_
GAM592  LOC221964 3'  TAGAGTATCTGATTTAGTA   15440     T  TT   A
                                TAGA GT  GTCT ATTTAGTA
                                |||| ||  |||| ||||||||
                                ATCT CA  TAGA TAAATCAT
                                  _ __   C
GAM592  LOC222008 3'  GTTTGTCCTTTAATTTGGTAA  15441        ___    A
                                GTTTGTCT   AATTT GTAA
                                ||||||||   ||||| ||||
                                CAAACAGG   TTAAA CATT
                                     AAA    C
GAM592  LOC254045 3'  AATGTTTGCATTTTTAGTA   15437        CTAA
                                GATGTTTGT   TTTAGTA
                                |||||||||   |||||||
                                TTACAAACG   AAATCAT
                                     TAA_
GAM592  LOC51184  3'  TAGATGGTTACTTTTAGTAAA  15442      T   T  AA
                                TAGATG TTG CT  TTTAGTAAA
                                |||||| ||| ||  |||||||||
                                ATCTAC AAT GA  AAATCATTT
                                   C   _ __
GAM592  LOC92573  5'  AATGTTTGTATTTTTAGTA   15438        CTAA
                                GATGTTTGT   TTTAGTA
                                |||||||||   |||||||
                                TTACAAACA   AAATCAT
                                     TAA_
GAM593  COL1A2    3'  CAGAAGAAATGGAAGGATTCAG 15445        _    A___
           CTTT                   CAGAAGAA TGGAA   TTAGCTTT
                                |||||||| |||||   |||||||||
                                GTCTTCTT ACCTT   AGTCGAAA
                                     T    CCTA
GAM593  HD        3'  TACGGAAGAATGGTGATT    15446     A       AA
                                TAC GAAGAATGG  ATT
                                ||| |||||||||  |||
                                ATG CTTCTTACC  TAA
                                  C        AC
GAM593  KIF3B     3'  TACAGAATTCAGATTAGCTTT  15447       GAA   AA
                                TACAGAA   TGGA  TTAGCTTT
                                |||||||   ||||  |||||||||
                                ATGTCTT   GTCT  AATCGAAA
                                     AA_   __
GAM593  MMP19     3'  GAACATGGAGTTAGCTTT    15448     GA    AA
                                GAA  ATGGA  TTAGCTTT
                                |||  |||||  |||||||||
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                                CTT  TACCT  AATCGAAA
                                  G_    C_
GAM593  MMP19    3' GAACATGGAGTTAGCTTT    15448    GA    AA
                                GAA  ATGGA  TTAGCTTT
                                |||  |||||  ||||||||
                                CTT  TACCT  AATCGAAA
                                  G_    C_
GAM593  MMP19    3' GAACATGGAGTTAGCTTT    15448    GA    AA
                                GAA  ATGGA  TTAGCTTT
                                |||  |||||  ||||||||
                                CTT  TACCT  AATCGAAA
                                  G_    C_
GAM593  MMP19    3' GAACATGGAGTTAGCTTT    15448    GA    AA
                                GAA  ATGGA  TTAGCTTT
                                |||  |||||  ||||||||
                                CTT  TACCT  AATCGAAA
                                  G_    C_
GAM593  PRELP    3' CAGAAGAATAGATGGCTTT    15449          AATTA
                                CAGAAGAATGGA    GCTTT
                                ||||||||||||    |||||
                                GTCTTCTTATCT    CGAAA
                                      AC___
GAM593  SLC38A2  3' GAAAAATAGGTTAGCTTT    15450        AAA
                                GAAGAATGG   TTAGCTTT
                                |||||||||   ||||||||
                                CTTTTTATC   AATCGAAA
                                    C__
GAM593  ABCA5    5' CAGAAGAAGCCTTAGCTTT    15451       AT  AAA
                                CAGAAGA  GG   TTAGCTTT
                                |||||||  ||   ||||||||
                                GTCTTCT  TC   AATCGAAA
                                   __  GG_
GAM593  AFAP     3' TAAGAAGAATGGCAGCTT    15452   C       AAAT
                                A AGAAGAATGG    TAGCTT
                                | ||||||||||    ||||||
                                A TCTTCTTACC    GTCGAA
                                 T        _____
GAM593  FARP1    3' TACAGAAGAAAGGAAACGTCTT 15453          T     TAG
                                TACAGAAGAA GGAAAT   CTT
                                |||||||||| ||||||   |||
                                ATGTCTTCTT CCTTTG   GAA
                                      T     CA_
GAM593  KIAA1817 3' TACAGAAGAAACATTGGCTTT  15454          TGGAA   A
                                TACAGAAGAA    ATT GCTTT
                                ||||||||||    ||| |||||
                                ATGTCTTCTT    TAA CGAAA
                                      TG___   C
GAM593  MGC26651 3' CAGAAGAATGCAAATGCT    15455          G    TA
                                CAGAAGAATG AAAT  GCT
                                |||||||||| ||||  |||
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                                GTCTTCTTAC TTTA  CGA
                                      G   __
GAM593  MGC5149   3'  TACAGACGAATGGAAATGAG   15456       A        T
                                TACAGA GAATGGAAAT AG
                                |||||| |||||||||| ||
                                ATGTCT CTTACCTTTA TC
                                    G         C
GAM593  PER3      3'  AAGAATGATACTAGCTTT     15457         AA
                                AAGAATGG  ATTAGCTTT
                                ||||||||  |||||||||
                                TTCTTACT  TGATCGAAA
                                     A_
GAM593  PRO1635   3'  TACAGAAAAAAAATTGGCTTT  15458          ATG      A
                                TACAGAAGA   GAAATT GCTTT
                                |||||||||   |||||| |||||
                                ATGTCTTTT   TTTTAA CGAAA
                                      ___      C
GAM593  SERP1     3'  CACAGGAGAATGGAAACATCTT 15459       A         TAG
                                TACAG AGAATGGAAAT   CTT
                                ||||| ||||||||||   |||
                                GTGTC TCTTACCTTTG   GAA
                                   C          TA_
GAM593  WWP1      3'  GAAGAACGGAAAACATACTTT  15460           TTA_
                                GAAGAATGGAAA    GCTTT
                                ||||||||||||    |||||
                                CTTCTTGCCTTT    TGAAA
                                       TGTA
GAM593  LOC144715 5'  AGAAGAATTGAATAACT     15461         G   AT
                                AGAAGAAT GAA  TAGCT
                                |||||||| |||  |||||
                                TCTTCTTA CTT  ATTGA
                                     A   __
GAM593  LOC200014 3'  TACAGAGGAATGGAAGTGTCCT 15462       A       ATTAG
          T                      TACAGA GAATGGAA     CTTT
                                ||||||| ||||||||     ||||
                                ATGTCT CTTACCTT     GGAA
                                   C       CACA_
GAM593  LOC91960  3'  TACAGAAGGTGGAGGGAACTT  15463         AA    AATT
                                TACAGAAG  TGGA    AGCTT
                                ||||||||  ||||    |||||
                                ATGTCTTC  ACCT    TTGAA
                                     C_    CCC_
GAM594  DSC3      3'  TTTACCAGTTGTCTGT      15466           CCCA
                                TTTACCGGTTG    TCTGT
                                ||||||||||    |||||
                                AAATGGTCAAC    AGACA
                                      ____
GAM594  DSC3      3'  TTTACCAGTTGTCTGT      15466           CCCA
                                TTTACCGGTTG    TCTGT
                                ||||||||||    |||||
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                                AAATGGTCAAC   AGACA
                                      ____
GAM594  LOC149773 3'  TTTACTGTTGCCCATCC     15467      CG
                                TTTAC  GTTGCCCATCT
                                |||||  ||||||||||
                                AAATG  CAACGGGTAGG
                                   A_
GAM595  CANX     3'  CTAAAATAATATCTAACTCT   15470          CGTT
                                CTAAAATAATATT   TTCT
                                ||||||||||||   ||||
                                GATTTTATTATAG   GAGA
                                       ATT_
GAM595  KIAA1229  3'  TAAAATAATACTCACATCT   15471           TTT
                                TAAAATAATATTCG   TCT
                                ||||||||||||||  |||
                                ATTTTATTATGAGT   AGA
                                       GT_
GAM595  LACE1    3'  TCTAAAATATTATCCCTTTT   15472        A    G
                                TCTAAAATA TATTC TTTT
                                ||||||||| ||||| ||||
                                AGATTTTAT ATAGG AAAA
                                     A    G
GAM595  My015    3'  TCTAGAATCAGTTCATTTTCTA 15473     A   AATA
           A                     TCTA AAT   TTCGTTTTCTAA
                                ||||| |||   ||||||||||||
                                AGAT TTA   AAGTAAAAGATT
                                  C  GTC_
GAM595  NPAS3    3'  TCTAAAATACTATTCCCCCTA  15474        A    GT TT
                                TCTAAAATA TATTC  T  CTA
                                ||||||||| |||||  |  |||
                                AGATTTTAT ATAAG  G  GAT
                                     G    __ GG
GAM595  PABPC5   3'  TCTAAAATGAATAAAGTTTTCT 15475       _   TTC
           A                     TCTAAAAT AATA   GTTTTCTA
                                ||||||||| ||||  ||||||||
                                AGATTTTA TTAT   CAAAAGAT
                                     C   TT_
GAM595  UBE1C    3'  TCTGCAATAATATTCATTT   15476    AA
                                TCT  AATAATATTCGTTT
                                |||  ||||||||||||||
                                AGA  TTATTATAAGTAAA
                                  CG
GAM595  YME1L1   3'  TCTAAAATAATTTTTCTA    15477         ATTCG
                                TCTAAAATAAT    TTTTCTA
                                ||||||||||    |||||||
                                AGATTTTATTA    AAAAGAT
                                      _____
GAM595  YME1L1   3'  TCTAAAATAATTTTTCTA    15477         ATTCG
                                TCTAAAATAAT    TTTTCTA
                                ||||||||||    |||||||
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                                AGATTTTATTA    AAAAGAT
                                       _____
GAM595  LOC256940 5'  TCTAAAATAGTTTTCTA    15478        ATATTC
                                TCTAAAATA    GTTTTCTA
                                |||||||||    ||||||||
                                AGATTTTAT    CAAAAGAT
                                       ______
GAM595  LOC257203 3'  TCTAAAACAATATTTTCTTT  15479           CG
                                TCTAAAATAATATT  TTTT
                                ||||||||||||||  ||||
                                AGATTTTGTTATAA  GAAA
                                        AA
GAM596  CXCL16   5'  TCAGGAGGCCGCCCGCCTGG  15482    AA      GC  G
                                TCG  GAGGCCGCC  CGC CTGG
                                |||  |||||||||  ||| ||||
                                AGT  CTCCGGCGG  GCG GACC
                                  C_       __  _
GAM596  GABRB3   5'  CCGCCGCCGCCGCCGCCGCGCT 15483    AAGAG
           GG                     TCG    GCCGCCGCCGCGCTGG
                                |||    ||||||||||||||||
                                GGC    CGGCGGCGGCGCGACC
                                  GGCGG
GAM596  GNA11    5'  GAAGAGGCGAGGCGCGCTGG  15484       CGCC  C
                                GAAGAGGC   GC GCGCTGG
                                ||||||||   || |||||||
                                CTTCTCCG   CG CGCGACC
                                     CTC_  _
GAM596  PTGFRN   5'  GGCGGGGGCCGCGCGCTGG   15485    C___    C
                                GGC   GCCGC GCGCTGG
                                |||   ||||| |||||||
                                CCG   CGGCG CGCGACC
                                  CCCC   _
GAM596  FLJ20640  5'  AAGAGGCGGCGCGCTG     15486       C  CGCC
                                AAGAGGC GC   GCGCTG
                                ||||||| ||   ||||||
                                TTCTCCG CG   CGCGAC
                                     C  ____
GAM596  MGC11061  5'  GAAGAGGCTGCGGCTG     15487       C  CGCC C
                                GAAGAGGC GC   G GCTG
                                |||||||| ||   | ||||
                                CTTCTCCG CG   C CGAC
                                     A  ____ _
GAM596  MGC15827  3'  CCGGGGAGGACTCGCGCTG   15488    AA   CCGCC  _
                                TCG  GAGG    GC CGCGCTG
                                |||  ||||    || |||||||
                                GGC  CTCC    TG GCGCGAC
                                  CC   _____  A
GAM596  WBSCR20A  5'  GAGGAGGCCGGCGCTG     15489    A     CCGCC
                                GA GAGGCCG    GCGCTG
                                || |||||||    ||||||
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                                CT CTCCGGC    CGCGAC
                                 C     _____
GAM596  LOC126129 3'  AGAGGCCAGCTGCCTGCTGG  15490       _ C  GC
                                AGAGGCC GC GCC  GCTGG
                                ||||||| || |||  |||||
                                TCTCCGG CG CGG  CGACC
                                   T  A   A_
GAM596  LOC150207 5'  TCGGAAGGCCTGCCCGCGCTGG 15491     AA    _  GC
                                TCG  GAGGCC GCC  CGCGCTGG
                                |||  |||||| |||  ||||||||
                                AGC  TTCCGG CGG  GCGCGACC
                                  C_     A  __
GAM596  LOC157280 3'  GAGGGGGCCGCCAGGAGGCTGG 15492     CC     C___
                                GAGG  GCCGCCG   GCTGG
                                ||||  |||||||   |||||
                                CTCC  CGGCGGT   CGACC
                                  CC      CCTC
GAM596  LOC253172 3'  TCGGGGGCGCCGCCGCCCG   15493    AAGA  C      G TG
                                TCG   GGC GCCGCCGC C  G
                                |||   ||| ||||||||  |  |
                                AGC   CCG CGGCGGCG G  C
                                  CC__  _      _ GT
GAM596  LOC255448 3'  GAGGGGGCCGCCAGGAGGCTGG 15492     CC     C___
                                GAGG  GCCGCCG   GCTGG
                                ||||  |||||||   |||||
                                CTCC  CGGCGGT   CGACC
                                  CC      CCTC
GAM597  HTR2C    3'  ATTGTAACACAACACTATATT  15496           T
                                ATTGTAACATAGTA CTATATT
                                |||||||||||||| |||||||
                                TAACATTGTGTTGT GATATAA
                                        _
GAM597  LOC221547 3'  TGACTGTAGCAGTCTATAT   15497       AACAT   _
                                TGATTGT    AGTA TCTATAT
                                |||||||    |||| |||||||
                                ACTGACA    TCGT AGATATA
                                   _____   C
GAM597  LOC257577 3'  TGACTGTAGCAGTCTATAT   15497       AACAT   _
                                TGATTGT    AGTA TCTATAT
                                |||||||    |||| |||||||
                                ACTGACA    TCGT AGATATA
                                   _____   C
GAM598  PPM1D    3'  TATTAGATGAATATATACCCAT 15500        _   _
          ATAA                    TATTAGATGA TATAT TTCGTATAA
                                |||||||||| ||||| |||||||||
                                ATAATCTACT ATATA GGGTATATT
                                     T    T
GAM598  SDCCAG1  3'  TATTAGATGTTATATACAGTA  15501        A    TTC
                                TATTAGATG TATAT   GTA
                                ||||||||| |||||   |||
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                                ATAATCTAC ATATA   CAT
                                     A    TGT
GAM598  SDCCAG1  3'  TATTAGATGTTATATACAGTA  15501        A    TTC
                                TATTAGATG TATAT   GTA
                                ||||||||| |||||   |||
                                ATAATCTAC ATATA   CAT
                                     A    TGT
GAM598  LOC220929 5'  TATTAATGATATATTTC     15502     A
                                TATT GATGATATATTTC
                                |||| ||||||||||||
                                ATAA TTACTATATAAAG
                                  _
GAM599  ANXA9    3'  TGAGATGGGAAAATTAAG    15505    GA       _
                                TG  ATGGGAAGAT AAG
                                ||  |||||||||| |||
                                AC  TACCCTTTTA TTC
                                 TC        A
GAM599  ASH1     3'  TGGGGTAGGAATAGGGATCCT  15506    AA    GATAA  A
                                TGG  TGGGAA    GA TCCT
                                |||  ||||||    || ||||
                                ACC  ATCCTT    CT AGGA
                                  CC     ATCC_  _
GAM599  CDH5     3'  GGAATGGGCTGCAGAGAATCCT 15507        AAGATA
                                GGAATGGG     AGAATCCT
                                ||||||||     ||||||||
                                CCTTACCC     TCTTAGGA
                                     GACGTC
GAM599  DMRT2    3'  TGGAATGGGGCGATAGCCT   15508        AA   AGAAT
                                TGGAATGGG  GATA    CCT
                                |||||||||  ||||    |||
                                ACCTTACCC  CTAT    GGA
                                     CG    C____
GAM599  GABRE    3'  AAAATGGGGATAAGAATCCT   15509       AA
                                GGAATGGG  GATAAGAATCCT
                                ||||||||  ||||||||||||
                                TTTTACCC  CTATTCTTAGGA
                                  __
GAM599  GABRE    3'  AAAATGGGGATAAGAATCCT   15509       AA
                                GGAATGGG  GATAAGAATCCT
                                ||||||||  ||||||||||||
                                TTTTACCC  CTATTCTTAGGA
                                  __
GAM599  GABRE    3'  AAAATGGGGATAAGAATCCT   15509       AA
                                GGAATGGG  GATAAGAATCCT
                                ||||||||  ||||||||||||
                                TTTTACCC  CTATTCTTAGGA
                                  __
GAM599  GABRE    3'  AAAATGGGGATAAGAATCCT   15509       AA
                                GGAATGGG  GATAAGAATCCT
                                ||||||||  ||||||||||||
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                                TTTTACCC  CTATTCTTAGGA
                                    __
GAM599  IL2RA    5'  TGGGATGGGAAGATCGGTCC   15510    A       AAGAA
                                TGG ATGGGAAGAT    TCC
                                ||| ||||||||||    |||
                                ACC TACCCTTCTA    AGG
                                  C        GCC__
GAM599  MYO1A    5'  GGAATGGGGCATAAGAGTCCT  15511       AAG     A
                                GGAATGGG   ATAAGA TCCT
                                ||||||||   |||||| ||||
                                CCTTACCC   TATTCT AGGA
                                     CG_    C
GAM599  SF3B3    3'  GGAATGGGGGACTCAGGTTC   15512       AA   A_  AA
                                GGAATGGG  GAT  AG  TC
                                ||||||||  |||  ||  ||
                                CCTTACCC  CTG  TC  AG
                                     C_   AG  CA
GAM599  SIAT7D   3'  TGGGGTGGGAAGGAACCT    15513    AA     ATAA   T
                                TGG  TGGGAAG    GAA CCT
                                |||  |||||||    ||| |||
                                ACC  ACCCTTC    CTT GGA
                                  CC      _____  _
GAM599  SORBS1   3'  GGGATGGGAAGCTGATGGGATC 15514    A      ATAAGA__
           CTA                    GG ATGGGAAG       ATCCTA
                                || ||||||||       ||||||
                                CC TACCCTTC       TAGGAT
                                 C       GACTACCC
GAM599  XK       3'  GGAGTAAGATGGTAAGAATTCT 15515    A    AGA     C
           A                     GGA TGGGA   TAAGAAT CTA
                                ||| |||||   ||||||| |||
                                CCT ATTCT   ATTCTTA GAT
                                  C    ACC      A
GAM599  ZNF278   3'  GGAAGGGAGGATGACGAAC   15516     T   A   AA_
                                GGAA GGGA GAT   GAAT
                                |||| |||| |||   ||||
                                CCTT CCCT CTA   CTTG
                                  _   C   CTG
GAM599  ZNF278   3'  GGAAGGGAGGATGACGAAC   15516     T   A   AA_
                                GGAA GGGA GAT   GAAT
                                |||| |||| |||   ||||
                                CCTT CCCT CTA   CTTG
                                  _   C   CTG
GAM599  ZNF278   3'  GGAAGGGAGGATGACGAAC   15516     T   A   AA_
                                GGAA GGGA GAT   GAAT
                                |||| |||| |||   ||||
                                CCTT CCCT CTA   CTTG
                                  _   C   CTG
GAM599  ARNTL2   3'  TGGAGTGGGAAGAGTGCCT   15517     A      TAAGAAT
                                TGGA TGGGAAGA      CCT
                                |||| ||||||||      |||
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                                ACCT ACCCTTCT      GGA
                                  C       CAC____
GAM599  C1orf17   3'  TGGAGTGGGAAGAAATC     15518      A       TAAG
                                TGGA TGGGAAGA    AATC
                                |||| ||||||||    ||||
                                ACCT ACCCTTCT    TTAG
                                  C       _____
GAM599  C21orf42  3'  TGGAATAGGGAAGATGAAA    15519       _       A
                                TGGAAT GGGAAGAT AGA
                                |||||| |||||||| |||
                                ACCTTA CCCTTCTA TTT
                                   T       C
GAM599  CCR5      3'  TGGGATGGGAAGGAAATC     15520      A       ATAA
                                TGG ATGGGAAG    GAATC
                                ||| ||||||||    |||||
                                ACC TACCCTTC    TTTAG
                                  C       C___
GAM599  DCNP1     3'  GGGGTGGGGACAAGAATTCTA  15521     AA    AA       C
                                GG  TGGG  GATAAGAAT CTA
                                ||  ||||  ||||||||| |||
                                CC  ACCC  CTGTTCTTA GAT
                                 CC    __        A
GAM599  DGS-A     3'  TGGAATGGCAGGGCCATCCTA  15522        GA  ATAAGA
                                TGGAATGG  AG     ATCCTA
                                ||||||||  ||     ||||||
                                ACCTTACC  TC     TAGGAT
                                     G_  CCGG__
GAM599  FLJ00001  3'  TGGGGTGGGAAGAAAGGCCT   15523     AA       T   AAT
                                TGG  TGGGAAGA AAG   CCT
                                |||  |||||||| |||   |||
                                ACC  ACCCTTCT TTC   GGA
                                  CC       _   C__
GAM599  FLJ10925  5'  GAGTGGGAAGATGACCT     15524     A       AA  AT
                                GA TGGGAAGAT  GA  CCT
                                || |||||||||  ||  |||
                                CT ACCCTTCTA  CT  GGA
                                 C        __  __
GAM599  FLJ20275  3'  TGGGAGGGAAGACAATCCT    15525     AAT       AGA
                                TGG   GGGAAGATA   ATCCT
                                |||   |||||||||   |||||
                                ACC   CCCTTCTGT   TAGGA
                                  CT_       ____
GAM599  FLJ22160  5'  TGGGACGGGGTCTCAGAATCCT 15526     A    AAGATA
                                TGG ATGGG     AGAATCCT
                                ||| |||||     ||||||||
                                ACC TGCCC     TCTTAGGA
                                  C    CAGAG_
GAM599  KIAA0179  3'  GAATGGGATGTGAGGATCCTA  15527        AGATA  A
                                GAATGGGA    AG ATCCTA
                                ||||||||    || ||||||
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                                CTTACCCT    TC TAGGAT
                                    ACAC_  C
GAM599  KIAA0774  5'  TGGTGTGGAGAGAATCCT    15528    AATG  A  TAA
                                TGG   GGA GA   GAATCCT
                                |||   ||| ||   |||||||
                                ACC   CCT CT   CTTAGGA
                                  ACA_  _ ___
GAM599  NAPA    3'  TGGGGTGGGGAGAATCCC    15529    AA   AAGATA
                                TGG  TGGG    AGAATCCT
                                |||  ||||    ||||||||
                                ACC  ACCC    TCTTAGGG
                                  CC   C_____
GAM599  ZNF339   3'  TGAAGTGGGAAGATTACCT   15530     A      AAGAAT
                                TGGA TGGGAAGAT     CCT
                                |||| |||||||||     |||
                                ACTT ACCCTTCTA     GGA
                                  C       AT____
GAM599  LOC142941 5'  GGAGGGGGCTAGAATCCTA   15531    AT   AAGATA
                                GGA  GGG    AGAATCCTA
                                |||  |||    |||||||||
                                CCT  CCC    TCTTAGGAT
                                  CC   GA____
GAM599  LOC150933 3'  TGAAATGGGGAGAGGAGAATCC 15532        A   TA
           TA                     TGGAATGGG AGA  AGAATCCTA
                                |||||||||  |||  |||||||||
                                ACTTTACCC TCT  TCTTAGGAT
                                     C   CC
GAM599  LOC197049 5'  TGGGGCGGGAATGAAATCCTA  15533    AA    GATAA
                                TGG  TGGGAA    GAATCCTA
                                |||  ||||||    ||||||||
                                ACC  GCCCTT    TTTAGGAT
                                  CC     AC___
GAM599  LOC255223 5'  TGGGGCGGGAATGAAATCCTA  15533    AA    GATAA
                                TGG  TGGGAA    GAATCCTA
                                |||  ||||||    ||||||||
                                ACC  GCCCTT    TTTAGGAT
                                  CC     AC___
GAM599  LOC90917  3'  TGGGGTGGGAAGATGTCC    15534    AA      AAGAA
                                TGG  TGGGAAGAT    TCC
                                |||  |||||||||    |||
                                ACC  ACCCTTCTA    AGG
                                  CC       C____
GAM599  LOC91585  3'  TGGAGGTGGGAAGATACAACTC 15535     A_       AGAA
           CT                     TGGA  TGGGAAGATA   TCCT
                                ||||  ||||||||||   ||||
                                ACCT  ACCCTTCTAT   AGGA
                                  CC       GTTG
GAM600  ABCC3    3'  GTGCAGGTGGGACAGCTC    15538       CCTAT   A
                                GTGTAGGT    GACA CTC
                                ||||||||    |||| |||
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                                CACGTCCA    CTGT GAG
                                    CC___   C
GAM600  ABCC3   3'  GTGCAGGTGGGACAGCTC    15538       CCTAT   A
                                GTGTAGGT    GACA CTC
                                ||||||||    |||| |||
                                CACGTCCA    CTGT GAG
                                    CC___   C
GAM600  ATP1B1  3'  GTGTAGGTCCCATACGTATGAC 15539       _______
          A                      GTGTAGGTCCT     ATGACA
                                ||||||||||     ||||||
                                CACATCCAGGG     TACTGT
                                      TATGCA
GAM600  DMC1    3'  GTGTGTGTCCTATAAACA    15540     AG      _
                                GTGT  GTCCTATGA CA
                                ||||  |||||||| ||
                                CACA  CAGGATATT GT
                                  CA        T
GAM600  IMPA2   3'  CACTGTAGCGTGACAACT    15541     G   _ CCTAT
                                CAC TGTAG GT    GACAACT
                                ||| ||||| ||    |||||||
                                GTG ACATC CA    CTGTTGA
                                  _     G _____
GAM600  KIF3C   3'  CACGGTAGGCCCAGACGGCTC  15542     T      TAT   AA
                                CACG GTAGGTCC   GAC  CTC
                                |||| ||||||||   |||  |||
                                GTGC CATCCGGG   CTG  GAG
                                  _       T__   CC
GAM600  RAPSN   5'  CACGTGGGGTGATCCCTGGTGG 15543      TA__     A  ACAA
          CTC                     CACGTG    GGTCCT TG    CTC
                                ||||||    |||||| ||    |||
                                GTGCAC    CTAGGG AC    GAG
                                   CCCA     _  CACC
GAM600  C6.1A   3'  ATGTAGGTCCATACAACT    15544         TATG
                                GTGTAGGTCC    ACAACT
                                ||||||||||    ||||||
                                TACATCCAGG    TGTTGA
                                      TA__
GAM600  FLJ12700 3'  CGTGTGAGGTGAGTGACAACTC 15545      _   CCTA
                                CGTGT AGGT    TGACAACTC
                                ||||| ||||    |||||||||
                                GCACA TCCA    ACTGTTGAG
                                  C    CTC_
GAM600  MGC14126 5'  GTGTAAGTTGCATAATGACT   15546       CC    CA
                                GTGTAGGT  TATGA  ACT
                                ||||||||  |||||  |||
                                CACATTCA  GTATT  TGA
                                    AC    AC
GAM600  TIX1    3'  CACTGTAGGTCCTGCATGAACT 15547     G       __   CA
                                CAC TGTAGGTCCT  ATGA  ACT
                                ||| ||||||||||  ||||  |||
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                                GTG ACATCCAGGA  TACT  TGA
                                  _       CG   __
GAM601  CPNE7    3'  CAGGATCCCAGGAGGAC    15550       GA  AA
                                CAGGATTT  CG  AGGAC
                                ||||||||  ||  |||||
                                GTCCTAGG  GT  TCCTG
                                    __  CC
GAM601  DAZ      3'  TCAGGATTTGCAGCAGAC    15551       A  AAA
                                TCAGGATTTG CG   GGAC
                                |||||||||| ||   ||||
                                AGTCCTAAAC GT   TCTG
                                    _ CG_
GAM601  DAZ      3'  TCAGGATTTGCAGCAGAC    15551       A  AAA
                                TCAGGATTTG CG   GGAC
                                |||||||||| ||   ||||
                                AGTCCTAAAC GT   TCTG
                                    _ CG_
GAM601  EFG1     3'  TCAGGTAATGAAAAGGAC    15552     ATT   CG
                                TCAGG   TGA  AAAGGAC
                                |||||   |||  |||||||
                                AGTCC   ACT  TTTCCTG
                                   ATT  __
GAM601  ICA1     3'  TCAGGATTTGAGAGTGG     15553       C  AA
                                TCAGGATTTGA GA  GG
                                |||||||||| ||  ||
                                AGTCCTAAACT CT  CC
                                    _ CA
GAM601  ICA1     3'  TCAGGATTTGAGAGTGG     15553       C  AA
                                TCAGGATTTGA GA  GG
                                |||||||||| ||  ||
                                AGTCCTAAACT CT  CC
                                    _ CA
GAM601  KIAA0442 3'  AGGATCTAGAAAGGAC     15554       AC
                                AGGATTTG  GAAAGGAC
                                ||||||||  ||||||||
                                TCCTAGAT  CTTTCCTG
                                    __
GAM601  MAP3K7IP2 3'  TCAGGATTAGAAATGGAC    15555       TGAC   _
                                TCAGGATT    GAAA GGAC
                                ||||||||    |||| ||||
                                AGTCCTAA    CTTT CCTG
                                    T___    A
GAM601  MAP3K9   3'  GGGGCTGACAAAGGGACC    15556    AT      A
                                GG  TTGACGAA GGACC
                                ||  |||||||| |||||
                                CC  GACTGTTT CCTGG
                                 CC       C
GAM601  OPHN1    3'  TCAGAACCTGGAAAGG      15557       AC
                                TCAGGATTTG  GAAAGG
                                ||||||||||  ||||||
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                                AGTCTTGGAC  CTTTCC
                                        __
GAM601  P53AIP1  3' TCAGGATTTGAACCCAGACC  15558         CGAAA
                                TCAGGATTTGA    GGACC
                                ||||||||||    |||||
                                AGTCCTAAACT    TCTGG
                                     TGGG_
GAM601  PCDH11X  3' TCAGGATTGAAAAGGA     15559       T  CG
                                TCAGGATT GA  AAAGGA
                                |||||||| ||  ||||||
                                AGTCCTAA CT  TTTCCT
                                      _ __
GAM601  PCDH11X  3' TCAGGATTGAAAAGGA     15559       T  CG
                                TCAGGATT GA  AAAGGA
                                |||||||| ||  ||||||
                                AGTCCTAA CT  TTTCCT
                                      _ __
GAM601  PCDH11Y  3' TCAGGATTGAAAAGGA     15559       T  CG
                                TCAGGATT GA  AAAGGA
                                |||||||| ||  ||||||
                                AGTCCTAA CT  TTTCCT
                                      _ __
GAM601  PCDHB15  3' TCAAGATTACTAAAGG     15560       TG  G
                                TCAGGATT  AC AAAGG
                                ||||||||  || |||||
                                AGTTCTAA  TG TTTCC
                                      __ A
GAM601  PSD      5' TCAGGATCTTGAAATCAGGA  15561        _  CGAA
                                TCAGGATTT GA   AGGA
                                ||||||||| ||   ||||
                                AGTCCTAGA CT   TCCT
                                     A  TTAG
GAM601  PSEN1    3' TCAGAATTTGGTGGAAAA    15562        AC_
                                TCAGGATTTG   GAAAG
                                ||||||||||   |||||
                                AGTCTTAAAC   CTTTT
                                      CAC
GAM601  PSEN1    3' TCAGAATTTGGTGGAAAA    15562        AC_
                                TCAGGATTTG   GAAAG
                                ||||||||||   |||||
                                AGTCTTAAAC   CTTTT
                                      CAC
GAM601  SAH      5' TCAGGATTTGCACAGAGACC  15563         A  AAA
                                TCAGGATTTG CG   GGACC
                                |||||||||| ||   |||||
                                AGTCCTAAAC GT   TCTGG
                                      _ GTC
GAM601  SIRPB2   5' TCAGAAGCAGGAAAGGACC  15564       TTTGAC
                                TCAGGA     GAAAGGACC
                                ||||||     |||||||||
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                                AGTCTT     CTTTCCTGG
                                   CGTC__
GAM601  SIRPB2   5'  TCAGAAGCAGGAAAGGACC   15564       TTTGAC
                                TCAGGA     GAAAGGACC
                                ||||||     |||||||||
                                AGTCTT     CTTTCCTGG
                                   CGTC__
GAM601  SLC4A7   3'  TCAGGATTTACTACAGAC    15565         A GAAA
                                TCAGGATTTG C    GGAC
                                |||||||||| |    ||||
                                AGTCCTAAAT G    TCTG
                                      _ ATG_
GAM601  UBE2A    3'  TCAGGATTTGAGTGGAAAA   15566          C__
                                TCAGGATTTGA   GAAAG
                                ||||||||||   |||||
                                AGTCCTAAACT   CTTTT
                                      CAC
GAM601  WBSCR1   3'  AGGAATGGAAAGGACC     15567     TT  AC
                                AGGA  TG  GAAAGGACC
                                ||||  ||  |||||||||
                                TCCT  AC  CTTTCCTGG
                                  T_  __
GAM601  WBSCR1   3'  AGGAATGGAAAGGACC     15567     TT  AC
                                AGGA  TG  GAAAGGACC
                                ||||  ||  |||||||||
                                TCCT  AC  CTTTCCTGG
                                  T_  __
GAM601  DKFZP434F0318 3'  AGGACTTGGAGAGGACC     15568        AC  A
                                AGGATTTG  GA AGGACC
                                ||||||||  || ||||||
                                TCCTGAAC  CT TCCTGG
                                     __  C
GAM601  DKFZp547A023 3'  TCAGAATTCACAGAGGA     15569         G   AA
                                TCAGGATTT ACG  AGGA
                                ||||||||| |||  ||||
                                AGTCTTAAG TGT  TCCT
                                     _   C_
GAM601  DKFZP564I1171 3'  TCAGGATTTCGGTGATGGGCC  15570         _ AC  AA  A
                                TCAGGATTT G  GA  GG CC
                                ||||||||| |  ||  || ||
                                AGTCCTAAA C  CT  CC GG
                                     G CA  AC  _
GAM601  FBP17    3'  GGATCCCTCAAAGGACC     15571       GA G
                                GGATTT  C AAAGGACC
                                ||||||  | ||||||||
                                CCTAGG  G TTTCCTGG
                                   GA _
GAM601  FLJ11362  3'  TCAGGATTTACCCCCAAGCC   15572          ACGAA   A
                                TCAGGATTTG    AGG CC
                                ||||||||||    ||| ||
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                                AGTCCTAAAT    TTC GG
                                     GGGGG  _
GAM601  FLJ12888  5'  CAGGATTTGATGACAGAA    15573         C  A
                                CAGGATTTGA GA AGGA
                                |||||||||| || ||||
                                GTCCTAAACT CT TCTT
                                     A  G
GAM601  FLJ21324  5'  TCAGGATTTACGGGAGGCGCC  15574         A  AA  A_
                                TCAGGATTTG CG  AGG  CC
                                |||||||||| ||  |||  ||
                                AGTCCTAAAT GC  TCC  GG
                                     _  CC   GC
GAM601  FLJ21820  3'  AGGATTTGAGCGGAGGGAC   15575         _  AAA
                                AGGATTTGA CG   GGAC
                                ||||||||| ||   ||||
                                TCCTAAACT GC   CCTG
                                     C  CTC
GAM601  FLJ22672  3'  GGAGCCAGATGAAAGGACC   15576     _ TT  C
                                GGA T  GA GAAAGGACC
                                ||| |  || |||||||||
                                CCT G  CT CTTTCCTGG
                                  C GT  A
GAM601  KIAA0007  3'  GGATTTGATGAAAGATACC   15577        C     _
                                GGATTTGA GAAAGG ACC
                                |||||||| |||||| |||
                                CCTAAACT CTTTCT TGG
                                     A     A
GAM601  KIAA0218  3'  TCAGGACTTGAGATGAC     15578         C  AAG
                                TCAGGATTTGA GA   GAC
                                |||||||||||| ||   |||
                                AGTCCTGAACT CT   CTG
                                     _  A__
GAM601  KIAA0226  3'  TCAGCATTATCAAAAGGAC   15579      G   TGA
                                TCAG ATT   CGAAAGGAC
                                |||| |||   |||||||||
                                AGTC TAA   GTTTTCCTG
                                  G   TA_
GAM601  KIAA0514  3'  TCAGGATCTTCACAATGGGGAC 15580         G_   AA_
          C                      TCAGGATTT  ACGA   GGACC
                                |||||||||  ||||   |||||
                                AGTCCTAGA  TGTT   CCTGG
                                     AG    ACC
GAM601  KIAA1198  3'  TCAAGAATGTGAAAGGACC   15581       TT  AC
                                TCAGGA  TG  GAAAGGACC
                                ||||||  ||  |||||||||
                                AGTTCT  AC  CTTTCCTGG
                                   T_  A_
GAM601  KIAA1328  3'  TCAGAATTAAAGGAC       15582         TGACG
                                TCAGGATT    AAAGGAC
                                ||||||||    |||||||
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                                AGTCTTAA    TTTCCTG
                                        _____
GAM601  KIAA1949 5' CCAGGAATCCCTGAAAGGACC 15583      T GAC
                                TCAGGA TT   GAAAGGACC
                                |||||| ||   |||||||||
                                GGTCCT AG   CTTTCCTGG
                                    T GGA
GAM601  KIAA1949 5' CCAGGAATCCCTGAAAGGACC 15583      T GAC
                                TCAGGA TT   GAAAGGACC
                                |||||| ||   |||||||||
                                GGTCCT AG   CTTTCCTGG
                                    T GGA
GAM601  KIAA1949 5' CCAGGAATCCCTGAAAGGACC 15583      T GAC
                                TCAGGA TT   GAAAGGACC
                                |||||| ||   |||||||||
                                GGTCCT AG   CTTTCCTGG
                                    T GGA
GAM601  LANO    5' CAGGCTGTGAAAGGAC     15584     AT  AC
                                CAGG  TTG  GAAAGGAC
                                ||||  |||  ||||||||
                                GTCC  GAC  CTTTCCTG
                                  __  A_
GAM601  MGC20496 3' TCAGCAATGAAAGGACC     15585     GATT  C
                                TCAG    TGA GAAAGGACC
                                ||||    ||| |||||||||
                                AGTC    GTT CTTTCCTGG
                                  ____  A
GAM601  MGC27171 3' AGGTTTGACAACAGAC      15586     A      AA
                                AGG TTTGACGA  GGAC
                                ||| ||||||||  ||||
                                TCC AAACTGTT  TCTG
                                  _      G_
GAM601  NLN     3' TCAAGATACAAGAAGGA     15587       TTG   _
                                TCAGGAT   ACGA AAGGA
                                |||||||   |||| |||||
                                AGTTCTA   TGTT TTCCT
                                    ___   C
GAM601  RALGPS1A 3' CAGGATTTATACTCAGGAC   15588        _ GAA
                                CAGGATTTG AC   AGGAC
                                ||||||||| ||   |||||
                                GTCCTAAAT TG   TCCTG
                                     A  AG_
GAM601  RERG    3' TCAGGGTTTGGTGAAAAGAC  15589      A   AC
                                TCAGG TTTG  GAAAGGAC
                                ||||| ||||  ||||||||
                                AGTCC AAAC  CTTTTCTG
                                  C   CA
GAM601  SLPI    3' TCAGGGTGGAAAGGACC     15590      ATT  AC
                                TCAGG   TG  GAAAGGACC
                                |||||   ||  |||||||||
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                                AGTCC   AC  CTTTCCTGG
                                  C__  __
GAM601   TFIP11    3'  TCAGGACTGTGAGGAC      15591         _   CGAAA
                                TCAGGATT TGA    GGAC
                                |||||||| |||    ||||
                                AGTCCTGA ACT    CCTG
                                    C  ______
GAM601   TFIP11    3'  TCAGATTTTAAAAGGAC     15592       A    CGA
                                TCAGG TTTGA   AAGGAC
                                ||||| |||||   ||||||
                                AGTCT AAATT   TTCCTG
                                  A    ____
GAM601   UQCRH     5'  TCAGGATCAAGAAGGAC     15593         TGAC   A
                                TCAGGATT    GAA GGAC
                                ||||||||    ||| ||||
                                AGTCCTAG    CTT CCTG
                                    TT__   _
GAM601   LOC127534 3'  CCAGGATCCACAAGGGACC    15594          G    AA
                                TCAGGATTT ACGA  GGACC
                                ||||||||| ||||  |||||
                                GGTCCTAGG TGTT  CCTGG
                                    _   C_
GAM601   LOC149469 3'  CCAGGCACTCGGAAGGGCC    15595       _    AC   A  A
                                TCAGG ATTTG  GAA GG CC
                                ||||| |||||  ||| || ||
                                GGTCC TGAGC  CTT CC GG
                                  G    __   C  _
GAM601   LOC149606 3'  TCAGGAGTTCCAAAGGACC    15596        T  GA G
                                TCAGGA TT  C AAAGGACC
                                ||||||  ||  | ||||||||
                                AGTCCT AA  G TTTCCTGG
                                  C  G_ _
GAM601   LOC149844 3'  TCAGGATCTTCCATAGGA     15597         GA  AA
                                TCAGGATTT  CG  AGGA
                                |||||||||  ||  ||||
                                AGTCCTAGA  GT  TCCT
                                    AG  A_
GAM601   LOC151959 5'  GGATTTAACAGGACC        15598         GAA
                                GGATTTGAC   AGGACC
                                |||||||||   ||||||
                                CCTAAATTG   TCCTGG
                                    ___
GAM601   LOC158476 3'  TCAGGATTTCAACATTCAGGA  15599          _   AA_
                                TCAGGATTT GACG   AGGA
                                ||||||||| ||||   ||||
                                AGTCCTAAA TTGT   TCCT
                                    G   AAG
GAM601   LOC221712 5'  TCAGGATTGGACCTGGGAC    15600         T   GAAA
                                TCAGGATT GAC    GGAC
                                |||||||| |||    ||||
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                                AGTCCTAA CTG    CCTG
                                     C  GAC_
GAM601  LOC221756 3'  TCAGGATTTCACGTGAGG    15601        G  AA
                                TCAGGATTT ACG  AGG
                                ||||||||| |||  |||
                                AGTCCTAAA TGC  TCC
                                     G  AC
GAM601  LOC253502 3'  CAGGATCCCAGGAGGAC     15550        GA  AA
                                CAGGATTT  CG  AGGAC
                                ||||||||  ||  |||||
                                GTCCTAGG  GT  TCCTG
                                     __  CC
GAM601  LOC256211 5'  AGACCTGATGAGAGGGCC    15602        C  A  A
                                GGATTTGA GA AGG CC
                                |||||||| || ||| ||
                                TCTGGACT CT TCC GG
                                     A  C  C
GAM601  LOC256542 5'  AGGATTTGACTAGGCC      15603        GAA  A
                                AGGATTTGAC  AGG CC
                                ||||||||||  ||| ||
                                TCCTAAACTG  TCC GG
                                     A__  _
GAM601  LOC56930  5'  TCAGGGGGTTGAGAGGAC    15604      AT_  C  AA
                                TCAGG  TTGA GA  GGAC
                                |||||  |||| ||  ||||
                                AGTCC  AACT CT  CCTG
                                   CCC  _ __
GAM601  LOC91097  3'  TCAGGATTTACGGGAGGCGCC  15574         A  AA  A_
                                TCAGGATTTG CG  AGG  CC
                                |||||||||| ||  |||  ||
                                AGTCCTAAAT GC  TCC  GG
                                     _  CC  GC
GAM602  APBA1     5'  GCTGGGCCCGGCTCACTGCGC  15607      ____      CA
                                GTTG   CGGCTCAC  CGC
                                ||||   ||||||||  |||
                                CGAC   GCCGAGTG  GCG
                                  CCGG       AC
GAM602  FGFR2     5'  CCTGTGTTGTCCCCGCGC    15608   _    CGGC  A  A
                                CC GTGTTG   TC CC CGC
                                || ||||||   || || |||
                                GG CACAAC   AG GG GCG
                                 A    ____  G  C
GAM602  FGFR2     5'  CCTGTGTTGTCCCCGCGC    15608   _    CGGC  A  A
                                CC GTGTTG   TC CC CGC
                                || ||||||   || || |||
                                GG CACAAC   AG GG GCG
                                 A    ____  G  C
GAM602  FGFR2     5'  CCTGTGTTGTCCCCGCGC    15608   _    CGGC  A  A
                                CC GTGTTG   TC CC CGC
                                || ||||||   || || |||
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                                GG CACAAC   AG GG GCG
                                 A    ____ G  C
GAM602  FGFR2   5' CCTGTGTTGTCCCCGCGC   15608   _   CGGC  A  A
                                CC GTGTTG   TC CC CGC
                                || ||||||   || || |||
                                GG CACAAC   AG GG GCG
                                 A    ____ G  C
GAM602  FGFR2   5' CCTGTGTTGTCCCCGCGC   15608   _   CGGC  A  A
                                CC GTGTTG   TC CC CGC
                                || ||||||   || || |||
                                GG CACAAC   AG GG GCG
                                 A    ____ G  C
GAM602  FGFR2   5' CCTGTGTTGTCCCCGCGC   15608   _   CGGC  A  A
                                CC GTGTTG   TC CC CGC
                                || ||||||   || || |||
                                GG CACAAC   AG GG GCG
                                 A    ____ G  C
GAM602  FGFR2   5' CCTGTGTTGTCCCCGCGC   15608   _   CGGC  A  A
                                CC GTGTTG   TC CC CGC
                                || ||||||   || || |||
                                GG CACAAC   AG GG GCG
                                 A    ____ G  C
GAM602  FGFR2   5' CCTGTGTTGTCCCCGCGC   15608   _   CGGC  A  A
                                CC GTGTTG   TC CC CGC
                                || ||||||   || || |||
                                GG CACAAC   AG GG GCG
                                 A    ____ G  C
GAM602  GNE     3' CACCATGTTTCACCA     15609       GCGGC
                                CACCGTGTT   TCACCA
                                |||||||||   ||||||
                                GTGGTACAA   AGTGGT
                                     _____
GAM602  HMGA2   3' CACAGTGTTACACACCGCG  15610   C     GCT   A
                                CAC GTGTTGCG  CACC CG
                                ||| ||||||||  |||| ||
                                GTG CACAATGT  GTGG GC
                                  T      ___   C
GAM602  MTMR3   3' CACCCTGTTTCACCACG    15611    G  GCGGC
                                CACC TGTT   TCACCACG
                                |||| ||||   ||||||||
                                GTGG ACAA   AGTGGTGC
                                  G  _____
GAM602  ZNF14   3' CACCATGTTGACCACG     15612        CGGCTC
                                CACCGTGTTG    ACCACG
                                ||||||||||    ||||||
                                GTGGTACAAC    TGGTGC
                                     ______
GAM602  CNOT7   5' CACCGTGCTGCCCTCGTGC  15613        GG  ACCAC
                                CACCGTGTTGC CTC   GC
                                ||||||||||| |||   ||
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                                GTGGCACGACG  GAG    CG
                                      G_  CA___
GAM602  FLJ10900  5'  CACCGAGCTACCTCGCCGCG  15614     T   GG  A  A
                                CACCG GTTGC  CTC CC CG
                                ||||| |||||  ||| || ||
                                GTGGC CGATG  GAG GG GC
                                   T   __  C  C
GAM602  FLJ10921  3'  ACCTGTCTTTCACCATGC   15615    G   GCGGC    C
                                ACC TGTT    TCACCA GC
                                ||| ||||    |||||| ||
                                TGG ACAG    AGTGGT CG
                                  _   AA___    A
GAM602  FLJ12577  3'  CCATTTAGCGGCTCATTGTGCC 15616    GTT     CCAC
                                CCGT  GCGGCTCA   GCC
                                ||||  ||||||||   |||
                                GGTA  CGCCGAGT   CGG
                                  AAT      AACA
GAM602  FLJ13189  5'  GCTGATGGGCTCACCGCGCC  15617   GT_ C     A
                                GT  TG GGCTCACC CGCC
                                ||  || |||||||| ||||
                                CG  AC CCGAGTGG GCGG
                                 ACT _      C
GAM602  KIAA0084  5'  CCGCGCTCTCGCTCGCTGCGCC 15618      GCG   ACCA
                                CCGTGTT  GCTC   CGCC
                                |||||||  ||||   ||||
                                GGCGCGA  CGAG   GCGG
                                    GAG   CGAC
GAM602  KIAA0555  5'  CACCGTGTGCTTGCGCTGGCGT 15619    ___   _______  TCACCAC
          GGTGG                 GTGT  TGCG    GC     G
                                ||||  ||||    ||     |
                                CACA  ACGC    CG     C
                                  CGA   GAIIIC  CACCACT
GAM602  KIAA0763  3'  CCGGCCACGGCTCACCACGC  15620    T  TG
                                CCG GT  CGGCTCACCACGC
                                ||| ||  ||||||||||||
                                GGC CG  GCCGAGTGGTGCG
                                  _  GT
GAM602  PNMA1    5'  CAACAGACTGTGGCTCACCGTG 15621   C  TG  C     AC
          C                     CA CG  TTG GGCTCACC  GC
                                || ||  ||| ||||||||  ||
                                GT GT  GAC CCGAGTGG  CG
                                 T  CT   A      CA
GAM602  SETBP1   3'  CCCCGCCCCGGCTCACTGCGC  15622   G   G     CA
                                CC TGTT CGGCTCAC  CGC
                                || |||| ||||||||  |||
                                GG GCGG GCCGAGTG  GCG
                                 G   G      AC
GAM602  SPUVE    5'  CCGGGCCGCGGCTCGCTGCGCC 15623    T       ACCA
                                CCG GTTGCGGCTC   CGCC
                                ||| ||||||||||   ||||
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                                GGC CGGCGCCGAG    GCGG
                                  C         CGAC
GAM602  LOC149175 3'  GTGTTGCACAGGCCCATGCC   15624        ___     CCAC
                                GTGTTGC   GGCTCA    GCC
                                |||||||   ||||||    |||
                                CACAACG   CCGGGT    CGG
                                    TGT     A___
GAM602  LOC221078 5'  CACTGCGTTACGCTACGC    15625     C       G  CACC
                                CAC GTGTTGCG CT    ACGC
                                ||| |||||||| ||    ||||
                                GTG CGCAATGC GA    TGCG
                                  A       _ _____
GAM603  DKFZp761B1514 3'  TGTCAGTATTTGGGGCAATTTT 15628            AAAC
           T                     TGTTAGTATTTG    TAATTTTT
                                ||||||||||||    ||||||||
                                ACAGTCATAAAC    GTTAAAAA
                                       CCC_
GAM603  KIAA0318  3'  TGTTGTATTTGAAACTA     15629      A
                                TGTT GTATTTGAAACTA
                                |||| ||||||||||||
                                ACAA CATAAACTTTGAT
                                  _
GAM603  LOC221078 3'  TGTTAGATTCACTAATTTT    15630       T    GAA
                                TGTTAG ATTT   ACTAATTTT
                                |||||| ||||   |||||||||
                                ACAATC TAAG   TGATTAAAA
                                  _   ____
GAM604  AQP6     3'  CTGTTTCACACACTCTCC     15633     G__   G
                                CTG   CAT ACACTCTCC
                                |||   ||| |||||||||
                                GAC   GTG TGTGAGAGG
                                  AAA  _
GAM604  CASP2    3'  TACCGGCATCACTCTCC      15634      T    GA
                                TACC GGCAT  CACTCTCC
                                |||| |||||  ||||||||
                                ATGG CCGTA  GTGAGAGG
                                  _    __
GAM604  CASP2    3'  TACCGGCATCACTCTCC      15634      T    GA
                                TACC GGCAT  CACTCTCC
                                |||| |||||  ||||||||
                                ATGG CCGTA  GTGAGAGG
                                  _    __
GAM604  CASP2    3'  TACCGGCATCACTCTCC      15634      T    GA
                                TACC GGCAT  CACTCTCC
                                |||| |||||  ||||||||
                                ATGG CCGTA  GTGAGAGG
                                  _    __
GAM604  CBS      3'  CTACCTGGCCGACTTCTC     15635         A   AC
                                CTACCTGGC TGAC  TCTC
                                ||||||||| ||||  ||||
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                                GATGGACCG GCTG  AGAG
                                      _   A_
GAM604  CD244   3'  CACTTACATAACACTTTC   15636    CTG       C
                                TAC   GCATGACACT TC
                                |||   |||||||||| ||
                                GTG   TGTATTGTGA AG
                                  AA_        A
GAM604  CDC27   3'  CTTCCTTCATGATACTTTCC  15637   A  GG   C  C
                                CT CCT  CATGA ACT TCC
                                || |||  ||||| ||| |||
                                GA GGA  GTACT TGA AGG
                                 A  A_    A  A
GAM604  FGF1    3'  TAACCTGGCATGAAGCTTCT  15638   T       CA  _
                                C ACCTGGCATGA  CT CT
                                | ||||||||||  || ||
                                A TGGACCGTACT  GA GA
                                 T         TC  A
GAM604  FGF1    3'  TAACCTGGCATGAAGCTTCT  15638   T       CA  _
                                C ACCTGGCATGA  CT CT
                                | ||||||||||  || ||
                                A TGGACCGTACT  GA GA
                                 T         TC  A
GAM604  FGF1    3'  TAACCTGGCATGAAGCTTCT  15638   T       CA  _
                                C ACCTGGCATGA  CT CT
                                | ||||||||||  || ||
                                A TGGACCGTACT  GA GA
                                 T         TC  A
GAM604  GRAF    3'  CACCCGGCCATGGCATTCT   15639       _  A  C
                                TACCTGGC ATG CA TCT
                                |||||||| ||| || |||
                                GTGGGCCG TAC GT AGA
                                     G   C  A
GAM604  MGEA5   3'  CTACCTGACATGTCAAATCC  15640         A  CTC
                                CTACCTGGCATG CA   TCC
                                |||||||||||| ||   |||
                                GATGGACTGTAC GT   AGG
                                       A  TT_
GAM604  MT3     3'  CCACCTGGCACTATCTCC    15641         GACAC
                                CTACCTGGCAT    TCTCC
                                ||||||||||    |||||
                                GGTGGACCGTG    AGAGG
                                       AT___
GAM604  MTL5    3'  CCGCCCTGCAGACACTCTCC  15642   TA  G  T
                                C  CCT GCA GACACTCTCC
                                |  ||| ||| ||||||||||
                                G  GGG CGT CTGTGAGAGG
                                 GC   A  _
GAM604  POU3F2  3'  CTAGCTATCACACACTCTCC  15643    C  G  G
                                CTA CTG CAT ACACTCTCC
                                ||| ||| ||| |||||||||
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                                GAT GAT GTG TGTGAGAGG
                                  C   A   _
GAM604  SUV39H1  3'  CCTGGCATCCACCTCC      15644         GA   T
                                CCTGGCAT  CAC CTCC
                                ||||||||  ||| ||||
                                GGACCGTA  GTG GAGG
                                    G_  _
GAM604  SYNGR1   3'  CACCTGCCACACTCTCC     15645       G ATG
                                TACCTG C   ACACTCTCC
                                |||||| |   |||||||||
                                GTGGAC G   TGTGAGAGG
                                   G ___
GAM604  TLX1     3'  CTGTCTGGTTGACACTCTCC   15646    AC    CA
                                CT  CTGG  TGACACTCTCC
                                ||  ||||  ||||||||||
                                GA  GACC  ACTGTGAGAGG
                                 CA    A_
GAM604  ADIR     3'  CCACCTGGCCCACTTTC      15647         ATGA    C
                                CTACCTGGC    CACT TC
                                |||||||||    |||| ||
                                GGTGGACCG    GTGA AG
                                     G___    A
GAM604  BAG3     3'  CCTGGCACATTTTACTCTC    15648         AC__
                                CCTGGCATG    ACTCTC
                                |||||||||    ||||||
                                GGACCGTGT    TGAGAG
                                     AAAA
GAM604  CCR5     3'  CTACTGTTGCACTCTC       15649      C  GCA  A
                                CTAC TG   TG CACTCTC
                                ||||  ||   ||  |||||||
                                GATG AC   AC GTGAGAG
                                  _  A__  _
GAM604  DDX33    3'  CTGGCATAAGCCAATGTTCTC  15650          __  C___
                                CTGGCATGA  CA    TCTC
                                |||||||||  ||    ||||
                                GACCGTATT  GT    AGAG
                                     CG  TACA
GAM604  DICER1   3'  CTACCTGGCAGGAGGACT     15651          T  C_
                                CTACCTGGCA GA  ACT
                                |||||||||| ||  |||
                                GATGGACCGT CT  TGA
                                     C  CC
GAM604  DKFZP564O1863 3'  TAACCATGTTTGACACTCT    15652    T   _  GCA
                                C ACC TG   TGACACTCT
                                | ||| ||   |||||||||
                                A TGG AC   ACTGTGAGA
                                 T   T  AA_
GAM604  DNAJC5   3'  CACCTGGCTTGAAACATTTTCC 15653         A   C  TC__
                                TACCTGGC TGA AC    TCC
                                |||||||| ||| ||    |||
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                                GTGGACCG ACT TG    AGG
                                     A   T  TAAA
GAM604   FLJ10811  3'  TGACCTGGCACCTTCTCC    15654    T       GACAC
                                C ACCTGGCAT     TCTCC
                                | |||||||||     |||||
                                A TGGACCGTG     AGAGG
                                 C        GA___
GAM604   FLJ20127  5'  CTACTGGCATACCTCT      15655      C      A A
                                CTAC TGGCATG C CTCT
                                |||| ||||||| | ||||
                                GATG ACCGTAT G GAGA
                                  _      _ _
GAM604   FLJ20340  3'  CACCTGGCCTGCCTACACTCT  15656         ATG___
                                TACCTGGC     ACACTCT
                                ||||||||     |||||||
                                GTGGACCG     TGTGAGA
                                     GACGGA
GAM604   GLIO703   3'  TAACCTGGCATGAAGCTTCT   15638    T         CA  _
                                C ACCTGGCATGA  CT CT
                                | ||||||||||  || ||
                                A TGGACCGTACT  GA GA
                                 T          TC  A
GAM604   HSJ001348 3'  CACCTGATCCCCACTCTCC    15657        CATGA
                                TACCTGG     CACTCTCC
                                |||||||     ||||||||
                                GTGGACT     GTGAGAGG
                                     AGGG_
GAM604   HSPC039   3'  CTACTGGCATGTCCTCT      15658      C      ACA
                                CTAC TGGCATG   CTCT
                                |||| |||||||   ||||
                                GATG ACCGTAC   GAGA
                                  _      AG_
GAM604   KIAA0247  3'  CTACCTAACTATGCTTTCC    15659         _   ACA  C
                                CTACCTGGC ATG   CT TCC
                                ||||||||| |||   || |||
                                GATGGATTG TAC   GA AGG
                                     A   ___  A
GAM604   KIAA0329  3'  CCTGGCATGGCCAGCGCTCTCC 15660         A_  ___
                                CCTGGCATG  CA   CTCTCC
                                |||||||||  ||   ||||||
                                GGACCGTAC  GT   GAGAGG
                                     CG  CGC
GAM604   KIAA0461  3'  CCACCTGGTATGCCCCCT     15661         C   ACA
                                CTACCTGG ATG   CTCT
                                ||||||||| |||   ||||
                                GGTGGACC TAC   GGGA
                                     A   GG_
GAM604   KIAA0514  3'  CACCTGGCACATCTC        15662           ACAC
                                TACCTGGCATG    TCTC
                                ||||||||||    ||||
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                              GTGGACCGTGT   AGAG
                                        ____
GAM604  KIAA0676 3' TGACCTGGCAGACCTTGCACTC 15663   T      _____ A
            T                  C ACCTGGCA    TG CACTCT
                               | ||||||||    || ||||||
                               A TGGACCGT    AC GTGAGA
                                C       CTGGA  _
GAM604  KIAA0683 3' CCTGCATCTGCACTCTCC    15664     G   GA_
                               CCTG CAT   CACTCTCC
                               |||| |||   ||||||||
                               GGAC GTA   GTGAGAGG
                                  _   GAC
GAM604  KIAA0937 3' CTACATTGACTCACTCTCC   15665     C_   ATGA
                               CTAC  TGGC   CACTCTCC
                               ||||  ||||   ||||||||
                               GATG  ACTG   GTGAGAGG
                                  TA   A___
GAM604  KIAA1010 3' CTACATAGAAACACTCT     15666     C   CAT
                               CTAC TGG   GACACTCT
                               |||| |||   ||||||||
                               GATG ATC   TTGTGAGA
                                  T   T__
GAM604  KIAA1040 3' CTATGTGGCATGAACTCC    15667     CC       C
                               CTA  TGGCATGA ACTCT
                               |||  |||||||| |||||
                               GAT  ACCGTACT TGAGG
                                 AC       _
GAM604  KIAA1086 3' CCACCTGGCCCTGTGGCTCTCC 15668         A_  ACA
                               CTACCTGGC  TG   CTCTCC
                               |||||||||  ||   ||||||
                               GGTGGACCG  AC   GAGAGG
                                     GG  ACC
GAM604  KIAA1677 3' TACCTGGCCTGATGGCTCT   15669         A   CA_
                               TACCTGGC TGA   CTCT
                               |||||||| |||   ||||
                               ATGGACCG ACT   GAGA
                                    G   ACC
GAM604  KIAA1701 3' CACCTGGCATGGACATGATCC  15670          _   CTC
                               TACCTGGCATG ACA   TCC
                               |||||||||||| |||   |||
                               GTGGACCGTAC TGT   AGG
                                      C   ACT
GAM604  KIAA1719 3' CACCTGCCCTAGACACTCTC   15671       G AT__
                               TACCTG C    GACACTCTC
                               |||||| |    |||||||||
                               GTGGAC G    CTGTGAGAG
                                  _ GGAT
GAM604  KIAA1719 3' CTGCCTGAGACACTCT      15672     A    CAT
                               CT CCTGG   GACACTCT
                               || |||||   ||||||||
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                                GA GGACT   CTGTGAGA
                                 C    ___
GAM604  LIP8    5'  CCACCTGGTTCCGCCTACTCTC 15673        CA_  AC_
              C                   CTACCTGG   TG   ACTCTCC
                                  ||||||||   ||   |||||||
                                  GGTGGACC   GC   TGAGAGG
                                      AAG  GGA
GAM604  OPRL1   3'  CCACCTGGACACTTTC      15674        CATG    C
                                  CTACCTGG    ACACT TC
                                  ||||||||    ||||| ||
                                  GGTGGACC    TGTGA AG
                                      ____     A
GAM604  PCBP4   3'  CTACCTGGCAGTGCCCCCTC   15675         _  ACA
                                  CTACCTGGCA TG   CTCTC
                                  ||||||||||  ||   |||||
                                  GATGGACCGT AC   GGGAG
                                        C  GG_
GAM604  PCBP4   3'  CTACCTGGCAGTGCCCCCTC   15675         _  ACA
                                  CTACCTGGCA TG   CTCTC
                                  ||||||||||  ||   |||||
                                  GATGGACCGT AC   GGGAG
                                        C  GG_
GAM604  PCBP4   3'  CTACCTGGCAGTGCCCCCTC   15675         _  ACA
                                  CTACCTGGCA TG   CTCTC
                                  ||||||||||  ||   |||||
                                  GATGGACCGT AC   GGGAG
                                        C  GG_
GAM604  RAB3GAP  3'  CTATCTGCATGACAGTCTC   15676    C   G     C
                                  CTA CTG CATGACA TCTC
                                  ||| ||| ||||||| ||||
                                  GAT GAC GTACTGT AGAG
                                    A   _      C
GAM604  RAI16   3'  CACCTGGCATGCCCATTCC   15677          A_  C
                                  TACCTGGCATG  CA TCT
                                  ||||||||||  ||  |||
                                  GTGGACCGTAC  GT AGG
                                        GG  A
GAM604  Rpo1-2   3'  CCTCCATGCACTCTCC      15678     GG    A
                                  CCT  CATG CACTCTCC
                                  |||  |||| ||||||||
                                  GGA  GTAC GTGAGAGG
                                    G_   _
GAM604  THEA    3'  CACCTGGCCTAAAACTCT    15679        A   C
                                  TACCTGGC TGA ACTCT
                                  |||||||| ||| |||||
                                  GTGGACCG ATT TGAGA
                                      G   T
GAM604  TREX2   5'  ACTTGGCAGCACTCTCC     15680    C    TGA
                                  AC TGGCA   CACTCTCC
                                  || |||||   ||||||||
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                                TG ACCGT   GTGAGAGG
                                 A    C__
GAM604   TREX2    5'  ACTTGGCAGCACTCTCC     15680    C    TGA
                                AC TGGCA   CACTCTCC
                                || |||||   ||||||||
                                TG ACCGT   GTGAGAGG
                                 A    C__
GAM604   TTTY2    5'  CCTGGCACTTGACCTCTC    15681        __   A
                                CCTGGCA  TGAC CTCTC
                                |||||||  |||| |||||
                                GGACCGT  ACTG GAGAG
                                    GA   _
GAM604   WDR13    5'  CCTTGCTTGACATTCTCC    15682     G  A    C
                                CCT GC TGACA TCTCC
                                ||| || ||||| |||||
                                GGA CG ACTGT AGAGG
                                  A A    A
GAM604   LOC121548 5'  CCACCTGGTGTGACATTC    15683        CA    C
                                CTACCTGG  TGACA TC
                                ||||||||  ||||| ||
                                GGTGGACC  ACTGT AG
                                     AC    A
GAM604   LOC126167 5'  CACCGCCCCGACACTCTC    15684      TG  A_
                                TACC  GC  TGACACTCTC
                                ||||  ||  ||||||||||
                                GTGG  CG  GCTGTGAGAG
                                  __  GG
GAM604   LOC126167 3'  CCACCTGGCATCTGATTTCTC  15685          __   CAC
                                CTACCTGGCA  TGA   TCTC
                                ||||||||||  |||   ||||
                                GGTGGACCGT  ACT   AGAG
                                      AG   AA_
GAM604   LOC131827 3'  CTACCTGGGCAGTGATGGCTTT 15686        _ _   CA_  C
            C                    CTACCTGG CA TGA   CT TC
                                ||||||| || |||   || ||
                                GATGGACC GT ACT   GA AG
                                     C  C   ACC  A
GAM604   LOC144289 5'  CTGGCCCAGGACACTCTCC    15687      AT__
                                CTGGC    GACACTCTCC
                                |||||    ||||||||||
                                GACCG    CTGTGAGAGG
                                   GGTC
GAM604   LOC146667 5'  CTACCCTGACTCACACTCTC   15688      _   ATG
                                CTACC TGGC   ACACTCTC
                                ||||| ||||   ||||||||
                                GATGG ACTG   TGTGAGAG
                                   G    AG_
GAM604   LOC148029 5'  CCTGGCATGCATCTCC      15689         A  C
                                CCTGGCATG CA TCTCC
                                ||||||||| || |||||
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                                GGACCGTAC GT AGAGG
                                      _ _
GAM604   LOC148147 5'  CTAGCTGTATTCACTCTCC   15690      A  A___
                                CTGGC TG    CACTCTCC
                                |||||| ||    ||||||||
                                GATCG AC    GTGAGAGG
                                  _  ATAA
GAM604   LOC149149 3'  CTACCTGGACAGAGTCT     15691        _  T  CAC
                                CTACCTGG CA GA   TCT
                                |||||||| || ||   |||
                                GATGGACC GT CT   AGA
                                     T  _  C__
GAM604   LOC149711 3'  CTACCTGGCACCTCC       15692          GACA
                                CTACCTGGCAT    CTCT
                                ||||||||||    ||||
                                GATGGACCGTG    GAGG
                                      ____
GAM604   LOC151657 5'  CCACCTGACATGCTTTCT    15693           ACAC
                                CTACCTGGCATG    TCT
                                ||||||||||    |||
                                GGTGGACTGTAC    AGA
                                      GAA_
GAM604   LOC157381 3'  CCTGGCATGTGACCTCC     15694         AC  T
                                CCTGGCATG  AC CTCC
                                |||||||||  || ||||
                                GGACCGTAC  TG GAGG
                                     AC  _
GAM604   LOC158373 5'  CCTGCGGGAGCACTCTCC    15695      G AT  _
                                CCTG C  GA CACTCTCC
                                |||| |  || ||||||||
                                GGAC G  CT GTGAGAGG
                                  _ CC  C
GAM604   LOC159148 5'  CCTGGCACTTGACCTCTC    15681        __   A
                                CCTGGCA  TGAC CTCTC
                                |||||||  |||| |||||
                                GGACCGT  ACTG GAGAG
                                     GA   _
GAM604   LOC200609 3'  CTACCTGGGATCACATCTC   15696         C  G   C
                                CTACCTGG AT ACA TCTC
                                |||||||| || ||| ||||
                                GATGGACC TA TGT AGAG
                                     C  G  _
GAM604   LOC206855 5'  TACCTGGAACACTCT       15697        CAT
                                TACCTGG   GACACTCT
                                |||||||   ||||||||
                                ATGGACC   TTGTGAGA
                                      ___
GAM604   LOC220776 3'  TAACCTGGCATGGGCTCC    15698    T        ACACT
                                C ACCTGGCATG    CTCC
                                | ||||||||||    ||||
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                                A TGGACCGTAC     GAGG
                                 T         CC___
GAM604  LOC222008 5'  CTACCTGGCAGCTCGTCC     15699          TGACA  _
                                CTACCTGGCA     CTC TCC
                                ||||||||||     ||| |||
                                GATGGACCGT     GAG AGG
                                      C____   C
GAM604  LOC256158 5'  CTAACCTGCACATTCTCC     15700       A  _  C
                                CTGGC TG ACA TCTCC
                                ||||| || ||| |||||
                                GATTG AC TGT AGAGG
                                   G  G   A
GAM605  CLCN4     3'  TCAACAAAGTAAGCGCAAA    15703          CA__
                                TCAACGAAG    TGTAAA
                                |||||||||    ||||||
                                AGTTGTTTC    GCGTTT
                                      ATTC
GAM605  DUSP6     5'  TCTCTCAATGAAGCTGC      15704         C     A
                                TCTCTCAA GAAGC TGT
                                |||||||| ||||| |||
                                AGAGAGTT CTTCG ACG
                                     A    _
GAM605  LIMD1     3'  TCTCAACAATATAAAAT      15705          AGCA
                                TCTCAACGA    TGTAAAAT
                                |||||||||    ||||||||
                                AGAGTTGTT    ATATTTTA
                                             _____
GAM605  VCP       3'  CTCAAAAGCATGTAAAAT     15706       AC
                                CTCA  GAAGCATGTAAAAT
                                ||||  ||||||||||||||
                                GAGT  TTTCGTACATTTTA
                                   __
GAM605  FLJ21168  3'  ACAATGCTATGTAAAATA     15707       A  _
                                ACGA GC ATGTAAAATA
                                |||| || ||||||||||
                                TGTT CG TACATTTTAT
                                  A  A
GAM605  HSPC129   3'  TCTTAACAAGCATACAAAATA  15708      C   G
                                TCT AAC AAGCATGTAAAATA
                                ||| ||| ||||||||||||||
                                AGA TTG TTCGTATGTTTTAT
                                  A  _
GAM605  KIAA0712  5'  TCTCTCAATGAATGCTGT     15709         C  _  A
                                TCTCTCAA GAA GC TGT
                                |||||||| ||| || |||
                                AGAGAGTT CTT CG ACA
                                     A   A  _
GAM605  KIAA1554  3'  TCTCTCAATGAACAGTA      15710         C   G  T
                                TCTCTCAA GAA CA GTA
                                |||||||| ||| || |||
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                                AGAGAGTT CTT GT CAT
                                    A  _ _
GAM605  MOV34-34KD 3'  TCTCTCAAGGAAGTGTA     15711        C    CA
                                TCTCTCAA GAAG  TGTA
                                |||||||| ||||  ||||
                                AGAGAGTT CTTC  ACAT
                                    C   __
GAM605  PRO2949   3'  TCTCTCATATGTAAAAT     15712        ACGAAGC
                                TCTCTCA      ATGTAAAAT
                                |||||||      |||||||||
                                AGAGAGT      TACATTTTA
                                    A_______
GAM605  Rpo1-2    3'  TCTCTCAACACCTTAAAAT    15713         GAA  ATG
                                TCTCTCAAC   GC   TAAAAT
                                |||||||||   ||   ||||||
                                AGAGAGTTG   TG   ATTTTA
                                     ___  GA_
GAM605  UBE2D1    3'  TCTCAATGCATACAAAAT     15714       CGAA
                                TCTCAA    GCATGTAAAAT
                                ||||||    ||||||||||||
                                AGAGTT    CGTATGTTTTA
                                    A___
GAM605  LOC219529 3'  CTCTTTCACATGTAAAAT     15715      CAACGAA
                                CTCT      GCATGTAAAAT
                                ||||      ||||||||||||
                                GAGA      TGTACATTTTA
                                  AAG_____
GAM605  LOC256940 3'  TCTCAAGACCATATAAAATA   15716       C  AG
                                TCTCAA GA  CATGTAAAATA
                                |||||| ||  ||||||||||||
                                AGAGTT CT  GTATATTTTAT
                                    _  G_
GAM606  HS2ST1    3'  TTTAGTTTTTCTTTAGTT     15719         _
                                TTTAGTTTT CTTTAGTT
                                |||||||| ||||||||
                                AAATCAAAA GAAATCAA
                                     A
GAM606  KLRC4     3'  TTTAGTTTTCTTTATATTTATT 15720            _  C
          T                      TTTAGTTTTCTTTA GTT ATTT
                                 |||||||||||||| ||| ||||
                                 AAATCAAAAGAAAT TAA TAAA
                                       A   A
GAM606  MIR16     3'  TTTAGTTTCCTCATTT       15721          TTTAGT
                                TTTAGTTTTC     TCATTT
                                ||||||||||     ||||||
                                AAATCAAAGG     AGTAAA
                                       _______
GAM606  C20orf45  3'  TTTAGTTCTCTTAAATTCATTT 15722            T
          GC                     TTTAGTTTTCTT AGTTCATTTGC
                                 |||||||||||| ||||||||||
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                                AAATCAAGAGAA TTAAGTAAACG
                                       T
GAM606  INVS     3'  TTTAGTTTTCCTTAGATTTTGC 15723             TTCA
                                TTTAGTTTTCTTTAG    TTTGC
                                ||||||||||||||    |||||
                                AAATCAAAAGGAATC    AAACG
                                      TA__
GAM606  TRIM4    3'  TTCAGTTTTCTCATTT      15724          TTTAGT
                                TTTAGTTTTC     TCATTT
                                ||||||||||     ||||||
                                AAGTCAAAAG     AGTAAA
                                      _______
GAM606  LOC221981 3'  AGTTTTCTTTTCATTTGC     15725          AGT
                                AGTTTTCTTT   TCATTTGC
                                ||||||||||   ||||||||
                                TCAAAAGAAA   AGTAAACG
                                      ___
GAM607  CARPX    3'  TGTGTGTGTGTGTAGGTATGTT 15728       C       TAG
           T                     TGTGTG GTGTGTGG   ATGTTT
                                ||||||| ||||||||   |||||||
                                ACACAC CACACATC   TACAAA
                                   A       CA_
GAM607  EFNB1    3'  TGTGTGTGTGTGTGGAAG    15729       C       T
                                TGTGTG GTGTGTGG AG
                                ||||||| |||||||| ||
                                ACACAC CACACACC TC
                                   A       T
GAM607  HS3ST4   3'  TGTGTGTGTGTGTGGGTGGGTG 15730       C       TAGA_
           T                     TGTGTG GTGTGTGG    TGT
                                ||||||| ||||||||    |||
                                ACACAC CACACACC    ACA
                                   A       CACCC
GAM607  NLGN3    3'  TGTGTGTGTGTGTGTGCA    15731       C      _
                                TGTGTG GTGTGTG GTA
                                ||||||| ||||||| |||
                                ACACAC CACACAC CGT
                                   A      A
GAM607  OXTR     3'  TGTGTGTGTGTGTGTGTGAGTT 15732       C      _ A  T
                                TGTGTG GTGTGTG GT GA GTT
                                ||||||| ||||||| || || |||
                                ACACAC CACACAC CA CT CAA
                                   A      A  _ _
GAM607  PACSIN3  3'  TGTGTGGGTGTGTGTCAAGTTT 15733       C      GTA  T
                                TGTGTG GTGTGTG   GA GTTT
                                ||||||| |||||||   || ||||
                                ACACAC CACACAC   TT CAAA
                                   C      AG_  _
GAM607  PCDH11X  3'  TGTGTGTGTGTGTGTGTAGAT    15734       C      G
                                TGTGTG GTGTGTG TAGAT
                                ||||||| ||||||| |||||
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                                ACACAC CACACAC ATCTA
                                   A      _
GAM607  PCDH11X  3'  TGTGTGTGTGTGTGTAGAT   15734       C      G
                                TGTGTG GTGTGTG TAGAT
                                |||||| ||||||| |||||
                                ACACAC CACACAC ATCTA
                                   A      _
GAM607  PLAG1    3'  TGTGTGTGTGTGTGTGTA    15735       C      _
                                TGTGTG GTGTGTG GTA
                                |||||| ||||||| |||
                                ACACAC CACACAC CAT
                                   A      A
GAM607  SHANK2   3'  TGTGTGGTGTGTGTTTTGTTT  15736       C      GTAGA
                                TGTGTG GTGTGTG    TGTTT
                                |||||| |||||||     |||||
                                ACACAC CACACAC    ACAAA
                                   _      AAA__
GAM607  SLC25A6  3'  TGTGTGTGTGTGTGGAG     15737       C       T
                                TGTGTG GTGTGTGG AG
                                |||||| |||||||| ||
                                ACACAC CACACACC TC
                                   A      _
GAM607  SRGAP2   3'  TGTGTGTGTGTGTGTAAA    15738       C      G
                                TGTGTG GTGTGTG TAGA
                                |||||| ||||||| ||||
                                ACACAC CACACAC ATTT
                                   A      _
GAM607  C1GALT1  3'  TGTGTGTGGGTGTGGTAG    15739       CGT
                                TGTGTG   GTGTGGTAG
                                ||||||   |||||||||
                                ACACAC   CACACCATC
                                   ACC
GAM607  C5orf5   3'  TGTGTGATGTGTGGTGTGTGTT 15740       C       AGA
           T                    TGTGTG GTGTGTGGT   TGTTT
                                |||||| |||||||||   |||||
                                ACACAC TACACACCA   ACAAA
                                   _       CAC
GAM607  CAMTA1   3'  TGTGTGCGTGTGTGCGTGTGTG 15741           _ AGA
           TT                    TGTGTGCGTGTGTG GT   TGTT
                                |||||||||||||| ||   ||||
                                ACACACGCACACAC CA   ACAA
                                      G  CAC
GAM607  CLIC6    3'  TGTGTGTGTGTGTGATAGA   15742       C
                                TGTGTG GTGTGTGGTAGA
                                |||||| ||||||||||||
                                ACACAC CACACACTATCT
                                   A
GAM607  COVA1    3'  TGTGTGCGTGCGTGTGTGTGTT 15743           _ AGA
           T                    TGTGTGCGTGTGTG GT   TGTTT
                                |||||||||||||| ||   |||||
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                                ACACACGCACGCAC CA   ACAAA
                                       A  C__
GAM607  CRMP5    3' TGTGTGTGTGTGGTGGCAG    15744       C    _
                                TGTGTG GTGTG TGGTAG
                                |||||| ||||| ||||||
                                ACACAC CACAC ACCGTC
                                   A    C
GAM607  FLJ10597 3' TGTGTGTGTGTGTACGCATGTT 15745       C      _ AG
           T                     TGTGTG GTGTGTG GT  ATGTTT
                                |||||| ||||||| ||  ||||||
                                ACACAC CACACAT CG  TACAAA
                                   A      G __
GAM607  FLJ13352 3' TGTGTGTGTGTGTGAAGCTGTT 15746       C       T  A
           T                     TGTGTG GTGTGTGG AG TGTTT
                                |||||| |||||||| || |||||
                                ACACAC CACACACT TC ACAAA
                                   A       _ G
GAM607  FLJ20043 3' TATGTGCGTGTGTGTGTGTGTG 15747            _ AGA
           TTT                     TGTGTGCGTGTGTG GT   TGTTT
                                |||||||||||||| ||   |||||
                                ATACACGCACACAC CA   ACAAA
                                       A  CAC
GAM607  FLJ22601 3' TGTGTGTGTGTGTGTTGGA   15748       C      GTA
                                TGTGTG GTGTGTG   GA
                                |||||| |||||||   ||
                                ACACAC CACACAC   CT
                                   A      AAC
GAM607  GRID1    3' TGTGTGCGAGTGTGTGTGGT   15749       ____
                                TGTGTGC    GTGTGTGGT
                                |||||||    |||||||||
                                ACACACG    CACACACCA
                                    CTCA
GAM607  KIAA0544 3' TGTGTGTGTGTGTGTGTA    15735       C      _
                                TGTGTG GTGTGTG GTA
                                |||||| ||||||| |||
                                ACACAC CACACAC CAT
                                   A      A
GAM607  KIAA1828 5' TGTGTGTGTGTGTGGGTGC   15750       C       TAGA
                                TGTGTG GTGTGTGG    TGT
                                |||||| ||||||||    |||
                                ACACAC CACACACC    ACG
                                   A       C___
GAM607  KIAA1854 3' TGTGTGTGTGTGTGTGAG    15751       C      GT
                                TGTGTG GTGTGTG  AG
                                |||||| |||||||  ||
                                ACACAC CACACAC  TC
                                   A      AC
GAM607  MAP3K2   3' TGTGTGTGTGTGTGTGTGTGTG 15752       C      _ AGA
           TTT                     TGTGTG GTGTGTG GT   TGTTT
                                |||||| ||||||| ||   |||||
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                                ACACAC CACACAC CA   ACAAA
                                   A      A  CAC
GAM607  MEGF11    3'  GTGTGTGTGTGTCTCTGTGTGT 15753      C     GGTAGA_
           TT                    GTGTG GTGTGT      TGTTT
                                 ||||| ||||||      |||||
                                 CACAC CACACA      ACAAA
                                    A     GAGACAC
GAM607  RAB9B     3'  TGTGTGCGTGTGTGTGCA    15754           _
                                 TGTGTGCGTGTGTG GTA
                                 |||||||||||||| |||
                                 ACACACGCACACAC CGT
                                       A
GAM607  SP192     3'  TGTGTGTGTGTGTGAGTGTGTT 15755       C      _ AGA
           T                     TGTGTG GTGTGTG GT   TGTTT
                                 |||||| ||||||| ||   |||||
                                 ACACAC CACACAC CA   ACAAA
                                    A      T  C__
GAM607  TRIP-Br2  3'  TGTGTGCATGTGTGTGCCTGTG 15756           _ AGA
           TTT                     TGTGTGCGTGTGTG GT   TGTTT
                                 |||||||||||||| ||   |||||
                                 ACACACGTACACAC CG   ACAAA
                                       A  GAC
GAM607  UBE4B     3'  TGTGTGCGCGTGTGGCTGTGTT 15757             AGA
           T                     TGTGTGCGTGTGTGGT   TGTTT
                                 ||||||||||||||   |||||
                                 ACACACGCGCACACCG   ACAAA
                                       AC_
GAM607  LOC132235 5'  TGTGTGTGTGTGTGTTAG     15758       C      G
                                 TGTGTG GTGTGTG TAG
                                 |||||| ||||||| |||
                                 ACACAC CACACAC ATC
                                    A      A
GAM607  LOC145135 5'  TGTGTGTGTGTGTGTGCAA    15759       C      _
                                 TGTGTG GTGTGTG GTAG
                                 |||||| ||||||| ||||
                                 ACACAC CACACAC CGTT
                                    A      A
GAM607  LOC149332 3'  TGTGTCCGTGTGTACCCAATGT 15760       G       GTA
           TT                     TGTGT CGTGTGTG   GATGTTT
                                 ||||| ||||||||   |||||||
                                 ACACA GCACACAT   TTACAAA
                                    G       GGG
GAM607  LOC150112 3'  TGTGTGTGTGTGTGTGCA     15731       C      _
                                 TGTGTG GTGTGTG GTA
                                 |||||| ||||||| |||
                                 ACACAC CACACAC CGT
                                    A      A
GAM607  LOC153218 5'  TGTGTGTGTGTGTGCCAAAT   15761       C      G
                                 TGTGTG GTGTGTG TAGAT
                                 |||||| ||||||| |||||
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                                ACACAC CACACAC GTTTA
                                   A      G
GAM607  LOC154215 3'  TGTGTGTGTGTGTGTCAGTGTT 15762       C      G   A
                                TGTGTG GTGTGTG TAG TGTT
                                |||||| ||||||| ||| ||||
                                ACACAC CACACAC GTC ACAA
                                   A      A  _
GAM607  LOC222008 3'  TGTGTGTGTGTGTGTGTA    15735       C      _
                                TGTGTG GTGTGTG GTA
                                |||||| ||||||| |||
                                ACACAC CACACAC CAT
                                   A      A
GAM607  LOC256112 3'  GTGTGTTCTTAGATGTTT    15763       GG_
                                GTGTGT   TAGATGTTT
                                ||||||   |||||||||
                                CACACA   ATCTACAAA
                                   AGA
GAM607  LOC92360  5'  TGTGTGTGTAATGTGTGT    15764       C  _   _
                                TGTGTG GTG TGTG GT
                                |||||| ||| |||| ||
                                ACACAC CAT ACAC CA
                                   A  T   A
GAM607  LOC92360  5'  TGTGTGTGTGTAATGTTGTGTT 15765      C       AGA_
          T                      TGTG GTGTGTGGT    TGTTT
                                |||| |||||||||    |||||
                                ACAC CACACATTA    ACAAA
                                  A        CAAC
GAM607  LOC92360  5'  TGTGTGTGTAATGTGTGT    15764       C  _   _
                                TGTGTG GTG TGTG GT
                                |||||| ||| |||| ||
                                ACACAC CAT ACAC CA
                                   A  T   A
GAM608  PDE7A     3'  TCATAATACAGCTAGGACA    15768        AA_   A
                                TCATAATA   CTAG GATG
                                ||||||||   |||| ||||
                                AGTATTAT   GATC CTGT
                                     GTC   _
GAM608  PRKRA     3'  TCAAAGTAAATTAGAGATATGT 15769     TAA   C      C
          AA                     TCA   TAAA TAGAGATG GTAA
                                |||   |||| |||||||| ||||
                                AGT   ATTT ATCTCTAT CATT
                                  TTC   A       A
GAM608  RECK      3'  TCATAATAAAATAGAAATA    15770          C
                                TCATAATAAA TAGAGATG
                                |||||||||| ||||||||
                                AGTATTATTT ATCTTTAT
                                       T
GAM608  B3GNT7    3'  TCATAATAGATCAAGTAAGCGT 15771        AACTA   AT_
                                TCATAATA    GAG   GCGT
                                ||||||||    |||   ||||
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                                AGTATTAT    TTC   CGCA
                                     CTAG_   ATT
GAM608  DCLRE1A  5' CATAATCAAAGAGATGTGTAA 15772       AAACT     C
                                CATAAT    AGAGATG GTAA
                                ||||||    ||||||| ||||
                                GTATTA    TCTCTAC CATT
                                   GTT__      A
GAM608  FLJ21916 3' TCATAATAAACATGCA      15773          TAGAG
                                TCATAATAAAC    ATGCG
                                ||||||||||    |||||
                                AGTATTATTTG    TACGT
                                      _____
GAM608  KIAA0630 3' TCATAATAGACAGAGAT     15774        A  T
                                TCATAATA AC AGAGAT
                                |||||||| || ||||||
                                AGTATTAT TG TCTCTA
                                     C  _
GAM608  SNRK     3' TCACAATGAACTAGAGCTGTA  15775       A       ATGC
                                TCATAAT AACTAGAG   GTA
                                ||||||| ||||||||   |||
                                AGTGTTA TTGATCTC   CAT
                                    C       GA__
GAM608  LOC90750 3' TCATATTAAACTAGGATG    15776      A       A
                                TCATA TAAACTAG GATG
                                ||||| |||||||| ||||
                                AGTAT ATTTGATC CTAC
                                   A      _
GAM608  LOC90906 3' TCATAATAGATCAAGTAAGCGT 15771        AACTA   AT_
                                TCATAATA    GAG   GCGT
                                ||||||||    |||   ||||
                                AGTATTAT    TTC   CGCA
                                     CTAG_   ATT
GAM609  SIGLEC6  3' TATGTTATTATAGTTTCT    15779     __
                                TATG  ATTATAGTTTCT
                                ||||  ||||||||||||
                                ATAC  TAATATCAAAGA
                                   AA
GAM609  KIAA0472 3' TATATGCATACACATTCTATTT 15780       AT    GT
           TT                    TATATG  TATA  TTCTATTTTT
                                ||||||  ||||  ||||||||||
                                ATATAC  ATGT  AAGATAAAAA
                                   GT    GT
GAM609  PTD012   3' TGAGATAATTTCTATTTTT   15781     TT
                                TGA  ATAGTTTCTATTTTT
                                |||  |||||||||||||||
                                ACT  TATTAAAGATAAAAA
                                  C_
GAM609  LOC154739 3'  TATAGTGATTATAGTTTATAAT 15782      _         C  T
           TTT                    TATA TGATTATAGTTT TA TTTT
                                |||| |||||||||||| || ||||
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                                ATAT ACTAATATCAAA AT AAAA
                                  C          T  T
GAM609  LOC203276 3'  TATAGTGATTATAGTTTATAAT 15782     _         C  T
           TTT                    TATA TGATTATAGTTT TA TTTT
                                  |||| ||||||||||| || ||||
                                ATAT ACTAATATCAAA AT AAAA
                                  C          T  T
GAM609  LOC203305 3'  TATAGTGATTATAGTTTATAAT 15782     _         C  T
           TTT                    TATA TGATTATAGTTT TA TTTT
                                  |||| ||||||||||| || ||||
                                ATAT ACTAATATCAAA AT AAAA
                                  C          T  T
GAM609  LOC221300 3'  CATATGATCATTCTATTTTT   15783          AGTT
                                TATATGATTAT    TCTATTTTT
                                ||||||||||    |||||||||
                                GTATACTAGTA    AGATAAAAA
                                      ____
GAM609  LOC254243 3'  TATAGTGATTATAGTTTATAAT 15782     _         C  T
           TTT                    TATA TGATTATAGTTT TA TTTT
                                  |||| ||||||||||| || ||||
                                ATAT ACTAATATCAAA AT AAAA
                                  C          T  T
GAM609  LOC90038  3'  TATAGTGATTATAGTTTATAAT 15782     _         C  T
           TTT                    TATA TGATTATAGTTT TA TTTT
                                  |||| ||||||||||| || ||||
                                ATAT ACTAATATCAAA AT AAAA
                                  C          T  T
GAM610  BTEB1    3'  TTTAAAATCTACCCAGTCT    15786          GT
                                TTTAAAATCTGCC  GTCT
                                ||||||||||||  ||||
                                AAATTTTAGATGG  CAGA
                                       GT
GAM610  DBY      3'  TCTAAAATCTGTTGTGTGCAAA 15787          CC__    C__
           TAGT                    TTTAAAATCTG    GTGT   TAGT
                                ||||||||||    ||||   ||||
                                AGATTTTAGAC    CACG   ATCA
                                      AACA    TTT
GAM610  KIF2     3'  TTTAAAACTGCTCAGTCT     15788        T   _ T
                                TTTAAAA CTGC CG GTCT
                                ||||||| |||| || ||||
                                AAATTTT GACG GT CAGA
                                   _    A  _
GAM610  CDC42BPB  3'  TTTAAAACTGCCGTCTTCT    15789        T     G_
                                TTTAAAA CTGCCGT  TCT
                                ||||||| |||||||  |||
                                AAATTTT GACGGCA  AGA
                                   _     GA
GAM610  DKFZP547N043 3'  CTTAAAATCTGCTGCCACTGT  15790          CG    TA_
                                TTTAAAATCTGC  TGTC   GT
                                ||||||||||||  ||||   ||
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                                GAATTTTAGACG  ACGG   CA
                                      __    TGA
GAM610  FLJ10803  3'  TTTAAAATCTGTTGTTTAGT   15791          CCG   C
                                TTTAAAATCTG   TGT TAGT
                                ||||||||||   ||| ||||
                                AAATTTTAGAC   ACA ATCA
                                      A__   A
GAM610  LOC221663 5'  TTTAAAATGTAAATTCTAGTCT 15792        CTGCCGTG
                                TTTAAAAT       TCTAGTCT
                                ||||||||       ||||||||
                                AAATTTTA       AGATCAGA
                                     CATTTA__
GAM610  LOC84549  3'  TTTAAGTTCTGTTCTAGTC    15793      AA    CCGTG
                                TTTAA  TCTG    TCTAGTC
                                |||||  ||||    |||||||
                                AAATT  AGAC    AGATCAG
                                   CA    A____
GAM611  KIAA1040  3'  TCTGAAAAACTGTAATCCACA  15796     A         A_
                                TCT AAAAATTGTAA  TACG
                                |||  ||||||||||  ||||
                                AGA TTTTTGACATT  GTGT
                                  C          AG
GAM612  AP3B1     3'  TACATGATAGATACAC      15799        ACA
                                TACATGA   TGGATACAC
                                |||||||   |||||||||
                                ATGTACT   ATCTATGTG
                                      ___
GAM612  CASP8AP2  3'  TACAGAAACACACATACA    15800      T      G
                                TACA GAACATG ATACA
                                ||||  ||||||| |||||
                                ATGT TTTGTGT TATGT
                                  C      G
GAM612  CERD4     3'  CACATGGACAGATACAC     15801       A   TG
                                TACATG ACA  GATACAC
                                ||||||  |||  |||||||
                                GTGTAC TGT  CTATGTG
                                   C   __
GAM612  DPYSL2    3'  TACATGGACCAGGATGACAC   15802       A  AT   _
                                TACATG AC  GGAT ACAC
                                ||||||  ||  ||||  ||||
                                ATGTAC TG  CCTA TGTG
                                   C  GT    C
GAM612  ESR1      3'  ACATGAATAGAAACAC      15803       AC     T
                                ACATGA  ATGGA ACAC
                                ||||||  |||||  ||||
                                TGTACT  TATCT TGTG
                                   __     T
GAM612  HCS       3'  ACATGAACACAAAACAC     15804          TG  T
                                ACATGAACA  GA ACAC
                                |||||||||  ||  ||||
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                                TGTACTTGT  TT TGTG
                                     GT  _
GAM612  HIVEP1   3'  TACATAAATATGGAGTTTACA  15805        C    ___
                                TACATGAA ATGGA   TACA
                                |||||||| |||||   ||||
                                ATGTATTT TACCT   ATGT
                                     A    CAA
GAM612  HNRPA1   3'  CACATGATAATGGATACAC   15806       AC
                                TACATGA  ATGGATACAC
                                |||||||  ||||||||||
                                GTGTACT  TACCTATGTG
                                     AT
GAM612  IRS2     3'  TACATAAACATCTACA      15807          GGA
                                TACATGAACAT   TACA
                                ||||||||||   ||||
                                ATGTATTTGTA   ATGT
                                      G__
GAM612  KCNS3    3'  ACATGAGCATGGATTTACA   15808       A    __
                                ACATGA CATGGA  TACA
                                |||||| ||||||  ||||
                                TGTACT GTACCT  ATGT
                                    C     AA
GAM612  KNSL2    3'  TACATAGACATAGGGACAC   15809       A   __
                                TACATG ACAT  GGATAC
                                |||||| ||||  ||||||
                                ATGTAT TGTA  CCTGTG
                                    C   TC
GAM612  LANCL1   3'  TACAGAACATAGAAATACA   15810     T      __
                                TACA GAACATGGA  TACA
                                |||| |||||||||  ||||
                                ATGT CTTGTATCT  ATGT
                                  _       TT
GAM612  LRAT     3'  TACATACAGAATACAC      15811      GA   T
                                TACAT  ACA GGATACAC
                                |||||  ||| ||||||||
                                ATGTA  TGT CTTATGTG
                                   __  _
GAM612  NAP1L3   3'  TACAAGAACATGAAAAAC    15812     T      T_
                                TACA GAACATGGA  AC
                                |||| |||||||||  ||
                                ATGT CTTGTACTT  TG
                                  T       TT
GAM612  NDUFS4   3'  TACATGGACTATAAATAC    15813      A  _
                                TACATG AC ATGGATAC
                                |||||| || ||||||||
                                ATGTAC TG TATTTATG
                                    C  A
GAM612  NEURL    3'  CACATGGACTACAGACAC    15814      A  _
                                TACATG AC ATGGATAC
                                |||||| || ||||||||
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                                GTGTAC TG TGTCTGTG
                                   C  A
GAM612  NF1     3'  TACATATACCAGATACAC    15815       A  A
                                TACATG AC TGGATACAC
                                |||||| || |||||||||
                                ATGTAT TG GTCTATGTG
                                   A  _
GAM612  POLH    3'  TACATAATTTGAATACA     15816        ACA
                                TACATGA   TGGATACA
                                |||||||   ||||||||
                                ATGTATT   ACTTATGT
                                   AA_
GAM612  PPIL1   3'  TACATAAACAACTGAACA    15817          __
                                TACATGAACA  TGGATA
                                ||||||||||  ||||||
                                ATGTATTTGT  ACTTGT
                                      TG
GAM612  PRKRA   3'  TACATGAATTCAAATACAC   15818         CA GG
                                TACATGAA  T  ATACAC
                                ||||||||  |  ||||||
                                ATGTACTT  G  TATGTG
                                   AA TT
GAM612  PTMA    3'  TAATGAACATGGTCACAC    15819   C        A
                                A ATGAACATGG TACAC
                                | ||||||||||| |||||
                                A TACTTGTACC GTGTG
                                 T        A
GAM612  RANBP2  3'  TACATAAACACAAGTACAC   15820          TG A
                                TACATGAACA  G TACAC
                                ||||||||||  | |||||
                                ATGTATTTGT  T ATGTG
                                      GT C
GAM612  REGL    3'  TACATAATAGATACA       15821        ACA
                                TACATGA   TGGATACA
                                |||||||   ||||||||
                                ATGTATT   ATCTATGT
                                   ___
GAM612  SLC4A4  3'  CATGAGCATAAAATACAC    15822       A     _
                                CATGA CATGGA TACAC
                                ||||| |||||| |||||
                                GTACT GTATTT ATGTG
                                   C     T
GAM612  SON     3'  TACAGATACAGAGATACA    15823      T _   T
                                TACA GA ACA GGATACA
                                |||| || ||| |||||||
                                ATGT CT TGT TCTATGT
                                  _ A   C
GAM612  STAU2   3'  TACATGATCATTCTACAC    15824        A   GGA
                                TACATGA CAT   TACAC
                                ||||||| |||   |||||
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                                ATGTACT GTA   ATGTG
                                    A   AG_
GAM612  TMEM1    3'  TACATAAACATTACA      15825         GGA
                                TACATGAACAT   TACA
                                ||||||||||   ||||
                                ATGTATTTGTA   ATGT
                                      ___
GAM612  YWHAZ    3'  TACATGAATTTAATACAC    15826        CATG
                                TACATGAA    GATACAC
                                ||||||||    |||||||
                                ATGTACTT    TTATGTG
                                    AAA_
GAM612  YWHAZ    3'  TACATGAAGTAATGAATAC   15827        C__
                                TACATGAA   ATGGATAC
                                ||||||||   ||||||||
                                ATGTACTT   TACTTATG
                                    CAT
GAM612  BZW2     3'  TACATGAGCAGATACAC     15828        A  TG
                                TACATGA CA  GATACAC
                                ||||||| ||  |||||||
                                ATGTACT GT  CTATGTG
                                    C  __
GAM612  C21orf7  3'  TACATGAATAGAAATGGACA  15829        C____
                                TACATGAA    ATGGATA
                                ||||||||    |||||||
                                ATGTACTT    TACCTGT
                                    ATCTT
GAM612  cerk     3'  TACGTGGGCACGGATACAC   15830     A  AA
                                TAC TG  CATGGATACAC
                                ||| ||  ||||||||||
                                ATG AC  GTGCCTATGTG
                                  C  CC
GAM612  COPB     3'  TACATGAAACATTATATAC   15831        _  GG_
                                TACATGAA CAT   ATAC
                                |||||||| |||   ||||
                                ATGTACTT GTA   TATG
                                    T   ATA
GAM612  DKFZp434G171 3'  ACATGACTGCATGGATACAC  15832       A__
                                ACATGA   CATGGATACAC
                                ||||||   ||||||||||
                                TGTACT   GTACCTATGTG
                                   GAC
GAM612  FLJ14735 3'  TACAGAACATCTTGGATA    15833     T    ___
                                TACA GAACA   TGGATA
                                |||| |||||   ||||||
                                ATGT CTTGT   ACCTAT
                                  _    AGA
GAM612  FLJ14803 3'  TACATAAACTTAATACA     15834         ATG
                                TACATGAAC   GATACA
                                |||||||||   ||||||
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                                ATGTATTTG  TTATGT
                                     AA_
GAM612  FLJ20666 3' TACATGAATATTCTAAATAC  15835       CA___
                                TACATGAA   TGGATAC
                                ||||||||   |||||||
                                ATGTACTT   ATTTATG
                                    ATAAG
GAM612  FLJ20666 3' TACATGAATATTCTAAATAC  15835       CA___
                                TACATGAA   TGGATAC
                                ||||||||   |||||||
                                ATGTACTT   ATTTATG
                                    ATAAG
GAM612  FLJ21302 3' TACATAAACAATTTGAACA   15836        ___
                                TACATGAACA  TGGATA
                                ||||||||||  ||||||
                                ATGTATTTGT  ACTTGT
                                     TAA
GAM612  FN5      3' ACATGAACATCTCTGAATA   15837        ____
                                ACATGAACA   TGGATA
                                |||||||||   ||||||
                                TGTACTTGT   ACTTAT
                                     AGAG
GAM612  GPR      3' CACTGAGATGGATACA     15838    A   AC
                                TAC TGA  ATGGATACA
                                ||| |||  |||||||||
                                GTG ACT  TACCTATGT
                                  _  C_
GAM612  KIAA0660 3' TACATGAAAAACAAAATACA  15839       CAT__
                                TACATGAA   GGATACA
                                ||||||||   |||||||
                                ATGTACTT   TTTATGT
                                    TTTGT
GAM612  KIAA0703 5' TACAACATGGATACAC      15840     TGA
                                TACA  ACATGGATACAC
                                ||||  ||||||||||||
                                ATGT  TGTACCTATGTG
                                   ___
GAM612  KIAA0798 3' ACAGTGAATGGATACAC     15841     _  AC
                                ACA TGA  ATGGATACAC
                                ||| |||  ||||||||||
                                TGT ACT  TACCTATGTG
                                  C  __
GAM612  KIAA0977 3' TACATAAAGAATACAC      15842       CAT
                                TACATGAA  GGATACAC
                                ||||||||  ||||||||
                                ATGTATTT  CTTATGTG
                                    ___
GAM612  KIAA1024 3' TACATAAACATGATAATAC   15843         __
                                TACATGAACATG  GATAC
                                ||||||||||||  |||||
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                                ATGTATTTGTAC  TTATG
                                      TA
GAM612  KIAA1209 3'  TACATGAAACATGAAGACAC   15844        _     T
                                TACATGAA CATGGA ACAC
                                |||||||| |||||| ||||
                                ATGTACTT GTACTT TGTG
                                     T     C
GAM612  KIAA1912 3'  ACACCAATGGATACAC      15845      G AC
                                ACAT A  ATGGATACAC
                                |||| |  ||||||||||
                                TGTG T  TACCTATGTG
                                  G __
GAM612  LCHN     3'  CACAGACATGGATGCACG    15846     GA       A   III
                                CAT  ACATGGAT CAC   G
                                |||  |||||||| |||   |
                                GTG  TGTACCTA GTG   C
                                  TC       C   III
GAM612  OPN4     3'  TACATGAAATGAATCAC     15847        C     A
                                TACATGAA ATGGAT CAC
                                |||||||| |||||| |||
                                ATGTACTT TACTTA GTG
                                      _     _
GAM612  RAI17    3'  CACATGAACACCTAATATAC   15848          GG___
                                TACATGAACAT    ATAC
                                ||||||||||    ||||
                                GTGTACTTGTG    TATG
                                      GATTA
GAM612  SCYA22   3'  TACATGAAATGGAATTAC    15849        C    __
                                TACATGAA ATGGA  TAC
                                |||||||| |||||  |||
                                ATGTACTT TACCT  ATG
                                     _    TA
GAM612  SMARCF1  3'  TACATGAAAGGGTCTACAC   15850        CAT  A_
                                TACATGAA   GG  TACAC
                                ||||||||   ||  |||||
                                ATGTACTT   CC  ATGTG
                                     TC_  AG
GAM612  SMARCF1  3'  TACATGAAAGGGTCTACAC   15850        CAT  A_
                                TACATGAA   GG  TACAC
                                ||||||||   ||  |||||
                                ATGTACTT   CC  ATGTG
                                     TC_  AG
GAM612  SMARCF1  3'  TACATGAAAGGGTCTACAC   15850        CAT  A_
                                TACATGAA   GG  TACAC
                                ||||||||   ||  |||||
                                ATGTACTT   CC  ATGTG
                                     TC_  AG
GAM612  SMC1L1   3'  TACATAAATGAATGAATACAC  15851        C__
                                TACATGAA   ATGGATACAC
                                ||||||||   ||||||||||
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                                ATGTATTT  TACTTATGTG
                                    ACT
GAM612  SS-56    3'  TACATGAACAGCCAATAC    15852        TG_
                                TACATGAACA  GATAC
                                ||||||||||  |||||
                                ATGTACTTGT  TTATG
                                    CGG
GAM612  STX3A    3'  CACATGAGTGAATACAC     15853       ACA
                                TACATGA  TGGATACAC
                                |||||||  |||||||||
                                GTGTACT  ACTTATGTG
                                   C__
GAM612  T2BP     3'  CACATGGACATCTGGACA    15854       A  __
                                TACATG ACA  TGGATA
                                |||||| |||  ||||||
                                GTGTAC TGT  ACCTGT
                                   C  AG
GAM612  LOC144363 3'  TACATAAACAGCTGGCAC    15855         __  A
                                TACATGAACA  TGG TAC
                                ||||||||||  ||| |||
                                ATGTATTTGT  ACC GTG
                                    CG  _
GAM612  LOC145123 3'  TAATGAACATGGTCACAC    15819   C       A
                                A ATGAACATGG TACAC
                                | ||||||||||| |||||
                                A TACTTGTACC GTGTG
                                 T        A
GAM612  LOC148932 3'  CACATGGTCAGATACAC     15856       AACA
                                TACATG   TGGATACAC
                                ||||||   |||||||||
                                GTGTAC   GTCTATGTG
                                   CA__
GAM612  LOC150928 3'  TAATGAACATGGTCACAC    15819   C       A
                                A ATGAACATGG TACAC
                                | ||||||||||| |||||
                                A TACTTGTACC GTGTG
                                 T        A
GAM612  LOC152300 3'  TACATGGCAGAAATACAC    15857       AA  TG
                                TACATG  CA  GATACAC
                                ||||||  ||  |||||||
                                ATGTAC  GT  TTATGTG
                                   C_  CT
GAM612  LOC158709 3'  TACATAGATGATAGATACA   15858      _  AC
                                TACAT GA  ATGGATACA
                                ||||| ||  |||||||||
                                ATGTA CT  TATCTATGT
                                   T  AC
GAM612  LOC219525 3'  TACGATGGCATAGATACA    15859     _  AA
                                TAC ATG  CATGGATACA
                                ||| |||  ||||||||||
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                                ATG TAC  GTATCTATGT
                                  C  C_
GAM612  LOC221711 5'  TACACGGAAATGAATACAC   15860      AAC
                                TACATG  ATGGATACAC
                                ||||||  ||||||||||
                                ATGTGC  TACTTATGTG
                                   CTT
GAM612  LOC222662 3'  TACTTGAACATAAGTAACAC  15861    A      AT_
                                TAC TGAACATGG  ACAC
                                ||| |||||||||  ||||
                                ATG ACTTGTATT  TGTG
                                  A       CAT
GAM612  LOC255098 3'  ACATGAACAACGGTGTAC    15862        _  A_
                                ACATGAACA TGG  TAC
                                ||||||||| |||  |||
                                TGTACTTGT GCC  ATG
                                     T  AC
GAM612  LOC55833  3'  TACATACATAAATACA     15863     GA
                                TACAT  ACATGGATACA
                                |||||  ||||||||||
                                ATGTA  TGTATTTATGT
                                  __
GAM613  LOC150407 5'  GATTGTGGTTTGTCTTCAG   15866    AC      GTA
                                GATT  GGTTTGTC  TAG
                                ||||  ||||||||  |||
                                CTAA  CCAAACAG  GTC
                                  CA      AA_
GAM614  CDK5R2   5'  TAATCCTGAGCTCCGC     15869       ATGGG  _
                                TAATTCTGA    GC CCGC
                                |||||||||    || ||||
                                ATTAGGACT    CG GGCG
                                     _____ A
GAM614  IRTA2    3'  TAATCCTGAGCCTATGCT    15870       ATGGG  C__
                                TAATTCTGA    GCC  GCT
                                |||||||||    |||  |||
                                ATTAGGACT    CGG  CGA
                                     _____  ATA
GAM614  LMO2     5'  CAATTCTGCTCAAGGCCCG   15871      AA
                                TAATTCTG  TGGGGCCCG
                                ||||||||  |||||||||
                                GTTAAGAC  GTTCCGGGC
                                   GA
GAM614  RLN2     3'  TAATTCTGAAGGACTGCT    15872       AT   CC
                                TAATTCTGA  GGGGC  GCT
                                |||||||||  |||||  |||
                                ATTAAGACT  TCCTG  CGA
                                     __   A_
GAM614  SPAG6    3'  ATTCTGAATTCTACCCTCGCT  15873       GGG  __
                                ATTCTGAAT  GCCC  GCT
                                |||||||||  ||||  |||
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                                TAAGACTTA  TGGG  CGA
                                     AGA   AG
GAM614  CBX6     3'  TCCCGGGGGCCCGCT      15874      AAT
                                TTCTG  GGGGCCCGCT
                                |||||  ||||||||||
                                AGGGC  CCCCGGGCGA
                                  ___
GAM614  DKFZP434A043 3'  TTCTGAATAAAGTGCT      15875          CCC
                                TTCTGAATGGGG  GCT
                                ||||||||||||  |||
                                AAGACTTATTTC  CGA
                                      A__
GAM614  FLJ10081  3'  TAATTCTGTGTGAATCCC     15876        AA   G
                                TAATTCTG  TGGG CCC
                                ||||||||  |||| |||
                                ATTAAGAC  ACTT GGG
                                     AC   A
GAM614  FLJ12707  5'  TTCTGAACCAAATGTCCGCT   15877        G  C__
                                TTCTGAAT GGG  CCGCT
                                |||||||| |||  |||||
                                AAGACTTG TTT  GGCGA
                                     G  ACA
GAM614  FLJ20136  3'  ATTCTCACAGGGCCTGCT     15878      GA      C
                                ATTCT  ATGGGGCC GCT
                                |||||  |||||||| |||
                                TAAGA  TGTCCCGG CGA
                                   G_      A
GAM614  FLJ20340  3'  TAATTATGAATGAAGCTGCT   15879      C       CC
                                TAATT TGAATGGGGC  GCT
                                ||||| ||||||||||  |||
                                ATTAA ACTTACTTCG  CGA
                                   T       A_
GAM614  GMEB2     3'  TAATTCTGAAGCTGGTTAGCGG 15880         __  _____  CCCG
          C                      TAATTCTGAA  TGG    GG   C
                                ||||||||||  |||    ||   |
                                ATTAAGACTT  ACC    TC   G
                                      CG   AAIII  GCCC
GAM614  GTF3C3    3'  TAATTCTGAAATGGTCATTAGC 15881       _  _________  CCCG
          GGGCC                    TTCTGAA TGG      GG   CT
                                ||||||| |||       ||   ||
                                AAGACTT ACC       TC   GG
                                    T   AGTAAIII  GCCC
GAM614  HDAC9-PENDING 3'  TAATTTGAATGGAGAC     15882      C       CCC
                                TAATT TGAATGGGG   GC
                                ||||| |||||||||   ||
                                ATTAA ACTTACCTC   TG
                                   _      ___
GAM614  MGC21738  3'  CAATTCTGACATTACCTGCT   15883        ATGGG   C
                                TAATTCTGA    GCC GCT
                                |||||||||    ||| |||
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                                GTTAAGACT    TGG CGA
                                     GTAA_  A
GAM614  TOLLIP   3'  TAATTCTGGGGACCGC     15884       AAT    C
                                TAATTCTG  GGGGCC GC
                                ||||||||  |||||| ||
                                ATTAAGAC  CCCTGG CG
                                     ____    _
GAM614  LOC120227 5'  TTCCCAGGGCCCGCT      15885     GAA
                                TTCT  TGGGGCCCGCT
                                ||||  ||||||||||
                                AAGG  GTCCCGGGCGA
                                   ____
GAM614  LOC148562 3'  TTCTGAATGACGAGTGCT    15886         _  CCC
                                TTCTGAATGG GG  GCT
                                |||||||||| ||  |||
                                AAGACTTACT CT  CGA
                                      G  CA_
GAM614  LOC151200 3'  TAATTCTAATGAGAAGCT    15887        A    CCC
                                TAATTCTGA TGGGG  GCT
                                |||||||| |||||  |||
                                ATTAAGATT ACTCT  CGA
                                     _    T__
GAM614  LOC221543 5'  TAATTCTAATTTTGCCTTCGCT 15888        ATGGG  __
                                TAATTCTGA    GCC  CGCT
                                |||||||||    |||  ||||
                                ATTAAGATT    CGG  GCGA
                                     AAAA_  AA
GAM614  LOC257596 5'  TAATTCTAATTTTGCCTTCGCT 15888        ATGGG  __
                                TAATTCTGA    GCC  CGCT
                                |||||||||    |||  ||||
                                ATTAAGATT    CGG  GCGA
                                     AAAA_  AA
GAM614  LOC93052  5'  TAATTCTGGGTAGGTCACGCT  15889       AA   GCC
                                TAATTCTG  TGGG  CGCT
                                ||||||||  ||||  ||||
                                ATTAAGAC  ATCC  GCGA
                                     CC   AGT
GAM615  RYR3     3'  ACGTATTACTTTATTGCA    15892       _     A
                                GCGTGT ACTTTATT CA
                                ||||||  |||||||| ||
                                TGCATA TGAAATAA GT
                                   A      C
GAM615  LOC146818 5'  TGGATGCGCCTTATTACAACG  15893    C   TA
                                TGG GTG  CTTTATTACAACG
                                |||  |||  ||||||||||||
                                ACC TAC  GGAATAATGTTGC
                                  _  GC
GAM616  PIK3R1   3'  TCTTTTTTGTGAAAGAAA    15896          A
                                TCTTTTTTGTGAAA AAA
                                ||||||||||||| |||
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                                AGAAAAAACACTTT TTT
                                       C
GAM616  RSN      3'  TCTTTTTTGTGATAAGAAAAT  15897          A  A
                                TCTTTTTTGTGA AA AAAAT
                                |||||||||||| || |||||
                                AGAAAAAACACT TT TTTTA
                                       A  C
GAM616  SCA1     5'  TCTTTCTCACGAAGAAAA    15898       TG   A
                                TCTTTTT  TGAA AAAA
                                |||||||  |||| ||||
                                AGAAAGA  GCTT TTTT
                                    GT   C
GAM616  TRAM     3'  TTTTTTGTGAAAGTAAAAAT  15899          A_
                                TTTTTTGTGAAA  AAAAAT
                                ||||||||||||  ||||||
                                AAAAAAACACTTT  TTTTTA
                                       CA
GAM616  FLJ20188 3'  TTTCTCGGGAAAAAAAAAT   15900       T
                                TTTTTTG GAAAAAAAAAT
                                ||||||| ||||||||||
                                AAAGAGC CTTTTTTTTTA
                                    C
GAM616  KIAA1870 3'  TCTTTCCCGGGTGAAAAAAAAA 15901        __
           TA                    TCTTTTTT  GTGAAAAAAAAATA
                                ||||||||  ||||||||||||||
                                AGAAAGGG  CACTTTTTTTTTAT
                                     CC
GAM616  MRPS17   3'  TTTTTTGTGAAAAACCATA   15902          AAA
                                TTTTTTGTGAAAAA   ATA
                                ||||||||||||||   |||
                                AAAAAAACACTTTTT   TAT
                                       GG_
GAM616  LOC222171 3'  CTTTTTGAAAAAAAAATAAT   15903      TTG
                                CTTTT   TGAAAAAAAAATAAT
                                |||||   ||||||||||||||||
                                GAAAA   ACTTTTTTTTTATTA
                                    ___
GAM617  CNNM1    3'  TTTTTTCCAGGAAAGGCATTTT 15906       GCC    _
                                TTTTTTC   GGAAAG CATTTT
                                |||||||   |||||| ||||||
                                AAAAAAG   CCTTTC GTAAAA
                                    GT_    C
GAM617  KIAA1796 3'  TATTTTTTCATTGGGAATATAC 15907        CC_   A__
           ATTTT                 TATTTTTTCG   GGAA   GCATTTT
                                ||||||||||   ||||   |||||||
                                ATAAAAAAGT   CCTT   TGTAAAA
                                      AAC   ATA
GAM617  LGALS9   3'  TTTTTTTGCCAACAAGCATTTT 15908      C    A
                                TTTTTT GCCGG AAGCATTTT
                                |||||| ||||| |||||||||
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                                AAAAAA CGGTT TTCGTAAAA
                                   A    G
GAM617  MGC2306   3'  TTTTTTCACAAAAAGTATTTT  15909        C     C
                                TTTTTTCGC GGAAAG ATTTT
                                ||||||||| |||||| |||||
                                AAAAAAGTG TTTTTC TAAAA
                                      _     A
GAM617  LOC162333 5'  TATTTTTTCCTTGGAAGGC   15910        GCC   A
                                TATTTTTTC   GGAA GC
                                |||||||||   |||| ||
                                ATAAAAAAG   CCTT CG
                                     GAA   C
GAM618  DMP1      3'  CATAATTTCAAAGTGCTTT   15913     C_
                                CAT  TTTCAAAGTGCTTT
                                |||  ||||||||||||||
                                GTA  AAAGTTTCACGAAA
                                  TT
GAM618  SFRS7     3'  TTGACATCTTTAATTACTTT   15914          CAAAG
                                TTGACATCTTT    TGCTTT
                                ||||||||||    ||||||
                                AACTGTAGAAA    ATGAAA
                                      TTA__
GAM618  SUSP1     3'  TTGATGTCTTCAAAAATGC   15915      CA    C
                                TTGA  TCTTT AAAGTGC
                                ||||  ||||| |||||||
                                AACT  AGAAG TTTTACG
                                  AC    T
GAM618  C6orf37   3'  TTGACATCTTCCAACTTT    15916           AAGT
                                TTGACATCTTTCA   GCTTT
                                ||||||||||||   |||||
                                AACTGTAGAAGGT   TGAAA
                                       ____
GAM618  FLJ23074  5'  TTGACATGTTTCAGTGCTTT  15917       C    AA
                                TTGACAT TTTCA  GTGCTTT
                                ||||||| |||||  |||||||
                                AACTGTA AAAGT  CACGAAA
                                   C    __
GAM618  KIAA1054  3'  TTGGTATCTTTCAAATGCATC  15918    AC       G   TT
                                TTG  ATCTTTCAAA TGC  TC
                                |||  |||||||||| |||  ||
                                AAC  TAGAAAGTTT ACG  AG
                                  CA        _   T_
GAM618  MRPL44    3'  TTGACATTTATCTCACTTTCG  15919       C__   AAAGT
                                TTGACAT   TTTC    GCTTTCG
                                |||||||   ||||    |||||||
                                AACTGTA   AGAG    TGAAAGC
                                   AAT   _____
GAM618  LOC139770 3'  TTGATTCTTTCAAAGTAAATC  15920     CA         CTT
                                TTGA  TCTTTCAAAGTG   TC
                                ||||  ||||||||||||   ||
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                                AACT  AGAAAGTTTCAT   AG
                                  A_          TT_
GAM618  LOC154877 3'  TTAACATCTTTTAAAAACTTT  15921          C    T
                                TTGACATCTTT AAAG GCTTT
                                |||||||||||  |||| |||||
                                AATTGTAGAAA TTTT TGAAA
                                      A   _
GAM619  CYP1A1   3'  TCCCAATTGTCAAAGATT    15924    G   GC
                                TT TAG  GTCAAAGATT
                                || |||  ||||||||||
                                AG GTT  CAGTTTCTAA
                                 G   AA
GAM619  MEN1     3'  TTGTAATATCAAAAGATTA    15925       GC     _
                                TTGTAG  GTCAAA GATTA
                                ||||||  |||||| |||||
                                AACATT  TAGTTT CTAAT
                                   A_     T
GAM619  MEN1     3'  TGTCCTGAATCAAAGATTAA   15926     AGGC_
                                TGT    GTCAAAGATTAA
                                |||    ||||||||||||
                                ACA    TAGTTTCTAATT
                                  GGACT
GAM619  PSEN1    5'  TTGCAGGCTCCCAGATTA    15927        G  AA
                                TTGTAGGC TC  AGATTA
                                |||||||| ||  ||||||
                                AACGTCCG AG  TCTAAT
                                     _ GG
GAM619  PSEN1    5'  TTGCAGGCTCCCAGATTA    15927        G  AA
                                TTGTAGGC TC  AGATTA
                                |||||||| ||  ||||||
                                AACGTCCG AG  TCTAAT
                                     _ GG
GAM619  TJP1     5'  TTGTAGACAAAAGATT      15928         TC
                                TTGTAGGCG  AAAGATT
                                |||||||||  |||||||
                                AACATCTGT  TTTCTAA
                                       __
GAM619  TTN      3'  TTGAGGCACAAAGATT      15929     T    T
                                TTG AGGCG CAAAGATT
                                ||| ||||| ||||||||
                                AAC TCCGT GTTTCTAA
                                  _    _
GAM619  TTN      3'  TTGAGGCACAAAGATT      15929     T    T
                                TTG AGGCG CAAAGATT
                                ||| ||||| ||||||||
                                AAC TCCGT GTTTCTAA
                                  _    _
GAM619  TTN      3'  TTGAGGCACAAAGATT      15929     T    T
                                TTG AGGCG CAAAGATT
                                ||| ||||| ||||||||
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                                AAC TCCGT GTTTCTAA
                                  _   _
GAM619  FLJ20445  3'  TTGCATTTCAAAGATTAA    15930      GGCG
                                TTGTA   TCAAAGATTAA
                                |||||   ||||||||||
                                AACGT   AGTTTCTAATT
                                  AA__
GAM619  UMP-CMPK  3'  TGTAGTTATGAAAGATTA    15931      GC  C
                                TGTAG  GT AAAGATTA
                                |||||  || ||||||||
                                ACATC  TA TTTCTAAT
                                  AA  C
GAM619  VDU1      3'  TGTAGTGTAAAGATTAA     15932      GC  C
                                TGTAG  GT AAAGATTAA
                                |||||  || |||||||||
                                ACATC  CA TTTCTAATT
                                  A_  _
GAM619  ZFP       3'  TTGTGAGGGACAAAGATTA   15933     _  CGT
                                TTGT AGG   CAAAGATTA
                                ||||  |||   |||||||||
                                AACA TCC   GTTTCTAAT
                                  C   CT_
GAM619  LOC120863 3'  CTGTAAACAGAAAGATTAA   15934        TC
                                TTGTAGGCG  AAAGATTAA
                                |||||||||  |||||||||
                                GACATTTGT  TTTCTAATT
                                     C_
GAM619  LOC126669 3'  TTATAAGCTACAAAGGTTAA  15935        GT    A
                                TTGTAGGC  CAAAG TTAA
                                ||||||||  |||||  ||||
                                AATATTCG  GTTTC AATT
                                     AT    C
GAM619  LOC143308 5'  CTGCAAACTCAAAGATT     15936        G
                                TTGTAGGC TCAAAGATT
                                |||||||| |||||||||
                                GACGTTTG AGTTTCTAA
                                  _
GAM619  LOC148085 3'  TTGTAGGAAAAGATTAA     15937        CGTC
                                TTGTAGG    AAAGATTAA
                                |||||||    |||||||||
                                AACATCC    TTTCTAATT
                                    T___
GAM619  LOC151242 3'  TAGGACATCAAGGATTAA    15938     _    A
                                TAGG CGTCAA GATTAA
                                |||| |||||| ||||||
                                ATCC GTAGTT CTAATT
                                  T     C
GAM620  FMO5      3'  ACTATTGTAGGAACATTA    15941     C    CGTTA
                                ACTG TGTAGG    AACATTA
                                |||| ||||||    |||||||
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                                TGAT ACATCC    TTGTAAT
                                  A    _____
GAM620  FLJ31737  3'  ACTGTTGCAGGCATTCATT   15942     C       AAA
                                ACTG TGTAGGCGTT  CATT
                                |||| ||||||||||  ||||
                                TGAC ACGTCCGTAA  GTAA
                                  A      ___
GAM620  KIAA0633  3'  ACTGCTGTAGTTAGACCTCATT 15943        GCGTTAAA
           AT                    ACTGCTGTAG      CATTAT
                                |||||||||||      ||||||
                                TGACGACATC      GTAATA
                                     AATCTGGA
GAM620  MGC10981  3'  ACTTTGTAAGCATAGGCATTAT 15944    GC       TAAA
                                ACT  TGTAGGCGT   CATTAT
                                |||  |||||||||   ||||||
                                TGA  ACATTCGTA   GTAATA
                                  A_       TCC_
GAM620  LOC145844 3'  TACTGTCACTTTTAAACATT   15945      AGGCG
                                TGCTGT    TTAAACATT
                                ||||||    |||||||||
                                ATGACA    AATTTGTAA
                                   GTGAA
GAM620  LOC154084 5'  CTGCTATACAAGAACATTAT   15946       AG   TTA
                                CTGCTGT  GCG   AACATTAT
                                |||||||  |||   ||||||||
                                GACGATA  TGT   TTGTAATA
                                   __   TC_
GAM620  LOC54516  3'  ACTGCTGTGTTGCTAACGTTA  15947       A_____
                                ACTGCTGT     GGCGTTA
                                ||||||||     |||||||
                                TGACGACA     TTGCAAT
                                     CAACGA
GAM620  LOC91263  3'  TGCTGTCTTTGAACATTAT   15948      AGGCG  A
                                TGCTGT    TT AACATTAT
                                ||||||    || ||||||||
                                ACGACA    AA TTGTAATA
                                   GA___  C
GAM621  CASP8AP2  3'  TAAAATGCTACAAAACTAT   15951          ___
                                TAAAGTGCTAT   ACTAT
                                ||||||||||   |||||
                                ATTTTACGATG   TGATA
                                      TTT
GAM621  CNGB3    3'  CAAAGTGCTGTAACAGTGACCA 15952        AT_  TATA
           TCT                   TAAAGTGCT   AC    ACCATCT
                                |||||||||   ||   |||||||
                                GTTTCACGA   TG    TGGTAGA
                                     CAT  TCAC
GAM621  SCD      3'  AAATGCTACAACCAT      15953          CTATA
                                AAGTGCTATA    ACCAT
                                ||||||||||    |||||
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                                TTTACGATGT    TGGTA
                                      _____
GAM621  SUV39H1  3'  AAGTGCTATCTACGGACTATCT 15954        A   A_  C
                                AAGTGCTAT CTAT  AC ATCT
                                ||||||||| ||||  || ||||
                                TTCACGATA GATG  TG TAGA
                                     _   CC  A
GAM621  TIMELESS 3'  AGTACTATATTCCAACCCTATC 15955        CTA   __
           T                     AGTGCTATA   TAACC  ATCT
                                 |||||||||   |||||  ||||
                                 TCATGATAT   GTTGG  TAGA
                                      AAG    GA
GAM621  VSX1     3'  TAAAGTGCCATTAAGGAACC   15956         ACTAT
                                 TAAAGTGCTAT    AACC
                                 ||||||||||     ||||
                                 ATTTCACGGTA    TTGG
                                       ATTCC
GAM621  UBXD2    3'  AGTGCTATCTTCCAATCT    15957        A  ATAA  _
                                 AGTGCTAT CT    CCA TCT
                                 |||||||| ||    ||| |||
                                 TCACGATA GA    GGT AGA
                                     _ A___   T
GAM621  ZAK      3'  TAAAGTGCTTTACATATA    15958         A  _
                                 TAAAGTGCT TAC TATA
                                 ||||||||| ||| ||||
                                 ATTTCACGA ATG ATAT
                                       A   T
GAM621  LOC146856 3'  TAAAGTGCTGGTGTCACCTGTC 15959         ATACTATA  A_
           T                     TAAAGTGCT       ACC  TCT
                                 |||||||||       |||  |||
                                 ATTTCACGA       TGG  AGA
                                      CCACAG__   AC
GAM622  KCNA7    3'  GTCTCTGTCTCTCTGGGT    15962           C
                                 GTCTCTGTCTCTC GGGT
                                 |||||||||||| ||||
                                 CAGAGACAGAGAG CCCA
                                       A
GAM622  CHL1     3'  GTTTTAGTTTCTGACTTAAAGG 15963        C   T  CTCC
           T                     GTTTTAGT TCTG CT    GGGT
                                 |||||||| |||| ||    ||||
                                 CAAAATCA AGAC GA    TCCA
                                     A   T  ATT_
GAM622  FOXP1    3'  GTTTTGGTCTCTGTAGAGG    15964       A       CTCTCC
                                 GTTTT GTCTCTGT     GGG
                                 ||||| ||||||||     |||
                                 CAAAA CAGAGACA     TCC
                                    C       TC____
GAM622  HN1L     3'  GTTTCTGGTCTGGCTCCGGGT  15965    C   _   __
                                 GT TCTG TCT  CTCCGGGT
                                 || |||| |||  ||||||||
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                                CA AGAC AGA  GAGGCCCA
                                 A   C   CC
GAM622  KIAA0848 3'  GTTTTAGTTTTGTTCAGGG   15966        CTC   CTC  C
                                GTTTTAGT   TGT   TC GGG
                                ||||||||   |||   || |||
                                CAAAATCA   ACA   AG CCC
                                     AA_   ___  T
GAM623  HCS      3'  TATATAAATCTAAATATAAA   15969     _
                                TATA AAATCTAAATATAAA
                                |||| ||||||||||||||
                                ATAT TTTAGATTTATATTT
                                  A
GAM623  AKAP6    3'  TAAAAAATCTAGTATAAATGTT 15970    T       AA
            T                    TA AAAATCTA  TATAAATGTTT
                                || ||||||||  ||||||||||
                                AT TTTTAGAT  ATATTTACAAA
                                 T       C_
GAM623  KIAA1571  3'  TATAAAATTTAAATATAAACCT 15971        C         G
            T                    TATAAAAT TAAATATAAAT TT
                                |||||||| |||||||||| ||
                                ATATTTTA ATTTATATTTG AA
                                     A         G
GAM624  CLN5     3'  GTACATTTACATATTAA     15974        CAA
                                GTACATT   TATATGTTGA
                                |||||||   ||||||||||
                                CATGTAA   ATGTATAATT
                                     ___
GAM624  ESR1     3'  TACATTCAATTGTCTGAT     15975          ATA  _
                                TACATTCAAT   TGT TGAT
                                ||||||||||   ||| ||||
                                ATGTAAGTTA   ACA ACTA
                                      ___  G
GAM624  NOTCH2   3'  ATACATTCAATGTATTG     15976          ATA
                                GTACATTCAAT   TGTTG
                                ||||||||||   |||||
                                TATGTAAGTTA   ATAAC
                                      C__
GAM624  NPAT     3'  TCAGAACATTCAATAAATG    15977      T        T
                                TCAG ACATTCAATA ATG
                                |||| |||||||||| |||
                                AGTC TGTAAGTTAT TAC
                                  T         T
GAM624  PSMD9    3'  TCAGTGCAAAGAAATATGTTG  15978      A  TTCAAT
                                TCAGT CA      ATATGTTG
                                ||||| ||      ||||||||
                                AGTCA GT      TATACAAC
                                   C  TTCTT_
GAM624  CHM-I    3'  TCAGTACATTTGCATATACTAA 15979          CAA
                                TCAGTACATT   TATATGTTGA
                                ||||||||||   ||||||||||
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                                AGTCATGTAA   GTATATGATT
                                     AC_
GAM624  DKFZP434O047 5'  TCAGTGGGTTCAATATCTGT   15980      ACA      A
                                TCAGT   TTCAATAT TGT
                                |||||   |||||||| |||
                                AGTCA   AAGTTATA ACA
                                   CCC      G
GAM624  DKFZp762K2015 3'  TCAGTCTGTTCAATATAC    15981      ACA
                                TCAGT   TTCAATATAT
                                |||||   ||||||||||
                                AGTCA   AAGTTATATG
                                   GAC
GAM624  FLJ23548  3'  TACATTCAAAATCTTGAT    15982        TAT  G
                                TACATTCAA   AT TTGAT
                                |||||||||   || |||||
                                ATGTAAGTT   TA AACTA
                                     T__  G
GAM624  KIAA0443  5'  TCAGTAATTCAATAATACAGAT 15983      C      T   TT
                                TCAGTA ATTCAATA ATG  GAT
                                |||||| |||||||| |||  |||
                                AGTCAT TAAGTTAT TAT  CTA
                                   _      _  GT
GAM624  KIAA1483  3'  AGTACATTCAAATTTGA     15984         TATATG
                                AGTACATTCAA     TTGA
                                ||||||||||      ||||
                                TCATGTAAGTT     AACT
                                     TA____
GAM624  LOC120939 3'  TCAGTGCATTAATGTCGA    15985      A   CAATAT
                                TCAGT CATT     ATGTTGA
                                ||||| ||||     |||||||
                                AGTCA GTAA     TACAGCT
                                   C   T_____
GAM624  LOC126669 3'  TCAGTACATTTGCATATG    15986        CAA
                                TCAGTACATT   TATATG
                                ||||||||||   ||||||
                                AGTCATGTAA   GTATAC
                                     AC_
GAM624  LOC221596 3'  TCAGTACATTTATACG      15987        CAA
                                TCAGTACATT   TATATG
                                ||||||||||   ||||||
                                AGTCATGTAA   ATATGC
                                     ___
GAM625  FLRT2    3'  GCAGGTGAGGCTGTAACA    15990     CAAC    CTT
                                GCA   GAGGC   TGTAACA
                                |||   |||||  |||||||
                                CGT   CTCCG   ACATTGT
                                  CCA_   ___
GAM625  JUND     3'  TGGCGTAACGAGACTTTA    15991      AC      C
                                TGGC  AACGAGGC TTTG
                                ||||  |||||||| ||||
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                                ACCG  TTGCTCTG AAAT
                                  CA      _
GAM625  KRTHA5   3'  GGCAGCCGGCCTTTGTGACA   15992      CAACGA       A
                                GGCA     GGCCTTTGT ACA
                                ||||     ||||||||| |||
                                CCGT     CCGGAAACA TGT
                                  CGG___       C
GAM625  TM4SF2   3'  TGGCACAACAGGGCTTCACA   15993         G   C   TG
                                TGGCACAAC AGG CTT  TA
                                ||||||||| ||| |||  ||
                                ACCGTGTTG TCC GAA  GT
                                      _  C   GT
GAM625  DKFZP434A0131 3'  TGGCAGGGTGAGGCCCCCAGGA 15994       CAAC      TT TA
           CA                     TGGCA   GAGGCCT  G  ACA
                                |||||   |||||||  |  |||
                                ACCGT   CTCCGGG  T  TGT
                                   CCCA      GG CC
GAM625  DKFZp434G179 3'  TGTACAGAGACTTTTTTTGTAA 15995    GC   AC    C___
           CA                     TG  ACA  GAGGC   TTTGTAACA
                                ||  |||  |||||   |||||||||
                                AC  TGT  CTCTG   AAACATTGT
                                 A_  __    AAAA
GAM625  FLJ11160  3'  TGGCACTGGCTTTGTAA     15996       AACGA   C
                                TGGCAC    GGC TTTGTAA
                                ||||||    ||| |||||||
                                ACCGTG    CCG AAACATT
                                   A____  _
GAM625  FLJ13952  3'  TGGCACAACTGGGCACTGGGTA 15997         GA   _  TT
                                TGGCACAAC  GGC CT  GTA
                                |||||||||  ||| ||  |||
                                ACCGTGTTG  CCG GA  CAT
                                      AC   T  CC
GAM625  FLJ21551  3'  GCACAGCAAGCTTTGTAACA   15998      A    GC
                                GCACA CGAG  CTTTGTAACA
                                ||||| ||||  ||||||||||
                                CGTGT GTTC  GAAACATTGT
                                  C   __
GAM625  KIAA0057  3'  TGGCACAACGCAGGCACCTGGC 15999          _   _  T
           A                     TGGCACAACG AGGC CTT GTA
                                ||||||||||| |||| ||| |||
                                ACCGTGTTGC TCCG GGA CGT
                                      G   T  C
GAM625  KIAA0644  3'  TGGCCAAGCCTCCTTTGTAA   16000     A   CGAGG
                                TGGC CAA    CCTTTGTAA
                                |||| |||    |||||||||
                                ACCG GTT    GGAAACATT
                                  _  CGGA_
GAM625  KIAA1450  3'  TGGCACAATGTGGCTTTCTTTG 16001        CGA  ___
                                TGGCACAA   GGC   CTTTG
                                ||||||||   |||   |||||
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                                ACCGTGTT  CCG  GAAAC
                                    ACA  AAA
GAM625  MAL2    3'  TGGCACATTTATGACTTTGTAA 16002       ACGA_  C
                                TGGCACA   GGC TTTGTAA
                                |||||||   ||| |||||||
                                ACCGTGT   CTG AAACATT
                                    AAATA  _
GAM625  SUI1    3'  TGGTCGAACAGACCTTTGT   16003    CAC  G
                                TGG  AAC AGGCCTTTGT
                                |||  ||| ||||||||||
                                ACC  TTG TCTGGAAACA
                                  AGC  _
GAM625  LOC148758 3'  GGCACAACGGGGAGCTGGCA  16004        A  CC  T
                                GGCACAACG GG  TT GTA
                                ||||||||| ||  || |||
                                CCGTGTTGC CC  GA CGT
                                     C  TC  C
GAM625  LOC202546 3'  TGGTCCAGCGAGGCCCGTG   16005    CA  A      T
                                TGG  CA CGAGGCCT TG
                                |||  || ||||||||  ||
                                ACC  GT GCTCCGGG AC
                                  AG  C       C
GAM625  LOC255971 5'  TGGAGCAGCGAGGCCTAGC   16006    CA  A      TT
                                TGG  CA CGAGGCCT  GT
                                |||  || ||||||||  ||
                                ACC  GT GCTCCGGA  CG
                                  TC  C       T_
GAM625  LOC257415 3'  TAGCACACCCTTTGTAAC    16007       A GAGG
                                TGGCACA C   CCTTTGTAAC
                                |||||||  |   ||||||||||
                                ATCGTGT G   GGAAACATTG
                                     _ _____
GAM625  LOC91050  3'  TGGCACAAATGAGGCAGCCTCA 16008       C_    CTTTG
          ACA                     TGGCACAA  GAGGC    TAACA
                                |||||||| |||||   |||||
                                ACCGTGTT  CTCCG    GTTGT
                                    TA    TCGGA
GAM626  ANXA4   3'  TGTGAAACACAAAGTAGAAA  16011    _     TCATT
                                TGT AAATACA    AGTAGAAA
                                |||  |||||||   ||||||||
                                ACA TTTGTGT    TCATCTTT
                                  C     T_____
GAM626  COG2    3'  TGTAAACTATAGTAGAAA    16012       ACATCAT
                                TGTAAAT     TAGTAGAAA
                                |||||||     |||||||||
                                ACATTTG     ATCATCTTT
                                    AT______
GAM626  EIF1A   3'  TAAATACAAATTAGTAGAA   16013        TC
                                TAAATACA  ATTAGTAGAA
                                ||||||||  ||||||||||
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                                ATTTATGT  TAATCATCTT
                                     T_
GAM626  IFRD1    3'  TAAATACATTGAAATAGAAAA  16014        CATT
                                TAAATACAT   AGTAGAAAA
                                |||||||||   |||||||||
                                ATTTATGTA   TTATCTTTT
                                     ACT_
GAM626  PCDHA12  5'  TGTAAGTACATATTTAGTAAA  16015      A    CA
                                TGTAA TACAT  TTAGTAGA
                                ||||| |||||  ||||||||
                                ACATT ATGTA  AATCATTT
                                   C    TA
GAM626  PCDHA12  5'  TGTAAGTACATATTTAGTAAA  16015      A    CA
                                TGTAA TACAT  TTAGTAGA
                                ||||| |||||  ||||||||
                                ACATT ATGTA  AATCATTT
                                   C    TA
GAM626  AK5      3'  TGAAATGCATCACCATGTAGA  16016    T   A      _
                                TG AAAT CATCATTA GTAGA
                                || |||| |||||||| |||||
                                AC TTTA GTAGTGGT CATCT
                                 _   C       A
GAM626  FLJ20275 3'  TGTAAATATTCTCAACAGAGAA 16017        CA_   T   T
                                TGTAAATA   TCA TAG AGAA
                                ||||||||   ||| ||| ||||
                                ACATTTAT   AGT GTC TCTT
                                     AAG   T   _
GAM626  KIAA0871 3'  TGTAAAGGCATCATTAGTA    16018       TA
                                TGTAAA  CATCATTAGTA
                                ||||||  ||||||||||
                                ACATTT  GTAGTAATCAT
                                   CC
GAM626  KIAA1078 3'  GTAAATACATCATATGAGA    16019           TAGT
                                GTAAATACATCAT    AGA
                                ||||||||||||    |||
                                CATTTATGTAGTA    TCT
                                       TAC_
GAM626  KIAA1430 3'  TATAAATACATCCTCAGGAAA  16020          A   TA
                                TGTAAATACATC TTAG  GAAA
                                |||||||||||| ||||  ||||
                                ATATTTATGTAG AGTC  CTTT
                                       G   __
GAM626  MGC5391  3'  TGTAAAACATCATTATAAAA   16021       T       G
                                TGTAAA ACATCATTA TAGAA
                                |||||| ||||||||| |||||
                                ACATTT TGTAGTAAT ATTTT
                                     _       _
GAM626  NEUGRIN  5'  TGAAATACGTCACTAATGAA   16022    T     A      A
                                TG AAATAC TCATTAGT GAA
                                || |||||| |||||||| |||
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                                AC TTTATG AGTGATTA CTT
                                 _     C      _
GAM626  POPX1    3'  TGTAGATACCATTAGTTAGA  16023     A   AT     _
                                TGTA ATAC  CATTAGT AGA
                                |||| ||||  ||||||| |||
                                ACAT TATG  GTAATCA TCT
                                  C   __      A
GAM626  PPP1R14C 3'  TGTAAATAAATCATTGGTAAA 16024       C     A
                                TGTAAATA ATCATT GTAGA
                                |||||||| |||||| |||||
                                ACATTTAT TAGTAA CATTT
                                     T     C
GAM626  RHOBTB1  3'  TGTAAATACACATTCTTGGA  16025        T   AGTA
                                TGTAAATACA CATT    GA
                                |||||||||| ||||    ||
                                ACATTTATGT GTAA    CT
                                      _   GAAC
GAM626  LOC145828 3' TGTAACATATCTTAGTAGAA  16026      ATAC   A
                                TGTAA    ATC TTAGTAGAA
                                |||||    ||| |||||||||
                                ACATT    TAG AATCATCTT
                                   GTA_  _
GAM626  LOC205851 5' TGTAAATATCTTCATCAGGAA 16027       CA_     TA
                                TGTAAATA   TCATTAG  GAA
                                ||||||||   |||||||  |||
                                ACATTTAT   AGTAGTC  CTT
                                     AGA     __
GAM626  LOC257109 3' TGTAAATGGGTCATTAGC    16028       ACA
                                TGTAAAT   TCATTAGT
                                |||||||   ||||||||
                                ACATTTA   AGTAATCG
                                    CCC
GAM627  RAB5A    3'  CAGCTGAAGATCGAATTTAAAA 16031    AAACTAA
                T                   TAG      ATCGAATTTAAAAT
                                    |||      ||||||||||||||
                                    GTC      TAGCTTAAATTTTA
                                      GACTTC_
GAM627  TNFSF4   3'  TAGTGGCTAAGTCAAATTTAAA 16032    AAA    A
                AT                    TAG   CTAA TCGAATTTAAAAT
                                      |||   |||| ||||||||||||
                                      ATC   GATT AGTTTAAATTTTA
                                        ACC    C
GAM627  BZW1     3'  TAGAAACTAAATGCAGAA    16033          _ _
                                TAGAAACTAAAT C GAA
                                |||||||||||| | |||
                                ATCTTTGATTTA G CTT
                                       C T
GAM627  CDC14A   3'  AAAACTAAACAGATTTAAAAT  16034         C  A
                                GAAACTAAAT GA TTTAAAAT
                                |||||||||| || ||||||||
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                                TTTTGATTTG CT AAATTTTA
                                      T  _
GAM627  LOC221830 3'  TAAAAACTGAATCGTGTTTAAA 16035        A     AA
              AT                  TAGAAACT AATCG  TTTAAAAT
                                  |||||||| |||||  ||||||||
                                  ATTTTTGA TTAGC  AAATTTTA
                                       C     AC
GAM628  ADRA2A   3'  TGACCACTCCATTCATATTTA  16038   C         ATC
                                  A ACCACTCCATT   TATTTA
                                  | ||||||||||   ||||||
                                  A TGGTGAGGTAA   ATAAAT
                                   C         GT_
GAM628  EPM2A    3'  CACTTCATCTATTTA       16039      CCA
                                  CACT   TTATCTATTTA
                                  ||||   ||||||||||
                                  GTGA   AGTAGATAAAT

                                    ___
GAM628  MTA1L1   3'  CACCACCTGTTATCTGTTTAC  16040        CCA     A
                                  CACCACT   TTATCT TTTAC
                                  |||||||   |||||| |||||
                                  GTGGTGG   AATAGA AAATG
                                      AC_     C
GAM628  NPM3     3'  CACACCACTTTATTTCAACCT  16041         CC   A  T
                                  TACACCACT  ATT TC ATTT
                                  |||||||||  ||| || ||||
                                  GTGTGGTGA  TAA AG TGGA
                                        AA   _  T
GAM628  CGI-203   5'  TACACCACCCGTCACCT     16042         T  A
                                  TACACCAC CC TTATCT
                                  |||||||| || ||||||
                                  ATGTGGTG GG AGTGGA
                                       _  C
GAM628  FLJ10498  3'  TACATTACCACCACTATTTAC  16043      CCACT     T
                                  TACA     CCATTA CTATTTAC
                                  ||||     |||||| ||||||||
                                  ATGT     GGTGGT GATAAATG
                                    AAT__      _
GAM628  FLJ10583  3'  TACAGCTACATCATCTATTT   16044      CCA  C
                                  TACA   CT CATTATCTATTT
                                  ||||   || ||||||||||||
                                  ATGT   GA GTAGTAGATAAA
                                    C__  T
GAM628  GCN2     3'  TACAACATTCCATTATTCCA   16045      C  C       _
                                  TACA CA TCCATTAT CTA
                                  |||| || |||||||| |||
                                  ATGT GT AGGTAATA GGT
                                    T  A       A
GAM628  GRID1    3'  TACCCCACTCCATTCTGTCATT 16046    A         ATC____
              ATTTAC                  AC CCACTCCATT       TATTTAC
                                  || ||||||||||       |||||||
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                                TG GGTGAGGTAA      ATAAATG
                                 G         GACAGTA
GAM628  KIAA1434  3'  CCACCACCATTTATTTA     16047      _    ATC
                                CCACT CCATT   TATTTA
                                ||||| |||||   ||||||
                                GGTGG GGTAA   ATAAAT
                                   T    ____
GAM628  MGC11034  3'  ACACCACTTTACGCTATTTAC  16048        CCA   _
                                ACACCACT   TTAT CTATTTAC
                                ||||||||   |||| ||||||||
                                TGTGGTGA   AATG GATAAATG
                                     ___    C
GAM628  MGC32104  3'  ACCTATTCCATTGATCTAT   16049     AC_     _
                                ACC   TCCATT ATCTAT
                                |||   |||||| ||||||
                                TGG   AGGTAA TAGATA
                                  ATA     C
GAM628  MGEA6     3'  CCACTCATGTCTATTTAC    16050       CATTA
                                CCACTC    TCTATTTAC
                                ||||||    |||||||||
                                GGTGAG    AGATAAATG
                                   TAC__
GAM628  SE57-1    3'  TACACTCTCCCTTCTATTTA  16051      CA    ATTA
                                TACAC  CTCC    TCTATTTA
                                |||||  ||||    ||||||||
                                ATGTG  GAGG    AGATAAAT
                                   A_    GA__
GAM628  LOC120939 3'  ACATCACTCCACTCCTATTTA  16052     C        A
                                ACA CACTCCATT TCTATTTA
                                ||| |||||||||| ||||||||
                                TGT GTGAGGTGA GGATAAAT
                                  A        _
GAM628  LOC220573 3'  CCACTCCTACCTATTT      16053        AT
                                CCACTCC  TATCTATTT
                                |||||||  |||||||||
                                GGTGAGG  ATGGATAAA
                                     __
GAM629  HSPA4     3'  TATTCATGAACATACTTTCAG  16056          GCCGA
                                TATTTATGAA     TTTCAG
                                ||||||||||     ||||||
                                ATAAGTACTT     AAAGTC
                                     GTATG
GAM629  MKI67     3'  TTTATGAAGCCGATTCAG     16057             T
                                TTTATGAAGCCGATT CAG
                                |||||||||||||| |||
                                AAATACTTCGGCTAA GTC
                                                _
GAM629  MKKS      5'  AATGTTTATGAAGCTAATC    16058     A        CG
                                GAT TTTATGAAGC  ATT
                                ||| ||||||||||  |||
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                                TTA AAATACTTCG  TAG
                                  C         AT
GAM629  Z39IG    3'  AGATATTTATTGAGCACCA    16059          _  A_
                                AGATATTTAT GA  GCCG
                                |||||||||| ||  ||||
                                TCTATAAATA CT  TGGT
                                     A  CG
GAM629  AUTL1    3'  AGATATTTGTGAAAATAAACAT 16060         A    CCG___
           TTCAG                    AGATATTT TGAAG     ATTTCAG
                                |||||||| |||||     |||||||
                                TCTATAAA ACTTT     TAAAGTC
                                     C    TATTTG
GAM629  KIAA0694 3'  AGATGTTTATGAAGATGACC   16061      A       CC
                                AGAT TTTATGAAG  GATT
                                |||| |||||||||  ||||
                                TCTA AAATACTTC  CTGG
                                  C        TA
GAM629  LOC116143 3'  TATTTATGAAGGTTAATTCAG  16062          CCGAT
                                TATTTATGAAG    TTCAG
                                ||||||||||    |||||
                                ATAAATACTTC    AAGTC
                                      CAATT
GAM629  LOC51333  3'  ATATTTATGGGCCCTTTCAG   16063         AA   GA
                                ATATTTATG  GCC  TTTCAG
                                |||||||||  |||  ||||||
                                TATAAATAC  CGG  AAAGTC
                                     C_   G_
GAM630  APOL1    3'  CAGCTCTTTCTTTTCCTGGCCT 16066      _ _____  C    C   III
           TCTCG                    CTCTT C    CC GGCCT CTC   G
                                ||||| |    || ||||| |||   |
                                GAGAA G    GG CCGGA GAG   C
                                   A AAAA  A     A   III
GAM630  ARSD     3'  GCGGCTCTTCCTCTCCT     16067    A       CCGGC
                                GC GCTCTTCC    CTCCT
                                || ||||||||    |||||
                                CG CGAGAAGG    GAGGA
                                 C       A_____
GAM630  CDH5     3'  TCTCAGCTCTTCCAGGCCTTCT 16068    G        CC    C
           C                     TC CAGCTCTTCC  GGCCT CTC
                                || ||||||||||  ||||| |||
                                AG GTCGAGAAGG  CCGGA GAG
                                 A         T_    A
GAM630  COL1A1   3'  TCGTGGCCCTTCCTGACTCTCC 16069     CA       CC  _
           TC                     TCG  GCTCTTCC  GGC CTCCTC
                                |||  ||||||||  ||| ||||||
                                AGC  CGGGAAGG  CTG GAGGAG
                                  AC       A_   A
GAM630  EYA4     5'  CCGCAGCTCTTTCCCCCTC    16070          C   GG
                                TCGCAGCTCTT CCC  CCTC
                                |||||||||| |||  ||||
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                                GGCGTCGAGAA GGG  GGAG
                                      A  __
GAM630  HUNK     5'  TCGCAGCTCCTCCTCCCCAGGC 16071          ___      C  C
             TCTTC                   TCGCAGCTCT   TCCCCGG CTC TC
                                |||||||||   |||||| ||| ||
                                AGCGTCGAGG   AGGGGTC GAG AG
                                      AGG      C   A
GAM630  IGFBP5   5'  GCAGCTCTTTCCTAGCTCT   16072         C  CG  _
                                GCAGCTCTT CC  GC CT
                                ||||||||| ||  || ||
                                CGTCGAGAA GG  CG GA
                                      A  AT  A
GAM630  IRTA1    3'  TCCAGCTCTTCTGATGTCCTC  16073    G       CCC  CC
                                TC CAGCTCTTC   GG  TCCTC
                                || |||||||||   ||  |||||
                                AG GTCGAGAAG   CT  AGGAG
                                 _       A__  AC
GAM630  NFATC1   3'  TCGCAGCCTTCCAGCATTCTC  16074       T    CC   CTC
                                TCGCAGC CTTCC  GGC   CTC
                                ||||||| |||||  |||   |||
                                AGCGTCG GAAGG  TCG   GAG
                                    _    __  TAA
GAM630  PBX2     3'  TCTGGCTTTTTGCAACCTCCTC 16075    GCA   C  CCC
                                TC   GCT TT   CGGCCTCCTC
                                ||   ||| ||   ||||||||||
                                AG   CGA AA   GTTGGAGGAG
                                 AC_   A  AC_
GAM630  PNUTL1   3'  GCAGCCTCTGGCCTCCT     16076      T   CCCC
                                GCAGC CTT    GGCCTCCT
                                ||||| |||    ||||||||
                                CGTCG GAG    CCGGAGGA
                                   _   A____
GAM630  PSD      5'  TCGATGGCCGAGTCGGCCTCCT 16077     CA_   CTTCCC
             C                   TCG   GCT     CGGCCTCCTC
                                |||   |||     ||||||||||
                                AGC   CGG     GCCGGAGGAG
                                  TAC   CTCA__
GAM630  SDC4     3'  TCTCAGCTCTTTTCCCCATCCT 16078    G      __     G
             C                   TC CAGCTCT  TCCCCG CCTC
                                || |||||||  |||||| ||||
                                AG GTCGAGA  AGGGGT GGAG
                                 A      AA     A
GAM630  SLC8A2   3'  TCGCTTTGATTCCCGGCCTCCT 16079      AGCTCTTC
             C                   TCGC       CCCGGCCTCCTC
                                ||||       ||||||||||||
                                AGCG       GGGCCGGAGGAG
                                  AAACTAA_
GAM630  SSPN     3'  CAGCTCTTCCCCCACCTC    16080           G
                                CAGCTCTTCCCC GCCTC
                                |||||||||||| |||||
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                                GTCGAGAAGGGG TGGAG
                                      G
GAM630  SYK      5'  CCGCGGCTCTTCCTCCTC    16081      A       CCGG
                                TCGC GCTCTTCC    CCTC
                                |||| ||||||||    ||||
                                GGCG CGAGAAGG    GGAG
                                  C       A___
GAM630  TACC1    5'  CCGCGTCCTCCTCGGCCTCCTC 16082      AGC     C
                                TCGC   TCTTCC CGGCCTCCTC
                                ||||   |||||| ||||||||||
                                GGCG   AGGAGG GCCGGAGGAG
                                  C__     A
GAM630  TRIM34   5'  GCAGCTCTCTCTGCTCCTC    16083          CCCCG  C
                                GCAGCTCTT    GC TCCTC
                                |||||||||    || |||||
                                CGTCGAGAG    CG AGGAG
                                      AGA__  _
GAM630  APOL2    3'  CAGCTCTTTCTTTTCCTGGCCT 16066      _ _____  C    C   III
           TCTCG                    CTCTT C    CC GGCCT CTC   G
                                |||||| |    || ||||| |||   |
                                GAGAA G    GG CCGGA GAG   C
                                   A AAAA  A     A   III
GAM630  APOL3    3'  CAGCTCTTTCTTTTCCTGGCCT 16066      _ _____  C    C   III
           TCTCG                    CTCTT C    CC GGCCT CTC   G
                                |||||| |    || ||||| |||   |
                                GAGAA G    GG CCGGA GAG   C
                                   A AAAA  A     A   III
GAM630  APOL4    3'  CAGCTCTTTCTTTTCCTGGTCT 16084      _ _____  C  C  C   III
           TCTCG                    CTCTT C    CC GG CT CTC   G
                                |||||| |    || || || |||   |
                                GAGAA G    GG CC GA GAG   C
                                   A AAAA  A  A  A   III
GAM630  ARHGEF4  5'  CCGCGCGGACCCTGGCCTCCT  16085      A  TCTT   C
                                TCGC GC    CCC GGCCTCCT
                                |||| ||    ||| ||||||||
                                GGCG CG    GGG CCGGAGGA
                                  _  CCT_   A
GAM630  ARL1     5'  GCAGCTCCGAGGCGGTTTCCTC 16086        TCCC   CC
                                GCAGCTCT    CGG  TCCTC
                                |||||||    |||  |||||
                                CGTCGAGG    GCC  AGGAG
                                     CTCC   AA
GAM630  C20orf38 3'  TCACAGCTCTTAAAATGGTTTC 16087          CCCC_  CC
           CT                    TCGCAGCTCTT    GG  TCCT
                                ||||||||||    ||  ||||
                                AGTGTCGAGAA    CC  AGGA
                                      TTTTA  AA
GAM630  C20orf51 5'  CCAAGCCTCCCTGGTCTCCTC  16088     C    CT    C  C
                                TCG AGCT  TCCC GG CTCCTC
                                |||  ||||  |||| ||  ||||||
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                                GGT TCGG  AGGG CC GAGGAG
                                  _   __   A  A
GAM630  CDC91L1   3'  TCCCAGTTCTTCCCCATAGGCC 16089    G   C      ___
             T                    TC CAG TCTTCCCC   GGCCT
                                  || ||| ||||||||   |||||
                                  AG GTC AGAAGGGG   CCGGA
                                   G   A       TAT
GAM630  CTRP5     5'  CCGGCTCCCCGATGGCCTCCT  16090     CA      CCC
                                  TCG  GCTCTTC   GGCCTCCT
                                  |||  |||||||   ||||||||
                                  GGC  CGAGGGG   CCGGAGGA
                                    __      CTA
GAM630  DKFZP727G051 3'  GCAGCTCTGTCCTGCTTCCT   16091         _   CCG  C
                                  GCAGCTCT TCC   GC TCCT
                                  |||||||| |||   || ||||
                                  CGTCGAGA AGG   CG AGGA
                                       C   A__  A
GAM630  EFA6R     3'  GCATAAACTCTTGGCCTCCT   16092     ___     CCCC
                                  GCA   GCTCTT    GGCCTCCT
                                  |||   ||||||    ||||||||
                                  CGT   TGAGAA    CCGGAGGA
                                    ATT     ____
GAM630  FBP17     5'  TCGCAGCTCCTCGCCCGGGGTC 16093           _    C__
             TCCTC                    TCGCAGCTCTTC CCCGG   CTCCTC
                                  |||||||||||| |||||   ||||||
                                  AGCGTCGAGGAG GGGCC   GAGGAG
                                         C     CCA
GAM630  FER1L4    3'  GCCGTTTCTCGGCCTCCTC    16094     C_   CC
                                  GCT  TTC  CGGCCTCCTC
                                  |||  |||  ||||||||||
                                  CGG  AAG  GCCGGAGGAG
                                    CA   A_
GAM630  FLJ10378  5'  CCCGTCCTCGGCCTCTTC     16095     T   C      C
                                  CTC TCC CGGCCTC TC
                                  ||| ||| ||||||| ||
                                  GGG AGG GCCGGAG AG
                                    C   A      A
GAM630  FLJ14641  3'  TCCCAGTCCCCGGCCTCCTC   16096    G   CTCT
                                  TC CAG    TCCCCGGCCTCCTC
                                  || |||    ||||||||||||||
                                  AG GTC    AGGGGCCGGAGGAG
                                   G   ____
GAM630  FLJ21687  3'  TCGCAGCTTGTCTTCACCGTTC 16097        ___     C   G_
             CTC                     TCGCAGC   TCTTC CCG  CCTC
                                  |||||||   ||||| |||  ||||
                                  AGCGTCG   AGAAG GGC  GGAG
                                      AAC    T   AA
GAM630  FLJ22501  5'  TCCAGCTCTTCCTCATCCTC   16098    G        C  G
                                  TC CAGCTCTTCC CG CCTC
                                  || |||||||||| || ||||
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                                AG GTCGAGAAGG GT GGAG
                                 _       A  A
GAM630  FLJ23112  3'  GCACTCCTGACTGGCCTCCTC  16099    G    CCCC
                                GCA CTCTT   GGCCTCCTC
                                ||| |||||   |||||||||
                                CGT GAGGA   CCGGAGGAG
                                  _   CTGA
GAM630  HCNGP     3'  TCACAGCCTGGCTTCC     16100       T  TCCCC  C
                                TCGCAGC CT    GGC TCC
                                ||||||| ||    ||| |||
                                AGTGTCG GA    CCG AGG
                                   _ _____  A
GAM630  HSA277841 3'  GCAGCCCTTTACTTCCT    16101        CCCCG  C
                                GCAGCTCTT    GC TCCT
                                |||||||||    || ||||
                                CGTCGGGAA    TG AGGA
                                     A____  A
GAM630  HT002     3'  GCAGCTCTTCCAGCCTTGTTTC 16102         CC  _____
           CTC                    GCAGCTCTTCC  GGCC    TCCTC
                                |||||||||||  ||||    |||||
                                CGTCGAGAAGG  TCGG    AGGAG
                                      __   AACAA
GAM630  KIAA0240  3'  TCATGGCTCTATCCCGGCCTCC 16103    CA    TC
           TC                     TCG  GCTCT  CCCGGCCTCCTC
                                |||  |||||  ||||||||||||
                                AGT  CGAGA  GGGCCGGAGGAG
                                  AC    TA
GAM630  KIAA0451  3'  TCGGCTTGGGATGGCCTCCTC  16104    CA   CTTCCCC
                                TCG  GCT     GGCCTCCTC
                                |||  |||     |||||||||
                                AGC  CGA     CCGGAGGAG
                                  __  ACCCTA_
GAM630  KIAA1078  3'  GCAGCTCTTTACAACACCTCCT 16105        CCCCG_
           C                     GCAGCTCTT     GCCTCCTC
                                |||||||||     ||||||||
                                CGTCGAGAA     TGGAGGAG
                                     ATGTTG
GAM630  KIAA1203  3'  TCACAGCTCTTCTCTGCTC   16106         CCCG  C
                                TCGCAGCTCTTC   GC TC
                                ||||||||||||   || ||
                                AGTGTCGAGAAG   CG AG
                                     AGA_ _
GAM630  KIAA1211  5'  TCCAGCTCTTCCCATCCCTC   16107    G       CGG
                                TC CAGCTCTTCCC   CCTC
                                || ||||||||||   ||||
                                AG GTCGAGAAGGG   GGAG
                                  _        TAG
GAM630  KIAA1274  3'  GCAGCTCCAGGCCTTGGCTTCC 16108       TC_  C_   C
           TC                     GCAGCTCT   CC  GGC TCCTC
                                ||||||||   ||  ||| |||||
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                                CGTCGAGG  GG  CCG AGGAG
                                    TCC  AA  A
GAM630  KIAA1277 3' TCGGGGCTTTTCCTGCCTC  16109    CA  C   CCG
                                TCG  GCT TTCC  GCCTC
                                |||  ||| ||||  |||||
                                AGC  CGA AAGG  CGGAG
                                  CC  A   A__
GAM630  KIAA1280 5' TCGTAGTCTCGCGCCTCCT  16110    C  C  TCCC  _
                                TCG AG TCT   CG GCCTCCT
                                ||| || |||   || |||||||
                                AGC TC AGA   GC CGGAGGA
                                  A  _  ____  G
GAM630  KIAA1377 5' GCAGCTCCGGCTTCCT     16111      CTTCC    C
                                GCAGCT    CCGGC TCCT
                                ||||||    ||||| ||||
                                CGTCGA    GGCCG AGGA
                                   _____    A
GAM630  KIAA1911 5' GCAGTTCTTATCTAACCTCCT 16112     C   CCCC
                                GCAG TCTT   GGCCTCCT
                                |||| ||||   ||||||||
                                CGTC AGAA   TTGGAGGA
                                  A   TAGA
GAM630  MSP     3'  TCCCAGCTCTTCCTTGGGCTC 16113    G       CC  C
                                TC CAGCTCTTCC  GG CTC
                                || ||||||||||  || |||
                                AG GTCGAGAAGG  CC GAG
                                 G        AA  C
GAM630  MYH7B   5'  GCAGCTCTGGCTTCCT     16114       TCCCC   C
                                GCAGCTCT    GGC TCCT
                                ||||||||    ||| ||||
                                CGTCGAGA    CCG AGGA
                                    _____  A
GAM630  NKX2C   3'  TCCTAGCCTCCTGGTCTCCTC 16115   GC   CT   CC  C
                                TC  AGCT  TCC  GG CTCCTC
                                ||  ||||  |||  || ||||||
                                AG  TCGG  AGG  CC GAGGAG
                                 GA   __   A_  A
GAM630  PC326   5'  TCGCAACTCTTCTCCTTCTC  16116          C  GGC
                                TCGCAGCTCTTC CC   CTC
                                ||||||||||| ||   |||
                                AGCGTTGAGAAG GG   GAG
                                      A  AA_
GAM630  PGR1    3'  TCCAGCTCTTCTCCAGATTC  16117   G       C   CC
                                TC CAGCTCTTC CCGG  TC
                                || |||||||| ||||  ||
                                AG GTCGAGAAG GGTC  AG
                                 _       A   TA
GAM630  PHT2    5'  CCGCGGCTCTTCTCTCCT    16118     A     CCCGGC
                                TCGC GCTCTTC     CTCCT
                                |||| |||||||     |||||
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                                GGCG CGAGAAG     GAGGA
                                  C      A_____
GAM630  RBM14    3'  ACCCTTTCCTGGCCTCCT    16119       C  C
                                GCTCTT CC GGCCTCCT
                                |||||| || ||||||||
                                TGGGAA GG CCGGAGGA
                                   A  A
GAM630  TCEB3L   5'  TCGCAGCTCTGTCTTTGGGGC  16120          _  CCC__
                                TCGCAGCTCT TC    GGC
                                |||||||||| ||    |||
                                AGCGTCGAGA AG    CCG
                                      C  AAACC
GAM630  TRIAD3   3'  TCGCAGCTCTCTCCGAACTC   16121          CC   GC
                                TCGCAGCTCTT  CCG  CTC
                                |||||||||||  |||  |||
                                AGCGTCGAGAG  GGC  GAG
                                      A_   TT
GAM630  TTTY9    3'  GCACTCTTAACCTCCT     16122     G    CCCC
                                GCA CTCTT    GGCCTCCT
                                ||| |||||    ||||||||
                                CGT GAGAA    TTGGAGGA
                                  _    _____
GAM630  LOC115073 5'  CAGCTCTTCTAGCATCTTC   16123        CCC   C  C
                                CAGCTCTTC   GGC TC TC
                                |||||||||   ||| || ||
                                GTCGAGAAG   TCG AG AG
                                     A__   T  A
GAM630  LOC129676 5'  AGTCTGTCCCTGGCCTCCTC   16124    C   _   C
                                AG TCT TCCC GGCCTCCTC
                                || ||| |||| |||||||||
                                TC AGA AGGG CCGGAGGAG
                                  _  C    A
GAM630  LOC130355 5'  GCAACTTCCGGCCTCT      16125       CTTCC       C
                                GCAGCT     CCGGCCTC T
                                ||||||     |||||||| |
                                CGTTGA     GGCCGGAG A
                                   A_____       A
GAM630  LOC143153 3'  GCAGCTCTTCCCCAAGCTCTTC 16126             C   C
                                GCAGCTCTTCCCCGG CTC TC
                                |||||||||||||| ||| ||
                                CGTCGAGAAGGGGTT GAG AG
                                      C   A
GAM630  LOC143154 3'  GCAGCTCTTCCCCAAGCTCTTC 16126             C   C
                                GCAGCTCTTCCCCGG CTC TC
                                |||||||||||||| ||| ||
                                CGTCGAGAAGGGGTT GAG AG
                                      C   A
GAM630  LOC145662 3'  AGTTCTTCCCCACCTTCTC   16127    C       G   C
                                AG TCTTCCCCG CCT CTC
                                || ||||||||| ||| |||
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                                TC AGAAGGGGT GGA GAG
                                 A        _  A
GAM630  LOC147004 3'  TCCAGCTCTTTCAACTCT    16128    G      CCC   _
                                TC CAGCTCTT   CGGC CT
                                || ||||||||   |||| ||
                                AG GTCGAGAA   GTTG GA
                                 _       A__    A
GAM630  LOC147077 3'  TCACAGCTGAACGGCCTCCT   16129        CTTCCC
                                TCGCAGCT     CGGCCTCCT
                                ||||||||     |||||||||
                                AGTGTCGA     GCCGGAGGA
                                     CTT___
GAM630  LOC148710 3'  TCGCCACCTCTGGCCTCCT    16130     _ G    TCCCC
                                TCGC A CTCT     GGCCTCCT
                                |||| | ||||     ||||||||
                                AGCG T GAGA     CCGGAGGA
                                  G G   _____
GAM630  LOC149422 3'  GCTCTTCCCACAGAGCCTC    16131         _ __
                                GCTCTTCCC C  GGCCTC
                                ||||||||| |  ||||||
                                CGAGAAGGG G  TCGGAG
                                     T TC
GAM630  LOC149711 5'  GCCCATTTCCCTGGCCTCCTC  16132      __     C
                                GCTC  TTCCC GGCCTCCTC
                                ||||  ||||| |||||||||
                                CGGG  AAGGG CCGGAGGAG
                                  TA     A
GAM630  LOC149935 3'  GCAGCTCCTTGGTCTTCTC    16133         CCCC  C  C
                                GCAGCTCTT    GG CT CTC
                                |||||||||    || || |||
                                CGTCGAGGA    CC GA GAG
                                     A___  A  A
GAM630  LOC150095 5'  TCGCAGCTCCTTGCTCCT     16134          TCCCCG  C
                                TCGCAGCTCT     GC TCCT
                                ||||||||||     || ||||
                                AGCGTCGAGG     CG AGGA
                                     AA____  _
GAM630  LOC151429 5'  CCGCACCCCTTGGCTTCT     16135      G    CCCC   C  C
                                TCGCA CTCTT    GGC TC T
                                ||||| |||||    ||| || |
                                GGCGT GGGAA    CCG AG A
                                  G     ____   A  A
GAM630  LOC154860 3'  GCAGCTCTGCGCGCTCCT     16136         TCCCCG  _
                                GCAGCTCT     GC CTCCT
                                ||||||||     || |||||
                                CGTCGAGA     CG GAGGA
                                     CG____  C
GAM630  LOC157860 5'  TCATAGCTTTTTCCCGTCCCCT 16137     C   C  C   GC
          C                      TCG AGCT TT CCCG  CTCCTC
                                ||| |||| || ||||  ||||||
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                                AGT TCGA AA GGGC  GGGGAG
                                  A   A A   A_
GAM630  LOC158055 3'  CCGCGGCTCTTCCCTGCCC   16138     A       CG
                                TCGC GCTCTTCCC  GCCT
                                |||| |||||||||  ||||
                                GGCG CGAGAAGGG  CGGG
                                  C       A_
GAM630  LOC163126 5'  TCGCGCCTTCCCCGGCCTCCTC 16139     A  T
                                TCGC GC CTTCCCCGGCCTCCTC
                                |||| || ||||||||||||||||
                                AGCG CG GAAGGGGCCGGAGGAG
                                  _ _
GAM630  LOC164714 5'  TCGCTGCTCCCGGCCTCCT   16140     A  CTTC
                                TCGC GCT   CCCGGCCTCCT
                                |||| |||   ||||||||||
                                AGCG CGA   GGGCCGGAGGA
                                  A  ____
GAM630  LOC199221 5'  CCGTAGCTCTTCTAACACCTCT 16141    C      CCCG    C
          TC                      TCG AGCTCTTC   GCCTC TC
                                ||| ||||||||   ||||| ||
                                GGC TCGAGAAG   TGGAG AG
                                  A      ATTG    A
GAM630  LOC201245 3'  GCAGCTCTTTTCCTCCAAGTCC 16142        __  _   CC
          TC                      GCAGCTCT  TCC CCGG  TCCTC
                                |||||||| ||| ||||  |||||
                                CGTCGAGA  AGG GGTT  AGGAG
                                    AA  A   C_
GAM630  LOC201705 3'  GCAGCACTGGCCTCCTC    16143      T  TCCCC
                                GCAGC CT    GGCCTCCTC
                                ||||| ||    |||||||||
                                CGTCG GA    CCGGAGGAG
                                  T  ______
GAM630  LOC219294 3'  GCAGCTCTTCCCCAAGCTCTTC 16126             C   C
                                GCAGCTCTTCCCCGG CTC TC
                                |||||||||||||| ||| ||
                                CGTCGAGAAGGGGTT GAG AG
                                         C   A
GAM630  LOC219295 3'  GCAGCTCTTCCCCAAGCTCTTC 16126             C   C
                                GCAGCTCTTCCCCGG CTC TC
                                |||||||||||||| ||| ||
                                CGTCGAGAAGGGGTT GAG AG
                                         C   A
GAM630  LOC219686 5'  CCGGCGCCTCGGCCTCCT   16144    CA  TCTT  C
                                TCG  GC   CC CGGCCTCCT
                                |||  ||   || |||||||||
                                GGC  CG   GG GCCGGAGGA
                                  __  C___  A
GAM630  LOC219686 5'  CCGGCGCCTCGGCCTCCT   16144    CA  TCTT  C
                                TCG  GC   CC CGGCCTCCT
                                |||  ||   || |||||||||
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                                GGC  CG    GG GCCGGAGGA
                                  __  C___  A
GAM630  LOC220045 3'  GCAGCTCTTCTCTCCTTCTC   16145          CCCGG   C
                                GCAGCTCTTC     CCT CTC
                                ||||||||||     ||| |||
                                CGTCGAGAAG     GGA GAG
                                     AGA__   A
GAM630  LOC254381 5'  TCCAGCTCTTCCTGTGGGTCTC 16146    G        CC__  C
                                TC CAGCTCTTCC    GG CTC
                                || ||||||||||    || |||
                                AG GTCGAGAAGG    CC GAG
                                  _        ACAC  A
GAM630  LOC255452 3'  CCGCGCGGACCCTGGCCTCCT  16085      A  TCTT   C
                                TCGC GC    CCC GGCCTCCT
                                |||| ||    ||| ||||||||
                                GGCG CG    GGG CCGGAGGA
                                  _  CCT_   A
GAM630  LOC256158 5'  GCAGGACCCGGCCTCCT     16147      CTCTTC
                                GCAG     CCCGGCCTCCT
                                ||||     ||||||||||
                                CGTC     GGGCCGGAGGA
                                  CT_____
GAM630  LOC256310 3'  GCTCCTCCTTGGCCTTCTC    16149         CC    C
                                GCTCTTCC  GGCCT CTC
                                ||||||||  ||||| |||
                                CGAGGAGG  CCGGA GAG
                                     AA    A
GAM630  LOC256310 3'  CGCAGCTGCTCGGCCTCCTC   16148         _  TCCC
                                CGCAGCT CT    CGGCCTCCTC
                                ||||||| ||    ||||||||||
                                GCGTCGA GA    GCCGGAGGAG
                                    C  _____
GAM630  LOC90589  5'  TCCAGGTGTCCTGGCCTCCTC  16150    G   CTCT   CC
                                TC CAG    TCC  GGCCTCCTC
                                || |||    |||  |||||||||
                                AG GTC    AGG  CCGGAGGAG
                                  _   CAC_   A_
GAM630  LOC92078  3'  TCACAGCAGGCTGGCCTCCT   16151        TCTTCCCC
                                TCGCAGC       GGCCTCCT
                                |||||||       ||||||||
                                AGTGTCG       CCGGAGGA
                                    TCCGA____
GAM631  ACADM     5'  GCGGGGTGGCAGCGGTCCCCGG 16154     AGC  _ _   GA
          C                      GCG   GTG C GCGG  TCCCCGGC
                                 |||   ||| | ||||  ||||||||
                                 CGC   CAC G CGCC  AGGGGCCG
                                   CC_   C T   __
GAM631  AMPD3     5'  GCGCAGCGCTGCGGATCCCCGG 16155     _    GC    G
          C                      GCG AGCGT  GCGG ATCCCCGGC
                                 ||| |||||  |||| |||||||||
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                                CGC TCGCG  CGCC TAGGGGCCG
                                  G    A_   _
GAM631  ATBF1   5' GCTGGCGTCCGGGTCCCCGGC  16156   GA   GCG   A
                                GC  GCGT   CGGG TCCCCGGC
                                ||  ||||   |||| ||||||||
                                CG  CGCA   GCCC AGGGGCCG
                                 AC   G__   _
GAM631  CALU    3' GAGGTATGAGGATCCCTGG   16157    C   CGC      C
                                GAG GTG   GGGATCCC GG
                                ||| |||   |||||||| ||
                                CTC CAT   TCCTAGGG CC
                                  _  AC_      A
GAM631  FGFR1   5' CGGGCGTGTGCCCGCGTCCCCG 16158   A   ____   GGA
          GC                    CG GCGTG   CGCG   TCCCCGGC
                                || |||||   ||||   ||||||||
                                GC CGCAC   GCGC   AGGGGCCG
                                 C    ACGG   ___
GAM631  FGFR1   5' CGGGCGTGTGCCCGCGTCCCCG 16158   A   ____   GGA
          GC                    CG GCGTG   CGCG   TCCCCGGC
                                || |||||   ||||   ||||||||
                                GC CGCAC   GCGC   AGGGGCCG
                                 C    ACGG   ___
GAM631  FGFR1   5' CGGGCGTGTGCCCGCGTCCCCG 16158   A   ____   GGA
          GC                    CG GCGTG   CGCG   TCCCCGGC
                                || |||||   ||||   ||||||||
                                GC CGCAC   GCGC   AGGGGCCG
                                 C    ACGG   ___
GAM631  FGFR1   5' CGGGCGTGTGCCCGCGTCCCCG 16158   A   ____   GGA
          GC                    CG GCGTG   CGCG   TCCCCGGC
                                || |||||   ||||   ||||||||
                                GC CGCAC   GCGC   AGGGGCCG
                                 C    ACGG   ___
GAM631  FGFR1   5' CGGGCGTGTGCCCGCGTCCCCG 16158   A   ____   GGA
          GC                    CG GCGTG   CGCG   TCCCCGGC
                                || |||||   ||||   ||||||||
                                GC CGCAC   GCGC   AGGGGCCG
                                 C    ACGG   ___
GAM631  FGFR1   5' CGGGCGTGTGCCCGCGTCCCCG 16158   A   ____   GGA
          GC                    CG GCGTG   CGCG   TCCCCGGC
                                || |||||   ||||   ||||||||
                                GC CGCAC   GCGC   AGGGGCCG
                                 C    ACGG   ___
GAM631  FOXG1B  5' GCGGGCGGCGCGGCGACCGG  16159    A  T   _ TCC
                                GCG GCG GCGCGG GA  CCGG
                                ||| ||| |||||| ||  ||||
                                CGC CGC CGCGCC CT  GGCC
                                  C  _    G ___
GAM631  HTR2C   5' GACCGTGCGCCCCCCGG    16160   G    GGGA
                                GA CGTGCGC   TCCCCGG
                                || |||||||   |||||||
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                                CT GCACGCG   GGGGGCC
                                 G     _____
GAM631  KCNS2   5' GCGAGTGTGTGCGCCCGG   16161     C  C  GGATC
                                GCGAG GTG GCG    CCCGG
                                ||||| ||| |||    |||||
                                CGCTC CAC CGC    GGGCC
                                  A  A  ______
GAM631  MGAT3   5' GCGGCCCCCGGGGTCCCCGGC 16162    T  G__   A
                                GCG GC   CGGG TCCCCGGC
                                ||| ||   |||| ||||||||
                                CGC CG   GCCC AGGGGCCG
                                  _ GGG   C
GAM631  NAGLU   5' GAGCGTGTGACCCCGG     16163       CGCGG  T
                                GAGCGTG    GA CCCCGG
                                |||||||    || ||||||
                                CTCGCAC    CT GGGGCC
                                    A_____ _
GAM631  NRIP1   5' GCGGGCGGGCGTGGGGCCGG  16164    A  T  C  ATCC
                                GCG GCG GCG GGG   CCGG
                                ||| ||| ||| |||   ||||
                                CGC CGC CGC CCC   GGCC
                                  C  C  A  C___
GAM631  PCDH7   5' GCGGGCGGAGAATCCCCGG   16165    T  C
                                GCG GCG GGGATCCCCGG
                                ||| ||| ||||||||||
                                CGC CGC TCTTAGGGGCC
                                  C  C
GAM631  PCDH7   5' GCGGGCGGAGAATCCCCGG   16165    T  C
                                GCG GCG GGGATCCCCGG
                                ||| ||| ||||||||||
                                CGC CGC TCTTAGGGGCC
                                  C  C
GAM631  PCDH7   5' GCGGGCGGAGAATCCCCGG   16165    T  C
                                GCG GCG GGGATCCCCGG
                                ||| ||| ||||||||||
                                CGC CGC TCTTAGGGGCC
                                  C  C
GAM631  SLC6A3  3' GCGAGGTGCGCTCCCG     16166      C    GGGATC
                                GCGAG GTGCGC     CCCG
                                ||||| ||||||     ||||
                                CGCTC CACGCG     GGGC
                                  _     A_____
GAM631  SMT3H1  5' GCGAGCGGCGCGGGGAGGCGGC 16167       T     ATCCC
                                GCGAGCG GCGCGGG    CGGC
                                ||||||| |||||||    ||||
                                CGCTCGC CGCGCCC    GCCG
                                    _      CTCC_
GAM631  ALTE    3' GCTGCCCTGCGTCCCCGGC   16168   G  ___  GGA
                                GC TGC   GCG   TCCCCGGC
                                || |||   |||   ||||||||
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                                CG ACG  CGC  AGGGGCCG
                                 _  GGA  ___
GAM631  C20orf39  5'  GCGAGCGTGCGGGGCG     16169        C  ATCCC
                                GCGAGCGTGCG GGG   CG
                                |||||||||| |||   ||
                                CGCTCGCACGC CCC   GC
                                      _  _____
GAM631  CENTG2   5'  GCGAGCGAGCGGGCCCCGG   16170      TGC   AT
                                GCGAGCG  GCGGG  CCCCGG
                                |||||||  |||||  ||||||
                                CGCTCGC  CGCCC  GGGGCC
                                   T__   __
GAM631  CNOT8    3'  GCGAGCGTGGTGGGACTGG   16171       CGC   CCCC
                                GCGAGCGTG  GGGAT  GG
                                |||||||||  |||||  ||
                                CGCTCGCAC  CCCTG  CC
                                     CA_   A___
GAM631  DKFZP434J1813 5'  GCGGTGTGCGCGGGATCCGGC  16172    AGC        CC
                                GCG  GTGCGCGGGATCC  GGC
                                |||  ||||||||||||  |||
                                CGC  CACGCGCCCTAGG  CCG
                                  CA_         __
GAM631  KIAA0620  5'  GCGGGCTGCGCGGCGCGG    16173    A  G     GATCCC
                                GCG GC TGCGCGG     CGG
                                ||| || |||||||     |||
                                CGC CG ACGCGCC     GCC
                                  C  _      GC____
GAM631  KIAA0876  5'  GCGGCGTGCGCGGCCCGG    16174    A       GATC
                                GCG GCGTGCGCGG   CCCGG
                                ||| ||||||||||   |||||
                                CGC CGCACGCGCC   GGGCC
                                  _       ____
GAM631  LRP16    5'  GCGGGCGGCGCGGGACGG    16175    A  T      TCCC
                                GCG GCG GCGCGGGA   CGG
                                ||| ||| ||||||||   |||
                                CGC CGC CGCGCCCT   GCC
                                  C  _      ____
GAM631  MGC2817  5'  GCGGGCGGCGCGGGCG     16176    A  T     ATCCC
                                GCG GCG GCGCGGG    CG
                                ||| ||| |||||||    ||
                                CGC CGC CGCGCCC    GC
                                  C  _     _____
GAM631  PSKH1    5'  GCGGGCGGCGGGCTCTTCGGC  16177    A  TGC    A  CC
                                GCG GCG   GCGGG TC  CGGC
                                ||| |||   ||||| ||  ||||
                                CGC CGC   CGCCC AG  GCCG
                                  C  ___    G  AA
GAM631  SCAP     5'  GCGGCGTGCGCGCTCTCGG   16178    A      GGA  CC
                                GCG GCGTGCGCG   TC  CGG
                                ||| |||||||||   ||  |||
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                                CGC CGCACGCGC   AG  GCC
                                  _       G__  A_
GAM631  TP53INP1  5'  GCGGGGTGCGCGGGGAAGGGAG 16179     AGC       ATCCCC
            C                    GCG   GTGCGCGGG     GGC
                                |||   |||||||||      |||
                                CGC   CACGCGCCC     TCG
                                  CC_       CTTCCC
GAM631  LOC126917 5'  GAGCGCGCGGATCTCCGGC   16180        GCG    C
                                GAGCGTGC   GGATC CCGGC
                                ||||||||   ||||| |||||
                                CTCGCGCG   CCTAG GGCCG
                                     ___     A
GAM631  LOC163412 5'  CGGCGACACAGGATCTTTGGC  16181    A   T        CCC
                                CG GCG GCGCGGGATC   GGC
                                || ||| ||||||||||   |||
                                GC CGC TGTGTCCTAG   CCG
                                 _  _        AAA
GAM631  LOC196761 3'  GCGGGCGCCCGGGATCCCCGG  16182     AGC    G
                                GCG   GTGC CGGGATCCCCGG
                                |||   |||| ||||||||||||
                                CGC   CGCG GCCCTAGGGGCC
                                  C__    G
GAM631  LOC221893 5'  GCGAGCGTGTGCAGCGGGACTG 16183        __   _      CCCC
            GC                    GCGAGC  GTGC GCGGGAT    GGC
                                ||||||  |||| |||||||    |||
                                CGCTCG  CACG CGCCCTG    CCG
                                   CA    T      A___
GAM632  ACPP     3'  GTCTTCTTTCGTAAGAA     16186     G       C
                                GTC TTCTTTCGT GGGA
                                ||| ||||||||| ||||
                                CAG AAGAAAGCA TCTT
                                  _       T
GAM632  ADAM23    3'  GTTCCTTCGTCCATTAGGGA   16187          _____
                                GTTCTTTCGTC    GGGA
                                ||||||||||     ||||
                                CAAGGAAGCAG    CCCT
                                       GTAAT
GAM632  BACH2     3'  GTTCTTTTTTTAAAAGAAGA   16188        CGTC
                                GTTCTTT    GGGAGAAGA
                                |||||||    |||||||||
                                CAAGAAA    TTTTCTTCT
                                    AAAA
GAM632  BCL9     5'  GTCCTTTTTTATGAGGAGAA   16189        C__  C
                                GTTCTTT   GT GGGAGAA
                                |||||||   || |||||||
                                CAGGAAA   TA TCCTCTT
                                    AAA  C
GAM632  CBFA2T3   3'  GTCTTCTTTCGGAGAG      16190     G       TC
                                GTC TTCTTTCG  GGGAG
                                ||| ||||||||  |||||
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                                CAG AAGAAAGC  CTCTC
                                  _     __
GAM632  GAK      3'  GTTCCTTCGGGAGGAGAA    16191         TC
                                GTTCTTTCG  GGGAGAA
                                |||||||||  |||||||
                                CAAGGAAGC  TCCTCTT
                                     CC
GAM632  PSA      3'  GTTGTTCTTTCAAAAAAGAAGA 16192    C       TC
              A                   GT GTTCTTTCG  GGGAGAAGAA
                                || |||||||||  ||||||||||
                                CA CAAGAAAGT  TTTTCTTCTT
                                 A        T_
GAM632  PSA      3'  GTTGTTCTTTCAAAAAAGAAGA 16192    C       TC
              A                   GT GTTCTTTCG  GGGAGAAGAA
                                || |||||||||  ||||||||||
                                CA CAAGAAAGT  TTTTCTTCTT
                                 A        T_
GAM632  ZNF76    3'  GTTCTTTAGGAGGAGA      16193        CGTC    A
                                GTTCTTT    GGGAG AGA
                                |||||||    ||||| |||
                                CAAGAAA    TCCTC TCT
                                   _____    C
GAM632  BTN3A1   3'  GTTCTTCCTATGGGGGAAGAA  16194         GTC   A
                                GTTCTTTC   GGG GAAGAA
                                ||||||||   ||| ||||||
                                CAAGAAGG   CCC CTTCTT
                                     ATA   C
GAM632  KIAA0545 3'  GTCGTGCCGGGAGGAG      16195       TCTTTC       A
                                GTCGT      GTCGGGAG AG
                                |||||      |||||||| ||
                                CAGCA      CGGCCCTC TC
                                  _______       C
GAM632  KIAA0853 5'  GTTCTTTTTCGACGAGGAGAAG 16196        __   T  _
                                GTTCTT  TCG CG GGAGAAG
                                ||||||  ||| || |||||||
                                CAAGAA  AGC GC CCTCTTC
                                    AA   T  T
GAM632  KIAA1280 5'  GTCGTCGGCTGGGAGAGGA    16197       CTTTC  C     A
                                GTCGTT     GT GGGAGA GA
                                ||||||     || |||||| ||
                                CAGCAG     CG CCCTCT CT
                                   C____  A     C
GAM632  LOC142941 5'  GTTTTTTTCAACAGGAGAA    16198     C_    T
                                GTT  TTTCG CGGGAGAA
                                |||  ||||| ||||||||
                                CAA  AAAGT GTCCTCTT
                                  AA     T
GAM632  LOC200734 3'  GTGCTTTGTAGAGAAGA      16199     T    C  CG
                                GT CTTT GT  GGAGAAGA
                                || |||| ||  ||||||||
```

```
                                CA GAAA CA  TCTCTTCT
                                 C   _ __
GAM632  LOC219649 5'  GTTCTGTCAAGAAGA      16200      TTC   GG
                                GTTCT   GTC  GAGAAGA
                                |||||   |||  |||||||
                                CAAGA   CAG  TTCTTCT
                                  ____   __
GAM632  LOC220097 5'  GTTGTTCTTAGTGGGAGAAGA  16201    C     TC  C
                                GT GTTCTT  GT GGGAGAAGA
                                || ||||||  || |||||||||
                                CA CAAGAA  CA CCCTCTTCT
                                 A     T_  _
GAM632  LOC91828  5'  GTCGCCGTCGTCGGGGGGAGAA 16202       CTT       AGA
                                GTCGTT   TCGTCGGG   AGAA
                                ||||||   ||||||||   ||||
                                CAGCGG   AGCAGCCC   TCTT
                                   C__       CCC
GAM632  LOC92017  5'  GTCGTCTTTCATCTGGGGGAGA 16203      T      ___
            A                    GTCGT CTTTCGTC   GGGAGAA
                                |||||| ||||||||   |||||||
                                CAGCA GAAAGTAG   CCCTCTT
                                   _       ACC
GAM633  BCL2     3'  GCAGGATAGCAGCACAGGA    16206       C       CAC
                                GCAGGAT AGCAGCGC   GA
                                ||||||| ||||||||   ||
                                CGTCCTA TCGTCGTG   CT
                                   _       TC_
GAM633  PPP2R1A  3'  GCAGGATCCAGTGACCCGGGAT 16207        AG   C_   A  A
                                GCAGGATC  CAG  GCC CG GAT
                                ||||||||  |||  ||| || |||
                                CGTCCTAG  GTC  TGG GC CTA
                                   __  AC   _  C
GAM633  RECQL5   3'  ACAGGATCATTCCATGAGA   16208         GCAGCG   C
                                GCAGGATCA     CCA GAGA
                                |||||||||     ||| ||||
                                TGTCCTAGT     GGT CTCT
                                   AA_____   A
GAM633  SCN4A    3'  GCAGGATCCAGTGGCCA     16209        AG   C_
                                GCAGGATC  CAG  GCCA
                                ||||||||  |||  ||||
                                CGTCCTAG  GTC  CGGT
                                   __  AC
GAM633  VIL2     3'  GCGGGGCTGGCAGCGCCCGCTA 16210    A  ATCA      A  AG
            T                    GC GG    GCAGCGCC CG  AT
                                || ||    |||||||| ||  ||
                                CG CC    CGTCGCGG GC  TA
                                 C  CGAC       _  GA
GAM633  CENTA1   3'  GGTCAGCAGCAGCATGACG    16211    A      _  C__
                                GG TCAGCAGC GC   ACG
                                || |||||||| ||   |||
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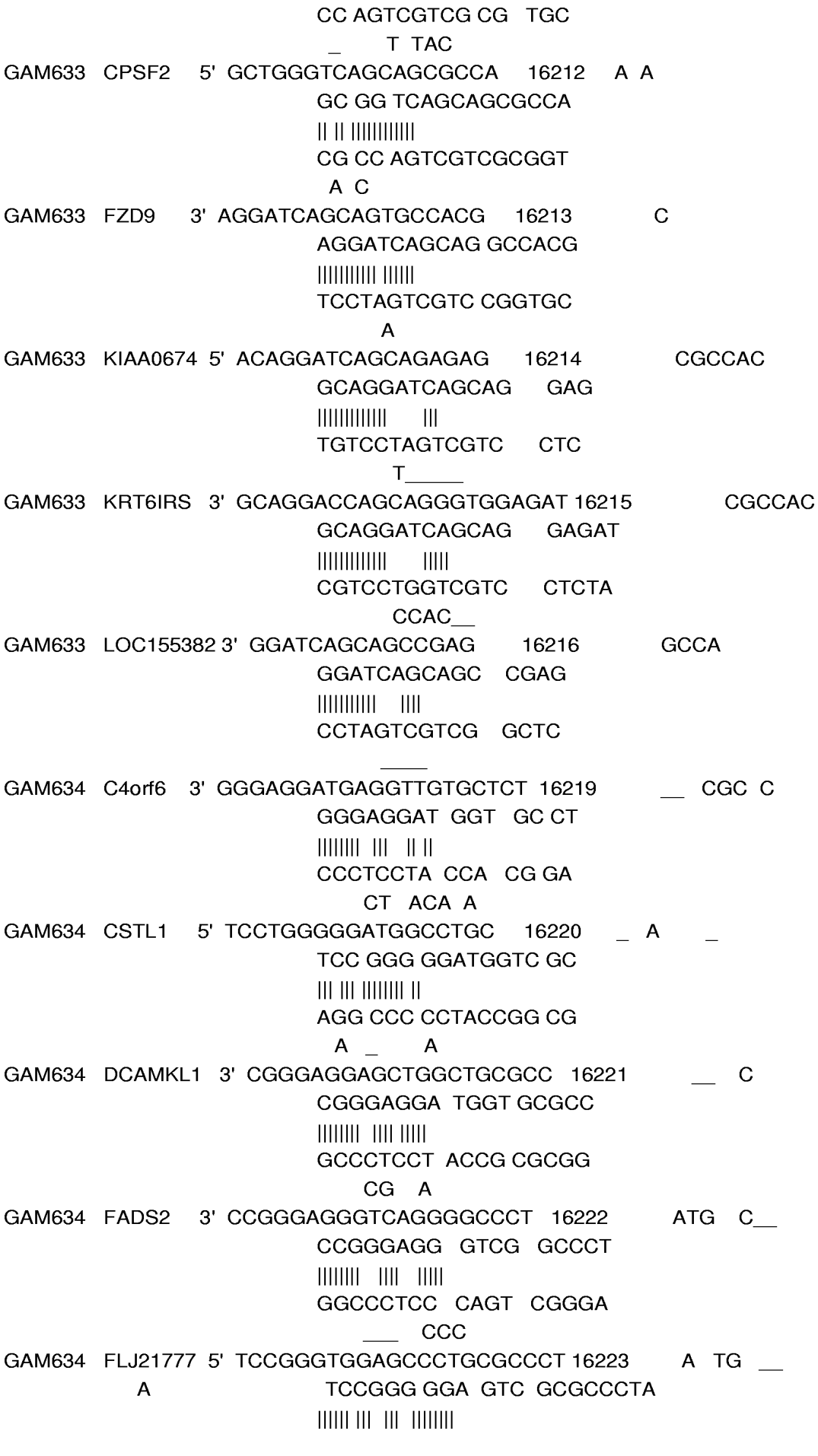
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_ T TAC
GAM633 CPSF2 5' GCTGGGTCAGCAGCGCCA 16212 A A
GC GG TCAGCAGCGCCA
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CG CC AGTCGTCGCGGT
A C
GAM633 FZD9 3' AGGATCAGCAGTGCCACG 16213 C
AGGATCAGCAG GCCACG
|||||||||| ||||||
TCCTAGTCGTC CGGTGC
A
GAM633 KIAA0674 5' ACAGGATCAGCAGAGAG 16214 CGCCAC
GCAGGATCAGCAG GAG
|||||||||||| |||
TGTCCTAGTCGTC CTC
T_____
GAM633 KRT6IRS 3' GCAGGACCAGCAGGGTGGAGAT 16215 CGCCAC
GCAGGATCAGCAG GAGAT
|||||||||||| |||||
CGTCCTGGTCGTC CTCTA
CCAC__
GAM633 LOC155382 3' GGATCAGCAGCCGAG 16216 GCCA
GGATCAGCAGC CGAG
|||||||||| ||||
CCTAGTCGTCG GCTC
____
GAM634 C4orf6 3' GGGAGGATGAGGTTGTGCTCT 16219 __ CGC C
GGGAGGAT GGT GC CT
|||||||| ||| || ||
CCCTCCTA CCA CG GA
CT ACA A
GAM634 CSTL1 5' TCCTGGGGGATGGCCTGC 16220 _ A _
TCC GGG GGATGGTC GC
||| ||| |||||||| ||
AGG CCC CCTACCGG CG
A _ A
GAM634 DCAMKL1 3' CGGGAGGAGCTGGCTGCGCC 16221 __ C
CGGGAGGA TGGT GCGCC
|||||||| |||| |||||
GCCCTCCT ACCG CGCGG
CG A
GAM634 FADS2 3' CCGGGAGGGTCAGGGGCCCT 16222 ATG C__
CCGGGAGG GTCG GCCCT
|||||||| |||| |||||
GGCCCTCC CAGT CGGGA
___ CCC
GAM634 FLJ21777 5' TCCGGGTGGAGCCCTGCGCCCT 16223 A TG __
A TCCGGG GGA GTC GCGCCCTA
|||||| ||| ||| ||||||||

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                                AGGCCC CCT  CGG  CGCGGGAT
                                   A  __  GA
GAM634  PPFIA4   3'  TCCGGGAGGAGGCAGTCCCT  16224        T  CGCG
                                TCCGGGAGGA GGT   CCCT
                                |||||||||| |||   ||||
                                AGGCCCTCCT CCG   GGGA
                                      _  TCA_
GAM634  SCAMP-4  3'  TCCGGGAGCAAGAGGGCGTCCT 16225       GAT  TC  C
                                TCCGGGAG  GG  GCG CCT
                                ||||||||  ||  ||| |||
                                AGGCCCTC  CT  CGC GGA
                                     GTT  CC  A
GAM634  LOC145547 3'  CCTGGGAGGATGGCCAGCCCT  16226   _        C
                                CC GGGAGGATGGTCG GCCCT
                                || ||||||||||||| |||||
                                GG CCCTCCTACCGGT CGGGA
                                 A         _
GAM634  LOC255042 3'  GGAAGGATGCACCCTA     16227       GGTC
                                GGGAGGAT   GCGCCCTA
                                ||||||||   ||||||||
                                CCTTCCTA   CGTGGGAT
                                     ____
GAM634  LOC256614 5'  GAGAGGAAGGCTGCCCT    16228       T  CGC
                                GGGAGGA GGT  GCCCT
                                ||||||| |||  |||||
                                CTCTCCT CCG  CGGGA
                                    T  A__
GAM635  WTAP     5'  GGCCTCGAGGCACAATGGA   16231       AA  AC
                                GGCCTCGA  CA  GTGGA
                                ||||||||  ||  |||||
                                CCGGAGCT  GT  TACCT
                                     CC  GT
GAM635  AIF1     5'  AGGTGGAGGAGACAACGTGGAA 16232    CCTC_  A
                                AGG    GA ACAACGTGGAA
                                |||    || ||||||||||
                                TCC    CT TGTTGCACCTT
                                  ACCTC  C
GAM635  FLJ11467  3'  GGCTTCAAACAACAGAA    16233    C  G      T
                                GGC TC AAACAACG GGA
                                ||| || |||||||| |||
                                CCG AG TTTGTTGT CTT
                                  A  _      _
GAM635  FLJ13322  5'  TAGAGGCCTCAGACACCCTGG  16234         AA  ACG
                                TAGAGGCCTCG  ACA  TGG
                                ||||||||||  |||  |||
                                ATCTCCGGAGT  TGT  ACC
                                      C_  GGG
GAM635  MIG      3'  GAGGCTGCAGTACGTGGAA   16235      CT  AAACA
                                GAGGC  CG    ACGTGGAA
                                |||||  ||    ||||||||
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                                CTCCG  GT    TGCACCTT
                                  AC  CA___
GAM635  TREX2    5'  TAGAGCACAACGTGG      16236      G CTCGAA
                                TAGAG C     ACAACGTGG
                                |||||  |     |||||||||
                                ATCTC G     TGTTGCACC
                                  _ _______
GAM635  TREX2    3'  TAGAGCACAACGTGG      16236      G CTCGAA
                                TAGAG C     ACAACGTGG
                                |||||  |     |||||||||
                                ATCTC G     TGTTGCACC
                                  _ _______
GAM635  TREX2    5'  TAGAGCACAACGTGG      16236      G CTCGAA
                                TAGAG C     ACAACGTGG
                                |||||  |     |||||||||
                                ATCTC G     TGTTGCACC
                                  _ _______
GAM635  LOC155382 3'  TAGAGGCCCCGGGGCACGGAA  16237          AAACA   T
                                TAGAGGCCTCG     ACG GGA
                                ||||||||||     ||| |||
                                ATCTCCGGGGC     TGC CTT
                                     CCCG_  _
GAM635  LOC199221 3'  GACCCCGAAACAACGTGG    16238
                                GGCCTCGAAACAACGTGG
                                ||||||||||||||||||
                                CTGGGGCTTTGTTGCACC

GAM635  LOC256158 5'  GAGGCCTCAAACGGG       16239         AACA   T
                                GAGGCCTCGA    ACG GG
                                ||||||||||    ||| ||
                                CTCCGGAGTT    TGC CC
                                     _____  _
GAM635  LOC90786  5'  TAGAGGCCTGGAGGCCATGG   16240        C  AACAA
                                TAGAGGCCT GA     CGTGG
                                |||||||| ||     |||||
                                ATCTCCGGA CT     GTACC
                                     C  CCG__
GAM636  APOE     3'  GGGGCGGGGACAGGGTCTCCC  16243       TC   A__   _
                                GGGGCGG  GGA   GGTC CCC
                                |||||||  |||   |||| |||
                                CCCCGCC  CCT   CCAG GGG
                                   __  GTC    A
GAM636  ATP6V0C   3'  GGGGGCGGCGGCCCC      16244        CGGAA
                                GGGGGCGGT    GGTCCC
                                |||||||||    ||||||
                                CCCCCGCCG    CCGGGG
                                     _____
GAM636  ATSV     3'  GGAGGTGGTTGGGGGTTCC    16245      C   C  AA   C
                                GGGGG GGT GG  GGT CC
                                |||||  ||| ||  |||  ||
```

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                                CCTCC CCA CC  CCA GG
                                  A  A C_  A
GAM636  AVPR2    3'  CGGAGACAGGAAGGTCCCC   16246       GTC
                                CGGGGGCG  GGAAGGTCCCC
                                ||||||||  ||||||||||
                                GCCTCTGT  CCTTCCAGGGG
                                   ___
GAM636  BCL7A    3'  GGGGCGTGCCTAAGGTCCCCC 16247      _  GG
                                GGGGCG GTC  AAGGTCCCCC
                                |||||| |||  ||||||||||
                                CCCCGC CGG  TTCCAGGGGG
                                  A  A_
GAM636  CACNG3   5'  CGGGGGCCGGCTGGTTTCCC  16248       _  C  AAGG
                                CGGGGGC GGT GG   TCCC
                                ||||||| ||| ||   ||||
                                GCCCCCG CCG CC   AGGG
                                   G  A  AA__
GAM636  CDH23    3'  GGCCTTGGAGGGTCCCCC   16249     __  A
                                GGTC  GGA GGTCCCCC
                                ||||  ||| ||||||||
                                CCGG  CCT CCAGGGGG
                                  AA  C
GAM636  CLCN7    3'  GGGGCGGTCGCAGCCTCC   16250        GAA   C
                                GGGGCGGTCG  GGTC CC
                                ||||||||||  |||| ||
                                CCCCGCCAGC  TCGG GG
                                     G__   A
GAM636  COL18A1  3'  GGGCACCCCGGGGTTCCCC  16251     G  _  AA  _
                                GGGCG TC GG  GGT CCCC
                                ||||| || ||  ||| ||||
                                CCCGT GG CC  CCA GGGG
                                  G  G  __  A
GAM636  COL18A1  3'  GGGCACCCCGGGGTTCCCC  16251     G  _  AA  _
                                GGGCG TC GG  GGT CCCC
                                ||||| || ||  ||| ||||
                                CCCGT GG CC  CCA GGGG
                                  G  G  __  A
GAM636  COL18A1  3'  GGGCACCCCGGGGTTCCCC  16251     G  _  AA  _
                                GGGCG TC GG  GGT CCCC
                                ||||| || ||  ||| ||||
                                CCCGT GG CC  CCA GGGG
                                  G  G  __  A
GAM636  COLQ     3'  GGGCATGTGGAAGGTTTTCC  16252     _  C     CC_
                                GGGCG GT GGAAGGT   CC
                                ||||| || |||||||   ||
                                CCCGT CA CCTTCCA   GG
                                  A  _      AAA
GAM636  COLQ     3'  GGGCATGTGGAAGGTTTTCC  16252     _  C     CC_
                                GGGCG GT GGAAGGT   CC
                                ||||| || |||||||   ||
```

```
                                CCCGT CA CCTTCCA   GG
                                  A _      AAA
GAM636  COLQ    3'  GGGCATGTGGAAGGTTTTCC  16252      _ C     CC_
                                GGGCG GT GGAAGGT   CC
                                ||||| || |||||||   ||
                                CCCGT CA CCTTCCA   GG
                                  A _      AAA
GAM636  COLQ    3'  GGGCATGTGGAAGGTTTTCC  16252      _ C     CC_
                                GGGCG GT GGAAGGT   CC
                                ||||| || |||||||   ||
                                CCCGT CA CCTTCCA   GG
                                  A _      AAA
GAM636  COLQ    3'  GGGCATGTGGAAGGTTTTCC  16252      _ C     CC_
                                GGGCG GT GGAAGGT   CC
                                ||||| || |||||||   ||
                                CCCGT CA CCTTCCA   GG
                                  A _      AAA
GAM636  COLQ    3'  GGGCATGTGGAAGGTTTTCC  16252      _ C     CC_
                                GGGCG GT GGAAGGT   CC
                                ||||| || |||||||   ||
                                CCCGT CA CCTTCCA   GG
                                  A _      AAA
GAM636  CUL3    5'  CGGCGGCTCCGCGGGGTCCCCC 16253    G  GGT_  AA
                                CGG GGC   CGG  GGTCCCCC
                                ||| |||   |||  ||||||||
                                GCC CCG   GCC  CCAGGGGG
                                  G  AGGC  __
GAM636  DYRK2   5'  CGGGAGCGGCGGCCGAAGGTTT 16254       T  ___   CC
          CC                    CGGGGGCGG CGG  AAGGT  CC
                                |||||||| |||  |||||  ||
                                GCCCTCGCC GCC  TTCCA  GG
                                    _  GGC   AA
GAM636  EFNA1   5'  CGGGGACGCGGGTCTCC    16255       GT  AAG  C
                                CGGGGGCG  CGG  GTC CC
                                |||||||  |||  ||| ||
                                GCCCCTGC  GCC  CAG GG
                                  __  ___  A
GAM636  FN14    3'  CAGACACCTTGGAAGGTTCCCC 16256    G  GGTC    _
                                CGGG GC   GGAAGGT CCCC
                                |||| ||   ||||||| ||||
                                GTCT TG   CCTTCCA GGGG
                                  G  GAA_     A
GAM636  FOXE1   3'  CGGGGGCGGTGGATAGAGTCC  16257       C  _ _
                                CGGGGGCGGT GGA AG GTCC
                                |||||||||| ||| || ||||
                                GCCCCCGCCA CCT TC CAGG
                                    _  A  T
GAM636  GALGT   5'  CGGGGGCGGTTGGCGGGGC   16258       C  AA_
                                CGGGGGCGGT GG  GGT
                                |||||||||| ||  |||
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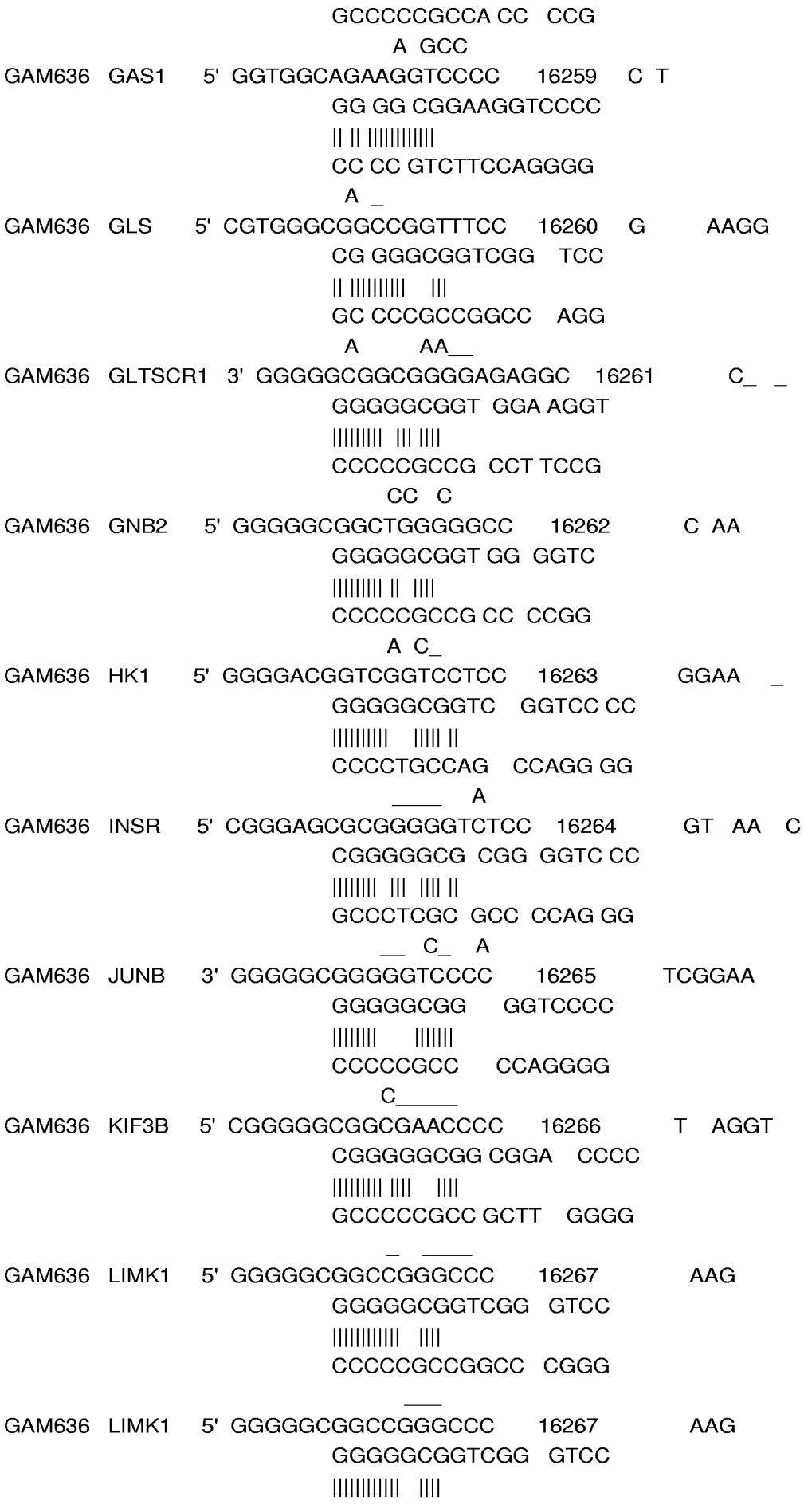
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A _
GAM636 GLS 5' CGTGGGCGGCCGGTTTCC 16260 G AAGG
CG GGGCGGTCGG TCC
|| |||||||||| |||
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A AA__
GAM636 GLTSCR1 3' GGGGGCGGCGGGGAGAGGC 16261 C_ _
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||||||||| ||| ||||
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CC C
GAM636 GNB2 5' GGGGGCGGCTGGGGGCC 16262 C AA
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||||||||| || ||||
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A C_
GAM636 HK1 5' GGGGACGGTCGGTCCTCC 16263 GGAA _
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|||||||||| ||||| ||
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_____ A
GAM636 INSR 5' CGGGAGCGCGGGGGTCTCC 16264 GT AA C
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|||||||| ||| |||| ||
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__ C_ A
GAM636 JUNB 3' GGGGGCGGGGGTCCCC 16265 TCGGAA
GGGGGCGG GGTCCCC
|||||||| |||||||
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C_____
GAM636 KIF3B 5' CGGGGGCGGCGAACCCC 16266 T AGGT
CGGGGGCGG CGGA CCCC
||||||||| |||| ||||
GCCCCCGCC GCTT GGGG
_ _____
GAM636 LIMK1 5' GGGGGCGGCCGGGCCC 16267 AAG
GGGGGCGGTCGG GTCC
|||||||||||| ||||
CCCCCGCCGGCC CGGG
___
GAM636 LIMK1 5' GGGGGCGGCCGGGCCC 16267 AAG
GGGGGCGGTCGG GTCC
|||||||||||| ||||

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                                CCCCCGCCGGCC  CGGG
                                      ___
GAM636  MAN1A2   5'  CAGGGAGGAAGGTCTCCC   16268      CGGTC     _
                                CGGGGG   GGAAGGTC CCC
                                ||||||   |||||||| |||
                                GTCCCT   CCTTCCAG GGG
                                  _____      A
GAM636  MAP3K11  3'  GGGGGCGCAGGTCCCC     16269      GTCGGA
                                GGGGGCG    AGGTCCCC
                                |||||||    ||||||||
                                CCCCCGC    TCCAGGGG
                                   G_____
GAM636  MAP4K5   5'  CGGGGGCGGCGGAGGC     16270       T   A
                                CGGGGGCGG CGGA GGT
                                ||||||||| |||| |||
                                GCCCCCGCC GCCT CCG
                                      _  _
GAM636  MOCS1    5'  CGGGGGCGGATGGTGATC    16271       TC  AA
                                CGGGGGCGG  GG  GGTC
                                |||||||||  ||  ||||
                                GCCCCCGCC  CC  CTAG
                                    TA  A_
GAM636  MYLK2    3'  CGGGGGCATGGAGGTCC     16272       GTC  A
                                CGGGGGCG   GGA GGTCC
                                ||||||||   ||| |||||
                                GCCCCCGT   CCT CCAGG
                                   A__   _
GAM636  PAX2     5'  CGGGGGCGGTCAGAGGGC    16273         A
                                CGGGGGCGGTCGGA GGT
                                |||||||||||||| |||
                                GCCCCCGCCAGTCT CCG
                                      C
GAM636  PAX2     5'  CGGGGGCGGTCAGAGGGC    16273         A
                                CGGGGGCGGTCGGA GGT
                                |||||||||||||| |||
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                                      C
GAM636  RELA     3'  GGGGGCAGTTGGAACACACCCC 16274       C   G TC
                                GGGGGCGGT GGAA G  CCCC
                                |||||||| |||| |  ||||
                                CCCCCGTCA CCTT T  GGGG
                                    A   G GT
GAM636  SDHB     5'  GGGAGGCGGCTTCCGGTTTCCC 16275    _    ___  AAGG
                                GGG GGCGGT  CGG   TCCC
                                ||| ||||||  |||   ||||
                                CCC CCGCCG  GCC   AGGG
                                  T    AAG  AA__
GAM636  SF1      5'  CGGGGGCGGCGGGGCC      16276       T  AA
                                CGGGGGCGG CGG  GGTC
                                |||||||| |||  ||||
```

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                                GCCCCCGCC GCC  CCGG
                                      _  __
GAM636  SLC1A5   3' AGGGCAGGGAAGGTCCC     16277       TC
                                GGGGCGG  GGAAGGTCCC
                                |||||||  ||||||||||
                                TCCCGTC  CCTTCCAGGG
                                     __
GAM636  SLC1A5   3' AGGGCAGGGAAGGTCCC     16277       TC
                                GGGGCGG  GGAAGGTCCC
                                |||||||  ||||||||||
                                TCCCGTC  CCTTCCAGGG
                                     __
GAM636  SPON2    5' CGGGGGCGGCGGGGGC      16278        T   AA
                                CGGGGGCGG CGG  GGT
                                ||||||||| |||  |||
                                GCCCCCGCC GCC  CCG
                                     _  C_
GAM636  THBD     3' GGGGTGCGGGGAGGGTC     16279     _   TC   A
                                GGGG GCGG  GGA GGTC
                                |||| ||||  ||| ||||
                                CCCC CGCC  CCT CCAG
                                  A   __  C
GAM636  THPO     3' GGGGGCGTTGGAAGGCC     16280       GTC
                                GGGGGCG   GGAAGGTC
                                |||||||   ||||||||
                                CCCCCGC   CCTTCCGG
                                    AA_
GAM636  TJP1     5' CGGGGGCGGACGGAAGGGCCC 16281        T     T
                                CGGGGGCGG CGGAAGG CCC
                                ||||||||| ||||||| |||
                                GCCCCCGCC GCCTTCC GGG
                                     T     C
GAM636  TMEPAI   5' CGGGGGCGGCCGGGGGGGGCTC 16282          AA__  TC
          C                      CGGGGGCGGTCGG   GG  CC
                                ||||||||||||    ||  ||
                                GCCCCCGCCGGCC   CC  GG
                                       CCCC  GA
GAM636  UPK1B    3' CAGAAGCATTGGAAGGT     16283       GTC
                                CGGGGGCG   GGAAGGT
                                ||||||||   |||||||
                                GTCTTCGT   CCTTCCA
                                    AA_
GAM636  USP6     5' GGGGGTGGCAGGTCCCC     16284      C   CGGA
                                GGGGG GGT   AGGTCCCC
                                ||||| |||   ||||||||
                                CCCCC CCG   TCCAGGGG
                                  A  _____
GAM636  AAMP     3' CAGGGGCAGGGGTCCC      16285        TCGGAA
                                CGGGGGCGG    GGTCCC
                                |||||||||    ||||||
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                                GTCCCCGTC     CCAGGG
                                     C_____
GAM636  ALDRL6   3'  GGGGGTGAGTGGGGTCCCCC  16286      C _  C  AA
                                GGGGG G GT GG  GGTCCCCC
                                ||||| | || ||  ||||||||
                                CCCCC C CA CC  CCAGGGGG
                                   A T  _  __
GAM636  C11orf11  5'  GGGGACAGGGTCCCC      16287        TCGGAA
                                GGGGGCGG     GGTCCCC
                                ||||||||     |||||||
                                CCCCTGTC     CCAGGGG
                                     _______
GAM636  C21orf93  3'  CGGGGGTGGTGCGGAAGCATTG 16288  C  _     ____ _   CIII
           TTCCCCG                  GGT CGGAAG   GT CCCC   G
                                 ||| ||||||   || ||||   |
                                 CCA GCCTTC   CA GGGG   C
                                A   C     GTAA  A   IIIC
GAM636  CECR2    5'  CGGGGGCGGCGGGGCGCTCC  16289        T   AA   CC_
                                CGGGGGCGG CGG  GGT   CC
                                ||||||||| |||  |||   ||
                                GCCCCCGCC GCC  CCG   GG
                                     _  __  CGA
GAM636  CNNM2    5'  CGGGGGCGGCGGGAGCCC    16290        T   AA
                                CGGGGGCGG CGG  GGTCC
                                ||||||||| |||  |||||
                                GCCCCCGCC GCC  TCGGG
                                     _  C_
GAM636  CPLX1    3'  CGAGGGCAGGGGTCCTCC    16291        TCGGAA   _
                                CGGGGGCGG     GGTCC CC
                                |||||||||     ||||| ||
                                GCTCCCGTC     CCAGG GG
                                     C_____     A
GAM636  CRF      3'  CGGGGGCGGTCAACCCCGGTTC 16292          AA__   C
           CC                     CGGGGGCGGTCGG   GGT CCC
                                ||||||||||||    ||| |||
                                GCCCCCGCCAGTT   CCA GGG
                                       GGGG   A
GAM636  DKFZp434C0923 3'  CGAGGGAAGGGAGGGTCTCC   16293       C  TC   A   C
                                CGGGGG GG  GGA GGTC CC
                                |||||| ||  ||| |||| ||
                                GCTCCC TC  CCT CCAG GG
                                   T  __   C   A
GAM636  DKFZp434J1015 3'  GGAGGCGGGTGGGGGGTCCCC  16294        TC  AA
                                GGGGGCGG  GG  GGTCCCC
                                ||||||||  ||  |||||||
                                CCTCCGCC  CC  CCAGGGG
                                     CA  CC
GAM636  DKFZP547L112 5'  CGGGGGCGGCGAGTCAGAGGTT 16295          ____   A  _ C
           CTCC                   CGGGGGCGGT   CGGA GGT C CC
                                ||||||||||   |||| ||| | ||
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                                GCCCCCGCCG   GTCT CCA G GG
                                     CTCA   _  A A
GAM636  DKFZp761O132 3'  GGGGGCAGGGGTCCCC     16296       TCGGAA
                                GGGGGCGG    GGTCCCC
                                ||||||||    |||||||
                                CCCCCGTC    CCAGGGG
                                    C_____
GAM636  DRIL2    3'  CGGGGGCGGTCAGAGAATGGTC 16297           A___
          C                      CGGGGGCGGTCGGA   GGTCC
                                ||||||||||||||   |||||
                                GCCCCCGCCAGTCT   CCAGG
                                       CTTA
GAM636  EDF1     3'  GGGCTGGGGAGGGTCCCCC   16298     _ TC  A
                                GGGC GG  GGA GGTCCCCC
                                |||| ||  ||| ||||||||
                                CCCG CC  CCT CCAGGGGG
                                  A __  C
GAM636  FLJ10650  3'  GGGGGCAAGGTCCCC      16299       GTCGGA
                                GGGGGCG    AGGTCCCC
                                |||||||    ||||||||
                                CCCCCGT    TCCAGGGG
                                     _______
GAM636  FLJ12242  5'  GGGGGCGGGCGGGGACC    16300       T  AA  T
                                GGGGGCGG CGG  GG CC
                                |||||||| |||  || ||
                                CCCCCGCC GCC  CC GG
                                    C  __ T
GAM636  FLJ12448  3'  GGTGGGGAAGGTCTCCC    16301    C  TC     _
                                GG GG  GGAAGGTC CCC
                                || ||  |||||||| |||
                                CC CC  CCTTCCAG GGG
                                 A __      A
GAM636  FLJ13322  5'  GGGGGCCTCCAGGGTCCCCC  16302      GG   AA
                                GGGGGC  TCGG  GGTCCCCC
                                ||||||  ||||  ||||||||
                                CCCCCG  GGTC  CCAGGGGG
                                   GA   __
GAM636  FLJ14596  3'  CGGGGAGCACAGGGTCC    16303     _  GT   AA
                                CGGGG GCG  CGG  GGTCC
                                ||||| |||  |||  |||||
                                GCCCC CGT  GTC  CCAGG
                                   T  __  __
GAM636  FLJ14596  3'  GGGAGGTTTTGGGGTCCCCC  16305    C  C__  AA
                                GGG GGT   GG  GGTCCCCC
                                ||| |||   ||  ||||||||
                                CCC CCA   CC  CCAGGGGG
                                  T  AAA  __
GAM636  FLJ14596  5'  CAGGGGCAGCATGAGGGTCC  16304        CG  A
                                CGGGGGCGGT  GA GGTCC
                                ||||||||||  || |||||
```

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                                GTCCCCGTCG  CT CCAGG
                                      TA  C
GAM636  FLJ20150  3'  GGGGGAGGACACGGTCCCCC  16306      C  T GGAA
                                GGGGG GG C    GGTCCCCC
                                ||||| || |    ||||||||
                                CCCCC CC G    CCAGGGGG
                                   T  T TG__
GAM636  FLJ25193  3'  CGGGAGGGAGGTCTCCC     16307      C  TCGGA    _
                                CGGGGG GG     AGGTC CCC
                                |||||| ||     ||||| |||
                                GCCCTC CC     TCCAG GGG
                                   _ ______    A
GAM636  FLJ32865  3'  CGGTGGTGGCAGAGGGTCC   16308    G  C  T   A
                                CGG GG GG CGGA GGTCC
                                ||| || || |||| |||||
                                GCC CC CC GTCT CCAGG
                                  A  A  _   C
GAM636  GBTS1     3'  GGGGGCGGTGGCCTCGGTTTCC 16309        C  AA__  CC
              C                  GGGGGCGGT GG    GGT  CCC
                                 |||||||||  ||    |||  |||
                                 CCCCCGCCA CC    CCA  GGG
                                      _ GGAG   AA
GAM636  HRLP5     5'  GGGGGCGGCTCGGGGAGGAACC 16310        _   A_  TC
                                 GGGGGCGG TCGG  AGG  CC
                                 |||||||| ||||  |||  ||
                                 CCCCCGCC AGCC  TCC  GG
                                      G   CC   TT
GAM636  KIAA0194  3'  CGGGGCCAGAAGAGGTTTCC   16311      G  TC  A  CC
                                 CGGGG CGG  GGA GGT  CC
                                 ||||| |||  ||| |||  ||
                                 GCCCC GTC  TCT CCA  GG
                                    G  T_  _  AA
GAM636  KIAA0337  3'  CAGGGGCGCATGGGTCCC    16312        GT  GAA
                                 CGGGGGCG  CG   GGTCCC
                                 ||||||||  ||   ||||||
                                 GTCCCCGC  GT   CCAGGG
                                      __ AC_
GAM636  KIAA0672  3'  GGGGGCGGCCTGAAAGGTTTTC 16313          _      CC_
              C                  GGGGGCGGTC GGAAGGT   CC
                                 ||||||||||  |||||||   ||
                                 CCCCCGCCGG CTTTCCA   GG
                                      A      AAA
GAM636  KIAA0964  3'  GGGGACGGGGGGGGGGGTCCCCC 16314        TC  AA
                                 GGGGGCGG  GG  GGTCCCCC
                                 ||||||||  ||  ||||||||
                                 CCCCTGCC  CC  CCAGGGGG
                                      CC  CC
GAM636  KIAA1016  5'  CGGGGGCGCCGGTTCC      16315        G    AAGG
                                 CGGGGGCG TCGG    TCC
                                 |||||||| ||||    |||
```

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                                GCCCCCGC GGCC   AGG
                                    _   A___
GAM636  KIAA1100 3' CGAGGGTGGTTGGAGCATCCC 16316      C  C  AG
                                CGGGGG GGT GGA  GTCCC
                                |||||| ||| |||  |||||
                                GCTCCC CCA CCT  TAGGG
                                   A  A  CG
GAM636  KIAA1514 3' CAGGGGTCAGTTGTGGGGGGT 16317      _  C__ AA
                                CGGGGG CGGT  GG  GGT
                                |||||| ||||  ||  |||
                                GTCCCC GTCA  CC  CCA
                                   A   ACA  CC
GAM636  KIF13B   3' GGGAGGCTGGGGGGTCCCCC  16318    C  C  AA
                                GGG GGT GG  GGTCCCCC
                                ||| ||| ||  ||||||||
                                CCC CCG CC  CCAGGGGG
                                  T  A  CC
GAM636  MARKL1   5' CGGGGGTCCCAGGGTCCCC  16319      CGG   AA
                                CGGGGG  TCGG  GGTCCCC
                                ||||||  ||||  |||||||
                                GCCCCC  GGTC  CCAGGGG
                                   AG_   __
GAM636  MGC10500 3' CGGGGGCGTCGTCCC      16320      G  GGAAG
                                CGGGGGC GTC    GTCCC
                                ||||||| |||    |||||
                                GCCCCCG CAG    CAGGG
                                   _  ______
GAM636  MGC15730 5' CGGTGGCGGCGGGTCCCC   16321    G   T  AAG
                                CGG GGCGG CGG  GTCCCC
                                ||| ||||| |||  ||||||
                                GCC CCGCC GCC  CAGGGG
                                  A   _  ___
GAM636  MGC15854 5' AGGGGCAGGGAGGTCCC    16322       TC  A
                                GGGGGCGG  GGA GGTCCC
                                ||||||||  ||| ||||||
                                TCCCCGTC  CCT CCAGGG
                                   __  _
GAM636  MGC4415  3' GGGGGCAGGTCGGGTGGCCACC 16323      _    AA  _
          CC                    GGGGGC GGTCGG  GGTC CCCC
                                |||||| ||||||  |||| ||||
                                CCCCCG CCAGCC  CCGG GGGG
                                   T    CA   T
GAM636  MGC5442  3' GGAGGCGGCTGGGTCCTCC  16324       C  AAG  _
                                GGGGGCGGT GG  GTCC CC
                                ||||||||| ||  |||| ||
                                CCTCCGCCG CC  CAGG GG
                                    A ___   A
GAM636  NIFU     5' CGGGGGCGGGCGGGGTC    16325       T  AA
                                CGGGGGCGG CGG  GGTC
                                ||||||||| |||  ||||
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                                GCCCCCGCC GCC  CCAG
                                     C   __
GAM636  NSE1     3'  GGGGCGGTGATGGTCCC     16326        CG  A
                                GGGGCGGT  GA GGTCCC
                                ||||||||  || ||||||
                                CCCCGCCA  CT CCAGGG
                                     __  A
GAM636  NT5C1B   3'  GAGGGTTCAAAAGGTTTTCC   16327      CGG       CC_
                                GGGGG   TCGGAAGGT   CC
                                |||||   |||||||||   ||
                                CTCCC   AGTTTTCCA   GG
                                   A__        AAA
GAM636  POPX1    3'  GGGGGCAGGGGGTTCC      16328        TC  AA   C
                                GGGGGCGG  GG  GGT CC
                                ||||||||  ||  ||| ||
                                CCCCCGTC  CC  CCA GG
                                     __  __  A
GAM636  PRKWNK2  5'  CGGGGGCGGCGGGGCGTCC   16329         T   AAG
                                CGGGGGCGG CGG   GTCC
                                |||||||||  |||   ||||
                                GCCCCCGCC GCC   CAGG
                                     _  CCG
GAM636  RGS11    5'  CGGGGGCGGCCGGGGGGC    16330           AA
                                CGGGGGCGGTCGG  GGT
                                ||||||||||||  |||
                                GCCCCCGCCGGCC  CCG
                                      CC
GAM636  SCOP     5'  CGGGGGCGGCGGAGGCGCC   16331         T   A   C
                                CGGGGGCGG CGGA GGT CC
                                |||||||||  ||||  |||  ||
                                GCCCCCGCC GCCT CCG GG
                                     _   _  C
GAM636  SIAT8A   5'  GGCAGCGGAGGGTCCCC     16332       T   A
                                GGCGG CGGA GGTCCCC
                                |||||  ||||  |||||||
                                CCGTC GCCT CCAGGGG
                                   _   C
GAM636  SMURF2   5'  CGGGGGCGGCGGGGGC      16278         T   AA
                                CGGGGGCGG CGG  GGT
                                |||||||||  |||  |||
                                GCCCCCGCC GCC  CCG
                                     _  C_
GAM636  TIGD5    5'  CGGGGGCGGCGGGGCC      16276         T   AA
                                CGGGGGCGG CGG  GGTC
                                |||||||||  |||  ||||
                                GCCCCCGCC GCC  CCGG
                                     _  __
GAM636  TINF2    5'  CGGAGGCGGTCCCTCCGGGTTC 16333           GGAA__   C
             C                   CGGGGGCGGTC     GGT CC
                                 ||||||||||      ||| ||
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                                GCCTCCGCCAG     CCA GG
                                      GGAGGC   A
GAM636  LOC116113 3'  GGGGGCGGCTGGAGGAGCCCCC 16334         C   A_
                                GGGGGCGGT GGA  GGTCCCC
                                ||||||||| |||  |||||||
                                CCCCCGCCG CCT  TCGGGGG
                                     A   CC
GAM636  LOC120072 3'  CGGAGGCAAGGTCCC       16335        GTCGGA
                                CGGGGGCG     AGGTCCC
                                ||||||||     |||||||
                                GCCTCCGT     TCCAGGG
                                      _______
GAM636  LOC124411 3'  GGGCCTCTGGGGGTCCCCC    16336      GG  _  AA
                                GGGC  TC GG  GGTCCCCC
                                ||||  || ||  ||||||||
                                CCCG  AG CC  CCAGGGGG
                                  G_  A  C_
GAM636  LOC132422 5'  GGGGGCGGCGGGGCCCCC    16337         T   AA
                                GGGGGCGG CGG  GGTCCCC
                                |||||||| |||  |||||||
                                CCCCCGCC GCC  CCGGGGG
                                      _   __
GAM636  LOC145801 5'  CGGGGGCGGATGGGGGAGAGGC 16338          TC___   _
                                CGGGGGCGG     GGA AGGT
                                |||||||||     ||| ||||
                                GCCCCCGCC     CCT TCCG
                                     TACCC   C
GAM636  LOC147791 3'  CAGGGGTCAGGGAAGGTCCC   16339        _   TC
                                CGGGGG CGG  GGAAGGTCCC
                                |||||| |||  ||||||||||
                                GTCCCC GTC  CCTTCCAGGG
                                   A   __
GAM636  LOC150183 5'  CGGGGGCGGTCAACTTTC     16340            AAGG
                                CGGGGGCGGTCGG    TC
                                ||||||||||||||   ||
                                GCCCCCGCCAGTT    AG
                                      GAA_
GAM636  LOC150184 5'  CGGGGGCGGTCAACTTTC     16340            AAGG
                                CGGGGGCGGTCGG    TC
                                ||||||||||||||   ||
                                GCCCCCGCCAGTT    AG
                                      GAA_
GAM636  LOC150185 5'  CGGGGGCGGTCAACTTTC     16340            AAGG
                                CGGGGGCGGTCGG    TC
                                ||||||||||||||   ||
                                GCCCCCGCCAGTT    AG
                                      GAA_
GAM636  LOC150225 3'  CGGGGGCGGTGGGGTGTCCC   16341          C  AAG
                                CGGGGGCGGT GG   GTCCC
                                |||||||||| ||   |||||
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                                GCCCCCGCCA CC   CAGGG
                                      C  CA_
GAM636   LOC150378 5'  GGGGCAGAAAGGTCCCCC    16342       TCG
                                GGGGCGG   GAAGGTCCCCC
                                |||||||   ||||||||||
                                CCCCGTC   TTTCCAGGGGG
                                    ___
GAM636   LOC151701 3'  CAGGGGCGGGCGAGGTCTTCC  16343        T  GA    CC
                                CGGGGGCGG CG  AGGTC  CC
                                |||||||||  ||  |||||  ||
                                GTCCCCGCC GC  TCCAG  GG
                                      C  __    AA
GAM636   LOC152941 3'  GGGAGCAAGTGGGGTCCC    16344       _  C  AA
                                GGGGGCG GT GG  GGTCCC
                                |||||||  ||  ||  ||||||
                                CCCTCGT CA CC  CCAGGG
                                     T  _  __
GAM636   LOC153769 5'  CGGGGGCAGAGCTGGTC     16345        TC  AA
                                CGGGGGCGG  GG  GGTC
                                |||||||||  ||  ||||
                                GCCCCCGTC  TC  CCAG
                                     __  GA
GAM636   LOC155382 3'  GGGGTGCGACAGGTCCCC    16346     _   T GGA
                                GGGG GCGG C   AGGTCCCC
                                ||||  |||| |   ||||||||
                                CCCC CGCT G   TCCAGGGG
                                  A   _ ____
GAM636   LOC163250 5'  GGGGCGGCAGGGGTTCCCC   16347       C  AA  _
                                GGGGCGGT GG  GGT CCCC
                                ||||||||  ||  |||  ||||
                                CCCCGCCG CC  CCA GGGG
                                     T  __   A
GAM636   LOC196985 5'  GGGAGTCCGGAGGGTCCCCC  16348      CGG    A
                                GGGGG   TCGGA GGTCCCCC
                                |||||   |||||  ||||||||
                                CCCTC   GGCCT CCAGGGGG
                                   A__    C
GAM636   LOC197414 3'  GAGGGTGACACCCAGGTCCCC  16349      C  T  GA_
                                GGGGG GG CG   AGGTCCCC
                                |||||  ||  ||   ||||||||
                                CTCCC CT GT   TCCAGGGG
                                   A  _  GGG
GAM636   LOC197416 3'  GGGCCTCTGGGGGTCCCCC   16336     GG  _  AA
                                GGGC  TC GG  GGTCCCCC
                                ||||  ||  ||  ||||||||
                                CCCG  AG CC  CCAGGGGG
                                  G_  A  C_
GAM636   LOC200230 5'  GGGGGCAGGGGCCGGTCC    16350       TC  AA
                                GGGGGCGG  GG  GGTCC
                                ||||||||  ||  |||||
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                                CCCCCGTC  CC  CCAGG
                                    C_  GG
GAM636  LOC200583 5'  CGGGGTGCAGGTCCCC      16351       _  GGTCGGA
                                CGGGG GC      AGGTCCCC
                                ||||| ||      ||||||||
                                GCCCC CG      TCCAGGGG
                                  A ________
GAM636  LOC201780 5'  CGGGGGCGGCGGGCCGGTCTCC 16352          C  AA   C
                                CGGGGGCGGT GG  GGTC CC
                                |||||||||| ||  |||| ||
                                GCCCCCGCCG CC  CCAG GG
                                     C  GG   A
GAM636  LOC203392 5'  CGTGGGCAAAGGTCCCC     16353    G   GGTCG
                                CG GGGC     GAAGGTCCCC
                                || ||||     ||||||||||
                                GC CCCG     TTTCCAGGGG
                                 A  _____
GAM636  LOC220001 5'  GGCGGCGGCGGGTCCCC     16354       T   AA
                                GGCGG CGG  GGTCCCC
                                ||||| |||  |||||||
                                CCGCC GCC  CCAGGGG
                                  _  GC
GAM636  LOC221943 5'  CGGGGTCCTGGTGGAGGTCCCC 16355       GC__   C   A
          C                      CGGGG   GGT GGA GGTCCCCC
                                |||||   ||| ||| ||||||||
                                GCCCC   CCA CCT CCAGGGGG
                                  AGGA  _  _
GAM636  LOC222962 3'  CGGGGGCGGTCCTCCCC     16356          GGAAGG
                                CGGGGGCGGTC     TCCCC
                                ||||||||||     |||||
                                GCCCCCGCCAG     AGGGG
                                     G_____
GAM636  LOC253216 3'  GGGGAGGAAGGTCCCCC     16357       CGGTC
                                GGGGG    GGAAGGTCCCCC
                                |||||    ||||||||||||
                                CCCCT    CCTTCCAGGGGG
                                  _____
GAM636  LOC254263 3'  CGGGGTGGGGGGGGTTCCCC  16358       GC  TC  AA  _
                                CGGGG  GG  GG  GGT CCCC
                                |||||  ||  ||  ||| ||||
                                GCCCC  CC  CC  CCA GGGG
                                  A_  CC  __  A
GAM636  LOC254381 5'  GGGGCCCGGGGTCTCC      16359       GG   AA   C
                                GGGGC  TCGG  GGTC CC
                                |||||  ||||  |||| ||
                                CCCCG  GGCC  CCAG GG
                                  __   __   A
GAM636  LOC256160 5'  CGGGGGCGGCGGGCCGGTCTCC 16352          C  AA   C
                                CGGGGGCGGT GG  GGTC CC
                                |||||||||| ||  |||| ||
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                                GCCCCCGCCG CC  CCAG GG
                                      C  GG    A
GAM636  LOC257479 5'  GGGGGAGGTTGGAAGGTCTTCC 16360      C   C       CC
                                GGGGG GGT GGAAGGTC  CC
                                ||||| ||| ||||||||  ||
                                CCCCC CCA CCTTCCAG  GG
                                   T   A       AA
GAM636  LOC51094  5'  GGGGGCCGCGGTCCCC      16361       G  CGGAA
                                GGGGGC GT    GGTCCCC
                                |||||| ||    |||||||
                                CCCCCG CG    CCAGGGG
                                   G  _____
GAM636  LOC64744  5'  CGGGGGCGTCCGTCCCC     16362         GT GGAAG
                                CGGGGGCG  C    GTCCCC
                                |||||||| |    ||||||
                                GCCCCCGC  G    CAGGGG
                                     AG _____
GAM636  LOC81691  5'  CGGGGAGCAGAGGTTCTCC    16363      _   TCGGA   _ C
                                CGGGG GCGG    AGGT C CC
                                ||||| ||||    |||| | ||
                                GCCCC CGTC    TCCA G GG
                                   T   _____   A A
GAM636  LOC91450  3'  GGGGGCAGGAAGGTCTTCC   16364       GTC       CC
                                GGGGGCG   GGAAGGTC  CC
                                |||||||   ||||||||  ||
                                CCCCCGT   CCTTCCAG  GG
                                     ___       AA
GAM637  AHSG     5'  GGCAGGCAGGCGTGCAGGTGG  16367      A   A  _    C
                                GGCAG CAG CG GCAGG GG
                                ||||| ||| || ||||| ||
                                CCGTC GTC GC CGTCC CC
                                   C   C  A    A
GAM637  AMN      3'  AGGTCGACGGTCAGGCGGCCG  16368     CAGACA    _
                                AGG     GACGG CAGGCGGCCG
                                |||     ||||| ||||||||||
                                TCC     CTGCC GTCCGCCGGC
                                  AG____     A
GAM637  APCS     5'  AGCAGACAACACAGTGGC    16369         A  G   GC
                                GGCAGACAG CG CAG  GGC
                                |||||||| || |||  |||
                                TCGTCTGTT GT GTC  CCG
                                     _ _  A_
GAM637  APOA4    3'  AGACAGACAGGTGGCAGG    16370         AC
                                AGGCAGACAG  GGCAGG
                                ||||||||||  ||||||
                                TCTGTCTGTC  CCGTCC
                                      CA
GAM637  ART1     3'  AGGCAGCAGGCGAGGC      16371       A  GAC  _
                                AGGCAG CA   GGC AGGC
                                |||||| ||   ||| ||||
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                                TCCGTC GT   CCG TCCG
                                  _ ____   C
GAM637  ATP2A3   3'  GCAGACAGCGCGGCGGCCG   16372        A  G A
                                GCAGACAG CG C GGCGGCCG
                                |||||||| || | ||||||||
                                CGTCTGTC GC G CCGCCGGC
                                  _  _ _
GAM637  BARX1    5'  GCAGGGGCCGGGCGGGCGGCCG 16373      ACAGAC   A
                                GCAG     GGC GGCGGCCG
                                ||||     ||| ||||||||
                                CGTC     CCG CCGCCGGC
                                  CCCGGC   C
GAM637  BLK      3'  GGCGCAGGCGGGCGCGGCC   16374     AGA   A   CAG
                                GGC   CAG CGG   GCGGCC
                                |||   ||| |||   ||||||
                                CCG   GTC GCC   CGCCGG
                                  C__   C   CG_
GAM637  BMP7     5'  GGCAGAGGGGGCAGGCGGCCG  16375       CAGAC
                                GGCAGA    GGCAGGCGGCCG
                                ||||||    ||||||||||||
                                CCGTCT    CCGTCCGCCGGC
                                   CCC__
GAM637  BMP8     5'  GGCGGGACGGGCGGGCAGCCG  16376     A_   AGAC   A
                                GGC  GAC   GGC GGCGGCCG
                                |||  |||   ||| ||||||||
                                CCG  CTG   CCG CCGTCGGC
                                  CC   C___   C
GAM637  CEP2     5'  AGGCGCGCAGACGGCAGAC   16377      AGA
                                AGGC   CAGACGGCAGGC
                                ||||   ||||||||||||
                                TCCG   GTCTGCCGTCTG
                                  CGC
GAM637  CLCN6    3'  GGCAGCCTCAGGGCAGGCGGC  16378      A__   AC
                                GGCAG   CAG  GGCAGGCGGC
                                |||||   |||  ||||||||||
                                CCGTC   GTC  CCGTCCGCCG
                                   GGA   __
GAM637  CLCN6    3'  GGCAGCCTCAGGGCAGGCGGC  16378      A__   AC
                                GGCAG   CAG  GGCAGGCGGC
                                |||||   |||  ||||||||||
                                CCGTC   GTC  CCGTCCGCCG
                                   GGA   __
GAM637  CLCN6    3'  GGCAGCCTCAGGGCAGGCGGC  16378      A__   AC
                                GGCAG   CAG  GGCAGGCGGC
                                |||||   |||  ||||||||||
                                CCGTC   GTC  CCGTCCGCCG
                                   GGA   __
GAM637  CSDA     5'  GGCGCAGGCGGCGGCGGCC   16379     AGA   A    A
                                GGC   CAG CGGC GGCGGCC
                                |||   ||| |||| |||||||
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                                CCG   GTC GCCG CCGCCGG
                                  C__   C   _
GAM637  CSF1R    5'  GGCAGGCAGGTGCAGGGC    16380      A  ACG    CG
                                GGCAG CAG   GCAGG  GC
                                ||||| |||   |||||  ||
                                CCGTC GTC   CGTCC  CG
                                   C  CA_    __
GAM637  CSNK1E   5'  GGCTGGCAGGCGGGGCGGGCCG 16381     AGA  A  CA   _
                                GGC   CAG CGG  GGCGG CCG
                                |||   ||| |||  ||||| |||
                                CCG   GTC GCC  CCGCC GGC
                                  ACC   C  __    C
GAM637  DES      5'  AGGCGGCGGGCAGGCGGCCG   16382     AGACAGAC
                                AGGC       GGCAGGCGGCCG
                                ||||       ||||||||||||
                                TCCG       CCGTCCGCCGGC
                                  CCGC____
GAM637  DES      5'  GGCGGGCAGGCGGCCG      16383     AGACAGAC
                                GGC       GGCAGGCGGCCG
                                |||       ||||||||||||
                                CCG       CCGTCCGCCGGC
                                  C________
GAM637  DLC1     5'  AGGCAGGCGGAGGCGGCC    16384       ACAGA  C     _
                                AGGCAG    CGG AGGCGGC C
                                ||||||    ||| ||||||| |
                                TCCGTC    GCC TCCGCCG G
                                   C____  _      A
GAM637  DYRK2    5'  AGGCGGCGGGAGCGGCGGCCG  16385     AGACAGAC  A
                                AGGC       GGC GGCGGCCG
                                ||||       ||| ||||||||
                                TCCG       TCG CCGCCGGC
                                  CCGCCC__  _
GAM637  E2F1     5'  GGTGACAGGCGGCGGCG     16386    CA    A   A
                                GG  GACAG CGGC GGCG
                                ||  ||||| |||| ||||
                                CC  CTGTC GCCG CCGC
                                 A_    C   _
GAM637  EIF2C1   3'  AGGCAGGCAGGCAGGCAG    16388       A  GAC
                                AGGCAG CA   GGCAGGCGG
                                |||||| ||   |||||||||
                                TCCGTC GT   CCGTCCGTC
                                   C  ___
GAM637  EIF2C1   3'  AGGCAGGCAGGCAGGCAGGCAG 16387       A   A _     _
           GCCG                  AGGCAG CAG C GGCAGGC GGCCG
                                |||||| ||| | ||||||| |||||
                                TCCGTC GTC G CCGTCCG CCGGC
                                   C   C T      T
GAM637  EIF2C1   3'  AGGCAGGCAGGCAGGCAG    16388       A  GAC
                                AGGCAG CA   GGCAGGCGG
                                |||||| ||   |||||||||
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                                TCCGTC GT   CCGTCCGTC
                                   C ___
GAM637  EIF2C1   3'  AGGCAGACAGGCAGGCAG    16389        GAC
                                AGGCAGACA   GGCAGGCGG
                                |||||||||   |||||||||
                                TCCGTCTGT   CCGTCCGTC
                                      ___
GAM637  GAA      3'  GGCAGCCGGGAAGCGGC     16390      ACAGA  C     C
                                GGCAG    CGG AGGCGG C
                                |||||    ||| |||||| |
                                CCGTC    GCC TTCGCC G
                                   G____  C     A
GAM637  GDF2     5'  AGGAGACTGCAGGCGGCC    16391     CAGAC   G
                                AGG    AGAC GCAGGCGGCC
                                |||    |||| ||||||||||
                                TCC    TCTG CGTCCGCCGG
                                  _____   A
GAM637  GLUL     5'  AGGGGACAGACAGCGGCC    16392     CA      GGCA
                                AGG  GACAGAC   GGCGGCC
                                |||  |||||||   |||||||
                                TCC  CTGTCTG   TCGCCGG
                                  C_     ____
GAM637  GNAI1    5'  GGCAGACAGCAACGGGCGGC  16393        A   A
                                GGCAGACAG CGGC GGCGGC
                                ||||||||| |||| ||||||
                                CCGTCTGTC GTTG CCGCCG
                                      _   C
GAM637  GPR44    5'  GGCAGACAGAGGTGGGCGGCCG 16394      A_________   AGGCG
            CCTGC                  AGACAG       CGGC    GC
                                ||||||       ||||    ||
                                TCTGTC       GCCG    CG
                                   TCCACCCIII   GCGGA
GAM637  GRM4     3'  GGCAAGACAGACGGCAGACG  16395     _
                                GGCA GACAGACGGCAGGCG
                                |||| ||||||||||||||
                                CCGT CTGTCTGCCGTCTGC
                                  T
GAM637  GTF2I    5'  GGCAGGCGGGCGGCCG      16396     GACAGAC  A
                                GGCA      GGC GGCGGCCG
                                ||||      ||| ||||||||
                                CCGT      CCG CCGCCGGC
                                  _______  C
GAM637  GTF2I    5'  GGCAGGCGGGCGGCCG      16396     GACAGAC  A
                                GGCA      GGC GGCGGCCG
                                ||||      ||| ||||||||
                                CCGT      CCG CCGCCGGC
                                  _______  C
GAM637  IDS      5'  GGCGCAGACGGGCGGCCA    16397     AGA     CAG
                                GGC   CAGACGG   GCGGCCG
                                |||   |||||||   |||||||
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                                CCG  GTCTGCC  CGCCGGT
                                 C__     ___
GAM637  IL13    3'  GGCAGACAGGAGCGGC     16398        ACGGCA
                                GGCAGACAG    GGCGGC
                                |||||||||    ||||||
                                CCGTCTGTC    TCGCCG
                                     C_____
GAM637  JUN     3'  GGCAGCCCGCAGGCGGCC    16399      ACAGA  G
                                GGCAG    CG CAGGCGGCC
                                |||||    || |||||||||
                                CCGTC    GC GTCCGCCGG
                                  GG___  _
GAM637  KIFC3   5'  GGGAAAGGGCGGGCGGCCG   16400    CA  C  AC   A
                                GG  GA AG  GGC GGCGGCCG
                                ||  || ||  ||| ||||||||
                                CC  CT TC  CCG CCGCCGGC
                                 __  T  __   C
GAM637  KRTHB6  3'  AGGCAGCGGGCGGCGGC    16401       ACAGAC   A
                                AGGCAG     GGC GGCGGC
                                ||||||     ||| ||||||
                                TCCGTC     CCG CCGCCG
                                   GC____   _
GAM637  LAG3    5'  AGCAGACAGAGCAAAGTGGCCG 16402          CG   _ C
                                GGCAGACAGA  GCAG G GGCCG
                                ||||||||||  |||| | |||||
                                TCGTCTGTCT  CGTT C CCGGC
                                     __    T A
GAM637  LAMB1   5'  GGCTGAAGGGGCGGGCGGCCG  16403    A  C  AC   A
                                GGC GA AG  GGC GGCGGCCG
                                ||| || ||  ||| ||||||||
                                CCG CT TC  CCG CCGCCGGC
                                 A  _  C_   C
GAM637  LMO1    3'  AGGCAGGTGGGCAGGCGG    16404       ACAGAC
                                AGGCAG     GGCAGGCGG
                                ||||||     |||||||||
                                TCCGTC     CCGTCCGCC
                                   CAC___
GAM637  LMO1    3'  AGGCGGGCAGATGGACAGACG  16405     AGA   C  _
                                AGGC   CAGA GG CAGGCG
                                ||||   |||| || ||||||
                                TCCG   GTCT CC GTCTGC
                                  CCC    A  T
GAM637  MADH7   3'  GGCAGGCAGGGGAGAGGC    16406      A   AC  C   C
                                GGCAG CAG  GG AGG GGC
                                ||||| |||  || ||| |||
                                CCGTC GTC  CC TCT CCG
                                  C   C_  _   _
GAM637  MAP2K2  5'  AGGCCGGCGTCGGGGCGGCCG  16407     AGACAGA   CA
                                AGGC     CGG  GGCGGCCG
                                ||||     |||  ||||||||
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                                TCCG      GCC  CCGCCGGC
                                  GCCGCA_  __
GAM637  MMP11    3'  AGGCAGACAGATGCAGG     16408          CG
                                AGGCAGACAGA  GCAGG
                                ||||||||||  |||||
                                TCCGTCTGTCT  CGTCC
                                      A_
GAM637  NLGN2    3'  GGCAGGCGGCGGGGGCCG    16409      ACAGA   A  C
                                GGCAG    CGGC GG GGCCG
                                |||||    |||| || |||||
                                CCGTC    GCCG CC CCGGC
                                  C____   C  _
GAM637  NRG2     5'  GGCAGGCGGCAAGCGGGCCG   16410      ACAGA        _
                                GGCAG    CGGCAGGCGG CCG
                                |||||    |||||||||| |||
                                CCGTC    GCCGTTCGCC GGC
                                  C____        C
GAM637  NRG2     5'  GGCAGGCGGCAAGCGGGCCG   16410      ACAGA        _
                                GGCAG    CGGCAGGCGG CCG
                                |||||    |||||||||| |||
                                CCGTC    GCCGTTCGCC GGC
                                  C____        C
GAM637  NRG2     5'  GGCAGGCGGCAAGCGGGCCG   16410      ACAGA        _
                                GGCAG    CGGCAGGCGG CCG
                                |||||    |||||||||| |||
                                CCGTC    GCCGTTCGCC GGC
                                  C____        C
GAM637  NRG2     5'  GGCAGGCGGCAAGCGGGCCG   16410      ACAGA        _
                                GGCAG    CGGCAGGCGG CCG
                                |||||    |||||||||| |||
                                CCGTC    GCCGTTCGCC GGC
                                  C____        C
GAM637  NRG2     5'  GGCAGGCGGCAAGCGGGCCG   16410      ACAGA        _
                                GGCAG    CGGCAGGCGG CCG
                                |||||    |||||||||| |||
                                CCGTC    GCCGTTCGCC GGC
                                  C____        C
GAM637  NRG2     5'  GGCAGGCGGCAAGCGGGCCG   16410      ACAGA        _
                                GGCAG    CGGCAGGCGG CCG
                                |||||    |||||||||| |||
                                CCGTC    GCCGTTCGCC GGC
                                  C____        C
GAM637  NRG2     5'  GGCAGGCGGCAAGCGGGCCG   16410      ACAGA        _
                                GGCAG    CGGCAGGCGG CCG
                                |||||    |||||||||| |||
                                CCGTC    GCCGTTCGCC GGC
                                  C____        C
GAM637  PACSIN1  3'  GGCGGCAGACGGCGGGCGG   16411     AGA      A
                                GGC   CAGACGGC GGCGG
                                |||   |||||||| |||||
                                CCG   GTCTGCCG CCGCC
                                  CC_      C
GAM637  PCTK3    3'  GGTGGACAGGCAGGAGCC    16412    CA   GAC     C
                                GG  GACA   GGCAGG GGCC
                                ||  ||||   |||||| ||||
```

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                                CC  CTGT   CCGTCC TCGG
                                 AC   ___    _
GAM637  PDE4A   3'  AGGTAGAGACTCCCCAGGCGGC 16413    C   CA   GG__
                                AGG AGA  GAC   CAGGCGGC
                                ||| |||  |||   ||||||||
                                TCC TCT  CTG   GTCCGCCG
                                  A  __  AGGG
GAM637  PHKG2   5'  GGCAGGCAGAGGAGCCAG   16414     A   C  C  G
                                GGCAG CAGA GG AG CGG
                                ||||| |||| || || |||
                                CCGTC GTCT CC TC GTC
                                   C   _ _ G
GAM637  PITX3   5'  GGCAGGCAGGGGCCAGGGGCCG 16415     A  AC  _  C
                                GGCAG CAG  GGC AGG GGCCG
                                ||||| |||  ||| ||| |||||
                                CCGTC GTC  CCG TCC CCGGC
                                   C  C_  G  _
GAM637  RGL     5'  AGGCAGGCAGGAGGCATTACG  16416     A  AC   G_
                                AGGCAG CAG  GGCA  GCG
                                |||||| |||  ||||  |||
                                TCCGTC GTC  CCGT  TGC
                                   C  CT   AA
GAM637  ROBO1   5'  GGCAGGCGCGGCGGCGGC   16417     ACAGA   A
                                GGCAG    CGGC GGCGGC
                                |||||    |||| ||||||
                                CCGTC    GCCG CCGCCG
                                   CGC__   _
GAM637  RRP22   5'  GGCAGACAGGTGGCGGGCG   16418       AC  A
                                GGCAGACAG  GGC GGCG
                                |||||||||  ||| ||||
                                CCGTCTGTC  CCG CCGC
                                      CA  C
GAM637  RRP22   5'  GGCAGACAGGTGGCGGGCG   16418       AC  A
                                GGCAGACAG  GGC GGCG
                                |||||||||  ||| ||||
                                CCGTCTGTC  CCG CCGC
                                      CA  C
GAM637  SIX1    5'  AGGCAGGGGGCGGCGGCC    16419      ACAGAC  A
                                AGGCAG     GGC GGCGGCC
                                ||||||     ||| |||||||
                                TCCGTC     CCG CCGCCGG
                                   CC_____  _
GAM637  SLC30A4 5'  AGGCGGACGGCCGGCGGC    16420     AGACA    A
                                AGGC    GACGGC GGCGGC
                                ||||    |||||| ||||||
                                TCCG    CTGCCG CCGCCG
                                  C_____    G
GAM637  SLC39A1 5'  GGCGGAGCAGGCGACC     16421    A  CAGACG
                                GGC GA     GCAGGCGGCC
                                ||| ||     ||||||||||
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                                CCG CT     CGTCCGCTGG
                                  C _______
GAM637  SMARCB1  5'  GGCAGAGGCGGGCGGCC     16422       CAGAC   A
                                GGCAGA     GGC GGCGGCC
                                ||||||     ||| |||||||
                                CCGTCT     CCG CCGCCGG
                                   ______  C
GAM637  SMTN     3'  AGGCAGGAGACGGTGCCC     16423       AC     CAG  GG
                                AGGCAG  AGACGG   GC  CC
                                ||||||  ||||||   ||  ||
                                TCCGTC  TCTGCC   CG  GG
                                   C_     A__  __
GAM637  SMTN     3'  AGGCAGGAGACGGTGCCC     16423       AC     CAG  GG
                                AGGCAG  AGACGG   GC  CC
                                ||||||  ||||||   ||  ||
                                TCCGTC  TCTGCC   CG  GG
                                   C_     A__  __
GAM637  SMTN     3'  AGGCAGGAGACGGTGCCC     16423       AC     CAG  GG
                                AGGCAG  AGACGG   GC  CC
                                ||||||  ||||||   ||  ||
                                TCCGTC  TCTGCC   CG  GG
                                   C_     A__  __
GAM637  SPARC    5'  AGGCAGGCAGGCGGCAGG     16424       A   A
                                AGGCAG CAG CGGCAGG
                                ||||||| ||| |||||||
                                TCCGTC GTC GCCGTCC
                                   C   C
GAM637  SPINT2   5'  GGCAGGCAGGGGGCGGGGC    16425       A   AC   A  C
                                GGCAG CAG  GGC GG GGC
                                ||||| |||  ||| || |||
                                CCGTC GTC  CCG CC CCG
                                  C   CC   _ _
GAM637  SQSTM1   3'  AGGCAGGGCAGGCGGTCC     16426       ACAGAC       _
                                AGGCAG     GGCAGGCGG CC
                                ||||||     ||||||||| ||
                                TCCGTC     CCGTCCGCC GG
                                   _______       A
GAM637  ST5      3'  AGGCAGGCAGGCAGGCAGGCCG 16427       A  GAC      _
                                AGGCAG CA   GGCAGGC GGCCG
                                |||||| ||   ||||||| |||||
                                TCCGTC GT   CCGTCCG CCGGC
                                   C ___       T
GAM637  ST5      3'  AGGCAGGCAGGCAGGCAGGCCG 16427       A  GAC      _
                                AGGCAG CA   GGCAGGC GGCCG
                                |||||| ||   ||||||| |||||
                                TCCGTC GT   CCGTCCG CCGGC
                                   C ___       T
GAM637  SUV39H1  3'  GGCAGGTGGAGGCAGGCG     16428       ACA  C
                                GGCAG   GA GGCAGGCG
                                |||||   || ||||||||
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                                CCGTC  CT CCGTCCGC
                                  CAC  _
GAM637  TAF15   5' AGCCAGGCGGCGCGGCGGCCG 16429    AGA  A   A_
                                GGC  CAG CGGC  GGCGGCCG
                                |||  ||| ||||  ||||||||
                                TCG  GTC GCCG  CCGCCGGC
                                 ___  C   CG
GAM637  TAF15   5' AGCCAGGCGGCGCGGCGGCCG 16429    AGA  A   A_
                                GGC  CAG CGGC  GGCGGCCG
                                |||  ||| ||||  ||||||||
                                TCG  GTC GCCG  CCGCCGGC
                                 ___  C   CG
GAM637  TBXA2R  5' AGGCAGATGTGCGGGCGCC  16430      CAGACG A   G
                                AGGCAGA    GC GGCG CC
                                |||||||    || |||| ||
                                TCCGTCT    CG CCGC GG
                                   ACA___  C   _
GAM637  TIMM23  3' AGGCCAAGGCAGGCGGC    16431    AGA  AC
                                AGGC  CAG  GGCAGGCGGC
                                ||||  |||  ||||||||||
                                TCCG  GTT  CCGTCCGCCG
                                 ___  __
GAM637  VIPR1   3' GGCAGACAGAGGAGGC     16432        C  C
                                GGCAGACAGA GG AGGC
                                |||||||||| || ||||
                                CCGTCTGTCT CC TCCG
                                  _  _
GAM637  WHN     3' AGGTGAGCCCGATGTGGGCGGC 16433    CA  CAGA  CA__
          CG                    AGG  GA   CGG   GGCGGCCG
                                |||  ||   |||   ||||||||
                                TCC  CT   GCT   CCGCCGGC
                                 A_  CGG_  ACAC
GAM637  YY1     5' GGCGGGCGAGGAGGCGGCCG  16434    AGACA  C  C
                                GGC    GA GG AGGCGGCCG
                                |||    || || |||||||||
                                CCG    CT CC TCCGCCGGC
                                 CCCG_  _  _
GAM637  ZAP70   3' AGGCAGGCAATGCAAGGCC   16435      A  GACG   GC
                                AGGCAG CA   GCAG  GGCC
                                ||||||  ||   ||||  ||||
                                TCCGTC GT   CGTT  CCGG
                                  C  TA__   __
GAM637  ZNF216  5' AGGTGGAGGGAGGACCGGCGGC 16436    CA  CA  C   A
          CG                    AGG  GA  GA GGC GGCGGCCG
                                |||  ||  || ||| ||||||||
                                TCC  CT  CT CTG CCGCCGGC
                                 AC  CC  C   G
GAM637  ZNF42   5' AGGCAGACGGAGGCGAC    16437        AGAC  C
                                AGGCAGAC   GG AGGCGGC
                                ||||||||   || |||||||
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                                TCCGTCTG   CC TCCGCTG
                                    ____ _
GAM637  13CDNA73 5' GGAGGACGGGCAGCGGCC   16438   C  ACA    CA
                                GG AG   GACGG  GGCGGCC
                                || ||   |||||  |||||||
                                CC TC   CTGCC  TCGCCGG
                                 _ ___    CG
GAM637  B7-H1    5' AGGCGGACAGAAGCGCGGC   16439     A     C   AG
                                AGGC GACAGA GGC  GCGGC
                                |||| |||||| |||  |||||
                                TCCG CTGTCT TCG  CGCCG
                                  C     _  __
GAM637  BA108L7.2 3' GGCAGGCAGGTGGACATGAGGC 16440      A   AC  _  GGC
                                GGCAG CAG  GG CA   GGC
                                ||||| |||  || ||   |||
                                CCGTC GTC  CC GT   CCG
                                   C   CA  T  ACT
GAM637  BCL2L1   5' AGGCAGGCAGGTGCAGCC   16441      GACAGAC    __
                                AGGCA      GGCAG  GCGGCC
                                |||||      |||||  ||||||
                                TCCGT      CCGTC  CGTCGG
                                  ________    CA
GAM637  C21orf80  3' GGCAGACAGGGGGCAGAAACCG  16442         AC     C
                                GGCAGACAG  GGCAGG GGCCG
                                |||||||||  |||||| |||||
                                CCGTCTGTC  CCGTCT TTGGC
                                     C_     _
GAM637  C22orf5   3' AGGCAGGCAGAGGTGTGCGGCC 16443    A  A__________   AGGCG
           GCCTGC                  AG CAG        CGGC    GC
                                || |||        ||||    ||
                                TC GTC        GCCG    CG
                                 C  TCCACACIII   GCGGA
GAM637  CECR6    5' GGCGAGGCGGGCTAGGCGGCCG 16444     A  CAGAC  _
                                GGC GA    GGC AGGCGGCCG
                                ||| ||    ||| |||||||||
                                CCG CT    CCG TCCGCCGGC
                                  _ CCGC_  A
GAM637  CHST3    3' AGACAGACAGATGGCAGA    16445          C
                                AGGCAGACAGA GGCAGG
                                |||||||||| ||||||
                                TCTGTCTGTCT CCGTCT
                                       A
GAM637  CMRF-35H 3' AGGTGACAGGCACTGGTGGC  16446    CA   GAC   __ C
                                AGG  GACA   GGCA  GG GGC
                                |||  ||||   ||||  || |||
                                TCC  CTGT   CCGT  CC CCG
                                  A_   ___   GA  A
GAM637  DDM36    3' AGGCAGGAGGATGGCAGGCG  16447       ACA  C
                                AGGCAG   GA GGCAGGCG
                                ||||||   || ||||||||
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                                TCCGTC   CT CCGTCCGC
                                   CTC  A
GAM637  DECR2    3'  AGGCGGCAGGAAGCAGCGGCCG 16448      AGA   AC    G
                                AGGC   CAG  GGCAG CGGCCG
                                ||||   |||  ||||| ||||||
                                TCCG   GTC  TCGTC GCCGGC
                                  CC_   CT    _
GAM637  DF       5'  GGCGGCGCCGCGCAGGCGGCCG 16449     AGACAGA  _
                                GGC      CG GCAGGCGGCCG
                                |||      || ||||||||||
                                CCG      GC CGTCCGCCGGC
                                  CCGCG__  G
GAM637  DGKD     3'  AGGCGGGCGAGAGCTGAGTGGC 16450      AGACA  C   A_  C
           CG                     AGGC    GA GGC  GG GGCCG
                                ||||    || |||  || |||||
                                TCCG    CT TCG  TC CCGGC
                                  CCCG_  C   AC  A
GAM637  dJ55C23.6 5'  GGCACTCTGGCGGGCGGCCG   16451      GACAGAC   A
                                GGCA      GGC GGCGGCCG
                                ||||      ||| ||||||||
                                CCGT      CCG CCGCCGGC
                                  GAGA___   C
GAM637  DJ726C3.2 5'  AGGCAGGCAGATGCAGA     16452       A    CG
                                AGGCAG CAGA  GCAGG
                                |||||| ||||  |||||
                                TCCGTC GTCT  CGTCT
                                   C    A_
GAM637  DKFZP434N1511 5'  GGCGGGCGGGACACCGGCGGCC 16453     AGACA_    G A
           G                     GGC     GACG C GGCGGCCG
                                |||     |||| | ||||||||
                                CCG     CTGT G CCGCCGGC
                                  CCCGCC    _ G
GAM637  DKFZP566J091 5'  GCAGACGGGCACGGCAGGCGGC 16454       AG__
           CG                     GCAGAC    ACGGCAGGCGGCCG
                                ||||||    ||||||||||||||
                                CGTCTG    TGCCGTCCGCCGGC
                                   CCCG
GAM637  DKFZP586J0619 3'  AGGCAGCCAGATGGCGGG    16455       A    C   A
                                AGGCAG CAGA GGC GG
                                |||||| |||| ||| ||
                                TCCGTC GTCT CCG CC
                                   G    A   C
GAM637  DKFZP727M111 5'  AGGCAGGCAGTGGCCAGGGC   16456       A   AC   A  C
                                AGGCAG CAG  GGC GG GGC
                                |||||| |||  ||| || |||
                                TCCGTC GTC  CCG TC CCG
                                   C   A_   G  _
GAM637  DLL1     3'  AGGCAGTGCCGCAGGCGGCCG  16457       ACAGA  G
                                AGGCAG    CG CAGGCGGCCG
                                ||||||    || ||||||||||
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                                TCCGTC    GC GTCCGCCGGC
                                   ACG__  _
GAM637  FAF1     5'  GGAGGCAGACGGCACCTCC   16458   C  A      AG  GG
                                GG AG CAGACGGC  GC  CC
                                || || ||||||||  ||  ||
                                CC TC GTCTGCCG  TG  GG
                                 _  C       __  GA
GAM637  FLJ10060 5'  AGGCAGACAGGCAGAAAGC   16459        GAC     C
                                AGGCAGACA   GGCAGG GGC
                                |||||||||   |||||| |||
                                TCCGTCTGT   CCGTCT TCG
                                      ___     T
GAM637  FLJ10140 3'  AGGCAGACGGCCCCAGCCG   16460        AGAC   AGG
                                AGGCAGAC    GGC   CGGCCG
                                ||||||||    |||   ||||||
                                TCCGTCTG    CCG   GTCGGC
                                     _____  GG_
GAM637  FLJ10743 3'  GGTGAGACAGACGGCAGG    16461    C_
                                GG  AGACAGACGGCAGG
                                ||  ||||||||||||||
                                CC  TCTGTCTGCCGTCC
                                 AC
GAM637  FLJ13265 3'  AGCAGGCAGGCGGCGGCAAGGC 16462      A   A    A   __
                                GGCAG CAG CGGC GGC  GGC
                                ||||| ||| |||| |||  |||
                                TCGTC GTC GCCG CCG  CCG
                                   C   C    _  TT
GAM637  FLJ14665 3'  AGCAGGCAGAGGAGGGCGGC   16463      A    C  CA
                                GGCAG CAGA GG  GGCGGC
                                |||||| |||| ||  ||||||
                                TCGTC GTCT CC  CCGCCG
                                   C    _  TC
GAM637  FLJ21156 3'  GGCAGACAGGGAGTCAGGC    16464         AC  _
                                GGCAGACAG  GG CAGGC
                                |||||||||  || |||||
                                CCGTCTGTC  TC GTCCG
                                      CC  A
GAM637  FLJ21276 3'  AGGTAGACAGACAGTGGGTACC 16465     C         CA  CG
                                AGG AGACAGACGG  GG  GCC
                                ||| ||||||||||  ||  |||
                                TCC TCTGTCTGTC  CC  TGG
                                  A         AC  A_
GAM637  FLJ22169 3'  AGGCAGACGGGATGGCAGG    16466        A_  C
                                AGGCAGAC  GA GGCAGG
                                ||||||||  || ||||||
                                TCCGTCTG  CT CCGTCC
                                     CC  A
GAM637  FLJ31547 5'  AGGCAGGCAGAGGCAGCAG    16467       A   C    G
                                AGGCAG CAGA GGCAG CGG
                                |||||| |||| ||||| |||
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                                TCCGTC GTCT CCGTC GTC
                                   C   _   _
GAM637  GRIN3A   5' AGCAGGCAGGCGGGCGGGCCG 16468      A  GAC   A    _
                                GGCAG CA   GGC GGCGG CCG
                                ||||| ||   ||| ||||| |||
                                TCGTC GT   CCG CCGCC GGC
                                   C ___   C    C
GAM637  HDAC10   5' GCAGGCGGGCGGCGGGCACCG 16469     ACAGA   A   G
                                GCAG    CGGC GGCG CCG
                                ||||    |||| |||| |||
                                CGTC    GCCG CCGT GGC
                                  CGCCC   C   _
GAM637  HSA249128 3' AGGCAGACAGGCAGGCAG   16389        GAC
                                AGGCAGACA   GGCAGGCGG
                                |||||||||   |||||||||
                                TCCGTCTGT   CCGTCCGTC
                                    ___
GAM637  IBTK     5' GGTCAGTTCGGCAGGCGGC   16470   _  ACAGA
                                GG CAG    CGGCAGGCGGC
                                || |||    ||||||||||
                                CC GTC    GCCGTCCGCCG
                                 A  AA___
GAM637  KCNT1    3' AGGCAGGAGGTGGCACAGGG  16471      AC  AC   _  C
                                AGGCAG  AG  GGCA GG GG
                                ||||||  ||  |||| || ||
                                TCCGTC  TC  CCGT TC CC
                                   C_  CA   G  _
GAM637  KIAA0014 5' GGCCGGGCAGACGGCCA    16472    AGACAGAC
                                GGC      GGCAGGCGGCCG
                                |||      ||||||||||||
                                CCG      CCGTCTGCCGGT
                                 GC_______
GAM637  KIAA0173 3' AGGCAGACAGGTGACAGA   16473         AC
                                AGGCAGACAG  GGCAGG
                                ||||||||||  ||||||
                                TCCGTCTGTC  CTGTCT
                                      CA
GAM637  KIAA0211 5' GGCAGGCGGAAGGCGACTCG  16474     ACAGA  C     _
                                GGCAG    CGG AGGCGGC CG
                                |||||    ||| ||||||| ||
                                CCGTC    GCC TCCGCTG GC
                                   C_____  T      A
GAM637  KIAA0346 3' GGCAGGCAGGCGGGCGGGGC  16475      A   A   CA  C
                                GGCAG CAG CGG  GG GGC
                                ||||| ||| |||  || |||
                                CCGTC GTC GCC  CC CCG
                                   C   C   CG  _
GAM637  KIAA0355 3' AGGCAGGCAGGCAGGCAGGCTG 16476       A   A _     _
            GC                    AGGCAG CAG C GGCAGGC GGC
                                ||||||| ||| | ||||||| |||
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                                TCCGTC GTC G CCGTCCG CCG
                                   C   C T      A
GAM637  KIAA0355 3' GGCAGGCAGGCAGGCAGGCAGG 16477      A   A _     _
             C                   GGCAG CAG C GGCAGGC GGC
                                 |||||| ||| | ||||||| |||
                                 CCGTC GTC G CCGTCCG CCG
                                    C   C T      T
GAM637  KIAA0450 5' GGTGGATAGACGGCAGGGGC   16478    CA  C        C
                                 GG  GA AGACGGCAGG GGC
                                 ||  || ||||||||||| |||
                                 CC  CT TCTGCCGTCC CCG
                                  AC  A        _
GAM637  KIAA0721 3' AGGCAGACAATGGTGGCC    16479          ACGGCA  C
                                 AGGCAGACAG     GG GGCC
                                 ||||||||||     || ||||
                                 TCCGTCTGTT     CC CCGG
                                       A_____  A
GAM637  KIAA0721 3' AGGCAGACAATGGTGGCC    16479          ACGGCA  C
                                 AGGCAGACAG     GG GGCC
                                 ||||||||||     || ||||
                                 TCCGTCTGTT     CC CCGG
                                       A_____  A
GAM637  KIAA0819 3' GGAGGCGGCAGGCGGC      16480    CAGAC  A
                                 GG     AG CGGCAGGCGGC
                                 ||     || ||||||||||
                                 CC     TC GCCGTCCGCCG
                                  _____  C
GAM637  KIAA1007 5' GGCGGAAGCAGGCGGCC     16481     A  CAGAC
                                 GGC GA     GGCAGGCGGCC
                                 ||| ||     ||||||||||
                                 CCG CT     TCGTCCGCCGG
                                   C  _____
GAM637  KIAA1016 5' AGGCAGGCAGGGCGGACAGC   16482       A   AC   A
                                 AGGCAG CAG  GGC GGCGGC
                                 |||||| |||  ||| ||||||
                                 TCCGTC GTC  CCG CTGTCG
                                    C   __   C
GAM637  KIAA1172 5' GGCGAGGCGGGCGGCCG     16483     AGACA  C   A
                                 GGC     GA GGC GGCGGCCG
                                 |||     || ||| ||||||||
                                 CCG     CT CCG CCGCCGGC
                                   _____  _   C
GAM637  KIAA1297 3' GGCAGGCAGAGCAGGGTGGC   16484      A   CG    C_
                                 GGCAG CAGA  GCAGG  GGC
                                 ||||| ||||  |||||  |||
                                 CCGTC GTCT  CGTCC  CCG
                                    C   __     CA
GAM637  KIAA1405 3' AGGCAGGCAATGGCAAGCAGC  16485       A   AC
                                 AGGCAG CAG  GGCAGGCGGC
                                 |||||| |||  ||||||||||
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                                TCCGTC GTT  CCGTTCGTCG
                                   C   A_
GAM637  KIAA1554  5'  GGCAGACAGACGGGGTCC    16486          CAGGC  _
                                GGCAGACAGACGG    GG CC
                                ||||||||||||    || ||
                                CCGTCTGTCTGCC    CC GG
                                      _____  A
GAM637  KIAA1634  5'  GGGAGACCCCGCGCGGGCGGCC 16487    C    AGA  _  A
           G                     GG AGAC   CG GC GGCGGCCG
                                || ||||   || || ||||||||
                                CC TCTG   GC CG CCGCCGGC
                                 C   GG_  G  C
GAM637  KIAA1821  3'  AGCCAGGCAGACGGTTTCTCCG 16488    G   A      CAGGCGG
                                AG CAG CAGACGG      CCG
                                || ||| |||||||      |||
                                TC GTC GTCTGCC      GGC
                                 G   C      AAAGA__
GAM637  KIAA1940  5'  AGGCAGCGGCGGCGGCGGCCG  16489       ACAGA   A
                                AGGCAG    CGGC GGCGGCCG
                                ||||||    |||| ||||||||
                                TCCGTC    GCCG CCGCCGGC
                                   GCC__   _
GAM637  KIF1C    3'  AGACAGACAGACGGACAGGGGC 16490            _   C
                                AGGCAGACAGACGG CAGG GGC
                                |||||||||||||| |||| |||
                                TCTGTCTGTCTGCC GTCC CCG
                                      T   _
GAM637  KPNB3    5'  GGTCAGACCTGCCCGGGCGGCC 16491    _    AGACG  A__
           G                     GG CAGAC    GC   GGCGGCCG
                                || |||||    ||   ||||||||
                                CC GTCTG    CG   CCGCCGGC
                                 A    GA___  GGC
GAM637  LUC7L    5'  AGGCAGGCGGTGGCAGC     16492       ACAGA   CA
                                AGGCAG    CGG  GGCGGC
                                ||||||    |||  ||||||
                                TCCGTC    GCC  CCGTCG
                                   C_____   A_
GAM637  MAD4     3'  AGGTGGACAGACGGACG     16493     CA       CAG
                                AGG  GACAGACGG   GCG
                                |||  |||||||||   |||
                                TCC  CTGTCTGCC   TGC
                                  AC        ___
GAM637  MAGEF1   5'  GGCAGGCAGGTGCAGAGCG   16494      A   ACG   _
                                GGCAG CAG   GCAG GCG
                                ||||| |||   |||| |||
                                CCGTC GTC   CGTC CGC
                                   C   CA_    T
GAM637  MAPKAP1  3'  GGCAGGCATTGAAGGTGGC   16495      A  GAC  C   C
                                GGCAG CA   GG AGG GGC
                                ||||| ||   || ||| |||
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                                CCGTC GT   CT TCC CCG
                                   C  AA_  _   A
GAM637  MARKL1   5'  GGCAGGCGGGCGGGCGGGGGCC 16496      ACAGAC   A  ___
             G                    GGCAG     GGC GGC   GGCCG
                                  |||||     ||| |||   |||||
                                  CCGTC     CCG CCG   CCGGC
                                     CGC___   C   CCC
GAM637  MGC16384 3'  AGGCAGGCAGATGTGTGCGGCC 16497    A   A__________   AGGCG
             GCCTGC                 AG CAG        CGGC    GC
                                  || |||        ||||    ||
                                  TC GTC        GCCG    CG
                                   C  TACACACIII   GCGGA
GAM637  MGC2487  5'  GACGGACGGATGGACGGCCG  16498    A    CA_
                                  GAC GACGG   GGCGGCCG
                                  ||| |||||   ||||||||
                                  CTG CTGCC   CTGCCGGC
                                    C    TAC
GAM637  MGC2594  3'  GGCAGGCGGGTGGGCGACCG  16499     ACAGA   CA_
                                  GGCAG    CGG   GGCGGCCG
                                  |||||    |||   ||||||||
                                  CCGTC    GCC   CCGCTGGC
                                     C____   CAC
GAM637  NEIL2    5'  GGCAGCACCTCCGCAGGCGGC  16500      _ AGA  G
                                  GGCAG AC   CG CAGGCGGC
                                  ||||| ||   || ||||||||
                                  CCGTC TG   GC GTCCGCCG
                                     G  GAG  _
GAM637  NIR3     3'  AGGCAGACAGGTGGGCAGGGTC 16501         AC_     CGG
             CG                    AGGCAGACAG   GGCAGG   CCG
                                  ||||||||||   ||||||   |||
                                  TCCGTCTGTC   CCGTCC   GGC
                                        CAC     CA_
GAM637  NPEPL1   3'  AGGCAGGCAGGAGGCC      16502      GACAGAC     C
                                  AGGCA      GGCAGG GGCC
                                  |||||      |||||| ||||
                                  TCCGT      CCGTCC CCGG
                                    _______     T
GAM637  NUDEL    3'  AGGCAGACGGAGGGGCACGGGG 16503        A  C_   _  C
             C                     AGGCAGAC GA  GGCA GG GGC
                                  |||||||| ||  |||| || |||
                                  TCCGTCTG CT  CCGT CC CCG
                                       C  CC    G  _
GAM637  PA26     3'  AGGCAGGCAGAGGCAGAGAGAC 16504       A    C    _ C
                                  AGGCAG CAGA GGCAG G GGC
                                  |||||| |||| ||||| | |||
                                  TCCGTC GTCT CCGTC C CTG
                                     C    _    T T
GAM637  PALM     3'  GGCAGGCGCCGGGAGGGGCCG  16505      ACAGA   C   C
                                  GGCAG    CGG AGG GGCCG
                                  |||||    ||| ||| |||||
```

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                                CCGTC    GCC TCC CCGGC
                                  CGCG_  C  _
GAM637  PIGQ    5'  GGCAGACGACGGCGCTCG    16506       A     AGG
                                GGCAGAC GACGGC  CG
                                ||||||| ||||||  ||
                                CCGTCTG CTGCCG  GC
                                   _    CGA
GAM637  PNMA1   5'  GGCGGGCGGCGAGGACGGCCG  16507    AGACAGA  _  _
                                GGC     CGGC AGG CGGCCG
                                |||     |||| ||| ||||||
                                CCG     GCCG TCC GCCGGC
                                 CCC____   C  T
GAM637  PODLX2  3'  GGCCAGGCGCGGGGGCGGCCG  16508    AGA  A__  CA
                                GGC  CAG  CGG  GGCGGCCG
                                |||  |||  |||  ||||||||
                                CCG  GTC  GCC  CCGCCGGC
                                 ___  CGC  C_
GAM637  PP1057  5'  AGACAGGCAGGTGGAGGC    16509      A  AC  C
                                AGGCAG CAG  GG AGGC
                                |||||| |||  || ||||
                                TCTGTC GTC  CC TCCG
                                   C  CA  _
GAM637  PP1665  3'  AGGAGGACAGATGGCACAGG  16510    CA    C   GGC
                                AGG  GACAGA GGCA  GG
                                |||  |||||| ||||  ||
                                TCC  CTGTCT CCGT  CC
                                 TC    A   GT_
GAM637  RAI1    3'  AGGCGGACGGACTGGCAGGGAC 16511     A  A  _    C
                                AGGC GAC GAC GGCAGG GGC
                                |||| ||| ||| |||||| |||
                                TCCG CTG CTG CCGTCC CTG
                                  C  C  A    _
GAM637  RBP7    5'  GACAAACCCGGCGGGCGGCCG  16512      AGA   A
                                GGCAGAC  CGGC GGCGGCCG
                                |||||||  |||| ||||||||
                                CTGTTTG  GCCG CCGCCGGC
                                   G__   C
GAM637  RPL3L   3'  GGCAGACAGTGCGGTGCG    16513       A_  CAG
                                GGCAGACAG  CGG  GCG
                                |||||||||  |||  |||
                                CCGTCTGTC  GCC  CGC
                                     AC  A__
GAM637  SCAMP-4 3'  GGAGGACGGGAGGGCGGCCG  16514   C  ACA   CA_
                                GG AG  GACGG  GGCGGCCG
                                || ||  |||||  ||||||||
                                CC TC  CTGCC  CCGCCGGC
                                 _ ___    CTC
GAM637  SCYA14  5'  GGCAGGCAGGGCTGGCC    16515    GACAGAC    _ _
                                GGCA     GGCAGG C GGCC
                                ||||     |||||| | ||||
```

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                                CCGT      CCGTCC G CCGG
                                  _______     C A
GAM637  SCYA14   5' GGCAGGCAGGGCTGGCC     16515     GACAGAC     _ _
                                GGCA      GGCAGG C GGCC
                                ||||      |||||| | ||||
                                CCGT      CCGTCC G CCGG
                                  _______     C A
GAM637  SCYA15   5' GGCAGGCAGGGCTGGCC     16515     GACAGAC     _ _
                                GGCA      GGCAGG C GGCC
                                ||||      |||||| | ||||
                                CCGT      CCGTCC G CCGG
                                  _______     C A
GAM637  SCYA23   5' GGCAGGCAGGGCTGGCC     16515     GACAGAC     _ _
                                GGCA      GGCAGG C GGCC
                                ||||      |||||| | ||||
                                CCGT      CCGTCC G CCGG
                                  _______     C A
GAM637  SH3BGRL3 5' GGTAGACAGACGGGCC      16516    C         CAGGCG
                                GG AGACAGACGG     GCC
                                || ||||||||||     |||
                                CC TCTGTCTGCC     CGG
                                 A        _______
GAM637  SKD3     3' GGCACATAGGAGCAGGCAGGTG 16517      GAC___  AC     C
           GC                     GGCA     AG  GGCAGG GGC
                                ||||     ||  |||||| |||
                                CCGT     TC  CCGTCC CCG
                                  GTATCC  GT     A
GAM637  SLC12A8  5' GGTCAGGCAGATGGCAGCCA  16518    _  A   C    G
                                GG CAG CAGA GGCAG CG
                                || ||| |||| ||||| ||
                                CC GTC GTCT CCGTC GT
                                 A  C    A    G
GAM637  SLC16A10 5' AGGCGGCCAGCGCGCAGGCGGC 16519      AGA   A  _
           CG                     AGGC   CAG CG GCAGGCGGCCG
                                ||||   ||| || ||||||||||
                                TCCG   GTC GC CGTCCGCCGGC
                                  CCG   _  G
GAM637  SLC2A4RG 3' GGCCGACAGGCGGGAGGGTGGC 16520     A    A  C   C_
                                GGC GACAG CGG AGG  GGC
                                ||| ||||| ||| |||  |||
                                CCG CTGTC GCC TCC  CCG
                                  G    C  C   CA
GAM637  SMARCF1  5' AGGCGGCGGCGGCGGCCG    16521     AGACAGA   A
                                AGGC      CGGC GGCGGCCG
                                ||||      |||| ||||||||
                                TCCG      GCCG CCGCCGGC
                                  CC_____   _
GAM637  SMARCF1  5' AGGCGGCGGCGGCGGCCG    16521     AGACAGA   A
                                AGGC      CGGC GGCGGCCG
                                ||||      |||| ||||||||
```

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                                TCCG      GCCG CCGCCGGC
                                  CC_____   _
GAM637  SMARCF1  5' AGGCGGCGGCGGCGGCCG    16521     AGACAGA   A
                                AGGC      CGGC GGCGGCCG
                                ||||      |||| ||||||||
                                TCCG      GCCG CCGCCGGC
                                  CC_____   _
GAM637  SPPL2A   5' GACAGGCGCGGGCGGCC     16522      A  G A
                                GACAG CG C GGCGGCC
                                ||||| || | |||||||
                                CTGTC GC G CCGCCGG
                                   C  _ C
GAM637  STK29    3' GGCGGCGGGCGGCGAGGCAGCC 16523     AGACAGA   _
           G                     GGC      CGGC AGGCGGCCG
                                |||      |||| |||||||||
                                CCG      GCCG TCCGTCGGC
                                  CCGCCC_   C
GAM637  SULT4A1  3' AGGTGGACAGACACGCAGGCGG 16524     CA      _
           CCG                    AGG  GACAGACG GCAGGCGGCCG
                                |||  |||||||| ||||||||||
                                TCC  CTGTCTGT CGTCCGCCGGC
                                  AC       G
GAM637  SYNJ2    3' AGCCGGACAGACGAGGC     16525     A_      GC
                                GGC  GACAGACG  AGGC
                                |||  ||||||||  ||||
                                TCG  CTGTCTGC  TCCG
                                  GC       __
GAM637  THG-1    3' AGGAAGAGGGGGGCAGGCGGC  16526     C   CAGAC
                                AGG AGA    GGCAGGCGGC
                                ||| |||    ||||||||||
                                TCC TCT    CCGTCCGCCG
                                  T  CCC__
GAM637  TREX1    5' AGGCAGGCAGGCAGGCAG     16388      A  GAC
                                AGGCAG CA   GGCAGGCGG
                                ||||||  ||   |||||||||
                                TCCGTC GT   CCGTCCGTC
                                   C  ____
GAM637  TREX1    5' AGGCAGGCAGGCAGGCAG     16388      A  GAC
                                AGGCAG CA   GGCAGGCGG
                                ||||||  ||   |||||||||
                                TCCGTC GT   CCGTCCGTC
                                   C  ____
GAM637  TREX1    5' AGGCAGGCAGGCAGGCAG     16388      A  GAC
                                AGGCAG CA   GGCAGGCGG
                                ||||||  ||   |||||||||
                                TCCGTC GT   CCGTCCGTC
                                   C  ____
GAM637  TRF4-2   3' AGTGGACGGACGGCAAAGCAGC 16527    CA   A      _
                                GG  GAC GACGGCAG GCGGC
                                ||  ||| |||||||| |||||
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                                TC  CTG CTGCCGTT CGTCG
                                 AC   C       T
GAM637   WSB1     5'  AGGAGACGGGCGGGGGCGGCCG 16528     C    AGA   CA
                                AGG AGAC   CGG  GGCGGCCG
                                ||| ||||   |||  ||||||||
                                TCC TCTG   GCC  CCGCCGGC
                                  _    CCC   C_
GAM637   WSB1     5'  AGGAGACGGGCGGGGGCGGCCG 16528     C    AGA   CA
                                AGG AGAC   CGG  GGCGGCCG
                                ||| ||||   |||  ||||||||
                                TCC TCTG   GCC  CCGCCGGC
                                  _    CCC   C_
GAM637   ZNF342   5'  AGGCAGGCAGGCGGGCGGGCG  16531       A   A   _ A
                                AGGCAG CAG CGG C GGCG
                                |||||| ||| ||| | ||||
                                TCCGTC GTC GCC G CCGC
                                    C   C   C C
GAM637   ZNF342   5'  GGCAGGCAGGCAGGCGGGCG   16529      A  GAC       C
                                GGCAG CA   GGCAGGCGG CG
                                ||||| ||   ||||||||| ||
                                CCGTC GT   CCGTCCGCC GC
                                   C  ___        C
GAM637   ZNF342   5'  GGCAGGCAGGCAGGCG      16530      A  GAC
                                GGCAG CA   GGCAGGCG
                                ||||| ||   ||||||||
                                CCGTC GT   CCGTCCGC
                                   C  ___
GAM637   LOC115399 3'  GGTGGAAGTGCTGGCGGCCG   16532    CA  C  ACG  A
                                GG  GA AG   GC GGCGGCCG
                                ||  || ||   || ||||||||
                                CC  CT TC   CG CCGCCGGC
                                 AC  _  A__  A
GAM637   LOC126917 3'  AGGCAGGCAGGCAGGCAGGCAG 16387       A   A _      _
            GCCG                    AGGCAG CAG C GGCAGGC GGCCG
                                |||||| ||| | ||||||| |||||
                                TCCGTC GTC G CCGTCCG CCGGC
                                    C   C T      T
GAM637   LOC129563 3'  AGGCAGGCGGGGCAGGCGGGGC 16533      A_____   AC__
            AGGCGGC                 GCAG     CAG    GGCAGGCGGC
                                ||||     |||    ||||||||||
                                CGTC     GTC    CCGTCCGCCG
                                  CGCCCC   CGCC
GAM637   LOC132573 3'  AGGCGGACAGGGCGGCC     16534      A    ACGGCA
                                AGGC GACAG     GGCGGCC
                                |||| |||||     |||||||
                                TCCG CTGTC     CCGCCGG
                                  C    _______
GAM637   LOC138399 5'  AGCAGGCAAGGTGCGGGTGGC  16535      A   ACG  A  C
                                GGCAG CAG   GC GG GGC
                                ||||| |||   || || |||
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                                TCGTC GTT   CG CC CCG
                                  C   CCA  C  A
GAM637   LOC144347 3'  GGCAGGCAGCGGGGAGCC    16536      A   A   CA  C
                                GGCAG CAG CGG  GG GGCC
                                ||||| ||| |||  || ||||
                                CCGTC GTC GCC  CC TCGG
                                  C  _  __  _
GAM637   LOC146280 5'  AGGCAGCAGACGGTGGACG   16537       A      CA
                                AGGCAG CAGACGG  GGCG
                                |||||| |||||||  ||||
                                TCCGTC GTCTGCC  CTGC
                                   _      AC
GAM637   LOC148018 5'  AGCAGGCAGGCGCCGAGCGGC  16538      A   A  GCA
                                GGCAG CAG CG   GGCGGC
                                ||||| ||| ||   ||||||
                                TCGTC GTC GC   TCGCCG
                                  C   C  GGC
GAM637   LOC148530 5'  AGGCAGACGGAGGCGGC     16539        AGAC  C
                                AGGCAGAC    GG AGGCGGC
                                ||||||||    || |||||||
                                TCCGTCTG    CC TCCGCCG
                                     ____  _
GAM637   LOC151512 5'  GGCGGGCAGGAGGCGGCCG    16540     AGA  GAC  C
                                GGC   CA   GG AGGCGGCCG
                                |||   ||   || |||||||||
                                CCG   GT   CC TCCGCCGGC
                                  CCC  ___  _
GAM637   LOC151534 5'  GGCGGGCGAGTACCTGGCGGCC 16541     AGACA  CG  A_
           G                     GGC    GA  GC  GGCGGCCG
                                |||    ||  ||  ||||||||
                                CCG    CT  TG  CCGCCGGC
                                  CCCG_  CA  GA
GAM637   LOC199953 5'  AGGCGGGCAGGCGGGCAGGCG  16542      AGA   A  _
                                AGGC   CAG CGG CAGGCG
                                ||||   ||| ||| ||||||
                                TCCG   GTC GCC GTCCGC
                                  CCC   C   C
GAM637   LOC199953 5'  AGGCGGGCAGGCGGGCAGGCG  16542      AGA   A  _
                                AGGC   CAG CGG CAGGCG
                                ||||   ||| ||| ||||||
                                TCCG   GTC GCC GTCCGC
                                  CCC   C   C
GAM637   LOC199953 5'  GGCAGGAGGCGGTGACGCCG   16543      AC  A   CA   G
                                GGCAG  AG CGG  GGCG CCG
                                |||||  || |||  |||| |||
                                CCGTC  TC GCC  CTGC GGC
                                  C_  C   A_   _
GAM637   LOC200269 5'  GGCAGCAGGCTCTCCGGGTGGC 16544      A  GAC   A_____  C
           CG                    GCAG CA   GGC     GG GGCCG
                                |||| ||   |||     || |||||
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                                CGTC GT   CCG     CC CCGGC
                                  _ ___   AGAGGC  A
GAM637   LOC202868 5'  AGGCAGGCAGGCAGGCAG    16388       A  GAC
                                AGGCAG CA   GGCAGGCGG
                                |||||| ||   |||||||||
                                TCCGTC GT   CCGTCCGTC
                                   C  ___
GAM637   LOC205143 5'  AGGCAGGCAGATGGGGGCACC  16545       A    C  CA    G
                                AGGCAG CAGA GG  GGCG CC
                                |||||| |||| ||  |||| ||
                                TCCGTC GTCT CC  CCGT GG
                                   C    A  C_   _
GAM637   LOC253358 5'  GGCAGGCAGGTGCGCGTCCG   16546       A   ACG  AG   G
                                GGCAG CAG   GC  GCG CCG
                                ||||| |||   ||  ||| |||
                                CCGTC GTC   CG  CGC GGC
                                   C   CA_  __   A
GAM637   LOC254381 5'  AGGCAGGCAGGGGCAAACG    16547       A   AC
                                AGGCAG CAG  GGCAGGCG
                                |||||| |||  ||||||||
                                TCCGTC GTC  CCGTTTGC
                                   C   C_
GAM637   LOC255251 3'  GCAGGCAACAGGGTGGCCG    16548      ACA    CA  C
                                GCAG   GACGG  GG GGCCG
                                ||||   |||||  || |||||
                                CGTC   TTGTC  CC CCGGC
                                  CG_    __  A
GAM637   LOC255565 3'  GGCAGACAGGTAAGCAGAGCCG 16549         AC_    GC
                                GGCAGACAG   GGCAG  GGCCG
                                |||||||||   |||||  |||||
                                CCGTCTGTC   TCGTC  TCGGC
                                     CAT    __
GAM637   LOC255704 5'  GGCACGCAGGCGGCGGGGCAGG 16550      GA   A    A_   __
            GC                    GGCA  CAG CGGC  GGC  GGC
                                ||||  ||| ||||  |||  |||
                                CCGT  GTC GCCG  CCG  CCG
                                  GC   C    CC   TC
GAM637   LOC256982 3'  AGGCGGACAGACGTCTGCGGCC 16551   A       __________  AGGCG
            GCCTGC                  GACAGACG        GC     GC
                                 ||||||||        ||     ||
                                 CTGTCTGC        CG     CG
                                C       AGACIIIGC  GCGGA
GAM637   LOC257054 5'  GGAGCAGACGGTGCTGGTGGC  16552    C  A      CA__  C
                                GG AG CAGACGG    GG GGC
                                || || |||||||    || |||
                                CC TC GTCTGCC    CC CCG
                                  _ _      ACGA  A
GAM637   LOC257364 3'  AGGCAGACAGAGGGCAGG    16553           C
                                AGGCAGACAGA GGCAGG
                                |||||||||| ||||||
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                                TCCGTCTGTCT CCGTCC
                                      C
GAM637  LOC64174  5' AGGCAGGCAGGGGTGGCAG   16554      A  AC  CA
                                AGGCAG CAG  GG  GGCGG
                                |||||| |||  ||  |||||
                                TCCGTC GTC  CC  CCGTC
                                   C  C_ A_
GAM637  LOC90010  3' GGCAGACAGGTAAGCAGAGCCG 16549        AC_   GC
                                GGCAGACAG  GGCAG  GGCCG
                                |||||||||  |||||  |||||
                                CCGTCTGTC  TCGTC  TCGGC
                                     CAT   __
GAM637  LOC90120  5' GCAGGCAGGTGGTGTGCGGGCC 16555    A  AC  CAG  _
          G                   GCAG CAG  GG  GCGG CCG
                              ||||  |||  ||  ||||  |||
                              CGTC GTC  CC  CGCC GGC
                                C  CA  ACA   C
GAM637  LOC90371  3' AGGCAGGCAGGCAGC      16556      GACAGAC
                                AGGCA     GGCAGGCGGC
                                |||||     ||||||||||
                                TCCGT     CCGTCCGTCG
                                  _______
GAM637  LOC92080  5' AGGCAGACAGAGGGGC     16557         C  CA
                                AGGCAGACAGA GG  GGC
                                |||||||||||  ||  |||
                                TCCGTCTGTCT CC  CCG
                                     _  __
GAM637  LOC92568  3' GGTAGATGGAGGTTTACGGCCG 16558   C  CA  C  CAG
                                GG AGA  GA GG  GCGGCCG
                                || |||  || ||  |||||||
                                CC TCT  CT CC  TGCCGGC
                                 A  AC  _  AAA
GAM638  MECP2     3'  TGCCGACTACGTTCCG     16561        A   GA
                                TGCCGACTG CGTT  CG
                                |||||||||  ||||  ||
                                ACGGCTGAT GCAA  GC
                                     _   G_
GAM639  APG5L     3'  GTGTCTGATACTGTAAGCCTT  16564       C  CCTCC
                                GTGTCTGA ACT    CCTT
                                |||||||| |||    ||||
                                CACAGACT TGA    GGAA
                                    A  CATTC
GAM639  BSN       3'  TGTGTCTGTTGCTCTCTACTTT 16565       ACA  C  CC  _
          CC                    TGTGTCTG  CTC TC  CTT CC
                                ||||||||  ||| ||  ||| ||
                                ACACAGAC  GAG AG  GAA GG
                                    AAC  _  AT  A
GAM639  CABC1     3'  TGTGTCTGGCATTCCCTGTTCC 16566       A  C   CCCC
                                TGTGTCTG CA TCCT   TTCC
                                |||||||| || ||||   ||||
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                                ACACAGAC GT AGGG    AAGG
                                    C  A    AC__
GAM639  CLOCK    3'  TGTCCTCTCCTCCCTTTC    16567      GACA       C
                                TGTCT    CTCCTCCC TTC
                                |||||    |||||||| |||
                                ACAGG    GAGGAGGG AAG
                                   A___       A
GAM639  ETV5     3'  TGTTCTGACTGCCCCCCTT    16568     G     ACTC
                                TGT TCTGAC    CTCCCCTT
                                ||| ||||||    ||||||||
                                ACA AGACTG    GGGGGGAA
                                  _     AC__
GAM639  FLG      5'  TGTGTCTGACTCTTCTGAATGT 16569          A  C  CCCCT
            CC                    TGTGTCTGAC CT CT     TCC
                                ||||||||||| || ||     |||
                                ACACAGACTG GA GA     AGG
                                      A  A  CTTAC
GAM639  HDAC4    3'  TGTGTCTGAACTTCTGCC    16570         C   C  C
                                TGTGTCTGA ACT CT CC
                                ||||||||| ||| || ||
                                ACACAGACT TGA GA GG
                                     _  A  C
GAM639  KL       3'  TGTATCTGCCATCTTCTTTTCC 16571         A  C  C  CCC
                                TGTGTCTG CA TC TC   TTCC
                                |||||||| || || ||   ||||
                                ACATAGAC GT AG AG   AAGG
                                     G  _  A  AA_
GAM639  NT5E     3'  GTCCTGTTCTTCCCCTTCC    16572      GACAC  C
                                GTCT    TC TCCCCTTCC
                                ||||    || |||||||||
                                CAGG    AG AGGGGAAGG
                                  ACA__  A
GAM639  PMX1     5'  TGTGCCTGACGTTTCACAGACC 16573          _____  TCC
            CCCTT                 TGTGTCTGAC    AC   TCCCCTT
                                ||||||||||    ||   |||||||
                                ACACGGACTG    TG   GGGGGAA
                                      CAAAG  TCT
GAM639  PMX1     5'  TGTGCCTGACGTTTCACAGACC 16573          _____  TCC
            CCCTT                 TGTGTCTGAC    AC   TCCCCTT
                                ||||||||||    ||   |||||||
                                ACACGGACTG    TG   GGGGGAA
                                      CAAAG  TCT
GAM639  PRG3     5'  TGTGTCTAGTATAGCCCCTTCC 16574         ACACTCCT
                                TGTGTCTG       CCCCTTCC
                                ||||||||       ||||||||
                                ACACAGAT       GGGGAAGG
                                     CATATC__
GAM639  PTGFRN   3'  TGTCCCCATCCTCCCCTTCC   16575      GA  C
                                TGTCT  CA TCCTCCCCTTCC
                                |||||  || ||||||||||||
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                                ACAGG  GT AGGAGGGGAAGG
                                  G_  _
GAM639  SPARC    3'  TGTGTCTGTTACTTCCCTT   16576        AC   CCTC
                                TGTGTCTG  ACT   CCCTT
                                ||||||||  |||   |||||
                                ACACAGAC  TGA   GGGAA
                                    AA   A___
GAM639  TCF19    3'  TGTATTTCCATCTCTCCCCTTC 16577      CTGA  C  _
          C                      TGTGT   CA TC CTCCCCTTCC
                                |||||   || || ||||||||||
                                ACATA   GT AG GAGGGGAAGG
                                  AAG_  _  A
GAM639  TCF19    3'  TGTATTTCCATCTCTCCCCTTC 16577      CTGA  C  _
          C                      TGTGT   CA TC CTCCCCTTCC
                                |||||   || || ||||||||||
                                ACATA   GT AG GAGGGGAAGG
                                  AAG_  _  A
GAM639  APOL4    3'  TGTGTCTGGCTCACCTTC    16578        ACACTC   C
                                TGTGTCTG     CTC CCTTC
                                ||||||||     ||| |||||
                                ACACAGAC     GAG GGAAG
                                    C_____   T
GAM639  CXYorf1  5'  TGTGTCTGATGCCCTGGGTCC  16579         CA   C___
                                TGTGTCTGA  CTC   TCC
                                |||||||||  |||   |||
                                ACACAGACT  GGG   AGG
                                     AC   ACCC
GAM639  DKFZP434I1735 3'  TGTGTCTACAATGTCCCTT   16580        A  CTCCTC
                                TGTGTCTG CA     CCCTT
                                ||||||||  ||     |||||
                                ACACAGAT GT     GGGAA
                                    _  TACA__
GAM639  DKFZP586B2420 3'  TGTGTCTGCAACCCGGCTTTCC 16581        AC   __  CC
          TTC                    TGTGTCTG  ACTC  CT  CCTTC
                                |||||||  ||||  ||  |||||
                                ACACAGAC  TGGG  GA  GGAAG
                                    GT   CC  AA
GAM639  FLJ10895  3'  TGTGTTGAGCCCCTTCCCTTCC 16582      C   CA    C
                                TGTGT TGA  CTCCT CCCTTCC
                                |||||  |||  |||||  |||||||
                                ACACA ACT  GGGGA GGGAAGG
                                  _  C_    A
GAM639  FLJ11715  3'  TGTGCCTGGCCCCCTCTTC   16583        ACACT    C
                                TGTGTCTG    CCTCC CTTC
                                ||||||||    |||||  ||||
                                ACACGGAC    GGGGG GAAG
                                    C____    A
GAM639  FLJ14957  3'  TCTGTTTCTTTCTTCCCTTCC  16584     ACA  C_  C
                                TCTG   CT  CT CCCTTCC
                                ||||   ||  ||  |||||||
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                                AGAC   GA  GA GGGAAGG
                                  AAA  AA  A
GAM639  FLJ20207  5'  TGGTCTGCCTCCTCCC      16585    T    ACA
                                TG GTCTG   CTCCTCCC
                                || |||||   ||||||||
                                AC CAGAC   GAGGAGGG
                                 _    G__
GAM639  FLJ20574  3'  TCACAACACGCTCTTCCCCTTC 16586    _     __ C
          C                      TC TGACAC  TC TCCCCTTCC
                                 || ||||||  || |||||||||
                                 AG GTTGTG  AG AGGGGAAGG
                                  T     CG  A
GAM639  FLJ22054  3'  TGTGTCTAAATAAAATCTCCCT 16587         CACTCC  _
          T                      TGTGTCTGA     TC CCCTT
                                 |||||||||     || |||||
                                 ACACAGATT     AG GGGAA
                                       TATTTT  A
GAM639  FLJ22612  3'  TGTTTGACACCCCCTTC     16588     C     TCCT
                                TGT TGACAC    CCCCTTC
                                ||| ||||||    |||||||
                                ACA ACTGTG    GGGGAAG
                                  A     _____
GAM639  FLJ23416  3'  TGTGTCTGACCTTCTGAGCTCC 16589          AC  _____
                                TGTGTCTGAC  TC    CTCC
                                ||||||||||  ||    ||||
                                ACACAGACTG  AG    GAGG
                                      GA  ACTC
GAM639  FLJ25193  3'  GCTGGCACTCCTCCCCTTCC   16590   T   A
                                G CTG CACTCCTCCCCTTCC
                                | ||| ||||||||||||||
                                C GAC GTGAGGAGGGGAAGG
                                 _  C
GAM639  HDAC9-PENDING 5'  TGTGTCTGTGCCTCTCTTC    16591        ACACT   CC
                                TGTGTCTG    CCTC  CTTC
                                ||||||||    ||||  ||||
                                ACACAGAC    GGAG  GAAG
                                     AC___    A_
GAM639  HDAC9-PENDING 5'  TGTGTCTGTGCCTCTCTTC    16591        ACACT   CC
                                TGTGTCTG    CCTC  CTTC
                                ||||||||    ||||  ||||
                                ACACAGAC    GGAG  GAAG
                                     AC___    A_
GAM639  HDAC9-PENDING 5'  TGTGTCTGTGCCTCTCTTC    16591        ACACT   CC
                                TGTGTCTG    CCTC  CTTC
                                ||||||||    ||||  ||||
                                ACACAGAC    GGAG  GAAG
                                     AC___    A_
GAM639  KIAA0350  3'  TGTGTCTGATGCATCTGGGTCC 16592         __  _  CC_
                                TGTGTCTGA  CA CT   TCC
                                |||||||||  || ||   |||
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                                ACACAGACT  GT GA   AGG
                                     AC  A  CCC
GAM639  KIAA0800 3' TGGCATGACATTCCTTCTCTT 16593    T  C    C   CCC
                                TG GT TGACA TCCT   CTT
                                || || ||||| ||||   |||
                                AC CG ACTGT AGGA   GAA
                                 _ T    A    AGA
GAM639  KIAA1789 3' TGTATCTACCTCTCCTT     16594        ACACT   C
                                TGTGTCTG    CCTC CCTT
                                ||||||||    |||| ||||
                                ACATAGAT    GGAG GGAA
                                     _____   A
GAM639  KIAA1789 3' TGTATCTACCTCTCCTT     16594        ACACT   C
                                TGTGTCTG    CCTC CCTT
                                ||||||||    |||| ||||
                                ACATAGAT    GGAG GGAA
                                     _____   A
GAM639  KIAA1881 3' TGTGTCTGGCATCCTAGCC   16595        A  C   CC
                                TGTGTCTG CA TCCT  CC
                                |||||||| || ||||  ||
                                ACACAGAC GT AGGA  GG
                                     C  _   TC
GAM639  KLHL4    3' TGCTCTTACTCCTCCTTTTCC 16596    G  GAC      CC
                                TGT TCT   ACTCCTCC  TTCC
                                ||| |||   ||||||||  ||||
                                ACG AGA   TGAGGAGG  AAGG
                                  _  A__       AA
GAM639  MGC15677 5' GCAAATACTCCTCCTCTTC   16597    CT  C      C
                                GT  GA ACTCCTCC CTTC
                                ||  || |||||||| ||||
                                CG  TT TGAGGAGG GAAG
                                 T_  A       A
GAM639  MGC15873 3' TGTGTCTGTGTCCTCATCTCTT 16598        ACA_  __  CC
           CTTC                   TGTGTCTG   CTC  CTC  CTTC
                                ||||||||   |||  |||  ||||
                                ACACAGAC   GAG  GAG  GAAG
                                     ACAG   TA   AA
GAM639  ODZ2     3' GTGCTCACTCCTCCTCTT    16599     CTGA       C
                                GTGT    CACTCCTCC CTT
                                ||||   ||||||||| |||
                                CACG    GTGAGGAGG GAA
                                  A___        A
GAM639  P450RAI-2 3' TGGGTTTGACCAGAGACCCCTT 16600    T  C   ACTCCT
           CC                     TG GT TGAC     CCCCTTCC
                                || || ||||     ||||||||
                                AC CA ACTG     GGGGAAGG
                                 C  A   GTCTCT
GAM639  PAK6     5' TGTGTCTGGCGTCCCCTC    16601        ACACTCC
                                TGTGTCTG      TCCCCTT
                                ||||||||      |||||||
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                                ACACAGAC      AGGGGAG
                                    CGC____
GAM639  PISD     5'  TGTTTTCCTCTTTCCTCCCCTT 16602     G_   GACAC
             CC                   TGT  TCT    TCCTCCCCTTCC
                                  |||  |||    ||||||||||||
                                  ACA  AGG    AGGAGGGGAAGG
                                   AA   AGAA_
GAM639  SRF      3'  TGTTTCTGAAAAAGCTCCCCTT 16603     G    CACTC
             C                    TGT TCTGA    CTCCCCTTC
                                  ||| |||||    |||||||||
                                  ACA AGACT    GAGGGGAAG
                                   A    TTTTC
GAM639  TUCAN    5'  TCTGGACACTCCTTTTTTTCC  16604     _      CCCC
                                  TCTG ACACTCCT    TTCC
                                  |||| ||||||||    ||||
                                  AGAC TGTGAGGA    AAGG
                                    C       AAAA
GAM639  WDR13    5'  TGTCTCTCCTCCCTTTC     16605      GACA       C
                                  TGTCT    CTCCTCCC TTC
                                  |||||    |||||||| |||
                                  ACAGA    GAGGAGGG AAG
                                     ____       A
GAM639  LOC126751 3'  TGTGTCTGATGCCTCGCTC    16606         CA_   _
                                  TGTGTCTGA   CTC CTC
                                  |||||||||   ||| |||
                                  ACACAGACT   GAG GAG
                                       ACG   C
GAM639  LOC134623 5'  TGACACTCATTCTTCCTCTTCC 16607         C____   C
                                  TGACACTC    TCC CTTCC
                                  ||||||||    ||| |||||
                                  ACTGTGAG    AGG GAAGG
                                       TAAGA   A
GAM639  LOC148758 5'  TGTATCTGTCTCTCCCTTTC   16608         ACA   C    C
                                  TGTGTCTG   CTC TCCC TTC
                                  ||||||||   ||| |||| |||
                                  ACATAGAC   GAG AGGG AAG
                                       A__   _    A
GAM639  LOC150035 5'  TGTGCCTGTCACCTTTCTCTT  16609         A    CC  CC
                                  TGTGTCTG CACT  TC  CTT
                                  |||||||| ||||  ||  |||
                                  ACACGGAC GTGG  AG  GAA
                                       A    AA  A_
GAM639  LOC152282 5'  TGTGTCTGAAGTTTCCTCC    16610         CAC_
                                  TGTGTCTGA    TCCTCC
                                  |||||||||    ||||||
                                  ACACAGACT    AGGAGG
                                       TCAA
GAM639  LOC153688 3'  TGTGGCTGCTTCCCCTTC     16611      T   ACACTCC
                                  TGTG CTG      TCCCCTTC
                                  |||| |||      ||||||||
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                                ACAC GAC      AGGGGAAG
                                  C   GA_____
GAM639   LOC158327 3'  ATCAGAATACTCCTCCTTTTTC 16612     T  C_      CC_
                                GTC GA  ACTCCTCC   TTC
                                ||| ||  ||||||||   |||
                                TAG CT  TGAGGAGG   AAG
                                  T  TA       AAA
GAM639   LOC158927 3'  TGTGTCTGGCTTTCCTTC    16613        ACACTC  CC
                                TGTGTCTG     CT  CCTTC
                                ||||||||     ||  |||||
                                ACACAGAC     GA  GGAAG
                                     C_____  AA
GAM639   LOC200093 5'  TGTGTCTGATGCCCTGGGTCC  16579         CA   C___
                                TGTGTCTGA  CTC    TCC
                                |||||||||  |||    |||
                                ACACAGACT  GGG    AGG
                                      AC   ACCC
GAM639   LOC202546 3'  TGTGCTCGCCCCTCCCCTTCC  16614     TC  ACA
                                TGTG  TG   CTCCTCCCCTTCC
                                ||||  ||   ||||||||||||
                                ACAC  GC   GGGGAGGGGAAGG
                                  GA  ___
GAM639   LOC203197 5'  TGTTTCTACTTCCCCTTC    16615     G   GAC   CC
                                TGT TCT   ACT  TCCCCTTC
                                ||| |||   |||  ||||||||
                                ACA AGA   TGA  AGGGGAAG
                                  A  ___   __
GAM639   LOC220469 3'  TGTGGCTAACTTCCCCTTC    16616      T    ACTCC
                                TGTG CTGAC     TCCCCTTC
                                |||| |||||     ||||||||
                                ACAC GATTG     AGGGGAAG
                                  C    A____
GAM639   LOC221042 3'  TGTGCCTGGTGTTCTCGGCTTC 16617         ACACTC   CC
                                TGTGTCTG     CTC  CTTC
                                ||||||||     |||  ||||
                                ACACGGAC     GAG  GAAG
                                     CACAA_   CC
GAM639   LOC254556 3'  TGTGCCTGACTCCCTTTC    16618         ACTCC    C
                                TGTGTCTGAC     TCCC TTC
                                ||||||||||     |||| |||
                                ACACGGACTG     AGGG AAG
                                       _____    A
GAM639   LOC255101 5'  TGCCCAACTCCTCCTCTTC    16619      TG  AC     C
                                TGTC  AC  TCCTCC CTTC
                                ||||  ||  |||||| ||||
                                ACGG  TG  AGGAGG GAAG
                                  GT  __      A
GAM639   LOC255152 5'  TGTGTCTTACAGAGATTCCTTT 16620        G   CTCC_   CC
            TC                   TGTGTCT ACA     TCC  TTC
                                ||||||| |||     |||  |||
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                                ACACAGA TGT    AGG  AAG
                                    A   CTCTA   AA
GAM639  LOC255527 5'  TGTCTACCAGGTTTCTCCCCTT 16621       A  CTC__
                                TGTCTG CA    CTCCCCTT
                                ||||||| ||    ||||||||
                                ACAGAT GT    GAGGGGAA
                                   G  CCAAA
GAM639  LOC256337 3'  TCTGACTCCTCCTCTT      16622       AC     C
                                TCTGAC  TCCTCC CTT
                                ||||||  |||||| |||
                                AGACTG  AGGAGG GAA
                                   __     A
GAM639  LOC257078 3'  TGTTTTCTGTCCCTTCCCTTCC 16623     G_   ACAC   C
                                TGT  TCTG   TCCT CCCTTCC
                                |||  ||||   |||| |||||||
                                ACA  AGAC   GGGA GGGAAGG
                                  AA   A___   A
GAM639  LOC257460 5'  TGTGCTCGCCCCTCCCCTTCC  16614     TC  ACA
                                TGTG  TG   CTCCTCCCCTTCC
                                ||||  ||   ||||||||||||
                                ACAC  GC   GGGGAGGGGAAGG
                                  GA  ___
GAM639  LOC91040  5'  TGTGTCTGATGCCCTGGGTCC  16579        CA   C___
                                TGTGTCTGA  CTC    TCC
                                |||||||||  |||   |||
                                ACACAGACT  GGG    AGG
                                     AC   ACCC
GAM639  LOC93613  5'  TGCGTCTCTTCTCCTCTTC   16624       GACA  C    C
                                TGTGTCT    CT CTCC CTTC
                                |||||||    || |||| ||||
                                ACGCAGA    GA GAGG GAAG
                                   ____ A    A
GAM640  MMP19    5'  ACCCGGCCTGAGACTGTCAT   16627        AC    _
                                ACCCGGCCT  GACTG CGT
                                |||||||||  ||||| |||
                                TGGGCCGGA  CTGAC GTA
                                     CT     A
GAM640  SECTM1   3'  CCCGGCCTGCGCTTGCCCCCT  16628        A  A  GC  G
                                CCCGGCCT CG CT  GT CTCT
                                |||||||| || ||  || ||||
                                GGGCCGGA GC GA  CG GGGA
                                     C  _  A_  G
GAM640  SLC26A4  3'  CCTGGCCTACATTCACTC    16629    C      ACTGCG
                                CC GGCCTACG     TGCTC
                                || |||||||      |||||
                                GG CCGGATGT     GTGAG
                                 A       AA____
GAM640  TNFRSF6B  3'  CGGCTGGCACTGCGTGTTCT   16630     CTACG       C
                                CGGC    ACTGCGTG TCT
                                ||||    |||||||| |||
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                                GCCG    TGACGCAC AGA
                                  ACCG_       A
GAM640  C17orf31  5'  ACACCGGTCAACTGTGTGCTCT 16631    _   CCTA     C
                                AC CCGG   CGACTG GTGCTCT
                                || ||||   |||||| |||||||
                                TG GGCC   GTTGAC CACGAGA
                                 T   A___     A
GAM640  FLJ11320  3'  ACCCGGCCTACGGCAT      16632          ACT
                                ACCCGGCCTACG   GCGT
                                ||||||||||||   ||||
                                TGGGCCGGATGC   CGTA
                                       ___
GAM640  FLJ12876  3'  GGCCCACGCCAGGTGCTCT   16633        A   C
                                GGCCTACG CTG GTGCTCT
                                |||||||| ||| |||||||
                                CCGGGTGC GGT CACGAGA
                                     _  C
GAM640  FLJ20457  5'  CCCGGACTGGGCGTGCTC    16634      CCT  GACT
                                CCCGG   AC    GCGTGCTC
                                |||||   ||    ||||||||
                                GGGCC   TG    CGCACGAG
                                   ___  ACC_
GAM640  FLJ21415  3'  CCCGGCCTCCGGTTTCATCT   16635        A  ACTG   G
                                CCCGGCCT CG    CGT CT
                                |||||||| ||    ||| ||
                                GGGCCGGA GC    GTA GA
                                     G  CAAA   _
GAM640  KIAA0014  3'  CCTGGCCCAGCTGCGCGTGCTC 16636    C     CGAC
           T                     CC GGCCTA    TGCGTGCTCT
                                || ||||||    ||||||||||
                                GG CCGGGT    GCGCACGAGA
                                 A     CGAC
GAM640  KIAA0329  3'  CCCGGCCTGGGGCTGCCTCT   16637        ACGA    GTG
                                CCCGGCCT    CTGC   CTCT
                                ||||||||    ||||   ||||
                                GGGCCGGA    GACG   GAGA
                                     CCCC    ___
GAM640  KIAA1871  3'  ACCTGGCCTACACTCATTACT  16638     C      G   GCG
                                ACC GGCCTAC ACT   TGCT
                                ||| ||||||| |||   ||||
                                TGG CCGGATG TGA   ATGA
                                  A      _  GTA
GAM640  PDZD2     3'  ACCTGGCTTGTAACTACATTTC 16639     C   CTAC       GC
           T                     ACC GGC    GACTGCGT  TCT
                                ||| |||    ||||||||  |||
                                TGG CCG    TTGATGTA  AGA
                                  A  AACA       A_
GAM640  RNB6      3'  CCCAGGCTCCTGTGCGTGCTCT 16640      C  ACGAC
                                CCCGG CT     TGCGTGCTCT
                                ||||| ||     ||||||||||
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                                GGGTC GA    ACGCACGAGA
                                   C  GGAC_
GAM640  SDC3    3'  CCTGGCCTGCCTCGTGCTCT  16641   C    ACGA  G
                                CC GGCCT   CT CGTGCTCT
                                || |||||   || ||||||||
                                GG CCGGA   GA GCACGAGA
                                 A    CG__  _
GAM640  STK29   3'  CCTGGCCTGCTGGGAAGGCTCT 16642   C    ACGA  CGT__
                                CC GGCCT   CTG    GCTCT
                                || |||||   |||    |||||
                                GG CCGGA   GAC    CGAGA
                                 A    C___  CCTTC
GAM640  TDP1    5'  CCCGGCCTTCGATTTGCC    16643       A  CTGCG
                                CCCGGCCT CGA    TGCT
                                |||||||| |||    ||||
                                GGGCCGGA GCT    ACGG
                                     A  AA___
GAM640  TEB4    3'  GCCTGCGCACTACTGCTCT   16644     A _   G
                                GCCT CG ACTGC TGCTCT
                                |||| || ||||| ||||||
                                CGGA GC TGATG ACGAGA
                                  C  G   _
GAM640  LOC153682 3'  CCCGGCCTAGATTCATTTCT  16645       C  CTG  GC
                                CCCGGCCTA GA  CGT  TCT
                                ||||||||| ||  |||  |||
                                GGGCCGGAT CT  GTA  AGA
                                     _ AA_  A_
GAM640  LOC200035 3'  CCCGGCCTATTGCTTGGGTCTC 16646       CGAC  GTG___
           T                    CCCGGCCTA   TGC    CTCT
                                |||||||||   |||    ||||
                                GGGCCGGAT   ACG    GAGA
                                     A___   AACCCA
GAM640  LOC222865 3'  CCCGGCCTTGACTCAACCTCT  16647       AC   G  TG
                                CCCGGCCT  GACT CG  CTCT
                                ||||||||  |||| ||  ||||
                                GGGCCGGA  CTGA GT  GAGA
                                     A_   _  TG
GAM640  LOC256158 5'  CCCGGCCCACGGCGT      16648         ACT
                                CCCGGCCTACG   GCGT
                                ||||||||||   ||||
                                GGGCCGGGTGC   CGCA
                                        ___
GAM640  LOC85479  5'  ACCCGGCCTATGATGGTTACT  16649        C  C  CG
                                ACCCGGCCTA GA TG  TGCT
                                |||||||||| || ||  ||||
                                TGGGCCGGAT CT AC  ATGA
                                     A  _  CA
GAM640  LOC93259  5'  ACCCAGCCTGTGGCTGCCC   16650       ACGACT  G
                                ACCCGGCCT    GC TGCTC
                                |||||||||    || |||||
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                                TGGGTCGGA     CG ACGGG
                                     CAC___ _
GAM641  ABCC5   5'  CAGCCGCTCAACCACGC     16653       G     C
                                CAGCCGC TCAACC CGT
                                ||||||| |||||| |||
                                GTCGGCG AGTTGG GCG
                                   _     T
GAM641  AMPD3   5'  CAGCCGCGTGCAGCCCCCGT  16654         _ A_
                                CAGCCGCGT CA  CCCCGT
                                ||||||||| ||  ||||||
                                GTCGGCGCA GT  GGGGCA
                                     C  CG
GAM641  BTEB1   5'  GCCTCGCGGTCCCGTGGCC   16655     G   CAAC
                                GCC CGT   CCCGTGGCC
                                ||| |||   |||||||||
                                CGG GCG   GGGCACCGG
                                  A  CCA_
GAM641  CDC34   3'  CAGCAGCGCCCCCGTGGC    16656     C   CAA
                                CAGC GCGT  CCCCGTGGC
                                |||| ||||  |||||||||
                                GTCG CGCG  GGGGCACCG
                                  T   ___
GAM641  CDKN2B  3'  GCGTCAGTCCCCCGTGGC    16657       A__
                                GCGTCA  CCCCGTGGC
                                ||||||  |||||||||
                                CGCAGT  GGGGCACCG
                                   CAG
GAM641  CELSR3  3'  CAGCCACTCTCCCCCGTGG   16658       G  AA
                                CAGCCGC TC  CCCCGTGG
                                ||||||| ||  ||||||||
                                GTCGGTG AG  GGGGCACC
                                   _  AG
GAM641  CHS1    5'  GCCGCGTCGACGCGGCC     16659       AACCC
                                GCCGCGTC    CGTGGCC
                                ||||||||    |||||||
                                CGGCGCAG    GCGCCGG
                                     CT___
GAM641  CSK     3'  GCCGCCCGCTCCGTGGCC    16660      G  AACC
                                GCCGC TC    CCGTGGCC
                                ||||| ||    ||||||||
                                CGGCG GG    GGCACCGG
                                  _  CGA_
GAM641  FRZB    5'  CAGCCGCGCAGTGGAC      16661       T  ACCCC   _
                                CAGCCGCG CA    GTGG C
                                |||||||| ||    |||| |
                                GTCGGCGC GT    CACC G
                                   _ _____   T
GAM641  GGA3    3'  CAACTCATCACTCCGTGGCC  16662     CG    A C
                                CAGC  CGTCA C CCGTGGCC
                                ||||  ||||| | ||||||||
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                                GTTG  GTAGT G GGCACCGG
                                  A_    _ A
GAM641  GGA3     3'  CAACTCATCACTCCGTGGCC  16662      CG    A C
                                CAGC  CGTCA C CCGTGGCC
                                ||||  ||||| | ||||||||
                                GTTG  GTAGT G GGCACCGG
                                  A_    _ A
GAM641  HIC1     5'  CAGTGCGTGTTGACCGCGGCC  16663     CC   CAACC
                                CAG  GCGT    CCGTGGCC
                                |||  ||||    ||||||||
                                GTC  CGCA    GGCGCCGG
                                 A_   CAACT
GAM641  HS3ST3A1 5'  GCCGTGCGCCCCTGTGGCC   16664      C  CAA   _
                                GCCG GT   CCCC GTGGCC
                                |||| ||   |||| ||||||
                                CGGC CG   GGGG CACCGG
                                  A  C__    A
GAM641  MMP14    3'  CAGCCCACCCTGTGGC      16665      G GTCA    C
                                CAGCC C    ACCC GTGGC
                                ||||| |    |||| |||||
                                GTCGG G    TGGG CACCG
                                  _ _____    A
GAM641  MXI1     5'  CAGCCGCGCCAGCCGCGCC    16666          ACC    G
                                CAGCCGCGTCA   CCGTG CC
                                ||||||||||   ||||| ||
                                GTCGGCGCGGT   GGCGC GG
                                      C__    _
GAM641  NAP1L4   5'  GCTGCGCCGCCGTGGCC     16667    C    AACC
                                GC GCGTC    CCGTGGCC
                                || |||||    ||||||||
                                CG CGCGG    GGCACCGG
                                 A    C___
GAM641  NDUFA8   5'  CAGCCGCGTCGCCCCCGT    16668         AA
                                CAGCCGCGTC  CCCCGT
                                ||||||||||  ||||||
                                GTCGGCGCAG  GGGGCA
                                      CG
GAM641  PIGA     3'  AGTCCAGGCACCCCGTGGCC   16669    _  C  CA
                                AG CCG GT  ACCCCGTGGCC
                                || ||| ||  ||||||||||
                                TC GGT CG  TGGGGCACCGG
                                 A  C  __
GAM641  PIGA     3'  AGTCCAGGCACCCCGTGGCC   16669    _  C  CA
                                AG CCG GT  ACCCCGTGGCC
                                || ||| ||  ||||||||||
                                TC GGT CG  TGGGGCACCGG
                                 A  C  __
GAM641  PITPN    5'  GCCGCTCTCCCCGTGGCC     16670      G  AA
                                GCCGC TC  CCCCGTGGCC
                                ||||| ||  ||||||||||
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                                CGGCG AG  GGGGCACCGG
                                  _ A_
GAM641  PITX1    3'  GCCCGCTGTCGCTCCGTGGCC  16671     _ _  AACC
                                GCC GC GTC   CCGTGGCC
                                ||| || |||   ||||||||
                                CGG CG CAG   GGCACCGG
                                  G  A  CGA_
GAM641  RNGTT    5'  AGCCGCCTCCCCGTGG      16672       G CAA
                                AGCCGC T  CCCCGTGG
                                |||||| |  ||||||||
                                TCGGCG A  GGGGCACC
                                   G ___
GAM641  TJP1     5'  CAGCAGCACCCGTGGC      16673     C  TCAAC
                                CAGC GCG    CCCGTGGC
                                |||| |||    ||||||||
                                GTCG CGT    GGGCACCG
                                  T  ______
GAM641  BRD3     3'  GCCGCGTCAGACACGAGG    16674         _ CC  T
                                GCCGCGTCA AC  CG GG
                                ||||||||| ||  || ||
                                CGGCGCAGT TG  GC CC
                                     C  T_  T
GAM641  C5orf7   5'  CAGCGCAGCGCCCCCCGTGGCC 16675     _ _    AA
                                CAGC C GCGTC  CCCCGTGGCC
                                |||| | |||||  ||||||||||
                                GTCG G CGCGG  GGGGCACCGG
                                  C T    __
GAM641  Cab45    3'  CAGCCGCGGTCGGTCGGCC   16676        _ AACCCCG
                                CAGCCGCG TC      TGGCC
                                |||||||| ||      |||||
                                GTCGGCGC AG      GCCGG
                                     C  CCA____
GAM641  CASKIN1  3'  AGCTGCAAGCCCGTGGCC    16677     C  TCAAC
                                AGC GCG    CCCGTGGCC
                                ||| |||    |||||||||
                                TCG CGT    GGGCACCGG
                                  A  TC___
GAM641  CDC42BPB 3'  CAGCCGCGTCATGACGGG    16678          ACCC  T
                                CAGCCGCGTCA   CG GG
                                ||||||||||   || ||
                                GTCGGCGCAGT   GC CC
                                      ACT_  _
GAM641  CENTB5   5'  CAGCCGCGCCGGCCCGGACC   16679         AAC   T
                                CAGCCGCGTC   CCCG GGCC
                                ||||||||||   |||| ||||
                                GTCGGCGCGG   GGGC CTGG
                                      CC_   _
GAM641  DKFZP564O123 5'  CAGCCGCGTCACCCGGAGC   16680          AC   TG
                                CAGCCGCGTCA  CCCG  GC
                                ||||||||||  ||||  ||
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                                GTCGGCGCAGT  GGGC  CG
                                      __    CT
GAM641  FLJ13910  5'  CAGCCGTTCGGCCCGGGCC   16681      CG  AAC   T
                                CAGCCG  TC   CCCG GGCC
                                ||||||  ||   |||| ||||
                                GTCGGC  AG   GGGC CCGG
                                   A_  CC_   _
GAM641  FLJ20718  5'  CAGCCGCCTCGGCCTGAC    16682       G  AACC  G
                                CAGCCGC TC    CC TGGC
                                |||||||  ||    || ||||
                                GTCGGCG AG    GG ACTG
                                    G  CC__  _
GAM641  FLJ22173  5'  CAGCCTCCCCATCCTGTGGCC  16683      GCG   A  CC
                                CAGCC   TCA CC  GTGGCC
                                |||||   |||  ||  ||||||
                                GTCGG   GGT GG  CACCGG
                                   AGG   A  A_
GAM641  KIAA1110  3'  TGACCTCGCGATCCCGTGGCC  16684   A   G   CAAC
                                C GCC CGT    CCCGTGGCC
                                | |||  |||    |||||||||
                                A TGG GCG    GGGCACCGG
                                 C   A   CTA_
GAM641  KIAA1405  5'  AGCCGCTCGCCCGTGGCC    16685      G  AAC
                                AGCCGC TC   CCCGTGGCC
                                ||||||  ||   |||||||||
                                TCGGCG AG   GGGCACCGG
                                   _  C__
GAM641  MGC14156  5'  CAGCCTCGCCACCCGTGGCC   16686      G    AC
                                CAGCC CGTCA  CCCGTGGCC
                                |||||  |||||  |||||||||
                                GTCGG GCGGT  GGGCACCGG
                                   A    __
GAM641  MGC2647   3'  CAGCCACAGCCTGTGGC     16687        TCAAC  C
                                CAGCCGCG     CC GTGGC
                                ||||||||     ||  |||||
                                GTCGGTGT     GG CACCG
                                     C____  A
GAM641  MGC9753   5'  AGCCACGTTGGCCACCAGG   16688        CAA  _   T
                                AGCCGCGT   CC CCG GG
                                ||||||||   ||  |||  ||
                                TCGGTGCA   GG GGT CC
                                     ACC  T   _
GAM641  MYH7B     3'  GCCGCATCAGTGATGGCC    16690        ACCCC
                                GCCGCGTCA    GTGGCC
                                |||||||||    ||||||
                                CGGCGTAGT    TACCGG
                                     CAC__
GAM641  MYH7B     3'  CAGCCTGGGCCTCTGTGGCC   16689      ___  G  AACCCC
                                CAGCC   GC TC     GTGGCC
                                |||||   ||  ||     ||||||
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                                GTCGG  CG AG    CACCGG
                                  ACC  G  A_____
GAM641  PASK    5'  GCCATGGCCCCCCAACTCTGTG 16691  C_  AA  _______    III
            GCCG                  GTC  CCCC    GTGGCC  G
                                  |||  ||||    ||||||  |
                                  CGG  GGGG    CACCGG  C
                                AC  __   TTGAGA    III
GAM641  PDE11A  5'  GCCGACCCCACCCCGTGG   16692    _ G  A
                                GCCG C TCA CCCCGTGG
                                |||| | ||| ||||||||
                                CGGC G GGT GGGGCACC
                                  T G  _
GAM641  RGC32   5'  CAGCCGCGCCGGTCGACGCGGC 16693        AACCC_
            C                   CAGCCGCGTC    CGTGGCC
                                ||||||||||    |||||||
                                GTCGGCGCGG    GCGCCGG
                                     CCAGCT
GAM641  SLC26A1  5'  GCGTCAGGTCCCGTGGCC   16694     AC_
                                GCGTCA  CCCGTGGCC
                                ||||||  |||||||||
                                CGCAGT  GGGCACCGG
                                   CCA
GAM641  SLC26A1  5'  GCGTCAGGTCCCGTGGCC   16694     AC_
                                GCGTCA  CCCGTGGCC
                                ||||||  |||||||||
                                CGCAGT  GGGCACCGG
                                   CCA
GAM641  SPPL2A  5'  GCTGCGCTGCCTCCGTGGCC  16695   C   CAA  _
                                GC GCGT  CC CCGTGGCC
                                || ||||  || ||||||||
                                CG CGCG  GG GGCACCGG
                                 A   AC_  A
GAM641  STK22D  3'  GCCCGCGAGCCCGTGGCC   16696   _  TCAAC
                                GCC GCG   CCCGTGGCC
                                ||| |||   |||||||||
                                CGG CGC   GGGCACCGG
                                  G  TC___
GAM641  TEX27   3'  CAGCAGCCTCCCGTGGC    16697    C  G CAAC
                                CAGC GC T   CCCGTGGC
                                |||| || |   ||||||||
                                GTCG CG A   GGGCACCG
                                  T  G _____
GAM641  TOR2A   3'  GCCATCTGTCCCGTGGCC   16698    GC  AAC
                                GCC  GTC  CCCGTGGCC
                                |||  |||  |||||||||
                                CGG  TAG  GGGCACCGG
                                  __  ACA
GAM641  ZNF263  5'  GCCACGCCGGCCCCGTGGCC  16699       AA
                                GCCGCGTC  CCCCGTGGCC
                                ||||||||  ||||||||||
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                                CGGTGCGG  GGGGCACCGG
                                    CC
GAM641  ZNF297B  3'  CAGCCACAACTTGTGGC    16700       TCA  CCC
                                CAGCCGCG  AC  GTGGC
                                ||||||||  ||  |||||
                                GTCGGTGT  TG  CACCG
                                    ___  AA_
GAM641  ZNF297B  3'  CAGCCACAACTTGTGGC    16700       TCA  CCC
                                CAGCCGCG  AC  GTGGC
                                ||||||||  ||  |||||
                                GTCGGTGT  TG  CACCG
                                    ___  AA_
GAM641  LOC142964 5'  GCCGATGTCCCGTGGCC    16701     C_  CAAC
                                GCCG  GT   CCCGTGGCC
                                ||||  ||   |||||||||
                                CGGC  CA   GGGCACCGG
                                  TA  _____
GAM641  LOC144486 5'  GCCGCTGTCACCCGTGGCC   16702      _   AC
                                GCCGC GTCA  CCCGTGGCC
                                ||||| ||||  |||||||||
                                CGGCG CAGT  GGGCACCGG
                                  A   __
GAM641  LOC145127 3'  GCCTCTCTGGCCCCGTGGCC  16703    GCG  AA_
                                GCC   TC   CCCCGTGGCC
                                |||   ||   ||||||||||
                                CGG   AG   GGGGCACCGG
                                  AG_  ACC
GAM641  LOC145853 5'  GCGCACAGCGGCCCCGTGGCC  16704    _   TCAA
                                GC CGCG    CCCCGTGGCC
                                || ||||    ||||||||||
                                CG GTGT    GGGGCACCGG
                                 C   CGCC
GAM641  LOC148018 5'  GCCGCCAGCCCCGTGGC     16705      GT  A
                                GCCGC  CA CCCCGTGGC
                                |||||  || |||||||||
                                CGGCG  GT GGGGCACCG
                                   __  C
GAM641  LOC152404 5'  GCACGGAGCCCCGTGGCC    16706    C   TCAA
                                GC GCG    CCCCGTGGCC
                                || |||    ||||||||||
                                CG TGC    GGGGCACCGG
                                 _   CTC_
GAM641  LOC160777 3'  CAGCTGGTCAACCCAGGCC   16707     CGC      CGT
                                CAGC   GTCAACCC   GGCC
                                ||||   ||||||||   ||||
                                GTCG   CAGTTGGG   CCGG
                                  AC_       T__
GAM641  LOC166341 3'  CAGCCGCATTCTGCTGCCTCGT 16708         _ AAC__  _
           GGCC                   CAGCCGCGT C     CC CGTGGCC
                                |||||||||  |     ||  |||||||
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                                GTCGGCGTA G    GG GCACCGG
                                     A ACGAC  A
GAM641  LOC197285 3'  GCCTCTCTGTCCCCGTGGCC  16709    GCG  AA_
                                GCC   TC   CCCCGTGGCC
                                |||   ||   ||||||||||
                                CGG   AG   GGGGCACCGG
                                  AG_  ACA
GAM641  LOC197350 3'  CAGCAGCGCCCCCGTGGCC   16710     C   CAA
                                CAGC GCGT   CCCCGTGGCC
                                |||| ||||   ||||||||||
                                GTCG CGCG   GGGGCACCGG
                                  T   ___
GAM641  LOC221937 5'  CAGCCGCGCCAGCGCCGGCC  16711          ACCC  _
                                CAGCCGCGTCA   CGT GGCC
                                ||||||||||    ||| ||||
                                GTCGGCGCGGT   GCG CCGG
                                      C___  G
GAM641  LOC65243  5'  GCCACCCGCTCCGTGGCC    16712      G  AACC
                                GCCGC TC    CCGTGGCC
                                |||||  ||   ||||||||
                                CGGTG GG    GGCACCGG
                                  _  CGA_
GAM641  LOC91917  3'  GCCTCTCTGGCCCCGTGGCC  16703    GCG  AA_
                                GCC   TC   CCCCGTGGCC
                                |||   ||   ||||||||||
                                CGG   AG   GGGGCACCGG
                                  AG_  ACC
GAM641  LOC92714  5'  CAGCCGCGCAGCGAC       16713        T  ACCCC
                                CAGCCGCG CA    GTGGC
                                ||||||||  ||    |||||
                                GTCGGCGC GT    CGCTG
                                     _  _____
GAM642  C3orf1    5'  GGTGAGAATCCGTGCATTTGAC 16716    ACCT_   C
                                GGT    TCCG GCATTTGAC
                                |||    |||| |||||||||
                                CCA    AGGC CGTAAACTG
                                  CTCTT    A
GAM642  FLJ11726  3'  CACAGTGCTTTGTTACATTTGA 16717      AC   CCGC
                                CACGGT  CTT    GCATTTGA
                                ||||||  |||    ||||||||
                                GTGTCA  GAA    TGTAAACT
                                   C_   ACAA
GAM642  FLJ21918  3'  GGTACCTTCTGAGAGCTTTGAC 16718        CGC__  A
                                GGTACCTTC     GC TTTGAC
                                |||||||||     || ||||||
                                CCATGGAAG     CG AAACTG
                                     ACTCT  _
GAM642  LOC146489 5'  ACAGTACCTTTCTATTTGAC   16719        CCGCGC
                                ACGGTACCTT     ATTTGAC
                                ||||||||||     |||||||
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                                TGTCATGGAA     TAAACTG
                                     AGA___
GAM643  PIGR     3'  GAGTGACAGAAATGGTGCGG  16722        TT_   A
                                GAGTGACG   GTGG TGCGG
                                ||||||||   |||| |||||
                                CTCACTGT   TACC ACGCC
                                    CTT   _
GAM644  F13A1    3'  TTTCTGGCTTTGCCAAAAATAA 16725          __
            AAA                   TTTCTGGCTTT  TAAAAATAAAAA
                                ||||||||||  ||||||||||||
                                AAAGACCGAAA  GTTTTTATTTTT
                                     CG
GAM644  KCNA5    3'  TTCCTGGGATAAAAATAAA   16726       CTTT
                                TTTCTGG    TAAAAATAAA
                                |||||||    ||||||||||
                                AAGGACC    ATTTTTATTT
                                    CT__
GAM644  PDE1A    3'  TCTGGCTTTTGTCTCAAAAA  16727         AAAAA
                                TCTGGCTTTT    TAAAAA
                                ||||||||||    ||||||
                                AGACCGAAAA    GTTTTT
                                     CAGA_
GAM644  PLAG1    3'  TTCTGGCCACTAGAGAATGAAA 16728        T   AA_   A
            AC                    TTCTGGCT TTA   AAT AAAAC
                                ||||||| |||   ||| |||||
                                AAGACCGG GAT   TTA TTTTG
                                     T   CTC   C
GAM644  RPP30    3'  TTTCTAGCTCCAAATGAAAAC  16729          TAA    A
                                TTTCTGGCTTT   AAAT AAAAC
                                ||||||||||   |||| |||||
                                AAAGATCGAGG   TTTA TTTTG
                                     ___    C
GAM644  ZNFN1A3  3'  TGGCTTTTAAATTCCATAAAA  16730          A___
                                TGGCTTTTAAA    ATAAAA
                                ||||||||||    ||||||
                                ACCGAAAATTT    TATTTT
                                     AAGG
GAM644  BRD1     3'  TACCTCTTAAAAATAAAAA    16731    G
                                TG CTTTTAAAAATAAAAA
                                || ||||||||||||||||
                                AT GAGAATTTTTATTTTT
                                  G
GAM644  FLJ13448 3'  TTTCTGGCTTCTGAAAAC    16732           A
                                TTTCTGGCTTTT AAAAT
                                |||||||||||| |||||
                                AAAGACCGAAGA TTTTG
                                     C
GAM644  HPRP8BP  3'  TGGCTTTTAATACAAAA     16733          AA
                                TGGCTTTTAA  ATAAAA
                                ||||||||||  ||||||
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                                ACCGAAAATT  TGTTTT
                                     A_
GAM644  KIAA1005 3'  GCTTATTAAAAATAAAAA    16734     _
                                GCTT TTAAAAATAAAAA
                                |||| ||||||||||||
                                CGAA AATTTTTATTTTT
                                   T
GAM644  KIAA1715 3'  TTTCTGTTTTTTAAAAAC    16735      GC
                                TTTCTG  TTTTAAAAAT
                                ||||||  ||||||||||
                                AAAGAC  AAAATTTTTG
                                    AA
GAM644  MCM10    3'  TTTCTAGCTTTTGAAAAC    16736          A
                                TTTCTGGCTTTT AAAAT
                                |||||||||||| |||||
                                AAAGATCGAAAA TTTTG
                                       C
GAM644  MDN1     3'  TTTCTGGCCAAGTAAAAAC    16737        TT_
                                TTTCTGGCT   TAAAAAT
                                |||||||||   |||||||
                                AAAGACCGG   ATTTTTG
                                     TTC
GAM644  MGC11034 3'  TAGCTTTTAAAAGAAAAAA    16738          AT
                                TGGCTTTTAAAA  AAAAA
                                ||||||||||||  |||||
                                ATCGAAAATTTT  TTTTT
                                       CT
GAM644  MGC11386 3'  TCTGTCAATTTAAAAATAAAAA 16739     GCT_
                                TCTG   TTTAAAAATAAAAA
                                ||||   ||||||||||||||
                                AGAC   AAATTTTTATTTTT
                                  AGTT
GAM644  MGC26655 3'  TGGCTTTTACACAAAAA     16740        AAA
                                TGGCTTTTA   ATAAAAA
                                |||||||||   |||||||
                                ACCGAAAAT   TGTTTTT
                                     G__
GAM644  PTK9     3'  TTTCTAGCTTTAACTCAAAAAT 16741         ____
           A                     TTTCTGGCTT   TTAAAAATA
                                 ||||||||||   |||||||||
                                 AAAGATCGAA   AGTTTTTAT
                                      ATTG
GAM644  RAB33B   3'  TGTTTTTTAAAAATAAAAAC  16742    GC
                                TG  TTTTAAAAATAAAAAC
                                ||  ||||||||||||||||
                                AC  AAAATTTTTATTTTTG
                                 AA
GAM644  LOC134111 3'  TTCTGGCTGGAGTAAAAAC   16743        TT__
                                TTCTGGCT    TAAAAAT
                                ||||||||    |||||||
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                                AAGACCGA    ATTTTTG
                                    CCTC
GAM644   LOC145957 3'  TTTCTGCCTTTGTAAAATAAAA 16744       G    TA
           AC                    TTTCTG CTTT  AAAATAAAAAC
                                 |||||| ||||  ||||||||||
                                 AAAGAC GAAA  TTTTATTTTTG
                                    G    CA
GAM644   LOC255082 5'  TTTCTGGCTCTTAGAAAT     16745            A
                                 TTTCTGGCTTTTA AAAT
                                 |||||||||||| ||||
                                 AAAGACCGAGAAT TTTA
                                         C
GAM644   LOC256295 3'  CTTCTGGAAGCCAAAAATAA   16746        CTT
                                 TTTCTGG   TTAAAAATAA
                                 |||||||   ||||||||||
                                 GAAGACC   GGTTTTTATT
                                     TTC
GAM645   LOC148549 5'  AAGATACTTCGTGGCTTTTCGT 16749     T       AAAATA
                                 AAG ATACTTCGT     TTCGT
                                 ||| |||||||||     |||||
                                 TTC TATGAAGCA     AAGCA
                                   _       CCGAA_
GAM646   CEACAM6   3'  AGTCTTGTTTTGACATC     16752    C       T
                                 AG CTTGTTTTG ATATT
                                 || ||||||||| |||||
                                 TC GAACAAAAC TGTAG
                                  A       _
GAM646   G6PC      3'  AAGTCTTGCTTTTGTATAT    16753    C       _
                                 AAG CTTGTTTT GTATAT
                                 ||| |||||||| ||||||
                                 TTC GAACGAAA CATATA
                                   A       A
GAM646   MSH3      3'  CAAAAGCTTGGGAATTATATTC 16754        C   TTTTG
           T                      CAAAAGC TTG     TATATTCT
                                  ||||||| |||     ||||||||
                                  GTTTTCG AAC     ATATAAGA
                                      _   CCTTA
GAM646   U2AF1     3'  CAGAAACCCATCTTTGTAT    16755    A     TG
                                 CA AAGCCT  TTTTGTAT
                                 || ||||||  ||||||||
                                 GT TTTGGG  GAAACATA
                                  C     TA
GAM646   UBE2V1    3'  TGAAAGCCCTGTTTAAAACTTC 16756    A         TGTATA
           T                      C AAAGCCTTGTTT     TTCT
                                  | ||||||||||||     ||||
                                  A TTTCGGGACAAA     AAGA
                                  C          TTTTG_
GAM646   UBE2V1    3'  TGAAAGCCCTGTTTAAAACTTC 16756    A         TGTATA
           T                      C AAAGCCTTGTTT     TTCT
                                  | ||||||||||||     ||||
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                                A TTTCGGGACAAA      AAGA
                                 C          TTTTG_
GAM646  UBE2V1    3'  TGAAAGCCCTGTTTAAAACTTC 16756    A          TGTATA
              T                   C AAAGCCTTGTTT      TTCT
                                  | ||||||||||||      ||||
                                A TTTCGGGACAAA      AAGA
                                 C          TTTTG_
GAM646  ZNF257    3'  AAAGGCCTTGTCACATTC    16757     A       TTGT
                                AAA GCCTTGTT    ATATTC
                                ||| ||||||||    ||||||
                                TTT CGGAACAG    TGTAAG
                                  C       _____
GAM646  C20orf38  3'  AGCCTTGTTTTGTCATATT    16758             _
                                AGCCTTGTTTTGT ATATT
                                |||||||||||| |||||
                                TCGGAACAAAACA TATAA
                                         G
GAM646  DKFZP566J091 3'  CAGAAGCCTCGTTTGACATT   16759     A         T T
                                CA AAGCCTTGTTT G ATATT
                                || ||||||||||| | |||||
                                GT TTCGGAGCAAA C TGTAA
                                 C          _ _
GAM646  KIAA1349  3'  AGCCTGGTGTATATTCT     16760       T  TTT
                                AGCCT GT   GTATATTCT
                                ||||| ||   |||||||||
                                TCGGA CA   CATATAAGA
                                   C  ___
GAM646  KIAA1655  5'  CAAAGGCCTTGTTATCCTCATC 16761       A       TTGTATAT
              T                   CAAA GCCTTGTT       TCT
                                  |||| ||||||||       |||
                                GTTT CGGAACAA       AGA
                                   C       TAGGAGT_
GAM646  LGALS8    3'  CAGAAGCCATTCTGTAT     16762     A     TT
                                CA AAGCC  GTTTTGTAT
                                || |||||  |||||||||
                                GT TTCGG  TAAGACATA
                                 C     __
GAM646  MGC32104  3'  TGAAGACCTTGTCATATTC    16763    A  _      TTGT
                                A AAG CCTTGTT    ATATTC
                                | ||| |||||||    ||||||
                                A TTC GGAACAG    TATAAG
                                 C  T     _____
GAM646  WBP4      3'  AAAGGCCCTGTTTCTCCAT    16764     A        GTA
                                AAA GCCTTGTTTT   TAT
                                ||| ||||||||||   |||
                                TTT CGGGACAAAG   GTA
                                  C         AG_
GAM646  LOC149194 5'  CAAAAGACTTGTTTTTGT     16765        C       _
                                CAAAAG CTTGTTTT GT
                                |||||| |||||||| ||
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                                GTTTTC GAACAAAA CA
                                   T       A
GAM646  LOC150157 3'  GCCTTGTCTTTATTAAATTCT  16766          GTAT__
                                GCCTTGTTTT     ATTCT
                                ||||||||||     |||||
                                CGGAACAGAA     TAAGA
                                     ATAATT
GAM646  LOC151171 5'  CAGGAGCCCTGCCTGATGTTCT 16767    AA        T T  A
                                CA  AGCCTTGTTT G AT TTCT
                                ||  |||||||||| | || ||||
                                GT  TCGGGACGGA C TA AAGA
                                 CC         _ _  C
GAM646  LOC151534 3'  CCTTGTTCTATGGTTCT     16768          ATA
                                CCTTGTTTTGT   TTCT
                                ||||||||||   ||||
                                GGAACAAGATA   AAGA
                                     CC_
GAM646  LOC196890 3'  GCCTTGTCTTTATTAAATTCT  16766          GTAT__
                                GCCTTGTTTT     ATTCT
                                ||||||||||     |||||
                                CGGAACAGAA     TAAGA
                                     ATAATT
GAM646  LOC253482 3'  CAAAAGCTTAGCATATTC    16769        C   TTTT
                                CAAAAGC TTG    GTATATTC
                                ||||||| |||    ||||||||
                                GTTTTCG AAT    CGTATAAG
                                   _   _____
GAM646  LOC256979 5'  AAAGCCTTGAACCATATTCT   16770         TTTTG
                                AAAGCCTTG     TATATTCT
                                |||||||||     ||||||||
                                TTTCGGAAC     GTATAAGA
                                     TTG__
GAM647  ALOX15    3'  GATTTATATAATTGTGGCTA   16773         GGTT    A
                                GATTTATA    TTGT GCTA
                                ||||||||    |||| ||||
                                CTAAATAT    AACA CGAT
                                     ATT_    C
GAM647  F8A       3'  ATGGATTTAGGGCTGTG     16774          TA    T
                                ATGGATTTA  GGTT TG
                                |||||||||  |||| ||
                                TACCTAAAT  CCGA AC
                                     C_    C
GAM647  FRK       3'  ATGGCTTTACCATCATTGTAG  16775      A    AGGTT
                                ATGG TTTAT     TTGTAG
                                ||||  |||||     ||||||
                                TACC AAATG     AACATC
                                  G     GTAGT
GAM647  MAPRE2    3'  TGAATGACAGTTTTGTGGCT   16776       TTATA       A
                                TGGAT     GGTTTTGT GCT
                                |||||     |||||||| |||
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                                ACTTA    TCAAAACA CGA
                                  CTG__      C
GAM647  MEOX1    3'  TGGATTTAAAAGGAGTAGCT  16777       T_  TTTT
                                TGGATTTA  AGG   GTAGCT
                                ||||||||  |||   ||||||
                                ACCTAAAT  TCC   CATCGA
                                    TT  T___
GAM647  MEOX1    3'  TGGATTTAAAAGGAGTAGCT  16777       T_  TTTT
                                TGGATTTA  AGG   GTAGCT
                                ||||||||  |||   ||||||
                                ACCTAAAT  TCC   CATCGA
                                    TT  T___
GAM647  NQO1     3'  TGGATTTATTGGTTTATCTCT  16778       A   T  AG
                                TGGATTTAT GGTTT GT  CT
                                |||||||||| ||||| ||  ||
                                ACCTAAATA CCAAA TA  GA
                                     A    _  GA
GAM647  PMP2     3'  ATAGATTAGAATTTTGTAG   16779       TATA
                                ATGGATT   GGTTTTGTAG
                                |||||||   ||||||||||
                                TATCTAA   TTAAAACATC
                                    TC__
GAM647  SERPINB5 3'  GATTTATAGGTTGCT      16780         TTGTA
                                GATTTATAGGTT    GCT
                                ||||||||||||    |||
                                CTAAATATCCAA    CGA
                                          _____
GAM647  ZNF253   3'  ATAGGTTTATAGGTTTTG    16781     A
                                ATGG TTTATAGGTTTTG
                                |||| ||||||||||||
                                TATC AAATATCCAAAAC
                                  C
GAM647  FLJ14564 3'  ATGGATTTATTGGTTAGCCA  16782       A  TTTG
                                ATGGATTTAT GGT   TAGCTA
                                |||||||||| |||   ||||||
                                TACCTAAATA CCA   ATCGGT
                                     A  ____
GAM647  KIAA1030 3'  ATGAGATTTATAGCCCTGGT  16783    _      G  T
                                ATG GATTTATAG TTT GT
                                ||| ||||||||| ||| ||
                                TAC CTAAATATC GGA CA
                                  T       G  C
GAM647  LOC200014 3' GATTTGGGTTGTAGCT      16784      ATA  TT
                                GATTT  GGT  TGTAGCT
                                |||||  |||  |||||||
                                CTAAA  CCA  ACATCGA
                                  C__  __
GAM647  LOC201283 3' ATGAATTTGTAGGTTTTG    16785       A
                                ATGGATTT TAGGTTTTG
                                |||||||| |||||||||
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                                TACTTAAA ATCCAAAAC
                                     C
GAM648  CDH11    3'  TGGCAATATCAAAGGCT     16788         ATAAG    A
                                TGGCAATAT    TAAA GCT
                                |||||||||    |||| |||
                                ACCGTTATA    GTTT CGA
                                      _____   C
GAM648  GJA1     5'  GCTGATACCTCGTAAAAGCT   16789    AAT    AA_
                                GC   ATAT   GTAAAAGCT
                                ||   ||||   |||||||||
                                CG   TATG   CATTTTCGA
                                 AC_    GAG
GAM648  MAPRE1   3'  GCTACAAGGTAAAAGCTC    16790    AATA     _
                                GC    TATAAG TAAAAGCTC
                                ||    |||||| |||||||||
                                CG    ATGTTC ATTTTCGAG
                                 ____     C
GAM648  PAX3     3'  TGGCAACAGAGTGAGAGCT    16791        TATA   AAA
                                TGGCAATA    AGT   AGCT
                                ||||||||    |||   ||||
                                ACCGTTGT    TCA   TCGA
                                     C___   CTC
GAM648  PUM1     3'  TGGAAATATACACAAGGCTC   16792     C       AGTAAAA
                                TGG AATATATA      GCTC
                                ||| ||||||||      ||||
                                ACC TTATATGT      CGAG
                                  T       GTTC___
GAM648  SOS2     3'  TGGCAAATAAAAGCT       16793       TATATAA
                                TGGCAA      GTAAAAGCT
                                ||||||      |||||||||
                                ACCGTT      TATTTTCGA
                                      ________
GAM648  WFS1     3'  TGGCAACATGCACTGGAAGCTC 16794         A  AGTAA
           C                     TGGCAATAT TA    AAGCTCC
                                |||||||||  ||    |||||||
                                ACCGTTGTA GT    TTCGAGG
                                     C  GACC_
GAM648  FLJ10898 5'  TGGACCACAGGGTAAAAGCTC  16795    CAA    TAA
                                TGG   TATA   GTAAAAGCTC
                                |||   ||||   ||||||||||
                                ACC   GTGT   CATTTTCGAG
                                  TG_    CC_
GAM648  KIAA1165 3'  TGGCAATAATAACTGGCTC    16796        TATAA    AA_
                                TGGCAATA    GTAA   GCTC
                                ||||||||    ||||   ||||
                                ACCGTTAT    TATT   CGAG
                                     _____    GAC
GAM648  KIAA1243 3'  TGACAATATAGTGAGAGCTC   16797         ATA   AAA
                                TGGCAATAT   AGT   AGCTC
                                |||||||||   |||   |||||
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                                ACTGTTATA  TCA  TCGAG
                                    ___  CTC
GAM648  KIAA1458  3'  GCAATATACAAAGGCT     16798          TAAAA
                                GCAATATATAAG   GCT
                                ||||||||||||   |||
                                CGTTATATGTTT   CGA
                                      C____
GAM648  NS1-BP   3'  GCAATATGCAAAAGCT     16799       ATAA
                                GCAATAT   GTAAAAGCT
                                |||||||   |||||||||
                                CGTTATA   CGTTTTCGA
                                     ____
GAM648  TRIM11   3'  TGGCAACATGCCCACGAAAGCT 16800         ATAA TA
                                TGGCAATAT   G  AAAGCT
                                |||||||||   |  ||||||
                                ACCGTTGTA   T  TTTCGA
                                     CGGG GC
GAM648  ZNF262   3'  TGGCAAACGTCATAAAAGCT  16801      TATATAA
                                TGGCAA      GTAAAAGCT
                                ||||||      |||||||||
                                ACCGTT      TATTTTCGA
                                   TGCAG__
GAM648  LOC152674 5'  TGAAATAATGTAAGTGAAAGCT 16802    C   TA_    A
          CC                     TGG AATA   TAAGT AAAGCTCC
                                ||| ||||   ||||| ||||||||
                                ACT TTAT   ATTCA TTTCGAGG
                                  _   TAC    C
GAM648  LOC154792 5'  TAGCAATATGATTAAGAGCTC  16803        ATAAG   A
                                TGGCAATAT    TAA AGCTC
                                |||||||||    ||| |||||
                                ATCGTTATA    ATT TCGAG
                                     CTA__   C
GAM648  LOC169270 3'  TGGTAAATATAAATAAAGGCT  16804    CAAT        A
                                TGG   ATATAAGTAAA GCT
                                |||   ||||||||||| |||
                                ACC   TATATTTATTT CGA
                                  ATT_         C
GAM648  LOC219940 5'  TGGCTGTGGGCCGTAAAAGCTC 16805     AATATATAA
          C                      TGGC       GTAAAAGCTCC
                                ||||       ||||||||||
                                ACCG       CATTTTCGAGG
                                  ACACCCGG_
GAM648  LOC257443 3'  GCAATATACAAAGGCT     16798          TAAAA
                                GCAATATATAAG   GCT
                                ||||||||||||   |||
                                CGTTATATGTTT   CGA
                                      C____
GAM649  FLJ20813  3'  TAGATATCATTGAAACTCCTAT 16808     T   AT  A
                                TAGAT TTA  TT AAACTCCTAT
                                ||||| |||  || ||||||||||
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                                ATCTA AGT  AA TTTGAGGATA
                                  T  __  C
GAM649  PRKRIR   3'  TAGATTTTTAACATACTTAAAA 16809    A_____          III
           CTCCTATA                TT     ATTTAAAACTCCTAT   A
                                ||     ||||||||||||||  |
                                AA     TGAATTTTGAGGATA   T
                                 ATTGTA           III
GAM649  PTP4A1   5'  GATTTCAATTCAACACTTCT   16810          A   C
                                GATTTTAATTTAA ACT CT
                                |||||||||||| ||| ||
                                CTAAAGTTAAGTT TGA GA
                                       G   A
GAM649  SPTLC2   3'  GATTTTATAGGACTCCTAT   16811       ATT  AA
                                GATTTTA   TA  ACTCCTAT
                                |||||||   ||  ||||||||
                                CTAAAAT   AT  TGAGGATA
                                   ___  CC
GAM649  LOC196424 3'  GATTCAGTATTTAAAACTCTTA 16812      TA_        C
           T                     GATTT   ATTTAAAACTC TAT
                                |||||   ||||||||||| |||
                                CTAAG   TAAATTTTGAG ATA
                                   TCA         A
GAM649  LOC199775 3'  TAGATTTTATTTACATTCCTAT 16813        A    AAAC
                                TAGATTTTA TTTA    TCCTAT
                                |||||||| ||||    ||||||
                                ATCTAAAAT AAAT    AGGATA
                                     _   GTA_
GAM649  LOC91923  5'  TACATCAAACTTTAAAACTCCT 16814    G   TTAA
                                TA ATT    TTTAAAACTCCT
                                || |||    ||||||||||||
                                AT TAG    AAATTTTGAGGA
                                 G   TTTG
GAM650  APM1     3'  GAACATAGCATATGAT      16817         ACA
                                GAATATAGCA   ATGAT
                                ||||||||||   |||||
                                CTTGTATCGT   TACTA
                                      A__
GAM650  CDKN2A   3'  TAAGAATATATAAAAAATGAT  16818         GCAAC
                                TAAGAATATA     AATGAT
                                ||||||||||     ||||||
                                ATTCTTATAT     TTACTA
                                      ATTTT
GAM650  CDKN2A   3'  TAAGAATATATAAAAAATGAT  16818         GCAAC
                                TAAGAATATA     AATGAT
                                ||||||||||     ||||||
                                ATTCTTATAT     TTACTA
                                      ATTTT
GAM650  CDKN2A   3'  TAAGAATATATAAAAAATGAT  16818         GCAAC
                                TAAGAATATA     AATGAT
                                ||||||||||     ||||||
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                                ATTCTTATAT    TTACTA
                                      ATTTT
GAM650  CDKN2A   3'  TAAGAATATATAAAAAATGAT  16818         GCAAC
                                TAAGAATATA    AATGAT
                                ||||||||||    ||||||
                                ATTCTTATAT    TTACTA
                                      ATTTT
GAM650  EGFL5    5'  AGCAGCACCACAACAATGAT   16819    AA_  A
                                AG   TAT GCAACAATGAT
                                ||   ||| ||||||||||
                                TC   GTG TGTTGTTACTA
                                 GTC   G
GAM650  FGF9     5'  CAAGAATAAACAATAATGAT   16820        T    C
                                TAAGAATA AGCAA AATGAT
                                |||||||| ||||| ||||||
                                GTTCTTAT TTGTT TTACTA
                                     _    A
GAM650  PTGIS    3'  AAAATATAGCAAATAAT     16821          CA
                                AGAATATAGCAA  ATGAT
                                ||||||||||||  |||||
                                TTTTATATCGTT  TATTA
                                              __
GAM650  C5orf4   3'  TAAGAATTTAGTAAAATGATAA 16822        A   C  C
           T                     TAAGAAT TAG AA AATGATAAT
                                 ||||||| ||| || |||||||||
                                 ATTCTTA ATC TT TTACTATTA
                                     A   A  _
GAM650  C5orf4   3'  TAAGAATTTAGTAAAATGATAA 16822        A   C  C
           T                     TAAGAAT TAG AA AATGATAAT
                                 ||||||| ||| || |||||||||
                                 ATTCTTA ATC TT TTACTATTA
                                     A   A  _
GAM650  DIO2     3'  TAAAAATATAGCACAAC     16823          A
                                TAAGAATATAGCA CAAT
                                |||||||||||| ||||
                                ATTTTTATATCGT GTTG
                                              _
GAM650  DIO2     3'  TAAAAATATAGCACAAC     16823          A
                                TAAGAATATAGCA CAAT
                                |||||||||||| ||||
                                ATTTTTATATCGT GTTG
                                              _
GAM650  DKFZp434G171 3'  GATAAAGCAACAATGAT     16824    A  T
                                GA TA AGCAACAATGAT
                                || || ||||||||||||
                                CT AT TCGTTGTTACTA
                                 _  T
GAM650  FLJ12649 3'  CAAGAATGAGAGACAATGAT   16825       AT  CA
                                TAAGAAT  AG  ACAATGAT
                                |||||||  ||  ||||||||
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                                GTTCTTA  TC  TGTTACTA
                                   C_  TC
GAM650  IPT      3'  AGAAAGACAGCAGTGATAAT  16826     T_    ACAA
                                AGAA  ATAGCA   TGATAAT
                                ||||  ||||||   |||||||
                                TCTT  TGTCGT   ACTATTA
                                  TC     C___
GAM650  PRO2958  5'  AAGAATATGGCAGCAATG   16827       A  A
                                AAGAATAT GCA CAATG
                                |||||||| ||| |||||
                                TTCTTATA CGT GTTAC
                                   C   C
GAM650  TRPM3    3'  TAAGAATAAAGCAGGTATGAT  16828       T   ACA
                                TAAGAATA AGCA   ATGAT
                                |||||||| ||||   |||||
                                ATTCTTAT TCGT   TACTA
                                   T    CCA
GAM650  LOC202934 5'  AGAGTCCAACACAATGATA   16829    ATA    A
                                AGA   TAGCA CAATGATA
                                |||   ||||| ||||||||
                                TCT   GTTGT GTTACTAT
                                  CAG    _
GAM650  LOC219627 3'  TAAGAGTATGACAACAGCAAT  16830     A  AG    AT
                                TAAGA TAT  CAACA  GAT
                                ||||| |||  |||||  |||
                                ATTCT ATA  GTTGT  TTA
                                   C  CT    CG
GAM651  MS4A7    3'  CAAAAGCTTTTTTTTTTTTAG  16833          GCGAC
                                CAAAAGCTTTTTT    TTTTAG
                                ||||||||||||    ||||||
                                GTTTTCGAAAAAA    AAAATC
                                       AA___
GAM651  SCP2     3'  CAAAAGCTTTTTTGTTTAC   16834          CG_
                                CAAAAGCTTTTTTG  AC
                                ||||||||||||||  ||
                                GTTTTCGAAAAAAC  TG
                                       AAA
GAM651  SLC7A8   3'  CAGAAGCTTTTTGGCTTCT   16835   A      T  GA
                                CA AAGCTTTTT GC  CT
                                || |||||||| ||  ||
                                GT TTCGAAAAA CG  GA
                                 C       C  AA
GAM651  BHLHB2   3'  CAAAAACTTTTTTGTTGCTTTT 16836          CGA
                                CAAAAGCTTTTTTG  CTTTT
                                ||||||||||||||  |||||
                                GTTTTTGAAAAAAC  GAAAA
                                       AAC
GAM651  LOC149910 3'  TGAAAGCTTTTATGCCAGATTT 16837   A      T  GACT
           AG                    C AAAGCTTTT TGC   TTTAG
                                | |||||||| |||   |||||
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                                A TTTCGAAAA ACG    AAATC
                                 C       T   GTCT
GAM651  LOC164955 3'  CAAAAGCTTCAGATGGTGATTT 16838          TT_  C_  C
          TTAG                    CAAAAGCTTT   TG  GA TTTTAG
                                |||||||||   ||  || ||||||
                                GTTTTCGAAG   AC  CT AAAATC
                                     TCT  CA  A
GAM651  LOC219690 3'  CAAAAGCTTTATTGTGGATCCA 16839          T   CGACT
          G                     CAAAAGCTTT TTG    TTTAG
                                |||||||||| |||    |||||
                                GTTTTCGAAA AAC    AGGTC
                                     T   ACCT_
GAM651  LOC222031 3'  CAAAAGCTTCCTGGGCTTTTAG 16840           T CGA
                                CAAAAGCTTTTT G   CTTTTAG
                                ||||||||||| |   |||||||
                                GTTTTCGAAGGA C   GAAAATC
                                      _ CC_
GAM652  TP73     5'  TCCCGGCTGGCCTGGCGCGGG  16843     ATTA __   C
                                TCTC    GC  GCC GGCGCGGG
                                ||||    ||  ||| ||||||||
                                AGGG    CG  CGG CCGCGCCC
                                  C___  AC   A
GAM652  FLJ20320  5'  CTCAGCCCGGCGCGG      16844      TTAGC
                                CTCA    GCCCGGCGCGG
                                ||||    ||||||||||
                                GAGT    CGGGCCGCGCC
                                  _____
GAM652  FLJ20435  3'  CAGCTCATTAGCGGGTGGGCCC 16845       G_________   GCG
          GCGCCGG                 CATTAGC       CCCG   CGG
                                |||||||        ||||  |||
                                GTAATCG       GGGC   GCC
                                    CCCACCCIII   GCG
GAM652  FLNC     5'  TCATCATGCTGGCGCGGG    16846      GC  CC
                                TCATTA  GC  GGCGCGGG
                                ||||||  ||  ||||||||
                                AGTAGT  CG  CCGCGCCC
                                   A_  A_
GAM652  KIAA1042  3'  ATCTCATTAGCGGCTTGG    16847         GCCC   GC
                                ATCTCATTAGC    GGC  GG
                                ||||||||||    |||  ||
                                TAGAGTAATCG    CCG  CC
                                      ____   AA
GAM652  NXN      3'  CAGCTCATTAGCGGGTGGGCCC 16845       G_________   GCG
          GCGCCGG                 CATTAGC       CCCG   CGG
                                |||||||        ||||  |||
                                GTAATCG       GGGC   GCC
                                    CCCACCCIII   GCG
GAM652  LOC132617 3'  CATCTCATGGTGCCCCCGG   16848        TA_  G
                                CATCTCAT   GC CCCGG
                                ||||||||   || |||||
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                                GTAGAGTA   CG GGGCC
                                     CCA  G
GAM652  LOC146562 5'  CTCATTGGCTACCGCGGG    16849       A  GC  GGC
                                CTCATT GC  CC   GCGGG
                                |||||| ||  ||   |||||
                                GAGTAA CG  GG   CGCCC
                                   C  AT  ___
GAM652  LOC222028 3'  TCATTAGCGTTTAGTCGTGGG  16850         CCC  _  C
                                TCATTAGCG   GG CG GGG
                                |||||||||   || || |||
                                AGTAATCGC   TC GC CCC
                                     AAA  A  A
GAM653  PTP4A2    3'  TCTATATTAATGGAATCTATTG 16853          A    ATA
          T                      TCTATATTAAT GGAG   GTTGT
                                ||||||||||| ||||   |||||
                                AGATATAATTA CCTT   TAACA
                                      _    AGA
GAM653  EIF4B     3'  TCTATTTTAATAGGGGGGACAA 16854       A       A__
                                TCTAT TTAATAGG   GATAG
                                ||||| ||||||||   |||||
                                AGATA AATTATCC   CTGTT
                                   A       CCC
GAM653  FLJ11040  3'  TCTATAATAATAGGAATGACTT 16855        T       ATAG
          GT                     TCTATA TAATAGGAG    TTGT
                                |||||| |||||||||    ||||
                                AGATAT ATTATCCTT    AACA
                                   T        ACTG
GAM654  DCN       3'  AATACAGAGCTAGTGTTTGG   16858       TA   A    CA
                                AATACAGA  CTA TGTTT  GG
                                ||||||||  ||| |||||  ||
                                TTATGTCT  GAT ACAAA  CC
                                     C_   C    __
GAM654  DCN       3'  AATACAGAGCTAGTGTTTGG   16858       TA   A    CA
                                AATACAGA  CTA TGTTT  GG
                                ||||||||  ||| |||||  ||
                                TTATGTCT  GAT ACAAA  CC
                                     C_   C    __
GAM654  DCN       3'  AATACAGAGCTAGTGTTTGG   16858       TA   A    CA
                                AATACAGA  CTA TGTTT  GG
                                ||||||||  ||| |||||  ||
                                TTATGTCT  GAT ACAAA  CC
                                     C_   C    __
GAM654  DCN       3'  AATACAGAGCTAGTGTTTGG   16858       TA   A    CA
                                AATACAGA  CTA TGTTT  GG
                                ||||||||  ||| |||||  ||
                                TTATGTCT  GAT ACAAA  CC
                                     C_   C    __
GAM654  DCN       3'  AATACAGAGCTAGTGTTTGG   16858       TA   A    CA
                                AATACAGA  CTA TGTTT  GG
                                ||||||||  ||| |||||  ||
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                                TTATGTCT  GAT ACAAA  CC
                                    C_  C    __
GAM654  DCN     3'  AATACAGAGCTAGTGTTTGG  16858       TA  A    CA
                                AATACAGA  CTA TGTTT  GG
                                ||||||||  ||| |||||  ||
                                TTATGTCT  GAT ACAAA  CC
                                    C_  C    __
GAM654  DLEC1   3'  CAGGTCCAGTTTCAGGG    16859    ATA  AT
                                CAG  CTA  GTTTCAGGG
                                |||  |||  |||||||||
                                GTC  GGT  CAAAGTCCC
                                  CA_  __
GAM654  DLEC1   3'  CAGGTCCAGTTTCAGGG    16859    ATA  AT
                                CAG  CTA  GTTTCAGGG
                                |||  |||  |||||||||
                                GTC  GGT  CAAAGTCCC
                                  CA_  __
GAM654  DVL3    3'  AATACAGATCTAAAGTCTGGG 16860       A   T   CA
                                AATACAGAT CTAA GTTT  GGG
                                ||||||||| |||| ||||  |||
                                TTATGTCTA GATT CAGA  CCC
                                    _   T   __
GAM654  LAPTM5  3'  GAACAGATGTGCCTGATTTCAG 16861   T    ACTAA  _
          GG                  A ACAGAT    TG TTTCAGGG
                              | ||||||    || ||||||||
                              C TGTCTA    AC AAAGTCCC
                               T    CACGG  T
GAM654  TERF1   3'  GATACTAAATGTGGCAGGG   16862       _  TT
                                GATACTAA TGT  CAGGG
                                |||||||| |||  |||||
                                CTATGATT ACA  GTCCC
                                    T  CC
GAM654  54TM    5'  TACGAATACTAATGAGG    16863    AG      TTTC
                                TAC  ATACTAATG   AGG
                                |||  |||||||||   |||
                                ATG  TATGATTAC   TCC
                                  CT       ____
GAM654  AP3M1   3'  ACAGATACTGGTTTGG     16864       AAT   CA
                                ACAGATACT   GTTT  GG
                                |||||||||   ||||  ||
                                TGTCTATGA   CAAA  CC
                                    C__   __
GAM654  BNIP-S  3'  ACAGTTCAGATGTTTCAGGG  16865    ATACTA
                                ACAG    ATGTTTCAGGG
                                ||||    ||||||||||
                                TGTC    TACAAAGTCCC
                                  AAGTC_
GAM654  C20orf124 5'  CAGGTACTATTTCCTCAGGG  16866    A    ATG
                                CAG TACTA   TTTCAGGG
                                ||| |||||   ||||||||
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                                GTC ATGAT   GGAGTCCC
                                  C     AAA
GAM654  COP9     3'  CAGATACTGTGCCTGGG     16867        AA    CA
                                CAGATACT  TGTTT  GGG
                                ||||||||  |||||  |||
                                GTCTATGA  ACGGA  CCC
                                    C_    __
GAM654  DDM36    3'  AACACAGATGCTTTCAGG    16868         A  AATGT
                                AATACAGAT CT    TTCAGG
                                |||||||||  ||    ||||||
                                TTGTGTCTA GA    AAGTCC
                                    C  _____
GAM654  FLJ13340 3'  TACAGTACAGTGTTTCAGGG  16869      A   TAA
                                TACAG TAC   TGTTTCAGGG
                                |||||  |||   ||||||||||
                                ATGTC ATG   ACAAAGTCCC
                                  _   TC_
GAM654  FLJ20716 3'  AATACAGATGACTCTTTTGGG 16870         _  AATG   CA
                                AATACAGAT ACT    TTT  GGG
                                |||||||||  |||    |||  |||
                                TTATGTCTA TGA    AAA  CCC
                                    C   GA__   __
GAM654  FLJ22671 3'  ATACAGATACAATCCATATCAG 16871          TAA_   T
          GG                    ATACAGATAC    TGT TCAGGG
                                ||||||||||    ||| ||||||
                                TATGTCTATG    GTA AGTCCC
                                    TTAG   T
GAM654  FLJ31846 5'  AGATTAGAGTTTCAGGG     16872      AC  AT
                                AGAT  TA  GTTTCAGGG
                                ||||  ||  |||||||||
                                TCTA  AT  CAAAGTCCC
                                  __  CT
GAM654  LBP-9    3'  TAAAGGTACCAGCTTTCAGGG  16873    C  A    ATG
                                TA AG TACTA   TTTCAGGG
                                || || |||||   ||||||||
                                AT TC ATGGT   AAAGTCCC
                                 T  C    CG_
GAM654  TBDN100  3'  TACAGTACAGTGTTTCAGGG   16869      A   TAA
                                TACAG TAC   TGTTTCAGGG
                                |||||  |||   ||||||||||
                                ATGTC ATG   ACAAAGTCCC
                                  _   TC_
GAM654  LOC149448 3'  CAGGTACCTCCTTCAGGG    16874     A    AATG
                                CAG TACT    TTTCAGGG
                                |||  ||||    ||||||||
                                GTC ATGG    GAAGTCCC
                                  C    AG__
GAM654  LOC152620 3'  GATACTAAATGTGGCAGGG    16862         _   TT
                                GATACTAA TGT  CAGGG
                                ||||||||  |||  |||||
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                                CTATGATT ACA  GTCCC
                                     T   CC
GAM654  LOC152698 5'  CAGGGCTATGCCTCAGGG    16875     ATA   A
                                CAG   CTA TGTTTCAGGG
                                |||   ||| ||||||||||
                                GTC   GAT ACGGAGTCCC
                                  CC_   _
GAM654  LOC158668 3'  GATACTAAATGTGGCAGGG    16862         _   TT
                                GATACTAA TGT  CAGGG
                                |||||||| |||  |||||
                                CTATGATT ACA  GTCCC
                                     T   CC
GAM654  LOC257078 5'  ATACATGATGCTGGTCCCAGGG 16876       _   A  AAT  TT
                                ATACA GAT CT   GT  CAGGG
                                ||||| ||| ||   ||  |||||
                                TATGT CTA GA   CA  GTCCC
                                   A   C  C__  GG
GAM654  LOC93380  3'  AATATAAATACTAATGGG     16877      C         TTTCA
                                AATA AGATACTAATG     GG
                                |||| ||||||||||     ||
                                TTAT TTTATGATTAC     CC
                                  A         _____
GAM655  ANKRD7    3'  GGAAGCGGCAAAGAAATTGTAG 16880     T   A       ACTA
          A                      GGA GCG CGAAGAAA    TAGA
                                ||| ||| ||||||||    ||||
                                CCT CGC GTTTCTTT    ATCT
                                  T   C       AAC_
GAM656  GSBS      3'  GGTTGACTCCCCCAGCTCA    16883        GCG_
                                GGTTGACT    CAGCTCA
                                ||||||||    |||||||
                                CCAACTGA    GTCGAGT
                                     GGGG
GAM656  INHBA     3'  TTGGTTGATTCAAGCTCAC    16884        CTG  C
                                TTGGTTGA   CG AGCTCAC
                                ||||||||   || |||||||
                                AACCAACT   GT TCGAGTG
                                     AA_  _
GAM656  ITGA5     3'  TTGGTTGATGAGCTCA      16885         C  CGC
                                TTGGTTGA TG   AGCTCA
                                |||||||| ||   ||||||
                                AACCAACT AC   TCGAGT
                                     _  ____
GAM656  MYCL2     5'  TTGCTTGCTCACGCAGCT    16886     G   AC
                                TTG TTG  TGCGCAGCT
                                ||| |||  |||||||||
                                AAC AAC  GTGCGTCGA
                                  G   GA
GAM656  PRKY      3'  TTGGTTGACTGCAGCCTCC    16887          _  AG
                                TTGGTTGACTGC GC  CT
                                |||||||||||| ||  ||
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                                AACCAACTGACG CG  GG
                                      T  GA
GAM656  SLC9A6   3'  TTAGTTGACTCAAGCT     16888         G  C
                                TTGGTTGACT CG AGCT
                                |||||||||| || ||||
                                AATCAACTGA GT TCGA
                                      _  _
GAM656  SPTB     3'  GGCGGGGCTGCGCAGCTCA   16889     TGA_
                                GGT   CTGCGCAGCTCA
                                |||   ||||||||||||
                                CCG   GACGCGTCGAGT
                                  CCCC
GAM656  BRD4     3'  TTGGTTGGTGGCCTCA      16890       AC  C  AG
                                TTGGTTG  TG GC  CTCA
                                |||||||  || ||  ||||
                                AACCAAC  AC CG  GAGT
                                    C_  _  __
GAM656  DKFZp434J0226 5'  GGTCGCTGCAGCTCA      16891      A   GC
                                GGTTG CTGC  AGCTCA
                                ||||| ||||  ||||||
                                CCAGC GACG  TCGAGT
                                   _   __
GAM656  DKFZP564O0423 5'  TTGGTGAAGACAGCTCA     16892      T  CTGC
                                TTGGT GA   GCAGCTCA
                                ||||| ||   ||||||||
                                AACCA CT   TGTCGAGT
                                   _  TC__
GAM656  DRIM     3'  CTGGTTGAGCAGGGTGGCTCAC 16893        CT   CA___
                                TTGGTTGA  GCG    GCTCAC
                                ||||||||  |||    ||||||
                                GACCAACT  CGT    CGAGTG
                                    __  CCCAC
GAM656  FLJ12476  3'  TTGGTTAACTAGATGCTGGCT  16894         C__  A_
                                TTGGTTGACTG   GC  GCT
                                ||||||||||   ||  |||
                                AACCAATTGAT   CG  CGA
                                      CTA  AC
GAM656  GGA2     3'  TTGGTTGAATGTCAGCT     16895       C  CG
                                TTGGTTGA TG  CAGCT
                                |||||||| ||  |||||
                                AACCAACT AC  GTCGA
                                     T  A_
GAM656  GNB4     5'  TGGAGAGCGCAGCTCAC     16896     TT  CT
                                TGG  GA  GCGCAGCTCAC
                                |||  ||  ||||||||||
                                ACC  CT  CGCGTCGAGTG
                                  T_  __
GAM656  IPLA2(GAMMA) 3'  TGGTTGACTGGAACTTCAC   16897         CGC   _
                                TGGTTGACTG   AGCT CAC
                                |||||||||   |||| |||
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                                ACCAACTGAC   TTGA GTG
                                     C__    A
GAM656  POLD3    3'  TTGGTTGCTAAAGAAGCTCA  16898       A  CGC_
                                TTGGTTG CTG    AGCTCA
                                ||||||| |||    ||||||
                                AACCAAC GAT    TCGAGT
                                   _  TTCT
GAM656  PRO1496  3'  TGGTGTGATTGCAGCTCAC   16899     _  CTGC
                                TGGT TGA    GCAGCTCAC
                                |||| |||    |||||||||
                                ACCA ACT    CGTCGAGTG
                                  C  AA__
GAM656  LOC130543 5'  TTAGTTGATGGCTCA       16900        C  CGCA
                                TTGGTTGA TG    GCTCA
                                |||||||| ||    |||||
                                AATCAACT AC    CGAGT
                                   _ ____
GAM656  LOC154215 3'  TTGGATGACTTCCCAGCTCAC  16901     T    GCG
                                TTGG TGACT   CAGCTCAC
                                |||| |||||   ||||||||
                                AACC ACTGA   GTCGAGTG
                                  T    AGG
GAM656  LOC197358 5'  TCGGTGTGCTGCAGCTCA    16902      TGAC  _
                                TTGGT    TGC GCAGCTCA
                                |||||    ||| ||||||||
                                AGCCA    ACG CGTCGAGT
                                   C___   A
GAM656  LOC205251 5'  TTGGCTGAGTGCGACAGCTCA  16903        C   _
                                TTGGTTGA TGCG CAGCTCA
                                |||||||| |||| |||||||
                                AACCGACT ACGC GTCGAGT
                                     C   T
GAM656  LOC221300 3'  TTGGTTGATGCCAGCT      16904        C  G
                                TTGGTTGA TGC CAGCT
                                |||||||| ||| |||||
                                AACCAACT ACG GTCGA
                                   _  _
GAM656  LOC90979  3'  TTAGTTAGCAGCTCA       16905       ACTGC
                                TTGGTTG    GCAGCTCA
                                |||||||    ||||||||
                                AATCAAT    CGTCGAGT
                                   _____
GAM657  DUSP6    3'  TTAGAAAAGAGCACAATTTTC  16908        T  A TG
                                TTAGAAAA AGC A  ATTTTC
                                |||||||| ||| |  ||||||
                                AATCTTTT TCG T  TAAAAG
                                     C  _ GT
GAM657  EDAR     3'  AAAGATATGACTGATTTTCCC  16909     A  GCAA
                                GAA ATA    TGATTTTCCC
                                ||| |||    ||||||||||
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                                TTT TAT   ACTAAAAGGG
                                  C  ACTG
GAM657  ESRRBL1  3' TTAAAAAATGCTTATTTTCCC 16910       A AATG
                                TTAGAAAAT GC   ATTTTCCC
                                ||||||||| ||   ||||||||
                                AATTTTTTA CG   TAAAAGGG
                                     _ AA__
GAM657  GCNT2    5' TAGAAAATAGCTTCTGTTTTCC 16911        AA_ A
                                TAGAAAATAGC  TG TTTTCC
                                |||||||||||  || ||||||
                                ATCTTTTATCG  AC AAAAGG
                                      AAG _
GAM657  GPR30    5' TTAGAAAGAAGCGTGATTCTC 16912      AT  AA
                                TTAGAAA AGC TGATTTTC
                                ||||||| ||| ||||||||
                                AATCTTT TCG ACTAAGAG
                                    CT  C_
GAM657  HLCS     3' AGAAAATATCTGAATTTTCCC 16913      GCAA  _
                                AGAAAATA   TGA TTTTCCC
                                ||||||||   ||| |||||||
                                TCTTTTAT   ACT AAAAGGG
                                    AG__  T
GAM657  KCNAB1   3' AGAAAATAGAATGGATTTTC  16914       C  _
                                AGAAAATAG AATG ATTTTC
                                ||||||||| |||| ||||||
                                TCTTTTATC TTAC TAAAAG
                                     _  C
GAM657  KCNJ1    5' TTAGAGAATGCAATGAT    16915     A  A
                                TTAGA AAT GCAATGAT
                                ||||| ||| ||||||||
                                AATCT TTA CGTTACTA
                                  C  _
GAM657  LARGE    3' TAGAGGCAGCTGATTTTCC  16916    AAA  AA
                                TAGA  TAGC TGATTTTCC
                                ||||  |||| |||||||||
                                ATCT  GTCG ACTAAAAGG
                                  CC_  __
GAM657  LARGE    3' TAGAGGCAGCTGATTTTCC  16916    AAA  AA
                                TAGA  TAGC TGATTTTCC
                                ||||  |||| |||||||||
                                ATCT  GTCG ACTAAAAGG
                                  CC_  __
GAM657  NKX3A    3' GAAAATACCACTTGATTTTCCC 16917      G A_
                                GAAAATA CA TGATTTTCCC
                                ||||||| ||  ||||||||||
                                CTTTTAT GT ACTAAAAGGG
                                    G GA
GAM657  NR4A2    3' TTAGGAAATAGCAACAGTTTT 16918     A      GA
                                TTAG AAATAGCAAT TTTT
                                |||| |||||||||  ||||
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                                AATC TTTATCGTTG  AAAA
                                  C         TC
GAM657  PIGA     3'  GAAAATAGCCTTTTCC      16919          AATGA
                                GAAAATAGC    TTTTCC
                                |||||||||    ||||||
                                CTTTTATCG    AAAAGG
                                     G____
GAM657  PIGA     3'  GAAAATAGCCTTTTCC      16919          AATGA
                                GAAAATAGC    TTTTCC
                                |||||||||    ||||||
                                CTTTTATCG    AAAAGG
                                     G____
GAM657  PIK3C2B  3'  TTAGAAAATACAATTC      16920          G    GATTT
                                TTAGAAAATA CAAT    TC
                                |||||||||| ||||    ||
                                AATCTTTTAT GTTA    AG
                                     _   _____
GAM657  PKNOX1   3'  TTAGAAAATGGCAGCGCTATTC 16921          A   A  ATT
          C                      TTAGAAAAT GCA TG   TTCC
                                |||||||| ||| ||   ||||
                                AATCTTTTA CGT GC   AAGG
                                     C   C  GAT
GAM657  PNN      3'  TAGAAAATAGCAAATGATTTT  16922           _
                                TAGAAAATAGCAA TGATTTT
                                |||||||||||| |||||||
                                ATCTTTTATCGTT ACTAAAA
                                       T
GAM657  RU2      3'  AGAAAATAGTACATGCTTTCC  16923         CA_   A
                                AGAAAATAG   ATG TTTTCC
                                |||||||||   ||| ||||||
                                TCTTTTATC   TAC GAAAGG
                                     ATG   _
GAM657  RXRB     3'  AAAAATAGCAGATCGGTTCC   16924          AT   __
                                GAAAATAGCA  GATT  TTCC
                                ||||||||||  ||||  ||||
                                TTTTTATCGT  CTAG  AAGG
                                     __    CC
GAM657  SCA1     3'  TTAGAAAATAGAATATGAATTC 16925          CA_    T
                                TTAGAAAATAG   ATGA TTT
                                ||||||||||   |||| |||
                                AATCTTTTATC   TACT AAG
                                      TTA    T
GAM657  SUFU     3'  GAAAACAGTAGCACCCCTCCC  16926         CAATGA
                                GAAAATAG     TTTTCCC
                                ||||||||     |||||||
                                CTTTTGTC     GGGAGGG
                                    ATCGTG
GAM657  TBX3     3'  TAGGAAATAGCACTTTCC     16927     A       ATGA
                                TAG AAATAGCA    TTTTCC
                                ||| ||||||||    ||||||
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                                ATC TTTATCGT    GAAAGG
                                  C       _____
GAM657  C20orf177 3'  AAAAATAGCAAGATTCT     16928          T
                                GAAAATAGCAA GATTTT
                                |||||||||||| ||||||
                                TTTTTATCGTT CTAAGA
                                                _
GAM657  FLJ11539  3'  GAAAATAGCGGTGAGGGTTTCC 16929         AA   T__
                                GAAAATAGC  TGA   TTTCC
                                |||||||||  |||   |||||
                                CTTTTATCG  ACT   AAAGG
                                      CC   CCC
GAM657  KCNJ9     3'  AGAAAATAGCTATCCCTGGTTT 16930         AA____  A
           TCC                    AGAAAATAGC     TG TTTTCC
                                |||||||||||      || ||||||
                                TCTTTTATCG     AC AAAAGG
                                      ATAGGG  C
GAM657  MGC3038   3'  TTAGGAAACAGACGATTTTCCC 16931      A     CA
                                TTAG AAATAG  ATGATTTTCCC
                                |||| ||||||  ||||||||||||
                                AATC TTTGTC  TGCTAAAAGGG
                                  C     __
GAM657  RACGAP1   5'  GAAAATAGTTGTAATTTTCC   16932        CAA
                                GAAAATAG   TGATTTTCC
                                ||||||||   |||||||||
                                CTTTTATC   ATTAAAAGG
                                     AAC
GAM657  SLAC2-B   3'  TAGAAAATAGCAGAGACTCTC  16933          AT
                                TAGAAAATAGCA  GATTTTC
                                ||||||||||||  |||||||
                                ATCTTTTATCGT  CTGAGAG
                                       CT
GAM657  SLC31A2   3'  TTAGTATACAGCAGTGATTTTC 16934      AAA     A
                                TTAG   ATAGCA TGATTTTC
                                ||||   |||||| ||||||||
                                AATC   TGTCGT ACTAAAAG
                                  ATA     C
GAM657  ZF5128    3'  TTAGGCAATAGCAAGTCTTTCC 16935      AA       TGA
                                TTAG  AATAGCAA   TTTTCC
                                ||||  ||||||||   ||||||
                                AATC  TTATCGTT   GAAAGG
                                  CG       CA_
GAM657  LOC123283 3'  CTAGAAAATAAGATTTTCC    16936          CAAT
                                TTAGAAAATAG    GATTTTCC
                                ||||||||||    ||||||||
                                GATCTTTTATT    CTAAAAGG
                                               ____
GAM657  LOC129446 3'  GAAAATGCAGTGATTTTC     16937        A   A
                                GAAAAT GCA TGATTTTC
                                |||||| ||| ||||||||
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                                CTTTTA CGT ACTAAAAG
                                   _  C
GAM657  LOC152317 3'  TTAGAAAATGCAATTGATTTTC 16938        A   _
          C                    TTAGAAAAT GCAAT GATTTTCC
                               ||||||||| ||||| ||||||||
                               AATCTTTTA CGTTA CTAAAAGG
                                   _   A
GAM657  LOC158376 3'  GAATATAGCAATAAAGTCTC  16939    A       T_
                               GAA ATAGCAATGA  TTTC
                               ||| ||||||||||  ||||
                               CTT TATCGTTATT  AGAG
                                 A        TC
GAM657  LOC158401 3'  CTAGAACCTAGTGATTTTCCC  16940      AA  CAA
                               TTAGAA  TAG  TGATTTTCCC
                               ||||||  |||  ||||||||||
                               GATCTT  ATC  ACTAAAAGGG
                                  GG  ___
GAM657  LOC169436 5'  TCAGAGTCAATGATTTTC    16941     AAATAG
                               TTAGA    CAATGATTTTC
                               |||||    ||||||||||
                               AGTCT    GTTACTAAAAG
                                  CA____
GAM657  LOC202986 3'  CTAGAGAATGGCAATGACTTT  16942     A  A
                               TTAGA AAT GCAATGATTTT
                               ||||| ||| ||||||||||
                               GATCT TTA CGTTACTGAAA
                                  C  C
GAM657  LOC219401 3'  TTAAACTCGTAGTGATTTTCCC 16943     AAA_  CAA
                               TTAGA   TAG  TGATTTTCCC
                               |||||   |||  ||||||||||
                               AATTT   ATC  ACTAAAAGGG
                                  GAGC  ___
GAM657  LOC221354 3'  CTAGAGAATGGCGATGACTTT  16944     A  A  A
                               TTAGA AAT GC ATGATTTT
                               ||||| ||| || ||||||||
                               GATCT TTA CG TACTGAAA
                                  C  C  C
GAM657  LOC90462  3'  TTAGAAAAGCTGATTTTC    16945      AT  AA
                               TTAGAAA  AGC  TGATTTTC
                               |||||||  |||  ||||||||
                               AATCTTT  TCG  ACTAAAAG
                                     __  __
GAM658  IRAK4    3'  GCTAAGTGTTGATATGGTGG  16948     A__  CT
                               GCTAA  TTG  TATGGTGG
                               |||||  |||  ||||||||
                               CGATT  AAC  ATACCACC
                                  CAC  T_
GAM658  PCDH9    5'  TTAAAGCTGAATTCTTTGG   16949       A  G  A
                               TTAAAGCT AATT CTT TGG
                               |||||||| |||| ||| |||
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                                AATTTCGA TTAA GAA ACC
                                    C   _  _
GAM658  MKRN4   3'  TTAAGGCTGGGCATGGTG   16950     A  AAATT  TT
                                TTAA GCT    GC  ATGGTG
                                |||| |||    ||  ||||||
                                AATT CGA    CG  TACCAC
                                  C  CC___  __
GAM659  ENPP3   3'  TCTTTATTAATTGTGCAT   16953          A_
                                TCTTTGTTAATT  GCGT
                                ||||||||||||  ||||
                                AGAAATAATTAA  CGTA
                                      CA
GAM660  CABC1   3'  TATCTGTTCATGTTTCTG   16956          _  CC
                                TATCTGTTCA GT  CTG
                                |||||||||| ||  |||
                                ATAGACAAGT CA  GAC
                                      A  AA
GAM660  CIT     3'  TGTTCAGTGCTACAGACT   16957        CC   CA
                                TGTTCAGT  CTGC  ACT
                                ||||||||  ||||  |||
                                ACAAGTCA  GATG  TGA
                                    C_   TC
GAM660  COG5    3'  TATGTGTTTAACTGCCAACTA  16958    C   CAGTCC
                                TAT TGTT    CTGCCAACTA
                                ||| ||||    ||||||||||
                                ATA ACAA    GACGGTTGAT
                                  C   ATT___
GAM660  DNMT2   3'  TATCTGTTCAAGTCCCTGC   16959         _
                                TATCTGTTCA GTCCCTGC
                                |||||||||| ||||||||
                                ATAGACAAGT CAGGGACG
                                      T
GAM660  FBXL7   3'  CATCTGTCTCTGCCAGCT   16960        CAGTCC    A
                                TATCTGTT    CTGCCA CT
                                ||||||||    |||||| ||
                                GTAGACAG    GACGGT GA
                                    A_____    C
GAM660  MAP1B   3'  TGTTCAGCGACTTAACTA   16961        CC  GCC
                                TGTTCAGT  CT   AACTA
                                ||||||||  ||   |||||
                                ACAAGTCG  GA   TTGAT
                                    CT  A__
GAM660  MAP1B   3'  TGTTCAGCGACTTAACTA   16961        CC  GCC
                                TGTTCAGT  CT   AACTA
                                ||||||||  ||   |||||
                                ACAAGTCG  GA   TTGAT
                                    CT  A__
GAM660  PTPN18  3'  TATCTGTCTAGTAATCTGACTA 16962       TC  CC_  CCA
                                TATCTGT  AGT   CTG   ACTA
                                |||||||  |||   |||   ||||
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                                ATAGACA  TCA   GAC   TGAT
                                   GA   TTA  ___
GAM660  PTPRM    3'  TATCTGTTAGTCCTGGAAAGCT 16963       C    C  CC  _
            A                    TATCTGTT AGTCC TG  AA CTA
                                 |||||||| ||||| ||  || |||
                                 ATAGACAA TCAGG AC  TT GAT
                                    _    _  CT  C
GAM660  RARB     3'  TATCTTTTCAGTCCAAAAACTA 16964      G      CTGCC
                                 TATCT TTCAGTCC    AACTA
                                 ||||| ||||||||    |||||
                                 ATAGA AAGTCAGG    TTGAT
                                    A       TTT__
GAM660  RARB     3'  TATCTTTTCAGTCCAAAAACTA 16964      G      CTGCC
                                 TATCT TTCAGTCC    AACTA
                                 ||||| ||||||||    |||||
                                 ATAGA AAGTCAGG    TTGAT
                                    A       TTT__
GAM660  TNFRSF6  3'  TATCTGCTTCAGTTTATAACTA 16965       _   CCCTGCC
                                 TATCTGTT CAGT      AACTA
                                 |||||||| ||||      |||||
                                 ATAGACGA GTCA      TTGAT
                                    A   AATA___
GAM660  ZNF36    3'  CTGTTCAGCAGCTAACT     16966        CCCT  C
                                 CTGTTCAGT   GC AACT
                                 |||||||||   || ||||
                                 GACAAGTCG   CG TTGA
                                    T___  A
GAM660  AD022    3'  TACCTGTTTGGAATCCAGC   16967       C__    CT
                                 TATCTGTT   AGTCC  GC
                                 ||||||||   |||||  ||
                                 ATGGACAA   TTAGG  CG
                                    ACC    T_
GAM660  C2F      3'  TGTTCAGTTTTTCACCACTA  16968       CCCT_   A
                                 TGTTCAGT    GCCA CTA
                                 ||||||||    |||| |||
                                 ACAAGTCA    TGGT GAT
                                    AAAAG   _
GAM660  CNNM4    3'  CTGTTCAGTCAGACAGGCTA  16969        CCT  CAA
                                 CTGTTCAGTC  GC  CTA
                                 ||||||||||  ||  |||
                                 GACAAGTCAG  TG  GAT
                                    TC_  TCC
GAM660  FLJ10759 3'  TGTCTTTCGGGCTGCCAACTA 16970     CAG  C__
                                 TGTT  TC  CTGCCAACTA
                                 ||||  ||  ||||||||||
                                 ACAG  AG  GACGGTTGAT
                                   AA_  CCC
GAM660  GAB3     3'  TATCTGCTTAGTTTCCAGC   16971       C  C_  T
                                 TATCTGTT AGT  CC GC
                                 |||||||| |||  || ||
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                                ATAGACGA TCA  GG CG
                                    A   AA  T
GAM660  KIAA0286  3'  TATATGTCTCTTTCCTGCCAAC 16972     C    CAGTC
           T                     TAT TGTT    CCTGCCAACT
                                 ||| ||||    ||||||||||
                                 ATA ACAG    GGACGGTTGA
                                   T   AGAAA
GAM660  SMCR5     3'  TATTGAGCCCCTGCCAGCT   16973     C         A
                                 TGTT AGTCCCTGCCA CT
                                 |||| |||||||||| ||
                                 ATAA TCGGGGACGGT GA
                                   C         C
GAM660  LOC144266 5'  CCTACACTCTTTGCCAGCT   16974     TT  G  CC    A
                                 TCTG  CA TC  TGCCA CT
                                 ||||  || ||  ||||| ||
                                 GGAT  GT AG  ACGGT GA
                                   __  G  AA    C
GAM660  LOC149559 5'  CTGTTTGTTCTCTGCCAACT   16975      CAG  C
                                 CTGTT   TC CTGCCAACT
                                 |||||   || |||||||||
                                 GACAA   AG GACGGTTGA
                                    ACA  A
GAM660  LOC149830 3'  ATCTGCTCCCTGTCAGCT    16976       TCAG     C  A
                                 ATCTGT    TCCCTG CA CT
                                 ||||||    |||||| || ||
                                 TAGACG    AGGGAC GT GA
                                     _____     A  C
GAM660  LOC203069 5'  TCTGGGTCCCTGCCAGCT    16977     TTCA        A
                                 TCTG    GTCCCTGCCA CT
                                 ||||    |||||||||| ||
                                 AGAC    CAGGGACGGT GA
                                   C___         C
GAM661  ADAM12    5'  TTAAAAAAGTTTCCCCCCGTGT 16980        A    GTG
                                 TTGAAAAA TTTTT   TCCGTGT
                                 |||||||| |||||   |||||||
                                 AATTTTTT AAAGG   GGGCACA
                                      C    G__
GAM661  RRAS2     3'  TTAAAAAAAGAGCATGTCTGTG 16981         TTTTT    C
           T                     TTGAAAAAA    GTGTC GTGT
                                 |||||||||    ||||| ||||
                                 AATTTTTTT    TACAG CACA
                                       CTCG_    A
GAM661  KIAA1577  3'  GAAAACATTTTGTGTTTTGTGT 16982      AAT      CC_
                                 GAAAA   TTTTGTGT   GTGT
                                 |||||   ||||||||   ||||
                                 CTTTT   AAAACACA   CACA
                                    GT_       AAA
GAM661  LOC196892 3'  TTGAGGAATTTTCATCCGTGT  16983     AAA      GT
                                 TTGA   AATTTTT  GTCCGTGT
                                 ||||   |||||||  ||||||||
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                                AACT   TTAAAAG  TAGGCACA
                                  CC_      __
GAM662  HNF3A    3'  TCTTGAGGGCAATTCCT     16986    A   AC  AA
                                TC TGA  GG  CGATTCCT
                                || |||  ||  ||||||||
                                AG ACT  CC  GTTAAGGA
                                 A   __  C_
GAM662  FLJ14816 3'  TCCTCATGGATGGATGCCT    16987       GAAC   AC   T
                                TTCTCAT    GGA  GAT CCT
                                |||||||    |||  ||| |||
                                AGGAGTA    CCT  CTA GGA
                                    _____  AC   C
GAM662  KIAA0121 3'  TTCTCATAGAATAACTGTTCCT 16988        AACGG   GA
                                TTCTCATG     AAC  TTCCT
                                ||||||||     |||  |||||
                                AAGAGTAT     TTG  AAGGA
                                     CTTA_   AC
GAM662  KIAA0417 3'  TTCTCATGGAAGCCCTCTTCCT 16989        AAC  AACGA
             A                    TTCTCATG   GG    TTCCTA
                                ||||||||   ||    ||||||
                                AAGAGTAC   TC    AAGGAT
                                     CT_  GGGAG
GAM662  KIAA1040 3'  TTCTCATGAATGACAATT    16990         CG  A
                                TTCTCATGAA  GA CGATT
                                ||||||||||  || |||||
                                AAGAGTACTT  CT GTTAA
                                      A_  _
GAM662  MGC16703 5'  TTCTCATGGTAAAGTTCCT    16991        AACG   CGA
                                TTCTCATG    GAA   TTCCT
                                ||||||||    |||   |||||
                                AAGAGTAC    TTT   AAGGA
                                     CA__   C__
GAM662  PPP1R3B  3'  TTCTTATGAACAGAGTGATCCT 16992      C       AC   T
                                TTCT ATGAACGGA  GAT CCT
                                |||| |||||||||  ||| |||
                                AAGA TACTTGTCT  CTA GGA
                                  A        CA  _
GAM662  LOC145786 3'  TTCTCATAATGGAGACAGCT   16993        AC   AC   TC
                                TTCTCATGA  GGA  GAT  CT
                                |||||||||  |||  |||  ||
                                AAGAGTATT  CCT  CTG  GA
                                     A_   __   TC
GAM662  LOC146745 5'  TTCTCATGGAGGGGGGGTCCTA 16994        AAC  AACGAT
                                TTCTCATG   GG     TCCTA
                                ||||||||   ||     |||||
                                AAGAGTAC   CC     AGGAT
                                     CT_  CCCCC_
GAM662  LOC162239 3'  TTCTCATGGGATCCTA      16995        AAC   ACGAT
                                TTCTCATG   GGA    TCCTA
                                ||||||||   |||    |||||
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                                AAGAGTAC   CCT    AGGAT
                                   ___   _____
GAM662  LOC219790 3'  TTCTTCTGAACAAAATGATT   16996      CA       C
                                TTCT  TGAACGGAA GATT
                                ||||  ||||||||| ||||
                                AAGA  ACTTGTTTT CTAA
                                  AG        A
GAM662  LOC91818  3'  TTCTCATGAACGGGCACCT    16997            AACGATT
                                TTCTCATGAACGG      CCT
                                ||||||||||||       |||
                                AAGAGTACTTGCC      GGA
                                       CGT____
GAM663  CELSR1    3'  CGTTCTGTTAAAAACCTCC    17000       C       G
                                CGTTC GTTAGAAAC TTT
                                ||||| ||||||||| |||
                                GCAAG CAATTTTTG AGG
                                   A        G
GAM663  DNAJB9    3'  ATTTCGTTAAGTTTTCAA     17001     C     AAAC
                                GTT CGTTAG    GTTTTCAA
                                ||| ||||||    ||||||||
                                TAA GCAATT    CAAAAGTT
                                  A     ____
GAM663  EHD2      3'  GTTCCGTTCAGAGGCCCCTCCC 17002        _    AACG_  TT
          A                      GTTCCGT TAGA     TT  CA
                                 |||||||  ||||     ||  ||
                                 CAAGGCA GTCT     GA  GT
                                     A    CCGGG  GG
GAM663  KERA      3'  GTTTTGTTAGAAAGCATTCAA  17003     CC       C  T
                                GTT  GTTAGAAA GT TTCAA
                                |||  |||||||| || |||||
                                CAA  CAATCTTT CG AAGTT
                                  AA        _  T
GAM663  ZHX1      3'  GCCCCAAAACGTTTTCAA     17004       GTTA
                                GTTCC    GAAACGTTTTCAA
                                |||||    ||||||||||||||
                                CGGGG    TTTTGCAAAAGTT
                                   ____
GAM663  C22orf20  3'  CCGCCATGGAGACGTTTT     17005        __  A
                                CCGTTA  GA ACGTTTT
                                ||||||  ||  |||||||
                                GGCGGT  CT TGCAAAA
                                    AC  C
GAM663  FLJ11181  3'  CCTTCCGTTAGGAAGTCCT    17006    G       A  C
                                C TTCCGTTAG AA GTTTT
                                | |||||||||  || |||||
                                G AAGGCAATC TT CAGGA
                                 G        C  _
GAM663  LOC152573 3'  GTCCAGTAAAACGTTTT      17007      C  TA
                                GTTC GT  GAAACGTTTT
                                ||||  ||  ||||||||||
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                                CAGG CA  TTTTGCAAAA
                                  T __
GAM664  DBN1     5'  CCCCGCCCTCGCTTTCCTTTG  17010       ___ AC_
                                CCCCGCC  G  TCCTTTG
                                |||||||  |  |||||||
                                GGGGCGG  C  AGGAAAC
                                   GAG GAA
GAM664  FHL2     5'  ACCCCGCCGTGTCATTTG    17011        AC  C
                                ACCCCGCCG  TC TTTG
                                |||||||||  || ||||
                                TGGGGCGGC  AG AAAC
                                     AC  T
GAM664  POU5F1   3'  CCCCTGCCCCCACCCTTTG   17012     _  G__  T
                                CCCC GCC   AC CCTTTG
                                |||| |||   || ||||||
                                GGGG CGG   TG GGAAAC
                                  A  GGG  _
GAM664  POU5F1   3'  CCCCTGCCCCCACCCTTTG   17012     _  G__  T
                                CCCC GCC   AC CCTTTG
                                |||| |||   || ||||||
                                GGGG CGG   TG GGAAAC
                                  A  GGG  _
GAM664  RANBP3   3'  CCCCGCTTCATTCCCTTTG   17013      __  AC
                                CCCCGC  CG  TCCTTTG
                                ||||||  ||  |||||||
                                GGGGCG  GT  GGGAAAC
                                   AA  AA
GAM664  TGIF     5'  CCCCTCTCCGCTCCTTTG    17014     G__  A
                                CCCC   CCG CTCCTTTG
                                ||||   ||| ||||||||
                                GGGG   GGC GAGGAAAC
                                  AGA  _
GAM664  BCL2L1   3'  TACCTGCCAGCCTCCTTTG   17015     CC   A_
                                TACC  GCCG  CTCCTTTG
                                ||||  ||||  ||||||||
                                ATGG  CGGT  GAGGAAAC
                                  A_   CG
GAM664  DCOHM    3'  CACCTTCTCCTGACTCCTTTG  17016     CCG_  _
                                TACC   CC GACTCCTTTG
                                ||||   || ||||||||||
                                GTGG   GG CTGAGGAAAC
                                  AAGA  A
GAM664  DKFZP434C1715 3'  TACCCCCTTACTGGCCCTTTG  17017       GCCG  ___
                                TACCCC   ACT  CCTTTG
                                ||||||   |||  ||||||
                                ATGGGG   TGA  GGAAAC
                                   GAA_  CCG
GAM664  ELF4     3'  TACCCCACTCGGCCTTTG    17018        _  ACT
                                TACCCCGC CG  CCTTTG
                                |||||||| ||  ||||||
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                                ATGGGGTG GC   GGAAAC
                                    A  C__
GAM664  FLJ10036  5'  CCCCGCCGGGACTATTTTG   17019       __   CC
                                CCCCGCC  GACT  TTTG
                                |||||||  ||||  ||||
                                GGGGCGG  CTGA  AAAC
                                    CC    TA
GAM664  FLJ12505  5'  CACCCCGCCGTCTTTG     17020         ACTC
                                TACCCCGCCG   CTTTG
                                ||||||||||   |||||
                                GTGGGGCGGC   GAAAC
                                    A___
GAM664  FLJ12687  5'  TACCCCTCCCTACTTTG    17021       G  GA  C
                                TACCCC CC  CT CTTTG
                                ||||||  ||  ||  |||||
                                ATGGGG GG  GA GAAAC
                                    A  __  T
GAM664  KIAA1100  5'  CCACACGTTGACTCCTTTG   17022    C   C__
                                CC CGC   GACTCCTTTG
                                ||  |||   ||||||||||
                                GG GTG   CTGAGGAAAC
                                 T   CAA
GAM664  KIAA1117  3'  TACCCCCTCCCAATACTCTTTT 17023       G_  G___    C
          G                      TACCCC  CC    ACTC TTTG
                                ||||||  ||    ||||  ||||
                                ATGGGG  GG    TGAG AAAC
                                    GA  GTTA    A
GAM664  KIAA1529  5'  CACCCAGACTCCTTTG     17024      CGCC
                                TACCC    GACTCCTTTG
                                |||||    ||||||||||
                                GTGGG    CTGAGGAAAC
                                   T___
GAM664  MGC12966  3'  CACCCGAGGCTCTCCTTTG   17025      C__  CGA
                                TACCC   GC   CTCCTTTG
                                |||||   ||   ||||||||
                                GTGGG   CG   GAGGAAAC
                                   CTC  A__
GAM664  SIMRP7    3'  CCTCCAGCCCCTCCTTTG    17026    _  _   GA
                                CC CC GCC  CTCCTTTG
                                ||  ||  |||  ||||||||
                                GG GG CGG  GAGGAAAC
                                 A  T   G_
GAM664  UXS1      5'  CACCCCCCTCTCCTTTG     17027       G  GA
                                TACCCC CC  CTCCTTTG
                                ||||||  ||  ||||||||
                                GTGGGG GG  GAGGAAAC
                                    _  A_
GAM664  LOC145660 5'  CACTTGCGCACTCCTTTG    17028     CC_   CG
                                TAC   CGC  ACTCCTTTG
                                |||   |||  |||||||||
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                                GTG   GCG  TGAGGAAAC
                                  AAC   __
GAM664   LOC146237 3'  CCTCGCCGACTCCACTTG    17029    C        _
                                CC CGCCGACTCC TTTG
                                || |||||||||| ||||
                                GG GCGGCTGAGG GAAC
                                 A         T
GAM664   LOC146821 3'  TACTTCACCTGCCCCTTTG   17030    CC    GA
                                TAC  CGCC  CTCCTTTG
                                |||  ||||  ||||||||
                                ATG  GTGG  GGGGAAAC
                                  AA    AC
GAM664   LOC147622 3'  TACCCAACTGCTCCTTTG    17031      C  CGA
                                TACCC GC   CTCCTTTG
                                ||||| ||   ||||||||
                                ATGGG TG   GAGGAAAC
                                   T  AC_
GAM664   LOC151760 5'  CCCCTCCAATGGCTCTTTTGC  17032     G   ___   C   III
                                CCCC CCGA   CTC TTTG   C
                                |||| ||||   ||| ||||   |
                                GGGG GGTT   GAG AAAC   G
                                  A    ACC   A    III
GAM664   LOC256806 3'  CACTCCCCCCTCCTTTG     17033    _  G  GA
                                TAC CCC CC  CTCCTTTG
                                ||| ||| ||  ||||||||
                                GTG GGG GG  GAGGAAAC
                                  A  _  __
GAM665   BTK      5'  CGCAGCAGACACTGGCCC    17036          ___
                                CGCAGCAGATA   GCCC
                                ||||||||||   ||||
                                GCGTCGTCTGT   CGGG
                                      GAC
GAM665   FBXW1B   5'  CCGCGCAGCAGCGAACGGCCC  17037          ATA___
                                CCGCGCAGCAG     GCCC
                                ||||||||||     ||||
                                GGCGCGTCGTC     CGGG
                                      GCTTGC
GAM665   FBXW1B   5'  CCGCGCAGCAGCGAACGGCCC  17037          ATA___
                                CCGCGCAGCAG     GCCC
                                ||||||||||     ||||
                                GGCGCGTCGTC     CGGG
                                      GCTTGC
GAM665   FBXW1B   5'  CCGCGCAGCAGCGAACGGCCC  17037          ATA___
                                CCGCGCAGCAG     GCCC
                                ||||||||||     ||||
                                GGCGCGTCGTC     CGGG
                                      GCTTGC
GAM665   GALR1    5'  CCGCGCAGGTGGAAAGACCC   17038        CA_  T  _
                                CCGCGCAG   GA AG CCC
                                ||||||||   || || |||
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                                GGCGCGTC  CT TC GGG
                                    CAC  T  T
GAM665  JAK2    5'  CCGCAGCAGCCCTCAGCCC   17039    _   AGA
                                CCGC GCAGC  TAGCCC
                                |||| |||||  ||||||
                                GGCG CGTCG  GTCGGG
                                  T   GGA
GAM665  LENG4   3'  CCGCACAGCAGCGCACCC   17040        ATA
                                CCGCGCAGCAG  GCCC
                                ||||||||||  ||||
                                GGCGTGTCGTC  TGGG
                                     GCG
GAM665  MADD    5'  CCGCGAGGACAGCCC     17041     C  CA
                                CCGCG AG  GATAGCCC
                                ||||| ||  ||||||||
                                GGCGC TC  CTGTCGGG
                                  _ __
GAM665  MOG     5'  CCCGCAGAAACAGCCC     17042   G   C
                                CC CGCAG AGATAGCCC
                                || ||||| |||||||||
                                GG GCGTC TTTGTCGGG
                                 _   _
GAM665  PDE9A   3'  CCGCGCAGCTCGGCCAGCCC  17043       AGA__
                                CCGCGCAGC   TAGCCC
                                |||||||||   ||||||
                                GGCGCGTCG   GTCGGG
                                     AGCCG
GAM665  RAB4A   5'  CCGCGCAGGCGCAGGGCCC   17044      ___   ATA
                                CCGCGCA  GCAG  GCCC
                                |||||||  ||||  ||||
                                GGCGCGT  CGTC  CGGG
                                   CCG   C__
GAM665  RAP1GA1 3'  CCTGCAGAGACAGCCC    17045   GC   C
                                CC  GCAG AGATAGCCC
                                ||  |||| |||||||||
                                GG  CGTC TCTGTCGGG
                                 A_   _
GAM665  SDC1    3'  CCACCAGACAGATAGTCC   17046    G  _    _
                                CCGC CAG CAGATAG CC
                                |||| ||| ||||||| ||
                                GGTG GTC GTCTATC GG
                                  _  T     A
GAM665  ARNTL2  5'  CGCGCAGCGGACGCCGCCC  17047       A  A__
                                CGCGCAGC GAT  GCCC
                                |||||||| |||  ||||
                                GCGCGTCG CTG  CGGG
                                    C  CGG
GAM665  BDG-29  5'  CGCGCAGCGAGTGGTAGTCC  17048       _ A__  _
                                CGCGCAGC AG  TAG CC
                                |||||||| ||  ||| ||
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                                GCGCGTCG TC   ATC GG
                                    C  ACC   A
GAM665  CDK5RAP1  5'  CCGCAGCAGCAACAGTGCCC  17049     _     ATA_
                                CCGC GCAGCAG    GCCC
                                |||| |||||||    ||||
                                GGCG CGTCGTT    CGGG
                                  T      GTCA
GAM665  DOK4      3'  CCCCGCAGCAGGCAGCCC    17050    G      A
                                CC CGCAGCAG TAGCCC
                                || |||||||| ||||||
                                GG GCGTCGTC GTCGGG
                                 G       C
GAM665  FLJ10597  3'  CCCCGCAGCAGGAGCCC     17051    G      AT
                                CC CGCAGCAG  AGCCC
                                || ||||||||  |||||
                                GG GCGTCGTC  TCGGG
                                 G       C_
GAM665  FLJ20371  3'  CCATGCCACAAATAGTCC    17052     C  A      _
                                CCG GC GCAGATAG CC
                                ||| || |||||||| ||
                                GGT CG TGTTTATC GG
                                  A G       A
GAM665  FLJ20548  3'  CCGCACAGGACGTGCCC     17053        CA   A_
                                CCGCGCAG  GAT  GCCC
                                ||||||||  |||  ||||
                                GGCGTGTC  CTG  CGGG
                                    __   CA
GAM665  FLJ21324  5'  CCGGGCAGCAGAGTACAGTCC  17054     C      ___   _
                                CCG GCAGCAGA   TAG CC
                                ||| ||||||||   ||| ||
                                GGC CGTCGTCT   GTC GG
                                  C       CAT   A
GAM665  FLJ21986  3'  CACTGTAACAGATAGCCC    17055     GC_
                                CGC   AGCAGATAGCCC
                                |||   ||||||||||||
                                GTG   TTGTCTATCGGG
                                  ACA
GAM665  FOXO3A    5'  GCGCAGCAGACACCGCCC     17056           __
                                GCGCAGCAGATA  GCCC
                                ||||||||||||  ||||
                                CGCGTCGTCTGT  CGGG
                                      GG
GAM665  KCNJ9     5'  CCGGCAGCAGAGACCC      17057     C      TA
                                CCG GCAGCAGA  GCCC
                                ||| ||||||||  ||||
                                GGC CGTCGTCT  TGGG
                                  _       C_
GAM665  KIAA0475  5'  CCGCGCAGAGCGGCAGTCC   17058        C  A__   _
                                CCGCGCAG AG   TAG CC
                                |||||||| ||   ||| ||
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                                GGCGCGTC TC   GTC GG
                                    _ GCC   A
GAM665  KIAA0537  3'  CCACGCAGCCAGACCTAGC   17059        _   __
                                CCGCGCAGC AGAT  AGC
                                ||||||||| ||||  |||
                                GGTGCGTCG TCTG  TCG
                                    G   GA
GAM665  KIAA0918  3'  CCGCGCAGCAAATTGGCC    17060          A_
                                CCGCGCAGCAGAT  GCC
                                ||||||||||||  |||
                                GGCGCGTCGTTTA  CGG
                                      AC
GAM665  KIAA1303  3'  CCGCAGCAGCCGACGCCC    17061     _    A  A
                                CCGC GCAGC GAT GCCC
                                |||| ||||| ||| ||||
                                GGCG CGTCG CTG CGGG
                                  T    G  _
GAM665  KIAA1817  3'  CCTGCAGCAACAGCCC      17062    GC     G
                                CC  GCAGCA ATAGCCC
                                ||  |||||| |||||||
                                GG  CGTCGT TGTCGGG
                                 A_     _
GAM665  KIAA1910  5'  CCGCACTGCAATAGCCC     17063       A   A
                                CCGCGC GCAG TAGCCC
                                |||||| |||| ||||||
                                GGCGTG CGTT ATCGGG
                                   A   _
GAM665  NIN       5'  CCGCACAGCCGGCAGCCC    17064         AGA
                                CCGCGCAGC   TAGCCC
                                |||||||||   ||||||
                                GGCGTGTCG   GTCGGG
                                     GCC
GAM665  RASGRP4   3'  CCGCGCAGCCAGCCC       17065         AGA
                                CCGCGCAGC   TAGCCC
                                |||||||||   ||||||
                                GGCGCGTCG   GTCGGG
                                     ___
GAM665  RBM12     5'  CCCCGCGGCCGACAGCCC    17066    G   A  A
                                CC CGC GC GATAGCCC
                                || ||| || ||||||||
                                GG GCG CG CTGTCGGG
                                 G   C  G
GAM665  TIP-1     5'  CCGGCAGCAGAGTACCC     17067     C       TA
                                CCG GCAGCAGA  GCCC
                                ||| ||||||||  ||||
                                GGC CGTCGTCT  TGGG
                                  _       CA
GAM665  TSSC1     3'  CCGTCGACAATAGCCC      17068     _  CA    A
                                CCG CG  GCAG TAGCCC
                                ||| ||  |||| ||||||
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                                GGC GC  TGTT ATCGGG
                                  A __   _
GAM665  LOC115708 3'  CCTGCGGCAGACAACCC     17069    GC  A
                                CC  GC GCAGATAGCCC
                                ||  || ||||||||||
                                GG  CG CGTCTGTTGGG
                                 A_  C
GAM665  LOC146713 3'  CCGGCAGCAGAGCCC       17070     C       TA
                                CCG GCAGCAGA  GCCC
                                ||| ||||||||  ||||
                                GGC CGTCGTCT  CGGG
                                  _      __
GAM665  LOC151438 5'  CCTGCCAGGGATAGCCC     17071    _ G   CA
                                CC GC CAG  GATAGCCC
                                || || |||  ||||||||
                                GG CG GTC  CTATCGGG
                                 A  _  C_
GAM665  LOC197414 3'  CCGTCGGTGCGACAGCCC    17072     _ CA  A
                                CCG CG  GC GATAGCCC
                                ||| ||  || ||||||||
                                GGC GC  CG CTGTCGGG
                                  A  CA  _
GAM665  LOC203668 5'  CCACGCAGCACAGCGCAGCCC  17073          GA___
                                CCGCGCAGCA    TAGCCC
                                ||||||||||    ||||||
                                GGTGCGTCGT    GTCGGG
                                      GTCGC
GAM665  LOC221755 5'  CCGCGCAGGAAGTAGCCC    17074        C  A
                                CCGCGCAG AG TAGCCC
                                |||||||| || ||||||
                                GGCGCGTC TT ATCGGG
                                     C  C
GAM665  LOC92714  5'  CCGCGCAGCGACGCCC      17075         A   A
                                CCGCGCAGC GAT GCCC
                                ||||||||| ||| ||||
                                GGCGCGTCG CTG CGGG
                                       _  _
GAM666  BUB3     3'  AAAGACCCTTCTCTGTA     17078     C    GTGCGG
                                AAA ACCC     TCTCTGTA
                                ||| ||||     ||||||||
                                TTT TGGG     AGAGACAT
                                  C   A_____
GAM666  FCMD     3'  CCCTACAAAATCTCTGTAT   17079     G   __
                                CCC TGCG  GTCTCTGTAT
                                ||| ||||  ||||||||||
                                GGG ATGT  TAGAGACATA
                                  _   TT
GAM666  KCNA6    3'  AACACCAGTGCCTCTGT     17080       C   GGT
                                AACACC GTGC   CTCTGT
                                |||||| ||||   ||||||
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                                TTGTGG CACG   GAGACA
                                   T   ___
GAM666  NEBL     3'  ACACCAGATCATCTCTGTAT  17081      CGTG  G
                                ACACC   CG TCTCTGTAT
                                ||||||   || |||||||||
                                TGTGG   GT AGAGACATA
                                   TCTA  _
GAM666  RFNG     3'  AAACATCTCTGTGGTCCCAGT  17082      CCCG  C     T
                                AAACA   TG GGTCTC GT
                                ||||||   || |||||| ||
                                TTTGT   AC CCAGGG CA
                                   AGAG  A     T
GAM666  SIL      3'  ACACCCTGTCCCTGTA      17083       GTGCG
                                ACACCC    GTCTCTGTA
                                ||||||    |||||||||
                                TGTGGG    CAGGGACAT
                                   A____
GAM666  TBXA2R   5'  GAACCCCTGGGCACATTTCTGT 17084   C   G  C   C____
             AT                   A ACCC TG GGT    TCTGTAT
                                | |||| || |||    |||||||
                                C TGGG AC CCG    AGACATA
                                 T   G  _   TGTAA
GAM666  BRD2     5'  GGACGACTCGAAGGCTCTGTAT 17085   A  _  C  TGC  T
                                A AC AC CG   GG CTCTGTAT
                                | || || ||   || ||||||||
                                C TG TG GC   CC GAGACATA
                                 C  C  A  TT_  _
GAM666  CDT6     3'  CGTGTCTCAGTTTCTGTAT   17086      ___    C
                                CGTG   CGGT TCTGTAT
                                ||||   |||| |||||||
                                GCAC   GTCA AGACATA
                                   AGA    A
GAM666  DKFZP564J047 3'  AAACACTGTTTGCTCTGTAT   17087       CC  GCG T
                                AAACAC  GT   G CTCTGTAT
                                ||||||  ||   | ||||||||
                                TTTGTG  CA   C GAGACATA
                                   A_  AA_ _
GAM666  DREV1    3'  CCCTGAAGTTCTGTAT      17088     G  C   C
                                CCC TG GGT TCTGTAT
                                ||| || ||| |||||||
                                GGG AC TCA AGACATA
                                  _  T   _
GAM666  FLJ12765 3'  ACACAGTGTTGGTTTCTGTAT  17089      CC   C_   C
                                ACAC  GTG  GGT TCTGTAT
                                ||||  |||  ||| |||||||
                                TGTG  CAC  CCA AGACATA
                                   T_   AA   A
GAM666  FLJ23132 3'  CCATCAGTTGTTTCTGTAT   17090      G    C___
                                CCGT CGGT    TCTGTAT
                                |||| ||||    |||||||
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                                GGTA GTCA    AGACATA
                                  _    ACAA
GAM666  FLJ23306  5'  GGACACCCGTGTGGCTTTGT   17091    A       C  T  C
                                A ACACCCGTG GG CT TGT
                                | ||||||||| || || |||
                                C TGTGGGCAC CC GA ACA
                                 C       A  _  A
GAM666  GBTS1     3'  AACTACCCACCTCTCTGTAT   17092     _    TGCGG
                                AAC ACCCG    TCTCTGTAT
                                ||| |||||    |||||||||
                                TTG TGGGT    AGAGACATA
                                  A    GG___
GAM666  HTMP10    3'  AACACCACCAGTCTCTGTAT   17093      CGTG
                                AACACC    CGGTCTCTGTAT
                                ||||||    ||||||||||||
                                TTGTGG    GTCAGAGACATA
                                    TG__
GAM666  P66       3'  AACAGCCGTTCCTCTGTAT    17094     C    GCGG
                                AACA CCGT    TCTCTGTAT
                                |||| ||||    |||||||||
                                TTGT GGCA    GGAGACATA
                                  C    A___
GAM666  PRO1914   5'  AAACAGTTGGCCCTCTGTAT   17095      CCC  GC   _
                                AAACA   GT  GGTC TCTGTAT
                                |||||   ||  |||| |||||||
                                TTTGT   CA  CCGG AGACATA
                                   ___  A_   G
GAM666  SPRY4     3'  CGTGGTGGTGGTCTCTGTAT   17096     C____
                                CGTG    GGTCTCTGTAT
                                ||||    ||||||||||||
                                GCAC    CCAGAGACATA
                                  CACCA
GAM666  LOC256158 5'  CACCCGTGTGGCTCTGC     17097        C  T
                                CACCCGTG GG CTCTGT
                                |||||||| || ||||||
                                GTGGGCAC CC GAGACG
                                    A  _
GAM666  LOC257457 3'  AAACACCCGGGCTTGGTTTGTG 17098         T  __  CTC
          T                      AAACACCCG GC  GGT   TGT
                                |||||||||  ||  |||   |||
                                TTTGTGGGC CG  CCA   ACA
                                     C  AA   AAC
GAM667  APPL      3'  TTCAAATCCAATTCTAAAGT   17101      T   TG A
                                TTCAA ATC  A TCTAAAGT
                                ||||| |||  | ||||||||
                                AAGTT TAG  T AGATTTCA
                                   _  GT A
GAM667  CASPR3    3'  CTCAATATCTTGGGGAAGTAA  17102          GAATCTA
                                TTCAATATCT      AAGTAA
                                ||||||||||      ||||||
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                                GAGTTATAGA      TTCATT
                                      ACCCC__
GAM667  KIAA0419  3'  TTCAATATTCTGTAAAAGTAAA 17103        _  AATCT
                                TTCAATAT CTG    AAAGTAAA
                                |||||||| |||    ||||||||
                                AAGTTATA GAC    TTTCATTT
                                     A   AT___
GAM667  MGC10981  3'  TTCAAATCTGAATCTGTGCAA  17104      T       AAA
                                TTCAA ATCTGAATCT   GTAA
                                ||||| ||||||||||   ||||
                                AAGTT TAGACTTAGA   CGTT
                                   _        CA_
GAM667  MGC2628   3'  CTCAATATTTGAGTCTCTGCA  17105       C   A   AAA
                                TTCAATAT TGA TCT   GTA
                                |||||||| ||| |||   |||
                                GAGTTATA ACT AGA   CGT
                                     A   C   GA_
GAM667  NSE1      3'  CAATATCTGAGAAAAATA    17106         ATCT
                                CAATATCTGA    AAAGTA
                                ||||||||||    ||||||
                                GTTATAGACT    TTTTAT
                                      CT__
GAM667  OIP5      3'  TTCAATAAGAATCTAAAGTAA  17107       TCT
                                TTCAATA   GAATCTAAAGTAA
                                |||||||   ||||||||||||
                                AAGTTAT   CTTAGATTTCATT
                                     T__
GAM667  ZNF177    3'  TCCAATATATGTTCTAAAGT   17108        C  AA
                                TTCAATAT TG  TCTAAAGT
                                |||||||| ||  ||||||||
                                AGGTTATA AC  AGATTTCA
                                     T  A_
GAM667  LOC154089 5'  TTCAATTTCTACAGATAAAGTA 17109       A    AATC
           A                     TTCAAT TCTG    TAAAGTAA
                                ||||||| ||||    ||||||||
                                AAGTTA AGAT    ATTTCATT
                                   A    GTCT
GAM667  LOC221585 3'  AATATCTGAGTTCCACTGGGGT 17110         A_    AA___
           AA                     AATATCTGA  TCTA    GTAA
                                |||||||||  ||||    ||||
                                TTATAGACT  AGGT    CATT
                                     CA    GACCC
GAM667  LOC57105  3'  TTCAATATCTGAAGAAAAGTA  17111           TCT
                                TTCAATATCTGAA   AAAGTA
                                ||||||||||||   ||||||
                                AAGTTATAGACTT   TTTCAT
                                       CT_
GAM668  FBXL5     5'  TTCAATCTGCTCATGCATT    17114    G       CTCC
                                TT AATCTGTTC    ATGCATT
                                || |||||||||    |||||||
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                                AA TTAGACGAG    TACGTAA
                                 G       _____
GAM668  MAP2     3'  TTGAATCTTTCTTCCCATT    17115        G   C   ATG
                                TTGAATCT TTC TCC   CATT
                                |||||||| ||| |||   ||||
                                AACTTAGA AAG AGG   GTAA
                                     _   A   ___
GAM668  FLJ10097 3'  TTGAACTGCTTTATGCATT    17116       T    CCTCC
                                TTGAA CTGTT    ATGCATT
                                ||||| |||||    |||||||
                                AACTT GACGA    TACGTAA
                                   _    AA___
GAM668  FLJ10330 3'  TTGAATCTGTTTCTCTAC     17117          C   CA
                                TTGAATCTGTT CTC  TGC
                                |||||||||||| |||  |||
                                AACTTAGACAA GAG  ATG
                                       A  __
GAM668  FLJ20313 5'  TTGTGTCTGTTGCAATGCATTT 17118     AA     CCTCC
                                TTG  TCTGTT    ATGCATTT
                                |||  ||||||    ||||||||
                                AAC  AGACAA    TACGTAAA
                                  AC     CGT__
GAM668  LOC120406 3'  TTGAATCATTTAATCTATGCAT 17119        TGTTCC  C
           TT                    TTGAATC     TC ATGCATTT
                                |||||||     || ||||||||
                                AACTTAG     AG TACGTAAA
                                    TAAATT  A
GAM668  LOC51334  5'  TTGATCTGTTCCTTCAC     17120      A       C
                                TTGA TCTGTTCCT CAT
                                |||| ||||||||| |||
                                AACT AGACAAGGA GTG
                                  _       A
GAM668  LOC90594  3'  TGAGTGCTTCCATGCATTT   17121     ATC   CC
                                TGA   TGTT  TCCATGCATTT
                                |||   ||||  ||||||||||
                                ACT   ACGA  AGGTACGTAAA
                                  C__   __
GAM669  MMP25    3'  TTCGTTTTTATTGTCCTGAGT  17124      G     CAA
                                TTCGT TTTATT   TTCTGAGT
                                ||||| ||||||   ||||||||
                                AAGCA AAATAA   AGGACTCA
                                   A     C__
GAM669  NR1I2    5'  TGTCTAAGTAATTCTGAGT    17125       TTC
                                TGTTTA   AATTCTGAGT
                                ||||||   ||||||||||
                                ACAGAT   TTAAGACTCA
                                    TCA
GAM669  TOX      3'  TGTCTGTTTAATTCTGAGT    17126       A  C
                                TGTTT TT AATTCTGAGT
                                ||||| || ||||||||||
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                                ACAGA AA TTAAGACTCA
                                  C  A
GAM669  TYROBP   3'  TTCATGTTTATTTTAGGAGAGT 17127          CAATTCT
           A                    TTCGTGTTTATT      GAGTA
                                ||||||||||||      |||||
                                AAGTACAAATAA      CTCAT
                                      AATCCT_
GAM669  C20orf11 3'  TTCGTGCTTTTCCTGTATTTTG 17128        A  A__  C
           AGT                   TTCGTGTTT TTC  ATT TGAGT
                                 |||||||||| |||  ||| |||||
                                 AAGCACGAA AGG  TAA ACTCA
                                     A  ACA  A
GAM669  RRP4     3'  TTCATGTTTATCTGAG      17129          TTCAAT
                                 TTCGTGTTTA     TCTGAG
                                 ||||||||||     ||||||
                                 AAGTACAAAT     AGACTC
                                        _______
GAM669  LOC145676 5'  CTCGTGTTTATTCAGTCACTG  17130           A  _
                                 TTCGTGTTTATTCA TT CTG
                                 |||||||||||||| || |||
                                 GAGCACAAATAAGT AG GAC
                                       C  T
GAM670  KIAA1229 3'  TAAATGTCTTAAAAGTTGAT   17133        G   CC
                                 TAAATGTC TAA  GTTGAT
                                 |||||||| |||  ||||||
                                 ATTTACAG ATT  CAACTA
                                     A   TT
GAM671  BVES     3'  CAGCATAAGTTTGGCCC     17136          TATTT
                                 CAGCATAAGTT    TGGTCT
                                 ||||||||||     ||||||
                                 GTCGTATTCAA    ACCGGG
                                        ______
GAM671  GPR87    5'  TTCAGCATAGGTTATTCCTGGT 17137         A   TA
                                 TTCAGCATA GTT  TTTTGGT
                                 |||||||| |||  |||||||
                                 AAGTCGTAT CAA  AGGACCA
                                     C   TA
GAM671  MAD2L1   3'  TTCAGTAAGTATCATTTTGGT  17138      CA    _
                                 TTCAG  TAAGT TTATTTTGGT
                                 |||||  ||||| ||||||||||
                                 AAGTC  ATTCA AGTAAAACCA
                                    __    T
GAM671  PDGFRA   3'  TTCAGCACAGGTTTATGCCT   17139        A     TTTG
                                 TTCAGCATA GTTTAT   GTCT
                                 |||||||| ||||||   ||||
                                 AAGTCGTGT CAAATA   CGGA
                                     C    _____
GAM671  DKFZp761D221 3'  GCATTTTCTATTTTGGT     17140      AAG
                                 GCAT   TTTATTTTGGT
                                 ||||   ||||||||||
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                                CGTA  AGATAAAACCA
                                  AA_
GAM671  FLJ10718  3'  TCCAGTGTAAGTTTATTGTCT  17141     CA       TTG
                                TTCAG  TAAGTTTATT  GTCT
                                |||||  ||||||||||  ||||
                                AGGTC  ATTCAAATAA  CAGA
                                  AC       ___
GAM671  FLJ13815  5'  TCAGCGTAATTCTTTGGTCT  17142     A  GTTTA
                                TCAGC TAA    TTTTGGTCT
                                ||||| |||    |||||||||
                                AGTCG ATT    GAAACCAGA
                                  C  AA___
GAM671  KIAA0712  3'  TTCAGCCTGAGTCTAAGTGGTC 17143      ATA    TTT
          T                      TTCAGC  AGTTTA  TGGTCT
                                ||||||  ||||||  ||||||
                                AAGTCG  TCAGAT  ACCAGA
                                   GAC    TC_
GAM671  RHOBTB1  3'  TTCAGCAGAAGTGGGTGGTCT  17144      T   TTATTT
                                TTCAGCA AAGT    TGGTCT
                                ||||||| ||||    ||||||
                                AAGTCGT TTCA    ACCAGA
                                   C   CCC___
GAM671  SLAM    3'  TTCAGTGTTCATTTTGGT   17145     CATAA
                                TTCAG   GTTTATTTTGGT
                                |||||   ||||||||||||
                                AAGTC   CAAGTAAAACCA
                                  A____
GAM671  LOC147837 3'  TCCAGTGTAAGTTTATTC   17146     CA
                                TTCAG  TAAGTTTATTT
                                |||||  ||||||||||
                                AGGTC  ATTCAAATAAG
                                  AC
GAM671  LOC150159 3'  TTCAATGTAAGTTTTTTCTGGT 17147     CA     A
          CT                     TTCAG  TAAGTTT TTTTGGTCT
                                |||||  ||||||| |||||||||
                                AAGTT  ATTCAAA AAGACCAGA
                                  AC     A
GAM671  LOC151195 5'  TTCAGCATAAGTTAAAAGCCT  17148          TATTTT
                                TTCAGCATAAGTT    GGTCT
                                ||||||||||||    |||||
                                AAGTCGTATTCAA    TCGGA
                                       TTT___
GAM671  LOC152687 5'  TTCAGTATAAGTTTGTGG   17149     C      ATTT
                                TTCAG ATAAGTTT   TGG
                                ||||| ||||||||   |||
                                AAGTC TATTCAAA   ACC
                                  A      C___
GAM671  LOC253981 3'  TTCATATAAGTTTTCAGTC   17150     GC      ATT TG
                                TTCA  ATAAGTTT  T  GTC
                                ||||  ||||||||  |  |||
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                                AAGT  TATTCAAA  A  CAG
                                  A_      ___ GT
GAM672  GRB10    3' TACCACAGTGACACCTTTT   17153       G__
                                TACCACAG  TACCTTTT
                                ||||||||  ||||||||
                                ATGGTGTC  GTGGAAAA
                                    ACT
GAM672  TPM1     3' ACCACAGGGGGACCTTTT    17154       T__
                                ACCACAGG  ACCTTTT
                                ||||||||  |||||||
                                TGGTGTCC  TGGAAAA
                                    CCC
GAM672  FLJ10110 3' TACCACAAATAAACTTTT    17155        C_
                                TACCACAGGTA  CTTTT
                                ||||||||||  |||||
                                ATGGTGTTTAT  GAAAA
                                      TT
GAM672  FLJ23191  5' ACCACAAAGAAATACCTTTT  17156      ____
                                ACCACAG   GTACCTTTT
                                |||||||   |||||||||
                                TGGTGTT   TATGGAAAA
                                   TCTT
GAM672  KIAA0555 3' CCACAAGCTCCACCTTTT    17157      ___
                                CCACAGGT  ACCTTTT
                                ||||||||  |||||||
                                GGTGTTCG  TGGAAAA
                                    AGG
GAM672  KIAA1679 3' TACCACAAGATGGCACCTTTT 17158      ____
                                TACCACA   GGTACCTTTT
                                |||||||   ||||||||||
                                ATGGTGT   CCGTGGAAAA
                                   TCTA
GAM672  KIAA1979 3' TACCACAAGTATTCTTTT    17159        C_
                                TACCACAGGTA  CTTTT
                                ||||||||||  |||||
                                ATGGTGTTCAT  GAAAA
                                      AA
GAM672  LOC202754 3' CACCACAGACTTTCCTTTT  17160       TA__
                                TACCACAGG   CCTTTT
                                |||||||||   ||||||
                                GTGGTGTCT   GGAAAA
                                    GAAA
GAM673  PPEF2    3' GAAGATTGTGAGGTGGGG    17163       ATA  TTC
                                GAAGATTGT  AG  GGGG
                                |||||||||  ||  ||||
                                CTTCTAACA  TC  CCCC
                                    C__  CA_
GAM673  PPP1R2   3' TAGAAGATTGTGTGCG      17164        ATAA  T
                                TAGAAGATTGT   GT CG
                                ||||||||||   || ||
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                                ATCTTCTAACA    CA GC
                                      ____  C
GAM673  C20orf108 3'  TAGAAGATTGTCTAAGAAAAGC 17165          A    TTC
                                TAGAAGATTGT TAAG   GGGGC
                                |||||||||||  ||||   |||||
                                ATCTTCTAACA ATTC   TTTCG
                                      G    T__
GAM673  H2AV      3'  TAGAAGATTGTGGAAAGG    17166          ATAAGTTC
                                TAGAAGATTGT       GGGG
                                ||||||||||        ||||
                                ATCTTCTAACA       TTCC
                                      CCT_____
GAM673  MGC16179  3'  TAGAAGGTTGTGAGTCAGG   17167       A   ATA   T
                                TAGAAG TTGT   AGT CGGG
                                ||||||  ||||   |||  ||||
                                ATCTTC AACA   TCA GTCC
                                    C   C__   _
GAM673  SPACA1    3'  TAGAAGATTTGTTGGGGG    17168        GTATAA   C
                                TAGAAGATT     GTT GGGG
                                |||||||||     |||  ||||
                                ATCTTCTAA     CAA CCCC
                                      A_____   C
GAM673  LOC221688 3'  TAGAAGATTGCATGTTAGGG   17169           AA   C
                                TAGAAGATTGTAT  GTT GGG
                                ||||||||||||  |||  |||
                                ATCTTCTAACGTA  CAA CCC
                                       __   T
GAM674  FLT1      3'  CAATTTTCAGTGCTATTTTAAT 17172        G   T     C
            G                    CAATTTTT AGT CTATTT AATG
                                ||||||||  |||  ||||||  ||||
                                GTTAAAAG TCA GATAAA TTAC
                                      _  C     A
GAM674  NFE2L3    3'  CAATTCTTGAAGCAGTTTCAAT 17173          _  TCTA
            G                    CAATTTTTGA GT    TTTCAATG
                                ||||||||||  ||    ||||||||
                                GTTAAGAACT CG    AAAGTTAC
                                      T  TC__
GAM674  MGC2488   5'  TTCTTGAGCTTCAAT       17174          TCTAT
                                TTTTTGAGT     TTCAAT
                                |||||||||     ||||||
                                AAGAACTCG     AAGTTA
                                      _____
GAM674  LOC114987 3'  AATCTTTGAATTTCAAT     17175           CTATT
                                AATTTTTGAGTT     TCAAT
                                ||||||||||||     |||||
                                TTAGAAACTTAA     AGTTA
                                      _____
GAM674  LOC147072 3'  AATTTTTGAAGCAGTTTCAATG 17176          _  TCTA
                                AATTTTTGA GT    TTTCAATG
                                |||||||||  ||    ||||||||
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                                TTAAAAACT CG   AAAGTTAC
                                     T  TC__
GAM674  LOC54103  3'  AATTTTTATGCCTATTATTTCA 17177       A  C__
            ATG                   AATTTTTG GTT   TATTTCAATG
                                |||||||| |||   ||||||||||
                                TTAAAAAT CGG   ATAAAGTTAC
                                     A   ATA
GAM675  CLCA2    3'  CAATGCATTTTAATACA    17180      TGTA
                                TAATGC   TTTAATACA
                                ||||||   |||||||||
                                GTTACG   AAATTATGT
                                   TA__
GAM675  GABRR1   3'  TAATGCTGTGTATTCAATA   17181        __
                                TAATGCTGT  ATTTAATA
                                |||||||||  ||||||||
                                ATTACGACA  TAAGTTAT
                                     CA
GAM675  PTTG1IP  3'  CAATGCTATTTAATACAA    17182       AT
                                TAATGCTGT  TTAATACAA
                                |||||||||  |||||||||
                                GTTACGATA  AATTATGTT
                                     __
GAM675  XK       3'  AATGCTGTATTTGACAA     17183         AAT
                                AATGCTGTATTT   ACAA
                                ||||||||||||   ||||
                                TTACGACATAAA   TGTT
                                     C__
GAM675  ARL1     3'  ATACTCTTTAATACAACT    17184      GTA
                                ATGCT   TTTAATACAACT
                                |||||   ||||||||||||
                                TATGA   AAATTATGTTGA
                                   G__
GAM675  DKFZp564K142 3'  TAATCCTGTATTTAGAGATAC  17185     G      ___
                                TAAT CTGTATTTA   ATAC
                                |||| |||||||||   ||||
                                ATTA GACATAAAT   TATG
                                   G       CTC
GAM675  FLJ13197  3'  TAATGCTGTTTTTAAACA    17186        A    T
                                TAATGCTGT TTTAA ACA
                                ||||||||| ||||| |||
                                ATTACGACA AAATT TGT
                                     A    _
GAM675  KIAA0186  3'  AATGCTGTGATTACAGATACA  17187       AT   ___
                                AATGCTGT  TTA   ATACA
                                ||||||||  |||   |||||
                                TTACGACA  AAT   TATGT
                                     CT   GTC
GAM675  MGC4562   3'  ATACTTTATTTAATGCAACT   17188      G      A
                                ATGCT TATTTAAT CAACT
                                ||||| |||||||| |||||
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                                TATGA ATAAATTA GTTGA
                                   A       C
GAM675  MLLT10   3'  TAATACTGAATCAATGCAACT  17189        TAT    A
                                TAATGCTG   TTAAT CAACT
                                ||||||||   ||||| |||||
                                ATTATGAC   AGTTA GTTGA
                                     TT_    C
GAM675  LOC151258 5'  CAATGCTGTATTTTTAC     17190           AA
                                TAATGCTGTATTT  TAC
                                ||||||||||||  |||
                                GTTACGACATAAA  ATG
                                       A_
GAM675  LOC157798 5'  GCTGTACTCAATACAACT    17191
                                GCTGTATTTAATACAACT
                                ||||||||||||||||||
                                CGACATGAGTTATGTTGA

GAM675  LOC200803 3'  TAATGTAATCCAATACAACT   17192      CTGT
                                TAATG    ATTTAATACAACT
                                |||||    ||||||||||||
                                ATTAC    TAGGTTATGTTGA
                                   AT__
GAM675  LOC256642 3'  TAATGCTGTAGTAGTAAAGTAC 17193         TT__  __
           AA                     TAATGCTGTA    TAA  TACAA
                                ||||||||||    |||  |||||
                                ATTACGACAT    ATT  ATGTT
                                      CATC   TC
GAM675  LOC89932  3'  TAATGCTGTTTTTAATGAC    17194        A    _
                                TAATGCTGT TTTAAT AC
                                ||||||||| ||||||  ||
                                ATTACGACA AAATTA TG
                                      A     C
GAM676  DEFA4    3'  TGAAGCTAACACCACCGATGA  17197    A    AT_       C
                                A GAGT   CGCCACCGA GA
                                | ||||   ||||||||| ||
                                A TTCG   GTGGTGGCT CT
                                 C    ATT        A
GAM676  HNF3A    3'  TAAGAGTATTGCCACAGA     17198         C    C
                                TAAGAGTAT GCCAC GA
                                ||||||||| ||||| ||
                                ATTCTCATA CGGTG CT
                                      A    T
GAM676  SP3      3'  GAGTATCGTCACTATGGTCGTC 17199       C  __________  ACGA
           GTCG                    GTATCG CAC        CG    CG
                                |||||| |||        ||    ||
                                CATAGC GTG        GC    GC
                                   A   ATACCIIIA  AGCA
GAM676  XRCC4    5'  AGAGTATCAGCTACTTCCGCCG 17200         _  C  CGA  A
                                AGAGTATC GC AC   CG CG
                                |||||||| || ||   || ||
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                                TCTCATAG CG TG   GC GC
                                     T  A  AAG  G
GAM676  XRCC4    5'  AGAGTATCAGCTACTTCCGCCG 17200        _  C  CGA  A
                                AGAGTATC GC AC   CG CG
                                |||||||| || ||   || ||
                                TCTCATAG CG TG   GC GC
                                     T  A  AAG  G
GAM676  XRCC4    5'  AGAGTATCAGCTACTTCCGCCG 17200        _  C  CGA  A
                                AGAGTATC GC AC   CG CG
                                |||||||| || ||   || ||
                                TCTCATAG CG TG   GC GC
                                     T  A  AAG  G
GAM676  CENTG2   3'  TAAGAGTATTGCAATCACATCG 17201         C  CACCG   A
                                TAAGAGTAT GC     ACG CG
                                ||||||||| ||     ||| ||
                                ATTCTCATA CG     TGT GC
                                      A  TTAG_   A
GAM676  LOC202868 5'  GAGCACCGGCCGGTGATGA   17202        CCA   AC  C
                                GAGTATCG   CCG  GA GA
                                ||||||||   |||  || ||
                                CTCGTGGC   GGC  CT CT
                                     C__   CA  A
GAM676  LOC257471 3'  GAGTATCGTCACTATGGTCGTC 17199       C  __________  ACGA
          GTCG                    GTATCG CAC        CG    CG
                                ||||||  |||        ||    ||
                                CATAGC GTG        GC    GC
                                   A   ATACCIIIA  AGCA
GAM677  AAAS     3'  CAAAAGGAAAACTTATTT    17205      T
                                CAAA GGAAAATTTGTTT
                                |||| ||||||||||||
                                GTTT CCTTTTGAATAAA
                                  T
GAM677  FGFR1    3'  CAAATGGAATGTTCTAT     17206         AATT
                                CAAATGGAA    TGTTTTAT
                                |||||||||    ||||||||
                                GTTTACCTT    ACAAGATA
                                     ____
GAM677  FGFR1    3'  CAAATGGAATGTTCTAT     17206         AATT
                                CAAATGGAA    TGTTTTAT
                                |||||||||    ||||||||
                                GTTTACCTT    ACAAGATA
                                     ____
GAM677  HOXD4    3'  CAAATAGAAAATTTGTCCT   17207
                                CAAATGGAAAATTTGTTTT
                                ||||||||||||||||||
                                GTTTATCTTTTAAACAGGA

GAM677  NYX      5'  CAAATGGACAGTTTGGATCTA  17208        AAA   TTTT
                                CAAATGGA   TTTG   ATCTA
                                ||||||||   ||||   |||||
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                                GTTTACCT  AAAC   TAGAT
                                    GTC   C___
GAM677  OTOR     3'  GAAAATCCTCTTTTATCT   17209       G_
                                GAAAATTT  TTTTATCT
                                ||||||||  ||||||||
                                CTTTTAGG  AAAATAGA
                                    AG
GAM677  RP2      3'  AAATGGGTAAAAGGTCTTATCT 17210      AA  TTT
          A                      AAATGG  AA   GTTTTATCTA
                                ||||||  ||   ||||||||||
                                TTTACC  TT   CAGAATAGAT
                                   CA  TTC
GAM677  CGGBP1   3'  TGAATAGAAAGTAATTTTATCT 17211   A      ATTT
                                C AATGGAAA   GTTTTATCT
                                | ||||||||   |||||||||
                                A TTATCTTT   TAAAATAGA
                                 C       CAT_
GAM677  CORTBP2  3'  AATGGAAAATAACTGTTT    17212         __
                                AATGGAAAAT  TTGTTT
                                ||||||||||  ||||||
                                TTACCTTTTA  GACAAA
                                      TT
GAM677  CPNE1    5'  TGAATGGAATATTTGCCT    17213   A     A
                                C AATGGAA ATTTGTTT
                                | ||||||| ||||||||
                                A TTACCTT TAAACGGA
                                 C      A
GAM677  DKFZP434A0225 3'  AAATGGAGTGTTGTACTTATCT 17214       AAAT   _
          A                      AAATGGA    TTGT TTTATCTA
                                |||||||    |||| ||||||||
                                TTTACCT    AACA GAATAGAT
                                    CAC_    T
GAM677  DKFZP434N1235 3'  GGAAAATCCACATTTATCT    17215       TG _
                                GGAAAATT  T TTTATCT
                                ||||||||  | |||||||
                                CCTTTTAG  G AAATAGA
                                    GT T
GAM677  KIAA0215  3'  AAATGGAAAATGGCCTCTTTTG 17216         ___  G   A
          TCT                     AAATGGAAAAT   TT TTTT TCT
                                ||||||||||   || |||| |||
                                TTTACCTTTTA   GA AAAA AGA
                                      CCG  G   C
GAM677  KIAA0266  5'  CAAATGGAATGTTTATTTTA   17217       AA
                                CAAATGGAA  TTTGTTTTA
                                |||||||||  |||||||||
                                GTTTACCTT  AAATAAAAT
                                      AC
GAM677  KIAA0976  3'  AATGGGAAATTTGTTTCA    17218     A
                                AATGG AAATTTGTTTTA
                                ||||| ||||||||||||
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                                TTACC TTTAAACAAAGT
                                   C
GAM677  KIAA1877 3'  CAAATGAAAACATGTTTTAT  17219         ATT
                                CAAATGGAAA  TGTTTTAT
                                ||||||||||  ||||||||
                                GTTTACTTTT  ACAAAATA
                                     GT_
GAM677  PEX12    3'  TGAATGAAAAATTTATTTTA  17220   A
                                C AATGGAAAATTTGTTTTA
                                | ||||||||||||||||||
                                A TTACTTTTTAAATAAAAT
                                 C
GAM677  PRO0611  5'  CAAATGGTAGGTTTGCTTTAT 17221       AAAA
                                CAAATGG   TTTGTTTTAT
                                |||||||   ||||||||||
                                GTTTACC   AAACGAAATA
                                    ATCC
GAM677  SS18L2   3'  CAAATGGAAGATTATTCTA   17222        AAT
                                CAAATGGAA  TTGTTTTA
                                |||||||||  ||||||||
                                GTTTACCTT  AATAAGAT
                                     CT_
GAM677  ZDHHC3   3'  CAAATGGAAAATCTATTCT   17223
                                CAAATGGAAAATTTGTTTT
                                ||||||||||||||||||
                                GTTTACCTTTTAGATAAGA

GAM677  LOC144535 3'  CAAATGGAAAATATCCTC    17224          TTG
                                CAAATGGAAAAT  TTTT
                                ||||||||||||  ||||
                                GTTTACCTTTTA  GGAG
                                       TA_
GAM677  LOC145623 5'  CAAATGGAAGGTGTGTTTT   17225        AATT
                                CAAATGGAA   TGTTTT
                                |||||||||   ||||||
                                GTTTACCTT   ACAAAA
                                     CCAC
GAM677  LOC150951 5'  GGAAAATTTGCATCT      17226         TTT
                                GGAAAATTTGT  ATCT
                                ||||||||||  ||||
                                CCTTTTAAACG  TAGA
                                      ___
GAM677  LOC153114 3'  CAAATGGAAAAATTAATTTTA  17227         TTT_
                                CAAATGGAAAA   GTTTTA
                                ||||||||||   ||||||
                                GTTTACCTTTT   TAAAAT
                                       TAAT
GAM677  LOC202754 3'  TGAAAGACCTGCTTTATCT   17228      A
                                TGGAA ATTTGTTTTATCT
                                ||||| ||||||||||||
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                                ACTTT TGGACGAAATAGA
                                  C
GAM677  LOC221354 3'  CAATTGGAAAATTTTATAATCT 17229     A        GTTTT
           A                     CAA TGGAAAATTT     ATCTA
                                 ||| ||||||||||     |||||
                                 GTT ACCTTTTAAA     TAGAT
                                   A         ATAT_
GAM678  ASPH     3'  TGATTTTAATCCTAAA      17232       GTTATG
                                 TGATTT     TGATCCTAAA
                                 ||||||     ||||||||||
                                 ACTAAA     ATTAGGATTT

                                 _______
GAM678  ASPH     3'  TGATTTTAATCCTAAA      17232       GTTATG
                                 TGATTT     TGATCCTAAA
                                 ||||||     ||||||||||
                                 ACTAAA     ATTAGGATTT

                                 _______
GAM678  HIP2     3'  TTTGTATTGGTCCTAAAAA    17233       TATG  A
                                 TTTGT    TG TCCTAAAAA
                                 |||||    || |||||||||
                                 AAACA    AC AGGATTTTT
                                    TA__  C
GAM678  IL12B    3'  TATCATTGTGATCCTAAAAA   17234        _
                                 TGTTAT GTGATCCTAAAAA
                                 |||||| ||||||||||||
                                 ATAGTA CACTAGGATTTTT
                                     A
GAM678  RAG1     3'  TGATTAGTTGTGAATCCTAAAA 17235       T  TA    _
           A                      TGATT GT  TGTGA TCCTAAAAA
                                  ||||| ||  ||||| |||||||||
                                  ACTAA CA  ACACT AGGATTTTT
                                     T  __     T
GAM678  FLJ11149 3'  TGTTTTGTTTTTCCTAAAA    17236      A   GA_
                                 TGTT TGT   TCCTAAAA
                                 |||| |||   ||||||||
                                 ACAA ACA   AGGATTTT
                                   A   AAA
GAM678  KIAA0286 3'  ATTTGTTATGTTGTCATAA    17237           GA  C
                                 ATTTGTTATGT  TC TAA
                                 ||||||||||  || |||
                                 TAAACAATACA  AG ATT
                                        AC  T
GAM678  KIAA0296 3'  TGGTTTGGTTGGATCCTAAAAA 17238    A    TTA  T
                                 TG TTTG   TG GATCCTAAAAA
                                 || ||||   || ||||||||||
                                 AC AAAC   AC CTAGGATTTTT
                                  C    CA_  _
GAM678  MAP3K2   3'  TGATTTGTTTGTACTAAAA    17239         A    ATC
                                 TGATTTGTT TGTG   CTAAAA
                                 ||||||||| ||||   ||||||
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                                ACTAAACAA ACAT   GATTTT
                                      _   ___
GAM678  LOC256158 5'  TGACTGCCGGTGATCCT     17240      T   AT
                                TGATT GTT  GTGATCCT
                                ||||| |||  ||||||||
                                ACTGA CGG  CACTAGGA
                                  _  C_
GAM679  ADAM19    3'  CCCGAAGGTCAGGACTGCTGAG 17243       ACCTT  __    A
           GGT                    TCCGAAG    GGA  GCTGA GGT
                                |||||||    |||  ||||| |||
                                GGGCTTC    CCT  CGACT CCA
                                   CAGT_  GA    C
GAM679  DRD3      3'  TCCGGAACTCGATATTGAAGGT 17244     AA  C    AGC
                                TCCG  GA CTTGG   TGAAGGT
                                ||||  || |||||   |||||||
                                AGGC  CT GAGCT   ACTTCCA
                                  __ T    ATA
GAM679  DRD3      3'  TCCGGAACTCGATATTGAAGGT 17244     AA  C    AGC
                                TCCG  GA CTTGG   TGAAGGT
                                ||||  || |||||   |||||||
                                AGGC  CT GAGCT   ACTTCCA
                                  __ T    ATA
GAM679  GPR85     5'  TCCGAAGAGTTTTGTTTGTGGA 17245       CC_  GAGC  A
           GGT                    TCCGAAGA   TTG    TG AGGT
                                |||||||   |||    || ||||
                                AGGCTTCT   AAC    AC TCCA
                                    CAA   AAAC  C
GAM679  MECP2     3'  CCCGGAGCGGGAGCTGGGGGT  17246     A  ACCTT      AA
                                TCCG AG    GGAGCTG  GGT
                                |||| ||    |||||||  |||
                                GGGC TC    CCTCGAC  CCA
                                  C  GC___      CC
GAM679  NPC2      3'  GAAGCAGCAGAGCTGGAGGT   17247      ACCTT      A
                                GAAG    GGAGCTG AGGT
                                ||||    ||||||| ||||
                                CTTC    TCTCGAC TCCA
                                  GTCG_      C
GAM679  RAB6A     5'  GAAGAGAAGCTGAGGGT     17248       CCTT       A
                                GAAGA   GGAGCTGA GGT
                                |||||   |||||||| |||
                                CTTCT   CTTCGACT CCA
                                   ____       C
GAM679  TNFAIP2   5'  GAGGCCTTGGAAGAAGGT    17249    A A       CT
                                GA G CCTTGGAG  GAAGGT
                                || | ||||||||  ||||||
                                CT C GGAACCTT  CTTCCA
                                 _ C       __
GAM679  TNXB      5'  TCTGAGAGAAGCTGAGGG    17250    C  A  CCTT       A
                                TC GA GA   GGAGCTGA GG
                                || || ||   |||||||| ||
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                                AG CT CT    CTTCGACT CC
                                 A  _ _____       C
GAM679  FLJ11539  3'  TCCGAGACGGAGCTGGGGGT  17251      A   CTT      AA
                                TCCGA GAC   GGAGCTG  GGT
                                ||||| |||   |||||||  |||
                                AGGCT CTG   CCTCGAC  CCA
                                   _  ____      CC
GAM679  FLJ12443  3'  GAAACGGAGCTGAAGG      17252      ACCT
                                GAAG    TGGAGCTGAAGG
                                ||||    ||||||||||||
                                CTTT    GCCTCGACTTCC
                                  _____
GAM679  FLJ14327  3'  AGACGCGGAGCTGAAGGT    17253      CT
                                AGAC  TGGAGCTGAAGGT
                                ||||  ||||||||||||
                                TCTG  GCCTCGACTTCCA
                                  C_
GAM679  INA       3'  GAAGCGTGAGCTGAAGGT    17254      ACCTTG
                                GAAG     GAGCTGAAGGT
                                ||||     ||||||||||
                                CTTC     CTCGACTTCCA
                                  GCA___
GAM679  KIAA0447  3'  CAGAGACAGCAAAGCTGAAGGT 17255    A    CT GG
                                CG AGAC  T  AGCTGAAGGT
                                || ||||  |  ||||||||||
                                GT TCTG  G  TCGACTTCCA
                                 C    TC TT
GAM679  KIAA1924  3'  CCGGGGCCTGAGCTGAAGGT   17256    AAGA   TG
                                CCG    CCT  GAGCTGAAGGT
                                |||    |||  ||||||||||
                                GGC    GGA  CTCGACTTCCA
                                  CCC_   __
GAM679  KPNA6     3'  GAAGGTTCCAGAGCTGAAGGT  17257      ACC TG
                                GAAG   T  GAGCTGAAGGT
                                ||||   |  ||||||||||
                                CTTC   G  CTCGACTTCCA
                                  CAA GT
GAM679  MKI67IP   3'  GAAAATCTTGTCAAAGGT    17258      C    GAGCT
                                GAAGA CTTG     GAAGGT
                                ||||| ||||     ||||||
                                CTTTT GAAC     TTTCCA
                                  A    AG___
GAM679  NBL1      3'  AACCTTGGGGCGAGGGAGGT   17259        A  T  ___
                                GACCTTGG GC GA   AGGT
                                |||||||| || ||   ||||
                                TTGGAACC CG CT   TCCA
                                     C  _  CCC
GAM679  LOC116211 5'  TCCAGGGCTGGACCTGAAGGT  17260      AAGACC    G
                                TCCG     TTGGA CTGAAGGT
                                ||||     ||||| ||||||||
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                                AGGT     GACCT GACTTCCA
                                  CCC___     G
GAM679  LOC200081 3'  TCTGCAGACTGGCCTGAAGGT  17261    CGA   CT   AG
                                TC   AGAC  TGG  CTGAAGGT
                                ||   ||||  |||  ||||||||
                                AG   TCTG  ACC  GACTTCCA
                                 ACG    __   G_
GAM679  LOC204200 5'  CCTGGAGACTTTGGGCGAAGG  17262    GA_   C    A  T
                                CC   AGAC TTGG GC GAAGG
                                ||   |||| |||| || |||||
                                GG   TCTG AACC CG CTTCC
                                 ACC    A   _ _
GAM679  LOC222236 3'  GAAGGCTCTTGCCGAAGGT   17263      AC   GGA
                                GAAG  CTT   GCTGAAGGT
                                ||||  |||   |||||||||
                                CTTC  GAG   CGGCTTCCA
                                  C_   AA_
GAM679  LOC90342  5'  CCGGCTCTGGGGCTGAGGGT   17264     AAGACC    A    A
                                CCG     TTGG GCTGA GGT
                                |||     |||| ||||| |||
                                GGC     GACC CGACT CCA
                                  CGA___    C    C
GAM680  SEL1L    3'  AGGAAGTTTTTGCGTATGT   17267    A      A
                                AG AAGTTTTT GCGTGTGT
                                || |||||||| ||||||||
                                TC TTCAAAAA CGCATACA
                                 C      _
GAM680  TIM3     3'  AGTAAGTTCCAATTGTGTGTCA 17268    A      TAGC
           AA                    AG AAGTTTT    GTGTGTCAAA
                                || |||||||    ||||||||||
                                TC TTCAAGG    CACACAGTTT
                                 A      TTAA
GAM680  TRIM8    3'  AGGAAGTTGCTGTGTCAA    17269    A    TTTA  G
                                AG AAGTT    GC TGTGTCAA
                                || |||||    || ||||||||
                                TC TTCAA    CG ACACAGTT
                                 C    _____  _
GAM680  FLJ12783  3'  AGAGAGATCACAGTGTGTCAA  17270     A  TTTTTA  _
                                AGA AG     GC GTGTGTCAA
                                ||| ||     || |||||||||
                                TCT TC     TG CACACAGTT
                                  C  TAG___  T
GAM680  FLJ20174  3'  AAAAAGTTTTTTACATGT    17271          A
                                AGAAAGTTTTT GCGTGT
                                |||||||||||| ||||||
                                TTTTTCAAAAA TGTACA
                                       A
GAM680  FLJ20232  5'  AGAAGTTTCTCCTGTGTC    17272      A     AGCG
                                AGAA GTTTTT    TGTGTC
                                |||| ||||||    ||||||
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                                TCTT CAAAGA   ACACAG
                                  _    GG__
GAM680  GMFB     3'  AAATTTTTAGCTAAAGTGTCA  17273         GT__
                                AAGTTTTTAGC   GTGTCA
                                ||||||||||   ||||||
                                TTTAAAAATCG   CACAGT
                                     ATTT
GAM680  GOLGA1   3'  AGAAAGTTTTATACAAGTCAAA 17274         TA  TGT
                                AGAAAGTTTT  GCG  GTCAAA
                                ||||||||||  |||  ||||||
                                TCTTTCAAAA  TGT  CAGTTT
                                     TA  T__
GAM680  KIAA0285 3'  AGAGAGCTTTTATTATGT    17275     A      GC
                                AGA AGTTTTTA  GTGT
                                ||| ||||||||  ||||
                                TCT TCGAAAAT  TACA
                                  C       AA
GAM680  KIAA1577 5'  AGGGAGTTTTCAGTGTCGTCA  17276    AA       C  G
                                AG  AGTTTTTAG GT TGTCA
                                ||  |||||||||| || |||||
                                TC  TCAAAAGTC CA GCAGT
                                 CC       A  _
GAM680  MAIL     3'  AAAAGGTTTTTAATGAGTCAAA 17277     A      GC   T
                                AGAA GTTTTTA  GTG GTCAAA
                                |||| |||||||  ||| ||||||
                                TTTT CAAAAAT  TAC CAGTTT
                                  C       __  T
GAM680  TCFL5    3'  GAAAATTTTTAGCACACA    17278           TG
                                GAAAGTTTTTAGCG  TG
                                ||||||||||||||  ||
                                CTTTTAAAAATCGT  GT
                                       GT
GAM680  LOC143162 3'  AAGTTTTTAGTAAATGTG    17279         C__
                                AAGTTTTTAG   GTGTG
                                ||||||||||   |||||
                                TTCAAAAATC   TACAC
                                     ATT
GAM680  LOC148356 3'  GAAAATTTTTAACAAATTGT   17280           TG_
                                GAAAGTTTTTAGCG   TGT
                                ||||||||||||||   |||
                                CTTTTAAAAATTGT   ACA
                                       TTA
GAM680  LOC196738 3'  AAGTTTTTAGTAAATGTG    17279         C__
                                AAGTTTTTAG   GTGTG
                                ||||||||||   |||||
                                TTCAAAAATC   TACAC
                                     ATT
GAM680  LOC257206 5'  AGAAAGTTTTTAATGC      17281           GC
                                AGAAAGTTTTTA  GTGT
                                ||||||||||||  ||||
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                                TCTTTCAAAAAT  TACG
                                      __
GAM680  LOC56181  3'  AGAAAGTTTTTAATCAGTG   17282          _  T
                                AGAAAGTTTTTAG CG GTG
                                |||||||||||| || |||
                                TCTTTCAAAAATT GT CAC
                                      A  _
GAM681  AGA       5'  TTGAAACCAAATATTTA     17285       G
                                TTGAAA CCAAATATTTG
                                |||||| ||||||||||
                                AACTTT GGTTTATAAAT
                                  _
GAM681  BRCA2     3'  TTGAAAGCAAGATATTTTCTCA 17286       CAA     GC_
           A                     TTGAAAGC   ATATTT   CAA
                                |||||||   ||||||  |||
                                AACTTTCG   TATAAA   GTT
                                     TTC     AGA
GAM681  CPE       3'  TTGAAAGCTAGAATTACTCAAA 17287       CAAATAT   _
           A                     TTGAAAGC      TTGC CAAAA
                                |||||||      |||| |||||
                                AACTTTCG      AATG GTTTT
                                     ATCTT__   A
GAM681  D10S170   3'  CTGAAAGCCAGATTTTCAAA   17288        AAT   GC
                                TTGAAAGCCA   ATTT  CAAA
                                |||||||||   ||||  ||||
                                GACTTTCGGT   TAAA  GTTT
                                     C__   A_
GAM681  GABRE     5'  TTAAAGGCCATCTGCCAA    17289      A   AATA
                                TTGAA GCCA    TTTGCCAA
                                ||||| ||||   ||||||||
                                AATTT CGGT    AGACGGTT
                                   C   ____
GAM681  GDF8      3'  TTGAAAGCCAACCTCTA     17290         ATA
                                TTGAAAGCCAA   TTTG
                                ||||||||||   ||||
                                AACTTTCGGTT   AGAT
                                      GG_
GAM681  SNAP23    3'  TTGAAAGCAAAAGAACCTGC   17291       C   T_
                                TTGAAAGC AAA  ATTTGC
                                |||||||| |||  ||||||
                                AACTTTCG TTT  TGGACG
                                     T   CT
GAM681  SNAP23    3'  TTGAAAGCAAAAGAACCTGC   17291       C   T_
                                TTGAAAGC AAA  ATTTGC
                                |||||||| |||  ||||||
                                AACTTTCG TTT  TGGACG
                                     T   CT
GAM681  TNFRSF10B 3'  TTGAAGCCAAAGTACATCTG   17292      A   ___
                                TTGAA GCCAA   ATATTTG
                                ||||| |||||   |||||||
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                                AACTT CGGTT   TGTAGAC
                                  _    TCA
GAM681  CCT4     3'  TTGAAACCAAATATTTA     17285       G
                                TTGAAA CCAAATATTTG
                                |||||| ||||||||||
                                AACTTT GGTTTATAAAT
                                  _
GAM681  CRMP5    3'  TTGAAACCACATCTGCTAAA  17293       G  AA     C
                                TTGAAA CCA  TATTTGC AAA
                                |||||| |||  ||||||| |||
                                AACTTT GGT  GTAGACG TTT
                                  _  __      A
GAM681  DKFZp547A023 5'  TTGAAAGCCTGATAATCGGCA  17294         AA  T  C
                                TTGAAAGCC  ATA TTG CA
                                |||||||||  ||| ||| ||
                                AACTTTCGG  TAT AGC GT
                                     AC  T  C
GAM681  DKFZp762A227 3'  TCGGAGCCAAACAGGCC     17295     AA       TTT
                                TTG  AGCCAAATA   GCC
                                |||  |||||||||   |||
                                AGC  TCGGTTTGT   CGG
                                  C_       C__
GAM681  DKFZp762A227 3'  TCGGAGCCAAACAGGCC     17295     AA       TTT
                                TTG  AGCCAAATA   GCC
                                |||  |||||||||   |||
                                AGC  TCGGTTTGT   CGG
                                  C_       C__
GAM681  FLJ10583  3'  TTAAAAGCTAAATTATATCCAA 17296       C   ATTTG
          A                      TTGAAAGC AAAT    CCAAA
                                |||||||| ||||    |||||
                                AATTTTCG TTTA    GGTTT
                                    A   ATATA
GAM681  FLJ12650  3'  TTGAAAGATTTGCCAA      17297       CCAAAT
                                TTGAAAG     ATTTGCCAA
                                |||||||     |||||||||
                                AACTTTC     TAAACGGTT
                                  _______
GAM681  FLJ20010  3'  TTGGAACCTTTGCCAA      17298     AA   AAATA
                                TTG  AGCC    TTTGCCAA
                                |||  ||||    ||||||||
                                AAC  TTGG    AAACGGTT
                                  C_   _____
GAM681  FLJ20511  3'  TTAAAAGCCAGAGCCAAA    17299         AATATTT
                                TTGAAAGCCA      GCCAAA
                                ||||||||||      ||||||
                                AATTTTCGGT      CGGTTT
                                     CT_____
GAM681  KIAA0227  3'  TTGAAAGCAAAGCACTTG    17300       C  A
                                TTGAAAGC AA TATTTG
                                |||||||| || ||||||
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                                AACTTTCG TT GTGAAC
                                     T  C
GAM681  KIAA0748  5'  CTGGAAGCCAAACTACAGCCAA 17301     A        ATTT
                                TTG AAGCCAAAT    GCCAA
                                ||| |||||||||    |||||
                                GAC TTCGGTTTG    CGGTT
                                  C        ATGT
GAM681  KIAA1069  3'  TCGGGAGCCAAATGCTGC    17302     AA       AT
                                TTG  AGCCAAAT  TTGC
                                |||  ||||||||  ||||
                                AGC  TCGGTTTA  GACG
                                  CC       C_
GAM681  KIAA1821  5'  TTGGGATCCAAATATTTCACAA 17303     AAAG        GC
                                TTG    CCAAATATTT  CAA
                                |||    ||||||||||  |||
                                AAC    GGTTTATAAA  GTT
                                  CCTA         GT
GAM681  KIAA1884  3'  TTGAAAGCCGAACTGCC     17304         A   ATT
                                TTGAAAGCC AAT   TGCC
                                ||||||||| |||   ||||
                                AACTTTCGG TTG   ACGG
                                     C   ___
GAM681  MGC30052  3'  TTGAAGCCAAATATCTG     17305       A
                                TTGAA GCCAAATATTTG
                                ||||| ||||||||||||
                                AACTT CGGTTTATAGAC
                                      _
GAM681  NXP-2     3'  TTGAAAGCTGTACAACCAAAA  17306         CAAA   TT
                                TTGAAAGC    TAT  GCCAAAA
                                ||||||||    |||  |||||||
                                AACTTTCG    ATG  TGGTTTT
                                     AC__    T_
GAM681  PDE1C     3'  TTGAAAGCCAGGTCATTAGCAA 17307          AA_    T  C
          A                      TTGAAAGCCA   TATT GC AAA
                                 ||||||||||   |||| || |||
                                 AACTTTCGGT   GTAA CG TTT
                                      CCA    T  _
GAM681  PSMD1     3'  TTGAAAACCAAGTTCTG     17308          ATA
                                TTGAAAGCCAA   TTTG
                                ||||||||||   ||||
                                AACTTTTGGTT   AGAC
                                      CA_
GAM681  RI58      3'  TTGATAGCTAAATATCCTCATC 17309      A  C       GC__
          AAA                    TTGA AGC AAATATTT    CAAA
                                 |||| ||| ||||||||    ||||
                                 AACT TCG TTTATAGG    GTTT
                                   A  A       AGTA
GAM681  LOC129566 3'  TTGGAGCCCAGATCTGCCA    17310     AA    AAAT
                                TTG  AGCC    ATTTGCCA
                                |||  ||||    ||||||||
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                                AAC  TCGG    TAGACGGT
                                  C_    GTC_
GAM681   LOC132720 3'  TTGAAATCCAAATATTTCCCAA 17311       G         G
             A                    TTGAAA CCAAATATTT CCAAA
                                  |||||| |||||||||| |||||
                                  AACTTT GGTTTATAAA GGTTT
                                     A         G
GAM681   LOC143286 5'  TTAAAAGCCAGCATGCTAAA   17312          AATATT   C
                                  TTGAAAGCCA      TGC AAA
                                  ||||||||||      ||| |||
                                  AATTTTCGGT      ACG TTT
                                        CGT___    A
GAM681   LOC144997 3'  TTGAAAGCCAAGCACCA      17313           ATATT
                                  TTGAAAGCCAA     TGCCA
                                  ||||||||||     |||||
                                  AACTTTCGGTT     GTGGT
                                        C____
GAM681   LOC145268 5'  TTGAAAGCCAGAAGACCAAAA  17314          AATATTT
                                  TTGAAAGCCA      GCCAAAA
                                  ||||||||||      |||||||
                                  AACTTTCGGT      TGGTTTT
                                        CTTC___
GAM681   LOC148697 3'  TGAAGGCCAAATAAGTCAAA   17315      A       TTTGC
                                  TGAA GCCAAATA     CAAA
                                  |||| ||||||||     ||||
                                  ACTT CGGTTTAT     GTTT
                                    C       TCA__
GAM681   LOC148824 3'  TTGAAGACCAAATATATGC    17316      AG       T
                                  TTGAA  CCAAATAT TGC
                                  |||||  |||||||| |||
                                  AACTT  GGTTTATA ACG
                                     CT       T
GAM681   LOC169611 3'  TTGAAGTACCTTTTGCCAAAA  17317       A_   AAATA
                                  TTGAA  GCC    TTTGCCAAAA
                                  |||||  |||    ||||||||||
                                  AACTT  TGG    AAACGGTTTT
                                     CA   A____
GAM681   LOC170393 3'  TTGAAAACCAAAAGCC       17318           TATTT
                                  TTGAAAGCCAAA    GCC
                                  ||||||||||||    |||
                                  AACTTTTGGTTT    CGG
                                        T____
GAM681   LOC196527 3'  TTGAGACTCATATTTGCCAAA  17319      AA  CAA
                                  TTGA  GC   ATATTTGCCAAA
                                  ||||  ||   ||||||||||||
                                  AACT  TG   TATAAACGGTTT
                                    C_  AG_
GAM681   LOC196860 5'  TTCAAAGCCAAACCACCA     17320    G        TAT TG
                                  TT AAAGCCAAA   T  CCA
                                  || |||||||||   |  |||
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                                AA TTTCGGTTT   G  GGT
                                 G        ___ GT
GAM681   LOC92973  5'  TTAAAAGCCAAAATATTTGC   17321          _
                                TTGAAAGCCAAA TATTTGC
                                |||||||||||| |||||||
                                AATTTTCGGTTT ATAAACG
                                       T
GAM682   CTSD     3'  AACAGATGGAGAGACAGACA   17324     G   T  A
                                AAC AGAT GA GAGACAGACA
                                ||| |||| || ||||||||||
                                TTG TCTA CT CTCTGTCTGT
                                  _   C  _
GAM682   G6PC     3'  GAGATTGAAAAACAGGCAA    17325        A      A
                                GAGATTGA GAGACAG CAA
                                |||||||| ||||||| |||
                                CTCTAACT TTTTGTC GTT
                                     _      C
GAM682   GLUL     5'  CGATGGAGAAGGGGACAGACA  17326     GATT    A_
                                CGA    GAAG  GACAGACA
                                |||    ||||  ||||||||
                                GCT    CTTC  CTGTCTGT
                                  ACCT    CC
GAM682   HOXB9    3'  GAGAGAAGAGAGAGACA     17327      TT      C
                                GAGA  GAAGAGA AGACA
                                ||||  ||||||| |||||
                                CTCT  CTTCTCT TCTGT
                                   __      C
GAM682   MADH3    3'  GAGAGGGGAGGGAGACAGACAA 17328      TT_  A_
                                GAGA   GA  GAGACAGACAA
                                ||||   ||  ||||||||||
                                CTCT   CT  CTCTGTCTGTT
                                   CCC  CC
GAM682   MAX      3'  GAGACGATGGAGACAGACA    17329       T  A_
                                GAGAT GA  GAGACAGACA
                                ||||| ||  ||||||||||
                                CTCTG CT  CTCTGTCTGT
                                   _  AC
GAM682   MAX      3'  GAGACGATGGAGACAGACA    17329       T  A_
                                GAGAT GA  GAGACAGACA
                                ||||| ||  ||||||||||
                                CTCTG CT  CTCTGTCTGT
                                   _  AC
GAM682   NR2E1     5'  ACAGATGGAGAGATGGACA    17330    G   T  A   CA
                                AC AGAT GA GAGA  GACA
                                || |||| || ||||  ||||
                                TG TCTA CT CTCT  CTGT
                                  _   C  _   AC
GAM682   PBX3     3'  TAATAAGATTGAAGAACATTCA 17331     CG         A  GA
            A                    TAA  AGATTGAAGAG CA  CAA
                                |||  |||||||||| ||  |||
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                                ATT  TCTAACTTCTT GT  GTT
                                  AT         _ AA
GAM682  SCD      3'  CAAAGAAAAGGGACAGACA   17332      ATT   A
                                CGAG   GAAG GACAGACA
                                ||||   |||| ||||||||
                                GTTT   TTTC CTGTCTGT
                                  CT_   C
GAM682  SERPINB13 3'  GAGAAGACAAGACAGACAA   17333      TT  A
                                GAGA  GA GAGACAGACAA
                                ||||  || ||||||||||
                                CTCT  CT TTCTGTCTGTT
                                  T_  G
GAM682  SLC20A2  3'  GAGGGTGGGAGACAGACAA   17334     AT  AA
                                GAG  TG  GAGACAGACAA
                                |||  ||  ||||||||||
                                CTC  AC  CTCTGTCTGTT
                                  CC  C_
GAM682  5T4      3'  GAGAGAGAGACAGACA      17335      TT  A
                                GAGA  GA GAGACAGACA
                                ||||  || ||||||||||
                                CTCT  CT CTCTGTCTGT
                                   __ _
GAM682  ASE-1    5'  GAAATTCTTGAAGAGACAG   17336       ___
                                GAGAT   TGAAGAGACAG
                                |||||   ||||||||||
                                CTTTA   ACTTCTCTGTC
                                   AGA
GAM682  CPR2     3'  AAGCTGGGAGAGACAGGCA   17337     A  A_      A
                                GAG TTG  AGAGACAG CA
                                ||| |||  |||||||| ||
                                TTC GAC  TCTCTGTC GT
                                  _  CC       C
GAM682  FLJ14768  3'  GAGGAAGACAGAGACAGACAA  17338     ATT  _
                                GAG   GA AGAGACAGACAA
                                |||   || ||||||||||||
                                CTC   CT TCTCTGTCTGTT
                                  CTT  G
GAM682  KIAA1243  3'  ACAGGTCGAGAGACAGACA   17339    G  A   A
                                AC AG TTGA GAGACAGACA
                                || || |||| ||||||||||
                                TG TC AGCT CTCTGTCTGT
                                 _ C   _
GAM682  KIAA1271  3'  GAGAAAACTAAGGGACAGACA  17340      TTG__  A
                                GAGA    AAG GACAGACA
                                ||||    ||| ||||||||
                                CTCT    TTC CTGTCTGT
                                  TTTGA  C
GAM682  KIAA1580  5'  CGAAGTGAGGGGACAGACA   17341     AT  AGA
                                CGAG  TGA   GACAGACA
                                ||||  |||   ||||||||
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                                GCTT  ACT   CTGTCTGT
                                  C_  CCC
GAM682  KIAA1715  3'  GAGATTCAGAGAGACAGA    17342       GA_
                                GAGATT   AGAGACAGA
                                ||||||   |||||||||
                                CTCTAA   TCTCTGTCT
                                   GTC
GAM682  KIAA1735  3'  AGATGAATTGGAGACAGA    17343     T  ___
                                AGAT GAA   GAGACAGA
                                |||| |||   ||||||||
                                TCTA CTT   CTCTGTCT
                                  _  AAC
GAM682  KIAA1751  3'  GAATGAGAAGAAGACAGACAA  17344     ATT    _
                                GAG   GAAGA GACAGACAA
                                |||   ||||| |||||||||
                                CTT   CTTCT CTGTCTGTT
                                  ACT    T
GAM682  MGC20255  3'  TAAAGGCTGAGAGACAGACA   17345   C   AT   A
                                A GAG  TGA GAGACAGACA
                                | |||  ||| ||||||||||
                                A TTC  ACT CTCTGTCTGT
                                 T   CG  _
GAM682  PCANAP7   5'  ACAGAGTGAAGAGACGGA    17346    G   T       A
                                AC AGA TGAAGAGAC GA
                                || ||| |||||||| ||
                                TG TCT ACTTCTCTG CT
                                  _  C        C
GAM682  LOC148758 5'  ACGGGATGCAGAGACAGACA   17347     A   TGA
                                ACG GAT   AGAGACAGACA
                                ||| |||   ||||||||||
                                TGC CTA   TCTCTGTCTGT
                                  C   CG_
GAM682  LOC151632 5'  GAGAGTGGAGACAGACAA    17348      T  AA
                                GAGA TG  GAGACAGACAA
                                |||| ||  ||||||||||
                                CTCT AC  CTCTGTCTGTT
                                  C  __
GAM682  LOC152271 5'  GAGAGTGGAGACAGACA     17349      T  AA
                                GAGA TG  GAGACAGACA
                                |||| ||  ||||||||||
                                CTCT AC  CTCTGTCTGT
                                  C  __
GAM682  LOC200269 3'  CAAGAGAGACAGGCAA      17350       TTGAA      A
                                CGAGA    GAGACAG CAA
                                |||||    ||||||| |||
                                GTTCT    CTCTGTC GTT
                                   _____      C
GAM682  LOC200904 5'  GAGAGTGGAGACAGACAA    17348      T  AA
                                GAGA TG  GAGACAGACAA
                                |||| ||  ||||||||||
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                                CTCT AC  CTCTGTCTGTT
                                  C __
GAM682  LOC203083 5'  GAGAGTGGAGACAGACAA    17348     T  AA
                                GAGA TG  GAGACAGACAA
                                |||| ||  ||||||||||
                                CTCT AC  CTCTGTCTGTT
                                  C __
GAM682  LOC219919 5'  GAGAGTGGAGACAGACAA    17348     T  AA
                                GAGA TG  GAGACAGACAA
                                |||| ||  ||||||||||
                                CTCT AC  CTCTGTCTGTT
                                  C __
GAM682  LOC254176 5'  GAGAGTGGAGACAGACAA    17348     T  AA
                                GAGA TG  GAGACAGACAA
                                |||| ||  ||||||||||
                                CTCT AC  CTCTGTCTGTT
                                  C __
GAM682  LOC256594 5'  GAGAGTGGAGACAGACA     17349     T  AA
                                GAGA TG  GAGACAGACA
                                |||| ||  |||||||||
                                CTCT AC  CTCTGTCTGT
                                  C __
GAM683  CYLN2    3'  ACGCCGCCACCCACAC      17353    A      GTAAAAC
                                AC CCGCCACC      CACGC
                                || ||||||||      |||||
                                TG GGCGGTGG      GTGTG
                                 C      _______
GAM683  LASS1    3'  CATACTGCCGCAGCACCACG   17354    CC  CA    AA
                                CA  GC  CCGTA  ACCACG
                                ||  ||  |||||  ||||||
                                GT  TG  GGCGT  TGGTGC
                                 A_  AC    CG
GAM683  MBTPS2   5'  CACCGCCAACAGCTGACCGCGC 17355        _ C  AAA   A
                                CACCGCCA C GT   ACC CGC
                                |||||||| | ||   ||| |||
                                GTGGCGGT G CG   TGG GCG
                                     T T  AC_   C
GAM683  PTBP1    3'  CACCATAAAAAACCGCGC    17356         __   A
                                CACCGTAAA  ACC CGC
                                |||||||||  ||| |||
                                GTGGTATTT  TGG GCG
                                     TT   C
GAM683  PTBP1    3'  CACCATAAAAAACCGCGC    17356         __   A
                                CACCGTAAA  ACC CGC
                                |||||||||  ||| |||
                                GTGGTATTT  TGG GCG
                                     TT   C
GAM683  C1orf25  5'  TACGACGCCACCACAAACTGCG 17357     AC      GTA    CA
            C                    TAC  CGCCACC   AAAC  CGC
                                |||  |||||||   ||||  |||
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                                ATG  GCGGTGG   TTTG  GCG
                                  CT      TG_   AC
GAM683  CCNE1    5'  TACACCGCGCTGGCGGCCGCGC 17358        CACC  AAAA  A
                                TACACCGC    GT    CC CGC
                                ||||||||    ||    || |||
                                ATGTGGCG    CG    GG GCG
                                    CGAC  CC__  C
GAM683  CIDEB    5'  ACCGCCACCTGTGGAGGGACCG 17359         _  AAA___   A
          CG                      ACCGCCACC GT     ACC CG
                                ||||||||| ||     ||| ||
                                TGGCGGTGG CA     TGG GC
                                    A  CCTCCC   C
GAM683  FLJ13057  5'  TACACCGCCACCTTCTCACGC  17360          GTAAAAC
                                TACACCGCCACC      CACGC
                                ||||||||||||      |||||
                                ATGTGGCGGTGG      GTGCG
                                      AAGA___
GAM683  FLJ13057  5'  TACACCGCCACCTTCTCACGC  17360          GTAAAAC
                                TACACCGCCACC      CACGC
                                ||||||||||||      |||||
                                ATGTGGCGGTGG      GTGCG
                                      AAGA___
GAM683  KIAA0191  5'  CACCGCCATGTCCGCCGCGC   17361        ___   TAAAA  A
                                CACCGCCA   CCG    CC CGC
                                ||||||||   |||    || |||
                                GTGGCGGT   GGC    GG GCG
                                    ACA   _____  C
GAM684  COL6A1    3'  AAGTAACTGTTAGGTGAGGATT 17364        ACGTCA_
          G                      AAGTAGCTG      AGGATTG
                                |||||||||      |||||||
                                TTCATTGAC      TCCTAAC
                                    AATCCAC
GAM684  FGF23    5'  AAGTAGCTGGTGTGAGGAT   17365         AC  CA
                                AAGTAGCTG  GT  AGGAT
                                |||||||||  ||  |||||
                                TTCATCGAC  CA  TCCTA
                                    CA  C_
GAM684  PCSK2    3'  AGTGGTGACTTTTGGGATTGAC 17366     AGC    GTCAA
                                AGT   TGAC    GGATTGAC
                                |||   ||||    ||||||||
                                TCA   ACTG    CCTAACTG
                                  CC_   AAAAC
GAM684  SLBP     3'  AAGTAGCTGACTCTCAATTGG  17367          G_   __
                                AAGTAGCTGAC  TCAA  GG
                                ||||||||||  ||||  ||
                                TTCATCGACTG  AGTT  CC
                                      AG   AA
GAM684  AVIL     3'  AAGTAGCTGAATGTCAGG    17368          C_   A
                                AAGTAGCTGA  GTCA GG
                                |||||||||  ||||  ||
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                                TTCATCGACT  CAGT CC
                                      TA   _
GAM684  C20orf160 3'  AAGTAGCCGATGTCCTGG    17369         C   AA
                                AAGTAGCTGA GTC  GG
                                |||||||||| |||  ||
                                TTCATCGGCT CAG  CC
                                      A   GA
GAM684  DKFZP667O116 3'  AGTAGCTACGTTGAAAGG    17370        A   C__
                                AGTAGCTG CGT   AAGG
                                |||||||| |||   ||||
                                TCATCGAT GCA   TTCC
                                     _  ACT
GAM684  FLJ20456  3'  AAGTAGCTGGTATCACAGAT   17371         AC    A
                                AAGTAGCTG  GTCA GGAT
                                |||||||||  |||| ||||
                                TTCATCGAC  TAGT TCTA
                                      CA    G
GAM684  KIAA0205  3'  ATAGTGGAAAGTTAAGGATTG  17372     CT  C_  C
                                GTAG  GA  GT AAGGATTG
                                ||||  ||  || ||||||||
                                TATC  CT  CA TTCCTAAC
                                  AC  TT  A
GAM684  KIAA0470  3'  AAATAGTTTGAAAGGATTGA   17373      C_   CGTC
                                AAGTAG  TGA    AAGGATTGA
                                ||||||  |||    |||||||||
                                TTTATC  ACT    TTCCTAACT
                                   AA  _____
GAM684  MGC10814  3'  AAGTAGCTGGCATTACAGG    17374        A   CA_
                                AAGTAGCTG CGT   AGG
                                |||||||||| |||   |||
                                TTCATCGAC GTA   TCC
                                      C   ATG
GAM684  N4BP3     3'  AAGAGCTGACGGAGATTG     17375     T      TCAA
                                AAG AGCTGACG    GGATTG
                                ||| ||||||||    ||||||
                                TTC TCGACTGC    TCTAAC
                                  _       C___
GAM684  TRIP-Br2  3'  AAGTAGCTGACTCAGGA     17376          G   A
                                AAGTAGCTGAC TCA GGA
                                |||||||||||| ||| |||
                                TTCATCGACTG AGT CCT
                                          _  _
GAM684  LOC145725 3'  AGAGGCTGACGTTGGAGGAT   17377    TA      CA_
                                AG  GCTGACGT   AGGAT
                                ||  ||||||||   |||||
                                TC  CGACTGCA   TCCTA
                                 TC       ACC
GAM684  LOC145732 3'  AGAGGCTGACGTTGGAGGAT   17377    TA      CA_
                                AG  GCTGACGT   AGGAT
                                ||  ||||||||   |||||
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                                TC  CGACTGCA   TCCTA
                                 TC       ACC
GAM684   LOC146227 5'  AAGTAGCTGGTGCGGTTG    17378         AC  CAA  A
                                AAGTAGCTG  GT   GG TTG
                                |||||||||  ||   || |||
                                TTCATCGAC  CG   CC AAC
                                    CA  ___  _
GAM684   LOC196957 3'  AGAGGCTGACGTTGGAGGAT   17377    TA      CA_
                                AG  GCTGACGT   AGGAT
                                ||  ||||||||   |||||
                                TC  CGACTGCA   TCCTA
                                 TC       ACC
GAM684   LOC196961 3'  AGAGGCTGACGTTGGAGGAT   17377    TA      CA_
                                AG  GCTGACGT   AGGAT
                                ||  ||||||||   |||||
                                TC  CGACTGCA   TCCTA
                                 TC       ACC
GAM684   LOC197138 3'  AGAGGCTGACGTTGGAGGAT   17377    TA      CA_
                                AG  GCTGACGT   AGGAT
                                ||  ||||||||   |||||
                                TC  CGACTGCA   TCCTA
                                 TC       ACC
GAM684   LOC220766 3'  AAATAGTTCGAAAGGATTGAC  17379       CTGA  TC
                                AAGTAG   CG  AAGGATTGAC
                                ||||||   ||  ||||||||||
                                TTTATC   GC  TTCCTAACTG
                                   AA__  T_
GAM684   LOC57118  3'  AAGTAGCTGACATTACAGG   17380           CA_
                                AAGTAGCTGACGT   AGG
                                ||||||||||||   |||
                                TTCATCGACTGTA   TCC
                                       ATG
GAM685   FLJ20123  5'  GGCCCCGTTGGCTCACC     17383        CACG  A
                                GGCCCCGT   TG CTTACC
                                ||||||||   || ||||||
                                CCGGGGCA   AC GAGTGG
                                    _____  C
GAM685   KIAA0721  3'  GGCTCTGTCACATATTAC    17384     CCC      AC
                                GGC  GTCACGTG  TTAC
                                |||  ||||||||  ||||
                                CCG  CAGTGTAT  AATG
                                  AGA      __
GAM685   KIAA0721  3'  GGCTCTGTCACATATTAC    17384     CCC      AC
                                GGC  GTCACGTG  TTAC
                                |||  ||||||||  ||||
                                CCG  CAGTGTAT  AATG
                                  AGA      __
GAM685   LOC144558 3'  GGGTTACGATGACTTACC    17385    CCCC  C  _
                                GG   GT ACG TGACTTACC
                                ||   || ||| |||||||||
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                                CC    CA TGC ACTGAATGG
                                 ____ A   T
GAM686  ADORA2A   3'  GGGCCTGCCCAGCAAAGATG   17388      _    AT
                                GGGCC GCCCG  CGAAGATG
                                ||||| |||||  ||||||||
                                CCCGG CGGGT  GTTTCTAC
                                   A     C_
GAM686  PRSS15    3'  GACCGAGCTGCTCGCTCG    17389        C  C  A
                                GACCGGGC GC CG TCG
                                |||||||| || || |||
                                CTGGCTCG CG GC AGC
                                     A  A  G
GAM686  KIAA0258  3'  CCGGGCCTCCGGCGGAT     17390        GC   AT  AA
                                CCGGGCC  CCG  CG  GAT
                                |||||||  |||  ||  |||
                                GGCCCGG  GGC  GC  CTA
                                    A_   C_  __
GAM686  KIAA1877  3'  GACCTGGTCGTTCAAAGAT    17391      G  C  CCCGA
                                GACC GG CG     TCGAAGAT
                                |||| || ||     ||||||||
                                CTGG CC GC     AGTTTCTA
                                  A  A  A____
GAM686  WBSCR16   3'  GACGGGGCCGCCCAAGCA     17392      C         T
                                GAC GGGCCGCCCGA CG
                                ||| ||||||||||| ||
                                CTG CCCGGCGGGTT GT
                                  C          C
GAM686  LOC147929 5'  GACCGGGATCGCCCCGCGAGAT 17393        C_    GAT   A
           G                     GACCGGG  CGCCC   CGA GATG
                                |||||||  |||||   ||| ||||
                                CTGGCCC  GCGGG   GCT CTAC
                                    TA     GC_  _
GAM686  LOC90768  5'  GACGGGCCGCCTACCG      17394     C       CG
                                GAC GGGCCGCC  ATCG
                                ||| ||||||||  ||||
                                CTG CCCGGCGG  TGGC
                                  _       A_
GAM687  ADAM21    3'  CAAGAGACTAAAGTGTACTAAT 17397        C   ACA   A____
           GCATG                    CAGGAGAC AAA   TAC     CATG
                                |||||||| |||   |||    ||||
                                GTTCTCTG TTT   ATG     GTAC
                                    A   CAC   ATTAC
GAM687  CLN2      3'  CAGGGAATCAAAACATTCAC   17398      AG C       A
                                CAGG  A CAAAACAT CAC
                                ||||  | |||||||| |||
                                GTCC  T GTTTTGTA GTG
                                  CT A       A
GAM687  GNAI3     3'  AGATTAAAAATGTACACATGA  17399     GACC    CA
                                GGA    AAAA  TACACATGA
                                |||    ||||  |||||||||
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                                TCT   TTTT  ATGTGTACT
                                  AAT_   AC
GAM687  MX2     3'  CAGGAGACTGGACATACA    17400        CAAA
                                CAGGAGAC   ACATACA
                                ||||||||   |||||||
                                GTCCTCTG   TGTATGT
                                    ACC_
GAM687  SORCS1   3'  AGAGGTCAGAGAGCACACATGA 17401     AC  AAACA
                                GGAG  CA    TACACATGA
                                ||||  ||    |||||||||
                                TCTC  GT    GTGTGTACT
                                  CA  CTCTC
GAM687  UGCG     3'  AGATACCAAAACATACATGTGA 17402     G          CA
                                GGA ACCAAAACATACA  TGA
                                ||| ||||||||||||  |||
                                TCT TGGTTTTGTATGT  ACT
                                  A           AC
GAM687  ZNF134   3'  GAGACCAAGAATATCCATGA   17403        AAC   CA
                                GAGACCAA   ATA  CATGA
                                ||||||||   |||  |||||
                                CTCTGGTT   TAT  GTACT
                                    CT_   AG
GAM687  ABLIM    3'  CAGGAACCACACACAT      17404       A   AAACA
                                CAGGAG CCA    TACACAT
                                ||||||  |||    |||||||
                                GTCCTT GGT    GTGTGTA
                                  _   _____
GAM687  ABLIM    3'  CAGGAACCACACACAT      17404       A   AAACA
                                CAGGAG CCA    TACACAT
                                ||||||  |||    |||||||
                                GTCCTT GGT    GTGTGTA
                                  _   _____
GAM687  ALK7     3'  GGAGACCAAGCACATG      17405         AACATA
                                GGAGACCAA     CACATG
                                |||||||||     ||||||
                                CCTCTGGTT     GTGTAC
                                    C_____
GAM687  B3GALT6  3'  AGAGACCAAAATCCCATG    17406          CATACA
                                GGAGACCAAAA     CATG
                                ||||||||||     ||||
                                TCTCTGGTTTT     GTAC
                                    AGG___
GAM687  CDH24    3'  CAGGAGACAGACACAGAGCATG 17407        CAAA    CA_
                                CAGGAGAC   ACATA   CATG
                                ||||||||   |||||  ||||
                                GTCCTCTG   TGTGT   GTAC
                                    TC__    CTC
GAM687  FLJ11598 3'  AGAGGACCAAAAGGACATGA   17408    GA      CATAC
                                AG  GACCAAAA    ACATGA
                                ||  ||||||||    ||||||
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                                TC  CTGGTTTT    TGTACT
                                 TC      CC___
GAM687  FLJ20321  3'  CAGGAAGCCGCACACATG    17409      GA  AAAACA
                                CAGGA  CC     TACACATG
                                |||||  ||     ||||||||
                                GTCCT  GG     GTGTGTAC
                                   TC  C_____
GAM687  FLJ20542  3'  CAGGAGACCAGCAGCACCTTG  17410         AAA  _  ACA
                                CAGGAGACCA   CA TAC   TG
                                ||||||||||   || |||   ||
                                GTCCTCTGGT   GT GTG   AC
                                      C__  C   GA_
GAM687  FLJ31709  3'  CAGGAGCTCAACACCTACATG  17411       ACCAA    AC
                                CAGGAG    AACAT  ACATG
                                ||||||    |||||  |||||
                                GTCCTC    TTGTG  TGTAC
                                   GAG__    GA
GAM687  KIAA0087  3'  CAGTAGAAACATACATATGA   17412     G   CCAA      C
                                CAG AGA    AACATACA ATGA
                                ||| |||    |||||||| ||||
                                GTC TCT    TTGTATGT TACT
                                  A  ____       A
GAM687  KIAA1511  3'  GGATAACAAGCATACACATG   17413     GAC   AA
                                GGA   CAA  CATACACATG
                                |||   |||  ||||||||||
                                CCT   GTT  GTATGTGTAC
                                  ATT   C_
GAM687  MGC4368   3'  CAGGAGACCAAGAGCACTG   17414         AACATA   A
                                CAGGAGACCAA     CAC TG
                                ||||||||||      ||| ||
                                GTCCTCTGGTT     GTG AC
                                      CTC___   _
GAM687  NPAS3     3'  GGCAGAGGCATATACACATGA  17415    _  CCAAAAC
                                GG AGA      ATACACATGA
                                || |||      ||||||||||
                                CC TCT      TATGTGTACT
                                 G   CCGTA__
GAM687  SDS3      3'  AGGAGGACAAAACACATG    17416      AC    ACAT
                                AGGAG  CAAA    ACACATG
                                |||||  ||||    |||||||
                                TCCTC  GTTT    TGTGTAC
                                  CT   _____
GAM687  WBP4      3'  AGGAACCAAAATAAATTTCACA 17417      A     CATA___
           TGA                    AGGAG CCAAAA      CACATGA
                                |||||  ||||||      |||||||
                                TCCTT GGTTTT      GTGTACT
                                  _     ATTTAAA
GAM687  LOC147160 5'  CAGGAGACCCAGCTCCAGCACG 17418         AAAACA  _  A
           TG                     CAGGAGACC     TA CAC TG
                                |||||||||     || ||| ||
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                                GTCCTCTGG     GT GTG AC
                                     GTCGAG  C   C
GAM687  LOC153442 3'  CAGGAAACTAAAGCACACAGTG 17419        C   A     CA
           A                    CAGGAGAC AAA CATACA  TGA
                                |||||||| ||| ||||||  |||
                                GTCCTTTG TTT GTGTGT  ACT
                                    A  C     C_
GAM688  CLCN6    3'  TATCCAGGAGTGCCCTGC    17422          AAA
                                TATCTAGGAGT   CCTGT
                                ||||||||||   |||||
                                ATAGGTCCTCA   GGACG
                                      CG_
GAM688  CLCN6    3'  TATCCAGGAGTGCCCTGC    17422          AAA
                                TATCTAGGAGT   CCTGT
                                ||||||||||   |||||
                                ATAGGTCCTCA   GGACG
                                      CG_
GAM688  CLCN6    3'  TATCCAGGAGTGCCCTGC    17422          AAA
                                TATCTAGGAGT   CCTGT
                                ||||||||||   |||||
                                ATAGGTCCTCA   GGACG
                                      CG_
GAM688  GM2A     3'  TCTAGGAGTAAACATTGAAACT 17423           C_  T_
           TT                    TCTAGGAGTAAAC  TG  ACTTT
                                 ||||||||||||  ||  |||||
                                 AGATCCTCATTTG  AC  TGAAA
                                       TA  TT
GAM688  PPP2R2B  3'  TCTAAGAGTAAACGGTGT    17424          C_
                                TCTAGGAGTAAAC  TGT
                                ||||||||||||  |||
                                AGATTCTCATTTG  ACA
                                      CC
GAM688  BCCIP    3'  CATCTAGGGTTTCTCACTT    17425        A  AAAC  G
                                TATCTAGG GT    CT TACTT
                                |||||||| ||    || |||||
                                GTAGATCC CA    GA GTGAA
                                    _  AA__  _
GAM688  ELL2     3'  CTAGGAGTAGCAGCTT      17426         AACCT  _
                                CTAGGAGTA     GTA CTT
                                |||||||||     ||| |||
                                GATCCTCAT     CGT GAA
                                     _____  C
GAM688  FLJ32658 3'  TATCTAGGGTAAGCCTGC    17427        A   A
                                TATCTAGG GTAA CCTGT
                                |||||||| |||| |||||
                                ATAGATCC CATT GGACG
                                    _   C
GAM688  KIAA1399 3'  TATCCACTGGAAATCTGTACTT 17428       __   TAAAC
           T                     TATCTA  GGAG    CTGTACTTT
                                 ||||||  ||||    |||||||||
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                                ATAGGT  CCTT    GACATGAAA
                                   GA    TA___
GAM688  SGT1     3'  TATCTAGGAGCAAATGACATGC 17429           ___  C
                                TATCTAGGAGTAA   AC TGT
                                ||||||||||||   || |||
                                ATAGATCCTCGTT   TG ACG
                                      TAC  T
GAM688  LOC129198 5'  TATCTGGGGGCGGGCCTGGGCC 17430      A  A  AAA    TA
          T                     TATCT GG GT   CCTG  CTT
                                |||||  || ||   ||||  |||
                                ATAGA CC CG   GGAC  GGA
                                   C  C  CCC    CC
GAM688  LOC151176 3'  TCTGGGACAGTCCTGTACTTT  17431     A  AG  AA
                                TCT GG  TA  CCTGTACTTT
                                |||  ||  ||  ||||||||||
                                AGA CC  GT  GGACATGAAA
                                  _  CT  CA
GAM688  LOC152048 3'  TAGGAGTAAATTTGGACT    17432          CC  T
                                TAGGAGTAAA  TG ACT
                                ||||||||||  || |||
                                ATCCTCATTT  AC TGA
                                      AA  C
GAM689  AP2B1    3'  TGGCGGTAACCTTTGTGCC    17435          GATC
                                TGGCGGTAGCC    GTGCC
                                ||||||||||    |||||
                                ACCGCCATTGG    CACGG
                                      AAA_
GAM689  CLECSF12  3'  GCGGTGAGCCGAGATCGTGCC  17436      _     __
                                GCGGT AGCCGA  TCGTGCC
                                |||||  ||||||  |||||||
                                CGCCA TCGGCT  AGCACGG
                                   C     CT
GAM689  EPHA2    3'  TGTGGCGGGGCTCCTGC     17437        TA  CGA  G
                                TGTGGCGG  GC   TC TGC
                                ||||||||  ||   || |||
                                ACACCGCC  CG   AG ACG
                                     C_  ___  G
GAM689  GM2A     5'  TGTGGCGGCAGAGGTGC     17438          CCGATC
                                TGTGGCGGTAG     GTGC
                                ||||||||||      ||||
                                ACACCGCCGTC     CACG
                                      TC_____
GAM689  MADH6    3'  GTGGCGGTGGCCGCGGCC    17439        A   AT  T
                                GTGGCGGT GCCG  CG GCC
                                ||||||||  ||||  || |||
                                CACCGCCA CGGC  GC CGG
                                     C    __  _
GAM689  MKI67    3'  TGTGGTGGTTGGAGGTGCC   17440      C   AGCC  TC
                                TGTGG GGT    GA  GTGCC
                                |||||  |||    ||  |||||
```

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                                ACACC CCA   CT  CACGG
                                  A  AC__  C_
GAM689  PTEN    5'  TGGCGGTAGCTGATGC     17441         C  TCG
                                TGGCGGTAGC GA  TGC
                                |||||||||| ||  |||
                                ACCGCCATCG CT  ACG
                                     A  ___
GAM689  PTGIS   3'  TGTGGTGAGCTGAGATCGTGCC 17442      C GT  C__
                                TGTGG G  AGC  GATCGTGCC
                                ||||| |  |||  |||||||||
                                ACACC C  TCG  CTAGCACGG
                                  A __  ACT
GAM689  RAMP1   3'  GTGGCGGTGGCCTCCAGCC   17443        A  GA  T
                                GTGGCGGT GCC  TCG GCC
                                |||||||| |||  ||| |||
                                CACCGCCA CGG  GGT CGG
                                     C  A_  _
GAM689  SEC13L1  5'  TGCGGCGGTGGCTGCCTCGTGC 17444         A  CGA_
            C                    TGTGGCGGT GC   TCGTGCC
                                |||||||||  ||   |||||||
                                ACGCCGCCA CG   AGCACGG
                                     C  ACGG
GAM689  SIX2    3'  TGTGGCGGGGCCTCGC     17445        TA  GA
                                TGTGGCGG  GCC  TCGT
                                ||||||||  |||  ||||
                                ACACCGCC  CGG  AGCG
                                     C_  ___
GAM689  VCP     3'  TGTGGCAGGTGGCAGTAGTGCC 17446       _  A  CGATC
                                TGTGGC GGT GC    GTGCC
                                ||||||  ||| ||    |||||
                                ACACCG CCA CG    CACGG
                                   T  C  TCAT_
GAM689  APOARGC  3'  TGTGACGGTGGTGAAGTATGTG 17447         AGCC  TC___
            CC                   TGTGGCGGT   GA   GTGCC
                                |||||||||   ||   |||||
                                ACACTGCCA   CT   CACGG
                                     CCA_  TCATA
GAM689  CARD6   3'  GCGGTGAGCCGAGATCGTGCC  17436      _    __
                                GCGGT AGCCGA  TCGTGCC
                                |||||  ||||||  |||||||
                                CGCCA TCGGCT  AGCACGG
                                   C     CT
GAM689  FLJ10506 3'  TGTGACGGTGGCCACAGCC   17448        A   ATCGT
                                TGTGGCGGT GCCG    GCC
                                |||||||||  ||||    |||
                                ACACTGCCA CGGT    CGG
                                     C   GT___
GAM689  FLJ10604 5'  TGTGGCGGAGGCCGCGC    17449        TA  GATC
                                TGTGGCGG  GCC   GTGC
                                ||||||||  |||   ||||
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                                ACACCGCC CGG   CGCG
                                    TC  ____
GAM689  FLJ13840 5' TGCGGCGGTCCTTGTGC    17450       AG GATC
                                TGTGGCGGT CC   GTGC
                                ||||||||| ||   ||||
                                ACGCCGCCA GG   CACG
                                    __ AA__
GAM689  FLJ14803 3' TGTAGTGAGCTAAGATCGTGCC 17451     C GT  C__
                                TGTGG G AGC  GATCGTGCC
                                ||||| | |||  |||||||||
                                ACATC C TCG  CTAGCACGG
                                   A __  ATT
GAM689  INA      3' TGGGGCGGTAGCATTGTG   17452   T     CG C
                                TG GGCGGTAGC AT GTG
                                || |||||||| || |||
                                AC CCGCCATCG TA CAC
                                 C       __ A
GAM689  KIAA0557 3' TGTGGTGAGCCAAGATCGTGCC 17453     C GT  __
                                TGTGG G AGCC GATCGTGCC
                                ||||| | |||| |||||||||
                                ACACC C TCGG CTAGCACGG
                                   A __   TT
GAM689  KIAA1712 3' GCGGTGAGCCAAGATCGTGC  17454     _  __
                                GCGGT AGCC GATCGTGC
                                ||||| |||| ||||||||
                                CGCCA TCGG CTAGCACG
                                   C   TT
GAM689  MRPL10   3' TGTGGCAGTGGCAGGTTGTGCC 17455       A CGATC
                                TGTGGCGGT GC    GTGCC
                                ||||||||| ||    |||||
                                ACACCGTCA CG    CACGG
                                     C TCCAA
GAM689  OVCA2    3' TGTGGCAGTCACCATCGTGCC 17456       A  G
                                TGTGGCGGT GCC ATCGTGCC
                                ||||||||| ||| ||||||||
                                ACACCGTCA TGG TAGCACGG
                                     G  _
GAM689  SEC61A1  3' TGTGGCGGTGGCCCTGTGC  17457       A  GATC
                                TGTGGCGGT GCC   GTGC
                                ||||||||| |||   ||||
                                ACACCGCCA CGG   CACG
                                     C  GA__
GAM689  SIMRP7   3' TGTGGTGTAGCTCAGCATGCC 17458     CG  _ AT
                                TGTGG GTAGC CG CGTGCC
                                |||||  ||||| ||  ||||||
                                ACACC  CATCG GT  GTACGG
                                   A_    A C_
GAM689  LOC146050 3' TGTGGCAGTGGCTTCTGC   17459       A CGA G
                                TGTGGCGGT GC  TC TGC
                                ||||||||| ||  || |||
```

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                                ACACCGTCA CG   AG ACG
                                     C  A__  _
GAM689  LOC146227 5'  GTGGCGGTGGCGGTGCC     17460        A  CGATC
                                GTGGCGGT GC     GTGCC
                                |||||||| ||     |||||
                                CACCGCCA CG     CACGG
                                     C  C____
GAM689  LOC154726 5'  TGTGGTGAGCTGAGATCGTGCC 17442       C GT   C__
                                TGTGG G  AGC   GATCGTGCC
                                ||||| |  |||   |||||||||
                                ACACC C  TCG   CTAGCACGG
                                   A __   ACT
GAM689  LOC157798 5'  TGAGGCGAGATCGTGC      17461    T    TAGCC
                                TG GGCGG     GATCGTGC
                                || |||||     ||||||||
                                AC CCGCT     CTAGCACG
                                 T    ______
GAM689  LOC196872 3'  TGTGGCGATAAGCTTGTG     17462          _  CGATC
                                TGTGGCGGTA GC     GTG
                                |||||||||| ||     |||
                                ACACCGCTAT CG     CAC
                                      T  AA___
GAM690  PRKAB1    3'  TGGAGAAATCCGGCAGCAG    17465      A     A  TAAT
                                TGGA AAATCC GC    GCAG
                                |||| |||||| ||    ||||
                                ACCT TTTAGG CG    CGTC
                                  C     C  T___
GAM690  RAG1      3'  GAAAAATCCATGACAGCAGAT  17466          GCTAAT
                                GAAAAATCCA      GCAGAT
                                ||||||||||      ||||||
                                CTTTTTAGGT      CGTCTA
                                      ACTGT_
GAM690  SLC6A12   5'  GGAAATCCAGGCCTTGGCAGAT 17467      AA     _  AAT
                                GGAA  ATCCAG CT   GCAGAT
                                ||||  |||||| ||   ||||||
                                CCTT  TAGGTC GG   CGTCTA
                                  __      C  AAC
GAM690  SMARCA2   3'  TGGAAAAATGTATATGCAG    17468         CCAGCTA
                                TGGAAAAAT       ATGCAG
                                |||||||||       ||||||
                                ACCTTTTTA       TACGTC
                                      CATA___
GAM690  KIAA0182  3'  TGGAGAAATCCAGTGAGA     17469      A       CTAA  C
                                TGGA AAATCCAG    TG AGA
                                |||| ||||||||    || |||
                                ACCT TTTAGGTC    AC TCT
                                  C       _____  _
GAM690  MGC14289  3'  TGGAAAAATTCAATATTCTGCA 17470          C   CTAA_
           GAT                    TGGAAAAAT CAG     TGCAGAT
                                |||||||||| |||     |||||||
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                                ACCTTTTTA GTT    ACGTCTA
                                     A  ATAAG
GAM690  P5      3'  TGGAAAAATCCACTGGC     17471          G  AAT
                                TGGAAAAATCCA CT  GC
                                |||||||||||| ||  ||
                                ACCTTTTTAGGT GA  CG
                                       _ C__
GAM690  LOC253765 3'  TGGTAAAATCCAGCTGCAG   17472    A        AAT
                                TGG AAAATCCAGCT  GCAG
                                ||| |||||||||||  ||||
                                ACC TTTTAGGTCGA  CGTC
                                  A       ___
GAM691  ADRB1   3'  CTCCTCGTTCCCCTGGG    17475     C      GA
                                CTCC CGTTCCCC  GGG
                                |||| ||||||||  |||
                                GAGG GCAAGGGG  CCC
                                  A      A_
GAM691  AXIN1   3'  CCCGTGCCCCGAGGCG     17476      T      GTCC
                                CCCGT CCCCGAGG   CG
                                ||||| ||||||||   ||
                                GGGCA GGGGCTCC   GC
                                  C      ____
GAM691  CIAO1   5'  CTCCCCGTTCCGCCGGAGGACC 17477          _  AG  T  C
           TGG                    CTCCCCGTTCC CCG  GG CC GG
                                ||||||||||| |||  || || ||
                                GAGGGGCAAGG GGC  CC GG CC
                                       C  CT  T  A
GAM691  DRD4    3'  CTCCTTGGTCCCTGAGGCCTGG 17478     CCGT   C   GT  C
                                CTCC   TCCC GAGG  CC GG
                                ||||   |||| ||||  || ||
                                GAGG   AGGG CTCC  GG CC
                                  AACC   A   __  A
GAM691  LASS1   3'  CCTGGTCTCCTGGGGGTCCCGG 17479   CC  TC  CGA
                                CC  GT  CC   GGGTCCCGG
                                ||  ||  ||   |||||||||
                                GG  CA  GG   CCCAGGGCC
                                 AC  GA  ACC
GAM691  MADH1   5'  CTCTCCGCTCCCCGAGCCTCGG 17480    C         GGT  _
                                CTC CCGTTCCCCGAG   CC CGG
                                ||| ||||||||||||   || |||
                                GAG GGCGAGGGGCTC   GG GCC
                                  A          ___  A
GAM691  MEN1    5'  GTCCCCCACAATTCCGG     17481        AG   C
                                GTTCCCCG  GGT CCGG
                                ||||||||  ||| ||||
                                CAGGGGGT  TTA GGCC
                                     G_   A
GAM691  MGAT2   5'  CTCATCCCGGGCCCCGGGGGTC 17482    __   TT    A    C
           CTGG                    CTC  CCCG  CCCCG GGGTCC GG
                                |||  ||||  ||||| |||||| ||
```

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                                GAG  GGGC  GGGGC CCCAGG CC
                                  TA   CC    C     A
GAM691  MPL     3'  CTGCCTGTGGAGAAAGGGTCCT 17483    C  C  TCCCC      C
           GG                     CT CC GT    GAGGGTCC GG
                                || || ||    |||||||| ||
                                GA GG CA    TTCCCAGG CC
                                 C  A  CCTCT       A
GAM691  PDE1B   3'  CTCCCCGCTCCCTGGCAGCCAC 17484          CGAG   _ _
           CTGG                   CTCCCCGTTCCC   GGTC CC GG
                                ||||||||||||   |||| || ||
                                GAGGGGCGAGGG   TCGG GG CC
                                      ACCG   T  A
GAM691  RNPEPL1  3'  CTCCCCATTCTCCCTGCCTGG  17485         _  GAGGGT  C
                                CTCCCCGTTC CCC     CC GG
                                |||||||||| |||     || ||
                                GAGGGGTAAG GGG     GG CC
                                      A   AC____  A
GAM691  SCG2    5'  CTCCCCGTTCTCCGGGCGAGCT 17486        _ ___   GG  C
           TCTCGG                 TCCCCGTTC CC   CGAG  TC CGG
                                ||||||||| ||   ||||  || |||
                                AGGGGCAAG GG   GCTC  AG GCC
                                     A  CCC   GA  A
GAM691  SIRT4   3'  TCCCTGTTCCAGGTTCTG    17487     C    CCG   G  CC
                                TCCC GTTCC   AGG TC  G
                                |||| |||||   ||| ||  |
                                AGGG CAAGG   TCC AG  C
                                  A    ___   A  A_
GAM691  TRPV3   3'  CTCCTTTTCCCCGAAGGGTTCC 17488     CCG      _   C
           GG                     CTCC   TTCCCCGA GGGT CCGG
                                ||||   |||||||| |||| ||||
                                GAGG   AAGGGGCT CCCA GGCC
                                  AA_       T   A
GAM691  WRN     5'  CTCCCCTTCCCTCCC      17489       G    CGAGGG
                                CTCCCC TTCCC     TCCC
                                |||||| |||||     ||||
                                GAGGGG AAGGG     AGGG
                                   _   _______
GAM691  ABLIM   3'  CTGCCCTGTTCCCTGATGG   17490   _  C    C  _
                                CT CCC GTTCCC GA GG
                                || ||| |||||| || ||
                                GA GGG CAAGGG CT CC
                                 C   A     A  A
GAM691  ABLIM   3'  CTGCCCTGTTCCCTGATGG   17490   _  C    C  _
                                CT CCC GTTCCC GA GG
                                || ||| |||||| || ||
                                GA GGG CAAGGG CT CC
                                 C   A     A  A
GAM691  C15orf15 5'  TCCCCCTTCCCCGACCG    17491      G      GGGTC
                                TCCCC TTCCCCGA    CCG
                                ||||| ||||||||    |||
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                                AGGGG AAGGGGCT    GGC
                                  G      _____
GAM691  C5orf5   5'  CCCCGTTCCCTGGCCGCGG   17492         CGAG   C
                                CCCCGTTCCC   GGTC CGG
                                ||||||||||   |||| |||
                                GGGGCAAGGG   CCGG GCC
                                     A___    C
GAM691  CBX6     3'  CTCCCTATTTCTGCATCCTGG  17493      CG_  CC GAGG   C
                                CTCCC  TTC  C   GTCC GG
                                |||||  |||  |   |||| ||
                                GAGGG  AAG  G   TAGG CC
                                  ATA  AC ____   A
GAM691  DKFZP434J154 3'  CTCTGCTCCCCGGGTCAGAGG  17494    CCC     GA    CC_
                                CTC  GTTCCCC  GGGTC  GG
                                |||  |||||||  |||||  ||
                                GAG  CGAGGGG  CCCAG  CC
                                 A__     __    TCT
GAM691  DKFZP434J154 3'  CTCTGCTCCCCGGGTCAGAGG  17494    CCC     GA    CC_
                                CTC  GTTCCCC  GGGTC  GG
                                |||  |||||||  |||||  ||
                                GAG  CGAGGGG  CCCAG  CC
                                 A__     __    TCT
GAM691  FLJ10482  5'  TCCCCGCAGGGGGGTCCCGG  17495       TCCCCGA
                                TCCCCGT     GGGTCCCGG
                                |||||||     |||||||||
                                AGGGGCG     CCCAGGGCC
                                    TCCC___
GAM691  FLJ11807  5'  CTCCCCGATCTCCCCCCG    17496       T  _  GAGGGT
                                CTCCCCG TC CCC     CCCG
                                ||||||| || |||     ||||
                                GAGGGGC AG GGG     GGGC
                                    T  A   _______
GAM691  HRIHFB2122 5'  CCTTTCCCCGACGCTGCCCCGG 17497    G      GG__
                                CC TTCCCCGA    GTCCCGG
                                || ||||||||    |||||||
                                GG AAGGGGCT    CGGGGCC
                                 A       GCGA
GAM691  HRIHFB2122 5'  CCTTTCCCCGACGCTGCCCCGG 17497    G      GG__
                                CC TTCCCCGA    GTCCCGG
                                || ||||||||    |||||||
                                GG AAGGGGCT    CGGGGCC
                                 A       GCGA
GAM691  KIAA0073  5'  CCGGTTCCTCCGGGTCCCGG   17498    C    _  GA
                                CC GTTCC CC  GGGTCCCGG
                                || ||||| ||  |||||||||
                                GG CAAGG GG  CCCAGGGCC
                                 C    A  __
GAM691  KIAA0296  3'  TCCCTTGTTCCCTGGCACCCGG 17499     C_     CGAG  _
                                TCCC  GTTCCC    GGT CCCGG
                                ||||  ||||||    ||| |||||
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                                AGGG  CAAGGG    CCG GGGCC
                                  AA     A___   T
GAM691  KIAA0450  5'  CTCCCCAGTTCTCCATCCCTGG 17500       _   C  GAGG    _
                                CTCCCC GTTC CC    GTCCC GG
                                |||||| |||| ||    ||||| ||
                                GAGGGG CAAG GG    TAGGG CC
                                   T    A ____     A
GAM691  KIAA0618  5'  CGCTCGGGGGTCCCGG      17501       CCC A
                                CGTTC   G GGGTCCCGG
                                |||||   | |||||||||
                                GCGAG   C CCCAGGGCC
                                   ___ C
GAM691  KIAA1036  3'  CTCTGCTCCCCAAACCCTGG   17502     CCC        GGT   _
                                CTC   GTTCCCCGAG   CCC GG
                                |||   ||||||||||   ||| ||
                                GAG   CGAGGGGTTT   GGG CC
                                  A__         ___   A
GAM691  KIAA1297  3'  CCTCCGTTTCCTGGGGGTCTGG 17503    _    C  CGA    CC
                                CC CCGTT CC   GGGTC  GG
                                || ||||| ||   |||||  ||
                                GG GGCAA GG   CCCAG  CC
                                 A    A  ACC    A_
GAM691  KIAA1737  5'  CTCTCCGTCCTCCGAAAGTCCC 17504     C     C
           GG                    CTC CCGTTC CCGAGGGTCCCGG
                                ||| |||||| ||||||||||||
                                GAG GGCAGG GGCTTTCAGGGCC
                                  A     A
GAM691  KIAA1821  3'  CTCCCCATTTCAAATATGTCCT 17505         CCCCGAGG    C
           GG                    CTCCCCGTT       GTCC GG
                                |||||||||       |||| ||
                                GAGGGGTAA       CAGG CC
                                     AGTTTATA    A
GAM691  MAGE-E1   3'  CCATTCCCGGGGGTCTCGG   17506        C A    C
                                CCGTTCCC G GGGTC CGG
                                |||||||| | ||||| |||
                                GGTAAGGG C CCCAG GCC
                                     _ C    A
GAM691  NOL4     5'  CTCCATGTTCCCCGCGCTCGG  17507     CC       AGG  CC
                                CTCC  GTTCCCCG   GT  CGG
                                ||||  ||||||||   ||  |||
                                GAGG  CAAGGGGC   CG  GCC
                                  TA       G__  A_
GAM691  OATL1    5'  TCCTGTCCTAGCCGGTCCCGG  17508    CC   C__  GAG
                                TCC  GTTC   CC   GGTCCCGG
                                |||  ||||   ||   ||||||||
                                AGG  CAGG   GG   CCAGGGCC
                                  A_   ATC  ___
GAM691  RAI17    3'  CTCTGTTCCCCAAGCCTGG   17509     CCC        GGT  C
                                CTC   GTTCCCCGAG   CC GG
                                |||   ||||||||||   || ||
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                                GAG   CAAGGGGTTC   GG CC
                                  A__         ___  A
GAM691  SEMA3B   3'  TCCCCGTCCCTTCCCTCCGG   17510          CCGAGGG  _
                                TCCCCGTTCC      TC CCGG
                                ||||||||||      || ||||
                                AGGGGCAGGG      GG GGCC
                                     AAG_____  A
GAM691  SEMA4G   5'  TCTCCGCAGTGAGGGTCCTGG  17511    C   TCCCC      C
                                TC CCGT    GAGGGTCC GG
                                || ||||    |||||||| ||
                                AG GGCG    CTCCCAGG CC
                                 A   TCA__      A
GAM691  TGIF2    3'  CTCTCGTTCCCCACACCG    17512    CC       AGGGT  C
                                CTC  CGTTCCCCG    CC G
                                |||  |||||||||    || |
                                GAG  GCAAGGGGT    GG C
                                  A_       GT___  A
GAM691  THG-1    5'  CCGTTCCCTGGGGCCTCCTGG  17513        CGA    _ _
                                CCGTTCCC   GGGTC CC GG
                                ||||||||   ||||| || ||
                                GGCAAGGG   CCCGG GG CC
                                     AC_    A  A
GAM691  TLN2     5'  CGCCCCAGCGAGGGTCCG    17514       C_       C
                                CGTTCC  CGAGGGTCC G
                                ||||||  |||||||||  |
                                GCGGGG  GCTCCCAGG C
                                    TC        A
GAM691  LOC127281 5'  CTCCCTGTTCCCCGCTCCCGG  17515      C       AGGG
                                CTCCC GTTCCCCG    TCCCGG
                                |||||  ||||||||    ||||||
                                GAGGG CAAGGGGC    AGGGCC
                                   A       G___
GAM691  LOC132422 5'  CTCCTGGGAACCGAGGGTCCTG 17516      CCGTTCC        C
           G                     CTCC       CCGAGGGTCC GG
                                ||||       |||||||||| ||
                                GAGG       GGCTCCCAGG CC
                                   ACCCTT_         A
GAM691  LOC143310 3'  CTCTTCCTTTCCCTCAGCCTGG 17517     C_  G    CGAG  T  C
                                CTC  CC TTCCC    GG CC GG
                                |||  || |||||    || || ||
                                GAG  GG AAGGG    TC GG CC
                                  AA  A    AG__  _  A
GAM691  LOC143666 5'  TCCCCGTCTCTCCGGCGTCGG  17518        _  C  GAG   CC
                                TCCCCGT TC CC   GGT  CGG
                                |||||||  || ||   |||  |||
                                AGGGGCA AG GG   CCG  GCC
                                    G  A  ___   CA
GAM691  LOC144583 3'  CCCGTGGGTCTGAGGGTCCTGG 17519       TCCCC_       C
                                CCCGT      GAGGGTCC GG
                                |||||      |||||||| ||
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                                GGGCA     CTCCCAGG CC
                                  CCCAGA       A
GAM691   LOC151516 5'  CTCCCCATTCTCCTTTGTTCTG 17520         C  GAGGG  CC
           G                     CTCCCCGTTC CC     TC  GG
                                 |||||||||| ||     ||  ||
                                 GAGGGGTAAG GG     AG  CC
                                      A  AAACA  A_
GAM691   LOC162048 5'  TCCCCGTTCCCTCTCCCG    17521          CGAGGG
                                 TCCCCGTTCCC     TCCCG
                                 ||||||||||      |||||
                                 AGGGGCAAGGG     AGGGC
                                       AG____
GAM691   LOC163682 5'  TCCCTGTTCCCCGGCCG     17522      C      GAG  T  C
                                 TCCC GTTCCCC   GG CC G
                                 |||| |||||||   || || |
                                 AGGG CAAGGGG   CC GG C
                                   A      ___  _  A
GAM691   LOC201102 3'  CTCCCCGTTTCTCTCCCCATCT 17523         _____     AG__
           TGG                     CTCCCCGT    TCCCCG    GG
                                 ||||||||     ||||||    ||
                                 GAGGGGCA    AGGGGT    CC
                                      AAGAG     AGAA
GAM691   LOC201164 3'  TCCCCGCTCTCCTCTCCTCCGG 17524         C  GAGGG  _
                                 TCCCCGTTC CC     TC CCGG
                                 |||||||| ||     || ||||
                                 AGGGGCGAG GG     GG GGCC
                                      A  AGA__  A
GAM691   LOC204804 3'  CTCCCCATTCTCCATCTTGG   17525         C   AG__
                                 CTCCCCGTTC CCG    GG
                                 |||||||||| |||    ||
                                 GAGGGGTAAG GGT    CC
                                      A   AGAA
GAM691   LOC204820 3'  GCTCCCCAGGTCCTGG      17526        GA     C
                                 GTTCCCC  GGGTCC GG
                                 |||||||  |||||| ||
                                 CGAGGGG  TCCAGG CC
                                     __      A
GAM691   LOC221466 5'  CTCCCCTTCCCCACTCTGG    17527       G      AG__
                                 CTCCCC TTCCCCG    GG
                                 ||||||| |||||||    ||
                                 GAGGGG AAGGGGT    CC
                                     _       GAGA
GAM691   LOC253258 3'  TCCCCGTCTCTCCGGCGTCGG  17518        _ C  GAG   CC
                                 TCCCCGT TC CC   GGT  CGG
                                 |||||||  || ||   |||  |||
                                 AGGGGCA AG GG   CCG  GCC
                                     G  A  ___   CA
GAM691   LOC253805 3'  GCTGGCCTGAGGGTCCTGG    17528     CC  _       C
                                 GTT  CC GAGGGTCC GG
                                 |||  ||  |||||||| ||
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                                CGA  GG CTCCCAGG CC
                                  CC  A       A
GAM691  LOC254381 5'  CTCCCCGCTCCCTGGGGTTGTG 17529      CGA   C_______   III
            TTTCCGGC                TTCCC   GGGT      CCGG   C
                                |||||   ||||      ||||  |
                                GAGGG   CCCA      GGCC   G
                                  AC_   ACACAAA   III
GAM691  LOC51177  5'  CTCCCCTTCTTTGTAGCTCCGG 17530       G   CCCGAG  TC
                                CTCCCC TTC     GG  CCGG
                                |||||| |||     ||  ||||
                                GAGGGG AAG     TC  GGCC
                                   _   AAACA_  GA
GAM691  LOC90835  5'  TCCCCGCTTCCCGCCGCAGCTC 17531        C    AG__   CC
            GG                    TCCCCGTT CCCG    GGT  CGG
                                |||||||| ||||    |||  |||
                                AGGGGCGA GGGC    TCG  GCC
                                    A    GGCG   A_
GAM691  LOC91768  5'  CTCCCACTCCCGGGGGTCCCGG 17532      CGTTC    A
                                CTCCC     CCCG GGGTCCCGG
                                |||||     |||| |||||||||
                                GAGGG     GGGC CCCAGGGCC
                                   TGA__    C
GAM692  ADAMTS3   3'  TGGTGATTTCTTCCAA      17535           AC
                                TGGTGATTTTTT  CCAA
                                ||||||||||||  ||||
                                ACCACTAAAGAA  GGTT
                                          __
GAM692  ETV5      3'  GTGATTTTTCAACAAA       17536         TACC
                                GTGATTTTT    CAACAAA
                                |||||||||    |||||||
                                CACTAAAAA    GTTGTTT
                                          ____
GAM692  MS4A3     3'  TGGTAATTTTTTATTTGACA   17537           CCCA
                                TGGTGATTTTTTA    ACA
                                ||||||||||||    |||
                                ACCATTAAAAAAT    TGT
                                        AAAC
GAM692  KIAA1136  3'  TGGGATTTGAGCCCAGCAA    17538     T    TTTA    A
                                TGG GATTT    CCCA CAA
                                ||| |||||    |||| |||
                                ACC CTAAA    GGGT GTT
                                  _    CTC_   C
GAM692  NUDT12    3'  TGCTGATTTTTTCCCAA      17539     G       A
                                TG TGATTTTTT CCCAA
                                || |||||||| |||||
                                AC ACTAAAAAA GGGTT
                                 G       _
GAM692  LOC157567 3'  TGACTTTACCCAATAAA      17540      TT       C
                                TGAT  TTTACCCAA AAA
                                ||||  |||||||| |||
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                                ACTG  AAATGGGTT TTT
                                  __        A
GAM692  LOC158297 3'  GGGAATTCTTTTTTGTCCAACA 17541    TG      AC___
           AAT                    GG  ATTTTTT    CCAACAAAT
                                || |||||||    |||||||||
                                CC  TAAGAAA    GGTTGTTTA
                                 CT       AAACA
GAM692  LOC196549 3'  TGGTGATCTCCTCCTCCAGCAA 17542           AC_   A
                                TGGTGATTTTTT   CCA CAA
                                ||||||||||||   ||| |||
                                ACCACTAGAGGA   GGT GTT
                                       GGA   C
GAM692  LOC253573 3'  TGGTGATTTCTTTAAAACAAA  17543           ACCC
                                TGGTGATTTTTT    AACAAA
                                ||||||||||||    ||||||
                                ACCACTAAAGAA    TTGTTT
                                       ATT_
GAM692  LOC51175  3'  TGGTATTACCAACAA       17544       ATTTT    C
                                TGGTG    TTACC AACAA
                                |||||    ||||| |||||
                                ACCAT    AATGG TTGTT
                                  ______    _
GAM692  LOC93550  3'  TGGTAATAGCACTCAACAAAT  17545        TTTT   C
                                TGGTGAT    TAC CAACAAAT
                                |||||||    ||| ||||||||
                                ACCATTA    GTG GTTGTTTA
                                     TC__   A
GAM693  CARD10    3'  GTCCCGGGACTCCCATAGGCTC 17548         _    C___
                                GTCCCGGG CTCCC    GTTC
                                |||||||| |||||    ||||
                                CAGGGCCC GAGGG    CGAG
                                     T     TATC
GAM693  CDKN2C    5'  GTCCCGGGACTCCCGGCAGCCC 17549         _    C  TC
           GA                     GTCCCGGG CTCCC GT  CCCGA
                                |||||||| ||||| ||  |||||
                                CAGGGCCC GAGGG CG  GGGCT
                                     T     C  TC
GAM693  CDKN2D    5'  GTCCCGGCTCCCCAGCCCGA   17550        G      TTC
                                GTCCCGG CTCCCCG   CCCGA
                                |||||||| |||||||   |||||
                                CAGGGCC GAGGGGT   GGGCT
                                   _      C__
GAM693  CDR2      5'  GCCCCGGGCTCTTCCCCG     17551           CCCG
                                GTCCCGGGCTC    TTCCCCG
                                ||||||||||    |||||||
                                CGGGGCCCGAG    AAGGGGC
                                        ____
GAM693  EMX2      5'  GCCCTGGGCTCCCAGCTCC    17552      C       C
                                GTCC GGGCTCCC GTTCC
                                |||| |||||||| |||||
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                                CGGG CCCGAGGG CGAGG
                                  A      T
GAM693  GALGT   5' GTGCCGGGCTCTCGCCCCG   17553   C     CC  TT
                                GT CCGGGCTC  CG  CCCCG
                                || ||||||||  ||  |||||
                                CA GGCCCGAG  GC  GGGGC
                                 C      A_  __
GAM693  GFPT2   5' TCTCGGGCTCCTTCGCGGCTCG 17554   C     C_  TCCC
          A                      TC CGGGCTCC  CGT   CGA
                                || ||||||||  |||   |||
                                AG GCCCGAGG  GCG   GCT
                                 A      AA  CCGA
GAM693  GNAS    5' TCCCGGGCTCCTCTCGCT    17555         C__
                                TCCCGGGCTCC   CGTT
                                ||||||||||   ||||
                                AGGGCCCGAGG   GCGA
                                      AGA
GAM693  GYPC    5' TCCCGGGCTCCTGACCCTCG   17556         CCGTT  _
                                TCCCGGGCTCC    CCC CG
                                ||||||||||    ||| ||
                                AGGGCCCGAGG    GGG GC
                                      ACT__   A
GAM693  GYPC    5' TCCCGGGCTCCTGACCCTCG   17556         CCGTT  _
                                TCCCGGGCTCC    CCC CG
                                ||||||||||    ||| ||
                                AGGGCCCGAGG    GGG GC
                                      ACT__   A
GAM693  HAP1    3' TCCCGGGCTTCTCCTGCCCCC  17557         _ _ C
                                TCCCGGGCT C CC GTTCCC
                                ||||||||| | || ||||||
                                AGGGCCCGA G GG CGGGGG
                                     A A  A
GAM693  IMPDH1  5' CCTGGGCTCCCCGCTCTCCCCG 17558   C       __
                                CC GGGCTCCCCGT  TCCCCG
                                || ||||||||||  ||||||
                                GG CCCGAGGGGCG  AGGGGC
                                 A         AG
GAM693  KNS2    3' GTCCCGGGCCAGCTCC      17559         CCCC
                                GTCCCGGGCT   GTTCC
                                |||||||||   |||||
                                CAGGGCCCGG   CGAGG
                                      T___
GAM693  MPST    5' GTCTCGGACTCCCGGCTTCC  17560    C      C  C
                                GTC CGGGCTCCC GTT CC
                                ||| ||||||||| ||| ||
                                CAG GCCTGAGGG CGA GG
                                  A       C  A
GAM693  NARS    3' CCCCGAACTTTGTTTCCCGA  17561         CCCC  C
                                TCCCGGGCT   GTT CCCGA
                                |||||||||   ||| |||||
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                                GGGGCTTGA   CAA GGGCT
                                    AA__  A
GAM693  NTSR1    5' GCCCCGGGCTCCGGGCTCC  17562         CC
                                GTCCCGGGCTCC GTTCC
                                |||||||||||| |||||
                                CGGGGCCCGAGG CGAGG
                                     CC
GAM693  POLA     3' ATCCCTCTCCCCGTTTTTCGA 17563     GGG      CCC
                                GTCCC  CTCCCCGTT  CGA
                                |||||  |||||||||  |||
                                TAGGG  GAGGGGCAA  GCT
                                  A__      AAA
GAM693  RANBP2L1 3' GTCTCGCTCTGTTCCCCGA  17564   CCGG  CCC
                                GTC  GCTC  GTTCCCCGA
                                |||  ||||  |||||||||
                                CAG  CGAG  CAAGGGGCT
                                 AG__  A__
GAM693  RGS3     3' GTCTTGGGCCCCCTCGTACCG  17565   CC     _  TCC
                                GTC GGGCTCCC CGT  CCG
                                ||| |||||||| |||  |||
                                CAG CCCGGGGG GCA  GGC
                                 AA     A  T__
GAM693  RGS3     3' GTCTTGGGCCCCCTCGTACCG  17565   CC     _  TCC
                                GTC GGGCTCCC CGT  CCG
                                ||| |||||||| |||  |||
                                CAG CCCGGGGG GCA  GGC
                                 AA     A  T__
GAM693  RGS3     3' GTCTTGGGCCCCCTCGTACCG  17565   CC     _  TCC
                                GTC GGGCTCCC CGT  CCG
                                ||| |||||||| |||  |||
                                CAG CCCGGGGG GCA  GGC
                                 AA     A  T__
GAM693  RGS3     3' GTCTTGGGCCCCCTCGTACCG  17565   CC     _  TCC
                                GTC GGGCTCCC CGT  CCG
                                ||| |||||||| |||  |||
                                CAG CCCGGGGG GCA  GGC
                                 AA     A  T__
GAM693  RGS3     3' GTCTTGGGCCCCCTCGTACCG  17565   CC     _  TCC
                                GTC GGGCTCCC CGT  CCG
                                ||| |||||||| |||  |||
                                CAG CCCGGGGG GCA  GGC
                                 AA     A  T__
GAM693  SACM2L   5' GTCCCGGCGAGTCCGTTCCCCG 17566      GCTCC
                                GTCCCGG   CCGTTCCCCG
                                |||||||   ||||||||||
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                                CAGGGCC    GGCAAGGGGC
                                    GCTCA
GAM693  SACM2L   5'  GTCCCGGCGAGTCCGTTCCCCG 17566       GCTCC
                                GTCCCGG    CCGTTCCCCG
                                |||||||    ||||||||||
                                CAGGGCC    GGCAAGGGGC
                                    GCTCA
GAM693  TP53BP2  5'  GCCCCGGGCTCCCCCGCCCCG  17567           GTT
                                GTCCCGGGCTCCCC   CCCCG
                                ||||||||||||||  |||||
                                CGGGGCCCGAGGGG   GGGGC
                                       GC_
GAM693  TULP1    3'  CCGGGCTCCTCCTGCCTCG    17568         _  GTT  C
                                CCGGGCTCC CC   CC CG
                                |||||||| ||   || ||
                                GGCCCGAGG GG   GG GC
                                     A  AC_  A
GAM693  ZIC3     5'  GTCCCGGGCACCCCTCCTCTCC 17569         T   GT___
            CCGA                    GTCCCGGGC CCCC     TCCCCGA
                                |||||||| ||||    |||||||
                                CAGGGCCCG GGGG    AGGGGCT
                                     T    AGGAG
GAM693  A2BP1    5'  CGGGTTTCCCCACCCGA     17570      C_     TTC
                                CGGG  TCCCCG   CCCGA
                                ||||  ||||||   |||||
                                GCCC  AGGGGT   GGGCT
                                  AA     ___
GAM693  AKAP9    5'  GTCCGGGGCTCCCCCGCCCGA  17571      C        GTTC
                                GTCC GGGCTCCCC    CCCGA
                                |||| |||||||||    |||||
                                CAGG CCCGAGGGG    GGGCT
                                  C        GC__
GAM693  APXL2    5'  GCCCCGGGCTCTGACTCC     17572           CCCG
                                GTCCCGGGCTC    TTCC
                                ||||||||||    ||||
                                CGGGGCCCGAG    GAGG
                                      ACT_
GAM693  CARD9    3'  CGGGCTCCCCCCGCCG      17573          GTT  _
                                CGGGCTCCCC   CC CCG
                                |||||||||   || |||
                                GCCCGAGGGG   GG GGC
                                     ___  C
GAM693  DEPP     3'  CCTGATTCCCGTTCCCTGA   17574     G GC    C     C
                                CC G  TCCC GTTCCC GA
                                || |  |||| |||||| ||
                                GG C  AGGG CAAGGG CT
                                 A TA   _     A
GAM693  DKFZp547D155 3'  ATCCTGGGCCCTTCCCTGA   17575      C     CCCG    C
                                GTCC GGGCTC    TTCCC GA
                                |||| ||||||    ||||| ||
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                                TAGG CCCGGG   AAGGG CT
                                  A    ____    A
GAM693  DKFZp564A176 3' GCTCCGGGCTCTCTCCCG   17576   TC      CCCGT _
                                G  CCGGGCTC    TC CCCG
                                |  ||||||||    || ||||
                                C  GGCCCGAG    AG GGGC
                                 GA      _____  A
GAM693  FLJ11700  5' GTCCCGGGCGCCCGCATGTCCC 17577         T  _  _
                                GTCCCGGGC CCC CGT TCCC
                                ||||||||| ||| ||| ||||
                                CAGGGCCCG GGG GTA AGGG
                                      C  C  C
GAM693  FLJ11807  5' GTCCCGGGTCAATGGCTCC   17578        C  CCC_
                                GTCCCGGG TC   GTTCC
                                |||||||| ||   |||||
                                CAGGGCCC AG   CGAGG
                                     _ TTAC
GAM693  FLJ13117  5' GCTCCGGGCTCCGCGTCCC   17579   TC      C
                                G  CCGGGCTCC CGTTCC
                                |  ||||||||| ||||||
                                C  GGCCCGAGG GCAGGG
                                 GA       C
GAM693  FLJ13725  5' GTCCCGGGCCTCTCGGCTTCCC 17580         _ CCC  C
           G                     GTCCCGGGC TC  GTT CCCG
                                |||||||| ||  ||| ||||
                                CAGGGCCCG AG  CGA GGGC
                                      G AGC  A
GAM693  FLJ13868  3' GTCCTGGCTCCCCTTCTCCCG  17581     CG      G  _
                                GTCC  GGCTCCCC TTC CCCG
                                ||||  |||||||| ||| ||||
                                CAGG  CCGAGGGG AAG GGGC
                                  A_      _  A
GAM693  FLJ20499  3' GTCCTGGGTCCTCCCCAAGCCT 17582     C  __     TT  C
           CG                    GTCC GGG  CTCCCCG  CC CG
                                |||| |||  |||||||  || ||
                                CAGG CCC  GAGGGGT  GG GC
                                  A  AG      TC  A
GAM693  FLJ21870  3' GTCCAGGGCTCCCACCAGGTTC 17583     C      C____
                                GTCC GGGCTCCC    GTTC
                                |||| ||||||||    ||||
                                CAGG CCCGAGGG    CAAG
                                  T       TGGTC
GAM693  FOXJ1    3' CCCGGGCTCCTCCAGGCCTCG  17584         _  TT  C
                                CCCGGGCTCC CCG  CC CG
                                |||||||||| |||  || ||
                                GGGCCCGAGG GGT  GG GC
                                      A  CC  A
GAM693  HSPC156  5' GCTCCGGGCTCCGGGCTCC   17585   TC      CC
                                G  CCGGGCTCC  GTTCC
                                |  |||||||||  |||||
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                              C  GGCCCGAGG  CGAGG
                               GA       CC
GAM693  JIK     5'  TCCTGTGGCTTGTTCCCCG   17586    CG_   CCCC
                              TCC   GGCT   GTTCCCCG
                              |||   ||||   ||||||||
                              AGG   CCGA   CAAGGGGC
                                ACA   A___
GAM693  KDELR1   3'  GTCCTGAGCTCCCCAAGACC   17587     C       TT_
                              GTCC GGGCTCCCCG   CC
                              |||| ||||||||||   ||
                              CAGG CTCGAGGGGT   GG
                                A        TCT
GAM693  KIAA0084  5'  GTCGCGGGCTCCCTGAGGTCGG 17588        __________  TTCCC
           GGAACG                 CGGGCTCCC       CG    CG
                              |||||||||       ||    ||
                              GCCCGAGGG       GC    GC
                                   ACTCCIIIA  CCCTT
GAM693  KIAA0205  5'  CCCGCGCCCGTTCCCCG     17589     G  TCC
                              CCCG GC   CCGTTCCCCG
                              |||| ||   ||||||||||
                              GGGC CG   GGCAAGGGGC
                                G  ___
GAM693  KIAA0285  5'  GTCCCAGGGCTTTCCC      17590      _    CCCCG
                              GTCCC GGGCT    TTCCC
                              ||||| |||||    |||||
                              CAGGG CCCGA    AAGGG
                                T    _____
GAM693  KIAA0296  3'  GCCCCATCCCTTGTTCCC    17591      GGC   C_
                              GTCCCG   TCCC  GTTCCC
                              ||||||   ||||  ||||||
                              CGGGGT   AGGG  CAAGGG
                                 ___    AA
GAM693  KIAA0336  3'  GTCTCGCTCTGTTCCCCGA   17564    CCGG   CCC
                              GTC   GCTC   GTTCCCCGA
                              |||   ||||   |||||||||
                              CAG   CGAG   CAAGGGGCT
                                AG__   A__
GAM693  KIAA1030  3'  GTCTAGGGCTCCCACACCTCCG 17592    CC      CGTT  _
                              GTC  GGGCTCCC    CC CCG
                              |||  ||||||||    || |||
                              CAG  CCCGAGGG    GG GGC
                                AT       TGT_  A
GAM693  KIAA1277  3'  GTCTCGGGCTCCCTTTC     17593     C       CG
                              GTC CGGGCTCCC  TTC
                              ||| |||||||||  |||
                              CAG GCCCGAGGG  AAG
                                A       A_
GAM693  KIAA1765  5'  GTCTCGGTCTCCCCACAGCG   17594     C   G     TTCCC
                              GTC CGG CTCCCCCG    CG
                              ||| ||| |||||||    ||
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                                CAG GCC GAGGGGT    GC
                                  A  A     GTC__
GAM693  MAP3K6   3' GTCCTGGGCCCCACTCGCC   17595     C   TC     C
                                GTCC GGGC  CCCGTTC CC
                                |||| ||||  ||||||| ||
                                CAGG CCCG  GGGTGAG GG
                                  A   __     C
GAM693  MGC4655  3' GTCTCAGGCTCCTATATGGTTC 17596    C      CC____
          C                      GTC CGGGCTCC     GTTCC
                                ||| ||||||||     |||||
                                CAG GTCCGAGG     CAAGG
                                  A       ATATAC
GAM693  MP1      3' GTCTCGGGCTCCTGTGCAGTCG 17597    C      CC_  TCCC
          A                      GTC CGGGCTCC   GT   CGA
                                ||| ||||||||   ||   |||
                                CAG GCCCGAGG   CG   GCT
                                  A       ACA  TCA_
GAM693  PLCL2    5' CCCGGGCTTCGTCCCCG     17598        CCC   T
                                CCCGGGCT   CGT CCCCG
                                ||||||||   ||| |||||
                                GGGCCCGA   GCA GGGGC
                                    A__   _
GAM693  RIPK2    5' GTCCCGGGCGCTCAGGCCG   17599        TCCCC   C__
                                GTCCCGGGC    GTTC   CCG
                                |||||||||    ||||   |||
                                CAGGGCCCG    CGAG   GGC
                                     _____   TCC
GAM693  RIS1     5' GGGTTCCCCGCCGCCCCCG   17600    C     __
                                GGG TCCCCGT  TCCCCG
                                ||| |||||||  ||||||
                                CCC AGGGGCG  GGGGGC
                                  A      GC
GAM693  RNASE6PL 5' GTCCCGGGCTCTGCTTCGCGA 17601         CCC   CCC
                                GTCCCGGGCTC   GTT   CGA
                                ||||||||||   |||   |||
                                CAGGGCCCGAG   CGA   GCT
                                     A__   AGC
GAM693  SCAND1   3' GTCCCAGGCTCAGGCCCCCG  17602         CCC  T
                                GTCCCGGGCTC   GT CCCCG
                                ||||||||||   || |||||
                                CAGGGTCCGAG   CG GGGGC
                                     TC_  _
GAM693  SCAND1   3' GTCCCAGGCTCAGGCCCCCG  17602         CCC  T
                                GTCCCGGGCTC   GT CCCCG
                                ||||||||||   || |||||
                                CAGGGTCCGAG   CG GGGGC
                                     TC_  _
GAM693  SIAT4B   3' GTCCCGGGCCGGAGCCCCG   17603         ____
                                GTCCCGGGCT    CCCCG
                                |||||||||    |||||
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                                CAGGGCCCGG    GGGGC
                                      CCTC
GAM693  SSB-4    5' GTCCTGGACTCCCTGGATCGGG 17604    C      _________ TTCCC
           GAC                   CC GGGCTCCC       CG    C
                                 || ||||||||       ||    |
                                 GG CCTGAGGG       GC    G
                                  A       ACCTIIIA  CCCTT
GAM693  LOC115343 5' TCCTGGGCTCCCATTGGTCGGG 17605  C      __________ TTCCC
           GAACG                    GGGCTCCC       CG    CG
                                    ||||||||       ||    ||
                                    CCCGAGGG       GC    GC
                                 A       TAACCIIIA  CCCTT
GAM693  LOC124093 3' TCTCGGGCTCCCTGCAGCTGCC 17606    C       C  TCC__
           G                     TC CGGGCTCCC GT    CCG
                                 || |||||||| ||    |||
                                 AG GCCCGAGGG CG    GGC
                                  A        A  TCGAC
GAM693  LOC126432 5' CCGGGCTCCAGATGAGTTCCTC 17607         CC____    C
           G                     CCGGGCTCC     GTTCC CG
                                 |||||||||     ||||| ||
                                 GGCCCGAGG     CAAGG GC
                                       TCTACT    A
GAM693  LOC127943 3' GTCTCGGGCGTTCCCC     17608    C    TCCCC
                                 GTC CGGGC    GTTCCCC
                                 ||| |||||    |||||||
                                 CAG GCCCG    CAAGGGG
                                   A   ______
GAM693  LOC145725 3' TCCTGGGCTTCCTCCTGCCG   17609    C    _ _ GTTCC
                                 TCC GGGCT CC CC    CCG
                                 ||| ||||| || ||    |||
                                 AGG CCCGA GG GG    GGC
                                   A    A  A  AC___
GAM693  LOC145732 3' TCCTGGGCTTCCTCCTGCCG   17609    C    _ _ GTTCC
                                 TCC GGGCT CC CC    CCG
                                 ||| ||||| || ||    |||
                                 AGG CCCGA GG GG    GGC
                                   A    A  A  AC___
GAM693  LOC150378 3' GCCCTGGTGTCCTGTTCCCCGA 17610     C  GC   CC
                                 GTCC GG  TCC  GTTCCCCGA
                                 |||| ||  |||  |||||||||
                                 CGGG CC  AGG  CAAGGGGCT
                                    A  AC   A_
GAM693  LOC153579 3' GTCACCGATCCCCGTTCCCCG  17611    _   GC
                                 GTC CCGG  TCCCCGTTCCCCG
                                 ||| ||||  |||||||||||||
                                 CAG GGCT  AGGGGCAAGGGGC
                                   T   __
GAM693  LOC157858 3' TCCTCATGCCCTCCGTTCCCTG 17612    _ G   C      C
           A                     TCC CG GCTC CCGTTCCC GA
                                 ||| || |||| |||||||| ||
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                                AGG GT CGGG GGCAAGGG CT
                                  A A   A       A
GAM693  LOC163682 5'  CAGGTCCCTGTTCCCCG     17613      C   C
                                CGGG TCCC GTTCCCCG
                                |||| |||| ||||||||
                                GTCC AGGG CAAGGGGC
                                  _   A
GAM693  LOC165476 5'  GCCCCGGGCTTCTGCCTTC   17614          _ C_  G
                                GTCCCGGGCT C  CC TTC
                                |||||||||| |  || |||
                                CGGGGCCCGA G  GG AAG
                                     A AC  _
GAM693  LOC170394 5'  GTCCCGGGACTCTCTGTCCAGC 17615        _  _____  C  T  C
           ACCTCG                   TCCCGGG CTC    CC GT CC CG
                                |||||||  |||    || || || ||
                                AGGGCCC GAG    GG CG GG GC
                                    T   AGACA  T  T  A
GAM693  LOC196957 3'  TCCTGGGCTTCCTCCTGCT   17616     C    _  _  _
                                TCC GGGCT CC CC GTT
                                |||  ||||| || || |||
                                AGG CCCGA GG GG CGA
                                  A    A  A  A
GAM693  LOC196961 3'  TCCTGGGCTTCCTCCTGCT   17616     C    _  _  _
                                TCC GGGCT CC CC GTT
                                |||  ||||| || || |||
                                AGG CCCGA GG GG CGA
                                  A    A  A  A
GAM693  LOC197138 3'  TCCTGGGCTTCCTCCTGCT   17616     C    _  _  _
                                TCC GGGCT CC CC GTT
                                |||  ||||| || || |||
                                AGG CCCGA GG GG CGA
                                  A    A  A  A
GAM693  LOC203339 3'  GTCCCAGGCTTCCTGGGTCGGG 17617        C  _________  TTCCC
           GAC                    CCCGGGCT CC       CG    C
                                |||||||| ||       ||    |
                                GGGTCCGA GG       GC    G
                                    A  ACCCIIIA  CCCTT
GAM693  LOC204084 5'  GTCTGGCCGTCCCCGTTTCCCG 17618     CCG  __      C
                                GTC   GGC  TCCCCGTT CCCG
                                |||   |||  |||||||| ||||
                                CAG   CCG  AGGGGCAA GGGC
                                  A__   GC       A
GAM693  LOC220692 3'  GTCTCGCTCTGTTCCCCGA   17564     CCGG    CCC
                                GTC    GCTC   GTTCCCCGA
                                |||    ||||   |||||||||
                                CAG    CGAG   CAAGGGGCT
                                  AG__    A__
GAM693  LOC220827 3'  TCCTGGGCTCCCTGAGGTCGGG 17619   C      __________  TTCCC
           GAACG                  GGGCTCCC       CG    CG
                                 ||||||||       ||    ||
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                                CCCGAGGG       GC    GC
                               A       ACTCCIIIA  CCCTT
GAM693  LOC253069 3'  GTCCAGGGCTCCCTGCACTTCC 17620     C      C ___  C_
          TTCGA                   GTCC GGGCTCCC GT   TCC  CGA
                               |||| |||||||| ||   |||  |||
                               CAGG CCCGAGGG CG   AGG  GCT
                                 T       A  TGA   AA
GAM693  LOC254099 5'  GCCCTGGGCTCCCCCAGCTCTC 17621     C       __   CC
          G                     GTCC GGGCTCCCC  GTTC  CG
                               |||| |||||||||  ||||  ||
                               CGGG CCCGAGGGG  CGAG  GC
                                 A       GT    A_
GAM693  LOC254102 5'  GTCCCAGGCTCCGACCCG    17622          CCGTTC
                               GTCCCGGGCTCC     CCCG
                               ||||||||||||     ||||
                               CAGGGTCCGAGG     GGGC
                                      CT_____
GAM693  LOC254552 5'  GCCCCGGGCTCCTGTAGCCTCC 17623          CC  T_ _
          G                     GTCCCGGGCTCC  GT  CC CCG
                               |||||||||||  ||  || |||
                               CGGGGCCCGAGG  CA  GG GGC
                                      A_  TC  A
GAM693  LOC257127 3'  GTCCTGGAGCTCCCCGGCTC   17624     C  _      _
                               GTCC GG GCTCCCCG TTC
                               |||| || |||||||| |||
                               CAGG CC CGAGGGGC GAG
                                 A  T       C
GAM693  LOC51281  3'  GTCCTGGGTCCTCCCCAAGCCT 17582     C  __     TT  C
          CG                    GTCC GGG  CTCCCCG  CC CG
                               |||| |||  |||||||  || ||
                               CAGG CCC  GAGGGGT  GG GC
                                 A  AG      TC  A
GAM693  LOC51637  3'  GGGCTTCCTCCCCCGA      17625      CC  G
                               GGGCT  CC TTCCCCGA
                               |||||  || ||||||||
                               CCCGA  GG AGGGGGCT
                                  A_  _
GAM693  LOC90190  5'  CCCGGGCTCCCCAGCTCC    17626          _
                               CCCGGGCTCCCC GTTCC
                               |||||||||||| |||||
                               GGGCCCGAGGGG CGAGG
                                      T
GAM693  LOC91421  3'  TCCCGGGCTCCCCACTCCCTCC 17627          _   _
          G                     TCCCGGGCTCCCCG TTCC CCG
                               |||||||||||||| |||| |||
                               AGGGCCCGAGGGGT AGGG GGC
                                      G   A
GAM693  LOC96652  3'  GCCCTGGGCTTCGAACCCG   17628     C    CCC  TTC
                               GTCC GGGCT   CG   CCCG
                               |||| |||||   ||   ||||
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                                CGGG CCCGA   GC   GGGC
                                  A    A__  TT_
GAM694  ADM     3'  GCTCCGGGGGTCTCAGC     17631      AT  A
                                GCTCC  GG GTCTCAGC
                                |||||  || ||||||||
                                CGAGG  CC CAGAGTCG
                                  CC  _
GAM694  ALPP    3'  CGCTCTGTCGCCCAGGCTGCA  17632      CA  GA   CA
                                CGCTC  TG  GTCT  GCTGCA
                                |||||  ||  ||||  ||||||
                                GCGAG  AC  CGGG  CGACGT
                                  __  AG   TC
GAM694  BRCA1   5'  TGGATGCCTCTCAGCTGCA   17633     G___
                                TGGA   TCTCAGCTGCA
                                ||||   ||||||||||
                                ACCT   AGAGTCGACGT
                                  ACGG
GAM694  BRCA1   3'  TGGATGCCTCTCAGCTGCA   17633     G___
                                TGGA   TCTCAGCTGCA
                                ||||   ||||||||||
                                ACCT   AGAGTCGACGT
                                  ACGG
GAM694  CELL    3'  CCGCTTCATGGAGCTGCTG   17634      C       CTCA
                                CCGCT CATGGAGT   GCTG
                                ||||| ||||||||   ||||
                                GGCGA GTACCTCG   CGAC
                                  A       A___
GAM694  CHST6   3'  CTCCTCTATCTCTCAGCTG   17635     A_  GAG
                                CTCC  TG   TCTCAGCTG
                                ||||  ||   |||||||||
                                GAGG  AT   AGAGTCGAC
                                  AG  AG_
GAM694  DDX24   5'  CCGCTGTACCTCAGCTGC    17636      CCAT GAG
                                CCGCT   G   TCTCAGCTGC
                                |||||   |   ||||||||||
                                GGCGA   C   GGAGTCGACG
                                  _____ AT_
GAM694  DLEC1   3'  GCTCCACACTTAGCTG      17637        GAGT  C
                                GCTCCATG   CT AGCTG
                                ||||||||   || |||||
                                CGAGGTGT   GA TCGAC
                                     _____  A
GAM694  DLEC1   3'  GCTCCACACTTAGCTG      17637        GAGT  C
                                GCTCCATG   CT AGCTG
                                ||||||||   || |||||
                                CGAGGTGT   GA TCGAC
                                     _____  A
GAM694  FBXW1B  3'  CCAGCTTCATAACTCAGCTG  17638   _   C    AGT
                                CC GCT CATGG   CTCAGCTG
                                || ||| |||||   ||||||||
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                                GG CGA GTATT   GAGTCGAC
                                 T   A    ___
GAM694  FBXW1B   3'  CCAGCTTCATAACTCAGCTG   17638    _  C    AGT
                                CC GCT CATGG   CTCAGCTG
                                || ||| |||||   ||||||||
                                GG CGA GTATT   GAGTCGAC
                                 T   A    ___
GAM694  FBXW1B   3'  CCAGCTTCATAACTCAGCTG   17638    _  C    AGT
                                CC GCT CATGG   CTCAGCTG
                                || ||| |||||   ||||||||
                                GG CGA GTATT   GAGTCGAC
                                 T   A    ___
GAM694  FUT6     5'  CCGCTCCTGGACACTGCTGC   17639       A   GT  CA
                                CCGCTCC TGGA  CT  GCTGC
                                ||||||| ||||  ||  |||||
                                GGCGAGG ACCT  GA  CGACG
                                    _   GT  __
GAM694  HMG20A   3'  TCCAAAGATCTCAGCTG     17640     T   G
                                TCCA GGA TCTCAGCTG
                                |||| ||| |||||||||
                                AGGT TCT AGAGTCGAC
                                  T   _
GAM694  IL1R1    3'  GCTCCATGGGCTTCTGGCTG   17641        A TC  A_
                                GCTCCATGG G  TC  GCTG
                                ||||||||| |  ||  ||||
                                CGAGGTACC C  AG  CGAC
                                     _ GA  AC
GAM694  IL5      3'  CTCCAAAATCTTTGGCTGCA   17642      TG     CA_
                                CTCCA  GAGTCT   GCTGCA
                                |||||  ||||||   ||||||
                                GAGGT  TTTAGA   CGACGT
                                   __     AAC
GAM694  JRK      3'  GCGTTCTGGAATCTCAGCTGCA 17643    TCCA
                                GC   TGGAGTCTCAGCTGCA
                                ||   ||||||||||||||||
                                CG   ACCTTAGAGTCGACGT
                                 CAAG
GAM694  PCDH11X  5'  CCGCTCCACGGAGACTGC    17644          TCTCA
                                CCGCTCCATGGAG    GCTGC
                                ||||||||||||    |||||
                                GGCGAGGTGCCTC    TGACG
                                      _____
GAM694  PCDH11Y  5'  CCGCTCCACGGAGACTGC    17644          TCTCA
                                CCGCTCCATGGAG    GCTGC
                                ||||||||||||    |||||
                                GGCGAGGTGCCTC    TGACG
                                      _____
GAM694  PXF      3'  GCCCCATGGGGCCTTGC     17645        A   CAGC
                                GCTCCATGG GTCT   TGC
                                |||||||| ||||   |||
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                                CGGGGTACC CGGA    ACG
                                     C   ____
GAM694  SCN1A    5'  GCCCATGAACAGCTGC      17646    T      GTCT
                                GC CCATGGA    CAGCTGC
                                || |||||||    |||||||
                                CG GGTACTT    GTCGACG
                                 _     ____
GAM694  SRGAP1   3'  CGTCCCATGGAGACAATTGCA  17647    CT       TCT   C
                                CG  CCATGGAG   CAG TGCA
                                ||  ||||||||   ||| ||||
                                GC  GGTACCTC   GTT ACGT
                                 AG       T__   A
GAM694  TNFSF11  3'  CCTCTCCACTTCAGCTGC    17648    G     GGAGTC
                                CC CTCCAT     TCAGCTGC
                                || ||||||     ||||||||
                                GG GAGGTG     AGTCGACG
                                 A     A_____
GAM694  TNFSF11  3'  CCTCTCCACTTCAGCTGC    17648    G     GGAGTC
                                CC CTCCAT     TCAGCTGC
                                || ||||||     ||||||||
                                GG GAGGTG     AGTCGACG
                                 A     A_____
GAM694  CIDEB    5'  CCAGCTCTGATTTCAGTTGCA  17649    _   CATG  GTC    C
                                CC GCTC    GA   TCAG TGCA
                                || ||||    ||   |||| ||||
                                GG CGAG    CT   AGTC ACGT
                                 T    A___  AA_    A
GAM694  CX46.6   3'  CCCTCCATGGGTTGCTGC    17650    G      A  CTCA
                                CC CTCCATGG GT    GCTGC
                                || |||||||| ||    |||||
                                GG GAGGTACC CA    CGACG
                                 _       _ A___
GAM694  CXYorf1  3'  GCTCTGACAGTCTCAGTTGCA  17651      CA  _      C
                                GCTC  TGG AGTCTCAG TGCA
                                ||||  ||| |||||||| ||||
                                CGAG  ACT TCAGAGTC ACGT
                                  __  G       A
GAM694  DKFZP434C131 3'  CCGCTCCAGGAGCCGCTGC    17652         T     TCA
                                CCGCTCCA GGAGTC   GCTGC
                                |||||||| ||||||   |||||
                                GGCGAGGT CCTCGG   CGACG
                                     _     ___
GAM694  DKFZp586I021 3'  GCTCATGGTCCAAGGCTG    17653      C   AG   CA_
                                GCTC ATGG  TCT   GCTG
                                |||| ||||  |||   ||||
                                CGAG TACC  AGG   CGAC
                                  _   __  TTC
GAM694  DNAJB11  3'  GCTCCTGGAGTCCTCTTGCA   17654       A       CAGC
                                GCTCC TGGAGTCT    TGCA
                                ||||| ||||||||    ||||
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                                CGAGG ACCTCAGG    ACGT
                                  _       AGA_
GAM694  FLJ10748  5'  CCCTCCACCCAGTCTCAGCTGC 17655    G     GG
            A                    CC CTCCAT  AGTCTCAGCTGCA
                                 || ||||||  ||||||||||||
                                 GG GAGGTG  TCAGAGTCGACGT
                                  _     GG
GAM694  FLJ11560  5'  TCCGTGGGTCCCGTTGCA    17656     A  A    AGC
                                 TCC TGG GTCTC   TGCA
                                 ||| ||| |||||   ||||
                                 AGG ACC CAGGG   ACGT
                                   C  _    CA_
GAM694  FLJ22035  5'  CCTTCCATCTGTTCAGCTGCA  17657    GC    GGA  C
                                 CC  TCCAT   GT TCAGCTGCA
                                 ||  |||||   || |||||||||
                                 GG  AGGTA   CA AGTCGACGT
                                  A_    GA_  _
GAM694  FLJ22814  3'  CGCTTCACGTTCAGCTGCA   17658     C    GAGTC
                                 CGCT CATG    TCAGCTGCA
                                 |||| ||||    |||||||||
                                 GCGA GTGC    AGTCGACGT
                                   A   A____
GAM694  GDF10     3'  GCTCTGTGTCTGCAGCTGCA   17659     CA  GA   _
                                 GCTC  TG  GTCT CAGCTGCA
                                 ||||  ||  |||| ||||||||
                                 CGAG  AC  CAGA GTCGACGT
                                   __ A_   C
GAM694  IKKE      3'  GCCCAGTCTCAGCTG       17660      CATGG
                                 GCTC    AGTCTCAGCTG
                                 ||||    ||||||||||
                                 CGGG    TCAGAGTCGAC
                                   _____
GAM694  KIAA1068  5'  GCTCCTTCTCAGCTGC      17661       ATGGAG
                                 GCTCC     TCTCAGCTGC
                                 |||||     ||||||||||
                                 CGAGG     AGAGTCGACG
                                   A_____
GAM694  KIAA1130  3'  CCAGCTCCACCCCTTCTCAGCT 17662    _     GGAG
            G                    CC GCTCCAT    TCTCAGCTG
                                 || |||||||    |||||||||
                                 GG CGAGGTG    AGAGTCGAC
                                  T      GGGA
GAM694  KIAA1161  5'  CTCCAGACTCAGCTGC      17663       TGGA T
                                 CTCCA    G CTCAGCTGC
                                 |||||    | |||||||||
                                 GAGGT    C GAGTCGACG
                                   ____ T
GAM694  KIAA1775  3'  GCTCCTGCTCTCAGCTGCA   17664      A  GAG
                                 GCTCC TG   TCTCAGCTGCA
                                 ||||| ||   ||||||||||
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                                CGAGG AC   AGAGTCGACGT
                                  _ G__
GAM694  KIAA1908  5'  CCCCTTCATGCCCAGCTGC   17665    G  C    GAGT
                                CC CT CATG    CTCAGCTGC
                                || || ||||    |||||||||
                                GG GA GTAC    GGGTCGACG
                                 G  A   ____
GAM694  TIZ       5'  TCCTGGAGTCTTAGCTG     17666     A       C
                                TCC TGGAGTCT AGCTG
                                ||| |||||||| |||||
                                AGG ACCTCAGA TCGAC
                                  _       A
GAM694  WBP11     3'  CTCCATGGGCCACTG       17667         A   TCA
                                CTCCATGG GTC   GCTG
                                |||||||| |||   ||||
                                GAGGTACC CGG   TGAC
                                    _   ___
GAM694  WNT10A    5'  CCGCTCCATGGGGCAGC     17668           A TCT
                                CCGCTCCATGG G   CAGC
                                |||||||||||  |   ||||
                                GGCGAGGTACC C   GTCG
                                      C ___
GAM694  LOC123435 3'  TCCATGAGATTCAGCTGCA   17669       G  TC
                                TCCATG AG  TCAGCTGCA
                                |||||| ||  |||||||||
                                AGGTAC TC  AGTCGACGT
                                   _ TA
GAM694  LOC144893 5'  GCTTCATGGAGTCTCATTGCA  17670     C          GC
                                GCT CATGGAGTCTCA  TGCA
                                ||| ||||||||||||  ||||
                                CGA GTACCTCAGAGT  ACGT
                                  A          A_
GAM694  LOC146988 5'  CCGCTCCAGGGAGTTTCA    17671         T    C
                                CCGCTCCA GGAGT TCA
                                |||||||| ||||| |||
                                GGCGAGGT CCTCA AGT
                                     C    A
GAM694  LOC148709 5'  CCGTGTGGGTCTCAGCTG    17672     CTCCA   A
                                CCG    TGG GTCTCAGCTG
                                |||    ||| ||||||||||
                                GGC    ACC CAGAGTCGAC
                                  AC___   _
GAM694  LOC152580 5'  TCTATGGTGCCGCAGCTGCA  17673    C    A   T
                                TC ATGG GTC CAGCTGCA
                                || |||| ||| ||||||||
                                AG TACC CGG GTCGACGT
                                 A   A   C
GAM694  LOC152762 3'  CCCTCAGCTTGGTCTCAGCTG  17674    G   CATGGA
                                CC CTC     GTCTCAGCTG
                                || |||     ||||||||||
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                                GG GAG     CAGAGTCGAC
                                 _  TCGAAC
GAM694  LOC154860 5'  CCCAGGCTCAGCTGC      17675     T  AGT
                                TCCA GG   CTCAGCTGC
                                |||| ||   |||||||||
                                GGGT CC   GAGTCGACG
                                  _ ___
GAM694  LOC163590 5'  CCGCTCCACACCGCTCGGCTGC 17676         GA T   A
          A                      CCGCTCCATG  G CTC GCTGCA
                                ||||||||||  | ||| ||||||
                                GGCGAGGTGT  C GAG CGACGT
                                      GG _  C
GAM694  LOC170261 3'  CCGCTTTGTGGATTAATTCATG 17677     CCA   GTC__  GC
          CA                     CCGCT   TGGA    TCA  TGCA
                                |||||   ||||    |||  ||||
                                GGCGA   ACCT    AGT  ACGT
                                   AAC    AATTA  __
GAM694  LOC196047 5'  CCCATGGAGTTCTCCCTG    17678         _  AG
                                TCCATGGAGT CTC  CTG
                                |||||||||| |||  |||
                                GGGTACCTCA GAG  GAC
                                     A  G_
GAM694  LOC200093 3'  GCTCTGACAGTCTCAGTTGCA  17651     CA  _      C
                                GCTC  TGG AGTCTCAG TGCA
                                ||||  ||| |||||||| ||||
                                CGAG  ACT TCAGAGTC ACGT
                                  __  G       A
GAM694  LOC257051 3'  CCGCTTTGTGGATTAATTCATG 17677     CCA   GTC__  GC
          CA                     CCGCT   TGGA    TCA  TGCA
                                |||||   ||||    |||  ||||
                                GGCGA   ACCT    AGT  ACGT
                                   AAC    AATTA  __
GAM694  LOC257364 3'  ACTCTATGGAGTCTTCCCTG   17679     C       _ AG
                                GCTC ATGGAGTCT C  CTG
                                |||| |||||||| |  |||
                                TGAG TACCTCAGA G  GAC
                                  A       A G_
GAM694  LOC55908  3'  CCGCTGTGTGGAGTCTCTCCTG 17680      CCA       AG
                                CCGCT   TGGAGTCTC  CTG
                                |||||   |||||||||  |||
                                GGCGA   ACCTCAGAG  GAC
                                   CAC       AG
GAM694  LOC56965  3'  GCTCCATGCAGCTGC      17681        GAGTCT
                                GCTCCATG     CAGCTGC
                                ||||||||     |||||||
                                CGAGGTAC     GTCGACG
                                     _______
GAM694  LOC91040  3'  GCTCTGACAGTCTCAGTTGCA  17651     CA  _      C
                                GCTC  TGG AGTCTCAG TGCA
                                ||||  ||| |||||||| ||||
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                                CGAG  ACT TCAGAGTC ACGT
                                  __  G       A
GAM694  LOC91179  5' CCGCGCCGTGGAGTCCGGGC  17682     T  A      CA
                                CCGC CC TGGAGTCT  GC
                                |||| || ||||||||  ||
                                GGCG GG ACCTCAGG  CG
                                  C  C       CC
GAM694  LOC92539  5' CTCTTTTATGGTAGGCAGCTGC 17683     C___   _ TCT
          A                      CTC   ATGG AG   CAGCTGCA
                                |||   |||| ||   ||||||||
                                GAG   TACC TC   GTCGACGT
                                  AAAA   A  C__
GAM694  LOC96597  5' CCGCCCCATGGAGTTGCTG   17684          CTCA
                                CCGCTCCATGGAGT   GCTG
                                ||||||||||||||   ||||
                                GGCGGGGTACCTCA   CGAC
                                       A___
GAM695  ABH       3'  TGGAAACTCACTTCTACCTTCC 17687          _ _  AC
                                TGGAAACTTACT C GCC  CC
                                |||||||||||| | |||  ||
                                ACCTTTGAGTGA G TGG  GG
                                       A A   AA
GAM695  BAK1      3'  AGAAGGCACTGTCACCCCCCA  17688     ACT   CGC
                                GGAA   TACT   CACCCCCCA
                                ||||   ||||   |||||||||
                                TCTT   GTGA   GTGGGGGGT
                                  CC_   CA_
GAM695  CDKN2D    3'  GGACGCTCCCCCCACCCCCCA  17689     AA  A   G
                                GGA  CTT CTC CCACCCCCCA
                                |||  ||| ||| ||||||||||
                                CCT  GAG GGG GGTGGGGGGT
                                  GC  _  _
GAM695  CDKN2D    3'  GGACGCTCCCCCCACCCCCCA  17689     AA  A   G
                                GGA  CTT CTC CCACCCCCCA
                                |||  ||| ||| ||||||||||
                                CCT  GAG GGG GGTGGGGGGT
                                  GC  _  _
GAM695  COL5A1    5'  TGGGGACCTCGGCACCCCCC   17690     AA  TTA   C
                                TGG  AC   CTCG CACCCCCC
                                |||  ||   |||| ||||||||
                                ACC  TG   GAGC GTGGGGGG
                                  CC  ___   C
GAM695  FBXL2     3'  TGGAAACCTATTAACATGCCTT 17691          ____ TC   AC
          CC                      TGGAAACTT   AC  GCC  CC
                                |||||||||   ||  |||  ||
                                ACCTTTGGA   TG  CGG  GG
                                     TAAT  TA   AA
GAM695  HTR2A     3'  TGAAAACTTGCTCAGTGTGCCT 17692          A  _____  AC
          TCC                       TGGAAACTT CTC    GCC  CC
                                |||||||||  |||    |||  ||
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                                ACTTTTGAA GAG    CGG  GG
                                     C   TCACA   AA
GAM695  IRS1     5'  GAAATCCACGCCGCCCCCC   17693      C  ACT    A
                                GAAA TT   CGCC CCCCCC
                                |||| ||   |||| ||||||
                                CTTT AG   GCGG GGGGGG
                                  _ GT_    C
GAM695  SPTA1    3'  TAGAAACTTTGACACCCCTCA  17694          ACTCGC     C
                                TGGAAACTT     CACCCC CA
                                |||||||||     |||||| ||
                                ATCTTTGAA     GTGGGG GT
                                     ACT___     A
GAM695  TDGF1    3'  TGGAAACTTGCCCTTCCA    17695         A   G_
                                TGGAAACTT CTC  CCA
                                ||||||||| |||  |||
                                ACCTTTGAA GGG  GGT
                                     C   AA
GAM695  C14orf4  5'  TGGGGGCCTCCGCCACCCCCC  17696     AAA   A T
                                TGG   CTT C CGCCACCCCCC
                                |||   ||| | ||||||||||
                                ACC   GGA G GCGGTGGGGGG
                                  CCC   _ _
GAM695  C6orf5   3'  TGAAAACTCAGTCACTCC    17697          C    CA
                                TGGAAACTTA TCGC  CC
                                |||||||||| ||||  ||
                                ACTTTTGAGT AGTG  GG
                                     C    A_
GAM695  ETR101   3'  TGGGAACCTACTGGGCACC   17698     A       CGC
                                TGG AACTTACT   CACC
                                ||| ||||||||   ||||
                                ACC TTGGATGA   GTGG
                                  C       CCC
GAM695  FAM8A1   3'  TGAAAACTTACTCCCC      17699           CGCCAC
                                TGGAAACTTACT     CCCC
                                ||||||||||||     ||||
                                ACTTTTGAATGA     GGGG
                                                 _______
GAM695  FLJ10540 5'  TGGCCGCCCCTCGCCACCCTCC 17700     AAA   A        C
                                TGG   CTT CTCGCCACCC CC
                                |||   ||| |||||||||| ||
                                ACC   GGG GAGCGGTGGG GG
                                  GGC   _         A
GAM695  FLJ21276 3'  TGGAAACTTGCCATTTTCCCA  17701         ACTC    CCC_
                                TGGAAACTT    GCCA    CCCA
                                |||||||||    ||||    ||||
                                ACCTTTGAA    CGGT    GGGT
                                     _____    AAAA
GAM695  KIAA0607 3'  GGAGGTTTCCCCACCCCCCA  17702     AACTTAC  G
                                GGA       TC CCACCCCCCA
                                |||       || ||||||||||
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                                CCT      AG GGTGGGGGGT
                                  CCAA___  G
GAM695  KIAA0660  3'  TGGAAACTCAAAGAATACTTTC 17703        _______  CG
              CA                   TGGAAACTT      ACT  CCA
                                   |||||||||      |||  |||
                                   ACCTTTGAG      TGA  GGT
                                        TTTCTTA   AA
GAM695  LGP1      3'  TGGGGACATTAACCCCCC    17704     AA  _  CTCGCC
                                   TGG  AC TTA     ACCCCCC
                                   |||  || |||     |||||||
                                   ACC  TG AAT     TGGGGGG
                                     CC  T  _______
GAM695  MGC10960  3'  TGGAAACTGCTTTCCTCCCC  17705       TA  CG  A
                                   TGGAAACT  CT  CC CCCC
                                   ||||||||  ||  || ||||
                                   ACCTTTGA  GA  GG GGGG
                                        C_  AA  A
GAM695  NME3      3'  TGGAGAGGCCTGCGCCACCCTC 17706     AACTTA  _      C
              CA                   TGGA     CT CGCCACCC CCA
                                   ||||     || |||||||| |||
                                   ACCT     GA GCGGTGGG GGT
                                     CTCCG_  C       A
GAM695  RBBP1     3'  TGAAAACTTATTCACAATTCCA 17707         C    CACCCC
                                   TGGAAACTTA TCGC     CCA
                                   |||||||||| ||||     |||
                                   ACTTTTGAAT AGTG     GGT
                                         A    TTAA__
GAM695  RBBP1     3'  TGAAAACTTATTCACAATTCCA 17707         C    CACCCC
                                   TGGAAACTTA TCGC     CCA
                                   |||||||||| ||||     |||
                                   ACTTTTGAAT AGTG     GGT
                                         A    TTAA__
GAM695  LOC138399 5'  TGGAAACCTGCTCCCTTCC   17708         A   G  AC
                                   TGGAAACTT CTC CC  CC
                                   ||||||||| ||| ||  ||
                                   ACCTTTGGA GAG GG  GG
                                        C   _  AA
GAM695  LOC144305 3'  TGGCAAACTTCACCACCTCC  17709     _    TAC       C
                                   TGG AAACT   TCGCCACC CC
                                   ||| |||||   |||||||| ||
                                   ACC TTTGA   AGTGGTGG GG
                                     G     ___        A
GAM695  LOC146669 3'  GGAAATCCCAGGCCACCCCC  17710      _   CTC
                                   GGAAA CTTA   GCCACCCCC
                                   ||||| ||||   |||||||||
                                   CCTTT GGGT   CGGTGGGGG
                                      A    C__
GAM695  LOC150372 3'  TGGAAACTCTGCTGCCAGAATC 17711         A_  C    CC__
              CCC                    TGGAAACTT  CT GCCA    CCCC
                                     |||||||||  || ||||    ||||
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                                ACCTTTGAG  GA CGGT   GGGG
                                     AC  _   CTTA
GAM695  LOC150418 5'  TGAAAGCTTGACCTGCGCCCCC 17712      A  _  TC  CA
          CA                    TGGAA CTT AC  GC  CCCCCCA
                                |||||| ||| ||  ||  |||||||
                                ACTTT GAA TG  CG  GGGGGGT
                                   C   C  GA  C_
GAM695  LOC219401 5'  TGGAAACTGCCGCAGCGCTCCC 17713        TAC   CACCC_
                                TGGAAACT   TCGC     CCC
                                ||||||||   ||||     |||
                                ACCTTTGA   GGCG     GGG
                                     C__   TCGCGA
GAM695  LOC221935 3'  GGAAACTTGCCATACCC     17714        ACTC   CC
                                GGAAACTT   GCCA  CCC
                                ||||||||   ||||  |||
                                CCTTTGAA   CGGT  GGG
                                     _____   AT
GAM695  LOC256021 3'  TGAAAGCTTAACCCCC      17715      A   CTCGCC
                                TGGAA CTTA     ACCCCC
                                ||||| ||||     ||||||
                                ACTTT GAAT     TGGGGG
                                   C   _______
GAM695  LOC90906  3'  TGGAAGCTCACTGGTGTCCTCC 17716      A     CGCCA  C
                                TGGAA CTTACT    CC CC
                                ||||| ||||||    || ||
                                ACCTT GAGTGA    GG GG
                                   C     CCACA  A
GAM695  LOC91561  5'  GGAAACTCACTCTACCC     17717          GCC
                                GGAAACTTACTC   ACCC
                                ||||||||||||   ||||
                                CCTTTGAGTGAG   TGGG
                                       A__
GAM696  WISP1     3'  TCGTGAAGATTCAGTGAGCT  17720         CA   AC
                                TCGTGGAGAT  TCG  GAGCT
                                ||||||||||  |||  |||||
                                AGCACTTCTA  AGT  CTCGA
                                     __  CA
GAM696  KIAA0252  3'  TCGTGGAGATCGGAGC      17721          ATCGAC
                                TCGTGGAGATC     GAGC
                                ||||||||||      ||||
                                AGCACCTCTAG     CTCG
                                       C_____
GAM696  KIAA0637  3'  CGTGGAGACACTGTGGTGAGCT 17722        T   CGAC__
                                CGTGGAGA CAT     GAGCT
                                |||||||| |||     |||||
                                GCACCTCT GTG     CTCGA
                                     _  ACACCA
GAM696  LOC148223 3'  GTGAAGATCAACGTGGCT    17723          T  ACGA
                                GTGGAGATCA CG    GCT
                                |||||||||| ||    |||
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                                CACTTCTAGT GC    CGA
                                      T  AC__
GAM696  LOC150113 3'  CCGTGGAGATTGGTGATGGAGC 17724          CATC  C_
             T                  TCGTGGAGAT    GA  GAGCT
                                ||||||||||    ||  |||||
                                GGCACCTCTA    CT  CTCGA
                                      ACCA  AC
GAM697  CDH1     3'  TACAGTGAGCTATGATCACAT  17727       TT  A  C
                                TACAGT  GC TA GATCACAT
                                ||||||  || || ||||||||
                                ATGTCA  CG AT CTAGTGTA
                                   CT  _  A
GAM697  GBE1     3'  GCTGTATTTGCATAAACCA   17728     ACA       C
                                GCT   GTTTGCATA GATCA
                                |||   ||||||||| |||||
                                CGA   TAAACGTAT TTGGT
                                  CA_       _
GAM697  GHR      3'  GCTATGGTTTGCATTCAAT   17729      CA       A
                                GCTA  GTTTGCAT CGAT
                                ||||  |||||||| ||||
                                CGAT  CAAACGTA GTTA
                                  AC       A
GAM697  MAP3K5   3'  CAGTGGTGCACGATCACAT   17730      T_   AT
                                CAGT  TGC  ACGATCACAT
                                ||||  |||  ||||||||||
                                GTCA  ACG  TGCTAGTGTA
                                  CC  __
GAM697  POLH     3'  GCTAAGTTTGCAACCAC     17731      C       TACG
                                GCTA AGTTTGCA    ATCAC
                                |||| ||||||||    |||||
                                CGAT TCAAACGT    TGGTG
                                  _      _____
GAM697  CENPJ    3'  TACTGTTACTTCATGATCACAT 17732     A   TG__   AC
                                TAC GTT    CAT  GATCACAT
                                ||| |||    |||  ||||||||
                                ATG CAA    GTA  CTAGTGTA
                                  A   TGAA  __
GAM697  KIAA0680 3'  GCTACAGTTTTCTAGGGTCACA 17733          GCA  CGA
             T                  GCTACAGTTT   TA   TCACAT
                                ||||||||||   ||   ||||||
                                CGATGTCAAA   AT   AGTGTA
                                     AG_  CCC
GAM697  KIAA1320 5'  GCTACAGTGAGCTGTGATCA   17734        TT  ATAC
                                GCTACAGT  GC    GATCA
                                ||||||||  ||    |||||
                                CGATGTCA  CG    CTAGT
                                     CT  ACA_
GAM697  KIAA1718 3'  GCTACAGTATTAAGATTACAT  17735        TTGCA  C   C
                                GCTACAGT    TA GAT ACAT
                                ||||||||    || ||| ||||
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                                CGATGTCA    AT CTA TGTA
                                    TA___  T  A
GAM697  KIAA1950  3'  GCAGTACAGTGGTATGATCACA 17736   __    TTGCA  C
          T                  GC  TACAGT    TA GATCACAT
                             ||  ||||||    || ||||||||
                             CG  ATGTCA    AT CTAGTGTA
                              TC     CC___  A
GAM697  MDS029    3'  GCTGCAGTTTGCAATATACCAC 17737    A       TACG
          AT                  GCT CAGTTTGCA   ATCACAT
                             |||  |||||||||   |||||||
                             CGA GTCAAACGT   TGGTGTA
                              C       TATA
GAM697  LOC145009 3'  GCTTACAGTGATGATCACA   17738    _    TTGCATAC
                             GCT ACAGT       GATCACA
                             |||  |||||       |||||||
                             CGA TGTCA       CTAGTGT
                              A    CTA_____
GAM697  LOC149182 5'  ACTGTAGTTTGCATCATCCCCA 17739    AC       ACGA_
          CAT                   GCT  AGTTTGCAT    TCACAT
                             |||  |||||||||    ||||||
                             TGA  TCAAACGTA    GGTGTA
                              CA       GTAGG
GAM698  CYP39A1   3'  AGATACGTTTACAATAAAGAA  17742    G       TAC_
                             AGA TACGTTTAC    GAGAA
                             |||  |||||||||   |||||
                             TCT ATGCAAATG    TTCTT
                              _       TTAT
GAM698  CYP3A43   3'  GAGATAGTCTTATGAGAACTA  17743    TAC    AC  C
                             GAG   GTTT  TA GAGAACTA
                             |||   ||||  || ||||||||
                             CTC   CAGA  AT CTCTTGAT
                              TAT    __  A
GAM698  CYP3A43   3'  GAGATAGTCTTATGAGAACTA  17743    TAC    AC  C
                             GAG   GTTT  TA GAGAACTA
                             |||   ||||  || ||||||||
                             CTC   CAGA  AT CTCTTGAT
                              TAT    __  A
GAM698  CYP3A43   3'  GAGATAGTCTTATGAGAACTA  17743    TAC    AC  C
                             GAG   GTTT  TA GAGAACTA
                             |||   ||||  || ||||||||
                             CTC   CAGA  AT CTCTTGAT
                              TAT    __  A
GAM698  IRS2      3'  AGGTAACATCTGCGAGAACT   17744    A  _    ACTA
                             AG GTA CGTTT    CGAGAACT
                             ||  ||| |||||   ||||||||
                             TC CAT GTAGA    GCTCTTGA
                              _  T    C___
GAM698  NDUFS2    5'  AGGGTCGTTTACCGTCGAACT  17745    A  A       ACGA
                             AG GT CGTTTACT    GAACT
                             ||  ||  ||||||||   |||||
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                                TC CA GCAAATGG   CTTGA
                                 C  _      CAG_
GAM698  PSKH1    3'  AGGATACGTTTACAAACT   17746   AG      TACGA
                                AG  TACGTTTAC   GAACT
                                ||  |||||||||   |||||
                                TC  ATGCAAATG   TTTGA
                                 CT      _____
GAM698  LOC204119 5'  GAGTGTTTGAGAACT     17747     AC   ACTAC
                                GAGT  GTTT   GAGAACT
                                ||||  ||||   |||||||
                                CTCA  CAAA   CTCTTGA
                                  __   _____
GAM699  MAP3K7   5'  GGGTGAGACCCGCGCCCACCCG 17750    CA     TA
                                GGG  AGACCCG  CGTTCATCCG
                                |||  |||||||  ||||||||||
                                CCC  TCTGGGC  GCGGGTGGGC
                                  AC     __
GAM699  NCOR2    3'  GGACAGGGCCTGCGTCCATC   17751      A AC  GTA
                                GGGCA G  CC   CGTTCATC
                                |||||  |  ||   ||||||||
                                CCTGT C  GG   GCAGGTAG
                                  _ CC  AC_
GAM699  TJP1     5'  GGGCAAGACCCGGTGTC     17752          TAC
                                GGGCAAGACCCG   GTT
                                ||||||||||||   |||
                                CCCGTTCTGGGC   CAG
                                       CA_
GAM699  GAL3ST2  3'  GGGCAGGACCCATACTCC    17753      A       G
                                GGGCA GACCCGTAC TTC
                                |||||  ||||||||| |||
                                CCCGT CTGGGTATG AGG
                                  C       _
GAM699  KIAA0561 3'  GGGCAAGACCTGGCAGCC    17754         C_  C
                                GGGCAAGACC  GTA GTT
                                ||||||||||  ||| |||
                                CCCGTTCTGG  CGT CGG
                                      AC  _
GAM699  LOC151429 3'  GGGAGACCCGTGGCAGTCCG   17755    CA      AC  TCA
                                GGG  AGACCCGT  GT   TCCG
                                |||  ||||||||  ||   ||||
                                CCC  TCTGGGCA  CG   AGGC
                                  __      C_  TC_
GAM700  ADH7     3'  AAATGTTTATAAAGGT     17758        AAG
                                AAGTGTTT   GTGGAGGT
                                ||||||||   ||||||||
                                TTTACAAA   TATTTCCA
                                     ___
GAM700  ATP7A    3'  TAAAGTCTTTTTGAGAGGTT   17759       G   AAGGT
                                TAAAGT TTT    GGAGGTT
                                ||||||  |||    |||||||
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                                ATTTCA AAA    TCTCCAA
                                   G  AAC__
GAM700  CR1     3' CGAGGCAGAAGGGTGGGGGTT 17760   A  T  TT   _  A
                                A AG GT  AAGG TGG GGTT
                                | || ||  |||| ||| ||||
                                G TC CG  TTCC ACC CCAA
                                 C _ TC   C  C
GAM700  FZD10   3' TGAGGTTTGATGGAGGT    17761   A  T   AA
                                A AG GTTT  GGTGGAGGT
                                | || ||||  |||||||||
                                A TC CAAA  CTACCTCCA
                                 C _   __
GAM700  PPP1R12B 3' GCCTGGGAGGTGGAGGTT   17762     A__
                                GTTT  AGGTGGAGGTT
                                ||||  ||||||||||
                                CGGA  TCCACCTCCAA
                                  CCC
GAM700  PRY     3' AAAGTGTTGTTGGAGGTT   17763       TAAGG
                                AAAGTGTT   TGGAGGTT
                                ||||||||   ||||||||
                                TTTCACAA   ACCTCCAA
                                    CA___
GAM700  SOS2    3' TAAAGAGTTTAAGAACAGTT  17764     T      TGGA
                                TAAAG GTTTAAGG   GGTT
                                ||||| ||||||||   ||||
                                ATTTC CAAATTCT   TCAA
                                   T      TG__
GAM700  BA108L7.2 3' AAAGAGGTTAAGGTGGGGGTT 17765     TGT      A
                                AAAG  TTAAGGTGG GGTT
                                ||||  ||||||||| ||||
                                TTTC  AATTCCACC CCAA
                                  TCC       C
GAM700  C12orf4  3' AAGTGTTTAAGTTAGGGGTT  17766        GT_ A
                                AAGTGTTTAAG  GG GGTT
                                ||||||||||  || ||||
                                TTCACAAATTC  CC CCAA
                                      AAT _
GAM700  CCR6    3' TAAAATGTTTAAAAGGT    17767         GGTG
                                TAAAGTGTTTAA   GAGGT
                                ||||||||||||   |||||
                                ATTTTACAAATT   TTCCA
                                     _____
GAM700  CCR6    3' TAAAATGTTTAAAAGGT    17767         GGTG
                                TAAAGTGTTTAA   GAGGT
                                ||||||||||||   |||||
                                ATTTTACAAATT   TTCCA
                                     _____
GAM700  CHERP   3' AAGTGTCTTAGGCTGGTT   17768       A   GGA
                                AAGTGTTT AGGT  GGTT
                                |||||||| ||||  ||||
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                                TTCACAGA TCCG   CCAA
                                    A    A__
GAM700  CHODL     3'  TAAAATGTTTGAGGAGGTT    17769          AA  T
                                TAAAGTGTTT  GG GGAGGTT
                                ||||||||||  || |||||||
                                ATTTTACAAA  CT CCTCCAA
                                    __  _
GAM700  FLJ10493  3'  TAAAGTGTTTTAGGAAAAGTT  17770          A   T
                                TAAAGTGTTT AGG GGAGGTT
                                |||||||||| ||| |||||||
                                ATTTCACAAA TCC TTTTCAA
                                    A   _
GAM700  FLJ12085  3'  AAATGTTTAAGAAAATAGTT   17771           TG A
                                AAGTGTTTAAGG  G GGTT
                                ||||||||||||  | ||||
                                TTTACAAATTCT  T TCAA
                                      TT A
GAM700  FLJ20420  3'  TACTTTGTTAGGGTGGAGGTT  17772    AAG    TAA
                                TA   TGTT   GGTGGAGGTT
                                ||   ||||   ||||||||||
                                AT   ACAA   CCACCTCCAA
                                  GAA    TC_
GAM700  FLJ23476  3'  TAAAGGATAGTGGAGGT     17773      TG TTAA
                                TAAAG  T    GGTGGAGGT
                                |||||  |    |||||||||
                                ATTTC  A    TCACCTCCA
                                   CT _____
GAM700  FLJ23548  3'  TAAAGTGTTTAGAAAATAG    17774           __
                                TAAAGTGTTTA  AGGTGG
                                ||||||||||  ||||||
                                ATTTCACAAAT  TTTATC
                                      CT
GAM700  FUK       3'  AGTAGGAGGTGGAGGTT     17775     TTTA
                                AGTG    AGGTGGAGGTT
                                ||||    ||||||||||
                                TCAT    TCCACCTCCAA
                                  CC__
GAM700  GTF2E1    3'  TAAACTGTTTCCTGAGGTT    17776     G    AAGGTG
                                TAAA TGTTT     GAGGTT
                                |||| |||||     ||||||
                                ATTT ACAAA     CTCCAA
                                  G    GGA___
GAM700  HSPC065   3'  AATCCCAGAGGTGGAGGTT    17777     G  TA
                                AGT TT  AGGTGGAGGTT
                                ||| ||  ||||||||||
                                TTA GG  TCCACCTCCAA
                                  G  TC
GAM700  KIAA1323  3'  TAAAGTATTTATAATTAGGTT  17778          AG  GG
                                TAAAGTGTTTA  GT  AGGTT
                                ||||||||||  ||  |||||
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                                ATTTCATAAAT  TA  TCCAA
                                      AT  A_
GAM700  KIAA1377  3'  AGGTTTAATAAAGAGGTT    17779    T     GGT
                                AG GTTTAA   GGAGGTT
                                || ||||||   |||||||
                                TC CAAATT   TCTCCAA
                                 _     ATT
GAM700  KIAA1906  3'  AAATGTTTGGTTCAGGTT    17780        AA   GG
                                AAGTGTTT  GGT  AGGTT
                                ||||||||  |||  |||||
                                TTTACAAA  CCA  TCCAA
                                    __  AG
GAM700  MGC9912   3'  ATCCAGGAGGTGGAGGTT    17781       __
                                GTTTA  AGGTGGAGGTT
                                |||||  ||||||||||
                                TAGGT  TCCACCTCCAA
                                   CC
GAM700  PRAX-1    3'  AAGGTCAAGGTGGGGGTT    17782     T  T      A
                                AAG GTT AAGGTGG GGTT
                                ||| ||| ||||||| ||||
                                TTC CAG TTCCACC CCAA
                                  _  _      C
GAM700  PREI3     3'  TAAAGTAGTTTGAAGATAAGGT 17783        _   _     G
          T                      TAAAGT GTTT AAGGTG AGGTT
                                ||||||| |||| |||||| |||||
                                ATTTCA CAAA TTCTAT TCCAA
                                   T   C    _
GAM700  RAI15     3'  AGGTCTGGTGGGGGTT      17784    T    AA    A
                                AG GTTT  GGTGG GGTT
                                || ||||  ||||| ||||
                                TC CAGA  CCACC CCAA
                                  _   __    C
GAM700  RNF8      3'  GTCTGGGAGGTGGAGGTT    17785      A__
                                GTTT   AGGTGGAGGTT
                                ||||   ||||||||||
                                CAGA   TCCACCTCCAA
                                  CCC
GAM700  RNO2      5'  ACACGCAAGGTGGAGGTT    17786   TG T
                                G  T TAAGGTGGAGGTT
                                |  | ||||||||||||
                                T  G GTTCCACCTCCAA
                                 GT C
GAM700  SCYA16    3'  GCCTGGGAGGTGGAGGTT    17762      A__
                                GTTT   AGGTGGAGGTT
                                ||||   ||||||||||
                                CGGA   TCCACCTCCAA
                                  CCC
GAM700  TRIP-Br2  3'  GTGTCTGCGTGGAGGTT     17787       AAG
                                GTGTTT   GTGGAGGTT
                                ||||||   ||||||||
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                                CACAGA   CACCTCCAA
                                   CG_
GAM700   LOC122258 3'  GGAGGCTGGTGGGTGGGGGTT  17788   A  T   TAA_    A
                                A AG GTT    GGTGG GGTT
                                | || |||    ||||| ||||
                                C TC CGA    CCACC CCAA
                                 C  _   CCAC     C
GAM700   LOC134265 3'  AAGTGTTTGTAAAAGGTT    17789        AAGGT
                                AAGTGTTT    GGAGGTT
                                ||||||||    |||||||
                                TTCACAAA    TTTCCAA
                                     CAT__
GAM700   LOC146901 3'  AGAATCTGGAAGGTGGAGGTT  17790    T    __
                                AG GTTT  AAGGTGGAGGTT
                                || ||||  ||||||||||||
                                TC TAGA  TTCCACCTCCAA
                                 T   CC
GAM700   LOC149401 5'  TAAAGTGTTTGAGATCAAA   17791         A   G
                                TAAAGTGTTT AGGT GAG
                                |||||||||| |||| |||
                                ATTTCACAAA TCTA TTT
                                      C   G
GAM700   LOC151201 3'  GCACCTGGGAGGTGGAGGTT   17792   TG   A__
                                G  TTT   AGGTGGAGGTT
                                |  |||   ||||||||||
                                C  GGA   TCCACCTCCAA
                                 GT   CCC
GAM700   LOC159160 3'  AAAGTGTTGTTGGAGGTT    17763        TAAGG
                                AAAGTGTT    TGGAGGTT
                                ||||||||    ||||||||
                                TTTCACAA    ACCTCCAA
                                     CA___
GAM700   LOC201304 3'  AAGTGTTTGAGGAAGTGGGTT  17793        A   T  A_
                                AAGTGTTT AGG GG  GGTT
                                |||||||| ||| ||  ||||
                                TTCACAAA TCC TC  CCAA
                                     C   T  AC
GAM700   LOC201627 3'  GCACCCGGGAGGTGGAGGTT   17794   TG   A__
                                G  TTT   AGGTGGAGGTT
                                |  |||   ||||||||||
                                C  GGG   TCCACCTCCAA
                                 GT   CCC
GAM700   LOC221663 5'  GCCCAGGAGGTGGAGGTT    17795      __
                                GTTTA  AGGTGGAGGTT
                                |||||  ||||||||||
                                CGGGT  TCCACCTCCAA
                                   CC
GAM700   LOC51652  3'  GTGTCAATGGAGGTT      17796      TAA
                                GTGTT   GGTGGAGGTT
                                |||||   ||||||||||
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                                CACAG   TTACCTCCAA
                                  ___
GAM701  AAT1    5'  CAGCGGGTCAGGCCTGGC    17799       A   AAGC
                                CAGCGGGT CAGG   GGT
                                |||||||| ||||   |||
                                GTCGCCCA GTCC   CCG
                                    _   GGA_
GAM701  ALAD    5'  CAGTGGGCACAGGGGCATCAG  17800    C      AA  G
                                CAG GGGTACAGG  GCG TAG
                                ||| |||||||||  ||| |||
                                GTC CCCGTGTCC  CGT GTC
                                  A       C_  A
GAM701  ARHGAP6  5'  AGGTCCAGGAGGCGGTAGCC  17801     A    A
                                GGGT CAGGA GCGGTAGCC
                                |||| ||||| |||||||||
                                TCCA GTCCT CGCCATCGG
                                  G    C
GAM701  BLMH    5'  GCGGGGTAACGGTAGC      17802      TACAG A
                                GCGGG    G AGCGGTAGC
                                |||||    | |||||||||
                                CGCCC    C TTGCCATCG
                                  _____ A
GAM701  CDK5R2   3'  GCGGTAACAGCGGCGGTGGC  17803     GT   GAA    A
                                GCGG  ACAG   GCGGT GC
                                ||||  ||||   ||||| ||
                                CGCC  TGTC   CGCCA CG
                                  AT   GC_    C
GAM701  CHRNA5   3'  CAGTGAGTACAGGAAAGT    17804    C       GC
                                CAG GGGTACAGGAA  GGT
                                ||| ||||||||||  |||
                                GTC CTCATGTCCTT  TCA
                                  A        __
GAM701  DCLRE1C  5'  CAGTGGGACAGGAAGTAGGC  17805    C  T     C_
                                CAG GGG ACAGGAAG  GGT
                                ||| ||| ||||||||  |||
                                GTC CCC TGTCCTTC  CCG
                                  A  _      AT
GAM701  GDF2    5'  AGCGGGCACGGGGAGGAGC   17806       A_  AGC  T
                                AGCGGGTAC  GGA   GG AGC
                                |||||||||  |||   || |||
                                TCGCCCGTG  CCT   CC TCG
                                    CC   ___  _
GAM701  GNAI2   3'  GGGTACAAAGTCGGCGGTGGCC 17807       AA__    A
                                GGGTACAGG   GCGGT GCC
                                |||||||||   ||||| |||
                                CCCATGTTT   CGCCA CGG
                                    CAGC    C
GAM701  GNG5    5'  GCGGGTACCAGGAGGT      17808       _   AGC
                                GCGGGTAC AGGA   GGT
                                |||||||| ||||   |||
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                                CGCCCATG TCCT   CCA
                                    G   ___
GAM701  HMGA1   3'  CAGCAGGTGCAGGGTGCGGC  17809       A   AA
                                CAGCGGGT CAGG  GCGGT
                                |||||||| ||||  |||||
                                GTCGTCCA GTCC  CGCCG
                                    C   CA
GAM701  HNF3B   3'  CAGCGGGTGAAGGAAGACTGC  17810       AC    _ G
                                CAGCGGGT  AGGAAG C GT
                                ||||||||  |||||| | ||
                                GTCGCCCA  TCCTTC G CG
                                    CT     T A
GAM701  LTA     5'  CAGCAGGTGCAGGAGGGAC   17811       A    A C  TA
                                CAGCGGGT CAGGA G GG  GC
                                |||||||| ||||| | ||  ||
                                GTCGTCCA GTCCT C CC  TG
                                    C   _ _ __
GAM701  MAF     5'  CAGCGGGCTGTGCTGGGTGGCC 17812       ACAGGAA __   A
                                CAGCGGGT      GC  GGT GCC
                                ||||||||      ||  ||| |||
                                GTCGCCCG      CG  CCA CGG
                                    ACA____  AC   C
GAM701  MBD3    3'  CAGCGGGCATGGGGAGGAGC  17813       CA_   AGC  T
                                CAGCGGGTA   GGA   GG AGC
                                |||||||||   |||   || |||
                                GTCGCCCGT   CCT   CC TCG
                                     ACC  ___  _
GAM701  MSN     3'  CAGGCACAGAGTGGGGGGTGGT 17814        AAGC_____   A
          GGCC                  CGGGTACAGG       GGT GCC
                                ||||||||||       ||| |||
                                GTCCGTGTCT       CCA CGG
                                   CACCCCCCA   C
GAM701  MYLK    5'  CAGTGGGACAGGAAAGGC   17815    C   T      C
                                CAG GGG ACAGGAAG GGT
                                ||| ||| |||||||| |||
                                GTC CCC TGTCCTTT CCG
                                  A  _      _
GAM701  MYLK    5'  CAGTGGGACAGGAAAGGC   17815    C   T      C
                                CAG GGG ACAGGAAG GGT
                                ||| ||| |||||||| |||
                                GTC CCC TGTCCTTT CCG
                                  A  _      _
GAM701  MYLK    5'  CAGTGGGACAGGAAAGGC   17815    C   T      C
                                CAG GGG ACAGGAAG GGT
                                ||| ||| |||||||| |||
                                GTC CCC TGTCCTTT CCG
                                  A  _      _
GAM701  PTK7    5'  GCGGGCACAGGAGGCGGAGC  17816         A   T
                                GCGGGTACAGGA GCGG AGC
                                |||||||||||| |||| |||
```

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                                CGCCCGTGTCCT CGCC TCG
                                      C   _
GAM701  PYGB     3'  CAGTGGTGGTCAGGGTGGTGGC 17817     CG__  A   AAGC  A
            C                    CAG   GGT CAGG   GGT GCC
                                 |||   ||| ||||   ||| |||
                                 GTC   CCA GTCC   CCA CGG
                                   ACCA  _   CA__  C
GAM701  AGS3     5'  GGGCACAGGGCCTTAGC     17818        AA  GG
                                 GGGTACAGG  GC  TAGC
                                 |||||||||  ||  ||||
                                 CCCGTGTCC  CG  ATCG
                                      __ GA
GAM701  FGD3     5'  GCGGGCACAGGCGCCTGGC   17819         AA  __
                                 GCGGGTACAGG  GC  GGT
                                 ||||||||||  ||  |||
                                 CGCCCGTGTCC  CG  CCG
                                       G_ GA
GAM701  FLJ00024 5'  CAGCGGGTGCAGCAGCC     17820        ACAGGAA
                                 CAGCGGGT      GCGGTAGCC
                                 ||||||||      |||||||||
                                 GTCGCCCA      CGTCGTCGG
                                      ________
GAM701  FLJ10901 3'  AGTGGGACAGGAGGGC      17821    C   T     A C
                                 AG GGG ACAGGA G GGT
                                 || ||| |||||| | |||
                                 TC CCC TGTCCT C CCG
                                   A  _     _ _
GAM701  FLJ32771 3'  GGGTACAGACAGTAGC      17822        GAA
                                 GGGTACAG   GCGGTAGC
                                 ||||||||   ||||||||
                                 CCCATGTC   TGTCATCG
                                      ____
GAM701  KCNT1    3'  CAGATGGCTTCCAGGAAGTGGT 17823     CG   A__      C
                                 CAG  GGT   CAGGAAG GGT
                                 |||  |||   ||||||| |||
                                 GTC  CCG   GTCCTTC CCA
                                   TA   AAG      A
GAM701  KIAA0673 5'  AGCGGGTGCAGGAGGGC     17824        A    A C
                                 AGCGGGT CAGGA G GGT
                                 ||||||| ||||| | |||
                                 TCGCCCA GTCCT C CCG
                                     C    _ _
GAM701  KIAA1089 3'  GGGCACAGGAGACCGTGC    17825          AG G  A
                                 GGGTACAGGA  C GT GC
                                 ||||||||||  | || ||
                                 CCCGTGTCCT  G CA CG
                                       CT G  _
GAM701  KIAA1190 3'  CAGCGGGTGCACGGGTGCAGC  17826         A  _  AA
                                 CAGCGGGT CA GG  GCGGT
                                 |||||||| || ||  |||||
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                                GTCGCCCA GT CC  CGTCG
                                    C  G  CA
GAM701  KIAA1322  3'  AGCGGGTATGGCAGGCATGGCT 17827      ___   AA_____ GGTA
           ACCGC                  GGGTA  CAGG     GC   GC
                                |||||  ||||     ||   ||
                                CCCAT  GTCC     CG   CG
                                  ACC   GTAIIIC  ATGG
GAM701  KIAA1643  5'  GCGGGTACGGGGGGCGCGCGGC  17828       A__  AA_
                                GCGGGTAC  GG  GCGGT
                                ||||||||  ||  |||||
                                CGCCCATG  CC  CGCCG
                                    CCC  GCG
GAM701  MGC15429  3'  CAGGGGGCAAAGCGGTGGC   17829    C   ACAG      A
                                CAG GGGT   GAAGCGGT GC
                                ||| ||||   |||||||| ||
                                GTC CCCG   TTTCGCCA CG
                                  C   ____      C
GAM701  MGC20806  5'  GCCGGGTACAGGAGACGGGGCC 17830   _       AG   TA
                                GC GGGTACAGGA  CGG  GCC
                                || ||||||||||  |||  |||
                                CG CCCATGTCCT  GCC  CGG
                                 G        CT   C_
GAM701  MGC34869  5'  CAGCTGGTGCAGGAAAGT   17831     G  A    GC
                                CAGC GGT CAGGAA  GGT
                                |||| ||| ||||||  |||
                                GTCG CCA GTCCTT  TCA
                                  A  C    __
GAM701  ST7L    3'  GCAGGTATAGGGCAATAGCC   17832       C  AA
                                GCGGGTA AGG  GCGGTAGCC
                                |||||||  |||  |||||||||
                                CGTCCAT TCC  CGTTATCGG
                                    A  __
GAM701  ST7L    3'  GCAGGTATAGGGCAATAGCC   17832       C  AA
                                GCGGGTA AGG  GCGGTAGCC
                                |||||||  |||  |||||||||
                                CGTCCAT TCC  CGTTATCGG
                                    A  __
GAM701  ST7L    3'  GCAGGTATAGGGCAATAGCC   17832       C  AA
                                GCGGGTA AGG  GCGGTAGCC
                                |||||||  |||  |||||||||
                                CGTCCAT TCC  CGTTATCGG
                                    A  __
GAM701  ZTL1    5'  CAGCGGGTGCAGGCGCG    17833        A  AA
                                CAGCGGGT CAGG  GCG
                                ||||||||  ||||  |||
                                GTCGCCCA GTCC  CGC
                                    C   G_
GAM701  ZTL1    5'  CAGCGGGTGCAGGCGCG    17833        A  AA
                                CAGCGGGT CAGG  GCG
                                ||||||||  ||||  |||
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                                GTCGCCCA GTCC  CGC
                                     C    G_
GAM701   LOC125268 3'  CAGCGAGTGCAGGCACCTGGC  17834        A    AAGC_
                                CAGCGGGT CAGG     GGT
                                |||||||| ||||     |||
                                GTCGCTCA GTCC     CCG
                                     C    GTGGA
GAM701   LOC128439 5'  GCGGGTACAGGGGTAAC     17835          AAGC
                                GCGGGTACAGG    GGTAGC
                                ||||||||||    ||||||
                                CGCCCATGTCC    CCATTG
                                          ____
GAM701   LOC146229 3'  CAGTGGGGCAGGGGACCACAGC 17836     C   TA    AA  G
            C                    CAG GGG  CAGG  GC GTAGCC
                                ||| |||  ||||  || ||||||
                                GTC CCC  GTCC  TG TGTCGG
                                  A  C_    CC  G
GAM701   LOC146712 5'  CAGCGGGCACGGGGGGT     17837          A  AAGC
                                CAGCGGGTAC GG    GGT
                                |||||||||| ||    |||
                                GTCGCCCGTG CC    CCA
                                      C  C___
GAM701   LOC149706 5'  AGCGGGGACAGGATGGGC     17838       T     AGC
                                AGCGGG ACAGGA   GGT
                                |||||| ||||||   |||
                                TCGCCC TGTCCT   CCG
                                    C     AC_
GAM701   LOC167040 5'  CAGCGGGTGTAAGGGCTGTGGG 17839        AC_   AA  G  A_
            C                    CAGCGGGT   AGG  GC GT  GC
                                ||||||||   |||  || ||  ||
                                GTCGCCCA   TCC  CG CA  CG
                                     CAT   __  A  CC
GAM701   LOC221935 3'  CAGTGGTGGAGAAGCGGTGGC  17840     C  GTACA       A
                                CAG GG     GGAAGCGGT GC
                                ||| ||     ||||||||| ||
                                GTC CC     TCTTCGCCA CG
                                  A  ACC__        C
GAM701   LOC245771 5'  AGTGGGACAGGAGGGC      17821     C   T     A C
                                AG GGG ACAGGA G GGT
                                || ||| |||||| | |||
                                TC CCC TGTCCT C CCG
                                 A   _     _ _
GAM701   LOC254057 3'  CAGCGGGTGCAGGGATGTGGCT 17841       A    AA________  GGTA
            ACG                    GCGGGT CAGG        GC    G
                                |||||| ||||        ||    |
                                CGCCCA GTCC        CG    C
                                    C    CTACAIIIC  ATGG
GAM701   LOC91353  3'  GGGTACAGGGAGAAGGGC    17842          ___   C
                                GGGTACAGG   AAG GGT
                                |||||||||   ||| |||
```

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                                CCCATGTCC   TTC CCG
                                     CTC  _
GAM701  LOC92573  5'  GGGTACAGAGTGGGACTAGC   17843        GA  C  ___
                                GGGTACAG  AG GG   TAGC
                                ||||||||  || ||   ||||
                                CCCATGTC  TC CC   ATCG
                                    __  A  CTG
GAM702  NYD-SP21  3'  TAATGAGGTGGCAACCACAGTT 17846        AA_   GAGATA
                                TAATGAGG   CAAC     AGTT
                                ||||||||   ||||     ||||
                                ATTACTCC   GTTG     TCAA
                                     ACC   GTG___
GAM702  SYNE-2    3'  TAATGAGAAACATCTGAG    17847          AC_
                                TAATGAGGAACA   GAG
                                ||||||||||||   |||
                                ATTACTCTTTGT   CTC
                                       AGA
GAM702  TJP2      3'  TAATGAGGAAAAATAG      17848         ACAAC     A
                                TAATGAGGA    GAGATA G
                                |||||||||    |||||| |
                                ATTACTCCT    TTTTAT C
                                     _____    _
GAM703  DBH       5'  TGAGGGCGGGCATGGCTGGGGT 17851        C   C   GTC
                                TGAGGGCG GCA GGC   GGT
                                |||||||| ||| |||   |||
                                ACTCCCGC CGT CCG   CCA
                                     C   A   ACC
GAM703  EGR4      5'  TGGGGGCGCGCGGGTGGC    17852    A      AC  C  C
                                TG GGGCGCGC  GG GT GGT
                                || ||||||||  || || |||
                                AC CCCGCGCG  CC CA CCG
                                 C      __  _  _
GAM703  EPHB1     5'  TGCGGGCGCGCGTGGGTG    17853    A      ACGGC  C
                                TG GGGCGCGC    GT GGTG
                                || ||||||||    || ||||
                                AC CCCGCGCG    CA CCAC
                                 G      _____  C
GAM703  FASN      5'  TGAGGGCGCGGGCGGCGGTGC  17854         CAC    T
                                TGAGGGCGCG   GGCG CGGTGC
                                ||||||||||   |||| ||||||
                                ACTCCCGCGC   CCGC GCCACG
                                     ___    C
GAM703  GNAO1     3'  GGGGGCAGGCGTCGGTG     17855     CGC   C
                                GGG   GCA GGCGTCGGTG
                                |||   ||| ||||||||||
                                CCC   CGT CCGCAGCCAC
                                 C__   _
GAM703  MAPT      5'  GAGGGCGCGCGCGGCGAGAGGG 17856          A    TC_  T
            C                    GAGGGCGCGC CGGCG   GG GC
                                ||||||||| |||||   || ||
```

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                                CTCCCGCGCG GCCGC   CC CG
                                      C    TCT  _
GAM703  MAPT    5'  GAGGGCGCGCGCGGCGAGAGGG 17856        A    TC_  T
           C                   GAGGGCGCGC CGGCG   GG GC
                               |||||||||| |||||   || ||
                               CTCCCGCGCG GCCGC   CC CG
                                      C    TCT  _
GAM703  MAPT    5'  GAGGGCGCGCGCGGCGAGAGGG 17856        A    TC_  T
           C                   GAGGGCGCGC CGGCG   GG GC
                               |||||||||| |||||   || ||
                               CTCCCGCGCG GCCGC   CC CG
                                      C    TCT  _
GAM703  MAPT    5'  GAGGGCGCGCGCGGCGAGAGGG 17856        A    TC_  T
           C                   GAGGGCGCGC CGGCG   GG GC
                               |||||||||| |||||   || ||
                               CTCCCGCGCG GCCGC   CC CG
                                      C    TCT  _
GAM703  SH3BP4  5'  CGGGGGCGCGCGCGGCTCCG  17857   A     A   GT
                               TG GGGCGCGC CGGC  CG
                               || |||||||| ||||  ||
                               GC CCCGCGCG GCCG  GC
                                C      C   AG
GAM703  ACAS2L  3'  TGAGGGCGGTGTGGGTCATGTG 17858       CGCAC  C   _
                               TGAGGGCG    GG GTCG GTG
                               ||||||||    || |||| |||
                               ACTCCCGC    CC CAGT CAC
                                    CACA_ _   A
GAM703  CPVL    5'  AGGGTGCGGCGCAGTCGGTGC  17859     C   CACG  _
                               AGGG GCG   GC GTCGGTGC
                               |||| |||   || ||||||||
                               TCCC CGC   CG CAGCCACG
                                 A  CG__  T
GAM703  FAM3A   5'  TGGGGGCGGGCGCGATCGGTGC 17860    A    C  ACG  _
                               TG GGGCG GC   GCG TCGGTGC
                               || ||||| ||   ||| |||||||
                               AC CCCGC CG   CGC AGCCACG
                                C    C  ___  T
GAM703  FLJ00024 3'  TGAGGGCGCACGTGGGGTCTGT 17861         AC  C   G
                               TGAGGGCGCGC  GG GTC GT
                               ||||||||||  || ||| ||
                               ACTCCCGCGTG  CC CAG CA
                                     CA  C   A
GAM703  FLJ20195 3'  TGGGGGCGCGCTTGGCGATCCG 17862    A      AC   _  G
           C                    TG GGGCGCGC  GGCG TC GT
                               || ||||||||  |||| || ||
                               AC CCCGCGCG  CCGC AG CG
                                C      AA   T  G
GAM703  PCYT2   3'  TGGGGGCGCACGCAGGAGCGGT 17863    A      A   CGT
           GC                    TG GGGCGCGC CGG   CGGTGC
                               || |||||||| |||   ||||||
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                                AC CCCGCGTG GTC   GCCACG
                                 C       C   CTC
GAM703  SLC37A1   5'  TGAGGGCGCCGCAGGT      17864         GCACGG   C
                                TGAGGGCGC     CGT GGT
                                |||||||||     ||| |||
                                ACTCCCGCG     GCG CCA
                                      _______   T
GAM703  LOC170370 5'  GAGTGCCCAGGGTGTCGGTGC  17865     C  G  C  C
                                GGG GC CA GG GTCGGTGC
                                ||| || || || ||||||||
                                CTC CG GT CC CAGCCACG
                                  A  G  C  A
GAM703  LOC255232 5'  TGAGGGCGTGCACAGCGC    17866         C
                                TGAGGGCG GCACGGCGT
                                |||||||| |||||||||
                                ACTCCCGC CGTGTCGCG
                                     A
GAM703  LOC51112  5'  TGGGGGCGCGCGCTGGCTGAAG 17867      AC_   GTC____    III
            ATGGTGCG                CGCGC   GGC      GGTGC   G
                                |||||   |||      |||||   |
                                GCGCG   CCG      CCACG   C
                                   CGA   ACTTCTA    III
GAM704  CENPF     3'  GATATAGTGCTTGTCA      17870        ACA  G
                                GATATAG   GC TTGTCA
                                |||||||   || ||||||
                                CTATATC   CG AACAGT
                                     A__  _
GAM704  NPAT      3'  TACAATATGGAATTGTC      17871         A  CAGC
                                TACGATAT GA    GTTGTC
                                |||||||| ||    ||||||
                                ATGTTATA CT    TAACAG
                                     C  _____
GAM705  ABR       3'  GCCCACGCCGGGCCG       17874     G GG
                                GCC C  ACGCCGGGCCG
                                ||| |  ||||||||||||
                                CGG G  TGCGGCCCGGC
                                  _ __
GAM705  ABR       3'  GCCCACGCCGGGCCG       17874     G GG
                                GCC C  ACGCCGGGCCG
                                ||| |  ||||||||||||
                                CGG G  TGCGGCCCGGC
                                  _ __
GAM705  ATP1A1    5'  GCCGGCGGCTCGGGCCGAT    17875     _   ACGC
                                GCCG CGG    CGGGCCGAT
                                |||| |||    |||||||||
                                CGGC GCC    GCCCGGCTA
                                  C   GA__
GAM705  BCL10     5'  GCCAGCCCGCGGGCCGAT     17876     _  GGA   C
                                GCC GC   CGC GGGCCGAT
                                ||| ||   ||| ||||||||
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                                CGG CG   GCG CCCGGCTA
                                 T  G__  _
GAM705  CMAR    5'  CGTGGACGCCAGGACGAT    17877    C        C
                                CG GGACGCCGGG CGAT
                                || |||||||||| ||||
                                GC CCTGCGGTCC GCTA
                                 A         T
GAM705  GAS1    5'  GCGGCGGACGCGGAGCCG    17878    C       C
                                GC GCGGACGC GGGCCG
                                || |||||||| ||||||
                                CG CGCCTGCG CTCGGC
                                 C       C
GAM705  HAP1    3'  GCCACGGAATGAGGCTGAT   17879        CGCC    C
                                GCCGCGGA    GGGC GAT
                                ||||||||    |||| |||
                                CGGTGCCT    TCCG CTA
                                     TAC_    A
GAM705  HCN2    3'  CGCGGACGGGGGGCCGGGCCG  17880        ____
                                CGCGGAC    GCCGGGCCG
                                |||||||    |||||||||
                                GCGCCTG    CGGCCCGGC
                                    CCCC
GAM705  PABPC1  5'  GCCGCAGAACGGGGTCGAT   17881        C  C   C
                                GCCGCGGA GC GGG CGAT
                                |||||||| || ||| ||||
                                CGGCGTCT TG CCC GCTA
                                     _ C   A
GAM705  PTEN    5'  GCCGCGGCCGCCGCCG      17882        A    GG
                                GCCGCGG CGCC  GCCG
                                ||||||| ||||  ||||
                                CGGCGCC GCGG  CGGC
                                    G   __
GAM705  SFRP5   5'  GCCGCGGAGGTCGCCCAGG   17883         ___   _
                                GCCGCGGA   CGCC GGG
                                ||||||||   |||| |||
                                CGGCGCCT   GCGG TCC
                                     CCA   G
GAM705  SORT1   5'  GCCGCCGACGCCGACACC    17884      G       _
                                GCCGC GACGCCGG GCC
                                ||||| |||||||| |||
                                CGGCG CTGCGGCT TGG
                                   G       G
GAM705  TARBP2  5'  GCCCGGAGTCGCGGCCG     17885     G   __  CG
                                GCC CGGA  CGC  GGCCG
                                ||| ||||  |||  |||||
                                CGG GCCT  GCG  CCGGC
                                  _   CA  __
GAM705  TARBP2  5'  GCCCGGAGTCGCGGCCG     17885     G   __  CG
                                GCC CGGA  CGC  GGCCG
                                ||| ||||  |||  |||||
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                                CGG GCCT  GCG  CCGGC
                                  _   CA  __
GAM705  APCL     3'  CGCGGCTGCGCCGGGCCGAT  17886     A__
                                CGCGG  CGCCGGGCCGAT
                                |||||  ||||||||||||
                                GCGCC  GCGGCCCGGCTA
                                   GAC
GAM705  ETAA16   5'  GCCACGAACCGCGGGCCGAT  17887       GC
                                GCCGCGGAC  CGGGCCGAT
                                |||||||||  ||||||||
                                CGGTGCTTG  GCCCGGCTA
                                      GC
GAM705  FLJ20584 3'  CCGGGCGCCGGGCGAT     17888    C  A     C
                                CCG GG CGCCGGGC GAT
                                ||| || |||||||| |||
                                GGC CC GCGGCCCG CTA
                                  _ _      _
GAM705  FLJ21313 5'  GCCGCGGACCTGGACACG    17889       GCC   _
                                GCCGCGGAC   GGGC CG
                                |||||||||   |||| ||
                                CGGCGCCTG   CCTG GC
                                     GA_    T
GAM705  FLJ22004 5'  GCCGCGGAGGCCCGGAGAT   17890       C   G  CC
                                GCCGCGGA GCC GG  GAT
                                |||||||| ||| ||  |||
                                CGGCGCCT CGG CC  CTA
                                     C   G  T_
GAM705  KIAA0476 5'  GCCGCGGGCGCCGCCG      17891       A   GG
                                GCCGCGG CGCC  GCCG
                                ||||||| ||||  ||||
                                CGGCGCC GCGG  CGGC
                                   C   __
GAM705  KIAA1822 3'  GCCACGGACCAGTACTGAT   17892       AC    _  C
                                GCCGCGG  GCCGG GC GAT
                                |||||||  ||||| || |||
                                CGGTGCC  TGGTC TG CTA
                                   __    A  A
GAM705  MGC19595 5'  CGCGGACGCTCACGAT      17893        _  GGC
                                CGCGGACGC CG   CGAT
                                |||||||||  ||   ||||
                                GCGCCTGCG GT   GCTA
                                     A  ___
GAM705  ZNF213   3'  GCCGATGGAGCGGGGCCGAT  17894     C_   C  C
                                GCCG  GGA GC GGGCCGAT
                                ||||  ||| || ||||||||
                                CGGC  CCT CG CCCGGCTA
                                  TA   _  C
GAM705  LOC129881 5'  GCCGCGGACGCCAGCCG     17895          G
                                GCCGCGGACGCCGG CCG
                                |||||||||||||| |||
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                                CGGCGCCTGCGGTC GGC
                                                _
GAM705  LOC130367 5'  GCTGCCACGCCGGGCCG     17896    C  GG
                                GC GC  ACGCCGGGCCG
                                || ||  ||||||||||
                                CG CG  TGCGGCCCGGC
                                 A  G_
GAM705  LOC138307 5'  GCTGCACAGCCTGGGCCGAT   17897    C   GAC  _
                                GC GCG   GCC GGGCCGAT
                                || |||   ||| ||||||||
                                CG CGT   CGG CCCGGCTA
                                 A  GT_   A
GAM705  LOC148534 5'  GCCGCGGGTTCCGGGCCG    17898       ACG
                                GCCGCGG   CCGGGCCG
                                |||||||   ||||||||
                                CGGCGCC   GGCCCGGC
                                    CAA
GAM705  LOC152559 5'  CCGCGGACGCTGCGCGA     17899         CGG  _
                                CCGCGGACGC   GC CGA
                                ||||||||||   || |||
                                GGCGCCTGCG   CG GCT
                                      A__  C
GAM705  LOC165257 5'  GCCGCGGACGCCCGCGCGCA  17900          _ G  _
                                GCCGCGGACGCC G GC CG
                                |||||||||||| | || ||
                                CGGCGCCTGCGG C CG GT
                                       G G  C
GAM705  LOC202781 5'  GCCGCGGAGGCCACCA      17901        C   GG
                                GCCGCGGA GCC  GCCG
                                |||||||| |||  ||||
                                CGGCGCCT CGG  TGGT
                                    C  __
GAM705  LOC256000 5'  GCGGCGGACGGGAAGCCGAT  17902    C      CC
                                GC GCGGACG  GGGCCGAT
                                || |||||||  ||||||||
                                CG CGCCTGC  TTCGGCTA
                                 C      CC
GAM706  ACP1     5'  GGCCCGGGCGCTGCG       17905          CCGTCG
                                GGCCCGGGCGCT     GCG
                                ||||||||||||     |||
                                CCGGGCCCGCGA     CGC
                                               _______
GAM706  ACP1     5'  GGCCCGGGCGCTGCG       17905          CCGTCG
                                GGCCCGGGCGCT     GCG
                                ||||||||||||     |||
                                CCGGGCCCGCGA     CGC
                                               _______
GAM706  CDK5R2   5'  GGCCCGGGCGCGCGGACTGGCG 17906          TC  TC__
            GG                    GGCCCGGGCGC  CG   GGCGGG
                                ||||||||||  ||   ||||||
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                                CCGGGCCCGCG  GC   CCGCCC
                                      C_  CTGA
GAM706  DIO3    3'  TGGTTTGAGGCGCTTGCACGTG 17907    CCC_     CC  _  GC
           GG                   TGG   GGGCGCT  GT CG  GGG
                                |||   |||||||  || ||  |||
                                ACC   TCCGCGA  CG GC  CCC
                                  AAAC      A_  T  A_
GAM706  EPB72   3'  TGGCCTGGGTGCTTAGGGCCCG 17908   C   C  T__________  TCGG
           CCGACG                C GGG GC        CCG   CG
                                | ||| ||        |||   ||
                                G CCC CG        GGC   GC
                                 A   A  AATCCCIIIG   GGCT
GAM706  LAMA4   5'  GGCTCGGGCGCTGTGGGCCCGC 17909   C     T__________  TCGG
           CGACG                 CGGGCGC        CCG   CG
                                 |||||||        |||   ||
                                 GCCCGCG        GGC   GC
                                A      ACACCCIIIG   GGCT
GAM706  LASS1   3'  GGCTCGGGCGCTCAGCGG    17910    C       CGTC
                                GGC CGGGCGCTC    GGCGG
                                ||| |||||||||    |||||
                                CCG GCCCGCGAG    TCGCC
                                  A       _____
GAM706  MARK3    5'  TGGCCCGGGCCGTCCCCCGGCG 17911          GC   G
           GG                   TGGCCCGGGC  TCC TCGGCGGG
                                ||||||||||  ||| ||||||||
                                ACCGGGCCCG  AGG GGCCGCCC
                                      GC   G
GAM706  PACE    5'  TGGCCCGGGGCTGACTGGTGGG 17912         C   CCGTC  C
                                TGGCCCGGG GCT    GG GGG
                                ||||||||| |||    || |||
                                ACCGGGCCC CGA    CC CCC
                                      _  CTGA_  A
GAM706  PIK3R3   5'  GGGCGCTCCCGCCGGG     17913         GT  G
                                GGGCGCTCC  CG CGGG
                                |||||||||  || ||||
                                CCCGCGAGG  GC GCCC
                                      __  G
GAM706  CENTA2   5'  TGGCCCGTGCGCTCCGCCCGG  17914        G        GG
                                TGGCCCG GCGCTCCGTC  CGG
                                |||||||  ||||||||||  |||
                                ACCGGGC CGCGAGGCGG  GCC
                                   A        __
GAM706  cerk    5'  TGGCCCGGGCGGCGGGCGGCGG 17915          CTC  T_
           G                    TGGCCCGGGCG   CG  CGGCGGG
                                ||||||||||   ||  |||||||
                                ACCGGGCCCGC   GC  GCCGCCC
                                      C__  CC
GAM706  CLIPR-59 3'  TGGCCCAGGTGCTGTGGGCCCG 17916      C  T__________  TCGG
           CCGACG                CCGGG GC        CCG   CG
                                |||||  ||        |||   ||
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                                GGTCC CG        GGC   GC
                                   A  ACACCCIIIG   GGCT
GAM706  DKFZp434A2417 5'  GGTCCCAAGGTCTGTCGGCGGG 17917    _     CGC  C
                                GG CCCGGG   TC GTCGGCGGG
                                || ||||||   || |||||||||
                                CC GGGTTC   AG CAGCCGCCC
                                 A     C__  A
GAM706  GOLPH3   5'  TGGCCGGGGCGTCGGCG      17918       C    GCTCC
                                TGGCC GGGC    GTCGGCG
                                ||||| ||||    |||||||
                                ACCGG CCCG    CAGCCGC
                                   _   _____
GAM706  MRF-1    3'  TGGCCCGGGTGTCCTGGGCCCG 17919       CG_ T_________   TCGG
           CCGACG                  CCGGG  C       CCG   CG
                                |||||  |       |||   ||
                                GGCCC  G       GGC   GC
                                   ACA GACCCIIIG   GGCT
GAM706  LOC149992 5'  GGCTTGGGCGCTCTGGGCCCGC 17920   CC      __________  TCGG
           CGACG                   GGGCGCTC       CG   CG
                                 ||||||||       ||   ||
                                 CCCGCGAG       GC   GC
                                AA       ACCCIIIGG  GGCT
GAM706  LOC253070 5'  TGGTCCGGGCGCCTGCGG    17921     C       CCGTCG
                                TGG CCGGGCGCT     GCGG
                                ||| |||||||||     ||||
                                ACC GGCCCGCGG     CGCC
                                  A       A_____
GAM707  BIN1     5'  CGGGGACAGAGGGAG       17924       CCAT
                                CGGGG   ACAGAGGGAG
                                |||||   ||||||||||
                                GCCCC   TGTCTCCCTC
                                   _____
GAM707  BIN1     5'  CGGGGACAGAGGGAG       17924       CCAT
                                CGGGG   ACAGAGGGAG
                                |||||   ||||||||||
                                GCCCC   TGTCTCCCTC
                                   _____
GAM707  BSN      3'  TCACAATACAGGGGGAG     17925       GGGCC     A
                                TCACG    ATACAG GGGAG
                                |||||    |||||| |||||
                                AGTGT    TATGTC CCCTC
                                   _____     C
GAM707  DLX2     3'  TCAAGGGGCCACGTGGGGGAG  17926     C       ACAGA
                                TCA GGGGCCAT    GGGAG
                                ||| ||||||||    |||||
                                AGT CCCCGGTG    CCCTC
                                  T       CACC_
GAM707  FOXO1A   5'  TCGCGGGGCCATCCACATCGAG 17927    A       __   GA
                                TC CGGGGCCAT  ACA  GGG
                                || |||||||||  |||  |||
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                              AG GCCCCGGTA  TGT  CTC
                               C       GG   AG
GAM707  GNA11    3'  CGAAGTGTACGGAGGGAGAG  17928      CCA   A
                              CGGGG   TAC GAGGGAGAG
                              |||||   ||| |||||||||
                              GCTTC   ATG CTCCCTCTC
                                 AC_   C
GAM707  MAP4     3'  GGGACCAGAGGGAGAG      17929       TACA
                              GGGGCCA    GAGGGAGAG
                              |||||||    |||||||||
                              CCCTGGT    CTCCCTCTC
                                   ____
GAM707  MAP4     3'  GGGACCAGAGGGAGAG      17929       TACA
                              GGGGCCA    GAGGGAGAG
                              |||||||    |||||||||
                              CCCTGGT    CTCCCTCTC
                                   ____
GAM707  NGB      3'  TCGCGGGGTCAGAGGGAG    17930    A    CCATA
                              TC CGGGG    CAGAGGGAG
                              || |||||    |||||||||
                              AG GCCCC    GTCTCCCTC
                               C    A____
GAM707  PRPH     3'  AGACACATGCAGAGGGAGAG   17931     _   A
                              GGGC CAT CAGAGGGAGAG
                              |||| ||| ||||||||||
                              TCTG GTA GTCTCCCTCTC
                                T   C
GAM707  PTPRS    5'  TCATGGAGGAGGCAGAGGGAG  17932    C   CCATA
                              TCA GGGG    CAGAGGGAG
                              ||| ||||    |||||||||
                              AGT CCTC    GTCTCCCTC
                                A   CTCC_
GAM707  PTPRS    5'  TCATGGAGGAGGCAGAGGGAG  17932    C   CCATA
                              TCA GGGG    CAGAGGGAG
                              ||| ||||    |||||||||
                              AGT CCTC    GTCTCCCTC
                                A   CTCC_
GAM707  PTPRS    5'  TCATGGAGGAGGCAGAGGGAG  17932    C   CCATA
                              TCA GGGG    CAGAGGGAG
                              ||| ||||    |||||||||
                              AGT CCTC    GTCTCCCTC
                                A   CTCC_
GAM707  PTPRS    5'  TCATGGAGGAGGCAGAGGGAG  17932    C   CCATA
                              TCA GGGG    CAGAGGGAG
                              ||| ||||    |||||||||
                              AGT CCTC    GTCTCCCTC
                                A   CTCC_
GAM707  RYR1     5'  CGGGGAACAGAGGGAG      17933      CCAT
                              CGGGG   ACAGAGGGAG
                              |||||   ||||||||||
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                              GCCCC   TGTCTCCCTC
                                T___
GAM707  SH3GL1   3' TCACTGGACCACAGAGGGAG  17934    G   AT
                              TCAC GGGCC  ACAGAGGGAG
                              |||| |||||  ||||||||||
                              AGTG CCTGG  TGTCTCCCTC
                                A   __
GAM707  TBL1X    3' GAGAAAGGTACAGAGGGAGAG 17935    CCA_
                              GGGG   TACAGAGGGAGAG
                              ||||   ||||||||||||
                              CTCT   ATGTCTCCCTCTC
                                TTCC
GAM707  C20orf51 5' TCCTGGGCTTGCAGAGGGAG  17936   ACG   CATA
                              TC   GGGC   CAGAGGGAG
                              ||   ||||   |||||||||
                              AG   CCCG   GTCTCCCTC
                               GA_   AAC_
GAM707  C9orf7   3' ACGGGGCCACACCAGGGAGAG 17937        AG
                              ACGGGGCCATAC  AGGGAGAG
                              ||||||||||||  ||||||||
                              TGCCCCGGTGTG  TCCCTCTC
                                    G_
GAM707  FLJ13441 3' TCACGGGGCTGTGTACAGAG  17938       CA__
                              TCACGGGGC   TACAGAG
                              |||||||||   |||||||
                              AGTGCCCCG   ATGTCTC
                                   ACAC
GAM707  FLJ13441 3' TCACGGGGCTGTGTACAGAG  17938       CA__
                              TCACGGGGC   TACAGAG
                              |||||||||   |||||||
                              AGTGCCCCG   ATGTCTC
                                   ACAC
GAM707  FLJ21939 5' CACGGGCCGGAGGGAG     17939      G  ATACA
                              CACGGG CC    GAGGGAG
                              |||||| ||    |||||||
                              GTGCCC GG    CTCCCTC
                                 _  C____
GAM707  FLJ22174 3' CAAGGACAGAGGGAG      17940     CCAT
                              CGGGG   ACAGAGGGAG
                              |||||   ||||||||||
                              GTTCC   TGTCTCCCTC
                                 ____
GAM707  KIAA1910 3' TCACGGGGCTAATCCACAGGG 17941       CATA_  G
                              TCACGGGGC    CA AGGG
                              |||||||||    || ||||
                              AGTGCCCCG    GT TCCC
                                   ATTAG  G
GAM707  MGC2541  3' ACAGGGCTGCTGATGGGAGAG 17942       CATACA  _
                              ACGGGGC     GA GGGAGAG
                              |||||||     || |||||||
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                                TGTCCCG     CT CCCTCTC
                                    ACGA__  A
GAM707  NKX2C    3'  CGCGGAAAGGCAGAGGGAGAG  17943    G  CCATA
                                CG GG    CAGAGGGAGAG
                                || ||    ||||||||||
                                GC CC    GTCTCCCTCTC
                                 G  TTTCC
GAM707  ORCTL3   3'  GGGGCCATACGTTAGCCAGAG  17944         ___  AG
                                GGGGCCATAC   AG  GGAG
                                ||||||||||   ||  ||||
                                CCCCGGTATG   TC  TCTC
                                      CAA  GG
GAM707  PSR      3'  GGGGGTAAGGAGGGAGAG    17945     CCA  CA
                                GGGG   TA  GAGGGAGAG
                                ||||   ||  |||||||||
                                CCCC   AT  CTCCCTCTC
                                  C__  TC
GAM707  RCD-8    3'  TCACGAGGCCATGCAGCATGAG 17946          A   AGG
                                TCACGGGGCCAT CAG   GAG
                                |||||||||||| |||   |||
                                AGTGCTCCGGTA GTC   CTC
                                       C   GTA
GAM707  LOC147495 3' TCAGGGGCTGGGAGGGAG    17947    C    CATACA
                                TCA GGGGC     GAGGGAG
                                ||| |||||     |||||||
                                AGT CCCCG     CTCCCTC
                                  _    ACC___
GAM707  LOC152137 5' CGTCCAGTACGGAGGGAGAG   17948    GGG  _   A
                                CG   CCA TAC GAGGGAGAG
                                ||   ||| ||| |||||||||
                                GC   GGT ATG CTCCCTCTC
                                 A__   C   C
GAM707  LOC154877 3' CAGGGTCCTAGAGGGAG     17949      _  ATAC
                                CGGGG CC    AGAGGGAG
                                ||||| ||    ||||||||
                                GTCCC GG    TCTCCCTC
                                   A  A___
GAM707  LOC160717 5' TCAGGGGCAGAGGGAG      17950    C    CATAC
                                TCA GGGGC    AGAGGGAG
                                ||| |||||    ||||||||
                                AGT CCCCG    TCTCCCTC
                                  _    _____
GAM707  LOC196337 5' CACGGGGCTGTGCAGCTCCAGG 17951        CATA  _____
          G                      CACGGGGC   CAG   AGGG
                                 ||||||||   |||   ||||
                                 GTGCCCCG   GTC   TCCC
                                      ACAC   GAGG
GAM707  LOC222865 3' TCAGGGGTGACAGAGAGGGAG  17952    C   CC   C
                                TCA GGGG  ATA AGAGGGAG
                                ||| ||||  ||| ||||||||
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                                AGT CCCC  TGT TCTCCCTC
                                  _   AC   C
GAM708  ATP1B2   3'  GGAATTTTCAGGCTG      17955     A      AT
                                GGAG TTTTCGGG  CTG
                                |||| ||||||||  |||
                                CCTT AAAAGTCC  GAC
                                  _      __
GAM708  EFNB2    3'  ACCTGGGGGGGAGGGGGATCTGA 17956    C  AGATTTTC
          C                      ACC GG       GGGATCTGAC
                                 ||| ||       ||||||||||
                                 TGG CC       CCCTAGACTG
                                   A  CCCCTCC_
GAM708  FEZ1     3'  CGGGATTTTCAAAATTCTG   17957    A         _
                                 CGG GATTTTCGGGAT CTG
                                 ||| ||||||||||| |||
                                 GCC CTAAAAGTTTTA GAC
                                  _          A
GAM708  P2RY1    3'  CAGAGATCCATTGATCTGA   17958         TCGG
                                 CGGAGATTT    GATCTGA
                                 |||||||||    |||||||
                                 GTCTCTAGG    CTAGACT
                                      TAA_
GAM708  SLC4A1AP 5'  CCAGCTTTCGGGGTCTGA    17959     AGA      A
                                 CCGG   TTTTCGGG TCTGA
                                 ||||   |||||||| |||||
                                 GGTC   GAAAGCCC AGACT
                                   ___       C
GAM708  VGF      3'  ACCCGGGAGGGGGGTCTG    17960      A  TTTTC   A
                                 ACCCGG GA     GGG TCTG
                                 |||||| ||     ||| ||||
                                 TGGGCC CT     CCC AGAC
                                    _ CC___    C
GAM708  FLJ22004 5'  CCCGGAGATCTGCTCTG     17961          TCGGGA
                                 CCCGGAGATTT     TCTG
                                 ||||||||||      ||||
                                 GGGCCTCTAGA     AGAC
                                       CG____
GAM708  MO25     3'  ACCTGAAGGTGCGCGATCTGAC 17962    C   ATTTT  G
                                 ACC GGAG     CG GATCTGAC
                                 ||| ||||     || ||||||||
                                 TGG CTTC     GC CTAGACTG
                                   A   CAC__  G
GAM708  MYRIP    3'  CCAGAGAAGGGGTCTGA     17963        TTTTC   A
                                 CCGGAGA     GGG TCTGA
                                 |||||||     ||| |||||
                                 GGTCTCT     CCC AGACT
                                     TC___   _
GAM708  RGS18    3'  ACCTGGAGATATGCAAAATCTG 17964     C      TTT
                                 ACC GGAGAT   CGGGATCTG
                                 ||| ||||||   |||||||||
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                                TGG CCTCTA   GTTTTAGAC
                                  A      TAC
GAM708  LOC151826 3'  GGTGATAAGGATCTGAC     17965     A   TTTC
                                GG GAT    GGGATCTGAC
                                || |||    ||||||||||
                                CC CTA    TCCTAGACTG
                                 A  T___
GAM708  LOC154789 5'  CCTGAGATTTTACTGAGTCTG  17966     G       CG_ GA
                                CC GAGATTTT   G  TCTG
                                || ||||||||   |  ||||
                                GG CTCTAAAA   C  AGAC
                                 A       TGA TC
GAM708  LOC200953 5'  CCTAGACTCCTGGGATCTG    17967     GG     TC
                                CC  AGATTT  GGGATCTG
                                ||  ||||||  ||||||||
                                GG  TCTGAG  CCCTAGAC
                                 A_     GA
GAM708  LOC204285 3'  CGGGATCCCGGGTCTGAC     17968     A  T TT    A
                                CGG GA T  CGGG TCTGAC
                                ||| || |  |||| ||||||
                                GCC CT A  GCCC AGACTG
                                  _ _ GG   _
GAM708  LOC253264 3'  GAAGATTCTCCATGGATTTGA  17969          G__    C
                                GGAGATTTTC   GGAT TGA
                                ||||||||||   |||| |||
                                CTTCTAAGAG   CCTA ACT
                                      GTA    A
GAM708  LOC51063  5'  CCGGAGATTATTCTGCCT     17970          _   GGGA
                                CCGGAGATT TTC    TCT
                                ||||||||| |||    |||
                                GGCCTCTAA AAG    GGA
                                     T   AC__
GAM709  ANK1      3'  GAGGTGCCAAAGCGGAG      17973     A    CGC
                                GAG TGCCG   GGGCGGAG
                                ||| |||||   ||||||||
                                CTC ACGGT   TTCGCCTC
                                  C    ____
GAM709  ANK1      3'  GAGGTGCCAAAGCGGAG      17973     A    CGC
                                GAG TGCCG   GGGCGGAG
                                ||| |||||   ||||||||
                                CTC ACGGT   TTCGCCTC
                                  C    ____
GAM709  ARHGEF1   3'  TGAGATGCTGCGGCAG       17974        C  GCG
                                TGAGATGC GC   GGCGG
                                |||||||| ||   |||||
                                ACTCTACG CG   CCGTC
                                     A  ____
GAM709  CELSR1    3'  TGAGATGCCCGCCTGGGCGGGG 17975          G   __     A
            C                    TGAGATGCC CGC  GGGCGG GC
                                ||||||||| |||  |||||| ||
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                                ACTCTACGG GCG  CCCGCC CG
                                      _  GA     C
GAM709  CTGF    5'  TGGCACTGCGGGCGGAGC    17976    C  _
                                TG CGC GCGGGCGGAGC
                                || ||| ||||||||||
                                AC GTG CGCCCGCCTCG
                                 C   A
GAM709  F2R     5'  CGCGGTCGCGCGGGCGGAGC   17977     ___
                                TGC   CGCGCGGGCGGAGC
                                |||   ||||||||||||||
                                GCG   GCGCGCCCGCCTCG
                                  CCA
GAM709  FUT6    5'  TGAGAGGCCGCGGACGA     17978      T    GC
                                TGAGA GCCGC  GGGCGG
                                ||||| |||||  ||||||
                                ACTCT CGGCG  CCTGCT
                                   C    __
GAM709  GALNT2  3'  GAGGGAGCTGCGGGCGGGGC   17979     AT_ CGC      A
                                GAG   GC   GCGGGCGG GC
                                |||   ||   |||||||| ||
                                CTC   CG   CGCCCGCC CG
                                  CCT  A__       C
GAM709  KLK13   5'  GAGGGCAGGGCGGGCGGGGC   17980     AT  CGC      A
                                GAG  GC   GCGGGCGG GC
                                |||  ||   |||||||| ||
                                CTC  CG   CGCCCGCC CG
                                  C_  TCC       C
GAM709  MAPK1   3'  TGAGATGCCAGTGACTAGAGC  17981          CGCG  _
                                TGAGATGCCG    GGC GGAGC
                                ||||||||||    ||| |||||
                                ACTCTACGGT    CTG TCTCG
                                      CA__   A
GAM709  MUS81   5'  TGGGACGCCGCCAGTTCTGGAG 17982    A       G   GC__
                                TG GATGCCGC CGG    GGAG
                                || |||||||| |||    ||||
                                AC CTGCGGCG GTC    CCTC
                                 C       _   AAGA
GAM709  PAX5    3'  GAGATGCATCATGGGTGGAGC  17983       CG  C   C
                                GAGATGC  CG GGG GGAGC
                                |||||||  || ||| |||||
                                CTCTACG  GT CCC CCTCG
                                    TA  A   A
GAM709  PFKL    5'  TGAGGTGCCACGCCTCTGGC   17984      A       G___
                                TGAG TGCCGCGC    GGC
                                |||| ||||||||    |||
                                ACTC ACGGTGCG    CCG
                                  C       GAGA
GAM709  REV3L   5'  CGAGGAACGGCGGGCGGGGC   17985      AT  C C       A
                                TGAG  GC G GCGGGCGG GC
                                ||||  || | |||||||| ||
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                                GCTC  TG C CGCCCGCC CG
                                  CT  _ _      C
GAM709  SLC16A2  3'  TGAAATGCTGTGTGCGCAGG  17986       C____
                                TGAGATGC    GCGCGGG
                                ||||||||    |||||||
                                ACTTTACG    CGCGTCC
                                    ACACA
GAM709  SMARCB1  3'  TGAGATGCTCCGTGGGAGC   17987       CG  C   CGG
                                TGAGATGC  CG GGG   AGC
                                ||||||||  || |||   |||
                                ACTCTACG  GC CCC   TCG
                                    AG  A  ___
GAM709  SYT4     3'  GAGATGCCGAGTGGAG     17988       CGCG  C
                                GAGATGCCG   GG GGAG
                                |||||||||   || ||||
                                CTCTACGGC   TC CCTC
                                    ____ A
GAM709  TCF20    3'  GCAGGCACGCGGGCGGGGC   17989   ___       A
                                GC   CGCGCGGGCGG GC
                                ||   ||||||||||| ||
                                CG   GTGCGCCCGCC CG
                                 TCC         C
GAM709  TEAD2    5'  GAGCCGCGGGCGGGCGGGGC  17990   T   __      A
                                GA GCCGC  GCGGGCGG GC
                                || |||||  |||||||| ||
                                CT CGGCG  CGCCCGCC CG
                                 _    CC       C
GAM709  ZNF219   5'  TGGGAGCCGCGCGGGAG    17991   A  T       CGG
                                TG GA GCCGCGCGGG   AG
                                || || ||||||||||   ||
                                AC CT CGGCGCGCCC   TC
                                 C  _        ___
GAM709  ZNF74    5'  TGAGGGGCCTGCAGCGGAGC  17992    AT   GC   G
                                TGAG  GCC  GCGG CGGAGC
                                ||||  |||  |||| ||||||
                                ACTC  CGG  CGTC GCCTCG
                                  CC   A_   _
GAM709  CACNG4   3'  TGAGATGCAGCGGGAGGGC   17993       CGC    C  A
                                TGAGATGC   GCGGG GG GC
                                |||||||   ||||| || ||
                                ACTCTACG   CGCCC CC CG
                                    T__    T  _
GAM709  CENTG2   5'  AGAAAGGCGCGGGCGGAGC   17994    TGCC
                                AGA   GCGCGGGCGGAGC
                                |||   |||||||||||||
                                TCT   CGCGCCCGCCTCG
                                 TTC_
GAM709  CRMP5    5'  GAGATGCTGCGGCCGCGGGGG  17995       C  ____    C
                                GAGATGC GC   GCGGG GG
                                |||||||  ||   ||||| ||
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                                CTCTACG CG   CGCCC CC
                                   A  CCGG   _
GAM709  FLJ12526  5'  TGAGGGGCCGCAGGCGG    17996     AT   GC
                                TGAG  GCCGC  GGGCGG
                                ||||  |||||  ||||||
                                ACTC  CGGCG  TCCGCC
                                  CC   __
GAM709  FLJ13215  3'  TGAAATGCCAGTGGAG     17997        GCGCG  C
                                TGAGATGCC    GG GGAG
                                |||||||||    || ||||
                                ACTTTACGG    TC CCTC
                                     _____ A
GAM709  FLJ20699  3'  TGAGGTTCTGCAGGGTGGAGC  17998     ATGCC   C   C
                                TGAG    GCG GGG GGAGC
                                ||||    ||| ||| |||||
                                ACTC    CGT CCC CCTCG
                                  CAAGA  _  A
GAM709  FLJ22087  5'  TGGATCTCGGTGCGGGCGGAGC 17999    A   GC  C_
                                TG GAT  CG  GCGGGCGGAGC
                                || |||  ||  ||||||||||
                                AC CTA  GC  CGCCCGCCTCG
                                 _  GA  CA
GAM709  FLJ22362  5'  GCCGAGCTGCGGGCGGAGC   18000     __ _
                                GCC  GC GCGGGCGGAGC
                                |||  || ||||||||||
                                CGG  CG CGCCCGCCTCG
                                 CT  A
GAM709  GSH-2     5'  TGGGAGCCGCGCAGACACGGGC 18001    A  T       __   A
                                TG GA GCCGCGCGG  GCGG GC
                                || || |||||||||  |||| ||
                                AC CT CGGCGCGTC  TGCC CG
                                 C  _       TG   _
GAM709  GTF3C1    3'  TGAGGTGTGCACAGGCGGGGC  18002     A  CC       A
                                TGAG TG  GCGCGGGCGG GC
                                |||| ||  |||||||||| ||
                                ACTC AC  CGTGTCCGCC CG
                                  C  A_        C
GAM709  HEMK      3'  TGAGATGCTGCTGAAGACAG   18003       C  GC_
                                TGAGATGC GC   GGGCGG
                                |||||||| ||   ||||||
                                ACTCTACG CG   TCTGTC
                                    A  ACT
GAM709  HOMER-2B  3'  TGGGACTCACGGGCGGGGC   18004    A   GCCG      A
                                TG GAT    CGCGGGCGG GC
                                || |||    ||||||||| ||
                                AC CTG    GTGCCCGCC CG
                                 C  A___       C
GAM709  KIAA0217  3'  TGAGATACTGCTGGGGG     18005       C  GC   C
                                TGAGATGC GC  GGG GG
                                |||||||| ||  ||| ||
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                                ACTCTATG CG  CCC CC
                                    A  A_  _
GAM709  KIAA0455  3'  TGAAATGCTGCAGCAGGGG   18006       C _   C
                                TGAGATGC GC GCGGG GG
                                |||||||| || ||||| ||
                                ACTTTACG CG CGTCC CC
                                    A  T   _
GAM709  LGI3    3'  TGAGCATGCAGACGGGGTGGGG 18007    _   C_  C  C  A
          C                      TGAG ATGC  GCG GGG GG GC
                                |||| ||||  ||| ||| || ||
                                ACTC TACG  TGC CCC CC CG
                                  G   TC  _  A  C
GAM709  MGC13114  3'  TGAGAGCACAGACTGGGTGGGG 18008     T  _  C  _  C  A
          C                      TGAGA GC CG GC GGG GG GC
                                ||||| || || || ||| || ||
                                ACTCT CG GT TG CCC CC CG
                                  _  T  C  A   A  C
GAM709  MLL4    3'  TGAGATGCTCTGGGAGGGGC  18009       CGCGC  C  A
                                TGAGATGC    GGG GG GC
                                ||||||||    ||| || ||
                                ACTCTACG    CCC CC CG
                                    AGA__   T  C
GAM709  OSBPL1A  5'  TGAGTGCCGCGCCGAGGC   18010    A     __
                                TGAG TGCCGCGC  GGGC
                                |||| ||||||||  ||||
                                ACTC ACGGCGCG  TCCG
                                  _      GC
GAM709  RAB6B   5'  GAGAGAGGCGCGGGCGGAGC  18011    TGCC
                                GAGA   GCGCGGGCGGAGC
                                ||||   ||||||||||||
                                CTCT   CGCGCCCGCCTCG
                                  CTC_
GAM709  SH3GLB1  5'  GAGGTGCCGCGGCCGGGC   18012    A     __
                                GAG TGCCGCG  CGGGC
                                ||| |||||||  |||||
                                CTC ACGGCGC  GCCCG
                                  C      CG
GAM709  TIP120B  3'  TGAGATGCCCGGCCTGAGC   18013       G GCG  G_
                                TGAGATGCC C   GGC  GAGC
                                |||||||| |   |||  ||||
                                ACTCTACGG G   CCG  CTCG
                                    _ ____   GA
GAM709  LOC125144 3'  TGAGATGCTGCTGCCAGC   18014       C  _  G
                                TGAGATGC GC GC GGC
                                |||||||| || || |||
                                ACTCTACG CG CG TCG
                                    A  A  G
GAM709  LOC148534 5'  TGAGATGCTCACGGGAGC   18015       _   C
                                TGAGATGC CGCG GGGC
                                |||||||| |||| ||||
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                                ACTCTACG GTGC CTCG
                                     A    C
GAM709   LOC149650 5'  GAGGGGAGCGCGGGCGGAGC   18016     ATGCC
                                GAG    GCGCGGGCGGAGC
                                |||    ||||||||||||
                                CTC    CGCGCCCGCCTCG
                                  CCCT_
GAM709   LOC150889 5'  TGAGATGCGTGTCAGTGAGC   18017        CGCG   GCG
                                TGAGATGC   CGG   GAGC
                                ||||||||   |||   ||||
                                ACTCTACG   GTC   CTCG
                                     CACA   A__
GAM709   LOC151194 5'  TGAGCTGCCCGGCGGAG     18018      A    G GCG
                                TGAG TGCC C   GGCGGAG
                                |||| |||| |   |||||||
                                ACTC ACGG G   CCGCCTC
                                  G   _ ____
GAM709   LOC152804 5'  TGAGACGCCGACTGGAG     18019          C  GGGC
                                TGAGATGCCG GC    GGAG
                                ||||||||||  ||    ||||
                                ACTCTGCGGC TG    CCTC
                                     _  A____
GAM709   LOC152804 5'  TGAGACGCCGACTGGAG     18019          C  GGGC
                                TGAGATGCCG GC    GGAG
                                ||||||||||  ||    ||||
                                ACTCTGCGGC TG    CCTC
                                     _  A____
GAM709   LOC152804 5'  TGAGACGCCGACTGGAG     18019          C  GGGC
                                TGAGATGCCG GC    GGAG
                                ||||||||||  ||    ||||
                                ACTCTGCGGC TG    CCTC
                                     _  A____
GAM709   LOC152804 5'  TGAGACGCCGACTGGAG     18019          C  GGGC
                                TGAGATGCCG GC    GGAG
                                ||||||||||  ||    ||||
                                ACTCTGCGGC TG    CCTC
                                     _  A____
GAM709   LOC152804 5'  TGAGACGCCGACTGGAG     18019          C  GGGC
                                TGAGATGCCG GC    GGAG
                                ||||||||||  ||    ||||
                                ACTCTGCGGC TG    CCTC
                                     _  A____
GAM709   LOC152804 5'  TGAGACGCCGACTGGAG     18019          C  GGGC
                                TGAGATGCCG GC    GGAG
                                ||||||||||  ||    ||||
                                ACTCTGCGGC TG    CCTC
                                     _  A____
GAM709   LOC152804 5'  TGAGACGCCGACTGGAG     18019          C  GGGC
                                TGAGATGCCG GC    GGAG
                                ||||||||||  ||    ||||
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                                ACTCTGCGGC TG    CCTC
                                      _  A___
GAM709   LOC152804 5'  TGAGACGCCGACTGGAG     18019         C  GGGC
                                TGAGATGCCG GC    GGAG
                                |||||||||| ||    ||||
                                ACTCTGCGGC TG    CCTC
                                      _  A___
GAM709   LOC152804 5'  TGAGACGCCGACTGGAG     18019         C  GGGC
                                TGAGATGCCG GC    GGAG
                                |||||||||| ||    ||||
                                ACTCTGCGGC TG    CCTC
                                      _  A___
GAM709   LOC152804 5'  TGAGACGCCGACTGGAG     18019         C  GGGC
                                TGAGATGCCG GC    GGAG
                                |||||||||| ||    ||||
                                ACTCTGCGGC TG    CCTC
                                      _  A___
GAM709   LOC152804 5'  TGAGACGCCGACTGGAG     18019         C  GGGC
                                TGAGATGCCG GC    GGAG
                                |||||||||| ||    ||||
                                ACTCTGCGGC TG    CCTC
                                      _  A___
GAM709   LOC152804 5'  TGAGACGCCGACTGGAG     18019         C  GGGC
                                TGAGATGCCG GC    GGAG
                                |||||||||| ||    ||||
                                ACTCTGCGGC TG    CCTC
                                      _  A___
GAM709   LOC197335 5'  TGAGATGCTGGCAGAGGC    18020         C_  C
                                TGAGATGC  GCG GGGC
                                ||||||||  ||| ||||
                                ACTCTACG  CGT TCCG
                                     AC   C
GAM709   LOC200014 5'  TGAGATGCTCCGGCCTGAGC  18021          CGCGCG   G_
                                TGAGATGC     GGC  GAGC
                                ||||||||     |||  ||||
                                ACTCTACG     CCG  CTCG
                                     AGG___   GA
GAM709   LOC254057 3'  TGAGGTGCCTGCACACAG    18022      A   GC   G
                                TGAG TGCC  GCG GCGG
                                |||| ||||  ||| ||||
                                ACTC ACGG  CGT TGTC
                                  C   A_   G
GAM709   LOC255465 3'  TGAGATGCCGAGGCGG      18023          CGC
                                TGAGATGCCG   GGGCGG
                                ||||||||||   ||||||
                                ACTCTACGGC   TCCGCC
                                      ___
GAM709   LOC257369 5'  TGAGATGCTGCTGTGAGAGG  18024         C  GC_   C
                                TGAGATGC GC   GGG GG
                                |||||||| ||   ||| ||
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                                ACTCTACG CG   CTC CC
                                    A  ACA   T
GAM709  LOC56270  3'  TGAGGATGCGGCGGAG     18025     _   CGCGCG
                                TGAG ATGC     GGCGGAG
                                |||| ||||     |||||||
                                ACTC TACG     CCGCCTC
                                  C   _______
GAM709  LOC90139  3'  TGGGATGCCATGGACAGAGC   18026    A     CGC
                                TG GATGCCG   GGGCGGAGC
                                || |||||||   |||||||||
                                AC CTACGGT   CCTGTCTCG
                                 C      A__
GAM709  LOC92421  3'  TGAGATACCGTGCCTGGC    18027         C  G_
                                TGAGATGCCG GC  GGC
                                |||||||||| ||  |||
                                ACTCTATGGC CG  CCG
                                      A  GA
GAM710  ALP       3'  TGCATCGAGTGGCATAATT    18030      AA
                                TGTA  GAGTGGCATAATT
                                ||||  ||||||||||||||
                                ACGT  CTCACCGTATTAA
                                  AG
GAM710  DDX6      3'  TGTTGGGAGGGGCACAATT    18031     AAA   T
                                TGT   GAG GGCATAATT
                                |||   ||| |||||||||
                                ACA   CTC CCGTGTTAA
                                  ACC   C
GAM710  KLHL2     3'  ACAATGTAGTACTGGCATAATT 18032     C    AAGAG
                                ACA TGTA     TGGCATAATT
                                ||| ||||     ||||||||||
                                TGT ACAT     ACCGTATTAA
                                  T    CATG_
GAM710  MADH6     3'  ACATTGTAAAAATGACTCCATA 18033     C       G   ___
            ATT                   ACA TGTAAAGA TGGC   ATAATT
                                ||| |||||||| ||||   ||||||
                                TGT ACATTTTT ACTG   TATTAA
                                  A       _   AGG
GAM710  NR3C2     3'  ACACTGTAAACGGTTCAT    18034         GA  GG
                                ACACTGTAAA  GT  CAT
                                |||||||||  ||  |||
                                TGTGACATTT  CA  GTA
                                      GC  A_
GAM710  FAM3C     3'  ACACTGTGAATGGCA       18035        AAA
                                ACACTGT   GAGTGGCA
                                |||||||   ||||||||
                                TGTGACA   CTTACCGT
                                           ___
GAM710  KIAA0537  3'  ACCTGTAAAAAGAAGTGTAATT 18036    A        T  CA
                                AC CTGTAAAGAG GG  TAATT
                                || ||||||||| ||  |||||
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                                TG GACATTTTTC TC  ATTAA
                                 _        T  AC
GAM710  LASP1    3'  CACACTGCAAAGGGCA      18037          AGT
                                CACACTGTAAAG   GGCA
                                ||||||||||||  ||||
                                GTGTGACGTTTC   CCGT
                                      ____
GAM710  OSBPL8   3'  ACTTGTAGAAGTTAGCATAATT 18038    _  AA   _
                                ACT GTA  GAGT GGCATAATT
                                ||| |||  |||| |||||||||
                                TGA CAT  TTCA TCGTATTAA
                                  A  C_   A
GAM710  PELI1    3'  CAAACTGTAAACTAACATA   18039    C    AA  G
                                CA ACTGTA  GA TGGCATA
                                || ||||||  || |||||||
                                GT TGACAT  TT ATTGTAT
                                 T     __  G
GAM710  TRIM36   3'  CACACTTTAAAATACATAATT  18040      GTAA    G
                                CACACT    AGAGTG CATAATT
                                ||||||    |||||| |||||||
                                GTGTGA    TTTTAT GTATTAA
                                   AA__     _
GAM710  UNC5D    3'  CACCATTTTGGTGGCATAATT  18041      AAAGA
                                CACTGT    GTGGCATAATT
                                ||||||    ||||||||||||
                                GTGGTA    CACCGTATTAA
                                   AAAC_
GAM710  LOC143872 3'  ACATTGTGGAGAGTTACATA   18042    C   AA    G
                                ACA TGT  AGAGT GCATA
                                ||| |||  ||||| |||||
                                TGT ACA  TCTCA TGTAT
                                  A  CC    A
GAM710  LOC201627 3'  CATCCTGTAGTGGCATAAT    18043    CA    AAAG
                                CA  CTGT    AGTGGCATAAT
                                ||  ||||    ||||||||||||
                                GT  GACA    TCACCGTATTA
                                 AG   _____
GAM710  LOC221271 3'  CTGTAAAGATACTATCATAATT 18044        GTGG__
                                CTGTAAAGA     CATAATT
                                |||||||||     |||||||
                                GACATTTCT     GTATTAA
                                     ATGATA
GAM710  LOC91445  3'  CACACTATAAAGCTGGTGG   18045          A__
                                CACACTGTAAAG   GTGG
                                ||||||||||||  ||||
                                GTGTGATATTTC   CACC
                                       GAC
GAM710  LOC92230  5'  ACACTGTGAGTAGCA       18046        AAA
                                ACACTGT   GAGTGGCA
                                |||||||   ||||||||
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                                TGTGACA   CTCATCGT
                                   ___
GAM711  ACCN2    3'  TGGTGGAGGGAGGGGGG     18049     AA        A
                                TGG  GAGGGAGGG GGG
                                |||  ||||||||| |||
                                ACC  CTCCCTCCC CCC
                                  AC        _
GAM711  ALDOC    3'  TGGAAGAGGTAGGGGGAG    18050          GA   A
                                TGGAAGAGG  GGG GGGAG
                                |||||||||  ||| |||||
                                ACCTTCTCC  TCC CCCTC
                                     A_   _
GAM711  ALMS1    5'  GGGGGAGGGAGGGGAAGGGGAG 18051    AA        __    A
            AG                    GG  GAGGGAGGG  AGGG GAGAG
                                ||  |||||||||  |||| |||||
                                CC  CTCCCTCCC  TCCC CTCTC
                                 CC        CT   _
GAM711  ALMS1    5'  GGAGGAGGGGGGGGAGGGAG   18052     A    A
                                GGA GAGGG GGGAGGGAG
                                |||  ||||| |||||||||
                                CCT CTCCC CCCTCCCTC
                                  C    C
GAM711  AMD1     3'  TGGGGGAGACACCAGGGAGAG  18053     AAGA     G___
                                TGG   GGGAGG   AGGGAGAG
                                |||   ||||||   ||||||||
                                ACC   CCCTCT   TCCCTCTC
                                  ____     GTGG
GAM711  ARIH1    5'  GGAGGAGGGAGGGAGGGAGCGA 18055     A           A
            G                     GGA GAGGGAGGGAGGGAG GAG
                                |||  |||||||||||||| |||
                                CCT CTCCCTCCCTCCCTC CTC
                                  C            G
GAM711  ARIH1    5'  GGAGGAGGGAGGGAGGGAG   18054     A
                                GGA GAGGGAGGGAGGGAG
                                |||  |||||||||||||
                                CCT CTCCCTCCCTCCCTC
                                  C
GAM711  B3GAT1   3'  GGAAGAGGGGCCGGAGGG    18056          AG_
                                GGAAGAGGG   GGAGGG
                                |||||||||   ||||||
                                CCTTCTCCC   CCTCCC
                                     CGG
GAM711  B3GAT1   3'  GGAAGAGGGGCCGGAGGG    18056          AG_
                                GGAAGAGGG   GGAGGG
                                |||||||||   ||||||
                                CCTTCTCCC   CCTCCC
                                     CGG
GAM711  B4GALT3  3'  TGGAAGAGGGAGGGGCTTGGG  18057            A___
                                TGGAAGAGGGAGGG   GGG
                                ||||||||||||||   |||
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                                ACCTTCTCCCTCCC  CCC
                                       CGAA
GAM711  B4GALT5  3' TGGGGTAGGAGATGGGGAGAGA 18058   AAGA   GA
           G                    TGG  GGGAGG GGGAGAGAG
                                |||  |||||| |||||||||
                                ACC  TCCTCT CCCTCTCTC
                                  CCA_   AC
GAM711  BAZ1B   5' TGGGGTGGGGGAAGGGAG   18059   AAGA A
                                TGG  GGG GGGAGGGAG
                                |||  ||| |||||||||
                                ACC  CCC CCTTCCCTC
                                  CCA_ _
GAM711  BAZ1B   5' TGGGGGAAGGGAGGGGTGAGAG 18060   AAGA      A_
                                TGG  GGGAGGGAGGG GAGAG
                                |||  |||||||||| |||||
                                ACC  CCTTCCCTCCC CTCTC
                                  C___       CA
GAM711  BCL2L2  5' GGAGCTGGGAGGGAGGGAGAGA 18061   AGA
           G                    GGA  GGGAGGGAGGGAGAGAG
                                |||  ||||||||||||||||
                                CCT  CCCTCCCTCCCTCTCTC
                                  CGA
GAM711  BCL7A   3' TGGGGGATGGGAGGGAGGG  18062   AA _
                                TGG GA GGGAGGGAGGG
                                ||| || ||||||||||
                                ACC CT CCCTCCCTCCC
                                  CC A
GAM711  BCL9    3' TGGGAGGGGGAGGAAAGG   18063   A A
                                TGG AG GGGAGGGAGGG
                                ||| || ||||||||||
                                ACC TC CCCTCCTTTCC
                                  C C
GAM711  BIN1    5' GGGGACAGAGGGAGGGAGAG  18064   AA G
                                GG GA GGAGGGAGGGAGAG
                                ||  || ||||||||||||||
                                CC CT TCTCCCTCCCTCTC
                                 C_ G
GAM711  BIN1    5' GGGGACAGAGGGAGGGAGAG  18064   AA G
                                GG GA GGAGGGAGGGAGAG
                                ||  || ||||||||||||||
                                CC CT TCTCCCTCCCTCTC
                                 C_ G
GAM711  BLAME   3' TGGGAGAGGGAAGGGGGAG  18065   A      A
                                TGG AGAGGGAGGG GGGAG
                                ||| |||||||||| |||||
                                ACC TCTCCCTTCC CCCTC
                                  C       _
GAM711  BTG2    3' GGAAGGGGGAGGGGAGGG   18066     A    _
                                GGAAG GGGAGGG AGGG
                                ||||| ||||||| ||||
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                                CCTTC CCCTCCC TCCC
                                   C      C
GAM711  CACNA1B  3' GGAGGAGGGGGAGGGAG     18068     A     AG
                                GGA GAGGG  GGAGGGAG
                                ||| |||||  ||||||||
                                CCT CTCCC  CCTCCCTC
                                  C    __
GAM711  CACNA1B  3' GGGGGAGGGAGGGGCCACAGGA 18067     AA        A____
          G                      GG  GAGGGAGGG    GGGAG
                                ||  |||||||||    |||||
                                CC  CTCCCTCCC    TCCTC
                                 CC        CGGTG
GAM711  CACNB1   3' GGGAGGGGGGGAAGGGAG     18069    AA    A
                                GG  GAGGG GGGAGGGAG
                                ||  ||||| |||||||||
                                CC  CTCCC CCTTCCCTC
                                 __     C
GAM711  CADPS    5' GGAGGAGGGGAAGGGAGAG    18070     A     AG
                                GGA GAGGG  GGAGGGAGAG
                                ||| |||||  ||||||||||
                                CCT CTCCC  CTTCCCTCTC
                                  C    __
GAM711  CALR     3' GGGAGGGGGTGGGGGAGAG    18071    A  A   AG  A
                                GG AG GGG  GG GGGAGAG
                                || || |||  || |||||||
                                CC TC CCC  CC CCCTCTC
                                 C  _   CA  _
GAM711  CASP10   3' GGAAGGGGGAGATCAGAGAGAG 18072       A     G_
                                GGAAG GGGAGG  AGGGAGAG
                                ||||| ||||||  ||||||||
                                CCTTC CCCTCT  TCTCTCTC
                                   C     AG
GAM711  CASP10   3' GGAAGGGGGAGATCAGAGAGAG 18072       A     G_
                                GGAAG GGGAGG  AGGGAGAG
                                ||||| ||||||  ||||||||
                                CCTTC CCCTCT  TCTCTCTC
                                   C     AG
GAM711  CCKAR    5' TGGAGGAGCAGGGAGGGAG    18073      A AG G
                                TGGA G  G AGGGAGGGAG
                                |||| |  | ||||||||||
                                ACCT C  C TCCCTCCCTC
                                  _ CT G
GAM711  CDC25B   5' GGGGGAAGGAGGGAGGGAG    18074    AA
                                GG  GAGGGAGGGAGGGAG
                                ||  ||||||||||||||
                                CC  CTTCCTCCCTCCCTC
                                 CC
GAM711  CDC25B   5' GGGGGAAGGAGGGAGGGAG    18074    AA
                                GG  GAGGGAGGGAGGGAG
                                ||  ||||||||||||||
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                                CC  CTTCCTCCCTCCCTC
                                 CC
GAM711  CDK5R2   3'  GGGAGAGGGAGGAAGAAAGAGA 18075    A         GG
           G                     GG AGAGGGAGGGAG  AGAGAG
                                 || ||||||||||||  ||||||
                                 CC TCTCCCTCCTTC  TCTCTC
                                  C          TT
GAM711  CENTD2   5'  TGGAGAGGGAGGCTGGGGAG  18076     A      GA  A
                                 TGGA GAGGGAGG  GGG GAG
                                 |||| ||||||||  ||| |||
                                 ACCT CTCCCTCC  CCC CTC
                                   _       GA  _
GAM711  CEP2     3'  TGGAGAGGGAGGGAGAG     18077     A
                                 TGGA GAGGGAGGGAGGG
                                 |||| ||||||||||||
                                 ACCT CTCCCTCCCTCTC
                                   _
GAM711  CHRNE    3'  GAGGGAGGGAGCAGGGAG    18078          ___
                                 GAGGGAGGGA   GGGAG
                                 ||||||||||   |||||
                                 CTCCCTCCCT   CCCTC
                                       CGT
GAM711  CLCN6    3'  GGAAGGGGCGGGGAGAG     18079      A  A  A
                                 GGAAG GGG GGG GGGAG
                                 ||||| ||| ||| |||||
                                 CCTTC CCC CCC CTCTC
                                   _  G  _
GAM711  CLCN6    3'  GGAAGGGGCGGGGAGAG     18079      A  A  A
                                 GGAAG GGG GGG GGGAG
                                 ||||| ||| ||| |||||
                                 CCTTC CCC CCC CTCTC
                                   _  G  _
GAM711  CLCN6    3'  GGAAGGGGCGGGGAGAG     18079      A  A  A
                                 GGAAG GGG GGG GGGAG
                                 ||||| ||| ||| |||||
                                 CCTTC CCC CCC CTCTC
                                   _  G  _
GAM711  CLOCK    3'  GGGAGAGGGGTTGGGGGAGGG  18080    A    A____
                                 GG AGAGGG    GGGAGGG
                                 || ||||||    |||||||
                                 CC TCTCCC    CCCTCCC
                                  C     CAACC
GAM711  COL11A1  5'  TGGGGAGGGAGAGGGG      18081     AA       A
                                 TGG  GAGGGAGGG GGG
                                 |||  ||||||||| |||
                                 ACC  CTCCCTCTC CCC
                                   C_       _
GAM711  COL11A1  5'  TGGGGAGGGAGAGGGG      18081     AA       A
                                 TGG  GAGGGAGGG GGG
                                 |||  ||||||||| |||
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                                ACC  CTCCCTCTC CCC
                                  C_       _
GAM711  COL1A2   3'  TGGGGGAGCGGGGGAAGGAG  18082     AA  _ A
                                TGG  GAG GG GGGAGGGAG
                                |||  ||| || |||||||||
                                ACC  CTC CC CCCTTCCTC
                                  CC   G _
GAM711  COL4A4   5'  TGGTAAGTTGGGAGGGAGGG  18083     _  A_
                                TGG AAG  GGGAGGGAGGG
                                ||| |||  ||||||||||
                                ACC TTC  CCCTCCCTCCC
                                  A  AA
GAM711  COL5A3   3'  TGGGGAGGGAGGGGAGAAAGAG 18084     AA       A
                                TGG  GAGGGAGGG GGGAGAGAG
                                |||  ||||||||| |||||||||
                                ACC  CTCCCTCCC CTCTTTCTC
                                  C_       _
GAM711  CRY2     3'  GAGGAGGGAGGGAAGGAG    18085    A
                                GA GAGGGAGGGAGGGAG
                                || ||||||||||||||
                                CT CTCCCTCCCTTCCTC
                                 C
GAM711  CSK      5'  GGAAGGGGGCGGGAGGGAG   18086      A  A
                                GGAAG GGG GGGAGGGAG
                                ||||| ||| |||||||||
                                CCTTC CCC CCCTCCCTC
                                   C  G
GAM711  DBN1     5'  GGAGGAGGGAGGGAAAGAGGGA 18087     A           A
          G                      GGA GAGGGAGGGAGGGAG GAG
                                ||| |||||||||||||| |||
                                CCT CTCCCTCCCTTTCTC CTC
                                  C           C
GAM711  DLG4     3'  TGGGAGGGAGGCCGGGGGGAG  18088     AA      GA  A_
                                TGG  GAGGGAGG  GGG  GAG
                                |||  ||||||||  |||  |||
                                ACC  CTCCCTCC  CCC  CTC
                                  __       GG   CC
GAM711  DLX4     3'  GGGAGAGGAGAAAGGGAGAGAG 18089    A    G  GG
                                GG AGAGG AG  AGGGAGAGAG
                                || ||||| ||  ||||||||||
                                CC TCTCC TC  TCCCTCTCTC
                                  C    _ TT
GAM711  DLX4     3'  GGGAGAGGAGAAAGGGAGAGAG 18089    A    G  GG
                                GG AGAGG AG  AGGGAGAGAG
                                || ||||| ||  ||||||||||
                                CC TCTCC TC  TCCCTCTCTC
                                  C    _ TT
GAM711  DPP6     3'  GGAAGAGGGAGGGCAGGG    18090           _
                                GGAAGAGGGAGGG AGGG
                                |||||||||||| ||||
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                                CCTTCTCCCTCCC TCCC
                                       G
GAM711  DUOX1   3'  TGGAGCAGGGAGAAGAGGG   18091     AG     _
                                TGGA  AGGGAGG GAGGG
                                |||| ||||||| |||||
                                ACCT  TCCCTCT CTCCC
                                  CG      T
GAM711  DUSP4   5'  GGAGGAGGTTGGGGAGGGAG  18092    A   GA_
                                GGA GAGG   GGGAGGGAG
                                ||| ||||   |||||||||
                                CCT CTCC   CCCTCCCTC
                                  C   AAC
GAM711  DYRK1A  5'  TGGGGGAAGGGAGGGAAGAG  18093    AAGA        _
                                TGG   GGGAGGGAGGGA GAG
                                |||   |||||||||||| |||
                                ACC   CCTTCCCTCCCT CTC
                                  C___          T
GAM711  DYRK1A  5'  TGGGGTGGGGGAAGGGAG    18059    AAGA  A
                                TGG   GGG GGGAGGGAG
                                |||   ||| |||||||||
                                ACC   CCC CCTTCCCTC
                                  CCA_  _
GAM711  DYRK1A  5'  TGGGGTGGGGGAAGGGAG    18059    AAGA  A
                                TGG   GGG GGGAGGGAG
                                |||   ||| |||||||||
                                ACC   CCC CCTTCCCTC
                                  CCA_  _
GAM711  DYRK1A  5'  TGGGGGAAGGGAGGGAAGAG  18093    AAGA        _
                                TGG   GGGAGGGAGGGA GAG
                                |||   |||||||||||| |||
                                ACC   CCTTCCCTCCCT CTC
                                  C___          T
GAM711  DYRK1A  5'  TGGGGTGGGGGAAGGGAG    18059    AAGA  A
                                TGG   GGG GGGAGGGAG
                                |||   ||| |||||||||
                                ACC   CCC CCTTCCCTC
                                  CCA_  _
GAM711  DYRK1A  5'  TGGGGGAAGGGAGGGAAGAG  18093    AAGA        _
                                TGG   GGGAGGGAGGGA GAG
                                |||   |||||||||||| |||
                                ACC   CCTTCCCTCCCT CTC
                                  C___          T
GAM711  ED1     5'  TGGGAAAGGGAGGAGGAGGG  18095    A       __
                                TGG AGAGGGAGG  GAGGG
                                ||| |||||||||  |||||
                                ACC TTTCCCTCC  CTCCC
                                  C        TC
GAM711  ED1     5'  AGGAGGAGGGGCGGGAGAGAG 18094    AG     A_
                                AG  GGAGGG  GGGAGAGAG
                                ||  ||||||  |||||||||
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                                TC  CCTCCC  CCCTCTCTC
                                 CT     CG
GAM711  EFNA3    3'  TGGGGGGACAAAGGGAGAG   18096     AAGA   G
                                TGG    GGGA GGAGGGAGAG
                                |||    |||| ||||||||||
                                ACC    CCCT TTTCCCTCTC
                                  C___    G
GAM711  EGLN1    5'  GGGAGGGCCGGGGGGAG     18097    AA    A_  A
                                GG  GAGGG  GGG GGGAG
                                ||  |||||  ||| |||||
                                CC  CTCCC  CCC CCCTC
                                 __     GG  _
GAM711  EGR3     5'  TGCGAGAGGGAAAGTTCGGGGG 18098    GA     __________
           GAGGG                    TG  AGAGGGA       GGGAGGG
                                ||  |||||||       |||||||
                                AC  TCTCCCT       CCCTCCC
                                 GC      TTCAAGCCC
GAM711  EGR3     5'  GAGGGGGGAGGGAAGAAG    18099      A       AG
                                GAGGG GGGAGGGAG  AG
                                ||||| |||||||||  ||
                                CTCCC CCCTCCCTT  TC
                                   _       CT
GAM711  EHD4     3'  TGGAAGGGAGGTTGGGAG    18100     AG      GA
                                TGGA  AGGGAGG  GGGAG
                                ||||  |||||||  |||||
                                ACCT  TCCCTCC  CCCTC
                                   __      AA
GAM711  EIF4EBP1 3'  GGAAGGAGGGGGAGGGAG    18101      AG  A
                                GGAAG  GG GGGAGGGAG
                                |||||  ||  |||||||||
                                CCTTC  CC CCCTCCCTC
                                   CT  _
GAM711  EIF4G2   5'  GGGGGAGGGAAGGGGGAG    18102    AA       A
                                GG  GAGGGAGGG GGGAG
                                ||  |||||||| |||||
                                CC  CTCCCTTCC CCCTC
                                 CC       _
GAM711  ELAVL4   5'  TGGGGGGGTGGGCGGGGGAGAG 18103     AAGA  A  A  A
                                TGG    GGG GGG GGG GAGAG
                                |||    ||| ||| ||| |||||
                                ACC    CCC CCC CCC CTCTC
                                  CC__   A  G  C
GAM711  EMX2     5'  GGAAAGGAGGGGGGAGGGAGAG 18104      __    A
                                GGAA  GAGGG GGGAGGGAGAG
                                ||||  ||||| ||||||||||
                                CCTT  CTCCC CCCTCCCTCTC
                                   TC    _
GAM711  ENSA     5'  GAAGGGGGAGGGGAAA      18105       A      A
                                GAGGG GGGAGGG GAGA
                                ||||| ||||||| ||||
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                                CTTCC CCCTCCC CTTT
                                  _     _
GAM711  ENTPD2   3'  TGGGGGAGGGATGGGGCAG   18106    AAGA      _  AG
                                TGG   GGGAGGGA GGG  AG
                                |||   |||||||| |||  ||
                                ACC   CCCTCCCT CCC  TC
                                  ____       A   CG
GAM711  EPB49    3'  TGGGGTGAGGGGCAGGGAGAG  18107    AAGA _    __
                                TGG   GG GAGGG  AGGGAGAG
                                |||   || |||||  ||||||||
                                ACC   CC CTCCC  TCCCTCTC
                                  ____ A    CG
GAM711  EPHB1    3'  GGAGAAGGGAGGGGACTCTCAG 18108    AG      ________
           GGAG                    GGA  AGGGAGGG      AGGGAG
                                |||  ||||||||      ||||||
                                CCT  TCCCTCCC      TCCCTC
                                  CT       CTGAGAG
GAM711  ERBB3    3'  TGGGAGAGAGAGGGAATAGGGA 18109    A        ___
           G                     TGG AGAGGGAGGGA   GGGAG
                                ||| ||||||||||   |||||
                                ACC TCTCTCTCCCT   CCCTC
                                  C         TAT
GAM711  EYA3     3'  GGGAGGGAGAGAGGGAGAGAG  18110    AA
                                GG  GAGGGAGGGAGGGAGAGAG
                                ||  ||||||||||||||||||
                                CC  CTCCCTCTCTCCCTCTCTC
                                  __
GAM711  F9       3'  GAGGGTAAAAGGGAGAGAG   18111      AG
                                GAGGG  GGAGGGAGAGAG
                                |||||  ||||||||||||
                                CTCCC  TTTCCCTCTCTC
                                   AT
GAM711  FGF12    3'  TGAGAGAGGGAAGAAGGGGAGA 18112    GA          A
           G                     TG  AGAGGGAGGGAGGG GAGAG
                                ||  ||||||||||||| |||||
                                AC  TCTCCCTTCTTCCC CTCTC
                                  TC          _
GAM711  FHIT     5'  TGAAAGGCAGAGGGAGGGAG   18113      AG
                                TGGAAG  GGAGGGAGGGAG
                                ||||||  ||||||||||||
                                ACTTTC  TCTCCCTCCCTC
                                   CG
GAM711  FOXF1    3'  TGGGGAGGGAGATCGGGAGGGA 18114    AA     ____
           G                     TGG  GAGGGA    GGGAGGGAG
                                |||  ||||||   |||||||||
                                ACC  CTCCCT    CCCTCCCTC
                                  C_     CTAG
GAM711  FOXF2    3'  GAGGAGGGGAGAGGAGAGAG   18115     GA    _
                                GAGG  GGGAG GGAGAGAG
                                ||||  ||||| ||||||||
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                                CTCC  CCCTC CCTCTCTC
                                  TC     T
GAM711  FXYD6    3'  TGGAAGGGGTAGGGTCCCAGAG 18116       A  _   AGGG
                                TGGAAG GGG AGGG    AGAG
                                |||||| ||| ||||    ||||
                                ACCTTC CCC TCCC    TCTC
                                   _  A    AGGG
GAM711  FZD1     3'  GGAGGGGACAGAAGGAGGGGGA 18117     A__  G        A
          G                      GGA   GA GGAGGGAGGG GAG
                                |||   || ||||||||| |||
                                CCT   CT TCTTCCTCCC CTC
                                  CCC  G         C
GAM711  GAS7     3'  TGGAAGATGGAGAGAGGG    18118        G
                                TGGAAGA GGAGGGAGGG
                                ||||||| ||||||||||
                                ACCTTCT CCTCTCTCCC
                                    A
GAM711  GJA5     3'  TGGAGGAGGGAGGGTGA     18119      AGAG        A
                                TGGA    GGAGGGAGGG GA
                                ||||    |||||||||| ||
                                ACCT    CCTCCCTCCC CT
                                  _____         A
GAM711  GRM4     3'  TGGGGAAGGGTGGCAGGGAGAG 18120     AA    A  G
                                TGG  GAGGG GG AGGGAGAG
                                |||  ||||| || ||||||||
                                ACC  TTCCC CC TCCCTCTC
                                  CC     A  G
GAM711  HAP1     3'  AGAAGAGGGAGGGAGGGAG    18121
                                GGAAGAGGGAGGGAGGGAG
                                ||||||||||||||||||
                                TCTTCTCCCTCCCTCCCTC

GAM711  HBA1     3'  GGAGGAGGGGCTGGGGGGAG   18122     A    A__   A
                                GGA GAGGG   GGG GGGAG
                                ||| |||||   ||| |||||
                                CCT CTCCC   CCC CCCTC
                                  C     CGA  _
GAM711  HHLA1    5'  TGGGGGGTGGTATGGAGAGAG  18123     AAGA   A  GAG
                                TGG    GGG GG   GGAGAGAG
                                |||    ||| ||   ||||||||
                                ACC    CCC CC   CCTCTCTC
                                  C___   A  ATA
GAM711  HLF      3'  TGAAGGAGGGAGGGGATGGGAG 18124      A        A__
                                TGGA GAGGGAGGG   GGGAG
                                |||| |||||||||   |||||
                                ACTT CTCCCTCCC   CCCTC
                                  C        CTA
GAM711  HMGA2    3'  AGGGAGAGGGAGAGAGAG    18125    A
                                AG GGGAGGGAGGGAGAG
                                || ||||||||||||||
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                                TC CTCTCCCTCTCTCTC
                                 C
GAM711  HOXB6   3'  TGGGGAGGGGGTGGGAGAG   18126    AA    A  GA
                                TGG  GAGGG GG  GGGAGAG
                                |||  ||||| ||  |||||||
                                ACC  CTCCC CC  CCCTCTC
                                  C_    _ A_
GAM711  HOXC4   5'  TGGGAGAGAGGAGGGGCGGAG  18127    A   _    AG
                                TGG AGAG GGAGGG  GGAG
                                ||| |||| ||||||  ||||
                                ACC TCTC CCTCCC  CCTC
                                  C   T     CG
GAM711  HPN     3'  TGGAAGAGAGGACCCTGGAGGG 18128        _  G___
            AG                    TGGAAGAG GGA    GGAGGGAG
                                ||||||||| |||    ||||||||
                                ACCTTCTC CCT    CCTCCCTC
                                     T   GGGA
GAM711  HYOU1   3'  TGGGAGAGGAAGGGAGGG    18129    A
                                TGG AGAGGGAGGGAGGG
                                ||| ||||||||||||||
                                ACC TCTCCTTCCCTCCC
                                  C
GAM711  IFITM2  5'  GGAGAGGGAGGAAAGAGGG   18130    A      ___
                                GGA GAGGGAGG   GAGGG
                                ||| ||||||||   |||||
                                CCT CTCCCTCC   CTCCC
                                  _       TTT
GAM711  IGF2    5'  TGAAAGGGGGGGGCCGAAGAGA 18131       A   A   AG
            G                    TGGAAG GGG GGG  GGAGAGAG
                                ||||||| ||| |||  ||||||||
                                ACTTTC CCC CCC  CTTCTCTC
                                   _  C   GG
GAM711  IGF2    5'  TGGGGGGGACGGGAGGGAG   18133    AAGA   _
                                TGG    GGGA GGGAGGGAG
                                |||    |||| |||||||||
                                ACC    CCCT CCCTCCCTC
                                  CC__    G
GAM711  IGF2    5'  GAGGGGGGGAGGGAGTCGGAG  18132      A       A__
                                GAGGG GGGAGGGAG   GAG
                                ||||| |||||||||   |||
                                CTCCC CCCTCCCTC   CTC
                                   C        AGC
GAM711  IKBKG   5'  TGGAGGAGGAGGGAGGA     18134      A AG
                                TGGA G  GGAGGGAGGG
                                |||| |  ||||||||||
                                ACCT C  CCTCCCTCCT
                                  _ CT
GAM711  IL2RG   3'  GGGAGGGAAAGAGGGAGGGAG  18135    AA           A
                                GG  GAGGGAGGGAGGGAG GAG
                                ||  |||||||||||||| |||
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                                CC  CTCCCTTTCTCCCTC CTC
                                 __            C
GAM711  KAI1    3'  TGGAGGAGGGAGCCAGGGAG  18136     A     GG
                                TGGA GAGGGAG  AGGGAG
                                |||| |||||||  ||||||
                                ACCT CTCCCTC  TCCCTC
                                  C      GG
GAM711  KCNA5   3'  TGGGGGGATCGAGGGAGGGAG 18137    AA_  GG
                                TGG   GA  GAGGGAGGGAG
                                |||   ||  ||||||||||
                                ACC   CT  CTCCCTCCCTC
                                  CCC  AG
GAM711  KCND3   3'  GGGAAAGGGGGGAGGGAG   18138   A    A
                                GG AGAGGG GGGAGGGAG
                                || |||||| |||||||||
                                CC TTTCCC CCCTCCCTC
                                 C    _
GAM711  KPNB1   5'  TGGGAAGGGAGGGTGGG    18139    AA       A
                                TGG  GAGGGAGGG GGG
                                |||  ||||||||| |||
                                ACC  TTCCCTCCC CCC
                                  C_       A
GAM711  KRTHA1  5'  TGGGAGGGAGGGAGGGAG   18140    AA
                                TGG  GAGGGAGGGAGGGAG
                                |||  ||||||||||||||
                                ACC  CTCCCTCCCTCCCTC
                                  __
GAM711  LAG3    5'  TGGAGAGAGGGTGGGGAGGG  18141    _    A_
                                TGGA AGAGGG  GGGAGGG
                                |||| ||||||  |||||||
                                ACCT TCTCCC  CCCTCCC
                                  C     AC
GAM711  LMO4    5'  GGAGCTGGAGGGAGGGAGGGAG 18142    A___
                                GGA   GAGGGAGGGAGGGAG
                                |||   ||||||||||||||
                                CCT   CTCCCTCCCTCCCTC
                                  CGAC
GAM711  MAF     5'  TGGAGGAGAGGGAGGG     18143     A A
                                TGGA G GGGAGGGAGGG
                                |||| | ||||||||||
                                ACCT C CTCTCCCTCCC
                                  _ _
GAM711  MAP4    3'  TGGGAGGAGGGAAGGGAGAG  18144    AA   GA
                                TGG  GAGG  GGGAGGGAGAG
                                |||  ||||  ||||||||||
                                ACC  CTCC  CCTTCCCTCTC
                                  __   TC
GAM711  MDFI    3'  GGAGAGGACCAGGGAGAG   18145    A    AGGG
                                GGA GAGGG   AGGGAGAG
                                ||| |||||   ||||||||
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                                CCT CTCCT    TCCCTCTC
                                  _    GG__
GAM711  MDK     3'  TGGGAGAGGGAGGGCGTGG   18146    A       AG_
                                TGG AGAGGGAGGG   GG
                                ||| ||||||||||   ||
                                ACC TCTCCCTCCC   CC
                                  C         GCA
GAM711  MFGE8   3'  TGGAGGGTGGGAAAGAGGGAGG 18147     AGA_          A
          GAG                     TGGA    GGGAGGGAGGGAG GAG
                                ||||    |||||||||||||| |||
                                ACCT    CCCTTTCTCCCTC CTC
                                  CCCA           C
GAM711  MFRP    3'  GGAGAAAGGAGGGGGAGAG   18148    AG      AG
                                GGA  AGGGAGGG  GGAGAG
                                |||  ||||||||  ||||||
                                CCT  TTCCTCCC  CCTCTC
                                  CT       ___
GAM711  MLF2    3'  TGGGCAGGAGGAGGGAGAGAG  18149    AAGA    G
                                TGG    GGGAGG AGGGAGAGAG
                                |||    |||||| ||||||||||
                                ACC    TCCTCC TCCCTCTCTC
                                  CG__     _
GAM711  MMP15   3'  TGTGAGTCGGGAGGGAGGGAG  18150    GA  A_
                                TG  AG  GGGAGGGAGGGAG
                                ||  ||  ||||||||||||||
                                AC  TC  CCCTCCCTCCCTC
                                 AC  AG
GAM711  MNT     3'  TGGAAGGGCTAGGGAGGGAG   18151       A  G_
                                TGGAAG GG  AGGGAGGGAG
                                ||||||  ||  ||||||||||
                                ACCTTC CC  TCCCTCCCTC
                                   _  GA
GAM711  MTMR3   3'  TGGAAAAGGTAGGGAGGGAG   18152         G
                                TGGAAGAGG AGGGAGGGAG
                                |||||||||  ||||||||||
                                ACCTTTTCC TCCCTCCCTC
                                      A
GAM711  MUC3B   3'  GGAGGAGGGAGACTGAGGG    18153    A       ___
                                GGA GAGGGAGG  GAGGG
                                |||  ||||||||  |||||
                                CCT CTCCCTCT  CTCCC
                                  C       GA
GAM711  NAV2    3'  GGAGGAGGAAGGGGAGGGAG   18154    A       _
                                GGA GAGGGAGGG AGGGAG
                                |||  |||||||||  ||||||
                                CCT CTCCTTCCC TCCCTC
                                  C       C
GAM711  NCOR2   3'  GGAAGGGAGGGAGGGAG     18156    AG
                                GGA  AGGGAGGGAGGGAG
                                |||  ||||||||||||||
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                              CCT  TCCCTCCCTCCCTC
                                ___
GAM711  NCOR2    3'  TGGGAGGCGGAGGGAGGG    18155     A  AG
                              TGG AG  GGAGGGAGGG
                              ||| ||  ||||||||||
                              ACC TC  CCTCCCTCCC
                                C  CG
GAM711  NDP      5'  GGGAGAGAGAGAGGGAGAGAG  18157    AA
                              GG  GAGGGAGGGAGGGAGAGAG
                              ||  ||||||||||||||||||
                              CC  CTCTCTCTCTCCCTCTCTC
                                ___
GAM711  NDST2    5'  GGGGGAGGAAGGGAGGGAG    18158    AA
                              GG  GAGGGAGGGAGGGAG
                              ||  ||||||||||||||
                              CC  CTCCTTCCCTCCCTC
                                CC
GAM711  NEUD4    3'  GGACAGAGAGGGAGGGAGGGAG 18159     ___            A
             GGAG                  GGA   AGAGGGAGGGAGGGAG GAG
                              |||   |||||||||||||||| |||
                              CCT   TCTCCCTCCCTCCCTC CTC
                                GTC             C
GAM711  NEUROD2  5'  GGGGGAGGGGGGCAAGAGAGAG  18160    AA    A _
                              GG  GAGGG GG GAGGGAGAG
                              ||  ||||| || |||||||||
                              CC  CTCCC CC TTCTCTCTC
                                CC    _ G
GAM711  NFIA     5'  TGAGAGAGGAGAAAGAGGGAGA 18161    GA    _
             GAG                    TG  AGAGG GAGGGAGGGAGAGAG
                              ||  ||||| ||||||||||||||
                              AC  TCTCC CTTTCTCCCTCTCTC
                                TC    T
GAM711  NHLH1    5'  TGGGAGGGGGAGGAAGGGGGAG 18162     A  A         A
                              TGG AG GGGAGGGAGGG GAG
                              ||| || |||||||||| |||
                              ACC TC CCCTCCTTCCC CTC
                                C  C          C
GAM711  NHP2L1   3'  TGGCAGAGGGAGGGAGGAAA   18163     A
                              TGG AGAGGGAGGGAGGGAG
                              ||| ||||||||||||||
                              ACC TCTCCCTCCCTCCTTT
                                G
GAM711  NLGN3    3'  TGGATCTGGGAGGGAGGGAG   18164      AGA
                              TGGA   GGGAGGGAGGGAG
                              ||||   ||||||||||||
                              ACCT   CCCTCCCTCCCTC
                                AGA
GAM711  NPTX1    3'  TGGGGAGGGGGAGAGGG     18165     AA    A
                              TGG  GAGGG GGGAGGG
                              |||  ||||| |||||||
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                                ACC  CTCCC CTCTCCC
                                  C_    C
GAM711  NRXN2   5'  TGGAGAGGGAGGGGAG      18166      A       A
                                TGGA GAGGGAGGG GGG
                                |||| ||||||||| |||
                                ACCT CTCCCTCCC CTC
                                  _       _
GAM711  NTSR1   3'  TGGGTGAGGATGGGAGGGAG  18168     AA    GA
                                TGG  GAGG  GGGAGGGAG
                                |||  ||||  |||||||||
                                ACC  CTCC  CCCTCCCTC
                                  CA    TA
GAM711  NTSR1   3'  TGGGGGAGGGGTGGGGAG    18167     AAGA      AG  A
                                TGG    GGGAGGG  GG GAG
                                |||    |||||||  || |||
                                ACC    CCCTCCC  CC CTC
                                  _____      CA  C
GAM711  NXF5    3'  GGAGAGGGAGGGCTCAGAG   18169     A       AG_
                                GGA GAGGGAGGG   GGAG
                                ||| |||||||||   ||||
                                CCT CTCCCTCCC   TCTC
                                  _       GAG
GAM711  NXF5    3'  GGAGAGGGAGGGCTCAGAG   18169     A       AG_
                                GGA GAGGGAGGG   GGAG
                                ||| |||||||||   ||||
                                CCT CTCCCTCCC   TCTC
                                  _       GAG
GAM711  NXF5    3'  GGAGAGGGAGGGCTCAGAG   18169     A       AG_
                                GGA GAGGGAGGG   GGAG
                                ||| |||||||||   ||||
                                CCT CTCCCTCCC   TCTC
                                  _       GAG
GAM711  NXF5    3'  GGAGAGGGAGGGCTCAGAG   18169     A       AG_
                                GGA GAGGGAGGG   GGAG
                                ||| |||||||||   ||||
                                CCT CTCCCTCCC   TCTC
                                  _       GAG
GAM711  NXF5    3'  GGAGAGGGAGGGCTCAGAG   18169     A       AG_
                                GGA GAGGGAGGG   GGAG
                                ||| |||||||||   ||||
                                CCT CTCCCTCCC   TCTC
                                  _       GAG
GAM711  NXF5    3'  GGAGAGGGAGGGCTCAGAG   18169     A       AG_
                                GGA GAGGGAGGG   GGAG
                                ||| |||||||||   ||||
                                CCT CTCCCTCCC   TCTC
                                  _       GAG
GAM711  OGDH    3'  TGGGGTGGGGAGGGAGTCCAAG 18170     AAGA       G__
            AGAG                  TGG   GGGAGGGAG   GAGAGAG
                                |||   |||||||||   |||||||
                                ACC   CCCTCCCTC   TTCTCTC
                                  CCAC       AGG
GAM711  OGG1    3'  GGGTGGGGATGGGGAGAGAG  18171     A_   __
                                GGG  GGGA  GGGAGAGAG
                                |||  ||||  |||||||||
```

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                                CCC  CCCT  CCCTCTCTC
                                  AC    AC
GAM711  OGG1     3'  GGGTGGGGATGGGGAGAGAG  18171     A_   __
                                GGG  GGGA  GGGAGAGAG
                                |||  ||||  |||||||||
                                CCC  CCCT  CCCTCTCTC
                                  AC    AC
GAM711  PAFAH1B1 5'  GGAGGAAGGAGGGAGGGAG   18174     A
                                GGA GAGGGAGGGAGGGAG
                                ||| ||||||||||||||
                                CCT CTTCCTCCCTCCCTC
                                  C
GAM711  PAFAH1B1 5'  GGGGGAGGGAGAGGGGAGGGAG 18173    AA       A    A
                                GG  GAGGGAGGG GGGAG GAG
                                ||  ||||||||| ||||| |||
                                CC  CTCCCTCTC CCCTC CTC
                                 CC       _    C
GAM711  PAFAH1B1 5'  GGGGGAGGGGGAGGGAGAG   18175    AA    AG
                                GG  GAGGG  GGAGGGAGAG
                                ||  |||||  ||||||||||
                                CC  CTCCC  CCTCCCTCTC
                                 CC    __
GAM711  PAFAH1B1 5'  GGAGGGGGAGGGAGAGGGGAG  18172     A A       _  A
                                GGA G GGGAGGGAG GG GAG
                                ||| | |||||||| || |||
                                CCT C CCCTCCCTC CC CTC
                                  _ C       T  C
GAM711  PAK1     5'  TGGGGGGGCGGGAGGGAG    18176     AAGA   A
                                TGG    GGG GGGAGGGAG
                                |||    ||| |||||||||
                                ACC    CCC CCCTCCCTC
                                  CC__   G
GAM711  PAX2     5'  TGGGGGAGGGAGGATGAG    18177     AAGA       GA
                                TGG    GGGAGGGAGG  GAG
                                |||    ||||||||||  |||
                                ACC    CCCTCCCTCC  CTC
                                  _____         TA
GAM711  PAX2     5'  TGGGGGAGGGAGGATGAG    18177     AAGA       GA
                                TGG    GGGAGGGAGG  GAG
                                |||    ||||||||||  |||
                                ACC    CCCTCCCTCC  CTC
                                  _____         TA
GAM711  PBX2     3'  TGGGAGAGGGAGAGAGAAAG   18178     A         GG
                                TGG AGAGGGAGGGAG  AG
                                ||| ||||||||||||  ||
                                ACC TCTCCCTCTCTC  TC
                                  C          TT
GAM711  PCDH11Y  5'  TGGCGAGGGGGAGGGACTTAAC 18179     A_  A      GG_  G
            AGAG                    TGG  AG GGGAGGGA   GA AGAG
                                ||| || ||||||||   || ||||
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                                ACC  TC CCCTCCCT   TT TCTC
                                  GC  C       GAA  G
GAM711  PCTK3    5'  GGGAGGGGAAGGGAGGGAG   18180    A  A
                                GG AG GGGAGGGAGGGAG
                                || || ||||||||||||
                                CC TC CCTTCCCTCCCTC
                                 C  C
GAM711  PDGFB    3'  TGGGAAGGGAGGTGGGAG    18181     AA      GA
                                TGG  GAGGGAGG  GGGAG
                                |||  ||||||||  |||||
                                ACC  TTCCCTCC  CCCTC
                                  C_       A_
GAM711  PEA15    3'  TGGAGGATGGGGGGAAGGGAG   18182      A  _  A
                                TGGA GA GGG GGGAGGGAG
                                |||| || ||| |||||||||
                                ACCT CT CCC CCTTCCCTC
                                  C  A  _
GAM711  PIK3R2   3'  TGGGGGAGGGAAGGAAAGA   18183     AAGA
                                TGG    GGGAGGGAGGGAGAGA
                                |||    ||||||||||||||||
                                ACC    CCCTCCCTTCCTTTCT
                                 _____
GAM711  PIM1     3'  TGAAGGAGGGGGTGAGGGAG   18184      A    A  _
                                TGGA GAGGG GG GAGGGAG
                                |||| ||||| || |||||||
                                ACTT CTCCC CC CTCCCTC
                                  C    _ A
GAM711  PKD2     3'  GGAAGAGATGAGGGGGGGAG   18185         _    A
                                GGAAGAGG GAGGG GGGAG
                                |||||||| ||||| |||||
                                CCTTCTCT CTCCC CCCTC
                                     A    C
GAM711  PLD2     3'  GGACAGGGAGGGGGTTCAAG   18186     AG       A  GA_
                                GGA  AGGGAGGG GG   GAG
                                |||  |||||||| ||   |||
                                CCT  TCCCTCCC CC   TTC
                                  G_       _ AAG
GAM711  PLOD     3'  TGGAAGAGGTGGGGGAAGG   18187         GA_
                                TGGAAGAGG   GGGAGGG
                                |||||||||   |||||||
                                ACCTTCTCC   CCCTTCC
                                     ACC
GAM711  PLXNB3   3'  GGAGAGGGGGAAGGAGGG    18188     _  A
                                GGA AG GGGAGGGAGGG
                                ||| || ||||||||||
                                CCT TC CCCTTCCTCCC
                                  C  C
GAM711  PMX1     5'  GGAAGAGGGAGGGAAGGAGAG  18189
                                GGAAGAGGGAGGGAGGGAGAG
                                |||||||||||||||||||||
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                                CCTTCTCCCTCCCTTCCTCTC

GAM711  PMX1     5'  GGAAGAGGGAGGGAAGGAGAG  18189
                                GGAAGAGGGAGGGAGGGAGAG
                                ||||||||||||||||||||
                                CCTTCTCCCTCCCTTCCTCTC

GAM711  POU2AF1  3'  TGGAAAGGAAGAAGGGAGGGAG 18190      __
                                TGGAA  GAGGGAGGGAGGGAG
                                |||||  ||||||||||||||
                                ACCTT  CTTCTTCCCTCCCTC
                                   TC
GAM711  POU2AF1  3'  GGGAGAGGGAGGAAGTGAGGGA 18191    A      _____      A
           GGGAG                    GG AGAGGGAGG    GAGGGAG GAG
                                || |||||||||    ||||||| |||
                                CC TCTCCCTCC    CTCCCTC CTC
                                 C        TTCA      C
GAM711  PPP2R5E  5'  TGGGGAGGGGGGGGAAGGGAGGG 18192     AA    A   _    A
           AG                     TGG  GAGGG GGGA GGGAG GAG
                                |||  ||||| |||| ||||| |||
                                ACC  CTCCC CCCT CCCTC CTC
                                  C_    C    T    C
GAM711  PRDM2    3'  GGGAGAGGGAAGGTGGGGAGAG 18193    A        A_
           AG                     GG AGAGGGAGGG  GGGAGAGAG
                                || ||||||||||  |||||||||
                                CC TCTCCCTTCC  CCCTCTCTC
                                 C         AC
GAM711  PRKACA   3'  TAGAGGAAGGAGGGAGGGAG   18194      A
                                TGGA GAGGGAGGGAGGGAG
                                |||| ||||||||||||||
                                ATCT CTTCCTCCCTCCCTC
                                   C
GAM711  PRKACA   3'  TGGGAGAGGGGGCAGGAGGG   18195     A     A__
                                TGG AGAGGG   GGGAGGG
                                ||| ||||||   |||||||
                                ACC TCTCCC   TCCTCCC
                                  C     CCG
GAM711  PTMS     3'  AGGGGAGGGAGAAAGAGA    18196    A       GG
                                AG GGGAGGGAG  AGAGA
                                || |||||||||  |||||
                                TC CCCTCCCTC  TCTCT
                                  _       TT
GAM711  PTPRA    3'  TGGGGGAGGGGACCAGGGAGAG 18197    AAGA     ____
           AG                     GG   GGGAGGG   AGGGAGAGAG
                                ||   |||||||   ||||||||||
                                CC   CCCTCCC   TCCCTCTCTC
                                  ____      CTGG
GAM711  PTPRA    3'  TGGGGGAGGGGACCAGGGAGAG 18197    AAGA     ____
           AG                     GG   GGGAGGG   AGGGAGAGAG
                                ||   |||||||   ||||||||||
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                                CC   CCCTCCC   TCCCTCTCTC
                                 ____     CTGG
GAM711  PTPRA    3'  TGGGGGAGGGGACCAGGGAGAG 18197    AAGA     ____
          AG                     GG   GGGAGGG   AGGGAGAGAG
                                 ||   |||||||   ||||||||||
                                CC   CCCTCCC   TCCCTCTCTC
                                 ____     CTGG
GAM711  PTPRS    5'  TGGAGGAGGCAGAGGGAG   18198    A   GAG
                                TGGA GAGG  GGAGGGAG
                                |||| ||||  ||||||||
                                ACCT CTCC  TCTCCCTC
                                  C   G__
GAM711  PTPRS    5'  TGGAGGAGGCAGAGGGAG   18198    A   GAG
                                TGGA GAGG  GGAGGGAG
                                |||| ||||  ||||||||
                                ACCT CTCC  TCTCCCTC
                                  C   G__
GAM711  PTPRS    5'  TGGAGGAGGCAGAGGGAG   18198    A   GAG
                                TGGA GAGG  GGAGGGAG
                                |||| ||||  ||||||||
                                ACCT CTCC  TCTCCCTC
                                  C   G__
GAM711  PTPRS    5'  TGGAGGAGGCAGAGGGAG   18198    A   GAG
                                TGGA GAGG  GGAGGGAG
                                |||| ||||  ||||||||
                                ACCT CTCC  TCTCCCTC
                                  C   G__
GAM711  PTPRZ1   5'  TGGAGAGGGAGGGGGAG    18199    A      AG
                                TGGA GAGGGAGGG  GGAG
                                |||| |||||||||  ||||
                                ACCT CTCCCTCCC  CCTC
                                  _      __
GAM711  PYGB     3'  TGGAAAGGGAGGGAGAATGGAG 18200     A       ___
                                TGGA GAGGGAGGGAG  GGAG
                                |||| ||||||||||  ||||
                                ACCT TTCCCTCCCTC  CCTC
                                  _        TTA
GAM711  RAD23A   3'  TAGAAGAGGATGGGGGGG   18201       GA  A
                                TGGAAGAGG  GGG GGG
                                |||||||||  ||| |||
                                ATCTTCTCC  CCC CCC
                                     TA  C
GAM711  RARG     3'  GGAAGGCACTAGGGAGAGAG  18202     G___
                                GGGAGG   AGGGAGAGAG
                                ||||||   ||||||||||
                                CCTTCC   TCCCTCTCTC
                                   GTGA
GAM711  RBP5     3'  GAGGAGGGACCCAGAGGGAG  18203   A    G__
                                GA GAGGGA  GGAGGGAG
                                || ||||||  ||||||||
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                                CT CTCCCT   TCTCCCTC
                                 C     GGG
GAM711   RCV1    3'  TGGACAGAGGGAGGGGTGG   18204     _       AG
                                TGGA AGAGGGAGGG  GG
                                |||| ||||||||||  ||
                                ACCT TCTCCCTCCC  CC
                                  G        CA
GAM711   RYR1    5'  CGGGGAACAGAGGGAGGG    18205    AA  G
                                TGG  GA GGAGGGAGGG
                                |||  || ||||||||||
                                GCC  TT TCTCCCTCCC
                                 CC  G
GAM711   SCA1    5'  GGAAGGGGGGGCAGAGGGAG  18206      A   A __
                                GGAAG GGG GG  GAGGGAG
                                ||||| ||| ||  |||||||
                                CCTTC CCC CC  CTCCCTC
                                  _  C  GT
GAM711   SCD     3'  GAGAGAGGGAGGGAGAGA    18207
                                GAGGGAGGGAGGGAGAGA
                                ||||||||||||||||||
                                CTCTCTCCCTCCCTCTCT

GAM711   SEPN1   3'  TGGGGGGGGAGGCAGAGAG   18208    AAGA  A     G
                                TGG    GGG GGGAGG AGAGAG
                                |||    ||| |||||| ||||||
                                ACC    CCC CCCTCC TCTCTC
                                 _____  _     G
GAM711   SEPN1   3'  TGGGGTGAGGGGGGTGGGGAGAG 18209    AA_    A  GA
                                TGG   GAGGG GG  GGGAGAG
                                |||   ||||| ||  |||||||
                                ACC   CTCCC CC  CCCTCTC
                                 CCA    _ AC
GAM711   SIX2    3'  GGAAGAGACAGAGGGAGAGAG  18210        GAG
                                GGAAGAGG   GGAGGGAGAGAG
                                ||||||||   ||||||||||||
                                CCTTCTCT   TCTCCCTCTCTC
                                     G__
GAM711   SIX3    5'  GGGAGAGGGAGAGGGAGAGAG  18213    A     GG
                                GG AGAGGGA  GAGGGAGAGAG
                                || |||||||  ||||||||||
                                CC TCTCCCT  CTCCCTCTCTC
                                 C     __
GAM711   SIX3    5'  GGGAGAGGGAGAGAGGAGAG   18214    A         G
                                GG AGAGGGAGGGAGG AGAG
                                || ||||||||||||| ||||
                                CC TCTCCCTCTCTCC TCTC
                                 C          _
GAM711   SIX3    5'  AGGAGGAGGGAGAGGAGAG    18211    AG      _
                                AG  GGAGGGAG GGAGAG
                                ||  |||||||| ||||||
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                                TC  CCTCCCTC CCTCTC
                                 CT       T
GAM711  SIX3     3'  TGGGGGAGGAGGGGAAGGAGAG 18212     AA    GA
                                TGG  GAGG  GGGAGGGAGAG
                                |||  ||||  ||||||||||
                                ACC  CTCC  CCCTTCCTCTC
                                  CC    TC
GAM711  SLC2A4   3'  TGGGGGAAGGAAGAGGGAG   18215     AA       G
                                TGG  GAGGGAGG AGGGAG
                                |||  |||||||| ||||||
                                ACC  CTTCCTTC TCCCTC
                                  CC       _
GAM711  SLC2A4   3'  GGAAGAGGGAGGGGAGAG    18216            A
                                GGAAGAGGGAGGG GGGAG
                                |||||||||||| |||||
                                CCTTCTCCCTCCC CTCTC

                                          _
GAM711  SLC39A1  3'  TGGGGGAGGGAAGGGAGAA   18217     AAGA       _
                                TGG    GGGAGGGA GGGAGAG
                                |||    |||||||| |||||||
                                ACC    CCCTCCCT CCCTCTT
                                  _____       T
GAM711  SLC6A3   3'  GGAGCAGGGAGGGAGGGAG   18218     AG
                                GGA  AGGGAGGGAGGGAG
                                |||  ||||||||||||||
                                CCT  TCCCTCCCTCCCTC
                                  CG
GAM711  SLC9A3R1 3'  TGGGGGAGGAAGGGAGGG    18219     AA
                                TGG  GAGGGAGGGAGGG
                                |||  ||||||||||||
                                ACC  CTCCTTCCCTCCC
                                  CC
GAM711  SOX10    5'  TGGGAGGGAGGGGCGGG      18220     AA       A_
                                TGG  GAGGGAGGG  GGG
                                |||  |||||||||  |||
                                ACC  CTCCCTCCC  CCC
                                  __        CG
GAM711  SOX11    3'  TGGAAAGGGAGGGCAGAGAG   18221      A       AG
                                TGGA GAGGGAGGG  GGAGAG
                                ||||  |||||||||  ||||||
                                ACCT TTCCCTCCC  TCTCTC
                                  _        G_
GAM711  SOX13    3'  TGGCAGAGCCAGGGAGGGAG   18222     A    GG
                                TGG AGAG  AGGGAGGGAG
                                |||  ||||  ||||||||||
                                ACC TCTC  TCCCTCCCTC
                                  G    GG
GAM711  SPTBN4   3'  GAGGGGGGAGGAGAGA      18223       A     G
                                GAGGG GGGAGG AGAGA
                                |||||  ||||||  |||||
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                                CTCCC CCCTCC TCTCT
                                  _    _
GAM711  STXBP1   3'  TGGGAGGGAGACGGGGAGAG  18224    AA      GA
                                TGG  GAGGGAGG  GGGAGAG
                                |||  ||||||||  |||||||
                                ACC  CTCCCTCT  CCCTCTC
                                  __       GC
GAM711  SUPT6H   3'  GGAGGGGCAGGGAGGGAG    18225    A A  _
                                GGA G GGG AGGGAGGGAG
                                ||| | ||| ||||||||||
                                CCT C CCC TCCCTCCCTC
                                  _ _  G
GAM711  TAL1     5'  GGCAAGAGGGAGGGAGAGAG  18226    _
                                GG AAGAGGGAGGGAGGGAG
                                || ||||||||||||||||
                                CC TTCTCCCTCCCTCTCTC
                                 G
GAM711  TBX5     5'  GGAAGGGGGAGAGGAGGG    18227      A    _
                                GGAAG GGGAG GGAGGG
                                ||||| ||||| ||||||
                                CCTTC CCCTC CCTCCC
                                   C    T
GAM711  TBX5     5'  GGAAGGGGGAGAGGAGGG    18227      A    _
                                GGAAG GGGAG GGAGGG
                                ||||| ||||| ||||||
                                CCTTC CCCTC CCTCCC
                                   C    T
GAM711  TCF21    5'  TGGGGGAGTGGACGAGGGAGAG 18229    AA  _  G G
          AG                    TGG  GAG GGA G AGGGAGAGAG
                                |||  ||| ||| | ||||||||||
                                ACC  CTC CCT C TCCCTCTCTC
                                  CC   A   G _
GAM711  TCF21    5'  TGGACGAGGGAGAGAGAG    18228      A
                                TGGA GAGGGAGGGAGGG
                                |||| ||||||||||||
                                ACCT CTCCCTCTCTCTC
                                  G
GAM711  TCF7L2   5'  GGGAGGGGAAAAGAGGGAG   18231    A  A
                                GG AG GGGAGGGAGGGAG
                                || || ||||||||||||
                                CC TC CCTTTTCTCCCTC
                                 C  C
GAM711  TCF7L2   5'  GGGAGGGGAAGGGGGGGGAG  18230    A  A     A   A
                                GG AG GGGAGGG GGG GAG
                                || || ||||||| ||| |||
                                CC TC CCCTTCC CCC CTC
                                 C  _      C   C
GAM711  TFAP4    5'  TGGGAGGGGCGGGAGGGAG   18232    AA    A_
                                TGG  GAGGG  GGGAGGGAG
                                |||  |||||  |||||||||
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                                ACC  CTCCC  CCCTCCCTC
                                  __    CG
GAM711  TGFB1    3'  GGAGGAGGCAGAGAGGGAGAGA 18233     A    G
            G                    GGA GAGG AGGGAGGGAGAGAG
                                 ||| |||| ||||||||||||||
                                 CCT CTCC TCTCTCCCTCTCTC
                                   C   G
GAM711  TIRAP    5'  GAAGGGGGAGGAGGGAG     18234      A   AG
                                 GAAG GGG  GGAGGGAG
                                 |||| |||  ||||||||
                                 CTTC CCC  CCTCCCTC
                                   _  CT
GAM711  TLR9     3'  TGGGGTGAGGGAGGCGAGCAGG 18235     AA_      _ ____
            GGAG                    TGG   GAGGGAGG GA    GGGAG
                                 |||   |||||||| ||    |||||
                                 ACC   CTCCCTCC CT    CCCTC
                                   CCA       G  CGTC
GAM711  TLX1     5'  GGGAGGGGAGGGGAGGGGGAGA 18236    A  A     _    A
            G                    GG AG GGGAGGG AGGG GAGAG
                                 || || ||||||| |||| |||||
                                 CC TC CCCTCCC TCCC CTCTC
                                  C  _      C    C
GAM711  TLX1     5'  AGGGGGAGGGGAGGGAGAGAG  18237    A     _
                                 AG GGGAGGG AGGGAGAGAG
                                 || ||||||| ||||||||||
                                 TC CCCTCCC TCCCTCTCTC
                                  C      C
GAM711  TMOD3    3'  TGGGGGGTGGGGAGGGAG    18238     AAGA  A_
                                 TGG   GGG  GGGAGGGAG
                                 |||   |||  |||||||||
                                 ACC   CCC  CCCTCCCTC
                                   C___   AC
GAM711  TNFAIP2  3'  TGGTGGAGGGAGGCAGGAGAG  18239     AA      GA
                                 TGG  GAGGGAGG  GGGAGAG
                                 |||  ||||||||  |||||||
                                 ACC  CTCCCTCC  TCCTCTC
                                   AC       G_
GAM711  TNFAIP2  3'  GAAGAGGGAGGGCTCAGGG   18240          ___
                                 GAAGAGGGAGGG   AGGG
                                 ||||||||||||   ||||
                                 CTTCTCCCTCCC   TCCC
                                        GAG
GAM711  TOP1     3'  TGGGAGAGAGGGAAGGGAG   18241     AA          A
                                 TGG  GAGGGAGGGAGGG GAG
                                 |||  |||||||||||| |||
                                 ACC  CTCTCTCCCTTCC CTC
                                   __          _
GAM711  TRPC5    5'  TGGAGAGAGAGGGGAGAGAG   18242      A       A
                                 TGGA GAGGGAGGG GGGAGAG
                                 |||| |||||||| |||||||
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                                ACCT CTCTCTCCC CTCTCTC
                                  _      _
GAM711  TULP3    3'  TGGGGCAGGGAGGGGAAGGGGA 18243     AAG      __    A
            G                    TGG   AGGGAGGG  AGGG GAG
                                 |||   ||||||||  |||| |||
                                 ACC   TCCCTCCC  TCCC CTC
                                   CCG       CT   _
GAM711  UBE2V1   3'  TGGGAGGCGGGAGGGTAAAGGG 18245     A  A_     ___
            AG                   TGG AG  GGGAGGG   AGGGAG
                                 ||| ||  |||||||   ||||||
                                 ACC TC  CCCTCCC   TCCCTC
                                   C  CG      ATT
GAM711  UBE2V1   3'  TGGGAGGCGGGAGGGTAAGGGG 18244     A  A_     __    A
            AG                   TGG AG  GGGAGGG  AGGG GAG
                                 ||| ||  |||||||  |||| |||
                                 ACC TC  CCCTCCC  TCCC CTC
                                   C  CG      AT   _
GAM711  UBE2V1   3'  TGGGAGGCGGGAGGGTAAAGGG 18245     A  A_     ___
            AG                   TGG AG  GGGAGGG   AGGGAG
                                 ||| ||  |||||||   ||||||
                                 ACC TC  CCCTCCC   TCCCTC
                                   C  CG      ATT
GAM711  UNRIP    5'  GGGAAAGGGAGGGAGGGAG   18246    A
                                 GG AGAGGGAGGGAGGGAG
                                 || ||||||||||||||||
                                 CC TTTCCCTCCCTCCCTC
                                  C
GAM711  VAT1     3'  CGGGGGAGGGAGGGCAGAG   18247     AAGA        _
                                 TGG    GGGAGGGAGGG AGAG
                                 |||    |||||||||||| ||||
                                 GCC    CCCTCCCTCCC TCTC
                                   _____          G
GAM711  VCP      3'  TGGATAGGGGGAAGGGAG    18248      AG   A
                                 TGGA  AGGG GGGAGGGAG
                                 ||||  |||| |||||||||
                                 ACCT  TCCC CCTTCCCTC
                                   A_   _
GAM711  VTN      3'  GGAGGAGGGAGCTACAGAGGG  18249     A     _____
                                 GGA GAGGGAG    GGAGGG
                                 ||| |||||||    ||||||
                                 CCT CTCCCTC    TCTCCC
                                   C      GATG
GAM711  WAS      3'  TGGAAGAGGAGAGTGGAGGG   18250          _  _
                                 TGGAAGAGG GAG GGAGGG
                                 ||||||||| ||| ||||||
                                 ACCTTCTCC CTC CCTCCC
                                       T   A
GAM711  XPNPEP2  5'  TGGATGGAGGGACAAGGGAGAG 18251      A_     G G
            AG                   TGGA  GAGGGA G AGGGAGAGAG
                                 ||||  |||||| | ||||||||||
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                                ACCT  CTCCCT T TCCCTCTCTC
                                  AC     G _
GAM711  ZFP36    3'  GGAAGAGGTGGGGGAGAG    18252        GAG  A
                                GGAAGAGG   GG GGGAGAG
                                ||||||||   || |||||||
                                CCTTCTCC   CC CCCTCTC
                                    A__  _
GAM711  ZIC3     5'  TGGCGGGGGGGAGGAGGAG    18253     AAGA  A     GA
                                TGG    GGG GGGAGG  GAG
                                |||    ||| ||||||  |||
                                ACC    CCC CCCTCC  CTC
                                  G___   _     TC
GAM711  ZIC3     5'  GGAGGAGGGAGGAGAAGGGAG  18254     A       _    A
                                GGA GAGGGAGG GAGGG GAG
                                ||| |||||||| ||||| |||
                                CCT CTCCCTCC CTTCC CTC
                                  C       T    _
GAM711  AD024    3'  TGGGGGAGGGGGGGAGGGATAG  18255     AA    A      G
                                TGG  GAGGG GGGAGGGA AG
                                |||  ||||| |||||||| ||
                                ACC  CTCCC CCCTCCCT TC
                                  CC    _       A
GAM711  AEBP1    5'  GGAAGGGGCGGGAGAGAG    18256      A  A
                                GGAAG GGG GGGAGGGAG
                                ||||| ||| |||||||||
                                CCTTC CCC CCCTCTCTC
                                   _  G
GAM711  APEG1    3'  TGGGGAGGGAGGGTCCACAGGG 18257     AA       _____
                                TGG  GAGGGAGGG    AGGG
                                |||  |||||||||    ||||
                                ACC  CTCCCTCCC    TCCC
                                  C_       AGGTG
GAM711  APOL3    5'  TGGACAGAGGGAGGTTGGAG   18258     _       GAG
                                TGGA AGAGGGAGG   GGAG
                                ||||  |||||||||  ||||
                                ACCT TCTCCCTCC   CCTC
                                  G       AA_
GAM711  ASB16    5'  TGGGAGGGGGAGAGAGGATTCT 18259        ________      AGIII
            GGGAGAGCC                GGAGGGA      GGGAGAG    C
                                |||||||      |||||||    |
                                CCTCTCT      CCCTCTC    G
                                    CCTAAGA      IIIGA
GAM711  ASB16    5'  TGGGAGAGAGAGTCCAAGGGAG 18260     A       G__
                                TGG AGAGGGAG   GAGGGAG
                                ||| ||||||||   |||||||
                                ACC TCTCTCTC   TTCCCTC
                                  C       AGG
GAM711  BCL2L12  5'  TGGAGGAGGGAGGCGGGCAGTC 18261      A       GA  _  A__
            GGAG                    TGGA GAGGGAGG  GGG AG   GAG
                                ||||  ||||||||  ||| ||   |||
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                                ACCT CTCCCTCC  CCC TC   CTC
                                  C       G_  G  AGC
GAM711  BSPECV   5' GGCTGTGGAGGGAGGGAGAG  18262    AAGAG
                                GG    GGAGGGAGGGAGAG
                                ||    ||||||||||||||
                                CC    CCTCCCTCCCTCTC
                                 GACA_
GAM711  C11orf11 3' TGGGGGTGGGAGGGAGGAAG  18263     AAGA
                                TGG   GGGAGGGAGGGAG
                                |||   |||||||||||||
                                ACC   CCCTCCCTCCTTC
                                  CCCA
GAM711  C14orf4  3' TGGGGGTGAGGGGAGGGAG   18264     AAGA  A
                                TGG   GGG GGGAGGGAG
                                |||   ||| |||||||||
                                ACC   CTC CCCTCCCTC
                                  CCCA  _
GAM711  C20orf27 3' TGGGAGAGGAGGACGAGGGAG 18265     A    GA  _
                                TGG AGAGG  GG GAGGGAG
                                ||| |||||  || |||||||
                                ACC TCTCC  CT CTCCCTC
                                  C    TC  G
GAM711  C21orf57 5' TGGAATGGGGGAGGGACAGGAG 18266       GA_      _
           AG                     TGGAA   GGGAGGGA GGGAGAG
                                |||||   |||||||| |||||||
                                ACCTT   CCCTCCCT TCCTCTC
                                   ACC       G
GAM711  C6orf28  3' TGAAAGAGGGAGGGGAAGAG  18267             AG
                                TGGAAGAGGGAGGG  GGAG
                                ||||||||||||||  ||||
                                ACTTTCTCCCTCCC  TCTC
                                         CT
GAM711  CASKIN1  3' TGGAGGGGGCAGGAGGAGAGAG 18268      A A  A     G
                                TGGA G GGG GGGAGG AGAGAG
                                |||| | ||| |||||| ||||||
                                ACCT C CCC TCCTCC TCTCTC
                                  _ C  G     _
GAM711  CCNI     5' TGAAAGGGGGGGAGGGGAG   18269       A  A     A
                                TGGAAG GGG GGGAGGG GAG
                                |||||| ||| ||||||| |||
                                ACTTTC CCC CCCTCCC CTC
                                     _  _      _
GAM711  CDH22    3' TGGGGGAGGGCAGGAAAG    18270     AAGA      A
                                TGG   GGGAGGG GGGAGAG
                                |||   ||||||| |||||||
                                ACC   CCCTCCC TCCTTTC
                                  _____      G
GAM711  CDH24    3' AGGAGGAGGGAGGTGAGAG   18271    AG        _
                                AG  GGAGGGAGG GAGAG
                                ||  ||||||||| |||||
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                                TC  CCTCCCTCC CTCTC
                                 CT        A
GAM711  CHPT1    5'  TGGGGGCAGGGAGAGGTGGAGG 18272     AAG_       AG    A
              GAG                    TGG    AGGGAGGG  GGAG GAG
                                |||    ||||||||  |||| |||
                                ACC    TCCCTCTC  CCTC CTC
                                  CCCG       CA    C
GAM711  CNNM1    3'  TGGGGAGGTGGGAGGGAG    18273     AA    GA
                                TGG  GAGG  GGGAGGGAG
                                |||  ||||  |||||||||
                                ACC  CTCC  CCCTCCCTC
                                  C_   A_
GAM711  CORO1B   3'  TGGGGAGGGAGCAGAGGG    18274     AA      _
                                TGG  GAGGGAG GGAGGG
                                |||  ||||||| ||||||
                                ACC  CTCCCTC TCTCCC
                                  C_      G
GAM711  ctm-1    3'  TGGAGCCCAGGAGGGAGGGAG  18275      AGA_
                                TGGA    GGGAGGGAGGGAG
                                ||||    ||||||||||||||
                                ACCT    TCCTCCCTCCCTC
                                   CGGG
GAM711  CXorf2   3'  AGGAGGAGGGAGGGAGCA    18276     AG          AG
                                AG  GGAGGGAGGGAG  A
                                ||  ||||||||||||  |
                                TC  CCTCCCTCCCTC  T
                                 CT           GA
GAM711  D15Wsu75e 5'  GGGAGAGGGGGGGGACCGAG    18277     A     A    GG
                                GG AGAGGG GGGA  GAG
                                || |||||| ||||  |||
                                CC TCTCCC CCCT  CTC
                                 C     C    GG
GAM711  dA141H5.1 3'  GAGGAGGGAGGATGGGGAG    18278     A       GA   A
                                GA GAGGGAGG  GGG GAG
                                || ||||||||  ||| |||
                                CT CTCCCTCC  CCC CTC
                                 C       TA  _
GAM711  dA141H5.1 3'  GAGAGAGGGAGGGAGAGAG    18280
                                GAGGGAGGGAGGGAGAGAG
                                ||||||||||||||||||
                                CTCTCTCCCTCCCTCTCTC

GAM711  dA141H5.1 3'  AGAAGGAGGGAGGGAGGGAG    18279       _
                                GGAAG AGGGAGGGAGGGAG
                                ||||| ||||||||||||||
                                TCTTC TCCCTCCCTCCCTC
                                   C
GAM711  DDX39    3'  TGGGAAGGGAGGTGGGAG    18181     AA       GA
                                TGG  GAGGGAGG  GGGAG
                                |||  ||||||||  |||||
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                                ACC  TTCCCTCC  CCCTC
                                  C_       A_
GAM711  DJ159A19.3 3'  TGGGAGGGGGTGGAGGGAG   18281     A  A   AG
                                TGG AG GGG  GGAGGGAG
                                ||| || |||  ||||||||
                                ACC TC CCC  CCTCCCTC
                                  C  _   CA
GAM711  DKFZP434B103 3'  GGAAGGGGCTTCTGAGGGAG   18282       A   AGG__
                                GGAAG GGG    GAGGGAG
                                ||||| |||    |||||||
                                CCTTC CCC    CTCCCTC
                                   _  GAAGA
GAM711  DKFZp434H2215 3'  TGGAGGAGGAGGGAGTCTAG   18283      A AG       GG_
                                TGGA G  GGAGGGAG   AG
                                |||| |  ||||||||   ||
                                ACCT C  CCTCCCTC   TC
                                  _ CT       AGA
GAM711  DKFZp434J0617 3'  GGGAGAGGGGGGGCACCCAGGG 18284    A     A  _____
           AG                     GG AGAGGG GGG    AGGGAG
                                || |||||| |||    ||||||
                                CC TCTCCC CCC    TCCCTC
                                 C     C   GTGGG
GAM711  DKFZp547J036 3'  GGGAGGGGTGGGGGAGAGAG   18285    AA    AG  A
                                GG  GAGGG  GG GGGAGAGAG
                                ||  |||||  || |||||||||
                                CC  CTCCC  CC CCCTCTCTC
                                  __     CA  _
GAM711  DKFZP564B147 5'  GGGGGAGGGAGGCGCGGAGGGA 18286    AA       ____
           G                      GG  GAGGGAGG    GAGGGAG
                                ||  ||||||||    |||||||
                                CC  CTCCCTCC    CTCCCTC
                                 CC       GCGC
GAM711  DKFZP564O1664 5'  TGGAAAGAGGGGGCAGAGGG   18287       _    A __
                                TGGAA GAGGG GG  GAGGG
                                ||||| ||||| ||  |||||
                                ACCTT CTCCC CC  CTCCC
                                   T    _ GT
GAM711  DKFZP586G1122 3'  TGGGGGGGGGGAAGGAGAG   18288     AAGA   A
                                TGG    GGG GGGAGGGAGAG
                                |||    ||| ||||||||||
                                ACC    CCC CCCTTCCTCTC
                                  CC__   _
GAM711  DKFZP761C169 3'  TGGGGGAAGGAGAGGGAG    18289     AAGA        A
                                TGG    GGGAGGGAGGG GAG
                                |||    |||||||||| |||
                                ACC    CCCTTCCTCTC CTC
                                  _____          C
GAM711  DKFZp761G2113 3'  TGGGTGGGGGTCAGGAGAGAG  18290     AAGA   A  GA
                                TGG    GGG GG  GGGAGAGAG
                                |||    ||| ||  |||||||||
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                                ACC    CCC CC  TCCTCTCTC
                                  CA__   _  AG
GAM711  E2-EPF    3'  GAGGGAGGGGACAGGAGAG    18291         A__
                                GAGGGAGGG   GGGAGAG
                                |||||||||   |||||||
                                CTCCCTCCC   TCCTCTC
                                     CTG
GAM711  EPB41L1   3'  GAGGGGAGGCGGGAGAGA    18292       AG  A
                                GAGGG  GG GGGAGAGA
                                |||||  || ||||||||
                                CTCCC  CC CCCTCTCT
                                   CT  G
GAM711  EPB41L1   3'  GGAAGGGGGAGGAGGGAG    18293       A   AG
                                GGAAG GGG  GGAGGGAG
                                ||||| |||  ||||||||
                                CCTTC CCC  CCTCCCTC
                                   _   CT
GAM711  EZF-2     3'  TGGAGGAGGGAGAGGGAG    18294      A     GG
                                TGGA GAGGGA  GAGGGAG
                                |||| ||||||  |||||||
                                ACCT CTCCCT  CTCCCTC
                                  C     __
GAM711  EZFIT     3'  GAAGAGGGAGGACCTTTGGGAG 18295           A____
                                GAAGAGGGAGGG    GGGAG
                                ||||||||||||    |||||
                                CTTCTCCCTCCT    CCCTC
                                      GGAAA
GAM711  FLJ10074  5'  GGGAGGGGAGGGACCGGG    18296    A  A      __
                                GG AG GGGAGGGA  GGG
                                || || ||||||||  |||
                                CC TC CCCTCCCT  CCC
                                 C  _       GG
GAM711  FLJ10193  3'  TGGGGGTGGGAGGAGAGA    18297     AAGA   A     G
                                TGG    GGG GGGAGG AGAGA
                                |||    ||| |||||| |||||
                                ACC    CCC CCCTCC TCTCT
                                  _____   A     _
GAM711  FLJ10246  3'  TGGGAGAGGGACAATGGGGAGG 18298     A      _____
          G                      TGG AGAGGGA     GGGAGGG
                                |||| |||||||     |||||||
                                ACC TCTCCCT     CCCTCCC
                                  C       GTTAC
GAM711  FLJ10330  5'  GGAGGGAAGGAGGGGGGGGAG  18299     A_       A   A
                                GGA  GAGGGAGGG GGG GAG
                                |||  ||||||||| ||| |||
                                CCT  CTTCCTCCC CCC CTC
                                  CC         _   C
GAM711  FLJ10597  3'  TGGGAGGGGGAGGGGCCAAG   18300     AA    A  GA   A_
                                TGG  GAGGG GG  GGG  GAG
                                |||  ||||| ||  |||  |||
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                                ACC  CTCCC CC  CCC  TTC
                                  __    _ TC   GG
GAM711  FLJ11320  3'  TGGAGAGGGAGGGGGGAG    18301     A       A
                                TGGA GAGGGAGGG GGGAG
                                |||| ||||||||| |||||
                                ACCT CTCCCTCCC CCCTC
                                  _       _
GAM711  FLJ11539  5'  TGGGAGGGAGTTGGGGGAGAGA 18302     AA      __ A
          G                      TGG  GAGGGAG  GG GGGAGAGAG
                                |||  |||||||  || |||||||||
                                ACC  CTCCCTC  CC CCCTCTCTC
                                  __      AA _
GAM711  FLJ11939  5'  TGGGGAGGGAAGGGGGAG    18303     AA       A
                                TGG  GAGGGAGGG GGGAG
                                |||  ||||||||| |||||
                                ACC  CTCCCTTCC CCCTC
                                  C_       _
GAM711  FLJ12229  3'  TGGAGGAGCGAGGGAGGCAGAG 18304     A  G      G
                                TGGA GAG GAGGGAGG AGAG
                                |||| ||| |||||||| ||||
                                ACCT CTC CTCCCTCC TCTC
                                  C  G       G
GAM711  FLJ12287  3'  GGAAAAGGGAGGGGGAGAG    18305           AG
                                GGAAGAGGGAGGG  GGAGAG
                                ||||||||||||  ||||||
                                CCTTTTCCCTCCC  CCTCTC
                                              __
GAM711  FLJ13055  3'  TGGAAGGGGGAGGGATAGAG   18306       A      G
                                TGGAAG GGGAGGGA GGAG
                                |||||| |||||||| ||||
                                ACCTTC CCCTCCCT TCTC
                                   C       A
GAM711  FLJ13158  3'  TGGCGGGGGGCGGGGGAGA    18307     AAGA  A  A  A
                                TGG    GGG GGG GGG GAGA
                                |||    ||| ||| ||| ||||
                                ACC    CCC CCC CCC CTCT
                                  G___   _  G  C
GAM711  FLJ13612  3'  GAAGAGGGAGGGACTGGG    18308           __
                                GAAGAGGGAGGGA  GGG
                                ||||||||||||  |||
                                CTTCTCCCTCCCT  CCC
                                       GA
GAM711  FLJ13881  3'  GGAAGGAGAGGGAGGGAGAGAG 18309       A
                                GGAAG GGGAGGGAGGGAGAGAG
                                ||||| ||||||||||||||||
                                CCTTC CTCTCCCTCCCTCTCTC
                                  _
GAM711  FLJ14299  3'  TGGGGAGGGAGGAGGAGGGAGA 18310     AA       __
          G                      TGG  GAGGGAGG  GAGGGAGAG
                                |||  ||||||||  |||||||||
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                                ACC  CTCCCTCC  CTCCCTCTC
                                  C_       TC
GAM711  FLJ14299  3'  GGAGGAGGGAGAGGGAG     18311     A     GG
                                GGA GAGGGA  GAGGGAG
                                ||| ||||||  |||||||
                                CCT CTCCCT  CTCCCTC
                                  C     __
GAM711  FLJ14816  3'  GGGAGAGGGAGGCTAGAGGG   18312    A       ___
                                GG AGAGGGAGG   GAGGG
                                || |||||||||   |||||
                                CC TCTCCCTCC   CTCCC
                                  C        GAT
GAM711  FLJ14816  3'  TGGTGGGGGATCAGGGAGAG   18313     AAGA   A   __
                                TGG    GGG GGG  AGGGAGAG
                                |||    ||| |||  ||||||||
                                ACC    CCC CCT  TCCCTCTC
                                  A___   _   AG
GAM711  FLJ20207  5'  TGGGAGGGAGGAAGCGGGAGGG 18314     AA        __     A
              AG                  TGG  GAGGGAGGGA  GGGAG GAG
                                ||| ||||||||||  ||||| |||
                                ACC  CTCCCTCCTT  CCCTC CTC
                                  __         CG    C
GAM711  FLJ21034  3'  TGGGAGAGGGAGAGGGCAG    18315     A        A  G
                                TGG AGAGGGAGGG GG AG
                                ||| |||||||||| || ||
                                ACC TCTCCCTCTC CC TC
                                  C         _ G
GAM711  FLJ21551  3'  GGAGAAAGTGGGGAGGGAGAGA 18316     AG   GA
              G                   GGA  AGG  GGGAGGGAGAGAG
                                |||  |||  ||||||||||||
                                CCT  TTC  CCCTCCCTCTCTC
                                  CT   AC
GAM711  FLJ22160  5'  TGGAGAGGGAAGAGGGG     18317      A       GA
                                TGGA GAGGGAGG  GGG
                                |||| ||||||||  |||
                                ACCT CTCCCTTC  CCC
                                  _       TC
GAM711  FLJ32926  3'  TGGGAGATGGAGATGAGGAGAG 18318     A  G    GA
              AG                  TGG AGA GGAGG  GGGAGAGAG
                                ||| ||| |||||  |||||||||
                                ACC TCT CCTCT  TCCTCTCTC
                                  C   A    AC
GAM711  FOXH1     3'  TGGGAGCGGGAGGGAGGA    18319     A  A
                                TGG AG GGGAGGGAGGG
                                ||| || ||||||||||
                                ACC TC CCCTCCCTCCT
                                  C  G
GAM711  FOXH1     5'  GGAAGGGAGGGGCAGAGA    18320          __
                                GGGAGGGAGGG  AGAGA
                                ||||||||||  |||||
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                                CCTTCCCTCCC  TCTCT
                                      CG
GAM711  FOXH1    5'  GGAAGGGGGAGGGGAGGG    18066      A     _
                                GGAAG GGGAGGG AGGG
                                ||||| ||||||| ||||
                                CCTTC CCCTCCC TCCC
                                   C      C
GAM711  FRAT1    3'  TGGGGGAGGGGCAGAGGGAG   18321     AA    AG
                                TGG  GAGGG  GGAGGGAG
                                |||  |||||  ||||||||
                                ACC  CTCCC  TCTCCCTC
                                  CC    CG
GAM711  GDF11    5'  TGGAGGGGAGGGGAGGGAG    18322     A A     _
                                TGGA G GGGAGGG AGGGAG
                                |||| | ||||||| ||||||
                                ACCT C CCCTCCC TCCCTC
                                  _ _     C
GAM711  GGTLA4   5'  TGGGGAGGGAGGGTGGGGAG   18323     AA       A  A
                                TGG  GAGGGAGGG GGG GAG
                                |||  ||||||||| ||| |||
                                ACC  CTCCCTCCC CCC CTC
                                  C_       A  _
GAM711  GOLGA1   3'  TGGGGTGGGATGAGGGAGAGAG 18324     AAGA   GG
                                TGG   GGGA  GAGGGAGAGAG
                                |||   ||||  ||||||||||
                                ACC   CCCT  CTCCCTCTCTC
                                  CCA_   A_
GAM711  GPR      5'  GGGAGGCGGGGAGGGAGGGAG  18325    A  A__
                                GG AG   GGGAGGGAGGGAG
                                || ||   ||||||||||||
                                CC TC   CCCTCCCTCCCTC
                                 C  CGC
GAM711  HIC      3'  TGGAGAAGGTAAGGGAGAGAG  18326      AG   _
                                TGGA  AGG GAGGGAGGGAG
                                ||||  ||| ||||||||||
                                ACCT  TCC TTCCCTCTCTC
                                   CT   A
GAM711  HNRPA0   5'  GGAAGGGGGAGGGAAGGGGAG  18327       A         A
                                GGAAG GGGAGGGAGGG GAG
                                ||||| |||||||||| |||
                                CCTTC CCCTCCCTTCC CTC
                                   C          C
GAM711  HTGN29   5'  GGAAGGATTGCAGGGAGGGAGG 18328      _______
           GAG                    GGAAG     AGGGAGGGAGGGAG
                                |||||     ||||||||||||||
                                CCTTC     TCCCTCCCTCCCTC
                                   CTAACG
GAM711  HU-K4    3'  GGGAGAGCAGGGGAGAGAG   18329        A__
                                GGGAGGG   GGGAGAGAG
                                |||||||   |||||||||
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                                CCCTCTC  CCCTCTCTC
                                   GTC
GAM711  JDD1    3' TGGGAGGGTGGAGGGAG    18330    AA   AG
                                TGG  GAGGG  GGAGGGAG
                                |||  |||||  ||||||||
                                ACC  CTCCC  CCTCCCTC
                                  __    A_
GAM711  K6HF    3' TGGAGGGAGGGAGGGAGGTGGA 18331     A_        GA
          G                      TGGA  GAGGGAGGGAGG  GAG
                                ||||  ||||||||||||  |||
                                ACCT  CTCCCTCCCTCC  CTC
                                  CC          AC
GAM711  KCNH8   5' GAGGGAGAAAGGGAGAGAG   18332       GG
                                GAGGGAG  AGGGAGAGAG
                                |||||||  ||||||||||
                                CTCCCTC  TCCCTCTCTC
                                   TT
GAM711  KIAA0057 3' TGGCAGGGGGGAGGGGGGG    18333    A A     A
                                TGG AG GGGAGGG GGG
                                ||| || ||||||| |||
                                ACC TC CCCTCCC CCC
                                  G  C     _
GAM711  KIAA0144 3' GGGAGAGGGAAATGGGGGAGGG 18334    A     _____
                                GG AGAGGGA    GGGAGGG
                                || |||||||    |||||||
                                CC TCTCCCT    CCCTCCC
                                 C      TTACC
GAM711  KIAA0237 3' CGGGGGGGAGGGGAGGGAG    18335    AAGA     _
                                TGG    GGGAGGG AGGGAG
                                |||    ||||||| ||||||
                                GCC    CCCTCCC TCCCTC
                                  C___      C
GAM711  KIAA0285 3' AGGGGGAGGGAGGGATGAG   18336    A        _
                                AG GGGAGGGAGGGA GAG
                                || ||||||||||| |||
                                TC CCCTCCCTCCCT CTC
                                 C          A
GAM711  KIAA0355 3' TGGAGGAGGGAGGAGAGGG   18337     A     _
                                TGGA GAGGGAGG GAGGG
                                |||| |||||||| |||||
                                ACCT CTCCCTCC CTCCC
                                  C       T
GAM711  KIAA0427 5' GGAAGGGAAACAGGGAGGGAG  18338      A  ___
                                GGAAG GGG   AGGGAGGGAG
                                ||||| |||   ||||||||||
                                CCTTC CCT   TCCCTCCCTC
                                   _  TTG
GAM711  KIAA0450 3' TGGGGGAGTGAGAGAGAG    18339    AAGA    G
                                TGG    GGGAG GAGGGAGAG
                                |||    ||||| |||||||||
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                                ACC    CCCTC CTCTCTCTC
                                 ____    A
GAM711  KIAA0450 5' TGCCAGGGGGAGGGAGGGAG  18340    GA  A
                                TG  AG GGGAGGGAGGGAG
                                ||  || ||||||||||||||
                                AC  TC CCCTCCCTCCCTC
                                 GG  C
GAM711  KIAA0450 5' GGGGGAGGGAGGGAGGCAG   18341    AA         G
                                GG  GAGGGAGGGAGG AG
                                ||  |||||||||||| ||
                                CC  CTCCCTCCCTCC TC
                                 CC          G
GAM711  KIAA0453 3' TGGGAGAGGAAAGGGAGGG   18342     A     _
                                TGG AGAGGGA GGGAGGG
                                ||| ||||||| |||||||
                                ACC TCTCCTT CCCTCCC
                                  C      T
GAM711  KIAA0514 5' GGGAGGGGAAGGGAGAGAG   18343       __
                                GGGAGGG  AGGGAGAGAG
                                |||||||  ||||||||||
                                CCCTCCC  TCCCTCTCTC
                                    CT
GAM711  KIAA0522 3' TGGAGAGGGGAGAGGGAG    18344     A    A
                                TGGA GAGGG GGGAGGGAG
                                |||| ||||| |||||||||
                                ACCT CTCCC CTCTCCCTC
                                  _    _
GAM711  KIAA0551 3' TGGGAGGGGCGGAGGGAG    18345     AA    AG
                                TGG  GAGGG  GGAGGGAG
                                |||  |||||  ||||||||
                                ACC  CTCCC  CCTCCCTC
                                  __    CG
GAM711  KIAA0552 3' TGGGGGTGGGAGGAAGAGA   18346     AAGA  A
                                TGG    GGG GGGAGGGAGAGA
                                |||    ||| ||||||||||||
                                ACC    CCC CCCTCCTTCTCT
                                  ____  A
GAM711  KIAA0721 3' GGGGGAGGGAGAGGGGAG    18347    AA       A
                                GG  GAGGGAGGG GGGAG
                                ||  ||||||||| |||||
                                CC  CTCCCTCTC CCCTC
                                 CC       _
GAM711  KIAA0721 3' TGGGAGGGAGAGGGGGAGGGAG 18348     AA    ____
           AG                     TGG  GAGGGA    GGGAGGGAGAG
                                |||  ||||||   ||||||||||
                                ACC  CTCCCT    CCCTCCCTCTC
                                  __     CTCC
GAM711  KIAA0721 3' TGGGAGGGAGAGGGGGAGGGAG 18348     AA    ____
           AG                     TGG  GAGGGA    GGGAGGGAGAG
                                |||  ||||||   ||||||||||
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                                ACC  CTCCCT    CCCTCCCTCTC
                                  __     CTCC
GAM711  KIAA0721  3'  GGGGGAGGGAGAGGGGAG    18347    AA       A
                                GG  GAGGGAGGG GGGAG
                                ||  ||||||||| |||||
                                CC  CTCCCTCTC CCCTC
                                 CC       _
GAM711  KIAA0775  3'  TGGAAGAAGGGTTGAGGG    18349         AGG
                                TGGAAGAGGG   GAGGG
                                ||||||||||   |||||
                                ACCTTCTTCC   CTCCC
                                      CAA
GAM711  KIAA0843  3'  GGGAGCAGTGAGGGAGAGAG   18350      __ _
                                GGGAG  G GAGGGAGAGAG
                                |||||  | ||||||||||
                                CCCTC  C CTCCCTCTCTC
                                   GT A
GAM711  KIAA0963  3'  GGAAGGGCTGGGGGAGGGAG   18351      AG__  A
                                GGAAG    GG GGGAGGGAG
                                |||||    || |||||||||
                                CCTTC    CC CCCTCCCTC
                                   CCGA  _
GAM711  KIAA0993  3'  TGGGGGAGGGAGAGTGTGGGGG 18352     AA       A___   A
          GAG                     TGG  GAGGGAGGG    GGG GAG
                                |||  |||||||||    ||| |||
                                ACC  CTCCCTCTC    CCC CTC
                                  CC        ACAC   C
GAM711  KIAA1016  5'  TGGAAGGAGGGGAGGAGGG    18353       _   AG
                                TGGAAG AGGG  GGAGGG
                                |||||| ||||  ||||||
                                ACCTTC TCCC  CCTCCC
                                   C    CT
GAM711  KIAA1034  3'  TGGGAGAGGGAAGGATGGAG   18354     A        G
                                TGG AGAGGGAGGGA GGAG
                                ||| ||||||||||| ||||
                                ACC TCTCCCTTCCT CCTC
                                  C          A
GAM711  KIAA1061  5'  TGGGCGGGAGGGAGGGAG    18355     AAGA
                                TGG    GGGAGGGAGGGAG
                                |||    ||||||||||||
                                ACC    CCCTCCCTCCCTC
                                  CG__
GAM711  KIAA1130  3'  GAGTGAAGGGAGGGGGAG    18356     _        A
                                GAG GGAGGGAGGG GAG
                                ||| |||||||||| |||
                                CTC CTTCCCTCCC CTC
                                  A         C
GAM711  KIAA1183  3'  GGAAGAGGGGAGGGGAGGG   18357         A__
                                GGAAGAGGG   GGGAGGG
                                |||||||||   |||||||
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                                CCTTCTCCC  CCCTCCC
                                     CTC
GAM711  KIAA1189 3' TGGTAGGTAGGGGGAGAGA  18358    AAGA  A  A
                                TGG   GGG GGG GGGAGAGA
                                |||   ||| ||| ||||||||
                                ACC   TCC TCC CCCTCTCT
                                  A___  A  _
GAM711  KIAA1196 3' TGGCAGAGGGAGGGCAGAAAGG 18359    A       _ GG  A
           AG                    TGG AGAGGGAGGG AG  AG GAG
                                |||  |||||||||| ||  || |||
                                ACC TCTCCCTCCC TC  TC CTC
                                  G        G  TT  _
GAM711  KIAA1205 3' TGGGAGGAATGGGGAGGGAG  18361    AA    __
                                TGG  GAGGGA  GGGAGGGAG
                                |||  ||||||  |||||||||
                                ACC  CTCCTT  CCCTCCCTC
                                  __     AC
GAM711  KIAA1205 3' TGGGGAGGGAGTGGAGGG   18360    AA    _
                                TGG  GAGGGAG GGAGGG
                                |||  |||||||  ||||||
                                ACC  CTCCCTC CCTCCC
                                  C_     A
GAM711  KIAA1238 5' TGGGGGAAGGAGAGGAGGGGGA 18362    AA    _    A
           G                     TGG  GAGGGAG GGAGGG GAG
                                |||  |||||||  ||||||  |||
                                ACC  CTTCCTC CCTCCC CTC
                                  CC      T     C
GAM711  KIAA1238 5' TGGAAGTGGGGGGAAGGAGAG  18363      AG  A
                                TGGAAG  GG GGGAGGGAGAG
                                ||||||  ||  ||||||||||
                                ACCTTC  CC CCCTTCCTCTC
                                   A_  _
GAM711  KIAA1384 5' GGAGAGGGAGAAAAGAGAG   18364    A     GG   G
                                GGA GAGGGAG  AGG AGAG
                                |||  |||||||  |||  ||||
                                CCT CTCCCTC  TTC TCTC
                                  _      TT   _
GAM711  KIAA1388 3' TGGAAGAGGGCAGGGGATAGAG 18365          _   A GG
                                TGGAAGAGGG AGGG G  AGAG
                                ||||||||||  ||||  |  ||||
                                ACCTTCTCCC TCCC C  TCTC
                                     G   _ TA
GAM711  KIAA1462 3' GGAAGAAAGGAAGGGAGGGAGG 18367  _______          A  III
           GAGGGAGC                   GGGAGGGAGGGAG GAG   C
                                   ||||||||||||| |||   |
                                   CCCTCCCTCCCTC CTC   G
                                TTCCTT           C  III
GAM711  KIAA1462 3' GGAAGGGAGGGAGGGAGGGAGG 18366     __           A
           GAG                    GGAA  GAGGGAGGGAGGGAG GAG
                                ||||  |||||||||||||| |||
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                                CCTT  CTCCCTCCCTCCCTC CTC
                                  CC            C
GAM711  KIAA1522 3' TGGAGGAGGGAGAGGGAAAGAG 18368     A     GG
                                TGGA GAGGGA  GAGGGAGAGAG
                                |||| ||||||  ||||||||||
                                ACCT CTCCCT  CTCCCTTTCTC
                                  C     __
GAM711  KIAA1536 3' TGGAGAGGGAGGGGGG      18369     A       A
                                TGGA GAGGGAGGG GGG
                                |||| ||||||||| |||
                                ACCT CTCCCTCCC CCC
                                  _       _
GAM711  KIAA1796 5' TGGCAGAGGGAGGGAAGGAG   18370     A
                                TGG AGAGGGAGGGAGGGAG
                                ||| ||||||||||||||
                                ACC TCTCCCTCCCTTCCTC
                                  G
GAM711  KIAA1922 3' TGGGAGAGAGAGGCAGGGGAGA 18371     A       G   A
          G                      TGG AGAGGGAGG AGGG GAGAG
                                ||| ||||||||| |||| |||||
                                ACC TCTCTCTCC TCCC CTCTC
                                  C       G   _
GAM711  KIAA1938 3' TGGCGGGAGGGAGGGAG     18372     AAGA
                                TGG    GGGAGGGAGGGAG
                                |||    ||||||||||||
                                ACC    CCCTCCCTCCCTC
                                  G___
GAM711  KIAA1938 3' TGGAAGGAGATTGGGAGGG    18373       A   __
                                TGGAAG GGGA  GGGAGGG
                                |||||| ||||  |||||||
                                ACCTTC CTCT  CCCTCCC
                                   _   AA
GAM711  KIAA1938 3' GGGAGGGGGAGGATGAGAG   18374        A_   _
                                GGGAGGG  GGGA GAGAG
                                |||||||  |||| |||||
                                CCCTCCC  TCCT CTCTC
                                    CC   A
GAM711  KIAA1949 5' GGAAGTGGAGGGGGAGAG    18377      AG     AG
                                GGAAG  GGAGGG  GGAGAG
                                |||||  ||||||  ||||||
                                CCTTC  CCTCCC  CCTCTC
                                  A_     __
GAM711  KIAA1949 5' GGAGGAGGGAGGGAGAG     18376     AGAG
                                GGA    GGAGGGAGGGAGAG
                                |||    ||||||||||||||
                                CCT    CCTCCCTCCCTCTC
                                  _____
GAM711  KIAA1949 5' GGAAGTGGAGGGGGAGAG    18377      AG     AG
                                GGAAG  GGAGGG  GGAGAG
                                |||||  ||||||  ||||||
```

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                                CCTTC  CCTCCC  CCTCTC
                                  A_     __
GAM711  KIAA1949  5'  TGGAGGGAGGGGAGGAGGGAGG 18375     A_    AG      A
            GAG                   TGGA  GAGGG  GGAGGGAG GAG
                                  ||||  |||||  |||||||| |||
                                  ACCT  CTCCC  CCTCCCTC CTC
                                    CC    CT      C
GAM711  KIAA1949  5'  TGGAGGGAGGGGAGGAGGGAGG 18375     A_    AG      A
            GAG                   TGGA  GAGGG  GGAGGGAG GAG
                                  ||||  |||||  |||||||| |||
                                  ACCT  CTCCC  CCTCCCTC CTC
                                    CC    CT      C
GAM711  KIAA1949  5'  GGAGGAGGGAGGGAGAG     18376     AGAG
                                  GGA   GGAGGGAGGGAGAG
                                  |||   ||||||||||||||
                                  CCT   CCTCCCTCCCTCTC
                                   _____
GAM711  KIAA1949  5'  TGGAGGGAGGGGAGGAGGGAGG 18375     A_    AG      A
            GAG                   TGGA  GAGGG  GGAGGGAG GAG
                                  ||||  |||||  |||||||| |||
                                  ACCT  CTCCC  CCTCCCTC CTC
                                    CC    CT      C
GAM711  KIAA1949  5'  GGAGGAGGGAGGGAGAG     18376     AGAG
                                  GGA   GGAGGGAGGGAGAG
                                  |||   ||||||||||||||
                                  CCT   CCTCCCTCCCTCTC
                                   _____
GAM711  KIAA1949  5'  GGAAGTGGAGGGGGAGAG     18377      AG     AG
                                  GGAAG  GGAGGG  GGAGAG
                                  |||||  ||||||  ||||||
                                  CCTTC  CCTCCC  CCTCTC
                                    A_     __
GAM711  KIAA1972  5'  TGGCAGTTCGGAGGGAGGG    18378     A  AG_
                                  TGG AG   GGAGGGAGGG
                                  ||| ||   ||||||||||
                                  ACC TC   CCTCCCTCCC
                                    G  AAG
GAM711  LASP1     3'  GAGGAGGGAGGTAGGGAGAGAG 18379     A       G
                                  GA GAGGGAGG AGGGAGAGAG
                                  || |||||||| ||||||||||
                                  CT CTCCCTCC TCCCTCTCTC
                                   C       A
GAM711  MAP2K5    5'  GGGGGAGGGAAGAGGGGAG    18380     AA      GA
                                  GG  GAGGGAGG  GGGAG
                                  ||  ||||||||  |||||
                                  CC  CTCCCTTC  CCCTC
                                   CC       TC
GAM711  MARK2     5'  TGGAGGAAGGGAGGGAAGG    18381     A_
                                  TGGA  GAGGGAGGGAGGG
                                  ||||  ||||||||||||
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```
                                ACCT  TTCCCTCCCTTCC
                                  CC
GAM711  MESDC2   3'  TGGATGGGCAGGGAGGG     18382      AGA  _
                                TGGA   GGG AGGGAGGG
                                ||||   ||| ||||||||
                                ACCT   CCC TCCCTCCC
                                  A__   G
GAM711  MGC11115 3'  GGGAGAGAGAGGGAGAGAG   18383    A
                                GG AGAGGGAGGGAGGGAG
                                || ||||||||||||||||
                                CC TCTCTCTCCCTCTCTC
                                 C
GAM711  MGC2487  3'  TGGAAGAGGTGAGGAAGGG   18384         _
                                TGGAAGAGG GAGGGAGGG
                                ||||||||| |||||||||
                                ACCTTCTCC CTCCTTCCC
                                      A
GAM711  MGC2705  3'  TGGGGGAGGGGAGGGAG     18385     AAGA      _
                                TGG    GGGAGGG AGGGAG
                                |||    ||||||| ||||||
                                ACC    CCCTCCC TCCCTC
                                  _____      C
GAM711  MGC4342  3'  TGGAAGGGAGCGGGGAGGG   18386       A  A_
                                TGGAAG GGG  GGGAGGG
                                |||||| |||  |||||||
                                ACCTTC CTC  CCCTCCC
                                   C   GC
GAM711  moblak   3'  TGGAAGAGATTGGGGAGGGAG  18387         GA_
                                TGGAAGAGG   GGGAGGGAG
                                |||||||||   |||||||||
                                ACCTTCTCT   CCCTCCCTC
                                      AAC
GAM711  MOST2    5'  GAAGAGGGAGAGGGAG      18388         GG
                                GAAGAGGGA  GAGGGAG
                                |||||||||  |||||||
                                CTTCTCCCT  CTCCCTC
                                      __
GAM711  N-PAC    3'  GGAAGAGGGGGTCAGAGGG   18389         A ____
                                GGAAGAGGG GG   GAGGG
                                ||||||||| ||   |||||
                                CCTTCTCCC CC   CTCCC
                                      _ AGT
GAM711  NAG73    3'  GGGGGAGAGTAGGAGGGAGAG  18390    AA    A
                                GG  GAGGG GGGAGGGAGAG
                                ||  ||||| ||||||||||
                                CC  CTCTC TCCTCCCTCTC
                                 CC    A
GAM711  NFAT5    3'  GGAGAAAGGAGGGAGGGAG   18391     AG
                                GGA  AGGGAGGGAGGGAG
                                |||  ||||||||||||||
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                                CCT  TTCCTCCCTCCCTC
                                  CT
GAM711  NFAT5    3'  GGGAGAGGGAGGGAGAATATGA 18393    A          A__
              G                    GG AGAGGGAGGGAGGG   GAG
                                   || |||||||||||||   |||
                                   CC TCTCCCTCCCTCTT   CTC
                                    C           ATA
GAM711  NFAT5    3'  GGAAGGGGAGAGGGAGGGAG   18392      A _
                                   GGAAG GG GAGGGAGGGAG
                                   ||||| || ||||||||||
                                   CCTTC CC CTCCCTCCCTC
                                      C  T
GAM711  NLI-IF   5'  GGGAGGGGTGGGAGGGAG    18394    A  A   A
                                   GG AG GGG GGGAGGGAG
                                   || || ||| |||||||||
                                   CC TC CCC CCCTCCCTC
                                    C  _   A
GAM711  NR5A1    3'  TGGGAGCAGGGAGGGGGCGGG  18395    A  _      A__
                                   TGG AG AGGGAGGG   GGG
                                   ||| || ||||||||   |||
                                   ACC TC TCCCTCCC   CCC
                                     C  G       CCG
GAM711  OS4      3'  GGAGGAGGGAGGGAGGGAGGAG 18396    A          _
              AG                     GGA GAGGGAGGGAGGGAG AGAG
                                   ||| |||||||||||||| ||||
                                   CCT CTCCCTCCCTCCCTC TCTC
                                     C             C
GAM711  P450RAI-2 3'  GGGAGGGGGAGCAAGGGAG   18397    A  A    G
                                   GG AG GGGAG GAGGGAG
                                   || || ||||| |||||||
                                   CC TC CCCTC TTCCCTC
                                    C  C    G
GAM711  PCDH17   5'  TGGGGGAGGGAGCAGGGAG   18398     AA     G G
                                   TGG  GAGGGA G AGGGAG
                                   |||  |||||| | ||||||
                                   ACC  CTCCCT C TCCCTC
                                     CC     _ G
GAM711  PFTK1    3'  GGAGAGAGGGAGGGAGGGAG   18399     _
                                   GGA AGAGGGAGGGAGGGAG
                                   ||| ||||||||||||||||
                                   CCT TCTCCCTCCCTCCCTC
                                     C
GAM711  PLSCR3   3'  TGGAAGGGGGTGGGAGAGAG   18400       A  A
                                   TGGAAG GGG GGGAGGGAG
                                   |||||| ||| |||||||||
                                   ACCTTC CCC CCCTCTCTC
                                      C  A
GAM711  PLSCR3   3'  TGGAAGGGGGTGGGAGAGAG   18400       A  A
                                   TGGAAG GGG GGGAGGGAG
                                   |||||| ||| |||||||||
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                                ACCTTC CCC CCCTCTCTC
                                   C   A
GAM711  PPM1A    5'  TGGAGAGGGAGGCAGAGAG   18401      A       G
                                TGGA GAGGGAGG AGGGAG
                                |||| |||||||| ||||||
                                ACCT CTCCCTCC TCTCTC
                                  _       G
GAM711  PRDM8    5'  TGGAAGAGTGGGCTGGAGAGAG 18402         GGA   AG
                                TGGAAGAG   GGG  GGAGAGAG
                                ||||||||   |||  ||||||||
                                ACCTTCTC   CCC  CCTCTCTC
                                     A__   GA
GAM711  PTK6     3'  TGGCAGAGACCAGGGAGAGAG  18403     A    G_
                                TGG AGAGG  AGGGAGGGAG
                                ||| |||||  ||||||||||
                                ACC TCTCT  TCCCTCTCTC
                                  G    GG
GAM711  QSCN6    3'  TGGGAGGGGAGGGAATGGG    18404     A  A      __
                                TGG AG GGGAGGGA  GGG
                                ||| || ||||||||  |||
                                ACC TC CCCTCCCT  CCC
                                  C  _       TA
GAM711  RAB-R    3'  GGACGAGGGAGGGGAGAGAG   18405     A       A
                                GGA GAGGGAGGG GGGAGAG
                                ||| ||||||||| |||||||
                                CCT CTCCCTCCC CTCTCTC
                                  G       _
GAM711  RAB3IL1  3'  GAAGGGGGAGGGAGGAAG    18406      A
                                GAAG GGGAGGGAGGGAG
                                |||| ||||||||||||
                                CTTC CCCTCCCTCCTTC
                                   C
GAM711  RBPMS    5'  TGGAGAGGGAGGGCGGGAG    18407      A       A
                                TGGA GAGGGAGGG GGGAG
                                |||| ||||||||| |||||
                                ACCT CTCCCTCCC CCCTC
                                  _       G
GAM711  RPL36    3'  GGGAGAGGGCAGGGGAGGG    18408    A     A__
                                GG AGAGGG   GGGAGGG
                                || ||||||   |||||||
                                CC TCTCCC   CCCTCCC
                                  C     GTC
GAM711  RPL36    3'  GGGAGAGGGCAGGGGAGGG    18408    A     A__
                                GG AGAGGG   GGGAGGG
                                || ||||||   |||||||
                                CC TCTCCC   CCCTCCC
                                  C     GTC
GAM711  SCYA22   3'  TGGGGGGGGGGGTGGGGAGAG   18409     AAGA  A  A  A
                                TGG    GGG GGG GGG GAGAG
                                |||    ||| ||| ||| |||||
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                                ACC    CCC CCC CCC CTCTC
                                  CC__  _  A  _
GAM711  SCYA3    3'  GGAAGGGGGAGGGGACAGGG  18410      A     ___
                                GGAAG GGGAGGG  AGGG
                                ||||| |||||||  ||||
                                CCTTC CCCTCCC  TCCC
                                   C      CTG
GAM711  SDC3     5'  AGGGGATGGGGGAGGGAG   18411   A   ___
                                AG GGGA  GGGAGGGAG
                                || ||||  |||||||||
                                TC CCCT  CCCTCCCTC
                                 _   ACC
GAM711  SDFR1    5'  GGAAGGGAGGGGAGGGAGGGAG 18412      A___
                                GGAAG   GGGAGGGAGGGAG
                                |||||   ||||||||||||
                                CCTTC   CCCTCCCTCCCTC
                                   CCTC
GAM711  SDFR1    5'  GGAAGGGAGGGGAGGGAGGGAG 18412      A___
                                GGAAG   GGGAGGGAGGGAG
                                |||||   ||||||||||||
                                CCTTC   CCCTCCCTCCCTC
                                   CCTC
GAM711  SEMA3E   3'  TGGGAGAGAGAGGGAGAAACTG 18413    A         GG GA
          AG                      TGG AGAGGGAGGGAG  A  GAG
                                ||| ||||||||||| | |||
                                ACC TCTCTCTCCCTC  T  CTC
                                  C          TT GA
GAM711  SEMA7A   3'  TGAGAGAGGGAGGGGAAGGAG  18414   GA       _
                                TG  AGAGGGAGGG AGGGAG
                                ||  |||||||||| ||||||
                                AC  TCTCCCTCCC TTCCTC
                                 TC        C
GAM711  SENP7    5'  TGGAGAGGGAGGGGGAGGG   18415     A    __
                                TGGA GAGGGA  GGGAGGG
                                |||| ||||||  |||||||
                                ACCT CTCCCT  CCCTCCC
                                   _     CC
GAM711  SH3BP1   3'  TGGGGAGGGAGGGGGTGCTGAG 18416    AA       A  GA__
                                TGG  GAGGGAGGG GG   GAG
                                |||  ||||||||| ||   |||
                                ACC  CTCCCTCCC CC   CTC
                                  C_        _  ACGA
GAM711  SIAT8C   5'  TGGTGGAGGGAGGGGGACTGAG 18417    AA       A  A_
                                TGG  GAGGGAGGG GGG  GAG
                                |||  ||||||||| |||  |||
                                ACC  CTCCCTCCC CCT  CTC
                                  AC        _  GA
GAM711  SIRPB1   3'  TGGCAGGAGGGAGAGAGAG   18418    AAGA
                                TGG   GGGAGGGAGGGAGAG
                                |||   ||||||||||||||
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                                ACC    TCCTCCCTCTCTCTC
                                  G___
GAM711  SLC26A10  5'  TGGGGGGTGGAGATAAGAGGGA 18419     AAGAG   ___
                G                  TGG    GGAG   GGAGGGAG
                                   |||    ||||   ||||||||
                                   ACC    CCTC   TCTCCCTC
                                     CCCCA    TAT
GAM711  SLC26A9   3'  GGAGGAGAGAGGGGGAGAG   18420     A       AG
                                   GGA GAGGGAGGG  GGAGAG
                                   ||| |||||||||  ||||||
                                   CCT CTCTCTCCC  CCTCTC
                                     C       __
GAM711  SLC2A4RG  3'  TGGAGGGGGTGGGGAGGGAG   18421     A A   A_
                                   TGGA G GGG  GGGAGGGAG
                                   |||| | |||  |||||||||
                                   ACCT C CCC  CCCTCCCTC
                                     _ C   AC
GAM711  SNPH      3'  GGAGAAGGGAGGGGGGAA    18422     AG      A
                                   GGA  AGGGAGGG GGGAG
                                   |||  |||||||| |||||
                                   CCT  TCCCTCCC CCCTT
                                     CT       _
GAM711  SPRY4     3'  GGCGGAGGGAGGGAGGGAG   18424     AA
                                   GG  GAGGGAGGGAGGGAG
                                   ||  ||||||||||||||
                                   CC  CTCCCTCCCTCCCTC
                                    GC
GAM711  SPRY4     3'  GGAAGGGGGGGGCGGAGGGAGG 18423      A  _______
                GAG                   GGAAG GGG     AGGGAGGGAG
                                      ||||| |||     ||||||||||
                                      CCTTC CCC     TCCCTCCCTC
                                        C   CCCGCC
GAM711  SR-A1     3'  GGGGGAGGGAGGTGGGGAG   18425     AA      GA
                                   GG  GAGGGAGG  GGGAG
                                   ||  ||||||||  |||||
                                   CC  CTCCCTCC  CCCTC
                                    CC       AC
GAM711  STX1B2    3'  TGGGGGAAGGGTCTGGGAGAGA 18426     AAGA      A__
                G                  TGG    GGGAGGG   GGGAGAGAG
                                   |||    |||||||   |||||||||
                                   ACC    CCTTCCC   CCCTCTCTC
                                     C___       AGA
GAM711  SV2       5'  TGGGGAAGGGACAGGGGGAG   18427     AA     G  A
                                   TGG  GAGGGA GG GGGAG
                                   |||  |||||| || |||||
                                   ACC  TTCCCT TC CCCTC
                                     CC     G  C
GAM711  SYT12     3'  GGGGGAGGGAGAGAGGGGAGAG 18429     AA          A
                                   GG  GAGGGAGGGAGGG GAGAG
                                   ||  ||||||||||||| |||||
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                                CC  CTCCCTCTCTCCC CTCTC
                                 CC          _
GAM711  SYT12    3'  GGGAGAGGGCAGGGGGGGAG  18428    A    _   A
                                GG AGAGGG AGGG GGGAG
                                || |||||| |||| |||||
                                CC TCTCCC TCCC CCCTC
                                 C     G   C
GAM711  TLOC1    3'  TGGGGAGGGAGGAGGGAG    18430    AA      G
                                TGG  GAGGGAGG AGGGAG
                                |||  |||||||| ||||||
                                ACC  CTCCCTCC TCCCTC
                                  C_      _
GAM711  TMPRSS5  3'  TGGAGAGGGAGAGTGGAGAG  18431     A       AG
                                TGGA GAGGGAGGG  GGAGAG
                                |||| |||||||||  ||||||
                                ACCT CTCCCTCTC  CCTCTC
                                   _       A_
GAM711  TNKS1BP1 5'  TGGAGTGGGGGGGGGTAGGAG  18432     AGA  A  A
                                TGGA   GGG GGG GGGAG
                                ||||   ||| ||| |||||
                                ACCT   CCC CCC TCCTC
                                  CAC   C   A
GAM711  TNKS1BP1 3'  TGGAGGAGGAAGCAGAGAGGGA 18433     A     ___
           GAG                    TGGA GAGGGAG   GGAGGGAGAG
                                |||| |||||||   ||||||||||
                                ACCT CTCCTTC   TCTCCCTCTC
                                  C      GTC
GAM711  TOMM40   3'  GGGGGAGGGAAGGGAGGG    18434    AA    _
                                GG  GAGGGA GGGAGGG
                                ||  |||||| |||||||
                                CC  CTCCCT CCCTCCC
                                 CC     T
GAM711  TPSG1    3'  GGGAGAGGGAGGGGGCGGAG   18435    A       A  GA
                                GG AGAGGGAGGG GG  GAG
                                || |||||||||| ||  |||
                                CC TCTCCCTCCC CC  CTC
                                 C         _ GC
GAM711  TRIM7    5'  TGGGAGAGGAAGGGCGGG    18436    A       A
                                TGG AGAGGGAGGG GGG
                                ||| |||||||||| |||
                                ACC TCTCCTTCCC CCC
                                  C         G
GAM711  TSC22    3'  TGGGGGGAGGAGAGGAGAGAG  18437    AAGA    GA
                                TGG   GGGAGG  GGGAGAGAG
                                |||   ||||||  |||||||||
                                ACC   CCCTCC  TCCTCTCTC
                                  C___     TC
GAM711  TSPEAR   3'  TGGAGGGGGCAGAGGGAG    18438     A A   AG
                                TGGA G GGG  GGAGGGAG
                                |||| | |||  ||||||||
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                                ACCT C CCC  TCTCCCTC
                                  _ _  CG
GAM711  VELI1    5'  TGGGGGCGGGGGTGGAGAG   18439    AAGA  A_  AG
                                TGG   GGG  GGG  GGAGAG
                                |||   |||  |||  ||||||
                                ACC   CCC  CCC  CCTCTC
                                  ____  GC   CA
GAM711  VIAAT    3'  GAGGGGAGAAGGGAGAGA    18440      AG
                                GAGGG  GGAGGGAGAGA
                                |||||  ||||||||||
                                CTCCC  CTTCCCTCTCT
                                   CT
GAM711  ZDHHC4   3'  TGGGGGAGAGAGGAGAATAGAG 18441     AAGA       _  _
                                TGG   GGGAGGGAGG GAG AGAG
                                |||   |||||||||| ||| ||||
                                ACC   CCCTCTCTCC CTT TCTC
                                  ____        T  A
GAM711  ZNF238   3'  GGGAGAGTAAGGGAGGGAG   18442   A   GG
                                GG AGAG  AGGGAGGGAG
                                || ||||  ||||||||||
                                CC TCTC  TCCCTCCCTC
                                 C   AT
GAM711  LOC115219 5'  TGGGGGTGGGGAGGAAGAGGAG 18443     AAGA_       _
           AGAG                   TGG    GGGAGGGAG GGAGAGAG
                                |||    ||||||||| ||||||||
                                ACC    CCCTCCTTC CCTCTCTC
                                  CCCAC       T
GAM711  LOC115574 3'  TGGGAGGGAGGGAGGGAG    18140    AA
                                TGG  GAGGGAGGGAGGGAG
                                |||  ||||||||||||||
                                ACC  CTCCCTCCCTCCCTC
                                  __
GAM711  LOC116113 3'  TGGAGGAGGGGTGGAGAGAG   18444     AGAG    AG
                                TGGA   GGAGGG  GGAGAGAG
                                ||||   ||||||  ||||||||
                                ACCT   CCTCCC  CCTCTCTC
                                  ____     CA
GAM711  LOC116411 5'  TGGAAAGAGCGGGGGGGGGGGG 18445      _  _ A  A  A
           AG                     TGGAA GAG GG GGG GGG GAG
                                ||||| ||| || ||| ||| |||
                                ACCTT CTC CC CCC CCC CTC
                                   T  G C  C  C
GAM711  LOC116411 5'  GGGGGGGGGGGGGAGGGGGAG   18446   AAGA  A     A
                                GG   GGG GGGAGGG GAG
                                ||   ||| ||||||| |||
                                CC   CCC CCCTCCC CTC
                                 CCCC  _     C
GAM711  LOC122664 5'  GGAGAAGGGGGAGGGAG    18447    A    A
                                GGA GAGGG GGGAGGGAG
                                ||| ||||| |||||||||
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                                CCT CTTCC CCCTCCCTC
                                  _   _
GAM711  LOC124446 5'  TGGAAGGGGGTTAAAGGGAGGG 18448       A  _____
                                TGGAAG GGG   AGGGAGGG
                                |||||| |||   ||||||||
                                ACCTTC CCC   TCCCTCCC
                                   C  AATT
GAM711  LOC124649 5'  TGGGAGAGAGTTGGAGGG    18449    A    AG
                                TGG AGAGGG  GGAGGG
                                ||| ||||||  ||||||
                                ACC TCTCTC  CCTCCC
                                  C     AA
GAM711  LOC124695 5'  TGGAGAGGGAGGGTCAGGG   18450     A      __
                                TGGA GAGGGAGGG  AGGG
                                |||| |||||||||  ||||
                                ACCT CTCCCTCCC  TCCC
                                  _       AG
GAM711  LOC128989 3'  GAGGGAAGAGGGAGAGAG    18451       G
                                GAGGGAGG AGGGAGAGAG
                                |||||||| ||||||||||
                                CTCCCTTC TCCCTCTCTC
                                  _
GAM711  LOC131583 5'  TGGGGGGAGGGGAGCAGAGAGA 18452    AAGA     _ _
           G                     TGG   GGGAGGG AG GGAGAGAG
                                |||   ||||||| || ||||||||
                                ACC   CCCTCCC TC TCTCTCTC
                                  C___      C  G
GAM711  LOC138389 5'  GAAAGAGGGAGGGAGGGAG   18453
                                GGAAGAGGGAGGGAGGGAG
                                ||||||||||||||||||
                                CTTTCTCCCTCCCTCCCTC

GAM711  LOC143879 3'  GAGAGGGGGGGAGGAGAGAG  18454    A    A  AG
                                GA GAGGG GGG  GGAGAGAG
                                || ||||| |||  ||||||||
                                CT CTCCC CCC  CCTCTCTC
                                  _   _  CT
GAM711  LOC144100 3'  TGGGGGAGGGATGTCCGAGGGA 18455    AA    GG___
           G                     TGG  GAGGGA    GAGGGAG
                                |||  ||||||    |||||||
                                ACC  CTCCCT    CTCCCTC
                                  CC     ACAGG
GAM711  LOC145216 3'  TGGAAGAGAGGGGCCTTGGAGA 18456         A  AG__
           G                     TGGAAGAGGG GGG   GGAGAG
                                |||||||||| |||   ||||||
                                ACCTTCTCTC CCC   CCTCTC
                                      _  GGAA
GAM711  LOC145468 3'  GAGGGGGGAGGGAAGGGAG   18457      A       A_
                                GAGGG GGGAGGGAG  GAG
                                ||||| |||||||||  |||
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                                CTCCC CCCTCCCTT  CTC
                                   _       CC
GAM711   LOC145623 3'  TGGAAGAGGGAGATGAGAG   18458           _
                                TGGAAGAGGGAGG GAGGG
                                |||||||||||| |||||
                                ACCTTCTCCCTCT CTCTC
                                        A
GAM711   LOC145719 5'  TGGAAAGGAAAGGGGAGGGAG  18459     A    __
                                TGGA GAGGGA  GGGAGGGAG
                                |||| ||||||  |||||||||
                                ACCT TTCCTT  CCCTCCCTC
                                   _     TC
GAM711   LOC145720 5'  TGGAAGGGAAAGGGGAGGGAG  18460      A   __
                                TGGAAG GGGA  GGGAGGGAG
                                |||||| ||||  |||||||||
                                ACCTTC CCTT  CCCTCCCTC
                                    _   TC
GAM711   LOC145919 3'  TGGGAAGGGAGGCAGGAGAG   18461    AA      GA
                                TGG  GAGGGAGG  GGGAGAG
                                |||  ||||||||  |||||||
                                ACC  TTCCCTCC  TCCTCTC
                                  C_      G_
GAM711   LOC145945 5'  TGGAGAGGGCTGAAAGGAGGGA 18462    A    ____
            GAGAG                   GGA GAGGG   AGGGAGGGAGAGAG
                                ||| |||||   ||||||||||||||
                                CCT CTCCC   TTCCTCCCTCTCTC
                                  _    GACT
GAM711   LOC146733 3'  TGGGGGAGTGGGGGAGGG    18463    AA  _ A
                                TGG  GAG GG GGGAGGG
                                |||  ||| || |||||||
                                ACC  CTC CC CCCTCCC
                                  CC   A  _
GAM711   LOC147495 3'  GGCTGGGAGGGAGGGAG     18464    AAGA
                                GG   GGGAGGGAGGGAG
                                ||   |||||||||||||
                                CC   CCCTCCCTCCCTC
                                 GA__
GAM711   LOC147645 3'  TGGGAGGGGAGGTCAGGGAG   18465    A A    G_
                                TGG AG GGGAGG  AGGGAG
                                ||| || ||||||  ||||||
                                ACC TC CCCTCC  TCCCTC
                                  C  _     AG
GAM711   LOC148529 5'  TGGGGGAGGAAGGGAGGCAAG  18466    AA        GA
                                TGG  GAGGGAGGGAGG  GAG
                                |||  ||||||||||||  |||
                                ACC  CTCCTTCCCTCC  TTC
                                  CC          G_
GAM711   LOC148645 3'  GAAGAGGGAGGGGCCAAGGGGA 18467          ____   A
            G                    GAAGAGGGAGGG   AGGG GAG
                                ||||||||||||   |||| |||
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                                CTTCTCCCTCCC   TCCC CTC
                                       CGGT   _
GAM711   LOC149301 5'  GGGAGGGGCAAGGGAGAG    18468       ___
                                GGGAGGG   AGGGAGAG
                                |||||||   ||||||||
                                CCCTCCC   TCCCTCTC
                                    CGT
GAM711   LOC149319 3'  TGGATAGAGGGAGGGAGGGAG  18469     _
                                TGGA AGAGGGAGGGAGGGAG
                                |||| ||||||||||||||||
                                ACCT TCTCCCTCCCTCCCTC
                                  A
GAM711   LOC149478 5'  TGGAGGAGGGAGCCTGGGAG   18470      A      GGA
                                TGGA GAGGGAG   GGGAG
                                |||| |||||||   |||||
                                ACCT CTCCCTC   CCCTC
                                  C      GGA
GAM711   LOC149711 3'  TGGTAGGGGGATGGAGGGAG   18471     A  A    G
                                TGG AG GGGA GGAGGGAG
                                ||| || |||| ||||||||
                                ACC TC CCCT CCTCCCTC
                                  A  C    A
GAM711   LOC149773 5'  TGGGAGGGAGGGGGGCAGGAG  18472     AA        A  _  A
                                TGG  GAGGGAGGG GGG AG GAG
                                |||  ||||||||| ||| || |||
                                ACC  CTCCCTCCC CCC TC CTC
                                  __        _  G  _
GAM711   LOC149912 5'  GGGAGTTGGAGGGAGAGAG    18473       __
                                GGGAG  GGAGGGAGAGAG
                                |||||  ||||||||||||
                                CCCTC  CCTCCCTCTCTC
                                   AA
GAM711   LOC150155 3'  GAGGGGGGAGGGAAGGGAG    18457       A        A_
                                GAGGG GGGAGGGAG  GAG
                                ||||| |||||||||  |||
                                CTCCC CCCTCCCTT  CTC
                                   _        CC
GAM711   LOC150319 3'  TGGCGGGGGGTGGGGGAGAGAG 18474     AAGA   AG  A
                                TGG    GGG  GG GGGAGAGAG
                                |||    |||  || |||||||||
                                ACC    CCC  CC CCCTCTCTC
                                  GCC_   CA  _
GAM711   LOC150538 5'  GGAAGGGGGTAAAGGGGAGAG  18475       A   AG     A
                                GGAAG GGG  GGAGGG GAGAG
                                ||||| |||  |||||| |||||
                                CCTTC CCC  TTTCCC CTCTC
                                   _  CA     _
GAM711   LOC150793 3'  TGGAGAGAGGGGGGAAAGGGAG  18476      _     A GG
                                TGGA AGAGGG G  AGGGAG
                                |||| |||||| |  ||||||
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                                ACCT TCTCCC C  TCCCTC
                                  C     C TT
GAM711  LOC151484 3'  AGGGCTGGGGAGGGAGAG    18477      A__
                                AGGG   GGGAGGGAGAG
                                ||||   ||||||||||
                                TCCC   CCCTCCCTCTC
                                  GAC
GAM711  LOC151516 5'  TGGAGAGGGAGGCAGAGGAG   18478      A      G    A
                                TGGA GAGGGAGG AGGG GAG
                                |||| |||||||| |||| |||
                                ACCT CTCCCTCC TCTC CTC
                                  _       G   _
GAM711  LOC152667 3'  TGGATAGAGAGGGGAGAGGG   18479      ___     A
                                TGGA   AGAGGG GGGAGGG
                                ||||   |||||| |||||||
                                ACCT   TCTCCC CTCTCCC
                                  ATC     _
GAM711  LOC153146 5'  TGGGAGGAGGATAAAGAGAGAG 18480     A  AG   GG
                                TGG AG  GGA  GAGGGAGAG
                                ||| ||  |||  |||||||||
                                ACC TC  CCT  TTCTCTCTC
                                  C  CT   AT
GAM711  LOC153339 5'  TGGAGGGTGGGAGGAGGGAG   18481      AGA_     G
                                TGGA    GGGAGG AGGGAG
                                ||||    |||||| ||||||
                                ACCT    CCCTCC TCCCTC
                                  CCCA     _
GAM711  LOC153811 3'  TGGGGGAGGGAGGAGGAAGGAG 18482     AA       G     A
                                TGG  GAGGGAGG AGGGAG GAG
                                |||  |||||||| |||||| |||
                                ACC  CTCCCTCC TCCTTC CTC
                                  CC       _     _
GAM711  LOC154877 3'  TGGTGGAGGGAGGGGACAGAG  18483     AA        A  G
                                TGG  GAGGGAGGG GG AGAG
                                |||  ||||||||| || ||||
                                ACC  CTCCCTCCC CT TCTC
                                  AC         _  G
GAM711  LOC157421 5'  TGGAAGAAGGAAGGAGGG    18484
                                TGGAAGAGGGAGGGAGGG
                                ||||||||||||||||||
                                ACCTTCTTCCTTCCTCCC

GAM711  LOC158062 3'  TGGAGGGGAGGGACAGAG    18485      A A       G
                                TGGA G GGGAGGGA GGAG
                                |||| | |||||||| ||||
                                ACCT C CCCTCCCT TCTC
                                  _ _       G
GAM711  LOC159090 5'  GGGAGAGGGCAGAGGGGAGGGA 18486     A     A____
              G                   GG AGAGGG     GGGAGGGAG
                                || ||||||     |||||||||
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                                CC TCTCCC    CCCTCCCTC
                                 C     GTCTC
GAM711   LOC159090 5'  GGAGGAGGGAGGGGAAGGGAGA 18487    A       __
            G                    GGA GAGGGAGGG  AGGGAGAG
                                 ||| |||||||||  ||||||||
                                 CCT CTCCCTCCC  TCCCTCTC
                                   C        CT
GAM711   LOC196410 3'  TGGCAGAGGTTGGGGAGAGAG  18488    A    GA   A
                                 TGG AGAGG  GGG GGGAGAG
                                 ||| |||||  ||| |||||||
                                 ACC TCTCC  CCC CTCTCTC
                                   G    AA  _
GAM711   LOC196484 5'  TGGAAAAGCTAGGGAGGGAG   18489        GG
                                 TGGAAGAG  AGGGAGGGAG
                                 ||||||||  ||||||||||
                                 ACCTTTTC  TCCCTCCCTC
                                      GA
GAM711   LOC196812 3'  AGAGCAGGGAGGGAGAGA    18490     _
                                 AGGG AGGGAGGGAGAGA
                                 |||| ||||||||||||
                                 TCTC TCCCTCCCTCTCT
                                   G
GAM711   LOC197419 3'  GAGAAGGGGAGGGAGAGA    18491     GA
                                 GAGG  GGGAGGGAGAGA
                                 ||||  ||||||||||||
                                 CTCT  CCCTCCCTCTCT
                                   TC
GAM711   LOC199232 5'  GGGGGAGGGAGACTGGGGAG   18492    AA      GA   A
                                 GG  GAGGGAGG  GGG GAG
                                 ||  ||||||||  ||| |||
                                 CC  CTCCCTCT  CCC CTC
                                  CC       GA  _
GAM711   LOC200032 5'  TGGAGGAGGGAGGGTGA     18119     AGAG        A
                                 TGGA   GGAGGGAGGG GA
                                 ||||   |||||||||| ||
                                 ACCT   CCTCCCTCCC CT
                                   ____         A
GAM711   LOC200734 3'  TGGAAGAGGCGGGGGAGGAG   18493        GA   AG
                                 TGGAAGAGG  GGG  GGAG
                                 |||||||||  |||  ||||
                                 ACCTTCTCC  CCC  CCTC
                                      GC   CT
GAM711   LOC200862 5'  TGGAAGAGGGAGGTAGAG    18494          G
                                 TGGAAGAGGGAGG AGGG
                                 |||||||||||| ||||
                                 ACCTTCTCCCTCC TCTC
                                        A
GAM711   LOC201702 5'  TGAAAGGCAGAGGGAGGGAG   18113       AG
                                 TGGAAG  GGAGGGAGGGAG
                                 ||||||  ||||||||||||
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                                ACTTTC  TCTCCCTCCCTC
                                   CG
GAM711   LOC201911 3'  GGGAGAGGGAGGGAGGGA    18495    A
                                GG AGAGGGAGGGAGGGA
                                || ||||||||||||||
                                CC TCTCCCTCCCTCCCT
                                 C
GAM711   LOC202134 3'  TGGAAGAGGGGGTGTCTGGAG  18496          A  GAG__
                                TGGAAGAGGG GG    GGAG
                                |||||||||| ||    ||||
                                ACCTTCTCCC CC    CCTC
                                      _  ACAGA
GAM711   LOC202347 3'  TGGAAGAGGTAGAGAGGG    18497         G
                                TGGAAGAGG AGGGAGGG
                                |||||||| ||||||||
                                ACCTTCTCC TCTCTCCC
                                      A
GAM711   LOC219818 3'  GGAAGGGGGAGGCCCGCTGGGA 18498      A     GA____
            GAG                    GGAAG GGGAGG     GGGAGAG
                                ||||| ||||||     |||||||
                                CCTTC CCCTCC     CCCTCTC
                                   C     GGGCGA
GAM711   LOC220549 5'  TGGGGGAGGAAGGCCGCGGGGA 18499     AA       GA__   A
            G                   TGG  GAGGGAGG    GGG GAG
                                |||  ||||||||    ||| |||
                                ACC  CTCCTTCC    CCC CTC
                                  CC       GGCG  _
GAM711   LOC220793 3'  TGGGAGAAGGAGAGGAGGG    18500     A      _
                                TGG AGAGGGAG GGAGGG
                                ||| |||||||| ||||||
                                ACC TCTTCCTC CCTCCC
                                  C       T
GAM711   LOC221191 3'  TGGGAGAGGGATAGAGGAGGGA 18501     A     ___
            G                   TGG AGAGGGA   GGGAGGGAG
                                ||| |||||||   |||||||||
                                ACC TCTCCCT   TCCTCCCTC
                                  C       ATC
GAM711   LOC221337 5'  GGGAGGGAGGGAGGGAGGGAG  18503    AA           A
                                GG  GAGGGAGGGAGGGAG GAG
                                ||  |||||||||||||| |||
                                CC  CTCCCTCCCTCCCTC CTC
                                  __             C
GAM711   LOC221337 5'  GGAAGAAAGGGAGGGAGGGAGG 18502      __          A   III
            GAGC                    AAGA  GGGAGGGAGGGAG GAG   C
                                ||||  |||||||||||| |||   |
                                TTCT  CCCTCCCTCCCTC CTC   G
                                  TT           C   III
GAM711   LOC221337 5'  GGGAGGGAGGGAGGGAGGGAG  18503    AA           A
                                GG  GAGGGAGGGAGGGAG GAG
                                ||  |||||||||||||| |||
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                                CC  CTCCCTCCCTCCCTC CTC
                                 __            C
GAM711   LOC221415 5'  TGGAAGAAGGGTTGGGAGGG   18504          A__
                                TGGAAGAGGG   GGGAGGG
                                ||||||||||   |||||||
                                ACCTTCTTCC   CCCTCCC
                                     CAA
GAM711   LOC221474 3'  TGGAGGGGAGGTCAGGGAGAG  18505      A A     G_
                                TGGA G GGGAGG  AGGGAGAG
                                |||| | ||||||  ||||||||
                                ACCT C CCCTCC  TCCCTCTC
                                  _ _     AG
GAM711   LOC221975 5'  GGGAGAGCAAGAGGGAGGGAGA 18506    A   __
            GAG                    GG AGAG  GGAGGGAGGGAGAGAG
                                || ||||  ||||||||||||||||
                                CC TCTC  TCTCCCTCCCTCTCTC
                                 C   GT
GAM711   LOC253367 3'  AGGGGTGGGAGGGAGAG     18507    A   A
                                AG GGG GGGAGGGAGAG
                                || ||| ||||||||||
                                TC CCC CCCTCCCTCTC
                                 _   A
GAM711   LOC253891 3'  TGGGGGATGGGGGGAAGGAAGA 18508     AA  _   A
            GAG                    TGG  GA GGG GGGAGGGAGAGAG
                                |||  || ||| ||||||||||||
                                ACC  CT CCC CCTTCCTTCTCTC
                                  CC  A   C
GAM711   LOC253980 3'  GGAAGGGGAGGGAAAGAGAGAG 18509       A
                                GGAAG GGGAGGGAGGGAGAGAG
                                ||||| ||||||||||||||||
                                CCTTC CCCTCCCTTTCTCTCTC
                                  _
GAM711   LOC254110 3'  GGAAGAGGCCATGGGGAGAGAG 18510         GAGGGA
                                GGAAGAGG     GGGAGAGAG
                                ||||||||     |||||||||
                                CCTTCTCC     CCCTCTCTC
                                     GGTAC_
GAM711   LOC254532 3'  GGAAGGAAGGGAGGGAGGGAG  18511       __
                                GGAAG  AGGGAGGGAGGGAG
                                |||||  ||||||||||||||
                                CCTTC  TCCCTCCCTCCCTC
                                   CT
GAM711   LOC254824 3'  TGGAAGAGCAGGGAGGG     18512        G G
                                TGGAAGA G AGGGAGGG
                                ||||||| | ||||||||
                                ACCTTCT C TCCCTCCC
                                    _ G
GAM711   LOC254873 3'  TGGGGGAAGGAAGAGGGAG    18215     AA       G
                                TGG  GAGGGAGG AGGGAG
                                |||  |||||||| ||||||
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                                ACC  CTTCCTTC TCCCTC
                                  CC       _
GAM711   LOC254873 3'  GGAAGAGGGAGGGGAGAG    18216            A
                                GGAAGAGGGAGGG GGGAG
                                ||||||||||||| |||||
                                CCTTCTCCCTCCC CTCTC
                                                 _
GAM711   LOC256809 5'  GGAAGGGAAGGGAGAGAG    18513       A
                                GGAAG GGGAGGGAGGGAG
                                ||||| ||||||||||||
                                CCTTC CCTTCCCTCTCTC
                                  _
GAM711   LOC257019 5'  TGGGAGGGGAGGAGGGAG    18514     AA    AG
                                TGG  GAGGG  GGAGGGAG
                                |||  |||||  ||||||||
                                ACC  CTCCC  CCTCCCTC
                                  __    CT
GAM711   LOC257048 3'  GGGGGAGGGAGGCGCGGAGGGA 18286    AA      ____
           G                     GG  GAGGGAGG    GAGGGAG
                                ||  ||||||||    |||||||
                                CC  CTCCCTCC    CTCCCTC
                                 CC       GCGC
GAM711   LOC257463 3'  TGGGAGGGAGGTTGGAGGGAG  18515     AA      ___
                                TGG  GAGGGAGG   GAGGGAG
                                |||  ||||||||   |||||||
                                ACC  CTCCCTCC   CTCCCTC
                                  __       AAC
GAM711   LOC51195  3'  TGGGAGAGGGAGGGAGTAAAG  18516     A         GG
                                TGG AGAGGGAGGGAG  AGAG
                                ||| ||||||||||||  ||||
                                ACC TCTCCCTCCCTC  TTTC
                                  C          A_
GAM711   LOC51277  5'  GGGAGCCGGGGGGAGGGAG    18517    A  AG  A
                                GG AG  GG GGGAGGGAG
                                || ||  || |||||||||
                                CC TC  CC CCCTCCCTC
                                 C  GG  _
GAM711   LOC51634  3'  GGAGGAGGGAGGAAACGGGGAG 18518     A       ___
                                GGA GAGGGAGGGA   GGGAG
                                ||| ||||||||||   |||||
                                CCT CTCCCTCCTT   CCCTC
                                  C          TGC
GAM711   LOC51762  5'  TGGAGAGAGGCGGGGAGGG    18519     _    GA
                                TGGA AGAGG  GGGAGGG
                                |||| |||||  |||||||
                                ACCT TCTCC  CCCTCCC
                                  C     GC
GAM711   LOC56961  5'  GGGAGAGGGAGAAGGAGGGGAG 18520    A      __     A
                                GG AGAGGGAG  GGAGGG GAG
                                || ||||||||  |||||| |||
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                                CC TCTCCCTC  CCTCCC CTC
                                 C       TT     _
GAM711  LOC57149  5'  TGGGAGAGGGAGGGAGGGAAGA 18521     A           _
              G                   TGG AGAGGGAGGGAGGGA GAG
                                  ||| |||||||||||||| |||
                                  ACC TCTCCCTCCCTCCCT CTC
                                    C            T
GAM711  LOC57149  5'  TGGGAGAGGGAGGGAGGG    18522     A
                                  TGG AGAGGGAGGGAGGG
                                  ||| ||||||||||||||
                                  ACC TCTCCCTCCCTCCC
                                    C
GAM711  LOC58486  5'  TGGAGGGGGAGGGGAGAGAG   18523      A A      A
                                  TGGA G GGGAGGG GGGAGAG
                                  |||| | ||||||| |||||||
                                  ACCT C CCCTCCC CTCTCTC
                                    _ C      _
GAM711  LOC90139  3'  GAAGAGGGACAGAGGGGAGAG  18524          G     A
                                  GAAGAGGGA GGAGGG GAGAG
                                  ||||||||| |||||| |||||
                                  CTTCTCCCT TCTCCC CTCTC
                                       G     _
GAM711  LOC90736  3'  GGGAGGGGGAAGGGAGAGAG   18525    AA     A
                                  GG  GAGGG GGGAGGGAGAGAG
                                  ||  ||||| ||||||||||||
                                  CC  CTCCC CCTTCCCTCTCTC
                                    __    _
GAM711  LOC90736  3'  GGAAGGGAGAGAGGGAGAGAG  18526     AG
                                  GGA  AGGGAGGGAGGGAGAGAG
                                  |||  ||||||||||||||||||
                                  CCT  TCCCTCTCTCCCTCTCTC
                                    __
GAM711  LOC91397  5'  TGGCAAGAGGAAGGGGGGGAG  18527     _         A
                                  TGG AAGAGGGAGGG GGGAG
                                  ||| |||||||||| |||||
                                  ACC TTCTCCTTCCC CCCTC
                                    G          C
GAM711  LOC91409  5'  TGGAGGAGGGAGGTCTGGGGAG 18528      A       GA_   A
                                  TGGA GAGGGAGG   GGG GAG
                                  |||| ||||||||   ||| |||
                                  ACCT CTCCCTCC   CCC CTC
                                    C       AGA   _
GAM711  LOC92578  3'  TGGAGAGGGAGGGCCAGACAGG 18529      A       _______
              GAG                   TGGA GAGGGAGGG      AGGGAG
                                  |||| |||||||||      ||||||
                                  ACCT CTCCCTCCC      TCCCTC
                                    _        GGTCTG
GAM711  LOC92697  5'  GGGAGAGGGAGAGGGAG     18531    A      GG
                                  GG AGAGGGA  GAGGGAG
                                  || |||||||  |||||||
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                                CC TCTCCCT  CTCCCTC
                                 C      __
GAM711  LOC92697  5'  GGGAGAGGGAGAGGGAGAG   18530   A     GG
                                GG AGAGGGA  GAGGGAGAG
                                || |||||||  |||||||||
                                CC TCTCCCT  CTCCCTCTC
                                 C      __
GAM711  LOC92697  5'  GGGAGAGGGAGAGGGAGAG   18530   A     GG
                                GG AGAGGGA  GAGGGAGAG
                                || |||||||  |||||||||
                                CC TCTCCCT  CTCCCTCTC
                                 C      __
GAM711  LOC95633  3'  TGGATAGAGGGGTGAGGAGAG 18532     _     AG GA
                                TGGA AGAGGG  G  GGGAGAG
                                |||| ||||||  |  |||||||
                                ACCT TCTCCC  C  TCCTCTC
                                   A     CA __
GAM712  BAZ2A    3'  GTGGCTCTTCAGTGCTGC    18535     CCC    CGA   C
                                GTGGC   CTTCG   TGC GC
                                |||||   |||||   ||| ||
                                CACCG   GAAGT   ACG CG
                                   A__    C__   A
GAM712  C10orf2  3'  TGGGTCCCCTTCGCCGGATG   18536   T  C       __
                                TG GG CCCCTTCGC  GATG
                                || || |||||||||  ||||
                                AC CC GGGGAAGCG  CTAC
                                 _ A        GC
GAM712  ICAM1    3'  TGGCCCCCTTCCCCACTGC    18537         _ G  A
                                TGGCCCCCTT C CG TGC
                                |||||||||| | || |||
                                ACCGGGGGAA G GT ACG
                                      G G  G
GAM712  LTBR     3'  TGTGCCCCCCTTCTTCTGCC   18538     G      GCGA
                                TGTG CCCCCTTC    TGCC
                                |||| ||||||||    ||||
                                ACAC GGGGGAAG    ACGG
                                  G       AAG_
GAM712  MBP      3'  GTGGCCCCCTCTCTGTGCTGCC 18539          CGCGA   C
                                GTGGCCCCCTT     TGC GCC
                                ||||||||||     ||| |||
                                CACCGGGGGAG     ACG CGG
                                      AGAC_   A
GAM712  ARHGEF16 3'  TGTGGCCCCCTCGAGCTTGCC  18540           C_  GA
                                TGTGGCCCCCTT  GC  TGCC
                                ||||||||||||  ||  ||||
                                ACACCGGGGGAG  CG  ACGG
                                       CT  A_
GAM712  C20orf64 5'  TGTGGCCCCCTCGTGCC     18541          T  CGA
                                TGTGGCCCCCT CG   TGCC
                                |||||||||| ||   ||||
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                                ACACCGGGGGA GC   ACGG
                                          _ ___
GAM712  CREB-H   3' TGTGGCCCTCTTTGCC     18542       C  CGCGA
                                TGTGGCCC CTT    TGCC
                                |||||||| |||    ||||
                                ACACCGGG GAA    ACGG
                                    A  _____
GAM712  FLJ12697 3' TGTGGTCCTTGTGCGGCCGC  18543     CCC   C_  AT
                                TGTGG  CCTT  GCG  GCCGC
                                |||||  ||||  |||  |||||
                                ACACC  GGAA  CGC  CGGCG
                                  A__   CA  __
GAM712  FLJ20487 3' TGTGGCCCTCATTCTGCCTGC 18544       CCT  CGA  _
                                TGTGGCCC  TCG  TGCC GC
                                ||||||||  |||  |||| ||
                                ACACCGGG  AGT  ACGG CG
                                    ___  AAG   A
GAM712  FLJ22408 5' TGGGGCCCCTCCGTGCCG   18545   T C     CGA
                                TG GG CCCCTTCG  TGCCG
                                || || ||||||||  |||||
                                AC CC GGGGAGGC  ACGGC
                                 _ C      ___
GAM712  KIAA0350 3' TGTGGCCCCCTTTCTGAGC   18546         _ GC  T
                                TGTGGCCCCCTT C  GA GC
                                |||||||||||| |  || ||
                                ACACCGGGGGAA G  CT CG
                                     A A_ _
GAM712  KIAA0514 3' TGTGGCCCTTTCTGCACCTGC 18547       CC  _  A_
                                TGTGGCCC  TTC GCG  TGC
                                ||||||||  ||| |||  |||
                                ACACCGGG  AAG CGT  ACG
                                    A_  A  GG
GAM712  KIAA0544 3' TGGGGTTCCCTCCACGGTGCTG 18548   T  CC      A  C
           CC                  TG GG  CCCTTCGCG TGC GCC
                               || ||  ||||||||| ||| |||
                               AC CC  GGGAGGTGC ACG CGG
                                C  AA       C  A
GAM712  KIAA1305 5' TGGTCCCCTTCGACCGC    18549    C     CGAT
                                TGG CCCCTTCG   GCCGC
                                ||| ||||||||   |||||
                                ACC GGGGAAGC   TGGCG
                                  A      ____
GAM712  KIAA1582 5' TGTAGTTCCAGAAGATGCCGC  18550     CC  CTTCGC
                                TGTGG  CC    GATGCCGC
                                |||||  ||    ||||||||
                                ACATC  GG    CTACGGCG
                                  AA  TCTT__
GAM712  UBE2E1   5' TGGCTCCTCCGTGCCGC    18551    CC    CGA
                                TGGC  CCTTCG   TGCCGC
                                ||||  ||||||   ||||||
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                                ACCG  GGAGGC   ACGGCG
                                  A_     ___
GAM712  LOC132228 3'  TGTGGCCCCTTCCTGTCGGCGG 18552      C  C_________  ATGC
            CATCG                  GGCCCC TT       GCG    CG
                                |||||| ||        |||    ||
                                CCGGGG AG        CGC    GC
                                   A  GACAGIIIC   CGTA
GAM712  LOC147599 3'  TGTGGCCCTTTCCTCTTGCC  18553        CC   GCGA
                                TGTGGCCC  TTC    TGCC
                                ||||||||  |||    ||||
                                ACACCGGG  AGG    ACGG
                                    AA   AGA_
GAM712  LOC204820 3'  TGTGGCCCTTTCCTGGCCCGCC 18554         ___   TC  GATG
                                TGTGGCCC   CCT  GC    CCGCC
                                ||||||||   |||  ||    |||||
                                ACACCGGG   GGA  CG    GGCGG
                                    AAA   C_  _____
GAM712  LOC254173 3'  TGTGGCCCCGTTGCTGCC    18555        C  C  GA
                                TGTGGCCCC TT GC  TGCC
                                ||||||||| || ||  ||||
                                ACACCGGGG AA CG  ACGG
                                    C  _  __
GAM712  LOC257127 3'  TGGGCTCCCTTCACCGCC    18556    T   C      GA
                                TG GGC CCCTTCGC  TGCC
                                || ||| ||||||||  ||||
                                AC CCG GGGAAGTG  GCGG
                                 _   A       __
GAM713  BCL11B   5'  GGCATCGCCCGGAGAG      18559     _  ACA
                                GGT TCG   CCCGGAGAG
                                ||| |||   |||||||||
                                CCG AGC   GGGCCTCTC
                                  T   ____
GAM713  BCL11B   5'  GGCATCGCCCGGAGAG      18559     _  ACA
                                GGT TCG   CCCGGAGAG
                                ||| |||   |||||||||
                                CCG AGC   GGGCCTCTC
                                  T   ____
GAM713  BMP1     3'  TCCCCGGGTGTGACAGAG    18560        TC   CCCG
                                TCCCCGGGT  GACA    GAG
                                |||||||||  ||||    |||
                                AGGGGCCCA  CTGT    CTC
                                    CA    _____
GAM713  ICMT     3'  TCCCCAGGTAACTCTGGAG   18561        TC   ACCC
                                TCCCCGGGT  GAC    GGAG
                                |||||||||  |||    ||||
                                AGGGGTCCA  TTG    CCTC
                                    __   AGA_
GAM713  MAP7     5'  CCGATGACGCGCCCGGAGAG  18562     GTT  ACA
                                CCGG   CG   CCCGGAGAG
                                ||||   ||   |||||||||
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                                GGCT  GC  GGGCCTCTC
                                  ACT GC_
GAM713  CKAP4    3' TCCTTGGTGACCTCCGGAGAG 18563    CCG  TC  AC
                                TCC  GGT GAC CCGGAGAG
                                |||  ||| ||| ||||||||
                                AGG  CCA CTG GGCCTCTC
                                  AA_  __  GA
GAM713  FLJ10829 3' CAACTCTGACGCCCGGGGAG  18564    G TC  A   A
                                CGG T  GAC CCCGG GAG
                                ||| |  ||| ||||| |||
                                GTT A  CTG GGGCC CTC
                                  G GA  C   C
GAM713  FLJ21687 3' CCCCAGCCGGTGCCCGGAGAG 18565      GT  ACA
                                CCCCGG  TCG  CCCGGAGAG
                                ||||||  |||  |||||||||
                                GGGGTC  GGC  GGGCCTCTC
                                   __  CAC
GAM713  HSJ001348 5' TCCCCGGGTCTGGCCGGTAG  18566        CGACAC  _
                                TCCCCGGGTT    CCGG AG
                                ||||||||||    |||| ||
                                AGGGGCCCAG    GGCC TC
                                     ACC___   A
GAM713  KIAA0720  3' TCCCCGGGGGGCACCTGGGGAG 18567       TTCGA  C  A
                                TCCCCGGG   CACC GG GAG
                                ||||||||   |||| || |||
                                AGGGGCCC   GTGG CC CTC
                                    CCC__  A  C
GAM713  KIAA1130  3' CCCCGGGTTTGACAAGGGGGAG 18568       C   CCC_
                                CCCCGGGTT GACA  GGAG
                                ||||||||| ||||  ||||
                                GGGGCCCAA CTGT  CCTC
                                     A  TCCC
GAM713  MGC2628   3' TCCACCGGAGAACACTTGGGGA 18569    _   TTC   CC  A
          G                      TCC CCGGG  GACAC  GG GAG
                                ||| |||||  |||||  || |||
                                AGG GGCCT  TTGTG  CC CTC
                                  T   C__   AA  C
GAM713  NEUROD4   5' CCCTGGTTAGCTCCCCGGAGAG 18570    G   CGACA
                                CCC GGTT   CCCGGAGAG
                                ||| ||||   |||||||||
                                GGG CCAA   GGGCCTCTC
                                  A  TCGAG
GAM713  LOC145945 5' CCCAAAGACACCTGGAGAG  18571      TTC    C
                                CCCGGG  GACACC GGAGAG
                                ||||||  |||||| ||||||
                                GGGTTT  CTGTGG CCTCTC
                                   ___    A
GAM713  LOC196746 3' TCCCCAGGGTTCGGGGGCGGAG 18572      _     ACACC
                                TCCCC GGGTTCG   CGGAG
                                ||||| |||||||   |||||
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                                AGGGG CCCAAGC    GCCTC
                                  T     CCCC_
GAM713  LOC219348 3'  TCCCCAGGTCTGAGCCTGGAG  18573        TC  CA  C
                                TCCCCGGGT  GA  CC GGAG
                                |||||||||  ||  || ||||
                                AGGGGTCCA  CT  GG CCTC
                                     GA  C_  A
GAM713  LOC256286 3'  CCCCCGGGCCGCCCGG      18574         T  ACA
                                TCCCCGGGT CG   CCCGG
                                |||||||||  ||   |||||
                                GGGGGCCCG GC   GGGCC
                                     _  ___
GAM713  LOC91748  5'  TCCCCGGGCTGCTCGGAG    18575         CGACACC
                                TCCCCGGGTT      CGGAG
                                ||||||||||      |||||
                                AGGGGCCCGA      GCCTC
                                     CGA____
GAM714  DHFR     3'  AACCCTTTGGTTCAAGCAACCA 18578       C_  AG  _
            T                    AGCCCT  GGT  TCA GCAACCAT
                                ||||||  |||  ||| ||||||||
                                TTGGGA  CCA  AGT CGTTGGTA
                                   AA  __  T
GAM714  LILRA1   5'  AGCCCTCGGTGCATGGCA    18579         A  CA_
                                AGCCCTCGGT GT   GCA
                                ||||||||||  ||   |||
                                TCGGGAGCCA CG   CGT
                                     _  TAC
GAM714  LILRB1   5'  AGCCCTCGGTGCATGGCA    18579         A  CA_
                                AGCCCTCGGT GT   GCA
                                ||||||||||  ||   |||
                                TCGGGAGCCA CG   CGT
                                     _  TAC
GAM714  LILRB2   5'  AGCCCTCGGTGCATGGCA    18579         A  CA_
                                AGCCCTCGGT GT   GCA
                                ||||||||||  ||   |||
                                TCGGGAGCCA CG   CGT
                                     _  TAC
GAM714  MKI67    3'  AAGCCCCCGGTGTTCAAC     18580         AG
                                AAGCCCTCGGT  TCAGC
                                ||||||||||  |||||
                                TTCGGGGGCCA  AGTTG
                                     CA
GAM714  PLCB2    3'  GCCCTCAGCCAGGGAGTGGCC  18581          _  TC  CAA
                                GCCCTCGGT AG  AG   CC
                                |||||||||  ||  ||   ||
                                CGGGAGTCG TC  TC   GG
                                     G  CC  ACC
GAM714  TEM1     3'  CCCTGGTGCAGCCCCGGCCAT  18582      C   A T   AA___
                                CCCT GGT G CAGC    CCAT
                                |||| ||| | ||||    ||||
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                                GGGA CCA C GTCG    GGTA
                                  _  _ _   GGGCC
GAM714  TMEFF2   3'  AAGCTCTCGGTAGTCCAGCCAC 18583     C       _  A
                                AAGC CTCGGTAGTC AGC AC
                                |||| |||||||||| ||| ||
                                TTCG GAGCCATCAG TCG TG
                                  A        G  G
GAM714  TNXB     3'  CCCTCAGTGCTCGGCAGTCAT  18584       AG  A  AC
                                CCCTCGGT  TC GCA  CAT
                                ||||||||  || |||  |||
                                GGGAGTCA  AG CGT  GTA
                                     CG  C   CA
GAM714  TNXB     3'  CCCTCAGTGCTCGGCAGTCAT  18584       AG  A  AC
                                CCCTCGGT  TC GCA  CAT
                                ||||||||  || |||  |||
                                GGGAGTCA  AG CGT  GTA
                                     CG  C   CA
GAM714  ALTE     3'  AGCCCTGAGAAGTCAGCAGCC  18585      C  T      A
                                AGCCCT GG AGTCAGCA CC
                                |||||| || |||||||| ||
                                TCGGGA TC TCAGTCGT GG
                                   C  T       C
GAM714  FLJ20396  5'  AAGTCCCCGGTAGCCGGGAGGC 18586     C        A____  AA
           GGCC                    AAG CCTCGGTAGTC    GC  CC
                                ||| ||||||||||    ||  ||
                                TTC GGGGCCATCGG    CG  GG
                                  A         CCCTC  CC
GAM714  FLJ23399  5'  AAACCCTCGGTGGTCGACA   18587         A  A
                                AAGCCCTCGGT GTC GCA
                                |||||||||| ||| |||
                                TTTGGGAGCCA CAG TGT
                                      C  C
GAM714  SFRS5    3'  AACCCCTTGGTGGTCCACA   18588    G   C  A  A
                                AA CCCT GGT GTC GCA
                                || |||| ||| ||| |||
                                TT GGGA CCA CAG TGT
                                 G   A  C  G
GAM714  LOC127702 3'  TCAGAAGTCAGCAGCCAT    18589     T      A
                                TCGG AGTCAGCA CCAT
                                |||| |||||||| ||||
                                AGTC TCAGTCGT GGTA
                                  T       C
GAM714  LOC151473 3'  GCCTCACAGCAACCA      18590     C  GTAGT
                                GCC TCG    CAGCAACCA
                                ||| |||    |||||||||
                                CGG AGT    GTCGTTGGT
                                  _  _____
GAM714  LOC221463 3'  GCTGACAGAGTCAGCAACCAT  18591    CCT   T
                                GC   CGG AGTCAGCAACCAT
                                ||   ||| ||||||||||||
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                                CG   GTC TCAGTCGTTGGTA
                                 ACT  _
GAM714  LOC256158 5'  AGCTCCTCGGCTGGGCGGCCAT 18592    _     AGTCA  AA
                                AGC CCTCGGT    GC  CCAT
                                ||| |||||||    ||  ||||
                                TCG GGAGCCG    CG  GGTA
                                  A      ACC__  CC
GAM714  LOC91373  3'  CCCGGATTAGTCAGCAACCAT  18593     __
                                CTCGG  TAGTCAGCAACCAT
                                |||||  ||||||||||||||
                                GGGCC  ATCAGTCGTTGGTA
                                   TA
GAM715  ADORA1   3'  CCTCTGCCTGCTGCAGCC    18596        CTAC T  A
                                CCTCTGCCT    G CT CAGCC
                                |||||||||    | || |||||
                                GGAGACGGA    C GA GTCGG
                                     _____ _  C
GAM715  BCRP2    3'  TCTGCCTTCATAGGCAGCC    18597      CTA   CTA
                                TCTGCCT   CGT   CAGCC
                                |||||||   |||   |||||
                                AGACGGA   GTA   GTCGG
                                    A__   TCC
GAM715  CERD4    3'  TCTGCCTCTGATCAGGCCC    18598       AC   TACA
                                TCTGCCTCT  GTC    GCCC
                                |||||||||  |||    ||||
                                AGACGGAGA  TAG    CGGG
                                     C_   TC__
GAM715  CMAR     3'  CTGCTGCCTCTGGGTGGCC    18599    _     AC  CTACA
                                CT CTGCCTCT  GT    GCC
                                || ||||||||  ||    |||
                                GA GACGGAGA  CA    CGG
                                 C       CC  C_____
GAM715  DNTT     5'  CTGCTGCCTCTGGCTGGCC    18600    _     AC T  ACA
                                CT CTGCCTCT  G CT   GCC
                                || ||||||||  | ||   |||
                                GA GACGGAGA  C GA   CGG
                                 C       C_ _  C__
GAM715  EMX2     3'  CCTCTGCCATCTTGGCGCGGCC 18601        _  A__   CTACA
                                CCTCTGCC TCT   CGT    GCC
                                ||||||| |||   |||    |||
                                GGAGACGG AGA   GCG    CGG
                                     T   ACC   C_____
GAM715  F2RL3    3'  CTCTGCCTCTGCCGCCACATGG 18602         A_  T    __
              C                  CTCTGCCTCT  CG CTACA  GC
                                ||||||||||  || |||||  ||
                                GAGACGGAGA  GC GGTGT  CG
                                     CG  _    AC
GAM715  FGFRL1   3'  CCCCTGCCTTCGTCTGCAGC   18603        CTA    A
                                CCTCTGCCT   CGTCT CAGC
                                |||||||||   ||||| ||||
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                                GGGGACGGA   GCAGA GTCG
                                     A__    C
GAM715  GOT2    3'  CCTCTGCCCTGTGTCAC    18604       T  AC   T
                                CCTCTGCC CT  GTC AC
                                |||||||| ||  ||| ||
                                GGAGACGG GA  CAG TG
                                    _ CA  _
GAM715  H1F0    5'  CCTCTGCCTCTGCCTCTGCC  18605         AC   ACA
                                CCTCTGCCTCT  GTCT   GCC
                                ||||||||||  ||||  |||
                                GGAGACGGAGA  CGGA   CGG
                                      __   GA_
GAM715  IL17E   5'  CCTCTCCCTCTCAGCACAGCCC 18606      G    A  TC
                                CCTCT CCTCT CG  TACAGCCC
                                ||||| ||||| ||  ||||||||
                                GGAGA GGAGA GT  GTGTCGGG
                                   G    _ C_
GAM715  JAM3    3'  CCTGCCTCTGCCAGGCGGCC  18607       AC   TACA_
                                TCTGCCTCT  GTC    GCC
                                |||||||||  |||    |||
                                GGACGGAGA  CGG    CGG
                                     __  TCCGC
GAM715  MAML1   3'  CTCTACCTTCCATATGTAGCC  18608       _  CG CTAC
                                CTCTGCCT CTA  T   AGCC
                                |||||||| |||  |   ||||
                                GAGATGGA GGT  A   TCGG
                                    A  AT CA__
GAM715  MAT1A   3'  CCCCTGCCTGAGCCTGTGGTCC 18609       CTAC   ACAG_
                                CCTCTGCCT   GTCT   CC
                                |||||||||   ||||   ||
                                GGGGACGGA   CGGA   GG
                                     CT__   CACCA
GAM715  MEOX1   3'  CCTTTTCTCTGGAGCACAGCCC 18610    CTGC   ACGTC
                                CCT   CTCT   TACAGCCC
                                |||   ||||   ||||||||
                                GGA   GAGA   GTGTCGGG
                                  AAA_   CCTC_
GAM715  MEOX1   3'  CCTTTTCTCTGGAGCACAGCCC 18610    CTGC   ACGTC
                                CCT   CTCT   TACAGCCC
                                |||   ||||   ||||||||
                                GGA   GAGA   GTGTCGGG
                                  AAA_   CCTC_
GAM715  MGAT2   5'  CCTCGCCTGGCAGCTACAGC  18611     T   CTA  T
                                CCTC GCCT   CG CTACAGC
                                |||| ||||  || |||||||
                                GGAG CGGA   GT GATGTCG
                                  _   CC_  C
GAM715  MMP8    3'  CTCTGCCTCTGTCTTCACACGG 18612        AC   __  __
            CC                  CTCTGCCTCT  GTCT  ACA  GCC
                                ||||||||||  ||||  |||  |||
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                                GAGACGGAGA  CAGA  TGT  CGG
                                     __   AG   GC
GAM715  MSX2     5'  CTCTGCCCTACGTAGC      18613        T     CTAC
                                CTCTGCC CTACGT    AGC
                                ||||||| ||||||    |||
                                GAGACGG GATGCA    TCG
                                    _     ____
GAM715  NDUFS2   5'  CTCTGCCTCTCCTGGGGCCC  18614          ACG   ACA
                                CTCTGCCTCT   TCT   GCCC
                                ||||||||||   |||   ||||
                                GAGACGGAGA   GGA   CGGG
                                     ___   CCC
GAM715  NEDD4L   3'  CCTCTGCCACTACCAGC     18615        T   GTCTA
                                CCTCTGCC CTAC     CAGC
                                |||||||| ||||     ||||
                                GGAGACGG GATG     GTCG
                                    T   _____
GAM715  NHLH1    3'  CTCTGCCTGTGCCCAGGGCC  18616        CTAC    CA
                                CTCTGCCT   GTCTA  GCC
                                ||||||||   |||||  |||
                                GAGACGGA   CGGGT  CGG
                                    CA__    CC
GAM715  Nrap     3'  CCTGCTGTCCGTCTACAGC   18617      CTCTA
                                TCTGC    CGTCTACAGC
                                |||||    ||||||||||
                                GGACG    GCAGATGTCG
                                   ACAG_
GAM715  Nrap     3'  CCTGCTGTCCGTCTACAGC   18617      CTCTA
                                TCTGC    CGTCTACAGC
                                |||||    ||||||||||
                                GGACG    GCAGATGTCG
                                   ACAG_
GAM715  OAS3     3'  CCTCTGCCTTCTGCTCCTCCAG 18618         _ ACG   A
            CC                    CCTCTGCCT CT   TCT CAGCC
                                |||||||| ||   ||| |||||
                                GGAGACGGA GA   GGA GTCGG
                                     A  CGA   G
GAM715  PABPN1   5'  CTGTGCCTCTAACATGTAGTCC 18619    C       _   C  CAG
                                CT TGCCTCTA CGT TA   CC
                                || |||||||| ||| ||   ||
                                GA ACGGAGAT GTA AT   GG
                                 C       T   C  CA_
GAM715  RAD23B   5'  CCGCTGCCTCCGCGACTGCGGC 18620    T      TA  T  ACA
            C                     CC CTGCCTC  CG CT   GCC
                                || |||||||  || ||   |||
                                GG GACGGAG  GC GA   CGG
                                 C      GC  T  CGC
GAM715  RANBP3   3'  CCTCTGCCTCTCACAGAAGCCC 18621           _   TCTAC
                                CCTCTGCCTCT ACG     AGCCC
                                |||||||||| |||     |||||
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                                GGAGACGGAGA TGT    TCGGG
                                      G  CT___
GAM715  SCA1    3'  CCTCTGCCCCAGTGTGGCC   18622        TAC  CTACA
                                CCTCTGCCTC  GT   GCC
                                ||||||||||  ||   |||
                                GGAGACGGGG  CA   CGG
                                     TCA  C____
GAM715  SLC22A1LS 5'  CCGCTGCCTCTTCATGCAG   18623   T      A   CTA
                                CC CTGCCTCT CGT   CAG
                                || |||||||| |||   |||
                                GG GACGGAGA GTA   GTC
                                 C      A  C__
GAM715  SPG7    3'  CTGCTGCCTCTGGGTGGCC   18599   _      AC  CTACA
                                CT CTGCCTCT  GT   GCC
                                || ||||||||  ||   |||
                                GA GACGGAGA  CA   CGG
                                 C      CC  C____
GAM715  SPR     3'  CTTTCCTCTACCCACAG    18624   CTG    GT
                                CT   CCTCTAC  CTACAG
                                ||   |||||||  ||||||
                                GA   GGAGATG  GGTGTC
                                 AA_     __
GAM715  TAL1    3'  CTCTGCCTTCACACAAAGCCC  18625       C   TC  C
                                CTCTGCCT TACG  TA AGCCC
                                |||||||| ||||  || |||||
                                GAGACGGA GTGT  GT TCGGG
                                     A   __ T
GAM715  TGFBR2   3'  TCTGCTTATCCCCACAGC    18626     CTC  CG
                                TCTGC   TA  TCTACAGC
                                |||||   ||  ||||||||
                                AGACG   AT  GGGTGTCG
                                   A__  AG
GAM715  TGM3    5'  CCTCTGCCTCTTCTCAG     18627         ACG   A
                                CCTCTGCCTCT   TCT CAG
                                ||||||||||   ||| |||
                                GGAGACGGAGA   AGA GTC
                                      ___  _
GAM715  TNFRSF10B 3'  TCTGCCTCTGTCCCAGCC    18628        AC   A
                                TCTGCCTCT  GTCT CAGCC
                                |||||||||  |||| |||||
                                AGACGGAGA  CAGG GTCGG
                                      __   _
GAM715  TNP2    3'  TCTGCCCCTGTGCAGGCCC   18629        AC  CTA  _
                                TCTGCCTCT  GT   CAG CCC
                                |||||||||  ||   ||| |||
                                AGACGGGGA  CA   GTC GGG
                                     __ C__   C
GAM715  VIL2    3'  CCTCTGCCCTTGGTCCTGGCC  18630       T  AC   ACA
                                CCTCTGCC CT  GTCT   GCC
                                ||||||| ||  ||||   |||
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                                GGAGACGG GA  CAGG   CGG
                                     _ AC    AC_
GAM715  ZFHX1B   3'  CCTTCTGTCCCTCTCTACAGC  18631     _  C    ACG
                                CCT CTG CTCT   TCTACAGC
                                ||| ||| ||||   ||||||||
                                GGA GAC GGGA   AGATGTCG
                                  A  A   G__
GAM715  APELIN   5'  CCTCCGCTCTTCTGCAGCC   18632       C   ACG   A
                                CCTCTGC TCT   TCT CAGCC
                                ||||||| |||   ||| |||||
                                GGAGGCG AGA   AGA GTCGG
                                     _  ____  C
GAM715  C17orf1A  3'  CTCTGCCTTTTTTCCAGCC    18633        CTACG  TA
                                CTCTGCCT    TC  CAGCC
                                ||||||||    ||  |||||
                                GAGACGGA    AG  GTCGG
                                     AAA__  __
GAM715  C20orf100 3'  CCTCTTTTCTGCTGTCAGCCC  18634      GCC   AC  CTA
                                CCTCT   TCT  GT   CAGCCC
                                |||||   |||  ||   ||||||
                                GGAGA   AGA  CG   GTCGGG
                                   AA_   __  ACA
GAM715  C6orf26   3'  CCTGCCTCTGTCAGC       18635         AC   TAC
                                TCTGCCTCT  GTC   AGC
                                |||||||||  |||   |||
                                GGACGGAGA  CAG   TCG
                                     __   ____
GAM715  CHK      3'  CTGCTGCCTCCCCATGCAGTCC 18636    _      TA   CTA   _
                                CT CTGCCTC  CGT   CAG CC
                                || |||||||  |||   ||| ||
                                GA GACGGAG  GTA   GTC GG
                                 C      GG   C__   A
GAM715  DKFZP434B103 3'  CCTCTGCCTGTGCCCTCCAGCC 18637          CTAC    A_
           C                     CCTCTGCCT    GTCT  CAGCCC
                                |||||||||    ||||  ||||||
                                GGAGACGGA    CGGG  GTCGGG
                                     CA__    AG
GAM715  DKFZP434G156 5'  TCTTCCTCTCACAGCC      18638     G    ACGTC
                                TCT CCTCT    TACAGCC
                                ||| |||||    |||||||
                                AGA GGAGA    GTGTCGG
                                  A    ______
GAM715  DKFZP586M1120 3'  CCTCTGCCATGCTGCAGCC    18639         TCTAC T  A
                                CCTCTGCC    G CT CAGCC
                                ||||||||    | || |||||
                                GGAGACGG    C GA GTCGG
                                     TA____ _  C
GAM715  DKFZp762K222 5'  CTCTGCCTCCGCTGCAGTCC   18640          TA  T  A  _
                                CTCTGCCTC  CG CT CAG CC
                                |||||||||  || || ||| ||
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                                GAGACGGAG  GC GA GTC GG
                                    __ _  C   A
GAM715  DPCR1    3' CTCTGCCCTTCCTGTAGTCC  18641        CTACG   AC  _
                                CTCTGCCT    TCT  AG CC
                                ||||||||    |||  || ||
                                GAGACGGG    GGA  TC GG
                                    AA___   CA  A
GAM715  FLJ11000 3' CTCTGCCTCTGTTTTCAG    18642         AC  CTA
                                CTCTGCCTCT  GT   CAG
                                ||||||||||  ||   |||
                                GAGACGGAGA  CA   GTC
                                    __ AAA
GAM715  FLJ11000 3' CCTCTGCCCTGTCTGGC     18643        T  AC    ACA
                                CCTCTGCC CT  GTCT   GC
                                ||||||||  ||  ||||   ||
                                GGAGACGG GA  CAGA   CG
                                    _ __    C__
GAM715  FLJ11850 3' CTCTCCCTTCTACAGCC     18644      G   CTACG
                                CTCT CCT    TCTACAGCC
                                ||||  |||    |||||||||
                                GAGA GGA    AGATGTCGG
                                  G  _____
GAM715  FLJ13072 5' CCTCTGTCACTGTGTACGGC  18645       CC  T  _  C   A
                                CCTCTG  TC AC GT TAC GC
                                ||||||  || || || ||| ||
                                GGAGAC  AG TG CA ATG CG
                                   __ _  A  C   C
GAM715  FLJ13769 3' CCTTGCCTCTGGTCTCAGCCC 18646    C      AC    A
                                CCT TGCCTCT  GTCT CAGCCC
                                |||  |||||||  ||||  ||||||
                                GGA ACGGAGA  CAGA GTCGGG
                                  _      C_   _
GAM715  FLJ14721 3' CCCTGCCTCTGCCAGC      18647          AC  CTA
                                CTCTGCCTCT  GT   CAGC
                                ||||||||||  ||   ||||
                                GGGACGGAGA  CG   GTCG
                                    __  ___
GAM715  FLJ20457 5' CCTCTACCTCTACGGTGCCAGG 18648            TCTA  _
           CC                    CCTCTGCCTCTACG    CAG CC
                                 ||||||||||||||    ||| ||
                                 GGAGATGGAGATGC    GTC GG
                                       CACG   C
GAM715  FLJ22353 3' CCATTTGTCAACCTCTACAGCC 18649    TCTGCC  T  G
                                CC     TC AC TCTACAGCC
                                ||     || || |||||||||
                                GG     AG TG AGATGTCGG
                                 TAAAC_  T  G
GAM715  FLJ31168 3' CCTCTCCCTCTATGAAGTCC   18650      G     C___
                                CCTCT CCTCTA    GTCT
                                |||||  ||||||    ||||
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                                GGAGA GGAGAT    CAGG
                                   G     ACTT
GAM715  FLNC     3'  CCTCTGCCCCTGAGCCTGGCCC 18651          AC    ACA
                                CCTCTGCCTCT  GTCT   GCCC
                                ||||||||||  ||||   ||||
                                GGAGACGGGGA  CGGA   CGGG
                                      CT    C__
GAM715  GENX-3414 3'  CCTTTGTTTCTACACCAGCC   18652     C  CC     TCTA
                                CCT TG  TCTACG    CAGCC
                                ||| ||  ||||||    |||||
                                GGA AC  AGATGT    GTCGG
                                  A  AA     G___
GAM715  GIT2     3'  CCTCTGCCCTATCAGC      18653        T   CGTCTA
                                CCTCTGCC CTA     CAGC
                                ||||||||  |||     ||||
                                GGAGACGG GAT     GTCG
                                     _   A_____
GAM715  GIT2     3'  CCTCTGCCCTATCAGC      18653        T   CGTCTA
                                CCTCTGCC CTA     CAGC
                                ||||||||  |||     ||||
                                GGAGACGG GAT     GTCG
                                     _   A_____
GAM715  GIT2     3'  CCTCTGCCCTATCAGC      18653        T   CGTCTA
                                CCTCTGCC CTA     CAGC
                                ||||||||  |||     ||||
                                GGAGACGG GAT     GTCG
                                     _   A_____
GAM715  HSPC155   3'  CCTCTGCCCTGCCTCAG     18654         T  AC    A
                                CCTCTGCC CT  GTCT CAG
                                ||||||||  ||  |||| |||
                                GGAGACGG GA  CGGA GTC
                                     _ __   _
GAM715  KIAA0125  3'  CCCTGCCTCCTCCTACAGCCC  18655          ACG
                                CTCTGCCTCT   TCTACAGCCC
                                ||||||||||   ||||||||||
                                GGGACGGAGG   GGATGTCGGG
                                     A__
GAM715  KIAA0446  5'  CTCTGCCTCTGTCTGGGCCC   18656          AC    ACA
                                CTCTGCCTCT  GTCT   GCCC
                                ||||||||||  ||||   ||||
                                GAGACGGAGA  CAGA   CGGG
                                     __    CC_
GAM715  KIAA0660  5'  CTCTGCCGCTACACCTCCGGC  18657        T    GT  ACA
                                CTCTGCC CTAC  CT   GC
                                |||||||  ||||  ||   ||
                                GAGACGG GATG  GA   CG
                                    C    TG  GGC
GAM715  KIAA0769  3'  TCTGCTTTAGCCACAGCC     18658       CTC  C T
                                TCTGC   TA G CTACAGCC
                                |||||   || | ||||||||
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                                AGACG   AT C GGTGTCGG
                                  AA_  _ _
GAM715  KIAA0800 3' TCTGCCTCCCTGTTATAGTCC  18659        AC  C  C  _
                                TCTGCCTCT  GT TA AG CC
                                |||||||||  || || || ||
                                AGACGGAGG  CA AT TC GG
                                     GA  _  A  A
GAM715  KIAA1140 5' CCTCCGCCTCTGCTGTAGCAGC 18660          ACGTCTA
                                CCTCTGCCTCT      CAGC
                                ||||||||||       ||||
                                GGAGGCGGAGA      GTCG
                                      CGACATC
GAM715  KIAA1140 3' CCTCTCCCTCTGGCCAGCC   18661      G    ACGTCTA
                                CCTCT CCTCT      CAGCC
                                ||||| |||||      |||||
                                GGAGA GGAGA      GTCGG
                                  G    CCG____
GAM715  KIAA1161 5' CCTCTGCCTGTTACCC      18662         CTAC  CTACA
                                CCTCTGCCT   GT    GCCC
                                |||||||||   ||    ||||
                                GGAGACGGA   CA    TGGG
                                     ____  A____
GAM715  KIAA1190 3' CCTGAGCGTACGTCTACAGC   18663     CT  CTC
                                CCT  GC   TACGTCTACAGC
                                |||  ||   ||||||||||||
                                GGA  CG   ATGCAGATGTCG
                                  CT  C__
GAM715  KIAA1193 3' CCTCTGCCCTCTGTGCCCTCAG 18664        _  AC   A
          C                      CCTCTGCC TCT  GTCT CAGC
                                 ||||||||  |||  ||||  ||||
                                 GGAGACGG AGA  CGGG GTCG
                                     G   CA   A
GAM715  KIAA1364 3' CCTCTGCCCCTCGGGTTTGCAG 18665          AC_  CTA
          CC                     CCTCTGCCTCT   GT   CAGCC
                                 ||||||||||   ||   |||||
                                 GGAGACGGGGA   CA   GTCGG
                                       GCC  AAC
GAM715  KIAA1464 3' CCTCTACCTCTGCTGTGTGGCC 18666          ACGTCTACA
          C                      CCTCTGCCTCT       GCCC
                                 ||||||||||        ||||
                                 GGAGATGGAGA       CGGG
                                       CGACACAC_
GAM715  KIAA1884 3' CCTGCCTCTGTCAGCC      18667         AC   TAC
                                TCTGCCTCT  GTC   AGCC
                                |||||||||  |||   ||||
                                GGACGGAGA  CAG   TCGG
                                     __   ___
GAM715  MAPK8IP3 3' CCTCTGCCTCTGCCCAGCC   18668          AC   TA
                                CCTCTGCCTCT  GTC  CAGCC
                                ||||||||||  |||  |||||
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                                GGAGACGGAGA  CGG  GTCGG
                                          __  __
GAM715  MAPKAPK3  3'  CTCTGCCCTACTCAGGCC    18669       T   G  TACA
                                CTCTGCC CTAC TC    GCC
                                ||||||| |||| ||    |||
                                GAGACGG GATG AG    CGG
                                   _   _ TC__
GAM715  MGC10814  5'  CCTCAGCCTCTTGAGTAGC    18670     T     AC_  CTAC
                                CCTC GCCTCT   GT    AGC
                                |||| ||||||   ||    |||
                                GGAG CGGAGA   CA    TCG
                                  T     ACT  ____
GAM715  MGC2488   5'  CCTCTCTTTCTGTTCTCAGCC  18671      GCC   ACG   A
                                CCTCT   TCT   TCT CAGCC
                                |||||   |||   ||| |||||
                                GGAGA   AGA   AGA GTCGG
                                   GAA   CA_   _
GAM715  MGC2780   5'  CCTCAGCTTCTGCCTCGGCC   18672     T  C   AC    ACA
                                CCTC GC TCT  GTCT   GCC
                                |||| || |||  ||||   |||
                                GGAG CG AGA  CGGA   CGG
                                  T  A   __    GC_
GAM715  MGC3035   5'  CCTCTGCCTCACTGGTGGCC   18673         T  GTCTACA
                                CCTCTGCCTC AC      GCC
                                |||||||||| ||      |||
                                GGAGACGGAG TG      CGG
                                     _  ACCAC__
GAM715  MRPS18B   3'  CCTCTCTTCCCAGTCTACAGC  18674      GCC    C
                                CCTCT   TCTA GTCTACAGC
                                |||||   |||| |||||||||
                                GGAGA   GGGT CAGATGTCG
                                   GAA   _
GAM715  MYH7B     3'  CCTCTGCCTCCTCCAGTGCAGC 18675         ACG   ___
          C                      CCTCTGCCTCT   TCTA   CAGCC
                                ||||||||||   ||||   |||||
                                GGAGACGGAGG   AGGT   GTCGG
                                     ___    CAC
GAM715  NPD009    3'  CCTCTGCCCTGGACAGCAGCC  18676        CT_   TCTA
                                CCTCTGCCT   ACG    CAGCC
                                |||||||||   |||    |||||
                                GGAGACGGG   TGT    GTCGG
                                     ACC   C___
GAM715  PCDH10    3'  TGCCTCTAAAGTTTCTACAG   18677        CG___
                                TGCCTCTA    TCTACAG
                                ||||||||    |||||||
                                ACGGAGAT    AGATGTC
                                   TTCAA
GAM715  PRO1163   3'  CCTCTGCCTCTCTGTCAGC   18678          AC   TAC
                                CCTCTGCCTCT  GTC   AGC
                                ||||||||||  |||   |||
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                                GGAGACGGAGA  CAG   TCG
                                      GA  ___
GAM715  PRO2949  5' CCTCTTCTCACCTTGCAGCCC 18679     GC   T  GTCTA
                                CCTCT  CTC AC    CAGCCC
                                |||||  ||| ||    ||||||
                                GGAGA  GAG TG    GTCGGG
                                  A_   _ GAAC_
GAM715  Rab11-FIP3 3' CCTCTGCCCCTTTGGCAGCCC 18680         ACGTCTA
                                CCTCTGCCTCT     CAGCCC
                                ||||||||||      ||||||
                                GGAGACGGGGA     GTCGGG
                                      AACC___
GAM715  RENT2    3' TCTGCCTCCTGGCCCCAGCC  18681        AC   A
                                TCTGCCTCT  GTCT CAGCC
                                |||||||||  |||| |||||
                                AGACGGAGG  CGGG GTCGG
                                      AC   _
GAM715  RENT2    3' TCTGCCTCCTGGCCCCAGCC  18681        AC   A
                                TCTGCCTCT  GTCT CAGCC
                                |||||||||  |||| |||||
                                AGACGGAGG  CGGG GTCGG
                                      AC   _
GAM715  RNF9     3' CCTCTGCCTTTGAGTTTGCACC 18682       CTAC  CTACA
          C                      CCTCTGCCT   GT    GCCC
                                |||||||||   ||    ||||
                                GGAGACGGA   CA    TGGG
                                      AACT  AACG_
GAM715  SEPT3    3' CTCTGCCTTCTCATGGCC    18683       _  A   CTACA
                                CTCTGCCT CT CGT    GCC
                                |||||||| || |||    |||
                                GAGACGGA GA GTA    CGG
                                     A  _   C____
GAM715  SH120    3' CTCCGCCTCTACACCAGCC   18684         TCTA
                                CTCTGCCTCTACG   CAGCC
                                ||||||||||||    |||||
                                GAGGCGGAGATGT   GTCGG
                                      G___
GAM715  SH120    3' CTCCGCCTCTACACCAGCC   18684         TCTA
                                CTCTGCCTCTACG   CAGCC
                                ||||||||||||    |||||
                                GAGGCGGAGATGT   GTCGG
                                      G___
GAM715  SLC1A7   3' CCTCGCCTGCCCCTGCAGC   18685     T   _ ACG   A
                                CCTC GCCT CT   TCT CAGC
                                ||||  |||| ||   ||| ||||
                                GGAG CGGA GG   GGA GTCG
                                  _   C  ___   C
GAM715  SLC6A14  5' CCTCGCCTCCTCTTGCAG    18686     T    ACG   A_
                                CCTC GCCTCT   TCT  CAG
                                ||||  ||||||   |||  |||
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                                GGAG CGGAGG   AGA  GTC
                                  _     ____   AC
GAM715  SV2      3'  CCTGCCTCTGCCCCAGC     18687         AC   A
                                TCTGCCTCT  GTCT CAGC
                                |||||||||  |||| ||||
                                GGACGGAGA  CGGG GTCG
                                      __   _
GAM715  TADA3L   5'  CCTCTACCTCCTCGCTGCGGCC 18688          A  T  ACA
                                CCTCTGCCTCT CG CT   GCC
                                |||||||||||| || ||   |||
                                GGAGATGGAGG GC GA   CGG
                                      A  _  CGC
GAM715  TADA3L   5'  CCTCTACCTCCTCGCTGCGGCC 18688          A  T  ACA
                                CCTCTGCCTCT CG CT   GCC
                                |||||||||||| || ||   |||
                                GGAGATGGAGG GC GA   CGG
                                      A  _  CGC
GAM715  TADA3L   5'  CCTCTACCTCCTCGCTGCGGCC 18688          A  T  ACA
                                CCTCTGCCTCT CG CT   GCC
                                |||||||||||| || ||   |||
                                GGAGATGGAGG GC GA   CGG
                                      A  _  CGC
GAM715  WASPIP   3'  CTCTGCCTATTACGACAAAAGC 18689        C_   TCTAC
          C                      CTCTGCCT  TACG    AGCC
                                |||||||  ||||    ||||
                                GAGACGGA  ATGC    TCGG
                                     TA   TGTTT
GAM715  ZNF313   3'  CTCTGCATCTACAAAGCAG   18690       C     TCTA
                                CTCTGC TCTACG   CAG
                                ||||||  ||||||   |||
                                GAGACG AGATGT   GTC
                                   T     TTC_
GAM715  LOC115219 3'  CCTATGTCTCTGCAAACAGTCC 18691     C  C   AC  CT   _
                                CCT TG CTCT  GT  ACAG CC
                                ||| || ||||  ||  |||| ||
                                GGA AC GAGA  CG  TGTC GG
                                  T  A   __  TT   A
GAM715  LOC125704 3'  CTCTGCCTCCTGCAGC      18692         TACGT  A
                                CTCTGCCTC    CT CAGC
                                |||||||||    || ||||
                                GAGACGGAG    GA GTCG
                                      _____  C
GAM715  LOC127294 3'  TCTGCCCCACCCCTGTAGCC   18693       T   G   AC
                                TCTGCC CTAC TCT  AGCC
                                ||||||  |||| |||  ||||
                                AGACGG GGTG GGA  TCGG
                                   _   G   CA
GAM715  LOC127534 3'  CCTCTGCCTTTGGGCACAGCCC 18694          CTACGTC
                                CCTCTGCCT      TACAGCCC
                                |||||||||      ||||||||
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                                GGAGACGGA      GTGTCGGG
                                     AACCC__
GAM715  LOC144079 5'  CCTCTCCTTTCTGCAGTCT   18695      G __  A _
                                CCTCT CC  TCT C GTCT
                                ||||| ||  ||| | ||||
                                GGAGA GG  AGA G CAGA
                                  _ AA   C T
GAM715  LOC144395 3'  CCTCTGCCCTCAGCAGCC    18696        CTACG  TA
                                CCTCTGCCT    TC  CAGCC
                                |||||||||    ||  |||||
                                GGAGACGGG    AG  GTCGG
                                     _____ TC
GAM715  LOC146050 3'  CTCTGCCTGCTGCACAGCCC   18697        _ ACGTC
                                CTCTGCCT CT    TACAGCCC
                                |||||||| ||    ||||||||
                                GAGACGGA GA    GTGTCGGG
                                     C  C____
GAM715  LOC146990 5'  CTCTGCCTATGCCCAGTCC    18698       CTAC    CAG
                                CTCTGCCT   GTCTA   CC
                                |||||||   |||||  ||
                                GAGACGGA   CGGGT   GG
                                     TA__    CA_
GAM715  LOC149529 3'  CCTCTGCCCTGCCAGC      18699       T  AC  CTA
                                CCTCTGCC CT  GT   CAGC
                                |||||||| ||  ||   ||||
                                GGAGACGG GA  CG   GTCG
                                     _  __  ___
GAM715  LOC150166 3'  CTCTGCCTCTCGTTAGC     18700         A   CTAC
                                CTCTGCCTCT CGT    AGC
                                |||||||||| |||    |||
                                GAGACGGAGA GCA    TCG
                                     _   A___
GAM715  LOC150197 3'  CTCTGCCTCTATGGCCAGC    18701          CGTCTA
                                CTCTGCCTCTA     CAGC
                                ||||||||||      ||||
                                GAGACGGAGAT     GTCG
                                     ACCG__
GAM715  LOC150622 5'  CCACTGCCTCTAAGGCATGCAG 18702    T       C_  CTA  _
           TCC                    CC CTGCCTCTA  GT   CAG CC
                                || |||||||||  ||   ||| ||
                                GG GACGGAGAT  CG   GTC GG
                                  T       TC  TAC   A
GAM715  LOC152220 3'  TCTGCCTCTGTCTTGGCAGC   18703        AC   A__
                                TCTGCCTCT  GTCT   CAGC
                                |||||||||  ||||   ||||
                                AGACGGAGA  CAGA   GTCG
                                     __    ACC
GAM715  LOC152274 5'  CCTCTGTTCTGCAAAGCCAGCC 18704       CC   A  TCTA
           C                     CCTCTG  TCT CG    CAGCCC
                                ||||||  ||| ||    ||||||
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                                GGAGAC  AGA GT    GTCGGG
                                   A_   C  TTCG
GAM715   LOC152627 5'  CCTCTGCCTCCACGTTCC    18705            _
                                CCTCTGCCTCTACGT CT
                                |||||||||||||| ||
                                GGAGACGGAGGTGCA GG
                                         A
GAM715   LOC154449 5'  CTCTGCCTCTGGTCATGCCC   18706         AC   TACA
                                CTCTGCCTCT  GTC    GCCC
                                ||||||||||  |||    ||||
                                GAGACGGAGA  CAG    CGGG
                                      C_   TA__
GAM715   LOC163682 5'  CTCTGCCTCTGTCCCTGGGTCC 18707          AC    ACAG__
                                CTCTGCCTCT  GTCT     CC
                                ||||||||||  ||||     ||
                                GAGACGGAGA  CAGG     GG
                                      __    GACCCA
GAM715   LOC196403 3'  CTCTGCCTCTTTTAGCAGCCC  18708         ACGTCTA
                                CTCTGCCTCT      CAGCCC
                                ||||||||||      ||||||
                                GAGACGGAGA      GTCGGG
                                      AAATC__
GAM715   LOC196410 3'  CCTCTGCCTCTTTGAGTCT    18709          AC__
                                CCTCTGCCTCT    GTCT
                                ||||||||||    ||||
                                GGAGACGGAGA    CAGA
                                       AACT
GAM715   LOC197085 5'  CCTCTCCCTCTCCAGCAGCC   18710      G    TACG   _
                                CCTCT CCTC    TCTA CAGCC
                                ||||| ||||    |||| |||||
                                GGAGA GGAG    AGGT GTCGG
                                   G    ____    C
GAM715   LOC197115 5'  CCTCTCCCTCTCCAGCAGCC   18710      G    TACG   _
                                CCTCT CCTC    TCTA CAGCC
                                ||||| ||||    |||| |||||
                                GGAGA GGAG    AGGT GTCGG
                                   G    ____    C
GAM715   LOC203052 3'  CCCTGCCTCTGCCGCAGTCC   18711         AC   TA   _
                                CTCTGCCTCT  GTC  CAG CC
                                ||||||||||  |||  ||| ||
                                GGGACGGAGA  CGG  GTC GG
                                      __   C_   A
GAM715   LOC221354 3'  CTCTGCCCTCGGGTAGCC    18712        T  A  TCTAC
                                CTCTGCC CT CG     AGCC
                                ||||||| || ||     ||||
                                GAGACGG GA GC     TCGG
                                   _ _  CCA__
GAM715   LOC221914 3'  CTCTACCCTCTCTGCAGCCC   18713        T  ACG   A
                                CTCTGCC CT   TCT CAGCCC
                                ||||||| ||   ||| ||||||
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                                GAGATGG GA   AGA GTCGGG
                                   _ G__   C
GAM715  LOC253142 3'  CTGCTGCCTCTCGCCACAGC   18714    _      A  T
                                CT CTGCCTCT CG CTACAGC
                                || |||||||| || |||||||
                                GA GACGGAGA GC GGTGTCG
                                 C      _ _
GAM715  LOC253228 3'  CTCTGCCTCAGTGTTACA    18715         TAC  C
                                CTCTGCCTC   GT TACA
                                |||||||||   || ||||
                                GAGACGGAG   CA ATGT
                                      TCA  _
GAM715  LOC253731 5'  CCTCTCCTCTGCACTGTGGC   18716      G    A  T  ACA
                                CCTCT CCTCT CG CT   GC
                                ||||| ||||| || ||   ||
                                GGAGA GGAGA GT GA   CG
                                   _    C  _  CAC
GAM715  LOC253782 3'  TCTGCTGTTGTCTTCACAGCCC 18717      CTCTAC   __
                                TCTGC     GTCT  ACAGCCC
                                |||||     ||||  |||||||
                                AGACG     CAGA  TGTCGGG
                                   ACAA__    AG
GAM715  LOC254517 5'  CCTCTCCCTCTCCAGCAGCC   18710      G   TACG   _
                                CCTCT CCTC    TCTA CAGCC
                                ||||| ||||    |||| |||||
                                GGAGA GGAG    AGGT GTCGG
                                   G    _____    C
GAM715  LOC254964 5'  CCTCTCCCTCTCCAGCAGCC   18710      G   TACG   _
                                CCTCT CCTC    TCTA CAGCC
                                ||||| ||||    |||| |||||
                                GGAGA GGAG    AGGT GTCGG
                                   G    _____    C
GAM715  LOC257127 3'  CCTCTGCCCTCTGCAGACTCTC 18718       _  _____  G_   A
            TGCAGCC                 TCTGCC TCT    AC  TCT CAGCC
                                |||||| |||    ||  ||| |||||
                                AGACGG AGA    TG  AGA GTCGG
                                   G   CGTC  AG   C
GAM715  LOC257142 5'  CCTCTGGTCTCTAAACCACAGC 18719       C_    CGT
            C                    CCTCTG  CTCTA   CTACAGCC
                                ||||||  |||||   ||||||||
                                GGAGAC  GAGAT   GGTGTCGG
                                   CA    TT_
GAM715  LOC51014  5'  CTCTGCCTCCGTTGCAGCC    18720        TA   CTA
                                CTCTGCCTC  CGT   CAGCC
                                |||||||||  |||   |||||
                                GAGACGGAG  GCA   GTCGG
                                      __   AC_
GAM715  LOC51207  3'  CCCTGCCTCTGCCTCAGCCC   18721         AC   A
                                CTCTGCCTCT  GTCT CAGCCC
                                ||||||||||  |||| ||||||
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                                GGGACGGAGA  CGGA GTCGGG
                                   __    _
GAM715  LOC51337  3'  TCTGCCTCTAGCCCCGGCC    18722          C    ACA
                                TCTGCCTCTA GTCT   GCC
                                |||||||||| ||||   |||
                                AGACGGAGAT CGGG   CGG
                                     _   GC_
GAM715  LOC55908  3'  CCTCTGCCGCTGCACGTGGCC  18723         T __    CTACA
                                CCTCTGCC CT  ACGT    GCC
                                |||||||| ||  ||||    |||
                                GGAGACGG GA  TGCA    CGG
                                     C  CG   C____
GAM715  LOC91266  5'  CCTCTGCTCACCTTGCAGC    18724        C  T  GTCTA
                                CCTCTGC TC AC    CAGC
                                ||||||| || ||    ||||
                                GGAGACG AG TG    GTCG
                                   _ _  GAAC_
GAM715  LOC91319  3'  CTCTGCCTTTCAGGAACAGCCC 18725         CTACGTCT
                                CTCTGCCT       ACAGCCC
                                ||||||||       |||||||
                                GAGACGGA       TGTCGGG
                                     AAGTCCT_
GAM715  LOC91408  5'  CCTCTCCCTCTCCGGGGCAGCC 18726       G    A  TCTA
                                CCTCT CCTCT CG    CAGCC
                                ||||| ||||| ||    |||||
                                GGAGA GGAGA GC    GTCGG
                                   G    G  CCC_
GAM715  LOC91421  3'  CTCTGCCTCCTGCGGCC     18727          A_  TCTACA
                                CTCTGCCTCT  CG     GCC
                                ||||||||||  ||     |||
                                GAGACGGAGG  GC     CGG
                                     AC  _______
GAM715  LOC92148  5'  TCTGCCTCTCACCCACAG    18728          A GT
                                TCTGCCTCT C  CTACAG
                                |||||||||  |  ||||||
                                AGACGGAGA G  GGTGTC
                                     _ TG
GAM716  ADD2      3'  GAACAAAGATTACTTTCTG   18731          CT
                                GAACAGAGGT  CTTTCTG
                                ||||||||||  |||||||
                                CTTGTTTCTA  GAAAGAC
                                     AT
GAM716  ADD2      3'  GAACAAAGATTACTTTCTG   18731          CT
                                GAACAGAGGT  CTTTCTG
                                ||||||||||  |||||||
                                CTTGTTTCTA  GAAAGAC
                                     AT
GAM716  ADD2      3'  GAACAAAGATTACTTTCTG   18731          CT
                                GAACAGAGGT  CTTTCTG
                                ||||||||||  |||||||
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                                CTTGTTTCTA  GAAAGAC
                                      AT
GAM716  ADD2     3'  GAACAAAGATTACTTTCTG   18731         CT
                                GAACAGAGGT  CTTTCTG
                                ||||||||||  |||||||
                                CTTGTTTCTA  GAAAGAC
                                      AT
GAM716  ASB2     3'  GAATAGAGGTTTCTGCC     18732     C     CTCT
                                GAA AGAGGT    TTCTGCC
                                |||  ||||||    |||||||
                                CTT TCTCCA    AAGACGG
                                  A     ____
GAM716  B4GALT1  3'  GAACAGAGGCTCCCTCTGCC  18733         T
                                GAACAGAGG CTCTTTCTGCC
                                |||||||||  ||||||||||
                                CTTGTCTCC GAGGGAGACGG

                                      _
GAM716  C18orf1  3'  GAACAAAGTCTTCTGC      18734         G   CTT
                                GAACAGAG TCT   TCTGC
                                ||||||||  |||   |||||
                                CTTGTTTC AGA   AGACG

                                      _  ___
GAM716  CDY1     3'  GAAAGAAGTTTCTGC       18735     C     CTCT
                                GAA AGAGGT    TTCTGC
                                |||  ||||||    ||||||
                                CTT TCTTCA    AAGACG

                                      _     _____
GAM716  CDY1     3'  GAAAGAAGTTTCTGC       18735     C     CTCT
                                GAA AGAGGT    TTCTGC
                                |||  ||||||    ||||||
                                CTT TCTTCA    AAGACG

                                      _     _____
GAM716  DPYSL3   3'  GAACAGAAGGTAGCTTGC    18736        _   CT  TTC
                                GAACAGA GGT  CT   TGC
                                |||||||  |||  ||   |||
                                CTTGTCT CCA  GA   ACG
                                     T   TC  ___
GAM716  DRIL1    3'  AAACGTCTGCCTCTTTCTG   18737      AGAG
                                GAAC    GTCTCTTTCTG
                                ||||    ||||||||||||
                                TTTG    CGGAGAAAGAC
                                  CAGA
GAM716  EGLN1     5'  CAAAGATGTTTCTTTCTGC   18738        C__
                                CAGAGGT   TCTTTCTGC
                                |||||||   |||||||||
                                GTTTCTA   AGAAAGACG
                                     CAA
GAM716  EPHB6     5'  AACAGCCACCCCTTTTTCTGCC 18739       AG      __
                                AACAG  GTCTCTT  TCTGCC
                                |||||  |||||||  ||||||
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                                TTGTC  TGGGGAA  AGACGG
                                  GG      AA
GAM716  EPHX2    3'  GAACGGCTGATTTTTCTGCC  18740     AGA  CTC__
                                GAAC  GGT    TTTCTGCC
                                ||||  |||    ||||||||
                                CTTG  CCG    AAAGACGG
                                  ___  ACTAA
GAM716  FACL4    3'  AAACAGAATTTCTGC      18741        GTCTC
                                GAACAGAG    TTTCTGC
                                ||||||||    |||||||
                                TTTGTCTT    AAAGACG
                                  _____
GAM716  FACL4    3'  AAACAGAATTTCTGC      18741        GTCTC
                                GAACAGAG    TTTCTGC
                                ||||||||    |||||||
                                TTTGTCTT    AAAGACG
                                  _____
GAM716  FADD     3'  ACAAAACATCCTTTCTGCC   18742      _  T
                                ACAGAG GTC CTTTCTGCC
                                |||||| ||| |||||||||
                                TGTTTT TAG GAAAGACGG
                                   G  _
GAM716  FMOD     3'  GAAAAGAGTGAGCTTCTGCC  18743    C   GTCTC
                                GAA AGAG    TTTCTGCC
                                ||| ||||    ||||||||
                                CTT TCTC    GAAGACGG
                                  T   ACTC_
GAM716  FZD7     3'  AAACACCCGTCTTTCTGCC   18744     GAGG  _
                                GAACA   TC TCTTTCTGCC
                                |||||   || ||||||||||
                                TTTGT   GG AGAAAGACGG
                                   G___  C
GAM716  HDAC8    3'  AAACCTGATCTCTTTCTG    18745     AGA
                                GAAC  GGTCTCTTTCTG
                                ||||  ||||||||||||
                                TTTG  CTAGAGAAAGAC
                                  GA_
GAM716  HMGCL    3'  CAGGAGGTCCTTCTGCC     18746    _    CT
                                CAG AGGTCT  TTCTGCC
                                ||| ||||||  |||||||
                                GTC TCCAGG  AAGACGG
                                  C    __
GAM716  HR       3'  GAACAGAGTGCCCTGC      18747       _  TCTTT
                                GAACAGAG GTC    CTGC
                                |||||||| |||    ||||
                                CTTGTCTC CGG    GACG
                                    A  _____
GAM716  HUS1     3'  GACAGAGGCTGTTCTTTCTG  18748   A     C__
                                GA CAGAGGT   TCTTTCTG
                                || |||||||  ||||||||
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                                CT GTCTCCG   AGAAAGAC
                                 _      ACA
GAM716  IKBKB    3'  CAGCAGATACCCTTTCTG    18749     _   _
                                CAG AGGT CTCTTTCTG
                                ||| |||| |||||||||
                                GTC TCTA GGGAAAGAC
                                  G   T
GAM716  KAI1     3'  GACGGAGTCTCTTTCTG     18750    ACA   G
                                GA   GAG TCTCTTTCTG
                                ||   ||| ||||||||||
                                CT   CTC AGAGAAAGAC
                                 GC_   _
GAM716  KCNMB1   5'  CAGACAGTTTCTTTCTGCC   18751      _   C
                                CAGA GGT TCTTTCTGCC
                                |||| ||| ||||||||||
                                GTCT TCA AGAAAGACGG
                                  G   A
GAM716  MASP1    3'  GAACACAGGTCTCCTGCC    18752      G      TTT
                                GAACA AGGTCTC   CTGCC
                                ||||| |||||||   |||||
                                CTTGT TCCAGAG   GACGG
                                   G     ___
GAM716  NPTX2    5'  CAGAAGTCTCCTGCC       18753          TTT
                                CAGAGGTCTC   CTGCC
                                ||||||||||   |||||
                                GTCTTCAGAG   GACGG
                                             ___
GAM716  PCLO     3'  GAACAGGGCCTTTCTGC     18754       A    CT
                                GAACAG GGTCT  TTCTGC
                                |||||| |||||  ||||||
                                CTTGTC CCGGA  AAGACG
                                   _    __
GAM716  PIAS1    3'  AAGTTCTCTTCTTTCTGCC   18755     G    ___
                                GAG TCTCTT   TCTGCC
                                ||| ||||||   ||||||
                                TTC AGAGAA   AGACGG
                                  A     GAA
GAM716  PLAG1    3'  AACAGAGTCTCTTTTTGC    18756       G      C
                                AACAGAG TCTCTTT TGC
                                ||||||| ||||||| |||
                                TTGTCTC AGAGAAA ACG
                                   _      A
GAM716  RAP1GA1  3'  CAGAGGTCTCGTCTGCC     18757          TT
                                CAGAGGTCTC  TCTGCC
                                ||||||||||  ||||||
                                GTCTCCAGAG  AGACGG
                                      C_
GAM716  SIGLEC6  3'  ACAGAAGTCCTGTGGTCTGCC 18758          CTT__
                                ACAGAGGTCT    TCTGCC
                                ||||||||||    ||||||
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                                TGTCTTCAGG    AGACGG
                                     ACACC
GAM716  SLC6A6   3' GGACAGAACTTTCTGCC    18759   A    GTCT
                                G ACAGAG   CTTTCTGCC
                                | ||||||   |||||||||
                                C TGTCTT   GAAAGACGG
                                 C    ____
GAM716  TLR4     3' GAACAATGTCTCTTTCTG    18760      AG
                                GAACAG  GTCTCTTTCTG
                                ||||||  ||||||||||
                                CTTGTT  CAGAGAAAGAC
                                   A_
GAM716  TLR4     3' GAACAATGTCTCTTTCTG    18760      AG
                                GAACAG  GTCTCTTTCTG
                                ||||||  ||||||||||
                                CTTGTT  CAGAGAAAGAC
                                   A_
GAM716  TLR4     3' GAACAATGTCTCTTTCTG    18760      AG
                                GAACAG  GTCTCTTTCTG
                                ||||||  ||||||||||
                                CTTGTT  CAGAGAAAGAC
                                   A_
GAM716  TNFRSF13C 3' CAGGGGCCACCTCCTGCC    18761    A   T
                                CAG GGTC CTTTCTGCC
                                ||| |||| |||||||||
                                GTC CCGG GGAGGACGG
                                  C   T
GAM716  VIPR1    3' CAGAACCTTTCTGCC      18762      GTC
                                CAGAG   TCTTTCTGCC
                                |||||   ||||||||||
                                GTCTT   GGAAAGACGG
                                   ___
GAM716  WBSCR14  3' GAACAGAGGTCTGTGC     18763          CTTTC
                                GAACAGAGGTCT    TGC
                                ||||||||||||    |||
                                CTTGTCTCCAGA    ACG
                                      C____
GAM716  WBSCR14  3' GAACAGAGGTCTGTGC     18763          CTTTC
                                GAACAGAGGTCT    TGC
                                ||||||||||||    |||
                                CTTGTCTCCAGA    ACG
                                      C____
GAM716  WEE1     5' CAGGGGTCCACCTCTGCC    18764    A   C
                                CAG GGTCT TTTCTGCC
                                ||| ||||| ||||||||
                                GTC CCAGG GGAGACGG
                                  C    T
GAM716  XT3      3' CAGAGGTCCCTGCAGCTTTCTG 18765          _______
             C                   CAGAGGTCTCT     TTCTGC
                                ||||||||||     ||||||
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                                GTCTCCAGGGA     AAGACG
                                      CGTCGA
GAM716  AKAP6    3'  AACAGAGGTCTAGAATGCC   18766          CTTTC
                                AACAGAGGTCT     TGCC
                                ||||||||||     ||||
                                TTGTCTCCAGA     ACGG
                                      TCTT_
GAM716  ANKRD7   3'  GACACAAATTTTTTTCTGCC  18767    A  G    CTC
                                GA CA AGGT   TTTCTGCC
                                || || ||||   ||||||||
                                CT GT TTTA   AAAGACGG
                                 _  G    AAA
GAM716  ARHF     3'  AGAAGCCATTTTTTCTGCC   18768        TC__
                                AGAGGTC    TTTCTGCC
                                |||||||    ||||||||
                                TCTTCGG    AAAGACGG
                                     TAAA
GAM716  ATP1B4   3'  GAACAGCAATTCTTTCTGCC  18769       AG  C
                                GAACAG  GT TCTTTCTGCC
                                ||||||  || ||||||||||
                                CTTGTC  TA AGAAAGACGG
                                   GT  _
GAM716  C11orf11 3'  ACAGAGGTCTCCAGCC      18770           TTCT
                                ACAGAGGTCTCT    GCC
                                ||||||||||||    |||
                                TGTCTCCAGAGG    CGG
                                      T___
GAM716  C1orf34  3'  CAGGGGTCCCCCATCTGC    18771     A       _
                                CAG GGTCTCTT TCTGC
                                ||| |||||||| |||||
                                GTC CCAGGGGG AGACG
                                  C       T
GAM716  C20orf60 3'  ACAGGGTTTTTCTGCC      18772      A   CTC
                                ACAG GGT   TTTCTGCC
                                |||| |||   ||||||||
                                TGTC CCA   AAAGACGG
                                  _   A__
GAM716  C21orf42 3'  GAATGGAGTTCTTCTGCC    18773     CA   G   CTT
                                GAA  GAG TCT   TCTGCC
                                |||  ||| |||   ||||||
                                CTT  CTC AGA   AGACGG
                                  AC   A   ___
GAM716  CNOT8    3'  AAACAAAAGTCTTTCTGC     18774           CT
                                GAACAGAGGTCT  TTCTGC
                                ||||||||||||  ||||||
                                TTTGTTTTCAGA  AAGACG
                                        __
GAM716  COPS7B   3'  GGAAGGAACCATTTCTGCC   18775   A   T_  C
                                C GAGG  CT TTTCTGCC
                                | ||||  ||  ||||||||
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                                C TTCC  GG AAAGACGG
                                 C    TT  T
GAM716  CSAD     3'  GAACAGAGTCTCGTACTG    18776        G    TTT
                                GAACAGAG TCTC   CTG
                                |||||||| ||||   |||
                                CTTGTCTC AGAG   GAC
                                     _   CAT
GAM716  CSRP2BP  5'  AACATCTTCTCTCTTTCTGC   18777     GAGG_
                                AACA    TCTCTTTCTGC
                                ||||    ||||||||||
                                TTGT    AGAGAAAGACG
                                  AGAAG
GAM716  CUL4A    5'  GAACAGAGATTTTCC       18778          CTC
                                GAACAGAGGT   TTTCT
                                ||||||||||   |||||
                                CTTGTCTCTA   AAAGG

                                     ___
GAM716  CYP2A13  3'  GAACTGAGCCCCTTCTG     18779     A   GT
                                GAAC GAG  CTCTTTCTG
                                |||| |||  |||||||||
                                CTTG CTC  GGGGAAGAC
                                  A   __
GAM716  D4ST-1   3'  GAGCAGCAGGTCTCCTGCC   18780    A  _     TTT
                                GA CAG AGGTCTC   CTGCC
                                || ||| |||||||   |||||
                                CT GTC TCCAGAG   GACGG
                                 C   G      ___
GAM716  DKFZP434C131 3'  CAGAGGTCCCCTGCC       18781          TTT
                                CAGAGGTCTC   CTGCC
                                ||||||||||   |||||
                                GTCTCCAGGG   GACGG

                                     ___
GAM716  DKFZP566G1424 5'  AACAGAGGGCTTCTGCC     18782        T  CTT
                                AACAGAGG CT   TCTGCC
                                |||||||| ||   ||||||
                                TTGTCTCC GA   AGACGG
                                     C  ___
GAM716  DKFZP566J091 3'  CAGAGGTCCCTTGCC       18783          TTC
                                CAGAGGTCTCT   TGCC
                                ||||||||||   ||||
                                GTCTCCAGGGA   ACGG

                                     ___
GAM716  DMRTC2   3'  GAACAAGTCCTTTCTG      18784      GA   T
                                GAACA  GGTC CTTTCTG
                                |||||  |||| |||||||
                                CTTGT  TCAG GAAAGAC

                                   __   _
GAM716  E2IG4    3'  GAACAAATGCAACCTTTTTCTG 18785        ___ GT  C
            C                    GAACAGA   G  CT TTTCTGC
                                |||||||   |  || |||||||
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                              CTTGTTT  T  GA AAAGACG
                                  ACG TG  A
GAM716  EPB41L1  3' GAGCATCTGGTTCTTTCTGC  18786   A  GA_  C
                              GA CA  GGT TCTTTCTGC
                              || ||  ||| |||||||||
                              CT GT  CCA AGAAAGACG
                               C  AGA  _
GAM716  FLJ12985 3' GAACAAAGGTCTTGC      18787          CTTTC
                              GAACAGAGGTCT    TGC
                              ||||||||||||    |||
                              CTTGTTTCCAGA    ACG
                                        _____
GAM716  FLJ14708 3' GAAAAACTCTTTTTCTGCC  18788    CA  G  C
                              GAA  GAG TCT TTTCTGCC
                              |||  ||| ||| ||||||||
                              CTT  TTT AGA AAAGACGG
                                __  G  A
GAM716  FLJ21016 3' AAACAGAGGTCGTCTGC    18789         TCTT
                              GAACAGAGGTC   TCTGC
                              ||||||||||   |||||
                              TTTGTCTCCAG   AGACG
                                    C___
GAM716  FLJ22671 3' GGACAGTACCCTTTCTGC   18790   A   AGGT
                              G ACAG   CTCTTTCTGC
                              | ||||   ||||||||||
                              C TGTC   GGGAAAGACG
                               C   AT__
GAM716  HAT     5' GAAGAGGTTCTTTTTTCTGCC 18791   C    _ C_
                              A AGAGGT CT  TTTCTGCC
                              | |||||| ||  ||||||||
                              C TCTCCA GA  AAAGACGG
                               T    A  AA
GAM716  KIAA0298 3' GAACAGAGGGTACTTTGCC  18792       TCT  TC
                              GAACAGAGG  CTT  TGCC
                              |||||||||  |||  ||||
                              CTTGTCTCC  GAA  ACGG
                                   CAT  __
GAM716  KIAA0884 5' GAACAAAGGTTTTTCCTCTTG 18793       C__   TC
                              GAACAGAGGT  TCTT  TG
                              ||||||||||  ||||  ||
                              CTTGTTTCCA  AGGA  AC
                                    AAA   GA
GAM716  KIAA1384 5' GAGCAGAGCTTTCTGC     18794   A   GTCT
                              GA CAGAG   CTTTCTGC
                              || |||||   ||||||||
                              CT GTCTC   GAAAGACG
                               C   ____
GAM716  KIAA1473 3' AAACAAATAATTTTTCTGCC  18795      GGTCTC
                              GAACAGA    TTTCTGCC
                              |||||||    ||||||||
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                                TTTGTTT     AAAGACGG
                                    ATTAA_
GAM716  KIAA1494  3'  GAACAGAGGTACTTCAATC   18796         _ _ TT
                                GAACAGAGGT CT C  TC
                                |||||||||| || |  ||
                                CTTGTCTCCA GA G  AG
                                     T  A TT
GAM716  KIAA1671  3'  AGGGCCTAGCTTTCTGCC    18797    A    __
                                AG GGTCT  CTTTCTGCC
                                || |||||  |||||||||
                                TC CCGGA  GAAAGACGG
                                 _    TC
GAM716  KIAA1755  3'  GAATGAAGGTCCCATGCC    18798    CA      TTTC
                                GAA  GAGGTCTC   TGCC
                                |||  ||||||||   ||||
                                CTT  TTCCAGGG   ACGG
                                  AC       T___
GAM716  KIAA1950  5'  CAGTGGCCACCTCTGCC     18799    A   T   T
                                CAG GGTC CTT CTGCC
                                ||| |||| ||| |||||
                                GTC CCGG GGA GACGG
                                  A   T   _
GAM716  LEAP-2    5'  AACAAATTCTTTCTGCC     18800      GGTC
                                AACAGA   TCTTTCTGCC
                                ||||||   ||||||||||
                                TTGTTT   AGAAAGACGG
                                   A___
GAM716  LRPPRC    3'  GAACAGAGGTGCTTGAAGCC  18801        CT   TCT
                                GAACAGAGGT  CTT   GCC
                                ||||||||||  |||   |||
                                CTTGTCTCCA  GAA   CGG
                                     C_   CTT
GAM716  MGC15634  5'  AAACAGGGGTCCCCTGC     18802      A     TTT
                                GAACAG GGTCTC   CTGC
                                |||||| ||||||   ||||
                                TTTGTC CCAGGG   GACG
                                   C     ___
GAM716  MGC16703  5'  GGACAGAGGTCTCCTGCC    18803   A       TTT
                                G ACAGAGGTCTC   CTGCC
                                | ||||||||||   |||||
                                C TGTCTCCAGAG   GACGG
                                 C         ___
GAM716  MGC17299  3'  AGAGCCCATATTCTTTCTGCC  18804     G  ____
                                AGAG TC   TCTTTCTGCC
                                ||||  ||   ||||||||||
                                TCTC GG   AGAAAGACGG
                                  G  TATA
GAM716  MGC7036   5'  CAGAGTCCCTACCTGCC     18805      G    T
                                CAGAG TCTCT TCTGCC
                                ||||| ||||| ||||||
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                                GTCTC AGGGA GGACGG
                                  _    T
GAM716  MLL3    3'  AAACAAAAATCTCTTTCTG   18806
                                GAACAGAGGTCTCTTTCTG
                                ||||||||||||||||||
                                TTTGTTTTTAGAGAAAGAC

GAM716  NAP1L1  3'  GAACAGAGGTACTTAACACC  18807        CT  TC
                                GAACAGAGGT  CTT  TGCC
                                ||||||||||  |||  ||||
                                CTTGTCTCCA  GAA  GTGG
                                      T_  TT
GAM716  NKX2B   3'  CAGAGGGCTCCCTGCC     18808      T   TT
                                CAGAGG CTCT  CTGCC
                                ||||||  ||||  |||||
                                GTCTCC GAGG  GACGG
                                   C   __
GAM716  PKNOX2  3'  GAACAGGTGTCTCCTTTGCC  18809     AG     C
                                GAACAG  GTCTCTTT TGCC
                                ||||||  ||||||||  ||||
                                CTTGTC  CAGAGGAA ACGG
                                   CA      _
GAM716  PRO2325 5'  GAACATAGAAGAATTTCTGCC  18810     G   TCTC
                                GAACA AGG    TTTCTGCC
                                |||||  |||    ||||||||
                                CTTGT TCT    AAAGACGG
                                  A   TCTT
GAM716  SCAMP5  3'  GAAGGGGCCAGTCTTTCTGC  18811   C  A   __
                                A AG GGTC  TCTTTCTGC
                                | || ||||  |||||||||
                                C TC CCGG  AGAAAGACG
                                 T  C    TC
GAM716  SEMA5B  3'  ACAGAGGCCAGACTTCTGCC  18812       TC_
                                ACAGAGGTC   TTTCTGCC
                                |||||||||   ||||||||
                                TGTCTCCGG   GAAGACGG
                                     TCT
GAM716  SYT13   3'  CAGTGTCTTTTTCTGCC    18813    AG   C
                                CAG  GTCT TTTCTGCC
                                |||  |||| ||||||||
                                GTC  CAGA AAAGACGG
                                  A_   A
GAM716  TBX19   3'  GAACAGAGATGCCTGC     18814        CTCTT
                                GAACAGAGGT    TCTGC
                                ||||||||||    |||||
                                CTTGTCTCTA    GGACG
                                     C_____
GAM716  TRAF3   5'  GAGCAGCGGTCTCTGGAATGC  18815   A  A     TTC_
                                GA CAG GGTCTCT    TGC
                                || ||| |||||||    |||
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                                CT GTC CCAGAGA   ACG
                                 C  G     CCTT
GAM716  UBCE7IP5  3'  CAGCAGGGGTCTTCCTGCC   18816    _  TC
                                CAG AGG  TCTTTCTGCC
                                ||| |||  ||||||||||
                                GTC TCC  AGAAGGACGG
                                  G  CC
GAM716  WSB1      3'  GAGATGCCACTCTTTCTGCC   18817     ____
                                GAGGT   CTCTTTCTGCC
                                |||||   ||||||||||
                                CTCTA   GAGAAAGACGG
                                   CGGT
GAM716  LOC127428 3'  GAACAGAGACTCTGC      18818        TCTCT
                                GAACAGAGG    TTCTGC
                                |||||||||    ||||||
                                CTTGTCTCT    GAGACG

                                      _____
GAM716  LOC146957 3'  GAACAGGGGTCTCTCCATG   18819      A      TC
                                GAACAG GGTCTCTT  TG
                                |||||| ||||||||  ||
                                CTTGTC CCAGAGAG  AC
                                   C       GT
GAM716  LOC147837 3'  GACAGAGGTTGTTTTGC     18820    A     CTC   C
                                GA CAGAGGT   TTT TGC
                                || |||||||   ||| |||
                                CT GTCTCCA   AAA ACG
                                 _      AC_  _
GAM716  LOC148397 5'  CAGAGCCACCTTCTGCC     18821      G  T
                                CAGAG TC CTTTCTGCC
                                ||||| || |||||||||
                                GTCTC GG GGAAGACGG
                                   _ T
GAM716  LOC150005 3'  GAGCAGGGCTACCCCTGCC   18822    A   A  T  C TT
                                GA CAG GG CT T  CTGCC
                                || ||| || || |  |||||
                                CT GTC CC GA G  GACGG
                                 C  _ _  T GG
GAM716  LOC150142 5'  GAACAGAGGCTCTGACT     18823        T   TT
                                GAACAGAGG CTCT  CT
                                ||||||||| ||||  ||
                                CTTGTCTCC GAGA  GA
                                      _   CT
GAM716  LOC150271 5'  GGAAGGGACCCTTCTGCC    18824   A   TC
                                C GAGG  TCTTTCTGCC
                                | ||||  ||||||||||
                                C TTCC  GGGAAGACGG
                                 C   CT
GAM716  LOC152829 5'  GACAGAGGCAGTCTGCC     18825    A     CTCTT
                                GA CAGAGGT    TCTGCC
                                || |||||||    ||||||
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                                CT GTCTCCG    AGACGG
                                 _      TC___
GAM716  LOC155032 3'  GAACAGAGATAACCTGCC    18826         CTCTT
                                GAACAGAGGT    TCTGCC
                                ||||||||||    ||||||
                                CTTGTCTCTA    GGACGG
                                      TT___
GAM716  LOC158714 5'  GATCAGCATGTTTCTTTCTGC  18827    A   AG_  C
                                GA CAG   GT TCTTTCTGC
                                || |||   || |||||||||
                                CT GTC   CA AGAAAGACG
                                 A   GTA  A
GAM716  LOC162333 5'  GAAATAGATATCTTTCTGCC   18828    CAG    C
                                GAA   AGGT TCTTTCTGCC
                                |||   |||| ||||||||||
                                CTT   TCTA AGAAAGACGG
                                  TA_    T
GAM716  LOC196283 3'  ACAGAGATTCTTTGC       18829        C    TC
                                ACAGAGGT TCTT  TGC
                                |||||||| ||||  |||
                                TGTCTCTA AGAA  ACG
                                     _    __
GAM716  LOC197125 3'  GACGGAGAGGCCTCTGCC    18830    AC_        TTCT
                                GA   AGAGGTCTCT    GCC
                                ||   ||||||||||    |||
                                CT   TCTCCGGAGA    CGG
                                 GCC         _____
GAM716  LOC203611 3'  GAAAGAAGTTTCTGC       18735     C     CTCT
                                GAA AGAGGT    TTCTGC
                                ||| ||||||    ||||||
                                CTT TCTTCA    AAGACG
                                  _     _____
GAM716  LOC219722 5'  GAACAGAGTTTCACC       18831        GTCTC    T
                                GAACAGAG     TTTC GCC
                                ||||||||     |||| |||
                                CTTGTCTC     AAAG TGG
                                     ______   _
GAM716  LOC219894 3'  GAAGAGAATGACATTTCTGCC  18832     C    GTCTC
                                GAA AGAG     TTTCTGCC
                                ||| ||||     ||||||||
                                CTT TCTT     AAAGACGG
                                  C    ACTGT
GAM716  LOC221463 3'  GAACAAAGCAGCCCCTTTCTG  18833          __
                                GAACAGAG  GTCTCTTTCTG
                                ||||||||  ||||||||||
                                CTTGTTTC  CGGGGAAAGAC
                                     GT
GAM716  LOC254494 5'  AACAGTGCCTTTCTGC      18834       AG    CT
                                AACAG  GTCT  TTCTGC
                                |||||  ||||  ||||||
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                                TTGTC  CGGA  AAGACG
                                  A_   __
GAM716  LOC254938 3'  GAACAGAAGTCTTCAGTC    18835          _ TT
                                GAACAGAGGTCT C  TC
                                |||||||||||| |  ||
                                CTTGTCTTCAGA G  AG
                                       A TC
GAM716  LOC255624 3'  GAACAAAGGTCTTGC       18787          CTTTC
                                GAACAGAGGTCT    TGC
                                ||||||||||||    |||
                                CTTGTTTCCAGA    ACG
                                      _____
GAM716  LOC255650 3'  GAAGGGTCAGACTTTCTGCC  18836   C  A   T__
                                A AG GGTC   CTTTCTGCC
                                | || ||||   |||||||||
                                C TC CCAG   GAAAGACGG
                                 T _    TCT
GAM716  LOC257445 5'  CAGAGGTCCCCTGCC       18781          TTT
                                CAGAGGTCTC   CTGCC
                                ||||||||||   |||||
                                GTCTCCAGGG   GACGG
                                     ___
GAM716  LOC51652  3'  GAGCAGAAGTCACTTCTGC   18837    A      T  T
                                GA CAGAGGTC CTT CTGC
                                || |||||||| ||| ||||
                                CT GTCTTCAG GAA GACG
                                 C       T  _
GAM716  LOC58489  3'  AAACAGAGGACTCTTCTG    18838         T    T
                                GAACAGAGG CTCTT CTG
                                ||||||||| ||||| |||
                                TTTGTCTCC GAGAA GAC
                                      T    _
GAM716  LOC91445  3'  ACAGTTTCTCTCTTTCTGCC  18839     AGG_
                                ACAG    TCTCTTTCTGCC
                                ||||    ||||||||||||
                                TGTC    AGAGAAAGACGG
                                  AAAG
GAM716  LOC92170  3'  CAGGGGTCTCTACTGCC     18840    A      TT
                                CAG GGTCTCT  CTGCC
                                ||| |||||||  |||||
                                GTC CCAGAGA  GACGG
                                  C      T_
GAM717  GRM6      3'  TTGGGAATCTCATGGG      18843        C    CTA   CA
                                TTGGGAA TCTCA   TGG  G
                                ||||||| |||||   |||  |
                                AACCCTT AGAGT   ACC  C
                                   _    ____  __
GAM717  PSEN2     3'  TTGGGAACACTCCTCGTAGG   18844         T   A  A  GC
                                TTGGGAAC CTC CT TG  AGG
                                |||||||| ||| || ||  |||
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                                AACCCTTG GAG GA GC  TCC
                                     T  _ _ A_
GAM717  PSEN2    3'  TTGGGAACACTCCTCGTAGG   18844        T  A  A  GC
                                TTGGGAAC CTC CT TG  AGG
                                |||||||| ||| || ||  |||
                                AACCCTTG GAG GA GC  TCC
                                     T  _ _ A_
GAM717  TEGT     3'  TTGGGGCTCTCACTGGTTTGG  18845      AA      AT  CA_
                                TTGGG  CTCTCACT  GG  GG
                                |||||  ||||||||  ||  ||
                                AACCC  GAGAGTGA  CC  CC
                                   C_       __ AAA
GAM717  TK2      3'  TTGGGAACTGCTCAATATTGGG 18846         _   C  GGCA
           A                     TTGGGAACT CTCA TAT   GGA
                                |||||||||  |||| |||   |||
                                AACCCTTGA GAGT ATA   CCT
                                     C   T  AC__
GAM717  ZNF274   5'  GGGGACTCTCAGCAGG     18847     A     CTATG
                                GGG ACTCTCA    GCAGG
                                ||| |||||||    |||||
                                CCC TGAGAGT    CGTCC
                                  C     _____
GAM717  BMF      3'  TTGGGAATTCTCACCATCACAG 18848        C       G
           A                     TTGGGAA TCTCACTAT GCAGG
                                |||||||  |||||||||  |||||
                                AACCCTT AGAGTGGTA TGTCT
                                     A       G
GAM717  C20orf44  3'  GGGGACTCTCACTCGGGG    18849     A       A  CA
                                GGG ACTCTCACT TGG  GG
                                ||| |||||||||  |||  ||
                                CCC TGAGAGTGA GCC  CC
                                  C       _  __
GAM717  CLSTN2   3'  TTGGGGACTCTGAGCCTGGGG  18850      A    CACTA  CA
                                TTGGG ACTCT    TGG  GG
                                |||||  |||||    |||  ||
                                AACCC TGAGA    ACC  CC
                                   C    CTCGG  __
GAM717  DKFZp434D0513 5'  TTGGGAACCTGGACAGTGGTGG 18851         CTC  TA  CA
           GA                     TTGGGAACT   AC  TGG  GGA
                                |||||||||   ||  |||  |||
                                AACCCTTGG   TG  ACC  CCT
                                     ACC  TC   AC
GAM717  KIAA0247  3'  TTGGAAACTCTCAACTCAACAG 18852           _  A
           G                     TTGGGAACTCTCA CT TGGCAGG
                                |||||||||||||  || |||||||
                                AACCTTTGAGAGT GA GTTGTCC
                                       T  _
GAM717  KIAA0478  3'  TTGGGAAGCTGTGGCAGG    18853        CTCTCA  A
                                TTGGGAA     CT TGGCAGG
                                |||||||      || |||||||
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                                AACCCTT     GA ACCGTCC
                                   C_____  C
GAM717  KIAA0557  3'  TTGGAAACTCTGGCAG      18854          CACTAT
                                TTGGGAACTCT     GGCAG
                                ||||||||||      |||||
                                AACCTTTGAGA     CCGTC
                                        _______
GAM717  KIAA1095  3'  TTGGGAACCTTAACCAGG    18855         CTC  TATGG
                                TTGGGAACT   AC    CAGG
                                |||||||||   ||    ||||
                                AACCCTTGG   TG    GTCC
                                     AAT  _____
GAM717  KIAA1737  3'  TTGGGAGGCTGTGGCAGG    18856       ACTCTCA  A
                                TTGGGA      CT TGGCAGG
                                ||||||      || |||||||
                                AACCCT      GA ACCGTCC
                                   CC_____  C
GAM717  L3MBTL2   3'  TTGGGAACTCTGGCG       18857          CACTAT   A
                                TTGGGAACTCT     GGC G
                                ||||||||||      ||| |
                                AACCCTTGAGA     CCG C
                                        _______  A
GAM717  PP5395    3'  CTGGGAAGGACTGTGGCAGGA  18858        CTCTC   A
                                TTGGGAA    ACT TGGCAGGA
                                |||||||    ||| ||||||||
                                GACCCTT    TGA ACCGTCCT
                                   CC___   C
GAM717  TTYH2     3'  TTGTGAACTCCAGGTTGGCAGG 18859     G     T  CTA
            A                    TTG GAACTC CA   TGGCAGGA
                                ||| |||||| ||   ||||||||
                                AAC CTTGAG GT   ACCGTCCT
                                  A     _  CCA
GAM717  LOC146895 5'  TTGGGAAGCTGAGATGGCAGGA 18860        _  CTCACT
                                TTGGGAA CT     ATGGCAGGA
                                ||||||| ||     |||||||||
                                AACCCTT GA     TACCGTCCT
                                   C  CTC___
GAM717  LOC169026 3'  TTGAGAACCCGATGTGGCAGGA 18861          TCACTA
                                TTGGGAACTC     TGGCAGGA
                                ||||||||||     ||||||||
                                AACTCTTGGG     ACCGTCCT
                                     CTAC__
GAM717  LOC90317  5'  TGGGAACTTTTACTAAAGGA   18862        CTC    TGGC
                                TGGGAACT   ACTA    AGGA
                                ||||||||   ||||    ||||
                                ACCCTTGA   TGAT    TCCT
                                   AAA    T___
GAM718  PTEN      3'  TAATGTTTCAAGCCC       18865           TTAT
                                TAATGTTTCAA    GCCT
                                ||||||||||    ||||
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                                ATTACAAAGTT   CGGG
                                      ____
GAM718  TK2      3'  TAATGCTTCCAGAGCCTTTATT 18866        AATTAT
                                TAATGTTTC     GCCTTTATT
                                |||||||||     |||||||||
                                ATTACGAAG     CGGAAATAA
                                    GTCT__
GAM718  DCLRE1A  3'  TAATGCTTCAAACTACTTTATT 18867          TTA  C
                                TAATGTTTCAA   TGC TTTATT
                                ||||||||||   ||| ||||||
                                ATTACGAAGTT   ATG AAATAA
                                     TG_  _
GAM718  KIAA1486 3'  ATATTTCAGTTTATGCCTTTAT 18868        A_
           T                     ATGTTTCA  TTATGCCTTTATT
                                ||||||||  ||||||||||||
                                TATAAAGT  AATACGGAAATAA
                                    CA
GAM718  MAIL     3'  ATGTTTCAATACTGACTTT    18869         TA  C
                                ATGTTTCAAT  TG CTTT
                                ||||||||||  || ||||
                                TACAAAGTTA  AC GAAA
                                     TG  T
GAM718  MAP      3'  GTTTTTAATTGTGCCTTTATT  18870     C_   A
                                GTTT  AATT TGCCTTTATT
                                ||||  |||| ||||||||||
                                CAAA  TTAA ACGGAAATAA
                                  AA   C
GAM718  MGC10955 3'  TAATGTTTCAGGTTCCTTTATT 18871          ATTATG
                                TAATGTTTCA     CCTTTATT
                                ||||||||||     ||||||||
                                ATTACAAAGT     GGAAATAA
                                     CCAA__
GAM718  MGC32104 3'  TGTAGGTATATGCCTTTATT   18872     TTCAAT
                                TGT     TATGCCTTTATT
                                |||     ||||||||||||
                                ACA     ATACGGAAATAA
                                  TCCAT_
GAM718  OSMR     3'  TAATGTCTCCTGTGGCCTTTAT 18873         AATTAT
           T                     TAATGTTTC     GCCTTTATT
                                |||||||||     |||||||||
                                ATTACAGAG     CGGAAATAA
                                    GACAC_
GAM718  LOC220047 3'  GTTTCAATTATGTCTTTATT   18874           C
                                GTTTCAATTATG CTTTATT
                                |||||||||||| |||||||
                                CAAAGTTAATAC GAAATAA
                                       A
GAM718  LOC221312 3'  TAATGATCCAATGCCTTTATT  18875      T   ATT
                                TAATG TTCA   ATGCCTTTATT
                                ||||| ||||   ||||||||||
```

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                                ATTAC AGGT   TACGGAAATAA
                                  T   ___
GAM719  ADD1    3'  CGGCCCCCTCCTCGACAGCT   18878          _  __
                                CGGCCCCCTCC CGA  GCT
                                |||||||||| |||  |||
                                GCCGGGGGAGG GCT  CGA
                                      A   GT
GAM719  ALDH8A1  3'  CAGCCTCCCAAGTAGCTGGGGC 18879      _  TCCCG
                                CGGCC CCC    AGCTGGGGC
                                ||||| |||    |||||||||
                                GTCGG GGG    TCGACCCCG
                                  A   TTCA_
GAM719  ARHGDIA  3'  GCTCCCTCCTGAAGCCAGGCC  18880    C     C_   TG  G
                                GC CCCTCC  GAGC  GG CC
                                || ||||||  ||||  || ||
                                CG GGGAGG  TTCG  CC GG
                                 A     AC    GT _
GAM719  ASC     5'  GGTCCCCTCCCACCCAGGCC   18881    C      GA   G
                                GG CCCCTCCC  GCT GGGCC
                                || ||||||||  ||| |||||
                                CC GGGGAGGG  TGG TCCGG
                                 A       __  G
GAM719  ASIC4    5'  GGTGCCCTCCCGAGTGG     18882    CC       C
                                GG  CCCTCCCGAG TGG
                                ||  ||||||||| |||
                                CC  GGGAGGGCTC ACC
                                 AC        _
GAM719  AXIN1    5'  CGGCCCCCATCTCGGCGGC   18883        _  C  A  TGG
                                CGGCCCCC TC CG GC   GGC
                                |||||||| || || ||   |||
                                GCCGGGGG AG GC CG   CCG
                                    T  A  _  ___
GAM719  BACH2    5'  CAGCCCCCTCCCGGCAGC    18884           A  TGG
                                CGGCCCCCTCCCG GC   GGC
                                |||||||||||| ||   |||
                                GTCGGGGGAGGGC CG   TCG
                                          _  ___
GAM719  BARHL1   3'  GGCCCCTTCCTGCCCCGCC   18885      C   CGA   GGG
                                GGCCCC TCC   GCT   GCC
                                |||||| |||   |||   |||
                                CCGGGG AGG   CGG   CGG
                                   A   A__   GG_
GAM719  CACNB1   3'  CGGGTCCTCTCCCCTGGGGCC  18886    CC  _    GAG
                                CGG  CC CTCCC   CTGGGGCC
                                |||  || |||||   ||||||||
                                GCC  GG GAGGG   GACCCCGG
                                  CA  A    ___
GAM719  CARKL    3'  GGCCCCCTCCTGGAAGC     18887         CGAGC   _
                                GGCCCCCTCC    TGGG GC
                                ||||||||||    |||| ||
```

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                                CCGGGGGAGG    ACCT CG
                                      _____   T
GAM719  CCNF    3'  GCCTCCCTCCCACGGGC    18888    _      AGCTG
                                GCC CCCTCCCG    GGGC
                                ||| ||||||||    ||||
                                CGG GGGAGGGT    CCCG
                                  A       G____
GAM719  CDA     3'  CAGTCCCTGTAGGCTGGGGCC  18889    CC    CCCGA
                                CGG  CCCT    GCTGGGGCC
                                |||  ||||    |||||||||
                                GTC  GGGA    CGACCCCGG
                                  A_   CATC_
GAM719  CELSR3   3'  CAGCCCTTCAAGAGCTGGGG   18890      CC  CC
                                CGGCCC  TC  GAGCTGGGG
                                ||||||  ||  |||||||||
                                GTCGGG  AG  CTCGACCCC
                                   A_  TT
GAM719  CLTC    5'  GGTCTCCTCCTGTCACTGGGGC 18891    CCC    CGA_
                                GG   CCTCC   GCTGGGGC
                                ||   |||||   ||||||||
                                CC   GGAGG   TGACCCCG
                                 AGA    ACAG
GAM719  COG4    3'  CAGCTCCTTGGCTGGGGC    18892     CCCC   CGA
                                CGGC   TCC   GCTGGGGC
                                ||||   |||   ||||||||
                                GTCG   AGG   CGACCCCG
                                  _____  AAC
GAM719  CSNK1G2  3'  CCCCCTCCCAGGAGGGCC    18893        G  CT
                                CCCCCTCCC AG  GGGGCC
                                |||||||||  ||  ||||||
                                GGGGGAGGG TC  TCCCGG
                                     _  C_
GAM719  DGCR2    3'  GGCCCCCTCCTGAGGGCGGCC  18894         C   CT  _
                                GGCCCCCTCC GAG  GG GGCC
                                |||||||||| |||  ||  ||||
                                CCGGGGGAGG CTC  CC CCGG
                                     A   __  G
GAM719  DUX4    5'  CGGCTCCCTCCCGCCCGC    18895     C      AG  GGG
                                CGGC CCCTCCCG  CT   GC
                                ||||  ||||||||  ||   ||
                                GCCG GGGAGGGC  GG   CG
                                  A       G_  ___
GAM719  ECH1    3'  CGGCCCCCTGGCTGGGGCC   18896        CCCGA
                                CGGCCCCCT    GCTGGGGCC
                                |||||||||    |||||||||
                                GCCGGGGGA    CGACCCCGG
                                     C____
GAM719  EGFL4    3'  CAGCCCCCTCCCATGGG     18897           AGC
                                CGGCCCCCTCCCG   TGGG
                                ||||||||||||   ||||
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                              GTCGGGGGAGGGT  ACCC
                                    ___
GAM719  FAT2    3'  GCCCCTCTCCTGGGAC     18898      _   CGAGC
                              GCCCC CTCC    TGGGGC
                              ||||| ||||    ||||||
                              CGGGG GAGG    ACCCTG
                                A   _____
GAM719  FGFR3   3'  CGGCCCCTCCCTGGAAACC   18899       C   GAGCT GG
                              CGGCCCC TCCC    G  GCC
                              ||||||| ||||    |  |||
                              GCCGGGG AGGG    C  TGG
                                 _   AC___ TT
GAM719  FMNL    3'  CGGTCCTCGGGGCTGGGGC   18900    CCC   CCGA
                              CGG   CCTC   GCTGGGGC
                              |||   ||||   ||||||||
                              GCC   GGAG   CGACCCCG
                                A__   CCC_
GAM719  FPGS    3'  CGGCCCCCCTTCCTCGAGGGCC 18901        __  _  GCTG
                              CGGCCCCC  TCC CGA   GGGCC
                              ||||||||  ||| |||   |||||
                              GCCGGGGG  AGG GCT   CCCGG
                                 GA  A  _____
GAM719  GCN5L2  3'  GGCCCCCTTCAGTTTGGGC   18902       CC G  CTG
                              GGCCCCCT  C AG   GGGC
                              ||||||||  | ||   ||||
                              CCGGGGGA  G TC   CCCG
                                 A_ _  AAA
GAM719  GGA1    3'  CAGCCCCTCGCTGGGGC    18903       C  CCGA
                              CGGCCCC TC   GCTGGGGC
                              ||||||| ||   ||||||||
                              GTCGGGG AG   CGACCCCG
                                 _ _____
GAM719  GPC1    3'  GGCCTCTGTCCCTGGGGCC   18904    CCC_   GAGC
                              GGCC   TCCC   TGGGGCC
                              ||||   ||||   |||||||
                              CCGG   AGGG   ACCCCGG
                                AGAC   _____
GAM719  GPR30   5'  GGCCTCTTCCCCACCAGGGCC 18905    CCC   GA  TG
                              GGCC   TCCC  GC  GGGCC
                              ||||   ||||  ||  |||||
                              CCGG   AGGG  TG  CCCGG
                                AGA   G_  GT
GAM719  GRB10   3'  GGCCAGCGAGCTGGGGC    18906    CCCTCC
                              GGCC    CGAGCTGGGGC
                              ||||    ||||||||||
                              CCGG    GCTCGACCCCG
                                TC_____
GAM719  HDAC5   3'  CAGCCCCCTCCTGGTCTTAGC 18907         CGAG  GG
                              CGGCCCCCTCC   CT  GGC
                              ||||||||||   ||  |||
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                                GTCGGGGGAGG   GA  TCG
                                      ACCA  A_
GAM719  HIP12   3'  GGTCCCCTCCCTGAGGGCC   18908   C      GAGCT
                                GG CCCCTCCC    GGGGCC
                                || ||||||||    ||||||
                                CC GGGGAGGG    TCCCGG
                                 A       AC___
GAM719  HR      5'  CGGCCCCCTCCCGGG      18909          GAGCTG
                                CGGCCCCCTCCC     GGG
                                ||||||||||||     |||
                                GCCGGGGGAGGG     CCC
                                      _______
GAM719  ICMT    3'  GGTCCCCTTGGCCTGGGGCC  18910   C    CCCGAG
                                GG CCCCT     CTGGGGCC
                                || |||||     ||||||||
                                CC GGGGA     GACCCCGG
                                 A    ACCG__
GAM719  IL15    5'  CAGTTCCCTCCCGGGGGGC   18911    CC      AGCT
                                CGG  CCCTCCCG   GGGGC
                                |||  ||||||||   |||||
                                GTC  GGGAGGGC   CCCCG
                                  AA       C___
GAM719  IL2RA   3'  GGTCTCCTAGGGAGCTGGGG  18912   CCCC   C___
                                GG   CTCC   GAGCTGGGG
                                ||   ||||   |||||||||
                                CC   GAGG   CTCGACCCC
                                 A___    ATCC
GAM719  ITGA5   3'  GGCTTCAGGGAGGCTGGGGCC 18913    CCCC  CC_  _
                                GGC   TC   GAG CTGGGGCC
                                |||   ||   ||| ||||||||
                                CCG   AG   CTC GACCCCGG
                                  A___  TCC   C
GAM719  KCNA7   3'  CGGCCTCCCAAAGTGCTGGGG 18914      CCC    ___
                                CGGCC   TCCCGA   GCTGGGG
                                |||||   ||||||   |||||||
                                GCCGG   AGGGTT   CGACCCC
                                   ___     TCA
GAM719  KCNH2   3'  GCCCCTCTCACTGGGGC    18915      _  CCGA
                                GCCCC CTC    GCTGGGGC
                                ||||| |||    ||||||||
                                CGGGG GAG    TGACCCCG
                                   A  _____
GAM719  LIM2    3'  CAGCTCCCTCCCATGGGC    18916     C     GAGCTG
                                CGGC CCCTCCC     GGGC
                                |||| |||||||     ||||
                                GTCG GGGAGGG     CCCG
                                  A      TA_____
GAM719  LIMK1   5'  GGCCCGGCGGGGCTGGGGC   18917      CCTCC  A_
                                GGCCC    CG  GCTGGGGC
                                |||||    ||  ||||||||
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                                CCGGG    GC  CGACCCCG
                                  CC___  CC
GAM719  LIMK1    5'  GGCCCGGCGGGGCTGGGGC   18917     CCTCC  A_
                                GGCCC    CG  GCTGGGGC
                                |||||    ||  ||||||||
                                CCGGG    GC  CGACCCCG
                                  CC___  CC
GAM719  LOXL1    5'  GGCCTTGTCCCGAGCGGGAC  18918     CCC      T
                                GGCC   TCCCGAGC GGGGC
                                ||||   |||||||| |||||
                                CCGG   AGGGCTCG CCCTG
                                  AAC      _
GAM719  MB       3'  GCTCTCTCTTGAACCCGGGGCC 18919    CCC   CC    _
                                GC   CTC  GAGCT GGGGCC
                                ||   |||  ||||| ||||||
                                CG   GAG  CTTGG CCCCGG
                                 AGA   AA    G
GAM719  MMP14    3'  GGCCCCCTGCTTGGCTTGGCC  18920       CCCGA   GG
                                GGCCCCCT    GCT  GGCC
                                ||||||||    |||  ||||
                                CCGGGGGA    CGA  CCGG
                                    CGAAC   A_
GAM719  MMP15    3'  CAGCCCCCTCTCCCTGGGGC   18921        _  GAG
                                CGGCCCCCTC CC   CTGGGGC
                                |||||||||| ||   |||||||
                                GTCGGGGGGAG GG   GACCCCG
                                     A  ____
GAM719  MUC5B    3'  GGCGCCCTCCCGAAAGGGG   18922    C       CT
                                GGC CCCTCCCGAG  GGGG
                                ||| ||||||||||  ||||
                                CCG GGGAGGGCTT  CCCC
                                  C        T_
GAM719  MYO1C    3'  CCTCCCAAAGTGCTGGGG    18923       ____
                                CCTCCCGA   GCTGGGG
                                ||||||||   |||||||
                                GGAGGGTT   CGACCCC
                                    TCA
GAM719  MYO1D    3'  GGCCTTCTCAGCAGCTGGGGC  18924     CC   CCG
                                GGCC  CTC   AGCTGGGGC
                                ||||  |||   |||||||||
                                CCGG  GAG   TCGACCCCG
                                  AA   TCG
GAM719  NBS1     5'  CGGCTCCTCAGGGCTGGGGCC  18925     CC    CCGA
                                CGGC  CCTC    GCTGGGGCC
                                ||||  ||||    |||||||||
                                GCCG  GGAG    CGACCCCGG
                                  A_    TCC_
GAM719  NGFR     3'  GGCCCCCTTCTGGCCAAGCT   18926        _ ____
                                GGCCCCCT C   CCGAGCT
                                |||||||| |   |||||||
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                                CCGGGGGA G   GGTTCGA
                                     A ACC
GAM719  NR2E3   3'  GGTCCCCACTCCCGGGGCC   18927   _   _    GAGCT
                                GG CCCC CTCCC    GGGGCC
                                || |||| |||||    ||||||
                                CC GGGG GAGGG    CCCCGG
                                 A   T   _____
GAM719  OTP     3'  GGCCTCGCGGGCTGGGGC    18928     CCC  C  A
                                GGCC   TC CG GCTGGGGC
                                ||||   || || ||||||||
                                CCGG   AG GC CGACCCCG
                                   ___  C  C
GAM719  PAX5    3'  GGCCTTCCCCAAGCTGGGCC  18929     CC T        G
                                GGCC  C CCCGAGCTGGG CC
                                ||||  | ||||||||||| ||
                                CCGG  G GGGTTCGACCC GG
                                  AA _        _
GAM719  PCDH7   5'  CGCCCCCCTCCTCCGGGGCC  18930   G     CGAG
                                CG CCCCCTCC   CTGGGGCC
                                || ||||||||   ||||||||
                                GC GGGGGAGG   GGCCCCGG
                                 G      A___
GAM719  PCDH7   5'  CGCCCCCCTCCTCCGGGGCC  18930   G     CGAG
                                CG CCCCCTCC   CTGGGGCC
                                || ||||||||   |||||||
                                GC GGGGGAGG   GGCCCCGG
                                 G      A___
GAM719  PCDH7   5'  CGCCCCCCTCCTCCGGGGCC  18930   G     CGAG
                                CG CCCCCTCC   CTGGGGCC
                                || ||||||||   ||||||||
                                GC GGGGGAGG   GGCCCCGG
                                 G      A___
GAM719  PFKFB3  5'  CGGCCCGCCTCCCGGGGC    18931      _    GAGCT
                                CGGCCC CCTCCC    GGGGC
                                |||||| ||||||    |||||
                                GCCGGG GGAGGG    CCCCG
                                   C    _____
GAM719  PLCB2   3'  CAGCCTCAGAAGGCTGGGGC  18932     CCC  CC  _
                                CGGCC  TC  GAG CTGGGGC
                                |||||  ||  ||| |||||||
                                GTCGG  AG  TTC GACCCCG
                                   ___  TC  C
GAM719  PLXNB2  3'  CGGCCGGAGGGAGCTGGGGC  18933     CCCTCCC
                                CGGCC     GAGCTGGGGC
                                |||||     ||||||||||
                                GCCGG     CTCGACCCCG
                                  CCTCC__
GAM719  PRDM2   3'  CGGCCCCCTTCCTGCCGC    18934       C  GA  GGG
                                CGGCCCCCT CC  GCT  GC
                                ||||||||| ||  |||  ||
```

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                                GCCGGGGGA GG  CGG   CG
                                     A  A_  ___
GAM719  PRX     3'  GGATTCCCACGGCTGGGGCC  18935    CCCCC    A_
                                GG    TCCCG  GCTGGGGCC
                                ||    |||||  |||||||||
                                CC    AGGGT  CGACCCCGG
                                 TA___    GC
GAM719  RAF1    3'  GGCTTCCTTCTCCCAGGGCC  18936    __ C_    GAGCT
                                GGC  CC  CTCCC    GGGGCC
                                |||  ||  |||||    ||||||
                                CCG  GG  GAGGG    TCCCGG
                                 AA  AA    _____
GAM719  RUNX1   3'  GCGTCCCCTGGGTGCTGGGGCC 18937    __    CCCGA
                                GC  CCCCT    GCTGGGGCC
                                ||  |||||    |||||||||
                                CG  GGGGA    CGACCCCGG
                                 CA    CCCA_
GAM719  RXRA    3'  CAGCTCCAGGGCTGGGGC    18938     CCCC   CGA
                                CGGC   TCC   GCTGGGGC
                                ||||   |||   ||||||||
                                GTCG   AGG   CGACCCCG
                                  ____  TCC
GAM719  SDC4    3'  GGCCCCAGCTGGGGC      18939       CTCCCG
                                GGCCCC     AGCTGGGGC
                                ||||||     |||||||||
                                CCGGGG     TCGACCCCG
                                  _______
GAM719  SEPN1   3'  GGCCCCTCCTGGCTGGGGC   18940       C   CGA
                                GGCCCC TCC   GCTGGGGC
                                |||||| |||   ||||||||
                                CCGGGG AGG   CGACCCCG
                                   _  AC_
GAM719  SLC29A1 3'  GGCTCCCTCCCCAGGGC     18941     C      GAGC
                                GGC CCCTCCC    TGGGGC
                                ||| |||||||    ||||||
                                CCG GGGAGGG    GTCCCG
                                 A     _____
GAM719  SMG1    5'  CGGCCCACGACGCTGGGGCC   18942       CCTCC  _
                                CGGCCC    CGA GCTGGGGCC
                                ||||||    ||| |||||||||
                                GCCGGG    GCT CGACCCCGG
                                   T_____   G
GAM719  SOLH    3'  CGGCCCCCGTCGGGTGTTGGGG 18943        _  CCGAGC
          C                     CGGCCCCC TC     TGGGGC
                                ||||||||  ||     ||||||
                                GCCGGGGG AG     ACCCCG
                                    C  CCCACA
GAM719  TCFL4   3'  GGCCCCTCCCTGAGATGGCC   18944       C   _   CTGG
                                GGCCCC TCCC GAG    GGCC
                                |||||| |||| |||    ||||
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                                CCGGGG AGGG CTC   CCGG
                                  _   A  TA__
GAM719  TK1     3'  CGACTTCCTCCTGGAGTGG   18945     CC    C_  C
                                CGGC  CCTCC  GAG TGG
                                ||||  |||||  ||| |||
                                GCTG  GGAGG  CTC ACC
                                  AA    AC  _
GAM719  TMEPAI  5'  CGGCCTCCCCTCGGCAGC    18946      C   C  A  TGG
                                CGGCC CCTC CG GC  GGC
                                ||||| |||| || ||  |||
                                GCCGG GGGG GC CG  TCG
                                  A   A  _ ___
GAM719  TMEPAI  5'  CGGCGCCCGGAGCTGGGGCC  18947     C  TCCC
                                CGGC CCC   GAGCTGGGGCC
                                |||| |||   ||||||||||
                                GCCG GGG   CTCGACCCCGG
                                  C  C___
GAM719  TNFSF7  5'  CAGCCCCCTCCCGGGGC     18948          GAGCT
                                CGGCCCCCTCCC    GGGGC
                                ||||||||||||    |||||
                                GTCGGGGGAGGG    CCCCG
                                                _____
GAM719  TRPV4   3'  GGTCCCTCGCCTCTGGGGCC  18949    CC    _  GAG
                                GG  CCCTC CC   CTGGGGCC
                                ||  ||||| ||   ||||||||
                                CC  GGGAG GG   GACCCCGG
                                 A_    C  A__
GAM719  USP11   5'  GGTCCCCTCCCTGCAGTATGCC 18950    C      GA  TGGG_
                                GG CCCCTCCC  GC    GCC
                                || ||||||||  ||    |||
                                CC GGGGAGGG  CG    CGG
                                 A       A_  TCATA
GAM719  VIPR2   3'  CGCGCCCCAGCTGGGG      18951    _    CTCCCG
                                CG GCCCC     AGCTGGGG
                                || |||||     ||||||||
                                GC CGGGG     TCGACCCC
                                 G    _______
GAM719  WBP2    3'  CGGCACCTCTCCCGAGGC    18952      _ C     GCTGG
                                CGGC CC CTCCCGA    GGC
                                |||| || |||||||    |||
                                GCCG GG GAGGGCT    CCG
                                  T  A     _____
GAM719  WHSC1   3'  GCTCCCTCCCGAGGAGGCC   18953    C       CT
                                GC CCCTCCCGAG  GGGGCC
                                || ||||||||||  ||||||
                                CG GGGAGGGCTC  CTCCGG
                                 A        __
GAM719  WHSC1   3'  GCTCCCTCCCGAGGAGGCC   18953    C       CT
                                GC CCCTCCCGAG  GGGGCC
                                || ||||||||||  ||||||
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```
                                CG GGGAGGGCTC  CTCCGG
                                 A       __
GAM719  WHSC1    3'  GCTCCCTCCCGAGGAGGCC   18953    C       CT
                                GC CCCTCCCGAG  GGGGCC
                                || ||||||||||  ||||||
                                CG GGGAGGGCTC  CTCCGG
                                 A       __
GAM719  WHSC1    3'  GCTCCCTCCCGAGGAGGCC   18953    C       CT
                                GC CCCTCCCGAG  GGGGCC
                                || ||||||||||  ||||||
                                CG GGGAGGGCTC  CTCCGG
                                 A       __
GAM719  WNT2     3'  GGCCCCCCCATCCTGGGGCC   18954        CCCGAG
                                GGCCCCCT     CTGGGGCC
                                ||||||||     ||||||||
                                CCGGGGGGG     GACCCCGG
                                     TAG___
GAM719  XYLB     3'  GGATCCCTCCTGTCTGGGGCC  18955    CC     CGAG
                                GG  CCCTCC    CTGGGGCC
                                ||  ||||||    ||||||||
                                CC  GGGAGG    GACCCCGG
                                 TA     ACA_
GAM719  ZNF76    3'  GGCCCCCTTCTTGAGCAGGGCC 18956         _ CC    T
                                GGCCCCCT C  GAGC GGGGCC
                                |||||||| |  |||| ||||||
                                CCGGGGGA G  CTCG TCCCGG
                                     A AA   _
GAM719  ARFRP1   3'  CAGCTCCCTCCCGGGGGG     18957      C       AGCT
                                CGGC CCCTCCCG    GGGG
                                |||| ||||||||    ||||
                                GTCG GGGAGGGC    CCCC
                                  A       _____
GAM719  ARHGAP8  5'  CGGCCCCCACCTGCGTGCCGGG 18958         T  __  A
                                CGGCCCCC CC  CG GCTGGG
                                |||||||| ||  || ||||||
                                GCCGGGGG GG  GC CGGCCC
                                     T  AC  A
GAM719  BRD3     3'  GGCTCCACGCTCCGGGCTGGGG 18959     _  C__    C A
             C                   GGC CC   CTCC G GCTGGGGC
                                ||| ||   |||| | ||||||||
                                CCG GG   GAGG C CGACCCCG
                                  A  TGC    _ C
GAM719  BRPF3    5'  GCCCCCTCCCGGCCCGCGCTGG 18960          A_____
             GGCC                   GCCCCCTCCCG     GCTGGGGCC
                                ||||||||||||     |||||||||
                                CGGGGGAGGGC     CGACCCCGG
                                       CGGGCG
GAM719  C14orf4  5'  GCGTCCTCTCCCCGACGGGCC  18962    C_  _    GA  TG
                                GC  CC CTCCC  GC  GGGCC
                                ||  || |||||  ||  |||||
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                                CG  GG GAGGG  TG  CCCGG
                                 CA  A    GC  __
GAM719  C14orf4   5'  GGCCCCCTCCCCGGAGTGG   18961          __  C
                                GGCCCCCTCCC  GAG TGG
                                ||||||||||  ||| |||
                                CCGGGGGAGGG  CTC ACC
                                      GC  _
GAM719  C20orf100 3'  CGGCCCACCTGGGCTGGGGC  18963       _  CCCGA
                                CGGCCC CCT    GCTGGGGC
                                ||||||| |||    ||||||||
                                GCCGGG GGA    CGACCCCG
                                   T  CC___
GAM719  C20orf110 3'  CGGTGCCCTGCTGGGGC    18964    CC   CCCGA
                                CGG  CCCT    GCTGGGGC
                                |||  ||||    ||||||||
                                GCC  GGGA    CGACCCCG
                                  AC  ______
GAM719  C20orf28  3'  GACCCCCTCCCTGGGG      18965          GAGC
                                GGCCCCCTCCC   TGGGG
                                ||||||||||   |||||
                                CTGGGGGAGGG   ACCCC
                                      ____
GAM719  C20orf51  5'  CGGCCCCCTCCAGCCTGGGG  18966          CG  _
                                CGGCCCCCTCC  AGC TGGGG
                                ||||||||||  ||| |||||
                                GCCGGGGGAGG  TCG ACCCC
                                      __  G
GAM719  CBCIP2    3'  CAGCCTCCCAAGTAGCTGGGGC 18879      _  TCCCG
                                CGGCC CCC    AGCTGGGGC
                                ||||| |||    |||||||||
                                GTCGG GGG    TCGACCCCG
                                   A  TTCA_
GAM719  CDC26     5'  AGCCCCTTCCCGGAACCTCGGC 18967      C   _   GG
                                GGCCCC TCCCG AGCT  GGC
                                |||||| ||||| ||||  |||
                                TCGGGG AGGGC TTGG  CCG
                                   A    C   AG
GAM719  CDH22     5'  GGCCTGCGCGGGGCTGGGGCC  18968    CCCTCC  A_
                                GGCC     CG  GCTGGGGCC
                                ||||     ||  |||||||||
                                CCGG     GC  CGACCCCGG
                                  ACGC__  CC
GAM719  CDT1      3'  GGCCTCCCAAAGTGCTGGGG   18969    CCC    ___
                                GGCC   TCCCGA   GCTGGGG
                                ||||   ||||||   |||||||
                                CCGG   AGGGTT   CGACCCC
                                  ___     TCA
GAM719  CECR6     3'  CGGCCTTCTCTGCTGGGGC   18970     CC   CCGA
                                CGGCC  CTC   GCTGGGGC
                                |||||  |||   ||||||||
```

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                                GCCGG  GAG   CGACCCCG
                                  AA  A___
GAM719  DDM36    5'  GGCCCGGGCCCGAGCTGGGGCC 18971      CCT
                                GGCCC  CCCGAGCTGGGGCC
                                |||||  ||||||||||||||
                                CCGGG  GGGCTCGACCCCGG
                                  CCC
GAM719  DKFZP434M154 5'  CGGCCTCCTCACGGCCCAGCC  18972      C   C A  G G
                                CGGCC CCTC CG GCT GG CC
                                ||||| |||| || ||| || ||
                                GCCGG GGAG GC CGG TC GG
                                  A   T _  G _
GAM719  DKFZP434M154 5'  CGGTCCCTGACGGCTGGGGC  18973    CC   CC  A
                                CGG  CCCT  CG GCTGGGGC
                                |||  ||||  || ||||||||
                                GCC  GGGA  GC CGACCCCG
                                  A_   CT  _
GAM719  DKFZP434P1750 5'  GGCTCCGGAGCTGGGG     18974    CCCC  C
                                GGC   TCC GAGCTGGGG
                                |||   ||| |||||||||
                                CCG   AGG CTCGACCCC
                                  _____  C
GAM719  DKFZP564O0823 3'  GGCCCCCTCCAGGGC      18975         CGAGCT
                                GGCCCCCTCC     GGGGC
                                ||||||||||     |||||
                                CCGGGGGAGG     TCCCG
                                       _______
GAM719  DKFZp586I021 3'  GGCCCCCTCTCCAGGGGC   18976        _  AGCT
                                GGCCCCCTC CCG   GGGGC
                                ||||||||| |||   |||||
                                CCGGGGGAG GGT   CCCCG
                                     A  _____
GAM719  DKFZP761C169 5'  GGCTATCTCCCGAATTAGCC  18977    CCC      CTGG
                                GGC  CTCCCGAG   GGCC
                                |||  ||||||||   ||||
                                CCG  GAGGGCTT   TCGG
                                  ATA      AA__
GAM719  DKFZP761E1824 5'  CGCGCCTCCTCCCGGGGC   18978   _  C    GAGCT
                                CG GCC CCTCCC    GGGGC
                                || ||| ||||||    |||||
                                GC CGG GGAGGG    CCCCG
                                 G  A    ______
GAM719  DKFZP761E1824 5'  CGGTCCCTCCCGGCGCGC   18979    CC      A  TGGG
                                CGG  CCCTCCCG GC   GC
                                |||  |||||||| ||   ||
                                GCC  GGGAGGGC CG   CG
                                  A_       _ CG__
GAM719  FADS2    3'  CGGCCCCTCCCTGAACGTGGCC 18980       C   _   TGG
                                CGGCCCC TCCC GAGC  GGCC
                                ||||||| |||| ||||  ||||
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                                GCCGGGG AGGG CTTG  CCGG
                                   _   A   CA_
GAM719  FAPP2   5' CGGCCCCCTCACTGCCCCAGGC 18981        CCGAG  G
            C                   CGGCCCCCTC    CT GGGCC
                                |||||||||     || |||||
                                GCCGGGGGAG    GG TCCGG
                                     TGACG  G
GAM719  FGF19   5' CAGCCCCCTCCCCGGGC    18982          GAGCTG
                                CGGCCCCCTCCC    GGGC
                                ||||||||||||    ||||
                                GTCGGGGGAGGG    CCCG
                                     G_____
GAM719  FKBP8   3' GGCCCCCTCCCTCTGGG    18983          GAG
                                GGCCCCCTCCC  CTGGG
                                ||||||||||  |||||
                                CCGGGGGAGGG  GACCC
                                     A__
GAM719  FLJ10244 3' CGGCCTCCCAAAGTGCTGGGG  18914     CCC    ___
                                CGGCC  TCCCGA  GCTGGGG
                                |||||  ||||||  |||||||
                                GCCGG  AGGGTT  CGACCCC
                                   ___    TCA
GAM719  FLJ10751 5' GCTTCTCACAAAAGGGCC   18984   CCC  C   CT
                                GC  CTC CGAG  GGGGCC
                                ||  ||| ||||  ||||||
                                CG  GAG GTTT  TCCCGG
                                 AA_  T   __
GAM719  FLJ10751 5' GCTTCTCACAAAAGGGCC   18984   CCC  C   CT
                                GC  CTC CGAG  GGGGCC
                                ||  ||| ||||  ||||||
                                CG  GAG GTTT  TCCCGG
                                 AA_  T   __
GAM719  FLJ10769 3' CGGTCTGCCCTGCTGGGGCC  18985    CCCC _  GA
                                CGG   CT CCC  GCTGGGGCC
                                |||   || |||  |||||||||
                                GCC   GA GGG  CGACCCCGG
                                  A___  C  A_
GAM719  FLJ10979 5' CGGCCCCCTGCCGACCCCCGCC 18986        C   G  GGG
                                CGGCCCCCT CCGA CT  GCC
                                ||||||||| |||| ||  |||
                                GCCGGGGGA GGCT GG  CGG
                                     C   G  GG_
GAM719  FLJ12078 5' CAGCCTCCCGAGTAGCTGGGGC 18987     CCC    ___
                                CGGCC  TCCCGA  GCTGGGGC
                                |||||  ||||||  ||||||||
                                GTCGG  AGGGCT  CGACCCCG
                                   ___    CAT
GAM719  FLJ12229 5' CGGTCACTCAGCTGGGGC   18988   CCCC  CCG
                                CGG   CTC  AGCTGGGGC
                                |||   |||  |||||||||
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                              GCC   GAG  TCGACCCCG
                                AGT_  ___
GAM719  FLJ13194  5' CGGCTCCCTCCCGCCGCT   18989     C      A_
                              CGGC CCCTCCCG  GCT
                              |||| ||||||||  |||
                              GCCG GGGAGGGC  CGA
                                A      GG
GAM719  FLJ13265  3' GGCCCCCTGGCGCTGGGGCC  18990       CCCGA
                              GGCCCCCT   GCTGGGGCC
                              ||||||||   |||||||||
                              CCGGGGGA   CGACCCCGG
                                  CCG__
GAM719  FLJ13868  3' CGGCCTTCCTCTGCCTGGGGCC 18991     C_   CCGAG
                              CGGCC  CCTC   CTGGGGCC
                              |||||  ||||   ||||||||
                              GCCGG  GGAG   GACCCCGG
                                 AA   ACG__
GAM719  FLJ13952  3' CAGCTTCCCGAGTAGCTGGGG  18992    CCCC    ___
                              CGGC   TCCCGA  GCTGGGG
                              ||||   ||||||  |||||||
                              GTCG   AGGGCT  CGACCCC
                                A___     CAT
GAM719  FLJ14050  3' CCTTTTCCGTGCCCGGGGCC  18993    C__  A  _
                              CCT   CCG GCT GGGGCC
                              |||   ||| ||| ||||||
                              GGA   GGC CGG CCCCGG
                                AAA  A  G
GAM719  FLJ14397  3' CAGCCTCCTGAGTAGCTGGGG  18994     C  CCCG
                              CGGCC CCT   AGCTGGGG
                              ||||| |||   ||||||||
                              GTCGG GGA   TCGACCCC
                                 A  CTCA
GAM719  FLJ21087  3' GGCTTTCTTTAGCTAAGGCC  18995    CCCC  CCG
                              GGC   TC  AGCTGGGGCC
                              |||   ||  ||||||||||
                              CCG   AG  TCGATTCCGG
                                AA__  AAA
GAM719  FLJ21709  3' CAGCCCTCTCCTGGGGC    18996      C   CGAGC
                              CGGCCC CTCC    TGGGGC
                              |||||| ||||    ||||||
                              GTCGGG GAGG    ACCCCG
                                 A  _____
GAM719  FLJ22329  3' GCCCCCTCCAGGGGGGC    18997       CG  CT
                              GCCCCCTCC  AG  GGGGC
                              |||||||||  ||  |||||
                              CGGGGGAGG  TC  CCCCG
                                   __  C_
GAM719  FLJ22349  3' CAGTCCCTTCAGCTGGGGC   18998    C  C  CCG
                              CGG CCC TC   AGCTGGGGC
                              ||| ||| ||   |||||||||
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                                GTC GGG AG   TCGACCCCG
                                  A   A ___
GAM719  FLJ22940  5'  CGGCCTCCGTCTCCTCCAGGGC 18999      _ __   CGAG TG
              C                    CGGCC CC  CTCC   C  GGGCC
                                   ||||| ||  ||||   |  |||||
                                   GCCGG GG  GAGG   G  CCCGG
                                     A  CA   A___ GT
GAM719  FLJ25409  5'  CAGCTCCTTCCCGGGAC     19000     C  C   GAGCT
                                   CGGC CC TCCC    GGGGC
                                   |||| || ||||    |||||
                                   GTCG GG AGGG    CCCTG
                                     A  A   _____
GAM719  FREQ     5'  CGGCCCCCGCCCCCCCGGGCC  19001        T   GAG  G
                                   CGGCCCCC CCC   CT GGGCC
                                   |||||||| |||   || |||||
                                   GCCGGGGG GGG   GG CCCGG
                                        C   G__  G
GAM719  GIPC3    3'  GGCTGGGCTCCGGGCTGGGGC  19002    CCC_   C A
                                   GGC   CTCC G GCTGGGGC
                                   |||   |||| | ||||||||
                                   CCG   GAGG C CGACCCCG
                                     ACCC   _ C
GAM719  GPT2     3'  GGTCTCCCGCTGGGGC     19003    CCCC    GA
                                   GG   CTCCC  GCTGGGGC
                                   ||   |||||  ||||||||
                                   CC   GAGGG  CGACCCCG
                                    A___    __
GAM719  KCNN1    3'  CGGACCCCTCCCCGGGC     19004    C      GAGCTG
                                   CGG CCCCTCCC     GGGC
                                   ||| ||||||||     ||||
                                   GCC GGGGAGGG     CCCG
                                     T      G_____
GAM719  KIAA0140 3'  GCCCCCAGCTGGGGC      19005      TCCCG
                                   GCCCCC    AGCTGGGGC
                                   ||||||    |||||||||
                                   CGGGGG    TCGACCCCG
                                             _____
GAM719  KIAA0173 3'  GGGCTCCTTCACTGGGGCC   19006   CCCC   CGA
                                   GG   CTCC   GCTGGGGCC
                                   ||   ||||   |||||||||
                                   CC   GAGG   TGACCCCGG
                                    C___    AAG
GAM719  KIAA0247 3'  GGCTCCTCCCCCAGGGCC   19007    CC     GAG TG
                                   GGC  CCTCCC   C  GGGCC
                                   |||  ||||||   |  |||||
                                   CCG  GGAGGG   G  CCCGG
                                     A_      ___ GT
GAM719  KIAA0363 5'  GGCTCCCTCGGGCTGGGGCC  19008    C    CCGA
                                   GGC CCCTC    GCTGGGGCC
                                   ||| |||||    |||||||||
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                                CCG GGGAG   CGACCCCGG
                                  A    CC__
GAM719  KIAA0397 3' GGTTGCTCCAGCTGGGGC   19009   CCCC   CG
                                GG   CTCC  AGCTGGGGC
                                ||   ||||  |||||||||
                                CC   GAGG  TCGACCCCG
                                 AAC_   __
GAM719  KIAA0444 3' CGGCCCCCTCTTAGCTGGGCC 19010        CCG     G
                                CGGCCCCCTC   AGCTGGG CC
                                ||||||||||   ||||||| ||
                                GCCGGGGGGAG   TCGACCC GG
                                      AA_     _
GAM719  KIAA0513 3' CCGTCCCTGAGGCTGGGGC   19011   C   _  _
                                CC TCCC GAG CTGGGGC
                                || |||| ||| |||||||
                                GG AGGG CTC GACCCCG
                                 C   A   C
GAM719  KIAA0556 3' AGTCCCCTCTTCCCAGCGGGC 19012   C    __ G   TG
                                GG CCCCTC  CC AGC  GGGC
                                || ||||||  || |||  ||||
                                TC GGGGAG  GG TCG  CCCG
                                 A     AA  G  __
GAM719  KIAA0557 3' GCCCCCTCCACTCCGGGGCC  19013        CGAG
                                GCCCCCTCC   CTGGGGCC
                                |||||||||   ||||||||
                                CGGGGGAGG   GGCCCCGG
                                      TGA_
GAM719  KIAA0618 5' GGCCCCCTCCTGGGGC     19014        CGAGC
                                GGCCCCCTCC    TGGGGC
                                ||||||||||    ||||||
                                CCGGGGGAGG    ACCCCG
                                      _____
GAM719  KIAA0672 5' CAGCTCCCTCCCGAGGGCGCC 19015    C       CT  G
                                CGGC CCCTCCCGAG  GG GCC
                                |||| ||||||||||  || |||
                                GTCG GGGAGGGCTC  CC CGG
                                  A        __ G
GAM719  KIAA0731 5' CGGCCCCCTCCCAGTTGGCCCC 19016          A______  TGGG
           G                   CGGCCCCCTCCCG      GC   G
                               ||||||||||||       ||   |
                               GCCGGGGGAGGGT      CG   C
                                     CAAIIIC  GGGT
GAM719  KIAA0876 3' CTCCCTGAGTCTGGGGCC   19017     _  _
                               CTCCC GAG CTGGGGCC
                               ||||| ||| ||||||||
                               GAGGG CTC GACCCCGG
                                  A  A
GAM719  KIAA1001 3' CAGCCTCCCAAGTAGCTGGGG 19018     _  TCCCG
                               CGGCC CCC    AGCTGGGG
                               ||||| |||    ||||||||
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                              GTCGG GGG    TCGACCCC
                                A  TTCA_
GAM719  KIAA1023 3' GGCTTCTGAGCCTGGGGCC  19019    CCCC CC  _
                              GGC   TC  GAGC TGGGGCC
                              |||   ||  |||| |||||||
                              CCG   AG  CTCG ACCCCGG
                               A___  A_   G
GAM719  KIAA1086 3' CGGCCCCTCCCCGGG      19020       C   GAGC
                              CGGCCCC TCCC   TGGG
                              ||||||| ||||   ||||
                              GCCGGGG AGGG   GCCC
                                 _   ____
GAM719  KIAA1115 3' CGGCCCCCACTCGGGAC    19021       TCCCGA  _
                              CGGCCCCC    GCT GGGGC
                              ||||||||    ||| |||||
                              GCCGGGGG    TGA CCCTG
                                 _______  G
GAM719  KIAA1160 3' CGGCCTCCCAAAGTGCTGGGG 18914     CCC    ___
                              CGGCC  TCCCGA  GCTGGGG
                              |||||  ||||||  |||||||
                              GCCGG  AGGGTT  CGACCCC
                                 ___    TCA
GAM719  KIAA1171 5' CAGCCCCCTTTCTGAGG    19022       CCCGAG
                              CGGCCCCCT    CTGGGG
                              |||||||||    ||||||
                              GTCGGGGGA    GACTCC
                                 AA____
GAM719  KIAA1196 3' CGGCCCCTCCCGGGG      19023       C    AGCT
                              CGGCCCC TCCCG   GGG
                              ||||||| |||||   |||
                              GCCGGGG AGGGC   CCC
                                 _   ____
GAM719  KIAA1238 5' CGACTGAGCCGGGCTGGGGCC 19024     CCCCTC  A
                              CGGC    CCG GCTGGGGCC
                              ||||    ||| |||||||||
                              GCTG    GGC CGACCCCGG
                                ACTC__  C
GAM719  KIAA1297 5' CAGCTTCGAGCTGGGGC    19025     CCCCTCC
                              CGGC     CGAGCTGGGGC
                              ||||     ||||||||||
                              GTCG     GCTCGACCCCG
                                AA_____
GAM719  KIAA1303 3' CGGCGCTCTCTCGAGCCGG   19026     CCC  C
                              CGGC  CTC CGAGCTGG
                              ||||  ||| ||||||||
                              GCCG  GAG GCTCGGCC
                                CGA  A
GAM719  KIAA1735 5' GGTCCCCCTCCTGTCTCGGGC 19027   _      CGAG  G
                              GG CCCCCTCC   CT GGGC
                              || ||||||||   || ||||
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                                CC GGGGGAGG   GA CCCG
                                 A       ACA_  G
GAM719  KIAA1813  5'  GGCCCCTCTGTAGGGCTGGGGC 19028       _  CCCGA
                                GGCCCC CT    GCTGGGGC
                                |||||| ||    ||||||||
                                CCGGGG GA    CGACCCCG
                                   A  CATCC
GAM719  KIAA1862  3'  GGCCACTTCCTGAGCCAGGCC  19029     CCC   C    TG  G
                                GGCC   TCC GAGC  GG CC
                                ||||   ||| ||||  || ||
                                CCGG   AGG CTCG  CC GG
                                  TGA   A    GT  _
GAM719  KIF13B   3'  CGGCCCCCGTCTGGGGC     19030        TCCCGAG
                                CGGCCCCC      CTGGGGC
                                ||||||||      |||||||
                                GCCGGGGG      GACCCCG
                                     CA_____
GAM719  MAPKAP1   3'  GGCCTCCCCCCGAGGAC     19031      C       GCTG
                                GGCC CCTCCCGA   GGGC
                                |||| ||||||||   ||||
                                CCGG GGGGGGCT   CCTG
                                  A      _____
GAM719  MGC11271  5'  CGTCTCCCTCCTCCTGGGGCC  19033    GCC     CGAG
                                CG   CCCTCC   CTGGGGCC
                                ||   ||||||   ||||||||
                                GC   GGGAGG   GACCCCGG
                                 AGA     AG__
GAM719  MGC11271  5'  GGGCCCCTCCCTCCTGGGG   19032    C       GAG
                                GG CCCCTCCC   CTGGGG
                                || ||||||||   ||||||
                                CC GGGGAGGG   GACCCC
                                 C       AG_
GAM719  MGC15631  5'  CGGTTCCCTCCACTGGGGCC   19034     CC     CGA
                                CGG  CCCTCC   GCTGGGGCC
                                |||  ||||||   |||||||||
                                GCC  GGGAGG   TGACCCCGG
                                  AA     ___
GAM719  MGC20258  3'  GGCCCCCTCCCATCCCTG     19035          AG_
                                GGCCCCCTCCCG   CTG
                                ||||||||||||   |||
                                CCGGGGGAGGGT   GAC
                                       AGG
GAM719  MGC2376   3'  GGACCCCAAGCTGGGGC     19036    C   TCCC
                                GG CCCC    GAGCTGGGGC
                                || ||||    ||||||||||
                                CC GGGG    TTCGACCCCG
                                 T   _____
GAM719  MGC29643  5'  GGCTGCCGAGGCTGCTGGGGCC 19037     CCCCTC   _____
                                GGC     CCGA    GCTGGGGCC
                                |||     ||||    |||||||||
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                                CCG     GGCT    CGACCCCGG
                                  AC____    CCGA
GAM719  MGC4368  3' CAGCCCCCTCCTGCCAGG    19038          CGA  TG
                                CGGCCCCCTCC   GC  GG
                                ||||||||||   ||  ||
                                GTCGGGGGAGG   CG  CC
                                      A__  GT
GAM719  MGC9753  3' GGCCCCTGCCTGCCCTGGGGCC 19039       CT  CGAG
                                GGCCCC  CC    CTGGGGCC
                                ||||||  ||    ||||||||
                                CCGGGG  GG    GACCCCGG
                                   AC  ACGG
GAM719  NLI-IF   5' CGGCCTCCCCCCCGGCTGGGGC 19040       _       A
            C                    CGGCC CCCTCCCG GCTGGGGCC
                                |||||  |||||||| |||||||||
                                GCCGG GGGGGGGC CGACCCCGG
                                   A       _
GAM719  NPEPL1   3' CGGTCCCCTCCCCGTGGC    19041     C       GAGC  G
                                CGG CCCCTCCC    TG GGC
                                |||  ||||||||    || |||
                                GCC GGGGAGGG    GC CCG
                                  A       _____  A
GAM719  P450RAI-2 3' CGGCCCCCTCCCACACACAGG  19042           A  _
                                CGGCCCCCTCCCG GC TGGG
                                ||||||||||||| || ||||
                                GCCGGGGGAGGGT TG GTCC
                                      G  T
GAM719  PCBP4    3' GGCCCCCTGCCCTGGGGC    19043        _  GAGC
                                GGCCCCCT CCC    TGGGGC
                                ||||||||  |||    ||||||
                                CCGGGGGA GGG    ACCCCG
                                   C  _____
GAM719  PCBP4    3' GGCCCCCTGCCCTGGGGC    19043        _  GAGC
                                GGCCCCCT CCC    TGGGGC
                                ||||||||  |||    ||||||
                                CCGGGGGA GGG    ACCCCG
                                   C  _____
GAM719  PCBP4    3' GGCCCCCTGCCCTGGGGC    19043        _  GAGC
                                GGCCCCCT CCC    TGGGGC
                                ||||||||  |||    ||||||
                                CCGGGGGA GGG    ACCCCG
                                   C  _____
GAM719  PCBP4    5' CGGCTCTCGCTGGGGC      19044      CCC   CCGA
                                CGGC   CTC    GCTGGGGC
                                ||||   |||    ||||||||
                                GCCG   GAG    CGACCCCG
                                  A__   _____
GAM719  PEPP3    5' GGCCCCCTTCTGCAGAGCGGGG 19045        _ CC__    T
            C                    GGCCCCCT C    GAGC GGGGC
                                |||||||| |    |||| |||||
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                                CCGGGGGA G   CTCG CCCCG
                                   A ACGT   _
GAM719  PIP5K2B  3'  GGCCCCTTCCTGGGGC     19046      C  CGAGC
                                GGCCCC TCC   TGGGGC
                                |||||| |||    ||||||
                                CCGGGG AGG    ACCCCG
                                   A  _____
GAM719  PIP5K2B  3'  GGCCCCTTCCTGGGGC     19046      C  CGAGC
                                GGCCCC TCC   TGGGGC
                                |||||| |||    ||||||
                                CCGGGG AGG    ACCCCG
                                   A  _____
GAM719  PLA2G6   3'  GGCCCTCAGGGAGGCTGGGGC  19047     CCTCCC  _
                                GGCCC    GAG CTGGGGC
                                |||||     ||| |||||||
                                CCGGG    CTC GACCCCG
                                   AGTCC_  C
GAM719  PRKWNK2  5'  GCCTCCTCCCTGGGGC     19048    C    GAGC
                                GCC CCTCCC   TGGGGC
                                ||| ||||||   ||||||
                                CGG GGAGGG   ACCCCG
                                  A    ____
GAM719  PRO0149  3'  CGGCCCCCTCTCAGCGAAGA  19049       C G  TG
                                CGGCCCCCTC C AGC  GGG
                                |||||||||| | |||  |||
                                GCCGGGGGAG G TCG  TCT
                                     A _  CT
GAM719  PRSS21   5'  GCCTCCTCTCGCGCCGGGCC  19050    C   C A    G
                                GCC CCTC CG GCTGGG CC
                                ||| |||| || |||||| ||
                                CGG GGAG GC CGGCCC GG
                                  A   A G    _
GAM719  PRSS21   5'  GCCTCCTCTCGCGCCGGGCC  19050    C   C A    G
                                GCC CCTC CG GCTGGG CC
                                ||| |||| || |||||| ||
                                CGG GGAG GC CGGCCC GG
                                  A   A G    _
GAM719  PTRF     3'  CGGCCTCCCAAAGTGCTGGGG  18914     CCC    ___
                                CGGCC  TCCCGA  GCTGGGG
                                |||||  ||||||  |||||||
                                GCCGG  AGGGTT  CGACCCC
                                   ___    TCA
GAM719  RASGRP4  5'  CAGCCCCTAGGGAGCTGGGGCC 19051       CTCCC
                                CGGCCCC   GAGCTGGGGCC
                                |||||||   ||||||||||
                                GTCGGGG   CTCGACCCCGG
                                   ATCC_
GAM719  RASSF2   3'  GGCTCCCTTGCTGAGGC    19052    CCCC   GA
                                GGC   TCCC  GCTGGGGC
                                |||   ||||  ||||||||
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                              CCG   AGGG  CGACTCCG
                                ____   AA
GAM719  RLUCL   3' CAGCTCCCAAGCTGGGG    19053     CCCC
                              CGGC   TCCCGAGCTGGGG
                              ||||   ||||||||||||
                              GTCG   AGGGTTCGACCCC
                                ____
GAM719  RNF40   3' GGCCCAGCGGCTGGGGC    19054     CCTCC  A
                              GGCCC    CG GCTGGGGC
                              |||||    || ||||||||
                              CCGGG    GC CGACCCCG
                                 TC___  _
GAM719  SCYA22  3' CAGCTTCCTCCCAGGGC    19055     CC     GAGCT
                              CGGC  CCTCCC    GGGGC
                              ||||  ||||||    |||||
                              GTCG  GGAGGG    TCCCG
                                AA    _____
GAM719  SEC24C  3' GCCCCCAAGCCAGTTGGGG   19056      TC_  G  C
                              GCCCCC   CC AG TGGGG
                              ||||||   || || |||||
                              CGGGGG   GG TC ACCCC
                                 TTC  _  A
GAM719  SEC61A1 3' CAGTCCCCTGGAAGCTGGGG  19057    C    CCC
                              CGG CCCCT   GAGCTGGGG
                              ||| |||||   |||||||||
                              GTC GGGGA   TTCGACCCC
                                A    CC_
GAM719  SH3BGRL2 5' GGCTCCCTCCCGGCGGG    19058    C      A  T
                              GGC CCCTCCCG GC GGG
                              ||| ||||||| || |||
                              CCG GGGAGGGC CG CCC
                                A      _ _
GAM719  SHANK3  3' GGCGAGGGGCCGAGCTGGGGCC 19059    CCCCTC
                              GGC     CCGAGCTGGGGCC
                              |||     ||||||||||||
                              CCG     GGCTCGACCCCGG
                                CTCCCC
GAM719  SIAT4A  3' CAGCCTCCCTAGTAGCTGGGGC 19060      _   CCCG
                              CGGCC CCCT    AGCTGGGGC
                              ||||| ||||    |||||||||
                              GTCGG GGGA    TCGACCCCG
                                 A    TCA_
GAM719  SPINT1  5' CGGTGCTCGGAGAGCTGGGGC  19061    CCCC   CC_
                              CGG   CTC   GAGCTGGGGC
                              |||   |||   ||||||||||
                              GCC   GAG   CTCGACCCCG
                                AC__   CCT
GAM719  SPRY4   3' CGACTCCCCTGCTGGGGC    19062     _    CCCGA
                              CGGC CCCCT    GCTGGGGC
                              |||| |||||    ||||||||
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                                GCTG GGGGA    CGACCCCG
                                  A   _____
GAM719  SPS     5' GCCTTCCTCCCGAAAACGGCC 19063    C_      CTGG
                                GCC CCTCCCGAG   GGCC
                                ||| |||||||||   ||||
                                CGG GGAGGGCTT   CCGG
                                  AA       TTG_
GAM719  SSBP3   5' CGGCCCCCTCCCCGGCGC   19064         GAGC  G
                                CGGCCCCCTCCC   TGG GC
                                ||||||||||||   ||| ||
                                GCCGGGGGAGGG   GCC CG
                                       _____  G
GAM719  SSH-3   3' CAGCCTCCCGCGGCTGGGGCC 19065     CCC   A_
                                CGGCC  TCCCG GCTGGGGCC
                                |||||  ||||| |||||||||
                                GTCGG  AGGGC CGACCCCGG
                                  ___    GC
GAM719  SSH-3   3' CAGCCTCCCGCGGCTGGGGCC 19065     CCC   A_
                                CGGCC  TCCCG GCTGGGGCC
                                |||||  ||||| |||||||||
                                GTCGG  AGGGC CGACCCCGG
                                  ___    GC
GAM719  STATI2  5' GGCCGCCCGAGCTGGGG    19066    CCCT
                                GGCC   CCCGAGCTGGGG
                                ||||   ||||||||||||
                                CCGG   GGGCTCGACCCC
                                  C___
GAM719  STATI2  5' GGCCGCCCGAGCTGGGG    19066    CCCT
                                GGCC   CCCGAGCTGGGG
                                ||||   ||||||||||||
                                CCGG   GGGCTCGACCCC
                                  C___
GAM719  STK17B  5' GCCCCCTCCAGGGGGC     19067       CG  CT
                                GCCCCCTCC  AG  GGGGC
                                |||||||||  ||  |||||
                                CGGGGGAGG  TC  CCCCG
                                       __  __
GAM719  STK29   3' GGCCTTCCTCCCACGGGCC   19068    C_    AGCTG
                                GGCC  CCTCCCG    GGGCC
                                ||||  |||||||    |||||
                                CCGG  GGAGGGT    CCCGG
                                  AA     G_____
GAM719  SYT12   3' GCTCTCCTCCTACTGGGGC   19069   CC_   CGA
                                GC   CCTCC   GCTGGGGC
                                ||   |||||   ||||||||
                                CG   GGAGG   TGACCCCG
                                 AGA    A__
GAM719  TETRAN  3' CGGCCCCCACCCACAGGG    19070       T   AGCT
                                CGGCCCCC CCCG   GGG
                                |||||||| ||||   |||
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                                GCCGGGGG GGGT   CCC
                                    T   GT__
GAM719  THG-1    3'  GGTTCCCTCCCAGAGGGGGC  19071   CC     _  CT
                                GG  CCCTCCC GAG  GGGGC
                                ||  ||||||| |||  |||||
                                CC  GGGAGGG CTC  CCCCG
                                 AA      T  __
GAM719  TIP-1    3'  AGCCCTTCTGAGCTGGGGCC  19072     CC  CC
                                GGCCC  TC  GAGCTGGGGCC
                                |||||  ||  ||||||||||
                                TCGGG  AG  CTCGACCCCGG
                                  A_  A_
GAM719  U5-116KD 3'  GCTCCTCTCTCACTGGGGC   19073   _  C   CCGA
                                GC CC CTC   GCTGGGGC
                                || || |||   ||||||||
                                CG GG GAG   TGACCCCG
                                 A  A   AG__
GAM719  UPLC1    3'  GGCCCATTCCTGCCAGGGCC  19074     CC   CGA  TG
                                GGCCC  TCC   GC  GGGCC
                                |||||  |||   ||  |||||
                                CCGGG  AGG   CG  CCCGG
                                   TA   A__  GT
GAM719  VI       3'  CAGCCTCCTCCTGAAGC     19075      C    CGAGC
                                CGGCC CCTCC    TGGGGC
                                ||||| |||||    ||||||
                                GTCGG GGAGG    ACTTCG
                                  A    _____
GAM719  ZAK      3'  CAGCCTCCCTAGTAGCTGGGG  19076      _   CCCG
                                CGGCC CCCT   AGCTGGGG
                                ||||| ||||   ||||||||
                                GTCGG GGGA   TCGACCCC
                                  A   TCA_
GAM719  ZNF263   3'  GGCTTCCCAACTGGGGC    19077    CCCC   G
                                GGC   TCCC AGCTGGGGC
                                |||   |||| |||||||||
                                CCG   AGGG TTGACCCCG
                                 A___   _
GAM719  LOC116071 3'  GGCCTCTACCCACCAGGGC   19078     CC  _  GA  TG
                                GGCC  CT CCC  GC  GGGC
                                ||||  || |||  ||  ||||
                                CCGG  GA GGG  TG  CCCG
                                  A_  T   __  GT
GAM719  LOC124222 3'  GCCCTTGAAAGCTGGGGCC   19080     CCTCCC
                                GCCC     GAGCTGGGGCC
                                ||||     ||||||||||
                                CGGG     TTCGACCCCGG
                                  AACT__
GAM719  LOC124222 5'  AGCCTCCTCCTCAGTGGGGCC  19079     C    CG  C
                                GGCC CCTCC  AG TGGGGCC
                                |||| |||||  || |||||||
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                                TCGG GGAGG  TC ACCCCGG
                                  A    AG  _
GAM719  LOC124944 5'  CAGCCCTCTCCACGGGGGCC  19081      C   CGA  T
                                CGGCCC CTCC  GC GGGGCC
                                |||||| ||||  || ||||||
                                GTCGGG GAGG  TG CCCCGG
                                   A   ___  C
GAM719  LOC127829 5'  CGGCCCCTCCCCGGTACGGCC  19082       CT   AGC  G
                                CGGCCCC  CCCG  TG GGCC
                                |||||||  ||||  || ||||
                                GCCGGGG  GGGC  AT CCGG
                                   AG   C__  G
GAM719  LOC127943 5'  GCCTCCCTCCCGGGGC      19083    _     GAGCT
                                GCC CCCTCCC    GGGGC
                                ||| |||||||    |||||
                                CGG GGGAGGG    CCCCG
                                  A     _____
GAM719  LOC128916 5'  CAGCCTTCTTGCTCTGGGGCC  19084      CC  CCCGAG
                                CGGCC  CT     CTGGGGCC
                                |||||  ||     ||||||||
                                GTCGG  GA     GACCCCGG
                                   AA  ACGA__
GAM719  LOC138311 3'  GCCTTTGCTCCGAGCTGGGG  19085     CC__   C
                                GCC   CTCC GAGCTGGGG
                                |||   |||| |||||||||
                                CGG   GAGG CTCGACCCC
                                  AAAC   _
GAM719  LOC138389 3'  GGCCCCTCCCTCCGAAACTGGG 19086       _  _   _
          GC                    GGCCCC CTC CCGAG CTGGGGC
                                |||||| ||| ||||| |||||||
                                CCGGGG GGG GGCTT GACCCCG
                                   A  A   T
GAM719  LOC138623 3'  CGGCCGTCGGGGCTGGGGC   19087      CCCTCC  A_
                                CGGCC     CG  GCTGGGGC
                                |||||     ||  ||||||||
                                GCCGG     GC  CGACCCCG
                                   CA____  CC
GAM719  LOC144543 5'  GCCCCTTCCCCGCGGGGC    19088      C   GA  T
                                GCCCC TCCC  GC GGGGC
                                ||||| ||||  || |||||
                                CGGGG AGGG  CG CCCCG
                                   A   G_  _
GAM719  LOC145225 3'  GGCCCTTTAGCAGAGCTGGGGC 19089      CCTCCC_
          C                     GGCCC      GAGCTGGGGCC
                                |||||      ||||||||||
                                CCGGG      CTCGACCCCGG
                                   AAATCGT
GAM719  LOC145438 3'  CAGCCTCCTGAGTAGCTGGGGC 19090      C   CCCG
                                CGGCC CCT    AGCTGGGGC
                                ||||| |||    |||||||||
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                                GTCGG GGA   TCGACCCCG
                                  A  CTCA
GAM719  LOC145566 5' GGCTCCCCCGAGGGGC     19091    CC  T    GCT
                                GGC  CC CCCGA  GGGGC
                                |||  || |||||  |||||
                                CCG  GG GGGCT  CCCCG
                                 A_  _   ___
GAM719  LOC145567 5' CGGACCTCAGTCAGCTGGGGC 19092    CCC   CCG_
                                CGG  CCTC   AGCTGGGGC
                                |||  ||||   |||||||||
                                GCC  GGAG   TCGACCCCG
                                 T__   TCAG
GAM719  LOC145858 5' GGTTCCCAGCTGGGGC     19093    CCCCC   G
                                GG    TCCC AGCTGGGGC
                                ||    |||| |||||||||
                                CC    AGGG TCGACCCCG
                                 A____  _
GAM719  LOC146433 3' GGTCCTCTCCCAAGGGGGGC  19094    C  C      CT
                                GG CC CTCCCGAG  GGGGC
                                || || ||||||||  |||||
                                CC GG GAGGGTTC  CCCCG
                                 A  A      C_
GAM719  LOC148166 3' CAGCCTCCCGAGTAGCTGGGGC 18987      CCC    ___
                                CGGCC  TCCCGA  GCTGGGGC
                                |||||  ||||||  ||||||||
                                GTCGG  AGGGCT  CGACCCCG
                                   ___    CAT
GAM719  LOC148223 3' GCCCCCTCCCCCAGGGC    19095        GAG TG
                                GCCCCCTCCC  C  GGGC
                                ||||||||||  |  ||||
                                CGGGGGAGGG  G  CCCG
                                      ___ GT
GAM719  LOC148254 3' CAGCCTCCCAAGTAGCTGGGG  19018     _  TCCCG
                                CGGCC CCC    AGCTGGGG
                                ||||| |||    ||||||||
                                GTCGG GGG    TCGACCCC
                                   A  TTCA_
GAM719  LOC148430 5' CGGTTCCCTATCCCAGGGCC  19096    CC  __   GAGCT
                                CGG  CCC  TCCC    GGGGCC
                                |||  |||  ||||    ||||||
                                GCC  GGG  AGGG    TCCCGG
                                 AA  AT   _____
GAM719  LOC149076 3' GGCCCCCGGAGGGAGCTGGGGC 19097       TCCC_
           C                     GGCCCCC    GAGCTGGGGCC
                                |||||||    ||||||||||
                                CCGGGGG    CTCGACCCCGG
                                    CCTCC
GAM719  LOC149668 3' GGCCCCCTCCTGCAAGGCC   19098        CGA  T
                                GGCCCCCTCC   GC GGGGCC
                                ||||||||||   || ||||||
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                                CCGGGGGAGG  CG TTCCGG
                                     A__  _
GAM719  LOC150150 5'  GCTCCTTCCTCGTTCTGGGGCC 19099    C  C  _  AG
                                GC CC TCC CG  CTGGGGCC
                                || || ||| ||  ||||||||
                                CG GG AGG GC  GACCCCGG
                                 A  A   A  AA
GAM719  LOC150225 3'  GGCTCCCTCCCCGGGGCC    19100     C      GAGC
                                GGC CCCTCCC    TGGGGCC
                                ||| |||||||    |||||||
                                CCG GGGAGGG    GCCCCGG
                                  A      _____
GAM719  LOC150517 5'  CGGCCCCCTCCCAGGCGC    19101           AGCT  G
                                CGGCCCCCTCCCG   GG GC
                                ||||||||||||    || ||
                                GCCGGGGGAGGGT   CC CG
                                      _____ G
GAM719  LOC151176 5'  CGGCCCCCTCCTCGGCGGC   19102          _  A  TGG
                                CGGCCCCCTCC CG GC   GGC
                                |||||||||| || ||   |||
                                GCCGGGGGAGG GC CG   CCG
                                      A  _  ___
GAM719  LOC151760 5'  CGGCTCTCCTGCTGGGGCC   19103     CCC    CGA
                                CGGC   CTCC   GCTGGGGCC
                                ||||   ||||   |||||||||
                                GCCG   GAGG   CGACCCCGG
                                  A__    A__
GAM719  LOC155179 3'  GGCTTCTGAGCCTGGGGCC   19019     CCCC  CC   _
                                GGC    TC  GAGC TGGGGCC
                                |||    ||  |||| |||||||
                                CCG    AG  CTCG ACCCCGG
                                  A___  A_   G
GAM719  LOC158987 3'  CAGCCTCCCAAGTAGCTGGGGC 18879      _  TCCCG
                                CGGCC CCC    AGCTGGGGC
                                ||||| |||    |||||||||
                                GTCGG GGG    TCGACCCCG
                                   A  TTCA_
GAM719  LOC196403 3'  GCTCCTCCCGAAGCCGGGCC   19104    CC      _     G
                                GC  CCTCCCGA GCTGGG CC
                                ||  |||||||| |||||| ||
                                CG  GGAGGGCT CGGCCC GG
                                 A_       T     _
GAM719  LOC203069 5'  GGGTCCCTGCCAGCTGGGGCC  19105    CC    C  G
                                GG  CCCT CC AGCTGGGGCC
                                ||  |||| || ||||||||||
                                CC  GGGA GG TCGACCCCGG
                                 CA   C  _
GAM719  LOC219654 5'  CGGCCCCTCCCCGGCCGC    19106       CT    A   GGG
                                CGGCCCC  CCCG GCT   GC
                                |||||||  |||| |||   ||
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                                GCCGGGG  GGGC CGG   CG
                                   AG   _  ___
GAM719  LOC219686 5'  GCCTCCTCCTCCGGGGC     19107     C    CGAG
                                GCC CCTCC    CTGGGGC
                                ||| |||||    |||||||
                                CGG GGAGG    GGCCCCG
                                  A    A___
GAM719  LOC219908 5'  CGGCGCCCTCTTTGCCGGG    19108     C    CCGA
                                CGGC CCCTC    GCTGGG
                                |||| |||||    ||||||
                                GCCG GGGAG    CGGCCC
                                  C    AAA_
GAM719  LOC220370 3'  CAGCCTCCCAAATAGCTGGGG  19109      _  TCCCG
                                CGGCC CCC    AGCTGGGG
                                ||||| |||    ||||||||
                                GTCGG GGG    TCGACCCC
                                   A   TTTA_
GAM719  LOC221271 5'  CGGCTCATTCTCCGCCGGGGCC 19110     CCC__   CGA
                                CGGC    CTCC   GCTGGGGCC
                                ||||    ||||   |||||||||
                                GCCG    GAGG   CGGCCCCGG
                                  AGTAA   ___
GAM719  LOC221465 3'  GGCCCCCTCCCTGGCGGGCC   19111         GA  TG
                                GGCCCCCTCCC  GC  GGGCC
                                ||||||||||  ||  |||||
                                CCGGGGGAGGG  CG  CCCGG
                                      AC  __
GAM719  LOC221935 3'  GGTCCCCTCTCCCTGGGGCC   19112    _   _    GAGC
                                GG CCCC CTCCC    TGGGGCC
                                || |||| |||||    |||||||
                                CC GGGG GAGGG    ACCCCGG
                                 A   A    _____
GAM719  LOC222066 3'  CAGCCTCCCAAGTAGCTGGGGC 18879      _  TCCCG
                                CGGCC CCC    AGCTGGGGC
                                ||||| |||    |||||||||
                                GTCGG GGG    TCGACCCCG
                                   A   TTCA_
GAM719  LOC222488 5'  CAGCCTCCCAGCTGGGG     19113      CCC   G
                                CGGCC   TCCC AGCTGGGG
                                |||||   |||| ||||||||
                                GTCGG   AGGG TCGACCCC
                                   ___   _
GAM719  LOC254100 3'  CGGCCTCCCAATGTGCTGGGG  19114      CCC    ___
                                CGGCC   TCCCGA   GCTGGGG
                                |||||   ||||||   |||||||
                                GCCGG   AGGGTT   CGACCCC
                                   ___     ACA
GAM719  LOC254158 5'  GCCCCCTCTCGGCAGC      19115        C  A  TGG
                                GCCCCCTC CG GC   GGC
                                |||||||| || ||   |||
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                                CGGGGGAG GC CG   TCG
                                    A  _ ___
GAM719  LOC254402 5'  GGCTCCCTGGCTCCCTGGGGCC 19116    _  ___    GAGC
                                GGC CCC   CTCCC    TGGGGCC
                                ||| |||   |||||    |||||||
                                CCG GGG   GAGGG    ACCCCGG
                                  A   ACC    ____
GAM719  LOC256277 3'  GGCCCCCTCCTCATCACTG    19117          _  A_
                                GGCCCCCTCC CG  GCTG
                                |||||||||| ||  ||||
                                CCGGGGGAGG GT  TGAC
                                      A  AG
GAM719  LOC256475 5'  GGCCCCCTCCAGTTGAGGCC   19118          CG  C
                                GGCCCCCTCC  AG TGGGGCC
                                ||||||||||  || |||||||
                                CCGGGGGAGG  TC ACTCCGG
                                      __  A
GAM719  LOC256740 5'  CGGCTCCGGCTGGGGC      19119      CCCCTC   A
                                CGGC      CCG GCTGGGGC
                                ||||      ||| ||||||||
                                GCCG      GGC CGACCCCG
                                  A_____   _
GAM719  LOC257054 3'  GGCCCTTGTCCGTGCCGGGGCC 19120       CCTC   A
                                GGCCC    CCG GCTGGGGCC
                                |||||    ||| |||||||||
                                CCGGG    GGC CGGCCCCGG
                                   AACA   A
GAM719  LOC51107  3'  GGACCCCGGGCTGGGGC     19121    C    TCCC A
                                GG CCCC    G GCTGGGGC
                                || ||||    | ||||||||
                                CC GGGG    C CGACCCCG
                                 T    _____ C
GAM719  LOC65243  5'  CAGCCCCCTCTCCCCGCTGGGC 19122          _  GA     G
          C                      CGGCCCCCTC CC  GCTGGG CC
                                |||||||||| ||  |||||| ||
                                GTCGGGGGAG GG  CGACCC GG
                                      A  GG     _
GAM719  LOC84528  5'  GCAGATTCTGAGCTGGGGCC   19123    CCCC  CC
                                GC    TC  GAGCTGGGGCC
                                ||    ||  ||||||||||
                                CG    AG  CTCGACCCCGG
                                 TCTA  A_
GAM719  LOC86010  5'  CGGCCCCCTCCCCGGCGC    19064          GAGC   G
                                CGGCCCCCTCCC    TGG GC
                                ||||||||||||    ||| ||
                                GCCGGGGGAGGG    GCC CG
                                       _____  G
GAM719  LOC90850  5'  CGGCCCCCCCTCTCGGCCGG   19124        _  C  A
                                CGGCCCCC TC CG GCTGG
                                |||||||| || || |||||
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                                GCCGGGGG AG GC CGGCC
                                    G  A  _
GAM719  LOC91301  5' CAGCCCCTTCCCGGAAGGCC  19125       C    AGCT
                                CGGCCCC TCCCG   GGGGCC
                                ||||||| |||||   ||||||
                                GTCGGGG AGGGC   TTCCGG
                                   A    C___
GAM719  LOC91813  5' AGCCCCCTTCTGGGAC     19126       CCCGAG
                                GGCCCCCT    CTGGGGC
                                ||||||||    |||||||
                                TCGGGGGA    GACCCTG
                                   A_____
GAM719  LOC92299  3' CAGCCTCCCGAGTAGCTGGGGC 18987     CCC    ___
                                CGGCC  TCCCGA  GCTGGGGC
                                |||||  ||||||  ||||||||
                                GTCGG  AGGGCT  CGACCCCG
                                  ___    CAT
GAM719  LOC92360  3' CAGCCTCCCGAGTAGCTGGGG  19127     CCC    ___
                                CGGCC  TCCCGA  GCTGGGG
                                |||||  ||||||  |||||||
                                GTCGG  AGGGCT  CGACCCC
                                  ___    CAT
GAM719  LOC92661  3' CAGCCCTTCAGGCTGGGGC   19128      CC  CCGA
                                CGGCCC  TC   GCTGGGGC
                                ||||||  ||   ||||||||
                                GTCGGG  AG   CGACCCCG
                                   A_  TC__
GAM719  LOC92840  3' CGGCCCCCTCCTCACCAGCC  19129        CGA  GG
                                CGGCCCCCTCC  GCT  GGCC
                                ||||||||||  |||  ||||
                                GCCGGGGGAGG  TGG  TCGG
                                      AG_  __
GAM720  CALCR   3'  CCTGGAAAAGCCTGAG     19132     A  AGCCC
                                CCTG AAA    GGCCTGAG
                                |||| |||    ||||||||
                                GGAC TTT    TCGGACTC
                                  C  _____
GAM720  CEACAM1  3'  CCCTGAAAGAGGTACCTGAG  19133       A  CCCG
                                CCCTGAAA AG   GCCTGAG
                                |||||||| ||   |||||||
                                GGGACTTT TC   TGGACTC
                                    C  CA__
GAM720  CMA1    5'  CCCAGAGAGGCTGCCTGAGC  19134    T  AAAA  CCG
                                CCC GA   GC   GCCTGAGC
                                ||| ||   ||   ||||||||
                                GGG CT   CG   CGGACTCG
                                  T  CTC_  A__
GAM720  CXorf6   3'  CTGAAGAAGCCCAGTTCTG   19135      A      C_
                                CTGAA AAGCCCGG  CTG
                                ||||| ||||||||  |||
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                                GACTT TTCGGGTC  GAC
                                  C       AA
GAM720  CYP46    3'  CCCCTGAAGAGGGCTTTAGGGA 19136        AA  CCC   CT____
              G                   CCCCTGAA  AG   GGC     GAG
                                  ||||||||  ||   |||     |||
                                  GGGGACTT  TC   CCG     CTC
                                      C_  ___   AAATCC
GAM720  EBF      3'  CCTCTTAAAAAGGCCTGAG   19137    _ G    GCCC
                                  CC CT AAAAA    GGCCTGAG
                                  || || |||||    ||||||||
                                  GG GA TTTTT    CCGGACTC
                                   A  A    _____
GAM720  ESRRG    3'  CCCTGAAAAAGTTACATAG    19138          CCCG  CTG
                                  CCCTGAAAAAG    GC   AG
                                  ||||||||||    ||   ||
                                  GGGACTTTTTC    TG   TC
                                        AA__   TA_
GAM720  FCN2     3'  CCCTGAGGCCGGCCTGG     19139       AAAA   C     A
                                  CCCTGA    GCC GGCCTG G
                                  ||||||    ||| |||||| |
                                  GGGACT    CGG CCGGAC C
                                     C___   _     C
GAM720  GAS11    3'  CCCCTGGAGAATCCCACTGGGC 19140       AAAAAG    GC   A
                                  CCCCTG     CCCG  CTG GC
                                  ||||||     ||||  ||| ||
                                  GGGGAC     GGGT  GAC CG
                                     CTCTTA   __   C
GAM720  GNAO1    3'  CTGGAAAGCCCGGCCTGAGC   19141     AA
                                  CTG  AAAGCCCGGCCTGAGC
                                  |||  ||||||||||||||||
                                  GAC  TTTCGGGCCGGACTCG
                                    C_
GAM720  GPRK5    3'  CCTCGGAAAACAGACCTGAG   19142     GAA    CC
                                  CCT   AAAGC  GGCCTGAG
                                  |||   |||||  ||||||||
                                  GGA   TTTTG  CTGGACTC
                                    GCC    T_
GAM720  GRM7     5'  CCTCCGGGAAAGCCCAGGGGC  19143    _   AA      ___
                                  CC CTG  AAAGCCC   GGC
                                  || |||  |||||||   |||
                                  GG GGC  TTTCGGG   CCG
                                   A  CC      TCC
GAM720  HCFC1    3'  CCCCAGCCTCGGAGCCTGGCCT 19144      TGAAAA__   C
              GAG                   CCCC       AGCC GGCCTGAG
                                    ||||       |||| ||||||||
                                    GGGG       TCGG CCGGACTC
                                      TCGGAGCC    A
GAM720  MAGEL2   5'  CCCTGAAAGGGCTGCTCCAGC  19145        AA___  _
                                  CCCTGAAA     GC CCGGC
                                  ||||||||     || |||||
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                                GGGACTTT    CG GGTCG
                                    CCCGA  A
GAM720  MHC2TA   3'  TGAGGAAGCCCAACTAGC    19146    AA       CTG
                                TGA  AAGCCCGGC   AGC
                                |||  |||||||||   |||
                                ACT  TTCGGGTTG   TCG
                                  CC       A__
GAM720  MIR16    3'  CCTAAAAAGCCTGGAAAAG   19147        A   C  CCT
                                CCTGAAAA GCC GG   GAG
                                |||||||| ||| ||   |||
                                GGATTTTT CGG CC   TTC
                                    _   A  TT_
GAM720  NPR1     3'  CCCAGCCCGGCCTGA      19148     TGAAAA
                                CCC     AGCCCGGCCTGA
                                |||     ||||||||||||
                                GGG     TCGGGCCGGACT
                                 _______
GAM720  RNF4     3'  CCCCTGAGAGAACCTGAG    19149       AAA  CCC
                                CCCCTGA   AG   GGCCTGAG
                                |||||||   ||   ||||||||
                                GGGGACT   TC   TTGGACTC
                                   C__  ___
GAM720  SHMT1    3'  CCCCTCAAAGGGCCCGAG    19150      G   AAGCCC
                                CCCCT AAA     GGCCTGAG
                                ||||| |||     ||||||||
                                GGGGA TTT     CCGGGCTC
                                  G   C_____
GAM720  SPOCK    3'  CCTTAGAAAAAGCCCTTGAG   19151     __        GGCC
                                CCT  GAAAAAGCCC    TGAG
                                |||  ||||||||||    ||||
                                GGA  CTTTTTCGGG    ACTC
                                  AT        A___
GAM720  TAP2     3'  CCTGGAAGACCTGAACCCTGAG 19152      AAA  _  C  __
                                CCTG   AAG CC GG  CCTGAG
                                ||||   ||| || ||  ||||||
                                GGAC   TTC GG CT  GGACTC
                                  C__   T  A  TG
GAM720  TEC      3'  CCTGAAAAACGTCCGGGAG   19153        GC_   CCT
                                CCTGAAAAA   CCGG   GAG
                                |||||||||   ||||   |||
                                GGACTTTTT   GGCC   CTC
                                    GCA    ___
GAM720  TMEPAI   3'  CCCTCGGGAAAGCCCGCC    19154     _ AA      G
                                CCCT G  AAAGCCCG CC
                                |||| |  |||||||| ||
                                GGGA C  TTTCGGGC GG
                                  G CC       _
GAM720  WHSC1    5'  CCTCCGGGAAAGCCCAAGGC   19155    _   AA      __
                                CC CTG  AAAGCCC  GGC
                                || |||  |||||||  |||
```

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                                GG GGC  TTTCGGG  CCG
                                 A  CC      TT
GAM720  WHSC1    3'  CCTCCGGGAAAGCCCAAGGC  19155   _  AA     __
                                CC CTG  AAAGCCC  GGC
                                || |||  |||||||  |||
                                GG GGC  TTTCGGG  CCG
                                 A  CC      TT
GAM720  WHSC1    3'  CCTCCGGGAAAGCCCAAGGC  19155   _  AA     __
                                CC CTG  AAAGCCC  GGC
                                || |||  |||||||  |||
                                GG GGC  TTTCGGG  CCG
                                 A  CC      TT
GAM720  ZNF24    3'  CTGAAGAAAAAGACCTGAG   19156      A  CCC
                                CTGAA AAG   GGCCTGAG
                                ||||| |||   ||||||||
                                GACTT TTT   CTGGACTC
                                   C   TT_
GAM720  7h3      3'  CCAGGAGCTCGGCCTGAGC   19157    TGAAAA  C
                                CC     AGC CGGCCTGAGC
                                ||     ||| ||||||||||
                                GG     TCG GCCGGACTCG
                                 TCC___   A
GAM720  ACTR1A   3'  CCCCCGAAAGGGGACTGG    19158        AAGCCC  C   A
                                CCCCTGAAA     GG CTG G
                                |||||||||     || ||| |
                                GGGGGCTTT     CC GAC C
                                      CC____  T   C
GAM720  BCAN     3'  CCCTTGGAAAACCCAGAAAGAG 19159     GAA       CCT
                                CCCT   AAAGCCCGG   GAG
                                ||||   |||||||||   |||
                                GGGA   TTTTGGGTC   CTC
                                  ACC        TTT
GAM720  BS69     3'  CCCCTGAAAAACTTCGGAGGAG 19160         GCC   CCT
           C                     CCCCTGAAAAA   CGG   GAGC
                                ||||||||||   |||   ||||
                                GGGGACTTTTT   GCC   CTCG
                                      GAA   TC_
GAM720  CLDN8    3'  CCCTGAAAAGCAATAGTTGAG  19161        A  CC_  CC
                                CCCTGAAAA GC   GG  TGAG
                                ||||||||| ||   ||  ||||
                                GGGACTTTT CG   TC  ACTC
                                     _  TTA  A_
GAM720  COLEC12  3'  CCCGCTGGGAGCAGCCTGAGC  19162    _  AAAA   CC
                                CCC CTG   AGC  GGCCTGAGC
                                ||| |||   |||  |||||||||
                                GGG GAC   TCG  TCGGACTCG
                                  C   CC__   __
GAM720  DKFZp434K2435 3'  CCTAGAAAAAGCATGTTGAGC  19163    _      CCGGCC
                                CCT GAAAAAGC     TGAGC
                                ||| ||||||||     |||||
```

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                                GGA CTTTTTCG     ACTCG
                                  T       TACA__
GAM720  DKFZP586M1120 3'  CCCCTGAGAGCCAGGCCTGAGC 19165        AAA   C
                                CCCCTGA   AGCC GGCCTGAGC
                                |||||||   |||| |||||||||
                                GGGGACT   TCGG CCGGACTCG
                                    C__   T
GAM720  DKFZP586M1120 3'  CCTGAAAAGGCTGGGAG     19164        A  CC  CCT
                                CCTGAAAA GC  GG   GAG
                                |||||||| ||  ||   |||
                                GGACTTTT CG  CC   CTC
                                     C  A_  ___
GAM720  DKFZp761F2014 3'  CCTGAAAAGCTCCACCTGGC   19166        A  _   G    A
                                CCTGAAAA GC CCG CCTG GC
                                |||||||| || ||| |||| ||
                                GGACTTTT CG GGT GGAC CG
                                     _  A   _   _
GAM720  FBP17    3'  CCTCTAAGAAGCCCGGCTGGGG 19167    _    AA       C  A_
              C                   CC CTGA  AAGCCCGGC TG  GC
                                || ||||  ||||||||| ||  ||
                                GG GATT  TTCGGGCCG AC  CG
                                 A   C_       _  CC
GAM720  FLJ12788  3'  CCCTTTGAAGGGTCCTGGGGC  19168     GAAA   CCC  _    A_
                                CCCT    AAG   GG CCTG  GC
                                ||||    |||   || ||||  ||
                                GGGA    TTC   CC GGAC  CG
                                  AAC_   ___  A    CC
GAM720  FLJ13111  3'  CCCCTGAAGATGCTCCTGGC   19169        AAA  _  _
                                CCCCTGAA   GC CC GGC
                                ||||||||   || || |||
                                GGGGACTT   CG GG CCG
                                     CTA  A  A
GAM720  FLJ13902  3'  CCCCTGGTGAAGTCCCTGGC   19170       AAA   _   _
                                CCCCTG   AAG CCC GGC
                                ||||||   ||| ||| |||
                                GGGGAC   TTC GGG CCG
                                    CAC   A   A
GAM720  FLJ14100  5'  CCCTGAGAAGGCCCAAGAG    19171       A  A     CCT
                                CCCTGA AA GCCCGG   GAG
                                |||||| || ||||||   |||
                                GGGACT TT CGGGTT   CTC
                                    C  C     ___
GAM720  FLJ32384  3'  CCTTGAGACCCAGCTGGCCTGA 19172    C   AAAA   ____
              G                   CC TGA    GCCC    GGCCTGAG
                                || |||    ||||    ||||||||
                                GG ACT    TGGG    CCGGACTC
                                 A  C___    TCGA
GAM720  GPS2     5'  CCTCTGGAACGCCACCTGAGC  19173    _   AAAAA   CG
                                CC CTG    GCC  GCCTGAGC
                                || |||    |||  ||||||||
```

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                              GG GAC    CGG  TGGACTCG
                               A  CTTG_  __
GAM720  KIAA0215 3' TGAAAAAGGACTGAG      19174        CCC  C
                              TGAAAAAG  GGC TGAG
                              ||||||||  ||| ||||
                              ACTTTTTC  CTG ACTC
                                  ___  _
GAM720  KIAA0229 3' CCCCTGAAAGGGACAGGAAGTT 19175         _________  CCC
           GGGC                  CCCCTGAAA      AAG  GGC
                              |||||||||      |||  |||
                              GGGGACTTT      TTC  CCG
                                   CCCTGTCC  AAC
GAM720  KIAA0356 3' CCTCTAAGCCAGGCCTGAG   19176    GAAA   C
                              CCT   AAGCC GGCCTGAG
                              |||   ||||| ||||||||
                              GGA   TTCGG CCGGACTC
                                GA__    T
GAM720  KIAA1136 3' CCCTTGAAAGTGCTATCAGGAG 19177    C    AA  C__  CCT
           C                   CCC TGAAA  GC  CGG  GAGC
                              ||| |||||  ||  |||  ||||
                              GGG ACTTT  CG  GTC  CTCG
                                A    CA  ATA  ___
GAM720  KIAA1655 3' CCCTGAAACGGAGGCCTGAG  19178       AAGCCC
                              CCCTGAAA    GGCCTGAG
                              ||||||||    ||||||||
                              GGGACTTT    CCGGACTC
                                   GCCT__
GAM720  KIAA1798 3' CCCTGAAAAAAACCT      19179         CCCG
                              CCCTGAAAAAG   GCCT
                              ||||||||||   ||||
                              GGGACTTTTTT   TGGA
                                   ____
GAM720  MGC10200 3' CCGCTGCAGTCCGGCCTG   19180   _  AAAA  C
                              CC CTG   AG CCGGCCTG
                              || |||   || ||||||||
                              GG GAC   TC GGCCGGAC
                               C  G___  A
GAM720  MGC10715 3' CCCCTGAAAAGGTCATCTGGGC 19181         A CC  GC  A
                              CCCCTGAAAA G  CG  CTG GC
                              |||||||||| |  ||  ||| ||
                              GGGGACTTTT C  GT  GAC CG
                                   _ CA  A_  C
GAM720  MGC11287 3' CCTGAAGAGCCCGAGGAAG   19182      AA     CCT
                              CCTGAA  AGCCCGG  GAG
                              ||||||  |||||||  |||
                              GGACTT  TCGGGCT  TTC
                                 C_     CC_
GAM720  MGC1842  3' CTGAAAAAGAACTTGAGC   19183        CCC  C
                              CTGAAAAAG  GGC TGAGC
                              |||||||||  ||| |||||
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                                GACTTTTTC   TTG ACTCG
                                    ___   A
GAM720  MGC20983  3'  CCCCTGAAGGGGCCCCGTGGGG 19184        AAA   _____
            C                    CCCCTGAA   GCCC    GGC
                                 ||||||||   ||||    |||
                                 GGGGACTT   CGGG    CCG
                                     CCC    GCACC
GAM720  MGC29654  3'  TGAAGGCCTGGCCTGAG     19185     AAA   C
                                 TGAA   GCC GGCCTGAG
                                 ||||   ||| ||||||||
                                 ACTT   CGG CCGGACTC
                                   C__   A
GAM720  MGC4415   3'  TGAGAAGGATGGACCTGAGC   19186     AA   CCC_
                                 TGA  AAG    GGCCTGAGC
                                 |||  |||    |||||||||
                                 ACT  TTC    CTGGACTCG
                                   C_   CTAC
GAM720  MGC5306   3'  CCCTAGAACGAGCCTGAG    19187     GAAAA  CC  _
                                 CCCT    AG  CG GCCTGAG
                                 ||||    ||  || |||||||
                                 GGGA    TC  GC CGGACTC
                                   _____  TT  T
GAM720  MRPL45    3'  CTGAAAAGACCTGAG       19188        AGCCC
                                 CTGAAAA    GGCCTGAG
                                 |||||||    ||||||||
                                 GACTTTT    CTGGACTC
                                            _____
GAM720  NTSR2     5'  CCCCCGAAAGGGTGTCCTGAGC 19189         AAGCCCGG
                                 CCCCTGAAA       CCTGAGC
                                 |||||||||       |||||||
                                 GGGGGCTTT       GGACTCG
                                     CCCACA__
GAM720  PIF1      5'  CTAGAGGAGCCTGGCCTGAGC  19190     AAAA    C
                                 CTG    AGCC GGCCTGAGC
                                 |||    |||| |||||||||
                                 GAT    TCGG CCGGACTCG
                                   CTCC    A
GAM720  RCD-8     3'  CCCCAGAGATGGGGCCTGAGC  19191      T  AAAAGCCC
                                 CCCC GA       GGCCTGAGC
                                 |||| ||       |||||||||
                                 GGGG CT       CCGGACTCG
                                   T  CTACC___
GAM720  SDC3      3'  CCTGGAAACCAGCCTGAG    19192     A   AGC
                                 CCTG AAA   CCGGCCTGAG
                                 |||| |||   ||||||||||
                                 GGAC TTT   GGTCGGACTC
                                   C   ___
GAM720  SEMA4G    3'  CCCCTGAAAGTGCCCCGG    19193         AA   _
                                 CCCCTGAAA  GCCC GG
                                 |||||||||  |||| ||
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                                GGGGACTTT  CGGG CC
                                     CA    G
GAM720  SMARCF1   3' CCTCTAGGAAGCCCAGGAG   19194    _  AAA      CCT
                                CC CTG   AAGCCCGG   GAG
                                || |||   ||||||||  |||
                                GG GAT   TTCGGGTC   CTC
                                 A  CC_      ___
GAM720  SMOC1     3' CCCTGGACAAGGCCGAGAGC  19195     AAAAA  CC   T_
                                CCCTG    GC  GGCC  GAGC
                                |||||    ||  ||||  ||||
                                GGGAC    TG  CCGG  CTCG
                                   C____  TT   CT
GAM720  LOC112817 5' CCACTGGGGCAGGCCTGAG   19196   _  AAAAA  CC
                                CC CTG    GC  GGCCTGAG
                                || |||    ||  ||||||||
                                GG GAC    CG  CCGGACTC
                                 T  CC___  T_
GAM720  LOC144524 5' CTGAAAAGGCCTAAA      19197       AGCCC
                                CTGAAAA    GGCCTGAG
                                |||||||    ||||||||
                                GACTTTT    CCGGATTT
                                     _____
GAM720  LOC149506 5' CCCCTGGCAGGGCCTGAG    19198      AAAAA  CC
                                CCCCTG    GC  GGCCTGAG
                                ||||||    ||  ||||||||
                                GGGGAC    CG  CCGGACTC
                                    _____  TC
GAM720  LOC149619 3' CTAAAAAAGCTTCCCAATGCTT 19199        ___  __  C
           GAG                    CTGAAAAAGC   CCG  GC TGAG
                                ||||||||||   |||  || ||||
                                GATTTTTTCG   GGT  CG ACTC
                                     AAG   TA  A
GAM720  LOC150372 3' CCCCTGAAAAAGACTGGAAAAT 19200          CCC  CCTGA
           GC                     CCCCTGAAAAAG   GG    GC
                                ||||||||||||  ||    ||
                                GGGGACTTTTTC   CC    CG
                                       TGA  TTTTA
GAM720  LOC151429 3' CCTCGTGATCCGCCGGCCTGGG 19201    CC_  AAAA   C     A
           C                     CC   TGA   GCC GGCCTG GC
                                ||   |||   ||| |||||| ||
                                GG   ACT   CGG CCGGAC CG
                                 AGC   AGG_  _     C
GAM720  LOC152794 5' CCTGAAAAACCTCCAAGAA   19202        GC  GG  T_
                                CCTGAAAAA  CC  CC  GAG
                                |||||||||  ||  ||  |||
                                GGACTTTTT  GG  GG  CTT
                                     __  A_  TT
GAM720  LOC170063 3' TGAAGAAGCCTCGTGGTGCTCA 19203     A    _  ________  CTGA
           GGC                     GAA AAGCC CG      GC   GC
                                ||| ||||| ||      ||   ||
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                                CTT TTCGG GC      CG    CG
                                  C    A  ACCAIII  AGTC
GAM720   LOC196955 5'  CCCCTGGTGTCAGGCCTGAGC  19204       AAAAAGCCC
                                CCCCTG        GGCCTGAGC
                                ||||||        |||||||||
                                GGGGAC        CCGGACTCG
                                   CACAGT___
GAM720   LOC200014 5'  CCCCTGAGATGCTCCGGCCTGA 19205        AAAA  _
           GC                     CCCCTGA    GC CCGGCCTGAGC
                                |||||||    || ||||||||||
                                GGGGACT    CG GGCCGGACTCG
                                   CTA_  A
GAM720   LOC219731 5'  CCTGAGACCAGCCTGG      19206       AAAA C       A
                                CCTGA    G CCGGCCTG G
                                |||||    | |||||||| |
                                GGACT    C GGTCGGAC C
                                  _____ T       C
GAM720   LOC220020 5'  CCCTGAGAGAGCCTAAG     19207       AAA  CCC
                                CCCTGA   AG   GGCCTGAG
                                ||||||   ||   ||||||||
                                GGGACT   TC   TCGGATTC
                                   C__  ___
GAM720   LOC221876 3'  CCCTGAAAGAGGCGTTTTGAGC 19208         A  CC  GCC
                                CCCTGAAA AG  CG   TGAGC
                                |||||||| ||  ||   |||||
                                GGGACTTT TC  GC   ACTCG
                                     C  C_  AAA
GAM720   LOC222832 3'  CCTTCAAAGAACCTGAG     19209     GAA    CCC
                                CCT   AAAG   GGCCTGAG
                                |||   ||||   ||||||||
                                GGA   TTTC   TTGGACTC
                                  AG_   ____
GAM720   LOC253675 3'  CCAGGAGAAAGGAAACCTGAGC 19210    T_  A    CCC
                                CC  GA AAAG   GGCCTGAGC
                                ||  || ||||   |||||||||
                                GG  CT TTTC   TTGGACTCG
                                 TC  C    CT_
GAM720   LOC254057 3'  CCCGACCCCCTGGCCTGAGC   19211       AAAAG  _
                                CCTGA     CCC GGCCTGAGC
                                |||||     ||| |||||||||
                                GGGCT     GGG CCGGACTCG
                                   GG____   A
GAM720   LOC255718 5'  CCGATGCCGGCCTGAG      19212      AAAA   C
                                CTGA    GCC GGCCTGAG
                                ||||    ||| ||||||||
                                GGCT    CGG CCGGACTC
                                  A____   _
GAM720   LOC256416 3'  CCCCTTAGACCCAGGCCTGAGC 19213       GAAAAA   _
                                CCCCT     GCCC GGCCTGAGC
                                |||||     |||| |||||||||
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                                GGGGA     TGGG CCGGACTCG
                                  ATC___    T
GAM720  LOC51673  3'  CCCCTTAGACCCAGGCCTGAGC 19213      GAAAAA   _
                                CCCCT     GCCC GGCCTGAGC
                                |||||     |||| |||||||||
                                GGGGA     TGGG CCGGACTCG
                                  ATC___    T
GAM720  LOC90297  3'  CCTGGGGGGAAGAGGTGCCTGAG 19214     AAA_   CCCG
          C                      CCTG    AAG    GCCTGAGC
                                ||||    |||    ||||||||
                                GGAC    TTC    CGGACTCG
                                  CCCC   TCCA
GAM720  LOC91069  3'  CCCCCAGCCTGGCTTGAG    19215      GAAAA   C   C
                                CCCCT    AGCC GGC TGAG
                                |||||    |||| ||| ||||
                                GGGGGG    TCGG CCG ACTC
                                  _____   A   A
GAM720  LOC91170  5'  CTGAAAAAGGCCCTTAAGC    19216        _   GGCC
                                CTGAAAAAG CCC    TGAGC
                                ||||||||| |||    |||||
                                GACTTTTTC GGG    ATTCG
                                     C   A___
GAM721  ABR       3'  CCCCAGCCCTGAGGGCCCGG   19219     G   ___
                                CCC AGCT   GGGGCCCGG
                                ||| ||||   |||||||||
                                GGG TCGG   TCCCGGGCC
                                  G    GAC
GAM721  ABR       3'  CCCCAGCCCTGAGGGCCCGG   19219     G   ___
                                CCC AGCT   GGGGCCCGG
                                ||| ||||   |||||||||
                                GGG TCGG   TCCCGGGCC
                                  G    GAC
GAM721  CACNA1A   3'  CCCGGCCCGCGGGGCCTGG    19220     A   ___     C
                                CCCG GCT   GGGGCC GG
                                |||| |||   |||||| ||
                                GGGC CGG   CCCCGG CC
                                  _   GCG     A
GAM721  CD1D      5'  CCCAAGCCCAGACCCCGG     19221        G     _
                                CCCGAGCT GGGCCC GG
                                |||||||| |||||| ||
                                GGGTTCGG TCTGGG CC
                                     G     G
GAM721  CDH11     5'  CCGAGCCGCCAGTCCCTGG    19222        G_  _   _
                                CCGAGCTG  GG CCC GG
                                ||||||||  || ||| ||
                                GGCTCGGC  TC GGG CC
                                     GG  A   A
GAM721  CDH16     3'  CCCAGCTAGAGCTGCCTGG    19223     G       __  _
                                CCC AGCTGGGGC  CC GG
                                ||| |||||||||  || ||
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                                GGG TCGATCTCG  GG CC
                                  _       AC  A
GAM721  CETP    5'  CCCGAGCCGTTCAGCCTGG   19224        G__   C
                                CCCGAGCTG   GGCC GG
                                |||||||||   |||| ||
                                GGGCTCGGC   TCGG CC
                                     AAG    A
GAM721  CRHR1   3'  CCAGAGGCCCTGGGCCCGG   19225   C  _ G_
                                CC GAG CT  GGGCCCGG
                                || ||| ||  ||||||||
                                GG CTC GG  CCCGGGCC
                                 T  C  GA
GAM721  DVL1    5'  CCGCGCGCTCAGGGCCCGG   19226   _ A  _
                                CC CG GCT GGGGCCCGG
                                || || ||| |||||||||
                                GG GC CGA TCCCGGGCC
                                 C  G  G
GAM721  E2F2    5'  CCTCGGCACCTGGGGTCCGG   19227   _ A_ _   C
                                CC CG  GC TGGGG CCGG
                                || ||  || ||||| ||||
                                GG GC  TG ACCCC GGCC
                                 A  CG  G    A
GAM721  EXTL3   3'  CCCCAGCTGGTGAGCCCTGG   19228    G    _ _   _
                                CCC AGCTGG G GCCC GG
                                ||| |||||| | |||| ||
                                GGG TCGACC C CGGG CC
                                  G     A T   A
GAM721  FGF2    5'  CCCAAGCTGCAGCGCCCGG   19229        _ _
                                CCCGAGCTG GG GCCCGG
                                ||||||||| || ||||||
                                GGGTTCGAC TC CGGGCC
                                     G  G
GAM721  FGFR1   5'  CCGGAGCTGGTGCCCCGG   19230   C     G   _
                                CC GAGCTGG GCCC GG
                                || ||||||| |||| ||
                                GG CTCGACC CGGG CC
                                 C     A   G
GAM721  FGFR1   5'  CCGGAGCTGGTGCCCCGG   19230   C     G   _
                                CC GAGCTGG GCCC GG
                                || ||||||| |||| ||
                                GG CTCGACC CGGG CC
                                 C     A   G
GAM721  FGFR1   5'  CCGGAGCTGGTGCCCCGG   19230   C     G   _
                                CC GAGCTGG GCCC GG
                                || ||||||| |||| ||
                                GG CTCGACC CGGG CC
                                 C     A   G
GAM721  FGFR1   5'  CCGGAGCTGGTGCCCCGG   19230   C     G   _
                                CC GAGCTGG GCCC GG
                                || ||||||| |||| ||
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                                GG CTCGACC CGGG CC
                                 C      A   G
GAM721  FGFR1   5' CCGGAGCTGGTGCCCCGG   19230   C     G   _
                                CC GAGCTGG GCCC GG
                                || ||||||| |||| ||
                                GG CTCGACC CGGG CC
                                 C      A   G
GAM721  FGFR1   5' CCGGAGCTGGTGCCCCGG   19230   C     G   _
                                CC GAGCTGG GCCC GG
                                || ||||||| |||| ||
                                GG CTCGACC CGGG CC
                                 C      A   G
GAM721  FMR2    5' CCCAGCTAAAAGTGTCCGG   19231    G     C___
                                CCC AGCTGGGG   CCGG
                                ||| ||||||||   ||||
                                GGG TCGATTTT   GGCC
                                  _      CACA
GAM721  GALR1   5' CCCGGAGCTGGACCTTCTCGG 19232     _     G ____
                                CCCG AGCTGGG CC   CGG
                                |||| ||||||| ||   |||
                                GGGC TCGACCT GG   GCC
                                  C      _ AAGA
GAM721  HPCAL1  3' CCCAGGCCCGGGGCCCGG   19233     A  _
                                CCCG GCT GGGGCCCGG
                                |||| ||| |||||||||
                                GGGT CGG CCCCGGGCC
                                  C  G
GAM721  HPCAL1  3' CCCAGGCCCGGGGCCCGG   19233     A  _
                                CCCG GCT GGGGCCCGG
                                |||| ||| |||||||||
                                GGGT CGG CCCCGGGCC
                                  C  G
GAM721  HYAL1   3' CCGGAGCTAGACAGCCTGG   19234   C     __   C
                                CC GAGCTGG  GGCC GG
                                || |||||||  |||| ||
                                GG CTCGATC  TCGG CC
                                 C      TG   A
GAM721  HYAL1   3' CCGGAGCTAGACAGCCTGG   19234   C     __   C
                                CC GAGCTGG  GGCC GG
                                || |||||||  |||| ||
                                GG CTCGATC  TCGG CC
                                 C      TG   A
GAM721  JUN     5' CCCGAACCACCAGCCCGG   19235       GG_
                                CCCGAGCT   GGCCCGG
                                ||||||||   |||||||
                                GGGCTTGG   TCGGGCC
                                     TGG
GAM721  LASS2   5' CCGAGGCCCCGAGGCCTGG   19236     ___     C
                                CCGAG   CTGGGGCC GG
                                |||||   |||||||| ||
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                                GGCTC   GGCTCCGG CC
                                  CGG       A
GAM721  LDLR    5'  CCTAGCTGGAAACCCTGG    19237    G      _  _
                                CC AGCTGGGG CCC GG
                                || |||||||| ||| ||
                                GG TCGACCTT GGG CC
                                 A       T   A
GAM721  LEPR    5'  CCCGAACTGGGGCCGCGG    19238           _
                                CCCGAGCTGGGGCC CGG
                                |||||||||||||| |||
                                GGGCTTGACCCCGG GCC
                                          C
GAM721  LTBR    5'  CCCGAGCCCAGAGCCTGG    19239        G _  C
                                CCCGAGCT GG GCC GG
                                |||||||| || ||| ||
                                GGGCTCGG TC CGG CC
                                     G T   A
GAM721  MFI2    5'  CCGGGCTGGGGCTGGGTCCGGC 19240     A      _____   III
                                CCG GCTGGGGC    CCGG   C
                                ||| ||||||||    ||||   |
                                GGC CGACCCCG    GGCC   G
                                  C       ACCCA   III
GAM721  MFI2    5'  CCGGGCTGGGGCTGGGTCCGGC 19240     A      _____   III
                                CCG GCTGGGGC    CCGG   C
                                ||| ||||||||    ||||   |
                                GGC CGACCCCG    GGCC   G
                                  C       ACCCA   III
GAM721  MLLT1   3'  CCCGGCGGTGGGGGCCCGG   19241     A  T___
                                CCCG GC   GGGGCCCGG
                                |||| ||   |||||||||
                                GGGC CG   CCCCGGGCC
                                  _ CCAC
GAM721  MMP25   3'  CCCAAGCTGGGTGGCCTGG   19242          __  C
                                CCCGAGCTGGG  GCC GG
                                |||||||||||  ||| ||
                                GGGTTCGACCC  CGG CC
                                       AC   A
GAM721  MYBBP1A 3'  CCAGAGCAGGATGCCCGG    19243   C   T  _
                                CC GAGC GGG GCCCGG
                                || |||| ||| ||||||
                                GG CTCG CCT CGGGCC
                                 T   T   A
GAM721  MYO1C   5'  CCCAGGGCCGACGCCCGG    19244     A_    G
                                CCCG  GCTGG GCCCGG
                                ||||  ||||| ||||||
                                GGGT  CGGCT CGGGCC
                                  CC    G
GAM721  NAGLU   5'  CCCGAAGGCTAAGCCCGG    19245      __     G
                                CCCGA  GCTGGG CCCGG
                                |||||  |||||| |||||
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                                GGGCT  CGATTC GGGCC
                                  TC     _
GAM721  NT5C     5'  CCGGAGCTGCGAGCTCTCGG   19246    C     _   C__
                                CC GAGCTG GGGC   CGG
                                || |||||| ||||   |||
                                GG CTCGAC CTCG   GCC
                                 C     G    AGA
GAM721  ONECUT2  3'  CCCCAGCTAGGAATCCGG    19247     G      C_
                                CCC AGCTGGGG  CCGG
                                ||| ||||||||  ||||
                                GGG TCGATCCT  GGCC
                                  G       TA
GAM721  PGF      5'  CCCGACGGGGAGCGGCCCGG   19248      G T  _____
                                CCCGA C GGG    GCCCGG
                                ||||| | |||    ||||||
                                GGGCT G CCC    CGGGCC
                                  _ C   TCGC
GAM721  PKIB     5'  CCCGGAGCTGCGACTCGG     19250     _    G   C
                                CCCG AGCTG GGC CGG
                                |||| ||||| ||| |||
                                GGGC TCGAC CTG GCC
                                  C     G   A
GAM721  PKIB     5'  CCCAAGCTCTGCGGCCCGG    19249        __ G
                                CCCGAGCT  G GGCCCGG
                                ||||||||  | |||||||
                                GGGTTCGA  C CCGGGCC
                                     GA G
GAM721  POU5F1   5'  CCCAAGCCGGGGGCCTGG    19251          _  C
                                CCCGAGCTGGGG CC GG
                                |||||||||||| || ||
                                GGGTTCGGCCCC GG CC
                                       C  A
GAM721  POU5F1   5'  CCCAAGCCGGGGGCCTGG    19251          _  C
                                CCCGAGCTGGGG CC GG
                                |||||||||||| || ||
                                GGGTTCGGCCCC GG CC
                                       C  A
GAM721  POV1     5'  CCCGAGCTCCGCAGGGCTCGG  19252        _____    C
                                CCCGAGCT    GGGGC CGG
                                ||||||||    ||||| |||
                                GGGCTCGA    TCCCG GCC
                                     GGCG     A
GAM721  PPP2R5D  3'  CCCTGGAACCTGGGTCCGG   19253     __    G   C
                                CCC  GAGCT GGG CCGG
                                |||  ||||| ||| ||||
                                GGG  CTTGG CCC GGCC
                                  AC     A   A
GAM721  REQ      3'  CCCGAGCTGCTGGCCTGG    19254         G_   C
                                CCCGAGCTG  GGCC GG
                                |||||||||  |||| ||
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                                GGGCTCGAC  CCGG CC
                                    GA   A
GAM721  RGS3    3' CCCGAGAGCCCAGGCCTGG   19255   __   G   C
                                CCC  GAGCT GGGCC GG
                                |||  ||||| ||||| ||
                                GGG  CTCGG TCCGG CC
                                  CT    G    A
GAM721  RGS3    3' CCCGAGAGCCCAGGCCTGG   19255   __   G   C
                                CCC  GAGCT GGGCC GG
                                |||  ||||| ||||| ||
                                GGG  CTCGG TCCGG CC
                                  CT    G    A
GAM721  RGS3    3' CCCGAGAGCCCAGGCCTGG   19255   __   G   C
                                CCC  GAGCT GGGCC GG
                                |||  ||||| ||||| ||
                                GGG  CTCGG TCCGG CC
                                  CT    G    A
GAM721  RGS3    3' CCCGAGAGCCCAGGCCTGG   19255   __   G   C
                                CCC  GAGCT GGGCC GG
                                |||  ||||| ||||| ||
                                GGG  CTCGG TCCGG CC
                                  CT    G    A
GAM721  RGS3    3' CCCGAGAGCCCAGGCCTGG   19255   __   G   C
                                CCC  GAGCT GGGCC GG
                                |||  ||||| ||||| ||
                                GGG  CTCGG TCCGG CC
                                  CT    G    A
GAM721  RGS3    3' CCCGAGAGCCCAGGCCTGG   19255   __   G   C
                                CCC  GAGCT GGGCC GG
                                |||  ||||| ||||| ||
                                GGG  CTCGG TCCGG CC
                                  CT    G    A
GAM721  SHOX    3' CCCGGGCTGGACGCACGG    19256    A   _ C
                                CCCG GCTGGG GC CGG
                                ||||  ||||||  ||  |||
                                GGGC CGACCT CG GCC
                                  C     G  T
GAM721  SLC20A1 5' CCACGGGCACACGGCCCGG   19257   _ A _ G
                                CC CG GC TG GGCCCGG
                                ||  ||  ||  ||  |||||||
                                GG GC CG GT CCGGGCC
                                 T  C  T  G
GAM721  SLC3A2  5' CCCGCGCTGAGACCCTGG    19258    A       _
                                CCCG GCTGGGGCCC GG
                                ||||  ||||||||||  ||
                                GGGC CGACTCTGGG CC
                                  G         A
GAM721  SLC7A4  3' CCCGAAGCCCAGCCCCTGG   19259     _  G  G  _
                                CCCGA GCT GG CCC GG
                                |||||  |||  ||  |||  ||
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                                GGGCT CGG TC GGG CC
                                  T  G G  A
GAM721  UBQLN1   5'  CCAGAGCCGGCAGGCCTGG   19260   C     __   C
                                CC GAGCTGG  GGCC GG
                                || |||||||  |||| ||
                                GG CTCGGCC  CCGG CC
                                 T      GT   A
GAM721  USP7     5'  CCGGGGCTGCGAGCCCGG    19261    A_   _
                                CCG  GCTG GGGCCCGG
                                |||  |||| ||||||||
                                GGC  CGAC CTCGGGCC
                                  CC   G
GAM721  ABTB1    5'  CCCGAGCCGAACGACCTCGG  19262         __   _
                                CCCGAGCTGG  GGCC CGG
                                ||||||||||  |||| |||
                                GGGCTCGGCT  CTGG GCC
                                      TG   A
GAM721  C1orf8   5'  CCCGAGTCCTCCAGGGCCTGGC 19263      _____ TG    C  III
                                CCCGAG   C  GGGCC GG  C
                                ||||||   |  ||||| ||  |
                                GGGCTC   G  CCCGG CC  G
                                   AGGA GT    A  III
GAM721  CDCA7    5'  CCCGGAGGGGCGGGGCTCGG  19264     _ C__    C
                                CCCG AG   TGGGGC CGG
                                |||| ||   |||||| |||
                                GGGC TC   GCCCCG GCC
                                  C  CCC     A
GAM721  CENTB5   3'  CCCGCCAGCAGGGGCCTGG   19265    __  T    C
                                CCCG  AGC GGGGCC GG
                                ||||  ||| |||||| ||
                                GGGC  TCG CCCCGG CC
                                  GG  T     A
GAM721  CENTG2   5'  CCGCGGGCCGCCGAGCCCGG  19266   _ A   __
                                CC CG GCTG  GGGCCCGG
                                || || ||||  ||||||||
                                GG GC CGGC  CTCGGGCC
                                 C  C   GG
GAM721  DKFZp434C0923 3'  CCCACACCAGGGGCCTGG    19267     A  _    C
                                CCCG GCT GGGGCC GG
                                |||| ||| |||||| ||
                                GGGT TGG CCCCGG CC
                                  G  T     A
GAM721  DKFZP434H0820 3'  CCAGAGCTGAGCCTGCCTGG  19268   C     ___  C
                                CC GAGCTGGG   GCC GG
                                || ||||||||   ||| ||
                                GG CTCGACTC   CGG CC
                                 T      GGA  A
GAM721  DKFZP434N1511 5'  CCCAAAGTGGAGGGTCCGG   19269      C   C__
                                CCCGAG TGGGG   CCGG
                                |||||| |||||   ||||
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                                GGGTTT ACCTC   GGCC
                                   C     CCA
GAM721  DKFZp762L0311 5'  CCCGGACTCACCACGGCCCGG  19270      A____    G
                                CCCG    GCTG GGCCCGG
                                ||||    |||| |||||||
                                GGGC    TGGT CCGGGCC
                                  CTGAG   G
GAM721  EMILIN   3'  CCTGAGCCGGCGCGCCCCGG  19271    C      G ___
                                CC GAGCTGG GC   CCGG
                                || ||||||| ||   ||||
                                GG CTCGGCC CG   GGCC
                                 A      G  CGG
GAM721  FLJ10375  3'  GAGCAGCGTGTGGGGCCCGGC  19272      _______        III
                                GAGC     TGGGGCCCGG   C
                                ||||     ||||||||||   |
                                CTCG     ACCCCGGGCC   G
                                  TCGCAC         III
GAM721  FLJ13782  3'  CCCAAGCTGCTGGTCCGG    19273         G_  C
                                CCCGAGCTG  GG CCGG
                                |||||||||  || ||||
                                GGGTTCGAC  CC GGCC
                                     GA  A
GAM721  FLJ14124  3'  CCCGGCTGAAGCGAGGCCCGG  19274      A   _____
                                CCCG GCTG    GGGCCCGG
                                |||| ||||    ||||||||
                                GGGC CGAC    TCCGGGCC
                                  _   TTCGC
GAM721  FLJ14957  3'  CCCAGCTGTGACTGGGCCTGG  19275     G    _____    C
                                CCC AGCTG    GGGCC GG
                                ||| |||||    ||||| ||
                                GGG TCGAC    CCCGG CC
                                  _    ACTGA    A
GAM721  FLJ20366  5'  CCCGGGGAGCCGGGCCCGG   19276     ___      G
                                CCC   GAGCTGGG CCCGG
                                |||   |||||||| |||||
                                GGG   CTCGGCCC GGGCC
                                  CCC       _
GAM721  FLJ22215  3'  CCCGGGCCTGCAACCCTGG   19277     A  _  G    _
                                CCCG GC TG GGCCC GG
                                |||| || || ||||| ||
                                GGGC CG AC TTGGG CC
                                  C  G  G    A
GAM721  FLJ22938  3'  CCCGCAGCAGCACCCTGG    19278     _  T  G   _
                                CCCG AGC GG GCCC GG
                                |||| ||| || |||| ||
                                GGGC TCG TC TGGG CC
                                  G   _  G   A
GAM721  FLJ30791  5'  CCCAGCCCTTACGGGCCCGG  19279     G   G____
                                CCC AGCT    GGGCCCGG
                                ||| ||||    ||||||||
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                                GGG TCGG    CCCGGGCC
                                  _   GAATG
GAM721  FLJ32734  3'  CCCGAGCTGGACTGACTGG   19280         ___   CC
                                CCCGAGCTGG  GGC  GG
                                ||||||||||  |||  ||
                                GGGCTCGACC  CTG  CC
                                      TGA  A_
GAM721  GS3955    5'  CCCGAGACCAAATTGCCCGG  19281       _ TG  __
                                CCCGAG C  GG  GCCCGG
                                ||||||  |  ||  ||||||
                                GGGCTC G  TT  CGGGCC
                                   T GT  AA
GAM721  GSK3A     5'  CCCAGGCTGCGGGGCTCGG   19282      A  __    C
                                CCCG GCT  GGGGC CGG
                                ||||  |||  |||||  |||
                                GGGT CGA  CCCCG GCC
                                  C  CG    A
GAM721  HSOBRGRP  5'  CCCGAACTGGGGCCGCGG    19238           _
                                CCCGAGCTGGGGCC CGG
                                ||||||||||||||  |||
                                GGGCTTGACCCCGG GCC
                                        C
GAM721  IRF5      3'  CCCGGGAAGGCAGGGGCTCGGC 19283      A____  T    C   III
                                CCCG    GC GGGGC CGG  C
                                ||||    ||  |||||  |||  |
                                GGGC    CG CCCCG GCC  G
                                  CCTTC  T    A  III
GAM721  KIAA0237  3'  CCCAAGCTCAGGGTTCGG    19284        _   CC
                                CCCGAGCT GGGG  CGG
                                ||||||||  ||||  |||
                                GGGTTCGA TCCC  GCC
                                    G   AA
GAM721  KIAA0444  3'  CCCTGGCTGGGACTCCTGG   19285     GA      _ _
                                CCC  GCTGGGGC CC GG
                                |||  ||||||||  ||  ||
                                GGG  CGACCCTG GG CC
                                  AC       A  A
GAM721  KIAA0995  5'  CCCGGAGCCGCGGCCCGG    19286     _    G
                                CCCG AGCTG GGCCCGG
                                ||||  |||||  |||||||
                                GGGC TCGGC CCGGGCC
                                  C    G
GAM721  KIAA1115  3'  CCCAGAGCCGGACTGGCCTGG  19288    _     ___   C
                                CCC GAGCTGG   GGCC GG
                                |||  |||||||   ||||  ||
                                GGG CTCGGCC   CCGG CC
                                  T      TGA   A
GAM721  KIAA1115  3'  CCTGAGCTAAAAGGCCGG    19287    C     __    C
                                CC GAGCTG  GGGCC GG
                                ||  ||||||  |||||  ||
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                                GG CTCGAT  TCCGG CC
                                 A     TT    _
GAM721  KIAA1233  5'  CCCGGGGCCGCGCGGGCTCGG  19289     A_   ___   C
                                CCCG  GCTG   GGGC CGG
                                ||||  ||||   |||| |||
                                GGGC  CGGC   CCCG GCC
                                  CC    GCG    A
GAM721  KIAA1340  5'  CCCGGCGCGCTGAGGCCCGG   19290     A___
                                CCCG   GCTGGGGCCCGG
                                ||||   ||||||||||||
                                GGGC   CGACTCCGGGCC
                                  CGCG
GAM721  KIAA1822  3'  CCAGAGCTGGACTACCTGG   19291    C      __  C
                                CC GAGCTGGG  GCC GG
                                || ||||||||  ||| ||
                                GG CTCGACCT  TGG CC
                                 T       GA   A
GAM721  MGC11257  3'  CCAAGGCCAGGGGTCCGG    19292      _ _   C
                                CCGAG CT GGGG CCGG
                                ||||| || |||| ||||
                                GGTTC GG CCCC GGCC
                                   C  T    A
GAM721  MGC15437  5'  CCCGAGCCGGATGGTTCGG   19293         __ CC
                                CCCGAGCTGG  GG  CGG
                                ||||||||||  ||  |||
                                GGGCTCGGCC  CC  GCC
                                      TA  AA
GAM721  MGC23280  5'  CCGAGCTGAGCTGAGCCCGG   19294         ____
                                CCGAGCTGGG   GCCCGG
                                ||||||||||   ||||||
                                GGCTCGACTC   CGGGCC
                                      GACT
GAM721  MGC2721   3'  CCCAGCCAGTCGGGTCCGG   19295    G   ___  C
                                CCC AGCTG   GGG CCGG
                                ||| |||||   ||| ||||
                                GGG TCGGT   CCC GGCC
                                  _    CAG   A
GAM721  MGC35570  5'  CCGGAGCGCGAAGCCCGG    19296   C   _
                                CC GAGC TGGGGCCCGG
                                || |||| ||||||||||
                                GG CTCG GCTTCGGGCC
                                 C   C
GAM721  MGC4368   3'  CCCGGCTGGAGCTCCCGG    19297    A     __
                                CCCG GCTGGGGC  CCGG
                                |||| ||||||||  ||||
                                GGGC CGACCTCG  GGCC
                                  _      AG
GAM721  MGC4614   5'  CCGCGCCGCCGGGCCCGG    19298    A   __
                                CCG GCTG  GGGCCCGG
                                ||| ||||  ||||||||
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                                GGC CGGC  CCCGGGCC
                                  G    GG
GAM721  PPP1R14C  5'  CCCGAGCCTCAGTGCGGCCCGG 19299        _____ G      III
             C                    CCCGAGCT    G GGCCCGG   C
                                  ||||||||    | |||||||   |
                                  GGGCTCGG    C CCGGGCC   G
                                      AGTCA G      III
GAM721  PRO0899   3'  CCCAGGCTCAAGGAGGCCTGG  19300     A  ____     C
                                  CCCG GCT    GGGGCC GG
                                  |||| |||    |||||| ||
                                  GGGT CGA    CTCCGG CC
                                    C   GTTC     A
GAM721  PTDSS2    5'  CCCGGAGCCACTCCGCCCGG   19301     _    GG__
                                  CCCG AGCTG    GCCCGG
                                  |||| |||||    ||||||
                                  GGGC TCGGT    CGGGCC
                                    C     GAGG
GAM721  RAB6C     5'  CCCGGCTGGAGAAGCCCGG    19302     A    ___
                                  CCCG GCTGG   GGCCCGG
                                  |||| |||||   |||||||
                                  GGGC CGACC   TCGGGCC
                                    _     TCT
GAM721  RAI17     3'  CCCATGCTGGGGCCCGGCC    19303     A         III
                                  CCCG GCTGGGGCCCGG   CC
                                  |||| ||||||||||||   ||
                                  GGGT CGACCCCGGGCC   GG
                                    A          III
GAM721  RLUCL     3'  CCCAAGCTGGGGTCCCGG     19304          _
                                  CCCGAGCTGGGG CCCGG
                                  |||||||||||| |||||
                                  GGGTTCGACCCC GGGCC
                                         A
GAM721  SHANK3    5'  CCCGAGGGCCCCAGGCTCGG   19305       ___ G    C
                                  CCCGAG   CT GGGC CGG
                                  ||||||   || |||| |||
                                  GGGCTC   GG TCCG GCC
                                     CCG  G    A
GAM721  SIAT4B    3'  CCCGGGCCGGAGCCCCGG     19306     A        _
                                  CCCG GCTGGGGCCC GG
                                  |||| ||||||||| ||
                                  GGGC CGGCCTCGGG CC
                                    C         G
GAM721  SPA17     5'  CCGAGCTGGTGCCGCCGG     19307         G  __
                                  CCGAGCTGG GCC  CGG
                                  |||||||| |||  |||
                                  GGCTCGACC CGG  GCC
                                       A  CG
GAM721  STAG3     3'  CCCAGGGCTGAAGCCTGG     19308     A_       C
                                  CCCG  GCTGGGGCC GG
                                  ||||  |||||||| ||
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                                GGGT  CGACTTCGG CC
                                  CC        A
GAM721   STRAIT11499 5'  CCCGCGCTGGGGGCCTGG    19309      A      _ C
                                CCCG GCTGGGG CC GG
                                |||| ||||||| || ||
                                GGGC CGACCCC GG CC
                                  G      C  A
GAM721   STX3A    5'  CCTGAAGCCCAGGCGCCCGG   19310    C_    __ G
                                CC  GAGCT  GG GCCCGG
                                ||  |||||  || ||||||
                                GG  TTCGG  CC CGGGCC
                                 AC     GT  G
GAM721   LOC113091 5'  CCCGGCCCAGAACCCCGG    19311      A   G   __
                                CCCG GCT GGG  CCCGG
                                |||| ||| |||  |||||
                                GGGC CGG TCT  GGGCC
                                  _   G   TG
GAM721   LOC115294 5'  CCGGAGCCGCCGGGGTCCGG   19312    C    ____   C
                                CC GAGCT   GGGG CCGG
                                || |||||   |||| ||||
                                GG CTCGG   CCCC GGCC
                                 C    CGG    A
GAM721   LOC116349 5'  CCCGAGCTGAAGTCGCTCGG   19313           ___ C
                                CCCGAGCTGGG   GC CGG
                                ||||||||||   || |||
                                GGGCTCGACTT   CG GCC
                                       CAG  A
GAM721   LOC125966 3'  CCCAGCTGGAATCTCCGG    19314     G       C__
                                CCC AGCTGGGG   CCGG
                                ||| ||||||||   ||||
                                GGG TCGACCTT   GGCC
                                  _       AGA
GAM721   LOC126031 5'  CCCAAGCTCGGGGCCTGG    19315         _     C
                                CCCGAGCT GGGGCC GG
                                |||||||| |||||| ||
                                GGGTTCGA CCCCGG CC
                                     G     A
GAM721   LOC138389 3'  CCCGAGCTCGTGACCCCGG   19316         _ _ G
                                CCCGAGCT G GG CCCGG
                                |||||||| | || |||||
                                GGGCTCGA C CT GGGCC
                                     G A  G
GAM721   LOC144305 5'  CCCCAGGGCCCCGGGGCCCGG  19317     G  ____
                                CCC AG    CTGGGGCCCGG
                                ||| ||    ||||||||||
                                GGG TC    GGCCCCGGGCC
                                  G  CCGG
GAM721   LOC146268 3'  CCCAGGCCCAAGTCCCGG    19318      A   G   _
                                CCCG GCT GGG CCCGG
                                |||| ||| ||| |||||
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                                GGGT CGG TTC GGGCC
                                  C   G   A
GAM721   LOC146774 3'  CCCGAGCCCGCGGGGTCCGG   19319        ___    C
                                CCCGAGCT   GGGG CCGG
                                ||||||||   |||| ||||
                                GGGCTCGG   CCCC GGCC
                                    GCG    A
GAM721   LOC147895 5'  CCCGAGCAGGCGACCTGG     19320        T _    C
                                CCCGAGC GG GGCC GG
                                ||||||| || |||| ||
                                GGGCTCG CC CTGG CC
                                    T G    A
GAM721   LOC148018 3'  CCCGGGGCCGCAGCCCGG     19321      A_   G
                                CCCG  GCTG GGCCCGG
                                ||||  |||| |||||||
                                GGGC  CGGC TCGGGCC
                                  CC    G
GAM721   LOC149372 3'  CCCGAACCTGAAGCCTGG     19322        _      C
                                CCCGAGC TGGGGCC GG
                                ||||||| ||||||| ||
                                GGGCTTG ACTTCGG CC
                                    G      A
GAM721   LOC149657 3'  CCCAGCTCCTGGGGCCTGG    19323     G   ___     C
                                CCC AGCT   GGGGCC GG
                                ||| ||||   |||||| ||
                                GGG TCGA   CCCCGG CC
                                  _   GGA     A
GAM721   LOC153277 3'  CCCAAGCTGGTGACCTGG     19324          _   C
                                CCCGAGCTGG GGCC GG
                                |||||||||| |||| ||
                                GGGTTCGACC CTGG CC
                                      A   A
GAM721   LOC154790 3'  CCCGGGGCGGGGCTGGCCCGG  19325      A_  T   ___
                                CCCG  GC GGG   GCCCGG
                                ||||  || |||   ||||||
                                GGGC  CG CCC   CGGGCC
                                  CC  C   GAC
GAM721   LOC162083 5'  CCCAAGCTGATGAAGCTGG    19326          ___   CC
                                CCCGAGCTGG   GGC  GG
                                ||||||||||   |||  ||
                                GGGTTCGACT   TCG  CC
                                      ACT   A_
GAM721   LOC201507 3'  CCCGGGCCGGATCCCCGG     19327      A     G_
                                CCCG GCTGGG  CCCGG
                                |||| ||||||  |||||
                                GGGC CGGCCT  GGGCC
                                  C     AG
GAM721   LOC201965 5'  CCGCGGCTGGTGGGGCCTGG   19328    _ A   ___     C
                                CC CG GCT   GGGGCC GG
                                || || |||   |||||| ||
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                                GG GC CGA   CCCCGG CC
                                 C _   CCA     A
GAM721   LOC221271 5'  CCGCAGCCGGGGGCCCGG    19329     _      _
                                CCG AGCTGGGG CCCGG
                                ||| |||||||| |||||
                                GGC TCGGCCCC GGGCC
                                  G       C
GAM721   LOC221463 3'  CCCAAGCTTAAAGGCTGG    19330        __    CC
                                CCCGAGCT  GGGGC  GG
                                ||||||||  |||||  ||
                                GGGTTCGA  TTCCG  CC
                                     AT    A_
GAM721   LOC221938 5'  CCGGAGCTGGAGGCGCCCGG   19331    C      ___
                                CC GAGCTGGG   GCCCGG
                                || ||||||||   ||||||
                                GG CTCGACCT   CGGGCC
                                 C       CCG
GAM721   LOC253181 5'  CCCGGAGCTACGACCTGG    19332     _    G    C
                                CCCG AGCTG GGCC GG
                                |||| ||||| |||| ||
                                GGGC TCGAT CTGG CC
                                  C    G    A
GAM721   LOC254102 3'  CCCGAGGCCGCCGGCCCGG    19333       _  G_
                                CCCGAG CTG  GGCCCGG
                                |||||| |||  |||||||
                                GGGCTC GGC  CCGGGCC
                                   C   GG
GAM721   LOC254986 5'  CCGGAGCCGCCGGGGTCCGG   19312    C    ___    C
                                CC GAGCT   GGGG CCGG
                                || |||||   |||| ||||
                                GG CTCGG   CCCC GGCC
                                 C    CGG    A
GAM721   LOC255452 3'  CCCAAGCTCTGCGGCCTGG    19334        __ G    C
                                CCCGAGCT  G GGCC GG
                                ||||||||  | |||| ||
                                GGGTTCGA  C CCGG CC
                                     GA G    A
GAM721   LOC257480 5'  CCCTGGAACCCGGGCCCGG    19335     __    G
                                CCC  GAGCT GGGCCCGG
                                |||  ||||| ||||||||
                                GGG  CTTGG CCCGGGCC
                                  AC    G
GAM721   LOC51104  5'  CCCGGGCCGAAGCGCCGG     19336      A      _
                                CCCG GCTGGGGC CCGG
                                |||| |||||||| ||||
                                GGGC CGGCTTCG GGCC
                                  C       C
GAM721   LOC90499  3'  CCTGAACTAAAATCCCGG     19337    C       _
                                CC GAGCTGGGG CCCGG
                                || |||||||| |||||
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                                GG CTTGATTTT GGGCC
                                 A       A
GAM721  LOC91409  3'  CCGGGCTGGGGCCTGGC    19338    A      C  III
                                CCG GCTGGGGCC GG   C
                                ||| ||||||||| ||   |
                                GGC CGACCCCGG CC   G
                                  C       A  III
GAM722  ATBF1     5'  GGCGTCCGGGTCCCCGGCC   19341    __   ATCC
                                GGC  CCGG   CCCCGGTT
                                |||  ||||   ||||||||
                                CCG  GGCC   GGGGCCGG
                                  CA   CA__
GAM722  BACE2     3'  GGGGCCTGTGGCTCTGGTTCC  19342     C__  A  CCCCC
                                GGGGCC   GG TC    GGTTCC
                                ||||||   || ||    ||||||
                                CCCCGG   CC AG    CCAAGG
                                   ACA  G  A_____
GAM722  BACE2     3'  GGGGCCTGTGGCTCTGGTTCC  19342     C__  A  CCCCC
                                GGGGCC   GG TC    GGTTCC
                                ||||||   || ||    ||||||
                                CCCCGG   CC AG    CCAAGG
                                   ACA  G  A_____
GAM722  BACE2     3'  GGGGCCTGTGGCTCTGGTTCC  19342     C__  A  CCCCC
                                GGGGCC   GG TC    GGTTCC
                                ||||||   || ||    ||||||
                                CCCCGG   CC AG    CCAAGG
                                   ACA  G  A_____
GAM722  BARX1     3'  TGGGACCTGGGTCTGGCT    19343      C  A  CCCCC
                                TGGGGCC GG TC    GGTT
                                ||||||| || ||    ||||
                                ACCCTGG CC AG    CCGA
                                   A  C  A_____
GAM722  LAMC2     3'  TGGGGTCCAGATCCTTGATCAT 19344     C      CCCCG_
          TC                      TGGGG CCGGATCC     GTTC
                                |||||  ||||||||     ||||
                                ACCCC GGTCTAGG     TAAG
                                   A       AACTAG
GAM722  NPTX1     3'  TGGGGCCCGGCTTCCCTGGT   19345        ATCC   C
                                TGGGGCCCGG    CCC GGT
                                ||||||||||    ||| |||
                                ACCCCGGGCC    GGG CCA
                                     GAA_   A
GAM722  OA1       3'  TGGGGTCTGGACCCCCAGC    19346      CCC   TC
                                TGGGG   GGA  CCCCCGGT
                                |||||   |||  ||||||||
                                ACCCC   CCT  GGGGGTCG
                                  AGA   __
GAM722  PCDHB2    5'  TAGGGCCCGGATTTCCCGG    19347          CCC
                                TGGGGCCCGGAT   CCCGG
                                ||||||||||||   |||||
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                                ATCCCGGGCCTA  GGGCC
                                      AA_
GAM722  PPP2R5E  5'  GGTACGGGGTCCCTCCGGTTCC 19348   CC  A_  C
                                GG  CGG  TCCC CCGGTTCC
                                ||  |||  |||| ||||||||
                                CC  GCC  AGGG GGCCAAGG
                                 AT  CC   A
GAM722  SEZ6L   5'  TGGGGTCCGGGTCCCCCGGT  19349     C   ATC
                                TGGGG CCGG  CCCCCGGT
                                ||||| ||||  ||||||||
                                ACCCC GGCC  GGGGGCCA
                                   A   CA_
GAM722  UCP2    5'  GGCCCGATCCCCTTGGTT   19350      G    CC
                                GGCCCG ATCCCC  GGTT
                                |||||| ||||||  ||||
                                CCGGGC TAGGGG  CCAA
                                   _     AA
GAM722  CDIPT   3'  TGAGGCCCGGGTCCTCAGGATC 19351        A  CCCC  T
            C                    TGGGGCCCGG TCC   GG TCC
                                ||||||||||| |||   || |||
                                ACTCCGGGCC AGG   CC AGG
                                      C  AGT_  T
GAM722  DGKZ    3'  TGGGGCCTAGGTCCCCCC   19352       CG A
                                TGGGGCC  G TCCCCCC
                                |||||||  | |||||||
                                ACCCCGG  C AGGGGGG
                                    AT C
GAM722  DKFZp434C0923 3'  TGGGGGATCCCCTTGGTTC   19353     CCCG     CC
                                TGGGG   GATCCCC  GGTTC
                                |||||   |||||||  |||||
                                ACCCC   CTAGGGG  CCAAG
                                   ____     AA
GAM722  FLJ12057  3'  TGGGGCCCCCCTCTGGTTC   19354       GGAT  CCC
                                TGGGGCCC   CCC  GGTTC
                                ||||||||   |||  |||||
                                ACCCCGGG   GGG  CCAAG
                                    ____  AGA
GAM722  FLJ21596  3'  TGGGGCCCAGATCTCTAAAGCC 19355          CCCCC
                                TGGGGCCCGGATC   GGTT
                                ||||||||||||   ||||
                                ACCCCGGGTCTAG   TCGG
                                      AGATT
GAM722  GMEB2   3'  TGGGGCTTGGAGCCCCTGCC  19356      CC  T  __
                                TGGGGC  GGA CCCC  CC
                                ||||||  ||| ||||  ||
                                ACCCCG  CCT GGGG  GG
                                   AA  C   AC
GAM722  KIAA1395  3'  TGAGGCCCGGGTGCTGGTTCC  19357        ATCCCCCC
                                TGGGGCCCGG      GGTTCC
                                ||||||||||      ||||||
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                                ACTCCGGGCC       CCAAGG
                                     CACGA___
GAM722  LOC123872 5'  TGGGGCCCCGATCTTCCC    19358        G   CC
                                TGGGGCCC GATC  CCC
                                |||||||| ||||  |||
                                ACCCCGGG CTAG  GGG
                                     G   AA
GAM722  LOC149657 3'  TGGGGCCTGGGCCCAGCTC    19359       C  ATCCC
                                TGGGGCC GG    CCCGGTTC
                                ||||||| ||    ||||||||
                                ACCCCGG CC    GGGTCGAG
                                    A  C____
GAM722  LOC151438 5'  TGGGGTCCAGGTTCCCCGGCC  19360      C   ATCC
                                TGGGG CCGG    CCCCGGTT
                                ||||| ||||    ||||||||
                                ACCCC GGTC    GGGGCCGG
                                   A    CAA_
GAM722  LOC166341 5'  TGGGGCCCGGGCCCTCGGCT   19361         ATC   C
                                TGGGGCCCGG   CCC CGGTT
                                ||||||||||   ||| |||||
                                ACCCCGGGCC   GGG GCCGA
                                     C__   A
GAM722  LOC92095  3'  TGGGGCCCGGGGCCTCAGCT   19362         ATCC  C
                                TGGGGCCCGG    CC CGGTT
                                ||||||||||    || |||||
                                ACCCCGGGCC    GG GTCGA
                                     CC__  A
GAM722  LOC92096  3'  TGGGGCCCGGGGCCTCAGCT   19362         ATCC  C
                                TGGGGCCCGG    CC CGGTT
                                ||||||||||    || |||||
                                ACCCCGGGCC    GG GTCGA
                                     CC__  A
GAM723  ABL2     5'  CCCTGGCCCTGAGCGGCTGGG  19365     C    CCTCC  A
                                CCC GGCCC     CG GCTGGG
                                ||| |||||     || ||||||
                                GGG CCGGG     GC CGACCC
                                  A    ACTC_  _
GAM723  ADCY2    3'  TCCTCGGCCTCCCAAAATATTG 19366     C    CCC      C___
           GG                     TCC CGGCC   TCCCGAG    TGGG
                                ||| |||||   |||||||    ||||
                                AGG GCCGG   AGGGTTT    ACCC
                                  A    ___       TATA
GAM723  AF1Q     5'  TCCCCGCCCCCTCCTGCC    19367       G      CGA
                                TCCCCG CCCCCTCC   GCT
                                |||||| ||||||||   |||
                                AGGGGC GGGGGAGG   CGG
                                   _       A__
GAM723  AK3      5'  CGGCCCCCTACCTCTGG     19368         C  GAG
                                CGGCCCCCT CC   CTGG
                                ||||||||| ||   ||||
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                                GCCGGGGGA GG   GACC
                                     T  A__
GAM723  AKAP13   5'  TCCCCCGCGGGCCGAGCTGGG  19369      G  CCCCTC
                                TCCCC GC     CCGAGCTGGG
                                ||||| ||     ||||||||||
                                AGGGG CG     GGCTCGACCC
                                   G  CCC___
GAM723  AKAP13   5'  TCCCCCGCGGGCCGAGCTGGG  19369      G  CCCCTC
                                TCCCC GC     CCGAGCTGGG
                                ||||| ||     ||||||||||
                                AGGGG CG     GGCTCGACCC
                                   G  CCC___
GAM723  ALDH3A2  5'  TCCCCGGCTCTGGCAGCGGGCT 19370        CCCCTCC_  A
           GGG                    TCCCCGGC       CG GCTGGG
                                  ||||||||       || ||||||
                                  AGGGGCCG       GC CGACCC
                                       AGACCGTC  C
GAM723  ANKH     3'  TCCTTGGCCTCCCAAAGTGTTG 19371     CC   CCC      C___
           GG                     TCC  GGCC   TCCCGAG   TGGG
                                  |||  ||||   |||||||   ||||
                                  AGG  CCGG   AGGGTTT   ACCC
                                    AA    ___      CACA
GAM723  AP2M1    5'  TCCTCGGCCCCCTGCTCTGCCG 19372     C       CCCGA
           G                      TCC CGGCCCCCT    GCTGG
                                  ||| |||||||||    |||||
                                  AGG GCCGGGGGA    CGGCC
                                    A       CGAGA
GAM723  ASC      5'  CCCTTGGTCCCCTCCCACCCAG 19373     C_  C       AG TG
           G                      CCC  GG CCCCTCCCG  C  GG
                                  |||  || |||||||||  |  ||
                                  GGG  CC GGGGAGGGT  G  CC
                                    AA  A       G_ GT
GAM723  BARHL1   3'  CCCTTGGCCCCTTCCTGCC   19374     C_     C   CGA
                                  CCC  GGCCCC TCC   GCT
                                  |||  |||||| |||   |||
                                  GGG  CCGGGG AGG   CGG
                                    AA     A   A__
GAM723  CD34     5'  CCCGCCCCCTCCGCCCGGG   19375      G       C AG
                                  CCCG CCCCCTCC G  CTGGG
                                  |||| ||||||| |  |||||
                                  GGGC GGGGGAGG C  GGCCC
                                    _       _ G_
GAM723  CYLN2    5'  CCCCGGCCTCCTCCTCTCGGG  19376        C    CGAGC
                                  CCCCGGCC CCTCC    TGGG
                                  |||||||| |||||    ||||
                                  GGGGCCGG GGAGG    GCCC
                                       A    AGA__
GAM723  CYP1A2   3'  CCCCGGCCTCCCAAAATGCTGG 19377        CCC     ___
           G                      CCCCGGCC   TCCCGA   GCTGGG
                                  ||||||||   ||||||   ||||||
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                                GGGGCCGG  AGGGTT  CGACCC
                                   ___     TTA
GAM723  DUX4    5'  TCCCCGGCTCCCTCCCGCCCG  19378        C      AG
                                TCCCCGGC CCCTCCCG  CTG
                                |||||||| ||||||||  |||
                                AGGGGCCG GGGAGGGC  GGC
                                    A       G_
GAM723  FBXW1B  3'  TCCCCTGCCCCCTCCCTTCCCC 19379      G       GAG___
          CTGGG                 TCCCC GCCCCCTCCC     CTGGG
                                ||||| ||||||||||     |||||
                                AGGGG CGGGGGAGGG     GACCC
                                   A         AAGGGG
GAM723  FBXW1B  3'  TCCCCTGCCCCCTCCCTTCCCC 19379      G       GAG___
          CTGGG                 TCCCC GCCCCCTCCC     CTGGG
                                ||||| ||||||||||     |||||
                                AGGGG CGGGGGAGGG     GACCC
                                   A         AAGGGG
GAM723  FBXW1B  3'  TCCCCTGCCCCCTCCCTTCCCC 19379      G       GAG___
          CTGGG                 TCCCC GCCCCCTCCC     CTGGG
                                ||||| ||||||||||     |||||
                                AGGGG CGGGGGAGGG     GACCC
                                   A         AAGGGG
GAM723  FOXD2   5'  CCCCGGGAATCCGAGCTGGG  19380       CCCCCTC
                                CCCCGG     CCGAGCTGGG
                                ||||||     ||||||||||
                                GGGGCC     GGCTCGACCC
                                   CTTA___
GAM723  GAS7    3'  CCTCGGCCTCCCAAAGAGCTGG 19381    C    _  TCCC
          G                      CC CGGCC CCC   GAGCTGGG
                                || ||||| |||   ||||||||
                                GG GCCGG GGG   CTCGACCC
                                 A    A  TTT_
GAM723  HUNK    5'  TCCCCGGCTTCTCCCGCCG   19382        CCC    GA
                                TCCCCGGC  CTCCC  GCTG
                                ||||||||  |||||  ||||
                                AGGGGCCG  GAGGG  CGGC
                                    AA_    __
GAM723  IL1RL1LG 3'  CCAGGCCCCCTTCCTGG     19383    C      C  GAGC
                                CC GGCCCCCT CC   TGG
                                || |||||||| ||   |||
                                GG CCGGGGGA GG   ACC
                                 T       A  ____
GAM723  ITGAL   3'  TCCTTGGCCTCCCAAAGTGCTG 19384     CC   CCC    ___
          GG                    TCC  GGCC  TCCCGA  GCTGGG
                                |||  ||||  ||||||  ||||||
                                AGG  CCGG  AGGGTT  CGACCC
                                  AA   ___     TCA
GAM723  KCNJ5   3'  CCTCGGCCTCCCAAAATGCTGG 19385    C    CCC    ___
          G                     CC CGGCC  TCCCGA  GCTGGG
                                || |||||  ||||||  ||||||
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                                GG GCCGG   AGGGTT   CGACCC
                                 A    ___     TTA
GAM723  LIM2    3'  CAGCTCCCTCCCATGGG     19386      C       AGC
                                CGGC CCCTCCCG   TGGG
                                |||| ||||||||   ||||
                                GTCG GGGAGGGT   ACCC
                                  A      ___
GAM723  LY6E    3'  GGCTTTCCTTCCTGAGCTGGG  19387     C__  C   C
                                GGC   CC TCC GAGCTGGG
                                |||   || ||| ||||||||
                                CCG   GG AGG CTCGACCC
                                  AAA  A   A
GAM723  MAFF    3'  TCCTTGGACTCCCAAAGTGCTG 19388     CC  CCCC      ___
            GG                    TCC  GG    CTCCCGA   GCTGGG
                                ||| ||    |||||||   ||||||
                                AGG  CC    GAGGGTT   CGACCC
                                  AA  T___      TCA
GAM723  MBD3    3'  TCTCCAGTCTCAAGGAGCTGGG 19389    C    CCCC   CC_
                                TC CCGG    CTC   GAGCTGGG
                                || ||||    |||   ||||||||
                                AG GGTC    GAG   CTCGACCC
                                 A    A___   TTC
GAM723  MS4A1   3'  CCTCGGCCTCCCAAAGGGCTGG 19390    C    CCC     ___
            G                    CC CGGCC   TCCCGA   GCTGGG
                                || |||||   ||||||   ||||||
                                GG GCCGG   AGGGTT   CGACCC
                                 A    ___     TCC
GAM723  MYO1C   3'  CCGCCTCCCAAAGTGCTGGG   19391    _      ___
                                CC CCTCCCGA   GCTGGG
                                || ||||||||   ||||||
                                GG GGAGGGTT   CGACCC
                                 C       TCA
GAM723  PCDHA9  3'  CCTTGGCCTCCCAAAATGTTGG 19392    CC    CCC      C___
            G                    CC  GGCC   TCCCGAG    TGGG
                                ||  ||||   |||||||    ||||
                                GG  CCGG   AGGGTTT    ACCC
                                 AA    ___      TACA
GAM723  PCOLN3  3'  GCCTTGGCTTCCAAGCTGGG   19393     CC__  C
                                GCC    CT CCGAGCTGGG
                                |||    || ||||||||||
                                CGG    GA GGTTCGACCC
                                  AACC  A
GAM723  PIP5K1A 5'  TCCCCGCCCCCTCCG       19394       G       CGAGCT
                                TCCCCG CCCCCTCC      G
                                |||||| ||||||||      |
                                AGGGGC GGGGGAGG      C
                                   _      _______
GAM723  PNOC    5'  TCCCCGGCTCCCTCCGATGG   19395         C     C  GC
                                TCCCCGGC CCCTCC GA  TGG
                                |||||||| |||||| ||  |||
```

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                                AGGGGCCG GGGAGG CT  ACC
                                    A     _ __
GAM723  POLR2E   3'  CCCCGGCTCAGCTGAGCTGGG  19396       CCCCTCCC
                                CCCCGGC       GAGCTGGG
                                |||||||       ||||||||
                                GGGGCCG       CTCGACCC
                                   AGTCGA__
GAM723  PRX      3'  TCCTCGGCCCCCTCCTTGG   19397     C        CGAGC
                                TCC CGGCCCCCTCC    TGG
                                ||| ||||||||||    |||
                                AGG GCCGGGGGAGG    ACC
                                  A         A____
GAM723  PTPRF    3'  CCCTGCCCCTCAGCAAGCTGGG 19398     G    C  C_
                                CCC GCCCC TC  CGAGCTGGG
                                ||| ||||| ||  |||||||||
                                GGG CGGGG AG  GTTCGACCC
                                  A    _ TC
GAM723  PTPRF    3'  CCCTGCCCCTCAGCAAGCTGGG 19398     G    C  C_
                                CCC GCCCC TC  CGAGCTGGG
                                ||| ||||| ||  |||||||||
                                GGG CGGGG AG  GTTCGACCC
                                  A    _ TC
GAM723  RNH      5'  TCCATGGCCCCCTTCTGG    19399     CC      CCCGAG
                                TCC  GGCCCCCT     CTGG
                                |||  ||||||||     ||||
                                AGG  CCGGGGGA     GACC
                                  TA       A_____
GAM723  RNH      5'  TCCATGGCCCCCTTCTGG    19399     CC      CCCGAG
                                TCC  GGCCCCCT     CTGG
                                |||  ||||||||     ||||
                                AGG  CCGGGGGA     GACC
                                  TA       A_____
GAM723  SFRS2IP  5'  CCTCGGCCTCCCAAACTGCTGG 19400    C    CCC     ___
            G                    CC CGGCC   TCCCGA   GCTGGG
                                || |||||   ||||||   ||||||
                                GG GCCGG   AGGGTT   CGACCC
                                 A    ___     TGA
GAM723  SLC1A5   5'  TCCTTGGCCCTAGGAGCTGGG  19401     CC    CCTCCC
                                TCC  GGCCC     GAGCTGGG
                                |||  |||||     ||||||||
                                AGG  CCGGG     CTCGACCC
                                  AA    ATC___
GAM723  SLC1A5   5'  TCCTTGGCCCTAGGAGCTGGG  19401     CC    CCTCCC
                                TCC  GGCCC     GAGCTGGG
                                |||  |||||     ||||||||
                                AGG  CCGGG     CTCGACCC
                                  AA    ATC___
GAM723  UBE2G2   3'  CCTTGGCCTCCCAAAGAGCTGG 19402    CC   _   TCCC
            G                    CC  GGCC CCC    GAGCTGGG
                                ||  |||| |||    ||||||||
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                                GG  CCGG GGG    CTCGACCC
                                 AA    A   TTT_
GAM723  WEE1     5'  CCGGGTCTCTGCGAGCTGGG  19403     CCCC   C_
                                CCGG   CTC  CGAGCTGGG
                                ||||   |||  |||||||||
                                GGCC   GAG  GCTCGACCC
                                  CA__   AC
GAM723  WHSC1    3'  CCTGGCGGCTCGAGCTGGG   19404    C   CCC   CC
                                CC GGC   CTC  GAGCTGGG
                                || |||   |||  ||||||||
                                GG CCG   GAG  CTCGACCC
                                 A   CC_   __
GAM723  WHSC1    3'  CCTGGCGGCTCGAGCTGGG   19404    C   CCC   CC
                                CC GGC   CTC  GAGCTGGG
                                || |||   |||  ||||||||
                                GG CCG   GAG  CTCGACCC
                                 A   CC_   __
GAM723  WHSC1    3'  CCTGGCGGCTCGAGCTGGG   19404    C   CCC   CC
                                CC GGC   CTC  GAGCTGGG
                                || |||   |||  ||||||||
                                GG CCG   GAG  CTCGACCC
                                 A   CC_   __
GAM723  WHSC1    3'  CCTGGCGGCTCGAGCTGGG   19404    C   CCC   CC
                                CC GGC   CTC  GAGCTGGG
                                || |||   |||  ||||||||
                                GG CCG   GAG  CTCGACCC
                                 A   CC_   __
GAM723  WW45     3'  CCTCGGCCTCCCAAAATGCTGG 19385    C    CCC    ___
          G                      CC CGGCC   TCCCGA   GCTGGG
                                 || |||||   ||||||   ||||||
                                 GG GCCGG   AGGGTT   CGACCC
                                  A    ___     TTA
GAM723  C20orf51  5'  TCCCCGGCCCCCTCCAGCCTGG 19405           CG  _
          G                      TCCCCGGCCCCCTCC  AGC TGGG
                                 ||||||||||||||  ||| ||||
                                 AGGGGCCGGGGGAGG  TCG ACCC
                                          __  G
GAM723  CFLAR    3'  TCCTTGGCCTCCCAAAGTGCTG 19384    CC   CCC    ___
          GG                      TCC  GGCC   TCCCGA   GCTGGG
                                 |||  ||||   ||||||   ||||||
                                 AGG  CCGG   AGGGTT   CGACCC
                                  AA    ___     TCA
GAM723  CNNM1    3'  CCTCGGTCTTCCAAACTG    19406    C   CCCC  C
                                CC CGG    CT CCGAGCTG
                                || |||    || ||||||||
                                GG GCC    GA GGTTTGAC
                                 A  A___  A
GAM723  CNOT3    3'  CCCGGCCCCCTCCCTGCTTCCT 19407           GAG___
          GGG                     CCCGGCCCCCTCCC     CTGGG
                                 ||||||||||||||     |||||
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                                GGGCCGGGGGAGGG     GACCC
                                      ACGAAG
GAM723  CRMP5    3' TCCCAGGCCCCCTTTTGGCCCA 19408   C     T_________  GAGCT
           GCTG                  C GGCCCCC       CCC    G
                                | |||||||       |||    |
                                G CCGGGGGG       GGG    C
                                 T      AAAACCIII   TCGAG
GAM723  DKFZP434J037 3'  CCCTCTCAGCCTTCTGAGCTGG 19409    ___    CC  CCC
           G                    CCC   CGGCC  CT   GAGCTGGG
                                |||   |||||  ||   ||||||||
                                GGG   GTCGG  GA   CTCGACCC
                                  AGA    AA  ___
GAM723  DKFZp586I021 3'  CCTGGCCCCCTCTCCAGGG   19410   C       _  AGCT
                                CC GGCCCCCTC CCG    GGG
                                || |||||||| |||    |||
                                GG CCGGGGGAG GGT    CCC
                                 A       A  _____
GAM723  FKBP14   3' TCCTTGGCCCCCAAAGTGCTGG 19411    CC     TCCCGA
           G                    TCC  GGCCCCC     GCTGGG
                                |||  |||||||     ||||||
                                AGG  CCGGGGG     CGACCC
                                  AA      TTTCA_
GAM723  FLJ10704  3' CCTCGGCCTCCCAAAATGCTGG 19385    C    CCC     ___
           G                    CC CGGCC   TCCCGA   GCTGGG
                                || |||||   ||||||   ||||||
                                GG GCCGG   AGGGTT   CGACCC
                                 A     ___      TTA
GAM723  FLJ11700  3' TCCTCGGCCTCCCAAAGTGCTG 19412    C    CCC     ___
           GG                     TCC CGGCC   TCCCGA   GCTGGG
                                |||  |||||   ||||||   ||||||
                                AGG GCCGG   AGGGTT   CGACCC
                                  A     ___      TCA
GAM723  FLJ11996  3' CCTCGGTCTCCCGAGTAGCTGG 19413    C   CCCC     ___
           G                    CC CGG    CTCCCGA   GCTGGG
                                || |||    |||||||   ||||||
                                GG GCC    GAGGGCT   CGACCC
                                 A  A___      CAT
GAM723  FLJ12949  3' TCCCCAGCCTCCTGAGTAGCTG 19414         C   CCCG
           GG                     TCCCCGGCC CCT    AGCTGGG
                                |||||||||  |||    |||||||
                                AGGGGTCGG GGA    TCGACCC
                                     A   CTCA
GAM723  FLJ13193  3' GGCCTCCCAAAGTGTTGGG    19415     CCC     C___
                                GGCC   TCCCGAG    TGGG
                                ||||   |||||||    ||||
                                CCGG   AGGGTTT    ACCC
                                  ___      CACA
GAM723  FLJ13194  5' CGGCTCCCTCCCGCCG     19416     C     GA
                                CGGC CCCTCCC  GCTG
                                |||| |||||||  ||||
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                              GCCG GGGAGGG  CGGC
                                A     __
GAM723  FLJ13305  3' CGGCCTCCCAAAATGCTGGG  19417     CCC    ___
                              CGGCC  TCCCGA  GCTGGG
                              |||||  ||||||  ||||||
                              GCCGG  AGGGTT  CGACCC
                                 ___    TTA
GAM723  FLJ14326  3' CCTCGGCCTCCCAAATTGCTGG 19418   C   CCC    ___
          G                    CC CGGCC  TCCCGA  GCTGGG
                               || |||||  ||||||  ||||||
                               GG GCCGG  AGGGTT  CGACCC
                                A    ___    TAA
GAM723  FLJ14641  3' CGGCCTCCCAAAATGTTGGG  19419     CCC     C___
                              CGGCC  TCCCGAG  TGGG
                              |||||  |||||||  ||||
                              GCCGG  AGGGTTT  ACCC
                                 ___    TACA
GAM723  FLJ20004  5' CCTGCAGCGCCTTCTTGAGCTG 19420   C_  C  C  CC
          GG                   CC  CGGC CC TC  GAGCTGGG
                               ||  |||| || ||  ||||||||
                               GG  GTCG GG AG  CTCGACCC
                                AC   C  A  AA
GAM723  FLJ20006  3' TCCTTGGCCTCCCAAAGTGCTG 19384    CC   CCC    ___
          GG                   TCC  GGCC  TCCCGA  GCTGGG
                               |||  ||||  ||||||  ||||||
                               AGG  CCGG  AGGGTT  CGACCC
                                 AA   ___    TCA
GAM723  FLJ20413  3' CCCGGCCCTCTCTCCGCTGG  19421       C  _  GA
                              CCCGGCCC CTC CC  GCTGG
                              ||||||||  ||| ||  |||||
                              GGGCCGGG GAG GG  CGACC
                                   A  A  __
GAM723  FLJ20584  5' TCCCCGGCGCCCTCCG     19422       C    CGAGCT
                              TCCCCGGC CCCTCC     G
                              ||||||||  ||||||     |
                              AGGGGCCG GGGAGG     C
                                   C     _______
GAM723  FLJ21135  3' TCCCTGGCCTCCTACAGGGCCC 19423     C  T__________  GAGCT
          AGCTCGG                GGCC CC       CCC    GG
                              ||||  ||        |||    ||
                              CCGG GG        GGG    CC
                                A  ATGTCCCIII   TCGAG
GAM723  FLJ21369  3' CCTCGGCCTCCCAAGTAGCTGG 19424    C    _  TCCCG
          G                    CC CGGCC CCC    AGCTGGG
                               || ||||| |||    |||||||
                               GG GCCGG GGG    TCGACCC
                                A    A  TTCA_
GAM723  FLJ21687  3' TCCCCGTCCCCTCCCCACAGGG 19425      GC      GA  T
                              TCCCCG  CCCCTCCC  GC GGG
                              ||||||  ||||||||  || |||
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                                AGGGGC  GGGGAGGG  TG CCC
                                   A_      G_  T
GAM723  FLJ22477  3'  TCCTGACCCCCTCCCAGAG   19426    CC       _
                                TCC  GGCCCCCTCCC GAG
                                |||  |||||||||||| |||
                                AGG  CTGGGGGAGGG CTC
                                  A_         T
GAM723  FLJ23416  3'  TCTCCGGCCCCTCCTG     19427    C      C   CGAGC
                                TC CCGGCCCC TCC    TG
                                || |||||||| |||    ||
                                AG GGCCGGGG AGG    AC
                                 A      _  ______
GAM723  FLJ23519  5'  TCCATGGCCCCCTTCTGG    19399    CC      CCCGAG
                                TCC  GGCCCCCT    CTGG
                                |||  ||||||||     ||||
                                AGG  CCGGGGGA    GACC
                                  TA       A_____
GAM723  FLJ25467  3'  TCCTCAGTCTAGAGCTGG    19428    C   CCCCC  CC
                                TCC CGG    TC  GAGCTGG
                                ||| |||    ||  |||||||
                                AGG GTC    AG  CTCGACC
                                  A  _____  AT
GAM723  FLJ30092  3'  TCCTCGGCCTCCCAAAGTGCTG 19412    C    CCC    ___
           GG                    TCC CGGCC   TCCCGA   GCTGGG
                                |||  |||||   ||||||   ||||||
                                AGG GCCGG   AGGGTT   CGACCC
                                  A   ___      TCA
GAM723  GABBR1   5'  TCCCCGGCTCTCCCCG     19429        CCC    GAGC
                                TCCCCGGC   CTCCC   TG
                                ||||||||   |||||   ||
                                AGGGGCCG   GAGGG   GC
                                     A__    _____
GAM723  GNB4     3'  CCTTGGCCTCCCAAATTGCTGG 19430    CC   CCC    ___
           G                     CC  GGCC   TCCCGA   GCTGGG
                                ||  ||||   ||||||   ||||||
                                GG  CCGG   AGGGTT   CGACCC
                                 AA   ___      TAA
GAM723  INE1     3'  CCTCGGCCCCACAAAGAGCTGG 19431    C     CTCCC
           G                     CC CGGCCCC    GAGCTGGG
                                || |||||||    ||||||||
                                GG GCCGGGG    CTCGACCC
                                 A      TGTTT
GAM723  KIAA0222 3'  TCCCCGGCTGTTCTTCCATGG  19432        CCC_  C   AGC
                                TCCCCGGC    CT CCG   TGG
                                ||||||||    || |||   |||
                                AGGGGCCG    GA GGT   ACC
                                     ACAA  A   ___
GAM723  KIAA0451 5'  GGCCTCCCAAAGAGCTGGG   19433     _   TCCC
                                GGCC CCC    GAGCTGGG
                                ||||  |||    ||||||||
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                              CCGG GGG   CTCGACCC
                                A  TTT_
GAM723  KIAA0495 5' TCCCCGGCTCCCATCTAG   19434       CCCC   AG
                              TCCCCGGC   TCCCG CTGG
                              ||||||||   ||||| ||||
                              AGGGGCCG   AGGGT GATC
                                  _____   A_
GAM723  KIAA0515 3' TCCCCGGCCCCCTCCTCTAGG 19435          CGAG
                              TCCCCGGCCCCCTCC   CTGGG
                              ||||||||||||||   |||||
                              AGGGGCCGGGGGAGG   GATCC
                                     A___
GAM723  KIAA0528 5' CCCGGCCCCACAAGGCTGGG  19436       CTCC  _
                              CCCGGCCCC   CGAG CTGGG
                              |||||||||   |||| |||||
                              GGGCCGGGG   GTTC GACCC
                                   T___   C
GAM723  KIAA0557 3' TCCCCTGCCCCCTCCACTCCGG 19437     G      CGAG
           G                   TCCCC GCCCCCTCC   CTGGG
                              ||||| |||||||||   |||||
                              AGGGG CGGGGGAGG   GGCCC
                                A       TGA_
GAM723  KIAA0618 3' CCTTGGCCTCCCAAAATGCTGG 19438   CC   CCC    ___
           G                   CC  GGCC  TCCCGA  GCTGGG
                              ||  ||||  ||||||  ||||||
                              GG  CCGG  AGGGTT  CGACCC
                               AA   ___    TTA
GAM723  KIAA0852 5' CGGCCTCCCAAAGTGCTGGG  19439     CCC    ___
                              CGGCC  TCCCGA  GCTGGG
                              |||||  ||||||  ||||||
                              GCCGG  AGGGTT  CGACCC
                                 ___    TCA
GAM723  KIAA0876 3' CCCCGGCCCTCTCCAGG    19440       C   CGAGCT
                              CCCCGGCCC CTCC    GG
                              ||||||||| ||||    ||
                              GGGGCCGGG GAGG    CC
                                   A  T_____
GAM723  KIAA0894 3' CCTCGGCCTCCCAAATTGCTGG 19418   C    CCC    ___
           G                   CC CGGCC  TCCCGA  GCTGGG
                              || |||||  ||||||  ||||||
                              GG GCCGG  AGGGTT  CGACCC
                               A   ___    TAA
GAM723  KIAA0945 3' TCCCCAGCTCCCTCCCCTGG  19441       C     GAG
                              TCCCCGGC CCCTCCC  CTGG
                              |||||||| |||||||  ||||
                              AGGGGTCG GGGAGGG  GACC
                                   A     ___
GAM723  KIAA1007 5' TCCTCGACCCCCTCTTCGGCCC 19442        _________ GAGCTG
           AGCTG                CGGCCCCCTC      CC    G
                              ||||||||||      ||    |
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                              GCTGGGGGAG      GG     C
                                   AAGCCIII  GTCGAG
GAM723  KIAA1164  3'  CCTTGGCCTCCCAAAATGTTGG 19392    CC    CCC      C___
            G                   CC  GGCC   TCCCGAG    TGGG
                              ||  ||||   |||||||    ||||
                              GG  CCGG   AGGGTTT    ACCC
                               AA    ___      TACA
GAM723  KIAA1196  3'  TCCCTTGCCCCAAGCTGG    19443      CG    CTCCC
                              TCCC  GCCCC    GAGCTGG
                              ||||  |||||    |||||||
                              AGGG  CGGGG    TTCGACC
                                AA    ______
GAM723  KIAA1228  5'  CCCGGCCGAGGCGGGCTGGG   19444        CCCTCC  A
                              CCCGGCC     CG GCTGGG
                              |||||||     || ||||||
                              GGGCCGG     GC CGACCC
                                   CTCC__  C
GAM723  KIAA1297  5'  TCTCCAGCTTCGAGCTGG    19445    C    CCCCTCC
                              TC CCGGC      CGAGCTGG
                              || |||||      ||||||||
                              AG GGTCG      GCTCGACC
                               A    AA_____
GAM723  KIAA1484  3'  CCCCGGCCCCGGGTGACGGGCT 19446          CTCC__  A
            GGG                   CCCCGGCCCC     CG GCTGGG
                              ||||||||||     || ||||||
                              GGGGCCGGGG     GC CGACCC
                                   CCCACT  C
GAM723  KIAA1754  3'  TCCCTGGCCCCCTGCAAGG    19447      C       CCCGA  T_
                              TCCC GGCCCCCT    GC  GG
                              |||| ||||||||    ||  ||
                              AGGG CCGGGGGA    CG  CC
                                A       ______ TT
GAM723  MAP4K1    5'  CCCTGGGGGCCTGAGCTGG   19448    C  CCC   CCC
                              CCC GG   CCT   GAGCTGG
                              ||| ||   |||   |||||||
                              GGG CC   GGA   CTCGACC
                                A  CCC   ___
GAM723  MAPK8IP3  3'  TCCCCGGCCTGCTCCTGA    19449        CC    C
                              TCCCCGGCC  CTCC GA
                              |||||||||  |||| ||
                              AGGGGCCGG  GAGG CT
                                   AC    A
GAM723  MAST205   3'  GGCCCCTCCTGAGGCTGGG   19450       C   C   _
                              GGCCCC TCC GAG CTGGG
                              |||||| ||| ||| |||||
                              CCGGGG AGG CTC GACCC
                                 _   A   C
GAM723  MGC23244  3'  CCTCGGCTTCCCAAACTGCTGG 19451    C    CCCC     ___
            G                   CC CGGC    TCCCGA   GCTGGG
                              || ||||    ||||||   ||||||
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                                GG GCCG   AGGGTT  CGACCC
                                 A   A___     TGA
GAM723  MGC2574  3' TCCCAGGCCCCCTCTG     19452     C      CCGAGC
                                TCCC GGCCCCCTC     TG
                                |||| |||||||||     ||
                                AGGG CCGGGGGAG     AC
                                  T      _______
GAM723  MGC4248  3' TCCCTGGTTATCCCTGAGCTGG 19453     C  CCCCC   _
           G                     TCCC GG    TCCC GAGCTGGG
                                |||| ||    |||| ||||||||
                                AGGG CC    AGGG CTCGACCC
                                  A  AAT__   A
GAM723  NICE-3   5' TCCCCGGCCATTTCCTTACGGG 19454        CCC  CGA  T
                                TCCCCGGCC  TCC  GC GGG
                                |||||||||  |||  || |||
                                AGGGGCCGG  AGG  TG CCC
                                     TAA  AA_  _
GAM723  NPEPL1   3' CCCGGTCCCCTCCCCGTGG   19455     C      GAGC
                                CCCGG CCCCTCCC   TGG
                                ||||| ||||||||   |||
                                GGGCC GGGGAGGG   ACC
                                  A      GC__
GAM723  NPTXR    3' CCTCGGCCTCCCGAGTAGCTGG 19456   C    CCC    ___
           G                     CC CGGCC  TCCCGA  GCTGGG
                                || |||||  ||||||  ||||||
                                GG GCCGG  AGGGCT  CGACCC
                                 A    ___     CAT
GAM723  NPTXR    3' CCTCGGCCTCCCGAGTAGCTGG 19456   C    CCC    ___
           G                     CC CGGCC  TCCCGA  GCTGGG
                                || |||||  ||||||  ||||||
                                GG GCCGG  AGGGCT  CGACCC
                                 A    ___     CAT
GAM723  PASK     5' GCCTTCCTCCCGAGCTCTGG  19457    C_       G_
                                GCC  CCTCCCGAGCT  GG
                                |||  ||||||||||  ||
                                CGG  GGAGGGCTCGA  CC
                                  AA         GA
GAM723  PP2447   5' TCCTTGGCCCCCTCCCCGACAG 19458    CC       GA  T
           G                     TCC  GGCCCCCTCCC  GC GG
                                |||  ||||||||||  || ||
                                AGG  CCGGGGGAGGG  TG CC
                                  AA         GC  T
GAM723  PRO2037  3' GCCTTGGTCTCCCAAAGCTGGG 19459    CC___     _
                                GCC    CTCCCGA GCTGGG
                                |||    ||||||| ||||||
                                CGG    GAGGGTT CGACCC
                                  AACCA      T
GAM723  RASGRP4  5' CAGCCCCTAGGGAGCTGGG   19460       CTCCC
                                CGGCCCC    GAGCTGGG
                                |||||||    ||||||||
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                              GTCGGGG    CTCGACCC
                                 ATCC_
GAM723  RoXaN    3'  CCTCGGCCTCCCAAATTGCTGG 19418    C    CCC    ___
           G                   CC CGGCC   TCCCGA   GCTGGG
                               || |||||   ||||||   ||||||
                               GG GCCGG   AGGGTT   CGACCC
                                A    ___     TAA
GAM723  RoXaN    3'  CCTTGGCCCTGGAGAGCTGGG  19461    CC    CCTCCC
                               CC  GGCCC    GAGCTGGG
                               ||  |||||    ||||||||
                               GG  CCGGG    CTCGACCC
                                AA    ACCT__
GAM723  SC65     3'  CCTTGGCCTCCCAAAATGCTGG 19438    CC    CCC    ___
           G                   CC  GGCC   TCCCGA   GCTGGG
                               ||  ||||   ||||||   ||||||
                               GG  CCGG   AGGGTT   CGACCC
                                AA   ___     TTA
GAM723  SEC14L2  3'  TCCCTGGCCCTCCCTGC     19462     C    CC    GA
                               TCCC GGCCC  TCCC  GC
                               |||| |||||  ||||  ||
                               AGGG CCGGG  AGGG  CG
                                 A    __   A_
GAM723  SEMA7A   3'  TCCCCGACCCATGGGCTCTTGG 19463         C____   CCGA
           GCTGGG                 CCCCGGCCC    CTC    GCTGGG
                               |||||||||    |||    ||||||
                               GGGGCTGGG    GAG    CGACCC
                                    TACCC   AACC
GAM723  SNAPC1   3'  CCTCGGCCTCCCAAAATGCTGG 19385    C    CCC    ___
           G                   CC CGGCC   TCCCGA   GCTGGG
                               || |||||   ||||||   ||||||
                               GG GCCGG   AGGGTT   CGACCC
                                A    ___     TTA
GAM723  SRF      3'  CCCCCGGCTTTCTCCTGG    19464        CCC    CGAGC
                               TCCCCGGC   CTCC    TGG
                               ||||||||   ||||    |||
                               GGGGGCCG   GAGG    ACC
                                    AAA   _____
GAM723  SSBP3    5'  CCCGGCCCCCTCCCCGG     19465           GAGC
                               CCCGGCCCCCTCCC   TGG
                               ||||||||||||||   |||
                               GGGCCGGGGGAGGG   GCC
                                                ____
GAM723  TIP-1    3'  AGCCCTTCTGAGCTGGG     19466      CC  CC
                               GGCCC  TC  GAGCTGGG
                               |||||  ||  ||||||||
                               TCGGG  AG  CTCGACCC
                                  A_  A_
GAM723  TNFSF13  3'  CCCTGGTCTTCCAAGCTGGG   19467     C  CCCC  C
                               CCC GG    CT CCGAGCTGGG
                               ||| ||    || ||||||||||
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                                GGG CC    GA GGTTCGACCC
                                  A  A___  A
GAM723  TRAF3    3'  TCCCCGGCCCTCCCTTGGGCTG 19468          CC    GA__
                                TCCCCGGCCC  TCCC    GCTG
                                ||||||||||  ||||    ||||
                                AGGGGCCGGG  AGGG    CGAC
                                      __    AACC
GAM723  ULK2     5'  TCCTCGGCCCTCCCCGCTCGGG 19469     C     CC    GA  _
                                TCC CGGCCC  TCCC  GCT GGG
                                |||  ||||||  ||||  |||  |||
                                AGG GCCGGG  AGGG  CGA CCC
                                  A      __    G_   G
GAM723  WDR13    5'  TCCCCGGCCTCCTCCTCTGG   19470         C     CGAG
                                TCCCCGGCC CCTCC    CTGG
                                |||||||||  |||||    ||||
                                AGGGGCCGG GGAGG    GACC
                                      A     A___
GAM723  ZFP106   3'  CCTCGGCCTCCCAAAGAGCTGG 19381    C    _   TCCC
                G                    CC CGGCC CCC    GAGCTGGG
                                || |||||  |||    ||||||||
                                GG GCCGG GGG    CTCGACCC
                                  A     A   TTT_
GAM723  LOC122509 5'  TCTCCGGCCTTTTCCCAAGCTG 19471    C      CCC
                G                    TC CCGGCC   TCCCGAGCTGG
                                || ||||||   ||||||||||
                                AG GGCCGG   AGGGTTCGACC
                                  A      AAA
GAM723  LOC124222 5'  TCCCCGAGCCTCCTCCTCAGTG 19472        _   C     CG  C
                GG                    TCCCCG GCC CCTCC  AG TGGG
                                ||||||  |||  |||||  ||  ||||
                                AGGGGC CGG GGAGG  TC ACCC
                                     T   A     AG  _
GAM723  LOC124871 5'  TCCCCGGCCCCTGCCTG     19473           CT  CGAGC
                                TCCCCGGCCCC  CC     TG
                                ||||||||||  ||     ||
                                AGGGGCCGGGG  GG     AC
                                      AC  _____
GAM723  LOC126432 3'  CCTTGGCCTCCCAAAATGTTGG 19392    CC    CCC      C___
                G                    CC  GGCC   TCCCGAG    TGGG
                                ||  ||||   |||||||    ||||
                                GG  CCGG   AGGGTTT    ACCC
                                  AA    ___       TACA
GAM723  LOC138241 3'  TCCTTGGCCTCCCAAAGTGTTG 19371     CC    CCC      C___
                GG                    TCC  GGCC   TCCCGAG    TGGG
                                |||  ||||   |||||||    ||||
                                AGG  CCGG   AGGGTTT    ACCC
                                  AA    ___       CACA
GAM723  LOC142901 5'  TCCCCGCCCCCTCCAG      19474        G       CGAGCT
                                TCCCCG CCCCCTCC      G
                                ||||||  ||||||||      |
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                                AGGGGC GGGGGAGG     C
                                  _       T_____
GAM723  LOC143451 3'  CCTCGGCCCCCTCCAGAATTTG 19475    C        C  C_
           GG                    CC CGGCCCCCTCC GAG  TGGG
                                 || |||||||||| |||  ||||
                                 GG GCCGGGGGAGG CTT  ACCC
                                  A         T  AA
GAM723  LOC145125 3'  CCTCGGCCCCCTCCAGAATTTG 19475    C        C  C_
           GG                    CC CGGCCCCCTCC GAG  TGGG
                                 || |||||||||| |||  ||||
                                 GG GCCGGGGGAGG CTT  ACCC
                                  A         T  AA
GAM723  LOC145258 3'  CGACCCCCTCCCGCAAGG    19476           AGCT
                                 CGGCCCCCTCCCG   GG
                                 ||||||||||||   ||
                                 GCTGGGGGAGGGC   CC
                                       GTT_
GAM723  LOC145566 5'  GGCTCCCCCGAGGGGCTGGG  19477    CC  T   ___
                                 GGC  CC CCCGA   GCTGGG
                                 |||  || |||||   ||||||
                                 CCG  GG GGGCT   CGACCC
                                  A_  _    CCC
GAM723  LOC146315 5'  CCCTGGCCTGGGCTCTGAGCTG 19478    C   CC__  CC
           GG                    CCC GGCC   CTC  GAGCTGGG
                                 ||| ||||   |||  ||||||||
                                 GGG CCGG   GAG  CTCGACCC
                                  A   ACCC   A_
GAM723  LOC148345 5'  CCCCTGGCCCCCTCCCTGG   19479     _       GAGC
                                 CCCC GGCCCCCTCCC   TGG
                                 |||| ||||||||||   |||
                                 GGGG CCGGGGGAGGG   ACC
                                  A        _____
GAM723  LOC149113 3'  TCCTCGGCCTCCCAAAGTGCTG 19412    C    CCC    ___
           GG                    TCC CGGCC   TCCCGA   GCTGGG
                                 ||| |||||   ||||||   ||||||
                                 AGG GCCGG   AGGGTT   CGACCC
                                  A   ___      TCA
GAM723  LOC149134 5'  TCCTAGGTCCCCCCCAAGAGCT 19480    CC  _     CC
           GGG                    TCC  GG CCCCCTC  GAGCTGGG
                                 |||  || |||||||  ||||||||
                                 AGG  CC GGGGGGG  CTCGACCC
                                  AT  A      TT
GAM723  LOC149668 3'  TCCTGGCCCCTCCCTGCTG   19481    CC    C   GA
                                 TCC  GGCCCC TCCC  GCTG
                                 |||  |||||| ||||  ||||
                                 AGG  CCGGGG AGGG  CGAC
                                  A_     _   A_
GAM723  LOC150095 3'  TCCTTGGCCTCCCAAAGTGCTG 19384    CC   CCC    ___
           GG                    TCC  GGCC   TCCCGA   GCTGGG
                                 |||  ||||   ||||||   ||||||
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                                AGG  CCGG   AGGGTT   CGACCC
                                  AA   ___     TCA
GAM723   LOC150998 3'  CGGCCTCCCAAAGTACTGGG   19482      CCC     ___
                                CGGCC   TCCCGA   GCTGGG
                                |||||   ||||||   ||||||
                                GCCGG   AGGGTT   TGACCC
                                   ___     TCA
GAM723   LOC151174 5'  TCCCCGGCTGTCCTCCTGCTG  19483       CC_    CGA
                                TCCCCGGC   CCTCC   GCTG
                                ||||||||   |||||   ||||
                                AGGGGCCG   GGAGG   CGAC
                                    ACA    A__
GAM723   LOC151429 3'  CCTCGGCCTCCCAAAGGGCTGG 19390    C    CCC     ___
           G                     CC CGGCC   TCCCGA   GCTGGG
                                || |||||   ||||||   ||||||
                                GG GCCGG   AGGGTT   CGACCC
                                 A    ___     TCC
GAM723   LOC151438 5'  TCCCCGGCCTCCTGTTGGGCCC 19484     C  T__________   GAGCT
           AGCTCGG                GGCC CC        CCC    GG
                                |||| ||        |||    ||
                                CCGG GG        GGG    CC
                                  A  ACAACCCIII   TCGAG
GAM723   LOC152263 3'  TCCTTGGCCTCCCAAAGTGCTG 19384    CC   CCC     ___
           GG                    TCC  GGCC   TCCCGA   GCTGGG
                                |||  ||||   ||||||   ||||||
                                AGG  CCGG   AGGGTT   CGACCC
                                  AA   ___     TCA
GAM723   LOC152627 5'  CAGCCTCCCAAATTGCTGGG   19485      CCC     ___
                                CGGCC   TCCCGA   GCTGGG
                                |||||   ||||||   ||||||
                                GTCGG   AGGGTT   CGACCC
                                   ___     TAA
GAM723   LOC152633 5'  CCCTTGGCCCCCTCCCTCCGGG 19486    C_        GAG
                                CCC  GGCCCCCTCCC   CTGGG
                                |||  ||||||||||   |||||
                                GGG  CCGGGGGAGGG   GGCCC
                                  AA         A__
GAM723   LOC154403 3'  TCCTCGGCCTCCCAAAGTGCTG 19412    C    CCC     ___
           GG                    TCC CGGCC   TCCCGA   GCTGGG
                                |||  |||||   ||||||   ||||||
                                AGG GCCGG   AGGGTT   CGACCC
                                  A    ___     TCA
GAM723   LOC154739 5'  CCTTGGTCTCCCAAAATGCTGG 19487    CC  CCCC     ___
           G                     CC  GG    CTCCCGA   GCTGGG
                                ||  ||    |||||||   ||||||
                                GG  CC    GAGGGTT   CGACCC
                                 AA  A___      TTA
GAM723   LOC154992 3'  TCCTCGGCCTCCCAAAGTGCTG 19412    C    CCC     ___
           GG                    TCC CGGCC   TCCCGA   GCTGGG
                                |||  |||||   ||||||   ||||||
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                                AGG GCCGG   AGGGTT   CGACCC
                                  A    ___      TCA
GAM723   LOC155006 3'  CCTCGGCCTCCCAAGTAGCTGG 19424    C    _  TCCCG
             G                     CC CGGCC CCC    AGCTGGG
                                || ||||| |||    |||||||
                                GG GCCGG GGG    TCGACCC
                                  A    A   TTCA_
GAM723   LOC157657 3'  CCTCGGCCTCCCGAGTAGTTGG 19488    C    CCC     C___
             G                     CC CGGCC   TCCCGAG   TGGG
                                || |||||   |||||||   ||||
                                GG GCCGG   AGGGCTC   ACCC
                                  A    ___      ATCA
GAM723   LOC157923 5'  CCCCCGGCCCTTTCCTCCTGTG 19489         ___    CGAGC
             G                     TCCCCGGCCC   CCTCC    TGG
                                ||||||||||   |||||    |||
                                GGGGGCCGGG   GGAGG    ACC
                                      AAA    AC___
GAM723   LOC158337 3'  TCCTCAGCCTCCCAAGCAGCTG 19490    C    _  TCCCG
             GG                      TCC CGGCC CCC    AGCTGGG
                                ||| ||||| |||    |||||||
                                AGG GTCGG GGG    TCGACCC
                                  A    A   TTCG_
GAM723   LOC159090 5'  CCCTGCCCCCCTCCCGCCT   19491    G    _    AG
                                CCC GCCCCC TCCCG  CT
                                ||| |||||| |||||  ||
                                GGG CGGGGG AGGGC  GA
                                  A     G    G_
GAM723   LOC168544 3'  TCCTAGGAGGTCCGAGCTGGG  19492    CC  CCCCCTC
                                TCC  GG     CCGAGCTGGG
                                |||  ||     ||||||||||
                                AGG  CC     GGCTCGACCC
                                  AT  TCCA___
GAM723   LOC196528 3'  TCCCTGGGCCCAAGCTGG    19493     C  CCCCCT
                                TCCC GG     CCCGAGCTGG
                                ||||  ||     ||||||||||
                                AGGG CC     GGGTTCGACC
                                  A  C_____
GAM723   LOC196989 3'  CCCCCGGCCCCCTCCCCGG   19494            GAGC
                                TCCCCGGCCCCCTCCC   TGG
                                ||||||||||||||||   |||
                                GGGGGCCGGGGGAGGG   GCC
                                          ____
GAM723   LOC199676 3'  TCCCCGAGCCTCCTCCTCCAGG 19495      _  C    CGAG TG
                                TCCCCG GCC CCTCC   C  GG
                                |||||| ||| |||||   |  ||
                                AGGGGC CGG GGAGG   G  CC
                                   T   A    A___ GT
GAM723   LOC199796 5'  CCCGGCCCTCTTCTCGTGGTTG 19496       C  _ C  AGC_
             GG                     CCCGGCCC CT C CG   TGGG
                                |||||||| || | ||   ||||
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                                GGGCCGGG GA G GC    ACCC
                                    A  A A  ACCA
GAM723  LOC201564 3'  CCTCGGCCTCCCAAGTAGCTGG 19424    C    _  TCCCG
              G                  CC CGGCC CCC    AGCTGGG
                                 || ||||| |||    |||||||
                                 GG GCCGG GGG    TCGACCC
                                  A    A   TTCA_
GAM723  LOC201780 5'  CCGGTCCCCTCCCGCCG     19497     C      GA
                                 CCGG CCCCTCCC  GCTG
                                 |||| ||||||||  ||||
                                 GGCC GGGGAGGG  CGGC
                                   A      __
GAM723  LOC201868 3'  TCCTCGGCCTCCCAAAGTGCTG 19412     C    CCC     ___
              GG                   TCC CGGCC   TCCCGA   GCTGGG
                                 ||| |||||   ||||||   ||||||
                                 AGG GCCGG   AGGGTT   CGACCC
                                   A    ___     TCA
GAM723  LOC202020 3'  CGGCCTCCCAAACTGCTGGG   19498      CCC     ___
                                 CGGCC   TCCCGA   GCTGGG
                                 |||||   ||||||   ||||||
                                 GCCGG   AGGGTT   CGACCC
                                    ___     TGA
GAM723  LOC203276 3'  CCTTGGCCTCCCAAATTGCTGG 19430    CC    CCC     ___
              G                   CC  GGCC   TCCCGA   GCTGGG
                                 ||  ||||   ||||||   ||||||
                                 GG  CCGG   AGGGTT   CGACCC
                                  AA   ___     TAA
GAM723  LOC203305 3'  CCTTGGCCTCCCAAATTGCTGG 19430    CC    CCC     ___
              G                   CC  GGCC   TCCCGA   GCTGGG
                                 ||  ||||   ||||||   ||||||
                                 GG  CCGG   AGGGTT   CGACCC
                                  AA   ___     TAA
GAM723  LOC219653 3'  GGCCCCTCCCTGAACTAG     19499       C   _
                                 GGCCCC TCCC GAGCTGG
                                 |||||| |||| |||||||
                                 CCGGGG AGGG CTTGATC
                                    _   A
GAM723  LOC219654 3'  TCTCCACGCACCTTCCGAGCTG 19500    C   _  CC   C
              GG                   TC CCG GC  CCT CCGAGCTGGG
                                 || ||| ||  ||| ||||||||||
                                 AG GGT CG  GGA GGCTCGACCC
                                  A  G  T_   A
GAM723  LOC253070 3'  TCCCCAGCTCCTTCGCTGG    19501         C  C  CCGA
                                 TCCCCGGC CC TC    GCTGG
                                 |||||||| || ||    |||||
                                 AGGGGTCG GG AG    CGACC
                                     A  A  ____
GAM723  LOC253239 3'  GGCGCTTCCGAGCTGGG     19502     CCC  C
                                 GGC   CT CCGAGCTGGG
                                 |||   || ||||||||||
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                                CCG   GA GGCTCGACCC
                                  C__  A
GAM723  LOC253758 5'  TCCCACGGCTCCACGGCTGGG  19503     _   CCCC  _ A
                                TCCC CGGC   TCC CG GCTGGG
                                |||| ||||   ||| || ||||||
                                AGGG GCCG   AGG GC CGACCC
                                  T   _____  T  _
GAM723  LOC253866 5'  CCCCGGCCTCCTCCGAAGGG  19504       C    C  CT
                                CCCCGGCC CCTCC GAG  GGG
                                |||||||| ||||| |||  |||
                                GGGGCCGG GGAGG CTT  CCC
                                    A    _  __
GAM723  LOC254243 3'  CCTTGGCCTCCCAAATTGCTGG 19430    CC   CCC    ___
          G                      CC  GGCC   TCCCGA   GCTGGG
                                ||  ||||   ||||||   ||||||
                                GG  CCGG   AGGGTT   CGACCC
                                 AA   ___     TAA
GAM723  LOC254440 3'  CCTCGGCCCCCTCCAGAATTTG 19475    C        C  C_
          GG                     CC CGGCCCCCTCC GAG  TGGG
                                || ||||||||||| |||  ||||
                                GG GCCGGGGGAGG CTT  ACCC
                                 A         T  AA
GAM723  LOC255937 3'  CCTCGGCCTCCAAAGAGCTGGG 19505    C    C  TCCC
                                CC CGGCC CC   GAGCTGGG
                                || ||||| ||   ||||||||
                                GG GCCGG GG   CTCGACCC
                                 A   A  TTT_
GAM723  LOC256052 3'  TCCCCGATCCCCTTTCCGCCGG 19506      GC    CCCGA
                                TCCCCG  CCCCT    GCTGG
                                ||||||  |||||    |||||
                                AGGGGC  GGGGA    CGGCC
                                   TA    AAGG_
GAM723  LOC256160 5'  CCGGTCCCCTCCCGCCG     19497     C      GA
                                CCGG CCCCTCCC  GCTG
                                |||| ||||||||  ||||
                                GGCC GGGGAGGG  CGGC
                                  A      __
GAM723  LOC51308  3'  TCCCCGTTCTCTCATGGGCTGG 19507      GCCCC  CCGA
          G                      TCCCCG    CTC   GCTGGG
                                ||||||    |||   ||||||
                                AGGGGC    GAG   CGACCC
                                   AAGA_  TACC
GAM723  LOC57406  5'  CCCTCGGTCTCTAGCCCCGGGC 19508    _  CCCCC__   A
          TGGG                    CCC CGG      TCCCG GCTGGG
                                ||| |||      ||||| ||||||
                                GGG GCC      GGGGC CGACCC
                                  A  AGAGATC    C
GAM723  LOC86010  5'  CCCGGCCCCCTCCCCGG     19465           GAGC
                                CCCGGCCCCCTCCC   TGG
                                ||||||||||||||   |||
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                                GGGCCGGGGGAGGG  GCC
                                     ____
GAM723  LOC90038  3' CCTTGGCCTCCCAAATTGCTGG 19430   CC  CCC   ___
           G                  CC  GGCC  TCCCGA  GCTGGG
                              ||  ||||  ||||||  ||||||
                              GG  CCGG  AGGGTT  CGACCC
                               AA   ___    TAA
GAM723  LOC91442  3' CCTCGGCCTCCCAAGTAGCTGG 19424   C   _  TCCCG
           G                  CC CGGCC CCC   AGCTGGG
                              || ||||| |||   |||||||
                              GG GCCGG GGG   TCGACCC
                               A   A  TTCA_
GAM723  LOC91978  3' CCCCGGCCTCCTCCGCAGGGCT 19509       C   _ A_
           GGG                  CCCCGGCC CCTCC CG  GCTGGG
                              |||||||| ||||| ||  ||||||
                              GGGGCCGG GGAGG GT  CGACCC
                                   A   C  CC
GAM723  LOC92405  3' TCCTCAGCCTCCCGAGTAGCTG 19510   C   CCC   ___
           GG                   TCC CGGCC  TCCCGA  GCTGGG
                              ||| |||||  ||||||  ||||||
                              AGG GTCGG  AGGGCT  CGACCC
                               A   ___    CAT
GAM723  LOC92661  5' CCTCGGCCTCCCAAATTGCTGG 19418   C   CCC   ___
           G                  CC CGGCC  TCCCGA  GCTGGG
                              || |||||  ||||||  ||||||
                              GG GCCGG  AGGGTT  CGACCC
                               A   ___    TAA
GAM724  CD7     3' GTGGGTGGGCCGGCACTGACAG 19513   C_  A_  AA
                              GTG  TG  CC  CACTGACAG
                              |||  ||  ||  |||||||||
                              CAC  AC  GG  GTGACTGTC
                                CC  CC  CC
GAM724  CYFIP2   5' TGACGTGCGTGGTCATGGCTGC 19514       _ AC  ACA  A
           AG                   TGACGTGC TG  CA  CTG CAG
                              |||||||| ||  ||  ||| |||
                              ACTGCACG AC  GT  GAC GTC
                                   C  CA  ACC  _
GAM724  DVL3    3' GAAGCACTGATACTGACAG   19515   C TG   CCAAC
                              GA G  CTGA   ACTGACAG
                              || |  ||||   ||||||||
                              CT C  GACT   TGACTGTC
                               T GT   A____
GAM724  HPSE    3' GTGCTAAATCTAGCACTGACAG 19516       CCAA__
                              GTGCTGA    CACTGACAG
                              |||||||    |||||||||
                              CACGATT    GTGACTGTC
                                  TAGATC
GAM724  RGL     5' TGCTGTCACACAGCACTGACAG 19517      __ _  A
                              TGCTG  AC CA CACTGACAG
                              |||||  || || |||||||||
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                                ACGAC  TG GT GTGACTGTC
                                   AG  T  C
GAM724  TXNIP    3'  TGACTGACCAAGTGCTGGCAG  19518   T       CA_   A
                                G GCTGACCAA   CTG CAG
                                | |||||||||   ||| |||
                                A TGACTGGTT   GAC GTC
                                 C       CAC   C
GAM724  FLJ10038  3'  GTGCTAACCACAACA       19519          ACAC
                                GTGCTGACCA    TGACA
                                ||||||||||    |||||
                                CACGATTGGT    GTTGT
                                      _____
GAM724  FLJ20040  3'  GCGTGACAAGGCACTGACAG   19520     C    CAA_
                                GTG TGAC    CACTGACAG
                                ||| ||||    |||||||||
                                CGC ACTG    GTGACTGTC
                                  _    TTCC
GAM724  ITGA8    5'  TGATATCTGCAACACTGGCAG  19521     CG G   AC       A
                                TGA  T CTG  CAACACTG CAG
                                |||  | |||  |||||||| |||
                                ACT  A GAC  GTTGTGAC GTC
                                  AT _  __       C
GAM724  KIAA0864  3'  TGCTGGGCCTTAATACTGACAG 19522       A_  AAC__
                                TGCTG  CC     ACTGACAG
                                |||||  ||    ||||||||
                                ACGAC  GG     TGACTGTC
                                   CC  AATTA
GAM724  KIAA1405  3'  TGAGGCAAAGACCAACACTG   19523     C   CT
                                TGA GTG  GACCAACACTG
                                ||| |||  ||||||||||
                                ACT CGT  CTGGTTGTGAC
                                  C   TT
GAM724  SDF1     3'  TGACATGTGAGGGAGCACTGA  19524        C   CCAA_
                                TGACGTG TGA     CACTGA
                                |||||||  |||    ||||||
                                ACTGTAC ACT     GTGACT
                                    _   CCCTC
GAM724  LOC130074 3'  ACGGGGGCCAACACTGACAG   19525     TGCTGA
                                ACG      CCAACACTGACAG
                                |||      ||||||||||||
                                TGC      GGTTGTGACTGTC
                                  CCCC__
GAM724  LOC143392 3'  CGTGCGTGGCTGGCACTGGCAG 19526       _  ACCAA     A
                                CGTGC TG     CACTG CAG
                                |||||  ||    ||||| |||
                                GCACG AC     GTGAC GTC
                                   C  CGACC     C
GAM724  LOC149910 3'  CGATGGTCAACACTGACAG    19527    C  AC
                                TG TG  CAACACTGACAG
                                ||  ||  ||||||||||||
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                                GC AC  GTTGTGACTGTC
                                 T  CA
GAM725  ADRBK2   3'  TGGCTGAGGGGGCCCCG     19530         C   T
                                TGGCTGGGG GGG CCCCG
                                ||||||||| ||| |||||
                                ACCGACTCC CCC GGGGC
                                      _   _
GAM725  AHR      5'  TGGCGGCCGGGTCCCCG     19531      TG  G
                                TGGC  GG CGGGTCCCCG
                                ||||  || ||||||||||
                                ACCG  CC GCCCAGGGGC
                                  __ G
GAM725  ANK1     5'  TGGCAGCCAGGTCCCCG     19532      TG  G
                                TGGC  GG CGGGTCCCCG
                                ||||  || ||||||||||
                                ACCG  TC GTCCAGGGGC
                                  __ G
GAM725  ANK1     5'  TGGCAGCCAGGTCCCCG     19532      TG  G
                                TGGC  GG CGGGTCCCCG
                                ||||  || ||||||||||
                                ACCG  TC GTCCAGGGGC
                                  __ G
GAM725  ANK1     5'  TGGCAGCCAGGTCCCCG     19532      TG  G
                                TGGC  GG CGGGTCCCCG
                                ||||  || ||||||||||
                                ACCG  TC GTCCAGGGGC
                                  __ G
GAM725  ATBF1    5'  TGGCGTCCGGGTCCCCG     19533      T GGG
                                TGGC G   CGGGTCCCCG
                                |||| |   ||||||||||
                                ACCG C   GCCCAGGGGC
                                  _ AG_
GAM725  BMP6     5'  TGGCGTGAGCAGTCCCCG    19534      TG     G
                                TGGC  GGGCGG TCCCCG
                                ||||  |||||| ||||||
                                ACCG  CTCGTC AGGGGC
                                  CA     _
GAM725  CDK10    3'  GGCTGGGAGCCCCCG       19535       GCG
                                GGCTGGG   GGTCCCCG
                                |||||||   ||||||||
                                CCGACCC   TCGGGGGC
                                     ____
GAM725  CDK10    3'  TGGCTGGGGCGGCCCG      19536          GTC
                                TGGCTGGGGCGG   CCCG
                                ||||||||||||   ||||
                                ACCGACCCCGCC   GGGC
                                     ____
GAM725  CDK10    3'  GGCTGGGAGCCCCCG       19535       GCG
                                GGCTGGG   GGTCCCCG
                                |||||||   ||||||||
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                              CCGACCC  TCGGGGGC
                                 ___
GAM725  CENTD2   5'  TGGCTGGGGCCCCCG      19537        GGGT
                              TGGCTGGGGC   CCCCG
                              ||||||||||   |||||
                              ACCGACCCCG   GGGGC
                                 _____
GAM725  CHD4     3'  TGGCTAGAGCCGCTGGGTTCC  19538        ____   C
                              TGGCTGGGGC   GGGT CC
                              ||||||||||   |||| ||
                              ACCGATCTCG   CCCA GG
                                    GCGA   A
GAM725  CKTSF1B1 5'  AGTGCGGCGGGTCCTCG    19539   C  G      C
                              GG TG GGCGGGTCC CG
                              || || |||||||||| ||
                              TC AC CCGCCCAGG GC
                               _  G       A
GAM725  COL5A1   3'  GGCTGGGGTCCCACACCCCG  19540       ___  G T
                              GGCTGGGG  CG G CCCCG
                              ||||||||  || | |||||
                              CCGACCCC  GT T GGGGC
                                   AGG  G _
GAM725  CRAT     5'  GGCTGGGGTCGGTGGGTCC   19541       _ ___
                              GGCTGGGG C   GGGTCC
                              |||||||| |   ||||||
                              CCGACCCC G   CCCAGG
                                   A CCA
GAM725  CSNK1A1  5'  GGCTGGGGCCAAGCCCCG   19542        G  T
                              GGCTGGGGC GG CCCCG
                              ||||||||| || |||||
                              CCGACCCCG TT GGGGC
                                    G  C
GAM725  CTNS     3'  GGCTGGGTACACTGGGTCCC  19543       ___  _
                              GGCTGGG   GC GGGTCCC
                              |||||||   || |||||||
                              CCGACCC   TG CCCAGGG
                                   ATG  A
GAM725  CXorf6   3'  TGGCTGAGGGGTGTTTTCCCCG 19544        C  _ ___
                              TGGCTGGGG GG G   TCCCCG
                              ||||||||| || |   ||||||
                              ACCGACTCC CC C   AGGGGC
                                    _  A AAA
GAM725  CYLN2    3'  GGCTGAAGGTCCCCG      19545       GGC
                              GGCTGG   GGGTCCCCG
                              ||||||   |||||||||
                              CCGACT   TCCAGGGGC
                                 ___
GAM725  DYSF     5'  GGCTAGGCTGGGTCCCCG    19546       GC
                              GGCTGGG  GGGTCCCCG
                              |||||||  |||||||||
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                                CCGATCC  CCCAGGGGC
                                   GA
GAM725  ENPP1    5'  GGCCGCCTGCGGGTCCCCG   19547      GG_
                                GGCTG  GCGGGTCCCCG
                                |||||  ||||||||||
                                CCGGC  CGCCCAGGGGC
                                  GGA
GAM725  EP300    5'  CGGCCCGGGGTCCCCG     19548      G  CGG
                                TGGCT GGG  GTCCCCG
                                ||||| |||  |||||||
                                GCCGG CCC  CAGGGGC
                                  G  ___
GAM725  FRK      5'  TGGCTGGAGGTGCTACCCCG  19549       CGG  __
                                TGGCTGGGG  GT  CCCCG
                                |||||||||  ||  |||||
                                ACCGACCTC  CG  GGGGC
                                     CA_  AT
GAM725  FTL      5'  GGCTGGAAGAGAGTCCCCG   19550      _ C
                                GGCTGGG G GGGTCCCCG
                                ||||||| | |||||||||
                                CCGACCT C CTCAGGGGC
                                   T T
GAM725  FXYD7    3'  TGGGTGGGGCGGCTCATTCCG  19551    C      G  C__
                                TGG TGGGGCGG TC  CCG
                                ||| ||||||| ||  |||
                                ACC ACCCCGCC AG  GGC
                                  C      G  TAA
GAM725  GLUL     5'  GGCTGGGGGAGGATCCCCG   19552      C_
                                GGCTGGGG  GGGTCCCCG
                                ||||||||  |||||||||
                                CCGACCCC  CCTAGGGGC
                                     CT
GAM725  HAP1     3'  TGGCTGGGGAGAGGAGACCC  19553       C__  TC
                                TGGCTGGGG  GGG  CCC
                                |||||||||  |||  |||
                                ACCGACCCC  CCT  GGG
                                     TCT  CT
GAM725  HAS2     5'  TGGCTGGGGCTGTTTCAAGTC  19554       _______
                                TGGCTGGGGC    GGGTC
                                ||||||||||    |||||
                                ACCGACCCCG    TTCAG
                                     ACAAAG
GAM725  HMX1     3'  TGGCTGAGGGCAGCTGCCCCG  19555     _    GT_
                                TGGCTG GGGCGG  CCCCG
                                |||||| ||||||  |||||
                                ACCGAC CCCGTC  GGGGC
                                   T    GAC
GAM725  HOXC5    3'  GGCTGGGGAGGTTCCCG    19556      C  C
                                GGCTGGGG GGGT CCCG
                                |||||||| |||| ||||
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                                CCGACCCC TCCA GGGC
                                    _   A
GAM725  HRH2    5'  GGCTGGGGTAGGTCTCCG   19557       CG   C
                                GGCTGGGG  GGTC CCG
                                ||||||||  |||| |||
                                CCGACCCC  CCAG GGC
                                    AT   A
GAM725  IFI27   3'  TGGCTGGGTGCCTTCTCCCC  19558       _ GGG_
                                TGGCTGGG GC   TCCCC
                                ||||||||  ||   |||||
                                ACCGACCC CG   AGGGG
                                    A  GAAG
GAM725  IKBKB   5'  GGCTGGGGCGGCCAAACCCG  19559        G ___
                                GGCTGGGGCGG TC  CCCG
                                ||||||||||  ||  ||||
                                CCGACCCCGCC GG  GGGC
                                    _ TTT
GAM725  IL11    3'  TGGCGGGGGGATCACC     19560     T   C   C
                                TGGC GGGG GGGTC CC
                                |||| |||| ||||| ||
                                ACCG CCCC CCTAG GG
                                  _   _    T
GAM725  IMPDH1  3'  TGGCTGAGGGGCACGGCCC  19561     __    _
                                TGGCT  GGGGCG GGTCC
                                |||||  |||||| |||||
                                ACCGA  CCCCGT CCGGG
                                   CT    G
GAM725  LMO1    5'  TGGCGGGGCGGCCGGTCCTCG 19562     T     ___   C
                                TGGC GGGGCGG   GTCC CG
                                |||| |||||||   |||| ||
                                ACCG CCCCGCC   CAGG GC
                                  _     GGC   A
GAM725  MAP3K10 5'  TGGCTGGGGCGCCCTCCG   19563       GG   _
                                TGGCTGGGGC  GTCC CCG
                                ||||||||||  |||| |||
                                ACCGACCCCG  CGGG GGC
                                    __   A
GAM725  MEF2B   5'  GGCTGGGGGGCCCCG      19564       CG  T
                                GGCTGGGG  GG CCCCG
                                ||||||||  || |||||
                                CCGACCCC  CC GGGGC
                                    __ _
GAM725  MIF     3'  AGCGTGCGGCGGGTTCCCG   19565    _ G     C
                                GGC TG GGCGGGT CCCG
                                ||| || ||||||| ||||
                                TCG AC CCGCCCA GGGC
                                  C G     A
GAM725  MSI1    3'  GGCTGGGGTGGGCAACCG    19566       C   CC
                                GGCTGGGG GGGT  CCG
                                |||||||| ||||  |||
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                                CCGACCCC CCCG  GGC
                                    A    TT
GAM725  MTMR2    5'  GGCTGAAGCAGTCTTCG     19567          G  CC
                                GGCTGGGGCGG TC  CG
                                |||||||||| ||  ||
                                CCGACTTCGTC AG  GC
                                      _  AA
GAM725  MYO1D    3'  TGGCTGAGGGGCTGGCCC    19568       __    G
                                TGGCT  GGGGC GGTCC
                                |||||  ||||| |||||
                                ACCGA  CCCCG CCGGG
                                   CT    A
GAM725  NPY2R    3'  GGCTGGAGAATCCCCG      19569        CG
                                GGCTGGGG  GGTCCCCG
                                ||||||||  ||||||||
                                CCGACCTC  TTAGGGGC
                                      __
GAM725  NPY2R    5'  GGCTGGAGAATCCCCG      19569        CG
                                GGCTGGGG  GGTCCCCG
                                ||||||||  ||||||||
                                CCGACCTC  TTAGGGGC
                                      __
GAM725  NR2E1    5'  GGCGAAGGGTCCCCG       19570     TG   C
                                GGC  GGG GGGTCCCCG
                                |||  ||| |||||||||
                                CCG  CTT CCCAGGGGC
                                     __  _
GAM725  PFKFB4   3'  GGCTGGGCAACCTCCG      19571       G   GT  _
                                GGCTGGG CGG  CC CCG
                                ||||||| |||  ||  |||
                                CCGACCC GTT  GG GGC
                                   _  __  A
GAM725  PIK3R2   3'  GCTTGGGGCGGGTCCTCG    19572     _         C
                                GCT GGGGCGGGTCC CG
                                ||| ||||||||||| ||
                                CGA CCCCGCCCAGG GC
                                  A          A
GAM725  PLG      3'  TAGCTGGGGACAGTGTCTTCG  19573          _  _  CC
                                TGGCTGGGG CGG GTC  CG
                                ||||||||| ||| |||  ||
                                ATCGACCCC GTC CAG  GC
                                      T   A   AA
GAM725  POLR2A   3'  GGCTGGGGGTGACGCCCCG   19574         CG  _
                                GGCTGGGG  GGT CCCCG
                                ||||||||  ||| |||||
                                CCGACCCC  CTG GGGGC
                                     CA   C
GAM725  PPP1R7   3'  TGGCTGGGCAGTTCTTCCG   19575         G   G  C_
                                TGGCTGGG CGG TC  CCG
                                |||||||| ||| ||  |||
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                                ACCGACCC GTC AG  GGC
                                    _  A  AA
GAM725  PPP2R5C  3'  TAGCTGGGGCAATCTTCG    19576          G  CC
                                TGGCTGGGGCGG TC  CG
                                |||||||||||| ||  ||
                                ATCGACCCCGTT AG  GC
                                      _ AA
GAM725  PRCC     5'  TGGCGGGGCGGGGAACCG    19577     T      TCC
                                TGGC GGGGCGGG  CCG
                                |||| ||||||||  |||
                                ACCG CCCCGCCC  GGC
                                  _      CTT
GAM725  RFXAP    5'  TGGCCGGGGTCCACGACCCCG  19578         __ _  T
                                TGGCTGGGG  CG GG CCCCG
                                |||||||||  || || |||||
                                ACCGGCCCC  GT CT GGGGC
                                     AG  G  _
GAM725  RGS14    5'  GCCGATCAGGGGTCCCCG     19579      __ C
                                GCTGG  GG GGGTCCCCG
                                |||||  || |||||||||
                                CGGCT  TC CCCAGGGGC
                                   AG  _
GAM725  SCRT1    3'  TGGCTGGGGGAGGCCCCG     19580        C  T
                                TGGCTGGGG GGG CCCCG
                                |||||||||  ||| |||||
                                ACCGACCCC TCC GGGGC
                                     C  _
GAM725  SECTM1   3'  TGGCTGGGGGCTCCCC      19581         CG G
                                TGGCTGGGG  G TCCCC
                                |||||||||  | |||||
                                ACCGACCCC  C AGGGG
                                     __ G
GAM725  SEPX1    3'  TGGCAGGGGCGGCCTCCG     19582      T     GT  _
                                TGGC GGGGCGG  CC CCG
                                |||| |||||||  || |||
                                ACCG CCCCGCC  GG GGC
                                  T      __  A
GAM725  SGCE     5'  TGGCTAGGCCGTCCGTCCTCG  19583        G  G__   C
                                TGGCTGGG CG   GTCC CG
                                ||||||||  ||   |||| ||
                                ACCGATCC GC   CAGG GC
                                     G  AGG    A
GAM725  SLC25A1  3'  TGCCTGGGGCGGTCCCC      19584    G       G
                                TG CTGGGGCGG TCCCC
                                ||  |||||||||  |||||
                                AC GACCCCGCC AGGGG
                                 G       _
GAM725  SNX6     5'  GGCTGGCGCGGTCCCCG      19585       G   G
                                GGCTGG GCGG TCCCCG
                                ||||||  |||| ||||||
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                                CCGACC CGCC AGGGGC
                                   G   _
GAM725  SOX15   5'  TGACTGGGGGACCCCCG     19586        CG GT
                                TGGCTGGGG  G  CCCCG
                                |||||||||  |  |||||
                                ACTGACCCC  C  GGGGC
                                      __ TG
GAM725  SOX4    3'  GGCTGGGCAGAGTGGGTCCCCG 19587        ____ C
                                GGCTGGG   G GGGTCCCCG
                                |||||||   | |||||||||
                                CCGACCC   C CCCAGGGGC
                                    GTCT A
GAM725  STAT5B  5'  TGCCTGCGCTGGGTCCCCG   19588   G   GG  _
                                TG CTG  GC GGGTCCCCG
                                || |||  || |||||||||
                                AC GAC  CG CCCAGGGGC
                                 G  G_  A
GAM725  TBX6    5'  GGCTGGGGTGGAGACCCC    19589       C  _ T
                                GGCTGGGG GG G CCCC
                                |||||||| || | ||||
                                CCGACCCC CC C GGGG
                                    A  T T
GAM725  TBX6    5'  GGCTGGGGTGGAGACCCC    19589       C  _ T
                                GGCTGGGG GG G CCCC
                                |||||||| || | ||||
                                CCGACCCC CC C GGGG
                                    A  T T
GAM725  TGFB1   5'  GGCTGGGGGTCTCCCG     19590       CGG  _
                                GGCTGGGG  GTC CCCG
                                ||||||||  ||| ||||
                                CCGACCCC  CAG GGGC
                                    ___  A
GAM725  TRPM2   5'  TGGCTGGGGCCCCCG      19537        GGGT
                                TGGCTGGGGC  CCCCG
                                ||||||||||  |||||
                                ACCGACCCCG  GGGGC
                                    _____
GAM725  UMOD    3'  TGGCTGGAGCACTGGCCC    19591         __
                                TGGCTGGGGCG GGTCC
                                |||||||||||  |||||
                                ACCGACCTCGT  CCGGG
                                     GA
GAM725  VASP    5'  GGCCGGGGCGGGTCTCCG    19592          C
                                GGCTGGGGCGGGTC CCG
                                |||||||||||||| |||
                                CCGGCCCCGCCCAG GGC
                                     A
GAM725  AGS3    5'  GGCTGAAGAAGTCCTCG     19593       C    C
                                GGCTGGGG GGGTCC CG
                                |||||||| |||||| ||
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                                CCGACTTC TTCAGG GC
                                   _     A
GAM725  ALTE     5' GCGAGCCCCCGGGTCCCCG   19594    T  G___
                                GC GGG   CGGGTCCCCG
                                || |||   ||||||||||
                                CG CTC   GCCCAGGGGC
                                 _  GGGG
GAM725  ATP6V1D  5' CGGCTCGGGTCCCCG      19595     GGGG
                                TGGCT   CGGGTCCCCG
                                |||||   ||||||||||
                                GCCGA   GCCCAGGGGC
                                  _____
GAM725  C11orf15 5' GGCTGGGGATCCTCCG      19596       CGG  _
                                GGCTGGGG  GTCC CCG
                                ||||||||  |||| |||
                                CCGACCCC  TAGG GGC
                                   ___   A
GAM725  C11orf24 5' GGCTGGGCGGTCCCCG      19597      G  G
                                GGCTGGG CGG TCCCCG
                                ||||||| ||| ||||||
                                CCGACCC GCC AGGGGC
                                   _  _
GAM725  C20orf102 3' GGCTGGGGGGCCCCG      19564       CG  T
                                GGCTGGGG  GG CCCCG
                                ||||||||  || |||||
                                CCGACCCC  CC GGGGC
                                   __  _
GAM725  C20orf18 5' GGCTGATCGCGGGTCCCCG   19598      G_
                                GGCTGG  GCGGGTCCCCG
                                ||||||  ||||||||||
                                CCGACT  CGCCCAGGGGC
                                   AG
GAM725  C20orf18 5' TGTTTGGGGCGACCCCACC   19599   GC      G  _
                                TG  TGGGGCGG TCC CC
                                ||  |||||||| ||| ||
                                AC  ACCCCGCT GGG GG
                                 AA       G  T
GAM725  C20orf18 5' GGCTGATCGCGGGTCCCCG   19598      G_
                                GGCTGG  GCGGGTCCCCG
                                ||||||  ||||||||||
                                CCGACT  CGCCCAGGGGC
                                   AG
GAM725  C20orf18 5' TGTTTGGGGCGACCCCACC   19599   GC      G  _
                                TG  TGGGGCGG TCC CC
                                ||  |||||||| ||| ||
                                AC  ACCCCGCT GGG GG
                                 AA       G  T
GAM725  CARD11   3' TGGCTGTCCGGGTCCCCG   19600      GGG
                                TGGCTG  CGGGTCCCCG
                                ||||||  ||||||||||
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                                ACCGAC  GCCCAGGGGC
                                   AG_
GAM725  CBX6    3' GCTGGGGCGGCACCTCCG   19601       GT _
                                GCTGGGGCGG  CC CCG
                                ||||||||||  || |||
                                CGACCCCGCC  GG GGC
                                     GT  A
GAM725  CDIPT   3' TGGCTGGGGGCGGAGGTC   19602       _  __
                                TGGCTGGGG CGG  GTC
                                ||||||||| |||  |||
                                ACCGACCCC GCC  CAG
                                     C   TC
GAM725  DCLRE1A 5' TGGCGGGAACAAGTTCCCG  19603    T      C
                                TGGC GGGGCGGGT CCCG
                                |||| ||||||||| ||||
                                ACCG CCTTGTTCA GGGC
                                  C       A
GAM725  DKFZP434C128 3' TGGCGGGAGGTGGTCCCCG  19604    T   CG
                                TGGC GGGG  GGTCCCCG
                                |||| ||||  ||||||||
                                ACCG CCTC  CCAGGGGC
                                  C   CA
GAM725  DKFZp761F2014 3' GGCTGGGGCAGGTAATCCCG  19605         C__
                                GGCTGGGGCGGGT  CCCG
                                ||||||||||||  ||||
                                CCGACCCCGTCCA  GGGC
                                      TTA
GAM725  DRIL2   3' GGCTGGGCAGCCCCG     19606      G  GT
                                GGCTGGG CGG  CCCCG
                                |||||||  |||  |||||
                                CCGACCC GTC  GGGGC
                                   _  __
GAM725  EHM2    5' TGGCTGGGGGCGCCCCC    19607       CGG
                                TGGCTGGGG  GTCCCC
                                |||||||||  ||||||
                                ACCGACCCC  CGGGGG
                                     CG_
GAM725  FLJ11099 3' TGGACTGGGAATCCCC    19608    _    CGG
                                TGG CTGGGG  GTCCCC
                                ||| ||||||  ||||||
                                ACC GACCCT  TAGGGG
                                  T   ____
GAM725  FLJ13639 3' TGGCTGGGTCCATGTCCC  19609      G_ G
                                TGGCTGGG  CG GTCCC
                                ||||||||  || |||||
                                ACCGACCC  GT CAGGG
                                     AG  A
GAM725  FLJ13902 3' GGCTGGGAATCCCTCG    19610       CGG   _
                                GGCTGGGG  GTCCC CG
                                ||||||||  ||||| ||
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                                CCGACCCT   TAGGG GC
                                   ___     A
GAM725  FLJ14816  3'  TGAGTCACTGGGTCCCCG    19611     __ _
                                TGGG  GC GGGTCCCCG
                                ||||  || |||||||||
                                ACTC  TG CCCAGGGGC
                                  AG  A
GAM725  FLJ20160  3'  TGGCTGGGGGGGCCTCACCC   19612        C  G_ _
                                TGGCTGGGG GG  TC CCC
                                ||||||||| ||  || |||
                                ACCGACCCC CC  AG GGG
                                     _ GG  T
GAM725  FLJ20257  5'  TGACTTAGGGGTCTCCG     19613      GG  C    C
                                TGGCT  GG GGGTC CCG
                                |||||  || ||||| |||
                                ACTGA  TC CCCAG GGC
                                   A_ _    A
GAM725  FLJ20330  5'  TGGCCGGCTCATCCCCG     19614      GG   GG
                                TGGCT  GGC  GTCCCCG
                                |||||  |||  |||||||
                                ACCGG  CCG  TAGGGGC
                                   __  AG
GAM725  FLJ20509  5'  TGGTGGGGGGGAGGGGTTCCCG 19615     C    C____   C
                                TGG TGGGG    GGGT CCCG
                                ||| |||||    |||| ||||
                                ACC ACCCC    CCCA GGGC
                                  _    CCCTC   A
GAM725  FLJ21135  5'  TGACGGGTCGCGGGTCCCCG   19616     T  __
                                TGGC GGG  GCGGGTCCCCG
                                |||| |||  ||||||||||
                                ACTG CCC  CGCCCAGGGGC
                                   _  AG
GAM725  FLJ21438  5'  TGGCGACGAAGGTCCTCG    19617     TGG  __   C
                                TGGC   GGCG  GGTCC CG
                                ||||   ||||  ||||| ||
                                ACCG   CTGC  CCAGG GC
                                  ___   TT    A
GAM725  FLJ22056  5'  GCTGGGACTTGGTCTCCG    19618       G_   C
                                GCTGGGGC  GGTC CCG
                                ||||||||  |||| |||
                                CGACCCTG  CCAG GGC
                                     AA   A
GAM725  FLJ22679  5'  TGTCTGGGGGAGCCCCC     19619    G    C
                                TG CTGGGG GGGTCCCC
                                || |||||| ||||||||
                                AC GACCCC CTCGGGGG
                                 A    _
GAM725  FLJ22795  3'  TGACTGAAGGCTGGGTCCC    19620       _  _
                                TGGCTGG GGC GGGTCCC
                                ||||||| ||| |||||||
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                                ACTGACT CCG CCCAGGG
                                    T  A
GAM725  GMEB1    5'  TAGCTGGGACTGCGTCTCCG  19621        GG_  C
                                TGGCTGGGGC  GTC CCG
                                ||||||||||  ||| |||
                                ATCGACCCTG  CAG GGC
                                     ACG  A
GAM725  KCNG3    5'  TGGCCGGGGAGTCCTCG    19622        CG   C
                                TGGCTGGGG  GGTCC CG
                                |||||||||  ||||| ||
                                ACCGGCCCC  TCAGG GC
                                     __   A
GAM725  KCNT1    3'  TGGATGCCGCAGGTCCCCG  19623    C  GG
                                TGG TG  GCGGGTCCCCG
                                ||| ||  ||||||||||
                                ACC AC  CGTCCAGGGGC
                                  T  GG
GAM725  KDELR1   5'  TGGCGGGGGGTGCCCCC    19624    T   C _
                                TGGC GGGG GG GTCCCC
                                |||| |||| || ||||||
                                ACCG CCCC CC CGGGGG
                                  _   _ A
GAM725  KIAA0189 3'  TGGCTGGTGGCAGCAGTC   19625      _   __
                                TGGCTGG GGCGG  GTC
                                ||||||| |||||  |||
                                ACCGACC CCGTC  CAG
                                    A   GT
GAM725  KIAA0227 3'  TGCCTGGAAGTCCCCG     19626   G   GCG
                                TG CTGGG   GGTCCCCG
                                || |||||   ||||||||
                                AC GACCT   TCAGGGGC
                                 G   ___
GAM725  KIAA0316 3'  TAGCTGAAGGGTCCCCG    19627       GC
                                TGGCTGGG  GGGTCCCCG
                                ||||||||  |||||||||
                                ATCGACTT  CCCAGGGGC
                                          __
GAM725  KIAA0322 5'  TGGCTGGGGAGGGGACCC   19628       C  TC
                                TGGCTGGGG GGG  CCC
                                ||||||||| |||  |||
                                ACCGACCCC CCC  GGG
                                     T  CT
GAM725  KIAA0415 3'  GGCTGGGGTCATGCCCTCCG  19629       _ G  _
                                GGCTGGGG CG GTCC CCG
                                |||||||| || |||| |||
                                CCGACCCC GT CGGG GGC
                                     A A  A
GAM725  KIAA0513 3'  TGTTGGGGTCAGGCCCCG   19630   GC   _  T
                                TG  TGGGG CGGG CCCCG
                                ||  ||||| |||| |||||
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                                AC  ACCCC GTCC GGGGC
                                 A_     A   _
GAM725  KIAA0618 3' TGGCTGAGGAGGACTTCC    19631         C  __
                                TGGCTGGGG GGG  TCC
                                ||||||||| |||  |||
                                ACCGACTCC CCT  AGG
                                     T  GA
GAM725  KIAA0672 5' TGCCTGGGGCCGTCCTCG    19632    G     GG   C
                                TG CTGGGGC  GTCC CG
                                || |||||||  |||| ||
                                AC GACCCCG  CAGG GC
                                 G      G_   A
GAM725  KIAA0939 3' TGGCTGGGGCTATCACACC    19633         GG  C__
                                TGGCTGGGGC  GTC   CC
                                ||||||||||  |||   ||
                                ACCGACCCCG  TAG   GG
                                     A_   TGT
GAM725  KIAA0940 3' TGGCTGGGTCGGCCCG      19634        G  GTC
                                TGGCTGGG CGG   CCCG
                                |||||||| |||   ||||
                                ACCGACCC GCC   GGGC
                                    A  ___
GAM725  KIAA1075 3' TGGCAGGGGCTGATCCCC    19635     T    G
                                TGGC GGGGC GGTCCCC
                                |||| ||||| |||||||
                                ACCG CCCCG CTAGGGG
                                  T    A
GAM725  KIAA1193 3' GGCTGGGGCAGCCCG       19636          GTC
                                GGCTGGGGCGG   CCCG
                                ||||||||||   ||||
                                CCGACCCCGTC   GGGC
                                      ___
GAM725  KIAA1238 5' TGGCCGGGCGTCCTCG      19637        G GG   C
                                TGGCTGGG C  GTCC CG
                                |||||||| |  |||| ||
                                ACCGGCCC G  CAGG GC
                                    _ __   A
GAM725  KIAA1529 5' TGACTGGGGTCAGGACCCC    19638         _   T
                                TGGCTGGGG CGGG CCCC
                                ||||||||| |||| ||||
                                ACTGACCCC GTCC GGGG
                                     A   T
GAM725  KIAA1691 3' TGGCTGTGGCGGGGCCTCCG   19639       G    T _
                                TGGCTG GGCGGG CC CCG
                                |||||| |||||| || |||
                                ACCGAC CCGCCC GG GGC
                                   A    C A
GAM725  KIAA1755 5' TGTCTGGGGCAGCCCTCG    19640    G       GT  _
                                TG CTGGGGCGG  CCC CG
                                || |||||||||  ||| ||
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                                AC GACCCCGTC  GGG GC
                                 A       __  A
GAM725  KIAA1766 5' CGGGAAGCGGGTCCCCG    19641    CT
                                TGG  GGGGCGGGTCCCCG
                                |||  ||||||||||||||
                                GCC  CTTCGCCCAGGGGC
                                  __
GAM725  KIAA1817 5' TGACTGGGGCAGCTTCCTCCG 19642         G_  _
                                TGGCTGGGGCGG  TCC CCG
                                ||||||||||||  ||| |||
                                ACTGACCCCGTC  AGG GGC
                                      GA  A
GAM725  KIAA1855 3' TGGCTGAGCCTTCCCCG    19643       G GGG
                                TGGCTGGG C   TCCCCG
                                ||||||||  |   ||||||
                                ACCGACTC G   AGGGGC
                                    _ GA_
GAM725  KIAA1881 5' TGCCTGGGGCGGCCCC     19644    G      GT
                                TG CTGGGGCGG  CCCC
                                || |||||||||  ||||
                                AC GACCCCGCC  GGGG
                                 G       __
GAM725  KIAA1909 5' TGGCTGGGGAAGTCTCC    19645       C    C
                                TGGCTGGGG GGGTC CC
                                |||||||||  |||||  ||
                                ACCGACCCC TTCAG GG
                                     _    A
GAM725  KIAA1924 3' GGCTGGGGGGGCCCCG     19646       C  T
                                GGCTGGGG GGG CCCCG
                                ||||||||  |||  |||||
                                CCGACCCC CCC GGGGC
                                     _  _
GAM725  LMOD1    3' GGCTGGGGTGGATGTGGTCCC 19647       C _____
                                GGCTGGGG GG    GTCCC
                                ||||||||  ||    |||||
                                CCGACCCC CC    CAGGG
                                    A  TACAC
GAM725  MGC10960 3' TGGCTGAGATGTCCTCG    19648       CGG   C
                                TGGCTGGGG   GTCC CG
                                |||||||||   ||||  ||
                                ACCGACTCT   CAGG GC
                                     A__   A
GAM725  MGC13057 5' GGCCCGGGGCGGGTCTCCG   19649    _       C
                                GGCT GGGGCGGGTC CCG
                                ||||  ||||||||||  |||
                                CCGG CCCCGCCCAG GGC
                                  G        A
GAM725  MGC15548 5' GCTGAGGCGGGGTCTCCG    19650         _ C
                                GCTGGGGCGGG TC CCG
                                ||||||||||  ||  |||
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                                CGACTCCGCCC AG GGC
                                      C  A
GAM725  MGC20486 5'  TGGCTGAGTGGCCCCG      19651        GCG  T
                                TGGCTGGG   GG CCCCG
                                ||||||||   || |||||
                                ACCGACTC   CC GGGGC
                                     A__  _
GAM725  MGC2628  3'  TGGCTGGGGAGCCCCG      19652         CG  T
                                TGGCTGGGG  GG CCCCG
                                |||||||||  || |||||
                                ACCGACCCC  TC GGGGC
                                     __ _
GAM725  MGC3130  3'  TGGCTGGAGAGCCAGTCTCCG  19653        _ _  G    C
                                TGGCTGG G GC GGTC CCG
                                ||||||| | || |||| |||
                                ACCGACC C CG TCAG GGC
                                     T T  G    A
GAM725  MGC4368  3'  GGGAGGCGGGTCCTCG      19654    CT         C
                                GG  GGGGCGGGTCC CG
                                ||  ||||||||||| ||
                                CC  CTCCGCCCAGG GC
                                __          A
GAM725  MMP28    3'  TGGCGGGGCAGGCCCCC      19655     T
                                TGGC GGGGCGGGTCCCC
                                |||| ||||||||||||
                                ACCG CCCCGTCCGGGGG
                                _
GAM725  moblak   3'  TGGCTGGGGGAGGGTGGTCTCC 19656         CG____    C
          G                      TGGCTGGGG     GGTC CCG
                                 |||||||||     |||| |||
                                 ACCGACCCC     CCAG GGC
                                       CTCCCA    A
GAM725  NIR3     3'  TGTCTGGGAGAACCTCCCG   19657    G     C GG  _
                                 TG CTGGGG G  TC CCCG
                                 || |||||| |  || ||||
                                 AC GACCCT C  GG GGGC
                                  A     _ TT  A
GAM725  OPN4     3'  GGCTGGGGCTGTGAATCCC    19658         ___
                                 GGCTGGGGC   GGGTCCC
                                 |||||||||   |||||||
                                 CCGACCCCG   CTTAGGG
                                       ACA
GAM725  P2RX1    3'  TGGCTGGGAGGGCTGTCC     19659         C    CC_
                                 TGGCTGGGG GGGT   CC
                                 |||||||||| ||||   ||
                                 ACCGACCCT CCCG   GG
                                       _    ACA
GAM725  PAPOLG   5'  TGGCTGAGGCATCCAACCG    19660         GG    __
                                 TGGCTGGGGC  GTCC  CCG
                                 ||||||||||  ||||  |||
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                                ACCGACTCCG  TAGG  GGC
                                     __    TT
GAM725  PLA2G12  5'  GGCTCTACGGGTCCCCG     19661      GGG
                                GGCT   GCGGGTCCCCG
                                ||||   ||||||||||
                                CCGA   TGCCCAGGGGC
                                  GA_
GAM725  PTPRT    3'  GGCCCAGTGGGGGTGGGTCCCC 19662      _____   C       III
           GC                     GGCT    GGGG GGGTCCCCG   C
                                ||||    |||| |||||||||   |
                                CCGG    CCCC CCCAGGGGC   G
                                  GTCAC   A       III
GAM725  RASSF2   3'  GGCGTGGTGGCGGGTCCC    19663     _  _
                                GGC TGG GGCGGGTCCC
                                ||| ||| ||||||||||
                                CCG ACC CCGCCCAGGG
                                  C   A
GAM725  SNTA1    3'  TGGCTGGGGTCAGGATCC    19664        _   _
                                TGGCTGGGG CGGG TCC
                                ||||||||| |||| |||
                                ACCGACCCC GTCC AGG
                                     A   T
GAM725  Spir-2   3'  TAGCTGGGATTACAGGTTCC   19665       ___     C
                                TGGCTGGG   GCGGGT CC
                                ||||||||   |||||| ||
                                ATCGACCC   TGTCCA GG
                                     TAA     A
GAM725  SSH2     3'  TGGCTGAGGCCTCCCC      19666        GGG
                                TGGCTGGGGC   TCCCC
                                ||||||||||   |||||
                                ACCGACTCCG   AGGGG
                                     G__
GAM725  TNKS1BP1 3'  TGGTGGGGCTCCAGCCG     19667    C     GGG  __
                                TGG TGGGGC   TCC  CCG
                                ||| ||||||   |||  |||
                                ACC ACCCCG   AGG  GGC
                                  _     ___   TC
GAM725  TReP-132 5'  TGGCTGGAGCCAGGTGTTCC   19668        _   CC_
                                TGGCTGGGGC GGGT   CC
                                |||||||||| ||||   ||
                                ACCGACCTCG TCCA   GG
                                     G    CAA
GAM725  TReP-132 5'  TGGCTGGAGCCAGGTGTTCC   19668        _   CC_
                                TGGCTGGGGC GGGT   CC
                                |||||||||| ||||   ||
                                ACCGACCTCG TCCA   GG
                                     G    CAA
GAM725  TReP-132 5'  TGGCTGGAGCCAGGTGTTCC   19668        _   CC_
                                TGGCTGGGGC GGGT   CC
                                |||||||||| ||||   ||
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                                ACCGACCTCG TCCA   GG
                                      G    CAA
GAM725  TREX1    5'  TGGCGCGGAGGTCCCCG     19669      T G  C
                                TGGC G GG GGGTCCCCG
                                |||| | || |||||||||
                                ACCG C CC TCCAGGGGC
                                  _ G  _
GAM725  UBE2D1   5'  TGGCTCCGCGCGGTGGGTCCCC 19670       ____ G  C        III
          GC                      TGGCT    G GG GGGTCCCCG   C
                                |||||    | || |||||||||   |
                                ACCGA    C CC CCCAGGGGC   G
                                   GGCG G  A        III
GAM725  ZNF213   3'  TGGCTGGGCCTCCCCCG     19671         G GGG
                                TGGCTGGG C   TCCCCG
                                |||||||| |   ||||||
                                ACCGACCC G   GGGGGC
                                     _ GA_
GAM725  ZNF282   3'  TGGCTGAGGACACCCG      19672        _    GGTC
                                TGGCTG GGGCG    CCCG
                                |||||| |||||    ||||
                                ACCGAC CCTGT    GGGC
                                   T    _____
GAM725  LOC114984 5'  TGGCTGGGGCCGCTCCTCCG   19673          GGG  _
                                TGGCTGGGGC   TCC CCG
                                ||||||||||   ||| |||
                                ACCGACCCCG   AGG GGC
                                      GCG   A
GAM725  LOC115708 3'  TGGGTGGGGGATGCCCCG    19674     C    C  GT
                                TGG TGGGG GG  CCCCG
                                ||| ||||| ||  |||||
                                ACC ACCCC CT  GGGGC
                                  C    _  AC
GAM725  LOC127702 3'  TGGCGGGGGCAGCCCG      19675      T      GTC
                                TGGC GGGGCGG   CCCG
                                |||| |||||||   ||||
                                ACCG CCCCGTC   GGGC
                                  C      ____
GAM725  LOC129676 5'  TGGCTGGGCTGCCAGCCTCC   19676         __ G   C
                                TGGCTGGG  GC GGTC CC
                                ||||||||  || |||| ||
                                ACCGACCC  CG TCGG GG
                                     GA  G    A
GAM725  LOC144563 5'  GGCTGGGACAGGGGTCCC     19677          __
                                GGCTGGGGC  GGGTCCC
                                |||||||||  |||||||
                                CCGACCCTG  CCCAGGG
                                      TC
GAM725  LOC145717 3'  TGACTGAAGGCTGGGTCCC    19620        _  _
                                TGGCTGG GGC GGGTCCC
                                ||||||| ||| |||||||
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                                ACTGACT CCG CCCAGGG
                                    T   A
GAM725   LOC145989 5'  GGTGGGTGGCGGGTCCCCG   19678    CT  _
                                GG  GG GGCGGGTCCCCG
                                ||  || ||||||||||||
                                CC  CC CCGCCCAGGGGC
                                 AC  A
GAM725   LOC147229 3'  TAGCTGGGCCTGTTTGGGTCCC 19679        G _______
                                TGGCTGGG C     GGGTCCC
                                |||||||| |     |||||||
                                ATCGACCC G     CCCAGGG
                                    _ GACAAA
GAM725   LOC148223 3'  TGGCTGGGAGACACCCG     19680        GC   TC
                                TGGCTGGG  GGG  CCCG
                                ||||||||  |||  ||||
                                ACCGACCC  TCT  GGGC
                                    __  GT
GAM725   LOC150225 3'  TGGCTGATGGTCCCCG      19681       GGCG
                                TGGCTGG   GGTCCCCG
                                |||||||   ||||||||
                                ACCGACT   CCAGGGGC
                                    A___
GAM725   LOC151632 5'  GGCTGGGACAGGGGTCCC    19677         __
                                GGCTGGGGC  GGGTCCC
                                |||||||||  |||||||
                                CCGACCCTG  CCCAGGG
                                     TC
GAM725   LOC154761 3'  GGCTGGAAAATCCTCG      19682        CG    C
                                GGCTGGGG  GGTCC CG
                                ||||||||  ||||| ||
                                CCGACCTT  TTAGG GC
                                    __    A
GAM725   LOC155032 3'  TGGCTGGGCCAAAACCCC    19683        G    T
                                TGGCTGGG CGGG CCCC
                                |||||||| |||| ||||
                                ACCGACCC GTTT GGGG
                                    G    T
GAM725   LOC158436 5'  TGGCGTGGGGCGAGGCCTCCG  19684     _     _   C
                                TGGC TGGGGCG GGTC CCG
                                |||| ||||||| |||| |||
                                ACCG ACCCCGC CCGG GGC
                                  C      T   A
GAM725   LOC169436 3'  GGCTGGCCAGTCCCCG      19685     GG   G
                                GGCT  GGC GGTCCCCG
                                ||||  ||| ||||||||
                                CCGA  CCG TCAGGGGC
                                  __  G
GAM725   LOC170394 5'  GGCTCACAGGGTCCCCG     19686     GGG  _
                                GGCT   GC GGGTCCCCG
                                ||||   || |||||||||
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                                CCGA   TG CCCAGGGGC
                                  G__  T
GAM725  LOC196047 5'  TGGCTGGGAGAGATTCTCC   19687        C   _ C
                                TGGCTGGGG GGGT C CC
                                ||||||||| |||| | ||
                                ACCGACCCT TCTA G GG
                                     C   A A
GAM725  LOC200904 5'  GGCTGGGACAGGGGTCCC    19677        __
                                GGCTGGGGC  GGGTCCC
                                |||||||||  |||||||
                                CCGACCCTG  CCCAGGG
                                     TC
GAM725  LOC201191 3'  TGGCTGGGAGTCTACCC     19688       GCG  __
                                TGGCTGGG   GGTC  CCC
                                ||||||||   ||||  |||
                                ACCGACCC   TCAG  GGG
                                    ___    AT
GAM725  LOC203083 5'  GGCTGGGACAGGGGTCCC    19677        __
                                GGCTGGGGC  GGGTCCC
                                |||||||||  |||||||
                                CCGACCCTG  CCCAGGG
                                     TC
GAM725  LOC205418 5'  TGGCTGGGCCCCCCG       19689       G GGG
                                TGGCTGGG C   TCCCCG
                                |||||||| |   ||||||
                                ACCGACCC G   GGGGGC
                                    _ ___
GAM725  LOC207089 3'  GGCTCTAGCTGGGTCCTCG   19690     GG  _    C
                                GGCT  GGC GGGTCC CG
                                ||||  ||| |||||| ||
                                CCGA  TCG CCCAGG GC
                                  GA  A     A
GAM725  LOC219919 5'  GGCTGGGACAGGGGTCCC    19677        __
                                GGCTGGGGC  GGGTCCC
                                |||||||||  |||||||
                                CCGACCCTG  CCCAGGG
                                     TC
GAM725  LOC220537 3'  TGACTGAAGGCTGGGTCCC   19620       _  _
                                TGGCTGG GGC GGGTCCC
                                ||||||| ||| |||||||
                                ACTGACT CCG CCCAGGG
                                    T   A
GAM725  LOC221641 5'  TGACTGGGGAGCTTGGGTCCC 19691        C____
                                TGGCTGGGG    GGGTCCC
                                |||||||||    |||||||
                                ACTGACCCC    CCCAGGG
                                     TCGAA
GAM725  LOC221795 5'  GGCTGGGACAGGGGTCCC    19677        __
                                GGCTGGGGC  GGGTCCC
                                |||||||||  |||||||
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                                CCGACCCTG  CCCAGGG
                                     TC
GAM725   LOC253298 5'  TGTTGGGGCGAGGCCTCCTCG  19692    GC     _   _ _
                                TG  TGGGGCG GGTC CC CG
                                ||  ||||||| |||| || ||
                                AC  ACCCCGC CCGG GG GC
                                 A_     T   A  A
GAM725   LOC253650 3'  TGGCTGGGCTGCCAGCATCC   19693       __ G   CC
                                TGGCTGGG  GC GGT  CC
                                ||||||||  || |||  ||
                                ACCGACCC  CG TCG  GG
                                     GA  G   TA
GAM725   LOC254020 5'  GCTGGGACTGAGGTTCCCG   19694       __   C
                                GCTGGGGC  GGGT CCCG
                                ||||||||  |||| ||||
                                CGACCCTG  TCCA GGGC
                                     AC   A
GAM725   LOC254176 5'  GGCTGGGACAGGGGTCCC    19677       __
                                GGCTGGGGC  GGGTCCC
                                |||||||||  |||||||
                                CCGACCCTG  CCCAGGG
                                     TC
GAM725   LOC254198 5'  TGACTGGGGGTGTCTTCCG   19695       CGG   C_
                                TGGCTGGGG   GTC  CCG
                                |||||||||   |||  |||
                                ACTGACCCC   CAG  GGC
                                     CA_   AA
GAM725   LOC256515 5'  GGCTGGGACAGGGGTCCC    19677       __
                                GGCTGGGGC  GGGTCCC
                                |||||||||  |||||||
                                CCGACCCTG  CCCAGGG
                                     TC
GAM725   LOC256906 3'  TGGCTGGGGCATGCATCCC   19696        G__
                                TGGCTGGGGCG   GTCCC
                                ||||||||||   |||||
                                ACCGACCCCGT   TAGGG
                                      ACG
GAM725   LOC256980 3'  TGGCTGTGGGGGGTCCCCG   19697      _  C
                                TGGCTG GGG GGGTCCCCG
                                ||||||  ||| |||||||||
                                ACCGAC CCC CCCAGGGGC
                                   A  _
GAM725   LOC257200 5'  TGGCTGGGATGGCCTTCC    19698       CG   C_
                                TGGCTGGGG  GGTC  CC
                                |||||||||  ||||  ||
                                ACCGACCCT  CCGG  GG
                                     A_    AA
GAM725   LOC257203 5'  TGTCCGGTGCGGGTCCCCG   19699    G   G
                                TG CTGG GCGGGTCCCCG
                                || |||| ||||||||||
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                                AC GGCC CGCCCAGGGGC
                                 A   A
GAM725  LOC257571 5'  TGTTGGGGCGAGGCCTCCTCG  19692    GC     _   _ _
                                TG  TGGGGCG GGTC CC CG
                                ||  ||||||| |||| || ||
                                AC  ACCCCGC CCGG GG GC
                                 A_     T   A A
GAM725  LOC51112  5'  TGGCTGGCGGCCGTGTCTCCG  19700       _  GG_  C
                                TGGCTGG GGC   GTC CCG
                                ||||||| |||   ||| |||
                                ACCGACC CCG   CAG GGC
                                    G   GCA   A
GAM725  LOC51608  3'  TGGCTGGGCTCTCAGGTCC   19701        G___
                                TGGCTGGG   CGGGTCC
                                ||||||||   |||||||
                                ACCGACCC   GTCCAGG
                                     GAGA
GAM725  LOC64182  5'  TGGCTGAGCATCCCCG      19702        G GG
                                TGGCTGGG C  GTCCCCG
                                |||||||| |  |||||||
                                ACCGACTC G  TAGGGGC
                                     _ __
GAM725  LOC90268  5'  GGCTGGGGCATAGTCCCC    19703         _
                                GGCTGGGGCG GGTCCCC
                                |||||||||| |||||||
                                CCGACCCCGT TCAGGGG
                                      A
GAM725  LOC90906  3'  TGCCTGGAAGTCCCCG      19626    G    GCG
                                TG CTGGG   GGTCCCCG
                                || |||||   ||||||||
                                AC GACCT   TCAGGGGC
                                 G   ___
GAM725  LOC91149  5'  TGGCCGGGGTCCCCG       19704        CGGG
                                TGGCTGGGG   TCCCCG
                                |||||||||   ||||||
                                ACCGGCCCC   AGGGGC
                                     ____
GAM725  LOC91974  5'  TGGCTGGAGCTGCCCTTCC   19705         GG   __
                                TGGCTGGGGC  GTCC  CC
                                ||||||||||  ||||  ||
                                ACCGACCTCG  CGGG  GG
                                      A_   AA
GAM725  LOC92719  5'  CGGCTCACTGGGTCCCCG    19706      GGG  _
                                TGGCT   GC GGGTCCCCG
                                |||||   || |||||||||
                                GCCGA   TG CCCAGGGGC
                                   G__  A
GAM726  LILRB4    3'  TCATTATTTTCTGTTTGA    19709          A
                                TTATTATTTTCT TTTGA
                                |||||||||||| |||||
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                                AGTAATAAAAGA AAACT
                                      C
GAM726  POU4F1   3'  CTATACATGATTTTCTATTTG  19710       T  T
                                CTATAT AT ATTTTCTATTTG
                                |||||| || ||||||||||||
                                GATATG TA TAAAAGATAAAC
                                   _  C
GAM726  ASCL3    3'  ATATTATTCATTTCTATTTG   19711         AT
                                ATATTATT  TTTCTATTTG
                                ||||||||  ||||||||||
                                TATAATAA  AAAGATAAAC
                                     GT
GAM726  KIAA0547 3'  TCTATATTTGTACAGCCCTATT 19712         AT   T_
           TGA                    TCTATATT  TAT  TTCTATTTGA
                                ||||||||  |||  ||||||||||
                                AGATATAA  ATG  GGGATAAACT
                                     AC   TC
GAM726  ZNF294   3'  TATATTATTATTTTTCTGCATA 19713          _ ____     III
           TTTGAT                 TTATTATTTT CT    ATTTGA   T
                                ||||||||||  ||    ||||||   |
                                AATAATAAAA GA    TAAACT   A
                                      A  CGTA     III
GAM726  LOC150358 3' TATTATTATTTTCTTTTTTTTG 19714            A___
           A                     TATTATTATTTTCT    TTTGA
                                ||||||||||||||    |||||
                                ATAATAATAAAAGA    AAACT
                                        AAAA
GAM726  LOC201910 3' TCTATATTATAATTTTCCTCTG 19715          T      A
           A                     TCTATATTAT ATTTTCT TTTGA
                                ||||||||||  |||||||  |||||
                                AGATATAATA TAAAAGG AGACT
                                      T      _
GAM726  LOC253443 5' TCAATATTATATATTCTATTTG 19716    T      TATT
           A                     TC ATATTAT    TTCTATTTGA
                                ||  |||||||    ||||||||||
                                AG TATAATA    AAGATAAACT
                                 T      TAT_
GAM726  LOC256113 3' TACTGGCATTTTCTATTTGA   19717      AT
                                TATT  TATTTTCTATTTGA
                                ||||  ||||||||||||||
                                ATGA  GTAAAAGATAAACT
                                  CC
GAM727  SOX11    3'  AGGTCAAACACTGCGGCGGCGT 19720         CG_ TA
           TC                     AGGTCAAGC   G  GCGGCGTTC
                                |||||||||   |  |||||||||
                                TCCAGTTTG   C  CGCCGCAAG
                                     TGA GC
GAM727  BPES     3'  AGGTCAGGCTGGCGGCGGC    19721       A  C  TA
                                AGGTCA GC GG  GCGGC
                                ||||||  ||  ||  |||||
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                                TCCAGT CG CC  CGCCG
                                   C  A  GC
GAM727  GTF2F2   5' AGGCGAAGAGCGGCGTT    19722     C   CCGGT
                                AGGT AAG    AGCGGCGTT
                                |||| |||    |||||||||
                                TCCG TTC    TCGCCGCAA
                                  C  _____
GAM727  LOC219540 3' AAGGTCAACCACCTAGGTGTT  19723       A    GTAGC  C
                                AAGGTC AGCCG    GG GTT
                                |||||| |||||    || |||
                                TTCCAG TTGGT    CC CAA
                                   _    GGAT_  A
GAM728  ANK1     3' GCAGCTCCTCCGACGCAGCC   19726   G       A  A  TG
                                G AGCTCCTCC AC CA  GCC
                                | |||||||||| || ||  |||
                                C TCGAGGAGG TG GT  CGG
                                 G        C  C  __
GAM728  ANK1     3' GCAGCTCCTCCGACGCAGCC   19726   G       A  A  TG
                                G AGCTCCTCC AC CA  GCC
                                | |||||||||| || ||  |||
                                C TCGAGGAGG TG GT  CGG
                                 G        C  C  __
GAM728  MYL1     5' GGAGTTCCTCCAAAAGAACC   19727     C       CACAT
                                GGAG TCCTCCAA    GGCC
                                |||| ||||||||    ||||
                                CCTC AGGAGGTT    TTGG
                                  A       TTC__
GAM728  RAD51L3  3' GGAGCTCCTGCAGCACAT    19728        C  A
                                GGAGCTCCT CA CACAT
                                ||||||||| || |||||
                                CCTCGAGGA GT GTGTA
                                     C  C
GAM728  RAD51L3  3' GGAGCTCCTGCAGCACAT    19728        C  A
                                GGAGCTCCT CA CACAT
                                ||||||||| || |||||
                                CCTCGAGGA GT GTGTA
                                     C  C
GAM728  CD109    3' GAAGCTCCTCCTGCTGGC    19729         AACACA
                                GGAGCTCCTCC     TGGC
                                ||||||||||     ||||
                                CTTCGAGGAGG     ACCG
                                      ACG___
GAM728  DKFZP547L112 5' GGAGTCCTCCAATGCCA     19730     C       CACATG
                                GGAG TCCTCCAA     GCCA
                                |||| ||||||||     ||||
                                CCTC AGGAGGTT     CGGT
                                  _       A_____
GAM728  FER1L4   5' GGAGCTCCTGCAGCGACGCAT  19731        C  ACACA   _
                                GGAGCTCCT CA    TGGC CAT
                                ||||||||| ||    |||| |||
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                                CCTCGAGGA GT    GCTG GTA
                                     C  C____    C
GAM728  KIAA0599  3'  GGGCTCCTCCATCTGGC    19732    A       ACACA
                                GG GCTCCTCCA    TGGC
                                || |||||||||    ||||
                                CC CGAGGAGGT    ACCG
                                 _       AG___
GAM728  KIAA1169  3'  GGAGCTCCTGCTGATGGCC   19733        CCAACAC
                                GGAGCTCCT      ATGGCC
                                |||||||||      ||||||
                                CCTCGAGGA      TACCGG
                                     CGAC___
GAM728  KIAA1432  5'  GGAGATCTTCCAACACAGAC   19734     C  C       T
                                GGAG TC TCCAACACA GGC
                                |||| || ||||||||| |||
                                CCTC AG AGGTTGTGT CTG
                                  T  A       _
GAM728  MGC20983  5'  GGAGCTCCTCCAGCC       19735          ACACATG
                                GGAGCTCCTCCA      GCC
                                ||||||||||||      |||
                                CCTCGAGGAGGT      CGG
                                          _______
GAM728  MMP24     3'  GGGCTCCTCCTGGCATGG    19736    A      AACA
                                GG GCTCCTCC    CATGG
                                || ||||||||    |||||
                                CC CGAGGAGG    GTACC
                                 _       ACC_
GAM728  MRPL16    5'  GGAGCTCCCCCAGCGACTCCGG 19737          AC_  A_
          C                      GGAGCTCCTCCA   AC  TGGC
                                |||||||||||   ||  ||||
                                CCTCGAGGGGGT   TG  GCCG
                                      CGC  AG
GAM728  TIGD5     3'  AGAGCTCCTCCAAGCC      19738          ACACAT
                                GGAGCTCCTCCA     GGCC
                                ||||||||||||     ||||
                                TCTCGAGGAGGT     TCGG
                                          _______
GAM728  ZNF211    5'  GGGTTTCTCCGACACATGGAC  19739    AGCTC    A      _
                                GG     CTCC ACACATGG C
                                ||     |||| |||||||| |
                                CC     GAGG TGTGTACC G
                                 CAAA_    C       T
GAM728  ZNF396    3'  GGAGCTCCTCTAAGCCA     19740          CAACACAT
                                GGAGCTCCTC       GGCCA
                                ||||||||||       |||||
                                CCTCGAGGAG       TCGGT
                                      AT_______
GAM728  LOC121536 5'  AGAGCTCCTCCAGGTCGGCCAT 19741          ACACA
                                GGAGCTCCTCCA     TGGCCAT
                                ||||||||||||     |||||||
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                                TCTCGAGGAGGT    GCCGGTA
                                      CCA__
GAM728  LOC143719 5'  GGAGCTCCTCCTGCAAAAGAGC 19742         AA  CAT_
           CAT                   GGAGCTCCTCC  CA   GGCCAT
                                 ||||||||||  ||   ||||||
                                 CCTCGAGGAGG  GT   TCGGTA
                                      AC  TTTC
GAM728  LOC147138 5'  GGAGTTCTCCCAGCACTGA   19743     C  CT   A   A
                                 GGAG TC  CCA CAC TGG
                                 |||| ||  ||| ||| |||
                                 CCTC AG  GGT GTG ACT
                                   A  AG   C   _
GAM728  LOC149722 5'  GGAGCTCCCCAAGCCAGGGC   19744       T   CA  T
                                 GGAGCTCC CCAA  CA GGC
                                 |||||||| ||||  || |||
                                 CCTCGAGG GGTT  GT CCG
                                      _   CG  C
GAM728  LOC150005 5'  GGAGCTCCCTCAGTCACTCCC  19745       TC  ACA   GG
                                 GGAGCTCC  CA   CAT  CC
                                 ||||||||  ||   |||  ||
                                 CCTCGAGG  GT   GTG  GG
                                      GA  CA_   AG
GAM728  LOC200138 3'  GGAGCTCCTCCAGCCATG    19746          ACA
                                 GGAGCTCCTCCA   CATG
                                 ||||||||||||   ||||
                                 CCTCGAGGAGGT   GTAC
                                      CG_
GAM728  LOC219513 5'  GGAGCCCCTCTGGCC       19747         CAACACA
                                 GGAGCTCCTC      TGGCC
                                 ||||||||||      |||||
                                 CCTCGGGGAG      ACCGG
                                      ________
GAM728  LOC51207  5'  GGAGCTCCTCCAGCTCCAGG   19748          ACA_  T
                                 GGAGCTCCTCCA    CA GG
                                 ||||||||||||    || ||
                                 CCTCGAGGAGGT    GT CC
                                      CGAG  _
GAM728  LOC90639  3'  GGAGCTCCGTCGGCATGG     19749        _  CAACA
                                 GGAGCTCC TC     CATGG
                                 |||||||| ||     |||||
                                 CCTCGAGG AG     GTACC
                                      C  CC___
GAM729  MADH7     3'  ATTTACAAGTAATAATATA    19752      T
                                 ATTT TAGGTAATAATATA
                                 |||| ||||||||||||||
                                 TAAA GTTCATTATTATAT
                                   T
GAM729  RAP1A     3'  TCTAAATTCTTCACATAATATA 19753          AGGTA
                                 TCTAAATTTTT    ATAATATA
                                 ||||||||||     ||||||||
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                                AGATTTAAGAA    TATTATAT
                                      GTG__
GAM729  FLJ13231  3'  CTAATCCAGGTAATAATAT   19754     ATT
                                CTAA   TTTAGGTAATAATAT
                                ||||   ||||||||||||||
                                GATT   AGGTCCATTATTATA
                                  ___
GAM729  FLJ23191  3'  TAAATTTTTAGGTAATAAAATA 19755              T
                                TAAATTTTTAGGTAATAA ATA
                                |||||||||||||||||| |||
                                ATTTAAAAATCCATTATT TAT
                                           T
GAM729  LOC158014 5'  TCTGTATTTTTAAGTAATA   19756     AA
                                TCT  ATTTTTAGGTAATA
                                |||  ||||||||||||||
                                AGA  TAAAAATTCATTAT
                                  CA
GAM729  LOC58492  3'  TCTGAATTTTTAGGTACAAAAT 19757     A         AT_
          A                      TCT AATTTTTAGGTA   AATA
                                ||| ||||||||||||   ||||
                                AGA TTAAAAATCCAT   TTAT
                                  C          GTT
GAM730  GAS7     3'  ACGAGCTGGATGAGGT      19760      A  CTC
                                ACGA CT   GGATGAGGT
                                |||| ||   |||||||||
                                TGCT GA   CCTACTCCA
                                  C ___
GAM730  GAS7     3'  ACGAGCTGGATGAGGT      19760      A  CTC
                                ACGA CT   GGATGAGGT
                                |||| ||   |||||||||
                                TGCT GA   CCTACTCCA
                                  C ___
GAM730  RUNX1    3'  TCAACGAATTTTAAGAGGT   19761        CTCTCG  T
                                TCAACGAA     GA GAGGT
                                ||||||||     || |||||
                                AGTTGCTT     TT CTCCA
                                     AAAA__  _
GAM730  BIRC5    3'  CCTCAACAACATGAG       19762        G   TCTCGG
                                CCTCAAC AAC     ATGAG
                                ||||||| |||     |||||
                                GGAGTTG TTG     TACTC
                                     _  _______
GAM730  FLJ13782  3'  CTCAGGGACAGATGAGG     19763     AC  ACTCT
                                CTCA  GA    CGGATGAGG
                                ||||  ||    |||||||||
                                GAGT  CT    GTCTACTCC
                                  CC _____
GAM730  KIAA0514  3'  TCAGCCGACAGAATGAGGT   19764     A_   ACTCTC
                                TCA  CGA     GGATGAGGT
                                |||  |||     |||||||||
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                                AGT  GCT     CTTACTCCA
                                  CG   GT____
GAM730  KIAA1843  3'  CTCAGCGCAACTTGAAGAGGT  19765      A  _   CTC   T
                                CTCA CG AACT   GGA GAGGT
                                |||| || ||||   ||| |||||
                                GAGT GC TTGA   CTT CTCCA
                                  C  G    A__   _
GAM730  PLA2G3    3'  CCTCAACAACCCTATGAGG    19766        G     CGG
                                CCTCAAC AACTCT   ATGAGG
                                |||||||| ||||||   ||||||
                                GGAGTTG TTGGGA   TACTCC
                                      _     ___
GAM730  LOC149276 5'  CCTGGGTGAACTCTCAAGG    19767     CAAC       GGAT
                                CCT    GAACTCTC    GAGG
                                |||    ||||||||    ||||
                                GGA    CTTGAGAG    TTCC
                                  CCCA       _____
GAM730  LOC221119 3'  TCGACGAGATCCAGGAGGT    19768    A    AC  T   AT
                                TC ACGA  TC CGG  GAGGT
                                || ||||  || |||  |||||
                                AG TGCT  AG GTC  CTCCA
                                 C    CT  _   __
GAM730  LOC256222 5'  TCAGCGACCGTGATGAGGT    19769     A   ACTC   _
                                TCA CGA    TCG GATGAGGT
                                ||| |||    ||| ||||||||
                                AGT GCT    GGC CTACTCCA
                                  C   _____   A
GAM731  ALEX2     5'  AAGGAAGACAGACCCTCCA    19772       A  CCA
                                AAGGAA AC   AGACCCTCCA
                                |||||| ||   ||||||||||
                                TTCCTT TG   TCTGGGAGGT
                                   C  ___
GAM731  APBB2     3'  TAAGAAAAAGACCTTCC      19773         ACCCA    C
                                TAAGGAAA     AGACC TCC
                                ||||||||     ||||| |||
                                ATTCTTTT     TCTGG AGG
                                     ______     A
GAM731  ARNT2     3'  TAAGAAAAGCCTCAACTCTCCT 19774         A  _   GAC_
            CCA                    TAAGGAAA CC CAA    CCTCCA
                                ||||||||| || |||    ||||||
                                ATTCTTTT GG GTT    GGAGGT
                                    C  A   GAGA
GAM731  C7        3'  AGGAAAACCACCCTC       19775          CAAG
                                AGGAAAACC    ACCCTC
                                |||||||||    ||||||
                                TCCTTTTGG    TGGGAG
                                      _____
GAM731  HOXD3     3'  GGCCAGGCCCAAGACTCTCCA  19776     AAAA_       C
                                GG     CCCAAGAC CTCCA
                                ||     |||||||| |||||
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                                CC    GGGTTCTG GAGGT
                                 GGTCC       A
GAM731  KRTHA5   3'  AAGGAAAACCTGACCC      19777          CAA
                                AAGGAAAACC   GACCC
                                ||||||||||   |||||
                                TTCCTTTTGG   CTGGG
                                     A__
GAM731  LAMC2    3'  TAAGGAAAGCTGAGACTCCCC  19778        ACCCA   C
                                TAAGGAAA     AGAC CTCC
                                ||||||||     |||| ||||
                                ATTCCTTT     TCTG GGGG
                                     CGAC_   A
GAM731  NORE1    3'  AAGGAAAATGACTCTCC      19779        CCCAA   C
                                AAGGAAAA     GAC CTCC
                                ||||||||     ||| ||||
                                TTCCTTTT     CTG GAGG
                                     A____   A
GAM731  PROK1    3'  TAAGGAAACACCCTAATTGCCT 19780         _   _ GAC
                                TAAGGAAA ACCC AA   CCT
                                |||||||| |||| ||   |||
                                ATTCCTTT TGGG TT   GGA
                                     G    A  AAC
GAM731  PRPS2    3'  AAGGAAAATTCAAAATCCA    19781        CC    CCC
                                AAGGAAAA  CAAGA   TCCA
                                ||||||||  |||||   ||||
                                TTCCTTTT  GTTTT   AGGT
                                     AA    ___
GAM731  RAD9     3'  CAAGGAAAACTTGTCAGCTCCA 19782          CCAAGACC
                                TAAGGAAAAC       CTCCA
                                ||||||||||       |||||
                                GTTCCTTTTG       GAGGT
                                      AACAGTC_
GAM731  SALL2    3'  TAAGGAAAATACAAGGGGCC   19783        CC    AC_
                                TAAGGAAAA  CAAG   CC
                                |||||||||  ||||   ||
                                ATTCCTTTT  GTTC   GG
                                      AT    CCC
GAM731  SERPINA3 3'  AGGAGGCCCAGGACCCTCCA   19784      AAA    A
                                AGGA   CCCA GACCCTCCA
                                ||||   |||| |||||||||
                                TCCT   GGGT CTGGGAGGT
                                  CC_    C
GAM731  TGFBR2   5'  AAGACCAAGACCCTCC       19785      AAAC
                                AGGA    CCAAGACCCTCC
                                ||||    ||||||||||||
                                TTCT    GGTTCTGGGAGG
                                        ____
GAM731  TM4SF6   3'  TAAGGAAAATACAACAATTCC  19786        CC   GACCC
                                TAAGGAAAA  CAA    TCC
                                |||||||||  |||    |||
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                                ATTCCTTTT  GTT    AGG
                                     AT   GTTA_
GAM731  WNT10B   3'  AGCTTCCCCTCAAGACCCTCCA 19787    AAAA_ _
                                GG    CC CAAGACCCTCCA
                                ||    || ||||||||||||
                                TC    GG GTTCTGGGAGGT
                                 GAAGG  A
GAM731  DKFZP434L0117 3'  TGAGAAAACCCAGAAAGCCA   19788   A       A  CCCT
                                A GGAAAACCCA GA    CCA
                                | ||||||||| ||    |||
                                A TCTTTTGGGT CT    GGT
                                 C         _ TTC_
GAM731  DKFZP564D0764 3'  TAAGGAAAACCTTGAACACTC  19789          CAA   C
                                TAAGGAAAACC   GAC CTC
                                ||||||||||   ||| |||
                                ATTCCTTTTGG   TTG GAG
                                      AAC   T
GAM731  DKFZP566G1424 5'  AGGAGAACCCAAGTGGCTCCTC 19790      A       AC___
           CA                     AGGA AACCCAAG     CCTCCA
                                ||||| ||||||||     ||||||
                                TCCT TTGGGTTC     GGAGGT
                                  C       ACCGA
GAM731  DOCK3    3'  GGAAGCCACAACCCTTCA    19791      AAC   A     C
                                GGAA   CCA GACCCT CA
                                ||||   ||| |||||| ||
                                CCTT   GGT TTGGGA GT
                                  C__   G     A
GAM731  FENS-1   3'  TAAGGAACAACAAAACCCTTCA 19792        AACC       C
                                TAAGGAA    CAAGACCCT CA
                                |||||||    ||||||||| ||
                                ATTCCTT    GTTTTGGGA GT
                                    GTT_       A
GAM731  FLJ10008  3'  AAGAAAACCATTCCTTCCA   19793         CAAGA  C
                                AGGAAAACC     CC TCCA
                                |||||||||     || ||||
                                TTCTTTTGG     GG AGGT
                                      TAA__  A
GAM731  FLJ10242  3'  AAGAAAATCCAACTCC      19794        C   GACC
                                AGGAAAA CCAA    CTCC
                                ||||||| ||||    ||||
                                TTCTTTT GGTT    GAGG
                                    A   _____
GAM731  FLJ10916  3'  TAAAGAAAGCCACCTCC     19795         AC   AGAC
                                TAAGGAAA  CCA    CCTCC
                                ||||||||  |||    |||||
                                ATTTCTTT  GGT    GGAGG
                                     C_  _____
GAM731  FLJ14166  3'  AAGGAGCACAGACCCTCCA   19796       AA  CCA
                                AAGGA  AC   AGACCCTCCA
                                |||||  ||   ||||||||||
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                                TTCCT  TG   TCTGGGAGGT
                                  CG  ___
GAM731  FLJ20375  3'  TAAAGAAAATCCAAGTTCCT   19797        C    AC
                                TAAGGAAAA CCAAG  CCT
                                ||||||||| |||||  |||
                                ATTTCTTTT GGTTC  GGA
                                    A    AA
GAM731  FLJ22195  3'  TAAGGAAAAACCTCCTC     19798        C  AAGAC
                                TAAGGAAAA CC    CCTC
                                ||||||||| ||    ||||
                                ATTCCTTTT GG    GGAG
                                    T  A____
GAM731  FLJ23360  3'  AGGAAAACTAGCTCCTTCCA   19799        CCA  AC  _
                                AGGAAAAC   AG  CCT CCA
                                ||||||||   ||  ||| |||
                                TCCTTTTG   TC  GGA GGT
                                    A__  GA   A
GAM731  GREB1     3'  AAAATAACCCAAGATTCT    19800      A       CC
                                AGGA AACCCAAGA  CT
                                |||| |||||||||  ||
                                TTTT TTGGGTTCT  GA
                                  A        AA
GAM731  GTF2F2    3'  TAAGAAAAACCCTCTTAATCCT 19801          AA__  C
        CCA                     TAAGGAAAACCC    GA CCTCCA
                                ||||||||||||    || ||||||
                                ATTCTTTTTGGG    TT GGAGGT
                                    AGAA  A
GAM731  KIAA0417  3'  AAGGAGAGAGTGAAGACCCTCC 19802      AAACCC_
        A                       AAGGA      AAGACCCTCCA
                                |||||      ||||||||||
                                TTCCT      TTCTGGGAGGT
                                  CTCTCAC
GAM731  KIAA0435  3'  TAAGGAAAACCTGAACACTC   19803          CAA   C
                                TAAGGAAAACC   GAC CTC
                                ||||||||||   ||| |||
                                ATTCCTTTTGG   TTG GAG
                                    AC_   T
GAM731  KIAA0514  3'  TAAAGAAAACTCAGGATCTCCC 19804         C  A  _____
        CTC                     TAAGGAAAAC CA GA    CCCTC
                                |||||||||| || ||    |||||
                                ATTTCTTTTG GT CT    GGGAG
                                    A  C  AGAG
GAM731  KIAA0537  3'  AAGGAAAACTTAACCCC     19805        CCAA
                                AAGGAAAAC    GACCCT
                                |||||||||    ||||||
                                TTCCTTTTG    TTGGGG
                                    AA__
GAM731  KIAA0924  3'  TAAGGAAATGCTCACCGACTCC 19806        _____   CAAGA
        CTC                     TAAGGAAA    ACC    CCCTC
                                ||||||||    |||    |||||
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                                ATTCCTTT    TGG    GGGAG
                                    ACGAG   CTGA_
GAM731  KIAA1143  3'  AAGGAAAACCCCCACCTCTCCA  19807          AAG  _
                                AAGGAAAACCC   ACC CTCCA
                                ||||||||||   ||| |||||
                                TTCCTTTTGGG   TGG GAGGT
                                     G__   A
GAM731  KIAA1157  3'  TAAGGAAAGCTGAGAACCTC   19808        ACCCA  C
                                TAAGGAAA    AGA CCTC
                                ||||||||    ||| ||||
                                ATTCCTTT    TCT GGAG
                                    CGAC_   T
GAM731  KIAA1557  3'  TAAGGAAAACCAAAAAATACCT 19809          C   C__  C
           TCA                    TAAGGAAAACC AAGA   CCT CA
                                ||||||||||| ||||   ||| ||
                                ATTCCTTTTGG TTTT   GGA GT
                                     T   TAT   A
GAM731  KIAA1560  3'  TAAGGAACACCCAAGACTCCC  19810       A       _
                                TAAGGAA ACCCAAGAC CCT
                                ||||||| ||||||||| |||
                                ATTCCTT TGGGTTCTG GGG
                                    G       A
GAM731  KIAA1710  3'  CAAGGAAAAAGCCCT      19811         CCCA  A
                                TAAGGAAAA   AG CCCT
                                |||||||||   || ||||
                                GTTCCTTTT   TC GGGA
                                    ____  _
GAM731  MGC11324  3'  CAAGGAAAACTAAGCTC     19812         CC   ACC
                                TAAGGAAAAC  AAG   CTC
                                ||||||||||  |||   |||
                                GTTCCTTTTG  TTC   GAG
                                    A_   ___
GAM731  MGC5297   3'  TAAGGAAAACTACAGATGCT   19813         CCA   CC
                                TAAGGAAAAC   AGA  CT
                                ||||||||||   |||  ||
                                ATTCCTTTTG   TCT  GA
                                     ATG   AC
GAM731  MUC13     3'  AAGAAAACCACCTCTC      19814         CAAG  _
                                AGGAAAACC    ACC CTC
                                |||||||||    ||| |||
                                TTCTTTTGG    TGG GAG
                                    ____   A
GAM731  OAZIN     3'  TAAAGAAAAAAACCCTC     19815         CCCA      C
                                TAAGGAAAA    AGACCCT C
                                |||||||||    ||||||| |
                                ATTTCTTTT    TTTGGGA G
                                    ____      A
GAM731  PB1       3'  AAGGAAAAAAGCATCCTC    19816        CCC   AC_
                                AAGGAAAA   AAG   CCTC
                                ||||||||   |||   ||||
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                                TTCCTTTT  TTC  GGAG
                                    ___  GTA
GAM731  PTD013   3' AAGGAAAATCATAACCCTC   19817       CC  A
                                AAGGAAAA  CA GACCCTC
                                ||||||||  || |||||||
                                TTCCTTTT  GT TTGGGAG
                                    A_  A
GAM731  sdolf    5' AAGAAAATCCAAGGAGCTCC  19818       C    ACC
                                AGGAAAA CCAAG  CTCC
                                ||||||| |||||  ||||
                                TTCTTTT GGTTC  GAGG
                                    A    CTC
GAM731  STMN3    3' TAAGGAAAGCTGCAGCCCCCA 19819       ACCCA  A   T
                                TAAGGAAA    AG CCC CCA
                                ||||||||    || ||| |||
                                ATTCCTTT    TC GGG GGT
                                    CGACG  _  _
GAM731  TIP120A  3' AAGAAAACCCAAGTCTC    19820          ACC
                                AGGAAAACCCAAG  CTC
                                ||||||||||||  |||
                                TTCTTTTGGGTTC  GAG
                                      A__
GAM731  TRIM29   3' AGGAGAAGCCACCCTCCA    19821     A  C  AAG
                                AGGA AA CC  ACCCTCCA
                                ||||  || ||  ||||||||
                                TCCT TT GG  TGGGAGGT
                                  C  C  ___
GAM731  URG4     3' AGGAGACTCCAAACCCTC    19822     AA  _  A
                                AGGA  AC CCA GACCCTC
                                ||||  || ||| |||||||
                                TCCT  TG GGT TTGGGAG
                                  C_  A  _
GAM731  LOC144893 3' AGGAAAACCCAATCC      19823          GACCC
                                AGGAAAACCCAA    TCC
                                ||||||||||||    |||
                                TCCTTTTGGGTT    AGG
                                      _____
GAM731  LOC145608 3' TAAGGAAAAACCAAGGACAATT 19824        C    _  CC_
          CCA                     TAAGGAAAA CCAAG AC  TCCA
                                ||||||||| ||||| ||  ||||
                                ATTCCTTTT GGTTC TG  AGGT
                                    T    C  TTA
GAM731  LOC146375 5' AGGAGCCGCGAGACCCTCCA  19825     AAA  CA_
                                AGGA  CC  AGACCCTCCA
                                ||||  ||  ||||||||||
                                TCCT  GG  TCTGGGAGGT
                                  C__  CGC
GAM731  LOC148918 5' CAAGGAAAGCCGGGTTCTCCA 19826       A  CAAGACC
                                TAAGGAAA CC      CTCCA
                                ||||||||  ||     |||||
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                                GTTCCTTT GG      GAGGT
                                    C  CCCAA__
GAM731   LOC149506 5'  AAGGGGACCCACCCTCCA    19827     AAA    AAG
                                AAGG   ACCC   ACCCTCCA
                                ||||   ||||   ||||||||
                                TTCC   TGGG   TGGGAGGT
                                  CC_   ___
GAM731   LOC149837 3'  TAAGGAAAATCCATGGTGCCT  19828        C   AGAC_
                                TAAGGAAAA CCA     CCT
                                ||||||||| |||     |||
                                ATTCCTTTT GGT     GGA
                                     A   ACCAC
GAM731   LOC150421 3'  GACACTCAAGACCCTCCA    19829    AA  C
                                GA  AC CAAGACCCTCCA
                                ||  || ||||||||||||
                                CT  TG GTTCTGGGAGGT
                                 G_  A
GAM731   LOC151196 5'  CAAGGAAAACCTGATCC     19830          CAA  CCC
                                TAAGGAAAACC   GA   TCC
                                ||||||||||   ||   |||
                                GTTCCTTTTGG   CT   AGG
                                      A__  ___
GAM731   LOC152925 3'  AAGGAAAATTCAAGGTCCT   19831        CC    AC
                                AAGGAAAA  CAAG  CCT
                                ||||||||  ||||  |||
                                TTCCTTTT  GTTC  GGA
                                     AA    CA
GAM731   LOC154860 5'  AAGGGGGAACCCAAGCACTCTC 19832      AA_       _  C
                                AAGG   AACCCAAG AC CTC
                                ||||   |||||||| || |||
                                TTCC   TTGGGTTC TG GAG
                                  CCC       G  A
GAM731   LOC157624 5'  AAGAAAACCCACAAAACT    19833          A  CC
                                AGGAAAACCCA GA  CT
                                |||||||||| ||  ||
                                TTCTTTTGGGT TT  GA
                                      G  TT
GAM731   LOC157753 3'  TAAGGAAAGCCCAACATCCTC  19834        A    GAC
                                TAAGGAAA CCCAA   CCTC
                                |||||||| |||||   ||||
                                ATTCCTTT GGGTT   GGAG
                                     C    GTA
GAM731   LOC158056 5'  AGGCCCAGGACCCTCCA     19835     AAAA   A
                                AGG   CCCA GACCCTCCA
                                |||   |||| |||||||||
                                TCC   GGGT CTGGGAGGT
                                  _____   C
GAM731   LOC158297 5'  AAGGAAAATTTAAGTGGCCCT  19836        CCC   A__
                                AAGGAAAA   AAG   CCCT
                                ||||||||   |||   ||||
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                                TTCCTTTT  TTC  GGGA
                                    AAA  ACC
GAM731  LOC201175 5'  AAGGAGGGCCACCCTCCA   19837     AAA  CAAG
                                AAGGA  CC   ACCCTCCA
                                |||||  ||   ||||||||
                                TTCCT  GG   TGGGAGGT
                                  CCC  ____
GAM731  LOC219855 3'  GGGACCCAACTGGGACCCTCCA 19838   AAA    ____
                                GG  ACCCAA   GACCCTCCA
                                ||  ||||||   |||||||||
                                CC  TGGGTT   CTGGGAGGT
                                 C__    GACC
GAM731  LOC51290  5'  AGGAAAACCTTCCTCTTCC   19839       CAAGA  _  _
                                AGGAAAACC    CC CT CC
                                |||||||||    || || ||
                                TCCTTTTGG    GG GA GG
                                     AA___  A  A
GAM731  LOC51301  5'  CAAGGAAAGCCCAGGGAACCCC 19840       A   A__
                                TAAGGAAA CCCA  GACCCT
                                |||||||| ||||  ||||||
                                GTTCCTTT GGGT  TTGGGG
                                     C   CCC
GAM731  LOC90268  3'  AGGAAAACCCAGGTCC     19841         A ACCC
                                AGGAAAACCCA G   TCC
                                |||||||||||  |   |||
                                TCCTTTTGGGT C   AGG
                                      _ C___
GAM732  ABCB9     3'  TCCTCTGCCCCACCGGG    19844    G  _  AG
                                TC TC GC  TCCACCGGG
                                || || ||  |||||||||
                                AG AG CG  GGGTGGCCC
                                 G  A  __
GAM732  CDKN2C    5'  TCGCCGCAGTTCCGGG     19845        CCA
                                TCGTCGCAGT   CCGGG
                                ||||||||||   |||||
                                AGCGGCGTCA   GGCCC
                                     A__
GAM732  DAG1      5'  TCGCGCGAGCACGTACCGGG  19846    T  _  CC__
                                TCG CGC AGT   ACCGGG
                                ||| ||| |||   ||||||
                                AGC GCG TCG   TGGCCC
                                  _  C  TGCA
GAM732  HRC       3'  CGTCGCAGTCGAGCGACTGGG  19847       C____  C
                                CGTCGCAGTC    AC GGG
                                ||||||||||    || |||
                                GCAGCGTCAG    TG CCC
                                      CTCGC  A
GAM732  ITPKB     3'  TCGTGCTCCACCGGG      19848     C  AG
                                TCGT GC  TCCACCGGG
                                ||||  ||  |||||||||
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                                AGCA CG  AGGTGGCCC
                                  _ __
GAM732  KIFC3    5'  TCGCCGCAGCGCCCGGG     19849         CCA
                                TCGTCGCAGT   CCGGG
                                ||||||||||  |||||
                                AGCGGCGTCG   GGCCC
                                     CG_
GAM732  MADD     5'  ATCGAAGTCTCCACCGGG    19850      C __
                                GTCG AG  TCCACCGGG
                                |||| ||  |||||||||
                                TAGC TC  AGGTGGCCC
                                  T  AG
GAM732  MLLT2    5'  TCGGCGCAGCCCCGGG      19851     T    T  A
                                TCG CGCAG CC CCGGG
                                ||| ||||| || |||||
                                AGC GCGTC GG GGCCC
                                  C    _ _
GAM732  SORCS2   5'  TCCTCGCCGCCACCGGG     19852    G    A T
                                TC TCGC G CCACCGGG
                                || |||| | ||||||||
                                AG AGCG C GGTGGCCC
                                 G   G _
GAM732  TDGF1    3'  TCATTGCAGTCCAGCCTGGG   19853      C      _ _
                                TCGT GCAGTCCA CC GGG
                                |||| |||||||| || |||
                                AGTA CGTCAGGT GG CCC
                                  A       C  A
GAM732  TP73     5'  CCGTCGCAGCCCCGGG      19854         T  A
                                TCGTCGCAG CC CCGGG
                                ||||||||| || |||||
                                GGCAGCGTC GG GGCCC
                                     _ _
GAM732  UCN      3'  TCGCAGCCCCAAACCGGG    19855         ____
                                TCGCAGTCC   ACCGGG
                                |||||||||   ||||||
                                AGCGTCGGG   TGGCCC
                                     GTT
GAM732  FLJ22160 3'  TCTCGCAGTCTCCATGG     19856    G      CA  _
                                TC TCGCAGTC  CCG GG
                                || ||||||||  ||| ||
                                AG AGCGTCAG  GGT CC
                                 _      A_  A
GAM732  KIAA0076 5'  CCTCAGAAGTCCACCGGG    19857   G  C_
                                C TCG  AGTCCACCGGG
                                | |||  ||||||||||
                                G AGT  TCAGGTGGCCC
                                 G   CT
GAM732  KIAA0415 3'  TCATCGCAGGCCGCGGG     19858         T  AC
                                TCGTCGCAG CC  CGGG
                                |||||||| ||  ||||
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                                AGTAGCGTC GG  GCCC
                                     C  C_
GAM732  KIAA0450  5'  TCGTCCACCACGCGGG     19859      G  GT   _
                                TCGTC CA  CCAC CGGG
                                ||||| ||  |||| ||||
                                AGCAG GT  GGTG GCCC
                                  _ __   C
GAM732  KIAA1076  3'  CCATCAGGGTCCACCGGG    19860       CA
                                TCGTCG  GTCCACCGGG
                                ||||||  ||||||||||
                                GGTAGT  CAGGTGGCCC
                                   CC
GAM732  KIAA1719  5'  TCGGCAGGGCCACCGGG     19861     TC   T_
                                TCG  GCAG  CCACCGGG
                                |||  ||||  ||||||||
                                AGC  CGTC  GGTGGCCC
                                  __   CC
GAM732  MGC4342   3'  TCGCCCACCACACTGGG     19862      G  G  _  C
                                TCGTC CA TC CAC GGG
                                ||||| || || ||| |||
                                AGCGG GT GG GTG CCC
                                  _ _ T  A
GAM732  TU3A      5'  TCCTCACTCCACCGGG      19863    G   AG
                                TC TCGC  TCCACCGGG
                                || ||||  |||||||||
                                AG AGTG  AGGTGGCCC
                                 G   __
GAM733  ACN       3'  CATTTGGTATGTATGTA     19866         CGTAA
                                TATTTGGTA    GTATGTA
                                |||||||||    |||||||
                                GTAAACCAT    CATACAT
                                     A____
GAM733  COL4A5    3'  ATTTGGTATGTAACATG     19867        C   G
                                ATTTGGTA GTAA TATG
                                |||||||| |||| ||||
                                TAAACCAT CATT GTAC
                                     A   _
GAM733  COL4A5    3'  ATTTGGTATGTAACATG     19867        C   G
                                ATTTGGTA GTAA TATG
                                |||||||| |||| ||||
                                TAAACCAT CATT GTAC
                                     A   _
GAM733  COL4A5    3'  ATTTGGTATGTAACATG     19867        C   G
                                ATTTGGTA GTAA TATG
                                |||||||| |||| ||||
                                TAAACCAT CATT GTAC
                                     A   _
GAM733  ESRRBL1   3'  TAATATGTGAGTATGTATA   19868       C  A
                                TGGTA GT AGTATGTATA
                                ||||| || ||||||||||
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                                ATTAT CA TCATACATAT
                                   A  C
GAM733  FGF13    3'  TATTCGGTGCGTATTTGGGTAT 19869        A    AGTAT
             A                   TATTTGGT CGTA    GTATA
                                 |||||||| ||||    |||||
                                 ATAAGCCA GCAT    CATAT
                                     C    AAACC
GAM733  PLSCR1   3'  TATTTGGTAGTAAAATG    19870        C    T
                                 TATTTGGTA GTAAG ATG
                                 ||||||||| ||||| |||
                                 ATAAACCAT CATTT TAC
                                       _    _
GAM733  SFRS7    3'  TCTGAATGTAGGTATGTAT   19871      TAC  A
                                 TTTGG   GTA GTATGTAT
                                 |||||   ||| ||||||||
                                 AGACT   CAT CATACATA
                                    TA_  C
GAM733  UQCRB    3'  TTAGCACAGGAGTATGTATA  19872        TA
                                 TTGGTACG  AGTATGTATA
                                 ||||||||  ||||||||||
                                 AATCGTGT  TCATACATAT
                                      CC
GAM733  DIO2     3'  TATTTGTATGTATGTATGTAT  19873       G  C   A
                                 TATTTG TA GTA GTATGTAT
                                 |||||| || ||| ||||||||
                                 ATAAAC AT CAT CATACATA
                                     _ A   A
GAM733  DIO2     3'  TATTTGTATGTATGTATGTAT  19873       G  C   A
                                 TATTTG TA GTA GTATGTAT
                                 |||||| || ||| ||||||||
                                 ATAAAC AT CAT CATACATA
                                    _ A   A
GAM733  FLJ14260 3'  TGTTACAGTAAGTATGTATA  19874    G  _
                                 TG TAC GTAAGTATGTATA
                                 || ||| ||||||||||||
                                 AC ATG CATTCATACATAT
                                  A   T
GAM733  INSM2    3'  TATTTGGTGGTAAGCAT     19875        AC
                                 TATTTGGT  GTAAGTAT
                                 ||||||||  ||||||||
                                 ATAAACCA  CATTCGTA
                                      C_
GAM733  PMAIP1   3'  TATAAGTATGTAAGTATGT   19876     TT   C
                                 TAT  GGTA GTAAGTATGT
                                 |||  |||| ||||||||||
                                 ATA  TCAT CATTCATACA
                                   T_   A
GAM734  LOC132625 3' TGGGGTTGCAATATTGA     19879       C  GAT
                                 TGGGGT GT   GATATTGA
                                 |||||| ||   ||||||||
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                                ACCCCA CG   TTATAACT
                                   A ____
GAM734   LOC221511 5'  TTGTGGGGTCTATAATTGAT   19880          _    _
                                TTGTGGGGTC GTGAT GAT
                                |||||||||| ||||| |||
                                AACACCCCAG TATTA CTA
                                      A     A
GAM734   LOC257569 5'  TTGTGGGGTCTATAATTGAT   19880          _    _
                                TTGTGGGGTC GTGAT GAT
                                |||||||||| ||||| |||
                                AACACCCCAG TATTA CTA
                                      A     A
GAM735   ACCN2     3'  CAGCAGAGCTTTCAACTCCTC  19883       _ CTAAGA
                                CAGCAG GC     AGCTCCTC
                                |||||| ||     ||||||||
                                GTCGTC CG     TTGAGGAG
                                   T  AAAG__
GAM735   AP1B1     3'  GCAGGCCCTGGGCTCCTC     19884        AAGAA
                                GCAGGCCT     GCTCCTC
                                ||||||||     |||||||
                                CGTCCGGG     CGAGGAG
                                     ACC__
GAM735   AP1G1     3'  CAGCAGTTCTCTTCAGCTCCTC 19885       GC  AAGA
                                CAGCAG  CT    AGCTCCTC
                                ||||||  ||    ||||||||
                                GTCGTC  GA    TCGAGGAG
                                   AA  GAAG
GAM735   APBB2     5'  CAGAAGGCAAGCTCCT      19886     C    CTAAG
                                CAG AGGC     AAGCTCCT
                                ||| ||||     ||||||||
                                GTC TCCG     TTCGAGGA
                                  T  ______
GAM735   ATP11A    3'  ACAGGCCTGGGGGGAATGGCCTC 19887         AA__   GCT
                                GCAGGCCT    GAA   CCTC
                                ||||||||    |||   ||||
                                TGTCCGGA    CTT   GGAG
                                     CCCC   ACC
GAM735   BACH2     3'  AGTAGGCCAAGAAATTC     19888    C    T     C
                                AG AGGCC AAGAAG TC
                                || ||||| |||||| ||
                                TC TCCGG TTCTTT AG
                                 A    _     A
GAM735   CERD4     3'  GCAGGCCTGAGCTTCCTC     19889        AA  A  _
                                GCAGGCCT  GA GCT CCTC
                                ||||||||  || ||| ||||
                                CGTCCGGA  CT CGA GGAG
                                     __ _  A
GAM735   CYP1A1    3'  CAGAGGCCTAAGGACCT     19890     C       AAGCT
                                CAG AGGCCTAAG     CCT
                                ||| |||||||||     |||
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                                GTC TCCGGATTC    GGA
                                  _       CT___
GAM735  DGCR2   3'  CAGCAGGCCAAGCTC       19891         TAAG
                                CAGCAGGCC   AAGCTC
                                |||||||||   ||||||
                                GTCGTCCGG   TTCGAG
                                     ____
GAM735  DGKE    5'  CAGCAGGCCTTGGCCGCCTC  19892         AAGAA  _
                                CAGCAGGCCT    GCT CCTC
                                ||||||||||    ||| ||||
                                GTCGTCCGGA    CGG GGAG
                                      AC___   C
GAM735  DTX1    5'  GCAGGCCCAGCTCCT       19893         AAGA
                                GCAGGCCT    AGCTCCT
                                ||||||||    |||||||
                                CGTCCGGG    TCGAGGA
                                     _____
GAM735  EBP     3'  GCAGGCAGAGAGCTCCTC    19894       CTA  _
                                GCAGGC   AGA AGCTCCTC
                                ||||||   ||| ||||||||
                                CGTCCG   TCT TCGAGGAG
                                   ___   C
GAM735  EHD3    3'  CAGCAGGCTAGCCCACTC    19895        CTAAGA    _
                                CAGCAGGC     AGCTC CTC
                                ||||||||     ||||| |||
                                GTCGTCCG     TCGGG GAG
                                     A_____     T
GAM735  EHF     3'  GGTTCTGAAAAGAAGCTCCTC  19896    C_  ___
                                GG  CT   AAGAAGCTCCTC
                                ||  ||   ||||||||||||
                                CC  GA   TTCTTCGAGGAG
                                  AA  CTT
GAM735  EIF2B5  3'  GCCGGGCCTGCTTAGCTCCTC  19897    A_    AAGA
                                GC  GGCCT    AGCTCCTC
                                ||  |||||    ||||||||
                                CG  CCGGA    TCGAGGAG
                                  GC     CGAA
GAM735  FASN    3'  CAGGGGCCCAGCTCCT      19898     CA    AAGA
                                CAG  GGCCT    AGCTCCT
                                |||  |||||    |||||||
                                GTC  CCGGG    TCGAGGA
                                  C_     _____
GAM735  GNAT1   3'  GCCAGACGGAAGCTCCT     19899    _   CTAA
                                GC AGGC    GAAGCTCCT
                                || ||||    |||||||||
                                CG TCTG    CTTCGAGGA
                                  G    C___
GAM735  GPX4    3'  CAGCAGGCCATGGGACCTTCCT 19900         TAA_  AGC
              C                  CAGCAGGCC    GA   TCCTC
                                 |||||||||    ||   |||||
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                                GTCGTCCGG   CT   AGGAG
                                     TACC  GGA
GAM735  GSTM1    3'  CAGCAGGCTGAGTATGGGCTCC 19901        CTAAGAA__
                TC                  CAGCAGGC       GCTCCTC
                                    ||||||||       |||||||
                                    GTCGTCCG       CGAGGAG
                                         ACTCATACC
GAM735  GSTM2    3'  CAGCAGGCTGAGTATGGGCTCC 19901        CTAAGAA__
                TC                  CAGCAGGC       GCTCCTC
                                    ||||||||       |||||||
                                    GTCGTCCG       CGAGGAG
                                         ACTCATACC
GAM735  GSTM4    3'  CAGCAGGCTGAGTATGGGCTCC 19901        CTAAGAA__
                TC                  CAGCAGGC       GCTCCTC
                                    ||||||||       |||||||
                                    GTCGTCCG       CGAGGAG
                                         ACTCATACC
GAM735  GTF2I    3'  AACAGGTCCGAAAAGCTCTTC  19902      C TA      C
                                    AGCAGG C  AGAAGCTC TC
                                    |||||| |  |||||||| ||
                                    TTGTCC G  TTTTCGAG AG
                                       A GC       A
GAM735  GTF2I    3'  AACAGGTCCGAAAAGCTCTTC  19902      C TA      C
                                    AGCAGG C  AGAAGCTC TC
                                    |||||| |  |||||||| ||
                                    TTGTCC G  TTTTCGAG AG
                                       A GC       A
GAM735  HOXC6    3'  CAGCAGGCCCAGGAGCCGGCTC 19903          A  A   C_
                                    CAGCAGGCCTA GA GCT  CTC
                                    |||||||||| || |||  |||
                                    GTCGTCCGGGT CT CGG  GAG
                                          C  _   CC
GAM735  HSF4     5'  CAGCGCGCCGCCAGCTCCTC   19904      AG   TAAGA
                                    CAGC  GCC    AGCTCCTC
                                    ||||  |||    ||||||||
                                    GTCG  CGG    TCGAGGAG
                                      CG   CGG__
GAM735  IRF1     3'  AGCAGGGTAGAGCTCCTC    19905       CCTA   A
                                    AGCAGG    AGA GCTCCTC
                                    ||||||    ||| |||||||
                                    TCGTCC    TCT CGAGGAG
                                       CA__   _
GAM735  KIF3C    3'  GCAGGCAGGAGCTCCTC     19906       CTA  A
                                    GCAGGC   AG AGCTCCTC
                                    ||||||   || ||||||||
                                    CGTCCG   TC TCGAGGAG
                                       ___  C
GAM735  KLHL3    3'  GCAGGCCTTTCCCTGAGGCTTC 19907        AA____  A   C
                TC                  GCAGGCCT     GA GCT CTC
                                    ||||||||     || ||| |||
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                                CGTCCGGA     CT CGA GAG
                                     AAGGGA  C   A
GAM735  KRT16    5'  CAGGTAGGCCAGCTCCT     19908     C_    TAAGA
                                CAG  AGGCC    AGCTCCT
                                |||  |||||    |||||||
                                GTC  TCCGG    TCGAGGA
                                  CA    _____
GAM735  LDHB     5'  GCAGGCCCAGGAGGACTC     19909         A  A_
                                GCAGGCCTA GA  GCTC
                                |||||||||  ||  ||||
                                CGTCCGGGT CT  TGAG
                                     C  CC
GAM735  MEOX1    3'  CAGCTGGTTCCAAAGCTCCTC  19910      A  CCTAA
                                CAGC GG    GAAGCTCCTC
                                ||||  ||    ||||||||||
                                GTCG CC    TTTCGAGGAG
                                  A  AAGG_
GAM735  MEOX1    3'  CAGCTGGTTCCAAAGCTCCTC  19910      A  CCTAA
                                CAGC GG    GAAGCTCCTC
                                ||||  ||    ||||||||||
                                GTCG CC    TTTCGAGGAG
                                  A  AAGG_
GAM735  MPO      3'  CAACAGGCCCAGTTCCT      19911          AAGA  C
                                CAGCAGGCCT   AG TCCT
                                ||||||||||   ||  ||||
                                GTTGTCCGGG   TC AGGA
                                     _____  A
GAM735  MPZ      3'  CAGCAGGCCGGAGCTC       19912         TAA  A
                                CAGCAGGCC   GA GCTC
                                |||||||||   ||  ||||
                                GTCGTCCGG   CT CGAG
                                     C__  _
GAM735  MYO15A   3'  CAGGGGCCTAAGGTAACTC   19913     CA       A_
                                CAG  GGCCTAAG  AGCTC
                                |||  ||||||||  |||||
                                GTC  CCGGATTC  TTGAG
                                  C_       CA
GAM735  MYO1E    3'  CAGCAGGCCAGCTTACCC     19914         TAAGA   __
                                CAGCAGGCC    AGCT  CCT
                                |||||||||    ||||  |||
                                GTCGTCCGG    TCGA  GGG
                                     _____    AT
GAM735  NPTX1    3'  GCAAAGCAGGAAGCTCCTC    19915     _  CTAA
                                GCAG GC    GAAGCTCCTC
                                ||||  ||    ||||||||||
                                CGTT CG    CTTCGAGGAG
                                  T  TC__
GAM735  NRXN2    3'  CAGGCCTGAGCCCCT       19916        AA  A
                                CAGGCCT  GA GCTCCT
                                |||||||  ||  ||||||
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                              GTCCGGA  CT CGGGGA
                                 __  _
GAM735  NRXN2    3'  CAGGCCTGAGCCCCT      19916       AA  A
                              CAGGCCT  GA GCTCCT
                              |||||||  || ||||||
                              GTCCGGA  CT CGGGGA
                                 __  _
GAM735  NRXN2    3'  CAGGCCTGAGCCCCT      19916       AA  A
                              CAGGCCT  GA GCTCCT
                              |||||||  || ||||||
                              GTCCGGA  CT CGGGGA
                                 __  _
GAM735  OSR1     3'  CAGCAGGCTCCCTCCT     19917       _  AAGAAG
                              CAGCAGGC CT     CTCCT
                              |||||||| ||     |||||
                              GTCGTCCG GG     GAGGA
                                  A  _______
GAM735  PIGN     3'  AGAAAAAAAAAAGAAGCTCCT  19918    C   CCT
                              AG AGG   AAGAAGCTCCT
                              || |||   ||||||||||
                              TC TTT   TTCTTCGAGGA
                               T   TTT
GAM735  PKD1     3'  CAGCAGGCCTGGGCGCTGCTC  19919         AAGAA   C
                              CAGCAGGCCT    GCT CTC
                              ||||||||||    ||| |||
                              GTCGTCCGGA    CGA GAG
                                   CCCG_   C
GAM735  PLAG1    3'  CAGGAGCCAAAGCTCCT     19920     CA    TAA
                              CAG  GGCC   GAAGCTCCT
                              |||  ||||   |||||||||
                              GTC  TCGG   TTTCGAGGA
                                C_   ___
GAM735  RAB3A    3'  GCAGGCCTGGCCACCTC     19921       AAGAA  _
                              GCAGGCCT    GCT CCTC
                              ||||||||    ||| ||||
                              CGTCCGGA    CGG GGAG
                                   C____   T
GAM735  RAI3     5'  CAGCAGGCGAGCTCCT      19922       CTAA  A
                              CAGCAGGC    GA GCTCCT
                              ||||||||    || ||||||
                              GTCGTCCG    CT CGAGGA
                                   _____  _
GAM735  RASSF1   3'  GCAGGCCTGGAGCAGCTTCTC  19923       A_  A   C
                              GCAGGCCT  AG AGCT CTC
                              ||||||||  || |||| |||
                              CGTCCGGA  TC TCGA GAG
                                   CC  G   A
GAM735  SH3BP2   3'  CAGTGGGCCCAAGTGCTGACCT 19924     CA      AA  __
          C                    CAG  GGCCTAAG  GCT  CCTC
                              |||  ||||||||  |||  ||||
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                                GTC  CCGGGTTC  CGA  GGAG
                                  AC       A_   CT
GAM735  TACC1    3'  CAGCAGCCTAAGGGAACCT   19925       G     AAGCT
                                CAGCAG CCTAAG    CCT
                                |||||| ||||||    |||
                                GTCGTC GGATTC    GGA
                                   _     CCTT_
GAM735  TAL1     3'  CAGCAGCCTAAGAACGCCCTC  19926       G      _ T
                                CAGCAG CCTAAGAA GC CCTC
                                |||||| |||||||| || ||||
                                GTCGTC GGATTCTT CG GGAG
                                   _      G  _
GAM735  TCF2     3'  CAGCAGGCCAGAGCTC      19927         TA   A
                                CAGCAGGCC  AGA GCTC
                                |||||||||  ||| ||||
                                GTCGTCCGG  TCT CGAG
                                     __   _
GAM735  TCF20    3'  ACAGGCCTGGACCTCCTC    19928         AA  AG
                                GCAGGCCT  GA  CTCCTC
                                ||||||||  ||  ||||||
                                TGTCCGGA  CT  GAGGAG
                                    C_  G_
GAM735  TCF8     3'  CAGCAGGCCAGGGATGCAGCCT 19929         TAA  A  T_
          C                      CAGCAGGCC   GA GC  CCTC
                                |||||||||   || ||  ||||
                                GTCGTCCGG   CT CG  GGAG
                                     TCC  A  TC
GAM735  TNS      3'  CAGCAGGCCCAGGAGCTC    19930          A  A
                                CAGCAGGCCTA GA GCTC
                                |||||||||||| || ||||
                                GTCGTCCGGGT CT CGAG
                                      C  _
GAM735  WBP2     3'  CAGTCAGGAAGCTCCT      19931     _   CCTAAG
                                CAG CAGG     AAGCTCCT
                                ||| ||||     ||||||||
                                GTC GTCC     TTCGAGGA
                                  A   _______
GAM735  ZNF41    3'  CAACAGGCCTTCCTCCT     19932          AAGAAG
                                CAGCAGGCCT     CTCCT
                                ||||||||||     |||||
                                GTTGTCCGGA     GAGGA
                                     AG____
GAM735  AQP10    3'  GCATGCCTAAGAACACAACCTC 19933     G       _ T_
                                GCA GCCTAAGAA GC  CCTC
                                ||| |||||||| ||  ||||
                                CGT CGGATTCTT TG  GGAG
                                  A       G  TT
GAM735  ATP10B   3'  CAGCAGACCTGGCTTCT     19934          AAGAA  C
                                CAGCAGGCCT    GCT CT
                                ||||||||||    ||| ||
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                                GTCGTCTGGA    CGA GA
                                     C____   A
GAM735  BRAP     5'  CAGCAGCAGCAGCTCCT     19935       G CTA  A
                                CAGCAG C   AG AGCTCCT
                                |||||| |   || |||||||
                                GTCGTC G   TC TCGAGGA
                                   _ ___  G
GAM735  BY55     5'  CAGCAGGCCCAGGAACT     19936          A   G
                                CAGCAGGCCTA GAA CT
                                |||||||||||| ||| ||
                                GTCGTCCGGGT CTT GA
                                      C   _
GAM735  C11orf11  3'  CAGCAGGCTGCCCAGGCTCCTC 19937         CTAAGAA
                                CAGCAGGC      GCTCCTC
                                ||||||||      |||||||
                                GTCGTCCG      CGAGGAG
                                     ACGGGTC
GAM735  CG012    5'  CAGCAGGCACTGGTCCCACT   19938        _ AAGAAG  _
                                CAGCAGGC CT     CTC CT
                                |||||||| ||     ||| ||
                                GTCGTCCG GA     GGG GA
                                     T  CCA___   T
GAM735  CNOT7    3'  CAGCAGTTACTAAGCTCCTC   19939       GCCTAAG
                                CAGCAG      AAGCTCCTC
                                ||||||      |||||||||
                                GTCGTC      TTCGAGGAG
                                   AATGA__
GAM735  CPR2     3'  CAGCTTCCCTGGGAAGCTCCTC 19940      AGG   AA
                                CAGC   CCT  GAAGCTCCTC
                                ||||   |||  ||||||||||
                                GTCG   GGA  CTTCGAGGAG
                                  AAG   CC
GAM735  DKFZP434L0117 3'  CAGCAGCCCAGCTCCT      19941       G  TAAGA
                                CAGCAG CC     AGCTCCT
                                |||||| ||     |||||||
                                GTCGTC GG     TCGAGGA
                                   G  _____
GAM735  DKFZP434L0718 3'  CAGTGGGTTCAACAACTCCTC  19942     CA  CC   GA
                                CAG  GG  TAA  AGCTCCTC
                                |||  ||  |||  ||||||||
                                GTC  CC  GTT  TTGAGGAG
                                  AC  AA   G_
GAM735  DKFZP434P0111 3'  CAGCAGCAGAAGCTCCT     19943       G CTA
                                CAGCAG C   AGAAGCTCCT
                                |||||| |   ||||||||||
                                GTCGTC G   TCTTCGAGGA
                                   _ ___
GAM735  DKFZP564D0478 3'  CAGCAGGCCCAACCCTGCCT   19944          GAAG  _
                                CAGCAGGCCTAA    CT CCT
                                ||||||||||||    || |||
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                                GTCGTCCGGGTT   GA GGA
                                      GG__  C
GAM735  DKFZp761A132 3'  GCGGCTCGGAGCTCCTC    19945    A   C AA  A
                                GC GGC T  GA GCTCCTC
                                || ||| |  || |||||||
                                CG CCG A  CT CGAGGAG
                                 _  _ GC  _
GAM735  DMWD     3'  AGCAGGCCTGCACTCCTC    19946        AAGAA
                                AGCAGGCCT    GCTCCTC
                                |||||||||    |||||||
                                TCGTCCGGA    TGAGGAG
                                     CG___
GAM735  FLJ00007  3'  CAGCAGCCTAACCCCT      19947       G   AGAA
                                CAGCAG CCTA   GCTCCT
                                |||||| ||||   ||||||
                                GTCGTC GGAT   TGGGGA
                                  _   _____
GAM735  FLJ10305  3'  GCAGGTCCTTGAGCTCCTC   19948      _  AAGA
                                GCAGG CCT   AGCTCCTC
                                ||||| |||   ||||||||
                                CGTCC GGA   TCGAGGAG
                                   A  AC__
GAM735  FLJ10922  3'  GCAGACACCCTCAGCTCCTC  19949       _ AAGA
                                GCAGGC CT   AGCTCCTC
                                |||||| ||   ||||||||
                                CGTCTG GG   TCGAGGAG
                                   T  GAG_
GAM735  FLJ12229  3'  AAGCCCAAGGGGGCTCCTC   19950        AA_
                                AGGCCTAAG   GCTCCTC
                                |||||||||   |||||||
                                TTCGGGTTC   CGAGGAG
                                     CCC
GAM735  FLJ12287  3'  GCAGAGTAGCAGAAGCTCCTC  19951      CCTA_
                                GCAGG    AGAAGCTCCTC
                                |||||    ||||||||||
                                CGTCT    TCTTCGAGGAG
                                   CATCG
GAM735  FLJ12666  5'  GCGACCCAAGAGGCTCCTC   19952    A       A
                                GC GGCCTAAGA GCTCCTC
                                || |||||||| |||||||
                                CG CTGGGTTCT CGAGGAG
                                 _       C
GAM735  FLJ12687  3'  CAGAGGCCTAATAGATTCT   19953    C     __  AG
                                CAG AGGCCTA  AGA  CT
                                ||| |||||||  |||  ||
                                GTC TCCGGAT  TCT  GA
                                  _     TA  AA
GAM735  FLJ13052  3'  GCGGCTGCGGGAAGCTCCTC  19954    A  CTAA_
                                GC GGC    GAAGCTCCTC
                                || |||    ||||||||||
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                              CG CCG    CTTCGAGGAG
                               _  ACGCC
GAM735  FLJ13782  3' CAACAGGCCTAAGGCACCT   19955          AA  T
                              CAGCAGGCCTAAG  GC CCT
                              ||||||||||||  || |||
                              GTTGTCCGGATTC  CG GGA
                                     __  T
GAM735  FLJ13852  3' CAGCAGCTCCTGCTCCT    19956      G_  AAGAA
                              CAGCAG  CCT    GCTCCT
                              ||||||  |||    ||||||
                              GTCGTC  GGA    CGAGGA
                                 GA  _____
GAM735  FLJ14803  3' AGTACTTAAAAGAAGCTCCT  19957    GC  ___
                              AG  CT   AAGAAGCTCCT
                              ||  ||   ||||||||||
                              TC  GA   TTCTTCGAGGA
                               AT  ATT
GAM735  FLJ20333  3' CAGCTTTTAAAGAAGCTTCTC  19958     AGGCCT      C
                              CAGC     AAGAAGCT CTC
                              ||||     |||||||| |||
                              GTCG     TTCTTCGA GAG
                                AAAAT_      A
GAM735  FLJ20452  3' ACAGGCCTGGAACACCCT    19959       AA   GC
                              GCAGGCCT  GAA  TCCT
                              ||||||||  |||  ||||
                              TGTCCGGA  CTT  GGGA
                                   C_   GT
GAM735  FLJ20507  3' GCTGGGGAAAGGAGCTCCTC  19960    A  CCT   A
                              GC GG   AAG AGCTCCTC
                              || ||   ||| ||||||||
                              CG CC   TTC TCGAGGAG
                               A  CCT   C
GAM735  FLJ20507  3' GCTGGGGAAAGGAGCTCCTC  19960    A  CCT   A
                              GC GG   AAG AGCTCCTC
                              || ||   ||| ||||||||
                              CG CC   TTC TCGAGGAG
                               A  CCT   C
GAM735  FLJ21276  5' GCACCCAGGAGCTCCTC     19961    AG    A  A
                              GC  GCCTA GA GCTCCTC
                              ||  ||||| || |||||||
                              CG  TGGGT CT CGAGGAG
                                __    C  _
GAM735  FLJ21919  3' CAGAGGAGAAAGCTCCT     19962     C   CCTAA
                              CAG AGG    GAAGCTCCT
                              ||| |||    |||||||||
                              GTC TCC    TTTCGAGGA
                                _  TC___
GAM735  FLJ22215  3' GCAGAGCTGGAGCTCCTC    19963      _  CTAA  A
                              GCAG GC    GA GCTCCTC
                              |||| ||    || |||||||
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                                CGTC CG    CT CGAGGAG
                                  T  AC__  _
GAM735  FLJ30681  3'  GCAGGCCTAGGAGGGGACTC   19964          A  A___
                                GCAGGCCTA GA    GCTC
                                |||||||||  ||    ||||
                                CGTCCGGAT CT    TGAG
                                     C  CCCC
GAM735  FLJ31952  3'  CAGCAAGCTAAAGTTCCT    19965         CTAA    C
                                CAGCAGGC    GAAG TCCT
                                ||||||||    |||| ||||
                                GTCGTTCG    TTTC AGGA
                                     A___    A
GAM735  GGA2      3'  CAGAGGAAAAGAAGCTCCT   19966     C   CCT
                                CAG AGG   AAGAAGCTCCT
                                ||| |||   ||||||||||
                                GTC TCC   TTCTTCGAGGA
                                  _  TT_
GAM735  GGA2      3'  CAGAGGAAAAGAAGCTCCT   19966     C   CCT
                                CAG AGG   AAGAAGCTCCT
                                ||| |||   ||||||||||
                                GTC TCC   TTCTTCGAGGA
                                  _  TT_
GAM735  GGA2      3'  CAGCCAGGTCTGGGAAGTCT   19967      _  C  AA   _
                                CAGC AGG CT  GAAG CT
                                |||| ||| ||  |||| ||
                                GTCG TCC GA  CTTC GA
                                  G   A  CC    A
GAM735  GNB1L     3'  CAGCAGGCCCAAGCCAACGTCT 19968           A_   TC
          C                      CAGCAGGCCTAAG  AGC  CTC
                                ||||||||||||  |||  |||
                                GTCGTCCGGGTTC  TTG  GAG
                                       GG   CA
GAM735  H-L(3)MBT 5'  CAGCAGGCCTCAAGACTC    19969          _  AA
                                CAGCAGGCCT AAG  GCTC
                                ||||||||||  |||  ||||
                                GTCGTCCGGA TTC  TGAG
                                     G  __
GAM735  H-L(3)MBT 5'  CAGCAGGCCTCAAGACTC    19969          _  AA
                                CAGCAGGCCT AAG  GCTC
                                ||||||||||  |||  ||||
                                GTCGTCCGGA TTC  TGAG
                                     G  __
GAM735  H2AFL     5'  CAGCGGCCTAAGCTC       19970      A     AGA
                                CAGC GGCCTA   AGCTC
                                ||||  ||||||   |||||
                                GTCG CCGGAT   TCGAG
                                  _    ____
GAM735  HSPC072   3'  CAGCAGGCTAGACCAGGCTTCT 19971         CTA   A___   C
                                CAGCAGGC   AGA    GCT CT
                                ||||||||   |||    ||| ||
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                                GTCGTCCG  TCT   CGA GA
                                    A__  GGTC  A
GAM735  HTMP10   5' CAGCTGGCCTGAGAGCT    19972    A   A  A
                                CAGC GGCCT AGA GCT
                                |||| ||||| ||| |||
                                GTCG CCGGA TCT CGA
                                  A   C  _
GAM735  KCNT1    3' CAGAGGTAGACGAGCTCCTC  19973    C  CCTAA  A
                                CAG AGG    GA GCTCCTC
                                ||| |||    || |||||||
                                GTC TCC    CT CGAGGAG
                                  _  ATCTG  _
GAM735  KIAA0040 5' GCAGGCCCAGGAGGACTC   19909       A  A_
                                GCAGGCCTA GA  GCTC
                                ||||||||| ||  ||||
                                CGTCCGGGT CT  TGAG
                                     C  CC
GAM735  KIAA0233 3' CAGCAGGCCGGCTCCT     19974       TAAGAA
                                CAGCAGGCC    GCTCCT
                                |||||||||    ||||||
                                GTCGTCCGG    CGAGGA
                                     C_____
GAM735  KIAA0247 3' CAGCAGGCCCAAGAGAAGCTC 19975          __
                                CAGCAGGCCTAAGA  AGCTC
                                |||||||||||||  |||||
                                GTCGTCCGGGTTCT  TCGAG
                                        CT
GAM735  KIAA0280 3' CAATCAGGAGGAAGCTCCTC  19976   _  CCTAA
                                CAG CAGG    GAAGCTCCTC
                                ||| ||||    ||||||||||
                                GTT GTCC    CTTCGAGGAG
                                  A   TC___
GAM735  KIAA0332 3' CAGGCCTAAGAAATCCTC    19977         C
                                CAGGCCTAAGAAG TCCTC
                                |||||||||||| |||||
                                GTCCGGATTCTTT AGGAG
                                          _
GAM735  KIAA0410 3' CAGCAGTCTAAGAAGCT     19978      GC
                                CAGCAG  CTAAGAAGCT
                                ||||||  ||||||||||
                                GTCGTC  GATTCTTCGA
                                   A_
GAM735  KIAA0418 3' CAGCAGGCTGGGAGCTGCCT  19979       CTAA  A  _
                                CAGCAGGC   GA GCT CCT
                                ||||||||   || ||| |||
                                GTCGTCCG   CT CGA GGA
                                     ACC_ _  C
GAM735  KIAA0481 3' CAGAGGCCTAAGGGCT      19980    C      AA
                                CAG AGGCCTAAG  GCT
                                ||| |||||||||  |||
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                                GTC TCCGGATTC  CGA
                                  _       C_
GAM735  KIAA0537  3'  CAGCAGGCCTGGGCAAAACTC  19981          AA__
                                CAGCAGGCCT    GAAGCTC
                                ||||||||||    |||||||
                                GTCGTCCGGA    TTTTGAG
                                     CCCG
GAM735  KIAA0628  3'  AGCAGGGCTGAGAAGATACT   19982       C  A    CTC
                                AGCAGG CT AGAAG   CT
                                ||||||  || |||||   ||
                                TCGTCC GA TCTTC   GA
                                   C  C    TAT
GAM735  KIAA0638  3'  ACAGGACCAAGCTCCT      19983       _  TAAG
                                GCAGG CC    AAGCTCCT
                                |||||  ||    ||||||||
                                TGTCC GG    TTCGAGGA
                                  T  _____
GAM735  KIAA0907  3'  CAGCAGACTAGCTCCT      19984         CTAAGA
                                CAGCAGGC     AGCTCCT
                                ||||||||     |||||||
                                GTCGTCTG     TCGAGGA
                                    A_____
GAM735  KIAA1138  3'  CAGCAGGCCCGCTCT       19985          AAGAA    C
                                CAGCAGGCCT    GCTC T
                                ||||||||||    |||| |
                                GTCGTCCGGG    CGAG A
                                     _____    A
GAM735  KIAA1184  3'  CAACAGGCCCGCTTCT      19986          AAGAA   C
                                CAGCAGGCCT    GCT CT
                                ||||||||||    ||| ||
                                GTTGTCCGGG    CGA GA
                                     _____    A
GAM735  KIAA1602  3'  CAGCTCGGGAGGAAGCTCCTC  19987      A_  CCTAA
                                CAGC  GG    GAAGCTCCTC
                                ||||  ||    ||||||||||
                                GTCG  CC    CTTCGAGGAG
                                  AG  CTC__
GAM735  KIAA1822  3'  CAACAGGCCTGGGACACTC    19988          AA  A
                                CAGCAGGCCT  GA GCTC
                                |||||||||  || ||||
                                GTTGTCCGGA  CT TGAG
                                     CC  G
GAM735  LSFR2     3'  CAGCAGGTTAGGAAACTC     19989        CC  A
                                CAGCAGG  TA GAAGCTC
                                |||||||  || |||||||
                                GTCGTCC  AT CTTTGAG
                                   A_  C
GAM735  MAD4      3'  GCAGGCAGGGGAAGCTCCT    19990        CTAA
                                GCAGGC    GAAGCTCCT
                                ||||||    |||||||||
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                                CGTCCG   CTTCGAGGA
                                   TCCC
GAM735  MAPK8IP3  3'  GCGGGCCAGAGCTCCTC     19991    A   TA  A
                                GC GGCC  AGA GCTCCTC
                                || ||||  ||| |||||||
                                CG CCGG  TCT CGAGGAG
                                 C   __  _
GAM735  MGC32043  3'  AGCAGGCTCAGCTCCTC     19992       CTAAGA
                                AGCAGGC     AGCTCCTC
                                |||||||     ||||||||
                                TCGTCCG     TCGAGGAG
                                   AG____
GAM735  MGC5149   3'  CAATAGGCAAAAGCTCTTC   19993    C   CTA      C
                                CAG AGGC   AGAAGCTC TC
                                ||| ||||   |||||||| ||
                                GTT TCCG   TTTTCGAG AG
                                  A   ___      A
GAM735  MGC5601   5'  CAGCAAGCACCTCTGGCTCTTC 19994       _ AAGAA   C
                                CAGCAGGC CT    GCTC TC
                                |||||||| ||    |||| ||
                                GTCGTTCG GG    CGAG AG
                                     T  AGAC_   A
GAM735  PER3      3'  AGCACTGGGTAAGAAGCTC   19995     __ CC
                                AGCA  GG  TAAGAAGCTC
                                ||||  ||  ||||||||||
                                TCGT  CC  ATTCTTCGAG
                                  GA  C_
GAM735  PINK1     3'  GCAGGCCTACCCCTCCTC    19996       AGAAG
                                GCAGGCCTA    CTCCTC
                                |||||||||    ||||||
                                CGTCCGGAT    GAGGAG
                                     GGG__
GAM735  POLD3     3'  CAGCACGGCAGCTCCT      19997      _  CTAAGA
                                CAGCA GGC     AGCTCCT
                                ||||| |||     |||||||
                                GTCGT CCG     TCGAGGA
                                  G  _______
GAM735  PP2447    3'  CAGCAGGCCGAAGAAGGCGGCC 19998        T    _ T_
           T                     CAGCAGGCC AAGAAG C  CCT
                                 ||||||||| |||||| |  |||
                                 GTCGTCCGG TTCTTC G  GGA
                                      C     C CC
GAM735  PRO0659   3'  CAACAGGCCTAGTGCTGCTTCT 19999         AGAA_  C
           C                     CAGCAGGCCTA    GCT CTC
                                 ||||||||||     ||| |||
                                 GTTGTCCGGAT    CGA GAG
                                       CACGA   A
GAM735  RNPC1     3'  GCGCCTGGGAGCTCCTC     20000    AG   AA  A
                                GC  GCCT  GA GCTCCTC
                                ||  ||||  || |||||||
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                                CG  CGGA  CT CGAGGAG
                                 __    CC  _
GAM735  SCAMP5   3'  CAGCATGTCCCAGCTCCTC   20001      GG_   AAGA
                                CAGCA   CCT    AGCTCCTC
                                |||||   |||    ||||||||
                                GTCGT   GGG    TCGAGGAG
                                  ACA   ____
GAM735  SCOP     3'  CAGTGGCCTAAGATCCATTTCC 20002     CA        AGC___
           TC                     CAG  GGCCTAAGA     TCCTC
                                |||  |||||||||     |||||
                                GTC  CCGGATTCT     AGGAG
                                 A_        AGGTAA
GAM735  SCYA5    3'  CAGCGCCTCAGAAGCTCTTC   20003     AG   A       C
                                CAGC  GCCT AGAAGCTC TC
                                ||||  |||| |||||||| ||
                                GTCG  CGGA TCTTCGAG AG
                                  __   G       A
GAM735  SEPT6    5'  CAGGAAACAGAGGAGCTCCTC  20004     CCTA  __
                                CAGG    AGA  AGCTCCTC
                                ||||    |||  ||||||||
                                GTCC    TCT  TCGAGGAG
                                  TTTG   CC
GAM735  SLC17A3  5'  CAGCAGCTTGTTAAGCTCCTC  20005       G CTAAG
                                CAGCAG C     AAGCTCCTC
                                |||||| |     |||||||||
                                GTCGTC G     TTCGAGGAG
                                   _ AACAA
GAM735  SMCR8    3'  GCTGGCTACCAGCTCCTC    20006    A   C  AGA
                                GC GGC TA   AGCTCCTC
                                || ||| ||   ||||||||
                                CG CCG AT   TCGAGGAG
                                 A   _  GG_
GAM735  STOML1   3'  CAGCAGGCCCTGCTCCT     20007          AAGAA
                                CAGCAGGCCT    GCTCCT
                                ||||||||||    ||||||
                                GTCGTCCGGG    CGAGGA
                                      A____
GAM735  TSGA     5'  GCAGGAAGAGCTCCT       20008       CCT    A
                                GCAGG   AAGA GCTCCT
                                |||||   |||| ||||||
                                CGTCC   TTCT CGAGGA
                                  ___    _
GAM735  LOC125268 3'  GCTGGCGCTGAAGCTCCT    20009    A   _  AA
                                GC GGC CT  GAAGCTCCT
                                || ||| ||  |||||||||
                                CG CCG GA  CTTCGAGGA
                                 A  C  __
GAM735  LOC126669 3'  CAGCAGGCCAAGTTTCTC    20010          T   AAG
                                CAGCAGGCC AAG   CTC
                                ||||||||| |||   |||
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                                GTCGTCCGG TTC   GAG
                                      _  AAA
GAM735  LOC132299 3'  CAGAGGTTTAAAAAACT     20011     C   CC
                                CAG AGG  TAAGAAGCT
                                ||| |||  |||||||||
                                GTC TCC  ATTTTTTGA
                                  _   AA
GAM735  LOC135892 3'  ACAGGCCTGAAGACCT      20012        AA    CT
                                GCAGGCCT  GAAG  CCT
                                ||||||||  ||||  |||
                                TGTCCGGA  CTTC  GGA
                                     __    T_
GAM735  LOC137695 5'  AGCGGCGACAGAAGCTCTTC   20013     A   CTA      C
                                AGC GGC   AGAAGCTC TC
                                ||| |||   |||||||| ||
                                TCG CCG   TCTTCGAG AG
                                  _  CTG       A
GAM735  LOC143437 5'  CAGCATAGAAGCTCCT      20014      GGCCTA
                                CAGCA     AGAAGCTCCT
                                |||||     ||||||||||
                                GTCGT     TCTTCGAGGA
                                   A_____
GAM735  LOC144348 5'  CAGCAAGCAGGCTCCT      20015        CTA  AA
                                CAGCAGGC   AG  GCTCCT
                                ||||||||   ||  ||||||
                                GTCGTTCG   TC  CGAGGA
                                     ___  __
GAM735  LOC144893 3'  CAGCAGGCCCAGGCTC      20016          AGAA
                                CAGCAGGCCTA    GCTC
                                ||||||||||    ||||
                                GTCGTCCGGGT    CGAG
                                      C___
GAM735  LOC146512 3'  AGCAGAACTGAGGCTCCTC   20017      GC  AA  A
                                AGCAG  CT  GA GCTCCTC
                                |||||  ||  || |||||||
                                TCGTC  GA  CT CGAGGAG
                                   TT  __  C
GAM735  LOC149086 3'  CAGCAGGCCAGGACCTGCCTC  20018         TAA  AG  _
                                CAGCAGGCC   GA  CT CCTC
                                |||||||||   ||  || ||||
                                GTCGTCCGG   CT  GA GGAG
                                     TC_  G_  C
GAM735  LOC149111 3'  CAGCAGGCTCAAGGCT      20019        C    AA
                                CAGCAGGC TAAG  GCT
                                |||||||| ||||  |||
                                GTCGTCCG GTTC  CGA
                                     A   __
GAM735  LOC149117 3'  CAGCAAGCCTAGATGTCT    20020          A  AG_
                                CAGCAGGCCTA GA   CT
                                |||||||||| ||   ||
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                                GTCGTTCGGAT CT   GA
                                      _  ACA
GAM735   LOC149414 5'  GCGGGCGCCTAGCTCCTC    20021    A  _  AAGA
                                GC GGC CT    AGCTCCTC
                                || ||| ||    ||||||||
                                CG CCG GG    TCGAGGAG
                                 C   C  A___
GAM735   LOC150951 5'  CAGCAGGACCAGCTCCT     20022       _  TAAGA
                                CAGCAGG CC     AGCTCCT
                                ||||||| ||     |||||||
                                GTCGTCC GG     TCGAGGA
                                    T _____
GAM735   LOC151176 3'  CAGCAGGCTTGGGACCAGCCCT 20023        CTAAGA__   T
           C                     CAGCAGGC       AGC CCTC
                                ||||||||       ||| ||||
                                GTCGTCCG       TCG GGAG
                                     AACCCTGG  _
GAM735   LOC153196 5'  CAGCAGGCCTAGGGCCT     20024          AAGA  CT
                                CAGCAGGCCT    AG  CCT
                                ||||||||||    ||  |||
                                GTCGTCCGGA    TC  GGA
                                      ____  CC
GAM735   LOC153205 5'  CAGCAGACTGAAAAAGTTCTTC 20025        CT     C  C
                                CAGCAGGC  AAGAAG TC TC
                                ||||||||  |||||| || ||
                                GTCGTCTG  TTTTTC AG AG
                                     AC     A  A
GAM735   LOC153688 3'  CAAAAAAGAAGCTCCT      20026      CCT
                                CAGG   AAGAAGCTCCT
                                ||||   ||||||||||||
                                GTTT   TTCTTCGAGGA
                                  T__
GAM735   LOC157247 5'  ACAGGCCTGCTTTACTCCTC   20027         AAGAA
                                GCAGGCCT    GCTCCTC
                                ||||||||    |||||||
                                TGTCCGGA    TGAGGAG
                                     CGAAA
GAM735   LOC158056 5'  ACAGGCCTGCTCGTCCTC    20028         AAGAA  ___
                                GCAGGCCT    GC   TCCTC
                                ||||||||    ||   |||||
                                TGTCCGGA    CG   AGGAG
                                     _____  AGC
GAM735   LOC158156 3'  ACAGAGCTTTAAGAAGCTTCTC 20029      _  C_       C
                                GCAG GC  TAAGAAGCT CTC
                                |||| ||  ||||||||| |||
                                TGTC CG  ATTCTTCGA GAG
                                  T  AA        A
GAM735   LOC158295 5'  AGCAGGCCAGAGCACC       20030         TA   A  T
                                AGCAGGCC  AGA GC CC
                                ||||||||  ||| || ||
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                                TCGTCCGG  TCT CG GG
                                   __  _ T
GAM735  LOC160414 3'  CAGAGGCTCTCAGGAGCTCCTC 20031    C   _ A  A
                                CAG AGGC CT AG AGCTCCTC
                                ||| |||| || || ||||||||
                                GTC TCCG GA TC TCGAGGAG
                                  _   A  G  C
GAM735  LOC160717 5'  CAGGCCCAGGGAGCTTCTC   20032       AGA   C
                                CAGGCCTA   AGCT CTC
                                ||||||||   |||| |||
                                GTCCGGGT   TCGA GAG
                                     CCC   A
GAM735  LOC163412 5'  GCAGGCCCAGCTCCT      19893       AAGA
                                GCAGGCCT   AGCTCCT
                                ||||||||   |||||||
                                CGTCCGGG   TCGAGGA
                                   _____
GAM735  LOC163695 5'  GCAGGTCTGGAAGCTCC    20033     C  AA
                                GCAGG CT  GAAGCTCC
                                ||||| ||  ||||||||
                                CGTCC GA  CTTCGAGG
                                   A  C_
GAM735  LOC196418 5'  CAGCAAGCAGGCTCCT     20015       CTA  AA
                                CAGCAGGC   AG  GCTCCT
                                ||||||||   ||  ||||||
                                GTCGTTCG   TC  CGAGGA
                                   ___  __
GAM735  LOC197342 3'  ACAGGACTTGAGCTCCTC   20034     C  AAGA
                                GCAGG CT   AGCTCCTC
                                ||||| ||   ||||||||
                                TGTCC GA   TCGAGGAG
                                   T  AC__
GAM735  LOC200081 3'  CAGCAGGCCTTGGCCCT    20035        AAGAA  T
                                CAGCAGGCCT    GC CCT
                                ||||||||||    || |||
                                GTCGTCCGGA    CG GGA
                                      AC___  _
GAM735  LOC200225 3'  CAGAGGGAAGCTCAAGCTCCTC 20036    C   CCTAAG_
                                CAG AGG      AAGCTCCTC
                                ||| |||      |||||||||
                                GTC TCC      TTCGAGGAG
                                  _  CTTCGAG
GAM735  LOC201139 3'  CAGGTAGGCCAGCTCCT    19908    C_    TAAGA
                                CAG  AGGCC    AGCTCCT
                                |||  |||||    |||||||
                                GTC  TCCGG    TCGAGGA
                                  CA    ______
GAM735  LOC204823 5'  CAGCAGCCCCAGCTCCT    20037      G   AAGA
                                CAGCAG CCT    AGCTCCT
                                |||||| |||    |||||||
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                                GTCGTC GGG    TCGAGGA
                                   G  _____
GAM735  LOC220020 5'  CAGCAGGCCTGGGCATGCCT  20038          AAGAA  T__
                                CAGCAGGCCT    GC   CCT
                                ||||||||||    ||   |||
                                GTCGTCCGGA    CG   GGA
                                      CC___  TAC
GAM735  LOC220776 3'  CAGACAGGACTCAAAGCTCTTC 20039    _   C  AA      C
                                CAG CAGG CT  GAAGCTC TC
                                ||| |||| ||  ||||||| ||
                                GTC GTCC GA  TTTCGAG AG
                                  T   T  G_      A
GAM735  LOC221002 3'  CAGCAGGCCCAGGGCTGCCTCC 20040          AGAA_  _
          TC                      CAGCAGGCCTA    GC TCCTC
                                ||||||||||    || |||||
                                GTCGTCCGGGT    CG AGGAG
                                      CCCGA  G
GAM735  LOC221540 3'  CAGCAGGCCAGAAAGTC    20041         TA    C
                                CAGCAGGCC  AGAAG TC
                                |||||||||  ||||| ||
                                GTCGTCCGG  TCTTT AG
                                     __    C
GAM735  LOC221922 5'  GCAGGCGTGAGCTCCTC    20042       CTAA  A
                                GCAGGC   GA GCTCCTC
                                ||||||   || |||||||
                                CGTCCG   CT CGAGGAG
                                   CA__  _
GAM735  LOC253531 5'  CAGCATAGAAGCTCCT     20014       GGCCTA
                                CAGCA     AGAAGCTCCT
                                |||||     ||||||||||
                                GTCGT     TCTTCGAGGA
                                  A_____
GAM735  LOC253538 5'  GCAGGCCTGAGCCTCCTC    20043         A  AAG
                                GCAGGCCT AG   CTCCTC
                                |||||||| ||   ||||||
                                CGTCCGGA TC   GAGGAG
                                     C  G__
GAM735  LOC254345 5'  CAGCAGGCTGAAGAGAGGGGCT 20044         CT    A____
                                CAGCAGGC  AAGA    GCT
                                ||||||||  ||||    |||
                                GTCGTCCG  TTCT    CGA
                                     AC    CTCCC
GAM735  LOC254556 5'  CAGAGAAGAAGCTCCT     20045      CCT
                                CAGG   AAGAAGCTCCT
                                ||||   ||||||||||
                                GTCT   TTCTTCGAGGA
                                  C__
GAM735  LOC255367 5'  CAGAAGGCACTAGAAGCTCCTC 20046     C   _   A
                                CAG AGGC CTA GAAGCTCCTC
                                ||| |||| ||| ||||||||||
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                                GTC TCCG GAT CTTCGAGGAG
                                  T   T  _
GAM735  LOC255718 5'  TGACAGGCCTGAGGGTCCTC  20047   A      A  AAGC
                                C GCAGGCCT AG   TCCTC
                                | ||||||| ||   |||||
                                A TGTCCGGA TC   AGGAG
                                 C       C  CC__
GAM735  LOC256218 3'  CAGGTAGGCCAGCTCCT     19908    C_    TAAGA
                                CAG  AGGCC    AGCTCCT
                                |||  |||||    |||||||
                                GTC  TCCGG    TCGAGGA
                                  CA    ______
GAM735  LOC256250 5'  AACATGAATAAGAAGCTCTTC  20048     GGCC        C
                                AGCA   TAAGAAGCTC TC
                                ||||   |||||||||| ||
                                TTGT   ATTCTTCGAG AG
                                   ACTT        A
GAM735  LOC257465 3'  CAGCAGGCTGAAAACTC     20049        CTAA
                                CAGCAGGC   GAAGCTC
                                ||||||||   |||||||
                                GTCGTCCG   TTTTGAG
                                     AC__
GAM735  LOC257545 3'  CAGCAGGCCAGAAAGTC     20041         TA    C
                                CAGCAGGCC  AGAAG TC
                                |||||||||  ||||| ||
                                GTCGTCCGG  TCTTT AG
                                     __    C
GAM735  LOC257598 3'  CAGCAGGCCAGAAAGTC     20041         TA    C
                                CAGCAGGCC  AGAAG TC
                                |||||||||  ||||| ||
                                GTCGTCCGG  TCTTT AG
                                     __    C
GAM735  LOC51020  5'  AGCAGGCCGCGGGAAGCTCCTC 20050         TAA_
                                AGCAGGCC   GAAGCTCCTC
                                ||||||||   ||||||||||
                                TCGTCCGG   CTTCGAGGAG
                                     CGCC
GAM735  LOC56920  3'  GCAGGCTGGAAGGCTTCTC   20051       CTAA   _  C
                                GCAGGC   GAAG CT CTC
                                ||||||   |||| || |||
                                CGTCCG   CTTC GA GAG
                                   AC__   C  A
GAM735  LOC56932  3'  CAGGCCTGGAGCTTCCTC    20052       AAGA   _
                                CAGGCCT   AGCT CCTC
                                |||||||   |||| ||||
                                GTCCGGA   TCGA GGAG
                                   CC__   A
GAM735  LOC90835  5'  CAGCAGGCCCTAGGTGCTC   20053         A  AA
                                CAGCAGGCCT AG  GCTC
                                |||||||||| ||  ||||
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                                GTCGTCCGGG TC  CGAG
                                     A  CA
GAM735  LOC91050  3'  CAGCCGGCTTAAGGCCCCT   20054     A  C   AA
                                CAGC GGC TAAG  GCTCCT
                                |||| ||| ||||  ||||||
                                GTCG CCG ATTC  CGGGGA
                                  G  A   __
GAM735  LOC96597  5'  CAGCAGGCACAGGCTCTTC   20055       CTA  AA   C
                                CAGCAGGC   AG  GCTC TC
                                ||||||||   ||  |||| ||
                                GTCGTCCG   TC  CGAG AG
                                     TG_  __   A
GAM736  DDX26     3'  TAGCCAACAATGCATGT     20058        CGACATC
                                TAGCCAACAA      CGTGT
                                ||||||||||      |||||
                                ATCGGTTGTT      GTACA
                                     AC_____
GAM736  GPR56     3'  GCCAGCAATCTACCCGTGT   20059     A  CGAC
                                GCCA CAA    ATCCGTGT
                                |||| |||    ||||||||
                                CGGT GTT    TGGGCACA
                                  C   AGA_
GAM736  ITGB1BP2  3'  GCCAACAATATCCTGGTA    20060       CGAC   GT
                                GCCAACAA    ATCC  GTA
                                |||||||    ||||  |||
                                CGGTTGTT    TAGG  CAT
                                     A___    AC
GAM736  RHD       3'  TAGCCAACATGGTGAAACCCTG 20061        AC__  C   G
          T                      TAGCCAACA    GA ATCC TGT
                                 |||||||||    || |||| |||
                                 ATCGGTTGT    CT TGGG ACA
                                      ACCA  T   _
GAM736  RHD       3'  TAGCCAACATGGTGAAACCCTG 20061        AC__  C   G
          T                      TAGCCAACA    GA ATCC TGT
                                 |||||||||    || |||| |||
                                 ATCGGTTGT    CT TGGG ACA
                                      ACCA  T   _
GAM736  SET       3'  GCCAGCAACTGTCCCGTGTA  20062     A   GACA
                                GCCA CAAC    TCCGTGTA
                                |||| ||||    ||||||||
                                CGGT GTTG    GGGCACAT
                                  C    ACA_
GAM736  EIF3S1    3'  TAGCAACAACGACAACAT    20063      C        TC
                                TAGC AACAACGACA  CGT
                                |||| ||||||||||  |||
                                ATCG TTGTTGCTGT  GTA
                                  _         T_
GAM736  LOC154877 3'  TAGCCAACATGGTGAGACCCTG 20064         AC__  C   G
          T                      TAGCCAACA    GA ATCC TGT
                                 |||||||||    || |||| |||
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                                ATCGGTTGT   CT TGGG ACA
                                     ACCA  C   _
GAM737  MME     3'  GAAGAATCTCAGCATCAGTCAA 20067      CC_  A
            A                    GAAGAA   CAG ATCAGTCAAA
                                 ||||||   ||| ||||||||||
                                 CTTCTT   GTC TAGTCAGTTT
                                    AGA   G
GAM737  MME     3'  GAAGAATCTCAGCATCAGTCAA 20067      CC_  A
            A                    GAAGAA   CAG ATCAGTCAAA
                                 ||||||   ||| ||||||||||
                                 CTTCTT   GTC TAGTCAGTTT
                                    AGA   G
GAM737  MME     3'  GAAGAATCTCAGCATCAGTCAA 20067      CC_  A
            A                    GAAGAA   CAG ATCAGTCAAA
                                 ||||||   ||| ||||||||||
                                 CTTCTT   GTC TAGTCAGTTT
                                    AGA   G
GAM737  MME     3'  GAAGAATCTCAGCATCAGTCAA 20067      CC_  A
            A                    GAAGAA   CAG ATCAGTCAAA
                                 ||||||   ||| ||||||||||
                                 CTTCTT   GTC TAGTCAGTTT
                                    AGA   G
GAM737  NLGN1   3'  TCAAAGAACTCAGAACTATAAT 20068        C    C__
            CA                    TCGAAGAAC CAGAAT   AGTCA
                                  ||||||||| ||||||   |||||
                                  AGTTTCTTG GTCTTG   TTAGT
                                       A     ATA
GAM737  COAS3   3'  TCAAAGAACCTAGAATAAG   20069        C    C
                                 TCGAAGAACC AGAAT AG
                                 |||||||||| ||||| ||
                                 AGTTTCTTGG TCTTA TC
                                       A    T
GAM737  FLJ13072 3' GAAGAGCTCCACAGTCAAA   20070      AC_  GAAT
                                 GAAGA   CCA   CAGTCAAA
                                 |||||   |||   ||||||||
                                 CTTCT   GGT   GTCAGTTT
                                    CGA  _____
GAM737  FLJ25442 5' TCGTAAGAAAGGTATCAGTCAA 20071    _    CCCAGA
            A                    TCG AAGAA     ATCAGTCAAA
                                 ||| |||||     ||||||||||
                                 AGC TTCTT     TAGTCAGTTT
                                   A    TCCA__
GAM737  GP      3'  TCAAGGCAAAATCAGTCA    20072    G   AACC
                                 TC AAG    CAGAATCAGTCA
                                 || |||    ||||||||||||
                                 AG TTC    GTTTTAGTCAGT
                                  _   C___
GAM737  KIAA1321 3' GAAAATTACAATATCAGTCAAA 20073      ACC   A
                                 GAAGA   CAG ATCAGTCAAA
                                 |||||   ||| ||||||||||
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                                CTTTT   GTT TAGTCAGTTT
                                   AAT   A
GAM737   KIAA1735  3'  TCAAGAACCCAGAACAG     20074    G         T
                                TC AAGAACCCAGAA CAG
                                || |||||||||||| |||
                                AG TTCTTGGGTCTT GTC
                                 _         _
GAM737   KRTHB4    3'  GAAAACCCAGGAACACAA     20075      A    _  _
                                GAAGA CCCAG AAT CAG
                                ||||| ||||| ||| |||
                                CTTTT GGGTC TTG GTT
                                   _    C   T
GAM737   LOC115343 5'  TCAAAGAGCCTGGACCAATCA  20076       A  CA  A
                                TCGAAGA CC  GA TCAGTCA
                                ||||||| ||  || |||||||
                                AGTTTCT GG  CT GGTTAGT
                                    C  AC  _
GAM737   LOC128582 5'  TCAAACCTCCAGGATCAGTCA  20077      GAAC    A
                                TCGAA    CCAG ATCAGTCA
                                |||||    |||| ||||||||
                                AGTTT    GGTC TAGTCAGT
                                   GGA_    C
GAM737   LOC152195 3'  TCGAAGAATATAAAACTTCAGT 20078        CCC    __
                                TCGAAGAA   AGAA  TCAGT
                                ||||||||   ||||  |||||
                                AGCTTCTT   TTTT  AGTCA
                                     ATA    GA
GAM737   LOC203523 3'  TCAAGAACCCCACCTTGTTGGT 20079    G       AGAATCA___
            CAAA                    TC AAGAACCC         GTCAAA
                                || ||||||||         ||||||
                                AG TTCTTGGG         CAGTTT
                                 _       GTGGAACAAC
GAM737   LOC220002 3'  GAAGGCTCCAGCCAGTCAA   20080      AAC    AA
                                GAAG   CCAG  TCAGTCAA
                                ||||   ||||  ||||||||
                                CTTC   GGTC  GGTCAGTT
                                  CGA   __
GAM737   LOC253816 3'  TCAAAGAATCCAGAGTCCTCA  20081        C     A  AG
                                TCGAAGAA CCAGA TC  TCA
                                ||||||| ||||| ||  |||
                                AGTTTCTT GGTCT AG  AGT
                                     A    C  G_
GAM737   LOC254594 3'  GAAGGCTCCAGCCAGTCAA   20080      AAC    AA
                                GAAG   CCAG  TCAGTCAA
                                ||||   ||||  ||||||||
                                CTTC   GGTC  GGTCAGTT
                                  CGA   __
GAM738   COL6A1    3'  TAGCACCGTTAATCTCGAGGGT 20084        CT_   CACTAT
            CT                    TAGCACCG   ATC     GTCT
                                ||||||||   |||     ||||
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                                ATCGTGGC  TAG    CAGA
                                    AAT  AGCTCC
GAM738  HIP12    3'  CAGCGCCCGGGCCGCTATGTCT 20085     A_  CTAT  A
            C                    TAGC  CCG   CC CTATGTCTC
                                 |||| |||   || |||||||||
                                 GTCG  GGC   GG GATACAGAG
                                   CG  CC__  C
GAM738  SFRS1    3'  GCATTGCTACCCACCTAAGTC  20086    CC       AT_
                                 GCA  GCTATCCACT  GTC
                                 |||  ||||||||||  |||
                                 CGT  CGATGGGTGG  CAG
                                   AA       ATT
GAM738  UBQLN3   3'  CAGCACCTCCACTATGT    20087      GCTA
                                 TAGCACC   TCCACTATGT
                                 |||||||   ||||||||||
                                 GTCGTGG   AGGTGATACA
                                    ____
GAM738  FLJ10648 3'  TAGCATCCTGCTTATGTCT   20088     _ _  ATCCAC
                                 TAGCA CC GCT    TATGTCT
                                 ||||| || |||    |||||||
                                 ATCGT GG CGA    ATACAGA
                                   A  A  _______
GAM738  FLJ20436 3'  GCCCAAAATATCCACTGTGTCT 20089   A  C__     A
                                 GC CCG   TATCCACT TGTCT
                                 || |||   |||||||| |||||
                                 CG GGT   ATAGGTGA ACAGA
                                  _  TTT      C
GAM738  KIAA1622 3'  TAACATCAGCTGTCATTATGTC 20090     C _  A  CAC
            TC                    TAGCA C GCT TC   TATGTCTC
                                 ||||| | ||| ||   ||||||||
                                 ATTGT G CGA AG   ATACAGAG
                                   A T   C  TA_
GAM738  SCHIP1   3'  TAGCACCGTCATTTACAGTTC  20091       C  CC  TATG
                                 TAGCACCG TAT  AC   TC
                                 |||||||| |||  ||   ||
                                 ATCGTGGC GTA  TG   AG
                                     A   AA  TCA_
GAM738  STK22B   5'  GCGCCGCTGCCGTCTACATC   20092   A    AT CA
                                 GC CCGCT  C  CTATGTC
                                 || |||||  |  |||||||
                                 CG GGCGA  G  GATGTAG
                                  C    CG CA
GAM738  ZNF212   3'  TAGCACCGTGTCCCCTGCTCTC 20093       CTA   ACTA  _
                                 TAGCACCG   TCC   TG TCTC
                                 ||||||||   |||   || ||||
                                 ATCGTGGC   AGG   AC AGAG
                                     AC_   GG__  G
GAM738  LOC145761 5'  ACCCCTTTTCACTGTGTCTC   20094    G  ATC   A
                                 ACC CT   CACT TGTCTC
                                 ||| ||   |||| ||||||
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                                TGG GA   GTGA ACAGAG
                                  G  AAA    C
GAM738  LOC146603 5'  ACAATGCTGTCCACTATGT   20095     CC   A
                                GCA  GCT TCCACTATGT
                                |||  ||| ||||||||||
                                TGT  CGA AGGTGATACA
                                  TA   C
GAM738  LOC202986 3'  TAGCAATCCAAATCGTTATGTC 20096      __  CT   CAC
           TC                     TAGCA  CCG  ATC   TATGTCTC
                                |||||  |||  |||   ||||||||
                                ATCGT  GGT  TAG   ATACAGAG
                                   TA   T_   CA_
GAM738  LOC51312  5'  GCTGCTATCCATATTTC    20097    ACC      C   G
                                GC   GCTATCCA TAT TC
                                ||   |||||||| ||| ||
                                CG   CGATAGGT ATA AG
                                 A__       _   A
GAM738  LOC57105  3'  TAGCGTCGTTAGTTGCTATATC 20098     AC  C  TCCA
           TC                     TAGC  CG TA    CTATGTCTC
                                ||||  || ||    |||||||||
                                ATCG  GC AT    GATATAGAG
                                  CA  A  CAAC
GAM739  CBFA2T3   3'  GAGAAAGTGTGTGATAGTCATA 20101      TGCCA  CT
           G                     GAGAA    TG  ATAGTCATAG
                                |||||    ||  ||||||||||
                                CTCTT    AC  TATCAGTATC
                                   TCAC_  AC
GAM739  DISC1    3'  GAGAATGCAGTGCTGTACAATA 20102        CA   __    CA
           CTAG                   GAGAATGC  TGCT  ATAGT  TAG
                                ||||||||  ||||  |||||  |||
                                CTCTTACG  ACGA  TGTTA  ATC
                                     TC    CA    TG
GAM739  EMS1     3'  GAGAGGCCATGCTGTGACAT   20103     AT      ATAGT
                                GAGA  GCCATGCT    CAT
                                ||||  ||||||||    |||
                                CTCT  CGGTACGA    GTA
                                  C_      CACT_
GAM739  EMS1     3'  GAGAGGCCATGCTGTGACAT   20103     AT      ATAGT
                                GAGA  GCCATGCT    CAT
                                ||||  ||||||||    |||
                                CTCT  CGGTACGA    GTA
                                  C_      CACT_
GAM739  PAX5     3'  GAGGATGCTCTGCCATAG    20104     A   CA
                                GAG ATGC  TGCTATAG
                                |||  ||||  ||||||||
                                CTC TACG  ACGGTATC
                                  C   AG
GAM739  STAC     3'  GATGCCATGTCAACATAG    20105    A     CTA   T
                                GA TGCCATG   TAG CATAG
                                ||  |||||||   ||| |||||
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                                CT ACGGTAC   GTT GTATC
                                 _      A__   _
GAM739   C8orf6    5'  GAGAATGCTTGCCTCTACCAT  20106        CA    A_  G
                                GAGAATGC  TGCT  TA TCAT
                                ||||||||  ||||  || ||||
                                CTCTTACG  ACGG  AT GGTA
                                    A_    AG  _
GAM739   ZFP95     3'  AAGGGTGCCAGAGCAGTCATAG 20107     AA    T_  TAT
                                GAG  TGCCA  GC   AGTCATAG
                                |||  |||||  ||   ||||||||
                                TTC  ACGGT  CG   TCAGTATC
                                  CC     CT  ___
GAM739   ZFP95     3'  AAGGGTGCCAGAGCAGTCATAG 20107     AA    T_  TAT
                                GAG  TGCCA  GC   AGTCATAG
                                |||  |||||  ||   ||||||||
                                TTC  ACGGT  CG   TCAGTATC
                                  CC     CT  ___
GAM740   CDK2      3'  CCAGTGGTTTTGTTTTACTTG  20110            C_
                                TCAGTGGTTTTGTTT  CTTG
                                ||||||||||||||  ||||
                                GGTCACCAAAACAAA  GAAC
                                        AT
GAM740   MEOX2     3'  ATGGTTTATTCTTGATA     20111        T   TC
                                GTGGTTT GTT  CTTGATA
                                |||||||  |||  |||||||
                                TACCAAA TAA  GAACTAT
                                    _   __
GAM740   SOX11     3'  AGTGGTTTGTTTCTCTGTAG   20112        T    C   A
                                AGTGGTTT GTTTC TTG TAG
                                |||||||| ||||| ||| |||
                                TCACCAAA CAAAG GAC ATC
                                    _     A   _
GAM740   ZNF83     3'  TCAGTGTTTTTGTTTCTCTCAA 20113       G       _  TG
                                TCAGTG TTTTGTTTC CT  A
                                |||||| |||||||| ||  |
                                AGTCAC AAAACAAAG GA  T
                                   A        A  GT
GAM740   BIRC1     3'  AGTGGTTTTGTTTTTTG     20114           CC
                                AGTGGTTTTGTTT  TTG
                                ||||||||||||  |||
                                TCACCAAAACAAA  AAC
                                        A_
GAM740   FLJ20651  3'  GTGGTTTTTTTCTCCTTG    20115        G_
                                GTGGTTTT  TTTCCTTG
                                ||||||||  ||||||||
                                CACCAAAA  AGAGGAAC
                                    AA
GAM740   KIAA0391  3'  AGGGTTTTGTTTCTAAAC    20116    T        CTT
                                AG GGTTTTGTTTC   GAT
                                || ||||||||||   |||
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                                TC CCAAAACAAAG   TTG
                                 _        AT_
GAM740  LATS1    3'  GTGGTGGTGGTCCTTGATA   20117      TT  TT
                                GTGGT  TG  TCCTTGATA
                                |||||  ||  |||||||||
                                CACCA  AC  AGGAACTAT
                                   CC  C_
GAM740  MGC2452  5'  AGTGGTTTTGTTATTTAA    20118          TCC
                                AGTGGTTTTGTT   TTGA
                                ||||||||||||  ||||
                                TCACCAAAACAA   AATT
                                       TA_
GAM740  LOC124961 3'  ATGTCCTTTCCTTGATA    20119     GTT  G
                                GTG   TT TTTCCTTGATA
                                |||   || ||||||||||
                                TAC   AG AAAGGAACTAT
                                 ___  G
GAM740  LOC144473 5'  CCAGTGGTGGTTCTTGGTA   20120        TTT   TC    A
                                TCAGTGGT   GTT  CTTG TA
                                ||||||||   |||  |||| ||
                                GGTCACCA   CAA  GAAC AT
                                     C__   __    C
GAM741  CNTN3    3'  GATTTTGTTTAATATTTGG   20123          __
                                GATTTTGTT  GTATTTGG
                                |||||||||  ||||||||
                                CTAAAACAA  TATAAACC
                                     AT
GAM741  IL1F5    3'  GATTTTGATTGTATCTTGGGTT 20124        _      __
                                GATTTTG TTGTATTT  GGTT
                                ||||||| ||||||||  ||||
                                CTAAAAC AACATAGA  CCAA
                                   T       AC
GAM741  KIAA0841  3'  GATTTTGTTGAGTTCAGTT   20125          TA  TG
                                GATTTTGTTG  TT  GTT
                                ||||||||||  ||  |||
                                CTAAAACAAC  AA  CAA
                                     TC  GT
GAM741  MGC4701   5'  AATTTTGTTGTATCTGATATG  20126              _
                                GATTTTGTTGTATTTGGT TG
                                |||||||||||||||||| ||
                                TTAAAACAACATAGACTA AC
                                          T
GAM741  RAB9A    3'  GATTTTGTGTATATGTGTGA   20127        T    T  GT
                                GATTTTGT GTAT TG  TGA
                                |||||||| |||| ||  |||
                                CTAAAACA CATA AC  ACT
                                     _   T  AC
GAM742  DHFR     3'  CCTATCCTGTACTTCTTTCTGC 20130        A  GG  ___  A
          C                      CCTATCCT TA  TC   CT CC
                                |||||||| ||  ||   || ||
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                                GGATAGGA AT  AG   GA GG
                                    C  GA  AAA  C
GAM742  DNAI2    5'  CCCTATCTCCACAGGTCCTGCC 20131       _        A
                                CCCTATC CTATAGGTCCT CC
                                ||||||| |||||||||| ||
                                GGGATAG GGTGTCCAGGA GG
                                    A         C
GAM742  DSS1     3'  CCCATCCTGGGTTCTCTGCC  20132       ATA  _ _  A
                                CCTATCCT   GGT C CT CC
                                ||||||||   ||| | || ||
                                GGGTAGGA   CCA G GA GG
                                    C__   A A  C
GAM742  DUSP6    3'  CCTACCCTATCATTTGGTTCTA 20133        A____   C
          CC                      CCTATCCTAT    GGT CTACC
                                ||||||||||    ||| |||||
                                GGATGGGATA    CCA GATGG
                                     GTAAA   A
GAM742  GAS11    3'  CCCCTGGTCCTACATCACCTAC 20134      A_     GGT
          C                       CCCCT  TCCTATA   CCTACC
                                |||||  |||||||  ||||||
                                GGGGA  AGGATGT   GGATGG
                                   CC      AGT
GAM742  MEFV     3'  TACTTCTATCCCAATCCAGTC  20135     CC      TA__
                                TAC  CTATCCTA    GGTC
                                |||  ||||||||   ||||
                                ATG  GATAGGGT    TCAG
                                  AA       TAGG
GAM742  MTA1L1   3'  CCAAGACATCTGTGGGTCCTAC 20136    CC__    CTATA
          C                       CC    TATC    GGTCCTACC
                                ||   ||||    |||||||||
                                GG   GTAG    CCAGGATGG
                                 TTCT   ACAC_
GAM742  OLIG2    3'  CCAATCCACAAGTGGTTCTAC  20137    T   T     C___
                                CC ATCC ATAGGT    CTAC
                                || |||| ||||||   ||||
                                GG TAGG TGTTCA    GATG
                                 T   _     CCAA
GAM742  TNC      3'  TACCCCTGTACATCCTAC    20138       ATCCTA  G
                                TACCCCT     TA GTCCTAC
                                |||||||     || |||||||
                                ATGGGGA     AT TAGGATG
                                    C_____  G
GAM742  FLJ10120 3'  CCCATTCTATCTCAGATGCC  20139     ___    CTA   _
                                CCC   CTATC   TAGGT CC
                                |||   |||||   ||||| ||
                                GGG   GATAG   GTCTA GG
                                  TAA    A__    C
GAM742  GPNMB    3'  CTATCCTACTAGTTACC     20140        A   CC
                                CTATCCTAT GGT  TACC
                                ||||||||| |||  ||||
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                                GATAGGATG TCA  ATGG
                                     A  __
GAM742  HSPC228  3'  CTTCCTATAGAAACACC    20141   A      TCC
                                CT TCCTATAGG   TACC
                                || |||||||||  ||||
                                GA AGGATATCT   GTGG
                                 _       TT_
GAM742  KIAA1431  3'  ACCCCTATTCTGGATCAGTTTA 20142       C  ATA   C___
          CC                     ACCCCTAT CT   GGTC   TACC
                                ||||||||  ||  ||||   ||||
                                TGGGGATA GA   CTAG   ATGG
                                    A  C__   TCAA
GAM742  MGC20255  3'  CCCCCATCCTCCCTC      20143         ATAGG   A
                                CCCCTATCCT    TCCT C
                                ||||||||||    |||| |
                                GGGGGTAGGA    GGGA G
                                      _____   C
GAM742  MGC3265  3'  CTTCCTTGGGTCCTACC    20144   A   ATA
                                CT TCCT   GGTCCTACC
                                || ||||   |||||||||
                                GA AGGA   CCAGGATGG
                                 _   AC_
GAM742  MYO18B   3'  CTATTCTAACAGTCCTACC   20145     C   TA
                                CTAT CTA  GGTCCTACC
                                |||| |||  |||||||||
                                GATA GAT  TCAGGATGG
                                  A  TG
GAM742  ST13    3'  CCCTACCCAGGTCCTAC    20146        TAT
                                CCCTATCC   AGGTCCTAC
                                ||||||||   |||||||||
                                GGGATGGG   TCCAGGATG
                                      ___
GAM742  WSB1    3'  TACTTCATCCTATGGTAAAGGT 20147    CCC      _____
          C                     TAC   TATCCTAT    AGGTC
                                |||   ||||||||    |||||
                                ATG   GTAGGATA    TCCAG
                                  AA_       CCATT
GAM742  LOC124470 3'  CTTCCCTGCAGGTCCTGCC   20148   A   A      A
                                CT TCCT TAGGTCCT CC
                                || |||| |||||||| ||
                                GA GGGA GTCCAGGA GG
                                 A   C       C
GAM742  LOC127428 3'  CCCCTATCCAAACTCCTGCC   20149        TAT  G   A
                                CCCCTATCC   AG TCCT CC
                                |||||||||   || |||| ||
                                GGGGATAGG   TT AGGA GG
                                      T__  G   C
GAM742  LOC142955 5'  CCTACCCTCTAATCTAC    20150        ATA   C
                                CCTATCCT   GGTC TAC
                                ||||||||   |||| |||
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                                GGATGGGA   TTAG ATG
                                    GA_   _
GAM742   LOC149317 3'  CTTGCCTATAGGTCCTGCC   20151    AT         A
                                CT  CCTATAGGTCCT CC
                                ||  ||||||||||| ||
                                GA  GGATATCCAGGA GG
                                 AC          C
GAM742   LOC149668 3'  TACCCCTCTCGGTCCT     20152       A  CTATA
                                TACCCCT TC    GGTCCT
                                |||||||  ||    ||||||
                                ATGGGGA AG    CCAGGA
                                    G  _____
GAM742   LOC151313 3'  CCCTCATCCTATGTCGGGCC   20153    C      A___
                                CCC TATCCTAT    GGTC
                                |||  ||||||||    ||||
                                GGG GTAGGATA    CCGG
                                  A       CAGC
GAM742   LOC153442 3'  CCCCTATTTTATAAACC     20154       CC     T
                                CCCCTAT  TATAGG CC
                                |||||||  ||||||  ||
                                GGGGATA  ATATTT GG
                                    AA     _
GAM742   LOC170082 3'  CCTATCCTGGAAGATTACC    20155        AT_   CC
                                CCTATCCT   AGGT  TACC
                                ||||||||   ||||  ||||
                                GGATAGGA   TCTA  ATGG
                                     CCT   __
GAM742   LOC254778 3'  TACTTCCATCCTATATAAATC  20156    CC        __
                                TAC  CTATCCTATA  GGTC
                                |||  ||||||||||  ||||
                                ATG  GGTAGGATAT  TTAG
                                  AA         AT
GAM742   LOC91250  5'  CCTCTATACTATAGGTCCTACC 20157    C    C
                                CC CTAT CTATAGGTCCTACC
                                || |||| ||||||||||||||
                                GG GATA GATATCCAGGATGG
                                 A    T
GAM743   CABC1     3'  CCTTTGGCTGGAACTGGTG    20160        _     CTA
                                CCTTTGG TGGAAC   GTG
                                |||||||  ||||||   |||
                                GGAAACC ACCTTG   CAC
                                    G     AC_
GAM743   CD69      5'  CTTTGCTGGAGCTCTTGTT    20161       G    AC  AG
                                CTTTG TGGA  CT  TGTT
                                |||||  ||||  ||  ||||
                                GAAAC ACCT  GA  ACAA
                                   G    C_  GA
GAM743   HDLBP     3'  ACCTTGGTTTAGTGTT      20162       T   GGAACC
                                ACCTT GGT     TAGTGTT
                                |||||  |||     |||||||
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                                TGGAA CCA     ATCACAA
                                  _  A_____
GAM743  SIAT4C   3'  CCTTGGTGGGGCCATCGCT   20163        AA  TAG
                                CTTTGGTGG  CC   TGTT
                                |||||||||  ||   ||||
                                GGAACCACC  GG   GCGA
                                     CC  TA_
GAM743  TXNIP    3'  ACCTTTGGTGGGGCAGT    20164         AACC
                                ACCTTTGGTGG    TAGT
                                ||||||||||    ||||
                                TGGAAACCACC    GTCA
                                      CC__
GAM743  CABYR    3'  ACTTTTGGTGGATGCTGC    20165    C       AC  A
                                AC TTTGGTGGA  CT GT
                                || |||||||||  || ||
                                TG AAACCACCT  GA CG
                                 A        AC  _
GAM743  MTHFD2   3'  CTTTGGTGGAAAAGTA     20166         CCT
                                CTTTGGTGGAA   AGTG
                                ||||||||||   ||||
                                GAAACCACCTT   TCAT
                                      T__
GAM743  OSBPL3   3'  AACCTTTGGAAAATTAGTGTTA 20167        T    CC
                                AACCTTTGG GGAA  TAGTGTTA
                                ||||||||| ||||  ||||||||
                                TTGGAAACC TTTT  ATCACAAT
                                     _   A_
GAM743  LOC149157 3'  CTTTAATTCATCTAGTGTTA   20168       GGAAC
                                CTTTGGT    CTAGTGTTA
                                |||||||    |||||||||
                                GAAATTA    GATCACAAT
                                    AGTA_
GAM743  LOC162333 5'  CCTCTTCAGCTTAGTGTTA    20169      GG   AACC
                                CCTTT  TGG    TAGTGTTA
                                |||||  |||   ||||||||
                                GGAGA  GTC    ATCACAAT
                                   A_   GA__
GAM743  LOC200488 5'  TTTGGTGGAGGCTAATGTTA   20170        AC
                                TTTGGTGGA  CTAGTGTTA
                                |||||||||  |||||||||
                                AAACCACCT  GATTACAAT
                                     CC
GAM744  DTNB     3'  ATGGTGCTAATATTGTAGATAA 20173     C       GC    A
                                ATG TGCTGGTGT  TGTA ATAA
                                ||| |||||||||  |||| ||||
                                TAC ACGATTATA  ACAT TATT
                                  C        __    C
GAM744  GGT2     5'  ATGCCGCTGGTGTGCCAGCTCA 20174             _  AA
             TA                   ATGCTGCTGGTGTGCT GT  ATA
                                ||||||||||||||| ||  |||
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                                TACGGCGACCACACGG CG  TAT
                                         T  AG
GAM744  GLP1R    3'  TGCTGCTGTGTGTCACCAT   20175        _   _
                                TGCTGCTG GTGT GCTGT
                                |||||||| |||| |||||
                                ACGACGAC CACA TGGTA
                                     A   G
GAM744  GPR23    5'  ATGTGCTGATGCCTGTAGATAA 20176    C       G    A
                                ATG TGCTGGTGT CTGTA ATAA
                                ||| ||||||||| ||||| ||||
                                TAC ACGACTACG GACAT TATT
                                  _       _    C
GAM744  H3F3B    3'  ATGATGCTGGTGTGAATAA   20177    C       CT
                                ATG TGCTGGTGTG  GTAA
                                ||| ||||||||||  ||||
                                TAC ACGACCACAC  TATT
                                  T        T_
GAM744  NEDD4    3'  ATGCTGTGGTGTTTGGAAA   20178      C    GC  T
                                ATGCTG TGGTGT  TG AAA
                                |||||| ||||||  || |||
                                TACGAC ACCACA  AC TTT
                                   _     A_  C
GAM744  DKFZP434N1817 5'  TGCTGGTGGTGGTGGAGGTA   20179      C    _ CT_
                                TGCTG TGGTG TG   GTA
                                ||||| ||||| ||   |||
                                ACGAC ACCAC AC   CAT
                                   C    C  CTC
GAM744  FAM3C    3'  TGCTGCCTTACACTGTGAAT   20180       GG  TG   A
                                TGCTGCT  TG  CTGT AAT
                                |||||||  ||  |||| |||
                                ACGACGG  AT  GACA TTA
                                    A_  GT   C
GAM744  FLJ10853  3'  TGCTGCTGTGGGTGTGAGTAA  20181        ___     CT
                                TGCTGCT   GGTGTG  GTAA
                                |||||||   ||||||  ||||
                                ACGACGA   CCACAC  CATT
                                    CAC     T_
GAM744  FLJ12838  3'  ATGACACACTGTGCTGTAGATA 20182    C   T G       A
                                ATG TGC G TGTGCTGTA ATA
                                ||| ||| | |||||||||| |||
                                TAC GTG T ACACGACAT TAT
                                  T   _ G        C
GAM744  GREB1    3'  TGCTGTTAGTGTGTCCATAA   20183      C     _
                                TGCTG TGGTGTG CTGTAA
                                ||||| ||||||| ||||||
                                ACGAC ATCACAC GGTATT
                                   A      A
GAM744  KALI     3'  ATGTGCTGGTGTGTTAT     20184     C        C
                                ATG TGCTGGTGTG TGT
                                ||| |||||||||| |||
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                                TAC ACGACCACAC ATA
                                  _       A
GAM744  KIAA0087 3' ATGTTACTTAACACTGTAAATA 20185    C   GGT TG
           A                     ATG TGCT  G  CTGTAAATAA
                                 ||| ||||  |  ||||||||||
                                 TAC ATGA  T  GACATTTATT
                                   A   AT_ GT
GAM744  KIAA0420 3' ATGCTGCTGGTTGGAGCAA   20186         G  CT
                                 ATGCTGCTGGT TG  GTAA
                                 |||||||||| ||  ||||
                                 TACGACGACCA AC  CGTT
                                       _ CT
GAM744  KIAA1218 5' TGCTGCTGGAGGTAAGTA    20187        T_  CT
                                 TGCTGCTGG  GTG  GTA
                                 |||||||||  |||  |||
                                 ACGACGACC  CAT  CAT
                                      TC  T_
GAM744  KIAA1271 3' TGTTTCTGGTGTTATTGTAGAT 20188   CTG     GC_   A
           AA                     TG  CTGGTGT  TGTA ATAA
                                 ||  |||||||  |||| ||||
                                 AC  GACCACA  ACAT TATT
                                  AAA      ATA   C
GAM744  KIAA1962 3' CTGCTGGTGACGAAAATAA   20189        T  TGT
                                 CTGCTGGTG GC   AAATAA
                                 |||||||||  ||  ||||||
                                 GACGACCAC TG   TTTATT
                                       _ CT_
GAM744  NAV3     3' TGTTGCTTGGTTGTAAAT    20190    C   _  GTGC
                                 TG TGCT GGT    TGTAAAT
                                 || |||| |||    |||||||
                                 AC ACGA CCA    ACATTTA
                                  A   A  _____
GAM744  RALGPS1A 3' TGCTAGTGCTGTGAAT      20191       GT    A
                                 TGCTGGT  GCTGT AAT
                                 |||||||  ||||| |||
                                 ACGATCA  CGACA TTA
                                     __     C
GAM744  STX1B2   3' ATGCATGTTGGTGTGCATGT   20192      _ C      _
                                 ATGC TG TGGTGTGC TGT
                                 |||| || |||||||| |||
                                 TACG AC ACCACACG ACA
                                   T  A       T
GAM744  TSGA     3' TGCATGTTCTGTAAATA     20193     TG   G
                                 TGC  GTGT CTGTAAATA
                                 |||  |||| |||||||||
                                 ACG  TACA GACATTTAT
                                   __    A
GAM744  LOC121512 5' TGCTGCTTGTGGAGCAA     20194       GG   CT
                                 TGCTGCT  TGTG  GTAA
                                 |||||||  ||||  ||||
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                                ACGACGA  ACAC  CGTT
                                   __    CT
GAM744   LOC149319 5'  ATGCTGCTGGTGTGCCAGCTCA 20195              _  AA
           TA                    ATGCTGCTGGTGTGCT GT  ATA
                                 ||||||||||||||| ||  |||
                                 TACGACGACCACACGG CG  TAT
                                          T  AG
GAM744   LOC150271 5'  TGCTGCTCTCTGTAAATA    20196       GGTGTG
                                 TGCTGCT     CTGTAAATA
                                 |||||||     |||||||||
                                 ACGACGA     GACATTTAT
                                    GA____
GAM744   LOC157247 5'  ATCCTGTTGTCTCACTGTAAAT 20197    G   C  GTG
           A                     AT CTG TG   TGCTGTAAATA
                                 || ||| ||   ||||||||||
                                 TA GAC AC   GTGACATTTAT
                                  G   A  AGA
GAM744   LOC200301 3'  TGCTAATCTGTAAAT       20198       GTG
                                 TGCTGGT   CTGTAAAT
                                 |||||||   ||||||||
                                 ACGATTA   GACATTTA
                                    ___
GAM744   LOC221486 3'  ATGCTGCTGGTGAAATAA    20199          TGCT
                                 ATGCTGCTGGTG    GTAA
                                 ||||||||||||    ||||
                                 TACGACGACCAC    TATT
                                       TT__
GAM744   LOC253443 3'  ACGCTGCTGGTAAAGGCTG   20200          T__
                                 ATGCTGCTGGTG   GCTG
                                 ||||||||||||   ||||
                                 TGCGACGACCAT   CGAC
                                       TTC
GAM744   LOC255330 5'  ATGTTGCTGCTGTAAATA    20201     C    GGTGT
                                 ATG TGCT    GCTGTAAATA
                                 ||| ||||    ||||||||||
                                 TAC ACGA    CGACATTTAT
                                   A   _____
GAM744   LOC256537 5'  TGCTGCTGAGTGTGGGGT    20202        _    CT
                                 TGCTGCTG GTGTG  GT
                                 |||||||| |||||  ||
                                 ACGACGAC CACAC  CA
                                      T    CC
GAM744   LOC257354 3'  ATGCTGCTGGTTGGAGCAA   20186          G  CT
                                 ATGCTGCTGGT TG  GTAA
                                 |||||||||||| ||  ||||
                                 TACGACGACCA AC  CGTT
                                       _ CT
GAM744   LOC92578  5'  TGCTGCTGGTTGTAGAGCTGTA 20203          _  ___
                                 TGCTGCTGGT GT   GCTGTA
                                 |||||||||| ||   ||||||
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                                ACGACGACCA CA   CGACAT
                                     A  TCT
GAM745  ABCC3    3'  CTGATGCCCTCCACCTGC    20206      _  TATC     C
                                CTGGT CCC    TCCACC GC
                                ||||| |||    |||||| ||
                                GACTA GGG    AGGTGG CG
                                   C  _____     A
GAM745  ABR      3'  CTGGTTCCACCACCCGCC    20207      C  TATCT
                                CTGGT CC    CCACCCGCC
                                ||||| ||    |||||||||
                                GACCA GG    GGTGGGCGG
                                   A  T____
GAM745  ABR      3'  CTGGTTCCACCACCCGCC    20207      C  TATCT
                                CTGGT CC    CCACCCGCC
                                ||||| ||    |||||||||
                                GACCA GG    GGTGGGCGG
                                   A  T____
GAM745  AGR2     5'  CTGGATTTCCTCACCCACCTGC 20208     TC__  ATC     C
              C                  CTGG   CCT   TCCACC GCC
                                 ||||   |||   |||||| |||
                                 GACC   GGA   GGGTGG CGG
                                   TAAA   GT_     A
GAM745  AP1B1    5'  TGGTCCCTTATCTGTAGCC    20209        _   CCACCC
                                TGGTCCCT ATCT     GCC
                                |||||||| ||||     |||
                                ACCAGGGA TAGA     CGG
                                     A   CAT___
GAM745  APAF1    5'  CTGGTTCTATCCCTTTTGCC   20210      CC      CACCC
                                CTGGT  CTATCTC    GCC
                                |||||  |||||||    |||
                                GACCA  GATAGGG    CGG
                                   A_      AAAA_
GAM745  APAF1    5'  CTGGTTCTATCCCTTTTGCC   20210      CC      CACCC
                                CTGGT  CTATCTC    GCC
                                |||||  |||||||    |||
                                GACCA  GATAGGG    CGG
                                   A_      AAAA_
GAM745  C18orf1  3'  TGGCCCCTATTTCCTGCC    20211         C   ACCC
                                TGGTCCCTAT TCC    GCC
                                |||||||||| |||    |||
                                ACCGGGGATA AGG    CGG
                                     A   A___
GAM745  COL4A4   5'  CTGGATCCGCGCCCACCTGCC  20212      _  CTATC     C
                                CTGG TCC     TCCACC GCC
                                |||| |||     |||||| |||
                                GACC AGG     GGGTGG CGG
                                  T   CGC__     A
GAM745  CPN1     5'  CTAGCCTCTTCACCCGC     20213       CCTA   C
                                CTGGTC    TCT CACCCGC
                                ||||||    ||| |||||||
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                                GATCGG   AGA GTGGGCG
                                   ____  A
GAM745  DES     3'  CTAGTCCCCCTGGCTACCTGCC 20214        ATCTCC  C
                                CTGGTCCCT     ACC GCC
                                |||||||||     ||| |||
                                GATCAGGGG     TGG CGG
                                    GACCGA  A
GAM745  FBXL7   5'  GGTCCCCATCCGCCCGCC    20215        TC  A
                                GGTCCCTA  TCC CCCGCC
                                ||||||||  ||| ||||||
                                CCAGGGGT  AGG GGGCGG
                                   __  C
GAM745  GAS11   3'  CTGGTCCCCATCTCTGCAGCC  20216           CACCC
                                CTGGTCCCTATCTC    GCC
                                ||||||||||||||    |||
                                GACCAGGGGTAGAG    CGG
                                      ACGT_
GAM745  GPC5    5'  CTGGTCCCCTTTACCCGCC   20217        ATCTCC
                                CTGGTCCCT     ACCCGCC
                                |||||||||     |||||||
                                GACCAGGGG     TGGGCGG
                                    AAA___
GAM745  GPT     5'  GGCCCCGCCCCACCCG      20218       TAT
                                GGTCCC  CTCCACCCG
                                ||||||  |||||||||
                                CCGGGG  GGGGTGGGC
                                  C__
GAM745  GPX3    5'  CTGATCCCTGGCCACCGTCC  20219        ATCT    CG
                                CTGGTCCCT   CCACC  CC
                                |||||||||   |||||  ||
                                GACTAGGGA   GGTGG  GG
                                    CC__    CA
GAM745  HIVEP1  5'  CCGGTCCCCCGCTCCGTCCGCC 20220        AT   AC
                                CTGGTCCCT  CTCC  CCGCC
                                |||||||||  ||||  |||||
                                GGCCAGGGG  GAGG  GGCGG
                                    GC   CA
GAM745  HMGA2   3'  CGGTTTTTCTCACCCGCC    20221     CCCTA   C
                                TGGT    TCTC ACCCGCC
                                ||||    |||| |||||||
                                GCCA    AGAG TGGGCGG
                                  AAA__   _
GAM745  HS3ST3A1 5' CTGGTCCCCTTGCCCGCC    20222        ATCTCCA
                                CTGGTCCCT     CCCGCC
                                |||||||||     ||||||
                                GACCAGGGG     GGGCGG
                                    AAC____
GAM745  KCNJ6   5'  GGTCTCCACCCCTCCGCCCGCC 20223     _ TA_    A
                                GGTC CC   TCTCC CCCGCC
                                |||| ||   ||||| ||||||
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                                CCAG GG   GGAGG GGGCGG
                                  A TGG    C
GAM745  KLF8    5'  CTGTTCCCCTCACACCCGCC  20224    G   TAT  _
                                CTG TCCC  CTC CACCCGCC
                                ||| ||||  ||| ||||||||
                                GAC AGGG  GAG GTGGGCGG
                                  A  ___  T
GAM745  MATK    5'  CTGGTGTCTTCCTGCCACCCGC 20225     CC  A  _
            C                    CTGGT  CT TCT CCACCCGCC
                                ||||||  || ||| |||||||||
                                GACCA  GA GGA GGTGGGCGG
                                   CA  A   C
GAM745  MGAT5   5'  CTAGTCCCACCACCTGC    20226       TATCT    C
                                CTGGTCCC    CCACC GC
                                ||||||||    ||||| ||
                                GATCAGGG    GGTGG CG
                                     T____    A
GAM745  NAGA    5'  CGGTCCCCAAGTTGCCCGCC  20227       TCTCCA
                                TGGTCCCTA    CCCGCC
                                |||||||||    ||||||
                                GCCAGGGGT    GGGCGG
                                     TCAAC_
GAM745  POLD1   3'  CTGGTCCCGCCCCCGC     20228       TATCT  A
                                CTGGTCCC    CC CCCGC
                                ||||||||    || |||||
                                GACCAGGG    GG GGGCG
                                     C____  _
GAM745  PPP2R2B  5'  CTGGTCCCGCCCGCCCGCC  20229       TATC   A
                                CTGGTCCC    TCC CCCGCC
                                ||||||||    ||| ||||||
                                GACCAGGG    GGG GGGCGG
                                     C___   C
GAM745  PTPRF   5'  CTGGTCCCGCTCCCGC     20230       TAT  CCA
                                CTGGTCCC   CT   CCCGC
                                ||||||||   ||   |||||
                                GACCAGGG   GA   GGGCG
                                     C__  ___
GAM745  PTPRF   5'  CTGGTCCCGCTCCCGC     20230       TAT  CCA
                                CTGGTCCC   CT   CCCGC
                                ||||||||   ||   |||||
                                GACCAGGG   GA   GGGCG
                                     C__  ___
GAM745  RAI14   5'  CTGCTCCACCCCGCCCGCC   20231    G  CTAT   A
                                CTG TCC    CTCC CCCGCC
                                ||| |||    |||| ||||||
                                GAC AGG    GGGG GGGCGG
                                  G  T___    C
GAM745  SLC9A5   3'  CTGATCCCTAGAAAGTCACCTG 20232         TCTC__   C
            CC                    CTGGTCCCTA     CACC GCC
                                ||||||||||     |||| |||
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                                GACTAGGGAT     GTGG CGG
                                     CTTTCA    A
GAM745  SLC9A5   3'  CTGATCCCTAGAAAGTCACCTG 20232         TCTC__    C
              CC                   CTGGTCCCTA     CACC GCC
                                   ||||||||||     |||| |||
                                   GACTAGGGAT     GTGG CGG
                                        CTTTCA    A
GAM745  STK11    3'  CTGGTCTCCACACCCGCC    20233       CCTA  TC
                                   CTGGTC   TC  CACCCGCC
                                   ||||||   ||  ||||||||
                                   GACCAG   AG  GTGGGCGG
                                      ____  GT
GAM745  WWOX     5'  CTGGCCCCCCTATCGCCCGC  20234        ATC  CA
                                   CTGGTCCCT  TC  CCCGC
                                   |||||||||  ||  |||||
                                   GACCGGGGG  AG  GGGCG
                                        GAT  C_
GAM745  WWOX     5'  CTGGCCCCCCTATCGCCCGC  20234        ATC  CA
                                   CTGGTCCCT  TC  CCCGC
                                   |||||||||  ||  |||||
                                   GACCGGGGG  AG  GGGCG
                                        GAT  C_
GAM745  WWOX     5'  CTGGCCCCCCTATCGCCCGC  20234        ATC  CA
                                   CTGGTCCCT  TC  CCCGC
                                   |||||||||  ||  |||||
                                   GACCGGGGG  AG  GGGCG
                                        GAT  C_
GAM745  WWOX     5'  CTGGCCCCCCTATCGCCCGC  20234        ATC  CA
                                   CTGGTCCCT  TC  CCCGC
                                   |||||||||  ||  |||||
                                   GACCGGGGG  AG  GGGCG
                                        GAT  C_
GAM745  WWOX     5'  CTGGCCCCCCTATCGCCCGC  20234        ATC  CA
                                   CTGGTCCCT  TC  CCCGC
                                   |||||||||  ||  |||||
                                   GACCGGGGG  AG  GGGCG
                                        GAT  C_
GAM745  ARFGAP1  3'  CCGGTCCCAGGCCCACCTGCC 20235        TATC     C
                                   CTGGTCCC   TCCACC GCC
                                   ||||||||   |||||| |||
                                   GGCCAGGG   GGGTGG CGG
                                      TCC_    A
GAM745  C8orf17  5'  CTGGTCCCACACCCGC     20236        TATCTC
                                   CTGGTCCC    CACCCGC
                                   ||||||||    |||||||
                                   GACCAGGG    GTGGGCG
                                      T_____
GAM745  CITED1   5'  CTGGTGCCCGCCCGCCCGCC  20237      _  TATC  A
                                   CTGGT CCC   TCC CCCGCC
                                   ||||| |||   ||| ||||||
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                                GACCA GGG   GGG GGGCGG
                                  C  C___  C
GAM745  DKFZP727G051 3' CTGGTCCCCATCTGGTGCC  20238          CCACCC
                                CTGGTCCCTATCT    GCC
                                ||||||||||||    |||
                                GACCAGGGGTAGA    CGG
                                      CCA___
GAM745  DKFZp761B0514 3' CTGCTCTCCACTCACCCGCC  20239    G  C  T  C
                                CTG TC CTA CTC ACCCGCC
                                ||| || ||| ||| |||||||
                                GAC AG GGT GAG TGGGCGG
                                  G  A  _  _
GAM745  DOK4    5' CTGCTCCTCACCTCACCCGCC 20240    G  C    C
                                CTG TCC TATCTC ACCCGCC
                                ||| ||| |||||| |||||||
                                GAC AGG GTGGAG TGGGCGG
                                  G  A    _
GAM745  FLJ10420 3' CTGGCTTCCAGCACCCGCC  20241     CC  TCTC
                                CTGGT  CTA   CACCCGCC
                                |||||  |||   ||||||||
                                GACCG  GGT   GTGGGCGG
                                  AA  C___
GAM745  FLJ11539 3' GGTCGCTTCCTCCACCCGCC  20242    C  A
                                GGTC CT TCTCCACCCGCC
                                |||| || ||||||||||||
                                CCAG GA GGAGGTGGGCGG
                                  C  A
GAM745  FLJ11856 3' CTGGTCCCTGGCTCCAAGCCTG 20243        AT   __ C
          C                      CTGGTCCCT  CTCCA  CC GC
                                |||||||||  |||||  || ||
                                GACCAGGGA  GAGGT  GG CG
                                     CC    TC  A
GAM745  FLJ14708 3' CTGGTCCCTTCCTTCTCTGCC  20244        A___   CA
                                CTGGTCCCT   TCTC  CC
                                |||||||||   ||||  ||
                                GACCAGGGA   AGAG  GG
                                     AGGA   AC
GAM745  FLJ14810 3' TGGTCCCTGTCCCTTGACCACT 20245      A  _____   C   III
          CGCCG                  TCCCT TCT    CCAC CGCC  G
                                |||||  |||    ||||  ||||  |
                                AGGGA AGG    GGTG GCGG  C
                                  C  GAACT   A   III
GAM745  FLJ20595 3' TGGTTCCCATCTCAGGTGCC  20246     C      CACCC
                                TGGT CCTATCTC    GCC
                                ||||  ||||||||    |||
                                ACCA GGGTAGAG    CGG
                                  A      TCCA_
GAM745  FLJ21709 3' CTGGCCCTACCTCCACC    20247     T
                                CTGG CCCTATCTCCACC
                                ||||  ||||||||||||
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                                GACC GGGATGGAGGTGG
                                   _
GAM745  FLJ22173  3'  TGGTCCCTATCTGGGACC    20248          CC_
                                TGGTCCCTATCT   ACC
                                ||||||||||||  |||
                                ACCAGGGATAGA   TGG
                                      CCC
GAM745  GSH-2     5'  CTGGTCCTCACGTCCACCCGCC 20249       C   C
                                CTGGTCC TAT TCCACCCGCC
                                ||||||| ||| ||||||||||
                                GACCAGG GTG AGGTGGGCGG
                                    A   C
GAM745  KIAA0152  3'  CTAGTCCCCAAATCACCTGC   20250         TCTC    C
                                CTGGTCCCTA    CACC GC
                                ||||||||||    |||| ||
                                GATCAGGGGT    GTGG CG
                                      TTA_    A
GAM745  KIAA0450  3'  CTGGCCCCGACACCCGC     20251        TATCTC
                                CTGGTCCC     CACCCGC
                                ||||||||     |||||||
                                GACCGGGG     GTGGGCG
                                    CT_____
GAM745  KIAA0544  3'  CTGGTGCCACGCCACCCGC    20252      C  TATCT
                                CTGGT CC     CCACCCGC
                                ||||| ||     ||||||||
                                GACCA GG     GGTGGGCG
                                   C  TGC__
GAM745  KIAA0599  3'  GGTCCTGTCCTCCACCTGC    20253      CTA      C
                                GGTCC   TCTCCACC GC
                                |||||   |||||||| ||
                                CCAGG   GGAGGTGG CG
                                   ACA       A
GAM745  KIAA0674  5'  CTGGCAAACTTCACCCGCC    20254      CCCTAT  C
                                CTGGT     CT CACCCGCC
                                |||||     || ||||||||
                                GACCG     GA GTGGGCGG
                                   TTT___  A
GAM745  KIAA0876  3'  CTGGTCCCAAACTCCTGCC    20255        TAT    ACCC
                                CTGGTCCC   CTCC    GCC
                                ||||||||   ||||    |||
                                GACCAGGG   GAGG    CGG
                                     TTT    A___
GAM745  KIAA0964  3'  GTCTCATTTCCACCCGCC     20256     CC   C
                                GTC  TAT TCCACCCGCC
                                |||  ||| ||||||||||
                                CAG  GTA AGGTGGGCGG
                                  A_   A
GAM745  KIAA1100  3'  TGGTCCCTATACCCGC       20257          CTCC
                                TGGTCCCTAT    ACCCGC
                                ||||||||||    ||||||
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                              ACCAGGGATA   TGGGCG
                                   ____
GAM745  KIAA1399 3' GGTCCCCCACCCTCTGCC   20258      TATCT    ___
                              GGTCCC   CCACCC  GCC
                              ||||||   ||||||  |||
                              CCAGGG   GGTGGG  CGG
                                 _____    AGA
GAM745  KIAA1553 3' CTGGTCCCTGCCCTCACAGC  20259       AT TC  CC
                              CTGGTCCCT  C  CAC  GC
                              |||||||||  |  |||  ||
                              GACCAGGGA  G  GTG  CG
                                    CG GA   T_
GAM745  KIAA1719 3' CTCGTTCCTATCTCAGGGCC  20261    G  C      CACCC
                              CT GT CCTATCTC    GCC
                              || || ||||||||    |||
                              GA CA GGATAGAG    CGG
                               G  A      TCC__
GAM745  KIAA1719 3' CTGGCTACACCTGCCCGCC   20260     CCC    CCA
                              CTGGT   TATCT   CCCGCC
                              |||||   |||||   ||||||
                              GACCG   GTGGA   GGGCGG
                                 AT_    C__
GAM745  LGI3    5' GGTCCCCTCCCCTGCTCGC   20262       A    ACC_
                              GGTCCCT TCTCC    CGC
                              ||||||| |||||    |||
                              CCAGGGG AGGGG    GCG
                                  _    ACGA
GAM745  MGC12921 3' CTGTTCCACCCACGCCCGCC  20263    G   CT   CCA
                              CTG TCC  ATCT   CCCGCC
                              ||| |||  ||||   ||||||
                              GAC AGG  TGGG   GGGCGG
                                A   __    TGC
GAM745  MGC13016 3' TGGTCCCTTCTTCAGGGC    20264       A  C  CCC
                              TGGTCCCT TCT CA   GC
                              |||||||| ||| ||   ||
                              ACCAGGGA AGA GT   CG
                                  _  A  CC_
GAM745  MGC14136 5' CTGGATCCCTATCGCCCCGCC 20265     _      TCCA
                              CTGG TCCCTATC    CCCGCC
                              |||| ||||||||    ||||||
                              GACC AGGGATAG    GGGCGG
                                 T       CG__
GAM745  MGC3048  3' CTGCTCCCTCCACCTGC     20266     G   TATC     C
                              CTG TCCC    TCCACC GC
                              ||| ||||    |||||| ||
                              GAC AGGG    AGGTGG CG
                                G    _____     A
GAM745  NY-REN-25 3' CTGGTCCCTTCTCCACCC    20267         A
                              CTGGTCCCT TCTCCACCC
                              ||||||||| |||||||||
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                                GACCAGGGA AGAGGTGGG
                                        _
GAM745  P2RXL1   3'  CTGGCCCTCCACAGCTTGCC  20268      CTATC    CC___
                                CTGGTCC    TCCAC    GCC
                                |||||||    |||||    |||
                                GACCGGG    AGGTG    CGG
                                    _____    TCGAA
GAM745  PIWIL2   3'  TGGTCCCCCAGAGTCACCCGC 20269      ATCTC_
                                TGGTCCCT     CACCCGC
                                ||||||||     |||||||
                                ACCAGGGG     GTGGGCG
                                     GTCTCA
GAM745  SMOC1    3'  CTGGACTCTCCACCTGCC    20270     TCCCTA      C
                                CTGG     TCTCCACC GCC
                                ||||     |||||||| |||
                                GACC     AGAGGTGG CGG
                                  TG____       A
GAM745  SOX30    5'  CTGGTCCCTACTCTCGC     20271        T   CACC
                                CTGGTCCCTA CTC    CGC
                                |||||||||| |||    |||
                                GACCAGGGAT GAG    GCG
                                     _   A___
GAM745  SPOP     5'  CTGGTCCCCGTCCCCCTGCGC 20272       TA    ACC
                                CTGGTCCC  TCTCC   CGC
                                ||||||||  |||||   |||
                                GACCAGGG  AGGGG   GCG
                                     GC    GAC
GAM745  ZF       3'  CTGGTCCCGTCTCTTCTGCC  20273       TA   CACCC
                                CTGGTCCC  TCTC    GCC
                                ||||||||  ||||    |||
                                GACCAGGG  AGAG    CGG
                                     C_    AAGA_
GAM745  LOC124470 3'  CTGCTCCCCACCACCTGC    20274    G     TCT    C
                                CTG TCCCTA   CCACC GC
                                ||| ||||||   ||||| ||
                                GAC AGGGGT   GGTGG CG
                                  G     ___     A
GAM745  LOC128402 3'  CTGCGCCTCTCCACCCG     20275    _   CCTA
                                CTG GTC    TCTCCACCCG
                                ||| |||    ||||||||||
                                GAC CGG    AGAGGTGGGC
                                  G  _____
GAM745  LOC134553 5'  CTGGCTCCCAGCACCCGCC   20276     TC    TCTC
                                CTGG  CCTA    CACCCGCC
                                ||||  ||||    ||||||||
                                GACC  GGGT    GTGGGCGG
                                  GA    C___
GAM745  LOC143241 5'  GTCCCTACACACGCGCC     20277       CTC   C
                                GTCCCTAT   CAC CGCC
                                ||||||||   ||| ||||
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                                CAGGGATG   GTG GCGG
                                    T__   C
GAM745   LOC143384 5'  CTGGCCCCCGGCACCCGCC   20278        ATCTC
                                CTGGTCCCT    CACCCGCC
                                |||||||||    ||||||||
                                GACCGGGGG    GTGGGCGG
                                     CC___
GAM745   LOC145553 5'  TGGCCCCTTCTATCTCAC    20280        ___    C
                                TGGTCCCT   ATCTC AC
                                ||||||||   ||||| ||
                                ACCGGGGA   TAGAG TG
                                    AGA    _
GAM745   LOC145553 5'  GTCCCTACCTCACCTGC     20279          C   C
                                GTCCCTATCTC ACC GC
                                |||||||||| ||| ||
                                CAGGGATGGAG TGG CG
                                      _   A
GAM745   LOC146733 3'  CTGGCTTGCTCCCCATTCGCC  20282      CCCTA     CC
                                CTGGT    TCTCCA  CGCC
                                |||||    ||||||  ||||
                                GACCG    AGGGGT  GCGG
                                   AACG_     AA
GAM745   LOC146733 3'  TGCTCCCCATTCGCCTGCC    20281    G      C  CA  C
                                TG TCCCTAT TC  CC GCC
                                || ||||||| ||  || |||
                                AC AGGGGTA AG  GG CGG
                                 G      _  C_  A
GAM745   LOC147807 3'  GGTCTCCACCCTCCACCTGC   20283     _  TA       C
                                GGTC CC  TCTCCACC GC
                                |||| ||  |||||||| ||
                                CCAG GG  GGAGGTGG CG
                                  A  TG       A
GAM745   LOC150606 3'  TGGCCCCTGTACTCCCCG    20284        AT_    AC
                                TGGTCCCT   CTCC  CCG
                                ||||||||   ||||  |||
                                ACCGGGGA   GAGG  GGC
                                    CAT    __
GAM745   LOC152586 5'  GGTCCCCAGCACACCCGCC   20285        TCTC
                                GGTCCCTA    CACCCGCC
                                ||||||||    ||||||||
                                CCAGGGGT    GTGGGCGG
                                    CGT_
GAM745   LOC153338 5'  CTGGTCCCTGCCTCTCACTGC  20286         AT   _   CC
                                CTGGTCCCT  CTC CAC  GC
                                |||||||||  ||| |||  ||
                                GACCAGGGA  GAG GTG  CG
                                     CG   A   A_
GAM745   LOC153811 3'  CTGGGTCCCATCAACACCCGCC 20287     TC     TC
                                CTGG  CCTATC  CACCCGCC
                                ||||  ||||||  ||||||||
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                                GACC  GGGTAG  GTGGGCGG
                                  CA     TT
GAM745  LOC163038 5'  CTGGACCCACCACCCGC     20288      T   TATCT
                                CTGG CCC     CCACCCGC
                                |||| |||     ||||||||
                                GACC GGG     GGTGGGCG
                                  T  T_____
GAM745  LOC220107 5'  CTGGTCCCCACGCCCCCGCC   20289          CT  A
                                CTGGTCCCTAT  CC CCCGCC
                                ||||||||||  || ||||||
                                GACCAGGGGTG  GG GGGCGG
                                      C_  _
GAM745  LOC220739 3'  CTGGCCCCTGACCCCACC     20290         AT
                                CTGGTCCCT  CTCCACC
                                |||||||||  |||||||
                                GACCGGGGA  GGGGTGG
                                     CT
GAM745  LOC222865 3'  CTGATCTCGTGATCCACCCGCC 20291       CCTATC
                                CTGGTC     TCCACCCGCC
                                ||||||     ||||||||||
                                GACTAG     AGGTGGGCGG
                                   AGCACT
GAM745  LOC51123  5'  TGGGCCTCCTCCACCCGC    20292     TC   A
                                TGG  CCT TCTCCACCCGC
                                |||  ||| ||||||||||
                                ACC  GGA GGAGGTGGGCG
                                  C_  _
GAM745  LOC90019  5'  CTGGCCCCTGTACCCGC     20293         ATCTCC
                                CTGGTCCCT     ACCCGC
                                |||||||||     ||||||
                                GACCGGGGA     TGGGCG
                                     CA____
GAM745  LOC92017  5'  CTGGTCCCCATCCTCCTCTCCA 20294       _______       C   III
           CCTGCCG                 CCCTA     TCTCCACC GCC   G
                                |||||     |||||||| |||   |
                                GGGGT     AGAGGTGG CGG   C
                                   AGGAGG       A   III
GAM746  ANGPT1    3'  TGTATATATTTCCCTTACAT   20297          C     TG
                                TGTATATATT CTCTTG  T
                                |||||||||| ||||||  |
                                ACATATATAA GGGAAT  A
                                     A     GT
GAM746  ARHGAP10  3'  TATATATGTTCTTCTGGCTGTA 20298        A   C   T T
                                TGTATAT TTC TCT G GTTGTA
                                ||||||| ||| ||| | ||||||
                                ATATATA AAG AGA C CGACAT
                                   C   A   _ _
GAM746  CAMP-GEFII 3'  TGTATATAATCCTGATTTGTA  20299        T    CTTGTG
                                TGTATATA TCCT      TTGTA
                                |||||||| ||||      |||||
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                                ACATATAT AGGA     AACAT
                                     T   CTA___
GAM746  DKFZp434A1520 3'  TGTGAATATTCCTCTCTGTG  20300     AT       _
                                TGT  ATATTCCTCT TGTG
                                |||  |||||||||| ||||
                                ACA  TATAAGGAGA ACAC
                                  CT        G
GAM746  DKFZp761B0514 3'  TGTATATATTATTCTTATA   20301         CC
                                TGTATATATT  TCTTGTG
                                ||||||||||  |||||||
                                ACATATATAA  AGAATAT
                                      TA
GAM746  KIAA0335  3'  TATATATTCCTTTTAAATTA  20302          C   T
                                TATATATTCCT TTG GTTG
                                |||||||||| ||| ||||
                                ATATATAAGGA AAT TAAT
                                      A   T
GAM746  KIAA0940  3'  TGTATATATTCTTAGTGTTTGT 20303         CTCTT    _
           A                     TGTATATATTC    GTGTT GTA
                                ||||||||||     ||||| |||
                                ACATATATAAG    CACAA CAT
                                      AAT__    A
GAM746  LOC127703 5'  TATATATTCCTTTTTGTG    20304          C_
                                TATATATTCCT  TTGTG
                                ||||||||||  |||||
                                ATATATAAGGA  AACAC
                                      AA
GAM746  LOC196424 3'  TGTATATATTTTTCTTTCCAGT 20305         CC    GTGTT
           A                     TGTATATATT  TCTT    GTA
                                ||||||||||  ||||    |||
                                ACATATATAA  AGAA    CAT
                                      AA    AGGT_
GAM747  FLJ13110  3'  AAAACGTCTGATAAGGCCTGT  20308         CACC_
                                AAAACGTCTG    GCCTGT
                                ||||||||||    ||||||
                                TTTTGCAGAC    CGGACA
                                      TATTC
GAM747  RBAK     3'  ACAAAACGACTGCCTCCTGT   20309        T    ACCG
                                ACAAAACG CTGC    CCTGT
                                |||||||| ||||    |||||
                                TGTTTTGC GACG    GGACA
                                     T    GA__
GAM747  LOC143384 5'  TCACAGGCACCTGCCGCCTGT  20310      AAA GT    AC
                                TCACA   C  CTGC  CGCCTGT
                                |||||   |  ||||  |||||||
                                AGTGT   G  GACG  GCGGACA
                                   CC_ TG    __
GAM747  LOC149153 5'  TCCTGAGACGTCTGCTGAACCT 20311    ACAAA       ___   GC
           CTGT                    TC     ACGTCTGC   ACC  CTGT
                                ||    ||||||||   |||  ||||
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                                AG    TGCAGACG  TGG  GACA
                                 GACTC       ACT  A_
GAM747  LOC169008 5'  TCCAAAACGTCTGGCTG     20312    A        CACC  C
                                TC CAAAACGTCTG   GC TG
                                || ||||||||||   || ||
                                AG GTTTTGCAGAC   CG AC
                                 _       ____  _
GAM748  PPP1CB    3'  TAAGTTAACAGGTTTCTCA    20315          A
                                TAAGTTAACAG GTTTTTTA
                                |||||||||| ||||||||
                                ATTCAATTGTC CAAAGAGT
                                          _
GAM748  PRO0082   3'  TAAGTTAAGGAGTTTTT     20316        CA
                                TAAGTTAA  GAGTTTTT
                                ||||||||  ||||||||
                                ATTCAATT  CTCAAAAA
                                     C_
GAM748  SPHAR     3'  AATTAACAGGATCGTTTATAAA 20317         AG  T
                                AGTTAACAG  TT TTTATAAA
                                |||||||||  || ||||||||
                                TTAATTGTC  AG AAATATTT
                                      CT  C
GAM749  NCALD     3'  TAGAATCACAGGACTGGAT    20320        AA_   A
                                TGGGGTCG   GACT GAT
                                ||||||||   |||| |||
                                ATCTTAGT   CTGA CTA
                                     GTC    C
GAM749  ROBO1     3'  TGGGGTCAGACCTGAT      20321        GA    A
                                TGGGGTC  AGACT GAT
                                |||||||  ||||| |||
                                ACCCCAG  TCTGG CTA
                                    __    A
GAM749  ROBO1     3'  TGGGGTCAGACCTGAT      20321        GA    A
                                TGGGGTC  AGACT GAT
                                |||||||  ||||| |||
                                ACCCCAG  TCTGG CTA
                                    __    A
GAM749  SCNN1G    3'  TGGTGGTCCTGACTAGAT    20322    _   GAA
                                TGG GGTC   GACTAGAT
                                ||| ||||   ||||||||
                                ACC CCAG   CTGATCTA
                                  A   GA_
GAM749  SP3       5'  TGGAATCTGGACTAGAT     20323        GAA
                                TGGGGTC   GACTAGAT
                                |||||||   ||||||||
                                ACCTTAG   CTGATCTA
                                    AC_
GAM749  HUMZD58C02 3'  TGGGGTCAACCAGAT      20324        GAA
                                TGGGGTC   GACTAGAT
                                |||||||   ||||||||
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                              ACCCCAG   TTGGTCTA
                                   ___
GAM749  KIAA0552  3'  TGGGGTCAGCCAAGCAGAT   20325       AA_  C
                              TGGGGTCG   GA TAGAT
                              ||||||||   || |||||
                              ACCCCAGT   TT GTCTA
                                   CGG  C
GAM749  KIAA0843  3'  TGGTGTAATGACTAGAT    20326    G  C  A
                              TGG GT GA GACTAGAT
                              ||| || || ||||||||
                              ACC CA TT CTGATCTA
                                A  _  A
GAM749  KIAA1940  3'  TGGGGCCAGACTGGAT     20327      GA    A
                              TGGGGTC  AGACT GAT
                              |||||||  ||||| |||
                              ACCCCGG  TCTGA CTA
                                   __    C
GAM749  MAD4      3'  TGGGGCCGGAAGGAGAT     20328       _  ACT
                              TGGGGTCG AAG   AGAT
                              |||||||| |||   ||||
                              ACCCCGGC TTC   TCTA
                                   C   C__
GAM749  MGC10200  3'  TGGGGTCAAAGACCAAAT    20329
                              TGGGGTCGAAGACTAGAT
                              ||||||||||||||||||
                              ACCCCAGTTTCTGGTTTA

GAM749  MGC15429  5'  TGGGGTCAGGAGGACATAG   20330       __ A  _
                              TGGGGTC  GA GAC TAG
                              |||||||  || ||| |||
                              ACCCCAG  CT CTG ATC
                                   TC  C   T
GAM749  LOC143392 3'  TGGGGTCAGAGCCGAC     20331       A  A  A
                              TGGGGTCG AG CT GAT
                              |||||||| || || |||
                              ACCCCAGT TC GG CTG
                                   C  _  _
GAM749  LOC150421 3'  GGGGTCGAGGAGACAGAT   20332       __   T
                              GGGGTCGA  AGAC AGAT
                              ||||||||  |||| ||||
                              CCCCAGCT  TCTG TCTA
                                   CC   _
GAM749  LOC254272 5'  TGGAGTCAGGGACTGGAT   20333       AA   A
                              TGGGGTCG  GACT GAT
                              ||||||||  |||| |||
                              ACCTCAGT  CTGA CTA
                                   CC   C
GAM749  LOC257471 5'  TGGAATCTGGACTAGAT    20323       GAA
                              TGGGGTC   GACTAGAT
                              |||||||   ||||||||
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                                ACCTTAG  CTGATCTA
                                   AC_
GAM749  LOC91179  3'  TGGGGTCAACCAGAT      20324       GAA
                                TGGGGTC  GACTAGAT
                                |||||||  ||||||||
                                ACCCCAG  TTGGTCTA
                                   ___
GAM750  AES       3'  TACCAGGGTGAGAGGGCTGTGG 20336       CCTCGA_   C
          C                      TATCAGGG     GCTG GGC
                                 ||||||||     |||| |||
                                 ATGGTCCC     CGAC CCG
                                    ACTCTCC   A
GAM750  CDK4      5'  TATCGGGGCCCCGGAGCCG   20337     A      _
                                TATC GGGCCTCG AGCTG
                                |||| |||||||| |||||
                                ATAG CCCGGGGC TCGGC
                                  C       C
GAM750  CDK4      5'  TATCGGGGCCCCGGAGCCG   20337     A      _
                                TATC GGGCCTCG AGCTG
                                |||| |||||||| |||||
                                ATAG CCCGGGGC TCGGC
                                  C       C
GAM750  CSF2      3'  TATCAGGGTCAGTGTGG     20338       CC  G  C  C
                                TATCAGGG  TC AG TG GG
                                ||||||||  || || || ||
                                ATAGTCCC  AG TC AC CC
                                   __  _  _  A
GAM750  DMPK      3'  TCAGGGCCTCAGCCTGGC    20339        G   GC
                                TCAGGGCCTC AGCT  GGC
                                |||||||||| ||||  |||
                                AGTCCCGGAG TCGG  CCG
                                    _   A_
GAM750  FAT       5'  CCGGGGCCTCGCCGGGC     20340    A     GA   C
                                TC GGGCCTC  GCTG GGC
                                || |||||||  |||| |||
                                GG CCCGGAG  CGGC CCG
                                 C      __   _
GAM750  RFX1      3'  TCAGAGTTTGCAGCTGCGGC  20341      CCTCG
                                TCAGGG    AGCTGCGGC
                                ||||||    |||||||||
                                AGTCTC    TCGACGCCG
                                   AAACG
GAM750  WTAP      5'  ATCGGGGCCTCGAGGC      20342    A       CT
                                ATC GGGCCTCGAG  GC
                                ||| ||||||||||  ||
                                TAG CCCGGAGCTC  CG
                                  C       __
GAM750  AKL3L     5'  TACCAGGGCTTTGGCCTGGC  20343        CTCGA  GC
                                TATCAGGGC    GCT  GGC
                                |||||||||    |||  |||
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                                ATGGTCCCG    CGG  CCG
                                     AAAC_  A_
GAM750  CPLX1    5'  GGCGCCCGGTGAGCTGCGGC  20344    _   C__
                                GG GCCT   GAGCTGCGGC
                                || ||||   ||||||||||
                                CC CGGG   CTCGACGCCG
                                 G   CCA
GAM750  DKFZP761I2123 5'  TATCAGGGTCTTGTAGACTGAG 20345       C  CG_ _  C
                                TATCAGGG CT   AG CTG GG
                                |||||||| ||   || ||| ||
                                ATAGTCCC GA   TC GAC TC
                                     A  ACA  T  _
GAM750  FLJ10737  3'  CAGGGCGGCGGGCTGCGG    20346      CT  A
                                CAGGGC  CG GCTGCGG
                                ||||||  || |||||||
                                GTCCCG  GC CGACGCC
                                    CC  C
GAM750  IGSF9    3'  TATCAGGGTCTGTGCCTGGGC  20347       C  CGAG   C
                                TATCAGGG CT    CTG GGC
                                |||||||| ||    ||| |||
                                ATAGTCCC GA    GAC CCG
                                     A  CACG  _
GAM750  KIAA1691  3'  CCAGGGCCTCTCTCCTGGC   20348        GAG  GC
                                TCAGGGCCTC   CT  GGC
                                ||||||||||   ||  |||
                                GGTCCCGGAG   GG  CCG
                                      AGA  A_
GAM750  MGC13102  3'  TCAGGGCCTTGGCTGTGGC   20349        CGA   C
                                TCAGGGCCT   GCTG GGC
                                |||||||||   |||| |||
                                AGTCCCGGA   CGAC CCG
                                     AC_   A
GAM750  N4BP3    3'  CAGGGCCCCCTGCGG      20350        GAG
                                CAGGGCCTC   CTGCGG
                                |||||||||   ||||||
                                GTCCCGGGG   GACGCC
                                     ___
GAM750  OBTP     3'  CATCAGGGCACATCTTGTGG   20351        CT  AGC  C
                                TATCAGGGC  CG   TG GG
                                |||||||||  ||   || ||
                                GTAGTCCCG  GT   AC CC
                                     T_  AGA  A
GAM750  PIP5K1C  3'  TCAGGGCCCCACTGCGGC    20352        GA
                                TCAGGGCCTC  GCTGCGGC
                                ||||||||||  ||||||||
                                AGTCCCGGGG  TGACGCCG
                                     __
GAM750  RoXaN    3'  CAGGGCCTCTGCCTGGC     20353        GA  GC
                                CAGGGCCTC  GCT  GGC
                                |||||||||  |||  |||
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                                GTCCCGGAG  CGG  CCG
                                     A_   A_
GAM750  SPTLC2    3'  TATCAGAGTCTTGAATCAGGC  20354        C  C   CT C
                                TATCAGGG CT GAG  G GGC
                                |||||||| || |||  | |||
                                ATAGTCTC GA CTT  T CCG
                                     A  A   AG _
GAM750  STOML1    3'  AGGGCCTCAACTCTCTGTGG   20355         G___   C
                                AGGGCCTCGA    CTG GG
                                ||||||||||    ||| ||
                                TCCCGGAGTT    GAC CC
                                      GAGA   A
GAM750  ZNF304    3'  TATCAGGGACTTGATCCTG    20356        C  C  G_
                                TATCAGGG CT GA  CTG
                                |||||||| || ||  |||
                                ATAGTCCC GA CT  GAC
                                     T  A  AG
GAM750  LOC147229 5'  ATCAGGGCAGGCACTGCGGC   20357         CTCGA
                                ATCAGGGC    GCTGCGGC
                                ||||||||    ||||||||
                                TAGTCCCG    TGACGCCG
                                     TCCG_
GAM750  LOC159199 5'  CAGGGCCTTGACCAGG      20358        C  G   C
                                CAGGGCCT GA CTG GG
                                |||||||| || ||| ||
                                GTCCCGGA CT GGT CC
                                     A  _   _
GAM750  LOC164397 3'  TCAGAGGACCAAGCTGTGG    20359       CC       C
                                TCAGGG  TCGAGCTG GG
                                ||||||  |||||||| ||
                                AGTCTC  GGTTCGAC CC
                                   CT       A
GAM750  LOC253256 5'  TATCAGGGCCCCGCTGGGG    20360          GA    C
                                TATCAGGGCCTC  GCTG GG
                                ||||||||||||  |||| ||
                                ATAGTCCCGGGG  CGAC CC
                                      __    C
GAM750  LOC96626  3'  CAGGGCCTAAATGCGGC      20361        C   C
                                CAGGGCCT GAG TGCGGC
                                |||||||| ||| ||||||
                                GTCCCGGA TTT ACGCCG
                                     _   _
GAM751  ADAMTS13  3'  CTGCAGCTGCTTTGGTCCA    20364          GC   AAAA
                                CTGCAGCTGCT  TGG    CCG
                                ||||||||||  |||    |||
                                GACGTCGACGA  ACC    GGT
                                      A_   A___
GAM751  ALEX1     5'  CTGCAGCTACTGCGGGCCG    20365          T  AAAA
                                CTGCAGCTGCTGC GG    CCG
                                ||||||||||||| ||    |||
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                                GACGTCGATGACG CC    GGC
                                        C _____
GAM751  AOC3    3'  TGAGCTGCTGCTGTCACG    20366    C        GAAAAC
                                TG AGCTGCTGCTG     CG
                                || ||||||||||      ||
                                AC TCGACGACGAC     GC
                                 _         AGT___
GAM751  APLP2   3'  GCGGCTGCTGCTTGGCAGTCGA 20367    A       _  AAAAC
                                GC GCTGCTGCT GG    CGA
                                || |||||||| ||     |||
                                CG CGACGACGA CC    GCT
                                 C        A  GTCA_
GAM751  ATRX    5'  CTGTAGCTGCTGCTGGAA    20368    C
                                CTG AGCTGCTGCTGGAA
                                ||| ||||||||||||||
                                GAC TCGACGACGACCTT
                                  A
GAM751  ATRX    5'  CTGTAGCTGCTGCTGGAA    20368    C
                                CTG AGCTGCTGCTGGAA
                                ||| ||||||||||||||
                                GAC TCGACGACGACCTT
                                  A
GAM751  BAZ1B   5'  CTGGCGGCTGCTGGGGCCG   20369    CA  T      AAAA
                                CTG  GC GCTGCTGG   CCG
                                |||  || ||||||||   |||
                                GAC  CG CGACGACC   GGC
                                  __ C       CC__
GAM751  CYP1A2  3'  CAGCTACTTGGGAGGCCGA   20370        GCT   AAA
                                CAGCTGCT   GGA   CCGA
                                ||||||||   |||   ||||
                                GTCGATGA   CCT   GGCT
                                     AC_   CC_
GAM751  DAAM2   3'  CTGCAGCTGTTCTGCCTGG   20371         __   _
                                CTGCAGCTG  CTGC TGG
                                |||||||||  |||| |||
                                GACGTCGAC  GACG ACC
                                      AA   G
GAM751  DGCR2   3'  CTGCGCTGCTGAGGAGGGGCCG 20372      A     CT   AAA_
                                CTGC GCTGCTG  GGA   CCG
                                |||| |||||||  |||   |||
                                GACG CGACGAC  CCT   GGC
                                  _      T_  CCCC
GAM751  EGFL5   5'  CTGCTGTTGCTGCTGCTGG   20373     A___
                                CTGC   GCTGCTGCTGG
                                ||||   ||||||||||
                                GACG   CGACGACGACC
                                  ACAA
GAM751  GLS     5'  CTGCTGCTGCTGCTGCGCGCCG 20374     A       GAAAA
          A                     CTGC GCTGCTGCTG    CCGA
                                |||| ||||||||||    ||||
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                                GACG CGACGACGAC    GGCT
                                  A        GCGC_
GAM751  GNAS    3'  TGTAGCTGCTGCTGGCCACCA 20375   C        AAA
                                TG AGCTGCTGCTGG   ACCG
                                || ||||||||||||   ||||
                                AC TCGACGACGACC   TGGT
                                 A         GG_
GAM751  HK1     5'  CAGCTGCTGTAGCCG      20376        C   AAAA
                                CAGCTGCTG TGG    CCG
                                ||||||||| |||    |||
                                GTCGACGAC ATC    GGC
                                      _  ____
GAM751  HPCAL1  5'  CCGCAGCTGCTGCGCCGG    20377          __
                                CTGCAGCTGCTGC  TGG
                                ||||||||||||  |||
                                GGCGTCGACGACG  GCC
                                       CG
GAM751  HRH1    3'  CTGCAGCTTCTGAAACCG    20378       G   CTGGA
                                CTGCAGCT CTG    AAACCG
                                |||||||| |||    ||||||
                                GACGTCGA GAC    TTTGGC
                                    A  _____
GAM751  HS3ST3B1 5'  CTGCAACTGGAACGGAAAGTCG 20379        CT  T    AC
                                CTGCAGCTG  GC GGAAA  CG
                                |||||||||  || |||||  ||
                                GACGTTGAC  TG CCTTT  GC
                                     CT  _    CA
GAM751  MTMR1   5'  CTGGGCTGCCGGGAGCCG    20380    CA     CT   AAA
                                CTG  GCTGCTG  GGA   CCG
                                |||  |||||||  |||   |||
                                GAC  CGACGGC  CCT   GGC
                                  C_      __   C__
GAM751  MYOZ1   5'  CTGAGCTGCTGTGACC     20381    C      C  GAAA
                                CTG AGCTGCTG TG    ACC
                                ||| |||||||| ||    |||
                                GAC TCGACGAC AC    TGG
                                   _      _ ____
GAM751  NEK6    5'  GCTGCCGCTGGGGGACCG    20382          AAA
                                GCTGCTGCTGG   ACCG
                                ||||||||||   ||||
                                CGACGGCGACC   TGGC
                                      CCC
GAM751  NPPB    5'  CTGCTGCTGCTGCTGCGA    20383     A       _
                                CTGC GCTGCTGCTG GA
                                |||| |||||||||| ||
                                GACG CGACGACGAC CT
                                  A        G
GAM751  NRAP    3'  CTGTGCTGCTGTGAAAC     20384    CAGC      GA
                                CTG   TGCTGCTG  AAAC
                                |||   ||||||||  ||||
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                                GAC   ACGACGAC  TTTG
                                 ____      AC
GAM751  P23     3'  GCGGCTGCTGCTAGGGAGTCGA 20385    A        AAAAC
                                GC GCTGCTGCTGG    CGA
                                || ||||||||||    |||
                                CG CGACGACGATC    GCT
                                 C         CCTCA
GAM751  PDGFB   3'  TGAGCTGCTGGGCAAGACCG  20386    C      CT  _  A
                                TG AGCTGCTG  GG AA ACCG
                                || ||||||||  || || ||||
                                AC TCGACGAC  CC TT TGGC
                                 _      __  G  C
GAM751  PDYN    3'  CTGCTGCTGCTGCTGCCG    20387     A       GAAAA
                                CTGC GCTGCTGCTG    CCG
                                |||| ||||||||||    |||
                                GACG CGACGACGAC    GGC
                                  A       _____
GAM751  PIM1    5'  CTGCTGCTGCTGCTGCTGCCG  20388     A       GAAAA
                                CTGC GCTGCTGCTG    CCG
                                |||| ||||||||||    |||
                                GACG CGACGACGAC    GGC
                                  A       GAC__
GAM751  PODXL   5'  CTGCCGCTGCAGCAGAGCCG  20389     A    T  T   AAA
                                CTGC GCTGC GC GGA   CCG
                                |||| ||||| || |||   |||
                                GACG CGACG CG TCT   GGC
                                  G    T  _   C__
GAM751  PRX     3'  GCAGCTGCACCTCGGGGAGTCG 20390        T   ____   AAAC
          A                      GCAGCTGC GCT    GGA    CGA
                                |||||||| |||    |||    |||
                                CGTCGACG TGG    CCT    GCT
                                    _   AGCC   CA__
GAM751  PXMP3   5'  CTGCAGCTCCCTCAAGACTGG  20391        G  _____
                                CTGCAGCT CT    GCTGG
                                |||||||| ||    |||||
                                GACGTCGA GG    TGACC
                                     G  AGTTC
GAM751  RAD52   3'  CTGCAGCTGCTTCTGCCGG   20392          ___
                                CTGCAGCTGCT   GCTGG
                                ||||||||||   |||||
                                GACGTCGACGA   CGGCC
                                      AGA
GAM751  RAD52   3'  CTGCAGCTGCTTCTGCCGG   20392          ___
                                CTGCAGCTGCT   GCTGG
                                ||||||||||   |||||
                                GACGTCGACGA   CGGCC
                                      AGA
GAM751  RAD52   3'  CTGCAGCTGCTTCTGCCGG   20392          ___
                                CTGCAGCTGCT   GCTGG
                                ||||||||||   |||||
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                                GACGTCGACGA  CGGCC
                                      AGA
GAM751  RALBP1   3'  CTGCACTGCCGGGGGCCGG   20393      G   ____
                                CTGCA CTGCT   GCTGG
                                ||||| |||||   |||||
                                GACGT GACGG   CGGCC
                                  _    CCCC
GAM751  RXRA     3'  CTGCAGCTCCAGGGCTGG    20394       G ___
                                CTGCAGCT CT   GCTGG
                                |||||||| ||   |||||
                                GACGTCGA GG   CGACC
                                    _ TCC
GAM751  SCA1     5'  TGCAGCTGCTGTTGCTCTGG  20395         _____
                                TGCAGCTGCTG    CTGG
                                ||||||||||    ||||
                                ACGTCGACGAC    GACC
                                      AACGA
GAM751  STAU     5'  CTGCTGGCTGCTGCTCCG    20396     A_      GGAAAA
                                CTGC  GCTGCTGCT     CCG
                                ||||  |||||||||     |||
                                GACG  CGACGACGA     GGC
                                  AC       _______
GAM751  STIM1    3'  CTGCAACTGCTAGGGGAA    20397          CT
                                CTGCAGCTGCTG  GGAA
                                ||||||||||||  ||||
                                GACGTTGACGAT  CCTT
                                      CC
GAM751  TARBP2   3'  CTGCAGCAGTAAAAACCG    20398       TGCTGCTG
                                CTGCAGC       GAAAACCG
                                |||||||       ||||||||
                                GACGTCG       TTTTTGGC
                                   TCA_____
GAM751  TTC3     3'  ACTTGCTGCTGCAAACTGA   20399     _     GA   C
                                GCT GCTGCTG  AAAC GA
                                ||| |||||||  |||| ||
                                TGA CGACGAC  TTTG CT
                                  A      G_   A
GAM751  WASF3    3'  CTACAGCTGCAGGGCTGA    20400         T__
                                CTGCAGCTGC   GCTGG
                                |||||||||   |||||
                                GATGTCGACG   CGACT
                                      TCC
GAM751  BRAL1    5'  CAGCTGCTTCAAGAAACCG   20401        GCT    A
                                CAGCTGCT   GGAAA CCG
                                ||||||||   ||||| |||
                                GTCGACGA   TCTTT GGC
                                     AGT    _
GAM751  C19orf7  3'  CTGGAGCTGTCCGGGGCTGG  20402     C    _ ___
                                CTG AGCTG CT   GCTGG
                                ||| ||||| ||   |||||
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                                GAC TCGAC GG   CGACC
                                  C     A  CCC
GAM751   C20orf162 5'  CTGCAGCTGGCAGGGGGCTGG  20403          _ T____
                                CTGCAGCTG C     GCTGG
                                |||||||||  |     |||||
                                GACGTCGAC G     CGACC
                                     C TCCCC
GAM751   C20orf172 3'  CTGCAGCTGTTTCACTGA     20404          C__
                                CTGCAGCTG   TGCTGG
                                |||||||||   ||||||
                                GACGTCGAC   GTGACT
                                     AAA
GAM751   CECR2     5'  CTGCGGCTGCGGCTGCCCG    20405      A    T    GAAAA
                                CTGC GCTGC GCTG     CCG
                                ||||  |||||  ||||     |||
                                GACG CGACG CGAC     GGC
                                  C     C    G____
GAM751   CIZ1      5'  CTGCAATTGCTGCTGCTGG    20407       ___
                                CTGCA   GCTGCTGCTGG
                                |||||   ||||||||||||
                                GACGT   CGACGACGACC
                                   TAA
GAM751   CIZ1      5'  CTGCTGCTGTAACTGCTGG    20406      A   ___
                                CTGC GCTG   CTGCTGG
                                ||||  ||||   |||||||
                                GACG CGAC   GACGACC
                                  A    ATT
GAM751   CL25022   5'  CTCCAGCTGTCCCAGAACCG   20408    G     CTG TG  AA
                                CT CAGCTG   C  GA  ACCG
                                ||  ||||||   |  ||  ||||
                                GA GTCGAC   G  CT  TGGC
                                 G      AG_ GT  __
GAM751   DC8       3'  CTGCATCTGCTGCTGTGCAGAA 20409       G        GA___    C
            ACTGA                    CTGCA CTGCTGCTG     AAAC GA
                                |||||  |||||||||     ||||  ||
                                GACGT GACGACGAC     TTTG CT
                                   A        ACGTC    A
GAM751   DJ667H12.2 5'  TGAGCTGCTGCTGGTCCG     20410    C          AAAA
                                TG AGCTGCTGCTGG    CCG
                                ||  ||||||||||||    |||
                                AC TCGACGACGACC    GGC
                                 _          A___
GAM751   DKFZP566C243 3'  CTGCAGCTGCGGGAAA      20411          TGCT
                                CTGCAGCTGC    GGAAA
                                ||||||||||    |||||
                                GACGTCGACG    CCTTT
                                      C___
GAM751   EDR2      5'  CTGTGGCTGCTGCTGGATCAC  20412     CA          AA
                                CTG  GCTGCTGCTGGA  AC
                                |||  ||||||||||||  ||
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                                GAC  CGACGACGACCT  TG
                                  AC          AG
GAM751  EFA6R    3'  CTGCAGCTCCTCAAGGGCCGA  20413        G  GCT  AAAA
                                CTGCAGCT CT   GG    CCGA
                                |||||||| ||   ||    ||||
                                GACGTCGA GA   CC    GGCT
                                    G  GTT  C___
GAM751  FLJ10043  5'  CCGCAGCTGCTCCACTGAGCTG 20414          _______
          G                      CTGCAGCTGCT      GCTGG
                                ||||||||||       |||||
                                GGCGTCGACGA      CGACC
                                      GGTGACT
GAM751  FLJ10101  3'  CTGCAGCTGCAGCTGGGCCCCA 20415          T    AAAA
                                CTGCAGCTGC GCTGG    CCG
                                |||||||||| |||||    |||
                                GACGTCGACG CGACC    GGT
                                      T    CGG_
GAM751  FLJ11151  3'  TGCAGCTGCTGTTTCTGG    20416          ___
                                TGCAGCTGCTG   CTGG
                                ||||||||||   ||||
                                ACGTCGACGAC   GACC
                                      AAA
GAM751  FLJ11783  3'  CTGCAGCTGCCTTCTGAAGGCT 20417          _________
          GG                     CTGCAGCTGCT       GCTGG
                                ||||||||||       |||||
                                GACGTCGACGG       CGACC
                                      AAGACTTC
GAM751  FLJ13153  3'  CTGCAGCTGGCTGGCTGG    20418         _  _
                                CTGCAGCTG CTG CTGG
                                ||||||||| ||| ||||
                                GACGTCGAC GAC GACC
                                      C   C
GAM751  FLJ20506  5'  CTGCTGCTGCTGCTGGCGCGA  20419      A         AAAAC
                                CTGC GCTGCTGCTGG    CGA
                                |||| ||||||||||    |||
                                GACG CGACGACGACC    GCT
                                  A         GC___
GAM751  FLJ20718  5'  TGCTGCTGCTCAGCTGGGCCG  20420     A    __    AAAA
                                TGC GCTGCT  GCTGG    CCG
                                ||| ||||||  |||||    |||
                                ACG CGACGA  CGACC    GGC
                                  A     GT    C___
GAM751  FLJ22969  5'  CTGCAGCTCTAAACC       20421         G   CTGGAA
                                CTGCAGCT CTG     AACC
                                ||||||||| |||     ||||
                                GACGTCGA GAT     TTGG
                                      _  _______
GAM751  FRAT1    5'  CTGCAGCCGCGGGAGCCGG   20422          T___
                                CTGCAGCTGC    GCTGG
                                ||||||||||    |||||
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                                GACGTCGGCG   CGGCC
                                     CCCT
GAM751  GRSF1    3'  GCAGTTGCTGCTAATAAAC   20423     C       A
                                GCAG TGCTGCTGG AAAC
                                |||| ||||||||| ||||
                                CGTC ACGACGATT TTTG
                                  A       A
GAM751  HRIHFB2436 5'  GCTGCTGCCTCTGAAGCCG   20424    A     G    AAA
                                GC GCTGCT CTGGA   CCG
                                || |||||| |||||   |||
                                CG CGACGG GACTT   GGC
                                 A     A    C__
GAM751  ICB-1    3'  CTGCGCTGCTGTCACCAA    20425     AGCT     GAAA
                                CTGC   GCTGCTG   ACCGA
                                ||||   |||||||   |||||
                                GACG   CGACGAC   TGGTT
                                  _____      AG__
GAM751  KIAA0125  5'  CTGTGGCTGCTGCCTGGGTCCA 20426     CA      _  AAAA
           A                     CTG  GCTGCTGC TGG   CCGA
                                ||| ||||||||| |||   ||||
                                GAC  CGACGACG ACC   GGTT
                                  AC       G   CA__
GAM751  KIAA0215  3'  CTGAGCTTATCTTGGAAAAC   20427    C   GCTGC
                                CTG AGCT    TGGAAAAC
                                ||| ||||    ||||||||
                                GAC TCGA    ACCTTTTG
                                  _   ATAGA
GAM751  KIAA0495  3'  TGCAAGAACTGGAAAACCG   20428     CTGCT
                                TGCAG    GCTGGAAAACCG
                                |||||    ||||||||||||
                                ACGTT    TGACCTTTTGGC
                                   CT___
GAM751  KIAA0542  3'  CTGCAGCTGCTGCCGGGAGGCC 20429             AAAA
                                CTGCAGCTGCTGCTGG   CC
                                ||||||||||||||||   ||
                                GACGTCGACGACGGCC   GG
                                          CTCC
GAM751  KIAA0630  5'  GCAGCTGCTGCAGTAGAA    20430          __
                                GCAGCTGCTGC  TGGAA
                                ||||||||||  |||||
                                CGTCGACGACG  ATCTT
                                       TC
GAM751  KIAA0757  5'  GCGGCTGCCGCCGGAGCCG   20431    A         AAA
                                GC GCTGCTGCTGGA   CCG
                                || ||||||||||||   |||
                                CG CGACGGCGGCCT   GGC
                                 C          C__
GAM751  KIAA0852  3'  CTGCAGCTACAGGGTTGATCGG 20432       TGC__________   AAAA
           TTTTCC                 AGCTGC         TGG   CC
                                ||||||          |||   ||
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                                TCGATG          GCC   GG
                                   TCCCAACTIIIA  AAAA
GAM751  KIAA1196  3'  CTGCAGTGCCAGAAGGCTGA  20433       C   _____
                                CTGCAG TGCT    GCTGG
                                |||||| ||||    |||||
                                GACGTC ACGG    CGACT
                                   _   TCTTC
GAM751  KIAA1399  3'  CTGCAGCTGCTCTCTTGG    20434         G_ _
                                CTGCAGCTGCT  CT GG
                                ||||||||||  || ||
                                GACGTCGACGA  GA CC
                                      GA  A
GAM751  KIAA1819  5'  CTGCTGTTGCTGCTGCTTGG  20435     A___       _
                                CTGC   GCTGCTGCT GG
                                ||||   ||||||||| ||
                                GACG   CGACGACGA CC
                                  ACAA       A
GAM751  KIAA1884  3'  CTGAGCTGCTGTTGGAA    20436    C      C
                                CTG AGCTGCTG TGGAA
                                ||| |||||||| |||||
                                GAC TCGACGAC ACCTT
                                  _       A
GAM751  KIAA1922  5'  TGCATCTGCTGCTGGGCCA   20437     G        AAAA
                                TGCA CTGCTGCTGG   CCG
                                |||| ||||||||||   |||
                                ACGT GACGACGACC   GGT
                                  A        C___
GAM751  KIAA1941  3'  CTGTGTGCTGCTGCTGGA    20438    CA_
                                CTG   GCTGCTGCTGGA
                                |||   ||||||||||||
                                GAC   CGACGACGACCT
                                  ACA
GAM751  LIN-28    3'  CTGGAGCTGCTGCTGGCTATCC 20439    C          AAAA_
            C                    CTG AGCTGCTGCTGG    CC
                                ||| ||||||||||||    ||
                                GAC TCGACGACGACC    GG
                                  C          GATAG
GAM751  MCAM      3'  CTGCAGCTGCTTCTGGATGCCG 20440          G    AAA
                                CTGCAGCTGCT CTGGA   CCG
                                |||||||||| |||||   |||
                                GACGTCGACGA GACCT   GGC
                                      A    AC_
GAM751  MGC10924  5'  CTGCGGCTTGGGAGCGCTGGGA 20441    A  _____ T    AAAA
            GGCCGA                 GC GCT    GC GCTGG   CCGA
                                || |||    || |||||   ||||
                                CG CGA    CG CGACC    GGCT
                                 C  ACCCT  _    CTCC
GAM751  MGC15429  5'  CTGCTGCTGCTGTGCTGG    20442     A    __
                                CTGC GCTGCT  GCTGG
                                |||| ||||||  |||||
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                                GACG CGACGA  CGACC
                                  A     CA
GAM751  PCDH16   5'  CTGCAGCTGTGTTTGCTGG   20443         C___
                                CTGCAGCTG   TGCTGG
                                |||||||||   ||||||
                                GACGTCGAC   ACGACC
                                     ACAA
GAM751  PDE11A   3'  TGCAGCTGCAGCTGACC    20444         T   GAAA
                                TGCAGCTGC GCTG   ACC
                                ||||||||| ||||   |||
                                ACGTCGACG CGAC   TGG
                                     T   ____
GAM751  QPRT     5'  TGCAGCTGTCTGGGCTGG    20445         _ __
                                TGCAGCTG CT  GCTGG
                                |||||||| ||  |||||
                                ACGTCGAC GA  CGACC
                                     A  CC
GAM751  SCAMP-4  3'  GCTCCGGCTGCTGGGAAACCG  20446    ___      A
                                GCT   GCTGCTGG AAACCG
                                |||   |||||||| ||||||
                                CGA   CGACGACC TTTGGC
                                  GGC       C
GAM751  SIMRP7   3'  CTGCAGCAGCTGCTGGAA    20447       T
                                CTGCAGC GCTGCTGGAA
                                ||||||| ||||||||||
                                GACGTCG CGACGACCTT
                                     T
GAM751  THG-1    5'  CTGCTGTTGCTGCTGAACTCCA 20448     AGC       AAA
                                CTGC   TGCTGCTGGA   CCG
                                ||||   ||||||||||   |||
                                GACG   ACGACGACTT   GGT
                                  ACA        GA_
GAM751  THG-1    5'  CTGCTGCTGTTGCTGCTGA   20449     A   ___
                                CTGC GCT   GCTGCTGG
                                |||| |||   ||||||||
                                GACG CGA   CGACGACT
                                  A   CAA
GAM751  USP20    3'  CTGCACTGCTGCTGCTGG    20450      __
                                CTGCA  GCTGCTGCTGG
                                |||||  ||||||||||
                                GACGT  CGACGACGACC
                                   GA
GAM751  ZNF222   5'  CTGCAGCTCTTTTAGAAA    20451        G  GC
                                CTGCAGCT CT  TGGAAA
                                |||||||| ||  ||||||
                                GACGTCGA GA  ATCTTT
                                     _  AA
GAM751  ZNF286   5'  TGAAGCTGTCCCTGGGGGAACC 20452    C    _  G   AA_
            G                    TG AGCTG CT CTGG   AACCG
                                || ||||| || ||||   |||||
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                                AC TCGAC GG GACC   TTGGC
                                 T    A  _   CCC
GAM751   LOC115051 3'  CTGCCAGTTGGCCCACGGAAGG 20453    _  CT_  GC    AA
           CCG                   CTG CAG   GCT  TGGAA  CCG
                                ||| |||   |||  |||||  |||
                                GAC GTC   CGG  GCCTT  GGC
                                  G   AAC   GT    CC
GAM751   LOC122330 5'  GCTGCTCTGGAAAACG      20454       G       C
                                GCTGCT CTGGAAAAC G
                                |||||| ||||||||| |
                                CGACGA GACCTTTTG C
                                   _       A
GAM751   LOC124977 5'  CTGCAGCTCTTGGCCTGAGACT 20455        ____  ____
           GG                    CTGCAGCT    GCT    GCTGG
                                ||||||||    |||    |||||
                                GACGTCGA    CGG    TGACC
                                     GAAC   ACTC
GAM751   LOC126661 5'  CCGCAGCGCCACCTGGGAAACT 20456       T  TG _   A    C
           GA                    CTGCAGC GC  C TGG AAAC GA
                                ||||||| ||  | ||| |||| ||
                                GGCGTCG CG  G ACC TTTG CT
                                   _ GT G   C    A
GAM751   LOC134301 5'  GCAGCTGCCCGGAGAACCG   20457        TG    A
                                GCAGCTGC  CTGGA AACCG
                                ||||||||  ||||| |||||
                                CGTCGACG  GGCCT TTGGC
                                    __     C
GAM751   LOC134328 5'  CTGTGCTGCTGACCAGCCG   20458    CA     _ TG AAAA
                                CTG  GCTGCTG C  G   CCG
                                |||  ||||||| |  |   |||
                                GAC  CGACGAC G  C   GGC
                                  A_      T GT ____
GAM751   LOC144193 5'  CTGCGCTGTCCGGGGCTGG   20459     A   _  ___
                                CTGC GCTG CT   GCTGG
                                |||| |||| ||   |||||
                                GACG CGAC GG   CGACC
                                  _    A  CCC
GAM751   LOC146062 5'  CCGTAGCTGCTGCCGACCG   20460    C        GAAA
                                CTG AGCTGCTGCTG   ACCG
                                ||| ||||||||||    ||||
                                GGC TCGACGACGGC   TGGC
                                  A        ____
GAM751   LOC146181 3'  CTGCAGCTCCTTGGTGAGCTGG 20461        G  _______
                                CTGCAGCT CT     GCTGG
                                |||||||| ||     |||||
                                GACGTCGA GA     CGACC
                                     G  ACCACT
GAM751   LOC146455 5'  CTGCAGCTGTTGCTGCTGG   20462        ___
                                CTGCAGCT   GCTGCTGG
                                ||||||||   ||||||||
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                                GACGTCGA   CGACGACC
                                     CAA
GAM751   LOC149117 3'  TGCAGCTGCTGTGACGACTGG  20463          _______
                                TGCAGCTGCTG      CTGG
                                ||||||||||      ||||
                                ACGTCGACGAC      GACC
                                      ACTGCT
GAM751   LOC149305 5'  CTGCTGCTGCTGCTGTCGCC   20464      A        GAAAA
                                CTGC GCTGCTGCTG     CC
                                |||| ||||||||||     ||
                                GACG CGACGACGAC     GG
                                  A         AGC__
GAM751   LOC150371 3'  CTACAGCTGGAGGGAAACCGA  20465          CTGCT  A
                                CTGCAGCTG     GG AAACCGA
                                |||||||||     || |||||||
                                GATGTCGAC     CC TTTGGCT
                                      CT___  C
GAM751   LOC151647 5'  CTGAAGCTGCTGCTGGAGAAGC 20466      C           A  C
           G                     CTG AGCTGCTGCTGGA AA CG
                                |||  ||||||||||||  ||  ||
                                GAC TCGACGACGACCT TT GC
                                  T           C  C
GAM751   LOC152200 3'  TGCAGCTGCTCTGCCCG     20467          G   GAAAA
                                TGCAGCTGCT CTG     CCG
                                |||||||||  |||     |||
                                ACGTCGACGA GAC     GGC
                                      _   G_____
GAM751   LOC152282 3'  CTGCTGTTGCTGCTACTGG    20468      A___
                                CTGC    GCTGCTGCTGG
                                ||||    ||||||||||
                                GACG    CGACGATGACC
                                  ACAA
GAM751   LOC152503 5'  CTACGGCTGCTGGGCTGA     20469      A     __
                                CTGC GCTGCT  GCTGG
                                |||| ||||||  |||||
                                GATG CGACGA  CGACT
                                  C      CC
GAM751   LOC158104 5'  CTGCAGCTGCAAGGGCCGG    20470          T___
                                CTGCAGCTGC    GCTGG
                                |||||||||    |||||
                                GACGTCGACG    CGGCC
                                      TTCC
GAM751   LOC159090 5'  CTGAGCTGCTGGGGACTGG    20471      C       ____
                                CTG AGCTGCTG    CTGG
                                ||| ||||||||    ||||
                                GAC TCGACGAC    GACC
                                  _       CCCT
GAM751   LOC170221 3'  CTGGTAGCTGCTGCGGGCCGA  20472      C_       T  AAAA
                                CTG  AGCTGCTGC GG    CCGA
                                |||  |||||||| ||    ||||
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                                GAC  TCGACGACG CC    GGCT
                                  CA       C  ____
GAM751   LOC200014 5'  CTGAGCTGCTGGGGCTGA    20473     C      ___
                                CTG AGCTGCT   GCTGG
                                ||| |||||||   |||||
                                GAC TCGACGA   CGACT
                                  _      CCC
GAM751   LOC200035 5'  CTGCAACTGCTGCTGTGA    20474             _
                                CTGCAGCTGCTGCTG GA
                                |||||||||||||| ||
                                GACGTTGACGACGAC CT
                                         A
GAM751   LOC200317 5'  CTGCAGCCGCTGCTCACCCCCG 20475             GGAAAA
                                CTGCAGCTGCTGCT     CCG
                                ||||||||||||||     |||
                                GACGTCGGCGACGA     GGC
                                         GTGGG_
GAM751   LOC200772 3'  CTGAGCTGCCAGAACTGG    20476     C      ___
                                CTG AGCTGCT   GCTGG
                                ||| |||||||   |||||
                                GAC TCGACGG   TGACC
                                  _      TCT
GAM751   LOC200860 3'  CTGCAGCTGCTGTTGTACACCC 20477           C  GAAAA
                   GA             CTGCAGCTGCTG TG    CCGA
                                ||||||||||| ||    ||||
                                GACGTCGACGAC AC    GGCT
                                       A  ATGTG
GAM751   LOC219404 3'  CAGACACTTTGGAAAAC     20478     C    GC
                                CAG TGCT  TGGAAAAC
                                ||| ||||  ||||||||
                                GTC GTGA  ACCTTTTG
                                  T   A_
GAM751   LOC220469 3'  CTGCAGCTGCCTAGGGCTGG   20479          ____
                                CTGCAGCTGCT    GCTGG
                                ||||||||||    |||||
                                GACGTCGACGG    CGACC
                                       ATCC
GAM751   LOC220914 5'  CTGTACTGCCTGAAGACCG    20480     CAGC      G   A
                                CTG    TGCTGCT GAA ACCG
                                |||    ||||||| ||| ||||
                                GAC    ATGACGG CTT TGGC
                                  ____      A   C
GAM751   LOC222057 3'  CTGCCAGCTGCTCAGCAGGA   20481      _      __  T
                                CTGC AGCTGCT  GC GGA
                                |||| |||||||  || |||
                                GACG TCGACGA  CG CCT
                                  G      GT  T
GAM751   LOC253955 5'  CTGGGCTGCTATGGAAAACTGA 20482     CA      C       C
                                CTG  GCTGCTG TGGAAAAC GA
                                |||  ||||||| |||||||| ||
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                                GAC  CGACGAT ACCTTTTG CT
                                  C_     _      A
GAM751   LOC255718 5'  CTGCAGCTGCAGCTCC      20483          T   GGAAAA
                                CTGCAGCTGC GCT     CC
                                |||||||||| |||     ||
                                GACGTCGACG CGA     GG
                                      T  _______
GAM751   LOC255975 5'  TGCTGAGGCTGCTGGGAGGCCG 20484     AGCT       AAAA
           A                     TGC    GCTGCTGG    CCGA
                                |||    ||||||||    ||||
                                ACG    CGACGACC    GGCT
                                  ACTC       CTCC
GAM751   LOC255988 5'  CTGCAGCTGGCTGGCTGG    20418          _  _
                                CTGCAGCTG CTG CTGG
                                ||||||||| ||| ||||
                                GACGTCGAC GAC GACC
                                      C   C
GAM751   LOC256158 5'  CTGTGGATGCTGCTGACCCCG  20485     CAGC       AAAA
                                CTG    TGCTGCTGG    CCG
                                |||    |||||||||    |||
                                GAC    ACGACGACT    GGC
                                  ACCT       GG__
GAM751   LOC51186  5'  CTGCGCTGCTGAAGGAA     20486      A      CT
                                CTGC GCTGCTG  GGAA
                                |||| |||||||  ||||
                                GACG CGACGAC  CCTT
                                   _      TT
GAM752   A1BG      3'  CAACTAAGCACTTGGGGAA    20489    C   TTT    _
                                A ACT   GCATT GGGGAA
                                | |||   ||||| ||||||
                                G TGA   CGTGA CCCCTT
                                 T   TT_    A
GAM752   ABCB4     5'  CACATTATGCTCCTTGGGGA   20490      C  T   A__
                                CACA TT TGC   TTGGGGA
                                |||| || |||   |||||||
                                GTGT AA ACG   AACCCCT
                                   _  T   AGG
GAM752   ABCB4     5'  CACATTATGCTCCTTGGGGA   20490      C  T   A__
                                CACA TT TGC   TTGGGGA
                                |||| || |||   |||||||
                                GTGT AA ACG   AACCCCT
                                   _  T   AGG
GAM752   ACAD8     3'  CACACCTTTGCTCTAGAA    20491          A
                                CACACTTTTGC TTGGGG
                                |||||||||||| ||||||
                                GTGTGGAAACG GATCTT
                                      A
GAM752   AP2B1     3'  CACACTTTTCCTTCTGGAA   20492         GCA  GG
                                CACACTTTT   TT  GGAA
                                |||||||||   ||  ||||
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                                GTGTGAAAA  AA  CCTT
                                    GG_  GA
GAM752  ARCN1   3'  ACACTCTTTGCAGGGA     20493       _  TTG
                                ACACTTTT GCA  GGGA
                                |||||||| |||  ||||
                                TGTGAGAA CGT  CCCT
                                   A  ___
GAM752  ATP5J   5'  CACACTTCTAGTCGCGGGA  20494       CA  _
                                CACACTTTTG  TTG GGGA
                                ||||||||||  ||| ||||
                                GTGTGAAGAT  AGC CCCT
                                    C_  G
GAM752  ATSV    3'  CACCCTTTCCTGGGGAA    20495      GCA
                                CACTTTT  TTGGGGAA
                                |||||||  ||||||||
                                GTGGGAA  GACCCCTT
                                   AG_
GAM752  AXL     3'  CACACCCCCACAGTTGGGGA  20496      TG  _
                                CACACTTT  CA TTGGGGA
                                ||||||||  || |||||||
                                GTGTGGGG  GT AACCCCT
                                    GT  C
GAM752  AXL     3'  CACACCCCCACAGTTGGGGA  20496      TG  _
                                CACACTTT  CA TTGGGGA
                                ||||||||  || |||||||
                                GTGTGGGG  GT AACCCCT
                                    GT  C
GAM752  B4GALT1  3'  CACATTCATGCTGGGGAA   20497    C  T   AT
                                CACA TT TGC  TGGGGAA
                                |||| || |||  |||||||
                                GTGT AG ACG  ACCCCTT
                                  A  T  __
GAM752  BAIAP3   3'  CACACTGGGCCTGGGGAA   20498     TTT  A
                                CACACT  GC TTGGGGAA
                                ||||||  || ||||||||
                                GTGTGA  CG GACCCCTT
                                   CC_  _
GAM752  BAZ2B   5'  ACACCTTTTTCGGGAA     20499      GCA
                                ACACTTTT  TTGGGGA
                                ||||||||  |||||||
                                TGTGGAAA  AGCCCTT
                                   A__
GAM752  BCAT1   3'  ACATTTTTGGCACCAGGGA  20500    C   _  TG
                                ACA TTTTG CAT  GGGA
                                ||| ||||| |||  ||||
                                TGT AAAAC GTG  CCCT
                                  A   C  GT
GAM752  BCL11B  3'  CACATTTTGCTTAGAG     20501    C    A
                                CACA TTTTGC TTGGGG
                                |||| |||||| ||||||
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                                GTGT AAAACG AATCTC
                                  _    _
GAM752  C18orf1  3'  CACACTTTGCTGGAA      20502       T  AT
                                CACACTTT GC  TGGGG
                                |||||||| ||  |||||
                                GTGTGAAA CG  ACCTT
                                  _  __
GAM752  CACNG3   5'  CACTGGAGCCCATTGGGGAA  20503     TTT __
                                CACT   GC  ATTGGGGAA
                                ||||   ||  |||||||||
                                GTGA   CG  TAACCCCTT
                                  CCT  GG
GAM752  CANX     3'  CACACATTTGCTTCAAGGA   20504      T    A TG
                                CACAC TTTGC T  GGGA
                                ||||| ||||| |  ||||
                                GTGTG AAACG A  TCCT
                                   T    A GT
GAM752  CD1D     3'  CACACCTTTGCACTTCTGA   20505          GGG
                                CACACTTTTGCATT   GA
                                ||||||||||||||   ||
                                GTGTGGAAACGTGA   CT
                                       AGA
GAM752  CDH6     3'  ACACTTTTGTTTAAGGGAA   20506        CATT
                                ACACTTTTG    GGGGAA
                                |||||||||    ||||||
                                TGTGAAAAC    TCCCTT
                                     AAAT
GAM752  CLN5     5'  CACACTTTGCAGTCCAGGAA  20507       T  _  G
                                CACACTTT GCA TT GGGAA
                                |||||||| ||| || |||||
                                GTGTGAAA CGT AG TCCTT
                                     _  C  G
GAM752  COL1A2   3'  CATACTTTTAATTGGGAA    20508    C      C
                                CA ACTTTTG ATTGGGGA
                                || ||||||| ||||||||
                                GT TGAAAAT TAACCCTT
                                 A      _
GAM752  DAF      3'  ACACTTTTAGGAAAGGAA    20509        CATT
                                ACACTTTTG    GGGGAA
                                |||||||||    ||||||
                                TGTGAAAAT    TTCCTT
                                     CCT_
GAM752  DAPP1    3'  CACAGTTTTGTCATTAGAA   20510     C    _
                                CACA TTTTG CATTGGGG
                                |||| ||||| ||||||||
                                GTGT AAAAC GTAATCTT
                                  C    A
GAM752  DDX11    3'  CACACTTTTATTTAAGGA    20511         CA
                                CACACTTTTG  TTGGGGA
                                |||||||||  |||||||
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                                GTGTGAAAAT  AATTCCT
                                     A_
GAM752  DDX11   3'  CACACTTTTATTTAAGGA    20511         CA
                                CACACTTTTG  TTGGGGA
                                ||||||||||  |||||||
                                GTGTGAAAAT  AATTCCT
                                     A_
GAM752  DYT1    3'  CACCTTTTGCAAAACGGAG   20512    A      T__
                                CAC CTTTTGCA   TGGGG
                                ||| ||||||||   |||||
                                GTG GAAAACGT   GCCTC
                                  _      TTT
GAM752  EPHA8   3'  CATTTTTGCATTGTCAGGA   20513    C       __
                                CA TTTTGCATTG  GGGA
                                || ||||||||||  ||||
                                GT AAAACGTAAC  TCCT
                                 A         AG
GAM752  EPHB2   3'  CACACTTTCTCTCCAGGGAA  20514        GCA TG
                                CACACTTTT   T  GGGAA
                                |||||||||   |  |||||
                                GTGTGAAAG   G  CCCTT
                                     AGA GT
GAM752  GAP43   3'  CACACTGTTTGACTTGGGA   20515      _   CA
                                CACACT TTTG  TTGGGG
                                ||||||| ||||  ||||||
                                GTGTGA AAAC  AACCCT
                                   C    TG
GAM752  IL12B   3'  CACATTTTGCATAATAGGGA  20516     C      __
                                CACA TTTTGCAT  TGGGGA
                                |||| ||||||||  ||||||
                                GTGT AAAACGTA  ATCCCT
                                  _      TT
GAM752  ITGBL1  5'  CACTTCTGCAAGGTGGGG    20517        T__
                                CACTTTTGCA   TGGGG
                                ||||||||||   |||||
                                GTGAAGACGT   ACCCC
                                     TCC
GAM752  ITPKB   3'  CACACTACATTGGGGAA     20518      TTT
                                CACACT   GCATTGGGGAA
                                ||||||   ||||||||||||
                                GTGTGA   TGTAACCCCTT
                                   ___
GAM752  KIF3B   3'  CACTTTTAGTACAGACGGGG  20519      ___   T_
                                CACTTT   TGCA  TGGGG
                                ||||||   ||||  |||||
                                GTGAAA   ATGT  GCCCC
                                   ATC    CT
GAM752  M17S2   3'  CACACTTCTGTAAACAGAG   20520        CAT_
                                CACACTTTTG    TGGGG
                                ||||||||||    |||||
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                                GTGTGAAGAC   GTCTC
                                     ATTT
GAM752  M17S2    3'  CACACTTCTGTAAACAGAG   20520        CAT_
                                CACACTTTTG   TGGGG
                                ||||||||||  |||||
                                GTGTGAAGAC   GTCTC
                                     ATTT
GAM752  M17S2    3'  CACACTTCTGTAAACAGAG   20520        CAT_
                                CACACTTTTG   TGGGG
                                ||||||||||  |||||
                                GTGTGAAGAC   GTCTC
                                     ATTT
GAM752  MAP3K7IP1 3'  CACGCCTGGCTCTGGGGAA   20521    A  TT  A
                                CAC CTT  GC TTGGGGAA
                                ||| |||  || ||||||||
                                GTG GGA  CG GACCCCTT
                                  C   C_  A
GAM752  MBL2     3'  CTTATTACATGTTGGGGAA   20522    _    __
                                CTT TTGCAT  TGGGGAA
                                ||| ||||||  |||||||
                                GAA AATGTA  ACCCCTT
                                  T     CA
GAM752  MBNL     3'  CACATTTTGCATTTTTGA    20523    C      GGG
                                CACA TTTTGCATT   GA
                                |||| |||||||||   ||
                                GTGT AAAACGTAA   CT
                                  _       AAA
GAM752  MVK      3'  CACACTTCTCCGGGAA     20524       GCA
                                CACACTTTT   TTGGGGA
                                |||||||||   |||||||
                                GTGTGAAGA   GGCCCTT
                                     ___
GAM752  NDUFS5   3'  CACACTTTGACAAGGAG    20525       T   TT
                                CACACTTT GCA  GGGG
                                |||||||| |||  ||||
                                GTGTGAAA TGT  CCTC
                                     C   T_
GAM752  OCA2     3'  ACATTTTGTCCTTGGGGA   20526    C    CA_
                                ACA TTTTG   TTGGGGA
                                ||| |||||   |||||||
                                TGT AAAAC   AACCCCT
                                  _    AGG
GAM752  PDE4D    3'  CACACTTTGGCAAGAG     20527       T   TT
                                CACACTTT GCA  GGGG
                                |||||||| |||  ||||
                                GTGTGAAA CGT  TCTC
                                     C   __
GAM752  PPP1R12B 3'  CACACTTTCGTGGGA      20528        CAT
                                CACACTTTTG   TGGGG
                                ||||||||||  |||||
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                                GTGTGAAAGC  ACCCT
                                    ___
GAM752  PRKCN   3' CACATCTTAAACTTTGGGGAA 20529    _  TT  A
                                CACA CTT  GC TTGGGGAA
                                |||| |||  || ||||||||
                                GTGT GAA  TG AACCCCTT
                                  A  TT  A
GAM752  PSEN2   3' CACACTCTTTGCGCATCTCAG 20530       ___   GG
                                CACACTTTT  GCATT  GG
                                |||||||||  |||||  ||
                                GTGTGAGAA  CGTAG  TC
                                     ACG   AG
GAM752  PSEN2   3' CACACTCTTTGCGCATCTCAG 20530       ___   GG
                                CACACTTTT  GCATT  GG
                                |||||||||  |||||  ||
                                GTGTGAGAA  CGTAG  TC
                                     ACG   AG
GAM752  PSMC1   3' CACGCTTTATTGGGAA    20531    A   TGC
                                CAC CTTT  ATTGGGGA
                                ||| ||||  ||||||||
                                GTG GAAA  TAACCCTT
                                 C  ___
GAM752  SERPINB13 3' CACAATATCTGTTGGGGAA  20532    CT_   CA
                                CACA  TTTG  TTGGGGAA
                                ||||  ||||  ||||||||
                                GTGT  AGAC  AACCCCTT
                                  TAT  __
GAM752  SERPINE1  3' CACCCTGTAATTGGGGAA   20533      TGC
                                CACTTT  ATTGGGGAA
                                ||||||  |||||||||
                                GTGGGA  TAACCCCTT
                                   CAT
GAM752  SLC1A2  3' CACATTTCTGCATCTTGGGA  20534    C      G_
                                CACA TTTTGCATT  GGGA
                                |||| |||||||||  ||||
                                GTGT AAGACGTAG  CCCT
                                  A       AA
GAM752  SNX9    3' ACACTTTTCCATCTAATGGGGA 20535       G  ____
                                ACACTTTT CAT   TGGGGA
                                |||||||| |||   ||||||
                                TGTGAAAA GTA   ACCCCT
                                    G  GATT
GAM752  SPARC   3' ACATTTTAAACATTGGGG   20536    C  T_
                                ACA TTT  GCATTGGGG
                                ||| |||  |||||||||
                                TGT AAA  TGTAACCCC
                                  A  TT
GAM752  TEM8    3' ACACTGTGAGCCTGGGGAA   20537     TTT_  A
                                ACACT   GC TTGGGGAA
                                |||||   || ||||||||
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                                TGTGA   CG GACCCCTT
                                  CACT  _
GAM752  TMEM2   3'  CAGACTTTTGCTGCAGGAA   20539   C      AT
                                CA ACTTTTGC  TGGGGA
                                || ||||||||  ||||||
                                GT TGAAAACG  GTCCTT
                                 C       AC
GAM752  TMEM2   3'  ACACTTTATGCGTCGGGG    20538       _  A
                                ACACTTT TGC TTGGGG
                                ||||||| ||| ||||||
                                TGTGAAA ACG AGCCCC
                                    T  C
GAM752  TRAF1   3'  CTCCTGCGTGTTGGGGAA    20540       A__
                                CTTTTGC  TTGGGGAA
                                |||||||  ||||||||
                                GAGGACG  AACCCCTT
                                    CAC
GAM752  TRIM14  3'  CACATTTCTGACTGGAG     20541     C   C
                                CACA TTTTG ATTGGGG
                                |||| ||||| |||||||
                                GTGT AAGAC TGACCTC
                                  A   _
GAM752  ZNF26   3'  CACACTTTCAATGGGAA     20542       GCAT
                                CACACTTTT   TGGGGA
                                |||||||||   ||||||
                                GTGTGAAAG   ACCCTT
                                     TT__
GAM752  AGMAT   3'  CACATTCTTTGCAGTGGGG   20543     C_     T
                                CACA  TTTTGCA TGGGG
                                ||||  ||||||| |||||
                                GTGT  GAAACGT ACCCC
                                  AA      C
GAM752  AK5     3'  CACAGTTTTGCATATGGG    20544     C      _
                                CACA TTTTGCAT TGGG
                                |||| |||||||| ||||
                                GTGT AAAACGTA ACCC
                                  C       T
GAM752  AP3D1   3'  CACTTCTGCTGACCAGGAA   20545       __ TG
                                CACTTTTGC  AT  GGGA
                                |||||||||  ||  ||||
                                GTGAAGACG  TG  CCTT
                                     AC  GT
GAM752  ARPP-21 3'  CAACTTTTGCAGTATTGAG   20546   C      ___
                                A ACTTTTGCA   TTGGG
                                | |||||||||   |||||
                                G TGAAAACGT   AACTC
                                 T       CAT
GAM752  BAG5    3'  ACACTTTTAAAGGGAA      20547       CATT
                                ACACTTTTG   GGGGAA
                                |||||||||   ||||||
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                                TGTGAAAAT   TCCCTT
                                     T___
GAM752  BTBD3    3'  CAGCCAGATACGTTGGGGAA  20548   _ TT_  A
                                CA CT  TGC TTGGGGAA
                                || ||  ||| ||||||||
                                GT GG  ATG AACCCCTT
                                 C  TCT  C
GAM752  C1orf24  3'  CACTTTTGTCTTGGGGAA   20549       CA
                                CACTTTTG  TTGGGGAA
                                ||||||||  ||||||||
                                GTGAAAAC  AACCCCTT
                                     AG
GAM752  C5orf4   3'  CACATTCTTTACTGGGAA   20550    C   GC
                                CACA TTTT  ATTGGGGA
                                |||| ||||  ||||||||
                                GTGT AGAA  TGACCCTT
                                  A   A_
GAM752  C5orf4   3'  CACATTCTTTACTGGGAA   20550    C   GC
                                CACA TTTT  ATTGGGGA
                                |||| ||||  ||||||||
                                GTGT AGAA  TGACCCTT
                                  A   A_
GAM752  CCR5     3'  ACACTTGTGTGCACTGGG   20551      T__
                                ACACTT  TGCATTGGG
                                ||||||  |||||||||
                                TGTGAA  ACGTGACCC
                                   CAC
GAM752  CG005    3'  TAACATTTGCTGGGGAA    20552   C  T   AT
                                A AC TTTGC  TGGGGAA
                                | || |||||  |||||||
                                A TG AAACG  ACCCCTT
                                 T  T   __
GAM752  CIC      3'  ACATGTTTTGTTCTGGGGAA  20553    C_   CA
                                ACA  TTTTG  TTGGGGAA
                                |||  |||||  ||||||||
                                TGT  AAAAC  GACCCCTT
                                  AC   AA
GAM752  COASTER  3'  CACACCTTTGTGTAGAA    20554        CAT  GG
                                CACACTTTTG  TG  GAA
                                ||||||||||  ||  |||
                                GTGTGGAAAC  AC  CTT
                                     ___  AT
GAM752  DKFZP434F0318 3'  CACATTTTTCCACTAGGAA   20555    C   G
                                CACA TTTT CATTGGGGA
                                |||| |||| |||||||||
                                GTGT AAAA GTGATCCTT
                                  A   G
GAM752  DKFZP434F091 3'  CACACCTTTTGCTAACCAGGA  20556     _    __ TG
                                CACAC TTTTGC  AT  GGG
                                ||||| ||||||  ||  |||
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                                GTGTG AAAACG  TG  CCT
                                   G     AT  GT
GAM752  DKFZp434G179 3'  CACACTGTTGCCCGGAG     20557       T   A
                                CACACT TTGC TTGGGG
                                |||||| |||| ||||||
                                GTGTGA AACG GGCCTC
                                   C   _
GAM752  DKFZP434H132 3'  CATTTTACACATGGGGAA    20558    C      _
                                CA TTTTGCAT TGGGGAA
                                || |||||||| |||||||
                                GT AAAATGTG ACCCCTT
                                 _       T
GAM752  DKFZP434H132 3'  CATTTTACACATGGGGAA    20558    C      _
                                CA TTTTGCAT TGGGGAA
                                || |||||||| |||||||
                                GT AAAATGTG ACCCCTT
                                 _       T
GAM752  DKFZp547I224 5'  CCTTGCTAGATTGGGGAA    20559       ___
                                TTTTGC   ATTGGGGAA
                                ||||||   |||||||||
                                GGAACG   TAACCCCTT
                                   ATC
GAM752  DKFZP564D166 3'  ACATTTCTGCTCTGGGGAA   20560     C     A
                                ACA TTTTGC TTGGGGAA
                                ||| |||||| ||||||||
                                TGT AAGACG GACCCCTT
                                  A     A
GAM752  DKFZP564F013 3'  ACACTTTGCACCAAGAA     20561       T   TG
                                ACACTTT GCAT  GGGA
                                ||||||| ||||  ||||
                                TGTGAAA CGTG  TCTT
                                    _   GT
GAM752  EIF3S8   3'  CACACCTTTGTGGCAA      20562          CAT   G
                                CACACTTTTG   TGG GA
                                ||||||||||   ||| ||
                                GTGTGGAAAC   ACC TT
                                     ___  G
GAM752  EIF4B    3'  CACACCTTTGTCCACTGGG   20563         __
                                CACACTTTTG  CATTGGG
                                ||||||||||  |||||||
                                GTGTGGAAAC  GTGACCC
                                     AG
GAM752  EPS8R1   3'  CGACTTCCGCTATTGGGGA   20564   C      _
                                A ACTTTTGC ATTGGGGA
                                | |||||||| ||||||||
                                G TGAAGGCG TAACCCCT
                                 C       A
GAM752  EPS8R1   3'  CGACTTCCGCTATTGGGGA   20564   C      _
                                A ACTTTTGC ATTGGGGA
                                | |||||||| ||||||||
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                                G TGAAGGCG TAACCCCT
                                 C       A
GAM752  EPS8R1   3' CGACTTCCGCTATTGGGGA   20564   C       _
                                A ACTTTTGC ATTGGGGA
                                | |||||||| ||||||||
                                G TGAAGGCG TAACCCCT
                                 C       A
GAM752  ETAA16   5' CACATTTTGCAAAGGGA    20565    C      TT
                                CACA TTTTGCA  GGGGA
                                |||| |||||||  |||||
                                GTGT AAAACGT  TCCCT
                                  _      T_
GAM752  ETL      5' CACATTTTGCATTTGGGA    20566    C       G
                                CACA TTTTGCATT GGGA
                                |||| ||||||||| ||||
                                GTGT AAAACGTAA CCCT
                                  _       A
GAM752  F-LAN-1  3' CACACTTTTGCAACAAAGGA  20567          TT_
                                CACACTTTTGCA   GGGGA
                                ||||||||||||   |||||
                                GTGTGAAAACGT   TTCCT
                                       TGT
GAM752  FLJ10514 3' TGACTTTAGCCTTGGGGAA   20568   C    T  A
                                A ACTTT GC TTGGGGAA
                                | ||||| || ||||||||
                                A TGAAA CG AACCCCTT
                                 C    T  G
GAM752  FLJ10587 3' CACATTTTGGATTTGGGAA   20569     C    C  G
                                CACA TTTTG ATT GGGAA
                                |||| ||||| ||| |||||
                                GTGT AAAAC TAA CCCTT
                                  _    C  A
GAM752  FLJ10597 3' ACACTTTTTCCCTGGGAA    20570        GCA
                                ACACTTTT   TTGGGGA
                                ||||||||   |||||||
                                TGTGAAAA   GACCCTT
                                     AGG
GAM752  FLJ12484 3' CAGACTTTTGCTTAAGA     20571    C       A
                                CA ACTTTTGC TTGGGG
                                || |||||||| ||||||
                                GT TGAAAACG AATTCT
                                 C       _
GAM752  FLJ13544 3' ACACTTTTTGGCCAAGGGA   20572        __ ATT
                                ACACTTTT  GC   GGGGA
                                ||||||||  ||   |||||
                                TGTGAAAA  CG   TCCCT
                                     AC  GT_
GAM752  FLJ13909 5' CAGCTTGGCCTGGGGAA     20573    C  T  A
                                CA TTT GC TTGGGGAA
                                || ||| || ||||||||
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                                GT GAA CG GACCCCTT
                                 C   C  _
GAM752  FLJ14146  3'  CACACCTTTGCAGGGA      20574          TTG
                                CACACTTTTGCA  GGGA
                                ||||||||||||  ||||
                                GTGTGGAAACGT  CCCT
                                              ____
GAM752  FLJ14251  3'  ACACTGCTTGGGGAA       20575       TTT  A
                                ACACT  GC TTGGGGAA
                                |||||  ||  ||||||||
                                TGTGA  CG AACCCCTT
                                  ____  _
GAM752  FLJ20257  3'  CACACTTTCTGTTTAGGG    20576        GCA
                                CACACTTTT  TTGGGG
                                |||||||||  ||||||
                                GTGTGAAAG  AATCCC
                                      ACA
GAM752  FLJ20261  3'  ACACTTTTGTTGATCTGGAA  20577         C__  GG
                                ACACTTTTG  ATT  GGAA
                                |||||||||  |||  ||||
                                TGTGAAAAC  TAG  CCTT
                                     AAC  A_
GAM752  FLJ20315  3'  CACACTCTTGGTTGGAG     20578         CA
                                CACACTTTTG  TTGGGG
                                ||||||||||  ||||||
                                GTGTGAGAAC  AACCTC
                                      C_
GAM752  FLJ21736  3'  CACCTTTTGCAGCCCGAG    20579     A      _  G
                                CAC CTTTTGCA TT GGG
                                ||| ||||||||  || |||
                                GTG GAAAACGT GG CTC
                                  _      C  G
GAM752  GABBR1    5'  ACACTTTTCCTGGGGA      20580        GCA
                                ACACTTTT  TTGGGGA
                                ||||||||  |||||||
                                TGTGAAAA  GACCCCT
                                     G__
GAM752  GDAP2     3'  CACACTGTTGAGATCGGAA   20581       T  C_
                                CACACT TTG  ATTGGGG
                                ||||||  |||  |||||||
                                GTGTGA AAC  TAGCCTT
                                    C  TC
GAM752  GPT2      3'  TAACTTCCCACTGGGGAA    20582   C     G
                                A ACTTTT CATTGGGGAA
                                | ||||||  ||||||||||
                                A TGAAGG GTGACCCCTT
                                 T     _
GAM752  GTF2A1    5'  CACCGCAAGATTGGGGAA    20583     TTT  ___
                                CACT  GCA  TTGGGGAA
                                ||||  |||  ||||||||
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                                GTGG  CGT  AACCCCTT
                                  ___  TCT
GAM752  HIC2     3' CACACTTCTGAATGGAG    20584        CAT
                                CACACTTTTG  TGGGG
                                ||||||||||  |||||
                                GTGTGAAGAC  ACCTC
                                      TT_
GAM752  HSAJ1454 3' CATTTTGTTATTGGGGAA   20585   C   C_
                                CA TTTTG  ATTGGGGAA
                                || |||||  |||||||||
                                GT AAAAC  TAACCCCTT
                                 _   AA
GAM752  HSCBCIP1 5' CACACTTTTGTCATTGGG   20586        _
                                CACACTTTTG CATTGGG
                                |||||||||| |||||||
                                GTGTGAAAAC GTAACCC
                                      A
GAM752  HSMPP8   3' CACCTTTTGTGCTTGGGGAA 20587    A    CA_
                                CAC CTTTTG  TTGGGGAA
                                ||| ||||||  ||||||||
                                GTG GAAAAC  AACCCCTT
                                  _    ACG
GAM752  HSU79252 5' CACACTTTATGATGAGGAA  20588       TGCAT
                                CACACTTT   TGGGGAA
                                ||||||||   |||||||
                                GTGTGAAA   ACTCCTT
                                     TACT_
GAM752  HTGN29   3' ACATTACAGTTTGGGGAA   20589   TT   __
                                AC  TTGCA  TTGGGGAA
                                ||  |||||  ||||||||
                                TG  AATGT  AACCCCTT
                                 T_   CA
GAM752  KIAA0014 3' CACACTTTTAGGCTGAGGGGA 20590       __ ATT
                                CACACTTTT  GC  GGGGA
                                |||||||||  ||  |||||
                                GTGTGAAAA  CG  CCCCT
                                      TC  ACT
GAM752  KIAA0016 3' ACACTTTTCACTGGGAA    20591       G
                                ACACTTTT CATTGGGGA
                                |||||||| |||||||||
                                TGTGAAAA GTGACCCTT
                                       _
GAM752  KIAA0222 5' CACCTTCTACATGGGGG    20592    A      T
                                CAC CTTTTGCAT GGGG
                                ||| ||||||||| ||||
                                GTG GAAGATGTA CCCC
                                  _       C
GAM752  KIAA0453 3' CACTCTTGGGATTTGGGGAA 20593       CA__
                                CACTTTTG   TTGGGGAA
                                ||||||||   ||||||||
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                                GTGAGAAC    AACCCCTT
                                    CCTA
GAM752  KIAA0776 3' CACCTTCAACCTTGGGG     20594     A    T  A
                                CAC CTTT GC TTGGGG
                                ||| |||| || ||||||
                                GTG GAAG TG AACCCC
                                  _    T  G
GAM752  KIAA0931 3' CACACTTTTTGGCTCCGAG   20595          __  A
                                CACACTTTT  GC TTGGG
                                |||||||||  || |||||
                                GTGTGAAAA  CG GGCTC
                                    AC  A
GAM752  KIAA1014 3' ACACTCTTGCCCAGGAA     20596          A TG
                                ACACTTTTGC T  GGGA
                                |||||||||| |  ||||
                                TGTGAGAACG G  CCTT
                                    _ GT
GAM752  KIAA1128 3' ACACTTTCAGTCTGGGGAA   20597          CA
                                ACACTTTTG  TTGGGGAA
                                |||||||||  ||||||||
                                TGTGAAAGT  GACCCCTT
                                    CA
GAM752  KIAA1462 3' CAGCTTCTACATGGGGAA    20598    _       T
                                CA CTTTTGCAT GGGGAA
                                || |||||||| ||||||
                                GT GAAGATGTA CCCCTT
                                 C       _
GAM752  KIAA1522 3' CACCTTTTGTGCTTTGGAA   20599       ___   A
                                CACTTT   TGC TTGGGG
                                ||||||   ||| ||||||
                                GTGGAA   ACG AACCTT
                                   AAC   A
GAM752  KIAA1635 3' CACACTCTTCCGGGA       20600         GCA
                                CACACTTTT   TTGGGG
                                |||||||||   ||||||
                                GTGTGAGAA   GGCCCT
                                    ___
GAM752  KIAA1641 3' CACACATTTAACGGGAA     20601      T   CAT
                                CACAC TTTG   TGGGGA
                                ||||| ||||   ||||||
                                GTGTG AAAT   GCCCTT
                                   T   T__
GAM752  MGC16121 3' CACATTTTTGTCCTTGGAG   20602     C    CA_
                                CACA TTTTG   TTGGGG
                                |||| |||||   ||||||
                                GTGT AAAAC   AACCTC
                                  A    AGG
GAM752  MGC17347 3' CACACTTATTGGGGAA      20603       TTGC
                                CACACTT    ATTGGGGAA
                                |||||||    |||||||||
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                                GTGTGAA   TAACCCCTT
                                      ____
GAM752  MGC2628  3' TGACTTTTGCAGTTAGGG   20604   C      _
                                A ACTTTTGCA TTGGGG
                                | ||||||||| ||||||
                                A TGAAAACGT AATCCC
                                 C       C
GAM752  MGC32104 3' CACATCTTTGCTATTGAG   20605    C    _
                                CACA TTTTGC ATTGGG
                                |||| |||||| ||||||
                                GTGT GAAACG TAACTC
                                  A     A
GAM752  MKRN4    3' CACACTCCTTGGGGAA     20606       TGCA
                                CACACTTT   TTGGGGAA
                                ||||||||   ||||||||
                                GTGTGAGG   AACCCCTT
                                      ____
GAM752  MY014    5' CACATGTTTGTATCTGGGGA  20607    CT   CA_
                                CACA  TTTG   TTGGGGA
                                ||||  ||||   |||||||
                                GTGT  AAAC   GACCCCT
                                  AC    ATA
GAM752  NDUFA3   3' CACATTTTTATTGGGA     20608    C   GC
                                CACA TTTT  ATTGGGG
                                |||| ||||  |||||||
                                GTGT AAAA  TAACCCT
                                  _   A_
GAM752  NPTXR    3' ACACTCTCTTGGGGAA     20609       GCA
                                ACACTTTT   TTGGGGAA
                                ||||||||   ||||||||
                                TGTGAGAG   AACCCCTT
                                     ___
GAM752  NPTXR    3' ACACTCTCTTGGGGAA     20609       GCA
                                ACACTTTT   TTGGGGAA
                                ||||||||   ||||||||
                                TGTGAGAG   AACCCCTT
                                     ___
GAM752  OATL1    3' CATACTTAGGCCTGGGGA   20610   C   TT  A
                                CA ACTT  GC TTGGGGA
                                || ||||  || |||||||
                                GT TGAA  CG GACCCCT
                                 A   TC  _
GAM752  PJA1     5' ACACGTTTTTGAGATGGGAA  20611    __    CAT
                                ACAC  TTTTG   TGGGGA
                                ||||  |||||   ||||||
                                TGTG  AAAAC   ACCCTT
                                  CA    TCT
GAM752  PREI3    3' ACACTTTTATCTCAATTGGGGA 20612        ___  _
            A                    ACACTTTTG   CA TTGGGGAA
                                 |||||||||   || ||||||||
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                                TGTGAAAAT  GT AACCCCTT
                                     AGA  T
GAM752  PRO2577  3'  CACACTGTTTAAGAGTGGGG  20613      _   CAT_
                                CACACT TTTG   TGGGG
                                |||||| ||||   |||||
                                GTGTGA AAAT   ACCCC
                                   C   TCTC
GAM752  RES4-25  3'  CACACCTATAATTGGGG    20614       T  C
                                CACACTT TG ATTGGGG
                                ||||||| || |||||||
                                GTGTGGA AT TAACCCC
                                    T  _
GAM752  RNF2     3'  CACACTTTGTGGGGA      20615       T CAT
                                CACACTTT G   TGGGGA
                                |||||||| |   ||||||
                                GTGTGAAA C   ACCCCT
                                     _ ___
GAM752  RNF9     3'  CACTGGGCATTGGGGAA    20616     TTT
                                CACT   GCATTGGGGAA
                                ||||   ||||||||||||
                                GTGA   CGTAACCCCTT
                                  CC_
GAM752  SCAMP5   3'  ACACTCAGCCTTGGGGAA   20617      TT  A
                                ACACTT  GC TTGGGGAA
                                ||||||  || ||||||||
                                TGTGAG  CG AACCCCTT
                                   T_  G
GAM752  SEMA4G   5'  CACATCTTCCTGGGGA     20618     _   TGCA
                                CACA CTTT   TTGGGGA
                                |||| ||||   |||||||
                                GTGT GAAG   GACCCCT
                                  A   _____
GAM752  STK3     3'  CACACTTTTTTGTGCAAGGG  20619       _____   TT
                                CACACTTT   TGCA  GGGG
                                ||||||||   ||||  ||||
                                GTGTGAAA   ACGT  TCCC
                                     AAAC   __
GAM752  TGIF2    3'  CATTTTACATAATGGGGAA   20620    C      __
                                CA TTTTGCAT  TGGGGAA
                                || ||||||||  |||||||
                                GT AAAATGTA  ACCCCTT
                                  _      TT
GAM752  TRIM5    3'  CACTCCAGCCTGGGGAA     20621      TT  A
                                CACTT  GC TTGGGGAA
                                |||||  || ||||||||
                                GTGAG  CG GACCCCTT
                                  GT  _
GAM752  TUSP     3'  CACACTTTTAGAATGGGAA   20622         CAT
                                CACACTTTTG   TGGGGA
                                ||||||||||   ||||||
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                                GTGTGAAAAT   ACCCTT
                                     CTT
GAM752  UNC5D    3'  CACTTTTGTGACATTGGA    20623       ___
                                CACTTTTG   CATTGGG
                                ||||||||   |||||||
                                GTGAAAAC   GTAACCT
                                    ACT
GAM752  UPLC1    3'  ACAATTTGGCTGGGGAA     20624     C   T  AT
                                ACA TTT GC  TGGGGAA
                                ||| ||| ||  |||||||
                                TGT AAA CG  ACCCCTT
                                  T   C  __
GAM752  VCY2     5'  CACACTTCTGTGGCTCTGG   20625       ___  A
                                CACACTTTT   GC TTGG
                                |||||||||   || ||||
                                GTGTGAAGA   CG GACC
                                     CAC  A
GAM752  VCY2     5'  CACACTTCTGTGGCTCTGG   20625       ___  A
                                CACACTTTT   GC TTGG
                                |||||||||   || ||||
                                GTGTGAAGA   CG GACC
                                     CAC  A
GAM752  VEZATIN  3'  ACACTTTTGTAAAAGGAA    20626       CATT
                                ACACTTTTG    GGGGAA
                                |||||||||    ||||||
                                TGTGAAAAC    TTCCTT
                                     ATT_
GAM752  ZNF294   3'  CACACTTTTATATTTTGGG   20627       CA__
                                CACACTTTTG    TTGGG
                                ||||||||||    |||||
                                GTGTGAAAAT    AACCC
                                      ATAA
GAM752  LOC112868 3'  CACACTGTTTGTAAACTGGA   20628      _   C__
                                CACACT TTTG   ATTGGG
                                ||||||  ||||   ||||||
                                GTGTGA AAAC   TGACCT
                                    C    ATT
GAM752  LOC115131 5'  CACACTTTGGCATCTCTCTGAA 20629       T    GGG__
                                CACACTTT GCATT     GAA
                                ||||||||  |||||     |||
                                GTGTGAAA CGTAG     CTT
                                     C     AGAGA
GAM752  LOC116123 3'  ACTTTTGCAGTCTTGGGGA   20630       ___
                                ACTTTTGCA   TTGGGGA
                                |||||||||   |||||||
                                TGAAAACGT   AACCCCT
                                     CAG
GAM752  LOC118976 3'  CACACATCCTCTGGGGAA    20631      T   GCAT
                                CACAC TTT    TGGGGAA
                                |||||  |||    |||||||
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                                GTGTG AGG    ACCCCTT
                                   T   AG__
GAM752   LOC127702 3'  ACAATTTTGTATTGAGAA    20632     C     C
                                ACA TTTTG ATTGGGGA
                                ||| ||||| ||||||||
                                TGT AAAAC TAACTCTT
                                  T     A
GAM752   LOC129676 5'  CACACTGTTGCTCTGGAA    20633       T    A
                                CACACT TTGC TTGGGG
                                |||||| |||| ||||||
                                GTGTGA AACG GACCTT
                                   C    A
GAM752   LOC130813 3'  CACACTGTTGCACTCCAG    20634       T      GG
                                CACACT TTGCATT  GG
                                |||||| |||||||  ||
                                GTGTGA AACGTGA  TC
                                   C      GG
GAM752   LOC145508 3'  CAACTTTTGCCTCAAGGGAA  20635    C      ATT_
                                A ACTTTTGC    GGGGAA
                                | ||||||||    ||||||
                                G TGAAAACG    TCCCTT
                                 T       GAGT
GAM752   LOC148764 5'  CACACTTTTTGATGTCTGGGG  20636         GCA___
                                CACACTTTT     TTGGGG
                                |||||||||     ||||||
                                GTGTGAAAA     GACCCC
                                     ACTACA
GAM752   LOC148894 5'  CACACTTTGCAGATTGGGAA   20637        T  __
                                CACACTTT GCA  TTGGGGA
                                |||||||| |||  |||||||
                                GTGTGAAA CGT  AACCCTT
                                     _  CT
GAM752   LOC149013 3'  CACACTTCTGTAGTGCTGGAA  20638         CAT  G_
                                CACACTTTTG   TG  GGAA
                                ||||||||||   ||  ||||
                                GTGTGAAGAC   AC  CCTT
                                     ATC  GA
GAM752   LOC150587 3'  ACATTTCTGCACTGTTTGA    20639     C       GG_
                                ACA TTTTGCATTG   GA
                                ||| ||||||||||   ||
                                TGT AAGACGTGAC   CT
                                  A         AAA
GAM752   LOC150933 3'  CACACTTTTCACCTGCTGAA   20640         G   GGG_
                                CACACTTTT CATT    GAA
                                ||||||||| ||||    |||
                                GTGTGAAAA GTGG    CTT
                                     _   ACGA
GAM752   LOC151126 3'  ACATTATTGCATTAGGGA    20641     CTT
                                ACA   TTGCATTGGGGA
                                |||   ||||||||||||
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                                TGT   AACGTAATCCCT
                                  AAT
GAM752   LOC151610 3'  CACATTCTTTGGGGA       20642      C    GCA
                                CACA TTTT   TTGGGGA
                                |||| ||||   |||||||
                                GTGT AAGA   AACCCCT
                                  _   ___
GAM752   LOC152059 3'  CACAATTTTGCATGGAA      20643      C       T
                                CACA TTTTGCAT GGGG
                                |||| |||||||| ||||
                                GTGT AAAACGTA CCTT
                                  T       _
GAM752   LOC152373 5'  CACAGTTTTACTGGGGA      20644      C     AT
                                CACA TTTTGC  TGGGGA
                                |||| ||||||  ||||||
                                GTGT AAAATG  ACCCCT
                                  C     __
GAM752   LOC154043 3'  CACATTCTATCTCTGGGGAA   20645      C     CA_
                                CACA TTTTG   TTGGGGAA
                                |||| |||||   ||||||||
                                GTGT AAGAT   GACCCCTT
                                  _     AGA
GAM752   LOC154739 5'  ACACTTTCTGCCCTAGGG     20646       _    A
                                ACACTT TTGC TTGGGG
                                |||||| |||| ||||||
                                TGTGAA GACG GATCCC
                                   A    G
GAM752   LOC157657 3'  CTGCTACAAGTTGGGGAA     20647     T    __
                                CT TTGCA  TTGGGGAA
                                || |||||  ||||||||
                                GA GATGT  AACCCCTT
                                 C     TC
GAM752   LOC158187 3'  CACCTTTTGTATATGCGGAA   20648      A     CAT_  G
                                CAC CTTTTG    TG GGAA
                                ||| ||||||    || ||||
                                GTG GAAAAC    AC CCTT
                                  _     ATAT  G
GAM752   LOC160646 3'  CACACTTCTGCTGCTGGAG    20649           A_
                                CACACTTTTGC  TTGGGG
                                ||||||||||  ||||||
                                GTGTGAAGACG  GACCTC
                                       AC
GAM752   LOC165693 5'  CACACTTTTGTTCTGGAA     20650          CA
                                CACACTTTTG  TTGGGG
                                ||||||||||  ||||||
                                GTGTGAAAAC  GACCTT
                                       AA
GAM752   LOC169026 3'  CACACATTTGAATAGGGA     20651       T    CAT
                                CACAC TTTG   TGGGGA
                                ||||| ||||   ||||||
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                                GTGTG AAAC   ATCCCT
                                   T    TT_
GAM752   LOC199858 5'  CATTCTGGCACTGGGGAA    20652    C   T
                                CA TTT GCATTGGGGAA
                                || ||| ||||||||||
                                GT AGA CGTGACCCCTT
                                 A   C
GAM752   LOC200812 3'  CACCCTTTCTCGGGGAA     20653       GCA
                                CACTTTT   TTGGGGAA
                                |||||||   ||||||||
                                GTGGGAA   AGCCCCTT
                                    AG_
GAM752   LOC200953 5'  CACACATTTGCCTCCGGG    20654      T    A  G
                                CACAC TTTGC TT GGG
                                ||||| ||||| || |||
                                GTGTG AAACG AG CCC
                                   T    G  G
GAM752   LOC201952 3'  CAACTTTTGCAATCAGGGAA  20655   C       _ TG
                                A ACTTTTGCA T  GGGAA
                                | |||||||||  |  |||||
                                G TGAAAACGT A  CCCTT
                                 T       T GT
GAM752   LOC203276 3'  ACACTTTCTGCCCTAGGGAA  20656      _   A
                                ACACTT TTGC TTGGGGAA
                                |||||| |||| ||||||||
                                TGTGAA GACG GATCCCTT
                                   A   G
GAM752   LOC203305 3'  ACACTTTCTGCCCTAGGGAA  20656      _   A
                                ACACTT TTGC TTGGGGAA
                                |||||| |||| ||||||||
                                TGTGAA GACG GATCCCTT
                                   A   G
GAM752   LOC203427 3'  ACACTCTTGTTGGGAA      20657        CA
                                ACACTTTTG  TTGGGGA
                                |||||||||  |||||||
                                TGTGAGAAC  AACCCTT
                                     __
GAM752   LOC221656 3'  CACACTTTGATTGGGG      20658        T C
                                CACACTTT G ATTGGGG
                                |||||||| | |||||||
                                GTGTGAAA C TAACCCC
                                     _ _
GAM752   LOC221749 5'  CACACTTGTGTGACCGAG    20659       T  C_
                                CACACTT TG  ATTGGG
                                ||||||| ||  ||||||
                                GTGTGAA AC  TGGCTC
                                    C  AC
GAM752   LOC221935 3'  CACACTTTCTGCATGTGG    20660       _    _
                                CACACTT TTGCAT TGG
                                ||||||| |||||| |||
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                                GTGTGAA GACGTA ACC
                                    A     C
GAM752   LOC254243 3'  ACACTTTCTGCCCTAGGGAA  20656       _   A
                                ACACTT TTGC TTGGGGAA
                                |||||| |||| ||||||||
                                TGTGAA GACG GATCCCTT
                                   A   G
GAM752   LOC254431 5'  CACATTTTGCTGGAG      20661     C     AT
                                CACA TTTTGC  TGGGG
                                |||| ||||||  |||||
                                GTGT AAAACG  ACCTC
                                  _     ___
GAM752   LOC254967 5'  ACATTTCTTGACAAGGGGA   20662     C_    _ TT
                                ACA  TTTTG CA  GGGGA
                                |||  ||||| ||  |||||
                                TGT  AGAAC GT  CCCCT
                                  AA    T  T_
GAM752   LOC255328 3'  CACTTTTCACCAGGGAA     20663       G   TG
                                CACTTTT CAT  GGGAA
                                ||||||| |||  |||||
                                GTGAAAA GTG  CCCTT
                                   _  GT
GAM752   LOC255779 3'  CACTTTGCATGGGGAA      20664       T   T
                                CACTTT GCAT GGGGAA
                                |||||| |||| ||||||
                                GTGAAA CGTA CCCCTT
                                  _   _
GAM752   LOC256529 5'  CACACTCTTGCCAGCAGAA   20665          ATTG
                                CACACTTTTGC   GGGA
                                ||||||||||    ||||
                                GTGTGAGAACG   TCTT
                                      GTCG
GAM752   LOC257457 3'  ACATTTTTGCATTGCAGGA   20666     C       _
                                ACA TTTTGCATTG GGGA
                                ||| |||||||||| ||||
                                TGT AAAACGTAAC TCCT
                                  A        G
GAM752   LOC257482 3'  CATCCTTCTTTGGGGAA     20667    CA    GCA
                                CA  CTTTT   TTGGGGAA
                                ||  |||||   ||||||||
                                GT  GAAGA   AACCCCTT
                                 AG    ____
GAM752   LOC51094  5'  CAGCTTCAGCTTGGGGAA    20668    _   T  A
                                CA CTTT GC TTGGGGAA
                                || |||| || ||||||||
                                GT GAAG CG AACCCCTT
                                 C   T  _
GAM752   LOC51336  5'  CACTTTTGGTGAGGAA      20669        CAT
                                CACTTTTG   TGGGGAA
                                ||||||||   |||||||
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                                GTGAAAAC   ACTCCTT
                                    C__
GAM752  LOC56906 3' CAAACTTTTGCCTTAGAG    20670    C      A
                                CA ACTTTTGC TTGGGG
                                || |||||||| ||||||
                                GT TGAAAACG AATCTC
                                 T       G
GAM752  LOC83468 3' CACATTTCTATACAGGGAA   20671     C    CAT
                                CACA TTTTG   TGGGGAA
                                |||| |||||   |||||||
                                GTGT AAGAT   GTCCCTT
                                  A    AT_
GAM752  LOC90038 3' ACACTTTCTGCCCTAGGGAA  20656       _   A
                                ACACTT TTGC TTGGGGAA
                                |||||| |||| ||||||||
                                TGTGAA GACG GATCCCTT
                                   A   G
GAM752  LOC90139 3' CACTCTTGGAGCTGGGGA    20672       CA_
                                CACTTTTG   TTGGGGA
                                ||||||||   |||||||
                                GTGAGAAC   GACCCCT
                                    CTC
GAM752  LOC90190 3' CACACTCTTGTGGCTAGAA   20673        CAT  __
                                CACACTTTTG   TGG  GGAA
                                ||||||||||   |||  ||||
                                GTGTGAGAAC   ACC  TCTT
                                     ____  GA
GAM752  LOC90288 3' CACACTTTGTCCATCTGGAA  20674       TG_   GG
                                CACACTTT   CATT  GGAA
                                ||||||||   ||||  ||||
                                GTGTGAAA   GTAG  CCTT
                                    CAG    A_
GAM752  LOC90379 5' CACACTTTCAATGGGGA     20675       GCAT
                                CACACTTTT    TGGGGA
                                |||||||||    ||||||
                                GTGTGAAAG    ACCCCT
                                     TT__
GAM752  LOC90750 5' CATTTTGCAGATGGGGAA    20676    C     T_
                                CA TTTTGCA  TGGGGAA
                                || |||||||  |||||||
                                GT AAAACGT  ACCCCTT
                                 _      CT
GAM752  LOC90835 3' CAGACCTTTATTGGGGAA    20677    C     GC
                                CA ACTTTT  ATTGGGGAA
                                || ||||||  |||||||||
                                GT TGGAAA  TAACCCCTT
                                 C     __
GAM752  LOC91263 5' CACACATTTGCTCACAGAA   20678      T    A  G
                                CACAC TTTGC TTG GGAA
                                ||||| ||||| ||| ||||
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                                GTGTG AAACG AGT TCTT
                                  T    _  G
GAM752  LOC91464  3' CACTTTTGCATCCTGTGGG   20679          __ _
                                CACTTTTGCAT  TG GGG
                                ||||||||||  || |||
                                GTGAAAACGTA  AC CCC
                                      GG  A
GAM752  LOC92299  3' ACACTTTTTGATAAGGAA   20680       GCAT
                                ACACTTTT   TGGGGAA
                                ||||||||   |||||||
                                TGTGAAAA   ATTCCTT
                                    ACT_
GAM752  LOC92697  3' CACAAGATTTATTGGGGAA   20681     CTT  GC
                                CACA   TT  ATTGGGGAA
                                ||||   ||  |||||||||
                                GTGT   AA  TAACCCCTT
                                  TCT  A_
GAM752  LOC93349  3' CACATTTCTGCAAAAGAA    20682     C      TT
                                CACA TTTTGCA  GGGG
                                |||| |||||||  ||||
                                GTGT AAGACGT  TCTT
                                  A      TT
GAM752  LOC93463  3' CAAACTCTCTTGGGGAA     20683    C     GCA
                                CA ACTTTT   TTGGGGAA
                                || ||||||   ||||||||
                                GT TGAGAG   AACCCCTT
                                 T    ____
GAM753  DLG5    3' ACAGAAATTGACCTTTATTTG  20686     TGTGGA
                                ACAG     GACCTTTATTTG
                                ||||     ||||||||||||
                                TGTC     CTGGAAATAAAC
                                  TTTAA_
GAM753  EPAC    3' GTGTGGAGACCTCTCTATTGC  20687           AT_
                                GTGTGGAGACCTTT   TTGC
                                ||||||||||||||   ||||
                                CACACCTCTGGAGA   AACG
                                       GAT
GAM753  FE65L2   3' CACTGAGGGATTTTTATTTGC  20688    G  T  A  CC
                                CA TG GG GA  TTTATTTGC
                                || || || ||  |||||||||
                                GT AC CC CT  AAATAAACG
                                 G  T  _  AA
GAM753  FE65L2   3' CACTGAGGGATTTTTATTTGC  20688    G  T  A  CC
                                CA TG GG GA  TTTATTTGC
                                || || || ||  |||||||||
                                GT AC CC CT  AAATAAACG
                                 G  T  _  AA
GAM753  FE65L2   3' CACTGAGGGATTTTTATTTGC  20688    G  T  A  CC
                                CA TG GG GA  TTTATTTGC
                                || || || ||  |||||||||
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                                GT AC CC CT  AAATAAACG
                                 G  T  _  AA
GAM753  FE65L2   3'  CACTGAGGGATTTTTATTTGC  20688    G  T  A  CC
                                CA TG GG GA  TTTATTTGC
                                || || || ||  |||||||||
                                GT AC CC CT  AAATAAACG
                                 G  T  _  AA
GAM753  MGAT4B   3'  CACAGTGTGGGGGGCCGCCTGC  20689         AGA  TTTA
                                TACAGTGTGG  CC   TTTGC
                                ||||||||||  ||   |||||
                                GTGTCACACC  GG   GGACG
                                      CCC  C___
GAM753  MGAT4B   3'  CACAGTGTGGGGGGCCGCCTGC  20689         AGA  TTTA
                                TACAGTGTGG  CC   TTTGC
                                ||||||||||  ||   |||||
                                GTGTCACACC  GG   GGACG
                                      CCC  C___
GAM753  PRKY     3'  TACAGTGTGGAATTCTGGTTGC 20690          AC  TTAT
                                TACAGTGTGGAG  CT   TTGC
                                ||||||||||||  ||   ||||
                                ATGTCACACCTT  GA   AACG
                                       AA  CC__
GAM753  TKTL1    3'  TACAGTGTGGAGGCTCT    20691          AC
                                TACAGTGTGGAG  CTTT
                                ||||||||||||  ||||
                                ATGTCACACCTC  GAGA
                                       C_
GAM753  TRPC6    3'  TAAGTGTGGGGATTCATCTG  20692   C     A  CC
                                A AGTGTGG GA  TTTATTTG
                                | |||||||  ||  ||||||||
                                A TCACACC CT  AAGTAGAC
                                 T     C  __
GAM753  EMILIN-2 3'  TACAGGTGGAGGCCTTT    20693     T    A
                                TACAG GTGGAG CCTTT
                                ||||| |||||| |||||
                                ATGTC CACCTC GGAAA
                                   _     C
GAM753  ISYNA1   3'  GTGGCAGCGCCTTTATTTG   20694    _  A_
                                GTGG AG  CCTTTATTTG
                                ||||  ||  ||||||||||
                                CACC TC  GGAAATAAAC
                                  G  GC
GAM753  KIAA1729 5'  GTGCATTTTGTCTTTATTTGC  20695     GAGAC_
                                GTGTG     CTTTATTTGC
                                |||||     ||||||||||
                                CACGT     GAAATAAACG
                                   AAAACA
GAM753  MGC10981 3'  CAGTGTGGGGATTTAC     20696       A  CC
                                CAGTGTGG GA  TTTAT
                                ||||||||  ||  |||||
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                                GTCACACC CT  AAATG
                                     C  __
GAM753  MGC12760 3'  CAGTGTGGGGAGCTGTTGC   20697        A  C  TTAT
                                CAGTGTGG GA CT    TTGC
                                |||||||| || ||    ||||
                                GTCACACC CT GA    AACG
                                     C  C  C___
GAM753  MGC14407 3'  ACAGTGCCTTAATTTTTATTTG 20698        GGAGACC
             C                   ACAGTGT      TTTATTTGC
                                |||||||      |||||||||
                                TGTCACG      AAATAAACG
                                    GAATTAA
GAM753  MGC16279 5'  TACAGTGTGAGGTTCAGCATTG 20699         G  ACCTTTAT
             C                   TACAGTGTG AG       TTGC
                                |||||||||| ||       ||||
                                ATGTCACAC TC       AACG
                                     _  CAAGTCGT
GAM753  MGC2452  5'  ATATGGAAACACTTTTATTTGC 20700          _   _
                                GTGTGGAGAC CTTT ATTTGC
                                |||||||||| |||| ||||||
                                TATACCTTTG GAAA TAAACG
                                      T   A
GAM753  MGC2734  3'  GTGTGGAGACCAATTTGC    20701          TTT
                                GTGTGGAGACC   ATTTGC
                                ||||||||||   ||||||
                                CACACCTCTGG   TAAACG
                                      T__
GAM753  MGC5391  3'  TACAGTGTGGATGTTGGCCACT 20702          GACCT_
             TG                   TACAGTGTGGA     TTATTTG
                                ||||||||||     |||||||
                                ATGTCACACCT     GGTGAAC
                                      ACAACC
GAM753  MGC8407  3'  GCAGGGTGATGTTTATTTGC   20703     T  A  CC
                                GTG GG GA  TTTATTTGC
                                ||| || ||  |||||||||
                                CGT CC CT  AAATAAACG
                                  C  A  AC
GAM753  MYOZ2    3'  TACGGTGTACTTTATTTG    20704     A    GAGAC
                                TAC GTGTG    CTTTATTTG
                                ||| |||||    |||||||||
                                ATG CACAT    GAAATAAAC
                                  C    _____
GAM753  LOC161527 5'  CAGGTGGCTTTTATTTG     20705     T    AGACC
                                CAG GTGG    TTTATTTG
                                ||| ||||    ||||||||
                                GTC CACC    AAATAAAC
                                  _   GA___
GAM753  LOC196484 5'  TACAGTGTGAGGTTCAGCATTG 20699         G  ACCTTTAT
             C                   TACAGTGTG AG       TTGC
                                |||||||||| ||       ||||
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                                ATGTCACAC TC       AACG
                                     _ CAAGTCGT
GAM753  LOC221715 3'  CAGTGTTCTTTATTTG      20706       GGAGAC
                                CAGTGT     CTTTATTTG
                                ||||||     |||||||||
                                GTCACA     GAAATAAAC
                                   A_____
GAM753  LOC222060 5'  TGAGTGTTTCCTTTATTTG    20707    C     GGAGA
                                A AGTGT    CCTTTATTTG
                                | |||||    ||||||||||
                                A TCACA    GGAAATAAAC
                                 C    AA___
GAM753  LOC57100  3'  TACAGTGTGGAGCTCTCTCCCT 20708           AC    A
          G                      TACAGTGTGGAG  CTTT TTTG
                                ||||||||||||  |||| ||||
                                ATGTCACACCTC  GAGA GGAC
                                      GA    G
GAM753  LOC91069  3'  TACAGTGTGAGGTTCAGCATTG 20699         G  ACCTTTAT
          C                      TACAGTGTG AG       TTGC
                                |||||||||  ||       ||||
                                ATGTCACAC TC       AACG
                                     _ CAAGTCGT
GAM754  NPY2R     5'  CAGAGCGGCTGGGCGGTTGGCG 20711         A  T  A_  A
          CT                       CAGAGCGGC GG CG  TG CGCT
                                |||||||||  ||  ||  ||  ||||
                                GTCTCGCCG CC GC  AC GCGA
                                     A  C  CA  C
GAM754  NR2E1     3'  CAGGGCGGCAGGTCATAGCT   20712     A        G   AC
                                CAG GCGGCAGGTC ATG  GCT
                                |||  ||||||||||  |||  |||
                                GTC CGCCGTCCAG TAT  CGA
                                  C        _   __
GAM754  EPI64     3'  GAGGACCTCGATGACGCT    20713     C   AGG
                                GAG GGC   TCGATGACGCT
                                |||  |||   ||||||||||
                                CTC CTG   AGCTACTGCGA
                                  _   G__
GAM754  FLJ20507  5'  CCAGGGCTGGGATGGTGC    20714     AGC   A  TC    AC
                                CCAG   GGC GG  GATG  GC
                                ||||   |||  ||  ||||  ||
                                GGTC   CCG CC  CTAC  CG
                                   ___   A  __    CA
GAM754  FLJ20507  5'  CCAGGGCTGGGATGGTGC    20714     AGC   A  TC    AC
                                CCAG   GGC GG  GATG  GC
                                ||||   |||  ||  ||||  ||
                                GGTC   CCG CC  CTAC  CG
                                   ___   A  __    CA
GAM754  FLJ23816  3'  GCGGGAGACGATGACGCT    20715     C   T
                                GCGG AGG CGATGACGCT
                                ||||  |||  ||||||||||
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                                CGCC TCT GCTACTGCGA
                                  C  _
GAM754  KIAA0265  3'  CAGGGCAGGAGATGACGC    20716    AGC    TC
                                CAG  GGCAGG  GATGACGC
                                |||  ||||||  ||||||||
                                GTC  CCGTCC  CTACTGCG
                                 ___    T_
GAM754  MGC2865   3'  GCGGCAGGTCGTGGGCT    20717         A  AC
                                GCGGCAGGTCG TG  GCT
                                |||||||||| ||  |||
                                CGCCGTCCAGC AC  CGA
                                      _ C_
GAM754  LOC157349 3'  GAGCAGCAGGTCCCCGCT    20718          GATGA
                                GAGCGGCAGGTC    CGCT
                                ||||||||||||    ||||
                                CTCGTCGTCCAG    GCGA
                                       GG___
GAM754  LOC169426 5'  CAGAGTGGCAGGTCACTGCT   20719      C       ATGAC
                                CAGAG GGCAGGTCG    GCT
                                ||||| |||||||||    |||
                                GTCTC CCGTCCAGT    CGA
                                  A       GA___
GAM754  LOC169696 5'  CCAGGGCTGCAGGTTCAAGATG 20720     A  G    _  T  C
          CT                    CCAG GC GCAGGT CGA GA GCT
                                |||| || |||||| ||| || |||
                                GGTC CG CGTCCA GTT CT CGA
                                  C A    A  _ A
GAM754  LOC221749 5'  CCGGAGCCGCAGGTCGGTGAC  20721    A   G      A
                                CC GAGC GCAGGTCG TGAC
                                || |||| |||||||| ||||
                                GG CTCG CGTCCAGC ACTG
                                 C   G      C
GAM754  LOC255497 3'  CCAGGGCGACAGAGCGACGCT  20722     A      TCGA
                                CCAG GCGGCAGG   TGACGCT
                                |||| ||||||||   |||||||
                                GGTC CGCTGTCT   GCTGCGA
                                  C      C___
GAM754  LOC64150  5'  CCGGGGCGGCAGGCGCACGGGA 20723    AGA      _ AT_
          CGCT                    CC  GCGGCAGGT CG  GACGCT
                                ||  ||||||||| ||  ||||||
                                GG  CGCCGTCCG GT  CTGCGA
                                 CCC       C  GCC
GAM755  PKDREJ   3'  ACCCATATGTACCTTTTTGT  20726      _     ATA
                                ACCCAT TGTACCT  TGT
                                |||||| |||||||  |||
                                TGGGTA ACATGGA  ACA
                                   T      AAA
GAM755  POP4     3'  TGTCCACATATGTATTGT    20727    A _
                                TGT CC TATATGTATTGT
                                ||| || ||||||||||||
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                                ACA GG GTATACATAACA
                                  _ T
GAM755  STC1     3'  TGTAGATATATGTATTGT    20728     CC
                                TGTA  TATATGTATTGT
                                ||||  ||||||||||||
                                ACAT  ATATACATAACA
                                  CT
GAM755  CEACAM7  3'  ACCCACTGTATTTATTTATGT  20729        CC __
                                ACCCATTGTA  TA  TATGT
                                ||||||||||  ||  |||||
                                TGGGTGACAT  AT  ATACA
                                      AA  AA
GAM755  MGC3180  3'  ACCCATTGTAATTTATTTGT   20730        CC_   A
                                ACCCATTGTA   TAT TGT
                                ||||||||||   ||| |||
                                TGGGTAACAT   ATA ACA
                                      TAA   A
GAM755  NR2F1    3'  CCACTTCCATATGTGTTGT   20731      GTAC      A
                                CCATT    CTATATGT TTGT
                                |||||    |||||||| ||||
                                GGTGA    GGTATACA AACA
                                   A___       C
GAM755  SBBI31   3'  CCCATTTTACCTATGTACT   20732      G     TA
                                CCCATT TACCTA  TGTATT
                                |||||| ||||||  ||||||
                                GGGTAA ATGGAT  ACATGA
                                   A     __
GAM755  STIP-1   3'  CTATACATTTTTATATGTATTG 20733      C_____
           T                     TTGTAC    TATATGTATTGT
                                ||||||    ||||||||||||
                                GATATG    ATATACATAACA
                                   TAAAA
GAM755  LOC221576 3'  CCCATTGTGCTGTGCCCTGC   20734       AC  ATA   A
                                CCCATTGT  CT   TGT TTGT
                                ||||||||  ||   ||| ||||
                                GGGTAACA  GA   ACG GACG
                                     C_  C__   G
GAM755  LOC257515 3'  CCCATTGTGCTGTGCCCTGC   20734       AC  ATA   A
                                CCCATTGT  CT   TGT TTGT
                                ||||||||  ||   ||| ||||
                                GGGTAACA  GA   ACG GACG
                                     C_  C__   G
GAM755  LOC257572 3'  CCCATTGTGCTGTGCCCTGC   20734       AC  ATA   A
                                CCCATTGT  CT   TGT TTGT
                                ||||||||  ||   ||| ||||
                                GGGTAACA  GA   ACG GACG
                                     C_  C__   G
GAM756  EPB41L2  3'  TATACATAGGGTCAAAGGCAAA 20737        CTAG    A
           G                     TATACGTAGG    GAAG CAAAG
                                ||||||||||    |||| |||||
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                                ATATGTATCC    TTTC GTTTC
                                      CAG_    C
GAM756  SRI      3'  TATACATATTACCGAAGGCAAA 20738        G_   AG    A
              G                  TATACGTA  GCT  GAAG CAAAG
                                 ||||||||  |||  |||| |||||
                                 ATATGTAT  TGG  CTTC GTTTC
                                     AA  __    C
GAM756  C1QTNF7   3'  GTATGGCAGGAAGATGAA    20739     _  T      CA
                                 GTA GGC AGGAAGA  AA
                                 ||| ||| |||||||  ||
                                 CAT CCG TCCTTCT  TT
                                   A  _      AC
GAM756  DKFZP434B205 3'  TGACGTCCAGGAAGATGAA    20740    T    AGG       CA
                                 A ACGT   CTAGGAAGA  AA
                                 | ||||   |||||||||  ||
                                 A TGCA   GGTCCTTCT  TT
                                  C   ___        AC
GAM756  DKFZp566D133 3'  CATAATTATCTAGGAAGGTAAA 20741      GG___       AC
              G                   CGTA    CTAGGAAG  AAAG
                                  ||||    ||||||||  ||||
                                  GTAT    GATCCTTC  TTTC
                                    TAATA       CA
GAM756  FLJ10352  3'  GTAGTGTAGAAAGATAAA    20742      GC       C
                                 GTAG  TAGGAAGA AAA
                                 ||||  |||||||| |||
                                 CATC  ATCTTTCT TTT
                                   AC       A
GAM756  KIAA0553  3'  GCCCCTAGGAAGGCAAAG    20743    AGG       A
                                 GT   CTAGGAAG CAAAG
                                 ||   |||||||| |||||
                                 CG   GATCCTTC GTTTC
                                  GG_       C
GAM756  MYH10     3'  TATGCATAGGCTGGAGA     20744     A       A   A
                                 TAT CGTAGGCT GGA GA
                                 ||| |||||||| ||| ||
                                 ATA GTATCCGA CCT CT
                                   C       _  _
GAM756  SLC12A8   5'  CGCCCAGGAGGAAGACGAAG   20745     __   CT       A
                                 CGT  AGG  AGGAAGAC AAG
                                 |||  |||  |||||||| |||
                                 GCG  TCC  TCCTTCTG TTC
                                   GG  __       C
GAM756  LOC253959 3'  CATAATTATCTAGGAAGGTAAA 20741      GG___       AC
              G                   CGTA    CTAGGAAG  AAAG
                                  ||||    ||||||||  ||||
                                  GTAT    GATCCTTC  TTTC
                                    TAATA       CA
GAM757  ARD1      5'  GCGCTCCGAAGCGACGCC    20748          AAA
                                 GCGCTCCGAA   CGACGCC
                                 ||||||||||   |||||||
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                                CGCGAGGCTT  GCTGCGG
                                      C__
GAM757  CACNA1C  3'  GCGCCCCGGGACCCTCGCCGCC 20749        AAAAACGA
                                GCGCTCCG      CGCCGCC
                                ||||||||      |||||||
                                CGCGGGGC      GCGGCGG
                                    CCTGGGA_
GAM757  CALCB    3'  GCTCCGAAAGAACCA      20750        AAC  C
                                GCTCCGAAA  GA GCCG
                                |||||||||  || ||||
                                CGAGGCTTT  CT TGGT
                                     ___ _
GAM757  CDC34    5'  GCGCTCCAGCAGCTCTGGCGCC 20751        AAAAACGA__
           GCC                    GCGCTCCG       CGCCGCC
                                ||||||||       |||||||
                                CGCGAGGT       GCGGCGG
                                    CGTCGAGACC
GAM757  CNTNAP2  5'  GCGCTCCAAGAGCTCGC    20752        AAAAC  C  _
                                GCGCTCCGA    GA GC CGC
                                |||||||||    || || |||
                                CGCGAGGTT    CT CG GCG
                                     _____ _  A
GAM757  EP300    5'  GCGCTCCGCGCCGCCGC    20753        AAAAA  A
                                GCGCTCCG    CG CGCCGC
                                ||||||||    || ||||||
                                CGCGAGGC    GC GCGGCG
                                     _____ G
GAM757  IGJ      5'  GCGCTCCGGCGCCATGGCCGC  20754        AAAAA  AC
                                GCGCTCCG    CG  GCCGC
                                ||||||||    ||  |||||
                                CGCGAGGC    GT  CGGCG
                                    CGCG_  AC
GAM757  IRS2     5'  GCGCTCCGGGAAGCCGGGGTGC 20755        A_  AA  A____
           GCC                    GCGCTCCG  AA  CG    CGCC
                                ||||||||  ||  ||    ||||
                                CGCGAGGC  TT  GC    GCGG
                                    CC  CG  CCCAC
GAM757  M11S1    5'  GCGCTCCGTGGGCGCAGGCCGC 20756        AAAAA  AC_
                                GCGCTCCG    CG   GCCGC
                                ||||||||    ||   |||||
                                CGCGAGGC    GC   CGGCG
                                    ACCC_  GTC
GAM757  RTN2     5'  GCGCCCACGACGCCG      20757       CGAAAA
                                GCGCTC     ACGACGCCG
                                ||||||     |||||||||
                                CGCGGG     TGCTGCGGC
                                     _______
GAM757  TCN2     5'  CGCTCCGAGAGACGCAGC    20758        AAAAC    C
                                CGCTCCGA    GACGC GC
                                ||||||||    ||||| ||
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                                GCGAGGCT    CTGCG CG
                                    CT___    T
GAM757  ZNF198   5'  GCGCTCCGCGGAACGAACC   20759       AAA    C
                                GCGCTCCG   AACGA GCC
                                ||||||||   ||||| |||
                                CGCGAGGC   TTGCT TGG
                                    GCC    _
GAM757  ARHU     5'  GCGCTCCGGCGGCGCCAGCC   20760       AAAAA  A   _
                                GCGCTCCG    CG CGCC GCC
                                ||||||||    || |||| |||
                                CGCGAGGC    GC GCGG CGG
                                    C____  C    T
GAM757  BRI3     3'  ACGCTCCGGGAAACCGCAGC   20761       AA   GA   C
                                GCGCTCCG  AAAC  CGC GC
                                ||||||||  ||||  ||| ||
                                TGCGAGGC  TTTG  GCG CG
                                    CC    __   T
GAM757  CECR7    5'  CGCTCTGACCACGCCGC     20762      C  AAAA G
                                CGCTC GA    C ACGCCGC
                                ||||| ||    | |||||||
                                GCGAG CT    G TGCGGCG
                                   A  ____ G
GAM757  Dlc2     5'  GCGCTCCGCCTCGCGCCGCC   20763       AAAAA  A
                                GCGCTCCG    CG CGCCGCC
                                ||||||||    || |||||||
                                CGCGAGGC    GC GCGGCGG
                                    GGA__  _
GAM757  FKBP5    5'  GCGCGCCGGACACCGCC     20764      T  AAAAAC
                                GCGC CCG     GACGCCGCC
                                |||| |||     |||||||||
                                CGCG GGC     CTGTGGCGG
                                  C  _______
GAM757  FLJ14681 5'  GCGCTCCGAGACGCCTGC    20765       AAAAC    _
                                GCGCTCCGA    GACGCC GC
                                |||||||||    |||||| ||
                                CGCGAGGCT    CTGCGG CG
                                    _____     A
GAM757  FLJ20464 5'  GCTCCGAAGGGTGGACGACGCC 20766       AA____
                                GCTCCGAA     ACGACGCC
                                ||||||||     ||||||||
                                CGAGGCTT     TGCTGCGG
                                    CCCACC
GAM757  FLJ22408 5'  GCGCTCCGGGACCACGGCGGCG 20767       AAAA_  A___  C
           CTGCC                GCGCTCCG    ACG   CGC GCC
                                ||||||||    |||   ||| |||
                                CGCGAGGC    TGC   GCG CGG
                                    CCTGG   CGCC  A
GAM757  HSA6591  5'  GCGCTCCGGGCAAACCTCGC  20768       AA_   GA
                                GCGCTCCG   AAAC  CGC
                                ||||||||   ||||  |||
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                                CGCGAGGC  TTTG  GCG
                                    CCG   GA
GAM757  HTCD37   5'  GCGCTCCGGAGTCCGGCGTCGC 20769       AAAAA  A  C
            C                    GCGCTCCG    CG CG CGCC
                                 ||||||||    || || ||||
                                 CGCGAGGC    GC GC GCGG
                                    CTCAG  C  A
GAM757  KIAA0014 3'  GCCTCCAACGCCGGCGGCGCTG 20770   G    AAAA__  A  C
            CC                    GC CTCCGA    CG CGC GCC
                                  || ||||||    || ||| |||
                                  CG GAGGTT    GC GCG CGG
                                   _    GCGGCC  C   A
GAM757  KIAA1893  5'  GCGCTCCGGCTCCCGCCGCC  20771       AAAAACGA
                                 GCGCTCCG      CGCCGCC
                                 ||||||||      |||||||
                                 CGCGAGGC      GCGGCGG
                                    CGAGG___
GAM757  MGC12945  5'  GCGCTCCGGGACGACGGCGACG 20772       AAAA    _ __
            CC                    GCGCTCCG   ACGACG C  CGCC
                                  ||||||||   |||||| |  ||||
                                  CGCGAGGC   TGCTGC G  GCGG
                                    CC__     C CT
GAM757  MGC5395   3'  GCTCCGAAAAGCCGC      20773         ACGAC
                                 GCTCCGAAAA    GCCGC
                                 ||||||||||    |||||
                                 CGAGGCTTTT    CGGCG
                                       _____
GAM757  PCYT2    5'  GCGACTCCGAACGCCGC    20774    _    AAAACG
                                 GCG CTCCGA    ACGCCGC
                                 ||| ||||||    |||||||
                                 CGC GAGGCT    TGCGGCG
                                   T    _______
GAM757  PTR4     5'  GCCCTCCATGCGACGCCGCC  20775   G    AAAAA
                                 GC CTCCG    CGACGCCGCC
                                 || |||||    ||||||||||
                                 CG GAGGT    GCTGCGGCGG
                                  G    AC___
GAM757  RAB32    5'  GCGCCCGCTGACGCCGC    20776    T  AAAAAC
                                 GCGC CCG    GACGCCGC
                                 |||| |||    ||||||||
                                 CGCG GGC    CTGCGGCG
                                   _   GA____
GAM757  SLC26A6  5'  ACGCTCCGGAAGGCGGCGCCG  20777       A  AA  A
                                 GCGCTCCG AA  CG CGCCG
                                 |||||||| ||  || |||||
                                 TGCGAGGC TT  GC GCGGC
                                    C  CC  C
GAM757  SLC26A6  5'  ACGCTCCGGAAGGCGGCGCCG  20777       A  AA  A
                                 GCGCTCCG AA  CG CGCCG
                                 |||||||| ||  || |||||
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                                TGCGAGGC TT  GC GCGGC
                                    C  CC  C
GAM757  SLC26A6   5'  ACGCTCCGGAAGGCGGCGCCG  20777        A  AA  A
                                GCGCTCCG AA  CG CGCCG
                                |||||||| ||  || |||||
                                TGCGAGGC TT  GC GCGGC
                                    C  CC  C
GAM757  TIGA1     5'  GCGCTATGGCGAGACGCCGCC  20778      C___  AAAAC
                                GCGCT   CGA    GACGCCGCC
                                |||||   |||    |||||||||
                                CGCGA   GCT    CTGCGGCGG
                                  TACC  _____
GAM757  TRAP95    3'  GCACTCCACGATGCTGC     20779       GAAAA   C  C
                                GCGCTCC    ACGA GC GC
                                |||||||    |||| || ||
                                CGTGAGG    TGCT CG CG
                                   _____   A  A
GAM757  LOC115110 3'  GCCTCCGAAAAGGCCG      20780    G       ACGAC
                                GC CTCCGAAAA    GCCG
                                || |||||||||    ||||
                                CG GAGGCTTTT    CGGC
                                 _       C____
GAM757  LOC138050 5'  GCGCCCCGAAGAGCCGC     20781         AAAC  C
                                GCGCTCCGAA   GA GCCGC
                                ||||||||||   || |||||
                                CGCGGGGCTT   CT CGGCG
                                     ____ _
GAM757  LOC147965 5'  GCGCCCCGCGACGCCGC     20782        AAAAA
                                GCGCTCCG    CGACGCCGC
                                ||||||||    |||||||||
                                CGCGGGGC    GCTGCGGCG
                                     _____
GAM757  LOC148753 5'  GCGCTCCGAGGACTGCC     20783        AAAAC  _
                                GCGCTCCGA    GAC GCC
                                |||||||||    ||| |||
                                CGCGAGGCT    CTG CGG
                                     C____   A
GAM757  LOC253070 5'  GCGCTCCAAAGACACCGTGCC  20784         AAAC    __
                                GCGCTCCGAA   GACGCC  GCC
                                ||||||||||   ||||||  |||
                                CGCGAGGTTT   CTGTGG  CGG
                                     ____    CA
GAM757  LOC255718 5'  GCGCTCCACCCCCGCGGCGTCG 20785       AAAAA_  A  C
          CC                   GCGCTCCG     CG CG CGCC
                               ||||||||     || || ||||
                               CGCGAGGT     GC GC GCGG
                                    GGGGGC  C  A
GAM757  LOC51659  5'  GCGTCCCGGGAGGAGACGCCGC 20786    CT   AAAAAC
          C                    GCG  CCG     GACGCCGCC
                               |||  |||     |||||||||
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                                CGC  GGC     CTGCGGCGG
                                  AG   CCTCCT
GAM757  LOC90378  5'  GCGCTCCGAGACGGGTGCGC   20787        AAAAC   C___
                                GCGCTCCGA    GACG    CGC
                                |||||||||    ||||    |||
                                CGCGAGGCT    CTGC    GCG
                                      _____   CCAC
GAM757  LOC90835  5'  GCGCCCCGGGCTCCCGCCGCC  20788        AAAAACGA
                                GCGCTCCG       CGCCGCC
                                ||||||||       |||||||
                                CGCGGGGC       GCGGCGG
                                     CCGAGG__
GAM757  LOC91960  5'  GCCTCCGGGTCCTAACGCCGCC 20789    G    AAAAAC
                                GC CTCCG     GACGCCGCC
                                || |||||     |||||||||
                                CG GAGGC     TTGCGGCGG
                                 _    CCAGGA
GAM758  C15orf5   3'  TTTCCTGTTGTGCTCTAGTGT  20792     G   AACG  CAC
                                TTT CTG    GC   TCTAGTGT
                                ||| |||    ||   ||||||||
                                AAA GAC    CG   AGATCACA
                                  G   AACA  ___
GAM758  DKFZP434K028 3'  TTTGCTCAGTGACCTAGTG    20793       GAA   CC  T
                                TTTGCT   CGG  AC CTAGTG
                                ||||||   |||  || ||||||
                                AAACGA   GTC  TG GATCAC
                                   ___   AC  _
GAM758  FLJ20419  3'  TTTGCTGAGGGGCCATGGCCAG 20794        AC    CT_   T
           GT                    TTTGCTGA  GGCCA   CTAG GT
                                ||||||||  |||||   |||| ||
                                AAACGACT  CCGGT   GGTC CA
                                     CC    ACC   _
GAM758  LOC199964 3'  TTTGCTGAGTGCCTACTGTGT  20795        ACG  _  CTA
                                TTTGCTGA   GCC ACT   GTGT
                                ||||||||   ||| |||   ||||
                                AAACGACT   CGG TGA   CACA
                                     CA_   A   ___
GAM759  CACNA2D2  3'  GAGTGTGTAAGGGCCAGA    20798    T      AACA
                                GA GTGTGTAA    CCGGA
                                || ||||||||    |||||
                                CT CACACATT    GGTCT
                                 _       CCC_
GAM759  CD1B     3'  AATGTGTGTAAAATCAGG    20799           _ CC
                                GATGTGTGTAAAA CA  GG
                                |||||||||||| ||  ||
                                TTACACACATTTT GT  CC
                                        A  __
GAM759  FMR1     3'  GATGTGTGCAAGGTACCAA   20800          AAC
                                GATGTGTGTAA   ACCGG
                                ||||||||||   |||||
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                                CTACACACGTT   TGGTT
                                      CCA
GAM759  KPNA1    3'  GATGTGTGTAAGAGA      20801         AAACACC
                                GATGTGTGTA      GGAGA
                                ||||||||||      |||||
                                CTACACACAT      TCTCT
                                      _______
GAM759  LARS2    3'  CGCTGTGGCTTGGACACCGGAG 20802    A    T  AAA_
                                CG TGTG GT    ACACCGGAG
                                || |||| ||    |||||||||
                                GC ACAC CG    TGTGGCCTC
                                 G    _  AACC
GAM759  OGT      3'  TGTGTTTAAAACACCCTAGGA  20803      G       ___
                                TGTGT TAAAACACC   GGA
                                ||||| |||||||||   |||
                                ACACA ATTTTGTGG   CCT
                                   A        GAT
GAM759  PTEN     3'  TGTGTGTAAATAGCTGGAGA   20804         ACACC
                                TGTGTGTAAA    GGAGA
                                ||||||||||    |||||
                                ACACACATTT    CCTCT
                                      ATCGA
GAM759  RET      3'  GATGTGGTGGGCCCGGGGGAC  20805       T  AAAACA   A_
                                GATGTG GT     CCGG  GAC
                                |||||| ||     ||||  |||
                                CTACAC CA     GGCC  CTG
                                   _  CCCG__    CC
GAM759  RET      3'  GATGTGGTGGGCCCGGGGGAC  20805       T  AAAACA   A_
                                GATGTG GT     CCGG  GAC
                                |||||| ||     ||||  |||
                                CTACAC CA     GGCC  CTG
                                   _  CCCG__    CC
GAM759  RFP      3'  GAAAGTATGAAACACTGGAG   20806    T_    TA     C
                                GA  GTGTG  AAACAC GGAG
                                ||  |||||  |||||| ||||
                                CT  CATAC  TTTGTG CCTC
                                 TT     __      A
GAM759  THBD     3'  TGTGCAAAGTGGATACTGGAGA 20807        AC_____  C
           C                     TGTGTAAA     AC GGAGAC
                                 ||||||||     || ||||||
                                 ACACGTTT     TG CCTCTG
                                      CACCTA  A
GAM759  ARHGAP5  3'  ATGTGTGTAAAAGAAA      20808         ACACC
                                ATGTGTGTAAA    GGAGA
                                ||||||||||     |||||
                                TACACACATTT    TCTTT
                                      ______
GAM759  C20orf97 3'  ATGTGTGTGGAACAAAGCAGA  20809        AA   C__
                                ATGTGTGT  AACA   CGGA
                                ||||||||  ||||   ||||
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                                TACACACA  TTGT   GTCT
                                     CC    TTC
GAM759  CSEN     3'  CGAGGTGGGCTCACACCGGAGA 20810     T   T  AAA
                                CGA GTG GT   ACACCGGAGA
                                ||| ||| ||   ||||||||||
                                GCT CAC CG   TGTGGCCTCT
                                  C   C  AG_
GAM759  KIAA1010 3'  TGTGTGCTGGACACTGGAG   20811       AAA   C
                                TGTGTGT   ACAC GGAG
                                |||||||   |||| ||||
                                ACACACG   TGTG CCTC
                                     ACC    A
GAM759  KIAA1795 3'  GAGTGTGTAACAAAGGAG    20812    T     AA   CC
                                GA GTGTGTA  ACA  GGAG
                                || |||||||  |||  ||||
                                CT CACACAT  TGT  CCTC
                                 _      __   TT
GAM759  KIAA1881 3'  TGTGTGCTAAGGCCGGAGAC   20813       A  ACA
                                TGTGTGT AA   CCGGAGAC
                                ||||||| ||   ||||||||
                                ACACACG TT   GGCCTCTG
                                     A  CC_
GAM759  NDRG4    3'  GATGTGTGTAGAGGAAA     20814         AAACACC
                                GATGTGTGTA      GGAGA
                                ||||||||||      |||||
                                CTACACACAT      CCTTT
                                      CT_____
GAM759  NDRG4    3'  GATGTGTGTAGAGGAAA     20814         AAACACC
                                GATGTGTGTA      GGAGA
                                ||||||||||      |||||
                                CTACACACAT      CCTTT
                                      CT_____
GAM759  NUDEL    3'  GATCATGAGCACTGGAGA    20815     G   TAAAA  C
                                GAT TGTG    CAC GGAGA
                                ||| ||||    ||| |||||
                                CTA GTAC    GTG CCTCT
                                  _   TC___   A
GAM759  PSMD10   3'  GTTTGTAGGACACTGGGGAC  20816    G   AA   C  A
                                GT TGTA  ACAC GG GAC
                                || ||||  |||| || |||
                                CA ACAT  TGTG CC CTG
                                 A   CC   A  C
GAM759  PSR      3'  ATGTGTGTGAAGCATGGA    20817        A  A  CC
                                ATGTGTGT AA CA  GGA
                                |||||||| || ||  |||
                                TACACACA TT GT  CCT
                                     C  C  A_
GAM759  UCK1     3'  TGTGTGTAAGAACCAGA     20818         AAC
                                TGTGTGTAA   ACCGGA
                                |||||||||   ||||||
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                                ACACACATT   TGGTCT
                                     CT_
GAM759   LOC127003 5'  GTGTGCAACATCGGAGA     20819        AA   C
                                GTGTGTA  ACA CGGAGA
                                |||||||  ||| ||||||
                                CACACGT  TGT GCCTCT
                                   __   A
GAM759   LOC149483 3'  GATGTGCTGGACACCGGAG    20820        GTAAA
                                GATGTGT    ACACCGGAG
                                |||||||    |||||||||
                                CTACACG    TGTGGCCTC
                                   ACC__
GAM759   LOC157869 5'  TGTGTGTAGACCAGTGTGGAGA 20821         AAAC  _____
            C                    TGTGTGTA   ACC    GGAGAC
                                |||||||   |||    ||||||
                                ACACACAT   TGG    CCTCTG
                                     C___   TCACA
GAM759   LOC255714 5'  GATGTGTGTAAGGTAGA     20822          AACACC  _
                                GATGTGTGTAA     GG AGA
                                ||||||||||     || |||
                                CTACACACATT     CC TCT
                                      _______ A
GAM760   PRKY     3'  AGACAAGGGTTTCATCATG    20825         GC   C
                                AGACAAGGGT  CATT TG
                                |||||||||  |||| ||
                                TCTGTTCCCA  GTAG AC
                                     AA   T
GAM760   TRIM9    3'  AGCAAGGGCCTTCTGCGTT    20826    A    GT   A
                                AG CAAGG  GCC TTCTGCGTT
                                || |||||  ||| |||||||||
                                TC GTTCC  CGG AAGACGCAA
                                 _    __  _
GAM760   FLJ20546  3'  AGACGGGGGTTTCTCCACGTTG 20827     AA   GCCA   TG
                                AGAC  GGGT   TTC  CGTTG
                                ||||  ||||   |||  |||||
                                TCTG  CCCA   GAG  GCAAC
                                  CC   AA__   GT
GAM760   KIAA0211  5'  AAACAAGGGTGTGGCGAGCGTT 20828          CCATTCT
            G                    AGACAAGGGTG      GCGTTG
                                ||||||||||      ||||||
                                TTTGTTCCCAC      CGCAAC
                                     ACCGCT_
GAM760   MGC10715  3'  AGACAAGGGTGCTTTCCCCTG  20829          CA__
                                AGACAAGGGTGC    TTCTG
                                ||||||||||||    |||||
                                TCTGTTCCCACG    GGGAC
                                     AAAG
GAM760   VMP1     3'  AGGCAAGGCTGCCATTCAGC   20830    A    G      T
                                AG CAAGG TGCCATTC GC
                                || ||||| |||||||| ||
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                                TC GTTCC ACGGTAAG CG
                                 C    G      T
GAM760  LOC89958  3'  AGATGGGGGTCTCTCACTGCGT 20831    CAA   GCCATT
           TG                    AGA  GGGT    CTGCGTTG
                                 |||  ||||    ||||||||
                                 TCT  CCCA    GACGCAAC
                                  ACC   GAGAGT
GAM761  CAV3    3'  AAGGGCCATTGTGCTTCTGTGG 20834    A  _  ATACGA
           C                     AAG GCC TTG    TCTGTGGC
                                 ||| ||| |||    ||||||||
                                 TTC CGG AAC    AGACACCG
                                  C  T  ACGA__
GAM761  ELK3    5'  AGGCGTCTGCAGACGGTCTGTG 20835   A  C_  AT_  A
           GC                    AG GC  TTG  ACG TCTGTGGC
                                 || ||  |||  ||| ||||||||
                                 TC CG  GAC  TGC AGACACCG
                                  _ CA  GTC  C
GAM761  FCGR2B  3'  AAGAGCCTTGATGTCAAGAAGA 20836          ACGATCTGT
           GC                    AAGAGCCTTGAT       GGC
                                 ||||||||||||       |||
                                 TTCTCGGAACTA       TCG
                                       CAGTTCTTC
GAM761  LIG4    5'  AAGAGTCTGTGACATCTTTGTG 20837      C  _   CGATC
           G                     AAGAG CT TGATA    TGTGG
                                 ||||| || |||||    |||||
                                 TTCTC GA ACTGT    ACACC
                                   A  C    AGAA_
GAM761  PPP2R5E  5'  AAGAATCCGAAGATGATCTGTG 20838      _  TT_  AC
           GC                    AAGAG CC  GAT  GATCTGTGGC
                                 ||||| ||  |||  ||||||||||
                                 TTCTT GG  CTA  CTAGACACCG
                                   A  CTT  __
GAM761  RGS2    3'  AACAGTACTGATGATCTGTGG  20839   G  CC   AC
                                 AA AG  TTGAT  GATCTGTGG
                                 || ||  |||||  |||||||||
                                 TT TC  GACTA  CTAGACACC
                                  G  AT   __
GAM761  SLC7A7  5'  AAGTGCCTTCCAGGATCTGTGG 20840    A   GA  C
                                 AAG GCCTT  TA GATCTGTGG
                                 ||| |||||  || |||||||||
                                 TTC CGGAA  GT CTAGACACC
                                  A   G_  C
GAM761  CHST3   3'  AAGAGCCTTGGATGGAGGTGGC 20841        ATAC  TCT
                                 AAGAGCCTTG   GA  GTGGC
                                 ||||||||||   ||  |||||
                                 TTCTCGGAAC   CT  CACCG
                                       CTAC  C__
GAM761  DKFZP434F1735 5'  AGGGCCTGGGACCTGTGG   20842   A   T ATAC
                                 AG GCCT G   GATCTGTGG
                                 || |||| |   |||||||||
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                                TC CGGA C    CTGGACACC
                                 C    _ C___
GAM761  FLJ10876  3'  AAGAGCCTTGACTATGAAGAGG 20843          AC_  TCTGT
           C                     AAGAGCCTTGAT   GA    GGC
                                 ||||||||||||  ||    |||
                                 TTCTCGGAACTG   CT    CCG
                                       ATA  TCT__
GAM761  FLJ13769  3'  GCCTAAGCGATCTGTGGC    20844     TGATA
                                 GCCT    CGATCTGTGGC
                                 ||||    ||||||||||||
                                 CGGA    GCTAGACACCG
                                   TTC__
GAM761  FLJ14154  3'  AAGAGCCTTTGTGTCTGCTGTG 20845        GATACGAT
           GC                    AAGAGCCTT       CTGTGGC
                                 |||||||||       |||||||
                                 TTCTCGGAA       GACACCG
                                      ACACAGAC
GAM761  FLJ22029  3'  AAAAGCCTTGATGCTG      20846          TACGATC  _
                                 AAGAGCCTTGA      TG TG
                                 ||||||||||||      || ||
                                 TTTTCGGAACT      AC AC
                                       ________  G
GAM761  KRTAP4-12 3'  GAGGCTTTAAGATCTGTGGC   20847     C   GATAC
                                 GAG CTT     GATCTGTGGC
                                 ||| |||     ||||||||||
                                 CTC GAA     CTAGACACCG
                                   C   ATT__
GAM761  MGC20253  3'  AGAGCCTTGGGACGGCAGGGAT 20848         AT   ATCT__
           GGC                     AGAGCCTTG  ACG     GTGGC
                                 |||||||||  |||     |||||
                                 TCTCGGAAC  TGC     TACCG
                                      CC   CGTCCC
GAM761  PDE8A     3'  AAGTGCTTTGTCATTTCTGTGG 20849     A  C   A  CGA
           C                      AAG GC TTG TA   TCTGTGGC
                                 ||| || ||| ||   ||||||||
                                 TTC CG AAC GT   AGACACCG
                                   A  A   A  AA_
GAM761  SEZ6      3'  GAGCCTTGCTGCTGGACTGTGG 20850        ATAC__  T
                                 GAGCCTTG     GA CTGTGG
                                 ||||||||     || ||||||
                                 CTCGGAAC     CT GACACC
                                      GACGAC  _
GAM761  LOC143915 3'  AGGGCTTTGGTATCTGTGG    20851    A  C   ATACG
                                 AG GC TTG     ATCTGTGG
                                 || || |||     ||||||||
                                 TC CG AAC     TAGACACC
                                  C  A   CA___
GAM761  LOC145371 3'  GAGCTTTGATACGAAACGC    20852      C        TC
                                 GAGC TTGATACGA  TGT
                                 |||| |||||||||  |||
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                                CTCG AACTATGCT  GCG
                                  A       TT
GAM761  LOC146733 3'  AGAGCCTTGACTGCGG     20853         TACGAT
                                AGAGCCTTGA    CTGTGG
                                ||||||||||    ||||||
                                TCTCGGAACT    GACGCC
                                      _______
GAM761  LOC157556 5'  GAGCCTTGGAGTGCAGGGC   20854       ATAC  TC  __
                                GAGCCTTG   GA  TGT  GGC
                                ||||||||   ||  |||  |||
                                CTCGGAAC   CT  ACG  CCG
                                     _____ C_   TC
GAM761  LOC196746 3'  GCCTTGATAACGGCCGGGC   20855        _ AT   T
                                GCCTTGATA CG  CTG GGC
                                ||||||||| ||  ||| |||
                                CGGAACTAT GC  GGC CCG
                                     T  C_   _
GAM761  LOC255012 5'  GAGCCTTGGAGCTCTGG     20856       ATAC  T  G
                                GAGCCTTG   GA CT TGG
                                ||||||||   || || |||
                                CTCGGAAC   CT GA ACC
                                     _____ C  G
GAM762  DSG2    3'  CTGTGTGTCTGTAAGGCTCA   20859     T  A  GC_
                                CTGT GT TC   AAGGCTCA
                                |||| || ||   ||||||||
                                GACA CA AG   TTCCGAGT
                                  _  C  ACA
GAM762  KRTHA7   5'  TACCTGTTGTGGTGCCATCA   20860        ATC  AAGGC
                                TACCTGTTGT   GC    TCA
                                ||||||||||   ||    |||
                                ATGGACAACA   CG    AGT
                                     CCA  GT___
GAM762  KRTHA8   5'  TACCTGTTGTGGTGCCATCA   20860        ATC  AAGGC
                                TACCTGTTGT   GC    TCA
                                ||||||||||   ||    |||
                                ATGGACAACA   CG    AGT
                                     CCA  GT___
GAM762  CALN1    3'  TACCTGTTCTGTTGGCTAAACT 20861       __  ATC  A
           CA                     TACCTGT  TGT   GC AGGCTCA
                                ||||||| |||   || |||||||
                                ATGGACA  ACA   CG TTTGAGT
                                   AG   AC_  A
GAM762  CD109    3'  TGTTGTATCCCTGGCTCAC   20862        GCAA
                                TGTTGTATC    GGCTCAC
                                |||||||||    |||||||
                                ACAACATAG    CCGAGTG
                                     GGA_
GAM762  DKFZP564D0764 3'  TACCTGTCACATTGCAAGGCT  20863       TG   C
                                TACCTGT  TAT GCAAGGCT
                                |||||||  ||| ||||||||
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                                ATGGACA  GTA CGTTCCGA
                                    GT   A
GAM762  ISL2     3'  TTGTTCGGCAAAGGCTCAC   20864      A  _  _
                                TTGT TCG CAA GGCTCAC
                                |||| ||| ||| |||||||
                                AACA AGC GTT CCGAGTG
                                  _  C   T
GAM762  LOC151121 5'  CCTGTTGTATTGTACACTTCA  20865          C__  AGGC
                                CCTGTTGTAT   GCA   TCA
                                ||||||||||   |||   |||
                                GGACAACATA   TGT   AGT
                                     ACA   GA__
GAM762  LOC153876 3'  TACCTGTTGAGTGACAGGCT   20866         TATC   A
                                TACCTGTTG    GCA GGCT
                                |||||||||    ||| ||||
                                ATGGACAAC    TGT CCGA
                                     TCAC   _
GAM762  LOC157931 3'  CCTTCCTTAGTCGCAAGGCT   20867     GTTG  _
                                CCT    TA TCGCAAGGCT
                                |||    || ||||||||||
                                GGA    AT AGCGTTCCGA
                                  AGGA  C
GAM762  LOC158088 3'  CCTTGTTGTATCATACAGCTC  20868      _       CAA
                                CCT GTTGTATCG   GGCTC
                                ||| |||||||||   |||||
                                GGA CAACATAGT   TCGAG
                                  A       ATG
GAM763  ADCY8    5'  CGGACAAAGCCTGCGGC     20871        AACC   CC   A
                                CGGACAA    AGTT  CGG C
                                |||||||    ||||  ||| |
                                GCCTGTT    TCGG  GCC G
                                    ____    AC   _
GAM763  CTBP2    5'  GATGAAACCCTCGTCCCGGACG 20872    CA    AGT_
                                GA  AAACC    TCCCGGACG
                                ||  |||||    |||||||||
                                CT  TTTGG    AGGGCCTGC
                                 AC    GAGC
GAM763  DDC      3'  CAGACAAAATCACAACCCTCTG 20873         C  GTT  ___
           GA                     CGGACAAAA CA   CCC   GGA
                                |||||||| ||   |||   |||
                                GTCTGTTTT GT   GGG   CCT
                                     A  GTT   AGA
GAM763  KCNK4    5'  CGGGCAAAACCAGGGA      20874     A       TTCCC
                                CGG CAAAACCAG     GGA
                                ||| |||||||||     |||
                                GCC GTTTTGGTC     CCT
                                  C       _____
GAM763  PRIM2A   5'  GGCAGCCAGCTGTTCCCGG    20875    A  AAA    ___
                                GG CA   CCAGT   TCCCGG
                                || ||   |||||   ||||||
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                                CC GT   GGTCG   AGGGCC
                                 _ C__     ACA
GAM763  DKFZp547H025 3'  GGGTAAGACCAGTTCAGAGA   20876    AC  A      CC
                                GG  AA ACCAGTTC  GGA
                                ||  || ||||||||  |||
                                CC  TT TGGTCAAG  TCT
                                 CA  C       TC
GAM763  DKFZp761G2113 3'  GGACAAACCAGTTCCCAA    20877        A
                                GGACAAA CCAGTTCCCGG
                                ||||||| ||||||||||
                                CCTGTTT GGTCAAGGGTT
                                      _
GAM763  FLJ10038  5'  CGGACAAAGCGCAGCGGC    20878        AC_   TTCC   A
                                CGGACAAA   CAG    CGG C
                                ||||||||   |||    ||| |
                                GCCTGTTT   GTC    GCC G
                                     CGC   ____   _
GAM763  KIAA0678  3'  GGACAAAACCTAATAGTCTTGG 20879          ____    CCC
           A                     GGACAAAACC    AGTT   GGA
                                ||||||||||    ||||   |||
                                CCTGTTTTGG    TCAG   CCT
                                      ATTA    AA_
GAM763  KIAA1260  3'  ACAGACGAAACCAACATGGA   20880       A      TTCCC
                                ACGGAC AAACCAG     GGA
                                |||||| |||||||     |||
                                TGTCTG TTTGGTT     CCT
                                   C      GTA__
GAM763  OAZ1      3'  CGGACAAACCCAGGCGA     20881         A    TTCC
                                CGGACAAA CCAG    CGG
                                |||||||| ||||    |||
                                GCCTGTTT GGTC    GCT
                                     G    C___
GAM763  TSPAN-1   5'  GGACAAAACAGCTCCCGG    20882          C
                                GGACAAAAC AGTTCCCGG
                                ||||||||| |||||||||
                                CCTGTTTTG TCGAGGGCC
                                      _
GAM763  LOC115110 3'  ACGGACGGGACCAGCTCCC    20883        AAA
                                ACGGAC   ACCAGTTCCC
                                ||||||   ||||||||||
                                TGCCTG   TGGTCGAGGG
                                   CCC
GAM763  LOC200734 3'  ACAGGCAGAACCAGTTGG     20884      A  A      CCC
                                ACGG CA AACCAGTT   GG
                                |||| || ||||||||   ||
                                TGTC GT TTGGTCAA   CC
                                  C  C       ___
GAM763  LOC257153 5'  ACAGGCAAAACCAGGGGCAGGA 20885      A       TTCCC
                                ACGG CAAAACCAG     GGA
                                |||| |||||||||     |||
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                                TGTC GTTTTGGTC    CCT
                                  C       CCCGT
GAM764  HMGA2    5'  TGAGTGTGTGTGAGTGTGTGTG 20889        _ _ CGC
             AGT                    TGAGTGTG GT AG   TGTGTGAGT
                                ||||||||| || ||  |||||||||
                                ACTCACAC CA TC   ACACACTCA
                                    A  C  AC_
GAM764  HMGA2    5'  TGAGTGTGTGTGAGTGTGAGT  20888        GTAGCGCT
                                TGAGTGTG       GTGTGAGT
                                ||||||||       ||||||||
                                ACTCACAC       CACACTCA
                                    ACACT___
GAM764  KCNK7    5'  GAGGAGGTGCTGTGTGG     20890     TGT   AGC       A
                                GAG   GGT   GCTGTGTG G
                                |||   |||   |||||||| |
                                CTC   CCA   CGACACAC C
                                  CT_   ___       C
GAM764  KCNK7    5'  GAGGAGGTGCTGTGTGG     20890     TGT   AGC       A
                                GAG   GGT   GCTGTGTG G
                                |||   |||   |||||||| |
                                CTC   CCA   CGACACAC C
                                  CT_   ___       C
GAM764  KCNK7    5'  GAGGAGGTGCTGTGTGG     20890     TGT   AGC       A
                                GAG   GGT   GCTGTGTG G
                                |||   |||   |||||||| |
                                CTC   CCA   CGACACAC C
                                  CT_   ___       C
GAM764  KCNK7    5'  GAGGAGGTGCTGTGTGG     20890     TGT   AGC       A
                                GAG   GGT   GCTGTGTG G
                                |||   |||   |||||||| |
                                CTC   CCA   CGACACAC C
                                  CT_   ___       C
GAM764  MICB     3'  TGGGTGTGGTGGTGCCTGT    20891     A      A__  G
                                TG GTGTGGT   GC CTGT
                                || |||||||   || ||||
                                AC CACACCA   CG GACA
                                 C      CCA  _
GAM764  MS4A1    3'  TGACTGTGACTGTGTGG     20892     G    GTAGC       A
                                TGA TGTG     GCTGTGTG G
                                ||| ||||     |||||||| |
                                ACT ACAC     TGACACAC C
                                  G    ______       C
GAM764  NPR1     3'  GCGTGTGCCTGTGTGAG     20893       GTA  G
                                GTGTG   GC CTGTGTGAG
                                |||||   || |||||||||
                                CGCAC   CG GACACACTC
                                  A__  _
GAM764  RHD      3'  TGGGTGTGGTAGTGCGCACTTG 20894     A        C  T TG GA
             T                   TG GTGTGGTAG GC G  T  GT
                                || |||||||| || |  |  ||
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                                AC CACACCATC CG C  G  CA
                                 C        A  _ GT AA
GAM764  RHD      3'  TGGGTGTGGTAGTGCGCACTTG 20894    A       C  T TG GA
              T                   TG GTGTGGTAG GC G  T  GT
                                || |||||||| || |  |  ||
                                AC CACACCATC CG C  G  CA
                                 C        A  _ GT AA
GAM764  BTN3A1   3'  TGGGTGTGGTGGCGTGCAC   20895    A      A  C  TG
                                TG GTGTGGT GCG TG  T
                                || ||||||| ||| ||  |
                                AC CACACCA CGC AC  G
                                 C      C  _ GT
GAM764  CARD6    3'  TGGGTGTGGTGGTGCATGCCTG 20896    A      A__  C  G
                                TG GTGTGGT   GCG TGT TG
                                || |||||||   ||| ||| ||
                                AC CACACCA   CGT ACG AC
                                 C      CCA  _  G
GAM764  DKFZP434K028 3'  TGATGCCAGTGCTGTGTGGGT  20897   T  G  C      A
                                G GTG TAG GCTGTGTG GT
                                | ||| ||| |||||||| ||
                                A TAC GTC CGACACAC CA
                                 C  G  A      C
GAM764  FLJ10535  3'  TGGGTGTGGTGGCGTGT     20898    A      A  C
                                TG GTGTGGT GCG TGT
                                || ||||||| ||| |||
                                AC CACACCA CGC ACA
                                 C      C  _
GAM764  FLJ12747  3'  TGGGTGTGGTGGCGCATGCCTG 20899    A      A  _  G
                                TG GTGTGGT GCGC TGT TG
                                || ||||||| |||| ||| ||
                                AC CACACCA CGCG ACG AC
                                 C      C   T  G
GAM764  FLJ23462  3'  TAGTAAGTGCTGTGTGAG    20900      _ C
                                TGGTA G GCTGTGTGAG
                                ||||| | ||||||||||
                                ATCAT C CGACACACTC
                                   T A
GAM764  GNG4     3'  TGGGTGTGGTGGCGCGTGC   20901    A      A  T
                                TG GTGTGGT GCGC GTGT
                                || ||||||| |||| ||||
                                AC CACACCA CGCG CACG
                                 C      C  _
GAM764  MGC1203  3'  TGAGGTGGTAGTGTAAAT    20902     T    GCGCT
                                TGAG GTGGTA    GTGTGAGT
                                |||| ||||||    ||||||||
                                ACTC CACCAT    CACATTTA
                                  _    _____
GAM764  MYRIP    3'  TGAGTGTGCATGTGTGAG    20903       GGTA  C
                                TGAGTGT   GCG TGTGTGAG
                                |||||||   ||| ||||||||
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                                ACTCACA   CGT ACACACTC
                                      ____  _
GAM764  NLI-IF   3'  TGAGTGTGGCGGCGGCCCATGG 20904        TA  _ G   A
            GT                    TGAGTGTGG  GCG CT TGTG GT
                                  |||||||||  ||| || |||| ||
                                  ACTCACACC  CGC GG GTAC CA
                                       GC  C _   C
GAM764  SLC12A8  3'  TGGGTGTGGAAACATGTGAGT  20905   A    T  GCT
                                  TG GTGTGG AGC   GTGTGAGT
                                  || |||||| |||   ||||||||
                                  AC CACACC TTG   TACACTCA
                                   C     T  ___
GAM764  SLC16A4  3'  TGGGTGTGGTGGCGTGT    20898   A     A  C
                                  TG GTGTGGT GCG TGT
                                  || ||||||| ||| |||
                                  AC CACACCA CGC ACA
                                   C      C  _
GAM764  TU12B1-TY 3'  TGGGTGTGGTAGTGCATGCCTG 20906   A       C _  G
                                  TG GTGTGGTAG GC TGT TG
                                  || ||||||||| || ||| ||
                                  AC CACACCATC CG ACG AC
                                   C       A T  G
GAM764  LOC115219 5'  TGGGTGTGGTGGCACGCACCAG 20907   A     A   T TG G
            T                     TG GTGTGGT GCGC G  T AGT
                                  || ||||||| |||| |  | |||
                                  AC CACACCA CGTG C  G TCA
                                   C      C   _ GT G
GAM764  LOC132241 3'  TGGGTGTGGTGGCGCATGCCTG 20899   A     A   _  G
                                  TG GTGTGGT GCGC TGT TG
                                  || ||||||| |||| ||| ||
                                  AC CACACCA CGCG ACG AC
                                   C      C   T  G
GAM764  LOC146346 5'  TGGGTGTGGTGGTGCATGCCTG 20896   A     A__  C  G
                                  TG GTGTGGT   GCG TGT TG
                                  || |||||||  ||| ||| ||
                                  AC CACACCA   CGT ACG AC
                                   C      CCA  _  G
GAM764  LOC147841 3'  TGGGTGTGGTGGCGCATGC   20908   A     A   T
                                  TG GTGTGGT GCGC GTGT
                                  || ||||||| |||| ||||
                                  AC CACACCA CGCG TACG
                                   C      C   _
GAM764  LOC150225 3'  TGGGTGTGGTGGCGTGT    20898   A     A  C
                                  TG GTGTGGT GCG TGT
                                  || ||||||| ||| |||
                                  AC CACACCA CGC ACA
                                   C      C  _
GAM764  LOC151701 3'  TGAGTGTGGTGGTGCATGCCTG 20909         A__  C  G
                                  TGAGTGTGGT   GCG TGT TG
                                  ||||||||||  ||| ||| ||
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                                ACTCACACCA   CGT ACG AC
                                      CCA   _   G
GAM764  LOC196264 3'  TGGGTGTGGTGGCGCATGCCTG 20899    A      A   _   G
                                TG GTGTGGT GCGC TGT TG
                                || ||||||| ||||| ||| ||
                                AC CACACCA CGCG ACG AC
                                  C      C    T   G
GAM764  LOC197358 3'  TGGGTGTGGTGGTGCGTGCCTG 20910    A      A__   C   G
                                TG GTGTGGT   GCG TGT TG
                                || |||||||   ||| ||| ||
                                AC CACACCA   CGC ACG AC
                                  C      CCA   _   G
GAM764  LOC51157  3'  TGAGTGACGCTGTGTGG     20911       TGGTA        A
                                TGAGTG    GCGCTGTGTG G
                                ||||||    |||||||||| |
                                ACTCAC    TGCGACACAC C
                                   ______         C
GAM765  CDT6     3'  AGACTTATTCTTTCTTTGGAGA 20914      CCG       GAGTC
                                AGAC   ATTCTTTT    GAGA
                                ||||   ||||||||    ||||
                                TCTG   TAAGAAAG    CTCT
                                  AA_       AAAC_
GAM765  FLJ10815  3'  AGACTGGATTCTTTCTTATGAG 20915      CC        GA  C
           A                     AGAC  GATTCTTTT  GT GAGA
                                ||||  |||||||||  || ||||
                                TCTG  CTAAGAAAG  TA CTCT
                                  AC        AA  _
GAM765  KIAA1184  3'  AGGCCCGCTTCTTTTGGCC    20916    A   A       A
                                AG CCCG TTCTTTTG GTC
                                || |||| |||||||| |||
                                TC GGGC AAGAAAAC CGG
                                 C   G       _
GAM765  MGC13007  5'  AGACTCCGTTCTTTCATGAGA  20917      _   A      GA  C
                                AGAC CCG TTCTTTT  GT GAGA
                                |||| ||| |||||||  || ||||
                                TCTG GGC AAGAAAG  TA CTCT
                                  A  _      __ _
GAM765  PTPRT    3'  AGGCCTGATTCTCTTGGCC    20918    A  C        A
                                AG CC GATTCTTTTG GTC
                                || || |||||||||| |||
                                TC GG CTAAGAGAAC CGG
                                 C  A        _
GAM765  LOC253946 3'  AGGCCCGGTCCTCCCGCGTCG  20919    A   A       A
                                AG CCCG TTCTTTTG GTCG
                                || |||| |||||||| ||||
                                TC GGGC AGGAGGGC CAGC
                                 C   C       G
GAM766  CHRNA4   3'  TACTGTAGCAGGAAGTCCT    20922     C         CGGCG
                                TAC GTAGCAGGAG    CCT
                                ||| ||||||||||    |||
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                                ATG CATCGTCCTT    GGA
                                  A        CA___
GAM766  IDH2     3'  GCAGCCATGGGTGGCGCCTCC  20923     A__  AGC
                                GTAGC   GG   GGCGCCTCC
                                |||||   ||   |||||||||
                                CGTCG   CC   CCGCGGAGG
                                   GTA  CA_
GAM766  WRN      5'  CCGAGTACAAGCCGGCGCCTCC 20924    TA_    AG
                                CCG   GCAGG  CGGCGCCTCC
                                |||   |||||  ||||||||||
                                GGC   TGTTC  GCCGCGGAGG
                                  TCA    G_
GAM766  FLJ20442  5'  TACCTGGCCTCGGCGCCTC   20925     GTA  AGGAG
                                TACC   GC    CGGCGCCTC
                                ||||   ||    |||||||||
                                ATGG   CG    GCCGCGGAG
                                  AC_  GA___
GAM766  FLJ20542  3'  CCGTGCAGGAGCCGAGGC    20926     A      ___
                                CCGT GCAGGAGC   GGC
                                |||| ||||||||   |||
                                GGCA CGTCCTCG   CCG
                                  _       GCT
GAM766  HS3ST1    5'  CCGCAGCAGGGAAGCCTCC   20927         AGC  C
                                CCGTAGCAGG   GG GCCTCC
                                ||||||||||   || ||||||
                                GGCGTCGTCC   CT CGGAGG
                                      ___  T
GAM766  OATPRP4   3'  TACCGTAGGGGAGCATGAGC   20928        CA     GC_
                                TACCGTAG  GGAGCG   GC
                                ||||||||  ||||||   ||
                                ATGGCATC  CCTCGT   CG
                                    C_     ACT
GAM766  LOC115123 3'  CCGTAGCAGGACAACCT     20929          G  GC
                                CCGTAGCAGGA CG  GCCT
                                |||||||||||  ||  ||||
                                GGCATCGTCCT GT  TGGA
                                      _  __
GAM766  LOC149076 3'  CCGGGTGGGGCGGCGCCTCC   20930     TAGCA  A
                                CCG    GG GCGGCGCCTCC
                                |||    ||  ||||||||||||
                                GGC    CC CGCCGCGGAGG
                                  CCAC_  _
GAM766  LOC159199 5'  GTAGCAGGCCAGCTCTCC    20931        AG   GC
                                GTAGCAGG  CGGC  CTCC
                                ||||||||  ||||  ||||
                                CATCGTCC  GTCG  GAGG
                                    G_    A_
GAM766  LOC170221 3'  CGAGCCAGGGAGCGGCGCCTC  20932    T   A__
                                CG AGC   GGAGCGGCGCCTC
                                || |||   ||||||||||||
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                                GC TCG   CCTCGCCGCGGAG
                                 _  GTC
GAM766  LOC220045 3'  GTGGCAGGCAGCGCCT     20933    A   GA
                                GT GCAG  GCGGCGCCT
                                || ||||  |||||||||
                                CA CGTC  CGTCGCGGA
                                 C   __
GAM766  LOC256586 5'  CCAAGGGGGCGGCGCCTCC   20934     T  CA  A
                                CCG AG  GG GCGGCGCCTCC
                                ||| ||  || ||||||||||
                                GGT TC  CC CGCCGCGGAGG
                                  _ C_ _
GAM767  ATP6V1A1  3'  AGGAGCTTGCTGAGGAAAA   20937     CCCC
                                AGGA   GCTGAGGAAGA
                                ||||   ||||||||||
                                TCCT   CGACTCCTTTT
                                  CGAA
GAM767  DYRK3    5'  GGACCCCGCTCGGGGAGAGGCG 20938         GA  A   C
                                GGACCCCGCT  GG AGA GCG
                                ||||||||||  || ||| |||
                                CCTGGGGCGA  CC TCT CGC
                                      GC  C   C
GAM767  FBXL4    5'  GACCCGGAAGGAAGACGCG   20939      CGCT
                                GACCC   GAGGAAGACGCG
                                |||||   ||||||||||||
                                CTGGG   TTCCTTCTGCGC
                                  CC__
GAM767  JUNB     3'  GGACCCCAGTGGGAGGCG    20940       C  A   AGAC
                                GGACCCCG TG GGA   GCG
                                |||||||| || |||   |||
                                CCTGGGGT AC CCT   CGC
                                     C  _  C___
GAM767  MYB      5'  GGCTCCGCCGAGAGCCGCG   20941    ACC       AAGA
                                GG  CCGCTGAGG   CGCG
                                ||  |||||||||   ||||
                                CC  GGCGGCTCT   GCGC
                                 GA_       CG__
GAM767  TFG      5'  CAGGTCTCCGCTGAATGGGCGG 20942     ACC      ___  AA
           ACGCG                  CAGG  CCGCTGA  GG  GACGCG
                                ||||  |||||||  ||  ||||||
                                GTCC  GGCGACT  CC  CTGCGC
                                  AGA     TAC  GC
GAM767  FLJ10458  3'  CAGGTCCCCACTGGTGGGGA  20943     A      A___
                                CAGG CCCCGCTG   GGA
                                |||| ||||||||   |||
                                GTCC GGGGTGAC   CCT
                                  A      CACC
GAM767  FLJ12387  3'  CAGGACCCCCTTGGGAGGC   20944        G  GA  AGAC
                                CAGGACCCC CT  GGA   GC
                                |||||||||  ||  |||   ||
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                                GTCCTGGGG GA  CCT    CG
                                      _ AC   C___
GAM767  FLJ14001  5'  GGCTTCGGGGACGAAGACGCG  20945    ACCC  CT  G
                                GG    CG  GA GAAGACGCG
                                ||    ||  || |||||||||
                                CC    GC  CT CTTCTGCGC
                                 GAA_  CC  G
GAM767  KIAA1243  5'  CAGGCTTTGCTGAGGACACA   20946     ACCCC      AG
                                CAGG    GCTGAGGA  ACG
                                ||||    ||||||||  |||
                                GTCC    CGACTCCT  TGT
                                  GAAA_       G_
GAM767  PALM      3'  CAGGACCCCGGTGGGCGC    20947          C  A  AAGA
                                CAGGACCCCG TG GG    CGC
                                |||||||||| || ||    |||
                                GTCCTGGGGC AC CC    GCG
                                      C  _  ____
GAM767  SIAT8C    5'  GGACCCCGTAGGCAGGGGCGCG 20948        CTG   A  A__
                                GGACCCCG   AGG AG   CGCG
                                ||||||||   ||| ||   ||||
                                CCTGGGGC   TCC TC   GCGC
                                     A__   G  CCC
GAM767  LOC255565 3'  GGGCCCCACCGGGAGA      20949    A       A   A
                                GG CCCCGCTG GGA GA
                                || |||||||| ||| ||
                                CC GGGGTGGC CCT CT
                                 C       _  _
GAM768  CIS4      3'  CCCGAGTTTAATTACAGAA    20952       C     ATA
                                CCCGAG TTTAAT   TATAGAA
                                |||||| ||||||   |||||||
                                GGGCTC AAATTA   ATGTCTT
                                     _     ____
GAM768  RERE      3'  AGCTTCAAGATATATAGAAA   20953         T
                                AGCTTTAA ATATATAGAAA
                                |||||||| ||||||||||
                                TCGAAGTT TATATATCTTT
                                     C
GAM768  TDG       3'  CCCAGCTTTAATATCTACCAGA 20954     G         ATA_
                                CCC AGCTTTAATAT    TAGA
                                ||| ||||||||||    ||||
                                GGG TCGAAATTATA    GTCT
                                  _          GATG
GAM768  BRD4      3'  AACAAAAAATATATATAGAAA  20955     TTT_
                                AGC    AATATATATAGAAA
                                |||    ||||||||||||||
                                TTG    TTATATATATCTTT
                                  TTTT
GAM768  C20orf72  3'  CCCAGCTGAAATATATAGAAA  20956     G    TTAAT
                                CCC AGCT    ATATATAGAAA
                                ||| ||||    ||||||||||
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                                GGG TCGA    TATATATCTTT
                                  _   CTT__
GAM768  CCNB3    3'  CCGAGCTTCTTCATGTAGA   20957        AATA  A
                                CCGAGCTTT   TAT TAGA
                                |||||||||   ||| ||||
                                GGCTCGAAG   GTA ATCT
                                     AA__   C
GAM768  CEP3     3'  CCTAAGCAATATATAGAA    20958    CG   TTTAAT
                                CC  AGC     ATATATAGAA
                                ||  |||     ||||||||||
                                GG  TCG     TATATATCTT
                                 AT   T_____
GAM768  CHCR     3'  CGAGAATATATATAGAA     20959     CTTT
                                CGAG   AATATATATAGAA
                                ||||   ||||||||||||
                                GCTC   TTATATATATCTT
                                  ____
GAM768  FLJ11116 3'  AGTTTTGATACATATAGAAA  20960    C   A
                                AG TTT ATATATATAGAAA
                                || ||| ||||||||||||
                                TC AAA TATGTATATCTTT
                                 A   C
GAM768  KIAA1005 3'  GAGCTTTAATGTGCATAAA   20961         ATA
                                GAGCTTTAAT   TATAGA
                                ||||||||||   ||||||
                                CTCGAAATTA   GTATTT
                                     CAC
GAM768  PRO1483  3'  GCTCTTTACTATATAGAAA   20962      AATA
                                GCTTT   TATATAGAAA
                                |||||   ||||||||||
                                CGAGA   ATATATCTTT
                                   AATG
GAM768  RERG     3'  CCCAAATCTTGATATATATAG  20963      C   A
                                CCCGAG TTT ATATATATAG
                                |||||| ||| ||||||||||
                                GGGTTT GAA TATATATATC
                                   A   C
GAM768  SYT13    3'  CCAGAGTTTTAATATTAATAGA 20964    C   C      AT
                                CC GAG TTTAATAT  ATAGA
                                || ||| ||||||||  |||||
                                GG CTC AAATTATA  TATCT
                                 T   A       AT
GAM768  TERE1    3'  GACTTTAATATATTCTAAGAAA 20965    G        AT__
                                GA CTTTAATATAT   AGAAA
                                || ||||||||||    |||||
                                CT GAAATTATATA   TCTTT
                                 _         AGAT
GAM768  LOC154739 5'  GAGCTTTATATAATAGAA    20966        A   T
                                GAGCTTTA TATA ATAGAA
                                |||||||| |||| ||||||
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                                CTCGAAAT ATAT TATCTT
                                   _   _
GAM768  LOC199907 3'  GAGTTTCATCATATATAGAAA  20967     C   A
                                GAG TTTA TATATATAGAAA
                                ||| |||| ||||||||||||
                                CTC AAGT GTATATATCTTT
                                  A   A
GAM768  LOC91149  5'  GAAACTTAATATATATAG    20968     C
                                GAG TTTAATATATATAG
                                ||| ||||||||||||||
                                CTT GAATTATATATATC
                                  T
GAM769  ADAM12    3'  CCAGTCCAGAAGACAGA     20971     C_       TAT
                                CCA  CCAGAAGAT   AGA
                                |||  |||||||||   |||
                                GGT  GGTCTTCTG   TCT
                                  CA        ____
GAM769  AIPL1     3'  CCAGAAGAATTAAAAACA    20972         TTATA
                                CCAGAAGA    GAAAACA
                                ||||||||    |||||||
                                GGTCTTCT    TTTTTGT
                                     TAA__
GAM769  ATP7A     3'  CACCCAGAGAAAAAAAC     20973         A  TTAT
                                CACCCAGA GA    AGAAAAC
                                |||||||| ||    |||||||
                                GTGGGTCT CT    TTTTTTG
                                   _ _____
GAM769  BIG1      3'  CCACCCAAAAGAAAAGAAAA  20974           TTAT
                                CCACCCAGAAGA    AGAAAA
                                ||||||||||||   ||||||
                                GGTGGGTTTTCT    TCTTTT
                                      TT__
GAM769  CKTSF1B1  3'  CCCAGGAGGGCACAAAAA    20975       A  AT
                                CCCAG AG  TATAGAAA
                                ||||| ||  ||||||||
                                GGGTC TC  GTGTTTTT
                                   C  CC
GAM769  CRADD     3'  CCATCTGAAGATCATCAAAAA  20976     CCCA       A
                                CCA    GAAGATTAT GAAAA
                                |||    ||||||||| |||||
                                GGT    CTTCTAGTA TTTTT
                                  AGA_        G
GAM769  CSF3      3'  CCACCCAGAAAAACAGGAGACA 20977           TT    AAA
                                CCACCCAGAAGA  ATAG   ACA
                                ||||||||||||  ||||   |||
                                GGTGGGTCTTTT  TGTC   TGT
                                      __    CTC
GAM769  DNASE1    5'  CACCTGAGAGTGCAGAAAACA  20978     CA  A  TTA
                                CACC  GA GA   TAGAAAACA
                                ||||  || ||   |||||||||
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                                GTGG  CT CT   GTCTTTTGT
                                  A_  _  CAC
GAM769  EGR2     3'  CCCAACCTATTGTAGAAAAC   20979       AAG   A
                                CCCAG   ATT TAGAAAAC
                                |||||   ||| ||||||||
                                GGGTT   TAA ATCTTTTG
                                   GGA   C
GAM769  ELK1     3'  CCACTGGGGGACTGACAGAAAA 20980      CCAGAA   _
           CA                     CCAC     GATT ATAGAAAACA
                                ||||     |||| ||||||||||
                                GGTG     CTGA TGTCTTTTGT
                                  ACCCC_   C
GAM769  ERBB2IP  3'  CCAGATTTTTATAGAAAA    20981       AGA
                                CCAGA   TTATAGAAAA
                                |||||   ||||||||||
                                GGTCT   AATATCTTTT
                                   AAA
GAM769  FRAT2    3'  CCACCAGAAAATAAGAAAA    20982       C      TAT
                                CCACC AGAAGAT   AGAAAA
                                ||||| |||||||   ||||||
                                GGTGG TCTTTTA   TCTTTT
                                  _      T__
GAM769  GFI1     3'  CCAGAAGATCTAAAAACA     20983          ATA
                                CCAGAAGATT   GAAAACA
                                ||||||||||   |||||||
                                GGTCTTCTAG   TTTTTGT
                                     A__
GAM769  GLRX     3'  CATCCAGAAGAAAACCAAGA   20984    C       TT  __
                                CA CCAGAAGA  AT  AGA
                                || ||||||||  ||  |||
                                GT GGTCTTCT  TG  TCT
                                 A       TT  GT
GAM769  HEM1     3'  CACCAGAAGATAGAAAA      20985      C     TTA
                                CACC AGAAGA   TAGAAAA
                                |||| ||||||   |||||||
                                GTGG TCTTCT   ATCTTTT
                                  _    ____
GAM769  HTR1D    3'  CAGAAGTTAAGAAAACA      20986        A   T
                                CAGAAG TTA AGAAAACA
                                |||||| ||| ||||||||
                                GTCTTC AAT TCTTTTGT
                                   _  _
GAM769  LETM1    3'  CCACCCAGAGGGCACAG      20987          A AT
                                CCACCCAGA G  TATAG
                                ||||||||| |  |||||
                                GGTGGGTCT C  GTGTC
                                     _ CC
GAM769  MEN1     5'  CCACCCAGGAGACAGA       20988          A    TAT
                                CCACCCAG AGAT   AGA
                                |||||||| ||||   |||
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                                GGTGGGTC TCTG   TCT
                                     C   ___
GAM769  MSX2    3'  GAAGATTACACCAAGAAAACA  20989        ____
                                GAAGATTAT   AGAAAACA
                                |||||||||   ||||||||
                                CTTCTAATG   TCTTTTGT
                                     TGGT
GAM769  MYO1C   3'  CCCCCAGAAGGGCATAGA   20990   A      AT
                                CC CCCAGAAG  TATAGA
                                || ||||||||  ||||||
                                GG GGGTCTTC  GTATCT
                                 _      CC
GAM769  NKTR    3'  CCACCCAAAGCCATGAAAA   20991        A A   A
                                CCACCCAGA G TTAT GAAAA
                                ||||||||| | |||| |||||
                                GGTGGGTTT C GGTA CTTTT
                                     _ _   _
GAM769  PPT2    3'  CCAGCCAGAAGACTCAG    20992    C       A
                                CCA CCAGAAGATT TAG
                                ||| |||||||||| |||
                                GGT GGTCTTCTGA GTC
                                  C       _
GAM769  PXF     3'  CCAGGAGAACTATAGAAA    20993    A  _
                                CCAG AGA TTATAGAAA
                                |||| ||| |||||||||
                                GGTC TCT GATATCTTT
                                  C  T
GAM769  SCP2    3'  CACCCAGAGCATAGGAAAAACA 20994       AGAT   __
                                CACCCAGA   TATAG  AAAACA
                                ||||||||   |||||  ||||||
                                GTGGGTCT   GTATC  TTTTGT
                                     C___    CT
GAM769  SLC35A1 3'  CCCATTAACATTATAGAAAACA 20995    G_  G
                                CCCA  AA ATTATAGAAAACA
                                ||||  || ||||||||||||||
                                GGGT  TT TAATATCTTTTGT
                                  AA  G
GAM769  SRY     3'  CCAGAGAAAAGAAAACA    20996     A  TTAT
                                CCAGA GA   AGAAAACA
                                ||||| ||   ||||||||
                                GGTCT CT   TCTTTTGT
                                  _  TT__
GAM769  TRPS1   5'  CAGAAGACACAGAAGACA   20997       T    A
                                CAGAAGAT ATAGAA ACA
                                |||||||| |||||| |||
                                GTCTTCTG TGTCTT TGT
                                     _    C
GAM769  UNC13   3'  CCACCCAAGAAGAAAATA   20998       _   TT
                                CCACCCA GAAGA  ATA
                                ||||||| |||||  |||
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                                GGTGGGT CTTCT  TAT
                                   T    TT
GAM769  ARHGAP9  5'  CCATCAGAAGATTCAG     20999     CC       A
                                CCA  CAGAAGATT TAG
                                |||  ||||||||| |||
                                GGT  GTCTTCTAA GTC
                                  A_       _
GAM769  BCAA     3'  CCAGGAAACAAAGAAAACA   21000     A    TAT
                                CCAG AGAT   AGAAAACA
                                |||| ||||   ||||||||
                                GGTC TTTG   TCTTTTGT
                                  C   TT_
GAM769  C8orf13  3'  CCACCCAGAGAATGAAGAAA  21001         A  TTAT
                                CCACCCAGA GA    AGAAA
                                ||||||||| ||    |||||
                                GGTGGGTCT CT    TCTTT
                                      _ TACT
GAM769  CG012    3'  CAGAGACATAGAAAACA     21002     A   T
                                CAGA GAT ATAGAAAACA
                                |||| ||| ||||||||||
                                GTCT CTG TATCTTTTGT
                                  _  _
GAM769  CNOT3    5'  CACCCACAAAGAAGGGAACA  21003       _    TTAT  AA
                                CACCCA GAAGA    AG  AACA
                                |||||| |||||    ||  ||||
                                GTGGGT TTTCT    TC  TTGT
                                   G    _____ CC
GAM769  DJ37E16.5 3'  CCACCCAGGGACCTAG     21004        AA   A
                                CCACCCAG  GATT TAG
                                ||||||||  |||| |||
                                GGTGGGTC  CTGG ATC
                                     C_    _
GAM769  DKFZP434A0225 3'  CCACCCAAAGATTAGGGA    21005         A    TA
                                CCACCCAGA GATTA  GA
                                ||||||||| |||||  ||
                                GGTGGGTTT CTAAT  CT
                                      _    CC
GAM769  DKFZP727M111 3'  CCAGGAGATAAAAAACA     21006     A   TTA
                                CCAG AGA   TAGAAAACA
                                |||| |||   |||||||||
                                GGTC TCT   ATTTTTTGT
                                  C  ___
GAM769  FLJ10246  3'  CCAGGAACACAGAAAACA    21007     AA  T
                                CCAG  GA TATAGAAAACA
                                ||||  || ||||||||||
                                GGTC  CT GTGTCTTTTGT
                                  __ T
GAM769  FLJ10697  3'  CACCCAGAACAGGAAAC     21008        AGATT   A
                                CACCCAGA    ATAG AAAC
                                ||||||||    |||| ||||
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                              GTGGGTCT    TGTC TTTG
                                  _____   C
GAM769  FLJ10813  3' CCACAGAAACACTAGGAAACA 21009   _    ATTA  A
                              CC CAGAAG   TAG AAACA
                              || ||||||   ||| |||||
                              GG GTCTTT   ATC TTTGT
                               T    GTG_  C
GAM769  FLJ11259  3' ACTTAGAAAATTATAAAAA  21010   CC
                              AC  AGAAGATTATAGAAA
                              ||  ||||||||||||||
                              TG  TCTTTTAATATTTTT
                               AA
GAM769  FLJ12700  3' CCCAGAAAACAACTGGAGGACA 21011        TATA_  AA
                              CCCAGAAGAT    GA  ACA
                              ||||||||||    ||  |||
                              GGGTCTTTTG    CT  TGT
                                    TTGAC  CC
GAM769  FLJ12768  3' CACCCAGAAGGCAGAA     21012        ATTA
                              CACCCAGAAG   TAGAA
                              ||||||||||   |||||
                              GTGGGTCTTC   GTCTT
                                   C___
GAM769  FLJ12969  5' CCAGTGATATAGAAAACA   21013     AA  T
                              CCAG  GAT ATAGAAAACA
                              ||||  ||| ||||||||||
                              GGTC  CTA TATCTTTTGT
                                A_  _
GAM769  FLJ14326  3' CCCAGAAGCCAGAAAA     21014       ATTA
                              CCCAGAAG   TAGAAAA
                              ||||||||   |||||||
                              GGGTCTTC   GTCTTTT
                                  G___
GAM769  FLJ14442  3' CCACCAGAAGAAGAA      21015      C    TTAT
                              CCACC AGAAGA   AGAA
                              ||||| ||||||   ||||
                              GGTGG TCTTCT   TCTT
                                _    _____
GAM769  FLJ23323  3' CACACAGAAGACTAGAA    21016    C      TA
                              CAC CAGAAGAT  TAGAA
                              ||| ||||||||  |||||
                              GTG GTCTTCTG  ATCTT
                                T      __
GAM769  FLJ30681  3' CCACCCAGAGGTGCTCTGAGAA 21017        AGA__  AT
          AACA                  CCACCCAGA    TT  AGAAAACA
                              |||||||||    ||  ||||||||
                              GGTGGGTCT    AG  TCTTTTGT
                                   CCACG  AC
GAM769  GGA2    3' CCATTTAGAAGATCTTCCAGAA 21018    CCC      A__
                              CCA   AGAAGATT   TAGAA
                              |||   ||||||||   |||||
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                                GGT   TCTTCTAG   GTCTT
                                  AAA       AAG
GAM769  GGA2     3'  CCATTTAGAAGATCTTCCAGAA 21018     CCC       A__
                                CCA   AGAAGATT   TAGAA
                                |||   ||||||||   |||||
                                GGT   TCTTCTAG   GTCTT
                                  AAA       AAG
GAM769  HIF1AN   3'  TGACCCAGAAGGAACAGGGAAC 21019   C       ATT    AA
           A                     C ACCCAGAAG   ATAG  AACA
                                | |||||||||   ||||  ||||
                                A TGGGTCTTC   TGTC  TTGT
                                 C       CT_   CC
GAM769  IL17D    3'  CCAGAAGAAGTAAAAAAC    21020        TTA
                                CCAGAAGA   TAGAAAAC
                                ||||||||   ||||||||
                                GGTCTTCT   ATTTTTTG
                                     TC_
GAM769  KIAA0036 3'  CAACCATTGCTTTATAGAAAAC 21021    C   GAAGA
           A                     CA CCA     TTATAGAAAACA
                                || |||     ||||||||||||
                                GT GGT     AATATCTTTTGT
                                 T   AACGA
GAM769  KIAA0125 3'  CCACCCAGGACATGCCCAGA   21022        AA   TA___
                                CCACCCAG  GAT     TAGA
                                ||||||||  |||     ||||
                                GGTGGGTC  CTG     GTCT
                                     __   TACGG
GAM769  KIAA0319 3'  ACCCTGAAGCATAAAGAAAACA 21023     A    ATTAT
                                ACCC GAAG     AGAAAACA
                                |||| ||||     ||||||||
                                TGGG CTTC     TCTTTTGT
                                  A    GTATT
GAM769  KIAA0410 3'  CCACCACAGAGGGCAAAGA    21024      _    A AT  T
                                CCACC CAGA G  TA AGA
                                ||||| |||| |  || |||
                                GGTGG GTCT C  GT TCT
                                   T    _ CC  T
GAM769  KIAA0418 3'  CCGCCCAGAAATACCCAAAA   21025    A       ATTA
                                CC CCCAGAAG    TAGAA
                                || ||||||||    |||||
                                GG GGGTCTTT    GTTTT
                                 C       ATGG
GAM769  KIAA0945 3'  CCACCCAGGGGAACCACAGAA  21026        AA_
                                CCACCCAG   GATTATAGAA
                                ||||||||   ||||||||||
                                GGTGGGTC   TTGGTGTCTT
                                     CCC
GAM769  KIAA1040 3'  CACCCAAATATAGAAAA     21027        AGAT
                                CACCCAGA    TATAGAAAA
                                ||||||||    |||||||||
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                                GTGGGTTT   ATATCTTTT
                                    ____
GAM769  KIAA1117 3' CCCCCAGGATTACAG      21028    A    AA
                                CC CCCAG  GATTATAG
                                || |||||  ||||||||
                                GG GGGTC  CTAATGTC
                                 _    __
GAM769  KIAA1649 3' CCACCCAGAGAATTCAG     21029        AG   A
                                CCACCCAGA  ATT TAG
                                |||||||||  ||| |||
                                GGTGGGTCT  TAA GTC
                                     CT  _
GAM769  KIAA1649 5' CCACCCAGAGAATTCAG     21029        AG   A
                                CCACCCAGA  ATT TAG
                                |||||||||  ||| |||
                                GGTGGGTCT  TAA GTC
                                     CT  _
GAM769  KRTAP4-7 3' CCACCAGAAGAAAAAGAAA   21030      C     TTAT
                                CCACC AGAAGA   AGAAA
                                ||||| ||||||   |||||
                                GGTGG TCTTCT   TCTTT
                                   _     TTT_
GAM769  KRTHB5   3' CATCCAGAAGATTCTGGAA   21031    C       ATA
                                CA CCAGAAGATT   GAA
                                || ||||||||||   |||
                                GT GGTCTTCTAA   CTT
                                 A         GAC
GAM769  MAPK8IP3 3' CCACCCGGCAGAGAGAAAACA 21032      AGA   TTAT
                                CCACCC   AGA   AGAAAACA
                                ||||||   |||   ||||||||
                                GGTGGG   TCT   TCTTTTGT
                                   CCG   C___
GAM769  MGC11115 3' CACCCGGGAGCCACAGAA    21033      AGA  A
                                CACCC   AG TTATAGAA
                                |||||   || ||||||||
                                GTGGG   TC GGTGTCTT
                                   CCC  _
GAM769  MGC14859 3' CCACCCAGGCCAAAGAAAACA 21034       AAGA   T
                                CCACCCAG    TTA AGAAAACA
                                ||||||||    ||| ||||||||
                                GGTGGGTC    GGT TCTTTTGT
                                     C___   T
GAM769  MGC5469  3' CACCCAGAAGCAGAGAAGACA 21035        ATTAT   A
                                CACCCAGAAG     AGAA ACA
                                ||||||||||     |||| |||
                                GTGGGTCTTC     TCTT TGT
                                      GTC__    C
GAM769  NYD-SP15 3' TAACCTAGGAGAGAACAGAAAA 21036   C   C  A   TT
                                C ACC AG AGA  ATAGAAAA
                                | ||| || |||  ||||||||
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                                A TGG TC TCT  TGTCTTTT
                                 T  A  C   CT
GAM769  PGRMC1   3' CCAGAAACACAGAAAA     21037       AT
                                CCAGAAG  TATAGAAAA
                                |||||||  |||||||||
                                GGTCTTT  GTGTCTTTT
                                   __
GAM769  POFUT1   3' CCCAGAAGAGCAGAAA     21038        TTA
                                CCCAGAAGA   TAGAAA
                                |||||||||   ||||||
                                GGGTCTTCT   GTCTTT
                                     C__
GAM769  PRRG1    3' CCAGTCAGAATTAGAAAAC   21039     A_  TTA
                                CCAG  AGA   TAGAAAAC
                                ||||  |||   ||||||||
                                GGTC  TCT   ATCTTTTG
                                  AG   TA_
GAM769  RAB17    5' CCTCCCAGAAGGTTTCAG    21040    A      A  A
                                CC CCCAGAAG TT TAG
                                || ||||||||  || |||
                                GG GGGTCTTC AA GTC
                                 A       C  A
GAM769  RAB3D    3' ACCCAGAAGAGACCTGGAAAA 21041         TTATA_
                                ACCCAGAAGA     GAAAA
                                ||||||||||     |||||
                                TGGGTCTTCT     CTTTT
                                     CTGGAC
GAM769  RNAC     3' CCATTCAGAAGATCAAAGA   21042     CC        T
                                CCA  CAGAAGATTA AGA
                                |||  ||||||||||  |||
                                GGT  GTCTTCTAGT TCT
                                  AA         T
GAM769  Rpo1-2   3' ACCACAGAAGACAAAAC     21043     _      TATAG
                                ACC CAGAAGAT    AAAAC
                                ||| ||||||||    |||||
                                TGG GTCTTCTG    TTTTG
                                  T      _____
GAM769  Rpo1-2   3' ACCACAGAAGACAAAAC     21043     _      TATAG
                                ACC CAGAAGAT    AAAAC
                                ||| ||||||||    |||||
                                TGG GTCTTCTG    TTTTG
                                  T      _____
GAM769  SOX17    3' AGAAGATTGAAAAAACA     21044        AT
                                AGAAGATT  AGAAAACA
                                ||||||||  ||||||||
                                TCTTCTAA  TTTTTTGT
                                     C_
GAM769  SSH2     3' CCACCAGGAAGATTAAGGAA  21045      CA       TA
                                CCACC  GAAGATTA  GAA
                                |||||  ||||||||  |||
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                                GGTGG  CTTCTAAT  CTT
                                  TC       TC
GAM769  TRIP-Br2  3'  CCTCCAGTTATAGAAA     21046    AC    AAGA
                                CC  CCAG    TTATAGAAA
                                ||  ||||    |||||||||
                                GG  GGTC    AATATCTTT
                                 A_   ____
GAM769  TRPC4     3'  CCACCCAGAGCACTACGGAAAA 21047         AG    TA
                                CCACCCAGA  ATTA  GAAAA
                                |||||||||  ||||  |||||
                                GGTGGGTCT  TGAT  CTTTT
                                     CG    GC
GAM769  U5-100K   3'  CAGAGAATAGAAAACA     21048     A  TT
                                CAGA GA  ATAGAAAACA
                                |||| ||  ||||||||||
                                GTCT CT  TATCTTTTGT
                                  _  __
GAM769  U5-116KD  3'  CCACCCAGAAGCAGCATGGA  21049          AT_   A
                                CCACCCAGAAG   TAT GA
                                ||||||||||   ||| ||
                                GGTGGGTCTTC   GTA CT
                                      GTC   C
GAM769  YME1L1    5'  CCTCCCAGAAACGGAAAA    21050    A      ATTATA
                                CC CCCAGAAG     GAAAA
                                || ||||||||     |||||
                                GG GGGTCTTT     CTTTT
                                 A       GC____
GAM769  YME1L1    5'  CCTCCCAGAAACGGAAAA    21050    A      ATTATA
                                CC CCCAGAAG     GAAAA
                                || ||||||||     |||||
                                GG GGGTCTTT     CTTTT
                                 A       GC____
GAM769  YME1L1    5'  CCTCCCAGAAACGGAAAA    21050    A      ATTATA
                                CC CCCAGAAG     GAAAA
                                || ||||||||     |||||
                                GG GGGTCTTT     CTTTT
                                 A       GC____
GAM769  ZFP91     3'  ACCTAGAATAAGAGAAAACA  21051     C    GATTAT
                                ACC AGAA     AGAAAACA
                                ||| ||||     ||||||||
                                TGG TCTT     TCTTTTGT
                                  A   ATTC__
GAM769  LOC121219 5'  CCGCCCAACCACCATAGAAAA 21052    A    AAG
                                CC CCCAG   ATTATAGAAAA
                                || |||||   ||||||||||
                                GG GGGTT   TGGTATCTTTT
                                 C    GG_
GAM769  LOC131000 5'  CACTGCAGAAGAAAAAAC    21053     C_     TTATA
                                CAC  CAGAAGA    GAAAAC
                                |||  |||||||    ||||||
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                                GTG  GTCTTCT    TTTTTG
                                  AC     _____
GAM769  LOC132617 3'  CCACCAGGAGATCATAG     21054      C  A
                                CCACC AG AGATTATAG
                                ||||| || |||||||||
                                GGTGG TC TCTAGTATC
                                  _  C
GAM769  LOC145134 5'  CATCCCGAAGGCTCACAA    21055    _  A   A_
                                CA CCC GAAG  TTATAG
                                || ||| ||||  ||||||
                                GT GGG CTTC  AGTGTT
                                 A  _   CG
GAM769  LOC146723 5'  CCCTTCAGATGCCATAGAAA  21056     AGA   __
                                CCC   AGAT  TATAGAAA
                                |||   ||||  ||||||||
                                GGG   TCTA  GTATCTTT
                                  AAG   CG
GAM769  LOC146728 5'  CCACCCAGCAAGCAGAA     21057        _  ATTA
                                CCACCCAG AAG    TAGAA
                                |||||||| |||    |||||
                                GGTGGGTC TTC    GTCTT
                                    G  ____
GAM769  LOC146990 5'  CCGCCCAGAAGGATACGAA   21058    A      AT   A
                                CC CCCAGAAG  TAT GAA
                                || ||||||||  ||| |||
                                GG GGGTCTTC  ATG CTT
                                 C       CT  _
GAM769  LOC149837 5'  CAATCAGAAAACTTTAGAAAAC 21059    CC       A
                                CA  CAGAAGATT TAGAAAAC
                                ||  ||||||||| ||||||||
                                GT  GTCTTTTGA ATCTTTTG
                                 TA       A
GAM769  LOC154562 3'  CCCAGAAGAAAAAAC       21060         TTATA
                                CCCAGAAGA    GAAAAC
                                |||||||||    ||||||
                                GGGTCTTCT    TTTTTG
                                     _____
GAM769  LOC166682 5'  CCAGGAAGAGAAAACA      21061      _   TTATA
                                CCAG AAGA    GAAAACA
                                |||| ||||    |||||||
                                GGTC TTCT    CTTTTGT
                                  C   _____
GAM769  LOC196812 3'  CCATCTGCAGAAACAGAAAACA 21062     CC__    GATT
                                CCA   CAGAA   ATAGAAAACA
                                |||   |||||   ||||||||||
                                GGT   GTCTT   TGTCTTTTGT
                                  AGAC   ____
GAM769  LOC203068 3'  CCCCCAGAAGAAAAAAC     21063    A       TTATA
                                CC CCCAGAAGA    GAAAAC
                                || |||||||||    ||||||
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                                GG GGGTCTTCT    TTTTTG
                                 _      _____
GAM769  LOC253233 5'  CCAGATTACCATAGAAGACA  21064      AG       A
                                CCAGA  ATTATAGAA ACA
                                |||||  ||||||||| |||
                                GGTCT  TGGTATCTT TGT
                                   AA       C
GAM769  LOC254263 3'  CCTCCAGGCGACATAGAAAA  21065    AC    AA   T
                                CC  CCAG  GAT ATAGAAAA
                                ||  ||||  ||| ||||||||
                                GG  GGTC  CTG TATCTTTT
                                 A_   CG  _
GAM769  LOC254532 5'  CCCCCAGAAGAGAGAA     21066    A       TTAT
                                CC CCCAGAAGA    AGAA
                                || |||||||||    ||||
                                GG GGGTCTTCT    TCTT
                                 _       C___
GAM769  LOC255242 3'  CACCCAGAAGCAGAGAAGACA  21035          ATTAT    A
                                CACCCAGAAG     AGAA ACA
                                ||||||||||     |||| |||
                                GTGGGTCTTC     TCTT TGT
                                      GTC__    C
GAM769  LOC256789 3'  CCTTCCAGGGGTTAAAGAAAAC 21067    AC    AAGA   T
          A                     CC  CCAG    TTA AGAAAACA
                                ||  ||||    ||| ||||||||
                                GG  GGTC    AAT TCTTTTGT
                                 AA    CCC_   T
GAM769  LOC257079 3'  CATCCAGAAGAAAATCAAGA   21068    C       TT  __
                                CA CCAGAAGA  AT  AGA
                                || ||||||||  ||  |||
                                GT GGTCTTCT  TA  TCT
                                 A       TT  GT
GAM769  LOC51064  3'  CCCAGGGCCACAGAAAA     21069       AAGA
                                CCCAG    TTATAGAAAA
                                |||||    ||||||||||
                                GGGTC    GGTGTCTTTT
                                   CC__
GAM769  LOC90249  3'  ACCCAGCAGGCACAGAAA    21070       A  AT
                                ACCCAG AG  TATAGAAA
                                |||||| ||  ||||||||
                                TGGGTC TC  GTGTCTTT
                                   G  C_
GAM769  LOC91574  3'  CCACCCAGGTGAAGAAA     21071        AA  TTAT
                                CCACCCAG  GA    AGAAA
                                ||||||||  ||    |||||
                                GGTGGGTC  CT    TCTTT
                                     CA  ____
GAM769  LOC91960  3'  CCACCACAGAAAACAGA     21072       _       TAT
                                CCACC CAGAAGAT   AGA
                                ||||| ||||||||   |||
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                                GGTGG GTCTTTTG   TCT
                                  T      ___
GAM769  LOC92230  5' CCACCCAGGAGCCAGAA     21073        A  ATTA
                                CCACCCAG AG    TAGAA
                                |||||||| ||    |||||
                                GGTGGGTC TC    GTCTT
                                    C  G___
GAM769  LOC92755  3' CCCAGAAGAAAAAAC       21060         TTATA
                                CCCAGAAGA    GAAAAC
                                |||||||||    ||||||
                                GGGTCTTCT    TTTTTG
                                     _____
GAM770  ADCY6     5'  TCCCCAATCAACAGG       21076     AGGAA
                                TCC    CCAATCAACAGG
                                |||    ||||||||||||
                                AGG    GGTTAGTTGTCC
                                 _____
GAM770  DSCR3     3'  TTTCTGGGAACCAAGTTTCAAG 21077      CA       TCAA
                                TTTC  GGAACCAA    CAGG
                                ||||  ||||||||    ||||
                                AAAG  CCTTGGTT    GTTC
                                  AC       CAAA
GAM770  NPY2R     3'  TTTCCAGGAATTAAACAG    21078          CCAATC
                                TTTCCAGGAA     AACAG
                                ||||||||||     |||||
                                AAAGGTCCTT     TTGTC
                                     AAT___
GAM770  ZNF175    5'  TTCCCAGGAGCCAGAAGC    21079         A   ATCAAC
                                TTTCCAGGA CCA     AGGC
                                ||||||||| |||     ||||
                                AAGGGTCCT GGT     TTCG
                                     C   C_____
GAM770  FLJ10081  3'  TTTCCAGGAGTCAGCAAG    21080         ACCAA   A
                                TTTCCAGGA    TCA CAGG
                                |||||||||    ||| ||||
                                AAAGGTCCT    AGT GTTC
                                     C____   C
GAM770  KIAA0010  3'  TCCAGGAAGACAAGTGGGCG  21081        CCAAT   CA_
                                TCCAGGAA    CAA   GGCG
                                ||||||||    |||   ||||
                                AGGTCCTT    GTT   CCGC
                                     CT___   CAC
GAM770  KIAA0153  3'  TCTCCAGGAGCTGCCAAAGGCG 21082         A___    TCAAC
                                TTTCCAGGA   CCAA    AGGCG
                                |||||||||   ||||    |||||
                                AGAGGTCCT   GGTT    TCCGC
                                     CGAC   _____
GAM770  KIAA1203  3'  TTTCCAGGAATCTGTCAAAGG  21083          CCAA    C
                                TTTCCAGGAA    TCAA AGG
                                ||||||||||    |||| |||
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                                AAAGGTCCTT    AGTT TCC
                                     AGAC    _
GAM770  MGC2776   5'  TTTCCAAGAACCAAGGGCTGCA 21084           TCAA__
           GGCG                   TTTCCAGGAACCAA     CAGGCG
                                |||||||||||||     ||||||
                                AAAGGTTCTTGGTT     GTCCGC
                                     CCCGAC
GAM770  LOC149606 3'  TTCCCAGGAGCTCACAGG    21085        ACCAA   A
                                TTTCCAGGA    TCA CAGG
                                |||||||||    ||| ||||
                                AAGGGTCCT    AGT GTCC
                                     CG___   _
GAM770  LOC150378 3'  TTTCCAAGAGCAAGGCAGG   21086        AC   TCAA
                                TTTCCAGGA  CAA    CAGG
                                |||||||||  |||    ||||
                                AAAGGTTCT  GTT    GTCC
                                     C_   CC__
GAM770  LOC152215 3'  TTTCCAGGAACCTAGTCCACA  21087          AA_  A
                                TTTCCAGGAACC   TC ACA
                                ||||||||||||   || |||
                                AAAGGTCCTTGG   AG TGT
                                      ATC  G
GAM770  LOC200197 3'  TTTCCAAGATTCACAACAGG   21088        AC  AT
                                TTTCCAGGA  CA  CAACAGG
                                |||||||||  ||  |||||||
                                AAAGGTTCT  GT  GTTGTCC
                                     AA  __
GAM770  LOC201475 3'  TTTCCAGGAATCATTTCCAC   21089        C  A_  A
                                TTTCCAGGAA CA  TC AC
                                |||||||||| ||  || ||
                                AAAGGTCCTT GT  AG TG
                                      A  AA  G
GAM770  LOC220581 5'  CTTCCAGGGGCCGTCTGCAGGC 21090        AA  AA  AA
           G                    TTTCCAGG  CC  TC  CAGGCG
                                ||||||||  ||  ||  ||||||
                                GAAGGTCC  GG  AG  GTCCGC
                                     CC  C_  AC
GAM770  LOC221087 3'  TTCCAGGAGCCTACAGGC    21091        A  AATCA
                                TTCCAGGA CC    ACAGGC
                                |||||||| ||    ||||||
                                AAGGTCCT GG    TGTCCG
                                     C  A____
GAM770  LOC91813  5'  TTCCAGGAATTCCAGACAGG   21092        __  ATCA
                                TTCCAGGAA  CCA   ACAGG
                                |||||||||  |||   |||||
                                AAGGTCCTT  GGT   TGTCC
                                     AA   C___
GAM770  LOC92521  3'  CTTCCAGGAAAAGCTGCAGTAG 21093        CCAAT_  AC
           G                    TTTCCAGGAA     CA  AGG
                                ||||||||||     ||  |||
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                                GAAGGTCCTT     GT  TCC
                                     TTCGAC  CA
GAM771  ATP11A   3'  TTCATGATATGTGCATATG   21096       GCCTCTCA
                                TTCATGA       TGCATATG
                                |||||||       ||||||||
                                AAGTACT       ACGTATAC
                                    ATAC____
GAM771  CLCN3    3'  ATGAGCCTTTGTTGTGGTGCAT 21097        CTCA_____    A
          GTG                     ATGAGCCT       TGCAT TG
                                |||||||||       ||||| ||
                                TACTCGGA       ACGTA AC
                                    AACAACACC    C
GAM771  PTGFR    3'  TCATGACCATGCATGTG     21098      GCCTC      A
                                TCATGA    TCATGCAT TG
                                ||||||    |||||||| ||
                                AGTACT    GGTACGTA AC
                                   _____      C
GAM771  FLJ20032 3'  ATGAGCCTTTACAAATTGC   21099       CTCA   TA_
                                ATGAGCCT   TGCA   TGC
                                ||||||||   ||||   |||
                                TACTCGGA   ATGT   ACG
                                    A___   TTA
GAM771  KIAA0555 3'  ATGATGGCATGCATATGC    21100     GCCTCT
                                ATGA     CATGCATATGC
                                ||||     ||||||||||
                                TACT     GTACGTATACG
                                  ACC___
GAM771  KIAA1254 3'  TTCATAAGTTTTCAATTATATG 21101       CCTC   TGC
          C                      TTCATGAG   TCA   ATATGC
                                ||||||||   |||   ||||||
                                AAGTATTC   AGT   TATACG
                                    AAA_   TAA
GAM771  KIAA1303 3'  TCATGGGCCTCTCACTGC    21102      A      _
                                TCATG GCCTCTCA TGC
                                ||||| |||||||| |||
                                AGTAC CGGAGAGT ACG
                                   C       G
GAM771  LOC151277 3'  ATGAGCCTTCTGATGTGC    21103       _  C   CATA
                                ATGAGCCT CT ATG    TGC
                                |||||||| || |||    |||
                                TACTCGGA GA TAC    ACG
                                    A  C  ____
GAM771  LOC197287 5'  TTCATGATATGTGCATATG   21096       GCCTCTCA
                                TTCATGA       TGCATATG
                                |||||||       ||||||||
                                AAGTACT       ACGTATAC
                                    ATAC____
GAM771  LOC221710 3'  TCACATCAATCTTGTGCATATG 21104     GAGCC   CA
                                TCAT    TCT  TGCATATG
                                ||||    |||  ||||||||
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                                AGTG    AGA  ACGTATAC
                                  TAGTT   AC
GAM771  LOC257463 3'  TTCATAAAAAATATGCATATG  21105        CCTCTC
                                TTCATGAG     ATGCATATG
                                ||||||||     |||||||||
                                AAGTATTT     TACGTATAC
                                    TTTA__
GAM772  ARHI     3'  TACGTATTGACAACATGGATGT 21108     A  G       _  CC
                                TAC TA TGACAACG GG  GT
                                ||| || |||||||| ||  ||
                                ATG AT ACTGTTGT CC  CA
                                  C  A       A  TA
GAM772  ATP8A2   3'  CACGTAGTGACAGCTG      21109     A       ACGG  CG
                                TAC TAGTGACA   GC  TG
                                ||| ||||||||   ||  ||
                                GTG ATCACTGT   CG  AC
                                  C       _____  __
GAM772  FOG2     3'  CATAGTAACAACATTTGTTAGC 21110        G__________  CGT
             ACGGCC                  GTGACAAC        GGC   GCT
                                ||||||||        |||   |||
                                CATTGTTG        TCG   CGG
                                    TAAACAAIII   TGC
GAM772  LHX2     3'  ACAGTGACACAAATGTTGTG   21111         A   CC__
                                ATAGTGACA CGGG   GTG
                                ||||||||| ||||   |||
                                TGTCACTGT GTTT   CAC
                                    _   ACAA
GAM772  POU2AF1  3'  TAATAGTGACGATGGTGC    21112   C       AAC  GCC
                                A ATAGTGAC   GG   GTGC
                                | ||||||||   ||   ||||
                                A TATCACTG   CT   CACG
                                 T       ___  AC_
GAM772  FLJ11274 3'  TACATGGTGGGAACCATG    21113       A   ACAAC
                                TACAT GTG    GGGCCGTG
                                ||||| |||    ||||||||
                                ATGTA CAC    CTTGGTAC
                                   C   C____
GAM772  FLJ14490 3'  TACATAGTAACAGCATAATTGC 21114           A  GGCCG
             T                   TACATAGTGACA CG     TGCT
                                ||||||||||||| ||     ||||
                                ATGTATCATTGT GT     ACGA
                                      C  ATTA_
GAM773  HUNK     3'  TAAGCGAGGTTGGGTTGTGCAG 21117       TAAT       CGC
                                TAGGT    GGTTGGGT   GCAG
                                |||||    ||||||||   ||||
                                ATTCG    CCAACCCA   CGTC
                                   CT__       ACA
GAM774  MPP6     3'  TCAACGCATTTCTTTA      21120          GAATCT
                                TCAATGCATT     TCTTTA
                                ||||||||||     ||||||
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                                AGTTGCGTAA     AGAAAT
                                       ______
GAM774  LOC145676 5'  TCAATGCAATTGAATCTT    21121        _
                                TCAATGCA TTGAATCTT
                                |||||||| |||||||||
                                AGTTACGT AACTTAGAA
                                     T
GAM774  LOC161580 5'  GCATTGATGTCTTTACG     21122       ATCT
                                GCATTGA   TCTTTACG
                                |||||||   ||||||||
                                CGTAACT   AGAAATGC
                                   AC__
GAM775  AICDA    3'  CGCAGCTTTATCATTCTGTTT  21125     G        GCAA
                                CGC AGCTTTATCA   GTTT
                                ||| ||||||||||   ||||
                                GCG TCGAAATAGT   CAAA
                                 _       AAGA
GAM775  APC10    3'  GAGCTTTATTACATGTT     21126        CA   A
                                GAGCTTTAT  GCA GTT
                                |||||||||  ||| |||
                                CTCGAAATA  TGT CAA
                                     A_   A
GAM775  SBBI26   5'  TCCCGAGCAGCAAGT      21127     G    TTTATC
                                TCC CGAGC     AGCAAGT
                                ||| |||||     |||||||
                                AGG GCTCG     TCGTTCA
                                 _    _______
GAM776  SCN3A    3'  GTAATTGCACAACTTTG     21130     C  A
                                GTAA TG CATAACTTTG
                                |||| || ||||||||||
                                CATT AC GTGTTGAAAC
                                  A  _
GAM776  TLR4     3'  TACTTAGTAGGCAATAACTTTG 21131        ACTGAC
                                TATTTAGTA     ATAACTTTG
                                |||||||||     |||||||||
                                ATGAATCAT     TATTGAAAC
                                     CCGT__
GAM776  TLR4     3'  TACTTAGTAGGCAATAACTTTG 21131        ACTGAC
                                TATTTAGTA     ATAACTTTG
                                |||||||||     |||||||||
                                ATGAATCAT     TATTGAAAC
                                     CCGT__
GAM776  TLR4     3'  TACTTAGTAGGCAATAACTTTG 21131        ACTGAC
                                TATTTAGTA     ATAACTTTG
                                |||||||||     |||||||||
                                ATGAATCAT     TATTGAAAC
                                     CCGT__
GAM776  GPCR150  3'  TATTTAATAACTGGTATA    21132          AC
                                TATTTAGTAACTG  ATA
                                |||||||||||||  |||
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                                ATAAATTATTGAC  TAT
                                       CA
GAM776  LOC50999  3'  TTTAGTAAGTGTAACTTT    21133        C  ACA
                                TTTAGTAA TG   TAACTTT
                                |||||||| ||   |||||||
                                AAATCATT AC   ATTGAAA
                                     C  ___
GAM777  AQP6     5'  GCCATGTGTATTGCACCC    21136     C  AC
                                GCCA GT  ATTGTACCT
                                |||| ||  |||||||||
                                CGGT CA  TAACGTGGG
                                  A  CA
GAM777  BCAS1    3'  GCCGTTGTCACTGAGCCTCAAA 21137     AC_  A    TA
             AG                   GCC   GT CATTG  CCTCAAAAG
                                |||   || |||||  |||||||||
                                CGG   CA GTGAC  GGAGTTTTC
                                  CAA  _    TC
GAM777  CLCA2    5'  GCTGCATACATTGTGTCA    21138    CA       ACC
                                GC  CGTACATTGT   TCA
                                ||  ||||||||||   |||
                                CG  GTATGTAACA   AGT
                                 AC        C__
GAM777  RNTRE    3'  ACATACTTTTGTACCTTGAAAG 21139       A_      CA
                                ACGTAC  TTGTACCT  AAAG
                                ||||||  ||||||||  ||||
                                TGTATG  AACATGGA  TTTC
                                   AA       AC
GAM777  TM4SF4   3'  GCCATGATGACAGCCTCAAAAG 21140     CGTACAT  _  _
                                GCCA      TG TA CCTCAAAAG
                                ||||      || || |||||||||
                                CGGT      AC GT GGAGTTTTC
                                  ACT_____  T  C
GAM777  ALS2CR19 3'  GCCACTTCTGTCTCAAAA    21141      GTACA   AC
                                GCCAC    TTGT  CTCAAAA
                                |||||    ||||  |||||||
                                CGGTG    GACA  GAGTTTT
                                   AA___   __
GAM777  CSAD     3'  GCCACTGCACCCGGCCTCAAA  21142      _   A   TA
                                GCCAC GTAC TTG  CCTCAAA
                                ||||| |||| |||  |||||||
                                CGGTG CGTG GGC  GGAGTTT
                                   A   _  C_
GAM777  KIAA0310 3'  CATGTGGATTGTACCACGAAAA 21143    C  AC      TC_
             G                    CA GT  ATTGTACC   AAAAG
                                || ||  ||||||||   |||||
                                GT CA  TAACATGG   TTTTC
                                 A  CC       TGC
GAM777  KIAA0809 3'  GCCAAGTGTCCTATTCTCAAAA 21144     C  ACA   AC
             G                    GCCA GT   TTGT  CTCAAAAG
                                |||| ||   ||||  ||||||||
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                                CGGT CA   GATA  GAGTTTTC
                                  T  CAG    A_
GAM777  MGC20253  3'  GTCCCACCCTCCTCAAAAG   21145    A_   GTA
                                GT  CATT   CCTCAAAAG
                                ||  ||||   |||||||||
                                CA  GTGG   GGAGTTTTC
                                 GG    GA_
GAM777  RGS12     3'  GCCACGTATCATTCCTGCAA  21146        _   GTA  _
                                GCCACGTA CATT   CCT CAA
                                |||||||| ||||   ||| |||
                                CGGTGCAT GTAA   GGA GTT
                                     A    ___   C
GAM777  LOC126964 3'  GTACATACCTCAAAAG     21147      TTG
                                GTACA   TACCTCAAAAG
                                |||||   ||||||||||||
                                CATGT   ATGGAGTTTTC

                                  ___
GAM777  LOC144577 3'  GTACATTACCCCAAAAG     21148       TG
                                GTACAT  TACCTCAAAAG
                                ||||||  ||||||||||||
                                CATGTA  ATGGGGTTTTC

                                  __
GAM777  LOC150481 3'  CCTGTACATTGTACTTCTC   21149    AC         __
                                CC  GTACATTGTAC  CTC
                                ||  ||||||||||||  |||
                                GG  CATGTAACATG  GAG
                                 A_          AA
GAM777  LOC153525 3'  CCACTTCATGTGCCTCAAAAG  21150     GTA   T  A
                                CCAC   CAT GT CCTCAAAAG
                                ||||   ||| || |||||||||
                                GGTG   GTA CA GGAGTTTTC
                                  AA_   _  C
GAM777  LOC158191 3'  CCTGTACATTGTACTTCTC   21149    AC         __
                                CC  GTACATTGTAC  CTC
                                ||  ||||||||||||  |||
                                GG  CATGTAACATG  GAG
                                 A_          AA
GAM778  ATP7A     3'  TTAAAGTTTTGGAAACATCTTG 21153        C  AC   C
                                TTGAAGTT TG  GAA TATCTTG
                                |||||||| ||  ||| |||||||
                                AATTTCAA AC  CTT GTAGAAC
                                     A  __   T
GAM778  DKFZP564B1162 5'  CTGAAGTTCTGAACC      21154          CGA
                                TTGAAGTTCTGA   ACT
                                ||||||||||||   |||
                                GACTTCAAGACT   TGG

                                     ___
GAM778  KIAA1529  3'  TTGAAGCTCTGGTGCCTAT    21155          ACGAA
                                TTGAAGTTCTG    CTAT
                                ||||||||||     ||||
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                                AACTTCGAGAC    GATA
                                      CACG_
GAM779  IL1R1    3'  GGCTTCTGCTGCAAAAT    21158    A  GAG
                                GGC TC   TGTTGCAAAAT
                                ||| ||   ||||||||||||
                                CCG AG   ACGACGTTTTA
                                  A  ___
GAM779  NET1     3'  TCCAGCATTTGCAAAA     21159        CGAGTG
                                TCCGGCAT     TTGCAAAA
                                ||||||||     ||||||||
                                AGGTCGTA     AACGTTTT
                                     _______
GAM779  AD-020   3'  CAGTATCAATTGCAAA     21160    C   AGT
                                CGG ATCG   GTTGCAAA
                                ||| ||||   ||||||||
                                GTC TAGT   TAACGTTT
                                  A   ___
GAM779  AD-020   3'  CAGTATCAATTGCAAA     21160    C   AGT
                                CGG ATCG   GTTGCAAA
                                ||| ||||   ||||||||
                                GTC TAGT   TAACGTTT
                                  A   ___
GAM779  EDG1     3'  GGCTCAGTGCAAAAT      21161    A  G   GTT
                                GGC TC AGT   GCAAAAT
                                ||| || |||   |||||||
                                CCG AG TCA   CGTTTTA
                                  _ _  ____
GAM779  KIAA0716 3'  TCCGACATTCAAAATTGTAAA  21162        _   T   C
                                TCCGGCAT CGAG GTTG AAA
                                |||||||| |||| |||| |||
                                AGGCTGTA GTTT TAAC TTT
                                     A   _   A
GAM779  MGC2452  5'  TCCAGCATTGAGTGGCAA    21163        C    TT
                                TCCGGCAT GAGTG  GCAA
                                |||||||| |||||  ||||
                                AGGTCGTA CTCAC  CGTT
                                     A    __
GAM779  LOC152048 3'  GGCACCGAAGACACAGAATC   21164         TGT   A
                                GGCATCGAG   TGCA AATC
                                |||||||||   |||| ||||
                                CCGTGGCTT   GTGT TTAG
                                     CT_   C
GAM779  LOC169505 3'  TCCAGCATTGATTACA      21165        C  GTG
                                TCCGGCAT GA   TTGCA
                                |||||||| ||   |||||
                                AGGTCGTA CT   AATGT
                                     A  ____
GAM780  ADRBK2   3'  GAGAAAACAAACTTCACAGG   21168           G  TT_
                                GAGGAAACAAACT TC   GG
                                |||||||||||| ||   ||
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                                CTCTTTTGTTTGA AG   CC
                                      _ TGT
GAM780  ATP10C   3'  GAGGAAACCAGGACTCTGTTTG 21169        AAA____   C
            GAA                  GAGGAAAC      CTGT TTGGAA
                                |||||||||      |||| ||||||
                                CTCCTTTG      GACA AACCTT
                                   GTCCTGA   _
GAM780  FCRH3    3'  GGAAACAAAATATTTGGA    21170         C   C
                                GGAAACAAA TGT TTGGA
                                ||||||||| ||| |||||
                                CCTTTGTTT ATA AACCT
                                      T   _
GAM780  FOXD2    3'  GAGGAAACGAACTTCCTTG   21171         A   GT
                                GAGGAAAC AACT  CTTG
                                |||||||| ||||  ||||
                                CTCCTTTG TTGA  GAAC
                                   C    AG
GAM780  GALC     3'  GAGGAAACAAATTGTGG     21172          C   CTT
                                GAGGAAACAAA TGT   GG
                                |||||||||||| |||   ||
                                CTCCTTTGTTT ACA   CC
                                      A   ___
GAM780  GAS7     3'  GAGGAAACACATTCATACCGG  21173         AACT_  C
                                GAGGAAACA    GT TTGG
                                |||||||||    || ||||
                                CTCCTTTGT    TA GGCC
                                      GTAAG  T
GAM780  KLF8     3'  GAGGAAAAAATTGTCCCA    21174        C   C
                                GAGGAAA AAA TGTCTTG
                                ||||||| ||| |||||||
                                CTCCTTT TTT ACAGGGT
                                   _   A
GAM780  MKI67    3'  GGAAACAAACGTGGAGACA    21175          TGTCT   _
                                GGAAACAAAC    TGGA ACA
                                ||||||||||    |||| |||
                                CCTTTGTTTG    ACCT TGT
                                      C____   C
GAM780  NCL      3'  AGGACTGTATACTGTCTTGGAA 21176      AACAA_
                                AGGA     ACTGTCTTGGAA
                                ||||     ||||||||||||
                                TCCT     TGACAGAACCTT
                                  GACATA
GAM780  PPARBP   5'  GAGGAAACAAGTTGGCTCG   21177          AC  T
                                GAGGAAACAA  TG CTTG
                                ||||||||||  || ||||
                                CTCCTTTGTT  AC GAGC
                                      CA  C
GAM780  RAI3     3'  GAGGCAAACTGTTCCCG     21178      AAA      _
                                GAGG   CAAACTGT CTTG
                                ||||   |||||||| ||||
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                                CTCC   GTTTGACA GGGC
                                  ___       A
GAM780  TAP2     3'  GAGACAGATGGGCTGGAACA  21179     GAA   AAC  TC
                                GAG   ACA   TG  TTGGAACA
                                |||   |||   ||  ||||||||
                                CTC   TGT   AC  GACCTTGT
                                  ___   CT_  CC
GAM780  TGFBR3   3'  GAGGGCAGCACCCATCTTGGGA 21180      AAACAAA       A
           CA                     GAGG      CTGTCTTGG ACA
                                ||||      ||||||||| |||
                                CTCC      GGTAGAACC TGT
                                  CGTCGTG        C
GAM780  ARL5     3'  GAGAAAGCAAACTGGAAGG   21181       A      TCTT
                                GAGGAA CAAACTG    GG
                                |||||| |||||||    ||
                                CTCTTT GTTTGAC    CC
                                   C      CTT_
GAM780  BBX      3'  GAGAGAACAAACTGGCCCAGGA 21182     GA       _   T
                                GAG  AACAAACTG TCT GGA
                                |||  ||||||||| ||| |||
                                CTC  TTGTTTGAC GGG CCT
                                  TC        C   T
GAM780  CALN1    3'  GAGGGCAAACTGCCCAGG    21183      AAA        T
                                GAGG   CAAACTGTCT GG
                                ||||   |||||||||| ||
                                CTCC   GTTTGACGGG CC
                                  C__         T
GAM780  CAMTA2   3'  GAGGAAACAGACGCAAAC    21184         A  T  CTTG
                                GAGGAAACA AC GT    GAAC
                                ||||||||| || ||    ||||
                                CTCCTTTGT TG CG    TTTG
                                     C  _  _____
GAM780  COVA1    3'  GAGAAAATAACTTTGGAAC   21185       CA    GTC
                                GAGGAAA  AACT   TTGGAAC
                                |||||||  ||||   |||||||
                                CTCTTTT  TTGA   AACCTTG
                                   A_    ___
GAM780  DKFZp434N074 5'  GAGGAAACAAGCGGGGGA    21186          ACT  CTT
                                GAGGAAACAA   GT   GGA
                                ||||||||||   ||   |||
                                CTCCTTTGTT   CG   CCT
                                     ___  CCC
GAM780  DLAD     5'  GAGGAAACTGAGGGATGGAA   21187       ACAA    TCT__
                                GAGGAA    ACTG     TGGAA
                                ||||||    ||||     |||||
                                CTCCTT    TGAC     ACCTT
                                   _____    TCCCT
GAM780  DNAJC5   3'  GAAGAAACAAAGAAAAGTGGGA 21188          CTGTCT   A
           CA                     GAGGAAACAAA      TGG ACA
                                ||||||||||      ||| |||
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                                CTTCTTTGTTT     ACC TGT
                                      CTTTTC   C
GAM780  FLJ10661 3' GAGGAAACGAGTGTGTCCAGGG 21189       AAAC_    T_
            A                    GAGGAAAC    TGTCT  GGA
                                 ||||||||    |||||  |||
                                 CTCCTTTG    ACAGG  CCT
                                     CTCAC    TC
GAM780  FLJ10661 3' GAGGAAACGAGTGTGTCCAGGG 21189       AAAC_    T_
            A                    GAGGAAAC    TGTCT  GGA
                                 ||||||||    |||||  |||
                                 CTCCTTTG    ACAGG  CCT
                                     CTCAC    TC
GAM780  FLJ10661 3' GAGGAAACGAGTGTGTCCAGGG 21189       AAAC_    T_
            A                    GAGGAAAC    TGTCT  GGA
                                 ||||||||    |||||  |||
                                 CTCCTTTG    ACAGG  CCT
                                     CTCAC    TC
GAM780  FLJ10849 3' GAGGAGACAGTCTGAA     21190      A  AACT   TG
                                 GAGGA ACA   GTCT  GAA
                                 ||||| |||   ||||  |||
                                 CTCCT TGT   CAGA  CTT
                                   C  _____   __
GAM780  FLJ12595 5' GAGTGAACAAACTGAGGA    21191     GA       TCTT
                                 GAG  AACAAACTG   GGA
                                 |||  |||||||||   |||
                                 CTC  TTGTTTGAC   CCT
                                   AC       T___
GAM780  FLJ13710 3' GAGGAACAGCACTTGGAAC   21192       A  AACT  _
                                 GAGGAA CA   GT CTTGGAAC
                                 ||||||  ||   ||  ||||||||
                                 CTCCTT GT   CG GAACCTTG
                                    _  _____  T
GAM780  FLJ14249 3' GAGGAGCAGAGGCCCTGGA   21193      AA  AACT
                                 GAGGA  CA   GTCTTGGA
                                 |||||  ||   ||||||||
                                 CTCCT  GT   CGGGACCT
                                    C_  CTC_
GAM780  FLJ14249 3' GAGGAGCAGAGGCCCTGGA   21193      AA  AACT
                                 GAGGA  CA   GTCTTGGA
                                 |||||  ||   ||||||||
                                 CTCCT  GT   CGGGACCT
                                    C_  CTC_
GAM780  FLJ20034 3' GAGGGGAGAACTCCCTGGAA  21194     AAACA   G
                                 GAGG    AACT TCTTGGAA
                                 ||||    |||| ||||||||
                                 CTCC    TTGA GGGACCTT
                                   CCTC_   _
GAM780  FLJ21596 3' AAAAACCAAACTGTCTTGGAAC 21195       A
            A                    AGGAA CAAACTGTCTTGGAACA
                                 ||||| ||||||||||||||||
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                                TTTTT GTTTGACAGAACCTTGT
                                   G
GAM780  GTF2F2   5' GAGGAGCGGGCGTCCGGAACA 21196      AACAAAC    T
                                GAGGA      TGTCT GGAACA
                                |||||      ||||| ||||||
                                CTCCT      GCAGG CCTTGT
                                   CGCCC__    _
GAM780  HIF1AN   3' AGGAGGCAGACTGACCTAA   21197     AA  A    T
                                AGGA  CA ACTG CTTGG
                                ||||  || |||| |||||
                                TCCT  GT TGAC GGATT
                                  CC  C    T
GAM780  KIAA0586 5' GGAAACAAACTCCGGA     21198          GTC
                                GGAAACAAACT   TTGGA
                                ||||||||||   |||||
                                CCTTTGTTTGA   GGCCT
                                      ___
GAM780  KIAA0638 3' GAGAAAACAGGCTGGGGA    21199         AA   TCTT
                                GAGGAAACA  CTG    GGA
                                |||||||||  |||    |||
                                CTCTTTTGT  GAC    CCT
                                     CC   C___
GAM780  KIAA1014 3' GAGGTGAATTTTGTTTTGGAAC 21200      AAACAAAC   C
          A                      GAGG       TGT TTGGAACA
                                ||||       ||| ||||||||
                                CTCC       ACA AACCTTGT
                                  ACTTAAA_   A
GAM780  KIAA1198 3' GAGTGAGACACCATCTTGG   21201     _  A  AA
                                GAG GA AC  ACTGTCTTGG
                                ||| || ||  ||||||||||
                                CTC CT TG  TGGTAGAACC
                                  A  C  __
GAM780  KIAA1272 3' GAAGAAACAACTTGG       21202          ACTGT
                                GAGGAAACAA    CTTGG
                                ||||||||||    |||||
                                CTTCTTTGTT    GAACC
                                      _____
GAM780  KIAA1437 3' GGAAACAAAGTCTGGG      21203         CT    T
                                GGAAACAAA  GTCT GG
                                |||||||||  |||| ||
                                CCTTTGTTT  CAGA CC
                                     __    C
GAM780  KIAA1673 3' GGAAAAACTGTCAGA       21204      CA      TT
                                GGAAA  AACTGTC  GGA
                                |||||  |||||||  |||
                                CCTTT  TTGACAG  TCT
                                   __      __
GAM780  KIAA1726 3' AAGGGGACAAACTGTCCT    21205      AA
                                GAGG  ACAAACTGTCTT
                                ||||  ||||||||||||
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                                TTCC  TGTTTGACAGGA
                                  CC
GAM780  LYPLA3    3'  GAGGAAATCAGGGCCCCTGGAA 21206       _  AACTG
            CA                    GAGGAAA CA    TCTTGGAACA
                                  ||||||| ||    ||||||||||
                                  CTCCTTT GT    GGGACCTTGT
                                     A  CCCG_
GAM780  MGC21675  5'  GAGAAGGCAGCGCTTGGAACA  21207      AA  AAC  T
                                  GAGGA  CA   TG CTTGGAACA
                                  |||||  ||   || |||||||||
                                  CTCTT  GT   GC GAACCTTGT
                                     CC  C__  _
GAM780  NDUFC2    3'  AGGAAACAAAAACTTTTGGGAC 21208         CTGTC    A
            A                     AGGAAACAAA    TTGG ACA
                                  ||||||||||    |||| |||
                                  TCCTTTGTTT    AACC TGT
                                        TTGAA    C
GAM780  PLSCR4    3'  GAGAAAACAAGCATGGAA    21209         ACT  CT
                                  GAGGAAACAA   GT  TGGAA
                                  ||||||||||   ||  |||||
                                  CTCTTTTGTT   CG  ACCTT
                                        ___  T_
GAM780  RP4-622L5 3'  AGGAAACAGTATGTTGG     21210        AAC   C
                                  AGGAAACA   TGT TTGG
                                  ||||||||   ||| ||||
                                  TCCTTTGT   ATA AACC
                                       C__   C
GAM780  SDS3      3'  AGAAACAATGACCTTTTGGAA  21211         __  GTC
                                  GGAAACAA  ACT   TTGGAA
                                  ||||||||  |||   ||||||
                                  TCTTTGTT  TGG   AACCTT
                                       AC   AA_
GAM780  SLC11A2   3'  GAGGAAACAGCTGTAGAGA   21212         AA   CTT
                                  GAGGAAACA  CTGT   GGA
                                  |||||||||  ||||   |||
                                  CTCCTTTGT  GACA   TCT
                                       C_   TC_
GAM780  LOC113386 3'  GAGTAAACAAACTGTGG     21213     G        CTT
                                  GAG AAACAAACTGT   GG
                                  ||| ||||||||||   ||
                                  CTC TTTGTTTGACA   CC
                                    A         ___
GAM780  LOC116150 3'  GAGGAAAAAAGCTGCCTTGG   21214        C  A
                                  GAGGAAA AA CTGTCTTGG
                                  ||||||| || |||||||||
                                  CTCCTTT TT GACGGAACC
                                       T  C
GAM780  LOC150407 3'  GAGGAAACAAAGTCAGAAGGA  21215          CT   TT__
                                  GAGGAAACAAA  GTC    GGA
                                  ||||||||||  |||    |||
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                                CTCCTTTGTTT  CAG    CCT
                                      __   TCTT
GAM780   LOC150538 3'  GAGGTAAACGACCATCCTTGGA 21216     _   AA     _
           ACA                    GAGG AAAC  ACTGTC TTGGAACA
                                  |||| ||||  |||||| ||||||||
                                  CTCC TTTG  TGGTAG AACCTTGT
                                    A   C_     G
GAM780   LOC151162 5'  GAGGAAAACCCTTGGAA     21217       CAA   GT
                                  GAGGAAA   ACT  CTTGGAA
                                  |||||||   |||  |||||||
                                  CTCCTTT   TGG  GAACCTT
                                       ___  __
GAM780   LOC151760 5'  GAGAACATGTCTTGG       21218      AA   AAC
                                  GAGG  ACA   TGTCTTGG
                                  ||||  |||   ||||||||
                                  CTCT  TGT   ACAGAACC
                                       __  ___
GAM780   LOC170425 5'  GAGAAGCAAACCACTGGGA   21219      AA     T  T
                                  GAGGA  CAAACTG CT GGA
                                  |||||  ||||||| || |||
                                  CTCTT  GTTTGGT GA CCT
                                     C_      _ C
GAM780   LOC196500 3'  AGAAACAAATGGTGTGGAA   21220        C  TCT
                                  GGAAACAAA TG   TGGAA
                                  |||||||||| ||   |||||
                                  TCTTTGTTT AC   ACCTT
                                       _ CAC
GAM780   LOC199786 3'  GAGGAAACGGTCTCCAGGGA   21221        AAACT    ___
                                  GAGGAAAC    GTCTT   GGA
                                  ||||||||    |||||   |||
                                  CTCCTTTG    CAGAG   CCT
                                       C____    GTC
GAM780   LOC203246 3'  GAGGAAACAGACTGAGAA    21222        A   TCTT
                                  GAGGAAACA ACTG    GGAA
                                  ||||||||| ||||    ||||
                                  CTCCTTTGT TGAC    TCTT
                                       C   ____
GAM780   LOC203377 5'  GAGGAAAACCCTTGGAA     21217       CAA   GT
                                  GAGGAAA   ACT  CTTGGAA
                                  |||||||   |||  |||||||
                                  CTCCTTT   TGG  GAACCTT
                                       ___  __
GAM780   LOC220073 5'  GAGGAAACGAGTGTGTCCAGGG 21189        AAAC_    T_
           A                       GAGGAAAC    TGTCT  GGA
                                  ||||||||    |||||  |||
                                  CTCCTTTG    ACAGG  CCT
                                       CTCAC    TC
GAM780   LOC220073 5'  GAGGAAACGAGTGTGTCCAGGG 21189        AAAC_    T_
           A                       GAGGAAAC    TGTCT  GGA
                                  ||||||||    |||||  |||
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                                CTCCTTTG    ACAGG  CCT
                                    CTCAC    TC
GAM780  LOC220980 3'  GAGAAAGTCTTGGAA      21223      ACAAACT
                                GAGGAA     GTCTTGGAA
                                ||||||     |||||||||
                                CTCTTT     CAGAACCTT
                                 _______
GAM780  LOC221755 3'  AGGAAACAACCCTTTTTGG   21224       A  GTC
                                AGGAAACAA CT   TTGG
                                ||||||||| ||   ||||
                                TCCTTTGTT GG   AACC
                                     G  AAA
GAM780  LOC253933 3'  GAGGAAACAATTTTAGA    21225        ACTGTC
                                GAGGAAACAA    TTGGA
                                ||||||||||    |||||
                                CTCCTTTGTT    AATCT
                                     AA____
GAM780  LOC57107  5'  GGGAAACAAACCAGGGG    21226   A        TCTT
                                G GGAAACAAACTG   GG
                                | ||||||||||||   ||
                                C CCTTTGTTTGGT   CC
                                _         CC__
GAM780  LOC90625  5'  GAGGAAGAAGCTGCCTTGG   21227      ACAAA
                                GAGGAA    CTGTCTTGG
                                ||||||    |||||||||
                                CTCCTT    GACGGAACC
                                   CTTC_
GAM780  LOC90841  5'  GAGGAAACCGAGGTCTGGA   21228       AAACT   T
                                GAGGAAAC    GTCT GGA
                                ||||||||    |||| |||
                                CTCCTTTG    CAGA CCT
                                     GCTC_   _
GAM780  LOC91069  3'  GAGGAAACGAGTGTGTCCAGGG 21189       AAAC_    T_
          A                      GAGGAAAC    TGTCT  GGA
                                ||||||||    |||||  |||
                                CTCCTTTG    ACAGG  CCT
                                     CTCAC    TC
GAM780  LOC91069  3'  GAGGAAACAAGTGTGTCC    21229        AC_
                                GAGGAAACAA   TGTCT
                                ||||||||||   |||||
                                CTCCTTTGTT   ACAGG
                                     CAC
GAM780  LOC92080  3'  GAGGAAAGAGCTGCCTCGG   21230      CAAA
                                GAGGAAA   CTGTCTTGG
                                |||||||   |||||||||
                                CTCCTTT   GACGGAGCC
                                    CTC_
GAM780  LOC93129  3'  GGGAAACAGACTGTCTCA    21231   A     A
                                G GGAAACA ACTGTCTTG
                                | |||||||  |||||||||
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                                C CCTTTGT TGACAGAGT
                                _      C
GAM781  FIGF     3'  TACAGTTTTCCTCATCTGCTCT 21234      ACACC        AA
                                TACA    TCCTCGTCT  CTCT
                                ||||    |||||||||  ||||
                                ATGT    AGGAGTAGA  GAGA
                                  CAAA_        C_
GAM781  NDRG2    3'  CAGCACCTCCCAGGTTAGCTCT 21235    A       C_  C  A
                                CA CACCTCCT  GT TA CTCT
                                || ||||||||  || || ||||
                                GT GTGGAGGG  CA AT GAGA
                                 C       TC  _  C
GAM781  PABPC4   5'  TACGGCCCTCCCCGCGACT   21236     AACA        CTA
                                TAC   CCTCCTCGT   ACT
                                |||   |||||||||   |||
                                ATG   GGAGGGGCG   TGA
                                  CCG_        C__
GAM781  PCDHA9   3'  TACAGCACCCCCTTTGCTC   21237      A       CGTCTAA
                                TACA CACCTCCT      CTC
                                |||| ||||||||      |||
                                ATGT GTGGGGGA      GAG
                                  C       AAC____
GAM781  CARM1    3'  CAGCCACCTGCTCTAACTCT   21238    _  T   CG
                                CA CC CCT  TCTAACTCT
                                || || |||  |||||||||
                                GT GG GGA  AGATTGAGA
                                 C  T   CG
GAM781  CDC14B   3'  CAACATCTTCCAACTC      21239       CCTCC  G
                                CAACA    TC TCTAACTC
                                |||||    || ||||||||
                                GTTGT    AG AGGTTGAG
                                   _____  A
GAM781  CDC14B   3'  CAACATCTTCCAACTC      21239       CCTCC  G
                                CAACA    TC TCTAACTC
                                |||||    || ||||||||
                                GTTGT    AG AGGTTGAG
                                   _____  A
GAM781  GRID1    3'  CACCTCCCCCAACTC       21240         CGT
                                CACCTCCT   CTAACTC
                                ||||||||   |||||||
                                GTGGAGGG   GGTTGAG
                                     ___
GAM781  KIAA0451 3'  TACAACACTCCTTGTACCCT   21241         C    C  CTA
                                TACAACAC TCCT GT   ACTCT
                                |||||||| |||| ||   |||||
                                ATGTTGTG AGGA CA   TGGGA
                                     _    A  ___
GAM781  LIMS1    5'  TACAGAACTTCCTCATCT    21242      AC  C
                                TACA  AC TCCTCGTCT
                                ||||  || |||||||||
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                                ATGT  TG AGGAGTAGA
                                  CT  A
GAM781  MAP3K3   3'  ACACCTCCTCGGGCTCT    21243         TCTAA
                                ACACCTCCTCG    CTCT
                                ||||||||||    ||||
                                TGTGGAGGAGC    GAGA
                                     CC___
GAM781  MBLL39   3'  TACAACCCTTTAATCCAACT  21244      A  CCTC
                                TACAAC CCT   GTCTAACT
                                |||||| |||   ||||||||
                                ATGTTG GGA   TAGGTTGA
                                   _  AAT_
GAM781  MKP-7    3'  TACAGTCTTTCCATCTAACT  21245     ACAC  CC
                                TACA   CT  TCGTCTAACT
                                ||||   ||  ||||||||||
                                ATGT   GA  GGTAGATTGA
                                  CA__  AA
GAM781  PTDSS1   3'  TACAACACTTCTCTCCCT   21246       C  _  G
                                TACAACAC TC CTC TCT
                                |||||||| || ||| |||
                                ATGTTGTG AG GAG GGA
                                     A  A  _
GAM781  TXI1     5'  ACCTCCTCGTAGCTGGCTCT  21247        __  AA
                                ACCTCCTCGT  CT  CTCT
                                ||||||||||  ||  ||||
                                TGGAGGAGCA  GA  GAGA
                                     TC  CC
GAM781  LOC256401 3'  CAACATCTTCCAACTC     21239     CCTCC  G
                                CAACA    TC TCTAACTC
                                |||||    || ||||||||
                                GTTGT    AG AGGTTGAG
                                  _____  A
GAM781  LOC90288  3'  CAACACCTGGCTAGCTC    21248       CCTC T   A
                                CAACACCT   G CTA CTC
                                ||||||||   | ||| |||
                                GTTGTGGA   C GAT GAG
                                     C___ _   C
GAM782  ABH      3'  CCATGTCAAACACTTCTCT   21251    A  T__
                                CCA GTT   TACTTCTCT
                                ||| |||   |||||||||
                                GGT CAG   GTGAAGAGA
                                  A   TTT
GAM782  ADCY7    3'  CCAAGTTGTCTCTAAACA    21252      TTACT
                                CCAAGTT    TCTCTAAACA
                                |||||||    ||||||||||
                                GGTTCAA    AGAGATTTGT
                                     C____
GAM782  ATRX     3'  CCAAGTTTTATTTCAAAC    21253       C   TCT
                                CCAAGTTTTA TTC   AAAC
                                |||||||||| |||   ||||
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                                GGTTCAAAAT AAG   TTTG
                                      A  ___
GAM782  ATRX    3'  CCAAGTTTTATTTCAAAC    21253        C   TCT
                                CCAAGTTTTA TTC   AAAC
                                |||||||||| |||   ||||
                                GGTTCAAAAT AAG   TTTG
                                      A  ___
GAM782  COL17A1  3'  CCCCAAGTGCCATTTTCT    21254       T   C_
                                CCCCAAGT TTA  TTCT
                                |||||||| |||  ||||
                                GGGGTTCA GGT  AAGA
                                     C   AA
GAM782  COL17A1  3'  CCCCAAGTGCCATTTTCT    21254       T   C_
                                CCCCAAGT TTA  TTCT
                                |||||||| |||  ||||
                                GGGGTTCA GGT  AAGA
                                     C   AA
GAM782  DISC1    3'  CCCAAGTTTTGCTTCACT    21255        A   T
                                CCCAAGTTTT CTTC CT
                                |||||||||| ||||  ||
                                GGGTTCAAAA GAAG GA
                                      C   T
GAM782  EFNA3    3'  CCCCAAGTTTGGTACCAAACA  21256         TACTTCT
                                CCCCAAGTTT      CTAAACA
                                ||||||||||      |||||||
                                GGGGTTCAAA      GGTTTGT
                                      CCAT___
GAM782  GALNT7   5'  CCCCAAGTCCTCTCT      21257        TTTA
                                CCCCAAGT    CTTCTCT
                                ||||||||    |||||||
                                GGGGTTCA    GGAGAGA
                                      ____
GAM782  KCNF1    5'  CCCGAGCCTTTTCTAAACA   21258    A   TTTA   C
                                CCC AGT    CTT TCTAAACA
                                ||| |||    ||| ||||||||
                                GGG TCG    GAA AGATTTGT
                                  C  ____  A
GAM782  LPHH1    3'  GTTTCACAATTTCTCTAAACA  21259       ___
                                GTTTTAC   TTCTCTAAACA
                                |||||||   ||||||||||
                                CAAAGTG   AAGAGATTTGT
                                    TTA
GAM782  PIAS1    3'  GCTTGTATACTTTTCTAAACA  21260     ___    C
                                GTTT   TACTT TCTAAACA
                                ||||   ||||| ||||||||
                                CGAA   ATGAA AGATTTGT
                                  CAT    A
GAM782  PIWIL1   3'  CCCAAGTTTCATCCA       21261          CTTC
                                CCCAAGTTTTA    TCTA
                                ||||||||||    ||||
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                              GGGTTCAAAGT   AGGT
                                    ____
GAM782  POU5F1   3' CCAGGTTTTCTTTCCCTA   21262    A   AC
                              CCA GTTTT  TTCTCTA
                              ||| |||||  |||||||
                              GGT CAAAA  AAGGGAT
                                C    GA
GAM782  POU5F1   3' CCAGGTTTTCTTTCCCTA   21262    A   AC
                              CCA GTTTT  TTCTCTA
                              ||| |||||  |||||||
                              GGT CAAAA  AAGGGAT
                                C    GA
GAM782  RNF28    3' CCCTAGTCCCTGCTCTCT   21263    A    AC
                              CCC AGTTTT  TTCTCT
                              ||| ||||||  ||||||
                              GGG TCAGGG  GAGAGA
                                A     AC
GAM782  SPTAN1   3' CCTAAGTCTTATTCCAAGCTAA 21264   C      C   ___
                              CC AAGTTTTA TTCT   CTAA
                              || ||||||||| ||||  ||||
                              GG TTCAGAAT AAGG   GATT
                               A       _   TTC
GAM782  TAF7     5' CCAAGTCTTTTCTCTAAA   21265        AC
                              CCAAGTTTT  TTCTCTAAA
                              |||||||||  |||||||||
                              GGTTCAGAA  AAGAGATTT
                                    __
GAM782  TNFSF4   3' CCCTTAAGCATTCTCTAAA   21266    __   TTTAC
                              CCC  AAGT    TTCTCTAAA
                              |||  ||||    |||||||||
                              GGG  TTCG    AAGAGATTT
                                AA   T____
GAM782  UNC13    3' CCCCAAATTTTTCCTTAAA   21267         ACT  TC
                              CCCCAAGTTTT   TC  TAAA
                              ||||||||||   ||  ||||
                              GGGGTTTAAAA   AG  ATTT
                                    ___  GA
GAM782  ABCA9    3' CCAAGTCTTTGCTATTGTAAAC 21268        A_  TCTC
           A                   CCAAGTTTT  CT    TAAACA
                              |||||||||  ||    ||||||
                              GGTTCAGAA  GA    ATTTGT
                                   AC  TAAC
GAM782  CNK2     3' CCGATCTAAATTCTCTAAACA 21269    AA   TAC
                              CC  GTTT   TTCTCTAAACA
                              ||  ||||   ||||||||||
                              GG  TAGA   AAGAGATTTGT
                               C_    TTT
GAM782  CXorf1   3' CAAGTTTCCTCTAAA      21270       TTAC
                              CAAGTT    TTCTCTAAA
                              ||||||    |||||||||
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                                GTTCAA   AGGAGATTT
                                    ____
GAM782  DKFZP566K0524 3'  CCCAAATCCAGTTTCTAAA   21271        TACTTC
                                CCCAAGTTT     TCTAAA
                                |||||||||     ||||||
                                GGGTTTAGG     AGATTT
                                     TCAA__
GAM782  EIF5     3'  CCCAAGTCTTACACCAAA    21272          TTCT
                                CCCAAGTTTTAC   CTAAA
                                ||||||||||||   |||||
                                GGGTTCAGAATG   GGTTT
                                       T___
GAM782  FLJ10759  3'  CCTCCAGTTCCCACCTCT    21273    _  AG
                                CC CCA  TTTTACTTCT
                                || |||  ||||||||||
                                GG GGT  AGGGTGGAGA
                                 A  CA
GAM782  FLJ11017  5'  CCCTGAGTTTTCCTTCCCCA   21274    CA     A
                                CCC  AGTTTT CTTCTCTA
                                |||  |||||| ||||||||
                                GGG  TCAAAA GAAGGGGT
                                  AC     G
GAM782  FLJ12439  3'  CCCAAGTTTTTTTGCTCCA    21275         ACTT
                                CCCAAGTTTT    CTCTA
                                ||||||||||   |||||
                                GGGTTCAAAA    GAGGT
                                      AAAC
GAM782  IGF2AS    3'  CCCTAGGTTTAGCTTCTCT    21276     A  T   _
                                CCC AG TTTA CTTCTCT
                                ||| || |||| |||||||
                                GGG TC AAAT GAAGAGA
                                  A  C    C
GAM782  KIAA0218  3'  CCAATCAGCTCTCTAAACA    21277     GTT   C
                                CCAA   TTA TTCTCTAAACA
                                ||||   ||| ||||||||||
                                GGTT   AGT GAGAGATTTGT
                                  ___   C
GAM782  MGC20253  3'  CCCCACAAACTTTTTTAAACA  21278      AGTTTT   CTC
                                CCCCA     ACTT   TAAACA
                                |||||     ||||   ||||||
                                GGGGT     TGAA   ATTTGT
                                   GTT___    AAA
GAM782  SCHIP1    3'  CCAACTTAAAATCTCTAAACA  21279     G  TTACT
                                CCAA TT    TCTCTAAACA
                                |||| ||    ||||||||||
                                GGTT AA    AGAGATTTGT
                                  G  TTTT_
GAM782  TEB4     3'  AAGTTTTATTCTGTAAACA   21280        C   C
                                AAGTTTTA TTCT TAAACA
                                |||||||| |||| ||||||
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                                TTCAAAAT AAGA ATTTGT
                                   _   C
GAM782  ZNF306   3'  CAGGTCTTACCTCTTCTAGACA 21281    A        _  A
                                CA GTTTTACTTCT CTA ACA
                                || |||||||||| ||| |||
                                GT CAGAATGGAGA GAT TGT
                                 C         A  C
GAM782  LOC122553 3' CCCTGAGCTTTGTTTCTCCA  21282    CA    AC
                                CCC  AGTTTT  TTCTCTA
                                |||  ||||||  |||||||
                                GGG  TCGAAA  AAGAGGT
                                  AC     CA
GAM782  LOC144465 3' GCTTCTAGTATTTCTCTAAACA 21283      AC____
                                GTTTT     TTCTCTAAACA
                                |||||     ||||||||||
                                CGAAG     AAGAGATTTGT
                                   ATCATA
GAM782  LOC146894 3' CCAAGTTTTGCATACTGAACA  21284         ACTTCT  A
                                CCAAGTTTT     CT AACA
                                |||||||||     || ||||
                                GGTTCAAAA     GA TTGT
                                      CGTAT_  C
GAM782  LOC151742 3' CCCAGCATTTTCTCTAAA    21285      A  TTTAC
                                CCCA GT     TTCTCTAAA
                                |||| ||     |||||||||
                                GGGT CG     AAGAGATTT
                                  _  TAA__
GAM782  LOC201910 3' CCCTAAGCTTTACTTTCCTA   21286     C         CT
                                CCC AAGTTTTACTT  CTA
                                ||| ||||||||||  |||
                                GGG TTCGAAATGAA  GAT
                                  A         AG
GAM782  LOC203378 5' CCAAATTTCTCTAAA       21287        TTACT
                                CCAAGTT    TCTCTAAA
                                |||||||    |||||||||
                                GGTTTAA    AGAGATTT
                                   _____
GAM782  LOC253070 3' CCCTGGAGTTGCTCTAAAC    21288     CA_   TTACTT
                                CCC   AGTT     CTCTAAAC
                                |||   ||||     ||||||||
                                GGG   TCAA     GAGATTTG
                                  ACC    C_____
GAM782  LOC51020  3' CCCCGGTTTATATCTCTAAA   21289      AA    TACT
                                CCCC  GTTT   TCTCTAAA
                                ||||  ||||   ||||||||
                                GGGG  CAAA   AGAGATTT
                                  C_   TAT_
GAM782  LOC92609  3' CCCAAGTTCTTGCTTCTTTTGA 21290          A_    CTA_
            ACA                   CCCAAGTTTT  CTTCT    AACA
                                ||||||||||  |||||   ||||
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                                GGGTTCAAGA  GAAGA    TTGT
                                      AC     AAAC
GAM783  PACE4    3'  GTGAGACAAAGGTCATCTT    21293      A
                                GTGA GGCAAAGGTCATCTT
                                |||| ||||||||||||||
                                CACT CTGTTTCCAGTAGAA
                                  _
GAM783  PROL4    3'  TGAAGGAAGTTATCTTCTT    21294       CAA    C
                                TGAAGG   AGGT ATCTTCTT
                                ||||||   |||| ||||||||
                                ACTTCC   TTCA TAGAAGAA
                                   ___    A
GAM783  ABLIM    3'  TATGAAGGTAAATTCAAATGTT 21295       C   GG   TC____
           TTCTT                 GTGAAGG AAA  TCA     TTCTT
                                |||||||  |||  |||     |||||
                                TACTTCC TTT  AGT     AAGAA
                                    A   A_   TTACAA
GAM783  ABLIM    3'  TATGAAGGTAAATTCAAATGTT 21295       C   GG   TC____
           TTCTT                 GTGAAGG AAA  TCA     TTCTT
                                |||||||  |||  |||     |||||
                                TACTTCC TTT  AGT     AAGAA
                                    A   A_   TTACAA
GAM783  DKFZp434O0515 3'  TGTGGAGGAAGGGCAACTT    21296      A   CA    T  T
                                TGTG AGG  AAGG CA CTT
                                |||| |||  |||| || |||
                                ACAC TCC  TTCC GT GAA
                                  C   __   C  T
GAM783  DKFZp564K142 3'  TGTTAAGGCACTACACATCTTC 21297     G     AAGGT
           TT                    TGT AAGGCA     CATCTTCTT
                                ||| ||||||     |||||||||
                                ACA TTCCGT     GTAGAAGAA
                                  A     GATGT
GAM783  FLJ21034  3'  GTGAAGGCAATCTCTTCT    21298         AAG   A
                                GTGAAGGCA   GTC TCTTCT
                                |||||||||   ||| ||||||
                                CACTTCCGT   TAG AGAAGA
                                     ___   _
GAM783  GPR105    5'  TGAAGGCAGAGGCCTCTT    21299         A    A
                                TGAAGGCA AGGTC TCTT
                                |||||||| ||||| ||||
                                ACTTCCGT TCCGG AGAA
                                    C    _
GAM783  HSU79303  3'  TGGAAGGTGCCCAGGATCTTCT 21300    T   __  AA   TC
           T                     TG GAAG  GC  AGG  ATCTTCTT
                                || ||||  ||  |||  ||||||||
                                AC CTTC  CG  TCC  TAGAAGAA
                                  _   CA  GG   __
GAM783  KIAA0557  3'  TGGAAGGTGAAGGCTTCT    21301    T    CA    TCAT
                                TG GAAGG  AAGG    CTTCT
                                || |||||  ||||    |||||
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                                AC CTTCC  TTCC    GAAGA
                                 _    AC   ____
GAM783  NS1-BP   3'  TGTGGAGGAGAGGGGACTTCTT 21302     A   CAA   TCAT
                                TGTG AGG   AGG    CTTCTT
                                |||| |||   |||    ||||||
                                ACAC TCC   TCC    GAAGAA
                                  C   TC_   CCT_
GAM783  PGLYRP   3'  TGTGAAGGCAAAAGGTCACAGC 21303          _     CT
          CT                     TGTGAAGGCAAA GGTCAT  TCT
                                ||||||||||| ||||||  |||
                                ACACTTCCGTTT CCAGTG  GGA
                                       T     TC
GAM783  WNT16    3'  TGTGGGGCAGGGAAACATTTCT 21304     AA    AA  T_   C
          T                     TGTG  GGCA  GG  CAT TTCTT
                                ||||  ||||  ||  ||| |||||
                                ACAC  CCGT  CT  GTA AAGAA
                                  C_    CC  TT   _
GAM783  WNT16    3'  TGTGGGGCAGGGAAACATTTCT 21304     AA    AA  T_   C
          T                     TGTG  GGCA  GG  CAT TTCTT
                                ||||  ||||  ||  ||| |||||
                                ACAC  CCGT  CT  GTA AAGAA
                                  C_    CC  TT   _
GAM783  LOC145623 3'  TGTGAAAGGCAAAATGGT    21305       _     __
                                TGTGAA GGCAAA  GGT
                                |||||| ||||||  |||
                                ACACTT CCGTTT  CCA
                                    T     TA
GAM783  LOC221914 3'  TGTGGGTGGCAGAGGTCAC    21306     AA_    A
                                TGTG   GGCA AGGTCAT
                                ||||   |||| |||||||
                                ACAC   CCGT TCCAGTG
                                  CCA    C
GAM783  LOC257466 3'  TGTGAAAGCAGGATTTCTT    21307          AA  TCA
                                TGTGAAGGCA  GG   TCTT
                                ||||||||||  ||   ||||
                                ACACTTTCGT  CC   AGAA
                                      __  TAA
GAM784  AF1Q     3'  TGGAGTAGACAGATA      21310    A    AACATT
                                TG GAGTA     GACGGATA
                                || |||||     ||||||||
                                AC CTCAT     CTGTCTAT
                                 _    _______
GAM784  AOC2     3'  TGAGAGGAACATTGAGGG    21311       TA       C
                                TGAGAG  AACATTGA GG
                                ||||||  |||||||| ||
                                ACTCTC  TTGTAACT CC
                                   C_       C
GAM784  KRT13    5'  TGAGAGCAGGTGCAGATA    21312        AACAT  A
                                TGAGAGTA    TG CGGATA
                                ||||||||    || ||||||
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                                ACTCTCGT    AC GTCTAT
                                    CC___  _
GAM784  MTMR8    3'  TGAGAATAAATGTAAATGGATA 21313         CATT  C
            AA                    TGAGAGTAAA   GA GGATAAA
                                  ||||||||||   || |||||||
                                  ACTCTTATTT   TT CCTATTT
                                      ACAT  A
GAM784  STXBP1   3'  TGAGAGCAGGCACTGAGGG   21314        AA    C
                                  TGAGAGTA  CATTGA GG
                                  ||||||||  |||||| ||
                                  ACTCTCGT  GTGACT CC
                                      CC    C
GAM784  SVIL     3'  TGAGAGTAAAATTGTAGA    21315         C   AC
                                  TGAGAGTAAA ATTG  GGA
                                  |||||||||| ||||  |||
                                  ACTCTCATTT TAAC  TCT
                                      _   A_
GAM784  SVIL     3'  TGAGAGTAAAATTGTAGA    21315         C   AC
                                  TGAGAGTAAA ATTG  GGA
                                  |||||||||| ||||  |||
                                  ACTCTCATTT TAAC  TCT
                                      _   A_
GAM784  AKL3L    3'  TAAGAGTAAATATGCCATGGA  21316         CAT  AC__
                                  TGAGAGTAAA  TG   GGA
                                  |||||||||  ||   |||
                                  ATTCTCATTT  AC   CCT
                                      AT_  GGTA
GAM784  CHIT1    3'  TGAGAGCAGAAAGCCTGGATAA 21317        AACATTGAC
            A                     TGAGAGTA       GGATAAA
                                  ||||||||       |||||||
                                  ACTCTCGT       CCTATTT
                                      CTTTCGGA_
GAM784  CL25084  3'  TGAGAGTAAACATACTCATAA  21318          TG  GG
                                  TGAGAGTAAACAT  AC  ATAA
                                  ||||||||||||  ||  ||||
                                  ACTCTCATTTGTA  TG  TATT
                                      __  AG
GAM784  CYLD     3'  TGAGAGTAGACTCTTAATAAA  21319        A  A_   CG
                                  TGAGAGTA AC  TTGA  GA
                                  |||||||| ||  ||||  ||
                                  ACTCTCAT TG  AATT  TT
                                      C  AG   AT
GAM784  OSBPL1A  3'  TGAGAATAAACATTGTATAGG 21320           AC__
                                  TGAGAGTAAACATTG   GG
                                  ||||||||||||||   ||
                                  ACTCTTATTTGTAAC   CC
                                       ATAT
GAM784  OSBPL1A  3'  TGAGAATAAACATTGTATAGG 21320           AC__
                                  TGAGAGTAAACATTG   GG
                                  ||||||||||||||   ||
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                                ACTCTTATTTGTAAC  CC
                                      ATAT
GAM784  OSBPL1A  3'  TGAGAATAAACATTGTATAGG  21320          AC__
                                TGAGAGTAAACATTG  GG
                                |||||||||||||||  ||
                                ACTCTTATTTGTAAC  CC
                                      ATAT
GAM784  RIP60    3'  TGGGAGGGGCGACAGATAA  21321   A  TAAACAT
                                TG GAG     TGACGGATAA
                                || |||     ||||||||||
                                AC CTC     GCTGTCTATT
                                 C  CCC____
GAM784  SDC3     3'  TGAGGATAAACATTCTTGGA  21322    AG     GAC
                                TGAG  TAAACATT  GGA
                                ||||  ||||||||  |||
                                ACTC  ATTTGTAA  CCT
                                   CT      GAA
GAM784  TINF2    3'  TGAGAGCAAGCAAAGAGGATA  21323       A  TT  C
                                TGAGAGTAA CA  GA GGATA
                                |||||||||  ||  ||  |||||
                                ACTCTCGTT GT  CT CCTAT
                                      C  TT  _
GAM784  LOC115297 3'  TGAGGTAAACAGATAGA    21324    A     TT  CG
                                TGAG GTAAACA  GA  GA
                                |||| |||||||  ||  ||
                                ACTC CATTTGT  CT  CT
                                  _     __  AT
GAM784  LOC128844 5'  TGAGAGTAGTGACTGTGATGGA 21325       A__  AT  C
                                TGAGAGTA  AC  TGA GGA
                                ||||||||  ||  ||| |||
                                ACTCTCAT  TG  ACT CCT
                                     CAC  AC  A
GAM784  LOC146489 5'  TGAGGAGTGGAGACTGCGGATA 21326    _  AAAC  A
          AA                    TGAG AGT   ATTG CGGATAAA
                                |||| |||   |||| ||||||||
                                ACTC TCA   TGAC GCCTATTT
                                  C  CCTC  _
GAM784  LOC160711 5'  TGAAAGTGAACACTGATAG   21327       A      CG
                                TGAGAGT AACATTGA  G
                                ||||||| ||||||||  |
                                ACTTTCA TTGTGACT  C
                                     C       AT
GAM784  LOC256594 5'  TGAGAGTGGAGACAGACA    21328       AAACATT
                                TGAGAGT      GACGGATA
                                |||||||      ||||||||
                                ACTCTCA      CTGTCTGT
                                     CCT_____
GAM784  LOC257466 5'  TGAGAGCAGCCAGTGGGTAA  21329       AA  T  AC  A
                                TGAGAGTA  CA TG  GG TAA
                                ||||||||  || ||  || |||
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                                ACTCTCGT  GT AC  CC ATT
                                    CG  C  __  _
GAM784  LOC89932  3'  TGAGGCTAAACACTGGGTGG  21330     AG       AC_
                                TGAG  TAAACATTG   GG
                                ||||  |||||||||   ||
                                ACTC  ATTTGTGAC   CC
                                  CG       CCA
GAM785  BSN     3'  TGGGGATTCCTTTTTACCTGCT 21333     AA   CA
                                TGG  GAT  TTTTTTTACCTGCT
                                |||  |||  ||||||||||||||
                                ACC  CTA  GGAAAAATGGACGA
                                  C_  A_
GAM785  GARP    3'  TGGGTGAGGCTTTTTACCTG  21334     AA  TCAT
                                TGG  GA   TTTTTTACCTG
                                |||  ||   ||||||||||
                                ACC  CT   GAAAAATGGAC
                                  CA  CC__
GAM785  SIM2    3'  TGGAAGCTCATTTTTTAAACAC 21335       A       T_  _
            TGCT                    TGGAAG TCATTTTTT  AC CTGCT
                                |||||| |||||||||  || |||||
                                ACCTTC AGTAAAAAA  TG GACGA
                                   G       TT  T
GAM785  SYT4    3'  TGGAGGACATTTTTTTA    21336     A  T
                                TGGA GA CATTTTTTTA
                                |||| || ||||||||||
                                ACCT CT GTAAAAAAAT
                                  C  _
GAM785  C8orf17  3'  TGGAAGATCATTTTG      21337           TTTTACC
                                TGGAAGATCATTT      TG
                                ||||||||||||      ||
                                ACCTTCTAGTAAA      AC
                                          ________
GAM785  DKFZp761J139 5'  TGGAGGATATTTTTTTCCT   21338     A  C      A
                                TGGA GAT ATTTTTTT CCT
                                |||| ||| |||||||| |||
                                ACCT CTA TAAAAAAA GGA
                                  C  _      _
GAM785  KIAA0820  3'  TGGCAGATCATTCAAAGCTATC 21339     A       TT__  C
            TG                    TGG AGATCATTT   TTA CTG
                                ||| |||||||||   ||| |||
                                ACC TCTAGTAAG   GAT GAC
                                  G       TTTC  A
GAM785  KIAA1200  3'  TGAAAGAAACTTTTTTTTACCT 21340       TCA_
            GCT                   TGGAAGA   TTTTTTTACCTGCT
                                |||||||   ||||||||||||||
                                ACTTTCT   AAAAAAATGGACGA
                                    TTGA
GAM785  KIAA1391  3'  TGGGTGAATGATTTTTTACCTG 21341     AA  TCAT
            CT                    TGG  GA   TTTTTTACCTGCT
                                |||  ||   ||||||||||||
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                                ACC  CT    AAAAAATGGACGA
                                  CA  TACT
GAM785  NT5C1B    5'  GACTCATTTTTTTACCTG    21342    _
                                GA TCATTTTTTTACCTG
                                || ||||||||||||||
                                CT AGTAAAAAAATGGAC
                                 G
GAM785  SS18L2    3'  TGGAAGATTATTCTATTGC    21343        C     TTTACC
                                TGGAAGAT ATTTT     TGC
                                |||||||| |||||     |||
                                ACCTTCTA TAAGA     ACG
                                     A     TA____
GAM785  TRIM2     3'  GGCAGCGATTTTTTACCTG    21344    A  ATCAT
                                GG AG     TTTTTTACCTG
                                || ||     ||||||||||
                                CC TC     AAAAAATGGAC
                                 G  GCT__
GAM785  LOC146714 5'  TGGAGGAGCATTCCCTGC    21345      A  T     TTTTA
                                TGGA GA CATTT     CCTGC
                                |||| || |||||     |||||
                                ACCT CT GTAAG     GGACG
                                  C  C    _____
GAM785  LOC152179 5'  TGGAAGATTTTCCCTCGTTTGC 21346         CA       ACC
           T                     TGGAAGAT  TTTTTTT   TGCT
                                |||||||  |||||||  ||||
                                ACCTTCTA  AAGGGAG   ACGA
                                     A_      CAA
GAM785  LOC157909 5'  TGGAGTGTCATTTTTTTGGTAG 21347      AGA        ACCT
           CT                     TGGA   TCATTTTTTT    GCT
                                ||||   ||||||||||   |||
                                ACCT   AGTAAAAAAA    CGA
                                  CAC         CCAT
GAM785  LOC220929 5'  TGGGGATCATTTTTTAC     21348     AA         T
                                TGG  GATCATTTTTT AC
                                |||  |||||||||| ||
                                ACC  CTAGTAAAAAA TG
                                  C_          _
GAM785  LOC253792 5'  GGAAGATCGTTTTACCACTTCT 21349         A    T    __
           GCT                     GGAAGATC TTTT TTAC  CTGCT
                                |||||||| |||| ||||  |||||
                                CCTTCTAG AAAA GGTG  GACGA
                                     C    T    AA
GAM785  LOC256965 3'  TGGGAATCATTCTTATGCTTGC 21350     AA         TTACC
           T                     TGG  GATCATTTTT     TGCT
                                |||  ||||||||||    ||||
                                ACC  TTAGTAAGAA    ACGA
                                  C_         TACGA
GAM786  GPRK6     3'  TGCTGGTGGGGGCCTCGGGCT  21353     CA  T    A_    CG
                                TGC  GT GGGG  TTGG  GCT
                                |||  || ||||  ||||  |||
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                                ACG  CA CCCC  AGCC  CGA
                                  AC  C    GG   __
GAM786  INHBB    3'  TGTCAGTTGAGGGTTCTCGCT  21354    C       A  GG  G
                                TG CAGTTGGGG TT  CG CT
                                || |||||||| ||  || ||
                                AC GTCAACTCC AA  GC GA
                                  A        C  GA  _
GAM786  PLTP     3'  TGCCAGCTTGGGGATTGA    21355         _
                                TGCCAGTT GGGGATTGG
                                |||||||| |||||||||
                                ACGGTCGA CCCCTAACT
                                     A
GAM786  DKFZp761G2113 5'  TGCTATTGGCAATCCGGCGG  21356     CA    G   _
                                TGC  GTTGG GATT GGCGG
                                |||  ||||| |||| |||||
                                ACG  TAACC TTAG CCGCC
                                  A_    G   G
GAM787  FLJ13840  5'  GTGTTTTCGGCGTCGTAG    21359     AGG    A
                                GTGT   TTTCG CGTCGTAG
                                ||||   ||||| ||||||||
                                CACA   AAAGC GCAGCATC
                                   ___    C
GAM788  ADH1A    5'  CAGGAGACTGGTGAGTCC    21362        G   A  GG
                                CAGGAGAC GGT AG  CC
                                |||||||| ||| ||  ||
                                GTCCTCTG CCA TC  GG
                                     A   C  A_
GAM788  IFITM2   3'  GAGGATAAAGGGCTGATGC   21363    C     _   C
                                GA GGGTAA GGGC GATGC
                                || |||||| |||| |||||
                                CT CCTATT CCCG CTACG
                                  _     T   A
GAM788  IGFBP1   5'  CAGCAGACAGGGGCCGATG   21364    G      TAAG
                                CAG AGACGGG    GGCCGATG
                                ||| |||||||    ||||||||
                                GTC TCTGTCC    CCGGCTAC
                                  G      ____
GAM788  LTBR     5'  GGGACGGGACTCAGGGCCGATG 21365    A     TA__
                                GG GACGGG    AGGGCCGATG
                                || ||||||    ||||||||||
                                CC CTGCCC    TCCCGGCTAC
                                  _     TGAG
GAM788  PPP2R5E  5'  GGAGACGGGCGAGGTGGCGCAT 21366         TA  ________  CGAT
          CG                    GAGACGGG  AGG      GC   G
                                ||||||||  |||      ||   |
                                CTCTGCCC  TCC      CG   C
                                     GC   ACCGIII  TAGC
GAM788  SOX12    3'  GGTGACAGGAAGGGCCGGTGC  21367    A     T      A
                                GG GACGGG AAGGGCCG TGC
                                || |||||| |||||||| |||
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                                CC CTGTCC TTCCCGGC ACG
                                 A     _      C
GAM788  TRPM2    5'  CAGGAAGATGAGGCTGATG   21368     GAC   AA   C
                                CAGGA  GGGT  GGGC GATG
                                |||||  ||||  |||| ||||
                                GTCCT  TCTA  TCCG CTAC
                                   ___   C_   A
GAM788  USH2A    3'  CAGGAGGAGGGTAAGGCCA   21369      AC      G
                                CAGGAG  GGGTAAGG CCG
                                ||||||  |||||||| |||
                                GTCCTC  CCCATTCC GGT
                                   CT      _
GAM788  XRCC3    3'  AGAGGTGGGTGAGGAGGAGC   21370     AC   A   CC  T
                                GGAG  GGGT AGGG  GA GC
                                ||||  |||| ||||  || ||
                                TCTC  CCCA TCCT  CT CG
                                  CA   C   C_ _
GAM788  B3GALT6  3'  TGAGAGACGGGCCTGGTGC   21371   A       AA  _
                                C GGAGACGGGT  GG GC
                                | ||||||||||  || ||
                                A TCTCTGCCCG  CC CG
                                 C        GA  A
GAM788  FLJ00001 3'  GGAGACGGAGGGGCTGGTGC   21372        TAA   CGA
                                GGAGACGGG   GGGC   TGC
                                |||||||||   ||||   |||
                                CCTCTGCCT   CCCG   ACG
                                     C__    ACC
GAM788  FLJ10101 3'  GGAGACAGGTGGGAGGACTGC  21373        AA   CC  _
                                GGAGACGGGT  GGG  GA TGC
                                ||||||||||  |||  || |||
                                CCTCTGTCCA  CCC  CT ACG
                                      __   TC  G
GAM788  FLJ14327 3'  GGGAGGCAGGACTGATG     21374    A  CG    A    C
                                GG GA  GGTA GGGC GATG
                                || ||  |||| |||| ||||
                                CC CT  CCGT CCTG CTAC
                                 _ __    _    A
GAM788  KIAA0773 3'  CAGGAGACGGGTGGGGAATAGC 21375          AA   CCGAT
                                CAGGAGACGGGT  GGG    GC
                                ||||||||||||  |||    ||
                                GTCCTCTGCCCA  CCC    CG
                                      __   CTTAT
GAM788  SDC3     5'  AGGGGATGGGGGAGGGAGAAGC 21376     A  C   TA    CC  T
                                AGG GA GGG  AGGG  GA GC
                                ||| || |||  ||||  || ||
                                TCC CT CCC  TCCC  CT CG
                                  C  A   CC    T_  T
GAM788  LOC130536 5'  GGCTACATGAAGGGCTGATG  21377    AG   GGT     C
                                GG  ACG   AAGGGC GATG
                                ||  |||   |||||| ||||
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                                CC  TGT   TTCCCG CTAC
                                 GA   AC_     A
GAM788   LOC145980 5'  GAGACGGGTGGTCCAGTGC   21378         AA  G   A
                                GAGACGGGT  GG CCG TGC
                                |||||||||  || ||| |||
                                CTCTGCCCA  CC GGT ACG
                                     __  A   C
GAM788   LOC221755 3'  AGGGGGTGGGTAAGGGGCTGC  21379     AGAC       CCGA
                                AGG   GGGTAAGGG   TGC
                                |||   |||||||||   |||
                                TCC   CCCATTCCC   ACG
                                  CCCA       CG__
GAM788   LOC222237 3'  CAGGAGGCTGGTGAAGGGTGC  21380       ACG  _    CCGA
                                CAGGAG   GGT AAGGG   TGC
                                ||||||   ||| |||||   |||
                                GTCCTC   CCA TTCCC   ACG
                                   CGA   C    _____
GAM788   LOC255030 3'  CAGTAGATGGGTGGCCAATG   21381     G   C   AAG
                                CAG AGA GGGT   GGCCGATG
                                ||| ||| ||||   ||||||||
                                GTC TCT CCCA   CCGGTTAC
                                  A   A   ___
GAM788   LOC255589 3'  CAGGAGACCCTGGGGCTGATG  21382         GGGTAA   C
                                CAGGAGAC     GGGC GATG
                                ||||||||     |||| ||||
                                GTCCTCTG     CCCG CTAC
                                     GGAC__    A
GAM788   LOC256000 5'  GGCGGACGGGAAGCCGATGC   21383    A_     TAA
                                GG  GACGGG   GGGCCGATGC
                                ||  ||||||   ||||||||||
                                CC  CTGCCC   TTCGGCTACG
                                 GC     ___
GAM788   LOC257000 3'  CAGGGGGTGGGCACAGGTG   21384     AGAC   AA   _  A_
                                CAGG   GGGT  GGGC CG  TG
                                ||||   ||||  |||| ||  ||
                                GTCC   CCCA  CCCG GT  AC
                                  _____   __    T  CC
GAM789   C5R1     3'  GAATAACATTCTTGAAATGA   21387         AAG      C
                                GAATAGCAT   TTTGAAA GA
                                |||||||||   ||||||| ||
                                CTTATTGTA   GAACTTT CT
                                     A__      A
GAM789   KIAA1691  3'  TCGAATTGCATAGTGAGA    21388       A    A  TT
                                TCGAAT GCATA GT  GA
                                ||||||  ||||| ||  ||
                                AGCTTA CGTAT CA  CT
                                   A     _  CT
GAM790   MIG2     5'  CTCGCGGGGCGGCGGT      21391       ACCA
                                TTTGC    GGGCGGCGGT
                                |||||    ||||||||||
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                                GAGCG   CCCGCCGCCA
                                  C___
GAM790  PEG10    3'  ACTTTTGCTTGCAGTGGT    21392        ACCAGG   C
                                ACTTTTGC     GCGG GGT
                                ||||||||     |||| |||
                                TGAAAACG     CGTC CCA
                                    AA____    A
GAM790  LOC220753 3'  TTTTGCACACAGTGGT     21393        CAGG   C
                                TTTTGCAC    GCGG GGT
                                ||||||||    |||| |||
                                AAAACGTG    TGTC CCA
                                    ____   A
GAM790  LOC90499  3'  AACTCTTGCACCACGTGGT   21394          AGG  GC
                                AACTTTTGCACC   GCG  GGT
                                ||||||||||||   |||  |||
                                TTGAGAACGTGG   TGC  CCA
                                     ___   A_
GAM791  SQLE     3'  TGGTACTATGCTATATATATCC 21397    A   G  A
            TC                    TG TAC AT CTATATGTATTCTT
                                || ||| || ||||||||||||||
                                AC ATG TA GATATATATAGGAG
                                 C   A  C
GAM791  LOC152925 3'  GATGCTAGCATGTATTCT    21398     A  _
                                GAT CTA TATGTATTCT
                                ||| ||| ||||||||||
                                CTA GAT GTACATAAGA
                                  C   C
GAM791  LOC252983 5'  GATACTACAGTAGATGTATT   21399        _____
                                GATACTAT    ATGTATT
                                ||||||||    |||||||
                                CTATGATG    TACATAA
                                    TCATC
GAM792  DNA2L    3'  TCTAGAATACTGAAATAC    21402         AA
                                TCTAGAATAC  AAATAT
                                ||||||||||  ||||||
                                AGATCTTATG  TTTATG
                                     AC
GAM792  DYRK2    3'  TAGAACACAAAAAGTTTCT   21403          TATGG
                                TAGAATACAAAAA    TCT
                                ||||||||||||    |||
                                ATCTTGTGTTTTT    AGA
                                     CAA__
GAM792  DYRK2    3'  TAGAACACAAAAAGTTTCT   21403          TATGG
                                TAGAATACAAAAA    TCT
                                ||||||||||||    |||
                                ATCTTGTGTTTTT    AGA
                                     CAA__
GAM792  PGK1     3'  TCTAGAATGCACAATGGT    21404        A  AAAAT
                                TCTAGAAT CA    ATGGT
                                ||||||| ||    |||||
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                                AGATCTTA GT    TACCA
                                    C  GT___
GAM792  SEPP1    3'  TCCATCATAAAAAATATGGT  21405    GA  C
                                TCTA  ATA AAAAATATGGT
                                ||||  ||| ||||||||||
                                AGGT  TAT TTTTTATACCA
                                  AG  _
GAM792  SEPP1    3'  TCCATCATAAAAAATATGGT  21405    GA  C
                                TCTA  ATA AAAAATATGGT
                                ||||  ||| ||||||||||
                                AGGT  TAT TTTTTATACCA
                                  AG  _
GAM792  SMARCA3  3'  TCTGGAATGCAAATATGGT  21406    A   ACAA
                                TCT GAAT   AAATATGGT
                                ||| ||||   |||||||||
                                AGA CTTA   TTTATACCA
                                  C   CG__
GAM792  STC1     3'  TCTAACTTAGAATATGGTCTA  21407     AATACAAA
                                TCTAG      AATATGGTCTA
                                |||||      ||||||||||
                                AGATT      TTATACCAGAT
                                   GAATC___
GAM792  UTY      3'  TAGAAACAAAAATCACAAATCT 21408     T      AT__
                                TAGAA ACAAAAAT   GGTCT
                                ||||| ||||||||   |||||
                                ATCTT TGTTTTTA   TTAGA
                                   _      GTGT
GAM792  FLJ20343 3'  TAAAATACAAAAATGGC    21409         AT
                                TAGAATACAAAA  ATGGT
                                ||||||||||||  |||||
                                ATTTTATGTTTT  TACCG
                                        __
GAM792  GMPPB    5'  CTAGAATACAGGACTTGG    21410        AAA  A
                                CTAGAATACA   AT TGG
                                ||||||||||   || |||
                                GATCTTATGT   TG ACC
                                      CC_  A
GAM792  KIAA0062 3'  GAATGCAGGAATACAGTCT   21411    A  AA
                                GAAT CA  AATATGGTCT
                                |||| ||  ||||||||||
                                CTTA GT  TTATGTCAGA
                                  C  CC
GAM792  KIAA0831 3'  CAGAATACAAGAAAATAGT   21412        A  T
                                TAGAATACAA AA ATGGT
                                |||||||||| || |||||
                                GTCTTATGTT TT TATCA
                                      C  T
GAM792  KIAA0940 3'  TCTAGAATACAAAAAGTAGT  21413           TA
                                TCTAGAATACAAAAA  TGGT
                                ||||||||||||||  ||||
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                                AGATCTTATGTTTTT  ATCA
                                       C_
GAM792  KIAA1729  3'  TCTAGAATATAAAAACGTTCTA 21414        C     ATGG
                                TCTAGAATA AAAAAT    TCTA
                                ||||||||| ||||||    ||||
                                AGATCTTAT TTTTTG    AGAT
                                     A     CA__
GAM792  PAK7      3'  TCTAGAATGCACAGGCCT    21415        A  AAAATAT
                                TCTAGAAT CA      GGTCT
                                |||||||| ||      |||||
                                AGATCTTA GT      CCGGA
                                    C  GT_____
GAM792  RERG      3'  CAGAATACAAGAGTCT      21416         AAATAT
                                TAGAATACAA     GGTCT
                                ||||||||||     |||||
                                GTCTTATGTT     TCAGA
                                     C_____
GAM792  TEX27     3'  TCTAGAACACAAAAGGGT    21417           ATAT
                                TCTAGAATACAAAA    GGT
                                ||||||||||||||    |||
                                AGATCTTGTGTTTT    CCA
                                       C___
GAM792  TIX1      3'  AGAATACAAAAATAGGC     21418           T
                                AGAATACAAAAATA GGT
                                |||||||||||||| |||
                                TCTTATGTTTTTAT CCG
                                       _
GAM792  TRNT1     3'  TCTAGAATACCAGAAACAT   21419         AA_
                                TCTAGAATAC   AAATAT
                                ||||||||||   ||||||
                                AGATCTTATG   TTTGTA
                                     GTC
GAM792  TU12B1-TY 3'  TCTAGAATAAATAGGTCT    21420         CAAA    T
                                TCTAGAATA    AATA GGTCT
                                |||||||||    |||| |||||
                                AGATCTTAT    TTAT CCAGA
                                     ____   _
GAM792  LOC150054 3'  CTAGAATACAAAATC       21421           AATATG
                                CTAGAATACAAA     GTC
                                ||||||||||||     |||
                                GATCTTATGTTT     TAG
                                       _______
GAM792  LOC152756 3'  AAATAAGAAAATATGGTCT   21422       CA
                                GAATA  AAAATATGGTCT
                                |||||  ||||||||||||
                                TTTAT  TTTTATACCAGA
                                   TC
GAM793  CYP1A1    5'  GGGTGGACTCTTGGAGCCT   21425    A       TCACA
                                GG TGGACTCTT    AGCCT
                                || |||||||||    |||||
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                                CC ACCTGAGAA    TCGGA
                                 C       CC___
GAM793  TAL1    3'  TGGATGGATCAACATAGGCCT  21426       C  TTT  CAA
                                TGGATGGA TC   CA   GCCT
                                |||||||| ||   ||   ||||
                                ACCTACCT AG   GT   CGGA
                                     _  TT_  ATC
GAM793  AQP9    3'  TGGGTGGATTCCACCTCAGGC  21427     A   C   T  A  A
                                TGG TGGA TCT TC CA GC
                                ||| |||| ||| || || ||
                                ACC ACCT AGG GG GT CG
                                  C   A   T  A  C
GAM793  BRAG    5'  ATGGGTGGGCCCCCCACGAGTC 21428     A   A T  TT   A  C
          T                      ATGG TGG C CT  CAC AG CT
                                |||| ||| | ||  ||| || ||
                                TACC ACC G GG  GTG TC GA
                                  C   C _  GG   C  A
GAM793  FLJ21916 3'  TGGACTGGACTCTTTTGTAGGC 21429      _       CACAA
          CT                     TGGA TGGACTCTTT    GCCT
                                |||| ||||||||||    ||||
                                ACCT ACCTGAGAAA    CGGA
                                  G         ACATC
GAM793  KIAA1594 3'  TGAATGGACTCTTTGACACCT  21430           C  AA
                                TGGATGGACTCTTT AC  GCCT
                                |||||||||||||| ||  ||||
                                ACTTACCTGAGAAA TG  TGGA
                                       C  __
GAM793  LHX6    3'  TGGGTGGACTCCTGGCCGCAGC 21431     A       TCACA_
                                TGG TGGACTCTT     AGC
                                ||| |||||||||     |||
                                ACC ACCTGAGGA     TCG
                                  C       CCGGCG
GAM793  MAP3K3   3'  ATGGAGTGGGCTCTGGCC    21432      _  A   TTCACAA
                                ATGGA TGG CTCT      GCC
                                ||||| ||| ||||      |||
                                TACCT ACC GAGA      CGG
                                  C  C   C_______
GAM793  PCDH20   3'  ATGGATGATTTCAAGC      21433        ACTC    CA
                                ATGGATGG   TTTCA  AGC
                                ||||||||   |||||  |||
                                TACCTACT   AAAGT  TCG
                                     _____   __
GAM793  LOC130985 3'  ATGGAAGGACACAAGC      21434      T   TCTTTC
                                ATGGA GGAC     ACAAGC
                                ||||| ||||     ||||||
                                TACCT CCTG     TGTTCG
                                  T   _______
GAM793  LOC145900 5'  GGGTGGACTCTGGGGGGTGAGC 21435    A       TTCACA__
          CT                     GG TGGACTCT       AGCCT
                                || ||||||||       |||||
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                                CC ACCTGAGA       TCGGA
                                 C       CCCCCCAC
GAM793   LOC151249 3'  ATGGATGATACACAAGC     21436        ACTCTTT
                                ATGGATGG      CACAAGC
                                ||||||||      |||||||
                                TACCTACT      GTGTTCG
                                    AT_____
GAM793   LOC153817 3'  ATGGATGATACACAAGC     21436        ACTCTTT
                                ATGGATGG      CACAAGC
                                ||||||||      |||||||
                                TACCTACT      GTGTTCG
                                    AT_____
GAM793   LOC157376 3'  ATGGATGGGTATTTTCTCAGCC 21437         ACTC    ACA
           T                     ATGGATGG    TTTC   AGCCT
                                ||||||||    ||||   |||||
                                TACCTACC    AAAG   TCGGA
                                    CATA    AG_
GAM793   LOC158662 3'  ATGGATGATACACAAGC     21436        ACTCTTT
                                ATGGATGG      CACAAGC
                                ||||||||      |||||||
                                TACCTACT      GTGTTCG
                                    AT_____
GAM793   LOC220840 3'  ATGGATGATACACAAGC     21436        ACTCTTT
                                ATGGATGG      CACAAGC
                                ||||||||      |||||||
                                TACCTACT      GTGTTCG
                                    AT_____
GAM793   LOC222256 3'  TGGCTGGACTCTTTCCA     21438     A         A
                                TGG TGGACTCTTTC CA
                                ||| |||||||||| ||
                                ACC ACCTGAGAAAG GT
                                  G         _
GAM793   LOC254936 5'  GGGTGGACTCTGGGGGGTGAGC 21435     A       TTCACA__
           CT                     GG TGGACTCT       AGCCT
                                || ||||||||       |||||
                                CC ACCTGAGA       TCGGA
                                 C       CCCCCCAC
GAM793   LOC90529  3'  ATGGAAGGGCCTGTAAGCC    21439      T  A T  TTCAC
                                ATGGA GG C CT     AAGCC
                                ||||| || | ||     |||||
                                TACCT CC G GA     TTCGG
                                   T  C _  CA___
GAM794   CDH19     3'  TAGATGACATTGAAAAAT     21442         CTA
                                TAGATGACA   AAGAAT
                                |||||||||   ||||||
                                ATCTACTGT   TTTTTA
                                      AAC
GAM794   LOC154442 3'  CAGATGGTTCACAGAATACT   21443       A__   TAA
                                TAGATG   CAC   AGAATACT
                                ||||||   |||   ||||||||
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                                GTCTAC  GTG  TCTTATGA
                                   CAA  ___
GAM795  KIAA0329  5'  GGCCGGCACCGGGGCCAGC   21446          AA  A
                                GGCCGGCACCGG  GC AGC
                                ||||||||||||  || |||
                                CCGGCCGTGGCC  CG TCG
                                      C_  G
GAM795  KIAA0574  3'  GGCCTGGTGTGTTACAAGCATT 21447     _  CACCGGAA
          T                     GGCC GG       GCAAGCATTT
                                ||||  ||       ||||||||||
                                CCGG CC       TGTTCGTAAA
                                  A  ACACAA__
GAM796  ALX3      3'  TGTCCAGGCGGGGGTG      21450        _  TCCCCGA
                                TGTCCAGG GG      GGGTG
                                ||||||||  ||      |||||
                                ACAGGTCC CC      CCCAC
                                   G  ________
GAM796  CCR9      3'  TGTCCAGGGGTTCACTGGCAAG 21451          CCC  AG  TG
                                TGTCCAGGGGT   CG  GG  AG
                                ||||||||||   ||  ||  ||
                                ACAGGTCCCCA   GT  CC  TC
                                      A__  GA  GT
GAM796  CCR9      3'  TGTCCAGGGGTTCACTGGCAAG 21451          CCC  AG  TG
                                TGTCCAGGGGT   CG  GG  AG
                                ||||||||||   ||  ||  ||
                                ACAGGTCCCCA   GT  CC  TC
                                      A__  GA  GT
GAM796  CORO2A    3'  GGTGTCCCTGAGGGTGAG    21452    G    C
                                GG GTCCC GAGGGTGAG
                                || ||||| |||||||||
                                CC CAGGG CTCCCACTC
                                 A    A
GAM796  CORO2A    3'  GGTGTCCCTGAGGGTGAG    21452    G    C
                                GG GTCCC GAGGGTGAG
                                || ||||| |||||||||
                                CC CAGGG CTCCCACTC
                                 A    A
GAM796  EGFL4     5'  TGTCGGGGGAGAAGGTGAGGGT 21453     CA   TCCCC__
            GAG                   TGTC  GGGG      GAGGGTGAG
                                ||||  ||||      |||||||||
                                ACAG  CCCC      CTCCCACTC
                                  C_    TCTTCCA
GAM796  FBXL3A    5'  TGTTCAGGGATCCCCGGCG   21454     C        GAG
                                TGT CAGGGGTCCCC   GGTG
                                ||| ||||||||||   ||||
                                ACA GTCCCTAGGGG   CCGC
                                  A         ___
GAM796  GPR61     3'  TGTCCAGGGGACTGGAGGTG  21455          TCCCC   G
                                TGTCCAGGGG    GAGG TG
                                ||||||||||    |||| ||
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                                ACAGGTCCCC    CTCC AC
                                      TGAC_   _
GAM796  JRK     3'  TGTCCAGGGGCGGTG      21456          CCCCGAG
                                TGTCCAGGGGT      GGTG
                                ||||||||||       ||||
                                ACAGGTCCCCG      CCAC
                                          _______
GAM796  MAP3K14  3'  TGGCCAGGGGCAGGGCAGGGTG 21457    T      CCCCG
          AG                      TG CCAGGGGT    AGGGTGAG
                                || ||||||||    ||||||||
                                AC GGTCCCCG    TCCCACTC
                                 C       TCCCG
GAM796  MTMR1    5'  TGTCCAGGGTCTCCACGCTGGG 21458         G_   C  A_
                                TGTCCAGGG  TCC CG  GGG
                                |||||||||  ||| ||  |||
                                ACAGGTCCC  AGG GC  CCC
                                      AG   T  GA
GAM796  SLC6A8   3'  TGTCCAGGGTCCCTTCCTGGG  21459         GT  __  GA
                                TGTCCAGGG  CC  CC  GGG
                                |||||||||  ||  ||  |||
                                ACAGGTCCC  GG  GG  CCC
                                      AG  AA  A_
GAM796  TNFAIP2  3'  TGTCCGGGGATCCCTGAG    21460       A       C
                                TGTCC GGGGTCCC GAG
                                |||||| |||||||| |||
                                ACAGG CCCTAGGG CTC
                                   C       A
GAM796  TRPM2    3'  TGTCCAGGGAAGGGTG      21461          GTCCCC
                                TGTCCAGGG     GAGGGTG
                                |||||||||     |||||||
                                ACAGGTCCC     TTCCCAC
                                          _______
GAM796  FLJ10375 3'  TGTCCACGGGTCCCTGGG    21462       G      CGA
                                TGTCCA GGGTCCC   GGG
                                |||||| |||||||   |||
                                ACAGGT CCCAGGG   CCC
                                   G      A__
GAM796  FLJ13659  5'  TCCAGGGGTTCCTGGCG     21463          C  CGAG
                                TCCAGGGGT CC    GGTG
                                |||||||||  ||    ||||
                                AGGTCCCCA GG    CCGC
                                      A  A___
GAM796  GRIN3A   3'  TGCCCAGGGATGGGGGTGA   21464          CCCCGA
                                TGTCCAGGGGT     GGGTGA
                                ||||||||||      ||||||
                                ACGGGTCCCTA     CCCACT
                                      CC_____
GAM796  HSJ1     3'  TGCCTAGTCTGAGGGTGA    21465      CAGG   CCC
                                TGTC   GGTC   GAGGGTGA
                                ||||   ||||   ||||||||
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                                ACGG   TCAG  CTCCCACT
                                  A___   A__
GAM796  KIAA0284  3'  TGTCCAGGGGCAGGCGGGGTG  21466         CCC  A
                                TGTCCAGGGGT  CG GGGTG
                                ||||||||||  || |||||
                                ACAGGTCCCCG  GC CCCAC
                                      TCC  _
GAM796  MGC5242  3'  TGTCCAGGGGCTTCTGGCCTGA 21467         C_____ C
          G                      TGTCCAGGGGT    CC GAG
                                ||||||||||    || |||
                                ACAGGTCCCCG    GG CTC
                                      AAGACC  A
GAM796  N4BP3   3'  TGCCAGGGGCTGGGGTG   21468   T     CCCCGA
                                TG CCAGGGGT    GGGTG
                                || ||||||||    |||||
                                AC GGTCCCCG    CCCAC
                                 _      AC____
GAM796  NET-5   3'  TGCCGGGGGTTCCTCCGGAG  21469   T  A   _  _  A
                                TG CC GGGGT CC CCG GGG
                                || || ||||| || ||| |||
                                AC GG CCCCA GG GGC CTC
                                 _ C    A  A  _
GAM796  SC65    3'  TGCCCAGGCTGGTGAGGGTG  21470       __  CCCC
                                TGTCCAGG  GGT   GAGGGTG
                                ||||||||  |||   |||||||
                                ACGGGTCC  CCA   CTCCCAC
                                     GA  ____
GAM796  SDC3    3'  TGTCCAGGGGCCCCCACCAGGA 21471           AG  T
          G                      TGTCCAGGGGTCCCCG  GG GAG
                                ||||||||||||||||  || |||
                                ACAGGTCCCCGGGGGGT  TC CTC
                                        GG  _
GAM796  SHANK3   5'  GTCCAGGGGTTTGCCGGTGAG  21472       CC_  GAG
                                GTCCAGGGGT  CC   GGTGAG
                                ||||||||||  ||   ||||||
                                CAGGTCCCCA  GG   CCACTC
                                      AAC  ___
GAM796  TOR2A   3'  TGACCAGGGGTTTCCCTGGG  21473   T     C_  GA
                                TG CCAGGGGT  CCC  GGG
                                || ||||||||  |||  |||
                                AC GGTCCCCA  GGG  CCC
                                 T      AA  A_
GAM796  LOC124044 3'  GTCTGGGTTCCGAGGGTG   21474    CAG   CC
                                GTC  GGGT  CCGAGGGTG
                                |||  ||||  |||||||||
                                CAG  CCCA  GGCTCCCAC
                                  A__   A_
GAM796  LOC124222 3'  GTCCAGGGGCTGGGGTG    21475       CCCCGA
                                GTCCAGGGGT    GGGTG
                                ||||||||||    |||||
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                                CAGGTCCCCG     CCCAC
                                     AC_____
GAM796  LOC146237 3'  TCCAGGGGTCCCTGGG      21476           CGA
                                TCCAGGGGTCCC   GGG
                                ||||||||||||  |||
                                AGGTCCCCAGGG   CCC
                                     A__
GAM796  LOC146488 3'  TGTCCGGGGTCCCTTCCCGGG  21477      A      CGA__
                                TGTCC GGGGTCCC    GGG
                                ||||| ||||||||    |||
                                ACAGG CCCCAGGG    CCC
                                   _      AAGGG
GAM796  LOC147054 5'  TGTTAGGGGTCCTTGTTAGGG  21478    CC      CCG__
                                TGT  AGGGGTCC    AGGG
                                |||  ||||||||    ||||
                                ACA  TCCCCAGG    TCCC
                                  A_      AACAA
GAM796  LOC149685 3'  TGTCAGGGGTCCCCCGGG    21479     C       GA
                                TGTC AGGGGTCCCC  GGG
                                |||| ||||||||||  |||
                                ACAG TCCCCAGGGG  CCC
                                   _       G_
GAM796  LOC151194 3'  TGTCCAGGTGTCTCCACTGTTG 21480       G   C   AGGG
          AG                      TGTCCAGG GTC CCG    TGAG
                                ||||||||| ||| |||    ||||
                                ACAGGTCC CAG GGT    ACTC
                                     A   A   GACA
GAM796  LOC153146 5'  AGTCTTCTCCCGAGGGTGA   21481    GGG  _
                                AG   TC CCCGAGGGTGA
                                ||   || ||||||||||
                                TC   AG GGGCTCCCACT
                                 AGA  A
GAM796  LOC158287 3'  TGTCCAGGGGCCTCCCAGGG   21482          _   G
                                TGTCCAGGGGTC CCC AGGG
                                |||||||||||| ||| ||||
                                ACAGGTCCCCGG GGG TCCC
                                      A   _
GAM796  LOC163682 3'  TGGCCGGGGGTCTCCATACCTG 21483    T  A     C   A_____
          GG                      TG CC GGGGTC CCG     GGG
                                || || |||||| |||     |||
                                AC GG CCCCAG GGT     CCC
                                 C  C      A   ATGGA
GAM796  LOC165614 5'  TGTCCAGGTGTCTCACTCTTGA 21484       G   CC  AGGG
          G                       TGTCCAGG GTC  CG    TGAG
                                ||||||||| |||  ||    ||||
                                ACAGGTCC CAG  GT    ACTC
                                     A   A_  GAGA
GAM796  LOC199678 5'  TGTCCAGGGGCCTCTCGAG   21485          CC_
                                TGTCCAGGGGTC   CGAG
                                ||||||||||||   ||||
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                                ACAGGTCCCCGG  GCTC
                                      AGA
GAM796  LOC199699 3'  TGTCTGGGGAGCAGGGTGA   21486     CA   TCCCCG
                                TGTC  GGGG     AGGGTGA
                                ||||  ||||     |||||||
                                ACAG  CCCC     TCCCACT
                                  A_   TCG___
GAM796  LOC201245 5'  TGTCCGAGGGCAGGGTG     21487      AG   CCCCG
                                TGTCC  GGGT    AGGGTG
                                |||||  ||||    ||||||
                                ACAGG  CCCG    TCCCAC
                                  CT   _____
GAM796  LOC219914 5'  GTCCAGGGGTCCTCGGTAG   21488          C  AG
                                GTCCAGGGGTCC CG  GG
                                ||||||||||||  ||  ||
                                CAGGTCCCCAGG GC  TC
                                      A  CA
GAM796  LOC253868 3'  TGTTCAGGGGTCCATGGAT   21489     C       CCGA
                                TGT CAGGGGTCC    GGGT
                                |||  |||||||||    ||||
                                ACA GTCCCCAGG    CCTA
                                  A        TA__
GAM796  LOC90120  5'  TGTCCAGGGGCCTCCCAGGG   21482          _  G
                                TGTCCAGGGGTC CCC AGGG
                                ||||||||||||  |||  ||||
                                ACAGGTCCCCGG GGG TCCC
                                      A  _
GAM796  LOC93538  5'  TGTCCAGGGTTCCTGAG     21490        G   CC
                                TGTCCAGGG TCC  GAG
                                |||||||||  |||  |||
                                ACAGGTCCC AGG  CTC
                                     A  A_
GAM797  ELOVL4    3'  TATGTTATAGCTTACAAAA   21493           TTA TG
                                TATGTTATAGCTT   A  GAA
                                ||||||||||||   |  |||
                                ATACAATATCGAA   T  TTT
                                      ___ GT
GAM797  ERBB4     3'  GTTATAACTTTAATGGA     21494          T
                                GTTATAGCTTT AATGGA
                                ||||||||||| ||||||
                                CAATATTGAAA TTACCT
                                      _
GAM797  F8        3'  TATGTTATAGTTTCCAAAGA  21495         C     T
                                TATGTTATAG TTTTAA GGA
                                |||||||||| ||||||  |||
                                ATACAATATC AAGGTT TCT
                                      A     _
GAM797  FLJ11184  3'  TATTTTAGCAACTTAATGGAAA 21496     A    T_
              T                  TGTT TAGC  TTTAATGGAAAT
                                ||||  ||||  ||||||||||||
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                                ATAA ATCG  GAATTACCTTTA
                                  A    TT
GAM797  FLJ13984  3'  TGTTGTAGCTTTCCCTGGAAAT 21497      A       AA
                                TGTT TAGCTTTT  TGGAAAT
                                |||| ||||||||  |||||||
                                ACAA ATCGAAAG  ACCTTTA
                                  C       GG
GAM797  SE57-1    3'  GTTATTCTAATGGAAA      21498       AGCT
                                GTTAT    TTTAATGGAAA
                                |||||    ||||||||||
                                CAATA    AGATTACCTTT
                                  _____
GAM797  ZF        3'  ATGTTATAGTTTTTAGAAA   21499         C    AA
                                ATGTTATAG TTTT  TGGAAA
                                ||||||||| ||||  ||||||
                                TACAATATC AAAA  ATCTTT
                                    _   __
GAM797  LOC145815 3'  TATGTTATAGTTTTTATTAAAA 21500          C     A
          AT                      TATGTTATAG TTTTA TGGAAAT
                                |||||||||| ||||| |||||||
                                ATACAATATC AAAAT ATTTTTA
                                     A    A
GAM797  LOC220662 3'  ATGTTTAGCATTTTAATGGAA  21501       A   _
                                ATGTT TAGC TTTTAATGGAA
                                ||||| |||| ||||||||||
                                TACAA ATCG AAAATTACCTT
                                  _    T
GAM797  LOC90167  3'  TATGTTATAAAAATGGAA    21502          CTTTT
                                TATGTTATAG    AATGGAA
                                ||||||||||    |||||||
                                ATACAATATT    TTACCTT
                                     T_____
GAM798  ADARB1    3'  GGAGGTACCTACGGAGAAA   21505    A         AAA
                                A AGGTACTTATG   AGGAA
                                | ||||||||||   |||||
                                C TCCATGGATGC   TCTTT
                                 C          C__
GAM798  ADARB1    3'  GGAGGTACCTACGGAGAAA   21505    A         AAA
                                A AGGTACTTATG   AGGAA
                                | ||||||||||   |||||
                                C TCCATGGATGC   TCTTT
                                 C          C__
GAM798  ALMS1     3'  AAAGGGACTTATTCTTGAGAAA 21506       T     GAAAA
                                AAAGG ACTTAT    GGAAA
                                ||||| ||||||    |||||
                                TTTCC TGAATA    TCTTT
                                   C     AGAAC
GAM798  AMPH      3'  AGCTACAATGGAAAGGAAA   21507    G   TT   A
                                AG TAC  ATG AAAGGAAA
                                || |||  ||| ||||||||
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                                TC ATG  TAC TTTCCTTT
                                 G   T_  C
GAM798  AP1G1    3'  AAAGGTACTTTTGATACAGA  21508          A   AAA
                                AAAGGTACTT TGA   GGA
                                |||||||||| |||   |||
                                TTTCCATGAA ACT   TCT
                                     A   ATG
GAM798  APLP2    3'  AAAGGGGAGGAAAAAGGAAAAA 21509       TACTTAT
                                AAAGG      GAAAAGGAAAAA
                                |||||      ||||||||||||
                                TTTCC      TTTTTCCTTTTT
                                   CCTCC__
GAM798  CACNG7   3'  AGGGACCAATGAAAAGGA    21510     T   T
                                AGG ACT ATGAAAAGGA
                                ||| ||| ||||||||||
                                TCC TGG TACTTTTCCT
                                  C   T
GAM798  CLCN4    3'  GGCACTTAGTGAAAAGGAA   21511         _
                                GGTACTTA TGAAAAGGAA
                                |||||||| ||||||||||
                                CCGTGAAT ACTTTTCCTT
                                     C
GAM798  CLCN5    5'  AAAGGATTTATGAAACAAAA  21512       TAC       AG
                                AAAGG  TTATGAAA  GAA
                                |||||  ||||||||  |||
                                TTTCC  AATACTTT  TTT
                                   TA_       GT
GAM798  CNN3     3'  AGGCAGAAAAAGGAAAA     21513       CTTAT
                                AGGTA    GAAAAGGAAAA
                                |||||    ||||||||||||
                                TCCGT    TTTTTCCTTTT
                                   C____
GAM798  COL19A1  3'  AAAGATGCTTAAAATTAGGAAA 21514        A    T  AA
           AA                     AAAGGT CTTA GA  AGGAAAAA
                                |||||| |||| ||  ||||||||
                                TTTCTA GAAT TT  TCCTTTTT
                                   C   T  AA
GAM798  CTBP2    3'  AAGGGACTGATAAAGGAAAAA  21515     T  T   AA
                                AAGG ACT ATGA  AGGAAAAA
                                |||| ||| ||||  ||||||||
                                TTCC TGA TATT  TCCTTTTT
                                  C  C   __
GAM798  CTBP2    3'  AAGGGACTGATAAAGGAAAAA  21515     T  T   AA
                                AAGG ACT ATGA  AGGAAAAA
                                |||| ||| ||||  ||||||||
                                TTCC TGA TATT  TCCTTTTT
                                  C  C   __
GAM798  CUGBP1   3'  AAAGGAAAAAAAAAGGAAA   21516      TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
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                                TTTCC      TTTTTCCTTT
                                   TTTT___
GAM798  CYP24    5'  GGTACCTCTTGAAAAGGGAAA  21517        A_       A
                                GGTACTT  TGAAAAGG AAA
                                |||||||  |||||||| |||
                                CCATGGA  ACTTTTCC TTT
                                    GA       C
GAM798  EHD4     3'  AAAGGTTTTATATGAAAGG   21518       ACT_      A
                                AAAGGT   TATGAAA GG
                                ||||||   ||||||| ||
                                TTTCCA   ATACTTT CC
                                   AAAT      _
GAM798  EMX2     5'  AAAGGAAAGGAAAAAGGAAA  21519       TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                   TTTCC__
GAM798  ESRRG    3'  AAAGGAAAGGGAAAAAGGAAA 21521       TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                   TTTCCC_
GAM798  ESRRG    3'  AAAGGAAAGGGAAAAGGAAA  21520       TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      CTTTTCCTTT
                                   TTTCC__
GAM798  FBXW1B   3'  AGTACTTATGAGAAAAAGA   21522          __
                                GGTACTTATGA  AAAGGA
                                ||||||||||  ||||||
                                TCATGAATACT  TTTTCT
                                      CT
GAM798  FBXW1B   3'  AGTACTTATGAGAAAAAGA   21522          __
                                GGTACTTATGA  AAAGGA
                                ||||||||||  ||||||
                                TCATGAATACT  TTTTCT
                                      CT
GAM798  FBXW1B   3'  AGTACTTATGAGAAAAAGA   21522          __
                                GGTACTTATGA  AAAGGA
                                ||||||||||  ||||||
                                TCATGAATACT  TTTTCT
                                      CT
GAM798  FCMD     3'  AAAGGTCACTTCAGGAAGGGGA 21523       _   AT_  AA
                                AAAGGT ACTT   GAA  GGA
                                |||||| ||||   |||  |||
                                TTTCCA TGAA   CTT  CCT
                                   G   GTC   CC
GAM798  FPGS     3'  AAGGCACTGGGAGGAGGAA   21524        TAT  AA
                                AAGGTACT   GA  AGGAA
                                ||||||||   ||  |||||
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                                TTCCGTGA  CT  TCCTT
                                    CC_  CC
GAM798  GNB3    3'  AAAGGTAGAAAAAGGA     21525       CTTAT
                                AAAGGTA    GAAAAGGA
                                |||||||    ||||||||
                                TTTCCAT    TTTTTCCT
                                    C____
GAM798  GRAF    3'  AAAGTGTACCAAAAAGG     21526     _    TAT
                                AAAG GTACT   GAAAAGG
                                |||| |||||   |||||||
                                TTTC CATGG   TTTTTCC
                                  A    ___
GAM798  GRIN2B  3'  AGAACTGTGAAAAGGA      21527     T   TA
                                AGG ACT  TGAAAAGGA
                                ||| |||  |||||||||
                                TCT TGA  ACTTTTCCT
                                  _  C_
GAM798  GRINL1A 3'  AGGTAAGAAAAAGGAAAAA   21528      CTTAT
                                AGGTA    GAAAAGGAAAAA
                                |||||    ||||||||||||
                                TCCAT    TTTTTCCTTTTT
                                   TC___
GAM798  IFIT4   5'  GCTTTTATGAAAGGGGAAA   21529    AC      A_
                                GT  TTATGAAA  GGAAA
                                ||  ||||||||  |||||
                                CG  AATACTTT  CCTTT
                                 AA       CC
GAM798  LAG3    5'  AAAGGAGGTCAGAAAAGGAAA 21530      TAC   T
                                AAAGG   TTA GAAAAGGAAA
                                |||||   ||| ||||||||||
                                TTTCC   AGT CTTTTCCTTT
                                   TCC  _
GAM798  MID1    3'  AAAGGAACTATTAAAAGGAA   21531      T   TATG
                                AAAGG ACT    AAAAGGAA
                                ||||| |||    ||||||||
                                TTTCC TGA    TTTTCCTT
                                   T   TAA_
GAM798  MID1    3'  AAAGGAACTATTAAAAGGAA   21531      T   TATG
                                AAAGG ACT    AAAAGGAA
                                ||||| |||    ||||||||
                                TTTCC TGA    TTTTCCTT
                                   T   TAA_
GAM798  MN1     3'  GGTAAGAAAAGGAAAAA     21532      CTTAT
                                GGTA    GAAAAGGAAAAA
                                ||||    ||||||||||||
                                CCAT    CTTTTCCTTTTT
                                  T____
GAM798  OAS2    3'  AAAGGCAGGCTCAGAAGGAAAA 21533        __   T  AA
                                AAAGGTA  CTTA GA  AGGAAAA
                                |||||||  |||| ||  |||||||
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                                TTTCCGT  GAGT CT  TCCTTTT
                                   CC   _ __
GAM798  PATE    3'  AAGGATAACACAGAAAGGAAAA 21534     TACT   GA
            A                   AAGG   TAT  AAAGGAAAAA
                                ||||   |||  ||||||||||
                                TTCC   GTG  TTTCCTTTTT
                                  TATT   TC
GAM798  PAX5    3'  AAAGATACTAAAGAAGGA    21535        TAT  AA
                                AAAGGTACT   GA  AGGA
                                |||||||||   ||  ||||
                                TTTCTATGA   CT  TCCT
                                     TTT __
GAM798  PIK3CG   3'  GGAGGCAGGGAAAAAGGAA   21536   A    CTTAT
                                A AGGTA    GAAAAGGAA
                                | |||||    |||||||||
                                C TCCGT    TTTTTCCTT
                                 C    CCC__
GAM798  PIK3R3   5'  GGAGGGAGAATGAAGAGGAAAA 21537   A   TACTT    A
            A                   A AGG    ATGAA AGGAAAAA
                                | |||    ||||| ||||||||
                                C TCC    TACTT TCCTTTTT
                                 C   CTCT_    C
GAM798  POU3F4   3'  AAAGGGAAAGAAAAAGGAAA   21538      TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                   CTTTC__
GAM798  POU3F4   3'  AAAGGGAAAAAAAGGAAA    21539      TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                   CTT_____
GAM798  PSCD4    3'  AGATATCCCTGAAAAGGAA   21540      _  A
                                AGGTA CTT TGAAAAGGAA
                                ||||| ||| ||||||||||
                                TCTAT GGG ACTTTTCCTT
                                   A  _
GAM798  PUM2     3'  AAAGGTTTCACGCAAAGGAAAA 21541       AC    A
            A                   AAAGGT  TTATG AAAGGAAAAA
                                ||||||  ||||| ||||||||||
                                TTTCCA  AGTGC TTTCCTTTTT
                                   A_    G
GAM798  RORC     3'  AGGGTTCATGGGAAAGGAAAA  21542    TAC    A_
                                AGG   TTATG  AAAGGAAAA
                                |||   |||||  |||||||||
                                TCC   AGTAC  TTTCCTTTT
                                  CA_    CC
GAM798  SIAH1    3'  GGTACAAAAAAAGGAAAAA   21543      TTAT
                                GGTAC    GAAAAGGAAAAA
                                |||||    ||||||||||||
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                              CCATG   TTTTTCCTTTTT
                                 TT__
GAM798  SIAT1    3'  AGGTATTGAAAAGGAA     21544      CTTA
                              AGGTA   TGAAAAGGAA
                              |||||   ||||||||||
                              TCCAT   ACTTTTCCTT
                                 A___
GAM798  SLC17A2  5'  AAGGCTAACTTGGAAAAGGA  21545      __   AT
                              AAGGT  ACTT  GAAAAGGA
                              |||||  ||||  ||||||||
                              TTCCG  TGAA  CTTTTCCT
                                 AT   C_
GAM798  SRC      3'  AGACGTATGAAAGGAAAA    21546    T  T     A
                              GG AC TATGAAA GGAAAA
                              || || ||||||| ||||||
                              TC TG ATACTTT CCTTTT
                               _ C      _
GAM798  STK24    3'  GGAGGAGGATGAAGAAGGAAAA 21547    A   TACTT    _
           A                   A AGG     ATGAA AAGGAAAAA
                              | |||     ||||| |||||||||
                              C TCC     TACTT TTCCTTTTT
                               C   TCC__    C
GAM798  TFDP1    3'  AAGATGCTTATGAAACAAA    21548      A       AG
                              AAGGT CTTATGAAA  GA
                              ||||| |||||||||  ||
                              TTCTA GAATACTTT  TT
                                 C        GT
GAM798  UBE2G2   3'  TGAGCCCCTTGTGAGAAGGAAA 21549    A   A_   A   A
           A                   A GGT  CTT TGA AAGGAAAA
                              | |||  ||| ||| ||||||||
                              A TCG  GAA ACT TTCCTTTT
                               C   GG   C   C
GAM798  UBE2V1   3'  AAAGGAACTTGAGGAGGA    21550      T   TA   AA
                              AAAGG ACT  TGA  AGGA
                              ||||| |||  |||  ||||
                              TTTCC TGA  ACT  TCCT
                                 T   __   CC
GAM798  UBE2V1   3'  AAAGGAACTTGAGGAGGA    21550      T   TA   AA
                              AAAGG ACT  TGA  AGGA
                              ||||| |||  |||  ||||
                              TTTCC TGA  ACT  TCCT
                                 T   __   CC
GAM798  UBE2V1   3'  AAAGGAACTTGAGGAGGA    21550      T   TA   AA
                              AAAGG ACT  TGA  AGGA
                              ||||| |||  |||  ||||
                              TTTCC TGA  ACT  TCCT
                                 T   __   CC
GAM798  VSX1     3'  AAAGGAAACGCAGGAAAGGAAA 21551      T_  T  T    A
                              AAAGG  AC TA GAAA GGAAA
                              |||||  || || |||| |||||
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                                TTTCC  TG GT CTTT CCTTT
                                   TT  C  C   _
GAM798  WHSC1    3'  AAAGGAAAAAGGAAA      21552       TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                  ________
GAM798  AMOT     3'  AAAGGCACTGAAGGA       21553         TAT  AA
                                AAAGGTACT   GA  AGGA
                                |||||||||   ||  ||||
                                TTTCCGTGA   CT  TCCT
                                    ___  __
GAM798  APMCF1   3'  AAAGGTACTTGTTTGAAAGG  21554          A__    A
                                AAAGGTACTT   TGAAA GG
                                ||||||||||   ||||| ||
                                TTTCCATGAA   ACTTT CC
                                     CAA    _
GAM798  ARHGEF4  5'  AAAGGTCTTATGAGCCAAGG  21555       A      A__
                                AAAGGT CTTATGA   AAGG
                                ||||||| |||||||   ||||
                                TTTCCA GAATACT   TTCC
                                   _      CGG
GAM798  ARL8     3'  AAAGGTACTAGGAAA       21556          TATGAAA
                                AAAGGTACT      AGGAAA
                                |||||||||      ||||||
                                TTTCCATGA      TCCTTT
                                  ________
GAM798  ASTN2    3'  AAAGGTTTAAAAAGGA      21557       ACTTA
                                AAAGGT    TGAAAAGGA
                                ||||||    |||||||||
                                TTTCCA    ATTTTTCCT
                                   A_____
GAM798  BLCAP    3'  AGGTACTCCCCAAAAAAGGAAA 21558         AT__
           A                     AGGTACTT    GAAAAGGAAAA
                                 ||||||||    ||||||||||||
                                 TCCATGAG    TTTTTCCTTTT
                                     GGGT
GAM798  CNOT8    3'  AAGGGTCAGAAAAGGAAA    21559      TAC   T
                                AAGG   TTA GAAAAGGAAA
                                ||||   ||| ||||||||||
                                TTCC   AGT CTTTTCCTTT
                                  C__   _
GAM798  CSMD1    3'  GGTTTAAAAAGGAAAA      21560     ACTTA
                                GGT    TGAAAAGGAAAA
                                |||    ||||||||||||
                                CCA    ATTTTTCCTTTT
                                  A_____
GAM798  CYB5-M   3'  GGTACTCATGGAAACCAG    21561          _   A_
                                GGTACTTATG AAA  GG
                                |||||||||| |||  ||
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                                CCATGAGTAC TTT  TC
                                     C   GG
GAM798  CYB5-M    3'  GGTACTCATGGAAACCAG    21561          _   A_
                                GGTACTTATG AAA  GG
                                |||||||||| |||  ||
                                CCATGAGTAC TTT  TC
                                     C   GG
GAM798  DKFZp547E052 3'  AGGCACTTTTATGAGGAAAAA  21562        __    AAA
                                AGGTACT  TATGA   GGAAAAA
                                |||||||  |||||   |||||||
                                TCCGTGA  ATACT   CCTTTTT
                                   AA    ___
GAM798  DKFZP564I0422 3'  GGTTTATGAAGAGGAAAAA   21563     AC      A
                                GGT  TTATGAA AGGAAAAA
                                |||  ||||||| ||||||||
                                CCA  AATACTT TCCTTTTT
                                  __      C
GAM798  FLJ10482  3'  AAAGGTACAGGAAAAGGA    21564         TTAT
                                AAAGGTAC    GAAAAGGA
                                ||||||||    ||||||||
                                TTTCCATG    CTTTTCCT
                                    TC__
GAM798  FLJ12484  3'  AGGTAGGCAACAAAAGGAA   21565       CT  TG
                                AGGTA  TA  AAAAGGAA
                                |||||  ||  ||||||||
                                TCCAT  GT  TTTTCCTT
                                   CC  TG
GAM798  FLJ12673  3'  AAAGTGGCTACAAAAGGAAAA  21566       AC    G
                                AAGGT  TTAT AAAAGGAAAA
                                |||||  |||| ||||||||||
                                TTTCA  GATG TTTTCCTTTT
                                   CC   _
GAM798  FLJ12899  3'  AAAGATACTAATGGGGAAA    21567         T   AAAA
                                AAAGGTACT ATG    GGAAA
                                ||||||||| |||    |||||
                                TTTCTATGA TAC    CCTTT
                                     T   C___
GAM798  FLJ13231  3'  AAAGGTACTTATCATTTTAAAA 21568           GAAAAG
          A                      AAAGGTACTTAT     GAAAA
                                 ||||||||||||     |||||
                                 TTTCCATGAATA     TTTTT
                                      GTAAAA
GAM798  FLJ13912  3'  AAAAGTTACTGAAGAGGAAAAA 21569        ACTTA    A
                                AAAGGT     TGAA AGGAAAAA
                                ||||||     |||| ||||||||
                                TTTTCA     ACTT TCCTTTTT
                                   ATG__    C
GAM798  FLJ20080  3'  AAGGGATGGAAAAAAGGAAAA  21570       TACTTAT
                                AAGG       GAAAAGGAAAA
                                ||||       ||||||||||
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                                TTCC      TTTTTCCTTTT
                                  CTACCT_
GAM798  FLJ20202  3'  GGTACACAAAGGAAAAA     21571      TTATGA
                                GGTAC     AAAGGAAAAA
                                |||||     ||||||||||
                                CCATG     TTTCCTTTTT
                                   TG____
GAM798  FLJ20373  3'  AGGCTAAGACGGGAAGGAAAAA 21572      ACTT   AA
                                AGGT    ATG  AAGGAAAAA
                                ||||    |||  |||||||||
                                TCCG    TGC  TTCCTTTTT
                                  ATTC   CC
GAM798  FLJ21736  3'  AAAGGCACTTCAGGGAGAGGGA 21573          AT__  AAA
           A                     AAAGGTACTT    GA   GGAA
                                ||||||||||    ||   ||||
                                TTTCCGTGAA    CT   CCTT
                                      GTCC  CTC
GAM798  GABARAP   3'  AAGGTAGTGAAAGGAA      21574       CTTA    A
                                AAGGTA    TGAAA GGAA
                                ||||||    ||||| ||||
                                TTCCAT    ACTTT CCTT
                                   C___     _
GAM798  GOLPH3    3'  GGAGGTACTTTGAAAGTCAAA  21575   A       A     A GA
                                A AGGTACTT TGAAA G  AAA
                                | ||||||| ||||| |  |||
                                C TCCATGAA ACTTT C  TTT
                                 C       _    _ AG
GAM798  GS3955    3'  AAGGTACTTAAAAAATAGG    21576          T    _
                                AAGGTACTTA GAAA AGG
                                |||||||||| |||| |||
                                TTCCATGAAT TTTT TCC
                                      T    A
GAM798  GTPBG3    3'  AAAGGGAAAGGGAAAAGGAAA  21577      TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      CTTTTCCTTT
                                   CTTTCC_
GAM798  HN1L      3'  AAGGCTGATGAGAGGAAAA    21578      ACTT    AA
                                AAGGT    ATGA  AGGAAAA
                                |||||    ||||  |||||||
                                TTCCG    TACT  TCCTTTT
                                   AC__    C_
GAM798  HPCAL4    3'  AAAGGTAATAAAAAGGAA     21579       CTT
                                AAAGGTA   ATGAAAAGGAA
                                |||||||   ||||||||||
                                TTTCCAT   TATTTTTCCTT
                                     ___
GAM798  HRI       3'  AAAGGAGCTTGTGGGGCAGGAA 21580      TA   A  AAA_
                                AAAGG  CTT TG    AGGAA
                                |||||  ||| ||    |||||
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                                TTTCC  GAA AC    TCCTT
                                   TC   C  CCCG
GAM798  KIAA0007 3' AGGTAATGAAAAGGAA     21581      CTT
                                AGGTA   ATGAAAAGGAA
                                ||||||  ||||||||||||
                                TCCAT   TACTTTTCCTT
                                  ___
GAM798  KIAA0062 3' AGGTGTGCACAAAAAGGGAAAA 21582      ACT  TG     _
                                AGGT   TA  AAAAGG AAAA
                                ||||   ||  |||||| ||||
                                TCCA   GT  TTTTCC TTTT
                                  CAC  GT     C
GAM798  KIAA0159 5' AGGCTGAAATGAAAAGGAAAAA 21583      ACTT
                                AGGT    ATGAAAAGGAAAAA
                                ||||    ||||||||||||||
                                TCCG    TACTTTTCCTTTTT
                                  ACTT
GAM798  KIAA0265 3' AGGCACTTAAAGGAAA      21584         TGAA
                                AGGTACTTA    AAGGAAA
                                |||||||||    |||||||
                                TCCGTGAAT    TTCCTTT
                                     ____
GAM798  KIAA0638 3' AAGGCACCAGTGGAAGGGA    21585         TA  A  A
                                AAGGTACT  TG AA GGA
                                ||||||||  || || |||
                                TTCCGTGG  AC TT CCT
                                     TC  C  C
GAM798  KIAA1165 3' AAAGATATAACCGAAAGGAAAA 21586        CTTA    A
           A                     AAAGGTA    TGAAA GGAAAAA
                                |||||||    ||||| |||||||
                                TTTCTAT    GCTTT CCTTTTT
                                    ATTG    _
GAM798  KIAA1430 3' AAAGGTGCTAAGGAAAA     21587       A  TATGAA
                                AAAGGT CT     AAGGAAAA
                                |||||| ||     ||||||||
                                TTTCCA GA     TTCCTTTT
                                   C _______
GAM798  KIAA1571 3' AAAGGTGGTTAAAAAAAAGG   21588       AC   T_
                                AAAGGT  TTA  GAAAAGG
                                ||||||  |||  |||||||
                                TTTCCA  AAT  TTTTTCC
                                   CC   TT
GAM798  KIAA1671 3' GGTATCTACTGAAGAGGAAAAA 21589      _  TA   A
                                GGTA CT  TGAA AGGAAAAA
                                ||||  ||  ||||  ||||||||
                                CCAT GA  ACTT TCCTTTTT
                                  A  TG   C
GAM798  KIAA1718 3' AAGGTTACTTATGAATCTTAAA 21590      _       _______
           AGGAA                 AAGGT ACTTATGAA     AAGGAA
                                |||||  |||||||||      ||||||
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                                TTCCA TGAATACTT     TTCCTT
                                   A        AGAATT
GAM798  KIAA1729  3'  AAAGGCACAGAAAGGAA     21591        TTATGA
                                AAAGGTAC     AAAGGAA
                                ||||||||     |||||||
                                TTTCCGTG     TTTCCTT
                                     TC_____
GAM798  KLK7      3'  AAAAGTACACAGAAGGAAGGA  21592        TTAT  __
                                AAAGGTAC    GAA  AAGGA
                                ||||||||    |||  |||||
                                TTTTCATG    CTT  TTCCT
                                     TGT_   CC
GAM798  KLK7      3'  AAAAGTACACAGAAGGAAGGA  21592        TTAT  __
                                AAAGGTAC    GAA  AAGGA
                                ||||||||    |||  |||||
                                TTTTCATG    CTT  TTCCT
                                     TGT_   CC
GAM798  MGC10646  3'  GGAGTTACCAGAGAAAGGAAAA 21593    A  G    TAT    A
                                A AG TACT   GAAA GGAAAA
                                | || ||||   |||| ||||||
                                C TC ATGG   CTTT CCTTTT
                                 C  A    TCT    _
GAM798  MGC13010  5'  GGAGATACTCAACTTTGGAGAG 21594    A       ____  AAA
           GAA                    A AGGTACTTA    TG   AGGAA
                                | |||||||||    ||   |||||
                                C TCTATGAGT    AC   TCCTT
                                 C        TGAA  CTC
GAM798  MGC2488   3'  AAAGGACTTATGACCAAGG    21595      T       A_
                                AAAGG ACTTATGA  AAGG
                                ||||| ||||||||  ||||
                                TTTCC TGAATACT  TTCC
                                   _       GG
GAM798  MGC2574   3'  AAGGCACTTGGAGAAGGA     21596        AT  A
                                AAGGTACTT  GA AAGGA
                                |||||||||  || |||||
                                TTCCGTGAA  CT TTCCT
                                     C_  C
GAM798  MGC4170   3'  GTCTTGTGAAGAGGAAAAA    21597    A  A    A
                                GT CTT TGAA AGGAAAAA
                                || ||| |||| ||||||||
                                CA GAA ACTT TCCTTTTT
                                 _   C    C
GAM798  MRPL48    3'  GGTACTTATGAAATCTAAGG   21598          ____
                                GGTACTTATGAAA    AGG
                                ||||||||||||    |||
                                CCATGAATACTTT    TCC
                                       AGAT
GAM798  NLI-IF    3'  AAGGCACTTAAATGGGAAGG   21599          __  AA
                                AAGGTACTTA  TG  AAGG
                                ||||||||||  ||  ||||
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                                TTCCGTGAAT  AC  TTCC
                                      TT  CC
GAM798  PFDN1    3'  AAAGGTACAGGAAGGGAAAA  21600        TTAT   AA
                                AAAGGTAC   GAA  GGAAAA
                                ||||||||   |||  ||||||
                                TTTCCATG   CTT  CCTTTT
                                     TC__   C_
GAM798  PRO0902  3'  AAGTACTTGTGGCAAAGG    21601        A  A_
                                AGGTACTT TG  AAAGG
                                |||||||| ||  |||||
                                TTCATGAA AC  TTTCC
                                     C  CG
GAM798  PRO1580  5'  GGAGGTACAAAGGAAAA     21602   A     TTATGA
                                A AGGTAC     AAAGGAAAA
                                | ||||||     |||||||||
                                C TCCATG     TTTCCTTTT
                                 C     _______
GAM798  PRO2325  5'  AAGGTAACTAACGGAAGGAAAA 21603       _  T   AA
          A                      AAGGTA CT ATG  AAGGAAAAA
                                ||||||| || |||  |||||||||
                                TTCCAT GA TGC  TTCCTTTTT
                                    T  T   C_
GAM798  TNFSF13  3'  GGTGGGAATGAAAAGGGAAAA  21604     ACTT       _
                                GGT    ATGAAAAGG AAAA
                                |||    ||||||||| ||||
                                CCA    TACTTTTCC TTTT
                                  CCCT        C
GAM798  TTLL1    3'  AGGGCTTAGGAAAGGAAAA   21605     TA   T   A
                                AGG  CTTA GAAA GGAAAA
                                |||  |||| |||| ||||||
                                TCC  GAAT CTTT CCTTTT
                                  C_   C   _
GAM798  YAP      5'  AAGGTACTTGCTGATTAGAGG  21606        A_  AA__
                                AAGGTACTT  TGA   AGG
                                |||||||||  |||   |||
                                TTCCATGAA  ACT   TCC
                                     CG   AATC
GAM798  ZNF323   3'  AGGTACCTTGTGAAGAA     21607        A  AA
                                AGGTACTT TG  AAGGA
                                |||||||| ||  |||||
                                TCCATGGA AC  TTCTT
                                     _  AC
GAM798  LOC115297 3'  AAAAGTGAAAAAAGGAAAA   21608       ACTTAT
                                AAAGGT     GAAAAGGAAAA
                                ||||||     ||||||||||
                                TTTTCA     TTTTTCCTTTT
                                   CT_____
GAM798  LOC130120 3'  AAGGTGAAGAAAAAGGAAAAA  21609      ACTTAT
                                AAGGT     GAAAAGGAAAAA
                                |||||     ||||||||||||
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                                TTCCA     TTTTTCCTTTTT
                                   CTTC__
GAM798  LOC130535 3'  GGTATGACTGGAAAGGAAAAA  21610      CTTA  A
                                GGTA    TG AAAGGAAAAA
                                ||||    || ||||||||||
                                CCAT    AC TTTCCTTTTT
                                  ACTG  C
GAM798  LOC134145 3'  AAGTACAAAAAGGAAA      21611       TTAT
                                AGGTAC    GAAAAGGAAA
                                ||||||    ||||||||||
                                TTCATG    TTTTTCCTTT
                                   ____
GAM798  LOC139420 3'  AAAGGTAACTGAAGGAAA    21612        CTTA   AA
                                AAAGGTA    TGA  AGGAAA
                                |||||||    |||  ||||||
                                TTTCCAT    ACT  TCCTTT
                                    TG__   __
GAM798  LOC144512 5'  AAAGGAAAAAAAAGGAAA    21613       TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                   TTT____
GAM798  LOC145826 5'  AGCACTATGAAAAGGGAAA    21614        T        A
                                GGTACT ATGAAAAGG AAA
                                |||||| ||||||||| |||
                                TCGTGA TACTTTTCC TTT
                                   _        C
GAM798  LOC148195 5'  AGGTACTTATGACTCAATGAGG 21615            AA_____
          A                      AGGTACTTATGA      AGGA
                                 ||||||||||||      ||||
                                 TCCATGAATACT      TCCT
                                       GAGTTAC
GAM798  LOC149705 3'  AGGGGGAAAAAAAAGGAAAAA  21616     TACTTAT
                                AGG      GAAAAGGAAAAA
                                |||      ||||||||||||
                                TCC      TTTTTCCTTTTT
                                  CCCTTT_
GAM798  LOC150311 5'  GGAAGTACATAGGAAAAGGAAA 21617    A     T  T
                                A AGGTAC TA GAAAAGGAAA
                                | |||||| || ||||||||||
                                C TTCATG AT CTTTTCCTTT
                                 C     T  C
GAM798  LOC152742 5'  AAAGGAACTGGCACAAAGGAAA 21618       T   TATGA
          AA                      AAAGG ACT     AAAGGAAAAA
                                  ||||| |||     ||||||||||
                                  TTTCC TGA     TTTCCTTTTT
                                     T   CCGTG
GAM798  LOC152925 3'  AAGGTCCTGAAAAGGAA      21619       ACTTA
                                AAGGT     TGAAAAGGAA
                                |||||     ||||||||||
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                                TTCCA    ACTTTTCCTT
                                   GG___
GAM798  LOC154562 3'  GGAGGTAGAGTTGGAAAGGAAA 21620   A    CTTA  A
                                A AGGTA   TG AAAGGAAA
                                | |||||   || ||||||||
                                C TCCAT   AC TTTCCTTT
                                 C    CTCA  C
GAM798  LOC155072 5'  AAGATACTGGAAGAGGAAA   21621       TAT   A
                                AAGGTACT   GAA AGGAAA
                                ||||||||   ||| ||||||
                                TTCTATGA   CTT TCCTTT
                                     C__   C
GAM798  LOC159090 5'  AAGGTGACAGAATGAAGGAAAA 21622      _  TT_   AA
                                AAGGT AC   ATGA  AGGAAAA
                                ||||| ||   ||||  |||||||
                                TTCCA TG   TACT  TCCTTTT
                                   C  TCT   __
GAM798  LOC197285 3'  AAAGGTACTTAGGCTCAGAA   21623         TGAAA
                                AAAGGTACTTA    AGGA
                                ||||||||||    ||||
                                TTTCCATGAAT    TCTT
                                      CCGAG
GAM798  LOC199953 3'  GGTGCCCGAAAGGAAAA    21624    A  TA    A
                                GGT CT  TGAAA GGAAAA
                                ||| ||  ||||| ||||||
                                CCA GG  GCTTT CCTTTT
                                  C  __    _
GAM798  LOC202134 5'  AAAGTACTTATGGAAAGA    21625          A
                                AAGGTACTTATG AAAGG
                                |||||||||||| |||||
                                TTTCATGAATAC TTTCT
                                      C
GAM798  LOC202868 5'  AAGATACTGGAAGAGGAAA   21621       TAT   A
                                AAGGTACT   GAA AGGAAA
                                ||||||||   ||| ||||||
                                TTCTATGA   CTT TCCTTT
                                     C__   C
GAM798  LOC207089 3'  GGCACCCAGAAGGAAGGA    21626       T   __
                                GGTACTTA GAA  AAGGA
                                |||||||| |||  |||||
                                CCGTGGGT CTT  TTCCT
                                     _   CC
GAM798  LOC254143 5'  AAAGGAAAAAAAAGGAAA    21613      TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                   TTT____
GAM798  LOC254170 5'  AAGGCGTACTGTAAGGAAAA   21627      ACT   GAA
                                AAGGT   TAT   AAGGAAAA
                                |||||   |||   ||||||||
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                                TTCCG   ATG   TTCCTTTT
                                  C__   ACA
GAM798  LOC254249 3'  GGTGCTTATAAGGAAAA     21628     A     AAA
                                GGT CTTATG   AGGAAAA
                                ||| ||||||   |||||||
                                CCA GAATAT   TCCTTTT
                                  C     ___
GAM798  LOC255452 3'  AAAGGTCTTATGAGCCAAGG   21555       A      A__
                                AAAGGT CTTATGA   AAGG
                                |||||| |||||||   ||||
                                TTTCCA GAATACT   TTCC
                                   _      CGG
GAM798  LOC257422 3'  AAAAGTGACAAAAAAGGAAAA  21629       ACTTAT
                                AAAGGT     GAAAAGGAAAA
                                ||||||     ||||||||||||
                                TTTTCA     TTTTTCCTTTT
                                   CTGT__
GAM798  LOC257465 3'  AAAGATAAAACAAAAAGGA    21630        CTT TG
                                AAAGGTA   A  AAAAGGA
                                |||||||   |  |||||||
                                TTTCTAT   T  TTTTCCT
                                    TT_ GT
GAM798  LOC51018  3'  AAAGTGTACATGAAAAGG     21631      _    TT
                                AAAG GTAC  ATGAAAAGG
                                |||| ||||  |||||||||
                                TTTC CATG  TACTTTTCC
                                  A   __
GAM798  LOC51064  3'  AAAGGCACTTGTGAGGCATAGA 21632          A   AAA__
          A                      AAAGGTACTT TGA     GGAA
                                ||||||||||| |||     ||||
                                TTTCCGTGAA ACT     TCTT
                                     C   CCGTA
GAM798  LOC90371  5'  AGGAGGATGAAGAGGAAAAA   21633     TACTT     A
                                AGG     ATGAA AGGAAAAA
                                |||     ||||| ||||||||
                                TCC     TACTT TCCTTTTT
                                  TCC__     C
GAM798  LOC91660  5'  GGTATATATGCACAGGAAAAA  21634      CT    AAA
                                GGTA  TATG   AGGAAAAA
                                ||||  ||||   ||||||||
                                CCAT  ATAC   TCCTTTTT
                                  AT    GTG
GAM799  CCNH      3'  TCTAGCTCTTTTGAAGATGG   21637    GC       CCC  CC
                                TC  AGCTCTTT   GG  TGG
                                ||  ||||||||   ||  |||
                                AG  TCGAGAAA   TC  ACC
                                 A_       ACT  T_
GAM799  HOXB9     3'  TCGGACTCTCCTGGCCTGGCT  21638     CAGCT     C
                                TCG     CTTTCC GGCCTGGCT
                                |||     |||||| |||||||||
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                                AGC    GAGAGG CCGGACCGA
                                  CT___     A
GAM799  IL17B    3'  TCGGGCTGCTGGCCTGGC    21639     CA  _  TTCCC
                                TCG  GCT CT    GGCCTGGC
                                |||  ||| ||    ||||||||
                                AGC  CGA GA    CCGGACCG
                                  C_   C _____
GAM799  PI3      5'  GCAGTCCAGCTTGGCCTGGCT  21640      C   TTCCC
                                GCAG TCT    GGCCTGGCT
                                ||||  |||    |||||||||
                                CGTC AGG    CCGGACCGA
                                  _  TCGAA
GAM799  REQ      3'  TCCCAGCTCCCTGGCCTGGCT  21641    G     TTT  C
                                TC CAGCTC   CC GGCCTGGCT
                                ||  ||||||   ||  |||||||||
                                AG GTCGAG   GG CCGGACCGA
                                  G     ___  A
GAM799  SIGLEC11  5'  TCTGGCTTCTGGGCCGGCCTGG 21642    GCA  _  TTC
              CT                  TC   GCT CT   CCGGCCTGGCT
                                ||   ||| ||   ||||||||||
                                AG   CGA GA   GGCCGGACCGA
                                  AC_   A  CCC
GAM799  WSX1     3'  TCCCAGCTCTGCCTGG      21643    G      TTCCCG
                                TC CAGCTCT     GCCTGG
                                ||  |||||||     ||||||
                                AG GTCGAGA     CGGACC
                                  G     _______
GAM799  FLJ10232  3'  TCCCAGCCCTTGGCCTGG    21644    G      TCCC
                                TC CAGCTCTT    GGCCTGG
                                ||  ||||||||    |||||||
                                AG GTCGGGAA    CCGGACC
                                  G      ____
GAM799  FLJ21709  3'  TCTCAGCTCCAAGGCCTGGCT  21645    G      TTCCC
                                TC CAGCTCT    GGCCTGGCT
                                ||  |||||||    |||||||||
                                AG GTCGAGG    CCGGACCGA
                                  A      TT___
GAM799  GCHFR    5'  GCACGCGTCCCGGCCTGGCT   21646     _  TCTT
                                GCA GC    TCCCGGCCTGGCT
                                |||  ||    ||||||||||||
                                CGT CG    AGGGCCGGACCGA
                                  G  C___
GAM799  KIAA0258  3'  GCAGCTCCTGGGTTTGGCT   21647         TCCC  CC
                                GCAGCTCTT    GG  TGGCT
                                |||||||||    ||  |||||
                                CGTCGAGGA    CC  ACCGA
                                     C___  AA
GAM799  KIAA1276  5'  CCGGGCCCTGGCCTGGC     21648     CA    TTCCC
                                TCG  GCTCT    GGCCTGGC
                                |||  |||||    ||||||||
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                                GGC  CGGGA    CCGGACCG
                                  C_   _____
GAM799  KIAA1598  5'  TCGCAGCCTTTCGAAGATTCTG 21649       T    CC  C__
              GCT                   TCGCAGC CTTTC  GG   CTGGCT
                                |||||||| |||||  ||   ||||||
                                AGCGTCG GAAAG  TC   GACCGA
                                    _    CT  TAA
GAM799  RALGPS1A  3'  GCAGCTCTGTGCCTGGC     21650        TTCCCG
                                GCAGCTCT     GCCTGGC
                                ||||||||     |||||||
                                CGTCGAGA     CGGACCG
                                     CA____
GAM799  SNPH      3'  CCGCAGCCAGTCCCGGCTTGGC 21651        T TT      C
              T                   TCGCAGC C  TCCCGGC TGGCT
                                ||||||| |  ||||||| |||||
                                GGCGTCG G  AGGGCCG ACCGA
                                    _ TC      A
GAM799  TCEB3L    5'  TCGCAGCTCTGTCTTTGGGGCT 21652          T  CC_  CCT
                                TCGCAGCTCT TC   GG   GGCT
                                |||||||||| ||   ||   ||||
                                AGCGTCGAGA AG   CC   CCGA
                                      C  AAA  ___
GAM799  LOC145644 5'  TCTCAGCTCTTGCTCTGGC    21653    G       TCCCG  _
                                TC CAGCTCTT     GC CTGGC
                                || ||||||||     || |||||
                                AG GTCGAGAA     CG GACCG
                                 A       _____  A
GAM799  LOC157860 5'  TCATAGCTTTTTCCCGTCCC   21654     C   C      G
                                TCG AGCT TTTCCCG CCT
                                ||| |||| ||||||| |||
                                AGT TCGA AAAGGGC GGG
                                  A   A      A
GAM799  LOC158696 3'  TCACAGCTCTTTTCATGGGCT  21655           CC  GCCT
                                TCGCAGCTCTTT  CG    GGCT
                                ||||||||||||  ||    ||||
                                AGTGTCGAGAAA  GT    CCGA
                                      A_  AC__
GAM799  LOC221943 5'  TCTTAGCTCTGCCAGGCCTGGC 21656    GC     TT  C
              T                   TC  AGCTCT  CC GGCCTGGCT
                                ||  ||||||  || |||||||||
                                AG  TCGAGA  GG CCGGACCGA
                                 AA     C_  T
GAM799  LOC254105 3'  GCTCTTAGGGCCTGGCT     21657       TCCC
                                GCTCTT    GGCCTGGCT
                                ||||||    |||||||||
                                CGAGAA    CCGGACCGA
                                    TC__
GAM800  CISH      5'  GGTGGGGACAGTGGCTGG    21660    AT     ___
                                GG  TGGGGA   TGGCTGG
                                ||  ||||||   |||||||
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                                CC  ACCCCT   ACCGACC
                                 __     GTC
GAM800  KPNB1    5'  TGGGGGTTGGGGGGTCGGGTG  21661    A  A     A_   C
                                TG GG TTGGGG  TGG TG
                                || || ||||||  ||| ||
                                AC CC AACCCC  GCC AC
                                 C  C     CA   C
GAM800  NPEPPS   3'  TGGGGGTTGGGGGGTGGAAC   21662    A  A     A   CT
                                TG GG TTGGGG TGG  GGC
                                || || |||||| |||  |||
                                AC CC AACCCC ACC  TTG
                                 C  C     C   __
GAM800  PLIN     3'  AGGGTTGGGGATGAACTG    21663     A         _
                                AGG TTGGGGATGG CTG
                                ||| |||||||||| |||
                                TCC AACCCCTACT GAC
                                  C         T
GAM800  SGCB     3'  TGAGAATTGGGGATATAAACAT 21664              GCT
                                TGAGGATTGGGGATG   GGCAT
                                ||||||||||||||   |||||
                                ACTCTTAACCCCTAT   TTGTA
                                          AT_
GAM800  XRCC3    5'  TGGGGCTTGGGGATGACCCGC  21665    A  A         G
                                TG GG TTGGGGATGGCT GC
                                || || ||||||||||| ||
                                AC CC AACCCCTACTGG CG
                                 C  G           G
GAM800  ACY-3    3'  TGAGGTTGGGGAGGTG      21666      A     T  C
                                TGAGG TTGGGGA GG TG
                                ||||| ||||||| || ||
                                ACTCC AACCCCT CC AC
                                    _      _ _
GAM800  AK5      3'  TGGGGGTTAGGGATGCT     21667    A  A       G
                                TG GG TTGGGGATG CT
                                || || |||||||| ||
                                AC CC AATCCCTAC GA
                                 C  C       _
GAM800  ALOXE3   3'  TGGGGATTGGGGAGGATG    21668    A        T  C
                                TG GGATTGGGGA GG TG
                                || |||||||| || ||
                                AC CCTAACCCCT CC AC
                                 C         _ T
GAM800  BC002942 3'  GGAGGGGCATGGCTGGC     21669     TT   _
                                GGA  GGGG ATGGCTGGC
                                |||  |||| |||||||||
                                CCT  CCCC TACCGACCG
                                  __    G
GAM800  BMF      3'  TGGGGGTGGGGGATGGAGTCTG 21670    A  ATT      ___
                                TG GG   GGGGATGG   CTG
                                || ||   ||||||||   |||
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                                AC CC   CCCCTACC   GAC
                                 C  CAC       TCA
GAM800  CLECSF9  3' GGAGCTGATGGCTGGCAT    21671     TTGGG
                                GGA    GATGGCTGGCAT
                                |||    ||||||||||||
                                CCT    CTACCGACCGTA
                                  CGA__
GAM800  CLIPR-59 3' TGGGGATTTGGGATTCCA    21672    A    G    GG
                                TG GGATT GGGAT  CTG
                                || ||||| |||||  |||
                                AC CCTAA CCCTA  GGT
                                 C    A    A_
GAM800  FLJ11222 3' TGAGGATGGGGATGCAAACA   21673       T      G TG
                                TGAGGAT GGGGATG C  GCA
                                ||||||| ||||||| |  |||
                                ACTCCTA CCCCTAC G  TGT
                                    _     _ TT
GAM800  KIAA1036 3' GAGGGATAGGGGTGGCTGGCAT 21674      AT    A
                                GAGG  TGGGG TGGCTGGCAT
                                ||||  ||||| ||||||||||
                                CTCC  ATCCC ACCGACCGTA
                                  CT    C
GAM800  P11      3' TGGGGTTGGGGACAAATGCATA 21675    A  A      TG CTG
                                TG GG TTGGGGA  G   GCATA
                                || || |||||||  |   |||||
                                AC CC AACCCCT  T   CGTAT
                                 _ C      GT TA_
GAM800  SPAG4L   5' AGGATTGGGGATGGAGA     21676            CT
                                AGGATTGGGGATGG  GG
                                ||||||||||||||  ||
                                TCCTAACCCCTACC  CT
                                        T_
GAM800  LOC149711 3' TGGGGATTGGGTATTTGCATA  21677    A      GATGGCTG
                                TG GGATTGGG       GCATA
                                || ||||||||       |||||
                                AC CCTAACCC       CGTAT
                                 C       ATAAA___
GAM800  LOC157503 3' TGAGGTTGGGTGGTG      21678      A    GA   C
                                TGAGG TTGGG  TGG TG
                                ||||| |||||  ||| ||
                                ACTCC AACCC  ACC AC
                                   _    __   _
GAM800  LOC220763 5' TGAGGGTTGGGGATGATG    21679      A        C
                                TGAGG TTGGGGATGG TG
                                ||||| ||||||||| ||
                                ACTCC AACCCCTACT AC
                                  C        _
GAM800  LOC254191 3' TGAGGGTGGGGGTGAGGGAT   21680      AT    A   CT  C
                                TGAGG  TGGGG TGG  GG AT
                                |||||  ||||| |||  || ||
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                                ACTCC  ACCCC ACT  CC TA
                                  C_    C   __ C
GAM800  LOC91748  3'  TGAGGATGGGGGGGCGGC    21681       T   AT   T
                                TGAGGAT GGGG  GGC GGC
                                ||||||| ||||  ||| |||
                                ACTCCTA CCCC  CCG CCG
                                    _   __  _
GAM801  GAN       3'  TGCTCATTGAGAAGGCAGAATG 21684    _   C  TATTA
                                TG TCAT TG    GCAGAATG
                                || |||| ||    ||||||||
                                AC AGTA AC    CGTCTTAC
                                 G   _ TCTTC
GAM801  LMO2      3'  TCTGTCATTTTTTATTAAGC   21685       CTG    _
                                TCTGTCAT   TATTA GC
                                ||||||||   ||||| ||
                                AGACAGTA   ATAAT CG
                                     AAA    T
GAM801  MBNL      3'  TCTGTCATTGTATTAGC     21686       C
                                TCTGTCAT TGTATTAGC
                                |||||||| |||||||||
                                AGACAGTA ACATAATCG
                                    _
GAM801  SLC1A1    3'  TCTTCATAAATTAGCAGAATG  21687    G   CTGT
                                TCT TCAT    ATTAGCAGAATG
                                ||| ||||    ||||||||||||
                                AGA AGTA    TAATCGTCTTAC
                                  _   TT__
GAM801  AMOT      3'  TGTCACCTTGCAGAAT      21688       GTATTA
                                TGTCATCT     GCAGAAT
                                ||||||||     |||||||
                                ACAGTGGA     CGTCTTA
                                     A_____
GAM801  C5orf5    3'  TCTGTAACAATGATTAGCAGAA 21689      C  C_  T
           TG                     TCTGT AT  TG ATTAGCAGAATG
                                ||||| ||  || ||||||||||||
                                AGACA TG  AC TAATCGTCTTAC
                                   T  TT  _
GAM801  ChGn      3'  TCTGTACGTCTGTATTAG    21690      CA_
                                TCTGT   TCTGTATTAG
                                |||||   ||||||||||
                                AGACA   AGACATAATC
                                   TGC
GAM801  FLJ12704  3'  TGTCTTCTGTATCAGTCAGGAA 21691     A       _  _
           TG                     TGTC TCTGTATTAG CAG AATG
                                |||| |||||||||| ||| ||||
                                ACAG AGACATAGTC GTC TTAC
                                  A        A  C
GAM801  MGC2574   3'  TCTATTGTCTGTATTTGC    21692      CA      A
                                TCTGT  TCTGTATT GC
                                |||||  |||||||| ||
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                                AGATA  AGACATAA CG
                                  AC       A
GAM801   PRO2859   3'  TCTGTCATCAGTATTAAC    21693         T
                                TCTGTCATC GTATTAGC
                                ||||||||| ||||||||
                                AGACAGTAG CATAATTG
                                     T
GAM801   ZNF333    3'  TCTGTCATTTGTGATAACA   21694        C   AT
                                TCTGTCAT TGT  TAGCA
                                |||||||| |||  |||||
                                AGACAGTA ACA  ATTGT
                                     A   CT
GAM801   LOC127255 3'  TCTGTCATTTGTGATGCAA   21695        C   ATTA
                                TCTGTCAT TGT    GCAG
                                |||||||| |||    ||||
                                AGACAGTA ACA    CGTT
                                     A   CTA_
GAM801   LOC146669 3'  TCGGTCATTCATCAGCAGGATG 21696    T    CTG       A
                                TC GTCAT   TATTAGCAG ATG
                                || |||||   ||||||||| |||
                                AG CAGTA   GTAGTCGTC TAC
                                 C    A__       C
GAM801   LOC150951 5'  TGCATCTGTAAAGAAT     21697    T      TTAGC
                                TG CATCTGTA    AGAAT
                                || ||||||||    |||||
                                AC GTAGACAT    TCTTA
                                 _      T_____
GAM801   LOC152263 3'  TCTGTCATCCTGGCTGGAATG  21698         GTATTA  A_
                                TCTGTCATCT     GC  GAATG
                                ||||||||||     ||  |||||
                                AGACAGTAGG     CG  CTTAC
                                      AC_____  AC
GAM801   LOC196485 5'  TCTTCATCTGTGTTTCCCAG   21699     G       A_  AG
                                TCT TCATCTGT  TT  CAG
                                ||| ||||||||  ||  |||
                                AGA AGTAGACA  AA  GTC
                                  _       CA  GG
GAM801   LOC202986 5'  TCTTCATCTGTGTTTCCCAG   21699     G       A_  AG
                                TCT TCATCTGT  TT  CAG
                                ||| ||||||||  ||  |||
                                AGA AGTAGACA  AA  GTC
                                  _       CA  GG
GAM801   LOC219688 3'  TGTTATTTTATTAGCAGGATG  21700     C  CTG       A
                                TGT AT   TATTAGCAG ATG
                                ||| ||   ||||||||| |||
                                ACA TA   ATAATCGTC TAC
                                  A  AA_       C
GAM802   CLCA1     5'  TACCATTATATATATACAGA   21703      C       C
                                TACCA TATATATA ACAGA
                                ||||| |||||||| |||||
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                                ATGGT ATATATAT TGTCT
                                   A       A
GAM802  EHHADH   3' CATTACTCTATCACAGAATTG 21704    C   A_   A
                                CA TAT  TAT CACAGAATTG
                                || |||  ||| ||||||||||
                                GT ATG  ATA GTGTCTTAAC
                                 A   AG  _
GAM802  EIF2C1   3' CTTTATAAAACACAGAATTG  21705    A    T_
                                CT TATA  ACACAGAATTG
                                || ||||  ||||||||||
                                GA ATAT  TGTGTCTTAAC
                                 A    TT
GAM802  CGGBP1   3' TACCACTAGATAAGAATT    21706        T   TACAC
                                TACCACTA ATA     AGAATT
                                |||||||| |||     ||||||
                                ATGGTGAT TAT     TCTTAA
                                     C  _____
GAM802  LOC51123 3' TACATTTACACAGAATTG    21707      A
                                TATAT TACACAGAATTG
                                ||||| ||||||||||||
                                ATGTA ATGTGTCTTAAC
                                   A
GAM803  PPP2CA   3' AGTTATATGGTTTTACAA    21710       T       T
                                AGTTAT TGGTTTTA CAA
                                |||||| |||||||| |||
                                TCAATA ACCAAAAT GTT
                                    T      _
GAM803  RNF6     3' GTTATTTGGTTCTAGCAA    21711            T
                                GTTATTTGGTTTTA CAA
                                |||||||||||||| |||
                                CAATAAACCAAGAT GTT
                                          C
GAM803  FLJ22843 5' TTTGGCTTTTATCAAGTACT  21712         _
                                TTTGGTTTT ATCAAGTACT
                                ||||||||| ||||||||||
                                AAACCGAAA TAGTTCATGA
                                     A
GAM803  KIAA1243 3' GTTACTTGAGGTCAAGTACT  21713         TTTTA
                                GTTATTTGG     TCAAGTACT
                                |||||||||     |||||||||
                                CAATGAACT     AGTTCATGA
                                     CC___
GAM803  KIAA1726 3' AGTATTTGGCCAATTGGGTACT 21714     T       TTATCAA
                                AGT ATTTGGTT      GTACT
                                ||| ||||||||      |||||
                                TCA TAAACCGG      CATGA
                                  _       TTAACC_
GAM803  LOC145942 3' ATTTGTTTACTATCAAGTACT 21715      GTT_
                                ATTTG    TTATCAAGTACT
                                |||||    ||||||||||||
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                                TAAAC    GATAGTTCATGA
                                  AAAT
GAM803  LOC151610 5'  AGTTATTTGACAATATTAAGTA 21716          TT   C
                                AGTTATTTGGT  TAT AAGTA
                                ||||||||||  ||| |||||
                                TCAATAAACTG  ATA TTCAT
                                     TT   A
GAM803  LOC200339 3'  AGTATTTACTCTGTCAAGTACT 21717     T    G   TA
                                AGT ATTTG TTT  TCAAGTACT
                                ||| ||||| |||  |||||||||
                                TCA TAAAT AGA  AGTTCATGA
                                  _    G   C_
GAM804  CXCL16   3'  CGCAAGGGCTGAGGCCAG    21720         CA    AG
                                CGCAAGGGC  AGGC  AG
                                |||||||||  ||||  ||
                                GCGTTCCCG  TCCG  TC
                                     AC    G_
GAM804  DDX11    3'  GCAGGGGCTGCAAGAGCTTC   21721     A    CAAG  _
                                GCA GGGC    GCA GAGCTTC
                                ||| ||||    ||| |||||||
                                CGT CCCG    CGT CTCGAAG
                                  C    A___   T
GAM804  MFNG     3'  TCGCAAGGGGTGGGGAGCAAGG 21722         CCAA__   __
           AGCTT                  TCGCAAGGG     GGCA  GAGCTT
                                |||||||||     ||||  ||||||
                                AGCGTTCCC     TCGT  CTCGAA
                                     CACCCC    TC
GAM804  MTA1L1   5'  TCGCGGGGGCAGGGCT     21723      AA   CCAA    A
                                TCGC  GGG    GGCAG GCT
                                ||||  |||    ||||| |||
                                AGCG  CCC    CCGTC CGA
                                  __   _____    C
GAM804  SRD5A1   3'  AAGGGCCACGAGGAGCTTC   21724         AGGCA
                                AAGGGCCA     GAGCTTC
                                ||||||||     |||||||
                                TTCCCGGT     CTCGAAG
                                     GCTC_
GAM804  BCL2L1   3'  GCAAGGGCCACCCTAGCTT   21725          AGGCAG
                                GCAAGGGCCA      AGCTT
                                ||||||||||      |||||
                                CGTTCCCGGT      TCGAA
                                     GGGA__
GAM804  DKFZP761F241 3'  GCGGGGGCGCAAAACTGCTT   21726    AA   _     AGA
                                GC  GGGC CAAGGC   GCTT
                                ||  |||| ||||||   ||||
                                CG  CCCG GTTTTG   CGAA
                                 CC    C     A__
GAM804  EREG     3'  AAGGGCCAGGGCCAGGACTT   21727         A   _  AG
                                AAGGGCCA GGC AG  CTT
                                |||||||| ||| ||  |||
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                                TTCCCGGT CCG TC  GAA
                                    C   G  CT
GAM804   FLJ00007  3'  AAGGGAACCCCAGAGCTTC   21728      __ AAGG
                                AAGGG  CC   CAGAGCTTC
                                |||||  ||   |||||||||
                                TTCCC  GG   GTCTCGAAG
                                  TT  G___
GAM804   FLJ10597  3'  GCACTGAGGGCAGAGCTTC   21729    AG  CCAA
                                GCA  GG   GGCAGAGCTTC
                                |||  ||   ||||||||||
                                CGT  CT   CCGTCTCGAAG
                                 GA  C___
GAM804   FLJ23053  3'  TCGCAAGAGGCTGAGGCAG   21730       _  CA
                                TCGCAAG GGC  AGGCAG
                                |||||||  |||  ||||||
                                AGCGTTC CCG  TCCGTC
                                    T   AC
GAM804   HEYL     3'  AAGGGCCAAGGTGCCT     21731          CAGA
                                AAGGGCCAAGG   GCTT
                                ||||||||||   ||||
                                TTCCCGGTTCC   CGGA
                                      A___
GAM804   HSU79274  5'  CGCAAGGATGCGGAGCTT   21732       CCAAG  A
                                CGCAAGGG    GC GAGCTT
                                ||||||||    || ||||||
                                GCGTTCCT    CG CTCGAA
                                    A____  C
GAM804   KIAA1656  3'  TCCAAGGGCCGGGGTCTT   21733   G      AA  CAGAG
                                TC CAAGGGCC  GG    CTT
                                || ||||||||  ||    |||
                                AG GTTCCCGG  CC    GAA
                                 _      C_  CA___
GAM804   LBP-9     3'  AGGGTGAAGCAGAGCTT    21734     CCA
                                AGGG   AGGCAGAGCTT
                                ||||   ||||||||||
                                TCCC   TTCGTCTCGAA
                                  AC_
GAM804   mPA-PLA1  5'  TCGCAGAGGCTTAAGAGTTTC  21735     AG   CAAGGC   C
                                TCGCA  GGC     AGAG TTC
                                |||||  |||     |||| |||
                                AGCGT  CCG     TCTC AAG
                                   CT   AAT___   A
GAM804   NT5C1B    5'  GCAGGGGCCAAGGGCT     21736    A       CAGA
                                GCA GGGCCAAGG   GCT
                                ||| |||||||||   |||
                                CGT CCCGGTTCC   CGA
                                  C       ____
GAM804   LOC145739 3'  GCAAAAAAAGGCAGAGCTTC  21737       CC
                                GCAAGGG  AAGGCAGAGCTTC
                                |||||||  ||||||||||||
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                                CGTTTTT  TTCCGTCTCGAAG
                                   __
GAM804  LOC147400 3'  TCATAGGGGCCAGAGCTT    21738     CAA     AGGCA
                                TCG   GGGCCA    GAGCTT
                                |||   ||||||    ||||||
                                AGT   CCCGGT    CTCGAA
                                  ATC     _____
GAM804  LOC151429 3'  TCTCAGAAGAAAAGGCAGAGCT 21739    G  AG  CC
          TC                     TC CA  GG  AAGGCAGAGCTTC
                                || ||  ||  ||||||||||||
                                AG GT  TC  TTCCGTCTCGAAG
                                 A  CT  TT
GAM804  LOC152245 3'  TCCAAGGGCCTAGAGCTT    21740    G       AAGGC
                                TC CAAGGGCC    AGAGCTT
                                || ||||||||    |||||||
                                AG GTTCCCGG    TCTCGAA
                                 _       A____
GAM804  LOC199796 5'  TCCCAAGAGGCGGCAGAGCTTC 21741    G   _   CAA
                                TC CAAG GGC   GGCAGAGCTTC
                                || |||| |||   ||||||||||
                                AG GTTC CCG   CCGTCTCGAAG
                                 G   T  ___
GAM804  LOC92716  3'  GCAGGGGGTTCACAGAGCTTC  21742     A   CCAAG
                                GCA GGG    GCAGAGCTTC
                                ||| |||    ||||||||||
                                CGT CCC    TGTCTCGAAG
                                  C   CAAG_
GAM804  LOC92716  3'  CAGGGGCCTCACAGAGCTTC   21743    A    AAG
                                CA GGGCC   GCAGAGCTTC
                                || |||||   ||||||||||
                                GT CCCGG   TGTCTCGAAG
                                 C    AG_
GAM805  BLAME     3'  GGAGTGCTGTGTATTTT     21746     CAC    GAG
                                GGA   TGCTG   GTATTTT
                                |||   |||||   |||||||
                                CCT   ACGAC   CATAAAA
                                  C__    A__
GAM805  FCER2     3'  AGGGTGCTGTTGGGGGCACT   21747     ACA   C   A
                                AGG   CTG TGG GGTATT
                                |||   ||| ||| ||||||
                                TCC   GAC ACC CCGTGA
                                  CAC   A   C
GAM805  KAI1      3'  GGACGCTGTGGGGAGCATTTTT 21748      A   CT  AG
                                GGAC CTG  GG  GTATTTTT
                                |||| |||  ||  ||||||||
                                CCTG GAC  CC  CGTAAAAA
                                  C   AC  CT
GAM805  LPIN2     3'  GGACACTGCTCGGGGGGCA    21749          _  A_
                                GGACACTGCT GG  GGTA
                                |||||||||| ||  ||||
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                                CCTGTGACGA CC  CCGT
                                      G  CC
GAM805  PIK3CG   3'  AGACACTGTTAACATAGTTTTT 21750        CTG  G  _
                                GGACACTG   GA GTA TTTTT
                                ||||||||   || ||| |||||
                                TCTGTGAC   TT TAT AAAAA
                                     AA_  G   C
GAM805  RANBP3   5'  AGGCATTGCTGGACTCATTTTT 21751     A  C      GG
                                AGG CA TGCTGGA  TATTTTT
                                ||| || |||||||  |||||||
                                TCC GT ACGACCT  GTAAAAA
                                  _ A      GA
GAM805  CTBS     3'  AGGACATTCGTGTGTATTTTT  21752       CTGC  GAG
                                AGGACA   TG   GTATTTTT
                                ||||||   ||   ||||||||
                                TCCTGT   GC   CATAAAAA
                                    AA__  ACA
GAM805  FLJ20694 3'  AAGGAGCTGAGACAGTATTTTT 21753       CACT   _ _
                                AAGGA   GCTG GA GGTATTTTT
                                |||||   |||| || |||||||||
                                TTCCT   CGAC CT TCATAAAAA
                                   _____   T  G
GAM805  KIAA0247 3'  AAGGGCACTGCTGTGGGT    21754      A       GA
                                AAGG CACTGCTG  GGT
                                |||| ||||||||  |||
                                TTCC GTGACGAC  CCA
                                  C       AC
GAM805  KIAA0435 3'  AGGAGCACTGCTGGGTATTT   21755      _       AG
                                AGGA CACTGCTGG  GTATTT
                                |||| |||||||||  ||||||
                                TCCT GTGACGACC  CATAAA
                                  C       __
GAM805  KIAA1143 3'  AGGAGTTGGGGAGGTATTTTT  21756      CAC  CT
                                AGGA   TG  GGAGGTATTTTT
                                ||||   ||  ||||||||||||
                                TCCT   AC  CCTCCATAAAAA
                                  CA_  C_
GAM805  KIAA1239 3'  GGAATACACTTGGGTATTTTT  21757     CAC    GGA
                                GGA   TGCT   GGTATTTTT
                                |||   ||||   |||||||||
                                CCT   GTGA   CCATAAAAA
                                  TAT    AC_
GAM805  KIAA1255 3'  GGATGTGTGAGGGTATTTTT   21758     CAC  C  GA
                                GGA   TG TG  GGTATTTTT
                                |||   || ||  |||||||||
                                CCT   AC AC  CCATAAAAA
                                  AC_  _  TC
GAM805  SSH2     3'  AGGACACTGCAGAGCACATTTT 21759          T   _
           T                     AGGACACTGC GGAG GTATTTTT
                                ||||||||| |||| ||||||||
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                                TCCTGTGACG TCTC TGTAAAAA
                                      _   G
GAM805  TAGAP    3'  AAGGACACGTTGAAGTGT    21760        T C    _
                                AAGGACAC G TGGAG GT
                                |||||||| | ||||| ||
                                TTCCTGTG C ACTTC CA
                                     _ A    A
GAM805  LOC158147 3'  AGGCACCAGGTATTTT     21761     A   GCTGG
                                AGG CACT    AGGTATTTT
                                ||| ||||    |||||||||
                                TCC GTGG    TCCATAAAA
                                 _   _____
GAM805  LOC220954 3'  AAGGATGCTCTTGGAGGTATT  21762      CA  GC
                                AAGGA  CT  TGGAGGTATT
                                |||||  ||  ||||||||||
                                TTCCT  GA  ACCTCCATAA
                                   AC  GA
GAM805  LOC221362 3'  GGAAACAAAGGTATTTT     21763     C  TGCT
                                GGA AC    GGAGGTATTTT
                                ||| ||    ||||||||||||
                                CCT TG    TTTCCATAAAA
                                  T _____
GAM806  BSN      3'  GCCAGATTGTAGATGTGT    21766      AG  _
                                GCCA  TT TAGATGTGT
                                ||||  || |||||||||
                                CGGT  AA ATCTACACA
                                  CT  C
GAM806  C18orf2   3'  TGCTGAGTTTAGAACCAGTGT  21767     CA      T___
                                TGC  AGTTTAGA    GTGT
                                |||  ||||||||    ||||
                                ACG  TCAAATCT    CACA
                                  AC       TGGT
GAM806  CYP8B1    3'  TGCCAAGTTCTGCAT      21768          AGA
                                TGCCAAGTTT   TGTGT
                                ||||||||||   |||||
                                ACGGTTCAAG   ACGTA
                                      ___
GAM806  E2F3     3'  TACCAAGTCCAGTGTGT     21769           A
                                TGCCAAGTTTAG TGTGT
                                |||||||||||| |||||
                                ATGGTTCAGGTC ACACA
                                      _
GAM806  EPB41L2   3'  TGCCAGCTTTAAATGGT     21770      AG      T
                                TGCCA  TTTAGATG GT
                                |||||  |||||||| ||
                                ACGGT  AAATTTAC CA
                                   CG       _
GAM806  GDI2     3'  TGCCAAATTTTAAATGTGT   21771          _
                                TGCCAAGTTT AGATGTGT
                                |||||||||| ||||||||
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                                ACGGTTTAAA TTTACACA
                                      A
GAM806  GNAZ     3'  TGCCATCTCCAGATGTGT    21772      AG
                                TGCCA  TTTAGATGTGT
                                |||||  ||||||||||
                                ACGGT  AGGTCTACACA
                                   AG
GAM806  KCNE1L   3'  TGCCAAGTGTTGGACGTGT   21773        _ A
                                TGCCAAGT TT GATGTGT
                                |||||||| || |||||||
                                ACGGTTCA AA CTGCACA
                                     C  C
GAM806  LIMD1    3'  TACCAAGTCCTTGTGT     21774         AGA
                                TGCCAAGTTT   TGTGT
                                ||||||||||   |||||
                                ATGGTTCAGG   ACACA
                                      A__
GAM806  PATE     3'  TGGCAAGCTCAAGTGTGT    21775    C       A
                                TG CAAGTTTAG TGTGT
                                || |||||||| |||||
                                AC GTTCGAGTT ACACA
                                 C       C
GAM806  TRIM     3'  TGCCAAGTCCTTCTGTGT    21776         AGA
                                TGCCAAGTTT   TGTGT
                                ||||||||||   |||||
                                ACGGTTCAGG   ACACA
                                      AAG
GAM806  XRCC3    3'  TGCAGCCAGATGTGT      21777     CA    T
                                TGC  AGTT AGATGTGT
                                |||  |||| ||||||||
                                ACG  TCGG TCTACACA
                                  __   _
GAM806  DIS3     3'  TGCCAAGTGACATGT      21778        TTA
                                TGCCAAGT   GATGTGT
                                ||||||||   |||||||
                                ACGGTTCA   CTGTACA
                                     ___
GAM806  DKFZP434L1435 5'  CGCCCGTGTAGATGTGT     21779      AA  T
                                TGCC  GT TAGATGTGT
                                ||||  || |||||||||
                                GCGG  CA ATCTACACA
                                  G_  C
GAM806  GR6      3'  TGCCAAATCTTGCTGTGT    21780         AGA
                                TGCCAAGTTT   TGTGT
                                ||||||||||   |||||
                                ACGGTTTAGA   ACACA
                                      ACG
GAM806  HTEX4    5'  TACCACTTCCTAGGTGTGT   21781      AG_    A
                                TGCCA   TTTAG TGTGT
                                |||||   ||||| |||||
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                                ATGGT   GGATC ACACA
                                   GAA    C
GAM806  HTEX4    5'  TACCACTTCCTAGGTGTGT   21781      AG_    A
                                TGCCA   TTTAG TGTGT
                                |||||   ||||| |||||
                                ATGGT   GGATC ACACA
                                   GAA    C
GAM806  HTEX4    5'  TACCACTTCCTAGGTGTGT   21781      AG_    A
                                TGCCA   TTTAG TGTGT
                                |||||   ||||| |||||
                                ATGGT   GGATC ACACA
                                   GAA    C
GAM806  KIAA0408 3'  TACCAATGTTAGATGTGT    21782       GT
                                TGCCAA  TTAGATGTGT
                                ||||||  ||||||||||
                                ATGGTT  AATCTACACA
                                    AC
GAM806  KIAA0594 3'  TACCAAGTTCTTCAATGT    21783         A__
                                TGCCAAGTTT   GATGT
                                ||||||||||   |||||
                                ATGGTTCAAG   TTACA
                                      AAG
GAM806  KIAA1348 5'  TACCAGCAAATGTGT       21784       A  TT
                                TGCCA GT  AGATGTGT
                                ||||| ||  ||||||||
                                ATGGT CG  TTTACACA
                                  _  __
GAM806  KIAA1458 3'  TGCTAAATTTAGGAATGT    21785     C       AT
                                TGC AAGTTTAG  GTGT
                                ||| ||||||||  ||||
                                ACG TTTAAATC  TACA
                                  A       CT
GAM806  LGI2     3'  TGCTGGGTCTAGACATGT    21786     CAA
                                TGC   GTTTAGATGTGT
                                |||   ||||||||||||
                                ACG   CAGATCTGTACA
                                  ACC
GAM806  MGC5139  5'  GCCAGGTTCCAGATGTGT    21787      A   _
                                GCCA GTTT AGATGTGT
                                |||| |||| ||||||||
                                CGGT CAAG TCTACACA
                                  C    G
GAM806  MTHFD2   3'  TACCAGACAGATGTGT      21788       A TT
                                TGCCA G  TAGATGTGT
                                ||||| |  |||||||||
                                ATGGT C  GTCTACACA
                                   _ T_
GAM806  NFAT5    3'  TGCCAAGTTCTGGAGTGTGT  21789          A_  _
                                TGCCAAGTTT  GA TGTGT
                                ||||||||||  || |||||
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                                ACGGTTCAAG  CT ACACA
                                      AC  C
GAM806  PEGASUS  3'  TGTCATGTTTAGATGCAT    21790    C  A
                                TG CA GTTTAGATGTGT
                                || || ||||||||||||
                                AC GT CAAATCTACGTA
                                 A  A
GAM806  PV1      3'  TGCCAAGTTCCCCATGT     21791         AGA
                                TGCCAAGTTT   TGTGT
                                ||||||||||   |||||
                                ACGGTTCAAG   GTACA
                                      GG_
GAM806  RCD-8    3'  TGCCAAGTGAGTTGTGT     21792        TT  A
                                TGCCAAGT  AG TGTGT
                                ||||||||  || |||||
                                ACGGTTCA  TC ACACA
                                     C_  A
GAM806  SNRPD1   3'  TGCCAAATTTAATTTGT     21793          ATG
                                TGCCAAGTTTAG   TGT
                                ||||||||||||   |||
                                ACGGTTTAAATT   ACA
                                       AA_
GAM806  LOC124145 3'  TACCAAGTTTGAATATGT    21794         AG
                                TGCCAAGTTT  ATGTGT
                                ||||||||||  ||||||
                                ATGGTTCAAA  TATACA
                                      CT
GAM806  LOC143437 5'  TGCCAGGTTTGAGCGT      21795      A   A  T
                                TGCCA GTTT GA GTGT
                                ||||| |||| || ||||
                                ACGGT CAAA CT CGCA
                                   C   _ _
GAM806  LOC144308 3'  TGCCAAGCTTACCATGT     21796         GA
                                TGCCAAGTTTA  TGTGT
                                ||||||||||   |||||
                                ACGGTTCGAAT  GTACA
                                       G_
GAM806  LOC146856 3'  TACCAAGTCCAGTGTGT     21769          A
                                TGCCAAGTTTAG TGTGT
                                ||||||||||| |||||
                                ATGGTTCAGGTC ACACA
                                            _
GAM806  LOC161635 5'  TGTCCAATCAAATGTGT     21797    _   GT
                                TG CCAA  TTAGATGTGT
                                || ||||  ||||||||||
                                AC GGTT  AGTTTACACA
                                 A   __
GAM806  LOC253531 5'  TGCCAGGTTTGAGCGT      21795      A   A  T
                                TGCCA GTTT GA GTGT
                                ||||| |||| || ||||
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                                ACGGT CAAA CT CGCA
                                  C   _ _
GAM806  LOC257103 5'  TGTCAAGTTTAGAAGCAGTGT  21798    C        T___
                                TG CAAGTTTAGA   GTGT
                                || ||||||||||   ||||
                                AC GTTCAAATCT   CACA
                                 A         TCGT
GAM806  LOC257443 3'  TGCTAAATTTAGGAATGT    21785    C       AT
                                TGC AAGTTTAG  GTGT
                                ||| ||||||||  ||||
                                ACG TTTAAATC  TACA
                                  A       CT
GAM806  LOC92249  5'  GCCAAGTAAGAAATGTGT    21799       TT_
                                GCCAAGT   AGATGTGT
                                |||||||   ||||||||
                                CGGTTCA   TTTACACA
                                    TTC
GAM807  ACAD8    3'  TCATGATTTACATTCAGAGGTG 21802    A      AAT     A
                                TCA TGATTTG   TTCAGA GTG
                                ||| |||||||   |||||| |||
                                AGT ACTAAAT   AAGTCT CAC
                                  _      GT_     C
GAM807  EMX2     3'  TCAAGGATTTGAAACAG     21803     T      TTT
                                TCAA GATTTGAA   CAG
                                |||| ||||||||   |||
                                AGTT CTAAACTT   GTC
                                  C       T__
GAM807  MPHOSPH9  3'  TCAAAGATTTGCAGAGGT    21804     T     AATTT    A
                                TCAA GATTTG    CAGA GT
                                |||| ||||||    |||| ||
                                AGTT CTAAAC    GTCT CA
                                  T     _____   C
GAM807  NEK6     3'  TCAAATGATTTCCTTCAGAGGT 21805     _     GAA      A
           G                     TCAA TGATTT   TTTCAGA GTG
                                |||| ||||||   ||||||| |||
                                AGTT ACTAAA   GAAGTCT CAC
                                  T     G__      C
GAM807  PPEF1    3'  TGACTATGAATTTCAGGGGTG  21806      _       AA
                                TGATT TGAATTTCAG  GTG
                                ||||| ||||||||||  |||
                                ACTGA ACTTAAAGTC  CAC
                                   T        CC
GAM807  CTCFL    3'  TCAATGATCTTGAAATACAGGG 21807         _  TTT   AA
           GTG                    TCAATGATTT GAA   CAG  GTG
                                |||||||||| |||   |||  |||
                                AGTTACTAGA CTT   GTC  CAC
                                      A   TAT   CC
GAM807  FLJ13456  3'  CCAATGATTTGAACAATGAGTG 21808           TTCA  A
                                TCAATGATTTGAAT    GA GTG
                                ||||||||||||||   || |||
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                                GGTTACTAAACTTG    CT CAC
                                      TTA_  _
GAM807  KIAA0831  3'  AATGATTTATCAGAGGT     21809         AATT    A
                                AATGATTTG    TCAGA GT
                                |||||||||    ||||| ||
                                TTACTAAAT    AGTCT CA
                                     ____    C
GAM807  MRPL53    3'  TGATTTGAATGATTAAGTG    21810          TTCAG
                                TGATTTGAAT    AAGTG
                                ||||||||||    |||||
                                ACTAAACTTA    TTCAC
                                     CTAA_
GAM807  PYPAF4    3'  TCAATGATTTGTATCTCCTGGG 21811           A    AGAA
          TG                      TCAATGATTTG ATTTC    GTG
                                ||||||||||| |||||    |||
                                AGTTACTAAAC TAGAG    CAC
                                      A     GACC
GAM807  LOC152674 3'  TCAATGATTTGCAGCAAGGAGG 21812           AATTTCA  A
          TG                      TCAATGATTTG      GA GTG
                                ||||||||||       || |||
                                AGTTACTAAAC      CT CAC
                                      GTCGTTC  C
GAM807  LOC158863 3'  GATTTGAACCAGTAAGTG    21813         TT   _
                                GATTTGAAT  CAG AAGTG
                                |||||||||  ||| |||||
                                CTAAACTTG  GTC TTCAC
                                     __   A
GAM807  LOC57105  3'  TAATAGAATTTCAGGAGTG   21814      TT       A
                                TGAT  GAATTTCAG AGTG
                                ||||  ||||||||| ||||
                                ATTA  CTTAAAGTC TCAC
                                  T_       C
GAM808  DNMT1     3'  ATCAGTGCATGTTGGGGA    21817      _  C  ATGACA
                                ATCA TGC TG     TTGGGGA
                                |||| ||| ||     |||||||
                                TAGT ACG AC     AACCCCT
                                  C   T _______
GAM808  SLC38A2   3'  ATGCCTGATGAGCGAAG     21818          CAT
                                ATGCCTGATGA   TGGGG
                                ||||||||||   |||||
                                TACGGACTACT   GCTTC
                                      C__
GAM808  DKFZP727G051 3'  TGTCTGGTGGGTCTGGGGAT   21819    C   A  ACA
                                TG CTG TG   TTGGGGAT
                                || ||| ||   ||||||||
                                AC GAC AC   GACCCCTA
                                 A   C  CCA
GAM808  MGC20255  3'  ATCAGCTGCCTTGTTGGGGAT  21820      __    GATGACA
                                ATCA  TGCCT      TTGGGGAT
                                ||||  |||||      ||||||||
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                                TAGT  ACGGA      AACCCCTA
                                  CG    AC_____
GAM808  MIG2     3'  CATGCCTGATTTATTTGGGG  21821          GACA
                                CATGCCTGAT    TTGGGG
                                ||||||||||    ||||||
                                GTACGGACTA    AACCCC
                                      AATA
GAM808  LOC148709 5'  ATCATGCCCTGGTGCCAGGGAT 21822          GATGACA TG
                                ATCATGCCT      T  GGGAT
                                |||||||||      |  |||||
                                TAGTACGGG      G  CCCTA
                                     ACCAC__ GT
GAM808  LOC200488 5'  ATCATACCTGATGGTATGAAG  21823           ACAT
                                ATCATGCCTGATG    TGGGG
                                ||||||||||||    |||||
                                TAGTATGGACTAC    ACTTC
                                       CAT_
GAM809  ABCC5    3'  TGCCACCTCAAAAAGCAG    21826      CT
                                TGCC  TTTCAAAAAGCAG
                                ||||  ||||||||||||||
                                ACGG  GGAGTTTTTCGTC
                                  T_
GAM809  ADARB1   3'  TGCCCTTTCCACTTACACAG   21827          AAAA_
                                TGCCCTTTTCA    GCAG
                                ||||||||||    ||||
                                ACGGGAAAGGT    TGTC
                                      GAATG
GAM809  ASB1     5'  GCCCCTCGGGCAGGAAGCAG   21828        T__  AA
                                GCCCTTT   CA  AAGCAG
                                |||||||   ||  ||||||
                                CGGGGAG   GT  TTCGTC
                                    CCC  CC
GAM809  CPNE7    3'  TGCCCCTTCTCATCGGGGCAG 21829      _     AAAA_
                                TGCCC TTTTCA    GCAG
                                ||||| ||||||    ||||
                                ACGGG AAGAGT    CGTC
                                   G     AGCCC
GAM809  CTPS     3'  TGCCCTTTCAACTGCAG     21830        T   AAA
                                TGCCCTTT CAA   GCAG
                                |||||||| |||   ||||
                                ACGGGAAA GTT   CGTC
                                     _   GA_
GAM809  ECHS1    3'  TGTCCTCTCCAAGCAG      21831    C       AAA
                                TG CCTTTTCA   AGCAG
                                || ||||||||   |||||
                                AC GGAGAGGT   TCGTC
                                 A       ___
GAM809  ENTPD6   5'  TGCCCTTTTCCGGGGAGCAG  21832          AAAA_
                                TGCCCTTTTC    AGCAG
                                ||||||||||    |||||
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                                ACGGGAAAAG    TCGTC
                                      GCCCC
GAM809  EPHB2    3'  TGTCCCTTTCATCAACAG    21833    C      AAA
                                TG CCTTTTCA   AGCAG
                                || ||||||||   |||||
                                AC GGGAAAGT   TTGTC
                                 A       AG_
GAM809  FGF7     3'  TACCCTTTCCACTTGAGCAG  21834          AAA_
                                TGCCCTTTTCA   AGCAG
                                ||||||||||    |||||
                                ATGGGAAAGGT   TCGTC
                                      GAAC
GAM809  HAS3     3'  TGCACTTTTAAAAGCAG     21835    C    CA
                                TGC CTTTT  AAAAGCAG
                                ||| |||||  ||||||||
                                ACG GAAAA  TTTTCGTC
                                 T    __
GAM809  HMGA1    5'  CCCTTCTCTAAGGAGCAG    21836        _  AA
                                CCCTTTTC AA  AGCAG
                                |||||||| ||  |||||
                                GGGAAGAG TT  TCGTC
                                     A  CC
GAM809  HSPA4    3'  TGCCCCAAAAAGCAG       21837      TTTT
                                TGCCC    CAAAAAGCAG
                                |||||    ||||||||||
                                ACGGG    GTTTTTCGTC
                                     ____
GAM809  JAG1     3'  CTTTTCAAGTCTAAAGCAG   21838        ____
                                CTTTTCAA    AAAGCAG
                                ||||||||    |||||||
                                GAAAAGTT    TTTCGTC
                                     CAGA
GAM809  MAGEA2   3'  TGCTCTCTTCAAAGAGGCAG  21839    C      AA_
                                TGC CTTTTCAAA   GCAG
                                ||| |||||||||   ||||
                                ACG GAGAAGTTT   CGTC
                                  A       CTC
GAM809  MAGEA8   3'  TGCTCTCTTCAAACACAG    21840    C      AA
                                TGC CTTTTCAAA  GCAG
                                ||| |||||||||  ||||
                                ACG GAGAAGTTT  TGTC
                                  A       G_
GAM809  MAGEA9   3'  TGCTCTCTTCAAACACAG    21840    C      AA
                                TGC CTTTTCAAA  GCAG
                                ||| |||||||||  ||||
                                ACG GAGAAGTTT  TGTC
                                  A       G_
GAM809  MAPK8IP1 3'  TGCCCCTCCTCAAGCAG     21841        CAAA
                                TGCCCTTTT    AAGCAG
                                |||||||||    ||||||
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                                ACGGGGAGG   TTCGTC
                                     AG__
GAM809  MFNG    3'  TGCCCTTTTTCAATTCAG    21842        _  AAAG
                                TGCCCTTTT CAA   CAG
                                ||||||||| |||   |||
                                ACGGGAAAA GTT   GTC
                                     A  AA__
GAM809  NFKBIL2 5'  GCTCTTCTCAAAGGCAG    21843   C       AA
                                GC CTTTTCAAA  GCAG
                                || |||||||||  ||||
                                CG GAAGAGTTT  CGTC
                                 A        C_
GAM809  NOS1    3'  TGCCTTTTCACTTTAACAG   21844     C     AAA_
                                TGCC TTTTCA   AGCAG
                                |||| ||||||   |||||
                                ACGG AAAAGT   TTGTC
                                  _     GAAA
GAM809  PLAU    3'  TGCCCTTTTTAACTCCTGCAG 21845        C  AAA__
                                TGCCCTTTT AA    GCAG
                                ||||||||| ||    ||||
                                ACGGGAAAA TT    CGTC
                                     A  GAGGA
GAM809  POLS    3'  CCTGCTTCAAAAGGGCAG    21846    _      A_
                                CCT TTTCAAAA  GCAG
                                ||| ||||||||  ||||
                                GGA GAAGTTTT  CGTC
                                  C       CC
GAM809  SMCX    3'  GCCCACCCCCCAAGAAGCAG  21847     __  TT   A
                                GCCC  TT  CAA AAGCAG
                                ||||  ||  ||| ||||||
                                CGGG  GG  GTT TTCGTC
                                   TG  GG   C
GAM809  TGFBR3  3'  TGCCCTTTCCAATCTCAG    21848          AAAG
                                TGCCCTTTTCAA   CAG
                                ||||||||||||   |||
                                ACGGGAAAGGTT   GTC
                                      AGA_
GAM809  TLX1    5'  TGCCCTTCTTTAAAACA     21849        CAA
                                TGCCCTTTT   AAAGCA
                                |||||||||   ||||||
                                ACGGGAAGA   TTTTGT
                                     AA_
GAM809  ZIC1    5'  TGCCCTTTTAAAGGCA      21850        CA   A
                                TGCCCTTTT  AAA GCA
                                |||||||||  ||| |||
                                ACGGGAAAA  TTT CGT
                                     __  C
GAM809  ZNF236  3'  TGCCCTTTCAAAATAACAG   21851        T    _
                                TGCCCTTT CAAAA AGCAG
                                |||||||| ||||| |||||
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                                ACGGGAAA GTTTT TTGTC
                                   _    A
GAM809  AGS3    3' TGCCCCTCCAGAAGCAG    21852       CAAA
                                TGCCCTTTT   AAGCAG
                                |||||||||   ||||||
                                ACGGGGAGG   TTCGTC
                                    TC__
GAM809  AKAP7   3' TGCTCTTTCAAACAGAAGCAG 21853    CC     ___
                                TGC TTTTCAAA  AAGCAG
                                |||  ||||||||  ||||||
                                ACG GAAAGTTT  TTCGTC
                                  A_      GTC
GAM809  AKAP7   3' TGCTCTTTCAAACAGAAGCAG 21853    CC     ___
                                TGC TTTTCAAA  AAGCAG
                                |||  ||||||||  ||||||
                                ACG GAAAGTTT  TTCGTC
                                  A_      GTC
GAM809  AKAP7   3' TGCTCTTTCAAACAGAAGCAG 21853    CC     ___
                                TGC TTTTCAAA  AAGCAG
                                |||  ||||||||  ||||||
                                ACG GAAAGTTT  TTCGTC
                                  A_      GTC
GAM809  AP1GBP1 3' CTTCTCCATAAAAAGCAG   21854      ___
                                CTTTTC  AAAAAGCAG
                                ||||||  |||||||||
                                GAAGAG  TTTTTCGTC
                                   GTA
GAM809  AP1GBP1 3' CTTCTCCATAAAAAGCAG   21854      ___
                                CTTTTC  AAAAAGCAG
                                ||||||  |||||||||
                                GAAGAG  TTTTTCGTC
                                   GTA
GAM809  BNIP2   5' GCCAGGTCGCAAAAAGCAG  21855    CT_ T
                                GCC  TT CAAAAAGCAG
                                |||  || ||||||||||
                                CGG  AG GTTTTTCGTC
                                  TCC  C
GAM809  COVA1   3' TGCCCTCCTTTAAAAGCAG  21856       CA
                                TGCCCTTTT  AAAAGCAG
                                |||||||||  ||||||||
                                ACGGGAGGA  TTTTCGTC
                                    AA
GAM809  DIO2    5' CCTCTTTCAAAGAAGCAG   21857   C     _
                                CC TTTTCAAA AAGCAG
                                || |||||||| ||||||
                                GG GAAAGTTT TTCGTC
                                 A      C
GAM809  DLAT    5' TGACCTCTCCAAGAGCAG   21858   C      AA
                                TG CCTTTTCAA  AGCAG
                                || |||||||||  |||||
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                                AC GGAGAGGTT  TCGTC
                                 T       C_
GAM809  FLJ10936  5'  GCCTCACCGCAAAAGCAG    21859     C  T  A_
                                GCC TT TC  AAAAGCAG
                                ||| || ||  ||||||||
                                CGG AG GG  TTTTCGTC
                                  _  T  CG
GAM809  FLJ11294  5'  GCTCCTCCAAAGGAGCAG    21860    _   TT   A_
                                GC CCTT  CAAA  AGCAG
                                || ||||  ||||  |||||
                                CG GGAG  GTTT  TCGTC
                                 A   __   CC
GAM809  FLJ11608  3'  TGCCCTCTTCGAACTCTCAG   21861         A  AAG_
                                TGCCCTTTTC AA   CAG
                                |||||||||| ||   |||
                                ACGGGAGAAG TT   GTC
                                      C  GAGA
GAM809  FLJ13194  3'  TGCCCTTCAATGTGAAAGCAG  21862        TCAA__
                                TGCCCTTT     AAAGCAG
                                ||||||||     |||||||
                                ACGGGAAG     TTTCGTC
                                     TTACAC
GAM809  FLJ20038  3'  TACCCCATTCAAAAGGCAG    21863       T      A
                                TGCCCT TTCAAAA GCAG
                                |||||| ||||||| ||||
                                ATGGGG AAGTTTT CGTC
                                   T      C
GAM809  FLJ20209  5'  TGGCCTTTTCAAACACACAG   21864    C        AA_
                                TG CCTTTTCAAA   GCAG
                                || ||||||||||   ||||
                                AC GGAAAAGTTT   TGTC
                                 C         GTG
GAM809  FLJ20275  3'  TACCCTCCCCCAAAAGCAG    21865       TT A
                                TGCCCTT  C AAAAGCAG
                                |||||||  | ||||||||
                                ATGGGAG  G TTTTCGTC
                                    GG G
GAM809  FLJ20793  3'  ACCACTTTTCAAAAAGCAG    21866     _
                                GCC CTTTTCAAAAAGCAG
                                ||| ||||||||||||||
                                TGG GAAAAGTTTTTCGTC
                                  T
GAM809  FLN29     3'  GCCCTCCCCATTAGAAAGCAG  21867      TT  A___
                                GCCCTT  CA    AAAGCAG
                                ||||||  ||    |||||||
                                CGGGAG  GT    TTTCGTC
                                   GG  AATC
GAM809  FOXP1     3'  TGCCCTTTATACAGAAAGCAG  21868       T__  A
                                TGCCCTTT   CA AAAGCAG
                                ||||||||   || |||||||
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                                ACGGGAAA   GT TTTCGTC
                                    TAT  C
GAM809  GR6      3'  CCCTTCTCACAGAAAGCAG   21869        A__
                                CCCTTTTCA   AAAGCAG
                                |||||||||   |||||||
                                GGGAAGAGT   TTTCGTC
                                     GTC
GAM809  HSPC133  3'  TGCCATTTCCAAAGCAG    21870     C      AA
                                TGCC TTTTCAA  AGCAG
                                |||| |||||||  |||||
                                ACGG AAAGGTT  TCGTC
                                  T      __
GAM809  HZFW1    3'  ACCCCCAAAAAGCAG      21871      TTT
                                GCCCT   CAAAAAGCAG
                                |||||   ||||||||||
                                TGGGG   GTTTTTCGTC
                                   ___
GAM809  KIAA0212 3'  TGCCCTCCAGAAAGCAG    21872       TT  A
                                TGCCCTT  CA AAAGCAG
                                |||||||  || |||||||
                                ACGGGAG  GT TTTCGTC
                                    __  C
GAM809  KIAA0914 3'  TGCCCTTTCAGAAGGCA    21873       T  A  A
                                TGCCCTTT CA AA GCA
                                |||||||| || || |||
                                ACGGGAAA GT TT CGT
                                     _  C  C
GAM809  KIAA0992 3'  TGCATTCAAAAAGCAG     21874     CCTT
                                TGC    TTCAAAAAGCAG
                                |||    ||||||||||||
                                ACG    AAGTTTTTCGTC
                                  T___
GAM809  KIAA1000 3'  TGTCCTTTCAAAGCAG     21875    C     CAA
                                TG CCTTTT   AAAGCAG
                                || ||||||   |||||||
                                AC GGAAAG   TTTCGTC
                                 A     ___
GAM809  KIAA1522 5'  TGCCTCTCCAGAGCAG     21876     C     AAA
                                TGCC TTTTCA   AGCAG
                                |||| ||||||   |||||
                                ACGG AGAGGT   TCGTC
                                  _     C__
GAM809  KIAA1649 5'  GCCCCTGGAAAAAGCAG    21877       TTC
                                GCCCTT   AAAAAGCAG
                                ||||||   |||||||||
                                CGGGGA   TTTTTCGTC
                                   CC_
GAM809  KIAA1649 3'  GCCCCTGGAAAAAGCAG    21877       TTC
                                GCCCTT   AAAAAGCAG
                                ||||||   |||||||||
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                                CGGGGA  TTTTTCGTC
                                   CC_
GAM809  KIAA1710 3' GCCTTTTTCCAAAGCAG    21878    C    AA
                                GCC TTTTC  AAAGCAG
                                ||| |||||  |||||||
                                CGG AAAAG  TTTCGTC
                                  A    G_
GAM809  KIAA1813 5' TGCTCCTTCCTGGAAGCAG  21879    _    CAAA
                                TGC CCTTTT   AAGCAG
                                ||| ||||||   ||||||
                                ACG GGAAGG   TTCGTC
                                  A    ACC_
GAM809  KIAA1918 5' TGCCCTTTTGAAGCAG     21880       CAAA
                                TGCCCTTTT   AAGCAG
                                |||||||||   ||||||
                                ACGGGAAAA   TTCGTC
                                     C___
GAM809  KLF12    3' TGCCCTTTTCAGGAAAAG    21881         __
                                TGCCCTTTTCA  AAAAG
                                ||||||||||  |||||
                                ACGGGAAAAGT  TTTTC
                                      CC
GAM809  KRTAP9-2 3' TGCCCTCCCTCAAGCAG    21882       CAAA
                                TGCCCTTTT   AAGCAG
                                |||||||||   ||||||
                                ACGGGAGGG   TTCGTC
                                     AG__
GAM809  KRTAP9-3 3' TGCCCTCCCTCAAGCAG    21882       CAAA
                                TGCCCTTTT   AAGCAG
                                |||||||||   ||||||
                                ACGGGAGGG   TTCGTC
                                     AG__
GAM809  LEC3     3' TGGCCTTTTAAAAAGCAG    21883    C    C
                                TG CCTTTT AAAAAGCAG
                                || |||||| |||||||||
                                AC GGAAAA TTTTTCGTC
                                 C    _
GAM809  MGC2742  5' TACCCTTTTGTTTCAAAGGGCA 21884       ____    AA
           G                     TGCCCTTT   TCAAA  GCAG
                                |||||||   |||||  ||||
                                ATGGGAAA   AGTTT  CGTC
                                     ACAA    CC
GAM809  MGC5590  5' GCCAGGCTCCAAAAAGCAG   21885    CT_
                                GCC   TTTCAAAAAGCAG
                                |||   ||||||||||||
                                CGG   GAGGTTTTTCGTC
                                  TCC
GAM809  NDST4    5' TGTCCTTTTCAAAACAAGCAG 21886    C       __
                                TG CCTTTTCAAAA  AGCAG
                                || ||||||||||  |||||
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                                AC GGAAAAGTTTT  TCGTC
                                 A          GT
GAM809  NEU4     3'  CCCCTTCCTAAAGAGCAG    21887        _  A
                                CCCTTTTC AAA AGCAG
                                |||||||| ||| |||||
                                GGGGAAGG TTT TCGTC
                                     A   C
GAM809  PCQAP    3'  GCCCTCCCTCCAAAAGGCAG  21888       __     A
                                GCCCTT  TTCAAAA GCAG
                                ||||||  ||||||| ||||
                                CGGGAG  AGGTTTT CGTC
                                   GG      C
GAM809  PELI2    3'  TGCTCTCTCAAAAGCAG     21889     C    CA
                                TGC CTTTT  AAAAGCAG
                                ||| |||||  ||||||||
                                ACG GAGAG  TTTTCGTC
                                  A    __
GAM809  POLD3    3'  CCCAACCTTAAAAAGCAG    21890     T_  C
                                CCC  TTT AAAAAGCAG
                                |||  ||| |||||||||
                                GGG  GGA TTTTTCGTC
                                  TT   A
GAM809  PSTPIP2  3'  TGCCCTTTCCATATCACAG   21891          AAAA
                                TGCCCTTTTCA    GCAG
                                ||||||||||    ||||
                                ACGGGAAAGGT    TGTC
                                       ATAG
GAM809  TBPL1    3'  TGTCCTTTTGTAAAAGCAG   21892    C     CA
                                TG CCTTTT  AAAAGCAG
                                || ||||||  ||||||||
                                AC GGAAAA  TTTTCGTC
                                 A     CA
GAM809  TERA     5'  TGCCTTCCAAAAGCAG      21893     CT      A
                                TGCC  TTTCAAAA GCAG
                                ||||  |||||||| ||||
                                ACGG  AAGGTTTT CGTC
                                   __      _
GAM809  TUSP     5'  GCCCCTTCACTCAAGAGGCAG 21894        ___   AAA
                                GCCCTTT   TCAA   GCAG
                                |||||||   ||||   ||||
                                CGGGGAA   AGTT   CGTC
                                    GTG    CTC
GAM809  UBCE7IP5 3'  GCTCCCCCTCAGGGAGCAG   21895    _      AAA
                                GC CCTTTTCA   AGCAG
                                || ||||||||   |||||
                                CG GGGGGAGT   TCGTC
                                 A       CCC
GAM809  ZIN      3'  TGCCCTCTGGAAAGCAG     21896         TCAA
                                TGCCCTTT    AAAGCAG
                                ||||||||    |||||||
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                                ACGGGAGA   TTTCGTC
                                    CC__
GAM809  LOC127702 3'  TGCCCCTTTCCTCCAGCAG   21897        AAAA
                                TGCCCTTTTC   AGCAG
                                ||||||||||   |||||
                                ACGGGGAAAG   TCGTC
                                   GAGG
GAM809  LOC144058 5'  GCCCTCCTCGCAAGGGCAG   21898        A_ AA
                                GCCCTTTTC AA GCAG
                                |||||||||  ||  ||||
                                CGGGAGGAG TT CGTC
                                     CG CC
GAM809  LOC144712 5'  CCCTTCTCTAAGGAGCAG    21836        _ AA
                                CCCTTTTC AA AGCAG
                                |||||||| ||  |||||
                                GGGAAGAG TT TCGTC
                                    A CC
GAM809  LOC145098 5'  GCCCTCCCCAGAAAGGCAG   21899       TT A  _
                                GCCCTT CA AAAG CAG
                                ||||||  || |||| |||
                                CGGGAG GT TTTC GTC
                                   GG C   C
GAM809  LOC148738 3'  TGCCATTCTTCAAAAGCAG   21900     C_       A
                                TGCC TTTTCAAAA GCAG
                                ||||  ||||||||| ||||
                                ACGG AGAAGTTTT CGTC
                                  TA       _
GAM809  LOC150378 3'  TGTCCTTTCCAAGAGCAA    21901    C       AA
                                TG CCTTTTCAA AGCAG
                                || |||||||||  |||||
                                AC GGAAAGGTT TCGTT
                                 A       C_
GAM809  LOC152315 5'  GCCTTCCAGGAAAAGCAG    21902    CT    __
                                GCC TTTCA AAAAGCAG
                                |||  |||||  ||||||||
                                CGG AAGGT TTTTCGTC
                                  __    CC
GAM809  LOC158055 3'  TGCCCTCTGGAAGGAGCAG   21903       TC AA
                                TGCCCTTT AA AGCAG
                                ||||||||  ||  |||||
                                ACGGGAGA TT TCGTC
                                    CC CC
GAM809  LOC158116 3'  TACCCTTTCCACTTGAGCAG  21834         AAA_
                                TGCCCTTTTCA   AGCAG
                                ||||||||||   |||||
                                ATGGGAAAGGT   TCGTC
                                    GAAC
GAM809  LOC159121 3'  CCCTTTTCAGCAGAAAGCAG  21904        A___
                                CCCTTTTCA   AAAGCAG
                                |||||||||   |||||||
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                                GGGAAAAGT   TTTCGTC
                                     CGTC
GAM809  LOC164714 3'  TGCCGTTTTCAAAGGGGCAG  21905     C      AA_
                                TGCC TTTTCAAA  GCAG
                                |||| ||||||||  ||||
                                ACGG AAAAGTTT  CGTC
                                  C       CCC
GAM809  LOC164945 5'  CCTTTTCAGAAAGGGCAG   21906       A  __
                                CCTTTTCA AAA  GCAG
                                |||||||| |||  ||||
                                GGAAAAGT TTT  CGTC
                                     C  CC
GAM809  LOC165140 5'  GCCTTTTCAGCAAAGGCAG  21907    C    A_  _
                                GCC TTTTCA  AAAG CAG
                                ||| ||||||  |||| |||
                                CGG AAAAGT  TTTC GTC
                                  _    CG   C
GAM809  LOC196746 3'  TGTCCTTTCCAGGAAGCAG  21908   C      AA
                                TG CCTTTTCA  AAGCAG
                                || ||||||||  ||||||
                                AC GGAAAGGT  TTCGTC
                                 A       CC
GAM809  LOC201475 5'  TGTCCCTAAGAAAAAGCAG  21909   _   TTTC
                                TG CCCT   AAAAAGCAG
                                || ||||   |||||||||
                                AC GGGA   TTTTTCGTC
                                 A   TTC_
GAM809  LOC201562 3'  TGCCCCCAAAAAAAGGCAG  21910      TTC    _
                                TGCCCTT   AAAAAG CAG
                                |||||||   |||||| |||
                                ACGGGGG   TTTTTC GTC
                                    TT_    C
GAM809  LOC202934 3'  TACCCTTTTCAAAACCATCAG  21911          AG__
                                TGCCCTTTTCAAAA   CAG
                                ||||||||||||||   |||
                                ATGGGAAAAGTTTT   GTC
                                       GGTA
GAM809  LOC203276 3'  ACCCCTTCAGAAAGCAG    21912      T  A
                                GCCCTTT CA AAAGCAG
                                ||||||| || |||||||
                                TGGGGAA GT TTTCGTC
                                    _ C
GAM809  LOC203305 3'  ACCCCTTCAGAAAGCAG    21912      T  A
                                GCCCTTT CA AAAGCAG
                                ||||||| || |||||||
                                TGGGGAA GT TTTCGTC
                                    _ C
GAM809  LOC219972 3'  GCCCTCAAAGTTAAAAAGCAG  21913      TTC___
                                GCCCTT    AAAAAGCAG
                                ||||||    |||||||||
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                                CGGGAG     TTTTTCGTC
                                   TTTCAA
GAM809   LOC221560 3'  GCCTTCCTCAAAGGCAG     21914     C       AA
                                GCC TTTTCAAA  GCAG
                                ||| ||||||||  ||||
                                CGG AGGAGTTT  CGTC
                                  A       C_
GAM809   LOC221935 3'  TGCGCCTTATAAAAGCAG    21915     _    TTCA
                                TGC CCTT    AAAAGCAG
                                ||| ||||    ||||||||
                                ACG GGAA    TTTTCGTC
                                  C    TA__
GAM809   LOC222484 5'  GCTCTCCTCAAAGGCAG     21916    C       AA
                                GC CTTTTCAAA  GCAG
                                || |||||||||  ||||
                                CG GAGGAGTTT  CGTC
                                  A        C_
GAM809   LOC253003 3'  TGCTCCCTTAAAAAGCAG    21917     _    TC
                                TGC CCTTT  AAAAAGCAG
                                ||| |||||  |||||||||
                                ACG GGGAA  TTTTTCGTC
                                  A    __
GAM809   LOC253038 5'  TACCCTTTTCACCCTGAGCAG  21918          AAA__
                                TGCCCTTTTCA     AGCAG
                                ||||||||||     |||||
                                ATGGGAAAAGT     TCGTC
                                      GGGAC
GAM809   LOC253502 3'  TGCCCCTTCTCATCGGGGCAG  21829      _     AAAA_
                                TGCCC TTTTCA     GCAG
                                ||||| ||||||     ||||
                                ACGGG AAGAGT     CGTC
                                   G     AGCCC
GAM809   LOC253539 3'  CCTTTTCCCAAAAAGGCAG   21919        __     _
                                CCTTTTC  AAAAAG CAG
                                |||||||  |||||| |||
                                GGAAAAG  TTTTTC GTC
                                    GG     C
GAM809   LOC254243 3'  ACCCCTTCAGAAAGCAG     21912        T  A
                                GCCCTTT CA AAAGCAG
                                ||||||| || |||||||
                                TGGGGAA GT TTTCGTC
                                   _ C
GAM809   LOC255452 3'  GCCCCACTCTGAAAAGCAG   21920      T   A_
                                GCCCT TTC  AAAAGCAG
                                ||||| |||  ||||||||
                                CGGGG GAG  TTTTCGTC
                                   T   AC
GAM809   LOC255465 3'  TACCCTTTTCAAAACCATCAG  21911           AG__
                                TGCCCTTTTCAAAA    CAG
                                ||||||||||||||    |||
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                                ATGGGAAAAGTTTT  GTC
                                      GGTA
GAM809  LOC257535 3'  GCCTTCCTCAAAGGCAG    21914    C      AA
                                GCC TTTTCAAA  GCAG
                                ||| ||||||||  ||||
                                CGG AGGAGTTT  CGTC
                                  A       C_
GAM809  LOC257595 3'  GCCTTCCTCAAAGGCAG    21914    C      AA
                                GCC TTTTCAAA  GCAG
                                ||| ||||||||  ||||
                                CGG AGGAGTTT  CGTC
                                  A       C_
GAM809  LOC90038  3'  ACCCCTTCAGAAAGCAG    21912       T  A
                                GCCCTTT CA AAAGCAG
                                ||||||| || |||||||
                                TGGGGAA GT TTTCGTC
                                    _ C
GAM809  LOC90982  5'  GCCCTTTCCCAAGCAG     21921        AAA
                                GCCCTTTTC   AAGCAG
                                |||||||||   ||||||
                                CGGGAAAGG   TTCGTC
                                     G__
GAM809  LOC91409  3'  TGCCCTCCAAAGGCAG     21922       TT   AA
                                TGCCCTT  CAAA  GCAG
                                |||||||  ||||  ||||
                                ACGGGAG  GTTT  CGTC
                                    __   C_
GAM809  LOC93070  5'  GCCTCACCGCAAAAGCAG   21859    C  T  A_
                                GCC TT TC  AAAAGCAG
                                ||| || ||  ||||||||
                                CGG AG GG  TTTTCGTC
                                  _ T  CG
GAM810  AF1Q      3'  TAGCACAAATCACCATCAATAT 21925         __  GAT
                                TAGCACAAAT  CCA   ATAT
                                ||||||||||  |||   ||||
                                ATCGTGTTTA  GGT   TATA
                                      GT   AGT
GAM810  LRRC2     3'  AGCCCCTCTTCAGATATATTTT 21926    ACAAATC       C
          C                      AGC      CAGATATAT TTC
                                 |||      ||||||||| |||
                                 TCG      GTCTATATA AAG
                                   GGGAGAA        A
GAM810  TBXA2R    5'  GCACTGGTTCAGGCACACCTTC 21927     AAATC   A
                                GCAC    CAG TATATCTTC
                                ||||    ||| |||||||||
                                CGTG    GTC GTGTGGAAG
                                  ACCAA   C
GAM810  TLR3      5'  TAGTCCAAATCCAGACATTTC  21928    CA          A
                                TAG  CAAATCCAGATAT TC
                                |||  |||||||||||| ||
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                                ATC  GTTTAGGTCTGTA AG
                                  AG           A
GAM810  AKAP3    3'  TAGCACAAGATGACATGTCTT  21929        ATCCA    A
                                TAGCACAA    GATAT TCTT
                                ||||||||    ||||| ||||
                                ATCGTGTT    CTGTA AGAA
                                    CTA__    C
GAM810  ATIP1    3'  TAGTACATATCCAGATATAT   21930    C   A
                                TAG ACA ATCCAGATATAT
                                ||| ||| ||||||||||||
                                ATC TGT TAGGTCTATATA
                                  A   A
GAM810  FACTP140 3'  GCACAACCTGATATATCTTC   21931      AT  A
                                GCACAA  CC GATATATCTTC
                                ||||||  || ||||||||||
                                CGTGTT  GG CTATATAGAAG
                                   __  A
GAM810  FIGN     3'  AGCACAAATGCTGATGTCTT   21932        CCA   ATA
                                AGCACAAAT   GAT   TCTT
                                |||||||||   |||   ||||
                                TCGTGTTTA   CTA   AGAA
                                     CGA   C__
GAM810  FLJ32861 3'  TAGCACATATCCAGTTCTT    21933        A     ATATA
                                TAGCACA ATCCAG    TCTT
                                |||||||| ||||||    ||||
                                ATCGTGT TAGGTC    AGAA
                                    A     A____
GAM810  PCDH10   3'  GCACAAATTTCCTTTATCTT   21934        __   AGATA
                                GCACAAA  TCC    TATCTT
                                |||||||  |||    ||||||
                                CGTGTTT  AGG    ATAGAA
                                    AA   AA___
GAM810  LOC144363 3'  ACACAACATGTATATCTT    21935       ATC  GA
                                GCACAA   CA  TATATCTT
                                ||||||   ||  ||||||||
                                TGTGTT   GT  ATATAGAA
                                   ___  AC
GAM810  LOC144699 3'  GCAGGTCATCCAGATGTATTTT 21936     CAA_      A   C
          C                      GCA    ATCCAGAT TAT TTC
                                |||    |||||||| ||| |||
                                CGT    TAGGTCTA ATA AAG
                                  CCAG       C   A
GAM810  LOC150291 3'  TAGTAAAATCCAGCACCTT    21937     CAC       ATA
                                TAG   AAATCCAG   TATCTT
                                |||   ||||||||   ||||||
                                ATC   TTTAGGTC   GTGGAA
                                  AT_       ____
GAM810  LOC253295 3'  TACCATAAATCCAGGCTACTCT 21938    G  C      A_   A
          TC                     TA CA AAATCCAG  TAT TCTTC
                                || || ||||||||  ||| |||||
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                                AT GT TTTAGGTC  ATG AGAAG
                                 G  A       CG  _
GAM811  BCRP2    3'  AAGGGGAAGAGAAACACACA  21941        A  TTC  _
                                AAGGGGAA GAG   CAC CA
                                |||||||| |||   ||| ||
                                TTCCCCTT CTC   GTG GT
                                     _  TTT   T
GAM811  CASP3    3'  AGGGAAATACAGTACCAAATA  21942       GAGTTCC
                                GGGGAAA      ACCAAATA
                                |||||||      ||||||||
                                TCCCTTT      TGGTTTAT
                                    ATGTCA_
GAM811  CASP3    3'  AGGGAAATACAGTACCAAATA  21942       GAGTTCC
                                GGGGAAA      ACCAAATA
                                |||||||      ||||||||
                                TCCCTTT      TGGTTTAT
                                    ATGTCA_
GAM811  CKM      3'  GGTGGAGAGAGCCCCCA     21943    _  A    T  A
                                GG GGA AGAGT CC CCA
                                || ||| ||||| || |||
                                CC CCT TCTCG GG GGT
                                 A  C    _ _
GAM811  EFEMP1   3'  AAAGAATCCAAGTTTCACCA  21944      AAA    C
                                AAGGGG   GAGTT CACCA
                                ||||||   ||||| |||||
                                TTTCTT   TTCAA GTGGT
                                   AGG    A
GAM811  EFEMP1   3'  AAAGAATCCAAGTTTCACCA  21944      AAA    C
                                AAGGGG   GAGTT CACCA
                                ||||||   ||||| |||||
                                TTTCTT   TTCAA GTGGT
                                   AGG    A
GAM811  ETS2     3'  AAGGAGAAAGCAGAGGCCA   21945        _  TT_
                                AAGGGGAAAG AG   CCA
                                |||||||||| ||   |||
                                TTCCTCTTTC TC   GGT
                                      G  TCC
GAM811  EVX1     5'  AGGGGAAAGCCCCAA      21946         AGTT  A
                                AGGGGAAAG   CC CCAA
                                |||||||||   || ||||
                                TCCCCTTTC   GG GGTT
                                     ____  _
GAM811  NR1I2    5'  AAGGGGAAGAGAGTGGCAAATA 21947        _    TCCAC
                                AAGGGGAA AGAGT    CAAATA
                                |||||||| |||||    ||||||
                                TTCCCCTT TCTCA    GTTTAT
                                     C    CC___
GAM811  PTGFRN   3'  GGGGAAAGACACTCAAATA   21948        GTTC  _
                                GGGGAAAGA   CAC CAAATA
                                |||||||||   ||| ||||||
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                                CCCCTTTCT   GTG GTTTAT
                                     ____   A
GAM811  DKFZP564I0422 3'  AAGGGAAAAGAGAACAAAT   21949          TTCCAC
                                AAGGGGAAAGAG     CAAAT
                                ||||||||||||     |||||
                                TTCCCTTTTCTC     GTTTA
                                      TT____
GAM811  FLJ13646  3'  AAGGGAAGCTGGTTACCAAATA 21950       AAGA   CC
                                AAGGGGA   GTT  ACCAAATA
                                |||||||   |||  ||||||||
                                TTCCCTT   CAA  TGGTTTAT
                                    CGAC   __
GAM811  FLJ20420  3'  AGGGTGGAGGTTCACCAAAT   21951     GAA  A    C
                                AGGG   AG GTTC ACCAAAT
                                ||||   || |||| |||||||
                                TCCC   TC CAAG TGGTTTA
                                  ACC  _   _
GAM811  FLJ21596  3'  AAGGGGAAAAAAATTACCA   21952          TTCC
                                AAGGGGAAAGAG   ACCA
                                ||||||||||||   ||||
                                TTCCCCTTTTTT   TGGT
                                      TAA_
GAM811  FLJ23129  3'  AAGGGGAAGTTATACATCAAAT 21953       AAG    C__  C
          A                      AAGGGGA   AGTT   CA CAAATA
                                |||||||   ||||   || ||||||
                                TTCCCCT   TCAA   GT GTTTAT
                                    ___    TAT  A
GAM811  HH114    3'  AAGAGGAAATTCTCATCAA   21954       AGA   _  C
                                AAGGGGAA   GTTC CA CAA
                                ||||||||   |||| || |||
                                TTCTCCTT   TAAG GT GTT
                                    ___    A  A
GAM811  KIAA0349  3'  GGGGAGAGAGGTGGACTCAAAT 21955      A   TTCC  _
                                GGGGA AGAG   AC CAAAT
                                ||||| ||||   || |||||
                                CCCCT TCTC   TG GTTTA
                                   C   CACC  A
GAM811  KIAA0830  3'  AGGAGAAAGAGAAGCAAAT   21956          TTCCAC
                                AGGGGAAAGAG     CAAAT
                                ||||||||||     |||||
                                TCCTCTTTCTC     GTTTA
                                      TTC___
GAM811  KIAA0923  3'  GGGGAAAATTGTTGCCAAAT   21957       A_   CCA
                                GGGGAAAG  GTT   CCAAAT
                                ||||||||  |||   ||||||
                                CCCCTTTT  CAA   GGTTTA
                                     AA   C__
GAM811  KIAA1157  3'  AAGGAAAGGAGTTTCACCA   21958       A    C
                                AGGGGAA GAGTT CACCA
                                ||||||| ||||| |||||
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                                TTCCTTT CTCAA GTGGT
                                    C    A
GAM811  KIAA1265  3'  AGGAGGAAAGAAGAGTACTAAA 21959    _      TTCC  C
           T                    AGG GGAAAGAG   AC AAAT
                                ||| ||||||||   || ||||
                                TCC CCTTTCTT   TG TTTA
                                  T      CTCA  A
GAM811  SCYD1    3'  AAGAGGAAAGTCACCA     21960         AGTTC
                                AAGGGGAAAG    CACCA
                                ||||||||||    |||||
                                TTCTCCTTTC    GTGGT
                                      A____
GAM811  ZDHHC5   5'  GGGGAAAGGTGATTCCAAAT  21961       A  TCCA
                                GGGGAAAG GT   CCAAAT
                                |||||||| ||   ||||||
                                CCCCTTTC CA   GGTTTA
                                    _ CTAA
GAM811  LOC112885 3'  AAGGAGAAAACCTGCCAAAT  21962        AGTT  A_
                                AAGGGGAAAG   CC  CCAAAT
                                ||||||||||   ||  ||||||
                                TTCCTCTTTT   GG  GGTTTA
                                     ____ AC
GAM811  LOC120406 3'  AAGGGGAAACAACCCAAAT   21963        G GTTCCA
                                AAGGGGAAA A    CCAAAT
                                |||||||| |    ||||||
                                TTCCCCTTT T    GGTTTA
                                     G TG____
GAM811  LOC120526 3'  GGGAATTCACCAAAT      21964     AAGA   C
                                GGGA   GTTC ACCAAAT
                                ||||   |||| |||||||
                                CCCT   TAAG TGGTTTA
                                   ____   _
GAM811  LOC123120 3'  GGGGAAGGGTTCTCCAA    21965       A A   CA
                                GGGGAA G GTTC  CCAA
                                |||||| | ||||  ||||
                                CCCCTT C CAAG  GGTT
                                   _ C   A_
GAM811  LOC126430 5'  AGGGGCTTCCACCAAAT    21966      AAAGAG
                                AGGGG     TTCCACCAAAT
                                |||||     ||||||||||
                                TCCCC     AAGGTGGTTTA
                                  G_____
GAM811  LOC134121 3'  AAGGGGAAAGGAGGCTCCA  21967        A__
                                AAGGGGAAAG   GTTCCA
                                ||||||||||   ||||||
                                TTCCCCTTTC   CGAGGT
                                     CTC
GAM811  LOC147858 3'  AAGGGTGGAGTTGCACCAAAT 21968      GAAA   C
                                AAGGG   GAGTT CACCAAAT
                                |||||   ||||| ||||||||
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                                TTCCC   CTCAA GTGGTTTA
                                  AC__    C
GAM811  LOC151996 3'  GGCGGAAGGAGTTTTCCCC   21969   _   A   __  A
                                GG GGAA GAGT  TCC CC
                                || |||| ||||  ||| ||
                                CC CCTT CTCA  AGG GG
                                 G   C   AA  _
GAM811  LOC152804 3'  GGGAAAAGAAAACACAAAT   21970        TTC  C
                                GGGGAAAGAG   CAC AAAT
                                ||||||||||   ||| ||||
                                CCCTTTTCTT   GTG TTTA
                                     TT_  _
GAM811  LOC154789 5'  AGAGGAAAGAGAAAGACAAATA 21971         TTCCAC
                                AGGGGAAAGAG    CAAATA
                                ||||||||||     ||||||
                                TCTCCTTTCTC    GTTTAT
                                     TTTCT_
GAM811  LOC196477 3'  AGGGGAAAACACCAAAT    21972        AGTTC
                                AGGGGAAAG    CACCAAAT
                                |||||||||    ||||||||
                                TCCCCTTTT    GTGGTTTA
                                      _____
GAM811  LOC197131 3'  GGGGAAAACACCAAAT     21973        AGTTC
                                GGGGAAAG    CACCAAAT
                                ||||||||    ||||||||
                                CCCCTTTT    GTGGTTTA
                                      _____
GAM811  LOC222068 3'  GGGGAAAGTACCAAAT     21974        AGTTCC
                                GGGGAAAG    ACCAAAT
                                ||||||||    |||||||
                                CCCCTTTC    TGGTTTA
                                    A_____
GAM811  LOC255045 3'  AAGGGAAGCTGGTTACCAAATA 21950       AAGA  CC
                                AAGGGGA   GTT  ACCAAATA
                                |||||||   |||  ||||||||
                                TTCCCTT   CAA  TGGTTTAT
                                    CGAC  __
GAM811  LOC51580  3'  AAGGGGAGAGACACTTCAAATA 21975       A  GTTC  __
                                AAGGGGA AGA   CAC  CAAATA
                                ||||||| |||   |||  ||||||
                                TTCCCCT TCT   GTG  GTTTAT
                                    C  ____   AA
GAM811  LOC90408  5'  AGAGGCCAGAGACCAAAT   21976     AA   TTCC
                                AGGGG  AGAG   ACCAAAT
                                |||||  ||||   |||||||
                                TCTCC  TCTC   TGGTTTA
                                  GG   ____
GAM812  FZD3    3'  TTTGATGCAATATAAAAA   21979    A
                                TTT ATGCAATGTAAAAG
                                ||| ||||||||||||||
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                                AAA TACGTTATATTTTT
                                  C
GAM812  LOC115073 3'  TACATCTGTAAAAGTTTATG  21980     A_      C
                                TGCA  TGTAAAAG TTATG
                                ||||  |||||||| |||||
                                ATGT  ACATTTTC AATAC
                                  AG       A
GAM813  ANGPT1    5'  AGGAATGCATGAGTGTGC    21983         AT  _
                                AGGAATGCAT  GGT TGC
                                ||||||||||  ||| |||
                                TCCTTACGTA  TCA ACG
                                      C_  C
GAM813  ANGPT1    5'  AGGAATGCATGAGTGTGC    21983         AT  _
                                AGGAATGCAT  GGT TGC
                                ||||||||||  ||| |||
                                TCCTTACGTA  TCA ACG
                                      C_  C
GAM813  HPRT1     3'  AGGAATGCAGCAACTGACA   21984        TATG  T  _
                                AGGAATGCA   GT GC GACA
                                |||||||||   || || ||||
                                TCCTTACGT   CG TG CTGT
                                     ____  T  A
GAM813  ITGA3     3'  AGGAATGCAGTGCACTCGGCG  21985         ___  GGTT
                                AGGAATGCA   TAT   GCG
                                |||||||||   |||   |||
                                TCCTTACGT   GTG   CGC
                                     CAC   AGC_
GAM813  ITGA3     3'  AGGAATGCAGTGCACTCGGCG  21985         ___  GGTT
                                AGGAATGCA   TAT   GCG
                                |||||||||   |||   |||
                                TCCTTACGT   GTG   CGC
                                     CAC   AGC_
GAM813  LZTFL1    3'  GGAATGCATAAGTACAAACA   21986         T  T   _
                                GGAATGCATA GGT GCGA CA
                                |||||||||| ||| |||| ||
                                CCTTACGTAT TCA TGTT GT
                                     _  _   T
GAM813  PTGIS     3'  AGAATGCATGAAATCGGCACC  21987         AT   CGA
                                GGAATGCAT  GGTTG  CACC
                                |||||||||  |||||  ||||
                                TCTTACGTA  TTAGC  GTGG
                                     CT    C__
GAM813  TPP2      3'  AGAGTGCATATGGTGTAC     21988     A       _
                                GGA TGCATATGGT TGC
                                ||| |||||||||| |||
                                TCT ACGTATACCA ATG
                                  C        C
GAM813  C20orf126 3'  AGGAATGCTGGAATGACAC    21989        ATA  TTGC
                                AGGAATGC   TGG   GACAC
                                ||||||||   |||   |||||
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                                TCCTTACG  ACC   CTGTG
                                   ___  TTA_
GAM813  CHST3    3' GGATGCATATGTACATACC   21990    A     GT   AC
                                GGA TGCATATG  TGCG  ACC
                                ||| ||||||||  ||||  |||
                                CCT ACGTATAC  ATGT  TGG
                                  _      __   A_
GAM813  FLJ23033 3' AGGGTGCATATGTGCA     21991    AA     GT
                                AGG  TGCATATG  TGCG
                                |||  ||||||||  ||||
                                TCC  ACGTATAC  ACGT
                                  C_      __
GAM813  KEO4     3' AGGAATACATATAGGATAC   21992          T_
                                AGGAATGCATATGG  TGC
                                ||||||||||||||  |||
                                TCCTTATGTATATC  ATG
                                        CT
GAM813  KIAA0143 3' AGGAATGCTATTCAACA    21993       ATATG  G
                                AGGAATGC    GTT CGACA
                                ||||||||    ||| |||||
                                TCCTTACG    TAA GTTGT
                                   A____  _
GAM813  KIAA0893 3' AGGAATGCATTGAATAC    21994        A  GT
                                AGGAATGCAT TG  TGC
                                |||||||||| ||  |||
                                TCCTTACGTA AC  ATG
                                   _ TT
GAM813  KIAA1164 3' GGAATGCAGTATGGCAGCA  21995       _    T
                                GGAATGCA TATGGT GCG
                                |||||||| |||||| |||
                                CCTTACGT ATACCG CGT
                                   C     T
GAM813  PADI1    3' AGAAATGCATGTCGACA     21996       ATGGTTG
                                AGGAATGCAT      CGACA
                                ||||||||||      |||||
                                TCTTTACGTA      GCTGT
                                   CA_____
GAM813  PPP1R3B  3' GGAATGCAGTGGTGTGA    21997       TA   T C
                                GGAATGCA  TGGT G GA
                                ||||||||  |||| | ||
                                CCTTACGT  ACCA C CT
                                   C_   _ A
GAM813  PRO0159  5' GGAATGCATATGGATGAGCA  21998         TT__
                                GGAATGCATATGG   GCG
                                ||||||||||||   |||
                                CCTTACGTATACC   CGT
                                      TACT
GAM813  LOC144563 5' GGAATGCAGGTGCGCGC    21999       TAT  T  ACA
                                GGAATGCA  GGT GCG  C
                                ||||||||  ||| |||  |
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                                CCTTACGT   CCA CGC   G
                                   ___   _   GC_
GAM813   LOC151632 5'  GGAATGCAGGTGTGCG      22000        TAT   _
                                GGAATGCA   GGT TGCG
                                ||||||||   ||| ||||
                                CCTTACGT   CCA ACGC
                                   ___   C
GAM813   LOC151888 3'  GGATGCATATTCTGTTGGTGC  22001     A     _______   T
                                GGA TGCATA     TGGT GC
                                ||| ||||||     |||| ||
                                CCT ACGTAT     ACCA CG
                                  _     AAGACA   _
GAM813   LOC157695 3'  AGGGACGCATAACTGGCAC    22002     A      __   TTGCGA
                                AGG ATGCATA  TGG     CAC
                                ||| |||||||  |||     |||
                                TCC TGCGTAT  ACC     GTG
                                  C      TG   _______
GAM813   LOC203536 3'  AGGAATGCAATGTTGGTGC    22003         TA__    T
                                AGGAATGCA    TGGT GC
                                |||||||||    |||| ||
                                TCCTTACGT    ACCA CG
                                     TACA    _
GAM813   LOC219404 3'  AGGAATGAGTGTGGTTACAA   22004        CATA
                                AGGAATG    TGGTTGCGA
                                |||||||    |||||||||
                                TCCTTAC    ACCAATGTT
                                    TCAC
GAM813   LOC51267  3'  AGGAATGCTTATAAGGCA    22005        A     TT
                                AGGAATGC TATGG  GCG
                                |||||||| |||||  |||
                                TCCTTACG ATATT  CGT
                                     A     C_
GAM814   SFRS7     3'  CCTCTTTCTAAACCGGAGG    22008    _      TGC    _
                                CC CTTTCTAA   GCCG AGG
                                || ||||||||   |||| |||
                                GG GAAAGATT   TGGC TCC
                                  A       ___    C
GAM814   TCF1      3'  CCCTTTCTGATGCATCAGAG   22009        A     C _
                                CCCTTTCT ATGCG C GAG
                                |||||||| ||||| | |||
                                GGGAAAGA TACGT G CTC
                                     C     A T
GAM814   FLJ20449  3'  CCTTTCTAATACCCATAGG    22010          G   _
                                CCTTTCTAATGC CCG AGG
                                |||||||||||| ||| |||
                                GGAAAGATTATG GGT TCC
                                       _   A
GAM814   FLJ22671  3'  TACCCTTTCTGCTGTGTATACC 22011          AA  C____   G
              CAG                    TACCCTTTCT  TG    GCC AG
                                |||||||||  ||    ||| ||
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                                ATGGGAAAGA  AC     TGG TC
                                     CG  ACATA   G
GAM814  KIAA0555  3'  CCCTTTCTGAGCCAGAG     22012         AAT C   _
                                CCCTTTCT   G GCC GAG
                                ||||||||   | ||| |||
                                GGGAAAGA   C CGG CTC
                                    ___ T   T
GAM814  KIAA0788  3'  CCCTTTCTGGTGCTGCCTCCCA 22013         AA___   G_  G
           GGAG                    CCCTTTCT     TGC  CC AGGAG
                                ||||||||     |||  || |||||
                                GGGAAAGA     ACG  GG TCCTC
                                     CCACG   GA  G
GAM814  PTPRT     3'  TACCCCTTCTAATGTTGATGAG 22014             CGCC_
                                TACCCTTTCTAATG     GAG
                                ||||||||||||||     |||
                                ATGGGGAAGATTAC     CTC
                                       AACTA
GAM814  SART3     3'  CCCTTTCTGTCTAAAGCCGAGG 22015         AATGC__
           AG                     CCCTTTCT      GCCGAGGAG
                                ||||||||      |||||||||
                                GGGAAAGA      CGGCTCCTC
                                     CAGATTT
GAM814  LOC157695 5'  CTTTCTAACGCGGAAAAG     22016           CC
                                CTTTCTAATGCG  GAGGAG
                                ||||||||||||  ||||||
                                GAAAGATTGCGC  CTTTTC
                                              __
GAM814  LOC167040 5'  CCCTTCCTGCACGTCCTGGGGA 22017         AAT   _  GA_
           G                      CCCTTTCT   GCG CC   GGAG
                                ||||||||   ||| ||   ||||
                                GGGAAGGA   TGC GG   CCTC
                                     CG_   A  ACC
GAM814  LOC91149  3'  TACTTTTTTAATGCGCGA     22018     CC   C       C
                                TAC  TTT TAATGCGC GA
                                |||  ||| |||||||| ||
                                ATG  AAA ATTACGCG CT
                                  A_   A       _
GAM815  C1orf24   3'  TAAAGTGTGAAGGCACATGT   22021       _  AAATA
                                TAAGG GT     AAGGCACATGT
                                ||||| ||     ||||||||||||
                                ATTTC CA     TTCCGTGTACA
                                   A  C_____
GAM815  DKFZP434P211 3'  TTAAGAGTGTGGCATATG     22022         AAATAAA    C
                                TTAAGGGT       GGCA ATG
                                ||||||||       |||| |||
                                AATTCTCA       CCGT TAC
                                     CA______    A
GAM815  MAPK6     3'  AGGTAGATAACACATG      22023       A   AAG
                                GGGTA ATA   GCACATG
                                ||||| |||   |||||||
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                                TCCAT TAT   TGTGTAC
                                  C  ___
GAM815  POU4F2   3'  TAAGGGTAAGTGAGAGCGCTCA 22024         ATAA_ _  A
                TGT                TAAGGGTAA    AG GC CATGT
                                   |||||||||    || || |||||
                                   ATTCCCATT    TC CG GTACA
                                     CACTC  G  A
GAM815  LOC121536 3'  GGTATTTGTAAGGGCACATGT  22025     AA__   A
                                   GGTA   TAA GGCACATGT
                                   ||||   ||| |||||||||
                                   CCAT   ATT CCGTGTACA
                                     AAAC   C
GAM815  LOC150174 3'  TTAAGAGTGTGGCATATG    22022        AAATAAA   C
                                   TTAAGGGT      GGCA ATG
                                   ||||||||      |||| |||
                                   AATTCTCA      CCGT TAC
                                     CA_____    A
GAM815  LOC150213 3'  TTAAGAGTGTGGCATATG    22022        AAATAAA   C
                                   TTAAGGGT      GGCA ATG
                                   ||||||||      |||| |||
                                   AATTCTCA      CCGT TAC
                                     CA_____    A
GAM815  LOC170372 3'  AGGTAGATAACACATG      22023      A  AAG
                                   GGGTA ATA   GCACATG
                                   ||||| |||   |||||||
                                   TCCAT TAT   TGTGTAC
                                     C  ___
GAM816  ACLY     3'  CACAGTTTCTAAGCATGTC    22028
                                   TACAGTTTCTAAGCGTGTT
                                   |||||||||||||||||||
                                   GTGTCAAAGATTCGTACAG

GAM816  BACH2    3'  TTTCTAACTGTTTTGT      22029        G G
                                   TTTCTAA C TGTTTTGT
                                   ||||||| | ||||||||
                                   AAAGATT G ACAAAACA
                                     _ _
GAM816  CYP4F3   3'  ACAGTTTGGCAGTGTTTTGT   22030       CTAA  _
                                   ACAGTTT    GC GTGTTTTGT
                                   |||||||    || |||||||||
                                   TGTCAAA    CG CACAAAACA
                                     C___  T
GAM816  DLG5     3'  TACAGTTTTTCATAGTTTGTC  22031        CTAAG    T
                                   TACAGTTT    CGTG TTTGTC
                                   ||||||||    |||| ||||||
                                   ATGTCAAA    GTAT AAACAG
                                     AA___    C
GAM816  LPL      3'  TACGTTTCTTTCTTGTTTTGT  22032     A     AAGCG
                                   TAC GTTTCT    TGTTTTGT
                                   ||| ||||||    ||||||||
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                                ATG CAAAGA    ACAAAACA
                                  _     AAGA_
GAM816  MTR     3'  TGAGTTTCTAGGCCCTTATTTT 22033   C      A  G__
            GT                    A AGTTTCTA GC   TGTTTTGT
                                | |||||||| ||   ||||||||
                                A TCAAAGAT CG   ATAAAACA
                                 C       C  GGA
GAM816  NR3C1   3'  TACAGCTTCTATTTTG     22034          AAGCGT
                                TACAGTTTCT     GTTTTG
                                ||||||||||     ||||||
                                ATGTCGAAGA     TAAAAC
                                       _______
GAM816  SNAI2   3'  TACATTCTCCTGTGTTTTGT  22035     G    AAGC
                                TACA TTTCT    GTGTTTTGT
                                |||| |||||    |||||||||
                                ATGT AGAGG    CACAAAACA
                                  A    A___
GAM816  TRIP15  3'  TACAATTTCTGAGCTGCACTGT 22036         A   G   T
                                TACAGTTTCT AGC TGT TTGT
                                |||||||||| ||| ||| ||||
                                ATGTTAAAGA TCG ACG GACA
                                      C   _   T
GAM816  AQP9    3'  CAGTTTCTGAATGCCACAATGT 22037        AAGC    T___
            C                    CAGTTTCT    GTGTT    TGTC
                                ||||||||    |||||    ||||
                                GTCAAAGA    TACGG    ACAG
                                     CT__     TGTT
GAM816  CRA     3'  ATTTCTAGGCCATCTTGT    22038        A  G
                                GTTTCTA GC TGTTTTGT
                                ||||||| || ||||||||
                                TAAAGAT CG GTAGAACA
                                    C  _
GAM816  FLJ20038 3'  CAGTTTCTAAGCACACCATGT  22039           TG TT
                                CAGTTTCTAAGCG  T  TGT
                                ||||||||||||  |  |||
                                GTCAAAGATTCGT  G  ACA
                                       GT GT
GAM816  KIAA1494 3'  ATTTCTAAATACATTTTGT   22040         CG
                                GTTTCTAAG  TGTTTTGT
                                |||||||||  ||||||||
                                TAAAGATTT  GTAAAACA
                                     AT
GAM816  KIAA1600 3'  TACAGTTTTCATATTTTGT   22041        CTAAG
                                TACAGTTT    CGTGTTTTGT
                                ||||||||    ||||||||||
                                ATGTCAAA    GTATAAAACA
                                    A____
GAM816  LOC130535 3'  CAGTATTTGAGCTTACTTTGTC 22042      TTCTA   G
                                CAGT    AGC TGTTTTGTC
                                ||||    ||| |||||||||
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                                GTCA    TCG ATGAAACAG
                                  TAAAC  A
GAM816  LOC136345 3'  CACAGTTTTGTTTTGTTTTGT  22043        CTAAGCG
                                TACAGTTT      TGTTTTGT
                                ||||||||      ||||||||
                                GTGTCAAA      ACAAAACA
                                    ACAAA__
GAM816  LOC145813 3'  TACAATTTCTCTGGTTTTGTC  22044          AAGCGT
                                TACAGTTTCT     GTTTTGTC
                                ||||||||||     ||||||||
                                ATGTTAAAGA     CAAAACAG
                                     GAC___
GAM816  LOC154930 3'  GTTTCTAATGTTTGT       22045        AGC     T
                                GTTTCTA   GTGTTT GT
                                |||||||   |||||| ||
                                CAAAGAT   TACAAA CA
                                   ___     _
GAM816  LOC155032 5'  CACAGTTTTGTTTTGTTTTGT  22043        CTAAGCG
                                TACAGTTT      TGTTTTGT
                                ||||||||      ||||||||
                                GTGTCAAA      ACAAAACA
                                    ACAAA__
GAM816  LOC170396 3'  ACAGTTTCTGGTGGTGCTTTTG 22046         AAGC     _
          TC                     ACAGTTTCT    GTGTTTT GTC
                                |||||||||    ||||||| |||
                                TGTCAAAGA    CACGAAA CAG
                                     CCAC      A
GAM816  LOC257152 3'  CACAGTTTTCTGTTTTGT    22047        _ AAGCGT
                                TACAGTTT CT     GTTTTGT
                                |||||||| ||     |||||||
                                GTGTCAAA GA     CAAAACA
                                    A _______
GAM817  PACSIN1   3'  GGGCTCAGGAGACTC       22050        AGAAAC
                                GGGCTCG     GGAGATTT
                                |||||||     ||||||||
                                CCCGAGT     CCTCTGAG
                                   _______
GAM817  DKFZP434G1411 3'  GGGTCAGATGGAGATTT     22051     C  G   AAC
                                GGG TC AGA   GGAGATTT
                                ||| || |||   ||||||||
                                CCC AG TCT   CCTCTAAA
                                  _  _  A__
GAM817  LOC221938 3'  GGACTCGAGGGATGATCT    22052         AAAC  _
                                GGGCTCGAG    GGA GATTT
                                |||||||||    ||| |||||
                                CCTGAGCTC    CCT CTAGA
                                     _____  A
GAM817  LOC222237 5'  GGGCTCGGGGACGGGAAAC    22053        A_  AAC
                                GGGCTCG  GA   GGAGAT
                                |||||||  ||   ||||||
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                                CCCGAGC  CT   CCTTTG
                                    CC  GC_
GAM818  ATRN     3'  TCCCAGGTGTCTCCAG      22056        T A
                                TCCCAGGT G TTTCCAG
                                |||||||| | |||||||
                                AGGGTCCA C AGAGGTC
                                     _ _
GAM818  BARX1    3'  TCCCAGGTTAGAGCCCAG    22057          ATT
                                TCCCAGGTTG   TCCAG
                                ||||||||||   |||||
                                AGGGTCCAAT   GGGTC
                                      CTC
GAM818  BRCA1    3'  TGGCCCAGACTCTTCCAG    22058    T    GT GA
                                TG CCCAG  T  TTTCCAG
                                || |||||  |  |||||||
                                AC GGGTC  A  GAAGGTC
                                 C    TG __
GAM818  CACNA1C  3'  TGTTCCGGTTAACTCCAG    22059     C  A      T
                                TGT CC GGTTGATT CCAG
                                ||| || |||||||| ||||
                                ACA GG CCAATTGA GGTC
                                  A  _       _
GAM818  CDC42    3'  TGTCCCAGATTACTCTCCAG   22060           A
                                TGTCCCAGGTTG TTTCCAG
                                |||||||||||| |||||||
                                ACAGGGTCTAAT AGAGGTC
                                      G
GAM818  CLTCL1   3'  TGTCCAGGTGTGGTCCAG    22061      C   _  ATT
                                TGTCC AGGT TG   TCCAG
                                ||||| |||| ||   |||||
                                ACAGG TCCA AC   AGGTC
                                   _   C  C__
GAM818  DLEC1    3'  TCACCTCGATTTCCAG      22062    _  AGG
                                TC CC   TTGATTTCCAG
                                || ||   ||||||||||
                                AG GG   AGCTAAAGGTC
                                 T  ____
GAM818  DLEC1    3'  TCACCTCGATTTCCAG      22062    _  AGG
                                TC CC   TTGATTTCCAG
                                || ||   ||||||||||
                                AG GG   AGCTAAAGGTC
                                 T  ____
GAM818  DYT1     3'  TGCTTGGGCTCATTTCCAG   22063     CCCA   G
                                TGT    GGTT ATTTCCAG
                                |||    |||| ||||||||
                                ACG    CCGA TAAAGGTC
                                  AAC_    G
GAM818  FAT2     3'  TGTTCCTGGTTTTCCAG     22064     C  A   GAT
                                TGT CC GGTT   TTCCAG
                                ||| || ||||   ||||||
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                                ACA GG CCAA   AAGGTC
                                  A  A   ___
GAM818  GLUD1    3'  TGTCCCAGACTCATCCAG    22065        GT G TT
                                TGTCCCAG  T A  TCCAG
                                ||||||||  | |  |||||
                                ACAGGGTC  A T  AGGTC
                                    TG G __
GAM818  ICMT     3'  TGTCCCAGGCTGCACAG     22066          ATTTC
                                TGTCCCAGGTTG    CAG
                                ||||||||||||    |||
                                ACAGGGTCCGAC    GTC
                                      GT___
GAM818  KCNH3    3'  TGCCCCAGGGATCCA      22067        TT  TT
                                TGTCCCAGG  GA  TCCA
                                |||||||||  ||  ||||
                                ACGGGGTCC  CT  AGGT
                                    __  __
GAM818  MAPK12   5'  TGTCCCAGGTGCCGACCCC   22068         __   TT
                                TGTCCCAGGT  TGAT  C
                                ||||||||||  ||||  |
                                ACAGGGTCCA  GCTG  G
                                     CG    GG
GAM818  MMP25    3'  GTCCCAGGTCCCCACCAG    22069         GA TT
                                GTCCCAGGTT  T  CCAG
                                ||||||||||  |  ||||
                                CAGGGTCCAG  G  GGTC
                                     G_ GT
GAM818  NRAP     3'  TGGCCCAGGCCATCTTCAG   22070    T      G    C
                                TG CCCAGGTT ATTT CAG
                                || ||||||||  |||| |||
                                AC GGGTCCGG TAGA GTC
                                 C       _    A
GAM818  OAS2     3'  TGTTACAGGGCTATTTCCAG  22071     CC    TTG
                                TGT  CAGG   ATTTCCAG
                                |||  ||||   ||||||||
                                ACA  GTCC   TAAAGGTC
                                  AT    CGA
GAM818  PHKB     3'  TATCTTTTGATTTCCAG     22072      CCAGG
                                TGTC    TTGATTTCCAG
                                ||||    ||||||||||
                                ATAG    AACTAAAGGTC
                                  AA___
GAM818  PIK3CG   3'  TCCAAAGAATTTCCAG      22073     C   TT
                                TCC AGG  GATTTCCAG
                                ||| |||  |||||||||
                                AGG TTC  TTAAAGGTC
                                  T  __
GAM818  PTK2B    3'  TGCCCCAGGTCCTCCCTCAG  22074          GA TT _
                                TGTCCCAGGTT  T  C CAG
                                ||||||||||  |  | |||
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                                ACGGGGTCCAG  A  G GTC
                                      G_ GG A
GAM818  RFP     3'  TGTCCCAGAATCCTTCCAG   22075        TTGA
                                TGTCCCAGG   TTTCCAG
                                |||||||||   |||||||
                                ACAGGGTCT   GAAGGTC
                                     TAG_
GAM818  RPE     3'  TCCCAGATCCTTTCCAG    22076        GA
                                TCCCAGGTT  TTTCCAG
                                |||||||||  |||||||
                                AGGGTCTAG  AAAGGTC
                                     G_
GAM818  SOX10   5'  TGTCCCAAGGTGTGCGGTCCAG 22077       _  _  ATT
                                TGTCCCA GGT TG   TCCAG
                                ||||||| ||| ||   |||||
                                ACAGGGT CCA AC   AGGTC
                                    T   C  GCC
GAM818  STAT6   5'  TGCCCCAGCCCGCTGTTTCC  22078        ___   A
                                TGTCCCAG   GTTG TTTCC
                                ||||||||   |||| |||||
                                ACGGGGTC   CGAC AAAGG
                                     GGG   _
GAM818  STC1    3'  GTTCCTGGAATTTCCAG    22079    C  A  TT
                                GT CC GG  GATTTCCAG
                                || || ||  |||||||||
                                CA GG CC  TTAAAGGTC
                                 A  A  __
GAM818  TOP3A   3'  TGTCCTCTAAGTTTCCAG   22080      CAGG   _
                                TGTCC   TTGA TTTCCAG
                                |||||   |||| |||||||
                                ACAGG   GATT AAAGGTC
                                   A___   C
GAM818  USF2    3'  TGTCTCAGTACCTCCAG    22081     C   GTTG
                                TGTC CAG   ATTTCCAG
                                |||| |||   ||||||||
                                ACAG GTC   TGGAGGTC
                                  A  A___
GAM818  ZK1     5'  TGCCTCAGAACTTCCAG    22082     C   GTT
                                TGTC CAG   GATTTCCAG
                                |||| |||   |||||||||
                                ACGG GTC   TTGAAGGTC
                                  A  ___
GAM818  ZNF136  5'  TGTCCCAGCTTCCTCCC    22083       G  GA
                                TGTCCCAG TT  TTTCC
                                |||||||| ||  |||||
                                ACAGGGTC AA  GAGGG
                                     G  G_
GAM818  AP4B1   5'  GTCCTCCGCCGGATTTCCAG  22084     CAG   _
                                GTCC   GTTG ATTTCCAG
                                ||||   |||| ||||||||
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                                CAGG  CGGC TAAAGGTC
                                  AGG   C
GAM818  BIRC5    3'  TGACCTCCAGAGGTTTCCAG  22085   _ _   TTGA
                                TG TC CCAGG   TTTCCAG
                                || || |||||   |||||||
                                AC GG GGTCT   AAAGGTC
                                 T  A    CC__
GAM818  C8orf13  3'  TGCCCAGGCCCTCCA     22086   T     GAT
                                TG CCCAGGTT  TTCCA
                                || ||||||||  |||||
                                AC GGGTCCGG  GAGGT
                                 _     ____
GAM818  CDC14B   3'  TGTGCCTATTCATTTCCAG   22087    C  AG  G
                                TGT CC  GTT ATTTCCAG
                                ||| ||  ||| ||||||||
                                ACA GG  TAA TAAAGGTC
                                  C  A_  G
GAM818  CHAF1B   3'  GTCTCAGGCACCTCCAG    22088    C    TG
                                GTC CAGGT  ATTTCCAG
                                ||| |||||  ||||||||
                                CAG GTCCG  TGGAGGTC
                                  A    __
GAM818  CIDEB    5'  TGTCCCAGCTCTGATTTC    22089       G_
                                TGTCCCAG  TTGATTTC
                                ||||||||  ||||||||
                                ACAGGGTC  GACTAAAG
                                     GA
GAM818  CMG1     5'  TGTCCCAGGTGGCATTGCAG  22090        TGAT  C
                                TGTCCCAGGT   TT CAG
                                ||||||||||   || |||
                                ACAGGGTCCA   AA GTC
                                      CCGT  C
GAM818  COL12A1  3'  TGTCCCAATTATTTCCAG   22091       GTTG
                                TGTCCCAG   ATTTCCAG
                                ||||||||   ||||||||
                                ACAGGGTT   TAAAGGTC
                                     AA__
GAM818  COL12A1  3'  TGTCCCAATTATTTCCAG   22091       GTTG
                                TGTCCCAG   ATTTCCAG
                                ||||||||   ||||||||
                                ACAGGGTT   TAAAGGTC
                                     AA__
GAM818  CYLD     5'  GTCCCAAAGCATGTTTTC    22092       _ _  A
                                GTCCCAG GT TG TTTC
                                ||||||| || || ||||
                                CAGGGTT CG AC AAAG
                                     T  T  A
GAM818  DIRC2    3'  TGTGCAGTATTGATTTCCAG  22093    CC  _
                                TGT  CAG GTTGATTTCCAG
                                |||  ||| ||||||||||||
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                                ACA  GTC TAACTAAAGGTC
                                  C_   A
GAM818  DKFZP434C131 3'  TGTCCCAGGCTCAAACTCCAG  22094          _  T
                                TGTCCCAGGTT GA TTCCAG
                                |||||||||| || ||||||
                                ACAGGGTCCGA TT GAGGTC
                                      G  T
GAM818  DKFZp761G0313 3'  TGCTTCCAGCACTTCCAG    22095    C_   GTTG
                                TGT  CCAG   ATTTCCAG
                                |||  ||||   ||||||||
                                ACG  GGTC   TGAAGGTC
                                  AA   G___
GAM818  FHOD2    5'  TCTCAAAGAAATTTCCAG    22096    C   TT
                                TC CAGG  GATTTCCAG
                                || ||||  |||||||||
                                AG GTTT  TTAAAGGTC
                                 A   CT
GAM818  FLJ10560  3'  TATCCTTGTATTTCCAG     22097      CAGG  _
                                TGTCC   TTG ATTTCCAG
                                |||||   ||| ||||||||
                                ATAGG   AAC TAAAGGTC
                                   _____  A
GAM818  FLJ13031  3'  TGATCCACTGTATTTCCAG   22098    TC   GG  _
                                TG  CCA  TTG ATTTCCAG
                                ||  |||  ||| ||||||||
                                AC  GGT  GAC TAAAGGTC
                                 TA  __  A
GAM818  FLJ20211  3'  GTCTCACAATTTCCAG     22099     C  GGT
                                GTC CA   TGATTTCCAG
                                ||| ||   ||||||||||
                                CAG GT   GTTAAAGGTC
                                  A  ___
GAM818  FLJ21019  3'  TGTCCCTGGGGCTCGTCCAG  22100       A__   GATT
                                TGTCCC   GGTT   TCCAG
                                ||||||   ||||   |||||
                                ACAGGG   CCGA   AGGTC
                                   ACC   GC__
GAM818  FLJ22215  3'  TGGCCCTTCCCGATTTCCAG  22101    T   AGG
                                TG CCC   TTGATTTCCAG
                                || |||   ||||||||||
                                AC GGG   GGCTAAAGGTC
                                 C   AAG
GAM818  FLJ31978  3'  TGTCCCAGTCAACCCAG     22102        G TG  TT
                                TGTCCCAG T  AT  CCAG
                                |||||||| |  ||  ||||
                                ACAGGGTC A  TG  GGTC
                                    _ GT  __
GAM818  FLJ32452  3'  TCCCCCAACATTTCCAG     22103   G     GTTG
                                T TCCCAG   ATTTCCAG
                                | ||||||   ||||||||
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                                A GGGGTT   TAAAGGTC
                                 G     G___
GAM818  FLJ32919  5'  GTTCCAGGTAGATCTCCAG   22104    C     T
                                GT CCAGGT GATTTCCAG
                                || |||||| |||||||||
                                CA GGTCCA CTAGAGGTC
                                 A     T
GAM818  FUT10     3'  TGTCCAGGCTGTCCA      22105      C     ATT
                                TGTCC AGGTTG   TCCA
                                ||||| ||||||   ||||
                                ACAGG TCCGAC   AGGT
                                  _    ___
GAM818  HSA250839 3'  TCCTAGGGCGACTTCCAG    22106     C   T
                                TCC AGG TGATTTCCAG
                                ||| ||| ||||||||||
                                AGG TCC GCTGAAGGTC
                                  A   C
GAM818  HUMNPIIY20 3'  TGGCCCAGGTCAGCCAG     22107    T       ATTT
                                TG CCCAGGTTG    CCAG
                                || |||||||||    ||||
                                AC GGGTCCAGT    GGTC
                                 C        C___
GAM818  KCNT1     3'  TGTCCAGGTTGTCCA      22108      C     ATT
                                TGTCC AGGTTG   TCCA
                                ||||| ||||||   ||||
                                ACAGG TCCAAC   AGGT
                                  _    ___
GAM818  KIAA0121  3'  TGCCCCAGGCCCCCCTCCAG  22109          GA
                                TGTCCCAGGTT  TTTCCAG
                                ||||||||||  |||||||
                                ACGGGGTCCGG  GGAGGTC
                                      GG
GAM818  KIAA0252  3'  TGCCCCAGGGGCTCCAG     22110         TTGAT
                                TGTCCCAGG    TTCCAG
                                |||||||||    ||||||
                                ACGGGGTCC    GAGGTC
                                     CC___
GAM818  KIAA0365  3'  TCTCTAAGTGATTTCCAG    22111   G  CC   T
                                T TC  AGGT GATTTCCAG
                                | ||  |||| |||||||||
                                A AG  TTCA CTAAAGGTC
                                 G  A_   _
GAM818  KIAA0590  3'  TGTCCCAGCTGTTGCTCAG   22112        __   ATTTC
                                TGTCCCAG  GTTG    CAG
                                ||||||||  ||||    |||
                                ACAGGGTC  CAAC    GTC
                                    GA   GA___
GAM818  KIAA0607  3'  TGCCCCAGGTTGCCC       22113          ATT
                                TGTCCCAGGTTG   TCC
                                ||||||||||||   |||
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                                ACGGGGTCCAAC  GGG
                                          ___
GAM818  KIAA1266 3'  TGTCCCAGGCTCCCA      22114        TGAT
                                TGTCCCAGGT   TTCCA
                                ||||||||||   |||||
                                ACAGGGTCCG   AGGGT
                                          _____
GAM818  KIAA1321 3'  TGCCCCAAAGAAAATTTCCAG 22115       _ TT
                                TGTCCCAG G  GATTTCCAG
                                |||||||| |  |||||||||
                                ACGGGGTT C  TTAAAGGTC
                                     T TT
GAM818  KIAA1908 5'  TGCCTCGGCTGAATTTCCAG  22116     CCA    _
                                TGTC  GGTTGA TTTCCAG
                                ||||  |||||| |||||||
                                ACGG  CCGACT AAAGGTC
                                  AG_     T
GAM818  MAD4     3'  TGCCCCAGGTGCTCACCCAG  22117        TGATT
                                TGTCCCAGGT    TCCAG
                                ||||||||||    |||||
                                ACGGGGTCCA    GGGTC
                                     CGAGT
GAM818  MCFP     3'  TGTTCCAAGTTGAACCAG    22118    C       TTT
                                TGT CCAGGTTGA  CCAG
                                ||| |||||||||  ||||
                                ACA GGTTCAACT  GGTC
                                  A       T__
GAM818  MCRS1    3'  TGCCCAGGTTTTTCCAG     22119    T      GA
                                TG CCCAGGTT  TTTCCAG
                                || ||||||||  |||||||
                                AC GGGTCCAA  AAAGGTC
                                _     __
GAM818  MGC13102 3'  TATCCTTAAGGCATTTCCAG  22120     C__   TG
                                TGTCC  AGGT  ATTTCCAG
                                |||||  ||||  ||||||||
                                ATAGG  TCCG  TAAAGGTC
                                   AAT   __
GAM818  MGC13114 3'  TCCCAGGTCCTCCAG      22121        GAT
                                TCCCAGGTT   TTCCAG
                                |||||||||   ||||||
                                AGGGTCCAG   GAGGTC
                                          ___
GAM818  MGC23284 3'  GTCCCGGGCCTGTTCCAG    22122     A   GAT
                                GTCCC GGTT   TTCCAG
                                ||||| ||||   ||||||
                                CAGGG CCGG   AAGGTC
                                   C   AC_
GAM818  MGC2452  5'  TGTCCCTGGAACCTCCAG    22123      A  TT
                                TGTCCC GG  GATTTCCAG
                                |||||| ||  |||||||||
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                                ACAGGG CC  TTGGAGGTC
                                   A __
GAM818  MGC2560  3' GTTTCAGGTATTCCCAG    22124   CC    TG
                                GT  CAGGT  ATTTCCAG
                                ||  |||||  ||||||||
                                CA  GTCCA  TAAGGGTC
                                 AA    __
GAM818  MGC2835  3' TGTCTTAGGCTGACGCAG   22125    CC      TTC
                                TGTC  AGGTTGAT   CAG
                                ||||  ||||||||   |||
                                ACAG  TCCGACTG   GTC
                                  AA       C__
GAM818  MGC4643  3' TGCCCTGATTATTTCCAG   22126     CA    A
                                TGTCC  GGTTG TTTCCAG
                                |||||  ||||| |||||||
                                ACGGG  CTAAT AAAGGTC
                                   A_    _
GAM818  MIDORI   3' TCCCACTTGATTTCCAG    22127     GG
                                TCCCA  TTGATTTCCAG
                                |||||  ||||||||||
                                AGGGT  AACTAAAGGTC
                                   G_
GAM818  MSP      3' TGTCTCCAGGTAATTTCCAG  22128     _     T
                                TGTC CCAGGT GATTTCCAG
                                ||||  ||||||  |||||||||
                                ACAG GGTCCA TTAAAGGTC
                                   A     _
GAM818  NPC1L1   3' TGTTCCTGCCAACTTCCAG   22129    C  AG  TG
                                TGT CC  GT  ATTTCCAG
                                |||  ||  ||  ||||||||
                                ACA GG  CG  TGAAGGTC
                                  A  A_  GT
GAM818  P2RXL1   3' TGCCCAGGCCTGTTCCAG   22130    T      GAT
                                TG CCCAGGTT   TTCCAG
                                ||  ||||||||   ||||||
                                AC GGGTCCGG   AAGGTC
                                 _       AC_
GAM818  PAI-RBP1 3' TGTCCCAGTTGACCA      22131        G   TTT
                                TGTCCCAG TTGA   CCA
                                |||||||| ||||   |||
                                ACAGGGTC AACT   GGT
                                      _   ____
GAM818  PASK     5' GTCCCAGGTCCAACCCAG    22132         GATT
                                GTCCCAGGTT    TCCAG
                                ||||||||||    |||||
                                CAGGGTCCAG    GGGTC
                                      GTT_
GAM818  PEG10    3' TGCCCAGGTCTTTCCAG     22133    T      GA
                                TG CCCAGGTT  TTTCCAG
                                ||  ||||||||  |||||||
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                                AC GGGTCCAG  AAAGGTC
                                 _     __
GAM818  POPX1    3'  TGTCCCAGTTCTATCCAG    22134       G  GATT
                                TGTCCCAG TT   TCCAG
                                |||||||| ||   |||||
                                ACAGGGTC AG   AGGTC
                                    A  AT__
GAM818  PRKRI    5'  TGCCTTTCTGATTTCCAG    22135     CCAGG
                                TGTC    TTGATTTCCAG
                                ||||    ||||||||||
                                ACGG    GACTAAAGGTC
                                  AAA__
GAM818  PRO0902  3'  TGTCCCAGGTACAACTTCCAG  22136         _
                                TGTCCCAGGT TGATTTCCAG
                                |||||||||| ||||||||||
                                ACAGGGTCCA GTTGAAGGTC
                                      T
GAM818  RAB3IL1  3'  TGCCCCAGTCCTTCCAG     22137       GTTGA
                                TGTCCCAG    TTTCCAG
                                ||||||||    |||||||
                                ACGGGGTC    GAAGGTC
                                    AG___
GAM818  RAI      3'  TGTCCCCAGTGATTTCCAG    22138      A  T
                                TGTCCC GGT GATTTCCAG
                                |||||| ||| |||||||||
                                ACAGGG TCA CTAAAGGTC
                                   G  _
GAM818  RHOBTB2  3'  TGTCCCAGCTGCTTCC      22139       G  A
                                TGTCCCAG TTG TTTCC
                                |||||||| ||| |||||
                                ACAGGGTC GAC GAAGG
                                      _  _
GAM818  RNAC     3'  TGTCCTGGATTAATCCA     22140     CA    TT
                                TGTCC  GGTTGA  TCCA
                                |||||  ||||||  ||||
                                ACAGG  CTAATT  AGGT
                                   AC     __
GAM818  SCDGF-B  3'  TATCCCACCTAATTTCCAG   22141       GG
                                TGTCCCA  TTGATTTCCAG
                                |||||||  ||||||||||
                                ATAGGGT  GATTAAAGGTC
                                    G_
GAM818  SCDGF-B  3'  TATCCCACCTAATTTCCAG   22141       GG
                                TGTCCCA  TTGATTTCCAG
                                |||||||  ||||||||||
                                ATAGGGT  GATTAAAGGTC
                                    G_
GAM818  SEZ6     3'  TGTTCCAGGCTGGTCCAG    22142     C      ATT
                                TGT CCAGGTTG   TCCAG
                                ||| ||||||||   |||||
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                                ACA GGTCCGAC   AGGTC
                                  A       C__
GAM818  SSH2     3'  TGTCCCAGAGATTCCAG     22143         TT    T
                                TGTCCCAGG  GATT CCAG
                                |||||||||  |||| ||||
                                ACAGGGTCT  CTAA GGTC
                                       __   _
GAM818  WBSCR21  5'  GTCCCAGGTTGCCTGCAG    22144          A   C
                                GTCCCAGGTTG TTT CAG
                                |||||||||||| ||| |||
                                CAGGGTCCAAC GGA GTC
                                       _  C
GAM818  ZNF238   3'  TGTCCCAGTGATCCCAG     22145         GT    T
                                TGTCCCAG  TGATT CCAG
                                ||||||||  ||||| ||||
                                ACAGGGTC  ACTAG GGTC
                                       __   _
GAM818  ZNF282   3'  TGCCTGTTGCCGATTTCCAG  22146     CCAG
                                TGTC   GTTGATTTCCAG
                                ||||   ||||||||||||
                                ACGG   CGGCTAAAGGTC
                                  ACAA
GAM818  LOC115442 3' TGTCCGGCCAATTCCAG     22147      CA   TG   T
                                TGTCC  GGT  ATT CCAG
                                |||||  |||  ||| ||||
                                ACAGG  CCG  TAA GGTC
                                  __  GT  _
GAM818  LOC116123 3' TGCCCACTGATTTCCAG     22148    T   GG
                                TG CCCA  TTGATTTCCAG
                                || ||||  ||||||||||
                                AC GGGT  GACTAAAGGTC
                                  _   __
GAM818  LOC121133 5' TGCCCACTCTCATTTCCAG   22149    T   GG  G
                                TG CCCA  TT ATTTCCAG
                                || ||||  || ||||||||
                                AC GGGT  GA TAAAGGTC
                                  _   GA  G
GAM818  LOC124512 3' TGTGCCAGGTTGCTCATCAG  22150     C      A  TC
                                TGT CCAGGTTG TT  CAG
                                ||| |||||||  ||  |||
                                ACA GGTCCAAC AG  GTC
                                  C       G  TA
GAM818  LOC127428 3' TGTCCCAGGCTCTGTTCCAG  22151          GAT
                                TGTCCCAGGTT   TTCCAG
                                ||||||||||   ||||||
                                ACAGGGTCCGA   AAGGTC
                                       GAC
GAM818  LOC127703 5' TGACCCAGGCCTTCCAG     22152    T     TGA
                                TG CCCAGGT   TTTCCAG
                                || |||||||   |||||||
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                                AC GGGTCCG   GAAGGTC
                                 T      ___
GAM818  LOC135138 5'  TGCCCAGGTTGATCCAG     22153    T        TT
                                TG CCCAGGTTGA  TCCAG
                                || ||||||||||  |||||
                                AC GGGTCCAACT  AGGTC
                                 _        __
GAM818  LOC143188 5'  TGTCCTGGTATCTCCAG     22154      CA   TG
                                TGTCC  GGT  ATTTCCAG
                                |||||  |||  ||||||||
                                ACAGG  CCA  TAGAGGTC
                                  A_   __
GAM818  LOC144596 3'  TGTCTCAGTACCTCCAG     22081      C   GTTG
                                TGTC CAG    ATTTCCAG
                                |||| |||    ||||||||
                                ACAG GTC    TGGAGGTC
                                  A   A___
GAM818  LOC145757 3'  GTCTCAGCCACTTCCAG     22155     CCA    G
                                GTC   GGTT ATTTCCAG
                                |||   |||| ||||||||
                                CAG   TCGG TGAAGGTC
                                  AG_   _
GAM818  LOC146378 3'  TGCTCAGGTTGAGTCCAG    22156     CC       TT
                                TGT  CAGGTTGA  TCCAG
                                |||  ||||||||  |||||
                                ACG  GTCCAACT  AGGTC
                                  A_       C_
GAM818  LOC146445 3'  TGCCCAGGTTGTCCC       22157    T       AT
                                TG CCCAGGTTG  TTCC
                                || |||||||||  ||||
                                AC GGGTCCAAC  AGGG
                                 _       __
GAM818  LOC147599 5'  TGTCCCAGGTCCACACAG    22158          G  TTC
                                TGTCCCAGGTT AT   CAG
                                |||||||||| ||   |||
                                ACAGGGTCCAG TG   GTC
                                       G  T__
GAM818  LOC149566 3'  GTCCCAGGTCATCCAG      22159          ATT
                                GTCCCAGGTTG   TCCAG
                                ||||||||||   |||||
                                CAGGGTCCAGT   AGGTC
                                       ___
GAM818  LOC149672 5'  TGCCCAAACCTTGATTTC    22160    T     __
                                TG CCCAGG  TTGATTTC
                                || ||||||  ||||||||
                                AC GGGTTT  AACTAAAG
                                 _     GG
GAM818  LOC149912 5'  TGTCCATGTCCTCTTTCCAG  22161      CAG   GA_
                                TGTCC   GTT   TTTCCAG
                                |||||   |||   |||||||
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                                ACAGG  CAG  AAAGGTC
                                  TA_  GAG
GAM818  LOC151031 5'  TGTCCCAGATTGGCCAG    22162         ATTT
                                TGTCCCAGGTTG  CCAG
                                ||||||||||||  ||||
                                ACAGGGTCTAAC  GGTC
                                      C___
GAM818  LOC151031 5'  TGTCCCAGGTCGACCAG    22163          TTT
                                TGTCCCAGGTTGA  CCAG
                                ||||||||||||  ||||
                                ACAGGGTCCAGCT  GGTC
                                     ___
GAM818  LOC153688 3'  TGTCTAAGGTATTCCCAG    22164     CC   TG
                                TGTC  AGGT  ATTTCCAG
                                ||||  ||||  ||||||||
                                ACAG  TCCA  TAAGGGTC
                                  AT   __
GAM818  LOC158527 5'  TGTCCCAGCTTCTCCAG    22165       G TGA
                                TGTCCCAG T  TTTCCAG
                                ||||||||  |  |||||||
                                ACAGGGTC A  AGAGGTC
                                    G ___
GAM818  LOC158969 5'  GTCCCAGGTTGGCATCCAG   22166         ATT
                                GTCCCAGGTTG  TCCAG
                                ||||||||||  |||||
                                CAGGGTCCAAC  AGGTC
                                      CGT
GAM818  LOC162540 3'  TGTCCCAGTGCCTCCAG    22167       GT  A
                                TGTCCCAG  TG TTTCCAG
                                ||||||||  || |||||||
                                ACAGGGTC  AC GGAGGTC
                                     __  _
GAM818  LOC169607 5'  GTCCCAGGCTGTCCAG     22168         ATT
                                GTCCCAGGTTG  TCCAG
                                ||||||||||  |||||
                                CAGGGTCCGAC  AGGTC
                                     ___
GAM818  LOC196394 5'  GTCCCAGGGCCTCCAG     22169       TTGA
                                GTCCCAGG   TTTCCAG
                                ||||||||   |||||||
                                CAGGGTCC   GGAGGTC
                                    C___
GAM818  LOC204010 5'  TCCCAGGTCCTCTTCAG    22170        GA  C
                                TCCCAGGTT  TTT CAG
                                |||||||||  ||| |||
                                AGGGTCCAG  AGA GTC
                                     G_  A
GAM818  LOC204084 5'  TGCTCAGGTACCACTTCCAG  22171    CC   TG_
                                TGT  CAGGT  ATTTCCAG
                                |||  |||||  ||||||||
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                                ACG  GTCCA   TGAAGGTC
                                  A_    TGG
GAM818  LOC219513 5'  TGACCCAGGTCTTGACTC    22172    T     __
                                TG CCCAGGT  TGATTT
                                || |||||||  ||||||
                                AC GGGTCCA  ACTGAG
                                 T      GA
GAM818  LOC219672 5'  TGCCTGGGTTCGATTTCCAG   22173    T  CA   _
                                TG CC  GGTT GATTTCCAG
                                || ||  |||| |||||||||
                                AC GG  CCAA CTAAAGGTC
                                 _ AC    G
GAM818  LOC221178 3'  TATCCCAGGGAAGCTCCAG    22174         TT  T_
                                TGTCCCAGG  GA  TTCCAG
                                |||||||||  ||  ||||||
                                ATAGGGTCC  CT  GAGGTC
                                      __  TC
GAM818  LOC221474 5'  TGTCTGAGTCTATTTCCAG    22175     CCA    G
                                TGTC   GGTT ATTTCCAG
                                ||||   |||| ||||||||
                                ACAG   TCAG TAAAGGTC
                                  AC_    A
GAM818  LOC221749 3'  TGACCCAAACCCAGTTTCCAG  22176    T    GG  GA_
                                TG CCCA  TT   TTTCCAG
                                || ||||  ||   |||||||
                                AC GGGT  GG   AAAGGTC
                                 T    TT  GTC
GAM818  LOC253286 5'  TGCCCCAGGTTTCTCAG     22177          GATT  _
                                TGTCCCAGGTT    TC CAG
                                ||||||||||    || |||
                                ACGGGGTCCAA    AG GTC
                                      ____  A
GAM818  LOC254263 3'  TGGCCCAGAATTTCCAG     22178    T    GTT
                                TG CCCAG   GATTTCCAG
                                || |||||   |||||||||
                                AC GGGTC   TTAAAGGTC
                                 C    ___
GAM818  LOC257445 3'  TGTCCCAGGCTCAAACTCCAG  22094          _  T
                                TGTCCCAGGTT GA TTCCAG
                                |||||||||| || ||||||
                                ACAGGGTCCGA TT GAGGTC
                                      G  T
GAM818  LOC58525  3'  TGCCCCAGGGTGTTTCCAG   22179         T  A
                                TGTCCCAGG TG TTTCCAG
                                ||||||||| || |||||||
                                ACGGGGTCC AC AAAGGTC
                                      C  _
GAM818  LOC90393  3'  TGCTCATCCTCATTTCCAG   22180     CC  GG  G
                                TGT  CA  TT ATTTCCAG
                                |||  ||  || ||||||||
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                              ACG  GT  GA TAAAGGTC
                                A_  AG  G
GAM818  LOC90507  3' GTCCTGGGTCCACCCCAG    22181     CA   G  T
                              GTCC  GGTT ATT CCAG
                              ||||  |||| ||| ||||
                              CAGG  CCAG TGG GGTC
                                AC   G  _
GAM818  LOC90576  5' TGTCCCAGGTCCTCC      22182         GAT
                              TGTCCCAGGTT   TTCC
                              ||||||||||   ||||
                              ACAGGGTCCAG   GAGG
                                   ___
GAM818  LOC90625  3' TGTTTGAAGCGATTTCCAG   22183    CCC   T
                              TGT   AGGT GATTTCCAG
                              |||   |||| |||||||||
                              ACA   TTCG CTAAAGGTC
                                AAC   _
GAM818  LOC91351  3' GTCCTCAGAAATTTCCAG    22184     _   TT
                              GTCC CAGG  GATTTCCAG
                              |||| ||||  |||||||||
                              CAGG GTCT  TTAAAGGTC
                                A   __
GAM818  LOC91522  3' TGTCCCAGGGACTCCAG     22185        TT   T
                              TGTCCCAGG  GATT CCAG
                              |||||||||  |||| ||||
                              ACAGGGTCC  CTGA GGTC
                                   __  _
GAM818  LOC92340  3' TGCCCCAGGCCTTCC       22186        TGA
                              TGTCCCAGGT   TTTCC
                              ||||||||||   |||||
                              ACGGGGTCCG   GAAGG
                                   ___
GAM818  LOC92521  3' TGCCCCAGGCCCTCCAG     22187         GAT
                              TGTCCCAGGTT   TTCCAG
                              ||||||||||   ||||||
                              ACGGGGTCCGG   GAGGTC
                                   ___
GAM818  LOC96597  5' TGTCCCAGTGGCTCTTCCAG  22188       GTTGA
                              TGTCCCAG    TTTCCAG
                              ||||||||    |||||||
                              ACAGGGTC    GAAGGTC
                                  ACCGA
GAM819  CFTR      3' CGAGCTCCAATTCCA      22191      TCA
                              CGAGT   TCCAATTCCA
                              |||||   ||||||||||
                              GCTCG   AGGTTAAGGT
                                   ___
GAM819  CFTR      3' CGAGCTCCAATTCCA      22191      TCA
                              CGAGT   TCCAATTCCA
                              |||||   ||||||||||
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                              GCTCG  AGGTTAAGGT
                                ___
GAM819  KHK     3'  GAGTTGGCCCCAATTCCA   22192     CA_
                              GAGTT  TCCAATTCCA
                              |||||  ||||||||||
                              CTCAA  GGGTTAAGGT
                                 CCG
GAM819  KHK     3'  GAGTTGGCCCCAATTCCA   22192     CA_
                              GAGTT  TCCAATTCCA
                              |||||  ||||||||||
                              CTCAA  GGGTTAAGGT
                                 CCG
GAM819  MARK3   5'  CGAGTCCACGGCAGTTCC   22193       C_ A
                              CGAGTTCAT  CA TTCC
                              |||||||||  || ||||
                              GCTCAGGTG  GT AAGG
                                    CC  C
GAM819  NDRG1   3'  CGAGTAACCCCAATTCCA   22194     TCA
                              CGAGT  TCCAATTCCA
                              |||||  ||||||||||
                              GCTCA  GGGTTAAGGT
                                 TTG
GAM819  NQO2    5'  CGAGTCCAGCAATCTTCC   22195       TC  __
                              CGAGTTCA  CAAT  TCC
                              ||||||||  ||||  |||
                              GCTCAGGT  GTTA  AGG
                                   C_   GA
GAM819  PRSS11  3'  CGTGCTCCCAATTCCA    22196   A   AT
                              CG GTTC  CCAATTCCA
                              || ||||  |||||||||
                              GC CGAG  GGTTAAGGT
                               A   __
GAM819  SIAH2   3'  CCAGCCATCCAATTTCA    22197   G  T      C
                              C AGT CATCCAATT CA
                              | ||| |||||||||  ||
                              G TCG GTAGGTTAA GT
                               G  _       A
GAM819  SLC4A5  5'  GAGCTCACAGCTGAATTCCA  22198       CC___
                              GAGTTCAT    AATTCCA
                              ||||||||    |||||||
                              CTCGAGTG    TTAAGGT
                                   TCGAC
GAM819  SLC4A5  5'  GAGCTCACAGCTGAATTCCA  22198       CC___
                              GAGTTCAT    AATTCCA
                              ||||||||    |||||||
                              CTCGAGTG    TTAAGGT
                                   TCGAC
GAM819  SLC4A5  5'  GAGCTCACAGCTGAATTCCA  22198       CC___
                              GAGTTCAT    AATTCCA
                              ||||||||    |||||||
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                                CTCGAGTG    TTAAGGT
                                    TCGAC
GAM819  THBD     3'  CAAGCTCCCAATTCCA     22199       AT
                                CGAGTTC  CCAATTCCA
                                |||||||  |||||||||
                                GTTCGAG  GGTTAAGGT
                                    __
GAM819  UTX      5'  CGAATTCACAACTCCA     22200       TC
                                CGAGTTCA  CAATTCCA
                                ||||||||  ||||||||
                                GCTTAAGT  GTTGAGGT
                                    __
GAM819  AF093680 3'  CGAGTCACAATTCCA      22201      T  TC
                                CGAGT CA  CAATTCCA
                                |||||  ||  ||||||||
                                GCTCA GT  GTTAAGGT
                                  _  __
GAM819  DKFZP761C169 5'  CAAGTCCAAATTCCA      22202       TCC
                                CGAGTTCA   AATTCCA
                                ||||||||   |||||||
                                GTTCAGGT   TTAAGGT
                                    ___
GAM819  EAT2     3'  CAAGTTCATTAAAAATTCCA  22203        CC__
                                CGAGTTCAT    AATTCCA
                                |||||||||    |||||||
                                GTTCAAGTA    TTAAGGT
                                     ATTT
GAM819  FTSJ1    3'  CAAGTTCATCAACAAGTTCC  22204         __  _
                                CGAGTTCATC  CAA TTCC
                                ||||||||||  ||| ||||
                                GTTCAAGTAG  GTT AAGG
                                     TT   C
GAM819  IDN3     5'  CAATGCATCCAATTCCA     22205     GTT
                                CGA   CATCCAATTCCA
                                |||   ||||||||||||
                                GTT   GTAGGTTAAGGT
                                  AC_
GAM819  IDN3     5'  CAATGCATCCAATTCCA     22205     GTT
                                CGA   CATCCAATTCCA
                                |||   ||||||||||||
                                GTT   GTAGGTTAAGGT
                                  AC_
GAM819  ORC6L    3'  CGGCCTCCAATTCCA      22206    A   CA
                                CG GTT  TCCAATTCCA
                                ||  |||  ||||||||||
                                GC CGG  AGGTTAAGGT
                                  _  __
GAM819  RBAK     3'  CAAGTCATCCAATTCCA     22207      T
                                CGAGT CATCCAATTCCA
                                |||||  ||||||||||||
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                                GTTCA GTAGGTTAAGGT
                                     _
GAM819  LOC124151 3'  CCAGTTCATCCAAGCCCA    22208   G        TT
                                C AGTTCATCCAA  CCA
                                | ||||||||||  |||
                                G TCAAGTAGGTT  GGT
                                 G          CG
GAM819  LOC145608 5'  CAGGCTTCCAATTCCA     22209    A   CA
                                CG GTT  TCCAATTCCA
                                || |||  ||||||||||
                                GT CGA  AGGTTAAGGT
                                 C  __
GAM819  LOC145609 3'  CAGGCTTCCAATTCCA     22209    A   CA
                                CG GTT  TCCAATTCCA
                                || |||  ||||||||||
                                GT CGA  AGGTTAAGGT
                                 C  __
GAM819  LOC149371 3'  CAAGCCCATGATTCCA     22210        CCA
                                CGAGTTCAT   ATTCCA
                                |||||||||   ||||||
                                GTTCGGGTA   TAAGGT
                                     C__
GAM819  LOC158927 3'  CAAGCCCATTCAGTTCCA    22211        C  A
                                CGAGTTCAT CA TTCCA
                                ||||||||| || |||||
                                GTTCGGGTA GT AAGGT
                                     A  C
GAM819  LOC202934 5'  CAAGTTCAAAATTCCA     22212        TCC
                                CGAGTTCA   AATTCCA
                                ||||||||   |||||||
                                GTTCAAGT   TTAAGGT
                                     T__
GAM819  LOC221712 5'  CAAGATCCAATTCCA      22213     TTC
                                CGAG   ATCCAATTCCA
                                ||||   ||||||||||||
                                GTTC   TAGGTTAAGGT
                                     ___
GAM819  LOC254007 3'  CGTGTCCTATCAATTCCA    22214    A   _  C
                                CG GTTC ATC AATTCCA
                                || |||| ||| |||||||
                                GC CAGG TAG TTAAGGT
                                 A   A  _
GAM819  LOC255465 5'  CAAGTTCAAAATTCCA     22212        TCC
                                CGAGTTCA   AATTCCA
                                ||||||||   |||||||
                                GTTCAAGT   TTAAGGT
                                     T__
GAM819  LOC256682 5'  CGTGTGACACCAATTCCA    22215    A  T_  T
                                CG GT  CA CCAATTCCA
                                || ||  || |||||||||
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                                GC CA  GT GGTTAAGGT
                                 A  CT  _
GAM819  LOC51076 3'  CCAGTTCATCAATTAATTCCA  22216   G      C___
                                C AGTTCATC    AATTCCA
                                | ||||||||    |||||||
                                G TCAAGTAG    TTAAGGT
                                 G       TTAA
GAM820  ALEX1    5'  TTAACCCGAGCACAAAACA   22219     T   A
                                TTG TTC AGCACAAAACA
                                ||| ||| ||||||||||
                                AAT GGG TCGTGTTTTGT
                                  T   C
GAM820  APPL     3'  TTTTGGTAAGCACAAAA     22220      TTTC
                                TTTTG    AAGCACAAAA
                                |||||    ||||||||||
                                AAAAC    TTCGTGTTTT
                                   CA__
GAM820  BCL11B   3'  GTTTTTTAAACACAAAACA   22221      GTTTC
                                GTTTT    AAGCACAAAACA
                                |||||    ||||||||||||
                                CAAAA    TTTGTGTTTTGT
                                   AA___
GAM820  FACL5    3'  GTTATGTTTATCACAAAACAAA 22222     T    CAAG
                                GTT TGTTT    CACAAAACAAA
                                ||| |||||    ||||||||||
                                CAA ACAAA    GTGTTTTGTTT
                                  T    TA__
GAM820  FGF5     3'  ATTTTGTTTCAGTCACACTGAA 22224          AG   ___
            ACAAA                  GTTTTGTTTCA  CACA   AAACAAA
                                ||||||||||  ||||  |||||||
                                TAAAACAAAGT  GTGT   TTTGTTT
                                      CA   GAC
GAM820  FGF5     3'  CCTCAAGCATAAAGCAAA    22223         C   A
                                TTTCAAGCA AAA CAAA
                                ||||||||| ||| ||||
                                GGAGTTCGT TTT GTTT
                                      A   C
GAM820  FGF5     3'  CCTCAAGCATAAAGCAAA    22223         C   A
                                TTTCAAGCA AAA CAAA
                                ||||||||| ||| ||||
                                GGAGTTCGT TTT GTTT
                                      A   C
GAM820  FGF5     3'  ATTTTGTTTCAGTCACATTGAA 22225          AG   ___
            ACAAA                  GTTTTGTTTCA  CACA   AAACAAA
                                ||||||||||  ||||  |||||||
                                TAAAACAAAGT  GTGT   TTTGTTT
                                      CA   AAC
GAM820  FOXD2    3'  TTTTCTTTTAAGCACAAAGCA  22226     G  C       A
                                TTTT TTT AAGCACAAA CA
                                |||| ||| ||||||||| ||
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                                AAAA AAA TTCGTGTTT GT
                                  G  A       C
GAM820  GAS7    3'  TTTGTTTCAGAGCGGCAA   22227        _  A_
                                TTTGTTTCA AGC  CAA
                                ||||||||| |||  |||
                                AAACAAAGT TCG  GTT
                                     C   CC
GAM820  IRS2    3'  ATTTTGTTAAAACAAAACAAA  22228       TCAAGC
                                GTTTTGTT     ACAAAACAAA
                                ||||||||     ||||||||||
                                TAAAACAA     TGTTTTGTTT
                                     TTT___
GAM820  ITSN1   3'  GCTTTGTTTCATGAAACA    22230         ___
                                GTTTTGTTTCA   AGCA
                                ||||||||||   ||||
                                CGAAACAAAGT   TTGT
                                       ACT
GAM820  ITSN1   3'  GCACATTCAAGCACAGAACA  22229    TTTGT       A
                                GT    TTCAAGCACA AACA
                                ||    |||||||||| ||||
                                CG    AAGTTCGTGT TTGT
                                 TGT__        C
GAM820  RPE65   3'  TGCTTTCAAGCATAAAACA   22231      _    C
                                TGTTT CAAGCA AAAACA
                                ||||| |||||| ||||||
                                ACGAA GTTCGT TTTTGT
                                   A     A
GAM820  ZFP37   3'  TGCTTAAGTACAAAACAA    22232      C  C
                                TGTTT AAG ACAAAACAA
                                ||||| ||| |||||||||
                                ACGAA TTC TGTTTTGTT
                                   _  A
GAM820  ABCA10  3'  TTATTTTTAAGCACAAAA    22233      C_
                                TTGTTT  AAGCACAAAA
                                ||||||  ||||||||||
                                AATAAA  TTCGTGTTTT
                                    AA
GAM820  C11orf23 3' GTTATGTTTCAAATACAA    22234    T      C
                                GTT TGTTTCAAG ACAA
                                ||| |||||||| ||||
                                CAA ACAAAGTTT TGTT
                                  T       A
GAM820  CARHSP1  3' GTCTCCTCAAGCACAGGACAA 22235      GT       AA
                                GTTTT  TTCAAGCACA  ACAA
                                |||||  ||||||||||  ||||
                                CAGAG  GAGTTCGTGT  TGTT
                                   __        CC
GAM820  DIRC2   3'  GTTTAGCACTGGCACAAAACA 22236     T  TTCAA
                                GTTT GT    GCACAAAACA
                                |||| ||    ||||||||||
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                                CAAA CG    CGTGTTTTGT
                                  T  TGAC_
GAM820  DKFZP564I0422 3'  GTTTTGTTTCAAGACAAA    22237           C
                                GTTTTGTTTCAAG ACAAA
                                ||||||||||||| |||||
                                CAAAACAAAGTTC TGTTT
                                          _
GAM820  ESDN     3'  TTTTGTTTCAAACATTTTGAAA 22238            CA___
           CAAA                  TTTTGTTTCAAGCA    AAACAAA
                                ||||||||||||||    |||||||
                                AAAACAAAGTTTGT    TTTGTTT
                                      AAAAC
GAM820  FLJ14297  3'  TTATTTTTAAGCACAAAA    22233       C_
                                TTGTTT  AAGCACAAAA
                                ||||||  ||||||||||
                                AATAAA  TTCGTGTTTT
                                   AA
GAM820  HCA4     3'  ATTTTGTTTCACACAAAA    22239         AA
                                GTTTTGTTTC  GCACAAAA
                                ||||||||||  ||||||||
                                TAAAACAAAG  TGTGTTTT
                                          __
GAM820  KDELR3    3'  TTTTGTTTCAAGACAAA     22240          C
                                TTTTGTTTCAAG ACAAA
                                ||||||||||| |||||
                                AAAACAAAGTTC TGTTT
                                          _
GAM820  KIAA0332  3'  CCGTTCAGGCACAAAACAAA   22241      T  A
                                TTGTT CA GCACAAAACAAA
                                ||||| || ||||||||||||
                                GGCAA GT CGTGTTTTGTTT
                                   _  C
GAM820  KIAA0391  3'  GTTTTGTTTTGAGACAA     22242         CA  C
                                GTTTTGTTT  AG ACAA
                                |||||||||  || ||||
                                CAAAACAAA  TC TGTT
                                      AC  _
GAM820  KIAA0603  3'  GCTTTGTTTCACTATAAAGACA 22243           AGCACAAA
           AA                    GTTTTGTTTCA       ACAAA
                                ||||||||||        |||||
                                CGAAACAAAGT       TGTTT
                                      GATATTTC
GAM820  KIAA0716  3'  ATTTTGTTTCAAGAACAAA    22244           C
                                GTTTTGTTTCAAG ACAAA
                                ||||||||||||| |||||
                                TAAAACAAAGTTC TGTTT
                                         T
GAM820  KIAA1280  5'  GTTTTATCATCAAAGACAAA   22245         _    C
                                GTTTTGTT TCAAG ACAAA
                                |||||||| ||||| |||||
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                                CAAAATAG AGTTT TGTTT
                                     T    C
GAM820  KIAA1915  3'  GTTTTGTGAGCACAAAACA   22246       TTCA
                                GTTTTGT   AGCACAAAACA
                                |||||||   ||||||||||
                                CAAAACA   TCGTGTTTTGT
                                   C___
GAM820  LRRN3     3'  GTTTTGTTTTTAGCACAA    22247        CA
                                GTTTTGTTT  AGCACAA
                                |||||||||  |||||||
                                CAAAACAAA  TCGTGTT
                                     AA
GAM820  SEPT3     3'  GCTTTGTTTTGGGACACAA   22248        CAA_
                                GTTTTGTTT   GCACAA
                                |||||||||   ||||||
                                CGAAACAAA   TGTGTT
                                     ACCC
GAM820  TA-KRP    3'  ATTTTGTTTCTGGAAAGCA   22249        ____
                                GTTTTGTTTC   AAGCA
                                ||||||||||   |||||
                                TAAAACAAAG   TTCGT
                                     ACCT
GAM820  LOC120534 3'  GTTTTATTTCATTGTAAAAACA 22250         AGCAC
          AA                    GTTTTGTTTCA    AAAACAAA
                                ||||||||||    ||||||||
                                CAAAATAAAGT    TTTTGTTT
                                     AACAT
GAM820  LOC148280 5'  GTTTTGCTTTTCCACGAAACAA 22251        CAAG   A
                                GTTTTGTTT   CAC AAACAA
                                |||||||||   ||| ||||||
                                CAAAACGAA   GTG TTTGTT
                                     AAG_   C
GAM820  LOC155037 5'  GTTTTGTTCAAGCTCAA     22252        T    A
                                GTTTTGTT CAAGC CAA
                                |||||||| ||||| |||
                                CAAAACAA GTTCG GTT
                                   _    A
GAM820  LOC159053 3'  GTTTTGTTTAGAGCAACCACCA 22253        CA   _ AAAA
          AA                    GTTTTGTTT  AGCA C   CAAA
                                |||||||||  |||| |   ||||
                                CAAAACAAA  TCGT G   GTTT
                                     TC   T GTG_
GAM820  LOC221477 3'  CTTTGTTTCGCAGCACAGACA  22254        A_    AA
                                TTTTGTTTC  AGCACA  ACA
                                |||||||||  ||||||  |||
                                GAAACAAAG  TCGTGT  TGT
                                     CG    C_
GAM820  LOC256537 3'  GTTTTGTTTTCAGCCAAA    22255        CA   A
                                GTTTTGTTT  AGC CAAA
                                |||||||||  ||| ||||
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                                CAAAACAAA  TCG GTTT
                                     AG   _
GAM820  LOC256568 5'  CTGTTTCAAGTACAAGACAAA  22256          C    A
                                TTGTTTCAAG ACAA ACAAA
                                |||||||||| |||| |||||
                                GACAAAGTTC TGTT TGTTT
                                      A    C
GAM820  LOC93166  5'  GTTTTACGACAGCACAAAA   22257       TTTCA
                                GTTTTG    AGCACAAAA
                                ||||||    |||||||||
                                CAAAAT    TCGTGTTTT
                                   GCTG_
GAM821  PSCD4    3'  TCTGTGTTACTTTCTGGCTC  22260     A        A_
                                TCT TGTTACTTTT  GTTC
                                ||| ||||||||||  ||||
                                AGA ACAATGAAAG  CGAG
                                  C         AC
GAM821  FLJ20184  3'  TCCATGTTATTTTTAGTC    22261         C
                                TCTATGTTA TTTTAGTT
                                ||||||||| ||||||||
                                AGGTACAAT AAAATCAG
                                     A
GAM821  MGC1842   3'  TCTATGCTACTTGCTGT     22262           TTA   C
                                TCTATGTTACTT   GTT GT
                                ||||||||||||   ||| ||
                                AGATACGATGAA   CGA CA
                                       ____   _
GAM821  MRPL50    3'  TATGTTTCTTTTATAGGTATC  22263       A     GTTC
                                TATGTT CTTTTA    GTATC
                                |||||| ||||||    |||||
                                ATACAA GAAAAT    CATAG
                                   A     ATC_
GAM821  LOC196027 3'  TCTATGTTACTTTTGAATC    22264            AGT
                                TCTATGTTACTTTT   TC
                                ||||||||||||||   ||
                                AGATACAATGAAAA   AG
                                       CTT
GAM822  ACCN2     5'  CTGTCCGCCCGCCCGCGCGC   22267           T  A
                                CTGTCCGCCTGT CC CGCGC
                                |||||||||||| || |||||
                                GACAGGCGGGCG GG GCGCG
                                       _  C
GAM822  BMX       5'  ACGCGTCCGCCCACGC      22268      T      TGTTC
                                ACGC GTCCGCC     CACGC
                                |||| |||||||     |||||
                                TGCG CAGGCGG     GTGCG
                                  _     ______
GAM822  DPYSL2    3'  CTGTCTGCGGTTCCACG     22269       C  CT
                                CTGTC GC  GTTCCACG
                                ||||| ||  ||||||||
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                                GACAG CG  CAAGGTGC
                                  A  C_
GAM822  HCN4     5'  GCTGTCCGTCTGTCTCGC    22270        C    CCA
                                GCTGTCCG CTGTT   CGC
                                |||||||| |||||   |||
                                CGACAGGC GACAG   GCG
                                    A    A__
GAM822  PXR1     5'  ACGCGTCCGCCCACGC      22268      T     TGTTC
                                ACGC GTCCGCC    CACGC
                                |||| |||||||    |||||
                                TGCG CAGGCGG    GTGCG
                                  _     ______
GAM822  BTN3A1   5'  ACGCGTCCGCCCACGC      22268      T     TGTTC
                                ACGC GTCCGCC    CACGC
                                |||| |||||||    |||||
                                TGCG CAGGCGG    GTGCG
                                  _     ______
GAM822  DKFZP586K0717 5'  ACGCGTCCGCCCACGC      22268      T     TGTTC
                                ACGC GTCCGCC    CACGC
                                |||| |||||||    |||||
                                TGCG CAGGCGG    GTGCG
                                  _     ______
GAM822  DKFZp762A227 5'  ACGCGTCCGCCCACGC      22268      T     TGTTC
                                ACGC GTCCGCC    CACGC
                                |||| |||||||    |||||
                                TGCG CAGGCGG    GTGCG
                                  _     ______
GAM822  DKFZp762A227 5'  ACGCGTCCGCCCACGC      22268      T     TGTTC
                                ACGC GTCCGCC    CACGC
                                |||| |||||||    |||||
                                TGCG CAGGCGG    GTGCG
                                  _     ______
GAM822  FLJ10704  3'  ACGCTGGTTCGCCTGACGCGC  22271       TC_    TTCC
                                ACGCTG   CGCCTG   ACGCGC
                                ||||||   ||||||   ||||||
                                TGCGAC   GCGGAC   TGCGCG
                                   CAA     _____
GAM822  FLJ14280  3'  CGCGTCCGCCTCCCGCG     22272     T     TGT   A
                                CGC GTCCGCC   TCC CGCG
                                ||| |||||||   ||| ||||
                                GCG CAGGCGG   AGG GCGC
                                  _     ____  _
GAM822  IRX4     3'  CGCCGTCCGCCTGAGCGC     22273           TTCCA
                                CGCTGTCCGCCTG    CGC
                                ||||||||||||     |||
                                GCGGCAGGCGGAC    GCG
                                        TC___
GAM822  KIAA1036  3'  ACACTGTCTGTACTCCATGCGC 22274        CGCC      C
                                ACGCTGTC    TGTTCCA GCGC
                                ||||||||    ||||||| ||||
```

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                                TGTGACAG   ATGAGGT CGCG
                                   AC__     A
GAM822  NUDT9    5'  ACGCGTCCGCCCACGC     22268     T     TGTTC
                                ACGC GTCCGCC    CACGC
                                |||| |||||||    |||||
                                TGCG CAGGCGG    GTGCG
                                  _     _____
GAM822  Sfmbt    5'  GCTGCCCGGAGTTTTCGCGC   22275       CCT   CCA
                                GCTGTCCG   GTT   CGCGC
                                ||||||||   |||   |||||
                                CGACGGGC   CAA   GCGCG
                                   CT_   AA_
GAM822  SLC21A6  5'  ACGCGTCCGCCCACGC     22268     T     TGTTC
                                ACGC GTCCGCC    CACGC
                                |||| |||||||    |||||
                                TGCG CAGGCGG    GTGCG
                                  _     _____
GAM822  LOC153364 5'  ACGCTGCCCGTAGCGTGCG   22276        CCT  TCCAC
                                ACGCTGTCCG   GT    GCG
                                ||||||||||   ||    |||
                                TGCGACGGGC   CG    CGC
                                   AT_  CA___
GAM822  LOC205095 3'  CGTTGCTGCCTGTTCCCGTGC  22277    C   CC       A  C
                                CG TGT  GCCTGTTCC CG GC
                                || |||  |||||||| || ||
                                GC ACG  CGGACAAGG GC CG
                                 A   A_       _ A
GAM822  LOC57116  5'  ACGCGTCCGCCCACGC     22268     T     TGTTC
                                ACGC GTCCGCC    CACGC
                                |||| |||||||    |||||
                                TGCG CAGGCGG    GTGCG
                                  _     _____
GAM822  LOC90381  3'  GCTGTTCCTCCACGCG     22278     _ GCCTGT
                                GCTGT CC     TCCACGCG
                                ||||| ||     ||||||||
                                CGACA GG     AGGTGCGC
                                   A _______
GAM823  CADPS    3'  TGATAGGATCGCCCCCTTG   22281     C
                                TGA AGGATCGTCCCCTTG
                                ||| ||||||||||||||
                                ACT TCCTAGCGGGGGAAC
                                  A
GAM823  SIM2     3'  TGACAGGATTTTTCCATGTTG  22282        CG_  CC_
                                TGACAGGAT   TCC   TTG
                                |||||||||   |||   |||
                                ACTGTCCTA   AGG   AAC
                                     AAA   TAC
GAM823  ZNF79    5'  ACAGCCACTCTTTGGCTCG   22283     GA  _  CCC
                                ACAG  TCG TC   TTGGCTCG
                                ||||  ||| ||   ||||||||
```

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                                TGTC  GGT AG   AACCGAGC
                                  __   G  A__
GAM823  FLJ10849  3'  TGCGGGAACATCCTTGGCT   22284    ACA   T    CC
                                TG   GGA CGTCC  TTGGCT
                                ||   ||| |||||  ||||||
                                AC   CCT GTAGG  AACCGA
                                 GC_   T    __
GAM823  FLJ14775  3'  TGGCAGGTTGTCCCCCCG    22285    A    ATC
                                TG CAGG   GTCCCCTTG
                                || ||||   |||||||||
                                AC GTCC   CAGGGGGGC
                                 C    AA_
GAM823  FLJ20209  3'  TGGCAGGATCGTTGCCCTTCAC 22286    A       C_    G
                                TG CAGGATCGT  CCCTT GC
                                || |||||||||  ||||| ||
                                AC GTCCTAGCA  GGGAA TG
                                 C        AC    G
GAM823  GDF10     5'  TGACAGGGTCGTCCCTGGCCCG 22287       A     CT
                                TGACAGG TCGTCCC  TGGCTCG
                                |||||||| |||||||  |||||||
                                ACTGTCC AGCAGGG  ACCGGGC
                                    C      __
GAM823  GOLGB1    3'  TGAAACCATCCTCTTGGCT    22288   A       C
                                C GGATCGTCC CTTGGCT
                                | |||||||||| |||||||
                                A TTTGGTAGG GAACCGA
                                 C        A
GAM823  GPA33     3'  TAACAGGATTGTTTCCACG    22289        C  CC  T
                                TGACAGGAT GT  CC TG
                                |||||||||  ||  || ||
                                ATTGTCCTA CA  GG GC
                                      A  AA  T
GAM823  HTR3A     3'  GAAGGGTTCAGACCTTGGCT   22290    CA  A   TCC
                                GA  GG TCG   CCTTGGCT
                                ||  || |||   ||||||||
                                CT  CC AGT   GGAACCGA
                                 TC  A   CT_
GAM823  KIAA0185  3'  TGACAGGATTTCCCCAAGC    22291        CG    TT
                                TGACAGGAT  TCCCC  GGC
                                |||||||||  |||||  |||
                                ACTGTCCTA  AGGGG  TCG
                                      A_    T_
GAM823  KIAA0534  3'  TGACAGGAATGTCCTCTACACT 22292        TC    C  TG
                                TGACAGGA  GTCC CT  GCT
                                ||||||||  |||| ||  |||
                                ACTGTCCT  CAGG GA  TGA
                                     TA    A  TG
GAM823  LOC152503 5'  TGACAAGGGTCCTTGGCT    22293       ATC    CC
                                TGACAGG   GTCC  TTGGCT
                                |||||||   ||||  ||||||
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                                ACTGTTC  CAGG  AACCGA
                                   C__   __
GAM823  LOC158337 3'  AGATGTTTCCCTTTGGCTC   22294     CG_   C
                                GGAT  TCCC TTGGCTC
                                ||||  |||| |||||||
                                TCTA  AGGG AACCGAG
                                  CAA   A
GAM824  ASIP    3'  CGAGAAGCGCCCCGCGTCCCCG 22297          GA   G_
                                CGAGAAGCGCCC  CGCG  CCTG
                                ||||||||||||  ||||  ||||
                                GCTCTTCGCGGG  GCGC  GGGC
                                      __   AG
GAM824  BACH1   5'  CGAGAGCGCCCGGCGG     22298      A     AC
                                CGAGA GCGCCCG  GCGG
                                |||||| |||||||  ||||
                                GCTCT CGCGGGC  CGCC
                                  _     __
GAM824  CACNG6  5'  CGGGAGCGAGGAGCGGCCTGG  22299    A  A   CCC  C
                                CG GA GCG   GA GCGGCCTGG
                                || || |||   || |||||||||
                                GC CT CGC   CT CGCCGGACC
                                 C  _   TC_  _
GAM824  CARKL   3'  CGGGGAGCATCTACGGCCTGG  22300    AGA   CCCGAC
                                CG   AGCG     GCGGCCTGG
                                ||   ||||     |||||||||
                                GC   TCGT     TGCCGGACC
                                 CCC    AGA___
GAM824  CD7     3'  GAGAAGCACCGTGGGGCCTGG  22301         CGACGC
                                GAGAAGCGCC     GGCCTGG
                                ||||||||||     |||||||
                                CTCTTCGTGG     CCGGACC
                                     CACC__
GAM824  CSNK1G2  3'  CGAGAAGCACCCGCCT      22302          GACGCG
                                CGAGAAGCGCCC     GCCT
                                ||||||||||||     ||||
                                GCTCTTCGTGGG     CGGA
                                      _______
GAM824  DLX2    3'  CGGGAAGCCTCGCGCGCCTGG  22303    A    GCC  A   G
                                CG GAAGC   CG CGCG CCTGG
                                || |||||   || |||| |||||
                                GC CTTCG   GC GCGC GGACC
                                 C    GA_  _   _
GAM824  EGFL6   5'  AGGGGCGCTCGCGGCCTG    22304    AA   CCGA
                                AG  GCGC   CGCGGCCTG
                                ||  ||||   |||||||||
                                TC  CGCG   GCGCCGGAC
                                 CC   A___
GAM824  GALNT2  3'  GAGGGGCGCTCCGGCCTG    22305     AA   _  GACGC
                                GAG  GCGC CC    GGCCTG
                                |||  |||| ||    ||||||
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                                CTC  CGCG GG    CCGGAC
                                  CC   A _____
GAM824  GAS11   3' AGAAGCGCCTGACTTACTGG  22306       C  GCG  C
                                AGAAGCGCC GAC  GC TGG
                                ||||||||| |||  || |||
                                TCTTCGCGG CTG  TG ACC
                                    A  AA_ _
GAM824  MATK    5' CGAGGCGCCGCGGCCTG    22307     AA   CGAC
                                CGAG  GCGCC   GCGGCCTG
                                ||||  |||||   ||||||||
                                GCTC  CGCGG   CGCCGGAC
                                  __   _____
GAM824  MATK    5' CGAGGCGCCGCGGCCTG    22307     AA   CGAC
                                CGAG  GCGCC   GCGGCCTG
                                ||||  |||||   ||||||||
                                GCTC  CGCGG   CGCCGGAC
                                  __   _____
GAM824  MGAM    3' GAGAGGCGTCCCTGCAGCCTGG 22308     A  _  GAC
                                GAGA GCG CCC  GCGGCCTGG
                                |||| ||| |||  |||||||||
                                CTCT CGC GGG  CGTCGGACC
                                  C  A  A__
GAM824  MTMR3   3' GAAGTGCTACACAGCCTGG   22309     C  CCG
                                GAAG GC  ACGCGGCCTGG
                                |||| ||  ||||||||||
                                CTTC CG  TGTGTCGGACC
                                  A  A__
GAM824  SLIT3   5' CGGGGAGCGCGGGCGGCCTGG  22310   AGA   CCGAC
                                CG  AGCGC   GCGGCCTGG
                                ||  |||||   |||||||||
                                GC  TCGCG   CGCCGGACC
                                 CCC   CC___
GAM824  SUV39H2  5' GAGGCGGGTCAGCGGCCTGG  22311    AA  CCCGAC
                                GAG  GCG    GCGGCCTGG
                                |||  |||    |||||||||
                                CTC  CGC    CGCCGGACC
                                  __  CCAGT_
GAM824  TOP3A   3' GAGAAGCCCTGGGCAGCCTGG  22312     GC   GAC
                                GAGAA  GCCC  GCGGCCTGG
                                |||||  ||||  |||||||||
                                CTCTT  CGGG  CGTCGGACC
                                   __   ACC
GAM824  TRPC6   5' CGGGAACGCCCGACTGGCCTGG 22313   A  G     GC
                                CG GAA CGCCCGAC  GGCCTGG
                                || ||| ||||||||  |||||||
                                GC CTT GCGGGCTG  CCGGACC
                                 C  _      A_
GAM824  TRPV1   5' CGGGGAGCATCTACGGCCTGG  22300   AGA   CCCGAC
                                CG  AGCG    GCGGCCTGG
                                ||  ||||    |||||||||
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                              GC  TCGT    TGCCGGACC
                               CCC   AGA___
GAM824  ASB13   3' GAGGCTCGGGCCGGCCTGG  22314    AAGC  C  ACG
                              GAG   GC CG   CGGCCTGG
                              |||   || ||   ||||||||
                              CTC   CG GC   GCCGGACC
                               _____ A  CCG
GAM824  C1orf2  5' GAGGAGGGGGCGGCGGCCTGG 22315    A  CGCC  AC
                              GAG AG   CG  GCGGCCTGG
                              ||| ||   ||  |||||||||
                              CTC TC   GC  CGCCGGACC
                               C  CCCC  __
GAM824  C1orf2  5' GAGGAGGGGGCGGCGGCCTGG 22315    A  CGCC  AC
                              GAG AG   CG  GCGGCCTGG
                              ||| ||   ||  |||||||||
                              CTC TC   GC  CGCCGGACC
                               C  CCCC  __
GAM824  CSEN    3' GAGGGGCCATGCGGCCTGG   22316    AAGC   CGAC
                              GAG   GCC   GCGGCCTGG
                              |||   |||   |||||||||
                              CTC   CGG   CGCCGGACC
                               CC__  TA__
GAM824  DVL2    3' CCAGGAGCGCCCGGCCCAGCCT 22317   G  A      ACG
           GG                  C AG AGCGCCCG   CGGCCTGG
                              | || ||||||||   ||||||||
                              G TC TCGCGGGC   GTCGGACC
                               G  C      CGG
GAM824  FLJ10748 5' AGCGCCCGGGCGCCGG     22318       ACGC  _
                              AGCGCCCG   GGC CTGG
                              ||||||||   ||| ||||
                              TCGCGGGC   CCG GGCC
                                   _____  C
GAM824  FLJ20005 5' CGGGGAAAGGGCGCGGCCTGG 22319   A__   C  CCGAC
                              CG   GAAG GC    GCGGCCTGG
                              ||   |||| ||    |||||||||
                              GC   TTTC CG    CGCCGGACC
                               CCC   C _____
GAM824  FLJ22202 5' CGGGGACCCCGGTGCGGCCTGG 22320   AGAA  G   AC
                              CG   GC CCCG  GCGGCCTGG
                              ||   || ||||  |||||||||
                              GC   TG GGGC  CGCCGGACC
                               CCC_  _   CA
GAM824  KCNT1   5' GAGTGGCATGCGGCCTGG   22321    AA  CCCGAC
                              GAG  GCG    GCGGCCTGG
                              |||  |||    |||||||||
                              CTC  CGT    CGCCGGACC
                               AC   A_____
GAM824  MGC13251 3' GAGGAGCGCGCAGCCTG    22322    A   CCGAC
                              GAG AGCGC   GCGGCCTG
                              ||| |||||   ||||||||
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                                CTC TCGCG    CGTCGGAC
                                  C   _____
GAM824  MGC15504  5'  CGAGAAGCATTCGGTGCCCA  22323        CCCGA  CG
                                CGAGAAGCG    CG  GCCTG
                                |||||||||    ||  |||||
                                GCTCTTCGT    GC  CGGGT
                                     AA___  CA
GAM824  PALM      5'  GAGGGGAGGGGGACGCGGCCTG 22324     AAGCGCCC
          G                      GAG       GACGCGGCCTGG
                                |||       ||||||||||||
                                CTC       CTGCGCCGGACC
                                  CCCTCCCC
GAM824  PP2447    3'  CGAGGCGCCGCGCGGCCTG   22325     AA    C A
                                CGAG  GCGCC G CGCGGCCTG
                                ||||  ||||| | |||||||||
                                GCTC  CGCGG C GCGCCGGAC
                                  __    _ _
GAM824  PRO2405   5'  GAGAAGCGCTTGACACTGG   22326        CC    _
                                GAGAAGCGC  GACGC GG
                                |||||||||  |||||  ||
                                CTCTTCGCG  CTGTG CC
                                     AA    A
GAM824  VI        5'  CGGGGAGCGCCCGGCCCCCCG  22327    AGA      AC  GG
                                CG   AGCGCCCG  GC  CCTG
                                ||   ||||||||  ||  ||||
                                GC   TCGCGGGC  CG  GGGC
                                 CCC       __  GG
GAM824  LOC113523 5'  CGAGAAGCGTCTCGTGTCGAAT 22328        CC_  ACG   CC_
          TTGG                    CGAGAAGCG   CG   CGG   TGG
                                |||||||||   ||   |||   |||
                                GCTCTTCGC   GC   GCT   ACC
                                     AGA  ACA   TAA
GAM824  LOC115708 3'  CGAGGAGAGCCCCCAGCCTGG  22329     A  C    GACG
                                CGAG AG GCCC    CGGCCTGG
                                |||| || ||||    ||||||||
                                GCTC TC CGGG    GTCGGACC
                                  C  T    G___
GAM824  LOC146733 3'  GCGCGTGAGGCGGCCTGG    22330     CC  C
                                GCGC  GA GCGGCCTGG
                                ||||  || |||||||||
                                CGCG  CT CGCCGGACC
                                  CA  C
GAM824  LOC149650 3'  CCAGAAGTGGAGGGCGGCCTGG 22331    G    CGCCCGAC
                                C AGAAG       GCGGCCTGG
                                | |||||       |||||||||
                                G TCTTC       CGCCGGACC
                                 G    ACCTCC__
GAM824  LOC166219 5'  CGAGAAGCGGCCCACGCGGCCT 22332         _  G
          GG                    CGAGAAGCG CCC ACGCGGCCTGG
                                ||||||||| ||| ||||||||||
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                                GCTCTTCGC GGG TGCGCCGGACC
                                     C  _
GAM824  LOC200081 3'  GAGAAGCATCATTGGCCTGG  22333        CC  ACGC
                                GAGAAGCG  CG   GGCCTGG
                                ||||||||  ||   |||||||
                                CTCTTCGT  GT   CCGGACC
                                    A_  AA__
GAM824  LOC203668 5'  CGAGAGGCCGCTCGACCTG   22334      A C   C ACG
                                CGAGA G GCC G   CGGCCTG
                                ||||| | ||| |   |||||||
                                GCTCT C CGG C   GCTGGAC
                                  _ _  _ GA_
GAM824  LOC220587 3'  CCAGGAGCGCCCGGCCCAGCCT 22317   G  A       ACG
           GG                     C AG AGCGCCCG   CGGCCTGG
                                | || ||||||||   ||||||||
                                G TC TCGCGGGC   GTCGGACC
                                 G  C       CGG
GAM824  LOC253015 5'  CGGGAAGGCGAGGGGCGGCCTG 22335    A    C  CCGAC
           G                     CG GAAG GC     GCGGCCTGG
                                || |||| ||     |||||||||
                                GC CTTC CG     CGCCGGACC
                                 C   _ CTCCC
GAM824  LOC255271 5'  CGAGGAGCGCCCAGTGCACGCT 22336      A       AC   G _
           GG                     CGAG AGCGCCCG  GCG C CTGG
                                |||| ||||||||  ||| | ||||
                                GCTC TCGCGGGT  CGT G GACC
                                  C       CA  _ C
GAM824  LOC256273 3'  GAGGAGCTGCCCACCAGCCTGG 22337     A  _   G  G
                                GAG AGC GCCC AC CGGCCTGG
                                ||| ||| |||| || ||||||||
                                CTC TCG CGGG TG GTCGGACC
                                  C  A   _ _
GAM825  AVPR1A   5'  TGGGATCGTGGCGCTTTCC   22340        CGCTC  A   C
                                TGGGATCG    GG GCT TCC
                                ||||||||    || ||| |||
                                ACCCTAGC    CC CGA AGG
                                    A____  G   A
GAM825  F2RL3    3'  TGGGATCACGTTTCTTCTGGGA 22341       CTC_________   GCTC
           GAGCTC                 ATCGCG         GGA   TC
                                ||||||         |||   ||
                                TAGTGC         CCT   AG
                                   AAAGAAGAIIIC  CTCG
GAM825  GAS1     3'  TGGGACGCGGGCTCTC      22342       T  GCTC  A
                                TGGGA CGC   GG GCTCTC
                                ||||| |||   || ||||||
                                ACCCT GCG   CC CGAGAG
                                  _  _____  _
GAM825  IL8      3'  TGGGGTCCAGACAGAGCTCTC  22343      A  G  CT
                                TGGG TC CG  CGGAGCTCTC
                                |||| || ||  ||||||||||
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                                ACCC AG GT  GTCTCGAGAG
                                  C  _  CT
GAM825  C20orf85  3'  CGGGATTCAGGGGAGCTCTTCC 22344       CG  CTC      _
                                TGGGAT  CG   GGAGCTCT CC
                                ||||||  ||   |||||||| ||
                                GCCCTA  GT   CCTCGAGA GG
                                   A_  CC_      A
GAM825  C22orf20  3'  TGGGATCATGCTATTCTCT   22345        C   CGGAG
                                TGGGATCG GCT    CTCT
                                |||||||| |||    ||||
                                ACCCTAGT CGA    GAGA
                                    A   TAA__
GAM825  FLJ10761  3'  TGGGATCCTGCCCAGGCTCTCC 22346        GC     A
          C                      TGGGATC  GCTCGG GCTCTCCC
                                |||||||  |||||| ||||||||
                                ACCCTAG  CGGGTC CGAGAGGG
                                   GA     _
GAM825  FLJ31564  5'  TGGGATCCTGCTCGGCGCTC   22347       GC     A
                                TGGGATC  GCTCGG GCTC
                                |||||||  |||||| ||||
                                ACCCTAG  CGAGCC CGAG
                                   GA     G
GAM825  FREQ     3'  TGGGATTGCCTGGAACTCT   22348       C  G  C
                                TGGGAT GC CT GGAGCTCT
                                |||||| || || ||||||||
                                ACCCTA CG GA CCTTGAGA
                                   A  _  _
GAM825  JM5      5'  TGGGATCGTGCTCCAGCTTCC  22349        C   GG   C
                                TGGGATCG GCTC  AGCT TCC
                                |||||||| ||||  |||| |||
                                ACCCTAGC CGAG  TCGA AGG
                                    A   G_   _
GAM825  LOC146506 3'  AGGATCTCGGAGCTTTCC    22350       GCGC       C
                                GGGATC    TCGGAGCT TCC
                                ||||||    |||||||| |||
                                TCCTAG    AGCCTCGA AGG
                                   ____       A
GAM825  LOC152464 5'  TGGGATCGTGCTCCAGCTTCC  22349        C   GG   C
                                TGGGATCG GCTC  AGCT TCC
                                |||||||| ||||  |||| |||
                                ACCCTAGC CGAG  TCGA AGG
                                    A   G_   _
GAM825  LOC159090 5'  TGGGATCGGTGCTTCTCC    22351      TCGCGC   A  _
                                TGGGA     TCGG GCT CTCC
                                |||||     |||| ||| ||||
                                ACCCT     AGCC CGA GAGG
                                   _______   A  A
GAM825  LOC159765 5'  TGGGGTCTCCAAGCTCTC    22352     ATCGCG   G
                                TGGG     CTC GAGCTCTC
                                ||||     ||| ||||||||
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                                ACCC     GAG TTCGAGAG
                                  CA____   G
GAM825  LOC196477 5'  TGGGATCACGTTTTCCTCTC   22353         CTCGGAG
                                TGGGATCGCG      CTCTC
                                ||||||||||      |||||
                                ACCCTAGTGC      GAGAG
                                     AAAAG__
GAM825  LOC253070 3'  TGGGACGCGGCGCTCTCC    22354      T  GCTC  A
                                TGGGA CGC    GG GCTCTCC
                                ||||| |||    || |||||||
                                ACCCT GCG    CC CGAGAGG
                                  _  ____  G
GAM825  LOC254107 5'  TGGGGTCCCGCTGCCGCTCTCC 22355     A  G   CGGA
          C                     TGGG TC CGCT    GCTCTCCC
                                |||| || ||||    ||||||||
                                ACCC AG GCGA    CGAGAGGG
                                  C  G    CGG_
GAM826  CSF3     3'  GACATGATTCCTCCTGTC    22358          G  C
                                GACATGATTCCT CC GTC
                                |||||||||||| || |||
                                CTGTACTAAGGA GG CAG
                                     _  A
GAM826  PIGR     3'  CGACATGATTCTGAAGGTGAT  22359          C  CCC  C
                                CGACATGATTC TG   GT GAT
                                |||||||||| ||   || |||
                                GCTGTACTAAG AC   CA CTA
                                     _  TTC  _
GAM826  FLJ14327  3'  GACGTGATCCCTGCTCGC    22360     A        C
                                GAC TGATTCCTGC CGT
                                ||| |||||||||| |||
                                CTG ACTAGGGACG GCG
                                  C        A
GAM826  KIAA1719  3'  CGACTGATTCCTGCTACCTC   22361      A        __  G
                                CGAC TGATTCCTGC  CC TC
                                |||| ||||||||||  || ||
                                GCTG ACTAAGGACG  GG AG
                                  _        AT  _
GAM826  LOC124460 3'  GACATGATTTCTGCCCAAGTC  22362         C     __
                                GACATGATT CTGCCC  GTC
                                |||||||| ||||||  |||
                                CTGTACTAA GACGGG  CAG
                                     A     TT
GAM826  LOC130813 3'  ACGAAATCCCTGCCTGTTGAT  22363    AT        C  C
                                AC  GATTCCTGCC GT GAT
                                ||  |||||||||| || |||
                                TG  TTAGGGACGG CA CTA
                                 CT        A  A
GAM827  ARHGDIA   3'  CCTGTCCGTCGTCCGTCCGTCA 22366    _    CCC   G_     C
                                CC GTCCG   TCG  TGTCCG CA
                                || |||||   |||  |||||| ||
```

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                                GG CAGGC  AGC  GCAGGC GT
                                 A   ___  AG    A
GAM827  HNRPDL   5' TCTGCCCTCGGTTCGCCA   22367   C      GTC
                                TC GCCCTCGGT  CGCCA
                                || |||||||||  |||||
                                AG CGGGAGCCA  GCGGT
                                 A       A__
GAM827  HPCAL1   5' TCAGTCCGCCCGTCCGC    22368   C     TCGGT
                                TC GTCCGCCC   GTCCGC
                                || ||||||||   ||||||
                                AG CAGGCGGG   CAGGCG
                                 T     _____
GAM827  PDGFB    5' TCCGTCTGCCCGCCTGCTCGCC 22369     C   TCGG TC
                                TCCGTC GCCC   TG  CGCC
                                |||||| ||||   ||  ||||
                                AGGCAG CGGG   AC  GCGG
                                   A   CGG_  GA
GAM827  RAD51L3  5' TCCGCCCGCCCGGGATCCGCC 22370       TC  TG
                                TCCGTCCGCCC  GG  TCCGCC
                                ||||||||||  ||  ||||||
                                AGGCGGGCGGG  CC  AGGCGG
                                      __ CT
GAM827  RAD51L3  5' TCCGCCCGCCCGGGATCCGCC 22370       TC  TG
                                TCCGTCCGCCC  GG  TCCGCC
                                ||||||||||  ||  ||||||
                                AGGCGGGCGGG  CC  AGGCGG
                                      __ CT
GAM827  RAD51L3  5' TCCGCCCGCCCGGGATCCGCC 22370       TC  TG
                                TCCGTCCGCCC  GG  TCCGCC
                                ||||||||||  ||  ||||||
                                AGGCGGGCGGG  CC  AGGCGG
                                      __ CT
GAM827  RAD51L3  5' TCCGCCCGCCCGGGATCCGCC 22370       TC  TG
                                TCCGTCCGCCC  GG  TCCGCC
                                ||||||||||  ||  ||||||
                                AGGCGGGCGGG  CC  AGGCGG
                                      __ CT
GAM827  UBE2B    5' TCCCTCCGCCCTCCGC    22371    G    TCGGTG
                                TCC TCCGCCC    TCCGC
                                ||| |||||||    |||||
                                AGG AGGCGGG    AGGCG
                                  G    _______
GAM827  XYLB     5' TCCGTCAGTCCGTCCGTCCGCC 22372     CG_  C  GG
           A                     TCCGTC  CC TC  TGTCCGCCA
                                 ||||||  || ||  |||||||||
                                 AGGCAG  GG AG  GCAGGCGGT
                                    TCA  C  __
GAM827  A2BP1    5' TCCGTCCGCCGTCCGCC    22373        CTCGGT
                                TCCGTCCGCC    GTCCGCC
                                |||||||||     |||||||
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                              AGGCAGGCGG     CAGGCGG
                                        _______
GAM827  AP1GBP1  3' GTCCACCCTTCACTGTGC    22374        _ G  CC
                              GTCCGCCCT CG TGT  GC
                              ||||||||| || |||  ||
                              CAGGTGGGA GT ACA  CG
                                   A  G  __
GAM827  AP1GBP1  3' GTCCACCCTTCACTGTGC    22374        _ G  CC
                              GTCCGCCCT CG TGT  GC
                              ||||||||| || |||  ||
                              CAGGTGGGA GT ACA  CG
                                   A  G  __
GAM827  AP1GBP1  3' GTCCACCCTTCACTGTGC    22374        _ G  CC
                              GTCCGCCCT CG TGT  GC
                              ||||||||| || |||  ||
                              CAGGTGGGA GT ACA  CG
                                   A  G  __
GAM827  cerk     5' TCCGCCGCCGGGCTCGTCCGCC 22375     T    CTC  __
           A                   TCCG CCGCC   GGT  GTCCGCCA
                              |||| |||||   |||  ||||||||
                              AGGC GGCGG   CCG  CAGGCGGT
                                _    C__   AG
GAM827  DKFZp434G171 5' GTTTGGCTCTGGGATCCGCCA  22376    CC_  C  C  TG
                              GT   GC CT GG  TCCGCCA
                              ||   || || ||  |||||||
                              CA   CG GA CC  AGGCGGT
                               AAC  A  _  CT
GAM827  DKFZp547I224 5'  TCCGTCCAGCTTTGTTCCG   22377       _ CCTCG  G
                              TCCGTCC GC     GT TCCG
                              ||||||| ||     || ||||
                              AGGCAGG CG     CA AGGC
                                  T  AAA__  _
GAM827  DOC2B    3'  TCCTCTGTTCCCACTGTCCGCC 22378     G  CGCC    G
           A                   TCC TC    CTCG TGTCCGCCA
                              ||| ||    |||| |||||||||
                              AGG AG    GGGT ACAGGCGGT
                                _  ACAA    G
GAM827  FLJ11539  3'  TCCTCCGCCCTCCGC      22379     G     TCGGTG
                              TCC TCCGCCC     TCCGC
                              ||| |||||||     |||||
                              AGG AGGCGGG     AGGCG
                                _     _______
GAM827  KIAA0802  5'  CCGTCCGCTCTAGCCGC     22380        CC  GGT T
                              CCGTCCGC  TC   G CCGC
                              ||||||||  ||   | ||||
                              GGCAGGCG  AG   C GGCG
                                   __  AT_ _
GAM827  KIAA1079  5'  TCCGTCCGTCCGTTCGCCCGTC 22381        C  TCGG     C
           A                   TCCGTCCG CC    TGTCCG CA
                              ||||||||  ||    ||||||  ||
```

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                                AGGCAGGC GG    GCGGGC GT
                                    A  CAA_     A
GAM827  KIAA1814  3'  CCCGTCCGTCCTTGCCTCTGCC 22382        C   CG  G  C
                                TCCGTCCG CCT  GT TC GCC
                                |||||||| |||  || || |||
                                GGGCAGGC GGA  CG AG CGG
                                    A   A_  G  A
GAM827  MGC2488   5'  TCTTTCTGTTCTCAGCCTCTGC 22383    CG  CGCC     G  C
           CA                    TC  TC    CTCGGT TC GCCA
                                ||  ||    |||||| || ||||
                                AG  AG    GAGTCG AG CGGT
                                 AA  ACAA     G  A
GAM827  MYOM1    3'  CGTCTGCCCTCTGACCA     22384      C     GG  T
                                CGTC GCCCTC  TG CCG
                                |||| ||||||  || |||
                                GCAG CGGGAG  AC GGT
                                  A     __  T
GAM827  SMOC2    5'  CGTCCGCCCTCGCTCC      22385          GTG
                                CGTCCGCCCTCG   TCC
                                ||||||||||||   |||
                                GCAGGCGGGAGC   AGG
                                       G__
GAM827  LOC116238 5'  CCGTCCGCCCTCGAGGCCG    22386            T T
                                CCGTCCGCCCTCGG G CCG
                                |||||||||||||| | |||
                                GGCAGGCGGGAGCT C GGC
                                       C _
GAM827  LOC130471 3'  TCCTCCGCCCTTGGGTGCC    22387     G       C_
                                TCC TCCGCCCT  GGTGTC
                                ||| ||||||||  ||||||
                                AGG AGGCGGGA  CCACGG
                                  _       AC
GAM827  LOC149707 5'  TCCTCTGTTTTCCGTATCCGCC 22388     G  CGCCC  G
           A                     TCC TC     TC GTGTCCGCCA
                                ||| ||     || ||||||||||
                                AGG AG     AG CATAGGCGGT
                                  _  ACAAA  G
GAM827  LOC150372 3'  TCCGTCCGTCCTGGAAGGTCCA 22389        C   C  T__
                                TCCGTCCG CCT GG   GTCCG
                                |||||||| ||| ||   |||||
                                AGGCAGGC GGA CC   CAGGT
                                    A   _  TTC
GAM827  LOC196074 5'  CCGTCTGCCTTTGGTTCCG    22390      C   CTC   G
                                CCGTC GCC   GGT TCCG
                                ||||| |||   ||| ||||
                                GGCAG CGG   CCA AGGC
                                   A   AAA   _
GAM827  LOC199923 3'  GCCCGCCTTGGCCTGCCA     22391        CTC   GT C
                                GTCCGCC   GGT  C GCCA
                                |||||||   |||  | ||||
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                                CGGGCGG  CCG  G CGGT
                                   AA_  __ A
GAM827  LOC200227 5'  TCCTCTGTTTTCCGTATCCGCC 22388    G  CGCCC  G
          A                     TCC TC    TC GTGTCCGCCA
                                ||| ||    || ||||||||||
                                AGG AG    AG CATAGGCGGT
                                 _ ACAAA  G
GAM827  LOC221312 5'  TCTCTCCGCCCCCTCCGCC   22392   CG      GGTG
                                TC  TCCGCCCTC   TCCGCC
                                ||  |||||||||   ||||||
                                AG  AGGCGGGGG   AGGCGG
                                 AG       _____
GAM827  LOC51629  5'  TCCGTCCGCCCTCGTGGCTCCG 22393           GT _
                                TCCGTCCGCCCTCG  G TCCG
                                ||||||||||||||  | ||||
                                AGGCAGGCGGGAGC  C AGGC
                                         AC G
GAM827  LOC95633  5'  TCCGTCCGTCCGTCCG     22394       C  TCGGT
                                TCCGTCCG CC    GTCCG
                                |||||||| ||    |||||
                                AGGCAGGC GG    CAGGC
                                   A  ______
GAM827  LOC95633  5'  TCCGTCCGTCCGTTGGTCCCA  22395       _ CTC   G
                                TCCGTCCG CC   GGT TCCG
                                |||||||| ||   ||| ||||
                                AGGCAGGC GG   CCA GGGT
                                   A  CAA  _
GAM828  CLASP1   3'  GAAAGGTCTCTGAGAGG    22398     ATTATTAC
                                GAAAG      CTCTGAGAGG
                                |||||      ||||||||||
                                CTTTC      GAGACTCTCC
                                  CA_______
GAM828  ECM2     3'  TGAGAGATTTTACCTTTACC   22399    A    A    T_______
                                TGA AGATT TTACC      CT
                                ||| ||||| |||||      ||
                                ACT TCTAA AATGG      GG
                                  C    _    AAATIII
GAM828  HS2ST1   3'  TGGAAGATAAAACACTGAGAGG 22400    A    TATT  CT
                                TG AAGAT   AC  CTGAGAGG
                                || |||||   ||  ||||||||
                                AC TTCTA   TG  GACTCTCC
                                 C    TTT_  T_
GAM828  KIR3DL2  3'  TGAAAGATAGTCTGAGG    22401       TATTACC    A
                                TGAAAGAT     TCTGAG G
                                ||||||||     |||||| |
                                ACTTTCTA     AGACTC C
                                   TC_____    _
GAM828  TNFSF15  3'  TGAAGGATTTTGCCTCTG    22402     A   A  A
                                TGAA GATT TT CCTCTG
                                |||| |||| || ||||||
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                                ACTT CTAA AA GGAGAC
                                  C   _ C
GAM828  VEGFB    3'  TGGCAGAAGAGCCCTCTGAGAG 22403    AA   TTATTA
            G                    TG  AGA     CCTCTGAGAGG
                                 ||  |||     ||||||||||
                                 AC  TCT     GGAGACTCTCC
                                  CG   TCTCG_
GAM828  C1orf25  3'  TGACAAATTTTACTTCTGAGAG 22404     A    A    C
            G                    TGA AGATT TTAC TCTGAGAGG
                                 |||  ||||| |||| |||||||||
                                 ACT TTTAA AATG AGACTCTCC
                                  G    _    A
GAM828  FLJ14454  3'  TGAGGAAGACTTTCTGAGAGG  22405     __     ATTACC
                                 TGA  AAGATT     TCTGAGAGG
                                 |||  ||||||     |||||||||
                                 ACT  TTCTGA     AGACTCTCC
                                  CC     A_____
GAM828  FLJ14950  5'  GAGAGACCCTCTGAGGG     22406    A    TATTA      A
                                 GA AGAT     CCTCTGAG GG
                                 ||  ||||     |||||||| ||
                                 CT TCTG     GGAGACTC CC
                                  C   _____       _
GAM828  FLJ21736  3'  TGAGAGAGCTCCTCTGAGGG   22407     A   TTATTA      A
                                 TGA AGA     CCTCTGAG GG
                                 |||  |||     |||||||| ||
                                 ACT TCT     GGAGACTC CC
                                  C   CGA___      _
GAM828  FLJ21816  5'  TGAGAGAAGTTTCTGAGAGG   22408     A   TTATTACC
                                 TGA AGA       TCTGAGAGG
                                 |||  |||       |||||||||
                                 ACT TCT       AGACTCTCC
                                  C   TCAA____
GAM828  JAM1     5'  AGAAGTACCTCTGGGAGG    22409     TTAT      A
                                 AGA    TACCTCTG GAGG
                                 |||    |||||||| ||||
                                 TCT    ATGGAGAC CTCC
                                  TC__       C
GAM828  KIAA0527  3'  AGGCCACTGCTTCTGAGAGG   22410    AT    ACC
                                 AG  TATT   TCTGAGAGG
                                 ||  ||||   |||||||||
                                 TC  GTGA   AGACTCTCC
                                  CG    CGA
GAM828  MAP2K6   3'  GAGAGAAAACCCTCTGAGAGG  22411    A   TTATTA
                                 GA AGA     CCTCTGAGAGG
                                 ||  |||     ||||||||||
                                 CT TCT     GGAGACTCTCC
                                  C   TTTG__
GAM828  MAP2K6   3'  GAGAGAAAACCCTCTGAGAGG  22411    A   TTATTA
                                 GA AGA     CCTCTGAGAGG
                                 ||  |||     ||||||||||
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                                CT TCT     GGAGACTCTCC
                                 C  TTTG__
GAM828  LOC131000 3'  TGAAAGATTGTTACATTAGCCT 22412     A  __________  TGA
          CTCAGAG                 GATT TTAC       CTC  GAG
                                |||| ||||       |||  |||
                                CTAA AATG       GAG  CTC
                                  C   TAATCIIIG  AGT
GAM828  LOC158130 3'  TGAGAATTATTAGCTGTGGGAG 22413     AA      C  C  A
          G                      TGA  GATTATTA CT TG GAGG
                                ||| |||||||| || || ||||
                                ACT  TTAATAAT GA AC CTCC
                                  C_      C  C  C
GAM829  PPARGC1   3'  TATTGCTCTTAATAGTCTTT  22416     A_    ATAT
                                TATT  TCTTA   ATAGTCTTT
                                ||||  |||||   |||||||||
                                ATAA  AGAAT   TATCAGAAA
                                  CG   _____
GAM829  FBXO22    3'  TATTATCTTAATAATTCTTTA  22417          TATAG
                                TATTATCTTAATA    TCTTTA
                                ||||||||||||    ||||||
                                ATAATAGAATTAT    AGAAAT
                                       TA___
GAM829  PRO1575   5'  TTATCTTCAATTGCAGTCTTTA 22418       AATATA
                                TTATCTT     TAGTCTTTA
                                |||||||     |||||||||
                                AATAGAA     GTCAGAAAT
                                    GTTAAC
GAM829  LOC90141  3'  CATTATCTTAGAGAAGTCTTTA 22419         ATATAT
                                TATTATCTTA     AGTCTTTA
                                ||||||||||     ||||||||
                                GTAATAGAAT     TCAGAAAT
                                      CTCT__
GAM830  TRHDE     3'  TGAGAATATCATTTCTGTTTT  22422     A       AAA
                                TGA AATATCATT   TTGTTTT
                                ||| |||||||||   |||||||
                                ACT TTATAGTAA   GACAAAA
                                  C       A__
GAM830  B3GNT5    3'  TGAAAACGTCATTAAAATCAGC 22423       TA      TT__
          TT                     TGAAAA  TCATTAAA   GTTT
                                ||||||  ||||||||   ||||
                                ACTTTT  AGTAATTT   CGAA
                                   GC       TAGT
GAM830  FLJ10607  3'  AAAACATTTAAATTGTTTTA   22424       CA
                                AAAATAT  TTAAATTGTTTTA
                                |||||||  ||||||||||||
                                TTTTGTA  AATTTAACAAAAT
                                       __
GAM830  FLJ20060  3'  TGAAGAATCATTAAGCCTGTTT 22425     AAT      A_
                                TGAA   ATCATTAA  TTGTTT
                                ||||   ||||||||  ||||||
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                                ACTT   TAGTAATT  GACAAA
                                  CT_       CG
GAM830  FLJ23563  3'  TGAAAATTATCATTAATGATTT 22426       _      ATT
            TA                    TGAAAAT ATCATTAA   GTTTTA
                                  ||||||| ||||||||   ||||||
                                  ACTTTTA TAGTAATT   TAAAAT
                                     A       AC_
GAM830  LOC148418 3'  GAAAATATCGTTACCCCATTT  22427         A   AA TG
                                  GAAAATATC TTA  T  TTT
                                  ||||||||| |||  |  |||
                                  CTTTTATAG AAT  G  AAA
                                        C   GG GT
GAM830  LOC222001 3'  TGAAGAATCATTAAGCCTGTTT 22425     AAT      A_
                                  TGAA   ATCATTAA  TTGTTT
                                  ||||   ||||||||  ||||||
                                  ACTT   TAGTAATT  GACAAA
                                    CT_       CG
GAM830  LOC56899  3'  AAAATTCACAAAATTGTTTT   22428      A    T
                                  AAAAT TCAT AAATTGTTTT
                                  ||||| |||| ||||||||||
                                  TTTTA AGTG TTTAACAAAA
                                     _    T
GAM831  RRM2      3'  GAATTGGCTCCCATTA      22431      GC    TCC
                                  GAATT  GGTT   CCCATTA
                                  |||||  ||||   |||||||
                                  CTTAA  CCGA   GGGTAAT
                                     __   ___
GAM831  SLC1A3    3'  GGAATACTTCCCCCATT     22432      T  GGT
                                  GGAAT GC   TTCCCCCATT
                                  ||||| ||   ||||||||||
                                  CCTTA TG   AAGGGGGTAA
                                     _ ___
GAM831  TEGT      3'  AGGAGCTGGAGATCCCCATTAG 22433      ATT  _  TTTC
                                  AGGA   GC GG    CCCCATTAG
                                  ||||   || ||    |||||||||
                                  TCCT   CG CC    GGGGTAATC
                                    ___  A  TCTA
GAM831  FLJ20069  3'  AGCAATTACAGTGTTTTCTTCA 22434    G       ___   CCC
            TTAG                    AG AATTGCGGT   TTC   CATTAG
                                  || |||||||||   |||   ||||||
                                  TC TTAATGTCA   AAG   GTAATC
                                   G       CAA   AA_
GAM831  KIAA1041  3'  GGAATATATTTCCCCATTAG   22435      TGCG      C
                                  GGAAT    GTTTCCCC ATTAG
                                  |||||    |||||||| |||||
                                  CCTTA    TAAAGGGG TAATC
                                     TA__       _
GAM831  PRO1905   5'  AGGGACTGTGGCTCTCATT    22436     A   C    CCCC
                                  AGG ATTG GGTTT    CATT
                                  ||| |||| |||||    ||||
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                                TCC TGAC CCGAG   GTAA
                                  C   A    A___
GAM831  LOC143098 5'  GGAATTGCCTTATCCTCATTAG 22437       GGTT  CC
                                GGAATTGC   TCC  CATTAG
                                ||||||||   |||  ||||||
                                CCTTAACG   AGG  GTAATC
                                    GAAT   A_
GAM831  LOC150622 3'  AGATGCAGTTTTTCCTATTAG  22438    AT     CC  C
                                GGA  TGCGGTTT  CC ATTAG
                                |||  ||||||||  || |||||
                                TCT  ACGTCAAA  GG TAATC
                                  __      AA  A
GAM832  VNN1    3'  TATCGGTACTATGTAATT    22441        A   AC
                                TATCGGTAC TAT  GTAATT
                                ||||||||| |||  ||||||
                                ATAGCCATG ATA  CATTAA
                                      _  __
GAM832  CYorf15B  3'  GGAAGTGTATATGTAATTCAC  22442    TACA_   C
                                GG    TATA GTAATTCAC
                                ||    |||| |||||||||
                                CC    ATAT CATTAAGTG
                                 TTCAC   A
GAM832  HNRPAB   3'  GGTACATAATTGTGTTCAC   22443       TAC  AA
                                GGTACATA   GT  TTCAC
                                ||||||||   ||  |||||
                                CCATGTAT   CA  AAGTG
                                    TAA  C_
GAM832  KIAA1054  3'  GGTACATACAGAATTCAC    22444        CGT
                                GGTACATATA   AATTCAC
                                ||||||||||   |||||||
                                CCATGTATGT   TTAAGTG
                                     C__
GAM832  KIAA1317  5'  GGTACATATGTGTTCA      22445        AC  AA
                                GGTACATAT  GT  TTCA
                                |||||||||  ||  ||||
                                CCATGTATA  CA  AAGT
                                    __  C_
GAM832  LOC92285  5'  TCGGTACATATATAGGGCTTCA 22446          CGTAA_
          C                      TCGGTACATATA     TTCAC
                                 ||||||||||||     |||||
                                 AGCCATGTATAT     AAGTG
                                      ATCCCG
GAM833  BPGM     3'  TCAATAATGATTTCTTGAA   22449    TAC       C
                                TC   AATGATTTC TGAA
                                ||   ||||||||| ||||
                                AG   TTACTAAAG ACTT
                                 TTA       A
GAM833  DRD1     5'  TCTCAAAGCCCCTGGAGCTTG  22450     A   TGAT     A
                                TCT CAA    TTCCTG AGCTTG
                                ||| |||    |||||| ||||||
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                                AGA GTT    GGGGAC TCGAAC
                                  _  TC__     C
GAM833  MALT1    3'  TCTCAAAGTCCTGAAGTTT   22451     A   TGATT      C
                                TCT CAA    TCCTGAAG TT
                                ||| |||    |||||||| ||
                                AGA GTT    AGGACTTC AA
                                  _  TC___      A
GAM833  FLJ11588  5'  TCTACATGATTAAGAGAAAGCT 22452       A    TCCT_
          TG                     TCTACA TGATT    GAAGCTTG
                                |||||| |||||    ||||||||
                                AGATGT ACTAA    TTTCGAAC
                                   _    TTCTC
GAM833  KIAA0280  3'  CAGTGACTCCCCAAGCTTG   22453    A       G
                                CA TGATTTCCT AAGCTTG
                                || |||||||| |||||||
                                GT ACTGAGGGG TTCGAAC
                                 C       _
GAM833  SLC26A7   5'  TACAATGTCAAAGCTT     22454       ATT  CT
                                TACAATG   TC  GAAGCTT
                                |||||||   ||  |||||||
                                ATGTTAC   AG  TTTCGAA
                                    ___  __
GAM833  SLC26A7   5'  TACAATGTCAAAGCTT     22454       ATT  CT
                                TACAATG   TC  GAAGCTT
                                |||||||   ||  |||||||
                                ATGTTAC   AG  TTTCGAA
                                    ___  __
GAM833  LOC151907 5'  ACGATTTCCTGGAGCTTG    22455          A
                                ATGATTTCCTG AGCTTG
                                |||||||||||| ||||||
                                TGCTAAAGGAC TCGAAC
                                       C
GAM833  LOC255452 5'  TCTGCCAGCTCCCTGAAGCTTG 22456     A_  ATGA
                                TCT  CA    TTTCCTGAAGCTTG
                                |||  ||    ||||||||||||||
                                AGA  GT    GAGGGACTTCGAAC
                                  CG  C___
GAM833  LOC255545 5'  ACGATTTCCTGGAGCTTG    22455          A
                                ATGATTTCCTG AGCTTG
                                |||||||||||| ||||||
                                TGCTAAAGGAC TCGAAC
                                       C
GAM833  LOC257196 5'  TCTCAATGATTCTGAAGTTTG  22457     A       TC     C
                                TCT CAATGATT  CTGAAG TTG
                                ||| ||||||||  |||||| |||
                                AGA GTTACTAA  GACTTC AAC
                                  _       __      A
GAM833  LOC92340  3'  TCCACAATGAGAAGT       22458          TTTCCT    C
                                TCTACAATGA     GAAG T
                                ||||||||||     |||| |
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                                AGGTGTTACT     CTTC A
                                       _______   A
GAM834  POLK     5'  CCTCCTGCTTTTCTACCCGTCG 22461    A   CC  __  C
                                CC TCC  CT  TC ACCCGTCG
                                || |||  ||  || ||||||||
                                GG AGG  GA  AG TGGGCAGC
                                 _   AC  AA  A
GAM834  USP6     5'  CACCTGTTCTCCTTCCACC    22462     CA_  CC
                                TACC   TC  CCTTCCACC
                                ||||   ||  |||||||||
                                GTGG   AG  GGAAGGTGG
                                  ACA  A_
GAM834  FLJ00026 3'  TACCCATCCTCCATCCCG    22463         CCCT   _
                                TACCCATCC    TCCA CCCG
                                |||||||||    |||| ||||
                                ATGGGTAGG    AGGT GGGC
                                     ____   A
GAM834  GMPPB    5'  CCTCATCCCCTCCCCTGT    22464    _     CT   A  C
                                CC CATCCCC  TCC CC GT
                                || |||||||  ||| || ||
                                GG GTAGGGG  AGG GG CA
                                 A      __   _ A
GAM834  GTF2E1   3'  TCCCCCTTCCACACACG     22465           C  T
                                TCCCCCTTCCAC CG CG
                                |||||||||||| || ||
                                AGGGGGAAGGTG GT GC
                                       T  _
GAM834  H3F3A    5'  TACTTACCCCCCTTCTCCTTCG 22466     CC         CAC  G
                                TAC  ATCCCCCTTC   CC TCG
                                |||  ||||||||||   || |||
                                ATG  TGGGGGGAAG   GG AGC
                                  AA         A__  A
GAM834  KIAA0212 3'  CCATCCCCCTTTCACCACG    22467           C   _
                                CCATCCCCCTT CACC CG
                                |||||||||| |||| ||
                                GGTAGGGGGAA GTGG GC
                                       A   T
GAM834  MAFB     3'  CCCGCCCGCGCACCCGCCCGTC 22468     AT   CCT__   A
           G                     CCC  CCC    TCC CCCGTCG
                                |||  |||    ||| |||||||
                                GGG  GGG    GGG GGGCAGC
                                  C_   CGCGT   C
GAM834  NGEF     3'  CCCACCCCCTTCCACCCCCTCG 22469      T          _ G
                                CCCA CCCCCTTCCACC C TCG
                                |||| |||||||||||| | |||
                                GGGT GGGGGAAGGTGG G AGC
                                  _          G G
GAM834  LOC145858 3'  CACCCATTCCTAGGGCCTCGTC 22470         CCC   TCCA  _
           G                     TACCCAT   CCT    CC CGTCG
                                |||||||   |||    || |||||
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                                GTGGGTA  GGA   GG GCAGC
                                   A__   TCCC  A
GAM834  LOC157621 3'  TACCCTCCCCCTTCTGCAC   22471      A       __
                                TACCC TCCCCCTTC  CAC
                                ||||| |||||||||  |||
                                ATGGG AGGGGGAAG  GTG
                                   _       AC
GAM834  LOC158117 3'  CCATCCCCCAACCCGTCG    22472        TTCC
                                CCATCCCCC   ACCCGTCG
                                |||||||||   ||||||||
                                GGTAGGGGGG   TGGGCAGC
                                     T___
GAM834  LOC203275 3'  CCATCCCCCAACCCGTCG    22472        TTCC
                                CCATCCCCC   ACCCGTCG
                                |||||||||   ||||||||
                                GGTAGGGGGG   TGGGCAGC
                                     T___
GAM834  LOC90183  3'  CCCGCCCGCGCACCCGCCCGTC 22468    AT   CCT__   A
          G                      CCC  CCC    TCC CCCGTCG
                                |||  |||    ||| |||||||
                                GGG  GGG    GGG GGGCAGC
                                  C_   CGCGT   C
GAM835  BDKRB2   3'  TGGGGGGTCTCAGCACTGTGAT 22475     AT       AGAC
                                TGGG  GTCTCAGCA   GTGAT
                                ||||  |||||||||   |||||
                                ACCC  CAGAGTCGT   CACTA
                                  CC       GA__
GAM835  CA9     5'  TGGGGTGTCCCAGCACACG   22476     A       AG
                                TGGG TGTCTCAGCA  ACG
                                |||| ||||||||||  |||
                                ACCC ACAGGGTCGT  TGC
                                  C        G_
GAM835  DSC3    3'  TGGGTGTTTCAGTAGCCGT   22477     A  C   CA  A
                                TGGG TGT TCAG  AG CGT
                                |||| ||| ||||  || |||
                                ACCC ACA AGTC  TC GCA
                                  _  A   A_  G
GAM835  DSC3    3'  TGGGTGTTTCAGTAGCCGT   22477     A  C   CA  A
                                TGGG TGT TCAG  AG CGT
                                |||| ||| ||||  || |||
                                ACCC ACA AGTC  TC GCA
                                  _  A   A_  G
GAM835  GJA1    3'  TGGAATGTTTTAGCAGGGAC  22478       CTC   A_
                                TGGGATGT   AGCA  GAC
                                ||||||||   ||||  |||
                                ACCTTACA   TCGT  CTG
                                     AAA   CC
GAM835  B3GNT5   3'  GGATGTGGTAAGACGTGA   22479      CTCAGC
                                GGATGT    AAGACGTGA
                                ||||||    |||||||||
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                                CCTACA     TTCTGCACT
                                   CCA___
GAM835  CPZ      3'  TGGGATGTCTGTGGCAGACA   22480          CA_   A
                                TGGGATGTCT   GCA GACG
                                ||||||||||   ||| ||||
                                ACCCTACAGA   CGT CTGT
                                     CAC   _
GAM835  P114-RHO-GEF 3'  TGGGATGTCCCAGCACCTTTGA 22481              AGACG
          T                      TGGGATGTCTCAGCA     TGAT
                                 ||||||||||||||     ||||
                                 ACCCTACAGGGTCGT     ACTA
                                       GGAA_
GAM835  LOC165254 5'  TGGGATGTCATCAGCGAAGCGA 22482          _    _  AC_
          GTG                     TGGGATGTC TCAGC AAG   GTG
                                  ||||||||| ||||| |||   |||
                                  ACCCTACAG AGTCG TTC   CAC
                                       T    C   GCT
GAM836  CDC25B   3'  TACCACGGTTCCTACAGAGAT  22485         GC__   C
                                TACCACGGT    ACA GAGAT
                                |||||||||    ||| |||||
                                ATGGTGCCA    TGT CTCTA
                                     AGGA   _
GAM836  CDC25B   3'  TACCACGGTTCCTACAGAGAT  22485         GC__   C
                                TACCACGGT    ACA GAGAT
                                |||||||||    ||| |||||
                                ATGGTGCCA    TGT CTCTA
                                     AGGA   _
GAM836  NOTCH3   3'  TACTCGGTACACGGGATC    22486     CA      ACGA
                                TAC  CGGTGCAC    GATC
                                |||  ||||||||    ||||
                                ATG  GCCATGTG    CTAG
                                  A_       CC__
GAM836  FLJ20716  3'  TACCACGGTGTGCCAGAT    22487          CACA G
                                TACCACGGTG    C AGAT
                                ||||||||||    | ||||
                                ATGGTGCCAC    G TCTA
                                     ACG_ _
GAM836  FLJ22283  5'  CCACACATACGAGATC      22488      GGT   C
                                CCAC   GCA ACGAGATC
                                ||||   ||| ||||||||
                                GGTG   TGT TGCTCTAG
                                   ___   A
GAM836  KIAA0415  3'  CCACGGTGCACCTCCGATC    22489          ACGA
                                CCACGGTGCAC    GATC
                                ||||||||||    ||||
                                GGTGCCACGTG    CTAG
                                     GAGG
GAM836  MGC12981  5'  CCAATAGGCACACGAGATC    22490     C_  T
                                CCA  GG GCACACGAGATC
                                |||  || ||||||||||||
```

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                                GGT  TC CGTGTGCTCTAG
                                  TA  _
GAM837  SSB      3'  TTAGTTTGTACTAATACATTCT 22493       C      AT
                                TTAGTT GTATTAG  TATATTCT
                                |||||| |||||||  ||||||||
                                AATCAA CATGATT  ATGTAAGA
                                   A      __
GAM838  CRSP9    3'  GAGGTTATCATCAAAGTTTT  22496     ACCAA  G
                                GAGG    GTC AAAGTTTT
                                ||||    ||| ||||||||
                                CTCC    TAG TTTCAAAA
                                  AATAG  _
GAM838  MGC27044 5'  CCAGGACCGACAGGAAAGTTTT 22497    G     AAGTC
                                CC AGGACC    GAAAGTTTT
                                || ||||||    |||||||||
                                GG TCCTGG    CTTTCAAAA
                                 _     CTGTC
GAM838  ZNF317   3'  ACCAAGGGTCGGCCAAGTTTT  22498       ACCAA   A__
                                ACCGAGG    GTCG   AAGTTTT
                                |||||||    ||||   |||||||
                                TGGTTCC    CAGC   TTCAAAA
                                    ______   CGG
GAM838  LOC144465 3'  CCTGGGACTCCCAAAGTTTT  22499    GA   CAAG  G
                                CC  GGAC    TC AAAGTTTT
                                ||  ||||    || ||||||||
                                GG  CCTG    GG TTTCAAAA
                                 AC    A___  G
GAM838  LOC146512 3'  GAGGATCTCATAAAGTTTT   22500      CCAAG  _
                                GAGGA    TCG AAAGTTTT
                                |||||    ||| ||||||||
                                CTCCT    AGT TTTCAAAA
                                   AG___   A
GAM839  ABCC3    3'  TCCGAAAAGTGGGAGTA     22503     AA       TC
                                TCC  AAGAGTGGG  GTA
                                |||  |||||||||  |||
                                AGG  TTTTCACCC  CAT
                                  C_       T_
GAM839  CMAR     5'  TCCAAGTGGAGTCATAC     22504      AAAG    _
                                TCCA    AGTGG GTCGTAC
                                ||||    ||||| |||||||
                                AGGT    TCACC CAGTATG
                                   ____    T
GAM839  DGCR2    3'  CCTGGAAGAGTGGGCCCCCA   22505    AA_       GTA
                                CC   AAGAGTGGGTC   CA
                                ||   ||||||||||   ||
                                GG   TTCTCACCCGG   GT
                                 ACC         GG_
GAM839  IL7R     3'  CAGGAAGAGTGGTCAAAGCAA  22506    A_      G   TA_
                                CA  AAGAGTGG TCG   CAA
                                ||  |||||||| |||   |||
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                                GT  TTCTCACC AGT   GTT
                                 CC       _  TTC
GAM839  NCYM     5'  TCCAAAAGGGCGGGAGGAGCA  22507        A    TC__
                                TCCAAAAG GTGGG   GTA
                                |||||||| |||||   |||
                                AGGTTTTC CGCCC   CGT
                                     C    TCCT
GAM839  PIP5K1B  3'  TCCAAAAAGGTGATTGGCA   22508        A   GTC
                                TCCAAAAG GTGG   GTA
                                |||||||| ||||  |||
                                AGGTTTTT CACT   CGT
                                     C   AAC
GAM839  RELN     3'  AAAAGAATGGAGAGCAACA   22509         TCGTA
                                AAAAGAGTGGG    CAACA
                                ||||||||||     |||||
                                TTTTCTTACCT    GTTGT
                                      CTC__
GAM839  SEPP1    3'  AAGAGTATGATACAACA     22510       GGTC
                                AAGAGTG   GTACAACA
                                |||||||   ||||||||
                                TTCTCAT   TATGTTGT
                                    AC__
GAM839  SEPP1    3'  AAGAGTATGATACAACA     22510       GGTC
                                AAGAGTG   GTACAACA
                                |||||||   ||||||||
                                TTCTCAT   TATGTTGT
                                    AC__
GAM839  TCF8     3'  TCCAAAAGAGGTTCCACA    22511         TGGG  G
                                TCCAAAAGAG   TC TACA
                                ||||||||||   || ||||
                                AGGTTTTCTC   AG GTGT
                                      CA__  _
GAM839  TEC      3'  TCCTGAGAGGCTGTACAAC   22512    AAAA  T   C
                                TCC   GAG GGGT GTACAAC
                                |||   ||| |||| |||||||
                                AGG   CTC TCCG CATGTTG
                                  A___  _   A
GAM839  WHSC1    3'  TCACAGGAGAGTGGGTGTCA  22513   _ AA      C  A
                                TC CA  AGAGTGGGT GT CA
                                || ||  |||||||||| || ||
                                AG GT  TCTCACCCA CA GT
                                 T  CC       _ _
GAM839  WHSC1    3'  TCACAGGAGAGTGGGTGTCA  22513   _ AA      C  A
                                TC CA  AGAGTGGGT GT CA
                                || ||  |||||||||| || ||
                                AG GT  TCTCACCCA CA GT
                                 T  CC       _ _
GAM839  WHSC1    3'  TCACAGGAGAGTGGGTGTCA  22513   _ AA      C  A
                                TC CA  AGAGTGGGT GT CA
                                || ||  |||||||||| || ||
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                                AG GT  TCTCACCCA CA GT
                                 T  CC       _ _
GAM839  ATP5I    3'  TCCAAAGAGTGGGTCGCA    22514       A
                                TCCAAA GAGTGGGTCGTA
                                |||||| ||||||||||||
                                AGGTTT CTCACCCAGCGT
                                   _
GAM839  ATP8A1   3'  TCCAAAAGAGATGGTGTTACA  22515         _  GTCG
                                TCCAAAAGAG TGG    TACA
                                |||||||||| |||    ||||
                                AGGTTTTCTC ACC    ATGT
                                      T   ACA_
GAM839  CASPR3   3'  AAAAGATGTTCTGTACAACA   22516       G  GG  _
                                AAAAGA TG  TC GTACAACA
                                |||||| ||  || ||||||||
                                TTTTCT AC  AG CATGTTGT
                                   _ A_  A
GAM839  DKFZP761C169 3'  AAAAGGTGAATAGTACAACA   22517      A     C
                                AAAAG GTGGGT GTACAACA
                                ||||| |||||| ||||||||
                                TTTTC CACTTA CATGTTGT
                                   _     T
GAM839  FLJ11011  3'  TCAAAAAGAGTGCAAC      22518    C       GGTCGTA
                                TC AAAAGAGTG      CAAC
                                || |||||||||      ||||
                                AG TTTTCTCAC      GTTG
                                 T       ________
GAM839  FLJ12688  3'  TCCAAGAGAGTGGGCAAT    22519      A       C
                                TCCAA AGAGTGGGT GT
                                ||||| ||||||||| ||
                                AGGTT TCTCACCCG TA
                                   C       T
GAM839  FLJ20034  3'  TCCAAAAGGCCAGGTACA    22520        A  G  TC
                                TCCAAAAG GT GG  GTACA
                                |||||||| || ||  |||||
                                AGGTTTTC CG TC  CATGT
                                     _ G  __
GAM839  FLJ20464  5'  TCCGAAGGGTGGACGAC     22521     AA  A    T  T
                                TCC  AAG GTGGG CG AC
                                |||  ||| ||||| || ||
                                AGG  TTC CACCT GC TG
                                  C_   C    _ _
GAM839  GIT1     3'  TCCAGAGGGTGGGACCACA   22522     AA  A    TCG
                                TCCA  AG GTGGG   TACA
                                ||||  || |||||   ||||
                                AGGT  TC CACCC   GTGT
                                  C_ C    TG_
GAM839  KIAA1069  3'  TCCAAAAAGTGGGAAGGGCA   22523       A      TC__
                                TCCAAA GAGTGGG    GTA
                                |||||| |||||||    |||
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                                AGGTTT TTCACCC   CGT
                                   _     TTCC
GAM839  KIAA1280  5'  CAAGGGAGTGAATGTGTACAA  22524    AA      C_
                                CAA  GAGTGGGT  GTACAA
                                |||  ||||||||  ||||||
                                GTT  CTCACTTA  CATGTT
                                  CC       CA
GAM839  KIAA1530  3'  TCCAGAAAGTGAAACAAC    22525     AA      TCGT
                                TCCA  AGAGTGGG   ACAAC
                                ||||  ||||||||   |||||
                                AGGT  TTTCACTT   TGTTG
                                  C_      ____
GAM839  MCAM      3'  TCCGGAGCGGGTGTGAACA   22526    AAAA      C __
                                TCC   GAGTGGGT GT  ACA
                                |||   |||||||| ||  |||
                                AGG   CTCGCCCA CA  TGT
                                  C___      _ CT
GAM839  MGC16491  3'  TCCAAAAGTGTGATGCAATA  22527       A   _ C
                                TCCAAAAG GTGG GT GTA
                                |||||||| |||| || |||
                                AGGTTTTC CACT CG TAT
                                     A   A  T
GAM839  Rpo1-2    3'  AAAGATCTGTTGTACAACA   22528     GTGG  C
                                AAAGA   GT GTACAACA
                                |||||   || ||||||||
                                TTTCT   CA CATGTTGT
                                   AGA_  A
GAM839  Rpo1-2    3'  AAAGATCTGTTGTACAACA   22528     GTGG  C
                                AAAGA   GT GTACAACA
                                |||||   || ||||||||
                                TTTCT   CA CATGTTGT
                                   AGA_  A
GAM839  LOC130576 5'  TCCAGGAGGGTTGCCAACA   22529     AAA  GT   C  A
                                TCCA   GA  GGGT GT CAACA
                                ||||   ||  |||| || |||||
                                AGGT   CT  CCCA CG GTTGT
                                  C__  __   A  _
GAM839  LOC150005 3'  TCTAAAAGAGAGAGCACAAC  22530   C     T   CGT
                                TC AAAAGAG GGGT   ACAAC
                                || ||||||| ||||   |||||
                                AG TTTTCTC CTCG   TGTTG
                                 A      T   ____
GAM839  LOC150223 5'  CCCAGGGGAGTGGGCCGGACA  22531     AAA       T
                                TCCA   GAGTGGGTCG ACA
                                ||||   |||||||||| |||
                                GGGT   CTCACCCGGC TGT
                                  CCC        C
GAM839  LOC200339 3'  CAGGAAGGGTGGGTCATTCA   22532    A_  A      A
                                CA  AAG GTGGGTCGT CA
                                ||  ||| |||||||||  ||
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                                GT  TTC CACCCAGTA GT
                                 CC   C        A
GAM839  LOC51195  3'  AAAAGGGTCTGTACAACA    22533      T    _
                                AGAG GGGTC GTACAACA
                                |||| ||||| ||||||||
                                TTTT CCCAG CATGTTGT
                                  _    A
GAM839  LOC90371  5'  TCCAAAAGTGTGGGCCAAGTCA 22534         A       TA_
          A                      TCCAAAAG GTGGGTCG   CAA
                                |||||||| ||||||||   |||
                                AGGTTTTC CACCCGGT   GTT
                                     A       TCA
GAM839  LOC91397  5'  CAGGAGAGTGGGCACAGACA   22535    AA       _  T
                                CA  AGAGTGGGT CG ACA
                                ||  ||||||||| || |||
                                GT  TCTCACCCG GT TGT
                                 CC        T  C
GAM840  PTBP1     3'  TCGAAGTCCAGGTACAGACT   22538      CG    A
                                TCGAAG  CCAG TACAGATT
                                ||||||  |||| ||||||||
                                AGCTTC  GGTC ATGTCTGA
                                   A_    C
GAM840  PTBP1     3'  TCGAAGTCCAGGTACAGACT   22538      CG    A
                                TCGAAG  CCAG TACAGATT
                                ||||||  |||| ||||||||
                                AGCTTC  GGTC ATGTCTGA
                                   A_    C
GAM840  KIAA1165  3'  GAACCTTACAGATTTG     22539    AGC   AGA
                                GA   GCC   TACAGATTTG
                                ||   |||   ||||||||||
                                CT   TGG   ATGTCTAAAC
                                 ___   A__
GAM840  MGC12466  3'  TCGGAGCATTTCAGATTTG   22540     A    CCAGATA
                                TCG AGCG      CAGATTTG
                                ||| ||||      ||||||||
                                AGC TCGT      GTCTAAAC
                                  C    AAA____
GAM841  BACH2     3'  TATCCTACTGCATGAACTGACA 22543      AC     ACGT
          A                      TATC  ACTGCG    GCTGACAA
                                ||||  ||||||   ||||||||
                                ATAG  TGACGT    TGACTGTT
                                  GA     ACT_
GAM841  OPHN1     3'  TATCACACTCTGGGGACTGTGG 22544          GC___   _   C
          TG                      TATCACACT    GAC GTG TG
                                |||||||||    ||| ||| ||
                                ATAGTGTGA    CTG CAC AC
                                     GACCC   A   C
GAM841  RGL       5'  TCACACAGCACTGACA      22545        T  GACGT
                                TCACAC GC    GCTGACA
                                ||||||  ||    |||||||
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                                AGTGTG CG    TGACTGT
                                   T _____
GAM841  TCF12    3'  TATCACACTACCTGCC     22546          GACG
                                TATCACACTGC   TGCT
                                ||||||||||   ||||
                                ATAGTGTGATG   ACGG
                                      G___
GAM841  TCF8     3'  CACACCTGTGCTGACA     22547       GCGAC
                                CACACT    GTGCTGACA
                                ||||||    |||||||||
                                GTGTGG    CACGACTGT
                                   A____
GAM841  SLC39A3  3'  TCACACTGTGGCCTGACA    22548        CGAC  G
                                TCACACTG   GT CTGACA
                                ||||||||   || ||||||
                                AGTGTGAC   CG GACTGT
                                     AC__  _
GAM841  ZNF225   3'  TATCACACTGTACCCCATA   22549         __ GA
                                TATCACACTG  C  CGTG
                                ||||||||||  |  ||||
                                ATAGTGTGAC  G  GTAT
                                      AT GG
GAM841  LOC149952 5'  TCACACTGAGATGTAAGAC   22550        C  C   CT
                                TCACACTG GA GTG  GAC
                                |||||||| || |||  |||
                                AGTGTGAC CT CAT  CTG
                                     T  A   T_
GAM841  LOC199729 3'  TATCACACTGTACCCCATA   22549         __ GA
                                TATCACACTG  C  CGTG
                                ||||||||||  |  ||||
                                ATAGTGTGAC  G  GTAT
                                      AT GG
GAM841  LOC256222 3'  TATCACACTGTTGCTGA     22551         CGACG
                                TATCACACTG    TGCTGA
                                ||||||||||    ||||||
                                ATAGTGTGAC    ACGACT
                                      A____
GAM842  ASPH     5'  GGTGGACCTCCTTCAGTG    22554        C  C  _
                                GGTGGATC CC TC GTG
                                |||||||| || || |||
                                CCACCTGG GG AG CAC
                                     A  A  T
GAM842  GPR17    3'  GATGGATCCCCTTTGTCAGTGT 22555       CTC__________  GTAA
           GTTACCA                 ATCCCC          GTG   CA
                                ||||||          |||   ||
                                TAGGGG          CAC   GT
                                   AAACAGTCAIII  AATG
GAM842  GRM3     5'  GGTTGGTCCTCCTCATCCGACA 22556     _ A  C     GGTA
           C                     GGT GG TCC CCTCGT    ACAC
                                ||| || ||| ||||||    ||||
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                                CCA CC AGG GGAGTA    TGTG
                                  A  _   A     GGC_
GAM842  PAH      5'  GGTGCATCTCCGCACAGTAAC  22557      G   CC  T  TG
                                GGTG ATC  CC CG  GTAAC
                                |||| |||  || ||  |||||
                                CCAC TAG  GG GT  CATTG
                                  G   A_  C  GT
GAM842  TJP1     5'  GGAGGATCCCCTTCTGGCGGTA 22558    T       C  __
                                GG GGATCCCC TC  GTGGTA
                                || |||||||| ||  ||||||
                                CC CCTAGGGG AG  CGCCAT
                                 T       A  AC
GAM842  ZRF1     5'  GATGGATCTTTCGTGGT     22559         CCCC
                                GGTGGATC    TCGTGGT
                                ||||||||    |||||||
                                CTACCTAG    AGCACCA
                                     AA__
GAM842  C20orf46 3'  GGTGGACCTTGTAGCA      22560       TCCC   C
                                GGTGGA    CCT GTGGTA
                                ||||||    ||| ||||||
                                CCACCT    GGA CATCGT
                                   ____   A
GAM842  GBA2     5'  GTGGATCCTCTTTGGCA     22561        CC  CG
                                GTGGATCC  CT  TGGTA
                                ||||||||  ||  |||||
                                CACCTAGG  GA  ACCGT
                                     A_  A_
GAM842  KIAA0193 3'  GGAGGGTCCCCTTGACAACAC  22562    T  A    CTCG  GT
                                GG GG TCCCC    TG  AACAC
                                || || |||||    ||  |||||
                                CC CC AGGGG    AC  TTGTG
                                 T  C    A___  TG
GAM842  KIAA0443 5'  GGTGGATCTTCACTTATGTGGT 22563        CCC_  C__
                                GGTGGATC    CT   GTGGT
                                ||||||||    ||   |||||
                                CCACCTAG    GA   CACCA
                                     AAGT  ATA
GAM842  KIAA1155 3'  GGTGAATCTCCTGCCTGACAC  22564        CC   C  GGTA
                                GGTGGATC  CCT GT    ACAC
                                ||||||||  ||| ||    ||||
                                CCACTTAG  GGA CG    TGTG
                                     A_   _  GAC_
GAM842  KIAA1634 3'  GGTGGATCCCTCTTACTCACA  22565         C  CG GGTA
                                GGTGGATCCC CT  T    ACA
                                |||||||||| ||  |    |||
                                CCACCTAGGG GA  G    TGT
                                      A  AT AG__
GAM842  MGC15435 5'  GGTAGATCCCCCTCCAGGC   22566            GT
                                GGTGGATCCCCCTC  GGT
                                ||||||||||||||  |||
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                                CCATCTAGGGGGAG  CCG
                                      GT
GAM842  LOC132617 3'  GCTGGATCCCTTTCCCTGTCGA 22567   G      ___  TC  _
          TA                    G TGGATCCC   CC  GT GGTA
                                | ||||||||   ||  || ||||
                                C ACCTAGGG   GG  CA CTAT
                                 G       AAA  GA  G
GAM842  LOC144594 3'  GGTGGGATCCCCCGTGGCA   22568      _      TC
                                GGTGG ATCCCCC  GTGGTA
                                ||||| |||||||  ||||||
                                CCACC TAGGGGG  CACCGT
                                   C      __
GAM842  LOC144747 5'  GGGGTCCCCCATCATGGTA   22569    T  A     _
                                GG GG TCCCCC TCGTGGTA
                                || || |||||| ||||||||
                                CC CC AGGGGG AGTACCAT
                                 _ _     T
GAM842  LOC148343 5'  GGAGGGTTTCCCTCGCGGTGAC 22570    T  ATCC        A
          AC                    GG GG    CCCTCGTGGT ACAC
                                || ||    |||||||||| ||||
                                CC CC    GGGAGCGCCA TGTG
                                 T  CAAA         C
GAM842  LOC152048 3'  GCTGGATCCCTCGTGACA    22571   G       CC     GT
                                G TGGATCCC  TCGTG  A
                                | ||||||||  |||||  |
                                C ACCTAGGG  AGCAC  T
                                 G       __     TG
GAM842  LOC221738 3'  GGTGAATCTTCCAAAACTGGCA 22572         CC  TCG__
                                GGTGGATC  CC     TGGTA
                                ||||||||  ||     |||||
                                CCACTTAG  GG     ACCGT
                                     AA  TTTTG
GAM843  PCOLCE2   3'  AGACAAGATTGTAACACCT   22575        A       C
                                AGACAA ATTGTAAC ACTT
                                |||||| |||||||| ||||
                                TCTGTT TAACATTG TGGA
                                   C       _
GAM843  LOC202781 3'  GACAAAACTGTAGTCACCT   22576           AC
                                GACAAAATTGTA  CACTT
                                ||||||||||||  |||||
                                CTGTTTTGACAT  GTGGA
                                      CA
GAM843  LOC253573 3'  AAACAAAATTGTAACCAGCC   22577              _
                                AGACAAAATTGTAACCA CT
                                |||||||||||||||| ||
                                TTTGTTTTAACATTGGT GG
                                         C
GAM843  LOC92140  3'  AGCAAAACTAAAACCATTTTGT 22578    A       T    C  C
          T                     AG CAAAATTG AACCA TT GTT
                                || |||||||| ||||| || |||
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                                TC GTTTTGAT TTGGT AA CAA
                                 _      T    A  A
GAM844  GABRE    3' TTTACATATTTCCCCATTTCA  22581         A   TC
                                TTTACATATT CCCT  TTCA
                                |||||||||| ||||  ||||
                                AAATGTATAA GGGG  AAGT
                                      A   TA
GAM844  GABRE    3' TTTACATATTTCCCCATTTCA  22581         A   TC
                                TTTACATATT CCCT  TTCA
                                |||||||||| ||||  ||||
                                AAATGTATAA GGGG  AAGT
                                      A   TA
GAM844  GABRE    3' TTTACATATTTCCCCATTTCA  22581         A   TC
                                TTTACATATT CCCT  TTCA
                                |||||||||| ||||  ||||
                                AAATGTATAA GGGG  AAGT
                                      A   TA
GAM844  GABRE    3' TTTACATATTTCCCCATTTCA  22581         A   TC
                                TTTACATATT CCCT  TTCA
                                |||||||||| ||||  ||||
                                AAATGTATAA GGGG  AAGT
                                      A   TA
GAM844  FLJ13197 3' CACACACTTCTTCAAAT    22582       TTACC
                                TACATA    CTTCTTCAAAT
                                ||||||    ||||||||||
                                GTGTGT    GAAGAAGTTTA
                                          _____
GAM844  FLJ20287 3' TTACATCAGTCTTTTTCTTCAA 22583       ATTACCC_
           AT                    TTACAT      TTCTTCAAAT
                                ||||||       ||||||||||
                                AATGTA       AAGAAGTTTA
                                   GTCAGAAA
GAM844  KIAA1911 5' ATATCACCTTTTTCTTCAA   22584        C__
                                ATATTACC   TTCTTCAA
                                ||||||||   ||||||||
                                TATAGTGG   AAGAAGTT
                                     AAA
GAM844  MGC32104 3' TCTACTGTTCCCTTCTT     22585      ATA  A
                                TTTAC   TT CCCTTCTT
                                |||||   || ||||||||
                                AGATG   AA GGGAAGAA
                                   AC_  _
GAM844  SNTG1    3' TTTACATACTTCTTCAAA    22586        TTACC
                                TTTACATA    CTTCTTCAAA
                                ||||||||    ||||||||||
                                AAATGTAT    GAAGAAGTTT
                                          _____
GAM845  CUL3     3' TCTAGATCTGATTTTTACA   22589     A      GT
                                TCTA ATCTGAT  TTTTGCA
                                |||| |||||||  |||||||
```

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                                AGAT TAGACTA  AAAATGT
                                  C     __
GAM845  FLJ13687  5'  TCTAAATCCAGGTTTTGTGTGG 22590         GAT    T CA
                                TCTAAATCT   GTTTT G  TGG
                                |||||||||   ||||| |  |||
                                AGATTTAGG   CAAAA C  ACC
                                     TC_    _ AC
GAM845  HSA250839 3'  TCTGCATCTGATGTTTTCA   22591     AA
                                TCT  ATCTGATGTTTTTG
                                |||  ||||||||||||||
                                AGA  TAGACTACAAAAGT
                                  CG
GAM845  KIAA0534  3'  TCTAAATCTGTATGTTTTTG   22592          _
                                TCTAAATCTG ATGTTTTTG
                                |||||||||| |||||||||
                                AGATTTAGAC TACAAAAAC
                                      A
GAM845  KIAA1210  3'  TCTGGATTTTTTTGCATG    22593      _ G
                                TCTG AT TTTTTGCATG
                                |||| || ||||||||||
                                AGAC TA AAAAACGTAC
                                  C  A
GAM845  MBLR     3'  TAAAACTGAAGTCTTTGCATGG 22594      T    T
                                TAAA CTGA GTTTTTGCATGG
                                |||| |||| ||||||||||||
                                ATTT GACT CAGAAACGTACC
                                  T    T
GAM845  LOC166824 3'  TAAATTTGAGTTCATTACATGG 22595       C   T    _
                                TAAAT TGA GTTT TTGCATGG
                                ||||| ||| |||| ||||||||
                                ATTTA ACT CAAG AATGTACC
                                   A   _    T
GAM845  LOC257486 3'  TCTGGATTTTTTTGCATG    22593      _ G
                                TCTG AT TTTTTGCATG
                                |||| || ||||||||||
                                AGAC TA AAAAACGTAC
                                  C  A
GAM846  AXIN1    3'  CCTGGCCGTGACACCCGTG    22598    C       G  GAG
                                CC GGCCGTGA CG   CCGTG
                                || |||||||| ||   |||||
                                GG CCGGCACT GT   GGCAC
                                 A       _ G__
GAM846  BAIAP3   3'  TCCCCGGCCTGGGAGCCCCG   22599          G  AGC     G
                                TCCCCGGCC TG   GGAGCC TG
                                ||||||||| ||   |||||| ||
                                AGGGGCCGG AC   CCTCGG GC
                                      _ ___      G
GAM846  INMT     3'  GGGCGTGAGCAAGCTGAGCTGT 22600    C       _____    C
             G                    GG CGTGAGCG    GAGC GTG
                                || ||||||||    |||| |||
```

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                                CC GCACTCGT   CTCG CAC
                                 C       TCGA   A
GAM846  NMB      5'  GCCCTGAGCAGCGGAGCCGTG  22601    G   ___
                                GCC TGAGC   GGAGCCGTG
                                ||| |||||   |||||||||
                                CGG ACTCG   CCTCGGCAC
                                  G    TCG
GAM846  TERF2    5'  TCCTCGGCTGTGACGCCGC   22602    C   C   GCGGA
                                TCC CGGC GTGA    GCCGT
                                ||| |||| ||||    |||||
                                AGG GCCG CACT    CGGCG
                                  A   A   G____
GAM846  KIAA1300 3'  TCCCCGGCTCTGCTGGCTGTG  22603       CGTGA  GGA  C
                                TCCCCGGC    GC   GC GTG
                                ||||||||    ||   || |||
                                AGGGGCCG    CG   CG CAC
                                     AGA__  AC_  A
GAM846  KIAA1602 3'  TCCCCAGCTCCAGCGGGGCCGT 22604       CGTG    A
             G                   TCCCCGGC   AGCGG GCCGTG
                                 ||||||||   ||||| ||||||
                                 AGGGGTCG   TCGCC CGGCAC
                                     AGG_    C
GAM846  KIAA1705 5'  CCGGCGGCGCGCGGAGCCGTG  22605     C   A
                                CCGGC GTG GCGGAGCCGTG
                                ||||| ||| ||||||||||
                                GGCCG CGC CGCCTCGGCAC
                                   C   G
GAM846  PRKCZ    3'  TCCCTGGCCGCCCTCGGAGCCG 22606     C     GAG
             TG                   TCCC GGCCGT   CGGAGCCGTG
                                  ||||  ||||||   ||||||||||
                                  AGGG CCGGCG   GCCTCGGCAC
                                    A     GGA
GAM846  LOC151438 5'  TCCCCGGCCTCCTGTTGGGCTG 22607       GTGAGC_  A  C
             TG                   TCCCCGGCC      GG GC GTG
                                  |||||||||      || || |||
                                  AGGGGCCGG      CC CG CAC
                                       AGGACAA  _  A
GAM846  LOC163126 5'  TCCCCGGCCTCCTCAGGCTGTG 22608       GTGAG   A  C
                                TCCCCGGCC    CGG GC GTG
                                |||||||||    ||| || |||
                                AGGGGCCGG    GTC CG CAC
                                     AGGA_   _  A
GAM846  LOC256477 5'  TCCCCAGCCGGAGGGTCGT   22609        T   C  AGC
                                TCCCCGGCCG GAG GG   CGT
                                |||||||||| ||| ||   |||
                                AGGGGTCGGC CTC CC   GCA
                                      _   _  A__
GAM847  ACCN2    5'  GACCGGTGGCGGGCTCAGCG   22612    A        G
                                GAC CGGTGGCGGGC CGGTG
                                ||| |||||||||| |||||
```

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                                CTG GCCACCGCCCG GTCGC
                                  _       A
GAM847  COG7    3'  GCATGGTGGCCACGGTGG    22613   A  C    GGG
                                G CA GGTGGC  CGCGGTGG
                                | || ||||||  ||||||||
                                C GT CCACCG  GTGCCACC
                                 _ A    ___
GAM847  CTBP2   5'  GGCGGCGGTGGCGGTGGC    22614       GC
                                GGTGGCGG  GCGGTGGC
                                ||||||||  ||||||||
                                CCGCCGCC  CGCCACCG
                                     AC
GAM847  CTGF    5'  GGAGCGGAGGGCGCGGTGGCG  22615   C    C
                                A GGTGG GGGCGCGGTGGCG
                                | ||||| ||||||||||||
                                C TCGCC CCCGCGCCACCGC
                                 C    T
GAM847  CYP26A1 5'  CAGAGGCGGCGCGGTGGCG   22616    T    G
                                CGG GGCGG CGCGGTGGCG
                                ||| ||||| ||||||||||
                                GTC CCGCC GCGCCACCGC
                                  T    _
GAM847  DRPLA   3'  CACGGTGGGGGGAGGGTG    22617       C   CGC
                                CACGGTGG GGG   GGTG
                                |||||||| |||   ||||
                                GTGCCACC CCC   CCAC
                                     _  CTC
GAM847  ELK1    5'  GGTGGTGGTGGCGGTGGCG   22618      C  GC
                                GGTGG GG  GCGGTGGCG
                                ||||| ||  |||||||||
                                CCACC CC  CGCCACCGC
                                   A  AC
GAM847  ENO2    5'  GGTGGCGGTGGCGGTGGC    22619       GC
                                GGTGGCGG  GCGGTGGC
                                ||||||||  ||||||||
                                CCACCGCC  CGCCACCG
                                     AC
GAM847  GAL     5'  GGTCCGGGTGCGGTGGC     22620     GG   C
                                GGT  CGGG GCGGTGGC
                                |||  |||| ||||||||
                                CCA  GCCC CGCCACCG
                                  G_   A
GAM847  IRS1    3'  GACACGGTGGTGGGCACATCAG 22621         C      GT
                                GACACGGTGG GGGCGCG  GG
                                |||||||||| |||||||  ||
                                CTGTGCCACC CCCGTGT  TC
                                      A      AG
GAM847  LGMN    5'  GACCGTGGTGGCAGTGGTGGCG 22622     AC_      GCGC
                                GAC   GGTGGCGG   GGTGGCG
                                |||   ||||||||   |||||||
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                                CTG  CCACCGTC   CCACCGC
                                  GCA      A___
GAM847  MAF     5'  CGGTGGCGGCGGTGG      22623        GGC
                                CGGTGGCG  GCGGTGG
                                ||||||||  |||||||
                                GCCACCGC  CGCCACC
                                     ___
GAM847  MAPRE3  5'  GACAGGTGGCGGGGGCG    22624     C       C
                                GACA GGTGGCGGG GCG
                                |||| ||||||||| |||
                                CTGT CCACCGCCC CGC
                                  _       C
GAM847  PKIG    3'  CACGGTGCGAAGGTGG     22625       G   CGC
                                CACGGTG CGGG  GGTGG
                                ||||||| ||||  |||||
                                GTGCCAC GCTT  CCACC
                                   _  ___
GAM847  PTMS    5'  CGGAACCTGGCGCGGTGGCG  22626    T  G_
                                CGG GGC  GGCGCGGTGGCG
                                ||| |||  ||||||||||||
                                GCC TTG  CCGCGCCACCGC
                                  _  GA
GAM847  PYGB    3'  CACAGTGGTGGTCAGGGTGG  22627       C  G  C
                                CACGGTGG GG CG GGTGG
                                |||||||| || || |||||
                                GTGTCACC CC GT CCACC
                                     A  A  C
GAM847  RRP22   5'  GACAGGTGGCGGGCGCG    22628     C
                                GACA GGTGGCGGGCGCG
                                |||| ||||||||||||
                                CTGT CCACCGCCCGCGC
                                  _
GAM847  SLC20A2 3'  GGTGTGGTGGCGGTGGCA   22629     GC  GC
                                GGTG  GG  GCGGTGGCG
                                ||||  ||  |||||||||
                                CCAC  CC  CGCCACCGT
                                  A_  AC
GAM847  SLC6A8  5'  GGTGGCGGCGGCGGCGGTGGCG 22630        __  _
                                GGTGGCGG  GCG CGGTGGCG
                                ||||||||  ||| ||||||||
                                CCACCGCC  CGC GCCACCGC
                                     GC  C
GAM847  SLC7A8  3'  GCACGGTGGGGCGGTGG    22631   A    GGC  C
                                G CACGGT  GGG GCGGTGG
                                | ||||||  ||| |||||||
                                C GTGCCA  CCC CGCCACC
                                  _    ___  _
GAM847  STK10   5'  GGCCGGGGGCGCGGTGGC   22632    _  C
                                GGT GG GGGCGCGGTGGC
                                ||| || ||||||||||||
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                                CCG CC CCCGCGCCACCG
                                  G  _
GAM847  USF2     3'  GGCGGCGGCTGCGTGGTGG   22633        __  C
                                GGTGGCGG  GCG GGTGG
                                ||||||||  ||| |||||
                                CCGCCGCC  CGC CCACC
                                    GA   A
GAM847  WNT1     5'  GACGCGGCGGTGGCGGCAGTGG 22634     A     CG   _
              CG                  GAC CGGTGG  GGCG CGGTGGCG
                                ||| ||||||  |||| ||||||||
                                CTG GCCGCC  CCGC GTCACCGC
                                  C     A_   C
GAM847  ASTN2    5'  GGCGGCGGTGGCGGCGGTGGCG 22635        __  _
                                GGTGGCGG  GCG CGGTGGCG
                                ||||||||  ||| ||||||||
                                CCGCCGCC  CGC GCCACCGC
                                    AC   C
GAM847  C6orf5   3'  CATGGTGGCAGGCGCCTATAG  22636    C         G_
                                CA GGTGGCGGGCGC  GTGG
                                || ||||||||||||  ||||
                                GT CCACCGTCCGCG  TATC
                                 A          GA
GAM847  CEP3     5'  GGCGCGGGGCGGGGC      22637     G   C   T
                                GGTG CGGG GCGG GGC
                                |||| |||| |||| |||
                                CCGC GCCC CGCC CCG
                                  _   _   _
GAM847  CNOT7    5'  CGGTGGCGGTGGCGGTGGCG   22638        GC
                                CGGTGGCGG  GCGGTGGCG
                                |||||||||  |||||||||
                                GCCACCGCC  CGCCACCGC
                                    AC
GAM847  CNOT7    5'  CGGTGGCGGTGGCGGTGGCG   22638        GC
                                CGGTGGCGG  GCGGTGGCG
                                |||||||||  |||||||||
                                GCCACCGCC  CGCCACCGC
                                    AC
GAM847  dJ383J4.3 5'  GACGCGGGGCGGGCCCTGCG   22639     A  T     GCG
                                GAC CGG GGCGGGC   GTG
                                ||| ||| |||||||   |||
                                CTG GCC CCGCCCG   CGC
                                  C   _      GGA
GAM847  DKFZP434N1817 5'  GACGTGGTGGTGCTGGTGG   22640     ACG   C  _  GC
                                GAC   GTGG GG GC  GGTGG
                                |||   |||| || ||  |||||
                                CTG   CACC CC CG  CCACC
                                  ____   A  A  A_
GAM847  DKFZp761B1514 3'  CAGGTGGCGGGTCGGTG     22641    C        CG
                                CA GGTGGCGGG  CGGTG
                                || |||||||||  |||||
```

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                                GT CCACCGCCC  GCCAC
                                 _       A_
GAM847  DPYSL4   3' GACTGGTGGTGGGGAGGCG   22642     AC    C   CGC
                                GAC  GGTGG GGG   GGTG
                                |||  ||||| |||   ||||
                                CTG  CCACC CCC   CCGC
                                  A_    A   CT_
GAM847  FLJ12750 3' ATGGGGGCGGGTGGCA      22643     C    C
                                GTGG GGGCG GGTGGCG
                                |||| ||||| |||||||
                                TACC CCCGC CCACCGT

                                  _    _
GAM847  FLJ14564 3' GGTGGGTGGTGTCCACGGTGG  22644      CG ____
                                GGTGG  GG    CGCGGTGG
                                |||||  ||    ||||||||
                                CCACC  CC    GTGCCACC
                                   CA  ACAG
GAM847  HUMAGCGB 5' GGCGTGCTGGCGGGCCTCG    22645     _ G    C   GG
                                GGTG GC GGCG GGT  CG
                                |||| || |||| |||  ||
                                CCGC CG CCGC CCG  GC
                                  A  A    _   GA
GAM847  HUMZD58C02 5' GGTGGCGGGGTCAGGTGGCG   22646         CG _
                                GGTGGCGGG  C GGTGGCG
                                |||||||||  | |||||||
                                CCACCGCCC  G CCACCGC
                                     CA T
GAM847  KIAA0664 3' GACACGGGGGGTGGGGTGGGGTG 22647        T  C   CGC_
                                GACACGG GG GGG    GGTG
                                ||||||| || |||    ||||
                                CTGTGCC CC CCC    CCAC
                                    C  A   CACC
GAM847  KIAA1817 3' CAGCGGTGGTGGCGGTGG    22649       C  GC
                                CGGTGG GG  GCGGTGG
                                ||||||  ||  |||||||
                                GTCGCC CC  CGCCACC
                                   A  AC
GAM847  KIAA1817 3' CGGTGGTGGTGGCAGCGGTGG  22648       CG__  _
                                CGGTGG    GGC GCGGTGG
                                ||||||    ||| |||||||
                                GCCACC    CCG CGCCACC
                                   ACCA   T
GAM847  KIAA1853 5' GGCAGCGGTGATGGCGGTGGCG 22650    TG   GC___
                                GG  GCGG    GCGGTGGCG
                                ||  ||||    |||||||||
                                CC  CGCC    CGCCACCGC
                                 GT    ACTAC
GAM847  KIAA1877 3' GGAATGACCGGGCGCGGTGG   22651   C     _
                                A GGTGGC GGGCGCGGTGG
                                | |||||| ||||||||||
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                                C TTACTG CCCGCGCCACC
                                 C     G
GAM847  KIAA1904  3'  GGGGTGGGCACAGGGCG     22652    T  C      T
                                GG GG GGGCGCGG GGCG
                                || || |||||||| ||||
                                CC CC CCCGTGTC CCGC
                                 _  A      _
GAM847  MGC35558  5'  GGTGGCGGGAGGGGCG      22653         CGC  T
                                GGTGGCGGG   GG GGCG
                                |||||||||   || ||||
                                CCACCGCCC   CC CCGC
                                      T__  _
GAM847  OSBPL10   5'  GACGCGGGTGCCCGCCGCGGTG 22654     A   TG  GG  _
           GCG                    GAC CGG  GC  GC GCGGTGGCG
                                ||| |||  ||  || |||||||||
                                CTG GCC  CG  CG CGCCACCGC
                                  C   CA  GG  G
GAM847  PDE8A     5'  GACACGCTGGCGGGTAGCCGCG 22655       G      CGC   G
                                GACACG TGGCGGG   GGT GCG
                                |||||| |||||||   ||| |||
                                CTGTGC ACCGCCC   TCG CGC
                                   G      A__   G
GAM847  RAB11B    3'  GATACCGTGGCGGGGGCG    22656    C  G       C
                                GA AC GTGGCGGG GCG
                                || || |||||||| |||
                                CT TG CACCGCCC CGC
                                 A  G       C
GAM847  SAST      5'  GACATGGTGGCAGGTGCG    22657      C        C
                                GACA GGTGGCGGG GCG
                                |||| ||||||||| |||
                                CTGT CCACCGTCC CGC
                                  A        A
GAM847  SUI1      5'  CGGTGGCGGGAGAAGGCG    22658          CGC  T
                                CGGTGGCGGG   GG GGCG
                                ||||||||||   || ||||
                                GCCACCGCCC   CT CCGC
                                      T__  T
GAM847  TBC1D1    5'  CATGGGGCGGGTTGGGGCG   22659    C  T     CGC  T
                                CA GG GGCGGG   GG GGCG
                                || || ||||||   || ||||
                                GT CC CCGCCC   CC CCGC
                                 A  _     AA_  _
GAM847  LOC130612 5'  GGTGTCGGCGCGGTGGCG    22660      GCG
                                GGTG   GGCGCGGTGGCG
                                ||||   ||||||||||||
                                CCAC   CCGCGCCACCGC
                                  AG_
GAM847  LOC131377 5'  GGTGGCCTAGGGTGCGGTGGCG 22661        ___   C
                                GGTGGC   GGG GCGGTGGCG
                                ||||||   ||| |||||||||
```

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                                CCACCG   CCC CGCCACCGC
                                   GAT   A
GAM847   LOC144596 3'  GGCGGCGGCTGCGTGGTGG   22633        __   C
                                GGTGGCGG  GCG GGTGG
                                ||||||||  ||| |||||
                                CCGCCGCC  CGC CCACC
                                    GA   A
GAM847   LOC146227 5'  GGTGGCGGTGGTGGCGGTGGCG 22662        GC___
                                GGTGGCGG    GCGGTGGCG
                                ||||||||    |||||||||
                                CCACCGCC    CGCCACCGC
                                    ACCAC
GAM847   LOC146950 5'  GACCGGTGGCGGGTGCAG    22663    A        C
                                GAC CGGTGGCGGG GCGG
                                ||| |||||||||| ||||
                                CTG GCCACCGCCC CGTC
                                  _        A
GAM847   LOC151816 5'  ACGGTGGTAGCACTGGTGG   22664       CG    _
                                ACGGTGG  GGCGC GGTGG
                                |||||||  ||||| |||||
                                TGCCACC  TCGTG CCACC
                                   A_    A
GAM847   LOC165721 3'  GCACGGTGGTGGTGGTG    22665   A      C  GCGC
                                G CACGGTGG GG    GGTG
                                | ||||||||  ||    ||||
                                C GTGCCACC CC    CCAC
                                _       A  A___
GAM847   LOC199786 3'  GGTGGCGGGTTGTGGGCG    22666        CGCG   _
                                GGTGGCGGG    GTGG CG
                                |||||||||    |||| ||
                                CCACCGCCC    CACC GC
                                     AA__    C
GAM847   LOC199964 5'  GCAGGTGAAGGTGTGGTGG   22667   A  C    C  GCGC
                                G CA GGTGG GG    GGTGG
                                | || |||||  ||    |||||
                                C GT CCACT CC    CCACC
                                _ _    T  ACA_
GAM847   LOC200491 5'  GTGACTGGGTGCGGTGGC    22668      _  C
                                GTGGC GGG GCGGTGGC
                                |||||  ||| ||||||||
                                CACTG CCC CGCCACCG
                                   A   A
GAM847   LOC219445 5'  CACGGTGGCGGGAGCCTATAG  22669          C  G_
                                CACGGTGGCGGG GC  GTGG
                                ||||||||||||  ||  ||||
                                GTGCCACCGCCC CG  TATC
                                       T  GA
GAM847   LOC219575 5'  GACGCGGGGCGCCAGCAGGTGG 22670    A  T   __   C
            CG                    GAC CGG GGCG  GGCG GGTGGCG
                                ||| ||| ||||  |||| |||||||
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                                CTG GCC CCGC  TCGT CCACCGC
                                  C  _   GG   _
GAM847  LOC219690 5'  GACACGGTGGCTGGCGTG    22671         G  GCG
                                GACACGGTGGC GGC  GTG
                                |||||||||| ||| |||
                                CTGTGCCACCG CCG  CAC
                                      A  ___
GAM847  LOC221692 3'  CACGGGGCGGGGCGGGGCG   22672      T    C   T
                                CACGG GGCGGG GCGG GGCG
                                ||||| |||||| |||| ||||
                                GTGCC CCGCCC CGCC CCGC
                                  _    _   _
GAM847  LOC222681 5'  CGTGTGGTGTTGCAGTGGCG  22673   _   CGGGC
                                CG GTGG    GCGGTGGCG
                                || ||||    |||||||||
                                GC CACC    CGTCACCGC
                                 A   ACAA_
GAM847  LOC257054 5'  GACACGGTGGGCGGGCCGTG  22674        _   G  G
                                GACACGGTGG CGGGC CG TG
                                |||||||||| ||||| || ||
                                CTGTGCCACC GCCCG GC AC
                                      C    _ _
GAM847  LOC257507 5'  CGTGTGGTGTTGCAGTGGCG  22673   _   CGGGC
                                CG GTGG    GCGGTGGCG
                                || ||||    |||||||||
                                GC CACC    CGTCACCGC
                                 A   ACAA_
GAM847  LOC257625 5'  CGTGTGGTGTTGCAGTGGCG  22673   _   CGGGC
                                CG GTGG    GCGGTGGCG
                                || ||||    |||||||||
                                GC CACC    CGTCACCGC
                                 A   ACAA_
GAM847  LOC56270  3'  CAGGTGGTGGGTGCTGTGGCG 22675   C    C   C  G
                                CA GGTGG GGG GC GTGGCG
                                || ||||| ||| || ||||||
                                GT CCACC CCC CG CACCGC
                                 _   A  A  A
GAM847  LOC91397  5'  GTGGGGGTGGGCGGTGGCG   22676    C  C__
                                GTGG GGG  GCGGTGGCG
                                |||| |||  |||||||||
                                CACC CCC  CGCCACCGC
                                  _  ACC
GAM848  AF5Q31    5'  TCGAGCCCGCCCAGGGGGCGG 22679       G G  AGAA
                                TCGGGCCCG C CGG   GGCGG
                                ||||||||| | |||   |||||
                                AGCTCGGGC G GTC   CCGCC
                                     _ G  CC__
GAM848  ARHGAP6   3'  GGGCCCGGGTATGGAGGCGG  22680       CGC_  GAA
                                GGGCCCGG   GGA  GGCGG
                                ||||||||   |||  |||||
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                                CCCGGGCC   CCT  CCGCC
                                    CATA  ___
GAM848  ATP6V0C  3' CGGGCCCGGCGGTGAGGGCGG 22681        CG  AA
                                CGGGCCCGGCG GAG GGCGG
                                |||||||||| ||| |||||
                                GCCCGGGCCGC CTC CCGCC
                                     CA  __
GAM848  CACNA1A  5' TCGGGTCGGGGGCTCAGAAGGC 22682     CC  C_ GG
          GG                  TCGGG CGG GC AGAAGGCGG
                              ||||| ||| || |||||||||
                              AGCCC GCC CG TCTTCCGCC
                                A_  CC AG
GAM848  CACNA1A  5' TCGGGTCGGGGGCTCAGAAGGC 22682     CC  C_ GG
          GG                  TCGGG CGG GC AGAAGGCGG
                              ||||| ||| || |||||||||
                              AGCCC GCC CG TCTTCCGCC
                                A_  CC AG
GAM848  CIAO1    5' GGCCCGACGCAGGGGGAGGTGG 22683         AGA_  C
                              GGCCCGGCGCGG   AGG GG
                              |||||||||||   ||| ||
                              CCGGGCTGCGTC   TCC CC
                                    CCCC  A
GAM848  CIAO1    5' GGCCCGACGCAGGGGGAGGTGG 22683         AGA_  C
                              GGCCCGGCGCGG   AGG GG
                              |||||||||||   ||| ||
                              CCGGGCTGCGTC   TCC CC
                                    CCCC  A
GAM848  DES      5' CGGGCGCACGGAGGAGGCGG  22684     CCG     A
                              CGGGC  GCGCGGAG AGGCGG
                              |||||  |||||||| ||||||
                              GCCCG  CGTGCCTC TCCGCC
                                 ___      C
GAM848  FES      5' TCAGGCCCGGTGCGGACCCCGG 22685        C   GAAGG
                              TCGGGCCCGG GCGGA   CGG
                              |||||||||| |||||   |||
                              AGTCCGGGCC CGCCT   GCC
                                    A   GGG__
GAM848  GRB14    5' GCAAGGCGCGGAGGGGGCG  22686   CC      AA
                              GC GGCGCGGAG GGCG
                              ||  |||||||||  ||||
                              CG CCGCGCCTC CCGC
                               TT       CC
GAM848  GUCY1A2  5' TCGCGCCCGGCGGGGC     22687    G     C AGAAG
                              TCG GCCCGGCG GG   GC
                              ||| |||||||| ||   ||
                              AGC CGGGCCGC CC   CG
                                G      _ ______
GAM848  GUK1     5' GGGCCCGGCCCAGGGCG     22688        G  AGAA
                              GGGCCCGGC CGG   GGCG
                              ||||||||| |||   ||||
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                                CCCGGGCCG GTC   CCGC
                                     G  ____
GAM848  HSF4    5'  TCGGGCCCGGCCGCTGCG   22689          G  GAGAAG
                                TCGGGCCCGGC CG     GCG
                                |||||||||| ||     |||
                                AGCCCGGGCCG GC     CGC
                                      _  GA____
GAM848  IGF2    5'  GGTTCGGCGAAGGCGAGAGGGC 22690   GCC    CG___   A
           GG                    GG   CGGCG    GAGA GGCGG
                                ||   |||||    |||| |||||
                                CC   GCCGC    CTCT CCGCC
                                 AA_    TTCCG   C
GAM848  LFNG    3'  GGGCCCAGCGGGGAGGTGG   22691          C  A  A  C
                                GGGCCCGGCG GG GA GG GG
                                |||||||||| || || || ||
                                CCCGGGTCGC CC CT CC CC
                                      _  _  _  A
GAM848  MAPK8IP1  5'  CGGAGCGCGGCGCGGAGGAGGC 22692    _  C        A
           GG                    CGG GC CGGCGCGGAG AGGCGG
                                ||| || |||||||||| ||||||
                                GCC CG GCCGCGCCTC TCCGCC
                                  T  C        C
GAM848  MPP1    5'  GCGGGGCTGCGGAGAAGGCGG  22693   CC  _
                                GC  GGC GCGGAGAAGGCGG
                                ||  ||| ||||||||||||
                                CG  CCG CGCCTCTTCCGCC
                                 CC   A
GAM848  RNMT    3'  GGGCTGCTAAAGAAGGTGG   22694    CCG  GC      C
                                GGGC   GC  GGAGAAGG GG
                                ||||   ||  |||||||| ||
                                CCCG   CG  TTTCTTCC CC
                                  A__  A_      A
GAM848  RNPEPL1   5'  CCGGGCGCCTCGGGGAAGGCGG 22695      _  GG  C  A
                                TCGGGC CC  CG GG GAAGGCGG
                                |||||| ||  || || ||||||||
                                GGCCCG GG  GC CC CTTCCGCC
                                    C  A_  _  _
GAM848  SH3GL1   3'  TCGGGTCAGGACGGAGGTGG   22696     CC   C    AA
                                TCGGG  CGG GCGGAG  GG
                                |||||  ||| ||||||  ||
                                AGCCC  GTC TGCCTC  CC
                                   A_   C     CA
GAM848  YWHAG    5'  GGCGGCTGCGCGGAGGAGGCGG 22697    CCG_      A
                                GGC    GCGCGGAG AGGCGG
                                |||    |||||||| ||||||
                                CCG    CGCGCCTC TCCGCC
                                  CCGA       C
GAM848  ZNF42    5'  GGGCCTGGAGAAGGCG      22698       CGGCGC
                                GGGCC     GGAGAAGGCG
                                |||||     ||||||||||
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                                CCCGG     CCTCTTCCGC
                                  A_____
GAM848  C20orf124 3'  GGTCCCGGCGCGGGTGTCTCGG 22699    G        AGAAGG
                                GG CCCGGCGCGG     CGG
                                || ||||||||||     |||
                                CC GGGCCGCGCC     GCC
                                 A         CACAGA
GAM848  FLJ20584  3'  CCGGGCCTGGCGTGCGGGAGGC 22700       C  __   A A
          GG                      TCGGGCC GGC  GCGG GA GGCGG
                                ||||||| |||  |||| || |||||
                                GGCCCGG CCG  CGCC CT CCGCC
                                   A  CA   _ _
GAM848  HSU24186  5'  TCAGGCTGAGGAGAAGGG    22701       CC  CGC       C
                                TCGGGC  GG   GGAGAAGG G
                                ||||||  ||   |||||||| |
                                AGTCCG  CT   CCTCTTCC C
                                   A_ ___       A
GAM848  KIAA0637  5'  GGCCCGGCCTCTGGGGCGG   22702       GC__  AGAA
                                GGCCCGGC   GG   GGCGG
                                ||||||||   ||   |||||
                                CCGGGCCG   CC   CCGCC
                                    GAGA  ____
GAM848  KIAA1297  3'  GGGCTTGGGCTCTGAAGGCGG  22703     CC  C  GGA
                                GGGC  GG GC   GAAGGCGG
                                ||||  || ||   ||||||||
                                CCCG  CC CG   CTTCCGCC
                                  AA  _  AGA
GAM848  LIM     5'  TCGGGTCCGGCGCGGCGCG   22704      C       AGAAG
                                TCGGG CCGGCGCGG    GCG
                                ||||| |||||||||    |||
                                AGCCC GGCCGCGCC    CGC
                                  A       G____
GAM848  MGC1842  3'  CGGGCCCGGCTGGGGG     22705        GC  AGAA  C
                                CGGGCCCGGC  GG   GG G
                                ||||||||||  ||   || |
                                GCCCGGGCCG  CC   CC C
                                    A_  ____  A
GAM848  PLCL2    5'  CGGGCCCGGGGAGGTGG     22706        CGC   AA
                                CGGGCCCGG   GGAG  GG
                                |||||||||   ||||  ||
                                GCCCGGGCC   CCTC  CC
                                    ___    CA
GAM848  TGIF2    5'  TCCGGCTCGGCGCGGGGCG   22707    G  C      AGAA
                                TC GGC CGGCGCGG    GGCG
                                || ||| ||||||||    ||||
                                AG CCG GCCGCGCC    CCGC
                                 G  A       _____
GAM848  TGOLN2   3'  CCGGGCCCCAGGGAGGGG    22708       GG  C   AA  C
                                TCGGGCCC  CG GGAG  GG G
                                ||||||||  || ||||  || |
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                                GGCCCGGG  GT CCTC  CC C
                                   __ C   __ A
GAM848  VPS4A    5'  GGGTCCGGCGCGGGAAGCCCGG 22709    C       A  ____
           CGG                    GGG CCGGCGCGG GAA   GGCGG
                                ||| ||||||||| |||   |||||
                                CCC GGCCGCGCC CTT   CCGCC
                                  A       _  CGGG
GAM848  LOC118987 5'  TCGGGCCGGCGCGCTGCG    22710       C    GAGAAG
                                TCGGGCC GGCGCG     GCG
                                |||||||| ||||||     |||
                                AGCCCGG CCGCGC     CGC
                                   _     GA____
GAM848  LOC133383 5'  CCAGGACGGCGCGGGGAAGGCG 22711      CC       A
           G                     TCGGG  CGGCGCGG GAAGGCGG
                                ||||||  |||||||| ||||||||
                                GGTCC  GCCGCGCC CTTCCGCC
                                  T_       C
GAM848  LOC148479 3'  GGTGCTTCAGTGGGAGAAGGTG 22712    _ C_   CGC       C
           G                     GG GC  CGG   GGAGAAGG GG
                                || ||  |||   |||||||| ||
                                CC CG  GTC   CCTCTTCC CC
                                 A  AA   AC_       A
GAM848  LOC149483 3'  GGGCCCGGGAGCAGGAGGTGG  22713        C_   A  A  C
                                GGGCCCGG  GCGG GA GG GG
                                ||||||||  |||| || || ||
                                CCCGGGCC  CGTC CT CC CC
                                     CT    _ _ A
GAM848  LOC93166  5'  CGGGCCCGGGGCCGGAGGTGG  22714         C  _   AA
                                CGGGCCCGG GC GGAG  GG
                                |||||||||| || ||||  ||
                                GCCCGGGCC CG CCTC  CC
                                     C  G    CA
GAM849  CENPC1    3'  TACATATATACATACATATA   22717      T      _
                                TACAT ATATACAT TATATA
                                ||||| |||||||| ||||||
                                ATGTA TATATGTA GTATAT
                                   _       T
GAM849  CRIM1     3'  TATATATATTATATACAC    22718       C
                                TATATA ATTATATACAT
                                |||||| ||||||||||
                                ATATAT TAATATATGTG
                                   A
GAM849  PCDH8     3'  CATTATATACAAACATTACATT 22719           TT   _
                                CATTATATACA  ATAT ACATT
                                ||||||||||  |||| |||||
                                GTAATATATGT  TGTA TGTAA
                                      T_   A
GAM849  PDE4B     5'  TACAAAACATTACATTATATAC 22720      TT   _
           ATT                    TACA  ATAT ACATTATATACATT
                                ||||  |||| ||||||||||||||
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                                ATGT  TGTA TGTAATATATGTAA
                                  TT    A
GAM849  PDE4B    3'  TACAAAACATTACATTATATAC 22720      TT    _
              ATT                  TACA  ATAT ACATTATATACATT
                                |||||  |||| ||||||||||||||
                                ATGT  TGTA TGTAATATATGTAA
                                  TT    A
GAM849  RNTRE    3'  CATTATATACATAAAATATA   22721           T__
                                CATTATATACAT   ATATA
                                ||||||||||||   |||||
                                GTAATATATGTA   TATAT
                                       TTT
GAM849  C1orf22  3'  TAATTATATACAGGATTATATA 22722    C        ___
              CATT                   A ATTATATACA   TTATATACATT
                                | ||||||||||   ||||||||||
                                A TAATATATGT   AATATATGTAA
                                 T         CCT
GAM849  CKS2     3'  TACCTTATATACACATATACAT 22723     A        T
              T                   TAC TTATATACAT ATATACATT
                                ||| |||||||||| |||||||||
                                ATG AATATATGTG TATATGTAA
                                  G         _
GAM849  FLJ10292 3'  TACATTCATACATACATATA   22724       A      _
                                TACATT TATACAT TATATA
                                |||||| ||||||| ||||||
                                ATGTAA GTATGTA GTATAT
                                    _       T
GAM849  FLJ11342 3'  ATTATATATACTTTATACATTA 22725         C   A       III
                                ATTATATA ATT TATACATT   A
                                |||||||| ||| ||||||||   |
                                TAATATAT TGA ATATGTAA   T
                                     A   A       III
GAM849  FLJ14011 3'  TACATTATAGACAAATACATA  22726          T   T_
                                TACATTATA ACA  TATATA
                                ||||||||| |||  ||||||
                                ATGTAATAT TGT  ATGTAT
                                     C   TT
GAM849  FLJ20729 3'  TACATTAATACATACATATA   22727        T     _
                                TACATTA ATACAT TATATA
                                ||||||| |||||| ||||||
                                ATGTAAT TATGTA GTATAT
                                    _     T
GAM849  H2AFJ    3'  TACAATATATACATATAT    22728      T       T
                                TACA TATATACAT ATAT
                                |||| ||||||||| ||||
                                ATGT ATATATGTA TATA
                                  T       _
GAM849  HYPH     3'  TTATATACAGATACACATT    22729          TT
                                TTATATACA  ATATACATT
                                |||||||||  |||||||||
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                                AATATATGT  TATGTGTAA
                                     C_
GAM849  KIAA0475  3'  CATATACGACTATATACATT  22730       _
                                TATATAC ATTATATACATT
                                ||||||| ||||||||||||
                                GTATATG TGATATATGTAA
                                    C
GAM849  MAN1      3'  TACATATATACACACACAT   22731      T      TAT
                                TACAT ATATACAT   ATACAT
                                ||||| ||||||||   ||||||
                                ATGTA TATATGTG   TGTGTA
                                  _      ____
GAM849  PDE10A    3'  CATATATACACATATGTATAC  22732    _       TA_
                                CAT TATATACAT   TATAC
                                ||| |||||||||   |||||
                                GTA ATATGTGTA   ATATG
                                  T       TAC
GAM849  SMBP      3'  TACATTATTTAATGTTATATAC 22733       A  CA_        III
           ATTA                    CATTAT TA   TTATATACATT   A
                                ||||||| ||   ||||||||||||   |
                                GTAATA AT   AATATATGTAA   T
                                    A  TAC         III
GAM849  STOML1    3'  TACATTGTAAACACCACAT    22734       A  T
                                TACATT TA ACATTATAT
                                |||||| || |||||||||
                                ATGTAA AT TGTGGTGTA
                                    C  T
GAM849  TOPBP1    3'  TACATATATACACACATAT    22735      _       T
                                TACAT TATATACAT ATAT
                                ||||| ||||||||| ||||
                                ATGTA ATATGTGTG TATA
                                   T       _
GAM849  LOC130619 3'  TACATTATGGTACAGGCACACA 22736        A_    TTA
           TT                     TACATTAT  TACA   TATACATT
                                ||||||||  ||||   ||||||||
                                ATGTAATA  ATGT   GTGTGTAA
                                     CC    CC_
GAM849  LOC154214 3'  TTATATACACACACAT      22737         TAT
                                TTATATACAT   ATACAT
                                ||||||||||   ||||||
                                AATATATGTG   TGTGTA
                                     ____
GAM849  LOC168537 3'  CACATTATATACATTAAACAT  22738             TAT
                                TACATTATATACATTA   ACAT
                                ||||||||||||||||   ||||
                                GTGTAATATATGTAAT   TGTA
                                          T__
GAM849  LOC199729 3'  TACATCATATACATATAT    22739             T
                                TACATTATATACAT ATAT
                                |||||||||||||| ||||
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                                ATGTAGTATATGTA TATA
                                              _
GAM849  LOC201810 3'  TATATACTTTATTATATACATT 22740       ___
                                TATATAC   ATTATATACATT
                                |||||||   ||||||||||||
                                ATATATG   TAATATATGTAA
                                    AAA
GAM849  LOC257130 3'  TACATCATATACGTATAT    22741          AT
                                TACATTATATAC  TATAT
                                ||||||||||||  |||||
                                ATGTAGTATATG  ATATA
                                      C_
GAM849  LOC51136  3'  TACATTAGGTTGAACATTATAT 22742       TAT___
          A                      TACATTA     ACATTATATA
                                |||||||     ||||||||||
                                ATGTAAT     TGTAATATAT
                                    CCAACT
GAM850  ANXA5     3'  GAAGGAAGGCAGTGGGGT    22745         ___
                                GAAGGGGGGT   GGGGT
                                ||||||||||   |||||
                                CTTCCTTCCG   CCCCA
                                     TCA
GAM850  C18orf1   3'  CAGGAGGGGGCGGCTTGGT   22746     AA      ___
                                TAG  GGGGGGTGG   GGT
                                |||  |||||||||   |||
                                GTC  TCCCCCGCC   CCA
                                  C_       GAA
GAM850  CAPN10    3'  AGAAGGGGAAGCAGGGGT    22747         _ _
                                AGAAGGGGG GT GGGGT
                                ||||||||| || |||||
                                TCTTCCCCT CG CCCCA
                                     T  T
GAM850  COL1A1    3'  GAGGGGAGGCCAAGGGGGGTA  22748    A     _____    III
                                GA GGGGGGT    GGGGT   A
                                || |||||||    |||||   |
                                CT CCCTCCG    CCCCA   T
                                 C      GTTCC    III
GAM850  COX10     3'  CAGAATAGAGGGTGGGGT    22749      _
                                TAGAA GGGGGGTGGGGT
                                ||||| ||||||||||||
                                GTCTT TCTCCCACCCCA
                                   A
GAM850  CYP11B1   3'  AGAGGGGTGGCCTGGGGT    22750     A   _  __
                                AGA GGGG GGT  GGGGT
                                ||| |||| |||  |||||
                                TCT CCCC CCG  CCCCA
                                  _   A  GA
GAM850  EPB41     3'  AGAAGGGCAGAGTTGGGGT   22751        G  ___
                                AGAAGGG GG   TGGGGT
                                |||||||  ||   ||||||
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                                TCTTCCC TC   ACCCCA
                                    G  TCA
GAM850  GLUL     3'  GAAGGAATAAAGGTGGGGT   22752      ____
                                GAAGGG   GGGTGGGGT
                                ||||||   |||||||||
                                CTTCCT   TCCACCCCA
                                   TATT
GAM850  H1F0     3'  CAGAAGGGGGCAAAAGGT   22753        GT_
                                TAGAAGGGGG  GGGGT
                                ||||||||||  |||||
                                GTCTTCCCCC  TTCCA
                                      GTT
GAM850  HDGF     3'  TAGAAGAGGAGAGCAGGT   22754         TG_
                                TAGAAGGGGGG  GGGT
                                ||||||||||  ||||
                                ATCTTCTCCTC  TCCA
                                       TCG
GAM850  HNF3A    3'  TAGAGAGGACAAAGGGGT   22755     _  G  T
                                TAGA AGGG GG GGGGT
                                |||| |||| || |||||
                                ATCT TCCT TT CCCCA
                                  C   G  T
GAM850  HOXC10   3'  TAGATGGGGGATGTGGGG   22756     A   __
                                TAGA GGGGG  GTGGGG
                                |||| |||||  ||||||
                                ATCT CCCCC  CACCCC
                                  A    TA
GAM850  HYOU1    3'  CAGAAGAGGTGGGGGTGGGGT  22757      ____
                                TAGAAG   GGGGGTGGGGT
                                ||||||   ||||||||||
                                GTCTTC   CCCCCACCCCA
                                   TCCA
GAM850  KCNC3    3'  CAGGCAGGGGGTGGGGTA   22758     AA        III
                                TAG  GGGGGGTGGGGT  A
                                |||  ||||||||||||  |
                                GTC  TCCCCCACCCCA  T
                                  CG         III
GAM850  KCNQ3    5'  AGAAGGGGCGCTCGGGGT   22759       G __
                                AGAAGGGG GT  GGGGT
                                |||||||| ||  |||||
                                TCTTCCCC CG  CCCCA
                                    G  AG
GAM850  KLK10    3'  TAGGTGGGGGAATGAGGT   22760     AA   _
                                TAG  GGGGGG TGGGGT
                                |||  |||||| ||||||
                                ATC  CCCCCT ACTCCA
                                  CA     T
GAM850  MTAP     3'  AGAAGAGAATGGTGGGGT   22761       __
                                AGAAGGGG  GGTGGGGT
                                ||||||||  ||||||||
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                                TCTTCTCT  CCACCCCA
                                    TA
GAM850  NFATC1   3'  CAGAAGGGCTGGGCGTGGGGT  22762       ___ _
                                TAGAAGGG   GG GTGGGGT
                                ||||||||   || |||||||
                                GTCTTCCC   CC CACCCCA
                                    GAC  G
GAM850  PDGFB    3'  TAGAGAGGAGTGACTGGGGT   22763     A     ____
                                TAGA GGGGGGT    GGGGT
                                |||| |||||||    |||||
                                ATCT CTCCTCA    CCCCA
                                  _      CTGA
GAM850  PEA15    3'  TAGGCAGGAGGCTGGGGT    22764     A_     G
                                TAG  AGGGGG TGGGGT
                                |||  |||||| ||||||
                                ATC  TCCTCC ACCCCA
                                  CG     G
GAM850  PPP2CA   3'  TAGAAGGGAGGCCTTGGT    22765          GG_
                                TAGAAGGGGGGT   GGT
                                ||||||||||||   |||
                                ATCTTCCCTCCG   CCA
                                       GAA
GAM850  PSD      3'  CAGAGGGGGACTGATGGT    22766     A    G  _
                                TAGA GGGGG TGG GGT
                                |||| ||||| ||| |||
                                GTCT CCCCT ACT CCA
                                  C    G   A
GAM850  PTGFRN   3'  GAAAACAGGGGGTGGGGT    22767     ___
                                GAA   GGGGGGTGGGGT
                                |||   ||||||||||||
                                CTT   TCCCCCACCCCA
                                  TTG
GAM850  PXN      3'  TAAAAGGGGAGTGCGGGT    22768          _
                                TAGAAGGGGGGTG GGGT
                                |||||||||||| ||||
                                ATTTTCCCCTCAC CCCA
                                       G
GAM850  RAC2     3'  TAGGTGGGAGCGCTGGGGT   22769     AA    _ _
                                TAG  GGGGG G TGGGGT
                                |||  ||||| | ||||||
                                ATC  CCCTC C ACCCCA
                                  CA    G G
GAM850  RARA     3'  TAAGGAGGGGGCACGGGGGT  22770     AA     ___
                                TAG  GGGGGGT   GGGGT
                                |||  |||||||   |||||
                                ATT  TCCCCCG   CCCCA
                                  CC      TGC
GAM850  RFX1     3'  AGAAGGGGAAGCAGTGGGGT  22771        ____
                                AGAAGGGG   GGTGGGGT
                                ||||||||   ||||||||
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                                TCTTCCCC   TCACCCCA
                                    TTCG
GAM850  RHCG     3'  GAAGGGGAGGGCAGGGGT   22772      __  _
                                GAAGGGG  GGT GGGGT
                                |||||||  ||| |||||
                                CTTCCCC  CCG CCCCA
                                    TC   T
GAM850  SELL     3'  TAAAAGAAGTGGTGGGGT   22773      _
                                TAGAAGGGG GGTGGGGT
                                ||||||||| ||||||||
                                ATTTTCTTC CCACCCCA
                                     A
GAM850  SERPINB2 3'  CAGAAGGGCATGGAGGGT   22774      G__  T
                                TAGAAGGG   GG GGGGT
                                ||||||||   || |||||
                                GTCTTCCC   CC TCCCA
                                    GTA  _
GAM850  SLC9A3R1 3'  AGAAGGAAAAAGGTGGGGT   22775      ___
                                AGAAGGG   GGGTGGGGT
                                |||||||   |||||||||
                                TCTTCCT   TCCACCCCA
                                    TTT
GAM850  SOD3     3'  CAGAGGGGGGCCTCGGGGGT  22776    A    ____
                                TAGA GGGGGGT   GGGGT
                                |||| |||||||   |||||
                                GTCT CCCCCCG   CCCCA
                                  _     GAGC
GAM850  STAT1    5'  TAGGCGGGGGCGCGGCGGT   22777    AA   _  _
                                TAG  GGGGG GTGG GGT
                                |||  ||||| |||| |||
                                ATC  CCCCC CGCC CCA
                                  CG    G   G
GAM850  STAT1    5'  TAGGCGGGGGCGCGGCGGT   22777    AA   _  _
                                TAG  GGGGG GTGG GGT
                                |||  ||||| |||| |||
                                ATC  CCCCC CGCC CCA
                                  CG    G   G
GAM850  TGFBR2   3'  GAAGGTAAAAAGTGGGGT   22778     ___
                                GAAGG   GGGGTGGGGT
                                |||||   ||||||||||
                                CTTCC   TTTCACCCCA
                                   ATT
GAM850  TP53     3'  AGGAGGGGAAGGGTGGGGT   22779   A   ___
                                AG AGGGG   GGTGGGGT
                                || |||||   ||||||||
                                TC TCCCC   CCACCCCA
                                 C    TTC
GAM850  UBE2I    5'  CAGAAATCGGGGGTGGGGT   22780     __
                                TAGAAG  GGGGGTGGGGT
                                ||||||  ||||||||||
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                                GTCTTT  CCCCCACCCCA
                                   AG
GAM850  USF2     3'  CAGAAACAAGAGGTGGGGT   22781      __
                                TAGAAG  GGGGGTGGGGT
                                ||||||  ||||||||||
                                GTCTTT  TCTCCACCCCA
                                   GT
GAM850  AKAP3    3'  AGAGGGGAAAGCAGTGGGGT  22782    A  _____
                                AGA GGGG    GGTGGGGT
                                ||| ||||    ||||||||
                                TCT CCCC    TCACCCCA
                                  _   TTTCG
GAM850  ARHGEF9  3'  TAGAGGAGAAGTGCGGGT    22783     A     _
                                TAGA GGGGGGTG GGGT
                                |||| |||||||| ||||
                                ATCT CTCTTCAC CCCA
                                  C       G
GAM850  BHLHB2   3'  AAAGGCAAAAGGGTGGGGT   22784     ____
                                GAAGG   GGGGTGGGGT
                                |||||   ||||||||||
                                TTTCC   TCCCACCCCA
                                   GTTT
GAM850  C21orf69 3'  TAGGGAGGGAAGCTAGGGGT  22785    A_     __
                                TAG  AGGGGGGT  GGGGT
                                |||  ||||||||  |||||
                                ATC  TCCCTTCG  CCCCA
                                  CC       AT
GAM850  CGI-203  5'  TACAAGGTAGGAATGGGGT   22786   G   __
                                TA AAGG  GGGGTGGGGT
                                || ||||  ||||||||||
                                AT TTCC  CCTTACCCCA
                                 G   AT
GAM850  DKFZP434K1772 5'  CAGGGGGCTCTGGGGTGGGGT  22787    AA  ____
                                TAG  GG   GGGGTGGGGT
                                |||  ||   ||||||||||
                                GTC  CC   CCCCACCCCA
                                  CC  GAGA
GAM850  DKFZP566J091 3'  GAAAGCAAAGGGTGGGGT    22788     ___
                                GAAGG   GGGGTGGGGT
                                |||||   ||||||||||
                                CTTTC   TCCCACCCCA
                                   GTT
GAM850  DKFZP761F241 3'  GAAGGGGCAGCGCGTGGGGTA  22789       G_____     III
                                GAAGGGG     GTGGGGT   A
                                |||||||     |||||||   |
                                CTTCCCC     CACCCCA   T
                                    GTCGCG      III
GAM850  DKFZp761J1523 3'  TACAAGGGGACTGATGGT    22790    G     G   _
                                TA AAGGGGG TGG GGT
                                || ||||||| ||| |||
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                                AT TTCCCCT ACT CCA
                                 G      G  A
GAM850  DMWD     3'  TAGCAAGGGCAGCTGGGGT   22791    _    G _
                                TAG AAGGG GG TGGGGT
                                ||| ||||| || ||||||
                                ATC TTCCC TC ACCCCA
                                  G    G  G
GAM850  DOK4     3'  GAGAGGGGGGCAGCAGGGGT  22792    _     ____
                                GA AGGGGGGT   GGGGT
                                || ||||||||   |||||
                                CT TCCCCCCG   CCCCA
                                 C       TCGT
GAM850  EDG1     3'  GAAGGGAGGGTGGGGTA    22793      _      III
                                GAAGGG GGGTGGGGT  A
                                |||||| |||||||||  |
                                CTTCCC CCCACCCCA  T
                                    T       III
GAM850  FHX      3'  GAAGGGACGGGCTGGGGT   22794      __  _
                                GAAGGG  GGG TGGGGT
                                ||||||  ||| ||||||
                                CTTCCC  CCC ACCCCA
                                    TG  G
GAM850  FLJ10701 3'  AGAAGGGGAAGGAGGGGT   22795       __ T
                                AGAAGGGG  GG GGGGT
                                ||||||||  || |||||
                                TCTTCCCC  CC CCCCA
                                     TT  T
GAM850  FLJ14549 3'  AGAGGGAAGTGGGGTA    22796    A        III
                                AGA GGGGGGTGGGGT  A
                                ||| ||||||||||||  |
                                TCT CCCTTCACCCCA  T
                                  _         III
GAM850  FLJ20701 3'  TAGAAGGGGAAAGAGGGT   22797         T_
                                TAGAAGGGGGG  GGGGT
                                ||||||||||  |||||
                                ATCTTCCCCTT  TCCCA
                                       TC
GAM850  IL1RAPL1 3'  TAGAGGTGGGGAATGAGGT   22798    A__
                                TAGA  GGGGGGTGGGGT
                                ||||  ||||||||||||
                                ATCT  CCCCTTACTCCA
                                   CCA
GAM850  KIAA0562 3'  CAGGAGGGGATGGCTGGT   22799    AA      __
                                TAG  GGGGGGTGG  GGT
                                |||  |||||||||  |||
                                GTC  TCCCCTACC  CCA
                                  C_       GA
GAM850  KIAA0674 3'  TAGAGGAGGGCTCCCAGGT   22800    A     G___
                                TAGA GGGGGGT   GGGT
                                |||| |||||||   ||||
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                                ATCT CCTCCCG    TCCA
                                  _      AGGG
GAM850  LGI4     3'  CAGAGGGACCAGCGGGGT    22801      A   __
                                TAGA GGGG  GGTGGGGT
                                |||| ||||  ||||||||
                                GTCT CCCT  TCGCCCCA
                                  _    GG
GAM850  MAFB     3'  CAGAAGGGACCTCAGGGT    22802         GG_
                                TAGAAGGGG   TGGGGT
                                |||||||||   ||||||
                                GTCTTCCCT   GTCCCA
                                     GGA
GAM850  MESDC1   3'  AGAAGGGGTATGGGGGTGGGGT 22803         _______       III
           A                     AGAAGGGG     GGTGGGGT   A
                                ||||||||     ||||||||   |
                                TCTTCCCC     CCACCCCA   T
                                    ATACCC       III
GAM850  MGC10485 3'  TAGATGGGGGTGCTGGGT    22804      A    _  G
                                TAGA GGGGG GT GGGT
                                |||| ||||| || ||||
                                ATCT CCCCC CG CCCA
                                  A    A  A
GAM850  MGC26914 3'  AGAGGGGGGGCACGGGGGT   22805     A      ___
                                AGA GGGGGGT   GGGGT
                                ||| |||||||   |||||
                                TCT CCCCCCG   CCCCA
                                  C      TGC
GAM850  MGC3040  3'  AGAAGGGAGGAAATGGGGT   22806          ___
                                AGAAGGGGGG   TGGGGT
                                ||||||||||   ||||||
                                TCTTCCCTCC   ACCCCA
                                     TTT
GAM850  NINJ2    3'  CAGAAGGAAGCAGTGGGGT   22807          __
                                TAGAAGGGGG  GTGGGGT
                                ||||||||||  |||||||
                                GTCTTCCTTC  CACCCCA
                                     GT
GAM850  NINJ2    3'  CAGAAGGAAGCAGTGGGGT   22807          __
                                TAGAAGGGGG  GTGGGGT
                                ||||||||||  |||||||
                                GTCTTCCTTC  CACCCCA
                                     GT
GAM850  P2RXL1   3'  TAGAAAGGGCAGCAGGGT    22808          _  TG
                                TAGAAGGGG GG  GGGT
                                |||||||||  ||  ||||
                                ATCTTTCCC TC  CCCA
                                     G  GT
GAM850  PFDN2    3'  TAGAAGTGGGAGTCAGGGT   22809       _     _
                                TAGAAG GGGGGT GGGGT
                                |||||| |||||| |||||
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                                ATCTTC CCCTCA TCCCA
                                   A     G
GAM850  PRIC285  3'  CAGAGGGTGGGGTGGGGT    22810     A  _
                                TAGA GG GGGGTGGGGT
                                |||| || ||||||||||
                                GTCT CC CCCCACCCCA
                                  C  A
GAM850  QSCN6    3'  GAGGGGAGGGAATGGGGTA   22811    A    ___    III
                                GA GGGGGG   TGGGGT   A
                                || ||||||   ||||||   |
                                CT CCCTCC   ACCCCA   T
                                 C     CTT     III
GAM850  RASAL2   3'  AGAGGGCCAGAGTGGGGT    22812    A   ___
                                AGA GGG   GGGTGGGGT
                                ||| |||   |||||||||
                                TCT CCC   CTCACCCCA
                                  _   GGT
GAM850  RNF11    5'  AGAAAGCAGCGGTGGGGT    22813      _ _
                                AGAAGG GG GGTGGGGT
                                |||||| || ||||||||
                                TCTTTC TC CCACCCCA
                                   G  G
GAM850  SAMHD1   3'  GACAGGGGGTGGGGTA     22814    A         III
                                GA GGGGGGTGGGGT   A
                                || ||||||||||||   |
                                CT TCCCCCACCCCA   T
                                 G          III
GAM850  SC65     3'  TAGAAGTGGCAGGATGGG    22815      _ __
                                TAGAAG GG  GGGTGGG
                                |||||| ||  |||||||
                                ATCTTC CC  CCTACCC
                                   A  GT
GAM850  SCYA21   3'  TACAAGGAAGAGGTGGGGT   22816    G   __
                                TA AAGG  GGGGTGGGGT
                                || ||||  ||||||||||
                                AT TTCC  CTCCACCCCA
                                 G   TT
GAM850  SELM     3'  GAAGGAAGAAAGTGGGGT    22817       ___
                                GAAGGGGG   GTGGGGT
                                ||||||||   |||||||
                                CTTCCTTC   CACCCCA
                                     TTT
GAM850  TA-LRRP  5'  TAAAAGGGCTTGAAGGGGT   22818       G__  T
                                TAGAAGGG   GG GGGGT
                                ||||||||   || |||||
                                ATTTTCCC   CT CCCCA
                                     GAA  T
GAM850  THG-1    3'  AGATGGGGGTGGGGTA     22819     AG        III
                                AGA  GGGGGTGGGGT   A
                                |||  ||||||||||   |
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                                TCT  CCCCCACCCCA   T
                                  A_          III
GAM850   TIMM10    3'  AAAGTGGGAAGGGGTGGGGT   22820      _____
                                GAAG     GGGGGTGGGGT
                                ||||     ||||||||||
                                TTTC     TCCCCACCCCA
                                  ACCCT
GAM850   WNT10A    3'  CAGAAGTGAGTGGTGGGGT    22821       _  _
                                TAGAAG GGG GGTGGGGT
                                |||||| ||| ||||||||
                                GTCTTC CTC CCACCCCA
                                   A   A
GAM850   LOC124753 5'  TAGAGGAGGGAATCGCGGGGT  22822      A    _____
                                TAGA GGGGG    GTGGGGT
                                |||| |||||    |||||||
                                ATCT CTCCC    CGCCCCA
                                  C     TTAG
GAM850   LOC126823 5'  AGAGGGAGGGCGGTGGGGT    22823     ___    G
                                AGA   AGGG GGTGGGGT
                                |||   |||| ||||||||
                                TCT   TCCC CCACCCCA
                                  CCC    G
GAM850   LOC129303 3'  AGAAGATATGGGGTGGGGT    22824       ___
                                AGAAGG   GGGGTGGGGT
                                ||||||   ||||||||||
                                TCTTCT   CCCCACCCCA
                                   ATA
GAM850   LOC144596 3'  CAGAAACAAGAGGTGGGGT    22781       __
                                TAGAAG  GGGGGTGGGGT
                                ||||||  ||||||||||
                                GTCTTT  TCTCCACCCCA
                                   GT
GAM850   LOC148014 3'  TAGGCAGGGGTGGGACGGGGT  22825     A_    _ __
                                TAG  AGGGG GG  TGGGGT
                                |||  ||||| ||  ||||||
                                ATC  TCCCC CC  GCCCCA
                                  CG     A  CT
GAM850   LOC150372 3'  AAGCGGGGGTGGGGTA      22826     _         III
                                AAG GGGGGTGGGGT   A
                                ||| ||||||||||   |
                                TTC CCCCCACCCCA   T
                                  G          III
GAM850   LOC150951 5'  TAGGCAGGGAGGGTGGGGT    22827     A_   _
                                TAG  AGGG GGGTGGGGT
                                |||  |||| |||||||||
                                ATC  TCCC CCCACCCCA
                                  CG    T
GAM850   LOC151521 3'  GAAGTGTGGGGGTGGGGT    22828      ___
                                GAAG   GGGGGTGGGGT
                                ||||   ||||||||||
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                                CTTC   CCCCCACCCCA
                                  ACA
GAM850   LOC196472 5'  AGAACAGGGAGGGTGGGGT   22829     __   _
                                AGA  AGGG GGGTGGGGT
                                |||  |||| |||||||||
                                TCT  TCCC CCCACCCCA
                                  TG    T
GAM850   LOC219513 5'  GAAGGAGGGGCACAGGGT    22830      _    __
                                GAAGG GGGGT  GGGGT
                                ||||| |||||  |||||
                                CTTCC CCCCG  TCCCA
                                   T    TG
GAM850   LOC221466 3'  AGAGGGCAAGGGGTGGGGT   22831     A ____
                                AGA GG   GGGGTGGGGT
                                ||| ||   ||||||||||
                                TCT CC   CCCCACCCCA
                                  C  GTT
GAM850   LOC222031 3'  CAGTAAATGGGGTGGGGT    22832     _  G
                                TAG AAG GGGGTGGGGT
                                ||| ||| ||||||||||
                                GTC TTT CCCCACCCCA
                                  A   A
GAM850   LOC51336  5'  TAGAGGACAATTTGGGGT    22833      A   G __
                                TAGA GGG GG  TGGGGT
                                |||| ||| ||  ||||||
                                ATCT CCT TT  ACCCCA
                                   _   G  AA
GAM851   COL4A2    3'  GATGCAAATTCCTTTGGT    22836     AG   GC
                                GAT  AGA  TCCTTTGGT
                                |||  |||  |||||||||
                                CTA  TTT  AGGAAACCA
                                  CG   A_
GAM851   SLA       3'  ACCAGGGAGGGGTTCCTTTGGT 22837      A ATA   AGC_
                                ACCA G   GAG    TCCTTTGGT
                                |||| |   |||   |||||||||
                                TGGT C   CTC    AGGAAACCA
                                  _ C__   CCCA
GAM851   C1QTNF6   3'  CCAAGATAGAAGCAGGG     22838          G   TCCTTT
                                CCAAGATAGA AGC      GG
                                |||||||||| |||     ||
                                GGTTCTATCT TCG      CC
                                      _   TC_____
GAM851   FLJ10718  3'  ACCAAGAAAGAGAGCTGGG    22839        T       CCTTT
                                ACCAAGA AGAGAGCT     GG
                                ||||||| ||||||||    ||
                                TGGTTCT TCTCTCGA     CC
                                    T       C_____
GAM851   GABBR1    3'  CAAGGGTGCCTTCCTTTGGT   22840      ATAGAGA __
                                CAAG      GC  TCCTTTGGT
                                ||||      ||  |||||||||
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                                GTTC      CG  AGGAAACCA
                                  CCA____  GA
GAM851  GABBR1   3'  CAAGGGTGCCTTCCTTTGGT  22840     ATAGAGA __
                                CAAG      GC  TCCTTTGGT
                                ||||      ||  |||||||||
                                GTTC      CG  AGGAAACCA
                                  CCA____  GA
GAM851  HIC2     3'  ACCAAGATGAGGGGCGAGAGGT 22841        A  A_  TCCTTT
                                ACCAAGAT GAG  GC     GGT
                                |||||||| |||  ||     |||
                                TGGTTCTA CTC  CG     CCA
                                    _  CC  CTCT__
GAM851  HSPC054  3'  CAAGACAGAGAGCTAGG    22842           CCTTT
                                CAAGATAGAGAGCT    GG
                                ||||||||||||||    ||
                                GTTCTGTCTCTCGA    CC
                                       T____
GAM851  KIAA0564 3'  GATAGGAGCATTTTGGT    22843      A    TCC
                                GATAG GAGC   TTTGGT
                                ||||| ||||   ||||||
                                CTATC CTCG   AAACCA
                                  _    TA_
GAM851  KIAA1026 3'  CAGGATAGAGAGCTGG     22844    A        CCTTT
                                CA GATAGAGAGCT    GG
                                || ||||||||||     ||
                                GT CTATCTCTCGA    CC
                                 C         _____
GAM851  SPRY4    3'  AAGATAAAGTCTTTTGGT    22845        AGC  C
                                AAGATAGAG   TC TTTGGT
                                |||||||||   || ||||||
                                TTCTATTTC   AG AAACCA
                                     ___  A
GAM851  LOC138128 5'  CCAAGGTAGAGGGCTCCT    22846      A    A
                                CCAAG TAGAG GCTCCT
                                ||||| ||||| ||||||
                                GGTTC ATCTC CGAGGA
                                  C    C
GAM851  LOC94976 3'  GATAGGTAGTTCCTTTGGT   22847      AG  C
                                GATAG  AG TCCTTTGGT
                                |||||  || |||||||||
                                CTATC  TC AGGAAACCA
                                  CA  A
GAM852  ATP7A    3'  TACACATTTATAAAATTTCT   22850      GCG  CT
                                TACACA   TA  GAATTTCT
                                ||||||   ||  ||||||||
                                ATGTGT   AT  TTTAAAGA
                                   AA_  AT
GAM852  DDX11    3'  CACAGCCACGAATTTCT     22851       G   T
                                CACAGC TAC GAATTTCT
                                |||||| ||| ||||||||
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                                GTGTCG GTG CTTAAAGA
                                     _  _
GAM852  EDNRA    3'  ACAGTGCACTGAAAGTCT    22852      C       TT
                                ACAG GTACTGAA  TCT
                                |||| ||||||||  |||
                                TGTC CGTGACTT  AGA
                                  A       TC
GAM852  EIF1AY   3'  TACACACTAAATGAATTTCT   22853       G GTAC
                                TACACA C    TGAATTTCT
                                |||||| |    |||||||||
                                ATGTGT G    ACTTAAAGA
                                   _ ATTT
GAM852  GRM6     3'  CACACGTGTATCTGAATTTCT  22854       AGC  _
                                TACAC   GTA CTGAATTTCT
                                |||||   ||| ||||||||||
                                GTGTG   CAT GACTTAAAGA
                                   CA_  A
GAM852  NAV2     3'  ACACAGCAGACTGGGTTTCT   22855        T   AA
                                ACACAGCG ACTG  TTTCT
                                |||||||| ||||  |||||
                                TGTGTCGT TGAC  AAAGA
                                     C   CC
GAM852  PLAG1    5'  TACACCGCCCGCGGAATTTCT  22856       A  GTACT
                                TACAC GC     GAATTTCT
                                ||||| ||     ||||||||
                                ATGTG CG     CTTAAAGA
                                   G  GGCGC
GAM852  PPP2CB   3'  ACATAGTGTACTAAATTT    22857     C  C
                                ACA AG GTACTGAATTT
                                ||| || ||||||||||
                                TGT TC CATGATTTAAA
                                  A  A
GAM852  RAB30    5'  TACACAGCTTCAATTTTCT    22858        GTAC   A
                                TACACAGC    TGA TTTCT
                                ||||||||    ||| |||||
                                ATGTGTCG    GTT AAAGA
                                     AA__   A
GAM852  RECQL5   3'  CACACAGCCCAAAGAGTTTCT  22859         G  CT  A
                                TACACAGC TA  GA TTTCT
                                |||||||| ||  || |||||
                                GTGTGTCG GT  CT AAAGA
                                     G  TT  C
GAM852  RNMT     3'  ACAGCAAATGTTGAATTTCT   22860       TAC__
                                ACAGCG     TGAATTTCT
                                ||||||     |||||||||
                                TGTCGT     ACTTAAAGA
                                   TTACA
GAM852  SEL1L    3'  TACACAGCAGTACCTCCTTT   22861         _    GAA
                                TACACAGC GTACT   TTT
                                |||||||| |||||   |||
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                                ATGTGTCG CATGG   AAA
                                     T    AGG
GAM852  BRD1     3'  TACACAGCATAACTTTATTCT  22862         _  GAAT
                                TACACAGCGTA CT   TTCT
                                |||||||||||  ||   ||||
                                ATGTGTCGTAT GA   AAGA
                                      T  AAT_
GAM852  C11orf23 3'  TACACTTCTGAATTTCT    22863      AGCGTA
                                TACAC    CTGAATTTCT
                                |||||    ||||||||||
                                ATGTG    GACTTAAAGA
                                   AA____
GAM852  C1orf25  3'  TACACAGCAGAATTT      22864        TACT
                                TACACAGCG   GAATTT
                                |||||||||   ||||||
                                ATGTGTCGT   CTTAAA

                                     _____
GAM852  C9orf5   3'  CACAGCCTGAATTTC      22865      GTA
                                CACAGC  CTGAATTTC
                                ||||||  |||||||||
                                GTGTCG  GACTTAAAG

                                     ___
GAM852  CNOT7    3'  CACAACGTGCTATATTCT    22866       A  AAT
                                CACAGCGT CTG   TTCT
                                |||||||| |||   ||||
                                GTGTTGCA GAT   AAGA
                                     C   AT_
GAM852  FHOD2    5'  ACACGCCGTCTGAATTTCT   22867     AG  A
                                ACAC  CGT CTGAATTTCT
                                ||||  ||| ||||||||||
                                TGTG  GCA GACTTAAAGA
                                  CG  _
GAM852  FLJ22865 5'  TACCAGCCAAGAATTTCT    22868     A   GTACT
                                TAC CAGC    GAATTTCT
                                ||| ||||    ||||||||
                                ATG GTCG    CTTAAAGA
                                  _   GTT__
GAM852  ICK      3'  ACAGCATAAATTCCT      22869       CTG
                                ACAGCGTA   AATTTCT
                                ||||||||   |||||||
                                TGTCGTAT   TTAAGGA

                                     ___
GAM852  KIAA1915 3'  CACCCTTACTGAATTTCT    22870     AGCG
                                CAC    TACTGAATTTCT
                                |||    ||||||||||||
                                GTG    ATGACTTAAAGA
                                  GGA_
GAM852  LIG-1    3'  TACACTGTACCAAAATTTCT  22871      AGC   TG  _
                                TACAC   GTAC  AA TTTCT
                                |||||   ||||  || |||||
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                                ATGTG  CATG  TT AAAGA
                                  A__   GT  T
GAM852  MGC14697  5'  TACAAAGGCATGAATTTCT   22872     C  C   C
                                TACA AG GTA TGAATTTCT
                                |||| || ||| |||||||||
                                ATGT TC CGT ACTTAAAGA
                                  T  _  _
GAM852  PP3501    3'  CACAGCGTACCCTTC      22873         GAA
                                CACAGCGTACT   TTTC
                                ||||||||||   ||||
                                GTGTCGCATGG   GAAG
                                      ___
GAM852  TP53INP1  3'  TACACAGCATATAAATCT    22874         C
                                TACACAGCGTA TGAATTT
                                |||||||||| |||||||
                                ATGTGTCGTAT ATTTAGA
                                      _
GAM852  TP53INP1  3'  TACACAGCATATAAATCT    22874         C
                                TACACAGCGTA TGAATTT
                                |||||||||| |||||||
                                ATGTGTCGTAT ATTTAGA
                                      _
GAM852  LOC125488 5'  ACAGACATGTTGAATTTCT   22875     _   AC
                                ACAG CGT  TGAATTTCT
                                |||| |||  |||||||||
                                TGTC GTA  ACTTAAAGA
                                  T   CA
GAM852  LOC136319 3'  GCATACTGGAATGGTTTCT   22876       _  ___
                                GCGTACTG AAT   TTCT
                                |||||||| |||   ||||
                                CGTATGAC TTA   AAGA
                                     C   CCA
GAM852  LOC146733 5'  CACGCAGCACTGAATTTCT   22877     A  _
                                CAC GC GTACTGAATTTCT
                                ||| || ||||||||||||
                                GTG CG CGTGACTTAAAGA
                                  _  T
GAM852  LOC151614 5'  CACACAGCGTACTGTCCT    22878          AAT
                                TACACAGCGTACTG   TTCT
                                ||||||||||||   ||||
                                GTGTGTCGCATGAC   AGGA
                                      ___
GAM852  LOC152464 3'  ACAGAGTTGAATTTCT      22879     C  AC
                                ACAG GT  TGAATTTCT
                                |||| ||  |||||||||
                                TGTC CA  ACTTAAAGA
                                  T  __
GAM852  LOC152715 3'  CACAGTTTATATGAATTTCT  22880      CG  C_
                                CACAG  TA  TGAATTTCT
                                |||||  ||  |||||||||
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                                GTGTC  AT  ACTTAAAGA
                                   AA  AT
GAM852  LOC155064 3'  ACAGCGCATGACCGTATTTCT  22881       ___   A
                                ACAGCGT   ACTG ATTTCT
                                |||||||   |||| ||||||
                                TGTCGCG   TGGC TAAAGA
                                    TAC    A
GAM852  LOC155376 3'  CACCCAGCCTGAATTTCT    22882     A   GTA
                                TAC CAGC   CTGAATTTCT
                                ||| ||||   ||||||||||
                                GTG GTCG   GACTTAAAGA
                                  G   ___
GAM852  LOC169026 3'  CACAGCGTGGAGAGGTTTCT  22884       ACT  A_
                                CACAGCGT   GA  TTTCT
                                ||||||||   ||  |||||
                                GTGTCGCA   CT  AAAGA
                                     CCT  CC
GAM852  LOC169026 3'  CACCATGACATGAATTTCT   22883    G  _  _
                                CA CGT AC TGAATTTCT
                                || ||| || |||||||||
                                GT GTA TG ACTTAAAGA
                                 G   C  T
GAM852  LOC219680 3'  TACACAGTGAATTTCT      22885       CGTAC
                                TACACAG    TGAATTTCT
                                |||||||    |||||||||
                                ATGTGTC    ACTTAAAGA
                                           _____
GAM852  LOC222174 3'  TACACAGTGCTAAACTT     22886       C TA
                                TACACAG G  CTGAATTT
                                ||||||| |  ||||||||
                                ATGTGTC C  GATTTGAA
                                    A __
GAM852  LOC253532 3'  CACCCAGCCTGAATTTCT    22882     A   GTA
                                TAC CAGC   CTGAATTTCT
                                ||| ||||   ||||||||||
                                GTG GTCG   GACTTAAAGA
                                  G   ___
GAM852  LOC254875 3'  CACCCAGCCTGAATTTCT    22882     A   GTA
                                TAC CAGC   CTGAATTTCT
                                ||| ||||   ||||||||||
                                GTG GTCG   GACTTAAAGA
                                  G   ___
GAM853  ASK     5'  AGAAAGTGTCGCACCG      22889       CCTA    A
                                AGAAAGTG    TGCAC CG
                                ||||||||    ||||| ||
                                TCTTTCAC    GCGTG GC
                                    A___    _
GAM853  CDKN2A   3'  AAGAAATGCCCACATGAA    22890       G   TATG   C
                                AAGAAA TGCC    CACA GAA
                                |||||| ||||    |||| |||
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                                TTCTTT ACGG   GTGT CTT
                                  _   ____   A
GAM853  CDKN2A   3'  AAGAAATGCCCACATGAA   22890      G   TATG   C
                                AAGAAA TGCC   CACA GAA
                                |||||| ||||   |||| |||
                                TTCTTT ACGG   GTGT CTT
                                  _   ____   A
GAM853  CDKN2A   3'  AAGAAATGCCCACATGAA   22890      G   TATG   C
                                AAGAAA TGCC   CACA GAA
                                |||||| ||||   |||| |||
                                TTCTTT ACGG   GTGT CTT
                                  _   ____   A
GAM853  CDKN2A   3'  AAGAAATGCCCACATGAA   22890      G   TATG   C
                                AAGAAA TGCC   CACA GAA
                                |||||| ||||   |||| |||
                                TTCTTT ACGG   GTGT CTT
                                  _   ____   A
GAM853  FPR1     3'  AGGAAATGCCTGTGCTCA   22891    A      A  A
                                AG AAGTGCCT TGC CA
                                || |||||||| ||| ||
                                TC TTTACGGA ACG GT
                                 C       C  A
GAM853  MTF1     3'  AGAATTTTTATGCACACGA   22892     AGTGCC
                                AGAA     TATGCACACGA
                                ||||     ||||||||||
                                TCTT     ATACGTGTGCT
                                  AAAA__
GAM853  PPP1R8   5'  AAGAAAGTGCCGTGTGTAC   22893          TA_  C
                                AAGAAAGTGCC   TG AC
                                ||||||||||   || ||
                                TTCTTTCACGG   AC TG
                                      CAC  A
GAM853  RNPEP    3'  AGGCAGGGGCCATGCACACGA  22894    AA  T_   T
                                AG  AG  GCC ATGCACACGA
                                ||  ||  ||| ||||||||||
                                TC  TC  CGG TACGTGTGCT
                                 CG  CC  _
GAM853  SPAG6    3'  AGAACAAATCCTATGCATGCGA 22895     AGTG_      CA
           A                     AGAA    CCTATGCA  CGAA
                                ||||    ||||||||  ||||
                                TCTT    GGATACGT  GCTT
                                  GTTTA       AC
GAM853  CLECSF9  3'  AAAGACACATGCACACGAA   22896     T  C
                                AAAG GC TATGCACACGAA
                                |||| || ||||||||||||
                                TTTC TG GTACGTGTGCTT
                                  _ T
GAM853  DKFZP434P0111 3'  GAAAAATGCACACGA      22897      TGCCT
                                GAAAG    ATGCACACGA
                                |||||    ||||||||||
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                                CTTTT    TACGTGTGCT
                                     _____
GAM853  FLJ14775  3'  AGAGAAGTGCCTGTGTCTAC  22898    _      A  CAC
                                AGA AAGTGCCT TG   AC
                                ||| |||||||| ||   ||
                                TCT TTCACGGA AC   TG
                                  C       C  AGA
GAM853  FLJ20489  3'  AAGAGAGTGCCTAGGGCA   22899     A      T_
                                AAGA AGTGCCTA  GCA
                                |||| ||||||||  |||
                                TTCT TCACGGAT  CGT
                                  C       CC
GAM853  HSPC067   5'  GAAAGCGCAGCCGCGCACG   22900        CTA   A
                                GAAAGTGC   TGC CACG
                                ||||||||   ||| ||||
                                CTTTCGCG   GCG GTGC
                                     TCG   C
GAM853  KIAA0682  3'  AGAAAATGTGAACACG     22901        CCTA  C
                                AGAAAGTG    TG ACACG
                                ||||||||    || |||||
                                TCTTTTAC    AC TGTGC
                                     ____  T
GAM853  KIAA1505  5'  AGTGTTATACACATGAA     22902     CC       C
                                AGTG  TATGCACA GAA
                                ||||  |||||||| |||
                                TCAC  ATATGTGT CTT
                                  A_       A
GAM853  KLHL6     3'  AAGGAAGTGCCTGGCACAGAA  22903     A      AT    C
                                AAG AAGTGCCT  GCACA GAA
                                ||| ||||||||  ||||| |||
                                TTC TTCACGGA  CGTGT CTT
                                  C       C_    _
GAM853  RPL32     3'  AGAAAACGTGCACATGA     22904        CCTA     C
                                AGAAAGTG    TGCACA GA
                                ||||||||    |||||| ||
                                TCTTTTGC    ACGTGT CT
                                     ____      A
GAM853  SEMA5A    3'  AGAAAGTGCCTATTTTCTTGAA 22905           GCACAC
                                AGAAAGTGCCTAT     GAA
                                ||||||||||||      |||
                                TCTTTCACGGATA     CTT
                                      AAAGAA
GAM853  LOC138654 5'  AAGAAAGCCTGGTGCGCATGA  22906       GT   A_  A  C
                                AAGAAA  GCCT  TGC CA GA
                                ||||||  ||||  ||| || ||
                                TTCTTT  CGGA  ACG GT CT
                                   __   CC   C  A
GAM853  LOC142955 5'  GAAGGTGCTGCACACG      22907     A   CTA
                                GAA GTGC   TGCACACG
                                ||| ||||   ||||||||
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                                CTT CACG   ACGTGTGC
                                  C   ___
GAM853  LOC147429 3'  AAGAAAGTGCCAGCCGA     22908          TAT  ACA
                                AAGAAAGTGCC   GC   CGA
                                ||||||||||   ||   |||
                                TTCTTTCACGG   CG   GCT
                                     T__  ___
GAM853  LOC162404 3'  AGAAAACATGCACACGA     22909       TGCC
                                AGAAAG   TATGCACACGA
                                ||||||   ||||||||||
                                TCTTTT   GTACGTGTGCT
                                    ____
GAM853  LOC200314 5'  AGAAAATGCTTATGACACAA   22910        C   C
                                AGAAAGTGC TATG ACACGA
                                ||||||||| |||| ||||||
                                TCTTTTACG ATAC TGTGTT
                                     A   _
GAM853  LOC203428 5'  GAAAGCGCAGCCGCGCACG    22900        CTA   A
                                GAAAGTGC   TGC CACG
                                ||||||||   ||| ||||
                                CTTTCGCG   GCG GTGC
                                    TCG   C
GAM854  ADD1     3'  CAGCTCTACCAAGGGCCTGTTG 22913    C    AG  TAA_    C
          GG                    CA CTCTA  CA    CCTGT GGG
                                || |||||  ||   ||||| |||
                                GT GAGAT  GT    GGACA CCC
                                 C    G_  TCCC    A
GAM854  ADD1     3'  CAGCTCTACCAAGGGCCTGTTG 22913    C    AG  TAA_    C
          GG                    CA CTCTA  CA    CCTGT GGG
                                || |||||  ||   ||||| |||
                                GT GAGAT  GT    GGACA CCC
                                 C    G_  TCCC    A
GAM854  LARS2    5'  CACCTTTAGGCGAGCACTGCCG 22914      C  A  ATAAC
          GG                    CACCT TA GC    CTGTCGGG
                                ||||| || ||    ||||||||
                                GTGGA AT CG    GACGGCCC
                                   A  C  CTCGT
GAM854  DKFZP564B1162 5'  CCTCTGAGCGAAACCCAACAG  22915      A   AT    T
                                CCTCT AGC  AACCTG CGG
                                ||||| |||  |||||| |||
                                GGAGA TCG  TTGGGT GTC
                                   C   CT     T
GAM854  FLJ14326  3'  CACTTCTAAGCAGCCCTTGGG  22916    C      TAA   GTC
                                CAC TCTAAGCA   CCT   GGG
                                ||| ||||||||   |||   |||
                                GTG AGATTCGT   GGG   CCC
                                  A       C__   AA_
GAM854  FLJ14351  3'  CACCTCTAAGCATATTCTGGG  22917           AC   TC
                                CACCTCTAAGCATA  CTG  GG
                                ||||||||||||||  |||  ||
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                                GTGGAGATTCGTAT  GAC  CC
                                      AA   __
GAM854  KIAA1191  3'  CACCTCTAAGCCATGATTTGCC 22918       ATAA__________  TGTC
          CGACAGG                 CTAAGC          CC    GG
                                |||||||          ||    ||
                                GATTCG          GG    CC
                                   GTACTAAACIIIG  CTGT
GAM854  KIAA1655  3'  CTCTAAGCATGGCCAGG     22919          AACCT
                                CTCTAAGCAT    GTCGGG
                                ||||||||||    ||||||
                                GAGATTCGTA    CGGTCC
                                      C_____
GAM854  PTD013    3'  CCTCTGAGCATAGCCACAG   22920       A     A  TGT
                                CCTCT AGCATA CC   CGG
                                ||||| |||||| ||   |||
                                GGAGA TCGTAT GG   GTC
                                   C     C  T__
GAM854  SDCCAG10  3'  CACCCCTAAGTGATGCTGTTGG 22921          CATAAC    C
          G                      CACCTCTAAG     CTGT GGG
                                ||||||||||     |||| |||
                                GTGGGGATTC     GACA CCC
                                      ACTAC_    A
GAM854  LOC144577 3'  TCTAAACATAATTTGTGGG   22922          CC   C
                                TCTAAGCATAA  TGT GGG
                                ||||||||||  ||| |||
                                AGATTTGTATT  ACA CCC
                                      AA   _
GAM855  C8orf1    3'  TGGACTGTTTAAATTAT     22925          TAC
                                TGGACTGTTTA   TTAT
                                ||||||||||   ||||
                                ACCTGACAAAT   AATA
                                      TT_
GAM855  PTGS2     3'  TGGATTGTTTACATAATATTCA 22926      C       CTT  C
                                TGGA TGTTTATA   AT TTCA
                                |||| ||||||||   || ||||
                                ACCT ACAAATGT   TA AAGT
                                   A       AT_  T
GAM855  RARRES3   3'  TGGCTGTTTATTGATCCTTCA  22927     A       ACTTA
                                TGG CTGTTTAT    TCTTCA
                                ||| ||||||||    ||||||
                                ACC GACAAATA    GGAAGT
                                  _       ACTA_
GAM855  CMG2      3'  TGGTTGTTGAACTTATCTT   22928     AC    TAT
                                TGG  TGTT   ACTTATCTT
                                |||  ||||   |||||||||
                                ACC  ACAA   TGAATAGAA
                                  A_    CT_
GAM855  FLJ12476  3'  TGGACTGTTGCTCCTCTTCAA  22929         TATA   A
                                TGGACTGTT    CTT TCTTCAA
                                |||||||||    ||| |||||||
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                                ACCTGACAA   GAG AGAAGTT
                                    C___  G
GAM855  JDD1     3'  GGACTGTTTAAATCTT     22930          TACTT
                                GGACTGTTTA    ATCTT
                                ||||||||||    |||||
                                CCTGACAAAT    TAGAA
                                    T____
GAM855  KLHL6    3'  ACATTTATATTTATCTTCAA  22931    T     C
                                AC GTTTATA TTATCTTCAA
                                || ||||||| ||||||||||
                                TG TAAATAT AATAGAAGTT
                                 _     A
GAM855  PORIMIN  3'  TGGCCTGTTTATACTATTTTCA 22932    A        T  C
            A                    TGG CTGTTTATACT AT TTCAA
                                ||| |||||||||| || |||||
                                ACC GACAAATATGA TA AAGTT
                                  G         _ A
GAM855  LOC113179 3'  TGGGCTGTTTATTTTCCCATC  22933    A      A__
                                TGG CTGTTTAT   CTTATC
                                ||| ||||||||   ||||||
                                ACC GACAAATA   GGGTAG
                                  C       AAA
GAM855  LOC152765 3'  TGGACTATTTGTGTACCTTCAA 22934         ATACT
                                TGGACTGTTT    TATCTTCAA
                                ||||||||||    |||||||||
                                ACCTGATAAA    ATGGAAGTT
                                    CAC__
GAM856  ACTN2    3'  TCTAACTCTGGCTTCTCCT   22937         ACC  AGG
                                TCTAACTCTG   CT   CCT
                                ||||||||||   ||   |||
                                AGATTGAGAC   GA   GGA
                                    C__  AGA
GAM856  ELF3     3'  CCTAACTCTGATTTTGTCAGAC 22938          CCC___
                                TCTAACTCTGA     TAGGC
                                ||||||||||     |||||
                                GGATTGAGACT     GTCTG
                                    AAAACA
GAM856  GAS11    3'  TCCAGCTCTCTGGGCCTAA   22939     A   GACC  A
                                TCTA CTCT    CT GGCCTAA
                                |||| ||||    || |||||||
                                AGGT GAGA    GA CCGGATT
                                  C    _____ C
GAM856  HEM1     3'  TCTGGCTCCTGACCCTCTCTCC 22940     AA  _     AGG_
            T                    TCT  CTC TGACCCT    CCT
                                |||  ||| |||||||    |||
                                AGA  GAG ACTGGGA    GGA
                                  CC   G      GAGA
GAM856  ITGAL    3'  TCTAACTCCTGACCTCAGG   22941         _    C
                                TCTAACTC TGACC TAGG
                                |||||||| ||||| ||||
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                                AGATTGAG ACTGG GTCC
                                     G    A
GAM856  KCNA7    3'  TCCAACTCTGGGTGTCTGAC  22943         ACC__  A
                                TCTAACTCTG    CT GGC
                                ||||||||||    || |||
                                AGGTTGAGAC    GA CTG
                                     CCACA  _
GAM856  KCNA7    3'  TCTAACTTGACCCAACATGGC  22942       C     TA___
                                TCTAACT TGACCC    GGC
                                ||||||| ||||||    |||
                                AGATTGA ACTGGG    CCG
                                    _    TTGTA
GAM856  MAP3K7IP1 3'  TCTAACTCAGGCCCTGGGC   22944        TGA   A
                                TCTAACTC   CCCT GGC
                                ||||||||   |||| |||
                                AGATTGAG   GGGA CCG
                                     TCC    C
GAM856  NINJ1    3'  TCCAGTTCTGACCCTCTGGGC  22945     AC       A__
                                TCTA  TCTGACCCT   GGC
                                ||||  |||||||||   |||
                                AGGT  AGACTGGGA   CCG
                                  CA        GAC
GAM856  PTPN18   3'  TAACTTTGATCCAGGCCCA   22946      C   CC
                                TAACT TGA  CTAGGCCTA
                                ||||| |||  |||||||||
                                ATTGA ACT  GGTCCGGGT
                                   A   A_
GAM856  RNMT     3'  TCTGCTCTGATCCTCTATTAAC 22947     AA     C   AGGCC
                                TCT  CTCTGA CCT    TAAC
                                |||  |||||| |||    ||||
                                AGA  GAGACT GGA    ATTG
                                  C_     A   GATA_
GAM856  TEGT     3'  TAACTCAAAATCTTAGGCCTA  22948       T  CC  _
                                TAACTC GA  CT AGGCCTA
                                ||||||  ||  || |||||||
                                ATTGAG TT  GA TCCGGAT
                                    T  TA  A
GAM856  TNFAIP1  3'  TCTAACCCTGGGTCTGGC    22949         ACC  A
                                TCTAACTCTG   CT GGC
                                ||||||||||   || |||
                                AGATTGGGAC   GA CCG
                                     CCA  _
GAM856  CLONE24945 3'  TCAGCTCTGACCTTCTCTGAC  22950    TAA       __  A_
                                TC   CTCTGACC  CT  GGC
                                ||   ||||||||  ||  |||
                                AG   GAGACTGG  GA  CTG
                                  TC_       AA  GA
GAM856  DKFZp761J139 3'  TCTAACTCGTGAAGCGGGCCT  22951         _   CCCTA
                                TCTAACTC TGA     GGCCT
                                ||||||| |||     |||||
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                                AGATTGAG ACT    CCGGA
                                     C   TCGC_
GAM856  FKSG42    3'  CTGACTTTGACCCCAAATTAAC 22952    A  C       CC
                                CT ACT TGACCCTAGG  TAAC
                                || ||| ||||||||||  ||||
                                GA TGA ACTGGGGTTT  ATTG
                                 C  A        A_
GAM856  FLJ20255  3'  TCTGACTCTGGCCTTTGCCT   22953    A    AC   AG
                                TCT ACTCTG  CCT  GCCT
                                ||| ||||||  |||  ||||
                                AGA TGAGAC  GGA  CGGA
                                  C     C_   AA
GAM856  KIAA0182  3'  TCTGACTCTGACTATATGAAGC 22954    A      CCT___
                                TCT ACTCTGAC     AGGC
                                ||| ||||||||     ||||
                                AGA TGAGACTG     TTCG
                                  C       ATATAC
GAM856  KIAA0445  3'  TCTGACCCCTGCCCTGGGCCT  22955    AA_    A   A
                                TCT   CTCTG CCCT GGCCT
                                |||   ||||| |||| |||||
                                AGA   GGGAC GGGA CCGGA
                                  CTG    _   C
GAM856  KIAA0551  3'  TCTGATTCTGCCTCTAGAC    22956    AAC    A  _
                                TCT   TCTG CC CTAGGC
                                |||   |||| || ||||||
                                AGA   AGAC GG GATCTG
                                  CTA   _  A
GAM856  KIAA1233  3'  TCTAGCTCTAATCCTAAA    22957     A     C
                                TCTA CTCTGA CCTAGG
                                |||| |||||| ||||||
                                AGAT GAGATT GGATTT
                                  C     A
GAM856  PRAX-1    3'  TAGCTCTGACCTTCACCAAGGC 22958    A      _____  _
                                TA CTCTGACC    CTA GGC
                                || ||||||||    ||| |||
                                AT GAGACTGG    GGT CCG
                                 C       AAGT   T
GAM856  ZDHHC1    3'  TCTAACTCGGCCCTCCGGC    22959        T A    A_
                                TCTAACTC G CCCT  GGC
                                |||||||| | ||||  |||
                                AGATTGAG C GGGA  CCG
                                     _ C    GG
GAM856  LOC158428 3'  TCTACTCTGACCCACCCTA    22960     A       TAGG
                                TCTA CTCTGACCC    CCTA
                                |||| |||||||||    ||||
                                AGAT GAGACTGGG    GGAT
                                  _       TG__
GAM856  LOC162083 5'  TCTAACTCGTGACAGTTCT    22961        _   CCT  GC
                                TCTAACTC TGAC   AG  CT
                                |||||||| ||||   ||  ||
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                                AGATTGAG ACTG   TC  GA
                                    C    ___  AA
GAM856  LOC196872 3'  ACGTTGATTAGGCCTAAC    22962    TC   CCC
                                AC  TGA   TAGGCCTAAC
                                ||  |||   ||||||||||
                                TG  ACT   ATCCGGATTG
                                 CA   A__
GAM856  LOC221312 3'  TCTGCTCTGACCCTAGA     22963     AA
                                TCT  CTCTGACCCTAGG
                                |||  ||||||||||||
                                AGA  GAGACTGGGATCT
                                  C_
GAM856  LOC221943 5'  TCTTAGCTCTGCCAGGCCT   22964     AA_    ACC
                                TCT   CTCTG   CTAGGCCT
                                |||   |||||   ||||||||
                                AGA   GAGAC   GGTCCGGA
                                  ATC    ___
GAM856  LOC255852 5'  TCTGCTTCTGACCCTCCT    22965     AAC       AGG
                                TCT   TCTGACCCT   CCT
                                |||   |||||||||   |||
                                AGA   AGACTGGGA   GGA
                                  CGA       ___
GAM856  LOC257473 3'  TCTAACTCGGCCCTCCGGC    22959        T A    A_
                                TCTAACTC G CCCT  GGC
                                ||||||||  |  ||||  |||
                                AGATTGAG C GGGA  CCG
                                     _ C    GG
GAM856  LOC90161  3'  TCTGGCCCTGACCCTGGC    22966     AA        A
                                TCT  CTCTGACCCT GGC
                                |||  ||||||||||  |||
                                AGA  GGGACTGGGA CCG
                                  CC        _
GAM857  DAZ      3'  GACTGTTTGCTTAGAATCTG   22969         CA  CGC
                                GACTGTTTGC  AG   AGTCTG
                                ||||||||||  ||   ||||||
                                CTGACAAACG  TC   TTAGAC
                                     AA  ___
GAM857  INPP5D   3'  AGACTGTTTGTTGCCCGTCTG  22970         CCAA  GCA
                                AGACTGTTTG   GC   GTCTG
                                ||||||||||   ||   |||||
                                TCTGACAAAC   CG   CAGAC
                                     AA__  GG_
GAM857  LIMK1    3'  CTGTTTGCTCAGCCACTG    22971        CA   G  GT
                                CTGTTTGC  AGC CA  CTG
                                ||||||||  ||| ||  |||
                                GACAAACG  TCG GT  GAC
                                     AG   _  __
GAM857  LIMK1    3'  CTGTTTGCTCAGCCACTG    22971        CA   G  GT
                                CTGTTTGC  AGC CA  CTG
                                ||||||||  ||| ||  |||
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                                GACAAACG  TCG GT  GAC
                                    AG  _ __
GAM857  AF9Q34   3' AGGCTGTTTCCCTGGACAGTCT 22972    A     G  AAGC
          G                      AG CTGTTT CC    GCAGTCTG
                                 || |||||| ||    ||||||||
                                 TC GACAAA GG    TGTCAGAC
                                  C     G  ACC_
GAM857  KIAA1191 5' AGGCTGTGGCGCAGTCT     22973    A   TTGCCAA
                                 AG CTGT      GCGCAGTCT
                                 || ||||      |||||||||
                                 TC GACA      CGCGTCAGA
                                  C   C_______
GAM857  MAD4     3' CTGTTTGCCAGATGACCCCTG  22974         AGC_  AG
                                 CTGTTTGCCA    GC  TCTG
                                 ||||||||||    ||  ||||
                                 GACAAACGGT    TG  GGAC
                                       CTAC  G_
GAM857  NR1H3    3' GAATGTTTGCCCTTCTCAGTCT 22975    C       AAGCG
          G                      GA TGTTTGCC     CAGTCTG
                                 || ||||||||     |||||||
                                 CT ACAAACGG     GTCAGAC
                                  T       GAAGA
GAM857  LOC112840 3' GACTGTTTGCTAACTGGC    22976         CA  __
                                 GACTGTTTGC  AGC  GC
                                 ||||||||||  |||  ||
                                 CTGACAAACG  TTG  CG
                                       A_   AC
GAM857  LOC160897 3' AAACTGTTTGTCAAAAAC    22977         C   C
                                 AGACTGTTTG CAAG GC
                                 |||||||||| |||| ||
                                 TTTGACAAAC GTTT TG
                                       A   T
GAM857  LOC56930  5' AGACTGTTGGCGCTAGTCT   22978        T CCAA   _
                                 AGACTGTT G    GCGC AGTCT
                                 |||||||| |    |||| |||||
                                 TCTGACAA C    CGCG TCAGA
                                    _ _____    A
GAM858  SERPINE2  5' GCCTGGTCTCGGCGGCGC    22981     CG       T  TTCA
                                 GCC  GGTCTCGG CG    CGC
                                 |||  |||||||| ||    |||
                                 CGG  CCAGAGCC GC    GCG
                                   A_       _  C___
GAM858  ARHV     5' GCCCGGGTCTCGGCTTCGCTGC 22982           __   CAC
          G                      GCCCGGGTCTCGGT  CGTT   GCG
                                 ||||||||||||||  ||||   |||
                                 CGGGCCCAGAGCCG  GCGA   CGC
                                       AA   ___
GAM858  HSP105B   5' CCTCGGGTCTCGGTCTGC    22983    _         _
                                 CC CGGGTCTCGGTC GT
                                 || ||||||||||||
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                                GG GCCCAGAGCCAG CG
                                 A          A
GAM858  KIAA0963  5'  GCCCGGGTCCGGCCGGGCGCG  22984         T     TTCA
                                GCCCGGGTC CGGTCG    CGCG
                                ||||||||| ||||||    ||||
                                CGGGCCCAG GCCGGC    GCGC
                                      _     CC__
GAM858  LOC253392 5'  CCGGGTCTCGGAGGCGC     22985          TC TTCA
                                CCGGGTCTCGG  G    CGC
                                ||||||||||  |    |||
                                GGCCCAGAGCC  C    GCG
                                       TC _____
GAM858  LOC255990 5'  CCGGGTCTTGGTCGGGACAAGC 22986         C     TT_  C
          G                      CCGGGTCT GGTCG   CA GCG
                                ||||||||| |||||   || |||
                                GGCCCAGA CCAGC   GT CGC
                                     A     CCT  T
GAM858  LOC256078 5'  GCCCGGGTCTCGTGTGTT    22987           _  C
                                GCCCGGGTCTCG GT GTT
                                |||||||||||| || |||
                                CGGGCCCAGAGC CA CAA
                                       A  _
GAM859  BCL2L11   3'  TCGTGGGTGGTCTTCG      22990         T  T
                                TCGTGGGTG GT CTTCG
                                ||||||||| || |||||
                                AGCACCCAC CA GAAGC

                                      _  _
GAM859  BCL2L11   3'  TCGTGGGTGGTCTTCG      22990         T  T
                                TCGTGGGTG GT CTTCG
                                ||||||||| || |||||
                                AGCACCCAC CA GAAGC

                                      _  _
GAM859  BCL2L11   3'  TCGTGGGTGGTCTTCG      22990         T  T
                                TCGTGGGTG GT CTTCG
                                ||||||||| || |||||
                                AGCACCCAC CA GAAGC

                                      _  _
GAM859  BCL2L11   3'  TCGTGGGTGGTCTTCG      22990         T  T
                                TCGTGGGTG GT CTTCG
                                ||||||||| || |||||
                                AGCACCCAC CA GAAGC

                                      _  _
GAM859  BCL2L11   3'  TCGTGGGTGGTCTTCG      22990         T  T
                                TCGTGGGTG GT CTTCG
                                ||||||||| || |||||
                                AGCACCCAC CA GAAGC

                                      _  _
GAM859  GPR62     3'  TGGGGGTGAAGTCGTCCAGC   22991      T   TTCT
                                TGGG GTG    TCGTCCAGC
                                |||| |||    |||||||||
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                                ACCC CAC    AGCAGGTCG
                                  C   TTC_
GAM859  NAGA     3'  TCCTGGGTGTGAGGCAAGTCTG 22992    G      TTCTTC   CA
            GC                    TC TGGGTGTG     GTC  GC
                                ||  ||||||||      |||  ||
                                AG ACCCACAC     CAG  CG
                                 G       TCCGTT   AC
GAM859  SEC15B   3'  TGTGTGTGCTCTTTTTGTCTGG 22993    G       C__   CA
            C                     TG GTGTGTTCTT   GTC  GC
                                ||  ||||||||||   |||  ||
                                AC CACACGAGAA   CAG  CG
                                 A        AAA   AC
GAM859  LOC145809 5'  GGGTGTGTTGCCCAG      22994        CTTC
                                GGGTGTGTT    GTCCAG
                                |||||||||    ||||||
                                CCCACACAA    CGGGTC
                                      _____
GAM860  GPX3     3'  GAGCTGGTTTTTCCTTTGG    22997     CA      AGA
                                GAGC  GTTTTTTC   TGG
                                ||||  ||||||||   |||
                                CTCG  CAAAAAGG   ACC
                                  AC       AA_
GAM860  MECP2    3'  TGGCTAGTTTGGCACTGATGGA 22998    A  C    TTTCA_
            TT                    TG GC AGTTT     GATGGATT
                                ||  ||  |||||     ||||||||
                                AC CG TCAAA     CTACCTAA
                                 _  A    CCGTGA
GAM860  FLJ12747  3'  TGGGCCAGTTCTTTCAGAT    22999    A
                                TG GCCAGTTTTTTCAGAT
                                ||  ||||||||||||||||
                                AC CGGTCAAGAAAGTCTA
                                 C
GAM860  KIAA1034  3'  TGGCCAGTTTAAAGCATGGATT 23000    A       TTTC  _
                                TG GCCAGTTT    AG ATGGATT
                                ||  ||||||||    ||  |||||||
                                AC CGGTCAAA    TC TACCTAA
                                 _       TT__  G
GAM860  ZFP106   3'  TGAGTCAGTTTTTGTCAG    23001      C       _
                                TGAG CAGTTTTT TCAG
                                ||||  ||||||||  ||||
                                ACTC GTCAAAAA AGTC
                                  A       C
GAM860  LOC151121 5'  TGGCTAGTTTTCTCTTGTGG   23002    A  C       AGA
                                TG GC AGTTTTTTC   TGG
                                ||  ||  |||||||||   |||
                                AC CG TCAAAAGAG   ACC
                                 _  A        AAC
GAM860  LOC256581 5'  TGACCAGTTTTCTACTGGATT  23003     G        CAGA
                                TGA CCAGTTTTTT    TGGATT
                                |||  ||||||||||    ||||||
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                                ACT GGTCAAAAGA   ACCTAA
                                  _       TG__
GAM860  LOC54103  5'  TGAGCAGTTTTCAGGAGATGG  23004     C     TC_
                                TGAGC AGTTTTT  AGATGG
                                ||||| |||||||  ||||||
                                ACTCG TCAAAAG  TCTACC
                                  _     TCC
GAM860  LOC91561  5'  GAACTTTTTTTTCAGATGGATT 23005     CAG
                                GAGC  TTTTTTCAGATGGATT
                                ||||  ||||||||||||||||
                                CTTG  AAAAAAGTCTACCTAA
                                  AA_
GAM861  ADD2      3'  TCTCCTTCTTTTTGCTCT    23008     G     CTG
                                TCT CTTCTTTT  TGTTCT
                                ||| ||||||||  ||||||
                                AGA GAAGAAAA  ACGAGA
                                  G      ___
GAM861  ANKRA2    5'  TCTCTCCTTTTTTTTAATATT  23009     G  C  CT
                                TCTCT CTT TTTT  GTGTT
                                ||||| ||| ||||  |||||
                                AGAGA GAA AAAA  TATAA
                                   G  A   AT
GAM861  BACH1     3'  TCTGCTTCTTTTATAATC    23010        TC   T
                                TCTGCTTCTTT  TGTG TC
                                ||||||||||  |||| ||
                                AGACGAAGAAA  ATAT AG
                                      __   T
GAM861  BICD1     3'  TCTGTGCTTCGTGTTC     23011     C     TTTTCT
                                TCT TGCTTC     GTGTTC
                                ||| ||||||     ||||||
                                AGA ACGAAG     CACAAG
                                  C     _______
GAM861  CA14      5'  TCTCTGCTTTTCTTGCTGTCTC 23012        C  _  G
                                TCTCTGCTT TTTT CTGT TTC
                                ||||||||| |||| |||| |||
                                AGAGACGAA AGAA GACA GAG
                                     A   C   _
GAM861  CALD1     3'  TCTCTCTTCTTTTCAATACTTT 23013     G      TGTG__
              C                  TCTCT CTTCTTTTC     TTC
                                 ||||| |||||||||     |||
                                 AGAGA GAAGAAAAG     AAG
                                   _       TTATGA
GAM861  CALD1     3'  TCTCTCTTCTTTTCAATACTTT 23013     G      TGTG__
              C                  TCTCT CTTCTTTTC     TTC
                                 ||||| |||||||||     |||
                                 AGAGA GAAGAAAAG     AAG
                                   _       TTATGA
GAM861  CBFA2T1   3'  TCTCTGCTCTCTTTTCAGTTCT 23014       _     TGT
              C                  TCTCTGCT TCTTTTC   GTTCTC
                                 ||||||| |||||||   ||||||
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                                AGAGACGA AGAAAAG   CAAGAG
                                    G      T__
GAM861  CKTSF1B1  3'  TCAGCTTCTTTCCCTTTTC   23015    T        GTG
                                TC GCTTCTTTTCT   TTC
                                || ||||||||||   |||
                                AG CGAAGAAAGGG   AAG
                                 T         AA_
GAM861  CPD     3'  TCTCTCTTCTTAATGCAGTGTT 23016      G     TTCT__
           CTC                   TCTCT CTTCTT     GTGTTCTC
                                ||||| ||||||     ||||||||
                                AGAGA GAAGAA     CACAAGAG
                                   _     TTACGT
GAM861  CREBL2   3'  TCTCTACTCCTGTGTT      23017         CTTTT
                                TCTCTGCTT    CTGTGTT
                                |||||||||    |||||||
                                AGAGATGAG    GACACAA

                                   _____
GAM861  CYP1B1   3'  TCTTTCCTTCTTTTCAGTGTT  23018     CTG       T
                                TCT   CTTCTTTTC GTGTT
                                |||   ||||||||| |||||
                                AGA   GAAGAAAAG CACAA
                                  AAG       T
GAM861  CYP4F3   3'  TCTTTTCTTTTCTTTCT     23019     GC       GTG
                                TCT  TTCTTTTCT   TTCT
                                |||  |||||||||  ||||
                                AGA  AAGAAAAGA   AAGA
                                  A_       ___
GAM861  DSG1     5'  TCTCTGTTCTTTTCCTTTCTC  23020       C       GTG
                                TCTCTG TTCTTTTCT   TTCTC
                                ||||||| |||||||||  |||||
                                AGAGAC AAGAAAAGG   AAGAG
                                   _       A__
GAM861  DYRK1A   3'  CTGCTTCTTTTCTAGGCTTCT  23021            T  _
                                CTGCTTCTTTTCTG GTT CT
                                |||||||||||||| ||| ||
                                GACGAAGAAAAGAT CGA GA
                                        C   A
GAM861  DYRK1A   3'  CTGCTTCTTTTCTAGGCTTCT  23021            T  _
                                CTGCTTCTTTTCTG GTT CT
                                |||||||||||||| ||| ||
                                GACGAAGAAAAGAT CGA GA
                                        C   A
GAM861  DYRK1A   3'  CTGCTTCTTTTCTAGGCTTCT  23021            T  _
                                CTGCTTCTTTTCTG GTT CT
                                |||||||||||||| ||| ||
                                GACGAAGAAAAGAT CGA GA
                                        C   A
GAM861  EGFL6    3'  TCTGTGCTTTTTTTTCTATTTT 23022     C    C_      G
           C                     TCT TGCTT  TTTTCTGT TTC
                                ||| |||||  |||||||| |||
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                                AGA ACGAA  AAAAGATA AAG
                                  C    AA      A
GAM861  FBXW7   3'  TCTCTTCTTCTTTTCCTTCT  23023      G       GTG
                                TCTCT CTTCTTTTCT  TTCT
                                ||||| ||||||||||  ||||
                                AGAGA GAAGAAAAGG  AAGA
                                   A       ___
GAM861  FBXW7   3'  TCTCTTCTTCTTTTCCTTCT  23023      G       GTG
                                TCTCT CTTCTTTTCT  TTCT
                                ||||| ||||||||||  ||||
                                AGAGA GAAGAAAAGG  AAGA
                                   A       ___
GAM861  GPC6    3'  TCTCTGTTTGCTTTTTTGT   23024      C _    C
                                TCTCTG TT CTTTT TGT
                                |||||| || ||||| |||
                                AGAGAC AA GAAAA ACA
                                    A C    A
GAM861  HUNK    3'  TCTCTGATTTCTCTGTGTTCT 23025      CTTC
                                TCTCTG   TTTTCTGTGTTCT
                                ||||||   ||||||||||||
                                AGAGAC   AAGAGACACAAGA
                                   TA__
GAM861  MBP     3'  TCTGTTTTCATGTTCT     23026     CTTC    T
                                TCTG   TTTTC GTGTTCT
                                ||||   ||||| |||||||
                                AGAC   AAAAG TACAAGA
                                  ____   _
GAM861  MOX2    3'  TCTCTGTATTCTTTCTTCT   23027      C_     CTGTG
                                TCTCTG  TTCTTTT    TTCT
                                ||||||  |||||||    ||||
                                AGAGAC  AAGAAAG    AAGA
                                   AT     _____
GAM861  MTMR6   3'  TCTCTTTTTTTTTCTATATT  23028      GC  C
                                TCTCT  TT TTTTCTGTGTT
                                |||||  || ||||||||||
                                AGAGA  AA AAAAGATATAA
                                   A_  A
GAM861  PSG1    5'  TCTCTGCTGCTTGTGTGTTCTC 23029       T   TTC
                                TCTCTGCT CTT   TGTGTTCTC
                                |||||||| |||   |||||||||
                                AGAGACGA GAA   ACACAAGAG
                                    C   C__
GAM861  PSG2    5'  TCTCTGCTGCCTGTGTGTTCTC 23030       T   TTC
                                TCTCTGCT CTT   TGTGTTCTC
                                |||||||| |||   |||||||||
                                AGAGACGA GGA   ACACAAGAG
                                    C   C__
GAM861  PSG4    5'  TCTCTGCTGCTTGTGTGTTCTC 23029       T   TTC
                                TCTCTGCT CTT   TGTGTTCTC
                                |||||||| |||   |||||||||
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                                AGAGACGA GAA   ACACAAGAG
                                     C   C__
GAM861   PSG6     5'  TCTCTGCTGTCTGTGTGTTCTC 23031        _   TTTC
                                TCTCTGCT TCT    TGTGTTCTC
                                |||||||| |||    |||||||||
                                AGAGACGA AGA    ACACAAGAG
                                     C   C___
GAM861   PSG9     5'  TCTCTGCTGCCTGTGTGTTCTC 23030         T   TTC
                                TCTCTGCT CTT   TGTGTTCTC
                                |||||||| |||   |||||||||
                                AGAGACGA GGA   ACACAAGAG
                                     C   C__
GAM861   RAP1     3'  TTCTTTTCTTTTTATCCCC    23032         G__
                                TTCTTTTCT   TGTTCTC
                                |||||||||   |||||||
                                AAGAAAAGA   ATAGGGG
                                      AAA
GAM861   SALL2    5'  TCTCTGATTCTCTGTTCT     23033       C     TTCTG
                                TCTCTG TTCTT     TGTTCT
                                ||||||| |||||     ||||||
                                AGAGAC AAGAG     ACAAGA
                                    T    _____
GAM861   SLC6A3   3'  TCTTCTGCTTTGTTGTTTGTGT 23034     _     CTTTTC_
            T                    TCT CTGCTT      TGTGTT
                                 ||| ||||||      ||||||
                                 AGA GACGAA      ACACAA
                                   A     ACAACAA
GAM861   TMPRSS3  3'  CTGCTTCTTTTGTTCT      23035          TCTG
                                CTGCTTCTTT    TGTTCT
                                ||||||||||    ||||||
                                GACGAAGAAA    ACAAGA
                                      ____
GAM861   TMPRSS3  3'  CTGCTTCTTTTGTTCT      23035          TCTG
                                CTGCTTCTTT    TGTTCT
                                ||||||||||    ||||||
                                GACGAAGAAA    ACAAGA
                                      ____
GAM861   TMPRSS3  3'  CTGCTTCTTTTGTTCT      23035          TCTG
                                CTGCTTCTTT    TGTTCT
                                ||||||||||    ||||||
                                GACGAAGAAA    ACAAGA
                                      ____
GAM861   ABCA5    5'  TCTTTTTTTCTTTTCTGAATTC 23036     GC__        T
            TC                    TCT    TTCTTTTCTG GTTCTC
                                  |||    |||||||||| ||||||
                                  AGA    AAGAAAAGAC TAAGAG
                                    AAAA         T
GAM861   ADAR3    5'  TCTCTGTCTCTCGAATTGTTCT 23037       CT    TTCTG
            C                     TCTCTG  TCTT     TGTTCTC
                                  ||||||  ||||     |||||||
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                                AGAGAC  AGAG    ACAAGAG
                                   AG   CTTA_
GAM861  AGTRL2    5'  TCTTTTGTGTGTTTTCTGTGTT 23038    GCTTC___
            CT                   TCT       TTTTCTGTGTTCT
                                 |||       ||||||||||||
                                 AGA       AAAAGACACAAGA
                                   AAACACAC
GAM861  ARHGAP11A 5'  TCTGATTCTTTCGGTTTCTC  23039     C      CTGTG
                                 TCTG TTCTTTT    TTCTC
                                 |||| |||||||    |||||
                                 AGAC AAGAAAG    AAGAG
                                   T      CCA__
GAM861  BHMT      3'  TCTCTACTTTTTTTTTAT    23040         C   C
                                 TCTCTGCTT TTTT TGT
                                 |||||||| |||| |||
                                 AGAGATGAA AAAA ATA
                                       A   A
GAM861  ChGn      3'  TCTTTTCTTTTCTGGTC     23041     GC        T
                                 TCT  TTCTTTTCTG GTT
                                 |||  |||||||||| |||
                                 AGA  AAGAAAAGAC CAG
                                   A_        _
GAM861  CNNM1     3'  TCTTTTCTTTTCTCTTTCT   23042     GC       GTG
                                 TCT  TTCTTTTCT   TTCT
                                 |||  |||||||||   ||||
                                 AGA  AAGAAAAGA   AAGA
                                   A_       GA_
GAM861  DKFZp761F2014 3'  TCTCTGCTCTTTTCTAT     23043         T
                                 TCTCTGCT CTTTTCTGT
                                 |||||||| |||||||||
                                 AGAGACGA GAAAAGATA
                                      _
GAM861  DKFZP761G1913 3'  TCTCTGCTCCTTTTTTGT    23044             C
                                 TCTCTGCTTCTTTT TGT
                                 |||||||||||||| |||
                                 AGAGACGAGGAAAA ACA
                                          A
GAM861  FLJ10898  3'  TCTGTTTTCTACTGGTTCT   23045     C_   TTT   T
                                 TCTG  TTCT   CTG GTTCT
                                 ||||  ||||   ||| |||||
                                 AGAC  AAGA   GAC CAAGA
                                   AA    T__   _
GAM861  FLJ12643  3'  TCTTTGCTTTTCTGGTT     23046     C    CTT    T
                                 TCT TGCTT   TTCTG GTT
                                 ||| |||||   ||||| |||
                                 AGA ACGAA   AAGAC CAA
                                   A    ____    _
GAM861  FLJ13910  3'  TCTCTTTGCTTCTGTGTT    23047      GCTTCT
                                 TCTCT     TTTCTGTGTT
                                 |||||     ||||||||||
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                                AGAGA     GAAGACACAA
                                  AAC___
GAM861  FLJ13984  3'  TCTCTTCTTTTTTTCTCATTGT 23048      G  C     G__
           C                     TCTCT CTT TTTTCT   TGTT
                                 ||||| ||| ||||||   ||||
                                 AGAGA GAA AAAAGA   ACAG
                                    A  A     GTA
GAM861  FLJ14457  3'  TCTCAGCTTCTTTTCAGCTC   23049     T        TGT
                                 TCTC GCTTCTTTTC   GTTC
                                 |||| ||||||||||   ||||
                                 AGAG CGAAGAAAAG   CGAG
                                   T        T__
GAM861  FLJ20150  5'  TCTCTGCTCTTTGATTCT    23050        T  TTC  T
                                 TCTCTGCT CTT   TG GTTCT
                                 |||||||| |||   || |||||
                                 AGAGACGA GAA   AC TAAGA
                                      _  ___  _
GAM861  FLJ20249  3'  TCTTCTGTTTCTTTTTGGCTTT 23051    _  C     CT  G
           C                     TCT CTG TTCTTTT  GT TTC
                                 ||| ||| |||||||  || |||
                                 AGA GAC AAGAAAA  CG AAG
                                   A  A      AC  A
GAM861  FLJ20309  3'  TCTCTTCTTCTTGTGTT     23052      G    TTTC
                                 TCTCT CTTCT    TGTGTT
                                 ||||| |||||    ||||||
                                 AGAGA GAAGA    ACACAA
                                   A    _____
GAM861  FLJ21159  3'  TCTTTGCTCTTTCATATTCTC  23053    C   T    CT
                                 TCT TGCT CTTTT  GTGTTCTC
                                 ||| |||| |||||  ||||||||
                                 AGA ACGA GAAAG  TATAAGAG
                                   A  _    __
GAM861  FLJ22418  3'  GCTTCTTTTTGTTTCT      23054         C  G
                                 GCTTCTTTT TGT TTCT
                                 ||||||||| ||| ||||
                                 CGAAGAAAA ACA AAGA
                                      _  _
GAM861  FOXP1     3'  TCTCTTTTTTTTTTCTGTCATT 23055      GC  C      _
           C                     TCTCT  TT TTTTCTGT GTTC
                                 |||||  || |||||||| ||||
                                 AGAGA  AA AAAAGACA TAAG
                                    AA  A       G
GAM861  HEMGN     5'  TCTCTGCTGCTTGCGTT     23056        T  TTTC
                                 TCTCTGCT CT    TGTGTT
                                 |||||||| ||    ||||||
                                 AGAGACGA GA    ACGCAA
                                      C  _____
GAM861  KIAA0494  3'  TCTCTTCTTTTGGTTCT     23057     G      TC  T
                                 TCT CTTCTTT  TG GTTCT
                                 ||| |||||||  || |||||
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                                AGA GAAGAAA  AC CAAGA
                                  _     __ _
GAM861  KIAA0625 5' TCTCTGTATCTTTCTTCT    23058       CT     CTGTG
                                TCTCTG  TCTTTT    TTCT
                                ||||||  ||||||    ||||
                                AGAGAC  AGAAAG    AAGA
                                   AT     _____
GAM861  KIAA0841 3' TCTGTTTCTTTTGTTC      23059      C     TCTG
                                TCTG TTCTTT    TGTTC
                                |||| ||||||    |||||
                                AGAC AAGAAA    ACAAG
                                  A     ____
GAM861  KIAA1026 3' TCTTTCTTCTTTTTCCGT    23060     CTG       _
                                TCT   CTTCTTTT CTGT
                                |||   |||||||| ||||
                                AGA   GAAGAAAA GGCA
                                  AA_       A
GAM861  LGI4     5' TCTGTTTCTCTTTCTCCCTGTC 23061      C     ___   G
                                TCTG TTCTTT   TCT TGTT
                                |||| ||||||   ||| ||||
                                AGAC AAGAGA   AGG ACAG
                                  A     AAG   G
GAM861  LZ16     3' CGTTTCTTTTCTGTAGTC    23062    C          T
                                TG TTCTTTTCTGTG TC
                                || ||||||||||| ||
                                GC AAGAAAAGACAT AG
                                 A          C
GAM861  MGC16153 3' TCTTCTTCTTTAGTGGTTCTC  23063     G      TC  T
                                TCT CTTCTTT  TG GTTCTC
                                ||| |||||||  || ||||||
                                AGA GAAGAAA  AC CAAGAG
                                  A      TC  _
GAM861  MGC20647 5' TCTCTTTTTCTTTTCTTTCT   23064      GC       GTG
                                TCTCT  TTCTTTTCT   TTCT
                                |||||  |||||||||   ||||
                                AGAGA  AAGAAAAGA   AAGA
                                   AA       ___
GAM861  NKX2B    3' TCTCTGTATTTTTAAAGTGTTC 23065       CTTC   TCT
           TC                    TCTCTG    TTT   GTGTTCTC
                                ||||||    |||   ||||||||
                                AGAGAC    AAA   CACAAGAG
                                   ATAA   TTT
GAM861  PPP1R3B  3' TCTCTTTTTTTTTCTGT     23066      GC  C
                                TCTCT  TT TTTTCTGT
                                |||||  || ||||||||
                                AGAGA  AA AAAAGACA
                                   A_  A
GAM861  PRDM7    3' TGCTTCTTTTTCCTTTTC     23067          _  GTG
                                TGCTTCTTTT CT   TTC
                                |||||||||| ||   |||
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                                ACGAAGAAAA GG   AAG
                                     A  AA_
GAM861  PRKCBP1   5'  TTCTTTTCTGGGCTGTTCTC  23068          ___
                                TTCTTTTCTG   TGTTCTC
                                ||||||||||   |||||||
                                AAGAAAAGAC   ACAAGAG
                                     CCG
GAM861  PRO0097   5'  TCTGCTTCTTTTTAAATTATTC 23069          CTG__
           T                    TCTGCTTCTTTT    TGTTCT
                                ||||||||||||    ||||||
                                AGACGAAGAAAA    ATAAGA
                                      ATTTA
GAM861  S164      5'  TCTCTTCTTCTTTCTTCT    23070      G      CTGTG
                                TCTCT CTTCTTTT    TTCT
                                ||||| ||||||||    ||||
                                AGAGA GAAGAAAG    AAGA
                                   A      _____
GAM861  SAMHD1    3'  TCTTTCTTTTCTTTCTC     23071     GC      GTG
                                TCT  TTCTTTTCT   TTCTC
                                |||  |||||||||   |||||
                                AGA  AAGAAAAGA   AAGAG
                                  __       ___
GAM861  SV2       5'  CCTGCTTCTTTTTCAGCT    23072          CT T
                                TCTGCTTCTTTT  G GTT
                                ||||||||||||  | |||
                                GGACGAAGAAAA  T CGA
                                      AG _
GAM861  TBL1Y     3'  TCTTTTCTTTTTTTCTATATT  23073    CTG   C
                                TCT   CTT TTTTCTGTGTT
                                |||   ||| ||||||||||||
                                AGA   GAA AAAAGATATAA
                                  AAA   A
GAM861  TBL1Y     3'  TCTTTTCTTTTTTTCTATATT  23073    CTG   C
                                TCT   CTT TTTTCTGTGTT
                                |||   ||| ||||||||||||
                                AGA   GAA AAAAGATATAA
                                  AAA   A
GAM861  TBL1Y     3'  TCTTTTCTTTTTTTCTATATT  23073    CTG   C
                                TCT   CTT TTTTCTGTGTT
                                |||   ||| ||||||||||||
                                AGA   GAA AAAAGATATAA
                                  AAA   A
GAM861  UST       3'  CTGCTTCTTTTTGATGTCTC  23074          CT    T
                                CTGCTTCTTTT  GTGT CTC
                                ||||||||||||  |||| |||
                                GACGAAGAAAA  TACA GAG
                                      AC    _
GAM861  LOC113612 3'  TCTTTTCTTTTTGTGCT     23075     GC      C
                                TCT  TTCTTTT TGTGTT
                                |||  ||||||| ||||||
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                                AGA  AAGAAAA ACACGA
                                  A_     _
GAM861   LOC123876 3'  TCTTTCTTCTTTCTCTTTCTC  23076     CTG      T  GTG
                                TCT   CTTCTTT CT   TTCTC
                                |||   ||||||| ||   |||||
                                AGA   GAAGAAA GA   AAGAG
                                  AA_      _ GA_
GAM861   LOC129526 3'  TCTTAGTTTCTTTTCTATGGCT 23077     GC__         _
             C                   TCT    TTCTTTTCTGTG TTC
                                |||    |||||||||||| |||
                                AGA    AAGAAAAGATAC GAG
                                  ATCA          C
GAM861   LOC139274 5'  CTGCTGCTTGTGTTCT      23078       T  TTTC
                                CTGCT CT    TGTGTTCT
                                ||||| ||    ||||||||
                                GACGA GA    ACACAAGA
                                   C  ____
GAM861   LOC145601 5'  TCTGCTTCTTTATTCCC     23079          TTCTG
                                TCTGCTTCTT     TGTTCTC
                                ||||||||||     |||||||
                                AGACGAAGAA     ATAAGGG
                                       _____
GAM861   LOC152190 5'  TCTCGCTTCTTTTTATCCT    23080      T        CTG
                                TCTC GCTTCTTTT   TGTTCT
                                |||| |||||||||   ||||||
                                AGAG CGAAGAAAA   ATAGGA
                                  _      ___
GAM861   LOC153761 5'  TCTATGCTTCTTTTTGTAGCCT 23081     C        C    TT
             C                   TCT TGCTTCTTTT TGTG  CTC
                                ||| |||||||||| ||||  |||
                                AGA ACGAAGAAAA ACAT  GAG
                                  T         _    CG
GAM861   LOC158714 5'  TCTCTCTTCTTTTCTAGGTT   23082       G         T
                                TCTCT CTTCTTTTCTG GTT
                                ||||| |||||||||| |||
                                AGAGA GAAGAAAAGAT CAA
                                   _          C
GAM861   LOC163944 5'  TCCTGCTGCACTTCTGTGTTCT 23083     T     TCT
                                TC CTGCT   TTTCTGTGTTCT
                                || |||||   ||||||||||||
                                AG GACGA   GAAGACACAAGA
                                  _    CGT
GAM861   LOC196374 5'  TCTGCTTCTTGAGGTTCTC    23084          TTCTGT
                                TCTGCTTCTT     GTTCTC
                                ||||||||||     ||||||
                                AGACGAAGAA     CAAGAG
                                       CTC___
GAM861   LOC199221 5'  TCCTGTTTCTTCTGTTTTC    23085    T  C    TT    G
                                TC CTG TTCT  TCTGT TTC
                                || ||| ||||  ||||| |||
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                                AG GAC AAGA  AGACA AAG
                                 _  A   __    A
GAM861  LOC201617 3'  TCTGTCTCTTTTCTCTACT   23086     CT      G
                                TCTG  TCTTTTCT TGTT
                                ||||  |||||||| ||||
                                AGAC  AGAAAAGA ATGA
                                  AG       G
GAM861  LOC202460 5'  TCTGTTTCTCTTCACTTTCT   23087     C      TGTG
                                TCTG TTCTTTTC    TTCT
                                |||| ||||||||    ||||
                                AGAC AAGAGAAG    AAGA
                                  A       TGA_
GAM861  LOC220515 5'  TCATACGTCCTTTTTTGTGTT  23088    _  _     C
                                TC TGC TTCTTTT TGTGTT
                                || ||| ||||||| ||||||
                                AG ATG AGGAAAA ACACAA
                                 T  C      A
GAM861  LOC220515 3'  TCTCTTCTTTTTTTTCTCATTGT 23048      G  C    G__
          C                      TCTCT CTT TTTTCT   TGTT
                                |||||| ||| ||||||   ||||
                                AGAGA GAA AAAAGA   ACAG
                                  A  A     GTA
GAM861  LOC220692 5'  TCTGCATTCTTCTTGTTCT    23089      _     CTG
                                TCTGC TTCTTTT   TGTTCT
                                ||||| |||||||   ||||||
                                AGACG AAGAAGA   ACAAGA
                                  T      ___
GAM861  LOC254221 5'  TCTCTGCTTTTTTTTCCTTCTC  23090         C     GTG
                                TCTCTGCTT TTTTCT   TTCTC
                                |||||||||| ||||||   |||||
                                AGAGACGAA AAAAGG   AAGAG
                                     A     ___
GAM861  LOC51290  3'  TCTGCTTATTTGTGTT      23091        C  TTC
                                TCTGCTT TT   TGTGTT
                                ||||||| ||   ||||||
                                AGACGAA AA   ACACAA
                                    T  ___
GAM861  LOC90288  3'  TCCTGTTTCTTTCCTCTTTCT  23092    T  C       GTG
                                TC CTG TTCTTTTCT   TTCT
                                || ||| |||||||||   ||||
                                AG GAC AAGAAAGGA   AAGA
                                 _  A        GA_
GAM861  LOC91012  5'  TCTCTGTTTCTTTGCCCAC    23093       C     _  TG
                                TCTCTG TTCTTT TC  T
                                |||||| |||||| ||  |
                                AGAGAC AAGAAA GG  G
                                   A     C  GT
GAM862  ABCD4     3'  TCCTCCTGGTCTCTCCT     23096     _    GT
                                TCC CCTGG  TTTCTCCT
                                ||| |||||  ||||||||
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                                AGG GGACC  AGAGAGGA
                                  A    __
GAM862  ADAMTS4  5' TCCTCCTGAGCCCTCCT    23097    _     TT
                                TCC CCTGGGT  TCTCCT
                                ||| |||||||  ||||||
                                AGG GGACTCG  GGAGGA
                                  A     __
GAM862  ASIC4    5' TCTCCTCGATCGTCTCCT    23098    C   G    T
                                TC CCT GGTT TCTCCT
                                || ||| |||| ||||||
                                AG GGA CTAG AGAGGA
                                 A  G    C
GAM862  B4GALT2  3' CCTCCTGGGGCTGCTCCT    23099    _     T  T
                                CC CCTGGG TT CTCCT
                                || |||||| || |||||
                                GG GGACCC GA GAGGA
                                 A     C  C
GAM862  B4GALT2  3' CCTCCTGGGGCTGCTCCT    23099    _     T  T
                                CC CCTGGG TT CTCCT
                                || |||||| || |||||
                                GG GGACCC GA GAGGA
                                 A     C  C
GAM862  BRF2     3' TCCCCAGTTCCCGCTCCT    23100      TG     __
                                TCCCC  GGTTTT  CTCCT
                                |||||  ||||||  |||||
                                AGGGG  TCAAGG  GAGGA
                                   __     GC
GAM862  CACNA1D  3' TCCCCTGGCTCTCCT      23101        GTT
                                TCCCCTGG   TTCTCCT
                                ||||||||   |||||||
                                AGGGGACC   GAGAGGA
                                    ___
GAM862  CCND1    3' TCCCCTCGGGAGCCTCCT    23102      _  TTT
                                TCCCCT GGG   TCTCCT
                                |||||| |||   ||||||
                                AGGGGA CCC   GGAGGA
                                   G   TC_
GAM862  CCR2     3' TCTCCCTCCTTCTCCT     23103    _   GGG
                                TC CCCT   TTTTCTCCT
                                || ||||   |||||||||
                                AG GGGA   GGAAGAGGA
                                 A   ___
GAM862  CDX2     5' TCCCTCTGGCCTGCCTCCT   23104     _   G  T
                                TCCC CTGG TT TCTCCT
                                |||| |||| || ||||||
                                AGGG GACC GA GGAGGA
                                  A   G  C
GAM862  CERD4    3' TCACCTGAATTCTCCT     23105    C      TT
                                TC CCTGGGT  TCTCCT
                                || |||||||  ||||||
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                                AG GGACTTA  AGAGGA
                                 T     __
GAM862  COL17A1  5'  TCTCCTGATGTTTTCTTCTA  23106   C   _     C  III
                                TC CCTGG GTTTTCT CT   A
                                || ||||| ||||||| ||   |
                                AG GGACT CAAAAGA GA   T
                                 A    A      A  III
GAM862  COL17A1  5'  TCTCCTGATGTTTTCTTCTA  23106   C   _     C  III
                                TC CCTGG GTTTTCT CT   A
                                || ||||| ||||||| ||   |
                                AG GGACT CAAAAGA GA   T
                                 A    A      A  III
GAM862  CYP4B1   3'  TCCCCTAAGCCATTCTTCT   23107         _   C
                                TCCCCTGGGTT TTCT CT
                                |||||||||| |||| ||
                                AGGGGATTCGG AAGA GA
                                       T   A
GAM862  DDX11    3'  TCCCCCATTTTCTCCT     23108      GG
                                TCCCCT  GTTTTCTCCT
                                ||||||  ||||||||||
                                AGGGGG  TAAAAGAGGA
                                   __
GAM862  DGCR6    3'  TCCACCTGGTCTCTCCT     23109    _   GT
                                TCC CCTGG  TTTCTCCT
                                ||| |||||  ||||||||
                                AGG GGACC  AGAGAGGA
                                 T    __
GAM862  DLG4     5'  TCCTCCTGGGCCTCCT      23110    _     TTT
                                TCC CCTGGGT   CTCCT
                                ||| |||||||   |||||
                                AGG GGACCCG   GAGGA
                                 A     ___
GAM862  DLX4     3'  TCCATTCCTTTTTCTCCT    23111    ___  GGG
                                TCC   CCT   TTTTCTCCT
                                |||   |||   |||||||||
                                AGG   GGA   AAAAGAGGA
                                  TAA  ___
GAM862  DLX4     3'  TCCATTCCTTTTTCTCCT    23111    ___  GGG
                                TCC   CCT   TTTTCTCCT
                                |||   |||   |||||||||
                                AGG   GGA   AAAAGAGGA
                                  TAA  ___
GAM862  DPH2L1   3'  TCCCCATGTCACCCTCCT    23112      TGG  _
                                TCCCC   GTT TTCTCCT
                                |||||   ||| |||||||
                                AGGGG   CAG GGGAGGA
                                   TA_   T
GAM862  DTNB     3'  TCCTCTGTGTCCGGCTCCT   23114    C  G   T_
                                TCC CTG GTTT  CTCCT
                                ||| ||| ||||  |||||
```

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                                AGG GAC CAGG  GAGGA
                                  A   A    CC
GAM862  DTNB    5'  TCTCCTGCGGCCTCACTCCT  23113    C   _     _
                                TC CCTG GGTTTT CTCCT
                                || |||| |||||| |||||
                                AG GGAC CCGGAG GAGGA
                                 A    G      T
GAM862  DTNB    3'  TCCTCTGTGTCCGGCTCCT   23114     C  G    T_
                                TCC CTG GTTT  CTCCT
                                ||| ||| ||||  |||||
                                AGG GAC CAGG  GAGGA
                                  A   A    CC
GAM862  DTNB    5'  TCTCCTGCGGCCTCACTCCT  23113    C   _     _
                                TC CCTG GGTTTT CTCCT
                                || |||| |||||| |||||
                                AG GGAC CCGGAG GAGGA
                                 A    G      T
GAM862  DTNB    5'  TCTCCTGCGGCCTCACTCCT  23113    C   _     _
                                TC CCTG GGTTTT CTCCT
                                || |||| |||||| |||||
                                AG GGAC CCGGAG GAGGA
                                 A    G      T
GAM862  DXS1283E  3'  CCCTGCACAAGTTTTCTTCTA  23115       ____       C  III
                                CCCTG    GGTTTTCT CT   A
                                |||||    |||||||| ||   |
                                GGGAC    TCAAAAGA GA   T
                                   GTGT       A  III
GAM862  EIF4G1    5'  TCCTCTGTGATATCCTTTCCT  23116     C   _   T   __
                                TCC CTG GGT TTC  TCCT
                                ||| ||| ||| |||  ||||
                                AGG GAC CTA AGG  AGGA
                                  A   A   T   AA
GAM862  EIF5A     3'  TCCCCTCCCCTCTCCT      23117        GGG
                                TCCCCT   TTTTCTCCT
                                ||||||   |||||||||
                                AGGGGA   GGGAGAGGA
                                   G__
GAM862  EMX2      3'  TCCCTCCCTCTTTCTCCT    23118      _ GGG
                                TCCC CT   TTTTCTCCT
                                |||| ||   |||||||||
                                AGGG GG   GAAAGAGGA
                                  A  GA_
GAM862  ENAM      3'  TCCTGCCTTCCCTTCTCCT   23119     __  GGG
                                TCC  CCT   TTTTCTCCT
                                |||  |||   |||||||||
                                AGG  GGA   GGAAGAGGA
                                  AC   AG_
GAM862  ENTPD1    3'  CCCTGGACGATTTTTTCCT   23120       ___    C
                                CCCTGG   GTTTT TCCT
                                ||||||   ||||| ||||
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                                GGGACC   TAAAA AGGA
                                   TGC     A
GAM862  FACL2    3'  TCCTCTGAGCTTTCTTCT    23121     C         C
                                TCC CTGGGTTTTCT CT
                                ||| |||||||||| ||
                                AGG GACTCGAAAGA GA
                                  A          A
GAM862  FCGR2B   3'  TCCCTCTCTGATTTTCTTCT  23122     _ G_      C
                                TCCC CT  GGTTTTCT CT
                                |||| ||  |||||||| ||
                                AGGG GA  CTAAAAGA GA
                                  A GA       A
GAM862  G6PD     5'  TCCTCTGGGCTGTCCCT     23123     C      T  T
                                TCC CTGGGTT TC CCT
                                ||| ||||||| || |||
                                AGG GACCCGA AG GGA
                                  A      C _
GAM862  GABRP    5'  TCCCCAGGGTTCTCCT      23124      T    TT
                                TCCCC GGGT  TCTCCT
                                ||||| ||||  ||||||
                                AGGGG CCCA  AGAGGA
                                   T   __
GAM862  GNG2     5'  TCCCTCTGTCTCTCCT      23125     _  GGT
                                TCCC CTG   TTTCTCCT
                                |||| |||   ||||||||
                                AGGG GAC   AGAGAGGA
                                  A  ____
GAM862  GNGT2    5'  TCGCCTGCTTTCTCCT      23126    C   GG
                                TC CCT  GTTTTCTCCT
                                || |||  ||||||||||
                                AG GGA  CGAAAGAGGA
                                 C  __
GAM862  IFI27    3'  TCCCCTGGCATGGTTCTCT   23127        _____
                                TCCCCTGG    GTTTTCT
                                ||||||||    |||||||
                                AGGGGACC    CAAGAGA
                                     GTAC
GAM862  KCNMB3   5'  TCACCCTCCTTCTCCT      23128    _   GGG
                                TC CCCT   TTTTCTCCT
                                || ||||   |||||||||
                                AG GGGA   GGAAGAGGA
                                 T   ____
GAM862  KLF8     5'  CCCCCTGCAGCTTTTCCT    23129       _     C
                                TCCCCTG GGTTTT TCCT
                                ||||||| |||||| ||||
                                GGGGGAC TCGAAA AGGA
                                    G     _
GAM862  KLK8     5'  TCCTCCTCCTTCTCCT      23130     _  GGG
                                TCC CCT   TTTTCTCCT
                                ||| |||   |||||||||
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                              AGG GGA   GGAAGAGGA
                                A  ___
GAM862  KLK8    5'  TCCTCCTCCTTCTCCT     23130    _  GGG
                              TCC CCT   TTTTCTCCT
                              ||| |||   |||||||||
                              AGG GGA   GGAAGAGGA
                                A  ___
GAM862  KLK8    5'  TCCTCCTCCTTCTCCT     23130    _  GGG
                              TCC CCT   TTTTCTCCT
                              ||| |||   |||||||||
                              AGG GGA   GGAAGAGGA
                                A  ___
GAM862  KLK8    5'  TCCTCCTCCTTCTCCT     23130    _  GGG
                              TCC CCT   TTTTCTCCT
                              ||| |||   |||||||||
                              AGG GGA   GGAAGAGGA
                                A  ___
GAM862  KPNB1   5'  TCCCCTTCCTCTCCT      23131      GGG
                              TCCCCT   TTTTCTCCT
                              ||||||   |||||||||
                              AGGGGA   AGGAGAGGA
                                  ___
GAM862  LOXL1   5'  CCCCCTGGGCGTGCTTCT   23132        ___
                              TCCCCTGGGT   TTTCT
                              ||||||||||   |||||
                              GGGGGACCCG   GAAGA
                                    CAC
GAM862  MGAT1   5'  TCCTCCTGGCCCGCCTCCT   23133    _    G TT
                              TCC CCTGG T  TCTCCT
                              ||| ||||| |  ||||||
                              AGG GGACC G  GGAGGA
                                A    G GC
GAM862  MRE11A  5'  TCCTCTGGGACCAGGTTCTTCT 23134    C    TT____   C  III
          A                    TCC CTGGG     TTCT CT   A
                              ||| |||||     |||| ||   |
                              AGG GACCC     AAGA GA   T
                                A    TGGTCC    A  III
GAM862  MRE11A  5'  TCCTCTGGGACCAGGTTCTTCT 23134    C    TT____   C  III
          A                    TCC CTGGG     TTCT CT   A
                              ||| |||||     |||| ||   |
                              AGG GACCC     AAGA GA   T
                                A    TGGTCC    A  III
GAM862  MUC4    5'  TCACCCTTTTCTCTCCT     23135    _  GGG
                              TC CCCT   TTTTCTCCT
                              || ||||   |||||||||
                              AG GGGA   AAGAGAGGA
                               T   A__
GAM862  MUC4    5'  TCACCCTTTTCTCTCCT     23135    _  GGG
                              TC CCCT   TTTTCTCCT
                              || ||||   |||||||||
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                                AG GGGA   AAGAGAGGA
                                 T   A__
GAM862  Nrap     3'  TCTCCTGGGTTCAGTTCCT   23136    C       TC_
                                TC CCTGGGTTT   TCCT
                                || |||||||||  ||||
                                AG GGACCCAAG   AGGA
                                 A        TCA
GAM862  Nrap     3'  TCTCCTGGGTTCAGTTCCT   23136    C       TC_
                                TC CCTGGGTTT   TCCT
                                || |||||||||  ||||
                                AG GGACCCAAG   AGGA
                                 A        TCA
GAM862  OXTR     5'  TCTGCTGGGTCCACCCTCCT  23137    CC      __
                                TC  CTGGGTTT  TCTCCT
                                ||  ||||||||  ||||||
                                AG  GACCCAGG  GGAGGA
                                 AC       TG
GAM862  PAFAH1B1 5'  TCCCCTCCTTCTCCT      23138      GGG
                                TCCCCT   TTTTCTCCT
                                ||||||   |||||||||
                                AGGGGA   GGAAGAGGA
                                   ___
GAM862  PATE     3'  TCCCAATCTTCTCCT      23139     CTG
                                TCCC   GGTTTTCTCCT
                                ||||   ||||||||||
                                AGGG   TTAGAAGAGGA
                                   ___
GAM862  PEX13    5'  TCCTCTCGGCTCCCGCTCCT  23140     C  G    __
                                TCC CT GGTTTT  CTCCT
                                ||| || ||||||  |||||
                                AGG GA CCGAGG  GAGGA
                                  A  G     GC
GAM862  PLAB     5'  TCCTCCTGGCTCTCCT      23141    _    GTT
                                TCC CCTGG   TTCTCCT
                                ||| |||||   |||||||
                                AGG GGACC   GAGAGGA
                                  A    ____
GAM862  POLR2E   3'  TCCCCTTGTCTCTCCT      23142      GG   T
                                TCCCCT  GTTT CTCCT
                                ||||||  |||| |||||
                                AGGGGA  CAGA GAGGA
                                   A_   _
GAM862  PRDM2    3'  TCCTCCTGAAGGCCTTCC    23143    _   __
                                TCC CCTG  GGTTTTCT
                                ||| ||||  ||||||||
                                AGG GGAC  CCGGAAGG
                                  A   TT
GAM862  PRKCN    3'  TCCCCTTGCCTCAGTTTTCT  23144      _ ____
                                TCCCCT G   GGTTTTCT
                                |||||| |   ||||||||
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                                AGGGGA C    TCAAAAGA
                                   A GGAG
GAM862  PVR      5'  TCCCCGGGGGGCCGCTCCT   23145      T__    TT
                                TCCCC   GGGTT  CTCCT
                                |||||   |||||  |||||
                                AGGGG   CCCGG  GAGGA
                                   CCC    C_
GAM862  RBM8A    3'  TCCTTTGGATCCTCTCCT    23146     CC
                                TCC  TGGGTTTTCTCCT
                                |||  ||||||||||||
                                AGG  ACCTAGGAGAGGA
                                  AA
GAM862  RFPL1    3'  TCCCATATTTTTCTCCT     23147      C  GG
                                TCCC TG  TTTTCTCCT
                                ||||  ||  |||||||||
                                AGGG AT  AAAAGAGGA
                                  T  A_
GAM862  RFPL3    3'  TCCCATATCTTTCTCCT     23148      C  GG
                                TCCC TG  TTTTCTCCT
                                ||||  ||  |||||||||
                                AGGG AT  GAAAGAGGA
                                  T  A_
GAM862  RING1    3'  TCCTCTGGCTGTCCCCT     23149      C    G  T
                                TCC CTGG TT TCTCCT
                                |||  ||||  ||  ||||||
                                AGG  GACC  GA AGGGGA
                                  A    _  C
GAM862  SDC2     5'  TCCTCCTCCTTCTCCT      23130     _   GGG
                                TCC CCT   TTTTCTCCT
                                |||  |||   |||||||||
                                AGG GGA   GGAAGAGGA
                                  A   ____
GAM862  SERPINF1 3'  TCCCTCGGGTTTTCTTCT    23150      C         C
                                TCCC TGGGTTTTCT CT
                                ||||  ||||||||||  ||
                                AGGG GCCCAAAAGA GA
                                   A         A
GAM862  STXBP1   5'  TCTCCCGGCTCCGATCTCCT  23151    C    G   __
                                TC CCTGG TTT  TCTCCT
                                ||  |||||  |||  ||||||
                                AG GGGCC AGG  AGAGGA
                                  A    G   CT
GAM862  TOMM22   3'  TCCCACTGGCATCGGTTCCT  23152      _   _  TTC
                                TCCC CTGG GTT   TCCT
                                ||||  ||||  |||   ||||
                                AGGG GACC TAG   AGGA
                                   T   G   CCA
GAM862  TRA1     5'  CCCCTGGGTTCGGATCCT    23153          TC_
                                CCCCTGGGTTT   TCCT
                                ||||||||||   ||||
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                                GGGGACCCAAG   AGGA
                                      CCT
GAM862  TREM2    3'  TCTCCTGGGCTTTTCCT    23154    C        C
                                TC CCTGGGTTTT TCCT
                                || |||||||||| ||||
                                AG GGACCCGAAA AGGA
                                 A        _
GAM862  UBE4A    3'  TCCTCCAGTTTTCTCCT    23155    _  TG
                                TCC CC  GGTTTTCTCCT
                                ||| ||  ||||||||||
                                AGG GG  TCAAAAGAGGA
                                 A  __
GAM862  VDR      3'  CCTCCTGGGTTCAATTCTTCT  23156    _       ___   C
                                CC CCTGGGTTT   TCT CT
                                || |||||||||   ||| ||
                                GG GGACCCAAG   AGA GA
                                 A        TTA   A
GAM862  WBSCR5   3'  CCCTCTGGGCCCCAGCTC    23157    _       __
                                CCC CTGGGTTTT  CTC
                                ||| |||||||||  |||
                                GGG GACCCGGGG  GAG
                                 A        TC
GAM862  WBSCR5   3'  CCCTCTGGGCCCCAGCTC    23157    _       __
                                CCC CTGGGTTTT  CTC
                                ||| |||||||||  |||
                                GGG GACCCGGGG  GAG
                                 A        TC
GAM862  WBSCR5   3'  CCCTCTGGGCCCCAGCTC    23157    _       __
                                CCC CTGGGTTTT  CTC
                                ||| |||||||||  |||
                                GGG GACCCGGGG  GAG
                                 A        TC
GAM862  ZNF138   3'  TCCCCAGTATGAATTTTCT   23158      ____
                                TCCCC   TGGGTTTTCT
                                |||||   ||||||||||
                                AGGGG   ACTTAAAAGA
                                   TCAT
GAM862  ZNF2     5'  TCTCCTGTGTGCTCTCCT    23159    C   G  T
                                TC CCTG GT TTCTCCT
                                || |||| || |||||||
                                AG GGAC CA GAGAGGA
                                 A   A  C
GAM862  ZNF83    5'  TCTCCTGTATTACTCTCCT   23160    C   GG  _
                                TC CCTG  TT TTCTCCT
                                || ||||  || |||||||
                                AG GGAC  AA GAGAGGA
                                 A   AT  T
GAM862  ACAA2    5'  CCTCCTGGGTTTTCTTCT    23161    _        C
                                CC CCTGGGTTTTCT CT
                                || ||||||||||| ||
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                                GG GGACCCAAAAGA GA
                                 A          A
GAM862  AGTRL2   5' TCCTCTGGGCCTCTCTCCT   23162     C     _
                                TCC CTGGGT TTTCTCCT
                                ||| |||||| ||||||||
                                AGG GACCCG AGAGAGGA
                                  A     G
GAM862  ALTE     3' CCTCCTGAAGTATTTTTCCT   23163    _    _ _  C
                                CC CCTGG GT TTT TCCT
                                || ||||| || ||| ||||
                                GG GGACT CA AAA AGGA
                                 A    T T   A
GAM862  ATIP1    3' TCCTCCCAGACTGTTTTCTTCT 23164     _ TG ___      C
                                TCC CC  G   GTTTTCT CT
                                ||| ||  |   ||||||| ||
                                AGG GG  C   CAAAAGA GA
                                  A  GT TGA      A
GAM862  ATP6V1G3 3' CCCTAGTGTTTGTTCTTCT   23165       _   __  C
                                CCCTGG GTTT  TCT CT
                                |||||| ||||  ||| ||
                                GGGATC CAAA  AGA GA
                                   A   CA  A
GAM862  BATF     5' TCCCTTCCTGACTTCTCCT   23166     ___   GT
                                TCCC   CTGG  TTTCTCCT
                                ||||   ||||  ||||||||
                                AGGG   GACT  GAAGAGGA
                                  AAG   __
GAM862  BHC80    3' TCCCGTGGCTTCTCCT     23167     C   GT
                                TCCC TGG  TTTCTCCT
                                |||| |||  ||||||||
                                AGGG ACC  GAAGAGGA
                                  C   __
GAM862  BTF3     3' CCCTGGGTAGTTTTTCCT    23168       __  C
                                CCCTGGGT  TTT TCCT
                                ||||||||  ||| ||||
                                GGGACCCA  AAA AGGA
                                     TC   A
GAM862  C17orf26 3' TCCCATGTAGTATCTCCT    23169     C _  TT
                                TCCC TG GGT  TCTCCT
                                |||| || |||  ||||||
                                AGGG AC TCA  AGAGGA
                                  T  A   T_
GAM862  C1QTNF7  3' TCTCCCTCCTTCTCCT     23103    _   GGG
                                TC CCCT   TTTTCTCCT
                                || ||||   |||||||||
                                AG GGGA   GGAAGAGGA
                                 A   ____
GAM862  C20orf124 5' CCCTACCAGCTTTCTTCT    23170      __      C
                                CCCTG  GGTTTTCT CT
                                |||||  |||||||| ||
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                                GGGAT  TCGAAAGA GA
                                  GG       A
GAM862  C22orf4   5'  TCCCCTAGCGGCCCTTTCCT  23171        __     C
                                TCCCCTG  GGTTTT TCCT
                                |||||||  |||||| ||||
                                AGGGGAT  CCGGGA AGGA
                                    CG     A
GAM862  C6.1A     3'  CCTGAAGATTTTTCTCCT    23172        ___
                                CCTGGG   TTTTCTCCT
                                ||||||   |||||||||
                                GGACTT   AAAAGAGGA
                                   CTA
GAM862  CCRL2     3'  TCCGCGCCTTAGTTTTCTTCT 23173     ___  G       C
                                TCC   CCT GGTTTTCT CT
                                |||   ||| |||||||| ||
                                AGG   GGA TCAAAAGA GA
                                  CGC   A       A
GAM862  CDC91L1   3'  TCACCTGCCTCTTCTCCT    23174    C    GG
                                TC CCTG  TTTTCTCCT
                                || ||||  |||||||||
                                AG GGAC  AGAAGAGGA
                                 T    GG
GAM862  CHFR      3'  TCCCTTGAAACTTTTCCT    23175      C    T   C
                                TCCC TGGG TTT TCCT
                                |||| |||| ||| ||||
                                AGGG ACTT GAA AGGA
                                  A    T   A
GAM862  CLONE24945 3'  CCCTCTAATGCTTTTCTCCT   23176     _    _    _
                                CCC CTGG GTTTT CTCCT
                                ||| |||| ||||| |||||
                                GGG GATT CGAAA GAGGA
                                  A    A    A
GAM862  DAMS      3'  TCCCCTTTTCCCCTCTCCT   23177       GGG_
                                TCCCCT    TTTTCTCCT
                                ||||||    |||||||||
                                AGGGGA    GGGAGAGGA
                                   AAAG
GAM862  DDX12     3'  TCACCTGGCCTCTCTCCT    23178    C    G
                                TC CCTGG TTTTCTCCT
                                || ||||| |||||||||
                                AG GGACC GAGAGAGGA
                                 T    G
GAM862  DGCR6L    3'  TCCACCTGGTCTCTCCT     23109     _    GT
                                TCC CCTGG  TTTCTCCT
                                ||| |||||  ||||||||
                                AGG GGACC  AGAGAGGA
                                  T    __
GAM862  DKFZp434J1015 3'  TCCTCCCCGAATTTCTCCT    23179     _   G GT
                                TCC CCT G  TTTCTCCT
                                ||| ||| |  ||||||||
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                                AGG GGG C  AAAGAGGA
                                  A   G TT
GAM862  DKFZP434O125 5'  TCCTCCTGATCCTTTCTCCT   23180    _    G_
                                TCC CCTGG  TTTTCTCCT
                                ||| |||||  |||||||||
                                AGG GGACT  GAAAGAGGA
                                  A     AG
GAM862  DKFZP586P0123 3'  TCCCCTTCCTCTCCT      23131       GGG
                                TCCCCT   TTTTCTCCT
                                ||||||   |||||||||
                                AGGGGA   AGGAGAGGA
                                   ___
GAM862  DKFZp761A132 3'  TCCTCCTGGGAGACCTCCT   23181    _     TTT
                                TCC CCTGGG   TCTCCT
                                ||| ||||||   ||||||
                                AGG GGACCC   GGAGGA
                                  A      TCT
GAM862  DKFZp761J1523 3'  CCTCCTTGGCTTTCTTCT    23182    _  G       C
                                CC CCT GGTTTTCT CT
                                || ||| |||||||| ||
                                GG GGA CCGAAAGA GA
                                 A  A       A
GAM862  ELSPBP1   3'  TCCTCTGAAGATATTTCTCCT  23183     C    T___
                                TCC CTGGG    TTTCTCCT
                                ||| |||||    ||||||||
                                AGG GACTT    AAAGAGGA
                                  A    CTAT
GAM862  ESM1     3'  TCCCCATCTTCTCCT      23184       TGG
                                TCCCC   GTTTTCTCCT
                                |||||   ||||||||||
                                AGGGG   TAGAAGAGGA
                                   ___
GAM862  FLJ10211  5'  TCCCCCGGGGCCCCATCCT   23185         T TT _
                                TCCCCTGGG T  C TCCT
                                ||||||||| |  | ||||
                                AGGGGGCCC G  G AGGA
                                      C GG T
GAM862  FLJ10300  5'  CCTCTCGATGTTTCTCCT    23186    C  G   _
                                CC CT GGT TTTCTCCT
                                || || ||| ||||||||
                                GG GA CTA AAAGAGGA
                                 A  G   C
GAM862  FLJ10563  5'  CCAGGTGAGTTTTCTCCT    23187    CC_
                                CC   TGGGTTTTCTCCT
                                ||   ||||||||||||
                                GG   ACTCAAAAGAGGA
                                 TCC
GAM862  FLJ10637  5'  TCCCCGATCATCTCCT      23188       TG    T
                                TCCCC  GGTT TCTCCT
                                |||||  |||| ||||||
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                                AGGGG  CTAG AGAGGA
                                  __   T
GAM862  FLJ10871  3' CCTCTTGGAAAACTTCTCCT  23189   C  _  T__
                                CC CT GGG   TTTCTCCT
                                || || |||   ||||||||
                                GG GA CCT   GAAGAGGA
                                 A  A   TTT
GAM862  FLJ10932  3' CCCTGAGCTTTTTTTCCT   23190         C__
                                CCCTGGGTTTT   TCCT
                                ||||||||||   ||||
                                GGGACTCGAAA   AGGA
                                      AAA
GAM862  FLJ11274  3' TCCTCCCACCTCTCCT     23191    _   GGT
                                TCC CCTG   TTTCTCCT
                                ||| ||||   ||||||||
                                AGG GGGT   GGAGAGGA
                                  A   ___
GAM862  FLJ12057  5' TCCTCCTGCCACCTCTCCT   23192    _   GGT
                                TCC CCTG   TTTCTCCT
                                ||| ||||   ||||||||
                                AGG GGAC   GGAGAGGA
                                  A   GGT
GAM862  FLJ12572  3' TCCCTTTATTAGCGTTTTCTTC 23193     C____  _     C  III
           TA                   TCCC    TGG GTTTTCT CT   A
                                ||||    ||| ||||||| ||   |
                                AGGG    ATC CAAAAGA GA   T
                                  AAATA   G      A  III
GAM862  FLJ14708  3' TCCCCTGGTCCCTTCCT    23194        G   TC
                                TCCCCTGG TTT  TCCT
                                |||||||| |||  ||||
                                AGGGGACC AGG  AGGA
                                     _   GA
GAM862  FLJ14840  5' TCCCCGTGGCCCCTGTCTCCT  23195      _  G  __
                                TCCCC TGG TTT  TCTCCT
                                ||||| ||| |||  ||||||
                                AGGGG ACC GGG  AGAGGA
                                   C   G   AC
GAM862  FLJ20234  5' TCCGCCTGGCCTCTCCT    23196    _    GT
                                TCC CCTGG  TTTCTCCT
                                ||| |||||  ||||||||
                                AGG GGACC  GGAGAGGA
                                  C    __
GAM862  FLJ21324  5' CCCCCGATTTCTTTCTCCT   23197       GT__
                                CCCCTGG    TTTCTCCT
                                |||||||    ||||||||
                                GGGGGCT    AAAGAGGA
                                    AAAG
GAM862  FLJ22169  3' TCTCCTGGGGGCCCATCCT   23198   C     TT  _
                                TC CCTGGG  TTC TCCT
                                || ||||||  ||| ||||
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                                AG GGACCC  GGG AGGA
                                 A     CC   T
GAM862  FLJ22672 3'  TCTCCTGTGCCCTCTCTCCT   23199    C    G __
                                TC CCTG GT  TTTCTCCT
                                || |||| ||  ||||||||
                                AG GGAC CG  AGAGAGGA
                                 A    A  GG
GAM862  GABBR1   5'  TCCCCCCTCCCTTCTCCT    23200       GGG
                                TCCCCT   TTTTCTCCT
                                ||||||   |||||||||
                                AGGGGG   GGAAGAGGA
                                   GAG
GAM862  HAND2    3'  TCCTCCTCCTCCTTCTCCT   23201     _   GGG
                                TCC CCT   TTTTCTCCT
                                ||| |||   |||||||||
                                AGG GGA   GGAAGAGGA
                                  A   GGA
GAM862  HDCMA18P 5'  TCCCCCAGAGGTTTTTTCCTA  23202       __      C    III
                                TCCCCT  GGGTTTT TCCT   A
                                ||||||  ||||||| ||||   |
                                AGGGGG  TCCAAAA AGGA   T
                                   TC      A    III
GAM862  HEMK     3'  TCCTTCTGGAGCAGCCTCCT   23203     C_    _ TT
                                TCC  CTGG GT  TCTCCT
                                |||  |||| ||  ||||||
                                AGG  GACC CG  GGAGGA
                                  AA    T  TC
GAM862  HOOK1    5'  CCTCCTACCGGCTCTCCT    23204    _    __   TT
                                CC CCTG  GGT  TCTCCT
                                || ||||  |||  ||||||
                                GG GGAT  CCG  AGAGGA
                                 A   GG   __
GAM862  HSP105B  5'  CCCCCTGCCTGCTTCTCCT   23205       GGT_
                                TCCCCTG    TTTCTCCT
                                |||||||    ||||||||
                                GGGGGAC    GAAGAGGA
                                    GGAC
GAM862  HSPC111  5'  TCCCGATTTTCTCCT      23206      CTG
                                TCCC   GGTTTTCTCCT
                                ||||   ||||||||||
                                AGGG   CTAAAAGAGGA
                                  ___
GAM862  HSU47926 3'  TCCTCTGAGTCCAGGCCCT   23207     C       TC_
                                TCC CTGGGTTT   TCCT
                                ||| ||||||||   ||||
                                AGG GACTCAGG   GGGA
                                  A       TCC
GAM862  ITGA8    5'  TCCGTCTGCTTTTCTCCT    23208     C_   GG
                                TCC  CTG  TTTTCTCCT
                                |||  |||  |||||||||
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                                AGG  GAC  AAAAGAGGA
                                  CA   G_
GAM862  KCNG3    5'  CCCTCGGGGCTCCGCTCCT   23209      __      _
                                CCCT  GGGTTTT CTCCT
                                ||||  ||||||| |||||
                                GGGA  CCCGAGG GAGGA
                                  GC      C
GAM862  KCNH7    5'  TCTCCCGGGATCTCTCCT    23210    C     T
                                TC CCTGGG TTTCTCCT
                                || |||||| ||||||||
                                AG GGGCCC AGAGAGGA
                                 A     T
GAM862  KIAA0280 3'  TCCTCCTCTTCCTCTCCT    23211     _  GGG
                                TCC CCT   TTTTCTCCT
                                ||| |||   |||||||||
                                AGG GGA   AGGAGAGGA
                                  A   GA_
GAM862  KIAA0280 3'  TCTCCTGGGCTCAGTCCT    23212    C       TC
                                TC CCTGGGTTT  TCCT
                                || |||||||||  ||||
                                AG GGACCCGAG  AGGA
                                 A        TC
GAM862  KIAA0317 3'  CCCTCCTTAGTTCTCCT     23213     _  G   TT
                                TCC CCT GGT  TCTCCT
                                ||| ||| |||  ||||||
                                GGG GGA TCA  AGAGGA
                                  A   A  __
GAM862  KIAA0553 3'  TCCCCTCCTTCTCCT       23138       GGG
                                TCCCCT   TTTTCTCCT
                                ||||||   |||||||||
                                AGGGGA   GGAAGAGGA
                                   ___
GAM862  KIAA0628 3'  TCTCCTGGACCCTATTTTCTTC 23214    C    _____      C  III
            TA                    TC CCTGG    GTTTTCT CT   A
                                || |||||    ||||||| ||   |
                                AG GGACC    TAAAAGA GA   T
                                 A    TGGGA      A  III
GAM862  KIAA0774 5'  TCCCCTGGGTTGACTCCT    23215          TT
                                TCCCCTGGGTT  CTCCT
                                ||||||||||  |||||
                                AGGGGACCCAA  GAGGA
                                      CT
GAM862  KIAA1029 5'  CCCCCTGGATGCTCCT      23216          TTT
                                TCCCCTGGGT   CTCCT
                                ||||||||||   |||||
                                GGGGGACCTA   GAGGA
                                      C__
GAM862  KIAA1464 3'  TCTCCTGGGCCTGTTTCCT    23217    C       TC_
                                TC CCTGGGTTT   TCCT
                                || |||||||||   ||||
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                                AG GGACCCGGA   AGGA
                                 A        CAA
GAM862  KIAA1719 3'  TCCCTCCCTCTTTCTCCT    23118     _ GGG
                                TCCC CT   TTTTCTCCT
                                |||| ||   |||||||||
                                AGGG GG   GAAAGAGGA
                                  A  GA_
GAM862  KIAA1855 3'  TCCCCTAGGTGACCCCCT    23218         TT
                                TCCCCTGGGT  TCTCCT
                                ||||||||||  ||||||
                                AGGGGATCCA  GGGGGA
                                      CT
GAM862  KIAA1908 3'  TCCTCATCCTAAATCTCCT   23219    _____     TTT
                                TCC    CCTGGG   TCTCCT
                                |||    ||||||   ||||||
                                AGG    GGATTT   AGAGGA
                                  AGTA     ___
GAM862  KIAA1912 5'  TCCCCTGCCCTCTCCT      23220       GG
                                TCCCCT  GTTTTCTCCT
                                ||||||  ||||||||||
                                AGGGGA  CGGGAGAGGA
                                   __
GAM862  KIAA1948 5'  TCCCATTGCTCAGGTTTTCT   23221      _____ _
                                TCCC    CT GGGTTTTCT
                                ||||    || |||||||||
                                AGGG    GA TCCAAAAGA
                                  TAAC  G
GAM862  LIM      3'  TCTCCTGGGTTCAAGAATTTTC 23222   C       TC_______   III
           CTA                    C CCTGGGTTT       TCCT   A
                                | |||||||||       ||||   |
                                G GGACCCAAG       AGGA   T
                                 A        TTCTTAAA    III
GAM862  LIN-28   3'  CCCCCTTTTTCTCCT       23223       GGG
                                TCCCCT   TTTTCTCCT
                                ||||||   |||||||||
                                GGGGGA   AAAAGAGGA
                                   ___
GAM862  MCC2     5'  CCTCTGAATGCTTCTCCT    23224    C     _
                                CC CTGGGT TTTCTCCT
                                || |||||| ||||||||
                                GG GACTTA GAAGAGGA
                                 A     C
GAM862  MGC11335 3'  TCCCCAGGGTGAGCCTTTCCT  23225      T   ___   C
                                TCCCC GGGT   TTT TCCT
                                ||||| ||||   ||| ||||
                                AGGGG CCCA   GGA AGGA
                                   T    CTC   A
GAM862  MGC19764 5'  TCCCGCTGGGTTCTCCT     23226      _     TT
                                TCCC CTGGGT  TCTCCT
                                |||| ||||||  ||||||
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                                AGGG GACCCA  AGAGGA
                                  C     __
GAM862  MGC20647 5'  TCCCCCTCTCCTTCTCCT    23227       GGG
                                TCCCCT   TTTTCTCCT
                                ||||||   |||||||||
                                AGGGGG   GGAAGAGGA
                                   AGA
GAM862  MGC4293  3'  TCCCCTGGCTCCCCT      23228        GTT
                                TCCCCTGG   TTCTCCT
                                ||||||||   |||||||
                                AGGGGACC   GAGGGGA
                                    ___
GAM862  MGC4309  3'  TCCCCTTGGCCCCCTCTCT   23229       G   TT  _
                                TCCCCT GGTT  CTC CT
                                |||||| ||||  ||| ||
                                AGGGGA CCGG  GAG GA
                                   A   GG   A
GAM862  MGC4655  5'  CCCCTTGCGTTGTTCTCCT   23230      _ G  _
                                CCCCT G GTT TTCTCCT
                                ||||| | ||| |||||||
                                GGGGA C CAA AAGAGGA
                                  A G   C
GAM862  NMT1     3'  TCCCCTCCTTCTCCT       23138       GGG
                                TCCCCT   TTTTCTCCT
                                ||||||   |||||||||
                                AGGGGA   GGAAGAGGA
                                    ___
GAM862  NRN1     3'  TCCCCTGGCCTTCTCCT     23231        G
                                TCCCCTGG TTTTCTCCT
                                |||||||| |||||||||
                                AGGGGACC GGAAGAGGA
                                    _
GAM862  OVCA2    3'  TCCCCATGTCACCCTCCT    23112       TGG  _
                                TCCCC   GTT TTCTCCT
                                |||||   ||| |||||||
                                AGGGG   CAG GGGAGGA
                                  TA_   T
GAM862  P450RAI-2 3'  CCCCCTCAGCTTTTCCT     23232       G     C
                                TCCCCT GGTTTT TCCT
                                |||||| |||||| ||||
                                GGGGGA TCGAAA AGGA
                                   G     _
GAM862  PDZD2    3'  TCACCCTGTTTCTCCT      23233    _    GGT
                                TC CCCTG   TTTCTCCT
                                || |||||   ||||||||
                                AG GGGAC   AAAGAGGA
                                 T    ___
GAM862  PIP5K2B  5'  TCCCCTGGCCCCGTCCT     23234        G   TC
                                TCCCCTGG TTT  TCCT
                                |||||||| |||  ||||
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                                AGGGGACC GGG  AGGA
                                     _  GC
GAM862  PIP5K2B  5'  TCCCCTGGCCCCGTCCT    23234       G  TC
                                TCCCCTGG TTT  TCCT
                                |||||||| |||  ||||
                                AGGGGACC GGG  AGGA
                                     _  GC
GAM862  PLAC3    3'  TCCTCCTGGGTCGGCCTCTC  23235    _     ___
                                TCC CCTGGGTT  TTCTC
                                ||| ||||||||  |||||
                                AGG GGACCCAG  GAGAG
                                  A       CCG
GAM862  PP1665   3'  TCCTCCTGGGCTGAACCTCCT  23236    _     T__
                                TCC CCTGGGTT  TCTCCT
                                ||| ||||||||  ||||||
                                AGG GGACCCGA  GGAGGA
                                  A       CTT
GAM862  QKI      5'  TCCTCCTCCTCCTTCTCCT   23201    _  GGG
                                TCC CCT   TTTTCTCCT
                                ||| |||   |||||||||
                                AGG GGA   GGAAGAGGA
                                  A  GGA
GAM862  RPS6KA4  3'  TCCCCCTGGAGGGGCCTTCT  23237      _____
                                TCCCCT    GGGTTTTCT
                                ||||||    |||||||||
                                AGGGGG    CCCGGAAGA
                                    ACCTC
GAM862  SEF      3'  TCTCCCTGGGGCCACTTTCT  23238   _     ____
                                TC CCCTGGG    TTTTCT
                                || |||||||    ||||||
                                AG GGGACCC    GAAAGA
                                 A      CGGT
GAM862  SLC22A6  5'  TCCCTTGCAGCTTCTCCT    23239     C  _    T
                                TCCC TG GGTTT CTCCT
                                |||| || ||||| |||||
                                AGGG AC TCGAA GAGGA
                                  A  G    _
GAM862  SRPUL    5'  TCCTCCTCTTTCTCCT     23240    _  GGG
                                TCC CCT   TTTTCTCCT
                                ||| |||   |||||||||
                                AGG GGA   GAAAGAGGA
                                  A  ___
GAM862  TCL6     5'  CTGGGCTTCGGTTTTCTCCTA  23241       _______      III
                                CTGGGT     TTTCTCCT   A
                                ||||||     ||||||||   |
                                GACCCG     AAAGAGGA   T
                                    AAGCCA       III
GAM862  TNFRSF13B 3'  TCCTCTGTCTCTCTCTCCT   23242     C   GG_
                                TCC CTG   TTTTCTCCT
                                ||| |||   |||||||||
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                                AGG GAC   GAGAGAGGA
                                  A   AGA
GAM862   TP53TG3   3'  TCCGCTGTGACGTTTTCTCCT  23243     C  _ __
                                TCC CTG G  GTTTTCTCCT
                                ||| ||| |  ||||||||||
                                AGG GAC C  CAAAAGAGGA
                                  C   A TG
GAM862   TROAP     5'  TCCTCCGCTTTTCTCCT     23244     C   GG
                                TCC CTG  TTTTCTCCT
                                ||| |||  |||||||||
                                AGG GGC  AAAAGAGGA
                                  A   G_
GAM862   UHRF1     3'  TCCCCTTGAGGCCATTTCT   23245       __   __
                                TCCCCT  GGGT  TTTCT
                                ||||||  ||||  |||||
                                AGGGGA  TCCG  AAAGA
                                    AC    GT
GAM862   UK114     3'  TCCACTATCTTCTCCT      23246     C  GG
                                TCC CT  GTTTTCTCCT
                                ||| ||  ||||||||||
                                AGG GA  TAGAAGAGGA
                                  T  __
GAM862   VI        3'  TCCTCCTGAAGCCCTTTCCT   23247     _    _    C
                                TCC CCTGG GTTTT TCCT
                                ||| ||||| ||||| ||||
                                AGG GGACT CGGGA AGGA
                                  A    T    A
GAM862   X123      3'  TCCCCTTGGAGTGGCCTTCT   23248       _ _____
                                TCCCCT GG    GTTTTCT
                                |||||| ||    |||||||
                                AGGGGA CC    CGGAAGA
                                    A  TCAC
GAM862   ZNF177    5'  TCCTCCTGTAGGTTTCCT    23249     _   __
                                TCC CCTG  GGTTTTCT
                                ||| ||||  ||||||||
                                AGG GGAC  CCAAAGGA
                                  A    AT
GAM862   ZNF185    3'  CCCCCTGGAGCTTTTCCT    23250         _    C
                                TCCCCTGG GTTTT TCCT
                                |||||||| ||||| ||||
                                GGGGGACC CGAAA AGGA
                                     T    _
GAM862   ZNF361    5'  TCCTCCGGGATGCTTTTCCT   23251     C    T__   C
                                TCC CTGGG   TTT TCCT
                                ||| |||||   ||| ||||
                                AGG GGCCC   GAA AGGA
                                  A    TAC   A
GAM862   LOC113730 5'  TCTCCCTGGTTCCCTCTCCT   23252     _     GT_
                                TC CCCTGG   TTTCTCCT
                                || ||||||   ||||||||
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                                AG GGGACC   GGAGAGGA
                                 A      AAG
GAM862   LOC127696 5'  TCCAGGCCTGGCTCTCCT    23253     ___     GTT
                                TCC   CCTGG   TTCTCCT
                                |||   |||||   |||||||
                                AGG   GGACC   GAGAGGA
                                  TCC    ___
GAM862   LOC129566 3'  TCCCTCGGGCTCCCCT      23254      C     TT
                                TCCC TGGGT  TCTCCT
                                |||| |||||  ||||||
                                AGGG GCCCG  AGGGGA
                                  A    __
GAM862   LOC133022 5'  TCCCCCTGGCTGCTCCT     23255       G    TT
                                TCCCCT GGTT  CTCCT
                                ||||||| ||||  |||||
                                AGGGGG CCGA  GAGGA
                                   A    C_
GAM862   LOC138311 3'  CCCCTTGGAGGACTCTCCT    23256       _ _ TT
                                CCCCT GG G  TTCTCCT
                                ||||| || |  |||||||
                                GGGGA CC C  GAGAGGA
                                   A  T CT
GAM862   LOC143243 3'  TCCCCTCCCCTCTCCT      23117       GGG
                                TCCCCT   TTTTCTCCT
                                ||||||   |||||||||
                                AGGGGA   GGGAGAGGA
                                   G__
GAM862   LOC143677 3'  CCCCTGGGTAAAAAGTCTCCT  23257         TT_____
                                CCCCTGGGT     TCTCCT
                                |||||||||     ||||||
                                GGGGACCCA     AGAGGA
                                      TTTTTC
GAM862   LOC146714 5'  CCCTCCTGGTTCTCCT      23258     _     GTT
                                TCC CCTGG   TTCTCCT
                                ||| |||||   |||||||
                                GGG GGACC   AAGAGGA
                                  A    ____
GAM862   LOC146953 3'  TCCCACCCCTTCTCCT      23259      _  GGG
                                TCCC CT   TTTTCTCCT
                                |||| ||   |||||||||
                                AGGG GG   GGAAGAGGA
                                  T  ____
GAM862   LOC147040 3'  TCCCCAGCTATCTCCT      23260       TG    T
                                TCCCC  GGTT TCTCCT
                                |||||  |||| ||||||
                                AGGGG  TCGA AGAGGA
                                   __    T
GAM862   LOC147093 5'  TCCACTGCAGGGCTCTCCT    23261     C   _  TT
                                TCC CTG GG  TTCTCCT
                                ||| ||| ||  |||||||
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                                AGG GAC TC  GAGAGGA
                                  T   G  CC
GAM862   LOC147685 3'  CCCCCATAGTTTCTCCT     23262       TG     T
                                TCCCC  GGTTT CTCCT
                                ||||| ||||| |||||
                                GGGGG  TCAAA GAGGA
                                   TA    _
GAM862   LOC148738 3'  TCTCCTAGGCCCTGCTTCCT   23263     C        _ _
                                TC CCTGGGTTTT CT CCT
                                || |||||||||| || |||
                                AG GGATCCGGGA GA GGA
                                 A         C  A
GAM862   LOC148758 5'  TCCCTCTGGCTCTCCT      23264      _    GTT
                                TCCC CTGG   TTCTCCT
                                |||| ||||   |||||||
                                AGGG GACC   GAGAGGA
                                  A   ___
GAM862   LOC150170 5'  TCCCCATGCACATATTTCTCCT 23265      TGG _____
                                TCCCC   GT    TTTCTCCT
                                |||||   ||    ||||||||
                                AGGGG   CG    AAAGAGGA
                                   TA_  TGTAT
GAM862   LOC150175 5'  TCCCCATGCACATATTTCTCCT 23265      TGG _____
                                TCCCC   GT    TTTCTCCT
                                |||||   ||    ||||||||
                                AGGGG   CG    AAAGAGGA
                                   TA_  TGTAT
GAM862   LOC150215 5'  TCCCCATGCACATATTTCTCCT 23265      TGG _____
                                TCCCC   GT    TTTCTCCT
                                |||||   ||    ||||||||
                                AGGGG   CG    AAAGAGGA
                                   TA_  TGTAT
GAM862   LOC150218 5'  TCCCCATGCACATATTTCTCCT 23265      TGG _____
                                TCCCC   GT    TTTCTCCT
                                |||||   ||    ||||||||
                                AGGGG   CG    AAAGAGGA
                                   TA_  TGTAT
GAM862   LOC151963 5'  CCCCCTGGGCCTCCT       23266         TTT
                                TCCCCTGGGT   CTCCT
                                ||||||||||   |||||
                                GGGGGACCCG   GAGGA
                                      ___
GAM862   LOC152283 3'  TCCCCTCCTCCTCTCCT     23267       GGG
                                TCCCCT   TTTTCTCCT
                                ||||||   |||||||||
                                AGGGGA   AGGAGAGGA
                                   GG_
GAM862   LOC152283 3'  TCCTCCTCCTTCTCCT      23130     _  GGG
                                TCC CCT   TTTTCTCCT
                                ||| |||   |||||||||
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                                AGG GGA   GGAAGAGGA
                                  A  ___
GAM862   LOC152762 5'  CCCTGGGTCTGTTTTCTTCT   23268        ____   C
                                CCCTGGGTT    TTCT CT
                                |||||||||    |||| ||
                                GGGACCCAG    AAGA GA
                                     ACAA    A
GAM862   LOC153727 5'  CCTCTTAACTTTTCTCCT    23269    C  _  G
                                CC CT GG TTTTCTCCT
                                || || || |||||||||
                                GG GA TT AAAAGAGGA
                                 A  A  G
GAM862   LOC154739 5'  CCCTGGGTCCCTTTTCCT    23270          C__
                                CCCTGGGTTTT   TCCT
                                ||||||||||   ||||
                                GGGACCCAGGG   AGGA
                                      AAA
GAM862   LOC154930 5'  TCCCCAGTATGAATTTTCT   23158      ____
                                TCCCC    TGGGTTTTCT
                                |||||    ||||||||||
                                AGGGG    ACTTAAAAGA
                                   TCAT
GAM862   LOC155081 3'  TCCCCTGGGTCCGGTGTTCTTC 23271          _____   C  III
           TA                    TCCCCTGGGTT    TTCT CT   A
                                ||||||||||    |||| ||   |
                                AGGGGACCCAG    AAGA GA   T
                                      GCCAC    A  III
GAM862   LOC155376 3'  TCCCCAGGTTCTCCT      23272      T    TT
                                TCCCC GGGT  TCTCCT
                                ||||| ||||  ||||||
                                AGGGG TCCA  AGAGGA
                                  _   __
GAM862   LOC157739 3'  CCTCCTGGGCCAGCTCCT    23273    _      TT
                                CC CCTGGGTT  CTCCT
                                || ||||||||  |||||
                                GG GGACCCGG  GAGGA
                                 A       TC
GAM862   LOC158947 5'  CCAGTGCAGTTTTCTCCT    23275    CC  _
                                CC  TG GGTTTTCTCCT
                                ||  || ||||||||||
                                GG  AC TCAAAAGAGGA
                                 TC  G
GAM862   LOC158947 5'  TCCTCTCCTTCCTTTCTCCT   23274     ___  GGG
                                TCC   CCT   TTTTCTCCT
                                |||   |||   |||||||||
                                AGG   GGA   GAAAGAGGA
                                  AGA   AG_
GAM862   LOC164944 5'  TCCCTCTGCTATAATTCTCCT  23276     _   G_  T_
                                TCCC CTG  GT  TTCTCCT
                                |||| |||  ||  |||||||
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                                AGGG GAC  TA  AAGAGGA
                                  A   GA  TT
GAM862   LOC167026 3'  TCCACTGGCTTCTCCT      23277     C    GT
                                TCC CTGG  TTTCTCCT
                                ||| ||||  ||||||||
                                AGG GACC  GAAGAGGA
                                  T   __
GAM862   LOC168576 5'  TCCTGCTGGGTCAGCCCCT   23278     C_      TT
                                TCC  CTGGGTT  CTCCT
                                |||  |||||||  |||||
                                AGG  GACCCAG  GGGGA
                                  AC       TC
GAM862   LOC197085 5'  TCCTCCTGCCGCCTCTCCT   23279     _    GGT
                                TCC CCTG   TTTCTCCT
                                ||| ||||   ||||||||
                                AGG GGAC   GGAGAGGA
                                  A    GGC
GAM862   LOC197115 5'  TCCTCCTGCCGCCTCTCCT   23279     _    GGT
                                TCC CCTG   TTTCTCCT
                                ||| ||||   ||||||||
                                AGG GGAC   GGAGAGGA
                                  A    GGC
GAM862   LOC197342 3'  TCCCCTGTGGCTTCTCCT    23280        _    T
                                TCCCCTG GGTTT CTCCT
                                ||||||| ||||| |||||
                                AGGGGAC CCGAA GAGGA
                                    A    _
GAM862   LOC201304 5'  TCACCAAGAGTTTCTCCT    23281     _ CT     T
                                TC CC  GGGTTT CTCCT
                                || ||  |||||| |||||
                                AG GG  CTCAAA GAGGA
                                 T  TT     _
GAM862   LOC202802 3'  TCCCCTGGGTCCGGTGTTCTTC 23271          _____    C  III
           TA                    TCCCCTGGGTT     TTCT CT   A
                                ||||||||||     |||| ||   |
                                AGGGGACCCAG     AAGA GA   T
                                      GCCAC    A  III
GAM862   LOC205827 5'  TCCCTCTAAATTTTTCCT    23282      _       C
                                TCCC CTGGGTTTT TCCT
                                |||| ||||||||| ||||
                                AGGG GATTTAAAA AGGA
                                  A       _
GAM862   LOC220954 3'  TCTCCTGGGCTCCAGGCCT   23283     C        CT_
                                TC CCTGGGTTTT   CCT
                                || ||||||||||   |||
                                AG GGACCCGAGG   GGA
                                 A         TCC
GAM862   LOC221756 3'  TCCCCGTCTGTCTCCT      23284       TGG    _
                                TCCCC   GTTT TCTCCT
                                |||||   |||| ||||||
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                                AGGGG  CAGA AGAGGA
                                  ___   C
GAM862  LOC222233 3'  TCCCCTGGGTCCGGTGTTCTTC 23271          _____   C  III
                TA                 TCCCCTGGGTT    TTCT CT   A
                                   ||||||||||    |||| ||  |
                                   AGGGGACCCAG    AAGA GA   T
                                         GCCAC    A  III
GAM862  LOC222256 3'  CCTACTGAGTTTTCTTCT    23285    CC        C
                                   TC  CTGGGTTTTCT CT
                                   ||  ||||||||||| ||
                                   GG  GACTCAAAAGA GA
                                    AT         A
GAM862  LOC245771 3'  TCTCCCTACCTCTCCT     23286    _    GGT
                                   TC CCCTG   TTTCTCCT
                                   || |||||   ||||||||
                                   AG GGGAT   GGAGAGGA
                                    A    ___
GAM862  LOC253181 5'  TCCCCTGGCGAGCCACCTCCT  23287        ___  TT
                                   TCCCCTGG   GT  TCTCCT
                                   ||||||||   ||  ||||||
                                   AGGGGACC   CG  GGAGGA
                                        GCT  GT
GAM862  LOC253532 3'  TCCCCAGGTTCTCCT      23272      T    TT
                                   TCCCC GGGT  TCTCCT
                                   ||||| ||||  ||||||
                                   AGGGG TCCA  AGAGGA
                                     _   __
GAM862  LOC253681 3'  TCCCCAGCTATCTCCT     23260      TG    T
                                   TCCCC  GGTT TCTCCT
                                   |||||  |||| ||||||
                                   AGGGG  TCGA AGAGGA
                                      __    T
GAM862  LOC253698 3'  TCACCCTTCCTCTCCT     23288    _   GGG
                                   TC CCCT   TTTTCTCCT
                                   || ||||   |||||||||
                                   AG GGGA   AGGAGAGGA
                                    T   ___
GAM862  LOC253815 3'  CCCCTGGGCTGTGGCTCCT   23289          TT__
                                   CCCCTGGGTT    CTCCT
                                   ||||||||||    |||||
                                   GGGGACCCGA    GAGGA
                                         CACC
GAM862  LOC254517 5'  TCCTCCTGCCGCCTCTCCT   23279     _   GGT
                                   TCC CCTG   TTTCTCCT
                                   ||| ||||   ||||||||
                                   AGG GGAC   GGAGAGGA
                                     A    GGC
GAM862  LOC254875 3'  TCCCCAGGTTCTCCT      23272      T    TT
                                   TCCCC GGGT  TCTCCT
                                   ||||| ||||  ||||||
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                                AGGGG TCCA  AGAGGA
                                  _   __
GAM862   LOC254876 3'  TCCCCTGGGTCCGGTGTTCTTC 23271          _____   C  III
                TA                  TCCCCTGGGTT    TTCT CT   A
                                    ||||||||||    |||| ||  |
                                    AGGGGACCCAG    AAGA GA   T
                                          GCCAC    A  III
GAM862   LOC254964 5'  TCCTCCTGCCGCCTCTCCT   23279    _   GGT
                                    TCC CCTG   TTTCTCCT
                                    ||| ||||   ||||||||
                                    AGG GGAC   GGAGAGGA
                                      A   GGC
GAM862   LOC255043 3'  TCCCCGAGGCCTCTCCT    23290      T     T
                                    TCCCC GGGTTT CTCCT
                                    ||||| |||||| |||||
                                    AGGGG TCCGGA GAGGA
                                       C     _
GAM862   LOC255101 5'  TCCTCCTCCTTCTCCT     23130    _  GGG
                                    TCC CCT   TTTTCTCCT
                                    ||| |||   |||||||||
                                    AGG GGA   GGAAGAGGA
                                      A  ___
GAM862   LOC256283 5'  TCCCCATGGCCTCTCCT    23291      TG    T
                                    TCCCC  GGTTT CTCCT
                                    |||||  ||||| |||||
                                    AGGGG  CCGGA GAGGA
                                       TA    _
GAM862   LOC256530 5'  TCCTCCTGAGCCTCCT     23292    _     TTT
                                    TCC CCTGGGT   CTCCT
                                    ||| |||||||   |||||
                                    AGG GGACTCG   GAGGA
                                      A     ___
GAM862   LOC256950 5'  TCCCCCGGGTGCCGCCT    23293         TT  T
                                    TCCCCTGGGT  TC CCT
                                    ||||||||||  || |||
                                    AGGGGGCCCA  GG GGA
                                          C_  C
GAM862   LOC256980 3'  CCCCCTGCCTCTCTCCT    23294       GG
                                    TCCCCTG  TTTTCTCCT
                                    |||||||  |||||||||
                                    GGGGGAC  GAGAGAGGA
                                       G_
GAM862   LOC257475 5'  TCCACTTTGTCCTTCTCCT   23295    C  GG  _
                                    TCC CT  GTT TTCTCCT
                                    ||| ||  ||| |||||||
                                    AGG GA  CAG AAGAGGA
                                      T  AA   G
GAM862   LOC257487 5'  TCTCCTAACTTTTCTTCT    23296    C    G    C
                                    TC CCTGG TTTTCT CT
                                    || ||||| |||||| ||
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                                AG GGATT AAAAGA GA
                                 A    G     A
GAM862  LOC51161  3' TCCCCATGGGGGCTTCCT    23297      _   TT  C
                                TCCCC TGGG  TT TCCT
                                ||||| ||||  || ||||
                                AGGGG ACCC  GA AGGA
                                   T   CC  _
GAM862  LOC84518  5' CCCCCCACTTCTCCT      23298       GGT
                                TCCCCTG   TTTCTCCT
                                |||||||   ||||||||
                                GGGGGGT   GAAGAGGA
                                    ___
GAM862  LOC90139  3' TCCCCTGGCCCTTCTCCT    23299        G
                                TCCCCTGG TTTTCTCCT
                                |||||||| |||||||||
                                AGGGGACC GGAAGAGGA
                                     G
GAM862  LOC90906  5' TCCCACTGGGGGTCGGTTCCT  23300     _    TT  C__
                                TCCC CTGGG  TT   TCCT
                                |||| |||||  ||   ||||
                                AGGG GACCC  AG   AGGA
                                   T    CC  CCA
GAM862  LOC90917  3' TCCCCTAGGCCTTTTCCT    23301           C
                                TCCCCTGGGTTTT TCCT
                                |||||||||||| ||||
                                AGGGGATCCGGAA AGGA
                                       A
GAM862  LOC91097  3' CCCCCGATTTCTTTCTCCT   23197       GT__
                                CCCCTGG    TTTCTCCT
                                |||||||    ||||||||
                                GGGGGCT    AAAGAGGA
                                    AAAG
GAM862  LOC91149  3' TCCTCTGACTTCTCCT     23302     C   GT
                                TCC CTGG  TTTCTCCT
                                ||| ||||  ||||||||
                                AGG GACT  GAAGAGGA
                                  A   __
GAM862  LOC91151  5' CCCCCTACCTCTCCT      23303       GGT
                                TCCCCTG   TTTCTCCT
                                |||||||   ||||||||
                                GGGGGAT   GGAGAGGA
                                    ___
GAM862  LOC91355  5' TCCCCAGGGCTCTCCT     23304      T   TT
                                TCCCC GGGT  TCTCCT
                                ||||| ||||  ||||||
                                AGGGG CCCG  AGAGGA
                                   T   __
GAM862  LOC91812  5' TCCTCCTGCCTTCTCCT    23306    _  GG
                                TCC CCT  GTTTTCTCCT
                                ||| |||  ||||||||||
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                                AGG GGA  CGGAAGAGGA
                                  A  __
GAM862  LOC91812 3' TCTCCTGTGTCAGCCTCCT   23305   C   G  T_
                                TC CCTG GTT  TCTCCT
                                || |||| |||  ||||||
                                AG GGAC CAG  GGAGGA
                                 A   A  TC
GAM862  LOC91813 3' TCTCCTGTGTCAGCCTCCT   23305   C   G  T_
                                TC CCTG GTT  TCTCCT
                                || |||| |||  ||||||
                                AG GGAC CAG  GGAGGA
                                 A   A  TC
GAM862  LOC92078 3' CCTTAAGTAGTTTCTCCT    23307   C   __
                                CC TGGGT  TTTCTCCT
                                || |||||  ||||||||
                                GG ATTCA  AAAGAGGA
                                 A    TC
GAM862  LOC92228 3' CCCTCCTGCCCTTTTTCCT   23308   _  GG   C
                                TCC CCTG  TTTT TCCT
                                ||| ||||  |||| ||||
                                GGG GGAC  GAAA AGGA
                                  A   GG   A
GAM862  LOC92299 5' TCCACCTTTCCCTTCTCCT   23309   _  GGG
                                TCC CCT   TTTTCTCCT
                                ||| |||   |||||||||
                                AGG GGA   GGAAGAGGA
                                  T  AAG
GAM862  LOC92579 5' TCCTCCTGCGCTCTCCT     23310   _  G  TT
                                TCC CCTG GT  TCTCCT
                                ||| |||| ||  ||||||
                                AGG GGAC CG  AGAGGA
                                  A   G  __
GAM862  LOC92710 3' TCTCCTGGATGGTTCTCCT   23311   C    T_
                                TC CCTGGGT  TTCTCCT
                                || |||||||  |||||||
                                AG GGACCTA  AAGAGGA
                                 A      CC
GAM863  CD83    3' TCACGGGCCAGCTGGGGG    23314    ATAAACA
                                TCAC      GCCAGCTGGGGG
                                ||||      ||||||||||||
                                AGTG      CGGTCGACCCCC
                                  CC_____
GAM863  COL6A3  3' TTCACATAAACACCAGC     23315          G
                                TTCACATAAACA CCAGC
                                |||||||||||| |||||
                                AAGTGTATTTGT GGTCG
                                           _
GAM863  COL6A3  3' TTCACATAAACACCAGC     23315          G
                                TTCACATAAACA CCAGC
                                |||||||||||| |||||
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                                AAGTGTATTTGT GGTCG
                                          _
GAM863  CXCR4    3'  CATAAACAGCTGGGG      23316         CAGC
                                CATAAACAGC   TGGGG
                                ||||||||||   |||||
                                GTATTTGTCG   ACCCC
                                          _____
GAM863  GBA      3'  TTCACATAAGCATGGGGGCTGG 23317         A  GCCA_
            GGG                   TTCACATAA CA    GCTGGGGG
                                ||||||||| ||    ||||||||
                                AAGTGTATT GT    CGACCCCC
                                     C  ACCCC
GAM863  ITGB3    3'  TTCACAAGGCAGCCAAGAGG  23318       TAAA      CT
                                TTCACA   CAGCCAG  GGGG
                                ||||||   |||||||  ||||
                                AAGTGT   GTCGGTT  CTCC
                                   TCC_     __
GAM863  JUN      3'  TTCCATATAGATACGCTGGGGG 23319     A    AACAGCCA
                                TTC CATA      GCTGGGGG
                                ||| ||||      ||||||||
                                AAG GTAT      CGACCCCC
                                  _   ATCTATG_
GAM863  KIF5C    3'  TTCATATAAACAGTCGCC    23320      C       CCA
                                TTCA ATAAACAG   GCT
                                |||| ||||||||   |||
                                AAGT TATTTGTC   CGG
                                  A       AG_
GAM863  LAMC3    3'  TCATGTAAACAGCAGGTGGGGG 23321     CA      C  C
                                TCA  TAAACAGC AG TGGGGG
                                |||  |||||||| || ||||||
                                AGT  ATTTGTCG TC ACCCCC
                                  AC       _ C
GAM863  FLJ10103 5'  TCACATAAGCGGCCGG     23322        AAC   CA
                                TCACATA   AGC  GCTGG
                                |||||||   |||  |||||
                                AGTGTAT   TCG  CGGCC
                                     ___   C_
GAM863  FLJ10650 3'  TTCGCATCAAGTAGCTGGG   23323     A   AAA   CC
                                TTC CAT   CAG  AGCTGGG
                                ||| |||   |||  |||||||
                                AAG GTA   GTT  TCGACCC
                                  C   ___   CA
GAM863  FLJ14494 3'  TTCACATAAATATCTAGG    23324          CAGCCAG
                                TTCACATAAA      CTGGG
                                ||||||||||      |||||
                                AAGTGTATTT      GATCC
                                     ATA____
GAM863  FLJ21562 5'  CTCACCACATGGCCAGCTGGGG 23325       ATAAACA
            G                    TTCAC      GCCAGCTGGGGG
                                |||||      ||||||||||||
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                                GAGTG      CGGTCGACCCCC
                                   GTGTAC_
GAM863  GC20     3'  TTCACAAGGCAGCCAAACCGGG 23326       TAAA      _
                                TTCACA    CAGCCAG CTGGG
                                ||||||    ||||||| |||||
                                AAGTGT    GTCGGTT GGCCC
                                   TCC_      T
GAM863  KIAA0757 3'  TTCACATGAGAAGCTGAAGG   23327       AAAC  CC
                                TTCACAT    AG  AGCTGGGGG
                                |||||||    ||  |||||||||
                                AAGTGTA    TC  TCGACTTCC
                                   C___  T_
GAM863  KIAA1036 3'  TTCACATAAAAAGTCAGAATTC 23328         C  C  _____
           TGG                     TTCACATAAA AG CAG    CTGG
                                |||||||||| || |||    ||||
                                AAGTGTATTT TC GTC    GACC
                                      T  A   TTAA
GAM863  LSFR2    3'  TTCACAGGGCAGCCACCGG    23329       TAAA     G
                                TTCACA    CAGCCA CTGG
                                ||||||    |||||| ||||
                                AAGTGT    GTCGGT GGCC
                                   CCC_     _
GAM863  MGC10882 3'  TTCACATAAATATCTGGGG    23330         CAGCCAG
                                TTCACATAAA      CTGGGG
                                ||||||||||      ||||||
                                AAGTGTATTT      GACCCC
                                      ATA_____
GAM863  NUP133   3'  ACATGTGAGCAGCTAGAA     23331      AAAC   C
                                ACAT    AGC AGCTGGGG
                                ||||    ||| ||||||||
                                TGTA    TCG TCGATCTT
                                  CAC_   _
GAM863  OSBPL3   3'  TTCATATAAACAATCAGGG    23332      C      GC  GCT
                                TTCA ATAAACA  CA   GGG
                                |||| |||||||  ||   |||
                                AAGT TATTTGT  GT   CCC
                                  A      TA  ____
GAM863  OSMR     5'  TTCAGGTAGGCAGGCCGGGGG  23333      CA  AA   CCA
                                TTCA  TA  CAG   GCTGGGGG
                                ||||  ||  |||   ||||||||
                                AAGT  AT  GTC   CGGCCCCC
                                  CC  CC  ____
GAM863  SIRPB1   3'  TTCAGATAGGCAGCCAGAGGG  23334      C   AA      CT
                                TTCA ATA  CAGCCAG  GGGG
                                |||| |||  |||||||  ||||
                                AAGT TAT  GTCGGTC  TCCC
                                  C   CC      __
GAM863  TNFRSF19L 3' CATTAAAAACAGCTGGGGG   23335     A  C   C
                                CAT AA AGC AGCTGGGGG
                                ||| || ||| |||||||||
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                                GTA TT TTG TCGACCCCC
                                  A  T  _
GAM863  LOC144363 3'  ACATAAACAGCTGGCACTG   23336          CA__
                                ACATAAACAGC   GCTG
                                ||||||||||   ||||
                                TGTATTTGTCG   TGAC
                                      ACCG
GAM863  LOC148508 3'  CATAAACAGCTGTGAAGG    23337         CAGC
                                CATAAACAGC   TGGGGG
                                ||||||||||   ||||||
                                GTATTTGTCG   ACTTCC
                                      AC__
GAM863  LOC152059 5'  TTCACATAAGTGCCAGGCTTGG 23338         ACA   _ _
           GGG                    TTCACATAA  GCCAG CT GGGGG
                                ||||||||||  ||||| || |||||
                                AAGTGTATT  CGGTC GA CCCCC
                                      CA_    C  A
GAM863  LOC167026 5'  TTCATATAAACAGCATGAAA  23339     C       CAGC  GG
                                TTCA ATAAACAGC   TG  G
                                |||| |||||||||   ||  |
                                AAGT TATTTGTCG   AC  T
                                  A       T___  TT
GAM863  LOC199704 3'  TTCACAAGACACGGTGCTGGGG 23340       TAA   GCCA
           G                     TTCACA  ACA   GCTGGGGGG
                                ||||||  |||   ||||||||
                                AAGTGT  TGT   CGACCCCC
                                   TC_  GCCA
GAM864  C1orf1    3'  AGTAAACAGTTCTTTTTCCAA  23343          CCA
                                AGTAAACAGTTTT  TTCTAA
                                ||||||||||||  ||||||
                                TCATTTGTCAAGA  AAGGTT
                                      AA_
GAM864  CHD1      3'  AGTAAACATTTTCCATTTCT  23344        G      _
                                AGTAAACA TTTTCCATT CT
                                |||||||| |||||||| ||
                                TCATTTGT AAAAGGTAA GA
                                   _       A
GAM864  DPYSL3    3'  AGCAAGCTTCCCTATTCTAA  23345     AAC      _
                                AGTA  AGTTTTCC ATTCTAA
                                ||||  |||||||| |||||||
                                TCGT  TCGAAGGG TAAGATT
                                  ___       A
GAM864  GRB10     3'  AGCAAACAAAAGAACATTCT  23346        TTTTC
                                AGTAAACAG    CATTCT
                                |||||||||    ||||||
                                TCGTTTGTT    GTAAGA
                                      TTCTT
GAM864  ITGA2     3'  AGAGAACAGTTTTCCCCCT   23347    TA        A
                                AG  AACAGTTTTCC TTCT
                                ||  ||||||||||| ||||
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                                TC  TTGTCAAAAGG GGGA
                                 TC        _
GAM864  MIC2    3'  GTAAACAGCCAAGATTCT    23348         TTCC
                                GTAAACAGTT   ATTCT
                                ||||||||||   |||||
                                CATTTGTCGG   TAAGA
                                      TTC_
GAM864  MME     3'  AGTAAACAGTTCTTTTCCA   23349          ___
                                AGTAAACAGTTT  TCCA
                                ||||||||||||  ||||
                                TCATTTGTCAAG  AGGT
                                      AAA
GAM864  MME     3'  AGTAAACAGTTCTTTTCCA   23349          ___
                                AGTAAACAGTTT  TCCA
                                ||||||||||||  ||||
                                TCATTTGTCAAG  AGGT
                                      AAA
GAM864  MME     3'  AGTAAACAGTTCTTTTCCA   23349          ___
                                AGTAAACAGTTT  TCCA
                                ||||||||||||  ||||
                                TCATTTGTCAAG  AGGT
                                      AAA
GAM864  MME     3'  AGTAAACAGTTCTTTTCCA   23349          ___
                                AGTAAACAGTTT  TCCA
                                ||||||||||||  ||||
                                TCATTTGTCAAG  AGGT
                                      AAA
GAM864  PMCHL1  3'  AGTAGTTCCTCCATTCT    23350     AACAG
                                AGTA    TTTTCCATTCT
                                ||||    ||||||||||||
                                TCAT    AGGAGGTAAGA
                                  CA___
GAM864  RNF14   3'  ATAAATTTCCATTCT      23351      CAGT
                                GTAAA   TTTCCATTCT
                                |||||   ||||||||||
                                TATTT   AAAGGTAAGA
                                  _____
GAM864  TACC1   3'  GTAAACAGTTTTTATTC    23352          CC
                                GTAAACAGTTTT  ATTC
                                ||||||||||||  ||||
                                CATTTGTCAAAA  TAAG
                                      A_
GAM864  TGFA    3'  AGTGAACAATTCATTTTCTAAA 23353    A      TCCA
                                AGT AACAGTTT   TTCTAAA
                                ||| ||||||||   |||||||
                                TCA TTGTTAAG   AAGATTT
                                  C       TAA_
GAM864  CHL1    3'  GTAAACAGTTTTTCT      23354          CCAT
                                GTAAACAGTTTT   TCT
                                ||||||||||||   |||
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                                CATTTGTCAAAA   AGA
                                       ____
GAM864  ESDN     3' AATAAACAGTTCTCTTTCT   23355          CA
                                AGTAAACAGTTTTC TTCT
                                |||||||||||||| ||||
                                TTATTTGTCAAGAG AAGA
                                       A_
GAM864  FLJ10008 3' AGTATACAGCAATTCTAAA   23356     A    TTTCC
                                AGTA ACAGT    ATTCTAAA
                                |||| |||||    ||||||||
                                TCAT TGTCG    TAAGATTT
                                  A    T____
GAM864  FLJ12876 3' AGTAGCAGCTTTATTCTAAAA 23357     AA     CC
                                AGTA  CAGTTTT  ATTCTAAAA
                                ||||  |||||||  |||||||||
                                TCAT  GTCGAAA  TAAGATTTT
                                  C_     __
GAM864  FLJ14909 3' GCAAACAGTTTTGTCTTTCT  23358          CCA_
                                GTAAACAGTTTT   TTCT
                                ||||||||||||   ||||
                                CGTTTGTCAAAA   AAGA
                                       CAGA
GAM864  KIAA0247 3' GTAAGATCTTCCATTTTAAAA 23359     ACA       C
                                GTAA   GTTTTCCATT TAAAA
                                ||||   |||||||||| |||||
                                CATT   TAGAAGGTAA ATTTT
                                  C__        A
GAM864  KIAA1795 5' AATAAACAGTTTTCATC     23360          C
                                AGTAAACAGTTTTC ATT
                                |||||||||||||| |||
                                TTATTTGTCAAAAG TAG
                                       _
GAM864  KIAA1975 5' AGTAGACATTTTCCATC     23361     A  G
                                AGTA ACA TTTTCCATT
                                |||| ||| |||||||||
                                TCAT TGT AAAAGGTAG
                                  C  _
GAM864  LAT1-3TM 3' ATAAACAGTTTTTCTA      23362          CCAT
                                GTAAACAGTTTT   TCTA
                                ||||||||||||   ||||
                                TATTTGTCAAAA   AGAT
                                       ____
GAM864  PABPC5   3' ATAAACAGTGATTTCCATT   23363        __
                                GTAAACAGT  TTTCCATT
                                |||||||||  ||||||||
                                TATTTGTCA  AAAGGTAA
                                      CT
GAM864  PEX12    3' GTAAATGCTTTCTTTTCTAAAA 23364     CA    CA
                                GTAAA  GTTTTC  TTCTAAAA
                                |||||  ||||||  ||||||||
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                                CATTT  CGAAAG  AAGATTTT
                                  A_     AA
GAM864  PIGPC1   3'  AGAAACAGTTTCTTCTTCT   23365    T        CCA
                                AG AAACAGTTTT   TTCT
                                || ||||||||||   ||||
                                TC TTTGTCAAAG   AAGA
                                 _         AAG
GAM864  SV2B     3'  AGTAAACATTTTAACCATT   23366        G   T_
                                AGTAAACA TTT  CCATT
                                |||||||| |||  |||||
                                TCATTTGT AAA  GGTAA
                                    A   TT
GAM864  ZNF262   3'  AGTAAGAAGTTTTCCAGTC   23367      AC        T
                                AGTAA  AGTTTTCCA TC
                                |||||  ||||||||| ||
                                TCATT  TCAAAAGGT AG
                                  CT        C
GAM864  LOC152940 3'  AGTAGGCAGTTTCTCCTTCTAA 23368      AA    _    A
          AA                     AGTA  CAGTT TTCC TTCTAAAA
                                |||||  ||||| |||| ||||||||
                                TCAT  GTCAA GAGG AAGATTTT
                                  CC     A   _
GAM864  LOC161742 3'  AGTTAACAGTCTATTCTA    23369     A       TCC
                                AGT AACAGTTT   ATTCTA
                                ||| ||||||||   ||||||
                                TCA TTGTCAGA   TAAGAT
                                  A       ___
GAM864  LOC163231 3'  AGTGAACAGGTTTCCATT    23370     A    T
                                AGT AACAG TTTCCATT
                                ||| ||||| ||||||||
                                TCA TTGTC AAAGGTAA
                                  C    C
GAM864  LOC196074 3'  AATAGACAGTTTTCTATTTCAA 23371      A        C   C
          A                      AGTA ACAGTTTTC ATT TAAA
                                |||| ||||||||| ||| ||||
                                TTAT TGTCAAAAG TAA GTTT
                                  C        A   A
GAM864  LOC197423 5'  ATAAACAGTTTTTCTA      23362           CCAT
                                GTAAACAGTTTT    TCTA
                                ||||||||||||    ||||
                                TATTTGTCAAAA    AGAT
                                          _____
GAM864  LOC199926 5'  AGTAAACAGTTTTTCTA     23372           CCAT
                                AGTAAACAGTTTT    TCTA
                                ||||||||||||    ||||
                                TCATTTGTCAAAA    AGAT
                                          _____
GAM864  LOC201411 3'  AGTAAACAGCTTTACTAAA    23373           CCATT
                                AGTAAACAGTTTT     CTAAA
                                ||||||||||||     |||||
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                                TCATTTGTCGAAA    GATTT
                                       T____
GAM864  LOC202316 5'  AGTAAACAGTTTTTCTA    23372          CCAT
                                AGTAAACAGTTTT   TCTA
                                ||||||||||||   ||||
                                TCATTTGTCAAAA   AGAT
                                      ____
GAM865  ALDH1A1   3'  GGATAGGACTTGGGGG     23376    A   TAAAC
                                GGA TAGG    GCTTGGGGG
                                ||| ||||    |||||||||
                                CCT ATCC    TGAACCCCC
                                  _   _____
GAM865  KIR2DL4   3'  TGGAGAGGTGGGCCAGGGG   23377    AT   AAAC   T
                                TGGA  AGGT   GCT GGGG
                                ||||  ||||   ||| ||||
                                ACCT  TCCA   CGG CCCC
                                  C_   CC__   T
GAM865  SLC6A8    3'  TGGAGAGGTGGGCAGGGGG   23378    AT   AAAC  TT
                                TGGA  AGGT   GC  GGGGG
                                ||||  ||||   ||  |||||
                                ACCT  TCCA   CG  CCCCC
                                  C_   CC__  T_
GAM865  TERF1     3'  TGGAACAGGATTTGGGGG    23379        TAAACGC
                                TGGAATAGG     TTGGGGG
                                |||||||||     |||||||
                                ACCTTGTCC     AACCCCC
                                     TA_____
GAM865  MACF1     3'  TGGATAGTGGCTTGGGGG    23380     A  GTAAAC
                                TGGA TAG     GCTTGGGGG
                                |||| |||     |||||||||
                                ACCT ATC     CGAACCCCC
                                  _  AC____
GAM865  MACF1     3'  TGGATAGTGGCTTGGGGG    23380     A  GTAAAC
                                TGGA TAG     GCTTGGGGG
                                |||| |||     |||||||||
                                ACCT ATC     CGAACCCCC
                                  _  AC____
GAM865  MGC10433  3'  GGATGGGTGGACAGCTGGGGGT 23381    ATA  AA  C
                                GGA  GGT  ACG TTGGGGGT
                                |||  |||  ||| ||||||||
                                CCT  CCA  TGT GACCCCCA
                                 AC_  CC  C
GAM865  RBP7      3'  TGGGATAGATAAACGTCTG   23382    A       CT
                                TGG ATAGGTAAACG  TG
                                ||| ||||||||||  ||
                                ACC TATCTATTTGC  AC
                                  C         AG
GAM865  TESK2     3'  TGGGGTGGGGAAAGAACCGGGG 23383    AATA  T  C_  T
                                TGG   GG AAA  GCT GGGG
                                |||   || |||  ||| ||||
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                                ACC    CC TTT  TGG CCCC
                                  CCAC  C   CT   _
GAM865  LOC126528 3'  TGGAATAGGCAGGCCGCAGGGT 23384          AA_   TTG
                                TGGAATAGGTA   CGC   GGGGT
                                ||||||||||   |||   |||||
                                ACCTTATCCGT   GCG   TCCCA
                                      CCG   ___
GAM865  LOC146488 3'  TGGAGAGGTGGGCAGGGGG   23378     AT    AAAC  TT
                                TGGA  AGGT    GC  GGGGG
                                ||||  ||||    ||  |||||
                                ACCT  TCCA    CG  CCCCC
                                  C_    CC__  T_
GAM865  LOC152620 3'  TGGAACAGGATTTGGGGG    23379         TAAACGC
                                TGGAATAGG      TTGGGGG
                                |||||||||      |||||||
                                ACCTTGTCC      AACCCCC
                                      TA_____
GAM865  LOC158668 3'  TGGAACAGGATTTGGGGG    23379         TAAACGC
                                TGGAATAGG      TTGGGGG
                                |||||||||      |||||||
                                ACCTTGTCC      AACCCCC
                                      TA_____
GAM865  LOC257000 3'  TGGGGAGGTATTTGGGGG    23385     AAT    AACGC
                                TGG   AGGTA    TTGGGGG
                                |||   |||||    |||||||
                                ACC   TCCAT    AACCCCC
                                  CC_    A____
GAM866  ABCG1     3'  TTGCAGCTTTAAATTCTGC    23388           AA
                                TTGCAGCTTTAGA  TCTGC
                                ||||||||||||  |||||
                                AACGTCGAAATTT  AGACG
                                        A_
GAM866  CDR1      3'  TCTTCCAGAAAAATCTG     23389      G   CTTT
                                TCTT CAG    AGAAATCTG
                                |||| |||    |||||||||
                                AGAA GTC    TTTTTAGAC
                                  G   ____
GAM866  D10S170   3'  TATTTTGCACCTTTAAAA    23390     C    G
                                TAT TTGCA CTTTAGAA
                                ||| ||||| ||||||||
                                ATA AACGT GAAATTTT
                                  A    G
GAM866  HTR2C     3'  TGCTAGTACTTTTGGAAATCTG 23391     A___    A_
                                TGC    GCTTT  GAAATCTG
                                |||    |||||  ||||||||
                                ACG    TGAAA  CTTTAGAC
                                  ATCA    AC
GAM866  IL4R      3'  TCTTCAAGTCTTTTGGAAATCT 23392      GC  _   A_
              GC                  TCTT  AG CTTT  GAAATCTGC
                                ||||  || ||||  |||||||||
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                                AGAA  TC GAAA  CTTTAGACG
                                  GT  A    AC
GAM866  FLJ20097  5'  TATCTTGCAGCTTTGAA     23393            A
                                TATCTTGCAGCTTT GAA
                                ||||||||||||||| |||
                                ATAGAACGTCGAAA CTT
                                                _
GAM866  KIAA1877  3'  TTCCAGCTCCATATCTGC     23394    G       GAA
                                TT CAGCTTTA   ATCTGC
                                || ||||||||   ||||||
                                AA GTCGAGGT   TAGACG
                                 G       A__
GAM866  KIAA1975  5'  TATCCTGTAGCTTTAAATG    23395        C        AATC
                                TATCTTG AGCTTTAGA    TG
                                ||||||| |||||||||    ||
                                ATAGGAC TCGAAATTT    AC
                                    A        ____
GAM866  PRRG1     3'  TATTTTGTTGCCTGGAAATCTG 23396     C   CA    TA
                                TAT TTG  GCTT  GAAATCTG
                                ||| |||  ||||  ||||||||
                                ATA AAC  CGGA  CTTTAGAC
                                  A  AA   C_
GAM866  SEP15     3'  TCTCTAATTTAGAAATCTG    23397      GCAGC
                                TCTT     TTTAGAAATCTG
                                ||||     ||||||||||||
                                AGAG     AAATCTTTAGAC
                                  ATT__
GAM866  LOC151199 3'  AACTCTTTGGAAATCTGC     23398       A__
                                AGCTTT   GAAATCTGC
                                ||||||   |||||||||
                                TTGAGA   CTTTAGACG
                                   AAC
GAM866  LOC200772 3'  TATCTGCAGCTTTGTTCTTCTG 23399       T       AGAAA
                                TATCT GCAGCTTT     TCTG
                                ||||| ||||||||     ||||
                                ATAGA CGTCGAAA     AGAC
                                  _       CAAGA
GAM867  AKAP2     3'  AACATAATAGAGCTT       23402        TACTC
                                AACATA     ATAGAGCTT
                                ||||||     |||||||||
                                TTGTAT     TATCTCGAA
                                           _____
GAM867  LILRB4    3'  AACAACACACACTGGGGCTT   23403            CATAGA
                                AACAACATATACT      GCTT
                                ||||||||||||||     ||||
                                TTGTTGTGTGTGA      CGAA
                                       CCC___
GAM867  NCKAP1    3'  AACAACATATGCTGCTGCTC   23404          A  CATAGA
                                AACAACATAT CT      GCTT
                                |||||||||| ||      ||||
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                                TTGTTGTATA GA     CGAG
                                      C  CGA___
GAM867  NEBL     3'  AACATGTACTACAAAAGCTTA  23405       A   _  T
                                AACAT TACT CA AGAGCTTA
                                ||||| |||| || ||||||||
                                TTGTA ATGA GT TTTCGAAT
                                   C    T  _
GAM867  SOX9     3'  ATATATCATAAAGCTTA     23406       C
                                ATATA TCATAGAGCTTA
                                ||||| ||||||||||||
                                TATAT AGTATTTCGAAT
                                   _
GAM867  WARS     3'  AACATACACAGGCTT       23407          TCAT  A
                                AACATATAC    AG GCTT
                                |||||||||    || ||||
                                TTGTATGTG    TC CGAA
                                     _____  _
GAM867  ALK7     3'  AACATTTTTATAGAGCTTA   23408       ATACTC
                                AACAT     ATAGAGCTTA
                                |||||      ||||||||||
                                TTGTA     TATCTCGAAT
                                   AAAA__
GAM867  DKFZp761P1010 3'  AACATATACTCATGC       23409            AGA
                                AACATATACTCAT   GC
                                ||||||||||||   ||
                                TTGTATATGAGTA   CG
                                      ___
GAM867  FLJ10057  5'  AACAAATACTGAAAGCTTA   23410      T    CAT
                                AACA ATACT   AGAGCTTA
                                |||| |||||   ||||||||
                                TTGT TATGA   TTTCGAAT
                                   T    C__
GAM867  GHITM    3'  CAACATATTTCATGCTT     23411         AC   AGA
                                CAACATAT  TCAT   GCTT
                                ||||||||  ||||   ||||
                                GTTGTATA  AGTA   CGAA
                                     A_   ___
GAM867  KIAA1829  3'  AACGGATACTCATGAACT    23412     AT       A
                                AAC  ATACTCAT GAGCT
                                |||  |||||||| |||||
                                TTG  TATGAGTA CTTGA
                                   CC       _
GAM867  XRN2     3'  AACAATATATACTCTAG     23413       C       A
                                AACAA ATATACTC TAG
                                ||||| |||||||| |||
                                TTGTT TATATGAG ATC
                                   A       _
GAM867  LOC158402 5'  AACAACATATACATATGAA   23414            TC  A
                                AACAACATATAC  AT GAG
                                ||||||||||||  || |||
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                                TTGTTGTATATG  TA CTT
                                       TA  _
GAM867  LOC221398 3'  AACAACATGTGCCTGCCCTCAT 23415   ATA_____    A     III
            GGAGCTTAT                T       CTCAT GAGCTTA  T
                                |       ||||| |||||||  |
                                A       GAGTA CTCGAAT  A
                                 CACGGACGG    C     III
GAM867  LOC93356  5'  ACAGCATATACTGGGAGGCTT  23416    A      CAT  A
                                ACA CATATACT  AG GCTT
                                ||| ||||||||  || ||||
                                TGT GTATATGA  TC CGAA
                                  C       CCC  _
GAM868  DIRC1    3'  TTTTCCTAGATGAAAGTCA   23419         TACA
                                TTTTCTTAG   AAAGTCA
                                |||||||||   |||||||
                                AAAAGGATC   TTTCAGT
                                      TAC_
GAM868  FLJ12078  3'  TATTTTCTTAGTTGCAAAGT  23420          ACA
                                TATTTTCTTAGT  AAAGT
                                ||||||||||||  |||||
                                ATAAAAGAATCA  TTTCA
                                       ACG
GAM868  FLJ12716  5'  TTTTCTTACACAAGTC     23421        G   AA
                                TTTTCTTA TACA  AGTC
                                |||||||| ||||  ||||
                                AAAAGAAT GTGT  TCAG
                                     _   __
GAM868  KIAA1843  3'  ATTTTCTGTAATAAAAGTCAAT 23422       _    CA
                                ATTTTCT TAGTA  AAAGTCAAT
                                ||||||| |||||  |||||||||
                                TAAAAGA ATTAT  TTTCAGTTA
                                    C    __
GAM868  TPD52    3'  TATTTTCTTAGTGTCAA     23423          ACAAAA
                                TATTTTCTTAGT     GTCAA
                                ||||||||||||     |||||
                                ATAAAAGAATCA     CAGTT
                                     _______
GAM868  LOC150935 3'  TATTCTCTTACCAGAAAGGGTC 23424         G  C   A_
            A                    TATTTTCTTA TA AAA  GTCA
                                ||||||||| || |||  ||||
                                ATAAGAGAAT GT TTT  CAGT
                                      G  C   CC
GAM868  LOC157798 5'  TATTTTCTAAGTACAAAGC   23425        T      A
                                TATTTTCT AGTACAAA GT
                                |||||||| |||||||| ||
                                ATAAAAGA TCATGTTT CG
                                     T      _
GAM869  BCL11B   3'  AGAAAAGGTAATAAAAATATTT 23428       AG_
            T                    AGAAAG   AATAAAAATATTTT
                                ||||||   ||||||||||||||
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                                TCTTTT  TTATTTTTATAAAA
                                   CCA
GAM869  NRG2    3' AGAAAATAAAAATATTTT   23429
                                AGAGAATAAAAATATTTT
                                ||||||||||||||||||
                                TCTTTTATTTTTATAAAA

GAM869  NRG2    3' AGAAAATAAAAATATTTT   23429
                                AGAGAATAAAAATATTTT
                                ||||||||||||||||||
                                TCTTTTATTTTTATAAAA

GAM869  NRG2    3' AGAAAATAAAAATATTTT   23429
                                AGAGAATAAAAATATTTT
                                ||||||||||||||||||
                                TCTTTTATTTTTATAAAA

GAM869  NRG2    3' AGAAAATAAAAATATTTT   23429
                                AGAGAATAAAAATATTTT
                                ||||||||||||||||||
                                TCTTTTATTTTTATAAAA

GAM869  SDPR    3' AGAAAATAAAAATATTTT   23429
                                AGAGAATAAAAATATTTT
                                ||||||||||||||||||
                                TCTTTTATTTTTATAAAA

GAM869  STMN1   3' AGAAAAAGAGTAAAACACTTT 23430       ATA
                                AGAAAGAGA  AAAATATTTT
                                |||||||||  ||||||||||
                                TCTTTTTCT  TTTTGTGAAA
                                     CA_
GAM869  BRPF3   3' TCAGAGAGAGACTAAAATATT 23431     A   ATA
                                TCAGA AGAGA  AAAATATT
                                ||||| |||||  ||||||||
                                AGTCT TCTCT  TTTTATAA
                                   C   GA_
GAM869  FLJ21657 3' TCAGGCAGAGTAAAATATTTT 23432    AA  AATA
                                TCAG  AGAG   AAAATATTTT
                                ||||  ||||   ||||||||||
                                AGTC  TCTC   TTTTATAAAA
                                  CG   A___
GAM869  FLJ23121 3' AGAAAGAGAAATTTCTATTTT 23433       TAAAAA
                                AGAAAGAGAA    TATTTT
                                ||||||||||    ||||||
                                TCTTTCTCTT    ATAAAA
                                     TAAAG_
GAM869  GABARAP  3' TCAGAAAGGGAACAGAAAC  23434       A   A
                                TCAGAAAG GAATA AAAT
                                |||||||| ||||| ||||
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                                AGTCTTTC CTTGT TTTG
                                    C    C
GAM869  KIAA0630  3'  TCAGAGAGACAAAATATTTT  23435     AA   ATA
                                TCAGA  GAGA   AAAATATTTT
                                |||||  ||||   ||||||||||
                                AGTCT  CTCT   TTTTATAAAA
                                   __   G__
GAM869  KIAA1786  3'  TCAGAGAGCATGAAAAAAATAT 23436     A  AGAAT_
          TTT                     TCAGA AG     AAAAATATTTT
                                |||||  ||     ||||||||||
                                AGTCT TC     TTTTTATAAAA
                                   C  GTACTT
GAM869  LCHN      3'  TCAGAAAGAAATGGGAAAACA  23437         ATA_
                                TCAGAAAGAGA    AAAATA
                                ||||||||||    ||||||
                                AGTCTTTCTTT    TTTTGT
                                      ACCC
GAM869  PTPRT     3'  TCAGAAAGTGGAATGCAAAT   23438       A_   AA
                                TCAGAAAG  GAAT  AAAT
                                ||||||||  ||||  ||||
                                AGTCTTTC  CTTA  TTTA
                                    AC    CG
GAM869  SV2B      3'  CAGAAGGAGAGTAAACATTTT  23439      A    ATAA
                                CAGAA GAGA    AAATATTTT
                                |||||  ||||    |||||||||
                                GTCTT CTCT    TTTGTAAAA
                                   C    CA__
GAM869  LOC145566 5'  TCAGAAAGGGAAAGGAGATACA 23440        A   TAAAA__
          TTTT                    TCAGAAAG GAA      ATATTTT
                                |||||||| |||      |||||||
                                AGTCTTTC CTT      TGTAAAA
                                    C   TCCTCTA
GAM869  LOC153396 3'  GAAAAAGAAGAGGAGTAAAAAT 23441      _______         III
          ATTTTA                    GAGAA     TAAAAATATTTT  A
                                |||||     ||||||||||||  |
                                TTCTT     ATTTTTATAAAA  T
                                   CTCCTC          III
GAM869  LOC257117 5'  TCATGGAGAGAATAAAAAC   23442     GAA
                                TCA   AGAGAATAAAAAT
                                |||   ||||||||||||||
                                AGT   TCTCTTATTTTTG
                                  ACC
GAM870  CYorf14   3'  ATGTCAATATTTTTATTAGGT  23445       _      C
                                ATGTTG TATTTTTA TAGGT
                                ||||||  ||||||||  |||||
                                TACAGT ATAAAAAT ATCCA
                                    T       A
GAM870  FLJ12704  3'  ATGCAGTGTTTTTTACTAGGT   23446     T  A
                                ATGT GT TTTTTTACTAGGT
                                ||||  ||  ||||||||||||
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                                TACG CA AAAAATGATCCA
                                  T  C
GAM870  TRIM36   3'  TTAAATTTGTATTTTTACT   23447       G
                                TTAAAT TTGTATTTTTACT
                                |||||| ||||||||||||
                                AATTTA AACATAAAAATGA
                                   _
GAM870  LOC125966 3'  TTAAATGTTGTTTCCAAAGGT  23448          AT    CT
                                TTAAATGTTGT  TTTTA  AGGT
                                ||||||||||  |||||  ||||
                                AATTTACAACA  AAGGT  TCCA
                                      __    T_
GAM870  LOC146253 3'  TTAAATGTTGTTTCCAAAGGT  23448          AT    CT
                                TTAAATGTTGT  TTTTA  AGGT
                                ||||||||||  |||||  ||||
                                AATTTACAACA  AAGGT  TCCA
                                      __    T_
GAM870  LOC151470 3'  TTAAATGTTGTTTCCAAAGGT  23448          AT    CT
                                TTAAATGTTGT  TTTTA  AGGT
                                ||||||||||  |||||  ||||
                                AATTTACAACA  AAGGT  TCCA
                                      __    T_
GAM870  LOC196477 3'  AATGATGTATTCTCCATAGGT  23449      T       AC
                                AATG TGTATTTTT  TAGGT
                                |||| |||||||||  |||||
                                TTAC ACATAAGAG  ATCCA
                                  T       GT
GAM871  AOX1     3'  AGCATATCTATCAAATCTAAAT 23452        C   TTT
                                AGCATATC ATCA   TTTAAAT
                                |||||||| ||||   |||||||
                                TCGTATAG TAGT   AGATTTA
                                    A   TT_
GAM871  EMX2     3'  CATCATCATCATTTTTTAA   23453     ATC
                                CAT   CATCATTTTTTAA
                                |||   ||||||||||||
                                GTA   GTAGTAAAAAATT
                                  GTA
GAM871  HDAC4    5'  TAGCAATGTCCACTCCTTTAA  23454      TA_    CA
                                TAGCA   TCCAT  TTTTTTAA
                                |||||   |||||  ||||||||
                                ATCGT   AGGTG  AGGAAATT
                                   TAC    __
GAM871  THBS1    3'  TAGCATATCTACACAATCT   23455        CAT   TT
                                TAGCATATC   CAT  TTT
                                |||||||||   |||  |||
                                ATCGTATAG   GTG  AGA
                                     AT_   TT
GAM871  UBL3     3'  TAGCATATCAATCTTTAAA   23456        C   ATTT
                                TAGCATATC ATC    TTTAAA
                                |||||||||  |||   ||||||
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                                ATCGTATAG TAG    AAATTT
                                     T  ____
GAM871  VNN1     3'  CATCCATCATTTTTTAAAT   23457
                                TATCCATCATTTTTTAAAT
                                ||||||||||||||||||
                                GTAGGTAGTAAAAAATTTA

GAM871  ZNF6     3'  TAGCATATCATATCTCCTAAAT 23458         C  C
                                TAGCATATC AT ATTTTTTAAAT
                                ||||||||| || ||||||||||
                                ATCGTATAG TA TAGAGGATTTA
                                     _ _
GAM871  C1QTNF7  3'  TAGCATATTTTATCATTTT   23459        CC_
                                TAGCATAT   ATCATTTT
                                ||||||||   ||||||||
                                ATCGTATA   TAGTAAAA
                                     AAA
GAM871  KIAA1910 3'  GCCTCAAAATCATTTTTTAAAT 23460    ATATCC
                                GC     ATCATTTTTTAAAT
                                ||     ||||||||||||||
                                CG     TAGTAAAAAATTTA
                                 GAGTTT
GAM871  MDS031   3'  AGCATAATCCATCATTTTTTAA 23461       _
           AT                    AGCATA TCCATCATTTTTTAAAT
                                ||||||| ||||||||||||||||
                                TCGTAT AGGTAGTAAAAAATTTA
                                   T
GAM871  LOC153139 5'  TAGCATACTTCAACTCTTTTAA 23462        C_  TCA
           AT                    TAGCATAT  CA   TTTTTTAAAT
                                ||||||||  ||   ||||||||||
                                ATCGTATG  GT   AGAAAATTTA
                                     AA  TG_
GAM871  LOC154184 5'  TAGCATACTTCAACTCTTTTAA 23462        C_  TCA
           AT                    TAGCATAT  CA   TTTTTTAAAT
                                ||||||||  ||   ||||||||||
                                ATCGTATG  GT   AGAAAATTTA
                                     AA  TG_
GAM871  LOC221601 5'  TAGCATACTTCAACTCTTTTAA 23462        C_  TCA
           AT                    TAGCATAT  CA   TTTTTTAAAT
                                ||||||||  ||   ||||||||||
                                ATCGTATG  GT   AGAAAATTTA
                                     AA  TG_
GAM872  DKFZP586A011 3'  TGGGCAGTAATTAGTACCT   23465     A  A
                                TGG TA TAATTAGTATTT
                                ||| || ||||||||||||
                                ACC GT ATTAATCATGGA
                                  C  C
GAM872  KIAA1384  3'  TGGATATACATATATTTATATA 23466       A  ATTA
                                TGGATA TA    GTATTTATATA
                                |||||| ||    ||||||||||||
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                                ACCTAT AT    TATAAATATAT
                                   _ GTA_
GAM872  KIAA1493  3'  TGGAAATAATTAGTATCCA    23467      T
                                TGGA AATAATTAGTATTTA
                                |||| ||||||||||||||
                                ACCT TTATTAATCATAGGT
                                   _
GAM872  LOC153346 3'  GGATAAAGTATTTATAT     23468       TAATT
                                GGATAA    AGTATTTATAT
                                ||||||    ||||||||||
                                CCTATT    TCATAAATATA
                                  _____
GAM873  KIAA0626  3'  TATTGGATGTATTATATTACAA 23471        _      AA
           AA                    TATTGGAT TATTATA  ATAAAA
                                |||||||| |||||||  ||||||
                                ATAACCTA ATAATAT  TGTTTT
                                     C      AA
GAM873  KIAA0853  3'  TATTGGGCTATATTAAAATAAA 23472       AT   TA
           AA                    TATTGG  TAT  TAAAATAAAAA
                                |||||| |||  ||||||||||
                                ATAACC  ATA  ATTTTATTTTT
                                   CG   TA
GAM873  KIAA1829  3'  TATTGGATCACAAAAAATGAAA 23473          TAT    A
           A                     TATTGGATTAT   AAAAT AAAA
                                ||||||||||   ||||| ||||
                                ATAACCTAGTG   TTTTA TTTT
                                      TT_    C
GAM873  MEF-2     3'  TATTGGAAATAATAAAATAA   23474       TTATT
                                TATTGGA    ATAAAATAA
                                |||||||    |||||||||
                                ATAACCT    TATTTTATT
                                    TTAT_
GAM873  LOC148534 3'  AGCCTTATTATAAAATAAAAA  23475    A_
                                GG  TTATTATAAAATAAAAA
                                ||  ||||||||||||||||
                                TC  AATAATATTTTATTTTT
                                 GG
GAM873  LOC164173 3'  TATTGGATTATTTAAAA     23476          A
                                TATTGGATTATT TAAAA
                                |||||||||||| |||||
                                ATAACCTAATAA ATTTT
                                      _
GAM874  AXUD1     5'  GCGCTCGGCCCGGCAGCCGTC  23479          _  A
                                GCGCTTGGCCTG CAG CCGTC
                                |||||||||||| ||| |||||
                                CGCGAGCCGGGC GTC GGCAG
                                      C  _
GAM874  CASP10    3'  GCTGGCCTGTAGATTGAGTC   23480     T    C   CC__
                                GCT GGCCTG AGA    GTC
                                ||| |||||| |||    |||
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```
                                CGA CCGGAC TCT    CAG
                                  _     A   AACT
GAM874  CASP10   3'  GCTGGCCTGTAGATTGAGTC  23480     T     C   CC__
                                GCT GGCCTG AGA    GTC
                                ||| |||||| |||    |||
                                CGA CCGGAC TCT    CAG
                                  _     A   AACT
GAM874  CCR9     3'  GGCAAGACCTGCAGATCGT   23481   C  TT        C
                                G GC  GGCCTGCAGA CGT
                                | ||  |||||||||| |||
                                C CG  CTGGACGTCT GCA
                                 _ TT         A
GAM874  CCR9     3'  GGCAAGACCTGCAGATCGT   23481   C  TT        C
                                G GC  GGCCTGCAGA CGT
                                | ||  |||||||||| |||
                                C CG  CTGGACGTCT GCA
                                 _ TT         A
GAM874  CNP      3'  GCTTGGCCCAGCCTCGTC    23482          _  AGAC
                                GCTTGGCCT GC    CGTC
                                ||||||||| ||    ||||
                                CGAACCGGG CG    GCAG
                                      T  GA__
GAM874  CTMP     3'  GCGCCTGGCCCGAGAGTTGTC  23483           C   CC_
                                GCGCTTGGCCTG AGA   GTC
                                |||||||||||| |||   |||
                                CGCGGACCGGGC TCT   CAG
                                      _  CAA
GAM874  EGR4     3'  GCCTTGGCCTGCCCCAGCCTGT 23484    G        ___  A  _
            C                    GC CTTGGCCTGC   AG CC GTC
                                || ||||||||||   || || |||
                                CG GAACCGGACG   TC GG CAG
                                 _        GGG  _  A
GAM874  EN1      5'  GCGTCTGGCCTGGATCGC    23485     CT      CA  C
                                GCG  TGGCCTG  GA CGT
                                |||  |||||||  || |||
                                CGC  ACCGGAC  CT GCG
                                  AG       __  A
GAM874  KCNK4    3'  CGCAGCGGTGCAGACCGT    23486     T_   CC
                                CGC  TGG  TGCAGACCGT
                                |||  |||  ||||||||||
                                GCG  GCC  ACGTCTGGCA
                                  TC   __
GAM874  KLK10    3'  GCACTTGGCTTGCCCAAAGTC  23487         C   AGACC
                                GCGCTTGGC TGC    GTC
                                ||||||||| |||    |||
                                CGTGAACCG ACG    CAG
                                      A  GGTTT
GAM874  MGAT2    5'  GCCTTGGCCTGTCACGGTC   23488    G       CAG  C
                                GC CTTGGCCTG   AC GTC
                                || |||||||||   || |||
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                                CG GAACCGGAC   TG CAG
                                 _       AG_  C
GAM874  NGFR     3'  GCACTTGGCCTCCCCGT     23489          GCAGA
                                GCGCTTGGCCT    CCGT
                                ||||||||||    ||||
                                CGTGAACCGGA    GGCA
                                      GG___
GAM874  PCDH9    3'  GCTTGGCCAGGTCAGGACTGT  23490        TG__  _  C
                                GCTTGGCC   CAG AC GT
                                ||||||||   ||| || ||
                                CGAACCGG   GTC TG CA
                                     TCCA  C  A
GAM874  SUDD     3'  GCCTGGCCCCCAAATTGT    23491         G   CC
                                GCTTGGCCT CAGA  GT
                                ||||||||| ||||  ||
                                CGGACCGGG GTTT  CA
                                      G   AA
GAM874  AGS3     5'  GCGCTTAGCCTGCACCCTC   23492          AG  G
                                GCGCTTGGCCTGC  ACC TC
                                ||||||||||||  ||| ||
                                CGCGAATCGGACG  TGG AG
                                       __  G
GAM874  BUP      3'  GCACTCGGGCGGATCGT     23493        CCT  A  C
                                GCGCTTGG   GC GA CGT
                                ||||||||   || || |||
                                CGTGAGCC   CG CT GCA
                                    ___  C  A
GAM874  CECR7    5'  CTTGGCCTCACCGTC       23494        G AG
                                CTTGGCCT C  ACCGTC
                                ||||||||| |  ||||||
                                GAACCGGA G  TGGCAG
                                      _ __
GAM874  COPS7B   5'  GCGCCTGCCCGCAGGTTGTC  23495        G      ACC
                                GCGCTTG CCTGCAG   GTC
                                ||||||| |||||||   |||
                                CGCGGAC GGGCGTC   CAG
                                    _      CAA
GAM874  EZFIT    5'  GCTGGGCCTGCACGCCGTC   23496     T      GA
                                GCT GGCCTGCA  CCGTC
                                ||| ||||||||  |||||
                                CGA CCGGACGT  GGCAG
                                  C       GC
GAM874  FLJ12684 5'  GCCTTGGCCTTCCAGTTGTC  23497    G      G_  ACC
                                GC CTTGGCCT  CAG   GTC
                                || ||||||||  |||   |||
                                CG GAACCGGA  GTC   CAG
                                 _       AG   AA_
GAM874  FLJ14966 3'  GCACTTGGCCTGATCCG     23498          CAGA
                                GCGCTTGGCCTG    CCG
                                ||||||||||||    |||
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                                CGTGAACCGGAC   GGC
                                       TA__
GAM874  FLJ20435  3'  ACGCTTGGCCGAAGCCGTC   23499        T C  A
                                GCGCTTGGCC G AG CCGTC
                                |||||||||| | || |||||
                                TGCGAACCGG C TC GGCAG
                                     _ T  _
GAM874  FLJ22686  3'  GCTTTGGCCCCAGGCCGTC   23500   GC     G   A
                                GC  TTGGCCT CAG CCGTC
                                ||  ||||||| ||| |||||
                                CG  AACCGGG GTC GGCAG
                                 A_      _  C
GAM874  FLJ30707  5'  GCGCTCGGCTTGCGGGCGCCGT 23501        C   AGA__
            C                    GCGCTTGGC TGC    CCGTC
                                ||||||||| |||    |||||
                                CGCGAGCCG ACG    GGCAG
                                     A  CCCGC
GAM874  HNRPA3   3'  GCACTTGGGACGACTGTC    23502       CCT  A   C
                                GCGCTTGG   GC GAC GTC
                                ||||||||   || ||| |||
                                CGTGAACC   TG CTG CAG
                                    C__  _   A
GAM874  KIAA0189  3'  GCTTGGCCTGGGCAGTGTC   23503        __   ACC
                                GCTTGGCCT  GCAG   GTC
                                |||||||||  ||||   |||
                                CGAACCGGA  CGTC   CAG
                                     CC    A__
GAM874  KIAA1510  5'  GCTGACCTGCAGGCTGTC    23504     T       ACC
                                GCT GGCCTGCAG   GTC
                                ||| |||||||||   |||
                                CGA CTGGACGTC   CAG
                                  _       CGA
GAM874  KIAA1550  3'  ACTTCCTCAGACCGTC      23505      GG   G
                                GCTT  CCT CAGACCGTC
                                ||||  ||| |||||||||
                                TGAA  GGA GTCTGGCAG
                                   __   _
GAM874  LAPTM4A   3'  GCTTAACCTAGATTGTC     23506        GC   CC
                                GCTTGGCCT  AGA  GTC
                                |||||||||  |||  |||
                                CGAATTGGA  TCT  CAG
                                     __   AA
GAM874  LYSAL1   3'  GCGCTCGGCCTGCATTTTGT   23507           GACC
                                GCGCTTGGCCTGCA   GT
                                ||||||||||||||   ||
                                CGCGAGCCGGACGT   CA
                                      AAAA
GAM874  MGC10870  5'  GCCTTGGCCTGCGCGT      23508    G       AGAC
                                GC CTTGGCCTGC    CGT
                                || ||||||||||    |||
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                                CG GAACCGGACG   GCA
                                 _       C___
GAM874  MGC15631  3'  GCGCTGGCCCAGACTGTC   23509     T   TG   C
                                GCGCT GGCC  CAGAC GTC
                                ||||| ||||  ||||| |||
                                CGCGA CCGG  GTCTG CAG
                                  _   __    A
GAM874  MGC20481  5'  ACGCTTGGCTCAGCTCTGTC  23510       CTG  ACC_
                                GCGCTTGGC   CAG   GTC
                                |||||||||   |||   |||
                                TGCGAACCG   GTC   CAG
                                     A__   GAGA
GAM874  MGC2562   3'  GCCTTGGCCTCCCAAATTGT  23511   G     G_   CC
                                GC CTTGGCCT  CAGA  GT
                                || ||||||||  ||||  ||
                                CG GAACCGGA  GTTT  CA
                                 _      GG   AA
GAM874  MIG       3'  GCGCTTAGTACTTCACCGT   23512       CC   AG_
                                GCGCTTGG  TGC   ACCGT
                                ||||||||  |||   |||||
                                CGCGAATC  ATG   TGGCA
                                     __   AAG
GAM874  NXN       3'  ACGCTTGGCCGAAGCCGTC   23499        T C  A
                                GCGCTTGGCC G AG CCGTC
                                |||||||||| | || |||||
                                TGCGAACCGG C TC GGCAG
                                     _ T  _
GAM874  RNB6      3'  GCACTTGGTTTCCTCACTGTC  23513        ___   G AG  C
                                GCGCTTGG   CCT C  AC GTC
                                ||||||||   ||| |  || |||
                                CGTGAACC   GGA G  TG CAG
                                     AAA   _ __  A
GAM874  SDS3      5'  GCGCTCGGTACTCGCCGTC   23514       CC   AGA
                                GCGCTTGG  TGC   CCGTC
                                ||||||||  |||   |||||
                                CGCGAGCC  ATG   GGCAG
                                     __   AGC
GAM874  SEMA4G    5'  GCGCTTGAGCAGCAGGGGCCGT 23515       _ CT   A__
          C                      GCGCTTG GC  GCAG   CCGTC
                                ||||||| ||  ||||   |||||
                                CGCGAAC CG  CGTC   GGCAG
                                    T  T_    CCC
GAM874  TRAF2     3'  GCCCTTGGCTAAGACCGTC   23516    G     C  C
                                GC CTTGGC TG AGACCGTC
                                || |||||| || ||||||||
                                CG GAACCG AT TCTGGCAG
                                 G      _  _
GAM874  LOC115219 3'  ACGTCTCCTGCGGACCGTC   23517     C  GG    A
                                GCG TT  CCTGC GACCGTC
                                ||| ||  ||||| |||||||
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                                TGC AG  GGACG CTGGCAG
                                  _ A_    C
GAM874  LOC122970 5'  GCGCCTGGCACAGCAGCCGTC  23518         CT_   A
                                GCGCTTGGC   GCAG CCGTC
                                |||||||||   |||| |||||
                                CGCGGACCG   CGTC GGCAG
                                     TGT   _
GAM874  LOC126382 5'  GCCTTGGCCTGAACGT      23519    G       CA   C
                                GC CTTGGCCTG  GAC GT
                                || |||||||||  ||| ||
                                CG GAACCGGAC  TTG CA
                                 _       __  _
GAM874  LOC144698 5'  GCTTCCACGCAGACCGT     23520      GG  _
                                GCTT  CC TGCAGACCGT
                                ||||  || ||||||||||
                                CGAA  GG GCGTCTGGCA
                                  __ T
GAM874  LOC150378 3'  GCCCTTGGCCTGAATGATGTC  23521    G       CA_  CC
                                GC CTTGGCCTG   GA  GTC
                                || |||||||||   ||  |||
                                CG GAACCGGAC   CT  CAG
                                 G        TTA  A_
GAM874  LOC152851 5'  GCGCATGGCCTGCCCTGAGTGT 23522      T       A__  CC
          C                      GCGC TGGCCTGC   GA  GTC
                                ||||  ||||||||   ||  |||
                                CGCG ACCGGACG   CT  CAG
                                  T       GGA  CA
GAM874  LOC219744 5'  GCTCTTGGCCTGAAGGGTC    23523    G       C  ACC
                                GC CTTGGCCTG AG   GTC
                                || |||||||||  ||   |||
                                CG GAACCGGAC TC   CAG
                                 A        T  C__
GAM874  LOC253070 3'  CTCGGCCTGCGGGCCGTC    23524          AGA
                                CTTGGCCTGC   CCGTC
                                ||||||||||   |||||
                                GAGCCGGACG   GGCAG
                                      CCC
GAM874  LOC93017  5'  GCCTTGGCCTAACTGT      23525    G      GCA   C
                                GC CTTGGCCT   GAC GT
                                || ||||||||   ||| ||
                                CG GAACCGGA   TTG CA
                                 _       ____  A
GAM874  LOC93166  5'  GCGCTTGGCCGCTGCCGC    23526          T  AGA
                                GCGCTTGGCC GC   CCGT
                                |||||||||| ||   ||||
                                CGCGAACCGG CG   GGCG
                                      _ AC_
GAM875  C20orf80  5'  AAGAGTACTAGGCCATGG    23529         C  A   _
                                AAGGGTAC AG CCG GG
                                |||||||| || ||| ||
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                                TTCTCATG TC GGT CC
                                    A C   A
GAM875  C22orf5   5' GGGCTGCCCTCGGGGATCACGG 23530     A_  AGACC
                                GGGT  CC    GGGATCACGG
                                ||||  ||    ||||||||||
                                CCCG  GG    CCCTAGTGCC
                                  AC  GAGC_
GAM875  CLSTN1    5' AGGGTACCCGGCCGGGGGCGG 23531        AGA    ATCA
                                AGGGTACC   CCGGG   CGG
                                ||||||||   |||||   |||
                                TCCCATGG   GGCCC   GCC
                                    GCC    CC__
GAM875  FLJ20294  3' GGGTACCAGGCTGGTCCCAGG 23532        ACC  GA   C
                                GGGTACCAG   GG  TCA GG
                                |||||||||   ||  ||| ||
                                CCCATGGTC   CC  GGT CC
                                    CGA  AG  _
GAM875  FLJ22362  3' GGGTACCAGGCCTGAGAT    23533        A  _
                                GGGTACCAG CC GGGAT
                                ||||||||| || |||||
                                CCCATGGTC GG CTCTA
                                    C  A
GAM875  IL18BP    5' AGGATACCAGACTGGGAT    23534          C
                                AGGGTACCAGAC GGGAT
                                |||||||||||| |||||
                                TCCTATGGTCTG CCCTA
                                     A
GAM875  KIAA0494  3' AAGGGTACCGGACTGTATCCAT 23535        A   CGGG   AC_
          GG                    AAGGGTACC GAC    ATC   GG
                                ||||||||| |||    |||   ||
                                TTCCCATGG CTG    TAG   CC
                                    C   ACA_   GTA
GAM875  KIAA1580  5' GGTCGGGGCCGGGATCACGG   23536    ACCAGA
                                GGT     CCGGGATCACGG
                                |||     ||||||||||||
                                CCA     GGCCCTAGTGCC
                                  GCCCC_
GAM875  PEG10     3' AAGGGTGCAGCGAGAGGATCAC 23537       AC   ACC_
          GG                    AAGGGT  CAG    GGGATCACGG
                                ||||||  |||    ||||||||||
                                TTCCCA  GTC    TCCTAGTGCC
                                   C_   GCTC
GAM875  LOC116113 3' GGTACCAGGCCTCTTCCCATGG 23538        A  GGGA_   C
                                GGTACCAG CC     TCA GG
                                ||||||||  ||    ||| ||
                                CCATGGTC GG     GGT CC
                                    C  AGAAG   A
GAM875  LOC145623 3' AAGGGTACCAGGACCATTCATG 23539          _    GGA   C
          G                     AAGGGTACCAG ACCG   TCA GG
                                |||||||||| ||||   ||| ||
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                                TTCCCATGGTC TGGT   AGT CC
                                      C    A__   A
GAM875  LOC57333  3'  AGGGGGCCAGACCACAGCGG  23540     TA      GGAT  _
                                AGGG  CCAGACCG    CA CGG
                                ||||  ||||||||    || |||
                                TCCC  GGTCTGGT    GT GCC
                                  CC       ____  C
GAM876  HDGF      3'  AAGGGTGTCAGGAGGTGG    23543     C  C   AC
                                GAG GT TCG  GGAGGTGG
                                ||| || |||  ||||||||
                                TTC CA AGT  CCTCCACC
                                  C  C   __
GAM876  IGFBP5    5'  GTGGAGATGGCGTTGGGGGTGG 23544    A   C  CT  AC  A
            G                    GT GAG GT  CG  GG GGTGGG
                                || ||| ||  ||  || ||||||
                                CA CTC TA  GC  CC CCACCC
                                 C   _  CC  AA  C
GAM876  SELPLG    3'  GAGAGCCCGTGGAGGTGG    23545     C   T  AC
                                GAG GTC CG  GGAGGTGG
                                ||| ||| ||  ||||||||
                                CTC CGG GC  CCTCCACC
                                  T   _  A_
GAM876  SP4       5'  ATAGAGGTGGGTGGGGGTGGG  23546       C  CTCGAC  A
                                GTAGAG GT     GG GGTGGG
                                |||||| ||     || ||||||
                                TATCTC CA     CC CCACCC
                                   _  CCCAC_  _
GAM876  SYN3      3'  GTCTGCGTTTGATGGAGGTGGG 23547    AGA    CTC  C
                                GT   GCGT   GA GGAGGTGGG
                                ||   ||||   || |||||||||
                                CA   CGCA   CT CCTCCACCC
                                 GA_    AA_  A
GAM876  SYN3      3'  GTCTGCGTTTGATGGAGGTGGG 23547    AGA    CTC  C
                                GT   GCGT   GA GGAGGTGGG
                                ||   ||||   || |||||||||
                                CA   CGCA   CT CCTCCACCC
                                 GA_    AA_  A
GAM876  SYN3      3'  GTCTGCGTTTGATGGAGGTGGG 23547    AGA    CTC  C
                                GT   GCGT   GA GGAGGTGGG
                                ||   ||||   || |||||||||
                                CA   CGCA   CT CCTCCACCC
                                 GA_    AA_  A
GAM876  ZFP36L1   3'  GTGGAATGTCTTGAGATGG   23548    A   C    CGACG
                                GT GAG GTCT    GAGGTGG
                                || ||| ||||    |||||||
                                CA CTT CAGA    CTCTACC
                                 C   A    A____
GAM876  CD109     3'  GTAGGGCTAGGTTGGAGGTGGG 23549      A  GTCTCGAC
                                GTAG GC       GGAGGTGGG
                                |||| ||       |||||||||
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                                CATC CG       CCTCCACCC
                                  C  ATCCAA__
GAM876  EFA6R    3'  GAGGTGGGCGACGGAGGTGGG  23550     C  CT_
                                GAG GT   CGACGGAGGTGGG
                                ||| ||   ||||||||||||||
                                CTC CA   GCTGCCTCCACCC
                                  _  CCC
GAM876  FLJ10898  3'  AGAGTGTGTGATGTGGGGGTGG 23551      C  CTC  C__  A
          G                      AGAG GT   GA   GG GGTGGG
                                ||||  ||   ||   || |||||||
                                TCTC CA   CT   CC CCACCC
                                  A  CA_  ACA  C
GAM876  KIAA0544  3'  CGTCTCCATGGAGGTGGG    23552       GAC
                                CGTCTC   GGAGGTGGG
                                ||||||   |||||||||
                                GCAGAG   CCTCCACCC
                                   GTA
GAM876  KIAA1719  3'  GAGACAGATGGAGGTGGG    23553     _  TCTC  C
                                GAG CG    GA GGAGGTGGG
                                ||| ||    || |||||||||
                                CTC GT    CT CCTCCACCC
                                  T  _____  A
GAM876  KIAA1853  3'  GCATCCGGGGAGGTGGG     23554       T  AC
                                GCGTC CG  GGAGGTGGG
                                ||||| ||  |||||||||
                                CGTAG GC  CCTCCACCC
                                  _  C_
GAM876  PTPNS1    3'  GTGGAGGTCAGGGGAGGTGGG  23555    A   C   TCGAC
                                GT GAG GTC    GGAGGTGGG
                                || ||| |||    |||||||||
                                CA CTC CAG    CCTCCACCC
                                 C   _   TCC__
GAM876  LOC126031 5'  AGAGCGTGGCCTGGAGGTGGG  23556        CTCGAC
                                AGAGCGT     GGAGGTGGG
                                |||||||     |||||||||
                                TCTCGCA     CCTCCACCC
                                   CCGGA_
GAM876  LOC158373 5'  TAGGCCGGCGGCGGAGGTGGG  23557     A  GTCT  A
                                TAG GC    CG CGGAGGTGGG
                                ||| ||    || ||||||||||
                                ATC CG    GC GCCTCCACCC
                                  _  GCC_  C
GAM876  LOC255981 3'  GGAGAGGCGGAGGTGG      23558    T    C TCTCGA
                                G AGAG G     CGGAGGTGG
                                | |||| |     |||||||||
                                C TCTC C     GCCTCCACC
                                 C   _ _______
GAM877  C20orf150 3'  TGTGGTGGCTGCGGTGG     23561        ATTT  C
                                TGTGGT    GC TGCGGTGG
                                ||||||    || ||||||||
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                                ACACCA   CG ACGCCACC
                                   C___  _
GAM877  DKFZp547H025 3'  AGAGTGGTATTTGCCATGG   23562    T        TGCG
                                AG GTGGTATTTGCC   GTGG
                                || ||||||||||||   ||||
                                TC CACCATAAACGG   TACC
                                 T        _____
GAM877  KIAA0329  3'  GTGTGGTGTGTTGTGTGG    23563       ATT  CC  CG
                                GTGTGGT   TG  TG  GTGG
                                |||||||   ||  ||  ||||
                                CACACCA   AC  AC  CACC
                                    C__   A_  A_
GAM877  KIAA1951  3'  AGTGTGGTGCTTGCCTCAGGT  23564        A      GC
                                AGTGTGGT TTTGCCT  GGT
                                |||||||| |||||||  |||
                                TCACACCA GAACGGA  CCA
                                     C      GT
GAM877  MGC10067  3'  AGTATGGTATTTGCTTCAGT   23565           CTG
                                AGTGTGGTATTTGC   CGGT
                                ||||||||||||||   ||||
                                TCATACCATAAACG   GTCA
                                       AA_
GAM877  PPY2     3'  GTGTGGTATTGTCCCCTGGGT  23566         __  G    C
                                GTGTGGTAT  TT CCTG GGT
                                |||||||||  || |||| |||
                                CACACCATA  AG GGAC CCA
                                     AC  G   _
GAM877  PRO2032   5'  AGTGTGGTGTTTGGTTTGCCT  23567        A_____
                                AGTGTGGT     TTTGCCT
                                ||||||||     |||||||
                                TCACACCA     AAACGGA
                                     CAAACC
GAM877  TLE4     3'  AGTTGGTATTTGTCTGGCTTGG 23568     G       C  _ GG
              T                  AGT TGGTATTTG CTG C  TGGT
                                ||| ||||||||| ||| |  ||||
                                TCA ACCATAAAC GAC G  ACCA
                                  _        A   C A_
GAM877  LOC139171 5'  AGTGTGGTTCTTTCCTTGTGGT 23569         A   G   _ C
              GGT                   AGTGTGGT TTT CCT G GGTGGT
                                ||||||||| ||| ||| | ||||||
                                TCACACCA GAA GGA C CCACCA
                                     A   A   A A
GAM877  LOC148709 5'  AGTTGGTGATGATGCGGTGGT  23570     G   ATT  CC
                                AGT TGGT   TG  TGCGGTGGT
                                ||| ||||   ||  |||||||||
                                TCA ACCA   AC  ACGCCACCA
                                  _   CT_  T_
GAM878  ESRRG    5'  ACACAAATGTTCTCCTAG    23573      TTAT
                                ACACG   ATGTTCTCCTAG
                                |||||   ||||||||||||
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                                TGTGT   TACAAGAGGATC
                                  T___
GAM878  ITGBL1   3'  TTCGCATTTATATGTTCT   23574    A  CG
                                TTC CA  TTATATGTTCT
                                ||| ||  ||||||||||||
                                AAG GT  AATATACAAGA
                                  C  A_
GAM878  RGS16    3'  TCCACACTTTGTTCTCCT   23575      GTTATA
                                TTCACAC     TGTTCTCCT
                                |||||||     |||||||||
                                AGGTGTG     ACAAGAGGA
                                    AA____
GAM878  dA141H5.1 3'  TTCACAGTTATTTACTCTCCT  23576      C    A
                                TTCACA GTTAT TGTTCTCCT
                                |||||| ||||| |||||||||
                                AAGTGT CAATA ATGAGAGGA
                                   _    A
GAM878  KIAA1679  3'  TTCACACATCTGATTTTCCTAG 23577         ATAT   C
                                TTCACACGTT    GTT TCCTAG
                                ||||||||||    ||| ||||||
                                AAGTGTGTAG    TAA AGGATC
                                      AC__   A
GAM878  LOC150150 5'  CACAGTTACTCCCCT      23578     C    ATGT
                                CACA GTTAT    TCTCCT
                                |||| |||||    ||||||
                                GTGT CAATG    AGGGGA
                                  _    ____
GAM878  LOC196528 3'  GTGCATGTGTCTTCTCCTAG   23579    _  A  __
                                GT TAT TGT  TCTCCTAG
                                || ||| |||  ||||||||
                                CA GTA ACA  AGAGGATC
                                 C  C   GA
GAM879  DCTN1    3'  TGAAGTCCTCAATCA      23582     G    ATGCC
                                TGAAG TCCTCA    ATCA
                                ||||| ||||||    ||||
                                ACTTC AGGAGT    TAGT
                                  _    _____
GAM879  DCTN1    3'  TGAAGTCCTCAATCA      23582     G    ATGCC
                                TGAAG TCCTCA    ATCA
                                ||||| ||||||    ||||
                                ACTTC AGGAGT    TAGT
                                  _    _____
GAM879  GALNT1   3'  TGAAAGTCCTTGATAATCAAA  23583        CA  CC
                                TGAAGGTCCT  ATG  ATCAAG
                                ||||||||||  |||  ||||||
                                ACTTTCAGGA  TAT  TAGTTT
                                      AC  __
GAM879  PLXNA1   3'  ATGAAGGTCCTTGGCCA    23584         CAAT
                                ATGAAGGTCCT   GCCA
                                ||||||||||   ||||
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                                TACTTCCAGGA   CGGT
                                      AC__
GAM879  TSSC4    5' ATGAAGGTCCTCAGCGGCAC  23585          A  C
                                ATGAAGGTCCTCA TG CAT
                                |||||||||||| || |||
                                TACTTCCAGGAGT GC GTG
                                      C  C
GAM879  UBE3A    3' ACGAAGGTCCCTTTCATCAAG 23586         CAATGC
                                ATGAAGGTCCT    CATCAAG
                                ||||||||||    |||||||
                                TGCTTCCAGGG    GTAGTTC
                                      AAA___
GAM879  UBE3A    3' ACGAAGGTCCCTTTCATCAAG 23586         CAATGC
                                ATGAAGGTCCT    CATCAAG
                                ||||||||||    |||||||
                                TGCTTCCAGGG    GTAGTTC
                                      AAA___
GAM879  UBE3A    3' ACGAAGGTCCCTTTCATCAAG 23586         CAATGC
                                ATGAAGGTCCT    CATCAAG
                                ||||||||||    |||||||
                                TGCTTCCAGGG    GTAGTTC
                                      AAA___
GAM879  DC-TM4F2 3' AGGGCTTAATGCTATCAAG   23587    TC  C    C
                                AGG  CT AATGC ATCAAG
                                |||  || ||||| ||||||
                                TCC  GA TTACG TAGTTC
                                  C_  A    A
GAM879  FLJ11040 3' TGAGGCGAATGCCATTAA    23588    A   CCTC      C
                                TGA GGT   AATGCCAT AA
                                ||| |||   |||||||| ||
                                ACT CCG   TTACGGTA TT
                                  _  C___      A
GAM879  FLJ14213 3' GAAGGGAAATGCCATCAA    23589      TCCTC
                                GAAGG    AATGCCATCAA
                                |||||    ||||||||||
                                CTTCC    TTACGGTAGTT
                                   CT___
GAM879  KIAA0682 3' ATGGAGTCCTCACCCAC     23590     AA      ATG
                                ATG  GGTCCTCA   CCAT
                                |||  ||||||||   ||||
                                TAC  TCAGGAGT   GGTG
                                  C_       G__
GAM879  KIAA1117 3' ATGACTAATGCCATCA      23591     AGGTC  C
                                ATGA    CT AATGCCATCA
                                ||||    || ||||||||||
                                TACT    GA TTACGGTAGT
                                  _____  _
GAM879  KIAA1950 3' ATGAAGGTCCTAATGCTACATC 23592          C    __
                                ATGAAGGTCCT AATGC  CATC
                                |||||||||| |||||  ||||
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                                TACTTCCAGGA TTACG  GTAG
                                      _    AT
GAM879  PRO0149   5'  ATGAAGGTGCTGCTTGACTGTC 23593       C  CAA  _ CA
           AAG                   ATGAAGGT CT   TG C  TCAAG
                                ||||||||  ||   || |  |||||
                                TACTTCCA GA   AC G  AGTTC
                                    C  CGA  T AC
GAM879  RPS6KC1   3'  TAAAGGTCCTTCTGTCAA    23594         CAA  CCA
                                TGAAGGTCCT   TG   TCAA
                                ||||||||||   ||   ||||
                                ATTTCCAGGA   AC   AGTT
                                     AG_  ___
GAM879  LOC143188 5'  ATGAAGGTTTGTCAATTACCAT 23595       CC_    _
                                ATGAAGGT   TCAAT GCCAT
                                ||||||||   ||||| |||||
                                TACTTCCA   AGTTA TGGTA
                                    AAC    A
GAM879  LOC145623 5'  ACGAAGGTCCCTTTCATCAAG  23586         CAATGC
                                ATGAAGGTCCT     CATCAAG
                                ||||||||||      |||||||
                                TGCTTCCAGGG     GTAGTTC
                                     AAA___
GAM879  LOC150605 5'  ATGAAGGCTTTGGTTACTCAAG 23596       CCTCAA   CA
                                ATGAAGGT     TGC  TCAAG
                                ||||||||     |||  |||||
                                TACTTCCG     ATG  AGTTC
                                    AAACCA   __
GAM879  LOC219333 3'  ATGAGGTCTTTCTACTGCCATC 23597     A   C_  AA_
           AAG                   ATGA GGTC  TC   TGCCATCAAG
                                |||| ||||  ||   ||||||||||
                                TACT CCAG  AG   ACGGTAGTTC
                                  _   AA  ATG
GAM879  LOC221943 5'  TGAGTGCGCCCAATGCCATC   23598     AG  C
                                TGA  GT CTCAATGCCATC
                                |||  || ||||||||||||
                                ACT  CG GGGTTACGGTAG
                                  CA  C
GAM879  LOC222166 3'  ATGAGGTCCTCACTCTCA    23599      A       ATGCCA
                                ATGA GGTCCTCA     TCA
                                |||| ||||||||     |||
                                TACT CCAGGAGT     AGT
                                  _       GAG___
GAM879  LOC63875  3'  GAAGGTTCTCAACCCCATCAAG 23600       C     G
                                GAAGGT CTCAAT CCATCAAG
                                |||||| |||||| ||||||||
                                CTTCCA GAGTTG GGTAGTTC
                                   A     G
GAM880  CGTHBA    3'  CTTGCTGGAGGGCCAG      23603     C       AAA
                                CTT GCTGGAGG   GCTAG
                                ||| ||||||||   |||||
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                                GAA CGACCTCC   CGGTC
                                  _     ___
GAM880  USH3A    3' CTTTCTGGAGGACAGCAG    23604     CG       A   T
                                CTT  CTGGAGGA AGC AG
                                |||  |||||||| ||| ||
                                GAA  GACCTCCT TCG TC
                                  A_       G   _
GAM880  FLJ10961 5' TTCGCTGGATCGCTGGAC    23605         GGAAA   A
                                TTCGCTGGA    GCT GAC
                                |||||||||    ||| |||
                                AAGCGACCT    CGA CTG
                                     AG___   C
GAM880  FLJ20584 3' TTCCTGGGGGGGCCCGGAC   23606     G    A  AAA   A_
                                TTC CTGG GG   GCT  GAC
                                ||| |||| ||   |||  |||
                                AAG GACC CC   CGG  CTG
                                  _   _ CC_   GC
GAM880  KIAA0445 3' TCCTAGAAGAGGGGGGCTGGAC 23607    G       AA___   A
                                TC CTGGAGGA    GCT GAC
                                || ||||||||    ||| |||
                                AG GATCTTCT    CGA CTG
                                 _       CCCCC   C
GAM880  KIAA0774 3' TTCCTGGGAAGCTAGA      23608     G    A  AA
                                TTC CTGG GG  AGCTAGA
                                ||| |||| ||  |||||||
                                AAG GACC CT  TCGATCT
                                  _   _ __
GAM880  PAXIP1L  3' CTTTTGGAAGAAGGCTGGAC   23609     CGC       A   A
                                CTT   TGGAGGAA GCT GAC
                                |||   |||||||| ||| |||
                                GAA   ACCTTCTT CGA CTG
                                  A__       C   C
GAM880  SLC22A6  5' CTTCGCTGGAGGAGCAGC    23610           A_
                                CTTCGCTGGAGGA  AGC
                                ||||||||||||  |||
                                GAAGCGACCTCCT  TCG
                                        CG
GAM880  ZNF300   3' CTTTGCTGGAAAAGTTAG    23611     C     GG    C
                                CTT GCTGGA  AAAG TAG
                                ||| ||||||  |||| |||
                                GAA CGACCT  TTTC ATC
                                  A     __    A
GAM880  ZNF304   3' TCCACTAGGAAAGTTAGA    23612       GG      C
                                TTCGCT  AGGAAAG TAGA
                                ||||||  ||||||| ||||
                                AGGTGA  TCCTTTC ATCT
                                   __       A
GAM880  LOC124895 5' ACTGGAGGGGGGCTAGAC    23613         AAA
                                GCTGGAGG   GCTAGAC
                                ||||||||   |||||||
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                                TGACCTCC  CGATCTG
                                    CCC
GAM880  LOC151178 5'  CTGGGCAGAGGGGAGCTAGAC  23614    TC  T    AA
                                CT  GC GGAGG  AGCTAGAC
                                ||  || |||||  ||||||||
                                GA  CG TCTCC  TCGATCTG
                                 CC  _    CC
GAM880  LOC221663 5'  CTTTGCTGGAGGAACTTGAC  23615     C       AA  A
                                CTT GCTGGAGGA  GCT GAC
                                ||| |||||||||  ||| |||
                                GAA CGACCTCCT  TGA CTG
                                  A        __  A
GAM880  LOC90342  5'  CACTGGTAGAGGAGAGCTGGA  23616       ___   A   A
                                CGCTGG   AGGA AGCT GA
                                ||||||   |||| |||| ||
                                GTGACC   TCCT TCGA CT
                                    ATC   C   C
GAM881  BTEB5    3'  GAGAGTACGGGAGTTCA    23619         CGCAA  A
                                GAGAGTACG    GGA TTCA
                                |||||||||    ||| ||||
                                CTCTCATGC    CCT AAGT
                                     _____  C
GAM882  TBXA2R   3'  GCGTGGTGGCGCGCGCCTATA  23622     TAC   AT
                                GCGT   GGCG  CGTCTATA
                                ||||   ||||  ||||||||
                                CGCA   CCGC  GCGGATAT
                                  CCA   GC
GAM882  DKFZp761O0113 5'  GCGTGGTGGTGCACGCCTATAA 23623     TAC  CGAT
                                GCGT   GG   CGTCTATAA
                                ||||   ||   |||||||||
                                CGCA   CC   GCGGATATT
                                  CCA  ACGT
GAM882  MGC5306  3'  GAGTGCTATGGCTTCCTATA  23624    C   C  GATCG
                                GAG GTTA GGC    TCTATA
                                ||| |||| |||    ||||||
                                CTC CGAT CCG    GGATAT
                                  A   A  AA___
GAM882  RAB21    3'  GCGTCGTGGTGGGCGCCTATA  23625      AC  CGAT
                                GCGTT  GG   CGTCTATA
                                |||||  ||   ||||||||
                                CGCAG  CC   GCGGATAT
                                   CA  ACCC
GAM882  LOC151057 3'  GCGTGGTGGCACGTGTCTATAA 23626     TAC   ATC
                                GCGT   GGCG   GTCTATAA
                                ||||   ||||   ||||||||
                                CGCA   CCGT   CAGATATT
                                  CCA    GCA
GAM883  ANGPT1   3'  TAATGAAGTTACATGTAT    23629   C   TTTA
                                A GTGA    TTACATGTAT
                                | ||||    ||||||||||
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                                A TACT    AATGTACATA
                                 T    TC__
GAM883  ELF2     3'  ATAAAATGTTACATGTATA    23630      TTTA
                                GTGA    TTACATGTATA
                                ||||    ||||||||||
                                TATT    AATGTACATAT
                                  TTAC
GAM883  FLJ22215  3'  TGACTTGGTTTATTACCGT    23631      G  A       A
                                TGAC TG TTTATTAC TGT
                                |||| || |||||||| |||
                                ACTG AC AAATAATG GCA
                                  A  C       _
GAM883  PCDH17    3'  TGACGTGAATTAGTCTACGTGT 23632         T   __    A
                                TGACGTGA TTA  TTAC TGT
                                |||||||| |||  |||| |||
                                ACTGCACT AAT  GATG ACA
                                     T   CA    C
GAM883  ZNF225    3'  TGATTTGATCATTACACATGTA 23633     CG     TAT_
             TAC                   TGA  TGATT    TACATGTATAC
                                |||  |||||   ||||||||||
                                ACT  ACTAG    GTGTACATATG
                                  AA    TAAT
GAM883  LOC145082 5'  TGACGTGATTTTTTAAAAGT   23634          A   CAT
                                TGACGTGATTT TTA   GT
                                |||||||||| |||   ||
                                ACTGCACTAAA AAT   CA
                                       A   TTT
GAM883  LOC149276 3'  TGATGGATTGCATACATGTAT  23635     CGT    TAT
                                TGA   GATT   TACATGTAT
                                |||   ||||   |||||||||
                                ACT   CTAA   ATGTACATA
                                  AC_    CGT
GAM883  LOC199775 3'  TGACGTGATTATTACATAT    23636          T
                                TGACGTGATT ATTACATGT
                                |||||||||| |||||||||
                                ACTGCACTAA TAATGTATA
                                          _
GAM884  CDKN1C    3'  TTGCACAGTTTTCAAAATT    23639           TGT
                                TTGCACAGTTTTT   ATT
                                ||||||||||||   |||
                                AACGTGTCAAAAG   TAA
                                       TTT
GAM884  MKNK2     3'  TTGCAAGTTTTTTGACTT     23640      C       TATT
                                TTGCA AGTTTTTTG    ACTT
                                ||||| |||||||||    ||||
                                AACGT TCAAAAAAC    TGAA
                                  _       _____
GAM884  NFYC      3'  GCACAGTTTTTAATGCATT    23641           __
                                GCACAGTTTTT  TGTATT
                                ||||||||||  ||||||
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                                CGTGTCAAAAA  ACGTAA
                                      TT
GAM884  SEDL     3'  GCACAGGCTGTATTACTT    23642       TTTT
                                GCACAG   TTGTATTACTT
                                ||||||   ||||||||||
                                CGTGTC   GACATAATGAA
                                   C___
GAM884  SLC3A2   3'  TTGCAACAGTTTGTTTGT    23643     _    _
                                TTGCA CAGTTT TTTGT
                                ||||| |||||| |||||
                                AACGT GTCAAA AAACA
                                   T     C
GAM884  ZFX      3'  TTGCCAGTTTTCCCTATT    23644     A       G
                                TTGC CAGTTTTTT TATT
                                |||| ||||||||| ||||
                                AACG GTCAAAAGG ATAA
                                  _       G
GAM884  FLJ11996 3'  TTGCATGTTTTTTGTAT     23645      CA
                                TTGCA  GTTTTTTGTAT
                                |||||  ||||||||||
                                AACGT  CAAAAAACATA
                                   A_
GAM884  KIAA1673 3'  TTGCACAGATTTACACAGTTAC 23646        T   TTGTA_
           TTA                    TTGCACAG TTT     TTACTTA
                                ||||||| |||     |||||||
                                AACGTGTC AAA     AATGAAT
                                     T   TGTGTC
GAM884  NETO2    3'  GCATGTCTGTATTACTT     23647     CA   TTT
                                GCA  GTT   TGTATTACTT
                                |||  |||   ||||||||||
                                CGT  CAG   ACATAATGAA
                                  A_  ____
GAM884  SFRS12   3'  CAGTTTTTTAATCCACTTA   23648         TA
                                CAGTTTTTTG  TTACTTA
                                ||||||||||  |||||||
                                GTCAAAAAAT  GGTGAAT
                                      TA
GAM884  SIRPB1   3'  TTGCACAGTCTTTTTGCAATCT 23649           _   TTA
           T                    TTGCACAGTTTTTT GTA   CTT
                                |||||||||||||| |||   |||
                                AACGTGTCAGAAAA CGT   GAA
                                        A   TA_
GAM884  SNTG1    3'  CTGCATAGTTGGCATTACTTA  23650      C    TTTT
                                TTGCA AGTT    GTATTACTTA
                                ||||| ||||    ||||||||||
                                GACGT TCAA    CGTAATGAAT
                                   A    C___
GAM884  LOC147229 5'  TTGCGCAGTCTACATTTGC    23651      A     ___
                                TTGC CAGTTT   TTTGT
                                |||| ||||||   |||||
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                                AACG GTCAGA   AAACG
                                  C     TGT
GAM884  LOC255158 3'  TTGTGCAGTTTTCTGTTTACTT 23652     CA         A
            A                      TTG  CAGTTTTTTGT TTACTTA
                                   |||  |||||||||||| |||||||
                                   AAC  GTCAAAAGACA AATGAAT
                                     AC         _
GAM885  KIAA1596  5'  GTTAGGTACTAAATTTTCA    23655      T       C
                                   GTTA GTACTAAAT TTTA
                                   |||| ||||||||| ||||
                                   CAAT CATGATTTA AAGT
                                     C        A
GAM885  LOC220573 3'  TTATGTACTGAAAATCTT     23656          __
                                   TTATGTACT  AAATCTT
                                   |||||||||  |||||||
                                   AATACATGA  TTTAGAA
                                        CT
GAM886  CALCRL    3'  TGTGTCAGCAAATGAGTAGA   23659     A        TACAT
                                   TGT TCAGCGAATG    GA
                                   ||| ||||||||||    ||
                                   ACA AGTCGTTTAC    CT
                                     C         TCAT_
GAM886  CHN2      3'  TGTATCAAGTACCTGTATGAAT 23660        CGAA_   CA
                                   TGTATCAG    TGTA  TGAAT
                                   ||||||||    ||||  |||||
                                   ACATAGTT    ACAT  ACTTA
                                        CATGG   __
GAM886  CREBBP    3'  TGTTAATACCATGTACATGAAT 23661     ATCA  GA
                                   TGT    GC  ATGTACATGAAT
                                   |||    ||  ||||||||||||
                                   ACA    TG  TACATGTACTTA
                                     ATTA  G_
GAM886  GAS2      3'  TATGTCAGCTCATGTATGAAT  23662     A    GA    CA
                                   TGT TCAGC  ATGTA  TGAAT
                                   ||| |||||  |||||  |||||
                                   ATA AGTCG  TACAT  ACTTA
                                     C    AG    __
GAM886  KIAA1323  3'  AACTGAGTGTACATGAAT    23663     _  A
                                   AGC GA TGTACATGAAT
                                   ||| || ||||||||||
                                   TTG CT ACATGTACTTA
                                     A  C
GAM886  UBE2G1    3'  TGTATTTGTGGATGTACATGAA 23664       CAGCGA
            C                       TGTAT     ATGTACATGAAT
                                   |||||     ||||||||||||
                                   ACATA     TACATGTACTTG
                                      AACACC
GAM886  LOC220045 3'  TGTATGAGCGAATGAGCATG   23665       C       TA
                                   TGTAT AGCGAATG  CATG
                                   ||||| ||||||||  ||||
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                                ACATA TCGCTTAC  GTAC
                                  C       TC
GAM887  ITGA1    3'  GGATAGATTATTGAATAATTGT 23668   A     C__   T
           TA                    A GTAGAT   TGA TAATTGTTA
                                | ||||||   ||| |||||||||
                                C TATCTA   ACT ATTAACAAT
                                 C     ATA   T
GAM887  C22orf20  3'  AAGTAGATTATCATCTTGTTAC 23669        CTG   A_
                                AAGTAGAT   ATTA  TTGTTAC
                                ||||||||   ||||  |||||||
                                TTCATCTA   TAGT  AACAATG
                                     A__    AG
GAM887  FLJ14775  3'  GATCTGATTGTTCTCCTGTTAC 23670         AA____
                                GATCTGATT     TTGTTAC
                                |||||||||     |||||||
                                CTAGACTAA     GACAATG
                                      CAAGAG
GAM887  KIAA0258  3'  AAGTAATCTGACCAGGTTAC   23671     A        ATT
                                AAGT GATCTGATTA   GTTAC
                                |||| ||||||||||   |||||
                                TTCA TTAGACTGGT   CAATG
                                  _        C__
GAM887  KIAA1243  3'  GTAGAGAGGTAATTGTTAC    23672      TCTGAT
                                GTAGA     TAATTGTTAC
                                |||||     |||||||||
                                CATCT     ATTAACAATG
                                   CTCC__
GAM887  RTVP1    3'  AAGTACACCTAATTGTTA    23673      G      TAAT
                                AAGTA ATCTGAT    TGTTA
                                ||||| |||||||    |||||
                                TTCAT TGGATTA    ACAAT
                                   G     ____
GAM887  ZID      3'  AAGTGAATCTGAATTGTTAC   23674      AG     TTA
                                AAGT  ATCTGA   ATTGTTAC
                                ||||  ||||||   ||||||||
                                TTCA  TAGACT   TAACAATG
                                  CT     ___
GAM887  LOC122830 3'  AAGTAGATTCAACTTGTTAC   23675        CT   TAA
                                AAGTAGAT  GAT   TTGTTAC
                                ||||||||  |||   |||||||
                                TTCATCTA  TTG   AACAATG
                                     AG   ___
GAM888  IL1B     5'  CAGAGCAGCCTGTTGT      23678        A   T
                                TAGAGCA GCTT GTTGT
                                ||||||| |||| |||||
                                GTCTCGT CGGA CAACA
                                     _   _
GAM889  TH1L     3'  GCACGAAGTCAGAGGTATA   23681    _
                                GT CGAAGTCAGAGGTATA
                                || ||||||||||||||||
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                                CG GCTTCAGTCTCCATAT
                                 T
GAM890  MMP8     3'  TATAATCCTTACTTCTAACCAA 23684        CC    ___   T
            AATCT                   TATAATCC  GCTTC   CTA AATCT
                                |||||||| |||||  ||| |||||
                                ATATTAGG  TGAAG   GGT TTAGA
                                     AA    ATT   T
GAM890  REGL     3'  TCTCCTCCTCTATAATCT    23685    C  G   C
                                TC CC CTTC TATAATCT
                                || || |||| ||||||||
                                AG GG GGAG ATATTAGA
                                 A  A   _
GAM890  C6orf37  3'  TATAATCTCTCTTCATATAGTC 23686       CCCG   C   A
            T                    TATAATC    CTTC TATA TCT
                                |||||||    |||| |||| |||
                                ATATTAG    GAAG ATAT AGA
                                     AGA_    T    C
GAM890  FLJ20445 3'  TATAATTACAGCCTATAATCT  23687       CCCC  TT
                                TATAAT    GC  CCTATAATCT
                                ||||||    ||  ||||||||||
                                ATATTA    TG  GGATATTAGA
                                    A___  TC
GAM890  PRO0245  5'  CCTCACGCCTATAATCT     23688    C   TT
                                CC CGC  CCTATAATCT
                                || |||  ||||||||||
                                GG GTG  GGATATTAGA
                                 A  C_
GAM890  SLC21A14 3'  TAATCCCCAATATAAT      23689         CTTCC
                                TAATCCCCG    TATAAT
                                |||||||||    ||||||
                                ATTAGGGGT    ATATTA
                                      T_____
GAM891  ALDH1A3  3'  TACAGCAGTCTTTCCAGTTG   23692     _      C
                                TGC GTAGTCTT CCAGTTG
                                ||| |||||||| |||||||
                                ATG CGTCAGAA GGTCAAC
                                  T       A
GAM891  FKBP14   3'  TCGTGGTATATTCCCAGTTG   23693      C   GTC
                                TCGTG GTA   TTCCCAGTTG
                                ||||| |||   ||||||||||
                                AGCAC CAT   AAGGGTCAAC
                                   _   AT_
GAM891  KIAA0410 3'  CATCTGTTCAACTTCCCAGTTG 23694      G  CG   T
                                CATC TG  TAG CTTCCCAGTTG
                                |||| ||  ||| ||||||||||
                                GTAG AC  GTT GAAGGGTCAAC
                                   _ AA  _
GAM891  LOC253868 3'  GTGGCCCCCCTTCCCAGTTG   23695     C  AG_
                                GTG GT   TCTTCCCAGTTG
                                ||| ||   ||||||||||||
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                                CAC CG   GGAAGGGTCAAC
                                  _ GGG
GAM892  EGR4     3'  TGCCTATTCACTGGGTGGTCT  23698       _  GAT  A
                                TGCCTAT TAT   GT GTCT
                                ||||||| |||   || ||||
                                ACGGATA GTG   CA CAGA
                                    A   ACC  C
GAM892  MAK      3'  TTAATGCCTATTCAGAGT    23699          AT  T
                                TTAATGCCTATT  GA GT
                                ||||||||||||  || ||
                                AATTACGGATAA  CT CA
                                       GT  _
GAM892  FLJ10352 3'  TTAATGCCTGGTTGTGAT    23700        A_  A
                                TTAATGCCT  TT TGAT
                                |||||||||  || ||||
                                AATTACGGA  AA ACTA
                                     CC  C
GAM892  KLF12    3'  ATGTCTATTCATATAGTCT   23701     C    ATG
                                ATG CTATT   ATGTAGTCT
                                ||| |||||   |||||||||
                                TAC GATAA   TATATCAGA
                                  A    G__
GAM892  LOC154089 3'  TTAATGCCAATTGTGATG    23702        T   A
                                TTAATGCC ATT TGATG
                                |||||||| ||| |||||
                                AATTACGG TAA ACTAC
                                     T   C
GAM892  LOC158476 3'  TTAATGCTGTGATAATGTAGT  23703       CTATT
                                TTAATGC    ATGATGTAGT
                                |||||||    ||||||||||
                                AATTACG    TATTACATCA
                                    ACAC_
GAM892  LOC255055 3'  TTAATGCCTGTTGTAAGTC   23704        ATTAT A   _
                                TTAATGCCT    G TGTA GTC
                                |||||||||    | |||| |||
                                AATTACGGA    C ACAT CAG
                                     _____ A   T
GAM893  CHD2     3'  TAAAATGCAAAGTACACTGGA  23707      A   A    AC
                                TAGAAT CAAA TGCGC  GGA
                                |||||| |||| |||||  |||
                                ATTTTA GTTT ATGTG  CCT
                                   C   C    A_
GAM893  EZH1     3'  GAATACAAACCACGGCGGA   23708        AT   CA
                                GAATACAAA  GCG  CGGA
                                |||||||||  |||  ||||
                                CTTATGTTT  TGC  GCCT
                                     GG  C_
GAM893  KDELR3   3'  TAGAACACAAGCATTGTGGA  23709         AAT   CAC_
                                TAGAATACAA   GCG   GGA
                                ||||||||||   |||   |||
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                                ATCTTGTGTT  CGT   CCT
                                      ___  AACA
GAM893  KIAA1317  3'  TAAAATACAGAGTTACATGGAC 23710        AAATGC  C
          G                    TAGAATACA    GCA GGACG
                               |||||||||    ||| |||||
                               ATTTTATGT    TGT CCTGC
                                    CTCAA_  A
GAM893  PRO1635  3'  AGAATGCAAAATGCAGGTATGG 23711      A       CAC__
          A                    AGAAT CAAAATGCG    GGA
                               ||||| |||||||||    |||
                               TCTTA GTTTTACGT    CCT
                                 C       CCATA
GAM893  SCYD1    3'  TAAAATACAAAATGGCACAGAC 23712           C
          G                    TAGAATACAAAATG GCACGGACG
                               |||||||||||||| |||||||||
                               ATTTTATGTTTTAC CGTGTCTGC
                                      _
GAM894  DGKI     3'  CACAGTTCCCACACAGGATT  23715     ___    G
                               CACAG  CTACG CGGGATT
                               |||||  ||||| |||||||
                               GTGTC  GGTGT GTCCTAA
                                 AAG   _
GAM894  EHD4     3'  CACACTAGGACAGGATT    23716     G  C
                               CACA CTA GGCGGGATT
                               |||| ||| |||||||||
                               GTGT GAT CTGTCCTAA
                                 _  C
GAM894  MYO7A    3'  CACAGCAAACTAGGATT    23717      TAC  _
                               CACAGC  GGC GGGATT
                               ||||||  ||| ||||||
                               GTGTCG  TTG TCCTAA
                                  T__  A
GAM894  PTGS1    3'  CACAGCCACACCTAGATT   23718        GCG
                               CACAGCTACG  GGATT
                               ||||||||||  |||||
                               GTGTCGGTGT  TCTAA
                                     GGA
GAM894  PTGS1    3'  CACAGCCACACCTAGATT   23718        GCG
                               CACAGCTACG  GGATT
                               ||||||||||  |||||
                               GTGTCGGTGT  TCTAA
                                     GGA
GAM894  RNMT     5'  CACAGCCAAACGCGATT    23719       C  G
                               CACAGCTA GGCG GATT
                               |||||||| |||| ||||
                               GTGTCGGT TTGC CTAA
                                    _  G
GAM894  SLC6A4   3'  CACAGCAGCACATGGATT   23720      TAC  ___
                               CACAGC  GGCG  GGATT
                               ||||||  ||||  |||||
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```
                                GTGTCG  TCGT  CCTAA
                                   ___   GTA
GAM894  TRHDE    3' CACAACTACTAAGAGATT   23721       GGC
                                CACAGCTAC  GGGATT
                                |||||||||  ||||||
                                GTGTTGATG  CTCTAA
                                     ATT
GAM894  USP9Y    5' CACAGCCACCAGAATT     23722       GG
                                CACAGCTAC  CGGGATT
                                |||||||||  |||||||
                                GTGTCGGTG  GTCTTAA
                                   __
GAM894  ARAP3    3' CACAGCACCACACTGGATT   23723      T  G  __
                                CACAGC AC GCG  GGATT
                                |||||| || |||  |||||
                                GTGTCG TG TGT  CCTAA
                                   _ G  GA
GAM894  ASB16    5' CACAGCAAGCTGAGATT    23724      TAC  _
                                CACAGC  GGC GGGATT
                                ||||||  ||| ||||||
                                GTGTCG  TCG CTCTAA
                                   T__  A
GAM894  CCR6     3' ACAGCTGTGAGCAAGATT   23725      AC_
                                ACAGCT  GGCGGGATT
                                ||||||  |||||||||
                                TGTCGA  TCGTTCTAA
                                   CAC
GAM894  CCR6     3' ACAGCTGTGAGCAAGATT   23725      AC_
                                ACAGCT  GGCGGGATT
                                ||||||  |||||||||
                                TGTCGA  TCGTTCTAA
                                   CAC
GAM894  CDV-1    5' CACAGCTATCATACTGGGATT 23726       CG__ _
                                CACAGCTA   GC GGGATT
                                ||||||||   || ||||||
                                GTGTCGAT   TG CCCTAA
                                     AGTA  A
GAM894  CPSF2    3' CACAACACGTAGGGATT    23727      T  GC
                                CACAGC ACG  GGGATT
                                |||||| |||  ||||||
                                GTGTTG TGC  CCCTAA
                                   _  AT
GAM894  FLJ10036 3' CAGAGCTGAGACAGGATT   23728   C   AC
                                CA AGCT  GGCGGGATT
                                || ||||  |||||||||
                                GT TCGA  CTGTCCTAA
                                 C   CT
GAM894  FLJ10751 3' CACGGCACACAGGATT     23729    A T  G
                                CAC GC ACG CGGGATT
                                ||| || ||| |||||||
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```
                                GTG CG TGT GTCCTAA
                                  C _  _
GAM894  FLJ10751  3'  CACGGCACACAGGATT     23729     A  T   G
                                CAC GC ACG CGGGATT
                                ||| || ||| |||||||
                                GTG CG TGT GTCCTAA
                                  C _  _
GAM894  FLJ23537  3'  CACAGCTCGACATGGGATT   23730       A   __
                                CACAGCT CGGC  GGGATT
                                ||||||| ||||  ||||||
                                GTGTCGA GCTG  CCCTAA
                                    _   TA
GAM894  GIOT-3    5'  ACAGGCCGGGGCGGGATT    23731     _ AC
                                ACAG CT  GGCGGGATT
                                |||| ||  |||||||||
                                TGTC GG  CCGCCCTAA
                                  C  CC
GAM894  KIAA0729  3'  CACAGCTAAAGAGGATT     23732       C  C
                                CACAGCTA GG GGGATT
                                |||||||| || ||||||
                                GTGTCGAT TC TCCTAA
                                    T  _
GAM894  KIAA1253  3'  CACAGCCATTCAAAATT     23733       CGG
                                CACAGCTA   CGGGATT
                                ||||||||   |||||||
                                GTGTCGGT   GTTTTAA
                                    AA_
GAM894  LYPLA3    3'  CACAGCCTGCGGGACT      23734       ACG
                                CACAGCT   GCGGGATT
                                |||||||   ||||||||
                                GTGTCGG   CGCCCTGA
                                   A__
GAM894  MBD2      3'  CACAGCAGCGGAGACT      23735       TAC    _
                                CACAGC   GGCGG GATT
                                ||||||   ||||| ||||
                                GTGTCG   TCGCC CTGA
                                   ___     T
GAM894  MGC29898  3'  CACAGCTACAAACTGATT    23736         CGG
                                CACAGCTACGG   GATT
                                ||||||||||   ||||
                                GTGTCGATGTT   CTAA
                                     TGA
GAM894  NFKBIE    3'  CACAGCTAGGGCAAGACT    23737       C
                                CACAGCTA GGCGGGATT
                                |||||||| |||||||||
                                GTGTCGAT CCGTTCTGA
                                    C
GAM894  RALGPS1A  3'  CACAGTTAGAACAAGATT    23738      C  CG
                                CACAG TA  GCGGGATT
                                ||||| ||  ||||||||
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                                GTGTC AT  TGTTCTAA
                                   A  CT
GAM894   LOC153937 5'  CACAGCTACTTCACTGGATT   23739        G__  G
                                CACAGCTAC   GC GGATT
                                |||||||||   || |||||
                                GTGTCGATG   TG CCTAA
                                     AAG  A
GAM894   LOC157918 3'  ACAGCTACGAGCTCTGGATT   23740        _  G__
                                ACAGCTACG GC   GGATT
                                ||||||||| ||   |||||
                                TGTCGATGC CG   CCTAA
                                     T  AGA
GAM894   LOC157919 5'  ACAGCTACGAGCTCTGGATT   23740        _  G__
                                ACAGCTACG GC   GGATT
                                ||||||||| ||   |||||
                                TGTCGATGC CG   CCTAA
                                     T  AGA
GAM894   LOC168966 5'  CACAGCAACACCACAGGATT   23741       __  G
                                CACAGC  TAC GCGGGATT
                                ||||||  ||| ||||||||
                                GTGTCG  GTG TGTCCTAA
                                   TT   G
GAM894   LOC199704 3'  CACAGTAAACAGGATT      23742       C  C
                                CACAG TA GGCGGGATT
                                ||||| || |||||||||
                                GTGTC AT TTGTCCTAA
                                  _  _
GAM894   LOC221929 5'  CACACTAGGCAGGATT      23743      G   C
                                CACA CTA GGCGGGATT
                                |||| ||| |||||||||
                                GTGT GAT CCGTCCTAA
                                  _   _
GAM894   LOC51002  5'  CACAGATAAGCAGGATT     23744       C  C
                                CACAG TA GGCGGGATT
                                ||||| || |||||||||
                                GTGTC AT TCGTCCTAA
                                   T  _
GAM894   LOC90092  5'  CAGAGCTACAGGTGGATT    23745    C       CG
                                CA AGCTACGG  GGATT
                                || ||||||||  |||||
                                GT TCGATGTC  CCTAA
                                 C       CA
GAM894   LOC92285  3'  CACAGTAAACAGGATT      23742       C  C
                                CACAG TA GGCGGGATT
                                ||||| || |||||||||
                                GTGTC AT TTGTCCTAA
                                  _  _
GAM895   FABP3     3'  GCTCTGCTTTATTGACCTCA   23748    C        A  AA
                                GC CTGTTTTATT AC  CA
                                || ||||||||| ||  ||
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                                CG GACGAAATAA TG  GT
                                 A         C  GA
GAM895  MAP3K7IP2 3'  GCCTTGTTTTATAAATACACAT 23749     C       TAACA_
                                GCC TGTTTTAT      ACAT
                                ||| ||||||||      ||||
                                CGG ACAAAATA      TGTA
                                  A       TTTATG
GAM895  CCR7     3'  GCCCTGTCTTTTTCGGCATT   23750          A  AACAA
                                GCCCTGTTTT TT     CATT
                                |||||||||| ||     ||||
                                CGGGACAGAA AA     GTAA
                                      A  GCC__
GAM895  COVA1    3'  GCCTTTCACCAGTAACAACATT 23751     CTG     ___
            AA                    GCC   TTTTAT   TAACAACATTAA
                                ||| ||||||  ||||||||||||
                                CGG  AAAGTG   ATTGTTGTAATT
                                 ___     GTC
GAM895  EVI5     3'  ACCTTGTTTTACACATTA    23752     C       TAACA
                                GCC TGTTTTAT     ACATTA
                                ||| ||||||||     ||||||
                                TGG ACAAAATG     TGTAAT
                                  A      _____
GAM895  KIAA0748  3'  GCCCTGTTTATTGACAA     23753          T   A
                                GCCCTGTTT ATT ACAA
                                ||||||||| ||| ||||
                                CGGGACAAA TAA TGTT
                                      _  C
GAM895  LOC256940 5'  GCTCTGTTTTATTACAA     23754    C         A
                                GC CTGTTTTATTA CAA
                                || ||||||||||| |||
                                CG GACAAAATAAT GTT
                                  A         _
GAM895  LOC92299  3'  GCTTTGTTTTATTAACGAC    23755    CC          A
                                GC  TGTTTTATTAAC AC
                                ||  ||||||||||| ||
                                CG  ACAAAATAATTG TG
                                  AA          C
GAM896  CGB      5'  TTTATACCTCGGGGTT      23758         ATG    A
                                TTTGTGCT   TCGG GTT
                                ||||||||   |||| |||
                                AAATATGG   AGCC CAA
                                     ___   C
GAM896  EIF2C1    3'  TTTGTGCTACGTTTTGTGAG   23759           CG___
                                TTTGTGCTATGT     GAG
                                ||||||||||||     |||
                                AAACACGATGCA     CTC
                                       AAACA
GAM896  HMGB1     3'  TTTGTGCTGTGCACCAACAA   23760         A   CGGAGTT
                                TTTGTGCT TGT      ACAA
                                |||||||| |||      ||||
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                                AAACACGA ACG      TGTT
                                    C   TGGT___
GAM896  OGT     5'  TGCTGTGGCAGTTACAAA    23762     AT  C  _
                                TGCT  GT GG AGTTACAAA
                                ||||  || || |||||||||
                                ACGA  CA CC TCAATGTTT
                                  __  _  G
GAM896  OGT     3'  TTTGTTAGTTGAGTTACA    23761      GCTAT  CG
                                TTTGT    GT  GAGTTACA
                                |||||    ||  ||||||||
                                AAACA    CA  CTCAATGT
                                   AT___  A_
GAM896  PUM2    3'  TTGTGCTATGGGGTT      23763         TC  A
                                TTGTGCTATG  GG GTT
                                ||||||||||  || |||
                                AACACGATAC  CC CAA
                                          __  _
GAM896  SP100   3'  TTTGTGCTGTGCACTAACAA  23764        A   CGGAGTT
                                TTTGTGCT TGT      ACAA
                                |||||||| |||      ||||
                                AAACACGA ACG      TGTT
                                    C   TGAT___
GAM896  BLZF1   3'  GTGCTAAAAGAGAGTTACA   23765       TGTC
                                GTGCTA    GGAGTTACA
                                ||||||    |||||||||
                                CACGAT    TCTCAATGT
                                   TTTC
GAM896  CGB5    5'  TTTATACCTCGGGGTT     23758        ATG   A
                                TTTGTGCT   TCGG GTT
                                ||||||||   |||| |||
                                AAATATGG   AGCC CAA
                                    ___    C
GAM896  DKFZp547I224 5'  TTTGTGCTATGTTTAGC    23766          CGG
                                TTTGTGCTATGT   AGT
                                ||||||||||||   |||
                                AAACACGATACA   TCG
                                      AA_
GAM896  FLJ12587  3'  TTTGTGCTATGTGATAAG    23767          CG_
                                TTTGTGCTATGT   GAG
                                ||||||||||||   |||
                                AAACACGATACA   TTC
                                      CTA
GAM896  GTF3C3  3'  CTATTTTGGAGTTACAAA    23768     GTC
                                CTAT   GGAGTTACAAA
                                ||||   ||||||||||||
                                GATA   CCTCAATGTTT
                                  AAA
GAM896  KIAA1804  3'  TTTGTGTATTCCAAGTTA    23769       C   G  G
                                TTTGTG TAT TC GAGTTA
                                |||||| ||| || ||||||
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                                  AAACAC ATA AG TTCAAT
                                    _  _ G
GAM896  LOC145508 3'  TCTGTGCTAGTATAAGTTGCAA 23770        T  CG    A
          A                    TTTGTGCTA GT  GAGTT CAAA
                               ||||||||| ||  ||||| ||||
                               AGACACGAT CA  TTCAA GTTT
                                     _ TA    C
GAM896  LOC253598 5'  TTTGGCAGCGGGAGTTACAAA  23771     T  TAT  C
                               TTTG GC   GT GGAGTTACAAA
                               |||| ||   || ||||||||||
                               AAAC CG   CG CCTCAATGTTT
                                  _ T__  C
GAM896  LOC257357 5'  TTTGTGCCTGTCTCAAAGTT   23772       A   __
                               TTTGTGCT TGTC  GGAGTT
                               |||||||| ||||  ||||||
                               AAACACGG ACAG  TTTCAA
                                     _   AG
GAM897  GFPT2    3'  GACACAGAGAAACAGTATC    23775       AAT  T
                               GACACAGA   AC GTATC
                               ||||||||   || |||||
                               CTGTGTCT   TG CATAG
                                    CTT  T
GAM897  LDHB     5'  AGGCACAGAAACTTGGTGTGTC 23776    A       AC__  A
                               AG CACAGAAAT    TGT TC
                               || |||||||||    ||| ||
                               TC GTGTCTTTG    ACA AG
                                C        AACC   C
GAM897  LIPA     3'  TAAGACACAAAATGAATCC    23777          ATAC  T
                               TAAGACACAGAA    TG ATCC
                               ||||||||||||    || ||||
                               ATTCTGTGTTTT    AC TAGG
                                      _____  T
GAM897  MAP3K9   3'  GACACAGAAAAGCTCCTATCTC 23778         TA  G_   _
          G                     GACACAGAAA  CT  TATC CG
                               ||||||||||  ||  |||| ||
                               CTGTGTCTTT  GA  ATAG GC
                                     TC  GG   A
GAM897  OLFM1    3'  TAAGACACAGGCATAGCC    23779         AA  _
                               TAAGACACAG  ATA CT
                               ||||||||||  ||| ||
                               ATTCTGTGTC  TAT GG
                                     CG   C
GAM897  UBQLN1   3'  CAAGATACAGAAATGCTG    23780      C       A
                               TAAGA ACAGAAAT CTG
                               ||||| |||||||| |||
                               GTTCT TGTCTTTA GAC
                                  A       C
GAM897  ARPC5    3'  TAAAACACAGAATGTGTAT   23781          ATAC
                               TAAGACACAGAA    TGTAT
                               ||||||||||||    |||||
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                                ATTTTGTGTCTT  ACATA
                                      AC__
GAM897  ATP6V1B2  3'  TAAGACACAGGAATCCCAATAC 23782        A  ACT_
                                TAAGACACAG AAT  GTAT
                                |||||||||| |||  ||||
                                ATTCTGTGTC TTA  TATG
                                     C  GGGT
GAM897  DDX31   3'  GACACAGAACTGACAT    23783       AAT  _
                                GACACAGA  ACTG TAT
                                ||||||||  |||| |||
                                CTGTGTCT  TGAC GTA
                                    ___  T
GAM897  DJ102H19.4 5'  TAAGACACAGGACTGT    23784         AAAT
                                TAAGACACAG  ACTGT
                                ||||||||||  |||||
                                ATTCTGTGTC  TGACA
                                     C___
GAM897  DKFZp434C0328 5'  AAGATACAGAAATATTTCAC  23785    C      CTG
                                AAGA ACAGAAATA  TAT
                                |||| |||||||||  |||
                                TTCT TGTCTTTAT  GTG
                                  A       AAA
GAM897  DORFIN   3'  TGAACACAGAAAATGTATC   23786   A       TAC
                                A GACACAGAAA  TGTATC
                                | ||||||||||  ||||||
                                A TTGTGTCTTT  ACATAG
                                 C       T__
GAM897  FLJ12704  3'  AGTGCACAGGAATACCAT   23787   A_   A
                                AG  CACAG AATACTGT
                                ||  ||||| ||||||||
                                TC  GTGTC TTATGGTA
                                 AC   C
GAM897  FLJ13456  3'  TAAGACACCTTAATTGTAT   23788       AGA  AC
                                TAAGACAC  AAT  TGTAT
                                ||||||||  |||  |||||
                                ATTCTGTG  TTA  ACATA
                                     GAA  __
GAM897  HDAC9-PENDING 3'  AGACACAATATTGTATC    23789       GAA  C
                                AGACACA  ATA TGTATC
                                |||||||  ||| ||||||
                                TCTGTGT  TAT ACATAG
                                    ___  A
GAM897  KIAA0040  3'  AGGCACAGAAACTTGGTGTGTC 23776   A       AC__  A
                                AG CACAGAAAT   TGT TC
                                || |||||||||   ||| ||
                                TC GTGTCTTTG   ACA AG
                                 C       AACC  C
GAM897  KIAA1143  3'  TAAGCCACAGAAATAGCCACAT 23790     A       _ TG
                                TAAG CACAGAAATA C  TAT
                                |||| |||||||||| |  |||
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                                ATTC GTGTCTTTAT G  GTA
                                  G        C GT
GAM897  KIAA1160  3'  TAAGACACAGGCAGCCA     23791         AAATACT   T
                                TAAGACACAG      GTA CCG
                                ||||||||||      ||| |||
                                ATTCTGTGTC      CGT GGT
                                      _______   C
GAM897  KIAA1243  3'  AGACACAAAAATGCA       23792          TAC
                                AGACACAGAAA   TGTA
                                ||||||||||||  ||||
                                TCTGTGTTTTT   ACGT
                                      ___
GAM897  KIAA1726  3'  TAAGACACAGAGACAACAGACT 23793          A _____
           G                     TAAGACACAGA AT     ACTG
                                ||||||||||| ||     ||||
                                ATTCTGTGTCT TG     TGAC
                                      C  TTGTC
GAM897  Rpo1-2    3'  TAAGGCACAGAAACAGTATC   23794      A        CT
                                TAAG CACAGAAATA  GTATC
                                |||| ||||||||||  |||||
                                ATTC GTGTCTTTGT  CATAG
                                  C        __
GAM897  LOC158310 5'  AAGGCACAGAAATGAAACTG   23795     A        ___
                                AAG CACAGAAAT   ACTG
                                ||| |||||||||   ||||
                                TTC GTGTCTTTA   TGAC
                                  C        CTT
GAM897  LOC158402 5'  AAGACACAGGGCCTCGTATC   23796         AAATA _
                                AAGACACAG     CT GTATC
                                |||||||||     || |||||
                                TTCTGTGTC     GA CATAG
                                      CCG__  G
GAM897  LOC205313 5'  TAAGCACAGAAAACATATC    23797      A       T  T
                                TAAG CACAGAAA AC GTATC
                                |||| |||||||| || |||||
                                ATTC GTGTCTTT TG TATAG
                                  _       _ _
GAM897  LOC254532 3'  TAAAACACAGAAAAGATCTG   23798           TA__
                                TAAGACACAGAAA    CTG
                                ||||||||||||    |||
                                ATTTTGTGTCTTT    GAC
                                      TCTA
GAM897  LOC56181  3'  TAAGAGGCAGAAACATCTG    23799       CA       _
                                TAAGA  CAGAAATA CTG
                                |||||  |||||||| |||
                                ATTCT  GTCTTTGT GAC
                                   CC       A
GAM898  ATP10B    3'  TATGTTATAGGGGAATAGT    23802         ATTCTA
                                TATGTTGTG     GAATAGT
                                |||||||||     |||||||
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                                ATACAATAT     CTTATCA
                                     CCC___
GAM899  TMPRSS4   5' TATTCCAGGAGTGATTGG    23805        T  ATA
                                TATTCCAG AG   GATTGG
                                |||||||| ||   ||||||
                                ATAAGGTC TC   CTAACC
                                     C  A__
GAM899  FLJ12439  3' GCTATACTCCAGTAGCTG    23806             ATAGA
                                GCTATATTCCAGTAG    TTG
                                ||||||||||||||    |||
                                CGATATGAGGTCATC    GAC
                                                  _____
GAM899  KIAA0390  3' GCTATATATACTGTAGATTGG  23807       TCCAGTAGA
                                GCTATAT       TAGATTGG
                                |||||||       ||||||||
                                CGATATA       ATCTAACC
                                    TATGAC___
GAM899  SPTLC2    3' TATTCCAGTGGGATTCTATGG  23808        A_  AGAT
                                TATTCCAGT  GAT   TGG
                                |||||||||  |||   |||
                                ATAAGGTCA  CTA   ACC
                                     CC   AGAT
GAM899  LOC149707 5' GCTATATCTGGTAGATGTTGTG 23809        CCA     AGAT
           G                     GCTATATT   GTAGAT    TGG
                                |||||||   ||||||   |||
                                CGATATAG   CATCTA    ACC
                                     AC_     CAAC
GAM899  LOC200227 5' GCTATATCTGGTAGATGTTGTG 23809        CCA     AGAT
           G                     GCTATATT   GTAGAT    TGG
                                |||||||   ||||||   |||
                                CGATATAG   CATCTA    ACC
                                     AC_     CAAC
GAM900  CD2AP     3' TAGTGACCTCATTAGAAG    23812     CAC    AAAG
                                TAG   ACCTT    ATTAGAAG
                                |||   |||||   ||||||||
                                ATC   TGGAG    TAATCTTC
                                  AC_    _____
GAM900  CLN5      3' GCATACCCCGGTTAGAAG    23813     C    AAAGA
                                GCA ACCTT    TTAGAAG
                                ||| |||||    |||||||
                                CGT TGGGG    AATCTTC
                                  A    CC___
GAM900  CPD       3' TAGCTCATCTTAAATTAAAAAG 23814      A  C     GATT
           A                     TAGC CA CTTAAA    AGAAGA
                                |||| || ||||||    ||||||
                                ATCG GT GAATTT    TTTTCT
                                  A A     AAT_
GAM900  DBY       3' TAGCATGCATTAAAGACCAGA  23815       CACC
                                TAGCA    TTAAAGATTAGA
                                |||||    ||||||||||||
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                                ATCGT   AATTTCTGGTCT
                                  ACGT
GAM900  ITGB1    3' ACATTAAAAGATTAGAAG   23816    CCTT
                                ACA   AAAGATTAGAAG
                                |||   ||||||||||||
                                TGT   TTTCTAATCTTC
                                 AAT_
GAM900  MEN1     3' CAGCACACTTTGAGATGGCTAG 23817       C  AA   ___
                                TAGCACAC TT  AGAT   TAG
                                |||||||| ||  ||||   |||
                                GTCGTGTG AA  TCTA   ATC
                                     _ AC   CCG
GAM900  SLC6A4   3' CAGCACATGGATTAGAAG   23818       CCTTAAA
                                TAGCACA     GATTAGAAG
                                |||||||     |||||||||
                                GTCGTGT     CTAATCTTC
                                    AC_____
GAM900  DCTD     3' TAGCAACCTCTTAGAA     23819      C    AAAGA
                                TAGCA ACCTT    TTAGAA
                                ||||| |||||    ||||||
                                ATCGT TGGAG    AATCTT
                                  _    _____
GAM900  FLJ20147 3' TAGCACACATTAGATAAAGAAG 23820       C  AA   T_
                                TAGCACAC TT  AGAT  AGAAG
                                |||||||| ||  ||||  |||||
                                ATCGTGTG AA  TCTA  TCTTC
                                     T __   TT
GAM900  FLJ20507 3' CACCTTAAAGGTTGGAAGA   23821         A  A
                                CACCTTAAAG TT GAAGA
                                |||||||||| || |||||
                                GTGGAATTTC AA CTTCT
                                      C  C
GAM900  FLJ20507 3' CACCTTAAAGGTTGGAAGA   23821         A  A
                                CACCTTAAAG TT GAAGA
                                |||||||||| || |||||
                                GTGGAATTTC AA CTTCT
                                      C  C
GAM900  IL1RAPL1 3' TAGCACACCTTTGGGTCTAGA 23822          AAAGA
                                TAGCACACCTT    TTAGA
                                ||||||||||    |||||
                                ATCGTGTGGAA    GATCT
                                       ACCCA
GAM900  SEC24A   3' GCATCTTTGATTAGAAGA    23823    CAC   AAA
                                GCA   CTT   GATTAGAAGA
                                |||   |||   ||||||||||
                                CGT   GAA   CTAATCTTCT
                                 A__   A__
GAM900  LOC145990 3' TAGGCACCTAATTAGAAG    23824    CA    TAAA
                                TAG  CACCT   GATTAGAAG
                                |||  |||||   |||||||||
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                                ATC  GTGGA    TTAATCTTC
                                  C_    ____
GAM900  LOC148354 3'  GCTATGCCTTAAACTAGAAGA  23825    ACA_    AA
                                GC    CCTTA  GATTAGAAGA
                                ||    |||||  ||||||||||
                                CG    GGAAT  TTGATCTTCT
                                 ATAC    __
GAM900  LOC154739 5'  GCACACCTTGGAGATATTGCAG 23826         AA    TAGA_
                                GCACACCTT  AGAT    AG
                                |||||||||  ||||    ||
                                CGTGTGGAA  TCTA    TC
                                     CC    TAACG
GAM900  LOC165229 5'  GCACACCTGGGAGAGCCAGA   23827        TAA   _
                                GCACACCT   AGA TTAGA
                                ||||||||   ||| |||||
                                CGTGTGGA   TCT GGTCT
                                    CCC   C
GAM900  LOC51107  3'  TAGCCCAAGGAGGTTAGAAGA  23828     ACA  TTAA  A
                                TAGC   CC    AG TTAGAAGA
                                ||||   ||    || ||||||||
                                ATCG   GG    TC AATCTTCT
                                  ___  TTCC  C
GAM901  FPGS     3'  TGATGTTGGTGCAGTCAT    23831      AC  C
                                TGAT  TG TGCAGTTAT
                                ||||  || |||||||||
                                ACTA  AC ACGTCAGTA
                                  CA  C
GAM901  SP3      3'  TGAACTGCTGCAGTTAC     23832     T
                                TGA ACTGCTGCAGTTAT
                                ||| ||||||||||||||
                                ACT TGACGACGTCAATG
                                 _
GAM901  BIKE     3'  TGATACTGCTGCATATAAGC   23833           GTTATT
                                TGATACTGCTGCA     GC
                                ||||||||||||      ||
                                ACTATGACGACGT     CG
                                       ATATT_
GAM901  FLJ11113  5'  TGCTACTGCTGCTACTG     23834    A       AGT
                                TG TACTGCTGC   TATTG
                                || |||||||||   |||||
                                AC ATGACGACG   ATGAC
                                 G       ___
GAM901  FLJ12891  3'  TGAGGCTGCTGCAGACCCA   23835     TA       TTATTG
                                TGA  CTGCTGCAG     CCA
                                |||  |||||||||     |||
                                ACT  GACGACGTC     GGT
                                  CC       TG____
GAM901  FLJ20309  3'  TGATCACTGCTGTATTGC    23836      _      CAGT
                                TGAT ACTGCTG    TATTGC
                                |||| |||||||    ||||||
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                                ACTA TGACGAC   ATAACG
                                  G     _____
GAM901  HSPC133  3' ATACTGCTGTTCTTGCCA   23837       CAGTTA
                                ATACTGCTG    TTGCCA
                                |||||||||    ||||||
                                TATGACGAC    AACGGT
                                     AAG___
GAM901  KIAA0298 3' TGGTACTGCTGCAGAGCTG  23838   A       TTA
                                TG TACTGCTGCAG  TTG
                                || ||||||||||  |||
                                AC ATGACGACGTC  GAC
                                 C        TC_
GAM901  KIAA0953 3' TGATACTGTTGTGTTAAGGC  23839      C  CA   TT
                                TGATACTG TG  GTTA  GC
                                |||||||| ||  ||||  ||
                                ACTATGAC AC  CAAT  CG
                                     A  A_   TC
GAM901  OSBPL1A  3' TGATACTGACTGCAGAAAACTG 23840       _    TT_
                                TGATACTG CTGCAG  ATTG
                                |||||||| ||||||  ||||
                                ACTATGAC GACGTC  TGAC
                                     T    TTT
GAM901  OSBPL1A  3' TGATACTGACTGCAGAAAACTG 23840       _    TT_
                                TGATACTG CTGCAG  ATTG
                                |||||||| ||||||  ||||
                                ACTATGAC GACGTC  TGAC
                                     T    TTT
GAM901  OSBPL1A  3' TGATACTGACTGCAGAAAACTG 23840       _    TT_
                                TGATACTG CTGCAG  ATTG
                                |||||||| ||||||  ||||
                                ACTATGAC GACGTC  TGAC
                                     T    TTT
GAM901  TCL6    5' TGACACTGTTCCAAATTGC  23841      CTG  TT
                                TGATACTG  CAG  ATTGC
                                ||||||||  |||  |||||
                                ACTGTGAC  GTT  TAACG
                                     AAG  __
GAM901  TCL6    5' TGACACTGTTCCAAATTGC  23841      CTG  TT
                                TGATACTG  CAG  ATTGC
                                ||||||||  |||  |||||
                                ACTGTGAC  GTT  TAACG
                                     AAG  __
GAM901  TCL6    5' TGACACTGTTCCAAATTGC  23841      CTG  TT
                                TGATACTG  CAG  ATTGC
                                ||||||||  |||  |||||
                                ACTGTGAC  GTT  TAACG
                                     AAG  __
GAM901  TCL6    5' TGACACTGTTCCAAATTGC  23841      CTG  TT
                                TGATACTG  CAG  ATTGC
                                ||||||||  |||  |||||
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                                ACTGTGAC  GTT  TAACG
                                    AAG  __
GAM901  LOC151360 3'  TAATATGTACTGTGGTTATTGC 23842     C_   CA
                                TGATA  TGCTG  GTTATTGC
                                |||||  |||||  ||||||||
                                ATTAT  ATGAC  CAATAACG
                                   AC    AC
GAM901  LOC151361 3'  TAATATGTACTGTGGTTATTGC 23842     C_   CA
                                TGATA  TGCTG  GTTATTGC
                                |||||  |||||  ||||||||
                                ATTAT  ATGAC  CAATAACG
                                   AC    AC
GAM901  LOC158292 5'  GATATTGCTGTGCCATGCCAT  23843     C    CA    T
                                GATA TGCTG  GTTAT GCCAT
                                |||| |||||  ||||| |||||
                                CTAT ACGAC  CGGTA CGGTA
                                  A    A_   _
GAM901  LOC196758 3'  TGATACTGATCATTGC      23844        CTGCA
                                TGATACTG    GTTATTGC
                                ||||||||    ||||||||
                                ACTATGAC    TAGTAACG
                                      _____
GAM901  LOC257471 3'  TGAACTGCTGCAGTTAC     23832     T
                                TGA ACTGCTGCAGTTAT
                                ||| ||||||||||||||
                                ACT TGACGACGTCAATG
                                  _
GAM902  CHML     5'  GTGATTATGCTGTAATAAAATC 23847        A  A   GTT_
           TG                    GTGATTAT TT TAA    ATCTG
                                ||||||||  ||  |||    |||||
                                CACTAATA GA ATT    TAGAC
                                    C  C   ATTT
GAM902  OCLN     3'  GTGATTATAAATAACAGTTATC 23848         TTATA_
           TG                    GTGATTATA     AGTTATCTG
                                |||||||||     |||||||||
                                CACTAATAT     TCAATAGAC
                                     TTATTG
GAM902  LOC144305 3'  GTGGATGCATATAAGTTGTCTG 23849     ATTATAT       A
                                GTG      TATAAGTT TCTG
                                |||      |||||||| ||||
                                CAC      ATATTCAA AGAC
                                  CTACGT_      C
GAM903  ENC1     3'  TCACAATGTAAAAGGTT     23852       GAT
                                TCACGG   TAAAAGGTT
                                ||||||   |||||||||
                                AGTGTT   ATTTTCCAA
                                   AC_
GAM903  RAB18    3'  TATCACAGGATTAAAACTCCAG 23853              ____
           TTA                   TATCACGGGATTAAAA    GGTTA
                                ||||||||||||||||   |||||
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                                ATAGTGTCCTAATTTT   TCAAT
                                       GAGG
GAM903  DOK4     3' TCATGGGATTAAAAAATT   23854    C
                                TCA GGGATTAAAAGGTT
                                ||| ||||||||||||||
                                AGT CCCTAATTTTTTAA
                                  A
GAM903  KIAA0825 3' TATTGCGGGATTATGATTA  23855    CA      AAA
                                TAT  CGGGATTA   GGTTA
                                |||  ||||||||   |||||
                                ATA  GCCCTAAT   CTAAT
                                  AC       A__
GAM903  MGC16179 3' ATCATGGGATTAGAAGGTT  23856     C      A
                                ATCA GGGATTA AAGGTT
                                |||| ||||||| ||||||
                                TAGT CCCTAAT TTCCAA
                                  A      C
GAM903  NSE1     3' TATCATGGATTAAAGCCAT   23857      CG     AA
                                TATCA  GGATTAA  GGTTAT
                                |||||  |||||||  ||||||
                                ATAGT  CCTAATT  TCGGTA
                                   A_      __
GAM903  PPP4R2   5' TATCATGGGATGAAGGT    23858      C    TAA
                                TATCA GGGAT   AAGGT
                                ||||| |||||   |||||
                                ATAGT CCCTA   TTCCA
                                   A    C__
GAM903  STAM2    3' ATCACTTGAAAAGGTTATTA  23859      GG  TTA
                                ATCAC  GA   AAAGGTTATTA
                                |||||  ||   ||||||||||||
                                TAGTG  CT   TTTCCAATAAT
                                   AA  ____
GAM903  LOC91660 5' TCATTAGGTTGAAAGGTTATTA 23860     C_   A  A
                                TCA  GGG TT AAAGGTTATTA
                                |||  ||| || ||||||||||||
                                AGT  TCC AA TTTCCAATAAT
                                  AA   _  C
GAM904  CLN2     3' GGCCATTGTTTCTGGATGTCAG 23863         CA  AGTGT
                                GGCCATTGT  TC    TGTCAG
                                |||||||||  ||    ||||||
                                CCGGTAACA  AG    ACAGTC
                                     A_  ACCT_
GAM904  NT5E     3' GGTCATTTCATCAGCAT     23864    C    G
                                GG CATT TCATCAGTGT
                                || |||| ||||||||||
                                CC GTAA AGTAGTCGTA
                                 A   _
GAM904  DKFZP434L0117 3'  GGCCATTGTCACTGGTACTTGC 23865           CA  _  _
           TCAG                    GGCCATTGTCAT  GTG TTG TCAG
                                ||||||||||||  ||| ||| ||||
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                                CCGGTAACAGTG  CAT AAC AGTC
                                      AC   G   G
GAM904  DKFZP434P211 3'  GGCCGTGGGTGGTGTTGTCAG  23866     ATT  CATCA
                                GGCC   GT    GTGTTGTCAG
                                ||||   ||    ||||||||||
                                CCGG   CA    CACAACAGTC
                                  ___  CCCAC
GAM904  FLJ22794  3'  CCATCTCATAGTGTTGT     23867      G    C
                                CCATT TCAT AGTGTTGT
                                ||||| |||| ||||||||
                                GGTAG AGTA TCACAACA
                                  _   _
GAM904  GOLPH2    3'  GGCCATTGATTGATTGATTGTC 23868        TCATCAGT
           AG                     GGCCATTG       GTTGTCAG
                                ||||||||       ||||||||
                                CCGGTAAC       TAACAGTC
                                    TAACTAAC
GAM904  GS3955    3'  GGCCATTGCTATCATCTCA    23869        TC    GTGTTG
                                GGCCATTG  ATCA     TCA
                                ||||||||  ||||     |||
                                CCGGTAAC  TAGT     AGT
                                    GA    AG____
GAM904  HEAB      5'  GGCTGTTGTCATTATTCGTGCA 23870     CA      CAGTG   _
           G                     GGC  TTGTCAT    TTGT CAG
                                |||  |||||||    |||| |||
                                CCG  AACAGTA    AGCA GTC
                                  AC      ATA__    C
GAM904  HERC1     3'  GGCCATTGTTTATAATGTTG   23871         CATC
                                GGCCATTGT    AGTGTTG
                                |||||||||    |||||||
                                CCGGTAACA    TTACAAC
                                    AATA
GAM904  KIAA0172  5'  GCTTGTTGTCATCACTGTTG   23872    CA_       G
                                GC   TTGTCATCA TGTTG
                                ||   ||||||||| |||||
                                CG   AACAGTAGT ACAAC
                                 AAC        G
GAM904  KIAA0247  3'  GCTTGTGCTCCTCAGTGTTGT  23873    CAT   CA_
                                GC   TGT   TCAGTGTTGT
                                ||   |||   ||||||||||
                                CG   ACG   AGTCACAACA
                                 AAC   AGG
GAM904  LOC123242 5'  GGCCATGTTGTCTGTAGTCAG  23874       __   ATCAG   T
                                GGCCAT  TGTC    TGT GTCAG
                                ||||||  ||||    ||| |||||
                                CCGGTA  ACAG    ACA CAGTC
                                   CA    _____   T
GAM904  LOC132617 3'  GATCATTGTCATTAACATCAG  23875   GC       CAGTGT
                                G  CATTGTCAT     TGTCAG
                                |  |||||||||     ||||||
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                                C  GTAACAGTA     GTAGTC
                                 TA        ATT___
GAM904   LOC145780 3'  GGTCCTTGTCATCAGGTGCAG  23876    _ A        T  T T
                                GG CC TTGTCATCAG GT G CAG
                                || || |||||||||| || | |||
                                CC GG AACAGTAGTC CA C GTC
                                 A _        _ _ _
GAM904   LOC169026 5'  AGCTTCCTACATCAGTGTTGT  23877     CA_   T
                                GGC   TTG CATCAGTGTTGT
                                |||   ||| ||||||||||||
                                TCG   GAT GTAGTCACAACA
                                  AAG   _
GAM904   LOC196955 3'  GGCCATGTTGTCTGTAGTCAG  23874       __    ATCAG   T
                                GGCCAT  TGTC    TGT GTCAG
                                ||||||  ||||    ||| |||||
                                CCGGTA  ACAG    ACA CAGTC
                                   CA    _____   T
GAM904   LOC204084 5'  GGCCATTGTTATCAGTAACCAG 23878         C      TTG
                                GGCCATTGT ATCAGTG   TCAG
                                |||||||||  |||||||   ||||
                                CCGGTAACA TAGTCAT   GGTC
                                     A      T__
GAM904   LOC219988 5'  GGCTGTTGTCATGAGAATGTCA 23879     CA      C  TGT
           G                     GGC  TTGTCAT AG   TGTCAG
                                |||  |||||| ||   ||||||
                                CCG  AACAGTA TC   ACAGTC
                                  AC      C  TT_
GAM904   LOC253001 5'  GGCCATGTTGTCTGTAGTCAG  23874       __    ATCAG   T
                                GGCCAT  TGTC    TGT GTCAG
                                ||||||  ||||    ||| |||||
                                CCGGTA  ACAG    ACA CAGTC
                                   CA    _____   T
GAM904   LOC256940 5'  GGCTGTTGTCAGCAGATGTC   23880     CA     T   TGT
                                GGC  TTGTCA CAG   TGTC
                                |||  |||||| |||   ||||
                                CCG  AACAGT GTC   ACAG
                                  AC     C  T__
GAM904   LOC257127 3'  GGCTGTGTTGCTCATGTTGTCA 23881     CAT   CA_   G
           G                     GGC   TGT   TCA TGTTGTCAG
                                |||   |||   ||| |||||||||
                                CCG   ACA   AGT ACAACAGTC
                                  AC_   ACG   _
GAM905   HSPG2    3'  GCCAGGGGCTGGGTGGAGGTG  23884      A       AA
                                GTTA GGGCTGGGT  AGGTG
                                |||| |||||||||  |||||
                                CGGT CCCGACCCA  TCCAC
                                  C        CC
GAM905   FLJ21125  3'  TGTTTTATGGGGGTGGAGGTG  23885     G   A   CTG   AA
                                TGT TTA GGG   GGT  AGGTG
                                ||| ||| |||   |||  |||||
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                                ACA AAT CCC   CCA  TCCAC
                                  A   A  ___   CC
GAM905  LOC221476 3'  TGTTTAGGGGCTGGGGACAGG  23886     G   A      TAA
                                TGT TTA GGGCTGGG   AGG
                                ||| ||| ||||||||   |||
                                ACA AAT CCCGACCC   TCC
                                  _  C       CTG
GAM905  LOC253933 3'  TATGTTAATGGTGAAGGT    23887        GGGC   GTA
                                TGTGTTAA   TGG   AAGGT
                                ||||||||   |||   |||||
                                ATACAATT   ACC   TTCCA
                                     _____  AC_
GAM905  LOC255105 3'  TATGTTAATGGTGAAGGT    23887        GGGC   GTA
                                TGTGTTAA   TGG   AAGGT
                                ||||||||   |||   |||||
                                ATACAATT   ACC   TTCCA
                                     _____  AC_
GAM906  IER5     3'  TCTCCAGATAAGCCAGAT    23890       _    TAGAT
                                TCTCCA ATAAG    CCAGAT
                                |||||| |||||    ||||||
                                AGAGGT TATTC    GGTCTA
                                   C    ______
GAM906  LPIN1    3'  TCTCCAATGTACCAG       23891        AA   GAT
                                TCTCCAAT  GTA   CCAG
                                ||||||||  |||   ||||
                                AGAGGTTA  CAT   GGTC
                                     __  ___
GAM906  MEIS2    5'  CTCCAATAAACTCCTGGAT   23892        GTAGA   A_
                                CTCCAATAA    TCC  GAT
                                |||||||||    |||  |||
                                GAGGTTATT    AGG  CTA
                                     TG___   AC
GAM906  C6orf32  5'  TCTCTGGTAGTACATCCAGAT  23893     CAATA    G
                                TCTC    AGTA ATCCAGAT
                                ||||    |||| ||||||||
                                AGAG    TCAT TAGGTCTA
                                  ACCA_   G
GAM906  CDA08    3'  TCCAATAATTACCATGGGATAC 23894        GTAGAT   ___
                                TCCAATAA    CCA   GATAC
                                ||||||||    |||   |||||
                                AGGTTATT    GGT   CTATG
                                     AAT___   ACC
GAM906  CECR2    3'  CCTCCAATGGAGACACCAG   23895        AAGT   _
                                TCTCCAAT   AGAT CCAG
                                ||||||||   |||| ||||
                                GGAGGTTA   TCTG GGTC
                                     CC__    T
GAM906  FLJ10565 5'  TCTCCAATGCAGTCAGGTA   23896        AA   ATC   A
                                TCTCCAAT  GTAG   CAG TA
                                ||||||||  ||||   ||| ||
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                                AGAGGTTA  CGTC   GTC AT
                                    __    A__   C
GAM906   LOC151643 3'  TCTCTAGTACCTTCCCAGATA  23897     CAATA   GA__
                                TCTC    AGTA   TCCAGATA
                                ||||    ||||   ||||||||
                                AGAG    TCAT   GGGTCTAT
                                  A_____   GGAA
GAM906   LOC154442 3'  TCCAGTAAGTCCAGATA     23898     A   TAGA
                                TCCA TAAG   TCCAGATA
                                |||| ||||   ||||||||
                                AGGT ATTC   AGGTCTAT
                                  C   _____
GAM906   LOC200197 3'  TCCAACAAGCTTCCAG      23899         AGA
                                TCCAATAAGT   TCCAG
                                ||||||||||   |||||
                                AGGTTGTTCG   AGGTC
                                     A__
GAM906   LOC202025 5'  TCTCAGAGGTCCAGAT      23900     CAATA  T  A
                                TCTC    AG AG TCCAGAT
                                ||||    || || |||||||
                                AGAG    TC TC AGGTCTA
                                  ______ _  C
GAM906   LOC220565 3'  TCTCCAGATATTCCAGATA   23901      ATAA   GA
                                TCTCCA   GTA  TCCAGATA
                                ||||||   |||  ||||||||
                                AGAGGT   TAT  AGGTCTAT
                                   C___   A_
GAM906   LOC254228 3'  TCTCCAATACCAACTGGATA  23902        AGTA   CCA
                                TCTCCAATA   GAT   GATA
                                |||||||||   |||   ||||
                                AGAGGTTAT   TTG   CTAT
                                     GG__   AC_
GAM906   LOC254749 5'  TCCAATAAATGGAATGATA   23903         A  TCCA
                                TCCAATAAGT GA   GATA
                                |||||||||| ||   ||||
                                AGGTTATTTA CT   CTAT
                                     C  TA__
GAM906   LOC255177 3'  TCTCTGTAATCCCAGATA    23904     CAATAA   A
                                TCTC     GTAG TCCAGATA
                                ||||     |||| ||||||||
                                AGAG     CATT GGGTCTAT
                                  A_____   A
GAM907   SLC1A4   3'  TTTCGAAGATTAACA       23907        A  GTTA
                                TTTCGAA GA   TTAACA
                                ||||||| ||   ||||||
                                AAAGCTT CT   AATTGT
                                   _ _____
GAM907   FAM8A1   3'  TATTTCGCAAGCTATTAATAGT 23908        AAA        C
                                TATTTCG   GAGTTATTAA AGT
                                |||||||   |||||||||| |||
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                                ATAAAGC   TTCGATAATT TCA
                                   G__        A
GAM907  KIAA1332  3'  TATTTTAAAGAGTTCCAACACA 23909      CG      ATTA_
            GT                    TATTT  AAAGAGTT    ACAGT
                                  |||||  ||||||||    |||||
                                  ATAAA  TTTCTCAA    TGTCA
                                    A_       GGTTG
GAM907  LZK1     3'  TTTCGAAAGAGAAGGCGCAGT  23910         TTATTAA
                                  TTTCGAAAGAG      CAGT
                                  ||||||||||       ||||
                                  AAAGCTTTCTC      GTCA
                                        TTCCGC_
GAM907  LOC144871 5'  TATTTCAAAGAGGTCACAG   23911       G     TTATTA
                                  TATTTC AAAGAG     ACAG
                                  ||||||  ||||||     ||||
                                  ATAAAG TTTCTC     TGTC
                                     _     CAG___
GAM907  LOC254672 3'  TATTTTTAAAGAGTCAAAAACA 23912      CG       TT
            GT                    TATTT  AAAGAGTTA  AACAGT
                                  |||||  |||||||||  ||||||
                                  ATAAA  TTTCTCAGT  TTGTCA
                                    AA        TT
GAM908  FOXO1A    3'  TAAGATTTTAACAGTGATTTT  23915        __    AC
                                  TAAGATTT  ACAG  GATTTT
                                  ||||||||  ||||  ||||||
                                  ATTCTAAA  TGTC  CTAAAA
                                       AT    A_
GAM908  LOC51200  3'  TAAGATTTACAAACATTTT    23916           G
                                  TAAGATTTACAGAC ATTTT
                                  |||||||||||||| |||||
                                  ATTCTAAATGTTTG TAAAA
                                                 _
GAM909  CDKN2B    3'  TCTCTGTGTTTCGCTTCATGGT 23919    C   CT   A   __  C  C
            GAG                     TC CTG  TTT CGC  CA GG GAG
                                  || |||  ||| |||  || || |||
                                  AG GAC  AAA GCG  GT CC CTC
                                   A   AC   _   AA  A  A
GAM909  KCNK5     3'  CCTGCTTTTGCTCACCTCAG   23920         A__    A
                                  CCTGCTTTT   CGCC CGG
                                  |||||||||   |||| |||
                                  GGACGAAAA   GTGG GTC
                                        CGA    A
GAM909  TEM5      3'  TCTCTGCTTTGCTGGTGA    23921    C      TAC  CAC  C
                                  TC CTGCTTT   GC   GG GA
                                  || |||||||   ||   || ||
                                  AG GACGAAA   CG   CC CT
                                   A       ___  A__  A
GAM909  WASF3     3'  TCTCTGCTTTTAGCTCCAG    23922    C       C  CA
                                  TC CTGCTTTTA GC  CGG
                                  || |||||||| ||  |||
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```
                                AG GACGAAAAT CG  GTC
                                 A       _ AG
GAM909  C22orf4   3'  CCGCTTCCAGGCTGCGGTGAG  23923        C  CA   C
                                CTGCTTTTA GC  CGG GAG
                                ||||||||| ||  ||| |||
                                GGCGAAGGT CG  GCC CTC
                                     C  AC   A
GAM909  PDE8B     5'  CCCCTGCTGGTGGTCGCGGCG  23924        TTTA__   CAC
                                TCCCTGCT     CGC   GGCG
                                ||||||||     |||   ||||
                                GGGGACGA     GCG   CCGC
                                    CCACCA   ___
GAM909  RAB10     5'  TCCCTGCTAGCACGCGGCGAG  23925        TT    CAC
                                TCCCTGCT  TACGC   GGCGAG
                                ||||||||  |||||   ||||||
                                AGGGACGA  GTGCG   CCGCTC
                                    TC    ___
GAM910  ADAMTS5   3'  TCACTGAAGCATGACTTTCTGT 23928    T      G
          G                      TC CTGGAGTG TGACTTTCTGTG
                                 || |||||||| ||||||||||||
                                 AG GACTTCGT ACTGAAAGACAC
                                  T      _
GAM910  ITSN1     3'  TCTAGATAATGACTTTCTGTG  23929       G
                                TCTGGA TGGTGACTTTCTGTG
                                |||||| ||||||||||||||
                                AGATCT ATTACTGAAAGACAC
                                    _
GAM910  SGCD      3'  TCTTTGATAGGCTTTCTGT   23930     C   AGT  TGA
                                TCT TGG   GG   CTTTCTGT
                                ||| |||   ||   ||||||||
                                AGA ACT   CC   GAAAGACA
                                  A   AT_  ___
GAM910  TIAL1     3'  TGGGGTGGTGACACCTGTG   23931     A      TT
                                TGG GTGGTGAC  TCTGTG
                                ||| ||||||||  ||||||
                                ACC CACCACTG  GGACAC
                                  C       T_
GAM910  DKFZP547E1010 3'  TCTGGGATGTTTCTGT     23932      AGT   AC
                                TCTGG   GGTG  TTTCTGT
                                |||||   ||||  |||||||
                                AGACC   CTAC  AAAGACA
                                    ____   __
GAM910  DKFZP547E1010 3'  TCTGGGATGTTTCTGT     23932      AGT   AC
                                TCTGG   GGTG  TTTCTGT
                                |||||   ||||  |||||||
                                AGACC   CTAC  AAAGACA
                                    ____   __
GAM910  DKFZP586F1318 5'  TCTGGAAGTTATTTCTGTG   23933       GT   GAC
                                TCTGGA  GGT   TTTCTGTG
                                ||||||  |||   ||||||||
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                                AGACCT  TCA   AAAGACAC
                                   __   AT_
GAM910  FLJ12700  3'  TCTCAGTGACTGGCTTTCTGTG 23934     TG_  G   TGA
                                TCTC   GA TGG   CTTTCTGTG
                                ||||   || |||   |||||||||
                                AGAG   CT ACC   GAAAGACAC
                                  TCA  G   ___
GAM910  FXYD3     3'  CCTGGAGTTCAAGTTTCTGTG  23935        GG   C
                                TCTGGAGT  TGA TTTCTGTG
                                ||||||||  ||| ||||||||
                                GGACCTCA  GTT AAAGACAC
                                     A_   C
GAM910  FXYD3     3'  CCTGGAGTTCAAGTTTCTGTG  23935        GG   C
                                TCTGGAGT  TGA TTTCTGTG
                                ||||||||  ||| ||||||||
                                GGACCTCA  GTT AAAGACAC
                                     A_   C
GAM910  GIOT-2    3'  TCTCTGTAGAGTTTTTTCTGTG 23936       G  T   GAC
                                TCTCTG AG GGT   TTTCTGTG
                                |||||| || |||   ||||||||
                                AGAGAC TC TCA   AAAGACAC
                                   A  _   AA_
GAM910  KIAA0218  3'  CCTGTCCTGGTTTTCTGT    23937      GAG    GAC
                                TCTG   TGGT   TTTCTGT
                                ||||   ||||   |||||||
                                GGAC   ACCA   AAAGACA
                                  AGG   ___
GAM910  KIAA1950  3'  TCTGGAGACAGTCTTTCTGTG  23938        _    GA
                                TCTGGAG TGGT  CTTTCTGTG
                                ||||||| ||||  |||||||||
                                AGACCTC GTCA  GAAAGACAC
                                     T   __
GAM910  PLCL1     3'  TGCATGTATGCTTTCTGTG   23939    GA  _  A
                                TG  GTG GTG CTTTCTGTG
                                ||  ||| ||| |||||||||
                                AC  TAC TAC GAAAGACAC
                                 G_  A  _
GAM910  LOC146443 5'  TCTCTGGGGGTGGTGCCCCTGT 23940        A_     AC TT
           G                     TCTCTGG  GTGGTG  T  CTGTG
                                |||||||  ||||||  |  |||||
                                AGAGACC  CACCAC  G  GACAC
                                    CC     __ GG
GAM910  LOC150135 5'  TCTCTGCAGTGGACAGTCTGTG 23941       G    TG  TT
                                TCTCTG AGTGG  AC  TCTGTG
                                ||||||  |||||  ||  ||||||
                                AGAGAC TCACC  TG  AGACAC
                                   G    __  TC
GAM910  LOC151959 5'  TCTTCTGGAGTGGTCCCTGTG  23942     _        GACT
                                TCT CTGGAGTGGT    TTCTGTG
                                ||| ||||||||||    |||||||
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                                AGA GACCTCACCA    GGGACAC
                                  A       _____
GAM910  LOC151996 5'  CCTCTGGACACTTTTTGT    23943        GTGGTG    C
                                TCTCTGGA     ACTTT TGT
                                ||||||||     ||||| |||
                                GGAGACCT     TGAAA ACA
                                    G_____    A
GAM910  LOC170063 3'  TCTCTGAAAATACTTTTTGTG  23944         TGGTG    C
                                TCTCTGGAG    ACTTT TGTG
                                |||||||||    ||||| ||||
                                AGAGACTTT    TGAAA ACAC
                                     TA___    A
GAM910  LOC221140 3'  TCTGAGTTTCTAATTTTCTGTG 23945     G  GG_  C
                                TCTG AGT   TGA TTTCTGTG
                                |||| |||   ||| ||||||||
                                AGAC TCA   ATT AAAGACAC
                                  _  AAG   A
GAM911  SCD     5'  GCGCTGAGCCGCGGCGCCTTGC 23948     CGT   ACAAA
                                GCGC   GCTG    CGCCTTGC
                                ||||   ||||    ||||||||
                                CGCG   CGGC    GCGGAACG
                                  ACT    GCC__
GAM911  CGI-51   3'  GTGTGGCATGGGCGCCTTGC   23949     C  A  AA__
                                GTG TG CA    CGCCTTGC
                                ||| || ||    ||||||||
                                CAC AC GT    GCGGAACG
                                  _  C  ACCC
GAM911  FLJ10647  3'  CCGGTACCCCGAGCGCCTTGC  23950     _   GACAAA
                                CCG TGCT     CGCCTTGC
                                ||| ||||     ||||||||
                                GGC ATGG     GCGGAACG
                                  C    GGCTC_
GAM911  HABP2    3'  GCTGTGCTGACTGCTTG     23951    C      AAAC  C
                                GC GTGCTGAC    GC TTG
                                || ||||||||    || |||
                                CG CACGACTG    CG AAC
                                 A       A___  _
GAM911  KIAA0562  3'  GCCTGTGCTGACCGTGGCCTTG 23952     _      AAAC
            C                    GCC GTGCTGAC    GCCTTGC
                                |||| ||||||||    |||||||
                                CGG CACGACTG    CGGAACG
                                  A       GCAC
GAM911  UBCE7IP5  3'  GCGCCGTGCTGACGCTGACTGC 23953           AAAC  C__
                                GCGCCGTGCTGAC    GC   TTGC
                                ||||||||||||    ||   ||||
                                CGCGGCACGACTG    CG   GACG
                                       _____  ACT
GAM911  LOC147525 5'  GCGCCGCGCCCCGGAATGCTTT 23954          GACAAAC  C
            GC                    GCGCCGTGCT      GC TTGC
                                ||||||||||      || ||||
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                                CGCGGCGCGG      CG AACG
                                      GGCCTTA  A
GAM911  LOC151512 3'  GCTTCCAATGACGGACGCCTTG 23955    G_  TGC   AA
          C                    GC  CCG   TGAC  ACGCCTTGC
                               ||  |||   ||||  |||||||||
                               CG  GGT   ACTG  TGCGGAACG
                                AA   T__    CC
GAM911  LOC167829 5'  GCACTGTGCTGACTTTCTTGC  23956     C       AAACGC
                               GCGC GTGCTGAC     CTTGC
                               |||| ||||||||      |||||
                               CGTG CACGACTG     GAACG
                                 A       AAA___
GAM911  LOC90936  5'  ACGCCGTGCTGACAGACG    23957            A
                               GCGCCGTGCTGACA ACG
                               |||||||||||||| |||
                               TGCGGCACGACTGT TGC
                                        C
GAM912  ARHGEF6   3'  TAGGTTGGAGTGCAGTGGT    23960        TA  C
                               TAGGTTG  AG GCAGTGGT
                               |||||||  || ||||||||
                               ATCCAAC  TC CGTCACCA
                                   C_  A
GAM912  FKRP      5'  TAGGTTGTAGGCTGGGGGAGTT 23961         A  GCAGT  TC
                               TAGGTTGTA GC     GG  GTT
                               |||||||| ||     ||  |||
                               ATCCAACAT CG     CC  CAA
                                     C  ACC__  CT
GAM912  LOC152579 3'  GGTTGCAAGTGGTTCGT     23962        AGCGC     _
                               GGTTGTA     AGTGGT CGT
                               |||||||     |||||| |||
                               CCAACGT     TCACCA GCA
                                   _____      A
GAM912  LOC162239 3'  TAGGTTGTAAGAGTA       23963           CGC
                               TAGGTTGTAAG   AGTG
                               ||||||||||   ||||
                               ATCCAACATTC   TCAT
                                             ___
GAM913  ARHA      3'  AGGGGTAATATGGCCATT    23966    T       ACCA    G
                               AG GGTAATATG    GCCGT T
                               || |||||||||    ||||| |
                               TC CCATTATAC    CGGTA A
                                C        ____     G
GAM913  KIAA1841  3'  ATGGTAACACTACCAGTTGTGT 23967          G    CC
          T                    GTGGTAATAT ACCAG  GTGTT
                               ||||||||||| |||||  |||||
                               TACCATTGTG TGGTC  CACAA
                                     A     AA
GAM913  KIAA1958  3'  AGTGGTAATGGTGTGGACTGTG 23968         ATGACCA  C
          TT                    AGTGGTAAT      GC GTGTT
                               |||||||||       || |||||
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                                TCACCATTA      TG CACAA
                                     CCACACC  A
GAM914  CLN5     5'  TGGGGGTTTTGCGGAG     23971         AA   T
                                TGGGGGTTT  TGT GAG
                                |||||||||  ||| |||
                                ACCCCCAAA  ACG CTC
                                     __   C
GAM914  PURA     3'  TGGGGGTTTCATTCAG     23972         AA   G
                                TGGGGGTTT  TGTT AG
                                |||||||||  |||| ||
                                ACCCCCAAA  GTAA TC
                                     __   G
GAM914  LOC158332 3'  GGGAGAATGTTGAGA      23973      TTT
                                GGGGG   AATGTTGAGA
                                |||||   ||||||||||
                                CCCTC   TTACAACTCT

                                     ___
GAM915  B3GALT5   3'  TGAGCCTTGGGACAAGTTTCTG 23976        ATGCCC  C
                                TGAGCTTT     AG TTCTG
                                ||||||||     || |||||
                                ACTCGGAA     TC AAGAC
                                     CCCTGT  A
GAM915  B3GALT5   3'  TGAGCCTTGGGACAAGTTTCTG 23976        ATGCCC  C
                                TGAGCTTT     AG TTCTG
                                ||||||||     || |||||
                                ACTCGGAA     TC AAGAC
                                     CCCTGT  A
GAM915  B3GALT5   3'  TGAGCCTTGGGACAAGTTTCTG 23976        ATGCCC  C
                                TGAGCTTT     AG TTCTG
                                ||||||||     || |||||
                                ACTCGGAA     TC AAGAC
                                     CCCTGT  A
GAM915  B3GALT5   3'  TGAGCCTTGGGACAAGTTTCTG 23976        ATGCCC  C
                                TGAGCTTT     AG TTCTG
                                ||||||||     || |||||
                                ACTCGGAA     TC AAGAC
                                     CCCTGT  A
GAM915  B3GALT5   3'  TGAGCCTTGGGACAAGTTTCTG 23976        ATGCCC  C
                                TGAGCTTT     AG TTCTG
                                ||||||||     || |||||
                                ACTCGGAA     TC AAGAC
                                     CCCTGT  A
GAM915  CACNB2    5'  CATGAGCAAATCACTTAGCTTC 23977        TTTAT  CC
          TG                     TATGAGC    GC  AGCTTCTG
                                |||||||    ||  ||||||||
                                GTACTCG    TG  TCGAAGAC
                                     TTTAG  AA
GAM915  LILRB4    3'  TGGCTTCTAAACAGCTTCTG   23978    A    A  CC
                                TG GCTTT TG  CAGCTTCTG
                                || ||||| ||  |||||||||
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                                AC CGAAG AT  GTCGAAGAC
                                 _    _ TT
GAM915  NEURL    3'  TATGAGCTTTGTGGCT      23979          A  CCCA
                                TATGAGCTTT TG    GCT
                                |||||||||| ||    |||
                                ATACTCGAAA AC    CGA
                                     C  ____
GAM915  FLJ11053 3'  ATGAGCTCTTCGGCTTCT    23980          A  CCCA
                                ATGAGCTTT TG    GCTTCT
                                ||||||||| ||    ||||||
                                TACTCGAGA GC    CGAAGA
                                     A  ____
GAM915  FLJ11342 3'  TGAACTTTATTATGCTTCTG  23981          GCCCA
                                TGAGCTTTAT    GCTTCTG
                                ||||||||||    |||||||
                                ACTTGAAATA    CGAAGAC
                                     ATA__
GAM915  FLJ11506 3'  TGAGCCTTATTTCTTTCTG   23982          GCCCAGC
                                TGAGCTTTAT     TTCTG
                                ||||||||||     |||||
                                ACTCGGAATA     AAGAC
                                     AAGA___
GAM915  KIAA1715 3'  ATGAGTTTACAGCTTCT     23983      C    TGCC
                                ATGAG TTTA    CAGCTTCT
                                ||||| ||||    ||||||||
                                TACTC AAAT    GTCGAAGA
                                  _    ____
GAM915  SMCR7    3'  AAGCTGGCCTTCAGCTTCTG   23984      TTAT  __
                                GAGCT    GCC  CAGCTTCTG
                                |||||    |||  |||||||||
                                TTCGA    CGG  GTCGAAGAC
                                   C___   AA
GAM915  LOC149935 3'  AGCTTCAATCAGCTTCTG    23985       TGCC
                                AGCTTTA    CAGCTTCTG
                                |||||||    |||||||||
                                TCGAAGT    GTCGAAGAC
                                    TA__
GAM915  LOC51279 3'  TGGGCTCACCTGGCTTCTG   23986    A   TAT   CA
                                TG GCTT   GCC  GCTTCTG
                                || ||||   |||  |||||||
                                AC CGAG   TGG  CGAAGAC
                                 C   ___   AC
GAM916  APM1     3'  ATTTTGCATCTATCATCCACTC 23989      A   CAG  _
          TC                     ATTTT CATC   TA CCACTCTC
                                |||||| ||||   || ||||||||
                                TAAAA GTAG   GT GGTGAGAG
                                   C   ATA  A
GAM916  ITGB1    3'  TATTTTACACCAGCAACTCTC  23990         T     CC
                                TATTTTACA CCAGTA  ACTCTC
                                ||||||||| ||||||  ||||||
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                                ATAAAATGT GGTCGT  TGAGAG
                                      _    __
GAM916  SURF6    3'  TATCTTGCATTCACTTCACTCT 23991      A   C  GTAC
            C                    TATTTT CAT CA    CACTCTC
                                 |||||| ||| ||    |||||||
                                 ATAGAA GTA GT    GTGAGAG
                                    C   A  GAA_
GAM916  FLJ10971 3'  TATTTTTCCAGTACCATTCTC  23992      ACA        C
                                 TATTTT   TCCAGTACCA TCTC
                                 ||||||   |||||||||| ||||
                                 ATAAAA   AGGTCATGGT AGAG
                                    ___         A
GAM916  KIAA0257 3'  TTTTACATTCATTCACCGTTCT 23993       C  G_   AC
                                 TTTTACAT CA  TACC  TCT
                                 |||||||| ||  ||||  |||
                                 AAAATGTA GT  GTGG  AGA
                                      A  AA    CA
GAM916  KIAA0648 3'  TACTTTACATTATACACACT   23994        CCA   _
                                 TATTTTACAT   GTAC CACT
                                 ||||||||||   |||| ||||
                                 ATGAAATGTA   TATG GTGA
                                      A__    T
GAM916  OSRF     3'  TATTTTACAACCAGGCGTTCTC 23995        T    TACCA
                                 TATTTTACA CCAG     CTC
                                 ||||||||| ||||     |||
                                 ATAAAATGT GGTC     GAG
                                      T    CGCAA
GAM916  SDS3     3'  TATTTTACATTCACCTCTC    23996        CCAG    A
                                 TATTTTACAT    TACC CTC
                                 ||||||||||    |||| |||
                                 ATAAAATGTA    GTGG GAG
                                      A___     A
GAM916  LOC200169 3'  TTTACATCCAACTCAAGCTCT  23997          TACCA_
                                 TTTACATCCAG     CTCT
                                 ||||||||||      ||||
                                 AAATGTAGGTT     GAGA
                                       GAGTTC
GAM916  LOC221035 3'  TATTTCACAAAAGCTACCA   23998        TCC   _
                                 TATTTTACA   AGT ACCA
                                 |||||||||   ||| ||||
                                 ATAAAGTGT   TCG TGGT
                                      TT_   A
GAM916  LOC221354 3'  TATTTTACAGCGTTTCACTCT  23999        TCCA  AC
                                 TATTTTACA    GT  CACTCT
                                 |||||||||    ||  ||||||
                                 ATAAAATGT    CA  GTGAGA
                                      CG__   AA
GAM917  LOC255925 3'  GAAGGTGTCACAACACGCAT   24002     A    C  G
                                 GGA GTGTC GC AGCACGCAT
                                 ||| ||||| || |||||||||
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                                CTT CACAG TG TTGTGCGTA
                                  C    _ _
GAM917  LOC55908  3'  GGAAGTGTTCCTTGCAGCAT  24003       _ GCGA  C
                                GGAAGTGT CC   GCA GCAT
                                |||||||| ||   ||| ||||
                                CCTTCACA GG   CGT CGTA
                                    A  AA__  _
GAM918  SURF4     3'  CGGCCTGCGCTTTCGAGACC  24006     C       CGTC
                                CGGTC GCGCTTTCG   GGCT
                                ||||| |||||||||   ||||
                                GCCGG CGCGAAAGC   CTGG
                                  A       T___
GAM918  MAPK6     5'  CGGACTGCCCCCAGTGTCGGCT 24007    TCC _  TT  C_
          C                      CGG  GC GCT  CG  GTCGGCTC
                                |||  || |||  ||  ||||||||
                                GCC  TG CGG  GT  CAGCCGAG
                                 ___ A  GG  CA
GAM919  RAB3GAP   3'  CATGAAACTAGAAATG     24010   C      TGGTC
                                CA GAAACTAG    GAATG
                                || ||||||||    |||||
                                GT CTTTGATC    TTTAC
                                 A      _____
GAM919  LOC163404 3'  GAAACTAAAGTGAATGT     24011       T  C
                                GAAACTAG GGT GAATGT
                                |||||||| ||| ||||||
                                CTTTGATT TCA CTTACA
                                    _  _
GAM920  LOC56965  3'  TGGATCGGGTCTGGGGGA    24014   AT      C  AC
                                TG  TCGGGTCT GG  GGGA
                                ||  |||||||| ||  ||||
                                AC  AGCCCAGA CC  CCCT
                                 CT      _ __
GAM920  LOC56965  3'  TGGATCGGGTCTGGGGGA    24014   AT      C  AC
                                TG  TCGGGTCT GG  GGGA
                                ||  |||||||| ||  ||||
                                AC  AGCCCAGA CC  CCCT
                                 CT      _ __
GAM921  C18orf1   3'  CAAGTGCAGGAGGGGGCGGC  24017     AC       _ T
                                CAAGT  CAGGAGGGG C GT
                                |||||  ||||||||| | ||
                                GTTCA  GTCCTCCCC G CG
                                  C_       C C
GAM921  CDKN1A    3'  CAAGAGCCAGGAGGGTACCA  24018     TA       _
                                CAAG  CCAGGAGGG GCTG
                                ||||  ||||||||| ||||
                                GTTC  GGTCCTCCC TGGT
                                  TC       A
GAM921  DNMT3B    3'  TGAGTATTGGAGAGCTGTCG  24019   A   CCA     G
                                C AGTA   GGAGGG CTGTCG
                                | ||||   |||||| ||||||
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                                A TCAT   CCTCTC GACAGC
                                 C   AA_    _
GAM921  FOXE3   3'  TGAGTCCAGGAGGCCACGA   24020   A  A    GG    T
                                C AGT CCAGGA  GGCTG CGA
                                | ||| ||||||  ||||| |||
                                A TCA GGTCCT  CCGGT GCT
                                 C  _    __   _
GAM921  HDAC4   5'  CAAGTACCGGGACGGTGAGGGC 24021       A  _____
                                CAAGTACC GGA    GGGGC
                                |||||||| |||    |||||
                                GTTCATGG CCT    TCCCG
                                     C  GCCAC
GAM921  HPCA    3'  AAGAGCCGGGAGGGGGCCG   24022    TA  A    CT
                                AAG  CC GGAGGGG  GTCG
                                |||  || |||||||  ||||
                                TTC  GG CCTCCCC  CGGC
                                  TC  C     __
GAM921  MECP2   3'  GTACTGGAAAGCTGTCG    24023    CA    G
                                GTAC  GGAGGG CTGTCG
                                ||||  |||||| ||||||
                                CATG  CCTTTC GACAGC
                                  A_    _
GAM921  MGA     3'  CAAGCACCAGGAGGCTG    24024         GG
                                CAAGTACCAGGA  GGCTG
                                ||||||||||||  |||||
                                GTTCGTGGTCCT  CCGAC
                                      __
GAM921  MGMT    5'  CAAGTACCAAGGGGCGGC   24025       GG    T
                                CAAGTACCA  AGGGGC GT
                                |||||||||  |||||| ||
                                GTTCATGGT  TCCCCG CG
                                     __    C
GAM921  NTSR1   3'  GCACTGGGAGGGCTGCC    24026    CA    G
                                GTAC  GGAGGG CTGTC
                                ||||  |||||| |||||
                                CGTG  CCTCCC GACGG
                                  AC    _
GAM921  RABL2A  3'  CAAGTACCAGAGAGGGGTG  24027         _   C
                                CAAGTACCAG GAGGGG TG
                                |||||||||| |||||| ||
                                GTTCATGGTC CTCCCC AC
                                      T    _
GAM921  RABL2A  3'  CAAGTACCAGAGAGGGGTG  24027         _   C
                                CAAGTACCAG GAGGGG TG
                                |||||||||| |||||| ||
                                GTTCATGGTC CTCCCC AC
                                      T    _
GAM921  RABL2B  3'  CAAGTACCAGAGAGGGGTG  24027         _   C
                                CAAGTACCAG GAGGGG TG
                                |||||||||| |||||| ||
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                                GTTCATGGTC CTCCCC AC
                                      T     _
GAM921  C20orf102 3'  TGAGTACCAGGGGGCCC     24028    A       A   G
                                C AGTACCAGG GGG CT
                                | |||||||||| ||| ||
                                A TCATGGTCC CCC GG
                                 C       _  G
GAM921  C7orf14   5'  AAGGCCAGGAAAATGTGGCTGT 24029     TA      ____     C
           TGA                    AAG  CCAGGAGG    GGCTGT GA
                                ||| ||||||||   |||||| ||
                                TTC  GGTCCTTT    CCGACA CT
                                  C_       TACA     A
GAM921  FLJ10748  5'  TGAGTTCCAGGAGGCGTGA   24030   A   A      GGC   C
                                C AGT CCAGGAGG   TGT GA
                                | ||| ||||||||   ||| ||
                                A TCA GGTCCTCC   GCA CT
                                 C   A      ___  _
GAM921  FLJ32332  3'  CAAGTCTGGGAGGGCCACG   24031      ACCA  AG     T
                                CAAGT    GG  GGGCTG CG
                                ||||||   ||  |||||| ||
                                GTTCA    CC  CCCGGT GC
                                   GA__  CT     _
GAM921  Grcc9     3'  CAAGTGGCTCTGGGGCTGTTGA 24032      ACCAGGA       C
                                CAAGT      GGGGCTGT GA
                                |||||      |||||||| ||
                                GTTCA      CCCCGACA CT
                                   CCGAGA_       A
GAM921  KIAA1198  3'  CAAGGTCAGGAGGGCGA     24033     TAC       GCTGT
                                CAAG   CAGGAGGG    CGA
                                ||||   ||||||||    |||
                                GTTC   GTCCTCCC    GCT
                                  CA_      _____
GAM921  KIAA1468  3'  CAAGTACAAGGAACCAGTCG   24034       CAG      _
                                CAAGTAC   GAGGGGCT GTCG
                                |||||||   |||||||| ||||
                                GTTCATG   TTCCTTGG CAGC
                                    ___       T
GAM921  KIAA1508  3'  CAGGTACTCAGGAGGCTGT   24035    A   _    GG
                                CA GTAC CAGGA  GGCTGT
                                || |||| |||||  ||||||
                                GT CATG GTCCT  CCGACA
                                 C   A   __
GAM921  KIAA1545  3'  CAAGTACCAAGGGGGGGCCA   24036        _ A
                                CAAGTACCA GG GGGGCTG
                                ||||||||| || |||||||
                                GTTCATGGT CC CCCCGGT
                                      T  C
GAM921  MGC2628   3'  CAAGGCCAGGGGGGGGTC     24037     TA    A   CT
                                CAAG  CCAGG GGGG  GTC
                                ||||  ||||| ||||  |||
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                                GTTC  GGTCC CCCC  CAG
                                  C_    _   __
GAM921  PALM     3'  CAGGCGCCGGGAGGGGCCG   24038    A TA  A
                                CA G  CC GGAGGGGCTG
                                || |  || ||||||||||
                                GT C  GG CCTCCCCGGC
                                 C GC  C
GAM921  PP1665   5'  AGGACCAGGAGGCCAGCGA   24039    T     GG    T
                                AG ACCAGGA  GGCTG CGA
                                || |||||||  ||||| |||
                                TC TGGTCCT  CCGGT GCT
                                 C       __    C
GAM921  SLC39A2  5'  TGAGTTTCAGGAGGCTGT    24040    A   AC    GG
                                C AGT  CAGGA  GGCTGT
                                | |||  |||||  ||||||
                                A TCA  GTCCT  CCGACA
                                 C   AA    __
GAM921  LOC143392 3'  TGAGTGCCAGGAGAGGCTGT   24041    A   A
                                C AGT CCAGGAGGGGCTGT
                                | ||| ||||||||||||||
                                A TCA GGTCCTCTCCGACA
                                 C   C
GAM921  LOC170221 3'  AAGTCCAGGAGGGCGCCGA    24042      A       G T
                                AAGT CCAGGAGGG C GTCGA
                                |||| ||||||||| | |||||
                                TTCA GGTCCTCCC G CGGCT
                                   _       _ _
GAM921  LOC219653 3'  TGAGTGCCAGGAGAGGTGC    24043    A   A       C
                                C AGT CCAGGAGGGG TGT
                                | ||| |||||||||| |||
                                A TCA GGTCCTCTCC ACG
                                 C   C        _
GAM921  LOC222169 3'  CGATACCAGGAGGCTATGA    24044    A       GG     C
                                A GTACCAGGA  GGCTGT GA
                                | |||||||||  |||||| ||
                                G TATGGTCCT  CCGATA CT
                                 C       __     _
GAM922  AGRN     3'  ACTGGGCTGGGGCTGGGGGTG  24047     TC_     A  AGA
                                ACT   CTGGGG CT   GGTG
                                |||   |||||| ||   ||||
                                TGA   GACCCC GA   CCAC
                                  CCC     _  CCC
GAM922  B3GNT3   3'  CTTCCTGGGAGGAAGGTG    24048          ACTA
                                CTTCCTGGGG    GAGGTG
                                ||||||||||    ||||||
                                GAAGGACCCT    TTCCAC
                                      CC__
GAM922  GCNT3    3'  AACTACTAGGGTTAGGGGTG   24049      TC     AC   A
                                AACT  CTGGGG  TAG GGTG
                                ||||  ||||||  ||| ||||
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                                TTGA  GATCCC  ATC CCAC
                                  T_     A_   C
GAM922   MEN1    3'  CTCCCCGGGCTGGAGGTG    24050        GA  A
                                CTTCCTGGG  CT GAGGTG
                                |||||||||  || ||||||
                                GAGGGGCCC  GA CTCCAC
                                     __  C
GAM922   MEN1    3'  CTCCCCGGGCTGGAGGTG    24050        GA  A
                                CTTCCTGGG  CT GAGGTG
                                |||||||||  || ||||||
                                GAGGGGCCC  GA CTCCAC
                                     __  C
GAM922   MEN1    3'  CTCCCCGGGCTGGAGGTG    24050        GA  A
                                CTTCCTGGG  CT GAGGTG
                                |||||||||  || ||||||
                                GAGGGGCCC  GA CTCCAC
                                     __  C
GAM922   MEN1    3'  CTCCCCGGGCTGGAGGTG    24050        GA  A
                                CTTCCTGGG  CT GAGGTG
                                |||||||||  || ||||||
                                GAGGGGCCC  GA CTCCAC
                                     __  C
GAM922   MEN1    3'  CTCCCCGGGCTGGAGGTG    24050        GA  A
                                CTTCCTGGG  CT GAGGTG
                                |||||||||  || ||||||
                                GAGGGGCCC  GA CTCCAC
                                     __  C
GAM922   MEN1    3'  CTCCCCGGGCTGGAGGTG    24050        GA  A
                                CTTCCTGGG  CT GAGGTG
                                |||||||||  || ||||||
                                GAGGGGCCC  GA CTCCAC
                                     __  C
GAM922   MEN1    3'  CTCCCCGGGCTGGAGGTG    24050        GA  A
                                CTTCCTGGG  CT GAGGTG
                                |||||||||  || ||||||
                                GAGGGGCCC  GA CTCCAC
                                     __  C
GAM922   MEN1    3'  CTCCCCGGGCTGGAGGTG    24050        GA  A
                                CTTCCTGGG  CT GAGGTG
                                |||||||||  || ||||||
                                GAGGGGCCC  GA CTCCAC
                                     __  C
GAM922   PAEP    3'  CTTCCTGGAGGCGGAGGTG   24051         ACTA
                                CTTCCTGGGG   GAGGTG
                                ||||||||||   ||||||
                                GAAGGACCTC   CTCCAC
                                   CGC_
GAM922   RABIF   3'  CCTCCTGAATAGTAGAGGTG  24052         GAC
                                CTTCCTGGG  TAGAGGTG
                                |||||||||  ||||||||
                                GGAGGACTT  ATCTCCAC
                                   ATC
GAM922   RAD54L  5'  TTCCCAGGGCTGGAGGTG    24053      TG  A  A
                                TTCC  GGG CT GAGGTG
                                ||||  ||| || ||||||
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                                AAGG  CCC GA CTCCAC
                                  GT   _  C
GAM922  C20orf38  3'  TTCCTGGGTGATCTTTGTG   24054        _  _  AGAG
                                TTCCTGGG GA CT   GTG
                                |||||||| || ||   |||
                                AAGGACCC CT GA   CAC
                                    A  A  AA__
GAM922  DKFZP434P211 3'  CTCCCTGGGGAGGGGGTG   24055          CTAGA
                                CTTCCTGGGGA    GGTG
                                ||||||||||     ||||
                                GAGGGACCCCT    CCAC
                                      CCC__
GAM922  MGC2744   5'  CTTCCTGGATCCAGGGGTG   24056        GA   A
                                CTTCCTGGG  CTAG GGTG
                                |||||||||  |||| ||||
                                GAAGGACCT  GGTC CCAC
                                    A_   C
GAM922  PHRET1    3'  CTTCCTGGGCTGGTGTAGAGGT 24057        GAC___
          G                      CTTCCTGGG     TAGAGGTG
                                 |||||||||     ||||||||
                                 GAAGGACCC     ATCTCCAC
                                     GACCAC
GAM922  PREI3     3'  TAAACTTCGTGGGAGAGG    24058        C   GACT
                                TAAACTTC TGGG   AGAGG
                                |||||||| ||||   |||||
                                ATTTGAAG ACCC   TCTCC
                                    C   _____
GAM922  SEMA5B    3'  ACTTCCAGGCAGAGGT      24059       T  GAC
                                ACTTCC GGG   TAGAGGT
                                |||||| |||   |||||||
                                TGAAGG TCC   GTCTCCA
                                  _   ___
GAM922  VCY2IP1   3'  ACTTTCTGGACAGGGGTG    24060     C    GAC  A
                                ACTT CTGGG   TAG GGTG
                                |||| |||||   ||| ||||
                                TGAA GACCT   GTC CCAC
                                  A    ___   C
GAM922  LOC133332 5'  TAAACTGCCTGGACAGAGGTG  24061      T    GAC
                                TAAACT CCTGGG   TAGAGGTG
                                |||||| ||||||   ||||||||
                                ATTTGA GGACCT   GTCTCCAC
                                   C     ___
GAM922  LOC150174 3'  CTCCCTGGGGAGGGGGTG    24055          CTAGA
                                CTTCCTGGGGA    GGTG
                                ||||||||||     ||||
                                GAGGGACCCCT    CCAC
                                      CCC__
GAM922  LOC150213 3'  CTCCCTGGGGAGGGGGTG    24055          CTAGA
                                CTTCCTGGGGA    GGTG
                                ||||||||||     ||||
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                                GAGGGACCCCT    CCAC
                                     CCC__
GAM922  LOC150236 5'  CTCCCTGGGGAGGGGGTG    24055         CTAGA
                                CTTCCTGGGGA    GGTG
                                ||||||||||    ||||
                                GAGGGACCCCT    CCAC
                                     CCC__
GAM922  LOC158263 3'  CTTCCTGGAGGAGGT      24062         ACTA
                                CTTCCTGGGG   GAGGT
                                |||||||||   |||||
                                GAAGGACCTC   CTCCA
                                     _____
GAM922  LOC196955 5'  ACTTCCTGGAGGAGGT     24063         ACTA
                                ACTTCCTGGGG   GAGGT
                                ||||||||||   |||||
                                TGAAGGACCTC   CTCCA
                                     _____
GAM922  LOC90297  3'  CTTCCTGGGGGAAGAGGTG   24064         ACT
                                CTTCCTGGGG  AGAGGTG
                                |||||||||  |||||||
                                GAAGGACCCC  TCTCCAC
                                     CT_
GAM922  LOC90668  3'  CCCTGGGGACTGGGGGTG    24065         AGA
                                TCCTGGGGACT  GGTG
                                ||||||||||  ||||
                                GGGACCCCTGA  CCAC
                                     CCC
GAM923  NRXN1     3'  TGATGCTGTAGTACTCCTTT  24068        AC    GA
                                TGATGCTG  AGTAT  TTTT
                                ||||||||  |||||  ||||
                                ACTACGAC  TCATG  GAAA
                                    A_    AG
GAM923  NRXN1     3'  TGATGCTGTAGTACTCCTTT  24068        AC    GA
                                TGATGCTG  AGTAT  TTTT
                                ||||||||  |||||  ||||
                                ACTACGAC  TCATG  GAAA
                                    A_    AG
GAM923  FBXO21    3'  TGATACTGAAGTAGATTTTTTA 24069        C    T
                                TGATGCTGA AGTA GATTTTTTA
                                ||||||||| |||| |||||||||
                                ACTATGACT TCAT CTAAAAAAT
                                     _   _
GAM923  FLJ12661  5'  TGATGCTGATGGATGATTAATT 24070        CAGT     TT
                                TGATGCTGA   ATGATT  TT
                                |||||||||   ||||||  ||
                                ACTACGACT   TACTAA  AA
                                     ACC_     TT
GAM923  LOC143888 3'  TGATGCTGATAATAGCAGTTTT 24071        C    TGAT
          TA                    TGATGCTGA AGTA   TTTTTA
                                |||||||||  ||||   ||||||
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                                ACTACGACT TTAT    AAAAAT
                                      A    CGTC
GAM923  LOC145501 3'  TGATGCTGGCAGCATGAC    24072        A
                                TGATGCTG CAGTATGAT
                                |||||||| |||||||||
                                ACTACGAC GTCGTACTG
                                     C
GAM923  LOC253626 3'  GATGCTGACAGTTATTTTT    24073           ATG
                                GATGCTGACAGT   ATTTTT
                                ||||||||||||   ||||||
                                CTACGACTGTCA   TAAAAA
                                       A__
GAM923  LOC257457 5'  TGATGCCGACGGTGTGGTTCT  24074          A  A  A
                                TGATGCTGAC GT TG TTTT
                                |||||||||| || || ||||
                                ACTACGGCTG CA AC AAGA
                                       C  C  C
GAM924  B4GALT5   3'  TGCTATAGCTTACCG       24077        AAGGC
                                TGCTATAG    TTTACCG
                                ||||||||    |||||||
                                ACGATATC    GAATGGC
                                            ______
GAM924  CDS2      3'  TGCATAGAAGGCTTACC     24078     T        T
                                TGC ATAGAAGGCTT ACC
                                ||| |||||||||| |||
                                ACG TATCTTCCGAA TGG
                                   _        _
GAM924  LIMD1     3'  TGCTAGGGGCTCCACTGAC   24079      TAGAA       C
                                TGCTA    GGCTTTAC GAC
                                |||||    |||||||| |||
                                ACGAT    CCGAGGTG CTG
                                   CC___       A
GAM924  MUCDHL    3'  TGCGTAGAAGGCTCCCG     24080     TA        TA
                                TGC  TAGAAGGCTT  CCG
                                |||  ||||||||||  |||
                                ACG  ATCTTCCGAG  GGC
                                  C_         __
GAM924  MUCDHL    3'  TGCGTAGAAGGCTCCCG     24080     TA        TA
                                TGC  TAGAAGGCTT  CCG
                                |||  ||||||||||  |||
                                ACG  ATCTTCCGAG  GGC
                                  C_         __
GAM924  PCDH11X   5'  TGCTGTAGCGGGCTCTAC    24081      A   AA
                                TGCT TAG  GGCTTTAC
                                |||| |||  ||||||||
                                ACGA ATC  CCGAGATG
                                  C   GC
GAM924  PCDH11Y   5'  TGCTGTAGCGGGCTCTAC    24081      A   AA
                                TGCT TAG  GGCTTTAC
                                |||| |||  ||||||||
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                                ACGA ATC  CCGAGATG
                                  C   GC
GAM924  PUM2     3'  TGTTATAAAAGGTTTCAC    24082    C       C
                                TG TATAGAAGG TTTAC
                                || ||||||||| |||||
                                AC ATATTTTCC AAGTG
                                 A       A
GAM924  TEM7     3'  TGCTACAGAGCAGACCATTGAC 24083         __    TTACC
                                TGCTATAGA  AGGCT    GAC
                                |||||||||  |||||    |||
                                ACGATGTCT  TCTGG    CTG
                                     CG    TAA__
GAM924  ACTL7A   3'  TGCTACAGGAATAAGCGCCG   24084        A___    TTTA
                                TGCTATAG    AGGC    CCG
                                ||||||||    ||||    |||
                                ACGATGTC    TTCG    GGC
                                     CTTA    C___
GAM924  FLJ11726 3'  TGCTATAGGAGCTAACTCTTGA 24085        AA    TTACC__
           C                     TGCTATAG  GGCT      GAC
                                |||||||  ||||      |||
                                ACGATATC  TCGA      CTG
                                     C_    TTGAGAA
GAM924  KIAA0779 3'  TATAGAAGAGCTCTGAC     24086         _    ACC
                                TATAGAAG GCTTT   GAC
                                |||||||| |||||   |||
                                ATATCTTC CGAGA   CTG
                                     T    ___
GAM924  RINZF    3'  TGCTATAAGGCTTTGA      24087        GA      ACC
                                TGCTATA  AGGCTTT   GA
                                |||||||  |||||||   ||
                                ACGATAT  TCCGAAA   CT
                                     __     ___
GAM924  LOC153243 5'  TGCTGCAGGAGGCTCCAC    24088      A   A
                                TGCT TAG AGGCTTTAC
                                |||| ||| |||||||||
                                ACGA GTC TCCGAGGTG
                                  C   C
GAM924  LOC255452 3'  TGCTATGGAATGGGCCCTGAC  24089       A   __     ACC
                                TGCTAT GAA  GGCTTT   GAC
                                |||||| |||  ||||||   |||
                                ACGATA CTT  CCGGGA   CTG
                                   C   AC     ___
GAM924  LOC256506 5'  TGTTCTAGAAGGCTTGGGGAGA 24090    CTA        TACC_
           C                     TG   TAGAAGGCTT    GAC
                                ||   ||||||||||    |||
                                AC   ATCTTCCGAA    CTG
                                 AAG        CCCCT
GAM924  LOC84549  3'  TGCTACAGGAGGCCACAGAC   24091        A    TT  C
                                TGCTATAG AGGCT  AC GAC
                                |||||||| |||||  || |||
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                                ACGATGTC TCCGG  TG CTG
                                    C    __  T
GAM925  FACL5    3'  CATAGACCCAATTTTTAA    24094          CC
                                TATAGACCCAAT  TTAA
                                ||||||||||||  ||||
                                GTATCTGGGTTA  AATT
                                   AA
GAM925  KIAA0252 3'  TATAGACCCATGACAGACTGAT 24095         ATCCT  A
                                TATAGACCCA    TA ACTGAT
                                ||||||||||    || ||||||
                                ATATCTGGGT    GT TGACTA
                                   ACT__  C
GAM925  LOC201245 5'  TAGACCCAGTTCTTAGACT   24096        ATC   A
                                TAGACCCA   CTTA ACT
                                ||||||||   |||| |||
                                ATCTGGGT   GAAT TGA
                                    CAA   C
GAM926  JDD1     3'  TGGATAATGTTGTGAAAGCT   24099         AT___
                                TGGGTAATGTT    AGCT
                                ||||||||||    ||||
                                ACCTATTACAA    TCGA
                                   CACTT
GAM927  EPHA2    3'  GCACAGCAGGGAGGCCAC    24102          ATT  A
                                GCACAGCAGGGA   GT GC
                                ||||||||||||  || ||
                                CGTGTCGTCCCT   CG TG
                                   C__  G
GAM927  FRAT2    3'  GCACAGCAATTGTAGCAC    24103        GGGA
                                GCACAGCA   ATTGTAGCAC
                                ||||||||   ||||||||||
                                CGTGTCGT   TAACATCGTG
                                    ____
GAM927  FZD7     3'  CCTGCAGCAGGGGGATCGC   24104    GCA      A_
                                CC  CAGCAGGG  ATTGT
                                ||  ||||||||  |||||
                                GG  GTCGTCCC  TAGCG
                                 AC_      CC
GAM927  GATA4    3'  CCGGCAGCAGGGGGAAGGCAC  24105    CA      AATTGTA
                                CCG  CAGCAGGG      GCAC
                                |||  ||||||||      ||||
                                GGC  GTCGTCCC      CGTG
                                  C_      CCTTC__
GAM927  KLK10    3'  CACACAGCGGGGAGTGGC    24106        A   ATT  A
                                CGCACAGC GGGA   GT GC
                                |||||||| ||||  || ||
                                GTGTGTCG CCCT   CA CG
                                    C   ___  C
GAM927  MCCC2    3'  GCACAGCAGTGTGAGGGCAC  24107        GGAAT  TA_
                                GCACAGCAG    TG   GCAC
                                |||||||||    ||   ||||
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                                CGTGTCGTC    AC  CGTG
                                     AC___  TCC
GAM927  PSEN1   3'  ACAGCAGGGCTGACAGCAC   24108        AA  _
                                ACAGCAGGG  TTG TAGCAC
                                |||||||||  ||| ||||||
                                TGTCGTCCC  GAC GTCGTG
                                     __  T
GAM927  PSEN1   3'  ACAGCAGGGCTGACAGCAC   24108        AA  _
                                ACAGCAGGG  TTG TAGCAC
                                |||||||||  ||| ||||||
                                TGTCGTCCC  GAC GTCGTG
                                     __  T
GAM927  SLC9A6  3'  GCATAGCAGGAAAGTCGC    24109    C       TT  A
                                GCA AGCAGGGAA  GT GC
                                ||| |||||||||  || ||
                                CGT TCGTCCTTT  CA CG
                                  A       __  G
GAM927  TRIM14  3'  AGCAGGGATTACAGGCAC    24110        A    _
                                AGCAGGGA TTGTAG CAC
                                |||||||| |||||| |||
                                TCGTCCCT AATGTC GTG
                                     _    C
GAM927  CARD14  5'  CCGTGCAGCAGGGTGGGGTCCA 24111    CA      AATT  AG
          C                      CCG  CAGCAGGG   GT  CAC
                                |||  ||||||||   ||  |||
                                GGC  GTCGTCCC   CA  GTG
                                  AC       ACCC  G_
GAM927  CBX6    3'  CCACGGCAGGTTCTCGTAGCAC 24112    ACA    GAA
                                CCGC   GCAGG   TTGTAGCAC
                                ||||   |||||  |||||||||
                                GGTG   CGTCC   AGCATCGTG
                                  C__    AAG
GAM927  CPR2    3'  CCGCAGCAGCAGGGAGGCTGC  24113     _       ATT  A
                                CCGCA CAGCAGGGA   GT GC
                                ||||| |||||||||   || ||
                                GGCGT GTCGTCCCT   CG CG
                                   C       C__  A
GAM927  CRA     3'  GCCAGCAGGGAAGGACTGT   24114    A       ___
                                GC CAGCAGGGA   ATTGT
                                || |||||||||   |||||
                                CG GTCGTCCCT   TGACA
                                 _       TCC
GAM927  DEFCAP  5'  CCGCAGAGCAGGGAATGGGC  24115     C       TGTA
                                CCGCA AGCAGGGAAT    GC
                                ||||| ||||||||||    ||
                                GGCGT TCGTCCCTTA    CG
                                   C        CC__
GAM927  DEFCAP  5'  CCGCAGAGCAGGGAATGGGC  24115     C       TGTA
                                CCGCA AGCAGGGAAT    GC
                                ||||| ||||||||||    ||
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                                GGCGT TCGTCCCTTA    CG
                                  C         CC__
GAM927  DKFZp547G183 3'  GCAAGTAGGCTTCCTGTAGCAC 24116     C  C   GAA_
                                GCA AG AGG    TTGTAGCAC
                                ||| || |||    |||||||||
                                CGT TC TCC    GACATCGTG
                                  _ A   GAAG
GAM927  E2IG4    3'  CCTGCAGCAGGGGGTCCCAC  24117    GCA      AATT  AG
                                CC   CAGCAGGG    GT  CAC
                                ||   ||||||||    ||  |||
                                GG   GTCGTCCC    CA  GTG
                                 AC_       C___  GG
GAM927  FLJ12895  5'  CGCACAGCGGGGGCTCGCA   24118         A   AA
                                CGCACAGC GGG  TTGTA
                                |||||||| |||  |||||
                                GCGTGTCG CCC  AGCGT
                                     C   CG
GAM927  FLJ13910  3'  CCGCACAGCACGGAGTAGC   24119          G   ATT
                                CCGCACAGCA GGA   GTAGC
                                |||||||||| |||   |||||
                                GGCGTGTCGT CCT   CATCG
                                      G  ____
GAM927  FLJ20280  3'  CCGAGTAGCAGGGATTACAGGC 24120     CAC       A     _
                                CCG   AGCAGGGA TTGTAG C
                                |||   |||||||| |||||| |
                                GGC   TCGTCCCT AATGTC G
                                  TCA       _     C
GAM927  FLJ20548  5'  CCGCGCAGCAGGGCGGTCGCGC 24121      A       AA_   A
                                CCGC CAGCAGGG   TTGT GC
                                |||| ||||||||   |||| ||
                                GGCG GTCGTCCC   AGCG CG
                                  C       GCC   _
GAM927  GPT2     3'  CCGCATGCTGGGGGATGGCAC  24122       CA  A   AAT  TA
                                CCGCA  GC GGG   TG  GCAC
                                |||||  || |||   ||  ||||
                                GGCGT  CG CCC   AC  CGTG
                                   A_  A   CCT  __
GAM927  GPT2     3'  CGCCAGCAGGGGGGCGATGTGC  24123     A       AAT__   A
                                CGC CAGCAGGG     TGT GC
                                ||| ||||||||     ||| ||
                                GCG GTCGTCCC     ACA CG
                                  _       CCGCT   _
GAM927  HSD-3.1   5'  GCAGCAGCAGGGAAACCGT    24124     _         _
                                GCA CAGCAGGGAA TTGT
                                ||| |||||||||| ||||
                                CGT GTCGTCCCTT GGCA
                                  C         T
GAM927  KCNS1     3'  ACACAGCAGGTCTTGGCGC    24125          GAA   TA
                                GCACAGCAGG   TTG  GC
                                ||||||||||   |||  ||
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                                TGTGTCGTCC   AAC  CG
                                     AG_   CG
GAM927  KIAA0169 5'  GCTACAGCAGGGAAGCGC    24126    _        T
                                GC ACAGCAGGGAA TGT
                                || |||||||||| |||
                                CG TGTCGTCCCTT GCG
                                 A         C
GAM927  KIAA0226 3'  CCGCAACAGCAGGGGATT    24127      _      A
                                CCGCA CAGCAGGG ATT
                                ||||| |||||||| |||
                                GGCGT GTCGTCCC TAA
                                   T       C
GAM927  KIAA0825 3'  CCGCACAGCAGGAGGTGAGC   24128           AAT  T
                                CCGCACAGCAGGG   TG AGC
                                ||||||||||||   || |||
                                GGCGTGTCGTCCT   AC TCG
                                       CC_  _
GAM927  MGC10870 5'  CCGCCAGCAGGGTCAGCA    24129     A      AATTG
                                CCGC CAGCAGGG    TAGCA
                                |||| ||||||||     |||||
                                GGCG GTCGTCCC    GTCGT
                                  _       A____
GAM927  MGC33345 3'  GCAGCAGCAGGGGCAGCAC    24130     _      AATT
                                GCA CAGCAGGG    GTAGCAC
                                ||| ||||||||    |||||||
                                CGT GTCGTCCC    CGTCGTG
                                 C       ____
GAM927  OATPRP4  5'  CCGCGCAGCAGGGCATCCTCAC 24131      A      A   GTA
                                CCGC CAGCAGGG ATT   GC
                                |||| |||||||| |||   ||
                                GGCG GTCGTCCC TAG   TG
                                  C       G   GAG
GAM927  OS-9     3'  GCCAGCAGGGGCAGCAGCA    24132    A      AATT
                                GC CAGCAGGG    GTAGCA
                                || ||||||||    ||||||
                                CG GTCGTCCC    CGTCGT
                                 _       CGT_
GAM927  OSMR     5'  CCGCACAGCACGGGGCTCGC   24133          _  AA
                                CCGCACAGCA GGG  TTGT
                                |||||||||| |||  ||||
                                GGCGTGTCGT CCC  AGCG
                                      G   CG
GAM927  P114-RHO-GEF 3'  CCCCATCCAAGGAATTGTGGCA 24134    G  CAG        A
                                CC CA   CAGGGAATTGT GCA
                                || ||   |||||||||| |||
                                GG GT   GTTCCTTAACA CGT
                                 G  AG_         C
GAM927  PNMA1    5'  CCTGCAGCAGGGGCGTCGC   24135    GCA      AAT   A
                                CC   CAGCAGGG   TGT GC
                                ||   ||||||||   ||| ||
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                                GG   GTCGTCCC   GCA CG
                                 AC_       C__   G
GAM927   PRO2605   3'  GCGCAGCAAGGAGGCTGC    24136    A       ATT  A
                                GC CAGCAGGGA   GT GC
                                || |||||||||   || ||
                                CG GTCGTTCCT   CG CG
                                 C        C__  A
GAM927   Rpo1-2    3'  CCGTCCAGCAGGACAGGGTAGC 24137     CA       AATT
            AC                    CCG  CAGCAGGG    GTAGCAC
                                ||| ||||||||   |||||||
                                GGC  GTCGTCCT    CATCGTG
                                  AG       GTCC
GAM927   LOC131377 3'  CCGCACTGGTAGGAAGGTGGCA 24138       AGCA    TT  A
            C                     CCGCAC    GGGAA  GT GCAC
                                ||||||    |||||  || ||||
                                GGCGTG    TCCTT  CA CGTG
                                    ACCA     C_  C
GAM927   LOC146603 5'  CAGCAATGGATTGTAGCA     24139       _   A
                                CAGCAG GGA TTGTAGCA
                                |||||| ||| ||||||||
                                GTCGTT CCT AACATCGT
                                   A   _
GAM927   LOC149668 3'  CCGCACAGCAGGCAGCAACAC  24140           GAATT
                                CCGCACAGCAGG     GTAGCAC
                                ||||||||||||     |||||||
                                GGCGTGTCGTCC     CGTTGTG
                                      GT___
GAM927   LOC153769 5'  CCGCGCAGCAGGGGTGCGC    24141      A       AAT   A
                                CCGC CAGCAGGG   TGT GC
                                |||| ||||||||   ||| ||
                                GGCG GTCGTCCC   ACG CG
                                  C       C__   _
GAM927   LOC157421 3'  CATACAGCAGAGTAGCA      24142     C       GAATT
                                CG ACAGCAGG     GTAGCA
                                || ||||||||     ||||||
                                GT TGTCGTCT     CATCGT
                                 A       ______
GAM927   LOC158678 3'  CGTCAGTAGGGAACTGC      24143     CA   C
                                CG  CAG AGGGAATTGT
                                ||  ||| ||||||||||
                                GC  GTC TCCCTTGACG
                                 A_   A
GAM927   LOC162333 5'  GCACGGCGGGGGACTCGGGCAC 24144      A  A_    A   TA
                                GCAC GC  GGGA TTG  GCAC
                                |||| ||  |||| |||  ||||
                                CGTG CG  CCCT AGC  CGTG
                                  C  CC    G   C_
GAM927   LOC196985 5'  CCGACAGCAGGGGGCGC      24145     C       AATT  A
                                CCG ACAGCAGGG    GT GC
                                ||| |||||||||    || ||
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                                GGC TGTCGTCCC    CG CG
                                  _        C___  _
GAM927   LOC196986 5'  CCGACAGCAGGGGGCGC     24145     C        AATT  A
                                CCG ACAGCAGGG    GT GC
                                ||| |||||||||    || ||
                                GGC TGTCGTCCC    CG CG
                                  _        C___  _
GAM927   LOC200382 3'  GCCACAGCAGGGAGGAAGGCA  24146    _         ATTGTA
                                GC ACAGCAGGGA     GCA
                                || ||||||||||     |||
                                CG TGTCGTCCCT     CGT
                                 G         CCTTC_
GAM927   LOC200597 3'  CGCACAGCAGGCGGCTGC    24147           GAATT  A
                                CGCACAGCAGG     GT GC
                                ||||||||||     || ||
                                GCGTGTCGTCC     CG CG
                                       GC___  A
GAM927   LOC202908 5'  GCAGTGGTCAACTTGTAGCAC  24148      _ AA___
                                GCAG GG     TTGTAGCAC
                                |||| ||     |||||||||
                                CGTC CC     AACATCGTG
                                  A  AGTTG
GAM927   LOC220595 5'  GCAGCAGCAGCTTCAGGTAGCA 24149     _     GGAATT
           C                     GCA CAGCAG      GTAGCAC
                                ||| ||||||      |||||||
                                CGT GTCGTC      CATCGTG
                                  C     GAAGTC
GAM927   LOC254830 5'  CCTGCAGCAGGGGTCCGTGC   24150    GCA       AA    A
                                CC   CAGCAGGG  TTGT GC
                                ||   ||||||||  |||| ||
                                GG   GTCGTCCC  GGCA CG
                                 AC_       CA    _
GAM927   LOC255758 5'  CCGGCAGCAGGGAAAGC     24151     CA        TTGT
                                CCG  CAGCAGGGAA    AGC
                                |||  ||||||||||    |||
                                GGC  GTCGTCCCTT    TCG
                                  C_         _____
GAM927   LOC51071  3'  CACAGCAGGAAATTAGTGC    24152             _ A
                                CACAGCAGGGAATT GT GC
                                |||||||||||||| || ||
                                GTGTCGTCCTTTAA CA CG
                                         T  _
GAM927   LOC90010  5'  CCTGCAGCAGGGTGGGGCA    24153    GCA       AAT  TA
                                CC   CAGCAGGG   TG  GCA
                                ||   ||||||||   ||  |||
                                GG   GTCGTCCC   AC  CGT
                                 AC_       ____  CC
GAM927   LOC91049  5'  CCGGCAGCAGGGGGAAGGCAC  24105     CA       AATTGTA
                                CCG  CAGCAGGG      GCAC
                                |||  ||||||||      ||||
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                                GGC  GTCGTCCC      CGTG
                                  C_       CCTTC__
GAM927  LOC93276  5'  GCAGTGGTCAACTTGTAGCAC  24148      _  AA___
                                GCAG GG     TTGTAGCAC
                                |||| ||     |||||||||
                                CGTC CC     AACATCGTG
                                  A  AGTTG
GAM928  HNRPH3    3'  TGTCAAGCTCTATTCCA     24156        CGGTACG
                                TGTCAAGT      TATTCCA
                                ||||||||      |||||||
                                ACAGTTCG      ATAAGGT
                                    AG_____
GAM928  PIGN      3'  TGTCAATTCGGAATTCCAA   24157       G    TACGT
                                TGTCAA TCGG     ATTCCAA
                                ||||||| ||||     |||||||
                                ACAGTT AGCC     TAAGGTT
                                   A    T____
GAM928  FLJ10619  3'  AGTCAGTATGTGTTCCAA    24158        C  A
                                AGTCGGTA GT TTCCAA
                                |||||||| || ||||||
                                TCAGTCAT CA AAGGTT
                                    A  C
GAM928  KIAA1754  3'  TGTCAAGTTGGTTATGCTCTC  24159         C   AC_  A
                                TGTCAAGT GGT   GT TTC
                                |||||||| |||   || |||
                                ACAGTTCA CCA   CG GAG
                                    A   ATA  A
GAM928  PRO2577   5'  TGTCAGGTCGAAGCAATTCCAA 24160       A     TA  T
          A                      TGTCA GTCGG  CG ATTCCAAA
                                ||||| |||||  || ||||||||
                                ACAGT CAGCT  GT TAAGGTTT
                                  C    TC  _
GAM928  LOC132880 5'  TGTCAAGTGGTGGCCCA     24161        C   AC  ATT
                                TGTCAAGT GGT  GT   CCA
                                |||||||| |||  ||   |||
                                ACAGTTCA CCA  CG   GGT
                                    _   C_  ___
GAM928  LOC255360 3'  GTCAAGGTCAGTGTGTTTC   24162       _    AC  A
                                GTCAAG TCGGT  GT TTC
                                |||||| |||||  || |||
                                CAGTTC AGTCA  CA AAG
                                   C    CA  _
GAM929  BCL2      3'  TTGGGAGTGAACGCTT      24165       CGAA  GC
                                TTGGGA   GT  GAACGCTT
                                ||||||   ||  ||||||||
                                AACCCT   CA  CTTGCGAA
                                   ____  __
GAM929  DAPP1     3'  TTGGGACGGAGTCTGACTCT  24166        A  GC  ACG
                                TTGGGACG AGT  GA   CT
                                |||||||| |||  ||   ||
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                                AACCCTGC TCA  CT   GA
                                    C   GA  GA_
GAM929  MGC2562  3'  TTGAGACGGAGTCTCGCTT   24167        A   GCGAA
                                TTGGGACG AGT    CGCTT
                                |||||||| |||    |||||
                                AACTCTGC TCA    GCGAA
                                    C   GA___
GAM930  NFKB1    3'  TGTCTTGTGGACAACGCAGTG  24170        A    A   _
                                TGTCTTGT GACAA CGCA TG
                                |||||||| ||||| |||| ||
                                ACAGAACA CTGTT GCGT AC
                                    C    _   C
GAM930  BRAG     3'  TCTTGAGAAAACGTATGAA   24171      T   C    C
                                TCTTG AGA AAACG ATGAA
                                ||||| ||| ||||| |||||
                                AGAAC TCT TTTGC TACTT
                                  _  _    A
GAM930  DKFZP434A236 3'  TGTCTTGTAGATGGGGCACA   24172          CAAAC
                                TGTCTTGTAGA    GCATG
                                ||||||||||    |||||
                                ACAGAACATCT    CGTGT
                                      ACCC_
GAM930  DKFZp761D0614 3'  TGTTTTGAGACAGAAACATGAA 24173    C   T    AAC
          A                      TGT TTG AGACA   GCATGAAA
                                ||| ||| |||||   ||||||||
                                ACA AAC TCTGT   TGTACTTT
                                  A  _    CTT
GAM930  DORFIN   3'  TGTTTTGTGGCAAACACACAAA 24174    C    AGA      TG
                                TGT TTGT   CAAACGCA  AA
                                ||| ||||   ||||||||  ||
                                ACA AACA   GTTTGTGT  TT
                                  A   CC_      GT
GAM930  EVI5     3'  TGTTTGTAGACAGCCACCTG   24175    C       AA   A
                                TGT TTGTAGACA  CGC TG
                                ||| |||||||||  ||| ||
                                ACA AACATCTGT  GTG AC
                                  _       CG   G
GAM930  FLJ14327  3'  GTTTTGTAGACAGAGATGA    24176    C       AACGC
                                GT TTGTAGACA    ATGA
                                || |||||||||    ||||
                                CA AACATCTGT    TACT
                                 A       CTC__
GAM930  FLJ20010  3'  TGTTTGTAGACATATCTGAAA  24177    C       AACGCA
                                TGT TTGTAGACA     TGAAA
                                ||| |||||||||     |||||
                                ACA AACATCTGT     ACTTT
                                  _       ATAG__
GAM930  KIAA1649  3'  TGTCCTGTAGACAACTGA    24178          AAC  A
                                TGTCTTGTAGACA   GC TGA
                                ||||||||||||   || |||
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                                ACAGGACATCTGT  TG ACT
                                       ___  _
GAM930  MGC5370  3'  TGTTTTGTAGACAGCA     24179    C       AAC
                                TGT TTGTAGACA  GCA
                                ||| |||||||||  |||
                                ACA AACATCTGT  CGT
                                  A      ___
GAM930  NCKX3    3'  TGTCTGTAACTCCTGCATGAAA 24180      T   ACAAAC
                                TGTCT GTAG     GCATGAAA
                                ||||| ||||     ||||||||
                                ACAGA CATT     CGTACTTT
                                   _   GAGGA_
GAM930  PSMD10   3'  TGTCTTGTGCACAAATACAT  24181        AG    CG
                                TGTCTTGT  ACAAA  CAT
                                ||||||||  |||||  |||
                                ACAGAACA  TGTTT  GTA
                                     CG    AT
GAM930  SFRS11   3'  TGTCTTATTTTAAAAGCGTATG 24182        AGAC  _  C
            AA                    TGTCTTGT   AAA CG ATGAA
                                ||||||||   ||| || |||||
                                ACAGAATA   TTT GC TACTT
                                     AAAT  C  A
GAM930  ZNF396   3'  TGTCTTGTGATGCTTGAA    24183        A  CAAAC  A
                                TGTCTTGT GA    GC TGAA
                                |||||||| ||    || ||||
                                ACAGAACA CT    CG ACTT
                                     _ A____  A
GAM930  LOC200300 3'  TGTTTAGTAGACAAATGA    24184    CTT      ACGC
                                TGT   GTAGACAA   ATGA
                                |||   ||||||||   ||||
                                ACA   CATCTGTT   TACT
                                  AAT     ____
GAM930  LOC200304 3'  TGTTTAGTAGACAAATGA    24184    CTT      ACGC
                                TGT   GTAGACAA   ATGA
                                |||   ||||||||   ||||
                                ACA   CATCTGTT   TACT
                                  AAT     ____
GAM930  LOC200305 3'  TGTTTAGTAGACAAATGA    24184    CTT      ACGC
                                TGT   GTAGACAA   ATGA
                                |||   ||||||||   ||||
                                ACA   CATCTGTT   TACT
                                  AAT     ____
GAM930  LOC255002 5'  TGTCTTGTAGGCACAAA     24185        ACAAAC   TG
                                TGTCTTGTAG     GCA  AA
                                ||||||||||     |||  ||
                                ACAGAACATC     CGT  TT
                                      _____  GT
GAM931  ATM      3'  GAGGATGCAGTGAGCCGTG   24188    A       _
                                GA GATGCAGTG GTTGTG
                                || ||||||||| ||||||
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                                CT CTACGTCAC CGGCAC
                                 C       T
GAM931  GRIN2A   5' CGAGGATGCAGTGGGGCGCG  24189    A       TTGT
                                CGA GATGCAGTGG   GCGCG
                                ||| ||||||||||   |||||
                                GCT CTACGTCACC   CGCGC
                                  C       C___
GAM931  KCNS2    5' CGCGGGTGCGAGTGTGTGCG  24190   AAGA  _   GT
                                CG   TGC AGTG  TGTGCG
                                ||   ||| ||||  ||||||
                                GC   ACG TCAC  ACACGC
                                 GCCC  C   __
GAM931  LAMP1    5' CGGAGAGCGGGGTCGCGTGCGC 24191   A  T  AGT   __
           G                     CG AGA GC   GGTT  GTGCGCG
                                || ||| ||   ||||  |||||||
                                GC TCT CG   CCAG  CACGCGC
                                 C  _  CC_   CG
GAM931  OTX1     3' CGGGATGCGGCTCTGTGCGCG 24192   AA    A  GG
                                CG  GATGC GT  TTGTGCGCG
                                ||  |||||  ||  |||||||||
                                GC  CTACG CG  GACACGCGC
                                 C_    C  A_
GAM931  TMEPAI   3' CGGGGACGTGGGTGCGC    24193   AA   GCA   TT
                                CG  GAT   GTGG  GTGCGC
                                ||  |||   ||||  ||||||
                                GC  CTG   CACC  CACGCG
                                 CC  ____   __
GAM931  TNXB     5' GAGGAGCAGTGGCAGTG    24194   A  T      T
                                GA GA GCAGTGGT GTG
                                || ||  |||||||| |||
                                CT CT CGTCACCG CAC
                                 C  _       T
GAM931  CDCA4    3' GAAGATGTGGCTGTGTGCG   24195      GCA       C
                                GAAGAT   GTGGTTGTG GCG
                                ||||||   ||||||||| |||
                                CTTCTA   CACCGACAC CGC
                                   ___         A
GAM931  CHRFAM7A 3' GAAGTGCAGTTGTGCG     24196     A     GGT
                                GAAG TGCAGT   TGTGCG
                                ||||  ||||||   ||||||
                                CTTC ACGTCA   ACACGC
                                   _     ____
GAM931  CNNM1    3' GAAGTGCAGTGGTGTG     24197     A       T
                                GAAG TGCAGTGGT GTG
                                ||||  ||||||||| |||
                                CTTC ACGTCACCA CAC
                                   _       _
GAM931  FLJ11175 3' ATGAGGGTGTGTGCACA    24198     C  T  _
                                ATG AG GGT TGTGCGCG
                                ||| || ||| ||||||||
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                                TAC TC CCA ACACGTGT
                                  _ _  C
GAM931  KIAA0977  3'  GAAGTGCAGTGGTGTG     24197     A       T
                                GAAG TGCAGTGGT GTG
                                |||| ||||||||| |||
                                CTTC ACGTCACCA CAC
                                  _       _
GAM931  MGC10471  5'  CGAAGATGTCGTGGGCCGTG  24199       CA   _
                                CGAAGATG  GTGG TTGTG
                                ||||||||  |||| |||||
                                GCTTCTAC  CACC GGCAC
                                     AG   C
GAM931  NYD-SP18  3'  CGAGGTGCAGTGGCGAGGACG  24200    A A      TGT_
                                CGA G TGCAGTGGT   GCG
                                ||| | |||||||||   |||
                                GCT C ACGTCACCG   TGC
                                  _ C       CTCC
GAM931  PPP1R3B   3'  CGGGAATGCAGTGGTGTG    24201    AA        T
                                CG  GATGCAGTGGT GTG
                                ||  ||||||||||| |||
                                GC  TTACGTCACCA CAC
                                 CC         _
GAM931  LOC135293 3'  GAAGGTGAGTGGTTGCG     24202      A  C
                                GAAG TG AGTGGTTGTG
                                |||| || ||||||||||
                                CTTC AC TCACCAACGC
                                  C  _
GAM931  LOC144308 5'  ACGGAGATGAGGTGGGTG    24203     A    CA    TT
                                ACG AGATG  GTGG  GTG
                                ||| |||||  ||||  |||
                                TGC TCTAC  CACC  CAC
                                  C    TC   __
GAM931  LOC145540 5'  CGGGATGCAGCTGCGC      24204    AA       GGTTG
                                CG  GATGCAGT    TGCGC
                                ||  ||||||||    |||||
                                GC  CTACGTCG    ACGCG
                                 C_       _____
GAM931  LOC146062 5'  GAAGATGGCGGCGGCTGCG   24205       _ A
                                GAAGATG C GTGGTTGTG
                                ||||||| | |||||||||
                                CTTCTAC G CGCCGACGC
                                    C C
GAM931  LOC148147 3'  GAAGTGCAGTGGCGCG      24206      A       TGT
                                GAAG TGCAGTGGT   GCG
                                |||| |||||||||   |||
                                CTTC ACGTCACCG   CGC
                                  _      ___
GAM931  LOC221935 3'  AGAAGCGGTGGCTGCTGCG   24207     T  A      GC
                                AGA GC GTGGTTGT  GCG
                                ||| || ||||||||  |||
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                                TCT CG CACCGACG  CGC
                                  T  C       A_
GAM931  LOC255481 3'  GAAGATGCAAGGGTGTGTG   24208          T  _
                                GAAGATGCAG GGT TGTG
                                |||||||||| ||| ||||
                                CTTCTACGTT CCA ACAC
                                      C   C
GAM931  LOC256414 3'  GAAGGATGCAGTCGTGTG    24209     _     G  T
                                GAAG ATGCAGT GT GTG
                                |||| ||||||| || |||
                                CTTC TACGTCA CA CAC
                                  C      G  _
GAM931  LOC92305  5'  AGATGCAGTCCCCGTGCG    24210         GG
                                AGATGCAGT  TTGTGCG
                                |||||||||  |||||||
                                TCTACGTCA  GGCACGC
                                      GG
GAM932  ACPT     3'  CAGCAGCTCGTGGTATCGGGGA 24213        GCTCG___  CAGA
           CAG                    CAGCAGCT       CG    GACAG
                                |||||||       ||    |||||
                                GTCGTCGA       GC    CTGTC
                                     GCACCATA  CC__
GAM932  ACPT     3'  CAGCAGCTCGTGGTATCGGGGA 24213        GCTCG___  CAGA
           CAG                    CAGCAGCT       CG    GACAG
                                |||||||       ||    |||||
                                GTCGTCGA       GC    CTGTC
                                     GCACCATA  CC__
GAM932  ACTA2    3'  ACAGTTGTGTGCTAGAGACAG  24214     C  CTC  GC
                                GCAG TG   GC  AGAGACAG
                                |||| ||   ||  ||||||||
                                TGTC AC   CG  TCTCTGTC
                                  A  ACA  A_
GAM932  ADARB1   3'  CAGTGCTGCCAGAGAC      24215     C    C  G
                                CAG TGCT GC CAGAGAC
                                ||| |||| || |||||||
                                GTC ACGA CG GTCTCTG
                                   _   _  _
GAM932  ALDOB    5'  CAGCAGCTGCCAAATAAGACAG 24216          CGCGCA
                                CAGCAGCTGCT     GAGACAG
                                ||||||||||      |||||||
                                GTCGTCGACGG     TTCTGTC
                                      TTTA__
GAM932  ARF3     5'  CAGCAGCTGCTTTCTGGGGACA 24217          CGCGCAGA
           G                     CAGCAGCTGCT       GACAG
                                ||||||||||        |||||
                                GTCGTCGACGA       CTGTC
                                      AAGACCC_
GAM932  CASP8    5'  CAGGGGCTGCTCAGACAG    24218     CA       C
                                CAG  GCTGCTCG GCAG
                                |||  |||||||| ||||
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                                GTC  CGACGAGT TGTC
                                  CC       C
GAM932  CASP8    5'  CAGGGGCTGCTCAGACAG    24218     CA       C
                                CAG  GCTGCTCG GCAG
                                |||  |||||||| ||||
                                GTC  CGACGAGT TGTC
                                  CC       C
GAM932  CD164    3'  CAGCAGCTATTTAAAATAAGAC 24219          CTCGCGCA
          AG                      CAGCAGCTG       GAGACAG
                                |||||||||       |||||||
                                GTCGTCGAT       TTCTGTC
                                     AAATTTTA
GAM932  CD22     3'  CAGCAGCTCCGGGTGGAGA    24220         G T  CGCA
                                CAGCAGCT C CG    GAGA
                                |||||||| | ||    ||||
                                GTCGTCGA G GC    CTCT
                                    _ _  CCAC
GAM932  DAP      3'  GCAGCTGCTCACGACACAG    24221           _  G
                                GCAGCTGCTCGCG CA AG
                                |||||||||||| || ||
                                CGTCGACGAGTGC GT TC
                                       T  G
GAM932  DES      3'  ACAGCTGGGGTCCGCAGAG    24222        C__  G
                                GCAGCTG   TC CGCAGAG
                                |||||||   || |||||||
                                TGTCGAC   AG GCGTCTC
                                   CCC  _
GAM932  DXYS155E 3'  CAGCAGCCGCTCGCGCAG    24223
                                CAGCAGCTGCTCGCGCAG
                                ||||||||||||||||||
                                GTCGTCGGCGAGCGCGTC

GAM932  JAM3     3'  CAGCAGCTCCTTGCTTTACAG  24224        G  C  ___
                                CAGCAGCT CT GC   GCAG
                                |||||||| || ||   ||||
                                GTCGTCGA GA CG   TGTC
                                     G  A  AAA
GAM932  KCNQ1    3'  CAGCAGCTGGCAAGGGGAG    24225         CTC   CA__
                                CAGCAGCTG   GCG    GAG
                                |||||||||   |||    |||
                                GTCGTCGAC   CGT    CTC
                                     ___   TCCC
GAM932  LAMP1    5'  GCGCTGGCGTTAGAGACAG    24226    A   CTC   C_
                                GC GCTG   GCG  AGAGACAG
                                || ||||   |||  ||||||||
                                CG CGAC   CGC  TCTCTGTC
                                 _   ___   AA
GAM932  RALBP1   3'  CAGGAGCTGCTCAGACAG    24227     C       C
                                CAG AGCTGCTCG GCAG
                                ||| |||||||| ||||
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                                GTC TCGACGAGT TGTC
                                  C       C
GAM932  RET     3'  CAGTGGCTGCTCGCCAG    24228    CA       G
                                CAG  GCTGCTCGC CAG
                                |||  ||||||||| |||
                                GTC  CGACGAGCG GTC
                                  AC       _
GAM932  TJP1    5'  AGTGGCCGCGCAGAGACA    24229    CT  T
                                AG  GC CGCGCAGAGACA
                                ||  || ||||||||||||
                                TC  CG GCGCGTCTCTGT
                                 AC  _
GAM932  TNFRSF8  3'  GCCGCTGCAGCAGAGACAG   24230       C  _
                                GCTGCT GC GCAGAGACAG
                                ||||||  || ||||||||||
                                CGGCGA CG CGTCTCTGTC
                                   _  T
GAM932  AASDHPPT  3'  CAGCAGCTCTTGTGATCGAGAG 24231        G  CG____  C
                                CAGCAGCT CT     CG AGAG
                                ||||||||  ||     || ||||
                                GTCGTCGA GA     GC TCTC
                                    _  ACACTA  _
GAM932  BIKE    3'  AGCAGCTGCTTCACTAGCAG   24232          _  __
                                AGCAGCTGCT CGC  GCAG
                                ||||||||||  |||  ||||
                                TCGTCGACGA GTG  CGTC
                                     A   AT
GAM932  BPESC1   3'  AGCAGCTGTGGTGGCAGGGGCA 24233        CTCGC   AGA
          G                      AGCAGCTG    GCAG   CAG
                                ||||||||    ||||  |||
                                TCGTCGAC    CGTC   GTC
                                    ACCAC    CCC
GAM932  C12orf22  3'  CAGCAGCTGCTTCTACAG    24234          _ GC
                                CAGCAGCTGCT C  GCAG
                                ||||||||||| |  ||||
                                GTCGTCGACGA G  TGTC
                                     A A_
GAM932  C6orf31   5'  CAGCCGGCAGCAGCGCAGAGA  24235     A_  T  TC
                                CAGC  GC GC  GCGCAGAGA
                                ||||  || ||  |||||||||
                                GTCG  CG CG  CGCGTCTCT
                                  GC  T  T_
GAM932  CBLN1    5'  CAGGGCTGCTCGCGCCAG    24236     CA        AG
                                CAG  GCTGCTCGCGC  AG
                                |||  ||||||||||  ||
                                GTC  CGACGAGCGCG  TC
                                  C_         G_
GAM932  CNTNAP1  3'  CAGCAGCTGGAACAGAGA    24237         CTCGC
                                CAGCAGCTG    GCAGAGA
                                |||||||||    |||||||
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                                GTCGTCGAC    TGTCTCT
                                     CT___
GAM932  DCOHM    3'  GCAGCTGCTCTAAGACA     24238         GCGCA
                                GCAGCTGCTC    GAGACA
                                ||||||||||    ||||||
                                CGTCGACGAG    TTCTGT
                                     A____
GAM932  DKFZP434C0826 5'  ACAGCTGCCACAGAGGCA    24239        TCG     A
                                GCAGCTGC   CGCAGAG CA
                                ||||||||   ||||||| ||
                                TGTCGACG   GTGTCTC GT
                                     ___      C
GAM932  DKFZP434P1750 3'  CAGCAGCTGGCGAGGAGA    24240        CTC   CA
                                CAGCAGCTG   GCG  GAGA
                                |||||||||   |||  ||||
                                GTCGTCGAC   CGC  CTCT
                                     ___  TC
GAM932  DKFZP564C103 3'  GCAGCTGCTCCCAGAGA     24241         GCG
                                GCAGCTGCTC   CAGAGA
                                ||||||||||   ||||||
                                CGTCGACGAG   GTCTCT
                                     G__
GAM932  FADS2    5'  GCCGGCTGCTCGCTGCACAGAC 24242    A_       _  G
                                GC  GCTGCTCGC GCA AGAC
                                ||  ||||||||| ||| ||||
                                CG  CGACGAGCG CGT TCTG
                                 GC        A   G
GAM932  FBXO21   3'  GGACAGACAGGTGCAGAGACAG 24243   A   CT  TCGC
                                C GCAG  GC    GCAGAGACAG
                                | ||||  ||    ||||||||||
                                C TGTC  TG    CGTCTCTGTC
                                 C    __  TCCA
GAM932  FLJ12387  3'  CAGGGGCTGTGGGAGAGACAG  24244     CA   CTCGCGC
                                CAG  GCTG      AGAGACAG
                                |||  ||||      ||||||||
                                GTC  CGAC      TCTCTGTC
                                  CC    ACCC___
GAM932  FLJ13114  3'  CAGCAGCTATTTCAGAGGCAG  24245        CTCGCG    A
                                CAGCAGCTG     CAGAG CAG
                                |||||||||     ||||| |||
                                GTCGTCGAT     GTCTC GTC
                                     AAA___    C
GAM932  FLJ20036  5'  ACAGCTGCACCGGGAGACAG   24246        _  CGCA
                                GCAGCTGC TCG    GAGACAG
                                |||||||| |||    |||||||
                                TGTCGACG GGC    CTCTGTC
                                     T   C___
GAM932  FLJ20619  3'  CAGTGGACTGCATCAAGAGACA 24247     CA_    TCG  C
             G                   CAG   GCTGC   CG AGAGACAG
                                |||   |||||   || ||||||||
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                                GTC   TGACG   GT TCTCTGTC
                                  ACC     TA_  _
GAM932   FLJ22021  3'  CAGCAGCTGACCCCAGAGACAG 24248         _   GCG
                                CAGCAGCTG CTC   CAGAGACAG
                                ||||||||| |||   |||||||||
                                GTCGTCGAC GGG   GTCTCTGTC
                                     T  ___
GAM932   GL004     3'  GCATACAATGCAGAGACAG    24249     GC   TCGC
                                GCA  TGC    GCAGAGACAG
                                |||  |||    ||||||||||
                                CGT  ATG    CGTCTCTGTC
                                  __   TTA_
GAM932   GPR72     3'  CAGCAGCTGCCCCACAGA     24250           G
                                CAGCAGCTGCTC CGCAGA
                                |||||||||||| ||||||
                                GTCGTCGACGGG GTGTCT

                                          _
GAM932   HELO1     5'  GCAGCCGGCGCAGAG       24251        CTC
                                GCAGCTG   GCGCAGAG
                                |||||||   ||||||||
                                CGTCGGC   CGCGTCTC

                                          ___
GAM932   HSSEXGENE 5'  GCAGCCGCGCCTGGGGACAG   24252       TGCT    AGA__
                                GCAGC    CGCGC    GACAG
                                |||||    |||||    |||||
                                CGTCG    GCGCG    CTGTC
                                   _____    GACCC
GAM932   KIAA0014  3'  CAGCGGCTGCTCACCTCCAGGG 24253      A       G__   A
            ACAG                    CAGC GCTGCTCGC   CAG GACAG
                                |||| |||||||||   ||| |||||
                                GTCG CGACGAGTG   GTC CTGTC
                                  C        GAG   C
GAM932   KIAA0545  3'  GCCGCTGCTCGGAGAGA     24254     A       CGC
                                GC GCTGCTCG   AGAGA
                                || ||||||||   |||||
                                CG CGACGAGC   TCTCT
                                 G       C__
GAM932   KIAA0630  5'  AGCAGCTGCTGCAGTAG     24255          CGC   _
                                AGCAGCTGCT   GCAG AG
                                ||||||||||   |||| ||
                                TCGTCGACGA   CGTC TC
                                     ___    A
GAM932   KIAA1280  5'  CAACAGCTGGGGCCTGGAGAC  24256         CTC  GCA
                                CAGCAGCTG   GC   GAGAC
                                |||||||||   ||   |||||
                                GTTGTCGAC   CG   CTCTG
                                     CC_  GAC
GAM932   KIAA1560  3'  CAGCAGCTCTTTGCAGCAATGA 24257         G  C_  _   A
            CAG                     CAGCAGCT CT  GC GCAG GACAG
                                |||||||| ||  || |||| |||||
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                                GTCGTCGA GA  CG CGTT CTGTC
                                     _ AA  T    A
GAM932  KIAA1668  3'  CAGGAGCTGCTCCAGGAG    24258     C       G  CA
                                CAG AGCTGCTC CG  GAG
                                ||| |||||||| ||  |||
                                GTC TCGACGAG GT  CTC
                                  C       _  C_
GAM932  KIAA1813  5'  AGGGGCTGCTCGGCGGCAG   24259    CA       _ _
                                AG  GCTGCTCG CG CAG
                                ||  |||||||| || |||
                                TC  CGACGAGC GC GTC
                                 CC       C  C
GAM932  MGC13251  3'  GCAGCTGCCAGGGACA      24260         TCGCG   A
                                GCAGCTGC    CAG GACA
                                ||||||||    ||| ||||
                                CGTCGACG    GTC CTGT
                                     ______  C
GAM932  NLI-IF    3'  GCAGCATGGACAGAGACAG   24261      TGCTCGC
                                GCAGC      GCAGAGACAG
                                |||||      ||||||||||
                                CGTCG      TGTCTCTGTC
                                   TACC___
GAM932  PAXIP1L   3'  CAGCAGCTCCTCGCCAGCCAGA 24262         G    G  __
          CAG                     CAGCAGCT CTCGC CAG  AGACAG
                                ||||||||  ||||| |||  ||||||
                                GTCGTCGA GAGCG GTC  TCTGTC
                                     G    _  GG
GAM932  PKNOX2    3'  GCTGTGCGCAGAGACAG     24263      CTC
                                GCTG   GCGCAGAGACAG
                                ||||   ||||||||||||
                                CGAC   CGCGTCTCTGTC
                                  A__
GAM932  SLC26A9   3'  CAGAGCTGCCAGAGAC      24264     C     TCGCG
                                CAG AGCTGC    CAGAGAC
                                ||| ||||||    |||||||
                                GTC TCGACG    GTCTCTG
                                   _    ______
GAM932  SLC26A9   3'  CAGAGCTGCCAGAGAC      24264     C     TCGCG
                                CAG AGCTGC    CAGAGAC
                                ||| ||||||    |||||||
                                GTC TCGACG    GTCTCTG
                                   _    ______
GAM932  TCL6      3'  GCAGCTGCTCTTGGCCCAG   24265          ___  G
                                GCAGCTGCTC   GC CAG
                                ||||||||||   || |||
                                CGTCGACGAG   CG GTC
                                      AAC  G
GAM932  TCL6      3'  GCAGCTGCTCTTGGCCCAG   24265          ___  G
                                GCAGCTGCTC   GC CAG
                                ||||||||||   || |||
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                                CGTCGACGAG   CG GTC
                                     AAC  G
GAM932  TPC2     3'  CAGCAGCTGTTCTGTAGAC    24266         C  GCGCAG
                                CAGCAGCTG TC     AGAC
                                |||||||||  ||     ||||
                                GTCGTCGAC AG     TCTG
                                     A  ACA___
GAM932  UBCE7IP5  3'  ACAGCTGCTTAAGGGGAGGCAG 24267          CGCGCA   A
                                GCAGCTGCT     GAG CAG
                                |||||||||     ||| |||
                                TGTCGACGA     CTC GTC
                                     ATTCCC   C
GAM932  ZDHHC4    5'  CAGCAGCTCCTCTTGGGCAG   24268        G   GC__
                                CAGCAGCT CTC    GCAG
                                ||||||||  |||   ||||
                                GTCGTCGA GAG    CGTC
                                     G   AACC
GAM932  LOC115399 3'  CAGCACCTGCAAGAGACA    24269      G    TCGCGC
                                CAGCA CTGC     AGAGACA
                                |||||  ||||     |||||||
                                GTCGT GACG     TCTCTGT
                                   G    T_____
GAM932  LOC129446 3'  CAGCAGCTGCTCTGTCAG    24270          GCG
                                CAGCAGCTGCTC   CAG
                                ||||||||||||   |||
                                GTCGTCGACGAG   GTC
                                       ACA
GAM932  LOC135932 3'  CAGCAGCTGTCCCTAGACAG   24271         _   GC_
                                CAGCAGCTG CTC   GCAG
                                |||||||||  |||   ||||
                                GTCGTCGAC GGG   TGTC
                                     A   ATC
GAM932  LOC139728 3'  GCTGGGGGCCAGAGACAG    24272      CTC  G
                                GCTG   GC CAGAGACAG
                                ||||   ||  |||||||||
                                CGAC   CG GTCTCTGTC
                                  CCC  _
GAM932  LOC144165 5'  CAATGGCTGCTCGCGCGAG    24273     CA         A
                                CAG  GCTGCTCGCGC GAG
                                |||  ||||||||||| |||
                                GTT  CGACGAGCGCG CTC
                                  AC         _
GAM932  LOC146108 5'  CAGCGGTGGCTGCAGAGACAG  24274      AGCT   CGC
                                CAGC    GCT   GCAGAGACAG
                                ||||    |||   ||||||||||
                                GTCG    CGA   CGTCTCTGTC
                                  CCAC   ___
GAM932  LOC146212 5'  CAGAGGCTGCTCAGGGGCAG   24275     CA       C__
                                CAG  GCTGCTCG   GCAG
                                |||  ||||||||   ||||
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                                GTC  CGACGAGT   CGTC
                                  TC       CCC
GAM932   LOC146325 3'  GCATGCTGCAGGCAGAGACAG  24276     _    TCGC
                                GCA GCTGC    GCAGAGACAG
                                ||| |||||    ||||||||||
                                CGT CGACG    CGTCTCTGTC
                                  A     TC__
GAM932   LOC147299 3'  GCAGCTGCTTTGCCCGTGAGCA 24277         C_  GCA_   A
           G                     GCAGCTGCT  GC    GAG CAG
                                |||||||||  ||    ||| |||
                                CGTCGACGA  CG    CTC GTC
                                     AA  GGCA   _
GAM932   LOC147669 5'  CAGCAGCTGTGTGACCTTGGGC 24278         CTC_  _____
           AG                     CAGCAGCTG    GC     GCAG
                                |||||||||    ||     ||||
                                GTCGTCGAC    TG     CGTC
                                     ACAC  GAACC
GAM932   LOC148696 5'  CAGCAGCCTCCCTGTGGGGACA 24279         G   GCGCAGA
           G                     CAGCAGCT CTC       GACAG
                                ||||||||| |||       |||||
                                GTCGTCGG GGG       CTGTC
                                     A   ACACCC_
GAM932   LOC150279 3'  ACAGCTGCAGCCCTGGGGACAG 24280         TC  GCAGA_
                                GCAGCTGC  GC     GACAG
                                ||||||||  ||     |||||
                                TGTCGACG  CG     CTGTC
                                     T_  GGACCC
GAM932   LOC150290 5'  CAGGGCTGCAGCCGAGAGACAG 24281     CA     TCG  C
                                CAG  GCTGC   CG AGAGACAG
                                |||  |||||   || ||||||||
                                GTC  CGACG   GC TCTCTGTC
                                  C_    TCG  _
GAM932   LOC150372 3'  CAGCTGAGACCCAGAGACAG   24282       CTC  G
                                CAGCTG   GC CAGAGACAG
                                ||||||   || |||||||||
                                GTCGAC   TG GTCTCTGTC
                                    TC_  G
GAM932   LOC151979 5'  ACAGCTGCACAGAGA       24283         TCGC
                                GCAGCTGC    GCAGAGA
                                ||||||||    |||||||
                                TGTCGACG    TGTCTCT
                                     _____
GAM932   LOC152195 5'  CAGTAACTGCTCCCAGGCAG   24284     C       G __
                                CAG AGCTGCTC C  GCAG
                                ||| |||||||| |  ||||
                                GTC TTGACGAG G  CGTC
                                  A       G TC
GAM932   LOC164397 5'  GCAGCTGCTCAGCAGGGCAG   24285          C    AGA
                                GCAGCTGCTCG GCAG   CAG
                                |||||||||| ||||   |||
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                                CGTCGACGAGT CGTC   GTC
                                      _    CC_
GAM932   LOC169693 3'  CAGTAGCTGCTCCCCACAG   24286     C      _ G
                                CAG AGCTGCT C CGCAG
                                ||| ||||||| | |||||
                                GTC TCGACGA G GTGTC
                                  A      G G
GAM932   LOC199704 5'  CAGAGCTGCTCTGAAGAGA   24287     C       GCGC
                                CAG AGCTGCTC    AGAGA
                                ||| ||||||||    |||||
                                GTC TCGACGAG    TCTCT
                                  _       ACT_
GAM932   LOC200081 3'  CAGCAACTGCTGCATGGAGACA 24288           C   CA
           G                     CAGCAGCTGCT GCG  GAGACAG
                                ||||||||||| |||  |||||||
                                GTCGTTGACGA CGT  CTCTGTC
                                      _   AC
GAM932   LOC200269 3'  GCTGTCAAGAGAGACAG     24289      C   CGC
                                GCTG TCG   AGAGACAG
                                |||| |||   ||||||||
                                CGAC AGT   TCTCTGTC
                                  _   TC_
GAM932   LOC219894 3'  CAGTACTGCAGAGAC       24290     C    CGC
                                CAG TGCT   GCAGAGAC
                                ||| ||||   ||||||||
                                GTC ATGA   CGTCTCTG
                                  _   ____
GAM932   LOC222057 3'  CAGCAGCTGCCTGGGAGGCAG  24291           CGC___
                                CAGCAGCTGCT     GCAG
                                ||||||||||      ||||
                                GTCGTCGACGG     CGTC
                                      ACCCTC
GAM932   LOC253595 5'  CAGAGCTGCTCGCGCATCAC   24292     C          GAG
                                CAG AGCTGCTCGCGCA   AC
                                ||| ||||||||||||   ||
                                GTC TCGACGAGCGCGT   TG
                                  _          AG_
GAM932   LOC254665 5'  CAGCAGCTGCTTTGCCACAG   24293          C_ _
                                CAGCAGCTGCT  GC GCAG
                                ||||||||||  || ||||
                                GTCGTCGACGA  CG TGTC
                                      AA  G
GAM932   LOC256352 5'  CAGAGGCTGCTCAGGGGCAG   24275     CA      C__
                                CAG  GCTGCTCG   GCAG
                                |||  ||||||||   ||||
                                GTC  CGACGAGT   CGTC
                                  TC       CCC
GAM932   LOC257144 5'  GCCACCCGTGCAGAGACAG   24294    TG   C
                                GC  CTCG GCAGAGACAG
                                ||  |||| ||||||||||
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                                CG  GGGC CGTCTCTGTC
                                 GT    A
GAM932  LOC96652  3'  CAGGGCCCTGCAGAGACA    24295     CT    GC
                                CAG  GCTC  GCAGAGACA
                                |||  ||||  |||||||||
                                GTC  CGGG  CGTCTCTGT
                                  C_    A_
GAM933  ARSB      3'  GTGCAGGCATTTTGCTGTTG  24298     A   A  CG_
                                GT CAG CA   TGCTGTTG
                                || ||| ||   ||||||||
                                CA GTC GT   ACGACAAC
                                 C   C  AAA
GAM933  BACH2     3'  TGTACAAATGCTATT       24299        ACAC
                                TGTACAG    GTGCTGTT
                                |||||||    ||||||||
                                ACATGTT    TACGATAA

                                     _____
GAM933  CARKL     3'  TGCACAGACATGCTCCTG    24300          CG    G
                                TGTACAGACA  TGCT TTG
                                ||||||||||  |||| |||
                                ACGTGTCTGT  ACGA GAC
                                      __    G
GAM933  ETV5      3'  CACAAATGTGCTGTTG      24301        CAC
                                TACAGA   GTGCTGTTG
                                ||||||   |||||||||
                                GTGTTT   CACGACAAC
                                   A__
GAM933  IL1RAP    3'  TGTACAGACACAAAATTG    24302           TGCT
                                TGTACAGACACG    GTTG
                                ||||||||||||    ||||
                                ACATGTCTGTGT    TAAC
                                       TT__
GAM933  KIR2DS1   3'  TGTACATGCTGGTATCTGTTG  24303       GACAC  _
                                TGTACA    GTG CTGTTG
                                ||||||    ||| ||||||
                                ACATGT    CAT GACAAC
                                   ACGAC   A
GAM933  KIR2DS2   3'  TGTACATGCTGGTATCTGTTG  24303       GACAC  _
                                TGTACA    GTG CTGTTG
                                ||||||    ||| ||||||
                                ACATGT    CAT GACAAC
                                   ACGAC   A
GAM933  KIR2DS4   3'  TGTACATGCTGGTATCTGTTG  24303       GACAC  _
                                TGTACA    GTG CTGTTG
                                ||||||    ||| ||||||
                                ACATGT    CAT GACAAC
                                   ACGAC   A
GAM933  LFNG      3'  TACAGACACGCCCACTG     24304          G TG
                                TACAGACACGT C  TTG
                                |||||||||| |  |||
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                                ATGTCTGTGCG G  GAC
                                      _ GT
GAM933  MEF2D   3'  TGCACTGAGTGTGCTGTTG   24305      A  CAC
                                TGTAC GA   GTGCTGTTG
                                ||||| ||   |||||||||
                                ACGTG CT   CACGACAAC
                                   A  CA_
GAM933  NR3C1   3'  TGACAGACTCACTGTTG     24306    T     A GT
                                TG ACAGAC C  GCTGTTG
                                || |||||| |  |||||||
                                AC TGTCTG G  TGACAAC
                                 _     A __
GAM933  PCDH7   3'  TGTAAAGAACTTTGCTGTTG  24307     C   CACG
                                TGTA AGA    TGCTGTTG
                                |||| |||    ||||||||
                                ACAT TCT    ACGACAAC
                                   T   TGAA
GAM933  PDHB    3'  TGTACAAAAATACCTGCTGTTG 24308        C__  G
                                TGTACAGA   AC TGCTGTTG
                                ||||||||   || ||||||||
                                ACATGTTT   TG ACGACAAC
                                     TTA  G
GAM933  PDLIM1  3'  TGTCAGACACGTTATATT    24309     A       GC
                                TGT CAGACACGT  TGTT
                                ||| |||||||||  ||||
                                ACA GTCTGTGCA  ATAA
                                  _       AT
GAM933  PKLR    3'  TGTACAATTGGTGCTGTTG   24310       ACAC
                                TGTACAG    GTGCTGTTG
                                |||||||    |||||||||
                                ACATGTT    CACGACAAC
                                    AAC_
GAM933  RNMT    3'  TGTACAGACCATTAAATGTTG  24311         A   GC__
                                TGTACAGAC CGT    TGTTG
                                ||||||||| |||    |||||
                                ACATGTCTG GTA    ACAAC
                                      _  ATTT
GAM933  RRM2B   3'  TGTACAGACAGTGACGATG   24312         C   C  T
                                TGTACAGACA GTG TG TG
                                |||||||||| ||| || ||
                                ACATGTCTGT CAC GC AC
                                      _  T  T
GAM933  TAL1    3'  TGTACAGATGCTATT      24313        CACG
                                TGTACAGA    TGCTGTT
                                ||||||||    |||||||
                                ACATGTCT    ACGATAA
                                     ____
GAM933  WHSC1   3'  GTGCAGATGATGCTGTTG    24314    A    CAC
                                GT CAGA   GTGCTGTTG
                                || ||||   |||||||||
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                                CA GTCT   TACGACAAC
                                 C    AC_
GAM933  WHSC1    3'  GTGCAGATGATGCTGTTG    24314    A    CAC
                                GT CAGA   GTGCTGTTG
                                || ||||   |||||||||
                                CA GTCT   TACGACAAC
                                 C    AC_
GAM933  WHSC1    3'  GTGCAGATGATGCTGTTG    24314    A    CAC
                                GT CAGA   GTGCTGTTG
                                || ||||   |||||||||
                                CA GTCT   TACGACAAC
                                 C    AC_
GAM933  WTAP     3'  TATACAGACATCATTGTGTTG  24315         _   GC
                                TGTACAGACA CGT  TGTTG
                                |||||||||| |||  |||||
                                ATATGTCTGT GTA  ACAAC
                                      A   AC
GAM933  C20orf54  5'  TGTAGAGACACGCCAACTG   24316     C      __
                                TGTA AGACACGT  GCTG
                                |||| ||||||||  ||||
                                ACAT TCTGTGCG  TGAC
                                  C       GT
GAM933  C22orf5   3'  TGTAGGGACACGTGTTGT    24317     CA      C
                                TGTA  GACACGTG TGT
                                ||||  |||||||| |||
                                ACAT  CTGTGCAC ACA
                                  CC       A
GAM933  DKFZp434F2322 3'  TGTCAGAGTTACTGTTG     24318     A    CACG
                                TGT CAGA    TGCTGTTG
                                ||| ||||    ||||||||
                                ACA GTCT    ATGACAAC
                                  _    CA__
GAM933  DKFZP434O047 5'  TGTGCAGATGCTGTTA      24319     A    CACG
                                TGT CAGA    TGCTGTTG
                                ||| ||||    ||||||||
                                ACA GTCT    ACGACAAT
                                  C    ____
GAM933  FLJ12425  3'  TGTACAGATGCCATT       24320         CACG
                                TGTACAGA    TGCTGTT
                                ||||||||    |||||||
                                ACATGTCT    ACGGTAA
                                             _____
GAM933  FLJ13241  3'  TGTATAAACACTGCCAGTTG   24321     C     G   _
                                TGTA AGACAC TGCT GTTG
                                |||| |||||| |||| ||||
                                ACAT TTTGTG ACGG CAAC
                                  A      _    T
GAM933  FLJ14957  3'  TGCACAGACACGCCTCTG    24322           G_
                                TGTACAGACACGT  CTG
                                ||||||||||||  |||
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                                ACGTGTCTGTGCG  GAC
                                       GA
GAM933  FLJ20297 3' TGTCACAGAGCGTAGCTGTTG 24323    _   CA  _
                                TGT ACAGA  CGT GCTGTTG
                                ||| |||||  ||| |||||||
                                ACA TGTCT  GCA CGACAAC
                                  G    C_  T
GAM933  FLJ20297 3' TGTCACAGAGCGTAGCTGTTG 24323    _   CA  _
                                TGT ACAGA  CGT GCTGTTG
                                ||| |||||  ||| |||||||
                                ACA TGTCT  GCA CGACAAC
                                  G    C_  T
GAM933  H2AV    3' TGTACAGATGTGGCCAT    24324       CAC  _
                                TGTACAGA   GTG CTGT
                                ||||||||   ||| ||||
                                ACATGTCT   CAC GGTA
                                     A__   C
GAM933  ICK     3' TATACAAAATGCTGTTG    24325       CAC
                                TGTACAGA   GTGCTGTTG
                                ||||||||   |||||||||
                                ATATGTTT   TACGACAAC
                                     ___
GAM933  ITGA10  3' TGTACAGAATGTCTCTTG   24326       CAC  _ G
                                TGTACAGA   GTG CT TTG
                                ||||||||   ||| || |||
                                ACATGTCT   TAC GA AAC
                                     ___   A  G
GAM933  KIAA0087 3' TGTCTAGACCTTGCTGTTG  24327    AC   ACG
                                TGT  AGAC   TGCTGTTG
                                |||  ||||   ||||||||
                                ACA  TCTG   ACGACAAC
                                  GA   GA_
GAM933  KIAA0237 3' TGTACAGAACAGCCTTTG   24328       C  T  G
                                TGTACAGA ACG GCT TTG
                                |||||||| ||| ||| |||
                                ACATGTCT TGT CGG AAC
                                     _  _  A
GAM933  KIAA0436 3' TGTACAGCATGCTGCT     24329       ACA
                                TGTACAG   CGTGCTGTT
                                |||||||   |||||||||
                                ACATGTC   GTACGACGA
                                     ___
GAM933  KIAA0574 3' TGTACAGACAGGTCTCTG   24330        C  G_
                                TGTACAGACA GT  CTG
                                |||||||||| ||  |||
                                ACATGTCTGT CA  GAC
                                      C  GA
GAM933  KIAA0674 5' TGCATGGACTGCTGTTG    24331     CA  ACG
                                TGTA  GAC   TGCTGTTG
                                ||||  |||   ||||||||
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                                ACGT  CTG   ACGACAAC
                                  AC  ___
GAM933  KIAA0748  3'  TGTCAGACCACATGCTGTTG  24332     A    _
                                TGT CAGAC ACGTGCTGTTG
                                ||| ||||| ||||||||||
                                ACA GTCTG TGTACGACAAC
                                  _    G
GAM933  KIAA1229  3'  TGTACAGAACGTACAGGTTG  24333        C     T_
                                TGTACAGA ACGTGC  GTTG
                                |||||||| ||||||  ||||
                                ACATGTCT TGCATG  CAAC
                                     _     TC
GAM933  KIAA1798  3'  TGTACAGATTAGTGTTTCTGTT 24334        CAC   ___
           G                     TGTACAGA   GTG   CTGTTG
                                |||||||   |||   ||||||
                                ACATGTCT   CAC   GACAAC
                                     AAT   AAA
GAM933  KIR3DS1   3'  TGTACATGCTGGTATCTGTTG  24303       GACAC  _
                                TGTACA    GTG CTGTTG
                                ||||||    ||| ||||||
                                ACATGT    CAT GACAAC
                                   ACGAC   A
GAM933  MGC15438  5'  TGTGGGACACACAGGCTTGTTG 24335     ACA     T__  _
                                TGT   GACACG   GCT GTTG
                                |||   ||||||   ||| ||||
                                ACA   CTGTGT   CGA CAAC
                                  CC_     GTC   A
GAM933  MGC15634  3'  ATACAGATGTGTGCTGTTG   24336       CAC
                                GTACAGA   GTGCTGTTG
                                |||||||   |||||||||
                                TATGTCT   CACGACAAC
                                   ACA
GAM933  MGC2477   5'  TGTGAGACAAGTACTGTTG   24337    AC    C
                                TGT  AGACA GTGCTGTTG
                                |||  ||||| |||||||||
                                ACA  TCTGT CATGACAAC
                                  C_    T
GAM933  MSTP028   3'  TGTAGACTTTGCTGTTG    24338    AC   ACG
                                TGT  AGAC   TGCTGTTG
                                |||  ||||   ||||||||
                                ACA  TCTG   ACGACAAC
                                  __    AA_
GAM933  NAV3      3'  TGCACAGATGTTTCGTGGTGTT 24339       CA___   C
           G                     TGTACAGA    CGTG TGTTG
                                ||||||||    |||| |||||
                                ACGTGTCT    GCAC ACAAC
                                     ACAAA   C
GAM933  PLAGL2    3'  TGTGTAAACGGTACCGTTG   24340    AC   AC
                                TGT  AGAC  GTGCTGTTG
                                |||  ||||  |||||||||
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                                ACA  TTTG  CATGGCAAC
                                  CA    C_
GAM933  PP1628    5'  TGTCAGGCAGGACGCTGTTG  24341     A   A  CG_
                                TGT CAG CA   TGCTGTTG
                                ||| ||| ||   ||||||||
                                ACA GTC GT   GCGACAAC
                                  _   C  CCT
GAM933  PRO2730   5'  TGTGACAGCTTTGCTGTTG   24342     _   ACACG
                                TGT ACAG     TGCTGTTG
                                ||| ||||     ||||||||
                                ACA TGTC     ACGACAAC
                                  C    GAA__
GAM933  SP2       3'  TGTGCAGGTGCTGTTA      24343     A   ACAC
                                TGT CAG    GTGCTGTTG
                                ||| |||    |||||||||
                                ACA GTC    CACGACAAT
                                  C  _____
GAM933  ZAK       3'  TGCAACATCTGCTGTTG     24344     ACA    CG
                                TGT   GACA  TGCTGTTG
                                |||   ||||  ||||||||
                                ACG   TTGT  ACGACAAC
                                  ____   AG
GAM933  ZNF294    3'  TGTACAGATGTGGTATT     24345        CAC   C
                                TGTACAGA   GTG TGTT
                                ||||||||   ||| ||||
                                ACATGTCT   CAC ATAA
                                     A__   C
GAM933  LOC144481 3'  TGTACAGGTGCTTACTGTTG  24346        ACACG
                                TGTACAG    TGCTGTTG
                                |||||||    ||||||||
                                ACATGTC    ATGACAAC
                                    CACGA
GAM933  LOC149372 5'  TGTACAAATGTGCCACCA    24347        CAC    TG
                                TGTACAGA   GTGC  TTG
                                ||||||||   ||||  |||
                                ACATGTTT   CACG  GGT
                                     A__    GT
GAM933  LOC149576 5'  TGTTTGGAACGGCTGTTG    24348     ACA  C   T
                                TGT   GA ACG GCTGTTG
                                |||   || ||| |||||||
                                ACA   CT TGC CGACAAC
                                  AAC  _   _
GAM933  LOC150139 3'  TGAACAGACACGGCCGT     24349     T       T
                                TG ACAGACACG GCTGT
                                || |||||||| |||||
                                AC TGTCTGTGC CGGCA
                                 T       _
GAM933  LOC150776 3'  TGTCACAGAGCGTGGCTGTTG  24350     _    CA   _
                                TGT ACAGA  CGTG CTGTTG
                                ||| |||||  |||| ||||||
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                                ACA TGTCT  GCAC GACAAC
                                  G    C_   C
GAM933  LOC199923 3'  GTACAGACATATGGGTTG    24351        CG  CT
                                GTACAGACA  TG  GTTG
                                |||||||||  ||  ||||
                                CATGTCTGT  AC  CAAC
                                     AT  C_
GAM933  LOC200339 3'  TGTACAGAAATACAATTG    24352       CAC    T
                                TGTACAGA   GTGC GTTG
                                ||||||||   |||| ||||
                                ACATGTCT   TATG TAAC
                                     T__    T
GAM933  LOC219401 3'  TGTACTGATGTACTATT     24353      A  CAC
                                TGTAC GA   GTGCTGTT
                                ||||| ||   ||||||||
                                ACATG CT   CATGATAA
                                   A  A__
GAM933  LOC219855 3'  TGCACAGAGAAGACTGTTG   24354        CACGT
                                TGTACAGA    GCTGTTG
                                ||||||||    |||||||
                                ACGTGTCT    TGACAAC
                                     CTTC_
GAM933  LOC254045 3'  TGTACAGGTGCTTACTGTTG  24346       ACACG
                                TGTACAG    TGCTGTTG
                                |||||||    ||||||||
                                ACATGTC    ATGACAAC
                                    CACGA
GAM933  LOC256055 3'  TGCATAGACACGTTGTTG    24355     C       GC
                                TGTA AGACACGT  TGTTG
                                |||| ||||||||  |||||
                                ACGT TCTGTGCA  ACAAC
                                  A       __
GAM934  BRCA1    3'  TAATACCTGCCTCAG      24358         CCTCT
                                TAATACCTGT    CTCAG
                                ||||||||||    |||||
                                ATTATGGACG    GAGTC
                                      _____
GAM934  BRCA1    3'  TAATACCTGCCTCAG      24358         CCTCT
                                TAATACCTGT    CTCAG
                                ||||||||||    |||||
                                ATTATGGACG    GAGTC
                                      _____
GAM934  BRCA1    3'  TAATACCTGCCTCAG      24358         CCTCT
                                TAATACCTGT    CTCAG
                                ||||||||||    |||||
                                ATTATGGACG    GAGTC
                                      _____
GAM934  BRCA1    3'  TAATACCTGCCTCAG      24358         CCTCT
                                TAATACCTGT    CTCAG
                                ||||||||||    |||||
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                                ATTATGGACG    GAGTC
                                          _____
GAM934  BRCA1   3' TAATACCTGCCTCAG     24358        CCTCT
                                TAATACCTGT    CTCAG
                                ||||||||||    |||||
                                ATTATGGACG    GAGTC
                                          _____
GAM934  BRCA1   3' TAATACCTGCCTCAG     24358        CCTCT
                                TAATACCTGT    CTCAG
                                ||||||||||    |||||
                                ATTATGGACG    GAGTC
                                          _____
GAM934  BRCA1   3' TAATACCTGCCTCAG     24358        CCTCT
                                TAATACCTGT    CTCAG
                                ||||||||||    |||||
                                ATTATGGACG    GAGTC
                                          _____
GAM934  BRCA1   3' TAATACCTGCCTCAG     24358        CCTCT
                                TAATACCTGT    CTCAG
                                ||||||||||    |||||
                                ATTATGGACG    GAGTC
                                          _____
GAM934  BRCA1   3' TAATACCTGCCTCAG     24358        CCTCT
                                TAATACCTGT    CTCAG
                                ||||||||||    |||||
                                ATTATGGACG    GAGTC
                                          _____
GAM934  BRCA1   3' TAATACCTGCCTCAG     24358        CCTCT
                                TAATACCTGT    CTCAG
                                ||||||||||    |||||
                                ATTATGGACG    GAGTC
                                          _____
GAM934  BRCA1   3' TAATACCTGCCTCAG     24358        CCTCT
                                TAATACCTGT    CTCAG
                                ||||||||||    |||||
                                ATTATGGACG    GAGTC
                                          _____
GAM934  BRCA1   3' TAATACCTGCCTCAG     24358        CCTCT
                                TAATACCTGT    CTCAG
                                ||||||||||    |||||
                                ATTATGGACG    GAGTC
                                          _____
GAM934  CALM1   3' ACACCTGTTTCACTCTAGA   24359         CC  T  _
                                ATACCTGT  TC CTC AGA
                                ||||||||  || ||| |||
                                TGTGGACA  AG GAG TCT
                                     A_  T   A
GAM934  CNGA1   3' TAATCATAGTATCTCTCAGA  24360      ACCT  CC
                                TAAT   GT  TCTCTCAGA
                                ||||   ||  |||||||||
                                ATTA   CA  AGAGAGTCT
                                  GTAT  T_
GAM934  DSCR1   3' TAATACCTATTTACCAGA    24361         CCTCT T
                                TAATACCTGT    C CAGA
                                ||||||||||    | ||||
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                                ATTATGGATA    G GTCT
                                      AAT__ _
GAM934  DTR     3'  TAATACCTTCTCCAG      24362        GTCC   T
                                TAATACCT   TCTC CAG
                                ||||||||   |||| |||
                                ATTATGGA   AGAG GTC
                                     _____   _
GAM934  FRK     3'  ATACCTATTTCTCAGA     24363        CCTC
                                ATACCTGT   TCTCAGA
                                ||||||||   |||||||
                                TATGGATA   AGAGTCT
                                     A___
GAM934  POP2    5'  TAATACTGTCCTCACATAG   24364      C      TCTC
                                TAATAC TGTCCTC   AG
                                |||||| |||||||   ||
                                ATTATG ACAGGAG   TC
                                   _     TGTA
GAM934  REG1A   5'  TAAAACCTCCTCTCAG     24365    T   GTCC
                                TAA ACCT   TCTCTCAG
                                ||| ||||   ||||||||
                                ATT TGGA   GGAGAGTC
                                  T  _____
GAM934  SIGLEC6 3'  TAACACCTTGTTCTCAGA    24366       _ CCTC
                                TAATACCT GT   TCTCAGA
                                |||||||| ||   |||||||
                                ATTGTGGA CA   AGAGTCT
                                     A _____
GAM934  SMTN    5'  CACCTGTCACCAGCTCAGA   24367       _ CT
                                TACCTGTC CT  CTCAGA
                                |||||||| ||  ||||||
                                GTGGACAG GG  GAGTCT
                                     T  TC
GAM934  SMTN    5'  CACCTGTCACCAGCTCAGA   24367       _ CT
                                TACCTGTC CT  CTCAGA
                                |||||||| ||  ||||||
                                GTGGACAG GG  GAGTCT
                                     T  TC
GAM934  SMTN    5'  CACCTGTCACCAGCTCAGA   24367       _ CT
                                TACCTGTC CT  CTCAGA
                                |||||||| ||  ||||||
                                GTGGACAG GG  GAGTCT
                                     T  TC
GAM934  ALS2CR3 3'  TAATGCCTGCCCCATTCAG   24368     A     T TC
                                TAAT CCTGTCC C  TCAG
                                |||| ||||||| |  ||||
                                ATTA GGACGGG G  AGTC
                                  C      _ TA
GAM934  ARAP3   3'  TACCTACCCTCTCAGA      24369       T  T
                                TACCTG CC CTCTCAGA
                                |||||| || ||||||||
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                                ATGGAT GG GAGAGTCT
                                    _ _
GAM934  CECR2     3'  ACAGGTGTTCTCTCTCAG    24370     CC   C
                                ATA  TGT CTCTCTCAG
                                |||  ||| |||||||||
                                TGT  ACA GAGAGAGTC
                                  CC   A
GAM934  CGI-85    3'  TAACTTCTGTCTCTCTCAGA  24371     AC    C
                                TAAT  CTGTC TCTCTCAGA
                                ||||  ||||| |||||||||
                                ATTG  GACAG AGAGAGTCT
                                  AA    _
GAM934  FLJ11320  3'  CCTGTCCCTGTCCTCAGA    24372       C__
                                CCTGTCCT   TCTCAGA
                                ||||||||   |||||||
                                GGACAGGG   GGAGTCT
                                     ACA
GAM934  FLJ21616  3'  AATACCTGGAAGCACTCTCTTG 24373       TC____    CA
          GA                    AATACCTG     CTCTCT  GA
                                ||||||||     ||||||  ||
                                TTATGGAC     GAGAGA  CT
                                     CTTCGT     AC
GAM934  MGC22014  3'  AATACCTGTTCATCTCAG    24374       CC  _
                                AATACCTGT  TC TCTCAG
                                |||||||||  || ||||||
                                TTATGGACA  AG AGAGTC
                                     __ T
GAM934  LOC132228 3'  CCTCTCCCCCTACTCAGA    24375     G     __
                                CCT TCCTCT  CTCAGA
                                |||  ||||||  ||||||
                                GGA AGGGGG  GAGTCT
                                  G     AT
GAM934  LOC145826 3'  TAATACCTTCTCTAG       24376       GTCC    C
                                TAATACCT    TCTCT AG
                                ||||||||    ||||| ||
                                ATTATGGA    AGAGA TC
                                     _____    _
GAM934  LOC151414 5'  TAATACCTGCTGGTCATCAGA  24377         CCTC  _
                                TAATACCTGT    TC TCAGA
                                ||||||||||    || |||||
                                ATTATGGACG    AG AGTCT
                                      ACC_  T
GAM934  LOC155411 3'  ATACCTACCTCTCAGA      24378       TCC
                                ATACCTG   TCTCTCAGA
                                |||||||   |||||||||
                                TATGGAT   GGAGAGTCT
                                     ____
GAM934  LOC157784 3'  ATATTTGTCCTCCTTTTCAGA  24379     CC      C__
                                ATA  TGTCCTCT   TCAGA
                                |||  ||||||||   |||||
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                                TAT  ACAGGAGG   AGTCT
                                  AA       AAA
GAM934  LOC222166 3'  CCTGGAGCCCCTCTCAGA    24380     T__
                                CCTG   CCTCTCTCAGA
                                ||||   ||||||||||
                                GGAC   GGGGAGAGTCT
                                  CTC
GAM934  LOC90906  5'  ATACTGCTGCTCTCTCAG    24381     C   C_
                                ATAC TGT  CTCTCTCAG
                                |||| |||  |||||||||
                                TATG ACG  GAGAGAGTC
                                  _  AC
GAM935  PRKRA     3'  TCATACTTAATAAAGGCCT   24384          T
                                TCATACTTAATA AGGCCT
                                |||||||||||| ||||||
                                AGTATGAATTAT TCCGGA
                                       T
GAM935  NFAT5     3'  TACTTAACATTGACCTTTAG   24385         A     _
                                TACTTAATAT GGCCTT AG
                                |||||||||| ||||||| ||
                                ATGAATTGTA CTGGAA TC
                                      A     A
GAM936  AIM1      3'  AGAAGATCAGCATTTTAGAAT  24388    T     A  CTA
                                AG AGATCA CA   TTTGGAAT
                                || |||||| ||   ||||||||
                                TC TCTAGT GT   AAATCTTA
                                 T     C  A__
GAM936  D10S170   3'  AAGTAGATTAACATTAAGGA   24389        C    CTATTT
                                AAGTAGAT AACA     GGA
                                |||||||| ||||     |||
                                TTCATCTA TTGT     CCT
                                     A    AATT__
GAM936  ZNF42     5'  AAGTGATCAACACAGGG     24390      A       TATTT
                                AAGT GATCAACAC    GG
                                |||| |||||||||    ||
                                TTCA CTAGTTGTG    CC
                                  _       TC___
GAM936  FLJ14824  3'  AAGTAGATTAGCCTGATTGGA  24391        CAACA  AT
                                AAGTAGAT    CT  TTGGA
                                ||||||||    ||  |||||
                                TTCATCTA    GA  AACCT
                                     ATCG_  CT
GAM936  KIAA0625  3'  AAGAGATCAACATTTCCAG    24392     T       CTA  TG
                                AAG AGATCAACA   TT  G
                                ||| |||||||||   ||  |
                                TTC TCTAGTTGT   AG  C
                                  _       AA_  GT
GAM936  KIAA1045  3'  TAGATCAGTACCTAGA      24393        ACAC
                                TAGATCA    TATTTGGA
                                |||||||    ||||||||
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                                ATCTAGT   ATGGATCT
                                   C___
GAM936  PRSC     3'  GTAGTATCTATTTGGAA     24394      _  AACAC
                                GTAG ATC    TATTTGGAA
                                |||| |||    |||||||||
                                CATC TAG    ATAAACCTT
                                  A  _____
GAM936  RIL      3'  GTAGATCCACGCGACCCGGA  24395       A  ACT
                                GTAGATC AC   ATTTGGA
                                ||||||| ||   |||||||
                                CATCTAG TG   TGGGCCT
                                   G  CGC
GAM936  SE57-1   3'  TAGAAGTACATTATTTGGAAT 24396     TCA   C
                                TAGA   ACA TATTTGGAAT
                                ||||   ||| ||||||||||
                                ATCT   TGT ATAAACCTTA
                                  TCA   A
GAM936  LOC133686 3'  AAGTAGATCAATAATTAGA   24397          CAC  T
                                AAGTAGATCAA   TA TTGGA
                                ||||||||||   || |||||
                                TTCATCTAGTT   AT AATCT
                                      ___  T
GAM936  LOC201516 3'  AAGTAGATAAATACTATAGGAA 24398        C  C    TT
          T                      AAGTAGAT AA ACTAT  GGAAT
                                ||||||||| || |||||  |||||
                                TTCATCTA TT TGATA  CCTTA
                                    T  A    T_
GAM936  LOC56851  3'  AAGAGATCAACGTCGG     24399     T      ACTAT
                                AAG AGATCAAC    TTGG
                                ||| ||||||||    ||||
                                TTC TCTAGTTG    AGCC
                                  _      C_____
GAM937  OSRF     3'  AGGGTTTTTAAAGCTTTGT   24402          _  G
                                AGGGTTTTTGAA CTT GT
                                |||||||||||| ||| ||
                                TCCCAAAAATTT GAA CA
                                      C   A
GAM937  ZFP106   3'  AGGGTTTGTGAATTTGGC    24403       T   C
                                AGGGTTT TGAA TTGGT
                                ||||||| |||| |||||
                                TCCCAAA ACTT AACCG
                                   C   A
GAM937  LOC164397 5'  AGAGCACTGGCTTGGTCTTG  24404      TT  AA
                                AGGGT  TTG  CTTGGTCTTG
                                |||||  |||  ||||||||||
                                TCTCG  GAC  GAACCAGAAC
                                  T_   C_
GAM937  LOC58525  5'  AGGGCTTTTGGGCTTGGCCCTG 24406         AA
                                AGGGTTTTTG  CTTGGTCTTG
                                ||||||||||  ||||||||||
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                                TCCCGAAAAC  GAACCGGGAC
                                     CC
GAM937  LOC58525  3'  GGGTCTTTGGGGTCTTTGCA  24405        AACTT    _
                                GGGTTTTTG    GGTCTT GCA
                                |||||||||    |||||| |||
                                CCCAGAAAC    CCAGAA CGT
                                     C____     A
GAM937  LOC90906  3'  GGGTTTTCTGGGCTTGGTCTTG 24407       GAA_
                                GGGTTTTT   CTTGGTCTTG
                                ||||||||   ||||||||||
                                CCCAAAAG   GAACCAGAAC
                                     ACCC
GAM937  LOC91266  5'  AGGGTTTTTGGCTTTGT    24408         AA  G
                                AGGGTTTTTG  CTT GT
                                ||||||||||  ||| ||
                                TCCCAAAAAC  GAA CA
                                     C_  A
GAM938  FLJ30046  3'  GAGTAAATTGAACAAGTTAC  24411       C    __
                                GAGTAAAT GAACGA  TAC
                                |||||||| ||||||  |||
                                CTCATTTA CTTGTT  ATG
                                     A     CA
GAM938  FUSIP1    3'  GAGTAAATGAATGATAC    24412       C  C
                                GAGTAAAT GAA GATAC
                                |||||||| ||| |||||
                                CTCATTTA CTT CTATG
                                     _  A
GAM938  LOC120856 3'  GAGTAAACTGAACGCTCT   24413       C    ATA
                                GAGTAAAT GAACG  CT
                                |||||||| |||||  ||
                                CTCATTTG CTTGC  GA
                                     A    GA_
GAM939  ATRN      3'  CAAGGCATAGGACTAACA    24416        TACATT
                                CAAGGCGTA    CTAACA
                                |||||||||    ||||||
                                GTTCCGTAT    GATTGT
                                     CCT___
GAM939  CYR61     3'  CCCCAAAAGCTACATT     24417       C  A
                                TCCCAAGG GT TACATT
                                |||||||| || ||||||
                                GGGGTTTT CG ATGTAA
                                     _ _
GAM939  DGAT2     3'  CAAGGCATATACAAAAGTCTGA 24418          T___  A
          CA                    CAAGGCGTATACA   TCT ACA
                                |||||||||||||   ||| |||
                                GTTCCGTATATGT   AGA TGT
                                      TTTC  C
GAM939  FANCC     3'  TCCCAAGATGTGTACAGCTC  24419       GC  A  _
                                TCCCAAG  GT TACA TTC
                                |||||||  || |||| |||
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                                AGGGTTC  CA ATGT GAG
                                    TA  C   C
GAM939  TDE1     5'  TCCTGAGGCTGCTTTCTAACA  24420     CA   GTATACA
                                TCC  AGGC      TTCTAACA
                                |||  ||||      ||||||||
                                AGG  TCCG      AAGATTGT
                                  AC    ACGA___
GAM939  ZNF146   3'  TCCCAAGGTCATATGCATT   24421        _    A
                                TCCCAAGG CGTAT CATT
                                |||||||| ||||| ||||
                                AGGGTTCC GTATA GTAA
                                    A    C
GAM939  C20orf18 3'  TCCCTGAGCTACATTCTAACA  24422     AA   GTA
                                TCCC  GGC   TACATTCTAACA
                                ||||  |||   ||||||||||||
                                AGGG  TCG   ATGTAAGATTGT
                                  AC  ___
GAM939  C20orf18 3'  TCCCTGAGCTACATTCTAACA  24422     AA   GTA
                                TCCC  GGC   TACATTCTAACA
                                ||||  |||   ||||||||||||
                                AGGG  TCG   ATGTAAGATTGT
                                  AC  ___
GAM939  CDIPT    3'  CATGGAGTTTACATTCTA    24423    A  C  A
                                CA GG GT TACATTCTA
                                || || || |||||||||
                                GT CC CA ATGTAAGAT
                                 A  T  A
GAM939  COQ7     3'  CCACAGGACATTCTAA      24424     _  CGTAT
                                CCA AGG     ACATTCTAA
                                ||| |||     |||||||||
                                GGT TCC     TGTAAGATT
                                  G  _____
GAM939  DKFZP434B205 3'  TCCTAAGGCGTAACTGCTA   24425     C       T  ATT
                                TCC AAGGCGTA AC   CTA
                                ||| |||||||| ||   |||
                                AGG TTCCGCAT TG   GAT
                                  A       _  AC_
GAM939  FLJ12363 3'  CAAGGCACACATTCTGACA   24426       GT       A
                                CAAGGC  ATACATTCT ACA
                                ||||||  ||||||||| |||
                                GTTCCG  TGTGTAAGA TGT
                                   __        C
GAM939  FLJ20073 3'  TCCCAGACATTCTAA       24427      A    ATACAT
                                TCCCA GGCGT     TCTAA
                                ||||| |||||     |||||
                                AGGGT CTGTA     AGATT
                                   _    _______
GAM939  KIAA1058 3'  AGGCCATCTATTCTAACA    24428      G   AC
                                AGGC TAT  ATTCTAACA
                                |||| |||  |||||||||
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                                TCCG GTA  TAAGATTGT
                                  _  GA
GAM939  KIAA1464  3'  TCCCAAGGCAGAATTCTGACA  24429         TATAC    A
                                TCCCAAGGCG    ATTCT ACA
                                ||||||||||    ||||| |||
                                AGGGTTCCGT    TAAGA TGT
                                      CT___    C
GAM939  KIAA1912  3'  TCCAGTACACACATTCTAA   24430    CAA  CG
                                TCC   GG  TATACATTCTAA
                                |||   ||  ||||||||||||
                                AGG   TC  GTGTGTAAGATT
                                  ___  AT
GAM939  SBBI31    3'  AAGAGCACCATTCTAA     24431     C    A
                                AAGG GTAT CATTCTAA
                                |||| |||| ||||||||
                                TTCT CGTG GTAAGATT

                                  _   _
GAM939  ST7L      3'  TCTCCATACCTTACATTCTGAC 24432    _  AG  GTA      A
            A                    TC CCA  GC   TACATTCT ACA
                                || |||  ||   |||||||| |||
                                AG GGT  TG   ATGTAAGA TGT
                                 A  A_  GA_      C
GAM939  ST7L      3'  TCTCCATACCTTACATTCTGAC 24432    _  AG  GTA      A
            A                    TC CCA  GC   TACATTCT ACA
                                || |||  ||   |||||||| |||
                                AG GGT  TG   ATGTAAGA TGT
                                 A  A_  GA_      C
GAM939  LOC160391 3'  CCTAGGCGTATGCCCAA    24433    A      ACAT
                                CC AGGCGTAT    TCTAA
                                || ||||||||    |||||
                                GG TCCGCATA    GGGTT
                                 A       C___
GAM939  LOC200609 3'  TCCTGAGGCCCATTCTAA    24434     CA   GTATA
                                TCC  AGGC    CATTCTAA
                                |||  ||||    ||||||||
                                AGG  TCCG    GTAAGATT
                                  AC   G____
GAM939  LOC92267  3'  CAAGGCACACATTCTGACA   24426       GT       A
                                CAAGGC  ATACATTCT ACA
                                ||||||  ||||||||| |||
                                GTTCCG  TGTGTAAGA TGT
                                    __        C
GAM940  ABCC1     5'  GGCGCAGGGAGCCGGGG     24437    _       AGCA
                                GG GCAGGGAGC    GGGG
                                || |||||||||    ||||
                                CC CGTCCCTCG    CCCC
                                 G        G___
GAM940  ABCC1     5'  GGCGCAGGGAGCCGGGG     24437    _       AGCA
                                GG GCAGGGAGC    GGGG
                                || |||||||||    ||||
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                                CC CGTCCCTCG    CCCC
                                 G        G___
GAM940  ABCC1    5'  GGCGCAGGGAGCCGGGG     24437    _       AGCA
                                GG GCAGGGAGC    GGGG
                                || |||||||||    ||||
                                CC CGTCCCTCG    CCCC
                                 G        G___
GAM940  ACP2     3'  GGGCTGGGGAGCAGCAACAG   24438      A_         G
                                GGGC  GGGAGCAGCAG GG
                                ||||  |||||||||||| ||
                                CCCG  CCCTCGTCGTT TC
                                  AC          G
GAM940  ADAMTS4  3'  AGGGCAGAGAGGAGGGG     24439          CAGC
                                AGGGCAGGGAG    AGGGG
                                ||||||||||    |||||
                                TCCCGTCTCTC    TCCCC
                                      C___
GAM940  ADCY9    3'  CAGTGCAGGGAGCGCGG     24440     G       A  A
                                CAG GCAGGGAGC GC GG
                                ||| ||||||||| || ||
                                GTC CGTCCCTCG CG CC
                                  A       _ _
GAM940  ADRA2A   5'  AGGGAGGGGGCCGCAGGG    24441     C    A  A
                                AGGG AGGG GC GCAGGG
                                |||| |||| || ||||||
                                TCCC TCCC CG CGTCCC
                                  _    C  G
GAM940  ADRA2B   3'  GGGCAGGGAGCAGAAAG     24442           C
                                GGGCAGGGAGCAG AGGG
                                |||||||||||| ||||
                                CCCGTCCCTCGTC TTTC

                                      _
GAM940  ALPPL2   3'  GGAGGTGGGGAGCAGGGG    24443    A   CA      GCA
                                C GGG  GGGAGCA   GGGG
                                | |||  |||||||   ||||
                                C TCC  CCCTCGT   CCCC
                                 C   AC      ___
GAM940  ANGPT4   3'  AGGCAGGGAGCCCCTGAAGGGG 24444          AGC___
           G                     GGGCAGGGAGC     AGGGGG
                                ||||||||||      ||||||
                                TCCGTCCCTCG     TCCCCC
                                      GGGACT
GAM940  AQP3     3'  CAGGGCAGCGGAGTGGGG    24445        _   CAGCA
                                CAGGGCAG GGAG    GGGG
                                |||||||| ||||    ||||
                                GTCCCGTC CCTC    CCCC
                                    G   A____
GAM940  AQP6     5'  CAGGGCAGCGGGGCTCATGGG  24446        _  A  AG  G
                                CAGGGCAG GG GC  CA GGG
                                |||||||| || ||  || |||
```

```
                                GTCCCGTC CC CG  GT CCC
                                    G  C  A_  A
GAM940  AR      5'  CAGGGTGGGGGGAGGCGGGG  24447     CA__    CA  A
                                CAGGG   GGGAG  GC GGGG
                                |||||   |||||  || ||||
                                GTCCC   CCCTC  CG CCCC
                                  ACCC    __  _
GAM940  ARHG    3'  CAAGGCACAACTGGTGGGGG  24448     A    A___
                                CAGGG GCAGC   GGGGG
                                ||||| |||||   |||||
                                GTTCC TGTTG   CCCCC
                                  G    ACCA
GAM940  ARHGAP6  3'  GGGCTCGGGGCAGGGGG    24449     A_  AGCA
                                GGGC  GGG   GCAGGGGG
                                ||||  |||   ||||||||
                                CCCG  CCC   CGTCCCCC
                                  AG  _____
GAM940  ARHGAP6  3'  GGGCTCGGGGCAGGGGG    24449     A_  AGCA
                                GGGC  GGG   GCAGGGGG
                                ||||  |||   ||||||||
                                CCCG  CCC   CGTCCCCC
                                  AG  _____
GAM940  ASIC4    3'  GGGTGGGGCTGGTGCAGGGGG  24451    CA  A  A___
                                GGG  GGG GC   GCAGGGGG
                                |||  ||| ||   ||||||||
                                CCC  CCC CG   CGTCCCCC
                                  A_  _  ACCA
GAM940  ASIC4    5'  CAGGGTGGGGGCCCGAGGTGGG 24450     CA  A  AGC  _
                                CAGGG  GGG GC  AGG GGG
                                |||||  ||| ||  ||| |||
                                GTCCC  CCC CG  TCC CCC
                                  AC  _  GGC  A
GAM940  ATP11A   3'  CAGGGCAGGGTGGCCCTGGGG  24452       A_  AGCA
                                CAGGGCAGGG  GC   GGGG
                                ||||||||||  ||   ||||
                                GTCCCGTCCC  CG   CCCC
                                     AC  GGA_
GAM940  AVP     5'  GGGCAGGGGACAGCCAGG    24453       AG   A
                                GGGCAGGG  CAGC GGG
                                ||||||||  |||| |||
                                CCCGTCCC  GTCG TCC
                                    CT   G
GAM940  B3GAT1   3'  CAGGGACAGGGAGCCAGGG   24454     _     AG
                                CAGGG CAGGGAGC  CAGGG
                                ||||| ||||||||  |||||
                                GTCCC GTCCCTCG  GTCCC
                                  T      __
GAM940  B3GAT1   3'  CAGGGACAGGGAGCCAGGG   24454     _     AG
                                CAGGG CAGGGAGC  CAGGG
                                ||||| ||||||||  |||||
```

```
                                GTCCC GTCCCTCG  GTCCC
                                  T      __
GAM940  BAT2    3'  GGGTAGGGGGCAAGAGG     24455     C    AGCA
                                GGG AGGG    GCAGGGGG
                                ||| ||||    ||||||||
                                CCC TCCC    CGTTCTCC
                                  A   C___
GAM940  BAT2    3'  GGGTAGGGGGCAAGAGG     24455     C    AGCA
                                GGG AGGG    GCAGGGGG
                                ||| ||||    ||||||||
                                CCC TCCC    CGTTCTCC
                                  A   C___
GAM940  BCL9    3'  AGGGTCACCAGCGGGGGG     24456      _ GGGAG    A
                                AGGG CA     CAGC GGGGG
                                |||| ||     |||| |||||
                                TCCC GT     GTCG CCCCC
                                  A  G_____    C
GAM940  BDP1    5'  GGAGGCAGGGGGCCCGGGG    24457    A       A  AGCA
                                C GGGCAGGG GC    GGGG
                                | ||||||||  ||    ||||
                                C TCCGTCCC CG    CCCC
                                 C       C  GG__
GAM940  BMPR2   5'  CAGGGTGCGGAGGGCGGGG    24458       CAG    CA  A
                                CAGGG   GGAG  GC GGGG
                                |||||   ||||  ||  ||||
                                GTCCC   CCTC  CG CCCC
                                   ACG    C_  _
GAM940  BST2    3'  CAGGGTGGGAGACAAGAGGGGG 24459       CA     _   C
                                CAGGG  GGGAG CAG AGGGGG
                                |||||  |||||  |||  ||||||
                                GTCCC  CCCTC GTT TCCCCC
                                   A_     T   C
GAM940  CALB2   3'  GGGCAGGGGTGGGTGCAGGGGG 24460         AGCA__
                                GGGCAGGG     GCAGGGGG
                                ||||||||     ||||||||
                                CCCGTCCC     CGTCCCCC
                                     CACCCA
GAM940  CCND3   5'  CAGGGCGGGAGTGCGGG     24461       A    CA  A
                                CAGGGC GGGAG  GC GGG
                                ||||||  |||||  ||  |||
                                GTCCCG CCCTC  CG CCC
                                   _    A_  _
GAM940  CD5     3'  GGGCAGGGAAAGGGG       24462          CAGC
                                GGGCAGGGAG    AGGGG
                                ||||||||||    |||||
                                CCCGTCCCTT    TCCCC
                                      _____
GAM940  CD5L    3'  AGGCGGGGCCAGGGG       24463      A   A  AG
                                GGGC GGG GC  CAGGGG
                                ||||  |||  ||  ||||||
```

```
                                TCCG CCC CG  GTCCCC
                                  _  _ __
GAM940  CD7     3'  GGGCAGGGAAGGTGCTGGGGG  24464         CA_  A
                                GGGCAGGGAG  GC GGGGG
                                ||||||||||  || |||||
                                CCCGTCCCTT  CG CCCCC
                                     CCA  A
GAM940  CDKN1A  3'  GGGCAGGGGGCGGCCAGGG  24465        A  A  A
                                GGGCAGGG GC GC GGGG
                                |||||||| || || ||||
                                CCCGTCCC CG CG TCCC
                                    C  C  G
GAM940  CDYL    3'  GGGCAGGGAGGCGAGG     24466         CA  A
                                GGGCAGGGAG  GC GGGG
                                ||||||||||  || ||||
                                CCCGTCCCTC  CG CTCC
                                  __  _
GAM940  CFL1    3'  AGGCAGGGGGCCAGAAGGGG  24467        A  _  C
                                GGGCAGGG GC AG AGGGG
                                |||||||| || || |||||
                                TCCGTCCC CG TC TCCCC
                                    C  G  T
GAM940  CGTHBA  3'  GGGGAGGGGGCCACAGGG   24468    C   A  A
                                GGG AGGG GC GCAGGG
                                ||| |||| || ||||||
                                CCC TCCC CG TGTCCC
                                  C   C  G
GAM940  CHRNE   3'  CAGGGTGGGGAAGAAAGGGG  24469     CA   C  C
                                CAGGG  GGGAG AG AGGGG
                                |||||  ||||| || |||||
                                GTCCC  CCCTT TT TCCCC
                                   AC    C  _
GAM940  CKMT1   3'  GGAGGCAGGGGATGCGGGGG  24470   A      AGCA  A
                                C GGGCAGGG   GC GGGGG
                                | ||||||||   || |||||
                                C TCCGTCCC   CG CCCCC
                                 C       CTA_  _
GAM940  CLCN7   3'  CAGGGCAGGGCAGCCCTCGGGG 24471          _  AGCA
                                CAGGGCAGGG AGC   GGGG
                                |||||||||| |||   ||||
                                GTCCCGTCCC TCG   CCCC
                                     G  GGAG
GAM940  CLN2    3'  AGAGGTAGGCACAGGGGG   24472     CAG  A  G
                                AGGG  GG GCA CAGGGGG
                                ||||  || ||| |||||||
                                TCTC  TC CGT GTCCCCC
                                  CA_  _  _
GAM940  CLN6    3'  GGAGTGGGAGCAGGGGG    24473    CA      CA
                                GGG  GGGAGCAG  GGGG
                                |||  ||||||||  ||||
```

```
                                CCT  CCCTCGTC  CCCC
                                  CA       __
GAM940  CNTFR    3'  CAGGGCAGAGGGGAGGGG    24474          AGCAGC
                                CAGGGCAGGG     AGGGG
                                ||||||||||     |||||
                                GTCCCGTCTC     TCCCC
                                     CCC___
GAM940  COL5A3   3'  GGGGAGGTGAGGGGCAGGGGG  24475     C  _  CA
                                GGG AGG GAG  GCAGGGGG
                                ||| ||| |||  ||||||||
                                CCC TCC CTC  CGTCCCCC
                                  C   A   CC
GAM940  COL6A1   3'  CAGGGCAGGAGAGCCCGGGG   24476         _   AGCA
                                CAGGGCAGG GAGC    GGGG
                                ||||||||| ||||    ||||
                                GTCCCGTCC CTCG    CCCC
                                     T    GG__
GAM940  CPSF4    3'  CAGGGCAGGGAGGGAG      24477           CAGCA
                                CAGGGCAGGGAG    GGGG
                                ||||||||||||    ||||
                                GTCCCGTCCCTC    CCTC
                                      _____
GAM940  CRABP2   3'  CAGGGCGGTGAGCATGG     24478       A _    GCA
                                CAGGGC GG GAGCA   GG
                                |||||| || |||||   ||
                                GTCCCG CC CTCGT   CC
                                   _ A    A__
GAM940  CSK      5'  AGGCAGAGGCAGGGG       24479         AGCA
                                GGGCAGGG    GCAGGGG
                                ||||||||    |||||||
                                TCCGTCTC    CGTCCCC
                                     ____
GAM940  CST3     3'  CAGGGGTGGGAATACAGGGGG  24480      CA    CA
                                CAGGG  GGGAG  GCAGGGGG
                                |||||  |||||  ||||||||
                                GTCCC  CCCTT  TGTCCCCC
                                   CA    A_
GAM940  CYP8B1   3'  AGGCAGAACAGAGGTAGGGGG  24482       GA   C___
                                GGGCAGG  GCAG    AGGGGG
                                |||||||  ||||    ||||||
                                TCCGTCT  TGTC    TCCCCC
                                   __    TCCA
GAM940  CYP8B1   3'  CAGAGGTAGGGGGTGCCACAGG 24481     _ C    A__  A
                                CAG GG AGGG   GC GCAGG
                                ||| || ||||   || |||||
                                GTC CC TCCC   CG TGTCC
                                  T  A    CCA  G
GAM940  DAXX     3'  GGAGGCAGGGAGAAGGGG    24483    A       CAGC
                                C GGGCAGGGAG    AGGGG
                                | ||||||||||    |||||
```

```
                                C TCCGTCCCTC    TCCCC
                                 C        T___
GAM940  DDAH2    5'  GGGCAGGGGCGCGACGG     24484        A  A  A  G
                                GGGCAGGG GC GC GG GG
                                |||||||| || || || ||
                                CCCGTCCC CG CG CT CC
                                    _ _ _ G
GAM940  DDX11    3'  CAGGATAGGGAGCAGGG     24486     GC      GCA
                                CAGG  AGGGAGCA  GGG
                                ||||  ||||||||  |||
                                GTCC  TCCCTCGT  CCC
                                  TA      ___
GAM940  DDX11    3'  CAGGACAGGGGGCCGGG     24485         A  AGCA
                                CAGGGCAGGG GC   GGG
                                |||||||||| ||   |||
                                GTCCTGTCCC CG   CCC
                                     C  G___
GAM940  DDX11    3'  CAGGATAGGGAGCAGGG     24486     GC      GCA
                                CAGG  AGGGAGCA  GGG
                                ||||  ||||||||  |||
                                GTCC  TCCCTCGT  CCC
                                  TA      ___
GAM940  DIA1     3'  CAGGGCGTGGGGTGCGCGGGGG 24487       A__  A  A  A
                                CAGGGC  GGG GC GC GGGGG
                                ||||||  ||| || || |||||
                                GTCCCG  CCC CG CG CCCCC
                                   CAC  A _ _
GAM940  DLEC1    3'  CAGGGCAGGAGGCATGTTGGG  24488        GA  GCAG
                                CAGGGCAGG  GCA   GGG
                                |||||||||  |||   |||
                                GTCCCGTCC  CGT   CCC
                                     TC  ACAA
GAM940  DLEC1    3'  CAGGGCAGGAGGCATGTTGGG  24488        GA  GCAG
                                CAGGGCAGG  GCA   GGG
                                |||||||||  |||   |||
                                GTCCCGTCC  CGT   CCC
                                     TC  ACAA
GAM940  DNAI2    5'  GGGCAGGAAGCAAGGGG     24489          GC
                                GGGCAGGGAGCA  AGGGG
                                ||||||||||||  |||||
                                CCCGTCCTTCGT  TCCCC
                                      __
GAM940  DPH2L2   3'  GGTGCAGGGAGCACTAAAGG  24490    _       GC
                                GG GCAGGGAGCA  AGGGG
                                || ||||||||||  |||||
                                CC CGTCCCTCGT  TTTCC
                                 A        GA
GAM940  DRIL1    5'  CAGTGCAGGGTGGCAGGGGG  24491    G     AGCA
                                CAG GCAGGG   GCAGGGGG
                                ||| ||||||   ||||||||
```

```
                                GTC CGTCCC   CGTCCCCC
                                  A     AC__
GAM940  DUSP2   3'  GGGCAGGCAGGCAGAGGGG   24492       G _  C
                                GGGCAGG AG CAG AGGGG
                                ||||||| || ||| |||||
                                CCCGTCC TC GTC TCCCC
                                    G  C  _
GAM940  DVL3    3'  TGAGGCAGCAGGCAGGGGG   24493   C  G   _
                                G AGG AGCAG CAGGGGG
                                | ||| ||||| |||||||
                                A TCC TCGTC GTCCCCC
                                 C  G   C
GAM940  E2F1    3'  CAGGGACAGGGGGCTCCAGGG  24494      _    A  AG
                                CAGGG CAGGG GC  CAGGG
                                ||||| ||||| ||  |||||
                                GTCCC GTCCC CG  GTCCC
                                   T    C  AG
GAM940  ECEL1   3'  AAGTGAGGGGCAGCAGGGGG  24495    GC   A
                                AGG  AGGG GCAGCAGGGGG
                                |||  |||| ||||||||||
                                TTC  TCCC CGTCGTCCCCC
                                  AC   _
GAM940  EDAR    3'  CAAGGCAGGGGGAAGGGGG   24496         AGCAGC
                                CAGGGCAGGG     AGGGGG
                                ||||||||||     ||||||
                                GTTCCGTCCC     TCCCCC
                                      CCT___
GAM940  EFNB1   3'  GGGCAGGGAAAAAGGGGG    24497         C  C
                                GGGCAGGGAG AG AGGGGG
                                |||||||||| || ||||||
                                CCCGTCCCTT TT TCCCCC
                                      _ _
GAM940  EGFL4   5'  CAGTCCCGGGAGCAGCGGGGGG 24498    GGCA       A
                                CAG   GGGAGCAGC GGGGG
                                |||   ||||||||| |||||
                                GTC   CCCTCGTCG CCCCC
                                  AGGG       C
GAM940  EGR3    3'  AGGGCAGGGGGCAAACTCAGG  24499        A   ___
                                AGGGCAGGG GCAG   CAGG
                                ||||||||| ||||   ||||
                                TCCCGTCCC CGTT   GTCC
                                    C   TGA
GAM940  FCGR2A  3'  CAGGACAGGGAGCTTTGGG   24500          AGCAG
                                CAGGGCAGGGAGC    GGG
                                ||||||||||||    |||
                                GTCCTGTCCCTCG    CCC
                                     AAA__
GAM940  FGFR4   3'  GGGCAGCAGCAGCAGGGGG   24501      G G
                                GGGCA G AGCAGCAGGGGG
                                ||||| | ||||||||||||
```

```
                                CCCGT C TCGTCGTCCCCC
                                   _ G
GAM940  FGFR4   3'  GGGCAGCAGCAGCAGGGGG   24501      G G
                                GGGCA G AGCAGCAGGGGG
                                ||||| | ||||||||||||
                                CCCGT C TCGTCGTCCCCC
                                   _ G
GAM940  FS      5'  CAGGGCAGGCAGCGGGG    24502        GGA    A
                                CAGGGCAG   GCAGC GGGG
                                ||||||||   ||||| ||||
                                GTCCCGTC   CGTCG CCCC
                                   ____    _
GAM940  FXYD7   5'  GGGCCGGAGCAGGGGG     24503     AG      CA
                                GGGC  GGAGCAG  GGGG
                                ||||  |||||||  ||||
                                CCCG  CCTCGTC  CCCC
                                  G_     __
GAM940  G6PD    3'  GGACAGGGGACATCCAGGGGG 24504        AG  G_
                                GGGCAGGG  CA  CAGGGGG
                                ||||||||  ||  |||||||
                                CCTGTCCC  GT  GTCCCCC
                                    CT  AG
GAM940  GAD1    5'  CAGAGTGGGGAGGCGGGG   24505      CA    CA  A
                                CAGGG  GGGAG  GC GGGG
                                |||||  |||||  || ||||
                                GTCTC  CCCTC  CG CCCC
                                   AC    __ _
GAM940  GATA4   3'  AAGGCCGGCAGCAGGGG    24506      AGGGA
                                AGGGC    GCAGCAGGGG
                                |||||    ||||||||||
                                TTCCG    CGTCGTCCCC
                                   GC___
GAM940  GCK     3'  GGGCAGAGGCTTGGGGG     24507        A  AGCA
                                GGGCAGGG GC    GGGGG
                                |||||||| ||    |||||
                                CCCGTCTC CG    CCCCC
                                    _  AA__
GAM940  GCK     3'  GGGCAGAGGCTTGGGGG     24507        A  AGCA
                                GGGCAGGG GC    GGGGG
                                |||||||| ||    |||||
                                CCCGTCTC CG    CCCCC
                                    _  AA__
GAM940  GCK     3'  GGGCAGAGGCTTGGGGG     24507        A  AGCA
                                GGGCAGGG GC    GGGGG
                                |||||||| ||    |||||
                                CCCGTCTC CG    CCCCC
                                    _  AA__
GAM940  GJA4    3'  GGGCAGGGGGCATCCCAGG   24508        A   G__
                                GGGCAGGG GCA   CAGG
                                |||||||| |||   ||||
```

```
                                CCCGTCCC CGT   GTCC
                                     C   AGG
GAM940  GNB2     5'  CAGGGTTGGGGGCGGCTGGGGG 24509      CA   A  A  A
                                CAGGG  GGG GC GC GGGGG
                                ||||||  ||| || || |||||
                                GTCCC  CCC CG CG CCCCC
                                   AA   C  C  A
GAM940  GPC1     3'  GGTGCAGGGAGCTGGGGG    24510    _       AGCA
                                GG GCAGGGAGC    GGGGG
                                || |||||||||    |||||
                                CC CGTCCCTCG    CCCCC
                                 A        A___
GAM940  GPRK6    3'  GAGCCCAGGGCAGCAGGGGG   24511     A_   A
                                GGGC  GGG GCAGCAGGGGG
                                ||||  ||| ||||||||||
                                CTCG  TCC CGTCGTCCCCC
                                   GG   _
GAM940  GRM4     5'  CAGGGCAGCTTCAGCAGCAGGG 24512        GG__
              GG                   CAGGGCAG    AGCAGCAGGGGG
                                |||||||||    ||||||||||||
                                GTCCCGTC    TCGTCGTCCCCC
                                     GAAG
GAM940  GUCY1B3  5'  CAGAGGCGGCAGCGGCGGGGGG 24513     _   A  G   A  A
                                CAG GGC GG AGC GC GGGGG
                                ||| ||| || ||| || |||||
                                GTC CCG CC TCG CG CCCCC
                                  T   _  G   C  C
GAM940  GUCY2D   3'  GGACAGGGAGCAGGG       24514           GCA
                                GGGCAGGGAGCA   GGG
                                ||||||||||||   |||
                                CCTGTCCCTCGT   CCC
                                          ____
GAM940  HCN2     3'  GGGCAGGGGCGATGGGGG    24515         A  AGCA
                                GGGCAGGG GC    GGGGG
                                ||||||||  ||    |||||
                                CCCGTCCC CG    CCCCC
                                     _  CTA_
GAM940  HD       3'  GGGTGGGGAGCAGCAACAG   24516     CA         G
                                GGG  GGGAGCAGCAG GG
                                |||  ||||||||||| ||
                                CCC  CCCTCGTCGTT TC
                                  AC          G
GAM940  HDAC5    3'  AAGGTGGGGAGCAGACCTGG   24517      CA       _ AG
                                AGGG  GGGAGCAG C  GG
                                ||||  |||||||| |  ||
                                TTCC  CCCTCGTC G  CC
                                  AC       T GA
GAM940  HDAC6    3'  AGGCAATGGGCAGGGG      24518       _  AGCA
                                GGGCAG GG    GCAGGGG
                                ||||||  ||    |||||||
```

```
                                TCCGTT CC    CGTCCCC
                                   A _____
GAM940  HIP12    3'  GGGGGGAGCAGGAGGG      24519     CA       C
                                GGG  GGGAGCAG AGGG
                                |||  |||||||| ||||
                                CCC  CCCTCGTC TCCC
                                  __       C
GAM940  HMGA1    3'  CAGGGCAGTGGAGTAGGG    24520         _   CAGC
                                CAGGGCAG GGAG    AGGG
                                |||||||| ||||    ||||
                                GTCCCGTC CCTC    TCCC
                                     A    A___
GAM940  HOXD4    3'  GGGCAGGGATGCAGTCAG    24521          _   _
                                GGGCAGGGA GCAG CAG
                                ||||||||| |||| |||
                                CCCGTCCCT CGTC GTC
                                      A    A
GAM940  HPCA     3'  CAGGGGGGGCGGTTGGGGG   24522      CA   A  AGCA
                                CAGGG  GGG GC    GGGGG
                                |||||  ||| ||    |||||
                                GTCCC  CCC CG    CCCCC
                                   __  _  CCAA
GAM940  HPCAL1   5'  CAGGGAGGGAGCAAGG      24523      C       GC
                                CAGGG AGGGAGCA  AGG
                                ||||| ||||||||  |||
                                GTCCC TCCCTCGT  TCC
                                   _       __
GAM940  HTR6     3'  GGAGATGGCAGCAGGGGG    24524    C   GA
                                GG AGG  GCAGCAGGGGG
                                || |||  ||||||||||
                                CC TCT  CGTCGTCCCCC
                                  _  AC
GAM940  HTRA3    3'  AGGGCAGAGGGAAGCTGGGG  24525         AGC   A
                                AGGGCAGGG   AGC GGGG
                                |||||||||   ||| ||||
                                TCCCGTCTC   TCG CCCC
                                      CCT   A
GAM940  HYAL2    3'  AGGGCAAGGGAGTAGGG     24526       _    CAGC
                                AGGGCA GGGAG    AGGG
                                ||||||| |||||    ||||
                                TCCCGT CCCTC    TCCC
                                   T    A___
GAM940  HYAL2    3'  AGGGCAAGGGAGTAGGG     24526       _    CAGC
                                AGGGCA GGGAG    AGGG
                                ||||||| |||||    ||||
                                TCCCGT CCCTC    TCCC
                                   T    A___
GAM940  IFI27    3'  CAGGGCGAGGGGCAGGG     24527       _   AGCA
                                CAGGGC AGGG    GCAGGG
                                |||||| ||||    ||||||
```

```
                                GTCCCG TCCC    CGTCCC
                                   C   ____
GAM940  IL11     5'  CAGGGCAGGGGGCAGGG     24529          AGCA
                                CAGGGCAGGG    GCAGGG
                                ||||||||||    ||||||
                                GTCCCGTCCC    CGTCCC
                                     C___
GAM940  IL11     5'  GGGCAGGGAGCCGGGGG     24528          AGCA
                                GGGCAGGGAGC    GGGGG
                                ||||||||||    |||||
                                CCCGTCCCTCG    CCCCC
                                      G___
GAM940  IL1R1    3'  CAGGGCAGGGAGGTGGTCTGGG 24530           CAGCAG_
                                CAGGGCAGGGAG      GGG
                                ||||||||||||      |||
                                GTCCCGTCCCTC      CCC
                                      CACCAGA
GAM940  IL27     5'  CAGGGCAGGGGCGGG       24531          A  AGCA
                                CAGGGCAGGG GC    GGG
                                |||||||||| ||    |||
                                GTCCCGTCCC CG    CCC
                                     _ _____
GAM940  ITGB4    5'  AGGGCGGGCGCGGGGG      24532       A   A  AGCA
                                AGGGC GGG GC    GGGGG
                                ||||| ||| ||    |||||
                                TCCCG CCC CG    CCCCC
                                   _  G _____
GAM940  ITPR1    5'  CAGGGCGAGGAGAGGGG     24533       AG    CAGC
                                CAGGGC  GGAG    AGGGG
                                ||||||  ||||    |||||
                                GTCCCG  CCTC    TCCCC
                                   CT    ____
GAM940  JUNB     3'  AGGGCAGGGGGCGGGG      24534          A  AGCA
                                AGGGCAGGG GC    GGGG
                                |||||||||  ||    ||||
                                TCCCGTCCC CG    CCCC
                                     C _____
GAM940  KCNC3    5'  GGGCGGGGCGTCAAGGG     24535      A   A  AG
                                GGGC GGG GC  CAGGGG
                                ||||  ||| ||  ||||||
                                CCCG CCC CG  GTTCCC
                                   _   _  CA
GAM940  KCNE1L   3'  CAGGGTTACAGAGCAGGGGGG  24536       CAGGG  C
                                CAGGG     AG AGCAGGGGG
                                |||||     ||  |||||||||
                                GTCCC     TC TCGTCCCCC
                                   AATG_  _
GAM940  KCNK5    3'  CAGGGCAGGAGGGCAGACACTA 24537          _ A    _  GG
                G                CAGGGCAGG G GCAG CA  GG
                                 |||||||||  |  ||||  ||  ||
```

```
                                GTCCCGTCC C CGTC GT  TC
                                     T C    T  GA
GAM940  KCNN4    5'  CAGGGGAGGCCCCAGGGTAGGG 24538      C   GAG   C__
              GG                   CAGGG AGG   CAG   AGGGGG
                                   ||||| |||   |||   ||||||
                                   GTCCC TCC   GTC   TCCCCC
                                     C   GGG   CCA
GAM940  KCNN4    5'  CAGGGCGGGGAGGGGCAGGGG  24539       A    CA
                                   CAGGGC GGGAG  GCAGGGG
                                   ||||||| |||||  |||||||
                                   GTCCCG CCCTC  CGTCCCC
                                      C     CC
GAM940  KCNQ3    5'  AGGCAGGGGGTCAGGGGG    24540         AGCAG
                                   GGGCAGGG    CAGGGGG
                                   ||||||||    |||||||
                                   TCCGTCCC    GTCCCCC
                                        CCA__
GAM940  KCNQ3    5'  GGGCAGGGGAGGCCAGGCAGGG 24541          _ __  _
              GG                   GGGCAGGG AG  CAG CAGGGGG
                                   |||||||| ||  ||| |||||||
                                   CCCGTCCC TC  GTC GTCCCCC
                                        C  CG   C
GAM940  KDR      5'  CAGGGCTAGGGAGCCCGGG   24542       _      AGCA
                                   CAGGGC AGGGAGC    GGG
                                   |||||| |||||||    |||
                                   GTCCCG TCCCTCG    CCC
                                      A      GG__
GAM940  KRT17    3'  GGGAAGGGACTGAAGCAGGGGG 24543     C    GC__
                                   GGG AGGGA    AGCAGGGGG
                                   ||| |||||    |||||||||
                                   CCC TCCCT    TCGTCCCCC
                                     T    GACT
GAM940  LASS2    3'  AGCGCAGGGAGCGGGG      24544    G       AGCA
                                   AG GCAGGGAGC    GGGG
                                   || |||||||||    ||||
                                   TC CGTCCCTCG    CCCC
                                    G       _____
GAM940  LCN1     3'  CAGGGCAGGGGGAAGGCGGGGG 24545          AGCA_  A
              G                    CAGGGCAGGG    GC GGGGG
                                   ||||||||||    || |||||
                                   GTCCCGTCCC    CG CCCCC
                                         CCTTC  C
GAM940  LCN1     3'  CAGGGCAGGGGGAAGGCGGGGG 24545          AGCA_  A
              G                    CAGGGCAGGG    GC GGGGG
                                   ||||||||||    || |||||
                                   GTCCCGTCCC    CG CCCCC
                                         CCTTC  C
GAM940  LCN1     3'  GGGCGCAGGGCAGGGGG     24546      A_   AGCA
                                   GGGC  GGG    GCAGGGGG
                                   ||||  |||    ||||||||
```

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                                CCCG  TCC   CGTCCCCC
                                  CG  ____
GAM940  LCN1    3' GGGCGCAGGGCAGGGGG    24546     A_  AGCA
                                GGGC  GGG   GCAGGGGG
                                ||||  |||   ||||||||
                                CCCG  TCC   CGTCCCCC
                                  CG  ____
GAM940  LCP1    3' CAGGGTAGGAAGAGGGG    24547     C    CAGC
                                CAGGG AGGGAG   AGGGG
                                ||||| ||||||   |||||
                                GTCCC TCCTTC   TCCCC
                                   A    ____
GAM940  LDLR    3' TGAGGCAGGGCCAGGGG    24548   A     AGCAG
                                C GGGCAGGG    CAGGGG
                                | ||||||||    ||||||
                                A TCCGTCCC    GTCCCC
                                 C      G____
GAM940  LDOC1   3' CAGGGCAGGTGGCAGCAG   24549       GA
                                CAGGGCAGG  GCAGCAG
                                |||||||||  |||||||
                                GTCCCGTCC  CGTCGTC
                                     AC
GAM940  LEF1    5' GGGCGGGCGAGCGCGGGG   24550    A _   A A
                                GGGC GG GAGC GC GGGG
                                |||| || |||| || ||||
                                CCCG CC CTCG CG CCCC
                                  C G   _ _
GAM940  LGR6    5' AGGGCAGGCAGAGTGGGG   24551      G  C  CA
                                AGGGCAGG AG AG  GGGG
                                |||||||| || ||  ||||
                                TCCCGTCC TC TC  CCCC
                                     G  _  A_
GAM940  LIMK1   3' GGGCAGGGAGCCTTGGGGG  24552        AGCA
                                GGGCAGGGAGC   GGGGG
                                ||||||||||    |||||
                                CCCGTCCCTCG   CCCCC
                                      GAA_
GAM940  LIMK1   3' GGGCAGGGAGCCTTGGGGG  24552        AGCA
                                GGGCAGGGAGC   GGGGG
                                ||||||||||    |||||
                                CCCGTCCCTCG   CCCCC
                                      GAA_
GAM940  LSP1    3' GGGTGGGGAGGGCGGGGG   24553    CA   CA  A
                                GGG  GGGAG  GC GGGGG
                                |||  |||||  || |||||
                                CCC  CCCTC  CG CCCCC
                                  AC    C_  _
GAM940  LY6E    3' CAGGGCAGGGGGCTACAGGG  24554       A  A
                                CAGGGCAGGG GC GCAGGG
                                |||||||||| || ||||||
```

```
                                GTCCCGTCCC CG TGTCCC
                                      C  A
GAM940  LY6E     3'  GGGCAGGTGGAGGTGCAGGGGG 24555       __  CA
                                GGGCAGG  GAG  GCAGGGGG
                                |||||||  |||  ||||||||
                                CCCGTCC  CTC  CGTCCCCC
                                    AC   CA
GAM940  MAFF     5'  GGGCGGGCGGCGCAGGGGG   24556     A  A_ A
                                GGGC GGG  GC GCAGGGGG
                                |||| |||  || ||||||||
                                CCCG CCC  CG CGTCCCCC
                                  _  GC  _
GAM940  MAP3K11  3'  AGGGCAGGTGAGCTGGGGG   24557       _   AGCA
                                AGGGCAGG GAGC   GGGGG
                                |||||||| ||||   |||||
                                TCCCGTCC CTCG   CCCCC
                                    A   A___
GAM940  MAP3K12  3'  GGGGTGGGGCAGGAAGGGG   24558    CA  A   C
                                GGG  GGG GCAG AGGGGG
                                |||  ||| |||| ||||||
                                CCC  CCC CGTC TTCCCC
                                 CA  _   C
GAM940  MAP3K9   3'  AGGGCTGGATCTCAGGGGG   24559     AG  GCAG
                                AGGGC  GGA   CAGGGGG
                                |||||  |||   |||||||
                                TCCCG  CCT   GTCCCCC
                                  A_  AGA_
GAM940  MAP4     3'  GGGCAGGGCAGCAAGAAGGG  24560       _   C
                                GGGCAGGG AGCAG AGGGG
                                |||||||| ||||| |||||
                                CCCGTCCC TCGTT TTCCC
                                    G   C
GAM940  MAP4     3'  GGGCAGGGCAGCAAGAAGGG  24560       _   C
                                GGGCAGGG AGCAG AGGGG
                                |||||||| ||||| |||||
                                CCCGTCCC TCGTT TTCCC
                                    G   C
GAM940  MAPRE3   3'  CAGGGAGGGAGGCACGGGG   24561     C    CA  G
                                CAGGG AGGGAG  GCA GGGG
                                |||||  ||||||  |||  ||||
                                GTCCC TCCCTC  CGT CCCC
                                  _    __  G
GAM940  MECP2    3'  CAGGGCAGGCAGGGG      24562       GGAGCA
                                CAGGGCAG    GCAGGGG
                                ||||||||    |||||||
                                GTCCCGTC    CGTCCCC
                                          _______
GAM940  MPP2     3'  GGGGAGGGGTGGCAGGGGG   24563    C   AGCA
                                GGG AGGG   GCAGGGGG
                                |||  ||||   ||||||||
```

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                                CCC TCCC    CGTCCCCC
                                  C    CAC_
GAM940   MPZ      3'  CAGGGCGGGGGAGCAAAGAGGG 24564       A_       C
                                CAGGGC  GGGAGCAG AGGGGG
                                ||||||  |||||||| ||||||
                                GTCCCG  CCCTCGTT TCTCCC
                                   CC       _
GAM940   MSF      3'  CAGGGCAGGGGTAGGGG     24565          AGCAGC
                                CAGGGCAGGG     AGGGG
                                ||||||||||     |||||
                                GTCCCGTCCC     TCCCC
                                      CA____
GAM940   MSI1     3'  CAGGGCAGGGGCCGGG      24568          A  AGCA
                                CAGGGCAGGG GC    GGG
                                |||||||||| ||    |||
                                GTCCCGTCCC CG    CCC
                                      _  G___
GAM940   MSI1     3'  CAGGGCCGGGAGAGGGG     24567       A    CAGC
                                CAGGGC GGGAG    AGGGG
                                |||||| |||||    |||||
                                GTCCCG CCCTC    TCCCC
                                   G    _____
GAM940   MSI1     3'  CAGGGGAGGGGGCGGCGG    24566       C   A  A  A
                                CAGGG AGGG GC GC GG
                                ||||| |||| || || ||
                                GTCCC TCCC CG CG CC
                                   C    C  C  _
GAM940   MUCDHL   3'  CAGGGCAGGAACCACGGGGG   24569          G  G A
                                CAGGGCAGGGA CA C GGGGG
                                |||||||||||| || | |||||
                                GTCCCGTCCTT GT G CCCCC
                                      G  _ _
GAM940   MUCDHL   3'  CAGGGCAGGAACCACGGGGG   24569          G  G A
                                CAGGGCAGGGA CA C GGGGG
                                |||||||||||| || | |||||
                                GTCCCGTCCTT GT G CCCCC
                                      G  _ _
GAM940   NDRG1    3'  AGGCAGGGGGCGAAAAGGGG   24570        A  _  C
                                GGGCAGGG GC AG AGGGG
                                |||||||| || || |||||
                                TCCGTCCC CG TT TCCCC
                                     C  C  T
GAM940   NGFR     3'  CAGGGTTGGGGAGGCAGCAGGG 24572       CA_    _
            G                    CAGGG   GGGAG CAGCAGGGG
                                |||||   ||||| |||||||||
                                GTCCC   CCCTC GTCGTCCCC
                                   AAC    C
GAM940   NGFR     3'  GGGTGGGGGGGCAAGAGGGG   24571     CA   A   C
                                GGG  GGG GCAG AGGGG
                                |||  ||| |||| |||||
```

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                                CCC  CCC CGTT TCCCC
                                  AC   C    C
GAM940  NINJ1    3'  CAGGGCAGGCAGCATCCAGGG  24573          G    G_
                                CAGGGCAGG AGCA  CAGGG
                                ||||||||| ||||  |||||
                                GTCCCGTCC TCGT  GTCCC
                                     G    AG
GAM940  NLGN2    3'  GGCGGGGAGCAGGGGG      24574     A       CA
                                GGC GGGAGCAG  GGGG
                                ||| ||||||||  ||||
                                CCG CCCTCGTC  CCCC
                                  C       __
GAM940  NONO     3'  CAGGAGCAGGGGGGCATGG    24575      _     A   GCA
                                CAGG GCAGGG GCA   GG
                                |||| |||||| |||   ||
                                GTCC CGTCCC CGT   CC
                                  T     C   A__
GAM940  NR2F6    5'  CAGGGCAGCGGGGCCGGGG   24576          _  A  AGCA
                                CAGGGCAG GG GC    GGGG
                                |||||||| || ||    ||||
                                GTCCCGTC CC CG    CCCC
                                     G  C  G___
GAM940  OLFM1    3'  CAGGGCGGGGAGGAAAACCGGG 24577        A     C__   A
          G                      CAGGGC GGGAG   AGC GGGG
                                ||||||| |||||   ||| ||||
                                GTCCCG CCCTC   TTG CCCC
                                   C     CTT   G
GAM940  PBX1     3'  GGGCAGAGGGTCAGCCGGG   24578        _  AG    A
                                GGGCAG GG  CAGC GGG
                                |||||| ||  |||| |||
                                CCCGTC CC  GTCG CCC
                                   T  CA    G
GAM940  PCTK3    3'  CAGGGCAGGGGGCCTGGG    24580           A  AGCAG
                                CAGGGCAGGG GC     GGG
                                |||||||||| ||     |||
                                GTCCCGTCCC CG     CCC
                                      C  GA___
GAM940  PCTK3    3'  GGGCAGGGCAGGGGG       24579         GAGCA
                                GGGCAGG    GCAGGGGG
                                |||||||    ||||||||
                                CCCGTCC    CGTCCCCC
                                           _____
GAM940  PDE4A    3'  AGGGCAAAAGGTAGGGGG    24581          G  CAGC
                                AGGGCAGG AG    AGGGGG
                                |||||||| ||    ||||||
                                TCCCGTTT TC    TCCCCC
                                     _  CA__
GAM940  PFKFB4   3'  CAGGGCAGAGGCCGGGGGG   24582           A  AGCA
                                CAGGGCAGGG GC    GGGGG
                                |||||||||| ||    |||||
```

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                                GTCCCGTCTC CG    CCCCC
                                      _ GC__
GAM940  PHB      3'  GGGGTGGGAGCAGAAGG     24583     CA       C
                                GGG  GGGAGCAG AGGG
                                |||  |||||||| ||||
                                CCC  CCCTCGTC TTCC
                                  CA       _
GAM940  PIGR     3'  AGAGCAGGGAGTGGGG      24584           CAGCA
                                AGGGCAGGGAG    GGGG
                                ||||||||||     ||||
                                TCTCGTCCCTC    CCCC
                                      A____
GAM940  PIK3R2   3'  CAGGGCAGAGGGTCAGGG    24585          AGCAG
                                CAGGGCAGGG    CAGGG
                                ||||||||||     |||||
                                GTCCCGTCTC    GTCCC
                                      CCA__
GAM940  PIN1L    3'  CAGTGGCAGGGAGTGGGGG   24586    _       CAGCA
                                CAG GGCAGGGAG    GGGGG
                                ||| |||||||||     |||||
                                GTC CCGTCCCTC    CCCCC
                                  A        A____
GAM940  PLAUR    3'  CAGGGCAGAGAGGGG       24587           CAGCA
                                CAGGGCAGGGAG    GGG
                                ||||||||||||    |||
                                GTCCCGTCTCTC    CCC
                                      _____
GAM940  PLD2     3'  GCACTGGGCAGCAGGGGG    24588     G_  A
                                GCA  GG GCAGCAGGGGG
                                |||  || ||||||||||
                                CGT  CC CGTCGTCCCCC
                                  GA  _
GAM940  PLD2     3'  CAGGGAGGGGGTTCAAGGG   24589      C    AGCAG
                                CAGGG AGGG    CAGGGG
                                ||||| ||||    ||||||
                                GTCCC TCCC    GTTCCC
                                   _    CCAA_
GAM940  PNUTL1   3'  GGGCAGGGAACAGACCCAGG  24590           _ AG
                                GGGCAGGGAGCAG C  GGG
                                |||||||||||| |  |||
                                CCCGTCCCTTGTC G  TCC
                                      T GG
GAM940  PPY      3'  GAGCAGGGAGCAAGCTTTGG  24591           _  AGG
                                GGGCAGGGAGCA GC   GG
                                |||||||||||| ||   ||
                                CTCGTCCCTCGT CG   CC
                                      T  AAA
GAM940  PRKACB   5'  CAGGGAAGGGAAGGGG      24592      C    GCAGC
                                CAGGG AGGGA    AGGGG
                                ||||| |||||    |||||
```

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                                GTCCC TCCCT    TCCCC
                                  T  _____
GAM940  PRKCG   5'  AGGCAGGGAGCGGCACCCCGGG 24593          A  G___
                                GGGCAGGGAGC GCA   GGG
                                |||||||||| |||   |||
                                TCCGTCCCTCG CGT   CCC
                                      C  GGGG
GAM940  PROC    3'  CAGGGGGGGGGGGGCGGGGGG  24594      CA  AGCA A
                                CAGGG  GGG   GC GGGGG
                                |||||  |||   || |||||
                                GTCCC  CCC   CG CCCCC
                                  CC  CC__  C
GAM940  PRPH    3'  CAGGGCAGGGAGAGG       24595          CAGC
                                CAGGGCAGGGAG   AGG
                                ||||||||||||   |||
                                GTCCCGTCCCTC   TCC
                                       _____
GAM940  PRX     3'  GGGCAGAGAGGAAGGGG     24596          CAGC
                                GGGCAGGGAG   AGGGG
                                ||||||||||   |||||
                                CCCGTCTCTC   TCCCC
                                     CT__
GAM940  PSMB10  5'  GGGCAGGCAGAGGGG      24597       GGA   C
                                GGGCAG  GCAG AGGGG
                                ||||||  |||| |||||
                                CCCGTC  CGTC TCCCC
                                   ___  _
GAM940  PTK7    3'  AGGGCAGGGGCCTCAGGG    24598         A  AG
                                AGGGCAGGG GC  CAGGG
                                ||||||||| ||  |||||
                                TCCCGTCCC CG  GTCCC
                                     _  GA
GAM940  PTPRN   3'  GGGCTGAGAAGCAGGGGG   24599      A   GC
                                GGGC GGGA  AGCAGGGGG
                                |||| ||||  |||||||||
                                CCCG CTCT  TCGTCCCCC
                                  A  __
GAM940  PYGB    3'  AGGGCAGGGGGCAGGGGG    24601         AGCA
                                AGGGCAGGG   GCAGGGGG
                                |||||||||   ||||||||
                                TCCCGTCCC   CGTCCCCC
                                     C___
GAM940  PYGB    3'  CAGGACAGAGGGCAGGGGG   24600         AGCA
                                CAGGGCAGGG   GCAGGGGG
                                ||||||||||   ||||||||
                                GTCCTGTCTC   CGTCCCCC
                                     C___
GAM940  RAB13   3'  GGGTGGGGAGGCAAGAAAGGG  24602     CA   _  C
                                GGG  GGGAG CAG AGGGGG
                                |||  ||||| ||| ||||||
```

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                                CCC  CCCTC GTT TTTCCC
                                  AC    C  C
GAM940  RANBP9   5'  TGAGGCAGGGGGAGGCGGGGG  24603   A      AGCA  A
                                C GGGCAGGG   GC GGGGG
                                | ||||||||   || |||||
                                A TCCGTCCC   CG CCCCC
                                 C       CCTC  _
GAM940  RAP1GA1  3'  AGGGTGGGGAGGCAGGGGG   24604     CA    CA
                                AGGG  GGGAG  GCAGGGGG
                                ||||  |||||  ||||||||
                                TCCC  CCCTC  CGTCCCCC
                                  AC    __
GAM940  RBP5     5'  CAGGGTGAGGAAGGAGGGGG  24605      CA   GC  C
                                CAGGG  GGGA  AG AGGGGG
                                |||||  ||||  || ||||||
                                GTCCC  TCCT  TC TCCCCC
                                   AC   __  C
GAM940  RNH      5'  CAGGGGTGGGGCAGGGG    24606      CA   AGCA
                                CAGGG  GGG   GCAGGGG
                                |||||  |||   |||||||
                                GTCCC  CCC   CGTCCCC
                                   CA  ____
GAM940  RNH      5'  CAGGGGTGGGGCAGGGG    24606      CA   AGCA
                                CAGGG  GGG   GCAGGGG
                                |||||  |||   |||||||
                                GTCCC  CCC   CGTCCCC
                                   CA  ____
GAM940  RORC     5'  AGGGCAGGGAGCAGGG     24607          GCA
                                AGGGCAGGGAGCA  GGG
                                ||||||||||||  |||
                                TCCCGTCCCTCGT  CCC
                                        ___
GAM940  SFN      3'  CAGGGCGGGGCGGTGGCGGG  24608       A   A  AGCA  _
                                CAGGGC GGG GC   GG GGG
                                |||||| ||| ||   || |||
                                GTCCCG CCC CG   CC CCC
                                   _  _  CCA_  G
GAM940  SFRP1    3'  AGGCTAGGGCCGCAGGGGG   24609     A   A  A
                                GGGC GGG GC GCAGGGGG
                                |||| ||| || ||||||||
                                TCCG TCC CG CGTCCCCC
                                  A  _  G
GAM940  SFRP4    3'  AGGGCAAGGGGCACATGG    24610        A   G  G
                                AGGGCAGGG GCA CA GG
                                ||||||||| ||| || ||
                                TCCCGTTCC CGT GT CC
                                     C   _  A
GAM940  SH3BP2   3'  AGGCAGAGATAAGGCAGGGGG  24611         GCA_
                                GGGCAGGGA   GCAGGGGG
                                |||||||||   ||||||||
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                                TCCGTCTCT   CGTCCCCC
                                     ATTC
GAM940  SIX1     5' CAGGGAGGGGGGCGCGG    24612      C   A_  A  A
                                CAGGG AGGG  GC GC GG
                                ||||| ||||  || || ||
                                GTCCC TCCC  CG CG CC
                                  _   CC  _  _
GAM940  SLC19A1  3' CAGGGCAGGGGGAATCCTAGGG 24613         AGCAGC__
           GG                    CAGGGCAGGG      AGGGGG
                                ||||||||||      ||||||
                                GTCCCGTCCC      TCCCCC
                                     CCTTAGGA
GAM940  SLC22A11 3' CAGGGCAGGGAGAAGAGG   24614          C  C
                                CAGGGCAGGGAG AG AGG
                                |||||||||||| || |||
                                GTCCCGTCCCTC TC TCC
                                      T  _
GAM940  SLC25A11 3' CAGGGCAAGCTGGAGCAGGGGG 24615        GAGC
                                CAGGGCAGG   AGCAGGGGG
                                |||||||||   |||||||||
                                GTCCCGTTC   TCGTCCCCC
                                     GACC
GAM940  SLC25A13 3' AGGGCAGGCAGCAACAGGG   24616       G
                                AGGGCAGG AGCAGCAGGG
                                |||||||| ||||||||||
                                TCCCGTCC TCGTTGTCCC
                                    G
GAM940  SLC6A3   3' GAGCAGGGAGCAGGG      24617          GCA
                                GGGCAGGGAGCA  GGG
                                ||||||||||||  |||
                                CTCGTCCCTCGT  CCC
                                      ___
GAM940  SLC6A8   3' CAGGGATGGGGAGAGGGG   24618     CA_   CAGC
                                CAGGG  GGGAG   AGGGG
                                |||||  |||||   |||||
                                GTCCC  CCCTC   TCCCC
                                   TAC   ____
GAM940  SLC8A2   3' CAGGGGAGGGGGCGGAG    24619     C   A  AGCA
                                CAGGG AGGG GC   GGGG
                                ||||| |||| ||   ||||
                                GTCCC TCCC CG   CCTC
                                   C   C ____
GAM940  SLC9A3R2 5' GGGCAGGGGCGCGGGG     24620       A  A  A
                                GGGCAGGG GC GC GGGG
                                |||||||| || || ||||
                                CCCGTCCC CG CG CCCC
                                      _  _  _
GAM940  SMT3H1   3' GGGGTGGGAGGGGTGGCAGGGG 24621    CA   CA___
           G                    GGG  GGGAG   GCAGGGGG
                                |||  |||||   ||||||||
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                                CCC  CCCTC    CGTCCCCC
                                  CA    CCCAC
GAM940  SMURF1   3'  GGGCAGAGGGGCAGGGGG    24622        AGCA
                                GGGCAGGG   GCAGGGGG
                                ||||||||   ||||||||
                                CCCGTCTC   CGTCCCCC
                                    CC__
GAM940  SNX1     3'  GGACAGGGAGGAAGGGG     24623         CAGC
                                GGGCAGGGAG   AGGGG
                                ||||||||||   |||||
                                CCTGTCCCTC   TCCCC
                                     CT__
GAM940  SOX10    3'  GGGCAGGGGCTGGGCGGGGGG 24624         A  A__  A
                                GGGCAGGG GC   GC GGGGG
                                |||||||| ||   || |||||
                                CCCGTCCC CG   CG CCCCC
                                    _ ACC  C
GAM940  SRC      3'  AGGGCAGGGTTTGAGGGGG   24625         AGCAGC
                                AGGGCAGGG    AGGGGG
                                |||||||||    ||||||
                                TCCCGTCCC    TCCCCC
                                     AAAC__
GAM940  STAT6    3'  CAGAGCAGGGGGTCAGGG    24626         AGCAG
                                CAGGGCAGGG    CAGGG
                                ||||||||||    |||||
                                GTCTCGTCCC    GTCCC
                                     CCA__
GAM940  SUPT6H   3'  GGTGGCAGCAGCAGGGGG    24627    CA  G
                                GG  GG AGCAGCAGGGGG
                                ||  || ||||||||||||
                                CC  CC TCGTCGTCCCCC
                                 A_  G
GAM940  SYN3     3'  GGGCAAGGCCTAGAGGGGG   24628         AGC  C
                                GGGCAGGG   AG AGGGGG
                                ||||||||   || ||||||
                                CCCGTTCC   TC TCCCCC
                                    GGA  _
GAM940  SYN3     3'  GGGCAAGGCCTAGAGGGGG   24628         AGC  C
                                GGGCAGGG   AG AGGGGG
                                ||||||||   || ||||||
                                CCCGTTCC   TC TCCCCC
                                    GGA  _
GAM940  SYN3     3'  GGGCAAGGCCTAGAGGGGG   24628         AGC  C
                                GGGCAGGG   AG AGGGGG
                                ||||||||   || ||||||
                                CCCGTTCC   TC TCCCCC
                                    GGA  _
GAM940  TCEB3    3'  AGGCAGGGAGGCGGGG      24629         CA  A
                                GGGCAGGGAG  GC GGGG
                                ||||||||||  || ||||
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                                TCCGTCCCTC  CG CCCC
                                   __  _
GAM940  TCF1     3'  CAGAGTGGGGAGCGAGG     24630      CA     AGCA
                                CAGGG  GGGAGC    GGGG
                                |||||  ||||||    ||||
                                GTCTC  CCCTCG    CTCC
                                  AC     _____
GAM940  TCIRG1   5'  AGGGCAGGGGCCTTGTGGGG   24631         A  AGCAG
                                AGGGCAGGG GC     GGGG
                                |||||||||  ||    ||||
                                TCCCGTCCC CG     CCCC
                                    _  GAACA
GAM940  TEM7     3'  CAGGGCAGTGAGTAAACCCGG  24632         G   C_   AG
                                CAGGGCAG GAG  AGC  GG
                                ||||||||  |||  |||  ||
                                GTCCCGTC CTC  TTG  CC
                                     A   AT   GG
GAM940  TERT     3'  CAGGGCGAGGGGTGAACAATGG 24633        _    AGC    G
                                CAGGGC AGGG   AGCAG GG
                                ||||||  ||||   |||||  ||
                                GTCCCG TCCC   TTGTT CC
                                   C    CAC    A
GAM940  TFAP4    3'  CAGAGGTGGGGGGCTGGGGGG   24634      CA   A  AGCA
                                CAGGG  GGG GC    GGGGG
                                |||||  |||  ||    |||||
                                GTCTC  CCC CG    CCCCC
                                  CA   C  A___
GAM940  TGM7     3'  GGGCAGGGGGTGCCAGGG     24635        A_  AG
                                GGGCAGGG  GC  CAGGG
                                ||||||||  ||  |||||
                                CCCGTCCC  CG  GTCCC
                                     CA  __
GAM940  THY1     3'  GGGCAGGGGGGCTGTCTGAGGGG 24636         A  AGC___
                                GGGCAGGG GC     AGGGG
                                |||||||  ||     |||||
                                CCCGTCCC CG     TCCCC
                                     C  ACAGAC
GAM940  TIMP3    5'  GGGCCGGGGGCAAGGGG     24637      A   AGCA
                                GGGC GGG    GCAGGGGG
                                ||||  |||    ||||||||
                                CCCG CCC    CGTTCCCC
                                  G   C___
GAM940  TNFAIP2  3'  CAGGGCAGGGGATGAACGG    24638         AGC_   A
                                CAGGGCAGGG    AGC GG
                                ||||||||||    |||  ||
                                GTCCCGTCCC    TTG CC
                                      CTAC   _
GAM940  TNFRSF14 5'  CAGGAGAGTGGGCAGCAGGGGG 24639       C  _  A
                                CAGGG AG GG GCAGCAGGGGG
                                |||||  ||  ||  ||||||||||
```

```
                                GTCCT TC CC CGTCGTCCCCC
                                   C  A  _
GAM940  TP53    3'  CAGGGGAGGGAGAGATGGGGG  24640      C     C  CA
                                CAGGG AGGGAG AG  GGGGG
                                ||||| |||||| ||  |||||
                                GTCCC TCCCTC TC  CCCCC
                                   C     _  TA
GAM940  TPS1    3'  AGGACAGGGAAGGGG       24642          GCAGC
                                AGGGCAGGGA    AGGGG
                                ||||||||||    |||||
                                TCCTGTCCCT    TCCCC
                                      _____
GAM940  TPS1    3'  GGGCAGGGAAGGTGTGGGGG  24641          CAGCA
                                GGGCAGGGAG    GGGGG
                                ||||||||||    |||||
                                CCCGTCCCTT    CCCCC
                                     CCACA
GAM940  TPSB1   3'  AGGACAGGGAAGGGG       24642          GCAGC
                                AGGGCAGGGA    AGGGG
                                ||||||||||    |||||
                                TCCTGTCCCT    TCCCC
                                      _____
GAM940  TPSB1   3'  GGGCAGGGAAGGTGTGGGGG  24641          CAGCA
                                GGGCAGGGAG    GGGGG
                                ||||||||||    |||||
                                CCCGTCCCTT    CCCCC
                                     CCACA
GAM940  TTYH1   3'  GGCAGGGGCAGCAGGGGG    24643        A
                                GGCAGGG GCAGCAGGGGG
                                ||||||| ||||||||||
                                CCGTCCC CGTCGTCCCCC
                                     _
GAM940  TULP1   3'  GGGCGCGGGGAGGAGGGGG   24644      A__    CAGC
                                GGGC  GGGAG   AGGGGG
                                ||||  |||||   ||||||
                                CCCG  CCCTC   TCCCCC
                                  CGC   C___
GAM940  TULP3   3'  GGGCAGGGAGGGGAAGGGG   24645          CAGC
                                GGGCAGGGAG    AGGGG
                                ||||||||||    |||||
                                CCCGTCCCTC    TCCCC
                                     CCCT
GAM940  TXNIP   3'  CAGGGCAGGAAGGGG       24646          CAGCA
                                CAGGGCAGGGAG    GGG
                                ||||||||||||    |||
                                GTCCCGTCCTTC    CCC
                                      _____
GAM940  UBE2I   5'  GGGCGGGGAGCAGGGG      24647      A      GCA
                                GGGC GGGAGCA   GGGG
                                |||| |||||||   ||||
```

```
                                CCCG CCCTCGT   CCCC
                                  C     ___
GAM940  VANGL2   3'  AGGCAGGGAGAAAAGGGG    24648         C  C
                                GGGCAGGGAG AG AGGGG
                                |||||||||| || |||||
                                TCCGTCCCTC TT TCCCC
                                      _  T
GAM940  WNT3A    3'  AGGGCAGGGAGGAGGGG     24649          CAGC
                                AGGGCAGGGAG   AGGGG
                                ||||||||||   |||||
                                TCCCGTCCCTC   TCCCC
                                      C___
GAM940  WNT5B    3'  TGAGGCAGAGTGCAGGGGG   24650   A      AGCA
                                C GGGCAGGG   GCAGGGGG
                                | ||||||||   ||||||||
                                A TCCGTCTC   CGTCCCCC
                                 C       A___
GAM940  WNT5B    3'  TGAGGCAGAGTGCAGGGGG   24650   A      AGCA
                                C GGGCAGGG   GCAGGGGG
                                | ||||||||   ||||||||
                                A TCCGTCTC   CGTCCCCC
                                 C       A___
GAM940  ZIC3     5'  CAGGGAGGGGGTGTTGGCGGGG 24651      C   AGCA___  A
           GG                    CAGGG AGGG      GC GGGGG
                                |||||  ||||      ||  |||||
                                GTCCC TCCC      CG CCCCC
                                   _   CCACAAC  C
GAM940  ZNF205   5'  GGGGTGGAGGCAGAGGGGG   24652    CA  GA   C
                                GGG  GG  GCAG AGGGGG
                                |||  ||  ||||  ||||||
                                CCC  CC  CGTC TCCCCC
                                  CA  TC   _
GAM940  ZNF219   5'  GGACAGGGAGCTGGGG     24653          AGCA
                                GGGCAGGGAGC   GGGG
                                ||||||||||   ||||
                                CCTGTCCCTCG   CCCC
                                      A___
GAM940  7h3      3'  GGGGGGGGGGCAAGGGGG    24654    CA   A   GC
                                GGG  GGG GCA  AGGGGG
                                |||  ||| |||  ||||||
                                CCC  CCC CGT  TCCCCC
                                  CC   C   __
GAM940  ABT1     3'  AAGGTGGGTGGCAGGGGG    24655     CA   AGCA
                                AGGG  GGG   GCAGGGGG
                                ||||  |||   ||||||||
                                TTCC  CCC   CGTCCCCC
                                  A_   AC__
GAM940  ACTR1A   3'  CAGGGCAGTGAGCAAGAGG   24656        G    GC
                                CAGGGCAG GAGCA  AGGGG
                                ||||||||  |||||  |||||
```

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                                GTCCCGTC CTCGT  TCTCC
                                   A    __
GAM940  APCL     3'  CAGAGGCAGGGAGCTGGG    24657    _       AGCA
                                CAG GGCAGGGAGC    GGG
                                ||| ||||||||||    |||
                                GTC CCGTCCCTCG    CCC
                                  T        A___
GAM940  APEG1    3'  GGCTCGGAGGGTAGCGGGGGG  24658    AG    C__   A
                                GGC  GGAG   AGC GGGGG
                                |||  ||||   ||| |||||
                                CCG  CCTC   TCG CCCCC
                                  AG    CCA   C
GAM940  ARHGEF2  3'  GGGCACGGGGCAGGGGG     24659      _  AGCA
                                GGGCA GGG    GCAGGGGG
                                ||||| |||    ||||||||
                                CCCGT CCC    CGTCCCCC
                                   G  _____
GAM940  ATP6V0A1 3'  CAGGACACCAGGGCAGGGGG  24660       __  AGCA
                                CAGGGCA  GGG    GCAGGGGG
                                |||||||  |||    ||||||||
                                GTCCTGT  TCC    CGTCCCCC
                                    GG  _____
GAM940  BCL2L1   3'  CAGGGGAGGGAGCATCAGG   24661      C       G
                                CAGGG AGGGAGCA CAGG
                                ||||| |||||||| ||||
                                GTCCC TCCCTCGT GTCC
                                   C       A
GAM940  BICD2    3'  CAGGGCAGAGAGCTGTGGG   24662           AGCAG
                                CAGGGCAGGGAGC     GGG
                                ||||||||||||     |||
                                GTCCCGTCTCTCG    CCC
                                       ACA__
GAM940  BIK      3'  CAGGGCAGTGGTCATGGGGG  24663        _  AG  GCA
                                CAGGGCAG GG  CA   GGGGG
                                |||||||| ||  ||   |||||
                                GTCCCGTC CC  GT   CCCCC
                                    A  A_  A__
GAM940  BRD1     5'  CAGGGAGGGAGCAGCAG     24664      C
                                CAGGG AGGGAGCAGCAG
                                ||||| ||||||||||||
                                GTCCC TCCCTCGTCGTC
                                  _
GAM940  C11orf9  3'  CAGGGCAGGGACAGGG      24665          AGCA
                                CAGGGCAGGG    GCAGGG
                                ||||||||||    ||||||
                                GTCCCGTCCC    TGTCCC
                                     _____
GAM940  C16orf5  3'  CAGGGCGGGGGAGTGAAAGGG  24666       A_    CAGC
                                CAGGGC  GGGAG    AGGGG
                                ||||||  |||||    |||||
```

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                                GTCCCG  CCCTC   TTCCC
                                   CC    ACT_
GAM940  C20orf46  3'  GGGCGGGAGCAGGGGG     24667     A      CA
                                GGGC GGGAGCAG  GGGG
                                |||| ||||||||  ||||
                                CCCG CCCTCGTC  CCCC
                                  _      __
GAM940  C20orf67  3'  CAGGGTGAGGGGCGGGG     24668     C_   A  AGCA
                                CAGGG  AGGG GC   GGGG
                                |||||  |||| ||   ||||
                                GTCCC  TCCC CG   CCCC
                                   AC   _ ____
GAM940  C21orf80  3'  CAGGGCAGGGGGCAGACAGGGG 24669         A   _
                                CAGGGCAGGG GCAG CAGGGG
                                |||||||||| |||| ||||||
                                GTCCCGTCCC CGTC GTCCCC
                                     C   T
GAM940  C22orf4   3'  CAGGGCAGGAGTGGTCCAGGG  24670         AGCAG_
                                CAGGGCAGGG     CAGGG
                                ||||||||||     |||||
                                GTCCCGTCCT     GTCCC
                                     CACCAG
GAM940  C2orf9    3'  CAGGGGAGGGGCGGGG      24671      C    A  AGCA
                                CAGGG AGGG GC    GGGG
                                ||||| |||| ||    ||||
                                GTCCC TCCC CG    CCCC
                                   C   _ ____
GAM940  C9orf16   3'  CAGAGTGGGGAGCGCCCAGG   24672      CA     A  AG
                                CAGGG  GGGAGC GC  GGG
                                |||||  |||||| ||  |||
                                GTCTC  CCCTCG CG  TCC
                                   AC     _ GG
GAM940  C9orf7    3'  CAGGGCAGAGGGAATATGGGGG 24673         AGCAGCA
                                CAGGGCAGGG      GGGGG
                                ||||||||||      |||||
                                GTCCCGTCTC      CCCCC
                                     CCTTATA
GAM940  C9orf9    3'  GGGCAAGGAGCAGATGG     24674           CAG
                                GGGCAGGGAGCAG   GG
                                ||||||||||||   ||
                                CCCGTTCCTCGTC   CC
                                      TA_
GAM940  CBX6      3'  GGGCAGGGCATAGGGGG     24676       GA   GC
                                GGGCAGG  GCA  AGGGGG
                                |||||||  |||  ||||||
                                CCCGTCC  CGT  TCCCCC
                                   __   A_
GAM940  CBX6      3'  CAGGGCAGGGTAGGGAGGGG  24675         _  CAGC
                                CAGGGCAGGG AG    AGGGG
                                |||||||||| ||    |||||
```

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                                GTCCCGTCCC TC    TCCCC
                                     A  CC__
GAM940  CDC42BPB 3'  CAGGGCGGGGCGGGGTGGGG  24677       A   A  AGCAG
                                CAGGGC GGG GC     GGGG
                                |||||| ||| ||     ||||
                                GTCCCG CCC CG     CCCC
                                   _  _  CCCCA
GAM940  CDIPT    3'  CAGGGCAGGTGGGCAGCCAGG  24678         GA_    A
                                CAGGGCAGG   GCAGC GGG
                                |||||||||   ||||| |||
                                GTCCCGTCC   CGTCG TCC
                                     ACC    G
GAM940  CES2     5'  GGGCAGGGAGTCAGCGGGG   24679          _   A
                                GGGCAGGGAG CAGC GGGG
                                |||||||||| |||| ||||
                                CCCGTCCCTC GTCG CCCC
                                     A   _
GAM940  CIC      3'  GGGCAAGGGCAGGGG       24680         AGCA
                                GGGCAGGG    GCAGGGG
                                ||||||||    |||||||
                                CCCGTTCC    CGTCCCC
                                     _____
GAM940  CLPTM1   3'  CAGGGAGGGGAGGCGAGGGGG  24681       CA    CA  _
                                CAGGG  GGGAG  GC AGGGGG
                                |||||  |||||  || ||||||
                                GTCCC  CCCTC  CG TCCCCC
                                   TC    __  C
GAM940  CLSTN1   5'  GGGCGGGAGCGGCAGGG     24682      A     A
                                GGGC GGGAGC GCAGGG
                                |||| |||||| ||||||
                                CCCG CCCTCG CGTCCC
                                   _     C
GAM940  CNNM3    3'  CAGGGAGGGAGCAGGG       24683       C       GCA
                                CAGGG AGGGAGCA   GGG
                                ||||| ||||||||   |||
                                GTCCC TCCCTCGT   CCC
                                     _      ____
GAM940  CNTNAP1  3'  CAGGGCAGGGGGGAGGCTGGGG 24684          AGCA_  A
           G                     CAGGGCAGGG    GC GGGGG
                                ||||||||||    || |||||
                                GTCCCGTCCC    CG CCCCC
                                     CCCTC  A
GAM940  CORO1B   3'  GGGGAGGGAGCAGAGGG     24685     C       C
                                GGG AGGGAGCAG AGGG
                                ||| |||||||| ||||
                                CCC TCCCTCGTC TCCC
                                  C       _
GAM940  CUL2     5'  CAGGGCAAGGGGCAGGGG    24686          AGCA
                                CAGGGCAGGG   GCAGGGG
                                ||||||||||   |||||||
```

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                                GTCCCGTTCC   CGTCCCC
                                     C___
GAM940  DDR1    3' GGGTGGGCGACAGGGGG    24687    CAG  A  A
                                GGG   GG GC GCAGGGGG
                                |||   || || ||||||||
                                CCC   CC CG TGTCCCCC
                                  A__  _  C
GAM940  DDR1    3' GGGTGGGCGACAGGGGG    24687    CAG  A  A
                                GGG   GG GC GCAGGGGG
                                |||   || || ||||||||
                                CCC   CC CG TGTCCCCC
                                  A__  _  C
GAM940  DDR1    3' GGGTGGGCGACAGGGGG    24687    CAG  A  A
                                GGG   GG GC GCAGGGGG
                                |||   || || ||||||||
                                CCC   CC CG TGTCCCCC
                                  A__  _  C
GAM940  DDX12   3' CAGGACAGGGGGGCCGGG    24485        A  AGCA
                                CAGGGCAGGG GC   GGG
                                |||||||||| ||   |||
                                GTCCTGTCCC CG   CCC
                                     C  G___
GAM940  DDX31   5' GGGCAGGGAAAAGGGGG    24688        CAGC
                                GGGCAGGGAG   AGGGGG
                                |||||||||   ||||||
                                CCCGTCCCTT   TCCCCC
                                     T___
GAM940  DDX31   5' GGGCAGGGAAAAGGGGG    24688        CAGC
                                GGGCAGGGAG   AGGGGG
                                |||||||||   ||||||
                                CCCGTCCCTT   TCCCCC
                                     T___
GAM940  DJ159A19.3 3' CAGGGTGGGAGGCAGAGGGG  24689     CA   _  C
                                CAGGG  GGGAG CAG AGGGG
                                |||||  ||||| ||| |||||
                                GTCCC  CCCTC GTC TCCCC
                                   A_    C  _
GAM940  DJ726C3.2 3' GGGCAGAGGAAGGAGGGGG   24690      _  GC  C
                                GGGCAG GGA  AG AGGGGG
                                ||||||  |||  ||  ||||||
                                CCCGTC CCT  TC TCCCCC
                                   T  __  C
GAM940  DKFZP434B103 3' GGGCAGGGGTTTCAGGGGG   24691       AGCAG
                                GGGCAGGG   CAGGGGG
                                ||||||||   |||||||
                                CCCGTCCC   GTCCCCC
                                     CAAA_
GAM940  DKFZp434C0923 3' AGGCAGGGAGTGCACCTGG   24692        CA  GG_
                                GGGCAGGGAG  GCA  GG
                                ||||||||||  |||  ||
```

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                                TCCGTCCCTC  CGT   CC
                                     A_   GGA
GAM940   DKFZP434H0820 3'  CAGGGGAGGGGGCCTGGGGG   24693      C    A  AGCA
                                CAGGG AGGG GC    GGGGG
                                ||||| |||| ||    |||||
                                GTCCC TCCC CG    CCCCC
                                   C    C  GA__
GAM940   DKFZp434I1916 3'  CAGGGCAGAGGGGCGGG     24694          AGCA  A
                                CAGGGCAGGG    GC GGG
                                ||||||||||    || |||
                                GTCCCGTCTC    CG CCC
                                     CC__  _
GAM940   DKFZP434K028 3'   CAGGGAGGGAGTAGAAG     24695      C     C  C
                                CAGGG AGGGAG AG AGG
                                ||||| |||||| || |||
                                GTCCC TCCCTC TC TTC
                                   _     A  _
GAM940   DKFZp434M0331 5'  CAGGGCAGGGAGAGGCGGGG   24696           CA  A
                                CAGGGCAGGGAG  GC GGGG
                                ||||||||||||  || ||||
                                GTCCCGTCCCTC  CG CCCC
                                      TC  _
GAM940   DKFZP434M154 5'   CAGGGCGGGCGAGGGCAGGGGG 24697       A  _   CA
                                CAGGGC GG GAG  GCAGGGGG
                                |||||| || |||  ||||||||
                                GTCCCG CC CTC  CGTCCCCC
                                    C  G   C_
GAM940   DKFZP434N1817 3'  CAGGGTGGGAGACCGGGG    24698      CA    CA  A
                                CAGGG  GGGAG  GC GGGG
                                |||||  |||||  || ||||
                                GTCCC  CCCTC  TG CCCC
                                   A_    __  G
GAM940   DKFZP434P211 3'   CAGGGCAGGGGTCAGGG     24699          AGCAG
                                CAGGGCAGGG    CAGGG
                                ||||||||||    |||||
                                GTCCCGTCCC    GTCCC
                                     CA___
GAM940   DKFZp564A176 3'   GGGCTGGGGAGCACAGGGG   24700      A_     G
                                GGGC  GGGAGCA CAGGGG
                                ||||  ||||||| ||||||
                                CCCG  CCCTCGT GTCCCC
                                   AC      _
GAM940   DKFZP564B147 3'   CAGGGAAGGGAGCAGGG     24701      C      GCA
                                CAGGG AGGGAGCA   GGG
                                ||||| ||||||||   |||
                                GTCCC TCCCTCGT   CCC
                                   T       ___
GAM940   DKFZp761G2113 3'  CAGGGAGGAGAGGCAGGGGG  24702      CA    CA
                                CAGGG  GGGAG  GCAGGGGG
                                |||||  |||||  ||||||||
```

```
                                GTCCC  TCCTC  CGTCCCCC
                                  __     TC
GAM940  DNAJC5   3'  AGGCAGGGGTGCTGGGGG    24703        AGCA  A
                                GGGCAGGG    GC GGGGG
                                ||||||||    || |||||
                                TCCGTCCC    CG CCCCC
                                    CA__  A
GAM940  EREG     5'  CAGGGCGGGAGCAGACGGG   24704       A       CA
                                CAGGGC GGGAGCAG  GGG
                                |||||| ||||||||  |||
                                GTCCCG CCCTCGTC  CCC
                                  _       TG
GAM940  ERF      3'  CAGGGCAGGCAGGGCTGGGG  24705         G  CA  A
                                CAGGGCAGG AG  GC GGGG
                                ||||||||| ||  || ||||
                                GTCCCGTCC TC  CG CCCC
                                     G  C_  A
GAM940  FBXO9    5'  GGGCAGGGGGCCAGATCGGGG  24706        A  _  CA_
                                GGGCAGGG GC AG   GGGG
                                |||||||| || ||   ||||
                                CCCGTCCC CG TC   CCCC
                                    C  G  TAG
GAM940  FKBP11   5'  GGGCAGGGAGCCGGGG     24707          AGCA
                                GGGCAGGGAGC   GGGG
                                ||||||||||    ||||
                                CCCGTCCCTCG   CCCC
                                     G___
GAM940  FKBP5    3'  GGGCAGCAGCAGGGG      24708      GGGA
                                GGGCA   GCAGCAGGGG
                                |||||   ||||||||||
                                CCCGT   CGTCGTCCCC
                                  _____
GAM940  FLJ00060 3'  CAGGGCGGTGGGGGGTAAGGGG 24709       A__   AGCAGC
          G                     CAGGGC   GGG     AGGGGG
                                ||||||   |||     ||||||
                                GTCCCG   CCC     TCCCCC
                                   CCA   CCCAT_
GAM940  FLJ10350 3'  AGGGCAGGGGGCATGGG    24710         A   GCA
                                AGGGCAGGG GCA   GGG
                                ||||||||| |||   |||
                                TCCCGTCCC CGT   CCC
                                    C   A__
GAM940  FLJ10432 3'  GGGCAGAGGAGCAGGG     24711        AGC
                                GGGCAGGG   AGCAGGG
                                ||||||||   |||||||
                                CCCGTCTC   TCGTCCC
                                    C__
GAM940  FLJ10583 3'  GGGTGGGGAAGCAGAGG    24712     CA   GC
                                GGG  GGGA  AGCAGGGG
                                |||  ||||  ||||||||
```

```
                                CCC  CCCT  TCGTCTCC
                                  AC   __
GAM940  FLJ10701  3' CAGGGCAGGGAGAAGGGG    24713          CAGC
                                CAGGGCAGGGAG   AGGGG
                                ||||||||||||  |||||
                                GTCCCGTCCCTC   TCCCC
                                       T___
GAM940  FLJ10748  3' GGGGAGGGGGTGGCAAAAGG  24714    C   AGCA
                                GGG AGGG   GCAGGGGG
                                ||| ||||   ||||||||
                                CCC TCCC   CGTTTTCC
                                  C   CCAC
GAM940  FLJ10922  3' GGGCAGGGAAGGTGGGGG    24715        CAGCA
                                GGGCAGGGAG    GGGGG
                                ||||||||||    |||||
                                CCCGTCCCTT    CCCCC
                                      CCA__
GAM940  FLJ10932  3' GGGCAGGAAGCCCGGGGG    24716         AGCA
                                GGGCAGGGAGC   GGGGG
                                ||||||||||   |||||
                                CCCGTCCTTCG   CCCCC
                                      GG__
GAM940  FLJ11078  3' CAGGCCAGGGAGTGGCAGGG  24717     G      CA
                                CAGG CAGGGAG  GCAGGG
                                |||| |||||||  ||||||
                                GTCC GTCCCTC  CGTCCC
                                  G      AC
GAM940  FLJ11362  3' GGGGTGGGAGAGTGGAGG    24718    CA    C  CA
                                GGG  GGGAG AG  GGGGG
                                |||  ||||| ||  |||||
                                CCC  CCCTC TC  CCTCC
                                  CA    _  A_
GAM940  FLJ12190  3' GGGGATGGAGCTGGCGGGGGG 24719    CAG    A_  A
                                GGG   GGAGC  GC GGGGG
                                |||   |||||  || |||||
                                CCC   CCTCG  CG CCCCC
                                  CTA    AC  C
GAM940  FLJ12577  3' CAGGACAGGGAGAGAGGGG   24720          C  C
                                CAGGGCAGGGAG AG AGGGG
                                |||||||||||| || |||||
                                GTCCTGTCCCTC TC TCCCC
                                       _  _
GAM940  FLJ13158  3' CAGGGCAGGGATAGGG      24721          GCAGC
                                CAGGGCAGGGA    AGGG
                                ||||||||||    ||||
                                GTCCCGTCCCT    TCCC
                                      A_____
GAM940  FLJ13725  5' GGGCAGGGCGGCAAACAGG   24722        A_   _
                                GGGCAGGG  GCAG CAGG
                                ||||||||  |||| ||||
```

```
                                CCCGTCCC  CGTT GTCC
                                    GC    T
GAM940  FLJ14100  5'  CAGGGCAGGGGGAGCACAGGG  24723       __      G
                                CAGGGCA  GGGAGCA CAGGG
                                |||||||  ||||||| |||||
                                GTCCCGT  CCCTCGT GTCCC
                                   CC     _
GAM940  FLJ14594  3'  AGGCAGGGCAGGGGG      24724       GAGCA
                                GGGCAGG    GCAGGGGG
                                |||||||    ||||||||
                                TCCGTCC    CGTCCCCC
                                      _____
GAM940  FLJ14675  3'  CAGGGCAGGAGGCAGCCTCCAG 24725        GA    AG__
          GG                     CAGGGCAGG  GCAGC    GGGG
                                |||||||||  |||||    ||||
                                GTCCCGTCC  CGTCG    TCCC
                                     TC    GAGG
GAM940  FLJ14810  3'  CAGGGCAGAGGGTGCCTGGGG  24726        AGCA  AG
                                CAGGGCAGGG   GC  GGGG
                                ||||||||||   ||  ||||
                                GTCCCGTCTC   CG  CCCC
                                     CCA_  GA
GAM940  FLJ20113  3'  CAAGGCAGGCACAGGCAGGGGG 24727        GA   _
                                CAGGGCAGG  GCAG CAGGGGG
                                |||||||||  |||| |||||||
                                GTTCCGTCC  TGTC GTCCCCC
                                     G_   C
GAM940  FLJ20487  3'  AGGGCGGGGAGCTGCAGGG   24728      A     A
                                AGGGC GGGAGC GCAGGG
                                |||||  ||||||  ||||||
                                TCCCG CCCTCG CGTCCC
                                   C     A
GAM940  FLJ20509  5'  GGGCGGGAAGCAGCCCCCGGGG 24729      A       A___
          G                     GGGC GGGAGCAGC    GGGGG
                                ||||  |||||||||   |||||
                                CCCG CCTTCGTCG    CCCCC
                                   C       GGGG
GAM940  FLJ20509  5'  GGGGTGGAGCTAGGCAGGGGG  24730    CAG    A__
                                GGG   GGAGC   GCAGGGGG
                                |||   |||||   ||||||||
                                CCC   CCTCG   CGTCCCCC
                                  CA_    ATC
GAM940  FLJ20539  3'  GGGCAGGGCAGAGGGGG     24731       GA   C
                                GGGCAGG  GCAG AGGGGG
                                |||||||  ||||  ||||||
                                CCCGTCC  CGTC TCCCCC
                                      __   _
GAM940  FLJ20699  3'  GGTGGATGCAGCAGCAGGGGG  24732    CA   ___
                                GG  GGG   AGCAGCAGGGGG
                                ||  |||   ||||||||||||
```

```
                                CC  CCT   TCGTCGTCCCCC
                                 A_   ACG
GAM940   FLJ21324  5' CAGAGTGGGGAGCTGCTCGGGG 24733      CA     A  A_
                                CAGGG  GGGAGC GC  GGGG
                                |||||  |||||| ||  ||||
                                GTCTC  CCCTCG CG  CCCC
                                   AC     A  AG
GAM940   FLJ21596  3' GGGCAGGGGGGCGACACAG    24734        A  A   G
                                GGGCAGGG GC GCA GG
                                |||||||| || ||| ||
                                CCCGTCCC CG TGT TC
                                     C  C   G
GAM940   FLJ21709  3' CAGGGCAGTGGGGCTCCAGGGG 24735        _  A  AG
                                CAGGGCAG GG GC  CAGGGG
                                |||||||| || ||  ||||||
                                GTCCCGTC CC CG  GTCCCC
                                     A  C  AG
GAM940   FLJ21870  3' CAGGGCAGGGAAGTGGAGGG   24736         GC  CA
                                CAGGGCAGGGA  AG  GGGGG
                                ||||||||||  ||  |||||
                                GTCCCGTCCCT  TC  CTCCC
                                      __  AC
GAM940   FLJ22056  3' AGGGCACACACCTGGCAGGGGG 24737      GGGA  A__
                                AGGGCA   GC   GCAGGGGG
                                ||||||   ||   ||||||||
                                TCCCGT   TG   CGTCCCCC
                                   GTG_  GAC
GAM940   FLJ22184  3' CAGGGCAGTGGAGGCGGGG   24738        _   CA  A
                                CAGGGCAG GGAG  GC GGGG
                                |||||||| ||||  || ||||
                                GTCCCGTC CCTC  CG CCCC
                                     A   __  _
GAM940   FLJ22215  3' CAGGGTAGGGGGCAGGGG    24739      C   AGCA
                                CAGGG AGGG   GCAGGGG
                                ||||| ||||   |||||||
                                GTCCC TCCC   CGTCCCC
                                   A   C___
GAM940   FLJ22679  3' GGGCAGGATGGGCAGTGGGGGG 24740        A__   CA
                                GGGCAGGG   GCAG  GGGGG
                                ||||||||   ||||  |||||
                                CCCGTCCT   CGTC  CCCCC
                                     ACC   AC
GAM940   FLJ22679  3' GGGCAGGATGGGCAGTGGGGGG 24740        A__   CA
                                GGGCAGGG   GCAG  GGGGG
                                ||||||||   ||||  |||||
                                CCCGTCCT   CGTC  CCCCC
                                     ACC   AC
GAM940   FLJ22865  3' CAAGGCAGGGGGCAGG      24741         AGCA
                                CAGGGCAGGG   GCAGG
                                ||||||||||   |||||
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                                GTTCCGTCCC   CGTCC
                                     C___
GAM940  FLJ22944  3'  CAGTGCAGAAAGGCAGGGGG  24742    G   GG  CA
                                CAG GCAG  AG  GCAGGGGG
                                ||| ||||  ||  ||||||||
                                GTC CGTC  TC  CGTCCCCC
                                  A   TT  __
GAM940  FLJ23058  3'  GGGCAGGCAGAGGGG      24597      GGA   C
                                GGGCAG   GCAG AGGGG
                                ||||||   |||| |||||
                                CCCGTC   CGTC TCCCC
                                   ___   _
GAM940  FLJ23360  5'  GGGCAGGGAGCCGGGG     24707         AGCA
                                GGGCAGGGAGC   GGGG
                                ||||||||||   ||||
                                CCCGTCCCTCG   CCCC
                                      G___
GAM940  FLJ23462  3'  GGGGAGGGAGCAGAAGG    24743    C       C
                                GGG AGGGAGCAG AGGG
                                ||| |||||||| ||||
                                CCC TCCCTCGTC TTCC
                                  C       _
GAM940  FLJ23519  5'  CAGGGGTGGGGCAGGGG    24606     CA   AGCA
                                CAGGG  GGG   GCAGGGG
                                |||||  |||   |||||||
                                GTCCC  CCC   CGTCCCC
                                   CA  _____
GAM940  FLJ23584  5'  CAGGACAGGGGGCAGAG    24744         A   C
                                CAGGGCAGGG GCAG AG
                                |||||||||| |||| ||
                                GTCCTGTCCC CGTC TC
                                      C   _
GAM940  FLJ30213  5'  CAGGGCAGGAGAAGTGTTGGGG 24745        _   CAGCA
          G                      CAGGGCAGG GAG    GGGGG
                                ||||||||| |||    |||||
                                GTCCCGTCC CTT    CCCCC
                                     T   CACAA
GAM940  FLJ32771  5'  GGGCAGGGCCCCAGGGGG   24746       AGCAG
                                GGGCAGGG    CAGGGGG
                                ||||||||    |||||||
                                CCCGTCCC    GTCCCCC
                                    GGG__
GAM940  FUK     3'  GGGCAAGGAAGGTGGGGG   24747         CAGCA
                                GGGCAGGGAG    GGGGG
                                ||||||||||    |||||
                                CCCGTTCCTT    CCCCC
                                      CCA__
GAM940  GIPC3    3'  CAGGGCCGGGGCAGGGGG   24748      A   AGCA
                                CAGGGC GGG   GCAGGGGG
                                |||||| |||   ||||||||
```

```
                                GTCCCG CCC   CGTCCCCC
                                   G  ____
GAM940  GIT1    3'  CAGGGCAGGGACATCCATGG  24749         G  G_  G
                                CAGGGCAGGGA CA  CA GG
                                |||||||||| ||  || ||
                                GTCCCGTCCCT GT  GT CC
                                      _  AG  A
GAM940  GIT2    3'  AGGCAGGGAGTTTTAAGGG  24750        CAGC
                                GGGCAGGGAG   AGGGG
                                ||||||||||   |||||
                                TCCGTCCCTC   TTCCC
                                      AAAA
GAM940  GIT2    3'  AGGCAGGGAGTTTTAAGGG  24750        CAGC
                                GGGCAGGGAG   AGGGG
                                ||||||||||   |||||
                                TCCGTCCCTC   TTCCC
                                      AAAA
GAM940  GIT2    3'  AGGCAGGGAGTTTTAAGGG  24750        CAGC
                                GGGCAGGGAG   AGGGG
                                ||||||||||   |||||
                                TCCGTCCCTC   TTCCC
                                      AAAA
GAM940  GOLPH3  5'  CAGGGCCGGGGGCAGTCA   24751       A  A   _
                                CAGGGC GGG GCAG CA
                                |||||| ||| |||| ||
                                GTCCCG CCC CGTC GT
                                   G  C   A
GAM940  GSK3A   3'  CAGGGCAGGAGCTTGATGGG  24752        G  AGCAG
                                CAGGGCAGG AGC    GGG
                                ||||||||| |||    |||
                                GTCCCGTCC TCG    CCC
                                      _  AACTA
GAM940  HEMK    3'  AAGTGCCAGGGTGGCAGGGGG  24753    _ _   AGCA
                                AGG GC AGGG   GCAGGGGG
                                ||| || ||||   ||||||||
                                TTC CG TCCC   CGTCCCCC
                                  A  G   AC__
GAM940  HES6    5'  GGACGGGGAGCGGCGGGG   24754     A    A  A
                                GGGC GGGAGC GC GGGG
                                |||| |||||| || ||||
                                CCTG CCCTCG CG CCCC
                                  C    C  _
GAM940  HGC6.1.1 5' CAGGGGGGACAGCGGGGGG  24755     CA   G   A
                                CAGGG  GGGA CAGC GGGGG
                                |||||  |||| |||| |||||
                                GTCCC  CCCT GTCG CCCCC
                                   __   _   C
GAM940  HIC2    3'  GGGCAGAGCAGCAGGGGG   24756     GG
                                GGGCA  GAGCAGCAGGGGG
                                |||||  ||||||||||||
```

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                                CCCGT  CTCGTCGTCCCCC
                                  __
GAM940  HIF1AN   3'  GGGCAGGGAGCATCATAGGG  24757          G  G
                                GGGCAGGGAGCA CA GGGG
                                |||||||||||| || ||||
                                CCCGTCCCTCGT GT TCCC
                                       A  A
GAM940  HOMER-2B 3'  GGGCGGGGGGGCAGGGGG    24758     A   AGCA
                                GGGC GGG    GCAGGGGG
                                |||| |||    ||||||||
                                CCCG CCC    CGTCCCCC
                                  C   C___
GAM940  HRH3     3'  AGGGTGGGCACCAGCAGGGGG 24759     CA   AG_
                                AGGG  GGG   CAGCAGGGGG
                                ||||  |||   ||||||||||
                                TCCC  CCC   GTCGTCCCCC
                                  A_   GTG
GAM940  HRH3     3'  GGGTAGGGGGCAGCAGGG    24760     C    A
                                GGG AGGG GCAGCAGGG
                                ||| |||| |||||||||
                                CCC TCCC CGTCGTCCC
                                  A    C
GAM940  HRMT1L3  5'  GGGCTGGGGGGGCTGGGAGGGG 24761     A__   A  AGC_
           G                     GGGC   GGG GC    AGGGGG
                                 ||||   ||| ||    ||||||
                                 CCCG   CCC CG    TCCCCC
                                   ACC   C  ACCC
GAM940  HSPC232  3'  GGGCAGGGAGCGGTGG      24762          AGCA  _
                                GGGCAGGGAGC    GG GG
                                ||||||||||    || ||
                                CCCGTCCCTCG    CC CC
                                       ____  A
GAM940  IGF2AS   3'  CAGGGGAGGGGCTAGAGGGGG  24763      C    A  _  C
                                CAGGG AGGG GC AG AGGGGG
                                ||||| |||| || || ||||||
                                GTCCC TCCC CG TC TCCCCC
                                   C    _  A  _
GAM940  IMP13    5'  CAGGGGAGGGAGGCCTGCGGGG 24764      C     _ A_  A
           G                     CAGGG AGGGAG C  GC GGGGG
                                 ||||| |||||| |  || |||||
                                 GTCCC TCCCTC G  CG CCCCC
                                   C     C GA  _
GAM940  ITPK1    3'  CAGGTCAGGGAGTGGGG     24765      G      CAGCA
                                CAGG CAGGGAG     GGGG
                                |||| |||||||     ||||
                                GTCC GTCCCTC     CCCC
                                  A      A____
GAM940  KCND1    3'  AGGGCAAGGAGGCCAGGGG   24766          CAG
                                AGGGCAGGGAG   CAGGGG
                                ||||||||||   ||||||
```

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                                TCCCGTTCCTC  GTCCCC
                                     CG_
GAM940  KIAA0057  3'  CAGGGAGGGTGGCAGGGGG  24767     C   AGCA
                                CAGGG AGGG   GCAGGGGG
                                ||||| ||||   ||||||||
                                GTCCC TCCC   CGTCCCCC
                                  _   AC__
GAM940  KIAA0140  3'  CAAGGCAGAGCCCGCAGCAGGG 24768        A__
          GG                  CAGGGCAGGG  GCAGCAGGGGG
                              ||||||||||  ||||||||||
                              GTTCCGTCTC  CGTCGTCCCCC
                                   GGG
GAM940  KIAA0179  3'  CAGGGAGGGAAACCGGGTAGGG 24769     C    _ AGC__
          GG                  CAGGG AGGGAG C    AGGGGG
                              ||||| |||||| |    ||||||
                              GTCCC TCCCTT G    TCCCCC
                                 _     T GCCCA
GAM940  KIAA0193  3'  GGGCAAGGGAGTGGGGG    24770      _    CAGCA
                              GGGCA GGGAG    GGGGG
                              ||||| |||||    |||||
                              CCCGT CCCTC    CCCCC
                                 T    A____
GAM940  KIAA0280  3'  AGGGCAGGGGCTAAGAGGGGG  24771        A  __  C
                              AGGGCAGGG GC  AG AGGGGG
                              ||||||||| ||  || ||||||
                              TCCCGTCCC CG  TC TCCCCC
                                   _ AT  _
GAM940  KIAA0295  3'  GGGCAGGAGGGGCTGGGG    24772       G  CA  A
                              GGGCAGG AG  GC GGGG
                              ||||||| ||  || ||||
                              CCCGTCC TC  CG CCCC
                                  _ CC  A
GAM940  KIAA0376  3'  AGGGTGGGCACAGGGG     24773     CAG  A   G
                              AGGG   GG GCA CAGGGG
                              ||||   || ||| ||||||
                              TCCC   CC CGT GTCCCC
                                A__  _   _
GAM940  KIAA0399  5'  AAGGCAGGGAGCAAGG     24774           GC
                              AGGGCAGGGAGCA  AGG
                              ||||||||||||  |||
                              TTCCGTCCCTCGT  TCC
                                      __
GAM940  KIAA0427  5'  CAGGGAGGGAGGGGCGGGTAGG 24775     C     CA  ____
          GGG                   CAGGG AGGGAG  GC    AGGGGG
                              ||||| ||||||  ||    ||||||
                              GTCCC TCCCTC  CG    TCCCCC
                                 _     CC  CCCA
GAM940  KIAA0447  3'  CAGGGTGTGGAAGAGGTAGGGG 24776     CA_    C  C_
          G                    CAGGG   GGGAG AG  AGGGGG
                              |||||   ||||| ||  ||||||
```

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                                GTCCC  CCTTC TC  TCCCCC
                                  ACA    _ CA
GAM940  KIAA0449 3' GGGCAGGGGACAGAACAAAGG 24777       AG  __
                                GGGCAGGG  CAG  CAGGGG
                                ||||||||  |||  ||||||
                                CCCGTCCC  GTC  GTTTCC
                                    CT   TT
GAM940  KIAA0469 3' CAGGGGGTAGGAGCAGGGGG  24778     CA  G  C
                                CAGGG  GG AG AGCAGGGGG
                                |||||  || || |||||||||
                                GTCCC  CC TC TCGTCCCCC
                                  __ A  C
GAM940  KIAA0478 3' CAAGGCAGGGAGTGGG     24779         CAGCA
                                CAGGGCAGGGAG    GGG
                                ||||||||||||    |||
                                GTTCCGTCCCTC    CCC
                                      A____
GAM940  KIAA0544 3' GGGCGGGCGGTGCAGGGGG  24780    A  AGCA
                                GGGC GGG   GCAGGGGG
                                |||| |||   ||||||||
                                CCCG CCC   CGTCCCCC
                                  _  GCCA
GAM940  KIAA0570 5' GGGCGGGGAGCAAGAG     24781     A     GC
                                GGGC GGGAGCA  AGGG
                                |||| |||||||  ||||
                                CCCG CCCTCGT  TCTC
                                  C     __
GAM940  KIAA0574 3' CAGGGCAGGGATAAAGG    24782         GCAGC
                                CAGGGCAGGGA    AGGG
                                ||||||||||    ||||
                                GTCCCGTCCCT    TTCC
                                      AT___
GAM940  KIAA0590 3' GGGCAGAGCCTAGCAGGGGG  24783       AGC
                                GGGCAGGG  AGCAGGGGG
                                ||||||||  |||||||||
                                CCCGTCTC  TCGTCCCCC
                                    GGA
GAM940  KIAA0682 3' GGACAGGGGGAGCAGGGG   24784       AGC
                                GGGCAGGG  AGCAGGGG
                                ||||||||  ||||||||
                                CCTGTCCC  TCGTCCCC
                                    CC_
GAM940  KIAA0767 3' CAGGGCGGGGGCTGGGGG   24785     A  A AGCA
                                CAGGGC GGG GC   GGGGG
                                ||||||| ||| ||   |||||
                                GTCCCG CCC CG   CCCCC
                                  C  _ A___
GAM940  KIAA0939 3' AGGCAGGGGGCCGCAGGGG  24786       A A
                                GGGCAGGG GC GCAGGGG
                                |||||||| || |||||||
```

```
                                TCCGTCCC CG CGTCCCC
                                    C  G
GAM940  KIAA0953  5'  GGGGAGGGAGCAGACGCGGGGG 24787     C       _ A_
                                GGG AGGGAGCAG C  GGGGG
                                ||| ||||||||| |  |||||
                                CCC TCCCTCGTC G  CCCCC
                                  C        T CG
GAM940  KIAA1030  3'  CAGGGAGGGAGCTGGGG     24788      C      AGCA
                                CAGGG AGGGAGC    GGGG
                                ||||| |||||||    ||||
                                GTCCC TCCCTCG    CCCC
                                   _      A___
GAM940  KIAA1052  3'  CAGGGCAGGGGTGGCACAGG   24789          A__   G
                                CAGGGCAGGG   GCA CAGG
                                ||||||||||   ||| ||||
                                GTCCCGTCCC   CGT GTCC
                                     CAC   _
GAM940  KIAA1068  3'  CAGGGCAGGGAGTGGGG     24790           CAGCA
                                CAGGGCAGGGAG    GGGG
                                ||||||||||||    ||||
                                GTCCCGTCCCTC    CCCC
                                     A____
GAM940  KIAA1115  5'  GGGCAGGGGGCGGCAAGG    24791         A  A
                                GGGCAGGG GC GCAGGG
                                |||||||| || ||||||
                                CCCGTCCC CG CGTTCC
                                    C  C
GAM940  KIAA1171  3'  CAGGGCAGGGGCCCAGGGG   24792          A  AG
                                CAGGGCAGGG GC  CAGGGG
                                |||||||||| ||  ||||||
                                GTCCCGTCCC CG  GTCCCC
                                     _  G_
GAM940  KIAA1184  3'  GGGCAGGGAGGCTGTGGG    24793          CA  AG_
                                GGGCAGGGAG  GC   GGG
                                ||||||||||  ||   |||
                                CCCGTCCCTC  CG   CCC
                                     __  ACA
GAM940  KIAA1205  3'  GGGCGGGGGCGAGAACGGGG  24794     A   A  _  CA_
                                GGGC GGG GC AG   GGGG
                                |||| ||| || ||   ||||
                                CCCG CCC CG TC   CCCC
                                  C   _  C  TTG
GAM940  KIAA1237  3'  CAGGACAGTAAGGCAGGGGG  24795        GG  CA
                                CAGGGCAG  AG  GCAGGGGG
                                ||||||||  ||  ||||||||
                                GTCCTGTC  TC  CGTCCCCC
                                    AT  __
GAM940  KIAA1271  3'  CAGGGGAGGGGGCCCAGTGGGG 24797      C    A  AG   _
                                CAGGG AGGG GC  CAG GGGG
                                ||||| |||| ||  ||| ||||
```

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                                GTCCC TCCC CG  GTC CCCC
                                   C    C  G_   A
GAM940  KIAA1271  3'  AGGGTAGGGGGACAGAGGG   24796     C    AGCA
                                AGGG AGGG    GCAGGGGG
                                |||| ||||    ||||||||
                                TCCC TCCC    TGTCTCCC
                                  A    CC__
GAM940  KIAA1402  5'  CAGGGACGGGGAAGGGG     24798      _ A    GCAGC
                                CAGGG C GGGA     AGGGG
                                ||||| | ||||     |||||
                                GTCCC G CCCT     TCCCC
                                   T C    _____
GAM940  KIAA1431  3'  AGGGCAGGGAGATGGGG     24799          CAGCA
                                AGGGCAGGGAG     GGGG
                                ||||||||||     ||||
                                TCCCGTCCCTC     CCCC
                                      TA___
GAM940  KIAA1443  5'  GGGGGAGAGGGCAGGGGG    24800     CA    CA
                                GGG  GGGAG  GCAGGGGG
                                |||  |||||  ||||||||
                                CCC  CTCTC  CGTCCCCC
                                  C_    C_
GAM940  KIAA1545  3'  GGGCAGGGCATGGGGGG     24801       GA   GCA
                                GGGCAGG  GCA   GGGGG
                                |||||||  |||   |||||
                                CCCGTCC  CGT   CCCCC
                                    __   AC_
GAM940  KIAA1553  3'  CAAGGCAGGGGGTGGCCAGG   24802          AGCA  A
                                CAGGGCAGGG    GC GGG
                                ||||||||||    || |||
                                GTTCCGTCCC    CG TCC
                                      CCAC  G
GAM940  KIAA1602  3'  GGGCAGAGGAGCAGCCGGG    24803       _       A
                                GGGCAG GGAGCAGC GGG
                                |||||| |||||||| |||
                                CCCGTC CCTCGTCG CCC
                                   T       G
GAM940  KIAA1649  5'  CAGGGTCCACTTCAGCAGGGGG 24804       CAGGGAG
                                CAGGG       CAGCAGGGGG
                                |||||       ||||||||||
                                GTCCC       GTCGTCCCCC
                                   AGGTGAA
GAM940  KIAA1656  3'  CAGGAGCAGGGGGGCACGG    24805     _     AGCA   G
                                CAGG GCAGGG    GCA GG
                                |||| ||||||    ||| ||
                                GTCC CGTCCC    CGT CC
                                  T     C___   G
GAM940  KIAA1668  3'  CAGGGTGAGGGGCGGAA     24806      C_   A  AGCA
                                CAGGG  AGGG GC    GGGG
                                |||||  |||| ||    ||||
```

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                                GTCCC  TCCC CG   CCTT
                                  AC   _ ____
GAM940  KIAA1674  3' GGGCAGGGAGCAGGGG     24808          GCA
                                GGGCAGGGAGCA  GGGG
                                ||||||||||||  ||||
                                CCCGTCCCTCGT  CCCC
                                     ___
GAM940  KIAA1674  3' GGGCAGGGAGCAGGG      24807          GCA
                                GGGCAGGGAGCA  GGG
                                ||||||||||||  |||
                                CCCGTCCCTCGT  CCC
                                     ___
GAM940  KIAA1751  3' CAGGGCAGGAGGCATGGGG  24809        GA  GCA
                                CAGGGCAGG GCA  GGGG
                                |||||||||  |||  ||||
                                GTCCCGTCC CGT  CCCC
                                     TC  A__
GAM940  KIAA1813  5' GGGCAGGAGCTGCGGGG    24810       G  A A
                                GGGCAGG AGC GC GGGG
                                ||||||| ||| || ||||
                                CCCGTCC TCG CG CCCC
                                   _  A  _
GAM940  KIAA1819  5' CAGGAGGGGCAGCAGGGGG  24811     GC   A
                                CAGG  AGGG GCAGCAGGGGG
                                ||||  |||| ||||||||||
                                GTCC  TCCC CGTCGTCCCCC
                                   __  _
GAM940  KIAA1870  5' CAGGGTGGGTGAGCAGAAAAGG 24812      CA _    C
          G                      CAGGG  GG GAGCAG AGGGGG
                                |||||  || |||||| ||||||
                                GTCCC  CC CTCGTC TTTCCC
                                  AC  A     T
GAM940  KIAA1922  3' AGGGCAGGGGGCAGGG     24813        AGCA
                                AGGGCAGGG   GCAGGG
                                |||||||||   ||||||
                                TCCCGTCCC   CGTCCC
                                     C___
GAM940  KIAA1922  3' CAGGGGAGAGGGCAGGGGG  24814     CA   CA
                                CAGGG  GGGAG  GCAGGGGG
                                |||||  |||||  ||||||||
                                GTCCC  CTCTC  CGTCCCCC
                                   __    C_
GAM940  KIAA1938  3' CAGGGTGGGGTGCACAGG   24815     CA  A  G
                                CAGGG  GGG GCA CAGG
                                |||||  ||| ||| ||||
                                GTCCC  CCC CGT GTCC
                                  AC  A  _
GAM940  KIAA1940  3' GGGGTAGGAGGCAAGGGG   24816    CA   CA
                                GGG  GGGAG  GCAGGGGG
                                |||  |||||  ||||||||
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                                CCC  TCCTC  CGTTCCCC
                                  CA    __
GAM940  KIAA1941  3'  GGGCAGGGGCAGCTTGG     24817         A     AG
                                GGGCAGGG GCAGC  GG
                                |||||||| |||||  ||
                                CCCGTCCC CGTCG  CC
                                     _    AA
GAM940  KIAA1949  5'  AGGGTAGGGAGCACTGGGG   24818     C       G A
                                AGGG AGGGAGCA C GGGG
                                |||| |||||||| | ||||
                                TCCC TCCCTCGT G CCCC
                                  A       _ A
GAM940  KIAA1949  5'  AGGGTAGGGAGCACTGGGG   24818     C       G A
                                AGGG AGGGAGCA C GGGG
                                |||| |||||||| | ||||
                                TCCC TCCCTCGT G CCCC
                                  A       _ A
GAM940  KIAA1949  5'  AGGGTAGGGAGCACTGGGG   24818     C       G A
                                AGGG AGGGAGCA C GGGG
                                |||| |||||||| | ||||
                                TCCC TCCCTCGT G CCCC
                                  A       _ A
GAM940  LHPP      3'  CAGGGCAGAGGGCAGAAGG   24819          A    C
                                CAGGGCAGGG GCAG AGGG
                                |||||||||| |||| ||||
                                GTCCCGTCTC CGTC TTCC
                                     C    _
GAM940  LOH12CR1  5'  CAGGGCAGGGGCCAGGG    24820          A  AG
                                CAGGGCAGGG GC  CAGGG
                                |||||||||| ||  |||||
                                GTCCCGTCCC CG  GTCCC
                                     _  __
GAM940  LYPLA2    3'  GGGCAGGGGCCTGGGGG     24821         A  AGCA
                                GGGCAGGG GC    GGGGG
                                |||||||| ||    |||||
                                CCCGTCCC CG    CCCCC
                                     _  GA__
GAM940  MAD3      3'  TGAGGCAAAGGCAGGGG     24822    A       AGCA
                                C GGGCAGGG    GCAGGGG
                                | ||||||||    |||||||
                                A TCCGTTTC    CGTCCCC
                                 C       _____
GAM940  MAD4      3'  AGGCCAGGAAGCAGGGGG    24823     G         CA
                                AGG CAGGGAGCAG  GGGG
                                ||| ||||||||||  ||||
                                TCC GTCCTTCGTC  CCCC
                                  G         __
GAM940  MAP4K3    5'  CAGGGGAGGGGGGCCGCTCAGG 24824       C    A_  AG__
              GGG                    CAGGG AGGG  GC    CAGGGGG
                                |||||  ||||  ||    |||||||
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                                GTCCC TCCC  CG   GTCCCCC
                                  C   CC  GCGA
GAM940  MARKL1   5' GGGCAGGGGCGGCCGGGTGGGG 24825       A  A  A____
            G                   GGGCAGGG GC GC    GGGGG
                                |||||||| || ||    |||||
                                CCCGTCCC CG CG    CCCCC
                                   _ C  GCCCA
GAM940  MCF2L    3' GGGTGGGAGGCAGGGGG    24826    CA    CA
                                GGG  GGGAG  GCAGGGGG
                                |||  |||||  ||||||||
                                CCC  CCCTC  CGTCCCCC
                                 A_    __
GAM940  MEGF11   5' AGGCAGGAGCAGGGG      24827       GAGC
                                GGGCAGG   AGCAGGGG
                                |||||||   ||||||||
                                TCCGTCC   TCGTCCCC
                                   ____
GAM940  MGC10902 3' CAGGGTACGGGGTGTGCTGGTG 24828     CA_  A___ AGCA
            GGGG                  CAGGG  GGG  GC   GGGGG
                                |||||  |||  ||  |||||
                                GTCCC  CCC  CG  CCCCC
                                  ATG  CACA ACCA
GAM940  MGC11303 3' GGGCAGAGGTCAGGAGGGGG  24829       AG  C
                                GGGCAGGG  CAG AGGGGG
                                ||||||||  ||| ||||||
                                CCCGTCTC  GTC TCCCCC
                                     CA  C
GAM940  MGC16332 3' AGGCAGGGAGTCAGGAGGGG  24830        _  C
                                GGGCAGGGAG CAG AGGGG
                                |||||||||| ||| |||||
                                TCCGTCCCTC GTC TCCCC
                                      A  C
GAM940  MGC16491 5' GGGCAGGGGCCAAGGCGGGGGG 24832       A  A___  A
                                GGGCAGGG GC   GC GGGGG
                                |||||||| ||   || |||||
                                CCCGTCCC CG   CG CCCCC
                                     _ GTTC  C
GAM940  MGC16491 5' CAAGGCGGGGGGCACGAAGG  24831      A  A  G AG
                                CAGGGC GGG GCA C  GGG
                                |||||| ||| ||| |  |||
                                GTTCCG CCC CGT G  TCC
                                   C  C  _ CT
GAM940  MGC17347 5' GGGCAGGGAGGCGGGGG    24833        CA  A
                                GGGCAGGGAG  GC GGGGG
                                ||||||||||  || |||||
                                CCCGTCCCTC  CG CCCCC
                                     __  _
GAM940  MGC20255 3' AGCCCAGGGCGGCAGGGGG  24834    A_  A  A
                                GGC  GGG GC GCAGGGGG
                                |||  ||| || ||||||||
```

```
                                TCG  TCC CG CGTCCCCC
                                  GG   _ C
GAM940   MGC2555   5' GCATGGGAGCAGCGGGGGG   24835     _       A
                                GCA GGGAGCAGC GGGGG
                                ||| ||||||||| |||||
                                CGT CCCTCGTCG CCCCC
                                  A        C
GAM940   MGC29654  5' CAGGGCCGGGGGCAGGG     24836       A   AGCA
                                CAGGGC GGG    GCAGGG
                                |||||| |||    ||||||
                                GTCCCG CCC    CGTCCC
                                   G   C___
GAM940   MGC3195   5' CAGGGCAGGAGGCTCGCGGGGG 24837         GA  A_  A
                                CAGGGCAGG  GC  GC GGGGG
                                |||||||||  ||  || |||||
                                GTCCCGTCC  CG  CG CCCCC
                                     TC  AG  _
GAM940   MGC35521  3' GGGCACAGCAGCAGGGGG    24838      GGG
                                GGGCA   AGCAGCAGGGGG
                                |||||   ||||||||||||
                                CCCGT   TCGTCGTCCCCC
                                  G__
GAM940   MGC4171   5' CAGGGCAGGGAGGGCATAG   24839           CA   G
                                CAGGGCAGGGAG  GCA GG
                                ||||||||||||  ||| ||
                                GTCCCGTCCCTC  CGT TC
                                      C_   A
GAM940   MGC4342   3' AGGCAGGGGGCAGTTAGGGG  24840        A    C_
                                GGGCAGGG GCAG  AGGGG
                                |||||||| ||||  |||||
                                TCCGTCCC CGTC  TCCCC
                                    C    AA
GAM940   MGC5149   3' AGGCTGGGGAGACGGGGGG   24841      A_    CA  A
                                GGGC  GGGAG  GC GGGGG
                                ||||  |||||  || |||||
                                TCCG  CCCTC  TG CCCCC
                                  AC     __  C
GAM940   MGC5508   3' CAGGGCAAGAAAAGGGCAGGGG 24842           CA_
            G                    CAGGGCAGGGAG   GCAGGGGG
                                ||||||||||||   ||||||||
                                GTCCCGTTCTTT   CGTCCCCC
                                      TCC
GAM940   moblak    3' CAGGGCAAGGAGTGACCCTGG  24843           CA  AGG
                                CAGGGCAGGGAG  GC   GG
                                ||||||||||||  ||   ||
                                GTCCCGTTCCTC  TG   CC
                                      AC  GGA
GAM940   MSP       3' CACGGCACCAGCAGGGG     24844    G   GGGAG
                                CA GGCA    CAGCAGGGG
                                || ||||    |||||||||
```

```
                                GT CCGT    GTCGTCCCC
                                 G   G____
GAM940  MSTP028  3'  CACGGCAGGGAGTGGGG    24845   G       CAGCA
                                CA GGCAGGGAG    GGGG
                                || |||||||||    ||||
                                GT CCGTCCCTC    CCCC
                                 G       A____
GAM940  N4BP3    3'  CAGGGCAGGGGACCGAGGG   24846         AG AGC
                                CAGGGCAGGG  C   AGGG
                                ||||||||||  |   ||||
                                GTCCCGTCCC  G   TCCC
                                      CT GC_
GAM940  NCUBE1   3'  GGCAGCAGAGGGCAGGGGG   24847      _   CA
                                GGCAG GGAG  GCAGGGGG
                                ||||| ||||  ||||||||
                                CCGTC TCTC  CGTCCCCC
                                   G   C_
GAM940  NECL1    3'  GGGCTGGGGAGCAAGCGGG   24848     A_     _ A
                                GGGC  GGGAGCA GC GGG
                                ||||  ||||||| || |||
                                CCCG  CCCTCGT CG CCC
                                  AC      T _
GAM940  NINJ2    3'  GGGTAGGGAGCAAGGG      24849     C      GC
                                GGG AGGGAGCA  AGGG
                                ||| ||||||||  ||||
                                CCC TCCCTCGT  TCCC
                                  A       __
GAM940  NINJ2    3'  GGGTAGGGAGCAAGGG      24849     C      GC
                                GGG AGGGAGCA  AGGG
                                ||| ||||||||  ||||
                                CCC TCCCTCGT  TCCC
                                  A       __
GAM940  NLI-IF   3'  CAGGGGATCAGGCAGGGGG   24850      AG_  _
                                CAGGG   CAG CAGGGGG
                                |||||   ||| |||||||
                                GTCCC   GTC GTCCCCC
                                   CTA   C
GAM940  NXPH3    3'  GGGCAGGGGCGAAAGGTGGGGG 24851        A ___  CA
                                GGGCAGGG GC   AG  GGGGG
                                |||||||| ||   ||  |||||
                                CCCGTCCC CG   TC  CCCCC
                                     _ CTT  CA
GAM940  OASIS    3'  GGGCAGCAGCAGGGG       24708       GGGA
                                GGGCA    GCAGCAGGGG
                                |||||    ||||||||||
                                CCCGT    CGTCGTCCCC
                                          _____
GAM940  OASIS    3'  GGGCCAGGGAGCAGCAAAG   24852      _
                                GGGC AGGGAGCAGCAGGG
                                |||| ||||||||||||||
```

```
                                CCCG TCCCTCGTCGTTTC
                                  G
GAM940  OATL1    3'  CAGGGAGGGAGGTGGGG     24853      C     CAGCA
                                CAGGG AGGGAG    GGGG
                                ||||| ||||||    ||||
                                GTCCC TCCCTC    CCCC
                                  _     CA___
GAM940  OSBPL7   5'  AGAGCAGGGAGCAGGG      24854           GCA
                                AGGGCAGGGAGCA  GGG
                                ||||||||||||  |||
                                TCTCGTCCCTCGT  CCC
                                      ___
GAM940  P450RAI-2 3'  CAGGGCGGAGGGCAAAGGGGG  24855       A  A   C
                                CAGGGC GGG GCAG AGGGGG
                                |||||| ||| |||| ||||||
                                GTCCCG CTC CGTT TCCCCC
                                   C  C   _
GAM940  P5CR2    3'  GGGCAGGGGGGGTGGCAGGGG  24856        AGCA_
                                GGGCAGGG    GCAGGGG
                                ||||||||    |||||||
                                CCCGTCCC    CGTCCCC
                                     CCCAC
GAM940  PAK7     5'  GGGTAGGGGCAAGGGGG     24857     C   A  GC
                                GGG AGGG GCA  AGGGGG
                                ||| |||| |||  ||||||
                                CCC TCCC CGT  TCCCCC
                                  A   _  __
GAM940  PALM     3'  AGGGCAGGGACCAAGTTGGGG  24858         G  CAG
                                AGGGCAGGGA CAG   GGGG
                                |||||||||| |||   ||||
                                TCCCGTCCCT GTT   CCCC
                                      G  CAA
GAM940  PEPP3    3'  GGGCAGGGGGCCAGGG      24860        A  AG
                                GGGCAGGG GC  CAGGG
                                |||||||| ||  |||||
                                CCCGTCCC CG  GTCCC
                                     C  __
GAM940  PEPP3    3'  CAGGGTGGGGAGCCAGG     24859      CA    AG
                                CAGGG  GGGAGC  CAGG
                                |||||  ||||||  ||||
                                GTCCC  CCCTCG  GTCC
                                   AC     __
GAM940  PHYHIP   3'  GGGCAAGGAGCAGCCAGGG   24861           A
                                GGGCAGGGAGCAGC GGGG
                                |||||||||||||| ||||
                                CCCGTTCCTCGTCG TCCC
                                        G
GAM940  PIK4CA   3'  CAGGGCAGGGAGGTCGCAGGG  24862          CA_
                                CAGGGCAGGGAG   GCAGGG
                                ||||||||||||   ||||||
```

```
                                GTCCCGTCCCTC  CGTCCC
                                      CAG
GAM940  PIK4CA   3' CAGGGCAGGGAGGTCGCAGGG 24862         CA_
                                CAGGGCAGGGAG  GCAGGG
                                ||||||||||||  ||||||
                                GTCCCGTCCCTC  CGTCCC
                                      CAG
GAM940  PIPPIN   3' AGGGTGGTAGGCAGGGGG   24863    CA  G  CA
                                AGGG  GG AG  GCAGGGGG
                                ||||  || ||  ||||||||
                                TCCC  CC TC  CGTCCCCC
                                  A_  A  __
GAM940  PISD     5' GGCGCAGGGAGGGCGGGG   24864   _     CA  A
                                GG GCAGGGAG  GC GGGG
                                || ||||||||  || ||||
                                CC CGTCCCTC  CG CCCC
                                 G       C_  _
GAM940  PP1057   3' GGGGAGGGGTGCAGGGGG   24865    C   AGCA
                                GGG AGGG   GCAGGGGG
                                ||| ||||   ||||||||
                                CCC TCCC   CGTCCCCC
                                  C   CA__
GAM940  PP1057   3' CAGGGCAGGGAGGCCAGG   24866         CAG
                                CAGGGCAGGGAG  CAGG
                                ||||||||||||  ||||
                                GTCCCGTCCCTC  GTCC
                                      CG_
GAM940  PPAP2C   3' CAGGGCAGGGGGCAGCGG   24867        A   A
                                CAGGGCAGGG GCAGC GG
                                |||||||||| ||||| ||
                                GTCCCGTCCC CGTCG CC
                                     C    _
GAM940  PPAP2C   3' CAGTGCAGGGCAGGGG     24868    G   GAGCA
                                CAG GCAGG    GCAGGGG
                                ||| |||||    |||||||
                                GTC CGTCC    CGTCCCC
                                  A   ______
GAM940  PSTPIP1  5' CAGGGCAGGGAGCAGGG    24869          GCA
                                CAGGGCAGGGAGCA  GGG
                                ||||||||||||||  |||
                                GTCCCGTCCCTCGT  CCC
                                          ___
GAM940  PTP4A1   5' CAGGGCAGGAGGCGGCGG   24870       GA  A  A
                                CAGGGCAGG  GC GC GG
                                |||||||||  || || ||
                                GTCCCGTCC  CG CG CC
                                     TC  C  _
GAM940  PTPRT    3' GGGTGGGAGAGCAGGGGG   24871    CA   C
                                GGG  GGGAG AGCAGGGGG
                                |||  ||||| |||||||||
```

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                                CCC  CCCTC TCGTCCCCC
                                  A_    _
GAM940  PV1      3'  CAGGGCTGGGAGTTGGGGG   24872       A    CAGCA
                                CAGGGC GGGAG    GGGGG
                                |||||| |||||    |||||
                                GTCCCG CCCTC    CCCCC
                                   A    AA___
GAM940  QSCN6    3'  CAAGGCAGGGGGGTAGCGTGGG  24873         AGC   AG
                                CAGGGCAGGG  AGC  GGG
                                ||||||||||  |||  |||
                                GTTCCGTCCC  TCG  CCC
                                      CCA  CA
GAM940  RAB-R    3'  GGGGGACCCCTTCAGCAGGGGG 24874     CA   AG____
                                GGG  GGG     CAGCAGGGGG
                                |||  |||     ||||||||||
                                CCC  CCT     GTCGTCCCCC
                                  __  GGGGAA
GAM940  RAB1B    3'  CAGGGCAGAGGGCGGCAGGAG  24875         A  A
                                CAGGGCAGGG GC GCAGGGG
                                |||||||||| || |||||||
                                GTCCCGTCTC CG CGTCCTC
                                      C  C
GAM940  RAB20    3'  GGGCAGAGAGCACCAGGGG   24876           G
                                GGGCAGGGAGCA CAGGGG
                                |||||||||||| ||||||
                                CCCGTCTCTCGT GTCCCC
                                       G
GAM940  RASGRP4  3'  GGGCAGGGAAGAGGGGG    24877         GC  C
                                GGGCAGGGA  AG AGGGGG
                                |||||||||  || ||||||
                                CCCGTCCCT  TC TCCCCC
                                      __  _
GAM940  RGS19    5'  GGGGTGGGGGCAGGAGGGG   24878     CA  A   C
                                GGG  GGG GCAG AGGGG
                                |||  ||| |||| |||||
                                CCC  CCC CGTC TCCCC
                                  CA   C   C
GAM940  RICH1    5'  CAGGGCGGGGGACAGCCTGG  24879       A  AG   AG
                                CAGGGC GGG  CAGC  GG
                                ||||||  |||  ||||  ||
                                GTCCCG CCC  GTCG  CC
                                   C   CT   GA
GAM940  RMP      5'  CAGGGCAGGGGCCGGGG     24880         A  AGCA
                                CAGGGCAGGG GC   GGGG
                                |||||||||| ||   ||||
                                GTCCCGTCCC CG   CCCC
                                      _  G___
GAM940  RoXaN    3'  GGGCAGGAGGCAGAAGG     24881        GA   C
                                GGGCAGG  GCAG AGGG
                                |||||||  |||| ||||
```

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                                CCCGTCC  CGTC TTCC
                                   TC   _
GAM940  RPS6KA4  3'  CAGGGGAGAACAGGGTAGGGGG 24882      CA      C__
                                CAGGG  GGGAGCAG   AGGGGG
                                |||||  ||||||||   ||||||
                                GTCCC  CTCTTGTC   TCCCCC
                                  __       CCA
GAM940  RTP801   3'  GGGCGGGAGCAGCCCAG     24883     A       AG
                                GGGC GGGAGCAGC  GG
                                ||||  |||||||||  ||
                                CCCG CCCTCGTCG  TC
                                  _       GG
GAM940  SARM     3'  AGGGTGGGGGACAGGGGG    24884     CA   AGCA
                                AGGG  GGG   GCAGGGGG
                                ||||  |||   ||||||||
                                TCCC  CCC   TGTCCCCC
                                  AC   C___
GAM940  SCMH1    3'  CAGGGCAAGGAGCTGTGGTGGG 24885           AGCA__
            GG                    CAGGGCAGGGAGC     GGGGG
                                |||||||||||||     |||||
                                GTCCCGTTCCTCG     CCCCC
                                      ACACCA
GAM940  SDC3     5'  CAGAGGTAGGGAGGGGG     24886    _ C     CAGCA
                                CAG GG AGGGAG    GGGG
                                ||| || ||||||    ||||
                                GTC CC TCCCTC    CCCC
                                  T  A    ______
GAM940  SDS3     3'  CAGGGCATGGGGGGAGGGG   24887       _  AGCAGC
                                CAGGGCA GGG     AGGGG
                                |||||||  |||     |||||
                                GTCCCGT CCC     TCCCC
                                   A   CCC___
GAM940  SIMRP7   3'  AGGGCACACATGCAGCAGGGGG 24888       GGGA_
                                AGGGCA    GCAGCAGGGGG
                                ||||||    ||||||||||||
                                TCCCGT    CGTCGTCCCCC
                                   GTGTA
GAM940  SLC2A13  5'  AGGGCAGGGGCCCGGGG     24889         A  AGCA
                                AGGGCAGGG GC    GGGG
                                |||||||||  ||    ||||
                                TCCCGTCCC CG    CCCC
                                     _  GG__
GAM940  SLC39A3  3'  CAGGGCCAGGGGTTGGGGG   24890       _   AGCAGCA
                                CAGGGC AGGG      GGGGG
                                ||||||  ||||      |||||
                                GTCCCG TCCC      CCCCC
                                   G    CAA_____
GAM940  SNPH     3'  CAGGGCAGGGGCCTATGGG    24891          A  AGCAG
                                CAGGGCAGGG GC     GGG
                                ||||||||||  ||     |||
```

```
                                GTCCCGTCCC CG    CCC
                                     _ GATA_
GAM940  SNTA1   5' CAGGGCAGAGGGCAGCGGGGG 24892        A   A
                                CAGGGCAGGG GCAGC GGGGG
                                |||||||||| ||||| |||||
                                GTCCCGTCTC CGTCG CCCCC
                                     C   _
GAM940  SR-A1   3' GGGCAGGGCAGGGCAGGGGG 24893       AGCA
                                GGGCAGGG   GCAGGGGG
                                ||||||||   ||||||||
                                CCCGTCCC   CGTCCCCC
                                    GTCC
GAM940  SRF     3' GGGCGGGAAGAAGGGG     24894     A   GC  C
                                GGGC GGGA  AG AGGGG
                                |||| ||||  || |||||
                                CCCG CCCT  TC TCCCC
                                  _   __  T
GAM940  SSH-3   3' CAGGGAGGGGGCGGGG     24895     C   A  AGCA
                                CAGGG AGGG GC   GGGG
                                ||||| |||| ||   ||||
                                GTCCC TCCC CG   CCCC
                                  _   C ____
GAM940  STMN3   3' CAGGGCAGAGGGCACAGG   24896       A   G
                                CAGGGCAGGG GCA CAGG
                                |||||||||| ||| ||||
                                GTCCCGTCTC CGT GTCC
                                     C  _
GAM940  SV2     3' CAGGTAGGGAGCATGGG    24897     GC     GCA
                                CAGG  AGGGAGCA  GGG
                                ||||  ||||||||  |||
                                GTCC  TCCCTCGT  CCC
                                  A_      A__
GAM940  SV2     3' CAGGGCAGGGAGGGGAA    24898         CAGCA
                                CAGGGCAGGGAG   GGGGG
                                ||||||||||||   |||||
                                GTCCCGTCCCTC   CCCTT
                                       _____
GAM940  TBX21   5' GGGCAGGGAGCAGGGGG    24899         CA
                                GGGCAGGGAGCAG  GGGG
                                ||||||||||||  ||||
                                CCCGTCCCTCGTC  CCCC
                                       __
GAM940  TERE1   5' GGGCGGGGCAGCAGGG     24900     A  A
                                GGGC GGG GCAGCAGGG
                                |||| ||| |||||||||
                                CCCG CCC CGTCGTCCC
                                  _  _
GAM940  TNFRSF19L 3' CAGGGCAGGCACGGGG     24901       GA  AGCA
                                CAGGGCAGG  GC   GGGG
                                |||||||||  ||   ||||
```

```
                                GTCCCGTCC TG   CCCC
                                    G_ ____
GAM940  TOB2     3' CAGGGCAGTGAGAAGGGG   24902       G  CAGC
                                CAGGGCAG GAG   AGGGG
                                |||||||| |||   |||||
                                GTCCCGTC CTC   TCCCC
                                    A  T___
GAM940  TOMM34   3' CAGGGCAGGGACAGCAG    24903         G
                                CAGGGCAGGGA CAGCAG
                                |||||||||||| ||||||
                                GTCCCGTCCCT GTCGTC
                                      _
GAM940  TRIAD3   3' GGGCAGGGGTGGCACCCAGGG 24904       A__  G_
                                GGGCAGGG  GCA CAGGG
                                ||||||||  |||  |||||
                                CCCGTCCC  CGT  GTCCC
                                    CAC  GG
GAM940  Ubc6p    3' CAGCGCAGGGGGCACGGG   24905    G    AGCA  G
                                CAG GCAGGG   GCA GGG
                                ||| ||||||   ||| |||
                                GTC CGTCCC   CGT CCC
                                  G    C___  G
GAM940  VI       3' CAGAGTGGGGAGTGATTGGGGG 24906     CA   CAGCA
                                CAGGG  GGGAG   GGGGG
                                |||||  |||||   |||||
                                GTCTC  CCCTC   CCCCC
                                   AC    ACTAA
GAM940  WBSCR17  3' CAGGGCAAGGGGGCAGCTACAG 24907       _  A   A__
          GG                    CAGGGCA GGG GCAGC  GGGG
                                ||||||| ||| |||||  ||||
                                GTCCCGT CCC CGTCG  TCCC
                                    T  C    ATG
GAM940  WBSCR18  3' GGGTCGGGGAGGGCAGGGGG  24908    CA_   CA
                                GGG  GGGAG  GCAGGGGG
                                |||  |||||  ||||||||
                                CCC  CCCTC  CGTCCCCC
                                  AGC   C_
GAM940  LOC112868 5' CAGTGCGGCTGGCAGGGGG   24909    G  AG  AGCA
                                CAG GC  GG   GCAGGGGG
                                ||| ||  ||   ||||||||
                                GTC CG  CC   CGTCCCCC
                                  A  __  GAC_
GAM940  LOC113730 5' GGGCAGGGGATGCGGCTGGGG  24910       A__  A  A
                                GGGCAGGG  GC GC GGGG
                                ||||||||  || || ||||
                                CCCGTCCC  CG CG CCCC
                                    CTA  C  A
GAM940  LOC115207 3' TGAGGCAGGGAGTAGAG    24911   A       C  C
                                C GGGCAGGGAG AG AG
                                | ||||||||| || ||
```

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                                A TCCGTCCCTC TC TC
                                 C        A  _
GAM940  LOC116113 3'  CAGGGCAGGGTGGGAGCTGGGG 24912          AGC_  A
                                CAGGGCAGGG   AGC GGGG
                                ||||||||||   ||| ||||
                                GTCCCGTCCC   TCG CCCC
                                     ACCC  A
GAM940  LOC116349 3'  CAGGGCACGGGGCAGGG    24913       _  AGCA
                                CAGGGCA GGG   GCAGGG
                                ||||||| |||   ||||||
                                GTCCCGT CCC   CGTCCC
                                   G  ____
GAM940  LOC120072 5'  CAGGGCAGGGATCACTGG    24914         GCA  A
                                CAGGGCAGGGA  GC GG
                                ||||||||||  || ||
                                GTCCCGTCCCT  TG CC
                                     AG_  A
GAM940  LOC120448 5'  AGGCCGGGGAGCGAGCGG    24915     A_    _  A
                                GGGC  GGGAGC AGC GG
                                ||||  |||||| ||| ||
                                TCCG  CCCTCG TCG CC
                                  GC     C  _
GAM940  LOC120939 3'  CAGGCCAGGAGCAGGGG     24916     G   GAGC
                                CAGG CAGG   AGCAGGGG
                                |||| ||||   ||||||||
                                GTCC GTCC   TCGTCCCC
                                  G   ____
GAM940  LOC123095 3'  GGGCACGCCCTGCAGGGGG   24917      GGGA  A__
                                GGGCA   GC  GCAGGGGG
                                |||||   ||  ||||||||
                                CCCGT   CG  CGTCCCCC
                                   G___  GGA
GAM940  LOC124044 3'  CAGGGTCAGGGAGTTGTGGG  24918      _     CAGCAG
                                CAGGG CAGGGAG     GGG
                                ||||| |||||||     |||
                                GTCCC GTCCCTC     CCC
                                   A      AACA__
GAM940  LOC124402 3'  GGGGAGGGGGCGGCGGGCAGGG 24919     C   A  A____
                                GGG AGGG GC    GCAGGG
                                ||| |||| ||    ||||||
                                CCC TCCC CG    CGTCCC
                                  C   C  CCGCC
GAM940  LOC124753 5'  GGGTTGGAAGACAGGGGG    24920     CA    CA
                                GGG  GGGAG  GCAGGGGG
                                |||  |||||  ||||||||
                                CCC  CCTTC  TGTCCCCC
                                  AA    __
GAM940  LOC124930 3'  GGGCAGGGGAGAGCCGGGGG  24921        _  C   A
                                GGGCAGGG AG AGC GGGGG
                                ||||||| || ||| |||||
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                                CCCGTCCC TC TCG CCCCC
                                     C  _  G
GAM940  LOC126208 3'  AGGGCGGGGAGCCGGGG    24922      A     AGCA
                                AGGGC GGGAGC   GGGG
                                ||||| ||||||   ||||
                                TCCCG CCCTCG   CCCC
                                   C     G___
GAM940  LOC126299 5'  AGGACAGCGCGCAGGGGG   24923       GGA  A
                                AGGGCAG  GC GCAGGGGG
                                |||||||  || ||||||||
                                TCCTGTC  CG CGTCCCCC
                                    G__  _
GAM940  LOC126353 3'  CAGGGCAGGGCAGGGG     24924        GAGCA
                                CAGGGCAGG    GCAGGGG
                                |||||||||    |||||||
                                GTCCCGTCC    CGTCCCC
                                      _____
GAM940  LOC126364 3'  CAGGGAGGGGGCGGCAG    24925      C   A  A
                                CAGGG AGGG GC GCAG
                                ||||| |||| || ||||
                                GTCCC TCCC CG CGTC
                                   _   C  C
GAM940  LOC126964 3'  GGGCAGAGAGCACAGCAGGG  24926          __
                                GGGCAGGGAGCA  GCAGGG
                                ||||||||||||  ||||||
                                CCCGTCTCTCGT  CGTCCC
                                       GT
GAM940  LOC127845 3'  CAGTGCAGGGGACTGAGGGGG  24927    G     AG AGC
                                CAG GCAGGG  C   AGGGGG
                                ||| ||||||  |   ||||||
                                GTC CGTCCC  G   TCCCCC
                                  A     CT AC_
GAM940  LOC129011 3'  CAGGGCAGGGGACAGG     24928         AGCA
                                CAGGGCAGGG   GCAGG
                                ||||||||||   |||||
                                GTCCCGTCCC   TGTCC
                                      C___
GAM940  LOC129138 3'  CAGGGTGGGGCAGTGGCAGG  24929      CA  A  ___
                                CAGGG  GGG GCA   GCAGG
                                |||||  ||| |||   |||||
                                GTCCC  CCC CGT   CGTCC
                                   A_  _  CAC
GAM940  LOC130470 5'  CAAGGCGGGGCAGGGG     24930       A  AGCA
                                CAGGGC GGG   GCAGGGG
                                ||||||| |||   |||||||
                                GTTCCG CCC    CGTCCCC
                                     _  _____
GAM940  LOC132200 3'  CAGGACAGCTTGAAGGTGGGGG 24931        ___   CAGCA
           G                    CAGGGCAG  GGAG    GGGGG
                                ||||||||  ||||    |||||
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                                GTCCTGTC  CTTC    CCCCC
                                    GAA   CAC__
GAM940  LOC138429 3'  CAGGAGCAGGGGGCCGGG   24932     _    A  AGCA
                                CAGG GCAGGG GC   GGG
                                |||| |||||| ||   |||
                                GTCC CGTCCC CG   CCC
                                  T     C  G___
GAM940  LOC138429 3'  CAGGCCAGGAGCAGGGG    24916     G   GAGC
                                CAGG CAGG   AGCAGGGG
                                |||| ||||   ||||||||
                                GTCC GTCC   TCGTCCCC
                                  G   ____
GAM940  LOC143310 5'  CAGGGTGGGGTGCAAACAAAGG 24933      CA  A   _
                                CAGGG  GGG GCAG CAGGGG
                                |||||  ||| |||| ||||||
                                GTCCC  CCC CGTT GTTTCC
                                   AC   A   T
GAM940  LOC144347 3'  CAGGGCAGGCAGCGGGG    24502       GGA    A
                                CAGGGCAG   GCAGC GGGG
                                ||||||||   ||||| ||||
                                GTCCCGTC   CGTCG CCCC
                                     ___    _
GAM940  LOC145195 3'  CAGGGCAGGGGACAGG     24928         AGCA
                                CAGGGCAGGG   GCAGG
                                ||||||||||   |||||
                                GTCCCGTCCC   TGTCC
                                      C___
GAM940  LOC145371 3'  CAGGGCCAGGCAGGGG     24934       A  GAGCA
                                CAGGGC GG    GCAGGGG
                                |||||| ||    |||||||
                                GTCCCG TC    CGTCCCC
                                   G  _____
GAM940  LOC145989 3'  GGGGAGACTGGCAGCAGGGGG  24935    C   GA_
                                GGG AGG   GCAGCAGGGGG
                                ||| |||   ||||||||||
                                CCC TCT   CGTCGTCCCCC
                                  C   GAC
GAM940  LOC146315 5'  CAGGTTAGGGAGCAAGG    24936     GC      GC
                                CAGG  AGGGAGCA  AGG
                                ||||  ||||||||  |||
                                GTCC  TCCCTCGT  TCC
                                  AA      __
GAM940  LOC146488 3'  CAGGGATGGGGAGAGGGG   24618      CA_   CAGC
                                CAGGG   GGGAG   AGGGG
                                |||||   |||||   |||||
                                GTCCC   CCCTC   TCCCC
                                   TAC    ____
GAM940  LOC146545 5'  AGGGCAGGCAGAGGGG     24937       GGA   C
                                AGGGCAG   GCAG AGGGG
                                |||||||   |||| |||||
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                                TCCCGTC  CGTC TCCCC
                                   ___   _
GAM940  LOC146728 5'  CAGGGCAGGGAGGGA      24938          CAGCA
                                CAGGGCAGGGAG    GGG
                                ||||||||||||    |||
                                GTCCCGTCCCTC    CCT
                                   _____
GAM940  LOC146733 3'  GGGTTAGTCAGCAGGGGG    24939    CAG  AG
                                GGG  GG  CAGCAGGGGG
                                |||  ||  ||||||||||
                                CCC  TC  GTCGTCCCCC
                                  AA_  A_
GAM940  LOC148046 3'  GGGCAGAGAGGCAGGGG     24940         CA
                                GGGCAGGGAG  GCAGGGG
                                ||||||||||  |||||||
                                CCCGTCTCTC  CGTCCCC
                                   __
GAM940  LOC148137 3'  GGGCAGCGGAGGATGGGGGG  24941      _   CAGCA
                                GGGCAG GGAG    GGGGG
                                ||||||| ||||    |||||
                                CCCGTC CCTC    CCCCC
                                   G   CTAC_
GAM940  LOC148223 3'  AGGGCAGGCTCCAGGGGG    24942        GAGCAG
                                AGGGCAGG     CAGGGGG
                                ||||||||     |||||||
                                TCCCGTCC     GTCCCCC
                                     GAG___
GAM940  LOC149182 3'  GGGCAGGGGCATTCCAGG    24943        A  G__
                                GGGCAGGG GCA   CAGG
                                |||||||| |||   ||||
                                CCCGTCCC CGT   GTCC
                                     _  AAG
GAM940  LOC149506 5'  CAGGGCGGCGGGCAAAGGGGG  24944       AG_ A   C
                                CAGGGC   GG GCAG AGGGGG
                                ||||||   || |||| ||||||
                                GTCCCG   CC CGTT TCCCCC
                                   CCG  _   _
GAM940  LOC149506 5'  TGAGGCAGGGAGCTCTGGGG  24945   A        AGCA
                                C GGGCAGGGAGC    GGGG
                                | ||||||||||    ||||
                                A TCCGTCCCTCG    CCCC
                                 C         AGA_
GAM940  LOC149603 3'  CAGGGCAGGGGGAAGAGG    24946         AGCAGC
                                CAGGGCAGGG     AGGGG
                                ||||||||||     |||||
                                GTCCCGTCCC     TCTCC
                                      CCT___
GAM940  LOC150111 5'  GGGGGGAGCTCGGGCAGGGGG  24947     CA     A___
                                GGG  GGGAGC    GCAGGGGG
                                |||  ||||||    ||||||||
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                                CCC  CCCTCG   CGTCCCCC
                                  __     AGCC
GAM940   LOC150150 5'  GGGCAGGGGACAGGGG      24948        AGCA
                                GGGCAGGG   GCAGGGG
                                ||||||||   |||||||
                                CCCGTCCC   TGTCCCC
                                    C___
GAM940   LOC150197 3'  CAAGGTAGGGGGACGGGG    24949      C   AGCA  A
                                CAGGG AGGG   GC GGGG
                                ||||| ||||   || ||||
                                GTTCC TCCC   TG CCCC
                                  A   CC__ _
GAM940   LOC150213 3'  CAGGGCAGGGGTCAGGG     24699         AGCAG
                                CAGGGCAGGG    CAGGG
                                ||||||||||    |||||
                                GTCCCGTCCC    GTCCC
                                     CA___
GAM940   LOC150236 3'  CAGGGCAGGGGTCAGGG     24699         AGCAG
                                CAGGGCAGGG    CAGGG
                                ||||||||||    |||||
                                GTCCCGTCCC    GTCCC
                                     CA___
GAM940   LOC150372 3'  AGGCAGGGATGCCTGGGGG   24950         _  AGCA
                                GGGCAGGGA GC   GGGGG
                                |||||||| ||   |||||
                                TCCGTCCCT CG   CCCCC
                                     A  GA__
GAM940   LOC150381 3'  AGAATCGGGGGTGGCAGGGGG 24951     CA   AGCA
                                AGGG  GGG   GCAGGGGG
                                ||||  |||   ||||||||
                                TCTT  CCC   CGTCCCCC
                                  AG   CCAC
GAM940   LOC150481 5'  AGGGGTGGAGGGCAGGGGG   24952     CAG   CA
                                AGGG   GGAG  GCAGGGGG
                                ||||   ||||  ||||||||
                                TCCC   CCTC  CGTCCCCC
                                  CA_   C_
GAM940   LOC151836 5'  GGGCAGGGGCGCAGTGGG    24953        A  A   _
                                GGGCAGGG GC GCAG GGG
                                |||||||| || |||| |||
                                CCCGTCCC CG CGTC CCC
                                    _ _   A
GAM940   LOC152189 5'  GGGCAGGAGGTGCGAGGGGG  24954       G  CA  _
                                GGGCAGG AG  GC AGGGGG
                                ||||||| ||  || ||||||
                                CCCGTCC TC  CG TCCCCC
                                    _ CA  C
GAM940   LOC152220 3'  CAGGATGGCAAGCAGGGGG   24955      A_   _
                                CAGGG  GCA GCAGGGGG
                                |||||  ||| ||||||||
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                                GTCCT  CGT CGTCCCCC
                                   AC   T
GAM940   LOC153196 3'  GGCCTGGGCAGCAGGGGG    24956     AG  A
                                GGC  GG GCAGCAGGGGG
                                |||  || ||||||||||
                                CCG  CC CGTCGTCCCCC
                                  GA  _
GAM940   LOC154428 5'  AGGCAGGGGGCCACGGG     24957        A  AG  G
                                GGGCAGGG GC  CA GGG
                                |||||||| ||  || |||
                                TCCGTCCC CG  GT CCC
                                     C  __  G
GAM940   LOC154807 3'  AGGGCAGGGGGCTAGGG     24958        A  AGC
                                AGGGCAGGG GC   AGGG
                                ||||||||| ||   ||||
                                TCCCGTCCC CG   TCCC
                                     C  A__
GAM940   LOC155066 3'  CAGGGCCAGGGGGCAGAGGG   24959       _   A   C
                                CAGGGC AGGG GCAG AGGG
                                |||||| |||| |||| ||||
                                GTCCCG TCCC CGTC TCCC
                                   G   C   _
GAM940   LOC157923 5'  CAGGAGTGGGGAGAGGGG    24960      CA_    CAGC
                                CAGGG   GGGAG    AGGGG
                                |||||   |||||    |||||
                                GTCCT   CCCTC    TCCCC
                                   CAC    _____
GAM940   LOC158056 5'  CAGGACGGGGGCCCGGGGG   24962       A   A  AGCA
                                CAGGGC GGG GC    GGGGG
                                |||||| ||| ||    |||||
                                GTCCTG CCC CG    CCCCC
                                   C   _  GG__
GAM940   LOC158056 3'  CAGGGCAGGGAACGCCCAGG   24961           A  AG
                                CAGGGCAGGGAGC GC  GGG
                                |||||||||||| ||  |||
                                GTCCCGTCCCTTG CG  TCC
                                       _  GG
GAM940   LOC158288 5'  CAGGGCAGGGAGGACACGGG   24963          CA   G
                                CAGGGCAGGGAG  GCA GGG
                                ||||||||||||  ||| |||
                                GTCCCGTCCCTC  TGT CCC
                                      C_   G
GAM940   LOC158314 5'  CAGTGGCAGGGGGCCGGG    24964     _     A  AGCA
                                CAG GGCAGGG GC    GGG
                                ||| ||||||| ||    |||
                                GTC CCGTCCC CG    CCC
                                  A      C  G___
GAM940   LOC159765 5'  GGGCTGGGGCACAGGGGG    24965     A   A   G
                                GGGC GGG GCA CAGGGGG
                                |||| ||| ||| |||||||
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                                CCCG CCC CGT GTCCCCC
                                  A  _  _
GAM940  LOC162048 5'  CAAGGTGGGGAGCAGGG    24966      CA      GCA
                                CAGGG  GGGAGCA   GGG
                                |||||  |||||||   |||
                                GTTCC  CCCTCGT   CCC
                                  AC      ____
GAM940  LOC163412 5'  CAGGGCAGGGGGTGGAGG    24967          AGCAGCA
                                CAGGGCAGGG      GGGGG
                                ||||||||||      |||||
                                GTCCCGTCCC      CCTCC
                                     CCA_____
GAM940  LOC164395 3'  CAGGGTGAGGGGCAGCCAG    24968      C_   A    A
                                CAGGG  AGGG GCAGC GG
                                |||||  |||| ||||| ||
                                GTCCC  TCCC CGTCG TC
                                  AC   _    G
GAM940  LOC164397 3'  CAGGGAGGGATCTGCGGGGGG  24969      C    GCA  A
                                CAGGG AGGGA   GC GGGGG
                                ||||| |||||   || |||||
                                GTCCC TCCCT   CG CCCCC
                                  _    AGA  C
GAM940  LOC164714 5'  GCGGGCAGCAGGGGG      24970    AG  A
                                GC  GG GCAGCAGGGGG
                                ||  || ||||||||||
                                CG  CC CGTCGTCCCCC
                                 __ _
GAM940  LOC165257 3'  GGGCAGGGAGGACGCAGGG   24971          CA_
                                GGGCAGGGAG   GCAGGG
                                ||||||||||   ||||||
                                CCCGTCCCTC   CGTCCC
                                     CTG
GAM940  LOC196484 5'  AGGGAGGGAGCAGAAG      24972      C       C
                                AGGG AGGGAGCAG AGG
                                |||| |||||||| |||
                                TCCC TCCCTCGTC TTC
                                  _       _
GAM940  LOC196489 3'  CAGGGCGGGAGCCAGCAGGG   24973       A     _
                                CAGGGC GGGAGC AGCAGGG
                                |||||| |||||| |||||||
                                GTCCCG CCCTCG TCGTCCC
                                  _     G
GAM940  LOC196759 3'  GGGCCGAGGTGGCAGGGGG    24974     A  AGCA
                                GGGC GGG    GCAGGGGG
                                |||| |||    ||||||||
                                CCCG CTC    CGTCCCCC
                                  G  CAC_
GAM940  LOC196860 3'  GGGCACGCCCTGCAGGGGG    24917      GGGA  A__
                                GGGCA   GC   GCAGGGGG
                                |||||   ||   ||||||||
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                                CCCGT   CG  CGTCCCCC
                                  G___  GGA
GAM940  LOC196955 3'  CAGGGTTAGGGATAGAGGGGG  24975     C_   GC  C
                                CAGGG  AGGGA  AG AGGGGG
                                ||||| |||||  || ||||||
                                GTCCC  TCCCT  TC TCCCCC
                                  AA    A_  _
GAM940  LOC197003 3'  CAGGTAGGGAGTGGAGAAGGGG 24976     GC    C__  C
                                CAGG  AGGGAG   AG AGGGG
                                ||||  ||||||   || |||||
                                GTCC  TCCCTC   TC TCCCC
                                  A_    ACC  T
GAM940  LOC197136 3'  CAGGGTCAGGGAGTTGTGGG  24918     _     CAGCAG
                                CAGGG CAGGGAG     GGG
                                ||||| |||||||     |||
                                GTCCC GTCCCTC     CCC
                                  A      AACA__
GAM940  LOC199796 5'  CAGGGCCAGGAGTCCAGGGGG  24977      A    CAG
                                CAGGGC GGGAG   CAGGGGG
                                |||||| |||||   |||||||
                                GTCCCG TCCTC   GTCCCCC
                                  G    AG_
GAM940  LOC200014 3'  GGGCAGGGGGGAGACAGCGGGG  24978     __   _   A
                                GGGCA  GGGAG CAGC GGGG
                                |||||  ||||| |||| ||||
                                CCCGT  CCCTC GTCG CCCC
                                  CC    T   _
GAM940  LOC200734 3'  GCAGTGTGGGCGGCAGGGGG  24979     ___  A  A
                                GCAG   GG GC GCAGGGGG
                                ||||   || || ||||||||
                                CGTC   CC CG CGTCCCCC
                                  ACA  _  C
GAM940  LOC201522 3'  CAGGGCAGGACAGGGG     24980        GAGCA
                                CAGGGCAGG    GCAGGGG
                                |||||||||    |||||||
                                GTCCCGTCC    TGTCCCC
                                             _____
GAM940  LOC201522 3'  GGGTGGGGGACGCAGGGGG   24981    CA   AG A
                                GGG  GGG  C GCAGGGGG
                                |||  |||  | ||||||||
                                CCC  CCC  G CGTCCCCC
                                  AC   CT _
GAM940  LOC204994 5'  GGTGTAGTAGGAGCAGGGGG  24982    GCAG  _  C
                                GG    GG AG AGCAGGGGG
                                ||    || || |||||||||
                                CC    TC TC TCGTCCCCC
                                 ACA_  A  C
GAM940  LOC204994 5'  AGGGCCGTGGGCAGGGGG    24984      AG_  AGCA
                                AGGGC   GG    GCAGGGGG
                                |||||   ||    ||||||||
```

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                                TCCCG  CC   CGTCCCCC
                                  GCA ____
GAM940  LOC204994 5' CAGGGGGGGCCGTGGGGGG  24983     CA  A AGCA
                                CAGGG GGG GC   GGGGG
                                ||||| ||| ||   |||||
                                GTCCC CCC CG   CCCCC
                                  __  _ GCAC
GAM940  LOC219920 5' CAGTGGCAGAGCAGGGG    24985    _   GGAGC
                                CAG GGCAG    AGCAGGGG
                                ||| |||||    ||||||||
                                GTC CCGTC    TCGTCCCC
                                 A   _____
GAM940  LOC220020 5' CAGGGCTGGGGGGCAGAGG   24986     A  A   C
                                CAGGGC GGG GCAG AGG
                                |||||| ||| |||| |||
                                GTCCCG CCC CGTC TCC
                                   A  C   _
GAM940  LOC220739 3' AGGGCAGGGAGGCATGGGGG  24987        CA  _
                                AGGGCAGGGAG  GCA GGGGG
                                ||||||||||  ||| |||||
                                TCCCGTCCCTC  CGT CCCCC
                                     __  A
GAM940  LOC220776 3' CAGGGCAGGGTGGGGAGGGG  24988        AGCAGC
                                CAGGGCAGGG    AGGGG
                                ||||||||||    |||||
                                GTCCCGTCCC    TCCCC
                                     ACCCC_
GAM940  LOC220776 3' GGGCAGGGCAGGGTGGGG   24990      GA   CAG
                                GGGCAGG  GCAG  GGGG
                                |||||||  ||||  ||||
                                CCCGTCC  CGTC  CCCC
                                   __   CCA
GAM940  LOC220776 3' CAGGGTGGGGAGGGGCGGGG  24989     CA   CA  A
                                CAGGG  GGGAG  GC GGGG
                                |||||  |||||  || ||||
                                GTCCC  CCCTC  CG CCCC
                                   AC   CC  _
GAM940  LOC220980 5' CAGGGCAGGGGCAGGGGG   24991        AGCA
                                CAGGGCAGGG   GCAGGGGG
                                ||||||||||   ||||||||
                                GTCCCGTCCC   CGTCCCCC
                                     _____
GAM940  LOC221336 5' GGGCGGGGCGCAGGG      24992     A  A  A
                                GGGC GGG GC GCAGGG
                                |||| ||| || ||||||
                                CCCG CCC CG CGTCCC
                                  _  _ _
GAM940  LOC221463 3' CAGGGCAGGCAGCACTGG   24993       GGA    GG
                                CAGGGCAG  GCAGCA  GG
                                ||||||||  ||||||  ||
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                                GTCCCGTC  CGTCGT  CC
                                   ___     GA
GAM940  LOC222682 5'  GCAGGTCTGGCGGCAGGGGG  24994      GA__  A
                                GCAGG   GC GCAGGGGG
                                |||||   || ||||||||
                                CGTCC   CG CGTCCCCC
                                  AGAC  C
GAM940  LOC222682 5'  GGCAGGGGGCACACAGGG    24995       A  _
                                GGCAGGG GCA GCAGGG
                                ||||||| ||| ||||||
                                CCGTCCC CGT TGTCCC
                                    C  G
GAM940  LOC253842 3'  GGGGTAGGGGGAGGCAGGGG  24996    CA___    CA
                                GGG    GGGAG  GCAGGGG
                                |||    |||||  |||||||
                                CCC    CCCTC  CGTCCCC
                                 CATCC    __
GAM940  LOC253926 5'  CAGGGCAGGGGAGCAAGCTGG  24997         _   _ A
                                CAGGGCAGGG AGCA GC GG
                                |||||||||| |||| || ||
                                GTCCCGTCCC TCGT CG CC
                                     C   T  A
GAM940  LOC254263 3'  CAGGGCTGGGGGTGCACAGG  24998      A__  A  G
                                CAGGGC  GGG GCA CAGG
                                ||||||  ||| ||| ||||
                                GTCCCG  CCC CGT GTCC
                                   ACC  A  _
GAM940  LOC255043 3'  CAGAGCAGCAGCAGGGG    24999       GGGA
                                CAGGGCA   GCAGCAGGGG
                                |||||||   ||||||||||
                                GTCTCGT   CGTCGTCCCC
                                   ____
GAM940  LOC255328 3'  CAGAGTAGATCGCAGGGGG   25000     C  GAGCA
                                CAGGG AGG    GCAGGGGG
                                ||||| |||    ||||||||
                                GTCTC TCT    CGTCCCCC
                                  A  AG___
GAM940  LOC255552 5'  CAGGGCGGCGAGCGGAA    25001      A  _   AGCA
                                CAGGGC GG GAGC   GGGG
                                |||||| || ||||   ||||
                                GTCCCG CC CTCG   CCTT
                                   _  G   ____
GAM940  LOC256867 5'  CAGGGCGATAAATGGCGGGGGG 25002      AGG  CA  A
                                CAGGGC  GAG  GC GGGGG
                                ||||||  |||  || |||||
                                GTCCCG  TTT  CG CCCCC
                                   CTA  AC  C
GAM940  LOC257309 5'  GGGCAGGAAGCAAGGGG    24489         GC
                                GGGCAGGGAGCA  AGGGG
                                ||||||||||||  |||||
```

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                                CCCGTCCTTCGT  TCCCC
                                      __
GAM940  LOC257426 3'  CAGGGCAGTGGGGCATGG    25003       _ A   GCA
                                CAGGGCAG GG GCA   GG
                                |||||||| || |||   ||
                                GTCCCGTC CC CGT   CC
                                     A  C   A__
GAM940  LOC257506 5'  GGCAGGGGGCACACAGGG    24995       A  _
                                GGCAGGG GCA GCAGGG
                                ||||||| ||| ||||||
                                CCGTCCC CGT TGTCCC
                                     C   G
GAM940  LOC257506 5'  GCAGGTCTGGCGGCAGGGGG  24994      GA__  A
                                GCAGG    GC GCAGGGGG
                                |||||    || ||||||||
                                CGTCC    CG CGTCCCCC
                                   AGAC  C
GAM940  LOC257624 5'  GGCAGGGGGCACACAGGG    24995       A  _
                                GGCAGGG GCA GCAGGG
                                ||||||| ||| ||||||
                                CCGTCCC CGT TGTCCC
                                     C   G
GAM940  LOC257624 5'  GCAGGTCTGGCGGCAGGGGG  24994      GA__  A
                                GCAGG    GC GCAGGGGG
                                |||||    || ||||||||
                                CGTCC    CG CGTCCCCC
                                   AGAC  C
GAM940  LOC51162  3'  GGGCAGGGGCATGGGGG     25004       A   GCA
                                GGGCAGGG GCA   GGGGG
                                |||||||| |||   |||||
                                CCCGTCCC CGT   CCCCC
                                     _   A__
GAM940  LOC51162  3'  GGGCAGGGGCATGGGGG     25004       A   GCA
                                GGGCAGGG GCA   GGGGG
                                |||||||| |||   |||||
                                CCCGTCCC CGT   CCCCC
                                     _   A__
GAM940  LOC51195  3'  GGGCAGGGAGCAGAAGGGGG  25006           C
                                GGGCAGGGAGCAG AGGGGG
                                |||||||||||| ||||||
                                CCCGTCCCTCGTC TCCCCC
                                        T
GAM940  LOC51195  3'  CAGGGAGGGGGCAGGG      25005      C   AGCA
                                CAGGG AGGG    GCAGGG
                                ||||| ||||    ||||||
                                GTCCC TCCC    CGTCCC
                                   _   C___
GAM940  LOC51667  3'  CAGGGCAGTGGGTGCAGG    25007       _ AGCA
                                CAGGGCAG GG    GCAGG
                                |||||||| ||    |||||
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                                GTCCCGTC CC    CGTCC
                                     A  CA__
GAM940  LOC85414  3' CAGGAGCGGGGAGCTGGG    25008     _ A     AGCA
                                CAGG GC GGGAGC    GGG
                                |||| || ||||||    |||
                                GTCC CG CCCTCG    CCC
                                  T  C     A___
GAM940  LOC90019  5' GGGGAGGGAGCACACCTGG   25009     C       _ AG
                                GGG AGGGAGCA GC  GG
                                ||| |||||||| ||  ||
                                CCC TCCCTCGT TG  CC
                                  C       G  GA
GAM940  LOC90249  5' GGGCAGGGAGCGGAAG      25010          AGCA
                                GGGCAGGGAGC    GGGGG
                                ||||||||||    |||||
                                CCCGTCCCTCG    CCTTC

                                      _____
GAM940  LOC90631  3' GGGCAGGGGGCAGGGG      25011        AGCA
                                GGGCAGGG    GCAGGGG
                                ||||||||    |||||||
                                CCCGTCCC    CGTCCCC
                                     C___
GAM940  LOC90668  3' AGGACAGGGGCTGGCAGGGGG  25012         A  A_
                                AGGGCAGGG GC  GCAGGGGG
                                ||||||||| ||  ||||||||
                                TCCTGTCCC CG  CGTCCCCC
                                     _  AC
GAM940  LOC91049  5' AAGGCCGGCAGCAGGGG     24506      AGGGA
                                AGGGC    GCAGCAGGGG
                                |||||    ||||||||||
                                TTCCG    CGTCGTCCCC
                                   GC___
GAM940  LOC91409  3' GGGCAGGATCATTGGGGG    25013        AG  GCA
                                GGGCAGGG  CA   GGGGG
                                ||||||||  ||   |||||
                                CCCGTCCT  GT   CCCCC
                                     A_  AA_
GAM940  LOC91796  3' GGGTAAGGAGCTGGGGG     25014     C      AGCA
                                GGG AGGGAGC    GGGGG
                                ||| |||||||    |||||
                                CCC TTCCTCG    CCCCC
                                  A      A___
GAM940  LOC91960  3' CAGGGCAGGGATGGCTTGG   25015          GCA  AG
                                CAGGGCAGGGA   GC  GG
                                ||||||||||   ||  ||
                                GTCCCGTCCCT   CG  CC
                                       AC_  AA
GAM940  LOC91978  3' GGGCAGGGGCTCCCGCGGGGG  25016        A  A___  A
                                GGGCAGGG GC    GC GGGGG
                                |||||||| ||    || |||||
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                                CCCGTCCC CG    CG CCCCC
                                    _ AGGG  _
GAM940  LOC92223  5' CAGGGAGGGGGCAGCGG     25017      C    A    A
                                CAGGG AGGG GCAGC GG
                                ||||| |||| ||||| ||
                                GTCCC TCCC CGTCG CC
                                   _   C    _
GAM940  LOC92230  5' GGAGATGGCAGCAGGGGGG    24524    C   GA
                                GG AGG  GCAGCAGGGGG
                                || |||  ||||||||||
                                CC TCT  CGTCGTCCCCC
                                 _  AC
GAM940  LOC93538  5' GGGCAGGGCAGCGTCGGGG    25018         _  AGCA
                                GGGCAGGG AGC    GGGG
                                |||||||| |||    ||||
                                CCCGTCCC TCG    CCCC
                                     G   CAG_
GAM941  AGL     3'  ACACAGTAGTTCAAGACATATC 25021         T          _
          AG                    ACACAGT AGTTCAAGACATA CAG
                                ||||||| |||||||||||| |||
                                TGTGTCA TCAAGTTCTGTAT GTC
                                   _           A
GAM941  AGL     3'  ACACAGTAGTTCAAGACATATC 25021         T          _
          AG                    ACACAGT AGTTCAAGACATA CAG
                                ||||||| |||||||||||| |||
                                TGTGTCA TCAAGTTCTGTAT GTC
                                   _           A
GAM941  AGL     3'  ACACAGTAGTTCAAGACATATC 25021         T          _
          AG                    ACACAGT AGTTCAAGACATA CAG
                                ||||||| |||||||||||| |||
                                TGTGTCA TCAAGTTCTGTAT GTC
                                   _           A
GAM941  AGL     3'  ACACAGTAGTTCAAGACATATC 25021         T          _
          AG                    ACACAGT AGTTCAAGACATA CAG
                                ||||||| |||||||||||| |||
                                TGTGTCA TCAAGTTCTGTAT GTC
                                   _           A
GAM941  AGL     3'  ACACAGTAGTTCAAGACATATC 25021         T          _
          AG                    ACACAGT AGTTCAAGACATA CAG
                                ||||||| |||||||||||| |||
                                TGTGTCA TCAAGTTCTGTAT GTC
                                   _           A
GAM941  AGL     3'  ACACAGTAGTTCAAGACATATC 25021         T          _
          AG                    ACACAGT AGTTCAAGACATA CAG
                                ||||||| |||||||||||| |||
                                TGTGTCA TCAAGTTCTGTAT GTC
                                   _           A
GAM941  CALB1    3'  CACAGTTATTTTTTAGATACAG 25022          GTTCA_  CA
                                CACAGTTA     AGA  TACAG
                                ||||||||     |||  |||||
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                                GTGTCAAT     TCT  ATGTC
                                    AAAAAA   __
GAM941   COL4A3   3'  AGCAGGTTTTAAGACATACAG  25023     TA   C_
                                AGT  GTT  AAGACATACAG
                                |||  |||  ||||||||||
                                TCG  CAA  TTCTGTATGTC
                                  TC   AA
GAM941   COL4A3   3'  AGCAGGTTTTAAGACATACAG  25023     TA   C_
                                AGT  GTT  AAGACATACAG
                                |||  |||  ||||||||||
                                TCG  CAA  TTCTGTATGTC
                                  TC   AA
GAM941   COL4A3   3'  AGCAGGTTTTAAGACATACAG  25023     TA   C_
                                AGT  GTT  AAGACATACAG
                                |||  |||  ||||||||||
                                TCG  CAA  TTCTGTATGTC
                                  TC   AA
GAM941   FBLN5    5'  ACACAGCTGGTTCAGATTACAG 25024         A    A  CA
                                ACACAGTT GTTCA GA  TACAG
                                |||||||| ||||| ||  |||||
                                TGTGTCGA CAAGT CT  ATGTC
                                    C    _  A_
GAM941   GATA6    3'  GTTAGTCACACTATACAG    25025       T  AG  _
                                GTTAGT CA  AC ATACAG
                                ||||||  ||  ||  ||||||
                                CAATCA GT  TG TATGTC
                                   _  G_  A
GAM941   HTRA3    3'  ACAGTAGAGAAACATACAG   25026       T  TTCA
                                ACAGT AG    AGACATACAG
                                |||||  ||    ||||||||||
                                TGTCA TC    TTTGTATGTC
                                  _  TC__
GAM941   IFI35    3'  CACTGTTGGTGAACATACAG  25027     A   A  TCAA
                                CAC GTT GT    GACATACAG
                                |||  |||  ||    |||||||||
                                GTG CAA CA    TTGTATGTC
                                  A   C  C___
GAM941   NAV2     3'  ACACAGTTAGTACAAAAC    25028           T
                                ACACAGTTAGT CAAGAC
                                ||||||||||  ||||||
                                TGTGTCAATCA GTTTTG
                                       T
GAM941   RAB4A    3'  CACTGGGCTACAGGACATACAG 25029     AGTTA  _  A
                                CAC     GTT CA GACATACAG
                                |||     |||  ||  |||||||||
                                GTG     CGA GT CTGTATGTC
                                  ACC__   T  C
GAM941   TIMP3    3'  ACACAGTCTGGTTGGGACATGC 25030         A_   CAA    A
            AG                    ACACAGTT  GTT   GACAT CAG
                                ||||||||  |||   |||||  |||
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                                TGTGTCAG  CAA   CTGTA GTC
                                     AC   CC_    C
GAM941  AKAP8    3'  AGTTAGCCCCTGGTATACAG   25031        AAGAC
                                AGTTAGTTC    ATACAG
                                |||||||||    ||||||
                                TCAATCGGG    TATGTC
                                     GACCA
GAM941  CRSP3    3'  ACAGTAAGTTCAAGTCCATA   25032      T       A_
                                ACAGT AGTTCAAG  CATA
                                ||||| ||||||||  ||||
                                TGTCA TCAAGTTC  GTAT
                                   T       AG
GAM941  KIAA0632 3'  ACATATTATAAATAGACATACA 25033     _   GTTCA
           G                     ACA GTTA    AGACATACAG
                                ||| ||||    ||||||||||
                                TGT TAAT    TCTGTATGTC
                                  A   ATTTA
GAM941  KIAA0981 3'  ACACAGTTGTTCAAGTCAT    25034        A      A
                                ACACAGTT GTTCAAG CAT
                                |||||||| ||||||| |||
                                TGTGTCAA CAAGTTC GTA
                                     _      A
GAM941  LEPROTL1 3'  CAGTTCAGAGGTATACAG    25035        _ AC
                                TAGTTCA AG  ATACAG
                                ||||||| ||  ||||||
                                GTCAAGT TC  TATGTC
                                     C  CA
GAM941  MAP3K3   3'  ACACAGCTGGTGGTAGCATA   25036        A  TCA  A
                                ACACAGTT GT   AG CATA
                                |||||||| ||   || ||||
                                TGTGTCGA CA   TC GTAT
                                     C  CCA  _
GAM941  NFAT5    3'  ACACAGTCTAAGGCATGCA    25037        AGTTC   A   A
                                ACACAGTT    AAG CAT CA
                                ||||||||    ||| ||| ||
                                TGTGTCAG    TTC GTA GT
                                     A____   C   C
GAM941  PPP1R9A  3'  CAGTTATTCAACACACAG    25038      G    AG
                                CAGTTA TTCA  ACATACAG
                                |||||| ||||  ||||||||
                                GTCAAT AAGT  TGTGTGTC
                                     _   __
GAM941  PRO2730  5'  CAGTAACAAGACATGCAG    25039     TAGTT       A
                                CAGT    CAAGACAT CAG
                                ||||    |||||||| |||
                                GTCA    GTTCTGTA GTC
                                  TT___       C
GAM941  LOC142973 3'  ACAGTTAGTCACAAATACAG  25040          _  GAC
                                ACAGTTAGTT CAA   ATACAG
                                |||||||||| |||   ||||||
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                                TGTCAATCAG GTT   TATGTC
                                      T  ___
GAM941  LOC145814 3'  CACAGTTGAGTGCTACATACAG 25041       _  TCAAG
                                CACAGTT AGT    ACATACAG
                                ||||||| |||    ||||||||
                                GTGTCAA TCA    TGTATGTC
                                   C  CGA__
GAM941  LOC148293 5'  CACATAGTTCAAAATCA    25042     GT       _
                                CACA  TAGTTCAAGA CA
                                ||||  |||||||||| ||
                                GTGT  ATCAAGTTTT GT
                                  __       A
GAM941  LOC152179 5'  ATCAGTTTTGGACATACA    25043       CAA
                                GTTAGTT   GACATACA
                                |||||||   ||||||||
                                TAGTCAA   CTGTATGT
                                   AAC
GAM941  LOC155434 3'  ACAGCTAGAACGCATACAG   25044       TTCAAGA
                                ACAGTTAG      CATACAG
                                ||||||||      |||||||
                                TGTCGATC      GTATGTC
                                   TTGC___
GAM941  LOC201595 3'  CAGTTAGTCCAAATTCTCAG  25045          ACATA
                                CAGTTAGTTCAAG    CAG
                                ||||||||||||    |||
                                GTCAATCAGGTTT    GTC
                                      AAGA_
GAM941  LOC221415 3'  ACACTGTCCCAGGACATACAG  25046    A  AGT  A
                                ACAC GTT   TCA GACATACAG
                                |||| |||   ||| |||||||||
                                TGTG CAG   GGT CTGTATGTC
                                  A  ___  C
GAM941  LOC90049  3'  CACATAGTTCAAAATCA    25042     GT       _
                                CACA  TAGTTCAAGA CA
                                ||||  |||||||||| ||
                                GTGT  ATCAAGTTTT GT
                                  __       A
GAM941  LOC92597  3'  CACAGTGGAAAAACATACAG  25047      TAGTTC
                                CACAGT     AAGACATACAG
                                ||||||     ||||||||||||
                                GTGTCA     TTTTGTATGTC
                                   CCT___
GAM941  LOC93109  3'  AGTTAGTTCCTGAAGCATACAG 25048       ___  A
                                AGTTAGTTC   AAG CATACAG
                                |||||||||   ||| |||||||
                                TCAATCAAG   TTC GTATGTC
                                      GAC  _
GAM942  CD80      5'  GCAAAACAGGCAGGGCTGATGA 25051       __  TTACCA
            C                   GCAAAACA  TAG     ATGAC
                                ||||||||  |||     |||||
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                                CGTTTTGT  GTC     TACTG
                                    CC   CCGAC_
GAM942  FNTB    3'  AGGTAATACATAGCCCAATA  25052    C  A     TA
                                AGG AA ACATAGT  CCAATG
                                ||| || |||||||  ||||||
                                TCC TT TGTATCG  GGTTAT
                                  A  A     __
GAM942  HD      3'  AGACAAAACACAGCTCAGTGAC 25053           AC  A
                                AGGCAAAACATAGTT  CA TGAC
                                ||||||||||||||  || ||||
                                TCTGTTTTGTGTCGA  GT ACTG
                                        __ C
GAM942  MME     3'  AGGCAAAGCTAGTGAATGA   25054       ACA   TACC
                                AGGCAAA   TAGT   AATGA
                                |||||||   ||||   |||||
                                TCCGTTT   ATCA   TTACT
                                    CG_   C___
GAM942  MME     3'  AGGCAAAGCTAGTGAATGA   25054       ACA   TACC
                                AGGCAAA   TAGT   AATGA
                                |||||||   ||||   |||||
                                TCCGTTT   ATCA   TTACT
                                    CG_   C___
GAM942  MME     3'  AGGCAAAGCTAGTGAATGA   25054       ACA   TACC
                                AGGCAAA   TAGT   AATGA
                                |||||||   ||||   |||||
                                TCCGTTT   ATCA   TTACT
                                    CG_   C___
GAM942  MME     3'  AGGCAAAGCTAGTGAATGA   25054       ACA   TACC
                                AGGCAAA   TAGT   AATGA
                                |||||||   ||||   |||||
                                TCCGTTT   ATCA   TTACT
                                    CG_   C___
GAM942  PPP1CC   5'  AGGCAGATCGTCTCCAATGAC  25055      AAACATA   A
                                AGGCA      GTT CCAATGAC
                                |||||      ||| ||||||||
                                TCCGT      CAG GGTTACTG
                                   CTAG___   A
GAM942  SRGAP2   3'  AGGCAAGAGCAAACACCAATGA 25056       AA_  TAGT
          C                      AGGCAA   CA   TACCAATGAC
                                ||||||   ||   ||||||||||
                                TCCGTT   GT   GTGGTTACTG
                                   CTC  TT__
GAM942  BAG5    3'  GGCCAAAACGTGGATTCCAATG 25057     _    ATA_  A
          AC                     GGC AAAAC    GTT CCAATGAC
                                ||| |||||    ||| ||||||||
                                CCG TTTTG    TAA GGTTACTG
                                  G    CACC   _
GAM942  BFAR    3'  AAGCAAAACAAAAGCCCAGTGA 25058         T_  TA  A
          C                      AGGCAAAACA  AGT  CCA TGAC
                                ||||||||||  |||  ||| ||||
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                                TTCGTTTTGT  TCG  GGT ACTG
                                      TT   __   C
GAM942  FBXW2    3'  GGCAAAACATAGATAAATGA   25059          TTACC
                                GGCAAAACATAG    AATGA
                                ||||||||||||    |||||
                                CCGTTTTGTATC    TTACT
                                       TAT__
GAM942  FLJ12439  3'  AGGCAAAACGAAGCCCACACCA 25060         AT   ___
            ATGA                    AGGCAAAAC  AGT   TACCAATGA
                                ||||||||||  |||  ||||||||||
                                TCCGTTTTG  TCG   GTGGTTACT
                                     CT   GGT
GAM942  FLJ14011  3'  AGGTCAAAATCACCAATGA   25061     _   ACATA
                                AGG CAAA    GTTACCAATGA
                                ||| ||||    ||||||||||||
                                TCC GTTT    TAGTGGTTACT
                                  A   ______
GAM942  FLJ20511  3'  GGGAAAATGAACACCAATGAC  25062    C    CATAGT
                                GG AAAA     TACCAATGAC
                                || ||||     ||||||||||
                                CC TTTT     GTGGTTACTG
                                 C   ACTT__
GAM942  GNB1L    5'  GGCAGGATGCAGTTACCTGA   25063     AAACA      AA
                                GGCA    TAGTTACC  TGA
                                ||||    ||||||||  |||
                                CCGT    GTCAATGG  ACT
                                  CCTAC       __
GAM942  KIAA1775  3'  GCAAAACAGGGGTCAGTGAC   25064        TA_   CCAA
                                GCAAAACA   GTTA    TGAC
                                ||||||||   ||||    ||||
                                CGTTTTGT   CAGT    ACTG
                                     CCC    C___
GAM942  KIAA1796  3'  AGGAAGATAGGATACCAATG   25065    CAA  C    T_
                                AGG   AA ATAG  TACCAATG
                                |||   || ||||  ||||||||
                                TCC   TT TATC  ATGGTTAC
                                  ___  C    CT
GAM942  MSC      3'  AGGCAAAACGTGGTCGCCCAGA 25066         ATA  TA  AAT
                                AGGCAAAAC   GT  CC   GA
                                |||||||||   ||  ||   ||
                                TCCGTTTTG   CA  GG   CT
                                     CAC  GC  GT_
GAM942  PDE4DIP   3'  GCAGGATATCTACCAATGA   25067    AAAC   G
                                GCA    ATA TTACCAATGA
                                |||    ||| ||||||||||
                                CGT    TAT GATGGTTACT
                                  CC__   A
GAM942  PDZ-GEF1  3'  AGCAGGACACATCCGCCAATGA 25068      AA     G TA
            C                    GGCA  ACATA T  CCAATGAC
                                ||||  ||||| |  ||||||||
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                                TCGT  TGTGT G  GGTTACTG
                                  CC     A GC
GAM942  SYNJ2    3'  GGCCAGGACAGCTACTAATG   25069     AAAAC       C
                                GGC     ATAGTTAC AATG
                                |||     |||||||| ||||
                                CCG     TGTCGATG TTAC
                                  GTCC_       A
GAM942  ZNF345   3'  AGGCAAAATATAATAAATGA   25070         C     TACC
                                AGGCAAAA ATAGT    AATGA
                                |||||||| |||||    |||||
                                TCCGTTTT TATTA    TTACT
                                     A    T___
GAM942  ZNF396   3'  AGGTAAAACATAGTTACTCA   25071     C           _
                                AGG AAAACATAGTTAC CA
                                ||| ||||||||||||| ||
                                TCC TTTTGTATCAATG GT
                                  A           A
GAM942  LOC118812 3'  GGAAAGACAGAACCACCAATGA 25072    C  A   T  TT
            C                    GG AA ACA AG  ACCAATGAC
                                || || ||| ||  |||||||||
                                CC TT TGT TT  TGGTTACTG
                                 T  C   C  GG
GAM942  LOC131377 3'  GGCAAAGCCACCAATG      25073       AACAT
                                GGCAA     AGTTACCAATG
                                |||||     ||||||||||
                                CCGTT     TCGGTGGTTAC
                                          _____
GAM942  LOC150481 3'  AGGCAAAATGCATGAGCAATGA 25074         CA  GTTAC
            C                    AGGCAAAA  TA     CAATGAC
                                ||||||||  ||    |||||||
                                TCCGTTTT  GT    GTTACTG
                                     AC  ACTC_
GAM942  LOC56899  5'  AAGTAAAACATAGTTTGCCA   25075     C         A_
                                AGG AAAACATAGTT  CCA
                                ||| ||||||||||  |||
                                TTC TTTTGTATCAA  GGT
                                  A          AC
GAM942  LOC57228  3'  GACAGAGTAGAGCAGCCAATGA 25076      AAACAT   TA
            C                    GGCA      AGT  CCAATGAC
                                ||||      |||  ||||||||
                                CTGT      TCG  GGTTACTG
                                  CTCATC   TC
GAM943  ATF6     3'  CTCAGTTTTCCAGCATAGCTGC 25079      A         CCCA__
            AGG                   CTCA TTTTCCAGTAT      AGG
                                |||| ||||||||||      |||
                                GAGT AAAAGGTCGTA      TCC
                                  C          TCGACG
GAM943  CDH6     3'  CCAATTTTCCTCTTCCAAGG   25080          AGTATC
                                TCAATTTTCC     CCAAGG
                                ||||||||||     ||||||
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                                GGTTAAAAGG     GGTTCC
                                     AGAA__
GAM943  CLECSF5  3'  CTCAGTTTCCCAAATGGGCAAG 25081      A       TATCC
           G                    CTCA TTTTCCAG     CAAGG
                                ||||  ||||||||     |||||
                                GAGT AAAGGGTT     GTTCC
                                  C       TACCC
GAM943  CYP51    3'  CCAATTTTATTACTCCCAAGG  25082         CCAGTA
                                TCAATTTT     TCCCAAGG
                                ||||||||     ||||||||
                                GGTTAAAA     AGGGTTCC
                                     TAATG_
GAM943  EGFL5    3'  TCAATTTTTCAATACCTTTTAA 25083         C      CC__
           GG                     TCAATTTT CAGTATC    AAGG
                                ||||||||  |||||||    ||||
                                AGTTAAAA GTTATGG    TTCC
                                     A      AAAA
GAM943  IL4R     3'  TCAATTTCTCATCGATTTCCCA 25084        TC  GTA___
           AGG                    TCAATTT  CA     TCCCAAGG
                                |||||||  ||     ||||||||
                                AGTTAAA  GT     AGGGTTCC
                                    GA  AGCTAA
GAM943  IL7      5'  ACTGCAGTTTCATCCATCCCAA 25085     _  A  __    GTA
           GG                     ACT CA TTT  TCCA   TCCCAAGG
                                |||  ||  |||  ||||   ||||||||
                                TGA GT AAA  AGGT   AGGGTTCC
                                  C  C   GT   ___
GAM943  PLXNA2   3'  CTCAGTTTCCAGCCAGCCAGGG 25086      AT       ATC   A
                                CTCA  TTTCCAGT   CCA GG
                                ||||  ||||||||   ||| ||
                                GAGT  AAAGGTCG   GGT CC
                                  C_       GTC   C
GAM943  RAB30    5'  TCAATTTTCTCTCGTCCTCAGG 25087         CAGTA   CA
                                TCAATTTTC    TCC  AGG
                                |||||||||    |||  |||
                                AGTTAAAAG    AGG  TCC
                                     AGAGC   AG
GAM943  ZNF179   3'  CTTAACTTTCCTACAATCCAGG 25088    C       AG  TC   A
           G                     CT AATTTTCC  TA  CCA GG
                                || ||||||||  ||  ||| ||
                                GA TTGAAAGG  GT  GGT CC
                                 A       AT  TA   C
GAM943  C9orf14  5'  ACTTGCTTTTCCAGCACCAGTA 25089     CAA         CC_
           AGG                    ACT   TTTTCCAGTATC   AAGG
                                |||   ||||||||||||   ||||
                                TGA   AAAAGGTCGTGG   TTCC
                                  ACG          TCA
GAM943  FLJ20273 5'  TCAATTTTTGCAGTGCCCTTTG 25090        C_   AT  CA__
           AGG                    TCAATTTT  CAGT  CC    AGG
                                ||||||||  ||||  ||    |||
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                                AGTTAAAA  GTCA  GG    TCC
                                    AC    CG  AAAC
GAM943  FLJ20371  3'  CTCAATTCCCATTTCAAG    25091        T   GTATCC
                                CTCAATTT CCA     CAAG
                                |||||||| |||     ||||
                                GAGTTAAG GGT     GTTC
                                    _   AAA___
GAM943  HPIP     3'  ACTCAATTTGCTACATCTCCCA 25092         TC__  GTA    A
          GGG                     ACTCAATTT    CA   TCCCA GG
                                |||||||||    ||   ||||| ||
                                TGAGTTAAA    GT   AGGGT CC
                                    CGAT  AG_    C
GAM943  KIAA0515  3'  TCGATTTCCCATCCAAG     25093     A      GTATC
                                TC ATTTTCCA     CCAAG
                                || ||||||||     |||||
                                AG TAAAGGGT     GGTTC
                                 C       A____
GAM943  KIAA1676  3'  TTTTCCATACTCCCAAGG     25094        GTA
                                TTTTCCA   TCCCAAGG
                                |||||||   ||||||||
                                AAAAGGT   AGGGTTCC
                                    ATG
GAM943  SCYA22    3'  ATTTTCCAGCAGTCCTGAGG   25095          _   CA
                                ATTTTCCAGTA TCC  AGG
                                |||||||||| |||  |||
                                TAAAAGGTCGT AGG  TCC
                                    C   AC
GAM943  LOC143425 3'  ATCCTCATTAGTATCCCAAGG  25096       C__
                                ATTTTC   AGTATCCCAAGG
                                ||||||   ||||||||||||
                                TAGGAG   TCATAGGGTTCC
                                   TAA
GAM943  LOC91464  5'  TCAATCTTCCAGAGAAG     25097          TATCCC
                                TCAATTTTCCAG     AAG
                                ||||||||||||     |||
                                AGTTAGAAGGTC     TTC
                                    TC____
GAM944  CYYR1     3'  CACCTTAAAATGCTTTGT     25100      G        C
                                CACC TAGAATGCTT GT
                                |||| ||||||||| ||
                                GTGG ATTTTACGAA CA
                                  A        A
GAM944  KIAA0775  3'  TCGCCGTAGAAGGCTCCCCA   25101    A       T    GT
                                TC CCGTAGAA GCTTC  CCA
                                || |||||||| |||||  |||
                                AG GGCATCTT CGAGG  GGT
                                 C       C    __
GAM944  KIAA1855  3'  TCTCACCGAGTTGTC       25102         T  AATGC  C
                                TCTCACCG AG    TT GTC
                                |||||||| ||    || |||
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                                AGAGTGGC TC     AA CAG
                                  _ ______ _
GAM944  MIP-T3    5'  TCTCGCCGCAGGGCGTTCG   25103      A     AAT _
                                TCTC CCGTAG   GC TTCG
                                |||| ||||||   || ||||
                                AGAG GGCGTC   CG AAGC
                                  C     C__  C
GAM944  LOC115297 3'  TCTCACCGTAGGATATCT    25104          A  _
                                TCTCACCGTAG ATG CT
                                |||||||||||| ||| ||
                                AGAGTGGCATC TAT GA
                                      C   A
GAM944  LOC150372 5'  TCTCACCGTGGAGTGTGGCCA  25105         A  A  CTTC T
                                TCTCACCGT GA TG    G CCA
                                ||||||||| || ||    | |||
                                AGAGTGGCA CT AC    C GGT
                                     C  C  AC__ _
GAM944  LOC255158 3'  CCTCATTGTAGAATTTTTCA   25106      CC      GC
                                TCTCA  GTAGAAT  TTCG
                                |||||  |||||||  ||||
                                GGAGT  CATCTTA  AAGT
                                   AA      AA
GAM945  DYT1      3'  CACTTGGAATTAAAACATAAT  25109     C_    CGAG
                                CAC  GGAAT    TAAAACATAAT
                                |||  |||||   ||||||||||
                                GTG  CCTTA    ATTTTGTATTA
                                  AA    ____
GAM945  FOXO1A    3'  GGAAAGTAATAAAACATAAT   25110      TCG
                                GGAA   AGTAAAACATAAT
                                ||||   ||||||||||||
                                CCTT   TTATTTTGTATTA
                                   TCA
GAM945  GPR44     3'  GGAGAGAAAACATAA       25111     ATC   T
                                GGA   GAG AAAACATAA
                                |||   ||| |||||||||
                                CCT   CTC TTTTGTATT
                                   ___  _
GAM945  LOC152137 5'  CACACGGGTCACCTAAAACATA 25112     _  AA   AG
                                CAC CGG  TCG  TAAAACATA
                                ||| |||  |||  |||||||||
                                GTG GCC  AGT  ATTTTGTAT
                                  T  C_   GG
GAM945  LOC202134 3'  CGGACATTTGTAAAACATAAT  25113      ATCGA
                                CGGA    GTAAAACATAAT
                                ||||    ||||||||||||
                                GCCT    CATTTTGTATTA
                                   GTAAA
GAM945  LOC203523 3'  CAGAATTTAATGGAACATAAT  25114       CG   AA
                                CGGAAT  AGT  AACATAAT
                                ||||||  |||  ||||||||
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                                GTCTTA  TTA  TTGTATTA
                                   AA   CC
GAM946  PLAC1     3'  TCAGACATTTGTACACT     25117     A       G
                                TCG ACATTTGTA CATT
                                ||| ||||||||| ||||
                                AGT TGTAAACAT GTGA
                                  C       _
GAM946  POU4F1    3'  TCAACATTTCTATAATTTCAT  25118    G      G  GC
                                TC AACATTT TA  ATTTCAT
                                || ||||||| ||  |||||||
                                AG TTGTAAA AT  TAAAGTA
                                 _      G  AT
GAM946  FLJ14751  3'  CATCATACATTTCATAT     25119      TGTA
                                CATT    GCATTTCATAT
                                ||||    ||||||||||
                                GTAG    TGTAAAGTATA
                                  TA__
GAM946  GDAP2     3'  GAACATTTCCATTTCATAT    25120        GTAG
                                GAACATTT    CATTTCATAT
                                ||||||||    ||||||||||
                                CTTGTAAA    GTAAAGTATA
                                     G___
GAM946  NR2C1     3'  ATTTGTAGTGTTTCATAT     25121        CA
                                ATTTGTAG  TTTCATAT
                                ||||||||  ||||||||
                                TAAACATC  AAAGTATA
                                     AC
GAM946  UBP1      3'  TCAATATGAAACATTTCATAT  25122      ACATT  T
                                TCGA    TG AGCATTTCATAT
                                ||||    || ||||||||||||
                                AGTT    AC TTGTAAAGTATA
                                  AT___  T
GAM946  LOC146952 5'  GAACACTGGCAATTTCATAT   25123        T   GC
                                GAACATT GTA  ATTTCATAT
                                ||||||| |||  |||||||||
                                CTTGTGA CGT  TAAAGTATA
                                     C  __
GAM946  LOC148562 3'  GATGATTTTAGCATTTCATAT  25124    AC   G
                                GA  ATTT TAGCATTTCATAT
                                ||  |||| ||||||||||||
                                CT  TAAA ATCGTAAAGTATA
                                 AC   _
GAM946  LOC151201 3'  GAGCATTTGCAGTATACATAT  25125    A       C  TT
                                GA CATTTGTAG AT  CATAT
                                || |||||||| ||  |||||
                                CT GTAAACGTC TA  GTATA
                                 C       A  T_
GAM947  NRG1      5'  TGGCGGCTCGCGTCCTGG    25128        CC     G_
                                TGGCGGT  CGCGTC  GG
                                |||||||  ||||||  ||
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                                ACCGCCG  GCGCAG  CC
                                   A_     GA
GAM947  NRG1     5'  TGGCGGCTCGCGTCCTGG    25128       CC     G_
                                TGGCGGT  CGCGTC  GG
                                |||||||  ||||||  ||
                                ACCGCCG  GCGCAG  CC
                                   A_     GA
GAM947  NRG1     5'  TGGCGGCTCGCGTCCTGG    25128       CC     G_
                                TGGCGGT  CGCGTC  GG
                                |||||||  ||||||  ||
                                ACCGCCG  GCGCAG  CC
                                   A_     GA
GAM947  NRG1     5'  TGGCGGCTCGCGTCCTGG    25128       CC     G_
                                TGGCGGT  CGCGTC  GG
                                |||||||  ||||||  ||
                                ACCGCCG  GCGCAG  CC
                                   A_     GA
GAM947  RAD54B   3'  TGGTGATTCTTATCTGGTCGTG 25129     C   CCCGC   G
          G                     TGG GGT    GTC GGTCGTGG
                                ||| |||    ||| ||||||||
                                ACC CTA    TAG CCAGCACC
                                  A   AGAA_   A
GAM947  HUMZD58C02 3'  TGGAGGTCCCGCGGCGTGTGG  25130     C       T  GGTC
                                TGG GGTCCCGCG CG    GTGG
                                ||| |||||||| ||    ||||
                                ACC CCAGGGCGC GC    CACC
                                  T       C  A___
GAM947  MGC33182 5'  TGGCGGTCGCTGCCTCGCTGTC 25131        CC_  G   G_
          GTGG                    TGGCGGTC   GC TCG  GTCGTGG
                                |||||||   || |||  |||||||
                                ACCGCCAG   CG AGC  CAGCACC
                                    CGA  G   GA
GAM947  LOC197342 3'  TGGTGGTCCCACGTGT      25132     C        CGGGTC
                                TGG GGTCCCGCGT     GT
                                ||| ||||||||||     ||
                                ACC CCAGGGTGCA     CA
                                  A        _______
GAM947  LOC91179  3'  TGGAGGTCCCGCGGCGTGTGG  25130     C       T  GGTC
                                TGG GGTCCCGCG CG    GTGG
                                ||| |||||||| ||    ||||
                                ACC CCAGGGCGC GC    CACC
                                  T       C  A___
GAM948  ARSB     3'  TTTTGCTGTTGACCTGAAC   25135        ACCC    CA
                                TTTTGCTG   TGACC  AAC
                                ||||||||   |||||  |||
                                AAAACGAC   ACTGG  TTG
                                    A___     AC
GAM948  ATP6V1C1  3'  TTTGTGTTCTGACCCAAA    25136     C  ACC
                                TTTG TG   CTGACCCAAA
                                ||||  ||   ||||||||||
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                                AAAC AC   GACTGGGTTT
                                  _ AA_
GAM948  CNR1    3'  TTTTGCTGAACTAAACAAA   25137        CC   CC
                                TTTTGCTGA  CTGA  CAAA
                                |||||||||  ||||  ||||
                                AAAACGACT  GATT  GTTT
                                     T_    T_
GAM948  DLX4    3'  TCTTGCTGATTTTGCACCCA   25138        CCC  _
                                TTTTGCTGA   TG ACCCA
                                |||||||||   || |||||
                                AGAACGACT   AC TGGGT
                                     AAA  G
GAM948  DLX4    3'  TCTTGCTGATTTTGCACCCA   25138        CCC  _
                                TTTTGCTGA   TG ACCCA
                                |||||||||   || |||||
                                AGAACGACT   AC TGGGT
                                     AAA  G
GAM948  DNASE2  3'  TCTTGCTATGTGACCCA     25139        ACCC
                                TTTTGCTG    TGACCCA
                                ||||||||    |||||||
                                AGAACGAT    ACTGGGT
                                     AC__
GAM948  GOLGA4  5'  TTTTGCAGCACTTTCTGACTCA 25140       TG_  C__    C
          A                      TTTTGC   AC   CTGAC CAA
                                 ||||||   ||   ||||| |||
                                 AAAACG   TG   GACTG GTT
                                    TCG  AAA    A
GAM948  LZTR1   3'  CTTTGCTGGCTTCTTCCCGGCC 25141        AC_____   A
          C                      TTTTGCTG      CCTG CCC
                                 ||||||||      |||| |||
                                 GAAACGAC      GGGC GGG
                                     CGAAGAA    C
GAM948  NCOA4   5'  CTTTACCCCTGACCC      25142       TGA
                                TTTTGC   CCCTGACCC
                                ||||||   |||||||||
                                GAAATG   GGGACTGGG
                                    ___
GAM948  NPY2R   3'  CTCTTTGATCCTGACCCAA   25143     GC   C
                                TTT  TGA CCTGACCCAA
                                |||  ||| ||||||||||
                                GAG  ACT GGACTGGGTT
                                  AA   A
GAM948  RAP1A   5'  TTCTGCTGACTCTTCCAAA   25144         C  GAC
                                TTTTGCTGAC CT   CCAAA
                                |||||||||| ||   |||||
                                AAGACGACTG GA   GGTTT
                                     A  A__
GAM948  RIMS2   5'  TTTGCTGACACCATCAAA    25145         _  TGACC
                                TTTGCTGAC CC    CAAA
                                |||||||| ||    ||||
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                                AAACGACTG GG    GTTT
                                     T  TA___
GAM948  RPL10    3'  TTTTGCTGCTCCCCCAAA    25146       AC  TGA
                                TTTTGCTG  CC   CCCAAA
                                ||||||||  ||   ||||||
                                AAAACGAC  GG   GGGTTT
                                     GA  ___
GAM948  SET      3'  TTCTGCTGATTCTCCCA     25147        CC  GA
                                TTTTGCTGA  CT  CCCA
                                |||||||||  ||  ||||
                                AAGACGACT  GA  GGGT
                                     AA  __
GAM948  TMOD     3'  TTTTGCTGGATCCCAA      25148        ACCCT  _
                                TTTTGCTG    GA CCCAA
                                ||||||||    || |||||
                                AAAACGAC    CT GGGTT
                                     _____  A
GAM948  ABLIM    3'  TTTTGCTGTTTTTCACCCCATT 25149    _______    ACC    III
           CAAACG                    CTG     ACCCTG   CAAAC   G
                                |||     ||||||  |||||  |
                                GAC     TGGGGT   GTTTG   C
                                  AAAAAG     AA_    III
GAM948  ABLIM    3'  TTTTGCTGTTTTTCACCCCATT 25149    _______    ACC    III
           CAAACG                    CTG     ACCCTG   CAAAC   G
                                |||     ||||||  |||||  |
                                GAC     TGGGGT   GTTTG   C
                                  AAAAAG     AA_    III
GAM948  C20orf173 3'  TTGCTATTCTGATCCAAA    25150       ACC    C
                                TTGCTG   CTGA CCAAA
                                ||||||   |||| |||||
                                AACGAT   GACT GGTTT
                                   AA_    A
GAM948  C8orf13  3'  TTGCTCCACCTTGACCCAAA   25151      G_   C
                                TTGCT  ACC TGACCCAAA
                                |||||  ||| |||||||||
                                AACGA  TGG ACTGGGTTT
                                   GG   A
GAM948  CUGBP2   3'  TTTTGCTGAACACAAA      25152        CCCTG  C
                                TTTTGCTGA    AC CAAA
                                |||||||||    || ||||
                                AAAACGACT    TG GTTT
                                     _____  T
GAM948  DKFZP434G072 5'  TCTTGCTGACAAGAACTCAA   25153         CCT   C
                                TTTTGCTGAC   GAC CAA
                                ||||||||||   ||| |||
                                AGAACGACTG   TTG GTT
                                     TTC   A
GAM948  DKFZP564I1171 3'  CTTTGCTGACTTTGGTAACC   25154         CC___
                                TTTTGCTGAC    TGACC
                                ||||||||||    |||||
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                                GAAACGACTG    ATTGG
                                     AAACC
GAM948  DKFZp761H079 3' TCTTGCTAATTTGGTCCAAA  25155        CCC  AC
                                TTTTGCTGA  TG  CCAAA
                                |||||||||  ||  |||||
                                AGAACGATT  AC  GGTTT
                                     AA_  CA
GAM948  EVI5    3' CTTTGCTGACCCTGGTCCA   25156           AC
                                TTTTGCTGACCCTG  CCA
                                ||||||||||||||  |||
                                GAAACGACTGGGAC  GGT
                                       CA
GAM948  FLJ11274 3' TTTTCCTGACCCTAATCCCA  25157     G       _
                                TTTT CTGACCCTGA CCCA
                                |||| |||||||||| ||||
                                AAAA GACTGGGATT GGGT
                                  G        A
GAM948  FLJ21603 5' TCTTGCTGGAGTAATCCTGACC 25158       AC_____
                                TTTTGCTG      CCTGACC
                                ||||||||      |||||||
                                AGAACGAC      GGACTGG
                                     CTCATTA
GAM948  FLJ22035 3' TTTTGCTGTCCCTACAAA    25159       A    ACC
                                TTTTGCTG CCCTG   CAAA
                                |||||||| |||||   ||||
                                AAAACGAC GGGAT   GTTT
                                     A    ___
GAM948  HSPC023  3' TTTTACTGACAAAGCCA     25160        CCT  C
                                TTTTGCTGAC   GA CCA
                                ||||||||||   || |||
                                AAAATGACTG   TT GGT
                                      T__  C
GAM948  KIAA0125 3' CTTTGCTGGCCCTGGCCC    25161       A    A
                                TTTTGCTG CCCTG CCC
                                |||||||| ||||| |||
                                GAAACGAC GGGAC GGG
                                     C    C
GAM948  KIAA0420 3' TTCTGCTGGTGCTCCCAAA   25162       ACC  GA
                                TTTTGCTG  CT  CCCAAA
                                ||||||||  ||  ||||||
                                AAGACGAC  GA  GGGTTT
                                     CAC  __
GAM948  KIAA0447 3' TTCTGCTGGTCTTCACCGACAA 25163       ACC  G_  __
           AC                    TTTTGCTG  CT  ACC  CAAAC
                                ||||||||  ||  |||  |||||
                                AAGACGAC  GA  TGG  GTTTG
                                     CA_  AG  CT
GAM948  KIAA0960 3' TCTTGCTGCCATCCAAA     25164       A  CTGAC
                                TTTTGCTG CC    CCAAA
                                |||||||| ||    |||||
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                                AGAACGAC GG    GGTTT
                                    _ TA___
GAM948  KIAA1735  3'  TTTTGCTGACTTTCCCAAAC  25165        CCTGA
                                TTTTGCTGAC    CCCAAAC
                                ||||||||||    |||||||
                                AAAACGACTG    GGGTTTG
                                    AAA__
GAM948  KIAA1826  5'  CTTTGCTGGCCCTTAGTTCAAA 25166       A   GACC_
                                TTTTGCTG CCCT    CAAA
                                |||||||| ||||    ||||
                                GAAACGAC GGGA    GTTT
                                    C   ATCAA
GAM948  MGC16025  5'  TTCTGCTGAGAAGGAGCCTGGA 25167       C_______  _
          C                      TTTTGCTGA     CCTG AC
                                |||||||||      |||| ||
                                AAGACGACT      GGAC TG
                                    CTTCCTC   C
GAM948  MT-ACT48  3'  TCTTGCTGTCACCCAGAC   25168       __   T
                                TTTTGCTG  ACCC GAC
                                ||||||||  |||| |||
                                AGAACGAC  TGGG CTG
                                    AG   T
GAM948  PFTK1     3'  TTTTGCTGAGTACTGCAAAC  25169       CC_  ACC
                                TTTTGCTGA  CTG  CAAAC
                                |||||||||  |||  |||||
                                AAAACGACT  GAC  GTTTG
                                    CAT  ___
GAM948  SC65      3'  TCTTGCTGCTGCCCA      25170       ACC  A
                                TTTTGCTG  CTG CCCA
                                ||||||||  ||| ||||
                                AGAACGAC  GAC GGGT
                                    ___  _
GAM948  LOC144395 5'  TTTGCTGACCGGTCCGTCCA  25171        ___  AC
                                TTTGCTGACC  CTG  CCA
                                ||||||||||  |||  |||
                                AAACGACTGG  GGC  GGT
                                    CCA  A_
GAM948  LOC145858 3'  CTTTGCTGTCACTACCTGAC  25172       __ __
                                TTTTGCTG  AC  CCTGAC
                                ||||||||  ||  ||||||
                                GAAACGAC  TG  GGACTG
                                    AG  AT
GAM948  LOC149910 3'  TTTTGCTGACTCTCCAGAC   25173        ___ T
                                TTTTGCTGAC  CC GAC
                                ||||||||||  || |||
                                AAAACGACTG  GG CTG
                                    AGA  T
GAM948  LOC150291 3'  TTCTGCTGGAAGACTGTCCAA  25174       ACCCT  ___
                                TTTTGCTG    GAC  CCAA
                                ||||||||    |||  ||||
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                                AAGACGAC    CTG   GGTT
                                    CTT__   ACA
GAM948  LOC153474 3'  CTTTGCTGACTTTGGTAACC  25154        CC___
                                TTTTGCTGAC    TGACC
                                ||||||||||    |||||
                                GAAACGACTG    ATTGG
                                     AAACC
GAM948  LOC157376 3'  TTTTCCTGGCCCAACCC     25175     G   A   T
                                TTTT CTG CCC GACCC
                                |||| ||| ||| |||||
                                AAAA GAC GGG TTGGG
                                  G   C   _
GAM948  LOC165246 3'  TTTTCTGACCCCACCC      25176     G      G
                                TTTT CTGACCCT ACCC
                                |||| |||||||| ||||
                                AAAA GACTGGGG TGGG

                                  _       _
GAM948  LOC166206 5'  TCTTGCTGATTCCGTTCTGA  25177        __ ___
                                TTTTGCTGA  CC   CTGA
                                |||||||||  ||   ||||
                                AGAACGACT  GG   GACT
                                     AA  CAA
GAM948  LOC196694 5'  TCTTGCTGAGCCACGGCCC   25178        _  C  A
                                TTTTGCTGA CC TG CCC
                                |||||||||  || || |||
                                AGAACGACT GG GC GGG
                                     C  T  C
GAM948  LOC254820 3'  TTTCGCTGATCTCCCAAA    25179        CC  GA
                                TTTTGCTGA  CT  CCCAAA
                                |||||||||  ||  ||||||
                                AAAGCGACT  GA  GGGTTT
                                     A_  __
GAM948  LOC257354 3'  TTCTGCTGGTGCTCCCAAA   25162        ACC  GA
                                TTTTGCTG   CT  CCCAAA
                                ||||||||   ||  ||||||
                                AAGACGAC   GA  GGGTTT
                                     CAC  __
GAM948  LOC51184  3'  TTCTGCTGGTTTGGCCACAA  25180        ACCC  A  _
                                TTTTGCTG    TG CC CAA
                                ||||||||    || || |||
                                AAGACGAC    AC GG GTT
                                     CAA_  C  T
GAM948  LOC51652  3'  TTCTGCTGAGCTTCCAAA    25181        CC  GAC
                                TTTTGCTGA  CT   CCAAA
                                |||||||||  ||   |||||
                                AAGACGACT  GA   GGTTT
                                     C_  A__
GAM948  LOC89231  3'  TTTTGCTACCAAGATTCAA   25182        A  CT  CC
                                TTTTGCTG CC  GA  CAA
                                ||||||||  ||  ||  |||
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                                AAAACGAT GG  CT  GTT
                                    _ TT  AA
GAM948  LOC90550  3'  TTTTGCTGACTCTGCAAA    25183         C   ACC
                                TTTTGCTGAC CTG   CAAA
                                |||||||||| |||   ||||
                                AAAACGACTG GAC   GTTT
                                    A  ___
GAM948  LOC92270  5'  TTTTGCTACCTACTCCCAA   25184        AC   A_
                                TTTTGCTG  CCTG  CCCAA
                                ||||||||  ||||  |||||
                                AAAACGAT  GGAT  GGGTT
                                    __   GA
GAM949  C18orf1   3'  TATTGTACATATTTTAAA    25187
                                TATTGTATATATTTTAAA
                                ||||||||||||||||||
                                ATAACATGTATAAAATTT

GAM949  CKAP2     3'  TATTTTAATTGTATATATATCA 25188        _        T
                                TATTTTA TTGTATATAT TTA
                                ||||||| |||||||||| |||
                                ATAAAAT AACATATATA AGT
                                    T        T
GAM949  DKFZP434L1717 3'  TATTCTATTGCTTACAATTTTA 25189          A   _
          AAA                   TATTTTATTGT TATA TTTTAAAA
                                |||||||||| |||| ||||||||
                                ATAAGATAACG ATGT AAAATTTT
                                    A   T
GAM949  FENS-1    3'  TTTTATTGTGTACATTTT    25190         A
                                TTTTATTGT TATATTTT
                                ||||||||| ||||||||
                                AAAATAACA ATGTAAAA
                                    C
GAM949  FLJ11040  3'  TTTTATTGTACTATTCTA    25191          A
                                TTTTATTGTAT TATTTTA
                                |||||||||| |||||||
                                AAAATAACATG ATAAGAT
                                    _
GAM949  KIAA1046  3'  TACTTTATTGTATTTTTTTTAA 25192           ATA
          A                      TATTTTATTGTAT   TTTTAAA
                                |||||||||||||   |||||||
                                ATGAAATAACATA   AAAATTT
                                    AAA
GAM949  NXP-2     3'  TATTTTATTATAAGATATTTTA 25193          T_
          AAA                     TATTTTATTGTA  ATATTTTAAAA
                                |||||||||||  ||||||||||
                                ATAAAATAATAT  TATAAAATTTT
                                    TC
GAM949  SLK       3'  TACTTTATAAAGATATATATTT 25194        T___
          TAAAA                    TATTTTAT   GTATATATTTTAAAA
                                ||||||||   ||||||||||||||
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                                ATGAAATA   TATATATAAAATTTT
                                     TTTC
GAM949  LOC129452 3'  TTTTATTGTATATCTTTAAAA  25195          A
                                TTTTATTGTATAT TTTTAAAA
                                |||||||||||| ||||||||
                                AAAATAACATATA GAAATTTT
                                          _
GAM949  LOC51136  3'  CATTATATATATTTTAAA    25196
                                TATTGTATATATTTTAAA
                                ||||||||||||||||||
                                GTAATATATATAAAATTT

GAM950  EDNRA     3'  TAATAGATTTGACTGCTA    25199        AA   T
                                TAATAGGTTT  GACT CTA
                                ||||||||||  |||| |||
                                ATTATCTAAA  CTGA GAT
                                     __   C
GAM950  PDZK1     3'  TAATAGGCTTATCTGCTA    25200        AGACT  A
                                TAATAGGTTTA    TCT CTA
                                ||||||||||     ||| |||
                                ATTATCCGAAT    AGA GAT
                                     _____  C
GAM950  FLJ20489  3'  GGTTTAAGAGGTCTCTGCTA  25201        C__   A
                                GGTTTAAGA   TTCT CTA
                                |||||||||   |||| |||
                                CCAAATTCT   GAGA GAT
                                     CCA   C
GAM950  KIAA0155  3'  TAGGTTTTTGCATTCTACTAA  25202       AAGAC
                                TAGGTTT    TTCTACTAA
                                |||||||    |||||||||
                                ATCCAAA    AAGATGATT
                                    AACGT
GAM950  MGC14407  3'  TAATAGGTGTTAAGGCTTC   25203        _   A
                                TAATAGGT TTAAG CTTC
                                |||||||| ||||| ||||
                                ATTATCCA AATTC GAAG
                                     C    C
GAM950  WNT16     3'  AGTTAAGACTTTTACTA     25204     T     C
                                GGTT AAGACTT TACTA
                                |||| ||||||| |||||
                                TCAA TTCTGAA ATGAT
                                  _      A
GAM950  WNT16     3'  AGTTAAGACTTTTACTA     25204     T     C
                                GGTT AAGACTT TACTA
                                |||| ||||||| |||||
                                TCAA TTCTGAA ATGAT
                                  _      A
GAM950  LOC113763 3'  AATAGGTTTAAGATTCT     25205          C
                                AATAGGTTTAAGA TTCT
                                |||||||||||| ||||
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                                TTATCCAAATTCT AAGA
                                           _
GAM950  LOC120103 3'  ATAGGTTTACCACTACT     25206        AAG   T
                                ATAGGTTT   ACT CTACT
                                ||||||||   ||| |||||
                                TATCCAAA   TGG GATGA
                                    ___   T
GAM951  C8A      3'  TAACATCCTGTAAGTTCTCCCT 25209        CA    AAAA__
           GG                     TAGCATCC  TAAG     CTGG
                                ||||||||  ||||     ||||
                                ATTGTAGG  ATTC     GACC
                                    AC    AAGAGG
GAM951  CD79B    3'  TAGCACCCCCAGAAGGCTGG  25210        ATA    AA
                                TAGCATCCC   AGAA  CTGG
                                |||||||||   ||||  ||||
                                ATCGTGGGG   TCTT  GACC
                                     G__    CC
GAM951  CD79B    3'  TAGCACCCCCAGAAGGCTGG  25210        ATA    AA
                                TAGCATCCC   AGAA  CTGG
                                |||||||||   ||||  ||||
                                ATCGTGGGG   TCTT  GACC
                                     G__    CC
GAM951  CLASP2   3'  TAGCCTTTCACCAAAACTGG  25211     ATCC   AAG
                                TAGC    CAT   AAAACTGG
                                ||||    |||   ||||||||
                                ATCG    GTG   TTTTGACC
                                  GAAA  G__
GAM951  CTNND2   3'  CATCATAAAGAAAACTGG    25212     CCAT
                                CATC    AAGAAAACTGG
                                ||||    ||||||||||
                                GTAG    TTCTTTTGACC
                                  TAT_
GAM951  DGKI     3'  GCATCCCATAAATCTGG      25213          AAAA
                                GCATCCCATAAG    CTGG
                                ||||||||||||    ||||
                                CGTAGGGTATTT    GACC
                                      A___
GAM951  DIAPH2   3'  GCAGCCACAAGAAACTGG    25214     TC        A
                                GCA  CCATAAGAAA CTGG
                                |||  |||||||||| ||||
                                CGT  GGTGTTCTTT GACC
                                  C_        _
GAM951  HMG20A   3'  CAGCTAGGTAAGAAAACTGG  25215     ATCCCA
                                TAGC     TAAGAAAACTGG
                                ||||     ||||||||||||
                                GTCG     ATTCTTTTGACC
                                  ATCC__
GAM951  PLA2G4A  3'  AACACACATAAGAAAGTTGG  25216      CC        AC
                                AGCAT  CATAAGAAA  TGG
                                |||||  |||||||||  |||
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                                TTGTG  GTATTCTTT  ACC
                                  T_       CA
GAM951  DKFZp434K1210 3'  TAGCATCCTTAAGGCTG     25217        CA    AAAA
                                TAGCATCC  TAAG    CTG
                                ||||||||  ||||    |||
                                ATCGTAGG  ATTC    GAC
                                    A_    C___
GAM951  FLJ20004  3'  GCATCCCAAAGTGCTGG     25218        T   AAAA
                                GCATCCCA AAG    CTGG
                                |||||||| |||    ||||
                                CGTAGGGT TTC    GACC
                                    _   AC__
GAM951  KIAA1677  3'  GCAAACAAGAAAACTGG     25219     TCCC
                                GCA    ATAAGAAAACTGG
                                |||    ||||||||||||
                                CGT    TGTTCTTTTGACC
                                 T___
GAM951  MGC16075  5'  CAGCATCCATGAAACTG     25220        CATAA    A
                                TAGCATCC     GAAA CTG
                                ||||||||     |||| |||
                                GTCGTAGG     CTTT GAC
                                    TA___    _
GAM951  MGC5149   3'  GCATCACAAGACAAAACTGG   25221      CC     __
                                GCATC  ATAAGA  AAACTGG
                                |||||  ||||||  |||||||
                                CGTAG  TGTTCT  TTTGACC
                                  __     GT
GAM951  SIMRP7    5'  GCACCCCACCTAGAGGTTGG   25222        A_   AAAC
                                GCATCCCAT  AGA    TGG
                                |||||||||  |||    |||
                                CGTGGGGTG  TCT    ACC
                                    GA   CCA_
GAM951  TBLR1     3'  TAGTATCCAAAAACTG      25223     C    CATAA
                                TAG ATCC     GAAAACTG
                                ||| ||||     ||||||||
                                ATC TAGG     TTTTTGAC
                                 A   _____
GAM951  TIMM22    3'  GCATCCCAGGAAAAGGCTGG   25224        TA    AA
                                GCATCCCA  AGAA  CTGG
                                ||||||||  ||||  ||||
                                CGTAGGGT  TTTT  GACC
                                    CC    CC
GAM951  LOC116411 5'  GCATGGCCAGAAAACTGG     25225     C_   TAA
                                GCAT  CCA   GAAAACTGG
                                ||||  |||   |||||||||
                                CGTA  GGT   CTTTTGACC
                                  CC   ___
GAM951  LOC124152 3'  CCACAAGTGGGAAAACTGG    25226       _____
                                CCATAA    GAAAACTGG
                                ||||||    |||||||||
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                                GGTGTT   CTTTTGACC
                                   CACC
GAM951  LOC144970 5'  CAGCATCCCATTTCCCACTGG  25227          AAGAAA
                                TAGCATCCCAT     ACTGG
                                ||||||||||     |||||
                                GTCGTAGGGTA     TGACC
                                      AAGGG_
GAM951  LOC150935 5'  AGCATCCCATGGGCACGTGG   25228          AAGAAA _
                                AGCATCCCAT     AC TGG
                                ||||||||||     || |||
                                TCGTAGGGTA     TG ACC
                                      CCCG__  C
GAM951  LOC158525 3'  CATTCCATAAGAAAGCTG    25229     C        A
                                CAT CCATAAGAAA CTG
                                ||| |||||||||| |||
                                GTA GGTATTCTTT GAC
                                  A         C
GAM951  LOC200138 3'  TAACATCCCAGAGCTG      25230          TAA  AAA
                                TAGCATCCCA   GA   CTG
                                ||||||||||   ||   |||
                                ATTGTAGGGT   CT   GAC
                                      ____  C__
GAM951  LOC220776 3'  AGCATCCCCCCAAAAAACTGG  25231        ATA
                                AGCATCCC   AGAAAACTGG
                                ||||||||   ||||||||||
                                TCGTAGGG   TTTTTTGACC
                                     GGG
GAM951  LOC91963  5'  GCCTCCCATAAGTGCTGG    25232    A       AAAA
                                GC TCCCATAAG    CTGG
                                || |||||||||    ||||
                                CG AGGGTATTC    GACC
                                 G        AC__
GAM951  LOC92573  5'  CAGCATCCCAAGAAGCTGG    25233          TA    AA
                                TAGCATCCCA  AGAA  CTGG
                                ||||||||||  ||||  ||||
                                GTCGTAGGGT  TCTT  GACC
                                      __    C_
GAM952  G22P1     5'  TCTTGTGAGATCTGTTCTAAA  25236    G    ACTAC
                                TC TTGT     CTGTTCTAAA
                                || ||||     ||||||||||
                                AG AACA     GACAAGATTT
                                 _    CTCTA
GAM952  RANBP3    3'  TTGTGAGACTGCCTGTTCT    25237      ___   A
                                TTGT   ACT CCTGTTCT
                                ||||   ||| ||||||||
                                AACA   TGA GGACAAGA
                                  CTC   C
GAM952  CDC14A    3'  GTTGTACCCTGTTTTAA      25238        TA     C
                                GTTGTAC  CCTGTT TAA
                                |||||||  |||||| |||
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                                CAACATG  GGACAA ATT
                                   __     A
GAM952  FLJ20417  3'  GATGTTGTGCTTGCTCTAA   25239    C    A  ACC
                                GAT GTTGT CT   TGTTCTAA
                                ||| ||||| ||   ||||||||
                                CTA CAACA GA   ACGAGATT
                                  _    C ___
GAM952  GRSF1    3'  GCACCCCTACTTGTTCTAAA  25240   TGTA   C
                                GT   CTAC TGTTCTAAA
                                ||   |||| |||||||||
                                CG   GATG ACAAGATTT
                                 TGGG   A
GAM952  LOC152503 5'  GATCGTTGTCTATTTCTTCT  25241        A  CCTG
                                GATCGTTGT CTA   TTCT
                                ||||||||| |||   ||||
                                CTAGCAACA GAT   AAGA
                                     _  AAAG
GAM953  FZD7     3'  TGCGCTGCTTTGCCTATAAAAG 25244        __ GAA
          T                      TGCGCTGCT  GC   ATAAAAGT
                                |||||||||  ||   ||||||||
                                ACGCGACGA  CG   TATTTTCA
                                     AA  GA_
GAM953  LOC254351 3'  TGCGGCTGCTGCGCGGTGAGGT 25245     _      AAATAAAA
          CG                     TGCG CTGCTGCG      GTCG
                                |||| ||||||||       ||||
                                ACGC GACGACGC       CAGC
                                  C       GCCACTC_
GAM954  CCNF     3'  TGAGGGGACAGTGGTGTG    25248        CA   A
                                TGAGGGGAC  TGGT TG
                                |||||||||  |||| ||
                                ACTCCCCTG  ACCA AC
                                     TC   C
GAM954  GNAT1    3'  CTGAGGGGAGTGCAAATTGT  25249        CCATG  ___
                                CTGAGGGGA    GTA   TGT
                                |||||||||    |||   |||
                                GACTCCCCT    CGT   ACA
                                     CA___   TTA
GAM954  MYO1D    3'  CTGAGGGGCTGGCCCTGT    25250       ACCA   A_
                                CTGAGGGG   TGGT  TGT
                                ||||||||   ||||  |||
                                GACTCCCC   ACCG  ACA
                                    G___   GG
GAM954  PBX2     3'  CTGAGGGGATCAGATGGTA   25251        C  __
                                CTGAGGGGA CA  TGGTA
                                ||||||||| ||  |||||
                                GACTCCCCT GT  ACCAT
                                     A  CT
GAM954  PML      3'  CTGGGGGGTGGTATGT     25252    A   ACCA
                                CTG GGGG   TGGTATGT
                                ||| ||||   ||||||||
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                                GAC CCCC   ACCATACA
                                  C   ____
GAM954  PML      3'  CTGGGGGGTGGTATGT     25252    A   ACCA
                                CTG GGGG   TGGTATGT
                                ||| ||||   ||||||||
                                GAC CCCC   ACCATACA
                                  C   ____
GAM954  CLDN4    5'  CTGAGGGGATCCGGCTGT    25253       _ AT  A
                                CTGAGGGGA CC  GGT TGT
                                ||||||||| ||  ||| |||
                                GACTCCCCT GG  CCG ACA
                                     A  __  _
GAM954  CMG2     3'  CTGAGGAGGCTGGTGTGT    25254       ACCA  A
                                CTGAGGGG   TGGT TGT
                                ||||||||   |||| |||
                                GACTCCTC   ACCA ACA
                                     CG__   C
GAM954  DKFZP564G092 5'  TAACTAAGTGATCATGGTATGT 25255       GG  C
                                TAACTGAG  GA CATGGTATGT
                                ||||||||  || ||||||||||
                                ATTGATTC  CT GTACCATACA
                                     A_  A
GAM954  FLJ14768  5'  GGGGAATACAGTGGTATGT   25256     C__ _
                                GGGGA   CA TGGTATGT
                                |||||   || ||||||||
                                CCCCT   GT ACCATACA
                                   TAT  C
GAM954  FLJ21290  3'  TGATGGGAGGTGGTATGT    25257    G   CCA
                                TGA GGGA   TGGTATGT
                                |||| ||||   ||||||||
                                ACT CCCT   ACCATACA
                                  A   CC_
GAM954  ITM3     3'  ACTGAGGGGACCCTGCTTGT   25258         ATG  A
                                ACTGAGGGGACC   GT TGT
                                ||||||||||||   || |||
                                TGACTCCCCTGG   CG ACA
                                       GA_  A
GAM954  SYNPO2   3'  GGGTGACAACATGGTGTGT   25259    _  __    A
                                GGG GAC  CATGGT TGT
                                ||| |||  |||||| |||
                                CCC CTG  GTACCA ACA
                                  A  TT     C
GAM954  LOC145788 5'  CTGGGTGGATCAGTATGT    25260    A  _  C  TG
                                CTG GG GGA CA  GTATGT
                                ||| || ||| ||  ||||||
                                GAC CC CCT GT  CATACA
                                  _  A  A  __
GAM954  LOC146445 3'  CCGAGGGGACCGGGTGTG    25261         AT  A
                                CTGAGGGGACC  GGT TG
                                ||||||||||  ||| ||
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                                GGCTCCCCTGG  CCA AC
                                      C_  C
GAM954  LOC149684 3'  TAACTGAGGTGACCATGG    25262         G
                                TAACTGAGG GACCATGG
                                ||||||||| ||||||||
                                ATTGACTCC CTGGTACC
                                     A
GAM955  DUSP4    5'  GAGCAGTCCATTTTTGTGGCCG 25265        CAC_________  GTCG
           CGACCG                  AGTCCGT         CCG   CG
                                |||||||         |||   ||
                                TCAGGTA         GGC   GC
                                   AAAACACCIII  GCTG
GAM955  ITGA3    3'  GAGCTGTTTATTGGTCGCG   25266     A  CC  CACCC
                                GAGC GT  GT    GGTCGCG
                                |||| ||  ||    |||||||
                                CTCG CA  TA    CCAGCGC
                                  A  AA  A____
GAM955  ITGA3    3'  GAGCTGTTTATTGGTCGCG   25266     A  CC  CACCC
                                GAGC GT  GT    GGTCGCG
                                |||| ||  ||    |||||||
                                CTCG CA  TA    CCAGCGC
                                  A  AA  A____
GAM955  MN1      5'  GCGGTTGTCACAGCCGCGG   25267    A  CC    CC
                                GC GT  GTCAC  GGTCGCGG
                                || ||  |||||  ||||||||
                                CG CA  CAGTG  TCGGCGCC
                                 C  A_    __
GAM955  PCTK1    5'  GAGCGGTCTGATCGCGG     25268     A   CGTCACCC
                                GAGC GTC       GGTCGCGG
                                |||| |||       ||||||||
                                CTCG CAG       CTAGCGCC
                                  C   A________
GAM955  PCTK1    5'  GAGCGGTCTGATCGCGG     25268     A   CGTCACCC
                                GAGC GTC       GGTCGCGG
                                |||| |||       ||||||||
                                CTCG CAG       CTAGCGCC
                                  C   A________
GAM955  PIGB     5'  GAGCAGTCGTCGCTCGCA    25269         C   ACCC G
                                GAGCAGTC GTC    G TCGCG
                                |||||||| |||    | |||||
                                CTCGTCAG CAG    C AGCGT
                                     _  ____ G
GAM955  C12orf4  5'  GCAGTCCGCTCACTCGAGCCGC 25270      _   _________  GTCG
           GACCG                   GTCCG TCAC       CCG   CG
                                ||||| ||||       |||   ||
                                CAGGC AGTG       GGC   GC
                                   G   AGCTCIII  GCTG
GAM955  DZIP1    5'  GCGGTCTTTACCCAGCCTGG  25271    A  CGTC      GC
                                GC GTC    ACCCGGTC  GG
                                || |||    ||||||||  ||
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                                CG CAG   TGGGTCGG  CC
                                 C  AAA_      A_
GAM955  ERO1L    5'  CAGTCCGCACGCTCGGTCGCGG 25272       T  C__
                                CAGTCCG CAC  CGGTCGCGG
                                ||||||| |||  |||||||||
                                GTCAGGC GTG  GCCAGCGCC
                                   _  CGA
GAM955  SERF2    5'  GAGGTCAGACGCTGGTCGCGG  25273    __  TC  CACCC
                                GAG  CAG  CGT   GGTCGCGG
                                |||  |||  |||   |||||||||
                                CTC  GTC  GCG   CCAGCGCC
                                 CA  T_  A____
GAM955  TRAP95   3'  GCTGTTTGTCGCCAACCACGG  25274   A  CC  AC  GT
                                GC GT  GTC  CCG  CGCGG
                                || ||  |||  |||  |||||
                                CG CA  CAG  GGT  GTGCC
                                 A  AA  C_  TG
GAM955  LOC147791 3'  GAGCAGTCCTTGCGTTAAGCGG 25275        GTCACC  GTC_
                                GAGCAGTCC    CG   GCGG
                                |||||||||    ||   ||||
                                CTCGTCAGG    GC   CGCC
                                     AAC___  AATT
GAM955  LOC149576 3'  GGCAGTCGCTCGGTCGCG   25276   A    C  CACC
                                G GCAGTC GT   CGGTCGCG
                                | |||||| ||   ||||||||
                                C CGTCAG CG   GCCAGCGC
                                _    _ A___
GAM955  LOC256227 3'  GAGCAGCCGTCACCTGCAGCA  25277      T      CG  C
                                GAGCAG CCGTCACC  GT GCG
                                |||||| ||||||||  || |||
                                CTCGTC GGCAGTGG  CG CGT
                                   _      A_  T
GAM955  LOC257479 5'  GCCGCCGCTGCCTGGTCGCGG  25278   A T   CA  C
                                GC G CCGT  CC GGTCGCGG
                                || | ||||  || ||||||||
                                CG C GGCG  GG CCAGCGCC
                                 G _   AC  A
GAM956  CROT     3'  TGTAATTCATACCCTT     25281         CCCAAC
                                TGTGATTCA    GCCCTT
                                |||||||||    ||||||
                                ACATTAAGT    TGGGAA
                                     A_____
GAM956  FLI1     3'  GTGATTCACCCGTCTTG    25282          AACGCC
                                GTGATTCACCC    CTTG
                                ||||||||||    ||||
                                CACTAAGTGGG    GAAC
                                      CA____
GAM956  HSPA5    3'  TGTGATCCACCCGCCTTG   25283          AAC  C
                                TGTGATTCACCC  GCC TTG
                                ||||||||||  ||| |||
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                                ACACTAGGTGGG  CGG AAC
                                      ___  _
GAM956  LUZP1    3' TGTGATCCGCCTGCCTTG   25284       A  CAAC  C
                                TGTGATTC CC   GCC TTG
                                |||||||| ||   ||| |||
                                ACACTAGG GG   CGG AAC
                                    C  A___  _
GAM956  RAB7L1   3' TGTGATCCGCCTGCCTTG   25284       A  CAAC  C
                                TGTGATTC CC   GCC TTG
                                |||||||| ||   ||| |||
                                ACACTAGG GG   CGG AAC
                                    C  A___  _
GAM956  RUNX1    5' TGTGATTCGTCCTGCCTGCTGA 25285       AC  AAC  C_
          C                      TGTGATTC  CC  GCC  TTGAC
                                |||||||| ||  |||  |||||
                                ACACTAAG  GG  CGG  GACTG
                                    CA  A__  AC
GAM956  SS18     3' TGTATCACAGTGCCCTTGA  25286     AT   CCAAC
                                TGTG  TCAC   GCCCTTGA
                                ||||  ||||   ||||||||
                                ACAT  AGTG   CGGGAACT
                                  __   TCA__
GAM956  TMEM2    3' TGTGATTCACCAGCAGGAGAC 25287        CAAC  CCTT
                                TGTGATTCACC   GC   GAC
                                ||||||||||   ||   |||
                                ACACTAAGTGG   CG   CTG
                                      T___  TCCT
GAM956  C21orf108 3' GTGATTCACCCGCCTTG    25288        AAC  C
                                GTGATTCACCC  GCC TTG
                                ||||||||||  ||| |||
                                CACTAAGTGGG  CGG AAC
                                      ___  _
GAM956  DKFZP586D0824 3' TGTGATTCACCCACTAAATGA 25289          ACGCCCT
                                TGTGATTCACCCA     TGA
                                ||||||||||||     |||
                                ACACTAAGTGGGT     ACT
                                      GATTT__
GAM956  DRF1     3' TGTGATCCACCCGCCTTG   25283        AAC  C
                                TGTGATTCACCC  GCC TTG
                                ||||||||||  ||| |||
                                ACACTAGGTGGG  CGG AAC
                                      ___  _
GAM956  FLJ20695 3' GTGATTCACCCACCTTG    25290         ACGC
                                GTGATTCACCCA  CCTTG
                                ||||||||||  |||||
                                CACTAAGTGGGT  GGAAC
                                      _____
GAM956  IMP-1    3' TGTGATCCACCCTCTTG    25291         AACGCC
                                TGTGATTCACCC    CTTG
                                ||||||||||    ||||
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                                ACACTAGGTGGG     GAAC
                                      A_____
GAM956  KIAA1393  3'  TGTGATTCATCCTTCACCTTG  25292        C  AA   C
                                TGTGATTCA CC  CGCC TTG
                                ||||||||| ||  |||| |||
                                ACACTAAGT GG  GTGG AAC
                                     A  AA   _
GAM956  LIM       3'  TGTGGTCCACCCACCTTG    25293     A      ACGC
                                TGTG TTCACCCA   CCTTG
                                |||| ||||||||   |||||
                                ACAC AGGTGGGT   GGAAC
                                  C      ____
GAM956  TPD52     3'  TGATTCACTCAGCCCTGAC   25294       C  AC    T
                                TGATTCAC CA  GCCCT GAC
                                |||||||| ||  ||||| |||
                                ACTAAGTG GT  CGGGA CTG
                                     A __    _
GAM956  LOC131744 3'  TGTGATTCACCCACCTCG    25295          ACGC
                                TGTGATTCACCCA   CCTTG
                                ||||||||||||   |||||
                                ACACTAAGTGGGT   GGAGC
                                      ____
GAM956  LOC158292 5'  TGTGATCCGCCCGCCTTG    25296       A   AAC   C
                                TGTGATTC CCC   GCC TTG
                                |||||||| |||   ||| |||
                                ACACTAGG GGG   CGG AAC
                                     C  ___   _
GAM956  LOC222828 5'  TATGATTCACGCTTCTTG    25297        CCAAC  C_
                                TGTGATTCAC    GC  CTTG
                                ||||||||||    ||  ||||
                                ATACTAAGTG    CG  GAAC
                                      _____  AA
GAM956  LOC253187 5'  TGTGATTCAGATTATGCCTTTG 25298        CCCAAC   C
                                TGTGATTCA     GCC TTG
                                |||||||||     ||| |||
                                ACACTAAGT     CGG AAC
                                      CTAATA   A
GAM957  DKFZP434C0826 3'  TTCATACAGTAAATGAAA    25301      _  A
                                TTCGT CA TAAATGAAA
                                ||||| || |||||||||
                                AAGTA GT ATTTACTTT
                                   T  C
GAM957  DOC-1R    3'  GTGCAACTCGGGATGAA     25302         TCAATAA
                                GTGCAATTCG      ATGAA
                                ||||||||||      |||||
                                CACGTTGAGC      TACTT
                                      CC_____
GAM957  MGC11115  3'  GTGCAGATCGCTGCAATGAAAG 25303      AT    CAATA
                                GTGCA  TCGT    AATGAAAG
                                |||||  ||||    ||||||||
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                                CACGT  AGCG    TTACTTTC
                                  CT    ACG__
GAM958  AKAP1    3'  GGCTTTGCGAAGAGAACCC   25306     CG      __
                                GGCT  TGTGAAGA  ACCC
                                ||||  ||||||||  ||||
                                CCGA  ACGCTTCT  TGGG
                                  A_       CT
GAM958  AKAP1    3'  GGCTTTGCGAAGAGAACCC   25306     CG      __
                                GGCT  TGTGAAGA  ACCC
                                ||||  ||||||||  ||||
                                CCGA  ACGCTTCT  TGGG
                                  A_       CT
GAM958  BAT4     5'  AAGCTCGTGGTGACCC      25307         _  AGAA
                                AGGCTCGTG TGA    CCC
                                |||||||||| |||    |||
                                TTCGAGCAC ACT    GGG
                                     C  _____
GAM958  CDX2     5'  AGGCTGGCGTGCGGAGCCC   25308      C    AA  A
                                AGGCT GTGTG  GA CCC
                                ||||| |||||  || |||
                                TCCGA CGCAC  CT GGG
                                  C    GC  C
GAM958  DDX24    5'  AGTCGCGAGTGAAGAACC    25309    C   __
                                GG TCGT  GTGAAGAACC
                                || ||||  ||||||||||
                                TC AGCG  CACTTCTTGG
                                 _   CT
GAM958  DIAPH2   3'  AAGCTTGTAAAGAACCC     25310      CG
                                AGGCT  TGTGAAGAACCC
                                |||||  ||||||||||||
                                TTCGA  ACATTTCTTGGG
                                   __
GAM958  DUSP5    3'  AGGTCAGTGAAGAACCC     25311     C   T
                                AGG TCG GTGAAGAACCC
                                ||| ||| ||||||||||
                                TCC AGT CACTTCTTGGG
                                  _  _
GAM958  GATA6    3'  AGGCCCGCGGCGGAGCCC    25312         _  AA  A
                                AGGCTCGTG TG  GA CCC
                                |||||||| ||  || |||
                                TCCGGGCGC GC  CT GGG
                                     C  __  C
GAM958  IL17     3'  AGGCATGTGAAATCGAGAAC  25313     TC    _____
                                AGGC  GTGTGA    AGAAC
                                ||||  ||||||    |||||
                                TCCG  TACACT    TCTTG
                                  __     TTAGC
GAM958  IRAK1    3'  GACTCGTGCACCATGAGAAC  25314         A____
                                GGCTCGTGTG    AGAAC
                                ||||||||||    |||||
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                                CTGAGCACGT    TCTTG
                                     GGTAC
GAM958  KCNK10   5' GGCTCGTGGAGGAACCC    25315       T  A
                                GGCTCGTG GA GAACCC
                                |||||||| || ||||||
                                CCGAGCAC CT CTTGGG
                                    _  C
GAM958  KIAA0442 3' GGCTTTTGTGAAAAGCCC   25316    CG      A
                                GGCT  TGTGAAGA CCC
                                ||||  |||||||| |||
                                CCGA  ACACTTTT GGG
                                  AA       C
GAM958  MADH6    5' AAGCTCGCGCGAACCC     25317          AGA
                                AGGCTCGTGTGA   ACCC
                                ||||||||||||   ||||
                                TTCGAGCGCGCT   TGGG
                                       ___
GAM958  MIPOL1   5' AGCTCACAGATAGAACCC   25318      TGT  _
                                GGCTCG   GA AGAACCC
                                ||||||   || |||||||
                                TCGAGT   CT TCTTGGG
                                   GT_  A
GAM958  MRPS12   3' AGGCCAGCATCGGAGGACCC  25319     C   _ A  A
                                AGGCT GTGT G AG ACCC
                                ||||| |||| | || ||||
                                TCCGG CGTA C TC TGGG
                                   T   G C  C
GAM958  MRPS12   3' AGGCCAGCATCGGAGGACCC  25319     C   _ A  A
                                AGGCT GTGT G AG ACCC
                                ||||| |||| | || ||||
                                TCCGG CGTA C TC TGGG
                                   T   G C  C
GAM958  MRPS12   3' AGGCCAGCATCGGAGGACCC  25319     C   _ A  A
                                AGGCT GTGT G AG ACCC
                                ||||| |||| | || ||||
                                TCCGG CGTA C TC TGGG
                                   T   G C  C
GAM958  PGF      5' AGGCTGTGGCTGGGGAACCC  25320     C   __  AA
                                AGGCT GTG  TG  GAACCC
                                ||||| |||  ||  ||||||
                                TCCGA CAC  AC  CTTGGG
                                   _  CG  CC
GAM958  PTGFRN   5' AGGCCCGGGTGGAACC     25321       T   AA
                                AGGCTCG GTG  GAACC
                                ||||||| |||  |||||
                                TCCGGGC CAC  CTTGG
                                    C  __
GAM958  RAD54L   5' GGCGTGTAAAAAACCC     25322    TC
                                GGC  GTGTGAAGAACCC
                                |||  ||||||||||||
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                                CCG  CACATTTTTTGGG
                                  __
GAM958  SACM1L   3'  AGACTTTAAAGAACCC      25323      CGTG
                                AGGCT   TGAAGAACCC
                                |||||   ||||||||||
                                TCTGA   ATTTCTTGGG
                                  A___
GAM958  SDC4     3'  AAGCTCAAGAAGAACC      25324       TGT
                                AGGCTCG   GAAGAACC
                                |||||||   ||||||||
                                TTCGAGT   CTTCTTGG
                                   T__
GAM958  STIP1    3'  AGGCTGGAAGAACCC       25325      CGT T
                                AGGCT   G GAAGAACCC
                                |||||   | |||||||||
                                TCCGA   C CTTCTTGGG
                                  ____ _
GAM958  SYNGR2   3'  AGGCTCATGGGAAAGTCC    25326        T   AA
                                AGGCTCGTG GAAG  CC
                                |||||||||| ||||  ||
                                TCCGAGTAC CTTT  GG
                                     C    CA
GAM958  TXK      3'  AGCCTTGTGAAGAAGAACC   25327    G  C   T_
                                AG CT GTG  GAAGAACC
                                || || |||  ||||||||
                                TC GA CAC  CTTCTTGG
                                 G  A   TT
GAM958  UBE3A    5'  GGCTCATGCGGGACCC      25328         AA  A
                                GGCTCGTGTG  GA CCC
                                ||||||||||  || |||
                                CCGAGTACGC  CT GGG
                                     C_  _
GAM958  ALLC     5'  AGACTCAGACAAGAGAACC   25329        T TG _
                                AGGCTCG G  A AGAACC
                                |||||||  |  | ||||||
                                TCTGAGT T  T TCTTGG
                                    C GT C
GAM958  C11orf21 3'  GGCCCACATGTGAGGGACCC  25330      __     AGA
                                GGCTC  GTGTGA   ACCC
                                |||||  ||||||   ||||
                                CCGGG  TACACT   TGGG
                                   TG     CCC
GAM958  CAPN13   3'  AGGCTCATTGTGCAGAGCCC  25331        _  A   A
                                AGGCTCGT GTG AGA CCC
                                |||||||| ||| ||| |||
                                TCCGAGTA CAC TCT GGG
                                     A   G   C
GAM958  DKFZP434B195 5'  GACCGCAAAGAAGAACCC    25332     T    T_
                                GGC CGTG  GAAGAACCC
                                ||| ||||  |||||||||
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                                CTG GCGT  CTTCTTGGG
                                  _   TT
GAM958  DKFZp547M072 3'  AAGCCCATGAAGAGTCC     25333       GT      AC
                                AGGCTC  GTGAAGA  CC
                                ||||||  |||||||  ||
                                TTCGGG  TACTTCT  GG
                                   __      CA
GAM958  DKFZP564M082 5'  AGCCTGAGCGGAAGAACCC    25334      C__   T
                                GGCT   GTG GAAGAACCC
                                ||||   ||| |||||||||
                                TCGG   CGC CTTCTTGGG
                                  ACT   _
GAM958  DKFZP564M182 5'  AGGCGCGTGTGCAACCC     25335      T     AAG
                                AGGC CGTGTG   AACCC
                                |||| ||||||   |||||
                                TCCG GCACAC   TTGGG
                                  C     G__
GAM958  DKFZP586L0724 3'  AGGTTCATGTGAAACC      25336     C       GA
                                AGG TCGTGTGAA  ACC
                                ||| |||||||||  |||
                                TCC AGTACACTT  TGG
                                  A       __
GAM958  DKFZP761C169 5'  AGTTTCGGCTGAAGAACCC    25337    GC   TG
                                AG  TCG  TGAAGAACCC
                                ||  |||  ||||||||||
                                TC  AGC  ACTTCTTGGG
                                 AA   CG
GAM958  FADS2    3'  GGCCCGTGAAAGCCC       25338         T   AA
                                GGCTCGTG GAAG  CCC
                                ||||||||| ||||  |||
                                CCGGGCAC TTTC  GGG
                                   _   __
GAM958  FLJ00058  5'  AGGCCCGTGGGAGACCC     25339         T  A  A
                                AGGCTCGTG GA GA CCC
                                ||||||||| || || |||
                                TCCGGGCAC CT CT GGG
                                     C  _  _
GAM958  FLJ10199  5'  GGCTGCGGTGGAAGGGCCC   25340     _  _  T   AA
                                GGCT CG TG GAAG  CCC
                                |||| || || ||||  |||
                                CCGA GC AC CTTC  GGG
                                  C  C  _    CC
GAM958  FLJ14824  3'  AGGATAAGAAGAACCC      25341     CTC   T
                                AGG   GTG GAAGAACCC
                                |||   ||| |||||||||
                                TCC   TAT CTTCTTGGG
                                  ____  T
GAM958  FLJ20371  5'  AGGCTGCGTAAAAGCC      25342       C       AA
                                AGGCT GTGTGAAG  CC
                                ||||| ||||||||  ||
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                                TCCGA CGCATTTT  GG
                                  _       C_
GAM958  FLJ20699  3'  AGACAGCAGAAGGACCC     25343     TC  T   A
                                AGGC  GTG GAAG ACCC
                                ||||  ||| |||| ||||
                                TCTG  CGT CTTC TGGG
                                  T_  _    C
GAM958  FLJ22865  5'  AGGCGGCGGGAAGAACCC    25344     TC  T
                                AGGC  GTG GAAGAACCC
                                ||||  ||| |||||||||
                                TCCG  CGC CTTCTTGGG
                                  C_  C
GAM958  FLJ23519  3'  AGGCTCACGGAGGGGACCC   25345        T  AGA_
                                AGGCTCGTG GA   ACCC
                                ||||||||| ||   ||||
                                TCCGAGTGC CT   TGGG
                                     _ CCCC
GAM958  HUMGT198A 5'  GGCTCGTGGAAAACCC     25346       T   A
                                GGCTCGTG GAAGA CCC
                                |||||||| ||||| |||
                                CCGAGCAC CTTTT GGG
                                  _    _
GAM958  IL17D     3'  AGGCCCGTGAAGACC       25347      GT     A
                                AGGCTC  GTGAAGA CC
                                ||||||  ||||||| ||
                                TCCGGG  CACTTCT GG
                                  __     _
GAM958  KCNK16    3'  AGGCTGTGTGAAGAGTCC    25348      C      AC
                                AGGCT GTGTGAAGA  CC
                                |||||  |||||||||  ||
                                TCCGA CACACTTCT  GG
                                  _       CA
GAM958  KIAA0451  3'  AGGCTTATGTGAAGAAGCCC  25349      CG      _
                                AGGCT  TGTGAAGAA CCC
                                |||||  ||||||||| |||
                                TCCGA  ACACTTCTT GGG
                                   AT       C
GAM958  KIAA0685  5'  AGGCCCGTGTGGAGGCCC    25350         A  AA
                                AGGCTCGTGTG AG  CC
                                ||||||||||| ||  ||
                                TCCGGGCACAC TC  GG
                                     C  CG
GAM958  KIAA0831  3'  AGCAGTGTAGAAGAACCC    25351     TC   _
                                GGC  GTGT GAAGAACCC
                                |||  |||| |||||||||
                                TCG  CACA CTTCTTGGG
                                  T_   T
GAM958  KIAA1183  3'  AGCGCCACGAAGAGCCC     25352     _  TG     A
                                GGC TCG  TGAAGA CCC
                                ||| |||  |||||| |||
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                                TCG GGT  GCTTCT GGG
                                  C  __     C
GAM958  KIAA1550 3'  AGGCCCATGAAGGGCCC    25353      GT     AA
                                AGGCTC  GTGAAG  CCC
                                ||||||  ||||||  |||
                                TCCGGG  TACTTC  GGG
                                   __     CC
GAM958  KIAA1828 5'  GGCCCGTGAAAGCCC      25338       T    AA
                                GGCTCGTG GAAG  CCC
                                |||||||| ||||  |||
                                CCGGGCAC TTTC  GGG
                                   _   __
GAM958  KIAA1872 3'  GACTCGCGCAGGACCC     25354        GA  A
                                GGCTCGTGT  AG ACCC
                                |||||||||  || ||||
                                CTGAGCGCG  TC TGGG
                                     __ C
GAM958  KIAA1904 3'  AGGCCCGTCTGGGAGCCC   25355       G  AA  A
                                AGGCTCGT TG  GA CCC
                                |||||||| ||  || |||
                                TCCGGGCA AC  CT GGG
                                    G  C_  C
GAM958  MGC21621 3'  AGGCATGTGAACCAGAAC   25356     TC     ___
                                AGGC  GTGTGA   AGAAC
                                ||||  ||||||   |||||
                                TCCG  TACACT   TCTTG
                                   __     TGG
GAM958  NFKBIE   3'  AGGCTCATGGAACAGAGCC  25357        T  __   A
                                AGGCTCGTG GA  AGA CC
                                |||||||||  ||  |||  ||
                                TCCGAGTAC CT  TCT GG
                                     _  TG   C
GAM958  PDE7B    5'  AGACTTGTGCTGCAGAATCC  25358      C   GA_   _
                                AGGCT GTGT   AGAA CC
                                |||||  ||||   ||||  ||
                                TCTGA CACG   TCTT GG
                                   A    ACG    A
GAM958  PI4KII   3'  AGGCTTGGCAAAAACCC    25359      CG  TG
                                AGGCT  TG  AAGAACCC
                                |||||  ||  ||||||||
                                TCCGA  AC  TTTTTGGG
                                   __  CG
GAM958  PRO0659  3'  AGGCACGAAACATGAGGACC  25360     T  ___    A  A
                                AGGC CG   TGTGA GA CC
                                ||||  ||   |||||  ||  ||
                                TCCG GC   GTACT CT GG
                                  T  TTT    C  _
GAM958  RNF9     3'  AGGCTGGTTCAAGAACCC    25361      C  GTG
                                AGGCT GT   AAGAACCC
                                |||||  ||   ||||||||
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                                TCCGA CA   TTCTTGGG
                                   C  AG_
GAM958  SLC38A5   5'  AGGCTCGTGGAAACACC     25362         T    A
                                AGGCTCGTG GAAG ACC
                                ||||||||| |||| |||
                                TCCGAGCAC CTTT TGG
                                      _   G
GAM958  LOC129566 3'  AGGCTCTGAAAAGCCC      25363       GTG     A
                                AGGCTC   TGAAGA CCC
                                ||||||   |||||| |||
                                TCCGAG   ACTTTT GGG
                                   ___     C
GAM958  LOC130617 5'  GGCTCGTGCTCGAAGTCC    25364          __    AA
                                GGCTCGTGT  GAAG  CC
                                |||||||||  ||||  ||
                                CCGAGCACG  CTTC  GG
                                     AG    A_
GAM958  LOC132946 5'  AGCCTGTGTGAAGAACCC    25365     TC
                                GGC  GTGTGAAGAACCC
                                |||  ||||||||||||
                                TCG  CACACTTCTTGGG
                                  GA
GAM958  LOC140380 5'  AGCTCAGCCCCAAGAGCCC   25366       T  G__    A
                                GGCTCG GT   AAGA CCC
                                |||||| ||   |||| |||
                                TCGAGT CG   TTCT GGG
                                   _ GGG    C
GAM958  LOC147525 3'  AAGCTCATCTTGGAGGACC   25367        G_  A  A
                                AGGCTCGT  TG AG ACC
                                ||||||||  || || |||
                                TTCGAGTA  AC TC TGG
                                     GA  C  C
GAM958  LOC147622 5'  AGCTTTACCCAAAGAACCC   25368      CG_ G
                                GGCT   T TGAAGAACCC
                                ||||   | ||||||||||
                                TCGA   G GTTTCTTGGG
                                  AAT G
GAM958  LOC148137 3'  GGCCCAGAAGAACCC       25369       TGT
                                GGCTCG   GAAGAACCC
                                ||||||   |||||||||
                                CCGGGT   CTTCTTGGG
                                   ___
GAM958  LOC150481 3'  AGCTCCTGGAAGAACCC     25370      G  T
                                GGCTC TG GAAGAACCC
                                ||||| || |||||||||
                                TCGAG AC CTTCTTGGG
                                  G  _
GAM958  LOC150951 5'  AGCCCATGTGGAGGGGCCC   25371          A  AA_
                                GGCTCGTGTG AG   CCC
                                |||||||||| ||   |||
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                                TCGGGTACAC TC   GGG
                                      C  CCC
GAM958   LOC151723 5'  GGCCCGTGGAGAGACCC     25372        T _   A
                                GGCTCGTG GA AGA CCC
                                |||||||| || ||| |||
                                CCGGGCAC CT TCT GGG
                                     _  C   _
GAM958   LOC158191 3'  AGCTCCTGTAAGAACCC     25373      G     A
                                GGCTC TGTGA GAACCC
                                ||||| ||||| ||||||
                                TCGAG ACATT CTTGGG
                                   G    _
GAM958   LOC158314 3'  AGGCTCGTTTGTGAACCC    25374        G  AA
                                AGGCTCGT TG  GAACCC
                                |||||||| ||  ||||||
                                TCCGAGCA AC  CTTGGG
                                     A  A_
GAM958   LOC159110 5'  GGCTCGCGGAAGGACCC     25375        T    A
                                GGCTCGTG GAAG ACCC
                                |||||||| |||| ||||
                                CCGAGCGC CTTC TGGG
                                     _    C
GAM958   LOC159116 5'  GGCTCGCGGAAGGACCC     25375        T    A
                                GGCTCGTG GAAG ACCC
                                |||||||| |||| ||||
                                CCGAGCGC CTTC TGGG
                                     _    C
GAM958   LOC165070 5'  AGGCTCGGTGTAGCAGACCC   25376         _    A_   A
                                AGGCTCG TGTG  AGA CCC
                                ||||||| ||||  ||| |||
                                TCCGAGC ACAT  TCT GGG
                                    C    CG   _
GAM958   LOC200734 3'  AGGCTCATAGAAACC       25377          T   GA
                                AGGCTCGTG GAA  ACC
                                ||||||||| |||  |||
                                TCCGAGTAT CTT  TGG
                                     _   ___
GAM958   LOC204970 3'  GGCTGCTGCTGAAGAACC     25378      CG  _
                                GGCT  TG TGAAGAACC
                                ||||  || |||||||||
                                CCGA  AC ACTTCTTGG
                                   CG  G
GAM958   LOC220135 5'  GGCGCCCGTGAAGAATCC     25379     _ G        _
                                GGC TC TGTGAAGAA CC
                                ||| || |||||||||  ||
                                CCG GG GCACTTCTT GG
                                  C  _         A
GAM958   LOC221431 3'  AGTCTCAGAAGAACCC       25380     G    TGT
                                AG CTCG   GAAGAACCC
                                || ||||   |||||||||
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                                TC GAGT   CTTCTTGGG
                                 A   ___
GAM958  LOC221931 3'  AGCGTCATCTGAAGAACC    25381     _   G
                                GGC TCGT TGAAGAACC
                                ||| |||| |||||||||
                                TCG AGTA ACTTCTTGG
                                  C   G
GAM958  LOC91291  5'  AGGCTCATGAAAGTCC      25382         T   AA
                                AGGCTCGTG GAAG  CC
                                ||||||||| ||||  ||
                                TCCGAGTAC TTTC  GG
                                     _   A_
GAM959  CCNT2     3'  AAGAGCCATATTACTGG     25385      TA  G
                                AAGA  TC ATATTACTGG
                                ||||  || ||||||||||
                                TTCT  GG TATAATGACC
                                  C_ _
GAM960  ARF3      5'  CACAGCAGCTGCTTTCTG    25388      A       GGA
                                CACA CAGCTGTT   TTCTG
                                |||| ||||||||   |||||
                                GTGT GTCGACGA   AAGAC
                                  C      ___
GAM960  HELZ      3'  TACATAAAAGCTGTCAAAGTTT 25389     C  C     TG  _  C
           TGA                    TACA AA AGCTGT  GA TT TGA
                                |||| || ||||||  || || |||
                                ATGT TT TCGACA  TT AA ACT
                                  A  T     GT  C  A
GAM960  ITGA2     3'  CACAGCAGCTGTCCTG      25390      A       GGATT
                                CACA CAGCTGTT     CTG
                                |||| ||||||||     |||
                                GTGT GTCGACAG     GAC
                                  C      _____
GAM960  LMO4      3'  TACACAGTAGCTGCTATGA    25391       AC       _
                                TACACA  AGCTGTTG GA
                                ||||||  |||||||| ||
                                ATGTGT  TCGACGAT CT
                                    CA       A
GAM960  MDM4      3'  ACAGCTACCTTGGATTTTGA   25392        __      C
                                ACAGCTG  TTGGATT TGA
                                |||||||  ||||||| |||
                                TGTCGAT  AACCTAA ACT
                                   GG      A
GAM960  MIC2      3'  AACAGCCAAGATTCTG      25393         TT
                                AACAGCTG  GGATTCTG
                                ||||||||  ||||||||
                                TTGTCGGT  TCTAAGAC
                                          __
GAM960  MSL3L1    3'  TACACAATACATAGAATTCTGA 25394        CA  TGTT
                                TACACAA  GC   GGATTCTGA
                                |||||||  ||   |||||||||
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                                ATGTGTT TG   CTTAAGACT
                                   A_ TAT_
GAM960  NAP1L3   3' TGACAACAGCTTACATATTTTG 25395  C      GTTGG  C
          A                     A ACAACAGCT    ATT TGA
                                | |||||||||    ||| |||
                                A TGTTGTCGA    TAA ACT
                                 C       ATGTA  A
GAM960  NEU3     3' TACACAAATAGGCCTGATTCTG 25396      CAGCT TG
          A                     TACACAA    GT GATTCTGA
                                |||||||    ||  ||||||||
                                ATGTGTT    CG CTAAGACT
                                   TATC_ GA
GAM960  RUNX1    3' ACAACAACTGCATTCTGA   25397        TGG
                                ACAACAGCTGT  ATTCTGA
                                ||||||||||  |||||||
                                TGTTGTTGACG  TAAGACT
                                     ___
GAM960  ARH2     3' CAACAGTTAGGATTCTGA   25398     CTGTT
                                CAACAG   GGATTCTGA
                                ||||||   |||||||||
                                GTTGTC   CCTAAGACT
                                   AAT__
GAM960  DKFZP761I2123 3' TACACAGAGCTGAATCTG   25399     AC   TTGGAT
                                TACACA AGCTG    TCTG
                                ||||||  |||||    ||||
                                ATGTGT  TCGAC    AGAC
                                   C_   TT____
GAM960  FLJ10738 3' AGCTCTTGTTGGATTCTG   25400    ___
                                AGCT  GTTGGATTCTG
                                ||||  ||||||||||
                                TCGA  CAACCTAAGAC
                                  GAA
GAM960  FLJ22693 3' CACACAGCAGCCACCTGTTCTG 25401      A   TG GGA
          A                     TACACA CAGC  TT   TTCTGA
                                |||||| ||||  ||   ||||||
                                GTGTGT GTCG  GG   AAGACT
                                   C   GT  AC_
GAM960  FLJ23598 3' TACGCAACATTAAATTCTG   25402    A   GCTG
                                TAC CAACA   TTGGATTCTG
                                ||| |||||   ||||||||||
                                ATG GTTGT   AATTTAAGAC
                                  C   _____
GAM960  FLJ32449 3' TAACAACAGCCTTGTTCTG   25403  C      G  GA
                                A ACAACAGCT TTG  TTCTG
                                | |||||||| |||  |||||
                                A TGTTGTCGG AAC  AAGAC
                                 T       _  __
GAM960  GGA2     3' CAGCCTGCTGGATTCTGA   25404    _
                                CAGC TGTTGGATTCTGA
                                |||| ||||||||||||
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                                GTCG ACGACCTAAGACT
                                  G
GAM960  HNK-1ST  3' TACACAGGCATGGATTCTG   25405      ACA  TGT
                                TACACA  GC  TGGATTCTG
                                ||||||  ||  |||||||||
                                ATGTGT  CG  ACCTAAGAC
                                   C__  T__
GAM960  HSPC177  3' CACAATAGAAAATGATTCTGA 25406      C  CTGTTG
                                CACAA AG    GATTCTGA
                                ||||| ||    ||||||||
                                GTGTT TC    CTAAGACT
                                   A  TTTTA_
GAM960  KIAA0212 3' ACAGCTGTTAACATTCTGA   25407          _
                                ACAGCTGTTGG ATTCTGA
                                |||||||||||| |||||||
                                TGTCGACAATT TAAGACT
                                      G
GAM960  KIAA0254 3' CACAGGGCCAGGATTCTG    25408     ACA  GTT
                                CACA  GCT  GGATTCTG
                                ||||  |||  ||||||||
                                GTGT  CGG  CCTAAGAC
                                  CC_  T__
GAM960  KIAA1036 3' TACTGACAGCTGTCCCTG    25409    ACA       GGAT
                                TAC  ACAGCTGTT   TCTG
                                |||  |||||||||   ||||
                                ATG  TGTCGACAG   GGAC
                                  AC_       _____
GAM960  MGC3113  3' TACACATAGCTGACTCTGA   25410      AC   GTTG
                                TACACA  AGCT   GATTCTGA
                                ||||||  ||||   ||||||||
                                ATGTGT  TCGA   CTGAGACT
                                   A_   _____
GAM960  NCK1     3' ACACAGCAGTCACTTCTG    25411    A   T   GA
                                ACA CAGC GTTG  TTCTG
                                ||| |||| ||||  |||||
                                TGT GTCG CAGT  AAGAC
                                  _   T   G_
GAM960  PRO1768  3' ACACAATAGCTGTTATCT    25412      C      GAT
                                ACACAA AGCTGTTG   TCT
                                |||||| ||||||||   |||
                                TGTGTT TCGACAAT   AGA
                                   A      ___
GAM960  LOC120105 5' ACAGTGGTTGCTGAAATTCTG 25413     C___     _
                                ACAG   TGTTGGA TTCTG
                                ||||   ||||||| |||||
                                TGTC   ACGACTT AAGAC
                                  ACCA     T
GAM960  LOC146307 3' CAGCAGCTGTCCTCCCTG   25414   A      GGA
                                CA CAGCTGTT   TTCTG
                                || ||||||||   |||||
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                                GT GTCGACAG   GGGAC
                                 C       GA_
GAM960  LOC255158 3'  TACATGGCAGGTGTAAATCCTG 25415      CAA   C   T
            A                     TACA   CAG TGT GGATTCTGA
                                  ||||   ||| ||| |||||||||
                                  ATGT   GTC ACA TTTAGGACT
                                    ACC   C  _
GAM961  AMMECR1  5'  AGGCTGGCGGGGCGCGCGCGC  25418     __   TT   A
                                  AGG  GGC  GGC CGCGCGC
                                  |||  |||  ||| |||||||
                                  TCC  CCG  CCG GCGCGCG
                                   GA   CC   C
GAM961  GPR4     3'  TGACCAGGGGCTTTGCAAAC   25419           G   C
                                  TGACCAGGGGCTT GCA GC
                                  |||||||||||| ||| ||
                                  ACTGGTCCCCGAA CGT TG
                                           A   T
GAM961  MARK3    5'  CCGGGGCTGCACGCGCGC    25420    A     TG
                                  CC GGGGCT  GCACGCGCGC
                                  || ||||||  ||||||||||
                                  GG CCCCGA  CGTGCGCGCG
                                   _     __
GAM961  MIC2     3'  ACCAGGGGTTTCAGACGTGC   25421        C_ TG C   C
                                  ACCAGGGG  T  G ACG GC
                                  ||||||||  |  | ||| ||
                                  TGGTCCCC  A  C TGC CG
                                       AA GT _   A
GAM961  NPR1     3'  TGGCCGTGGGCTTGGCTCAGC  25422    A  AG       A  C
                                  TG CC  GGGCTTGGC CG GC
                                  || ||  |||||||||| || ||
                                  AC GG  CCCGAACCG GT CG
                                   C  CA        A  _
GAM961  TEM6     3'  TGGCCAGGGGCCTGCGGTGC   25423    A         GCAC
                                  TG CCAGGGGCTTG    GC
                                  || ||||||||||    ||
                                  AC GGTCCCCGGAC    CG
                                   C          GCCA
GAM961  USP21    3'  TGGGCAGGGGCTTGGTGAGC   25424    AC         CAC
                                  TG  CAGGGGCTTGG   GC
                                  ||  ||||||||||   ||
                                  AC  GTCCCCGAACC   CG
                                   CC          ACT
GAM961  USP21    3'  TGGGCAGGGGCTTGGTGAGC   25424    AC         CAC
                                  TG  CAGGGGCTTGG   GC
                                  ||  ||||||||||   ||
                                  AC  GTCCCCGAACC   CG
                                   CC          ACT
GAM961  CRYL1    3'  TGATTAAGGGCTTGCAGTGTGC 25425          __________  ACGCGC
              GCGCGG                  AGGGGCTTG        GC     G
                                  |||||||||        ||     |
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                                TTCCCGAAC       CG     C
                                     GTCACAIII  CGCGCA
GAM961  DKFZP434J154 5'  CGGCCGGGGAGGGCGCGCGCGC 25426    A  A    CTT   A
                                TG CC GGGG   GGC CGCGCGC
                                || || ||||   ||| |||||||
                                GC GG CCCC   CCG GCGCGCG
                                 C  _   TC_  C
GAM961  KIAA1719  5'  TGGCCAGGAGCTTGGTGGC   25427    A         CAC
                                TG CCAGGGGCTTGG   GC
                                || ||||||||||||   ||
                                AC GGTCCTCGAACC   CG
                                 C          AC_
GAM961  LY117    5'  TGATCAGGGGCTGGTGACTTGC 25428     C       __    AC
                                TGA CAGGGGCT  TGGC  GC
                                ||| ||||||||  ||||  ||
                                ACT GTCCCCGA  ACTG  CG
                                  A       CC    AA
GAM961  LY117    5'  TGATCAGGGGCTGGTGACTTGC 25428     C       __    AC
                                TGA CAGGGGCT  TGGC  GC
                                ||| ||||||||  ||||  ||
                                ACT GTCCCCGA  ACTG  CG
                                  A       CC    AA
GAM961  LY117    5'  TGATCAGGGGCTGGTGACTTGC 25428     C       __    AC
                                TGA CAGGGGCT  TGGC  GC
                                ||| ||||||||  ||||  ||
                                ACT GTCCCCGA  ACTG  CG
                                  A       CC    AA
GAM961  MGC2494   5'  TGGCCTGGGGCTGGCGGTGTGC 25429    A  A     T   ACGC_
                                TG CC GGGGCT GGC     GC
                                || || |||||| |||     ||
                                AC GG CCCCGA CCG     CG
                                 C  A      _   CCACA
GAM961  LOC115264 3'  AGGTGCCGGCACGTGCGC    25430     _  T     C
                                GGG GCT GGCACG GCGC
                                ||| ||| |||||| ||||
                                TCC CGG CCGTGC CGCG
                                  A  _     A
GAM961  LOC131583 5'  GGGGGAGACACGCGCGC     25431     CTT
                                GGGG   GGCACGCGCGC
                                ||||   ||||||||||
                                CCCC   CTGTGCGCGCG
                                  CT_
GAM961  LOC149318 3'  AGGTGCCGGCACGTGCGC    25430     _  T     C
                                GGG GCT GGCACG GCGC
                                ||| ||| |||||| ||||
                                TCC CGG CCGTGC CGCG
                                  A  _     A
GAM961  LOC155061 3'  CCAGGGGCTTGGTGCGC     25432          CAC
                                CCAGGGGCTTGG   GCGC
                                ||||||||||||   ||||
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                                GGTCCCCGAACC  CGCG
                                      A__
GAM961  LOC157254 5'  TGGGCAGGGGCTTCTGCGC   25433    AC       GGCAC
                                TG  CAGGGGCTT    GCGC
                                ||  |||||||||    ||||
                                AC  GTCCCCGAA    CGCG
                                 CC       GA___
GAM961  LOC159201 5'  CGGCCAGGGGCTTGGGGTAGCC 25434          CA____      III
          GCGCGCG                 AGGGGCTTGG     CGCGCGC   G
                                ||||||||||     |||||||  |
                                TCCCCGAACC     GCGCGCG   C
                                      CCATCG      III
GAM961  LOC221463 3'  GACCAGGGGCTTGGCCA     25435            A
                                GACCAGGGGCTTGGC CG
                                |||||||||||||| ||
                                CTGGTCCCCGAACCG GT

                                      _
GAM962  GABRE    3'  TAGTGGGCTTCTGGAAAA    25438    CA   C
                                TAG  GGC TTCTGGAAAG
                                |||  ||| ||||||||||
                                ATC  CCG AAGACCTTTT
                                  AC  _
GAM962  GABRE    3'  TAGTGGGCTTCTGGAAAA    25438    CA   C
                                TAG  GGC TTCTGGAAAG
                                |||  ||| ||||||||||
                                ATC  CCG AAGACCTTTT
                                  AC  _
GAM962  GABRE    3'  TAGTGGGCTTCTGGAAAA    25438    CA   C
                                TAG  GGC TTCTGGAAAG
                                |||  ||| ||||||||||
                                ATC  CCG AAGACCTTTT
                                  AC  _
GAM962  GABRE    3'  TAGTGGGCTTCTGGAAAA    25438    CA   C
                                TAG  GGC TTCTGGAAAG
                                |||  ||| ||||||||||
                                ATC  CCG AAGACCTTTT
                                  AC  _
GAM962  HSPA1A   5'  AGGTTCGCTCTGGGAAGCCTTG 25439    CC__     A
                                AGG   TTCTGG AAGCCTTG
                                |||   |||||| ||||||||
                                TCC   GAGACC TTCGGAAC
                                  AAGC     C
GAM962  HSPA1B   5'  AGGTTCGCTCTGGAAAGCCTTG 25440    CC__
                                AGG   TTCTGGAAAGCCTTG
                                |||   ||||||||||||||||
                                TCC   GAGACCTTTCGGAAC
                                  AAGC
GAM962  KCNK5    3'  GGCCCACAGAAAGCCTTG    25441      TCT
                                GGCCT   GGAAAGCCTTG
                                |||||   ||||||||||
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                                CCGGG  TCTTTCGGAAC
                                  TG_
GAM962  RAPSN    3'  GCAGGCCCCAAGGCCTT    25442        CT  AAA
                                GCAGGCCTT  GG  GCCTT
                                |||||||||  ||  |||||
                                CGTCCGGGG  TC  CGGAA
                                     T_  ___
GAM962  SYNGR1   3'  CAGTGGGCCTTCTGGAAGGCC  25443    CA         A
                                TAG  GGCCTTCTGGAA GCC
                                |||  |||||||||||| |||
                                GTC  CCGGAAGACCTT CGG
                                  AC          C
GAM962  BG1      5'  GCAGGCCTCTGGGGAGC    25444        T    AA
                                GCAGGCCT CTGG  AGC
                                |||||||| ||||  |||
                                CGTCCGGA GACC  TCG
                                     _   CC
GAM962  FLJ22635 3'  ACAGGCAGAAAGCCT      25445       CTTCT
                                GCAGGC    GGAAAGCCT
                                ||||||    |||||||||
                                TGTCCG    TCTTTCGGA
                                     _____
GAM962  KIAA0854 3'  GGCAGTTCAGAAAGCCTT    25446    C_   T
                                GGC  TTC GGAAAGCCTT
                                |||  ||| ||||||||||
                                CCG  AAG TCTTTCGGAA
                                  TC  _
GAM962  MOST2    3'  CAGCAGGTCTTGCAGCCTT   25447       CCT   GGAA
                                TAGCAGG   TCT   AGCCTT
                                |||||||   |||   ||||||
                                GTCGTCC   AGA   TCGGAA
                                     ___  ACG_
GAM962  NDST3    3'  GGTAGCTTCTGGAAGCTTTG  25448    C__       A  C
                                GG   CTTCTGGAA GC TTG
                                ||   ||||||||| || |||
                                CC   GAAGACCTT CG AAC
                                  ATC        _  A
GAM962  LOC145601 3'  GCGGGCTCCCCCAGGCCTTG  25449    A  _    TG AAA
                                GC GGC CTTC  G   GCCTTG
                                || ||| ||||  |   ||||||
                                CG CCG GGGG  C   CGGAAC
                                  C   A    GT ___
GAM962  LOC148046 3'  TAGAGGGCCCCCCAGAGGCTTT 25450     CA      TG  AA  C
           G                     TAG  GGCCTTC  GA  GC TTG
                                |||  |||||||  ||  || |||
                                ATC  CCGGGGG  CT  CG AAC
                                  TC      GT  C_  A
GAM962  LOC148147 3'  GGGCTCCCAAAGCCTTG     25451    C    GG
                                GG CTTCT  AAAGCCTTG
                                || |||||  |||||||||
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                                CC GAGGG  TTTCGGAAC
                                 C    __
GAM962  LOC149711 3'  AGTAGGTTGAAAAGCCTT    25452    C   CCTTC
                                AG AGG    TGGAAAGCCTT
                                || |||    ||||||||||
                                TC TCC    ACTTTTCGGAA
                                 A  A____
GAM962  LOC157503 5'  GGTCTGGAAAGCCTT      25453    CCT
                                GG  TCTGGAAAGCCTT
                                ||  ||||||||||||
                                CC  AGACCTTTCGGAA
                                 ___
GAM962  LOC158969 5'  GCAGGGTGGAGGAAGCCTTG  25454      CCTTCT   A
                                GCAGG     GGAA GCCTTG
                                |||||     |||| ||||||
                                CGTCC     CCTT CGGAAC
                                   CACCT_   _
GAM962  LOC162333 5'  ACTGGGCCTTCTGGGGCCCTG  25455    A_       AAA
                                GC  GGCCTTCTGG   GCCTTG
                                ||  ||||||||||   ||||||
                                TG  CCGGAAGACC   CGGGAC
                                 AC        C__
GAM962  LOC196382 5'  GGGCTTCAATGGAAGCCTTG   25456    C   __    A
                                GG CTTC  TGGAA GCCTTG
                                || ||||  ||||| ||||||
                                CC GAAG  ACCTT CGGAAC
                                 C   TT    _
GAM962  LOC90529  3'  ACAGGCCTTGGAGGCTTT    25457       TC   AA  C
                                GCAGGCCT  TGGA  GC TT
                                ||||||||  ||||  || ||
                                TGTCCGGA  ACCT  CG AA
                                     __   C_  A
GAM963  CNTNAP2   3'  TGCTGTTGCTTTTAGAGA    25460    A       CTT
                                TG TGTTGCTTTT   GGA
                                || ||||||||||   |||
                                AC ACAACGAAAA   TCT
                                 G        TC_
GAM963  EFNB2     3'  TGATGTTGTTTTTCCCAGAA   25461       C     TG
                                TGATGTTG TTTTCT  GAA
                                |||||||| ||||||  |||
                                ACTACAAC AAAAGG  CTT
                                     A     GT
GAM963  EGLN1     3'  TGATGTTATTTTGAGGAA    25462       C   CTT
                                TGATGTTG TTTT   GGAA
                                |||||||| ||||   ||||
                                ACTACAAT AAAA   CCTT
                                     _   CT_
GAM963  GATA3     5'  TGATTTGCTTTCGGTGG     25463     G      CT
                                TGAT TTGCTTTT  TGG
                                |||| ||||||||  |||
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                                ACTA AACGAAAG  ACC
                                  _      CC
GAM963  GCLM     3'  TAATGAATTTTTTTTGGAAATA 25464      TTGC   C
              A                   TGATG   TTTT TTGGAAATAA
                                  ||||||   |||| ||||||||||
                                  ATTAC   AAAA AACCTTTATT
                                     TTA_   A
GAM963  GRIN2A   3'  GATGTGTCTTGGAAAT     25465      T CTTT
                                  GATGT G   TCTTGGAAAT
                                  ||||| |   ||||||||||
                                  CTACA C   AGAACCTTTA
                                    _ ____
GAM963  MKPX     3'  ATGTTGCTTTTCTTTTTGG   25466          ___
                                  ATGTTGCTTTTCT   TGG
                                  ||||||||||||   |||
                                  TACAACGAAAAGA   ACC
                                         AAA
GAM963  PKIA     5'  GATCTCTTTTTTCTTGGA    25467    G  GC
                                  GAT TT  TTTTCTTGGA
                                  ||| ||  ||||||||||
                                  CTA AG  AAAAGAACCT
                                    G  AA
GAM963  SFRP1    3'  TGTGTTGCTGTTGGAAAT    25468    A     TTTC
                                  TG TGTTGCT   TTGGAAAT
                                  || |||||||   ||||||||
                                  AC ACAACGA   AACCTTTA
                                  _     C___
GAM963  TEM6     3'  TGATGTTGTTTGTTCTTG    25469       C  _
                                  TGATGTTG TT TTCTTG
                                  |||||||| || ||||||
                                  ACTACAAC AA AAGAAC
                                       A  C
GAM963  ALK7     3'  TGTTGCTTTCAAAATA      25470         CTTG
                                  TGTTGCTTTT   GAAATA
                                  ||||||||||   ||||||
                                  ACAACGAAAG   TTTTAT
                                       ____
GAM963  DKFZp434E2220 5'  TGATATTGCTTTGAAATA    25471          TCTTG
                                  TGATGTTGCTTT    GAAATA
                                  ||||||||||||    ||||||
                                  ACTATAACGAAA    CTTTAT
                                       _____
GAM963  DKFZp761G0313 3'  TGATGTTGTCTTTCATGA    25472       CT   T
                                  TGATGTTG  TTTC TGG
                                  ||||||||  |||| |||
                                  ACTACAAC  AAAG ACT
                                       AG   T
GAM963  DKFZP762D096 3'  TGATGTTGGCTTTACCGAGG   25473       _   _ TT
                                  TGATGTTG CTTT TC  GG
                                  |||||||| |||| ||  ||
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                                ACTACAAC GAAA GG  CC
                                    C    T  CT
GAM963  FLJ20079  3'  TGATGTGCAAGCTGGAAATAA  25474       T  TTTTC
                                TGATGT GC    TTGGAAATAA
                                |||||| ||    ||||||||||
                                ACTACA CG    GACCTTTATT
                                   _  TTC__
GAM963  MGC17299  3'  GATGTGAGGGGTCTTGGAAAT  25475      TGCTTT
                                GATGT     TCTTGGAAAT
                                |||||     ||||||||||
                                CTACA     AGAACCTTTA
                                  CTCCCC
GAM963  MGC3265   3'  TGATGTTGACAGGCTTGGA   25476        _ TTTT
                                TGATGTTG C    CTTGGA
                                |||||||| |    ||||||
                                ACTACAAC G    GAACCT
                                     T TCC_
GAM963  LOC143719 5'  TGATGTTGCTCTTCTTCATGG  25477             ___
                                TGATGTTGCTTTTCT   TGG
                                ||||||||||||||   |||
                                ACTACAACGAGAAGA   ACC
                                         AGT
GAM963  LOC145820 3'  TGTGTTGCTTTTGATAGA    25478    A        CT
                                TG TGTTGCTTTT  TGGA
                                || ||||||||||  ||||
                                AC ACAACGAAAA  ATCT
                                 _         CT
GAM963  LOC149670 5'  TGAGGTCCCTCTTCTTGGGAAT 25479     T   G        A
                                TGA GTT CTTTTCTTGG AAT
                                ||| ||| ||||||||||| |||
                                ACT CAG GAGAAGAACC TTA
                                  C   G         C
GAM963  LOC154739 5'  TGCAATACTTTTTTTGGAAATA 25480     __      C
                                TGT  TGCTTTT TTGGAAATA
                                |||  ||||||| |||||||||
                                ACG  ATGAAAA AACCTTTAT
                                  TT      A
GAM963  LOC170425 5'  TGTTGTTGACATTTTGGAAATA 25481    A    _ TTTTC
                                TG TGTTG C    TTGGAAATA
                                || ||||| |    |||||||||
                                AC ACAAC G    AACCTTTAT
                                 A    T TAA__
GAM963  LOC201685 5'  TAATGTTGCTTGGAA       25482          TTTCT
                                TGATGTTGCT    TGGAA
                                ||||||||||    |||||
                                ATTACAACGA    ACCTT
                                              _____
GAM963  LOC203276 3'  TGCAATACTTTTTTTTGGAAAT 25483     __      C_
            A                    TGT  TGCTTTT  TTGGAAATA
                                |||  |||||||  |||||||||
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                                ACG  ATGAAAA  AACCTTTAT
                                  TT      AA
GAM963   LOC203305 3'  TGCAATACTTTTTTTTGGAAAT 25483     __      C_
             A                    TGT  TGCTTTT  TTGGAAATA
                                  |||  |||||||  |||||||||
                                  ACG  ATGAAAA  AACCTTTAT
                                    TT      AA
GAM963   LOC219578 5'  TGGAGTTGCTTTTCTATGG   25484    AT        _
                                  TG  GTTGCTTTTCT TGG
                                  ||  |||||||||||| |||
                                  AC  CAACGAAAAGA ACC
                                   CT         T
GAM963   LOC220883 3'  TGAAGTTGCTTTTGGA      25485     T      TCT
                                  TGA GTTGCTTT   TGGA
                                  ||| ||||||||   ||||
                                  ACT CAACGAAA   ACCT
                                    T      ____
GAM963   LOC221981 3'  TGGTATTGCTTTTTAATGG   25486    A        CT_
                                  TG TGTTGCTTTT   TGG
                                  || ||||||||||   |||
                                  AC ATAACGAAAA   ACC
                                   C         ATT
GAM963   LOC253129 3'  TGATTTGCTTTCGGTGG     25463     G       CT
                                  TGAT TTGCTTTT  TGG
                                  |||| ||||||||  |||
                                  ACTA AACGAAAG  ACC
                                     _       CC
GAM963   LOC253715 3'  TGAGGTCCCTCTTCTTGGGAAT 25479     T   G        A
                                  TGA GTT CTTTTCTTGG AAT
                                  ||| ||| |||||||||| |||
                                  ACT CAG GAGAAGAACC TTA
                                    C   G         C
GAM963   LOC254243 3'  TGCAATACTTTTTTTTGGAAAT 25483     __      C_
             A                    TGT  TGCTTTT  TTGGAAATA
                                  |||  |||||||  |||||||||
                                  ACG  ATGAAAA  AACCTTTAT
                                    TT      AA
GAM963   LOC255098 5'  TGATGTTTTTTTCTACTGG   25487        GC     __
                                  TGATGTT  TTTTCT  TGG
                                  |||||||  ||||||  |||
                                  ACTACAA  AAAAGA  ACC
                                      A_     TG
GAM963   LOC90038  3'  TGCAATACTTTTTTTTGGAAAT 25483     __      C_
             A                    TGT  TGCTTTT  TTGGAAATA
                                  |||  |||||||  |||||||||
                                  ACG  ATGAAAA  AACCTTTAT
                                    TT      AA
GAM963   LOC92285  5'  TGAAGTTGTGACTTGGAAAT   25488    T   CTTTT
                                  TGA GTTG    CTTGGAAAT
                                  ||| ||||    |||||||||
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                                ACT CAAC    GAACCTTTA
                                  T   ACT__
GAM964  MMP16    3'  TAGTAGTGTTTTGTTGTT    25491       C_
                                TGGTGGT  TTTGTTGTT
                                |||||||  |||||||||
                                ATCATCA  AAACAACAA
                                    CA
GAM964  LOC147180 3'  TTTGATGGTGGTTGTAGT    25492     A      CTT   T
                                TTT ATGGTGGT   TGT GT
                                ||| ||||||||   ||| ||
                                AAA TACCACCA   ACA CA
                                  C       ___   T
GAM964  LOC163882 3'  TGGTTTTTCTTTGTTGTT    25493     GG_
                                TGGT   TCTTTGTTGTT
                                ||||   ||||||||||
                                ACCA   AGAAACAACAA
                                   AAA
GAM964  LOC221178 3'  TTTGATGGTGGTGAAATGTT   25494     A      CTT_
                                TTT ATGGTGGT    TGTT
                                ||| ||||||||    ||||
                                AAA TACCACCA    ACAA
                                  C       CTTT
GAM965  ACHE     3'  GTGGGGATGGGCAGAGTCT   25497     TC  CCGTA
                                GTGG  GT    GGCAGAGTCT
                                ||||  ||    ||||||||||
                                CACC  TA    CCGTCTCAGA
                                  CC  C_____
GAM965  ACHE     3'  GTGGGGATGGGCAGAGTCT   25497     TC  CCGTA
                                GTGG  GT    GGCAGAGTCT
                                ||||  ||    ||||||||||
                                CACC  TA    CCGTCTCAGA
                                  CC  C_____
GAM965  MAPRE3   3'  TGGGGTCCAGGCAGAGT     25498     TC    GT
                                TGG  GTCC  AGGCAGAGT
                                |||  ||||  |||||||||
                                ACC  CAGG  TCCGTCTCA
                                  C_   __
GAM965  TM4SF4   3'  TGTAGTCGTCATGCTGTAGAGT 25499          CGTAG  ___
           CT                     TGTGGTCGTC    GC   AGAGTCT
                                ||||||||||    ||   |||||||
                                ACATCAGCAG    CG   TCTCAGA
                                     TA___  ACA
GAM965  DKFZp761J139 5'  TGTGGTCGTTGTTGAGACGGAG 25500         CC  __   A
           TCT                    TGTGGTCGT  GT  AGGC GAGTCT
                                |||||||||  ||  |||| ||||||
                                ACACCAGCA  CA  TCTG CTCAGA
                                     A_  AC   C
GAM965  FLJ22418  3'  TGTGGCCAGGCAGGGT      25501       GTCCGT     A
                                TGTGGTC     AGGCAG GT
                                |||||||     |||||| ||
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                                ACACCGG     TCCGTC CA
                                   _____     C
GAM965  KIAA1710  3'  TGTGGCAATTTAGGCAGAGTCT 25502       CGTCCG
                                TGTGGT     TAGGCAGAGTCT
                                ||||||     ||||||||||||
                                ACACCG     ATCCGTCTCAGA
                                   TTAA__
GAM965  LHPP      3'  TGGTCAAGGCAGAGT       25503       TCCGT
                                TGGTCG     AGGCAGAGT
                                ||||||     |||||||||
                                ACCAGT     TCCGTCTCA
                                   _____
GAM965  LOC200014 3'  TGTGTTTGTTTTGAGACAGAGT 25504     GTC  CCGT
             CT                   TGTG   GT    AGGCAGAGTCT
                                ||||   ||    ||||||||||||
                                ACAC   CA    TCTGTCTCAGA
                                  AAA  AAAC
GAM965  LOC222066 3'  TGTTGTTGTTTTGAGACAGAGT 25505     G  C  CCGT
             CT                   TGT GT GT    AGGCAGAGTCT
                                ||| || ||    ||||||||||||
                                ACA CA CA    TCTGTCTCAGA
                                  A  A  AAAC
GAM966  ABL1      3'  CTGTGAAATACGTGAGGC    25508     GC   C
                                TTG  GAA ACGTGAGGC
                                |||  ||| |||||||||
                                GAC  TTT TGCACTCCG
                                  AC   A
GAM966  ABL1      3'  CTGTGAAATACGTGAGGC    25508     GC   C
                                TTG  GAA ACGTGAGGC
                                |||  ||| |||||||||
                                GAC  TTT TGCACTCCG
                                  AC   A
GAM966  CAPN10    3'  ACCCTCTGGGTGTGAGGC    25509      C   CGAACAC
                                ACCC TTGG      GTGAGGC
                                |||| ||||      |||||||
                                TGGG GACC      CACTCCG
                                  A    CA_____
GAM966  CAPN10    3'  ACCCTCTGGGTGTGAGGC    25509      C   CGAACAC
                                ACCC TTGG      GTGAGGC
                                |||| ||||      |||||||
                                TGGG GACC      CACTCCG
                                  A    CA_____
GAM966  CAPN10    3'  ACCCTCTGGGTGTGAGGC    25509      C   CGAACAC
                                ACCC TTGG      GTGAGGC
                                |||| ||||      |||||||
                                TGGG GACC      CACTCCG
                                  A    CA_____
GAM966  CAPN10    3'  ACCCTCTGGGTGTGAGGC    25509      C   CGAACAC
                                ACCC TTGG      GTGAGGC
                                |||| ||||      |||||||
```

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                                TGGG GACC      CACTCCG
                                  A   CA_____
GAM966  CAPN10   3'  ACCCTCTGGGTGTGAGGC   25509     C   CGAACAC
                                ACCC TTGG      GTGAGGC
                                |||| ||||      |||||||
                                TGGG GACC      CACTCCG
                                  A   CA_____
GAM966  CAPN10   3'  ACCCTCTGGGTGTGAGGC   25509     C   CGAACAC
                                ACCC TTGG      GTGAGGC
                                |||| ||||      |||||||
                                TGGG GACC      CACTCCG
                                  A   CA_____
GAM966  CELL     3'  CCCCTTGGTGATTGTGAA    25510       C  ACAC
                                CCCCTTGG GA    GTGAG
                                |||||||| ||    |||||
                                GGGGAACC CT    CACTT
                                    A  AA__
GAM966  CKAP1    5'  TTGGCGAAGCACCTAGGCC   25511       _   G G
                                TTGGCGAA CAC T AGGCC
                                |||||||| ||| | |||||
                                AACCGCTT GTG A TCCGG
                                    C   G _
GAM966  CLC      3'  CCTTGGCAACATGAAG      25512       AAC
                                CCTTGGCG   ACGTGAGG
                                ||||||||   ||||||||
                                GGAACCGT   TGTACTTC
                                     ___
GAM966  DNM2     3'  CCTGCGCCGCGGGTGCGTGAGG 25513     _  G  AACA__
            CC                    CCT TG CG     CGTGAGGCC
                                ||| || ||     |||||||||
                                GGA GC GC     GCACTCCGG
                                  C  G  GCCCAC
GAM966  EGLN2    5'  ACCCCTTGGTGACCAGCGC   25514       C  A  _
                                ACCCCTTGG GA CA CGT
                                ||||||||| || || |||
                                TGGGGAACC CT GT GCG
                                    A  G  C
GAM966  F9       3'  CCATGGTGAACACGAAACC   25515    T   C     GT
                                CC TGG GAACAC  GAGGCC
                                || ||| ||||||  ||||||
                                GG ACC CTTGTG  CTTTGG
                                 T   A     __
GAM966  GCK      3'  CCCCTTGGGGCAGAGGC     25516       CGAA  CGT
                                CCCCTTGG   CA   GAGGC
                                ||||||||   ||   |||||
                                GGGGAACC   GT   CTCCG
                                    CC__  ___
GAM966  GCK      3'  CCCCTTGGGGCAGAGGC     25516       CGAA  CGT
                                CCCCTTGG   CA   GAGGC
                                ||||||||   ||   |||||
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                              GGGGAACC   GT  CTCCG
                                 CC__ ___
GAM966  GCK     3' CCCCTTGGGGCAGAGGC    25516      CGAA CGT
                              CCCCTTGG   CA  GAGGC
                              ||||||||   ||  |||||
                              GGGGAACC   GT  CTCCG
                                 CC__ ___
GAM966  GOLGA4  3' TTGGCTACATGAGGGGCC   25517     GAAC   __
                              TTGGC   ACGTGA GGCC
                              |||||   ||||||  ||||
                              AACCG   TGTACT  CCGG
                                 A___    CC
GAM966  KCNN3   5' CCTCTAGGAGCGTGTGAGGCC 25518    ____  AACAC
                              CCTT   GGCG   GTGAGGCC
                              ||||   ||||   ||||||||
                              GGAG   TCGC   CACTCCGG
                                ATCC   A____
GAM966  MAT1A   3' CCCCTTGGGAGCAGACC    25519      C ACAC G
                              CCCCTTGG GA   GT AGGCC
                              |||||||| ||   || |||||
                              GGGGAACC CT   CG TCTGG
                                 _ ____ _
GAM966  PACSIN3 5' CCCCTCGGCGGGTGGGG    25520       AACAC  A
                              CCCCTTGGCG    GTG GG
                              ||||||||||    ||| ||
                              GGGGAGCCGC    CAC CC
                                 C____  C
GAM966  PDGFB   3' CCCCTTGGTGGAGCAGAC   25521      C_ ACAC G
                              CCCCTTGG  GA   GT AGGC
                              ||||||||  ||   || ||||
                              GGGGAACC  CT   CG TCTG
                                 AC ____ _
GAM966  SCA1    3' CCCCTTACCCCATGTGGGGCC 25522      G GAA  C  A
                              CCCCTTG C  CA GTG GGCC
                              ||||||| |  || ||| ||||
                              GGGGAAT G  GT CAC CCGG
                                 _ GG_  A  C
GAM966  SECTM1  3' CCCCCTGGCGGTGGGGC    25523       AACAC  A
                              CCCCTTGGCG    GTG GGC
                              ||||||||||    ||| |||
                              GGGGGACCGC    CAC CCG
                                 _____  C
GAM966  SHC1    3' ACCCCTTGGGGTGAGGGGC   25524       CGAACAC  __
                              ACCCCTTGG     GTGA  GGC
                              |||||||||     ||||  |||
                              TGGGGAACC     CACT  CCG
                                 C_______  CC
GAM966  SLC7A8  3' CCCTGGTGAACAGATAGGG   25525     C   C  A
                              CCTTGG GAACA GTG GG
                              |||||| ||||| ||| ||
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                                GGGACC CTTGT TAT CC
                                   A    C  C
GAM966  TMPRSS2  3' ACCCCTTGCGGACAAGG    25526       G  A  CGTG
                                ACCCCTTG CG ACA   AGG
                                |||||||| || |||   |||
                                TGGGGAAC GC TGT   TCC
                                   _  C  _____
GAM966  ACTR1A   3' CCCTGGTGAACATGAGGGCC  25527      C    CG   _
                                CCTTGG GAACA  TGAGG CC
                                |||||| |||||  ||||| ||
                                GGGACC CTTGT  ACTCC GG
                                   A    __    C
GAM966  ARHGEF9  3' CCTTTTGGAGAGCAAATCCTGG 25528   CC   C  A  C  GA_
           CC                     CC  TTGG GA CA GT   GGCC
                                ||  |||| || || ||   ||||
                                GG  AACC CT GT TA   CCGG
                                 AA   T  C  T  GGA
GAM966  BDG-29   3' CTTGTTACAACGCACGTGAGGC 25529    __   A_
           C                     CTTG  GCGA  CACGTGAGGCC
                                ||||  ||||  ||||||||||
                                GAAC  TGTT  GTGCACTCCGG
                                  AA   GC
GAM966  C20orf81  5' CCCACTTGGCGGGCGCGAAGCC 25530    _     AACA
                                CCC CTTGGCG   CGTGAGGCC
                                ||| |||||||   |||||||||
                                GGG GAACCGC   GCGCTTCGG
                                  T     CC__
GAM966  C3IP1    3' ACTCCTTGGCAGACATGTG   25531   C      A  C
                                AC CCTTGGCG ACA GTG
                                || |||||||| ||| |||
                                TG GGAACCGT TGT CAC
                                 A      C  A
GAM966  DKFZP434B0335 5' CCCTTGGGCTCGTGAGGC   25532       CGAACA
                                CCCTTGG     CGTGAGGC
                                |||||||     ||||||||
                                GGGAACC     GCACTCCG
                                    CGA___
GAM966  DNAJA4   3' CCCTTGGCATAATGTGGGGCC  25533        AACAC  A
                                CCCTTGGCG    GTG GGCC
                                |||||||||    ||| ||||
                                GGGAACCGT    CAC CCGG
                                     ATTA_  C
GAM966  FLJ13265  3' CCCCCTGGCGCTGGGGC    25534         AACACG  A
                                CCCCTTGGCG     TG GGC
                                ||||||||||     || |||
                                GGGGGACCGC     AC CCG
                                     G_____  C
GAM966  FLJ13639  5' CCCCTTGGCGAACCACACGACG 25535          _    G
           C                     CCCCTTGGCGAAC ACGTGA GC
                                |||||||||||| |||||| ||
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                                GGGGAACCGCTTG TGTGCT CG
                                      G     G
GAM966  FLJ21478  3'  CCCCTTGGTGACACAATCAGAG 25536        C  A   T___
            GC                   CCCCTTGG GA CACG   GAGGC
                                 |||||||| || ||||   |||||
                                 GGGGAACC CT GTGT   CTCCG
                                     A  _   TAGT
GAM966  FLJ32884  3'  CCCTTGGCAACATCAGC    25537        AAC   GA
                                 CCCTTGGCG  ACGT  GGC
                                 |||||||||  ||||  |||
                                 GGGAACCGT  TGTA  TCG
                                     ___   G_
GAM966  GTPBP5    3'  ACCCCTTGCGCAGCAGTGAGGC 25538        _  AA  C
            C                    ACCCCTTG GCG  CA GTGAGGCC
                                 |||||||| |||  || ||||||||
                                 TGGGGAAC CGT  GT CACTCCGG
                                     G  C_  _
GAM966  KIAA0161  3'  CCTCTTAGTGAACACATG    25539    C    C
                                 CC CTTGG GAACACGTG
                                 || ||||| |||||||||
                                 GG GAATC CTTGTGTAC
                                  A    A
GAM966  KIAA1016  3'  ACTCCTCCACGTGAGG      25540    C   GGCGAA
                                 AC CCTT     CACGTGAGG
                                 || ||||     |||||||||
                                 TG GGAG     GTGCACTCC
                                  A  _______
GAM966  KIAA1196  3'  ACCCCTTGGGAGGAGG      25541        C  ACACGT
                                 ACCCCTTGG GA     GAGG
                                 ||||||||| ||     ||||
                                 TGGGGAACC CT     CTCC
                                     _ C_____
GAM966  KIAA1881  5'  CCCCTTGGGTGAACGTCGC   25542        C_   A_
                                 CCCCTTGG  GAAC  CGT
                                 ||||||||  ||||  |||
                                 GGGGAACC  CTTG  GCG
                                     CA   CA
GAM966  MGC2562   3'  CCCCTTAGGAAGATGTGGGGC  25543        C  CAC   A
                                 CCCCTTGG GAA   GTG GGC
                                 |||||||| |||   ||| |||
                                 GGGGAATC CTT   CAC CCG
                                     _  CTA   C
GAM966  MSC       5'  CCCTGGCGGAGGCGGAGGCC   25544        AACA  T
                                 CCTTGGCG   CG GAGGCC
                                 ||||||||   || ||||||
                                 GGGACCGC   GC CTCCGG
                                     CTCC  _
GAM966  NAF1      3'  CCCCTCGGCGGACGTGGC    25545        AAC   GA
                                 CCCCTTGGCG  ACGT  GGC
                                 |||||||||  ||||  |||
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                                GGGGAGCCGC  TGCA  CCG
                                     C__   __
GAM966  Rab11-FIP2 5'  CCTGCGGGCACGTGAGGCC   25546    TG  AA
                                CCT  GCG  CACGTGAGGCC
                                |||  |||  ||||||||||
                                GGA  CGC  GTGCACTCCGG
                                  __   CC
GAM966  RASSF2   3'  CCCTTGGCGAAATGCCAGGGGC 25547         CAC  G __
          C                      CCCTTGGCGAA   GT A  GGCC
                                ||||||||||   || |  ||||
                                GGGAACCGCTT   CG T  CCGG
                                      TA_  G CC
GAM966  SETBP1   3'  CCTTGGCAGCGTGAGG     25548        AACA
                                CCTTGGCG    CGTGAGG
                                ||||||||    |||||||
                                GGAACCGT    GCACTCC
                                     C___
GAM966  SLC16A10  5'  CCCCTGGCGGGCGGGCGGGC   25549        AACAC   A
                                CCCTTGGCG    GTG GGC
                                |||||||||    ||| |||
                                GGGGACCGC    CGC CCG
                                     CCGCC  _
GAM966  LOC114928 3'  TTGGGAACATAAGGC      25550     C    CG
                                TTGG GAACA  TGAGGC
                                |||| |||||  ||||||
                                AACC CTTGT  ATTCCG
                                  _    __
GAM966  LOC122726 3'  CTTGGCAAAATGAGA      25551         CAC
                                CTTGGCGAA   GTGAGG
                                |||||||||   ||||||
                                GAACCGTTT   TACTCT
                                     ___
GAM966  LOC131583 5'  ACTCCTCGGCGAACGTGAGG   25552    C       AC
                                AC CCTTGGCGA  ACGTGAGG
                                || |||||||||  ||||||||
                                TG GGAGCCGCT  TGCACTCC
                                 A        __
GAM966  LOC132617 3'  ACCCCTTGGGGAACAGGGC    25553         C    CGTGA
                                ACCCCTTGG GAACA    GGC
                                ||||||||| |||||    |||
                                TGGGGAACC CTTGT    CCG
                                     C    C_____
GAM966  LOC134637 3'  CTGGTGGAACGGCGAGGCC    25554     C_   AC
                                TTGG  GAAC  GTGAGGCC
                                ||||  ||||  ||||||||
                                GACC  CTTG  CGCTCCGG
                                  AC   C_
GAM966  LOC143153 3'  ACCCCTCGGTGAAGGAGAGG   25555         C   CACGT
                                ACCCCTTGG GAA    GAGG
                                ||||||||| |||    ||||
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                                TGGGGAGCC CTT    CTCC
                                     A  CCT__
GAM966  LOC197342 3'  CCTACACGGGTGCGTGAGGCC  25556    TG  AACA
                                CCT  GCG   CGTGAGGCC
                                |||  |||   |||||||||
                                GGA  TGC   GCACTCCGG
                                  TG  CCAC
GAM966  LOC253822 5'  CTGTGGCGGGAGCGAGGCC   25557   _   AACAC
                                CT TGGCG    GTGAGGCC
                                || |||||    ||||||||
                                GA ACCGC    CGCTCCGG
                                 C    CCT__
GAM966  LOC254173 3'  CCTTGGCGAGGCCCCGGGCC  25558       ACACG  A
                                CCTTGGCGA    TG GGCC
                                |||||||||    || ||||
                                GGAACCGCT    GC CCGG
                                     CCGGG  _
GAM966  LOC254387 3'  CCCCTGGCCCATGTGGGGCC  25559       GAA  C   A
                                CCCTTGGC   CA GTG GGCC
                                ||||||||   || ||| ||||
                                GGGGACCG   GT CAC CCGG
                                     G__  A   C
GAM966  LOC254532 3'  CCCTTGGGGCAGCGTGTGAGGC 25560       CGAACAC_
          C                      CCCTTGG       GTGAGGCC
                                |||||||       ||||||||
                                GGGAACC       CACTCCGG
                                   CCGTCGCA
GAM966  LOC254556 3'  CTTGGCAAATGTGCAGG     25561        CAC   _
                                CTTGGCGAA   GTG AGG
                                |||||||||   ||| |||
                                GAACCGTTT   CAC TCC
                                     A__   G
GAM966  LOC64744  5'  CCCCTTGGCGGGCTTAGGGACA 25562        AACACGTG___
            GGCC                   CCCCTTGGCG         AGGCC
                                |||||||||          |||||
                                GGGGAACCGC         TCCGG
                                     CCGAATCCCTG
GAM966  LOC90371  3'  CCCCCTGGGAGCTGTGGGGC   25563       C  ACAC   A
                                CCCCTTGG GA    GTG GGC
                                |||||||| ||    ||| |||
                                GGGGGACC CT    CAC CCG
                                   _  CGA_   C
GAM966  LOC91064  5'  CCCCTTGGAGAGAAAGAGGGCC 25564       C  ACACGT   _
                                CCCCTTGG GA     GAGG CC
                                |||||||| ||     |||| ||
                                GGGGAACC CT     CTCC GG
                                     T  CTTT__    C
GAM966  LOC92399  3'  CCCTTGGCAACATCAAG     25565        AAC    G
                                CCCTTGGCG   ACGT AGG
                                |||||||||   |||| |||
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                                GGGAACCGT   TGTA TTC
                                   ___    G
GAM967  RAB5A    3'  TTGAATATACATAATTGTTAGT 25568          CG  ACAA
              G                  TTGAATATACA  AT    TGGTG
                                 ||||||||||  ||    |||||
                                 AACTTATATGT  TA    ATCAC
                                       AT  ACA_
GAM967  PCMF     3'  TTGAATGTACACAATGTAACAA 25569       A       ___
                                 TTGAAT TACACGAT   ACAA
                                 ||||||  ||||||||   ||||
                                 AACTTA ATGTGTTA   TGTT
                                    C       CAT
GAM968  RGL      5'  TAGCAGCGCACAGTCTGA    25572        G   A  CC
                                 TAGCAGCG ACA TC  GA
                                 ||||||||  ||| ||  ||
                                 ATCGTCGC TGT AG  CT
                                      G   C  A_
GAM968  ALS2CR8  5'  CAGCAGCATTTTCTCGGTCT  25573        GACAA  C  A
                                 TAGCAGCG    TC CG TCT
                                 ||||||||    || || |||
                                 GTCGTCGT    AG GC AGA
                                      AAA__  A  C
GAM968  FLJ21802 3'  GCAGCGGAGAATCACTA     25574        C    CCGAT
                                 GCAGCGGA AATC    CTA
                                 ||||||||  ||||    |||
                                 CGTCGCCT TTAG    GAT
                                      C    T____
GAM968  SIAT8A   5'  GCAGCGGAGGGTCCCCCAC   25575        CAA    GAT
                                 GCAGCGGA   TCCC   CTAC
                                 ||||||||   ||||   ||||
                                 CGTCGCCT   AGGG   GGTG
                                      CCC    ___
GAM968  LOC152941 3'  AGCAGCAACATTCTTGGTCTA  25576        G   A  CCGA
                                 AGCAGCG ACA TC    TCTA
                                 |||||||  ||| ||    ||||
                                 TCGTCGT TGT AG    AGAT
                                      _   A  AACC
GAM969  COL15A1  3'  AAGAAAACATGAAGGAC     25579       CATT      A
                                 AAGAAA    GCATGAA GAC
                                 ||||||    |||||||  |||
                                 TTCTTT    TGTACTT CTG
                                      ____       C
GAM969  CRI1     3'  TACAGCAAACAAATATGAAAGA 25580      AG     TTGC
                                 TACA  AAACA    ATGAAAGA
                                 ||||  |||||    ||||||||
                                 ATGT  TTTGT    TACTTTCT
                                   CG    TTA_
GAM969  DIAPH2   3'  CACAAGAAACTGGAAG      25581          ATTGCA  A
                                 TACAAGAAAC     TG AAG
                                 ||||||||||     || |||
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                                GTGTTCTTTG     AC TTC
                                       _______ C
GAM969  DLEU1    3'  AGAAACATGCTGGAAAGA    25582        T  AT
                                AGAAACAT GC  GAAAGA
                                |||||||| ||  ||||||
                                TCTTTGTA CG  CTTTCT
                                     _  AC
GAM969  FLG      3'  TACGCAGAATCTTGTGAAAGAC 25583    A_   ACA   CA
                                TAC  AGAA   TTG  TGAAAGAC
                                |||  ||||   |||  ||||||||
                                ATG  TCTT   AAC  ACTTTCTG
                                  CG    AG_  __
GAM969  FMR2     3'  TACAGAAACATCTGAAGA    25584      A      GCA    A
                                TACA GAAACATT   TGAA GA
                                |||| ||||||||   |||| ||
                                ATGT CTTTGTAG   ACTT CT
                                  _       ____   _
GAM969  HEBP1    3'  AAGAATCACAGATGAAAGA    25585      A   TGC
                                AAGAA CAT   ATGAAAGA
                                ||||| |||   ||||||||
                                TTCTT GTG   TACTTTCT
                                   A   TC_
GAM969  IRF6     3'  TACAAGAACAATGCAGAAGGA  25586        A  T    T   A
                                TACAAGAA CA TGCA GAA GA
                                |||||||| || |||| ||| ||
                                ATGTTCTT GT ACGT CTT CT
                                     _  T    _   C
GAM969  PPP1R8   3'  CAGGAGACATTCTGAAAGAC   25587    A  A    GCA
                                CA GA ACATT   TGAAAGAC
                                || || |||||   ||||||||
                                GT CT TGTAA   ACTTTCTG
                                 C  C    G__
GAM969  PPP1R8   3'  CAGGAGACATTCTGAAAGAC   25587    A  A    GCA
                                CA GA ACATT   TGAAAGAC
                                || || |||||   ||||||||
                                GT CT TGTAA   ACTTTCTG
                                 C  C    G__
GAM969  PPP1R8   3'  CAGGAGACATTCTGAAAGAC   25587    A  A    GCA
                                CA GA ACATT   TGAAAGAC
                                || || |||||   ||||||||
                                GT CT TGTAA   ACTTTCTG
                                 C  C    G__
GAM969  TCEA1    3'  TACAAGAAATTACAAGA     25588        AC     T
                                TACAAGAA  ATTGCA GA
                                ||||||||  |||||| ||
                                ATGTTCTT  TAATGT CT
                                     __     T
GAM969  TCERG1   3'  TACAAGAAACACCCAGAAAG   25589           G  T
                                TACAAGAAACATT CA GAAAG
                                |||||||||||| || |||||
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                                ATGTTCTTTGTGG GT CTTTC
                                        _ _
GAM969  AFAP     3' CAAGAAATATTGCACAGAAG  25590       C      GA
                                CAAGAAA ATTGCAT  AAG
                                ||||||| |||||||  |||
                                GTTCTTT TAACGTG  TTC
                                    A      TC
GAM969  C1QTNF7  3' AAGAAACATTTAAAAGA    25591         GCA
                                AAGAAACATT   TGAAAGA
                                |||||||||   |||||||
                                TTCTTTGTAA   ATTTTCT
                                       ___
GAM969  CCRL2    3' TACATGAAATAATGCAGAAAGA 25592     A   CAT   T
                                TACA GAAA   TGCA GAAAGA
                                |||| ||||   |||| ||||||
                                ATGT CTTT   ACGT CTTTCT
                                  A   ATT   _
GAM969  DNAJC5   3' AGAAACACCGCGGAGGAC    25593         AT  AA
                                AGAAACATTGC  GA  GAC
                                ||||||||||  ||  |||
                                TCTTTGTGGCG  CT  CTG
                                     C_  C_
GAM969  EPSIN    5' TACAAGAACATGGGAAGA    25594       AACATT    A_
                                TACAAGA     GCATG  AAGA
                                |||||||     |||||  ||||
                                ATGTTCT     TGTAC  TTCT
                                   _______    CC
GAM969  ERO1L    3' TACAGAGAAAGCATGAAAGA   25595     _    CATT
                                TACA AGAAA    GCATGAAAGA
                                |||| |||||    ||||||||||
                                ATGT TCTTT    CGTACTTTCT
                                  C    ____
GAM969  FLJ10242 3' TACAAGAAATATAGCACA    25596         C  T
                                TACAAGAAA AT GCATG
                                ||||||||| || |||||
                                ATGTTCTTT TA CGTGT
                                     A  T
GAM969  FLJ10583 3' AGAAACACTAATTGTATGAAGG 25597         ____ C    A
          A                      AGAAACAT    TG ATGAA GA
                                |||||||    || ||||| ||
                                TCTTTGTG    AC TACTT CT
                                    ATTA  A    C
GAM969  FLJ12649 3' ACAAGAGCATGAAAG       25598       AACATT
                                ACAAGA     GCATGAAAG
                                ||||||     |||||||||
                                TGTTCT     CGTACTTTC
                                      _______
GAM969  FLJ13841 3' GAAACATTTATAAAAGA     25599         GC
                                GAAACATT  ATGAAAGA
                                ||||||||  ||||||||
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                                CTTTGTAA  TATTTTCT
                                    A_
GAM969  FLJ20725  3'  TACAGGAAACATTCATA     25600      A       G
                                TACA GAAACATT CATG
                                |||| |||||||| ||||
                                ATGT CTTTGTAA GTAT
                                  C       _
GAM969  FLJ22002  3'  AGAGATATTTACATAAAAGAC  25601     AACA_
                                AGA     TTGCATGAAAGAC
                                |||     ||||||||||||||
                                TCT     AATGTATTTTCTG
                                  CTATA
GAM969  GORASP2   3'  TACAAGAAATGTTGCGTG    25602          CA    A
                                TACAAGAAA  TTGC TG
                                |||||||||  |||| ||
                                ATGTTCTTT  AACG AC
                                      AC    C
GAM969  GPR64     3'  CAAGAGAACCTTAGTGAAAGAC 25603       _   ATTGCA
                                CAAGA AAC      TGAAAGAC
                                ||||| |||      ||||||||
                                GTTCT TTG      ACTTTCTG
                                   C   GAATC_
GAM969  KIAA0268  3'  TAAAGAAACATTGTTTTAAAGA 25604    C          CATG
            C                    A AAGAAACATTG    AAAGAC
                                | ||||||||||    ||||||
                                A TTCTTTGTAAC    TTTCTG
                                 T          AAAA
GAM969  KIAA0321  3'  AGAAACATGGCACTTGCGTGAA 25605         _______   A
            AG                     AGAAACAT     TGC TGAAAG
                                ||||||||      ||| ||||||
                                TCTTTGTA      ACG ACTTTC
                                     CCGTGA   C
GAM969  KIAA1040  3'  ACAAGAAACAAGAAAGA      25606          TTGCAT
                                ACAAGAAACA      GAAAGA
                                ||||||||||      ||||||
                                TGTTCTTTGT      CTTTCT
                                      T_____
GAM969  KIAA1143  3'  TACAGGAAACATTGTCAAGTGT 25607      A       _ _____
            GA                     TACA GAAACATTG CA    TGA
                                |||| ||||||||| ||    |||
                                ATGT CTTTGTAAC GT    ACT
                                  C        A  TCAC
GAM969  KIAA1272  3'  ACAAGAAACATTTCTGA      25608          GCA
                                ACAAGAAACATT   TGA
                                ||||||||||||   |||
                                TGTTCTTTGTAA   ACT
                                       AG_
GAM969  KRTAP4-12 3'  TACAAAAATGTTTGCAAAAGAC 25609         ACA     TG
                                TACAAGAA   TTGCA  AAAGAC
                                ||||||||   |||||  ||||||
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                                ATGTTTTT  AACGT  TTTCTG
                                    ACA   __
GAM969  LHX6    3'  TACAAAGCACGACATGAAAG  25610      AAA  T
                                TACAAG  CAT GCATGAAAG
                                ||||||  ||| |||||||||
                                ATGTTT  GTG TGTACTTTC
                                   C__  C
GAM969  MGC14258 3'  TACAAGAATATAAAAGAAAGAC 25611       ACATTGCAT
                                TACAAGAA       GAAAGAC
                                ||||||||       |||||||
                                ATGTTCTT       CTTTCTG
                                    ATATTTT__
GAM969  MGC5528  3'  AGAAACATTTATTGAAAGAC  25612       GCA
                                AGAAACATT  TGAAAGAC
                                |||||||||  ||||||||
                                TCTTTGTAA  ACTTTCTG
                                     ATA
GAM969  NCOA2   3'  GAGACATTGCTATGAAGA   25613   A    _   A
                                GA ACATTGC ATGAA GA
                                || ||||||| ||||| ||
                                CT TGTAACG TACTT CT
                                 C     A   _
GAM969  PLA2G2E  5'  CACAAGGAGCATAAAAG    25614      AAACATT
                                TACAAG     GCATGAAAG
                                ||||||     |||||||||
                                GTGTTC     CGTATTTTC
                                   CT_____
GAM969  VIT1    3'  TACCAGAAACATTGCTG    25615    A       A
                                TAC AGAAACATTGC TG
                                ||| ||||||||||| ||
                                ATG TCTTTGTAACG AC
                                  G        _
GAM969  LOC129526 3'  TACAGAAAACATTTCATTTGAA 25616    AG     G __
          AG                    TACA  AAACATT CA  TGAAAG
                                ||||  ||||||| ||  ||||||
                                ATGT  TTTGTAA GT  ACTTTC
                                  CT     A  AA
GAM969  LOC144455 3'  CAAGGGACACTGAAAGAC   25617    AA   TGCA
                                CAAG  ACAT   TGAAAGAC
                                ||||  ||||   ||||||||
                                GTTC  TGTG   ACTTTCTG
                                  CC   ____
GAM969  LOC151258 5'  TACAGAAACATGCTGTAGA   25618    A     T  A  AA
                                TACA GAAACAT GC TG  AGA
                                |||| ||||||| || ||  |||
                                ATGT CTTTGTA CG AC  TCT
                                  _     _ _  A_
GAM969  LOC200312 3'  ACAAGAAGTATCCTGAAAGAC  25619       ACATTGCA
                                ACAAGAA       TGAAAGAC
                                |||||||       ||||||||
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                                TGTTCTT       ACTTTCTG
                                    CATAGG__
GAM969  LOC202781 3'  CAAGAGACAAATGAAAGAC   25620      A   TTGC
                                CAAGA ACA    ATGAAAGAC
                                ||||| |||    |||||||||
                                GTTCT TGT    TACTTTCTG
                                   C   T___
GAM969  LOC221849 3'  GAAACATCCCAAAAGAC     25621        G  TG
                                GAAACATT CA  AAAGAC
                                |||||||| ||  ||||||
                                CTTTGTAG GT  TTTCTG
                                     G  __
GAM969  LOC51580  5'  TACAACTTTTGCATGAAGGA  25622      GAAACA       A
                                TACAA      TTGCATGAA GA
                                |||||      ||||||||| ||
                                ATGTT      AACGTACTT CT
                                   GAA___        C
GAM969  LOC91796  5'  AGAAACATAACACAAAGAC   25623        T    G
                                AGAAACAT GCAT AAAGAC
                                |||||||| |||| ||||||
                                TCTTTGTA TGTG TTTCTG
                                     T   _
GAM970  CDH1      5'  CGCCGGGTGCGGTCGGG     25626        CTTGTC    C
                                CGCCGGGT     GCGG CGGG
                                ||||||||     |||| ||||
                                GCGGCCCA     CGCC GCCC
                                     _______    A
GAM970  CDH16     3'  GCTGGATCTTGGGTGCTGGGC  25627    C       TCGCG  C
                                GC GGGTCTTG     GC GGGC
                                || |||||||     || ||||
                                CG CCTAGAAC     CG CCCG
                                 A       CCA__  A
GAM970  FASN      3'  CGCTGGGTGTGGCCGGG     25628     C    CTT  CGC
                                CGC GGGT   GT   GGCCGGG
                                ||| ||||   ||   |||||||
                                GCG CCCA   CA   CCGGCCC
                                  A    ___  ___
GAM970  GNAS      5'  CGGCGGGGCGCGGCCGGG    25629    C    TCTT T
                                CG CGGG    G CGCGGCCGGG
                                || ||||    | ||||||||||
                                GC GCCC    C GCGCCGGCCC
                                 C    _____ _
GAM970  GNAS      5'  CGGCGGGGCGCGGCCGGG    25629    C    TCTT T
                                CG CGGG    G CGCGGCCGGG
                                || ||||    | ||||||||||
                                GC GCCC    C GCGCCGGCCC
                                 C    _____ _
GAM970  HMX1      5'  CGCCGGGCTGGGCTGG      25630        CT  TCGC   C
                                CGCCGGGT  TG    GGC GG
                                ||||||||  ||    ||| ||
```

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                                GCGGCCCG  AC    CCG CC
                                   __  _____   A
GAM970  MADH1    5'  CCGGGTCCGGACGGCCGGGC  25631        TGTC
                                CCGGGTCT   GCGGCCGGGC
                                ||||||||   ||||||||||
                                GGCCCAGG   TGCCGGCCCG
                                    CC__
GAM970  MAN1A1   5'  CGCCGGGTCTTCTCCCCGGG  25632          G  GCGG
                                CGCCGGGTCTT TC   CCGGG
                                |||||||||| ||   |||||
                                GCGGCCCAGAA AG   GGCCC
                                      G  G___
GAM970  MARK1    5'  GCCGGGGTCTAGACCGGCCGGG 25633       _  TGTCG
          C                      GCCGGG TCT    CGGCCGGGC
                                |||||| |||    |||||||||
                                CGGCCC AGA    GCCGGCCCG
                                   C   TCTG_
GAM970  MGAT1    5'  CGCCGGGGCCGGACGGCCGGGC 25634        TCTT   __
                                CGCCGGG   GTCG  CGGCCGGGC
                                |||||||   ||||  |||||||||
                                GCGGCCC   CGGC  GCCGGCCCG
                                    _____   CT
GAM970  MMP14    5'  GGGCTCCGCGGCCGGG     25635     T   GT
                                GGG CTT  CGCGGCCGGG
                                ||| |||  ||||||||||
                                CCC GAG  GCGCCGGCCC
                                  _  __
GAM970  NTN2L    5'  GCGGGTCAGCCAGTGGCCGGGC 25636    C    TT   C_
                                GC GGGTC  GTCG  GGCCGGGC
                                || |||||  ||||  ||||||||
                                CG CCCAG  CGGT  CCGGCCCG
                                 _    T_   CA
GAM970  NUP50    5'  CGCTGGGTCTTGGTTGCGGC   25637     C      TC_
                                CGC GGGTCTTG   GCGGC
                                ||| ||||||||   |||||
                                GCG CCCAGAAC   CGCCG
                                  A       CAA
GAM970  PAX2     5'  CGGGGCTCGGGGCTGGGC    25638     T   TCGC   C
                                CGGG CTTG    GGC GGGC
                                |||| ||||    ||| ||||
                                GCCC GAGC    CCG CCCG
                                  C   C___   A
GAM970  PAX2     5'  CGGGGCTCGGGGCTGGGC    25638     T   TCGC   C
                                CGGG CTTG    GGC GGGC
                                |||| ||||    ||| ||||
                                GCCC GAGC    CCG CCCG
                                  C   C___   A
GAM970  PFKFB3   5'  CGCCGGCGCGCGGCCGGG    25639       GTCT  T
                                CGCCGG   TG CGCGGCCGGG
                                ||||||   || ||||||||||
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                                GCGGCC   GC GCGCCGGCCC
                                    ____ _
GAM970  RPIP8    5' CGCTGGATCACGGCTGGG   25640    C   TTGTC   C
                                CGC GGGTC    GCGGC GGG
                                ||| |||||    ||||| |||
                                GCG CCTAG    TGCCG CCC
                                  A   _____   A
GAM970  SLC6A8   5' CGTCGGGGCCCGGCCGGG   25641   C   TCTT  G
                                CG CGGG   GTC CGGCCGGG
                                || ||||   ||| ||||||||
                                GC GCCC   CGG GCCGGCCC
                                 A  ____ _
GAM970  ATP6V1D  5' CGGGTCCCCGGCCGGG     25642       GTCG
                                CGGGTCTT   CGGCCGGG
                                ||||||||   ||||||||
                                GCCCAGGG   GCCGGCCC
                                    ____
GAM970  BAG3     5' CGCCGAGTCTCTGGCCGGG   25643        GTCGC
                                CGCCGGGTCTT    GGCCGGG
                                ||||||||||    |||||||
                                GCGGCTCAGAG    CCGGCCC
                                      A____
GAM970  Cab45    3' CGCGGGGCGCGGCCGG     25644    C  TCTTGT
                                CGC GGG    CGCGGCCGG
                                ||| |||    |||||||||
                                GCG CCC    GCGCCGGCC
                                  C _______
GAM970  Cab45    3' CGCGGGGCGCGGCCGG     25644    C  TCTTGT
                                CGC GGG    CGCGGCCGG
                                ||| |||    |||||||||
                                GCG CCC    GCGCCGGCC
                                  C _______
GAM970  CENTB5   3' CGCAGGGCCGCGGCCGGG   25645    C   CTTGT
                                CGC GGGT   CGCGGCCGGG
                                ||| ||||   ||||||||||
                                GCG CCCG   GCGCCGGCCC
                                  T  ______
GAM970  DKFZP434A236 3' CCTGGGCCTTGCGGTTGGG   25646   _    GTC   CC
                                CC GGGTCTT  GCGG  GGG
                                || |||||||  ||||  |||
                                GG CCCGGAA  CGCC  CCC
                                 A     ___   AA
GAM970  DKFZP434M154 5' CGCCAGGTCCTTGGTGGCCGGG 25647         GTCGC
                                CGCCGGGTCTT    GGCCGGG
                                ||||||||||    |||||||
                                GCGGTCCAGGA    CCGGCCC
                                      ACCA_
GAM970  FLJ10751 3' GCCGGGTCTGGAGGGCTGGGC  25648        TGTCGC  C
                                GCCGGGTCT    GGC GGGC
                                |||||||||    ||| ||||
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                                CGGCCCAGA     CCG CCCG
                                     CCTC__   A
GAM970  FLJ10751  3'  GCCGGGTCTGGAGGGCTGGGC  25648        TGTCGC   C
                                GCCGGGTCT     GGC GGGC
                                |||||||||     ||| ||||
                                CGGCCCAGA     CCG CCCG
                                     CCTC__   A
GAM970  FLJ13081  5'  CGCGGGCCGAGCGCGGCCGGGC 25649     C    TT T
                                CGC GGGTC  G CGCGGCCGGGC
                                ||| |||||  | ||||||||||
                                GCG CCCGG  C GCGCCGGCCCG
                                  _    CT _
GAM970  FLJ20005  5'  GCTGGTGGAGCGGCCGGG    25650    C  GTCT  TC
                                GC GG   TG  GCGGCCGGG
                                || ||   ||  |||||||||
                                CG CC   AC  CGCCGGCCC
                                 A  ____  CT
GAM970  KIAA0350  3'  GCCGGGACAGCTGGCTGGGC   25651      TCTTGTC  _   C
                                GCCGGG      GC GGC GGGC
                                ||||||      || ||| ||||
                                CGGCCC      CG CCG CCCG
                                   TGT____  A   A
GAM970  KIAA1026  5'  GCGCGGGGGGCGCGCGGCCGGG 25652    _   TCT  T
           C                     GC CGGG   TG CGCGGCCGGGC
                                || ||||   || ||||||||||
                                CG GCCC   GC GCGCCGGCCCG
                                 C   CCC  _
GAM970  KIAA1091  5'  CGCCGGGGCCGAGACCGGCCGG 25653      TCTT   ____
           GC                     GCCGGG   GTCG   CGGCCGGGC
                                ||||||   ||||   |||||||||
                                CGGCCC   CGGC   GCCGGCCCG
                                   ____   TCTG
GAM970  MGC10526  5'  CGCGGGCGCGGCCGG      25654     C   TCTTGT
                                CGC GGG     CGCGGCCGG
                                ||| |||     |||||||||
                                GCG CCC     GCGCCGGCC
                                  _  _______
GAM970  MGC14353  5'  CGTCCGGTCGCCGCGGTTGGG  25655    _   GTC       CC
                                CG CCGG   TTGTCGCGG  GGG
                                || ||||   |||||||||  |||
                                GC GGCC   AGCGGCGCC  CCC
                                 A   ___        AA
GAM970  MGC4399   5'  CGCCGGGTCTTGTCTCCCCG   25656           GCGG
                                CGCCGGGTCTTGTC    CCG
                                ||||||||||||||    |||
                                GCGGCCCAGAACAG    GGC
                                        AGG_
GAM970  moblak    3'  CCTGGGAAGCTGCGTGGCCGGG 25657    _   TC_   T  C
           C                     CC GGG   TTG CG GGCCGGGC
                                || |||   ||| || ||||||||
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                                GG CCC   GAC GC CCGGCCCG
                                 A   TTC   _  A
GAM970  NR6A1    5'  CGCCGGGTTTGTTGCTCCG   25658        C    C  GG
                                CGCCGGGT TTGT GC  CCG
                                |||||||| |||| ||  |||
                                GCGGCCCA AACA CG  GGC
                                     _    A  A_
GAM970  NR6A1    5'  CGCCGGGTTTGTTGCTCCG   25658        C    C  GG
                                CGCCGGGT TTGT GC  CCG
                                |||||||| |||| ||  |||
                                GCGGCCCA AACA CG  GGC
                                     _    A  A_
GAM970  NR6A1    5'  CGCCGGGTTTGTTGCTCCG   25658        C    C  GG
                                CGCCGGGT TTGT GC  CCG
                                |||||||| |||| ||  |||
                                GCGGCCCA AACA CG  GGC
                                     _    A  A_
GAM970  PLSCR4   5'  CGCCGGGTCTAGTTGTACTGGC 25659          ___   C  _
                                CGCCGGGTCT   TGT GC GGC
                                ||||||||||   ||| || |||
                                GCGGCCCAGA   ACA TG CCG
                                      TCA   _  A
GAM970  PRAM-1   3'  CGCTGGGTCTTGTGGTGGC   25660     C        CGC
                                CGC GGGTCTTGT   GGC
                                ||| |||||||||   |||
                                GCG CCCAGAACA   CCG
                                  A        CCA
GAM970  RASD2    5'  CGCCGGGCTGGGCGCGGCCGGG 25661         CTT T
          C                      CGCCGGGT   G CGCGGCCGGGC
                                ||||||||   | ||||||||||
                                GCGGCCCG   C GCGCCGGCCCG
                                     ACC _
GAM970  SHANK3   5'  CGCCGGTCCTTGGCCGGG    25662       GT   GTCGC
                                CGCCGG  CTT    GGCCGGG
                                ||||||  |||    |||||||
                                GCGGCC  GAA    CCGGCCC
                                   AG  _____
GAM970  SSB-4    3'  GCCAGGTCTGCGGTTGGG    25663         TGTC   CC
                                GCCGGGTCT   GCGG  GGG
                                |||||||||   ||||  |||
                                CGGTCCAGA   CGCC  CCC
                                      ____    AA
GAM970  ZFP36L2  5'  GGGCGGCGTGGCCGGGC     25664      CTT T  C
                                GGGT   G CG GGCCGGGC
                                ||||   | || ||||||||
                                CCCG   C GC CCGGCCCG
                                  C__ _  A
GAM970  LOC132241 5'  GCTGAGTCTTGGGCTGGG    25665    C       TCGC   C
                                GC GGGTCTTG    GGC GGG
                                || ||||||||    ||| |||
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                                CG CTCAGAAC   CCG CCC
                                 A      ____  A
GAM970  LOC148114 3'  GGGTCTTGGGCTCTGGGC   25666       TCGC  C__
                                GGGTCTTG   GGC  GGGC
                                ||||||||   |||  ||||
                                CCCAGAAC   CCG  CCCG
                                    ____  AGA
GAM970  LOC200261 3'  GCGGGTCTTGGGAGCTGGGC  25667   C      TCGC  C
                                GC GGGTCTTG   GGC GGGC
                                || ||||||||   ||| ||||
                                CG CCCAGAAC   TCG CCCG
                                 _      CC__  A
GAM970  LOC219401 5'  CGCTGGGACCGCGGCTGGGC  25668    C  T TTGT    C
                                CGC GGG C   CGCGGC GGGC
                                ||| ||| |   |||||| ||||
                                GCG CCC G   GCGCCG CCCG
                                  A  T ____    A
GAM970  LOC219908 5'  GCCGGGTCTTTTGCTCGC   25669        __ _
                                GCCGGGTCT  TG TCGC
                                |||||||||  || ||||
                                CGGCCCAGA  AC AGCG
                                     AA  G
GAM970  LOC253256 5'  CGCTGGGGTTGCAGGGCTGGGC 25670    C  TC  T C  C
                                CGC GGG  TTG CG GGC GGGC
                                ||| |||  ||| || ||| ||||
                                GCG CCC  AAC GT CCG CCCG
                                  A  C_  _ C  A
GAM970  LOC254866 5'  GCCGGGTAAGCGGCCGGGC   25671       CTTGTC
                                GCCGGGT    GCGGCCGGGC
                                |||||||    ||||||||||
                                CGGCCCA    CGCCGGCCCG
                                   TT____
GAM970  LOC90485  3'  CCGGGTGTGGTGGCCGGG   25672      CTT  CGC
                                CCGGGT  GT  GGCCGGG
                                ||||||  ||  |||||||
                                GGCCCA  CA  CCGGCCC
                                   ___  CCA
GAM970  LOC91149  5'  GGGCGCAGCGCGGCCGGGC   25673    CTT T
                                GGGT  G CGCGGCCGGGC
                                ||||  | ||||||||||
                                CCCG  C GCGCCGGCCCG
                                  CGT _
GAM971  ACAT1    5'  CAGAGGGCTGAGTATCGG    25676    AGT    TGCT
                                CAGA  CTGAGTA   TCGG
                                ||||  |||||||   ||||
                                GTCT  GACTCAT   AGCC
                                  CCC     ____
GAM971  CELSR3   3'  CAGAAGTTTGGCCTTTGG    25677       C  A  ATG  C
                                CAGAAGT TG GT  CTT GG
                                ||||||| || ||  ||| ||
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                                GTCTTCA AC CG   GAA CC
                                   A  _  ___   A
GAM971  FGR      3'  ACAAGGTCTGAGCACTTTTGGG 25678     AA        GC  C
                                ACAG  GTCTGAGTAT  TT GG
                                ||||  ||||||||||  || ||
                                TGTT  CAGACTCGTG  AA CC
                                  C_        AA  C
GAM971  FXR2     5'  CAGCAGTCTGAGTGCGGG    25679     A       AT  TTC
                                CAG AGTCTGAGT  GC   GG
                                ||| |||||||||  ||   ||
                                GTC TCAGACTCA  CG   CC
                                  G        __ C__
GAM971  KCNA6    3'  ACAGAAGCTGGGCATGATTGGG 25680       T   A    C  C
                                ACAGAAG CTG GTATG TT GG
                                ||||||| ||| ||||| || ||
                                TGTCTTC GAC CGTAC AA CC
                                   _  C    T  C
GAM971  PDE1A    3'  ACAGAAGTCTTTAAGGTGTTTC 25681         GAGTA_  C
           GG                    ACAGAAGTCT     TG TTCGG
                                ||||||||||     || |||||
                                TGTCTTCAGA     AC AAGCC
                                     AATTCC  A
GAM971  PMM2     3'  AAAGTCTGGGTGAAGGCCTGGG 25682        A  AT__   C
                                GAAGTCTG GT    GCTT GG
                                |||||||| ||    |||| ||
                                TTTCAGAC CA    CGGA CC
                                   C  CTTC    C
GAM971  PPP1R12B 3'  AGAAGTCTTACATGTTTGGA   25683       GAG   C  C
                                AGAAGTCT   TATG TT GGA
                                ||||||||   |||| || |||
                                TCTTCAGA   GTAC AA CCT
                                   AT_    _  A
GAM971  PPP1R12B 3'  AGAAGTCTTACATGTTTGGA   25683       GAG   C  C
                                AGAAGTCT   TATG TT GGA
                                ||||||||   |||| || |||
                                TCTTCAGA   GTAC AA CCT
                                   AT_    _  A
GAM971  PPP1R12B 3'  AGAAGTCTTACATGTTTGGA   25683       GAG   C  C
                                AGAAGTCT   TATG TT GGA
                                ||||||||   |||| || |||
                                TCTTCAGA   GTAC AA CCT
                                   AT_    _  A
GAM971  SHANK2   3'  GAAGTCTGAGAAACAAGTTTGG 25684         TAT  TTC___
           A                    GAAGTCTGAG   GC     GGA
                                ||||||||||   ||     |||
                                CTTCAGACTC   TG     CCT
                                     TT_  TTCAAA
GAM971  CHAF1A   3'  AGAACTCTGCACACTTTGG   25685     G   GA      C
                                AGAA TCT  GTATGCTT GG
                                |||| |||  |||||||| ||
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                                TCTT AGA  CGTGTGAA CC
                                  G  __      A
GAM971  FLJ14642  3'  CAGAAGTCTGTGCTGGGTCGG  25686        A  A  CT
                                CAGAAGTCTG GT TG  TCGG
                                |||||||||| || ||  ||||
                                GTCTTCAGAC CG AC  AGCC
                                     A  _  CC
GAM971  GOLGA1   3'  GAAATCTGGGTAGTGCCAGGA  25687       A  _   TC
                                GAAGTCTG GTA TGCT  GGA
                                |||||||| ||| ||||  |||
                                CTTTAGAC CAT ACGG  CCT
                                     C  C   T_
GAM971  IRLB     5'  CAGGGATCTGAATACTTCGG  25688     AA     GT
                                CAG  GTCTGA  ATGCTTCGG
                                |||  ||||||  |||||||||
                                GTC  TAGACT  TATGAAGCC
                                  CC     __
GAM971  KIAA1396  3'  ACAGGAGTTTGAGACCACCCTG 25689     A  C   TA   TC
           G                     ACAG AGT TGAG  TGCT  GG
                                |||| ||| ||||  ||||  ||
                                TGTC TCA ACTC  GTGG  CC
                                  C  A   TG   GA
GAM971  KIAA1655  3'  ACGGAGGCCTGAGTGACCGGA  25690    A  A      ATGCT
                                AC GA GTCTGAGT    TCGGA
                                || || ||||||||    |||||
                                TG CT CGGACTCA    GGCCT
                                 C  C      CT___
GAM971  NLI-IF   3'  CAGAAGTCTGAGGTCATTGCTT 25691          TA___    C
           GGA                   CAGAAGTCTGAG    TGCTT GGA
                                ||||||||||||    ||||| |||
                                GTCTTCAGACTC    ACGAA CCT
                                      CAGTA    _
GAM971  LOC133258 5'  GAAGTCTGAGGACTTGGG    25692         TAT   C
                                GAAGTCTGAG   GCTT GG
                                ||||||||||   |||| ||
                                CTTCAGACTC   TGAA CC
                                      C__   C
GAM971  LOC146667 5'  CAGAAGTCTGCGTTACTGGA  25693        A  A   TC
                                CAGAAGTCTG GT TGCT  GGA
                                |||||||||| || ||||  |||
                                GTCTTCAGAC CA ATGA  CCT
                                     G  _   __
GAM971  LOC150862 5'  AGAGCTCTGAGTAGGCAGTCGG 25694    AG      T  T_
           A                     AGA  TCTGAGTA GC  TCGGA
                                |||  |||||||| ||  |||||
                                TCT  AGACTCAT CG  AGCCT
                                  CG      C  TC
GAM971  LOC253296 5'  GAGGTCTGAGCGCGCGACCGG  25695    A     TA   T_
                                GA GTCTGAG  TGC  TCGG
                                || |||||||  |||  ||||
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                                CT CAGACTC  GCG  GGCC
                                 C      GC   CT
GAM971  LOC257570 5'  GAGGTCTGAGCGCGCGACCGG  25695    A      TA   T_
                                GA GTCTGAG  TGC  TCGG
                                || |||||||  |||  ||||
                                CT CAGACTC  GCG  GGCC
                                 C      GC   CT
GAM972  C8orf17   5'  TTCTACCGCATGGCACT     25698     G      GCC
                                TTC TACCGCAT   GGCGCT
                                ||| ||||||||   ||||||
                                AAG ATGGCGTA   CCGTGA
                                  _      ___
GAM972  LOC199906 3'  TTCATACCGCATGCACT     25699             CGGC
                                TTCGTACCGCATGC    GCT
                                ||||||||||||||    |||
                                AAGTATGGCGTACG    TGA
                                        _____
GAM973  AMT       3'  ATCAGCCTCCACCTTAACTGCC 25702     T       CC____
           CACCCC                   TCA CCTCCACCT     CCCACCCC
                                ||| |||||||||      ||||||||
                                AGT GGAGGTGGA     GGGTGGGG
                                  C        ATTGAC
GAM973  ASTN      3'  ACCATCCTAAGATTTTCCCCTG 25703         CCACC__    CA
           CCC                    ATCATCCT      TCCCC  CCC
                                ||||||||      |||||  |||
                                TGGTAGGA      AGGGG  GGG
                                     TTCTAAA     AC
GAM973  B4GALT2   3'  ATCATCCTCGCCACCCC     25704         CA  T
                                ATCATCCTC  CC CCCC
                                |||||||||  || ||||
                                TAGTAGGAG  GG GGGG
                                     C_  T
GAM973  C1orf6    3'  TCAGGCTGTCTCCCCCATTCC  25705     TC  CCAC      CC
                                TCA  CT    CTCCCCCA  CC
                                |||  ||    ||||||||  ||
                                AGT  GA    GAGGGGGT  GG
                                  CC  CA__       AA
GAM973  CD79B     3'  ACCAGTCTCTGCCTCCCCCATC 25706      TC   CA       _
           CC                     ATCA  CTC  CCTCCCCCA CCC
                                ||||  |||  ||||||||| |||
                                TGGT  GAG  GGAGGGGGT GGG
                                  CA   AC        A
GAM973  CD79B     3'  ACCAGTCTCTGCCTCCCCCATC 25706      TC   CA       _
           CC                     ATCA  CTC  CCTCCCCCA CCC
                                ||||  |||  ||||||||| |||
                                TGGT  GAG  GGAGGGGGT GGG
                                  CA   AC        A
GAM973  CFTR      3'  ATCACCCTAGGTTCTCCCCTGT 25707         CCAC_     CA_
           CCC                    ATCATCCT    CTCCCC   CCC
                                ||||||||    ||||||   |||
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                                TAGTGGGA    GAGGGG  GGG
                                    TCCAA     ACA
GAM973  CHST1    5'  CATCCTCCGCCTCCCGCGCCC  25708        A     CCA
                                CATCCTCC CCTCCC   CCC
                                |||||||| ||||||   |||
                                GTAGGAGG GGAGGG   GGG
                                    C     CGC
GAM973  DBN1     5'  CATCCTTCCACCTCACTCC    25709       _     CC_
                                CATCCT CCACCTC   CC
                                |||||| |||||||   ||
                                GTAGGA GGTGGAG   GG
                                   A      TGA
GAM973  DLEC1    3'  ACCATTTTCCACCTCCAGCTCC 25710      CC       CCCA
                                ATCAT  TCCACCTCC    CC
                                |||||  |||||||||    ||
                                TGGTA  AGGTGGAGG    GG
                                   AA        TCGA
GAM973  DLEC1    3'  ACCATTTTCCACCTCCAGCTCC 25710      CC       CCCA
                                ATCAT  TCCACCTCC    CC
                                |||||  |||||||||    ||
                                TGGTA  AGGTGGAGG    GG
                                   AA        TCGA
GAM973  DNMT2    3'  ACCATCCTCCCCATCCACC    25711         A  TCCC
                                ATCATCCTCC CC    CCACC
                                |||||||||| ||    |||||
                                TGGTAGGAGG GG    GGTGG
                                     _  TA__
GAM973  DYSF     5'  TCATCTTCCACCCCCGCCGCCC 25712      C       C  A
                                TCATC TCCACCTCC CC CCC
                                ||||| ||||||||| || |||
                                AGTAG AGGTGGGGG GG GGG
                                   A        C  C
GAM973  E2F1     3'  TCCCCCACTCACCTCTCCCA   25713       ____    C
                                TCCTCC    ACCTC CCCA
                                ||||||    ||||| ||||
                                AGGGGG    TGGAG GGGT
                                    TGAG    A
GAM973  ELAVL3   3'  TCTTCCCCTCCCACCCC     25714    C  A     CC
                                TC TCC CCTCCC  ACCCC
                                || ||| ||||||  |||||
                                AG AGG GGAGGG  TGGGG
                                 A  _     __
GAM973  EPHA1    3'  ATCATCCTTTTACTTCTACCCC 25715        CC_  C  __
                                ATCATCCT   AC TC  CCCC
                                ||||||||   || ||  ||||
                                TAGTAGGA   TG AG  GGGG
                                     AAA  A  AT
GAM973  GP1BA    3'  ATCACCCTGTGTTCCTTACCCC 25716        CCACC   CCC
                                ATCATCCT    TCC   ACCCC
                                ||||||||    |||   |||||
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                                TAGTGGGA    AGG   TGGGG
                                    CACA_   AA_
GAM973  HR      5'  CCATCTTCCACCCCAAAGCCGT 25717      C      C___  CAC
             TCC                    TCATC TCCACCTC    CC   CC
                                    ||||| ||||||||    ||   ||
                                    GGTAG AGGTGGGG    GG   GG
                                       A       TTTC  CAA
GAM973  IL1F5   3'  TCTCCTCCACTCACCCC     25718    A      C  _
                                    TC TCCTCCAC TC CCCC
                                    || |||||||| || ||||
                                    AG AGGAGGTG AG GGGG
                                     _       _  T
GAM973  JRK     3'  TCACCTCCCAAAGGCCCCACC  25719     T    ACCTC_
                                    TCA CCTCC     CCCCACC
                                    ||| |||||     |||||||
                                    AGT GGAGG     GGGGTGG
                                      _    GTTTCC
GAM973  MAPK8IP1  3'  CCCCACCCTCCCCTACCC    25720       TC   _
                                    CTCCACC  CCCC ACCC
                                    |||||||  |||| ||||
                                    GGGGTGG  GGGG TGGG
                                        GA   A
GAM973  MBL2    3'  TCATCCTCTACCAGTTCCACTC 25721        C   TCCC   _
             C                      TCATCCTC ACC    CCAC CC
                                    |||||||| |||    |||| ||
                                    AGTAGGAG TGG    GGTG GG
                                         A   TCAA    A
GAM973  MPZ     3'  TCATTTGCCCCCTCCCCCACTC 25722     CC_   A       _
             C                      TCAT   TCC CCTCCCCCAC CC
                                    ||||   ||| ||||||||||  ||
                                    AGTA   GGG GGAGGGGGTG GG
                                      AAC   _        A
GAM973  MYBL1   5'  ATCATCCTCGTCCCTTGTCCA  25723        CA_   CCC
                                    ATCATCCTC   CCT   CCA
                                    |||||||||   |||   |||
                                    TAGTAGGAG   GGA   GGT
                                         CAG   ACA
GAM973  NEFH    3'  CATCCAGACCTCCCCTGCCC   25724      TCC      CA
                                    CATCC   ACCTCCCC  CCC
                                    |||||   ||||||||  |||
                                    GTAGG   TGGAGGGG  GGG
                                       TC_       AC
GAM973  PDE7A   3'  TCTTCCCCTCCCACCCC     25714    C   A     CC
                                    TC TCC CCTCCC  ACCCC
                                    || ||| ||||||  |||||
                                    AG AGG GGAGGG  TGGGG
                                     A   _     __
GAM973  PHF1    3'  ATCATCCTCCCTCCTCAGTCTC 25725        A_   _________
             TGCCCC                 TCATCCTCC  CCTC      CCCC
                                    |||||||||  ||||      ||||
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                                AGTAGGAGG  GGAG      GGGG
                                    GA    TCAGAGAC
GAM973  PHF1     3'  ATCATCCTCCCTCCTCAGTCTC 25725        A_   _________
           TGCCCC                  TCATCCTCC  CCTC      CCCC
                                |||||||||  ||||      ||||
                                AGTAGGAGG  GGAG      GGGG
                                    GA    TCAGAGAC
GAM973  PPP1R8   3'  ATCACCCTTCCACCCCATTCC  25726        _     CC_
                                ATCATCCT CCACCTC   CC
                                |||||||| |||||||   ||
                                TAGTGGGA GGTGGGG   GG
                                    A      TAA
GAM973  PPP1R8   3'  ATCACCCTTCCACCCCATTCC  25726        _     CC_
                                ATCATCCT CCACCTC   CC
                                |||||||| |||||||   ||
                                TAGTGGGA GGTGGGG   GG
                                    A      TAA
GAM973  PPP1R8   3'  ATCACCCTTCCACCCCATTCC  25726        _     CC_
                                ATCATCCT CCACCTC   CC
                                |||||||| |||||||   ||
                                TAGTGGGA GGTGGGG   GG
                                    A      TAA
GAM973  PRX      3'  ATCATCCCCACTTCTTGCC   25727       T   C  CC_
                                ATCATCC CCAC TC   CC
                                ||||||| |||| ||   ||
                                TAGTAGG GGTG AG   GG
                                    _   A  AAC
GAM973  PYGO2    3'  CATGCCTGCCTTCCCCACCCC  25728    _  CCA   C
                                CAT CCT   CCT CCCCACCCC
                                ||| |||   ||| |||||||||
                                GTA GGA   GGA GGGGTGGGG
                                  C   C__   A
GAM973  RAB5A    3'  ACCATTAATACTCTTCCCCACC 25729      CCTCC  _  C
           CC                     ATCAT    AC CT CCCCACCCC
                                |||||    || || |||||||||
                                TGGTA    TG GA GGGGTGGGG
                                   ATTA_  A  A
GAM973  RASD1    3'  CATCCCTCCCCCACC      25730      TCCAC
                                CATCC    CTCCCCCACC
                                |||||    ||||||||||
                                GTAGG    GAGGGGGTGG
                                    _____
GAM973  REGL     3'  ATCATCCTTCCATTTCTTGAAT 25731        _  CC  CCCCAC
           CC                     ATCATCCT CCA  TC     CC
                                |||||||| |||  ||     ||
                                TAGTAGGA GGT  AG     GG
                                    A   AA  AACTTA
GAM973  RRM2B    5'  CCCGGCCCCGCCTCCCCCGCC  25732    ATC   A      A
                                TC   CTCC CCTCCCCC CC
                                ||   |||| |||||||| ||
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                                GG  GGGG GGAGGGGG GG
                                 GCC   C      C
GAM973  SCD     3'  ATCCTCCACTCAGGCCCC   25733        C ___
                                ATCCTCCAC TC  CCCC
                                ||||||||| ||  ||||
                                TAGGAGGTG AG  GGGG
                                     _ TCC
GAM973  SDC4    3'  TCATCAGCCCTCCCCCATTCC  25734     CTCCA      CC
                                TCATC   CCTCCCCCA  CC
                                |||||   |||||||||  ||
                                AGTAG   GGAGGGGGT  GG
                                   TCG__      AA
GAM973  SHOC2   5'  CCATCCTCCTCGCTCGCCC   25735       AC_  C
                                TCATCCTCC  CTC CCC
                                |||||||||  ||| |||
                                GGTAGGAGG  GAG GGG
                                     AGC  C
GAM973  TCAP    3'  ACCATCCTTGCCTCTGCCC   25736      CCA   C_
                                ATCATCCT  CCTC  CCC
                                ||||||||  ||||  |||
                                TGGTAGGA  GGAG  GGG
                                    AC_   AC
GAM973  TCL1A   3'  TCATCCTCTGTCTGTCCATTCC 25737      CAC  CCC   CC
                                TCATCCTC  CT  CCA CC
                                ||||||||  ||  ||| ||
                                AGTAGGAG  GA  GGT  GG
                                    ACA  CA_  AA
GAM973  TGFB3   3'  ACCATCCCTTTCCTCTATCCC  25738      CCA   C__
                                ATCATCCT  CCTC  CCC
                                ||||||||  ||||  |||
                                TGGTAGGG  GGAG  GGG
                                    AAA   ATA
GAM973  TIMP3   3'  TCACATCCACCTCCCCTAC   25739    CC       C
                                TCAT  TCCACCTCCCC AC
                                ||||  |||||||||| ||
                                AGTG  AGGTGGAGGGG TG
                                  T_       A
GAM973  TLL2    3'  ATCATCCTCTACACTTCTC   25740       __  __
                                ATCATCCTC  CAC  CTC
                                |||||||||  |||  |||
                                TAGTAGGAG  GTG  GAG
                                    AT   AA
GAM973  TNFRSF6B 5'  CATGCCACCTCCTTTGCCCC  25741    CCT     CCCA
                                CAT   CCACCTCC   CCCC
                                |||   ||||||||   ||||
                                GTA   GGTGGAGG   GGGG
                                  C__      AAAC
GAM973  VANGL2  3'  ATCCTTTCCCTCTCCCCCACCC 25742     __  AC
            C                    ATCC  TCC  CTCCCCCACCCC
                                ||||  |||  ||||||||||||
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                                TAGG  AGG  GAGGGGGTGGGG
                                  AA   GA
GAM973  XRCC5    3'  CTCCCCTTCCCACCCC      25743      A   CC
                                CTCC CCT  CCCACCCC
                                |||| |||  ||||||||
                                GAGG GGA  GGGTGGGG
                                  _   A_
GAM973  ADAM9    5'  TCGCCTCCACCTCCGCC     25744    AT        C
                                TC  CCTCCACCTCC CC
                                ||  ||||||||||| ||
                                AG  GGAGGTGGAGG GG
                                 C_          C
GAM973  AMOT     3'  CACCCCCCACTTCCCTCACCC  25745          C    C
                                CATCCTCCAC TCCC CACCC
                                |||||||||| |||| |||||
                                GTGGGGGGTG AGGG GTGGG
                                      A    A
GAM973  APCL     3'  CCTCTGCCCCTCCCACCCC    25746      CA    C
                                CCTC  CCTC CCCACCCC
                                ||||  |||| ||||||||
                                GGAG  GGGG GGGTGGGG
                                  AC    A
GAM973  AQP10    3'  ATCCTCCTCCACTTCTCC     25747     A       __
                                ATC TCCTCCAC  CTCC
                                ||| ||||||||  ||||
                                TAG AGGAGGTG  GAGG
                                  G       AA
GAM973  ARHGEF2  3'  TCATTCTCTCCCCCACCCC    25748      C   CACC
                                TCAT CTC    TCCCCCACCCC
                                |||| |||    ||||||||||
                                AGTA GAG    AGGGGGTGGGG
                                  A   _____
GAM973  ATP6V0A1 3'  ATCATCTTCCTGGACCCACCCC 25749       C   ACCTCC
                                ATCATC TCC      CCCACCCC
                                |||||| |||     ||||||||
                                TAGTAG AGG      GGGTGGGG
                                   A   ACCT__
GAM973  C20orf124 3'  TCCTCCTCCCCACCTCATCCC  25750       A    _  C  _
                                TCCTCC CCTC CC CA CCC
                                |||||| |||| || || |||
                                AGGAGG GGGG GG GT GGG
                                   A    T  A  A
GAM973  C20orf150 3'  TCATCCTCCAGTCTGTCCC    25751          C_  CC
                                TCATCCTCCA  CT  CCC
                                ||||||||||  ||  |||
                                AGTAGGAGGT  GA  GGG
                                      CA  CA
GAM973  C20orf164 3'  ATCATCCTCATTCCCTTTGTCC 25752          CACC    CCA__
            C                   ATCATCCTC    TCCC    CCC
                                |||||||||    ||||    |||
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                                TAGTAGGAG   AGGG    GGG
                                    TA__   AAACA
GAM973  C22orf19  3'  TCCCCCTCCACCTCCCCCAC  25753   AT
                                TC  CCTCCACCTCCCCCAC
                                ||  ||||||||||||||||
                                AG  GGAGGTGGAGGGGGTG
                                 GG
GAM973  CAMKK2   3'  ATCAATGTGGGTCTCCCCCACC 25754     TCCTCCAC
          CC                     ATCA      CTCCCCCACCCC
                                ||||       ||||||||||||
                                TAGT       GAGGGGGTGGGG
                                  TACACCCA
GAM973  CHDH     3'  ACCATCCTCCCCTTCTGTCCC  25755        A  _ C__
                                ATCATCCTCC CCT C   CCC
                                |||||||||| ||| |   |||
                                TGGTAGGAGG GGA G   GGG
                                     _  A ACA
GAM973  DF       3'  TCATCCTCCCACCTCAGCC   25756        _    CC
                                TCATCCTCC ACCTC  CC
                                |||||||||  |||||  ||
                                AGTAGGAGG TGGAG  GG
                                     G    TC
GAM973  DF       3'  TCATCCTCCCACCTCAGCC   25756        _    CC
                                TCATCCTCC ACCTC  CC
                                |||||||||  |||||  ||
                                AGTAGGAGG TGGAG  GG
                                     G    TC
GAM973  DKFZP564J0863 3'  ATCCTCCATCCCCTCCCC    25757       CC    CA
                                ATCCTCCA  TCCCC  CCC
                                ||||||||  |||||  |||
                                TAGGAGGT  AGGGG  GGG
                                     __    AG
GAM973  DKFZp761O17121 3'  CATCTCCCTTCCCCCAC    25758     C   ACC
                                CATC TCC   TCCCCCAC
                                |||| |||   ||||||||
                                GTAG AGG   AGGGGGTG
                                  _  GA_
GAM973  DNAL4    3'  TCATCTCCCACCTCCTCTACCC 25759      CT      CCC
                                TCATC  CCACCTCC   ACCC
                                |||||  ||||||||   ||||
                                AGTAG  GGTGGAGG   TGGG
                                   AG       AGA
GAM973  EVI5     3'  ATCCTCCCTGCCCCCACC    25760       ACCT
                                ATCCTCC    CCCCCACC
                                |||||||    ||||||||
                                TAGGAGG    GGGGGTGG
                                    GAC_
GAM973  FABP7    3'  ACCATTTTCCACCTCCACACC  25761      CC       CC
                                ATCAT  TCCACCTCC  CACC
                                |||||  |||||||||  ||||
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                                TGGTA  AGGTGGAGG  GTGG
                                  AA       T_
GAM973  FKBP8    5'  TCATCCTCTTCCTCCTCTTCC  25762       CA    CCCA
                                TCATCCTC  CCTCC    CC
                                ||||||||  |||||    ||
                                AGTAGGAG  GGAGG    GG
                                    AA    AGAA
GAM973  FLJ10276 3'  TCTCTCCATCCCACCCC     25763    _    CCTCC
                                TC CTCCA    CCCACCCC
                                || |||||    ||||||||
                                AG GAGGT    GGGTGGGG
                                 A    A____
GAM973  FLJ11101 3'  TCATCCTCCACCACCACCCC  25764          TCCC
                                TCATCCTCCACC   CCACCCC
                                ||||||||||||   |||||||
                                AGTAGGAGGTGG   GGTGGGG
                                       T___
GAM973  FLJ11274 3'  TCCTCCCACCTCTCCTGCTCC  25765       _    _  CCAC
                                TCCTCC ACCTC CC    CC
                                ||||||  ||||| ||    ||
                                AGGAGG TGGAG GG    GG
                                   G    A  ACGA
GAM973  FLJ12089 3'  ATCAGCCTTCCCACCCACCCC  25766     T   __    TC
                                ATCA CCT  CCACC  CCCC
                                ||||  |||  |||||  ||||
                                TAGT GGA  GGTGG  GGGG
                                  C   AG    GT
GAM973  FLJ12409 3'  CCATCCTCCCACCTCTGCCC   25767         _    C_
                                TCATCCTCC ACCTC  CCC
                                |||||||||  |||||  |||
                                GGTAGGAGG TGGAG  GGG
                                     G    AC
GAM973  FLJ12572 3'  ATCACCTCTCCAAGACCCCACC 25768       _    CCTC
            CC                    ATCATC CTCCA    CCCCACCCC
                                ||||||  |||||    |||||||||
                                TAGTGG GAGGT    GGGGTGGGG
                                   A    TCT_
GAM973  FLJ14525 3'  ATCCTCCTCCACCACACCAC   25769     A       TCCC
                                ATC TCCTCCACC    CCAC
                                |||  |||||||||    ||||
                                TAG AGGAGGTGG    GGTG
                                  G        TGT_
GAM973  FLJ14936 3'  ACCATCCTCTAATTCTCTGCCC 25770         CAC__   __
            C                    ATCATCCTC    CTC  CCCC
                                |||||||||    |||  ||||
                                TGGTAGGAG    GAG  GGGG
                                     ATTAA   AC
GAM973  FLJ20311 3'  ATCTCCTCCATAACCCCCACC  25771     A      CCT
                                ATC TCCTCCA   CCCCCACC
                                |||  |||||||   ||||||||
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                                TAG AGGAGGT   GGGGGTGG
                                  _      ATT
GAM973   FLJ20446  3'  ATCATTTCCACCTCCCCACATC 25772       CC         _ _
              CC                    ATCAT  TCCACCTCCCC CA CCC
                                    |||||  |||||||||||| || |||
                                    TAGTA  AGGTGGAGGGG GT GGG
                                      A_         T  A
GAM973   FLJ20546  3'  CCATCCCTTCCTTCCCTGTTCC 25773        CCA  _  CCAC
                                    TCATCCT   CCT CCC    CC
                                    |||||||   ||| |||    ||
                                    GGTAGGG   GGA GGG    GG
                                       AA_   A   ACAA
GAM973   FLJ20871  3'  TCTCCTTTGGCCAACCCACCCC 25774    A    CCAC  CC
                                    TC TCCT    CT  CCCACCCC
                                    || ||||    ||  ||||||||
                                    AG AGGA    GG  GGGTGGGG
                                     _    AACC  TT
GAM973   FLJ22688  3'  TCTCCTCCCCTCCCACCC    25775    A     A     CC
                                    TC TCCTCC CCTCCC  ACCC
                                    || |||||| ||||||  ||||
                                    AG AGGAGG GGAGGG  TGGG
                                     _     _     __
GAM973   FLJ23120  3'  ACCATTCTCCTGAACCCCCACC 25776       C    ACCT
              CC                    ATCAT CTCC    CCCCCACCCC
                                    ||||| ||||    ||||||||||
                                    TGGTA GAGG    GGGGGTGGGG
                                      A    ACTT
GAM973   GTPBP5    3'  CATCCTCGGCCCCACCC     25777        CACCTC
                                    CATCCTC     CCCCACCC
                                    |||||||     ||||||||
                                    GTAGGAG     GGGGTGGG
                                       CC_____
GAM973   HEYL      3'  ATCATCCTTTCTCTTGCCCC   25778        CCAC  ___
                                    ATCATCCT    CTC   CCCC
                                    ||||||||    |||   ||||
                                    TAGTAGGA    GAG   GGGG
                                       AA__    AAC
GAM973   HPIP      3'  CCTTCCCCAGACCCCACCCC   25779     _  A  TC_
                                    CCT CC CC   CCCCACCCC
                                    ||| || ||   |||||||||
                                    GGA GG GG   GGGGTGGGG
                                      A  _  TCT
GAM973   HSA243396 5'  TCGCCTCCCCGCCCACCC    25780    AT    A  TCC
                                    TC  CCTCC CC   CCCACCC
                                    ||  ||||| ||   |||||||
                                    AG  GGAGG GG   GGGTGGG
                                     C_     _  C__
GAM973   HTEX4     5'  ATCATCCTTCACTCTAAATCC  25781        C  _  CCC_
                                    ATCATCCT CAC CT    CC
                                    |||||||| ||| ||    ||
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                                TAGTAGGA GTG GA    GG
                                    A   A  TTTA
GAM973  HTEX4     5'  ATCATCCTTCACTCTAAATCC  25781        C   _  CCC_
                                ATCATCCT CAC CT    CC
                                |||||||| ||| ||    ||
                                TAGTAGGA GTG GA    GG
                                    A   A  TTTA
GAM973  HTEX4     5'  ATCATCCTTCACTCTAAATCC  25781        C   _  CCC_
                                ATCATCCT CAC CT    CC
                                |||||||| ||| ||    ||
                                TAGTAGGA GTG GA    GG
                                    A   A  TTTA
GAM973  IMAGE:4907098 3'  CATTTTCCACACCCCCCACCCC 25782     CC     C
                                CAT  TCCAC TCCCCCACCCC
                                |||  ||||| ||||||||||
                                GTA  AGGTG GGGGGGTGGGG
                                  AA     T
GAM973  KIAA0040  5'  CCTCTGCACTCCCACCCC    25783      __   CTCC
                                CCTC  CAC    CCCACCCC
                                ||||  |||    ||||||||
                                GGAG  GTG    GGGTGGGG
                                  AC   A___
GAM973  KIAA0237  3'  TCCTTCCTTCCCCACCCC    25784      CCA   C
                                TCCT   CCT CCCCACCCC
                                ||||   ||| |||||||||
                                AGGA   GGA GGGGTGGGG
                                  A__   A
GAM973  KIAA0275  3'  CATCCTTAACAACCCCCACCCC 25785       CC  CT
                                CATCCT  AC  CCCCCACCCC
                                ||||||  ||  ||||||||||
                                GTAGGA  TG  GGGGGTGGGG
                                   AT  TT
GAM973  KIAA0599  3'  CATCCTCCTGCCCCACC     25786        ACCTC
                                CATCCTCC     CCCCACC
                                ||||||||     |||||||
                                GTAGGAGG     GGGGTGG
                                    AC___
GAM973  KIAA1181  3'  CCATCCTCTACTTTCCCCCCAC 25787        C  C__
                                TCATCCTC AC   TCCCCCAC
                                |||||||| ||   ||||||||
                                GGTAGGAG TG   GGGGGGTG
                                    A  AAA
GAM973  KIAA1254  3'  ATCCTCCAGCTCTACCC     25788        C   CCCC
                                ATCCTCCA CTC    ACCC
                                |||||||| |||    ||||
                                TAGGAGGT GAG    TGGG
                                    C   A___
GAM973  KIAA1613  3'  ATCATGCTCCACCTTTGCCC   25789      C       CC_
                                ATCAT CTCCACCT   CCC
                                ||||| ||||||||   |||
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                                TAGTA GAGGTGGA   GGG
                                  C       AAC
GAM973  KIAA1649 3' ATCACCCTTCATCTCTTAATGC 25790        C  C  _______
           CCC                    ATCATCCT CA CTC     CCCC
                                  |||||||| || |||      ||||
                                  TAGTGGGA GT GAG     GGGG
                                     A  A   AATTAC
GAM973  KIAA1649 3' ATCACCCTTCATCTCTTAATGC 25790        C  C  _______
           CCC                    ATCATCCT CA CTC     CCCC
                                  |||||||| || |||      ||||
                                  TAGTGGGA GT GAG     GGGG
                                     A  A   AATTAC
GAM973  KIAA1719 3' ATCATCCCCATGGCACCTACCC 25791         _____    C
           C                      ATCATCCTC    CACCT CCCC
                                  |||||||||    ||||| ||||
                                  TAGTAGGGG    GTGGA GGGG
                                       TACC     T
GAM973  KIAA1784 3' ATCTTCCTCCACACTGCTCC   25792     A      _____
                                  ATC TCCTCCAC    CTCC
                                  ||| ||||||||    ||||
                                  TAG AGGAGGTG    GAGG
                                    A       TGAC
GAM973  KIAA1938 3' CATCCATCCTACCTCCCCTATC 25793      _  _       CA_
           CC                     CATCC TCC ACCTCCCC   CCC
                                  ||||| ||| ||||||||   |||
                                  GTAGG AGG TGGAGGGG   GGG
                                     T   A       ATA
GAM973  MGC17299 5' TCACCCTCACCTCTCTGCC   25794        C    CC__
                                  TCATCCTC ACCTC    CC
                                  |||||||| |||||    ||
                                  AGTGGGAG TGGAG    GG
                                       _    AGAC
GAM973  MGC17998 3' ATCATCCCTCCGCCTTTCATTG 25795        _  A   CCC____
           CCA                    ATCATCC TCC CCT      CCA
                                  ||||||| ||| |||      |||
                                  TAGTAGG AGG GGA      GGT
                                     G   C   AAGTAAC
GAM973  MGC5356  5' ATCCTCCTCATCTCCACCC   25796       ACC  CC
                                  ATCCTCC   TC  CCACCC
                                  |||||||   ||  ||||||
                                  TAGGAGG   AG  GGTGGG
                                     AGT  A_
GAM973  MGC5508  3' ATCCTCAGGTCCCCTTACCCC  25797      CACC    C_
                                  ATCCTC    TCCCC  ACCCC
                                  ||||||    |||||  |||||
                                  TAGGAG    AGGGG  TGGGG
                                     TCC_     AA
GAM973  OBSCN    3' TCTCCTCCACCTCCACCC    25798    A        _
                                  TC TCCTCCACCTCC CCC
                                  || ||||||||||| |||
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                                AG AGGAGGTGGAGG GGG
                                 _         T
GAM973  PHYHIP   3' TCATCTCTCCCTCGCCCC    25799      C  CA   _
                                TCATC TC  CCTC CCCC
                                ||||| ||  |||| ||||
                                AGTAG AG  GGAG GGGG
                                  _ AG   C
GAM973  PKNOX2   3' ACCATCCTTTTGCTCTACCCC  25800        CCAC  __
                                ATCATCCT   CTC  CCCC
                                ||||||||   |||  ||||
                                TGGTAGGA   GAG  GGGG
                                    AAAC   AT
GAM973  PLUNC    5' TCTCCTCTCTCTCCCCCACTCC 25801    A    CAC       _
                                TC TCCTC   CTCCCCCAC CC
                                || |||||   ||||||||| ||
                                AG AGGAG   GAGGGGGTG GG
                                 _    AGA        A
GAM973  PLUNC    5' TCTCCTCTCTCTCCCCCACTCC 25801    A    CAC       _
                                TC TCCTC   CTCCCCCAC CC
                                || |||||   ||||||||| ||
                                AG AGGAG   GAGGGGGTG GG
                                 _    AGA        A
GAM973  PRO1584  5' TCCTCTCCACCCCACCCC    25802      CA  TC
                                TCCTC  CC  CCCCACCCC
                                |||||  ||  |||||||||
                                AGGAG  GG  GGGGTGGGG
                                  A_  T_
GAM973  PTPN4    5' TCACCCCCCTCCTTCTCCACC  25803        A   CCC
                                TCATCCTCC CCT   CCACC
                                ||||||||| |||   |||||
                                AGTGGGGGG GGA   GGTGG
                                    A   AGA
GAM973  RAB40A   5' ATCATCCTTACCGAGCTGTCCC 25804        CC  _______
                                ATCATCCT  ACC     TCCC
                                ||||||||  |||     ||||
                                TAGTAGGA  TGG     AGGG
                                    A_   CTCGAC
GAM973  RASSF2   5' ATCACTCTCCACCCCTTCGCC  25805     TC       CC__
                                ATCA  CTCCACCTC    CC
                                ||||  |||||||||    ||
                                TAGT  GAGGTGGGG    GG
                                  GA        AAGC
GAM973  RINZF    5' TCGTCCTCCACCCCCGCCC    25806    A         _
                                TC TCCTCCACCTCC CCC
                                || ||||||||||||| |||
                                AG AGGAGGTGGGGG GGG
                                 C          C
GAM973  RODH-4   3' CATCCTCCAGGCCATTTCCACC 25807          __  TCCC
            CC                    CATCCTCCA  CC    CCACCCC
                                ||||||||  ||   |||||||
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                                GTAGGAGGT GG   GGTGGGG
                                     CC TAAA
GAM973 SDCCAG33 5' CATCCTCCTTCCCCTCCA   25808       AC   C
                                CATCCTCC CTCC CCA
                                |||||||| |||| |||
                                GTAGGAGG GGGG GGT
                                     AA   A
GAM973 SDOS    3' CATCCTCCACCCACACATCCC 25809         CCCC _
                                CATCCTCCACCT   CA CCC
                                |||||||||||   || |||
                                GTAGGAGGTGGG   GT GGG
                                      TGT_ A
GAM973 SEC15B  3' ATCACCTCCCAAGGCCTCACC 25810     T   ACCTC C
                                ATCA CCTCC    CC CACC
                                |||| |||||    || ||||
                                TAGT GGAGG    GG GTGG
                                  _   GTTCC A
GAM973 SFXN5   3' CCTCAGCACACTTCCCCTACCC 25811    ____ C   C
                                CCTC   CAC TCCCC ACCC
                                ||||   ||| ||||| ||||
                                GGAG   GTG AGGGG TGGG
                                  TCGT  A    A
GAM973 SMARCA4 5' TCCCGGCGCCTCCCCCGCCCC 25812    CCA_     A
                                TCCT   CCTCCCCC CCCC
                                ||||   |||||||| ||||
                                AGGG   GGAGGGGG GGGG
                                  CCGC      C
GAM973 SMARCF1 5' CTCCCCCCCTCCCACCCC   25813    A   _
                                CTCC CCTCC CCCACCCC
                                |||| ||||| ||||||||
                                GAGG GGGGG GGGTGGGG
                                  _   A
GAM973 SMARCF1 3' TCTTCTTCTTCTTCCCCACCC 25814   A C CAC C
                                TC TC TC  CT CCCCACCC
                                || || ||  || ||||||||
                                AG AG AG  GA GGGGTGGG
                                 A A AA_ A
GAM973 SMARCF1 5' CTCCCCCCCTCCCACCCC   25813    A   _
                                CTCC CCTCC CCCACCCC
                                |||| ||||| ||||||||
                                GAGG GGGGG GGGTGGGG
                                  _   A
GAM973 SMARCF1 5' CTCCCCCCCTCCCACCCC   25813    A   _
                                CTCC CCTCC CCCACCCC
                                |||| ||||| ||||||||
                                GAGG GGGGG GGGTGGGG
                                  _   A
GAM973 UNC5D   3' TCCCCACCTCCCCCCATTCC   25815    T       CC
                                TCC CCACCTCCCCCA CC
                                ||| |||||||||||  ||
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                                AGG GGTGGAGGGGGT  GG
                                  _          AA
GAM973  VEST1    5'  ATCTCTCTCCTCCCCCACCCC  25816     _  CA
                                ATC CTC  CCTCCCCCCACCCC
                                ||| |||  ||||||||||||||
                                TAG GAG  GGAGGGGGTGGGG
                                  A  A_
GAM973  WIRE     3'  ACCATTCTCCACCCTGCCC    25817      C       CC
                                ATCAT CTCCACCT  CCC
                                ||||| ||||||||  |||
                                TGGTA GAGGTGGG  GGG
                                   A       AC
GAM973  ZNF212   5'  ATCCTCCAGATTCTCCCATTCC 25818        C___    CCA
                                ATCCTCCA   CTCCC   CC
                                ||||||||   |||||  ||
                                TAGGAGGT   GAGGG   GG
                                     CTAA    TAA
GAM973  LOC115110 3'  CCATCCTCAATGGGCCTCCACC 25819        CACCTC  _
          CC                      TCATCCTC     CC CCACCCC
                                ||||||||     || |||||||
                                GGTAGGAG     GG GGTGGGG
                                     TTACCC  A
GAM973  LOC126755 3'  ATCACCTCCCAAAAGCCCCACC 25820      T    ACCTC_
                                ATCA CCTCC     CCCCACC
                                |||| |||||     |||||||
                                TAGT GGAGG     GGGGTGG
                                  _    GTTTTC
GAM973  LOC126917 3'  CATCTTATATTCTCCCCCACCC 25821      CTCCAC_
          C                      CATC      CTCCCCCACCCC
                                ||||      ||||||||||||
                                GTAG      GAGGGGGTGGGG
                                  AATATAA
GAM973  LOC127703 3'  ATCATCTTCATCACTACTCC   25822       C  __  __
                                ATCATC TC  CAC  CTCC
                                |||||| ||  |||  ||||
                                TAGTAG AG  GTG  GAGG
                                   A  TA   AT
GAM973  LOC130074 3'  TCATCCTCTGTCTCCCCTTCC  25823        CAC     CA
                                TCATCCTC   CTCCCC  CC
                                ||||||||   ||||||  ||
                                AGTAGGAG   GAGGGG  GG
                                     ACA     AA
GAM973  LOC135932 3'  ATCACCTCCCTACCTCATCC   25824      T    __    CC
                                ATCA CCTCC  ACCTC  CC
                                |||| |||||  |||||  ||
                                TAGT GGAGG  TGGAG  GG
                                  _    GA     TA
GAM973  LOC139770 3'  TCATCCTCCATCTTTCATCC   25825         C  CCCC  C
                                TCATCCTCCA CT    CA CC
                                |||||||||| ||    || ||
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                                AGTAGGAGGT GA    GT GG
                                      A  AA__  A
GAM973   LOC143785 3'  ATCTTCTGTCCCCCACCC    25826     C  CACC
                                ATC TC    TCCCCCACCC
                                ||| ||    ||||||||||
                                TAG AG    AGGGGGTGGG
                                  A  AC__
GAM973   LOC144289 5'  TCATCCCCATTCCCCCACTCC  25827       T   CC       _
                                TCATCC CCA  TCCCCCAC CC
                                |||||| |||  |||||||| ||
                                AGTAGG GGT  AGGGGGTG GG
                                   _  A_       A
GAM973   LOC145333 5'  ACCATCCTCTGTCTCTCTCCCT 25828         CAC__  _  C
            AC                    ATCATCCTC    CTC CCC AC
                                |||||||||    ||| ||| ||
                                TGGTAGGAG    GAG GGG TG
                                      ACAGA   A   A
GAM973   LOC145368 5'  TCATCCTCGCTTCCTTCACC   25829       CACC   CC
                                TCATCCTC    TCC  CACC
                                ||||||||    |||  ||||
                                AGTAGGAG    AGG  GTGG
                                     CGA_   AA
GAM973   LOC147137 3'  TCCTCTGACCTCCCCATTCC   25830      C_      CAC
                                TCCTC  ACCTCCCC   CC
                                |||||  ||||||||   ||
                                AGGAG  TGGAGGGG   GG
                                   AC       TAA
GAM973   LOC147343 5'  TCATCCCCTCCTCCACC     25831       TCCA    C
                                TCATCC    CCTCC CCACC
                                ||||||    ||||| |||||
                                AGTAGG    GGAGG GGTGG
                                     ____     A
GAM973   LOC147650 5'  ATCCTCCTGACTCTCCATCC   25832       AC_  CC   C
                                ATCCTCC   CTC  CCA CC
                                |||||||   |||  ||| ||
                                TAGGAGG   GAG  GGT GG
                                     ACT   A_   A
GAM973   LOC148710 3'  TCCCCTCCACCTTCCCCAC    25833    A        C
                                TC TCCTCCACCT CCCCAC
                                || ||||||||| ||||||
                                AG GGGAGGTGGA GGGGTG
                                  _        A
GAM973   LOC149910 5'  TCATCCTCTTCCTTCACC     25834       CACC   CC
                                TCATCCTC    TCC  CACC
                                ||||||||    |||  ||||
                                AGTAGGAG    AGG  GTGG
                                     A___   AA
GAM973   LOC150423 5'  TCATCCTCGCTTCCTTCACC   25829       CACC   CC
                                TCATCCTC    TCC  CACC
                                ||||||||    |||  ||||
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                                AGTAGGAG   AGG  GTGG
                                    CGA_   AA
GAM973   LOC150596 3'  TCATCCCCTCCTTCACC     25835       TCCA    CC
                                TCATCC   CCTCC  CACC
                                ||||||   |||||  ||||
                                AGTAGG   GGAGG  GTGG
                                   ____    AA
GAM973   LOC150759 3'  ATCATTCCTCCCTCTACCCC   25836      _    AC  C
                                ATCAT CCTCC  CT CCCC
                                ||||| |||||  || ||||
                                TAGTA GGAGG  GA GGGG
                                   A    GA  T
GAM973   LOC150889 3'  ATCACCCCAGTTTCCCACCC   25837        CCACCTCC
                                ATCATCCT       CCCACCC
                                ||||||||       |||||||
                                TAGTGGGG       GGGTGGG
                                    TCAAA___
GAM973   LOC151057 3'  ACCATCCTTTCCCCACCC     25838        CCACCTC
                                ATCATCCT      CCCCACCC
                                ||||||||      ||||||||
                                TGGTAGGA      GGGGTGGG
                                    AA_____
GAM973   LOC151178 5'  ATCATCCTTACAGCTCCTGTCC 25839        C_  C    C__
                                ATCATCCT  CA CTCC   CC
                                ||||||||  || ||||   ||
                                TAGTAGGA  GT GAGG   GG
                                    AT  C    ACA
GAM973   LOC151323 3'  ATCATTCCTCCCTCTACCCC   25836      _    AC  C
                                ATCAT CCTCC  CT CCCC
                                ||||| |||||  || ||||
                                TAGTA GGAGG  GA GGGG
                                   A    GA  T
GAM973   LOC152179 5'  ATCCTCCACCTCCTCCCCCACT 25840          ___      _
            CC                    ATCCTCCACC   TCCCCCAC CC
                                ||||||||||   |||||||| ||
                                TAGGAGGTGG   AGGGGGTG GG
                                     AGG       A
GAM973   LOC152215 3'  CATCCTACCTTCCCACCC    25841       CC    CC
                                CATCCT  ACCT  CCCACCC
                                ||||||  ||||  |||||||
                                GTAGGA  TGGA  GGGTGGG
                                   __    A_
GAM973   LOC152283 5'  ATCCTCCTCTGCCTCCCC    25842     A     CA
                                ATC TCCTC  CCTCCCC
                                ||| |||||  |||||||
                                TAG AGGAG  GGAGGGG
                                  G    AC
GAM973   LOC154849 3'  TCATCTTCCACCTCCTGCA    25843      C        CC
                                TCATC TCCACCTCC  CA
                                ||||| |||||||||  ||
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                                AGTAG AGGTGGAGG  GT
                                  A       AC
GAM973  LOC169436 5'  TCCTCCACCACCAGGTTCACCC 25844        T  CC___
          C                    TCCTCCACC CC    CACCCC
                               ||||||||| ||    ||||||
                               AGGAGGTGG GG    GTGGGG
                                   T  TCCAA
GAM973  LOC200014 3'  ATCACCCTCAAGTTCTCCCATC 25845        CACC  C   _
          CC                   ATCATCCTC   TC CCCA CCC
                               |||||||||   || |||| |||
                               TAGTGGGAG   AG GGGT GGG
                                   TTCA  A   A
GAM973  LOC200312 5'  CCATCCTCCATAGCCATCC   25846         ___  _
                               TCATCCTCCA   CC TCC
                               ||||||||||   || |||
                               GGTAGGAGGT   GG AGG
                                    ATC  T
GAM973  LOC200399 3'  ATCATTCCTCCCTCTACCCC   25836      _    AC  C
                               ATCAT CCTCC  CT CCCC
                               ||||| |||||  || ||||
                               TAGTA GGAGG  GA GGGG
                                  A    GA  T
GAM973  LOC200942 3'  CCCCCATGCCTCTCTCATCCC  25847      __   CCC  _
                               CCTCCA  CCTC   CA CCC
                               ||||||  ||||   || |||
                               GGGGGT  GGAG   GT GGG
                                   AC    AGA  A
GAM973  LOC201689 3'  ACCATCCTCCCCTTCTGTCCC  25755        A   _ C__
                               ATCATCCTCC CCT C   CCC
                               |||||||||| ||| |   |||
                               TGGTAGGAGG GGA G   GGG
                                    _   A ACA
GAM973  LOC205095 5'  CCATCCTCCACTGCCCACC    25848         CTCC
                               TCATCCTCCAC    CCCACC
                               ||||||||||    ||||||
                               GGTAGGAGGTG    GGGTGG
                                     AC__
GAM973  LOC219942 3'  ATCACCTCCCAAAGGTCCCACC 25849     T    ACCTCC_
                               ATCA CCTCC      CCCACC
                               |||| |||||      ||||||
                               TAGT GGAGG      GGGTGG
                                  _    GTTTCCA
GAM973  LOC220538 3'  CATCCTCCATCTCCTGGTGCC  25850        C   CCCAC
                               CATCCTCCA CTCC    CC
                               ||||||||| ||||    ||
                               GTAGGAGGT GAGG    GG
                                    A   ACCAC
GAM973  LOC220549 3'  CCATCCTCCCCTCTCTGCC    25851        A   CC__
                               TCATCCTCC CCTC   CC
                               ||||||||| ||||   ||
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                                GGTAGGAGG GGAG    GG
                                      _    AGAC
GAM973   LOC221712 5'  CCATCTCCACCTTCCTTGCTCC 25852       C      _  CCCAC
                                TCATC TCCACCT CC     CC
                                ||||| ||||||| ||     ||
                                GGTAG AGGTGGA GG     GG
                                   _      A  AACGA
GAM973   LOC245744 3'  CATCGCCCCTCCCCCGTTCC   25853      CT  A       AC_
                                CATC  CC CCTCCCCC   CC
                                ||||  || ||||||||   ||
                                GTAG  GG GGAGGGGG   GG
                                  C_ _       CAA
GAM973   LOC253220 5'  TCATCCTCACTCTGTCCC     25854         C  _  CC
                                TCATCCTC AC CT  CCC
                                |||||||| || ||  |||
                                AGTAGGAG TG GA  GGG
                                      _ A  CA
GAM973   LOC253358 5'  TCCAAGCACCTTCCCCGTCCC  25855     TC_    C    AC
                                TCC   CACCT CCCC  CCC
                                |||   ||||| ||||  |||
                                AGG   GTGGA GGGG  GGG
                                  TTC     A    CA
GAM973   LOC253805 5'  TCTTCCACTCACCCCACCC    25856    C     C  _
                                TC TCCAC TC CCCCACCC
                                || ||||| || ||||||||
                                AG AGGTG AG GGGGTGGG
                                 A     _ T
GAM973   LOC254128 3'  CATCCTCCATGTCATCCCTAC  25857          CC  __   C
                                CATCCTCCA  TC  CCC AC
                                |||||||||  ||  ||| ||
                                GTAGGAGGT  AG  GGG TG
                                      AC  TA   A
GAM973   LOC254532 5'  TCTCCTCCACCCAGAGCGCCCC 25858     A         CCCCCA
                                TC TCCTCCACCT      CCCC
                                || ||||||||||      ||||
                                AG AGGAGGTGGG      GGGG
                                 _         TCTCGC
GAM973   LOC256277 5'  ATCCTCCAGCTTCCTCCGCCCC 25859         C  C  _  A
                                ATCCTCCA CT CC CC CCCC
                                |||||||| || || || ||||
                                TAGGAGGT GA GG GG GGGG
                                     C  A  A  C
GAM973   LOC256310 3'  TCCTCCTCCACCTTCTGCC    25860     A        _ CC
                                TC TCCTCCACCT C  CC
                                || ||||||||||  |  ||
                                AG AGGAGGTGGA G  GG
                                 G         A AC
GAM973   LOC256982 5'  TCTGGCCCCGCCTCCCCCGCC  25861     ATC    A       A
                                TC   CTCC CCTCCCCC CC
                                ||   |||| ||||||||  ||
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                                AG   GGGG GGAGGGGG GG
                                 ACC    C       C
GAM973  LOC257428 5'  ATCATCCTGCATCAGGCAC    25862        C  CC  CCC
                                ATCATCCT CA  TC   CAC
                                ||||||||  ||  ||   |||
                                TAGTAGGA GT  AG   GTG
                                     C  __  TCC
GAM973  LOC257451 3'  CATGCCTGCCTTCCCCACCCC  25728     _  CCA   C
                                CAT CCT   CCT CCCCACCCC
                                |||  |||   |||  |||||||||
                                GTA GGA   GGA GGGGTGGGG
                                  C   C__   A
GAM973  LOC51195  3'  CCATCCCCCTCCCCCAC     25863        CCA
                                TCATCCT   CCTCCCCCAC
                                |||||||   ||||||||||
                                GGTAGGG   GGAGGGGGTG
                                     ___
GAM973  LOC58525  5'  ATCATCCTGTTATCCAACCGTC 25864        ______   _ _
           CC                     ATCATCC    TCCA CC TCCC
                                |||||||     ||||  ||  ||||
                                TAGTAGG     AGGT GG AGGG
                                    ACAAT    T  C
GAM973  LOC90297  5'  TCTCCCACCTCCCCCACC    25865    CT
                                TC  CCACCTCCCCCACC
                                ||  ||||||||||||||
                                AG  GGTGGAGGGGGGTGG
                                 AG
GAM973  LOC90550  3'  ATCATCCTTTCCATCCTGCCCC 25866        __   _   C
                                ATCATCC  TCCA CCT CCCC
                                |||||||  ||||  |||  ||||
                                TAGTAGG  AGGT GGA GGGG
                                    AA    A   C
GAM973  LOC90841  3'  CATCCTCCCACAGGCCCCTGCC 25867        _  CT_   CA
           CC                     CATCCTCC AC   CCCC  CCCC
                                |||||||  ||   ||||  ||||
                                GTAGGAGG TG   GGGG  GGGG
                                     G  TCC    AC
GAM973  LOC92235  5'  ATCATCCTCCCGCACCCTGCTC 25868         ACCT   CCAC
           C                      ATCATCCTCC    CCC    CC
                                ||||||||||    |||    ||
                                TAGTAGGAGG    GGG    GG
                                      GCGT   ACGA
GAM973  LOC92771  3'  CATTTTCCACCCCACCCC    25869     CC      _
                                CAT  TCCACCTC CCCC
                                |||  ||||||||  ||||
                                GTA  AGGTGGGG GGGG
                                  AA       T
GAM974  APPL      3'  GCATTGTAGAAGTAGGCAGGC  25872     C  _  CGTC
                                GCA TG AG    TAGGCAGGC
                                ||| ||  ||   |||||||||
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                                CGT AC TC   ATCCGTCCG
                                  A  A  TTC_
GAM974  CTGF    3'  CACTGGGGCTACAGGCAGG   25873     A_  GTC
                                CACTG  GC   TAGGCAGG
                                |||||  ||   ||||||||
                                GTGAC  CG   GTCCGTCC
                                   CC  AT_
GAM974  FBXL7   5'  GCGCTGAGCCGGGCAGGCC   25874   A    GTCTA
                                GC CTGAGC    GGCAGGCC
                                || ||||||    ||||||||
                                CG GACTCG    CCGTCCGG
                                 C     GC___
GAM974  MSF     3'  ACATTGAGGCTGGGCAGGCC   25875    C   C T  A
                                GCA TGAG G CT GGCAGGCC
                                ||| |||| | || ||||||||
                                TGT ACTC C GA CCGTCCGG
                                  A   _ _  C
GAM974  MUC4    3'  GCGTTGAACGTCTCCTGGCC   25876   AC       AGGCA
                                GC  TGAGCGTCT    GGCC
                                ||  |||||||||    ||||
                                CG  ACTTGCAGA    CCGG
                                 CA       GGA__
GAM974  P53AIP1  3'  ACACTGAGACTCAGGCAGGCC  25877        CG  T
                                GCACTGAG  TC AGGCAGGCC
                                ||||||||  || |||||||||
                                TGTGACTC  AG TCCGTCCGG
                                     TG  _
GAM974  PHF1    3'  CTGAGCGTCTAGGAAGACC   25878          C
                                CTGAGCGTCTAGG AGGCC
                                |||||||||||| |||||
                                GACTCGCAGATCC TCTGG
                                       T
GAM974  RGS3    5'  GCACTGAGTGGGGAGCGGGCC  25879        CGTCTA  A
                                GCACTGAG     GGC GGCC
                                ||||||||     ||| ||||
                                CGTGACTC     TCG CCGG
                                     ACCCC_  C
GAM974  SCA1    3'  GCCTAGAGTTTAGGCAGG    25880    A  G  C  C
                                GC CT AG GT TAGGCAGG
                                || || || || ||||||||
                                CG GA TC CA ATCCGTCC
                                 _ _  T  A
GAM974  SORCS3  3'  GCATTGAGCAGGCCTGGCGGG  25881     C    __    A  A
                                GCA TGAGC  GTCT GGC GG
                                ||| |||||  |||| ||| ||
                                CGT ACTCG  CGGA CCG CC
                                  A    TC    _  C
GAM974  ABLIM   3'  CACTGCAATCTTAGGCAGGCC  25882      AGC   _
                                CACTG   GTCT AGGCAGGCC
                                |||||   |||| |||||||||
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                                GTGAC   TAGA TCCGTCCGG
                                  GT_   A
GAM974  ABLIM    3'  CACTGCAATCTTAGGCAGGCC  25882      AGC   _
                                CACTG   GTCT AGGCAGGCC
                                |||||   |||| |||||||||
                                GTGAC   TAGA TCCGTCCGG
                                  GT_   A
GAM974  CGI-51   5'  GCTGCTGAGGGCAGAAGGCGGG 25883    A_    C  CT_   A
                                GC  CTGAG GT   AGGC GG
                                ||  ||||| ||   |||| ||
                                CG  GACTC CG   TCCG CC
                                 AC    C  TCT   C
GAM974  DKFZP434A0131 3'  CAGCACTGGGTGTCCAGGGCC  25884        AGC     CAG
                                TAGCACTG   GTCTAGG   GCC
                                ||||||||   |||||||   |||
                                GTCGTGAC   CAGGTCC   CGG
                                     CCA     ___
GAM974  DKFZp434N035 3'  GCGCTGGTTGAGGCAGGC    25885    A   AGC  CT
                                GC CTG   GT  AGGCAGGC
                                || |||   ||  ||||||||
                                CG GAC   CA  TCCGTCCG
                                 C   ___  AC
GAM974  DKFZP564D0478 3'  GCACTGGCTGTGCTGGCAGGCC 25886       A  _  _  A
                                GCACTG GC GT CT GGCAGGCC
                                |||||| || || || ||||||||
                                CGTGAC CG CA GA CCGTCCGG
                                   _  A  C  _
GAM974  DMWD     3'  GCGCTGGGCTGGGAGCAGGCC  25887    A   A  GTCTA
                                GC CTG GC    GGCAGGCC
                                || ||| ||    ||||||||
                                CG GAC CG    TCGTCCGG
                                 C   C  ACCC_
GAM974  FLJ32796  5'  CAGCACTGGTGAGGCAGG    25888        AGC  CT
                                TAGCACTG   GT  AGGCAGG
                                ||||||||   ||  |||||||
                                GTCGTGAC   CA  TCCGTCC
                                     ___  C_
GAM974  HSPC121   5'  GCGCGAGCAGAAAGCAGGCC   25889    AC     TCT
                                GC  TGAGCG   AGGCAGGCC
                                ||  ||||||   |||||||||
                                CG  GCTCGT   TTCGTCCGG
                                 C_     CT_
GAM974  KIAA0450  5'  CAGCACTGGGCCTGGGCAGGCC 25890        AGC   A
                                TAGCACTG   GTCT GGCAGGCC
                                ||||||||   |||| ||||||||
                                GTCGTGAC   CGGA CCGTCCGG
                                     C__    C
GAM974  KIAA0819  3'  GCATCATCTGGGCAGGC     25891     CTGAG    A
                                GCA    CGTCT GGCAGGC
                                |||    ||||| |||||||
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                                CGT    GTAGA CCGTCCG
                                  A____    C
GAM974  KIAA1755  3'  GCTCTGAGGCAGGCAGGCC   25892    A    C  CT
                                GC CTGAG GT  AGGCAGGCC
                                || ||||| ||  |||||||||
                                CG GACTC CG  TCCGTCCGG
                                 A    _ __
GAM974  MAD4      3'  CAGCACTAGCTGGGCAGGC   25893       G   GTCTA
                                TAGCACT AGC    GGCAGGC
                                ||||||| |||    |||||||
                                GTCGTGA TCG    CCGTCCG
                                    _  AC___
GAM974  MAPKAP1   3'  GCCCTGGCAGGCAGGC     25894    A   A  GTCT
                                GC CTG GC    AGGCAGGC
                                || ||| ||    ||||||||
                                CG GAC CG    TCCGTCCG
                                 G  _ _____
GAM974  SCLY      3'  GCGCTGAGCAGAGCAGGCC   25895    A     TCTA
                                GC CTGAGCG    GGCAGGCC
                                || |||||||    ||||||||
                                CG GACTCGT    TCGTCCGG
                                 C      C___
GAM974  SP2       3'  CACAGTCTGGGCAGGCC     25896     TGAGC    A
                                CAC    GTCT GGCAGGCC
                                |||    |||| ||||||||
                                GTG    CAGA CCGTCCGG
                                  T____    C
GAM974  USP19     3'  GCCTGGGGCAGGCAGGTAGGCC 25897    A   A_   TC    C
                                GC CTG  GCG  TAGG AGGCC
                                || |||  |||  |||| |||||
                                CG GAC  CGT  GTCC TCCGG
                                 _  CC   CC    A
GAM974  WDR7      3'  GCACTGGGGTGGGCAGGCC   25898       AGC  CTA
                                GCACTG   GT   GGCAGGCC
                                ||||||   ||   ||||||||
                                CGTGAC   CA   CCGTCCGG
                                   CC_  C__
GAM974  LOC126528 3'  CAGCACTGGGTGGAACAGGCC  25899         AGC  CTA
                                TAGCACTG   GT   GGCAGGCC
                                ||||||||   ||   ||||||||
                                GTCGTGAC   CA   TTGTCCGG
                                    C__  CC_
GAM974  LOC127348 3'  TAGCATGACATCCAGGTGGG   25900      C   G      CA
                                TAGCA TGA CGTCTAGG  GG
                                ||||| ||| ||||||||  ||
                                ATCGT ACT GTAGGTCC  CC
                                   _  _       AC
GAM974  LOC130617 5'  AGTGCTGAGCGTCTTTAGGGC  25901    CA        A___
                                AG  CTGAGCGTCT    GGC
                                ||  ||||||||||    |||
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                                TC  GACTCGCAGA    CCG
                                 AC         AATC
GAM974   LOC138389 5'  GCGCTGAACGTGCCCACGGGCC 25902     A       _  AG  A
                                GC CTGAGCGT CT  GC GGCC
                                || |||||||| ||  || ||||
                                CG GACTTGCA GG  TG CCGG
                                 C       C  G_  C
GAM974   LOC145601 3'  CAGCACTGGGTGTTTTCCTGGG 25903         AGCG___   A  CA
           G                     TAGCACTG      TCT GG  GG
                                ||||||||      ||| ||  ||
                                GTCGTGAC      AGG CC  CC
                                     CCACAAA   A  __
GAM974   LOC196374 5'  GCCTGAGCGTCCTTGAGGGCC  25904     A         AGGCA
                                GC CTGAGCGTCT     GGCC
                                || ||||||||||     ||||
                                CG GACTCGCAGG     CCGG
                                 _         AACTC
GAM974   LOC196463 3'  GCCCTGAGGTGAGGGGCAGGCC 25905     A     C  CTA_
                                GC CTGAG GT    GGCAGGCC
                                || ||||| ||    ||||||||
                                CG GACTC CA    CCGTCCGG
                                 G    _  CTCC
GAM974   LOC202781 3'  AGCACTGAGTGTTTTTATTACA 25906          C  CTAG___
           GG                    AGCACTGAG GT      GCAGG
                                |||||||| ||      |||||
                                TCGTGACTC CA      TGTCC
                                     A  AAAATAA
GAM974   LOC203274 5'  GCGCTGAGCGTGCCCACGGGCC 25907     A       _  AG  A
                                GC CTGAGCGT CT  GC GGCC
                                || |||||||| ||  || ||||
                                CG GACTCGCA GG  TG CCGG
                                 C       C  G_  C
GAM974   LOC220776 3'  GCACTGAAGTCAGGCAGGCC   25908         C   T
                                GCACTGAG GTC AGGCAGGCC
                                |||||||| ||| |||||||||
                                CGTGACTT CAG TCCGTCCGG
                                     _  _
GAM974   LOC253980 3'  TAACGCTGAGCTGGGCAGGCC  25909      A     GTCTA
                                TAGC CTGAGC     GGCAGGCC
                                |||| ||||||     ||||||||
                                ATTG GACTCG     CCGTCCGG
                                  C     AC___
GAM974   LOC255650 3'  TAGAACTGAACACTTCTGGGCG 25910     C       __   A   A
           GGC                    TAG ACTGAGCG  TCT GGC GGC
                                ||| ||||||||  ||| ||| |||
                                ATC TGACTTGT  AGA CCG CCG
                                  T       GA   C   C
GAM974   LOC93190  3'  GCCCTACCTAGGCAGGC     25911     A   AGCG
                                GC CTG    TCTAGGCAGGC
                                || |||    ||||||||||
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                                CG GAT    GGATCCGTCCG
                                 G  ____
GAM975  ABAT     5'  TCTCCGATCTGCGGGATC    25914     T   AGGACCA
                                TCTC CGGT      CGGGATC
                                |||| ||||      |||||||
                                AGAG GCTA      GCCCTAG
                                  _    GAC____
GAM975  ITGAM    3'  TCTCTCGGTGGTGCAGTGGTTC 25915        A  AC  CG  A
                                TCTCTCGGT GG  CA  GG TC
                                ||||||||| ||  ||  || ||
                                AGAGAGCCA CC  GT  CC AG
                                     _ AC  CA  A
GAM975  LFG      5'  TCTCTCGGGGAAGGGGTC    25916        TA   CCAC   A
                                TCTCTCGG  GGA    GGG TC
                                ||||||||  |||    ||| ||
                                AGAGAGCC  CCT    CCC AG
                                     __   T___   C
GAM975  RANBP3   3'  TCTCTCGGGAGGGCCTCTGGTT 25917        T   A  ACG  A
             C                   TCTCTCGG AGG CC   GG TC
                                ||||||||| ||| ||   || ||
                                AGAGAGCC TCC GG   CC AG
                                     C   C  AGA  A
GAM975  MGC2306  3'  CTTTCATACTAGGGCTGTGGGA 25918    C   G__    ACCAC
             TCC                  CT TCG   TAGG    GGGATCC
                                || |||   ||||    |||||||
                                GA AGT   ATCC    CCCTAGG
                                 A   ATG    CGACA
GAM975  PPP1R15B 5'  TCTCTCAGGTAGGGCCGCGG   25919       _     A  A
                                TCTCTC GGTAGG CC CGG
                                |||||| |||||| || |||
                                AGAGAG CCATCC GG GCC
                                   T     C  C
GAM975  LOC126917 3'  TCCGGTAGGATCAGTAGTC    25920    T      C  CG  A
                                TC CGGTAGGA CA  GG TC
                                || |||||||| ||  || ||
                                AG GCCATCCT GT  TC AG
                                 _       A  CA  _
GAM975  LOC158668 5'  CCTCGGTAGGGTCGGCATCC   25921         ACCA   G
                                TCTCGGTAGG    CGG ATCC
                                ||||||||||    ||| ||||
                                GGAGCCATCC    GCC TAGG
                                      CA__   G
GAM975  LOC222709 5'  TCTGTCGGCCCGCGGGATC    25922     C    AGGA  A
                                TCT TCGGT    CC CGGGATC
                                ||| |||||    || |||||||
                                AGA AGCCG    GG GCCCTAG
                                  C     _____ C
GAM975  LOC90917  3'  TCTTTGGGTGGGAGCAAGATCC 25923     CTC   A   CCA
                                TCT   GGT GGA   CGGGATCC
                                |||   ||| |||   ||||||||
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                                AGA  CCA CCT  GTTCTAGG
                                  AAC  C  C__
GAM976  AFP     5'  TTGTTATTGGCAGTG      25926          CGGGACGA
                                TTGTTATTGGC      AGTG
                                ||||||||||       ||||
                                AACAATAACCG      TCAC
                                          _________
GAM976  LASS2   3'  TTGTTATTGAGGATGGGGTGG  25927        GCC   CGAA
                                TTGTTATTG  GGGA  GTGG
                                |||||||||  ||||  ||||
                                AACAATAAC  TCCT  CACC
                                     ___  ACCC
GAM976  SLC22A11 3'  TCGTTATTGGTTGGGCATG   25928         CC  A GAA
                                TTGTTATTGG  GGG C  GTG
                                ||||||||||  ||| |  |||
                                AGCAATAACC  CCC G  TAC
                                     AA  _ ___
GAM976  LOC124649 5'  TTGTTATTGGCTGGTGAGGTGG 25929          C  GAC  A
                                TTGTTATTGGC GG  GA GTGG
                                |||||||||| ||  || ||||
                                AACAATAACCG CC  CT CACC
                                     A  A__  C
GAM977  NPTX2   3'  GATTCCTGGGGAATGAGC   25932     G   TAAA
                                GATT TTTG   GAATGAGC
                                |||| ||||   ||||||||
                                CTAA GGAC   CTTACTCG
                                  _   CC__
GAM977  SLC4A5  5'  GATTGTTTGTGCCAAGC    25933         AAAGAA
                                GATTGTTTGT    TGAGC
                                ||||||||||    |||||
                                CTAACAAACA    GTTCG
                                     CG____
GAM977  SLC4A5  5'  GATTGTTTGTGCCAAGC    25933         AAAGAA
                                GATTGTTTGT    TGAGC
                                ||||||||||    |||||
                                CTAACAAACA    GTTCG
                                     CG____
GAM977  SLC4A5  5'  GATTGTTTGTGCCAAGC    25933         AAAGAA
                                GATTGTTTGT    TGAGC
                                ||||||||||    |||||
                                CTAACAAACA    GTTCG
                                     CG____
GAM977  FLJ00001 3'  TTGTTGCACAGATGAGCCC   25934     T  A  A
                                TTGTT GTA AGA TGAGCCC
                                ||||| ||| ||| |||||||
                                AACAA CGT TCT ACTCGGG
                                  _  G  _
GAM977  FLJ14457 3'  TGCTTAATAAGGGATGAGCCC 25935      TA  A_
                                TGTTTG  AAG  ATGAGCCC
                                ||||||  |||  ||||||||
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                                ACGAAT  TTC  TACTCGGG
                                   TA   CC
GAM977  IL1RAPL1  5'  GATTGTTTGCTGAAGATACAAT 25936          A_   _ TG G
           CC                    GATTGTTTGT  AAGA A  A CC
                                 ||||||||||  |||| |  | ||
                                 CTAACAAACG  TTCT T  T GG
                                      AC    A GT A
GAM977  KIAA1954  5'  TGTTTATAAAGGGATGGGC   25937          A_   A
                                 TGTTTGTAAAG  ATG GC
                                 ||||||||||  ||| ||
                                 ACAAATATTTC  TAC CG
                                       CC   C
GAM977  NRM       3'  GCTTGTAACCAGAGTGAGCTCC 25938          __   A    _
                                 GTTTGTAA  AGA TGAGC CC
                                 ||||||||  ||| ||||| ||
                                 CGAACATT  TCT ACTCG GG
                                      GG   C    A
GAM977  NRM       3'  GCTTGTAACCAGAGTGAGCTCC 25938          __   A    _
                                 GTTTGTAA  AGA TGAGC CC
                                 ||||||||  ||| ||||| ||
                                 CGAACATT  TCT ACTCG GG
                                      GG   C    A
GAM977  NRM       3'  GCTTGTAACCAGAGTGAGCTCC 25938          __   A    _
                                 GTTTGTAA  AGA TGAGC CC
                                 ||||||||  ||| ||||| ||
                                 CGAACATT  TCT ACTCG GG
                                      GG   C    A
GAM977  PELI2     3'  AATTGTTTGTGAAGTCC     25939          AAA   TGAG
                                 GATTGTTTGT   GAA    CC
                                 ||||||||||   |||    ||
                                 TTAACAAACA   CTT    GG
                                       ___   CA__
GAM977  ZNF226    5'  GTAGGCTCAAGAATGAGCC    25940    TT  A_
                                 GT  GT  AAGAATGAGCC
                                 ||  ||  ||||||||||||
                                 CA  CG  TTCTTACTCGG
                                  TC  AG
GAM977  LOC126364 3'  ATTGTCCTCTGAAGGGTGAGCC 25941        GTA_   AA
           CC                     ATTGTTT    AAG  TGAGCCCC
                                  |||||||    |||  ||||||||
                                  TAACAGG    TTC  ACTCGGGG
                                     AGAC   CC
GAM977  LOC221641 5'  GACTGTTTAATAATGAG     25942          TAAAG
                                 GATTGTTTG    AATGAG
                                 |||||||||    ||||||
                                 CTGACAAAT    TTACTC
                                       TA___
GAM977  LOC255975 3'  CTGTTGTGAGGAATGAGCCCC  25943       T  AAA
                                 TTGTT GT   GAATGAGCCCC
                                 ||||| ||   ||||||||||
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                                GACAA CA   CTTACTCGGGG
                                   _ CTC
GAM977  LOC91252  3'  TGTTGGCCAGGAATGAGCTCC  25944     T  AAA      _
                                TGTT GT   GAATGAGC CC
                                |||| ||   |||||||| ||
                                ACAA CG   CTTACTCG GG
                                  C  GTC       A
GAM978  AKAP8     3'  TCAGTGGCTGTATTGAACAAGT 25947       CGCGGATAT
           A                     TCAGTGGC       ACAAGTA
                                 ||||||||       |||||||
                                 AGTCACCG       TGTTCAT
                                     ACATAACT_
GAM978  LOC151475 3'  TCAGTAGGCTTCCTATACAAGT 25948       CC  GGA_
           A                     TCAGTGG  GC    TATACAAGTA
                                 |||||||  ||    ||||||||||
                                 AGTCATC  CG    ATATGTTCAT
                                    __  AAGG
GAM978  LOC203378 3'  TCAGTAGCTGGAACTACAGGT  25949       CGC   TA    A
                                 TCAGTGGC   GGA  TACA GT
                                 ||||||||   |||  |||| ||
                                 AGTCATCG   CCT  ATGT CA
                                     A__   TG    C
GAM979  KIAA0984  3'  TGGTACAATGCATGCATGTTAT 25952       CAAA     A__
           TG                     TGGTACAA    CATGTA   TATTG
                                  ||||||||    ||||||   |||||
                                  ACCATGTT    GTACGT   ATAAC
                                      AC__     ACA
GAM980  F2RL3     3'  GTTTGATCCTGTTTCAGATTC  25955      TA   ___
                                 GTTTG  ATCT   TTCAGATTC
                                 |||||  ||||   |||||||||
                                 CAAAC  TAGG   AAGTCTAAG
                                    __    ACA
GAM980  PHKB      3'  AAATGTTTGATAAGGTACAGAT 25956        TAATCTTT
           T                      AAATGTTTG       CAGATT
                                  |||||||||       ||||||
                                  TTTACAAAC       GTCTAA
                                       TATTCCAT
GAM980  SECTM1    3'  ACGTTTCTTTCAGATT      25957      TGTAA
                                 ATGTT    TCTTTCAGATT
                                 |||||    ||||||||||
                                 TGCAA    AGAAAGTCTAA
                                    _____
GAM980  GAB3      3'  AAATGTTTGGTAGAAACAGATT 25958        TAATCTTT
                                 AAATGTTTG       CAGATT
                                 |||||||||       ||||||
                                 TTTACAAAC       GTCTAA
                                      CATCTTT_
GAM980  KIAA0546  3'  AAATGTCTGTAGCAGATT    25959          ATCTTT
                                 AAATGTTTGTA     CAGATT
                                 ||||||||||     ||||||
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                                TTTACAGACAT     GTCTAA
                                      C_____
GAM980  KIAA1265  3'  GTCAGAAATAATTTTTCAGATT 25960     T___    C
              C                    GTT    GTAAT TTTCAGATTC
                                   |||    ||||| ||||||||||
                                   CAG    TATTA AAAGTCTAAG
                                     TCTT     A
GAM980  KIAA1854  3'  AAATGGTTGTTTCTCAGATTC  25961      T    AATC
                                   AAATG TTGT    TTTCAGATTC
                                   ||||| ||||    ||||||||||
                                   TTTAC AACA    AGAGTCTAAG
                                      C    A___
GAM980  LOC122773 3'  AAATGTATGTAATCTTTC     25962       T
                                   AAATGT TGTAATCTTTC
                                   |||||| ||||||||||
                                   TTTACA ACATTAGAAAG
                                       T
GAM980  LOC145748 3'  AAATGTTTGTAGTCAACAGTTC 25963          A  TTT   A
                                   AAATGTTTGTA TC   CAG TTC
                                   |||||||||| ||   ||| |||
                                   TTTACAAACAT AG   GTC AAG
                                         C  TT_   _
GAM980  LOC145757 3'  AACGTCTTCATTTTTCAGATT  25964       GTA  C
                                   AATGTTT   AT TTTCAGATT
                                   |||||||   || |||||||||
                                   TTGCAGA   TA AAAGTCTAA
                                       AG_  A
GAM980  LOC150208 5'  TTGTTCTTTTCAGATTC     25965      AA    _
                                   TTGT  TCTTT CAGATTC
                                   ||||  ||||| |||||||
                                   AACA  AGAAA GTCTAAG
                                     __     A
GAM980  LOC203378 3'  TGTTTGGATTTTTTCAGATT   25966       TAATC
                                   TGTTTG    TTTCAGATT
                                   ||||||    |||||||||
                                   ACAAAC    AAAGTCTAA
                                       CTAAA
GAM981  ELOVL4    3'  CAAGTTTAAGTGTATACACATT 25969         CATAAT_
              T                    CAAGTTTAA      CACATTT
                                   |||||||||      |||||||
                                   GTTCAAATT      GTGTAAA
                                         CACATAT
GAM981  FGF7      3'  CAAGACATAGTCACATTT    25970      TTTA    A
                                   CAAG    ACATA TCACATTT
                                   ||||    ||||| ||||||||
                                   GTTC    TGTAT AGTGTAAA
                                     ____     C
GAM981  IGSF8     3'  ACAAGTTTATTCACATT     25971          ACATAA
                                   ACAAGTTTA     TCACATT
                                   |||||||||     |||||||
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                                TGTTCAAAT     AGTGTAA
                                     A_____
GAM981  NOV      3'  CAAGTTTACAGTTAATTACATT 25972        ACA_   C
              T                   CAAGTTTA   TAAT ACATTT
                                  ||||||||   |||| ||||||
                                  GTTCAAAT   ATTA TGTAAA
                                       GTCA   A
GAM981  RPL10    3'  GTTAACTATAATCACATT    25973    T  _
                                  GTT AAC ATAATCACATT
                                  ||| ||| ||||||||||
                                  CAA TTG TATTAGTGTAA
                                    _  A
GAM981  SLC4A7   3'  TACAGGCTTAACAACATT    25974     A      TAATC
                                  TACA GTTTAACA    ACATT
                                  |||| ||||||||    |||||
                                  ATGT CGAATTGT    TGTAA
                                    C      _____
GAM981  TRAM     3'  GTATAACATAAAGCACATT   25975    T      T_
                                  GT TAACATAA  CACATT
                                  || ||||||||  ||||||
                                  CA ATTGTATT  GTGTAA
                                   T       TC
GAM981  IL1F10   3'  CTTAACATAATCACATTT    25976
                                  TTTAACATAATCACATTT
                                  ||||||||||||||||||
                                  GAATTGTATTAGTGTAAA

GAM981  KIAA1069 3'  TACAAGTTTAAAAATACATTT  25977          CAT   C
                                  TACAAGTTTAA   AAT ACATTT
                                  ||||||||||   ||| ||||||
                                  ATGTTCAAATT   TTA TGTAAA
                                         T__   _
GAM981  KIAA1265 3'  GCAGGACCATAATCACATTT   25978    TTAA_
                                  GT    CATAATCACATTT
                                  ||    ||||||||||||
                                  CG    GTATTAGTGTAAA
                                   TCCTG
GAM981  PEPP2    3'  CACAATGAACATAATTACATTT 25979      GTTT      C
                                  TACAA    AACATAAT ACATTT
                                  |||||    |||||||| ||||||
                                  GTGTT    TTGTATTA TGTAAA
                                     AC__       A
GAM981  LOC158116 3'  CAAGACATAGTCACATTT    25970     TTTA    A
                                  CAAG    ACATA TCACATTT
                                  ||||    ||||| ||||||||
                                  GTTC    TGTAT AGTGTAAA
                                     ____    C
GAM982  GPR61    3'  TCCTGTCCAGTTTGCA      25982          CA
                                  TCCTGTCCAG  TTTGCA
                                  ||||||||||  ||||||
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                                AGGACAGGTC  AAACGT
                                          __
GAM982  RFP      3'  ACATCCTGTCTCCCACTGCA   25983          CAG    T
                                ACATCCTGTC   CATT GCA
                                ||||||||||   |||| |||
                                TGTAGGACAG   GTGA CGT
                                     AGG   _
GAM982  UBE4A    3'  ACATTCTGGCATTTGC      25984      C   TCCA
                                ACAT CTG    GCATTTGC
                                |||| |||    ||||||||
                                TGTA GAC    CGTAAACG
                                  A  ____
GAM982  APOARGC  3'  CATCCTGTCAGGTTGCA     25985          C  CAT
                                CATCCTGTC AG   TTGCA
                                |||||||||  ||   |||||
                                GTAGGACAG TC   AACGT
                                     _  C__
GAM982  DKFZP434J046 5'  TACGTATCCTGCCTGGGGTGTG 25986         CA__________  ATTT
           CAAATGC                  ATCCTGTC         GC    GC
                                |||||||          ||    ||
                                TAGGACGG         CG    CG
                                    ACCCCACIIIA  TTTA
GAM982  FLJ21615 3'  ACACATTCTCATTTGC      25987       C  GTCCAG
                                ACACAT CT     CATTTGC
                                ||||||  ||     |||||||
                                TGTGTA GA     GTAAACG
                                   A  _______
GAM982  KIAA0252 3'  CACATGCTTGAAACATTTGCA  25988      C  GTCC
                                CACAT CT    AGCATTTGCA
                                |||||  ||    ||||||||||
                                GTGTA GA    TTGTAAACGT
                                   C  ACT_
GAM982  KIAA1391 3'  CACATTTTAACAGCATTTG    25989      CC  TC
                                CACAT  TG  CAGCATTTG
                                |||||  ||  |||||||||
                                GTGTA  AT  GTCGTAAAC
                                   AA  T_
GAM982  LSFR2    3'  CATCCTGTCCATCCTGCA     25990          GCAT
                                CATCCTGTCCA    TTGCA
                                ||||||||||    |||||
                                GTAGGACAGGT    GACGT
                                     AG__
GAM982  Nup43    5'  TACACATCCTGTTGATGAAGCA 25991           CC____
                                TACACATCCTGT     AGCA
                                ||||||||||||     ||||
                                ATGTGTAGGACA     TCGT
                                     ACTACT
GAM982  PRO0097  5'  CACACATCCTGTTTTGTGTGCA 25992          CCA_______  ATTT
           AAG                    CACATCCTGT        GC    G
                                |||||||||          ||    |
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                              GTGTAGGACA        CG   C
                                   AAACACIIIA  TTTA
GAM982  PTD002   3'  TACACATCTTATCTTGTATGCA 25993       C   CA_______  ATTT
          AAG                   CACATC TGTC       GC   G
                              |||||| ||||       ||   |
                              GTGTAG ATAG       CG   C
                                 A   AACATIIIA  TTTA
GAM982  TRIM2    3'  ACATGTGCTGACATTTGC    25994     CC   CCA
                              ACAT  TGT   GCATTTGC
                              ||||  |||   ||||||||
                              TGTA  ACG   TGTAAACG
                                C_  AC_
GAM982  WDR7     3'  TACACTCCTGAACATTTG    25995      A    TCC
                              TACAC TCCTG   AGCATTTG
                              ||||| |||||   ||||||||
                              ATGTG AGGAC   TTGTAAAC
                                 _    ___
GAM982  LOC118672 3'  CATCTTTGTCCATTTGCA    25996     C_     GCA
                              CATC  TGTCCA   TTTGCA
                              ||||  ||||||   ||||||
                              GTAG  ACAGGT   AAACGT
                                AA     ___
GAM982  LOC129080 3'  CATCTGTCACAAGCATTTGCA  25997     C   _ _
                              CATC TGTC CA GCATTTGCA
                              |||| |||| || |||||||||
                              GTAG ACAG GT CGTAAACGT
                                _   T  T
GAM982  LOC146784 3'  TACACATCCGTCTCCTCTGC   25998        T   CAGCA
                              TACACATCC GTC     TTTGC
                              ||||||||| |||     |||||
                              ATGTGTAGG CAG     AGACG
                                   _  AGG__
GAM982  LOC147353 3'  CACATGCTAACATTTGC     25999      C   TCCA
                              CACAT CTG    GCATTTGC
                              ||||| |||    ||||||||
                              GTGTA GAT    TGTAAACG
                                C  _____
GAM982  LOC148930 3'  ACACCTAGCCAGCATTTG    26000     T   T
                              ACA CCTG CCAGCATTTG
                              ||| |||| ||||||||||
                              TGT GGAT GGTCGTAAAC
                                _   C
GAM982  LOC158014 5'  TACACATCTTGTTCTAAGATTG 26001        C   CCAGCAT
          CA                    TACACATC TGT      TTGCA
                              |||||||| |||      |||||
                              ATGTGTAG ACA      AACGT
                                   A   AGATTCT
GAM982  LOC170394 5'  CACGTGTCTTGCGGCATTTGCA 26002     A__  C   CCA
                              CAC   TC TGT   GCATTTGCA
                              |||   || |||   |||||||||
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                                GTG   AG ACG   CGTAAACGT
                                  CAC  A   C__
GAM982  LOC196890 3'  TACACATCTTTCTGCCCGCA   26003        ___     A
                                TACACATC   CTGTCC GCA
                                ||||||||   |||||| |||
                                ATGTGTAG   GACGGG CGT
                                    AAA     _
GAM982  LOC201685 3'  TACAACATCTTGTCCTTCAATT 26004      _   C    AG  T
          GCA                     TACA CATC TGTCC  CA TTGCA
                                |||| |||| |||||  || |||||
                                ATGT GTAG ACAGG  GT AACGT
                                  T   A    AA  T
GAM982  LOC51266  3'  ATCCTGTCCACCTCTTTGCA   26005         GCA_
                                ATCCTGTCCA    TTTGCA
                                ||||||||||    ||||||
                                TAGGACAGGT    AAACGT
                                    GGAG
GAM983  IDH3A    3'  CCAGTGAAAATGAAGTACT    26008      C       TAAT
                                TCAG GAAAATGAA    TGCT
                                |||| |||||||||    ||||
                                GGTC CTTTTACTT    ATGA
                                  A        C___
GAM983  P53AIP1   3'  TCAGCAAAGTGATGACGCT    26009        AA   ATAAT
                                TCAGCGAA  TGA    TGCT
                                ||||||||  |||    ||||
                                AGTCGTTT  ACT    GCGA
                                    C_   ACT__
GAM983  PTP4A2    5'  TCAGCGAAAATGCTGTGCT    26010          AATAAT
                                TCAGCGAAAATG     TGCT
                                ||||||||||||     ||||
                                AGTCGCTTTTAC     ACGA
                                      GAC___
GAM983  PTP4A2    5'  TCAGCGAAAATGCTGTGCT    26010          AATAAT
                                TCAGCGAAAATG     TGCT
                                ||||||||||||     ||||
                                AGTCGCTTTTAC     ACGA
                                      GAC___
GAM983  RAP1     3'  AGCAAAATGAATACAGC     26011     G       ATT
                                AGC AAAATGAATA   GC
                                ||| ||||||||||   ||
                                TCG TTTTACTTAT   CG
                                  _        GT_
GAM983  B3GNT5    3'  TCAGCAAATAAATAATTG    26012       AA
                                TCAGCGA  ATGAATAATTG
                                |||||||  ||||||||||
                                AGTCGTT  TATTTATTAAC
                                       __
GAM983  ESDN     3'  TCAGCGAATAAACCCATTG    26013       AA     A_
                                TCAGCGA  ATGAAT  ATTG
                                |||||||  ||||||  ||||
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                                AGTCGCT  TATTTG  TAAC
                                   __     GG
GAM983  ICK      3'  TCAGCTGACTAATTGC      26014       GAAAA   A
                                TCAGC    TGA TAATTGC
                                |||||    ||| |||||||
                                AGTCG    ACT ATTAACG
                                   _____  G
GAM983  KIAA0826 3'  TCAGCTAAAATGAAACAGCC   26015       G       TAATT
                                TCAGC AAAATGAA    GCT
                                ||||| ||||||||    |||
                                AGTCG TTTTACTT    CGG
                                   A       TGT__
GAM983  KIAA1211 3'  CAGTGAAATACTAATTGCT   26016     C    ATGAA
                                CAG GAAA    TAATTGCT
                                ||| ||||    ||||||||
                                GTC CTTT    ATTAACGA
                                  A   ATG__
GAM983  POPX1    3'  GAACAAATGAATAGTTGCT    26017     __       A
                                GAA  AATGAATA TTGCT
                                |||  |||||||| |||||
                                CTT  TTACTTAT AACGA
                                  GT       C
GAM983  PTD012   3'  CCAGTGAAATAAAAATTGCT   26018      C    A    T
                                TCAG GAAA TGAA AATTGCT
                                |||| |||| |||| |||||||
                                GGTC CTTT ATTT TTAACGA
                                  A   _   _
GAM983  SNX10    3'  AGTGAAAATGAAAAGGTTGCT  26019    C       TAA_
                                AG GAAAATGAA    TTGCT
                                || |||||||||    |||||
                                TC CTTTTACTT    AACGA
                                 A        TTCC
GAM983  UBE2D1   3'  TCAGCAAAAAATAATTTGGTTG 26020          _   ATAA_
            CT                    TCAGCGAAAA TGA     TTGCT
                                |||||||||| |||     |||||
                                AGTCGTTTTT ATT     AACGA
                                      T   AAACC
GAM983  LOC151610 3'  TCAGCAAAGATGCAATGCT    26021        A   AATAAT
                                TCAGCGAA ATG      TGCT
                                |||||||| |||      ||||
                                AGTCGTTT TAC      ACGA
                                    C   GTT___
GAM983  LOC91496  5'  TCAGCAAAAGTGGATAACC    26022        A  A
                                TCAGCGAAA TG ATAATT
                                ||||||||| || ||||||
                                AGTCGTTTT AC TATTGG
                                      C  C
GAM984  HOXB2    3'  GGATTAAACGCTAATTCAGTAA 26025          GGGCCAC
            T                    GGATTAGACG      CAGTAAT
                                ||||||||||      |||||||
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                                CCTAATTTGC      GTCATTA
                                     GATTAA_
GAM984  LOC150378 3'  GGATTAGATGGGCTTGAGT   26026        CG   CACC
                                GGATTAGA  GGGC   AGT
                                ||||||||  ||||   |||
                                CCTAATCT  CCCG   TCA
                                    A_   AAC_
GAM984  LOC220930 3'  AGATTTGGGCTACCAGTAA   26027     CG_   C
                                AGA   GGGC ACCAGTAA
                                |||   |||| ||||||||
                                TCT   CCCG TGGTCATT
                                  AAA   A
GAM985  ARHGEF12  3'  TCAAAACCCTCAATACCAGTGG 26030        _   AAA_  C
                                TCAAAACC TCAA   GG GG
                                |||||||| ||||   || ||
                                AGTTTTGG AGTT   TC CC
                                    G   ATGG  A
GAM985  DIA1     3'  CCAAAACCCTGAGGCGG     26031        CAAAA
                                TCAAAACCT    AGGCGG
                                |||||||||    ||||||
                                GGTTTTGGG    TCCGCC
                                     AC___
GAM985  EPHB2    3'  TCAAGTCCTCAAAAGGTAG   26032     AA      A  CG
                                TCAA  CCTCAAAA GG  G
                                ||||  |||||||| ||  |
                                AGTT  GGAGTTTT CC  C
                                  CA       _  AT
GAM985  FBN2     3'  AAAACCTCAAAATACTGG    26033          AG  _
                                AAAACCTCAAAA  GC GG
                                ||||||||||||  || ||
                                TTTTGGAGTTTT  TG CC
                                       A_  A
GAM985  GRM7     3'  CAAAACCTCAAGACA       26034         AAA
                                CAAAACCTCA   AGGCG
                                ||||||||||   |||||
                                GTTTTGGAGT   TCTGT
                                     ____
GAM985  MBNL     3'  TCCAAACCTCAAAAAAAGG   26035    A          C
                                TC AAACCTCAAAAAGG GG
                                || ||||||||||||| ||
                                AG TTTGGAGTTTTTTT CC
                                 G          _
GAM985  PABPN1   5'  TCAAAACCGTAAATCACGG   26036       TCA   AG
                                TCAAAACC   AAA  GCGG
                                ||||||||   |||  ||||
                                AGTTTTGG   TTT  TGCC
                                     CA_   AG
GAM985  SAS      3'  CAAAACCTTAAAGACTGG    26037       CAA     _
                                CAAAACCT   AAAGGC GG
                                ||||||||   |||||| ||
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                                GTTTTGGA  TTTCTG CC
                                    A__     A
GAM985  DOCK3    3'  TCAAACCCCAGAGGGCGG    26038      A    AAAA
                                TCAAA CCTCA   GGCGG
                                ||||| |||||   |||||
                                AGTTT GGGGT   CCGCC
                                  _    CTC_
GAM985  FLJ11560 3'  TCAGGACCCCAAAACAAGG   26039     AA       __
                                TCA  ACCTCAAAA  AGG
                                |||  |||||||||  |||
                                AGT  TGGGGTTTT  TCC
                                  CC        GT
GAM985  FLJ13263 3'  AAACCACAAAAAAGGTGG    26040      T     _ C
                                AAACC CAAAAA GG GG
                                ||||| |||||| || ||
                                TTTGG GTTTTT CC CC
                                   T     T  A
GAM985  FLJ23017 3'  AAAACCTCAGCAAGCGG     26041         AAA
                                AAAACCTCA   AGGCGG
                                |||||||||   ||||||
                                TTTTGGAGT   TTCGCC
                                     CG_
GAM985  FLJ23790 5'  CAAAACCTTCAAGAGGTGG   26042        CA  A   C
                                CAAAACCT  AA AGG GG
                                ||||||||  || ||| ||
                                GTTTTGGA  TT TCC CC
                                     AG  C   A
GAM985  KIAA1034 3'  CAAAAAAAAAAAAAGGCGG   26043      CCTC
                                CAAAA   AAAAAGGCGG
                                |||||   ||||||||||
                                GTTTT   TTTTTCCGCC
                                   TTTT
GAM985  KIAA1913 5'  AAAGCCCCGAAGAGGCGG    26044     A   A  A
                                AAA CCTC AA AGGCGG
                                ||| |||| || ||||||
                                TTT GGGG TT TCCGCC
                                  C   C  C
GAM985  MGC2835  3'  TCAGAACCTCAAACAGGGGG  26045     A       A  C
                                TCA AACCTCAAA AGG GG
                                ||| ||||||||| ||| ||
                                AGT TTGGAGTTT TCC CC
                                  C       G  C
GAM985  RGS19    5'  TCAGCGACCCAAAGGCGG    26046     AA_   CAA
                                TCA   ACCT   AAAGGCGG
                                |||   ||||   ||||||||
                                AGT   TGGG   TTTCCGCC
                                  CGC   ___
GAM985  SLC15A2  3'  TCAGCACCTCAAAAATTAGG  26047     AA       GGC
                                TCA  ACCTCAAAAA  GG
                                |||  ||||||||||  ||
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                                AGT  TGGAGTTTTT   CC
                                  CG         AAT
GAM985   LOC143381 3'  TCAAAAACCTCAGGAGG     26048        _     AAAA  C
                                TCAAAA CCTCA    GG GG
                                |||||| |||||    || ||
                                AGTTTT GGAGT    CC CC
                                   T     _____  T
GAM985   LOC254773 3'  AAAACTCTCAAAGGCGG      26049       _     AA
                                AAAAC CTCAA  AGGCGG
                                ||||| |||||  ||||||
                                TTTTG GAGTT  TCCGCC
                                  A     __
GAM985   LOC255704 3'  TCAAGACCTCAAAATTCAG    26050      A        AGG
                                TCAA ACCTCAAAA   CGG
                                |||| |||||||||   |||
                                AGTT TGGAGTTTT   GTC
                                  C        AA_
GAM986   B4GALT1   3'  AGTGGTTTGGGGTCCGACACGA 26053      CCG    C  A    G
            G                    AGTGG   GGGG CC GACG GAG
                                |||||   |||| || |||| |||
                                TCACC   CCCC GG CTGT CTC
                                   AAA   A  _    G
GAM986   CDK5     3'  GGCCGGGGGGTCCCGGG      26054         _  AGAC
                                GGCCGGGGGG CCC    GGG
                                |||||||| |||    |||
                                CCGGCCCCC GGG    CCC
                                     A  _____
GAM986   CGTHBA    5'  GGCCGGGGGGCGGAGGGG     26055         CCA  C
                                GGCCGGGGGC   GA GGG
                                ||||||||||   || |||
                                CCGGCCCCCG   CT CCC
                                     C__  C
GAM986   CKB      5'  GCGGCCGGGCGGGGGCGGG    26056         _ CCCAGA
                                GTGGCCGGG GG     CGGG
                                ||||||||| ||     ||||
                                CGCCGGCCC CC     GCCC
                                     G  CCC___
GAM986   CLCN6    3'  AGGGCCGGGGGGCCCATTGG    26057    T         GACG
                                AG GGCCGGGGGGCCCA    GG
                                || ||||||||||||    ||
                                TC CCGGCCCCCGGGT    CC
                                  _          AA__
GAM986   CLCN6    3'  AGGGCCGGGGGGCCCATTGG    26057    T         GACG
                                AG GGCCGGGGGGCCCA    GG
                                || ||||||||||||    ||
                                TC CCGGCCCCCGGGT    CC
                                  _          AA__
GAM986   CLCN6    3'  AGGGCCGGGGGGCCCATTGG    26057    T         GACG
                                AG GGCCGGGGGGCCCA    GG
                                || ||||||||||||    ||
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                                TC CCGGCCCCCGGGT   CC
                                 _          AA__
GAM986  COL6A2   3'  GTGACCGGGGGCTCGCCGCCAG 26058          _______
                                GTGGCCGGGGGC     CCAG
                                ||||||||||||     ||||
                                CACTGGCCCCCG     GGTC
                                      AGCGGC
GAM986  DYRK1B   3'  AGGGCCCCCAGATGGG     26059    T   GGGGG     C
                                AG GGCC    CCCAGA GGG
                                || ||||    |||||| |||
                                TC CCGG    GGGTCT CCC
                                 _  ______    A
GAM986  ENO1     3'  TGGTCGGGGGCCTCGAG     26060    C       CAGA
                                TGG CGGGGGCC    CGGG
                                ||| ||||||||    ||||
                                ACC GCCCCCGG    GCTC
                                  A       A___
GAM986  ESPN     3'  AGGGCTGGGGATACGGG     26061    T  C    CCCAG
                                AG GGC GGGGG    ACGGG
                                || ||| |||||    |||||
                                TC CCG CCCCT    TGCCC
                                 _  A    A____
GAM986  FGD1     5'  GGCCGGGGGCCGCTGGGGAG   26062          CAGAC
                                GGCCGGGGGCC    GGGAG
                                ||||||||||    |||||
                                CCGGCCCCCGG    CCCTC
                                      CGAC_
GAM986  HDAC7A   3'  AGTGGCCGAGGGGTCCCAGGGG 26063        _   _    AC
                                AGTGGCCG GGGG CCCAG  GGG
                                |||||||| |||| |||||  |||
                                TCACCGGC CCCC GGGTC  CCC
                                     T   A    __
GAM986  HDAC7A   3'  AGTGGCCGAGGGGTCCCAGGGG 26063        _   _    AC
                                AGTGGCCG GGGG CCCAG  GGG
                                |||||||| |||| |||||  |||
                                TCACCGGC CCCC GGGTC  CCC
                                     T   A    __
GAM986  HSPG2    3'  AGGGGCTGGGTGGAGGTGGG   26064    T  C  _  CCC  AC
                                AG GGC GGG GG   AG  GGG
                                || ||| ||| ||   ||  |||
                                TC CCG CCC CC   TC  CCC
                                 C   A   A ___  CA
GAM986  LASS2    5'  GGCTGGGCGTGACGGGAG    26065    CGG   CCA
                                GGC   GGGC   GACGGGAG
                                |||   ||||   ||||||||
                                CCG   CCCG   CTGCCCTC
                                  A__    CA_
GAM986  LDB1     5'  GGCCGGGGGGCCAGGGGG     26066          C  AC
                                GGCCGGGGGCC AG  GGG
                                |||||||||| ||  |||
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                                CCGGCCCCCGG TC  CCC
                                      _  C_
GAM986  LETM1    5'  GCGGCTGGCCTCGGACGGGAG  26067      CGGG   CA_
                                GTGGC   GGCC  GACGGGAG
                                |||||   ||||  ||||||||
                                CGCCG   CCGG  CTGCCCTC
                                  A___   AGC
GAM986  MAP3K10  5'  AGGGGCCGGGGGGCTGCGGGAG  26068   T       CCAGA
                                AG GGCCGGGGGGC    CGGGAG
                                || ||||||||||    ||||||
                                TC CCGGCCCCCG    GCCCTC
                                 C        AC___
GAM986  OTP      3'  GCGGCCGGGAGACGGG      26069         GGCCC
                                GTGGCCGGG    AGACGGG
                                |||||||||    |||||||
                                CGCCGGCCC    TCTGCCC
                                      _____
GAM986  PAX2     3'  GGCTGGGAGGGGATGGGAG   26070    C    CCCA  C
                                GGC GGGGG   GA GGGAG
                                ||| |||||   || |||||
                                CCG CCCTC   CT CCCTC
                                  A    CC__  A
GAM986  PAX2     3'  GGCTGGGAGGGGATGGGAG   26070    C    CCCA  C
                                GGC GGGGG   GA GGGAG
                                ||| |||||   || |||||
                                CCG CCCTC   CT CCCTC
                                  A    CC__  A
GAM986  PCDH7    5'  TGGCCGGGAATGGGGGTGGGAG 26071         CCCAGAC
                                TGGCCGGGGGG     GGGAG
                                ||||||||||     |||||
                                ACCGGCCCTT     CCCTC
                                      ACCCCCA
GAM986  PCDH7    5'  TGGCCGGGAATGGGGGTGGGAG 26071         CCCAGAC
                                TGGCCGGGGGG     GGGAG
                                ||||||||||     |||||
                                ACCGGCCCTT     CCCTC
                                      ACCCCCA
GAM986  PCDH7    5'  TGGCCGGGAATGGGGGTGGGAG 26071         CCCAGAC
                                TGGCCGGGGGG     GGGAG
                                ||||||||||     |||||
                                ACCGGCCCTT     CCCTC
                                      ACCCCCA
GAM986  PRG3     3'  AGAGGTTGGGGGACGGGA    26072    T  CCG   CCCA
                                AG GG   GGGG   GACGGGA
                                || ||   ||||   |||||||
                                TC CC   CCCC   CTGCCCT
                                 T  AA_   _____
GAM986  PTPRS    3'  GCGGCCGGGGCCGGTGGGG   26073         G  CAGAC
                                GTGGCCGGGG CC    GGG
                                |||||||||| ||    |||
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                                CGCCGGCCCC GG    CCC
                                      _ CCAC_
GAM986  PTPRS    3'  GCGGCCGGGGCCGGTGGGG   26073        G  CAGAC
                                GTGGCCGGGG CC    GGG
                                |||||||||| ||    |||
                                CGCCGGCCCC GG    CCC
                                      _ CCAC_
GAM986  PTPRS    3'  GCGGCCGGGGCCGGTGGGG   26073        G  CAGAC
                                GTGGCCGGGG CC    GGG
                                |||||||||| ||    |||
                                CGCCGGCCCC GG    CCC
                                      _ CCAC_
GAM986  PTPRS    3'  GCGGCCGGGGCCGGTGGGG   26073        G  CAGAC
                                GTGGCCGGGG CC    GGG
                                |||||||||| ||    |||
                                CGCCGGCCCC GG    CCC
                                      _ CCAC_
GAM986  SHB      3'  AGTGGCTGGGGGCTGGTTGGTG 26074      C     CCAGAC__
          GG                      AGTGGC GGGGGC       GGG
                                |||||| ||||||       |||
                                TCACCG CCCCCG       CCC
                                   A     ACCAACCA
GAM986  SIGLECL1 3'  AGAGGCCGGGGGGCGGGGA    26075    T       CCAGAC
                                AG GGCCGGGGGC     GGGA
                                || ||||||||||     ||||
                                TC CCGGCCCCCG     CCCT
                                 T        C_____
GAM986  SIGLECL1 3'  AGAGGCCGGGGGGCGGGGA    26075    T       CCAGAC
                                AG GGCCGGGGGC     GGGA
                                || ||||||||||     ||||
                                TC CCGGCCCCCG     CCCT
                                 T        C_____
GAM986  SYN3     3'  AGTGGCCGAGTGTGATGGG    26076         GGCCCA  C
                                AGTGGCCGGG     GA GGG
                                ||||||||||     || |||
                                TCACCGGCTC     CT CCC
                                      ACA___  A
GAM986  SYN3     3'  AGTGGCCGAGTGTGATGGG    26076         GGCCCA  C
                                AGTGGCCGGG     GA GGG
                                ||||||||||     || |||
                                TCACCGGCTC     CT CCC
                                      ACA___  A
GAM986  SYN3     3'  AGTGGCCGAGTGTGATGGG    26076         GGCCCA  C
                                AGTGGCCGGG     GA GGG
                                ||||||||||     || |||
                                TCACCGGCTC     CT CCC
                                      ACA___  A
GAM986  TEM6     3'  AGTGGCCAGGGGCCTGCGG    26077           CAGA
                                AGTGGCCGGGGGCC    CGG
                                ||||||||||||||    |||
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                                TCACCGGTCCCCGG   GCC
                                      AC__
GAM986  TUFT1    3'  AGTGGCCAGGGGCTTGGG    26078          CCAGAC
                                AGTGGCCGGGGGC    GGG
                                ||||||||||||     |||
                                TCACCGGTCCCCG    CCC
                                      AA____
GAM986  VAT1     3'  GTGGCGGGGCAGGGACGGGAG  26079     CG    CCA
                                GTGGC  GGGGC   GACGGGAG
                                |||||  |||||   ||||||||
                                CACCG  CCCCG   CTGCCCTC
                                   __    TCC
GAM986  BRD1     3'  GTGGGCGGGACGACGGGA    26080     C    G CCA
                                GTGG CGGGG C   GACGGGA
                                |||| ||||| |   |||||||
                                CACC GCCCT G   CTGCCCT
                                  C    _ ___
GAM986  C8orf17  3'  AGCGGCCGCGGTGGGCGGGAG  26081       G  GCCCAGA
                                AGTGGCCG GG      CGGGAG
                                |||||||| ||      ||||||
                                TCGCCGGC CC      GCCCTC
                                     G  ACCC___
GAM986  C9orf10  3'  AGTGGCTGGGGGCCCTGGCG   26082      C       AGA
                                AGTGGC GGGGGCCC   CG
                                ||||||| ||||||||   ||
                                TCACCG CCCCCGGG   GC
                                   A       ACC
GAM986  CCNI     5'  GGCCGGGGAGAGGCGGG     26083        CCC  A
                                GGCCGGGGG   AG CGGG
                                |||||||||   || ||||
                                CCGGCCCCT   TC GCCC
                                     C__  C
GAM986  CLSTN1   3'  GTGGCCGGGGGCACGGG     26084          CCAG
                                GTGGCCGGGGGC    ACGGG
                                ||||||||||||    |||||
                                CACCGGCCCCCG    TGCCC
                                          _____
GAM986  FLJ20413 3'  GTGGTCAGGGGTCAGGGG    26085     C     CC   AC
                                GTGG CGGGGG  CAG  GGG
                                |||| ||||||  |||  |||
                                CACC GTCCCC  GTC  CCC
                                  A     A_   __
GAM986  FLJ20552 3'  GGCTGGGGGCCCACGTGG    26086     C       AG  _
                                GGC GGGGGCCC  ACG GG
                                ||| ||||||||  ||| ||
                                CCG CCCCCGGG  TGC CC
                                  A       __   A
GAM986  FLJ21477 3'  GGTTGGGGGCTAGGGGAG    26087    CC     CC  AC
                                GG  GGGGGC  AG  GGGAG
                                ||  ||||||  ||  |||||
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                                CC  CCCCCG  TC  CCCTC
                                 AA     A_ __
GAM986  FLJ21742  3'  AGTGGCCGGGGGGCCAGGG   26088          C   GAC
                                AGTGGCCGGGGG CCA   GGG
                                |||||||||||| |||   |||
                                TCACCGGCCCCC GGT   CCC
                                       C  ___
GAM986  FLJ22415  5'  AGCTGGCGCCCGGACGGGA   26089    CG  G   A
                                GGC  GG GCCC GACGGGA
                                |||  || |||| |||||||
                                TCG  CC CGGG CTGCCCT
                                  A_ G   C
GAM986  GFPT1    5'  AGTGGCTGGCGGGATCGGG   26090      C  G  CCCA  _
                                AGTGGC GG GG    GA CGGG
                                |||||| || ||    || ||||
                                TCACCG CC CC    CT GCCC
                                   A  G  _____  A
GAM986  GMEB2    3'  GGCCGGGGGCCAGGGA     26091          CAGAC
                                GGCCGGGGGCC    GGGA
                                ||||||||||     ||||
                                CCGGCCCCCGG    CCCT
                                       T_____
GAM986  HIC2     3'  AGTGGCCGGGGGCCAGG     26092           CAGAC
                                AGTGGCCGGGGGCC    GGG
                                ||||||||||||||    |||
                                TCACCGGCCCCCGG    TCC
                                          ______
GAM986  KIAA0607  5'  AGAGGCTGGGGGCCCAGA    26093    T   C
                                AG GGC GGGGGCCCAGA
                                || ||| ||||||||||
                                TC CCG CCCCCGGGTCT
                                 T   A
GAM986  KIAA1115  5'  GGCCGGGGGCAGGGGG      26094          CC  AC
                                GGCCGGGGGC  AG  GGG
                                |||||||||  ||  |||
                                CCGGCCCCCG  TC  CCC
                                      __  C_
GAM986  MGC15906  5'  GCGGACCGAGGGCCCAGGTGGG 26095      _          AC
                                GTGG CCGGGGGCCCAG  GGG
                                ||||  ||||||||||||  |||
                                CGCC GGCTCCCGGGTC  CCC
                                  T          CA
GAM986  MGC29654  5'  AGGGCCGGGGGCAGGG      26096    T        CCAGAC
                                AG GGCCGGGGGC     GGG
                                || ||||||||||     |||
                                TC CCGGCCCCCG     CCC
                                 _        T_____
GAM986  MGC3020   3'  AGAGGCCGGAGAAAGGTGGG   26097    T       CCC  AC
                                AG GGCCGGGGGG   AG  GGG
                                || |||||||||   ||  |||
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                                TC CCGGCCTCT   TC  CCC
                                 T       T__  CA
GAM986  NAF1    5' AGTGCCGGGGGCCCGGACA   26098     G       A
                                AGTG CCGGGGGCCC GACG
                                |||| |||||||||| ||||
                                TCAC GGCCCCCGGG CTGT
                                  _       C
GAM986  NBL1    5' GCGGCCGGCAGGGCGGG    26099       __   CCAGAC
                                GTGGCCGG  GGGC    GGG
                                ||||||||  ||||    |||
                                CGCCGGCC  CCCG    CCC
                                    GT   ______
GAM986  NET-5   3' AGTGCCGGGGGTTCCTCCGGA 26100     G     C_ AGA
                                AGTG CCGGGGGG  CC  CGGG
                                |||| |||||||  ||  ||||
                                TCAC GGCCCCC  GG  GCCT
                                  _     AA  AG_
GAM986  NFASC   3' AGGGGCTGGGGGGCCAGGGGAG  26101   T  C     C  AC
                                AG GGC GGGGGCC AG  GGGAG
                                || ||| ||||||| ||  |||||
                                TC CCG CCCCCGG TC  CCCTC
                                 C  A     _ __
GAM986  NR6A1   3' GTAGCTGGGGGGCCCCGAGGGAG 26102      C      A  C
                                GTGGC GGGGGCCC GA GGGAG
                                ||||| |||||||| || |||||
                                CATCG CCCCCGGG CT CCCTC
                                   A      G  _
GAM986  NR6A1   3' GTAGCTGGGGGGCCCCGAGGGAG 26102      C      A  C
                                GTGGC GGGGGCCC GA GGGAG
                                ||||| |||||||| || |||||
                                CATCG CCCCCGGG CT CCCTC
                                   A      G  _
GAM986  NR6A1   3' GTAGCTGGGGGGCCCCGAGGGAG 26102      C      A  C
                                GTGGC GGGGGCCC GA GGGAG
                                ||||| |||||||| || |||||
                                CATCG CCCCCGGG CT CCCTC
                                   A      G  _
GAM986  PIPPIN  3' GTGGCCAGGGGTCTTGGGAG  26103        CCCAGAC
                                GTGGCCGGGGG     GGGAG
                                ||||||||||      |||||
                                CACCGGTCCCC     CCCTC
                                     AGAA___
GAM986  RAGA    5' AGGGGTCGGGGGGCTGCCGGG  26104   T  C     CCAGA
                                AG GG CGGGGGGC    CGGG
                                || || |||||||    ||||
                                TC CC GCCCCCG    GCCC
                                 C  A     ACG__
GAM986  RHOBTB1 5' AGGGCCGGGGGGGAGCGGG   26105   T      CCC  A
                                AG GGCCGGGGGG  AG CGGG
                                || |||||||||  || ||||
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                                TC CCGGCCCCC  TC GCCC
                                 _       C__  _
GAM986  SEC14L1  5'  GGCCGGGGAGGCGGGA     26106       GCCC  A
                                GGCCGGGG   AG CGGGA
                                ||||||||   || |||||
                                CCGGCCCC   TC GCCCT
                                    _____  C
GAM986  SEMA3C   5'  AGTGGCCGGAGGCCGGG    26107          CAGAC
                                AGTGGCCGGGGGCC   GGG
                                ||||||||||||||   |||
                                TCACCGGCCTCCGG   CCC
                                         ______
GAM986  STAG1    5'  GTCGCCGGGGGTTCGGGA   26108   G      CCCAGA
                                GT GCCGGGGG    CGGGA
                                || ||||||||    |||||
                                CA CGGCCCCC    GCCCT
                                 G      AA_____
GAM986  VTS58635 5'  AGGGGCTGGGGGCTCAGCCA  26109   T  C    C  A
                                AG GGC GGGGGC CAG CG
                                || ||| |||||| ||| ||
                                TC CCG CCCCCG GTC GT
                                 C  A    A  G
GAM986  LOC115110 3' AGGGGCCGGGGGTCCACAG   26110   T       _ _
                                AG GGCCGGGGG CC CAG
                                || |||||||| || |||
                                TC CCGGCCCCC GG GTC
                                 C       A  T
GAM986  LOC115574 3' AGGGGCTGGGGGAGCTGGG   26111   T  C   CCC  AC
                                AG GGC GGGGG  AG  GGG
                                || ||| |||||  ||  |||
                                TC CCG CCCCC  TC  CCC
                                 C  A    ___  GA
GAM986  LOC121536 5' GGCAGAGGGCTCAGGCGGGAG 26112    C    C  A
                                GGC GGGGGC CAG CGGGAG
                                ||| |||||| ||| ||||||
                                CCG CTCCCG GTC GCCCTC
                                  T    A  C
GAM986  LOC131583 3' AGTGCTGGGGCGGGAGCGGG  26113    GCCG   CC_ A
                                AGTG   GGGGC  AG CGGG
                                ||||   |||||  || ||||
                                TCAC   CCCCG  TC GCCC
                                  GA__    CCC  _
GAM986  LOC132228 3' GTAGCTGGGGGCCCGGACACTT 26114     C      A  ____
           GGG                    GTGGC GGGGGCCC GAC   GGG
                                |||||  |||||||| |||   |||
                                CATCG CCCCCGGG CTG   CCC
                                   A      C  TGAA
GAM986  LOC146378 3' GGTCGGGGGGACCCTGGGAG  26115   C    _  AGAC
                                GG CGGGGG CCC   GGGAG
                                || |||||| |||   |||||
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                                CC GCCCCC GGG    CCCTC
                                 A     T  A___
GAM986  LOC146958 5'  AGGGCTGGGGGCCTCCAGGGAG 26116    T  C      CAGAC
                                AG GGC GGGGGCC     GGGAG
                                || ||| |||||||     |||||
                                TC CCG CCCCCGG     CCCTC
                                 _  A      AGGT_
GAM986  LOC155036 5'  AGTGGTGGACCAGGCGGGA   26117      CCGG    C  A
                                AGTGG   GGGCC AG CGGGA
                                |||||   ||||| || |||||
                                TCACC   CCTGG TC GCCCT
                                   A___    _  C
GAM986  LOC221272 3'  AGTAGCCACTTTCTGGATGGGA 26118        GGGGCCCA  C
           G                     AGTGGCCG       GA GGGAG
                                |||||||       || |||||
                                TCATCGGT       CT CCCTC
                                     GAAAGAC_  A
GAM986  LOC253991 5'  GTGACCGGGCGGCGGCGGGAG  26119         _  CCAGA
                                GTGGCCGGG GGC    CGGGAG
                                ||||||||| |||    ||||||
                                CACTGGCCC CCG    GCCCTC
                                     G  CC___
GAM986  LOC255536 3'  GCGGCCGGGGGACCTCGGG   26120          C  AGA
                                GTGGCCGGGGG CC   CGGG
                                |||||||||| ||   ||||
                                CGCCGGCCCCC GG   GCCC
                                       T  A__
GAM986  LOC256072 3'  TGGTCGGGGGCCTCGAG    26060    C      CAGA
                                TGG CGGGGGCC   CGGG
                                ||| ||||||||   ||||
                                ACC GCCCCCGG   GCTC
                                  A       A___
GAM986  LOC256158 5'  GGCCGGGGGCCGTGAGGAG   26121          CAGAC
                                GGCCGGGGGCC    GGGAG
                                ||||||||||     |||||
                                CCGGCCCCCGG    TCCTC
                                       CAC__
GAM986  LOC51133  5'  GCGGCCGGAGGGCGGG      26122        _   CCAGAC
                                GTGGCCGG GGGC     GGG
                                |||||||| ||||     |||
                                CGCCGGCC CCCG     CCC
                                     T   _______
GAM986  LOC91149  5'  GTGGCCGGGGTCCCCGAGCGGG 26123         G  A  _
                                GTGGCCGGGG CCC GA CGGG
                                |||||||||| ||| || ||||
                                CACCGGCCCC GGG CT GCCC
                                       A  G  C
GAM987  SRGAP2    3'  GAACTACAGAAAATAATAA   26126     ATT
                                GAAT   TAGAAAATAATAA
                                ||||   ||||||||||||
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                                CTTG  GTCTTTTATTATT
                                  AT_
GAM987  MRS2L    3' ATACAAGAAAATAATAAA   26127     TT
                                ATAT  AGAAAATAATAAA
                                ||||  ||||||||||||
                                TATG  TCTTTTATTATTT
                                  T_
GAM988  ADAM19   3' CATGCAGTCACTATGGC    26130    C  CC
                                CA GTA  TCACTATGGC
                                || |||  ||||||||||
                                GT CGT  AGTGATACCG
                                 A  C_
GAM988  PPP2R5A  3' TACAATATACTATGGCCAT   26131     C  CCTC
                                TACA GTA   ACTATGGCCAT
                                |||| |||   ||||||||||
                                ATGT TAT   TGATACCGGTA
                                  _  A___
GAM988  SOX13    3' TACAGTGTCCCCTGGCCAT   26132     C_ A   ACTA
                                TACA  GT CCTC   TGGCCAT
                                ||||  || ||||   |||||||
                                ATGT  CA GGGG   ACCGGTA
                                  CA  _   _____
GAM988  FOXP1    5' TAACGTGTCTCACAGCCAT   26133   C   AC    TAT
                                A ACGT  CTCAC   GGCCAT
                                | ||||  |||||  ||||||
                                A TGCA  GAGTG   TCGGTA
                                 T   CA   ___
GAM988  KIAA0150 3' ACACGTACACGTGGCTAT    26134       CTC  TA   C
                                ACACGTAC   AC  TGGC AT
                                ||||||||   ||  |||| ||
                                TGTGCATG   TG  ACCG TA
                                     ___  C_   A
GAM988  MGC5457  3' TACACGTACCTGCCACCATG  26135         __
                                TACACGTACCT  CACTATG
                                ||||||||||  |||||||
                                ATGTGCATGGA  GTGGTAC
                                       CG
GAM988  UBE2G1   3' TACATATACTGCCATGGCCAT 26136     CG   CTCA
                                TACA  TAC   CTATGGCCAT
                                ||||  |||   ||||||||||
                                ATGT  ATG   GGTACCGGTA
                                  AT   AC__
GAM988  ZNF397   3' CGTGGTCCCATGGCCAT    26137    ACC  A
                                CGT   TC CTATGGCCAT
                                |||   || ||||||||||
                                GCA   AG GGTACCGGTA
                                 CC_  _
GAM988  LOC125488 3' TACAGGTACCTCATCATG   26138     C       C
                                TACA GTACCTCA TATG
                                |||| |||||||| ||||
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                                ATGT CATGGAGT GTAC
                                  C       A
GAM988  LOC152633 5'  TACACGTGCTCACGCATG    26139        AC    _
                                TACACGT  CTCAC TATG
                                |||||||  ||||| ||||
                                ATGTGCA  GAGTG GTAC
                                    C_    C
GAM988  LOC196996 3'  ACACGTACTTCAGATCTCTCAT 26140         C   CTATGGC
          A                      ACACGTAC TCA      CATA
                                |||||||| |||      ||||
                                TGTGCATG AGT      GTAT
                                     A   CTAGAGA
GAM988  LOC199786 3'  GCACTGCCACGCCTGGCCATA  26141      C_    TA_
                                GTAC  TCAC   TGGCCATA
                                ||||  ||||   ||||||||
                                CGTG  GGTG   ACCGGTAT
                                  AC    CGG
GAM989  CDS2     3'  TACATTCTGCAGGATTTTGGTG 26144          _    CG_ _  A
          TGGAT                    TACATTCTG AGGAT   GG GT GAT
                                |||||||||  |||||   || || |||
                                ATGTAAGAC TCCTA   CC CA CTA
                                     G    AAA  A  C
GAM989  GYG2     3'  TAATTCTGAATAGGGTAG    26145   C       GATC
                                A ATTCTGAG    GGGGTAG
                                | ||||||||    |||||||
                                A TAAGACTT    TCCCATC
                                 T       A___
GAM989  NUP98    3'  TTCTGGAAGGGGTAGA      26146       A   TC
                                TTCTG GGA  GGGGTAGA
                                |||||  |||  ||||||||
                                AAGAC CTT  CCCCATCT
                                   _  __
GAM989  PCDHB7   3'  TTCTGAGACTAGGGTAG     26147        G  CG
                                TTCTGAG AT  GGGTAG
                                |||||||  ||  ||||||
                                AAGACTC TG  CCCATC
                                    _  AT
GAM989  LOC92230  5'  CATTCTGAGGGTTAAAGAT   26148          ATC_
                                CATTCTGAGG    GGGGT
                                |||||||||    |||||
                                GTAAGACTCC    TTCTA
                                     CAAT
GAM990  ACP2     3'  GAGGCCCAACCCAGGATCT    26151        G G     C
                                GGGGCCCG G TTAGGA CT
                                |||||||| | |||||| ||
                                CTCCGGGT T GGTCCT GA
                                    _ G     A
GAM990  ANK1     5'  AGGGGCCCGCCGAAGGGCCT   26152         GGGTT   A
                                AGGGGCCCG    AGG CCT
                                |||||||||    ||| |||
```

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                                TCCCCGGGC    TCC GGA
                                     GGCT_  C
GAM990  ANK1     5' AGGGGCCCGCCGAAGGGCCT  26152       GGGTT  A
                                AGGGGCCCG    AGG CCT
                                |||||||||    ||| |||
                                TCCCCGGGC    TCC GGA
                                     GGCT_  C
GAM990  ARHGEF7  5' GGGGCTCGGGGTAGACCT   26153     C    TA
                                GGGGC CGGGGT  GGACCT
                                ||||| ||||||  ||||||
                                CCCCG GCCCCA  TCTGGA
                                  A     __
GAM990  ATP2B3   3' GGGGCCCGGAGGCGCTCCT   26154       _  TAGGA
                                GGGGCCCGG GGT    CCT
                                ||||||||| |||    |||
                                CCCCGGGCC CCG    GGA
                                     T  CGA__
GAM990  B3GNT3   5' AGGGTCTGGGGTCGGCCT   26155    GCCC    A  A
                                AGGG   GGGGTT GG CCT
                                ||||   |||||| || |||
                                TCCC   CCCCAG CC GGA
                                  AGA_    _ _
GAM990  BAZ2A    3' AGGGGCTGCCCCAGGACCT   26156     __ GGGG
                                AGGGGC  CC   TTAGGACCT
                                ||||||  ||   |||||||||
                                TCCCCG  GG   GGTCCTGGA
                                  AC  _____
GAM990  BCL2L2   5' AGGAGCCCCCAGCTGGGGCCT 26157       GG   A  A
                                AGGGGCCC  GGTT GG CCT
                                ||||||||  |||| || |||
                                TCCTCGGG  TCGA CC GGA
                                     GG   C  C
GAM990  BDP1     5' GGGGCCCGGGGAGGCAGCCT  26158        TTA_  A
                                GGGGCCCGGGG   GG CCT
                                ||||||||||   || |||
                                CCCCGGGCCCC   TC GGA
                                      TCCG  _
GAM990  BRCA1    3' GGGGCTAGGGAAGACCT    26159     CC   TT
                                GGGGC  GGGG  AGGACCT
                                |||||  ||||  |||||||
                                CCCCG  TCCC  TTCTGGA
                                  A_   __
GAM990  BRCA1    3' GGGGCTAGGGAAGACCT    26159     CC   TT
                                GGGGC  GGGG  AGGACCT
                                |||||  ||||  |||||||
                                CCCCG  TCCC  TTCTGGA
                                  A_   __
GAM990  BRCA1    3' GGGGCTAGGGAAGACCT    26159     CC   TT
                                GGGGC  GGGG  AGGACCT
                                |||||  ||||  |||||||
```

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                                CCCCG TCCC TTCTGGA
                                  A_   __
GAM990  BRCA1    3' GGGGCTAGGGAAGACCT    26159     CC   TT
                                GGGGC GGGG AGGACCT
                                ||||| |||| |||||||
                                CCCCG TCCC TTCTGGA
                                  A_   __
GAM990  BRCA1    3' GGGGCTAGGGAAGACCT    26159     CC   TT
                                GGGGC GGGG AGGACCT
                                ||||| |||| |||||||
                                CCCCG TCCC TTCTGGA
                                  A_   __
GAM990  BRCA1    3' GGGGCTAGGGAAGACCT    26159     CC   TT
                                GGGGC GGGG AGGACCT
                                ||||| |||| |||||||
                                CCCCG TCCC TTCTGGA
                                  A_   __
GAM990  BRCA1    3' GGGGCTAGGGAAGACCT    26159     CC   TT
                                GGGGC GGGG AGGACCT
                                ||||| |||| |||||||
                                CCCCG TCCC TTCTGGA
                                  A_   __
GAM990  BRCA1    3' GGGGCTAGGGAAGACCT    26159     CC   TT
                                GGGGC GGGG AGGACCT
                                ||||| |||| |||||||
                                CCCCG TCCC TTCTGGA
                                  A_   __
GAM990  BRCA1    3' GGGGCTAGGGAAGACCT    26159     CC   TT
                                GGGGC GGGG AGGACCT
                                ||||| |||| |||||||
                                CCCCG TCCC TTCTGGA
                                  A_   __
GAM990  BRCA1    3' GGGGCTAGGGAAGACCT    26159     CC   TT
                                GGGGC GGGG AGGACCT
                                ||||| |||| |||||||
                                CCCCG TCCC TTCTGGA
                                  A_   __
GAM990  BRCA1    3' GGGGCTAGGGAAGACCT    26159     CC   TT
                                GGGGC GGGG AGGACCT
                                ||||| |||| |||||||
                                CCCCG TCCC TTCTGGA
                                  A_   __
GAM990  C21orf2  3' AAGGGCCCAGGGACC      26160        TTAGG
                                AGGGGCCCGGGG   ACC
                                ||||||||||||   |||
                                TTCCCGGGTCCC   TGG
                                        _____
GAM990  CACNG3   3' AGGATGGAGGGGTTAGGAC  26161    GCCC
                                AGGG   GGGGTTAGGAC
                                ||||   ||||||||||
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                                TCCT   CCCCAATCCTG
                                  ACCT
GAM990  CDK5R2   5'  GGGACCCGGCGGTGGGGGGCCT 26162        _  TA_ A
                                GGGGCCCGG GGT  GG CCT
                                ||||||||| |||  || |||
                                CCCTGGGCC CCA  CC GGA
                                     G  CCC  C
GAM990  CEP2     3'  AGGGCGCCTGGGCTGAC    26163     _ G    AG
                                GGGGC CC GGGTT  GAC
                                ||||| || |||||  |||
                                TCCCG GG CCCGA  CTG
                                  C  A   __
GAM990  CLDN3    5'  AGGGGCCGGGGCCGCTGGGCCT 26164      C    A__ A
                                AGGGGCC GGGGTT  GG CCT
                                ||||||| ||||||  || |||
                                TCCCCGG CCCCGG  CC GGA
                                   _    CGA  C
GAM990  CTSD     3'  AGGGCCCGGGAGGACGGCCT  26165        TTA_ A
                                GGGGCCCGGGG   GG CCT
                                ||||||||||   || |||
                                TCCCGGGCCCT   CC GGA
                                     CCTG  _
GAM990  DGKG     5'  GGTGGCCCGGGGCGCTCCT   26166   _      TAGGA
                                GG GGCCCGGGGT   CCT
                                || ||||||||||   |||
                                CC CCGGGCCCCG   GGA
                                 A       CGA__
GAM990  DTX1     5'  AGGAGGCCTGGGCCACAGCCT  26167    _  CG    _ A
                                AGG GGCC  GGGTTA GG CCT
                                ||| ||||  |||||| || |||
                                TCC CCGG  CCCGGT TC GGA
                                  T   A_    G  _
GAM990  DUSP4    5'  GGTGGCCTAACCAGGACCT   26168   _  CG GG
                                GG GGCC  G  TTAGGACCT
                                || ||||  |  |||||||||
                                CC CCGG  T  GGTCCTGGA
                                 A   AT __
GAM990  FBXO7    5'  GGCGGCCCGAGGGGCC     26169   _      TTA  A
                                GG GGCCCGGGG  GG CC
                                || |||||||||  || ||
                                CC CCGGGCTCC  CC GG
                                 G       ___ _
GAM990  FGR      3'  AGGGGTCCAGCCAAGAC    26170      C  GG
                                AGGGG CC  GGTTAGGAC
                                ||||| ||  |||||||||
                                TCCCC GG  TCGGTTCTG
                                  A  __
GAM990  FXYD7    3'  AGGGGCCAGGGGGACGGATCT  26171       C   TTA  C
                                AGGGGCC GGGG  GGA CT
                                ||||||| ||||  ||| ||
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                                TCCCCGG CCCC   CCT GA
                                   T   CTG   A
GAM990  GALR1    5'  GGAGCCCGGAGCTGGACCT   26172          A
                                GGGGCCCGGGGTT GGACCT
                                |||||||||||| ||||||
                                CCTCGGGCCTCGA CCTGGA
                                                _
GAM990  GNAZ     3'  AGGGTCCCAGCAGGGCCT    26173     G    GGT   A
                                AGGG CCCGG   TAGG CCT
                                |||| |||||   |||| |||
                                TCCC GGGTC   GTCC GGA
                                  A    ___   C
GAM990  GYS1     3'  GGTGGCCCGCATGCCGGGCCT 26174    _    GG_ TA  A
                                GG GGCCCG   GT  GG CCT
                                || ||||||   ||  || |||
                                CC CCGGGC   CG  CC GGA
                                 A     GTA  GC  _
GAM990  H4FM     3'  AGGGGCCCTAAAAAGGGCCT  26175       GG  TT   A
                                AGGGGCCC  GG  AGG CCT
                                ||||||||  ||  ||| |||
                                TCCCCGGG  TT  TCC GGA
                                    A_  TT   C
GAM990  HNRPDL   5'  GGGGCGCGGCGGGGCCT    26176     C   _  TTA  A
                                GGGGC CGG GG   GG CCT
                                ||||| ||| ||   || |||
                                CCCCG GCC CC   CC GGA
                                  C   G  ___  _
GAM990  HOXC6    3'  GGGGTCCAGAGCTGAC     26177     C      AG
                                GGGG CCGGGGTT  GAC
                                |||| ||||||||  |||
                                CCCC GGTCTCGA  CTG
                                  A      __
GAM990  HYAL1    5'  GGGGCCTAAGCAGGGCCT    26178      CG  GT   A
                                GGGGCC  GG  TAGG CCT
                                ||||||  ||  |||| |||
                                CCCCGG  TC  GTCC GGA
                                   AT  __   C
GAM990  HYAL1    5'  GGGGCCTAAGCAGGGCCT    26178      CG  GT   A
                                GGGGCC  GG  TAGG CCT
                                ||||||  ||  |||| |||
                                CCCCGG  TC  GTCC GGA
                                   AT  __   C
GAM990  JUP      3'  AGGGGTCAGGGGCTCGGTGGAC 26179     CCC    A___
           CT                    AGGGG  GGGGTT   GGACCT
                                |||||  ||||||   ||||||
                                TCCCC  CCCCGA   CCTGGA
                                  AGT    GCCA
GAM990  KIAA0857 3'  AGGGGTCAGGGAGCAGCCT   26180     CC    TTA  A
                                AGGGG  CGGGG   GG CCT
                                |||||  |||||   || |||
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                                TCCCC  GTCCC   TC GGA
                                  A_    TCG  _
GAM990  KLK10   5'  AGGGGCCCTGGAATACAGG   26181       _   _
                                AGGGGCCC GGGGT TAGG
                                |||||||| ||||| ||||
                                TCCCCGGG CCTTA GTCC
                                   A    T
GAM990  LDB1    5'  GGGGCCAGGGGGCCGGCCT   26182      C   TTA  A
                                GGGGCC GGGG   GG CCT
                                |||||| ||||   || |||
                                CCCCGG CCCC   CC GGA
                                   T   CGG  _
GAM990  MAPK4   3'  GGGGCCAGGAGACTGGGA    26183      C   _  A
                                GGGGCC GGGG TT GGA
                                |||||| |||| || |||
                                CCCCGG CCTC GA CCT
                                   T   T  C
GAM990  MEOX1   3'  AGGAGGCCTGGCTGACCT    26184    _   CGG   AG
                                AGG GGCC   GGTT  GACCT
                                ||| ||||   ||||  |||||
                                TCC CCGG   CCGA  CTGGA
                                  T   A__   __
GAM990  MEOX1   3'  AGGAGGCCTGGCTGACCT    26184    _   CGG   AG
                                AGG GGCC   GGTT  GACCT
                                ||| ||||   ||||  |||||
                                TCC CCGG   CCGA  CTGGA
                                  T   A__   __
GAM990  MMP2    3'  AGGGGTCTGGAGTGGCCACCT  26185      CCC    TA __
                                AGGGG   GGGGT  GG  ACCT
                                |||||   |||||  ||  ||||
                                TCCCC   CCTCA  CC  TGGA
                                   AGA    __  GG
GAM990  MUC4    5'  AGGGGCCAGGGAACC       26186       C   TTAG
                                AGGGGCC GGGG   GACC
                                ||||||| ||||   ||||
                                TCCCCGG TCCC   TTGG
                                   _   ____
GAM990  MUC4    5'  AGGGGCCAGGGAACC       26186       C   TTAG
                                AGGGGCC GGGG   GACC
                                ||||||| ||||   ||||
                                TCCCCGG TCCC   TTGG
                                   _   ____
GAM990  NOL3    3'  GGGGCTAGGTTTGGGATCT   26187      CCG   A_  C
                                GGGGC   GGGTT  GGA CT
                                |||||   |||||  ||| ||
                                CCCCG   TCCAA  CCT GA
                                   A__    AC   A
GAM990  NPAS1   5'  GGGGCCAGGGGCAACGCT    26188      C   TAG  _
                                GGGGCC GGGGT   GAC CT
                                |||||| |||||   ||| ||
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                                CCCCGG CCCCG  TTG GA
                                   T    ___  C
GAM990  P2RX3    5' GGGGCCCAGTGGTGGCCT   26189       _  TA  A
                                GGGGCCCGG GGT  GG CCT
                                ||||||||| |||  || |||
                                CCCCGGGTC CCA  CC GGA
                                    A  __ _
GAM990  PCOLCE   3' AGGGGCCGGGGCTGGCCT   26190      C    A  A
                                AGGGGCC GGGGTT GG CCT
                                ||||||| |||||| || |||
                                TCCCCGG CCCCGA CC GGA
                                  _    _ _
GAM990  PIGR     3' AGGGACCCATGAGGACCT   26191       GGGTT
                                AGGGGCCCG    AGGACCT
                                |||||||||    |||||||
                                TCCCTGGGT    TCCTGGA
                                    AC___
GAM990  PTBP1    3' GGGGCCCGGCCGTGGGGGCCT 26192       G_  TA  A
                                GGGGCCCGG  GT  GG CCT
                                |||||||||  ||  || |||
                                CCCCGGGCC  CA  CC GGA
                                    GG  CC  C
GAM990  PTBP1    3' GGGGCCCGGCCGTGGGGGCCT 26192       G_  TA  A
                                GGGGCCCGG  GT  GG CCT
                                |||||||||  ||  || |||
                                CCCCGGGCC  CA  CC GGA
                                    GG  CC  C
GAM990  RET      3' AGGGGTCTGGGGGAACCT   26193     CCC   TTA
                                AGGGG  GGGG  GGACCT
                                |||||  ||||  ||||||
                                TCCCC  CCCC  CTTGGA
                                  AGA  ___
GAM990  SLC1A5   5' GGGGCCGGGAAGCGGACCT   26194      C   TTA
                                GGGGCC GGGG  GGACCT
                                |||||| ||||  ||||||
                                CCCCGG CCCT  CCTGGA
                                   _  TCG
GAM990  SLC1A5   5' GGGGCCGGGAAGCGGACCT   26194      C   TTA
                                GGGGCC GGGG  GGACCT
                                |||||| ||||  ||||||
                                CCCCGG CCCT  CCTGGA
                                   _  TCG
GAM990  SLC22A12 5' GGGGCCAGGGCCGGCCT    26195      C    A  A
                                GGGGCC GGGGTT GG CCT
                                |||||| |||||| || |||
                                CCCCGG TCCCGG CC GGA
                                  _    _ _
GAM990  SORCS2   3' GGGGTCTGGGGGGCAGAACCT 26196    CCC_   T
                                GGGG   GGGG TAGGACCT
                                ||||   |||| ||||||||
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                                CCCC   CCCC GTCTTGGA
                                  AGAC   C
GAM990  SOX10   3'  GGAGCCAAGGGTTAGGGCCT  26197      C      A
                                GGGGCC GGGGTTAGG CCT
                                |||||| ||||||||| |||
                                CCTCGG TCCCAATCC GGA
                                   T       C
GAM990  SOX12   3'  AGGGGTCCGGAGGACTCT   26198     C   GGTT   _
                                AGGGG CCGG   AGGAC CT
                                ||||| ||||   ||||| ||
                                TCCCC GGCC   TCCTG GA
                                  A   ____   A
GAM990  TCF7    3'  GGGACCCGGGGCAGCCT    26199         TA  A
                                GGGGCCCGGGGT  GG CCT
                                ||||||||||||  || |||
                                CCCTGGGCCCCG  TC GGA
                                       __ _
GAM990  TCIRG1  3'  AGGAGGTCTGGCAGGACCT  26200     CCCGG  T
                                AGGGG   GGT AGGACCT
                                |||||   ||| |||||||
                                TCCTC   CCG TCCTGGA
                                  CAGA_  _
GAM990  TCIRG1  3'  AGGAGGTCTGGCAGGACCT  26200     CCCGG  T
                                AGGGG   GGT AGGACCT
                                |||||   ||| |||||||
                                TCCTC   CCG TCCTGGA
                                  CAGA_  _
GAM990  THRA    5'  GGGGCCCGGGCCGCCCGCCT  26201        __  AGGA
                                GGGGCCCGGG  GTT   CCT
                                ||||||||||  |||   |||
                                CCCCGGGCCC  CGG   GGA
                                     GG  GC__
GAM990  TNFRSF8 3'  AGGGGCCCCGGGAGCTGGCCT 26202       _  _  A  A
                                AGGGGCCC GGG GTT GG CCT
                                |||||||| ||| ||| || |||
                                TCCCCGGG CCC CGA CC GGA
                                    G  T  _ _
GAM990  VIPR1   3'  GGGGCCGGGGGCAGCCT    26203      C   TA  A
                                GGGGCC GGGGT  GG CCT
                                |||||| |||||  || |||
                                CCCCGG CCCCG  TC GGA
                                  C    __ _
GAM990  VIPR2   3'  AGGGGCCCGCAGGCC      26204       GGGT   A
                                AGGGGCCCG   TAGG CC
                                |||||||||   |||| ||
                                TCCCCGGGC   GTCC GG
                                      ____   _
GAM990  WNT3A   3'  GGAGCCCGGGCAGGGCGGGCCT 26205        GTTA__  A
                                GGGGCCCGGG    GG CCT
                                ||||||||||    || |||
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                                CCTCGGGCCC     CC GGA
                                      GTCCCG  C
GAM990  ACAS2L   3'  AGGGACCCGGCTCACTGGGCCT 26206         GGTTA_  A
                                AGGGGCCCGG     GG CCT
                                ||||||||||     || |||
                                TCCCTGGGCC     CC GGA
                                      GAGTGA  C
GAM990  ADAR3    3'  AGGGTTCTGGGGCCAGCGATCT 26207      GCCC       _ C
                                AGGG    GGGGTTAG GA CT
                                ||||    |||||||| || ||
                                TCCC    CCCCGGTC CT GA
                                  AAGA       G  A
GAM990  AP1M2    3'  AGGGGCCAGCGGGACC      26208        CGG   TA
                                AGGGGCC   GGT  GGACC
                                |||||||   |||  |||||
                                TCCCCGG   TCG  CCTGG
                                   ___   C_
GAM990  ARTN     5'  GGGGCCCGAGGGACC       26209          TTAG
                                GGGGCCCGGGG   GACC
                                ||||||||||    ||||
                                CCCCGGGCTCC    CTGG
                                      ____
GAM990  BAT8     3'  AGGGCCTGGCTGGGATCT    26210       CGG    A   C
                                GGGGCC   GGTT GGA CT
                                ||||||   |||| ||| ||
                                TCCCGG   CCGA CCT GA
                                   A__    C   A
GAM990  C12orf6  5'  AGGGGCTAGCCGCGGGGCCT   26211       ___   G  TTA  A
                                AGGGGC   CCG GG   GG CCT
                                ||||||   ||| ||   || |||
                                TCCCCG   GGC CC   CC GGA
                                   ATC   G  ___  _
GAM990  C16orf5  3'  AGGGGCCCGGCACTTAGGTCCT 26212          __________   TAGG
           AAC                    GGGGCCCGG       GGT    AC
                                |||||||||       |||    ||
                                CCCCGGGCC       CCA    TG
                                      GTGAAIIIT   GGAT
GAM990  C19orf7  3'  AGGGTCCCCATTGTTGGGGCCT 26213      G_    GG   A  A
                                AGGG  CCCG  GTT GG CCT
                                ||||  ||||  ||| || |||
                                TCCC  GGGT  CAA CC GGA
                                  AG    AA   C  C
GAM990  C20orf27 3'  AGGGGCCCGGGGGCAGGCGGGGC 26214           TA__  A_
           CT                    AGGGGCCCGGGGT   GG  CCT
                                ||||||||||||    ||  |||
                                TCCCCGGGCCCCG    CC  GGA
                                      TCCG  CC
GAM990  C21orf51 3'  AGGTGGTCCCAGTTAGGACCT  26215     _  _   GG
                                AGG GG CCC  GGTTAGGACCT
                                ||| || |||  ||||||||||
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                                TCC CC GGG  TCAATCCTGGA
                                  A A  __
GAM990  C21orf69  3'  AGGAGCCCCCAGAAGGACCT  26216       GG  TT
                                AGGGGCCC  GG  AGGACCT
                                ||||||||  ||  |||||||
                                TCCTCGGG  TC  TCCTGGA
                                    GG  T_
GAM990  C22orf20  5'  GGGGCGCGGGTTAGGATCT  26217     C   G    C
                                GGGGC CGGG TTAGGA CT
                                ||||| |||| |||||| ||
                                CCCCG GCCC AATCCT GA
                                  C   _    A
GAM990  C5orf6    3'  GGGGACCAATATAGGGCCT  26218     C   GGT   A
                                GGGG CCGG   TAGG CCT
                                |||| ||||   |||| |||
                                CCCC GGTT   ATCC GGA
                                  T   AT_   C
GAM990  CABP2     5'  GGTGGCCCGGGTGGGCCT  26219   _     GTTA  A
                                GG GGCCCGGG   GG CCT
                                || ||||||||   || |||
                                CC CCGGGCCC   CC GGA
                                 A      AC__  _
GAM990  CABP2     5'  GGTGGCCCGGGTGGGCCT  26219   _     GTTA  A
                                GG GGCCCGGG   GG CCT
                                || ||||||||   || |||
                                CC CCGGGCCC   CC GGA
                                 A      AC__  _
GAM990  CACNG4    3'  AGGGGCCCTGGCAGGCCT  26220       GG  T   A
                                AGGGGCCC  GGT AGG CCT
                                ||||||||  ||| ||| |||
                                TCCCCGGG  CCG TCC GGA
                                    A_  _  _
GAM990  CLSTN3    3'  AGGGGCCGGGGCTGCAGGACCT 26221       C    __
                                AGGGGCC GGGGT  TAGGACCT
                                ||||||| |||||  ||||||||
                                TCCCCGG CCCCG  GTCCTGGA
                                    _   AC
GAM990  CNK2      3'  AGGAGAAAGTTAGGA      26222      CCC
                                AGGGG  GGGGTTAGGA
                                |||||  ||||||||||
                                TCCTC  TTTCAATCCT
                                   ___
GAM990  DEFCAP    5'  AGGAGCCCAGAGGGGCCT   26223         TTA  A
                                AGGGGCCCGGGG  GG CCT
                                ||||||||||||  || |||
                                TCCTCGGGTCTC  CC GGA
                                      C__  _
GAM990  DGKZ      3'  GGGGCCCAGGAAGCC      26224         TTA  A
                                GGGGCCCGGGG  GG CC
                                ||||||||||  || ||
```

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                                CCCCGGGTCCT   TC GG
                                      ___  _
GAM990  DKFZp434G171 3'  AGGGCCCAAGTAGGAC      26225          GT
                                GGGGCCCGGG  TAGGAC
                                ||||||||||  ||||||
                                TCCCGGGTTC  ATCCTG
                                     __
GAM990  DKFZp547F072 5'  GGGGCCCAGGAGCCCTGGATCT 26226          _  A_  C
                                GGGGCCCGGG GTT  GGA CT
                                |||||||||| |||  ||| ||
                                CCCCGGGTCC CGG  CCT GA
                                      T   GA   A
GAM990  DKFZp547I014 5'  AGGGACCTGGGGCAACC     26227        C    TAG
                                AGGGGCC GGGGT   GACC
                                ||||||| |||||   ||||
                                TCCCTGG CCCCG   TTGG
                                    A    ___
GAM990  DKFZP564B147 5'  AGGGGCCCGGCCAGGAGGGCCT 26228         GG      ___
                                AGGGGCCC  GGTTAGGA   CCT
                                ||||||||  ||||||||   |||
                                TCCCCGGG  CCGGTCCT   GGA
                                     __       CCC
GAM990  DKFZP566G1424 5'  AGAGGCCCTGGGGGCC      26229         G   TTA  A
                                AGGGGCCC GGG   GG CC
                                |||||||| |||   || ||
                                TCTCCGGG CCC   CC GG
                                    A   ___  _
GAM990  FADS2    3'  AGGGGCCCTGCCCGACTAGGAC 26230         GG___ GT
           CT                    AGGGGCCC    G  TAGGACCT
                                ||||||||    |  ||||||||
                                TCCCCGGG    C  ATCCTGGA
                                    ACGGG TG
GAM990  FAM3A    5'  GGGGTCAGGGGCAAGCCT    26231      CC    T    A
                                GGGG  CGGGG TAGG CCT
                                ||||  ||||| |||| |||
                                CCCC  GTCCC GTTC GGA
                                  A_    C   _
GAM990  FBX30    3'  AGGGGGCCGGGCCTGGA     26232      C    G  A
                                AGGGG CCGGG TT GGA
                                ||||| ||||| || |||
                                TCCCC GGCCC GA CCT
                                  C    G  _
GAM990  FBXO27   3'  AGGGCCCGTCAGGGCC      26233        GGG     A
                                GGGGCCC   GTTAGG CC
                                |||||||   |||||| ||
                                TCCCGGG   CAGTCC GG
                                     ___      C
GAM990  FLJ00007 3'  GGGGCACTGATAGGACCT    26234      CCGG   T
                                GGGGC    GGT AGGACCT
                                |||||    ||| |||||||
```

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                                CCCCG   CTA TCCTGGA
                                  TGA_  _
GAM990  FLJ00058  5' GGGGCTCGGGGATTAAGGCCT  26235     C   _   A
                                GGGGC CGGGG TTAGG CCT
                                ||||| ||||| ||||| |||
                                CCCCG GCCCC AATTC GGA
                                  A   T   C
GAM990  FLJ10232  3' AGGAGTTCGGGACCAGCCT   26236     CC   GT  GA
                                AGGGG  CGGG  TAG  CCT
                                |||||  ||||  |||  |||
                                TCCTC  GCCC  GTC  GGA
                                  AA   TG  __
GAM990  FLJ10305  5' AGGTGGCAGTTTAGGACCT   26237    _  CC  GG
                                AGG GGC  GG  TTAGGACCT
                                ||| |||  ||  |||||||||
                                TCC CCG  TC  AATCCTGGA
                                 A  __  A_
GAM990  FLJ10700  3' AGAGGTCTGGATTAGGGGCCT  26238     CCCG      A_
                                AGGGG   GGGTTAGG  CCT
                                |||||   ||||||||  |||
                                TCTCC   CCTAATCC  GGA
                                  AGA_      CC
GAM990  FLJ10900  3' AGAGGCCCGGACAGTGACCT   26239         GT  _
                                AGGGGCCCGGG  TAG GACCT
                                ||||||||||  ||| |||||
                                TCTCCGGGCCT  GTC CTGGA
                                      __  A
GAM990  FLJ11783  3' AGGGGCCAGGGTCCTTGGGATC 26240       C     A___  C
          T                     AGGGGCC GGGGTT   GGA CT
                                ||||||| ||||||   ||| ||
                                TCCCCGG TCCCAG   CCT GA
                                   _    GAAC  A
GAM990  FLJ12355  5' GGGTCCGGGACAGGCCT    26241    GC     T  A
                                GGG  CCGGGGT AGG CCT
                                |||  ||||||| ||| |||
                                CCC  GGCCCTG TCC GGA
                                 A_     _  _
GAM990  FLJ12666  3' GGGGCCTGGCCCAGGCCT   26242      CG  G   A
                                GGGGCC  GG TTAGG CCT
                                ||||||  || ||||| |||
                                CCCCGG  CC GGTCC GGA
                                  A_  G   _
GAM990  FLJ12800  3' AGGGGCCCAGGAGCTGCCT   26243        _  AGGA
                                AGGGGCCCGGG GTT   CCT
                                |||||||||| |||   |||
                                TCCCCGGGTCC CGA   GGA
                                      T  C___
GAM990  FLJ13102  3' AGGGTTTTGGGGAGAACTCT  26244    GCCC   TT   _
                                AGGG   GGGG  AGGAC CT
                                ||||   ||||  ||||| ||
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                                TCCC   CCCC  TCTTG GA
                                  AAAA   __    A
GAM990  FLJ13241  3'  GGGGCCCGGGGAGGCCT    26245         TT   A
                                GGGGCCCGGGG  AGG CCT
                                ||||||||||  ||| |||
                                CCCCGGGCCCC  TCC GGA
                                          __  _
GAM990  FLJ20533  5'  AGAGGCCCGGGGACC      26246          TTAGG
                                AGGGGCCCGGGG    ACC
                                ||||||||||||    |||
                                TCTCCGGGCCCC    TGG
                                          _____
GAM990  FLJ20979  5'  GGGGCCCGAAGGGGCCT    26247          TTA  A
                                GGGGCCCGGGG   GG CCT
                                ||||||||||   || |||
                                CCCCGGGCTTC   CC GGA
                                       C__  _
GAM990  FLJ21919  3'  AGGGGCCAGGGGGCTGAGGAC  26248       C_     _
                                AGGGGCC  GGGGTT AGGAC
                                |||||||  |||||| |||||
                                TCCCCGG  CCCCGA TCCTG
                                    TC     C
GAM990  FLJ23058  3'  AGGGGGCCAAGGGGACCT    26249      C     TTA
                                AGGGG CCGGGG   GGACCT
                                |||||  ||||||   ||||||
                                TCCCC GGTTCC   CCTGGA
                                  C     ___
GAM990  FLJ23058  3'  GGGGCCCAGAAAGGGGCCT   26250          TTA  A
                                GGGGCCCGGGG   GG CCT
                                ||||||||||   || |||
                                CCCCGGGTCTT   CC GGA
                                       TCC  _
GAM990  FLJ32356  3'  AGGGCCTGGGGGCCAGCCT   26251       C_      GA
                                GGGGCC  GGGGTTAG  CCT
                                ||||||  ||||||||  |||
                                TCCCGG  CCCCGGTC  GGA
                                   AC       __
GAM990  GIOT-3    5'  AGGGGCCCGGGCCGGGCCT   26252          G TA  A
                                AGGGGCCCGGG T  GG CCT
                                |||||||||| |  || |||
                                TCCCCGGGCCC G  CC GGA
                                      _ GC  _
GAM990  HT002     3'  AGGTGCTTCAAGTTAGGAC   26253     G  CCG
                                AGG GC   GGGTTAGGAC
                                ||| ||   ||||||||||
                                TCC CG   TTCAATCCTG
                                  A  AAG
GAM990  HU-K4     3'  GGGGCCCAGCAGGCC       26254         GGT   A
                                GGGGCCCGG   TAGG CC
                                |||||||||   |||| ||
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                              CCCCGGGTC  GTCC GG
                                   ___   _
GAM990  IGFALS   3' GGGGCTTGAGTCCGGGGACCT 26255     CCG   A__
                              GGGGC  GGGTT  GGACCT
                              |||||  |||||  ||||||
                              CCCCG  CTCAG  CCTGGA
                                 AA_   GCC
GAM990  KIAA0323 3' AGGGCCTGGAAAAGATCT   26256     C   TT   C
                              GGGGCC GGGG  AGGA CT
                              |||||| ||||  |||| ||
                              TCCCGG CCTT  TTCT GA
                                 A   __   A
GAM990  KIAA0339 3' GGGGCCTCCAGGACCT     26257      CGGGG
                              GGGGCC   TTAGGACCT
                              ||||||   |||||||||
                              CCCCGG   GGTCCTGGA
                                 A____
GAM990  KIAA0376 3' AGGGGCCCGAGGCAAGCCT  26258         T  A
                              AGGGGCCCGGGGT AGG CCT
                              |||||||||||| ||| |||
                              TCCCCGGGCTCCG TTC GGA
                                      _  _
GAM990  KIAA0515 3' GGGGCCTGGGATGGGCCT   26259      C   TA  A
                              GGGGCC GGGGT  GG CCT
                              |||||| |||||  || |||
                              CCCCGG CCCTA  CC GGA
                                 A    __ C
GAM990  KIAA0544 3' AAGGGCCCGGGGACTCCCT  26260         TTAGGA
                              AGGGGCCCGGGG    CCT
                              ||||||||||||    |||
                              TTCCCGGGCCCC    GGA
                                    TGAG__
GAM990  KIAA0561 3' AGGTGCCTGGGGCAAGACCT 26261    G  C   T
                              AGG GCC GGGGT AGGACCT
                              ||| ||| ||||| |||||||
                              TCC CGG CCCCG TTCTGGA
                                A  A   _
GAM990  KIAA0618 5' AGGGGCCCGGGCCGGGCCT  26252         G TA  A
                              AGGGGCCCGGG T  GG CCT
                              |||||||||| |  || |||
                              TCCCCGGGCCC G  CC GGA
                                    _ GC  _
GAM990  KIAA0711 3' GGGCCCAAAGGGACCT     26262        TTA
                              GGGCCCGGGG  GGACCT
                              ||||||||||  ||||||
                              CCCGGGTTTC  CCTGGA
                                   ___
GAM990  KIAA0789 5' AGGCGCCCGGGGTCCC     26263    G       AGGA
                              AGG GCCCGGGGTT   CC
                              ||| ||||||||||   ||
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                                TCC CGGGCCCCAG   GG
                                  G       ____
GAM990  KIAA0793 3' AGGGGCCTGGGAGCTGTGG   26264       C  _  A_
                                AGGGGCC GGG GTT  GG
                                ||||||| ||| |||  ||
                                TCCCCGG CCC CGA  CC
                                    A  T  CA
GAM990  KIAA0876 3' AGGGGCCCCGAAGGCC     26265       G  GTT  A
                                AGGGGCCC GG  AGG CC
                                |||||||| ||  ||| ||
                                TCCCCGGG CT  TCC GG
                                    G  ___  _
GAM990  KIAA1029 3' AGGGACCCGGGGAGAA     26266         TT
                                AGGGGCCCGGGG  AGGA
                                ||||||||||||  ||||
                                TCCCTGGGCCCC  TCTT

                                    __
GAM990  KIAA1045 3' GGGGCCCATTAGGATCT    26267       GGG     C
                                GGGGCCC  GTTAGGA CT
                                |||||||  ||||||| ||
                                CCCCGGG  TAATCCT GA
                                   ___     A
GAM990  KIAA1196 3' AGGGACCCGGCAGGGCCT   26268         GGT   A
                                AGGGGCCCGG  TAGG CCT
                                ||||||||||  |||| |||
                                TCCCTGGGCC  GTCC GGA
                                   ___  C
GAM990  KIAA1200 3' AGGGGTCAGATTGGACCT   26269      CC   GTTA
                                AGGGG  CGGG   GGACCT
                                |||||  ||||   ||||||
                                TCCCC  GTCT   CCTGGA
                                  A_   AA__
GAM990  KIAA1297 3' AGGGGCCCTGGGCGTGGCCT  26270       G   TA  A
                                AGGGGCCC GGGT  GG CCT
                                |||||||| ||||  || |||
                                TCCCCGGG CCCG  CC GGA
                                    A   CA  _
GAM990  KIAA1545 3' GGGGCCAGGGCTGGCCT    26271      C    A  A
                                GGGGCC GGGGTT GG CCT
                                |||||| |||||| || |||
                                CCCCGG TCCCGA CC GGA

                                  _    _ _
GAM990  KIAA1643 3' AGGGGCCCTGTCGCTGGCCT  26272       GGG_  A  A
                                AGGGGCCC   GTT GG CCT
                                ||||||||   ||| || |||
                                TCCCCGGG   CGA CC GGA
                                    ACAG  _ _
GAM990  KIAA1822 3' AGAGGCCCTGGAGGAC     26273       GG  TT
                                AGGGGCCC  GG  AGGAC
                                ||||||||  ||  |||||
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                                TCTCCGGG  CC  TCCTG
                                    A_ __
GAM990  KIAA1854 3'  AGGGGCCCTGCTAATGGCCT  26274       GGG   __ A
                                AGGGGCCC  GTTA  GG CCT
                                ||||||||  ||||  || |||
                                TCCCCGGG  CGAT  CC GGA
                                    A__   TA  _
GAM990  KLF5     3'  GGAGCCCAGGGGACC      26275         TTAG
                                GGGGCCCGGGG   GACC
                                ||||||||||   ||||
                                CCTCGGGTCCC   CTGG
                                     ____
GAM990  LYPLA3   3'  AGGAGCCGATCCCTGGGACCT  26276       C  GGTTA_
                                AGGGGCC GG    GGACCT
                                ||||||| ||    ||||||
                                TCCTCGG CT    CCTGGA
                                   _  AGGGAC
GAM990  MGC15523 5'  AGGGGCCCGGGGCGAGAGGCCT 26277          T__  A
                                AGGGGCCCGGGGT  AGG CCT
                                ||||||||||||  ||| |||
                                TCCCCGGGCCCCG  TCC GGA
                                      CTC  _
GAM990  MGC17998 5'  AGGGGCACCCAGGACC     26278      _ GGGGT
                                AGGGGC CC    TAGGACC
                                ||||||| ||   |||||||
                                TCCCCG GG    GTCCTGG
                                   T ______
GAM990  MGC1842  3'  AGGGGTTCGAGACCAGCCT   26279     CC   GT   GA
                                AGGGG  CGGG  TAG  CCT
                                |||||  ||||  |||  |||
                                TCCCC  GCTC  GTC  GGA
                                  AA   TG  __
GAM990  MGC4825  5'  GAGGCCCGGTAGGGCCT    26280       GGT   A
                                GGGGCCCGG  TAGG CCT
                                |||||||||  |||| |||
                                CTCCGGGCC  ATCC GGA
                                     ___   C
GAM990  MICAL    5'  GGCGGCCCGGGGCGTGCGCCT  26281   _       TAGGA
                                GG GGCCCGGGGT    CCT
                                || ||||||||||    |||
                                CC CCGGGCCCCG    GGA
                                 G        CACGC
GAM990  MLZE     5'  AGGGCCCTGGGAAGCACCT   26282      G   TT  G
                                GGGGCCC GGG  AG ACCT
                                ||||||| |||  || ||||
                                TCCCGGG CCC  TC TGGA
                                    A  T_  G
GAM990  NEIL1    5'  AGGGACCCGGTGGGGATCT   26283        _  TTA   C
                                AGGGGCCCGG GG   GGA CT
                                |||||||||| ||   ||| ||
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                                TCCCTGGGCC CC   CCT GA
                                     A ___  A
GAM990  NGEF     3' AGGGGCATGGGGGGCCCT   26284      CC   TTA  A
                                AGGGGC  GGGG   GG CCT
                                ||||||  ||||   || |||
                                TCCCCG  CCCC   CC GGA
                                   TA   ___  G
GAM990  NRM      3' AGGGCCTGGATGTTAAGGA   26285      C  _   _
                                GGGGCC GGG GTTA GGA
                                |||||| ||| |||| |||
                                TCCCGG CCT CAAT CCT
                                   A  A   T
GAM990  NRM      3' AGGGCCTGGATGTTAAGGA   26285      C  _   _
                                GGGGCC GGG GTTA GGA
                                |||||| ||| |||| |||
                                TCCCGG CCT CAAT CCT
                                   A  A   T
GAM990  NRM      3' AGGGCCTGGATGTTAAGGA   26285      C  _   _
                                GGGGCC GGG GTTA GGA
                                |||||| ||| |||| |||
                                TCCCGG CCT CAAT CCT
                                   A  A   T
GAM990  NUBP2    3' GAGGCCCGGGGTCACCT    26286          AGG
                                GGGGCCCGGGGTT  ACCT
                                ||||||||||||  ||||
                                CTCCGGGCCCCAG  TGGA
                                      ___
GAM990  OKL38    5' GGGGCTTTGGGATCGGCCT   26287      CC_    A  A
                                GGGGC  GGGGTT GG CCT
                                |||||  |||||| || |||
                                CCCCG  CCCTAG CC GGA
                                  AAA    _ _
GAM990  OSBPL5   3' GGGGCTCTGCAGGAGGCCT   26288      C___   GTT  A
                                GGGGC   CGGG  AGG CCT
                                |||||   ||||  ||| |||
                                CCCCG   GTCC  TCC GGA
                                  AGAC   ___  _
GAM990  P114-RHO-GEF 3' AGGAGCCTGGGGACACCT   26289       C   TTAGG
                                AGGGGCC GGGG   ACCT
                                ||||||| ||||   ||||
                                TCCTCGG CCCC   TGGA
                                   A   TG___
GAM990  PHYHIP   3' GAGGCCCGGGAAGGAC    26290          TT
                                GGGGCCCGGGG  AGGAC
                                ||||||||||  |||||
                                CTCCGGGCCCT  TCCTG
                                      __
GAM990  PPP1R16A 5' GGGGCCAGGCTGGGCCT    26291      CG   A  A
                                GGGGCC  GGGTT GG CCT
                                ||||||  ||||| || |||
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                                CCCCGG  TCCGA CC GGA
                                  __    C  _
GAM990  PPP1R16B  3'  AGGAGCTGCCATAGGACCT   26292      __  GGGT
                                AGGGGC  CCG   TAGGACCT
                                ||||||  |||   ||||||||
                                TCCTCG  GGT   ATCCTGGA
                                  AC  _____
GAM990  PPP1R16B  5'  GGGGCCAGGGCAGCGCGGGGCC 26293      C    TA___  A_
          T                     GGGGCC GGGGT    GG  CCT
                                ||||||  |||||    ||  |||
                                CCCCGG TCCCG    CC  GGA
                                  _    TCGCG  CC
GAM990  PRAX-1   3'  GGGGCCCTGGGGACCC     26294      GG  TTA
                                GGGGCCC  GG   GGACCT
                                |||||||  ||   ||||||
                                CCCCGGG  CC   CCTGGG
                                  A_  ___
GAM990  PSK      5'  AGGGGCCTGAGCTGTAGG    26295      CG   __
                                AGGGGCC  GGGT  TAGG
                                |||||||  ||||  ||||
                                TCCCCGG  CTCG  ATCC
                                  A_   AC
GAM990  QSCN6    3'  AGGGCCCGGGGTGGTCCT    26296        TA  A
                                GGGGCCCGGGGT  GG CCT
                                ||||||||||||  || |||
                                TCCCGGGCCCCA  CC GGA
                                    __  A
GAM990  RAB3GAP  3'  AGGGCCCTCTCCAGGACCT   26297      GGGG
                                GGGGCCC   TTAGGACCT
                                |||||||   |||||||||
                                TCCCGGG   GGTCCTGGA
                                  AGA_
GAM990  RBAK     5'  AGGGGCCCGGGCCGGGCCT   26252        G TA  A
                                AGGGGCCCGGG T  GG CCT
                                ||||||||||| |  || |||
                                TCCCCGGGCCC G  CC GGA
                                    _ GC  _
GAM990  REM      5'  AGGGGTCCAGGGTCCC      26298      C      AGGA
                                AGGGG CCGGGGTT   CC
                                |||||  ||||||||   ||
                                TCCCC GGTCCCAG   GG
                                  A      _____
GAM990  RNF10    5'  GGAGTCCGGGCCGGGCCT    26299     C    G TA  A
                                GGGG CCGGG T  GG CCT
                                ||||  ||||| |  || |||
                                CCTC GGCCC G  CC GGA
                                  A   _ GC  _
GAM990  SEC61A1  3'  GGGTGCTCATCTCCAGGACCT  26300    _  C  GGG
                                GGG GC CG   TTAGGACCT
                                |||  ||  ||  |||||||||
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                                CCC CG GT   GGTCCTGGA
                                  A  A  AGA
GAM990  SEMA4F   5'  AGGGCCCCGGGGCTACTGGCCT 26301      G        __  A
                                AGGG CCCGGGGTTA  GG CCT
                                |||| ||||||||||  || |||
                                TCCC GGGCCCCGAT  CC GGA
                                  G        GA  _
GAM990  SEMA6C   3'  AGGGGCCTCGGGAGACTCT   26302       _   GTTA   _
                                AGGGGCC CGGG   GGAC CT
                                ||||||| ||||   |||| ||
                                TCCCCGG GCCC   TCTG GA
                                   A   ____   A
GAM990  SES2     3'  GGGGCCAGCCAGGGACT    26303      CGG      AC
                                GGGGCC   GGTTAGG  CT
                                ||||||   |||||||  ||
                                CCCCGG   TCGGTCC  GA
                                   ___      CT
GAM990  SH3BP1   3'  GGTGGCTCCCCTAGGACCT   26304   _  _ GGGG
                                GG GGC CC   TTAGGACCT
                                || ||| ||   |||||||||
                                CC CCG GG   GATCCTGGA
                                 A   A  G___
GAM990  SHC3     5'  GGGGCCCCGGGACAGCCT    26305      G   TTA  A
                                GGGGCCC GGG   GG CCT
                                ||||||| |||   || |||
                                CCCCGGG CCC   TC GGA
                                   G   TG_  _
GAM990  STATI2   5'  AGGGGCTTGGTGACTGGCCT   26306      CC  _ GT A  A
                                AGGGGC  GG G  T GG CCT
                                ||||||  || |  | || |||
                                TCCCCG  CC C  A CC GGA
                                   AA  A TG _  _
GAM990  STX11    3'  GGCGGCCCGGGCCGGCCT    26307   _      GTTA  A
                                GG GGCCCGGG    GG CCT
                                || ||||||||    || |||
                                CC CCGGGCCC    CC GGA
                                 G       GG__  _
GAM990  TGIF2    5'  AGGGGCTAGGCTGGACCT    26308      CCG    A
                                AGGGGC   GGGTT GGACCT
                                ||||||   ||||| ||||||
                                TCCCCG   TCCGA CCTGGA
                                   A__    _
GAM990  TIGA1    5'  AGGAGCCCAAAGGAC       26309         GGTT
                                AGGGGCCCGG   AGGAC
                                ||||||||||   |||||
                                TCCTCGGGTT   TCCTG
                                             ____
GAM990  TRAF3    3'  GGGGCCACACCAGGAC      26310       _ GGG
                                GGGGCC CG   TTAGGAC
                                |||||| ||   |||||||
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                                CCCCGG GT   GGTCCTG
                                   T ___
GAM990  URG4     3' AGGGGTCAGGGAAGCC     26311      CC    TT   A
                                AGGGG  CGGGG  AGG CC
                                |||||  |||||  ||| ||
                                TCCCC  GTCCC  TTC GG
                                  A_    __  _
GAM990  USP2     5' GGGGCCCAGAAGGGACCT    26312         TTA
                                GGGGCCCGGGG  GGACCT
                                ||||||||||  ||||||
                                CCCCGGGTCTT  CCTGGA
                                      C__
GAM990  ZWINT    3' AGAGGCCTTTTCTAGGATCT  26313       CGGGG     C
                                AGGGGCC    TTAGGA CT
                                |||||||    |||||| ||
                                TCTCCGG    GATCCT GA
                                    AAAA_     A
GAM990  LOC113386 3' AGGGGTCAGGGGGCTCCT    26314      CC    TTA  A_
                                AGGGG  CGGGG  GG  CCT
                                |||||  |||||  ||  |||
                                TCCCC  GTCCC  CC  GGA
                                  A_    ___  GA
GAM990  LOC116071 3' AGGGCTTGGACTCTGGACCT  26315      CC   G  A
                                GGGGC  GGG TT GGACCT
                                |||||  ||| || ||||||
                                TCCCG  CCT AG CCTGGA
                                  AA   G  A
GAM990  LOC124857 5' GGGGCCCACCAGGGCCT     26316       GGG    A
                                GGGGCCCG   TTAGG CCT
                                ||||||||   ||||| |||
                                CCCCGGGT   GGTCC GGA
                                     ___     C
GAM990  LOC130617 3' AGGGGCTAAGAGTAGGGCCT  26317       CC    T   A
                                AGGGGC  GGGGT AGG CCT
                                ||||||  ||||| ||| |||
                                TCCCCG  TCTCA TCC GGA
                                   AT    _  C
GAM990  LOC138429 3' AGGGGGCCGGGAGGCC      26318      C    GTT   A
                                AGGGG CCGGG   AGG CC
                                |||||  |||||  ||| ||
                                TCCCC GGCCC   TCC GG
                                  C    ___  _
GAM990  LOC144501 3' AGGGGCCTTGGCAGAGCCT   26319       CGG   T  GA
                                AGGGGCC   GGT AG  CCT
                                |||||||   ||| ||  |||
                                TCCCCGG   CCG TC  GGA
                                    AA_   _ TC
GAM990  LOC145134 5' GGGGCCCTGCTAGGCCT     26320       GGG     A
                                GGGGCCC   GTTAGG CCT
                                |||||||   |||||| |||
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                                CCCCGGG  CGATCC GGA
                                   A__    _
GAM990  LOC145694 5'  GGGGTCCCGGGACAGCCT   26321     _     TTA  A
                                GGGG CCCGGGG  GG CCT
                                |||| |||||||  || |||
                                CCCC GGGCCCT  TC GGA
                                  A     G__  _
GAM990  LOC146667 3'  GGGGCTCTGGGCAAGCCT   26322     CCG   T  A
                                GGGGC  GGGT AGG CCT
                                |||||  |||| ||| |||
                                CCCCG  CCCG TTC GGA
                                  AGA   _  _
GAM990  LOC148029 5'  AGGGACCTCAGGACC      26323       CGGGG
                                AGGGGCC    TTAGGACC
                                |||||||    ||||||||
                                TCCCTGG    AGTCCTGG
                                   _____
GAM990  LOC148397 3'  AGGTGGCCCGGGTCTCAGCCT  26324    _      GTTA  A
                                AGG GGCCCGGG   GG CCT
                                ||| ||||||||   || |||
                                TCC CCGGGCCC   TC GGA
                                  A      AGAG  _
GAM990  LOC148397 5'  GGGACCCAGGAGGACCT    26325        GTT
                                GGGGCCCGGG  AGGACCT
                                ||||||||||  |||||||
                                CCCTGGGTCC  TCCTGGA
                                   ___
GAM990  LOC149668 3'  AGGGCCCTGGGAGCACCT   26326      G  TT  G
                                GGGGCCC GGG  AG ACCT
                                ||||||| |||  || ||||
                                TCCCGGG CCC  TC TGGA
                                   A  __  G
GAM990  LOC152137 3'  AGGGGTTCGAGACCAGCCT  26279     CC   GT   GA
                                AGGGG  CGGG  TAG  CCT
                                |||||  ||||  |||  |||
                                TCCCC  GCTC  GTC  GGA
                                  AA   TG  __
GAM990  LOC152330 5'  AGGTGGCCCCAGGACC     26327    _   GGGGT
                                AGG GGCCC    TAGGACC
                                ||| |||||    |||||||
                                TCC CCGGG    GTCCTGG
                                  A   _____
GAM990  LOC154790 5'  AGGGCCTGGGAGAGGGGCCT  26328      C   TTA  A
                                GGGGCC GGGG  GG CCT
                                |||||| ||||  || |||
                                TCCCGG CCCT  CC GGA
                                   A  CTC  C
GAM990  LOC154982 5'  GGGCGCCCGGGGGACCC    26329    _     TTAG
                                GGG GCCCGGGG   GACCT
                                ||| ||||||||   |||||
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                                CCC CGGGCCCC   CTGGG
                                  G      ____
GAM990  LOC155435 3'  AGCGGCCCGGAGAGACCT    26330    G       TTA
                                AG GGCCCGGGG   GGACCT
                                || |||||||||   ||||||
                                TC CCGGGCCTC   TCTGGA
                                 G       ___
GAM990  LOC158402 5'  GGGGCCAAGAAGGACCT     26331       C   GTT
                                GGGGCC GGG   AGGACCT
                                |||||| |||   |||||||
                                CCCCGG TCT   TCCTGGA
                                   T  ___
GAM990  LOC158629 5'  AGGAGTTTGGGGCTAGCCT   26332      CCC       GA
                                AGGGG   GGGGTTAG  CCT
                                |||||   ||||||||  |||
                                TCCTC   CCCCGATC  GGA
                                  AAA       __
GAM990  LOC163682 3'  GGGGCCCGGGGCCGCAGG    26333           __
                                GGGGCCCGGGGT  TAGG
                                ||||||||||||  ||||
                                CCCCGGGCCCCG  GTCC
                                     GC
GAM990  LOC170394 5'  GGGGTCCGGGGCTGGCCT    26334      C       A  A
                                GGGG CCGGGGTT GG CCT
                                |||| |||||||| || |||
                                CCCC GGCCCCGA CC GGA
                                  A       _  _
GAM990  LOC199953 3'  AGGGGCCCGCTTCGGACCT   26335         GGGTTA
                                AGGGGCCCG     GGACCT
                                |||||||||     ||||||
                                TCCCCGGGC     CCTGGA
                                     GAAG__
GAM990  LOC201191 3'  GGGGCCCGGCCTCAGGGCCT  26336         GG    A
                                GGGGCCCGG  TTAGG CCT
                                |||||||||  ||||| |||
                                CCCCGGGCC  AGTCC GGA
                                     GG    C
GAM990  LOC203503 5'  AGGGGCCCGGCCAGGAGGGCCT 26228         GG       ___
                                AGGGGCCC  GGTTAGGA   CCT
                                ||||||||  ||||||||   |||
                                TCCCCGGG  CCGGTCCT   GGA
                                     __       CCC
GAM990  LOC203636 3'  AGGGGCCCCGAGGACC      26337         G GGTT
                                AGGGGCCC G    AGGACC
                                |||||||| |    ||||||
                                TCCCCGGG C    TCCTGG
                                     G _____
GAM990  LOC219688 3'  AGGGGCCCAGGTACTGATCT   26338           GTTAG  C
                                AGGGGCCCGGG    GA CT
                                ||||||||||     || ||
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                                TCCCCGGGTCC    CT GA
                                      ATGA_  A
GAM990  LOC220995 3'  AGAGGCTCGACTCGGGCCT   26339      C  G G TA  A
                                AGGGGC CG G T  GG CCT
                                |||||| || | |  || |||
                                TCTCCG GC T A  CC GGA
                                   A  _ G GC  _
GAM990  LOC221122 5'  GGGACTCACTCAGGACCT    26340     C  GGG
                                GGGGC CG   TTAGGACCT
                                ||||| ||   |||||||||
                                CCCTG GT   AGTCCTGGA
                                  A  G__
GAM990  LOC221833 3'  AGGGCCCAAGAGGAC       26341        GTT
                                GGGGCCCGGG   AGGAC
                                ||||||||||   |||||
                                TCCCGGGTTC   TCCTG

                                      ___
GAM990  LOC253609 5'  GAGGCCCGGGCTCCTGGCCT  26342        G  A_  A
                                GGGGCCCGGG TT  GG CCT
                                |||||||||| ||  || |||
                                CTCCGGGCCC AG  CC GGA
                                      G  GA  _
GAM990  LOC253841 5'  AGGGGCCCGCCGAAGGGCCT  26152        GGGTT  A
                                AGGGGCCCG    AGG CCT
                                |||||||||    ||| |||
                                TCCCCGGGC    TCC GGA
                                     GGCT_  C
GAM990  LOC253842 3'  AGGGGCCCAGAGAGGAGGGCCT 26343          TT_  A
                                AGGGGCCCGGGG   AGG CCT
                                ||||||||||||   ||| |||
                                TCCCCGGGTCTC   TCC GGA
                                       TCC  C
GAM990  LOC253982 5'  AGAGGCCTGGGGCGTCCT    26344       C    TAGGA
                                AGGGGCC GGGGT    CCT
                                ||||||| |||||    |||
                                TCTCCGG CCCCG    GGA
                                    A    CA___
GAM990  LOC256056 5'  GGGGCCCAGCAGGGCCT     26345        GGT   A
                                GGGGCCCGG   TAGG CCT
                                |||||||||   |||| |||
                                CCCCGGGTC   GTCC GGA
                                      ___   C
GAM990  LOC256980 3'  GGGACCCTGGGGACCT      26346       GG  TTA
                                GGGGCCC  GG   GGACCT
                                |||||||  ||   ||||||
                                CCCTGGG  CC   CCTGGA
                                    A_  ___
GAM990  LOC257020 5'  AGGGCTCCTGCAGGACCT    26347      _  GGGGT
                                GGGGC CC    TAGGACCT
                                ||||| ||    ||||||||
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                                TCCCG GG    GTCCTGGA
                                   A  AC___
GAM990  LOC257457 5'  AGGGGCCGGGGCCAGCCT   26348       C      GA
                                AGGGGCC GGGGTTAG  CCT
                                ||||||| ||||||||  |||
                                TCCCCGG CCCCGGTC  GGA
                                      _      __
GAM990  LOC51236  3'  GGGACCCAGGGGGCC      26349         TTA  A
                                GGGGCCCGGGG   GG CC
                                |||||||||||   || ||
                                CCCTGGGTCCC   CC GG
                                        ___ _
GAM990  LOC51337  3'  GGTCCGAGCCAGGATCT    26350   C    G    C
                                GG CCGGG TTAGGA CT
                                || ||||| |||||| ||
                                CC GGCTC GGTCCT GA
                                 A    _    A
GAM990  LOC55924  3'  AGGGGCCCAGCACTGGGACCT 26351        G   A
                                AGGGGCCCGG GTT GGACCT
                                |||||||||| ||| ||||||
                                TCCCCGGGTC TGA CCTGGA
                                     G   C
GAM990  LOC58512  3'  AGGGACCCGGCCCGGCCT    26352        GGTTA  A
                                AGGGGCCCGG    GG CCT
                                ||||||||||    || |||
                                TCCCTGGGCC    CC GGA
                                     GGG__ _
GAM990  LOC92249  3'  AGGGGTTAGGCCTGGGACCT  26353     CCC   G  A
                                AGGGG   GGG TT GGACCT
                                |||||   ||| || ||||||
                                TCCCC   TCC GA CCTGGA
                                   AA_   G  C
GAM990  LOC92497  5'  GGGGCTCAGGCAAAACCT    26354     C    GT
                                GGGGC CGGG  TAGGACCT
                                ||||| ||||  ||||||||
                                CCCCG GTCC  GTTTTGGA
                                   A   __
GAM990  LOC92716  3'  AGAGGCCCCTAGGAC       26355       GGGG
                                AGGGGCCC    TTAGGAC
                                ||||||||    |||||||
                                TCTCCGGG    GATCCTG
                                      _____
GAM990  LOC93259  5'  AGGGGCCCGGGAGGAATTGACC 26356          TTAG__
          T                    AGGGGCCCGGGG     GACCT
                               ||||||||||||     |||||
                               TCCCCGGGCCCT     CTGGA
                                     CCTTAA
GAM991  GPR17     3'  GCGTGGGGTTACAGCAGGAGA  26359     A_  C   CT  C
                                GTGT  GG TAC  GC GGAGA
                                ||||  || |||  || |||||
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                                CGCA  CC ATG  CG CCTCT
                                  CC  A   T_  T
GAM991  AGPAT1   3'  GTGTAGGCTGAGTCACTGGAGA 26360        ACCT_  C
                                GTGTAGGCT    GC GGAGA
                                |||||||||    || |||||
                                CACATCCGA    TG CCTCT
                                     CTCAG  A
GAM991  AGPAT1   3'  GTGTAGGCTGAGTCACTGGAGA 26360        ACCT_  C
                                GTGTAGGCT    GC GGAGA
                                |||||||||    || |||||
                                CACATCCGA    TG CCTCT
                                     CTCAG  A
GAM991  FLJ12681 3'  CGTGTAGGCTGTGGCGG     26361         ACC  C
                                CGTGTAGGCT   TG CGG
                                ||||||||||   || |||
                                GCACATCCGA   AC GCC
                                     C__  C
GAM991  FLJ22390  5'  GTGTAGGCTGCACTGAGA    26362        ACCT  CG_
                                GTGTAGGCT   GC   GAGA
                                |||||||||   ||   ||||
                                CACATCCGA   CG   CTCT
                                     ____  TGA
GAM991  HSPC055   3'  TACTGTGGGTTGCTGCTCAGGA 26363     G   A  CTAC   _ _
          G                      TAC TGT GG    CTGC C GGAG
                                 ||| ||| ||    |||| | ||||
                                 ATG ACA CC    GACG G CCTC
                                   _   C  AAC_    A T
GAM991  UQCR     3'  TACGTGTGGGTGACTTGTTAAG 26364       A  CT  C  CCG
                                TACGTGT GG  AC TG   GAG
                                ||||||| ||  || ||   |||
                                ATGCACA CC  TG AC   TTC
                                    C  AC  A  AA_
GAM991  LOC128954 5'  TGCTGGGTGTACTTGCCGGAG  26365     A  C__   C
                                TGT GG   TAC TGCCGGAG
                                ||| ||   ||| ||||||||
                                ACG CC   ATG ACGGCCTC
                                  A  CAC   A
GAM991  LOC144305 3'  TACTTGTAGGCTGAGGTGGGAG 26366     G       ACCTGCC
                                TAC TGTAGGCT      GGAG
                                ||| ||||||||      ||||
                                ATG ACATCCGA      CCTC
                                  A       CTCCAC_
GAM992  GABRP    3'  AGAACAATGGTTGGAGCTT   26369     TCC   GC
                                AGA   GTGG  TGGAGCTT
                                |||   ||||  ||||||||
                                TCT   TACC  ACCTCGAA
                                  TGT   A_
GAM992  LLT1     3'  CTAAAGATTAGTTGGGGCT   26370        CC  __
                                TTAAAGAT  GT  GGGCT
                                ||||||||  ||  |||||
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                                GATTTCTA  CA  CCCGA
                                    AT  AC
GAM992  RRP22    3'  AGACTGGGTTGGAGCTT    26371     CCG   C
                                AGAT   TGGG TGGAGCTT
                                ||||   |||| ||||||||
                                TCTG   ACCC ACCTCGAA
                                  ___    A
GAM992  DKFZp761D0614 3'  TCAAAGATTTGTGGGTTGG   26372        CC    C
                                TTAAAGAT  GTGGG TGG
                                ||||||||  ||||| |||
                                AGTTTCTA  CACCC ACC
                                    AA    A
GAM992  KIAA0532  3'  TTAAAGATCAGTGGGTG     26373         C    C
                                TTAAAGATC GTGGG TG
                                |||||||||| ||||| ||
                                AATTTCTAG CACCC AC
                                     T    _
GAM992  LOC120196 3'  TTAAAGACTCACCGGTTGG    26374        TC   G  C
                                TTAAAGA  CGT GG TGG
                                |||||||  ||| || |||
                                AATTTCT  GTG CC ACC
                                    GA   G  A
GAM993  DKFZp434A1010 3'  GGGGTAGTGGTCGGG      26377         TCGTT
                                GGGGTAGTG    GTCGGG
                                |||||||||    ||||||
                                CCCCATCAC    CAGCCC
                                      _____
GAM994  IGF1R    3'  GCGCGTGCGCACACGTT     26380      A      AG
                                GCGC TGCGCAC  ACGTT
                                |||| |||||||  |||||
                                CGCG ACGCGTG  TGCAA
                                  C      __
GAM994  ELF4     3'  GCATGCGCATCAAAGCGTTC   26381          _   _
                                GCATGCGCA CAGA CGTTC
                                ||||||||| |||| |||||
                                CGTACGCGT GTTT GCAAG
                                     A   C
GAM994  HUMNPIIY20 3'  GCACGCGCGCGTAGGTGTTC   26382      A    AC  AC
                                GCGC TGCGC  AG  GTTC
                                |||| |||||  ||  ||||
                                CGTG GCGCG  TC  CAAG
                                  C    CA  CA
GAM994  WBSCR17   3'  GCATGCACACGCGTTC      26383          AGA
                                GCATGCGCAC   CGTTC
                                ||||||||||   |||||
                                CGTACGTGTG   GCAAG
                                      C__
GAM994  LOC124626 3'  GCGCAATTACTGTGTAGACGTT 26384      __  GCAC_
            C                    GCGCA  TGC    AGACGTTC
                                |||||  |||    ||||||||
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                                CGCGT  ATG    TCTGCAAG
                                   TA   ACACA
GAM994  LOC146136 5'  CATGGCACACAGGTGTTC    26385     _     AC
                                CATG CGCACAG  GTTC
                                |||| |||||||  ||||
                                GTAC GTGTGTC  CAAG
                                  C      CA
GAM994  LOC220565 3'  CATGGCACACAGGTGTTC    26385     _     AC
                                CATG CGCACAG  GTTC
                                |||| |||||||  ||||
                                GTAC GTGTGTC  CAAG
                                  C      CA
GAM995  ACVR1B    3'  TGCGGGCCAGGGCTCCTGGCCA 26388    ACA    TGAG_
           CA                     TGC   GCCAG    CTGGCCACA
                                |||   |||||    |||||||||
                                ACG   CGGTC    GACCGGTGT
                                  CC_    CCGAG
GAM995  ALDOC     5'  TGCGCAGCCAGTTAGCAGCCGC 26389    A      G   T   A
           A                      TGC CAGCCAGT AGC GGCC CA
                                ||| |||||||| ||| |||| ||
                                ACG GTCGGTCA TCG TCGG GT
                                  C       A   _   C
GAM995  CASP3     3'  TGACAGCCAGTGAGACTTGG   26390    C          _ _
                                TG ACAGCCAGTGAG CT GG
                                || |||||||||||| || ||
                                AC TGTCGGTCACTC GA CC
                                  _          T  A
GAM995  CASP3     3'  TGACAGCCAGTGAGACTTGG   26390    C          _ _
                                TG ACAGCCAGTGAG CT GG
                                || |||||||||||| || ||
                                AC TGTCGGTCACTC GA CC
                                  _          T  A
GAM995  CPSF4     3'  GCAGGCGTGAGCTGGCCACA   26391     CA  CA
                                GCA  GC  GTGAGCTGGCCACA
                                |||  ||  ||||||||||||||
                                CGT  CG  CACTCGACCGGTGT
                                  C_  __
GAM995  DSCAM     5'  TGCGCAGCCAGCGGCCTCCC   26392     A       A   GG
                                TGC CAGCCAGTG GCT  CC
                                ||| |||||||| |||  ||
                                ACG GTCGGTCGC CGG  GG
                                  C        _  AG
GAM995  EGR1      5'  TGCGGCGGCGGAAGCTGGC    26393     ACA  CA   __
                                TGC   GC  GTG  AGCTGGC
                                |||   ||  |||  |||||||
                                ACG   CG  CGC  TCGACCG
                                  C__   C_   CT
GAM995  FOXO1A    3'  TACATGGCCACCCCTGGCCACA 26394      CA   GTGAG
                                TGCA  GCCA    CTGGCCACA
                                ||||  ||||    |||||||||
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                                ATGT  CGGT    GACCGGTGT
                                  AC   GGG__
GAM995  HDAC4    3'  GCCAGGCTCGGCTGGCCACA  26395      ___ A
                                GCCAG   TG GCTGGCCACA
                                |||||   || ||||||||||
                                CGGTC   GC CGACCGGTGT
                                   CGA  _
GAM995  KCNK10   3'  TGTACGGCCAGAACCGGCTAC  26396    C  A   GT      C
                                TG AC GCCA  GAGCTGGC AC
                                || || ||||  |||||||| ||
                                AC TG CGGT  CTTGGCCG TG
                                 A  C   __      A
GAM995  KCNK10   3'  TGTACGGCCAGAACCGGCTAC  26396    C  A   GT      C
                                TG AC GCCA  GAGCTGGC AC
                                || || ||||  |||||||| ||
                                AC TG CGGT  CTTGGCCG TG
                                 A  C   __      A
GAM995  KCNK10   3'  TGTACGGCCAGAACCGGCTAC  26396    C  A   GT      C
                                TG AC GCCA  GAGCTGGC AC
                                || || ||||  |||||||| ||
                                AC TG CGGT  CTTGGCCG TG
                                 A  C   __      A
GAM995  MPL      3'  TGCACAGCTAGTAAATG     26397        C     C
                                TGCACAGC AGTGAG TG
                                |||||||| |||||| ||
                                ACGTGTCG TCATTT AC
                                     A    _
GAM995  NGFR     5'  TGCCCGCCGGAGCTGGCC    26398     ACA   AGT
                                TGC   GCC   GAGCTGGCC
                                |||   |||   |||||||||
                                ACG   CGG   CTCGACCGG
                                  GG_   C__
GAM995  NPR2L    3'  TGCACTGGCCAGTGGGCCGCA  26399      A_     AGCT    A
                                TGCAC  GCCAGTG    GGCC CA
                                |||||  |||||||    |||| ||
                                ACGTG  CGGTCAC    CCGG GT
                                   AC      _____    C
GAM995  NTSR1    3'  GCACCCCATCCTGGCCAC    26400     AG   GTGAG
                                GCAC  CCA    CTGGCCAC
                                ||||  |||    ||||||||
                                CGTG  GGT    GACCGGTG
                                  G_   AG___
GAM995  P2RY1    3'  TGCACAGCAGTGGGGC      26401        C   AGCT
                                TGCACAGC AGTG    GGC
                                |||||||| ||||    |||
                                ACGTGTCG TCAC    CCG
                                     _    C___
GAM995  PABPN1   5'  TGCCAGCTAGTGAGCTG     26402     A   C
                                TGC CAGC AGTGAGCTG
                                ||| |||| |||||||||
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                                ACG GTCG TCACTCGAC
                                  _   A
GAM995  PACE4    3'  TGCACAGCAGCAGTTGG     26403        C  G  C
                                TGCACAGC AGT AG TGG
                                |||||||| ||| || |||
                                ACGTGTCG TCG TC ACC
                                     _  _ A
GAM995  PGC      5'  TGCTGGTCCCCAACTGGCCACA 26404     ACAG  AGTG
                                TGC   CC   AGCTGGCCACA
                                |||   ||   ||||||||||
                                ACG   GG   TTGACCGGTGT
                                  ACCA  GG__
GAM995  PIK4CB   3'  GCATGGCCAGTGGCCAACCACA 26405     CA      A  TG
                                GCA  GCCAGTG GC  GCCACA
                                |||  ||||||| ||  ||||||
                                CGT  CGGTCAC CG  TGGTGT
                                  AC      _  GT
GAM995  PPP1R12B 3'  TGCCAGCCAGTGGTAGGCACA  26406     A       AGCT   C
                                TGC CAGCCAGTG   GGC ACA
                                ||| |||||||||   ||| |||
                                ACG GTCGGTCAC   CCG TGT
                                  _       CAT_  _
GAM995  RANBP3   3'  TGCAAGCTGGCTCTTGGCCA   26407     C   CA  GAGC
                                TGCA AGC  GT   TGGCCA
                                |||| |||  ||   ||||||
                                ACGT TCG  CG   ACCGGT
                                  _  AC  AGA_
GAM995  TRPM1    5'  TGCTGGTTGGTGAACTGGCCAC 26408     ACAGCCA
           A                     TGC      GTGAGCTGGCCACA
                                |||      ||||||||||||||
                                ACG      CACTTGACCGGTGT
                                  ACCAAC_
GAM995  C11orf11 3'  TGCCTGGGCCCGGCTGGCCAC  26409     ACA_  AG  A
                                TGC   GCC  TG GCTGGCCAC
                                |||   |||  || |||||||||
                                ACG   CGG  GC CGACCGGTG
                                  GACC  __ _
GAM995  CAMKK2   3'  TGTCCAGCCAGCCAGCGGCCAC 26410    CA      G   T
                                TG  CAGCCAGT AGC GGCCAC
                                ||  |||||||| ||| ||||||
                                AC  GTCGGTCG TCG CCGGTG
                                  AG       G  _
GAM995  CLIC4    5'  CCGGAGTCGAGCTGGCCAC   26411    __  _
                                CC  AGT GAGCTGGCCAC
                                ||  ||| ||||||||||
                                GG  TCA CTCGACCGGTG
                                  CC   G
GAM995  DKFZP434I216 3'  CAGCCACACCCTGGTCACA   26413       G  AG   C
                                CAGCCA TG  CTGG CACA
                                ||||||  ||  |||| ||||
```

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                                GTCGGT GT  GACC GTGT
                                   _ GG    A
GAM995  DKFZP434I216 3'  GCCAGTTAGTCCAATGGCCACA 26412       G  _  ___
                                GCCAGT AG CT   GGCCACA
                                |||||| || ||   |||||||
                                CGGTCA TC GG   CCGGTGT
                                   A  A  TTA
GAM995  FLJ11126  3'  TGCACAGCGGTGGGGCTCACA  26414        CA   AGCT  _
                                TGCACAGC  GTG   GGC CACA
                                ||||||||  |||   ||| ||||
                                ACGTGTCG  CAC   CCG GTGT
                                     C_  C___   A
GAM995  FLJ12800  3'  TGGGCAGCCAGTGATGGACTAC 26415    CA        GCT   C
          A                      TG  CAGCCAGTGA   GGC ACA
                                ||  ||||||||||   ||| |||
                                AC  GTCGGTCACT   CTG TGT
                                 CC         AC_   A
GAM995  FLJ14326  3'  TGCACAGCCATCTGGCTG    26417         G_  A
                                TGCACAGCCA  TG GCTG
                                ||||||||||  || ||||
                                ACGTGTCGGT  AC CGAC
                                      AG  _
GAM995  FLJ14326  3'  CACAGCCACTTTGGTCACA   26416        GTGAGC   C
                                CACAGCCA     TGG CACA
                                ||||||||     ||| ||||
                                GTGTCGGT     ACC GTGT
                                     GAA___   A
GAM995  FLJ14549  5'  TGAACAGCTGGTGAGCCA    26418    C    CA
                                TG ACAGC  GTGAGCTG
                                || |||||  ||||||||
                                AC TGTCG  CACTCGGT
                                 T    AC
GAM995  FLJ21478  3'  TGCAAGCCAGGAGGCCAC    26419     C     T  GCT
                                TGCA AGCCAG GA   GGCCAC
                                |||| |||||| ||   ||||||
                                ACGT TCGGTC CT   CCGGTG
                                   _     _ ___
GAM995  FLJ22501  5'  TGTACAGCCAGTGGCTCCC   26420    C        A   GG
                                TG ACAGCCAGTG GCT  CC
                                || ||||||||| |||  ||
                                AC TGTCGGTCAC CGA  GG
                                 A        _   G_
GAM995  GBTS1     3'  TACATAGTCCCACCTGGCCACA 26421      C  _  AGTGAG
                                TGCA AG CC     CTGGCCACA
                                |||| || ||     |||||||||
                                ATGT TC GG     GACCGGTGT
                                  A  A  GTG___
GAM995  H17       3'  TGCAAGCCAGTGGAGCCAG   26422      C       _   TG
                                TGCA AGCCAGTG AGC  G
                                |||| |||||||| |||  |
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                                ACGT TCGGTCAC TCG  C
                                  _      C  GT
GAM995  KIAA1822  3'  GCACAGCCAGGGGCCA     26423         TGAGCT
                                GCACAGCCAG    GGCCA
                                ||||||||||    |||||
                                CGTGTCGGTC    CCGGT
                                    C_____
GAM995  KIAA1957  3'  CACGGCCCCGCCCTGGCCACA  26424    A  AG  AG
                                CAC GCC  TG  CTGGCCACA
                                ||| |||  ||  |||||||||
                                GTG CGG  GC  GACCGGTGT
                                  C  G_  GG
GAM995  MGC10870  5'  TGCGCTGCCAGTGACCAC    26425    ACA     AGCTG
                                TGC  GCCAGTG    GCCAC
                                |||  |||||||    |||||
                                ACG  CGGTCAC    TGGTG
                                  CGA     _____
GAM995  MKP-7     3'  TGCACAACTAGTGAGGTCTG   26426       C    __
                                TGCACAGC AGTGAG  CTG
                                |||||||| ||||||  |||
                                ACGTGTTG TCACTC  GAC
                                    A     CA
GAM995  NIFU      3'  TGCACAGCAGGTGGGAAAC   26427       CA  AGCT  CC
                                TGCACAGC  GTG   GG  AC
                                ||||||||  |||   ||  ||
                                ACGTGTCG  CAC   CC  TG
                                    TC  _____ TT
GAM995  PSMD13    3'  TGAGCAGCCAGCTTCATTGGCT 26428    CA      GAGC_   CA
          GCA                     TG  CAGCCAGT    TGGC  CA
                                ||  ||||||||    ||||  ||
                                AC  GTCGGTCG    ACCG  GT
                                 TC       AAGTA   AC
GAM995  SIMRP7    3'  TGTGCAGCAGGTGGTTGGCCAC 26429    CA   CA   AGC
          A                      TG  CAGC  GTG   TGGCCACA
                                ||  ||||  |||   ||||||||
                                AC  GTCG  CAC   ACCGGTGT
                                 AC   TC   CA_
GAM995  SLC39A3   3'  GCATGGCCAGGGCTGGTCACA  26430    CA    TGA    C
                                GCA  GCCAG   GCTGG CACA
                                |||  |||||   ||||| ||||
                                CGT  CGGTC   CGACC GTGT
                                  AC    C__    A
GAM995  TU12B1-TY 3'  TACACAGTCAGTGAGCCTTGG  26431       C       __
                                TGCACAG CAGTGAGCT  GG
                                |||||||  |||||||||  ||
                                ATGTGTC GTCACTCGG  CC
                                    A        AA
GAM995  ZDHHC7    3'  TACACAGCCGGTAAATGTTACA 26432         A    C  GCC
                                TGCACAGCC GTGAG TG   ACA
                                |||||||| ||||| ||   |||
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                                ATGTGTCGG CATTT AC   TGT
                                    C    _ AA_
GAM995  LOC113763 3'  TGCCAGCCAGTGAGAGC    26433    A       CT
                                TGC CAGCCAGTGAG  GGC
                                ||| ||||||||||  |||
                                ACG GTCGGTCACTC  TCG
                                  _       __
GAM995  LOC123242 5'  CAGTCAGAGCCATGGCCACA  26434     __   __
                                CAGT  GAGCT  GGCCACA
                                ||||  |||||  |||||||
                                GTCA  CTCGG  CCGGTGT
                                  GT    TA
GAM995  LOC145678 3'  TGCACAGCTGTGGCTGATCA  26435       CA  A   GC
                                TGCACAGC  GTG GCTG  CA
                                ||||||||  ||| ||||  ||
                                ACGTGTCG  CAC CGAC  GT
                                    A_  _   TA
GAM995  LOC146332 3'  TGCACAGCTGTGTCCCTCACA 26436       CA  AG  GGC
                                TGCACAGC  GTG  CT   CACA
                                ||||||||  |||  ||   ||||
                                ACGTGTCG  CAC  GG   GTGT
                                    A_  AG  A__
GAM995  LOC147664 3'  AGCCAGTGTAGCCAC      26437       AGC
                                AGCCAGTG   TGGCCAC
                                ||||||||   |||||||
                                TCGGTCAC   ATCGGTG
                                   ___
GAM995  LOC147727 3'  TGCACAGCTGTTGGCC     26438       CA  GAGC
                                TGCACAGC  GT   TGGCC
                                ||||||||  ||   |||||
                                ACGTGTCG  CA   ACCGG
                                    A_ ____
GAM995  LOC162417 5'  TGCGTGAGCCAGTGGCGC    26439    AC_     A  TG
                                TGC   AGCCAGTG GC  GC
                                |||   |||||||| ||  ||
                                ACG   TCGGTCAC CG  CG
                                  CAC      _ __
GAM995  LOC163682 5'  TGCACAGCTAATGAGCTGA   26440       C
                                TGCACAGC AGTGAGCTGG
                                |||||||| ||||||||||
                                ACGTGTCG TTACTCGACT
                                    A
GAM995  LOC196955 5'  CAGTCAGAGCCATGGCCACA  26434     __   __
                                CAGT  GAGCT  GGCCACA
                                ||||  |||||  |||||||
                                GTCA  CTCGG  CCGGTGT
                                  GT    TA
GAM995  LOC196955 3'  GCTAGACCAGCTGGCCAC    26441    C  _ G
                                GC AG T AGCTGGCCAC
                                || || | ||||||||||
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                                CG TC G TCGACCGGTG
                                 A  T G
GAM995  LOC204820 3'  GCCCGGTGCTGCTGGCCAC   26442     A_  A_
                                GCC  GTG  GCTGGCCAC
                                |||  |||  |||||||||
                                CGG  CAC  CGACCGGTG
                                  GC   GA
GAM995  LOC254249 3'  CATCTAGTGAGCTGGCCACA  26443    GCC
                                CA   AGTGAGCTGGCCACA
                                ||   ||||||||||||||
                                GT   TCACTCGACCGGTGT
                                 AGA
GAM995  LOC257472 3'  CAGCCACACCCTGGTCACA   26413       G  AG    C
                                CAGCCA TG  CTGG CACA
                                ||||||  ||  |||| ||||
                                GTCGGT GT  GACC GTGT
                                    _  GG    A
GAM995  LOC257472 3'  GCCAGTTAGTCCAATGGCCACA 26412       G  _  ___
                                GCCAGT AG CT   GGCCACA
                                ||||||  || ||   |||||||
                                CGGTCA TC GG   CCGGTGT
                                   A  A  TTA
GAM995  LOC51706  3'  TGCACAGCCAGGGGTTCCTGCC 26444          TGAG_  G
          ACA                    TGCACAGCCAG     CT GCCACA
                                ||||||||||     ||  ||||||
                                ACGTGTCGGTC     GG CGGTGT
                                      CCCAA  A
GAM995  LOC90850  3'  TGCGACAGCTCTGGCCAC    26445     _     CAGTGAG
                                TGC ACAGC      CTGGCCAC
                                |||  |||||      |||||||||
                                ACG TGTCG      GACCGGTG
                                  C    A_____
GAM996  ANGPT2    3'  AATCACAATTATGGATGTT    26448      TGGGA   C
                                GATC     AAT ATGGATGTT
                                ||||     |||  |||||||||
                                TTAG     TTA TACCTACAA
                                  TG___    A
GAM996  GASC1     5'  AGATTTGGGAAATTTGG      26449      C       CA
                                AGAT TGGGAAAT  TGG
                                ||||  ||||||||  |||
                                TCTA ACCCTTTA  ACC
                                  A       A_
GAM996  PPP2R5C   3'  TCTGGGAAGTCACCATTGTTT  26450         A    GGA
                                TCTGGGAA TCAT   TGTTT
                                ||||||||  ||||   |||||
                                AGACCCTT AGTG   ACAAA
                                     C    GTA
GAM996  RP2       3'  AGATTTGGGAAACAGTGCTT   26451      C       CAT  A
                                AGAT TGGGAAAT   GG TGTTT
                                ||||  ||||||||   ||  |||||
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                                TCTA ACCCTTTG   TC ACGAA
                                  A      ___ _
GAM996  FLJ20487  3'  AGGGCTGGGAAATTGTAAAT   26452    AT       CA
                                AG  CTGGGAAAT  TGGAT
                                ||  |||||||||  |||||
                                TC  GACCCTTTA  ATTTA
                                 CC        AC
GAM996  FLJ23045  3'  AGATTTGGGAGAATGTT     26453     C    AATCAT
                                AGAT TGGGA     GGATGTT
                                |||| |||||     |||||||
                                TCTA ACCCT     CTTACAA
                                  A    _______
GAM996  FLJ23537  3'  TCTGGGAAGGAGGTGTTT    26454        ATCAT  A
                                TCTGGGAA    GG TGTTT
                                ||||||||    || |||||
                                AGACCCTT    CC ACAAA
                                     CCT__ _
GAM996  GPS1      3'  TCTGGGAAATGGTGCC      26455        ATC    A
                                TCTGGGAA   ATGG TGTT
                                ||||||||   |||| ||||
                                AGACCCTT   TACC ACGG
                                     ___   _
GAM996  RFX4      3'  AGATTGTGGGAGAAGAATGTTT 26456      C_    AATCAT
                                AGAT  TGGGA     GGATGTTT
                                ||||  |||||     ||||||||
                                TCTA  ACCCT     CTTACAAA
                                  AC    CTT___
GAM996  LOC150951 5'  AGATCTGGGTGATTAT      26457        AAATCA   A
                                AGATCTGGG     TGG TGT
                                |||||||||     ||| |||
                                TCTAGACCC     ACT ATA
                                     _______  A
GAM996  LOC253015 5'  AGGCTCTGGGGGGGATGTT    26458    A_     AAATCAT
                                AG  TCTGGG      GGATGTT
                                ||  ||||||      |||||||
                                TC  AGACCC      CCTACAA
                                 CG     C_______
GAM997  BSN       3'  TCCATGGACCAGAGGCCTGC   26461    G        TA_
                                TC CATGGACCAGG   TTGC
                                || ||||||||||   ||||
                                AG GTACCTGGTCT   GACG
                                 _         CCG
GAM997  PTK2B     3'  GCATGGACCAGGCTGGCT    26462           AT  C
                                GCATGGACCAGGT  TG GCT
                                ||||||||||||  || |||
                                CGTACCTGGTCCG  AC CGA
                                     __ _
GAM997  SMAP      3'  TCGTGTGGCCCAGGTACC    26463     CA   A
                                TCG  TGG CCAGGTATT
                                |||  ||| |||||||||
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                                AGC  ACC GGTCCATGG
                                  AC   G
GAM997  TGFBR2   3'  TCGCATGGATGGGGACATC   26464        CCA  _
                                TCGCATGGA   GG TATT
                                |||||||||   || ||||
                                AGCGTACCT   CC GTAG
                                     ACC  T
GAM997  ZFHX1B   5'  TCGCATGGACTCGGCGCCCT  26465        CA   ATT  G
                                TCGCATGGAC  GGT   GC CT
                                ||||||||||  |||   || ||
                                AGCGTACCTG  CCG   CG GA
                                     AG   ___  G
GAM997  BZW2     3'  TGGTAACCTAGGTATTGTGCT  26466    __  _      C
                                TGG  ACC AGGTATTG GCT
                                |||  ||| |||||||| |||
                                ACC  TGG TCCATAAC CGA
                                  AT   A       A
GAM997  CNOT8    5'  TCGCGTGATTAGTTGCGCT   26467     A   ACCA   AT
                                TCGC TGG    GGT  TGCGCT
                                |||| |||    |||  ||||||
                                AGCG ACT    TCA  ACGCGA
                                  C   AA__   __
GAM997  DUSP9    3'  CCGCGTGAGGTATTGCGCT   26468     A  GACC
                                TCGC TG    AGGTATTGCGCT
                                |||| ||    ||||||||||||
                                GGCG AC    TCCATAACGCGA
                                  C  _____
GAM997  FLJ23563 3'  TCACATGGATCTCCGTCTGTGC 26469         ___  AG  A   C
           TC                     TCGCATGGA   CC  GT TTG GCTC
                                |||||||||   ||  || ||| ||||
                                AGTGTACCT   GG  CA GAC CGAG
                                     AGA  __  _   A
GAM997  KIAA0472 3'  TCGCATTGGGTTGGTTTTGC   26470       _  ACCA   A
                                TCGCAT GG    GGT TTGC
                                |||||| ||    ||| ||||
                                AGCGTA CC    CCA AACG
                                   A  CAA_   A
GAM997  KIAA0769 3'  TAGTCCCTAGGTATTGTGCTC  26471     A_  _      C
                                TGG  CC AGGTATTG GCTC
                                |||  || ||||||||| ||||
                                ATC  GG TCCATAAC CGAG
                                  AG  A       A
GAM997  MGC20470 5'  TGTCTCAGGTATTGTGCTC   26472    GAC       C
                                TG   CAGGTATTG GCTC
                                ||   ||||||||| ||||
                                AC   GTCCATAAC CGAG
                                  AGA        A
GAM997  SYTL3    5'  GCATGGACCAAGCGCT      26473          GTATT
                                GCATGGACCAG    GCGCT
                                ||||||||||     |||||
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                                CGTACCTGGTT    CGCGA
                                      _____
GAM998  NXF2    3' GGGTGGTTATGTCACGTG    26476    C  A  CGC
                                GGG GG TTA  GTTACGTG
                                ||| || |||  ||||||||
                                CCC CC AAT  CAGTGCAC
                                  A  _  A__
GAM998  NXF2    3' GGGTGGTTATGTCACGTG    26476    C  A  CGC
                                GGG GG TTA  GTTACGTG
                                ||| || |||  ||||||||
                                CCC CC AAT  CAGTGCAC
                                  A  _  A__
GAM998  DKFZP572C163 3' TTCTGCACTACGTGTTATGTG  26477    GG  GG    C   C
                                TTC  GC  ATTACG GTTA GTG
                                |||  ||  |||||| |||| |||
                                AAG  CG  TGATGC CAAT CAC
                                  A_  __    A   A
GAM999  CSE1L   5'  CCAGAGCGCATGAGCGAGCGGC 26480       AC G       A
                                TCAGAGC  G ATGAGCGAGC GC
                                |||||||  | ||||||||||  ||
                                GGTCTCG  C TACTCGCTCG CG
                                    __ G        C
GAM999  DDX6    3' CAGTGCGGATGAACTGCAG   26481    A  AC     GA
                                CAG GC  GGATGAGC  GCAG
                                ||| ||  ||||||||  ||||
                                GTC CG  CCTACTTG  CGTC
                                  A  __      A_
GAM999  DVL3    3' TCGCAGCACCCTGCGAGCAG  26482   AG   GGATGA
                                TC  AGCAC    GCGAGCAG
                                ||  |||||    ||||||||
                                AG  TCGTG    CGCTCGTC
                                 CG   GGA___
GAM999  EXT1    5' CCAGGGCGGGCGAGCA     26483     A  AC  ATGA
                                TCAG GC  GG   GCGAGCA
                                ||||  ||  ||   |||||||
                                GGTC CG  CC   CGCTCGT
                                  C  __  _____
GAM999  FTSJ2   3' TCAGAGCAGGGGTGGAAAGC  26484       C  A  AGC
                                TCAGAGCA GG TG  GAGC
                                |||||||  || ||  ||||
                                AGTCTCGT CC AC  TTCG
                                    C  C  CT_
GAM999  KCNS2   5' GAGCACGGGTGCCCGCGGC   26485       A  A__  A
                                GAGCACGG TG  GCG GC
                                ||||||||  ||  ||| ||
                                CTCGTGCC AC  CGC CG
                                    C  GGG  _
GAM999  KIFC3   3' CCAGGCAGGTGAGCGAGCAGC  26486     A  C  A
                                TCAG GCA GG TGAGCGAGCAGC
                                |||| ||| || ||||||||||||
```

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                                GGTC CGT CC ACTCGCTCGTCG
                                  _  _ _
GAM999  VCP      5'  CCAGGCGGTGGGCGAGCAGC  26487     A  AC  A  A
                                TCAG GC  GG TG GCGAGCAGC
                                |||| ||  || || |||||||||
                                GGTC CG  CC AC CGCTCGTCG
                                  _ __  _ C
GAM999  FLJ10846 5'  TCAGGGTGCTATTGGCGAGCAG 26488     A__  ACGGA  A
                                TCAG   GC    TG GCGAGCAG
                                ||||   ||    || ||||||||
                                AGTC   CG    AC CGCTCGTC
                                  CCA  ATA__  _
GAM999  FLJ13881 3'  CAGAGCATGGGCAGCAG     26489       C  ATGA  G
                                CAGAGCA GG    GC AGCAG
                                ||||||| ||    || |||||
                                GTCTCGT CC    CG TCGTC
                                    A  ____  _
GAM999  FLJ20333 5'  GCACGCCGACCGCGAGCAGC  26490      __  GA
                                GCACG  GAT  GCGAGCAGC
                                |||||  |||  |||||||||
                                CGTGC  CTG  CGCTCGTCG
                                   GG   G_
GAM999  FLJ22969 3'  TCAGAGCAGGGGTGAGGAAGC  26491       C  A   C
                                TCAGAGCA GG TGAG GAGC
                                |||||||| || |||| ||||
                                AGTCTCGT CC ACTC TTCG
                                    C  C   C
GAM999  GFR      3'  TCAGAGCATGGATGCTAGC   26492       C    AGCG
                                TCAGAGCA GGATG   AGC
                                |||||||| |||||   |||
                                AGTCTCGT CCTAC   TCG
                                    A    GA__
GAM999  HEMK     3'  TCAGAGCACTGATGGGGC    26493        G   A_
                                TCAGAGCAC GATG  GC
                                ||||||||| ||||  ||
                                AGTCTCGTG CTAC  CG
                                    A   CC
GAM999  KIAA0352 3'  TCAGGGCTGGGGACAAGCAGC  26494     A  AC_  TG  G
                                TCAG GC   GGA  AGC AGC
                                |||| ||   |||  ||| |||
                                AGTC CG   CCT  TCG TCG
                                  C  ACC   GT  _
GAM999  KIAA1881 3'  AGAGCACGGGGGCCCGGCGGC  26495       A___  A  A
                                AGAGCACGG   TG GCG GC
                                |||||||||   || ||| ||
                                TCTCGTGCC   GC CGC CG
                                    CCGG  _  _
GAM999  MGC2452  5'  CAGGGTACATCAGAGCGAGCAG 26496    AGC  GAT
            C                   CAG  ACG  GAGCGAGCAGC
                                |||  |||  ||||||||||
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                                GTC  TGT  CTCGCTCGTCG
                                  CCA  AGT
GAM999  PIP3-E   3'  TCAGAGCATGGGGCAGC    26497       C  ATGA  G
                                TCAGAGCA GG   GC AGC
                                |||||||| ||   || |||
                                AGTCTCGT CC   CG TCG
                                     A  C___  _
GAM999  SLC12A5  3'  CCAGAGCACGGAGAAGGCGGC  26498          T  _  A
                                TCAGAGCACGGA GAG CG GC
                                |||||||||||| ||| || ||
                                GGTCTCGTGCCT TTC GC CG
                                       C  C  _
GAM999  SLC16A8  3'  GCACAGATGAGGGAGGCAG   26499         C  _
                                GCACGGATGAG GAG CAG
                                |||||||||| ||| |||
                                CGTGTCTACTC CTC GTC
                                       C  C
GAM999  TOB2     3'  CAGGCCGGTGGGCGAGC    26500    A  A  A  A
                                CAG GC CGG TG GCGAGC
                                ||| || ||| || ||||||
                                GTC CG GCC AC CGCTCG
                                  _  _  _  C
GAM999  ZNF212   3'  TCAGAGCAGGGCTAAGCA   26501       C  A
                                TCAGAGCA GG TGAGCG
                                |||||||| || ||||||
                                AGTCTCGT CC ATTCGT
                                     C  G
GAM999  LOC146733 3'  TCAGAGCAGGCTGCGGGCAG  26502       C  ATGA  A
                                TCAGAGCA GG   GCG GCAG
                                |||||||| ||   ||| ||||
                                AGTCTCGT CC   CGC CGTC
                                     _  GA__  C
GAM999  LOC149711 3'  TCAGAGCATAGAAAAAGTAGC  26503       CG  T_  CG
                                TCAGAGCA  GA  GAG  AGC
                                ||||||||  ||  |||  |||
                                AGTCTCGT  CT  TTC  TCG
                                     AT  TT  A_
GAM999  LOC200583 3'  TCAGAGTGGTGGTTACGAGCAG 26504      CAC  A  A__
           C                     TCAGAG  GG TG  GCGAGCAGC
                                ||||||  || ||  |||||||||
                                AGTCTC  CC AC  TGCTCGTCG
                                   A__  _  CAA
GAM999  LOC201522 3'  TCAGGGCCGTGGCGAGCAG   26505    A  A  GA  A
                                TCAG GC CG  TG GCGAGCAG
                                |||| || ||  || ||||||||
                                AGTC CG GC  AC CGCTCGTC
                                  C  _  __  _
GAM1000  MADH7   5'  AGTCGTTTGCCTGCTAAGGAG  26508   C      C  GGTGCC
                                AG CGTTTGCC GT    GGAG
                                || |||||||| ||    ||||
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                                TC GCAAACGG CG     CCTC
                                 A      A  ATT___
GAM1000  RNF4     3'  GCCGTTTGTTTGGCGTGA    26509       CCCG    CCG
                                GCCGTTTG   TGGTG   GA
                                ||||||||   |||||  ||
                                CGGCAAAC   ACCGC   CT
                                    AA__    A__
GAM1000  C20orf46 3'  GCTGCTTGCCCGTGTGGG    26510    C        G  CC
                                GC GTTTGCCCGTG TG  GG
                                || ||||||||||| ||  ||
                                CG CGAACGGGCAC AC  CC
                                 A         _ __
GAM1000  KIAA0930 3'  GCCGTCTGCTCAGCTGGA    26511        C  TGGT  C
                                GCCGTTTGC CG   GC GGA
                                ||||||||| ||   || |||
                                CGGCAGACG GT   CG CCT
                                     A  ____  A
GAM1000  KIAA1535 3'  AGCCATTTGCCCCTCCACCGG  26512          GTGGT
                                AGCCGTTTGCCC    GCCGG
                                ||||||||||||    |||||
                                TCGGTAAACGGG    TGGCC
                                      GAGG_
GAM1000  MGC20576 5'  GCTGTTTGCCCCAGCTGGG   26513    C      G   GCC
                                GC GTTTGCCC TGGT   GG
                                || |||||||| ||||   ||
                                CG CAAACGGG GTCG   CC
                                 A       _   AC_
GAM1000  LOC146375 5'  AGCTGTTGCCCGTGACCAG   26514     C   T     GT
                                AGC GTT GCCCGTG  GCCGG
                                ||| ||| |||||||  |||||
                                TCG CAA CGGGCAC  TGGTC
                                 A  _     __
GAM1000  LOC253776 5'  ATTTGTGGTGGTGGTGCTGGAG 26515      CCC__     C
                                GTTTG    GTGGTGC GGAG
                                |||||    ||||||| ||||
                                TAAAC    CACCACG CCTC
                                   ACCAC      A
GAM1001  ACY1     3'  TGTCCTTGTGTTAGTACTTCAG 26518     G   ACA_   CC
            A                    TGT CCT    TTAG  ATTTCAGA
                                ||| |||    ||||  ||||||||
                                ACA GGA    AATC  TGAAGTCT
                                 _   ACAC    A_
GAM1001  BTEB1    3'  TATGTTTACACATTTCAG    26519     CC    TTAGC
                                TGTG  TACA    CATTTCAG
                                ||||  ||||    ||||||||
                                ATAC  ATGT    GTAAAGTC
                                  AA   _____
GAM1001  DUSP5    3'  GTGTCTACACAACATTTCAG   26520     C     TAGC
                                GTG CTACAT    CATTTCAG
                                ||| ||||||    ||||||||
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                                CAC GATGTG   GTAAAGTC
                                  A     TT__
GAM1001 E2F3     3' TGTGCCTACCATTGGGTCAG  26521       ACATTA    ___
                                TGTGCCT     GCCATT   TCAG
                                |||||||     ||||||   ||||
                                ACACGGA     TGGTAA   AGTC
                                    _______     CCC
GAM1001 TRPC6    3' TGTGTCCACATTAGCCAC    26522     C
                                TGTG CTACATTAGCCAT
                                |||| ||||||||||||
                                ACAC GGTGTAATCGGTG
                                  A
GAM1001 DKFZP564A022 3' TGTTCTACATTAGCTCAG    26523     GC        CATT
                                TGT  CTACATTAGC    TCAG
                                |||  ||||||||||    ||||
                                ACA  GATGTAATCG    AGTC
                                  A_        _____
GAM1001 FLJ10980  3' TGTGCTACATTAGAACACTAGA 26524      C       C_    TC
                                TGTGC TACATTAG  CATT  AGA
                                ||||| ||||||||  ||||  |||
                                ACACG ATGTAATC  GTGA  TCT
                                   _       TT   __
GAM1001 KIAA1554  3' TGTGTCCAGTGAAGTCATTTCA 26525      _  TACATT  C
          G                      TGTG CC     AG CATTTCAG
                                |||| ||     || ||||||||
                                ACAC GG     TC GTAAAGTC
                                  A  TCACT_  A
GAM1001 SEC15B   3' TGCTTACAAATGAATTTCAGA  26526     C    TTAGCC
                                TGC TACA     ATTTCAGA
                                ||| ||||     ||||||||
                                ACG ATGT     TAAAGTCT
                                  A    TTACT_
GAM1001 SRPK1    3' TGCTTACATTAAAAATCAGA   26527     C       CCATT
                                TGC TACATTAG     TCAGA
                                ||| ||||||||     |||||
                                ACG ATGTAATT     AGTCT
                                  A       TTT__
GAM1001 LOC132332 3' TGTGCCTATATGGTTACCAT   26528        C  TA__
                                TGTGCCTA AT    GCCAT
                                |||||||| ||    |||||
                                ACACGGAT TA    TGGTA
                                     A  CCAA
GAM1001 LOC143310 5' GTGTCTATCTTCATTTCAGA   26529     C   CA  AGC
                                GTG CTA  TT   CATTTCAGA
                                ||| |||  ||   |||||||||
                                CAC GAT  AA   GTAAAGTCT
                                  A   AG  ___
GAM1001 LOC146856 3' TGTGCCTACCATTGGGTCAG   26521       ACATTA    ___
                                TGTGCCT     GCCATT   TCAG
                                |||||||     ||||||   ||||
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                                ACACGGA     TGGTAA   AGTC
                                   _______     CCC
GAM1001  LOC147042 5'  TGTGTCACATTAGCCCAGTCAG 26530      CC        ATT
                                TGTG  TACATTAGCC   TCAG
                                ||||  ||||||||||   ||||
                                ACAC  GTGTAATCGG   AGTC
                                  A_        GTC
GAM1001  LOC148189 5'  TGTTCCTACACCAGTTTCAGA  26531     G        CCA
                                TGT CCTACATTAG   TTTCAGA
                                ||| ||||||||||   |||||||
                                ACA GGATGTGGTC   AAAGTCT
                                  A        ___
GAM1001  LOC149684 5'  TGTGCCTATTTCCTTCAG    26532        CATTAG  AT
                                TGTGCCTA     CC  TTCAG
                                ||||||||     ||  |||||
                                ACACGGAT     GG  AAGTC
                                     AAA___  __
GAM1001  LOC196890 3'  TGTGGCTGCCACCCATTTCAG  26533     C  A_   TAG
                                TGTG CT  CAT   CCATTTCAG
                                |||| ||  |||   |||||||||
                                ACAC GA  GTG   GGTAAAGTC
                                  C  CG   ___
GAM1001  LOC222256 3'  TGTTCCTGTATCATTTCAG    26534     G   ACAT  GC
                                TGT CCT    TA  CATTTCAG
                                ||| |||    ||  ||||||||
                                ACA GGA    AT  GTAAAGTC
                                  A   C___  A_
GAM1001  LOC254778 3'  TGTGCCTGTCATCCCAGCTTTC 26535       A_    __   CA
           AG                     TGTGCCT  CATT  AGC  TTTCAG
                                ||||||| ||||  |||  ||||||
                                ACACGGA  GTAG  TCG  AAAGTC
                                    CA    GG   __
GAM1001  LOC81034  3'  TGTGTTGATGGCAGCCATTTCA 26536     CCTACAT
           G                      TGTG      TAGCCATTTCAG
                                ||||      ||||||||||||
                                ACAC      GTCGGTAAAGTC
                                  AACTACC
GAM1002  UNC13     5'  CAGCTCCTCATGGTCCCGGTCG 26539       GA  TAGA
                                CGGCTCC  TC    TCCCGGTCG
                                |||||||  ||    |||||||||
                                GTCGAGG  AG    AGGGCCAGC
                                    __  TACC
GAM1002  CNTNAP1   5'  CGGCTCCGGCTAGGGC      26540        AT   ATCCC
                                CGGCTCCG  CTAG    GGT
                                ||||||||  ||||    |||
                                GCCGAGGC  GATC    CCG
                                     C_   _____
GAM1002  DKFZP434H0820 5'  CGGCTCCGCTCCCGGT      26541        ATCTAGA
                                CGGCTCCG      TCCCGGT
                                ||||||||      |||||||
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                                GCCGAGGC      AGGGCCA
                                    G_______
GAM1002  FLJ10925  5'  GGCTCCGAATCCTGGTC     26542        TCTAG    C
                                GGCTCCGA    ATCC GGTC
                                ||||||||    |||| ||||
                                CCGAGGCT    TAGG CCAG
                                    ______    A
GAM1002  KIAA0982  5'  GCTCCGCCTTGGTCCCGGTCG  26543       A   AGA
                                GCTCCG TCT   TCCCGGTCG
                                |||||| |||   |||||||||
                                CGAGGC GGA   AGGGCCAGC
                                   _   ACC
GAM1002  KIAA1887  5'  CGGCTCCGTCTAGGGGT     26544        A    ATCCC
                                CGGCTCCG TCTAG    GGT
                                |||||||| |||||    |||
                                GCCGAGGC AGATC    CCA
                                    _    C_____
GAM1002  LOC145644 5'  CGTTCTGATCTAGATGGCC   26545    GC  C       CCC
                                CG  TC GATCTAGAT   GGTC
                                ||  || |||||||||   ||||
                                GC  AG CTAGATCTA   CCGG
                                 A_  A       ___
GAM1002  LOC201707 5'  CGGCCTCGAGGTCCCGGTC   26546     TC   TCTA A
                                CGGC  CGA    G TCCCGGTC
                                ||||  |||    | ||||||||
                                GCCG  GCT    C AGGGCCAG
                                  GA  _____ C
GAM1003  ACT      5'  CCTGCATTTCCTCCAAGTC   26549    CC  CC      AAC
                                CC  CA  TCCTCCA   GGTC
                                ||  ||  |||||||   ||||
                                GG  GT  AGGAGGT   TCAG
                                 AC  AA      ___
GAM1003  ACTR1B    3'  CCCCCACCCCCTTTTAGGTC  26550          CCAAAC
                                CCCCCACCTCCT     GGTC
                                ||||||||||||     ||||
                                GGGGGTGGGGGA     CCAG
                                      AAAT__
GAM1003  ADCY6     3'  CCCCCACCCCCCACAGT     26551          TCCAA
                                CCCCCACCTCC    ACGGT
                                ||||||||||    |||||
                                GGGGGTGGGGG    TGTCA
                                    _____
GAM1003  ADCY6     3'  CCCCCACCCCCCACAGT     26551          TCCAA
                                CCCCCACCTCC    ACGGT
                                ||||||||||    |||||
                                GGGGGTGGGGG    TGTCA
                                    _____
GAM1003  ANXA6     3'  CCCCTGCCCCTTCCTTAGTC  26552      CA   C   AAAC
                                CCCC  CCTC TCC    GGTC
                                ||||  |||| |||    ||||
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                                GGGG  GGGG AGG    TCAG
                                  AC    A   AA__
GAM1003  AP2B1    3'  CCCCATTTCTTTCCAGAGTC   26553      CC  C_    AAC
                                CCCCA  TC  TCCA   GGTC
                                |||||  ||  ||||   ||||
                                GGGGT  AG  AGGT   TCAG
                                  AA  AA    C__
GAM1003  BAT1     3'  CCTCTCCTGAAGGACAGACGGT 26554    AC     C_____  A
             C                   CC  CTCCT     CA ACGGTC
                                 ||  |||||     || ||||||
                                 GG  GAGGA     GT TGCCAG
                                  A_     CTTCCT  C
GAM1003  BAT1     3'  CCTCTCCTGAAGGACAGACGGT 26554    AC     C_____  A
             C                   CC  CTCCT     CA ACGGTC
                                 ||  |||||     || ||||||
                                 GG  GAGGA     GT TGCCAG
                                  A_     CTTCCT  C
GAM1003  BCAS1    3'  CCTCCACCTCCTGGGTACAAGC 26555    _       C____   A
             GGT                   CC CCACCTCCT     CAA CGGT
                                 || |||||||||     ||| ||||
                                 GG GGTGGAGGA     GTT GCCA
                                  A        CCCAT   C
GAM1003  BMP1     3'  CCCCCACCTCCTATGGACAGTC 26556           CCAA
                                 CCCCCACCTCCT    ACGGTC
                                 ||||||||||||    ||||||
                                 GGGGGTGGAGGA    TGTCAG
                                       TACC
GAM1003  CACNA2D2 3'  CCTCCCCCTCCTCCCAGTC    26557    _  A       AAA
                                 CC CCC CCTCCTCC   CGGTC
                                 || ||| ||||||||   |||||
                                 GG GGG GGAGGAGG   GTCAG
                                  A  _       ____
GAM1003  CCND1    3'  CCTCACACCTCCTCCCGCCTGT 26558    CC_        AAACG
             C                   CC   CACCTCCTCC     GTC
                                 ||   ||||||||||     |||
                                 GG   GTGGAGGAGG     CAG
                                  AGT         GCGGA
GAM1003  CSRP1    3'  CCCCCCTCCTCATCTTGGTC   26559      A      CAAAC
                                 CCCC CCTCCTC     GGTC
                                 ||||  |||||||    ||||
                                 GGGG GGAGGAG     CCAG
                                   _      TAGAA
GAM1003  DIO3     3'  CCCCCACCTCTCTTTGACCGTT 26560          _ T________  AAAC
             TGG                   CCCCACCTC C       CC    GG
                                 |||||||||  |       ||    ||
                                 GGGGTGGAG G       GG    CC
                                      A AAAIIICT  CAAA
GAM1003  DLEC1    3'  CCTCCAGCTCCAGGACGGTC   26561    A  TC     A_
                                 CC CC  CTCCA  ACGGTC
                                 || ||  |||||  ||||||
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                                GG GG  GAGGT  TGCCAG
                                 A  TC    CC
GAM1003  DLEC1    3'  CCTCCAGCTCCAGGACGGTC  26561    A  TC    A_
                                CC CC  CTCCA  ACGGTC
                                || ||  |||||  ||||||
                                GG GG  GAGGT  TGCCAG
                                 A  TC    CC
GAM1003  DYRK1B   3'  CCCCCACCCCCTCCTAGGGTC  26562            AAAC
                                CCCCCACCTCCTCC   GGTC
                                ||||||||||||||   ||||
                                GGGGGTGGGGGAGG   CCAG
                                       ATC_
GAM1003  EN1      5'  CCTCCCCCTCCTTCAGGC    26563    _  A    C  AAC
                                CC CCC CCTCCT CA   GGT
                                || ||| |||||| ||   |||
                                GG GGG GGAGGA GT   CCG
                                 A  _     A  ___
GAM1003  EPHA1    3'  CCCCCACCTCCCTTTGACCGTT 26564         T_________  AAAC
              TGG                  CCCCACCTCC       CC   GG
                                |||||||||        ||   ||
                                GGGGTGGAGG       GG   CC
                                     GAAAIIICT  CAAA
GAM1003  FABP2    3'  CCTCCAACTCTTCCAAGTC   26565    _  C  C   AAC
                                CC CCA CTC TCCA   GGTC
                                || ||| ||| ||||   ||||
                                GG GGT GAG AGGT   TCAG
                                 A  T  A   ___
GAM1003  FN14     3'  CCCCCACCCCCCTTGTGGT   26566          CCAAAC
                                CCCCCACCTCCT     GGT
                                ||||||||||||     |||
                                GGGGGTGGGGGG     CCA
                                      AACA__
GAM1003  FOSB     3'  CCTCCTCCTCCTCTTCCAAGTC 26567    _ A      CAAAC
                                CC CC CCTCCTC    GGTC
                                || || |||||||    ||||
                                GG GG GGAGGAG    TCAG
                                 A  A      AAGGT
GAM1003  FOSB     3'  CCTCCTCCTCTTCCAAGTC   26568    _ A   C   AAC
                                CC CC CCTC TCCA   GGTC
                                || || |||| ||||   ||||
                                GG GG GGAG AGGT   TCAG
                                 A  A   A   ___
GAM1003  FOXD2    5'  CCCCCACCTTCCTGGC      26569         _  CCAAAC
                                CCCCCACCT CCT     GGT
                                |||||||||  |||     |||
                                GGGGGTGGA GGA     CCG
                                     A  _______
GAM1003  GABRG2   5'  CCCCCACCTGCCTCTAGTAGGT 26570         _   CAAAC
              C                   CCCCCACCT CCTC    GGTC
                                |||||||||  ||||    ||||
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                                GGGGGTGGA GGAG    CCAG
                                     C   ATCAT
GAM1003  GALGT    3'  CCCCACCCCCTCGGT      26571          CAAAC
                                CCCCACCTCCTC    GGT
                                ||||||||||||    |||
                                GGGGTGGGGGAG    CCA
                                      _____
GAM1003  GATA2    3'  CCCCACCTGGGCAGCGGTC   26572       CCTC  AA
                                CCCCACCT   CA  CGGTC
                                ||||||||   ||  |||||
                                GGGGTGGA   GT  GCCAG
                                    CCC_  C_
GAM1003  GDF2     3'  CCCTTTCCTCCTCCAGGC    26573    CCA       AAC
                                CCC   CCTCCTCCA   GGT
                                |||   |||||||||   |||
                                GGG   GGAGGAGGT   CCG
                                  AAA       ___
GAM1003  GLTSCR1  3'  CCCCCACCCCCTCTCCGGT   26574          CAAA
                                CCCCCACCTCCTC    CGGT
                                ||||||||||||    ||||
                                GGGGGTGGGGGAG    GCCA
                                      AG__
GAM1003  HDGF     5'  CCTCCACCCCCCGCCCGGTC   26575    _       _ AAA
                                CC CCACCTCCT CC   CGGTC
                                || |||||||| ||   |||||
                                GG GGTGGGGGG GG   GCCAG
                                 A        C ___
GAM1003  INHBB    3'  CCCCGCCATTTCCTCCTGCGGT 26576     A ___     AAA
              C                  CCCC CC   TCCTCC   CGGTC
                                ||||  ||   ||||||   |||||
                                GGGG GG   AGGAGG   GCCAG
                                  C  TAA     AC_
GAM1003  KCNJ4    3'  CCCCCACCTTCCTCCAGAAGGT 26577         _     AAC
              C                  CCCCCACCT CCTCCA   GGTC
                                |||||||| ||||||   ||||
                                GGGGGTGGA GGAGGT   CCAG
                                     A     CTT
GAM1003  KCNK5    3'  CCTCCACCCCACTACGGT    26578    _     _ CCAA
                                CC CCACCTC CT    ACGGT
                                || |||||| ||    |||||
                                GG GGTGGGG GA    TGCCA
                                 A      T _____
GAM1003  KLF4     5'  CCCCCACCACTGTCGCGGTC  26579        TC  CCAAA
                                CCCCCACC  CT    CGGTC
                                ||||||||  ||    |||||
                                GGGGGTGG  GA    GCCAG
                                    T_  CAGC_
GAM1003  LEP      3'  CCCTCACCTCCTTCAAAC    26580    _       C
                                CCC CACCTCCT CAAAC
                                ||| |||||||| |||||
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                                GGG GTGGAGGA GTTTG
                                  A       A
GAM1003  MEIS1    3'  CCATGCCTCCTCCTACCAGTC  26581     __       AAA
                                CCA  CCTCCTCC   CGGTC
                                |||  ||||||||   |||||
                                GGT  GGAGGAGG   GTCAG
                                  AC       ATG
GAM1003  MGAT3    5'  CCCCCACTTCCACCCCGTC   26582       C   T  AAACG
                                CCCCCAC TCC CC    GTC
                                ||||||| ||| ||    |||
                                GGGGGTG AGG GG    CAG
                                    A  T  GG___
GAM1003  MMP9     3'  CCTCCCTTTCCTCCAGAAC   26583    _  ACC      _
                                CC CCC   TCCTCCA AAC
                                || |||   ||||||| |||
                                GG GGG   AGGAGGT TTG
                                 A  AA_     C
GAM1003  NGB      5'  CCCCCGCCCCCTCCAGGC    26584      A       AAC
                                CCCCC CCTCCTCCA   GGT
                                ||||| |||||||||   |||
                                GGGGG GGGGGAGGT   CCG
                                  C       ___
GAM1003  PFKFB2   3'  CCTCCTCCTCCAGATC      26585    A       AAC
                                CC CCTCCTCCA   GGTC
                                || |||||||||   ||||
                                GG GGAGGAGGT   CTAG
                                 A       ___
GAM1003  PHGDH    5'  CCTCCTCCTCCTCTTACAGTC  26586    _ A      CAA
                                CC CC CCTCCTC   ACGGTC
                                || || |||||||   ||||||
                                GG GG GGAGGAG   TGTCAG
                                 A A      AA_
GAM1003  PIP5K1A  5'  CCCCGCCCCCTCCGGGCC    26587     A       AAAC
                                CCCC CCTCCTCC    GGTC
                                |||| ||||||||    ||||
                                GGGG GGGGGAGG    CCGG
                                  C       C___
GAM1003  PTPRJ    5'  CCGCTGCCTCCTCCGCGCGTC  26588    CCCA       AAA _
                                CC    CCTCCTCC   CG GTC
                                ||    ||||||||   || |||
                                GG    GGAGGAGG   GC CAG
                                 CGAC       C__  G
GAM1003  RAB5B    3'  CCTCCACCTCCGCCCAGT    26589    _      T  AAA
                                CC CCACCTCC CC   CGGT
                                || |||||||| ||   ||||
                                GG GGTGGAGG GG   GTCA
                                 A       C  ___
GAM1003  RENBP    5'  CCTCCCCCTCCTCTTCAGGGT  26590    _  A      CAAAC
                                CC CCC CCTCCTC    GGT
                                || ||| |||||||    |||
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                                GG GGG GGAGGAG    CCA
                                 A  _      AAGTC
GAM1003  RFC2    3'  CCTCCACCTCCTCCTCCTGGGT 26591    _        AAAC_
                                CC CCACCTCCTCC    GGT
                                || ||||||||||    |||
                                GG GGTGGAGGAGG    CCA
                                 A         AGGAC
GAM1003  SDHC    3'  CCCCCACCTCTCTTCGACCGTT 26592        _ T_______  AAAC
             TGG                  CCCCACCTC C       CC   GG
                                |||||||| |       ||   ||
                                GGGGTGGAG G       GG   CC
                                     A AAGIIICT  CAAA
GAM1003  SLC6A2  3'  CCTCCTTCTCCTCCAGGC    26593    _ AC       AAC
                                CC CC  CTCCTCCA   GGT
                                || ||  ||||||||   |||
                                GG GG  GAGGAGGT   CCG
                                 A  AA       ___
GAM1003  SP3     5'  CCTCCTCCTCCTCCTGGTC    26594    _ A       AAAC
                                CC CC CCTCCTCC    GGTC
                                || || ||||||||    ||||
                                GG GG GGAGGAGG    CCAG
                                 A  A       A___
GAM1003  STARD5   5'  CCCACACCTCCTCTAGTGTC   26595     _       CAAACG
                                CCC CACCTCCTC     GTC
                                ||| |||||||||     |||
                                GGG GTGGAGGAG     CAG
                                  T        ATCA__
GAM1003  SURF5    3'  CCCCTCCAGCTCAAACGGTC   26596     A  TC   C
                                CCCC CC  CTC AAACGGTC
                                |||| ||  ||| ||||||||
                                GGGG GG  GAG TTTGCCAG
                                  A  TC  _
GAM1003  TEAD3    3'  CCCCACCTCTCTGAGGTC     26597         C  CAAAC
                                CCCCACCTC TC     GGTC
                                ||||||||| ||     ||||
                                GGGGTGGAG AG     CCAG
                                     _  ACT__
GAM1003  TMEPAI   3'  CCCTCATGCTCTCCTCTGGTC  26598     _ C___     CAAAC
                                CCC CA    CTCCTC     GGTC
                                ||| ||    ||||||     ||||
                                GGG GT    GAGGAG     CCAG
                                  A  ACGA     A____
GAM1003  USP7     5'  CCTCCTCCTCCTCCCGCGCGTC 26599    _ A       AAA  _
                                CC CC CCTCCTCC   CG GTC
                                || || ||||||||   || |||
                                GG GG GGAGGAGG   GC CAG
                                 A  A       GC_  G
GAM1003  VAT1     3'  CCTCCACCTCCCATTGCAATGG 26600    _       CCA__  C
             T                    CC CCACCTCCT     AA GGT
                                || |||||||||     || |||
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                                GG GGTGGAGGG    TT CCA
                                 A       TAACG  A
GAM1003  VEGF     5'  CCTCCCCCTCCTCCGGC     26601    _  A      AAAC
                                CC CCC CCTCCTCC    GGT
                                || ||| ||||||||    |||
                                GG GGG GGAGGAGG    CCG
                                 A  _      _____
GAM1003  ZNF219   5'  CCCCCGCCCCCTCCCCGGTC   26602      A      AAA
                                CCCCC CCTCCTCC   CGGTC
                                ||||| ||||||||   |||||
                                GGGGG GGGGGAGG   GCCAG
                                   C       G__
GAM1003  54TM     5'  CCCCCACCCCGCCGGT      26603        T  T  AAAC
                                CCCCCACC CC CC    GGT
                                |||||||| || ||    |||
                                GGGGGTGG GG GG    CCA
                                     _  C  _____
GAM1003  AF9Q34   3'  CCTCCCATCTTCCTGTGGTC   26604    _   CC  C   AAAC
                                CC CCCA  TC TCC    GGTC
                                || ||||  || |||    ||||
                                GG GGGT  AG AGG    CCAG
                                 A    __  A   ACA_
GAM1003  ARHGAP11A 5'  CCCCCTTCCTCCAAAC      26605      ACC
                                CCCCC   TCCTCCAAAC
                                |||||   ||||||||||
                                GGGGG   AGGAGGTTTG
                                   A__
GAM1003  ARHGAP9  5'  CCACCACCTCCTCTGCAGTC   26606    _        CAAA
                                CC CCACCTCCTC    CGGTC
                                || ||||||||||    |||||
                                GG GGTGGAGGAG    GTCAG
                                 T        AC__
GAM1003  B3GNT6   3'  CCCTTCCCTCCTCCAGAAC    26607     CCA       _
                                CCC   CCTCCTCCA AAC
                                |||   ||||||||| |||
                                GGG   GGAGGAGGT TTG
                                  AAG        C
GAM1003  BHMT     3'  CCTCCCCTCCTCCCCATTGGTC 26608    _ A       AAAC_
                                CC CC CCTCCTCC     GGTC
                                || || ||||||||     ||||
                                GG GG GGAGGAGG     CCAG
                                 A  _       GGTAA
GAM1003  C14orf4  5'  CCCCCACCTCCTACTGCGGT   26609          CCAAA
                                CCCCCACCTCCT    CGGT
                                ||||||||||||    ||||
                                GGGGGTGGAGGA    GCCA
                                       TGAC_
GAM1003  C1QTNF6  3'  CCCCCACACTCCTGGGT     26610        _    CCAAAC
                                CCCCCAC CTCCT     GGT
                                ||||||| |||||     |||
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                                GGGGGTG GAGGA     CCA
                                   T    C_____
GAM1003  C6orf11   3'  CCCCCACCTCCTTGTTGACCGT 26611          T__________  AAAC
                TTGG                  CCCACCTCC        CC   GG
                                      |||||||||        ||   ||
                                      GGGTGGAGG        GG   CC
                                         AACAAIIICT  CAAA
GAM1003  C8orf13   3'  CCTCCACTTCTCATCTTGGGTC 26613    _   __  C  CAAAC
                                      CC CCAC  CTC TC    GGTC
                                      || ||||  ||| ||    ||||
                                      GG GGTG  GAG AG    CCAG
                                       A   AA  T  AAC__
GAM1003  C8orf13   5'  CCGCCGCCTCCTCCTGCGCGGG 26612    _ A       AAAC__
                TC                     CC CC CCTCCTCC     GGTC
                                      || || ||||||||     ||||
                                      GG GG GGAGGAGG     CCAG
                                       C  C       ACGCGC
GAM1003  CFLAR     5'  CCTACACCTCCTCCCGTGGTC  26614    CC        AAAC
                                      CC  CACCTCCTCC    GGTC
                                      ||  ||||||||||    ||||
                                      GG  GTGGAGGAGG    CCAG
                                       AT        GCA_
GAM1003  CSEN      3'  CCCCTGCCCCCCAGCTGGTC   26615     ACC      AAC
                                      CCCC   TCCTCCA   GGTC
                                      ||||   |||||||   ||||
                                      GGGG   GGGGGGT   CCAG
                                        AC_      CGA
GAM1003  D6S2654E  3'  CCCCCACCCCCGGTTGACCGTT 26616          T_________  AAAC
                TGG                    CCCCACCTCC        CC   GG
                                      ||||||||||        ||   ||
                                      GGGGTGGGGG        GG   CC
                                           CCAAIIICT  CAAA
GAM1003  DJ1042K10.2 3'  CCCCCACCTCCTCACAAGGT   26617           _   AC
                                      CCCCCACCTCCTC CAA  GGT
                                      |||||||||||| |||  |||
                                      GGGGGTGGAGGAG GTT  CCA
                                               T   __
GAM1003  DKFZP434A0225 5'  CCCCACCCACCCGGACGGT    26618        TC T  AA
                                      CCCCACC  C CC  ACGGT
                                      |||||||  | ||  |||||
                                      GGGGTGG  G GG  TGCCA
                                         GT _  CC
GAM1003  DKFZP434B205 3'  CCTCACCTCCCGCATGGTC    26619     C       C  AAC
                                      CC CACCTCCT CA   GGTC
                                      || ||||||||  ||   ||||
                                      GG GTGGAGGG GT   CCAG
                                       A       C  A__
GAM1003  DKFZP566G1424 5'  CCCCCATCCCTCCTTGACCGTT 26620       __     T_______  AAAC
                TGG                    CCCCA  CCTCC      CC    GG
                                      |||||  |||||      ||    ||
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                                GGGGT GGAGG     GG   CC
                                  AG    AAIIICT CAAA
GAM1003 DKFZp586I021 3' CCTGCCCCCTCCAAGAAGT  26621   CA       AC
                                CC CCTCCTCCAA GGT
                                || |||||||||| |||
                                GG GGGGGAGGTT TCA
                                 AC       CT
GAM1003 DKFZP586I2223 3' CCCACCTCCCTTCAAAAC  26622       __ C
                                CCCACCTCC TC AAAC
                                ||||||||| || ||||
                                GGGTGGAGG AG TTTG
                                     GA T
GAM1003 DKFZP586I2223 3' CCCACCTCCCTTCAAAAC  26622       __ C
                                CCCACCTCC TC AAAC
                                ||||||||| || ||||
                                GGGTGGAGG AG TTTG
                                     GA T
GAM1003 DKFZP586I2223 3' CCCACCTCCCTTCAAAAC  26622       __ C
                                CCCACCTCC TC AAAC
                                ||||||||| || ||||
                                GGGTGGAGG AG TTTG
                                     GA T
GAM1003 ERN1    3' CCCCCACCTCTCAATTCCGGTC 26623        C CAAA_
                                CCCCCACCTC TC    CGGTC
                                |||||||||| ||    |||||
                                GGGGGTGGAG AG    GCCAG
                                     _ TTAAG
GAM1003 FADS1   3' CCTCCACCTCCCCGGT     26624   _      CCAAA
                                CC CCACCTCCT    CGGT
                                || |||||||||    ||||
                                GG GGTGGAGGG    GCCA
                                 A      _____
GAM1003 FAP48   5' CCGCCACCTCCTCCGGC    26625   _       AAAC
                                CC CCACCTCCTCC   GGT
                                || ||||||||||   |||
                                GG GGTGGAGGAGG   CCG
                                 C       ____
GAM1003 FAP48   5' CCGCCACCTCCTCCGGC    26625   _       AAAC
                                CC CCACCTCCTCC   GGT
                                || ||||||||||   |||
                                GG GGTGGAGGAGG   CCG
                                 C       ____
GAM1003 FLJ10506 3' CCCATCTGCCTTCCAGGTC  26626    C _ _  AAC
                                CCCA CT CCT CCA  GGTC
                                |||| || ||| |||  ||||
                                GGGT GA GGA GGT  CCAG
                                  A C  A  ___
GAM1003 FLJ10521 3' CCTCAGCCTCCTCCTGGTC  26627   C _     AAAC
                                CC CA CCTCCTCC   GGTC
                                || || ||||||||   ||||
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                                GG GT GGAGGAGG    CCAG
                                 A  C       A___
GAM1003  FLJ10597  3'  CCCCCACCTCCCTGCGACCGTT 26628          T_________  AAAC
               TGG                  CCCCACCTCC        CC    GG
                                    ||||||||||        ||    ||
                                    GGGGTGGAGG        GG    CC
                                          GACGIIICT  CAAA
GAM1003  FLJ10709  3'  CCTCCCTCCTCTCTCAGGGTC  26629    _   A    _   CAAAC
                                    CC CCC CCTC CTC     GGTC
                                    || ||| |||| |||     ||||
                                    GG GGG GGAG GAG     CCAG
                                     A  A    A  TC___
GAM1003  FLJ11000  3'  CCCCACCTCCTCTGTAGTGGGT 26630           CAAAC__
                                    CCCCACCTCCTC       GGT
                                    ||||||||||||       |||
                                    GGGGTGGAGGAG       CCA
                                           ACATCAC
GAM1003  FLJ12056  3'  CCTGCCCCCAAAATGGTC    26631     _       C_
                                    CCT CCTCCAAA  GGTC
                                    ||| ||||||||  ||||
                                    GGA GGGGGTTT  CCAG
                                      C       TA
GAM1003  FLJ12770  3'  CCACTACTTCCTCCAAAGGT   26632      C___        C
                                    CCAC    TCCTCCAAA GGT
                                    ||||    ||||||||| |||
                                    GGTG    AGGAGGTTT CCA
                                      ATGA        _
GAM1003  FLJ20151  3'  CCCACCTCCTCCAGGGTC    26633            AAC
                                    CCCACCTCCTCCA   GGTC
                                    ||||||||||||   ||||
                                    GGGTGGAGGAGGT   CCAG
                                           C__
GAM1003  FLJ20330  3'  CCCCACATTCCCCATGGTC    26634       C_   T   AAC
                                    CCCCAC  TCC CCA   GGTC
                                    ||||||  ||| |||   ||||
                                    GGGGTG  AGG GGT   CCAG
                                       TA   _   A__
GAM1003  FLJ22349  3'  CCTGCCTCCCCCAGCAGTC    26635    CA        AA
                                    CC  CCTCCTCCA  CGGTC
                                    ||  |||||||||  |||||
                                    GG  GGAGGGGGT  GTCAG
                                     AC        C_
GAM1003  FLJ22940  5'  CCTCCGTCTCCTCCAGGGC    26636    _ AC       AAC
                                    CC CC  CTCCTCCA   GGT
                                    || ||  ||||||||   |||
                                    GG GG  GAGGAGGT   CCG
                                     A  CA       C__
GAM1003  FLJ30058  3'  CCCCCACCCTTTTCCCCTGTC  26637          CC_   AAACG
                                    CCCCCACCT   TCC    GTC
                                    |||||||||   |||    |||
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                                GGGGGTGGG  AGG    CAG
                                     AAA  GGA__
GAM1003  FLJ32332  3'  CCCTGCCTCCTCCAAGAAGC  26638    CA       AC
                                CCC  CCTCCTCCAA  GGT
                                |||  ||||||||||  |||
                                GGG  GGAGGAGGTT  TCG
                                  AC        CT
GAM1003  FRAT1    3'  CCCCCACCTCCTTTCGACCGTT 26639         T_________  AAAC
           TGG                    CCCCACCTCC       CC   GG
                                ||||||||||       ||   ||
                                GGGGTGGAGG       GG   CC
                                     AAAGIIICT  CAAA
GAM1003  GREB1    3'  CCCACCTCCTCTCTAGTC    26640          CAAAC
                                CCCACCTCCTC    GGTC
                                ||||||||||    ||||
                                GGGTGGAGGAG    TCAG
                                     AGA__
GAM1003  GS3955   3'  CCTCTCCTCCTCCAAGGT    26641    CCA       AC
                                CC   CCTCCTCCAA  GGT
                                ||   ||||||||||  |||
                                GG   GGAGGAGGTT  CCA
                                 AGA        __
GAM1003  HEMK     3'  CCCCCACCTCTTCAGAAC    26642          C  CA
                                CCCCCACCTC TC  AAC
                                |||||||||| ||  |||
                                GGGGGTGGAG AG  TTG
                                     A  TC
GAM1003  HSPB7    5'  CCTCCCCTCCAGACTCTGGT   26643    A  T     A ___
                                CC CC CCTCCA AC   GGT
                                || || |||||| ||   |||
                                GG GG GGAGGT TG   CCA
                                 A  _     C  AGA
GAM1003  HSPC003  3'  CCCCGCCCCTCCAAATGGTC   26644      A  T      C
                                CCCC CC CCTCCAAA GGTC
                                |||| || |||||||| ||||
                                GGGG GG GGAGGTTT CCAG
                                  C  _       A
GAM1003  HT002    3'  CCCTCACCTCCCTTTCAGT    26645     _      CCAAA
                                CCC CACCTCCT    CGGT
                                ||| ||||||||    ||||
                                GGG GTGGAGGG    GTCA
                                  A       AAA__
GAM1003  IL10RB   3'  CCTCCTCCTCCTCCTCCCGG   26646    _ A       AAA
                                CC CC CCTCCTCC   CGG
                                || || ||||||||   |||
                                GG GG GGAGGAGG   GCC
                                 A  A       AGG
GAM1003  jdp2     3'  CCTCCACCTCCTCCCAGC    26647    _         AAA
                                CC CCACCTCCTCC   CGGT
                                || ||||||||||   ||||
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                                GG GGTGGAGGAGG   GTCG
                                 A        ___
GAM1003  JM4      3'  CCCCACCTCACCCCTTGGT   26648         _   AAAC
                                CCCCACCTC CTCC    GGT
                                ||||||||| ||||    |||
                                GGGGTGGAG GGGG    CCA
                                     T    AA__
GAM1003  KCNJ9    3'  CCTCCTCCTCCTCCACCAC    26649    _ A       A_
                                CC CC CCTCCTCCA  AC
                                || || |||||||||  ||
                                GG GG GGAGGAGGT  TG
                                 A  A        GG
GAM1003  KIAA0082 5'  CCGCCGCCTCCTCCCTCAGT   26650    _ A       AAA
                                CC CC CCTCCTCC   CGGT
                                || || ||||||||   ||||
                                GG GG GGAGGAGG   GTCA
                                 C  C       GA_
GAM1003  KIAA0237 3'  CCCCATCTCTATGCACCCAATG 26651       C   C_____    AC
              GTC                   CCCCA CTC     TCCAA  GGTC
                                ||||| |||     |||||  ||||
                                GGGGT GAG     GGGTT  CCAG
                                   A   ATACGT    A_
GAM1003  KIAA0258 3'  CCCCACCTGCCTCCATACAGTC 26652         _     A
                                CCCCACCT CCTCCA ACGGTC
                                |||||||| |||||| ||||||
                                GGGGTGGA GGAGGT TGTCAG
                                     C     A
GAM1003  KIAA0321 3'  CCCCCACCGCCTCCCCTGTATC 26653         T    AAACG
                                CCCCCACC CCTCC    GTC
                                |||||||| |||||    |||
                                GGGGGTGG GGAGG    TAG
                                     C    GGACA
GAM1003  KIAA0354 5'  CCCCTAGCTCCTCCAGCCAGT  26654      CAC       AA
                                CCCC   CTCCTCCA  CGGT
                                ||||   ||||||||  ||||
                                GGGG   GAGGAGGT  GTCA
                                   ATC       CG
GAM1003  KIAA0537 5'  CCCCCACCTCCCTGCGACCGTT 26628          T_________  AAAC
              TGG                   CCCCACCTCC        CC    GG
                                ||||||||||        ||    ||
                                GGGGTGGAGG        GG    CC
                                      GACGIIICT  CAAA
GAM1003  KIAA0543 3'  CCTCCCCCTCTAACAAGGTGGT 26655    _  A    CTC   AC_
              C                    CC CCC CCTC   CAA   GGTC
                                || ||| ||||   |||   ||||
                                GG GGG GGAG   GTT   CCAG
                                 A  _    ATT   CCA
GAM1003  KIAA0596 3'  CCTCCACCTCCACCTCCAG   26656    _      T  AAA
                                CC CCACCTCC CC   CGG
                                || |||||||| ||   |||
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                                GG GGTGGAGG GG   GTC
                                 A       T  AG_
GAM1003  KIAA0607  5' CCCCTCCTCCCCCTTGGTC   26657      A       AAAC
                                CCCC CCTCCTCC    GGTC
                                |||| ||||||||    ||||
                                GGGG GGAGGGGG    CCAG
                                  A       AA__
GAM1003  KIAA0664  3' CCCCACCCCTCCCCACCGG    26658       T     AAA_
                                CCCCACC CCTCC    CGG
                                ||||||| |||||    |||
                                GGGGTGG GGAGG    GCC
                                    _    GGTG
GAM1003  KIAA0937  3' CCCCACCTCCTACTGCC     26659          CCAA  G
                                CCCCACCTCCT    AC GTC
                                ||||||||||    || |||
                                GGGGTGGAGGA    TG CGG
                                      _____  A
GAM1003  KIAA1001  3' CCTCCACCTCCCCGGT      26624    _       CCAAA
                                CC CCACCTCCT    CGGT
                                || |||||||||    ||||
                                GG GGTGGAGGG    GCCA
                                 A       ______
GAM1003  KIAA1110  3' CCACCTCCTCCCAAGTC     26660          AAAC
                                CCACCTCCTCC    GGTC
                                ||||||||||    ||||
                                GGTGGAGGAGG    TCAG
                                      GT__
GAM1003  KIAA1464  3' CCCTTTCCTCCTCCAGGGC    26661     CCA       AAC
                                CCC   CCTCCTCCA   GGT
                                |||   |||||||||   |||
                                GGG   GGAGGAGGT   CCG
                                  AAA       C__
GAM1003  KIAA1855  3' CCCCCACCTCTCCTGGT     26662          C   AAAC
                                CCCCCACCTC TCC    GGT
                                |||||||||| |||    |||
                                GGGGGTGGAG AGG    CCA
                                      _   A___
GAM1003  KIAA1906  3' CCTTCACCTCCTCCCCAGT    26663    CC        AAA
                                CC  CACCTCCTCC   CGGT
                                ||  ||||||||||   ||||
                                GG  GTGGAGGAGG   GTCA
                                 AA        G__
GAM1003  LENG9     3' CCATTGTCTCCTCCAGAGGTC  26664     C___      AAC
                                CCA    CTCCTCCA   GGTC
                                |||    ||||||||   ||||
                                GGT    GAGGAGGT   CCAG
                                  AACA       CT_
GAM1003  MAP2K5    3' CCTTTACCTCTCTGCCAGTGTC 26665    CCC    _ _   AACG
                                CC   ACCTC CT CCA    GTC
                                ||   ||||| || |||    |||
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                                GG   TGGAG GA GGT    CAG
                                 AAA    A  C   CA__
GAM1003  MGC10772  3'  CCCCCGCCCCTCCCCGCAGTC  26666      A  T    AAA
                                CCCCC CC CCTCC   CGGTC
                                ||||| || |||||   |||||
                                GGGGG GG GGAGG   GTCAG
                                   C  _    GGC
GAM1003  MGC21621  3'  CCCCTGCCTCCTCCAGGC    26667     CA       AAC
                                CCCC  CCTCCTCCA   GGT
                                ||||  |||||||||   |||
                                GGGG  GGAGGAGGT   CCG
                                  AC       ___
GAM1003  MGC2941   5'  CCCTCCCCTCCTCCCGGTC    26668    _ A      AAA
                                CCC CC CCTCCTCC   CGGTC
                                ||| || ||||||||   |||||
                                GGG GG GGAGGAGG   GCCAG
                                 A  _      ____
GAM1003  MGC5139   5'  CCTCATCCTCCTCCTGGTC    26669    C  _      AAAC
                                CC CA CCTCCTCC    GGTC
                                || || ||||||||    ||||
                                GG GT GGAGGAGG    CCAG
                                 A  A       A___
GAM1003  N4BP2     3'  CCTCCACCTCCCAGGTTTAAGC 26670    _       CCAAA____
            GGT                   CC CCACCTCCT        CGGT
                                || |||||||||        ||||
                                GG GGTGGAGGG        GCCA
                                 A        TCCAAATTC
GAM1003  NAV1      3'  CCTGCCTCCCCCAGATC     26671    CA       AAC
                                CC  CCTCCTCCA   GGTC
                                ||  |||||||||   ||||
                                GG  GGAGGGGGT   CTAG
                                 AC       ___
GAM1003  NXPH3     3'  CCTCCTCCTTCCTGCAGTC   26672    A     _ AAA
                                CC CCTCCT CC   CGGTC
                                || |||||| ||   |||||
                                GG GGAGGA GG   GTCAG
                                 A     A  AC_
GAM1003  OSBPL8    5'  CCCCCACCTTCCCTCAGTC   26673        CC   AAA
                                CCCCCCACCT  TCC   CGGTC
                                |||||||||  |||   |||||
                                GGGGGGTGGA  AGG   GTCAG
                                      __   GA_
GAM1003  p25       3'  CCCCCGCCTTCCCCAGGC    26674      A  C    AAC
                                CCCCC CCT CTCCA   GGT
                                ||||| ||| |||||   |||
                                GGGGG GGA GGGGT   CCG
                                   C  A    ___
GAM1003  PADI3     3'  CCCCCATCCCCTGAATTCAGT  26675       C    CCAAA
                                CCCCCA CTCCT     CGGT
                                |||||| |||||     ||||
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                                GGGGGT GGGGA    GTCA
                                   A    CTTAA
GAM1003  PGRMC2   3'  CCCCCACCTCCCCTGAT    26676          CAAAC
                                CCCCCACCTCCTC    GGT
                                ||||||||||||    |||
                                GGGGGTGGAGGGG    CTA
                                      A____
GAM1003  PLPL     3'  CCTGCCTCCCCCTCCAGGTC  26677    C_ A       AAC
                                CC  CC CCTCCTCCA   GGTC
                                ||  || |||||||||   ||||
                                GG  GG GGGGGAGGT   CCAG
                                 AC  A       ___
GAM1003  PP5395   3'  CCTTCACCTCCCCAGGCC    26678    CC      T   AAC
                                CC  CACCTCC CCA   GGTC
                                ||  ||||||| |||   ||||
                                GG  GTGGAGG GGT   CCGG
                                 AA      _  ___
GAM1003  PPP1R16B 3'  CCCCCTCCACCCCTGGATGGTC 26679      A  T    CAAAC
                                CCCCC CC CCTC    GGTC
                                ||||| || ||||    ||||
                                GGGGG GG GGGG    CCAG
                                   A  T    ACCTA
GAM1003  PRO0971  5'  CCTCCTCCTCCTCCCGCTC   26680    _ A       AAA  G
                                CC CC CCTCCTCC   CG TC
                                || || ||||||||   || ||
                                GG GG GGAGGAGG   GC AG
                                 A  A       ___  G
GAM1003  PRO1855  3'  CCCCCAGTTCCTCCTGATC   26681       CC     AAAC
                                CCCCCA  TCCTCC   GGTC
                                ||||||  ||||||   ||||
                                GGGGGT  AGGAGG   CTAG
                                   CA     A___
GAM1003  PRO2900  3'  CCCACCTCCCTCCTGCCAGT   26682         _  AAA
                                CCCACCTCC TCC   CGGT
                                |||||||| |||   ||||
                                GGGTGGAGG AGG   GTCA
                                      G   ACG
GAM1003  RPS6KC1  3'  CCCCCATTTCCTATAACGGTC  26683       CC    CCA
                                CCCCCA  TCCT   AACGGTC
                                ||||||  ||||   |||||||
                                GGGGGT  AGGA   TTGCCAG
                                   AA    TA_
GAM1003  STIM2    5'  CCCCCGCCCCCTCCGGC     26684       A      AAAC
                                CCCCC CCTCCTCC    GGT
                                ||||| ||||||||    |||
                                GGGGG GGGGGAGG    CCG
                                   C       _____
GAM1003  STX1B2   5'  CCTCCTCCTCCTCCTAGTC   26685    _ A       AAAC
                                CC CC CCTCCTCC    GGTC
                                || || ||||||||    ||||
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                                GG GG GGAGGAGG    TCAG
                                 A  A       A___
GAM1003  TTYH2    3'  CCCGTCTCCTCCAGATC     26686     AC       AAC
                                CCC  CTCCTCCA   GGTC
                                |||  ||||||||   ||||
                                GGG  GAGGAGGT   CTAG
                                  CA       ___
GAM1003  LOC124602 5'  CCCCCACCGCCTCCGGGTC    26687         T     AAAC
                                CCCCCACC CCTCC    GGTC
                                |||||||| |||||    ||||
                                GGGGGTGG GGAGG    CCAG
                                     C     C___
GAM1003  LOC138724 3'  CCCCACCTTCCCCCTGGT     26688          _     AAAC
                                CCCCACCT CCTCC    GGT
                                |||||||| |||||    |||
                                GGGGTGGA GGGGG    CCA
                                     A     A___
GAM1003  LOC142901 5'  CCCCGCCCCCTCCAGGGC     26689      A        AAC
                                CCCC CCTCCTCCA   GGT
                                ||||  |||||||||   |||
                                GGGG GGGGGAGGT   CCG
                                  C        C__
GAM1003  LOC145225 3'  CCTGCATCTCCTCCAGGTC    26690     CC  C       AAC
                                CC  CA CTCCTCCA   GGTC
                                ||  ||  ||||||||   ||||
                                GG  GT GAGGAGGT   CCAG
                                 AC  A       ___
GAM1003  LOC147645 5'  CCTCTGCCTCCCCCAACCGTGT 26691     CCCA         A  _
            C                    CC    CCTCCTCCAA CG GTC
                                ||    ||||||||||  ||  |||
                                GG    GGAGGGGGTT GC CAG
                                 AGAC         G  A
GAM1003  LOC148018 3'  CCCCCAGCCCCGGGGCTCCAGG 26692        _   _____     AA
            CGGT                    CCCCCA CCTC    CTCCA  CGGT
                                ||||||  ||||    |||||  ||||
                                GGGGGT GGGG    GAGGT  GCCA
                                   C    CCCC     CC
GAM1003  LOC149276 3'  CCTCCTCCTCCTCCGAAC     26693     _  A       A
                                CC CC CCTCCTCC AAC
                                || ||  |||||||  |||
                                GG GG GGAGGAGG TTG
                                 A  A       C
GAM1003  LOC149319 3'  CCACCACCTCCTCCAAGAAGTC 26694     _           AC
                                CC CCACCTCCTCCAA  GGTC
                                ||  ||||||||||||  ||||
                                GG GGTGGAGGAGGTT  TCAG
                                 T           CT
GAM1003  LOC150166 5'  CCCTCTCCTCCTCCTACCTGGT 26695     CCA       AAAC_
            C                    CCC   CCTCCTCC     GGTC
                                |||   ||||||||     ||||
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                                GGG  GGAGGAGG   CCAG
                                  AGA      ATGGA
GAM1003  LOC150319 3'  CCCCCTCCTCCCGGGTTCAAGC 26696     A    C____  A
                GGT                CCCCC CCTCCT    CAA CGGT
                                   ||||| ||||||    ||| ||||
                                   GGGGG GGAGGG    GTT GCCA
                                     A     CCCAA   C
GAM1003  LOC150372 3'  CCCCCACCTCCTTGGCGACCGT 26698        T__________  AAAC
                TTGG               CCCACCTCC        CC   GG
                                   |||||||||        ||   ||
                                   GGGTGGAGG        GG   CC
                                        AACCGIIICT  CAAA
GAM1003  LOC150372 3'  CCTCCTCCTCCTCCCTGCC   26697   _ A      AAACG
                                   CC CC CCTCCTCC    GTC
                                   || || ||||||||    |||
                                   GG GG GGAGGAGG    CGG
                                    A  A      GA___
GAM1003  LOC151009 3'  CCTTTCCCTCCTCCTAAAGT  26699   CCCA      A  C
                                   CC   CCTCCTCC AA GGT
                                   ||   |||||||| || |||
                                   GG   GGAGGAGG TT TCA
                                    AAAG      A  _
GAM1003  LOC152179 5'  CCTCCACCTCCTCCCCCACTC 26700   _        AAA  G
                                   CC CCACCTCCTCC   CG TC
                                   || ||||||||||   || ||
                                   GG GGTGGAGGAGG   GT AG
                                    A         GG_  G
GAM1003  LOC152426 5'  CCTAACCTCCTCCAGGC    26701   CC        AAC
                                   CC  ACCTCCTCCA   GGT
                                   ||  ||||||||||   |||
                                   GG  TGGAGGAGGT   CCG
                                    AT       ___
GAM1003  LOC152620 3'  CCCTACCTCCCCAGTGTC    26702    C    T   AACG
                                   CCC ACCTCC CCA    GTC
                                   ||| |||||| |||    |||
                                   GGG TGGAGG GGT    CAG
                                     A     _   CA__
GAM1003  LOC154092 3'  CCACCTCCTCACAGT       26703         CAA
                                   CCACCTCCTC   ACGGT
                                   ||||||||||   |||||
                                   GGTGGAGGAG   TGTCA
                                                ___
GAM1003  LOC154222 3'  CCCCTTCTCCTCCACCATGTC  26704     AC       AACG
                                   CCCC  CTCCTCCA    GTC
                                   ||||  ||||||||    |||
                                   GGGG  GAGGAGGT    CAG
                                     AA       GGTA
GAM1003  LOC157254 5'  CCCGCCTCCTCCCACCACTC   26705    A       AAA  G
                                   CCC CCTCCTCC   CG TC
                                   ||| ||||||||   || ||
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                                GGG GGAGGAGG   GT AG
                                  C       GTG  G
GAM1003  LOC158402 5'  CCCTCACCTCCTCTCCCTATC  26706     _       CAAACG
                                CCC CACCTCCTC     GTC
                                ||| |||||||||     |||
                                GGG GTGGAGGAG     TAG
                                  A       AGGGA_
GAM1003  LOC164714 5'  CCCGGCCTCCTCCCTCTGGTC  26707     CA      AAAC
                                CCC  CCTCCTCC    GGTC
                                |||  ||||||||   ||||
                                GGG  GGAGGAGG    CCAG
                                  CC       GAGA
GAM1003  LOC200316 3'  CCTCCACCTCCCCGGC      26708    _       CCAAA
                                CC CCACCTCCT     CGGT
                                ||  |||||||||    ||||
                                GG GGTGGAGGG     GCCG
                                 A       _____
GAM1003  LOC200953 5'  CCCCAGCCTCCTCCTGACCTGG 26709      _       AA __
              TC                  CCCCA CCTCCTCC  AC  GGTC
                                |||||  ||||||||  ||  ||||
                                GGGGT GGAGGAGG  TG  CCAG
                                   C       AC  GA
GAM1003  LOC201175 5'  CCCCCACCCCCTCTTGATC    26710           CAAAC
                                CCCCCACCTCCTC     GGTC
                                ||||||||||||     ||||
                                GGGGGTGGGGGAG     CTAG
                                       AA___
GAM1003  LOC201230 3'  CCCGCCTCCTCCGCCGGTC    26711     A       AAA
                                CCC CCTCCTCC   CGGTC
                                |||  ||||||||   |||||
                                GGG GGAGGAGG   GCCAG
                                  C       CG_
GAM1003  LOC203209 5'  CCAGCTCCTCCAAGATC      26712     C       AC
                                CCA CTCCTCCAA  GGTC
                                |||  |||||||||  ||||
                                GGT GAGGAGGTT  CTAG
                                  C       __
GAM1003  LOC203397 5'  CCCCCACCGCCTCCGGGTC    26687         T     AAAC
                                CCCCCACC CCTCC    GGTC
                                |||||||| |||||    ||||
                                GGGGGTGG GGAGG    CCAG
                                     C     C___
GAM1003  LOC219686 5'  CCGCCGCCTCCTCCCGCTC    26713    _ A       AAA  G
                                CC CC CCTCCTCC   CG TC
                                ||  ||  ||||||||   ||  ||
                                GG GG GGAGGAGG   GC AG
                                 C  C       ___  G
GAM1003  LOC221078 3'  CCCCCTACTTCCTCTATGTC   26714       _  C     CAAACG
                                CCCCC AC TCCTC      GTC
                                |||||  ||  |||||      |||
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                                GGGGG TG AGGAG     CAG
                                  A  A    ATA___
GAM1003  LOC221218 5'  CCTCCTCCTCTTCCTCCAGGTC 26716    _  A  ___      AAC
                                CC CC CC   TCCTCCA   GGTC
                                || || ||   |||||||   ||||
                                GG GG GG   AGGAGGT   CCAG
                                 A  A  AGA      ___
GAM1003  LOC221218 5'  CCTCCTCTTCCTCCAGGTC   26715    _  ACC      AAC
                                CC CC   TCCTCCA   GGTC
                                || ||   |||||||   ||||
                                GG GG   AGGAGGT   CCAG
                                 A  AGA      ___
GAM1003  LOC221914 3'  CCCCCACCCCTCCCCAC     26717         T     AA
                                CCCCCACC CCTCC  AC
                                |||||||| |||||  ||
                                GGGGGTGG GGAGG  TG
                                     _    GG
GAM1003  LOC245744 3'  CCCCCACCACCTCCCGCTC   26718         T    AAA  G
                                CCCCCACC CCTCC   CG TC
                                |||||||| |||||   || ||
                                GGGGGTGG GGAGG   GC AG
                                     T     ___  G
GAM1003  LOC254532 5'  CCCCCTCCTCCTCCAGGC    26719       A        AAC
                                CCCCC CCTCCTCCA   GGT
                                ||||| |||||||||   |||
                                GGGGG GGAGGAGGT   CCG
                                  A       ___
GAM1003  LOC254896 5'  CCTCCACGTCCTCCAGGGC   26720    _   C      AAC
                                CC CCAC TCCTCCA   GGT
                                || |||| |||||||   |||
                                GG GGTG AGGAGGT   CCG
                                 A   C      C__
GAM1003  LOC255480 3'  CCTTCACCTCCTCAAGATC   26721    CC        CAAAC
                                CC  CACCTCCTC    GGTC
                                ||  |||||||||    ||||
                                GG  GTGGAGGAG    CTAG
                                 AA       TT___
GAM1003  LOC257471 5'  CCTCCTCCTCCTCCTGGTC   26594    _  A       AAAC
                                CC CC CCTCCTCC    GGTC
                                || || ||||||||    ||||
                                GG GG GGAGGAGG    CCAG
                                 A  A       A___
GAM1003  LOC257479 5'  CCGCCGCCTCCTCCGAT     26722    _  A       AAAC
                                CC CC CCTCCTCC    GGT
                                || || ||||||||    |||
                                GG GG GGAGGAGG    CTA
                                 C  C       _____
GAM1003  LOC51291  3'  CCCACCTCCTCCAGGAAGGTC  26723            AAC_
                                CCCACCTCCTCCA    GGTC
                                ||||||||||||    ||||
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                                GGGTGGAGGAGGT   CCAG
                                      CCTT
GAM1003  LOC54466  3'  CCCCTGCCCCCTCCAGAC    26724     CA       A
                                CCCC  CCTCCTCCA AC
                                |||| ||||||||| ||
                                GGGG  GGGGGAGGT TG
                                  AC        C
GAM1003  LOC56996  3'  CCTCCTCCTCCAAGGATC    26725    A        AC
                                CC CCTCCTCCAA  GGTC
                                || ||||||||||  ||||
                                GG GGAGGAGGTT  CTAG
                                 A         C_
GAM1003  LOC89985  5'  CCCCCTCCTCCTCCAGAGGT   26726      A       AAC
                                CCCCC CCTCCTCCA   GGT
                                ||||| |||||||||   |||
                                GGGGG GGAGGAGGT   CCA
                                   A        CT_
GAM1003  LOC90190  3'  CCCACCTCCCCAGAT       26727         T   AAC
                                CCCACCTCC CCA   GGT
                                ||||||||| |||   |||
                                GGGTGGAGG GGT   CTA
                                      _  ____
GAM1003  LOC90288  3'  CCTCCATCTCCTCCAGGGTC   26729    _  C       AAC
                                CC CCA CTCCTCCA   GGTC
                                || ||| ||||||||   ||||
                                GG GGT GAGGAGGT   CCAG
                                 A  A       C__
GAM1003  LOC90288  3'  CCACTGCCTCCTCCAGGGC    26728    ___       AAC
                                CCA   CCTCCTCCA   GGT
                                |||   |||||||||   |||
                                GGT   GGAGGAGGT   CCG
                                  GAC        C__
GAM1003  LOC90631  3'  CCCCTGCCCCCTCCAACCAGT  26730     CA        A
                                CCCC  CCTCCTCCAA CGGT
                                |||| ||||||||| ||||
                                GGGG  GGGGGAGGTT GTCA
                                  AC         G
GAM1003  LOC90784  5'  CCCCACTGTCCTCTCCACTC   26731      C_    CAAA  G
                                CCCCAC  TCCTC    CG TC
                                ||||||  |||||    || ||
                                GGGGTG  AGGAG    GT AG
                                   AC    AG__  G
GAM1003  LOC92492  5'  CCCACCTCCTCCAAGAAGC    26732           AC
                                CCCACCTCCTCCAA  GGT
                                ||||||||||||||  |||
                                GGGTGGAGGAGGTT  TCG
                                      CT
GAM1004  ATP2B4    5'  TGTCACGATGATTGGTGTC    26735    C       CGA
                                TG CATGATGAT   TGTC
                                || |||||||||   ||||
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                                AC GTGCTACTA   ACAG
                                 A        ACC
GAM1004  REV3L    5'  TGCCATGATGATGATGTCAC   26736          C
                                TGCCATGATGAT GATGTCAT
                                |||||||||||| ||||||||
                                ACGGTACTACTA CTACAGTG
                                          _
GAM1004  ZNF157   3'  TGCCCTGGTGATCATATG    26737     A  A    _
                                TGCC TG TGATCG ATG
                                |||| || |||||| |||
                                ACGG AC ACTAGT TAC
                                  G  C     A
GAM1004  DKFZP434K046 3'  TGCAATGCATGCTGGTGTCAT  26738    C  _  ATCGA
                                TGC ATG ATG    TGTCAT
                                ||| ||| |||    ||||||
                                ACG TAC TAC    ACAGTA
                                  T   G   GACC_
GAM1004  TRIM4    3'  TGATGAGAGTCATATG     26739       TC  T
                                TGATGA  GA GTCATATG
                                ||||||  || ||||||||
                                ACTACT  CT CAGTATAC
                                   __  _
GAM1004  LOC164971 5'  TGGCATGATTTGTCATAT    26740    C     GATCGA
                                TG CATGAT     TGTCATAT
                                || ||||||     ||||||||
                                AC GTACTA     ACAGTATA
                                 C     A_____
GAM1005  CPSF6    3'  CTTTTTAAATCACACAGG    26743      CATT   A
                                CTTTT    AAT CACACAGG
                                |||||    ||| ||||||||
                                GAAAA    TTA GTGTGTCC
                                   AT__   _
GAM1005  CRK      3'  CCCTTCTGATACACACAG    26744       CATTA
                                CCTTTT    ATACACACAG
                                ||||||    ||||||||||
                                GGGAAG    TATGTGTGTC
                                    AC___
GAM1005  CYLN2    3'  TTTCCACCACGCACAGG     26745       TAA   A
                                TTTTCAT   TAC CACAGG
                                |||||||   ||| ||||||
                                AAAGGTG   GTG GTGTCC
                                    ___   C
GAM1005  MAX      3'  TTTCTTAGAAATACACACGGG  26746     ATT__       A
                                TTTC    AATACACAC GG
                                ||||    ||||||||| ||
                                AAAG    TTATGTGTG CC
                                  AATCT        C
GAM1005  MAX      3'  TTTCTTAGAAATACACACGGG  26746     ATT__       A
                                TTTC    AATACACAC GG
                                ||||    ||||||||| ||
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                                AAAG    TTATGTGTG CC
                                  AATCT       C
GAM1005  TOMM22    3'  CTTTTTTTAAACACACACACAG 26747      CATTA__
             G                    CTTTT      ATACACACAGG
                                  |||||      ||||||||||
                                  GAAAA      TGTGTGTGTCC
                                    AAATTTG
GAM1005  13CDNA73  3'  CCTTTTCACATACACAG     26748        TAATAC
                                  CCTTTTCAT     ACACAG
                                  |||||||||     ||||||
                                  GGAAAAGTG     TGTGTC
                                        TA____
GAM1005  DKFZp566D133 5'  TTTTCAGAAATGCACACAGG   26749       TT   A
                                  TTTTCA  AAT CACACAGG
                                  ||||||  ||| ||||||||
                                  AAAAGT  TTA GTGTGTCC
                                     CT   C
GAM1005  FLJ14641  5'  CCTTCTCATTTCACGCGG    26750        AATA   ACA
                                  CCTTTTCATT    CAC   GG
                                  ||||||||||    |||   ||
                                  GGAAGAGTAA    GTG   CC
                                        A___   CG_
GAM1005  FLJ20209  5'  CCTTTTCAAACACACAGG    26751       TTAAT
                                  CCTTTTCA    ACACACAGG
                                  ||||||||    |||||||||
                                  GGAAAAGT    TGTGTGTCC
                                        T_____
GAM1005  FLJ23563  3'  TACCTTCTCATTTTAGCACAGG 26752          AATACA
                                  TACCTTTTCATT     CACAGG
                                  ||||||||||||     ||||||
                                  ATGGAAGAGTAA     GTGTCC
                                         AATC__
GAM1005  KIAA0319  3'  TACCTTGTCAACACATAG    26753      T   TTAAT    C
                                  TACCTT TCA     ACACA AG
                                  |||||| |||     ||||| ||
                                  ATGGAA AGT     TGTGT TC
                                     C   ______     A
GAM1005  KIAA0802  3'  TACCTTTTCGTTTAATATAC   26754        A_     C
                                  TACCTTTTC  TTAATA AC
                                  |||||||||  |||||| ||
                                  ATGGAAAAG  AATTAT TG
                                        CA      A
GAM1005  KIAA1383  3'  TTTTCACTAACAGTACACATAG 26755          ___    C
             G                     TTTTCATTAAT   ACACA AGG
                                   ||||||||||||  ||||| |||
                                   AAAAGTGATTG   TGTGT TCC
                                         TCA     A
GAM1005  MGC23918  3'  TTTTCGCCACACACAGG     26756      ATTAA
                                  TTTTC    TACACACAGG
                                  |||||    ||||||||||
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                                AAAAG    GTGTGTGTCC
                                  CG___
GAM1005  RASSF2   3'  TCTTCACCAATACGTACAGG   26757          AC
                                TTTTCATTAATAC  ACAGG
                                ||||||||||||  |||||
                                AGAAGTGGTTATG  TGTCC
                                    CA
GAM1005  SEMA4F   3'  TTTTCATTGGTACAGACAGG   26758       AA   C
                                TTTTCATT  TACA ACAGG
                                ||||||||  |||| |||||
                                AAAAGTAA  ATGT TGTCC
                                   CC   C
GAM1005  LOC149707 5'  CCTTTCCATTGATTCCCAGG   26759        A  ACACA
                                CCTTTTCATT AT    CAGG
                                ||||||||||  ||    ||||
                                GGAAAGGTAA TA    GTCC
                                    C  AGG__
GAM1005  LOC200227 5'  CCTTTCCATTGATTCCCAGG   26759        A  ACACA
                                CCTTTTCATT AT    CAGG
                                ||||||||||  ||    ||||
                                GGAAAGGTAA TA    GTCC
                                    C  AGG__
GAM1005  LOC253959 5'  TTTTCAGAAATGCACACAGG   26749      TT   A
                                TTTTCA  AAT CACACAGG
                                ||||||  ||| ||||||||
                                AAAAGT  TTA GTGTGTCC
                                  CT   C
GAM1006  ACVR1    3'  CTGCAGTGTGAACAGTTC    26762       C    AG
                                CTGCAG GTGA  GCAGTTT
                                |||||| ||||  |||||||
                                GACGTC CACT  TGTCAAG
                                   A   __
GAM1006  ATP6V0D1  3'  CCTTAGAGAGGGCAGTTT    26763     GC  CGT  A
                                CCT  AG   GA GGCAGTTT
                                |||  ||   || ||||||||
                                GGA  TC   CT CCGTCAAA
                                  A_  T__  C
GAM1006  BRCA1    3'  CTGAGCATGGCAGTTT     26764     C    GAA
                                CTG AGCGT   GGCAGTTT
                                ||| |||||   ||||||||
                                GAC TCGTA   CCGTCAAA
                                  _    ____
GAM1006  CDH5     3'  CCCTTGCAGTGTGAGGGGC   26765     C    C   A_
                                CCC TGCAG GTGA  GGC
                                ||| ||||| ||||  |||
                                GGG ACGTC CACT  CCG
                                  A    A   CC
GAM1006  HMGA2    3'  CCCCTGTGTTTACAGCAGTTT  26766       CAGC  GAA_
                                CCCCTG   GT   GGCAGTTT
                                ||||||   ||   ||||||||
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                                GGGGAC   CA   TCGTCAAA
                                   A___  AATG
GAM1006 HTRA3   3' CTCCATGGAAGGCAGTTT   26767   G GCGT
                                CT CA   GAAGGCAGTTT
                                || ||   ||||||||||
                                GA GT   CTTCCGTCAAA
                                 G AC__
GAM1006 MAP3K11 3' CCCTTCCAGTGTGAAGGC   26768    G_  C
                                CCCT CAG GTGAAGGC
                                ||||  ||| ||||||||
                                GGGA GTC CACTTCCG
                                  AG  A
GAM1006 NKX3A   3' CCCTGGGGAAGGCAGTTT   26769     CAGCGT
                                CCCTG    GAAGGCAGTTT
                                |||||    ||||||||||
                                GGGAC    CTTCCGTCAAA
                                   CC____
GAM1006 PLAUR   5' CCTCAGGAAGGAGGCAGTTT 26770    G  CGTGA
                                CCT CAG    AGGCAGTTT
                                ||| |||    |||||||||
                                GGA GTC    TCCGTCAAA
                                  _  CTTCC
GAM1006 SEZ6L   5' CTGCTTGAGCGAAGGCAGTTTC 26771     AGC_
                                CTGC   GTGAAGGCAGTTTC
                                ||||   ||||||||||||||
                                GACG   CGCTTCCGTCAAAG
                                  AACT
GAM1006 SNX13   3' TGCTTGAGATGGGGGCAGTTT 26772    ___ C  AA
                                TGC  AG GTG  GGCAGTTT
                                |||  || |||  ||||||||
                                ACG  TC TAC  CCGTCAAA
                                  AAC  _  CC
GAM1006 STXBP1  3' CTTCAGTGTGTCCAGCAGTTTC 26773   G  C  AA_
                                CT CAG GTG  GGCAGTTTC
                                || ||| |||  |||||||||
                                GA GTC CAC  TCGTCAAAG
                                 A  A  AGG
GAM1006 TP73    3' CCTGCCTCCTGAGGCAGTTT  26774     AGCG  A
                                CCTGC   TGA GGCAGTTT
                                |||||   ||| ||||||||
                                GGACG   ACT CCGTCAAA
                                   GAGG  _
GAM1006 ZNF137  3' CCTGGGAGTAATAGGCAGTTT 26775    CAGC  _
                                CCTG   GTGA AGGCAGTTT
                                ||||   |||| |||||||||
                                GGAC   CATT TCCGTCAAA
                                  CCT_   A
GAM1006 ZNF76   3' CCCTTCAGTTAGGCAGTTT  26776    G  CGTGA
                                CCCT CAG    AGGCAGTTT
                                |||| |||    |||||||||
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                                GGGA GTC    TCCGTCAAA
                                  A  AA___
GAM1006 ARL1    5' CTGCAGCTCCGAGGCGGTTTC 26777      G_  A  A
                                CTGCAGC  TGA GGC GTTTC
                                |||||||  ||| ||| |||||
                                GACGTCG  GCT CCG CAAAG
                                    AG  _  C
GAM1006 CLSP    3' CCTCCCAGGGGGAGGCAGTTTC 26778   _ TG  CGT  A
                                CC CC  CAG  GA GGCAGTTTC
                                || ||  |||  || |||||||||
                                GG GG  GTC  CT CCGTCAAAG
                                 A  __  CCC  _
GAM1006 ELF2    3' CCTACTGTAAGAGGCAGTTT  26779     AGC  _
                                CCTGC  GTGA AGGCAGTTT
                                |||||  |||| |||||||||
                                GGATG  CATT TCCGTCAAA
                                   A__  C
GAM1006 FLJ10408 3' CCTGCGCGTCATGCAGTTTC  26780     A  GAAG
                                CCTGC GCGT   GCAGTTTC
                                ||||| ||||   ||||||||
                                GGACG CGCA   CGTCAAAG
                                   _  GTA_
GAM1006 FLJ10648 3' CCCTACACAGGCAGTTT    26781      G GTGA
                                CCCTGCA C   AGGCAGTTT
                                ||||||| |   |||||||||
                                GGGATGT G   TCCGTCAAA
                                   _ _____
GAM1006 KIAA0712 5' CCCCTGCAGCAGCAGTTT   26782       GTGAA
                                CCCCTGCAGC   GGCAGTTT
                                ||||||||||   ||||||||
                                GGGGACGTCG   TCGTCAAA
                                     ______
GAM1006 KIAA1695 5' CTGCAGCGTCGGTTGTTT   26783       GAA  CA
                                CTGCAGCGT  GG  GTTT
                                |||||||||  ||  ||||
                                GACGTCGCA  CC  CAAA
                                     G__  AA
GAM1006 KIAA1729 5' CTTCCAGCGGAAACAGTTTC  26784   G_   T   G
                                CT  CAGCG GAAG CAGTTTC
                                ||  ||||| |||| |||||||
                                GA  GTCGC CTTT GTCAAAG
                                 AG   _  _
GAM1006 KRTHB2  3' TGCAGCGTGCATGTTTC    26785      GAAG  _
                                TGCAGCGT   GCA GTTTC
                                ||||||||   ||| |||||
                                ACGTCGCA   CGT CAAAG
                                    ____  A
GAM1006 MGC11349 3' TGCTCACAAAGGCAGTTTC  26786    AG  TG
                                TGC  CG  AAGGCAGTTTC
                                |||  ||  ||||||||||
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                                ACG  GT  TTCCGTCAAAG
                                  A_  GT
GAM1006 MGC29762 3' CCCCTTAGTCAAAGGCAGTTT 26787      GC  CG
                                CCCCT  AG  TGAAGGCAGTTT
                                |||||  ||  ||||||||||||
                                GGGGA  TC  GTTTCCGTCAAA
                                   A_  A_
GAM1006 MGC3262  3' TGCAGCACAGGCAGTTT    26788      GTGA
                                TGCAGC   AGGCAGTTT
                                ||||||   |||||||||
                                ACGTCG   TCCGTCAAA
                                   TG__
GAM1006 MGC4248  3' CCCTGAGCTGGGCAGTTT   26789      C  G  AA
                                CCCTG AGC TG  GGCAGTTT
                                ||||| ||| ||  ||||||||
                                GGGAC TCG AC  CCGTCAAA
                                  _  _  __
GAM1006 NCOR1    3' CCTGTATCAAAGGCAGTTT   26790     CAGCG
                                CCTG    TGAAGGCAGTTT
                                ||||    ||||||||||||
                                GGAC    GTTTCCGTCAAA
                                  ATA__
GAM1006 OAZ3     5' CCTCTTACAAGGCAGTTT    26791    GCA  TGA
                                CCT  GCG  AGGCAGTTT
                                |||  |||  |||||||||
                                GGA  TGT  TCCGTCAAA
                                 GAA  ___
GAM1006 OSBPL3   3' CCTGCAGCGTGGGGTAGTC   26792        AA  C
                                CCTGCAGCGTG  GG AGTT
                                ||||||||||  || ||||
                                GGACGTCGCAC  CC TCAG
                                      C_  A
GAM1006 SETBP1   3' CCCTGCAGCGGGGGATTC    26793        TGAA  CA
                                CCCTGCAGCG   GG  GTTT
                                ||||||||||   ||  ||||
                                GGGACGTCGC   CC  TAAG
                                     ____  CC
GAM1006 SMOC1    3' CCTCTCCCAGGGCAGTTTC   26794    _  G_  CGTGAA
                                CC CT  CAG    GGCAGTTTC
                                || ||  |||    |||||||||
                                GG GA  GTC    CCGTCAAAG
                                 A  GG  _______
GAM1006 ZNF211   5' CCCTGCAGGTAAAGGGTTTC  26795       C     CA
                                CCCTGCAG GTGAAGG  GTTTC
                                |||||||| |||||||  |||||
                                GGGACGTC CATTTCC  CAAAG
                                   _     __
GAM1006 LOC126669 3' TGCATATGGGGCAGTTT    26796     GC  AA
                                TGCA  GTG  GGCAGTTT
                                ||||  |||  ||||||||
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                                ACGT  TAC  CCGTCAAA
                                  A_  C_
GAM1006  LOC137964 3'  CCCCTGCAGATGACAGTTT   26797        C   AAG
                                CCCCTGCAG GTG   GCAGTTT
                                ||||||||| |||   |||||||
                                GGGGACGTC TAC   TGTCAAA
                                     _  ____
GAM1006  LOC137991 5'  CCCGTGCAGCGTGGAGGC    26798    C       A
                                CCC TGCAGCGTG AGGC
                                ||| ||||||||| ||||
                                GGG ACGTCGCAC TCCG
                                  C       C
GAM1006  LOC145231 3'  CCTTTGAAGCTAGGGCAGTTTC 26799    CC  C   GTGAA
                                CC  TG AGC    GGCAGTTTC
                                ||  || |||    |||||||||
                                GG  AC TCG    CCGTCAAAG
                                 AA  T   ATC__
GAM1006  LOC145758 5'  CTGGGTGAAACAGTTT     26800    CAGC     G
                                CTG   GTGAAG CAGTTT
                                |||   |||||| ||||||
                                GAC   CACTTT GTCAAA
                                  C___    _
GAM1006  LOC147837 3'  CTCCAGTGTGAGATATTTC   26801    G   C    A  CA
                                CT CAG GTGA GG  GTTTC
                                || ||| |||| ||  |||||
                                GA GTC CACT CT  TAAAG
                                 G   A   _ A_
GAM1006  LOC150538 5'  CCGCAGGCCGAGGGCAGTTT   26802       C  _  A
                                CTGCAG GT GA GGCAGTTT
                                |||||| || || ||||||||
                                GGCGTC CG CT CCGTCAAA
                                   _ G  C
GAM1006  LOC151273 3'  CCTACTGTAAGAGGCAGTTT   26779      AGC   _
                                CCTGC   GTGA AGGCAGTTT
                                |||||   |||| |||||||||
                                GGATG   CATT TCCGTCAAA
                                   A__   C
GAM1006  LOC152698 3'  CCTGCGCGTCACGCAGTTTC   26803      A   GAAG
                                CCTGC GCGT    GCAGTTTC
                                ||||| ||||   ||||||||
                                GGACG CGCA    CGTCAAAG
                                   _   GTG_
GAM1006  LOC155435 3'  CCCCTGCAGCGTGCAGT     26804          GAAG
                                CCCCTGCAGCGT    GCAGT
                                ||||||||||||   |||||
                                GGGGACGTCGCA    CGTCA
                                     _____
GAM1006  LOC157280 3'  CCTGCGCGTCACGCAGTTTC   26803      A   GAAG
                                CCTGC GCGT    GCAGTTTC
                                ||||| ||||   ||||||||
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                                GGACG CGCA   CGTCAAAG
                                  _   GTG_
GAM1006  LOC158056 5'  CCCCTGTGGGTGGCATTT   26805      CAGC  GAA   G
                                CCCCTG   GT   GGCA TTT
                                ||||||   ||   |||| |||
                                GGGGAC   CA   CCGT AAA
                                   ACC_  ____   _
GAM1006  LOC196906 5'  CTGTAACACAGCAGTTTC   26806    C   TGAA
                                CTG AGCG   GGCAGTTTC
                                ||| ||||   |||||||||
                                GAC TTGT   TCGTCAAAG
                                  A   G___
GAM1006  LOC199988 5'  CCTGCCTCCTGAGGCAGTTT  26774     AGCG   A
                                CCTGC   TGA GGCAGTTT
                                |||||   ||| ||||||||
                                GGACG   ACT CCGTCAAA
                                   GAGG  _
GAM1006  LOC203286 3'  CCTCTTGCCGGAGGCAGTTTC 26807    GCA  G  A
                                CCT   GC TG AGGCAGTTTC
                                |||   || || ||||||||||
                                GGA   CG GC TCCGTCAAAG
                                  GAA  _  C
GAM1006  LOC219376 3'  TGCTTGTGTGCCAGGCAGTTT 26808    AGC_   A_
                                TGC   GTG  AGGCAGTTT
                                |||   |||  |||||||||
                                ACG   CAC  TCCGTCAAA
                                  AACA   GG
GAM1006  LOC221002 3'  CCTCTCAGTATTGGGCAGTTT 26809    G_   CG GAA
                                CCT  CAG  T   GGCAGTTT
                                |||  |||  |   ||||||||
                                GGA  GTC  A   CCGTCAAA
                                  GA   AT AC_
GAM1006  LOC255448 3'  CCTGCGCGTCACGCAGTTTC  26803     A   GAAG
                                CCTGC GCGT   GCAGTTTC
                                ||||| ||||   ||||||||
                                GGACG CGCA   CGTCAAAG
                                   _   GTG_
GAM1007  ARHGEF7   5'  TCCGGGGCTCGGGGTAGACCTG 26812      T  C  TC
                                TCCGG GC TG  GTAGACCTG
                                ||||| || ||  |||||||||
                                AGGCC CG GC  CATCTGGAC
                                   C  A  CC
GAM1007  GHR      3'  GGTGCCTGGTAAGTTGATCTG  26813       TC__  A  C
                                GGTGCCTG   GT GA CTG
                                ||||||||   || || |||
                                CCACGGAC   CA CT GAC
                                     CATT  A  A
GAM1007  KCNK6    3'  GGTGCCTGAAATGAGGTCTG   26814       TC  _  AC
                                GGTGCCTG  GT AG  CTG
                                |||||||  || ||  |||
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                                CCACGGAC  TA TC  GAC
                                    TT  C  CA
GAM1007  MGAT4B   5'  CCTGGTGCCTGTGTCTCTG   26815   _      C  AGAC
                                CC GGTGCCTGT GT   CTG
                                || |||||||| ||   |||
                                GG CCACGGACA CA   GAC
                                 A       _ GA__
GAM1007  NEBL     3'  CGGTTTTGTCATAGCTG    26816    GCC      AC
                                CGGT  TGTCGTAG  CTG
                                ||||  ||||||||  |||
                                GCCA  ACAGTATC  GAC
                                  AA_       __
GAM1007  UBE2L3   3'  CGGGGCCACCACAGACCTG   26817    T  TGT
                                CGG GCC   CGTAGACCTG
                                ||| |||   ||||||||||
                                GCC CGG   GTGTCTGGAC
                                  C  TG_
GAM1007  UBTF     3'  TCCGGTGCTGGCTTAGTCTG  26818       C  TCG  AC
                                TCCGGTGC TG   TAG  CTG
                                |||||||| ||   |||  |||
                                AGGCCACG AC   ATC  GAC
                                    _ CGA   A_
GAM1007  USP6     5'  TCCTGTGCCTGCAAAC     26819    G      CGT
                                TCC GTGCCTGT   AGAC
                                ||| ||||||||   ||||
                                AGG CACGGACG   TTTG
                                  A      ____
GAM1007  WEE1     5'  TCCGGTGCTGGGGGATCTG   26820       C  TCGTA  C
                                TCCGGTGC TG    GA CTG
                                |||||||| ||    || |||
                                AGGCCACG AC    CT GAC
                                    _ CCC__  A
GAM1007  ZNF278   3'  GGTTCCTGAGCAGACCTG    26821    G   TC
                                GGT CCTG  GTAGACCTG
                                ||| ||||  |||||||||
                                CCA GGAC  CGTCTGGAC
                                  A   T_
GAM1007  ARHGEF9  5'  TCCGGCGCCTGCTCAGTCTG  26822         CG   AC
                                TCCGGTGCCTGT  TAG  CTG
                                ||||||||||||  |||  |||
                                AGGCCGCGGACG  GTC  GAC
                                      A_   A_
GAM1007  CAPN13   3'  TCAGGTGCCTGTCACTGTCTG 26823    C        TAGAC
                                TC GGTGCCTGTCG    CTG
                                || ||||||||||    |||
                                AG CCACGGACAGT    GAC
                                 T         GACA_
GAM1007  CLIPR-59 3'  CCTGGTGCCTGTGAATAGGGCT 26824    _      C_   AC
                                CC GGTGCCTGT  GTAG  CT
                                || |||||||||  ||||  ||
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                                GG CCACGGACA  TATC  GA
                                 A        CT    CC
GAM1007  HT002    3'  TCAGGTGCCTGTCCAAGCC   26825    C        GT  A
                                TC GGTGCCTGTC  AG CC
                                || ||||||||||  || ||
                                AG CCACGGACAG  TC GG
                                 T         GT  _
GAM1007  KIAA0290  5'  TCCAGTGCCTGTCTGGTGTCTG 26826            GTAGAC
                                TCCGGTGCCTGTC     CTG
                                ||||||||||||      |||
                                AGGTCACGGACAG     GAC
                                       ACCACA
GAM1007  KIAA1190  3'  GGGGCCTGCCAGCCTG     26827    T      GT  A
                                GG GCCTGTC  AG CCTG
                                || |||||||  || ||||
                                CC CGGACGG  TC GGAC
                                 C      __  _
GAM1007  KIAA1357  3'  TCCGTGCTCACCAGACCTG   26828     G   C GT GT
                                TCCG TGC T  C  AGACCTG
                                |||| ||| |  |  |||||||
                                AGGC ACG G  G  TCTGGAC
                                  _   A TG __
GAM1007  KIAA1814  5'  CCGAGTGGTTGTAGACCTG   26829     _  CCT  C
                                CCG GTG   GT GTAGACCTG
                                ||| |||   || |||||||||
                                GGC CAC   CA CATCTGGAC
                                  T   ____  A
GAM1007  MAP-1    5'  TCCAGGTGCCTGTGGTACTG   26830     _       C   GAC
                                TCC GGTGCCTGT GTA   CTG
                                ||| |||||||| |||   |||
                                AGG CCACGGACA CAT   GAC
                                  T       C   ____
GAM1007  MDS025   5'  TCCGGCGCCTGTTTCCT     26831          CGTAGA
                                TCCGGTGCCTGT     CCT
                                ||||||||||||     |||
                                AGGCCGCGGACA     GGA
                                       AA_____
GAM1007  TCL6     5'  CGGTGCCCTTAGATCTG     26832        GTCG    C
                                CGGTGCCT    TAGA CTG
                                ||||||||    |||| |||
                                GCCACGGG    ATCT GAC
                                     A___    A
GAM1007  TCL6     5'  CGGTGCCCTTAGATCTG     26832        GTCG    C
                                CGGTGCCT    TAGA CTG
                                ||||||||    |||| |||
                                GCCACGGG    ATCT GAC
                                     A___    A
GAM1007  LOC152024 5'  GTGCTGATAGTAGACCTG    26833     C  TC_
                                GTGC TG   GTAGACCTG
                                |||| ||   |||||||||
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                                CACG AC   CATCTGGAC
                                  _ TAT
GAM1007  LOC158972 3'  TCTTGTGCCTGGAGCCGCCTG  26834    CG      TC  AGA
                                TC  GTGCCTG  GT   CCTG
                                ||  |||||||  ||   ||||
                                AG  CACGGAC  CG   GGAC
                                 AA      CT  GC_
GAM1007  LOC203286 5'  TCCGGTTCTGACCCCAGATCTG 26835       GC  _  G   C
                                TCCGGT  CTG TC TAGA CTG
                                ||||||  ||| || |||| |||
                                AGGCCA  GAC GG GTCT GAC
                                   A_  T  G   A
GAM1007  LOC206426 5'  GGGGCCTCCCTCAGACCTG   26836    T   G  G
                                GG GCCT TC TAGACCTG
                                || |||| || ||||||||
                                CC CGGA GG GTCTGGAC
                                 C   G  A
GAM1007  LOC221100 5'  GGTGCCTGTACACAGGCCTG   26837         _    A
                                GGTGCCTGT CGTAG CCTG
                                ||||||||| ||||| ||||
                                CCACGGACA GTGTC GGAC
                                     T    C
GAM1007  LOC255925 5'  GGCGTTTCCGCAGACCTG    26838      CCTG
                                GGTG   TCGTAGACCTG
                                ||||   ||||||||||
                                CCGC   GGCGTCTGGAC
                                  AAA_
GAM1008  LAMA3    3'  GTGCATTGGGTAATCAGTGCTT 26841         AGA__   A
            T                    GTGCATTGG    TAGT GCTTT
                                |||||||||    |||| |||||
                                CACGTAACC    GTCA CGAAA
                                     CATTA   _
GAM1008  FLJ13154  3'  GTGCATTGGAGGCCTGGCTTTC 26842          ATAGTA
            A                    GTGCATTGGAG     GCTTTCA
                                ||||||||||     |||||||
                                CACGTAACCTC     CGAAAGT
                                      CGGAC_
GAM1008  KIAA0062  3'  GTGCATTGTGGATGGTAAGTCC 26843        GA   A  _ _
            TC                    GTGCATTG  GAT GTA G CTTT
                                ||||||||  ||| ||| | ||||
                                CACGTAAC  CTA CAT C GGAG
                                    AC   C   T A
GAM1008  LOC129868 5'  GTGCAGTGCTGGTAGCTTTC   26844      T  GAGATA
                                GTGCA TG     GTAGCTTTC
                                ||||| ||     |||||||||
                                CACGT AC     CATCGAAAG
                                  C  GAC___
GAM1008  LOC130633 5'  GTGCAGTGCTGGTAGCTTTC   26844      T  GAGATA
                                GTGCA TG     GTAGCTTTC
                                ||||| ||     |||||||||
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                                CACGT AC     CATCGAAAG
                                  C  GAC___
GAM1008  LOC149448 3'  GTGTTTGGAGATGGCATCTTT  26845     CA       A   G
                                GTG  TTGGAGAT GTA CTTT
                                |||  |||||||| ||| ||||
                                CAC  AACCTCTA CGT GAAA
                                  A_       C   A
GAM1008  LOC158308 3'  GCATTGGGCAGCTTT       26846        AGATA
                                GCATTGG    GTAGCTTT
                                |||||||    ||||||||
                                CGTAACC    CGTCGAAA

                                      _____
GAM1009  IRS1     3'  GCAGACTCATTATTCTGGT    26849         __    C
                                GTAGATTT  TATTC GGT
                                ||||||||  ||||| |||
                                CGTCTGAG  ATAAG CCA
                                     TA    A
GAM1009  PHB      3'  TTTCACAGTGATTTCTGGGGT  26850         A     ATTCC
                                TTTCACAGT GATTTT    GGT
                                |||||||||| ||||||    |||
                                AAAGTGTCA CTAAAG    CCA
                                     _     ACC__
GAM1009  GLTP     3'  TTCACAGTGATTCTG       26851         A     ATTCC
                                TTCACAGT GATTTT    G
                                |||||||| ||||||    |
                                AAGTGTCA CTAAGA    C

                                     _    _____
GAM1009  TM9SF1   3'  TTTCTTAATAAATTTTATTTTG 26852      AC          CC
            GT                    TTTC  AGTAGATTTTATT  GGT
                                ||||  ||||||||||||  |||
                                AAAG  TTATTTAAAATAA  CCA
                                  AA          AA
GAM1009  LOC126669 3'  TTTCACAGTAAATAAACTGGT  26853           TTT   CC
                                TTTCACAGTAGAT   ATT  GGT
                                ||||||||||||   |||  |||
                                AAAGTGTCATTTA   TGA  CCA
                                       TT_  __
GAM1009  LOC149117 3'  CTTCACAGTAGGTGCTGTATTT 26854          ATTT__   CC
            GGT                   TTTCACAGTAG     TATT  GGT
                                ||||||||||     ||||  |||
                                GAAGTGTCATC     ATAA  CCA
                                     CACGAC    A_
GAM1009  LOC166929 5'  TTTCACAGTGGATGTACAGATG 26855         A   TT   TCC_
            GT                    TTTCACAGT GAT  TAT    GGT
                                |||||||| |||  |||   |||
                                AAAGTGTCA CTA  ATG    CCA
                                     C   C_   TCTA
GAM1010  COLQ     3'  CTTGAGGTCTGCTGTGGGGGTG 26858         ATAC   TTA_
                                CTTGAGGTC   GTT   GGGTG
                                |||||||||   |||   |||||
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                                GAACTCCAG   CGA   CCCAC
                                     A___   CACC
GAM1010 COLQ    3' CTTGAGGTCTGCTGTGGGGGTG 26858       ATAC  TTA_
                                CTTGAGGTC   GTT   GGGTG
                                |||||||||   |||   |||||
                                GAACTCCAG   CGA   CCCAC
                                     A___   CACC
GAM1010 COLQ    3' CTTGAGGTCTGCTGTGGGGGTG 26858       ATAC  TTA_
                                CTTGAGGTC   GTT   GGGTG
                                |||||||||   |||   |||||
                                GAACTCCAG   CGA   CCCAC
                                     A___   CACC
GAM1010 COLQ    3' CTTGAGGTCTGCTGTGGGGGTG 26858       ATAC  TTA_
                                CTTGAGGTC   GTT   GGGTG
                                |||||||||   |||   |||||
                                GAACTCCAG   CGA   CCCAC
                                     A___   CACC
GAM1010 COLQ    3' CTTGAGGTCTGCTGTGGGGGTG 26858       ATAC  TTA_
                                CTTGAGGTC   GTT   GGGTG
                                |||||||||   |||   |||||
                                GAACTCCAG   CGA   CCCAC
                                     A___   CACC
GAM1010 COLQ    3' CTTGAGGTCTGCTGTGGGGGTG 26858       ATAC  TTA_
                                CTTGAGGTC   GTT   GGGTG
                                |||||||||   |||   |||||
                                GAACTCCAG   CGA   CCCAC
                                     A___   CACC
GAM1010 TLX1    5' TTGGGGTCTGCTGCCAGGGTG  26859    A   ATAC  _
                                TTG GGTC   GTT TTAGGGTG
                                ||| ||||   ||| ||||||||
                                AAC CCAG   CGA GGTCCCAC
                                  C   A___   C
GAM1010 FLJ21162 5' CTTAAGGTATATTTTAGGGTG  26860       CATAC
                                CTTGAGGT   GTTTTAGGGTG
                                ||||||||   ||||||||||
                                GAATTCCA   TAAAATCCCAC
                                     TA___
GAM1010 TRAP95   3' CTTGAGGTCGGTGTTGGT   26861       ATAC  TTAG
                                CTTGAGGTC   GTT   GGT
                                |||||||||   |||   |||
                                GAACTCCAG   CAA   CCA
                                     CCA_  _____
GAM1010 WNT10A   3' TGAGGCTTGTTTTAGGGT   26862      CATAC
                                TGAGGT   GTTTTAGGGT
                                ||||||   ||||||||||
                                ACTCCG   CAAAATCCCA
                                   AA___
GAM1010 WSB1    3' CTTGAGGTTTGTGTTAAG   26863       CATAC  T
                                CTTGAGGT   GT TTAGG
                                ||||||||   || |||||
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                                GAACTCCA    CA AATTC
                                    AA___  C
GAM1010 WSB1    3' CTTGAGGTTTGTGTTAAG   26863       CATAC  T
                                CTTGAGGT    GT TTAGG
                                ||||||||    || |||||
                                GAACTCCA    CA AATTC
                                    AA___  C
GAM1010 LOC149373 3' CTTGAGGCAGGCCTTTGGGGTG 26864       T  TAC    A_
                                CTTGAGG CA   GTTTT  GGGTG
                                ||||||| ||   |||||  |||||
                                GAACTCC GT   CGGAA  CCCAC
                                   _ C__    AC
GAM1011 ROBO1   3' ACTGCACGCCTTTTCTAT   26867        GTATAC
                                ATTGCACGCC     TCTAT
                                ||||||||||     |||||
                                TGACGTGCGG     AGATA
                                     AAA___
GAM1011 ROBO1   3' ACTGCACGCCTTTTCTAT   26867        GTATAC
                                ATTGCACGCC     TCTAT
                                ||||||||||     |||||
                                TGACGTGCGG     AGATA
                                     AAA___
GAM1012 AHR     5' GGCACGCTCTCGGAACAG   26870     AACC  A   A
                                GGCA    CT TTC GGAACAG
                                ||||    || ||| |||||||
                                CCGT    GA GAG CCTTGTC
                                  GC__  _   _
GAM1012 AQP2    3' AGGCAAACCTGTTCACACTCAG 26871        C_____
            G                    AGGCAAACC     TATTCAGG
                                |||||||||     ||||||||
                                TCCGTTTGG     GTGAGTCC
                                     ACAAGT
GAM1012 BLAME   3' AGACAGAATCATTCAGGGGCAG 26872      AACCC      AA
            A                    AGGCA    TATTCAGG  CAGA
                                |||||    ||||||||  ||||
                                TCTGT    GTAAGTCC  GTCT
                                   CTTA_       CC
GAM1012 CHRNB2  3' GGCTAAACCCTACTTGGCAGG  26873    _       ___
                                GGC AAACCCTATT   CAGG
                                ||| ||||||||||   ||||
                                CCG TTTGGGATGA   GTCC
                                  A         ACC
GAM1012 CYP4A11  3' AGGAAACTAATATAGGAACAGA 26874    C   CCT  TC
                                AGG AAAC   AT  AGGAACAGA
                                ||| ||||   ||  |||||||||
                                TCC TTTG   TA  TCCTTGTCT
                                  _   AT_  TA
GAM1012 EPHX1   3' AGGCAAACTCATTCCTCAG   26875       CC    AGGAA
                                AGGCAAAC  TATTC    CAG
                                ||||||||  |||||    |||
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                                TCCGTTTG GTAAG   GTC
                                   A_   GA___
GAM1012 FACL5   3' AGCAAACTGTAGGGAACAG  26876      CC TTCA
                                GGCAAAC TA  GGAACAG
                                ||||||| ||  |||||||
                                TCGTTTG AT  CCTTGTC
                                   AC C___
GAM1012 FGFR2   3' AGGAAATAGATGCCAGGAACAG 26877    C  CCCTAT
           A                     AGG AAA    TCAGGAACAGA
                                ||| |||    ||||||||||
                                TCC TTT    GGTCCTTGTCT
                                  _ ATCTAC
GAM1012 FUS1    3' AGGCAAACTTGGAAGAAAGCAG 26878       CCTATTC   _
           A                     AGGCAAAC     AGGAA CAGA
                                ||||||||     ||||| ||||
                                TCCGTTTG     TCTTT GTCT
                                   AACCT__   C
GAM1012 GBF1    3' AGGCTGAACCCCCAGGAATGGA 26879    A_    ATT    CA
                                AGGC AACCCT  CAGGAA GA
                                ||||  ||||||  ||||||  ||
                                TCCG TTGGGG  GTCCTT CT
                                  AC    ___    AC
GAM1012 KRTHA8  3' AGGCATGTCCAAGGAACAG  26880     AAC TATTC
                                AGGCA  CC   AGGAACAG
                                |||||  ||   ||||||||
                                TCCGT  GG   TCCTTGTC
                                  ACA T____
GAM1012 MAX     3' AGCAAATGCCAGGAACG    26881      CCCTAT     A
                                GGCAAA    TCAGGAAC G
                                ||||||    |||||||| |
                                TCGTTT    GGTCCTTG C
                                   AC____     C
GAM1012 MAX     3' AGCAAATGCCAGGAACG    26881      CCCTAT     A
                                GGCAAA    TCAGGAAC G
                                ||||||    |||||||| |
                                TCGTTT    GGTCCTTG C
                                   AC____     C
GAM1012 MBTPS1  3' GGCAGGCCCATGTAGAACAGA 26882    AA  TATTCA
                                GGCA CCC    GGAACAGA
                                |||| |||    ||||||||
                                CCGT GGG    TCTTGTCT
                                  CC  TACA__
GAM1012 NPTX1   3' AGGTGGCCCTAGAAGGAACAGA 26883    CAAA   TTC
                                AGG  CCCTA  AGGAACAGA
                                |||  |||||  |||||||||
                                TCC  GGGAT  TCCTTGTCT
                                  ACC_   CT_
GAM1012 POLS    3' AGCAAACCGCGAAGGAACAGA 26884      CTATTC
                                GGCAAACC    AGGAACAGA
                                ||||||||    |||||||||
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                                TCGTTTGG     TCCTTGTCT
                                    CGCT__
GAM1012 PRIM2A   3' AGGCAAAATCTTAAAAACAG  26885       CC  ATTC
                                AGGCAAA  CT   AGGAACAG
                                |||||||  ||   ||||||||
                                TCCGTTT  GA   TTTTTGTC
                                   TA  A___
GAM1012 RANBP3   5' GGCAGACCTAGGAACAG    26886     A   CTATTC
                                GGCA ACC     AGGAACAG
                                |||| |||     ||||||||
                                CCGT TGG     TCCTTGTC
                                  C   A_____
GAM1012 TLE1     3' AGGTGAACTGCAAGGAACAGA 26887    CA   CC  TTC
                                AGG  AAC  TA   AGGAACAGA
                                |||  |||  ||   |||||||||
                                TCC  TTG  GT   TCCTTGTCT
                                  AC   AC  ___
GAM1012 CLSTN2   3' AGGCAAACTCTGCAGACAG   26888       C  ATT   GA
                                AGGCAAAC CT   CAG  ACAG
                                |||||||| ||   |||  ||||
                                TCCGTTTG GA   GTC  TGTC
                                    A  C__   __
GAM1012 DKFZp564A176 5' AGGCGCACCCAGGAACAG    26889     AA    TATTC
                                AGGC  ACCC    AGGAACAG
                                ||||  ||||    ||||||||
                                TCCG  TGGG    TCCTTGTC
                                  CG   _____
GAM1012 FLJ00060 3' AGCAAACTAATGCAGGAACAGA 26890       CCT  T
                                GGCAAAC   AT CAGGAACAGA
                                |||||||   || ||||||||||
                                TCGTTTG   TA GTCCTTGTCT
                                   AT_  C
GAM1012 FLJ10101 3' GGCAAACCATTAGGGAATGGA  26891       CT   CA   CA
                                GGCAAACC  ATT  GGAA  GA
                                ||||||||  |||  ||||  ||
                                CCGTTTGG  TAA  CCTT  CT
                                    __  TC   AC
GAM1012 FLJ10546 5' AGGCAAACCATTGATAACAGA  26892        CTATTCAGG
                                AGGCAAACC       AACAGA
                                |||||||||       ||||||
                                TCCGTTTGG       TTGTCT
                                    TAACTA___
GAM1012 FLJ13322 3' AGGCAAACACTGACAGGA    26893       C  ATT
                                AGGCAAAC CT   CAGGA
                                |||||||| ||   |||||
                                TCCGTTTG GA   GTCCT
                                   T  CT_
GAM1012 FLJ20128 3' AGACAAACTCTTCCCAGGAACA 26894        C  A
          GA                    AGGCAAAC CT TTCAGGAACAGA
                                |||||||| || ||||||||||||
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                                TCTGTTTG GA GGGTCCTTGTCT
                                    A  A
GAM1012  FLJ22578  3'  AGGCAGGGCCTGGGAACAG   26895      AAC   ATTCA
                                AGGCA   CCT    GGAACAG
                                |||||   |||    |||||||
                                TCCGT   GGA    CCTTGTC
                                  CCC   C____
GAM1012  GMFB      3'  AGCCAAACAGTGTTGGGAACAG 26896    G    CCTATTCA
             A                   AG CAAAC       GGAACAGA
                                || |||||       ||||||||
                                TC GTTTG       CCTTGTCT
                                 G    TCACAAC_
GAM1012  GSK3A     3'  AGGCAAACCTTACTGTGGA   26897         C   CA
                                AGGCAAACC TATT  GGA
                                ||||||||| ||||  |||
                                TCCGTTTGG ATGA  CCT
                                     A   CA
GAM1012  HRH3      3'  AGGCAAACTGCTAGGGCAGG   26898        C_   TT_
                                AGGCAAAC  CTA   CAGG
                                ||||||||  |||   ||||
                                TCCGTTTG  GAT   GTCC
                                    AC   CCC
GAM1012  HRIHFB2436 3'  AGGCAGGCCCATCCAAATGGA  26899      AAC      ___
                                AGGCA   CCTATTCA   GGA
                                |||||   ||||||||   |||
                                TCCGT   GGGTAGGT   CCT
                                  CC_      TTA
GAM1012  KIAA0057  3'  AGCTAGACCCTATCAGGTGAAC 26900     AA_      T   __
             AG                   GGC   ACCCTAT CAGG  AACAG
                                |||   ||||||| ||||  |||||
                                TCG   TGGGATA GTCC  TTGTC
                                 ATC      _   AC
GAM1012  KIAA0668  3'  GGCAGGCCCTAGCAGGAACAG  26901     AA    TT
                                GGCA  CCCTA  CAGGAACAG
                                ||||  |||||  |||||||||
                                CCGT  GGGAT  GTCCTTGTC
                                  CC    C_
GAM1012  KIAA0759  3'  AGGCAGTGTCCAGGGAACAGA  26902      AACCCTA    _
                                AGGCA      TTCAGG AACAGA
                                |||||      |||||| ||||||
                                TCCGT      AGGTCC TTGTCT
                                  CAC____     C
GAM1012  KIAA0775  5'  GGGGAACCCTACGAGGGGGCAG 26903    CA      TC   AA_
                                GG  AACCCTAT  AGG   CAG
                                ||  ||||||||  |||   |||
                                CC  TTGGGATG  TCC   GTC
                                 CC       C_   CCC
GAM1012  KIAA1045  3'  GGCTGAGCTGTCAGGAACAG   26904     AAACC  AT
                                GGC    CT  TCAGGAACAG
                                |||    ||  ||||||||||
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                              CCG    GA  AGTCCTTGTC
                                ACTC_  C_
GAM1012 KIAA1145 5' AGCAAACCCAGGAGCA     26905        TATTC   A
                              GGCAAACCC    AGGA CA
                              |||||||||    |||| ||
                              TCGTTTGGG    TCCT GT
                                   _____   C
GAM1012 KIAA1854 3' AGGCAAACCTTAGGTGGGGGCA 26906        C  TTCA  AA
          G                    AGGCAAACC TA   GG  CAG
                              ||||||||| ||   ||  |||
                              TCCGTTTGG AT   CC  GTC
                                   A  CCAC  CC
GAM1012 LRP1B   5' GACAAGCCAAGGAACAG     26907      A  CTATTC
                              GGCAA CC     AGGAACAG
                              ||||| ||     ||||||||
                              CTGTT GG     TCCTTGTC
                                 C  T_____
GAM1012 N4BP3   3' AGGTAAGCCCTATCAGGGCAG  26908    C  A     T   AA
                              AGG AA CCCTAT CAGG  CAG
                              ||| || |||||| ||||  |||
                              TCC TT GGGATA GTCC  GTC
                                A  C     _   C_
GAM1012 SEMA6B  3' AGGCAAACTCCAGAGAGGGCAG 26909        _  TATTC   AA
          A                    AGGCAAAC CC    AGG  CAGA
                              |||||||| ||    |||  ||||
                              TCCGTTTG GG    TCC  GTCT
                                   A  TCTC_   C_
GAM1012 SEMA6B  3' AGGCAAACTCCAGAGAGGGCAG 26909        _  TATTC   AA
          A                    AGGCAAAC CC    AGG  CAGA
                              |||||||| ||    |||  ||||
                              TCCGTTTG GG    TCC  GTCT
                                   A  TCTC_   C_
GAM1012 SEMA6B  3' AGGCAAACTCCAGAGAGGGCAG 26909        _  TATTC   AA
          A                    AGGCAAAC CC    AGG  CAGA
                              |||||||| ||    |||  ||||
                              TCCGTTTG GG    TCC  GTCT
                                   A  TCTC_   C_
GAM1012 SLC2A10  3' AAGCAAACCACCTTTGGGGGCA 26910        _  ATTCA  AA
          G                    AGGCAAACC CT    GG  CAG
                              ||||||||| ||    ||  |||
                              TTCGTTTGG GG    CC  GTC
                                   T  AAAC_  CC
GAM1012 SLC38A5  5' AGGCAGACTCAGAAACAAA   26911      A  CCTAT
                              AGGCA AC    TCAGGAACAGA
                              ||||| ||    ||||||||||
                              TCCGT TG    AGTCTTTGTTT
                                C  _____
GAM1012 SQV7L   5' AGCAAACTAACACAGGAACAGA 26912       CCT  T
                              GGCAAAC   AT CAGGAACAGA
                              |||||||   || ||||||||||
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                                TCGTTTG   TG GTCCTTGTCT
                                   AT_  T
GAM1012  UHRF1    3'  AGACAAACCTTTTTAGGGAACG 26913        CTATTCA    A
              GA                  AGGCAAACC      GGAAC GA
                                  |||||||||      ||||| ||
                                  TCTGTTTGG      CCTTG CT
                                      AAAAATC    C
GAM1012  USP25    3'  AAGCAAACCCTGTGACAGG   26914         ATT_
                                  AGGCAAACCCT    CAGG
                                  ||||||||||    ||||
                                  TTCGTTTGGGA    GTCC
                                        CACT
GAM1012  LOC139673 3'  GGTCAAAGCATCAGGAACAG   26915    _   CCCTAT
                                  GG CAAA     TCAGGAACAG
                                  || ||||     ||||||||||
                                  CC GTTT     AGTCCTTGTC
                                   A   CGT___
GAM1012  LOC144231 5'  AGGCAGACAGAGAAGGAACAGA 26916      A  CCTATTC
                                  AGGCA AC      AGGAACAGA
                                  ||||| ||      |||||||||
                                  TCCGT TG      TCCTTGTCT
                                     C  TCTCT__
GAM1012  LOC145813 5'  GGCAGGCTCCAGGAAGACAG   26917     AACCCTA     __
                                  GGCA      TTCAGGA  ACAG
                                  ||||      |||||||  ||||
                                  CCGT      AGGTCCT  TGTC
                                    CCG____      TC
GAM1012  LOC154877 3'  GGCGACTGTGCAGGAACAGA   26918    AAACC  ATT
                                  GGC    CT   CAGGAACAGA
                                  |||    ||   ||||||||||
                                  CCG    GA   GTCCTTGTCT
                                    CT___  CAC
GAM1012  LOC164862 5'  AGGAAGGCCTGGTGGAACAGA  26919    C  AC   ATTCA
                                  AGG AA  CCT    GGAACAGA
                                  ||| ||  |||    ||||||||
                                  TCC TT  GGA    CCTTGTCT
                                    _  CC   CCA__
GAM1012  LOC196382 3'  AGGAAACCCTGCCCCAGCAG   26920    C      A_    GAA
                                  AGG AAACCCT  TTCAG   CAG
                                  ||| |||||||  |||||   |||
                                  TCC TTTGGGA  GGGTC   GTC
                                    _      CG    ___
GAM1012  LOC196932 5'  GGCTAAACCCCAGGGACAG    26921    _    TATT   A
                                  GGC AAACCC    CAGG ACAG
                                  ||| ||||||    |||| ||||
                                  CCG TTTGGG    GTCC TGTC
                                    A     _____    C
GAM1012  LOC199858 5'  AGGCAAACCCATATCTGGAGTA 26922          TAT  A   AC
              GA                  AGGCAAACCC   TC GGA  AGA
                                  ||||||||||   || |||  |||
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                                TCCGTTTGGG  AG CCT  TCT
                                      TAT  A   CA
GAM1012  LOC203248 3'  AGGCTAACCCAGAAGGAACAGA 26923     A    TATTC
                                AGGC AACCC    AGGAACAGA
                                |||| |||||    |||||||||
                                TCCG TTGGG    TCCTTGTCT
                                  A    TCT__
GAM1012  LOC51014  3'  AAACCCTATAGTCTACAGA   26924        TC  GA_
                                AAACCCTAT  AG   ACAGA
                                |||||||||  ||   |||||
                                TTTGGGATA  TC   TGTCT
                                     __  AGA
GAM1012  LOC51634  3'  AGGCAAACCCATAAACAGG   26925         _  TT
                                AGGCAAACCC TA  CAGG
                                |||||||||| ||  ||||
                                TCCGTTTGGG AT  GTCC
                                      T  TT
GAM1012  LOC57019  3'  AGACAAGCCCTATTCTAAGCGT 26926      A      _   AAC
            AG                    AGGCAA CCCTATTC AGG   AG
                                |||||| |||||||| |||   ||
                                TCTGTT GGGATAAG TTC   TC
                                   C       A   GCA
GAM1012  LOC57107  5'  AAACAAACCAGGGGCAGA    26927        CTATTC   AA
                                AGGCAAACC     AGG  CAGA
                                |||||||||     |||  ||||
                                TTTGTTTGG     TCC  GTCT
                                      _______  CC
GAM1013  KIAA0061  3'  AAAAAAATTAAGTAACTA    26930          TT
                                AAAAAAATTAAGT  CTA
                                ||||||||||||  |||
                                TTTTTTTAATTCA  GAT
                                       TT
GAM1014  PLA2G1B   3'  GGAGAGTACAGTGTGAGAT   26933       AA   T  AC
                                GGAGAGT  ACA TG  GGAT
                                |||||||  ||| ||  ||||
                                CCTCTCA  TGT AC  TCTA
                                    __   C  AC
GAM1014  BPESC1    3'  TCGGGGAGTAAACAGGAGG   26934     A       TT  C
                                TCGG GAGTAAACA  GA GG
                                |||| |||||||||  || ||
                                AGCC CTCATTTGT  CT CC
                                  C        C_  _
GAM1014  DKFZP434K2235 3'  TCAGAGAGTAAAGCTGGTGGAT 26935          CA   AC
                                TCGGAGAGTAAA  TTG  GGAT
                                ||||||||||||  |||  ||||
                                AGTCTCTCATTT  GAC  CCTA
                                       C_   CA
GAM1014  KIAA1061  3'  GGGAGTAAACATAACA      26936    A        T
                                GG GAGTAAACAT GACG
                                || ||||||||||  ||||
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                                CC CTCATTTGTA TTGT
                                  _       _
GAM1014  LOC131034 5'  TCGGAGAGTAAAGAGGA     26937          CATT  C
                                TCGGAGAGTAAA    GA GGA
                                ||||||||||||    || |||
                                AGCCTCTCATTT    CT CCT
                                      _____  _
GAM1014  LOC255506 5'  TCGGAGAGCTGGGCAAAGGAT  26938         AAACATT  C
                                TCGGAGAGT       GA GGAT
                                |||||||||       || ||||
                                AGCCTCTCG       TT CCTA
                                     ACCCGT_  _
GAM1015  NT5C3     3'  TGTAATGATTAGCAACATTGT  26941       A   AAACAT
                                TGTAA GAT     CAACATTGT
                                ||||| |||     |||||||||
                                ACATT CTA     GTTGTAACA
                                   A   ATC___
GAM1015  C20orf42  5'  TAAAGATAAACCAATATTGT   26942          AT   C
                                TAAAGATAAAC  CAA ATTGT
                                ||||||||||  ||| |||||
                                ATTTCTATTTG  GTT TAACA
                                      __   A
GAM1015  DKFZP434N1235 3'  TAAAGATAAACATCAGCA    26943             A
                                TAAAGATAAACATCA CA
                                |||||||||||||| ||
                                ATTTCTATTTGTAGT GT
                                       C
GAM1015  DKFZP586B0923 3'  TATAAAGGTAAACATCACA   26944        A       A
                                TGTAAAG TAAACATCA CA
                                ||||||| ||||||||| ||
                                ATATTTC ATTTGTAGT GT
                                    C       _
GAM1015  FLJ13188  3'  TGTAAAGATAATATCAAC    26945          AC
                                TGTAAAGATAA  ATCAAC
                                ||||||||||  ||||||
                                ACATTTCTATT  TAGTTG
                                      A_
GAM1015  FLJ14082  3'  TGTAATCAGTAGCATCAACATT 26946       AGATAAA
            GT                    TGTAA      CATCAACATTGT
                                |||||      ||||||||||||
                                ACATT      GTAGTTGTAACA
                                   AGTCATC
GAM1015  LOC144317 3'  TGTAAAGATACAGCAATCTAAA 26947         AA_  _  __
            CATTGT                  GTAAAGATA   CA TC  AACATTGT
                                |||||||||   || ||  ||||||||
                                CATTTCTAT   GT AG  TTGTAACA
                                      GTC  T  AT
GAM1016  FLJ21168  3'  TCCTAAAATTTCCTAGAAGTGT 26950     _        _   A
            ATTT                    TCC AAAATTTTTTA AAGT TATTT
                                ||| ||||||||||| |||| |||||
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                                AGG TTTTAAAGGAT TTCA ATAAA
                                  A         C   C
GAM1016  GMFB     3'  TCCAAACATTTTTTAAGTACAC 26951       _       A
                CT                  TCCAAA ATTTTTTAA GTATATTT
                                    |||||| ||||||||| ||||||||
                                    AGGTTT TAAAAAATT CATGTGGA
                                       G       _
GAM1016  KIAA1674  3'  TCCAAAAATTTTTGCAATATAT 26952        T    AA
                                    TCCAAAA TTTTT  AGTATAT
                                    ||||||| |||||  |||||||
                                    AGGTTTT AAAAA  TTATATA
                                        T    CG
GAM1016  LOC152220 3'  CAAAATTAACCAAAGTATATTT 26953        TT
                                    CAAAATT  TTAAAGTATATTT
                                    |||||||  |||||||||||||
                                    GTTTTAA  GGTTTCATATAAA
                                        TT
GAM1016  LOC170395 3'  TCCAAAAATTTTTGCAATATAT 26952        T    AA
                                    TCCAAAA TTTTT  AGTATAT
                                    ||||||| |||||  |||||||
                                    AGGTTTT AAAAA  TTATATA
                                        T    CG
GAM1016  LOC220933 5'  TCCAAAATTTTTGAGTCCATTT 26954           TAA  A
                                    TCCAAAATTTTT   AGT TATTT
                                    ||||||||||||   ||| |||||
                                    AGGTTTTAAAAA   TCA GTAAA
                                          C__   G
GAM1017  CHCR     3'  GGTAGAATAAGACATACG    26957    C   TGC  C
                                    GG AGA   GA GACATACG
                                    || |||   || ||||||||
                                    CC TCT   TT CTGTATGC
                                     A  TA_  _
GAM1018  AF1Q     3'  TTTGTGTTTACTGCCCTG    26960      A  AC
                                    TTTG TG  TTACTGCCCTG
                                    |||| ||  ||||||||||
                                    AAAC AC  AATGACGGGAC
                                      _  A_
GAM1018  C14orf1  3'  CCCTTGGTCACAGCTGCTCTG  26961       ATG  TTA   C
                                    CCTTTG   AC   CTGC CTG
                                    ||||||   ||   |||| |||
                                    GGGAAC   TG   GACG GAC
                                        CAG  TC_   A
GAM1018  JAG1     3'  CTTGTTCCCTTACTGCTCTG   26962      ATGA       C
                                    TTTG    CTTACTGC CTG
                                    ||||    |||||||| |||
                                    GAAC    GAATGACG GAC
                                      AAGG       A
GAM1018  MEN1     5'  ACCCTCTGAAACAGGCTGTCT  26963         T   TTA   CC
                                    ACCCTTTGA GAC   CTG  CT
                                    ||||||||| |||   |||  ||
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                                TGGGAGACT TTG   GAC  GA
                                      _  TCC   A_
GAM1018  NHP2L1   3'  CTTTGGTATGCTGCTGCCCTG  26964      __  A  TA
                                CTTTG  ATG CT  CTGCCCTG
                                |||||  ||| ||  ||||||||
                                GAAAC  TAC GA  GACGGGAC
                                   CA   _  C_
GAM1018  PTGFRN   3'  CCCTTCTTACTGCCCT      26965       TGATGA
                                CCCTT     CTTACTGCCCT
                                |||||     ||||||||||
                                GGGAA     GAATGACGGGA
                                   _______
GAM1018  ZNF10    5'  CTTGATGATACTTCCT      26966         CT    GC
                                TTTGATGA  TACT  CCT
                                ||||||||  ||||  |||
                                GAACTACT  ATGA  GGA
                                     __    A_
GAM1018  ANXA13   3'  ACCCTGTGTTCCTATTGCCCTG 26967       T  ATGA    C
                                ACCCT TG    CTTA TGCCCTG
                                ||||| ||    |||| |||||||
                                TGGGA AC    GGAT ACGGGAC
                                   C  AA__    A
GAM1018  ELOVL1   3'  ACCCTTTGTGGGGCCAGCCCTG 26968         A  ACTTACT
                                ACCCTTTG TG      GCCCTG
                                |||||||| ||      ||||||
                                TGGGAAAC AC      CGGGAC
                                     _  CCCGGT_
GAM1018  FLJ11413 5'  CCTTTTGATGATGACTCCCTG  26969    C       CTT   G
                                CC TTTGATGA   ACT CCCTG
                                || ||||||||   ||| |||||
                                GG AAACTACT   TGA GGGAC
                                 A       AC_  _
GAM1018  FLJ12671 3'  CCATTGGTCCACTGCCCTG    26970    T   ATGAC
                                CC TTG     TTACTGCCCTG
                                || |||     ||||||||||
                                GG AAC     GGTGACGGGAC
                                 T   CA___
GAM1018  FLJ13111 3'  CTCTGGACTTGCTGCCCTG    26971      AT    A
                                CTTTG  GACTT CTGCCCTG
                                |||||  ||||| ||||||||
                                GAGAC  CTGAA GACGGGAC
                                   __     C
GAM1018  FLJ20420 3'  CCTTTAATGACTGATCCCTG   26972           TACTG
                                CCTTTGATGACT    CCCTG
                                ||||||||||||    |||||
                                GGAAATTACTGA    GGGAC
                                      CTA__
GAM1018  FLJ22301 3'  CCCCTTGATCTGCCC       26973         GACTTA
                                CCCTTTGAT     CTGCCC
                                |||||||||     ||||||
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                                GGGGAACTA     GACGGG
                                          _______
GAM1018 FLJ31168 3' CCCTTCTGACCTCTACTGCCCT 26974       GA    __
             G                   CCCTTT  TGACT  TACTGCCCTG
                                 ||||||  |||||  ||||||||||
                                 GGGAAG  ACTGG  ATGACGGGAC
                                    __     AG
GAM1018 FUSIP1   3' ACCCTTTGGTCGCTTGAACTG  26975        A_  A   __
                                 ACCCTTTG  TG CTT  ACTG
                                 ||||||||  || |||  ||||
                                 TGGGAAAC  GC GAA  TGAC
                                      CA  _   CT
GAM1018 KIAA0674  5' CCCTTGATGACTTTTCCT    26976           ACTGC
                                 CCTTTGATGACTT     CCT
                                 ||||||||||||     |||
                                 GGGAACTACTGAA     GGA
                                       AA___
GAM1018 KIAA1828  5' CCTTTGATGGAATCCCCTGCTC 26977         ACTTA__    C
             TG                   CCTTTGATG      CTGC CTG
                                  |||||||||      |||| |||
                                  GGAAACTAC      GACG GAC
                                       CTTAGGG    A
GAM1018 KR19     5' CTTTGATGCCCTGCTCTG    26978         ACTTA    C
                                 CTTTGATG     CTGC CTG
                                 ||||||||     |||| |||
                                 GAAACTAC     GACG GAC
                                      GG___     A
GAM1018 MGC16385  3' CTTTGGATGACTTAAACCCTG  26979       _       CT
                                 CTTTG ATGACTTA  GCCCTG
                                 |||||  ||||||||  ||||||
                                 GAAAC TACTGAAT  TGGGAC
                                    C       T_
GAM1018 MGC4707   3' ACCCTTGATGGTGCAAGGCCCT 26980       T    ACTTACT
             G                    ACCCTT GATG      GCCCTG
                                  ||||||  ||||      ||||||
                                  TGGGAA CTAC      CGGGAC
                                     _    CACGTTC
GAM1018 PDE4DIP   3' CCCTTCGATGACTCCCT     26981           TACTG
                                 CCCTTTGATGACT     CCCT
                                 ||||||||||||     ||||
                                 GGGAAGCTACTGA     GGGA
                                           _____
GAM1018 PRO0246   5' ACCCTTTAATGACTCCCT     26982           TACTG
                                 ACCCTTTGATGACT     CCCT
                                 ||||||||||||||     ||||
                                 TGGGAAATTACTGA     GGGA
                                           _____
GAM1018 PRO2533   3' CCTTTGGGTCACTTACTGTCT  26983       ATG_       CC
                                 CCTTTG    ACTTACTG  CT
                                 ||||||    ||||||||  ||
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                                GGAAAC   TGAATGAC  GA
                                   CCAG      A_
GAM1018  SCYA28   3' CTTTGATGATTTAGCTTCTG  26984       C  CT  C_
                                CTTTGATGA TTA  GC  CTG
                                ||||||||| |||  ||  |||
                                GAAACTACT AAT  CG  GAC
                                     A  __  AA
GAM1018  LOC118611 5' CTTTTGTGTGTACTGCCCTG  26985    GA  ACT
                                CTTT  TG  TACTGCCCTG
                                ||||  ||  ||||||||||
                                GAAA  AC  ATGACGGGAC
                                  AC  AC_
GAM1018  LOC143914 5' ACCCTAACCTCTTGCTGC   26986     TT  GA  A
                                ACCCT  GAT  CTT CTGC
                                |||||  |||  ||| ||||
                                TGGGA  TTG  GAA GACG
                                   __  GA  C
GAM1018  LOC151534 5' CCCTTGGTGACTCACGCC   26987      A      T
                                CCTTTG TGACTTAC GCC
                                |||||| |||||||| |||
                                GGGAAC ACTGAGTG CGG
                                   C      _
GAM1018  LOC151827 5' CCTTTGTCACCCTGCCCTG   26988      ATG  TA
                                CCTTTG  ACT  CTGCCCTG
                                ||||||  |||  ||||||||
                                GGAAAC  TGG  GACGGGAC
                                   AG_  __
GAM1018  LOC155046 3' ACCCTTGGGCCACTGCCCT   26989     TTGA  AC
                                ACCCT   TG  TTACTGCCCT
                                |||||   ||  ||||||||||
                                TGGGA   AC  GGTGACGGGA
                                   ____  CC
GAM1018  LOC200312 3' ACCCACTGGGCTTGCTGTCCTG 26990     T  ATGA  A  C
                                ACCC TTG   CTT CTG CCTG
                                |||| |||   ||| ||| ||||
                                TGGG GAC   GAA GAC GGAC
                                  T  CC__  C  A
GAM1018  LOC202759 5' CTTTGATGCCCTGCTCTG   26978       ACTTA   C
                                CTTTGATG   CTGC CTG
                                ||||||||   |||| |||
                                GAAACTAC   GACG GAC
                                     GG___   A
GAM1018  LOC220766 5' CTCTCCATTTACTGCCCTG   26991     GATGAC
                                CTTT    TTACTGCCCTG
                                ||||    ||||||||||
                                GAGA    AATGACGGGAC
                                  GGTA__
GAM1018  LOC221272 3' CCCTTTTGATGATAACAGCTCC 26992      _   CTT  T  _
            TG                   CCCTTT GATGA  AC GC CCTG
                                ||||||| |||||  || || ||||
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                                GGGAAA CTACT   TG CG GGAC
                                   A    AT_  T  A
GAM1018  LOC254057 5'  CCCCTTGGCGCTGCCCT    26993       A  ACTTA
                                CCCTTTG TG    CTGCCCT
                                ||||||| ||    |||||||
                                GGGGAAC GC    GACGGGA
                                   C  _____
GAM1018  LOC255718 5'  CCCTTGACAGCTGCCCT    26994     TTGA   TTA
                                CCCT   TGAC   CTGCCCT
                                ||||   ||||  |||||||
                                GGGA   ACTG   GACGGGA
                                  _____   TC_
GAM1018  LOC256946 3'  ACCCTTTGGTCGCTTGAACTG  26975       A_  A  __
                                ACCCTTTG  TG CTT  ACTG
                                ||||||||  || |||  ||||
                                TGGGAAAC  GC GAA  TGAC
                                     CA  _   CT
GAM1019  BRCA1    3'  TGGACACCTGTGCCAAG    26997        CG
                                TGGACACTTG  GTTAGG
                                ||||||||||  ||||||
                                ACCTGTGGAC  CGGTTC
                                      A_
GAM1019  BRCA1    3'  TGGACACCTGTGCCAAG    26997        CG
                                TGGACACTTG  GTTAGG
                                ||||||||||  ||||||
                                ACCTGTGGAC  CGGTTC
                                      A_
GAM1019  LPIN1    5'  TGGCTGCTGTTAGGAC     26998    ACAC   G
                                TGG   TTGC GTTAGGAC
                                |||   |||| ||||||||
                                ACC   GACG CAATCCTG
                                  _____   A
GAM1019  MAK      3'  AAATAGACATTTGTAGAC    26999        C  CGGTTA
                                AAATGGACA TTG     GGAC
                                ||||||||| |||     ||||
                                TTTATCTGT AAC     TCTG
                                     A  A_____
GAM1019  SRGAP2   3'  GGATGGACACTGATCAAG    27000   A      TGC
                                A ATGGACACT   GGTTAGG
                                | |||||||||   |||||||
                                C TACCTGTGA   CTAGTTC
                                 C       ___
GAM1019  TBP      3'  TGGGCACTTACAGAAGGGCA  27001    A      TT  A
                                TGG CACTTGCGG  AGG CA
                                ||| |||||||||  ||| ||
                                ACC GTGAATGTC  TCC GT
                                  C       T_  C
GAM1019  ABLIM    3'  GGATGGACATTTTGAGGACA  27002   A     C_  CGGTT
                                A ATGGACA  TTG    AGGACA
                                | |||||||  |||    ||||||
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                                C TACCTGT  AAC    TCCTGT
                                 C      AA  _____
GAM1019  ABLIM    3'  GGATGGACATTTTGAGGACA  27002   A     C_  CGGTT
                                A ATGGACA  TTG    AGGACA
                                | |||||||  |||    ||||||
                                C TACCTGT  AAC    TCCTGT
                                 C      AA  _____
GAM1019  CLDN6    3'  TGGACGTCTTATCAGGAC    27003      AC  GCG
                                TGGAC  TT   GTTAGGAC
                                |||||  ||  ||||||||
                                ACCTG  AG   TAGTCCTG
                                   C_  AA_
GAM1019  CYLD     3'  AAATGGACATTTGGGGAC    27004        C   C  TTAG
                                AAATGGACA TTG GG    GAC
                                ||||||||| ||| ||    |||
                                TTTACCTGT AAC CC    CTG
                                      A  _  ____
GAM1019  DKFZP586P0123 5'  AATGGAGGTTTGGGAGGACA  27005       CAC   C  TT
                                AATGGA   TTG GG  AGGACA
                                ||||||   ||| ||  ||||||
                                TTACCT   AAC CC  TCCTGT
                                    CCA  _  __
GAM1019  DKFZP586P0123 3'  TGGACACTGGACTGGTTTGG   27006        T_  _   A
                                TGGACACT  GC GGTT GG
                                ||||||||  || |||| ||
                                ACCTGTGA  TG CCAA CC
                                     CC  A   A
GAM1019  FLJ12525  3'  GGATGAACACTTGCACCAGG   27007   A         G TT
                                A ATGGACACTTGC G  AGG
                                | ||||||||||| |  |||
                                C TACTTGTGAACG T  TCC
                                 C          _ GG
GAM1019  KIAA1199  3'  TAGACACTTGAGTAGG      27008         C   T
                                TGGACACTTG GGT AGG
                                |||||||||| ||| |||
                                ATCTGTGAAC TCA TCC
                                      _  _
GAM1019  OSBPL3   5'  GGATGGCCACTTGCAGAC    27009   A   A     GGTTA
                                A ATGG CACTTGC    GGAC
                                | |||| |||||||    ||||
                                C TACC GTGAACG    TCTG
                                 C   G     _____
GAM1019  P37NB    3'  AAATGGACATTGTAGTGG    27010        C   CG  TA
                                AAATGGACA TTG  GT  GG
                                ||||||||| |||  ||  ||
                                TTTACCTGT AAC  CA  CC
                                      _  AT  __
GAM1019  PAFAH2   5'  AAATGGACGCTTGGAAGC    27011        A   C_
                                AAATGGAC CTTG  GGT
                                |||||||| ||||  |||
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                                TTTACCTG GAAC  TCG
                                    C    CT
GAM1019  POF1B    3'  TGGATACTTGCAAAGA      27012      C      GTT
                                TGGA ACTTGCG   AGGA
                                |||| |||||||   ||||
                                ACCT TGAACGT   TTCT
                                  A      ___
GAM1019  SEC61A1  3'  ATGGACACTTGGGGAC      27013          C  TTAG
                                ATGGACACTTG GG    GAC
                                |||||||||||  ||    |||
                                TACCTGTGAAC CC    CTG
                                          _ _____
GAM1019  LOC134637 3'  TGGGCACTTGTGGCTAGAA   27014     A     C
                                TGG CACTTG GGTTAGGA
                                |||  ||||||  ||||||||
                                ACC GTGAAC CCGATCTT
                                  C      A
GAM1019  LOC202934 3'  GACACTTGGATGGGGACA    27015        C   TA
                                GACACTTG GGT  GGACA
                                ||||||||  |||  |||||
                                CTGTGAAC CTA  CCTGT
                                     _   CC
GAM1019  LOC220477 3'  AAATGGACATCTGATTGGGA   27016         C  GC    A
                                AAATGGACA TT  GGTT GGA
                                |||||||||  ||  ||||  |||
                                TTTACCTGT AG  CTAA CCT
                                      _  A_    C
GAM1019  LOC221490 5'  TGGACACTTGTGAAAACA    27017          C  TTA
                                TGGACACTTG GG   GGACA
                                ||||||||||  ||   |||||
                                ACCTGTGAAC CT   TTTGT
                                      A  ___
GAM1019  LOC92340  3'  GGATGGGCACCTACGGGG    27018    A    A       TTA
                                A ATGG CACTTGCGG   GG
                                |  ||||  |||||||||   ||
                                C TACC GTGGATGCC   CC
                                 C    C        ___
GAM1020  MAP3K7    3'  TCTTTTGCCTTTTAATTT    27021         AAAA
                                TCTTTTGCT    TTTTAATTT
                                |||||||||    |||||||||
                                AGAAAACGG    AAAATTAAA
                                          _____
GAM1020  POLR2K    3'  ATCTCTTGCTATGCTTAATTT  27022          AAAT
                                ATCTTTTGCTA    TTTAATTT
                                ||||||||||    ||||||||
                                TAGAGAACGAT    GAATTAAA
                                      AC__
GAM1020  DKFZp566D133 3'  ATCTTTTGCTGTAACTTT    27023          AA
                                ATCTTTTGCT  AATTTT
                                |||||||||  ||||||
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                                TAGAAAACGA  TTGAAA
                                     CA
GAM1020  KIAA0972  3'  ATCTCTTGCTGTGCCTAATTT  27024          AAAAT
                                ATCTTTTGCT    TTTAATTT
                                ||||||||||    ||||||||
                                TAGAGAACGA    GGATTAAA
                                     CAC__
GAM1020  TREX1     5'  TCTCGCAAAATTTTAATTT   27025       T
                                TTTTGC AAAATTTTAATTT
                                |||||| ||||||||||||
                                AGAGCG TTTTAAAATTAAA
                                   _
GAM1020  LOC150421 3'  ATCTTTTACTCAGGTAATTTTA 27026          AA___
              ATTT                 ATCTTTTGCT    AATTTTAATTT
                                ||||||||||    ||||||||||
                                TAGAAAATGA    TTAAAATTAAA
                                     GTCCA
GAM1020  LOC152024 3'  TTTTGCTAGGACTCTAATTT   27027        AA
                                TTTTGCTA  ATTTTAATTT
                                ||||||||  ||||||||||
                                AAAACGAT  TGAGATTAAA
                                    CC
GAM1020  LOC253959 3'  ATCTTTTGCTGTAACTTT    27023          AA
                                ATCTTTTGCT  AATTTT
                                ||||||||||  ||||||
                                TAGAAAACGA  TTGAAA
                                     CA
GAM1020  LOC255762 3'  ATCTTTTGCCAGCTCAATTT   27028          AAAT
                                ATCTTTTGCTA    TTTAATTT
                                ||||||||||||   ||||||||
                                TAGAAAACGGT    GAGTTAAA
                                     C___
GAM1021  ITK       3'  TGTACAAAATTCTAAAAAGTA  27031      AATTTGT
                                TGTA      ATTCTAAAAAGTA
                                ||||      ||||||||||||||
                                ACAT      TAAGATTTTTCAT
                                  GTTT___
GAM1021  OSBPL8    3'  TGTATATTTAGCATGCTAAAAA 27032      A   _   T
              GT                  TGTA ATTT GTAT CTAAAAAGT
                                |||| |||| |||| |||||||||
                                ACAT TAAA CGTA GATTTTTCA
                                  A   T   C
GAM1021  LOC157867 5'  TGTAAATTCTACAGCTGAAAAG 27033          GTATT  A
              TA                  TGTAAATTT    CT AAAAGTA
                                |||||||||    || |||||||
                                ACATTTAAG    GA TTTTCAT
                                     ATGTC  C
GAM1022  GRAF      3'  CACAAAATTTGAAAACTAG   27036      C  G
                                TACAA GT TGAAAACTAG
                                ||||| || ||||||||||
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                                GTGTT TA ACTTTTGATC
                                   T  A
GAM1022  HS3ST2    3'  ACAGACTGATGAAAACTAG   27037     _ GT
                                ACA AC  GTGAAAACTAG
                                ||| ||  ||||||||||
                                TGT TG  TACTTTTGATC
                                  C  AC
GAM1022  KNSL1     3'  TACTTTATATGAAAACTAG   27038     AAC
                                TAC   GTGTGAAAACTAG
                                |||   ||||||||||||
                                ATG   TATACTTTTGATC
                                  AAA
GAM1022  DNAJC5    3'  ACAACATAGAGAACTAG     27039        T  A
                                ACAACGTG GA AACTAG
                                |||||||| || ||||||
                                TGTTGTAT CT TTGATC
                                     _  C
GAM1022  KIAA1143  3'  ACACCACCTGAAAACTAG    27040     A  TG
                                ACA CG  TGAAAACTAG
                                ||| ||  ||||||||||
                                TGT GT  ACTTTTGATC
                                  G  GG
GAM1022  TP53INP1  3'  TACAAAGCATAAAAAACTAG   27041      C       _
                                TACAA GTGTGAAAA CTAG
                                ||||| |||||||| ||||
                                ATGTT CGTATTTTT GATC
                                   T       T
GAM1022  TP53INP1  3'  TACAAAGCATAAAAAACTAG   27041      C       _
                                TACAA GTGTGAAAA CTAG
                                ||||| |||||||| ||||
                                ATGTT CGTATTTTT GATC
                                   T       T
GAM1022  LOC144317 3'  ACATGTGAACCTAAACTAG    27042         ____
                                ACGTGTGAA    AACTAG
                                |||||||||    ||||||
                                TGTACACTT    TTGATC
                                     GGAT
GAM1022  LOC222174 3'  CACAACATGATGAGCTAG     27043         _  AAA
                                TACAACGTG TGA   CTAG
                                |||||||| |||   ||||
                                GTGTTGTAC ACT   GATC
                                     T  C__
GAM1023  TMPO      3'  CTGGAAACTAAAACAACCT    27046          C
                                CTGGAAACTAAA TAACTT
                                |||||||||||| ||||||
                                GACCTTTGATTT GTTGGA
                                       T
GAM1023  FLJ21616  3'  TACGTCTAAACTAAGTTAACTT 27047      _  GA     AC
                                TACG CTG  AACTAA  TAACTT
                                |||| |||  ||||||  ||||||
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                                ATGC GAT  TTGATT  ATTGAA
                                  A  __     CA
GAM1023  LOC148508 3'  CACTTTAAACTAACTT     27048      GGAAAC
                                CGCT     TAAACTAACTT
                                ||||     ||||||||||
                                GTGA     ATTTGATTGAA
                                  A_____
GAM1024  D12S2489E 3'  TGGAGAATAATGCCTTTA    27051        TATTT  GA
                                TGGAGAAT    TG  CCTTTA
                                ||||||||    ||  ||||||
                                ACCTCTTA    AC  GGAAAT
                                     TT___  __
GAM1024  MSH3      3'  TGGAGAGTTATTTTGTAC    27052       A       G
                                TGGAGA TTATTTTG AC
                                |||||| |||||||| ||
                                ACCTCT AATAAAAC TG
                                   C       A
GAM1024  C1orf24   3'  TGGGGAATTGTGAAACCTTT  27053     A    ATTTT
                                TGG GAATT    GGACCTTT
                                ||| |||||    ||||||||
                                ACC CTTAA    TTTGGAAA
                                  C    CAC__
GAM1024  COE2      3'  GGGAATTATTCCGTTTTTTAA 27054    A        GACC
                                GG GAATTATTTTG    TTTAA
                                || ||||||||||    |||||
                                CC CTTAATAAGGC    AAATT
                                 _         AAA_
GAM1024  FLJ20312  3'  AAGTTATTTTGGACCTTTAA  27055     AA
                                GAG  TTATTTTGGACCTTTAA
                                |||  ||||||||||||||||
                                TTC  AATAAAACCTGGAAATT
                                  __
GAM1024  SDCBP     3'  TAGAGAACTACATTTTGG    27056          __
                                TGGAGAATTAT  TTTGG
                                ||||||||||  |||||
                                ATCTCTTGATG  AAACC
                                       TA
GAM1024  SS18L2    3'  TGGAAGATTATTCTATTGCTTT 27057      GA       GAC
                                TGGA  ATTATTTTG   CTTT
                                ||||  |||||||||   ||||
                                ACCT  TAATAAGAT   GAAA
                                  TC        AAC
GAM1024  ZNF271    3'  TGGAGAATTTTTCTTAATTTTA 27058        _______
              G                  TGGAGAATT      ATTTTGG
                                 |||||||||      |||||||
                                 ACCTCTTAA      TAAAATC
                                      AAAGAAT
GAM1024  LOC158527 5'  GGAGATCATTTTGGACTTTTAA 27059       A        C
                                GGAGA TTATTTTGGAC TTTAA
                                ||||| |||||||||| |||||
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                                CCTCT AGTAAAACCTG AAATT
                                  _       A
GAM1025 ADAM19   3' CCAGTGAGGGAAATCCAG   27062    CC   C__
                                CCA  GTGA   AAATCCAG
                                |||  ||||   ||||||||
                                GGT  CACT   TTTAGGTC
                                  __   CCC
GAM1025 BACE     5' CCACCATAATCCAGC      27063        CAAA
                                CCACCGTGA   TCCAGC
                                |||||||||   ||||||
                                GGTGGTATT   AGGTCG
                                    ____
GAM1025 BACE     5' CCACCATAATCCAGC      27063        CAAA
                                CCACCGTGA   TCCAGC
                                |||||||||   ||||||
                                GGTGGTATT   AGGTCG
                                    ____
GAM1025 BLAME    3' CCCCAGAAAAAATCCAG    27064    A  T  C
                                CC CCG GA AAATCCAG
                                || ||| || ||||||||
                                GG GGT TT TTTAGGTC
                                 _  C  T
GAM1025 DBI      3' CACAGTAACCAAATCCAG   27065    C   _
                                CAC GTGAC AAATCCAG
                                ||| ||||| ||||||||
                                GTG CATTG TTTAGGTC
                                  T    G
GAM1025 EZH1     3' CACCCACAAATCCAGC     27066     GTG
                                CACC   ACAAATCCAGC
                                ||||   ||||||||||
                                GTGG   TGTTTAGGTCG
                                  G__
GAM1025 GPC6     5' CAACATACAAATCCAGC    27067    C   A
                                CA CGTG CAAATCCAGC
                                || |||| ||||||||||
                                GT GTAT GTTTAGGTCG
                                 T   _
GAM1025 HNF3A    3' ACCACGTTTTGAAATCCAGC  27068      C  GAC_
                                ACCAC GT    AAATCCAGC
                                ||||| ||    |||||||||
                                TGGTG CA    TTTAGGTCG
                                  _ AAAC
GAM1025 HS2ST1   3' ACCAATGGGAAAATCCAG   27069     CC   AC_
                                ACCA  GTG   AAATCCAG
                                ||||  |||   ||||||||
                                TGGT  TAC   TTTAGGTC
                                  __  CCT
GAM1025 LIF      3' ACCCCTGCTGCAGGTCCAGC  27070    A  _  GA  AA
                                ACC CC GT  CA  TCCAGC
                                ||| || ||  ||  ||||||
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                                TGG GG CG  GT  AGGTCG
                                  _ A  AC  CC
GAM1025 LZTS1    3' ACCCCGTGACAGTCCAG     27071     A       AA
                                ACC CCGTGACA  TCCAG
                                ||| ||||||||  |||||
                                TGG GGCACTGT  AGGTC
                                  _       C_
GAM1025 PAFAH1B1 3' CCGTGACCTGTAAATCCAGC  27072        ____
                                CCGTGAC   AAATCCAGC
                                |||||||   |||||||||
                                GGCACTG   TTTAGGTCG
                                    GACA
GAM1025 PCDH9    5' ACCACCATGGCACCGGC     27073         A  AAT  A
                                ACCACCGTG CA   CC GC
                                ||||||||| ||   || ||
                                TGGTGGTAC GT   GG CG
                                     C  ___  C
GAM1025 PIK3C2B  3' CACCACTCCAATCCAGC     27074       GA   A
                                CACCGT  CAA TCCAGC
                                ||||||  ||| ||||||
                                GTGGTG  GTT AGGTCG
                                   AG   _
GAM1025 RRM2B    3' ACCAGTGCATTAAAAATCCAG 27075      CC   AC____
                                ACCA  GTG     AAATCCAG
                                ||||  |||     ||||||||
                                TGGT  CAC     TTTAGGTC
                                  __  GTAATT
GAM1025 SFRS1    3' CACTGTGACAAATTAGC     27076     C       CC
                                CAC GTGACAAAT  AGC
                                ||| |||||||||  |||
                                GTG CACTGTTTA  TCG
                                  A       A_
GAM1025 SIX3     5' ACCGCCGAGTCAAGATTCAGC 27077     A   TGA  _  C
                                ACC CCG   CAA AT CAGC
                                ||| |||   ||| || ||||
                                TGG GGC   GTT TA GTCG
                                  C   TCA   C  A
GAM1025 STAU     3' ACCCCAGCACAGTCCAGC    27078     A   TG   AA
                                ACC CCG  ACA  TCCAGC
                                ||| |||  |||  ||||||
                                TGG GGT  TGT  AGGTCG
                                  _  CG   C_
GAM1025 STAU     3' ACCCCAGCACAGTCCAGC    27078     A   TG   AA
                                ACC CCG  ACA  TCCAGC
                                ||| |||  |||  ||||||
                                TGG GGT  TGT  AGGTCG
                                  _  CG   C_
GAM1025 STAU     3' ACCCCAGCACAGTCCAGC    27078     A   TG   AA
                                ACC CCG  ACA  TCCAGC
                                ||| |||  |||  ||||||
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                                TGG GGT  TGT  AGGTCG
                                  _  CG  C_
GAM1025 STAU    3' ACCCCAGCACAGTCCAGC    27078    A  TG  AA
                                ACC CCG  ACA  TCCAGC
                                ||| |||  |||  ||||||
                                TGG GGT  TGT  AGGTCG
                                  _  CG  C_
GAM1025 TADA2L  3' CACCATGAGAATTCAGC     27079       CA  C
                                CACCGTGA  AAT CAGC
                                ||||||||  ||| ||||
                                GTGGTACT  TTA GTCG
                                     C_  A
GAM1025 TGFB3   3' ACCACCGTGATTCTCAG     27080        CAAA _
                                ACCACCGTGA   TC CAG
                                ||||||||||   || |||
                                TGGTGGCACT   AG GTC
                                      A___  A
GAM1025 THBS1   3' CATCATGAAATCCAGC      27081   C   CA
                                CA CGTGA  AATCCAGC
                                || |||||  ||||||||
                                GT GTACT  TTAGGTCG
                                 A   __
GAM1025 TPMT    3' CAGCCATGAATCCAGC      27082   _    CAA
                                CA CCGTGA  ATCCAGC
                                || ||||||  |||||||
                                GT GGTACT  TAGGTCG
                                 C    ___
GAM1025 Z39IG   3' CCAGAGCCAAATCCAGC     27083    CC  GA
                                CCA  GT  CAAATCCAGC
                                |||  ||  ||||||||||
                                GGT  CG  GTTTAGGTCG
                                  CT  __
GAM1025 AKR1B10 5' CCACCGTGACTCCCAGC     27084        AAA
                                CCACCGTGAC  TCCAGC
                                ||||||||||  ||||||
                                GGTGGCACTG  GGGTCG
                                      A__
GAM1025 ARHGEF11 5' ACCATCCTTTAAATCCAGC  27085    _ GTGAC
                                ACCA CC    AAATCCAGC
                                |||| ||    |||||||||
                                TGGT GG    TTTAGGTCG
                                  A  AAA__
GAM1025 ARP5    5' CCAAGACCCTGAATCCAGC   27086   ___  G  CAA
                                CC  ACC TGA  ATCCAGC
                                ||  ||| |||  |||||||
                                GG  TGG ACT  TAGGTCG
                                 TTC  G  ___
GAM1025 C21orf18 3' ACCACCATGGTTCGCCATCAGC 27087        ACAA___  C
                                ACCACCGTG     ATC AGC
                                |||||||||     ||| |||
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                                TGGTGGTAC      TAG TCG
                                     CAAGCGG  _
GAM1025  CHRAC1    3'  CCACCGCAATCCAGC      27088        GACA
                                CCACCGT    AATCCAGC
                                |||||||    ||||||||
                                GGTGGCG    TTAGGTCG
                                     ____
GAM1025  DKFZp434C0923 3'  ACCACCATGAGACACCAGC    27089          CAAAT
                                ACCACCGTGA     CCAGC
                                ||||||||||     |||||
                                TGGTGGTACT     GGTCG
                                     CTGT_
GAM1025  DKFZP434J1813 3'  CCATGGACTGAATCCAGC     27090       _ A_
                                CCGTG AC  AATCCAGC
                                ||||| ||  ||||||||
                                GGTAC TG  TTAGGTCG
                                   C  AC
GAM1025  DKFZP566N034 3'  CCTACCGTGACATCAGC      27091    _       AATC
                                CC ACCGTGACA    CAGC
                                || |||||||||    ||||
                                GG TGGCACTGT    GTCG
                                 A        A___
GAM1025  FLJ13114  3'  CCACCAGCTCCAAATCCAGC   27092       _ GA
                                CCACC GT  CAAATCCAGC
                                ||||| ||  ||||||||||
                                GGTGG CG  GTTTAGGTCG
                                   T  AG
GAM1025  FLJ20040  3'  CACCGTGACGCAGACCTTCAGC 27093         AA__  __
                                CACCGTGAC    ATC  CAGC
                                |||||||||    |||  ||||
                                GTGGCACTG    TGG  GTCG
                                     CGTC   AA
GAM1025  FLJ21415  3'  ACCACCGTGAGCCCGGC     27094          CAAA   A
                                ACCACCGTGA    TCC GC
                                ||||||||||    ||| ||
                                TGGTGGCACT    GGG CG
                                     C___   C
GAM1025  FLJ22637  3'  CCACCATGGACTCCAG      27095        _ AAA
                                CCACCGTG AC   TCCAG
                                |||||||| ||   |||||
                                GGTGGTAC TG   AGGTC
                                     C  ___
GAM1025  FLJ32356  3'  CCACTCAGAATCCAGC      27096     _ T  CAA
                                CCAC CG GA   ATCCAGC
                                |||| || ||   |||||||
                                GGTG GT CT   TAGGTCG
                                  A  _  ___
GAM1025  FLJ32784  3'  ACCACCGTGGCCCACAGC    27097         ACAAA  _
                                ACCACCGTG     TC CAGC
                                |||||||||     || ||||
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                              TGGTGGCAC    GG GTCG
                                   CG___  T
GAM1025 KIAA0077 3' ACCACCTAAATCCAGC     27098      GTGAC
                              ACCACC    AAATCCAGC
                              ||||||    |||||||||
                              TGGTGG    TTTAGGTCG
                                 A____
GAM1025 KIAA1014 5' CACCGTGACACCGCCTCCAGC 27099         AA___
                              CACCGTGACA    TCCAGC
                              ||||||||||    ||||||
                              GTGGCACTGT    AGGTCG
                                    GGCGG
GAM1025 KIAA1668 3' CCCCAGGACAAATCCAG    27100    A   T
                              CC CCG GACAAATCCAG
                              || ||| ||||||||||
                              GG GGT CTGTTTAGGTC
                               _  C
GAM1025 KIAA1805 3' CCCCGTGACAACAGC      27101    A       ATC
                              CC CCGTGACAA   CAGC
                              || |||||||||   ||||
                              GG GGCACTGTT   GTCG
                               _       ___
GAM1025 KIAA1826 3' ACCACAGCTAATCCAGC    27102      C  GACA
                              ACCAC GT    AATCCAGC
                              ||||| ||    ||||||||
                              TGGTG CG    TTAGGTCG
                                 T  A___
GAM1025 MDS029   3' ACCACATTTAGAATCCAGC   27103      C  GACA
                              ACCAC GT    AATCCAGC
                              ||||| ||    ||||||||
                              TGGTG TA    TTAGGTCG
                                 _ AATC
GAM1025 MGC10966 5' CACCGCGACGAGTCCAGC    27104        AAA
                              CACCGTGAC   TCCAGC
                              |||||||||   ||||||
                              GTGGCGCTG   AGGTCG
                                    CTC
GAM1025 MGC3248  3' CCACCATGGAGACAGAGTCCAG 27105       ___   AA_
           C                   CCACCGT   GACA   TCCAGC
                              |||||||   ||||   ||||||
                              GGTGGTA   CTGT   AGGTCG
                                  CCT    CTC
GAM1025 OCLM     5' CCAATCATAGAATCCAGC    27106    C_   ACA
                              CCA  CGTG   AATCCAGC
                              |||  ||||   ||||||||
                              GGT  GTAT   TTAGGTCG
                                TA   C__
GAM1025 PDE11A   3' CACTTGTGGTAAATCCAGC   27107    C_  AC
                              CAC  GTG  AAATCCAGC
                              |||  |||  |||||||||
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                                GTG  CAC  TTTAGGTCG
                                  AA   CA
GAM1025  PHYHIP   3'  CATCACGAAAATCCAGC     27108    C    C
                                CA CGTGA AAATCCAGC
                                || ||||| |||||||||
                                GT GTGCT TTTAGGTCG
                                 A    _
GAM1025  PIGQ     3'  CCACCATGGTGACCGCAGC   27109        ACAA  _
                                CCACCGTG    ATC CAGC
                                ||||||||    ||| ||||
                                GGTGGTAC    TGG GTCG
                                     CAC_   C
GAM1025  PPP1R10  3'  CCAGAACTCAAATCCAGC    27110     T ____
                                CCG GA   CAAATCCAGC
                                ||| ||   ||||||||||
                                GGT CT   GTTTAGGTCG
                                  _ TGA
GAM1025  SCAND2   5'  CCCCGTGACATGTTCTTAGC  27111    A      AA_  C_
                                CC CCGTGACA   TC  AGC
                                || ||||||||   ||  |||
                                GG GGCACTGT   AG  TCG
                                 _      ACA  AA
GAM1025  SCAND2   5'  CCCCGTGACATGTTCTTAGC  27111    A      AA_  C_
                                CC CCGTGACA   TC  AGC
                                || ||||||||   ||  |||
                                GG GGCACTGT   AG  TCG
                                 _      ACA  AA
GAM1025  SCAND2   5'  CCCCGTGACATGTTCTTAGC  27111    A      AA_  C_
                                CC CCGTGACA   TC  AGC
                                || ||||||||   ||  |||
                                GG GGCACTGT   AG  TCG
                                 _      ACA  AA
GAM1025  SCAND2   5'  CCCCGTGACATGTTCTTAGC  27111    A      AA_  C_
                                CC CCGTGACA   TC  AGC
                                || ||||||||   ||  |||
                                GG GGCACTGT   AG  TCG
                                 _      ACA  AA
GAM1025  SCAND2   5'  CCCCGTGACATGTTCTTAGC  27111    A      AA_  C_
                                CC CCGTGACA   TC  AGC
                                || ||||||||   ||  |||
                                GG GGCACTGT   AG  TCG
                                 _      ACA  AA
GAM1025  SCAND2   5'  CCCCGTGACATGTTCTTAGC  27111    A      AA_  C_
                                CC CCGTGACA   TC  AGC
                                || ||||||||   ||  |||
                                GG GGCACTGT   AG  TCG
                                 _      ACA  AA
GAM1025  SEC14L2  3'  CCACCGTAACTCTAGC      27112         AAA  C
                                CCACCGTGAC   TC AGC
                                ||||||||||   || |||
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                                GGTGGCATTG   AG TCG
                                      ___  A
GAM1025  SGKL     3'  ACCACCTTAAAAAATCCAG   27113       G   C
                                ACCACC TGA AAATCCAG
                                |||||| ||| ||||||||
                                TGGTGG ATT TTTAGGTC
                                   A   T
GAM1025  WBSCR16  3'  ACTGCCATGACAGACAGAGC  27114    CA      A  CC
                                AC  CCGTGACA AT  AGC
                                ||  |||||||| ||  |||
                                TG  GGTACTGT TG  TCG
                                 AC       C  TC
GAM1025  LOC123872 5'  CCTGCGCGCAATCCAGC     27115    AC   A   A
                                CC  CGTG CAA TCCAGC
                                ||  |||| ||| ||||||
                                GG  GCGC GTT AGGTCG
                                 AC   _  _
GAM1025  LOC128977 5'  ACCACCGCGACGACAGC     27116          AAATC
                                ACCACCGTGAC    CAGC
                                ||||||||||     ||||
                                TGGTGGCGCTG    GTCG
                                      CT___
GAM1025  LOC129011 3'  CCACCATGGGTGACCGTCCAGC 27117       ____    AAA
                                CCACC   GTGAC   TCCAGC
                                |||||   |||||   ||||||
                                GGTGG   CACTG   AGGTCG
                                   TACC    GC_
GAM1025  LOC143310 3'  CACCGTGACTTCCTTCCAGC   27118        AAA__
                                CACCGTGAC    TCCAGC
                                |||||||||    ||||||
                                GTGGCACTG    AGGTCG
                                     AAGGA
GAM1025  LOC147093 5'  CCACCATGAATTCAGC      27119         CAA  C
                                CCACCGTGA   AT CAGC
                                |||||||||   || ||||
                                GGTGGTACT   TA GTCG
                                      ___  A
GAM1025  LOC147172 3'  CAACGGAGAAATCCAGC     27120    C  T  C
                                CA CG GA AAATCCAGC
                                || || || |||||||||
                                GT GC CT TTTAGGTCG
                                 T  _  C
GAM1025  LOC147991 5'  ACCCTGGCTCCAAATCCAGC   27121     ACC  GA
                                ACC   GT  CAAATCCAGC
                                |||   ||  ||||||||||
                                TGG   CG  GTTTAGGTCG
                                  GAC  AG
GAM1025  LOC151963 3'  CCAAAATAAATAAATCCAGC   27122     CC   C_
                                CCA  GTGA  AAATCCAGC
                                |||  ||||  |||||||||
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                                GGT  TATT  TTTAGGTCG
                                  TT    TA
GAM1025  LOC158376 3'  CCACCGTGCACTCCGGC     27123         A  AA   A
                                CCACCGTG CA  TCC GC
                                |||||||| ||  ||| ||
                                GGTGGCAC GT  AGG CG
                                     _ G_   C
GAM1025  LOC219920 5'  CCTCATGAAAATCCAGC     27124     AC     C
                                CC  CGTGA AAATCCAGC
                                ||  ||||| |||||||||
                                GG  GTACT TTTAGGTCG
                                 A_     _
GAM1025  LOC220766 5'  CCACTGTGAAACCCAGC     27125      C    CA
                                CCAC GTGA  AATCCAGC
                                |||| ||||  ||||||||
                                GGTG CACT  TTGGGTCG
                                  A   __
GAM1025  LOC222224 5'  ACCACCATAATCCAGC      27126          CAAA
                                ACCACCGTGA    TCCAGC
                                ||||||||||    ||||||
                                TGGTGGTATT    AGGTCG
                                      _____
GAM1025  LOC254182 5'  CCATCCCCAGAATCCAGC    27127     _  G  ACA
                                CCA CC TG   AATCCAGC
                                ||| || ||   ||||||||
                                GGT GG GT   TTAGGTCG
                                  A  G  C__
GAM1025  LOC51647  5'  ACCACCGCTGATCCTAGC    27128        GACAA   _
                                ACCACCGT    ATCC AGC
                                ||||||||    |||| |||
                                TGGTGGCG    TAGG TCG
                                     AC___    A
GAM1026  ABCC5     3'  CACCAAACCACACAGCAACCAG 27131        A_   AAA
              C                   CACCAAA  ACA   CAACCAGC
                                |||||||  |||   ||||||||
                                GTGGTTT  TGT   GTTGGTCG
                                     GG   GTC
GAM1026  BCL11B    3'  TCACCAAAAGAAAACAA     27132         AC
                                TCACCAAAA  AAAACAA
                                |||||||||  |||||||
                                AGTGGTTTT  TTTTGTT
                                     C_
GAM1026  CERD4     3'  TCACCAAAGCCACTGGACCAGC 27133         AA  AAACA
                                TCACCAAA  CA    ACCAGC
                                ||||||||  ||    ||||||
                                AGTGGTTT  GT    TGGTCG
                                     CG  GACC_
GAM1026  CHRNE     3'  AAAGACAATTCAACCAGC    27134     A    AA
                                AAA ACAA  CAACCAGC
                                ||| ||||  ||||||||
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                                TTT TGTT  GTTGGTCG
                                  C    AA
GAM1026  COL13A1   5'  CCGAAAAAGCACAACCAGC   27135   _    CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1026  COL13A1   5'  CCGAAAAAGCACAACCAGC   27135   _    CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1026  COL13A1   5'  CCGAAAAAGCACAACCAGC   27135   _    CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1026  COL13A1   5'  CCGAAAAAGCACAACCAGC   27135   _    CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1026  COL13A1   5'  CCGAAAAAGCACAACCAGC   27135   _    CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1026  COL13A1   5'  CCGAAAAAGCACAACCAGC   27135   _    CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1026  COL13A1   5'  CCGAAAAAGCACAACCAGC   27135   _    CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1026  COX7A2L   3'  CCAAAAAACAAACCAG     27136      _  AACA
                                CCAAAAA CAA   ACCAG
                                ||||||| |||   |||||
                                GGTTTTT GTT   TGGTC
                                    T  _____
GAM1026  DPYD      3'  CACCAAAAATAAGCAATTTCAG 27137       CAAAA  C__
           C                    CACCAAAAA    CAA  CAGC
                                |||||||||    |||  ||||
                                GTGGTTTTT    GTT  GTCG
                                     ATTC_   AAA
GAM1026  HMGN1     3'  ACCAAAAAAATAAACAACCAGC 27138       CA
                                ACCAAAAA  AAACAACCAGC
                                ||||||||  ||||||||||
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                                TGGTTTTT  TTTGTTGGTCG
                                    TA
GAM1026  MYOM2    3'  TCACCAAATGCAAAAATCAAAA 27139        AA    __  CC
                GC                   TCACCAAA  CAAAA  CAA  AGC
                                     ||||||||  |||||  |||  |||
                                     AGTGGTTT  GTTTT  GTT  TCG
                                         AC    TA   T_
GAM1026  PIM2     3'  TCACCAAAATAAACTTCCTTAG 27140        ACA   AA  __
                C                    TCACCAAAA   AAAC  CC  AGC
                                     |||||||||   ||||  ||  |||
                                     AGTGGTTTT   TTTG  GG  TCG
                                         A__    AA  AA
GAM1026  PON1     3'  CAAAAACAAAACAAAAGC    27141           CC
                                     CAAAAACAAAACAA  AGC
                                     ||||||||||||||  |||
                                     GTTTTTGTTTTGTT  TCG
                                           T_
GAM1026  ROR2     3'  TCACCAAATACAAAGCTGTCAG 27142        A    ACAAC
                                     TCACCAAA ACAAA    CAG
                                     ||||||||  |||||    |||
                                     AGTGGTTT TGTTT    GTC
                                         A    CGACA
GAM1026  SEL1L    3'  CAGAAACAAAATATCCAGC   27143    A      CAA
                                     CA AAACAAAA   CCAGC
                                     ||  ||||||||   |||||
                                     GT TTTGTTTT   GGTCG
                                      C       ATA
GAM1026  TAF1C    3'  TCACCAAACACGAGGAGCCAGC 27144        A  AAAACAA
                                     TCACCAAA AC       CCAGC
                                     ||||||||  ||      |||||
                                     AGTGGTTT TG       GGTCG
                                         G  CTCCTC_
GAM1026  TTN      5'  CCTAAAAACAAAACTACACAG  27145    _        A  _
                                     CC AAAAACAAAAC AC CAG
                                     ||  ||||||||||  ||  |||
                                     GG TTTTTGTTTTG TG GTC
                                      A          A  T
GAM1026  TTN      5'  CCTAAAAACAAAACTACACAG  27145    _        A  _
                                     CC AAAAACAAAAC AC CAG
                                     ||  ||||||||||  ||  |||
                                     GG TTTTTGTTTTG TG GTC
                                      A          A  T
GAM1026  TTN      5'  CCTAAAAACAAAACTACACAG  27145    _        A  _
                                     CC AAAAACAAAAC AC CAG
                                     ||  ||||||||||  ||  |||
                                     GG TTTTTGTTTTG TG GTC
                                      A          A  T
GAM1026  TTN      5'  CCTAAAAACAAAACTACACAG  27145    _        A  _
                                     CC AAAAACAAAAC AC CAG
                                     ||  ||||||||||  ||  |||
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                                GG TTTTTGTTTTG TG GTC
                                 A         A  T
GAM1026  VIPR2    3'  CCACCGACCATCAACAACCAG  27146      AAAAA  A_
                                TCACC    CA  AACAACCAG
                                |||||    ||  |||||||||
                                GGTGG    GT  TTGTTGGTC
                                   CTG__  AG
GAM1026  ASB16    3'  CCACCAAAAATACAAAATCAGC 27147          __     CAAC
                                TCACCAAAA  ACAAAA    CAGC
                                |||||||||  ||||||    ||||
                                GGTGGTTTT  TGTTTT    GTCG
                                      TA     A___
GAM1026  C1orf17  3'  CCACTAAGAACAAAACAA    27148      C  A
                                TCAC AA AACAAAACAA
                                |||| || ||||||||||
                                GGTG TT TTGTTTTGTT
                                  A  C
GAM1026  C1orf24  3'  CCACCAAAAATACAAAAATTAG 27149          __     CAACC
              C                  TCACCAAAA  ACAAAA     AGC
                                |||||||||  ||||||    |||
                                GGTGGTTTT  TGTTTT    TCG
                                      TA     TAA__
GAM1026  C20orf112 3'  CAAAAACAAAATGTACCAAC   27150          CA_
                                CAAAAACAAAA   ACCAGC
                                ||||||||||   ||||||
                                GTTTTTGTTTT   TGGTTG
                                       ACA
GAM1026  CAT56    3'  TCACAGAAAACAACCAG     27151      CAAAAAC
                                TCAC      AAAACAACCAG
                                ||||      ||||||||||
                                AGTG      TTTTGTTGGTC
                                  TC_____
GAM1026  DKFZP434I216 3'  CACCAAAGGCCTAACAACCAG  27152        AACAA
                                CACCAAA    AACAACCAG
                                |||||||    |||||||||
                                GTGGTTT    TTGTTGGTC
                                    CCGGA
GAM1026  DKFZP434P0721 3'  CACCAAAATTAACAGCCAG    27153        ACAA    A
                                CACCAAAA    AACA CCAG
                                ||||||||    |||| ||||
                                GTGGTTTT    TTGT GGTC
                                     AA__    C
GAM1026  DKFZP586M1120 3'  TCCTCAAAATTTAGCAACCAGC 27154     AC     ACAAAA
                                TC  CAAAA     CAACCAGC
                                ||  |||||     ||||||||
                                AG  GTTTT     GTTGGTCG
                                 GA    AAATC_
GAM1026  FLJ10587  3'  ACCAAAAACAAAAACCAGC   27155           CA
                                ACCAAAAACAAAA  ACCAGC
                                ||||||||||||  ||||||
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                                TGGTTTTTGTTTT  TGGTCG
                                           __
GAM1026  FLJ11252  3'  TCACTCAAAACAACAACAG   27156     CA     AA    C
                                TCAC  AAAACA  ACAAC AG
                                ||||  ||||||  ||||| ||
                                AGTG  TTTTGT  TGTTG TC
                                  AG     __    _
GAM1026  FLJ20097  3'  CAAAAACAAGCAGCCAGC    27157         AA  A
                                CAAAAACAA  CA CCAGC
                                |||||||||  || |||||
                                GTTTTTGTT  GT GGTCG
                                      C_  C
GAM1026  FLJ20984  3'  TCACCAAAAGAAAGCAGCCA   27158         AC   A  A
                                TCACCAAAA  AAA CA CCA
                                |||||||||  ||| || |||
                                AGTGGTTTT  TTT GT GGT
                                      C_   C  C
GAM1026  FLJ23186  3'  TCCCAACAAAACAATCAG    27159    A   AAA       C
                                TC CCA   ACAAAACAA CAG
                                || |||   |||||||||| |||
                                AG GGT   TGTTTTGTT GTC
                                 _  ___       A
GAM1026  GAL3ST2   3'  CAAAATCACCAACCAGC     27160      A  AAA
                                CAAAA CA   CAACCAGC
                                ||||| ||   ||||||||
                                GTTTT GT   GTTGGTCG
                                   A  G__
GAM1026  GG2-1     3'  TCAATCTTAACAAAACAGTCAG 27161     CCAAA       AC
              C                  TCA    AACAAAACA  CAGC
                                |||    |||||||||  ||||
                                AGT    TTGTTTTGT  GTCG
                                  TAGAA       CA
GAM1026  HUMGT198A 3'  ACCAAAAACAAGGTAGCCAG  27162          AACAA
                                ACCAAAAACAA    CCAG
                                ||||||||||    ||||
                                TGGTTTTTGTT    GGTC
                                      CCATC
GAM1026  HUMGT198A 3'  ACCAAAAACAAGGTAGCCAG  27162          AACAA
                                ACCAAAAACAA    CCAG
                                ||||||||||    ||||
                                TGGTTTTTGTT    GGTC
                                      CCATC
GAM1026  KIAA0317  3'  CCAAAAACAGCAGAACCAG   27163         AAAC
                                CCAAAAACA   AACCAG
                                |||||||||   ||||||
                                GGTTTTTGT   TTGGTC
                                      CGTC
GAM1026  KIAA0367  3'  TCACCAAAAGGAAATCCAGC  27164         AC   ACAA
                                TCACCAAAA  AAA   CCAGC
                                |||||||||  |||   |||||
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                                AGTGGTTTT  TTT    GGTCG
                                     CC   A___
GAM1026  KIAA0376  3'  TCACCAAAGGGCATCCAGCCAG 27165        AACAAAA  A
              C                   TCACCAAA      CA CCAGC
                                  ||||||||      || |||||
                                  AGTGGTTT      GT GGTCG
                                       CCCGTAG  C
GAM1026  KIAA0453  3'  CACCAAAAACAAGACCCAG   27166          A  AA
                                  CACCAAAAACAA AC  CCAG
                                  ||||||||||||| ||  ||||
                                  GTGGTTTTTGTT TG  GGTC
                                         C  __
GAM1026  KIAA1257  3'  ACCAAAAATACAAAATCAGC   27167        __     CAAC
                                  ACCAAAA  ACAAAA    CAGC
                                  |||||||  ||||||    ||||
                                  TGGTTTT  TGTTTT    GTCG
                                      TA     A___
GAM1026  KIAA1361  3'  TCCCCAAAAACAAACAAACCCG 27168    A         AC    A_
              GC                    TC CCAAAAACAAA  AACC  GC
                                  || ||||||||||  ||||  ||
                                  AG GGTTTTTGTTT  TTGG  CG
                                   G         GT    GC
GAM1026  KIAA1784  5'  CCAAAGTCAGCAACCAGC    27169       AA  AAA
                                  CCAAA  CA   CAACCAGC
                                  |||||  ||   ||||||||
                                  GGTTT  GT   GTTGGTCG
                                     CA  C__
GAM1026  KIAA1922  5'  CCACCAAAAATACAAAAATTAG 27149          __     CAACC
              C                    TCACCAAAA  ACAAAA     AGC
                                  |||||||||  ||||||    |||
                                  GGTGGTTTT  TGTTTT    TCG
                                       TA     TAA__
GAM1026  KIAA1975  5'  TCACCAATAACAAAACAA    27170        A
                                  TCACCAA AACAAAACAA
                                  ||||||| ||||||||||
                                  AGTGGTT TTGTTTTGTT
                                      A
GAM1026  ORCTL3    3'  CACCAGAAAGAACTGCAACCAG 27171       A   C  AA_
              C                    CACCA AAA AA   CAACCAGC
                                  ||||| ||| ||   ||||||||
                                  GTGGT TTT TT   GTTGGTCG
                                     C   C  GAC
GAM1026  RAB14    3'  CCAAAACAAAACAAAAGC    27172       A       CC
                                  CCAAAA CAAAACAA  AGC
                                  |||||| ||||||||  |||
                                  GGTTTT GTTTTGTT  TCG
                                      _       T_
GAM1026  RAB40A   5'  TCCCAAAAACCACAGTCAG   27173    A      AAA   AC
                                  TC CCAAAAAC   ACA  CAG
                                  || ||||||||   |||  |||
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                                AG GGTTTTTG   TGT  GTC
                                 _      G__   CA
GAM1026  SKIP     3'  CAGTCACAAAACAGCCAGC   27174    AAA       A
                                CA   ACAAAACA CCAGC
                                ||   |||||||| |||||
                                GT   TGTTTTGT GGTCG
                                 CAG       C
GAM1026  SKIP     3'  CAGTCACAAAACAGCCAGC   27174    AAA       A
                                CA   ACAAAACA CCAGC
                                ||   |||||||| |||||
                                GT   TGTTTTGT GGTCG
                                 CAG       C
GAM1026  SSBP4    3'  ACCAAAAACCAAAACCAGC   27175         AAAAC
                                ACCAAAAAC    AACCAGC
                                |||||||||    |||||||
                                TGGTTTTTG    TTGGTCG
                                     GTT__
GAM1026  STK17A   3'  CCAAAAACAAATCCAA      27176          ACAA
                                CCAAAAACAAA   CCAG
                                ||||||||||    ||||
                                GGTTTTTGTTT   GGTT
                                      A___
GAM1026  LOC150848 5'  TCACCAAAAACAACAACAAC   27177           _
                                TCACCAAAAACAA AACAAC
                                |||||||||||| ||||||
                                AGTGGTTTTTGTT TTGTTG
                                       G
GAM1026  LOC153514 3'  ACCAAAGGCCAACAACCAGC   27178       AACAA
                                ACCAAA    AACAACCAGC
                                ||||||    ||||||||||
                                TGGTTT    TTGTTGGTCG
                                   CCGG_
GAM1026  LOC158956 3'  ACCAAAAAATAAACAACCAGC  27138        CA
                                ACCAAAAA  AAACAACCAGC
                                ||||||||  ||||||||||
                                TGGTTTTT  TTTGTTGGTCG
                                     TA
GAM1026  LOC161357 3'  TCATTTGAAACAAAACCAGC   27179     CCAA      ACA
                                TCA   AAACAAA   ACCAGC
                                |||   |||||||   ||||||
                                AGT   TTTGTTT   TGGTCG
                                  AAAC      ___
GAM1026  LOC200059 3'  TCATCCAAAACAAAACAA    27180     _     A
                                TCA CCAAAA CAAAACAA
                                ||| |||||| ||||||||
                                AGT GGTTTT GTTTTGTT
                                  A     _
GAM1026  LOC200942 3'  CCAAGGTCATACAACCAGC    27181      AAA  AA
                                CCAA   CA  ACAACCAGC
                                ||||   ||  |||||||||
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                                GGTT   GT  TGTTGGTCG
                                  CCA  A_
GAM1026  LOC204804 3'  AAAAACAAAACAAGGACCCAGC 27182          ____
                                AAAAACAAAACAA   CCAGC
                                |||||||||||||   |||||
                                TTTTTGTTTTGTT   GGTCG
                                     CCTG
GAM1026  LOC253019 5'  TCCTCAAAAACAAAACAA   27183   AC
                                TC  CAAAAACAAAACAA
                                ||  ||||||||||||||
                                AG  GTTTTTGTTTTGTT
                                 GA
GAM1026  LOC253975 5'  TCCTCAAAAACAAAACAA   27183   AC
                                TC  CAAAAACAAAACAA
                                ||  ||||||||||||||
                                AG  GTTTTTGTTTTGTT
                                 GA
GAM1026  LOC255480 3'  TCACCAAAGGCCAGAAACCCAG 27184       AA_ _   AA
           C                     TCACCAAA   CA AAAC  CCAGC
                                ||||||||   || ||||  |||||
                                AGTGGTTT   GT TTTG  GGTCG
                                     CCG  C   __
GAM1026  LOC257472 3'  CACCAAAGGCCTAACAACCAG  27152       AACAA
                                CACCAAA    AACAACCAG
                                |||||||    |||||||||
                                GTGGTTT    TTGTTGGTC
                                     CCGGA
GAM1026  LOC51652  3'  TCCCACGCACAAGACAACCAGC 27185   A  AAA   A
                                TC CCA   ACAA ACAACCAGC
                                || |||   |||| |||||||||
                                AG GGT   TGTT TGTTGGTCG
                                 _  GCG   C
GAM1026  LOC91759  3'  CCACCAAAGGCATTTTCCAGC  27186       AA  AAACAA
                                TCACCAAA  CA    CCAGC
                                ||||||||  ||    |||||
                                GGTGGTTT  GT    GGTCG
                                     CC  AAAA__
GAM1027  FCAR     3'  ACTTCACTCTCAGTGCACGT   27189         ATACC
                                ACTTCACTCTCG    CACGT
                                ||||||||||||    |||||
                                TGAAGTGAGAGT    GTGCA
                                     CAC__
GAM1027  FCAR     3'  ACTTCACTCTCAGTGCACGT   27189         ATACC
                                ACTTCACTCTCG    CACGT
                                ||||||||||||    |||||
                                TGAAGTGAGAGT    GTGCA
                                     CAC__
GAM1027  FLJ10508  3'  ACTTCACTTGATCCATCCATGT 27190       CTC   AC__   C
                                ACTTCACT   GAT   CCA GT
                                ||||||||   |||   ||| ||
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                                TGAAGTGA  CTA   GGT CA
                                    A__   GGTA  A
GAM1027 KIAA1430 3' TAACCTCACTGTGCCCAG    27191        CTCGATA   C
                                TAACTTCACT      CCCA G
                                ||||||||||      |||| |
                                ATTGGAGTGA      GGGT C
                                    CAC____     A
GAM1027 KIAA1924 3' CTTCACACACTACCCACGT   27192      TCTCGA
                                CTTCAC     TACCCACGT
                                ||||||     |||||||||
                                GAAGTG     ATGGGTGCA
                                   TGTG__
GAM1027 LOC149711 5' TAACTTCACCTCTCTGAC   27193        _   _
                                TAACTTCAC TCTC GAT
                                ||||||||| |||| |||
                                ATTGAAGTG AGAG CTG
                                    G   A
GAM1027 LOC163341 3' TAACTTGCTCAGCCCACG   27194      CACT   ATA
                                TAACTT   CTCG   CCCACG
                                ||||||   ||||   ||||||
                                ATTGAA   GAGT   GGGTGC
                                   C___   C__
GAM1028 FLJ20374 5' ACACCCCCACCTTTTTTCCGCT 27197       T  C_____
                                ATACCCCT CC     CCGCT
                                |||||||| ||     |||||
                                TGTGGGGG GG     GGCGA
                                    T  AAAAAA
GAM1028 FLJ20984 3' TGGGACACACCCCTCCGC    27198    AA       TCCC
                                TG  ACATACCCCT   CCGC
                                ||  ||||||||||   ||||
                                AC  TGTGTGGGGA   GGCG
                                 CC       _____
GAM1028 IR1899308 5' TGAAGTGGCCCCTTCCAGCC 27199     ACATA      CCC
                                TGAA    CCCCTTCC   GCT
                                ||||    ||||||||   |||
                                ACTT    GGGGAAGG   CGG
                                  CACC_      T__
GAM1028 KIAA1393 3' TGACACATACCCCTTCCC    27200    A
                                TGA ACATACCCCTTCCC
                                ||| ||||||||||||||
                                ACT TGTATGGGGAAGGG
                                  G
GAM1028 PHF3    3' ATAAATGTACCCCTTGGGC    27201      ACA      CCCCC
                                ATGAA   TACCCCTT    GC
                                |||||   ||||||||    ||
                                TATTT   ATGGGGAA    CG
                                  AC_      CC___
GAM1028 SEMA3E   3' ATGAAACATATCCTTGGAAACT 27202         CC   CCCCC__
            GCT                   ATGAAACATA  CCTT     GCT
                                ||||||||||  ||||     |||
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                                TACTTTGTAT  GGAA      CGA
                                     A_    CCTTTGA
GAM1028  LOC113612 3'  ATGAAACATACCCTTCTCTGCT 27203           C   CCCC
                                ATGAAACATACCC TTC    GCT
                                |||||||||||| |||    |||
                                TACTTTGTATGGG AAG    CGA
                                      _   AGA_
GAM1028  LOC149722 5'  TGAAACATGCCCCTTGC     27204         A     CCCCC
                                TGAAACAT CCCCTT     GC
                                |||||||| ||||||     ||
                                ACTTTGTA GGGGAA     CG
                                     C     _____
GAM1028  LOC166424 5'  GAAATACCCCCTGGCTGCT    27205     AC        CCCCC
                                GAA  ATACCCCTT     GCT
                                |||  |||||||||     |||
                                CTT  TATGGGGGA     CGA
                                  __        CCGA_
GAM1028  LOC203429 3'  ATGAAACAGCAAATCTCTCCTG 27206         TACCCC   C  C
              CT                   ATGAAACA     TTC CC GCT
                                |||||||||     ||| || |||
                                TACTTTGT     GAG GG CGA
                                     CGTTTA   A  A
GAM1028  LOC257277 5'  ATGAAAAATGCCCCTTCC    27207       C  A
                                ATGAAA AT CCCCTTCC
                                |||||| || ||||||||
                                TACTTT TA GGGGAAGG
                                   T  C
GAM1029  AIM1     3'  TCAGTTGTTAAGCAGTTTGT   27210           GTTCA
                                TCAGTTGTTAAG    TTGT
                                ||||||||||||    ||||
                                AGTCAACAATTC    AACA
                                       GTCA_
GAM1029  AK1      3'  TCAGGTGTTAAGGACAC     27211      T       TT
                                TCAG TGTTAAGG  CAT
                                |||| ||||||||  |||
                                AGTC ACAATTCC  GTG
                                  C       T_
GAM1029  GBAS     3'  TCAGTTATTGGGTACACT    27212         AA   T
                                TCAGTTGTT  GGT CATT
                                |||||||||  ||| ||||
                                AGTCAATAA  CCA GTGA
                                     C_   T
GAM1029  NEBL     3'  TCAGTTTTAGTCTTCATTGT   27213       GTTA  G_
                                TCAGTT   AG  TTCATTGT
                                ||||||   ||  ||||||||
                                AGTCAA   TC  AAGTAACA
                                   AA__  AG
GAM1029  SLC7A6   3'  ATCTTTAAGGTTCATTGT    27214     G
                                GTT TTAAGGTTCATTGT
                                ||| ||||||||||||||
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                                TAG AATTCCAAGTAACA
                                  A
GAM1029  SYT4     3'  GTTGTTGGTTTCATTGT     27215       AA   _
                                GTTGTT  GGTT CATTGT
                                ||||||  |||| ||||||
                                CAACAA  CCAA GTAACA
                                   __    A
GAM1029  COAS3    3'  CAGTTGTTAGGGAGGCCTGT   27216         A  TTCA
                                CAGTTGTTA GG    TTGT
                                ||||||||| ||    ||||
                                GTCAACAAT CC    GACA
                                      C  TCCG
GAM1029  DJ122O8.2 3'  TCAGTGTTAAGGCAACTGT    27217       T       TC
                                TCAGT GTTAAGGT  ATTGT
                                ||||| ||||||||  |||||
                                AGTCA CAATTCCG  TGACA
                                   _       T_
GAM1029  ESDN     3'  TCAGTTGTTACTTGATTGT    27218          AGGTTC
                                TCAGTTGTTA     ATTGT
                                ||||||||||     |||||
                                AGTCAACAAT     TAACA
                                      GAAC__
GAM1029  FLJ11004 3'  TCAGCTGTTGGTTTTTGT    27219         AA    CA
                                TCAGTTGTT  GGTT  TTGT
                                |||||||||  ||||  ||||
                                AGTCGACAA  CCAA  AACA
                                     __    A_
GAM1029  GMFB     3'  TCAGTTGTTGGTTTTG      27220         AA    CA
                                TCAGTTGTT  GGTT  TTG
                                |||||||||  ||||  |||
                                AGTCAACAA  CCAA  AAC

                                     __    __
GAM1029  KIAA0416 3'  TCACTTGGATTCATTG      27221     G   TTAA
                                TCA TTG    GGTTCATTG
                                ||| |||    |||||||||
                                AGT AAC    CTAAGTAAC
                                  G  ____
GAM1029  KIAA1069 3'  TCATTTGTTAAAGTGACATTGT 27222     G         T_
                                TCA TTGTTAAGGT  CATTGT
                                ||| ||||||||||  ||||||
                                AGT AACAATTTCA  GTAACA
                                  A         CT
GAM1029  KIAA1371 3'  AGTTGTTAACCACTGT      27223         GGT
                                AGTTGTTAA   TCATTGT
                                |||||||||   |||||||
                                TCAACAATT   GGTGACA

                                     ___
GAM1029  KIAA1795 3'  TCAAAGTCAAAGGTTCATTGT  27224      TT    _
                                TCAG  GTTAA GGTTCATTGT
                                ||||  ||||| ||||||||||
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                                AGTT  CAGTT CCAAGTAACA
                                  T_    T
GAM1029  KIAA1887  5'  ATTGCCCCCATTCATTGT    27225       AAG
                                GTTGTT   GTTCATTGT
                                ||||||   |||||||||
                                TAACGG   TAAGTAACA
                                   GGG
GAM1029  OLFM3     3'  TCAGTTGTATGAAATCAGTTGT 27226        TAAGGT  _
                                TCAGTTGT     TCA TTGT
                                ||||||||     ||| ||||
                                AGTCAACA     AGT AACA
                                     TACTTT   C
GAM1029  TSPAN-2   3'  TCAGTTTTAACACTCCATTGT  27227       G   G _
                                TCAGTT TTAA G TTCATTGT
                                |||||| |||| | ||||||||
                                AGTCAA AATT T AGGTAACA
                                   _   G G
GAM1029  LOC144766 3'  AGTGGTTGGGTTCATTGT    27228     T   AA
                                AGT GTT  GGTTCATTGT
                                ||| |||  ||||||||||
                                TCA CAA  CCAAGTAACA
                                  C   C_
GAM1029  LOC157464 5'  TCAATTGTCCTTCATTGT    27229         AAGG
                                TCAGTTGTT    TTCATTGT
                                |||||||||    ||||||||
                                AGTTAACAG    AAGTAACA
                                     G___
GAM1029  LOC196812 3'  CAGTTCAGGTTCATTGT     27230       GTTA
                                CAGTT    AGGTTCATTGT
                                |||||    ||||||||||
                                GTCAA    TCCAAGTAACA
                                   G___
GAM1029  LOC199699 3'  AGTTGTCAATCATTGT      27231         GGT
                                AGTTGTTAA   TCATTGT
                                |||||||||   |||||||
                                TCAACAGTT   AGTAACA
                                     ___
GAM1029  LOC254978 3'  TCAGTTATTAATTTATTGT    27232          GG  C
                                TCAGTTGTTAA  TT ATTGT
                                ||||||||||  || |||||
                                AGTCAATAATT  AA TAACA
                                     A_  _
GAM1029  LOC90591  3'  AATTGTTTACATTCATTGT    27233       AAG
                                AGTTGTT   GTTCATTGT
                                |||||||   |||||||||
                                TTAACAA   TAAGTAACA
                                   ATG
GAM1029  LOC90826  5'  TCAGTTGTATAAGGTTCAATTG 27234         _       _
            T                   TCAGTTGT TAAGGTTCA TTGT
                                |||||||| ||||||||| ||||
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                                AGTCAACA ATTCCAAGT AACA
                                     T        T
GAM1030  CYP7A1    3'  TTAAAATATTTTATCAAAGCAT 27237         CTAC
                                TTAAAATAT    ATCAGAGCAT
                                |||||||||    ||||||||||
                                AATTTTATA    TAGTTTCGTA
                                   AAA_
GAM1030  C15orf5   3'  TTAAAATATCTGAATCAAAA   27238          AC
                                TTAAAATATCT  ATCAGAG
                                ||||||||||  |||||||
                                AATTTTATAGA  TAGTTTT
                                     CT
GAM1030  FAM3C     3'  TTAAAATATTTACACATAGC   27239         C    CAG
                                TTAAAATAT TACAT   AGC
                                ||||||||| |||||   |||
                                AATTTTATA ATGTG   TCG
                                   A    TA_
GAM1030  KIAA1724  3'  CTAAAATGTCCAGAGCAT    27240        A  TACAT
                                TTAAAAT TC    CAGAGCAT
                                ||||||| ||    ||||||||
                                GATTTTA AG    GTCTCGTA
                                   C _____
GAM1030  LOC257206 3'  TAAAATATTTACATCACATC   27241         C     AGA
                                TAAAATAT TACATC   GCATC
                                |||||||| ||||||   |||||
                                ATTTTATA ATGTAG   TGTAG
                                   A    ___
GAM1030  LOC91496  5'  TCAAAATATCTGAGC       27242          ACATCA
                                TTAAAATATCT     GAGC
                                ||||||||||     ||||
                                AGTTTTATAGA     CTCG
                                        _______
GAM1031  ABCC5     3'  CACCAAACCACACAGCAACCAG 27131        A_   AAA
            C                    CACCAAA  ACA   CAACCAGC
                                |||||||  |||   ||||||||
                                GTGGTTT  TGT   GTTGGTCG
                                   GG   GTC
GAM1031  BCL11B    3'  TCACCAAAAGAAAACAA     27132         AC
                                TCACCAAAA  AAAACAA
                                |||||||||  |||||||
                                AGTGGTTTT  TTTTGTT
                                   C_
GAM1031  CERD4     3'  TCACCAAAGCCACTGGACCAGC 27133         AA  AAACA
                                TCACCAAA  CA    ACCAGC
                                ||||||||  ||    ||||||
                                AGTGGTTT  GT    TGGTCG
                                   CG  GACC_
GAM1031  CHRNE     3'  AAAGACAATTCAACCAGC    27134     A    AA
                                AAA ACAA  CAACCAGC
                                ||| ||||  ||||||||
```

```
                                TTT TGTT  GTTGGTCG
                                  C    AA
GAM1031  COL13A1   5' CCGAAAAAGCACAACCAGC   27135   _   CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1031  COL13A1   5' CCGAAAAAGCACAACCAGC   27135   _   CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1031  COL13A1   5' CCGAAAAAGCACAACCAGC   27135   _   CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1031  COL13A1   5' CCGAAAAAGCACAACCAGC   27135   _   CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1031  COL13A1   5' CCGAAAAAGCACAACCAGC   27135   _   CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1031  COL13A1   5' CCGAAAAAGCACAACCAGC   27135   _   CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1031  COL13A1   5' CCGAAAAAGCACAACCAGC   27135   _   CAAA
                                CC AAAAA   ACAACCAGC
                                || |||||   |||||||||
                                GG TTTTT   TGTTGGTCG
                                 C    CG__
GAM1031  COX7A2L   3' CCAAAAAACAAACCAG     27136     _  AACA
                                CCAAAAA CAA   ACCAG
                                ||||||| |||   |||||
                                GGTTTTT GTT   TGGTC
                                    T  ____
GAM1031  DPYD      3' CACCAAAAATAAGCAATTTCAG 27137      CAAAA  C__
           C                    CACCAAAAA   CAA  CAGC
                                |||||||||   |||  ||||
                                GTGGTTTTT   GTT  GTCG
                                     ATTC_  AAA
GAM1031  HMGN1     3' ACCAAAAAAATAAACAACCAGC 27138      CA
                                ACCAAAAA  AAACAACCAGC
                                ||||||||  ||||||||||
```

```
                                TGGTTTTT  TTTGTTGGTCG
                                    TA
GAM1031  MYOM2    3'  TCACCAAATGCAAAAATCAAAA 27139        AA    __  CC
              GC                  TCACCAAA  CAAAA  CAA  AGC
                                  ||||||||  |||||  |||  |||
                                  AGTGGTTT  GTTTT  GTT  TCG
                                      AC    TA   T_
GAM1031  PIM2     3'  TCACCAAAATAAACTTCCTTAG 27140        ACA   AA  __
              C                   TCACCAAAA   AAAC  CC  AGC
                                  |||||||||   ||||  ||  |||
                                  AGTGGTTTT   TTTG  GG  TCG
                                      A__    AA  AA
GAM1031  PON1     3'  CAAAAACAAAACAAAAGC    27141           CC
                                  CAAAAACAAAACAA  AGC
                                  ||||||||||||||  |||
                                  GTTTTTGTTTTGTT  TCG
                                        T_
GAM1031  ROR2     3'  TCACCAAATACAAAGCTGTCAG 27142        A    ACAAC
                                  TCACCAAA ACAAA    CAG
                                  ||||||||  |||||    |||
                                  AGTGGTTT TGTTT    GTC
                                      A    CGACA
GAM1031  SEL1L    3'  CAGAAACAAAATATCCAGC   27143    A      CAA
                                  CA AAACAAAA   CCAGC
                                  ||  ||||||||   |||||
                                  GT TTTGTTTT   GGTCG
                                   C       ATA
GAM1031  TAF1C    3'  TCACCAAACACGAGGAGCCAGC 27144        A  AAAACAA
                                  TCACCAAA AC       CCAGC
                                  ||||||||  ||      |||||
                                  AGTGGTTT TG       GGTCG
                                      G  CTCCTC_
GAM1031  TTN      5'  CCTAAAAACAAAACTACACAG  27145   _        A  _
                                  CC AAAAACAAAAC AC CAG
                                  ||  ||||||||||  ||  |||
                                  GG TTTTTGTTTTG TG GTC
                                   A          A  T
GAM1031  TTN      5'  CCTAAAAACAAAACTACACAG  27145   _        A  _
                                  CC AAAAACAAAAC AC CAG
                                  ||  ||||||||||  ||  |||
                                  GG TTTTTGTTTTG TG GTC
                                   A          A  T
GAM1031  TTN      5'  CCTAAAAACAAAACTACACAG  27145   _        A  _
                                  CC AAAAACAAAAC AC CAG
                                  ||  ||||||||||  ||  |||
                                  GG TTTTTGTTTTG TG GTC
                                   A          A  T
GAM1031  TTN      5'  CCTAAAAACAAAACTACACAG  27145   _        A  _
                                  CC AAAAACAAAAC AC CAG
                                  ||  ||||||||||  ||  |||
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                                GG TTTTTGTTTTG TG GTC
                                 A         A  T
GAM1031  VIPR2    3'  CCACCGACCATCAACAACCAG  27146      AAAAA  A_
                                TCACC    CA  AACAACCAG
                                |||||    ||  |||||||||
                                GGTGG    GT  TTGTTGGTC
                                   CTG__  AG
GAM1031  ASB16    3'  CCACCAAAAATACAAAATCAGC 27147          __     CAAC
                                TCACCAAAA  ACAAAA    CAGC
                                |||||||||  ||||||    ||||
                                GGTGGTTTT  TGTTTT    GTCG
                                      TA     A___
GAM1031  C1orf17  3'  CCACTAAGAACAAAACAA    27148      C  A
                                TCAC AA AACAAAACAA
                                |||| || ||||||||||
                                GGTG TT TTGTTTTGTT
                                  A  C
GAM1031  C1orf24  3'  CCACCAAAAATACAAAAATTAG 27149          __     CAACC
              C                  TCACCAAAA  ACAAAA     AGC
                                |||||||||  ||||||    |||
                                GGTGGTTTT  TGTTTT    TCG
                                      TA     TAA__
GAM1031  C20orf112 3'  CAAAAACAAAATGTACCAAC   27150          CA_
                                CAAAAACAAAA   ACCAGC
                                ||||||||||   ||||||
                                GTTTTTGTTTT   TGGTTG
                                       ACA
GAM1031  CAT56    3'  TCACAGAAAACAACCAG     27151      CAAAAAC
                                TCAC      AAAACAACCAG
                                ||||      ||||||||||
                                AGTG      TTTTGTTGGTC
                                  TC_____
GAM1031  DKFZP434I216 3'  CACCAAAGGCCTAACAACCAG  27152        AACAA
                                CACCAAA    AACAACCAG
                                |||||||    |||||||||
                                GTGGTTT    TTGTTGGTC
                                    CCGGA
GAM1031  DKFZP434P0721 3'  CACCAAAATTAACAGCCAG    27153        ACAA    A
                                CACCAAAA    AACA CCAG
                                ||||||||    |||| ||||
                                GTGGTTTT    TTGT GGTC
                                     AA__    C
GAM1031  DKFZP586M1120 3'  TCCTCAAAATTTAGCAACCAGC 27154     AC     ACAAAA
                                TC  CAAAA     CAACCAGC
                                ||  |||||     ||||||||
                                AG  GTTTT     GTTGGTCG
                                 GA    AAATC_
GAM1031  FLJ10587  3'  ACCAAAAACAAAAACCAGC   27155           CA
                                ACCAAAAACAAAA  ACCAGC
                                ||||||||||||  ||||||
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                                TGGTTTTTGTTTT TGGTCG
                                          __
GAM1031 FLJ11252 3' TCACTCAAAACAACAACAG  27156     CA    AA    C
                                TCAC AAAACA ACAAC AG
                                |||| |||||| ||||| ||
                                AGTG TTTTGT TGTTG TC
                                  AG    __   _
GAM1031 FLJ20097 3' CAAAAACAAGCAGCCAGC   27157        AA A
                                CAAAAACAA CA CCAGC
                                ||||||||| || |||||
                                GTTTTTGTT GT GGTCG
                                     C_ C
GAM1031 FLJ20984 3' TCACCAAAAGAAAGCAGCCA 27158        AC  A A
                                TCACCAAAA AAA CA CCA
                                ||||||||| ||| || |||
                                AGTGGTTTT TTT GT GGT
                                     C_  C C
GAM1031 FLJ23186 3' TCCCAACAAAACAATCAG   27159   A  AAA      C
                                TC CCA  ACAAAACAA CAG
                                || |||  ||||||||| |||
                                AG GGT  TGTTTTGTT GTC
                                 _  ___      A
GAM1031 GAL3ST2  3' CAAAATCACCAACCAGC    27160     A AAA
                                CAAAA CA  CAACCAGC
                                ||||| ||  ||||||||
                                GTTTT GT  GTTGGTCG
                                  A G__
GAM1031 GG2-1    3' TCAATCTTAACAAAACAGTCAG 27161    CCAAA      AC
           C                     TCA    AACAAAACA CAGC
                                |||    ||||||||| ||||
                                AGT    TTGTTTTGT GTCG
                                 TAGAA       CA
GAM1031 HUMGT198A 3' ACCAAAAACAAGGTAGCCAG  27162         AACAA
                                ACCAAAAACAA    CCAG
                                ||||||||||    ||||
                                TGGTTTTTGTT    GGTC
                                      CCATC
GAM1031 HUMGT198A 3' ACCAAAAACAAGGTAGCCAG  27162         AACAA
                                ACCAAAAACAA    CCAG
                                ||||||||||    ||||
                                TGGTTTTTGTT    GGTC
                                      CCATC
GAM1031 KIAA0317 3' CCAAAAACAGCAGAACCAG   27163        AAAC
                                CCAAAAACA   AACCAG
                                |||||||||   ||||||
                                GGTTTTTGT   TTGGTC
                                      CGTC
GAM1031 KIAA0367 3' TCACCAAAAGGAAATCCAGC  27164        AC  ACAA
                                TCACCAAAA AAA   CCAGC
                                ||||||||| |||   |||||
```

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                                AGTGGTTTT  TTT   GGTCG
                                     CC   A___
GAM1031  KIAA0376  3'  TCACCAAAGGGCATCCAGCCAG 27165        AACAAAA  A
             C                    TCACCAAA      CA CCAGC
                                  ||||||||      || |||||
                                  AGTGGTTT      GT GGTCG
                                       CCCGTAG  C
GAM1031  KIAA0453  3'  CACCAAAAACAAGACCCAG   27166          A  AA
                                  CACCAAAAACAA AC  CCAG
                                  ||||||||||||| ||  ||||
                                  GTGGTTTTTGTT TG  GGTC
                                         C  __
GAM1031  KIAA1257  3'  ACCAAAAATACAAAATCAGC   27167        __     CAAC
                                  ACCAAAA  ACAAAA   CAGC
                                  |||||||  ||||||   ||||
                                  TGGTTTT  TGTTTT   GTCG
                                       TA     A___
GAM1031  KIAA1361  3'  TCCCCAAAAACAAACAAACCCG 27168    A        AC    A_
             GC                     TC CCAAAAACAAA  AACC  GC
                                  || ||||||||||  ||||  ||
                                  AG GGTTTTTGTTT  TTGG  CG
                                   G         GT    GC
GAM1031  KIAA1784  5'  CCAAAGTCAGCAACCAGC    27169      AA  AAA
                                  CCAAA  CA   CAACCAGC
                                  |||||  ||   ||||||||
                                  GGTTT  GT   GTTGGTCG
                                     CA  C__
GAM1031  KIAA1922  5'  CCACCAAAAATACAAAAATTAG 27149          __     CAACC
             C                     TCACCAAAA  ACAAAA    AGC
                                   |||||||||  ||||||    |||
                                   GGTGGTTTT  TGTTTT    TCG
                                        TA     TAA__
GAM1031  KIAA1975  5'  TCACCAATAACAAAACAA    27170        A
                                  TCACCAA AACAAAACAA
                                  ||||||| ||||||||||
                                  AGTGGTT TTGTTTTGTT
                                       A
GAM1031  ORCTL3    3'  CACCAGAAAGAACTGCAACCAG 27171      A   C  AA_
             C                     CACCA AAA AA   CAACCAGC
                                   ||||| ||| ||   ||||||||
                                   GTGGT TTT TT   GTTGGTCG
                                      C   C  GAC
GAM1031  RAB14    3'  CCAAAACAAAACAAAAGC    27172       A       CC
                                  CCAAAA CAAAACAA  AGC
                                  |||||| ||||||||  |||
                                  GGTTTT GTTTTGTT  TCG
                                      _       T_
GAM1031  RAB40A   5'  TCCCAAAAACCACAGTCAG   27173    A      AAA   AC
                                  TC CCAAAAAC   ACA  CAG
                                  || ||||||||   |||  |||
```

```
                                AG GGTTTTTG   TGT  GTC
                                 _      G__   CA
GAM1031  SKIP     3'  CAGTCACAAAACAGCCAGC   27174    AAA       A
                                CA   ACAAAACA CCAGC
                                ||   |||||||| |||||
                                GT   TGTTTTGT GGTCG
                                 CAG       C
GAM1031  SKIP     3'  CAGTCACAAAACAGCCAGC   27174    AAA       A
                                CA   ACAAAACA CCAGC
                                ||   |||||||| |||||
                                GT   TGTTTTGT GGTCG
                                 CAG       C
GAM1031  SSBP4    3'  ACCAAAAACCAAAACCAGC   27175         AAAAC
                                ACCAAAAAC    AACCAGC
                                |||||||||    |||||||
                                TGGTTTTTG    TTGGTCG
                                     GTT__
GAM1031  STK17A   3'  CCAAAAACAAATCCAA      27176          ACAA
                                CCAAAAACAAA   CCAG
                                ||||||||||    ||||
                                GGTTTTTGTTT   GGTT
                                      A___
GAM1031  LOC150848 5'  TCACCAAAAACAACAACAAC   27177           _
                                TCACCAAAAACAA AACAAC
                                |||||||||||| ||||||
                                AGTGGTTTTTGTT TTGTTG
                                       G
GAM1031  LOC153514 3'  ACCAAAGGCCAACAACCAGC   27178       AACAA
                                ACCAAA    AACAACCAGC
                                ||||||    ||||||||||
                                TGGTTT    TTGTTGGTCG
                                   CCGG_
GAM1031  LOC158956 3'  ACCAAAAAATAAACAACCAGC  27138        CA
                                ACCAAAAA  AAACAACCAGC
                                ||||||||  ||||||||||
                                TGGTTTTT  TTTGTTGGTCG
                                     TA
GAM1031  LOC161357 3'  TCATTTGAAACAAAACCAGC   27179     CCAA      ACA
                                TCA   AAACAAA   ACCAGC
                                |||   |||||||   ||||||
                                AGT   TTTGTTT   TGGTCG
                                  AAAC      ___
GAM1031  LOC200059 3'  TCATCCAAAACAAAACAA    27180     _     A
                                TCA CCAAAA CAAAACAA
                                ||| |||||| ||||||||
                                AGT GGTTTT GTTTTGTT
                                  A     _
GAM1031  LOC200942 3'  CCAAGGTCATACAACCAGC    27181      AAA  AA
                                CCAA   CA  ACAACCAGC
                                ||||   ||  |||||||||
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                                GGTT   GT  TGTTGGTCG
                                  CCA  A_
GAM1031  LOC204804 3'  AAAAACAAAACAAGGACCCAGC 27182            ____
                                AAAAACAAAACAA    CCAGC
                                |||||||||||||    |||||
                                TTTTTGTTTTGTT    GGTCG
                                     CCTG
GAM1031  LOC253019 5'  TCCTCAAAAACAAAACAA    27183    AC
                                TC  CAAAAACAAAACAA
                                ||  ||||||||||||||
                                AG  GTTTTTGTTTTGTT
                                 GA
GAM1031  LOC253975 5'  TCCTCAAAAACAAAACAA    27183    AC
                                TC  CAAAAACAAAACAA
                                ||  ||||||||||||||
                                AG  GTTTTTGTTTTGTT
                                 GA
GAM1031  LOC255480 3'  TCACCAAAGGCCAGAAACCCAG 27184         AA_ _   AA
           C                     TCACCAAA   CA AAAC  CCAGC
                                ||||||||   || ||||  |||||
                                AGTGGTTT   GT TTTG  GGTCG
                                     CCG  C   __
GAM1031  LOC257472 3'  CACCAAAGGCCTAACAACCAG  27152        AACAA
                                CACCAAA     AACAACCAG
                                |||||||     |||||||||
                                GTGGTTT     TTGTTGGTC
                                     CCGGA
GAM1031  LOC51652  3'  TCCCACGCACAAGACAACCAGC 27185    A   AAA    A
                                TC CCA   ACAA ACAACCAGC
                                || |||   |||| |||||||||
                                AG GGT   TGTT TGTTGGTCG
                                 _  GCG    C
GAM1031  LOC91759  3'  CCACCAAAGGCATTTTCCAGC  27186        AA  AAACAA
                                TCACCAAA  CA     CCAGC
                                ||||||||  ||     |||||
                                GGTGGTTT  GT     GGTCG
                                     CC  AAAA__
GAM1032  GCMB      3'  GAAAAGCTGTAGATACACACG  27246       ACAAAA
                                GAGAAG     ATACACACG
                                ||||||     |||||||||
                                CTTTTC     TATGTGTGC
                                   GACATC
GAM1032  MXI1      3'  GAAAGACAAAGGGAACACA   27247      A     AAT_
                                GAGA GACAAA    ACACA
                                |||| ||||||    |||||
                                CTTT CTGTTT    TGTGT
                                  _     CCCT
GAM1032  MXI1      3'  GAAAGACAAAGGGAACACA   27247      A     AAT_
                                GAGA GACAAA    ACACA
                                |||| ||||||    |||||
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                                CTTT CTGTTT    TGTGT
                                  _     CCCT
GAM1032 ARL8     3' TTCAGAAGACATCACGCA    27248     G       AAAA   A
                                TTC AGAAGACA    TAC CA
                                ||| ||||||||    ||| ||
                                AAG TCTTCTGT    GTG GT
                                  _       A___   C
GAM1032 GPCR150  5' TTCAAGAAGACCTGCTGAAATA 27249           AA____
              CACA                   TTCGAGAAGAC     AAATACACA
                                ||||||||||      |||||||||
                                AAGTTCTTCTG     TTTATGTGT
                                      GACGAC
GAM1032 MGC20496 3' GAAGGCAAAAATATGCACG   27250      A       CA
                                GAAG CAAAAATA  CACG
                                |||| ||||||||  ||||
                                CTTC GTTTTTAT  GTGC
                                  C       AC
GAM1032 PEG10    3' TTCGGACAGTGAATACACA   27251     AGAA    AA_
                                TTCG    GACA   AATACACA
                                ||||    ||||   ||||||||
                                AAGC    CTGT   TTATGTGT
                                  _____    CAC
GAM1033 RECQL    3' TAATATTGCTTTCAAAAAGAT  27254           _    _
                                TAATATTGCTT CAAAG GAT
                                |||||||||| ||||| |||
                                ATTATAACGAA GTTTT CTA
                                      A     T
GAM1033 AKAP9    3' TAATGATGTTTCAAAGGA    27255     AT  C
                                TAAT  TG TTCAAAGGA
                                ||||  || |||||||||
                                ATTA  AC AAGTTTCCT
                                  CT  A
GAM1033 DGKD     3' TTGTTTCAAAGGTAGC      27256     C       ATT
                                TTG TTCAAAGG   TAGC
                                ||| ||||||||   ||||
                                AAC AAGTTTCC   ATCG
                                  A       ___
GAM1033 KIAA0191 5' ATTGCTTCAAGTCCAG      27257         AA  A
                                ATTGCTTCA  GG TTTAG
                                |||||||||  || |||||
                                TAACGAAGT  TC AGGTC
                                      __ _
GAM1033 KIAA1726 3' TAATTACACTGAAGGATTTAG 27258    T    TTCA
                                A ATTGC    AAGGATTTAG
                                | |||||    ||||||||||
                                A TAATG    TTCCTAAATC
                                 T    TGAC
GAM1033 PRC1     3' TAATAGTGCTTCAAGAAGA   27259      T      _
                                TAATA TGCTTCAA AGGA
                                ||||| |||||||| ||||
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                                ATTAT ACGAAGTT TTCT
                                  C       C
GAM1033  PRO1600   3'  TAATATTGCTGTGGTAGTCATT 27260          TCAA_  G_
            TAGC                   TAATATTGCT    AG  ATTTAGC
                                   ||||||||||    ||  |||||||
                                   ATTATAACGA    TC  TAAATCG
                                      CACCA  AG
GAM1033  Rab11-FIP2 3'  TAATACTGCTTTAAAAATAATA 27261          C     ATT
            GC                     TAATATTGCTT AAAGG   TAGC
                                   ||||||||||| |||||   ||||
                                   ATTATGACGAA TTTTT   ATCG
                                       A     ATT
GAM1033  STK38L    3'  ATATTGCTTTAAAAAAATAGC  27262         C      TT
                                   ATATTGCTT AAAGGA  TAGC
                                   |||||||| ||||||  ||||
                                   TATAACGAA TTTTTT  ATCG
                                       A     T_
GAM1033  VR22      3'  ATATTGCTTTTGTTGATTTAGC 27263          CAAAG
                                   ATATTGCTT    GATTTAGC
                                   |||||||||    ||||||||
                                   TATAACGAA    CTAAATCG
                                       AACAA
GAM1033  LOC121536 3'  TAATATTTCTTTAAAAAATTTA 27264        G   C
            G                       TAATATT CTT AAAGGATTTAG
                                   ||||||| ||| ||||||||||
                                   ATTATAA GAA TTTTTTAAATC
                                      A   A
GAM1033  LOC143274 3'  CAATATTACATGAAGGATTTGG 27265          TTCA       A
            C                       TAATATTGC    AAGGATTT GC
                                   |||||||||    |||||||| ||
                                   GTTATAATG    TTCCTAAA CG
                                       TAC_       C
GAM1033  LOC202052 3'  TATTGCTTCTATTTAG      27266          AAAGG
                                   TATTGCTTC    ATTTAG
                                   |||||||||    ||||||
                                   ATAACGAAG    TAAATC
                                       A____
GAM1034  FLJ20360  3'  TATAGTTTTTACAAGGGT    27269            CTAC
                                   TATAGTTTTTATA    GGT
                                   ||||||||||||    |||
                                   ATATCAAAAATGT    CCA
                                        TC__
GAM1034  LOC145258 3'  CTATAAATACTACGGT      27270        TTTTT
                                   CTATAG    ATACTACGGT
                                   ||||||    ||||||||||
                                   GATATT    TATGATGCCA
                                             _____
GAM1035  GRLF1     3'  CTGCTGTCCCCTCACAC     27273          A   A
                                   CTGCTGTCC CCT TGCAC
                                   ||||||||| ||| |||||
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                                GACGACAGG GGA GTGTG
                                      _  _
GAM1035 KLF7     3' GGACTGCCGTCCACCTGCAC  27274   A          AT
                                A ACTGCTGTCCACCT  GCAC
                                | ||||||||||||||  ||||
                                C TGACGGCAGGTGGA  CGTG
                                 C           __
GAM1035 PIGH     3' GGACTGTGTCCACCTGATG   27275   A   C       _
                                A ACTG TGTCCACCT ATG
                                | |||| ||||||||| |||
                                C TGAC ACAGGTGGA TAC
                                 C   _       C
GAM1035 RNF7     3' AAACTGCTTCCACTGC      27276        G    CTA
                                AAACTGCT TCCAC   TGC
                                |||||||| |||||   |||
                                TTTGACGA AGGTG   ACG
                                      _   ____
GAM1035 ZNF79    5' AACCGCTGTCCAAGTACC    27277          CCTATGC
                                AACTGCTGTCCA      ACC
                                ||||||||||||      |||
                                TTGGCGACAGGT      TGG
                                      TCA_____
GAM1035 CDT6     3' ACTCTGTCCACCTCCTGC    27278    G       A_
                                ACT CTGTCCACCT  TGC
                                ||| ||||||||||  |||
                                TGA GACAGGTGGA  ACG
                                  _        GG
GAM1035 FLJ12287 3' ACTGCTGTGCATCACCCTGC  27279       C___    A
                                ACTGCTGT    CACCT TGC
                                ||||||||    ||||| |||
                                TGACGACA    GTGGG ACG
                                     CGTA    _
GAM1035 FLJ23598 5' CTGCTGCCCATCATCCG     27280        CC   GCA
                                CTGCTGTCCA  TAT   CCG
                                ||||||||||  |||   |||
                                GACGACGGGT  GTA   GGC
                                      A_   ___
GAM1035 KIAA0674 5' GGACTGCTGTTGCGACCA    27281   A      CCACCTA  _
                                A ACTGCTGT      TGC ACCG
                                | ||||||||      ||| ||||
                                C TGACGACA      ACG TGGT
                                 C       ________   C
GAM1035 KIAA1303 3' CTGCTGTCCCCGCGCC      27282        A  TAT  A
                                CTGCTGTCC CC   GC CC
                                ||||||||| ||   || ||
                                GACGACAGG GG   CG GG
                                      _ ___  C
GAM1035 MGC10870 5' AACTGCTGCCCATCCGC     27283          _  TAT
                                AACTGCTGTCCA CC   GC
                                |||||||||||| ||   ||
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                                TTGACGACGGGT GG   CG
                                      A  ___
GAM1035  P2RX1    3'  AAACTGCTCTCTGCCTGGC   27284        G  CA   AT
                                AAACTGCT TC  CCT  GC
                                |||||||| ||  |||  ||
                                TTTGACGA AG  GGA  CG
                                     G  AC   C_
GAM1035  SMCR5    3'  AAACTGCTCTTTATCCGTGCAC 27285        ____   ACCTA
                                AAACTGCT   GTCC    TGCAC
                                ||||||||   ||||    |||||
                                TTTGACGA   TAGG    ACGTG
                                     GAAA   C____
GAM1035  SUI1     3'  CTCTGTCCACCTAGTCA     27286    G        TG
                                CT CTGTCCACCTA  CA
                                || ||||||||||  ||
                                GA GACAGGTGGAT  GT
                                 _         CA
GAM1035  TERE1    5'  GCCGCCATCTTGTGCGCCG   27287     T   C  A_  A
                                GCTG CCA CT  TGC CCG
                                |||| ||| ||  ||| |||
                                CGGC GGT GA  ACG GGC
                                  _  A  AC   C
GAM1035  ZF       5'  AAACTGCTGCTTGCGGCC    27288         CCACCTA   A_
                                AAACTGCTGT      TGC  CC
                                ||||||||||      |||  ||
                                TTTGACGACG      ACG  GG
                                     A_______   CC
GAM1035  LOC122704 3'  AAACTGCTGTCCCCTTTTCAC  27289          A   ATG
                                AAACTGCTGTCC CCT   CAC
                                |||||||||||| |||   |||
                                TTTGACGACAGG GGA   GTG
                                      _  AAA
GAM1035  LOC144587 5'  GGACTGCTGCTGCCTGCACC   27290   A      CCA   AT
                                A ACTGCTGT   CCT  GCACC
                                | ||||||||   |||  |||||
                                C TGACGACG   GGA  CGTGG
                                 C       AC_  __
GAM1035  LOC146517 3'  CTGCTGCCACACACAC      27291       T    CT
                                CTGCTG CCAC  ATGCAC
                                |||||| ||||  ||||||
                                GACGAC GGTG  TGTGTG
                                     _   __
GAM1035  LOC147174 5'  CTGCTGCCATAGCCACCG    27292       T   CCTAT  _
                                CTGCTG CCA    GC ACCG
                                |||||| |||    || ||||
                                GACGAC GGT    CG TGGC
                                   _  AT___  G
GAM1035  LOC150370 3'  GGACTGCTGTCCTCCACG    27293   A        A  T
                                A ACTGCTGTCC CC ATG
                                | ||||||||| || |||
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                                C TGACGACAGG GG TGC
                                 C         A  _
GAM1035  LOC150384 5'  TGCTGCCCACTGACC       27294          CTA  C
                                TGCTGTCCAC   TG ACC
                                ||||||||||   || |||
                                ACGACGGGTG   AC TGG
                                      ____  _
GAM1035  LOC163412 5'  CTGCTGCCGTCTCCGACCG    27295       T  AC  A  C
                                CTGCTG CC  CT TG ACCG
                                ||||||  ||  || || ||||
                                GACGAC GG  GA GC TGGC
                                   _  CA  G  _
GAM1035  LOC200225 5'  AACTGCTTCCGCTCCATCCG   27296        G   AC_   GCA
                                AACTGCT TCC   CTAT   CCG
                                |||||||  |||   ||||   |||
                                TTGACGA AGG   GGTA   GGC
                                   _   CGA    ___
GAM1035  LOC201702 3'  AAACTGCTTTCCACAGTGGC   27297         G    CTAT
                                AAACTGCT TCCAC    GC
                                |||||||| |||||    ||
                                TTTGACGA AGGTG    CG
                                     A     TCAC
GAM1035  LOC221344 3'  GGACTGCTGTTATTTGCCCA   27298    A      CCACCTA   A
                                A ACTGCTGT      TGC CCG
                                | ||||||||      ||| |||
                                C TGACGACA      ACG GGT
                                 C       ATAA___   _
GAM1035  LOC255452 3'  AACTGCTGTCCACGTAGC     27299           C  T
                                AACTGCTGTCCAC TA GC
                                |||||||||||| || ||
                                TTGACGACAGGTG AT CG
                                       C  _
GAM1035  LOC256950 3'  ACTGCTGCAGGCTGTGCGCCG  27300         CCAC  A   A
                                ACTGCTGT    CT TGC CCG
                                ||||||||    || ||| |||
                                TGACGACG    GA ACG GGC
                                     TCC_  C   C
GAM1035  LOC89932  5'  GGACTGCTGCCGCCACCATCCG 27301    A       __     TATGCA
                                A ACTGCTGT  CCACC     CCG
                                | ||||||||  |||||     |||
                                C TGACGACG  GGTGG     GGC
                                 C       GC    TA_____
GAM1036  CHD4     3'  GAAGGTCACTGCTCAGCGG    27304     TAA       CGAA
                                GAA   TCACTGCTT    CGG
                                |||   |||||||||    |||
                                CTT   AGTGACGAG    GCC
                                  CC_        TC__
GAM1036  METTL1    3'  TCACTGCCTGGAGGACGG     27305         C  __
                                TCACTGCTT GA  ACGG
                                |||||||| ||  ||||
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```
                                AGTGACGGA CT  TGCC
                                     C  CC
GAM1036  METTL1    3'  TCACTGCCTGGAGGACGG    27305        C  __
                                TCACTGCTT GA  ACGG
                                |||||||||  ||  ||||
                                AGTGACGGA CT  TGCC
                                     C  CC
GAM1036  KIAA0089  3'  GAATAATCACTGGCTCTTGG   27306          C   GAAC
                                GAATAATCACTG TTC    GG
                                ||||||||||||  |||    ||
                                CTTATTAGTGAC GAG    CC
                                       C   AA__
GAM1036  SSH-3     3'  AGGGTAACCACTGACTGGCGG  27307    AA       _  TCGAA
                                AG  TAATCACTG CT    CGG
                                ||  |||||||||  ||     |||
                                TC  ATTGGTGAC GA    GCC
                                 CC        T  CC___
GAM1036  LOC145138 5'  AGAATAACTGTTGCTTCCAG   27308        CAC     GAA
                                AGAATAAT   TGCTTC   CGG
                                ||||||||   ||||||   |||
                                TCTTATTG   ACGAAG   GTC
                                     ACA     ___
GAM1037  FGFR1     3'  AGGGGTTGTGAGTGGAGACAGT 27311       A   TTCAT
                                AGGGGT TGT    GAGACAGT
                                ||||||  |||    ||||||||
                                TCCCCA ACA    CTCTGTCA
                                   _  CTCAC
GAM1037  FGFR1     3'  AGGGGTTGTGAGTGGAGACAGT 27311       A   TTCAT
                                AGGGGT TGT    GAGACAGT
                                ||||||  |||    ||||||||
                                TCCCCA ACA    CTCTGTCA
                                   _  CTCAC
GAM1037  GSTM1     3'  AGGGGATGTTCACGAAGGATAG 27312       T    T    __  C
            T                    AGGGG ATGTT CATGA  GA AGT
                                |||||  |||||  |||||  ||  |||
                                TCCCC TACAA GTGCT  CT TCA
                                   _    _     TC  A
GAM1037  GSTM2     3'  AGGGGATGTTCACGAAGGATAG 27312       T    T    __  C
            T                    AGGGG ATGTT CATGA  GA AGT
                                |||||  |||||  |||||  ||  |||
                                TCCCC TACAA GTGCT  CT TCA
                                   _    _     TC  A
GAM1037  KIF5C     3'  AGGGCGTACAGATGGGACAGT  27313      _    TTTC   A
                                AGGG GTATG    ATG GACAGT
                                ||||  |||||    |||  ||||||
                                TCCC CATGT    TAC CTGTCA
                                  G    C___   C
GAM1037  SMARCC1   3'  GGTATGTTCTGCCAGGCAGT   27314         CATG  A
                                GGTATGTTT    AG CAGT
                                |||||||||    ||  ||||
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                                CCATACAAG   TC GTCA
                                     ACGG  C
GAM1037 ZNF261   3' AGGGATATGCGGTGGTGAGATG 27315         TTCA_   CA
            GT                   AGGGGTATGT    TGAGA  GT
                                ||||||||||    |||||  ||
                                TCCCTATACG    ACTCT  CA
                                     CCACC    AC
GAM1037 BPESC1   3' GGGGTATTAAAGACAGT    27316       GTTTCAT
                                GGGGTAT      GAGACAGT
                                |||||||      ||||||||
                                CCCCATA      TTCTGTCA
                                   AT_____
GAM1037 FLJ11773 3' AGGGCTATGGAGAGACAGT   27317     G   TTTCAT
                                AGGG TATG     GAGACAGT
                                |||| ||||     ||||||||
                                TCCC ATAC     CTCTGTCA
                                  G   CT____
GAM1037 PIP5K1C  3' AGGGCTGTGGAGACAG     27318      A  TTCAT
                                GGGGT TGT    GAGACAG
                                ||||| |||    |||||||
                                TCCCG ACA    CTCTGTC
                                  _  C____
GAM1037 LOC120939 3' GGTGGTATGTTTTGTGGA    27319   _       CA  A
                                GG GGTATGTTT  TG GA
                                || |||||||||  || ||
                                CC CCATACAAA  AC CT
                                 A        AC  _
GAM1037 LOC152048 3' GGGGTGATGGGAGACAGT    27320      _  TTTCAT
                                GGGGT ATG     GAGACAGT
                                ||||| |||     ||||||||
                                CCCCA TAC     CTCTGTCA
                                  C  C_____
GAM1038 CHD4     3' TGTAACAGGCGTTACAGTG   27323       ATAA  _
                                TGTAACA   CGT ACAGTG
                                |||||||   ||| ||||||
                                ACATTGT   GCA TGTCAC
                                    CC__  A
GAM1038 EGR2     5' TATTATAACAGTCAGT     27324         ATAAC  A
                                TATTGTAACA    GT CAGT
                                ||||||||||    || ||||
                                ATAATATTGT    CA GTCA
                                      _____ _
GAM1038 PCDHB4   3' CTGCAAAGTAATGTACAGTGA 27325       CAA  C
                                TTGTAA   TAA GTACAGTGA
                                ||||||   ||| |||||||||
                                GACGTT   ATT CATGTCACT
                                   TC_   A
GAM1038 ARHGEF9  3' TATCGTAATAATGACAAGGCAG 27326       C  A  TA_
            TGA                  TATTGTAA AAT ACG   CAGTGA
                                |||||||| ||| |||   ||||||
```

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                                ATAGCATT TTA TGT   GTCACT
                                    A   C   TCC
GAM1038  DKFZp434G179 3'  TTGTAACACTCATTACAGTGA  27327        ATAACG
                                TTGTAACA     TACAGTGA
                                ||||||||     ||||||||
                                AACATTGT     ATGTCACT
                                    GAGTA_
GAM1038  FLJ13611  3'  TTGTAACAGTAACACATGA   27328        A   GT   G
                                TTGTAACA TAAC  ACA TGA
                                |||||||| ||||  ||| |||
                                AACATTGT ATTG  TGT ACT
                                    C   __  _
GAM1038  LOC142941 3'  TATTGTGAATAGCACAGTG   27329       AAC   AC
                                TATTGT   AATA  GTACAGTG
                                ||||||   ||||  ||||||||
                                ATAACA   TTAT  CGTGTCAC
                                   C__   __
GAM1038  LOC158819 5'  TATTGTAAAAGCCACAGTG   27330        CAAT  CG
                                TATTGTAA   AA  TACAGTG
                                ||||||||   ||  |||||||
                                ATAACATT   TT  GTGTCAC
                                    _____ CG
GAM1039  DUX4    5'  TCCCGGAGGCCGAGGACCG   27333       TC   AAAA
                                TCCCGGG  CCGA   ACCG
                                |||||||  ||||   ||||
                                AGGGCCT  GGCT   TGGC
                                    CC   CC__
GAM1039  IL12RB2  5'  TCCCGGGCCTGCGGGGACCG  27334        C_  AAAAA
                                TCCCGGGTC  CG    ACCG
                                |||||||||  ||    ||||
                                AGGGCCCGG  GC    TGGC
                                     AC  CCC__
GAM1039  NAGA    5'  CCTGGGTCCCCAAAACCG   27335   C     GAA
                                CC GGGTCCC   AAAACCG
                                || |||||||   |||||||
                                GG CCCAGGG   TTTTGGC
                                 A     G__
GAM1039  SIAH2   5'  TCCCGGGCCCCGAACCCCA   27336          AAAA
                                TCCCGGGTCCCGAA   CCG
                                ||||||||||||||   |||
                                AGGGCCCGGGGCTT   GGT
                                      GG__
GAM1039  T       5'  TCCCGGGTCCCGGGTCCCG   27337          AAAAAA
                                TCCCGGGTCCCG    CCG
                                ||||||||||||    |||
                                AGGGCCCAGGGC    GGC
                                      CCAG__
GAM1039  FLJ10204  5'  CCCGGGCCGGAGGAAGACCG  27338      T  C  A_  A
                                CCCGGG CC GA  AA ACCG
                                |||||| || ||  || ||||
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                                GGGCCC GG CT  TT TGGC
                                   _ C  CC  C
GAM1039  FLJ12132  5'  TCCCGGGCCCTGAGCCCCG   27339         C  AAAAA
                                TCCCGGGTCC GA    CCG
                                |||||||||| ||    |||
                                AGGGCCCGGG CT    GGC
                                     A  CGG__
GAM1039  FLJ20979  5'  TCCCGGGCCCCGCCCAAGCCG  27340          AAA  A
                                TCCCGGGTCCCG   AA CCG
                                ||||||||||||   || |||
                                AGGGCCCGGGGC   TT GGC
                                      GGG  C
GAM1039  FLJ22596  5'  TCCCGAGTTACAGAAAAA    27341        CC _
                                TCCCGGGT  C GAAAAA
                                ||||||||  | ||||||
                                AGGGCTCA  G CTTTTT
                                     AT T
GAM1039  KIAA0227  5'  TCCCGGGTTTAAAAGCCG    27342        CCCGA   A
                                TCCCGGGT    AAAA CCG
                                ||||||||    |||| |||
                                AGGGCCCA    TTTT GGC
                                     AA___   C
GAM1039  KIAA1649  5'  TCCCAGGTCCTCAGGAGGCCG  27343         _  AAAAAA
                                TCCCGGGTCC CG    CCG
                                |||||||||| ||    |||
                                AGGGTCCAGG GT    GGC
                                     A  CCTCC_
GAM1039  KIAA1681  5'  CCCCGGGCAAGGAAACCG    27344        CCC  AA
                                TCCCGGGT   GA  AAACCG
                                ||||||||   ||  ||||||
                                GGGGCCCG   TT  TTTGGC
                                     ___  CC
GAM1039  KIAA1981  3'  TCCCGGGCCTGCTCCAGGGCCG 27345         ____   AAAAAA
                                TCCCGGGTC   CCG    CCG
                                |||||||||   |||    |||
                                AGGGCCCGG   GGT    GGC
                                     ACGA  CCC___
GAM1039  MGC23284  3'  TCCCGGGCCTGTTCCAGAGCCG 27346         ____   AAAAAA
                                TCCCGGGTC   CCG    CCG
                                |||||||||   |||    |||
                                AGGGCCCGG   GGT    GGC
                                     ACAA  CTC___
GAM1039  MUC13    3'  TCCCAGGCACGCCTCCTGAAAA 27347        _______  C
           A                     TCCCGGGT     CC GAAAAA
                                 ||||||||     || ||||||
                                 AGGGTCCG     GG CTTTTT
                                      TGCGGA  A
GAM1039  NIR1     5'  TCCCGGGCCCGGCCCCGACCG  27348        T   AAAAA_
                                TCCCGGG CCCG     ACCG
                                ||||||| ||||     ||||
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                                AGGGCCC GGGC     TGGC
                                   _   CGGGGC
GAM1039  PDCD7    5'  TCCCGGGCCCTCTCGCGAAGCC 27349         _____   AAAA
                G                  TCCCGGGTCC    CGAA   CCG
                                   ||||||||||    ||||   |||
                                   AGGGCCCGGG    GCTT   GGC
                                         AGAGC   C___
GAM1039  TNFAIP3  3'  CCGGGTCCTCAGGAAAGGAACC 27350        _ __   A_
                G                  CCGGGTCC C  GAAA  AACCG
                                   |||||||| |  ||||  |||||
                                   GGCCCAGG G  CTTT  TTGGC
                                        A TC   CC
GAM1039  TRAF3    3'  CCACGGTGTCCTGAAGAAAC  27351   _  _   C   A
                                   CC CGG GTCC GAA AAAC
                                   || ||| |||| ||| ||||
                                   GG GCC CAGG CTT TTTG
                                    T   A   A   C
GAM1039  LOC131000 5'  CCAGGTGGAAAAACCG     27352      CCC     A
                                   CCGGGT   GAAAAA CCG
                                   ||||||   |||||| |||
                                   GGTCCA   CTTTTT GGC
                                      C__     _
GAM1039  LOC131831 5'  CCCCGGGTCTCCGAAGCCG   27353        _    AAAA
                                   TCCCGGGTC CCGAA   CCG
                                   |||||||| |||||   |||
                                   GGGGCCCAG GGCTT   GGC
                                         A    C___
GAM1039  LOC138429 3'  CCCGGGCCCGGGGGAACCG   27354      T   AAAA
                                   CCCGGG CCCG   AACCG
                                   |||||| ||||   |||||
                                   GGGCCC GGGC   TTGGC
                                      _   CCCC
GAM1039  LOC147859 5'  CCCTGGGTCCCAAAGGCCG   27355    _       AAAA
                                   CCC GGGTCCCGAA   CCG
                                   ||| ||||||||||   |||
                                   GGG CCCAGGGTTT   GGC
                                     A        CC__
GAM1039  LOC163033 5'  TCCCAGGTCCTAGAGGGGGGCC 27356         C_  AAAAA_
                G                  TCCCGGGTCC  GA     CCG
                                   ||||||||||  ||     |||
                                   AGGGTCCAGG  CT     GGC
                                         AT  CCCCCC
GAM1039  LOC203427 5'  CCCGGGCCCGGAAGACCG   27357        C   AAA
                                   CCCGGGTCC GAA   ACCG
                                   |||||||||  |||   ||||
                                   GGGCCCGGG CTT   TGGC
                                         C   C__
GAM1039  LOC221463 3'  CCCCGAAGGAAAGAACCG   27358      TCCC   A
                                   TCCCGGG   GAAA AACCG
                                   |||||||   |||| |||||
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                                GGGGCTT   CTTT TTGGC
                                   C___   C
GAM1039  LOC221749 5'  TCCCGGGTCTGTCCGTGGCCG  27359        ___  AAAAAA
                                TCCCGGGTC  CCG    CCG
                                |||||||||  |||    |||
                                AGGGCCCAG  GGC    GGC
                                     ACA  ACC___
GAM1039  LOC254013 5'  TCCGGGGTCCCGCTACCAAAAC 27360    C      AA___
                                TCC GGGTCCCG    AAAAC
                                ||| ||||||||    |||||
                                AGG CCCAGGGC    TTTTG
                                  C      GATGG
GAM1039  LOC254120 3'  TCCCAGGTCTCGGCACCG    27361        C  AAAAA
                                TCCCGGGTC CG    ACCG
                                ||||||||| ||    ||||
                                AGGGTCCAG GC    TGGC
                                     A  CG___
GAM1040  ANPEP    3'  GAGGGGAGGACACTGGTGCC  27364   T     G  GC   A
                                GA GGGGAGGG GC  GGT CC
                                || |||||||| ||  ||| ||
                                CT CCCCTCCT TG  CCA GG
                                 _      G  A_  C
GAM1040  C1QG     3'  CCATGGGGAGGGGGGTGCAGT  27365   G        C
                                C ATGGGGAGGGGG GCGGT
                                | ||||||||||| |||||
                                G TACCCCTCCCCC CGTCA
                                 G          A
GAM1040  CELSR1   3'  GAGGGGAGGGGGTGGTGGT   27366   T       CGC_
                                GA GGGGAGGGGG   GGT
                                || ||||||||||   |||
                                CT CCCCTCCCCC   CCA
                                 _       ACCA
GAM1040  CNP      3'  GAAGGGGAGGGGGCAGGGAC  27367   T        C  T
                                GA GGGGAGGGGGCG GG AC
                                || |||||||||||| || ||
                                CT CCCCTCCCCCGT CC TG
                                 T          C  _
GAM1040  EZH1     3'  TGGGGAGGGGTTGAGACCC   27368         GCGC  T
                                TGGGGAGGGG   GG ACCC
                                ||||||||||   || ||||
                                ACCCCTCCCC   TC TGGG
                                     AAC_  _
GAM1040  LPIN2    3'  TGGGGAGGGGGACCAAGCCC  27369         C  GGTA
                                TGGGGAGGGGG GC   CCC
                                |||||||||| ||   |||
                                ACCCCTCCCCC TG   GGG
                                      _ GTTC
GAM1040  NPY2R    5'  CGTGGGGAGGGGGGCAAACCC  27370   A        C   T
                                CG TGGGGAGGGGG GCGG ACCC
                                || |||||||||| |||| ||||
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                                GC ACCCCTCCCCC CGTT TGGG
                                 _       _   _
GAM1040 NRCAM    3' GGGGAGGGGGGAACC      27371         CGC  T
                                GGGGAGGGGG  GG ACC
                                |||||||||  || |||
                                CCCCTCCCCC  CT TGG
                                    ___ _
GAM1040 PKD2L1   5' GGTGGGGGGGCCCGGTACCC  27372   _ A    G
                                GG GG GGGGGC CGGTACCC
                                || || |||||| ||||||||
                                CC CC CCCCCG GCCATGGG
                                 A _    G
GAM1040 PPP3R1   5' CGGCGGGGAGGGGGCGCG    27373   A
                                CG TGGGGAGGGGGCGCG
                                || ||||||||||||||
                                GC GCCCCTCCCCCGCGC
                                 C
GAM1040 PSD      5' GGGGGGAGGACCAGGTATCC  27374    A    GC   _
                                GGGG GGGGGC  GGTA CC
                                |||| ||||||  |||| ||
                                CCCC CTCCTG  CCAT GG
                                  C    GT   A
GAM1040 SLC39A4  5' TGGGGAGGGTCAGGGTGCCC  27375       GG  C   A
                                TGGGGAGGG  CG GGT CCC
                                |||||||||  || ||| |||
                                ACCCCTCCC  GT CCA GGG
                                     A_  C   C
GAM1040 SLC7A1   3' TGGGGAGGGTGGGGTGCC    27376       _ CGC   A
                                TGGGGAGGG GG   GGT CC
                                |||||||||  ||   ||| ||
                                ACCCCTCCC CC   CCA GG
                                     A  ___   C
GAM1040 SOST     3' CGGTGGGGAGGGGCGCGG    27377    A       G
                                CG TGGGGAGGGG CGCGG
                                || |||||||||| |||||
                                GC ACCCCTCCCC GCGCC
                                 C       _
GAM1040 ABTB1    3' GGGGAGGGGGCTCATCC     27378         G  GTA
                                GGGGAGGGGGC CG   CC
                                ||||||||||  ||   ||
                                CCCCTCCCCCG GT   GG
                                      A  A__
GAM1040 ARHGAP10 3' GAAGGGGGGGGGGGGCCC    27379    T   A    CGC  TA
                                GA GGGG GGGGG   GG  CC
                                || |||| |||||   ||  ||
                                CT CCCC CCCCC   CC  GG
                                 T   _    ___  CG
GAM1040 C14orf4  5' CGAGGGGAGGGGGCGAGGGTGC 27380    T         C_  A
             CC                   CGA GGGGAGGGGGCG  GGT CCC
                                ||| ||||||||||||  ||| |||
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                                GCT CCCCTCCCCCGC  CCA GGG
                                  _         TC   C
GAM1040  C20orf54  3'  CGATGGGGGCGGGGTCGGCGGC 27381        A_    GC_
                                CGATGGGG  GGGG   GCGGT
                                ||||||||  ||||   |||||
                                GCTACCCC  CCCC   CGCCG
                                     CG    AGC
GAM1040  CSR1      3'  GGTGGAGGGGGGTGGTGCC    27382    _      CGC   A
                                GG GGAGGGGGG   GGT CC
                                || ||||||||   ||| ||
                                CC CCTCCCCC   CCA GG
                                 A       A__   C
GAM1040  DKFZP434I2117 3'  TGGGGAGGGGGGAGGGTCC    27383          CGC   A
                                TGGGGAGGGGG   GGT CC
                                ||||||||||   ||| ||
                                ACCCCTCCCCC   CCA GG
                                      TC_   _
GAM1040  DPYSL4    3'  TGGGGAGGCGGCAGCAAATGCC 27384        G   _    TA_
              C                  TGGGGAGG GGC GCGG   CCC
                                 ||||||||  ||| ||||   |||
                                 ACCCCTCC CCG CGTT   GGG
                                      G   T    TAC
GAM1040  FLJ10079  3'  GATGGGGAGGAGGTGAGGCTGC 27385           CGC   A_
              CC                   GATGGGGAGGGGG   GGT  CCC
                                   ||||||||||||   |||  |||
                                   CTACCCCTCCTCC   CCG  GGG
                                         ACT   AC
GAM1040  FLJ10246  3'  CAATGGGGAGGGGTGGATA   27386          GCGC
                                CGATGGGGAGGGG    GGTA
                                ||||||||||||    ||||
                                GTTACCCCTCCCC    CTAT
                                      AC__
GAM1040  GGTLA4    5'  TGGGGAGGGGGCACAGGT    27387           _
                                TGGGGAGGGGGCGC GGT
                                |||||||||||||| |||
                                ACCCCTCCCCCGTG CCA
                                       T
GAM1040  GPS1      3'  TGGGGAGGGGGTGCAGATGTCC 27388          C   TA__
                                TGGGGAGGGGG GCGG    CC
                                |||||||||| ||||    ||
                                ACCCCTCCCCC CGTC    GG
                                      A    TACA
GAM1040  GPS2      3'  CGATGGGGTGGGGGGTGTGGT  27389        A    CGC_
                                CGATGGGG GGGGG    GGT
                                |||||||| |||||    |||
                                GCTACCCC CCCCC    CCA
                                     A     CACA
GAM1040  ITPK1     3'  CGATGGGGGGCGGGTGGC    27390         A  _   CGC
                                CGATGGGG GG GGG   GGT
                                |||||||| || |||   |||
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                                GCTACCCC CC CCC   CCG
                                    _ G   A__
GAM1040  KIAA0892  3'  GATGGAGAGTCAGGCGTGGTGC 27391         G_    C   A
              CC                  GATGGGGAG  GGGCG GGT CCC
                                  |||||||||  ||||| ||| |||
                                  CTACCTCTC  TCCGC CCA GGG
                                      AG    A   C
GAM1040  KIAA1190  5'  TGGGGAGGGGGGGTCTGCCC   27392          CGCG  A
                                  TGGGGAGGGGG   GT CC
                                  ||||||||||    || ||
                                  ACCCCTCCCCC   CG GG
                                       CAGA  _
GAM1040  KIAA1453  3'  TGGTGGAGGAGACATGGT    27393     _        C
                                  TGG GGAGGGGGCG GGT
                                  ||| ||||||||| |||
                                  ACC CCTCCTCTGT CCA
                                    A         A
GAM1040  KIAA1937  5'  GATGGTGGGGGGGGCCTGGT   27394       _ A     GC
                                  GATGG GG GGGGGC  GGT
                                  ||||| || ||||||  |||
                                  CTACC CC CCCCCG  CCA
                                     A  _     GA
GAM1040  MGC15523  5'  CGGTGGGGAGGGGATGGGCAGC 27395    A         C__
                                  CG TGGGGAGGGGG   GCGGT
                                  || ||||||||||   |||||
                                  GC ACCCCTCCCCT   CGTCG
                                   C          ACC
GAM1040  MGC4549   3'  CCATGGGGAGGGGGGCGGC   27396   G         C
                                  C ATGGGGAGGGGG GCGGT
                                  | ||||||||||| |||||
                                  G TACCCCTCCCCC CGCCG
                                   G          _
GAM1040  NECL1     5'  GATGGGGAGGGGGTGGAC    27397           CGC  T
                                  GATGGGGAGGGGG   GG AC
                                  ||||||||||||   || ||
                                  CTACCCCTCCCCC   CC TG
                                        A__  _
GAM1040  OBTP      3'  TGGGGACGGGGCTGTCC     27398       G    GCG  A
                                  TGGGGA GGGGC   GT CC
                                  ||||||  |||||   || ||
                                  ACCCCT CCCCG   CA GG
                                     G    A__  _
GAM1040  P450RAI-2 3'  GGGGAGGGGGGTACAGGTCC   27399         CG   TA
                                  GGGGAGGGGG  CGG  CC
                                  ||||||||||  |||  ||
                                  CCCCTCCCCC  GTC  GG
                                        AT   CA
GAM1040  PRDM12    3'  GAAGGGGAGGGGGCATTGGTCC 27400    T         C_  A
                                  GA GGGGAGGGGGCG  GGT CC
                                  || ||||||||||||  ||| ||
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                                  CT CCCCTCCCCCGT  CCA GG
                                   T          AA  _
GAM1040  PSK      5'  GAGGGGAGGGGGGTGACAACC  27401    T        C_  GT
                                  GA GGGGAGGGGG  GCG  ACC
                                  || ||||||||||  |||  |||
                                  CT CCCCTCCCCC  TGT  TGG
                                   _         AC  __
GAM1040  PTPNS1    3'  GGGGAGGGGGGCCGTGGCTGCCC 27402          _ C   A_
                                  GGGGAGGGGGC G GGT  CCC
                                  |||||||||||| | |||  |||
                                  CCCCTCCCCCG C CCG  GGG
                                         G A   AC
GAM1040  SCAMP-4   3'  CGTGGGGAGGGGGGCGAGGC   27403    A          C
                                  CG TGGGGAGGGGGGCG GGT
                                  || ||||||||||||| |||
                                  GC ACCCCTCCCCCGC CCG
                                   _           T
GAM1040  SEMA6B    3'  GATGGGGAGGGGGGCTGG     27404            GC
                                  GATGGGGAGGGGGGC  GG
                                  ||||||||||||||  ||
                                  CTACCCCTCCCCCG  CC
                                         A_
GAM1040  SEMA6B    3'  GATGGGGAGGGGGGCTGG     27404            GC
                                  GATGGGGAGGGGGGC  GG
                                  ||||||||||||||  ||
                                  CTACCCCTCCCCCG  CC
                                         A_
GAM1040  SEMA6B    3'  GATGGGGAGGGGGGCTGG     27404            GC
                                  GATGGGGAGGGGGGC  GG
                                  ||||||||||||||  ||
                                  CTACCCCTCCCCCG  CC
                                         A_
GAM1040  TAO1      5'  GAGGGGAGGGGGGTGACAACC  27401    T        C_  GT
                                  GA GGGGAGGGGG  GCG  ACC
                                  || ||||||||||  |||  |||
                                  CT CCCCTCCCCC  TGT  TGG
                                   _         AC  __
GAM1040  TSPEAR    3'  CGTGGGGAGGGGGGTGCGACCC  27405    A        C   GT
                                  CG TGGGGAGGGGG GCG  ACCC
                                  || ||||||||||| |||  ||||
                                  GC ACCCCTCCCCC CGC  TGGG
                                   _          A  __
GAM1040  LOC116113 3'  ATGGGGAGGGGGGCGGAGGGCCC 27406            C  TA
                                  ATGGGGAGGGGGGCG GG  CCC
                                  |||||||||||||| ||  |||
                                  TACCCCTCCCCCGC TC  GGG
                                         C  CC
GAM1040  LOC127281 3'  GATGGGGAGGGAGCCAGT    27407             G
                                  GATGGGGAGGGGGGC CGGT
                                  |||||||||||||| ||||
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                                CTACCCCTCCCTCG GTCA
                                              _
GAM1040  LOC142941 5'  GATGGGAGGGGGCTAGAATCC  27408       G      GC  TA_
                                GATGGG AGGGGGC  GG   CC
                                |||||| |||||||  ||   ||
                                CTACCC TCCCCCG  TC   GG
                                   _      A_  TTA
GAM1040  LOC146733 3'  GAGGGGGAGGAGCTGGTACC   27409    T    AG     GC
                                GA GGGG  GGGGC  GGTACC
                                || ||||  |||||  ||||||
                                CT CCCC  CCTCG  CCATGG
                                 _   CT    A_
GAM1040  LOC147077 3'  GAGGGGAGGGGAGGAGTGCCC  27410    T        CGC   A
                                GA GGGGAGGGGG   GGT CCC
                                || ||||||||||   ||| |||
                                CT CCCCTCCCCT   TCA GGG
                                 _        CC_   C
GAM1040  LOC149506 3'  GATGGGGAGGGGGCCTAAGCCC 27411             GCGGTA
                                GATGGGGAGGGGGC     CCC
                                ||||||||||||||     |||
                                CTACCCCTCCCCCG     GGG
                                         GATTC_
GAM1040  LOC206480 5'  CGGTGGGGAGGGGCTTCTGTAC 27412    A        G GCG_
                                CG TGGGGAGGGG C    GTAC
                                || |||||||||| |    ||||
                                GC ACCCCTCCCC G    CATG
                                 C         _ AAGA
GAM1040  LOC221463 3'  CGGTGGGGGCGGGGGGTGGT   27413    A    A_    CGC
                                CG TGGGG  GGGGG   GGT
                                || |||||  |||||   |||
                                GC ACCCC  CCCCC   CCA
                                 C    CG    CA_
GAM1040  LOC255146 3'  TGGTGGTGGGGGGGGCACC    27414     _ A    CGC
                                TGG GG GGGGG   GGTACC
                                ||| || |||||   ||||||
                                ACC CC CCCCC   CCGTGG
                                  A  A    ____
GAM1040  LOC91301  5'  GAGGGGAGGGGGCGGCAGC    27415    T         _
                                GA GGGGAGGGGGCG CGGT
                                || ||||||||||| ||||
                                CT CCCCTCCCCCGC GTCG
                                 _          C
GAM1041  ANGPT1    3'  CAATCATGTATTATGTATATT  27418      TG  _
                                CAAT  TGT TTATGTATATT
                                ||||  ||| ||||||||||
                                GTTA  ACA AATACATATAA
                                  GT   T
GAM1041  HOXD3     5'  ACCACAATTATGTATGT     27419     C       TT
                                ACC CAATTGTGT  ATGT
                                ||| |||||||||  ||||
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                                TGG GTTAATACA  TACA
                                  T       __
GAM1041  PDE4D    3'  CCCCAGTTGTGTTTCCGAGT   27420      A      AT__
                                CCCCA TTGTGTTT   GT
                                ||||| ||||||||   ||
                                GGGGT AACACAAA   CA
                                   C       GGCT
GAM1041  PLOD2    3'  CCTCGGTTGTGTTTTGTAC   27421    CCAA      A
                                CC   TTGTGTTT TGTAT
                                ||   |||||||| |||||
                                GG   AACACAAA ACATG
                                 AGCC       _
GAM1041  PRKY     3'  CTGTGAAGTATGTATATT    27422      TT_
                                TTGTG   TATGTATATT
                                |||||   ||||||||||
                                GACAC   ATACATATAA
                                   TTC
GAM1041  TPM1     3'  ACACCTGATTGTGTTTCCAACA 27423    _  CA       ATGT
              TT                  AC CC  ATTGTGTTT   ATATT
                                || ||  |||||||||   |||||
                                TG GG  TAACACAAA   TGTAA
                                 T  AC       GGT_
GAM1041  WIF1     3'  ATTGTGTTTAGAATATATT   27424         T_
                                ATTGTGTTTA  GTATATT
                                ||||||||||  |||||||
                                TAACACAAAT  TATATAA
                                      CT
GAM1041  bA430M15.1 3'  CCAAATGTCTTGTGTATATT   27425     T   G   A
                                CCAA TGT TTT TGTATATT
                                |||| ||| ||| ||||||||
                                GGTT ACA GAA ACATATAA
                                  T   _   C
GAM1041  KIAA1271  3'  ACCCCAATGTGTTTCTG     27426        T     A
                                ACCCCAAT GTGTTT TG
                                |||||||| |||||| ||
                                TGGGGTTA CACAAA AC
                                     _     G
GAM1041  PGRMC2   3'  AATTGAGTTTGTGTATATT   27427      T   A
                                AATTG GTTT TGTATATT
                                ||||| |||| ||||||||
                                TTAAC CAAA ACATATAA
                                   T   C
GAM1042  MEN1     3'  TTAGATCAGATTCTTTTG    27430        T   C
                                TTAGATCAG TTC TTTG
                                ||||||||| ||| ||||
                                AATCTAGTC AAG AAAC
                                      T   A
GAM1042  TACC1    3'  TTACATCAGTTTCTTTA     27431     G       C
                                TTA ATCAGTTTC TTTG
                                ||| ||||||||| ||||
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                                AAT TAGTCAAAG AAAT
                                  G       _
GAM1042  FLJ13646  3'  TTAGGTTGGTTTCCTTTAG   27432     ATCA
                                TTAG   GTTTCCTTTGG
                                ||||   ||||||||||
                                AATC   CAAAGGAAATC
                                  CAAC
GAM1042  LOC152620 3'  TTAGACCAGTTTCCCTCTCCGT 27433              GGG
                                TTAGATCAGTTTCCTTT   CCGT
                                |||||||||||||||||  ||||
                                AATCTGGTCAAAGGGAG   GGCA
                                          A__
GAM1042  LOC255045 3'  TTAGGTTGGTTTCCTTTAG   27432     ATCA
                                TTAG   GTTTCCTTTGG
                                ||||   ||||||||||
                                AATC   CAAAGGAAATC
                                  CAAC
GAM1043  ACTN2    3'  CTCCTACTCTAACTCT     27436        CTAG     CC
                                CTCCTACTC   TGGCTC  T
                                |||||||||   ||||||  |
                                GAGGATGAG   ATTGAG  A
                                      ____     __
GAM1043  ARHGAP6  5'  CTCCTCCTCCCTCCCT     27437      A   TAGTGG
                                CTCCT CTCC     CTCCCT
                                ||||| ||||     ||||||
                                GAGGA GAGG     GAGGGA
                                  G   _______
GAM1043  ARHGAP6  5'  CTCCTCCTCCCTCCCT     27437      A   TAGTGG
                                CTCCT CTCC     CTCCCT
                                ||||| ||||     ||||||
                                GAGGA GAGG     GAGGGA
                                  G   _______
GAM1043  ASTN     3'  CCTGCTTCACCCTCTCCCTGG  27438     A _ _  AGTGG
                                CCT CT C CT    CTCCCTGG
                                ||| || | ||    ||||||||
                                GGA GA G GG    GAGGGACC
                                  C  A T  GA___
GAM1043  ATP7B    3'  CTCCTTTTCTGAAGCCCCTGG  27439      AC  CTAGT   T
                                CTCCT  TC    GGC CCCTGG
                                |||||  ||    ||| ||||||
                                GAGGA  AG    TCG GGGACC
                                  AA  ACT__   _
GAM1043  AVPR1A   5'  CCTACTCCCCGCTCCCTGG   27440        AGTG
                                CCTACTCCT   GCTCCCTGG
                                |||||||||   |||||||||
                                GGATGAGGG   CGAGGGACC
                                     G___
GAM1043  B4GALT5  3'  CTCCCTATTTGAGTGCTCCTTG 27441      ACTCCT   G   C
            G                    CTCCT     AGTG CTCC TGG
                                |||||     |||| |||| |||
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                                GAGGG     TCAC GAGG ACC
                                  ATAAAC   _   A
GAM1043  CA14     3'  CTACTCCTACAGTGTTTCTGG  27442        __   GCTCC
                                CTACTCCT  AGTG    CTGG
                                ||||||||  ||||    ||||
                                GATGAGGA  TCAC    GACC
                                    TG   AAA__
GAM1043  CAPZA1   5'  CTACTCCTACAAGTTTTTCTGG 27443        GT  CTCC_
                                CTACTCCTA  GG    CTGG
                                |||||||||  ||    ||||
                                GATGAGGAT  TC    GACC
                                    GT  AAAAA
GAM1043  CHRNB4   3'  CTCCTACTGGGGCTTCCTGG  27444        CCTAGT   C
                                CTCCTACT     GGCT CCTGG
                                ||||||||     |||| |||||
                                GAGGATGA     CCGA GGACC
                                    CC_____   A
GAM1043  DGUOK    3'  TCCTTTCTCCTCCTCCCTGG  27445     A_    AGTGG
                                TCCT  CTCCT    CTCCCTGG
                                ||||  |||||    ||||||||
                                AGGA  GAGGA    GAGGGACC
                                  AA    G_____
GAM1043  DGUOK    3'  TCCTTTCTCCTCCTCCCTGG  27445     A_    AGTGG
                                TCCT  CTCCT    CTCCCTGG
                                ||||  |||||    ||||||||
                                AGGA  GAGGA    GAGGGACC
                                  AA    G_____
GAM1043  DTNB     3'  CTCTGGCTCCCCTCTCCCTGG  27446    CTA    AGTGG
                                CTC   CTCCT    CTCCCTGG
                                |||   |||||    ||||||||
                                GAG   GAGGG    GAGGGACC
                                  ACC    GA____
GAM1043  DTNB     3'  CTCTGGCTCCCCTCTCCCTGG  27446    CTA    AGTGG
                                CTC   CTCCT    CTCCCTGG
                                |||   |||||    ||||||||
                                GAG   GAGGG    GAGGGACC
                                  ACC    GA____
GAM1043  FGF2     5'  CCCCTACTCGCTCGGGTTTTCT 27447        _  AGT  CTCC
              GG                  CTCCTACTC CT   GG    CTGG
                                ||||||||| ||   ||    ||||
                                GGGGATGAG GA   CC    GACC
                                    C  GC_  AAAA
GAM1043  FZD7     3'  CCTACTCCACGTCTCCTTGG  27448        TAGTGG   C
                                CCTACTCC     CTCC TGG
                                ||||||||     |||| |||
                                GGATGAGG     GAGG ACC
                                    TGCA__    A
GAM1043  KLK3     3'  CTTTTCCTAGCAACCCTGG   27449    AC     TG CT
                                CT  TCCTAG  G  CCCTGG
                                ||  ||||||  |  ||||||
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                                GA  AGGATC  T  GGGACC
                                 AA     GT __
GAM1043  MNAT1    3'  TACTTTTGCTAGCTCCCTGG   27450      CCTAG
                                TACT    TGGCTCCCTGG
                                ||||    ||||||||||
                                ATGA    ATCGAGGGACC
                                  AAACG
GAM1043  OGDH     3'  TCCTATCCTAGTGGGTGAGACT 27451       C       CTCC__
              GG                  TCCTA TCCTAGTGG     CTGG
                                ||||| |||||||||     ||||
                                AGGAT AGGATCACC     GACC
                                  _       CACTCT
GAM1043  PMM2     3'  CTCCTCTTACTGTTCTCTG   27452      A  CC  G  GC  C
                                CTCCT CT  TA TG  TC CTG
                                ||||| ||  || ||  || |||
                                GAGGA GA  AT AC  AG GAC
                                  _ __  G  A_  A
GAM1043  RFX5     3'  CCCTGCTCCTAGTTTCCACTTG 27453      A       GGC  _ _
              G                   TCCT CTCCTAGT   TCC CT GG
                                |||| ||||||||   ||| || ||
                                GGGA GAGGATCA   AGG GA CC
                                  C       A__   T  A
GAM1043  CSR1     3'  TCCCACTCCTAGTCCAGCTGG  27454           GG  CC
                                TCCTACTCCTAGT  CT  CTGG
                                ||||||||||||  ||  ||||
                                AGGGTGAGGATCA  GG  GACC
                                        __  TC
GAM1043  DKFZP434C1715 3'  CTCAGAGTGGCTCTCTGG    27455     CT       C
                                CTC  AGTGGCTC CTGG
                                |||  |||||||| ||||
                                GAG  TCACCGAG GACC
                                  TC       A
GAM1043  DKFZp547G183 3'  CTCCTACTTGTGTGATCTTGG  27456        CCTA    C  CC
                                CTCCTACT    GTGG TC  TGG
                                ||||||||    |||| ||  |||
                                GAGGATGA    CACT AG  ACC
                                     ACA_    _  A_
GAM1043  FADS2    3'  CTCCCGCTCTGCCTCCCTG   27457      TA   CTAG  G
                                CTCC  CTC    TG CTCCCTG
                                ||||  |||    || |||||||
                                GAGG  GAG    AC GAGGGAC
                                  GC   ____  G
GAM1043  FLJ10743 3'  TCCTTCTCCCTCCCTGG     27458      A    TAGTGG
                                TCCT CTCC     CTCCCTGG
                                |||| ||||     ||||||||
                                AGGA GAGG     GAGGGACC
                                  A   _______
GAM1043  FLJ14800 3'  CTCCTGCTGCCTCTTCCTCCCT 27459       A  _   AGTGG
              GG                  CTCCT CT CCT     CTCCCTGG
                                ||||| || |||     ||||||||
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                              GAGGA GA GGA    GAGGGACC
                                C  C  GAAG_
GAM1043  FLJ14816  3'  CTCCAGCTCCTGCCTTCTTGG  27460     TA    AGTG  CC  _
                              CTCC  CTCCT   GCT  CT GG
                              ||||  |||||   |||  || ||
                              GAGG  GAGGA   CGG  GA CC
                                TC    _____  AA  A
GAM1043  FLJ22690  3'  TACTTCAGTAGCTCTGG    27461     CC       CC
                              TACT  TAGTGGCTC  TGG
                              ||||  |||||||||  |||
                              ATGA  GTCATCGAG  ACC
                                A_       __
GAM1043  IMPACT    3'  CTCCTAACTTCTGTTCCCTCCC 27462       _  C  A  GG_
            TGG                 CTCCTA CT CT GT   CTCCCTGG
                              ||||||  || || ||   ||||||||
                              GAGGAT GA GA CA   GAGGGACC
                                 T  A  _  AGG
GAM1043  KIAA0237  3'  CTCCTTTCCTAGTAGAATTGG  27463      AC       CTCCC
                              CTCCT  TCCTAGTGG    TGG
                              |||||  |||||||||    |||
                              GAGGA  AGGATCATC    ACC
                                A_       TTA__
GAM1043  KIAA0295  3'  TCCTGCTCCTAGTCACTTTTGG 27464      A      G   CCC
                              TCCT CTCCTAGT GCT   TGG
                              |||| ||||||| |||   |||
                              AGGA GAGGATCA TGA   ACC
                                C       G   AA_
GAM1043  KIAA0415  3'  CTCCACTCAGGTGGCTCCCTGG 27465     T    CTA
                              CTCC ACTC   GTGGCTCCCTGG
                              |||| ||||   ||||||||||||
                              GAGG TGAG   CACCGAGGGACC
                                _    TC_
GAM1043  KIAA0972  5'  CTCCTGTTCCTGGGGCTCCCT  27466      AC    AGT
                              CTCCT  TCCT   GGCTCCCT
                              |||||  ||||   ||||||||
                              GAGGA  AGGA   CCGAGGGA
                                 CA    CC_
GAM1043  KIAA1169  5'  CTGCTGCTCTTGCTCCCTG   27467    C  A   CTAGTG
                              CT CT CTC     GCTCCCTG
                              || || |||     ||||||||
                              GA GA GAG     CGAGGGAC
                               C  C   AA____
GAM1043  KIAA1171  3'  CTCCAGCTCCCACCCTCCCTGG 27468      TA     GTGG
                              CTCC  CTCCTA    CTCCCTGG
                              ||||  ||||||    ||||||||
                              GAGG  GAGGGT    GAGGGACC
                                TC     GG__
GAM1043  KIAA1399  3'  TCCTCTTGGCCCCCTTGG    27469      AG       _
                              TCCT  TGGCTCCCT GG
                              ||||  ||||||||| ||
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                                AGGA  ACCGGGGGA CC
                                  GA        A
GAM1043  KIAA1453  3'  CTCCACTCCTGGGGGTCTG   27470     T     AGT  CTCC
                                CTCC ACTCCT   GG    CTG
                                |||| ||||||   ||    |||
                                GAGG TGAGGA   CC    GAC
                                  _     ____  CCCA
GAM1043  KIAA1655  5'  CTCCTACCTGTTCTCTTCTCTG 27471       CT   A  GG   C___
            G                    CTCCTA  CCT GT  CTC    CTGG
                                |||||||  ||| ||  |||    ||||
                                GAGGAT  GGA CA  GAG    GACC
                                   __   _ A_   AAGA
GAM1043  KIAA1904  3'  CTCCTGCTGCTGGGAACCCTCC 27472      A  C  AGT  ____
            CTGG                    TCCT CT CT   GG    CTCCCTGG
                                |||| || ||   ||    ||||||||
                                AGGA GA GA   CC    GAGGGACC
                                  C  C  C__  TTGG
GAM1043  LATS1    3'  CTCCTATTCCTAGTGTCT    27473       C       G
                                CTCCTA TCCTAGTG CT
                                |||||| |||||||| ||
                                GAGGAT AGGATCAC GA
                                   A       A
GAM1043  MEGF10   3'  CTGCTCCCCTTCTCCCTGG   27474    A    AGTGG
                                CT CTCCT    CTCCCTGG
                                || |||||    ||||||||
                                GA GAGGG    GAGGGACC
                                 C    GAA__
GAM1043  MGC11335  3'  CTCCTGTTCCCCTCCCTG    27475      AC   AGTGG
                                CTCCT  TCCT    CTCCCTG
                                |||||  ||||    |||||||
                                GAGGA  AGGG    GAGGGAC
                                   CA   ______
GAM1043  MGC19556  5'  CTCCTACTCCCAACCT      27476          TGGCTC
                                CTCCTACTCCTAG     CCT
                                ||||||||||||      |||
                                GAGGATGAGGGTT     GGA
                                                  _______
GAM1043  PEX16    3'  CTCCTAGTGAAGGCTTCTTGG  27477        ___   CCC
                                CTCCTAGT   GGCT   TGG
                                ||||||||   ||||   |||
                                GAGGATCA   CCGA   ACC
                                     CTT    AGA
GAM1043  SCYA21   3'  CTCCTCTCATGCTCCCTG    27478      A  CTAGTG
                                CTCCT CTC     GCTCCCTG
                                ||||| |||     ||||||||
                                GAGGA GAG     CGAGGGAC
                                   _  TA____
GAM1043  LOC138399 5'  CTCCCACTCTACCAACTTTCTG 27479         C  G    CC
            G                    CTCCTACTC TA TGGCT  CTGG
                                |||||||| || |||||  ||||
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                                GAGGGTGAG AT GTTGA  GACC
                                     _ G    AA
GAM1043  LOC143719 5'  CTCTTAAAAGCTCCCTGG    27480    C   T
                                CTC TAG GGCTCCCTGG
                                ||| ||| ||||||||||
                                GAG ATT TCGAGGGACC
                                  A   T
GAM1043  LOC147515 3'  CTCCTACTCCCCCTTCCTG   27481         AGTGG  C
                                CTCCTACTCCT    CT CCTG
                                ||||||||||    || ||||
                                GAGGATGAGGG    GA GGAC
                                      G____  A
GAM1043  LOC147664 3'  CTCCTACCTTGGTAACCTCTGG 27482       CCTA    CC
                                CTCCTACT   GTGGCT  CTGG
                                ||||||||   ||||||  ||||
                                GAGGATGG   CATTGG  GACC
                                     AAC_    A_
GAM1043  LOC149157 5'  CTCTGGCTCCCCCTTTGGCTCC 27483    CTA    AG__
            CTGG                 CTC   CTCCT   TGGCTCCCTGG
                                |||   |||||   ||||||||||
                                GAG   GAGGG   ACCGAGGGACC
                                  ACC    GGAA
GAM1043  LOC149995 3'  CTCCTACTCCCCCTTCCTG   27481         AGTGG  C
                                CTCCTACTCCT    CT CCTG
                                ||||||||||    || ||||
                                GAGGATGAGGG    GA GGAC
                                      G____  A
GAM1043  LOC151102 3'  TCCTTCTTTCCAGCCCTCCCTG 27484    A  C_    GG
            G                   TCCT CT  CTAGT  CTCCCTGG
                                |||| ||  |||||  ||||||||
                                AGGA GA  GGTCG  GAGGGACC
                                  A  AA    G_
GAM1043  LOC151283 3'  CTCCTACCCTTACCTCTG    27485       T   AGTGGCT  _
                                CTCCTAC CCT      CC CTG
                                ||||||| |||      || |||
                                GAGGATG GGA      GG GAC
                                     _  AT_____  A
GAM1043  LOC151429 3'  CTACTCCCTGCTTTCCCTGG   27486       A  GGC
                                CTACTCCT GT   TCCCTGG
                                |||||||| ||   |||||||
                                GATGAGGG CG   AGGGACC
                                     A  AA_
GAM1043  LOC153769 3'  CTCCCACTTTTGCTTTCCTGG  27487       CCTAGTG   C_
                                CTCCTACT      GCT  CCTGG
                                ||||||||      |||  |||||
                                GAGGGTGA      CGA  GGACC
                                     AAA____   AA
GAM1043  LOC158117 3'  CTCCTAATCCTCTATTCTTGG  27488      C    AGTGG  CCC
                                CTCCTA TCCT    CT   TGG
                                |||||| ||||    ||   |||
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                                GAGGAT AGGA    GA   ACC
                                   T   GATAA  ___
GAM1043  LOC166341 3'  CTTGCCCTACAGCTCCTGG   27489    AC    G     C
                                CT  TCCTA TGGCTCC TGG
                                ||  ||||| ||||||| |||
                                GA  GGGAT GTCGAGG ACC
                                 AC    _     _
GAM1043  LOC199958 3'  TCTTATTCCTGGGGCTCCCTA  27490    C  C   AGT
                                TC TA TCCT   GGCTCCCTG
                                || || ||||   |||||||||
                                AG AT AGGA   CCGAGGGAT
                                 A  A   CC_
GAM1043  LOC201617 5'  TCCTACCCCTGCCTCCTCTGG  27491          AGT G   _
                                TCCTACTCCT   G CTCC CTGG
                                ||||||||||   | |||| ||||
                                AGGATGGGGA   C GAGG GACC
                                      ___ G   A
GAM1043  LOC203275 3'  CTCCTAATCCTCTATTCTTGG  27488      C   AGTGG  CCC
                                CTCCTA TCCT    CT   TGG
                                |||||| ||||    ||   |||
                                GAGGAT AGGA    GA   ACC
                                   T   GATAA  ___
GAM1043  LOC204084 5'  CTCCACTTCTGCTCCT     27492     T   C  AGTG    C
                                CTCC ACT CT    GCTCC T
                                |||| ||| ||    ||||| |
                                GAGG TGA GA    CGAGG A
                                  _   A  ____    _
GAM1043  LOC221893 3'  CTCCTGCTTTATCAGCTCCCTG 27493      A  CCTAG
            G                    CTCCT CT    TGGCTCCCTGG
                                |||||  ||    ||||||||||
                                GAGGA GA    GTCGAGGGACC
                                   C  AATA_
GAM1043  LOC254132 5'  CTCCCGCTTCTCCTCCCTG   27494     TA  C  AGTGG
                                CTCC  CT CT    CTCCCTG
                                ||||  || ||    |||||||
                                GAGG  GA GA    GAGGGAC
                                  GC  A  G____
GAM1043  LOC254901 5'  CTCCCACTTCTCTTTCCTTGG  27495       C  AGTGGC   C
                                CTCCTACT CT     TCC TGG
                                |||||||| ||     ||| |||
                                GAGGGTGA GA     AGG ACC
                                    A  GAA___   A
GAM1043  LOC255069 5'  CTCCTGTCTCCCTCCCTG    27496      A_   TAGTGG
                                CTCCT  CTCC     CTCCCTG
                                |||||  ||||     |||||||
                                GAGGA  GAGG     GAGGGAC
                                   CA   _______
GAM1043  LOC51066  5'  CCTTTGCTCCTGGGGCCTCCCT 27497     A__    AGT  _
            GG                   CCT   CTCCT   GGC TCCCTGG
                                |||   |||||   ||| |||||||
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                                GGA   GAGGA   CCG AGGGACC
                                  AAC     CC_   G
GAM1043  LOC91064  3'  CTCCTGCCTCAGCCTCCCTGG  27498      A_   CT   GG
                                CTCCT  CTC  AGT  CTCCCTGG
                                |||||  |||  |||  ||||||||
                                GAGGA  GAG  TCG  GAGGGACC
                                   CG   __   __
GAM1043  LOC91156  3'  TCTCACTCCCATTTTCCTGG   27499    C      GTGGCTC
                                TC TACTCCTA      CCTGG
                                || ||||||||      |||||
                                AG GTGAGGGT      GGACC
                                 A       AAAA___
GAM1044  FLJ14525  3'  TTACTTTTGAAAATGTTAAT   27502            A
                                TTATTTTTGAAAAT TTAAT
                                |||||||||||||| |||||
                                AATGAAAACTTTTA AATTA
                                         C
GAM1044  HCNGP     3'  TTTTATTTTTGAAACCTCA    27503            ATA
                                TTTTATTTTTGAAA   TTA
                                ||||||||||||||   |||
                                AAAATAAAAACTTT   AGT
                                         GG_
GAM1044  MOCS3     3'  TATTCTATCATCTGAAATATTA 27504          _      A
                AT                  TATTTTATT TTTGAAA TATTAAT
                                |||||||||  |||||||  |||||||
                                ATAAGATAG AGACTTT ATAATTA
                                      T      _
GAM1044  PABPC5    3'  TTTACACATTGAAAATATTAAT 27505       TT_
                                TTTAT   TTGAAAATATTAAT
                                |||||   ||||||||||||||
                                AAATG   AACTTTTATAATTA
                                   TGT
GAM1045  CDH18     5'  TCCATCAGGGAAAGGTCAGATC 27508         AA      TA___
                ATATT                 TCCATCAG  AGAGGTT    ATATT
                                |||||||||  |||||||    |||||
                                AGGTAGTC  TTTCCAG    TATAA
                                     CC      TCTAG
GAM1045  FBXW1B    3'  TCCACGGGAAGAGGTTT     27509       CA   A
                                TCCAT  GAA GAGGTTT
                                |||||  |||  |||||||
                                AGGTG  CTT CTCCAAA
                                   CC   _
GAM1045  FBXW1B    3'  TCCACGGGAAGAGGTTT     27509       CA   A
                                TCCAT  GAA GAGGTTT
                                |||||  |||  |||||||
                                AGGTG  CTT CTCCAAA
                                   CC   _
GAM1045  FBXW1B    3'  TCCACGGGAAGAGGTTT     27509       CA   A
                                TCCAT  GAA GAGGTTT
                                |||||  |||  |||||||
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                                AGGTG  CTT CTCCAAA
                                  CC   _
GAM1045  IRTA1    3'  TCCATCAGGAGACCTCTAATAT 27510        AA   GG
                T                  TCCATCAG  AGA  TTTAATATT
                                   ||||||||  |||  |||||||||
                                   AGGTAGTC  TCT  AGATTATAA
                                       C_   GG
GAM1045  KERA     3'  AGAAAGCATTCAATATT     27511       AG
                                   AGAAAG  GTTTAATATT
                                   ||||||  ||||||||||
                                   TCTTTC  TAAGTTATAA
                                      G_
GAM1045  PCMT1    3'  CCATCTTAAGGTTTAATATT   27512      AGAAA
                                   CCATC    GAGGTTTAATATT
                                   |||||    ||||||||||||
                                   GGTAG    TTCCAAATTATAA
                                      AA___
GAM1045  EML4     3'  AGAAAGAGGAAACATT      27513        TTT
                                   AGAAAGAGG   AATATT
                                   |||||||||   ||||||
                                   TCTTTCTCC   TTGTAA
                                        T__
GAM1045  KIAA1492  3'  ATCAGAAACTATAATTTAATAT 27514        GA__
                T                  ATCAGAAA    GGTTTAATATT
                                   ||||||||    ||||||||||
                                   TAGTCTTT    TTAAATTATAA
                                       GATA
GAM1045  LOC120939 5'  CATCAGAAAACTGGTAATATT  27515         A_   TT
                                   CATCAGAAAG  GGT  AATATT
                                   ||||||||||  |||  ||||||
                                   GTAGTCTTTT  CCA  TTATAA
                                        GA   __
GAM1045  LOC129676 5'  TCCATGGGAAGGAGGCTCA    27516      CA   A
                                   TCCAT  GAA GAGGTTTA
                                   |||||  ||| ||||||||
                                   AGGTA  CTT CTCCGAGT
                                      CC   C
GAM1045  LOC148145 5'  ATCAGGTCCAGGTTTAATATT  27517      AAAG
                                   ATCAG    AGGTTTAATATT
                                   |||||    ||||||||||||
                                   TAGTC    TCCAAATTATAA
                                      CAGG
GAM1045  LOC152464 3'  TCCATCAGGAGTGAAGACATAT 27518        AAA_   TTTA
                T                  TCCATCAG    GAGG    ATATT
                                   ||||||||    ||||    |||||
                                   AGGTAGTC    CTTC    TATAA
                                        CTCA    TG__
GAM1045  LOC196027 3'  TCCATTAAAAGAGGTAAAA   27519      CA       TT
                                   TCCAT  GAAAGAGGT  AA
                                   |||||  |||||||||  ||
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                                AGGTA  TTTTCTCCA  TT
                                  A_       TT
GAM1045  LOC196205 3'  TCAGTGGGGGGAGGTTTAATA  27520     AAA___
                                TCAG     GAGGTTTAATA
                                ||||     ||||||||||
                                AGTC     CTCCAAATTAT
                                  ACCCCC
GAM1045  LOC196527 3'  ATCAGAAAAAGGTAACATT   27521          TT
                                ATCAGAAAGAGGT  AATATT
                                ||||||||||||  ||||||
                                TAGTCTTTTTCCA  TTGTAA
                                          __
GAM1045  LOC96652  3'  TCCGTCAGCAAGAGGTTCA   27522     A   A
                                TCC TCAG AAGAGGTTTA
                                ||| |||| ||||||||||
                                AGG AGTC TTCTCCAAGT
                                  C   G
GAM1046  ADARB1    3'  CTGGGTGCACCCACTC     27525       CC  GACT
                                CTGGGT  GT   ACCCACTC
                                ||||||  ||   ||||||||
                                GACCCA  CG   TGGGTGAG
                                   __  _____
GAM1046  AGTR1     5'  CTGGGTCCGCTCCAGCCGCTCC 27526         GA   C  A
           C                     CTGGGTCCGT  CTA CC CTCCC
                                 ||||||||||  ||| || |||||
                                 GACCCAGGCG  GGT GG GAGGG
                                      A_   C  C
GAM1046  AGTR1     5'  CTGGGTCCGCTCCAGCCGCTCC 27526         GA   C  A
           C                     CTGGGTCCGT  CTA CC CTCCC
                                 ||||||||||  ||| || |||||
                                 GACCCAGGCG  GGT GG GAGGG
                                      A_   C  C
GAM1046  AGTR1     5'  CTGGGTCCGCTCCAGCCGCTCC 27526         GA   C  A
           C                     CTGGGTCCGT  CTA CC CTCCC
                                 ||||||||||  ||| || |||||
                                 GACCCAGGCG  GGT GG GAGGG
                                      A_   C  C
GAM1046  AGTR1     5'  CTGGGTCCGCTCCAGCCGCTCC 27526         GA   C  A
           C                     CTGGGTCCGT  CTA CC CTCCC
                                 ||||||||||  ||| || |||||
                                 GACCCAGGCG  GGT GG GAGGG
                                      A_   C  C
GAM1046  ATP8B2    5'  CTGGGCCCGGGCCCACT     27527         TGACTA
                                CTGGGTCCG     CCCACT
                                |||||||||     ||||||
                                GACCCGGGC     GGGTGA
                                     CC____
GAM1046  CD79B     3'  TGGGTCCATGGCCCTTCC     27528         ACTA  AC
                                TGGGTCCGTG   CCC  TCC
                                ||||||||||   |||  |||
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                                ACCCAGGTAC   GGG  AGG
                                     C___   A_
GAM1046  CD79B    3'  TGGGTCCATGGCCCTTCC    27528         ACTA  AC
                                TGGGTCCGTG   CCC  TCC
                                ||||||||||   |||  |||
                                ACCCAGGTAC   GGG  AGG
                                     C___   A_
GAM1046  CELSR3   3'  TGGGATCTGCCCCCACTCC   27529     _  CG  A  A
                                TGGG TC  TG CT CCCACTCC
                                |||| ||  || || ||||||||
                                ACCC AG  AC GG GGGTGAGG
                                  T  __  _ _
GAM1046  CHC1     3'  TGGGTCCGTGACAGATGGCTC  27530          TACCCA
                                TGGGTCCGTGAC     CTC
                                ||||||||||||     |||
                                ACCCAGGCACTG     GAG
                                       TCTACC
GAM1046  CTSH     3'  AGGCCCAGGCTGCCCGTTCC   27531        TGA  A   AC
                                GGGTCCG   CT CCC  TCC
                                |||||||   || |||  |||
                                TCCGGGT   GA GGG  AGG
                                    CC_  C   CA
GAM1046  EGLN2    5'  CTGGGCCTCAAGAGCCCACTCC 27532        _  T  CTA
              C                  CTGGGTC CG GA   CCCACTCCC
                                 ||||||| || ||   |||||||||
                                 GACCCGG GT CT   GGGTGAGGG
                                    A  T  C__
GAM1046  HCR      3'  GGTCTGTCCCCACCCACT    27533      C  GA
                                GGTC GT  CTACCCACT
                                |||| ||  |||||||||
                                CCAG CA  GGTGGGTGA
                                  A  GG
GAM1046  ITGB4    3'  CTGGGTCCTTGTGCTGCTCCC  27534         __   A  ACCCA
                                CTGGGTCC  GTG CT    CTCCC
                                ||||||||  ||| ||    |||||
                                GACCCAGG  CAC GA    GAGGG
                                     AA   _  C_____
GAM1046  MGAM     3'  GGGGACACTGCCCACTCC    27535     TC GTG   A
                                GGG  C   ACT CCCACTCC
                                |||  |   ||| ||||||||
                                CCC  G   TGA GGGTGAGG
                                  CT ___   C
GAM1046  NFRKB    5'  CTGGGTCCGCCACTCCCGCTCC 27536          G   A   A
                                CTGGGTCCGT ACT CCC CTCC
                                |||||||||| ||| ||| ||||
                                GACCCAGGCG TGA GGG GAGG
                                       G   _   C
GAM1046  NSEP1    5'  GGGTCCGCTCTCCGCTCCC   27537         GA  AC  A
                                GGGTCCGT  CT  CC CTCCC
                                ||||||||  ||  || |||||
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                                CCCAGGCG  GA  GG GAGGG
                                    A_  __  C
GAM1046  PAFAH1B3  5'  CTGGCTCCGCCACGCCCACTCC 27538     G    G  TA
                                CTGG TCCGT AC  CCCACTCC
                                |||| ||||| ||  ||||||||
                                GACC AGGCG TG  GGGTGAGG
                                  G    G  C_
GAM1046  RAB5C    3'  TGGTTCCGTCCCCTCCCACTCC 27539     G    GA  A
            C                    TGG TCCGT  CT CCCACTCCC
                                ||| |||||  || |||||||||
                                ACC AGGCA  GG GGGTGAGGG
                                  A    GG  A
GAM1046  RBBP2    3'  CTGGATCCATGTACCTGCTC   27540          AC   CA
                                CTGGGTCCGTG  TACC  CTC
                                ||||||||||  ||||  |||
                                GACCTAGGTAC  ATGG  GAG
                                      __   AC
GAM1046  RDX      3'  GGGTCCACCATCCATTCC    27541       GTG   C  C
                                GGGTCC   ACTA CCA TCC
                                ||||||   |||| ||| |||
                                CCCAGG   TGGT GGT AGG
                                   ___   A  A
GAM1046  RNPEPL1  3'  CTGGGTCCTGGGACTCCC    27542        GT_   A
                                CTGGGTCC   GACT CCC
                                ||||||||   |||| |||
                                GACCCAGG   CTGA GGG
                                    ACC   _
GAM1046  SFTPA2   5'  CTGGGTCCAGTCGCTGCTCC   27543        _  GA  ACCCA
                                CTGGGTCC GT  CT    CTCC
                                |||||||| ||  ||    ||||
                                GACCCAGG CA  GA    GAGG
                                    T  GC  C____
GAM1046  ZNF266   5'  TGGGTCCAGTAAAGTCCATTC  27544        _   CTAC   C
                                TGGGTCC GTGA   CCA TC
                                ||||||| ||||   ||| ||
                                ACCCAGG CATT   GGT AG
                                    T   TCA_   A
GAM1046  C14orf4  5'  TGGGCTTGCTGGCCCACTCC   27545      CC  GACTA
                                TGGGT  GT    CCCACTCC
                                |||||  ||    ||||||||
                                ACCCG  CG    GGGTGAGG
                                  AA  ACC__
GAM1046  C20orf60  3'  CTGGGTGTGTCCCCACCCACTC 27546       CC  GA
                                CTGGGT  GT  CTACCCACTC
                                ||||||  ||  ||||||||||
                                GACCCA  CA  GGTGGGTGAG
                                   CA  GG
GAM1046  FLJ13962  3'  CTGGGTCCTGCTTGTTCC    27547        G  A  ACCCAC
                                CTGGGTCC TG CT     TCC
                                |||||||| || ||     |||
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                                GACCCAGG AC GA     AGG
                                    _ _  ACA___
GAM1046  FLJ14936  3'  CTGAGTCCATTACTCATTCCC  27548        GAC   C  C
                                CTGGGTCCGT   TAC CA TCCC
                                ||||||||||   ||| || ||||
                                GACTCAGGTA   ATG GT AGGG
                                    ___   A  A
GAM1046  KIAA0418  3'  CTGGGACTCCCTGGTCCATTCC 27549     __   G  ACTAC   C
            C                    CTGGG  TCC TG    CCA TCCC
                                |||||  ||| ||    ||| ||||
                                GACCC  AGG AC    GGT AGGG
                                   TG   G  CA___   A
GAM1046  KIAA0427  3'  TGGGTCTGGGAGACCCCACTCC 27550      CGT__   TA
            C                    TGGGTC    GAC  CCCACTCCC
                                ||||||    |||  |||||||||
                                ACCCAG    CTG  GGGTGAGGG
                                   ACCCT   __
GAM1046  KIAA0683  5'  CTGGGTCCGGGCGAGGCTCCC  27551        __   __  A
                                CTGGGTCC  GTGA  CT CCC
                                ||||||||  ||||  || |||
                                GACCCAGG  CGCT  GA GGG
                                    CC    CC  _
GAM1046  KIAA1196  3'  CCGGGTCTCCACACCCACTCCC 27552       CGTG  T
                                CTGGGTC    AC ACCCACTCCC
                                |||||||    || ||||||||||
                                GGCCCAG    TG TGGGTGAGGG
                                    AGG_  _
GAM1046  LIP8     5'  CTGGTTCCGCCTACTCTC    27553     G    GA   CCA
                                CTGG TCCGT  CTAC   CTC
                                |||| |||||  ||||   |||
                                GACC AGGCG  GATG   GAG
                                  A    __   A__
GAM1046  MAPK8IP3  3'  CTGGGTCCCCGGCCTGCTCC   27554        G  ACTA  CA
                                CTGGGTCC TG    CC  CTCC
                                |||||||| ||    ||  ||||
                                GACCCAGG GC    GG  GAGG
                                    G  C___  AC
GAM1046  MGC3295  5'  GGGTCCGCTCTCATTCC     27555        GA  ACC  C
                                GGGTCCGT  CT   CA TCC
                                ||||||||  ||   || |||
                                CCCAGGCG  GA   GT AGG
                                    A_  ___  A
GAM1046  RHOBTB2  3'  CTGGGTCCTGGTTACGTGGGCC 27556        G  AC   CCACT
            C                    CTGGGTCC TG  TAC    CCC
                                ||||||||| ||  |||    |||
                                GACCCAGG AC  ATG    GGG
                                    _ CA   CACCC
GAM1046  SEZ6     3'  CTGGGTCCTTGGACCTCTGCTC 27557        GT_   ACCCA
            C                    CTGGGTCC   GACT    CTCC
                                ||||||||   ||||    ||||
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                                GACCCAGG  CTGG    GAGG
                                    AAC   AGAC_
GAM1046  SPEC1    5'  CTGGTGTTTGGACAACCCACTC 27558     GTCCGT  T
             C                   CTGG     GAC ACCCACTCC
                                 ||||     ||| |||||||||
                                 GACC     CTG TGGGTGAGG
                                   ACAAAC  T
GAM1046  STX4A    3'  CTGGGTTCCTGGTGCTCC    27559      _ __  A A
                                 CTGGGT CC  GTG CT CC
                                 |||||| ||  ||| || ||
                                 GACCCA GG  CAC GA GG
                                    A AC  _ _
GAM1046  THG-1    5'  CTGGGTCCGTGTCTCCGCTCC  27560         A AC  A
                                 CTGGGTCCGTG CT  CC CTCC
                                 |||||||||||| ||  || ||||
                                 GACCCAGGCAC GA  GG GAGG
                                       A __  C
GAM1046  LOC126964 3'  CTGTGTCCGCATCCCCACTCCC 27561    G     ACTA
                                 CTG GTCCGTG   CCCACTCCC
                                 ||| |||||||   |||||||||
                                 GAC CAGGCGT   GGGTGAGGG
                                   A     AG__
GAM1046  LOC147381 5'  CTGGGTCCAGTTTGCCATTCCC 27562       _ GACTAC  C
                                 CTGGGTCC GT    CCA TCCC
                                 |||||||| ||    ||| ||||
                                 GACCCAGG CA    GGT AGGG
                                      T  AAC___  A
GAM1046  LOC150111 3'  CTGGTTTGTGACCAGCTCC   27563    GTCC     CCCA
                                 CTGG   GTGACTA   CTCC
                                 ||||   |||||||   ||||
                                 GACC   CACTGGT   GAGG
                                   AAA_     C___
GAM1046  LOC150245 5'  CTGGGTCCTGACTGGGGGCTGC 27564       G    ACCCA___
             TCCC                  CTGGGTCC TGACT      CTCCC
                                 |||||||| |||||      |||||
                                 GACCCAGG ACTGA      GAGGG
                                      _    CCCCCGAC
GAM1046  LOC151174 5'  CTGGGTGTGGAGTGGCCCACTC 27565      CC  ACTA__
             C                   CTGGGT  GTG    CCCACTCC
                                 ||||||  |||    ||||||||
                                 GACCCA  CAC    GGGTGAGG
                                    __  CTCACC
GAM1046  LOC151568 5'  CTGGGTCCTGGCTTAGGCACTC 27566       G  A  ACC_
             C                   CTGGGTCC TG CT   CACTCC
                                 |||||||| || ||   ||||||
                                 GACCCAGG AC GA   GTGAGG
                                      _ C  ATCC
GAM1046  LOC157226 5'  GGGTCCGCTCTCCGCTCCC   27537       GA  AC  A
                                 GGGTCCGT  CT  CC CTCCC
                                 ||||||||  ||  || |||||
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                                CCCAGGCG  GA  GG GAGGG
                                    A_  __  C
GAM1046  LOC158364 3'  CTGGGTCCTGTGGCCAGCATGC 27567        _  A  CCCA_
              TC                  CTGGGTCC GTG CTA    CTC
                                  |||||||| ||| |||    |||
                                  GACCCAGG CAC GGT    GAG
                                    A  C  CGTAC
GAM1046  LOC162137 3'  CTGGGTCCTGAGCGCTATTCTC 27568        ___  A  CCCA
                                  CTGGGTCC  GTG CTA   CTC
                                  ||||||||  ||| |||   |||
                                  GACCCAGG  CGC GAT   GAG
                                    ACT  _  AA__
GAM1046  LOC163595 5'  GGGTCCAGGCATGCCCACTCC  27569       TGACTA
                                  GGGTCCG    CCCACTCC
                                  |||||||    ||||||||
                                  CCCAGGT    GGGTGAGG
                                    CCGTAC
GAM1046  LOC164537 5'  CTGGATCCGGCTTGCTCC    27570        TGA  ACCCA
                                  CTGGGTCCG  CT   CTCC
                                  |||||||||  ||   ||||
                                  GACCTAGGC  GA   GAGG
                                    C__  AC___
GAM1046  LOC200473 5'  GGGTCCGCAGTCCACTCC    27571        GACTAC
                                  GGGTCCGT    CCACTCC
                                  ||||||||    |||||||
                                  CCCAGGCG    GGTGAGG
                                    TCA___
GAM1046  LOC220739 3'  TGGGTCCAAGAGCTGCTTACT  27572        T  _  ACCC
                                  TGGGTCCG GA CT   ACT
                                  |||||||| || ||   |||
                                  ACCCAGGT CT GA   TGA
                                    T  C  CGAA
GAM1046  LOC253613 3'  CTGGGTCCTGTGGCCAGCATGC 27567        _  A  CCCA_
              TC                  CTGGGTCC GTG CTA    CTC
                                  |||||||| ||| |||    |||
                                  GACCCAGG CAC GGT    GAG
                                    A  C  CGTAC
GAM1046  LOC257547 3'  GGTCTGTCCCCACCCACT    27533     C  GA
                                  GGTC GT  CTACCCACT
                                  |||| ||  |||||||||
                                  CCAG CA  GGTGGGTGA
                                    A  GG
GAM1046  LOC257607 3'  GGTCTGTCCCCACCCACT    27533     C  GA
                                  GGTC GT  CTACCCACT
                                  |||| ||  |||||||||
                                  CCAG CA  GGTGGGTGA
                                    A  GG
GAM1046  LOC90631  3'  CTGTGTCCCCGTGCCCACTCCC 27573    G   G  ACTA
                                  CTG GTCC TG   CCCACTCCC
                                  ||| |||| ||   |||||||||
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                                GAC CAGG GC   GGGTGAGGG
                                  A   G  AC__
GAM1046  LOC91252  3'  TGGGCTGCTCTCACTCC    27574     CCG  A  ACC
                                TGGGT  TG CT  CACTCC
                                |||||  || ||  ||||||
                                ACCCG  AC GA  GTGAGG
                                  ___ _ GA_
GAM1047  AVPR2   3'  GTCCCAGCCTCGGGG     27577        TCTA
                                GTCCCGGCCT  CGGGG
                                ||||||||||  |||||
                                CAGGGTCGGA  GCCCC
                                     _____
GAM1047  DTX1    5'  CGCCCGGCTTCAGTGGGG   27578   T    C  TAC
                                CG CCCGGC TTC  GGGG
                                || |||||| |||  ||||
                                GC GGGCCG AAG  CCCC
                                 _    _  TCA
GAM1047  KCNK5   3'  CGTCCCGGTCATCTCGGGA  27579      CCT  A
                                CGTCCCGG  TCT CGGGG
                                ||||||||  ||| |||||
                                GCAGGGCC  AGA GCCCT
                                    AGT  _
GAM1047  KPNB1   5'  CGGCCCGGCCTTTCGGG    27580   T     CTA
                                CG CCCGGCCTT  CGGG
                                || |||||||||  ||||
                                GC GGGCCGGAA  GCCC
                                 C       A__
GAM1047  PC      3'  CGGCCCGGCCTTCCTGG    27581   T       AC
                                CG CCCGGCCTTCT  GG
                                || ||||||||||  ||
                                GC GGGCCGGAAGG  CC
                                 C        A_
GAM1047  PC      3'  CGGCCCGGCCTTCCTGG    27581   T       AC
                                CG CCCGGCCTTCT  GG
                                || ||||||||||  ||
                                GC GGGCCGGAAGG  CC
                                 C        A_
GAM1047  PDGFRB  3'  CGTCTGGCCTTCTAGA    27582    CC     ACGG
                                CGTC  GGCCTTCT  GGA
                                ||||  ||||||||  |||
                                GCAG  CCGGAAGA  TCT
                                  A_     ____
GAM1047  PDK4    5'  CGCCCCGGCCTGGGCTGGGG  27583       TCTAC
                                CGTCCCGGCCT   GGGG
                                ||||||||||    ||||
                                GCGGGGCCGGA   CCCC
                                      CCCGA
GAM1047  PLXNA1  3'  GTCCTGGTCTCAAGGGGAC  27584    C  C  CTAC
                                GTCC GG CTT   GGGGAC
                                |||| || |||   ||||||
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                                CAGG CC GAG   CCCCTG
                                  A A  TT__
GAM1047  PRKCH   5'  GCCCCGGCCCCGGGG     27585        TCTA
                                GTCCCGGCCT   CGGGG
                                ||||||||||   |||||
                                CGGGGCCGGG   GCCCC
                                     _____
GAM1047  PSCD4   5'  GTCCTGGCCCACGGGG     27586     C    TCT
                                GTCC GGCCT   ACGGGG
                                |||| |||||   ||||||
                                CAGG CCGGG   TGCCCC
                                  A    ___
GAM1047  RRM2B   3'  TCCCGGCCTTTCATCAGA    27587         C  _
                                TCCCGGCCTT TA CGGG
                                |||||||||| || ||||
                                AGGGCCGGAA GT GTCT
                                      A  A
GAM1047  SLC1A2  5'  CGTCCCGGCTCTCCACGG    27588        C
                                CGTCCCGGC TTCTACGG
                                ||||||||| ||||||||
                                GCAGGGCCG GAGGTGCC
                                     A
GAM1047  SNX6    5'  CGTCCAGGCCTTCCTGTGGGG  27589      C       AC_
                                CGTCC GGCCTTCT   GGGG
                                ||||| ||||||||   ||||
                                GCAGG CCGGAAGG   CCCC
                                   T       ACA
GAM1047  SPINT2  5'  CGCCCGGCCTTCTCGG     27590    T        A
                                CG CCCGGCCTTCT CGG
                                || ||||||||||| |||
                                GC GGGCCGGAAGA GCC
                                _         _
GAM1047  VGF     3'  CCGGTTTCCGACGGGGAC    27591     CC   _
                                CCGG  TTCT ACGGGGAC
                                ||||  |||| ||||||||
                                GGCC  AAGG TGCCCCTG
                                  A_   C
GAM1047  WT1     5'  CGTCCCGGCTCTGGG      27592        CT   AC
                                CGTCCCGGC  TCT  GGG
                                |||||||||  |||  |||
                                GCAGGGCCG  AGA  CCC
                                     __   __
GAM1047  WT1     5'  CGTCCCGGCTCTGGG      27592        CT   AC
                                CGTCCCGGC  TCT  GGG
                                |||||||||  |||  |||
                                GCAGGGCCG  AGA  CCC
                                     __   __
GAM1047  WT1     5'  CGTCCCGGCTCTGGG      27592        CT   AC
                                CGTCCCGGC  TCT  GGG
                                |||||||||  |||  |||
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                              GCAGGGCCG AGA CCC
                                       __ __
GAM1047 WT1     5' CGTCCCGGCTCTGGG      27592       CT  AC
                              CGTCCCGGC TCT GGG
                              ||||||||| ||| |||
                              GCAGGGCCG AGA CCC
                                       __ __
GAM1047 XT3     5' CGCTCGGCTCCGGCTCGGGG 27593    CC  _ T_ A
                              CGT CGGC CT CT CGGGG
                              ||| |||| ||  || |||||
                              GCG GCCG GG GA GCCCC
                                A_  A CC _
GAM1047 ARPC4   3' GTCCCGGCCCAGGGGA     27594       TCTAC
                              GTCCCGGCCT   GGGGA
                              ||||||||||   |||||
                              CAGGGCCGGG   CCCCT
                                   T____
GAM1047 C1QTNF2 5' CGTCCCGGCTTTCCTCAG   27595       C   A
                              CGTCCCGGC TTCT CGG
                              ||||||||| |||| |||
                              GCAGGGCCG AAGG GTC
                                   A   A
GAM1047 C20orf18 5' CGTCCCGGGTTTCAAGG   27596       CC  TAC
                              CGTCCCGG TTC  GGGG
                              |||||||| |||  ||||
                              GCAGGGCC AAG  TTCC
                                   CA ___
GAM1047 C20orf18 5' CGTCCCGGGTTTCAAGG   27596       CC  TAC
                              CGTCCCGG TTC  GGGG
                              |||||||| |||  ||||
                              GCAGGGCC AAG  TTCC
                                   CA ___
GAM1047 CD36L1  5' CGCCTGGCAGGAGACGGGGAC 27597   T C  CTTCT
                              CG CC GGC   ACGGGGAC
                              || || |||   ||||||||
                              GC GG CCG   TGCCCCTG
                               _ A  TCCTC
GAM1047 CNNM2   5' GTCTCGGCCCACGGGG     27598    C    TCT
                              GTC CGGCCT  ACGGGG
                              ||| ||||||  ||||||
                              CAG GCCGGG  TGCCCC
                                A    ___
GAM1047 CXYorf1 3' CGCCTTGGCCTACAGGG    27599    CC   TCT
                              CGTC GGCCT  ACGGGG
                              |||| |||||  ||||||
                              GCGG CCGGA  TGTCCC
                                AA   ___
GAM1047 DGS-A   3' GTCCCGGCCCCGGGG      27600       TCTA
                              GTCCCGGCCT  CGGGG
                              |||||||||   |||||
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                                CAGGGCCGGG   GCCCC
                                     ____
GAM1047 FLJ11939 5' CGCCCCGGCGGGGAC      27601        CTTCTAC
                                CGTCCCGGC     GGGGAC
                                |||||||||     ||||||
                                GCGGGGCCG     CCCCTG
                                     _______
GAM1047 FLJ12150 3' TCCTGGCCTTCCTAGGG    27602    C      AC
                                TCC GGCCTTCT  GGGG
                                ||| ||||||||  ||||
                                AGG CCGGAAGG  TCCC
                                  A      A_
GAM1047 FLJ14249 3' GCCTGGCCTCCCCTGGGG   27603   T C      AC
                                G CC GGCCTTCT  GGGG
                                | || ||||||||  ||||
                                C GG CCGGAGGG  CCCC
                                _ A       GA
GAM1047 FLJ14466 3' CGCCTTGGCCTTCCAAAGGG  27604     CC       C
                                CGTC  GGCCTTCTA GGGG
                                ||||  |||||||||| ||||
                                GCGG  CCGGAAGGT TCCC
                                  AA        T
GAM1047 FLJ20477 5' CGTCCCGACCTCCCCGGCGGGG 27605           A__
          AC                    CGTCCCGGCCTTCT   CGGGGAC
                                ||||||||||||||   |||||||
                                GCAGGGCTGGAGGG   GCCCCTG
                                      GCC
GAM1047 FLJ21313 5' CGTCCCGGCTTCTAGG     27606        C    C
                                CGTCCCGGC TTCTA GG
                                ||||||||| ||||| ||
                                GCAGGGCCG AAGAT CC
                                     _    _
GAM1047 FLJ23537 3' GTCCCGGCCTCCCAAAGGG   27607           C
                                GTCCCGGCCTTCTA GGGG
                                |||||||||||||| ||||
                                CAGGGCCGGAGGGT TCCC
                                      T
GAM1047 GCHFR    5' CGGCCTGGCTCCCACCGGGG  27608   T C  C    _
                                CG CC GGC TTCTAC GGGG
                                || || ||| |||||| ||||
                                GC GG CCG AGGGTG CCCC
                                 C  A  _     G
GAM1047 GPS2     5' GTCCCAGCCTCCAGGCGGGGA 27609          TA_
                                GTCCCGGCCTTC   CGGGGA
                                ||||||||||||   ||||||
                                CAGGGTCGGAGG   GCCCCT
                                      TCC
GAM1047 HB-1     5' CGCCTCGGCCTCCTGGGA    27610     C       ACG
                                CGTC CGGCCTTCT   GGGA
                                |||| |||||||||   ||||
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                                GCGG GCCGGAGGA  CCCT
                                  A       ___
GAM1047 HEAB     5' CGCTCGGCCTTCTGGGA    27611    CC       ACG
                                CGT  CGGCCTTCT  GGGA
                                |||  |||||||||  ||||
                                GCG  GCCGGAAGA  CCCT
                                 A_       ___
GAM1047 KIAA0140 3' CGCCCCGGCTTTCCTGCAGG  27612        C   A_
                                CGTCCCGGC TTCT  CGGG
                                ||||||||| ||||  ||||
                                GCGGGGCCG AAGG  GTCC
                                     A   AC
GAM1047 KIAA0637 5' CGGCCCGGCCTCTGGGG    27613   T      T  AC
                                CG CCCGGCCT CT  GGGG
                                || ||||||| ||  ||||
                                GC GGGCCGGA GA  CCCC
                                 C      _ __
GAM1047 KIAA0721 3' CGTTCCAGCCTTGCTTTGGG  27614    C      _ ACG
                                CGT CCGGCCTT CT  GGG
                                ||| ||||||| ||  |||
                                GCA GGTCGGAA GA  CCC
                                  A      C  AA_
GAM1047 KIAA0721 3' CGTTCCAGCCTTGCTTTGGG  27614    C      _ ACG
                                CGT CCGGCCTT CT  GGG
                                ||| ||||||| ||  |||
                                GCA GGTCGGAA GA  CCC
                                  A      C  AA_
GAM1047 KIAA0794 3' CGCCCGGCCTTCCTGG     27615   T       AC
                                CG CCCGGCCTTCT  GG
                                || ||||||||||  ||
                                GC GGGCCGGAAGG  CC
                                 _       A_
GAM1047 KIAA1069 3' GCCCCGGCCTTCAAGG     27616          TAC
                                GTCCCGGCCTTC  GGGG
                                ||||||||||||  ||||
                                CGGGGCCGGAAG  TTCC
                                          ___
GAM1047 KIAA1691 3' CGCCCCGGCTTGGGG      27617        C  CTAC
                                CGTCCCGGC TT   GGGG
                                ||||||||| ||   ||||
                                GCGGGGCCG AA   CCCC
                                      _ ____
GAM1047 MGC14844 5' CGGCCCGGCCTGGGCGCGGGG 27618   T      TCTA_
                                CG CCCGGCCT   CGGGG
                                || ||||||||   |||||
                                GC GGGCCGGA   GCCCC
                                 C      CCCGC
GAM1047 SRPUL    5' GTCCCGGCCTCCGGGA     27619          TACG
                                GTCCCGGCCTTC  GGGA
                                ||||||||||||  ||||
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                                CAGGGCCGGAGG   CCCT
                                      ____
GAM1047  LOC118471 3'  CGCCCGGCCTGCTGGGG    27620   T      T  AC
                                CG CCCGGCCT CT  GGGG
                                || |||||||| ||  ||||
                                GC GGGCCGGA GA  CCCC
                                 _       C  __
GAM1047  LOC123591 5'  CGTCCCAGCCTGGGGGA    27621          TCTAC
                                CGTCCCGGCCT    GGGGA
                                ||||||||||    |||||
                                GCAGGGTCGGA    CCCCT
                                       C____
GAM1047  LOC144017 3'  GTCCCGGCGCTGCGCCCGGGG  27622        _  TCTA_
                                GTCCCGGC CT    CGGGG
                                |||||||| ||    |||||
                                CAGGGCCG GA    GCCCC
                                     C  CGCGG
GAM1047  LOC146901 3'  GCCTCGGCCTTCCAAAGTGCGG 27623    C       _____
            GGA                   GTC CGGCCTTCTA    CGGGGA
                                ||| ||||||||||    ||||||
                                CGG GCCGGAAGGT    GCCCCT
                                  A         TTCAC
GAM1047  LOC147063 5'  CGCCTTGGCCTTCCAAGTAATG 27624  CC       C_____    III
            GGGACG                  GGCCTTCTA    GGGGAC  G
                                 |||||||||    ||||||  |
                                 CCGGAAGGT    CCCCTG  C
                                AA        TCATTA    III
GAM1047  LOC147671 5'  GCCTGGCCTCCTGGGG    27625   T  C      AC
                                G CC GGCCTTCT  GGGG
                                | || ||||||||  ||||
                                C GG CCGGAGGA  CCCC
                                 _ A       __
GAM1047  LOC147993 5'  CCTCCTGGTCTTCTGGGGG   27626   G  C  C    AC
                                C TCC GG CTTCT  GGGG
                                | ||| || |||||  ||||
                                G AGG CC GAAGA  CCCC
                                 G  A A    C_
GAM1047  LOC148426 5'  GCCCGGCCCCAGGGGG    27627   T     TT  C
                                G CCCGGCC  CTA GGGG
                                | |||||||  ||| ||||
                                C GGGCCGG  GGT CCCC
                                 _      __  C
GAM1047  LOC153571 3'  CGCCCCGGCCTTCTCAG    27628           A
                                CGTCCCGGCCTTCT CGG
                                |||||||||||||| |||
                                GCGGGGCCGGAAGA GTC
                                          _
GAM1047  LOC158056 3'  GTCCCAGCCTGGGCGGGG   27629         TCTA
                                GTCCCGGCCT   CGGGG
                                |||||||||   |||||
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                                CAGGGTCGGA   GCCCC
                                     CCC_
GAM1047  LOC158292 5'  GCCTCGGCCTTCTGAG     27630    C       AC
                                GTC CGGCCTTCT  GGG
                                ||| |||||||||  |||
                                CGG GCCGGAAGA  CTC
                                  A       __
GAM1047  LOC196047 5'  CGCCCTGGCCTTCCGG     27631     C      TA
                                CGTCC GGCCTTC  CGG
                                ||||| |||||||  |||
                                GCGGG CCGGAAG  GCC
                                   A     __
GAM1047  LOC200093 3'  CGCCTTGGCCTACAGGG    27599     CC    TCT
                                CGTC  GGCCT   ACGGGG
                                ||||  |||||   ||||||
                                GCGG  CCGGA   TGTCCC
                                  AA    ___
GAM1047  LOC200301 3'  GCCCGGCCCTGGGGA      27632   T      CTAC
                                G CCCGGCCTT   GGGGA
                                | |||||||||   |||||
                                C GGGCCGGGA   CCCCT
                                _      _____
GAM1047  LOC203235 5'  CCTCCCGGCCTCCAAGGGG   27633   G        TAC
                                C TCCCGGCCTTC   GGGG
                                | ||||||||||   ||||
                                G AGGGCCGGAGG   CCCC
                                 G         TT_
GAM1047  LOC220020 3'  CGTCCTGACCTTCCTAGG    27634     C      AC
                                CGTCC GGCCTTCT  GGG
                                ||||| ||||||||  |||
                                GCAGG CTGGAAGG  TCC
                                   A       A_
GAM1047  LOC221069 5'  GTGTCGGCCTTCTGGGG     27635    CC       AC
                                GT  CGGCCTTCT  GGGG
                                ||  |||||||||  ||||
                                CA  GCCGGAAGA  CCCC
                                 CA       __
GAM1047  LOC256980 3'  GCCCGGCCTTCTATAAGA    27636   T        CG
                                G CCCGGCCTTCTA  GGG
                                | ||||||||||||  |||
                                C GGGCCGGAAGAT  TCT
                                _         AT
GAM1047  LOC55974  3'  CGCCCGGCCTTTTAAGG     27637    T      C  C
                                CG CCCGGCCTT TA GGG
                                || |||||||| || |||
                                GC GGGCCGGAA AT TCC
                                 _       A  _
GAM1047  LOC90120  5'  CGTCCCGGACCTCGGGG     27638        _  TCTA
                                CGTCCCGG CCT    CGGGG
                                |||||||| |||   |||||
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                                GCAGGGCC GGA    GCCCC
                                    T  ____
GAM1047  LOC90637  5'  GCCCGCGGCCTACGGGGA    27639      _     TCT
                                GTCC CGGCCT   ACGGGGA
                                |||| ||||||   |||||||
                                CGGG GCCGGA   TGCCCCT
                                  C     ___
GAM1047  LOC91040  3'  CGCCTTGGCCTACAGGG     27599     CC    TCT
                                CGTC  GGCCT   ACGGGG
                                ||||  |||||   ||||||
                                GCGG  CCGGA   TGTCCC
                                  AA    ___
GAM1048  DKK1      3'  TCAGAAAATAAGCTAGTATTTT 7183         _    TAA
                                TCAGAAAG AGGTT   TATTTT
                                |||||||| |||||   ||||||
                                AGTCTTTT TTCGA   ATAAAA
                                     A    TC_
GAM1048  KERA      3'  AGAAAGCATTCAATATTTT    7184        AG
                                AGAAAG  GTTTAATATTTT
                                ||||||  ||||||||||||
                                TCTTTC  TAAGTTATAAAA
                                   G_
GAM1048  PPP1R12A  3'  CCAGAAAGATGTAGTATTTT   7185         G  TTAA
                                TCAGAAAGA GT    TATTTT
                                ||||||||| ||    ||||||
                                GGTCTTTCT CA    ATAAAA
                                     A  TC__
GAM1048  S100B     3'  GAAAGAGGTTTTCAATTTT    7186          AAT
                                GAAAGAGGTTT   ATTTT
                                ||||||||||   |||||
                                CTTTCTCCAAA   TAAAA
                                      AGT
GAM1048  DKFZP564I0422 3'  ATCAGAAGAATGCAATATTTT  7187        A   GTT
                                ATCAGAA GAG   TAATATTTT
                                ||||||| |||   |||||||||
                                TAGTCTT CTT   GTTATAAAA
                                   _  AC_
GAM1048  EML4      3'  AGAAAGAGGAAACATTTT    7188         TTT
                                AGAAAGAGG   AATATTTT
                                |||||||||   ||||||||
                                TCTTTCTCC   TTGTAAAA
                                     T__
GAM1048  FLJ21657  3'  ATCAGGCAGAGTAAAATATTTT 7189       AA   GTTT
                                ATCAG  AGAG    AATATTTT
                                |||||  ||||    ||||||||
                                TAGTC  TCTC    TTATAAAA
                                  CG    ATT_
GAM1048  KIAA1054  3'  GAAAGAGGTACCATTTT     7190         TTAA
                                GAAAGAGGT    TATTTT
                                |||||||||    ||||||
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                                CTTTCTCCA   GTAAAA
                                    TG__
GAM1048 SEMA3E   5' TCAGGAAGAAGCTGTATTTT  7191      A      TAA
                                TCAG AAGAGGTT  TATTTT
                                |||| ||||||||  ||||||
                                AGTC TTCTTCGA  ATAAAA
                                  C      C__
GAM1048 LOC130507 3' CAGAAAGTTATCTTAATATTTT 7192       AGG_
                                CAGAAAG   TTTAATATTTT
                                |||||||   ||||||||||
                                GTCTTTC   GAATTATAAAA
                                    AATA
GAM1048 LOC148145 5' ATCAGGTCCAGGTTTAATATTT 7193      AAAG
            T                    ATCAG   AGGTTTAATATTTT
                                |||||   ||||||||||||||
                                TAGTC   TCCAAATTATAAAA
                                   CAGG
GAM1049 DKK1     3' TCAGAAAATAAGCTAGTATTTT 7183        _    TAA
                                TCAGAAAG AGGTT  TATTTT
                                |||||||| |||||  ||||||
                                AGTCTTTT TTCGA  ATAAAA
                                    A    TC_
GAM1049 KERA     3' AGAAAGCATTCAATATTTT   7184       AG
                                AGAAAG  GTTTAATATTTT
                                ||||||  ||||||||||||
                                TCTTTC  TAAGTTATAAAA
                                   G_
GAM1049 PPP1R12A 3' CCAGAAAGATGTAGTATTTT  7185        G  TTAA
                                TCAGAAAGA GT   TATTTT
                                ||||||||| ||   ||||||
                                GGTCTTTCT CA   ATAAAA
                                    A  TC__
GAM1049 S100B    3' GAAAGAGGTTTTCAATTTT   7186          AAT
                                GAAAGAGGTTT  ATTTT
                                ||||||||||  |||||
                                CTTTCTCCAAA  TAAAA
                                    AGT
GAM1049 DKFZP564I0422 3' ATCAGAAGAATGCAATATTTT 7187       A  GTT
                                ATCAGAA GAG  TAATATTTT
                                ||||||| |||  |||||||||
                                TAGTCTT CTT  GTTATAAAA
                                   _  AC_
GAM1049 EML4     3' AGAAAGAGGAAACATTTT    7188        TTT
                                AGAAAGAGG  AATATTTT
                                |||||||||  ||||||||
                                TCTTTCTCC  TTGTAAAA
                                    T__
GAM1049 FLJ21657 3' ATCAGGCAGAGTAAAATATTTT 7189      AA   GTTT
                                ATCAG  AGAG   AATATTTT
                                |||||  ||||   ||||||||
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                                TAGTC  TCTC    TTATAAAA
                                  CG    ATT_
GAM1049  KIAA1054  3'  GAAAGAGGTACCATTTT     7190          TTAA
                                GAAAGAGGT    TATTTT
                                |||||||||    ||||||
                                CTTTCTCCA    GTAAAA
                                     TG__
GAM1049  SEMA3E    5'  TCAGGAAGAAGCTGTATTTT   7191      A       TAA
                                TCAG AAGAGGTT   TATTTT
                                |||| ||||||||   ||||||
                                AGTC TTCTTCGA   ATAAAA
                                  C       C__
GAM1049  LOC130507 3'  CAGAAAGTTATCTTAATATTTT 7192         AGG_
                                CAGAAAG    TTTAATATTTT
                                |||||||    ||||||||||
                                GTCTTTC    GAATTATAAAA
                                     AATA
GAM1049  LOC148145 5'  ATCAGGTCCAGGTTTAATATTT 7193       AAAG
           T                     ATCAG    AGGTTTAATATTTT
                                 |||||    ||||||||||||||
                                 TAGTC    TCCAAATTATAAAA
                                   CAGG
GAM1050  DAAM2     3'  TGATGGAGTTTTAGAAAAATTT 7469         CG  AA
           T                     TGATGGAGT  TA  AAAAGTTTT
                                 |||||||||  ||  |||||||||
                                 ACTACCTCA  AT  TTTTTAAAA
                                       AA  C_
GAM1050  BY55      3'  TGATGAAGAGGGAGGAAAAGTT 27644        TCGTAAA
           TT                     TGATGGAG      AAAAGTTTT
                                  ||||||||      |||||||||
                                  ACTACTTC      TTTTCAAAA
                                       TCCCTCC
GAM1050  FLJ23056  3'  TAGGTGTAAAAAAAGTTT    27645     A  C
                                TGG GT GTAAAAAAAGTTT
                                ||| || ||||||||||||
                                ATC CA CATTTTTTTCAAA
                                  _  _
GAM1050  ZDHHC3    3'  GAGACATAAAAAAAGTTT    27646     T
                                GAG CGTAAAAAAAGTTT
                                ||| ||||||||||||||
                                CTC GTATTTTTTTCAAA
                                  T
GAM1050  LOC220930 3'  TGATAGAGCTGGAAAGTTT    27647         CGTAAAA
                                TGATGGAGT      AAAGTTT
                                |||||||||      |||||||
                                ACTATCTCG      TTTCAAA
                                       ACC_____
GAM1051  DAAM2     3'  TGATGGAGTTTTAGAAAAATTT 7469         CG  AA
           T                     TGATGGAGT  TA  AAAAGTTTT
                                 |||||||||  ||  |||||||||
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                                ACTACCTCA  AT  TTTTTAAAA
                                     AA  C_
GAM1051  BY55     3'  TGATGAAGAGGGAGGAAAAGTT 27644        TCGTAAA
              TT                   TGATGGAG      AAAAGTTTT
                                   ||||||||      |||||||||
                                   ACTACTTC      TTTTCAAAA
                                       TCCCTCC
GAM1051  FLJ23056 3'  TAGGTGTAAAAAAAGTTT    27645     A  C
                                   TGG GT GTAAAAAAAGTTT
                                   ||| || ||||||||||||
                                   ATC CA CATTTTTTTCAAA
                                     _  _
GAM1051  ZDHHC3   3'  GAGACATAAAAAAAGTTT    27646     T
                                   GAG CGTAAAAAAAGTTT
                                   ||| ||||||||||||||
                                   CTC GTATTTTTTTCAAA
                                     T
GAM1051  LOC220930 3'  TGATAGAGCTGGAAAGTTT   27647         CGTAAAA
                                   TGATGGAGT      AAAGTTT
                                   |||||||||      |||||||
                                   ACTATCTCG      TTTCAAA
                                        ACC____
GAM1052  EBF      3'  AGAATAAATATATCCCC     27651      A
                                   AGAA TAAATATATCTTT
                                   |||| ||||||||||||
                                   TCTT ATTTATATAGGGG
                                     _
GAM1052  GBP1     3'  AGAGGTAAATGCATCTTTGTT  27652     AA    A
                                   AGA  TAAAT TATCTTTGTT
                                   |||  ||||| ||||||||||
                                   TCT  ATTTA GTAGAAACAA
                                     CC    C
GAM1052  GNA11    3'  GAAATAAAAACCATTTGTTAAA 27653         T  ATC
                                   GAAATAAA AT   TTTGTTAAA
                                   |||||||| ||   |||||||||
                                   CTTTATTT TG   AAACAATTT
                                        T  GT_
GAM1052  BIRC2    5'  TAAACTCTATCTTTGTTAAA   27654      A_
                                   TAAAT  TATCTTTGTTAAA
                                   |||||  ||||||||||||||
                                   ATTTG  ATAGAAACAATTT
                                      AG
GAM1052  C6orf5   3'  AGAAGAAAATGTCTCTGTTAA  27655     AT    ATA
                                   AGAA  AAAT   TCTTTGTTAA
                                   ||||  ||||   ||||||||||
                                   TCTT  TTTA   AGAGACAATT
                                     CT    C__
GAM1052  FLJ10961 3'  AGAGGTAAATGCATCTTTGTT  27652     AA    A
                                   AGA  TAAAT TATCTTTGTT
                                   |||  ||||| ||||||||||
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                                TCT  ATTTA GTAGAAACAA
                                  CC    C
GAM1052  GTF3C3    3'  AAAAATAAATACACTGTTTGTT 27656            C_
              A                   AGAAATAAATATAT  TTTGTTA
                                  ||||||||||||||  |||||||
                                  TTTTTATTTATGTG  AAACAAT
                                        AC
GAM1052  KIAA0828  3'  AAATAAATATACTCTGCTTTGT 27657          ____
              TA                   AAATAAATATAT   CTTTGTTA
                                  ||||||||||||   ||||||||
                                  TTTATTTATATG   GAAACAAT
                                        AGAC
GAM1052  KIAA1462  3'  AGAAATATAGTCACTTTGTTAA 27658        AATATAT
              A                   AGAAATA      CTTTGTTAAA
                                  |||||||      ||||||||||
                                  TCTTTAT      GAAACAATTT
                                     ATCAGT_
GAM1052  MGC15504  3'  GAAATAAATATTTCCCCA    27659          A   TT
                                  GAAATAAATAT TCT  G
                                  |||||||||||  |||  |
                                  CTTTATTTATA AGG  T
                                        A   GG
GAM1052  MYT1L     3'  AGAAATAGATATACCCCCA    27660        A       TT
                                  AGAAATA ATATATCT  G
                                  |||||||  ||||||||  |
                                  TCTTTAT TATATGGG  T
                                     C       GG
GAM1052  LOC153020 3'  GAAATAAATATCTTTGATTAA  27661        AT       _
                                  GAAATAA  ATATCTTTG TTAA
                                  |||||||  |||||||| ||||
                                  CTTTATT  TATAGAAAC AATT
                                     __        T
GAM1052  LOC201115 3'  GAAATATATACACCTTTG     27662        A
                                  GAAATA ATATATCTTTG
                                  ||||||  ||||||||||
                                  CTTTAT TATGTGGAAAC
                                     A
GAM1052  LOC56965  5'  AGAAATAAGGATATCATGCTTT 27663         AT    ____
              GTTA                   AGAAATAA  ATATC    TTTGTTA
                                  ||||||||  |||||    |||||||
                                  TCTTTATT  TATAG    AAACAAT
                                     CC     TACG
GAM1053  AKAP2     3'  CCAGATCCATGAGTCA      27666       AG       C
                                  CCAGA  TTTATGAG CA
                                  |||||  ||||||||  ||
                                  GGTCT  AGGTACTC GT
                                     __       A
GAM1053  BACH2     3'  CCAGAAATTGCACTTCCA     27667          _  GAG
                                  CCAGAAGTT TAT   CCA
                                  |||||||||  |||   |||
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                                GGTCTTTAA GTG   GGT
                                     C   AA_
GAM1053  BCRP2    3'  CCAGGAGTCATAAGCCA     27668      A    T
                                CCAG AGTT ATGAGCCA
                                |||| |||| ||||||||
                                GGTC TCAG TATTCGGT
                                  C   _
GAM1053  CAMP     3'  CCAGAAGCCTGAGCCA      27669         TA
                                CCAGAAGTT  TGAGCCA
                                |||||||||  |||||||
                                GGTCTTCGG  ACTCGGT
                                    __
GAM1053  CANX     3'  CCGGAGCTCACGTGCCA     27670    A  A      A
                                CC GA GTTTATG GCCA
                                || || ||||||| ||||
                                GG CT CGAGTGC CGGT
                                 C  _      A
GAM1053  CYP4F3   3'  CCAGAAATTTATCCA       27671           GAG
                                CCAGAAGTTTAT   CCA
                                ||||||||||||   |||
                                GGTCTTTAAATA   GGT
                                    ____
GAM1053  CYP8B1   3'  TGAGAAGTTTGGAGACCA    27672   C       AT  _
                                C AGAAGTTT  GAG CCA
                                | ||||||||  ||| |||
                                A TCTTCAAA  CTC GGT
                                 C       C_  T
GAM1053  DBN1     3'  CCAGAGCCCACGAGCCA     27673      A
                                CCAGA GTTTATGAGCCA
                                ||||| ||||||||||||
                                GGTCT CGGGTGCTCGGT
                                  _
GAM1053  DBN1     3'  CCAGAGCCCACGAGCCA     27673      A
                                CCAGA GTTTATGAGCCA
                                ||||| ||||||||||||
                                GGTCT CGGGTGCTCGGT
                                  _
GAM1053  DLEC1    3'  CCAGAACATGAGCCA       27674       GTT
                                CCAGAA   TATGAGCCA
                                ||||||   |||||||||
                                GGTCTT   GTACTCGGT
                                   ____
GAM1053  EDN2     3'  CCACAAGCCCTGGCCA      27675     G     A  A
                                CCA AAGTTT TG GCCA
                                ||| |||||| || ||||
                                GGT TTCGGG AC CGGT
                                  G     _ _
GAM1053  HGD      5'  CCAGAGGATATAAAGCCA     27676      A TT    _
                                CCAGA G  TATGA GCCA
                                ||||| |  ||||| ||||
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                                GGTCT C  ATATT CGGT
                                  _ CT    T
GAM1053  HYAL1    5'  CCAGAAATCCTGGCAGCCA   27677         ATG_
                                CCAGAAGTTT   AGCCA
                                ||||||||||   |||||
                                GGTCTTTAGG   TCGGT
                                     ACCG
GAM1053  INSM1    3'  CCAGCAGTTCACAAGCCA    27678     A     TG
                                CCAG AGTTTA  AGCCA
                                |||| ||||||  |||||
                                GGTC TCAAGT  TCGGT
                                  G     GT
GAM1053  JUP      3'  CCAGAAGCTCAAGCCA      27679         AT
                                CCAGAAGTTT  GAGCCA
                                ||||||||||  ||||||
                                GGTCTTCGAG  TTCGGT
                                     __
GAM1053  NDUFV3   5'  CCAGAAGTCTGAAGTCA     27680         AT   C
                                CCAGAAGTTT  GAG CA
                                ||||||||||  ||| ||
                                GGTCTTCAGA  TTC GT
                                     C_   A
GAM1053  OAS3     3'  CCAAAAGTTACAGTGGGGCCA 27681         TA__  A_
                                CCAGAAGTT   TG  GCCA
                                |||||||||   ||  ||||
                                GGTTTTCAA   AC  CGGT
                                     TGTC  CC
GAM1053  PHKA2    3'  CCTGGAAGACCATGAGCCA   27682    A_   T
                                CC  GAAG TTATGAGCCA
                                ||  |||| ||||||||||
                                GG  CTTC GGTACTCGGT
                                 AC    T
GAM1053  PRKR     3'  CAGAAGTTGCAGTGAGCCA   27683        _ _
                                CAGAAGTT TA TGAGCCA
                                |||||||| || |||||||
                                GTCTTCAA GT ACTCGGT
                                     C  C
GAM1053  RPA2     3'  CCTAGAAGCCCCCTGGCCA   27684    _      A_  A
                                CC AGAAGTTT  TG GCCA
                                || ||||||||  || ||||
                                GG TCTTCGGG  AC CGGT
                                 A       GG  _
GAM1053  SLC24A1  5'  CCATGAAGCCCAGCCA     27685    _     ATG
                                CCA GAAGTTT   AGCCA
                                ||| |||||||   |||||
                                GGT CTTCGGG   TCGGT
                                 A      ___
GAM1053  SORCS3   3'  TGAGAGGTTCACAAAGAGCCA 27686   C   A     ___
                                C AGA GTTTAT   GAGCCA
                                | ||| ||||||   ||||||
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                                A TCT CAAGTG   CTCGGT
                                 C   C     TTT
GAM1053  SPARC    3'  CCAAAAGTTTGAACCA      27687         TA
                                CCAGAAGTT  TGAGCCA
                                |||||||||  |||||||
                                GGTTTTCAA  ACTTGGT
                                     __
GAM1053  SRP14    3'  CCAGGAGTATATAACCA     27688      A  T    G
                                CCAG AGT TATGA CCA
                                |||| ||| ||||| |||
                                GGTC TCA ATATT GGT
                                  C  T    _
GAM1053  SVIL     3'  CCAGAGTCCATGCCA       27689       A     GA
                                CCAGA GTTTAT  GCCA
                                ||||| ||||||  ||||
                                GGTCT CAGGTA  CGGT
                                  _     __
GAM1053  SVIL     3'  CCAGAGTCCATGCCA       27689       A     GA
                                CCAGA GTTTAT  GCCA
                                ||||| ||||||  ||||
                                GGTCT CAGGTA  CGGT
                                  _     __
GAM1053  TCF8     3'  CCTGAGCCATGAGCCA      27691     A  A   T
                                CC GA GTT ATGAGCCA
                                || || ||| ||||||||
                                GG CT CGG TACTCGGT
                                 A  _  _
GAM1053  TCF8     3'  CCATGAGCCATGAGCCA     27690      GA    T
                                CCA  AGTT ATGAGCCA
                                |||  |||| ||||||||
                                GGT  TCGG TACTCGGT
                                  AC   _
GAM1053  AD7C-NTP 3'  CCAGAAGTTTGAGACCA     27692          TA   _
                                CCAGAAGTT  TGAG CCA
                                |||||||||  |||| |||
                                GGTCTTCAA  ACTC GGT
                                     __   T
GAM1053  ALLC     5'  CCAAAAGCGATGGCCA      27693        TT   A
                                CCAGAAGT  ATG GCCA
                                ||||||||  ||| ||||
                                GGTTTTCG  TAC CGGT
                                     C_  _
GAM1053  BAGE     5'  CCAGAGTGAGACGAGCCA    27694       A  TT_
                                CCAGA GT   ATGAGCCA
                                ||||| ||   ||||||||
                                GGTCT CA   TGCTCGGT
                                  _ CTC
GAM1053  C20orf18 3'  CCACGAAGCTCCCTGAGC    27695     _      A_
                                CCA GAAGTTT  TGAGC
                                ||| |||||||  |||||
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                                GGT CTTCGAG  ACTCG
                                  G      GG
GAM1053  C20orf18  3'  CCACGAAGCTCCCTGAGC    27695    _      A_
                                CCA GAAGTTT  TGAGC
                                ||| |||||||  |||||
                                GGT CTTCGAG  ACTCG
                                  G      GG
GAM1053  COLEC12   3'  CCAGAAGTTTGAAACCA     27696         AT
                                CCAGAAGTTT  GAGCCA
                                ||||||||||  ||||||
                                GGTCTTCAAA  TTTGGT
                                      C_
GAM1053  FHOD2     3'  CCAAGAAGATAAGCCA      27697     _   TTT
                                CCA GAAG   ATGAGCCA
                                ||| ||||   ||||||||
                                GGT CTTC   TATTCGGT
                                  T   ___
GAM1053  FLJ10081  3'  CCAGAAGTTTCCAGGAGTCA  27698         AT__   C
                                CCAGAAGTTT    GAG CA
                                ||||||||||    ||| ||
                                GGTCTTCAAA    CTC GT
                                      GGTC   A
GAM1053  FLJ10287  3'  CCAAAGTTTAATGAGGCCA   27699      A    _   _
                                CCAGA GTTTA TGAG CCA
                                ||||| ||||| |||| |||
                                GGTTT CAAAT ACTC GGT
                                   _    T   C
GAM1053  FLJ20312  5'  CAGAAGTTTTCATGGGCC    27700        __    A
                                CAGAAGT  TTATG GCC
                                |||||||  ||||| |||
                                GTCTTCA  AGTAC CGG
                                    AA    C
GAM1053  FLJ20335  3'  CCAAAAGCCTGGCCA       27701         TA  A
                                CCAGAAGTT  TG GCCA
                                |||||||||  ||  ||||
                                GGTTTTCGG  AC CGGT
                                      __  _
GAM1053  FLJ20356  3'  CCAGAAAATGAGCCA       27702        TTT
                                CCAGAAG   ATGAGCCA
                                |||||||   ||||||||
                                GGTCTTT   TACTCGGT
                                     ____
GAM1053  FLJ22529  5'  CCAGAGCTGACAGCCA      27703      A   T  G
                                CCAGA GTT AT AGCCA
                                ||||| ||| || |||||
                                GGTCT CGA TG TCGGT
                                   _  C  _
GAM1053  GBTS1     3'  CCAGAAGCTACTGCCA      27704         T  GA
                                CCAGAAGTT AT  GCCA
                                |||||||||  ||  ||||
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                                GGTCTTCGA TG  CGGT
                                     _ A_
GAM1053  GFR      3'  CCAGAAATTAAACAATGAGTCA 27705         T____     C
                                CCAGAAGTT     ATGAG CA
                                |||||||||     ||||| ||
                                GGTCTTTAA     TACTC GT
                                     TTTGT    A
GAM1053  GTPBP2   3'  CCAGGTTTGATGAGCCA     27706      AA   _
                                CCAG  GTTT ATGAGCCA
                                ||||  |||| ||||||||
                                GGTC  CAAA TACTCGGT
                                  __   C
GAM1053  H2BFQ    3'  CCAAAAGCCCTTAGCCA     27707          ATG
                                CCAGAAGTTT   AGCCA
                                ||||||||||   |||||
                                GGTTTTCGGG   TCGGT
                                     AA_
GAM1053  HSPC055  5'  CCTAAGAATTATGAGCCA    27708    AG   T_
                                CC  AAG  TTATGAGCCA
                                ||  |||  ||||||||||
                                GG  TTC  AATACTCGGT
                                 A_   TT
GAM1053  HUMAGCGB 5'  CCGGAAATTCACGTAGCCA   27709    A        _
                                CC GAAGTTTATG AGCCA
                                || |||||||||| |||||
                                GG CTTTAAGTGC TCGGT
                                 C         A
GAM1053  IL18BP   5'  CCAAAGTTCAGTGGCCA     27710      A    _ A
                                CCAGA GTTTA TG GCCA
                                ||||| ||||| || ||||
                                GGTTT CAAGT AC CGGT
                                  _    C  _
GAM1053  KCNH4    3'  CCAGAAATCCAGAGCCA     27711          T
                                CCAGAAGTTTA GAGCCA
                                |||||||||||  ||||||
                                GGTCTTTAGGT CTCGGT
                                     _
GAM1053  KIAA0350 3'  CCACGAAGCATGAGTCA     27712    _    TT    C
                                CCA GAAGT  ATGAG CA
                                |||  |||||  ||||| ||
                                GGT CTTCG  TACTC GT
                                  G    __    A
GAM1053  KIAA0737 3'  CCAGAATCTATGCCA       27713       G    GA
                                CCAGAA TTTAT  GCCA
                                ||||||  |||||  ||||
                                GGTCTT AGATA  CGGT
                                     _    __
GAM1053  KIAA1243 3'  CCAAAAGTCTTCAGCCA     27714          ATG
                                CCAGAAGTTT   AGCCA
                                ||||||||||   |||||
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                                GGTTTTCAGA   TCGGT
                                      AG_
GAM1053  KIAA1254  3'  CCAGAAATCTAGAAGTCA    27715          T   C
                                CCAGAAGTTTA GAG CA
                                |||||||||| ||| ||
                                GGTCTTTAGAT TTC GT
                                       C   A
GAM1053  KIAA1287  3'  CAGAAGTTGCAGTGAGCCA   27683        _ _
                                CAGAAGTT TA TGAGCCA
                                |||||||| || |||||||
                                GTCTTCAA GT ACTCGGT
                                     C  C
GAM1053  KIAA1372  5'  CCAGAAGCTTTGGCTCCA    27716          A  AG_
                                CCAGAAGTTT TG   CCA
                                |||||||||| ||   |||
                                GGTCTTCGAA AC   GGT
                                       _  CGA
GAM1053  MGC16386  3'  CCAGAGGCCATGAGCCA     27717       A   T
                                CCAGA GTT ATGAGCCA
                                ||||| ||| ||||||||
                                GGTCT CGG TACTCGGT
                                   C   _
GAM1053  MGC17303  3'  CCACAAGTCCTCCTGAGCCA   27718     G    TA__
                                CCA AAGTT    TGAGCCA
                                ||| |||||    |||||||
                                GGT TTCAG    ACTCGGT
                                  G    GAGG
GAM1053  MGC3113   3'  CCAGAAGTTTGAGACCA     27692         TA   _
                                CCAGAAGTT  TGAG CCA
                                |||||||||  |||| |||
                                GGTCTTCAA  ACTC GGT
                                       __   T
GAM1053  MGC4251   3'  CCAGAAATTTGGACAAATGAGC 27719          _______
                                CCAGAAGTTT     ATGAGC
                                ||||||||||     ||||||
                                GGTCTTTAAA     TACTCG
                                       CCTGTT
GAM1053  moblak    3'  CCAGGAGCCTGGGAGCCA    27720      A    AT
                                CCAG AGTTT  GAGCCA
                                |||| |||||  ||||||
                                GGTC TCGGA  CTCGGT
                                   C    CC
GAM1053  MSTP032   3'  CCAGAAGCATGAGTCA      27721        TT    C
                                CCAGAAGT  ATGAG CA
                                ||||||||  ||||| ||
                                GGTCTTCG  TACTC GT
                                       __    A
GAM1053  NK4       5'  CCAAAAGTTCAAGGAGCCA   27722          T_
                                CCAGAAGTTTA  GAGCCA
                                ||||||||||  ||||||
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                                GGTTTTCAAGT  CTCGGT
                                      TC
GAM1053  NY-REN-25 3'  CAGAAATTACCTATGAGTCA  27723        ___     C
                                CAGAAGTT   TATGAG CA
                                ||||||||   |||||| ||
                                GTCTTTAA   ATACTC GT
                                     TGG     A
GAM1053  P115     3'  CCAAAGTTTAGAGTCCA     27724       A    T  _
                                CCAGA GTTTA GAG CCA
                                ||||| ||||| ||| |||
                                GGTTT CAAAT CTC GGT
                                  _    _  A
GAM1053  PP1628   5'  CAGAAGCTGCACTGGCCA    27725         _  GA
                                CAGAAGTT TAT  GCCA
                                |||||||| |||  ||||
                                GTCTTCGA GTG  CGGT
                                     C   AC
GAM1053  PPIL2    3'  CCAGGTGGTTCACAGCCA    27726      AA_     G
                                CCAG   GTTTAT AGCCA
                                ||||   |||||| |||||
                                GGTC   CAAGTG TCGGT
                                  CAC     _
GAM1053  PRO1163  3'  CCAGACAGCTGGAGCCA     27727       _   TAT
                                CCAGA AGTT   GAGCCA
                                ||||| ||||   ||||||
                                GGTCT TCGA   CTCGGT
                                   G    C__
GAM1053  PRO1163  3'  CCAAAAGCCCTAGAGTCA    27728          AT   C
                                CCAGAAGTTT  GAG CA
                                ||||||||||  ||| ||
                                GGTTTTCGGG  CTC GT
                                      AT   A
GAM1053  PRO2730  3'  TAAGAAGGCCATGAGCCA    27729   C    TT
                                C AGAAG  TATGAGCCA
                                | |||||  |||||||||
                                A TCTTC  GTACTCGGT
                                 T    CG
GAM1053  PTD002   3'  TAAGAAGTGATAAGCCA     27730   C     TT
                                C AGAAGT  ATGAGCCA
                                | ||||||  ||||||||
                                A TCTTCA  TATTCGGT
                                 T     C_
GAM1053  RNF24    3'  CCAGAAGTATGGGCCA      27731        TT   A
                                CCAGAAGT  ATG GCCA
                                ||||||||  ||| ||||
                                GGTCTTCA  TAC CGGT
                                     __  C
GAM1053  SIAT8C   5'  CCAAAAGCTGAGGCCA      27732        TTA   _
                                CCAGAAGT   TGAG CCA
                                ||||||||   |||| |||
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                                GGTTTTCG   ACTC GGT
                                    ___    C
GAM1053  SPRY4    3'  CCAGAAGTTTGAGACCA     27692         TA   _
                                CCAGAAGTT  TGAG CCA
                                |||||||||  |||| |||
                                GGTCTTCAA  ACTC GGT
                                    __    T
GAM1053  TRIP3    3'  CCTGAAACATGAGCCA      27733    A    TT
                                CC GAAG  TATGAGCCA
                                || ||||  |||||||||
                                GG CTTT  GTACTCGGT
                                 A   __
GAM1053  LOC125268 3'  CCAGAGTCCTCTGGCCA     27734      A   A_  A
                                CCAGA GTTT  TG GCCA
                                ||||| ||||  || ||||
                                GGTCT CAGG  AC CGGT
                                   _    AG  _
GAM1053  LOC129566 5'  CCAGAAGCTCCCTGCAGC    27735          A_  _
                                CCAGAAGTTT  TG AGC
                                ||||||||||  || |||
                                GGTCTTCGAG  AC TCG
                                     GG  G
GAM1053  LOC133418 3'  CCAGGAAACCATGAGCCA    27736      A  T
                                CCAG AG TTATGAGCCA
                                |||| || ||||||||||
                                GGTC TT GGTACTCGGT
                                  C  T
GAM1053  LOC143689 3'  CCAGTAGTTCATGCCA      27737      A      GA
                                CCAG AGTTTAT  GCCA
                                |||| |||||||  ||||
                                GGTC TCAAGTA  CGGT
                                  A      __
GAM1053  LOC144308 5'  CCAGGGATTTATACGCCA    27738      AA      A
                                CCAG  GTTTATG GCCA
                                ||||  ||||||| ||||
                                GGTC  TAAATAT CGGT
                                  CC       G
GAM1053  LOC144583 3'  CCACGAGGCTGTGTGTGAGCCA 27739     _  A   TA___
                                CCA GA GTT     TGAGCCA
                                ||| || |||     |||||||
                                GGT CT CGA     ACTCGGT
                                 G  C   CACAC
GAM1053  LOC145622 3'  CAGAAGTTGCAGTGAGCC     27740         _  _
                                CAGAAGTT TA TGAGCC
                                |||||||| || ||||||
                                GTCTTCAA GT ACTCGG
                                     C  C
GAM1053  LOC145758 5'  CCAAAGAGTCTATGGGCCA    27741       _       A
                                CCAGA AGTTTATG GCCA
                                ||||| |||||||| ||||
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                                GGTTT TCAGATAC CGGT
                                   C       C
GAM1053  LOC146346 5'  CAGAAGTTGCAGTGAGCC    27740        _ _
                                CAGAAGTT TA TGAGCC
                                |||||||| || ||||||
                                GTCTTCAA GT ACTCGG
                                     C  C
GAM1053  LOC146783 5'  CCAGGAGTTTGAGACCA     27742     A    TA   _
                                CCAG AGTT  TGAG CCA
                                |||| ||||  |||| |||
                                GGTC TCAA  ACTC GGT
                                  C    __    T
GAM1053  LOC147093 3'  CCAGAAGCTCAGCCA       27743          ATG
                                CCAGAAGTTT   AGCCA
                                ||||||||||   |||||
                                GGTCTTCGAG   TCGGT

                                      ____
GAM1053  LOC147136 3'  CCAAAAGCTGTGGCCA      27744         TA  A
                                CCAGAAGTT  TG GCCA
                                |||||||||  || ||||
                                GGTTTTCGA  AC CGGT
                                     C_ _
GAM1053  LOC147525 3'  CCGAAGTTTAAGCTCA      27745    A     TA    _
                                CC GAAGTT  TGAGC CA
                                || ||||||  ||||| ||
                                GG CTTCAA  ATTCG GT
                                 _     __     A
GAM1053  LOC148918 5'  TAAGAAGTAAATAAGCCA    27746   C     TT
                                C AGAAGT  ATGAGCCA
                                | ||||||  ||||||||
                                A TCTTCA  TATTCGGT
                                 T     TT
GAM1053  LOC149606 3'  CCAGAGTGAAATGAGCCA    27747      A  TT_
                                CCAGA GT   ATGAGCCA
                                ||||| ||   ||||||||
                                GGTCT CA   TACTCGGT
                                   _ CTT
GAM1053  LOC150580 3'  CCAGAAATCAGAAAGCCA    27748         TAT
                                CCAGAAGTT   GAGCCA
                                |||||||||   ||||||
                                GGTCTTTAG   TTCGGT
                                     TCT
GAM1053  LOC153339 5'  CCAGAAATTAGAGCCA      27749         TAT
                                CCAGAAGTT   GAGCCA
                                |||||||||   ||||||
                                GGTCTTTAA   CTCGGT
                                     T__
GAM1053  LOC159199 5'  CCACAAGTTTACGTGGCC    27750     G       A_
                                CCA AAGTTTATG  GCC
                                ||| |||||||||  |||
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                                GGT TTCAAATGC  CGG
                                  G        AC
GAM1053  LOC160414 5'  CCACGAAGTCATGGCCA     27751     _     T   A
                                CCA GAAGTT ATG GCCA
                                ||| |||||| ||| ||||
                                GGT CTTCAG TAC CGGT
                                  G     _  _
GAM1053  LOC170082 3'  CAGAAGTCGATATTGAGCCA   27752         TA___
                                CAGAAGTT     TGAGCCA
                                ||||||||     |||||||
                                GTCTTCAG     ACTCGGT
                                     CTATA
GAM1053  LOC200448 5'  CCAAAAGTTATGAATCA     27753          T    GC
                                CCAGAAGTT ATGA  CA
                                ||||||||| ||||  ||
                                GGTTTTCAA TACT  GT
                                     _    TA
GAM1053  LOC203636 3'  CCAAAAGTCAGAGGCCA     27754          TAT   _
                                CCAGAAGTT   GAG CCA
                                |||||||||   ||| |||
                                GGTTTTCAG   CTC GGT
                                     T__   C
GAM1053  LOC220020 5'  CCAGAAGTACATGGAGCCA    27755         T    _
                                CCAGAAGT TATG AGCCA
                                |||||||| |||| |||||
                                GGTCTTCA GTAC TCGGT
                                     T    C
GAM1053  LOC221035 3'  CCAGAAGTTTGGGAGGCC     27756          AT   _
                                CCAGAAGTTT  GAG CC
                                ||||||||||  ||| ||
                                GGTCTTCAAA  CTC GG
                                      CC   C
GAM1053  LOC221576 3'  CCAGAAATTAAGCCA       27757         TTA
                                CCAGAAGT   TGAGCCA
                                ||||||||   |||||||
                                GGTCTTTA   ATTCGGT
                                     ____
GAM1053  LOC256167 5'  CCGAGAGTTTACAGCCA     27758    _  A     G
                                CC AGA GTTTAT AGCCA
                                || ||| |||||| |||||
                                GG TCT CAAATG TCGGT
                                 C  _     _
GAM1053  LOC257515 3'  CCAGAAATTAAGCCA       27757         TTA
                                CCAGAAGT   TGAGCCA
                                ||||||||   |||||||
                                GGTCTTTA   ATTCGGT
                                     ____
GAM1053  LOC257572 3'  CCAGAAATTAAGCCA       27757         TTA
                                CCAGAAGT   TGAGCCA
                                ||||||||   |||||||
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                                GGTCTTTA  ATTCGGT
                                    ___
GAM1053 LOC63875 3' CCAGAAGCATAAGCCA     27759       TT
                                CCAGAAGT  ATGAGCCA
                                ||||||||  ||||||||
                                GGTCTTCG  TATTCGGT
                                    __
GAM1053 LOC90072 3' CCAAAGGCATGAGCCA     27760      A  TT
                                CCAGA GT  ATGAGCCA
                                |||||  ||  ||||||||
                                GGTTT CG  TACTCGGT
                                  C  __
GAM1053 LOC90485 3' CAGAAGTTTCAGTGAGCC    27761        A__
                                CAGAAGTTT   TGAGCC
                                |||||||||   ||||||
                                GTCTTCAAA   ACTCGG
                                     GTC
GAM1053 LOC90591 3' CCAGAAGTTGTGAGACA     27762        TA   C
                                CCAGAAGTT  TGAG CA
                                |||||||||  ||||  ||
                                GGTCTTCAA  ACTC GT
                                     C_   T
GAM1053 LOC90906 5' CCAGAAATCCAAGCCA      27763        AT
                                CCAGAAGTTT  GAGCCA
                                ||||||||||  ||||||
                                GGTCTTTAGG  TTCGGT
                                    __
GAM1053 LOC90917 3' CCAGAAATGCATGGGCCA    27764        T   A
                                CCAGAAGT TATG GCCA
                                |||||||| |||| ||||
                                GGTCTTTA GTAC CGGT
                                     C   C
GAM1054 ABCC5    3' AGCGGCTGTGGGGAGGCG    27767        C  AA   G
                                AGCGGCTG TGG  GAGG CG
                                |||||||| |||  |||| ||
                                TCGCCGAC ACC  CTCC GC
                                    _  C_   _
GAM1054 ALDH3B1  3' GGCTGCTGTTGGAGAAGGCG  27768        GA__
                                GGCTGCTG   AGAGGGCG
                                ||||||||   ||||||||
                                CCGACGAC   TCTTCCGC
                                     AACC
GAM1054 AREG     5' AGCGGGTGTTGGAAGAGCG   27769      C  C     GG
                                AGCGG TG TGGAAGA  GCG
                                |||||  || |||||||  |||
                                TCGCC AC ACCTTCT  CGC
                                  C  A     __
GAM1054 BSN      3' GCGGCTGTGGGAAGTACG    27770       CT    AGG
                                GCGGCTG  GGAAG   GCG
                                |||||||  |||||   |||
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                                CGCCGAC  CCTTC   TGC
                                   AC    A__
GAM1054  CAPON    5'  GCGGCTGCAGGAAGGGGC    27771       T    A
                                GCGGCTGC GGAAG GGGC
                                |||||||| ||||| ||||
                                CGCCGACG CCTTC CCCG
                                     T    _
GAM1054  CCR9     5'  AGGGCTTGTGGAGGGCGA    27772    C   GC   AGA
                                AG GGCT  TGGA   GGGCGA
                                || ||||  ||||   ||||||
                                TC CCGA  ACCT   CCCGCT
                                 _   AC   ____
GAM1054  CDK2AP1  5'  GCGGCTGCGGGAGGCCAGGGCG 27773       T   AG__
                                GCGGCTGC GGA    AGGGCG
                                |||||||| |||    ||||||
                                CGCCGACG CCT    TCCCGC
                                     C   CCGG
GAM1054  CHST5    5'  AGGGCTGCTGGGAGAGC     27774    C       AA
                                AG GGCTGCTGG  GAGGGC
                                || |||||||||  ||||||
                                TC CCGACGACC  CTCTCG
                                 _       __
GAM1054  CHST6    5'  AGGGCTGCTGGGAGAGC     27774    C       AA
                                AG GGCTGCTGG  GAGGGC
                                || |||||||||  ||||||
                                TC CCGACGACC  CTCTCG
                                 _       __
GAM1054  CUL3     5'  GCGGCGGCGGGGGCGC      27775      T  T  AAGA    A
                                GCGGC GC GG    GGGCG C
                                ||||| || ||    ||||| |
                                CGCCG CG CC    CCCGC G
                                   C  _ _____    C
GAM1054  EN2      3'  GCGGCTGCTGGTGAGCA     27776          AAGA
                                GCGGCTGCTGG    GGGCG
                                ||||||||||    |||||
                                CGCCGACGACC    CTCGT
                                      A___
GAM1054  ENO2     5'  GCGGCTGCGGCTCCCGGGCGGC 27777       T  AAGA_    A
            G                    GCGGCTGC GG    GGGCG CG
                                 |||||||| ||    ||||| ||
                                 CGCCGACG CC    CCCGC GC
                                     _ GAGGG    C
GAM1054  FXYD7    5'  GGCTGCTGGATGCTTTGGCGGC 27778         AGAG__   A
            G                    GGCTGCTGGA     GGCG CG
                                 ||||||||||     |||| ||
                                 CCGACGACCT     CCGC GC
                                      ACGAAA    C
GAM1054  GLUL     5'  AGCTTTCTGGGAGAGGGCGA  27779     G_   A
                                GGCT  CTGG AGAGGGCGA
                                ||||  |||| |||||||||
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                                TCGA  GACC TCTCCCGCT
                                  AA    C
GAM1054  GRM7     5'  GCGGCGCTGGAGGGAAC     27780       T     AGA   C
                                GCGGC GCTGGA   GGG GAC
                                ||||| ||||||   ||| |||
                                CGCCG CGACCT   CCC TTG
                                  _     ___   _
GAM1054  HNF4A    3'  GGTGTTGGAGAAGACG      27781     C  C    A
                                GG TG TGGA GAGGGCG
                                || || |||| |||||||
                                CC AC ACCT CTTCTGC
                                 _ A   _
GAM1054  INSM1    5'  GCGGCTGCGGGACTCGCGTGGC 27782         T   AGAG___
              G                  GCGGCTGC GGA      GGCG
                                |||||||| |||       ||||
                                CGCCGACG CCT      CCGC
                                     C   GAGCGCA
GAM1054  IRF1     3'  AGGGCTGCTGGGGCTTGAGGG  27783    C       AA___
                                AG GGCTGCTGG    GAGGG
                                || |||||||||    |||||
                                TC CCGACGACC    CTCCC
                                 _       CCGAA
GAM1054  KCNQ1    3'  GCTGGCTGCTGGGACTGGGCG  27784    _       AAGA
                                GC GGCTGCTGG    GGGCG
                                || |||||||||    |||||
                                CG CCGACGACC    CCCGC
                                 A        CTGA
GAM1054  MPG      5'  GCTGCTGCTGGGGGCA      27785    G      AAGA
                                GC GCTGCTGG    GGGCG
                                || ||||||||    |||||
                                CG CGACGACC    CCCGT
                                 A      _____
GAM1054  NFKB1    5'  GCGGCTGCGGCCTCGGCGGCG  27786         T  AAGAG    A
                                GCGGCTGC GG    GGCG CG
                                |||||||| ||    |||| ||
                                CGCCGACG CC    CCGC GC
                                     _  GGAG_    C
GAM1054  PODXL    5'  GCGGCTGCGTCCTGGGCGGCG  27787         T GAAGA    A
                                GCGGCTGC G    GGGCG CG
                                |||||||| |    ||||| ||
                                CGCCGACG C    CCCGC GC
                                     _ AGGA_    C
GAM1054  PPP2R5B  5'  GGCTGCCCGTAGGGAGGGCGAC 27788        _____  AA
              G                  GGCTGCT   GG  GAGGGCGACG
                                |||||||   ||  ||||||||||
                                CCGACGG   CC  CTCCCGCTGC
                                    GCAT  __
GAM1054  RFNG     3'  GCGGCAGAGAGGGCGC      27789       TGCT  A      A
                                GCGGC   GGA GAGGGCG C
                                |||||   ||| ||||||| |
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                                CGCCG    TCT CTCCCGC G
                                  _____  _      C
GAM1054  SGT      3'  AGCGGCTGCAGGGCCGCGGCG  27790         T  AAGAG
                                AGCGGCTGC GG     GGCG
                                ||||||||| ||     ||||
                                TCGCCGACG CC     CCGC
                                     T  CGGCG
GAM1054  SNL      3'  AGGGCTCCCGGAGGGGGCGACG 27791     C    G     A A
                                AG GGCT CTGGA G GGGCGACG
                                || |||| ||||| | ||||||||
                                TC CCGA GGCCT C CCCGCTGC
                                  _   G    _ C
GAM1054  SOX12    3'  GGCTGTGCAGGAGGGGGCGACG 27792       CT__   A A
                                GGCTG    GGA G GGGCGACG
                                |||||    ||| | ||||||||
                                CCGAC    CCT C CCCGCTGC
                                   ACGT   _ C
GAM1054  SPTBN2   3'  AGTGGCAGCTGGAGTTACAGGG 27793     C   T     AG___
                                AG GGC GCTGGA     AGGG
                                || ||| ||||||     ||||
                                TC CCG CGACCT     TCCC
                                 A   T     CAATG
GAM1054  TRC8     5'  AGCGATGGCCGAGAGGGCGGCG 27794       CT    GA       A
                                AGCGG  GCTG  AGAGGGCG CG
                                |||||  ||||  |||||||| ||
                                TCGCT  CGGC  TCTCCCGC GC
                                   AC   __       C
GAM1054  AGPAT1   5'  CGGTGCCAAGGGGGCGACG   27795     C    GG   A
                                CGG TGCT  AAG GGGCGACG
                                ||| ||||  ||| ||||||||
                                GCC ACGG  TTC CCCGCTGC
                                  _   __   C
GAM1054  DCAMKL1  5'  AGCAGCTGCTGGAGCGCGGCG  27796            A AG_
                                AGCGGCTGCTGGA G   GGCG
                                |||||||||||| |   ||||
                                TCGTCGACGACCT C   CCGC
                                       _ GCG
GAM1054  DKFZP434J1813 5'  GCGGTGGGGTGGAGAGGGCG   27797      C  C__    A
                                GCGG TG   TGGA GAGGGCG
                                |||| ||   |||| |||||||
                                CGCC AC   ACCT CTCCCGC
                                  _  CCC   _
GAM1054  DKFZP434N014 5'  GGCTGCTGGAGCCCGGAGGTGG 27798          _______  AG
            CG                    GGCTGCTGGA     AG  GGCG
                                ||||||||||     ||  ||||
                                CCGACGACCT     TC  CCGC
                                      CGGGCC  CA
GAM1054  DKFZp761B0514 3'  GGCTGCTGGGAGGAGAGGA   27799          AA_    C
                                GGCTGCTGG   GAGGG GA
                                |||||||||   ||||| ||
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                                CCGACGACC   CTCTC CT
                                     CTC    _
GAM1054  DNAJC5   3'  GGCTGCTGAGGGCAA      27800       GGAA
                                GGCTGCT   GAGGGCGA
                                |||||||   ||||||||
                                CCGACGA   CTCCCGTT
                                    _____
GAM1054  ELOVL2   5'  AGCGGCTGTGGCGCGGCG   27801       C   AAGAG
                                AGCGGCTG TGG    GGCG
                                |||||||| |||    ||||
                                TCGCCGAC ACC    CCGC
                                    _  GCG__
GAM1054  EZF-2    3'  AGTGGCGCTGGGAGAGAG   27802    C  T    A
                                AG GGC GCTGG AGAGGG
                                || ||| ||||| ||||||
                                TC CCG CGACC TCTCTC
                                 A  _    C
GAM1054  FLJ12229 3'  GCAGCTGTTGGAGGAGCG   27803       C   A A
                                GCGGCTG TGGA G GGGCG
                                ||||||| |||| | |||||
                                CGTCGAC ACCT C CTCGC
                                    A   _ _
GAM1054  FLJ14126 5'  AGTGGCTGCTGTGGGACA   27804    C      GAAGA
                                AG GGCTGCTG    GGGCG
                                || ||||||||    |||||
                                TC CCGACGAC    CCTGT
                                 A       AC___
GAM1054  FLJ14950 3'  GCTGGCTGCTGGGAGGG    27805    _      AA
                                GC GGCTGCTGG  GAGGG
                                || |||||||||  |||||
                                CG CCGACGACC  CTCCC
                                 A       __
GAM1054  FLJ20195 3'  GCGGCGCTGGAGGCG      27806      T    AGAG
                                GCGGC GCTGGA   GGCG
                                ||||| ||||||   ||||
                                CGCCG CGACCT   CCGC
                                   _    _____
GAM1054  FLJ20397 3'  AGTGGCTGCGGGAGGAGCG   27807    C    T  A A
                                AG GGCTGC GGA G GGGCG
                                || |||||| ||| | |||||
                                TC CCGACG CCT C CTCGC
                                 A     C  _ _
GAM1054  FLJ20898 5'  AGTGGCTGCTGCAGGGACG   27808    C      GA  A
                                AG GGCTGCTG  AG GGGCG
                                || ||||||||  || |||||
                                TC CCGACGAC  TC CCTGC
                                 A       G_ _
GAM1054  FLJ22167 5'  AGGGCTGCTGGGAGAGC     27774    C      AA
                                AG GGCTGCTGG  GAGGGC
                                || |||||||||  ||||||
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                                TC CCGACGACC  CTCTCG
                                 _      __
GAM1054  FLJ25132  5'  GCGGCTGCCGGAGGGCGGCG  27809          AGA    A
                                GCGGCTGCTGGA  GGGCG CG
                                ||||||||||||  ||||| ||
                                CGCCGACGGCCT  CCCGC GC
                                      ___    C
GAM1054  FLJ30678  5'  GCCGCTGCTGGGGCAGGCG  27810   G      AAGA
                                GC GCTGCTGG   GGGCG
                                || ||||||||   |||||
                                CG CGACGACC   TCCGC
                                 G      CCG_
GAM1054  HRD1      3'  AGTGGCTGCTGGGTGAGACA  27811   C       AA   G
                                AG GGCTGCTGG  GAGG CG
                                || |||||||||  |||| ||
                                TC CCGACGACC  CTCT GT
                                 A       CA   _
GAM1054  KIAA0326  3'  AGGGCTGCTGGGAGAGAACA  27812   C       A
                                AG GGCTGCTGG AGAGGGCG
                                || ||||||||| ||||||||
                                TC CCGACGACC TCTCTTGT
                                 _       C
GAM1054  KIAA1030  3'  GGCTGCTGGGAGAATAGGG   27813         A  ___
                                GGCTGCTGG AGA   GGG
                                ||||||||| |||   |||
                                CCGACGACC TCT   CCC
                                      C   TAT
GAM1054  KIAA1033  3'  AGCAGCTGTTGGAGGTTAA   27814        C   AGA  GC
                                AGCGGCTG TGGA   GG  GA
                                |||||||| ||||   ||  ||
                                TCGTCGAC ACCT   CC  TT
                                     A   ___  AA
GAM1054  KIAA1169  5'  GCGGCTGCCTGGGGGCTGCTGG 27815     ____  AAGA_    A  III
            GCGGCGC                 TGCT   GG    GGGCG CG   C
                                ||||   ||    ||||| ||   |
                                ACGG   CC    CCCGC GC   G
                                  ACCC  GACGA    C  III
GAM1054  KIAA1255  3'  AGCAGCTGCTGGGGAGG     27816          AA
                                AGCGGCTGCTGG  GAGG
                                ||||||||||||  ||||
                                TCGTCGACGACC  CTCC
                                      C_
GAM1054  KIAA1511  5'  GCGGCTGCTCGGGCTGCGGCG  27817        _  AAGAG
                                GCGGCTGCT GG    GGCG
                                |||||||||  ||    ||||
                                CGCCGACGA CC    CCGC
                                     G  CGACG
GAM1054  KIAA1884  3'  AGCTGCTGTTGGAAGCAAAGTG 27818    G   C    ___  _
            GCG                   AGC GCTG TGGAAG   AG GGCG
                                ||| |||| ||||||   || ||||
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                                TCG CGAC ACCTTC   TC CCGC
                                  A   A     GTT  A
GAM1054  MGC15716  5'  GCGGCTGCAGCTTAGGCGGCG  27819        T  AAGA    A
                                GCGGCTGC GG    GGGCG CG
                                |||||||| ||    ||||| ||
                                CGCCGACG TC    TCCGC GC
                                     _  GAA_    C
GAM1054  MGC20460  5'  GGCTGCTGCTGAGGCGGCG   27820        GAA   __
                                GGCTGCTG   GAGG  GCG
                                ||||||||   ||||  |||
                                CCGACGAC   CTCC  CGC
                                     GA_   GC
GAM1054  MGC4737   5'  GGCCGCCAGGGAGGGCGA    27821       TG AA
                                GGCTGC  G  GAGGGCGA
                                ||||||  |  ||||||||
                                CCGGCG  C  CTCCCGCT
                                    GT C_
GAM1054  NCE2      5'  GCGGCTGCTGCGAGACG     27822         GAA   G
                                GCGGCTGCTG   GAGG CG
                                ||||||||||   |||| ||
                                CGCCGACGAC   CTCT GC
                                     G__   _
GAM1054  NMU       5'  GCGGCTGCGGGAGGCTCG    27823        T  AA   G_
                                GCGGCTGC GG  GAGG  CG
                                |||||||| ||  ||||  ||
                                CGCCGACG CC  CTCC  GC
                                     _ ___   GA
GAM1054  OPTC      3'  GCGGCTGCTGGAGAATGTGA   27824          A   GGC
                                GCGGCTGCTGGA GAG   GA
                                |||||||||||| |||   ||
                                CGCCGACGACCT CTT   CT
                                      _   ACA
GAM1054  PIP5K1C   3'  AGCGCTGCCCTCTTGGAGGGTG 27825      G    GGAA__    C
              A                  AGCG CTGCT     GAGGG GA
                                 |||| |||||     ||||| ||
                                 TCGC GACGG     CTCCC CT
                                   _    GAGAAC     A
GAM1054  PIP5K2B   5'  GCGGCGGCGAAAGAGGGGGGCG 27826      T  T    ___    A
              GCG                  GCGGC GC GGAAGA   GGGCG CG
                                   ||||| || ||||||   ||||| ||
                                   CGCCG CG CTTTCT   CCCGC GC
                                     C  _     CCC    C
GAM1054  PIP5K2B   5'  GCGGCGGCGAAAGAGGGGGGCG 27826      T  T    ___    A
              GCG                  GCGGC GC GGAAGA   GGGCG CG
                                   ||||| || ||||||   ||||| ||
                                   CGCCG CG CTTTCT   CCCGC GC
                                     C  _     CCC    C
GAM1054  PMX2B     3'  GGGTTGAAATGAGGGCGACG   27827    CTGC    _
                                GG    TGGAA GAGGGCGACG
                                ||    ||||| ||||||||||
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                                CC    ACTTT CTCCCGCTGC
                                 CA__     A
GAM1054  PP1201    3'  AGTGGCTGGCTGGAGAGA    27828    C    _    A
                                AG GGCTG CTGGA GAGG
                                || ||||| ||||| ||||
                                TC CCGAC GACCT CTCT
                                 A    C    _
GAM1054  RCD-8     3'  AGCGCCTGCTGGAAGGC     27829      G      AGA
                                AGCG CTGCTGGA   GGGC
                                |||| ||||||||   ||||
                                TCGC GACGACCT   TCCG
                                  G       ___
GAM1054  RER1      3'  GCGGCTGCTGGGGAAGGCG   27830          AA
                                GCGGCTGCTGG  GAGGGCG
                                ||||||||||  |||||||
                                CGCCGACGACC  CTTCCGC
                                       C_
GAM1054  SCGN      5'  AGCGCTGCTGGCCGTGGCG   27831      G      AAGAG
                                AGCG CTGCTGG    GGCG
                                |||| |||||||    ||||
                                TCGC GACGACC    CCGC
                                  _      GGCA_
GAM1054  ZNF-U69274 5'  GCGGCTGCAGGAGGAGCGGCG  27832        T   A   _
                                GCGGCTGC GGA GAG GGCG
                                |||||||| ||| ||| ||||
                                CGCCGACG CCT CTC CCGC
                                     T   C   G
GAM1054  LOC126364 5'  AGCGCTGCTGGGGTCGCTGGCG 27833      G      AAGAG__
                                AGCG CTGCTGG      GGCG
                                |||| |||||||      ||||
                                TCGC GACGACC      CCGC
                                  _      CCAGCGA
GAM1054  LOC133957 3'  GCTGCTGAAGGGTGACG     27834        GAA    C
                                GCTGCTG   GAGGG GACG
                                |||||||   ||||| ||||
                                CGACGAC   TTCCC CTGC
                                    ___     A
GAM1054  LOC145717 5'  AGCGGCTGCGGCTAAAGCGGCG 27835         T  A_   _
                                AGCGGCTGC GG  AGAG GGCG
                                ||||||||| ||  |||| ||||
                                TCGCCGACG CC  TTTC CCGC
                                     _ GA    G
GAM1054  LOC145989 3'  AGGGCTCCCCGAGGGGGCGACG 27836    C    G  G  A A
                                AG GGCT CT GA G GGGCGACG
                                || |||| || || | ||||||||
                                TC CCGA GG CT C CCCGCTGC
                                 _   G  G  _ C
GAM1054  LOC147057 5'  GCGGCTGCGGGGACCGGCG   27837        T_   AGAG
                                GCGGCTGC  GGA    GGCG
                                ||||||||  |||    ||||
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                                CGCCGACG  CCT    CCGC
                                     CC   GG__
GAM1054  LOC148018 5'  AGCGGCTGCTGGCAGAGG    27838           A
                                AGCGGCTGCTGG AGAGG
                                |||||||||||| |||||
                                TCGCCGACGACC TCTCC
                                       G
GAM1054  LOC148534 5'  GCCGAGCCGGGAGAGGGCGGCG 27839    __    A      A
                                GCT  GCTGG AGAGGGCG CG
                                |||  ||||| |||||||| ||
                                CGG  CGGCC TCTCCCGC GC
                                  CT    C      C
GAM1054  LOC148759 3'  AGGGCTGCTGGGGGTGGGCGA  27840    C       AAGA
                                AG GGCTGCTGG    GGGCGA
                                || |||||||||    ||||||
                                TC CCGACGACC    CCCGCT
                                 _       CCCA
GAM1054  LOC152009 3'  AGGGCTGCTGGAGGGAGGG    27841    C       A_
                                AG GGCTGCTGGA  GAGGG
                                || ||||||||||  |||||
                                TC CCGACGACCT  CTCCC
                                 _       CC
GAM1054  LOC153243 5'  AGTGGCTGCTGAAGGC      27842    C       AAGA
                                AG GGCTGCTGG    GGGC
                                || |||||||||    ||||
                                TC CCGACGACT    TCCG
                                 A       _____
GAM1054  LOC157349 5'  AGGGGCTGCTGGAGACGGGCG  27843    C       A _
                                AG GGCTGCTGGA GA GGGCG
                                || |||||||||| || |||||
                                TC CCGACGACCT CT CCCGC
                                 C         _ G
GAM1054  LOC163412 5'  AGGGGCTGCTGGGGCTCCAGAC 27844    C       AAGA__
           G                     AG GGCTGCTGG     GGGCG
                                || |||||||||     |||||
                                TC CCGACGACC     TCTGC
                                 C        CCGAGG
GAM1054  LOC196761 3'  GACCTGGTGGAGAGGGCGGCG  27845     GC_   A     A
                                GGCT   TGGA GAGGGCG CG
                                ||||   |||| ||||||| ||
                                CTGG   ACCT CTCCCGC GC
                                   ACC    _      C
GAM1054  LOC200470 5'  AGCGGCTGTTTGGGTCTGGCG  27846        C_   AAGAG
                                AGCGGCTG  TGG    GGCG
                                ||||||||  |||    ||||
                                TCGCCGAC  ACC    CCGC
                                     AA   CAGA_
GAM1054  LOC201780 5'  GCGGCGTCGGGGGCGC      27847       T C   AAGA    A
                                GCGGC G TGG    GGGCG C
                                ||||| | |||    ||||| |
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                                CGCCG C GCC    CCCGC G
                                  _ A  ____     C
GAM1054  LOC245727 5'  AGCGGCTGCGGCTAAAGCGGCG 27835         T  A_   _
                                AGCGGCTGC GG  AGAG GGCG
                                ||||||||| ||  |||| ||||
                                TCGCCGACG CC  TTTC CCGC
                                    _ GA    G
GAM1054  LOC255718 5'  AGCGGCTGCTGGCGGGGC    27848           AAGA
                                AGCGGCTGCTGG    GGGC
                                ||||||||||||    ||||
                                TCGCCGACGACC    CCCG
                                      GC__
GAM1054  LOC256160 5'  GCGGCGTCGGGGGCGC      27847       T C   AAGA    A
                                GCGGC G TGG    GGGCG C
                                ||||| | |||    ||||| |
                                CGCCG C GCC    CCCGC G
                                  _ A  ____     C
GAM1054  LOC91035  3'  AGCAGCTGCTGGGGC       27849           AAGAG
                                AGCGGCTGCTGG     GGC
                                ||||||||||||     |||
                                TCGTCGACGACC     CCG
                                                 _____
GAM1054  LOC92405  5'  AGTGGTTGCGGGGGCGCGGGCGA 27850    C  C   T  AAGA
           CG                     AG GG TGC GG    GGGCGACG
                                || || ||| ||    ||||||||
                                TC CC ACG CC    CCCGCTGC
                                 A  A   C  CGCG
GAM1054  LOC92912  5'  AGCGCTGCTGGAAAATGGCG   27851      G         G
                                AGCG CTGCTGGAAGA GGCG
                                |||| |||||||||| ||||
                                TCGC GACGACCTTTT CCGC
                                  _         A
GAM1055  ZNF236    3'  TGTGGACAGCTGAATCCTTATT 27854         ACAAAC  AA
                                TGTGGACA      AT  TTATT
                                ||||||||      ||  |||||
                                ACACCTGT      TA  AATAA
                                     CGACT_  GG
GAM1055  DKFZp434O0515 5'  TGTCGATAACAAACATCACTA  27855     G  C        A
                                TGT GA AACAAACAT ATTA
                                ||| || |||||||| ||||
                                ACA CT TTGTTTGTA TGAT
                                  G  A        G
GAM1055  RNB6      3'  TGCGGACAGTAAACCGTTTATT 27856         AC    ATAA
           A                     TGTGGACA  AAAC    TTATTA
                                ||||||||  ||||    ||||||
                                ACGCCTGT  TTTG    AATAAT
                                     CA    GCA_
GAM1056  HUNK      3'  GTTCGATCCTTGGAGAAAG   27859      A   GATATC
                                GTTC GTCC      GGAGAAAG
                                |||| ||||      ||||||||
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                                CAAG TAGG     CCTCTTTC
                                  C   AA____
GAM1056  DNAL4    3'  GTTCAGCCTGGGGTCAAGTTGG 27860        _______  TATC  A
                GGGAA                GTTCAGTC     CGA    GG GAA
                                |||||||||     |||    || |||
                                CAAGTCGG     GTT    CC CTT
                                    ACCCCA   CAAC  C
GAM1056  FLJ22555  5'  CTCAGCGGTGTCGGAGAAAG   27861       CCGATA
                                TTCAGT     TCGGAGAAAG
                                ||||||     ||||||||||
                                GAGTCG     AGCCTCTTTC
                                   CCAC__
GAM1056  FLJ22649  3'  ATTTAGTCTTTAAGTGGAGAAA 27862     C    CGATATC
                G                    GTT AGTC      GGAGAAAG
                                ||| ||||      ||||||||
                                TAA TCAG      CCTCTTTC
                                  A    AAATTCA
GAM1056  KIAA0222  3'  CGCTCAGTTCGAATGGTGGGAA 27863        C   TATC_  A
                                CGTTCAGT CGA     GG GAA
                                |||||||| |||     || |||
                                GCGAGTCA GCT     CC CTT
                                    A   TACCA  _
GAM1056  KIAA1580  5'  CGTTCGGTTCCAGGAGAAAG   27864      AG_    ATATC
                                CGTTC   TCCG    GGAGAAAG
                                |||||   ||||    ||||||||
                                GCAAG   AGGT    CCTCTTTC
                                   CCA   _____
GAM1056  PTPRT    3'  GTTCAGTCTATGACCTCAAAG  27865        C__   A
                                GTTCAGTC   GAT TCGGAG
                                ||||||||   ||| ||||||
                                CAAGTCAG   CTG AGTTTC
                                    ATA   G
GAM1056  RICH1    3'  GTTCGGTCTGCAAAGAAA    27866      A   CGATAT
                                GTTC GTC     CGGAGAAA
                                |||| |||     ||||||||
                                CAAG CAG     GTTTCTTT
                                  C   AC____
GAM1056  SKD3     3'  GCTCAGTCTGAGTAGGGGAG   27867        C  _  TC
                                GTTCAGTC GA TA  GGAG
                                |||||||| || ||  ||||
                                CGAGTCAG CT AT  CCTC
                                    A  C  CC
GAM1056  LOC152018 3'  TTCAGTCTGATATCAGAG    27868        C
                                TTCAGTC GATATCGGAG
                                ||||||| ||||||||||
                                AAGTCAG CTATAGTCTC
                                    A
GAM1056  LOC196337 3'  CGTTCAGTCTGGATAGAAG   27869         C_    TC
                                CGTTCAGTC  GATA  GGAG
                                |||||||||  ||||  ||||
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                                GCAAGTCAG  CTAT  CTTC
                                     AC   __
GAM1057  DAG1     5'  TCCAAGTTTGCTCAAGTCGATA 27872        CAC  A  ___
                                TCCAAGTT   TG CTC   TTGATA
                                ||||||||   || |||   ||||||
                                AGGTTCAA   AC GAG   AGCTAT
                                     ___  _   TTC
GAM1057  IL5RA    3'  TCCAAGTTCATGGTTCACTCC  27873         C  ____
                                TCCAAGTTCA TG    ACTCT
                                |||||||||| ||    |||||
                                AGGTTCAAGT AC    TGAGG
                                     _  CAAG
GAM1057  KCNK2    3'  TCCAAATTCTCTTGAT      27874         ACTGAC
                                TCCAAGTTC     TCTTGAT
                                |||||||||     |||||||
                                AGGTTTAAG     AGAACTA

                                     _______
GAM1057  MEOX2    3'  CATAGTTTGCTCTTGATA    27875    _   CAC  A
                                CA AGTT   TG CTCTTGATA
                                || ||||   || |||||||||
                                GT TCAA   AC GAGAACTAT
                                 A   ___  _
GAM1057  PLAG1    3'  TCTCAGTTCACTAATTTGAT  27876    CA        CTC
                                TC  AGTTCACTGA   TTGAT
                                ||  ||||||||||   |||||
                                AG  TCAAGTGATT   AACTA
                                 AG         A__
GAM1057  TPTE     5'  GTTCACTCCTGATAA       27877       TGAC
                                GTTCAC    TCTTGATAA
                                ||||||    |||||||||
                                CAAGTG    AGGACTATT

                                     _____
GAM1057  ZNF35    5'  CCTGAGTTCACTGGCTCT    27878    A_       A
                                CC  AGTTCACTG CTCT
                                ||  ||||||||| ||||
                                GG  TCAAGTGAC GAGA
                                 AC        C
GAM1057  C8orf13  3'  CAAGTTCATTGACATGTGA   27879         C    TCT
                                CAAGTTCA TGAC   TGA
                                |||||||| ||||   |||
                                GTTCAAGT ACTG   ACT
                                     A    TAC
GAM1057  DKFZP434J154 3'  CAAGTTCATTTGCTGCCTGA  27880         C_  A  _
                                CAAGTTCA  TG CT CTTGA
                                ||||||||  || || |||||
                                GTTCAAGT  AC GA GGACT
                                     AA  _  C
GAM1057  FLJ00024 5'  TCCGAGTCGCTGATGGCTTG  27881     A   T A    CT_
                                TCC AGT C CTGA   CTTG
                                ||| ||| | ||||   ||||
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                                AGG TCA G GACT   GAAC
                                  C   _ C    ACC
GAM1057  FLJ10898  5'  TCCAGTTTCACTGACTCT    27882      AG
                                TCCA  TTCACTGACTCT
                                ||||  ||||||||||||
                                AGGT  AAGTGACTGAGA
                                   CA
GAM1057  KIAA0252  3'  TCCAAGTTCATCATGATA    27883          CTGAC  T
                                TCCAAGTTCA    TC TGATA
                                ||||||||||    || |||||
                                AGGTTCAAGT    AG ACTAT
                                      _____  T
GAM1057  KIAA0391  3'  AAGTTCTCCAACTCTTGATAA  27884       A TG
                                AAGTTC C  ACTCTTGATAA
                                ||||||  |  ||||||||||
                                TTCAAG G  TGAGAACTATT
                                    A GT
GAM1057  KLF12     3'  CATGTTCACTGACTTTGCCTG  27885    A         ___
                                CA GTTCACTGACT   CTTG
                                ||  ||||||||||   ||||
                                GT CAAGTGACTGA   GGAC
                                 A          AAC
GAM1057  PRO1386   5'  TCCAAGTCACTGGCCTGGAT   27886        T    A T  T
                                TCCAAGT CACTG C CT GAT
                                |||||||  |||||  |  ||  |||
                                AGGTTCA GTGAC G GA CTA
                                     _    C _  C
GAM1057  TPIP      5'  GTTCACTCCTGATAA      27877        TGAC
                                GTTCAC    TCTTGATAA
                                ||||||    |||||||||
                                CAAGTG    AGGACTATT
                                     ____
GAM1057  WDR5B     3'  TCCAAGTTTTTTGGCCAACTTG 27887         CAC  A  __
                                TCCAAGTT   TG CT  CTTG
                                ||||||||   ||  ||  ||||
                                AGGTTCAA   AC GG  GAAC
                                     AAA  C  TT
GAM1057  ZNF294    3'  TCTGAGTTTCATAACCCTTGAT 27888    CA    _  C
              AA                  TC  AGTT CA TGACTCTTGATAA
                                  ||  |||| ||  ||||||||||||
                                  AG  TCAA GT ATTGGGAACTATT
                                   AC    A  _
GAM1057  LOC153886 3'  CCAGGTTCACTGTGGATA    27889     A       ACTCTT
                                CCA GTTCACTG      GATA
                                |||  ||||||||      ||||
                                GGT CAAGTGAC      CTAT
                                  C       AC____
GAM1057  LOC154215 3'  TCTGAGTTCCTGATAAGCCTGA 27890    CA     A    CT__
                                TC  AGTTC CTGA    CTTGA
                                ||  |||||  ||||    |||||
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                                AG  TCAAG GACT    GGACT
                                 AC     _    ATTC
GAM1057  LOC196202 5'  TCCAAGATTCCAGGTCTTGATA 27891       _   ACTGAC
              A                   TCCAAG TTC     TCTTGATAA
                                  |||||| |||     |||||||||
                                  AGGTTC AAG     AGAACTATT
                                     T   GTCC__
GAM1057  LOC199907 3'  TCCAAGTTCACCTGGACT    27892           __
                                  TCCAAGTTCACT  GACT
                                  ||||||||||||  ||||
                                  AGGTTCAAGTGG  CTGA
                                        AC
GAM1057  LOC203297 5'  TCCGAGTCGCTGATGGCTTG   27881     A   T A    CT_
                                  TCC AGT C CTGA   CTTG
                                  ||| ||| | ||||   ||||
                                  AGG TCA G GACT   GAAC
                                    C   _ C    ACC
GAM1057  LOC253019 3'  AAGTTCAACTCTTGAT      27893        CTG
                                  AAGTTCA   ACTCTTGAT
                                  |||||||   |||||||||
                                  TTCAAGT   TGAGAACTA
                                      ___
GAM1057  LOC254710 5'  TCCGCAGTACATTCTTGATAA  27894     A_   T  CTGAC
                                  TCC  AGT CA    TCTTGATAA
                                  |||  ||| ||    |||||||||
                                  AGG  TCA GT    AGAACTATT
                                    CG   T  A____
GAM1057  LOC56898  3'  CCAGGTTCACTGTGGATA    27889     A       ACTCTT
                                  CCA GTTCACTG     GATA
                                  ||| ||||||||     ||||
                                  GGT CAAGTGAC     CTAT
                                    C       AC____
GAM1058  FGF12     3'  CCAAATGCTAAGAGCAAGT    27897     T      A   TATG
                                  CCA ATGCTAA AGT    GAGT
                                  ||| ||||||| |||    ||||
                                  GGT TACGATT TCG    TTCA
                                    T      C  _____
GAM1058  TAF4      3'  CATGTGCCAAAAGTTATG    27898     A
                                  CAT TGCTAAAAGTTATG
                                  ||| ||||||||||||||
                                  GTA ACGGTTTTCAATAC
                                    C
GAM1058  TAP2      3'  CCATATGCAAAGGCACAAAG   27899        TA    T  TG
                                  CCATATGC  AAAG TA  GAG
                                  ||||||||  |||| ||  |||
                                  GGTATACG  TTTC GT  TTC
                                       __    C  GT
GAM1058  FLJ23416  3'  CCATATGTTGACAGGATGGAGT 27900        CTAAA  TT
              A                    CCATATG    AG  ATGGAGTA
                                   |||||||    ||  ||||||||
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                                GGTATAC    TC  TACCTCAT
                                    AACTG  C_
GAM1058  NSG-X     3'  ATATACTAGGCACTGGAGTA   27901        AAA  TA
                                ATATGCTA   GT  TGGAGTA
                                ||||||||   ||  |||||||
                                TATATGAT   CG  ACCTCAT
                                    C__  TG
GAM1058  LOC151610 3'  CATATGCTGGGAAGAACCTAGT 27902        AA_   TT  GG
                                CATATGCT   AAG  AT  AGT
                                ||||||||   |||  ||  |||
                                GTATACGA   TTC  TG  TCA
                                    CCC   T_  GA
GAM1058  LOC158402 5'  CATGGCTAAGAGCTATAGGT   27903     AT    A      A
                                CAT  GCTAA AGTTATGG GT
                                |||  ||||| |||||||| ||
                                GTA  CGATT TCGATATC CA
                                  C_    C       _
GAM1058  LOC158435 3'  TGATATGCTAAACAAGGGGT   27904    C        AGTTAT  A
                                C ATATGCTAAA     GG GT
                                | ||||||||||     || ||
                                A TATACGATTT     CC CA
                                 C        GTT___  C
GAM1058  LOC220827 3'  ATATGCTAAACAAAGGGTA    27905         AGTTAT  A
                                ATATGCTAAA     GG GTA
                                ||||||||||     || |||
                                TATACGATTT     CC CAT
                                     GTTT__  _
GAM1058  LOC253795 5'  TATGCTAAAAGTTTTCAAAGT  27906          AT_
                                TATGCTAAAAGTT   GGAGT
                                ||||||||||||   |||||
                                ATACGATTTTCAA   TTTCA
                                       AAG
GAM1059  ACTN1     3'  TCCCACACCAAAATGGACA   27909          ___
                                TCTCACACCAG   GGACA
                                ||||||||||   |||||
                                AGGGTGTGGTT   CCTGT
                                      TTA
GAM1059  C14orf1   3'  CTCTTAGCCTGGACAACATA   27910     ACA_  AG
                                CTC    CC  GGACAACATA
                                |||    ||  ||||||||||
                                GAG    GG  CCTGTTGTAT
                                  AATC  A_
GAM1059  DBH       3'  CCCACAGGGACAGCAT      27911       CCA     A
                                CTCACA   GGGACA CAT
                                ||||||   |||||| |||
                                GGGTGT   CCCTGT GTA
                                    ___      C
GAM1059  KIT       3'  TCAACAATTGGACAACATA   27912     _  CCAG
                                TCA CA    GGACAACATA
                                ||| ||    ||||||||||
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                                AGT GT    CCTGTTGTAT
                                  T  TAA_
GAM1059  MAGEA8   3'  CCTCACACCCAACAT      27913        AGGGA
                                TCTCACACC    CAACAT
                                |||||||||    ||||||
                                GGAGTGTGG    GTTGTA
                                           _____
GAM1059  MTMR3    3'  TCCCACGGGGGACAACAT    27914      ACCA
                                TCTCAC   GGGACAACAT
                                ||||||   ||||||||||
                                AGGGTG   CCCTGTTGTA
                                   CC__
GAM1059  RP42     3'  CTCACATCAACAACATA     27915      C  GGG
                                CTCACA CA   ACAACATA
                                |||||| ||   ||||||||
                                GAGTGT GT   TGTTGTAT
                                   A ___
GAM1059  SDC1     3'  TCTCACACGGGCTTCTCCAAC 27916       CA  A_____
                                TCTCACAC  GGG     CAAC
                                ||||||||  |||     ||||
                                AGAGTGTG  CCC     GTTG
                                     __  GAAGAG
GAM1059  SLC6A3   3'  CCTCACACAGACAGCAT     27917       CAG    A
                                TCTCACAC   GGACA CAT
                                ||||||||   ||||| |||
                                GGAGTGTG   TCTGT GTA
                                     ___    C
GAM1059  SMT3H1   3'  TCTTATACACGACAACATA   27918    C__   CAGG
                                TCT   ACAC   GACAACATA
                                |||   ||||   |||||||||
                                AGA   TGTG   CTGTTGTAT
                                  ATA   ____
GAM1059  TMEPAI   3'  TCCCACGCCAGGAACCAAC   27919      A      _
                                TCTCAC CCAGGGAC AAC
                                |||||| |||||||| |||
                                AGGGTG GGTCCTTG TTG
                                   C       G
GAM1059  AP3D1    3'  TCTACACGGCGGACAACATA  27920    C   CAG
                                TCT ACAC   GGACAACATA
                                ||| ||||   ||||||||||
                                AGA TGTG   CCTGTTGTAT
                                  _   CCG
GAM1059  ARG99    3'  TCTCCACCAAAATAACAATATA 27921     A     __    C
                                TCTC CACCAGG  GACAA ATA
                                |||| |||||||  ||||| |||
                                AGAG GTGGTTT  TTGTT TAT
                                  _      TA    A
GAM1059  FHOD2    3'  TCACATAAGCACAACATA    27922      CC   G
                                TCACA  AGG ACAACATA
                                |||||  ||| ||||||||
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                                AGTGT  TTC TGTTGTAT
                                  A_   G
GAM1059  FLJ11294  3'  TCTTCACAAAACAACAT     27923     _   CCAG
                                TCT CACA    GGACAACAT
                                ||| ||||    |||||||||
                                AGA GTGT    TTTGTTGTA
                                  A   ____
GAM1059  FLJ13456  3'  TCACAACACTACAACATA    27924      C  GGG
                                TCACA CA   ACAACATA
                                ||||| ||   ||||||||
                                AGTGT GT   TGTTGTAT
                                  T  GA_
GAM1059  FLJ14251  3'  TCTCTACCAAACAACATA    27925     AC   GG
                                TCTC  ACCA  GACAACATA
                                ||||  ||||  |||||||||
                                AGAG  TGGT  TTGTTGTAT
                                  A_   __
GAM1059  FLJ14957  3'  TCTCACACTGGGCCCCATA   27926        CA   ACAA
                                TCTCACAC  GGG   CATA
                                ||||||||  |||   ||||
                                AGAGTGTG  CCC   GTAT
                                    A_   GGG_
GAM1059  FLJ20574  3'  TCCCACAGGACAACAT      27927       CCAG
                                TCTCACA   GGACAACAT
                                |||||||   |||||||||
                                AGGGTGT   CCTGTTGTA
                                          ____
GAM1059  FLJ22056  5'  CCTCACACAGCAGCAT      27928       CAG  A  A
                                TCTCACAC   GG CA CAT
                                ||||||||   || || |||
                                GGAGTGTG   TC GT GTA
                                    ___  _  C
GAM1059  GMEB2     5'  TCTCCACATCCACACAACATA  27929     _  _  GGG
                                TCTC ACA CCA   ACAACATA
                                |||| ||| |||   ||||||||
                                AGAG TGT GGT   TGTTGTAT
                                  G   A   G__
GAM1059  KIAA0218  3'  TCTGCAGCACAGACAACATA   27930    CA  C  G
                                TCT  CA CA GGACAACATA
                                |||  || || ||||||||||
                                AGA  GT GT TCTGTTGTAT
                                  C_  C  G
GAM1059  KIAA0960  5'  TCTAACACCAGGGAACAA     27931     C        _
                                TCT ACACCAGGGA CAA
                                ||| |||||||||| |||
                                AGA TGTGGTCCCT GTT
                                  T         T
GAM1059  KIAA1766  3'  TCACACCCCGACAACAT      27932       AGG
                                TCACACC   GACAACAT
                                |||||||   ||||||||
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                                AGTGTGG  CTGTTGTA
                                   GG_
GAM1059  MAGEB2   3'  TCTCACACATTCTTGAATAACA 27933       CAG___  C
             TA                  TCTCACAC    GGA AACATA
                                 ||||||||    ||| |||||||
                                 AGAGTGTG    CTT TTGTAT
                                     TAAGAA  A
GAM1059  TTY7     5'  CCTCACACTAACCACAT    27934       CAGG  A
                                 TCTCACAC   GAC ACAT
                                 ||||||||   ||| ||||
                                 GGAGTGTG   TTG TGTA
                                     A___  G
GAM1059  YAP1     3'  ACATTAGGAACAAGGACATA  27935    CC     ___
                                 ACA  AGGGACA  ACATA
                                 |||  |||||||  |||||
                                 TGT  TCCTTGT  TGTAT
                                   AA     TCC
GAM1059  LOC158563 5'  CCACATTCAAAACAACAT   27936     CCA
                                 TCACA  GGGACAACAT
                                 |||||  ||||||||||
                                 GGTGT  TTTTGTTGTA
                                    AAG
GAM1059  LOC200830 3'  TCACAAGAACAGCATA     27937     CCA    A
                                 TCACA  GGGACA CATA
                                 |||||  ||||||  ||||
                                 AGTGT  TCTTGT GTAT
                                    ___    C
GAM1059  LOC253443 3'  CACACCAACACAAAGCATA   27938       G G   __
                                 CACACCA G ACAA  CATA
                                 |||||||  |  ||||  ||||
                                 GTGTGGT T TGTT  GTAT
                                     _ G   TC
GAM1059  LOC255870 5'  TCCCACACGCAAACCAACAT  27939        _   GA
                                 TCTCACAC CAGG  CAACAT
                                 ||||||||  ||||  ||||||
                                 AGGGTGTG GTTT  GTTGTA
                                     C   G_
GAM1059  LOC51246  3'  CTCACGCACACACACAACATA  27940     __ _  GGG
                                 CTCAC  AC CA   ACAACATA
                                 |||||  ||  ||   ||||||||
                                 GAGTG  TG GT   TGTTGTAT
                                    CG  T  G__
GAM1060  IL16     3'  GTTTGTGTCAGCTCTAACT   27943       G  AT   C
                                 GTTTGTGT GG  CTC AACT
                                 ||||||||  ||  ||| ||||
                                 CAAACACA TC  GAG TTGA
                                     G  __   A
GAM1060  ITPKB    3'  GTTTTGTGCCCCAAC      27944     G   GGAT
                                 GTTT TGTG   CTCCAAC
                                 ||||  ||||   |||||||
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                                CAAA ACAC    GGGGTTG
                                  _   _____
GAM1060  GLUC     5'  GTCTACTGGGATCTTCA     27945       G       C
                                GTTTGT TGGGATCT CA
                                |||||| |||||||| ||
                                CAGATG ACCCTAGA GT
                                   _       A
GAM1060  MFN1     3'  GTTTTGTATTTTCTCCAACT   27946     G   GGA
                                GTTT TGTG   TCTCCAACT
                                |||| ||||   |||||||||
                                CAAA ACAT   AGAGGTTGA
                                  _   AAA
GAM1060  MGC13125 3'  GTCTGTGTGGGCTCCAA     27947          AT
                                GTTTGTGTGGG  CTCCAA
                                ||||||||||  ||||||
                                CAGACACACCC  GAGGTT
                                      __
GAM1060  MGC3123   5'  TAGTTTGTTTAGGTTCTAACT  27948        G   A   CC
                                TAGTTTGT TGGG TCT  AACT
                                |||||||| |||| |||  ||||
                                ATCAAACA ATCC AGA  TTGA
                                    A   A  __
GAM1060  ZDHHC7    3'  GTTTGTGTAGGTTCCA      27949          ATC
                                GTTTGTGTGGG   TCCA
                                ||||||||||   ||||
                                CAAACACATCC   AGGT
                                    A__
GAM1060  LOC144587 5'  TAGTTTGTTTAGGTTCTAACT  27948        G   A   CC
                                TAGTTTGT TGGG TCT  AACT
                                |||||||| |||| |||  ||||
                                ATCAAACA ATCC AGA  TTGA
                                    A   A  __
GAM1060  LOC165229 5'  TAGCTTGTGTGGCTC       27950          GAT
                                TAGTTTGTGTGG   CTC
                                ||||||||||   |||
                                ATCGAACACACC   GAG
                                      ___
GAM1060  LOC219649 5'  CAGTTTGCCCATCTCTGACT   27951        G GGG    CA
                                TAGTTTGT T   ATCTC  ACT
                                |||||||| |   |||||  |||
                                GTCAAACG G   TAGAG  TGA
                                    G ___     AC
GAM1061  RRAD     3'  CTGTCCATGACCATGAGGT    27954       AT  T
                                CTGTCCA  TG CTGTGAGGT
                                |||||||  || |||||||||
                                GACAGGT  AC GGTACTCCA
                                   __ T
GAM1061  BM-002    3'  TACCTGTTTGTGTTGTGAGGT  27955       CCAA   C_
                                TACCTGT   TTGT  TGTGAGGT
                                |||||||   ||||  ||||||||
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                                ATGGACA   AACA  ACACTCCA
                                   ____   CA
GAM1061  CREB-H   3'  CTGTCTGTTTGTCTGGGT   27956     CAA     TGA
                                CTGTC   TTGTCTG   GGT
                                |||||   |||||||   |||
                                GACAG   AACAGAC   CCA
                                  ACA     ___
GAM1061  CREB-H   3'  CTGTCTGTTTGTCTGGGT   27956     CAA     TGA
                                CTGTC   TTGTCTG   GGT
                                |||||   |||||||   |||
                                GACAG   AACAGAC   CCA
                                  ACA     ___
GAM1061  DCOHM    3'  CTGTCTATGGATGGTGAGGT  27957     CAAT  TC  _
                                CTGTC    TG  TG TGAGGT
                                |||||    ||  || ||||||
                                GACAG    AC  AC ACTCCA
                                  AT__   CT  C
GAM1061  HCGIV.9  5'  TGTCTGTCTGCGACGT     27958     CAAT       G
                                TGTC    TGTCTGTGA GT
                                ||||    ||||||||| ||
                                ACAG    ACAGACGCT CA
                                  ____        G
GAM1061  KHDRBS1  3'  TACTTGTCTGTTGTGG     27959     C   CAAT   C    A
                                TAC TGTC    TGT TGTG G
                                ||| ||||    ||| |||| |
                                ATG ACAG    ACA ACAC C
                                  A   ____  _   _
GAM1061  KIAA1719 3'  TACTTGTTGATTGTCTGC    27960     C   CCA
                                TAC TGT   ATTGTCTGT
                                ||| |||   |||||||||
                                ATG ACA   TAACAGACG
                                  A   AC_
GAM1061  TRIP-Br2 3'  CTGTCCAATTGTTTAGAT    27961          CTGTG
                                CTGTCCAATTGT    AGGT
                                ||||||||||||    ||||
                                GACAGGTTAACA    TCTA
                                      AA___
GAM1061  LOC118851 5'  CTGTGCAGTTGTGTGGAGGT   27962     C  A    C  T
                                CTGT CA TTGT TG GAGGT
                                |||| || |||| || |||||
                                GACA GT AACA AC CTCCA
                                  C  C    C  _
GAM1061  LOC136345 3'  CTGCTTGGCTGTCTGTGAGGT  27963      CCAA
                                CTGT    TTGTCTGTGAGGT
                                ||||    ||||||||||||
                                GACG    GACAGACACTCCA
                                  AACC
GAM1061  LOC149721 3'  TGCGTGCTTGTCTGTGGGGT   27964     CCAA       A
                                TGT    TTGTCTGTG GGT
                                |||    ||||||||| |||
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                                ACG    AACAGACAC CCA
                                  CACG        C
GAM1061  LOC155032 5'  CTGCTTGGCTGTCTGTGAGGT  27963      CCAA
                                CTGT    TTGTCTGTGAGGT
                                ||||    |||||||||||||
                                GACG    GACAGACACTCCA
                                  AACC
GAM1061  LOC197342 3'  CCTGCCTTGTCTGTGGGGT    27965       CAA        A
                                CCTGTC   TTGTCTGTG GGT
                                ||||||   ||||||||| |||
                                GGACGG   AACAGACAC CCA
                                   ___         C
GAM1061  LOC199733 3'  TACCTGTCTAATTTTCTGT    27966         C    G
                                TACCTGTC AATT TCTGT
                                |||||||| |||| |||||
                                ATGGACAG TTAA AGACA
                                     A    A
GAM1062  DKFZP434H132 5'  TGGCATGCTCCACAGAAC     27969          G_  C
                                TGGCATGCT  AC GAAC
                                |||||||||  || ||||
                                ACCGTACGA  TG CTTG
                                     GG  T
GAM1063  ABCC5     3'  ATATAGGCTATGTACAGAATTA 27972      C        __  AG  C
           TAT                    ATA AGGCTATG  CA  GT ATAT
                                ||| ||||||||  ||  || ||||
                                TAT TCCGATAC  GT  TA TATA
                                  A       AT  CT  A
GAM1063  EGFL5     5'  TGACAGGCTATGTTCACAT    27973    T        CAAGG
                                A ACAGGCTATG     TCATAT
                                | ||||||||||     ||||||
                                A TGTCCGATAC     AGTGTA
                                 C         A____
GAM1063  ITGA9     3'  TGACAGGCTAGTGATCAGGTCA 27974    T       _  CA_
           T                     A ACAGGCTA TG   AGGTCAT
                                | ||||||||  ||   |||||||
                                A TGTCCGAT AC   TCCAGTA
                                 C       C  TAG
GAM1063  MYCN      3'  TATACAGGCAGTGTAAGA     27975          TA  C
                                TATACAGGC  TG AAGG
                                |||||||||  || ||||
                                ATATGTCCG  AC TTCT
                                     TC  A
GAM1063  SH3BP5    3'  TATACAGGCTGTGACAGAAT   27976          A  _  AG
                                TATACAGGCT TG CA  GT
                                ||||||||||  ||  ||  ||
                                ATATGTCCGA AC GT  TA
                                     C  T  CT
GAM1063  ZNF8      3'  TACACAGGTGGGTAGGTTATAT 27977         CTATGCA    C
                                TATACAGG      AGGT ATAT
                                ||||||||      |||| ||||
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                                ATGTGTCC      TCCA TATA
                                    ACCCA__    A
GAM1063 ARFGEF2  3' TATACAGCTATGTTCAGT    27978       G    CAA
                                TATACAG CTATG   GGT
                                ||||||| |||||   |||
                                ATATGTC GATAC   TCA
                                    _    AAG
GAM1063 EIF5     3' AGGACACTGAGGTCATAT    27979     C   GCA
                                AGG TAT   AGGTCATAT
                                ||| |||   |||||||||
                                TCC GTG   TCCAGTATA
                                  T   AC_
GAM1063 PDZD2    3' TACAGGCTATTTCATA      27980          GCAAGG
                                TACAGGCTAT     TCATA
                                ||||||||||     |||||
                                ATGTCCGATA     AGTAT
                                     A_____
GAM1064 CABC1    5' GAGCGTCTGTTTGTGCTGCTT 27983      ATATAC
                                GAGTG     TTGTGCTGCTT
                                |||||     ||||||||||
                                CTCGC     AACACGACGAA
                                   AGACA_
GAM1064 EGLN2    5' GGGTAATAAACACTGCT     27984    A     T  TTGT
                                GG GTGATA AC    GCTGCT
                                || |||||| ||    ||||||
                                CC CATTAT TG    TGACGA
                                 _     T  _____
GAM1064 DOCK3    3' GGAGTGATTGGCAAGCTGCTTA 27985        ATACTTGT
                                GGAGTGAT       GCTGCTTA
                                ||||||||       ||||||||
                                CCTCACTA       CGACGAAT
                                     ACCGTT__
GAM1064 EPI64    3' GGAGTGATGGGTTGGGGGCTTA 27986        ATAC   TGCT
                                GGAGTGAT    TTG    GCTTA
                                |||||||    |||    |||||
                                CCTCACTA    AAC    CGAAT
                                     CCC_   CCC_
GAM1064 FLJ22569 5' GGATGATAATTTGCTGCTT   27987     G    TACTTG
                                GGA TGATA     TGCTGCTT
                                ||| |||||     ||||||||
                                CCT ACTAT     ACGACGAA
                                  _     TAA___
GAM1064 KIAA0532 3' GGTGGTGTAGTCCCAGCTGCTT 27988    A_   A  TA    T
                                GG  GTG TA  CTTG GCTGCTT
                                ||  ||| ||  |||| |||||||
                                CC  CAC AT  GGGT CGACGAA
                                 AC   _  CA   _
GAM1064 LOC123872 5' GGGTAATATAAAGCTTGTGCTG 27989    A       ___
             CTT                   GG GTGATATA   CTTGTGCTGCTT
                                || ||||||||   ||||||||||||
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                                CC CATTATAT   GAACACGACGAA
                                 _      TTC
GAM1065  B3GALT2   3'  TTTGGCAGACATGCATCTTA   27992     A      _  G
                                TTTG CAGACATG AT TTG
                                |||| |||||||| || |||
                                AAAC GTCTGTAC TA AAT
                                  C       G  G
GAM1065  MAGEL2    3'  TTTGGCAGATACGAAACCAAGT 27993     A    C    TG TG
           T                     TTTG CAGA ATGA  T  GGTT
                                |||| |||| ||||  |  ||||
                                AAAC GTCT TGCT  G  TCAA
                                  C    A    TT GT
GAM1065  DKFZP586F1318 5'  TTGATAGACAATTGGGTT    27994     C    TGAT
                                TTGA AGACA    GTTGGGTT
                                |||| |||||    ||||||||
                                AACT TCTGT    TAACCCAA
                                  A    ____
GAM1065  FLJ14327  3'  TTTGACAGACAGATGCTG    27995          T
                                TTTGACAGACA GATGTTG
                                |||||||||||| |||||||
                                AAACTGTCTGT CTACGAC
                                           _
GAM1065  ICT1      3'  TTTGACAACATGGTGACTG    27996        A    A  _
                                TTTGACAG CATG TG TTG
                                |||||||| |||| || |||
                                AAACTGTT GTAC AC GAC
                                     _   C  T
GAM1065  KIAA0574  3'  TTTGTCAGGCATGATGGCT    27997     A   A     GTTG
                                TTTG CAG CATGAT    GGTT
                                |||| ||| ||||||    ||||
                                AAAC GTC GTACTA    CCGA
                                  A  C     ____
GAM1065  KIAA1303  3'  TTTGACAGGTGGTGATTTTG   27998        ACA_   G
                                TTTGACAG    TGAT TTG
                                ||||||||    |||| |||
                                AAACTGTC    ACTA AAC
                                     CACC    A
GAM1065  TRIP10    3'  TGACAGGTAGGACTGGGTT    27999       ACAT   GT
                                TGACAG    GAT  TGGGTT
                                ||||||    |||  ||||||
                                ACTGTC    CTG  ACCCAA
                                   CATC   __
GAM1065  LOC143384 3'  TTTGACAACATGGTCACACAGT 28000        A    AT   ___
           T                     TTTGACAG CATG  GTTG   GGTT
                                |||||||| ||||  ||||   ||||
                                AAACTGTT GTAC  CAGT   TCAA
                                     _   __    GTG
GAM1065  LOC149722 5'  TTTGGCAGACATGGGGTC    28001     A      ATGTT
                                TTTG CAGACATG    GGGTT
                                |||| ||||||||    |||||
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                                AAAC GTCTGTAC    CCCAG
                                  C      _____
GAM1065  LOC150517 5'  TTTGGCAAACATGGTTTG    28002     A      ATG
                                TTTG CAGACATG   TTG
                                |||| ||||||||   |||
                                AAAC GTTTGTAC   AAC
                                  C      CA_
GAM1065  LOC221931 3'  TTTGACAGATGAGGACGTTG   28003       CAT_
                                TTTGACAGA   GATGTTG
                                |||||||||   |||||||
                                AAACTGTCT   CTGCAAC
                                     ACTC
GAM1066  ARHGEF12  3'  AGGAAAGAAAAATTTTGTAGA  28006    T   CC
                                AG GAAG  GAAAAATTTTGTAGA
                                || ||||  ||||||||||||||
                                TC CTTT  CTTTTTAAAACATCT
                                 _   __
GAM1066  DCTN1     3'  AGTGAAGCTGAACGGGGCAG   28007       C   AAATTTT
                                AGTGAAGC GAA      GTAG
                                |||||||| |||      ||||
                                TCACTTCG CTT      CGTC
                                    A   GCCC___
GAM1066  DCTN1     3'  AGTGAAGCTGAACGGGGCAG   28007       C   AAATTTT
                                AGTGAAGC GAA      GTAG
                                |||||||| |||      ||||
                                TCACTTCG CTT      CGTC
                                    A   GCCC___
GAM1066  LFG       3'  AGTGAAGCTAGAAGAGATGTGG 28008       C_   AAATTT   A
           A                     AGTGAAGC  GAA     TGT GA
                                |||||||| |||     ||| ||
                                TCACTTCG  CTT     ACA CT
                                    AT   CTCT__   C
GAM1066  MMP19     5'  AGTGGGGCCGGTAGCCCTCGTA 28009     AA    AAAAA
           GA                    AGTG  GCCG    TTTTGTAGA
                                ||||  ||||    |||||||||
                                TCAC  CGGC    GGAGCATCT
                                  CC    CATCG
GAM1066  MMP19     5'  AGTGGGGCCGGTAGCCCTCGTA 28009     AA    AAAAA
           GA                    AGTG  GCCG    TTTTGTAGA
                                ||||  ||||    |||||||||
                                TCAC  CGGC    GGAGCATCT
                                  CC    CATCG
GAM1066  SLC38A2   3'  AGTGAAACTGAAAACATTAG   28010       C    ATTTTG
                                AGTGAAGC GAAAA     TAG
                                |||||||| |||||     |||
                                TCACTTTG CTTTT     ATC
                                    A    GTA___
GAM1066  ABCC13    3'  AGTAAGGCCTTTTTGTAG    28011      A   GAAAAA
                                AGTGA GCC     TTTTGTAG
                                ||||| |||     ||||||||
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                                TCATT CGG     AAAACATC
                                  C   A_____
GAM1066 COVA1    3' GTGGAGCTGACCTATTTGTAGA 28012     A   C  AAAAT
                                GTG AGC GA    TTTGTAGA
                                ||| ||| ||    ||||||||
                                CAC TCG CT    AAACATCT
                                  C   A  GGAT_
GAM1066 CTCFL    3' AGCTTTAAATTTTGTAGA    28013     CGAA
                                AGC    AAATTTTGTAGA
                                |||    ||||||||||||
                                TCG    TTTAAAACATCT
                                  AAA_
GAM1066 DIS3     3' AATGGAGCTGAAAAATTCC    28014      A   C
                                AGTG AGC GAAAAATTTT
                                |||| ||| ||||||||||
                                TTAC TCG CTTTTTAAGG
                                  C   A
GAM1066 DKFZp761J139 5' AATGGAGCTGAAAAATTCC    28014      A   C
                                AGTG AGC GAAAAATTTT
                                |||| ||| ||||||||||
                                TTAC TCG CTTTTTAAGG
                                  C   A
GAM1066 FLJ10876  3' AGTGAACTGAAAAATTTCTTAG 28015       G C         G
             A                   AGTGAA C GAAAAATTTT TAGA
                                ||||||  | ||||||||||  ||||
                                TCACTT G CTTTTTAAAG ATCT
                                   _ A         A
GAM1066 KIAA0186  3' AGTGAAGCCTGGAAGTGCCTCG 28016         __   AAA
                                AGTGAAGCC  GAA   TTTTG
                                |||||||||  |||   |||||
                                TCACTTCGG  CTT   GGAGC
                                     AC   CAC
GAM1066 KIAA1034  3' AGGAAGCCGAAAGAGATCTG   28017    T        AAT_
                                AG GAAGCCGAAA    TTTG
                                || ||||||||||    ||||
                                TC CTTCGGCTTT    AGAC
                                 _         CTCT
GAM1066 KIAA1332  3' AGTGAAGCAGAAGGAAACCCAG 28018        C   __     TTG
             A                   AGTGAAGC GAA  AAATT   TAGA
                                |||||||| |||  |||||   ||||
                                TCACTTCG CTT  TTTGG   GTCT
                                     T   CC    ___
GAM1066 MGC15476  5' GTGAATCTGGACCTCCTGTAGA 28019      GCC_  AAAA
                                GTGAA    GA    TTTTGTAGA
                                |||||    ||    |||||||||
                                CACTT    CT    AGGACATCT
                                   AGAC  GG__
GAM1066 MGC15705  5' AGAGAAGCCGATTTGTG     28020    T      AAAAT    A
                                AG GAAGCCGA    TTTGT G
                                || ||||||||    ||||| |
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                                TC CTTCGGCT     AAACA C
                                 T       _____     C
GAM1066  MRF2     5'  GTGGAATTGAAAAGCCTTGTAG 28021     _  GCC     A
                A                GTG AA   GAAAA TTTTGTAGA
                                 ||| ||   ||||| |||||||||
                                 CAC TT   CTTTT GGAACATCT
                                   C  AA_     C
GAM1066  TCL6     3'  ATGAGGCCCATTTTGTAG     28022      A   GAAAA
                                 GTGA GCC     ATTTTGTAG
                                 |||| |||     |||||||||
                                 TACT CGG     TAAAACATC
                                   C   G____
GAM1066  TCL6     3'  ATGAGGCCCATTTTGTAG     28022      A   GAAAA
                                 GTGA GCC     ATTTTGTAG
                                 |||| |||     |||||||||
                                 TACT CGG     TAAAACATC
                                   C   G____
GAM1066  ZTL1     3'  AGTGAGGCCAAAAAACCACAAG 28023       A         TTGT
                A                AGTGA GCCGAAAAATT    AGA
                                 ||||| ||||||||||    |||
                                 TCACT CGGTTTTTTGG    TCT
                                    C          TGT_
GAM1066  LOC148760 3'  AGTGGAGCCAAAAAATTTTG   28024      A
                                 AGTG AGCCGAAAAATTTTG
                                 |||| ||||||||||||||
                                 TCAC TCGGTTTTTTAAAAC
                                   C
GAM1066  LOC151405 5'  AGTAAGGCTGAGAGGCCTTGTA 28025       A  C  AAAA
                GA               AGTGA GC GA    TTTTGTAGA
                                 ||||| || ||    |||||||||
                                 TCATT CG CT    GGAACATCT
                                    C  A  CTCC
GAM1066  LOC162333 5'  ATGAAGCTGGTGGTTTGTAGA  28026        CGAAAAAT
                                 GTGAAGC       TTTGTAGA
                                 |||||||       ||||||||
                                 TACTTCG       AAACATCT
                                     ACCACC__
GAM1066  LOC203080 3'  AGCGAGGCTGTATTTTGTAG   28027      A  CGAAAA
                                 AGTGA GC     ATTTTGTAG
                                 ||||| ||     |||||||||
                                 TCGCT CG     TAAAACATC
                                    C  ACA___
GAM1066  LOC221943 5'  AGTGAAGCAGGAAGGTTTAGCA 28028         C_   AAA   T
                G                 AGTGAAGC  GAA   TTT GTAG
                                  ||||||||  |||   ||| ||||
                                  TCACTTCG  CTT   AAA CGTC
                                      TC   CC_   T
GAM1066  LOC222057 3'  GTAGAGGCCGGGCCTGTAGA   28029    _  A    AAAAAT
                                 GT GA GCCG     TTTGTAGA
                                 || || ||||     ||||||||
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                                CA CT CGGC     GGACATCT
                                 T  C   CC____
GAM1066  LOC254413 5'  AGTGATGGAAGTTTTGTAGA  28030      AGCC   AAA
                                AGTGA   GAA   TTTTGTAGA
                                |||||   |||   |||||||||
                                TCACT   CTT   AAAACATCT
                                  AC__   C__
GAM1067  KIAA1829  3'  AAAATATAATCCAAATTA    28033         A
                                AAAATATAAT CCGAATTA
                                |||||||||| ||||||||
                                TTTTATATTA GGTTTAAT
                                          _
GAM1067  LOC221399 5'  AATATTAAATACCGAATTA   28034      __
                                AATAT  AATACCGAATTA
                                |||||  ||||||||||||
                                TTATA  TTATGGCTTAAT
                                  AT
GAM1068  CLCN4     3'  TATGCTCCAATAGTTCAT    28037      AA   T
                                TATGCT  AAT AGTTCAT
                                ||||||  ||| |||||||
                                ATACGA  TTA TCAAGTA
                                   GG   _
GAM1068  FACL6     3'  TAATATTGCTAGACAGTTCAT  28038      A    AAAT
                                TAATAT TGCTA   TAGTTCAT
                                |||||| |||||   ||||||||
                                ATTATA ACGAT   GTCAAGTA
                                   _    CT__
GAM1068  GABRB3    3'  ATATATGCTGAGAAGTTCAC   28039        AAAATT
                                ATATATGCT     AGTTCAT
                                |||||||||     |||||||
                                TATATACGA     TCAAGTG
                                     CTCT__
GAM1068  GABRB3    3'  ATATATGCTGAGAAGTTCAC   28039        AAAATT
                                ATATATGCT     AGTTCAT
                                |||||||||     |||||||
                                TATATACGA     TCAAGTG
                                     CTCT__
GAM1068  ACYP2     3'  ATATATGCTGTAATGTTCAT   28040        AA   TA
                                ATATATGCT  AAT  GTTCAT
                                |||||||||  |||  ||||||
                                TATATACGA  TTA  CAAGTA
                                     CA   __
GAM1068  KIAA0923  3'  TAATATTTGCTAAAATAAG    28041      A       T
                                TAATAT TGCTAAAAT AG
                                |||||| ||||||||| ||
                                ATTATA ACGATTTTA TC
                                   A        T
GAM1069  PRKY      3'  GTGCATCTGCCATAATGAC    28044       _      G
                                GTGCATC GCCATGG TGAC
                                ||||||| ||||||| ||||
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                                CACGTAG CGGTATT ACTG
                                    A     _
GAM1069 PSTPIP2  3' GTGTGTCGCCGTGGAAACTC  28045    CA    A   TGAC
                                GTG  TCGCC TGGG   GACTC
                                |||  ||||| ||||   |||||
                                CAC  AGCGG ACCT   TTGAG
                                  AC    C  ____
GAM1069 LOC56926 3' GTGCATCCATCATGACGACTC 28046      CG   GG
                                GTGCAT  CCAT  GTGACGACTC
                                ||||||  ||||  ||||||||||
                                CACGTA  GGTA  TACTGCTGAG
                                   __   G_
GAM1070 HDAC9-PENDING 3' AAATATAAATATTTTAAT   28049
                                AAATATAAATATTTTAAT
                                ||||||||||||||||||
                                TTTATATTTATAAAATTA

GAM1071 BCL6    5' TCGGACTTTACCACTGCTACG 28052         A  TTCCC
                                TCGGACTTTG CCG    ACG
                                |||||||||| |||    |||
                                AGCCTGAAAT GGT    TGC
                                      _  GACGA
GAM1071 LANCL1   5' AACCCCGTTCCCACG      28053     TTGA
                                GACT   CCGTTCCCACG
                                ||||   ||||||||||
                                TTGG   GGCAAGGGTGC
                                  ____
GAM1071 NPY2R    5' CCTGGACCTCGCGTT      28054    C      AC
                                CCT GGACTTTG  CGTT
                                ||| ||||||||  ||||
                                GGA CCTGGAGC  GCAA
                                  _      __
GAM1071 FLJ13841 5' CCTTGGACTCTGGCTGTCC   28055    C      ACC
                                CCT GGACTTTG   GTTC
                                ||| ||||||||   ||||
                                GGA CCTGAGAC   CAGG
                                  A       CGA
GAM1072 AIPL1    3' GATTTAAACAGATTACTT    28058    ___
                                GAT   AGCAGATTACTT
                                |||   ||||||||||||
                                CTA   TTGTCTAATGAA
                                  AAT
GAM1072 ESR1     3' TAATAGAGGCAGCAATTACTTA 28059      T  A    A
                                TAATA AG TAGCAG TTACTTA
                                ||||| || |||||| |||||||
                                ATTAT TC GTCGTT AATGAAT
                                   C  C    _
GAM1072 PCDH11X  3' TAACATAGATAGTAACCA    28060          CA
                                TAATATAGATAG  GATTA
                                ||||||||||||  |||||
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                                ATTGTATCTATC  TTGGT
                                      A_
GAM1072 PCDH11X  3' TAACATAGATAGTAACCA    28060          CA
                                TAATATAGATAG  GATTA
                                ||||||||||||  |||||
                                ATTGTATCTATC  TTGGT
                                      A_
GAM1072 PCDH11Y  3' TAACATAGATAGTAACCA    28060          CA
                                TAATATAGATAG  GATTA
                                ||||||||||||  |||||
                                ATTGTATCTATC  TTGGT
                                      A_
GAM1072 VSNL1    3' ATATAGATAGATATACTTAA  28061         CAGAT
                                ATATAGATAG    TACTTAA
                                ||||||||||    |||||||
                                TATATCTATC    ATGAATT
                                      TAT__
GAM1072 FLJ20445 3' TAGAGTGCAAACAGATTACTTA 28062      T____
                                TAGA    AGCAGATTACTTA
                                ||||    |||||||||||||
                                ATCT    TTGTCTAATGAAT
                                  CACGT
GAM1072 FLJ23045 3' TAATATTGATAGCAGCTCA   28063       A       A
                                TAATAT GATAGCAG TTA
                                |||||| |||||||| |||
                                ATTATA CTATCGTC AGT
                                    A       G
GAM1072 KIAA0318 3' TAGAGGCAGGGTTACTTAA   28064     TA   A_
                                TAGA  GCAG  TTACTTAA
                                ||||  ||||  ||||||||
                                ATCT  CGTC  AATGAATT
                                  C_   CC
GAM1072 PFDN4    3' TAATATAGAAACATAAAAGATT 28065       T  _____   A
            GCTTAA                ATATAGA AGCA    GATT CTTAA
                                |||||||  ||||    |||| |||||
                                TATATCT TTGT    CTAA GAATT
                                    _   ATTTT   C
GAM1072 ZF       3' GGATAAAGAGCAGATTACTT  28066   T    T
                                A ATAGA AGCAGATTACTT
                                | ||||| ||||||||||||
                                C TATTT TCGTCTAATGAA
                                 C    C
GAM1072 LOC51026 3' ATATAGACAGATACTTA    28067      ATA     T
                                ATATAG   GCAGAT ACTTA
                                ||||||   |||||| |||||
                                TATATC   TGTCTA TGAAT
                                    ___    _
GAM1073 HEPH     3' GCTGGGAGTGCACTACAGA   28070        A   C_
                                GCTGGGAGT CAC  CGGA
                                |||||||||  |||  ||||
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                                CGACCCTCA GTG  GTCT
                                     C   AT
GAM1073  HEPH     3'  GCTGGGAGTGCACTACAGA   28070         A   C_
                                GCTGGGAGT CAC  CGGA
                                ||||||||| |||  ||||
                                CGACCCTCA GTG  GTCT
                                     C   AT
GAM1073  HIF1A    5'  TCGCCGGGGTCCGGGCCC    28071         A  ACAC    A
                                TCGCTGGG GT    CCGG CCC
                                |||||||| ||    |||| |||
                                AGCGGCCC CA    GGCC GGG
                                     _ ____    C
GAM1073  IGFBP4   5'  CCTGGAGGACCCGGACCC    28072    G    TAC
                                CT GGAG   ACCCGGACCC
                                || ||||   ||||||||||
                                GG CCTC   TGGGCCTGGG
                                 A   C__
GAM1073  PDGFB    5'  TCGCTGGGGGGCAGGGGAGGAC 28073         A_   CACCC
              C                  TCGCTGGG  GTA    GGACC
                                |||||||  |||    |||||
                                AGCGACCC  CGT    CCTGG
                                     CC   CCCCT
GAM1073  SLIT3    5'  TCGCTGGGAGTGCCCAG     28074          ACA
                                TCGCTGGGAGT   CCCGG
                                ||||||||||   |||||
                                AGCGACCCTCA   GGGTC
                                      C__
GAM1073  ZNF76    3'  GCTGGGAGGGCAGGACAGGGCC 28075         TA  CCC   ____
                                GCTGGGAG  CA   GGAC   CC
                                ||||||||  ||   ||||   ||
                                CGACCCTC  GT   CCTG   GG
                                     CC  ___   TCCC
GAM1073  DDX36    5'  CCGCTGGAAATGGCGTCCGGGC 28076          ACAC_   A
              CCG                   TCGCTGGGAGT    CCGG CCCG
                                |||||||||||    |||| ||||
                                GGCGACCTTTA    GGCC GGGC
                                      CCGCA   C
GAM1073  EFNA2    3'  CGCTGGGAGTGCAACCGGCCCG 28077          A  C   A
                                CGCTGGGAGT CA CCGG CCCG
                                |||||||||| || |||| ||||
                                GCGACCCTCA GT GGCC GGGC
                                      C  T   _
GAM1073  KIAA1075 5'  GCTGGGAGTGTCAGCCTGCGGG 28078         A_  _  _____  GACC
              TC                   CTGGGAGT  CA CC    CG   C
                                ||||||||  || ||    ||   |
                                GACCCTCA  GT GG    GC   G
                                     CA  C  ACIII  CCAG
GAM1073  KIAA1887 5'  TCGCTGAGGAGGTAGCTCCGG  28079       _   _  CAC
                                TCGCTG GGAG TA   CCGG
                                |||||| |||| ||   ||||
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                                AGCGAC CCTC AT   GGCC
                                   T   C  CGA
GAM1073  phospho1  3'  ACTGGCTGTCCGGACCC     28080      GA  ACAC
                                GCTGG  GT   CCGGACCC
                                |||||  ||   ||||||||
                                TGACC  CA   GGCCTGGG
                                  GA  ____
GAM1073  WBSCR20A  5'  GCTGGAGTACACCAGCCC    28081      G      C  A
                                GCTGG AGTACACC GG CCC
                                ||||| |||||||| || |||
                                CGACC TCATGTGG TC GGG
                                  _      _ _
GAM1073  LOC125943 3'  TCACTGGGAGTACAAGA     28082           CCC
                                TCGCTGGGAGTACA   GGA
                                ||||||||||||||   |||
                                AGTGACCCTCATGT   TCT
                                     ___
GAM1073  LOC144193 5'  TCGCCGGGAGGCCACCGGG    28083         TA   C
                                TCGCTGGGAG  CACC GG
                                ||||||||||  |||| ||
                                AGCGGCCCTC  GTGG CC
                                    CG   C
GAM1073  LOC144245 5'  GCTGGGAGAGCGCGGATCCG   28084        TACACC   C
                                GCTGGGAG     CGGA CCG
                                ||||||||     |||| |||
                                CGACCCTC     GCCT GGC
                                   TCGC__    A
GAM1073  LOC157506 3'  TCGCTGGGAGGCAGACC     28085         TACACC
                                TCGCTGGGAG     CGGACC
                                ||||||||||     ||||||
                                AGCGACCCTC     GTCTGG
                                    C_____
GAM1073  LOC199990 3'  TCCCTCACACCTGGGCCC    28086    G  GGGAG     C  A
                                TC CT    TACACC GG CCC
                                || ||    |||||| || |||
                                AG GA    GTGTGG CC GGG
                                 G  _____     A  C
GAM1074  TMEM2     3'  TAAGTGAATAAAAATAGCACAT 28089         TTAAT    A
                                TGAGTGAAT    GATA CACAT
                                |||||||||    |||| |||||
                                ATTCACTTA    TTAT GTGTA
                                   TTT__    C
GAM1074  C20orf180 3'  TGGGTGAATCTGTGGCTGACAC 28090    A       AATGATA
            AT                   TG GTGAATTT      ACACAT
                                || ||||||||      ||||||
                                AC CACTTAGA      TGTGTA
                                 C       CACCGAC
GAM1074  FBP17     3'  GAGTAAATGATGATACA     28091         TTA     A
                                GAGTGAAT   ATGATA CA
                                ||||||||   |||||| ||
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                                CTCATTTA   TACTAT GT
                                    C__     _
GAM1074  FUSIP1    3'  TGAGTAAATGAATGATACA    28092         TT      A
                                TGAGTGAAT  AATGATA CA
                                |||||||||  ||||||| ||
                                ACTCATTTA  TTACTAT GT
                                    C_      _
GAM1074  SPAF      3'  ATGAATTTTAATGATAACACAT 28093         _
                                GTGAATTT AATGATAACACAT
                                |||||||| ||||||||||||||
                                TACTTAAA TTACTATTGTGTA
                                    A
GAM1074  UMP-CMPK  3'  TAAGTGAATTTCATAACACAT  28094           AATG
                                TGAGTGAATTT    ATAACACAT
                                ||||||||||    |||||||||
                                ATTCACTTAAA    TATTGTGTA
                                     G___
GAM1074  LOC123879 3'  TGAGTGAAGTTAAGGAACA    28095        T    T  TA
                                TGAGTGAA TTAA GA  ACA
                                |||||||| |||| ||  |||
                                ACTCACTT AATT CT  TGT
                                    C    C  __
GAM1074  LOC163231 3'  TGAGTGAGTTAATGACA     28097        AT
                                TGAGTGA  TTAATGATA
                                |||||||  |||||||||
                                ACTCACT  AATTACTGT
                                    C_
GAM1074  LOC163231 5'  TGAGTGAATTGATGACA     28096          TA
                                TGAGTGAATT  ATGATA
                                ||||||||||  ||||||
                                ACTCACTTAA  TACTGT
                                     C_
GAM1074  LOC257465 3'  TGAATGAGTTTATTTAACACAT 28098        A    ATGA
                                TGAGTGA TTTA    TAACACAT
                                ||||||| ||||    ||||||||
                                ACTTACT AAAT    ATTGTGTA
                                    C    AA__
GAM1075  GP1BA     3'  TTTGGCTGGGACTGAAATTGTG 28101      A_  A    GTC
                                TTTG  TG GGAC   GAAATTGTG
                                ||||  || ||||   |||||||||
                                AAAC  AC CCTG   CTTTAACAC
                                  CG  _    A__
GAM1075  LOC91049  5'  TTTGATGAGGCTGTGCTGT   28102          AC  CGAAA
                                TTTGATGAGG  GT    TTGT
                                ||||||||||  ||    ||||
                                AAACTACTCC  CA    GACA
                                     GA  C_____
GAM1076  ATP6V1E1  5'  GGCTCGAGTTTAGGTTTG    28105     A   A CC
                                GGT TGA G  TAGGTTTG
                                ||| ||| |  ||||||||
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                                CCG GCT C  ATCCAAAC
                                  A  _ AA
GAM1076 DISC1    3' TGGGGTGAATAGGTTTG    28106    TA   GCC
                                TGG  TGAA   TAGGTTTG
                                |||  ||||   ||||||||
                                ACC  ACTT   ATCCAAAC
                                  CC   ___
GAM1076 KLK8     3' TGGTATAGACGCCAGGTTTG  28107      _ A  T
                                TGGTAT GA GCC AGGTTTG
                                |||||| || ||| |||||||
                                ACCATA CT CGG TCCAAAC
                                   T  G  _
GAM1076 LAMP1    3' TGGATGAAGCAGATTTG    28108    T     CT
                                TGG ATGAAGC  AGGTTTG
                                ||| |||||||  |||||||
                                ACC TACTTCG  TCTAAAC
                                  _     __
GAM1076 MEF2C    3' TGATATGCCTGCAGGTTTG  28109     GAA   __
                                TGGTAT   GCCT  AGGTTTG
                                ||||||   ||||  |||||||
                                ACTATA   CGGA  TCCAAAC
                                   ___   CG
GAM1076 PTPRM    3' TGGTATGAAAGGGATTGTTTG 28110        CCTAG_
                                TGGTATGAAG     GTTTG
                                ||||||||||     |||||
                                ACCATACTTT     CAAAC
                                     CCCTAA
GAM1076 SCO1     3' TGGTATGAAGGCCATTCTG   28111        _ TAGG
                                TGGTATGAAG CC    TTTG
                                |||||||||| ||    ||||
                                ACCATACTTC GG    AGAC
                                     C  TA__
GAM1076 STARD4   3' GGTATGAAGAACTTTG     28112       CCT  G
                                GGTATGAAG   AG TTTG
                                |||||||||   || ||||
                                CCATACTTC   TT AAAC
                                     ___  G
GAM1076 TCL1B    3' GGTATGAAGGGGATTTG    28113       CCTA
                                GGTATGAAG   GGTTTG
                                |||||||||   ||||||
                                CCATACTTC   CTAAAC
                                     CC__
GAM1076 ZNFN1A3  3' TGGTATGAAAAGAAGTTTG  28114        CCT
                                TGGTATGAAG   AGGTTTG
                                ||||||||||   |||||||
                                ACCATACTTT   TTCAAAC
                                     TC_
GAM1076 BRI3     3' TGGTATGAATCTCATTTA    28115       GC  AG
                                TGGTATGAA  CT  GTTTG
                                |||||||||  ||  |||||
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                                ACCATACTT  GA  TAAAT
                                     A_  G_
GAM1076 DIS3     3' GGTATACCATCTAGGTTTG   28116      AAGC
                                GGTATG   CTAGGTTTG
                                ||||||   |||||||||
                                CCATAT   GATCCAAAC
                                   GGTA
GAM1076 FLJ20254 5' GGAACTTGCCTAGGTTTG    28117    T  GAA
                                GG AT   GCCTAGGTTTG
                                || ||   ||||||||||
                                CC TG   CGGATCCAAAC
                                 T  AA_
GAM1076 FLJ22104 3' TGGTATGAGACCCATCTTTG  28118       AG   GG
                                TGGTATGA  CCTA  TTTG
                                ||||||||  ||||  ||||
                                ACCATACT  GGGT  AAAC
                                     CT   AG
GAM1076 KIAA0721 3' TGGAGTGAGGCTAAGTTT    28119    TA   A  C
                                TGG  TGA GC TAGGTTT
                                |||  ||| || |||||||
                                ACC  ACT CG ATTCAAA
                                  TC   C  _
GAM1076 KIAA0721 3' TGGAGTGAGGCTAAGTTT    28119    TA   A  C
                                TGG  TGA GC TAGGTTT
                                |||  ||| || |||||||
                                ACC  ACT CG ATTCAAA
                                  TC   C  _
GAM1076 KIAA0789 3' TGGATGGTGCAGGTTTG     28120    T   AA  CT
                                TGG ATG  GC  AGGTTTG
                                ||| |||  ||  |||||||
                                ACC TAC  CG  TCCAAAC
                                  _   CA  __
GAM1076 KIAA1032 3' TGATATGAGGACTGGGTTTG  28121       AGC  A
                                TGGTATGA   CT GGTTTG
                                ||||||||   || ||||||
                                ACTATACT   GA CCAAAC
                                     CCT  C
GAM1076 KIAA1553 3' TGGTATGACACACTGTTTG   28122       A  CTAG
                                TGGTATGA GC    GTTTG
                                |||||||| ||    |||||
                                ACCATACT TG    CAAAC
                                     G  TGA_
GAM1076 KRTAP1-3 5' TGGTATGAAGTCTGGGTT    28123        C  A
                                TGGTATGAAG CT GGTT
                                |||||||||| || ||||
                                ACCATACTTC GA CCAA
                                      A  C
GAM1076 LY75     3' TGGTATGAAATAACTTTG    28124        CC   G
                                TGGTATGAAG  TAG TTTG
                                |||||||||  ||| ||||
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                                ACCATACTTT  ATT AAAC
                                      __  G
GAM1076  MUF1     3'  GGTATGAAAGGGTTTG      28125         CCTA
                                GGTATGAAG   GGTTTG
                                |||||||||   ||||||
                                CCATACTTT   CCAAAC
                                     C___
GAM1076  P5       3'  TGGTCTGAAGCCTCTGTT    28126      A      AG
                                TGGT TGAAGCCT  GTT
                                |||| ||||||||  |||
                                ACCA ACTTCGGA  CAA
                                  G       GA
GAM1076  TAF2     3'  TGGTATGAGAGCCAAATT    28127         _   T
                                TGGTATGA AGCC AGGTT
                                |||||||| |||| |||||
                                ACCATACT TCGG TTTAA
                                     C   _
GAM1076  TSPAN-2  3'  TGGTATGAAAGCTTTAGATT  28128         _ C_
                                TGGTATGAA GC  TAGGTT
                                ||||||||| ||  ||||||
                                ACCATACTT CG  ATCTAA
                                      T  AA
GAM1076  LOC121457 3'  GGTATGAGACATAGGTTTG   28129        AG C
                                GGTATGA  C TAGGTTTG
                                |||||||  | ||||||||
                                CCATACT  G ATCCAAAC
                                    CT T
GAM1076  LOC124930 3'  GGTATGAAGCCTCTTTTATTTG 28130           AG___
                                GGTATGAAGCCT    GTTTG
                                ||||||||||||    |||||
                                CCATACTTCGGA    TAAAC
                                       GAAAA
GAM1076  LOC150370 3'  TGGATGAAGCCAGGCT     28131     T      T
                                TGG ATGAAGCC AGGTT
                                ||| |||||||| |||||
                                ACC TACTTCGG TCCGA
                                  _      _
GAM1076  LOC221876 5'  TGGGATGAGGCTCAGATTTG  28132     T   A  C
                                TGG ATGA GC TAGGTTTG
                                ||| |||| || ||||||||
                                ACC TACT CG GTCTAAAC
                                  C   C  A
GAM1076  LOC57333  3'  TGGTGGAGGCTCAGATTTG   28133     AT  A  C
                                TGGT  GA GC TAGGTTTG
                                ||||  || || ||||||||
                                ACCA  CT CG GTCTAAAC
                                  C_  C  A
GAM1077  ADRB1    3'  ACGAGGATTGTGGGCTTCGAGT 28136        CGCGA  GG
                                ACGGGGAT    GC  TCGAGT
                                ||||||||    ||  ||||||
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                                TGCTCCTA    CG  AGCTCA
                                     ACACC  A_
GAM1077  SPON2    5'  CGCGGCCGGCAGCGGTCGGGTC 28137    G  A   CG      A
                                CG GG TCG  AGCGGTCG GTC
                                || || |||  |||||||| |||
                                GC CC GGC  TCGCCAGC CAG
                                 G  _   CG       C
GAM1077  C1QTNF4  5'  GGGGGCGGCGGTCGAGTC    28138     ATC   A
                                GGGG   GCG GCGGTCGAGTC
                                ||||   ||| ||||||||||
                                CCCC   CGC CGCCAGCTCAG
                                  ___   _
GAM1077  KIAA0310  3'  ACGGAGATCGCGGAGGTCGGTC 28139          _ __     A
              GGGT                   ACGGGGATCGCG AG  CGGTCG GT
                                |||||||||||| ||  |||||| ||
                                TGCCTCTAGCGC TC  GCCAGC CA
                                       C  CA     C
GAM1077  NIFIE14   5'  CGGGGATCGCGAGGCGGCGTC  28140           _   CGA
                                CGGGGATCGCGAG CGGT   GTC
                                |||||||||||| ||||   |||
                                GCCCCTAGCGCTC GCCG   CAG
                                       C   ___
GAM1077  LOC200531 5'  CGGGGATGCGCGGGCGTC    28141        _   A   G
                                CGGGGAT CGCG GCG TC
                                ||||||| |||| ||| ||
                                GCCCCTA GCGC CGC AG
                                    C   C   _
GAM1077  LOC201514 5'  GGGGATCGCGAGGAAGTC    28142          C_
                                GGGGATCGCGAG  GGTC
                                ||||||||||||  ||||
                                CCCCTAGCGCTC  TCAG
                                       CT
GAM1078  HTR4     3'  TTCCCGGGACTTCTGC      28145          TA   C
                                TTCCCGGGACT  TCT GT
                                ||||||||||  ||| ||
                                AAGGGCCCTGA  AGA CG
                                     __  _
GAM1078  SCNN1G   3'  TCCCGGGATTTATCTCAGCC   28146        C      _
                                TCCCGGGA TTATCTC GTC
                                |||||||| ||||||| |||
                                AGGGCCCT AATAGAG CGG
                                    A      T
GAM1078  FLJ22626  5'  TTCCCGGGACCTGCCGCTGCG  28147          ATC    CA
                                TTCCCGGGACTT   TCGT  CG
                                ||||||||||||   ||||  ||
                                AAGGGCCCTGGA   GGCG  GC
                                       C__    AC
GAM1078  KIAA0227  5'  TTCCCGGGTTTAAAAGCCGCG  28148        AC   TCTC   A
                                TTCCCGGG  TTA    GTC CG
                                ||||||||  |||    ||| ||
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                                AAGGGCCC  AAT   CGG GC
                                    A_   TTT_   C
GAM1078  LOC132948 5'  TTCCCGGATAGCTCGTCGCG   28149       ACT  T    A
                                TTCCCGGG   TA CTCGTC CG
                                ||||||||   || |||||| ||
                                AAGGGCCT   AT GAGCAG GC
                                    ____  C     C
GAM1078  LOC158835 3'  TTCTTGGGACTATCTCA     28150     CC     T
                                TTC  GGGACT ATCTCG
                                |||  |||||| ||||||
                                AAG  CCCTGA TAGAGT
                                  AA     _
GAM1078  LOC254571 3'  TTCCCGGAGCTGGATGTCACG  28151       GA  TATCTC
                                TTCCCGG  CT     GTCACG
                                |||||||  ||     ||||||
                                AAGGGCC  GA     CAGTGC
                                    TC  CCTA__
GAM1078  LOC256207 3'  TTCCTGAGGCTGTGTCACG    28152      C   A  TATCTC
                                TTCC GGG CT     GTCACG
                                |||| ||| ||     ||||||
                                AAGG CTC GA     CAGTGC
                                  A   C  CA____
GAM1079  ADAM22    3'  TGCCTTAGCCCTGCATGCTCAT 28155      A       _
           T                     TGCC TTAGCTCT TATGCTCATT
                                |||| |||||||| ||||||||||
                                ACGG AATCGGGA GTACGAGTAA
                                  _       C
GAM1079  ADAM22    3'  TGCCTTAGCCCTGCATGCTCAT 28155      A       _
           T                     TGCC TTAGCTCT TATGCTCATT
                                |||| |||||||| ||||||||||
                                ACGG AATCGGGA GTACGAGTAA
                                  _       C
GAM1079  PCDHB14   3'  TGACATTAGCTCTTAATACT   28156    C         _
                                TG CATTAGCTCTTA TGCT
                                || ||||||||||| ||||
                                AC GTAATCGAGAAT ATGA
                                 T          T
GAM1079  DEFCAP    5'  TGCCTTGGCTCTTACCGTCTC  28157      A  A       _ _
                                TGCC TT GCTCTTAT G CTC
                                |||| || |||||||| | |||
                                ACGG AA CGAGAATG C GAG
                                  _ C       G A
GAM1079  FLJ10921  3'  TGCCATCAGTTCTCCAATG    28158         __    T
                                TGCCATTAG  CTCT ATG
                                |||||||||  |||| |||
                                ACGGTAGTC  GAGG TAC
                                     AA    T
GAM1079  FLJ23342  3'  TGCCATTATCTATTGCTTATT  28159        GC   TA    C
                                TGCCATTA  TCT  TGCT ATT
                                ||||||||  |||  |||| |||
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                                ACGGTAAT  AGA  ACGA TAA
                                    __  TA   A
GAM1079  FLJ23537  3'  TGCTTTAGCTCTCTGCC    28160    CA       A
                                TGC  TTAGCTCTT TGCT
                                |||  ||||||||| ||||
                                ACG  AATCGAGAG ACGG
                                  A_       _
GAM1079  KIAA1724  3'  ATTAGCTCTCTTATCATT    28161         A  C
                                ATTAGCTCTT TG TCATT
                                |||||||||| || |||||
                                TAATCGAGAG AT AGTAA
                                     A  _
GAM1079  LEC3    3'  TGCCATTAGTTTTATCATC   28162        CTC   GC
                                TGCCATTAG   TTAT  TC
                                |||||||||   ||||  ||
                                ACGGTAATC   AATA  AG
                                     AA_   GT
GAM1079  WNT16   3'  TGCCTTAGCTCTTAGGCT    28163     A       T
                                TGCC TTAGCTCTTA GCT
                                |||| ||||||||||| |||
                                ACGG AATCGAGAAT CGA
                                  _        C
GAM1079  WNT16   3'  TGCCTTAGCTCTTAGGCT    28163     A       T
                                TGCC TTAGCTCTTA GCT
                                |||| ||||||||||| |||
                                ACGG AATCGAGAAT CGA
                                  _        C
GAM1079  LOC200349 3'  TGTCATCAGCTGACTTAT    28164    C      __
                                TG CATTAGCT  CTTAT
                                || ||||||||  |||||
                                AC GTAGTCGA  GAATA
                                 A       CT
GAM1080  GCA     5'  GAGCGAGCGTCACCCTCGAGTC 28167         ACTG
           G                     GAGCGAGCG   TCTCGAGTCG
                                |||||||||   ||||||||||
                                CTCGCTCGC   GGAGCTCAGC
                                     AGTG
GAM1080  LIPA    5'  CGGGCCGCTGTCTCGAGTC   28168    A  GA
                                CG GC  CTGTCTCGAGTC
                                || ||  ||||||||||||
                                GC CG  GACAGAGCTCAG
                                 C  GC
GAM1081  APAF1   3'  GTATGTATTCACATTTTCATT  28171        GGAGG_
                                GTATGTAT    TTTCATT
                                ||||||||    |||||||
                                CATACATA    AAAGTAA
                                    AGTGTA
GAM1081  APAF1   3'  GTATGTATTCACATTTTCATT  28171        GGAGG_
                                GTATGTAT    TTTCATT
                                ||||||||    |||||||
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                                CATACATA     AAAGTAA
                                     AGTGTA
GAM1081  PURA     3'  GTGTGTGTGGGGGTTTCATT   28172    A   A   A
                                GT TGT TGG GGTTTCATT
                                || ||| ||| |||||||||
                                CA ACA ACC CCAAAGTAA
                                 C   C   C
GAM1081  TERF1    3'  TAAGGTATGTATGACCTTGTT  28173     A        AG__
                                TAA GTATGTATGG    GTT
                                ||| ||||||||||    |||
                                ATT CATACATACT    CAA
                                  C         GGAA
GAM1081  TRIM9    3'  AAAGTATGTGTGTGAACTTT   28174         A  _   G
                                AAAGTATGT TG GAG TTT
                                ||||||||| || ||| |||
                                TTTCATACA AC CTT AAA
                                     C  A   G
GAM1081  AP1S3    3'  TAAAGTATGTACAAATTGTTT  28175          TG  G_
                                TAAAGTATGTA  GA  GTTT
                                ||||||||||  ||  ||||
                                ATTTCATACAT  TT  CAAA
                                      GT  AA
GAM1081  C1orf16  5'  AAGTGTGCTGCTCGGTTTCATT 28176      A   ATGGA
                                AAGT TGT     GGTTTCATT
                                |||| |||     |||||||||
                                TTCA ACG     CCAAAGTAA
                                  C   ACGAG
GAM1081  DKFZP564O0423 3'  AAAGTGGTAGGGGGTTTCATT  28177       AT   T  A
                                AAAGT  GTA GG GGTTTCATT
                                |||||  ||| || |||||||||
                                TTTCA  CAT CC CCAAAGTAA
                                   C_   C  _
GAM1081  EPHA7    3'  AGTATGTATGGATCAT      28178           GGTT
                                AGTATGTATGGA    TCAT
                                ||||||||||||    ||||
                                TCATACATACCT    AGTA
                                                ____
GAM1081  FLJ14442 3'  TAAGGTGTGTATGGGGC     28179     A  A      A
                                TAA GT TGTATGG GGT
                                ||| || ||||||| |||
                                ATT CA ACATACC CCG
                                  C  C      _
GAM1081  GC20     3'  TAAAGACAATATGAGGTTT    28180       TAT    G
                                TAAAG   GTATG AGGTTT
                                |||||   ||||| ||||||
                                ATTTC   TATAC TCCAAA
                                   TGT     _
GAM1081  RAB21    3'  TAAAGTATGTATGAAAATT    28181
                                TAAAGTATGTATGGAGGTT
                                |||||||||||||||||||
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                                ATTTCATACATACTTTTAA

GAM1081  USP25    3'  TAAAGTATGGATTTTGATTTTC 28182        TATG__  GG
              ATT                  TAAAGTATG     GA  TTTCATT
                                   |||||||||     ||  |||||||
                                   ATTTCATAC     CT  AAAGTAA
                                       CTAAAA  A_
GAM1081  LOC151178 3'  AAAGCTGTTGGAGGTTTCATT  28183      A   A
                                   AAAGT TGT TGGAGGTTTCATT
                                   ||||| ||| ||||||||||||
                                   TTTCG ACA ACCTCCAAAGTAA
                                     _  _
GAM1081  LOC158668 3'  TAAGGTATGTATGACCTTGTT  28173     A        AG__
                                   TAA GTATGTATGG    GTT
                                   ||| ||||||||||    |||
                                   ATT CATACATACT    CAA
                                     C         GGAA
GAM1081  LOC201304 3'  AAGTATGTATTTTCAT      28184          GGAGG
                                   AAGTATGTAT    TTTCAT
                                   ||||||||||    ||||||
                                   TTCATACATA    AAAGTA
                                         _____
GAM1081  LOC203292 5'  ATGGAAAAGAGGTTTCATT   28185     TAT_
                                   ATG   GGAGGTTTCATT
                                   |||   ||||||||||||
                                   TAC   TCTCCAAAGTAA
                                     CTTT
GAM1081  LOC51068  3'  TAAAGTATGTACCTCATT    28186           GGAGGT
                                   TAAAGTATGTAT     TTCATT
                                   ||||||||||||     ||||||
                                   ATTTCATACATG     GAGTAA
                                         _______
GAM1082  CDC42     3'  TACTGGATCTACTCAAGGGTG 28189        AA  AG   A
                                   TATTGGAT  AC  CAA GGTG
                                   ||||||||  ||  ||| ||||
                                   ATGACCTA  TG  GTT CCAC
                                       GA  A_   C
GAM1082  ITGAL     3'  TATTGGATAAATACATGCA   28190          __   _
                                   TATTGGATAA  ACA GCA
                                   ||||||||||  ||| |||
                                   ATAACCTATT  TGT CGT
                                       TA   A
GAM1082  PON2      3'  TTGGAAGGCAAAGGTGA     28191       TAAACA
                                   TTGGA     GCAAAGGTGA
                                   |||||     ||||||||||
                                   AACCT     CGTTTCCACT
                                     TC____
GAM1082  SDC4      3'  TATTGGATAGCACAGCCCTAGA 28192         A_    AA_
                                   TATTGGATA  ACAGC   AGG
                                   |||||||||  |||||   |||
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                                ATAACCTAT  TGTCG   TCT
                                     CG    GGA
GAM1082  TRPS1    3'  TTGGATAAGGCAGGCTCTATGA 28193        A_  CAAAG
            A                    TTGGATAA  CAG    GTGAA
                                 ||||||||  |||    |||||
                                 AACCTATT  GTC    TACTT
                                     CC   CGAGA
GAM1082  ANAPC11  3'  TATTGGATAAAAGTG      28194          CAGCAAA
                                 TATTGGATAAA     GGTG
                                 ||||||||||      ||||
                                 ATAACCTATTT     TCAC
                                              _______
GAM1082  DKFZP434L0117 3'  CATTGGATGGAGAAGAAAGGTG 28195        AAAC_  C
                                 TATTGGAT    AG AAAGGTG
                                 ||||||||    || |||||||
                                 GTAACCTA    TC TTTCCAC
                                     CCTCT  _
GAM1082  FLJ12666 3'  TATTGGATGAGCAGAAAAGA   28196        AAA   C
                                 TATTGGAT   CAG AAAGG
                                 ||||||||   ||| |||||
                                 ATAACCTA   GTC TTTCT
                                     CTC   T
GAM1082  FLJ30567 3'  TGGATAAATCACAGGTGAA   28197        CA   AA
                                 TGGATAAA  GCA  GGTGAA
                                 ||||||||  |||  ||||||
                                 ACCTATTT  TGT  CCACTT
                                     AG  __
GAM1082  KIAA0254 3'  TTGGGAAACAGCAACACATGA  28198     AT       AG_
                                 TTGG  AAACAGCAA   GTGA
                                 ||||  |||||||||   ||||
                                 AACC  TTTGTCGTT   TACT
                                   C_       GTG
GAM1082  KIAA0429 3'  TTGGATTCCATAAAGGTGA   28199      AAA  GC
                                 TTGGAT   CA  AAAGGTGA
                                 ||||||   ||  ||||||||
                                 AACCTA   GT  TTTCCACT
                                    AG_  A_
GAM1082  KIAA0552 3'  TATTGGAAGAAAAGGTGA    28200       TAAAC  C
                                 TATTGGA    AG AAAGGTGA
                                 |||||||    || ||||||||
                                 ATAACCT    TC TTTCCACT
                                      _____  T
GAM1082  KIAA0931 3'  TATTGGATAGATAGAGAAGGTG 28201         AAC  CA
            A                    TATTGGATA   AG  AAGGTGA
                                 |||||||||   ||  |||||||
                                 ATAACCTAT   TC  TTCCACT
                                      CTA  TC
GAM1082  OSBPL11   3'  TACTGGATATTAACCTAAAGGT 28202         __   AGC
            GAA                    TATTGGATA  AAC   AAAGGTGAA
                                 |||||||||  |||   |||||||||
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                                ATGACCTAT  TTG   TTTCCACTT
                                     AA   GA_
GAM1082  LOC133418 3'  TATTAAGAAATGGCAAAGGTGA 28203      _  TAAACA
                                TATTG GA     GCAAAGGTGA
                                ||||| ||     ||||||||||
                                ATAAT CT     CGTTTCCACT
                                   T  TTAC__
GAM1082  LOC146958 3'  GGATAAACTGCAGGGGGTGA   28204        A   AA_
                                GGATAAAC GCA   GGTGA
                                |||||||| |||   |||||
                                CCTATTTG CGT   CCACT
                                     A   CCC
GAM1082  LOC158527 3'  GGAGTGAAACAGCAAGGGTG   28205     T__       A
                                GGA   AAACAGCAA GGTG
                                |||   ||||||||| ||||
                                CCT   TTTGTCGTT CCAC
                                  CAC       C
GAM1082  LOC51339  3'  TTGGATAAACGGCCCTAGA    28206         A  AA_
                                TTGGATAAAC GC   AGG
                                |||||||||| ||   |||
                                AACCTATTTG CG   TCT
                                      C  GGA
GAM1082  LOC91149  5'  GGAGACAGCAAAGGTGA     28207     TAA
                                GGA   ACAGCAAAGGTGA
                                |||   ||||||||||||
                                CCT   TGTCGTTTCCACT
                                  C__
GAM1082  LOC92249  3'  TATTAGACGTGGCAAAGGTGAA 28208        AAACA
                                TATTGGAT    GCAAAGGTGAA
                                ||||||||    ||||||||||
                                ATAATCTG    CGTTTCCACTT
                                     CAC__
GAM1083  ADRA2A    3'  GTGAAATAAGAGTGCAGGCCTT 28211      TCTT_  CA
            AA                    GTGAA    GG  CAGGCCTTAA
                                |||||    ||  ||||||||||
                                CACTT    TC  GTCCGGAATT
                                   TATTC  AC
GAM1083  ETV3      3'  TGCGAATCTACTAGGGGTCTTA 28212         TGGCACA  C
                                TGTGAATCT      GG CTTA
                                |||||||||      || ||||
                                ACGCTTAGA      CC GAAT
                                     TGATCC_  A
GAM1083  F7        3'  TGAATCTTGGAGTCTC     28213          CAC  GC
                                TGAATCTTGG   AG  CTT
                                ||||||||||   ||  |||
                                ACTTAGAACC   TC  GAG
                                     ____  A_
GAM1083  F7        3'  TGAATCTTGGAGTCTC     28213          CAC  GC
                                TGAATCTTGG   AG  CTT
                                ||||||||||   ||  |||
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                                ACTTAGAACC  TC  GAG
                                      ___  A_
GAM1083 LYAAT1   5'  TGTCAGTCTTGGCACAAG    28214    GAA
                                TGT  TCTTGGCACAGG
                                |||  ||||||||||||
                                ACA  AGAACCGTGTTC
                                  GTC
GAM1083 MTF1     3'  TGTGAGCCAGGCCTT      28215      ATCTTG  A
                                TGTGA    GC CAGGCCTT
                                |||||    || ||||||||
                                ACACT    CG GTCCGGAA
                                  _______ _
GAM1083 DKFZP434O125 3'  TGTGAATCTTAGCAGAC    28216           CA
                                TGTGAATCTTGGCA  GGC
                                ||||||||||||||  |||
                                ACACTTAGAATCGT  CTG
                                      __
GAM1083 DKFZp566H0824 5'  ATGAAACCACACAGGCCTT   28217      T  TG
                                GTGAA CT  GCACAGGCCTT
                                ||||| ||  ||||||||||
                                TACTT GG  TGTGTCCGGAA
                                   T  __
GAM1083 DOC2B    3'  TGTGGGGGCCACAGGCCTT   28218     AATCTT  _
                                TGTG    GGC ACAGGCCTT
                                ||||    ||| |||||||||
                                ACAC    CCG TGTCCGGAA
                                   CC_____  G
GAM1083 FLJ10232 3'  TGAGAGTCACTGCTGCAGGTCT 28219   T  A  TTG  A_   C
            TAA                  TG GA TC   GC  CAGG CTTAA
                                || || ||   ||  |||| |||||
                                AC CT AG   CG  GTCC GAATT
                                 T  C  TGA  AC    A
GAM1083 KIAA0800 3'  TGTGAACTCTCAGGCCTT    28220       T   GGCA
                                TGTGAA CTT    CAGGCCTT
                                |||||| |||    ||||||||
                                ACACTT GAG    GTCCGGAA
                                   _   A___
GAM1083 KIAA0841 3'  GTGAAATGCACAGGCCTTAA   28221      TCTTG
                                GTGAA    GCACAGGCCTTAA
                                |||||    ||||||||||||
                                CACTT    CGTGTCCGGAATT
                                   TA___
GAM1083 OMD      3'  TGTGAATCTGTATGCCTT    28222         T GCACAG
                                TGTGAATCT G     GCCTT
                                |||||||| |     |||||
                                ACACTTAGA C     CGGAA
                                     _ ATA___
GAM1083 PPP1R1A  3'  TGGACACGGCACAGGCCTTA  28223    T  ATCT
                                TG GA    TGGCACAGGCCTTA
                                || ||    ||||||||||||||
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                                AC CT    GCCGTGTCCGGAAT
                                 _ GT__
GAM1083  LOC148293 5'  TGTGGATCTTGATTGGGCCTTA 28224      A      CACA
             A                    TGTG ATCTTGG    GGCCTTAA
                                  |||| |||||||    ||||||||
                                  ACAC TAGAACT    CCGGAATT
                                    C      AAC_
GAM1083  LOC51231  3'  TGTGATTAAACAGCAGGCCTT  28225      ATCTT   _
                                  TGTGA    GGCA CAGGCCTT
                                  |||||    |||| ||||||||
                                  ACACT    TTGT GTCCGGAA
                                    AAT__   C
GAM1083  LOC90049  3'  TGTGGATCTTGATTGGGCCTTA 28224      A      CACA
             A                    TGTG ATCTTGG    GGCCTTAA
                                  |||| |||||||    ||||||||
                                  ACAC TAGAACT    CCGGAATT
                                    C      AAC_
GAM1084  DAZ      5'  GCGCGTGGTATCGGCCTGAGCC 28228       A  CCAGCA
             A                    GCGCGT GG     CCTGAGCCA
                                  |||||| ||     |||||||||
                                  CGCGCA CC     GGACTCGGT
                                     _ ATAGCC
GAM1084  GRB10    3'  GCGCGAGGCCAGCGAGC     28229      T      ACCT
                                  GCGCG AGGCCAGC    GAGC
                                  ||||| ||||||||    ||||
                                  CGCGC TCCGGTCG    CTCG
                                     _      _____
GAM1084  MTMR3    5'  GCGCTGGGCAGCGCCTGAGCC  28230     GTA   C   A
                                  GCGC   GGC AGC CCTGAGCC
                                  ||||   ||| ||| ||||||||
                                  CGCG   CCG TCG GGACTCGG
                                    AC_   _   C
GAM1084  NRF1     3'  GGCAAGGTCAGCACCTGGGCCA 28231    C   T   C       A
                                  G GCG AGG CAGCACCTG GCCA
                                  | ||| ||| ||||||||| ||||
                                  C CGT TCC GTCGTGGAC CGGT
                                  _   _   A        C
GAM1084  PIK3CD   3'  CAGAGCTGGCACCTGAGCC    28232     _  CA
                                  TAG GC  GCACCTGAGCC
                                  ||| ||  ||||||||||||
                                  GTC CG  CGTGGACTCGG
                                    T  AC
GAM1084  RAB2L    5'  GCAGCGTGGGTCCTGAGCC    28233    _    A  CCAGCA
                                  GC GCGT GG     CCTGAGCC
                                  || |||| ||     |||||||||
                                  CG CGCA CC     GGACTCGG
                                   T   C  A_____
GAM1084  APELIN   3'  GCGGTAGTCTCAGTGCCTGAGC 28234     C    GC_   CA
             C                    GCG GTAG   CAG  CCTGAGCC
                                  ||| ||||   |||  ||||||||
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                                CGC CATC   GTC  GGACTCGG
                                  _   AGA   AC
GAM1084  DKFZp761N1114 3'  GTGAGCCAGCACTTGAGCCA  28235    AG      C
                                GT  GCCAGCAC TGAGCCA
                                ||  |||||||| |||||||
                                CA  CGGTCGTG ACTCGGT
                                 CT       A
GAM1084  FLJ10922  3'  GCGCGTAGGCCAGGGTGTCCT  28236          CA___
                                GCGCGTAGGCCAG    CCT
                                ||||||||||||     |||
                                CGCGCATCCGGTC    GGA
                                       CCACA
GAM1084  FLJ11252  5'  GCGCGTAGGCAGCAGCGGCC  28237         C   CC  A
                                GCGCGTAGGC AGCA  TG GCC
                                |||||||||| ||||  || |||
                                CGCGCATCCG TCGT  GC CGG
                                     _   C_  _
GAM1084  FLJ13868  3'  GTAGACAGACCTGAGC     28238       C  C
                                GTAGGC AG ACCTGAGC
                                |||||| || ||||||||
                                CATCTG TC TGGACTCG
                                   _ _
GAM1084  MCF2L    3'  GCACGTGGGCCTTACCTGAGC  28239       A   AGC
                                GCGCGT GGCC   ACCTGAGC
                                |||||| ||||   ||||||||
                                CGTGCA CCGG   TGGACTCG
                                   C   AA_
GAM1084  OSBPL5   3'  GCGGGGCCAGCTAAGCC    28240    TA     ACC
                                GCG  GGCCAGC   TGAGCC
                                |||  |||||||   ||||||
                                CGC  CCGGTCG   ATTCGG
                                  C_     ___
GAM1084  SLC16A3  3'  GCCGTGGCCCTGCCTGAGCCA  28241    G   A   AGCA
                                GC CGT GGCC    CCTGAGCCA
                                || ||| ||||    |||||||||
                                CG GCA CCGG    GGACTCGGT
                                 _  _    GAC_
GAM1084  TRIM22   3'  GCGGTGGGCCCTGAGC     28242     C  A   AGCAC
                                GCG GT GGCC    CTGAGC
                                ||| || ||||    ||||||
                                CGC CA CCGG    GACTCG
                                  _ C   _____
GAM1084  LOC131583 5'  GCGAGGCCCGCTGAGCC     28243     T    AGCAC
                                GCG AGGCC    CTGAGCC
                                ||| |||||    |||||||
                                CGC TCCGG    GACTCGG
                                  _    GC___
GAM1084  LOC144165 5'  GCGCGAGGCTGGCATGTTCC  28244      T   CA   CC  AG
                                GCGCG AGGC  GCA  TG  CC
                                ||||| ||||  |||  ||  ||
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                                CGCGC TCCG  CGT  AC  GG
                                  _    AC   __ AA
GAM1084  LOC144278 3'  GCGCGTAGGCAGCATCGCC   28245         C   CCTGA
                                GCGCGTAGGC AGCA    GCC
                                |||||||||| ||||    |||
                                CGCGCATCCG TCGT    CGG
                                     _   AG___
GAM1084  LOC147072 5'  GCGTCCGGCACCTGAGCC    28246     AGG  A
                                GCGT   CC GCACCTGAGCC
                                ||||   || ||||||||||
                                CGCA   GG CGTGGACTCGG
                                  ___  C
GAM1084  LOC151174 5'  GCGCGGGGCCAGCAGAGAAGCC 28247      TA      CCT
                                GCGCG  GGCCAGCA   GAGCC
                                |||||  ||||||||   |||||
                                CGCGC  CCGGTCGT   TTCGG
                                   C_       CTC
GAM1084  LOC158158 3'  GCGTAGGACCCTCTGAGCCA   28248       _  AGCAC
                                GCGTAGG CC    CTGAGCCA
                                ||||||| ||    ||||||||
                                CGCATCC GG    GACTCGGT
                                    T  GA___
GAM1084  LOC196489 3'  GCCGTAGGCCAGGGCGGGAGCC 28249    G        CACCT
           A                     GC CGTAGGCCAG     GAGCCA
                                || ||||||||||     ||||||
                                CG GCATCCGGTC     CTCGGT
                                 _         CCGCC
GAM1084  LOC255535 5'  GGCCTAGCACCTGGGCCA    28250     _      A
                                GGCC AGCACCTG GCCA
                                |||| |||||||| ||||
                                CCGG TCGTGGAC CGGT
                                  A       C
GAM1084  LOC256849 5'  GTTGCCACACCTGAGCC     28251    AG   G
                                GT  GCCA CACCTGAGCC
                                ||  |||| ||||||||||
                                CA  CGGT GTGGACTCGG
                                 A_   _
GAM1084  LOC55885  5'  GTTGACCGCATCTGAGCCA   28252    A   A   C
                                GT GGCC GCA CTGAGCCA
                                || |||| ||| ||||||||
                                CA CTGG CGT GACTCGGT
                                 A   _   A
GAM1084  LOC91974  5'  GCGCGTAGTGTCAGACCAGC   28253       GC_   C   TG
                                GCGCGTAG   CAG ACC  AGC
                                ||||||||   ||| |||  |||
                                CGCGCATC   GTC TGG  TCG
                                     ACA   _   ___
GAM1085  CUGBP1    3'  TACTTCAAAGTTGTCTTTAAAA 28256         CTT  AT
                                TACTTCAGAG   TC  TTTAAAA
                                ||||||||||   ||  |||||||
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                                ATGAAGTTTC  AG  AAATTTT
                                      AAC  __
GAM1085  GRM6    3'  CTTTAGAGCTCTCATCCCA   28257    C
                                CTT AGAGCTTTCATTTTA
                                ||| ||||||||||||||
                                GAA TCTCGAGAGTAGGGT
                                  A
GAM1085  ITGAM   3'  TTCAGAACTGTATTTTA    28258       TTC
                                TTCAGAGCT  ATTTTA
                                |||||||||  ||||||
                                AAGTCTTGA  TAAAAT
                                     CA_
GAM1085  NEBL    3'  TACTTCAGAGACTTTTATTTTA 28259        _   C
                                TACTTCAGAG CTTT ATTTTA
                                |||||||||| |||| ||||||
                                ATGAAGTCTC GAAA TAAAAT
                                      T   A
GAM1085  PTPRK   3'  TTCATCAGCTTTCATTTTA   28260     G_
                                TTCA  AGCTTTCATTTTA
                                ||||  ||||||||||||||
                                AAGT  TCGAAAGTAAAAT
                                  AG
GAM1085  RBM8A   3'  CTTTAGAACTTTCAATTTTA  28261    C       _
                                CTT AGAGCTTTCA TTTTA
                                ||| |||||||||| |||||
                                GAA TCTTGAAAGT AAAAT
                                  A        T
GAM1085  SCD     3'  CTTCAGAGTTTTTTCCAAA   28262       C  CA
                                CTTCAGAG TTT  TTTTAAA
                                |||||||| |||  |||||||
                                GAAGTCTC AAA  AAGGTTT
                                     A  __
GAM1085  ZNF18   3'  CTCTAGAACTCATTTTAA   28263   TC   TT
                                CT  AGAGC  TCATTTTAA
                                ||  |||||  |||||||||
                                GA  TCTTG  AGTAAAATT
                                 GA   __
GAM1085  ABLIM   3'  ACTTCAGAGCTTTTGTTCT  28264         CA
                                ACTTCAGAGCTTT  TTTT
                                ||||||||||||  ||||
                                TGAAGTCTCGAAA  AAGA
                                      AC
GAM1085  ABLIM   3'  ACTTCAGAGCTTTTGTTCT  28264         CA
                                ACTTCAGAGCTTT  TTTT
                                ||||||||||||  ||||
                                TGAAGTCTCGAAA  AAGA
                                      AC
GAM1085  ARTS-1  3'  TTCAGAGCAATTTTAAA    28265       TTTC
                                TTCAGAGC   ATTTTAAA
                                ||||||||   ||||||||
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                                AAGTCTCG   TAAAATTT
                                   T___
GAM1085 C20orf39 3' CTTTGGAGCTTTCCTTT    28266    CA      A
                                CTT  GAGCTTTC TTTT
                                |||  |||||||| ||||
                                GAA  CTCGAAAG GAAA
                                  AC      _
GAM1085 DKFZp434I1117 3' ACTTCAGAGCCCCACTTT    28267          T
                                ACTTCAGAGCTT CATTTT
                                |||||||||||| ||||||
                                TGAAGTCTCGGG GTGAAA
                                           _
GAM1085 DKFZP564I0422 3' TTCAGTGTTCATTTTAAA    28268      AGCT
                                TTCAG    TTCATTTTAAA
                                |||||    ||||||||||
                                AAGTC    AAGTAAAATTT
                                   AC__
GAM1085 FLJ10853 3' TTCAGAGCTGGTTCATTTTAAA 28269         __
                                TTCAGAGCT  TTCATTTTAAA
                                |||||||||  ||||||||||
                                AAGTCTCGA  AAGTAAAATTT
                                     CC
GAM1085 FLJ20060 3' AGAGCTTTTCCAGTCTTAAAA  28270       __   _
                                AGAGCT  TTCA TTTTAAAA
                                ||||||  |||| ||||||||
                                TCTCGA  AGGT AGAATTTT
                                   AA   C
GAM1085 FLJ20265 3' TTCATATCTTTCATTTTA    28271     GAG
                                TTCA   CTTTCATTTTA
                                ||||   ||||||||||
                                AAGT   GAAAGTAAAAT
                                  ATA
GAM1085 FLJ23322 3' TCAGAGCTTTTGTTTTAAA   28272         CA
                                TCAGAGCTTT  TTTTAAA
                                ||||||||||  |||||||
                                AGTCTCGAAA  AAAATTT
                                     AC
GAM1085 KIAA0635 5' TACTTCAAAAAACTATATTTTA 28273        __  TTC
           AAA                    TACTTCAGA  GCT   ATTTTAAAA
                                |||||||||  |||  |||||||||
                                ATGAAGTTT  TGA   TAAAATTTT
                                     TT   TA_
GAM1085 KIAA0831 3' TTCAGTAAATCATTTTAAAA  28274      AGCTT
                                TTCAG    TCATTTTAAAA
                                |||||    ||||||||||
                                AAGTC    AGTAAAATTTT
                                   ATTT_
GAM1085 KIAA1100 3' AGCAACTTTCATTTTAAAA   28275    _
                                AG AGCTTTCATTTTAAAA
                                || ||||||||||||||||
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                                TC TTGAAAGTAAAATTTT
                                 G
GAM1085  KIAA1610  3'  TACTTCAAATACATTTTAAA  28276        GCTTT
                                TACTTCAGA    CATTTTAAA
                                |||||||||    |||||||||
                                ATGAAGTTT    GTAAAATTT
                                     AT___
GAM1085  KIAA1969  3'  CTTCAGAGTTTTCCTCTA    28277        C    A
                                CTTCAGAG TTTC TTTTA
                                |||||||| |||| |||||
                                GAAGTCTC AAAG GAGAT
                                     A    _
GAM1085  PCDH10    5'  TACTCCTTTTGCTTCATTTTA  28278       AGA_    T
                                TACTTC    GCTT CATTTTA
                                ||||||    |||| |||||||
                                ATGAGG    CGAA GTAAAAT
                                    AAAA    _
GAM1085  PCDH10    5'  TACTCCTTTTGCTTCATTTTA  28278       AGA_    T
                                TACTTC    GCTT CATTTTA
                                ||||||    |||| |||||||
                                ATGAGG    CGAA GTAAAAT
                                    AAAA    _
GAM1085  RASSF2    3'  CTACAGAGCTTTGACATAAAA  28279    T       C  TT
                                CT CAGAGCTTT AT  TAAAA
                                || |||||||| ||  |||||
                                GA GTCTCGAAA TG  ATTTT
                                 T        C  T_
GAM1085  SLC28A3   3'  TACTTCAGAGTTCCACT     28280         C
                                TACTTCAGAG TTTCATT
                                |||||||||| |||||||
                                ATGAAGTCTC AAGGTGA
                                      _
GAM1085  TCF6L1    3'  AGATTTCTCATTTTAAAA    28281     GC
                                AGA  TTTCATTTTAAAA
                                |||  ||||||||||||
                                TCT  AGAGTAAAATTTT
                                  AA
GAM1085  LOC125488 3'  CCTCTGCTTTTATTTTAAA   28282      AGA    C
                                CTTC   GCTTT ATTTTAAA
                                ||||   ||||| ||||||||
                                GGAG   CGAAA TAAAATTT
                                  A__    A
GAM1085  LOC131368 3'  CACTTCAAAGTTATTTTAAA  28283         CTTTC
                                TACTTCAGAG    ATTTTAAA
                                ||||||||||    ||||||||
                                GTGAAGTTTC    TAAAATTT
                                      AA___
GAM1085  LOC134265 3'  TTCAGAGCTCTGATTTTAAAA 28284          C
                                TTCAGAGCTTT ATTTTAAAA
                                |||||||||| |||||||||
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                                AAGTCTCGAGA TAAAATTTT
                                      C
GAM1085  LOC196812 3'  TACTTCAGGACTTCAACTAAA  28285        AG   T  TT
                                TACTTCAG  CTT CA  TTAAA
                                ||||||||  ||| ||  |||||
                                ATGAAGTC  GAA GT  GATTT
                                     CT   _  T_
GAM1085  LOC222001 3'  AGAGCTTTTCCAGTCTTAAAA  28270       __   _
                                AGAGCT  TTCA TTTTAAAA
                                ||||||  |||| ||||||||
                                TCTCGA  AGGT AGAATTTT
                                   AA   C
GAM1085  LOC51336  3'  CTCAGAGCTGATTTTTAAAA   28286        TTCA
                                TTCAGAGCT    TTTTAAAA
                                |||||||||    ||||||||
                                GAGTCTCGA    AAAATTTT
                                     CTA_
GAM1086  ID4       3'  GTGTAAAATGAAGAGTA     28289    A    CC
                                GT TGAA  TGAAGAGTA
                                || ||||  |||||||||
                                CA ATTT  ACTTCTCAT
                                 C    T_
GAM1086  RAG1      3'  ACTGTGTATGAAGAGTA     28290      A  AACC
                                ACTGT TG    TGAAGAGTA
                                ||||| ||    |||||||||
                                TGACA AT    ACTTCTCAT
                                   C  ____
GAM1086  SCA7      3'  CAGCCAATCTAACTTGAAGAGT 28291    A   TATG   C
                                CA CTG    AAC TGAAGAGT
                                || |||    ||| ||||||||
                                GT GGT    TTG ACTTCTCA
                                 C  TAGA   A
GAM1086  GPR64     3'  ACTGTATGAGCTAACTGT    28292         AC    AGA
                                ACTGTATGA  CTGA   GT
                                |||||||||  ||||   ||
                                TGACATACT  GATT   CA
                                     C_    GA_
GAM1086  KIAA0441  3'  CAACTGTAGAAAATACAGAGTA 28293         T   CCTGA
                                CAACTGTA GAA     AGAGTA
                                |||||||| |||     ||||||
                                GTTGACAT CTT     TCTCAT
                                     _   TTATG
GAM1086  MRPS14    3'  CAACTGTACTGGGCCCCTGTAG 28294         GAA___    A
                                CAACTGTAT      CCTG AG
                                |||||||||      |||| ||
                                GTTGACATG      GGAC TC
                                     ACCCGG    A
GAM1086  PC326     5'  TATATGTAATCTGAAGAGTAA  28295       _  C
                                TGTATG AA CTGAAGAGTAA
                                |||||| || ||||||||||
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                                ATATAC TT GACTTCTCATT
                                   A  A
GAM1086  POR1     3'  ACCCCAGCCTGAAGAGT     28296     G  TGAA
                                ACT TA    CCTGAAGAGT
                                ||| ||    ||||||||||
                                TGG GT    GGACTTCTCA
                                  G  C___
GAM1086  R3HDM    5'  CAACTGTAGTGAACCATCTGTA 28297         _     TGAAGA
              A                  CAACTGTA TGAACC      GTAA
                                ||||||||| ||||||      ||||
                                GTTGACAT ACTTGG      CATT
                                     C     TAGA__
GAM1086  LOC149837 3'  GAGTGTACCTTTGAAGAGTAA  28298    TA  A   __
                                G  TG ACCT  GAAGAGTAA
                                |  || ||||  |||||||||
                                C  AC TGGA  CTTCTCATT
                                 TC  A    AA
GAM1086  LOC153727 5'  CAGCTGTTTGGTGGAAGAGTA  28299    A    A  AACCT
                                CA CTGT TG     GAAGAGTA
                                || |||| ||     ||||||||
                                GT GACA AC     CTTCTCAT
                                 C    A  CAC__
GAM1087  CEBPA    3'  ATCGGCTGATAAAGCA      28302       GTACA
                                ATCGG     TGATAAAGCA
                                |||||     ||||||||||
                                TAGCC     ACTATTTCGT
                                   G____
GAM1087  PLAGL1   3'  TTAAATTTGGTACAAAGC    28303        CG     TGATA
                                TTAAAT  GGTACA     AAGC
                                ||||||  ||||||     ||||
                                AATTTA  CCATGT     TTCG
                                   AA     _____
GAM1087  FLJ22875  3'  TTAAATTGAGTACATTTGGGCA 28304        C       GATAAA
                                TTAAAT GGGTACAT      GCA
                                |||||| ||||||||      |||
                                AATTTA CTCATGTA      CGT
                                   A       AACC__
GAM1087  HNRPAB   3'  TTAAATTTGGTACATAAT    28305       CG
                                TTAAAT  GGTACATGAT
                                |||||||  ||||||||||
                                AATTTA  CCATGTATTA
                                   AA
GAM1087  KIAA0419  3'  TCAGAATGATAAAGCA      28306       TAC
                                TCGGG   ATGATAAAGCA
                                |||||   ||||||||||||
                                AGTCT   TACTATTTCGT
                                   ___
GAM1087  RAB40B   3'  CAGTGCAATCATGATAAAG   28307     _   __
                                CGG GTA  CATGATAAAG
                                ||| |||  ||||||||||
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                                GTC CGT  GTACTATTTC
                                  A   TA
GAM1088  COIL     3'  TTACTTAAAACTTATTGAG   28310       TAAT
                                TTATTT   AAACTTATTGAG
                                ||||||   ||||||||||||
                                AATGAA   TTTGAATAACTC
                                   T___
GAM1088  MBL2     3'  TTAAGAAATAAACTTATTGAG  28311     TTTT
                                TTA   AATAAACTTATTGAG
                                |||   ||||||||||||||||
                                AAT   TTATTTGAATAACTC
                                  TCT_
GAM1088  LOC126964 3'  ATTATTTTAATAAACTAACCA  28312              T
                                ATTATTTTAATAAACT ATTG
                                |||||||||||||||| ||||
                                TAATAAAATTATTTGA TGGT
                                          T
GAM1088  LOC221929 3'  TTATTTTAATAAACATTCAGAG 28313            TTATT
                                TTATTTTAATAAAC    GAG
                                |||||||||||||    |||
                                AATAAAATTATTTG    CTC
                                       TAAGT
GAM1089  TIM3     3'  TACCGTCTTGAAATTTAAGTT  28316    G     ATTA
                                TA CGTCTT   AAGTTTAAGTT
                                || ||||||   ||||||||||
                                AT GCAGAA   TTTAAATTCAA
                                 G     C___
GAM1089  AASDHPPT  3'  GCATCTTATATATTAAGTT   28317        TAAAGT
                                GCGTCTTAT     TTAAGTT
                                |||||||||     |||||||
                                CGTAGAATA     AATTCAA
                                      TAT___
GAM1089  MGC16279  3'  GTCTTATTAGAGGGCAGTT   28318         A  TTTA
                                GTCTTATTA AG   AGTT
                                ||||||||| ||   ||||
                                CAGAATAAT TC   TCAA
                                      C  CCG_
GAM1089  MGC16279  5'  GTCTTATTAGAGGGCAGTT   28318         A  TTTA
                                GTCTTATTA AG   AGTT
                                ||||||||| ||   ||||
                                CAGAATAAT TC   TCAA
                                      C  CCG_
GAM1089  LOC219917 3'  GTCTTATTAGAGGGCAGTT   28318         A  TTTA
                                GTCTTATTA AG   AGTT
                                ||||||||| ||   ||||
                                CAGAATAAT TC   TCAA
                                      C  CCG_
GAM1090  M11S1    3'  ATTGTTTTACTCCTAAGCAA   28321       G       ATTT
                                ATTGT TTTACTTT   AGCAA
                                ||||| ||||||||   |||||
```

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                                TAACA AAATGAGG   TCGTT
                                  _      AT__
GAM1090  MAPK9    3'  CATTGTGTTTCTTACATGCA  28322        A  T  TTA
                                CATTGTGTTT CTT AT  GCA
                                |||||||||| ||| ||  |||
                                GTAACACAAA GAA TG  CGT
                                     _  _  TA_
GAM1090  MAPK9    3'  CATTGTGTTTCTTACATGCA  28322        A  T  TTA
                                CATTGTGTTT CTT AT  GCA
                                |||||||||| ||| ||  |||
                                GTAACACAAA GAA TG  CGT
                                     _  _  TA_
GAM1090  MAPK9    3'  CATTGTGTTTCTTACATGCA  28322        A  T  TTA
                                CATTGTGTTT CTT AT  GCA
                                |||||||||| ||| ||  |||
                                GTAACACAAA GAA TG  CGT
                                     _  _  TA_
GAM1090  MAPK9    3'  CATTGTGTTTCTTACATGCA  28322        A  T  TTA
                                CATTGTGTTT CTT AT  GCA
                                |||||||||| ||| ||  |||
                                GTAACACAAA GAA TG  CGT
                                     _  _  TA_
GAM1090  NEDD4    3'  ATTGTAGTTTACTCAATAG   28323     _     TATT
                                ATTGT GTTTACTT   TAG
                                ||||| ||||||||   |||
                                TAACA CAAATGAG   ATC
                                   T      TT__
GAM1090  NFIB     3'  TTGTGTTTCTTTTTCCCTCA  28324       A   A  AG
                                TTGTGTTT CTTT TTT  CA
                                |||||||| |||| |||  ||
                                AACACAAA GAAA AGG  GT
                                     _   A  GA
GAM1090  PPP2R5C  3'  TTGTGTTACTTTATGC     28325       T     TTA
                                TTGTGTT ACTTTAT  GC
                                ||||||| |||||||  ||
                                AACACAA TGAAATA  CG
                                     _    ____
GAM1090  PTGFR    3'  ATTGTGTCTACCTCCCATTGGC 28326          AT_  A
              AA                  ATTGTGTTTACTTT  TT GCAA
                                  ||||||||||||||  || ||||
                                  TAACACAGATGGAG  AA CGTT
                                        GGT  C
GAM1090  SLC2A8   3'  TGTGTCAGTCTTTATTTGGCAA 28327      TA_     A
                                TGTGTT  CTTTATTT GCAA
                                ||||||  |||||||| ||||
                                ACACAG  GAAATAAA CGTT
                                   TCA      C
GAM1090  TSG101   3'  TATGCAACAAATTTTATTTAGC 28328     TT ____
              A                  TGTGT  AC   TTTATTTAGCA
                                 |||||  ||   ||||||||||
```

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                                ATACG  TG    AAATAAATCGT
                                  T_  TTTA
GAM1090  C21orf25  3'  CTGTGCTCTTGTTTAGCAA   28329        ACT  A
                                TTGTGTTT   TT TTTAGCAA
                                ||||||||   || ||||||||
                                GACACGAG   AA AAATCGTT
                                    ___  C
GAM1090  ELF1      3'  ATTCTGTTTAGCACTTAGCAA  28330     G     CTT
                                ATT TGTTTA   TATTTAGCAA
                                ||| ||||||   ||||||||||
                                TAA ACAAAT   GTGAATCGTT
                                  G     C__
GAM1090  FLJ13273  3'  ATCATAATTATTTTATTTAGCA 28331    TG  T   C
              A                  AT  TG TTA TTTATTTAGCAA
                                 ||  || ||| ||||||||||||
                                 TA  AT AAT AAATAAATCGTT
                                  GT  T   A
GAM1090  FLJ14824  3'  ATTGTGTTAATAACTGCTTAGC 28332        TACT_  A
              A                  ATTGTGTT     TT TTTAGCA
                                 ||||||||     || |||||||
                                 TAACACAA     GA GAATCGT
                                     TTATT  C
GAM1090  FYCO1     3'  CATAGTGTTTACTTTATTTAA  28333     T
                                 CAT GTGTTTACTTTATTTAG
                                 ||| ||||||||||||||||
                                 GTA CACAAATGAAATAAATT
                                   T
GAM1090  MGC2217   3'  ATTGTGTTTATATCATAAAG   28334         CT    TT
                                 ATTGTGTTTA  TTAT  AG
                                 ||||||||||  ||||  ||
                                 TAACACAAAT  AGTA  TC
                                       AT    TT
GAM1090  MGC2477   5'  GTGTTTACTCTTTGGCA     28335         TA   A
                                 GTGTTTACTT  TTT GCA
                                 ||||||||||  ||| |||
                                 CACAAATGAG  AAA CGT
                                       __  C
GAM1090  NR1H4     3'  CATTATGTTTGCTTTATTGC   28336         A      TA
                                 CATTGTGTTT CTTTATT  GC
                                 |||||||||| |||||||  ||
                                 GTAATACAAA GAAATAA  CG
                                       C      __
GAM1090  PRO0800   3'  GTTTAAATTTATTTAGCA    28337      C_
                                 GTTTA  TTTATTTAGCA
                                 |||||  ||||||||||
                                 CAAAT  AAATAAATCGT
                                    TT
GAM1090  LOC142948 3'  TGTGTTTATAATCCTTTAGCAA 28338         CT_  A
                                 TGTGTTTA   TT TTTAGCAA
                                 ||||||||   || ||||||||
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                                ACACAAAT   AG AAATCGTT
                                    ATT  G
GAM1090  LOC147381 3'  CATTGTGTTACTTTTACTT   28339        T    _
                                CATTGTGTT ACTTT ATTT
                                ||||||||| ||||| ||||
                                GTAACACAA TGAAA TGAA
                                     _    A
GAM1090  LOC253573 3'  TTGGTTTACTTTACGC     28340    T       TTA
                                TTG GTTTACTTTAT   GC
                                ||| ||||||||||   ||
                                AAC CAAATGAAATG   CG
                                  _       ___
GAM1091  CX3CR1    3'  TATGTGAAAGGTACCTTA    28343       TAGAT
                                TATGTGAA    AGGTATTTTA
                                ||||||||    ||||||||||
                                ATACACTT    TCCATGGAAT
                                     _____
GAM1091  GAD1      3'  TATGTTGGTAGAAGTATTTTAT 28344     GAA   TA
                                TATGT   TAGA  GGTATTTTAT
                                |||||   ||||  ||||||||||
                                ATACA   ATCT  TCATAAAATA
                                   ACC   __
GAM1091  C8orf2    3'  GTGAATAGAGTCCTTTTAT   28345       TAG  A_
                                GTGAATAGA   GT  TTTTAT
                                |||||||||   ||  ||||||
                                CACTTATCT   CA  AAAATA
                                     ___  GG
GAM1091  FLJ11011  3'  TATGTGAAAAGGTAATTTA   28346       TAGAT    T
                                TATGTGAA    AGGTA TTTA
                                ||||||||    ||||| ||||
                                ATACACTT    TCCAT AAAT
                                     T____    T
GAM1091  FLJ21272  3'  TGTGAGTAGTAATTATTTTAT  28347     A   A   G
                                TGTGA TAG TAG TATTTTAT
                                ||||| ||| ||| ||||||||
                                ACACT ATC ATT ATAAAATA
                                   C   _   A
GAM1091  LANCL2    3'  TATGTGAAGAAGTCATATTTTA 28348      AT   TAG_
              T                  TATGTGA  AGA   GTATTTTAT
                                 |||||||  |||   |||||||||
                                 ATACACT  TCT   TATAAAATA
                                     __   TCAG
GAM1091  LOC91149  3'  TATGTGAATAATAGGCAT    28349        A
                                TATGTGAAT GATAGGTAT
                                ||||||||| |||||||||
                                ATACACTTA TTATCCGTA
                                     _
GAM1091  LOC93297  3'  TGTGGGATAGAGGCATTTT   28350     A_    TA
                                TGTG  ATAGA  GGTATTTT
                                ||||  |||||  ||||||||
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                                ACAC  TATCT  CCGTAAAA
                                  CC    __
GAM1092  OAS3     3'  CCTAGGTCTCGACTCC      28353      A    AATC
                                CCTA GGTC    CGACTCC
                                |||| ||||    |||||||
                                GGAT CCAG    GCTGAGG
                                  _    A___
GAM1092  DKFZp761J139 5'  TATCCTAACACTAATGATTTGG 28354         G TC   CCGA___
           CTCCA                    TATCCTAA G  AAT      CTCCA
                                |||||||| |  |||      |||||
                                ATAGGATT T  TTA      GAGGT
                                    G GA   CTAAACC
GAM1092  FLJ14437  3'  TATCCTAAGGTCACTACT    28355            ATCCG
                                TATCCTAAGGTCA    ACT
                                ||||||||||||    |||
                                ATAGGATTCCAGT    TGA
                                      GA___
GAM1092  KIAA1336  3'  TATCCTAAGCTCATCTAGGCTC 28356         G   A  CGA_
                                TATCCTAAG TCA TC    CTC
                                ||||||||| ||| ||    |||
                                ATAGGATTC AGT AG    GAG
                                    G   _  ATCC
GAM1092  LYPLA3    3'  TCCTAAGGTCACAGCAGTTCCA 28357          ATC  AC
                                TCCTAAGGTCA   CG  TCCA
                                ||||||||||   ||  ||||
                                AGGATTCCAGT   GT  AGGT
                                    GTC  CA
GAM1092  MGC16202  3'  TATCCTGAGGTCAACGGGA   28358       A       CC
                                TATCCT AGGTCAAT  GA
                                ||||||  ||||||||  ||
                                ATAGGA TCCAGTTG  CT
                                   C       CC
GAM1092  SCAMP-4   3'  CCTGGGTCCCCGACTC      28359     AA   AA
                                CCT  GGTC  TCCGACTC
                                |||  ||||  ||||||||
                                GGA  CCAG  GGGCTGAG
                                  C_   __
GAM1092  ZNF317    5'  CTCGGGGCAATCGACTCCA    28360    AA  T    C
                                CT  GG CAATC GACTCCA
                                ||  || ||||| |||||||
                                GA  CC GTTAG CTGAGGT
                                 GC  C    _
GAM1092  LOC144363 3'  CAAGGTCAGAAGTAATGACTCC 28361         ATCC____
           A                     TAAGGTCA       GACTCCA
                                ||||||||       |||||||
                                GTTCCAGT       CTGAGGT
                                    CTTCATTA
GAM1092  LOC146159 5'  CTAAACAATCCGACTTCA    28362       GT        C
                                CTAAG  CAATCCGACT CA
                                |||||  |||||||||| ||
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                                GATTT  GTTAGGCTGA GT
                                  __         A
GAM1092  LOC152179 5'  TCTTAAGGTCAATCTTCTC    28363     C         CGA
                                TC TAAGGTCAATC   CTC
                                || ||||||||||   |||
                                AG ATTCCAGTTAG   GAG
                                 A         AA_
GAM1092  LOC154739 5'  TATCCTGAGATCAACCCTCCA  28364       A         GAC
                                TATCCT AGGTCAATCC   TCCA
                                |||||| ||||||||||   ||||
                                ATAGGA TCTAGTTGGG   AGGT
                                   C        ___
GAM1092  LOC203276 3'  TATCCTGAGATCAACCCTCCA  28364       A         GAC
                                TATCCT AGGTCAATCC   TCCA
                                |||||| ||||||||||   ||||
                                ATAGGA TCTAGTTGGG   AGGT
                                   C        ___
GAM1092  LOC203305 3'  TATCCTGAGATCAACCCTCCA  28364       A         GAC
                                TATCCT AGGTCAATCC   TCCA
                                |||||| ||||||||||   ||||
                                ATAGGA TCTAGTTGGG   AGGT
                                   C        ___
GAM1092  LOC221755 3'  TATCCTAAGGTGATGGACGCC  28365           CAATCC   T
                                TATCCTAAGGT     GAC CC
                                ||||||||||      ||| ||
                                ATAGGATTCCA     CTG GG
                                      CTAC__   C
GAM1092  LOC254243 3'  TATCCTGAGATCAACCCTCCA  28364       A         GAC
                                TATCCT AGGTCAATCC   TCCA
                                |||||| ||||||||||   ||||
                                ATAGGA TCTAGTTGGG   AGGT
                                   C        ___
GAM1092  LOC51003  3'  CTAAAGTCAAGAGTCCA     28366          TCC  C
                                CTAAGGTCAA   GA TCCA
                                ||||||||||   || ||||
                                GATTTCAGTT   CT AGGT
                                      ___  C
GAM1092  LOC90038  3'  TATCCTGAGATCAACCTTCCA  28367       A         CGAC
                                TATCCT AGGTCAATC    TCCA
                                |||||| |||||||||    ||||
                                ATAGGA TCTAGTTGG    AGGT
                                   C        A___
GAM1092  LOC90321  3'  TCCTAAAGTCATGGCGTGCTC  28368          ATC  A_
                                TCCTAAGGTCA   CG  CTC
                                ||||||||||   ||  |||
                                AGGATTTCAGT   GC  GAG
                                      ACC  AC
GAM1093  ITPR1     3'  TTCATCTTTATATGGATGTATA 28371          TATCACC___
              TAGTT                  TTCATCTTT        ATATAGTT
                                |||||||||         ||||||||
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                                AAGTAGAAA        TATATCAA
                                     TATACCTACA
GAM1093  KRT12    3'  TTCATCTTTTATTACAAT    28372          CACCA
                                TTCATCTTTTAT    TATAGT
                                ||||||||||||    ||||||
                                AAGTAGAAAATA    ATGTTA
                                      _____
GAM1093  NRIP1    5'  TTCATCTTTTGTTCCCCAT    28373         A_  A
                                TTCATCTTTT  TC CCAT
                                |||||||||  || ||||
                                AAGTAGAAAA  AG GGTA
                                     CA  G
GAM1093  PLAB     3'  TTTTATCACCAGAGTT      28374          TAT
                                TTTTATCACCA   AGTT
                                ||||||||||   ||||
                                AAAATAGTGGT   TCAA
                                      C__
GAM1093  ZNF236   3'  TTCATCTTTTATTTATAGT   28375          CACCA
                                TTCATCTTTTAT    TATAGT
                                ||||||||||||    ||||||
                                AAGTAGAAAATA    ATATCA
                                      A____
GAM1093  DKFZp566D133 5'  TTCATCTCTTATTGTATCCCAA 28376          CA____   TAT
           GTT                    TCATCTTTTAT     CCA   AGTT
                                ||||||||||     |||   ||||
                                AGTAGAGAATA     GGT   TCAA
                                      ACATAG  ___
GAM1093  KIAA1977  5'  TTCATCCTTTGTCACCTCAC   28377         A    A
                                TTCATCTTTT TCACC TAT
                                |||||||||| ||||| |||
                                AAGTAGGAAA AGTGG GTG
                                     C    A
GAM1093  LRMP     5'  TCTTGACCACCATATAGT    28378     TT
                                TCTT  ATCACCATATAGT
                                ||||  ||||||||||||
                                AGAA  TGGTGGTATATCA
                                  C_
GAM1093  MRPL35   3'  TTCATCTTATTATTACCA    28379        _   C
                                TTCATCTT TTAT ACCA
                                |||||||| |||| ||||
                                AAGTAGAA AATA TGGT
                                     T   A
GAM1093  LOC253959 5'  TTCATCTCTTATTGTATCCCAA 28376          CA____   TAT
           GTT                    TCATCTTTTAT     CCA   AGTT
                                ||||||||||     |||   ||||
                                AGTAGAGAATA     GGT   TCAA
                                      ACATAG  ___
GAM1093  LOC254228 3'  TTCACCTTTTATCAATGCAGTT 28380           CC  A
                                TTCATCTTTTATCA  AT TAGTT
                                ||||||||||||||  || |||||
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                                AAGTGGAAAATAGT  TA GTCAA
                                        __ C
GAM1093  LOC257313 3'  TTCATCTTTTATTCCACAGCAA 28381          CA   ____
             TAGTT                 TCATCTTTTAT  CCAT    ATAGTT
                                   ||||||||||  ||||   ||||||
                                   AGTAGAAAATA  GGTG    TATCAA
                                         A_   TCGT
GAM1094  ADORA2B  3'  CACCATAAACAAGGCAGACTTT 28384     TGATTT   AA
                                   CACC     ACAA  CAGACTTT
                                   ||||     ||||  ||||||||
                                   GTGG     TGTT  GTCTGAAA
                                     TATT__   CC
GAM1094  ATP7A    3'  CACCTGATTTTAAGACT     28385          ACAAAAC
                                   CACCTGATTT      AGACT
                                   ||||||||||      |||||
                                   GTGGACTAAA      TCTGA
                                         AT_____
GAM1094  CELSR1   3'  CACCTGATTTGAAGAACAA   28386          ACAA
                                   CACCTGATTT    AACAG
                                   ||||||||||    |||||
                                   GTGGACTAAA    TTGTT
                                         CTTC
GAM1094  EXTL3    5'  CACCCTGGAATCAGACAGACTT 28387      GATTTA  AA
             T                      CACCT     CA  ACAGACTTT
                                   |||||     ||  |||||||||
                                   GTGGG     GT  TGTCTGAAA
                                      ACCTTA  C_
GAM1094  FRK      3'  ACCTATTTCTCAGACTT     28388      A   ACAAAA
                                   ACCTG TTT     CAGACTT
                                   ||||| |||     |||||||
                                   TGGAT AAA     GTCTGAA
                                      _  GA____
GAM1094  GDF8     3'  CACTTATTTACAAAACAA    28389     CTG
                                   CAC   ATTTACAAAACAG
                                   |||   ||||||||||||||
                                   GTG   TAAATGTTTTGTT
                                     AA_
GAM1094  NR5A2    3'  TGTTCTACAGCAGACTTT    28390    A     AAA
                                   TG TTTACA   CAGACTTT
                                   || ||||||   ||||||||
                                   AC AGATGT   GTCTGAAA
                                    A     C__
GAM1094  PIK3R3   3'  CCCAATGAAACAGACTTT    28391    TG  TTACA
                                   CC  AT    AAACAGACTTT
                                   ||  ||    ||||||||||
                                   GG  TA    TTTGTCTGAAA
                                    GT  C____
GAM1094  PODXL    3'  CACCTGATCTACAAGACAAATA 28392           A   __
             CTTT                    CACCTGATTTACAA ACAG  ACTTT
                                   |||||||||||||| ||||  |||||
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                                GTGGACTAGATGTT TGTT  TGAAA
                                       C    TA
GAM1094  PRKCN    3'  TGATATAAACAGACTTT     28393      TTACA
                                TGAT     AAACAGACTTT
                                ||||     ||||||||||
                                ACTA     TTTGTCTGAAA
                                  TA___
GAM1094  AFAP     3'  CACACTTTTTGAAACAGACTTT 28394     _  GATTTACA
                                CAC CT       AAACAGACTTT
                                ||| ||       ||||||||||
                                GTG GA       TTTGTCTGAAA
                                  T  AAAAC___
GAM1094  ALS2CR3  3'  CATCTGATGAGAAGCAGACTTT 28395    C    TTACAAAA
                                CA CTGAT       CAGACTTT
                                || |||||       ||||||||
                                GT GACTA       GTCTGAAA
                                 A    CTCTTC__
GAM1094  CKLFH1   5'  CCTGATTTGTACGGGACTTT   28396        ACAAA  A_
                                CCTGATTT    AC  GACTTT
                                ||||||||    ||  ||||||
                                GGACTAAA    TG  CTGAAA
                                     CA___  CC
GAM1094  DIS3     3'  CTGATTTACTTGGCAGGCTTT  28397         AAAA   A
                                CTGATTTAC    CAG CTTT
                                |||||||||    ||| ||||
                                GACTAAATG    GTC GAAA
                                      AACC   C
GAM1094  FLJ20054 3'  ACCTGATTTAAAAGCACAG    28398          C  A_
                                ACCTGATTTA AA  ACAG
                                |||||||||| ||  ||||
                                TGGACTAAAT TT  TGTC
                                      T  CG
GAM1094  FLJ20701 3'  ACCAGGATTGAAAACAGACTTT 28399     T_    TAC
                                ACC  GATT   AAAACAGACTTT
                                |||  ||||   ||||||||||||
                                TGG  CTAA   TTTTGTCTGAAA
                                  TC    C__
GAM1094  FLJ21032 3'  CTAATAAAACAGACTTT     28400       TTAC
                                CTGAT    AAAACAGACTTT
                                |||||    ||||||||||||
                                GATTA    TTTTGTCTGAAA
                                     _____
GAM1094  HIG2     3'  CACCTGTGCATTAAACAGGCTT 28401        ATTTACA     A
           T                     CACCTG       AAACAG CTTT
                                 ||||||       |||||| ||||
                                 GTGGAC       TTTGTC GAAA
                                    ACGTAA_     C
GAM1094  KIAA0063 3'  TGATGTCAAAAGCAGACTTT   28402      TTA    _
                                TGAT   CAAAA CAGACTTT
                                ||||   ||||| ||||||||
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                                ACTA   GTTTT GTCTGAAA
                                  CA_    C
GAM1094  KIAA0202  3'  TGATGTCACAAAGCAGACTTT  28403     _     A
                                TGAT TTACAAA CAGACTTT
                                |||| ||||||| ||||||||
                                ACTA AGTGTTT GTCTGAAA
                                  C      C
GAM1094  KIAA0534  3'  CAACTGATCGCTGGACAGACTT 28404    C     TACAAA
           T                     CA CTGATT     ACAGACTTT
                                || ||||||     |||||||||
                                GT GACTAG     TGTCTGAAA
                                 T     CGACC_
GAM1094  MKNK1     3'  CCTGCTCAGCAGACTT      28405      A    CAAAA
                                CCTG TTTA     CAGACTT
                                |||| ||||     |||||||
                                GGAC GAGT     GTCTGAA
                                  _    C____
GAM1094  PRO0082   3'  TGCTTAAAAACAGACTTT    28406    A    C
                                TG TTTA AAAACAGACTTT
                                || |||| ||||||||||||
                                AC GAAT TTTTGTCTGAAA
                                 _    _
GAM1094  PTPRR     3'  CCATTCACAAGACAGA      28407    TG       A
                                CC  ATTTACAA ACAGA
                                ||  |||||||| |||||
                                GG  TAAGTGTT TGTCT
                                 __       C
GAM1094  PTPRR     3'  CCATTCACAAGACAGA      28407    TG       A
                                CC  ATTTACAA ACAGA
                                ||  |||||||| |||||
                                GG  TAAGTGTT TGTCT
                                 __       C
GAM1094  Rab11-FIP3 3'  CTGATTTACACCCAAGGCTTT  28408          AAA   A_
                                CTGATTTACA   CAG  CTTT
                                ||||||||||   |||  ||||
                                GACTAAATGT   GTT  GAAA
                                      GG_   CC
GAM1094  RI58      3'  CCTGATTTATAAAAACAA     28409         C_
                                CCTGATTTA  AAAACAG
                                |||||||||  |||||||
                                GGACTAAAT  TTTTGTT
                                     AT
GAM1094  SERPINA10 3'  CCTAATTTATAAATTAAACTTT 28410         C   AC
                                CCTGATTTA AAA  AGACTTT
                                ||||||||| |||  |||||||
                                GGATTAAAT TTT  TTTGAAA
                                     A   AA
GAM1094  ZNF313    3'  ACTTACGGATAAACAGACTTT  28411       A___
                                ATTTAC    AAACAGACTTT
                                ||||||    ||||||||||
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                                TGAATG    TTTGTCTGAAA
                                   CCTA
GAM1094  LOC147166 5'  CACCGACACCAGAACAGACTTT 28412      T   TTA  A
                                CACC GAT   CA AACAGACTTT
                                |||| |||   || ||||||||||
                                GTGG CTG   GT TTGTCTGAAA
                                  _   TG_  C
GAM1094  LOC163992 5'  ACCTGATTTGCAGTGACAACCT 28413          A  AAACA
                                ACCTGATTT CA     GACTT
                                ||||||||| ||     |||||
                                TGGACTAAA GT     TTGGA
                                     C  CACTG
GAM1094  LOC200854 5'  TGATCCAGGACAGGACAGACTT 28414        ___   AA
                   T                 TGATTT   ACA  ACAGACTTT
                                |||||   |||  |||||||||
                                ACTAGG   TGT  TGTCTGAAA
                                   TCC   CC
GAM1094  LOC202754 3'  CTGAATCACCACAGACTTT    28415      T    AAA
                                CTGA TTAC   ACAGACTTT
                                |||| ||||   |||||||||
                                GACT AGTG   TGTCTGAAA
                                  T   G__
GAM1094  LOC221092 5'  ACCTTTGCCTCAAAGCAGACTT 28416      GATTTA    A
                   T                 ACCT      CAAA CAGACTTT
                                ||||      |||| ||||||||
                                TGGA      GTTT GTCTGAAA
                                  AACGGA    C
GAM1094  LOC91664  3'  ACTTGATTTACAACTGTAAACT 28417    C         AAC_
                   TT                 AC TGATTTACAA    AGACTTT
                                || ||||||||||    |||||||
                                TG ACTAAATGTT    TTTGAAA
                                 A         GACA
GAM1094  LOC93206  3'  CACTTGATTACAGACTT     28418     C     TACAAA
                                CAC TGATT      ACAGACTT
                                ||| |||||      ||||||||
                                GTG ACTAA      TGTCTGAA
                                  A    _______
GAM1095  EPS8      3'  TCTAAATATTCTTCCAT      28421      A
                                TCTA GATATTCTTCCAT
                                |||| ||||||||||||
                                AGAT TTATAAGAAGGTA
                                  _
GAM1095  RNASE4    3'  TCTCAATTCTTCCATTAACTT  28422      AAGAT         C
                                TCT     ATTCTTCCAT AACTT
                                |||     |||||||||| |||||
                                AGA     TAAGAAGGTA TTGAA
                                  GT___         A
GAM1095  SOX11     3'  TAAGATATTCTGTCAA       28423           TCCA
                                TAAGATATTCT    TCAA
                                ||||||||||    ||||
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                                ATTCTATAAGA   AGTT
                                      C___
GAM1095 ATP1B4   3' CAAGATATTTTTCCTCA     28424        C   A
                                TAAGATATT TTCC TCA
                                ||||||||| |||| |||
                                GTTCTATAA AAGG AGT
                                    A   _
GAM1095 FLJ10648 3' TAAAATAATTTTCCATCAGCTT 28425       TTC      A
                                TAAGATA   TTCCATCA CTT
                                |||||||   |||||||| |||
                                ATTTTAT   AAGGTAGT GAA
                                    TAA      C
GAM1095 FLJ20701 3' CCTAAGATATCATCAA      28426         TCTTC
                                TCTAAGATAT    CATCAA
                                ||||||||||    ||||||
                                GGATTCTATA    GTAGTT

                                     _____
GAM1095 LOC145945 5' CTAAAATTTTCCATCA      28427       ATTC
                                CTAAGAT    TTCCATCA
                                |||||||    ||||||||
                                GATTTTA    AAGGTAGT
                                    A___
GAM1095 LOC152059 3' TCCAAGACTCCATTAACT    28428       ATTCT    C
                                TCTAAGAT    TCCAT AACT
                                ||||||||    ||||| ||||
                                AGGTTCTG    AGGTA TTGA
                                     _____    A
GAM1095 LOC153339 5' TCTAGAATATTCTTCCTC    28429     AG        A
                                TCTA  ATATTCTTCC TC
                                ||||  |||||||||| ||
                                AGAT  TATAAGAAGG AG
                                  CT        _
GAM1095 LOC256476 5' CTAAGATATTCTTAAACT    28430          CCATC
                                CTAAGATATTCTT    AACT
                                ||||||||||||    ||||
                                GATTCTATAAGAA    TTGA
                                       T____
GAM1096 ABCC3    3' CACGAGCTGCCTCTGG      28433       GC   CTGCG
                                CACGAGCTG  CCTC    GG
                                |||||||||  ||||    ||
                                GTGCTCGAC  GGAG    CC
                                     __   A____
GAM1096 ABCC3    3' CACGAGCTGCCTCTGG      28433       GC   CTGCG
                                CACGAGCTG  CCTC    GG
                                |||||||||  ||||    ||
                                GTGCTCGAC  GGAG    CC
                                     __   A____
GAM1096 BRCA1    3' CACGAGCTGACTCTGGGGC   28434         CCTC  C
                                CACGAGCTGGC   CTG GGGC
                                ||||||||||   ||| ||||
```

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                                GTGCTCGACTG   GAC CCCG
                                    A___  _
GAM1096 CAPN10   3' CACCAGCTGGCCCCCAGGGC  28435    G       CTGC
                                CAC AGCTGGCCCTC   GGGC
                                ||| ||||||||||   ||||
                                GTG TCGACCGGGGGG   CCCG
                                  G        T___
GAM1096 CAPN10   3' CACCAGCTGGCCCCCAGGGC  28435    G       CTGC
                                CAC AGCTGGCCCTC   GGGC
                                ||| ||||||||||   ||||
                                GTG TCGACCGGGGGG   CCCG
                                  G        T___
GAM1096 CAPN10   3' CACCAGCTGGCCCCCAGGGC  28435    G       CTGC
                                CAC AGCTGGCCCTC   GGGC
                                ||| ||||||||||   ||||
                                GTG TCGACCGGGGGG   CCCG
                                  G        T___
GAM1096 CAPN10   3' CACCAGCTGGCCCCCAGGGC  28435    G       CTGC
                                CAC AGCTGGCCCTC   GGGC
                                ||| ||||||||||   ||||
                                GTG TCGACCGGGGGG   CCCG
                                  G        T___
GAM1096 CAPN10   3' CACCAGCTGGCCCCCAGGGC  28435    G       CTGC
                                CAC AGCTGGCCCTC   GGGC
                                ||| ||||||||||   ||||
                                GTG TCGACCGGGGGG   CCCG
                                  G        T___
GAM1096 CAPN10   3' CACCAGCTGGCCCCCAGGGC  28435    G       CTGC
                                CAC AGCTGGCCCTC   GGGC
                                ||| ||||||||||   ||||
                                GTG TCGACCGGGGGG   CCCG
                                  G        T___
GAM1096 CCND1    3' GAGCTGGCTGCAGGGC     28436       CCTCC  _
                                GAGCTGGC    TGC GGGC
                                ||||||||    ||| ||||
                                CTCGACCG    ACG CCCG
                                    _____   T
GAM1096 FBP1     5' CGGGCGGCAGGTGCGGGCC   28437    A  T   CCTCC
                                CG GC GGC    TGCGGGCC
                                || || |||    ||||||||
                                GC CG CCG    ACGCCCGG
                                 C  _   TCC__
GAM1096 FOXE1    5' CGGGCTGGCCCCGAGAGCC   28438    A       CCT C
                                CG GCTGGCCCT   G GGGCC
                                || |||||||||   | |||||
                                GC CGACCGGGG   C CTCGG
                                 C        ___ T
GAM1096 G6PC     3' GAGCTGGCCCTACCTGGAAG  28439          _   CG
                                GAGCTGGCCCT CCTG  GG
                                |||||||||| ||||  ||
```

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                                CTCGACCGGGA GGAC  TC
                                      T    CT
GAM1096  GYPE     5'  CACGAGCTGGCTCCTGAAG   28440          CC    C
                                CACGAGCTGGC  TCCTG GG
                                |||||||||||  ||||| ||
                                GTGCTCGACCG  AGGAC TC
                                      __     T
GAM1096  HSD17B1  5'  CAAGGATAAGCCTTCCTGCGGG 28441      CT__   C
                                CGAG   GGCC TCCTGCGGG
                                ||||   |||| |||||||||
                                GTTC   TCGG AGGACGCCC
                                  CTAT   A
GAM1096  KIAA0857 5'  CGGGCTGGGCTGGGCCGGGCC  28442    A    CCCTC  ___
                                CG GCTGG    CTG   CGGGCC
                                || |||||    |||   ||||||
                                GC CGACC    GAC   GCCCGG
                                 C    C____   CCG
GAM1096  MECP2    3'  GAGCTGGCCCCGGATGTGGGCC 28443          CC_  C
                                GAGCTGGCCCT   TG GGGCC
                                ||||||||||   || |||||
                                CTCGACCGGGG   AC CCCGG
                                      CCT  A
GAM1096  MKNK2    3'  GAGCTGGCCTGGGGC      28444         CTCC  C
                                GAGCTGGCC    TG GGGC
                                |||||||||    || ||||
                                CTCGACCGG    AC CCCG
                                     ____  _
GAM1096  PIK4CB   3'  CACAGCTGGCTCTCCCAC    28445     G     C   TG
                                CAC AGCTGGC CTCC  C
                                ||| ||||||| ||||  |
                                GTG TCGACCG GAGG  G
                                  _     A   GT
GAM1096  PRX2     5'  CGAGCGGCCCCGGGGGGGCC  28446      T     CCTGC
                                CGAGC GGCCCT    GGGCC
                                ||||| ||||||    |||||
                                GCTCG CCGGGG    CCCGG
                                   _     CCCC_
GAM1096  RGS14    3'  ACCGGCTCTTCCTGCGGGCC  28447      C  _
                                GCTGGC CT CCTGCGGGCC
                                |||||| || ||||||||||
                                TGGCCG GA GGACGCCCGG
                                   A  A
GAM1096  RNPEPL1  3'  CGGGCTGGCCCCAGGGC    28448    A       CCTGC
                                CG GCTGGCCCT    GGGC
                                || |||||||||    ||||
                                GC CGACCGGGG    CCCG
                                 C       T____
GAM1096  SDC1     5'  CGGGCCGGCTTCGCGGG    28449    A    CC  CT
                                CG GCTGGC  TC  GCGGG
                                || ||||||  ||  |||||
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                                GC CGGCCG  AG  CGCCC
                                 C     A_ __
GAM1096  SLC6A3   3'  GACTGGCCCTGCACGGCC    28450    G      CCT  _
                                GA CTGGCCCT   GCG GGCC
                                || ||||||||   ||| ||||
                                CT GACCGGGA   CGT CCGG
                                 _      ____  G
GAM1096  SURF5    5'  CACGGCCTGGCCCTCCCGC    28451     AG
                                CACG  CTGGCCCTCCTGC
                                ||||  ||||||||||||
                                GTGC  GACCGGGAGGGCG
                                  CG
GAM1096  SURF5    5'  CACGGCCTGGCCCTCCCGC    28451     AG
                                CACG  CTGGCCCTCCTGC
                                ||||  ||||||||||||
                                GTGC  GACCGGGAGGGCG
                                  CG
GAM1096  TCN2     5'  GCTGGCCCTGCTGAGGC     28452        C   C
                                GCTGGCCCT CTG GGGC
                                ||||||||| ||| ||||
                                CGACCGGGA GAC TCCG
                                     C  _
GAM1096  VIPR2    3'  CGCAGCTGGCCTGGGG      28453    _      CTCC  C
                                CG AGCTGGCC    TG GGG
                                || ||||||||    || |||
                                GC TCGACCGG    AC CCC
                                 G      _____ _
GAM1096  ARFGAP3  5'  CGCAGCTGGCCCTCGTGC    28454    _        C
                                CG AGCTGGCCCTC TGC
                                || ||||||||||| |||
                                GC TCGACCGGGAG ACG
                                 G         C
GAM1096  ATIP1    3'  GAGCTGGCTCTGGGGC      28455        CCTC   C
                                GAGCTGGC    CTG GGGC
                                ||||||||    ||| ||||
                                CTCGACCG    GAC CCCG
                                     A___   _
GAM1096  BLR1     3'  AGCTGGCCTTTCCTCAGCC    28456        C_   G   G
                                AGCTGGCC  TCCT CGG CC
                                ||||||||  |||| ||| ||
                                TCGACCGG  AGGA GTC GG
                                     AA   _  _
GAM1096  BLR1     3'  AGCTGGCCTTTCCTCAGCC    28456        C_   G   G
                                AGCTGGCC  TCCT CGG CC
                                ||||||||  |||| ||| ||
                                TCGACCGG  AGGA GTC GG
                                     AA   _  _
GAM1096  C11orf9  3'  GAGCTGGCCTGCAGCGGGC    28457         CTCCT
                                GAGCTGGCC    GCGGGC
                                |||||||||    ||||||
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                                CTCGACCGG    CGCCCG
                                     ACGT_
GAM1096 C1QR1    3' GCTGGCCCTTCCTGAAGCC   28458        _   C
                                GCTGGCCCT CCTG GGGCC
                                ||||||||| |||| |||||
                                CGACCGGGA GGAC TTCGG
                                     A   _
GAM1096 C1QTNF4  5' CGGGCTGCGGGCTGCGGGC   28459    A   G CCTC
                                CG GCTG C   CTGCGGGC
                                || |||| |   ||||||||
                                GC CGAC G   GACGCCCG
                                 C   _ CCC_
GAM1096 C20orf51 5' CACGAGCTTGTCTTCCTGGG  28460       GGCCC    C
                                CACGAGCT    TCCTG GG
                                ||||||||    ||||| ||
                                GTGCTCGA    AGGAC CC
                                     ACAGA   _
GAM1096 CENTG2   5' CGGGGCTGGCCCGCGGGC    28461    A_      TCCT
                                CG  GCTGGCCC   GCGGGC
                                ||  ||||||||   ||||||
                                GC  CGACCGGG   CGCCCG
                                 CC      _____
GAM1096 DOC2B    3' CGGGGCTGGCCCTCTAGAAGGG 28462    A_       CTGC_
                                CG  GCTGGCCCTC    GGG
                                ||  ||||||||||    |||
                                GC  CGACCGGGAG    CCC
                                 CC        ATCTT
GAM1096 FBP17    3' CACGAGGTGGCCCGGG     28463      C     TCCTGC
                                CACGAG TGGCCC     GGG
                                |||||| ||||||     |||
                                GTGCTC ACCGGG     CCC
                                   C    _______
GAM1096 FLJ10079 3' CACGAGCTGCCCCTCAGGGC  28464        G    CTGC
                                CACGAGCTG CCCTC   GGGC
                                ||||||||| |||||   ||||
                                GTGCTCGAC GGGAG   CCCG
                                     G    T___
GAM1096 FLJ13940 5' CGAGCTGGCCCTCTCCAGCC  28465          _ GCG
                                CGAGCTGGCCCTC CT  GGCC
                                |||||||||||| ||  ||||
                                GCTCGACCGGGAG GG  TCGG
                                       A ___
GAM1096 FLJ14326 3' CACAAGCTGGCCTTTCTGGAC 28466          CTC  GC
                                CACGAGCTGGCC  CT  GGGC
                                ||||||||||||  ||  ||||
                                GTGTTCGACCGG  GA  CCTG
                                       AAA __
GAM1096 FLJ14641 5' CACGAGCTGGTTTCCTGAC   28467        CCC   _
                                CACGAGCTGG   TCCTG C
                                ||||||||||   ||||| |
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                                GTGCTCGACC   AGGAC G
                                      AA_    T
GAM1096  FLJ20457  3'  AGTTGGCCCTTTGGAACC    28468    C      CC  C
                                AG TGGCCCT  TG GGGCC
                                || |||||||  || |||||
                                TC ACCGGGA  AC CTTGG
                                 A      A_  _
GAM1096  FLJ21087  3'  CACAGCTCCTGCGGG       28469     G   TGGCCC
                                CAC AGC     TCCTGCGGG
                                ||| |||     |||||||||
                                GTG TCG     AGGACGCCC
                                  _  _______
GAM1096  FLJ22559  5'  CGACCTGGCCCTTCCGGCG   28470     G       _  T
                                CGA CTGGCCCT CC GCG
                                ||| |||||||| || |||
                                GCT GACCGGGA GG CGC
                                  G       A  C
GAM1096  FLJ23042  3'  CGAGCTGGTGCCTGCCTGGCC  28471         CCCT    G_
                                CGAGCTGG    CCTGC  GGCC
                                ||||||||    |||||  ||||
                                GCTCGACC    GGACG  CCGG
                                     AC__     GA
GAM1096  KIAA0450  3'  CGAAGCCCCTCCTGTGGGCC   28472     _  TGG       C
                                CGA GC   CCCTCCTG GGGCC
                                ||| ||   |||||||| |||||
                                GCT CG   GGGAGGAC CCCGG
                                  T  ____       A
GAM1096  KIAA0964  3'  GAGCTGGCTTCGGGGC      28473         CC  CT C
                                GAGCTGGC  TC  G GGGC
                                ||||||||  ||  | ||||
                                CTCGACCG  AG  C CCCG
                                     A_  __ _
GAM1096  LSR7      5'  GAGCTGGTCCTGCAACAGGGC  28474        CCC     _____
                                GAGCTGG   TCCTGC   GGGC
                                |||||||   ||||||   ||||
                                CTCGACC   AGGACG   CCCG
                                     ___     TTGT
GAM1096  MGC16186  5'  GCTGCGTCTCCTGCGGGC    28475     GCC
                                GCTG   CTCCTGCGGGC
                                ||||   ||||||||||
                                CGAC   GAGGACGCCCG
                                  GCA
GAM1096  MGC17998  3'  GACCTGTTTCTCCTGCGGG   28476    G   GCC
                                GA CTG   CTCCTGCGGG
                                || |||   ||||||||||
                                CT GAC   GAGGACGCCC
                                 G   AAA
GAM1096  PPIE      3'  GAGCTGGCTCCTGGGC      28477         CC    GC
                                GAGCTGGC  TCCT  GGGC
                                ||||||||  ||||  ||||
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                                CTCGACCG  AGGA  CCCG
                                   __   __
GAM1096  PSIP2    5'  CGGGCGGCGGACGCGGGCC   28478    A  T   CCTCC
                                CG GC GGC    TGCGGGCC
                                || || |||    ||||||||
                                GC CG CCG    GCGCCCGG
                                 C  _   CCT__
GAM1096  PTDSS2   5'  CGGCGCTGGCCCGCGGG    28479    A_      TCCT
                                CG  GCTGGCCC   GCGGG
                                ||  ||||||||   |||||
                                GC  CGACCGGG   CGCCC
                                 CG       ____
GAM1096  TOLLIP   3'  CACGGGCTGCTCAAGGGC    28480     A   GCC   CTGC
                                CACG GCTG   CTC   GGGC
                                |||| ||||   |||   ||||
                                GTGC CGAC   GAG   CCCG
                                  C   ___   TT__
GAM1096  UHRF1    3'  CACGGGCTGCCACGGG     28481     A   G  CTCCT
                                CACG GCTG CC    GCGGG
                                |||| |||| ||    |||||
                                GTGC CGAC GG    TGCCC
                                  C   _ _____
GAM1096  LOC122700 5'  GAGCTGGCCCTGGGGC     28482          CCT C
                                GAGCTGGCCCT   G GGGC
                                ||||||||||   | ||||
                                CTCGACCGGGA   C CCCG
                                     ___ _
GAM1096  LOC126823 5'  ACGGCCTGGCCCCTAGCTGGG  28483     AG      CCT  _
                                ACG  CTGGCCCT   GC GGG
                                |||  ||||||||   || |||
                                TGC  GACCGGGG   CG CCC
                                  CG       AT_  A
GAM1096  LOC143287 3'  GAGCCTGGGGCTGCGGGCC   28484     _   CCCTC
                                GAGC TGG    CTGCGGGCC
                                |||| |||    |||||||||
                                CTCG ACC    GACGCCCGG
                                  G   CC___
GAM1096  LOC148479 3'  GAGCTGGCCCTCACAGGGGCC  28485          CTGC
                                GAGCTGGCCCTC    GGGCC
                                ||||||||||||   |||||
                                CTCGACCGGGAG    CCCGG
                                      TGTC
GAM1096  LOC151174 5'  GAGATGGCCCTCAACGCC    28486     C       CT  GG
                                GAG TGGCCCTC  GC  GCC
                                ||| ||||||||  ||  |||
                                CTC ACCGGGAG  TG  CGG
                                  T       T_  __
GAM1096  LOC151534 5'  CGAATTGAAGCTCTGTGGGC   28487     C   CC   C  C
                                CGAG TGG  CTC TG GGGC
                                |||| |||  ||| || ||||
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                                GCTT ACT  GAG AC CCCG
                                  A   TC   _ A
GAM1096  LOC163682 3'  GAGTGGACTCTCTTGTGGGC   28488    C   _ C   C  C
                                GAG TGG C CTC TG GGGC
                                ||| ||| | ||| || ||||
                                CTC ACC G GAG AC CCCG
                                  _   T A   A  A
GAM1096  LOC170394 5'  GCTGCCCAGCCTCCTGCGGGCC 28489     G  ___
                                GCTG CC   CTCCTGCGGGCC
                                |||| ||   ||||||||||||
                                CGAC GG   GAGGACGCCCGG
                                  G  TCG
GAM1096  LOC200349 3'  GACCTGGCCCTTTCAGCC    28490    G      CCTG   G
                                GA CTGGCCCT    CGG CC
                                || ||||||||    ||| ||
                                CT GACCGGGA    GTC GG
                                 G       AA__   _
GAM1096  LOC203052 3'  GAGCTGGCCCTCCCCCTGCC   28491           GCGG
                                GAGCTGGCCCTCCT    GCC
                                ||||||||||||||    |||
                                CTCGACCGGGAGGG    CGG
                                        GGA_
GAM1096  LOC255506 5'  GAGCTGGCTGCCCTGGGC    28492        CC    GC
                                GAGCTGGC  TCCT  GGGC
                                ||||||||  ||||  ||||
                                CTCGACCG  GGGA  CCCG
                                     AC   __
GAM1096  LOC255975 3'  GAGCTGGCCCTGGACAGGCC   28493          CCT
                                GAGCTGGCCCT   GCGGGCC
                                ||||||||||   |||||||
                                CTCGACCGGGA   TGTCCGG
                                       CC_
GAM1096  LOC256158 5'  CACGGGCTGGCCGTCCCGC    28495     A      C
                                CACG GCTGGCC TCCTGC
                                |||| ||||||| ||||||
                                GTGC CGACCGG AGGGCG
                                  C      C
GAM1096  LOC256158 5'  CGGCTGGCCCGCAAGGG     28494    A      TCCT  __
                                CG GCTGGCCC    GC  GGG
                                || ||||||||    ||  |||
                                GC CGACCGGG    CG  CCC
                                 _       _____  TT
GAM1096  LOC256586 5'  ACGAGCGGGTCTTGGTGCGGGC 28496       T  CC  CC_
            C                    ACGAGC GG  CT   TGCGGGCC
                                ||||||  ||  ||   ||||||||
                                TGCTCG CC  GA   ACGCCCGG
                                   C  A_  ACC
GAM1096  LOC257019 3'  CACGGGCAGGTTCTGCTGGG   28497      A  T  CCCTC   _
                                CACG GC GG    CTGC GGG
                                |||| || ||    |||| |||
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                                GTGC CG CC    GACG CCC
                                  C  T  AA___   A
GAM1096 LOC51285 3' CGTAGCTGGCCTGTGGG    28498   _     CTCC  C
                                CG AGCTGGCC   TG GGG
                                || ||||||||   || |||
                                GC TCGACCGG   AC CCC
                                 A      ____ A
GAM1096 LOC90050 5' CGAGCTGACCTTGCGGGC   28499       CTCC
                                CGAGCTGGCC   TGCGGGC
                                ||||||||||   |||||||
                                GCTCGACTGG   ACGCCCG
                                     A___
GAM1096 LOC90768 5' CGATCTGGCCCTTCTCGC   28500    G      C  _
                                CGA CTGGCCCT CT GC
                                ||| |||||||| || ||
                                GCT GACCGGGA GA CG
                                  A       A  G
GAM1097 CAPN10   3' GGGCTCCAGTCACCTGA    28503    TTCACC   AC
                                GGGC    TCCA  CACCTGA
                                ||||    ||||  |||||||
                                CCCG    AGGT  GTGGACT
                                  _______   CA
GAM1097 CAPN10   3' GGGCTCCAGTCACCTGA    28503    TTCACC   AC
                                GGGC    TCCA  CACCTGA
                                ||||    ||||  |||||||
                                CCCG    AGGT  GTGGACT
                                  _______   CA
GAM1097 CAPN10   3' GGGCTCCAGTCACCTGA    28503    TTCACC   AC
                                GGGC    TCCA  CACCTGA
                                ||||    ||||  |||||||
                                CCCG    AGGT  GTGGACT
                                  _______   CA
GAM1097 CAPN10   3' GGGCTCCAGTCACCTGA    28503    TTCACC   AC
                                GGGC    TCCA  CACCTGA
                                ||||    ||||  |||||||
                                CCCG    AGGT  GTGGACT
                                  _______   CA
GAM1097 CAPN10   3' GGGCTCCAGTCACCTGA    28503    TTCACC   AC
                                GGGC    TCCA  CACCTGA
                                ||||    ||||  |||||||
                                CCCG    AGGT  GTGGACT
                                  _______   CA
GAM1097 CAPN10   3' GGGCTCCAGTCACCTGA    28503    TTCACC   AC
                                GGGC    TCCA  CACCTGA
                                ||||    ||||  |||||||
                                CCCG    AGGT  GTGGACT
                                  _______   CA
GAM1097 CAPN10   3' GGGCTCCAGTCACCTGA    28503    TTCACC   AC
                                GGGC    TCCA  CACCTGA
                                ||||    ||||  |||||||
                                CCCG    AGGT  GTGGACT
                                  _______   CA
GAM1097 GCH1     5' GGGCTGTGGCCGGAGTCACCTG 28504      TCA_  TCCAAC
           AG                   GGGCT   CC    CACCTGAG
                                |||||   ||    ||||||||
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                                CCCGA   GG     GTGGACTC
                                  CACC  CCTCA_
GAM1097 MMP14    3'  GGGCCTCAGCCCCAGCTGCCTG 28505        C    ACCA
            AG                    GGGCTTCA CTCCA    CCTGAG
                                  |||||||| |||||    ||||||
                                  CCCGGAGT GGGGT    GGACTC
                                      C    CGAC
GAM1097 ARFGAP3  3'  GGACTTCACTGCCGCCTGA   28506        CTCCAA  A
                                  GGGCTTCAC     CC CCTGA
                                  |||||||||     || |||||
                                  CCTGAAGTG     GG GGACT
                                       AC____  C
GAM1097 BTF3     5'  GGGTCTCGGGTGGACCACCTGA 28507     CT  ACCTCCA
            G                     GGG  TC      ACCACCTGAG
                                  |||  ||      ||||||||||
                                  CCC  AG      TGGTGGACTC
                                    AG  CCCACC_
GAM1097 FLJ10094 5'  AGGCTTCATCCCTTTACCTGAG 28508        CC   AACC
                                  GGGCTTCA  TCC    ACCTGAG
                                  ||||||||  |||    |||||||
                                  TCCGAAGT  AGG    TGGACTC
                                       __   GAAA
GAM1097 FLJ13204 5'  GGGTTTTACCTCCAGCCCA    28509     C  C      A_
                                  GGG TT ACCTCCA  CCA
                                  ||| || |||||||  |||
                                  CCC AA TGGAGGT  GGT
                                    A  A      CG
GAM1097 FLJ20003 3'  GGACTTCACTATCCATTTGAG  28510        CTCCAA   CC
                                  GGGCTTCAC     CCA  TGAG
                                  |||||||||     |||  ||||
                                  CCTGAAGTG     GGT  ACTC
                                       ATA___   AA
GAM1097 HEI10    5'  GGATTTCATCTCCAACCA    28511    GC   C
                                  GG  TTCA CTCCAACCA
                                  ||  |||| |||||||||
                                  CC  AAGT GAGGTTGGT
                                   TA    A
GAM1097 KIAA0869 3'  GGCTTCACTGGGCATCTGAG   28512        CTCCAAC  C
                                  GGCTTCAC      CA CTGAG
                                  ||||||||      || |||||
                                  CCGAAGTG      GT GACTC
                                       ACCC___  A
GAM1097 KIAA1028 3'  GGGCATCACAGGTCCACCTGAG 28513     T    CTCCAA
                                  GGGC TCAC     CCACCTGAG
                                  |||| ||||     |||||||||
                                  CCCG AGTG     GGTGGACTC
                                    T   TCCA__
GAM1097 NIP30    3'  GGGCTCCATTTCATTACCTG   28514        CC  CAACC
                                  GGGCTTCA  TC    ACCTG
                                  ||||||||  ||    |||||
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                                CCCGAGGT  AG    TGGAC
                                    AA  TAA__
GAM1097  PALM     3'  GGCCTCACCCCAACTGCCTGAG 28515        T    CA
                                GGCTTCACC CCAAC  CCTGAG
                                ||||||||| |||||  ||||||
                                CCGGAGTGG GGTTG  GGACTC
                                    _    AC
GAM1097  PNMA5    3'  GGGCTTCACTTCTGCCCCAC  28516        C  CAA_
                                GGGCTTCAC TC   CCAC
                                ||||||||| ||   ||||
                                CCCGAAGTG AG   GGTG
                                    A  ACGG
GAM1097  LOC147632 3'  GGGCTTCACCTTCAATCA    28517         C   C
                                GGGCTTCACCT CAA CA
                                |||||||||| ||| ||
                                CCCGAAGTGGA GTT GT
                                     A   A
GAM1097  LOC147922 5'  GGGCTTCACCTTGACCAC    28518         CCA
                                GGGCTTCACCT   ACCAC
                                ||||||||||   |||||
                                CCCGAAGTGGA   TGGTG
                                     AC_
GAM1097  LOC196746 3'  GGGCTCCACACCAGCTGCCTG  28519        CT   ACCA
                                GGGCTTCAC  CCA   CCTG
                                |||||||| |||   ||||
                                CCCGAGGTG  GGT   GGAC
                                    T_   CGAC
GAM1097  LOC219988 5'  GCTCCAGTTTGGCCACCTGAG  28520      CCTCCAA
                                GCTTCA      CCACCTGAG
                                ||||||      |||||||||
                                CGAGGT      GGTGGACTC
                                   CAAACC_
GAM1097  LOC93052  3'  GGGCTCCAGTAACCACCTG   28521        CCTCC
                                GGGCTTCA    AACCACCTG
                                ||||||||    |||||||||
                                CCCGAGGT    TTGGTGGAC
                                    CA___
GAM1098  MDM1     3'  ATGTGCTCACAGGGACCTGCTG 28524     _ _  CTTTA
                                GTG GC CAC    ACCTGCTG
                                ||| || |||    ||||||||
                                TAC CG GTG    TGGACGAC
                                  A  A   TCCC_
GAM1098  TGM4     3'  TGGCCTTTTTGACCTGCTG   28525      ACC   A
                                TGGCC   TTT ACCTGCTG
                                |||||   ||| ||||||||
                                ACCGG   AAA TGGACGAC
                                   AA_   C
GAM1098  VPS26    3'  GCAACCATCTTTAACCTGCTG  28526   TG    C
                                G  GCCA CTTTAACCTGCTG
                                |  |||| ||||||||||||
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                                C  TGGT GAAATTGGACGAC
                                 GT    A
GAM1098  CACNG4    3'  CACGTGGCCGCCATTCCCCTG  28527         A  T  AA
                                CACGTGGCC CC TT  CCTG
                                ||||||||| || ||  ||||
                                GTGCACCGG GG AA  GGAC
                                     C  T  GG
GAM1098  FADS2     3'  ACGTGGCCACTGCCTCTGCTG  28528         CTTTAAC
                                ACGTGGCCAC      CTGCTG
                                ||||||||||      ||||||
                                TGCACCGGTG      GACGAC
                                     ACGGA__
GAM1098  FLJ12610  3'  CACGTGGTAGTTTAACCTG    28529        CCACC
                                CACGTGG    TTTAACCTG
                                |||||||    |||||||||
                                GTGCACC    AAATTGGAC
                                    ATC__
GAM1098  GGA2      3'  GTGGCCACTGGACTTGCTG    28530        CTTTA  C
                                GTGGCCAC    AC TGCTG
                                ||||||||    || |||||
                                CACCGGTG    TG ACGAC
                                     ACC__  A
GAM1098  GGA2      3'  GTGGCCACTGGACTTGCTG    28530        CTTTA  C
                                GTGGCCAC    AC TGCTG
                                ||||||||    || |||||
                                CACCGGTG    TG ACGAC
                                     ACC__  A
GAM1098  MGC15873  3'  TGATGGCCTCTTTTAACCTGCT 28531   C     ACC
            G                    A GTGGCC   TTTAACCTGCTG
                                | ||||||   ||||||||||||
                                A TACCGG   AAATTGGACGAC
                                 C     AGA
GAM1098  MGC4737   5'  ACGTGGCCACCTTCCCAGGCTG 28532           AA  T_
                                ACGTGGCCACCTTT  CC  GCTG
                                ||||||||||||||  ||  ||||
                                TGCACCGGTGGAAG  GG  CGAC
                                       __  TC
GAM1098  SYT12     3'  CACGTGGCCGGTAGGCTGCTG  28533         ACCTTTAAC
                                CACGTGGCC        CTGCTG
                                |||||||||        ||||||
                                GTGCACCGG        GACGAC
                                     CCATCC____
GAM1098  TSPEAR    3'  CACCTGGCCACCCCAGTTGCTG 28534     G        TAACC
                                CAC TGGCCACCTT     TGCTG
                                ||| ||||||||||     |||||
                                GTG ACCGGTGGGG     ACGAC
                                  G        TCA__
GAM1098  LOC149840 3'  GTGGCCACCAACACTGCTG    28535         TTT  _
                                GTGGCCACC   AAC CTGCTG
                                |||||||||   ||| ||||||
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                                CACCGGTGG   TTG GACGAC
                                    ___   T
GAM1098  LOC152345 5'  CGCGGGGCTGGTCAACCTGCTG 28536      CCACCT
                                CGTGG     TTAACCTGCTG
                                |||||     ||||||||||
                                GCGCC     AGTTGGACGAC
                                   CCGACC
GAM1098  LOC158376 5'  CACGTGGCCCCACTGC      28537         A  TTTAAC
                                CACGTGGCC CC     CTGC
                                ||||||||| ||     ||||
                                GTGCACCGG GG     GACG
                                    _ T_____
GAM1098  LOC161424 3'  TGGCCACCGCACCCTGCTG    28538        TTTAA
                                TGGCCACC    CCTGCTG
                                ||||||||    |||||||
                                ACCGGTGG    GGACGAC
                                     CGTG_
GAM1098  LOC219700 5'  GTGGCTGCTCGGAGACCTGCTG 28539      CAC   TA__
                                GTGGC   CTT    ACCTGCTG
                                |||||   |||    ||||||||
                                CACCG   GAG    TGGACGAC
                                   AC_   CCTC
GAM1098  LOC256118 5'  GCCACCTTTAATCTGCTG    28540          C
                                GCCACCTTTAA CTGCTG
                                |||||||||| ||||||
                                CGGTGGAAATT GACGAC
                                      A
GAM1098  LOC51659  3'  CACATGGCCACTCCTGCT    28541          CTTTAA
                                CACGTGGCCAC     CCTGCT
                                ||||||||||     ||||||
                                GTGTACCGGTG     GGACGA
                                      A_____
GAM1098  LOC51659  3'  CACATGGCCACTCCTGCT    28541          CTTTAA
                                CACGTGGCCAC     CCTGCT
                                ||||||||||     ||||||
                                GTGTACCGGTG     GGACGA
                                      A_____
GAM1099  CX3CR1    3'  TATGTGAAAGGTACCTTA    28343        TAGAT
                                TATGTGAA    AGGTATTTTA
                                ||||||||    ||||||||||
                                ATACACTT    TCCATGGAAT
                                    _____
GAM1099  GAD1      3'  TATGTTGGTAGAAGTATTTTAT 28344      GAA   TA
                                TATGT   TAGA  GGTATTTTAT
                                |||||   ||||  ||||||||||
                                ATACA   ATCT  TCATAAAATA
                                   ACC   __
GAM1099  C8orf2    3'  GTGAATAGAGTCCTTTTAT    28345        TAG  A_
                                GTGAATAGA   GT  TTTTAT
                                |||||||||   ||  ||||||
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                                CACTTATCT  CA  AAAATA
                                    ___  GG
GAM1099  FLJ11011  3'  TATGTGAAAAGGTAATTTA   28346       TAGAT    T
                                TATGTGAA    AGGTA TTTA
                                ||||||||    ||||| ||||
                                ATACACTT    TCCAT AAAT
                                   T____    T
GAM1099  FLJ21272  3'  TGTGAGTAGTAATTATTTTAT  28347     A  A  G
                                TGTGA TAG TAG TATTTTAT
                                ||||| ||| ||| ||||||||
                                ACACT ATC ATT ATAAAATA
                                  C  _  A
GAM1099  LANCL2   3'  TATGTGAAGAAGTCATATTTTA 28348      AT  TAG_
           T                     TATGTGA  AGA   GTATTTTAT
                                |||||||  |||   |||||||||
                                ATACACT  TCT   TATAAAATA
                                   __  TCAG
GAM1099  LOC91149  3'  TATGTGAATAATAGGCAT    28349       A
                                TATGTGAAT GATAGGTAT
                                ||||||||| |||||||||
                                ATACACTTA TTATCCGTA
                                    _
GAM1099  LOC93297  3'  TGTGGGATAGAGGCATTTT   28350     A_   TA
                                TGTG  ATAGA  GGTATTTT
                                ||||  |||||  ||||||||
                                ACAC  TATCT  CCGTAAAA
                                  CC   __
GAM1100  BTG1     3'  TTAAAAATGCCAAGATAAGAA  28545         ATCT
                                TTAGAAATGCCAA   ATAAGAA
                                ||||||||||||   |||||||
                                AATTTTTACGGTT   TATTCTT
                                       C___
GAM1100  CKTSF1B1  3'  TTAGAAATGTTAACCTTTAAG  28546       CCA   A
                                TTAGAAATG   AATCT TAAG
                                |||||||||   ||||| ||||
                                AATCTTTAC   TTGGA ATTC
                                     AA_    A
GAM1100  DKFZp434C0328 3'  TTAAAAATATCTATAAGA   28547       GCCAA
                                TTAGAAAT    ATCTATAAGA
                                ||||||||    ||||||||||
                                AATTTTTA    TAGATATTCT
                                    _____
GAM1100  FLJ10898  3'  TTAGGACCTATCTATAAGA   28548     AAAT  AA
                                TTAG   GCC  ATCTATAAGA
                                ||||   |||  ||||||||||
                                AATC   TGG  TAGATATTCT
                                  C___   A_
GAM1100  FLJ23042  3'  AGAAATGCTGGGTCCACAGA  28549       CAAA    A
                                AGAAATGC   TCTATA GA
                                ||||||||   |||||| ||
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                                TCTTTACG    AGGTGT CT
                                    ACCC     _
GAM1100  FLJ23403  3'  CTAGAAATGCTTAGCTCTTATG 28550          CAAA_   _  A
             AGAA                   TTAGAAATGC     TCT AT AGAA
                                ||||||||||     ||| || ||||
                                GATCTTTACG     AGA TA TCTT
                                    AATCG   A  C
GAM1100  KIAA0630  3'  GAAATGCCAAGTTCTGAGA   28551          A_   ATA
                                GAAATGCCAA  TCT   AGA
                                ||||||||||  |||   |||
                                CTTTACGGTT  AGA   TCT
                                    CA   C__
GAM1100  KIAA0970  3'  TTAGAAAGTTTTTCTATAAGAA 28552        TGCCAAA
                                TTAGAAA      TCTATAAGAA
                                |||||||      ||||||||||
                                AATCTTT      AGATATTCTT
                                    CAAAA__
GAM1100  OSBPL8    3'  CTAGAAATGCTAAACACT    28553          C   _
                                TTAGAAATGC AAAT CT
                                |||||||||| |||| ||
                                GATCTTTACG TTTG GA
                                    A   T
GAM1100  TU3A      3'  TTAGAAATGCAGGATCTCCCAG 28554          CAA   ATA
                                TTAGAAATGC   ATCT   AG
                                |||||||||   ||||   ||
                                AATCTTTACG   TAGA   TC
                                    TCC   GGG
GAM1100  UBCE7IP5  3'  TTAGAAATGCAGATCCCCAG   28555          CAA   ATA
                                TTAGAAATGC   ATCT   AG
                                |||||||||   ||||   ||
                                AATCTTTACG   TAGG   TC
                                    TC_   GG_
GAM1100  LOC151098 5'  TTAGAAATGCCAACATCTA    28556           _
                                TTAGAAATGCCAA ATCTA
                                |||||||||||| |||||
                                AATCTTTACGGTT TAGAT
                                      G
GAM1100  LOC152274 3'  TAGAAGTGCCAAATTTATAA   28557       A       C
                                TAGAA TGCCAAAT TATAA
                                ||||| |||||||| |||||
                                ATCTT ACGGTTTA ATATT
                                   C       A
GAM1100  LOC152903 3'  AAAGTGCCAAACACCAAAGAA  28558      A       _   T
                                GAA TGCCAAAT CTA AAGAA
                                ||| |||||||| ||| |||||
                                TTT ACGGTTTG GGT TTCTT
                                  C       T   _
GAM1100  LOC158230 5'  GAAATGCCAAACAGGCAAG    28559           CTA
                                GAAATGCCAAAT   TAAG
                                ||||||||||||   ||||
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                                CTTTACGGTTTG  GTTC
                                      TCC
GAM1100 LOC254827 3'  TCAGAAATGTAGATATAAGAA 28560        CCAAATC
                                TTAGAAATG     TATAAGAA
                                |||||||||     ||||||||
                                AGTCTTTAC     ATATTCTT
                                    ATCT___
GAM1100 LOC85479 5'  TTAGCAATGCCAAGTACCT   28561     A      __
                                TTAG AATGCCAA  ATCT
                                |||| ||||||||  ||||
                                AATC TTACGGTT  TGGA
                                  G       CA
GAM1100 LOC90982 3'  GAAATGCCATTCCCATGAGA  28562        AA    A
                                GAAATGCCA  TCTAT AGA
                                |||||||||  ||||| |||
                                CTTTACGGT  GGGTA TCT
                                    AA    C
GAM1101 KCNQ1    5'  TGTTGGCGCGCACCCAC    28565    TA   _
                                TGT  TGGT TGCACCCAC
                                |||  |||| |||||||||
                                ACA  ACCG GCGTGGGTG
                                  __   C
GAM1101 PHLDA3   5'  TGCTCCGCGCACCCACA    28566     ATG  T
                                TGTT   GT GCACCCACA
                                ||||   || |||||||||
                                ACGA   CG CGTGGGTGT
                                  GG_  _
GAM1101 SOD3     5'  TGTATGCCGGGCACCCACA   28567    TA__  TT
                                TGT   TGG  GCACCCACA
                                |||   |||  |||||||||
                                ACA   GCC  CGTGGGTGT
                                  TACG  __
GAM1101 IRF7     5'  TGTCACAGGTGTCCACA     28568       T  CAC
                                TGTTATGG TG   CCACA
                                |||||||| ||   |||||
                                ACAGTGTC AC   GGTGT
                                    C  A__
GAM1101 IRF7     5'  TGTCACAGGTGTCCACA     28568       T  CAC
                                TGTTATGG TG   CCACA
                                |||||||| ||   |||||
                                ACAGTGTC AC   GGTGT
                                    C  A__
GAM1101 IRF7     5'  TGTCACAGGTGTCCACA     28568       T  CAC
                                TGTTATGG TG   CCACA
                                |||||||| ||   |||||
                                ACAGTGTC AC   GGTGT
                                    C  A__
GAM1101 IRF7     5'  TGTCACAGGTGTCCACA     28568       T  CAC
                                TGTTATGG TG   CCACA
                                |||||||| ||   |||||
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                                ACAGTGTC AC   GGTGT
                                    C  A__
GAM1101  KIAA1975  5'  TGTTAATGTCACACCCACA   28569      TG  TG
                                TGTTA  GT  CACCCACA
                                |||||  ||  ||||||||
                                ACAAT  CA  GTGGGTGT
                                   TA  GT
GAM1101  MGC15631  5'  TGTCACGGCCGCCCAC     28570          AC
                                TGTTATGGTTGC  CCAC
                                ||||||||||||  ||||
                                ACAGTGCCGGCG  GGTG
                                              __
GAM1101  LOC138399 5'  TGTTCATGGCACCCAC     28571     _   GTT
                                TGT TATG   GCACCCAC
                                ||| ||||   ||||||||
                                ACA GTAC   CGTGGGTG
                                  A   ___
GAM1101  LOC145474 5'  TGTCATGGCACCTACA     28572       GTT    C
                                TGTTATG   GCACC ACA
                                |||||||   ||||| |||
                                ACAGTAC   CGTGG TGT
                                    ___    A
GAM1101  LOC147515 5'  TGTCATGGCCACCTCCACA   28573        TG AC
                                TGTTATGGT  C  CCACA
                                |||||||||  |  |||||
                                ACAGTACCG  G  GGTGT
                                     GT GA
GAM1101  LOC149995 5'  TGTCATGGCCACCTCCACA   28573        TG AC
                                TGTTATGGT  C  CCACA
                                |||||||||  |  |||||
                                ACAGTACCG  G  GGTGT
                                     GT GA
GAM1101  LOC151258 5'  TGCTACAGTTGCCTACA     28574          ACCC
                                TGTTATGGTTGC   ACA
                                ||||||||||||   |||
                                ACGATGTCAACG   TGT
                                      GA__
GAM1101  LOC221715 5'  TGTCATGGTCATCCGCA     28575        TG  C  A
                                TGTTATGGT  CA CC CA
                                |||||||||  || || ||
                                ACAGTACCA  GT GG GT
                                     __  A  C
GAM1101  LOC256222 5'  TGCTATGGTCTTCCTTACA   28576        GCA  C_
                                TGTTATGGTT   CC  ACA
                                ||||||||||   ||  |||
                                ACGATACCAG   GG  TGT
                                      AA_  AA
GAM1102  DXS1283E  3'  CGAGTCTCAAGAGATCCG    28579     A_
                                CGA  TTTAAGAGATCCG
                                |||  ||||||||||||
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                                GCT  GAGTTCTCTAGGC
                                  CA
GAM1102  VHL      3'  CCGGGTTCAAGAGATTCG    28580     AA        C
                                TCG  TTTAAGAGAT CG
                                |||  |||||||||| ||
                                GGC  AAGTTCTCTA GC
                                  CC         A
GAM1102  FLJ20070  5'  CCGAACCTCAGATCCG      28581         AAG
                                TCGAATTT   AGATCCG
                                ||||||||   |||||||
                                GGCTTGGA   TCTAGGC
                                     G__
GAM1103  BRPF1     3'  ACGCAGTGTCCTAACT      28584    A   ATAT A
                                AC CAGT    G TCCTAACT
                                || ||||    | ||||||||
                                TG GTCA    C AGGATTGA
                                 C   _____ _
GAM1103  DACH      3'  CACAGCACATTTTAACT      28585         GATCC
                                CACAGTATAT     TAACT
                                ||||||||||     |||||
                                GTGTCGTGTA     ATTGA
                                     AA___
GAM1103  KCNAB1    3'  ACACAGTATAGTCTCACAA    28586          TGA  C
                                ACACAGTATA   TC TAA
                                ||||||||||   || |||
                                TGTGTCATAT   AG GTT
                                     CAG  T
GAM1103  MNT       3'  TAACACAGAGCCCCTGACT    28587        TATATGA    A
                                TAACACAG      TCCT ACT
                                ||||||||      |||| |||
                                ATTGTGTC      GGGA TGA
                                     TCG____    C
GAM1103  USP9Y     3'  TAACATAGTATATATACCT    28588      C       AT
                                TAACA AGTATATG  CCT
                                ||||| ||||||||  |||
                                ATTGT TCATATAT  GGA
                                   A       AT
GAM1103  C20orf142 3'  CAGTGGCGTGATCCTAGCTC   28589      ATA_      A
                                CAGT    TGATCCTA CTC
                                ||||    |||||||| |||
                                GTCA    ACTAGGAT GAG
                                  CCGC       C
GAM1103  CPSF2     3'  TAACACAGGACCTAAC       28590        TATAT  T
                                TAACACAG     GA CCTAAC
                                ||||||||     || ||||||
                                ATTGTGTC     CT GGATTG
                                     _____  _
GAM1103  DKFZP434G1411 3'  TAACACAGTATTTGATACT    28591          A   C
                                TAACACAGTAT TGAT CT
                                |||||||||| |||| ||
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                                ATTGTGTCATA ACTA GA
                                      A   T
GAM1103  DKFZP564I052 3'  CAGTGGCATGATCCTGGCTC  28592     A_      AA
                                CAGT  TATGATCCT  CTC
                                ||||  |||||||||  |||
                                GTCA  GTACTAGGA  GAG
                                  CC       CC
GAM1103  DKFZP564I1171 3'  ACACAGTATATTGAACT    28593         GATCCT
                                ACACAGTATAT     AACT
                                ||||||||||     ||||
                                TGTGTCATATA     TTGA
                                      AC____
GAM1103  FLJ11280  5'  ACACAGTAGAAATCTGGCTC  28594       TAT   CTAA
                                ACACAGTA  GATC   CTC
                                ||||||||  ||||   |||
                                TGTGTCAT  TTAG   GAG
                                    CT_   ACC_
GAM1103  KIAA0087  3'  CAGTAGCCTAGTCCTAACT   28595     TA_ A
                                CAGTA   TG TCCTAACT
                                |||||   || ||||||||
                                GTCAT   AT AGGATTGA
                                  CGG  C
GAM1103  KIAA1084  3'  TAACACAGTATCTAC      28596         ATGATC   A
                                TAACACAGTAT     CTA C
                                ||||||||||     ||| |
                                ATTGTGTCATA     GAT G
                                      _______  C
GAM1103  KIAA1271  3'  CAGTGGCACGATCCTAGCTC  28597     A_       A
                                CAGT  TATGATCCTA CTC
                                ||||  |||||||||| |||
                                GTCA  GTGCTAGGAT GAG
                                  CC        C
GAM1103  MGC13138  3'  ACACAGTCACAGGATTTTAACT 28598       _  T   CC
                                ACACAGT ATA GAT  TAACT
                                ||||||| ||| |||  |||||
                                TGTGTCA TGT CTA  ATTGA
                                    G   C   AA
GAM1103  PROL2    3'  CAGTGGCCTGATCCTAGCTC  28599     ATA_      A
                                CAGT    TGATCCTA CTC
                                ||||    |||||||| |||
                                GTCA    ACTAGGAT GAG
                                  CCGG       C
GAM1103  SCN12A   3'  CAGTGACACGATCTTGGCTC  28600     _      CTAA
                                CAGT ATATGATC    CTC
                                |||| ||||||||    |||
                                GTCA TGTGCTAG    GAG
                                  C       AACC
GAM1103  STAG1    3'  CACAGTATATAGGCCTCTAGCT 28601         AT   AA__
            C                    CACAGTATATG  CCT    CTC
                                ||||||||||  |||    |||
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                                GTGTCATATAT  GGA   GAG
                                     CC   GATC
GAM1103  LOC143872 3'  TAACACAGTATTTGAAACT   28602         A   TC
                                TAACACAGTAT TGA  CT
                                |||||||||||  |||  ||
                                ATTGTGTCATA ACT  GA
                                     A   TT
GAM1103  LOC152220 3'  TAACAACAGCTGGTCCTAACT  28603      _   ATA  A
                                TAACA CAGT   TG TCCTAACT
                                |||||  ||||   || ||||||||
                                ATTGT GTCG   AC AGGATTGA
                                   T   ___  C
GAM1103  LOC158696 5'  ACAGTATATAATTTTAGCTC   28604          CC  A
                                ACAGTATATGAT  TA CTC
                                ||||||||||||  || |||
                                TGTCATATATTA  AT GAG
                                      AA  C
GAM1103  LOC161742 3'  TAACACAGCTGAACATATTC   28605        ___    A
                                TAACACAGT   ATATG TC
                                |||||||||   |||||  ||
                                ATTGTGTCG   TGTAT AG
                                     ACT    A
GAM1103  LOC257017 5'  ACACAGTAATTCCTAACT    28606        TATGA
                                ACACAGTA    TCCTAACT
                                ||||||||    ||||||||
                                TGTGTCAT    AGGATTGA
                                    TA___
GAM1103  LOC56899  5'  AGTATGACTTGATCCTAGCTC  28607      A___      A
                                AGTAT   TGATCCTA CTC
                                |||||   |||||||| |||
                                TCATA   ACTAGGAT GAG
                                   CTGA       C
GAM1103  LOC89985  3'  CACAGAAGATTCTAACTC    28608      TATAT   C
                                CACAG    GAT CTAACTC
                                |||||    ||| |||||||
                                GTGTC    CTA GATTGAG
                                   TT___   A
GAM1104  NPHP1     3'  CATGGTATCTTTACTGGGAATA 28611        _____   C
            TTA                   CATGGTATC   CTGG GAATATTA
                                |||||||||   |||| ||||||||
                                GTACCATAG   GACC CTTATAAT
                                     AAAT   _
GAM1104  AP1S3     3'  TGGTATTGGCTTTGAATATTA  28612      CC   ___
                                TGGTAT  TGGC   GAATATTA
                                ||||||  ||||   ||||||||
                                ACCATA  ACCG   CTTATAAT
                                   __   AAA
GAM1104  KIAA0712  5'  TTCATGGCGTAGTCTCTGGATA 28613        A___  _   CGA
            TT                   TTCATGGT   TC CTGG   ATATT
                                ||||||||   || ||||   |||||
```

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                                AAGTACCG   AG GACC   TATAA
                                    CATC  A   ___
GAM1104  LOC147400 3'  TTCATGGTTTGGCAAAGTATT  28614       ATCC     _
                                TTCATGGT   TGGCGAA TATT
                                ||||||||   ||||||| ||||
                                AAGTACCA   ACCGTTT ATAA
                                    A___     C
GAM1105  ATP11A   3'  TGTGTGCATGTGTGCAGT    28617         _   T
                                TGTGTGCATGT TGTA GT
                                |||||||||||| |||| ||
                                ACACACGTACA ACGT CA
                                      C   _
GAM1105  ATP11A   3'  TGTGTGCATGTGTGTAGGAGCC 28618         _   TGT_
            TGT                   TGTGTGCATGT TGTA   TTTGT
                                ||||||||||| ||||   |||||
                                ACACACGTACA ACAT   GGACA
                                      C   CCTC
GAM1105  ATP8A2   3'  TGTGTGCATGTGTGTGTT    28619         T  A
                                TGTGTGCATGT GT TGTT
                                |||||||||| || ||||
                                ACACACGTACA CA ACAA
                                      _ C
GAM1105  CPNE3    3'  TGAGTGCATGCTGTTTTGT   28620    T      TGTA
                                TG GTGCATGT   TGTTTTGT
                                || ||||||||   ||||||||
                                AC CACGTACG   ACAAAACA
                                 T      ____
GAM1105  CSF2RB   3'  TGTGTGTGTGTGTGTCTGT   28621      CA   T  A    T
                                TGTGTG  TGT GT TGTTT GT
                                ||||||  ||| || ||||| ||
                                ACACAC  ACA CA ACAGA CA
                                   __  _ C   _
GAM1105  CX3CR1   3'  TGTGTGGCATTTGTTTTGT   28622      _  GTTGTA
                                TGTGTG CAT     TGTTTTGT
                                |||||| |||     ||||||||
                                ACACAC GTA     ACAAAACA
                                   C   A_____
GAM1105  DGKG     3'  TGTGTGCATGTGTGAGTGT   28623         _  TA
                                TGTGTGCATGT TG  TGT
                                |||||||||| ||  |||
                                ACACACGTACA AC  ACA
                                      C  TC
GAM1105  DIAPH2   3'  TGTGTGCATTTGTGTATGT   28625       GT_
                                TGTGTGCAT   TGTATGT
                                |||||||||   |||||||
                                ACACACGTA   ACATACA
                                      AAC
GAM1105  DIAPH2   3'  TGTGTGCATGTGTGTGCATTTG 28624         T  A  _
            T                  TGTGTGCATGT GT TGT TTTGT
                                |||||||||| || ||| |||||
```

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                                ACACACGTACA CA ACG AAACA
                                     _ C   T
GAM1105  DMD    3' TGTGTGTGTGTTTGTTTTG   28626      CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                   __   _  A
GAM1105  DMD    3' TGTGTGTGTGTTTGTTTTG   28626      CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                   __   _  A
GAM1105  DMD    3' TGTGTGTGTGTTTGTTTTG   28626      CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                   __   _  A
GAM1105  DMD    3' TGTGTGTGTGTTTGTTTTG   28626      CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                   __   _  A
GAM1105  DMD    3' TGTGTGTGTGTTTGTTTTG   28626      CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                   __   _  A
GAM1105  DMD    3' TGTGTGTGTGTTTGTTTTG   28626      CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                   __   _  A
GAM1105  DMD    3' TGTGTGTGTGTTTGTTTTG   28626      CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                   __   _  A
GAM1105  DMD    3' TGTGTGTGTGTTTGTTTTG   28626      CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                   __   _  A
GAM1105  DMD    3' TGTGTGTGTGTTTGTTTTG   28626      CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                   __   _  A
GAM1105  DMD    3' TGTGTGTGTGTTTGTTTTG   28626      CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
```

```
                                ACACAC  ACA CA ACAAAAC
                                  __  _ A
GAM1105  DMD     3'  TGTGTGTGTGTTTGTTTTG   28626       CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                  __  _ A
GAM1105  DMD     3'  TGTGTGTGTGTTTGTTTTG   28626       CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                  __  _ A
GAM1105  DMD     3'  TGTGTGTGTGTTTGTTTTG   28626       CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                  __  _ A
GAM1105  EGR3    3'  TGTGTGTATGTTATGTATATGT 28627       C     A  TT
              A                  TGTGTG ATGTTGT TGT  TGTA
                                ||||||| ||||||| |||  ||||
                                ACACAC TACAATA ATA  ACAT
                                   A      C  T_
GAM1105  EHD3    3'  TGTGTGCATGTTTGTGTGTGTG 28628          _ A  TT
              T                  TGTGTGCATGTT GT TGT  TGT
                                |||||||||||| || |||  |||
                                ACACACGTACAA CA ACA  ACA
                                      A  C  C_
GAM1105  FOSB    3'  TGTGTTTGTTTGTTTTGT    28629      GCATG   A
                                TGTGT    TTGT TGTTTTGT
                                |||||    |||| ||||||||
                                ACACA    AACA ACAAAACA
                                  _____   A
GAM1105  GLS     3'  TGTGTGCATGTGTGTGT     28630          T  A
                                TGTGTGCATGT GT TGT
                                |||||||||| || |||
                                ACACACGTACA CA ACA
                                      _ C
GAM1105  GNAZ    3'  TGTGTGCATGTGTGTGT     28630          T  A
                                TGTGTGCATGT GT TGT
                                |||||||||| || |||
                                ACACACGTACA CA ACA
                                      _ C
GAM1105  GTF2H1  3'  TGTGTGTGTGTGTATAT     28631       CA  T
                                TGTGTG  TGT GTATGT
                                ||||||  ||| ||||||
                                ACACAC  ACA CATATA
                                   AC  _
GAM1105  KIF5A   3'  TGTGTGCGTGTGTGCGTGT   28632        A  _ TA
                                TGTGTGC TGT TG  TGT
                                ||||||| ||| ||  |||
```

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                                ACACACG ACA AC  ACA
                                    C   C  GC
GAM1105 KIF5A    3'  TGTGTGCGTGTGTGTATG    28634        A  _
                                TGTGTGC TGT TGTATG
                                ||||||| ||| ||||||
                                ACACACG ACA ACATAC
                                    C   C
GAM1105 KIF5A    3'  TGTGTGCATGTTTGTGTGCGTG 28633          _ A  TT
              T                  TGTGTGCATGTT GT TGT  TGT
                                ||||||||||| || |||  |||
                                ACACACGTACAA CA ACG  ACA
                                      A  C   C_
GAM1105 MHC2TA   3'  TGTGTGTATGTGTGTGT     28635       C   T  A
                                TGTGTG ATGT GT TGT
                                |||||| |||| || |||
                                ACACAC TACA CA ACA
                                    A   _ C
GAM1105 NLGN3    3'  TGTGTGTGTGTGTGTCTGCGTG 28636       CA  _  A  TT
              T                  TGTGTG  TGT TGT TGT  TGT
                                |||||| ||| ||| |||  |||
                                ACACAC  ACA ACA ACG  ACA
                                    AC  C  G  C_
GAM1105 NLGN3    3'  TGTGTGTGTGTGTGTGTCT   28637       CA  T  A
                                TGTGTG  TGT GT TGTTT
                                |||||| ||| || |||||
                                ACACAC  ACA CA ACAGA
                                    AC  _ C
GAM1105 PCDH11Y  3'  TGTGTGTATGTGTGTGT     28635       C   T  A
                                TGTGTG ATGT GT TGT
                                |||||| |||| || |||
                                ACACAC TACA CA ACA
                                    A   _ C
GAM1105 PCDH11Y  3'  TGTGTGTGTGTGTGTATGT   28638       CA  _
                                TGTGTG  TGT TGTATGT
                                ||||||  ||| |||||||
                                ACACAC  ACA ACATACA
                                    AC  C
GAM1105 PCDH11Y  3'  TGTGTGTGTGTATGTGTGT   28639       CA  T   TT
                                TGTGTG  TGT GTATGT  TGT
                                ||||||  ||| ||||||  |||
                                ACACAC  ACA CATACA  ACA
                                    __  _    C_
GAM1105 PLAG1    3'  TGTGTGCATGTGTGTGT     28630         T  A
                                TGTGTGCATGT GT TGT
                                |||||||||| || |||
                                ACACACGTACA CA ACA
                                      _ C
GAM1105 RCV1     3'  TGTGTGCATGTGTGTGT     28630         T  A
                                TGTGTGCATGT GT TGT
                                |||||||||| || |||
```

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                                ACACACGTACA CA ACA
                                      _ C
GAM1105 SLC1A4   3' TGTGTGTGTGTTGTGTAT    28640      CA    A
                                TGTGTG  TGTTGT TGT
                                ||||||  |||||| |||
                                ACACAC  ACAACA ATA
                                   AC     C
GAM1105 SNAP25   3' TGTGTGTGTGTTGTCTCATCAG 28641      CA    ATGT  T
           TA                    TGTGTG  TGTTGT   TT GTA
                                ||||||  ||||||   || |||
                                ACACAC  ACAACA   AG CAT
                                   AC     GAGT  T
GAM1105 SNAP25   3' TGTGTGTGTGTTGTCTCATCAG 28641      CA    ATGT  T
           TA                    TGTGTG  TGTTGT   TT GTA
                                ||||||  ||||||   || |||
                                ACACAC  ACAACA   AG CAT
                                   AC     GAGT  T
GAM1105 WHSC1    3' TGTGTGCGTGTGTATAAAAAGT 28642       A  T   TTTT
                                TGTGTGC TGT GTATG   GT
                                ||||||| ||| |||||   ||
                                ACACACG ACA CATAT   CA
                                   C  _    TTTT
GAM1105 XKRY     5' TGTGGGCATGTTTTTGTTTGT  28643     T     GTA   T
                                TGTG GCATGTT   TGTTT GT
                                |||| |||||||   ||||| ||
                                ACAC CGTACAA   ACAAA CA
                                  C      AA_   _
GAM1105 XKRY     5' TGTGGGCATGTTTTTGTTTGT  28643     T     GTA   T
                                TGTG GCATGTT   TGTTT GT
                                |||| |||||||   ||||| ||
                                ACAC CGTACAA   ACAAA CA
                                  C      AA_   _
GAM1105 C5orf4   3' TGTGTGTATGTTTGTGTGT   28644      C   _ A
                                TGTGTG ATGTT GT TGT
                                |||||| ||||| || |||
                                ACACAC TACAA CA ACA
                                   A    A  C
GAM1105 C5orf4   3' TGTGTGTATGTTTGTGTGT   28644      C   _ A
                                TGTGTG ATGTT GT TGT
                                |||||| ||||| || |||
                                ACACAC TACAA CA ACA
                                   A    A  C
GAM1105 caspr5   3' TGTGTGTGTGTGTGTATA    28645      CA  _
                                TGTGTG  TGT TGTATG
                                ||||||  ||| ||||||
                                ACACAC  ACA ACATAT
                                   AC   C
GAM1105 caspr5   3' TGTGTGTGTGTGTATAT     28631      CA  T
                                TGTGTG  TGT GTATGT
                                ||||||  ||| ||||||
```

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                                ACACAC  ACA CATATA
                                   AC  _
GAM1105  CBX1     3'  TGTGTGTATGTGTGTGTT    28646       C   T  A
                                TGTGTG ATGT GT TGTT
                                |||||| |||| || ||||
                                ACACAC TACA CA ACAA
                                   A   _ C
GAM1105  CSR1     3'  TGTGTGCATGTGTGTGCATG  28647           ___
                                TGTGTGCATGT  TGTATG
                                ||||||||||  ||||||
                                ACACACGTACA  ACGTAC
                                      CAC
GAM1105  CSR1     3'  TGTGTGCATGTGTATGT     28648          T
                                TGTGTGCATGT GTATGT
                                |||||||||| ||||||
                                ACACACGTACA CATACA
                                      _
GAM1105  CSR1     3'  TGTGTGCATGTGTGTGT     28630          T  A
                                TGTGTGCATGT GT TGT
                                |||||||||| || |||
                                ACACACGTACA CA ACA
                                      _ C
GAM1105  CSR1     3'  TGTGTGCATGTGTGTGT     28630          T  A
                                TGTGTGCATGT GT TGT
                                |||||||||| || |||
                                ACACACGTACA CA ACA
                                      _ C
GAM1105  DKFZp761K1423 5'  TGTGTGCATGTGTGCAAGCATG 28649          _   T  TT
            T                    TGTGTGCATGT TGTA GT  TGT
                                |||||||||| |||| ||  |||
                                ACACACGTACA ACGT CG  ACA
                                      C   T  T_
GAM1105  DKFZp762A227 3'  TGTGTGTGTGTGTGTGTTTTG  28650       CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                   AC  _ C
GAM1105  FLJ11175  3'  TGTGTGTATGTCTGTGCACGT  28651       C   ___
                                TGTGTG ATGT   TGTATGT
                                |||||| ||||   |||||||
                                ACACAC TACA   ACGTGCA
                                   A   GAC
GAM1105  FLJ11598  3'  TGTGTGTGTGTGTATGC     28652       CA  T
                                TGTGTG  TGT GTATGT
                                ||||||  ||| ||||||
                                ACACAC  ACA CATACG
                                   AC  _
GAM1105  FLJ14686  3'  TGTGTGTGTGTGTGTGTTTTA  28653       CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
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                                ACACAC  ACA CA ACAAAAT
                                   AC  _ C
GAM1105  FLJ21290  3'  TGTGTGCATGTGTGTGT     28630          T  A
                                TGTGTGCATGT GT TGT
                                |||||||||| || |||
                                ACACACGTACA CA ACA
                                      _ C
GAM1105  FLJ21290  3'  TGTGTGCTTGTGTGTGTGT    28654        A  _  A
                                TGTGTGC TGT TGT TGT
                                ||||||| ||| ||| |||
                                ACACACG ACA ACA ACA
                                   A  C  C
GAM1105  FLJ21290  3'  TGTGTGTGTGTGTGTGTTTTG  28650       CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                   AC  _ C
GAM1105  KIAA0869  3'  TGTGTGTGTGTGTGTTTTG   28655       CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                   __  _ C
GAM1105  KIAA0971  3'  TGTGTGTGTGTGTGTCCAGT  28656       CA  T  A   TT
                                TGTGTG  TGT GT TGTT  GT
                                ||||||  ||| || ||||  ||
                                ACACAC  ACA CA ACAG  CA
                                   __  _ C   GT
GAM1105  KIAA1309  3'  TGTGTGTATGTGTATGT    28657       C   T
                                TGTGTG ATGT GTATGT
                                |||||| |||| ||||||
                                ACACAC TACA CATACA
                                   A  _
GAM1105  KIAA1399  3'  TGTGTGTGTGTGTGTGTCCTGT 28658       CA  T  A
            A                    TGTGTG  TGT GT TGTTTTGTA
                                ||||||  ||| || |||||||||
                                ACACAC  ACA CA ACAGGACAT
                                   AC  _ C
GAM1105  KIAA1550  3'  TGTGTGTATGCTTGTCAGTGT  28659       C   GTA   T_
                                TGTGTG ATGTT  TGTT  TGT
                                |||||| |||||  ||||  |||
                                ACACAC TACGA  ACAG  ACA
                                   A   ____  TC
GAM1105  KIAA1553  3'  TGTGTGCATGCTGTGTGCATGT 28660          A  TT
                                TGTGTGCATGTTGT TGT  TGT
                                |||||||||||||| |||  |||
                                ACACACGTACGACA ACG  ACA
                                      C  T_
GAM1105  KIAA1594  3'  TGTGTGTGTGTGTGTGTC   28661       CA  T  A
                                TGTGTG  TGT GT TGTT
                                ||||||  ||| || ||||
```

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                                ACACAC  ACA CA ACAG
                                   AC   _  C
GAM1105  KIAA1615  3'  TGTGTGTGTGTGTATAT     28631       CA   T
                                TGTGTG  TGT GTATGT
                                ||||||  ||| ||||||
                                ACACAC  ACA CATATA
                                   AC   _
GAM1105  KIAA1615  3'  TGTGTGTGTGTGTGTATA    28645       CA   _
                                TGTGTG  TGT TGTATG
                                ||||||  ||| ||||||
                                ACACAC  ACA ACATAT
                                   AC   C
GAM1105  KIAA1671  3'  TGTGTGTGTGTGTGTCTCTGT  28662       CA   T  A    _
                                TGTGTG  TGT GT TGTTT TGT
                                ||||||  ||| ||  ||||| |||
                                ACACAC  ACA CA ACAGA ACA
                                   __   _ C    G
GAM1105  KIAA1762  3'  TGTGTGCATGTATGTGTATG   28663          ___
                                TGTGTGCATGT   TGTATG
                                ||||||||||   ||||||
                                ACACACGTACA   ACATAC
                                      TAC
GAM1105  KIAA1918  3'  TGTGTGCATGTGTATGT     28648          T
                                TGTGTGCATGT GTATGT
                                ||||||||||| ||||||
                                ACACACGTACA CATACA
                                            _
GAM1105  PPP1R16B  3'  TGTGTGTGTGTGTATATGT   28664       CA   _
                                TGTGTG  TGT TGTATGT
                                ||||||  ||| |||||||
                                ACACAC  ACA ATATACA
                                   AC   C
GAM1105  TRIP-Br2  3'  TGTGTGCATGTGTGTGCCTGT  28665          T  A    T
                                TGTGTGCATGT GT TGTTT GT
                                |||||||||| || ||||| ||
                                ACACACGTACA CA ACGGA CA
                                      _ C    _
GAM1105  USP25     3'  TGTGTGTATGTGTATATATGT  28666       C   T    TT
                                TGTGTG ATGT GTATGT  TGT
                                ||||||  |||| ||||||  |||
                                ACACAC  TACA CATATA  ACA
                                   A    _     T_
GAM1105  ZNF387    3'  GTGTGTGTGTATATTTTGTA   28667       CA   T
                                GTGTG  TGT GTATGTTTTGTA
                                |||||  ||| ||||||||||||
                                CACAC  ACA CATATAAAACAT
                                   __   _
GAM1105  LOC128989 3'  TGTGTGTGTGTCTGTGCAACTG 28668       CA   GTA   T_
            T                   TGTGTG  TGTT   TGT  TTGT
                                ||||||  ||||   |||  ||||
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                                ACACAC  ACAG   ACG  GACA
                                   AC    AC_   TT
GAM1105  LOC146227 3'  TGTGTGCACGCCTTTGT     28669          GTA
                                TGTGTGCATGTT   TGT
                                ||||||||||||  |||
                                ACACACGTGCGG   ACA
                                      AA_
GAM1105  LOC147054 5'  TGTGTGTGTGTGTGTGTCCTA  28670       CA   T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAGGAT
                                   AC   _  C
GAM1105  LOC147054 5'  TGTGTGCATGTTTGTGTGTGTG 28628           _  A   TT
            T                   TGTGTGCATGTT GT TGT  TGT
                                ||||||||||||| || |||  |||
                                ACACACGTACAA CA ACA  ACA
                                      A  C   C_
GAM1105  LOC148529 3'  TGTGTGTGTGTGTGTGGTGT   28672       CA   T  A   TT
                                TGTGTG  TGT GT TGT  TGT
                                ||||||  ||| || |||  |||
                                ACACAC  ACA CA ACA  ACA
                                   __   _  C   CC
GAM1105  LOC148529 3'  TGTGTGTGTGTGGTGTGTT   28671       CA   T  A
                                TGTGTG  TGT GT TGTT
                                ||||||  ||| || ||||
                                ACACAC  ACA CA ACAA
                                   AC   C  C
GAM1105  LOC149711 3'  TGTGTGCATGTGTGTGT     28630          T  A
                                TGTGTGCATGT GT TGT
                                |||||||||||| || |||
                                ACACACGTACA CA ACA
                                      _  C
GAM1105  LOC150147 3'  TGTGTGCGTGTTTTGT      28673        ATGTTGTA
                                TGTGTGC       TGTTTTGT
                                |||||||       ||||||||
                                ACACACG       ACAAAACA
                                   C________
GAM1105  LOC151127 3'  TGTGTGTATGTGTGTGT     28635       C   T  A
                                TGTGTG ATGT GT TGT
                                |||||| |||| || |||
                                ACACAC TACA CA ACA
                                   A   _  C
GAM1105  LOC153711 5'  TGTGTGTATGTATGTATAT   28674       C   _
                                TGTGTG ATGT TGTATGT
                                |||||| |||| |||||||
                                ACACAC TACA ACATATA
                                   A   T
GAM1105  LOC219988 3'  TGTGTGTGTGTGTATCTATGT  28675       CA   T   G  T
                                TGTGTG  TGT GTAT TT TGT
                                ||||||  ||| |||| || |||
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                                ACACAC  ACA CATA GA ACA
                                   AC  _   _ T
GAM1106  CPSF6    3'  TTTGACCCCTTACACAT     28678      T    A
                                TTTG CCTT TTACACAT
                                |||| |||| ||||||||
                                AAAC GGGG AATGTGTA
                                  T   _
GAM1106  HAO1     3'  CTCTTTGTCAAGTAATACA   28679         CT_  T
                                TTCTTTGTC   TA TACA
                                |||||||||   || ||||
                                GAGAAACAG   AT ATGT
                                      TTC  T
GAM1106  HCS      3'  TCTTTAATATTACACAT     28680       TCCT
                                TCTTTG   TATTACACAT
                                ||||||   ||||||||||
                                AGAAAT   ATAATGTGTA
                                   T___
GAM1106  INMT     3'  TTCCTTGTCCTTAACA      28681           TT
                                TTCTTTGTCCTTA  ACA
                                ||||||||||||  |||
                                AAGGAACAGGAAT  TGT
                                       __
GAM1106  INMT     3'  TTCCTTGTCCTTAACA      28681           TT
                                TTCTTTGTCCTTA  ACA
                                ||||||||||||  |||
                                AAGGAACAGGAAT  TGT
                                       __
GAM1106  NRXN2    3'  TTCTTTTTCCCACACA      28682       G    TATT
                                TTCTTT TCCT    ACACA
                                |||||| ||||    |||||
                                AAGAAA AGGG    TGTGT
                                   A   ____
GAM1106  NRXN2    3'  TTCTTTTTCCCACACA      28682       G    TATT
                                TTCTTT TCCT    ACACA
                                |||||| ||||    |||||
                                AAGAAA AGGG    TGTGT
                                   A   ____
GAM1106  NRXN2    3'  TTCTTTTTCCCACACA      28682       G    TATT
                                TTCTTT TCCT    ACACA
                                |||||| ||||    |||||
                                AAGAAA AGGG    TGTGT
                                   A   ____
GAM1106  PTPRM    3'  TCTTTGTTCATTACACAT    28683        CC
                                TCTTTGT  TTATTACACAT
                                |||||||  ||||||||||
                                AGAAACA  AGTAATGTGTA
                                      __
GAM1106  RAD21    3'  TTCTGTGTCCCCTACACAT   28684      T     TA
                                TTCT TGTCCT  TTACACAT
                                |||| ||||||  ||||||||
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                                AAGA ACAGGG  GATGTGTA
                                  C     __
GAM1106  RP1      3'  TTCTTGTCCTTAGCACA     28685       T      T
                                TTCTT GTCCTTA TACA
                                ||||| ||||||| ||||
                                AAGAA CAGGAAT GTGT
                                  _      C
GAM1106  USP6     5'  TTCCTTGTCCTGATGCCACAT  28686           T  TA
                                TTCTTTGTCCT AT  CACAT
                                |||||||||||  ||  |||||
                                AAGGAACAGGA TA  GTGTA
                                     C  CG
GAM1106  WBSCR1   3'  TTCTTTATCTTATCCACAT    28687         C     A
                                TTCTTTGTC TTATT CACAT
                                ||||||||| ||||| |||||
                                AAGAAATAG AATAG GTGTA

                                  _    _
GAM1106  WBSCR1   3'  TTCTTTATCTTATCCACAT    28687         C     A
                                TTCTTTGTC TTATT CACAT
                                ||||||||| ||||| |||||
                                AAGAAATAG AATAG GTGTA

                                  _    _
GAM1106  C5orf5   3'  TTCTTTATTCCCCAACTACACA 28688          _    _
            T                    TTCTTTGT CCTTA TTACACAT
                                ||||||||  ||||| ||||||||
                                AAGAAATA GGGGT GATGTGTA
                                    A    T
GAM1106  ENPP4    3'  TTCTTGTCCCATCAACAT     28689       T    T   C
                                TTCTT GTCCT ATTA ACAT
                                ||||| ||||| |||| ||||
                                AAGAA CAGGG TAGT TGTA

                                  _    _   _
GAM1106  FLJ10101 5'  TCCTTTGTCTACTACA       28690          CT
                                TTCTTTGTC  TATTACA
                                |||||||||  |||||||
                                AGGAAACAG  ATGATGT

                                  __
GAM1106  FLJ12875 3'  TTCTTTTGTCCTCTACACACAC 28691          _     AT
                                TTCTTT GTCCTT  TACACAT
                                ||||||  ||||||  |||||||
                                AAGAAA CAGGAG  GTGTGTG
                                   A     AT
GAM1106  FLJ14753 3'  TTCTTTGTCCATAAAACA     28692          T  TT
                                TTCTTTGTCC TA  ACA
                                ||||||||||  ||  |||
                                AAGAAACAGG AT  TGT
                                     T  TT
GAM1106  HSU84971 3'  TTCTTTGCATAATTACACAT   28693         CCTT
                                TTCTTTGT    ATTACACAT
                                ||||||||    |||||||||
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                                AAGAAACG   TAATGTGTA
                                    TAT_
GAM1106 KIAA0934 3' TTCTTTGTCACACTACA    28694       CT
                                TTCTTTGTC  TATTACA
                                |||||||||  |||||||
                                AAGAAACAG  GTGATGT
                                     T_
GAM1106 KIAA0976 5' TTCTTTGTCTTAGAACA    28695       C   TT
                                TTCTTTGTC TTA  ACA
                                ||||||||| |||  |||
                                AAGAAACAG AAT  TGT
                                     _  CT
GAM1106 KIAA1831 3' TTCTCTGTTCCTTTACAC   28696       _   AT
                                TTCTTTGT CCTT  TACAC
                                |||||||| ||||  |||||
                                AAGAGACA GGAA  ATGTG
                                    A   __
GAM1106 KIAA1948 5' TTCTTTGTCTCTACAC     28697       CTTA
                                TTCTTTGTC   TTACAC
                                |||||||||   ||||||
                                AAGAAACAG   GATGTG
                                    A___
GAM1106 NUDT11   3' TTCTTGTCCTCAAACA     28698     T     TT
                                TTCTT GTCCTTA  ACA
                                ||||| |||||||  |||
                                AAGAA CAGGAGT  TGT
                                  _     T_
GAM1106 PELI2    3' TTCCTTGTGTATACACAT   28699       CCTTAT
                                TTCTTTGT    TACACAT
                                ||||||||    |||||||
                                AAGGAACA    ATGTGTA
                                    CAT___
GAM1106 PRO2015  5' TCTTTTAACATTACACAT   28700     GTCCT
                                TCTTT   TATTACACAT
                                |||||   ||||||||||
                                AGAAA   GTAATGTGTA
                                  ATT__
GAM1106 PTPRT    3' TTCTTTGCCATTGCACAT   28701       CTT  A
                                TTCTTTGTC  ATT CACAT
                                |||||||||  ||| |||||
                                AAGAAACGG  TAA GTGTA
                                    ___  C
GAM1106 RASGRP4  3' TTCTTTGCCCTATAGCACAT  28702         T  TA
                                TTCTTTGTCCT AT  CACAT
                                |||||||||| ||  |||||
                                AAGAAACGGGA TA  GTGTA
                                     _ TC
GAM1106 SIRPB1   3' TTCATTGTCCTCTACA     28703     T     AT
                                TTC TTGTCCTT  TACA
                                ||| ||||||||  ||||
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                                AAG AACAGGAG  ATGT
                                 T      __
GAM1106  SPARCL1   5'  TTCTTTGCCCAGAGGCACAT  28704        TTATTA
                                TTCTTTGTCC     CACAT
                                ||||||||||     |||||
                                AAGAAACGGG     GTGTA
                                     TCTCC_
GAM1106  ZNF-U69274 3'  TTCTTTATCCTTAAAGCCAT  28705          TTACA
                                TTCTTTGTCCTTA    CAT
                                ||||||||||||    |||
                                AAGAAATAGGAAT    GTA
                                      TTCG_
GAM1106  LOC128344 3'  TCTGTCCTTCACCAT      28706        TA   A
                                TTTGTCCT  TTAC CAT
                                ||||||||  |||| |||
                                AGACAGGA  AGTG GTA
                                   __   _
GAM1106  LOC149830 3'  CTTTGTAACCTTTACACAT   28707      __   AT
                                CTTTGT  CCTT  TACACAT
                                ||||||  ||||  |||||||
                                GAAACA  GGAA  ATGTGTA
                                   TT   __
GAM1106  LOC150935 3'  TTCTTTGTCCTTCCCCTCTACA 28708          AT____
                                TTCTTTGTCCTT     TACA
                                ||||||||||||     ||||
                                AAGAAACAGGAA     ATGT
                                      GGGGAG
GAM1106  LOC157317 3'  TCTTTAATATTACACAT     28680       TCCT
                                TCTTTG    TATTACACAT
                                ||||||    ||||||||||
                                AGAAAT    ATAATGTGTA
                                   T___
GAM1106  LOC200743 3'  TTTGCTTCATCACACAC     28709       CC
                                TTTGT  TTATTACACAT
                                |||||  ||||||||||
                                AAACG  AGTAGTGTGTG
                                  A_
GAM1106  LOC219673 5'  CTCTTTGCCATTATACA     28710         C   T
                                TTCTTTGTC TTAT ACA
                                ||||||||| |||| |||
                                GAGAAACGG AATA TGT
                                     T   _
GAM1106  LOC221322 3'  TTCTTTGTCTCCCAACA     28711         _   TT
                                TTCTTTGTC CTTA  ACA
                                ||||||||| ||||  |||
                                AAGAAACAG GGGT  TGT
                                     A   __
GAM1106  LOC255937 5'  TTCTTTGTTTTCACAGCAC   28712         CC   TA
                                TTCTTTGT  TTAT  CAC
                                ||||||||  ||||  |||
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                                AAGAAACA  AGTG  GTG
                                    AA    TC
GAM1106  LOC92691  3'  TTCTTTATTCTCCCTGACACAT 28713        C   ATT_
                                TTCTTTGT CTT    ACACAT
                                |||||||| |||    ||||||
                                AAGAAATA GAG    TGTGTA
                                    A   GGAC
GAM1107  WARS      3'  TCATTGTTAAAAGCAGCT    28716    T       A
                                TC TTGTTAAAA CAGTT
                                || ||||||||| |||||
                                AG AACAATTTT GTCGA
                                 T       C
GAM1107  C20orf108 3'  TCCTTGTCTTCTCCGGTTATTT 28717        AAAAACA
             TC                   TCTTTGTT      GTTATTTTC
                                |||||||       |||||||||
                                AGGAACAG      CAATAAAAG
                                    AAGAGGC
GAM1107  C6orf37   3'  TCTTTGTTACAGCTGTTTT   28718        AAAA     A
                                TCTTTGTT    ACAGTT TTTT
                                ||||||||    ||||||| ||||
                                AGAAACAA    TGTCGA AAAA
                                    _____     C
GAM1107  DDX28     5'  TCTTTTCTTCACAGTTATTTTC 28719      GTTAAAA
                                TCTTT      ACAGTTATTTTC
                                |||||      ||||||||||||
                                AGAAA      TGTCAATAAAAG
                                   AGAAG__
GAM1107  KIAA0495  3'  TCTTTGTTTAAAAGGTTAGTTA 28720        A   C___
             TTTT                 TCTTTGTT AAAA    AGTTATTTT
                                |||||||| ||||    |||||||||
                                AGAAACAA TTTT    TCAATAAAA
                                    A    CCAA
GAM1107  TLN2      3'  TCTTTGTTGGTAACAGTC    28721        AAA
                                TCTTTGTT   AACAGTT
                                ||||||||   |||||||
                                AGAAACAA   TTGTCAG
                                    CCA
GAM1107  LOC143425 3'  CTTGGGGCACAGTTATTTTC   28722     TTAAAA
                                TTTG     ACAGTTATTTTC
                                ||||     ||||||||||||
                                GAAC     TGTCAATAAAAG
                                  CCCG__
GAM1107  LOC220906 5'  TCTTTGCTAAAAATGTGACATT 28723          CAGT_
             TT                   TCTTTGTTAAAAA    TATTTT
                                ||||||||||||||    ||||||
                                AGAAACGATTTTT    GTAAAA
                                        ACACT
GAM1108  ARHGEF7   5'  AGGAACTGAGGACCTTGTT   28726        C  TT   CC
                                AGGAACTG GG  GCC  GTT
                                |||||||| ||  |||  |||
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                                TCCTTGAC CC  TGG  CAA
                                     T __   AA
GAM1108 BMPR2    3' GGAATGAACTGCCCTGTT    28727     C  C GT    C
                                GGAA TG G  TGCCC GTT
                                |||| || |  ||||| |||
                                CCTT AC T  ACGGG CAA
                                  _ _ TG    A
GAM1108 CTNND2   3' AGAAACTGCTGAATGCCTTGTT 28728         _ GT   CC
                                AGGAACTGC G  TGCC  GTT
                                ||||||||| |  ||||  |||
                                TCTTTGACG C  ACGG  CAA
                                     A TT   AA
GAM1108 RAB3A    3' AGGAACTGGGGGGGCACGTT   28729        C  TT  CC
                                AGGAACTG GG  GC  CGTT
                                |||||||| ||  ||  ||||
                                TCCTTGAC CC  CG  GCAA
                                     _ CC  T_
GAM1108 SCA1     3' AGGCACTGTGAAGCCCCGTT   28730     A   C  TT
                                AGG ACTG GG  GCCCCGTT
                                ||| |||| ||  ||||||||
                                TCC TGAC CT  CGGGGCAA
                                  G   A  T_
GAM1108 SHC1     3' AGGAACTGCAGGTTTTGCGTT  28731         _   GCCC
                                AGGAACTGC GGTT   CGTT
                                ||||||||| ||||   ||||
                                TCCTTGACG CCAA   GCAA
                                     T   AAC_
GAM1108 WNT3A    3' AGGAGTACTGCCCCGTT     28732     AC   GGT
                                AGGA  TGC   TGCCCCGTT
                                ||||  |||   |||||||||
                                TCCT  ATG   ACGGGGCAA
                                  C_  ___
GAM1108 CDC14B   3' AGGAGCTGCCCGTGCCTGCCCT 28733      A  __ _ _   C
           GTT                    AGGA CTGC  G GT TGCCC GTT
                                ||||  ||||  | || ||||| |||
                                TCCT GACG  C CG ACGGG CAA
                                  C   GG A  G    A
GAM1108 DJ159A19.3 5' GGGGCCCAGTGCTCCGTT    28734    AA  G   T  C
                                GG  CT CGGT GC CCGTT
                                ||  || |||| || |||||
                                CC  GG GTCA CG GGCAA
                                 CC  _   _  A
GAM1108 DKFZp434G179 3' GAACTGGCTTGCTCCGTT    28735       CGG   C
                                GAACTG   TTGC CCGTT
                                ||||||   |||| |||||
                                CTTGAC   AACG GGCAA
                                   CG_   A
GAM1108 EPS8R1   3' AGGGACTGCAGCAAGGATCGTT 28736     A       TGCCC_
                                AGG ACTGCGGT     CGTT
                                ||| ||||||||     ||||
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                                TCC TGACGTCG     GCAA
                                  C       TTCCTA
GAM1108  EPS8R1   3'  AGGGACTGCAGCAAGGATCGTT 28736     A       TGCCC_
                                AGG ACTGCGGT     CGTT
                                ||| ||||||||     ||||
                                TCC TGACGTCG     GCAA
                                  C       TTCCTA
GAM1108  EPS8R1   3'  AGGGACTGCAGCAAGGATCGTT 28736     A       TGCCC_
                                AGG ACTGCGGT     CGTT
                                ||| ||||||||     ||||
                                TCC TGACGTCG     GCAA
                                  C       TTCCTA
GAM1108  FLJ13639 3'  AGGAACTGCCTCTCCCGTT   28737         GG  GC
                                AGGAACTGC  TT  CCCGTT
                                |||||||||  ||  ||||||
                                TCCTTGACG  AG  GGGCAA
                                     G_  A_
GAM1108  FLJ20123 5'  GGGACTGGGCCCCGTT     28738    A    C GTT
                                GG ACTG G   GCCCCGTT
                                || |||| |   ||||||||
                                CC TGAC C   CGGGGCAA
                                 C   _ ___
GAM1108  KIAA0227 3'  AGGAACTACTACCTGT      28739         GGT    CC
                                AGGAACTGC   TGCC  GT
                                |||||||||   ||||  ||
                                TCCTTGATG   ATGG  CA
                                     ___    A_
GAM1108  KIAA0450 3'  GGGGCCTGGCTGCCCTGTT   28740    AA  GC      C
                                GG  CT  GGTTGCCC GTT
                                ||  ||  |||||||| |||
                                CC  GG  CCGACGGG CAA
                                 CC  A_       A
GAM1108  KIAA0599 3'  AGGAATGCAACCCTGT      28741      C    GTT    C
                                AGGAA TGCG   GCCC GT
                                ||||| ||||   |||| ||
                                TCCTT ACGT   TGGG CA
                                   _   ___    A
GAM1108  KIAA1719 3'  GGAGTGGGTGCCCCGTT     28742     AC  C   T
                                GGA  TG GGT GCCCCGTT
                                |||  || ||| ||||||||
                                CCT  AC CCA CGGGGCAA
                                  C_  _   _
GAM1108  MAGEE1   3'  AGAACCTAAACTGCCCTGTT   28743       GCGG     C
                                GGAACT    TTGCCC GTT
                                ||||||    |||||| |||
                                TCTTGG    GACGGG CAA
                                   ATTT     A
GAM1108  MGC13007 5'  AGGAACTGTGATCTTTTTCTCG 28744         C    GCCC___
            TT                   AGGAACTG GGTT      CGTT
                                ||||||||  ||||      ||||
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                                TCCTTGAC CTAG      GCAA
                                    A   AAAAAGA
GAM1108 MGC20255 3' GGAATCAGCTGCCTTGTT   28745     CTG      CC
                                GGAA  CGGTTGCC  GTT
                                ||||  ||||||||  |||
                                CCTT  GTCGACGG  CAA
                                  A__       AA
GAM1108 MGC29761 3' AGGACTTCACGGCCCCGTT   28746     AC_   GTT
                                AGGA  TGCG  GCCCCGTT
                                ||||  ||||  ||||||||
                                TCCT  GTGC  CGGGGCAA
                                  GAA   ___
GAM1108 NAV1     3' AGGAACTGCTGCAGTGTT    28747        GGT  CCC
                                AGGAACTGC  TGC  GTT
                                |||||||||  |||  |||
                                TCCTTGACG  ACG  CAA
                                     ___  TCA
GAM1108 SCYA22   3' AGGACGCTTGAGGGCCCCGTT 28748     AC__  C  TT
                                AGGA   TG GG  GCCCCGTT
                                ||||   || ||  ||||||||
                                TCCT   AC CC  CGGGGCAA
                                  GCGA  T  __
GAM1108 TIP120A  3' AGGTACTGCAAAAGCTTTGTT  28749     A      TT  CCC
                                AGG ACTGCGG  GC   GTT
                                ||| |||||||  ||   |||
                                TCC TGACGTT  CG   CAA
                                  A      TT  AAA
GAM1108 TOMM34   3' AGGGGTTCCAGTTGCCCTGTT  28750     AACTG       C
                                AGG    CGGTTGCCC GTT
                                |||    ||||||||| |||
                                TCC    GTCAACGGG CAA
                                  CCAAG        A
GAM1108 LOC147093 5' AGGAACTGATTTTATTCCTGTT 28751        CGG   CC  _
                                AGGAACTG   TTG  CC GTT
                                ||||||||   |||  || |||
                                TCCTTGAC   AAT  GG CAA
                                     TAA   AA  A
GAM1108 LOC196741 3' AGGCCCGAGTTGCCCTGTT   28752     AA  C      C
                                AGG  CTG GGTTGCCC GTT
                                |||  ||| ||||||||| |||
                                TCC  GGC TCAACGGG CAA
                                  G_  _       A
GAM1108 LOC201115 5' GGAGCTGCGGTTCCCCG     28753     A      G
                                GGA CTGCGGTT CCCCG
                                ||| |||||||| |||||
                                CCT GACGCCAA GGGGC
                                  C       _
GAM1108 LOC201522 3' GGGGCTGGGGGCCCCGTT    28754    AA  C  TT
                                GG  CTG GG  GCCCCGTT
                                ||  ||| ||  ||||||||
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                                CC  GAC CC  CGGGGCAA
                                 CC   _ C_
GAM1108  LOC219690 3'  AGAACTCAGCCCCGT      28755       G  GTT
                                GGAACT CG   GCCCCGT
                                ||||||  ||   |||||||
                                TCTTGA GT   CGGGGCA
                                   _  ____
GAM1108  LOC221354 3'  GGAACTGCGTACTCACCTGTT  28756         G__ TG  CC
                                GGAACTGCG   T  CC  GTT
                                |||||||||   |  ||  |||
                                CCTTGACGC   A  GG  CAA
                                     ATG GT  A_
GAM1108  LOC92231  3'  AGAAACTGTGTCTCCGCT    28757        CG   GCC
                                AGGAACTG  GTT   CCGTT
                                ||||||||  |||   |||||
                                TCTTTGAC  CAG   GGCGA
                                    A_   A__
GAM1109  ARHGEF4   3'  AGAAGGAATAGTGCAAG     28760         CGA  T
                                AGAAGGAATA   GC AAG
                                ||||||||||   || |||
                                TCTTCCTTAT   CG TTC
                                     CA_  _
GAM1109  GT650     3'  GAGGAAGGGACTCACTGAGT   28761     A    AAT  GA   A
                                GA GAAGG   AC  GCT AGT
                                || |||||   ||  ||| |||
                                CT CTTCC   TG  TGA TCA
                                 C    C__  AG   C
GAM1109  SPRY1     3'  GAAGAAGGAAGGTGGCTGAGT  28762         TACGA   A
                                GAAGAAGGAA    GCT AGT
                                ||||||||||    ||| |||
                                CTTCTTCCTT    CGA TCA
                                     CCAC_   C
GAM1109  LOC146237 3'  TCTGGGAAGGAATGTGAGAGCT 28763    GAA      AC__
                                TC   GAAGGAAT   GAGCT
                                ||   ||||||||   |||||
                                AG   CTTCCTTA   CTCGA
                                 ACC       CACT
GAM1110  ADAM28    3'  AACTTGTTAATTTTAAGT    28766
                                AACTTGTTAATTTTAAGT
                                ||||||||||||||||||
                                TTGAACAATTAAAATTCA

GAM1110  ATRX      3'  TTATTAATTTTATGACAAT   28767          AA
                                TTGTTAATTTT  GTGACAAT
                                ||||||||||  ||||||||
                                AATAATTAAAA  TACTGTTA
                                      __
GAM1110  ATRX      3'  TTATTAATTTTATGACAAT   28767          AA
                                TTGTTAATTTT  GTGACAAT
                                ||||||||||  ||||||||
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                                AATAATTAAAA  TACTGTTA
                                           __
GAM1110  CNGB3    3'  AACTTGTTATATTTTGTGA   28768        _    AA
                                AACTTGTTA ATTTT  GTGA
                                |||||||||  |||||  ||||
                                TTGAACAAT TAAAA  CACT
                                     A    __
GAM1110  FMR2     3'  CTTGTTAAGAACAGTGACA   28769       TTTTA
                                CTTGTTAA    AGTGACA
                                ||||||||    |||||||
                                GAACAATT    TCACTGT
                                     CTTG_
GAM1110  KIAA0410 3'  AACTTGTTCACAAAAAGTGA  28770       A  TTT
                                AACTTGTT AT   AAGTGA
                                ||||||||  ||   ||||||
                                TTGAACAA TG   TTCACT
                                     G  TTT
GAM1110  NAV3     3'  CTTAGGTTTTAAGTGAC     28771     TTAA
                                CTTG   TTTTAAGTGAC
                                ||||   ||||||||||
                                GAAT   AAAATTCACTG
                                  CC__
GAM1110  PTBP2    3'  CTTGTTAATTTTAACTAA    28772          G
                                CTTGTTAATTTTAA TGA
                                ||||||||||||| |||
                                GAACAATTAAAATT ATT
                                       G
GAM1110  LOC253883 3'  ACTTGTTAATCTTGTCAC   28773          AA  G
                                ACTTGTTAATTTT  GT AC
                                ||||||||||||  || ||
                                TGAACAATTAGAA  CA TG
                                       __  G
GAM1110  LOC256380 3'  CTGTTAATTTTAAGAGGA   28774          T_
                                TTGTTAATTTTAAG  GA
                                ||||||||||||  ||
                                GACAATTAAAATTC  CT
                                       TC
GAM1110  LOC257235 3'  AACTTGTTAGTCTGCAAGTA  28775       A  _
                                AACTTGTTA TTT TAAGTG
                                |||||||||  ||| ||||||
                                TTGAACAAT AGA GTTCAT
                                     C  C
GAM1111  BLAME    3'  TACTGATTCCCAAGTGCCAAG  28778     ATG  TT
                                TACT   TTT  AGTGCCAAG
                                ||||   |||  |||||||||
                                ATGA   AGG  TCACGGTTC
                                  CTA   GT
GAM1111  DRD2     3'  CTGCATCTTTGGTGCCAAG   28779    AT     A
                                CT  GTTTTT GTGCCAAG
                                ||  |||||| ||||||||
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                                GA  TAGAAA CACGGTTC
                                 CG     C
GAM1111  GPC4     3'  TACATGTTACGTGCCAAG    28780     T    TTTA
                                TAC ATGTT   GTGCCAAG
                                ||| |||||   ||||||||
                                ATG TACAA   CACGGTTC
                                  _    TG__
GAM1111  HEPH     3'  TACTCCCTTAGTGCCA      28781     ATG
                                TACT  TTTTTAGTGCCA
                                ||||  ||||||||||||
                                ATGA  GGGAATCACGGT
                                  ___
GAM1111  HEPH     3'  TACTCCCTTAGTGCCA      28781     ATG
                                TACT  TTTTTAGTGCCA
                                ||||  ||||||||||||
                                ATGA  GGGAATCACGGT
                                  ___
GAM1111  HRH1     3'  TACTAGTTTTTGCTTACCA   28782      T    AG_
                                TACTA GTTTTT  TGCCA
                                ||||| ||||||  |||||
                                ATGAT CAAAAA  ATGGT
                                   _    CGA
GAM1111  POLR2C   3'  TACTGATGTCCTGCCAAG    28783     _    TTAG
                                TACT ATGTTT   TGCCAAG
                                |||| ||||||   |||||||
                                ATGA TACAGG   ACGGTTC
                                  C    _____
GAM1111  RAI3     5'  CTGGACCCTAGTGCCAAG    28784    ATGT
                                CT   TTTTAGTGCCAAG
                                ||   ||||||||||||
                                GA   GGGATCACGGTTC
                                 CCT_
GAM1111  RNMT     3'  CACTATGTTTTTAAAACAAG  28785          TGC
                                TACTATGTTTTTAG  CAAG
                                ||||||||||||||  ||||
                                GTGATACAAAAATT  GTTC
                                        TT_
GAM1111  SCN1A    5'  TACTATGTTCCTCCAA      28786         AGTG
                                TACTATGTTTTT   CCAA
                                ||||||||||||   ||||
                                ATGATACAAGGA   GGTT
                                        _____
GAM1111  SMARCA5  3'  TACTATGTTTCTAGCTCA    28787           GC
                                TACTATGTTTTTAGT  CA
                                ||||||||||||||| ||
                                ATGATACAAAGATCG  GT
                                        A_
GAM1111  STAU2    3'  TACATGTTTTTCTACCA     28788     T     AG
                                TAC ATGTTTTT  TGCCA
                                ||| ||||||||  |||||
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                                ATG TACAAAAA  ATGGT
                                  _      G_
GAM1111  CG012    3'  TACTTGTTGACTGTGCCAAG  28789     A   TTTA
                                TACT TGTT   GTGCCAAG
                                |||| ||||   ||||||||
                                ATGA ACAA   CACGGTTC
                                  _   CTGA
GAM1111  DKFZp761I1011 3'  CCAGGCATAGTGCCAAG    28790     T  TTT
                                CTA GT   TAGTGCCAAG
                                ||| ||   ||||||||||
                                GGT CG   ATCACGGTTC
                                  C  T__
GAM1111  DNAH8    5'  TACTATGTCCAGGCCAAG    28791        TT   T
                                TACTATGTT  TAG GCCAAG
                                |||||||||  ||| ||||||
                                ATGATACAG  GTC CGGTTC
                                     __  _
GAM1111  DNAJA4   5'  TACCATGAGACAGTGCCA    28792       TTTT
                                TACTATG    TAGTGCCA
                                |||||||    ||||||||
                                ATGGTAC    GTCACGGT
                                    TCT_
GAM1111  FLJ14494  3'  CACTGTGCTCCCAGGTGCCA  28793     A       _
                                TACT TGTTTTTAG TGCCA
                                |||| ||||||||| |||||
                                GTGA ACGAGGGTC ACGGT
                                  C        C
GAM1111  FLJ14957  3'  CTGTATTCTGTGTGCCAAG   28794    A     TA
                                CT TGTTTT  GTGCCAAG
                                || ||||||  ||||||||
                                GA ATAAGA  CACGGTTC
                                 C     CA
GAM1111  FLJ20079  5'  TGTCTTTCTTGATGCCAAG   28795       A___
                                TGTTTTT    GTGCCAAG
                                |||||||    ||||||||
                                ACAGAAA    TACGGTTC
                                    GAAC
GAM1111  H2AV     3'  TACTCTGTCCTCTGCCAAG   28796     A     AG
                                TACT TGTTTTT  TGCCAAG
                                |||| |||||||  |||||||
                                ATGA ACAGGAG  ACGGTTC
                                  G     __
GAM1111  KIAA1750  3'  TATGTGTGCGCAGTGCCAAG  28797      TTT__
                                TATGT    TAGTGCCAAG
                                |||||    ||||||||||
                                ATACA    GTCACGGTTC
                                   CACGC
GAM1111  MGC1136   3'  TATGTTTTTGGCCCAAG    28798        A  G
                                TATGTTTTT GT CCAAG
                                ||||||||| || |||||
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                                ATACAAAAA CG GGTTC
                                     C  _
GAM1111  LOC143437 5'  TACAGTGCCCTGTGCCA     28799     TA     TA
                                TAC  TGTTTT  GTGCCA
                                |||  ||||||  ||||||
                                ATG  ACGGGA  CACGGT
                                  TC     __
GAM1111  LOC146435 3'  TACATAAATTTTAGTGCCAAG  28800     TATGT
                                TAC    TTTTAGTGCCAAG
                                |||    ||||||||||||
                                ATG    AAAATCACGGTTC
                                  TATTT
GAM1111  LOC151610 3'  CTAATCTTTAGTGCCAAG    28801     T
                                CTA GTTTTTAGTGCCAAG
                                ||| ||||||||||||||
                                GAT TAGAAATCACGGTTC
                                  _
GAM1111  LOC253531 5'  TACAGTGCCCTGTGCCA     28799     TA     TA
                                TAC  TGTTTT  GTGCCA
                                |||  ||||||  ||||||
                                ATG  ACGGGA  CACGGT
                                  TC     __
GAM1111  LOC54103  5'  TACTTGAGATCCAGTGCCA    28802      A  TT_
                                TACT TG   TTTAGTGCCA
                                |||| ||   ||||||||||
                                ATGA AC   AGGTCACGGT
                                  _ TCT
GAM1111  LOC92249  3'  TGCTATTCCAGTGCCAAG    28803     __
                                TGT  TTTTAGTGCCAAG
                                |||  ||||||||||||
                                ACG  AAGGTCACGGTTC
                                  AT
GAM1112  CRI1      3'  AGATATAGCGCTTTTTACTT   28806        GA__
                                AGATATGG    TTTTACTT
                                ||||||||    ||||||||
                                TCTATATC    AAAATGAA
                                     GCGA
GAM1112  FMR2      3'  TCTGGATGTGGGATTTCA     28807     AA   A
                                TCT  GAT TGGGATTTTA
                                |||  ||| ||||||||||
                                AGA  CTA ACCCTAAAGT
                                  C_   C
GAM1112  ITGA1     3'  TAAAATACATTTCTGGGATTTT 28808    _______        C    III
              ATTTAAT                TA     TGGGATTTTA TTAA   T
                                ||     |||||||||| ||||   |
                                AT     ACCCTAAAAT AATT   A
                                 GTAAAG         A    III
GAM1112  OSR1      3'  TCTAGGATTTGGTTCAAAACTT 28809      A   A   GATTTT
              AA                   TCTA GAT TGG     ACTTAA
                                |||| ||| |||     ||||||
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                                AGAT CTA ACC     TGAATT
                                  C   A  AAGTTT
GAM1112  PCDHA9   3'  TCTAAGATATTGGGTGACAACT 28810        _  ATTTT
             TA                   TCTAAGATAT GGG    ACTTA
                                  |||||||||| |||    |||||
                                  AGATTCTATA CCC    TGAAT
                                       A   ACTGT
GAM1112  AKAP3    5'  TCTGAGATATGAGGAAAGCTCT 28811    A     _  TTTTA
             T                    TCT AGATATG GGA    CTT
                                  ||| ||||||| |||    |||
                                  AGA TCTATAC CCT    GAA
                                    C      T  TTCGA
GAM1112  DKFZP434C131 3'  TCTGGGATATGGGGGTCTCA  28812    AA      A_
                                  TCT  GATATGGG  TTTTA
                                  |||  ||||||||  |||||
                                  AGA  CTATACCC  AGAGT
                                    CC       CC
GAM1112  KIAA0266  5'  AGATATGGCATTACTTAA   28813       G  TT
                                  AGATATGG AT  TACTTAA
                                  |||||||| ||  |||||||
                                  TCTATACC TA  ATGAATT
                                       G  __
GAM1112  SCDGF-B   3'  TCTAGGACTGATTTTACTT   28814     A   ATGG
                                  TCTA GAT    GATTTTACTT
                                  |||| |||    ||||||||||
                                  AGAT CTG    CTAAAATGAA
                                    C   A___
GAM1112  SCDGF-B   3'  TCTAGGACTGATTTTACTT   28814     A   ATGG
                                  TCTA GAT    GATTTTACTT
                                  |||| |||    ||||||||||
                                  AGAT CTG    CTAAAATGAA
                                    C   A___
GAM1112  UPB1     3'  TCTGAGATAATCTCACTTA   28815     A    TGGG
                                  TCT AGATA    ATTTTACTTA
                                  ||| |||||    ||||||||||
                                  AGA TCTAT    TAGAGTGAAT
                                    C    _____
GAM1112  LOC126917 3'  TCTAAGACATTTCACTT     28816         GGGAT
                                  TCTAAGATAT     TTTACTT
                                  ||||||||||     |||||||
                                  AGATTCTGTA     AAGTGAA
                                                 ______
GAM1112  LOC149830 3'  CTTAGAGATGGGTTTTACTTA  28817    A  T    A
                                  CT AGA ATGGG TTTTACTTA
                                  || ||| ||||| |||||||||
                                  GA TCT TACCC AAAATGAAT
                                   A  C    _
GAM1112  LOC200918 3'  CTGAGAATGGTTTTACTTAA   28818    A  T   GA
                                  CT AGA ATGG  TTTTACTTAA
                                  || ||| ||||  ||||||||||
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                                GA TCT TACC  AAAATGAATT
                                 C  _   __
GAM1113  E2F3     3'  GGAAAGCCATTCTTGGACA   28821     TCCTA       A
                                GGA    CCATTCTTG ACA
                                |||    ||||||||| |||
                                CCT    GGTAAGAAC TGT
                                  TTC__       C
GAM1113  GDI2     3'  ATGGATCCAGCTCTTGA     28822        TACCA
                                ATGGATCC    TTCTTGA
                                ||||||||    |||||||
                                TACCTAGG    GAGAACT
                                    TC___
GAM1113  C20orf162 5'  TGGATTAAACTTCTTGAA    28823      CCT  CA
                                TGGAT   AC  TTCTTGAA
                                |||||   ||  ||||||||
                                ACCTA   TG  AAGAACTT
                                   ATT  __
GAM1113  DKFZp762P2111 3'  AATGGATCTTACACACCCATGA 28824        C  _    T
            ACA                    AATGGATC TAC CATTC TGAACA
                                |||||||| ||| ||||| ||||||
                                TTACCTAG ATG GTGGG ACTTGT
                                    A  T    T
GAM1113  FLJ10619  3'  GACTTACTATTCTTGAA     28825     CC   C
                                GAT  TAC ATTCTTGAA
                                |||  ||| |||||||||
                                CTG  ATG TAAGAACTT
                                  A_   A
GAM1113  FLJ14825  3'  AATGGATCCTGTCTGAA     28826          ACCAT   T
                                AATGGATCCT    TCT GAA
                                ||||||||||    ||| |||
                                TTACCTAGGA    AGA CTT
                                    C_____   _
GAM1113  FLJ20986  3'  AGAGGGTACCATTCTTGA    28827     TCC
                                GGA   TACCATTCTTGA
                                |||   ||||||||||||
                                TCT   ATGGTAAGAACT
                                  CCC
GAM1113  KIAA1036  3'  TGGATCCTGGCCCCCAAGA   28828        A_  A   TT
                                TGGATCCT  CC TTC  GA
                                ||||||||  || |||  ||
                                ACCTAGGA  GG GGG  CT
                                    CC  _   TT
GAM1113  PRDM10    3'  AATGGATCCTGCAAGGCAGAAC 28829          AC  TTCTT
            A                    AATGGATCCT  CA    GAACA
                                ||||||||||  ||    |||||
                                TTACCTAGGA  GT    CTTGT
                                    C_  TCCGT
GAM1113  SLC25A21  3'  AATAGATTTTGTTCTTGAACA  28830        CCTACCA
                                AATGGAT      TTCTTGAACA
                                |||||||      ||||||||||
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                                TTATCTA      AAGAACTTGT
                                    AAAC___
GAM1113  ZNF339    3'  AATGGACCCTACTGCTGA    28831          CATTC
                                AATGGATCCTAC    TTGA
                                ||||||||||||    ||||
                                TTACCTGGGATG    GACT
                                      AC___
GAM1113  LOC146856 3'  GGAAAGCCATTCTTGGACA   28821     TCCTA       A
                                GGA    CCATTCTTG ACA
                                |||    ||||||||| |||
                                CCT    GGTAAGAAC TGT
                                  TTC__        C
GAM1113  LOC147804 5'  TGGATCCTACCGTTCACG    28832          A   T
                                TGGATCCTACC TTC TG
                                |||||||||| ||| ||
                                ACCTAGGATGG AAG GC
                                      C   T
GAM1113  LOC152313 3'  ATGGATCCTTCATGAA      28833         ACCAT  T
                                ATGGATCCT    TC TGAA
                                |||||||||    || ||||
                                TACCTAGGA    AG ACTT
                                     _____ T
GAM1114  ANKTM1    3'  CATCTCTAGAAAAGTCCA    28836      C       A
                                CATC CTAGAAGA GTTTA
                                |||| |||||||| |||||
                                GTAG GATCTTTT CAGGT
                                  A       _
GAM1114  GRLF1     3'  TCCCCAGAGGGAGCTCGGGAGC 28837        AGA    AT
                                TCCCTAGA   AGTTT  GAGC
                                ||||||||   |||||  ||||
                                AGGGGTCT   TCGAG  CTCG
                                     CCC    CC
GAM1114  HOXA3     3'  CATCCCCAGAGGAGACCAGGAG 28838         A  AG  TAT
                                CATCCCTAGA GA  TT   GAG
                                |||||||||| ||  ||   |||
                                GTAGGGGTCT CT  GG   CTC
                                      C  CT  TC_
GAM1114  LDB3      3'  TCCTTAGAAGAAAAGAG     28839     C       TTTAT
                                TCC TAGAAGAAG     GAG
                                ||| |||||||||     |||
                                AGG ATCTTCTTT     CTC
                                  A        T____
GAM1114  LEF1      3'  CATCTCCAGAAGAGGTCC    28840      C       A
                                CATC CTAGAAGA GTTT
                                |||| |||||||| ||||
                                GTAG GGTCTTCT CAGG
                                  A       C
GAM1114  OCRL      3'  CATCCCTAGGTGAAGGAG    28841         AA    TTTAT
                                CATCCCTAG  GAAG    GAG
                                |||||||||  ||||    |||
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                                GTAGGGATC  CTTC    CTC
                                     CA   _____
GAM1114  OCRL     3'  CATCCCTAGGTGAAGGAG    28841        AA   TTTAT
                                CATCCCTAG  GAAG    GAG
                                |||||||||  ||||    |||
                                GTAGGGATC  CTTC    CTC
                                     CA   _____
GAM1114  PNOC     3'  CCCCTAGAAGGGGCAAGAG   28842        AA  TTAT
                                TCCCTAGAAG  GT   GAG
                                ||||||||||  ||   |||
                                GGGGATCTTC  CG   CTC
                                     CC  TT__
GAM1114  RECQL5   3'  CATCCCAGAAGAGGGTGGAG   28843      T    A_  TTAT
                                CATCCC AGAAGA  GT   GAG
                                ||||||  ||||||  ||   |||
                                GTAGGG TCTTCT  CA   CTC
                                   _    CC  C___
GAM1114  EDG1     3'  CATCCCTAAAGAAGCAGAAG   28844        A    TTAT
                                CATCCCTAGA GAAGT   GAG
                                ||||||||||  |||||   |||
                                GTAGGGATTT CTTCG   TTC
                                     _    TC__
GAM1114  FLJ10849 3'  CATCCTTAGAAGAAGATT    28845      C       T
                                CATCC TAGAAGAAG TT
                                |||||  |||||||||  ||
                                GTAGG ATCTTCTTC AA
                                   A       T
GAM1114  FLJ20371 3'  CCTTTTGAAGGGTTTATGAG   28846    A__   AA
                                CCT   GAAG  GTTTATGAG
                                |||   ||||  |||||||||
                                GGA   CTTC  CAAATACTC
                                  AAA   C_
GAM1114  KIAA0125 3'  CATCCCCAGGGGAGGACACAGC 28847        AA  A TT   G
                                CATCCCTAG  GA G  TAT AGC
                                |||||||||  || |  ||| |||
                                GTAGGGGTC  CT C  GTG TCG
                                     CC  _ CT   _
GAM1114  KIAA0125 3'  CATCCCTAGGGGAGGACACAGC 28848        AA  A TT   G
                                CATCCCTAG  GA G  TAT AGC
                                |||||||||  || |  ||| |||
                                GTAGGGATC  CT C  GTG TCG
                                     CC  _ CT   _
GAM1114  KIAA0125 3'  CATCCCCAGGGGAGGACACAGC 28847        AA  A TT   G
                                CATCCCTAG  GA G  TAT AGC
                                |||||||||  || |  ||| |||
                                GTAGGGGTC  CT C  GTG TCG
                                     CC  _ CT   _
GAM1114  KIAA0143 3'  CCTAAGAGAATTTTATGAG   28849     GA   G
                                CCTA  AGAA TTTATGAG
                                ||||  |||| ||||||||
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                                GGAT  TCTT AAATACTC
                                  TC    A
GAM1114  KIAA0773  3'  CATCCCAGAAGTGTGA      28850       TAGA     TTA
                                CATCCC   AGAAGT   TGA
                                ||||||   ||||||   |||
                                GTAGGG   TCTTCA   ACT
                                   ____     C__
GAM1114  KIAA1695  3'  CACTCCTGGGAGTAACCTATGA 28851    TC   AGA  A  TT
             G                   CA  CCT   AG AG  TATGAG
                                 ||  |||   || ||  ||||||
                                 GT  GGA   TC TT  ATACTC
                                  GA   CCC  A  GG
GAM1114  MGC955    3'  TCCAAGAAGTTTGTGAG     28852     CTAG       A
                                TCC    AAGAAGTTT TGAG
                                |||    ||||||||| ||||
                                AGG    TTCTTCAAA ACTC
                                  ____        C
GAM1114  PDE1C     3'  CATCCCCTGGAAGGAGATG    28853        A_    A  TTT
                                CATCCCT  GAAG AG   ATG
                                |||||||  |||| ||   |||
                                GTAGGGG  CTTC TC   TAC
                                    AC    C  ___
GAM1114  SEMA4G    3'  CATTCCTAAAGAAGTGTAG    28854     C     A    TTATG
                                CAT CCTAGA GAAGT     AG
                                ||| |||||| |||||     ||
                                GTA GGATTT CTTCA     TC
                                  A     _     CA___
GAM1114  SEMA4G    3'  CATTCCTAAAGAAGTGTAG    28854     C     A    TTATG
                                CAT CCTAGA GAAGT     AG
                                ||| |||||| |||||     ||
                                GTA GGATTT CTTCA     TC
                                  A     _     CA___
GAM1114  LOC146237 3'  CCTACAAGAAATTGAG      28855      G      TTA
                                CCTA AAGAAGT   TGAG
                                |||| |||||||   ||||
                                GGAT TTCTTTA   ACTC
                                  G      ___
GAM1114  LOC148438 3'  CTATTTTCAGGGGTTTATGAGC 28856     GA___  AA
                                CTA     AG  GTTTATGAGC
                                |||     ||  ||||||||||
                                GAT     TC  CAAATACTCG
                                  AAAAG  CC
GAM1114  LOC149276 5'  ATCCCAGAGCTTATG       28857       T   AGAA
                                ATCCC AGA    GTTTATG
                                ||||| |||    |||||||
                                TAGGG TCT    CGAATAC
                                   _  _____
GAM1114  LOC151429 3'  TCTCAGAAGAAAAGGCAGAGC  28858     CC        TTTAT
                                TC  TAGAAGAAG     GAGC
                                ||  |||||||||     ||||
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                                AG  GTCTTCTTT    CTCG
                                 A_       TCCGT
GAM1114  LOC152674 5'  ATCCCTAGAAGTGTGTATTATG 28859          AA_  _
                                ATCCCTAGAAG   GT TTATG
                                ||||||||||   || |||||
                                TAGGGATCTTC   CA AATAC
                                      ACA  T
GAM1114  LOC155061 3'  CATCCCCAGGAGTCAGTGGGC  28860        AAGA   TA  A
                                CATCCCTAG    AGTT  TG GC
                                |||||||||    ||||  || ||
                                GTAGGGGTC    TCAG  AC CG
                                     C___    TC  C
GAM1114  LOC204084 5'  CATTCCTAGAAGGAGCTGAGC  28861     C       A   TTA
                                CAT CCTAGAAG AGT   TGAGC
                                ||| ||||||| |||   |||||
                                GTA GGATCTTC TCG   ACTCG
                                  A       C  ___
GAM1114  LOC219649 5'  ATCCCTAGAGCGTATGAG    28862         AGAA  T
                                ATCCCTAGA    GT TATGAG
                                |||||||||    || ||||||
                                TAGGGATCT    CG ATACTC
                                     _____ C
GAM1114  LOC253292 5'  ATCCCTTGAAGGGATGAG    28863       A    AAGTTT
                                ATCCCT GAAG     ATGAG
                                |||||| ||||     |||||
                                TAGGGA CTTC     TACTC
                                   A   CC_____
GAM1115  CTNNB1    3'  ATGAATTAATTAGTGTTCTACA 28866          AA_
                                ATGAATTAATTA   TTCTACA
                                ||||||||||||   |||||||
                                TACTTAATTAAT   AAGATGT
                                       CAC
GAM1115  FOXO1A    3'  ATGAACACAAATTCTACA    28867       TAAT
                                ATGAAT    TAAATTCTACA
                                ||||||    ||||||||||
                                TACTTG    GTTTAAGATGT
                                   T___
GAM1115  IL7       3'  CATGATTAATTAAATCTCT    28868       A       _
                                CATGA TTAATTAAAT TCT
                                ||||| |||||||||| |||
                                GTACT AATTAATTTA AGA
                                   _        G
GAM1115  SFRS2IP   5'  TCCATGAATTAATAAAGACTC  28869          TAA_
                                TCCATGAATTAAT    ATTC
                                ||||||||||||    ||||
                                AGGTACTTAATTA    TGAG
                                       TTTC
GAM1115  FAM3C     3'  CATGAATTAATTACATTC    28870           A
                                CATGAATTAATTA ATTC
                                |||||||||||| ||||
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                                GTACTTAATTAAT TAAG
                                      G
GAM1115 KLHL4    3' TCCATGAATGGATTAATCCA  28871        TA    AT
                                TCCATGAAT  ATTAA  TCTA
                                |||||||||  |||||  ||||
                                AGGTACTTA  TAATT  AGGT
                                     CC    __
GAM1115 MGC4827  3' TCCAGGAATAATTCTA     28872     T   TAATTA
                                TCCA GAAT     AATTCTA
                                |||| ||||     |||||||
                                AGGT CTTA     TTAAGAT
                                  C   ______
GAM1115 SEF      3' CCCATGGCAATGTAAATTCTAC 28873       AAT   _
             A                   TCCATG   TAAT TAAATTCTACA
                                ||||||   |||| ||||||||||
                                GGGTAC   GTTA ATTTAAGATGT
                                   C__    C
GAM1115 SLC26A7  3' CATGTGAGCACTAGATTCTACA 28874     AATTA    A
                                CATG     ATTA ATTCTACA
                                ||||     |||| ||||||||
                                GTAC     TGAT TAAGATGT
                                  ACTCG    C
GAM1115 LOC158668 5' CCTGAATTTTAATTAAATTCT  28875    A    __
                                CC TGAAT  TAATTAAATTCT
                                || |||||  ||||||||||||
                                GG ACTTA  ATTAATTTAAGA
                                 _    AA
GAM1115 LOC158668 5' TCCATGAATAATAGCCTCT    28876        T   TAAA
                                TCCATGAAT AAT    TTCT
                                ||||||||| |||    ||||
                                AGGTACTTA TTA    GAGA
                                     _  TCG_
GAM1115 LOC257017 5' CATGAATTAATAAATTACA    28877         T    TC
                                CATGAATTAAT AAAT  TACA
                                |||||||||| ||||  ||||
                                GTACTTAATTA TTTA  ATGT
                                          _   __
GAM1116 SCN3A    3' AGTTTAGATGCTTATAG     28880         ATACC
                                AGTTTAGATG    TATAG
                                ||||||||||    |||||
                                TCAAATCTAC    ATATC
                                     GA___
GAM1116 FLJ32884 5' CACAAGTTGATGGCCTGTA    28881        TA   ATA   A
                                CACAAGTT  GATG   CCT TA
                                ||||||||  ||||   ||| ||
                                GTGTTCAA  CTAC   GGA AT
                                     __    C__   C
GAM1116 PDZD2    3' CACAAGCTTGGAGATTTTTATA 28882         A  T   ACC
             G                   CACAAGTTT GA GAT   TATAG
                                |||||||||  || |||   |||||
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                                GTGTTCGAA CT CTA   ATATC
                                     C  _   AAA
GAM1116 SEC22C   3' ACAAGTTTAGGTTGTACTAC  28883         A_  A   C
                                ACAAGTTTAG  TG TAC TAT
                                ||||||||||  || ||| |||
                                TGTTCAAATC  AC ATG ATG
                                     CA  _   _
GAM1116 ZNF272   3' CACAGAGATGATACTTAT    28884      A TTT       C
                                CACA G   AGATGATAC TAT
                                ||||  |   ||||||||| |||
                                GTGT C   TCTACTATG ATA
                                  _ ___       A
GAM1117 ARHGEF12 3' GCAGTCACCTCCAGGACA    28887         C   T  TA
                                GCAGTCACC CCG GG  ACA
                                ||||||||| ||| ||  |||
                                CGTCAGTGG GGT CC  TGT
                                     A   _  __
GAM1117 CAPN10   3' TCCAGTCACCTGAGCTGGCA  28888    G      CCC _
                                TC CAGTCACC   G TGGTA
                                || ||||||||   | |||||
                                AG GTCAGTGG   C ACCGT
                                 _       ACT G
GAM1117 CAPN10   3' TCCAGTCACCTGAGCTGGCA  28888    G      CCC _
                                TC CAGTCACC   G TGGTA
                                || ||||||||   | |||||
                                AG GTCAGTGG   C ACCGT
                                 _       ACT G
GAM1117 CAPN10   3' TCCAGTCACCTGAGCTGGCA  28888    G      CCC _
                                TC CAGTCACC   G TGGTA
                                || ||||||||   | |||||
                                AG GTCAGTGG   C ACCGT
                                 _       ACT G
GAM1117 CAPN10   3' TCCAGTCACCTGAGCTGGCA  28888    G      CCC _
                                TC CAGTCACC   G TGGTA
                                || ||||||||   | |||||
                                AG GTCAGTGG   C ACCGT
                                 _       ACT G
GAM1117 CAPN10   3' TCCAGTCACCTGAGCTGGCA  28888    G      CCC _
                                TC CAGTCACC   G TGGTA
                                || ||||||||   | |||||
                                AG GTCAGTGG   C ACCGT
                                 _       ACT G
GAM1117 CAPN10   3' TCCAGTCACCTGAGCTGGCA  28888    G      CCC _
                                TC CAGTCACC   G TGGTA
                                || ||||||||   | |||||
                                AG GTCAGTGG   C ACCGT
                                 _       ACT G
GAM1117 CENTD1   5' CCGCAGTCGCCTCTGCTGCGTG 28889     A  CCC_________  GTAA
             TTACCA                 AGTC CC         GTG   CA
                                |||| ||         |||   ||
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                                TCAG GG         CAC    GT
                                  C  AGACGACGIII   AATG
GAM1117 HMGCR    3' ACAGTCACTTTTTTGAACAC   28890        CCCCG   TA
                                GCAGTCAC    TGG  ACAC
                                ||||||||    |||  ||||
                                TGTCAGTG    ACT  TGTG
                                    AAAAA   __
GAM1117 HPS4     3' TCCCAGTCACCTCCTGGGT    28891    G      C  GT
                                TC CAGTCACC CC  GGT
                                || |||||||| ||  |||
                                AG GTCAGTGG GG  CCA
                                 G       A  AC
GAM1117 MYCL2    3' GCATCACCCCAGAGACA     28892     G      CGT  TA
                                GCA TCACCCC   GG  ACA
                                ||| |||||||   ||  |||
                                CGT AGTGGGG   TC  TGT
                                 _      ___  TC
GAM1117 APEG1    3' TCGCAGCCGCCCCTTCCCAGCA 28893        A    CG__
                                TCGCAGTC CCCC    TGGTA
                                |||||||| ||||    |||||
                                AGCGTCGG GGGG    GTCGT
                                    C    AAGG
GAM1117 APXL2    5' TCGCAGCCGCGCGGTGACA    28894        ACCCC     A
                                TCGCAGTC    CGTGGT ACA
                                ||||||||    |||||| |||
                                AGCGTCGG    GCGCCA TGT
                                    C_____     C
GAM1117 BOLL     5' TCGCAGTCACTGCCTCGGC    28895         CC  G
                                TCGCAGTCAC  CC TGGT
                                ||||||||||  || ||||
                                AGCGTCAGTG  GG GCCG
                                     AC  A
GAM1117 C20orf20 3' TCGCAGTCACACGAAAGTGGCA 28896         CCCC__
                                TCGCAGTCAC     GTGGTA
                                ||||||||||     ||||||
                                AGCGTCAGTG     CACCGT
                                     TGCTTT
GAM1117 C20orf82 5' TCCAGTCACCCTCGCCAT    28897    G      C   G
                                TC CAGTCACCC CGT GT
                                || |||||||| ||| ||
                                AG GTCAGTGGG GCG TA
                                 _       A   G
GAM1117 DATF1    5' TCGCAGCCATTTCCCCGAACGC 28898         C__    TG_
                                TCGCAGTCA   CCCCG   GT
                                |||||||||   |||||   ||
                                AGCGTCGGT   GGGGC   CG
                                    AAA     TTG
GAM1117 E2IG4    3' CCACAACTCCTGTGGTGAC    28899      GTC  C  C    A
                                TCGCA   AC CC GTGGT AC
                                |||||   || || ||||| ||
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                              GGTGT  TG GG CACCA TG
                                 ___ A A    C
GAM1117 FLJ10569 5' TCGCAGTCCCCCTGGGCAGACA 28900       A   CGT   _
                              TCGCAGTC CCCC  GGTA ACA
                              |||||||| ||||  |||| |||
                              AGCGTCAG GGGG  CCGT TGT
                                   _   AC_   C
GAM1117 FLJ20626 3' GCAGTCACCCCACAGGCA   28901         _ T
                              GCAGTCACCCC CG GGTA
                              |||||||||| || ||||
                              CGTCAGTGGGG GT CCGT
                                     T _
GAM1117 FLJ20758 5' GTCACCATAGTAACAC     28902      CCC
                              GTCACC  GTGGTAACAC
                              ||||||  ||||||||||
                              CAGTGG  TATCATTGTG

                                 ___
GAM1117 FLJ23514 3' TCGCAATCACCCCCAAACA  28903          TGGT
                              TCGCAGTCACCCCCG   AACA
                              ||||||||||||||   ||||
                              AGCGTTAGTGGGGGT   TTGT

                                   ____
GAM1117 KIAA0089 5' TCGCGGCCACCCCCGCCCGGC 28904     A       __
                              TCGC GTCACCCCCGT  GGT
                              |||| ||||||||||  |||
                              AGCG CGGTGGGGGCG  CCG
                                C         GG
GAM1117 KIAA0644 3' GCAGTGACCTCCATGGTA   28905     C  C
                              GCAGT ACC CCGTGGTA
                              ||||| ||| ||||||||
                              CGTCA TGG GGTACCAT
                                 C  A
GAM1117 MGC4796  3' GCAGTCACCCTTCCAGGCA  28906       __  T
                              GCAGTCACCC  CCG GGTA
                              ||||||||||  ||| ||||
                              CGTCAGTGGG  GGT CCGT
                                   AA  _
GAM1117 SARM     3' GCAGTCACCTCTGAACA    28907       CCCG  TA
                              GCAGTCACC   TGG  ACA
                              |||||||||   |||  |||
                              CGTCAGTGG   ACT  TGT
                                   AG__  __
GAM1117 SV2B     3' GCAGCCACCCCAGCA      28908        CGT
                              GCAGTCACCCC  GGTA
                              ||||||||||  ||||
                              CGTCGGTGGGG  TCGT

                                   ___
GAM1117 YEA      5' TCGCAGTCAGCTTCGGTCCCA 28909       CCCCCG  AA
                              TCGCAGTCA    TGGT  CA
                              |||||||||    ||||  ||
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                                AGCGTCAGT     GCCA  GT
                                     CGAA__    GG
GAM1117  LOC152426 3'  TCCCAGTCACCCTTGGAGAGGA 28910    G       CCGT___  T
              AC                    TC CAGTCACCC      GG AAC
                                ||  |||||||||       ||  |||
                                AG GTCAGTGGG      CC TTG
                                 G        AACCTCT  _
GAM1117  LOC158055 3'  TCGCAGTCAGTCACCTGAT    28911         CCC_  G
                                TCGCAGTCA    CC TGGT
                                |||||||||    ||  ||||
                                AGCGTCAGT    GG ACTA
                                     CAGT  _
GAM1117  LOC203069 5'  TCGCAGCCGCCCTCGGC     28912         A   CCG
                                TCGCAGTC CCC   TGGT
                                |||||||| |||   ||||
                                AGCGTCGG GGG   GCCG
                                     C   A__
GAM1117  LOC203504 3'  TCCAGTCACCCAGAGGGTGACA 28913    G       CCGT   A
              C                     TC CAGTCACCC    GGT ACAC
                                ||  |||||||||    |||  ||||
                                AG GTCAGTGGG    CCA TGTG
                                 _        TCTC   C
GAM1117  LOC220537 3'  CGCGGTCATCCCACAACA    28914     A    CC    TGG
                                CGC GTCA  CCCG   TAACA
                                |||  ||||  ||||   |||||
                                GCG CAGT  GGGT   GTTGT
                                  C    A_   ___
GAM1117  LOC256158 5'  TCACGGTCACCTCCTCATCTGC 28915      A     _  _   G_
              A                     TCGC GTCACC CC CGT  GTA
                                ||||  ||||||  ||  |||  |||
                                AGTG CAGTGG GG GTA  CGT
                                  C      A  A   GA
GAM1117  LOC91818  5'  GCGGTCACCACAGTAACAC   28916    A     CCC TG
                                GC GTCACC   G  GTAACAC
                                ||  ||||||   |  |||||||
                                CG CAGTGG   T  CATTGTG
                                 C      ___ GT
GAM1118  CNTN3     3'  AAAAAGCCTGCCAGACTCA    28919         A__    T
                                AAAAAGCC   CAGA CTCA
                                ||||||||   ||||  ||||
                                TTTTTCGG   GTCT GAGT
                                     ACG   _
GAM1118  DHCR24    3'  AAAAAGCCATGAACTCA     28920         CA  T
                                AAAAAGCCA  GA CTCA
                                |||||||||  ||  ||||
                                TTTTTCGGT  CT GAGT
                                     A_  T
GAM1118  DMD       3'  AAAAAGCCATGAATTTCA    28921         CA   C
                                AAAAAGCCA  GAT TCA
                                |||||||||  |||  |||
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                          TTTTTCGGT  TTA AGT
                               AC   A
GAM1118  DMD     3' AAAAAGCCATGAATTTCA    28921        CA   C
                          AAAAAGCCA  GAT TCA
                          |||||||||  ||| |||
                          TTTTTCGGT  TTA AGT
                               AC   A
GAM1118  DMD     3' AAAAAGCCATGAATTTCA    28921        CA   C
                          AAAAAGCCA  GAT TCA
                          |||||||||  ||| |||
                          TTTTTCGGT  TTA AGT
                               AC   A
GAM1118  DMD     3' AAAAAGCCATGAATTTCA    28921        CA   C
                          AAAAAGCCA  GAT TCA
                          |||||||||  ||| |||
                          TTTTTCGGT  TTA AGT
                               AC   A
GAM1118  DMD     3' AAAAAGCCATGAATTTCA    28921        CA   C
                          AAAAAGCCA  GAT TCA
                          |||||||||  ||| |||
                          TTTTTCGGT  TTA AGT
                               AC   A
GAM1118  DMD     3' AAAAAGCCATGAATTTCA    28921        CA   C
                          AAAAAGCCA  GAT TCA
                          |||||||||  ||| |||
                          TTTTTCGGT  TTA AGT
                               AC   A
GAM1118  DMD     3' AAAAAGCCATGAATTTCA    28921        CA   C
                          AAAAAGCCA  GAT TCA
                          |||||||||  ||| |||
                          TTTTTCGGT  TTA AGT
                               AC   A
GAM1118  DMD     3' AAAAAGCCATGAATTTCA    28921        CA   C
                          AAAAAGCCA  GAT TCA
                          |||||||||  ||| |||
                          TTTTTCGGT  TTA AGT
                               AC   A
GAM1118  DMD     3' AAAAAGCCATGAATTTCA    28921        CA   C
                          AAAAAGCCA  GAT TCA
                          |||||||||  ||| |||
                          TTTTTCGGT  TTA AGT
                               AC   A
GAM1118  DMD     3' AAAAAGCCATGAATTTCA    28921        CA   C
                          AAAAAGCCA  GAT TCA
                          |||||||||  ||| |||
                          TTTTTCGGT  TTA AGT
                               AC   A
GAM1118  DMD     3' AAAAAGCCATGAATTTCA    28921        CA   C
                          AAAAAGCCA  GAT TCA
                          |||||||||  ||| |||
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                                TTTTTCGGT  TTA AGT
                                     AC   A
GAM1118  DMD      3'  AAAAAGCCATGAATTTCA    28921        CA   C
                                AAAAAGCCA  GAT TCA
                                |||||||||  ||| |||
                                TTTTTCGGT  TTA AGT
                                     AC   A
GAM1118  DMD      3'  AAAAAGCCATGAATTTCA    28921        CA   C
                                AAAAAGCCA  GAT TCA
                                |||||||||  ||| |||
                                TTTTTCGGT  TTA AGT
                                     AC   A
GAM1118  GNA11    5'  AAAAAGCCACCTCCCCA     28922         AGA
                                AAAAAGCCAC   TCTCA
                                ||||||||||   |||||
                                TTTTTCGGTG   GGGGT
                                      GA_
GAM1118  HOXD4    3'  AAAAAACCACTATTCTCA    28923         AGA
                                AAAAAGCCAC   TCTCA
                                ||||||||||   |||||
                                TTTTTTGGTG   AGAGT
                                      ATA
GAM1118  MAN2A1   3'  AAAAGCCAATGATTCTCA    28925        CA  _
                                AAAAGCCA  GAT CTCA
                                ||||||||  ||| ||||
                                TTTTCGGT  CTA GAGT
                                     TA   A
GAM1118  MAN2A1   3'  AAAAACCCACAGAATCA     28924      G      TC
                                AAAAA CCACAGA  TCA
                                ||||| |||||||  |||
                                TTTTT GGTGTCT  AGT
                                   G      T_
GAM1118  PBP      3'  AAAAAACACAGATCTCA     28926        C
                                AAAAAGC ACAGATCTCA
                                ||||||| ||||||||||
                                TTTTTTG TGTCTAGAGT
                                        _
GAM1118  SLC4A1AP 3'  AAAAGCCAGTCACCAGATCT  28927        _____
                                AAAAGCCA    CAGATCT
                                ||||||||    |||||||
                                TTTTCGGT    GTCTAGA
                                     CAGTG
GAM1118  ALS2CR3  3'  AAAAAACCACAATCTCA     28928          A
                                AAAAAGCCACAG TCTCA
                                |||||||||||| |||||
                                TTTTTTGGTGTT AGAGT
                                         _
GAM1118  BCAS4    3'  GGAAGACCACAAAGCTCA    28929    A  _     T
                                A AAG CCACAGA CTCA
                                | ||| ||||||| ||||
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                                C TTC GGTGTTT GAGT
                                 C   T      C
GAM1118 CAT56    3' AAAAAACCTCATTCTCA     28930         A  GA
                                AAAAAGCC CA  TCTCA
                                |||||||| ||  |||||
                                TTTTTTGG GT  AGAGT
                                     A  A_
GAM1118 DKFZP564D0462 3' AAAAACCCACTACCTCA     28931       G    AG
                                AAAAA CCAC  ATCTCA
                                ||||| ||||  ||||||
                                TTTTT GGTG  TGGAGT
                                   G    A_
GAM1118 DNAJA4   3' GGAAAGCCACAGAATCA     28932   A         TC
                                A AAAGCCACAGA  TCA
                                | ||||||||||  |||
                                C TTTCGGTGTCT  AGT
                                 C          T_
GAM1118 EIF4B    3' AAAAACCCACAACCCA      28933       G     AT
                                AAAAA CCACAG  CTCA
                                ||||| ||||||  ||||
                                TTTTT GGTGTT  GGGT
                                   G     __
GAM1118 FLJ10377 3' AAAAAGCCACACAATATCTCA 28934          G___
                                AAAAAGCCACA    ATCTCA
                                ||||||||||    ||||||
                                TTTTTCGGTGT    TAGAGT
                                      GTTA
GAM1118 FLJ20716 3' AAAAGCCACAATAATCTCA   28935          __
                                AAAAGCCACA  GATCTCA
                                |||||||||  |||||||
                                TTTTCGGTGT  TTAGAGT
                                      TA
GAM1118 FLJ22671 3' AAAAAACCAGATCTCA      28936         CA
                                AAAAAGCCA  GATCTCA
                                |||||||||  |||||||
                                TTTTTTGGT  CTAGAGT
                                          __
GAM1118 GALNAC4ST-2 3' AAAAAGCCACAGCCTCA     28937           A
                                AAAAAGCCACAG TCTCA
                                |||||||||||| |||||
                                TTTTTCGGTGTC GGAGT
                                          _
GAM1118 HSPC067   3' AAAAAACCACCCTCA      28938          AGA
                                AAAAAGCCAC   TCTCA
                                ||||||||||   |||||
                                TTTTTTGGTG   GGAGT
                                          ___
GAM1118 KIAA0077 3' AAAAAACCCCCACATCTCA    28939         A  G
                                AAAAAGCC CA ATCTCA
                                |||||||| || ||||||
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                                TTTTTTGG GT TAGAGT
                                     G  G
GAM1118 KIAA0285 3' AAAAAGCCCAGACTTCA     28940        A    TC
                                AAAAAGCC CAGA  TCA
                                |||||||| ||||  |||
                                TTTTTCGG GTCT  AGT
                                     _   GA
GAM1118 KIAA0286 3' AAAAAGCCCAGTACATCTCA  28941        A  ___
                                AAAAAGCC CAG   ATCTCA
                                |||||||| |||   ||||||
                                TTTTTCGG GTC   TAGAGT
                                     _  ATG
GAM1118 KIAA1393 3' TGAAACAACAAGATCTCA    28942    A   C  _
                                A AAGC ACA GATCTCA
                                | |||| ||| |||||||
                                A TTTG TGT CTAGAGT
                                 C   T  T
GAM1118 MGC12335 3' AAAAAACCAAGAGTTCTCA   28943        C  __
                                AAAAAGCCA AGA  TCTCA
                                ||||||||| |||  |||||
                                TTTTTTGGT TCT  AGAGT
                                     _  CA
GAM1118 PELI2    3' AAAAAGCCCCAGATTTCA    28944        A    C
                                AAAAAGCC CAGAT TCA
                                |||||||| ||||| |||
                                TTTTTCGG GTCTA AGT
                                     G    A
GAM1118 PSP1     3' AAAAAGCCAAAACCCTCA    28945        C  AT
                                AAAAAGCCA AG  CTCA
                                ||||||||| ||  ||||
                                TTTTTCGGT TT  GAGT
                                      T  GG
GAM1118 RIS1     3' AAAAAACCACAAATTTCA    28946           C
                                AAAAAGCCACAGAT TCA
                                |||||||||||||| |||
                                TTTTTTGGTGTTTA AGT
                                        A
GAM1118 S164     3' AAAAAATTACAGATCTCA    28947       CC
                                AAAAAG  ACAGATCTCA
                                ||||||  ||||||||||
                                TTTTTT  TGTCTAGAGT
                                   AA
GAM1118 SERF2    5' AAAAAGCCCAGGCGCTGTCTC 28948        A  A_____
                                AAAAAGCC CAG     TCTC
                                |||||||| |||     ||||
                                TTTTTCGG GTC     AGAG
                                     _  CGCGAC
GAM1118 SERP1    3' AAAAACCACAAGACTTCA    28949         _ TC
                                AAAAGCCACA GA  TCA
                                |||||||||| ||  |||
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                                TTTTTGGTGT CT  AGT
                                      T  GA
GAM1118  SIRPB1    3'  AAAAAACCAGATCTCA     28936        CA
                                AAAAAGCCA  GATCTCA
                                |||||||||  |||||||
                                TTTTTTGGT  CTAGAGT
                                      __
GAM1118  UBE4B     3'  AAAAAACCCAACCCTCA     28950        A   AT
                                AAAAAGCC CAG  CTCA
                                |||||||| |||  ||||
                                TTTTTTGG GTT  GAGT
                                     _  GG
GAM1118  LOC112885 3'  AAAAAACCTAACAATCTCA   28951        ACA_
                                AAAAAGCC   GATCTCA
                                ||||||||   |||||||
                                TTTTTTGG   TTAGAGT
                                     ATTG
GAM1118  LOC150343 5'  AAAAATCCCAGCTCTCA     28952      G  A   A
                                AAAAA CC CAG TCTCA
                                ||||| || ||| |||||
                                TTTTT GG GTC AGAGT
                                   A  _   G
GAM1118  LOC162962 3'  AAAAAACAAGATCTCA      28953       CAC
                                AAAAAGC   AGATCTCA
                                |||||||   ||||||||
                                TTTTTTG   TCTAGAGT
                                     T__
GAM1118  LOC203428 3'  AAAAAACCACCCTCA       28938         AGA
                                AAAAAGCCAC   TCTCA
                                ||||||||||   |||||
                                TTTTTTGGTG   GGAGT
                                      ___
GAM1118  LOC254013 3'  AAAAAGCCCAGAGTTCA     28954        A    TC
                                AAAAAGCC CAGA  TCA
                                |||||||| ||||  |||
                                TTTTTCGG GTCT  AGT
                                     _   CA
GAM1118  LOC255851 3'  AAAAACCCACAACCCA      28933      G     AT
                                AAAAA CCACAG  CTCA
                                ||||| ||||||  ||||
                                TTTTT GGTGTT  GGGT
                                   G    __
GAM1118  LOC93626  5'  AAAAAGCCACCTCCCCA     28922         AGA
                                AAAAAGCCAC   TCTCA
                                ||||||||||   |||||
                                TTTTTCGGTG   GGGGT
                                      GA_
GAM1119  COL13A1   5'  CTCCCGGGCCAGTCAGTT    28957         AACCCT  _
                                CTCCCGGGC     TAG CAGTT
                                |||||||||     ||| |||||
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                              GAGGGCCCG     GTC GTCAA
                                    _______  A
GAM1119 COL13A1  5' CTCCCGGGCCAGTCAGTT    28957        AACCCT  _
                              CTCCCGGGC     TAG CAGTT
                              |||||||||     ||| |||||
                              GAGGGCCCG     GTC GTCAA
                                    _______  A
GAM1119 COL13A1  5' CTCCCGGGCCAGTCAGTT    28957        AACCCT  _
                              CTCCCGGGC     TAG CAGTT
                              |||||||||     ||| |||||
                              GAGGGCCCG     GTC GTCAA
                                    _______  A
GAM1119 COL13A1  5' CTCCCGGGCCAGTCAGTT    28957        AACCCT  _
                              CTCCCGGGC     TAG CAGTT
                              |||||||||     ||| |||||
                              GAGGGCCCG     GTC GTCAA
                                    _______  A
GAM1119 COL13A1  5' CTCCCGGGCCAGTCAGTT    28957        AACCCT  _
                              CTCCCGGGC     TAG CAGTT
                              |||||||||     ||| |||||
                              GAGGGCCCG     GTC GTCAA
                                    _______  A
GAM1119 COL13A1  5' CTCCCGGGCCAGTCAGTT    28957        AACCCT  _
                              CTCCCGGGC     TAG CAGTT
                              |||||||||     ||| |||||
                              GAGGGCCCG     GTC GTCAA
                                    _______  A
GAM1119 COL13A1  5' CTCCCGGGCCAGTCAGTT    28957        AACCCT  _
                              CTCCCGGGC     TAG CAGTT
                              |||||||||     ||| |||||
                              GAGGGCCCG     GTC GTCAA
                                    _______  A
GAM1119 COL13A1  5' CTCCCGGGCCAGTCAGTT    28957        AACCCT  _
                              CTCCCGGGC     TAG CAGTT
                              |||||||||     ||| |||||
                              GAGGGCCCG     GTC GTCAA
                                    _______  A
GAM1119 EZH1     3' TCCTGGGCCCAAGCTTAGCAGT 28958     C    AACC_
          T                    TCC GGGC     CTTAGCAGTT
                               |||  ||||    ||||||||||
                               AGG CCCG     GAATCGTCAA
                                 A   GGTTC
GAM1119 GAN      3' CTCCCAGGTAGTTTTTCAACAG 28959        CAACCC_
          TT                   CTCCCGGG     TTAGCAGTT
                               ||||||||     |||||||||
                               GAGGGTCC     AGTTGTCAA
                                  ATCAAAA
GAM1119 HNRPDL   5' TCCTGGGGTCAGCAGTT     28960     C  CAACCC
                               TCC GGG     TTAGCAGTT
                               |||  |||     |||||||||
                               AGG CCC     AGTCGTCAA
                                 A  C_____
GAM1119 MSF      5' CTCCCGGGCGGATCAGGTT    28961        AACCC   CA
                               CTCCCGGGC    TTAG  GTT
                               |||||||||    ||||  |||
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                                GAGGGCCCG    AGTC  CAA
                                     CCT__   __
GAM1119 AF9Q34   3' CTCCCGGGAACTCAGGTT    28962       C  CC   CA
                                CTCCCGGG AAC  TTAG  GTT
                                |||||||| |||  ||||  |||
                                GAGGGCCC TTG  AGTC  CAA
                                     _  __   __
GAM1119 C20orf18 5' CTCCCGGGAGGCCCCAGTT   28963       CAA  TTAG
                                CTCCCGGG  CCC   CAGTT
                                ||||||||  |||   |||||
                                GAGGGCCC  GGG   GTCAA
                                     TCC  ____
GAM1119 C20orf18 5' CTCCCGGGAGGCCCCAGTT   28963       CAA  TTAG
                                CTCCCGGG  CCC   CAGTT
                                ||||||||  |||   |||||
                                GAGGGCCC  GGG   GTCAA
                                     TCC  ____
GAM1119 FLJ21044 5' CTCCCGGGCGCCCTTCGGTT  28964        AA   AGCA
                                CTCCCGGGC  CCCTT   GTT
                                |||||||||  |||||   |||
                                GAGGGCCCG  GGGAA   CAA
                                     C_    GC__
GAM1119 KIAA0365  3' TCCCGGGAATGGGAAAGCAGTT 28965      CAACCCTT
             C                   TCCCGGG      AGCAGTTC
                                 |||||||      ||||||||
                                 AGGGCCC      TCGTCAAG
                                     TTACCCTT
GAM1119 MGC12760  5' CTCCTGGGCAACCTGCAGCT  28966    C      CTTA
                                CTCC GGGCAACC   GCAGTT
                                |||| ||||||||   ||||||
                                GAGG CCCGTTGG   CGTCGA
                                  A      A___
GAM1119 MGC23427  3' TCTCAGGCAACAGTAGCAGTTC 28967   C      CCT
                                TC CGGGCAAC   TAGCAGTTC
                                || ||||||||   |||||||||
                                AG GTCCGTTG   ATCGTCAAG
                                 A      TC_
GAM1119 LOC149722 5' CTCCCGGGCCATCTGGAGTTC  28968       AACC  TAGC
                                CTCCCGGGC   CT   AGTTC
                                |||||||||   ||   |||||
                                GAGGGCCCG   GA   TCAAG
                                     GTA_  CC__
GAM1119 LOC150113 5' CTCCTGGCCAGTCCAAAGTGTT 28969    C  G  AC  TT  CA
             C                   CTCC GG CA  CC  AG  GTTC
                                 |||| || ||  ||  ||  ||||
                                 GAGG CC GT  GG  TC  CAAG
                                   A  G  CA  TT  A_
GAM1119 LOC151429 3' CTCCTGAGCAGCCCCCTCTGTT 28970    C    A_    AGCA
             C                   CTCC GGGCA  CCCTT   GTTC
                                 |||| |||||  |||||   ||||
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                                GAGG CTCGT  GGGGA   CAAG
                                  A    CG    GA__
GAM1119  LOC166713 5'  CTCCTTGGACCCTTGGTAGTT  28971     CG  CA    AGC
                                CTCC  GG  ACCCTT   AGTT
                                ||||  ||  ||||||   ||||
                                GAGG  CC  TGGGAA   TCAA
                                  AA  __     CCA
GAM1119  LOC221543 3'  GGACATTTAGCAGTTC     28972      ACCC
                                GGGCA   TTAGCAGTTC
                                |||||   ||||||||||
                                CCTGT   AATCGTCAAG
                                  A___
GAM1119  LOC257596 3'  GGACATTTAGCAGTTC     28972      ACCC
                                GGGCA   TTAGCAGTTC
                                |||||   ||||||||||
                                CCTGT   AATCGTCAAG
                                  A___
GAM1119  LOC90019  3'  CTCCCGGGCAGCACTTGC    28973        ACC   A
                                CTCCCGGGCA   CTT GC
                                ||||||||||   ||| ||
                                GAGGGCCCGT   GAA CG
                                     CGT   _
GAM1120  CDK2AP1   5'  GCGGCGGCGAGGCCGGGCGG   28976         G   CT
                                GCGGCGGCGAGG CTG  GCGG
                                ||||||||||||| |||  ||||
                                CGCCGCCGCTCC GGC  CGCC
                                      _   C_
GAM1120  CDK5R2    3'  CAGCGGCGGTGGCTTTGG    28977       AG    GC  C
                                CGGCGGCG  GGCT  TG G
                                ||||||||  ||||  || |
                                GTCGCCGC  CCGA  AC C
                                    CA    A_  A
GAM1120  CHAD      5'  GCGGCGGCGGGGCGCG     28978        A    TGCT
                                GCGGCGGCG GGGC   GCG
                                ||||||||| ||||   |||
                                CGCCGCCGC CCCG   CGC
                                      _   _____
GAM1120  CPT2      5'  CTGCGGCGGCGAGAACGCG   28979           TGCT
                                CTGCGGCGGCGAGGGC   GCG
                                ||||||||||||||||   |||
                                GACGCCGCCGCTCTTG   CGC
                                          _____
GAM1120  CRKL      5'  CTGCGGCGGTAGGGGC     28980        CG   CTGCT
                                CTGCGGCGG  AGGG    GC
                                |||||||||  ||||    ||
                                GACGCCGCC  TCCC    CG
                                    A_   ______
GAM1120  EGFL4     5'  TGCGGCAGTGGCTGTG     28981        CGAG    C
                                TGCGGCGG   GGCTG TG
                                ||||||||   ||||| ||
```

```
                                ACGCCGTC   CCGAC AC
                                   A___   _
GAM1120 EGR1    5' CTGCGGCGGCGGAAGCTGGCTG 28982         AG   _
            CGG                  CTGCGGCGGCG  GGCTG CTGCGG
                                 ||||||||||  ||||| ||||||
                                 GACGCCGCCGC  TCGAC GACGCC
                                      CT    C
GAM1120 ELOVL4  5' CCGCGGCGGCGGGGATGCG   28983         A  CTGC
                                 CTGCGGCGGCG GGG   TGCG
                                 ||||||||||| |||   ||||
                                 GGCGCCGCCGC CCC   ACGC
                                      _  T___
GAM1120 FBXL7   5' GCGGCGGCCACTTGTTGCGG  28984       GAGG  GC_
                                 GCGGCGGC   GCT  TGCGG
                                 ||||||||   |||  |||||
                                 CGCCGCCG   TGA  ACGCC
                                    G___  ACA
GAM1120 FHL1    5' CGGTGGCGGCGGCGGCTGCGG 28985    C   AG  T
                                 CGG GGCG  GGC GCTGCGG
                                 ||| ||||  ||| |||||||
                                 GCC CCGC  CCG CGACGCC
                                   A   CG  C
GAM1120 FMR2    5' CTGCGGCGGCAGCCGCTGCGG 28986        GAG
                                 CTGCGGCGGC  GGCTGCTGCGG
                                 ||||||||||  ||||||||||
                                 GACGCCGCCG  TCGGCGACGCC
                                     ___
GAM1120 GMPR    5' CTGCGGCGGCGGCGACGGCGG 28987        GAG  T T
                                 CTGCGGCGGC  GGC GC GCGG
                                 ||||||||||  ||| || ||||
                                 GACGCCGCCG  CCG TG CGCC
                                      ___  C C
GAM1120 GNAS    5' GCGGCGGCGGGGCGCG     28978        A   TGCT
                                 GCGGCGGCG GGGC   GCG
                                 ||||||||| ||||   |||
                                 CGCCGCCGC CCCG   CGC
                                     _  _____
GAM1120 GNAS    5' GCGGCGGCGGGGCGCG     28978        A   TGCT
                                 GCGGCGGCG GGGC   GCG
                                 ||||||||| ||||   |||
                                 CGCCGCCGC CCCG   CGC
                                     _  _____
GAM1120 GPC1    3' CTGCGGCGGTGCAGGGAGCTG 28988       CG_  CT
                                 CTGCGGCGG  AGGG  GCTG
                                 |||||||||  ||||  ||||
                                 GACGCCGCC  TCCC  CGAC
                                     ACG   T_
GAM1120 HHIP    5' GCGGCGGCGGGGCAGGCGG   28989        A   TGCT
                                 GCGGCGGCG GGGC   GCGG
                                 ||||||||| ||||   ||||
```

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                                CGCCGCCGC CCCG   CGCC
                                     _   TC__
GAM1120 INHBB   5' CTGCGGCGGGCGCTGC     28990       GGCGA   T
                                CTGCGGC    GGGC GCTGC
                                |||||||    |||| |||||
                                GACGCCG    CCCG CGACG
                                      ______   _
GAM1120 ITGA11  5' GCGGCGGCGGGGGGCG     28991        A  CTGCT
                                GCGGCGGCG GGG    GCG
                                ||||||||| |||    |||
                                CGCCGCCGC CCC    CGC
                                     C  _____
GAM1120 ITPKB   3' CTGTGGTGACGAGGGCTG   28992    C  C
                                CTG GG GGCGAGGGCTG
                                ||| || ||||||||||
                                GAC CC CTGCTCCCGAC
                                  A  A
GAM1120 KCNS3   5' CCGCGGCGGCGAGGAGAGCGG 28993           CTGCT
                                CTGCGGCGGCGAGGG   GCGG
                                ||||||||||||||    ||||
                                GGCGCCGCCGCTCCT   CGCC
                                        CT___
GAM1120 KPNA3   5' CTGCGGCGGCGGCGGC     28994         AGGGCT  T
                                CTGCGGCGGCG    GC GC
                                ||||||||||     || ||
                                GACGCCGCCGC    CG CG
                                      _______ C
GAM1120 LEF1    5' CTGGGCGGCGAGGGCTGC   28995    C
                                CTG GGCGGCGAGGGCTGC
                                ||| ||||||||||||||
                                GAC CCGCCGCTCCCGACG
                                 _
GAM1120 NFKBIA  5' CTGCGGGCGCTGCTGC     28996      CG  GAGG
                                CTGCGG  GC   GCTGCTGC
                                ||||||  ||   ||||||||
                                GACGCC  CG   CGACGACG
                                  __ _____
GAM1120 NPR1    3' GGCGATGGGGCTGCTGTGG  28997      __       C
                                GGCGA  GGGCTGCTG GG
                                |||||  ||||||||| ||
                                CCGCT  CCCGACGAC CC
                                   AC       A
GAM1120 PABPC4  5' CTGCGGCGGCGGGCGC     28998        GA   TGCT
                                CTGCGGCGGC  GGGC   GC
                                ||||||||||  ||||   ||
                                GACGCCGCCG  CCCG   CG
                                      __   _____
GAM1120 PDAP1   5' CTGCGGCGGCGGCGGC     28994         AGGGCT  T
                                CTGCGGCGGCG    GC GC
                                ||||||||||     || ||
```

```
                                GACGCCGCCGC     CG CG
                                       _______ C
GAM1120  PK428    5'  CTGCGGCGGCGGCGCGGGCGG  28999         GAG   T  T_
                                CTGCGGCGGC   GGC GC  GCGG
                                ||||||||||   ||| ||  ||||
                                GACGCCGCCG   CCG CG  CGCC
                                    ____   _ CC
GAM1120  PPP3R1   5'  CGGCGGCGGCGGCCCAGCTGCG 29000        AG   __
              G                  CGGCGGCG  GGCT  GCTGCGG
                                 ||||||||  ||||  |||||||
                                 GCCGCCGC  CCGG  CGACGCC
                                      CG   GT
GAM1120  SCN8A    5'  GCGGCGGCGAGGGAGGCAGCGG 29001           CT  T
                                GCGGCGGCGAGGG  GC GCGG
                                ||||||||||||  || ||||
                                CGCCGCCGCTCCC  CG CGCC
                                       TC  T
GAM1120  SP3      5'  GCGGCGGCGGGGGCCCCGG   29002         A  CT   G
                                GCGGCGGCG GGG  GCT CGG
                                |||||||| |||  ||| |||
                                CGCCGCCGC CCC  CGG GCC
                                     _  __   G
GAM1120  TBL1X    5'  CTGCGGCGGCGGCGGGGCG   29003          A_  CTGCT
                                CTGCGGCGGCG  GGG    GCG
                                ||||||||||  |||    |||
                                GACGCCGCCGC  CCC    CGC
                                      CG  _____
GAM1120  TPM1     5'  GCGGCGGCGAGGGGCCCTG   29004           _ G
                                GCGGCGGCGAGGG CT CTG
                                |||||||||||| || |||
                                CGCCGCCGCTCCC GG GAC
                                      C  _
GAM1120  WDR4     3'  GGCGAGCAGCTACTGCGG    29005       _
                                GGCGAG GGCTGCTGCGG
                                |||||| ||||||||||
                                CCGCTC TCGATGACGCC
                                   G
GAM1120  WDR4     3'  GGCGAGCAGCTACTGCGG    29005       _
                                GGCGAG GGCTGCTGCGG
                                |||||| ||||||||||
                                CCGCTC TCGATGACGCC
                                   G
GAM1120  WEE1     5'  CTGCGCGGCGGCGGCCTGCGG  29006      G    AG   TG
                                CTGCG CGGCG  GGC  CTGCGG
                                ||||| |||||  |||  ||||||
                                GACGC GCCGC  CCG  GACGCC
                                   _    CG  __
GAM1120  ANP32B   5'  CTGGGTGGCGGGCGGCGTGCGG 29007     C  C   GA   T  _
                                CTG GG GGC  GGGC GC TGCGG
                                ||| || |||  |||| || |||||
```

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                                GAC CC CCG  CCCG CG ACGCC
                                  _ A  __   C  C
GAM1120 BACH    5' CTGCGGCGGCGGATGC     29008          A  GCTGC
                                CTGCGGCGGCG GG    TGC
                                |||||||||| ||    |||
                                GACGCCGCCGC CT    ACG
                                      _ _____
GAM1120 C5orf4  5' GGTGGCTGTTGCTGCTGCGG  29009   C  GAGG
                                GG GGC   GCTGCTGCGG
                                || |||   ||||||||||
                                CC CCG   CGACGACGCC
                                 A  ACAA
GAM1120 CRMP5   5' CTGCGGCCGCGGGGGCCCGTGG 29010       G  A   TG  C
                                CTGCGGC GCG GGGC  CTG GG
                                ||||||| ||| ||||  ||| ||
                                GACGCCG CGC CCCG  GGC CC
                                    G  C   __  A
GAM1120 DGKD    3' CGGCGGCGGGGATGTG     29011        A  C  C
                                CGGCGGCG GGG TG TG
                                |||||||| ||| || ||
                                GCCGCCGC CCC AC AC
                                    _  T  _
GAM1120 DKFZp762K222 5' CTGCGGCGGGCGGGCTCCTGCG 29012         CGA   G
          G                      CTGCGGCGG  GGGCT CTGCGG
                                |||||||||  ||||| ||||||
                                GACGCCGCC  CCCGA GACGCC
                                     CG_   G
GAM1120 DLGAP1  3' GGCGGCGGCGGCCGGGCTGCGG 29013       AG  __
                                GGCGGCG  GGCT  GCTGCGG
                                |||||||  ||||  |||||||
                                CCGCCGC  CCGG  CGACGCC
                                    CG   CC
GAM1120 DLGAP1  3' GGCGGCGGCGGCCGGGCTGCGG 29013       AG  __
                                GGCGGCG  GGCT  GCTGCGG
                                |||||||  ||||  |||||||
                                CCGCCGC  CCGG  CGACGCC
                                    CG   CC
GAM1120 EDR2    5' CTGGGGCGGCGGCTGCTGC  29014    C    GAG
                                CTG GGCGGC  GGCTGCTGC
                                ||| ||||||  |||||||||
                                GAC CCGCCG  CCGACGACG
                                  C    ___
GAM1120 GDBR1   3' CCGCACCAGGGGGCTGCTGTGG 29015     G  CGA      C
                                CTGCG CGG  GGGCTGCTG GG
                                ||||| |||  ||||||||| ||
                                GGCGT GTC  CCCGACGAC CC
                                   G  C__      A
GAM1120 HNRPU   5' GGTGGCGGCTGCTGCG     29016   C  GAG
                                GG GGC  GGCTGCTGCG
                                || |||  ||||||||||
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                                CC CCG   CCGACGACGC
                                 A  ___
GAM1120 HNRPU    5' GGTGGCGGCTGCTGCG     29016    C   GAG
                                GG GGC   GGCTGCTGCG
                                || |||   ||||||||||
                                CC CCG   CCGACGACGC
                                 A  ___
GAM1120 KCNG3    5' CGCGGCGGCGGGGGCG     29017         A   CTGCT
                                TGCGGCGGCG GGG    GCG
                                |||||||||| |||    |||
                                GCGCCGCCGC CCC    CGC
                                     _  _____
GAM1120 KIAA0258 3' CTCCGGCGGCGGGGGTCG    29018    G      A   CTGCTG
                                CT CGGCGGCG GGG     CG
                                || ||||||| |||     ||
                                GA GCCGCCGC CCC     GC
                                 G       _   CA____
GAM1120 KIAA1026 5' GCGGTGGCGAGGCGGCG     29019     C      G TGCT
                                GCGG GGCGAGG C    GCG
                                |||| ||||||| |    |||
                                CGCC CCGCTCC G    CGC
                                  A      _ C___
GAM1120 KIAA1169 5' CTGGGCGGCGGGGGCTG     29020     C      A
                                CTG GGCGGCG GGGCTG
                                ||| ||||||| ||||||
                                GAC CCGCCGC CCCGAC
                                  _      C
GAM1120 KIAA1243 3' CTGGGGTGGCGGGGGGTGAACTA 29021     C  C    A   CT_   C
             GG                   CTG GG GGCG GGG   GCTG GG
                                ||| || |||| |||   |||| ||
                                GAC CC CCGC CCC   TGAT CC
                                  C  A    C   ACT   _
GAM1120 KIAA1483 5' CTGCTGCGGCGGGGGGTGTG   29022     G     A   C  C
                                CTGC GCGGCG GGG TG TG
                                |||| |||||| ||| || ||
                                GACG CGCCGC CCC AC AC
                                  A     C   C  _
GAM1120 LBP-32   5' CGGCGGCGGCGGCTGC      29023       GAG   T
                                CGGCGGC   GGC GCTGC
                                |||||||   ||| |||||
                                GCCGCCG   CCG CGACG
                                    ___   C
GAM1120 MAP2K3   5' CGGCGGCGGCGGCGACTGCGG  29024        AG   T
                                CGGCGGCG  GGC GCTGCGG
                                ||||||||  ||| |||||||
                                GCCGCCGC  CCG TGACGCC
                                     CG   C
GAM1120 MAP2K5   5' CTGCGGCGGCGGCGACGGCGG  28987         GAG   T  T
                                CTGCGGCGGC   GGC GC GCGG
                                ||||||||||   ||| || ||||
```

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                                GACGCCGCCG  CCG TG CGCC
                                    ___  C  C
GAM1120 MAPK8IP2 5' CTGCGGCGGGGGGTGC     29025       CGA  CTGC
                                CTGCGGCGG  GGG   TGC
                                |||||||||  |||   |||
                                GACGCCGCC  CCC   ACG
                                    C__  ____
GAM1120 MAPK8IP2 5' CTGCGGCGGGGGGGTGC     29025       CGA  CTGC
                                CTGCGGCGG  GGG   TGC
                                |||||||||  |||   |||
                                GACGCCGCC  CCC   ACG
                                    C__  ____
GAM1120 MESDC1   5' CTGCGGCGGCGGGAGCCCGGGC 29026         A    GCT
           GG                    CTGCGGCGGCG GGGCT  GCGG
                                |||||||||| |||||  ||||
                                GACGCCGCCGC CTCGG  CGCC
                                      C    GCC
GAM1120 MGC2668  3' CTGCTGGCGGTGGGGGGAGTCG 29027    _   CGA  CTGCTG
           G                     CTGC GGCGG  GGG    CGG
                                |||| |||||  |||    |||
                                GACG CCGCC  CCC    GCC
                                  A    A__  CCCTCA
GAM1120 MGC3265  5' GCGGCGGCGAGGAGCGCGG   29028         CT  T
                                GCGGCGGCGAGGG  GC GCGG
                                ||||||||||||  || ||||
                                CGCCGCCGCTCCT  CG CGCC
                                          __ _
GAM1120 NOVA2    5' CTGCTGCGGCGGCTGC     29030     G    AGGGCT
                                CTGC GCGGCG    GCTGC
                                |||| ||||||    |||||
                                GACG CGCCGC    CGACG
                                  A    _______
GAM1120 NOVA2    5' GCGGCGGCTGCTGCTGCTGCGG 29029       GAGG
                                GCGGCGGC   GCTGCTGCGG
                                ||||||||   ||||||||||
                                CGCCGCCG   CGACGACGCC
                                     ACGA
GAM1120 PCBP4    5' CTGCGGCGGCGGCGGCGGCGG  29031        GAG  T  T
                                CTGCGGCGGC  GGC GC GCGG
                                |||||||||  ||| || ||||
                                GACGCCGCCG  CCG CG CGCC
                                    ___  C  C
GAM1120 PDE10A   5' CCGCGGCGGCGAGGGCGAACG  29032           TGCT
                                CTGCGGCGGCGAGGGC   GCG
                                ||||||||||||||||   |||
                                GGCGCCGCCGCTCCCG   TGC
                                       CT__
GAM1120 PEG10    3' CTGTGGCGGCGGGTACTGTGG  29033    C    GA  C    C
                                CTG GGCGGC  GGG TGCTG GG
                                ||| ||||||  ||| ||||| ||
```

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                                GAC CCGCCG  CCC ATGAC CC
                                  A     __  _    A
GAM1120  PPP1R1A  5'  CTGCGGCGGGAGGGAAGGCGG  29034        C    CTGCT
                                CTGCGGCGG GAGGG    GCGG
                                ||||||||| |||||    ||||
                                GACGCCGCC CTCCC    CGCC
                                     _    TTC__
GAM1120  RAB6B    5'  GGGGCTGGGCTGCTGCG    29035    C   GA
                                GG GGC  GGGCTGCTGCG
                                || |||  ||||||||||
                                CC CCG  CCCGACGACGC
                                 _  A_
GAM1120  SCAP     5'  CTGCGGCGGCGGCGGCGGCGG  29031        GAG   T  T
                                CTGCGGCGGC   GGC GC GCGG
                                ||||||||||   ||| || ||||
                                GACGCCGCCG   CCG CG CGCC
                                     ___   C  C
GAM1120  SHARP    5'  CGGCGGCGGCGGCGGCTGCGG  29036       AG   T
                                CGGCGGCG  GGC GCTGCGG
                                ||||||||  ||| |||||||
                                GCCGCCGC  CCG CGACGCC
                                    CG   C
GAM1120  SMOC1    5'  CGCGGCGGCGGGGAGCG    29037         A   CTGCT
                                TGCGGCGGCG GGG    GCG
                                |||||||||| |||    |||
                                GCGCCGCCGC CCC    CGC
                                     _   T____
GAM1120  UBE2E1   5'  CCGCGGCGGCTGCTGCTGCGG  29038         GAGG
                                CTGCGGCGGC   GCTGCTGCGG
                                ||||||||||   ||||||||||
                                GGCGCCGCCG   CGACGACGCC
                                     A___
GAM1120  ZDHHC7   5'  CTGCGGCGGCGGCGGC     28994          AGGGCT  T
                                CTGCGGCGGCG    GC GC
                                ||||||||||     || ||
                                GACGCCGCCGC    CG CG
                                     ______  C
GAM1120  LOC158172 5'  CTGCGGTGCCAGGAGCTGCTGT 29039       CG  G  _     C
           GG                    CTGCGG  GC AGG GCTGCTG GG
                                ||||||  || ||| ||||||| ||
                                GACGCC  CG TCC CGACGAC CC
                                   A_  G   T     A
GAM1120  LOC196453 5'  TGCGGCAGGTGGGGTGCTTCTT 29040        CGA   C   ____
           GCGG                   TGCGGCGG   GGG TGCT    GCGG
                                ||||||||   ||| ||||    ||||
                                ACGCCGTC   CCC ACGA    CGCC
                                    CA_   C    AGAA
GAM1120  LOC201707 5'  CTGCGGCGGCGGCGGAGCG   29041          A_   CTGCT
                                CTGCGGCGGCG  GGG    GCG
                                ||||||||||  |||    |||
```

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                                GACGCCGCCGC  CCT    CGC
                                      CG  _____
GAM1120  LOC221424 5'  CTGCGGCGGAGGCTGC     29043        CGA
                                CTGCGGCGG   GGGCTGC
                                |||||||||   |||||||
                                GACGCCGCC   TCCGACG
                                    ___
GAM1120  LOC221424 5'  CTGTGGCGGAGGCTGC     29042    C    CGA
                                CTG GGCGG   GGGCTGC
                                ||| |||||   |||||||
                                GAC CCGCC   TCCGACG
                                  A   ___
GAM1120  LOC253822 5'  CTGCGGCGGCGGCGTGCTGCGG 29044         GAG  _
                                CTGCGGCGGC   GGC TGCTGCGG
                                ||||||||||   ||| ||||||||
                                GACGCCGCCG   CCG ACGACGCC
                                     ___  C
GAM1120  LOC253868 5'  CTGTGGGGCGAGGGCTGTG   29045    C  C        C
                                CTG GG GGCGAGGGCTG TG
                                ||| || ||||||||||| ||
                                GAC CC CCGCTCCCGAC AC
                                  A  _         _
GAM1120  LOC256477 5'  CTGCGGCGCGTGAGGGCAGCGG 29046        GC_    TGCT
                                CTGCGGCG   GAGGGC   GCGG
                                ||||||||   ||||||   ||||
                                GACGCCGC   CTCCCG   CGCC
                                     GCA     T___
GAM1120  LOC256855 3'  CGTGGCGCTGCTGCTGTGG   29047    GC   AGG     C
                                CG  GGCG   GCTGCTG GG
                                ||  ||||   ||||||| ||
                                GC  CCGC   CGACGAC CC
                                 A_   GA_      A
GAM1120  LOC257442 5'  CTGTGTGCATGGGCTGCTGTGG 29048     CGGCG   A       C
                                CTG    GCG GGGCTGCTG GG
                                |||    ||| |||||||||| ||
                                GAC    CGT CCCGACGAC CC
                                  ACA__   A        A
GAM1120  LOC257471 5'  GCGGCGGCGGGGGGCCCCGG   29002         A   CT   G
                                GCGGCGGCG GGG  GCT CGG
                                ||||||||| |||  ||| |||
                                CGCCGCCGC CCC  CGG GCC
                                     _  __   G
GAM1120  LOC90987  5'  CTGTGTGCATGGGCTGCTGTGG 29048     CGGCG   A       C
                                CTG    GCG GGGCTGCTG GG
                                |||    ||| |||||||||| ||
                                GAC    CGT CCCGACGAC CC
                                  ACA__   A        A
GAM1120  LOC91585  5'  CTCCGGCGGCGGGGTCGGTG   29049    G       A   C  C
                                CT CGGCGGCG GGG TG TG
                                || |||||||| ||| || ||
```

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                                GA GCCGCCGC CCC GC AC
                                 G      _  A  C
GAM1121  DXYS155E  3'  TGACCGGGTGTCCTTTCTGG  29052         T  GAAG
                                TGACCGGGTGT CCT   GG
                                |||||||||| |||   ||
                                ACTGGCCCACA GGA   CC
                                      _  AAGA
GAM1121  FGF1      3'  TGCCTCTGTTCTGAAGGGGG  29053   A  GGG   C
                                TG CC  TGTTC TGAAGGGGG
                                || ||  ||||| |||||||||
                                AC GG  ACAAG ACTTCCCCC
                                 _ AG_   _
GAM1121  FGF1      3'  TGCCTCTGTTCTGAAGGGGG  29053   A  GGG   C
                                TG CC  TGTTC TGAAGGGGG
                                || ||  ||||| |||||||||
                                AC GG  ACAAG ACTTCCCCC
                                 _ AG_   _
GAM1121  FGF1      3'  TGCCTCTGTTCTGAAGGGGG  29053   A  GGG   C
                                TG CC  TGTTC TGAAGGGGG
                                || ||  ||||| |||||||||
                                AC GG  ACAAG ACTTCCCCC
                                 _ AG_   _
GAM1121  HCFC1     3'  CGGGTGTTCCTGAAGCAGGGG  29054          __
                                CGGGTGTTCCTGAAG  GGGG
                                ||||||||||||||  ||||
                                GCCCACAAGGACTTC  CCCC
                                      GT
GAM1121  MAPK4     3'  CCGGGTGTGGGGTGAAGGGGG  29055       TCC_
                                CCGGGTGT   TGAAGGGGG
                                ||||||||   |||||||||
                                GGCCCACA   ACTTCCCCC
                                    CCCC
GAM1121  PUNC      3'  TGATGGGTGTTAGGGCCGGGGG 29056    CC     CCTGAA
                                TGA  GGGTGTT    GGGGG
                                |||  |||||||    |||||
                                ACT  CCCACAA    CCCCC
                                  A_     TCCCGG
GAM1121  CLIPR-59  3'  TGATTGGGTTTCCTGGGG   29057    CC   G   GAA
                                TGA  GGGT TTCCT   GGGG
                                |||  |||| |||||   ||||
                                ACT  CCCA AAGGA   CCCC
                                  AA   _   ____
GAM1121  FLJ13782  3'  GAGTGTTTCTCTTGAAGGGGG  29058       _ _ _
                                GGGTGTT C CT GAAGGGGG
                                ||||||| | || ||||||||
                                CTCACAA G GA CTTCCCCC
                                    A A  A
GAM1121  FLJ21347  3'  TGAGTGGGTGCCCAAGGGGG  29059    CC     CTG
                                TGA  GGGTGTTC   AAGGGGG
                                |||  ||||||||   |||||||
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                                ACT  CCCACGGG   TTCCCCC
                                  CA       ___
GAM1121  KIAA0445  3'  GACCGGGCTCTGGGGGGGG   29060        GTTC   AA
                                GACCGGGT   CTG  GGGGG
                                ||||||||   |||  |||||
                                CTGGCCCG   GAC  CCCCC
                                    A___   CC
GAM1121  TRIP-Br2  3'  CGGGTGTTGGTGCCAGGGGG  29061        CC  A_
                                CGGGTGTT  TG  AGGGGG
                                ||||||||  ||  ||||||
                                GCCCACAA  AC  TCCCCC
                                    CC  GG
GAM1121  LOC257464 5'  TGCCGGGTGTTCCTCAGGG   29062    A         GA
                                TG CCGGGTGTTCCT  AGGG
                                || ||||||||||||  ||||
                                AC GGCCCACAAGGA  TCCC
                                 _         G_
GAM1122  AP3M1     3'  GGGCATGAGGCATTTAGGT   29065        CCTC    CTC
                                GGGCATGA   GGCA   AGGT
                                ||||||||   ||||   ||||
                                CCCGTACT   CCGT   TCCA
                                    _____    AAA
GAM1122  LOC145951 3'  GGGCATGAGCTTGGTGGT    29066        C  C  CACTCA
                                GGGCATGA CT GG     GGT
                                |||||||| || ||     |||
                                CCCGTACT GA CC     CCA
                                    C  A  A_____
GAM1122  LOC151146 5'  AGGCATTCTGGCACTCAGGTT  29067       GAC  C
                                GGGCAT   CT GGCACTCAGGTT
                                ||||||   || ||||||||||||
                                TCCGTA   GA CCGTGAGTCCAA
                                   A__  _
GAM1122  LOC219287 3'  AGGCATGACTCTTACTTAGGTT 29068         C  GGC   C
                                GGGCATGAC TC   ACT AGGTT
                                |||||||||  ||   ||| |||||
                                TCCGTACTG AG   TGA TCCAA
                                     _  AA_   A
GAM1123  B3GALT2   3'  TTTGGGAAACCTTTTTTG    29071     CCT
                                TTTG   GGACCTTTTTTG
                                ||||   ||||||||||||
                                AAAC   TTTGGAAAAAAC
                                  CC_
GAM1123  RAI14     3'  TCACATTTCTTTGGAGCATTTT 29072        GCC    CCT
            TG                   TCACATTT   TGGA   TTTTTG
                                ||||||||   ||||   ||||||
                                AGTGTAAA   ACCT   AAAAAC
                                    GAA    CGT
GAM1123  KIAA1143  3'  ATTTGCCTTGGTTTTTG     29073         _  ACCT
                                ATTTGCCT GG    TTTTTG
                                |||||||| ||    ||||||
```

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                                TAAACGGA CC    AAAAAC
                                    A _____
GAM1123 KIAA1854 3' CATATTTGCCTGGACTCT    29074    C         _
                                CA ATTTGCCTGGAC CT
                                || ||||||||||| ||
                                GT TAAACGGACCTG GA
                                 A          A
GAM1123 KIAA1878 3' TTTGTGGCCTTTTTTG      29075     CC   A
                                TTTG  TGG CCTTTTTTG
                                ||||  ||| |||||||||
                                AAAC  ACC GGAAAAAAC
                                  __  _
GAM1123 PRRG1    3' ACATTTGCAACACTTTTTT    29076        CTG  _
                                ACATTTGC   GAC CTTTTTT
                                ||||||||   ||| |||||||
                                TGTAAACG   TTG GAAAAAA
                                    ___  T
GAM1123 TCF6L1   3' TCACATTTGCTTGGATTACTCT 29077         C   C__
                                TCACATTTGC TGGA   CTTT
                                |||||||||| ||||   ||||
                                AGTGTAAACG ACCT   GAGA
                                     A   AAT
GAM1123 LOC152179 3' CACATTTGGGGGCCTTTTTTG  29078        CCT  A
                                CACATTTG   GG CCTTTTTTG
                                ||||||||   || |||||||||
                                GTGTAAAC   CC GGAAAAAAC
                                    CC_  _
GAM1123 LOC157697 3' TCACATTTGTCTTTTAAGTTTT 29079        C  GGACC__
             TTTG                  TCACATTTG CT      TTTTTTG
                                ||||||||| ||      |||||||
                                AGTGTAAAC GA      AAAAAAC
                                     A  AAATTCA
GAM1124 DUSP3    3' ATGTGCTCCCCAGGGTGGGG   29082     C      GTA  C
                                GTG GCTTCTT   GG GGGG
                                ||| |||||||   || ||||
                                TAC CGAGGGG   CC CCCC
                                  A      TC_  A
GAM1124 C20orf38 3' TCTTTGTGCTTCTTGTATTTGG 29083    CG  C        GGCG
                                TC  TG GCTTCTTGTA    GG
                                ||  || ||||||||||    ||
                                AG  AC CGAAGAACAT    CC
                                 AA  A         AAA_
GAM1124 DED      3' GTGGCGTTTAAAGGCGGGG    29084     C  TTC   T
                                GTG GC   TTG AGGCGGGG
                                ||| ||   ||| ||||||||
                                CAC CG   AAT TCCGCCCC
                                  _  CA_   T
GAM1124 KIAA0513 3' TCCTGTGCTTCTTGCGAGGG   29085     G  C       A  C
                                TCC TG GCTTCTTGT GG GGG
                                ||| || ||||||||| || |||
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                                AGG AC CGAAGAACG CT CCC
                                  _ A       _ _
GAM1124 ZNF387   5' TCTGTGTTTCTTGTAGG    29086    C   CGC
                                TC GTG   TTCTTGTAGG
                                || |||   ||||||||||
                                AG CAC   AAGAACATCC
                                 A  A__
GAM1125 DRD3     3' GCAGTGTCCTGGCAGATGCTG 29089     CGCC  CC
                                GCAG   CC  GCGGATGCTG
                                ||||   ||  ||||||||||
                                CGTC   GG  CGTCTACGAC
                                  ACA_  AC
GAM1125 GGT2     5' GCGGGCCAGCTGGATGCTG   29090    CCC  C  _
                                GCG   CC GC GGATGCTG
                                |||   || || ||||||||
                                CGC   GG CG CCTACGAC
                                  CC_  T  A
GAM1125 GJB3     5' TAGTAAGTGCCCCATAAATGCT 29091    C_  C    CC CG
              G                  TAG  AG GCCCC  G  GATGCTG
                                ||| || |||||  |  |||||||
                                ATC  TC CGGGG  T  TTACGAC
                                  AT  A    __ AT
GAM1125 HMGN3    5' GCGCCGCCGCTGGATGCTG   29092     CC   _
                                GCGCC  CCGC GGATGCTG
                                |||||  |||| ||||||||
                                CGCGG  GGCG CCTACGAC
                                   C_   A
GAM1125 ITGA4    5' TAGCAGCAGCCTCTCAGGCTG 29093      _  CCCCG  AT
                                TAGCAGC GCC    CGG  GCTG
                                ||||||| |||    |||  ||||
                                ATCGTCG CGG    GTC  CGAC
                                    T   AGA__   __
GAM1125 TGFB1    5' GCGGCGCCCCCCGGCACTG   29094    A      GC  A
                                GC GCGCCCCCC  GG TGCTG
                                || |||||||||  || |||||
                                CG CGCGGGGGG  CC GTGAC
                                 C       __  _
GAM1125 TPST1    5' CAGCAGCGTCTCCCGCGG    29095       CCC
                                TAGCAGCG   CCCGCGG
                                ||||||||   |||||||
                                GTCGTCGC   GGGCGCC
                                     AGA
GAM1125 CRA      3' TAGCAGCGTCTCCAGAGCC   29096       CCC  CGC   T
                                TAGCAGCG   CC   GGA GCT
                                ||||||||   ||   ||| |||
                                ATCGTCGC   GG   TCT CGG
                                     AGA  ____  _
GAM1125 FLJ21865 3' GCAGCAAGGCGTGGATGCTG  29097      CCCCC  C
                                GCAGCG    CG GGATGCTG
                                ||||||    || ||||||||
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                                CGTCGT    GC CCTACGAC
                                   TCC__  A
GAM1125 KIAA0415 3' GCGGCGCCCCCTGGCGGCTG  29098    A      C_   A
                                GC GCGCCCCC  GCGG TG
                                || ||||||||  |||| ||
                                CG CGCGGGGG  CGCC AC
                                 C       AC    G
GAM1125 KIAA0450 3' CAGCAGCCGCGGATGCT     29099       GCCCCC
                                TAGCAGC     CGCGGATGCT
                                |||||||     ||||||||||
                                GTCGTCG     GCGCCTACGA
                                   _______
GAM1125 KIAA1952 5' TAGCAGTTCCTGGATGCT    29100       CG  CCCCGC
                                TAGCAG  CC     GGATGCT
                                ||||||  ||     |||||||
                                ATCGTC  GG     CCTACGA
                                   AA  A_____
GAM1125 MGC16332 5' TAGCAGATGCTTCCCGGGCTG 29101       C_  CC    C  A
                                TAGCAG  GC  CCCG GG TG
                                ||||||  ||  |||| || ||
                                ATCGTC  CG  GGGC CC AC
                                   TA  AA    _  G
GAM1125 SCAP     5' GCAGCACCTCCCAAGCT     29102        C    CGGAT
                                GCAGCGCC CCCG     GCT
                                |||||||| ||||     |||
                                CGTCGTGG GGGT     CGA
                                    A    T____
GAM1125 LOC118668 5' GCAGCGCCCTCTGGCACT   29103         CCCGC  A
                                GCAGCGCCC     GG TGCT
                                |||||||||     || ||||
                                CGTCGCGGG     CC GTGA
                                    AGA__  _
GAM1125 LOC146227 5' GCCTGTCCCTGCGGATGCTG  29104     ___   C
                                GCC   CCC GCGGATGCTG
                                |||   ||| ||||||||||
                                CGG   GGG CGCCTACGAC
                                  ACA   A
GAM1125 LOC149319 5' GCGGGCCAGCTGGATGCTG   29090     CCC  C  _
                                GCG   CC GC GGATGCTG
                                |||   || || ||||||||
                                CGC   GG CG CCTACGAC
                                  CC_  T  A
GAM1125 LOC154007 3' TAGCAGTGCCCCCCGGTAG   29105       C       C_
                                TAGCAG GCCCCCCG  GG
                                |||||| ||||||||  ||
                                ATCGTC CGGGGGGC  TC
                                   A       CA
GAM1125 LOC256866 5' CAGGATCCCCTCGCGGATGCTG 29106     CG_    C
                                CAG   CCCC CGCGGATGCTG
                                |||   |||| ||||||||||
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                                GTC   GGGG GCGCCTACGAC
                                  CTA    A
GAM1125  LOC51071  3'  CAGCAGCGCTTGCGAGATG   29107        CCCCC  _
                                TAGCAGCGC    GCG GATG
                                |||||||||    ||| ||||
                                GTCGTCGCG    CGC CTAC
                                     AA___   T
GAM1126  C18orf1   3'  AGCTGAACAAAGTCTTCTGCT  29110       AGTC_
                                AGCTGAA    TCTTCTGCT
                                |||||||    |||||||||
                                TCGACTT    AGAAGACGA
                                    GTTTC
GAM1126  CD3G      3'  GCTGAAAGTCTCTCTGCT    29111          T
                                GCTGAAAGTCTCT CTGCT
                                |||||||||||| |||||
                                CGACTTTCAGAGA GACGA
                                                _
GAM1126  CYP24     5'  GAAAGCTGGGAGTCCTCCTG  29112       AA   T
                                GAAAGCTG  AGTC CTTCTG
                                ||||||||  |||| ||||||
                                CTTTCGAC  TCAG GAGGAC
                                     CC   _
GAM1126  DEDD      3'  AAACTGAAGTTCTGC      29113        A  CTCT
                                AAGCTGAA GT   TCTGC
                                |||||||| ||   |||||
                                TTTGACTT CA   AGACG
                                     _ _____
GAM1126  DGSI      3'  GAAGGCTGGAGTCCTCTGCT  29114    A   AA    CT
                                GAA GCTG  AGTCT  TCTGCT
                                ||| ||||  |||||  ||||||
                                CTT CGAC  TCAGG  AGACGA
                                  C   C_    __
GAM1126  IRTA1     3'  GAAAGTGAATATCCTTTTGCT  29115     C   A   T   C
                                GAAAG TGAA GTC CTT TGCT
                                ||||| |||| ||| ||| ||||
                                CTTTC ACTT TAG GAA ACGA
                                   _   A  _   A
GAM1126  MCC       3'  GAAAGCAGAAACGAGGCTCTGC 29116      T   GTCTC
              T                  GAAAGC GAAA    TTCTGCT
                                 ||||||  ||||    |||||||
                                 CTTTCG CTTT    GAGACGA
                                    T   GCTCC
GAM1126  PCDHA9    3'  GAAAGTGTCTCTTCTGC     29117      CTGAAA
                                GAAAG     GTCTCTTCTGC
                                |||||     ||||||||||
                                CTTTC     CAGAGAAGACG
                                  A_____
GAM1126  SCN8A     3'  CGGCAGCCTCTCTTCTG     29118    AA   GAAAG
                                CG  AGCT    TCTCTTCTG
                                ||  ||||    |||||||||
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                                GC  TCGG    AGAGAAGAC
                                 CG   _____
GAM1126  Apg4B    3'  GCTGGGGGTGTCCTCTGCT   29119     AAA  C
                                GCTG   GT TCTTCTGCT
                                ||||   || |||||||||
                                CGAC   CA AGGAGACGA
                                  CCC  C
GAM1126  APOL3    3'  AGCCGCTGTTTCTTCTGCT   29120     AAA  C
                                AGCTG   GT TCTTCTGCT
                                |||||   || |||||||||
                                TCGGC   CA AGAAGACGA
                                  GA_  A
GAM1126  C20orf45 3'  GAACAGCTGTTCTTCTG     29121     _    AAAGTC
                                GAA AGCTG     TCTTCTG
                                ||| |||||     |||||||
                                CTT TCGAC     AGAAGAC
                                  G    A_____
GAM1126  C20orf64 3'  GAAAGCTGTAAGTCTGC     29122       A     CTTCT
                                GAAAGCTG AAGTCT    GC
                                |||||||| ||||||    ||
                                CTTTCGAC TTCAGA    CG
                                    A    _____
GAM1126  CHST3    3'  CGAGGGCTGCAAATCTCTGCT 29123     AA   A      TCT
                                CGA  GCTG AAGTCTCT   GCT
                                |||  |||| ||||||||   |||
                                GCT  CGAC TTTAGAGA   CGA
                                  CC   G      ___
GAM1126  COLEC12  3'  GAGAGCTGAAAATTTGC     29124    A       CTCTTC
                                GA AGCTGAAAGT     TGC
                                || ||||||||||     |||
                                CT TCGACTTTTA     ACG
                                 C        A_____
GAM1126  COLEC12  3'  GAGAGCTGAAAATTTGC     29124    A       CTCTTC
                                GA AGCTGAAAGT     TGC
                                || ||||||||||     |||
                                CT TCGACTTTTA     ACG
                                 C        A_____
GAM1126  D2S448   3'  GACAGCTGAAAGCAAACCTG   29125    A       CTCT
                                GA AGCTGAAAGT    TCTG
                                || ||||||||||    ||||
                                CT TCGACTTTCG    GGAC
                                 G        TTT_
GAM1126  DKFZp761J1523 3'  CGTGAGCTGGAAGGGGCTGCT  29126    AA    A   TCTCTT
                                CG  AGCTG AAG     CTGCT
                                ||  ||||| |||     |||||
                                GC  TCGAC TTC     GACGA
                                 AC    C   CCC___
GAM1126  FLJ10604 3'  GAAAGCTGGAGTGGGTCTGCT  29127       AA   CTCT
                                GAAAGCTG  AGT    TCTGCT
                                ||||||||  |||    ||||||
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                                CTTTCGAC  TCA   AGACGA
                                    C_   CCC_
GAM1126 FLJ10956 3' CGAAAGCTGGAATCTTGTATCT 29128        AA    CT__
            GCT                   CGAAAGCTG  AGTCT   TCTGCT
                                  |||||||||  |||||   ||||||
                                  GCTTTCGAC  TTAGA   AGACGA
                                      C_    ACAT
GAM1126 G3A     3' AGCTGGAAGTCTCCAGCT   29129      A      TCT
                                  AGCTG AAGTCTCT   GCT
                                  ||||| ||||||||   |||
                                  TCGAC TTCAGAGG   CGA
                                    C       T__
GAM1126 KIAA0316 3' GAAAGCTGGAAGTCATAGCT  29130        A    TCTTCT
                                  GAAAGCTG AAGTC     GCT
                                  |||||||| |||||     |||
                                  CTTTCGAC TTCAG     CGA
                                      C    TAT___
GAM1126 KIAA0447 3' AAAGCTGAAGGTTTCTGTGCT 29131         A  C   TC
                                  AAAGCTGAA GT TCT  TGCT
                                  ||||||||| || |||  ||||
                                  TTTCGACTT CA AGA  ACGA
                                       C  A   C_
GAM1126 KIAA1161 5' AAGCTAAAGTTCACCCTG   29132        AG  T  T
                                  AAGCTGAA  TC CT CTG
                                  ||||||||  || || |||
                                  TTCGATTT  AG GG GAC
                                       CA  T  _
GAM1126 MOV10    5' GAAACTGAAAGTCGCCGC    29133     G       TCTT
                                  GAAA CTGAAAGTC    CTGC
                                  |||| |||||||||    ||||
                                  CTTT GACTTTCAG    GGCG
                                    _       C___
GAM1126 RHO6     3' GAAGCTGAAGGTGAGGCTGCT 29134     A     A  CTCTT
                                  GAA GCTGAA GT     CTGCT
                                  ||| |||||| ||     |||||
                                  CTT CGACTT CA     GACGA
                                    _     C  CTCC_
GAM1126 SCAND1   5' CGGAAGCGAAAGTCTCT     29135    A   T
                                  CG AAGC GAAAGTCTCT
                                  || |||| ||||||||||
                                  GC TTCG CTTTCAGAGA
                                   C   _
GAM1126 SCAND1   5' CGGAAGCGAAAGTCTCT     29135    A   T
                                  CG AAGC GAAAGTCTCT
                                  || |||| ||||||||||
                                  GC TTCG CTTTCAGAGA
                                   C   _
GAM1126 SCYB10   5' GAGACTGGAGGTTCCTCTGCT 29136    AA   AA  TC
                                  GA  GCTG  AG  TCTTCTGCT
                                  ||  ||||  ||  |||||||||
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                                CT  TGAC  TC  AGGAGACGA
                                 C_    C_  CA
GAM1126  SEC24A    5'  GAGAGCTGAAAGACCACTGCT  29137    A       T  CTT
                                GA AGCTGAAAG CT   CTGCT
                                || ||||||||| ||   |||||
                                CT TCGACTTTC GG   GACGA
                                 C        T  T__
GAM1126  SH3BGRL2  3'  GCTGTAATTCTTCTGCT     29138      AA   C
                                GCTG  AGT TCTTCTGCT
                                ||||  ||| |||||||||
                                CGAC  TTA AGAAGACGA
                                  A_  _
GAM1126  TUCAN     3'  CGGAAGCTAAAAGGAAACTGCT 29139    A        TCTCTT
                                CG AAGCTGAAAG     CTGCT
                                || ||||||||||      |||||
                                GC TTCGATTTTC     GACGA
                                 C         CTTT__
GAM1126  ZNF294    3'  GAAGGCTGAAAAACATTTGCT  29140    A       TCTCTTC
                                GAA GCTGAAAG      TGCT
                                ||| ||||||||      ||||
                                CTT CGACTTTT      ACGA
                                  C       TGTAA__
GAM1126  LOC146435 5'  CGAAACTTGAGGCCTCTGC    29141      GC   AAGTCT
                                CGAAA  TGA     CTTCTGC
                                |||||  |||     |||||||
                                GCTTT  ACT     GGAGACG
                                   GA   CC____
GAM1126  LOC150889 5'  CGAGGGCTGGCAGTCTCCC    29142     AA   AA
                                CGA  GCTG  AGTCTCTT
                                |||  ||||  ||||||||
                                GCT  CGAC  TCAGAGGG
                                  CC    CG
GAM1126  LOC153688 5'  GAAAGATGAGGTCAATCTGCT  29143      C   AA   TCT
                                GAAAG TGA  GTC   TCTGCT
                                ||||| |||  |||   ||||||
                                CTTTC ACT  CAG   AGACGA
                                   T   C_   TT_
GAM1126  LOC168489 5'  GAAAGCAGAAAGTCTCTTCT   29144       T
                                GAAAGC GAAAGTCTCTTCT
                                |||||| ||||||||||||
                                CTTTCG CTTTCAGAGAAGA
                                    T
GAM1126  LOC201689 5'  GAAAGCTGAAAATCTCCCCT   29145
                                GAAAGCTGAAAGTCTCTTCT
                                ||||||||||||||||||
                                CTTTCGACTTTTAGAGGGGA

GAM1126  LOC203378 3'  CGAAGGCTGAAAGCTCCT    29146      A       T
                                CGAA GCTGAAAG CTCTT
                                |||| |||||||| |||||
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                                GCTT CGACTTTC GAGGA
                                  C      _
GAM1126  LOC206777 5'  GAGAGCAGAATTCTTCTGCT  29147    A  T  AGTC
                                GA AGC GAA   TCTTCTGCT
                                || ||| |||   |||||||||
                                CT TCG CTT   AGAAGACGA
                                 C  T  A___
GAM1126  LOC221773 3'  GAGAGCTACGCAATCTTCTGCT 29148    A    AAAGTC
                                GA AGCTG     TCTTCTGCT
                                || |||||     |||||||||
                                CT TCGAT     AGAAGACGA
                                 C    GCGTT_
GAM1126  LOC256158 5'  CGGAGCTGGAAGTCCCTGGCCT 29149    AA    A      __
            GCT                   CG  AGCTG AAGTCTCT  TCTGCT
                                ||  ||||| ||||||||  ||||||
                                GC  TCGAC TTCAGGGA  GGACGA
                                 C_    C       CC
GAM1126  LOC257553 3'  AGCTGGAAGTCTCCAGCT    29129      A      TCT
                                AGCTG AAGTCTCT   GCT
                                ||||| ||||||||   |||
                                TCGAC TTCAGAGG   CGA
                                   C       T__
GAM1126  LOC257604 3'  AGCTGGAAGTCTCCAGCT    29129      A      TCT
                                AGCTG AAGTCTCT   GCT
                                ||||| ||||||||   |||
                                TCGAC TTCAGAGG   CGA
                                   C       T__
GAM1126  LOC91300  5'  AAGCCGAGAGTCTCTTCACC  29150       A       T
                                AAGCTGA AGTCTCTTC GCT
                                ||||||| ||||||||| |||
                                TTCGGCT TCAGAGAAG TGG
                                    C       _
GAM1126  LOC91300  5'  AAGCCGAGAGTCTCTTCACC  29150       A       T
                                AAGCTGA AGTCTCTTC GCT
                                ||||||| ||||||||| |||
                                TTCGGCT TCAGAGAAG TGG
                                    C       _
GAM1127  HS2ST1    3'  TATGTTAAAGATGTTTC     29153        AAAT
                                TATGTTAA    AGGTGTTTT
                                ||||||||    |||||||||
                                ATACAATT    TCTACAAAG
                                            _____
GAM1127  ITGA1     3'  TGTTTTGAAAATAGATGTTTC  29154      A__
                                TGTT   AAAATAGGTGTTTT
                                ||||   ||||||||||||||
                                ACAA   TTTTATCTACAAAG
                                  AAC
GAM1127  C6orf5    3'  TGTTAAAAATGGGTGTTTT    29155          A
                                TGTTAAAAAT GGTGTTTT
                                |||||||||| ||||||||
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                                ACAATTTTTA CCACAAAA
                                      C
GAM1127 CNNM1    3' TATTTAAAATAGTAGTGTTTTT 29156      A      __
             T                   TGTT AAAATAG  GTGTTTTTT
                                 |||| |||||||  |||||||||
                                 ATAA TTTTATC  CACAAAAAA
                                   A       AT
GAM1127 KIAA1280 5' TATGTATAGATATACGTGTTTT 29157       TAAAA_  G
             TT                   TATGT     ATA GTGTTTTTT
                                  |||||      ||| |||||||||
                                  ATACA      TAT CACAAAAAA
                                    TATCTA   G
GAM1127 KIAA1373 3' TATGTTAAAGATGCTTTT    29158         AAAT
                                 TATGTTAA    AGGTGTTTTT
                                 ||||||||    ||||||||||
                                 ATACAATT    TCTACGAAAA
                                      _____
GAM1127 PRO1942  3' TATGCTTGGAAATAGGGCGTTT 29159       AA_      _
             C                    TATGTT   AAATAGG TGTTTT
                                  ||||||   ||||||| ||||||
                                  ATACGA   TTTATCC GCAAAG
                                     ACC      C
GAM1127 PRO2086  5' CATGTTAAAAATATGCTTTTTC 29160           AG
                                 TATGTTAAAAAT  GTGTTTTTTC
                                 ||||||||||||  |||||||||
                                 GTACAATTTTTA  TACGAAAAAG
                                      __
GAM1127 SEF      3' ATGTTAAAAGTGCCTTTT    29161         AATA
                                 ATGTTAAA    GGTGTTTTTT
                                 ||||||||    ||||||||||
                                 TACAATTT    TCACGGAAAA
                                      _____
GAM1127 LOC201161 3' ATGTTAAAAATATTTATTTTTT 29162           GG
                                 ATGTTAAAAATA  TGTTTTTT
                                 ||||||||||||  ||||||||
                                 TACAATTTTTAT  ATAAAAAA
                                       AA
GAM1128 HMGCR    3' TTCAAGAATTTCATCAAAACT  29165      T        TTT
                                 TTCA GAATTTCATT   AGAACT
                                 |||| ||||||||||   ||||||
                                 AAGT CTTAAAGTAG   TTTTGA
                                   T       ___
GAM1128 POLQ     3' TTCATGAATATTCATTCCTACA 29166          _        GA
             CT                    TTCATGAAT TTCATTTTTA  ACT
                                   ||||||||| ||||||||||  |||
                                   AAGTACTTA AAGTAAGGAT  TGA
                                         T        G_
GAM1128 SSPN     3' TTCATGAATTTCCATTTTTAG  29167           _
                                 TTCATGAATTTC ATTTTTAG
                                 |||||||||||| ||||||||
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                                AAGTACTTAAAG TAAAAATC
                                      G
GAM1128 VAPA     3' ATGAATTTCATAAAGGACT   29168          TTTT  A
                                ATGAATTTCAT   AG ACT
                                ||||||||||   || |||
                                TACTTAAAGTA   TC TGA
                                      TT__  C
GAM1128 FLJ11273 3' TTCTGAATTTCATTTTC    29169     A
                                TTC TGAATTTCATTTTT
                                ||| ||||||||||||||
                                AAG ACTTAAAGTAAAAG
                                  _
GAM1128 KIAA1559 3' TTCATGAAATTCATTTTT    29170         T
                                TTCATGAA TTCATTTTT
                                |||||||| |||||||||
                                AAGTACTT AAGTAAAAA
                                     T
GAM1128 ULK2     3' TTCATGAATTTACATTTT    29171          _
                                TTCATGAATTT CATTTT
                                |||||||||| ||||||
                                AAGTACTTAAA GTAAAA
                                      T
GAM1128 LOC220906 3' TTCATGTATTTCATCAAAG   29172       A       TTT
                                TTCATG ATTTCATT   AG
                                |||||| ||||||||   ||
                                AAGTAC TAAAGTAG   TC
                                   A       TT_
GAM1128 LOC222128 5' TGAATTTCATTTCTCTTTAGAA 29173           ____
                                TGAATTTCATTTT   TAGAA
                                ||||||||||||   |||||
                                ACTTAAAGTAAAG   ATCTT
                                      AGAA
GAM1128 LOC90167  3' TTCATGAATTTCCTAGGTTTAG 29174          ATT__
             AA                   TTCATGAATTTC    TTTAGAA
                                ||||||||||||    |||||||
                                AAGTACTTAAAG    AAATCTT
                                      GATCC
GAM1129 ABCB9    3' CGGAGGGCAGCTGGGGGC    29177     AA _  C
                                TGGA  GT GTT GGGGGC
                                ||||  || ||| ||||||
                                GCCT  CG CGA CCCCCG
                                  CC  T  _
GAM1129 ACY1     3' TGGAAGCCCCAGGGGC      29178      A  G
                                TGGAA GT TTCGGGGGC
                                ||||| || |||||||||
                                ACCTT CG GGGTCCCCG
                                  _ _
GAM1129 ALK      5' TGGAAGCTCAGGGGC       29179      AGT
                                TGGAA   GTTCGGGGGC
                                |||||   ||||||||||
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                                ACCTT  CGAGTCCCCG
                                  ___
GAM1129 ARHC    5' TGGGTGCCCCAGGGGGC    29180    AAA    __
                                TGG  GTGTTC GGGGGC
                                |||  |||||| ||||||
                                ACC  CACGGG CCCCCG
                                  ___    GT
GAM1129 CCND2   3' TAGAAGGACCCAGGGGC    29181     A TG
                                TGGAA G  TTCGGGGGC
                                ||||| |  |||||||||
                                ATCTT C  GGGTCCCCG
                                  _ CT
GAM1129 CDH6    3' TGGAAAATGAAAAAGGC    29182       TTC
                                TGGAAAGTG  GGGGGC
                                |||||||||  ||||||
                                ACCTTTTAC  TTTCCG
                                     TT_
GAM1129 CDKN2B  3' TGGTGAGTGTCGAGGGC    29183    AA   T
                                TGG  AGTGT CGGGGGC
                                |||  ||||| |||||||
                                ACC  TCACA GCTCCCG
                                  AC   _
GAM1129 CHN1    5' TGGGGTGCCCGATGGGGC    29184    AAA    __
                                TGG  GTGTTCG GGGGC
                                |||  ||||||| |||||
                                ACC  CACGGGC CCCCG
                                  C__     TA
GAM1129 DPYSL3  3' CGGAAGTCCCAAGGGC     29185     A  G
                                TGGAA GT TTCGGGGGC
                                ||||| || |||||||||
                                GCCTT CA GGGTTCCCG
                                  _ _
GAM1129 DR1     5' CGGAGAGTGATCCCGGGGG   29186     A   __
                                TGGA AGTG  TTCGGGGG
                                |||| ||||  ||||||||
                                GCCT TCAC  GGGCCCCC
                                  C   TA
GAM1129 DRD1    5' TGGAGATTGTTCAAAGGGC   29187     AAG    _
                                TGGA  TGTTCGG GGGC
                                ||||  ||||||| ||||
                                ACCT  ACAAGTT CCCG
                                  CTA     T
GAM1129 EFNA3   3' TGGAGAGGCCAAAGGC     29188     A  T  T
                                TGGA AG GT CGGGGGC
                                |||| || || |||||||
                                ACCT TC CG GTTTCCG
                                  C  _  _
GAM1129 EIF2C1  3' TGGAAAGGCCAGGGGC     29189       T  T
                                TGGAAAG GT CGGGGGC
                                ||||||| || |||||||
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                                ACCTTTC CG GTCCCCG
                                      _ _
GAM1129  EXTL3    3'  TGGAAAGTGGTAACTCGGG   29190        ____
                                TGGAAAGTG   TTCGGG
                                |||||||||   ||||||
                                ACCTTTCAC   GAGCCC
                                     CATT
GAM1129  FANCD2   3'  TGGAAAATGAGAGGC      29191        TTC
                                TGGAAAGTG  GGGGGC
                                |||||||||  ||||||
                                ACCTTTTAC  TCTCCG
                                      ___
GAM1129  GPX4     3'  TGGAAGGCTCCAAGGGC    29192      A  G
                                TGGAA GT TTCGGGGGC
                                |||||  ||  |||||||||
                                ACCTT CG AGGTTCCCG
                                   C  _
GAM1129  HDAC4    5'  TGGAAAGGTCCAGAAGGGGC  29193       T   ___
                                TGGAAAG GTTC  GGGGGC
                                |||||||  ||||  ||||||
                                ACCTTTC CAGG  TCCCCG
                                     _   TCT
GAM1129  HDAC7A   5'  TGGAAAGTTTGTCCTCGGGGGC 29194       GT____
                                TGGAAAGT    TCGGGGGC
                                ||||||||    ||||||||
                                ACCTTTCA    AGCCCCCG
                                     AACAGG
GAM1129  HDAC7A   5'  TGGAAAGTTTGTCCTCGGGGGC 29194       GT____
                                TGGAAAGT    TCGGGGGC
                                ||||||||    ||||||||
                                ACCTTTCA    AGCCCCCG
                                     AACAGG
GAM1129  ITGA11   3'  CGGGAGCCCCAGGGGC     29195     AA  G
                                TGG  AGT TTCGGGGGC
                                |||  ||| |||||||||
                                GCC  TCG GGGTCCCCG
                                  C_  _
GAM1129  JPH3     3'  TGGAAGGCCGGGGGC      29196      A T  T
                                TGGAA G GT CGGGGGC
                                |||||  |  ||  |||||||
                                ACCTT C CG GCCCCCG
                                      _ _  _
GAM1129  MAF      5'  TGGAAGGCGCGGCGGGC    29197      A   TT  _
                                TGGAA GTG  CGG GGGC
                                |||||  |||  |||  ||||
                                ACCTT CGC  GCC CCCG
                                   C   __  G
GAM1129  MEN1     5'  TGGAAAGTTTCTAAGC     29198        G   GG
                                TGGAAAGT TTC  GGGC
                                |||||||| |||  ||||
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                                ACCTTTCA AAG  TTCG
                                    _  A_
GAM1129  MMP19    3'  CGGAAGTGTTAGAGGC      29199       A    C
                                TGGAA GTGTT GGGGGC
                                ||||| ||||| ||||||
                                GCCTT CACAA TCTCCG
                                  _    _
GAM1129  NAGA     5'  TGGGAGTCCCGAGGGC      29200     AA   G
                                TGG  AGT TTCGGGGGC
                                |||  ||| |||||||||
                                ACC  TCA GGGCTCCCG
                                  C_  _
GAM1129  NFATC1   5'  GGAAAGTCATCGAGGGGC    29201        GT   _
                                GGAAAGT  TCG GGGGC
                                |||||||  ||| |||||
                                CCTTTCA  AGC CCCCG
                                    GT   T
GAM1129  NPTX1    3'  TGGGAAGGTCGAGGGC      29202     A   T  T
                                TGG AAG GT CGGGGGC
                                ||| ||| || |||||||
                                ACC TTC CA GCTCCCG
                                  C  _ _
GAM1129  OTOF     3'  TGAAAAGTGGACGCTGGGC    29203         TT  G_
                                TGGAAAGTG  CG  GGGC
                                |||||||||  ||  ||||
                                ACTTTTCAC  GC  CCCG
                                     CT  GA
GAM1129  PLS3     3'  TGGGAAATGTCAAGGGC     29204     A     T
                                TGG AAGTGT CGGGGGC
                                ||| |||||| |||||||
                                ACC TTTACA GTTCCCG
                                  C     _
GAM1129  PPP1R14B 3'  TGGAAAACTGAGGGGGC     29205        _  TTC
                                TGGAAAG TG   GGGGGC
                                ||||||| ||   ||||||
                                ACCTTTT AC   CCCCCG
                                    G  T__
GAM1129  PRKY     3'  TGGAAATGTCCTCAGGC     29206       G    GG
                                TGGAAA TGTTC  GGGC
                                |||||| |||||  ||||
                                ACCTTT ACAGG  TCCG
                                   _    AG
GAM1129  RAB36    3'  TGGAGGCCCGAAGGGGC     29207      AA T    __
                                TGGA  G GTTCG  GGGGC
                                ||||  | |||||  |||||
                                ACCT  C CGGGC  CCCCG
                                  __ _    TT
GAM1129  RGS19IP1 3'  TGGAAAGTGGTGGAGGCGGGGG 29208          TT_____
                                TGGAAAGTG      CGGGGG
                                |||||||||      ||||||
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                                ACCTTTCAC      GCCCCC
                                     CACCTCC
GAM1129 SLC19A1  5' TGGAGATGTGCCAGGGGC   29209     AA_   T
                                TGGA  GTGT CGGGGGC
                                ||||  |||| |||||||
                                ACCT  CACG GTCCCCG
                                  CTA   _
GAM1129 TBL1X    5' TGGAAAGTTTCGGTGGC    29210       G    G
                                TGGAAAGT TTCGG GGC
                                |||||||| ||||| |||
                                ACCTTTCA AAGCC CCG
                                     _    A
GAM1129 TCF15    3' TGGAGATGTCCCGAGGGC   29211     AA     _
                                TGGA  GTGTTC GGGGGC
                                ||||  |||||| ||||||
                                ACCT  TACAGG CTCCCG
                                  C_     G
GAM1129 XPNPEP2  3' TGGAAAGTTCAAAGGGC    29212       G  CG
                                TGGAAAGT TT  GGGGC
                                |||||||| ||  |||||
                                ACCTTTCA AG  TCCCG
                                     _ TT
GAM1129 ZNF144   3' TGGAAGGAGTGGAGAGGC   29213      __   TTC
                                TGGAA  AGTG   GGGGGC
                                |||||  ||||   ||||||
                                ACCTT  TCAC   TCTCCG
                                   CC    C__
GAM1129 APEX2    3' TGGAAAGTGGTGTAAGGGGC  29214       TTC__
                                TGGAAAGTG    GGGGGC
                                |||||||||    ||||||
                                ACCTTTCAC    TCCCCG
                                     CACAT
GAM1129 BPESC1   3' TGGAAGTTCCAAAGGGC    29215     AGT   __
                                TGGAA   GTTC  GGGGGC
                                |||||   ||||  ||||||
                                ACCTT   CAAG  TTCCCG
                                   ____   GT
GAM1129 C14orf4  5' TGGAAGCTCGAAAGGGGC   29216     AGT   ____
                                TGGAA   GTTCG   GGGGC
                                |||||   |||||   |||||
                                ACCTT   CGAGC   CCCCG
                                   ____    TTT
GAM1129 C14orf4  5' GGAGCAGGCGTCGGGGGC   29217    A_  T  _
                                GGA  AG GT TCGGGGGC
                                |||  || || ||||||||
                                CCT  TC CG AGCCCCCG
                                  CG  _  C
GAM1129 C5orf6   3' TGAAAAGTGTTCCAGGGC   29218         G
                                TGGAAAGTGTTC GGGGC
                                |||||||||||| |||||
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                                ACTTTTCACAAG TCCCG
                                       G
GAM1129 CASPR3   3' TGGAAAGTTCATGGGC     29219        GT   G
                                TGGAAAGT  TCG GGGC
                                ||||||||  ||| ||||
                                ACCTTTCA  AGT CCCG
                                     __   A
GAM1129 CHRFAM7A 5' TGGAAAATGGCAAGGGGC    29220        TTC
                                TGGAAAGTG   GGGGGC
                                |||||||||   ||||||
                                ACCTTTTAC   TCCCCG
                                     CGT
GAM1129 CRMP5    3' TGGGAGTGATCAGGGGC     29221     AA    T
                                TGG  AGTG TCGGGGGC
                                |||  |||| ||||||||
                                ACC  TCAC AGTCCCCG
                                  C_    T
GAM1129 DDX34    3' TGGAGGGTTTCGAGGGC     29222     AA  G
                                TGGA  GT TTCGGGGGC
                                ||||  || |||||||||
                                ACCT  CA AAGCTCCCG
                                   CC  _
GAM1129 DKFZP564C186 3' TGGAAGGGCCAGGGGC      29223      A T  T
                                TGGAA G GT CGGGGGC
                                ||||| | || |||||||
                                ACCTT C CG GTCCCCG
                                   _ C  _
GAM1129 DKFZP761E2110 3' TGGAAAGTGAGAGGC      29224        TTC
                                TGGAAAGTG   GGGGGC
                                |||||||||   ||||||
                                ACCTTTCAC   TCTCCG
                                      ___
GAM1129 FLJ00001  3' TGGGATGTCCAAAGGGC     29225     AAA      _
                                TGG   GTGTTCGG GGGC
                                |||   |||||||| ||||
                                ACC   TACAGGTT CCCG
                                  C__       T
GAM1129 FLJ10241  3' TGGAGGGTGCCAAGGGC     29226     AA    T
                                TGGA  GTGT CGGGGGC
                                ||||  |||| |||||||
                                ACCT  CACG GTTCCCG
                                   CC   _
GAM1129 FLJ10620  3' TGGAGAGATTCAGAAGGGGC  29227     A  T   ___
                                TGGA AG GTTC   GGGGGC
                                |||| || ||||   ||||||
                                ACCT TC TAAG   TCCCCG
                                  C  _    TCT
GAM1129 FLJ11773  5' CGGGTGTCTCGGGGGC      29228     AAA   _
                                TGG   GTGT TCGGGGGC
                                |||   |||| ||||||||
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                                GCC   CACA AGCCCCCG
                                  ___   G
GAM1129  FLJ13153  5'  TGGGGAGTGCTCGACAGC    29229    AA       G
                                TGG  AGTGTTCGG GGC
                                |||  ||||||||| |||
                                ACC  TCACGAGCT TCG
                                  CC       G
GAM1129  FLJ20225  3'  TGGAAGTCCGGGGGC      29230     AGT
                                TGGAA  GTTCGGGGGC
                                |||||  ||||||||||
                                ACCTT  CAGGCCCCCG
                                   ___
GAM1129  FLJ21347  3'  TGGGTGCCCAAGGGGGGC   29231    AAA    ___
                                TGG  GTGTTC  GGGGGC
                                |||  ||||||  ||||||
                                ACC  CACGGG  CCCCCG
                                  ___    TTC
GAM1129  FLJ22479  3'  TGGAAAGTGGGGGAGGC    29232       TTC
                                TGGAAAGTG  GGGGGC
                                |||||||||  ||||||
                                ACCTTTCAC  CCTCCG
                                     CC_
GAM1129  FLJ32334  3'  TGAAAAGTGGGGGGC      29233       TTC
                                TGGAAAGTG  GGGGGC
                                |||||||||  ||||||
                                ACTTTTCAC  CCCCCG
                                   ___
GAM1129  GTPBP1    5'  GGGGAGCTGGGCTCGGGGGC  29234    AA  ___
                                GG  AGT  GTTCGGGGGC
                                ||  |||  ||||||||||
                                CC  TCG  CGAGCCCCCG
                                 CC  ACC
GAM1129  HSSEXGENE 3'  TGGGTGTGCCGGGGGC     29235    AAA  _
                                TGG  GTGT TCGGGGGC
                                |||  |||| ||||||||
                                ACC  CACA GGCCCCCG
                                  ___   C
GAM1129  KCND1     5'  TGGGGAATTCCAAGGGC     29236    AA  G
                                TGG  AGT TTCGGGGGC
                                |||  ||| |||||||||
                                ACC  TTA AGGTTCCCG
                                  CC  _
GAM1129  KIAA0870  3'  TGGGTGCCCAGGGGGC     29237    AAA   _
                                TGG  GTGTTC GGGGGC
                                |||  |||||| ||||||
                                ACC  CACGGG CCCCCG
                                  ___    T
GAM1129  KIAA0984  3'  GGAGAGTGTTCACAGGGC   29238    A     _
                                GGA AGTGTTCG GGGGC
                                ||| |||||||| |||||
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                                CCT TCACAAGT TCCCG
                                  C       G
GAM1129 KIAA1280 5' TGGAAGCCCGAGGGGC     29239      AGT    _
                                TGGAA   GTTCG GGGGC
                                |||||   ||||| |||||
                                ACCTT   CGGGC CCCCG
                                   ____    T
GAM1129 KIAA1655 3' TGGGAGGCCCAGGGGC     29240     AA  T
                                TGG  AG GTTCGGGGGC
                                |||  || ||||||||||
                                ACC  TC CGGGTCCCCG
                                  C_ _
GAM1129 KIAA1887 5' TGTAAAGTGCTGGGAGGGGG  29241    G      C___
                                TG AAAGTGTT    GGGGG
                                || ||||||||    |||||
                                AC TTTCACGA    CCCCC
                                 A       CCCT
GAM1129 KIAA1940 3' TGGAAGGTCCCTGGGGC    29242      A T    G_
                                TGGAA G GTTC  GGGGC
                                ||||| | ||||  |||||
                                ACCTT C CAGG  CCCCG
                                   _ _   GA
GAM1129 MCF2L    3' CGGGGCGTCCGGGGGC     29243     AAA
                                TGG   GTGTTCGGGGGC
                                |||   ||||||||||||
                                GCC   CGCAGGCCCCCG
                                  C__
GAM1129 MFN2     3' GAAAGTGTCCTTTGGGGG    29244         ___
                                GAAAGTGTTC   GGGGG
                                ||||||||||   |||||
                                CTTTCACAGG   CCCCC
                                      AAA
GAM1129 MGC13010 3' GGAAAGTGTTCGGCAGGGC   29245          __
                                GGAAAGTGTTCGG  GGGC
                                ||||||||||||  ||||
                                CCTTTCACAAGCC  CCCG
                                        GT
GAM1129 MGC14128 3' TGGAATGTTCAGCCGGGC    29246     AA      __
                                TGGA  GTGTTCGG  GGGC
                                ||||  ||||||||  ||||
                                ACCT  TACAAGTC  CCCG
                                   __       GG
GAM1129 MGC16025 5' TGGAGCGTTCACAGGGC     29247     AA     _
                                TGGA  GTGTTCG GGGGC
                                ||||  ||||||| |||||
                                ACCT  CGCAAGT TCCCG
                                   __      G
GAM1129 MGC34869 3' TGGCAAGTGCCGGGGGC     29248     A     T
                                TGG AAGTGT CGGGGGC
                                ||| |||||| |||||||
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                                ACC TTCACG GCCCCCG
                                  G     _
GAM1129  OSBPL5   5'  TGGGCGCTCGGGGGC      29249     AAA
                                TGG   GTGTTCGGGGGC
                                |||   ||||||||||||
                                ACC   CGCGAGCCCCCG
                                      ____
GAM1129  PKMYT1   3'  TGGGAGTTCCCGAGGGGC    29250     AA   G   _
                                TGG  AGT TTCG GGGGC
                                |||  ||| |||| |||||
                                ACC  TCA GGGC CCCCG
                                  C_   A    T
GAM1129  PNMA5    3'  TGGAAAGTAAGGGGGC      29251         TTC
                                TGGAAAGTG   GGGGGC
                                |||||||||   ||||||
                                ACCTTTCAT   CCCCCG
                                      T__
GAM1129  PP1628   5'  TGGCAGGTCCCAGGGGGGC   29252     AA  T   ____
                                TGG  AG GTTC   GGGGGC
                                |||  || ||||   ||||||
                                ACC  TC CAGG   CCCCCG
                                  G_  _    GTC
GAM1129  SGKL     3'  TGAAAAGTGCAGTGGC      29253         TC  G
                                TGGAAAGTGT  GG GGC
                                ||||||||||  || |||
                                ACTTTTCACG  TC CCG
                                      __  A
GAM1129  SMPD2    5'  TGGGGAGCTCCAGGGGC     29254     AA   G
                                TGG  AGT TTCGGGGGC
                                |||  ||| |||||||||
                                ACC  TCG AGGTCCCCG
                                  CC   _
GAM1129  TUBB5    3'  TGGAAGAGCTCAAGGGGG    29255      A T   __
                                TGGAA G GTTC  GGGGG
                                ||||| | ||||  |||||
                                ACCTT C CGAG  CCCCC
                                   _ T    TT
GAM1129  YAF2     3'  TGGAAATGTTTGGTAGGC    29256      G   C  _
                                TGGAAA TGTT GG GGGC
                                |||||| |||| || ||||
                                ACCTTT ACAA CC TCCG
                                   _    A  A
GAM1129  LOC129052 5'  TGGAAAGCAAGGGGC      29257         TTC
                                TGGAAAGTG   GGGGGC
                                |||||||||   ||||||
                                ACCTTTCGT   TCCCCG
                                      ____
GAM1129  LOC129892 5'  TGGAAAGCGGCAAAGGC    29258          TT
                                TGGAAAGTG  CGGGGGC
                                |||||||||  |||||||
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                                ACCTTTCGC  GTTTCCG
                                     C_
GAM1129  LOC130471 3'  GGAAAGTGGCAGAAGGGC    29259        _ TC
                                GGAAAGTG T  GGGGGC
                                |||||||| |  ||||||
                                CCTTTCAC G  TTCCCG
                                     C TC
GAM1129  LOC142941 5'  TGGGATGTCCCGGGGGC     29260     AAA    _
                                TGG   GTGTTC GGGGGC
                                |||   |||||| ||||||
                                ACC   TACAGG CCCCCG
                                  C__     G
GAM1129  LOC146083 5'  TGGGAGTCTCAGGGGC      29261     AA   G
                                TGG  AGT TTCGGGGGC
                                |||  ||| |||||||||
                                ACC  TCA GAGTCCCCG
                                  C_  _
GAM1129  LOC146669 5'  TAGAAAGCAGGGGGC       29262         TTC
                                TGGAAAGTG   GGGGGC
                                |||||||||   ||||||
                                ATCTTTCGT   CCCCCG
                                     ___
GAM1129  LOC147040 5'  TGGGAGTGTCCGAGGGC     29263     AA
                                TGG  AGTGTTCGGGGGC
                                |||  ||||||||||||
                                ACC  TCACAGGCTCCCG
                                  C_
GAM1129  LOC147700 3'  TGGCGAGGCTCGGGGGC     29264     AA  T
                                TGG  AG GTTCGGGGGC
                                |||  || ||||||||||
                                ACC  TC CGAGCCCCCG
                                  GC  _
GAM1129  LOC148195 5'  TGGAAAGTGGAAGGGC      29265         TTC
                                TGGAAAGTG   GGGGGC
                                |||||||||   ||||||
                                ACCTTTCAC   TTCCCG
                                     C__
GAM1129  LOC149422 3'  TGCAAAGTGCTGGAGGGC    29266    G       C
                                TG AAAGTGTT GGGGGC
                                || |||||||| ||||||
                                AC TTTCACGA CTCCCG
                                  G       C
GAM1129  LOC150311 5'  TGGAAAATGCCTATGGGC    29267          CGG
                                TGGAAAGTGTT   GGGC
                                ||||||||||   ||||
                                ACCTTTTACGG   CCCG
                                       ATA
GAM1129  LOC151534 5'  TAGAAACGCTCCCGGGGGC   29268       _  G
                                TGGAAA GT TTCGGGGGC
                                |||||| || |||||||||
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                                ATCTTT CG GGGCCCCCG
                                   G  A
GAM1129  LOC151723 5'  TGGAAAGCAGGGGGC       29269          TTC
                                TGGAAAGTG   GGGGGC
                                |||||||||   ||||||
                                ACCTTTCGT   CCCCCG
                                    ____
GAM1129  LOC152002 3'  TGGAGGCCCCGGGGGC      29270      AA  G
                                TGGA  GT TTCGGGGGC
                                ||||  || |||||||||
                                ACCT  CG GGGCCCCCG
                                  C_  _
GAM1129  LOC158382 5'  TGGAAGGCCAGGGGC       29271       A T  T
                                TGGAA G GT CGGGGGC
                                ||||| | || |||||||
                                ACCTT C CG GTCCCCG
                                   _ _  _
GAM1129  LOC197320 5'  GGAAGCGGTGCCGGGGGC    29272      A__    T
                                GGAA   GTGT CGGGGGC
                                ||||   |||| |||||||
                                CCTT   CACG GCCCCCG
                                  CGC   _
GAM1129  LOC203221 5'  TGCAAAGTGTCCACAGGGC   29273    G        _
                                TG AAAGTGTTCG GGGGC
                                || ||||||||| |||||
                                AC TTTCACAGGT TCCCG
                                 G         G
GAM1129  LOC219401 5'  TGGGCGTCCGGGGGC       29274     AAA
                                TGG   GTGTTCGGGGGC
                                |||   ||||||||||||
                                ACC   CGCAGGCCCCCG
                                   ____
GAM1129  LOC220074 3'  TGAAAAGTACAAAGGGGC    29275          TC
                                TGGAAAGTGT  GGGGGC
                                ||||||||||  ||||||
                                ACTTTTCATG  TCCCCG
                                      TT
GAM1129  LOC220705 3'  TGTGAAGTGCCCTGGGGGC   29276    GA       _
                                TG  AAGTGTTC GGGGGC
                                ||  |||||||| ||||||
                                AC  TTCACGGG CCCCCG
                                 AC       A
GAM1129  LOC221405 5'  TGGAAAGCTGCCAGTGGGGC  29277        _   CG_
                                TGGAAAG TGTT   GGGGC
                                ||||||| ||||   |||||
                                ACCTTTC ACGG   CCCCG
                                   G   TCA
GAM1129  LOC253681 5'  TGGGAGTGTCCGAGGGC     29263     AA
                                TGG  AGTGTTCGGGGGC
                                |||  ||||||||||||
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                                ACC  TCACAGGCTCCCG
                                  C_
GAM1129  LOC255452 3'  TGGGTGGTCTCAGGGGC    29278    AAA  __
                                TGG   GTG  TTCGGGGGC
                                |||   |||  |||||||||
                                ACC   CAC  GAGTCCCCG
                                  ___   CA
GAM1129  LOC257017 5'  TGAAAAGTGTAAAAGGGG    29279        TC_
                                TGGAAAGTGT   GGGGG
                                ||||||||||   |||||
                                ACTTTTCACA   TCCCC
                                      TTT
GAM1129  LOC51213  3'  TGGAATGTCCAAGGGGC    29280     AA     _
                                TGGA  GTGTTCG GGGGC
                                ||||  ||||||| |||||
                                ACCT  TACAGGT CCCCG
                                  __      T
GAM1129  LOC58525  5'  TGTGAAGGTCCGAGGGGC    29281    GA  T    _
                                TG  AAG GTTCG GGGGC
                                ||  ||| ||||| |||||
                                AC  TTC CAGGC CCCCG
                                 AC   _    T
GAM1129  LOC90139  3'  TGGGTGGTTCAAGAGGGGC   29282     AAA  _  ___
                                TGG   GTG TTC   GGGGGC
                                |||   ||| |||   ||||||
                                ACC   CAC AAG   TCCCCG
                                  ___   C   TTC
GAM1129  LOC91145  3'  TGGAAGGTTCCAAAGGC    29283     A  G
                                TGGAA GT TTCGGGGGC
                                ||||| || |||||||||
                                ACCTT CA AGGTTTCCG
                                   C  _
GAM1129  LOC92912  5'  TGGAAAATGGCGAGGGGC    29284        TT  _
                                TGGAAAGTG  CG GGGGC
                                |||||||||  ||  |||||
                                ACCTTTTAC  GC CCCCG
                                      C_  T
GAM1130  CLCA3    3'  TAGATGCCATCATTCTTGA   29287        C  GCTAG
                                TAGATGCCG CA    TTGA
                                |||||||||  ||    ||||
                                ATCTACGGT GT    AACT
                                      A  AAG__
GAM1130  CLTCL1   3'  TAGATGCCCTTAAGCCCTGA  29288       GCC_   AG
                                TAGATGCC   AGCT  TTGA
                                ||||||||   ||||  ||||
                                ATCTACGG   TCGG  GACT
                                     GAAT   __
GAM1130  ESR1     3'  TAAATGGAGCTAGTTG     29289       CCGCC
                                TAGATG    AGCTAGTTG
                                ||||||    |||||||||
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                                ATTTAC    TCGATCAAC
                                   C____
GAM1130 FOSB    5' GATGCCGCTGTACCTCTTGA  29290       CA_  AG
                                GATGCCGC  GCT  TTGA
                                ||||||||  |||  ||||
                                CTACGGCG  TGG  AACT
                                    ACA  AG
GAM1130 GEMIN5  5' TAGATACCAGCTGTGTTG   29291     GCC     A_
                                TAGAT  GCCAGCT  GTTG
                                |||||  |||||||  ||||
                                ATCTA  TGGTCGA  CAAC
                                   ___     CA
GAM1130 IL1RAP  3' TAGATGCCGTCAGGCTAG   29292       C  _
                                TAGATGCCG CAG CTAG
                                ||||||||| ||| ||||
                                ATCTACGGC GTC GATC
                                     A  C
GAM1130 PIR51   3' GATCAGAAGCTAGTTGA    29293    GC  CC
                                GAT  CG  AGCTAGTTGA
                                |||  ||  ||||||||||
                                CTA  GT  TCGATCAACT
                                  __ CT
GAM1130 TPS1    3' TAGATGCCAGGCCGGTTG   29294       CCA  TA
                                TAGATGCCG  GC  GTTG
                                |||||||||  ||  ||||
                                ATCTACGGT  CG  CAAC
                                     C__ GC
GAM1130 DKFZP434C1715 3' GATGCCAAACTCTAGTTGA  29295       CCAG
                                GATGCCG   CTAGTTGA
                                |||||||   ||||||||
                                CTACGGT   GATCAACT
                                    TTGA
GAM1130 FLJ12684 5' AGATGTTTCAGCTAGTTG   29296     CCGC
                                AGATG   CAGCTAGTTG
                                |||||   ||||||||||
                                TCTAC   GTCGATCAAC
                                   AAA_
GAM1130 FLJ14213 3' TAGATACAGGCCAGTTGGTTG 29297       C_   CTA
                                TAGATGC  GCCAG  GTTG
                                |||||||  |||||  ||||
                                ATCTATG  CGGTC  CAAC
                                    TC    AAC
GAM1130 GMPPA   5' TAGATGCCGCAGTTG      29298        CAGCT
                                TAGATGCCGC    AGTTG
                                ||||||||||    |||||
                                ATCTACGGCG    TCAAC
                                      _____
GAM1130 KIAA0603 3' TAGATGCAACATGCTAGTTG  29299       C  CA
                                TAGATGC GC  GCTAGTTG
                                |||||||  ||  ||||||||
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                                ATCTACG TG  CGATCAAC
                                    T  TA
GAM1130  KIAA0819  3'  CAGATGCCGCTGTGGTCAACTA 29300          __________  CTAG
              GCT                   AGATGCCGC       CAG    TT
                                    |||||||||       |||    ||
                                    TCTACGGCG       GTT    GA
                                        ACACCIIIA   GATC
GAM1130  KIAA1497  5'  TAGATGCCTGCTAGTC     29301        GCCA
                                    TAGATGCC    GCTAGTT
                                    ||||||||    |||||||
                                    ATCTACGG    CGATCAG
                                        A___
GAM1130  LOC149421 5'  TAGATGCCACCACGGCTGA   29302           GCTA
                                    TAGATGCCGCCA    GTTGA
                                    ||||||||||||    |||||
                                    ATCTACGGTGGT    CGACT
                                          GC__
GAM1130  LOC219690 3'  CAGATGCCGCTTTGGTCAACTA 29303          __________  CTAG
              GCT                   AGATGCCGC       CAG    TT
                                    |||||||||       |||    ||
                                    TCTACGGCG       GTT    GA
                                        AAACCIIIA   GATC
GAM1130  LOC221922 5'  AGATGCCGCCAGGTATGTG   29304           C  GT
                                    AGATGCCGCCAG TA  TG
                                    ||||||||||||  ||  ||
                                    TCTACGGCGGTC AT  AC
                                          C  AC
GAM1131  DKFZP566G1424 5'  GGGGTTACAGCTGTTCA     29307         A  AAA
                                    GGGGTTACA CT   TTCG
                                    |||||||||  ||   ||||
                                    CCCCAATGT GA   AAGT
                                        C  C__
GAM1131  HSJ1     3'  GGGGGTCTGCAGCTGGTCCA   29308        A_  A  AAA
                                    GGGGGTT  CA CT   TTCG
                                    |||||||  ||  ||   ||||
                                    CCCCCAG  GT GA   AGGT
                                        AC  C  CC_
GAM1131  KIAA0844  3'  GGGGGTTATAATAAAATTC   29309         C  CT
                                    GGGGGTTA AA  AAATTC
                                    ||||||||  ||  ||||||
                                    CCCCCAAT TT  TTTAAG
                                        A  AT
GAM1132  MBTPS1   3'  TCTATGTTGTTCCTCATGA   29312      A       G  GC
                                    TCTG TGTTGTTC CT  TATGA
                                    ||||  ||||||||  ||  |||||
                                    AGAT ACAACAAG GA  GTACT
                                      _       _  __
GAM1132  TFPI2    3'  TCTTATGTTGTTTCAGTTATGA 29313     G       _  CTGC
              T                      TCT ATGTTGTT CG    TATGAT
                                    |||  ||||||||  ||    ||||||
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                                AGA TACAACAA GT    ATACTA
                                  A       A  CA__
GAM1132  KIAA1155  3'  TGATGCTGCAGTGAGCTATG   29314         TCGCT
                                TGATGTTGT     GCTATG
                                |||||||||     ||||||
                                ACTACGACG     CGATAC
                                     TCACT
GAM1132  PRO1600   3'  GATGTGTTTGCTATGA      29315       T   CGC
                                GATGT GTT   TGCTATGA
                                ||||| |||   ||||||||
                                CTACA CAA   ACGATACT
                                  _   ____
GAM1132  SSB-4     3'  TCTGATATCCCACTGCTGTGAT 29316         GT       A
                                TCTGATGTT  TCGCTGCT TGAT
                                |||||||||  |||||||| ||||
                                AGACTATAG  GGTGACGA ACTA
                                     __       C
GAM1132  LOC142964 5'  TGATGCCGAAGTTGCTATG    29317         TTCGC
                                TGATGTTG     TGCTATG
                                ||||||||     |||||||
                                ACTACGGC     ACGATAC
                                     TTCA_
GAM1132  LOC152313 3'  TGGTGCTGTTCTCATGA      29318    A       GCTGC
                                TG TGTTGTTC     TATGA
                                || ||||||||     |||||
                                AC ACGACAAG     GTACT
                                  C       A_____
GAM1132  LOC152804 3'  TGAGGTTGCAGTGAGCTATGAT 29319     T     TCGCT
                                TGA GTTGT     GCTATGAT
                                ||| |||||     ||||||||
                                ACT CAACG     CGATACTA
                                  C     TCACT
GAM1132  LOC51134  3'  TGATGTTGTTCCTCCTGC     29320          G__
                                TGATGTTGTTC   CTGC
                                ||||||||||   ||||
                                ACTACAACAAG   GACG
                                      GAG
GAM1132  LOC51277  3'  TCTGATGTTGTTTGCTTCCAT  29321           C   G
                                TCTGATGTTGTT GCT CTAT
                                |||||||||||| ||| ||||
                                AGACTACAACAA CGA GGTA
                                      A   A
GAM1133  DLX2      3'  TGAGTATTTTTATACAAA     29324          __
                                TGAGTATTTT  TACAAA
                                ||||||||||  ||||||
                                ACTCATAAAA  ATGTTT
                                      AT
GAM1133  PDE4D     3'  TGGGTATCTTTACAACAC     29325     A        AAAAT
                                TG GTATTTTTACA     GCAT
                                || ||||||||||     ||||
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                                AC CATAGAAATGT     TGTG
                                 C         _____
GAM1133  C20orf9   3'  TGAGTATTACAGAAGATGCATA 29326        TTT   _  A
                                TGAGTAT   TACA AA ATGCATA
                                |||||||   |||| || |||||||
                                ACTCATA   ATGT TT TACGTAT
                                    ___    C  C
GAM1133  EML4      3'  TGAGTATTTTCAACGTGGTGCA 29327           CAAAAA
                TA                   TGAGTATTTTTA     TGCATA
                                |||||||||||||     ||||||
                                ACTCATAAAAGT     ACGTAT
                                       TGCACC
GAM1133  FLJ10512  3'  TGAGTAATGAAGGAAAATGCAT 29328       TTTTTACA
                                TGAGTA       AAAATGCAT
                                ||||||       |||||||||
                                ACTCAT       TTTTACGTA
                                    TACTTCC_
GAM1133  KLF12     3'  TGAGTATATTTACAATACATA  29329       T     AAA
                                TGAGTAT TTTACA   ATGCATA
                                ||||||| ||||||   |||||||
                                ACTCATA AAATGT   TATGTAT
                                     T     ___
GAM1133  MOT8      3'  TGAGCATTTTTACAAAAATA   29330
                                TGAGTATTTTTACAAAAATG
                                ||||||||||||||||||||
                                ACTCGTAAAAATGTTTTTAT

GAM1133  QKI       3'  TGAGTATTTATATGCAC     29331          TTACAAAA
                                TGAGTATTT       ATGCAT
                                |||||||||       ||||||
                                ACTCATAAA       TACGTG
                                      TA_______
GAM1133  WSB1      3'  TGAGCATTTTACATAATGCATA 29332          T   AA
                                TGAGTATTTT ACA  AATGCATA
                                |||||||||| |||  ||||||||
                                ACTCGTAAAA TGT  TTACGTAT
                                      _   A_
GAM1133  WSB1      3'  TGAGCATTTTACATAATGCATA 29332          T   AA
                                TGAGTATTTT ACA  AATGCATA
                                |||||||||| |||  ||||||||
                                ACTCGTAAAA TGT  TTACGTAT
                                      _   A_
GAM1133  LOC113523 3'  TAAGTATTTTTACACCCTG   29333            AAAA
                                TGAGTATTTTTACA   TG
                                ||||||||||||||   ||
                                ATTCATAAAAATGT   AC
                                       GGG_
GAM1133  LOC153139 3'  TGGATAAAACAAAAATGCATA  29334    AG  TTTTT
                                TG  TA    ACAAAAATGCATA
                                ||  ||    ||||||||||||
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                                AC  AT    TGTTTTTACGTAT
                                 CT  TT___
GAM1133  LOC154184 3'  TGGATAAAACAAAAATGCATA  29334    AG  TTTTT
                                TG  TA    ACAAAAATGCATA
                                ||  ||    |||||||||||||
                                AC  AT    TGTTTTTACGTAT
                                 CT  TT___
GAM1133  LOC220992 3'  GAGTATTTCTGTTAAATGCATA 29335         ACAA
                                GAGTATTTTT    AAATGCATA
                                ||||||||||    |||||||||
                                CTCATAAAGA    TTTACGTAT
                                      CAA_
GAM1134  ANKTM1    3'  TATTATGTAATTAACAAGCA   29338         A  T
                                TATTATGTGA TG TAAGCA
                                |||||||||| || ||||||
                                ATAATACATT AT GTTCGT
                                      A  T
GAM1134  BCL11A    3'  TATTGTGTCAATGTTAAG    29339     A   G
                                TATT TGT AATGTTAAG
                                |||| ||| |||||||||
                                ATAA ACA TTACAATTC
                                  C   G
GAM1134  BCL11A    3'  TATTGTGTCAATGTTAAG    29339     A   G
                                TATT TGT AATGTTAAG
                                |||| ||| |||||||||
                                ATAA ACA TTACAATTC
                                  C   G
GAM1134  C4BPA     3'  TGTGTGTTGAAAAGCAAAAA   29340     AA_  TT
                                TGTG   TG  AAGCAAAAA
                                ||||   ||  |||||||||
                                ACAC   AC  TTCGTTTTT
                                  ACA  TT
GAM1134  CA1       3'  TATTATTTGAATTAAGCA    29341       G   AT
                                TATTAT TGA  GTTAAGCA
                                |||||| |||  ||||||||
                                ATAATA ACT  TAATTCGT
                                   A  __
GAM1134  CYP7A1    3'  TATTTGTAAAATAAGCAAAAA  29342     A     TGT
                                TATT TGTGAA   TAAGCAAAAA
                                |||| ||||||   ||||||||||
                                ATAA ACATTT   ATTCGTTTTT
                                  _     T__
GAM1134  VIL2      3'  TATTCTAAAACTGTTAAGCAAA 29343      ATGTGAA
              AA                  TATT      TGTTAAGCAAAAA
                                ||||      ||||||||||||||
                                ATAA      ACAATTCGTTTTT
                                  GATTTTG
GAM1134  C15orf15  3'  TATTATGTAGATGGCAATGCA  29344         A   T  _
                                TATTATGTG ATG TAA GCA
                                ||||||||| ||| ||| |||
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                                ATAATACAT TAC GTT CGT
                                     C   C   A
GAM1134  dA141H5.1 3'  TATTGATGTGAAAGCAAAA   29345     _      TGTTA
                                TATT ATGTGAA     AGCAAAA
                                |||| |||||||     |||||||
                                ATAA TACACTT     TCGTTTT
                                  C      _____
GAM1134  DKFZp761K1824 3'  CATTATGTGACAGCAAAA    29346          ATGTTA
                                TATTATGTGA      AGCAAAA
                                ||||||||||      |||||||
                                GTAATACACT      TCGTTTT
                                     G_____
GAM1134  HRH4     3'  TATTATTGAATGTTAAA     29347       G
                                TATTAT TGAATGTTAAG
                                |||||| ||||||||||
                                ATAATA ACTTACAATTT

                                  _
GAM1134  HSPC154   5'  CATTACATGGGGTGTTAGGCAA 29348          AA_     A
              AAA                   TATTATGTG   TGTTA GCAAAAA
                                |||||||||   ||||| |||||||
                                GTAATGTAC   ACAAT CGTTTTT
                                     CCC    C
GAM1134  KIAA1016  3'  TACTATGTGATGTGGCAAAAA  29349          A   TAA
                                TATTATGTGA TGT   GCAAAAA
                                |||||||||| |||   |||||||
                                ATGATACACT ACA   CGTTTTT
                                     _   C__
GAM1134  KIAA1795  3'  TATTATGTAGGATGCCAAA   29350         A_
                                TATTATGTG  ATGTTAAG
                                |||||||||  ||||||||
                                ATAATACAT  TACGGTTT
                                     CC
GAM1134  PRO0456   5'  TTATGTGAGTTTTATCGCAA   29351         ATG   A_
                                TTATGTGA   TTA  GCAA
                                ||||||||   |||  ||||
                                AATACACT   AAT  CGTT
                                     CAA   AG
GAM1134  USP24     3'  ATTATGTTTTAAGCAAAA    29352        GAATG
                                ATTATGT    TTAAGCAAAA
                                |||||||    ||||||||||
                                TAATACA    AATTCGTTTT
                                   A_____
GAM1134  LOC145891 3'  TATGTGTGTGTCTGAGCAAA   29353       AA    A_
                                TATGTG  TGTT  AGCAAA
                                ||||||  ||||  ||||||
                                ATACAC  ACAG  TCGTTT
                                   AC    AC
GAM1134  LOC201895 3'  TACTATGTGGATTATATCAGCA 29354          A___      A
              AA                    TATTATGTG    ATGTTA GCAAA
                                |||||||||    |||||| |||||
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                                ATGATACAC   TATAGT CGTTT
                                     CTAA    _
GAM1134 LOC257017 5' TATTATGTGATAAAGGCAAAA 29355        A  TTAA
                                TATTATGTGA TG   GCAAAA
                                |||||||||| ||   ||||||
                                ATAATACACT AT   CGTTTT
                                     _ TTC_
GAM1134 LOC92710 3' TATGTGATCTTGAGCAAAA  29356      A G  A
                                TATGTGA T TT AGCAAAA
                                ||||||| | || |||||||
                                ATACACT A AA TCGTTTT
                                    _ G  C
GAM1135 GRB10   5' TATCACATTTCCACGGCTGG  29359      C   AGAAA
                                TATCACGT TCTA    GCTGG
                                |||||||| ||||    |||||
                                ATAGTGTA AGGT    CGACC
                                     A   GC___
GAM1135 RP2     3' TATCACCTTTTTAAAAACTGCT 29360     GTCTC    A_
           GG                    TATCAC    TAAGAA  GCTGG
                                |||||||   ||||||  |||||
                                ATAGTG    ATTTTT  CGACC
                                   GAAAA     GA
GAM1135 WFDC1   3' TCCTGTCTCTAAGCATCTCTGG 29361    AC       AAAG_
                                TC  GTCTCTAAG    CTGG
                                ||  |||||||||    ||||
                                AG  CAGAGATTC    GACC
                                 GA       GTAGA
GAM1135 FLJ20898 3' CGCTAACCAGGAAAGCTGG   29362    CT_   A
                                CGT   CTA GAAAGCTGG
                                |||   ||| |||||||||
                                GCG   GGT CTTTCGACC
                                  ATT   C
GAM1135 KIAA1054 3' TATCGCGTCTCCAAGGTCTG  29363     A        AAAG
                                TATC CGTCTCTAAG    CTG
                                |||| ||||||||||    |||
                                ATAG GCAGAGGTTC    GAC
                                  C        CA__
GAM1135 KIAA1243 3' TACCACGTCTCTAAGGCCA   29364           AAA  TG
                                TATCACGTCTCTAAG   GC  G
                                ||||||||||||||   ||  |
                                ATGGTGCAGAGATTC   CG  T
                                       ___  GT
GAM1135 RIN3    5' TCAGCGTTCTCTAAGGGAGCTG 29365    _  _     AA
           G                     TCA CGT CTCTAAG  AGCTGG
                                ||| ||| |||||||  ||||||
                                AGT GCA GAGATTC  TCGACC
                                  C  A      CC
GAM1135 LOC115330 3' TCACGTCTCCCCAGGAGGGCTG 29366         AA__  AA
           G                     TCACGTCTCT    GA  GCTGG
                                ||||||||||   ||  |||||
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                                AGTGCAGAGG   CT  CGACC
                                     GGTC  CC
GAM1136  CD2AP    3'  TCAGGTGAGAAAGCTGG     29369     C  CTCTA
                                TCA GT    AGAAAGCTGG
                                ||| ||    ||||||||||
                                AGT CA    TCTTTCGACC
                                  C  C____
GAM1136  WFDC1    3'  TCCTGTCTCTAAGCATCTCTGG 29361    AC       AAAG_
                                TC  GTCTCTAAG    CTGG
                                ||  |||||||||    ||||
                                AG  CAGAGATTC    GACC
                                 GA       GTAGA
GAM1136  FLJ14641 5'  ATCTGACATGAGGGAAGCTGGA 29370     C_  A  ___
                                GTCT  TA GA   AAGCTGGA
                                ||||  || ||   ||||||||
                                TAGA  GT CT   TTCGACCT
                                  CT  A  CCC
GAM1136  FLJ20898 3'  CGCTAACCAGGAAAGCTGGA   29371     CT_   A
                                CGT   CTA GAAAGCTGGA
                                |||   ||| ||||||||||
                                GCG   GGT CTTTCGACCT
                                  ATT   C
GAM1136  FLJ31168 3'  CCACGTTGGGGAAGCTGGA    29372       CTCTAA   A
                                TCACGT     GAA GCTGGA
                                ||||||     ||| ||||||
                                GGTGCA     CTT CGACCT
                                   ACCC__   _
GAM1136  RIN3     5'  TCAGCGTTCTCTAAGGGAGCTG 29365     _   _      AA
           G                     TCA CGT CTCTAAG  AGCTGG
                                ||| ||| |||||||  ||||||
                                AGT GCA GAGATTC  TCGACC
                                  C   A      CC
GAM1136  LOC115330 3'  TCACGTCTCCCCAGGAGGGCTG 29366          AA__  AA
           G                     TCACGTCTCT    GA  GCTGG
                                ||||||||||    ||  |||||
                                AGTGCAGAGG    CT  CGACC
                                     GGTC  CC
GAM1136  LOC96597  5'  TATCTTGTCTCTAAGAGCTCCA 29373     AC        AAG TG
           GA                    TATC  GTCTCTAAGA   C  GA
                                ||||  ||||||||||   |  ||
                                ATAG  CAGAGATTCT   G  CT
                                  AA         CGA GT
GAM1137  B29      3'  TGTTAGCTTTCTCATCTAT    29376      TA  A
                                TGTT  TT TCTCATCTAT
                                ||||  ||  ||||||||||
                                ACAA  GA AGAGTAGATA
                                  TC  A
GAM1137  BAZ2B    3'  CACATTGCTGGTCTCAT     29377         TATTA
                                TACATTGTT    TCTCAT
                                |||||||||    ||||||
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                                GTGTAACGA    AGAGTA
                                     CC___
GAM1137 CCNA1    3' TACATTTTTAAAATGTCATCTA 29378      G   TT  C
             T                    TACATT TTTA  AT TCATCTAT
                                  ||||||| ||||  || ||||||||
                                  ATGTAA AAAT  TA AGTAGATA
                                     _   TT  C
GAM1137 PCDHGA8  5' TACATTGTTTATATTTTTCTAT 29379          TATCTCA
                                  TACATTGTTTAT      TCTAT
                                  ||||||||||||      |||||
                                  ATGTAACAAATA      AGATA
                                        TAAAA__
GAM1137 PCDHGA8  5' TACATTGTTTATATTTTTCTAT 29379          TATCTCA
                                  TACATTGTTTAT      TCTAT
                                  ||||||||||||      |||||
                                  ATGTAACAAATA      AGATA
                                        TAAAA__
GAM1137 PRKY     3' TGATTGTTTCACGATCATCTAT 29380    C      ATTATC
                                  A ATTGTTT     TCATCTAT
                                  | |||||||     ||||||||
                                  A TAACAAA     AGTAGATA
                                   C      GTGCT_
GAM1137 KIAA0961 3' ACGTTGTCAGTCTCATCTAT   29381    A    TATTA
                                  AC TTGTT     TCTCATCTAT
                                  || |||||     ||||||||||
                                  TG AACAG     AGAGTAGATA
                                   C     TC___
GAM1137 PRO2893  3' TACATTATTTATTATTAGTCAT 29382            C__
                                  TACATTGTTTATTAT   TCAT
                                  ||||||||||||||   ||||
                                  ATGTAATAAATAATA   AGTA
                                           ATC
GAM1137 ZBRK1    3' ACACCAATTATCTCATCT    29383       TTT
                                  ACATTG   ATTATCTCATCT
                                  ||||||   ||||||||||||
                                  TGTGGT   TAATAGAGTAGA
                                     ___
GAM1137 LOC147711 3' TGTGTACTGTGTCTCATCTAT  29384     T   A__
                                  TGT TATT   TCTCATCTAT
                                  ||| ||||   ||||||||||
                                  ACA ATGA   AGAGTAGATA
                                    C    CAC
GAM1137 LOC158401 5' TACATAGTTTATTATTTC    29385      T       C
                                  TACAT GTTTATTAT TC
                                  ||||| ||||||||| ||
                                  ATGTA CAAATAATA AG
                                     T       A
GAM1137 LOC200931 3' ACATTGTTCACCTTCATCT   29386          ATC
                                  ACATTGTTTATT   TCATCT
                                  ||||||||||||   ||||||
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                                TGTAACAAGTGG  AGTAGA
                                      A__
GAM1138 RHCE    3' TGTCATGAGCGTTTCTCAC  29389      AC  ATGCGA
                                TGTCATGA CGT   TCAC
                                |||||||| |||    ||||
                                ACAGTACT GCA   AGTG
                                    C_  AAG___
GAM1138 RHCE    3' TGTCATGAGCGTTTCTCAC  29389      AC  ATGCGA
                                TGTCATGA CGT   TCAC
                                |||||||| |||    ||||
                                ACAGTACT GCA   AGTG
                                    C_  AAG___
GAM1138 RHCE    3' TGTCATGAGCGTTTCTCAC  29389      AC  ATGCGA
                                TGTCATGA CGT   TCAC
                                |||||||| |||    ||||
                                ACAGTACT GCA   AGTG
                                    C_  AAG___
GAM1138 RHCE    3' TGTCATGAGCGTTTCTCAC  29389      AC  ATGCGA
                                TGTCATGA CGT   TCAC
                                |||||||| |||    ||||
                                ACAGTACT GCA   AGTG
                                    C_  AAG___
GAM1138 RHD     3' TGTCATGAGCGTTTCTCAC  29389      AC  ATGCGA
                                TGTCATGA CGT   TCAC
                                |||||||| |||    ||||
                                ACAGTACT GCA   AGTG
                                    C_  AAG___
GAM1138 RHD     3' TGTCATGAGCGTTTCTCAC  29389      AC  ATGCGA
                                TGTCATGA CGT   TCAC
                                |||||||| |||    ||||
                                ACAGTACT GCA   AGTG
                                    C_  AAG___
GAM1138 C5orf4  3' TGTCATGAATTGAGACC    29390      CCGTA  C
                                TGTCATGAA   TG GATC
                                |||||||||   || ||||
                                ACAGTACTT   AC CTGG
                                    A____  T
GAM1138 C5orf4  3' TGTCATGAATTGAGACC    29390      CCGTA  C
                                TGTCATGAA   TG GATC
                                |||||||||   || ||||
                                ACAGTACTT   AC CTGG
                                    A____  T
GAM1138 C6.1A   3' TGTTATATAAATGCGATCA  29391    C  AACCGT
                                TGT ATG    ATGCGATCA
                                ||| |||    |||||||||
                                ACA TAT    TACGCTAGT
                                  A  ATT___
GAM1138 FLJ11040 3' TGTTATGAACCATGCAAC  29392    C     GT
                                TGT ATGAACC  ATGCGAT
                                ||| |||||||  |||||||
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                                ACA TACTTGG  TACGTTG
                                  A     __
GAM1138  LOC201252 3'  TGTCATGACCGTGTGCG     29393        A   A
                                TGTCATGA CCGT TGCG
                                |||||||| |||| ||||
                                ACAGTACT GGCA ACGC
                                     _   C
GAM1138  LOC91050  3'  TGTCATGAGCCTGGTATA    29394        A __
                                TGTCATGA CC  GTATG
                                |||||||| ||  |||||
                                ACAGTACT GG  CATAT
                                     C  AC
GAM1139  AP1G1     3'  ATACAGAGTCTGATC       29397        GGT
                                ATACGGAG   TCTGATC
                                ||||||||   |||||||
                                TATGTCTC   AGACTAG
                                     ___
GAM1139  MADD      3'  TAATACGGAGTAGCAGAT    29398         _  TCT
                                TAATACGGAG GGT   GAT
                                |||||||||| |||   |||
                                ATTATGCCTC TCG   CTA
                                      A  T__
GAM1139  PGD       3'  ATACAGAGGTTCCAGTTGATC 29399         G  ___
                                ATACGGAGG TTC   TGATC
                                ||||||||| |||   |||||
                                TATGTCTCC AGG   ACTAG
                                     A   TCA
GAM1139  FIGNL1    3'  TAATACAGAGATGCCTTGAT   29400          _ TC
                                TAATACGGAGG GT  TGAT
                                |||||||||| ||  ||||
                                ATTATGTCTCT CG  ACTA
                                      A  GA
GAM1139  FLJ22969  3'  TAATGCAGGGGGCCACTG    29401      A  A   _
                                TAAT CGG GGGTT CTG
                                |||| ||| ||||| |||
                                ATTA GTC CCCGG GAC
                                  C  C    T
GAM1139  LOC145813 3'  TAACATGGCCATTCTGATC    29402      C  AGG
                                TAATA GG   GTTCTGATC
                                ||||| ||   |||||||||
                                ATTGT CC   TAAGACTAG
                                   A  GG_
GAM1140  CHIC2     5'  CCGCGGAGTTCGCTGTCGGC   29405   _      A   ATC
                                CC CGGAGTTC CTGT   GT
                                || |||||||| ||||   ||
                                GG GCCTCAAG GACA   CG
                                 C       C   GC_
GAM1140  DKFZP566D1346 3'  CCCATTTCACTGTATCGTA   29406     GGAG
                                CCC    TTCACTGTATCGTA
                                |||    ||||||||||||||
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                                GGG   AAGTGACATAGCAT
                                  TA__
GAM1140 GALNT12  5' CCCCGGAGTTCCCCAGGTAT  29407          A __
                                CCCCGGAGTTC CT  GTAT
                                |||||||||| ||  ||||
                                GGGGCCTCAAG GG  CATA
                                      G  TC
GAM1140 TRIM31   5' CCCCGGAGTCCACTGTGGATAC 29408             ATC
           T                    CCCCGGAGTTCACTGT   GTACT
                                |||||||||||||||   |||||
                                GGGGCCTCAGGTGACA   TATGA
                                         CC_
GAM1140 LOC151068 5' GGATTCACTGTTTCTGTGCT  29409    G      A _ A
                                GGA TTCACTGT TC GT CT
                                ||| |||||||| || || ||
                                CCT AAGTGACA AG CA GA
                                  _      A  A  C
GAM1140 LOC221037 5' GGTGGTTCATTGACCACACT  29410    A_    C  T
                                GG  GTTCA TG ATCGTACT
                                ||  |||||| || ||||||||
                                CC  CAAGT AC TGGTGTGA
                                 AC    A  _
GAM1140 LOC256158 5' CCCGGAGTCCGACAGCCGTGCT 29411          _ T  AT   A
                                CCCGGAGTTC AC GT  CGT CT
                                |||||||||| || ||  ||| ||
                                GGGCCTCAGG TG CG  GCA GA
                                      C  T __   C
GAM1140 LOC257608 5' CCCCGGAGTCCACTGTGGATAC 29408             ATC
           T                    CCCCGGAGTTCACTGT   GTACT
                                |||||||||||||||   |||||
                                GGGGCCTCAGGTGACA   TATGA
                                         CC_
GAM1141 IL18R1   3' TCTTTTTAGTCATCCAGTT   29414      A      TTC
                                TCTTT TTAGTTAT   CCAGTT
                                ||||| ||||||||   ||||||
                                AGAAA AATCAGTA   GGTCAA
                                  _      ___
GAM1141 PDE4D    3' TCTTTATTAGTGCAGT     29415          TATTTCC
                                TCTTTATTAGT      CAGT
                                ||||||||||       ||||
                                AGAAATAATCA      GTCA
                                      C_______
GAM1141 SMURF1   3' TTATATAGTTATTTTCCAGTT  29416     _       C
                                TTAT TAGTTATTT CCAGTT
                                |||| ||||||||| ||||||
                                AATA ATCAATAAA GGTCAA
                                  T       A
GAM1141 FLJ10769 3' TCTTCATTTCCGTCTTCCCAGT 29417        AGTTA
           TA                     TCTTTATT    TTTCCCAGTTA
                                  ||||||||    ||||||||||
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                                AGAAGTAA    GAAGGGTCAAT
                                    AGGCA
GAM1141 KIAA0303 5' TCCTTATTGAGTCCCAGTT   29418       _ TTATT
                                TCTTTATT AG    TCCCAGTT
                                |||||||| ||    ||||||||
                                AGGAATAA TC    AGGGTCAA
                                    C _____
GAM1141 KIAA0318 3' TCTTTATCGGTATCTTCAGTT 29419       TA T   CC
                                TCTTTAT  GT ATTT  CAGTT
                                |||||||  || ||||  |||||
                                AGAAATA  CA TAGA  GTCAA
                                    GC _   A_
GAM1141 NDRG4    3' TCTTTATTAGTTTTTCAGCACA 29420          A   C___
            GTTA                TCTTTATTAGTT TTTC   CAGTTA
                                |||||||||||| ||||   ||||||
                                AGAAATAATCAA AAAG   GTCAAT
                                      _   TCGT
GAM1141 NDRG4    3' TCTTTATTAGTTTTTCAGCACA 29420          A   C___
            GTTA                TCTTTATTAGTT TTTC   CAGTTA
                                |||||||||||| ||||   ||||||
                                AGAAATAATCAA AAAG   GTCAAT
                                      _   TCGT
GAM1141 RNAH     3' TCTATATTTTATTTCCCAGTTA 29421     T   AG
                                TCT TATT  TTATTTCCCAGTTA
                                ||| ||||  ||||||||||||||
                                AGA ATAA  AATAAAGGGTCAAT
                                  T   __
GAM1141 ULK2     3' TCTTTGGTAGTCACCAGTT   29422      AT    TTTC
                                TCTTT  TAGTTA   CCAGTT
                                |||||  ||||||   ||||||
                                AGAAA  ATCAGT   GGTCAA
                                   CC    _____
GAM1141 LOC220980 5' CTCAGAAAGTTGTTTCTCAGTT 29423    TATT   A   C
                                CTT   AGTT TTTC CAGTT
                                |||   |||| |||| |||||
                                GAG   TCAA AAAG GTCAA
                                  TCTT   C   A
GAM1141 LOC55580 3' TCCTTATCCCTTTTCCCAGTT  29424       AGTTA
                                TCTTTATT    TTTCCCAGTT
                                ||||||||    ||||||||||
                                AGGAATAG    AAAGGGTCAA
                                    GGA__
GAM1142 FLJ11186 3' TTCATGGAACCTGGAAGACCTG 29427     CCGTC   C
                                TTCG    GCC GGAAGACCTG
                                ||||    ||| ||||||||||
                                AAGT    TGG CCTTCTGGAC
                                  ACCT_   A
GAM1142 FLJ21709 3' TCCGCTGTCGCCCAGCAGGTTT 29428      C       A  ACC
            GC                  TTCGC GTCGCCCGG AG   TGC
                                ||||| ||||||||| ||   |||
```

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                                AGGCG CAGCGGGTC TC   ACG
                                  A       G  CAA
GAM1142  KIAA0450  3'  CTCGCCGTTGCACGGCCGAGGC 29429       C  C   AA __
           CTGC                  TTCGCCGT GC CGG  GA  CCTGC
                                 |||||||| || |||  ||  |||||
                                 GAGCGGCA CG GCC  CT  GGACG
                                    A  T   GG  CC
GAM1142  KIAA1878  3'  TTCGTTTCGCCTCTCAGACCTG 29430     CCG    CGGA
           C                    TTCG   TCGCC    AGACCTGC
                                ||||   |||||    ||||||||
                                AAGC   AGCGG    TCTGGACG
                                  AA_    AGAG
GAM1142  MAPK8IP3  3'  GCCTCGCCCGACACCCTGC   29431    G      AAGA
                                GCC TCGCCCGG    CCTGC
                                ||| ||||||||    |||||
                                CGG AGCGGGCT    GGACG
                                  _      GTG_
GAM1142  LOC155435 3'  TCGCAGGGTCTGGAAGACCTGC 29432     C__   GCCC
                                TCGC   GTC    GGAAGACCTGC
                                ||||   |||    ||||||||||
                                AGCG   CAG    CCTTCTGGACG
                                  TCC   A___
GAM1142  LOC219513 5'  TTCGCCGTCTCCCATCCTTGC  29433       G   GAAGA  _
                                TTCGCCGTC CCCG    CCT GC
                                ||||||||| ||||    ||| ||
                                AAGCGGCAG GGGT    GGA CG
                                    A   A____   A
GAM1142  LOC90719  5'  CTCGCCGTCGTCTGGGCGCTCT 29434        CCC  AAGAC
           GC                   TTCGCCGTCG   GG    CTGC
                                ||||||||||   ||    ||||
                                GAGCGGCAGC   CC    GACG
                                     AGA  CGCGA
GAM1143  ABCC1    5'  GGCGGCGGCGGGCACCGGGCGG 29437     A    AGGA  _
           CG                   GGCGG GGCGG    CGG CGGCG
                                ||||| |||||    ||| |||||
                                CCGCC CCGCC    GCC GCCGC
                                  G    CGTG   C
GAM1143  ABCC1    5'  GGCGGCGGCGGGCACCGGGCGG 29437     A    AGGA  _
           CG                   GGCGG GGCGG    CGG CGGCG
                                ||||| |||||    ||| |||||
                                CCGCC CCGCC    GCC GCCGC
                                  G    CGTG   C
GAM1143  ABCC1    5'  GGCGGCGGCGGGCACCGGGCGG 29437     A    AGGA  _
           CG                   GGCGG GGCGG    CGG CGGCG
                                ||||| |||||    ||| |||||
                                CCGCC CCGCC    GCC GCCGC
                                  G    CGTG   C
GAM1143  ABCC1    5'  GGCGGCGGCGGGCACCGGGCGG 29437     A    AGGA  _
           CG                   GGCGG GGCGG    CGG CGGCG
                                ||||| |||||    ||| |||||
```

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                                CCGCC CCGCC    GCC GCCGC
                                  G    CGTG   C
GAM1143 ABCC1    5' GGCGGCGGCGGGCACCGGGCGG 29437      A    AGGA  _
            CG                    GGCGG GGCGG    CGG CGGCG
                                |||||  |||||    |||  |||||
                                CCGCC CCGCC    GCC GCCGC
                                  G    CGTG   C
GAM1143 ABCC1    5' GGCGGCGGCGGGCACCGGGCGG 29437      A    AGGA  _
            CG                    GGCGG GGCGG    CGG CGGCG
                                |||||  |||||    |||  |||||
                                CCGCC CCGCC    GCC GCCGC
                                  G    CGTG   C
GAM1143 ACTN2    5' AGGCGGCGGGCGGCGGGCGGCG 29438       A_    A  A
                                AGGCGG  GGCGG GG CGGCG
                                ||||||  |||||  ||  |||||
                                TCCGCC  CCGCC CC GCCGC
                                   GC    G  C
GAM1143 ADRA2A   5' GCGGAGCTCGGGGACGGCGGCG 29439       G_   A
                                GCGGAG  CGG GGACGGCGGCG
                                ||||||  |||  ||||||||||
                                CGCCTC  GCC CCTGCCGCCGC
                                   GA   _
GAM1143 AF5Q31   5' AGGCGGCGTCGGCGGCGGC   29440     GGA   GA  A
                                AGGC   GGCG  GG CGGCGGC
                                ||||   ||||  ||  |||||||
                                TCCG   CCGC  CC GCCGCCG
                                  ___    AG  _
GAM1143 AMPH     5' AGCGGGGCTGGCGGCGGC    29441      A   GGA  A
                                GGCGG GGC   GG CGGCGGC
                                |||||  |||   ||  |||||||
                                TCGCC CCG   CC GCCGCCG
                                  _   A__  _
GAM1143 AP1M1    5' AGCGGCCGAGGGCGGTGGC   29442     GGA   G    A   C
                                GGC   GGC GAGG CGG GGC
                                |||   |||  ||||  |||  |||
                                TCG   CCG CTCC GCC CCG
                                  ___   G    C   A
GAM1143 AP2B1    5' AGGCGAGGGCGGGGGTGGCGGC 29443      GA    A  AC      III
            GC                    GGCG  GGCGG GG  GGCGGCG   C
                                ||||  |||||  ||  |||||||   |
                                CCGC  CCGCC CC  CCGCCGC   G
                                  TC    _  CA      III
GAM1143 APOBEC3B 5' AGGCGGGCGGCGGAGATGG   29444       A_      AC
                                AGGCGG  GGCGGAGG  GG
                                ||||||  ||||||||  ||
                                TCCGCC  CCGCCTCT  CC
                                   CG       A_
GAM1143 AQP3     5' GGCGGGGCAGGCGGCGGC    29445      A   GG   A
                                GGCGG GGC  AGG CGGCGGC
                                |||||  |||  |||  |||||||
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                                CCGCC CCG  TCC GCCGCCG
                                  _  __  _
GAM1143 ATP12A   5' GGTGGAGATACCGGCGGCGGCG 29446    C    CGGA  A
                                GG GGAGG   GG CGGCGGCG
                                || |||||   || ||||||||
                                CC CCTCT   CC GCCGCCGC
                                 A    ATGG  _
GAM1143 B4GALT7  5' GCGGAGAGGCGGCGGC     29447      GGCG   A
                                GCGGA   GAGG CGGCGGC
                                |||||   |||| |||||||
                                CGCCT   CTCC GCCGCCG
                                  _____  _
GAM1143 BACE2    5' AGGCGGAGGCCGGGGAGGCG  29448         _ A  C
                                AGGCGGAGGC GG GGA GGCG
                                |||||||||| || ||| ||||
                                TCCGCCTCCG CC CCT CCGC
                                     G  _  _
GAM1143 BACE2    5' AGGCGGAGGCCGGGGAGGCG  29448         _ A  C
                                AGGCGGAGGC GG GGA GGCG
                                |||||||||| || ||| ||||
                                TCCGCCTCCG CC CCT CCGC
                                     G  _  _
GAM1143 BACE2    5' AGGCGGAGGCCGGGGAGGCG  29448         _ A  C
                                AGGCGGAGGC GG GGA GGCG
                                |||||||||| || ||| ||||
                                TCCGCCTCCG CC CCT CCGC
                                     G  _  _
GAM1143 BARX1    5' GGCGGAGGCGCAGGGGCCGGGC 29449         G  AC  __
           G                     GGCGGAGGCG AGG  GGC  GGCG
                                |||||||||| |||  |||  ||||
                                CCGCCTCCGC TCC  CCG  CCGC
                                     G  __  GC
GAM1143 BAZ1B    3' AGGCAGGGGAAGCTGGCGG   29450     GG  C    AC
                                AGGC  AGG GGAGG  GGCGG
                                ||||  ||| |||||  |||||
                                TCCG  TCC CCTTC  CCGCC
                                  __  _    GA
GAM1143 BCL10    5' GGTGGAGGCGGGAGATGGCG  29451    C      AG  C
                                GG GGAGGCGG  GA GGCG
                                || ||||||||  || ||||
                                CC CCTCCGCC  CT CCGC
                                 A       CT  A
GAM1143 BCL11A   5' GGCGGCGGCGGCGGCGGC    29453      A    AGGA
                                GGCGG GGCGG   CGGCGGC
                                ||||| |||||   |||||||
                                CCGCC CCGCC   GCCGCCG
                                   G   _____
GAM1143 BCL11A   5' GGCGGCGGCGGCGGCGGC    29453      A    AGGA
                                GGCGG GGCGG   CGGCGGC
                                ||||| |||||   |||||||
```

```
                                CCGCC CCGCC   GCCGCCG
                                  G   ____
GAM1143 BCL11A   5' GGCGGGCGGCGGCGG     29452     AG   AGGA
                                GGCGG GCGG   CGGCGG
                                ||||| ||||   ||||||
                                CCGCC CGCC   GCCGCC
                                  __  ____
GAM1143 BCL11A   5' GGCGGGCGGCGGCGG     29452     AG   AGGA
                                GGCGG GCGG   CGGCGG
                                ||||| ||||   ||||||
                                CCGCC CGCC   GCCGCC
                                  __  ____
GAM1143 BCL11A   5' GGCGGGCGGCGGCGG     29452     AG   AGGA
                                GGCGG GCGG   CGGCGG
                                ||||| ||||   ||||||
                                CCGCC CGCC   GCCGCC
                                  __  ____
GAM1143 BCL11A   5' GGCGGCGGCGGCGGCGGC   29453     A    AGGA
                                GGCGG GGCGG   CGGCGGC
                                ||||| |||||   |||||||
                                CCGCC CCGCC   GCCGCCG
                                  G   ____
GAM1143 BCR      5' AGGCGGAGCGGGGCGCTCGGCG 29454       G  A  A  G_
                                AGGCGGAG CGG GG CG  CGGCG
                                |||||||| ||| || ||  |||||
                                TCCGCCTC GCC CC GC  GCCGC
                                   _  _ _ GA
GAM1143 BCR      5' AGGTGAGGCGGAGCGGGGC   29455    CG      GA  C
                                AGG  GAGGCGGAG  CGG GGC
                                |||  |||||||||  ||| |||
                                TCC  CTCCGCCTC  GCC CCG
                                  A_       __  _
GAM1143 BCR      5' AGGTGAGGCGGAGCGGGGC   29455    CG      GA  C
                                AGG  GAGGCGGAG  CGG GGC
                                |||  |||||||||  ||| |||
                                TCC  CTCCGCCTC  GCC CCG
                                  A_       __  _
GAM1143 BCR      5' AGGCGGAGCGGGGCGCTCGGCG 29454       G  A  A  G_
                                AGGCGGAG CGG GG CG  CGGCG
                                |||||||| ||| || ||  |||||
                                TCCGCCTC GCC CC GC  GCCGC
                                   _  _ _ GA
GAM1143 CACNA2D2 5' AGGGGGGGCAGTGGCGGCG   29457    C A    A A
                                AGG GG GGCGG GG CGGCG
                                ||| || ||||| || |||||
                                TCC CC CCGTC CC GCCGC
                                  _ C    A _
GAM1143 CACNA2D2 3' AGGTGGGAGTGGAGGTGGGG  29456    C  AG C    AC  C
                                AGG GG  G GGAGG  GG GG
                                ||| ||  | |||||  || ||
```

```
                                TCC CC  C CCTCC  CC CC
                                  A  CT A    A_ _
GAM1143  CALCA    5'  AGGCGGTGGCAGCGGCGGC   29458       A    AGGA
                                AGGCGG GGCGG   CGGCGGC
                                |||||| |||||   |||||||
                                TCCGCC CCGTC   GCCGCCG
                                   A    ____
GAM1143  CDH2     5'  AGCCGGAGGAGGCGGCGGC   29459    G   GGC    A
                                AG CGGA   GGAGG CGGCGGC
                                || ||||   ||||| |||||||
                                TC GCCT   CCTCC GCCGCCG
                                 G   ___    _
GAM1143  CDH2     5'  AGGCGGCGGCGGCGGCGGC   29460       A    AGGA
                                AGGCGG GGCGG   CGGCGGC
                                |||||| |||||   |||||||
                                TCCGCC CCGCC   GCCGCCG
                                   G    ____
GAM1143  CDK2AP1  5'  GGCGGCGGCGGCGGCGGC   29453      A    AGGA
                                GGCGG GGCGG   CGGCGGC
                                ||||| |||||   |||||||
                                CCGCC CCGCC   GCCGCCG
                                   G    ____
GAM1143  CDK2AP1  5'  AGGCCGCGAGGGCGGCGGC   29461     GGAG   GA  A
                                AGGC   GCG  GG CGGCGGC
                                ||||   |||  || |||||||
                                TCCG   CGC  CC GCCGCCG
                                  G___   TC  _
GAM1143  CGB      5'  GGGTGAGGCGGAGACCACGG   29462    CG       G  G
                                GG  GAGGCGGAG AC GCGG
                                ||  ||||||||| || ||||
                                CC  CTCCGCCTC TG TGCC
                                 CA       _ G
GAM1143  CHAC     5'  GGCTGGAGGCGGAGCGCGG   29463    _        GACG
                                GGC GGAGGCGGAG   GCGG
                                ||| ||||||||||   ||||
                                CCG CCTCCGCCTC   CGCC
                                  A        G___
GAM1143  CHAC     5'  GGCTGGAGGCGGAGCGCGG   29463    _        GACG
                                GGC GGAGGCGGAG   GCGG
                                ||| ||||||||||   ||||
                                CCG CCTCCGCCTC   CGCC
                                  A        G___
GAM1143  CHAD     5'  GGCTGGGGGCAGCAGCGGCGGC 29464    _ A    A  A
              G                  GGC GG GGCGG GG CGGCGGCG
                                ||| || ||||| || ||||||||
                                CCG CC CCGTC TC GCCGCCGC
                                  A  C    G  _
GAM1143  CHRNA4   5'  GCGGTGCGGCGGCGGCG    29465     AG   AGGA
                                GCGG  GCGG   CGGCGGCG
                                ||||  ||||   ||||||||
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                                CGCC  CGCC   GCCGCCGC
                                  A_  ____
GAM1143  CNN2     3'  AGGCGGAGGCGGGCGGATCACA 29466        A_  CG
                                AGGCGGAGGCGG  GGA  GCG
                                ||||||||||||  |||  |||
                                TCCGCCTCCGCC  CCT  TGT
                                      CG   AG
GAM1143  COL13A1  5'  GGCAGAGGTGGGTCGTGGCG  29467      C  AGGA  GC
                                GGCGGAGG GG   CG  GGCG
                                |||||||| ||   ||  ||||
                                CCGTCTCC CC   GC  CCGC
                                    A  CA__  A_
GAM1143  COL13A1  5'  GGCAGAGGTGGGTCGTGGCG  29467      C  AGGA  GC
                                GGCGGAGG GG   CG  GGCG
                                |||||||| ||   ||  ||||
                                CCGTCTCC CC   GC  CCGC
                                    A  CA__  A_
GAM1143  COL13A1  5'  GGCAGAGGTGGGTCGTGGCG  29467      C  AGGA  GC
                                GGCGGAGG GG   CG  GGCG
                                |||||||| ||   ||  ||||
                                CCGTCTCC CC   GC  CCGC
                                    A  CA__  A_
GAM1143  COL13A1  5'  GGCAGAGGTGGGTCGTGGCG  29467      C  AGGA  GC
                                GGCGGAGG GG   CG  GGCG
                                |||||||| ||   ||  ||||
                                CCGTCTCC CC   GC  CCGC
                                    A  CA__  A_
GAM1143  COL13A1  5'  GGCAGAGGTGGGTCGTGGCG  29467      C  AGGA  GC
                                GGCGGAGG GG   CG  GGCG
                                |||||||| ||   ||  ||||
                                CCGTCTCC CC   GC  CCGC
                                    A  CA__  A_
GAM1143  COL13A1  5'  GGCAGAGGTGGGTCGTGGCG  29467      C  AGGA  GC
                                GGCGGAGG GG   CG  GGCG
                                |||||||| ||   ||  ||||
                                CCGTCTCC CC   GC  CCGC
                                    A  CA__  A_
GAM1143  COL13A1  5'  GGCAGAGGTGGGTCGTGGCG  29467      C  AGGA  GC
                                GGCGGAGG GG   CG  GGCG
                                |||||||| ||   ||  ||||
                                CCGTCTCC CC   GC  CCGC
                                    A  CA__  A_
GAM1143  CORO2A   5'  GGTGGCGGTGGCGGCGGC   29468   A   A  A
                                GG GGCGG GG CGGCGGC
                                || ||||| || |||||||
                                CC CCGCC CC GCCGCCG
                                 A   A  _
GAM1143  CSNK2A2  5'  GGGGCGCAGAGGGTGGCGGCG  29469   C  AG     AC
                                GG GG  GCGGAGG  GGCGGCG
                                || ||  |||||||  |||||||
```

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                                CC CC  CGTCTCC  CCGCCGC
                                 _ G_      CA
GAM1143  CTGF     5'  GGCGGAGCGGAGGGCGCGGTGG 29470        G     A__   C
              CG                  GGCGGAG CGGAGG   CGG GGCG
                                  ||||||| ||||||   ||| ||||
                                  CCGCCTC GCCTCC   GCC CCGC
                                     _     CGC   A
GAM1143  CUL3     5'  GGCGGCGGCGGCGGCGGC    29453      A    AGGA
                                  GGCGG GGCGG    CGGCGGC
                                  ||||| |||||    |||||||
                                  CCGCC CCGCC    GCCGCCG
                                     G    ____
GAM1143  CUL3     5'  GGCGGGGGCGGCGGCGGCG    29471      A    AGGA
                                  GGCGG GGCGG    CGGCGGCG
                                  ||||| |||||    ||||||||
                                  CCGCC CCGCC    GCCGCCGC
                                     C    ____
GAM1143  CUL3     5'  GGCGGCGGCGGGGGGCGGCGGCG 29472      A    A  A
                                  GGCGG GGCGG GG CGGCGGCG
                                  ||||| ||||| || ||||||||
                                  CCGCC CCGCC CC GCCGCCGC
                                     G    C  _
GAM1143  CUL3     5'  GGCGACGCTGGGGGGCGGCGGCG 29473      AG  _  A  A
                                  GGCGG  GC GG GG CGGCGGCG
                                  |||||  || || || ||||||||
                                  CCGCT  CG CC CC GCCGCCGC
                                     G_  A  C  _
GAM1143  CYP26A1   5'  AGGCAGAGGCGGCGCGGTGGCG 29474           AGGA   C
                                  AGGCGGAGGCGG    CGG GGCG
                                  ||||||||||||    ||| ||||
                                  TCCGTCTCCGCC    GCC CCGC
                                        GC__   A
GAM1143  ELAVL1   5'  GGCGGGCGGGAGGCGGCGGCG  29475      AG   _   A
                                  GGCGG  GCGG AGG CGGCGGCG
                                  |||||  |||| ||| ||||||||
                                  CCGCC  CGCC TCC GCCGCCGC
                                     __    C   _
GAM1143  ELAVL1   5'  AGGCGGCGGCGGCGCGGCG   29476      A    AGGA
                                  AGGCGG GGCGG    CGGCG
                                  |||||| |||||    |||||
                                  TCCGCC CCGCC    GCCGC
                                     G    GC__
GAM1143  EMD      5'  AGGCGGAGGCCTGGCGGC    29477        AC_
                                  AGGCGGAGG   GGCGGC
                                  |||||||||   ||||||
                                  TCCGCCTCC   CCGCCG
                                        GGA
GAM1143  EN1      3'  GGCCGGGAGACGACGGCGGCG  29478    __     GGAG
                                  GGC  GGAGGC   GACGGCGGCG
                                  |||  ||||||   ||||||||||
```

```
                                CCG  CCTCTG    CTGCCGCCGC
                                  GC     _____
GAM1143  EN1      3'  GGCGGGGGCAGCGAGGCGG   29479       A     AG  C
                                GGCGG GGCGG  GA GGCGG
                                ||||| |||||  || |||||
                                CCGCC CCGTC  CT CCGCC
                                   C     G_ _
GAM1143  EPS15    5'  GGAGGAGGCGGAGGGAGCG   29480    C         AC
                                GG GGAGGCGGAGG  GGCG
                                || ||||||||||  ||||
                                CC CCTCCGCCTCC  TCGC
                                 T          C_
GAM1143  ESPN     3'  GGCTGGGGCGGAGGGCCCCACG 29481     _ A       ACG__
                                GGC GG GGCGGAGG     GCG
                                ||| || ||||||||     |||
                                CCG CC CCGCCTCC     TGC
                                  A _       CGGGG
GAM1143  EXT1     5'  GGCTGGAGGCGGCGGCGGC   29482     _       AGGA
                                GGC GGAGGCGG    CGGCGGC
                                ||| ||||||||    |||||||
                                CCG CCTCCGCC    GCCGCCG
                                  A       _____
GAM1143  EXT1     5'  AGGCGGCGGCGGCGGCGGC   29460       A     AGGA
                                AGGCGG GGCGG    CGGCGGC
                                |||||| |||||    |||||||
                                TCCGCC CCGCC    GCCGCCG
                                   G    _____
GAM1143  F2RL3    3'  AGGCGGGGCTGGAGGAGCG   29483       A  _     CG
                                AGGCGG GGC GGAGGA  GCG
                                |||||| ||| ||||||  |||
                                TCCGCC CCG CCTCCT  CGC
                                   _  A     ___
GAM1143  F8A      3'  AGGCGGAGGCAGGAGGCTGCG  29484          _    ACG
                                AGGCGGAGGC GGAGG   GCG
                                |||||||||| |||||   |||
                                TCCGCCTCCG CCTCC   CGC
                                      T    GA_
GAM1143  FBXO7     5'  AAGCGGCGACGGGGACGGCGGC 29485       A    A
              G                  AGGCGG GGCGG GGACGGCGGCG
                                 |||||| ||||| ||||||||||
                                 TTCGCC CTGCC CCTGCCGCCGC
                                   G    _
GAM1143  FDX1     5'  AGGCGGGGGCGGCAGCTGCGGC 29486       A    A  ACG
              G                  AGGCGG GGCGG GG   GCGGCG
                                 |||||| ||||| ||   ||||||
                                 TCCGCC CCGCC TC   CGCCGC
                                   C    G  GA_
GAM1143  FGD1     5'  AGGCGCGGGCGGAGGAGGCCCG 29487      GA       C  ___
              GCG                  AGGCG  GGCGGAGGA GGC  GGCG
                                 |||||  ||||||||| |||  ||||
```

```
                                TCCGC  CCGCCTCCT CCG  CCGC
                                  GC       _  GG
GAM1143  FHL1    5'  AGGCGCGGCGGTGGCGGCG   29488      GA    A  A
                                AGGCG  GGCGG GG CGGCG
                                |||||  ||||| || |||||
                                TCCGC  CCGCC CC GCCGC
                                  G_    A  _
GAM1143  FMNL    5'  GGCCGGGCAGTGGGGGCGGCGG 29489    _ A_  C  A  A
           CG                    GGC GG  GG GG GG CGGCGGCG
                                ||| ||  || || || ||||||||
                                CCG CC  TC CC CC GCCGCCGC
                                 G  CG  A  C  _
GAM1143  FMNL    5'  AGTGGGGGCGGCGGCGGTGGCG 29490    C  A    A  A   C
                                GG GG GGCGG GG CGG GGCG
                                || || ||||| || ||| ||||
                                TC CC CCGCC CC GCC CCGC
                                 A  C    G  _  A
GAM1143  FMNL    5'  AGGCGGCGGCGGCGGCGGC   29460       A    AGGA
                                AGGCGG GGCGG   CGGCGGC
                                |||||| |||||   |||||||
                                TCCGCC CCGCC   GCCGCCG
                                  G    ____
GAM1143  FMR2    5'  GGCGGCAGCGGCGGCGGC    29491      A    AGGA
                                GGCGG GGCGG   CGGCGGC
                                ||||| |||||   |||||||
                                CCGCC TCGCC   GCCGCCG
                                  G    ____
GAM1143  FOXE1   5'  AGGCGAGGCGGGGGCAGCG   29492      G    A  A
                                AGGCG AGGCGG GG CGGCG
                                ||||| |||||| || |||||
                                TCCGC TCCGCC CC GTCGC
                                  _     C  _
GAM1143  FOXG1B  5'  GGCGGCGGGCGGCAGCGGCG  29493      A_    AGGA
                                GGCGG  GGCGG   CGGCGGCG
                                |||||  |||||   ||||||||
                                CCGCC  CCGCC   GTCGCCGC
                                  GC    ____
GAM1143  FTH1    5'  AGGCGGCGGCGGCGGCGG    29494       A    AGGA
                                AGGCGG GGCGG   CGGCGG
                                |||||| |||||   ||||||
                                TCCGCC CCGCC   GCCGCC
                                  G    ____
GAM1143  GNAO1   3'  AGGCAGGGGTGGGGAGGGGCG  29495      A  C  A   C  C
                                AGGCGG GG GG GGA GG GGCG
                                |||||| || || ||| || ||||
                                TCCGTC CC CC CCT CC CCGC
                                  C  A  _  _  _
GAM1143  GNB2    5'  GGCGGAGGCGGCGGCGGCG   29496          AGGA
                                GGCGGAGGCGG   CGGCGGCG
                                ||||||||||   ||||||||
```

```
                                CCGCCTCCGCC   GCCGCCGC
                                      ____
GAM1143 GNB2     5' AGGCGGCGGCGGCGGCGGC   29460      A    AGGA
                                AGGCGG GGCGG   CGGCGGC
                                |||||| |||||   |||||||
                                TCCGCC CCGCC   GCCGCCG
                                   G   ____
GAM1143 GRB14    5' GGAGGGGGCGGAGGAGGAGG  29497    C A      C C
                                GG GG GGCGGAGGA GG GG
                                || || ||||||||| || ||
                                CC CC CCGCCTCCT CC CC
                                 T C       _ T
GAM1143 GRM6     3' AGGTGGAGGCAGGAGGATCG  29498    C    _    _
                                AGG GGAGGC GGAGGA CG
                                ||| |||||| |||||| ||
                                TCC CCTCCG CCTCCT GC
                                  A    T    A
GAM1143 GTF2IRD1 5' AGGCAGAGGGAGGCGAGGACGG 29499    ____     G
             CGGCG                 GGC   GGAGGCG AGGACGGCGGCG
                                |||   ||||||| ||||||||||||
                                CCG   CCTCCGC TCCTGCCGCCGC
                                  TCTC     _
GAM1143 GUCY1A2  5' GGCGGAGGCGGCGGTGGCG   29500         A  AC
                                GGCGGAGGCGG GG  GGCG
                                |||||||||| ||  ||||
                                CCGCCTCCGCC CC  CCGC
                                      G  A_
GAM1143 GUCY1B3  5' AGGCAGAGGCGGCAGCGGC   29501         AGGA
                                AGGCGGAGGCGG   CGGCGGC
                                ||||||||||||   |||||||
                                TCCGTCTCCGCC   GTCGCCG
                                      ____
GAM1143 HD       5' GGCGGAGGCGGGGCCGCGCCGG 29502         A  A__  G
             CG                   GGCGGAGGCGG GG   CG CGGCG
                                |||||||||| ||   || |||||
                                CCGCCTCCGCC CC   GC GCCGC
                                      _  GGC  G
GAM1143 HDAC4    5' GGCGGCGGCGGCGGCGGC    29453      A    AGGA
                                GGCGG GGCGG   CGGCGGC
                                ||||| |||||   |||||||
                                CCGCC CCGCC   GCCGCCG
                                   G   ____
GAM1143 HDAC4    5' GGCGGCGGCGGGGACGG     29503      A    A
                                GGCGG GGCGG GGACGG
                                ||||| ||||| ||||||
                                CCGCC CCGCC CCTGCC
                                   G   _
GAM1143 HDAC5    5' GGCGGCGGCAGCAGCGGCGGCG 29504      A    A  A
                                GGCGG GGCGG GG CGGCGGCG
                                ||||| ||||| || ||||||||
```

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                                CCGCC CCGTC TC GCCGCCGC
                                   G    G  _
GAM1143  HDAC5    5'  GGCGGCGGCAGCAGCGGCGGCG 29504      A    A  A
                                GGCGG GGCGG GG CGGCGGCG
                                ||||| ||||| || ||||||||
                                CCGCC CCGTC TC GCCGCCGC
                                   G    G  _
GAM1143  HK2      5'  AGGGGAGGCGGGCGG      29505    C      AGGACG
                                AGG GGAGGCGG     GCGG
                                ||| ||||||||     ||||
                                TCC CCTCCGCC     CGCC
                                  _      _______
GAM1143  HUNK     5'  GGTGGGGCGCGGTCCGGCGGCG 29506    C  A   GA  A_
                                GG GG GGCG  GG  CGGCGGCG
                                || || ||||  ||  ||||||||
                                CC CC CCGC  CC  GCCGCCGC
                                 A  _   G_  AG
GAM1143  HYOU1    3'  AGGTGGGGGTGGGGTGAGGGG  29507    C  A  C  A  AC_  C
                                AGG GG GG GG GG   GG GG
                                ||| || || || ||   || ||
                                TCC CC CC CC CC   CC CC
                                 A  C  A  _  ACT  _
GAM1143  IFRD1    5'  GGCGGGGGTAAGAGTGGGCGGT 29508      A  C_   GA__   C
            GGCG                   GGCGG GG  GGAG   CGG GGCG
                                ||||| ||  ||||   ||| ||||
                                CCGCC CC  TCTC   GCC CCGC
                                   C  AT   ACCC   A
GAM1143  IGF2R    5'  AGGCGGAGGTGGAGACGGAGCG 29509         C   G   C
                                AGGCGGAGG GGAG ACGG GGCG
                                ||||||||| |||| |||| ||||
                                TCCGCCTCC CCTC TGCC TCGC
                                     A   _   _
GAM1143  IGFBP1   5'  GGTGGCGGCGGCGCGGC     29510    A    A  A  G
                                GG GGCGG GG CG CGGC
                                || ||||| || || ||||
                                CC CCGCC CC GC GCCG
                                 A    G  _  _
GAM1143  INHBB    5'  GGCGGGGCGGAGGTCGCG    29511      A      A  G
                                GGCGG GGCGGAGG CG CG
                                ||||| |||||||| || ||
                                CCGCC CCGCCTCC GC GC
                                   _      A  _
GAM1143  INS      3'  AGGCGGCGGGTGGGGGGC    29512       A_  C  A  AC
                                AGGCGG  GG GG GG  GGC
                                ||||||  || || ||  |||
                                TCCGCC  CC CC CC  CCG
                                   GC  A  _  ___
GAM1143  INSM1    3'  GGCCGGGGTGGAGGGCG     29513     _  A  C    ACG
                                GGC GG GG GGAGG   GCG
                                ||| || || |||||   |||
```

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                                CCG CC CC CCTCC   CGC
                                  G  _  A    ___
GAM1143  ISL1     5'  AGCGGAGGCGCTGCGGCGGCG  29514         GAGGA
                                GGCGGAGGCG    CGGCGGCG
                                ||||||||||    ||||||||
                                TCGCCTCCGC    GCCGCCGC
                                     GAC__
GAM1143  JAG2     5'  AGGCGGCGGCGGCGGCGGC   29460       A    AGGA
                                AGGCGG GGCGG   CGGCGGC
                                ||||||| |||||   |||||||
                                TCCGCC CCGCC   GCCGCCG
                                   G   _____
GAM1143  KCNC3    3'  GGTCGGGGGGTGGGGGGCGG   29515   _  A  C  A  AC
                                GG CGG GG GG GG  GGCGG
                                || ||| || || ||  |||||
                                CC GCC CC CC CC  CCGCC
                                 A  C  A  _  __
GAM1143  KIF3B    5'  GGCGGCGGCGGCGGCGGC    29453      A    AGGA
                                GGCGG GGCGG   CGGCGGC
                                ||||| |||||   |||||||
                                CCGCC CCGCC   GCCGCCG
                                   G   _____
GAM1143  KIF5A    5'  AGGCCGAGGCGGAGGACAG   29516     G
                                AGGC GAGGCGGAGGACGG
                                |||| ||||||||||||||
                                TCCG CTCCGCCTCCTGTC
                                  G
GAM1143  KPNB1    5'  GGCGGAGGTGGCGGCGGC    29517        C  AGGA
                                GGCGGAGG GG   CGGCGGC
                                |||||||| ||   |||||||
                                CCGCCTCC CC   GCCGCCG
                                     A  _____
GAM1143  LATS2    5'  GGGGGAGCCCCGGGCGGCGGCG 29518    C  AG  GGA  A
                                GG GG  GC   GG CGGCGGCG
                                || ||  ||   || ||||||||
                                CC CC  CG   CC GCCGCCGC
                                 _  CT  GGG  C
GAM1143  LEF1     5'  GGCGGAAGCGGGGCGGGCG   29519          A  AC
                                GGCGGAGGCGG GG  GGCG
                                |||||||||| ||  ||||
                                CCGCCTTCGCC CC  CCGC
                                      _  GC
GAM1143  LIMK1    5'  AGGCGGGGGCGGAGGGCG    29520       A      ACG
                                AGGCGG GGCGGAGG   GCG
                                |||||| ||||||||   |||
                                TCCGCC CCGCCTCC   CGC
                                   C       ___
GAM1143  LIMK1    5'  AGGCGGGGGCGGAGGGCG    29520       A      ACG
                                AGGCGG GGCGGAGG   GCG
                                |||||| ||||||||   |||
```

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                                TCCGCC CCGCCTCC   CGC
                                   C      ___
GAM1143  LMO2     5'  AGGCGGGGTGCCGGGCGGCG  29521       A  CGGA  A
                                AGGCGG GG    GG CGGCG
                                |||||| ||    || |||||
                                TCCGCC CC    CC GCCGC
                                   _  ACGG  C
GAM1143  LMO4     5'  AGGCGGCGGCGGCGGCGGC   29460       A    AGGA
                                AGGCGG GGCGG    CGGCGGC
                                |||||| |||||    |||||||
                                TCCGCC CCGCC    GCCGCCG
                                   G    _____
GAM1143  LRP1     5'  AGGGGGGGTGGGGGGCG     29522     C  A  C  A  AC
                                AGG GG GG GG GG  GGCG
                                ||| || || || ||  ||||
                                TCC CC CC CC CC  CCGC
                                  _  C  A  _  __
GAM1143  LU       3'  GGTGGGGCGGAGGTAGGGCG  29524    C  A       AC_
                                GG GG GGCGGAGG   GGCG
                                || || ||||||||   ||||
                                CC CC CCGCCTCC   CCGC
                                 A  _       ATC
GAM1143  LU       3'  AGGCGGGGGCGGGCATGGCG  29523       A    AGGAC
                                AGGCGG GGCGG    GGCG
                                |||||| |||||    ||||
                                TCCGCC CCGCC    CCGC
                                   C    CGTA_
GAM1143  MAPRE3   5'  AGGCGGAGGGGGAGGGGACAGG 29525         C  __   _  C
            TGGCG                   AGGCGGAGG GGA  GGAC GG GGCG
                                |||||||||  |||  ||||  ||  ||||
                                TCCGCCTCC CCT  CCTG CC CCGC
                                     C   CC    T  A
GAM1143  MAPT     5'  AGGTGGGCGGTGGCAGCGGCG  29526     C  AG   A  A
                                AGG GG  GCGG GG CGGCGGCG
                                |||  ||  ||||  ||  ||||||||
                                TCC CC  CGCC CC GTCGCCGC
                                  A  __   A  _
GAM1143  MAPT     5'  AGGTGGGCGGTGGCAGCGGCG  29526     C  AG   A  A
                                AGG GG  GCGG GG CGGCGGCG
                                |||  ||  ||||  ||  ||||||||
                                TCC CC  CGCC CC GTCGCCGC
                                  A  __   A  _
GAM1143  MAPT     5'  AGGTGGGCGGTGGCAGCGGCG  29526     C  AG   A  A
                                AGG GG  GCGG GG CGGCGGCG
                                |||  ||  ||||  ||  ||||||||
                                TCC CC  CGCC CC GTCGCCGC
                                  A  __   A  _
GAM1143  MAPT     5'  AGGTGGGCGGTGGCAGCGGCG  29526     C  AG   A  A
                                AGG GG  GCGG GG CGGCGGCG
                                |||  ||  ||||  ||  ||||||||
```

```
                                TCC CC  CGCC CC GTCGCCGC
                                  A __   A _
GAM1143  MAZ     5'  GGCGGAGGCGGGGGGCG     29528          A  AC
                                GGCGGAGGCGG GG  GGCG
                                |||||||||| ||  ||||
                                CCGCCTCCGCC CC  CCGC
                                      _ __
GAM1143  MAZ     5'  AGGTTGGGGCTACGACGGCGG  29527     C_  A   GGAG
                                AGG  GG GGC    GACGGCGG
                                |||  || |||    ||||||||
                                TCC  CC CCG    CTGCCGCC
                                  AA  _   ATG_
GAM1143  MSI1    5'  AGCGGAGCGGCGGCGG      29529        G   AGGA
                                GGCGGAG CGG    CGGCGG
                                |||||||| |||    ||||||
                                TCGCCTC GCC    GCCGCC
                                   _  _____
GAM1143  MYO1E   5'  AGGTGAGGGCGAGACGGCGGCG 29530     C GA    GA
                                AGG G  GGCG  GGACGGCGGCG
                                ||| |  ||||  ||||||||||
                                TCC C  CCGC  TCTGCCGCCGC
                                  A TC   __
GAM1143  NFATC2  5'  GGCGGAGGCGGCTCGAGCGGCG 29531          AGGA  _
                                GGCGGAGGCGG    CG GCGGCG
                                ||||||||||    || ||||||
                                CCGCCTCCGCC    GC CGCCGC
                                      GA__  T
GAM1143  NME2    5'  AGCTGGAGGGGCCGGGCGGCGG 29532     _    C  A_  A
            CG                    GGC GGAGG GG  GG CGGCGGCG
                                ||| ||||| ||  || ||||||||
                                TCG CCTCC CC  CC GCCGCCGC
                                  A    _ GG  C
GAM1143  NPEPPS  5'  GGAGGAGGCGGAGGGCCG    29533    C         A_
                                GG GGAGGCGGAGG  CG
                                || ||||||||||  ||
                                CC CCTCCGCCTCC  GC
                                 T          CG
GAM1143  NR2F2   5'  GGCGGCGGCGGGGCGGCGGCG  29534      A    A  A
                                GGCGG GGCGG GG CGGCGGCG
                                ||||| ||||| || ||||||||
                                CCGCC CCGCC CC GCCGCCGC
                                   G    _ _
GAM1143  NRG2    3'  GGCGGAGGGGCGCGCGGC    29535        CGGA  A  _
                                GGCGGAGG    GG CG GCGGC
                                ||||||||    || || |||||
                                CCGCCTCC    CC GC CGCCG
                                     _____  _  G
GAM1143  NRG2    3'  GGCGGGGCGGAGGGGCG     29536      A       AC
                                GGCGG GGCGGAGG  GGCG
                                ||||| ||||||||  ||||
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                                CCGCC CCGCCTCC  CCGC
                                  _     __
GAM1143  NRG2    3'  GGCGGGGCGGAGGGGCG    29536      A      AC
                                GGCGG GGCGGAGG  GGCG
                                ||||| ||||||||  ||||
                                CCGCC CCGCCTCC  CCGC
                                  _     __
GAM1143  NRG2    3'  GGCGGAGGGGCGCGCGGC    29535       CGGA  A  _
                                GGCGGAGG   GG CG GCGGC
                                ||||||||   || || |||||
                                CCGCCTCC   CC GC CGCCG
                                    _____  _  G
GAM1143  NRG2    3'  GGCGGGGCGGAGGGGCG    29536      A      AC
                                GGCGG GGCGGAGG  GGCG
                                ||||| ||||||||  ||||
                                CCGCC CCGCCTCC  CCGC
                                  _     __
GAM1143  NRG2    3'  GGCGGAGGGGCGCGCGGC    29535       CGGA  A  _
                                GGCGGAGG   GG CG GCGGC
                                ||||||||   || || |||||
                                CCGCCTCC   CC GC CGCCG
                                    _____  _  G
GAM1143  NRG2    3'  GGCGGAGGGGCGCGCGGC    29535       CGGA  A  _
                                GGCGGAGG   GG CG GCGGC
                                ||||||||   || || |||||
                                CCGCCTCC   CC GC CGCCG
                                    _____  _  G
GAM1143  NRG2    3'  GGCGGGGCGGAGGGGCG    29536      A      AC
                                GGCGG GGCGGAGG  GGCG
                                ||||| ||||||||  ||||
                                CCGCC CCGCCTCC  CCGC
                                  _     __
GAM1143  OTP     3'  AGGCGGAGGGGAGGCCTCGCG  29537        C    ACG_
                                AGGCGGAGG GGAGG   GCG
                                ||||||||| |||||   |||
                                TCCGCCTCC CCTCC   CGC
                                    _   GGAG
GAM1143  PACE4   5'  AGGAGGAGGCGGCCGCGGC   29538     C      AGGACG
                                AGG GGAGGCGG    GCGGC
                                ||| ||||||||    |||||
                                TCC CCTCCGCC    CGCCG
                                  T      GG____
GAM1143  PACE4   5'  AGGAGGAGGCGGCCGCGGC   29538     C      AGGACG
                                AGG GGAGGCGG    GCGGC
                                ||| ||||||||    |||||
                                TCC CCTCCGCC    CGCCG
                                  T      GG____
GAM1143  PACE4   5'  AGGAGGAGGCGGCCGCGGC   29538     C      AGGACG
                                AGG GGAGGCGG    GCGGC
                                ||| ||||||||    |||||
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                                TCC CCTCCGCC     CGCCG
                                  T       GG____
GAM1143  PACE4    5'  AGGAGGAGGCGGCCGCGGC   29538     C       AGGACG
                                AGG GGAGGCGG     GCGGC
                                ||| ||||||||     |||||
                                TCC CCTCCGCC     CGCCG
                                  T       GG____
GAM1143  PACE4    5'  AGGAGGAGGCGGCCGCGGC   29538     C       AGGACG
                                AGG GGAGGCGG     GCGGC
                                ||| ||||||||     |||||
                                TCC CCTCCGCC     CGCCG
                                  T       GG____
GAM1143  PACE4    5'  AGGAGGAGGCGGCCGCGGC   29538     C       AGGACG
                                AGG GGAGGCGG     GCGGC
                                ||| ||||||||     |||||
                                TCC CCTCCGCC     CGCCG
                                  T       GG____
GAM1143  PAX2     3'  GGCGGAGGGGGAGGGG     29539         C     AC
                                GGCGGAGG GGAGG  GG
                                |||||||| |||||  ||
                                CCGCCTCC CCTCC  CC
                                     C    __
GAM1143  PAX2     3'  GGCGGAGGGGGAGGGG     29539         C     AC
                                GGCGGAGG GGAGG  GG
                                |||||||| |||||  ||
                                CCGCCTCC CCTCC  CC
                                     C    __
GAM1143  PCTK1    5'  AGGAGGAGGCGGCGGCGGCGGC 29540     C       A  A
              G                   AGG GGAGGCGG GG CGGCGGCG
                                ||| |||||||| || ||||||||
                                TCC CCTCCGCC CC GCCGCCGC
                                  T       G  _
GAM1143  PCTK1    5'  AGGAGGAGGCGGCGGCGGCGGC 29540     C       A  A
              G                   AGG GGAGGCGG GG CGGCGGCG
                                ||| |||||||| || ||||||||
                                TCC CCTCCGCC CC GCCGCCGC
                                  T       G  _
GAM1143  PCTK1    5'  GGAGGAGGAGGCGGCGGC    29541       C     A
                                GGAGG GGAGG CGGCGGC
                                ||||| ||||| |||||||
                                CCTCC CCTCC GCCGCCG
                                   T    _
GAM1143  PCTK1    5'  AGGCGGCGGCGGCGGCGG    29494        A     AGGA
                                AGGCGG GGCGG   CGGCGG
                                |||||| |||||   ||||||
                                TCCGCC CCGCC   GCCGCC
                                   G    _____
GAM1143  PCTK1    5'  GGAGGAGGAGGCGGCGGC    29541       C     A
                                GGAGG GGAGG CGGCGGC
                                ||||| ||||| |||||||
```

```
                                CCTCC CCTCC GCCGCCG
                                  T    _
GAM1143  PCTK1    5'  AGGCGGCGGCGGCGGCGG    29494       A    AGGA
                                AGGCGG GGCGG   CGGCGG
                                |||||| |||||   ||||||
                                TCCGCC CCGCC   GCCGCC
                                  G    _____
GAM1143  PDE4A    5'  GGTGGAGGCGGTGGGGGG    29542    C      A  AC  C
                                GG GGAGGCGG GG  GG GG
                                || |||||||| ||  || ||
                                CC CCTCCGCC CC  CC CC
                                 A       A __ _
GAM1143  PLOD3    5'  AGGCGGGGGAGGGGCGGC    29543       A  CG   AC
                                AGGCGG GG  GAGG  GGCGGC
                                |||||| ||  ||||  ||||||
                                TCCGCC CC  CTCC  CCGCCG
                                  _ __   __
GAM1143  PLXNB2   3'  GGCGGAGGCGGAGGCCAGC   29544            A
                                GGCGGAGGCGGAGG CGGC
                                |||||||||||||| ||||
                                CCGCCTCCGCCTCC GTCG
                                        G
GAM1143  PPP2R5A  5'  AGGAGGAGGCGGGGGAGAGGCG 29545    C      A   C_
                                AGG GGAGGCGG GGA  GGCG
                                ||| |||||||| |||  ||||
                                TCC CCTCCGCC CCT  CCGC
                                  T       C   CT
GAM1143  PPP2R5A  5'  GGCGGGGGCGGAGGGGGG    29546      A      AC  C
                                GGCGG GGCGGAGG  GG GG
                                ||||| ||||||||  || ||
                                CCGCC CCGCCTCC  CC CC
                                   C       __ _
GAM1143  PRKACA   3'  GGGGAGGCGGAAGCTGG     29547    C        AC
                                GG GGAGGCGGAGG  GG
                                || ||||||||||  ||
                                CC CCTCCGCCTTC  CC
                                 _         GA
GAM1143  PRKCM    5'  AGGGCGGGGGCTGGCGGC    29548    A    A  AC
                                GG GGCGG GG  GGCGGC
                                || ||||| ||  ||||||
                                TC CCGCC CC  CCGCCG
                                 _    C  GA
GAM1143  PROS1    5'  AGGCGCCGGCAGGGACGGTGGC 29549     GA    A    C   III
            GC                    GGCG  GGCGG GGACGG GGCG   C
                                ||||  ||||| |||||| ||||   |
                                CCGC  CCGTC CCTGCC CCGC   G
                                  GG    _     A   III
GAM1143  PROS1    5'  AGCCGGGGGCGGAGGAGAC   29550    G  A       C
                                AG CGG GGCGGAGGA GGC
                                || ||| ||||||||| |||
```

```
                                TC GCC CCGCCTCCT CTG
                                 G   C       _
GAM1143  PRX      3'  GGGGGGAGGAGCGGCGGC    29551    A  C     _
                                GG GG GGAGGA CGGCGGC
                                || || |||||| |||||||
                                CC CC CCTCCT GCCGCCG
                                 _ _     C
GAM1143  PTGER3   5'  GGCGGCGGCGGAGGTCGGCG   29552      A       A
                                GGCGG GGCGGAGG CGGCG
                                ||||| |||||||| |||||
                                CCGCC CCGCCTCC GCCGC
                                   G       A
GAM1143  PTGFRN   5'  AGGCGGAGGCGGCGGTGCAGCG 29553           A  ACG
                                AGGCGGAGGCGG GG   GCGGCG
                                |||||||||||| ||   ||||||
                                TCCGCCTCCGCC CC   CGTCGC
                                       G  A__
GAM1143  PTMA     5'  GGCGGAGGCGGCTGCGGCG   29554          AGGACG
                                GGCGGAGGCGG     GCGGCG
                                ||||||||||      ||||||
                                CCGCCTCCGCC     CGCCGC
                                      GA____
GAM1143  PTPRG    5'  GGCGGCGGCGGGGCTGAGCGCG 29555       A    A  ACG___
            GCG                   GGCGG GGCGG GG     GCGGCG
                                ||||| ||||| ||     ||||||
                                CCGCC CCGCC CC     CGCCGC
                                   G    _  GACTCG
GAM1143  RAB5C    5'  AGGCGGCTCCGGGGCGGCGGCG 29556       AGG   A  A
                                AGGCGG   CGG GG CGGCGGCG
                                ||||||   ||| || ||||||||
                                TCCGCC   GCC CC GCCGCCGC
                                   GAG   _  _
GAM1143  RAC3     5'  GGCGCGGGCCGGGCGGCGGCG  29557     GA   GGA  A
                                GGCG  GGC   GG CGGCGGCG
                                ||||  |||   || ||||||||
                                CCGC  CCG   CC GCCGCCGC
                                  GC   GC_  _
GAM1143  RANBP9   5'  AGGGGGAGGCGGGGGCGACGGC 29558     C       A  A
            G                    AGG GGAGGCGG GG CGGCGGCG
                                ||| |||||||| || ||||||||
                                TCC CCTCCGCC CC GCTGCCGC
                                  C       C  _
GAM1143  RFXANK   5'  GGCGGGGGGCAGAGGGC      29559       A       ACG
                                GGCGG GGCGGAGG   GC
                                ||||| ||||||||   ||
                                CCGCC CCGTCTCC   CG
                                   C       ____
GAM1143  RFXANK   5'  GGCGGGGGGCAGAGGGC      29559       A       ACG
                                GGCGG GGCGGAGG   GC
                                ||||| ||||||||   ||
```

```
                                CCGCC CCGTCTCC   CG
                                  C      ___
GAM1143 RNPEPL1   5' AGGCGGGCAGCGGGGGCGGCGG 29560       A_    A A
                CG                  AGGCGG  GGCGG GG CGGCGGCG
                                    ||||||  ||||| || ||||||||
                                    TCCGCC  TCGCC CC GCCGCCGC
                                      CG    C  _
GAM1143 RXRA      3' AGGCAGGGGTGGAGGGCGGCG  29561       A  C    A
                                    AGGCGG GG GGAGG CGGCG
                                    |||||| || ||||| |||||
                                    TCCGTC CC CCTCC GCCGC
                                      C  A    C
GAM1143 SALL1     3' GGCGGGGTGGGGGGCAA     29562       A  C  A  AC
                                    GGCGG GG GG GG  GGCGG
                                    ||||| || || ||  |||||
                                    CCGCC CC CC CC  CCGTT
                                      _  A  _  __
GAM1143 SH3GL1    3' GGCGGGGCGGGGACACGG    29563       A    A    G
                                    GGCGG GGCGG GGACG CGG
                                    ||||| ||||| ||||| |||
                                    CCGCC CCGCC CCTGT GCC
                                      _    _    _
GAM1143 SLBP      5' AGGCTGAGGCGGCGGCGGC   29565       G      AGGA
                                    AGGC GAGGCGG    CGGCGGC
                                    |||| |||||||    |||||||
                                    TCCG CTCCGCC    GCCGCCG
                                      A      _____
GAM1143 SLBP      5' GGCCGAGGCTGAGGCGGCGGCG 29564     G    G    A
                                    GGC GAGGC GAGG CGGCGGCG
                                    ||| ||||| |||| ||||||||
                                    CCG CTCCG CTCC GCCGCCGC
                                      G    A   _
GAM1143 SLC30A4   5' GGGGAGGCGGACGGCCGGCGGC 29566     C        _ A
                G                    GG GGAGGCGGA GG CGGCGGCG
                                    || |||||||| || ||||||||
                                    CC CCTCCGCCT CC GCCGCCGC
                                      _       G  G
GAM1143 SLC6A8    5' GGCGGCGGGCGGACGGCG    29568     GGA    A_
                                    GGC   GGCGG  GGACGGCG
                                    |||   |||||  ||||||||
                                    CCG   CCGCC  CCTGCCGC
                                      ___     CG
GAM1143 SLC6A8    5' GGCGGCGGCGGCGGCGGC    29453       A    AGGA
                                    GGCGG GGCGG    CGGCGGC
                                    ||||| |||||    |||||||
                                    CCGCC CCGCC    GCCGCCG
                                      G    _____
GAM1143 SLC6A8    5' GGCGGCGGCGGCTGCGGC    29567       A    AGGACG
                                    GGCGG GGCGG     GCGGC
                                    ||||| |||||     |||||
```

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                                CCGCC CCGCC     CGCCG
                                  G    GA____
GAM1143  SLC9A3R2  5'  GGGGAGCTCGGGGGCGGCGGCG 29569    C   G_  A  A
                                GG GGAG  CGG GG CGGCGGCG
                                || ||||  ||| || ||||||||
                                CC CCTC  GCC CC GCCGCCGC
                                 _   GA  C  _
GAM1143  SLIT3    5'  AGCGGGGCGCTCCGGGCGGCGG 29570      A   GA__  A
                CG                GGCGG GGCG   GG CGGCGGCG
                                ||||| ||||   || ||||||||
                                TCGCC CCGC   CC GCCGCCGC
                                  _   GAGG  C
GAM1143  SMG1     5'  GGAGGAGGAGGCGGCGGC    29541      C    A
                                GGAGG GGAGG CGGCGGC
                                ||||| ||||| |||||||
                                CCTCC CCTCC GCCGCCG
                                  T   _
GAM1143  SMG1     5'  AGGCGGCGGCGGAGGGCG    29571       A      ACG
                                AGGCGG GGCGGAGG  GCG
                                |||||| ||||||||  |||
                                TCCGCC CCGCCTCC  CGC
                                  G      ___
GAM1143  SNL      5'  GGTGGCGGGTCCCTGCGGCGGC 29572    A    AGGA___
                G                GG GGCGG     CGGCGGCG
                                || |||||     ||||||||
                                CC CCGCC     GCCGCCGC
                                 A    CAGGGAC
GAM1143  SOX12    5'  GGTGGGGGAGGAGGCAGCGGCG 29574    C  A  C    A
                                GG GG GG GGAGG CGGCGGCG
                                || || || ||||| ||||||||
                                CC CC CC CCTCC GTCGCCGC
                                 A  C  T   _
GAM1143  SOX12    3'  GGCGGGGCAGAGAGATGGCGGC 29573      A     _  C
                G                GGCGG GGCGGAG GA GGCGGCG
                                ||||| ||||||| || |||||||
                                CCGCC CCGTCTC CT CCGCCGC
                                  _     T  A
GAM1143  SOX18    5'  GGATGGCGGTGGGGACGGCGG  29575    _    A__
                                GGA GGCGG   GGACGGCGG
                                ||| |||||   |||||||||
                                CCT CCGCC   CCTGCCGCC
                                  A    ACC
GAM1143  TBL1X    5'  AGGCGGGCGCGGCGGCGGC   29577      AG   GA  A
                                AGGCGG  GCG  GG CGGCGGC
                                ||||||  |||  || |||||||
                                TCCGCC  CGC  CC GCCGCCG
                                   __   G_  _
GAM1143  TBL1X    5'  GGCGCGGCGGCGGCGGC     29576     GA    AGGA
                                GGCG  GGCGG   CGGCGGC
                                ||||  |||||   |||||||
```

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                                CCGC  CCGCC   GCCGCCG
                                  G_   _____
GAM1143  TLX1    5'  GGGGGGCCCGGGCGGCGGC   29578   C  A   GGA  A
                                GG GG GGC   GG CGGCGGC
                                || || |||   || |||||||
                                CC CC CCG   CC GCCGCCG
                                 _ _   GG_  C
GAM1143  TP53BP2  5'  AGGCGGCGGCGGCGGCAGCGGC 29579       A    A  A
            G                    AGGCGG GGCGG GG CGGCGGCG
                                ||||||| ||||| || ||||||||
                                TCCGCC CCGCC CC GTCGCCGC
                                   G    G  _
GAM1143  TRAF5   5'  GGCGCGGGCGGAGGGGCG    29581     GA      AC
                                GGCG  GGCGGAGG  GGCG
                                ||||  ||||||||  ||||
                                CCGC  CCGCCTCC  CCGC
                                  GC       __
GAM1143  TRAF5   5'  GGCGGGGCCGGGGCGCGGGCG  29580      A  _  A  A  G  _
                                GGCGG GGC GG GG CG CGG CG
                                ||||| ||| || || || ||| ||
                                CCGCC CCG CC CC GC GCC GC
                                   _  G  _ _ _  C
GAM1143  TRC8    5'  GGCCGAGAGGGCGGCGGC    29582    G  GC  A  A
                                GGC GAG  GG GG CGGCGGC
                                ||| |||  || || |||||||
                                CCG CTC  TC CC GCCGCCG
                                  G  __  _  _
GAM1143  USF2    3'  AGGCCGGCGTGGGCGGCGGCG  29583     GGA   GA  A
                                AGGC   GGCG  GG CGGCGGCG
                                ||||   ||||  || ||||||||
                                TCCG   CCGC  CC GCCGCCGC
                                  G__    AC  _
GAM1143  USP14   5'  AGGCGGAGGCGCGGTGG     29585          GAGGA  C
                                AGGCGGAGGCG    CGG GG
                                ||||||||||     ||| ||
                                TCCGCCTCCGC    GCC CC
                                      _____  A
GAM1143  USP14   5'  AGGCGCGGTGGTGGCGGC    29584     GGAG   A  AC
                                AGGC   GCGG GG  GGCGGC
                                ||||   |||| ||  ||||||
                                TCCG   CGCC CC  CCGCCG
                                  ____   A  A_
GAM1143  USP7    5'  GGCGGCGGCGGCGGCGGC    29453      A    AGGA
                                GGCGG GGCGG   CGGCGGC
                                ||||| |||||   |||||||
                                CCGCC CCGCC   GCCGCCG
                                  G   ____
GAM1143  USP7    5'  AGCCGGGGCGGCGGCGGC    29586   G  A   AGGA
                                AG CGG GGCGG   CGGCGGC
                                || ||| |||||   |||||||
```

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                                TC GCC CCGCC    GCCGCCG
                                 G  _    _____
GAM1143  USP7     5'  GGCGGGCGGGCGGCGGC     29587      AG    AG A
                                GGCGG  GCGG  G CGGCGGC
                                |||||  ||||  | |||||||
                                CCGCC  CGCC  C GCCGCCG
                                  __   __ _
GAM1143  WNT6     5'  AGGCGAGGGATCCGGCGGCGGC 29588      GA  CGGA  A
              G                  AGGCG  GG   GG CGGCGGCG
                                |||||  ||   || ||||||||
                                TCCGC  CC   CC GCCGCCGC
                                  TC  TAGG  _
GAM1143  YY1      5'  GGCGGGCGCCGCGGCGGC    29589      AG   GAGGA
                                GGCGG  GCG    CGGCGGC
                                |||||  |||    |||||||
                                CCGCC  CGC    GCCGCCG
                                  __  GGC__
GAM1143  ZNF219   5'  GGCGGCGGCGGAGCGGGCGGCG 29590     A     __ A       III
              GCGC                  CGG GGCGGA  GG CGGCGGCG   C
                                ||| ||||||  || ||||||||  |
                                GCC CCGCCT  CC GCCGCCGC   G
                                  G     CG  C       III
GAM1143  ZNF219   5'  GGCGGCGGCGGCGGCGGC    29453      A    AGGA
                                GGCGG GGCGG    CGGCGGC
                                ||||| |||||    |||||||
                                CCGCC CCGCC    GCCGCCG
                                  G    _____
GAM1143  ZNF278   5'  GGAGCGGGCGGGCGGCGGC    29591      G   A_  A
                                GGAG CGG  GG CGGCGGC
                                |||| |||  || |||||||
                                CCTC GCC  CC GCCGCCG
                                  _  CG  C
GAM1143  ZNF278   5'  GGAGCGGGCGGGCGGCGGC    29591      G   A_  A
                                GGAG CGG  GG CGGCGGC
                                |||| |||  || |||||||
                                CCTC GCC  CC GCCGCCG
                                  _  CG  C
GAM1143  ZNF278   5'  GGCGGGCGGCGGCGG       29452      AG    AGGA
                                GGCGG  GCGG   CGGCGG
                                |||||  ||||   ||||||
                                CCGCC  CGCC   GCCGCC
                                  __   _____
GAM1143  ZNF278   5'  GGCGGTGGCGGCGGCGGC    29593      A    AGGA
                                GGCGG GGCGG    CGGCGGC
                                ||||| |||||    |||||||
                                CCGCC CCGCC    GCCGCCG
                                  A    _____
GAM1143  ZNF278   5'  AGGCGAAGGCGAAGGCGGCGGC 29594             A
              G                  AGGCGGAGGCGGAGG CGGCGGCG
                                |||||||||||||| ||||||||
```

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                              TCCGCTTCCGCTTCC GCCGCCGC
                                          _
GAM1143 ZNF278  5' AGGCGAAGGCGGCGGCGGC  29592         AGGA
                              AGGCGGAGGCGG  CGGCGGC
                              ||||||||||||  |||||||
                              TCCGCTTCCGCC  GCCGCCG
                                          ____
GAM1143 ZNF278  5' AGGCGAAGGCGGCGGCGGC  29592         AGGA
                              AGGCGGAGGCGG  CGGCGGC
                              ||||||||||||  |||||||
                              TCCGCTTCCGCC  GCCGCCG
                                          ____
GAM1143 ZNF278  5' GGAGCGGGCGGGCGGCGGC  29591    G  A_ A
                              GGAG CGG  GG CGGCGGC
                              |||| |||  || |||||||
                              CCTC GCC  CC GCCGCCG
                                _  CG  C
GAM1143 ZNF278  5' GGCGGGCGGCGGCGG     29452    AG  AGGA
                              GGCGG  GCGG  CGGCGG
                              |||||  ||||  ||||||
                              CCGCC  CGCC  GCCGCC
                                __  ____
GAM1143 ZNF278  5' AGGCGAAGGCGGCGGCGGC  29592         AGGA
                              AGGCGGAGGCGG  CGGCGGC
                              ||||||||||||  |||||||
                              TCCGCTTCCGCC  GCCGCCG
                                          ____
GAM1143 ZNF278  5' GGCGGGCGGCGGCGG     29452    AG  AGGA
                              GGCGG  GCGG  CGGCGGC
                              |||||  ||||  ||||||
                              CCGCC  CGCC  GCCGCC
                                __  ____
GAM1143 ZNF278  5' GGAGCGGGCGGGCGGCGGC  29591    G  A_ A
                              GGAG CGG  GG CGGCGGC
                              |||| |||  || |||||||
                              CCTC GCC  CC GCCGCCG
                                _  CG  C
GAM1143 ZNF278  5' GGCGGTGGCGGCGGCGGC  29593    A  AGGA
                              GGCGG GGCGG  CGGCGGC
                              ||||| |||||  |||||||
                              CCGCC CCGCC  GCCGCCG
                                A  ____
GAM1143 ZNF278  5' GGCGGTGGCGGCGGCGGC  29593    A  AGGA
                              GGCGG GGCGG  CGGCGGC
                              ||||| |||||  |||||||
                              CCGCC CCGCC  GCCGCCG
                                A  ____
GAM1143 ZNF278  5' GGCGGTGGCGGCGGCGGC  29593    A  AGGA
                              GGCGG GGCGG  CGGCGGC
                              ||||| |||||  |||||||
```

```
                                CCGCC CCGCC    GCCGCCG
                                  A   ____
GAM1143  ZNF278   5'  AGGCGAAGGCGGCGGCGGC   29592          AGGA
                                AGGCGGAGGCGG   CGGCGGC
                                ||||||||||||  |||||||
                                TCCGCTTCCGCC   GCCGCCG
                                      ____
GAM1143  ZNF278   5'  AGGCGAAGGCGAAGGCGGCGGC 29594           A
              G                  AGGCGGAGGCGGAGG CGGCGGCG
                                ||||||||||||||| ||||||||
                                TCCGCTTCCGCTTCC GCCGCCGC
                                      _
GAM1143  ZNF278   5'  AGGCGAAGGCGAAGGCGGCGGC 29594           A
              G                  AGGCGGAGGCGGAGG CGGCGGCG
                                ||||||||||||||| ||||||||
                                TCCGCTTCCGCTTCC GCCGCCGC
                                      _
GAM1143  ZNF278   5'  AGGCGAAGGCGAAGGCGGCGGC 29594           A
              G                  AGGCGGAGGCGGAGG CGGCGGCG
                                ||||||||||||||| ||||||||
                                TCCGCTTCCGCTTCC GCCGCCGC
                                      _
GAM1143  ZNF278   5'  GGCGGGCGGCGGCGG      29452      AG   AGGA
                                GGCGG  GCGG   CGGCGG
                                |||||  ||||   ||||||
                                CCGCC  CGCC   GCCGCC
                                  __   ____
GAM1143  ADAMTS18 5'  AGGCGGAGCGCACGGGCGGCG  29595       _  GA  A
                                AGGCGGAG GCG  GG CGGCG
                                |||||||| |||  || |||||
                                TCCGCCTC CGT  CC GCCGC
                                    G  GC  _
GAM1143  ADNP     5'  GGCGGATGGCGGCGGCACGGCG 29597      _    A  _
              G                  GGCGGA GGCGG GG ACGGCGG
                                |||||| ||||| || |||||||
                                CCGCCT CCGCC CC TGCCGCC
                                   A    G  G
GAM1143  ADNP     5'  GGCGGGCGGATGGCGGC     29596      AG    GGAC
                                GGCGG  GCGGA   GGCGGC
                                |||||  |||||   ||||||
                                CCGCC  CGCCT   CCGCCG
                                  __    A___
GAM1143  ANP32B   5'  GGCGGAGGGGGGGAGAGGCG   29598       C  A  C_
                                GGCGGAGG GG GGA  GGCG
                                |||||||| || |||  ||||
                                CCGCCTCC CC CCT  CCGC
                                    _ _  CT
GAM1143  ASTN2    5'  GGCGGCGGCGGCGGTGGCG   29599      A    A  AC
                                GGCGG GGCGG GG  GGCG
                                ||||| ||||| ||  ||||
```

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                                CCGCC CCGCC CC  CCGC
                                   G    G  A_
GAM1143 ATF3    5' GGGTGCGCTCGGGCGGCGGCG 29600   AG  GA_  A
                                GG  GCG   GG CGGCGGCG
                                ||  |||   || ||||||||
                                CC  CGC   CC GCCGCCGC
                                 CA  GAG  C
GAM1143 BCAA    5' AGGCGGTGGCCGTGGCGGCG  29601      A  GGA  A
                                AGGCGG GGC   GG CGGCG
                                |||||| |||   || |||||
                                TCCGCC CCG   CC GCCGC
                                   A  GCA  _
GAM1143 C1orf17  5' GGCTGCCTGAGGGCGGCGGCG 29602   AG  G_   A
                                GG  GC  GAGG CGGCGGCG
                                ||  ||  |||| ||||||||
                                CC  CG  CTCC GCCGCCGC
                                 GA  GA   C
GAM1143 C20orf177 5' AGCTGGAGGCGGAGGCGCG   29603    _       A  G
                                GGC GGAGGCGGAGG CG CG
                                ||| |||||||||| || ||
                                TCG CCTCCGCCTCC GC GC
                                 A        _ _
GAM1143 C3F     3' AGGCGGAGGCGGGTGGATCAC 29604          A_  CG
                                AGGCGGAGGCGG  GGA  GC
                                ||||||||||||  |||  ||
                                TCCGCCTCCGCC  CCT  TG
                                      CA  AG
GAM1143 CACNA1H  5' GGCGGAGGCGACGGCGGC   29605        GGAG
                                GGCGGAGGC   GACGGCGGC
                                |||||||||   |||||||||
                                CCGCCTCCG   CTGCCGCCG
                                     ____
GAM1143 CECR2   5' GGCGCCGGGCGGGGGGCGGCGG 29606     GA_   A  A
          CG                    GGCG  GGCGG GG CGGCGGCG
                                ||||  ||||| || ||||||||
                                CCGC  CCGCC CC GCCGCCGC
                                  GGC   C  C
GAM1143 CEGP1   5' GGCGGTGGCGGCGGCGGC   29593      A   AGGA
                                GGCGG GGCGG   CGGCGGC
                                ||||| |||||   |||||||
                                CCGCC CCGCC   GCCGCCG
                                  A   ____
GAM1143 CEGP1   5' GGCGGAGTGCGGGCGGTGGCG 29607       _  AG A  C
                                GGCGGAG GCGG  G CGG GGCG
                                ||||||| ||||  | ||| ||||
                                CCGCCTC CGCC  C GCC CCGC
                                   A   __ _  A
GAM1143 CEP3    5' GGCGGGGCGGAGGGCG     29608      A      ACG
                                GGCGG GGCGGAGG  GCG
                                ||||| ||||||||  |||
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                                CCGCC CCGCCTCC   CGC
                                  _     ___
GAM1143  CGB5     5'  GGGTGAGGCGGAGACCACGG   29462    CG       G  G
                                GG  GAGGCGGAG AC GCGG
                                ||  |||||||| || ||||
                                CC  CTCCGCCTC TG TGCC
                                 CA       _ G
GAM1143  CGB8     5'  GGGTGAGGCGGAGACCACGG   29462    CG       G  G
                                GG  GAGGCGGAG AC GCGG
                                ||  |||||||| || ||||
                                CC  CTCCGCCTC TG TGCC
                                 CA       _ G
GAM1143  CPLX1    5'  GGCGCGGGCGGTCAGCGGCG   29609     GA    AGGA
                                GGCG  GGCGG   CGGCGGCG
                                ||||  |||||   ||||||||
                                CCGC  CCGCC   GTCGCCGC
                                  GC    A___
GAM1143  CTHRC1   5'  AGCTGGAGGCGGAGGAGAC   29610     _        C
                                GGC GGAGGCGGAGGA GGC
                                ||| |||||||||||| |||
                                TCG CCTCCGCCTCCT CTG
                                 A         _
GAM1143  CUL2     5'  AGGTGGGCGGAGGCGGCGGCG  29612     C  AG      A
                                AGG GG  GCGGAGG CGGCGGCG
                                ||| ||  ||||||| ||||||||
                                TCC CC  CGCCTCC GCCGCCGC
                                 A  __      _
GAM1143  CUL2     5'  GGCGGAGGCGGCGGCGGCGGCG 29611          A  A
                                GGCGGAGGCGG GG CGGCGGCG
                                |||||||||| || ||||||||
                                CCGCCTCCGCC CC GCCGCCGC
                                      G  _
GAM1143  DCAMKL1  5'  CAGGGCTGGGGGGCGGCGGCG  29613     A  _  A  A
                                CGG GGC GG GG CGGCGGCG
                                ||| ||| || || ||||||||
                                GTC CCG CC CC GCCGCCGC
                                  _  A  C  C
GAM1143  DEGS     5'  GGTGGCGGCGGCGGCGGC    29614    A    A  A
                                GG GGCGG GG CGGCGGC
                                || ||||| || |||||||
                                CC CCGCC CC GCCGCCG
                                 A    G  _
GAM1143  DEGS     5'  GGTGGCGGCGGCGGCGGC    29614    A    A  A
                                GG GGCGG GG CGGCGGC
                                || ||||| || |||||||
                                CC CCGCC CC GCCGCCG
                                 A    G  _
GAM1143  DKFZP434I0714 5'  AGGCGGCAGCGGCGGTGGCG   29615       A    A  AC
                                AGGCGG GGCGG GG  GGCG
                                |||||| ||||| ||  ||||
```

```
                                TCCGCC TCGCC CC  CCGC
                                   G    G  A_
GAM1143  DKFZP434N1511 5'  AGGCGGCGGGCGGGACACCGGC 29616       A_    AG   G
              G                     AGGCGG  GGCGG  GACG CGGCG
                                    ||||||  |||||  |||| |||||
                                    TCCGCC  CCGCC  CTGT GCCGC
                                       GC    __    G
GAM1143  DKFZp547M072 3'  GGCGGGGCGGAGGGCAG     29617      A      ACG
                                    GGCGG GGCGGAGG   GCGG
                                    |||||  ||||||||   ||||
                                    CCGCC CCGCCTCC   CGTC
                                       _      ____
GAM1143  DKFZP564D0478 5'  GGCGGGGGGTGGCGGCGGCG   29618      A  C  AGGA
                                    GGCGG GG GG    CGGCGGCG
                                    |||||  ||  ||    ||||||||
                                    CCGCC CC CC    GCCGCCGC
                                       C  A  _____
GAM1143  DKFZP586G1122 3'  AGTCGGGGGGTGGGGGAGAGG   29619    G   A  C  A   C  C
                                    AG CGG GG GG GGA GG GG
                                    ||  |||  ||  ||  |||  ||  ||
                                    TC GCC CC CC CCT CT CC
                                     A   C  A  C   _  _
GAM1143  DKFZp761A052 5'  AGGCGGCGGCGGCGGCGGC    29460       A     AGGA
                                    AGGCGG GGCGG    CGGCGGC
                                    ||||||  |||||    |||||||
                                    TCCGCC CCGCC    GCCGCCG
                                       G    _____
GAM1143  DKFZp761A052 5'  GGCGGAGGCGGCGGCGGCG    29496          AGGA
                                    GGCGGAGGCGG    CGGCGGCG
                                    ||||||||||    ||||||||
                                    CCGCCTCCGCC    GCCGCCGC
                                                _____
GAM1143  DKFZP761F241 5'  GGCGCACGGGGCGGCGGC    29620      GAG    A  A
                                    GGCG   GCGG GG CGGCGGC
                                    ||||   ||||  ||  |||||||
                                    CCGC   TGCC CC GCCGCCG
                                      G__   _  _
GAM1143  DOK4     5'  GGCGGGGGCGGCAGGGCGGCGG 29621       A     _   A
              CG                      GGCGG GGCGG AGG CGGCGGCG
                                      |||||  |||||  |||  ||||||||
                                      CCGCC CCGCC TCC GCCGCCGC
                                        C    G   C
GAM1143  FLJ10211  5'  CAGGGTCGGGGGGACGGCGG    29622     A  _   A
                                      CGG GG CGG GGACGGCGG
                                      |||  ||  |||  |||||||||
                                      GTC CC GCC CCTGCCGCC
                                        _  A   C
GAM1143  FLJ10607  5'  AGCGGAGGCGGAGGCCAAGGCG 29623             A   C
                                      GGCGGAGGCGGAGG CGG GGCG
                                      ||||||||||||| ||| ||||
```

```
                                TCGCCTCCGCCTCC GTT CCGC
                                       G  _
GAM1143  FLJ10904  5' GGCGGGGGCGGCTGCGGCG   29624      A    AGGACG
                                GGCGG GGCGG     GCGGCG
                                ||||| |||||     ||||||
                                CCGCC CCGCC     CGCCGC
                                   C    GA____
GAM1143  FLJ11280  3' GGTGGAGGCGGGGGAGCAA   29625    C      A   CG
                                GG GGAGGCGG GGA  GCGG
                                || |||||||| |||  ||||
                                CC CCTCCGCC CCT  CGTT
                                 A       C  __
GAM1143  FLJ11730  5' AGGCGGGCGGCGGCGG     29627      AG   AGGA
                                AGGCGG  GCGG   CGGCGG
                                ||||||  ||||   ||||||
                                TCCGCC  CGCC   GCCGCC
                                  __   _____
GAM1143  FLJ11730  5' GGCTGAGGCGGGCGGCGGCG  29626    G     AG A
                                GGC GAGGCGG  G CGGCGGCG
                                ||| |||||||  | ||||||||
                                CCG CTCCGCC  C GCCGCCGC
                                  A      __ _
GAM1143  FLJ11743  5' GGTCGGGGCGGAGGGGTCCCAG 29628   _  A      AC  C____
           GCG                    G CGG GGCGGAGG  GG    GGCG
                                | ||| ||||||||  ||    ||||
                                C GCC CCGCCTCC  CC    CCGC
                                 A  _       __  AGGGT
GAM1143  FLJ14280  3' AGGCGGGGGGTAGGGGAGCGG  29629      A  CG A   CG
                                AGGCGG GG  G GGA  GCGG
                                |||||| ||  | |||  ||||
                                TCCGCC CC  C CCT  CGCC
                                   C  AT C  __
GAM1143  FLJ20506  5' GGCAGCTGAGGGGGCGGCGGCG 29630      AGGC  A  A
                                GGCGG   GG GG CGGCGGCG
                                |||||   || || ||||||||
                                CCGTC   CC CC GCCGCCGC
                                   GACT  C  _
GAM1143  FLJ22477  5' AGCGCGGGGGCGGCGG     29631    GGAG   A  A
                                GGC   GCGG GG CGGCGG
                                |||   |||| || ||||||
                                TCG   CGCC CC GCCGCC
                                  _____   C  _
GAM1143  FLJ23231  5' GGGGCAAGGACGGCGGC     29632    A   G
                                GG GGCG AGGACGGCGGC
                                || |||| ||||||||||
                                CC CCGT TCCTGCCGCCG
                                  _   _
GAM1143  FLJ23231  3' GGCGGAAGTGGGGTGGCG    29633       C  A  AC
                                GGCGGAGG GG GG  GGCG
                                |||||||| || ||  ||||
```

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                                CCGCCTTC CC CC  CCGC
                                    A  _  A_
GAM1143  GABARAP   5'  GGCGGCGACGACGGCGGC    29634      A  GGAG
                                GGCGG GGC    GACGGCGGC
                                ||||| |||    |||||||||
                                CCGCC CTG    CTGCCGCCG
                                  G  ____
GAM1143  GC20      5'  AGGAGGAGGCGGAGGAAGAGGC 29636     C         C  C
              G                   AGG GGAGGCGGAGGA GG GGCG
                                ||| ||||||||||| || ||||
                                TCC CCTCCGCCTCCT TC CCGC
                                  T          _ T
GAM1143  GC20      5'  AGGCTGGAGTGGCGGCGGC    29635      _    GC  AGGA
                                AGGC GGAG  GG    CGGCGGC
                                |||| ||||  ||    |||||||
                                TCCG CCTC  CC    GCCGCCG
                                  A   A_  ____
GAM1143  GIT2      5'  AGGCGGCGGTGGCGGCGGC    29637      GGA    A  A
                                AGGC   GGCGG GG CGGCGGC
                                ||||   ||||| || |||||||
                                TCCG   CCGCC CC GCCGCCG
                                  ___     A  _
GAM1143  GIT2      5'  AGGCGGCGGTGGCGGCGGC    29637      GGA    A  A
                                AGGC   GGCGG GG CGGCGGC
                                ||||   ||||| || |||||||
                                TCCG   CCGCC CC GCCGCCG
                                  ___     A  _
GAM1143  GIT2      5'  AGGCGGCGGTGGCGGCGGC    29637      GGA    A  A
                                AGGC   GGCGG GG CGGCGGC
                                ||||   ||||| || |||||||
                                TCCG   CCGCC CC GCCGCCG
                                  ___     A  _
GAM1143  GIT2      5'  AGGCGGCGGTGGCGGCGGC    29637      GGA    A  A
                                AGGC   GGCGG GG CGGCGGC
                                ||||   ||||| || |||||||
                                TCCG   CCGCC CC GCCGCCG
                                  ___     A  _
GAM1143  HSPBAP1   5'  AGGCGGAGCGGAGCTGGGG    29638        G    GAC  C
                                AGGCGGAG CGGAG   GG GG
                                |||||||| |||||   || ||
                                TCCGCCTC GCCTC   CC CC
                                    _    GA_  _
GAM1143  HSPC051   5'  GGCGAAGGTGGAGGTCCTGCG  29639        C    ACG_
                                GGCGGAGG GGAGG    GCG
                                |||||||| |||||    |||
                                CCGCTTCC CCTCC    CGC
                                    A     AGGA
GAM1143  HUMAGCGB  5'  GGGGAGGCGTGGAAGCGGCGGC 29641    C     __     A
              G                   GG GGAGGC  GGAGG CGGCGGCG
                                || ||||||  ||||| ||||||||
```

```
                                CC CCTCCG  CCTTC GCCGCCGC
                                 _     CA    _
GAM1143 HUMAGCGB 5' GGCGGAGGCCGGAGGCACGCG 29642         _    _  G
                                GGCGGAGGC GGAGG ACG CG
                                ||||||||| ||||| ||| ||
                                CCGCCTCCG CCTCC TGC GC
                                    G    G  _
GAM1143 HUMAGCGB 5' AGGCGAAGGCTGCGGCGGC   29640          GGAGGA
                                AGGCGGAGGC     CGGCGGC
                                ||||||||||     |||||||
                                TCCGCTTCCG     GCCGCCG
                                    AC____
GAM1143 HYPH     5' GGCGAGGCGGAGGGCG      29643      G       ACG
                                GGCG AGGCGGAGG   GCG
                                |||| |||||||||   |||
                                CCGC TCCGCCTCC   CGC

                                 _       ____
GAM1143 IMP-2    3' GGCGGGAGGCGGGGCTCGG   29644      _     A  ACGG
                                GGCGG AGGCGG GG    CGG
                                ||||| |||||| ||    |||
                                CCGCC TCCGCC CC    GCC
                                  C     _ GA__
GAM1143 KHSRP    5' AGGCGGCGGCGGCGGCGGC   29460       A    AGGA
                                AGGCGG GGCGG    CGGCGGC
                                |||||| |||||    |||||||
                                TCCGCC CCGCC    GCCGCCG
                                  G    _____
GAM1143 KIAA0215 5' AGGCGGTTGGGCGGCGGC    29645       A_  A
                                AGGCGG  GG CGGCGGC
                                ||||||  || |||||||
                                TCCGCC  CC GCCGCCG
                                  AA  C
GAM1143 KIAA0339 3' GGTGGGGGCGGAGGGCGGCGGC 29646    C  A       A
            G                    GG GG GGCGGAGG CGGCGGCG
                                || || |||||||| ||||||||
                                CC CC CCGCCTCC GCCGCCGC
                                 A  C       C
GAM1143 KIAA0350 5' AAGCGGAGGATGCGGCGGC   29647          __
                                AGGCGGAGGA  CGGCGGC
                                ||||||||||  |||||||
                                TTCGCCTCCT  GCCGCCG
                                    AC
GAM1143 KIAA0562 3' AGGCGGAGGTGGGTGGATCACA 29648         C  A_  CG
            A                    AGGCGGAGG GG  GGA  GCGG
                                ||||||||| ||  |||  ||||
                                TCCGCCTCC CC  CCT  TGTT
                                    A  CA   AG
GAM1143 KIAA0669 5' GGAGGAGGAGGCGGTGGC    29650       C    A   C
                                GGAGG GGAGG CGG GGC
                                ||||| ||||| ||| |||
```

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                                CCTCC CCTCC GCC CCG
                                  T    _  A
GAM1143  KIAA0669  5'  AGGAGGAGGCGGTGGCGGCGGC 29649     C       A  A
                G                  AGG GGAGGCGG GG CGGCGGCG
                                   ||| |||||||| || ||||||||
                                   TCC CCTCCGCC CC GCCGCCGC
                                     T       A  _
GAM1143  KIAA0995  5'  AGGAGGAGGCGGCGAGCGGCG  29651     C       A GA
                                   AGG GGAGGCGG G  CGGCG
                                   ||| |||||||| |  |||||
                                   TCC CCTCCGCC C  GCCGC
                                     T       G TC
GAM1143  KIAA1170  3'  AGGTGGAGGCGGGCGGATCAC  29652     C       A_   CG
                                   AGG GGAGGCGG  GGA  GC
                                   ||| ||||||||  |||  ||
                                   TCC CCTCCGCC  CCT  TG
                                     A       CG   AG
GAM1143  KIAA1172  5'  AGGCAGAGGCGGAGAGGTGGCG 29653              AC  C
                                   AGGCGGAGGCGGAGG  GG GGCG
                                   ||||||||||||||  || ||||
                                   TCCGTCTCCGCCTCT  CC CCGC
                                            __ A
GAM1143  KIAA1402  5'  GGCGGAGGCGTGGGGACCAAGA 29654       GA_   ____      III
                GCGGCGC                AGGCG   GGAC    GGCGGCG   C
                                   |||||   ||||   |||||||  |
                                   TCCGC   CCTG    TCGCCGC   G
                                      ACC    GTTC      III
GAM1143  KIAA1706  5'  AGGCGGCGGCAGCGGCGGC    29655       A    AGGA
                                   AGGCGG GGCGG    CGGCGGC
                                   |||||| |||||    |||||||
                                   TCCGCC CCGTC    GCCGCCG
                                      G    ____
GAM1143  KIAA1884  3'  AGGCGGGGCTCTCGGTGGCGG  29656       A   GGA_  AC
                                   AGGCGG GGC    GG  GGCGG
                                   |||||| |||    ||  |||||
                                   TCCGCC CCG    CC  CCGCC
                                      _   AGAG  A_
GAM1143  KIAA1910  5'  GGCGGAGGGCGGGGGGCG    29657         _   A  AC
                                   GGCGGAGG CGG GG  GGCG
                                   |||||||| ||| ||  ||||
                                   CCGCCTCC GCC CC  CCGC
                                        C   _  __
GAM1143  KIAA1913  5'  GGTTGGGGGGCGGGGGCCGGGGC 29658    C_  A    A  A   C
                G                   GG  GG GGCGG GG CGG GGCG
                                    ||  || ||||| || ||| ||||
                                    CC  CC CCGCC CC GCC CCGC
                                     AA  C    C  G  _
GAM1143  KIAA1940  5'  GGCCGGGGCCAGGCGGCGGCG  29659     _  A   GG   A
                                    GGC GG GGC  AGG CGGCGGCG
                                    ||| || |||  ||| ||||||||
```

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                                CCG CC CCG  TCC GCCGCCGC
                                  G _  G_  _
GAM1143 KIAA1972 5' GGAGGGGGCGGCGGCGGCGGCG 29660    C A    A A
                                GG GG GGCGG GG CGGCGGCG
                                || || ||||| || ||||||||
                                CC CC CCGCC CC GCCGCCGC
                                 T C    G _
GAM1143 KIAA1972 5' AGGGAGGGGGCGGCGG      29661    C    C AG A
                                GG GGAGG GG  G CGGCGG
                                || ||||| ||  | ||||||
                                TC CCTCC CC  C GCCGCC
                                 _    _ __ _
GAM1143 KIAA1975 5' AGGTGGAGGCGGGCGGATCACG 29662     C      A_  CG
                                AGG GGAGGCGG  GGA  GCG
                                ||| ||||||||  |||  |||
                                TCC CCTCCGCC  CCT  TGC
                                  A       CG   AG
GAM1143 LBP-32   5' GGGGGGAGGAGGCGGCGGC   29663    C A C    A
                                GG GG GG GGAGG CGGCGGC
                                || || || ||||| |||||||
                                CC CC CC CCTCC GCCGCCG
                                 _ _ T    _
GAM1143 LBP-32   5' GGAGGAGGCGGCGGCGGC    29664    C      AGGA
                                GG GGAGGCGG    CGGCGGC
                                || ||||||||    |||||||
                                CC CCTCCGCC    GCCGCCG
                                 T      _____
GAM1143 LCP      5' AGCGGAGCCGGGCGGCGGCG   29665       G   AG A
                                GGCGGAG CGG  G CGGCGGCG
                                ||||||| |||  | ||||||||
                                TCGCCTC GCC  C GCCGCCGC
                                    G  __ _
GAM1143 LHPP     3' AGGCAGGGGTGGAGGAGG    29667       A C     C
                                AGGCGG GG GGAGGA GG
                                |||||| || |||||| ||
                                TCCGTC CC CCTCCT CC
                                   C A     _
GAM1143 LHPP     3' AGGCAGGGGTGGAGGAGGCG   29666       A C     C
                                AGGCGG GG GGAGGA GGCG
                                |||||| || |||||| ||||
                                TCCGTC CC CCTCCT CCGC
                                   C A     _
GAM1143 LHPP     3' GGTGGAGGGGAGGCAGGGG   29668    C    C    A  C
                                GG GGAGG GGAGG CGG GG
                                || ||||| ||||| ||| ||
                                CC CCTCC CCTCC GTC CC
                                 A    _    _  C
GAM1143 LIMK2    5' AGGAGGAGGCGGGGGACACAG  29669     C      A    G
                                AGG GGAGGCGG GGACG CGG
                                ||| |||||||| ||||| |||
```

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                                TCC CCTCCGCC CCTGT GTC
                                  T       C    _
GAM1143 MAP     5' GGCGGCGGCTGCTGCGGCGGCG 29670      A   GGAGGA
                                GGCGG GGC     CGGCGGCG
                                ||||| |||     ||||||||
                                CCGCC CCG     GCCGCCGC
                                   G   ACGAC_
GAM1143 MAP     5' GCGGGGATCTGGGCGGCGGCG  29671     A  CGGA  A
                                GCGG GG    GG CGGCGGCG
                                |||| ||    || ||||||||
                                CGCC CC    CC GCCGCCGC
                                  _ TAGA  C
GAM1143 MAP2K5   5' GGAGGAGGAAGGCGGCGGCG   29672      C    A
                                GGAGG GGAGG CGGCGGCG
                                ||||| ||||| ||||||||
                                CCTCC CCTTC GCCGCCGC
                                   T    C
GAM1143 MGC10818 5' GGCGGCGGCGGCGGCGGC    29453      A    AGGA
                                GGCGG GGCGG    CGGCGGC
                                ||||| |||||    |||||||
                                CCGCC CCGCC    GCCGCCG
                                   G    ____
GAM1143 MGC10940 5' AGGTGGCGGCGACAGCGGCGGC 29673     C  A    GA  A
            G                    AGG GG GGCG  GG CGGCGGCG
                                ||| || ||||  || ||||||||
                                TCC CC CCGC  TC GCCGCCGC
                                  A  G    TG  _
GAM1143 MGC14376 3' GGCGGAGGTGGAAGTAGGGCGG 29674        C    AC_
                                GGCGGAGG GGAGG   GGCGG
                                |||||||| |||||   |||||
                                CCGCCTCC CCTTC   CCGCC
                                     A    ATC
GAM1143 MGC15730 5' GGTGGAGGCGGTGGCGGCG   29675    C      A  A
                                GG GGAGGCGG GG CGGCG
                                || |||||||| || |||||
                                CC CCTCCGCC CC GCCGC
                                  A       A  _
GAM1143 MGC2601  5' GGCGCGGGTCCGGGCGGCGGCG 29676     GA  CGGA  A
                                GGCG  GG    GG CGGCGGCG
                                ||||  ||    || ||||||||
                                CCGC  CC    CC GCCGCCGC
                                  G_  CAGG  C
GAM1143 MGC2817  5' GGCGCGGGCGGCGCGGGCGGCG 29677      GA    AGGAC
                                GGCG  GGCGG    GGCGGCG
                                ||||  |||||    |||||||
                                CCGC  CCGCC    CCGCCGC
                                  GC    GCGC_
GAM1143 MGC2817  5' GGCGGCGCGGGCGGCGGC    29678      AG    AG A
                                GGCGG  GCGG  G CGGCGGC
                                |||||  ||||  | |||||||
```

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                                CCGCC  CGCC  C GCCGCCG
                                  G_   __ _
GAM1143  MGC3329   3'  GGGGAGGTGGGGGACAG     29679    C    C  A
                                GG GGAGG GG GGACGG
                                || ||||| || |||||||
                                CC CCTCC CC CCTGTC
                                 _    A  C
GAM1143  MGC4415   5'  GGCGCGGTGGCGGCGGC     29681     GGAG    A  A
                                GGC    GCGG GG CGGCGGC
                                |||    |||| || |||||||
                                CCG    CGCC CC GCCGCCG
                                 _____   A  _
GAM1143  MGC4415   3'  GGCTGGGATTCTGGGCGGCGGC 29680     __   GGCGGA  A
            G                    GGC  GGA     GG CGGCGGCG
                                |||  |||     || ||||||||
                                CCG  CCT     CC GCCGCCGC
                                  AC   AAGAC_  _
GAM1143  MIC2L1    3'  GGCTGGTTCGGGCGGCGGCG   29682     _  AGG   AG A
                                GGC GG   CGG  G CGGCGGCG
                                ||| ||   |||  | ||||||||
                                CCG CC   GCC  C GCCGCCGC
                                  A  AA_   __ _
GAM1143  ORCTL3    3'  AGGAGGAGGCGGGGTGAGGCG  29683     C       A  AC_
                                AGG GGAGGCGG GG   GGCG
                                ||| |||||||| ||   ||||
                                TCC CCTCCGCC CC   CCGC
                                  T       _  ACT
GAM1143  PARVA     5'  GGCGGACGCAGCGGGCGGCGGC 29684       G    A  A
            G                    GGCGGA GCGG GG CGGCGGCG
                                |||||| |||| || ||||||||
                                CCGCCT CGTC CC GCCGCCGC
                                   G   G  C
GAM1143  PARVB     3'  AGGCAGGGGGTGGGGCAGGCG  29685       A  C  A  AC   _
                                AGGCGG GG GG GG  GGC GGCG
                                |||||| || || ||  ||| ||||
                                TCCGTC CC CC CC  CCG CCGC
                                   _  _  A  __   T
GAM1143  PEG10     3'  GGTGGAGGCGGCGGCTGTGGCG 29688    C       A  AC__
            GCG                    GG GGAGGCGG GG    GGCGGCG
                                || ||||||||  ||    |||||||
                                CC CCTCCGCC CC    CCGCCGC
                                 A       G  GACA
GAM1143  PEG10     3'  AGATGGAGGCGGCGGCGG    29686    GC       AGGA
                                AG  GGAGGCGG    CGGCGG
                                ||  ||||||||    ||||||
                                TC  CCTCCGCC    GCCGCC
                                 TA       _____
GAM1143  PEG10     3'  AGGCGGCGGCGGTGGTGG    29687       A    A  AC
                                AGGCGG GGCGG GG  GG
                                |||||| ||||| ||  ||
```

```
                                TCCGCC CCGCC CC  CC
                                   G    A  A_
GAM1143  PIP5K2B  5'  GGCGGCGGCGGCGGCGGC    29453      A    AGGA
                                GGCGG GGCGG   CGGCGGC
                                ||||| |||||   |||||||
                                CCGCC CCGCC   GCCGCCG
                                   G   ____
GAM1143  PIP5K2B  5'  GGCGGCGGCGGCGGCGGC    29453      A    AGGA
                                GGCGG GGCGG   CGGCGGC
                                ||||| |||||   |||||||
                                CCGCC CCGCC   GCCGCCG
                                   G   ____
GAM1143  PLAGL2   3'  AGGCGGGGGTGGGGGCACAG  29689       A  C  A  _
                                AGGCGG GG GG GG ACGG
                                |||||| || || || ||||
                                TCCGCC CC CC CC TGTC
                                   C  A  C  G
GAM1143  PNMA1    5'  GGCGAGGAGCGACGGCGGCG  29690       AGGC   _
                                GGCGG   GGAG GACGGCGGCG
                                |||||   |||| ||||||||||
                                CCGCT   CCTC CTGCCGCCGC
                                   ____  G
GAM1143  PPIL2    5'  GGCGGAGCGGCGGCGG     29691       G  AGGA
                                GGCGGAG CGG   CGGCGG
                                ||||||| |||   ||||||
                                CCGCCTC GCC   GCCGCC
                                   _  ____
GAM1143  PPM1A    5'  GGAGGGGGTCACCGCGGCGGCG 29692       C  AGGA__
                                GGAGG GG     CGGCGGCG
                                ||||| ||     ||||||||
                                CCTCC CC     GCCGCCGC
                                   C  AGTGGC
GAM1143  PTP4A1   5'  AGGCGGCGGCGACACAGGCGGT 29694       A   ___  A  C
            GGCG                 AGGCGG GGCGG  AGG CGG GGCG
                                ||||||| |||||  ||| ||| ||||
                                TCCGCC CCGCT  TCC GCC CCGC
                                   G    GTG  _  A
GAM1143  PTP4A1   5'  GGCGGAGCGGCGGTGGCG    29693       G  A  AC
                                GGCGGAG CGG GG  GGCG
                                ||||||| ||| ||  ||||
                                CCGCCTC GCC CC  CCGC
                                   _  G  A_
GAM1143  PTP4A1   5'  AGGCGGCGGTGGTCGTGGC   29695     GGA   A  A  GC
                                AGGC  GGCGG GG CG  GGC
                                ||||  ||||| || ||  |||
                                TCCG  CCGCC CC GC  CCG
                                   ___   A  A  A_
GAM1143  RAB6B    5'  AGGGGAGGCGGCCGGCGG    29697    C      AGGA
                                AGG GGAGGCGG   CGGCGG
                                ||| ||||||||   ||||||
```

```
                                TCC CCTCCGCC   GCCGCC
                                  _      G___
GAM1143  RAB6B    5'  AGGCGGAGGCGGAGGAAGGC  29696            C
                                AGGCGGAGGCGGAGGA GGC
                                |||||||||||||||| |||
                                TCCGCCTCCGCCTCCT CCG
                                          T
GAM1143  RANBP1   5'  GGCGCGGCGGCGGCGGC    29576     GA    AGGA
                                GGCG  GGCGG   CGGCGGC
                                ||||  |||||   |||||||
                                CCGC  CCGCC   GCCGCCG
                                  G_   _____
GAM1143  RINZF    5'  GGCGGGCGGCGGAGAGG    29698      A_      AC
                                GGCGG  GGCGGAGG  GG
                                |||||  ||||||||  ||
                                CCGCC  CCGCCTCT  CC
                                   CG       __
GAM1143  SAST     5'  AGGCGGCGGCGGCGGCGGC   29460       A    AGGA
                                AGGCGG GGCGG   CGGCGGC
                                ||||||| |||||   |||||||
                                TCCGCC CCGCC   GCCGCCG
                                   G    _____
GAM1143  SAST     5'  GGCGGAGGCGGCGGCGGCG   29496          AGGA
                                GGCGGAGGCGG   CGGCGGCG
                                ||||||||||   ||||||||
                                CCGCCTCCGCC   GCCGCCGC
                                             _____
GAM1143  SHARP    5'  AGGCGGGTGCCGGGGCGGCGGC 29699       AG  _  A  A
             G                   AGGCGG  GC GG GG CGGCGGCG
                                ||||||  || || || ||||||||
                                TCCGCC  CG CC CC GCCGCCGC
                                   CA  G  _  _
GAM1143  SMARCF1  5'  GGAGGAGGAGGCGGCGGC    29541      C    A
                                GGAGG GGAGG CGGCGGC
                                ||||| ||||| |||||||
                                CCTCC CCTCC GCCGCCG
                                   T    _
GAM1143  SMARCF1  5'  AGGAGGAGGCGGCGGCGGC   29700    C      AGGA
                                AGG GGAGGCGG   CGGCGGC
                                ||| ||||||||   |||||||
                                TCC CCTCCGCC   GCCGCCG
                                  T      _____
GAM1143  SMARCF1  5'  GGAGGAGGAGGCGGCGGC    29541      C    A
                                GGAGG GGAGG CGGCGGC
                                ||||| ||||| |||||||
                                CCTCC CCTCC GCCGCCG
                                   T    _
GAM1143  SMARCF1  5'  AGGAGGAGGCGGCGGCGGC   29700    C      AGGA
                                AGG GGAGGCGG   CGGCGGC
                                ||| ||||||||   |||||||
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                                TCC CCTCCGCC   GCCGCCG
                                  T      ____
GAM1143  SMARCF1  5'  GGAGGAGGAGGCGGCGGC    29541      C    A
                                GGAGG GGAGG CGGCGGC
                                ||||| ||||| |||||||
                                CCTCC CCTCC GCCGCCG
                                  T    _
GAM1143  SMARCF1  5'  AGGAGGAGGCGGCGGCGGC   29700    C      AGGA
                                AGG GGAGGCGG   CGGCGGC
                                ||| ||||||||   |||||||
                                TCC CCTCCGCC   GCCGCCG
                                  T      ____
GAM1143  SMPD2    5'  GACGGGGGCGGCCGGCGGCG  29701     A    AGGA
                                GGCGG GGCGG   CGGCGGCG
                                ||||| |||||   ||||||||
                                CTGCC CCGCC   GCCGCCGC
                                   C    G___
GAM1143  SPS      5'  GGCGGCGGCGGGGCCCGGGCG 29702     A    A A_  _
                                GGCGG GGCGG GG  CGG CG
                                ||||| ||||| ||  ||| ||
                                CCGCC CCGCC CC  GCC GC
                                   G    _ GG   C
GAM1143  SPTLC2   5'  AGGCGGTGGCAGCGGCGGC   29458      A    AGGA
                                AGGCGG GGCGG   CGGCGGC
                                |||||| |||||   |||||||
                                TCCGCC CCGTC   GCCGCCG
                                   A    ____
GAM1143  STAT5A   5'  GGCCGGGGTTCCTGGCGGCGGC 29703    _ A  CGGA_  A
            G                   GGC GG GG    GG CGGCGGCG
                                ||| || ||    || ||||||||
                                CCG CC CC    CC GCCGCCGC
                                  G  _  AAGGA  _
GAM1143  STX3A    5'  AGGCGGCGGCGGGCGG     29705       A    AGGACG
                                AGGCGG GGCGG     GCGG
                                |||||| |||||     ||||
                                TCCGCC CCGCC     CGCC
                                   G    _______
GAM1143  STX3A    5'  AGCTGGAGGCGCAGGCGGCGGC 29704    _     G   A
            G                   GGC GGAGGCG AGG CGGCGGCG
                                ||| ||||||| ||| ||||||||
                                TCG CCTCCGC TCC GCCGCCGC
                                  A      G  _
GAM1143  SUI1     5'  AGGCGGCGGCGGCGGTGGCG  29706      A    A  AC
                                AGGCGG GGCGG GG  GGCG
                                |||||| ||||| ||  ||||
                                TCCGCC CCGCC CC  CCGC
                                   G    G  A_
GAM1143  SV2      5'  GGCGGAGGCGGCAGCGGCG   29707          AGGA
                                GGCGGAGGCGG   CGGCGGCG
                                ||||||||||   ||||||||
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                                CCGCCTCCGCC   GTCGCCGC
                                      ____
GAM1143  TAF6L   5'  ACGGCGGCGGGGGCGGTGGCG  29708     A    A  A   C
                                GCGG GGCGG GG CGG GGCG
                                |||| ||||| || ||| ||||
                                TGCC CCGCC CC GCC CCGC
                                  G    C  _   A
GAM1143  TAF6L   5'  GGCGGGGGCGGTGGCGGCG   29709      A    A  A
                                GGCGG GGCGG GG CGGCG
                                ||||| ||||| || |||||
                                CCGCC CCGCC CC GCCGC
                                  C    A  _
GAM1143  TEX27   3'  AGGAGGGGGCGGGGGGC     29710     C  A    A  AC
                                AGG GG GGCGG GG  GGC
                                ||| || ||||| ||  |||
                                TCC CC CCGCC CC  CCG
                                  T  C    _  __
GAM1143  TIAF1   3'  GGTGGGGGCTGGAGGTGCG   29711    C  A  _    ACG
                                GG GG GGC GGAGG   GCG
                                || || ||| |||||   |||
                                CC CC CCG CCTCC   CGC
                                 A  C   A    A__
GAM1143  TIEG2   5'  ACGTGGGCTGCGGGCGGCGGCG 29712     GA   GGA  A
                                GCG  GGC   GG CGGCGGCG
                                |||  |||   || ||||||||
                                TGC  CCG   CC GCCGCCGC
                                  AC   ACG  C
GAM1143  TUBB5   5'  GGTGGACGCGGCGGCGG     29713    C   G   AGGA
                                GG GGA GCGG    CGGCGG
                                || ||| ||||    ||||||
                                CC CCT CGCC    GCCGCC
                                 A  G   _____
GAM1143  USP22   5'  GCGCGCGGGGGGCGGCGGCG  29714     GAG   A  A
                                GCG   GCGG GG CGGCGGCG
                                |||   |||| || ||||||||
                                CGC   CGCC CC GCCGCCGC
                                  G__    C  C
GAM1143  USP3    5'  AGGTGGGGGGCGGAGGAACTCCG 29715     C  A       _ GG
                                AGG GG GGCGGAGGA C  CG
                                ||| || |||||||| |  ||
                                TCC CC CCGCCTCCT G  GC
                                  A  C        T AG
GAM1143  VEGFC   5'  AGGCGGGGGCGGGGGACACCAG  29716       A    A    G
                                AGGCGG GGCGG GGACG CGG
                                |||||| ||||| ||||| |||
                                TCCGCC CCGCC CCTGT GTC
                                   _    C    G
GAM1143  VIAAT   5'  GGCGGAGCGGCGGCGGC     29717        G  AGGA
                                GGCGGAG CGG   CGGCGGC
                                ||||||| |||   |||||||
```

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                                CCGCCTC GCC    GCCGCCG
                                   _  _____
GAM1143  WAC      5'  GGCGGGCGCGCAGGCGGCG   29718      AG   G   A
                                GGCGG  GCG AGG CGGCG
                                |||||  ||| ||| |||||
                                CCGCC  CGC TCC GCCGC
                                   CG   G  _
GAM1143  WAC      5'  GGCGGGCGCGCAGGCGGCG   29718      AG   G   A
                                GGCGG  GCG AGG CGGCG
                                |||||  ||| ||| |||||
                                CCGCC  CGC TCC GCCGC
                                   CG   G  _
GAM1143  YWHAQ    5'  GGCCGGGGCGGAGGGCG     29719     _  A       ACG
                                GGC GG GGCGGAGG   GCG
                                ||| || ||||||||   |||
                                CCG CC CCGCCTCC   CGC
                                  G  _      ___
GAM1143  ZDHHC2   5'  AGGCGGAGGGGGGCGG      29724         C  AGGAC
                                AGGCGGAGG GG    GGCGG
                                |||||||||  ||    |||||
                                TCCGCCTCC CC    CCGCC
                                   _  _____
GAM1143  ZDHHC2   5'  GGCGGAGGCGGAGGCGGCG   29721            A
                                GGCGGAGGCGGAGG CGGCG
                                |||||||||||||| |||||
                                CCGCCTCCGCCTCC GCCGC
                                      _
GAM1143  ZDHHC2   5'  GGCGGTGAGGCGGCGGC     29723      AGGCG   A
                                GGCGG    GAGG CGGCGGC
                                |||||    |||| |||||||
                                CCGCC    CTCC GCCGCCG
                                   A____   _
GAM1143  ZDHHC2   5'  AGGCGGAGGCGGCGGCTGC   29720          AGGA   G
                                AGGCGGAGGCGG   CGGC GC
                                ||||||||||||   |||| ||
                                TCCGCCTCCGCC   GCCG CG
                                      ____   A
GAM1143  ZDHHC2   5'  GACGGGCTCCTGGGCGGCGGCG 29722      AG  GGA_  A
                                GGCGG  GC   GG CGGCGGCG
                                |||||  ||   || ||||||||
                                CTGCC  CG   CC GCCGCCGC
                                   __  AGGA  C
GAM1143  ZFP91    5'  AGGCGGAGGCGGCGGCCTCGGC 29725          A  ACGG
            G                    AGGCGGAGGCGG GG   CGGCG
                                ||||||||||||  ||   |||||
                                TCCGCCTCCGCC CC   GCCGC
                                      G  GGA_
GAM1143  ZFP91    5'  GGCGGAGGCGGAGGCGGCG   29721            A
                                GGCGGAGGCGGAGG CGGCG
                                |||||||||||||| |||||
```

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                                CCGCCTCCGCCTCC GCCGC
                                      _
GAM1143  LOC124044 3'  GGTGGGGCGGAGGGTCAG    29726    C  A      ACGG
                                GG GG GGCGGAGG    CGG
                                || || ||||||||    |||
                                CC CC CCGCCTCC    GTC
                                 A  _      CA__
GAM1143  LOC132573 3'  GGCGGGCGAGCGGCGGC     29727      AG   GA  A
                                GGCGG  GCG  GG CGGCGGC
                                |||||  |||  || |||||||
                                CCGCC  CGC  TC GCCGCCG
                                  __  __ _
GAM1143  LOC134553 5'  AGGCAGCGAGGGCGGCGGC   29728     GGA   GA  A
                                AGGC   GGCG  GG CGGCGGC
                                ||||   ||||  || |||||||
                                TCCG   TCGC  CC GCCGCCG
                                  ___    TC  _
GAM1143  LOC138428 5'  GGCGGAAGCGGCGAGGCGG   29729          AG  C
                                GGCGGAGGCGG  GA GGCGG
                                ||||||||||  || |||||
                                CCGCCTTCGCC  CT CCGCC
                                      G_  _
GAM1143  LOC143903 5'  AGGCGGGGGGGAGGGCG     29730       A  C    ACG
                                AGGCGG GG GGAGG   GCG
                                ||||||| || |||||   |||
                                TCCGCC CC CCTCC   CGC
                                   C  _    ____
GAM1143  LOC144165 5'  GGCGCGCTGTCGGGCGGCGGCG 29731      GAG  GGA_  A
                                GGCG   GC    GG CGGCGGCG
                                ||||   ||    || ||||||||
                                CCGC   CG    CC GCCGCCGC
                                  G__  ACAG  C
GAM1143  LOC144596 3'  AGGCCGGCGTGGGCGGCGGCG  29583      GGA   GA  A
                                AGGC   GGCG  GG CGGCGGCG
                                ||||   ||||  || ||||||||
                                TCCG   CCGC  CC GCCGCCGC
                                  G__    AC  _
GAM1143  LOC145123 5'  GGCGGAGGCGGCTGCGGCG   29554          AGGACG
                                GGCGGAGGCGG     GCGGCG
                                ||||||||||      ||||||
                                CCGCCTCCGCC     CGCCGC
                                      GA_____
GAM1143  LOC145989 5'  GGTGGCGGGTCCCCGCGGCGGC 29732    A    AGGA___
            G                    GG GGCGG      CGGCGGCG
                                 || |||||      ||||||||
                                 CC CCGCC      GCCGCCGC
                                  A    CAGGGGC
GAM1143  LOC147057 5'  AGGCGGAGGCGCGGGCCGC   29733          GA  ACG  G
                                AGGCGGAGGCG  GG   GC GC
                                ||||||||||  ||   || ||
```

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                                TCCGCCTCCGC  CC   CG CG
                                      G_ ___  G
GAM1143  LOC147429 3'  AGGCGGGGGCGGGCGGATCACA 29734       A    A_  CG
              A                    AGGCGG GGCGG  GGA  GCGG
                                   |||||| |||||  |||  ||||
                                   TCCGCC CCGCC  CCT  TGTT
                                      C    CG   AG
GAM1143  LOC148479 5'  GGCGGCGGCGGCGGCGG     29735      A    AGGA
                                   GGCGG GGCGG    CGGCGG
                                   ||||| |||||    ||||||
                                   CCGCC CCGCC    GCCGCC
                                     G    ____
GAM1143  LOC148479 5'  CGGGCGGGGGGCGGCGGCG    29736     AG    A  A
                                   CGG  GCGG GG CGGCGGCG
                                   |||  |||| || ||||||||
                                   GCC  CGCC CC GCCGCCGC
                                     __   C  C
GAM1143  LOC148479 5'  AGTGGCTGCAGGGGGCGGCGGC 29737    C  AG    A  A
              G                     GG GG  GCGG GG CGGCGGCG
                                   || ||  |||| || ||||||||
                                   TC CC  CGTC CC GCCGCCGC
                                    A  GA    C  C
GAM1143  LOC148946 5'  AGCGGAGGCGGTGGTGGTGGCG 29738           A  AC  C
                                   GGCGGAGGCGG GG  GG GGCG
                                   |||||||||| ||  || ||||
                                   TCGCCTCCGCC CC  CC CCGC
                                         A  A_  A
GAM1143  LOC149297 5'  AGGAGGAGGCGGCAGCGGCGGC 29739     C       A  A
              G                     AGG GGAGGCGG GG CGGCGGCG
                                   ||| |||||||| || ||||||||
                                   TCC CCTCCGCC TC GCCGCCGC
                                     T       G  _
GAM1143  LOC150067 5'  AGCCGGGGGGGGTGGCGGCG    29740    G   A  C  A  A
                                   AG CGG GG GG GG CGGCG
                                   || ||| || || || |||||
                                   TC GCC CC CC CC GCCGC
                                    G   C  _  A  _
GAM1143  LOC150155 3'  AGGTGGAGGCGGAGGTGGAATC 29741     C          AC  CGG
              G                     AGG GGAGGCGGAGG  GG   CG
                                   ||| ||||||||||  ||   ||
                                   TCC CCTCCGCCTCC  CC   GC
                                     A          A_  TTA
GAM1143  LOC150928 5'  GGCGGAGGCGGCTGCGGCG    29554           AGGACG
                                   GGCGGAGGCGG      GCGGCG
                                   ||||||||||      ||||||
                                   CCGCCTCCGCC      CGCCGC
                                         GA____
GAM1143  LOC151512 5'  AGGCGCAGGCGGAGAGGCG    29742       G        AC
                                   AGGCG AGGCGGAGG  GGCG
                                   ||||| |||||||||  ||||
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                                TCCGC TCCGCCTCT  CCGC
                                  G       __
GAM1143  LOC152106 5'  GCGGAGGCAGCGGCGGCG    29743          AGGA
                                GCGGAGGCGG   CGGCGGCG
                                ||||||||||   ||||||||
                                CGCCTCCGTC   GCCGCCGC
                                     _____
GAM1143  LOC153546 5'  GGCTGGGCGGGGGGCGGCGGCG 29744     GGA    A  A
                                GGC   GGCGG GG CGGCGGCG
                                |||   ||||| || ||||||||
                                CCG   CCGCC CC GCCGCCGC
                                  AC_    C  C
GAM1143  LOC157254 3'  GACGGGGCAGGGCGGCGGCG   29746      A    A  A
                                GGCGG GGCGG GG CGGCGGCG
                                ||||| ||||| || ||||||||
                                CTGCC CCGTC CC GCCGCCGC
                                  _    _ _
GAM1143  LOC157254 3'  GGGTGAGGCGGTGTGGCGGCG  29745    CG      AGGAC
                                GG  GAGGCGG    GGCGGCG
                                ||  |||||||    |||||||
                                CC  CTCCGCC    CCGCCGC
                                 CA      ACA__
GAM1143  LOC195977 3'  GGCGGAGGCGGGAGTGGAGGTG 29747           A___   C  C
           G                     GGCGGAGGCGG    GGA GG GG
                                ||||||||||    ||| || ||
                                CCGCCTCCGCC    CCT CC CC
                                       CTCA  _  A
GAM1143  LOC195977 3'  AGGCGGAGGCGGTGGTGGTGG  29749           A  AC  C
                                AGGCGGAGGCGG GG  GG GG
                                |||||||||||| ||  || ||
                                TCCGCCTCCGCC CC  CC CC
                                       A  A_  A
GAM1143  LOC195977 3'  GGTGGAGGCGGAGGCGGTGG   29748    C         A   C
                                GG GGAGGCGGAGG CGG GG
                                || |||||||||| ||| ||
                                CC CCTCCGCCTCC GCC CC
                                 A          _   A
GAM1143  LOC196500 5'  GGCGCGGGGCGGCGGC      29751     GGAG    A  A
                                GGC    GCGG GG CGGCGGC
                                |||    |||| || |||||||
                                CCG    CGCC CC GCCGCCG
                                  _____   _ _
GAM1143  LOC196500 5'  GGCGCGGGGCGGCGG       29750     GGAG    A  A
                                GGC    GCGG GG CGGCGG
                                |||    |||| || ||||||
                                CCG    CGCC CC GCCGCC
                                  _____   _ _
GAM1143  LOC197136 3'  GGTGGGGCGGAGGGTCAG    29726    C  A       ACGG
                                GG GG GGCGGAGG    CGG
                                || || ||||||||    |||
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                                CC CC CCGCCTCC    GTC
                                 A  _       CA__
GAM1143  LOC197423 5'  GGAGGAGGAGGCGGCGGC    29541       C     A
                                GGAGG GGAGG CGGCGGC
                                ||||| ||||| |||||||
                                CCTCC CCTCC GCCGCCG
                                   T    _
GAM1143  LOC199986 3'  AGGCGGAGGTGAAGCTGAGG   29752          C   __ C
                                AGGCGGAGG GGAG  GA GG
                                ||||||||| ||||  || ||
                                TCCGCCTCC CTTC  CT CC
                                     A   GA  _
GAM1143  LOC199994 5'  AGCGGAGGCGGAGGACGCG    29753              G
                                GGCGGAGGCGGAGGACG CG
                                |||||||||||||||| ||
                                TCGCCTCCGCCTCCTGC GC
                                                 _
GAM1143  LOC200169 3'  AGGTGGAGGCGGAGACAG     29754     C         G
                                AGG GGAGGCGGAG ACGG
                                ||| |||||||||| ||||
                                TCC CCTCCGCCTC TGTC
                                  A         _
GAM1143  LOC201595 5'  GGGGTGGAGGAAGCGGCGGCG  29755    C  A  C     A
                                GG GG GG GGAGG CGGCGGCG
                                || || || ||||| ||||||||
                                CC CC CC CCTTC GCCGCCGC
                                 _  A  T    _
GAM1143  LOC202518 5'  AGGCGGGGGGTAGGGGGCG     29756        A  CG A  AC
                                AGGCGG GG  G GG  GGCG
                                |||||| ||  | ||  ||||
                                TCCGCC CC  C CC  CCGC
                                    C  AT _  __
GAM1143  LOC220565 5'  GGAGGAGGAGGCGGCGGC     29541       C     A
                                GGAGG GGAGG CGGCGGC
                                ||||| ||||| |||||||
                                CCTCC CCTCC GCCGCCG
                                   T    _
GAM1143  LOC220565 5'  AGGCGGCGGCGGAGGGCG     29571        A       ACG
                                AGGCGG GGCGGAGG   GCG
                                |||||| ||||||||   |||
                                TCCGCC CCGCCTCC   CGC
                                   G       ___
GAM1143  LOC220932 3'  GGCTGGGGCGGACGGCG      29757     _  A   GGA
                                GGC GG GGC   GGACGGCG
                                ||| || |||   ||||||||
                                CCG CC CCG   CCTGCCGC
                                  A  _  ____
GAM1143  LOC221424 5'  GGTGGAGGCGGCGGCTGTGGCG 29758     C       A  AC__
                                GG GGAGGCGG GG    GGCG
                                || |||||||| ||    ||||
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                                CC CCTCCGCC CC    CCGC
                                 A       G  GACA
GAM1143  LOC222510 5'  AGGCGGCGGCGACCACAGACGG 29759       A    A___
                CGGCG                    AGGCGG GGCGG    GGACGGCGGCG
                                |||||| |||||    ||||||||||
                                TCCGCC CCGCT    TCTGCCGCCGC
                                   G     GGTG
GAM1143  LOC254100 5'  AGGGGAGGCGGAGGCCAGCG   29760     C         A
                                AGG GGAGGCGGAGG CGGCG
                                ||| |||||||||| |||||
                                TCC CCTCCGCCTCC GTCGC
                                  _         G
GAM1143  LOC254345 5'  GGGGAGGCGGGGGCCGG     29761    C       A  A
                                GG GGAGGCGG GG CGG
                                || |||||||| || |||
                                CC CCTCCGCC CC GCC
                                 _       C  G
GAM1143  LOC254351 5'  AGGCGGAGGCGGGTGGATCAC  29604           A_   CG
                                AGGCGGAGGCGG  GGA  GC
                                ||||||||||||  |||  ||
                                TCCGCCTCCGCC  CCT  TG
                                       CA   AG
GAM1143  LOC254552 5'  GGCGAGGCGGGGCGGGGC    29762      G     A  A   C
                                GGCG AGGCGG GG CGG GGC
                                |||| |||||| || ||| |||
                                CCGC TCCGCC CC GCC CCG
                                  _     _ _  _
GAM1143  LOC254892 5'  AGGCGGAGGCGGCAAAACCGGC 29763            _    _
                G                    AGGCGGAGGCGG AGGAC GGCG
                                |||||||||||| ||||| ||||
                                TCCGCCTCCGCC TTTTG CCGC
                                       G    G
GAM1143  LOC255271 5'  AGGCGAGGCGGGCGCGG     29764       G     AGGACG
                                AGGCG AGGCGG     GCGG
                                ||||| ||||||     ||||
                                TCCGC TCCGCC     CGCC
                                   _     CG____
GAM1143  LOC257619 5'  AGGCGGGGGTAGGGGGCG    29756        A  CG A  AC
                                AGGCGG GG  G GG  GGCG
                                |||||| ||  | ||  ||||
                                TCCGCC CC  C CC  CCGC
                                   C  AT _  __
GAM1143  LOC51072  5'  AGCCGGGGCGGTGGCGGCG   29765    G   A    A  A
                                AG CGG GGCGG GG CGGCG
                                || ||| ||||| || |||||
                                TC GCC CCGCC CC GCCGC
                                 G   _    A  _
GAM1143  LOC51104  5'  GGCGAAGAAGGACGGCGGCG  29766        GCG
                                GGCGGAG   GAGGACGGCGGCG
                                |||||||   ||||||||||||||
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                                CCGCTTC  TTCCTGCCGCCGC
                                   ___
GAM1143 LOC51112 5' AGGGGAGGCGGGCTGGCG   29767    C      AG AC
                                AGG GGAGGCGG  G  GGCG
                                ||| ||||||||  |  ||||
                                TCC CCTCCGCC  C  CCGC
                                  _      __ GA
GAM1143 LOC56926 5' AGCTGGGACGGGACGGCGGCG 29768    _ A    AG
                                GGC GG GGCGG  GACGGCGGCG
                                ||| || |||||  ||||||||||
                                TCG CC CTGCC  CTGCCGCCGC
                                  A _    __
GAM1143 LOC91272 5' GGTGGGGGCGGCGGCGGCG   29770   C A    AGGA
                                GG GG GGCGG   CGGCGGCG
                                || || |||||   ||||||||
                                CC CC CCGCC   GCCGCCGC
                                 A  C   _____
GAM1143 LOC91272 5' GGCGGTGGTGGGGGCGGCGGCG 29769      A  C  A  A
                                GGCGG GG GG GG CGGCGGCG
                                ||||| || || || ||||||||
                                CCGCC CC CC CC GCCGCCGC
                                   A  A  C  _
GAM1144 DAF     3' TGTGTGTATTTTCTTCT    29773         CCC
                                TGTGTGTATT   CTTCT
                                ||||||||||   |||||
                                ACACACATAA   GAAGA
                                     AA_
GAM1144 SMAC    3' TGCACCCCTTCTCTTAG    29774     TT      CC
                                TGTA  CCCCTTCTC  AG
                                ||||  |||||||||  ||
                                ACGT  GGGGAAGAG  TC
                                  __       AA
GAM1144 SMAC    3' TGCACCCCTTCTCTTAG    29774     TT      CC
                                TGTA  CCCCTTCTC  AG
                                ||||  |||||||||  ||
                                ACGT  GGGGAAGAG  TC
                                  __       AA
GAM1144 SMAC    3' TGCACCCCTTCTCTTAG    29774     TT      CC
                                TGTA  CCCCTTCTC  AG
                                ||||  |||||||||  ||
                                ACGT  GGGGAAGAG  TC
                                  __       AA
GAM1144 DIO2    5' TCTGTGCTTCTCTTTCTCCCAG 29775   G    A  CCC
           T                     T TGTGT TTC   TTCTCCCAGT
                                | ||||| |||   ||||||||||
                                A ACACG AAG   AAGAGGGTCA
                                 G    _  AGA
GAM1144 DIO2    3' TATGTGTATTCTCTATGCCA  29776         CC  TCTC
                                TGTGTGTATTC  CT   CCA
                                ||||||||||  ||   |||
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                                ATACACATAAG  GA   GGT
                                      A_  TAC_
GAM1144  DIO2    5'  TCTGTGCTTCTCTTTCTCCCAG 29775   G    A  CCC
             T                   T TGTGT TTC   TTCTCCCAGT
                                 | ||||| |||   ||||||||||
                                 A ACACG AAG   AAGAGGGTCA
                                  G    _  AGA
GAM1144  DIO2    3'  TATGTGTATTCTCTATGCCA  29776         CC  TCTC
                                 TGTGTGTATTC  CT   CCA
                                 ||||||||||  ||   |||
                                 ATACACATAAG  GA   GGT
                                       A_  TAC_
GAM1144  FADS1   3'  TGAGGTTCTCTTCTCCCAGT  29777   TA_  CC
                                 TG   TTC  CTTCTCCCAGT
                                 ||   |||  ||||||||||
                                 AC   AAG  GAAGAGGGTCA
                                   TCC   A_
GAM1144  FLJ11218 3'  TGTGTGTATTTTTTCCCA   29778         CCCC  C
                                 TGTGTGTATT    TT TCCCA
                                 |||||||||    || |||||
                                 ACACACATAA    AA AGGGT
                                       _____  A
GAM1144  FLJ14966 5'  GTACTCCCTTTTTCCCG    29779        C  C    A
                                 GTATTCCC TT TCCC G
                                 |||||||| || |||| |
                                 CATGAGGG AA AGGG C
                                      A  A    C
GAM1144  FLJ22644 3'  TATGTGTATGTTTCCCAG    29780        TCCCCTTC
                                 TGTGTGTAT       TCCCAG
                                 |||||||||       ||||||
                                 ATACACATA       AGGGTC
                                       CAA_____
GAM1144  KIAA0924 5'  TGTGTGCAATTCTTCCAG    29781        TTCCCC    C
                                 TGTGTGTA     TTCT CCAG
                                 ||||||||     |||| ||||
                                 ACACACGT     AAGA GGTC
                                      T_____    A
GAM1144  RPS6KC1  3'  TGTGTATATTCTTTTTTCT   29782          CCC_
                                 TGTGTGTATTC    TTCT
                                 ||||||||||    ||||
                                 ACACATATAAG    AAGA
                                        AAAA
GAM1144  LOC170395 3'  TGTGGTGGGTCTTCTCCCAGT  29783      T  ATTCCC
                                 TGTG GT     CTTCTCCCAGT
                                 |||| ||     ||||||||||
                                 ACAC CA     GAAGAGGGTCA
                                   _ CCCA__
GAM1144  LOC90639 3'  TGTGTTCCCCTCACATCCTGGT 29784       AT      C__   CA
                                 TGTGT  TCCCCTT   TCC  GT
                                 |||||  |||||||   |||  ||
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                                ACACA  AGGGGAG   AGG  CA
                                  __      TGT   AC
GAM1145  GRM1     3'  TACGTAGGAGAAATAAT     29787        TA
                                TACGTAG  AGAAATAAT
                                |||||||  |||||||||
                                ATGCATC  TCTTTATTA
                                   C_
GAM1145  FLJ20073 3'  TAGTAAGAATAAATGTT     29788         A   T
                                TAGTAAGAA TAA ATGTT
                                ||||||||| ||| |||||
                                ATCATTCTT ATT TACAA
                                     _  _
GAM1145  TCEA3    3'  TACGTAGTATGGAAGTAATAT  29789         A_  A
                                TACGTAGTA  GAA TAATAT
                                |||||||||  ||| ||||||
                                ATGCATCAT  CTT ATTATA
                                     AC   C
GAM1146  CRI1     3'  GAAACTTTTTAATTAAGG    29792      G       C
                                GAAA TTTTTAGTT AGG
                                |||| ||||||||| |||
                                CTTT AAAAATTAA TCC
                                  G        T
GAM1146  GRB10    3'  GAAAGTTTACAATTAGG     29793         T    C
                                GAAAGTTT TAGTT AGG
                                |||||||| ||||| |||
                                CTTTCAAA GTTAA TCC
                                     T    _
GAM1146  IGF2R    3'  GAAAGTTTCTGTTAAAGG    29794          A   C_
                                GAAAGTTTTT GTT  AGG
                                |||||||||| |||  |||
                                CTTTCAAAGA CAA  TCC
                                     _  TT
GAM1146  ITSN1    3'  GAAAGTTTCTAACTACAGG   29795          GT _
                                GAAAGTTTTTA  T CAGG
                                |||||||||||  | ||||
                                CTTTCAAAGAT  A GTCC
                                      TG T
GAM1146  KIAA0442 3'  GAAGCTTTCTTTCAGG      29796     A     AG
                                GAA GTTTTT  TTCAGG
                                ||| ||||||  ||||||
                                CTT CGAAAG  AAGTCC
                                  _     A_
GAM1146  P23      3'  GAGGTTTTCAGCCCGGG     29797    AA         A
                                GA  GTTTTTAGTTC GG
                                ||  ||||||||||| ||
                                CT  CAAAAGTCGGG CC
                                 C_          C
GAM1146  TEM7     3'  TCCAAAGTTTAGAGCAGG    29798    G     TT   TT
                                TC AAAGTT  TAG  CAGG
                                || ||||||  |||  ||||
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                                AG TTTCAA  ATC  GTCC
                                 G     __  TC
GAM1146  TM7SF3   3'  CCGAAAGTTTAGACAGG     29799        TT   TT
                                TCGAAAGTT  TAG  CAGG
                                |||||||||  |||  ||||
                                GGCTTTCAA  ATC  GTCC
                                     __  T_
GAM1146  ARFGAP3  3'  GAAGCCTCCTGGTTCAGG    29800     A     A_
                                GAA GTTTTT  GTTCAGG
                                |||  ||||||  |||||||
                                CTT CGGAGG  CAAGTCC
                                  _     AC
GAM1146  ARHGAP11A 3'  AAAAGCCAGTTCAGG       29801       TTT
                                GAAAGT   TAGTTCAGG
                                ||||||   |||||||||
                                TTTTCG   GTCAAGTCC
                                    ___
GAM1146  BHC80    3'  CGAAAGTTTAGAAACAGG    29802        TT   TT_
                                CGAAAGTT  TAG   CAGG
                                ||||||||  |||   ||||
                                GCTTTCAA  ATC   GTCC
                                     __  TTT
GAM1146  CEZANNE  3'  AAAAGTTTCCAGCCAGG     29803           T
                                GAAAGTTTTTAGT CAGG
                                |||||||||||| ||||
                                TTTTCAAAGGTCG GTCC
                                        _
GAM1146  DKFZP434P1750 5'  GAGAGTTTTCAGCAGG      29804    A       TT
                                GA AGTTTTTAG  CAGG
                                || |||||||||  ||||
                                CT TCAAAAGTC  GTCC
                                 C       __
GAM1146  FLJ14906  3'  GAAAGTTTTAAATTAAGG    29805        T   C
                                GAAAGTTTT AGTT AGG
                                ||||||||| |||| |||
                                CTTTCAAAA TTAA TCC
                                      T   T
GAM1146  FLJ20487  3'  GAAGGATTCAGCTCAGG     29806     A TT
                                GAA G  TTTAGTTCAGG
                                ||| |  ||||||||||
                                CTT C  AAGTCGAGTCC
                                  _ CT
GAM1146  FLJ23040  3'  TCAAAAGTTTTCCAG       29807         TTAG
                                TCGAAAGTTT   TTCAG
                                ||||||||||   |||||
                                AGTTTTCAAA   AGGTC
                                     _____
GAM1146  IL1RAPL1  3'  TCGAGGATTTAGTTCCAGG   29808      AA TT      _
                                TCGA  G  TTTAGTTC AGG
                                ||||  |  |||||||| |||
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                                AGCT  C  AAATCAAG TCC
                                  __ CT       G
GAM1146 KIAA0173  3'  TCAAGGGTTTCTCCTCAGG   29809      AA     AG
                                TCGA  GTTTTT  TTCAGG
                                ||||  ||||||  ||||||
                                AGTT  CAAAGA  GAGTCC
                                  CC     G_
GAM1146 KIAA1911  3'  TCAAAGTATAGTTCAGG     29810    G    TTT
                                TC AAAGT   TAGTTCAGG
                                || |||||   |||||||||
                                AG TTTCA   ATCAAGTCC
                                 _    T__
GAM1146 NYD-SP29  3'  TCAAAAGTTTTAATAGCAGG   29811          TAGTT
                                TCGAAAGTTTT    CAGG
                                ||||||||||     ||||
                                AGTTTTCAAAA    GTCC
                                      TTATC
GAM1146 P450RAI-2 3'  TCAAAAACAATTGGTTCAGG   29812        TT  A
                                TCGAAAGT  TT GTTCAGG
                                ||||||||  || |||||||
                                AGTTTTTG  AA CAAGTCC
                                     TT  C
GAM1146 SCIN      3'  CGAAAGTTTCCTTCAGG     29813          AG
                                CGAAAGTTTTT  TTCAGG
                                ||||||||||  ||||||
                                GCTTTCAAAGG  AAGTCC
                                          __
GAM1146 SPRY1     3'  GAAAGCTAAAAGTTCAGG    29814       TTT
                                GAAAGTT   AGTTCAGG
                                |||||||   ||||||||
                                CTTTCGA   TCAAGTCC
                                    TTT
GAM1146 LOC134957 3'  GAAAGTTTAATACAGG      29815       TT   T
                                GAAAGTT  TAGT CAGG
                                |||||||  |||| ||||
                                CTTTCAA  ATTA GTCC
                                    __   T
GAM1146 LOC146795 3'  TCCAAAGTTTCCTGTTTTCAGG 29816    G      TA __
                                TC AAAGTTTT  GT  TCAGG
                                || ||||||||  ||  |||||
                                AG TTTCAAAG  CA  AGTCC
                                 G       GA  AA
GAM1146 LOC154872 3'  TCGAAAATTCTTCAG       29817         TTAG
                                TCGAAAGTTT    TTCAG
                                ||||||||||    |||||
                                AGCTTTTAAG    AAGTC
                                          _____
GAM1146 LOC157651 5'  GAAAGTCTTGTTCAGG      29818         TA
                                GAAAGTTTT  GTTCAGG
                                |||||||||  |||||||
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                                CTTTCAGAA  CAAGTCC
                                    __
GAM1146  LOC165614 5'  TCTGAAGTTTTCCTCAGG    29819    GA      AG
                                TC  AAGTTTTT  TTCAGG
                                ||  ||||||||  ||||||
                                AG  TTCAAAAG  GAGTCC
                                 AC      __
GAM1146  LOC219722 3'  GAAAGTCTGTAGCAGG     29820        T   TT
                                GAAAGTTT TAG  CAGG
                                |||||||| |||  ||||
                                CTTTCAGA ATC  GTCC
                                     C  __
GAM1146  LOC257282 5'  GAAAGTTCAGGAGGGTTCAGG  29821        TTA___
                                GAAAGTTT     GTTCAGG
                                ||||||||     |||||||
                                CTTTCAAG     CAAGTCC
                                     TCCTCC
GAM1146  LOC257466 3'  GAAATTTTTTCAACTCAGG   29822     G_     GT
                                GAAA  TTTTTA  TCAGG
                                ||||  ||||||  |||||
                                CTTT  AAAAGT  AGTCC
                                  AA     TG
GAM1147  ADD2     3'  TGTCAGCACTGGTGGTCAT   29825          A  A
                                TGTCAGCACTG TG TTAT
                                |||||||||||| || ||||
                                ACAGTCGTGAC AC AGTA
                                      C  C
GAM1147  CHRNA3   3'  TGTCAGTGGTGATGATCACGT  29826       CAC
                                TGTCAG   TGATGATTATGT
                                ||||||   ||||||||||||
                                ACAGTC   ACTACTAGTGCA
                                   ACC
GAM1147  LAPTM5   3'  TCAGCAGAACAATTGTGTGT   29827       CT  TG   A
                                TCAGCA  GA  ATT TGTGT
                                ||||||  ||  ||| |||||
                                AGTCGT  TT  TAA ACACA
                                   C_  GT   C
GAM1147  DKFZp434B0417 3'  TGTTAACACCATTTATGTGT   29828     C      ATGA
                                TGT AGCACTG    TTATGTGT
                                ||| |||||||    ||||||||
                                ACA TTGTGGT    AATACACA
                                  A      A___
GAM1147  DKFZp761O0113 3'  TGTTAGCATTGATGATCTTTGT 29829     C    C       ATG
                                TGT AGCA TGATGATT   TGT
                                ||| |||| ||||||||   |||
                                ACA TCGT ACTACTAG   ACA
                                  A   A       AA_
GAM1147  DKFZp762L0311 3'  TGTCGACACTGATGGCACGTGT 29830      A        AT
                                TGTC GCACTGATG  TATGTGT
                                |||| |||||||||  |||||||
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                                ACAG TGTGACTAC  GTGCACA
                                  C       C_
GAM1147  LOC149837 5'  TGTCGGGGCTGCTCATGTGTC  29831     AGCA   ATGA
                                TGTC   CTG   TTATGTGTC
                                ||||   |||   |||||||||
                                ACAG   GAC   AGTACACAG
                                  CCCC  G___
GAM1147  LOC153883 3'  TGCAGCACTGATGTG      29832    T       TGATTA
                                TG CAGCACTGA     TGTG
                                || |||||||||     ||||
                                AC GTCGTGACT     ACAC
                                 _      _______
GAM1147  LOC256568 5'  GCACTGACTATGTGT      29833        GAT
                                GCACTGAT   TATGTGT
                                ||||||||   |||||||
                                CGTGACTG   ATACACA
                                    ___
GAM1148  IL8      3'  GTATATTCTCCCGTGCAATA   29836        TA   A
                                GTATATTTT  CGT CAATA
                                |||||||||  ||| |||||
                                CATATAAGA  GCA GTTAT
                                     GG   C
GAM1148  FAM8A1    3'  ACTCATATATAGAAAATGTGCA 29837         TTTTAC_  A
           ATA                    ACTCGTATAT      GT CAATA
                                |||||||||||      || |||||
                                TGAGTATATA      CA GTTAT
                                     TCTTTTA  C
GAM1148  PELI2     3'  TATTTCCACAGGTACAATA   29838        __
                                TATTTTTAC  GTACAATA
                                |||||||||  ||||||||
                                ATAAAGGTG  CATGTTAT
                                     TC
GAM1148  TAF1B     3'  ACTTTTATATTTTTACATA   29839     CG
                                ACT  TATATTTTTACGTA
                                |||  ||||||||||||||
                                TGA  ATATAAAAATGTAT
                                  AA
GAM1148  LOC126917 3'  CATATATCTTTTATGTACA   29840         AC_
                                CGTATATTTTT   GTACA
                                ||||||||||   |||||
                                GTATATAGAAA   CATGT
                                      ATA
GAM1148  LOC133634 5'  GTATGTTCAACATACAAT    29841      A   TT
                                GTAT TTT  ACGTACAAT
                                |||| |||  |||||||||
                                CATA AAG  TGTATGTTA
                                  C   T_
GAM1148  LOC146909 3'  CGTGTATCCTATGTACAATA   29842     A     TAC
                                CGT TATTTT   GTACAATA
                                ||| ||||||   ||||||||
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                                GCA ATAGGA   CATGTTAT
                                  C     TA_
GAM1148 LOC92218 3' ACTCGTTATTTTCACTTTGCAA 29843       A       GTA_
            TA                    ACTCGT TATTTTTAC    CAATA
                                  |||||| |||||||||    |||||
                                  TGAGCA ATAAAAGTG    GTTAT
                                    _       AAAC
GAM1149 MEN1    5' AGATACATCCAAAGTCGT    29846       ATA
                                  AGATATG   AAAGTCGT
                                  ||||||| ||||||||
                                  TCTATGT   TTTCAGCA
                                     AGG
GAM1149 MLLT2   3' AGATATGACTACAGCTGTC   29847        AAA   C
                                  AGATATGAT   AGT GTC
                                  ||||||||| ||| |||
                                  TCTATACTG   TCG CAG
                                       ATG   A
GAM1149 NSF     3' AGATATGACATCCAAGTC    29848         A__
                                  AGATATGATA   AAGTC
                                  ||||||||||  |||||
                                  TCTATACTGT   TTCAG
                                       AGG
GAM1149 XRCC4   3' AATATGATAAATGTGTC     29849          A  C
                                  GATATGATAAA GT GTC
                                  |||||||||||| || |||
                                  TTATACTATTT CA CAG
                                        A  _
GAM1149 XRCC4   3' AATATGATAAATGTGTC     29849          A  C
                                  GATATGATAAA GT GTC
                                  |||||||||||| || |||
                                  TTATACTATTT CA CAG
                                        A  _
GAM1149 XRCC4   3' AATATGATAAATGTGTC     29849          A  C
                                  GATATGATAAA GT GTC
                                  |||||||||||| || |||
                                  TTATACTATTT CA CAG
                                        A  _
GAM1149 ZFP36   3' AGAATAAATAAAGTCGTC    29850     TAT     A
                                  AGA   GATAAA GTCGTC
                                  |||   |||||| ||||||
                                  TCT   TTATTT CAGCAG
                                    TAT     _
GAM1149 C20orf100 3' AAATAGACAAAAGTCGTC    29851       T
                                  AGATA GATAAAAGTCGTC
                                  ||||| ||||||||||||
                                  TTTAT CTGTTTTCAGCAG
                                     _
GAM1149 KIAA0237 5' GATGTGATAAAAGGGTC     29852     A       TC
                                  GAT TGATAAAAG  GTC
                                  ||| |||||||||  |||
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                                CTA ACTATTTTC  CAG
                                  C       C_
GAM1149  KIAA0628  3'  GACATTGATAAAAGTTGT    29853      _       C
                                GATAT GATAAAAGT GT
                                ||||| ||||||||| ||
                                CTGTA CTATTTTCA CA
                                   A       A
GAM1149  MGC13071  5'  GATGTCGACTAAGTCGTC    29854     A_   AA
                                GAT  TGAT  AAGTCGTC
                                |||  ||||  ||||||||
                                CTA  GCTG  TTCAGCAG
                                  CA   A_
GAM1149  MYH10     5'  AGATATGAAAAGTACGT     29855        TA    _
                                AGATATGA  AAAGT CGT
                                ||||||||  ||||| |||
                                TCTATACT  TTTCA GCA
                                    __    T
GAM1149  PRO2435   5'  AAATATGATAAAAGAAGC    29856           TC
                                AGATATGATAAAAG  GT
                                ||||||||||||||  ||
                                TTTATACTATTTTC  CG
                                        TT
GAM1149  ZNF384    5'  GATATAATAACAGCAGTC    29857         A   C
                                GATATGATAA AGT GTC
                                |||||||||| ||| |||
                                CTATATTATT TCG CAG
                                     G   T
GAM1150  FABP1     3'  ACACACTAAAATAATAT     29860      TTT
                                ACGCA   CTAAAATAATAT
                                |||||   ||||||||||||
                                TGTGT   GATTTTATTATA
                                  ____
GAM1150  KCNAB1    3'  CGCATTTTAAAATAATAT    29861       C
                                CGCATTT TAAAATAATAT
                                ||||||| ||||||||||
                                GCGTAAA ATTTTATTATA
                                  _
GAM1150  MGC5521   3'  TCACATTCTAAAATAATAT   29862      CAT
                                TCACG   TTCTAAAATAATAT
                                |||||   ||||||||||||||
                                AGTGT   AAGATTTTATTATA
                                  ____
GAM1150  SEC24A    3'  ACACCGTATCTAAAATAATAT 29863     ATT_
                                ACGC    TCTAAAATAATAT
                                ||||    ||||||||||||
                                TGTG    AGATTTTATTATA
                                  GCAT
GAM1151  P2RY6     3'  ATGTTGCTGTGCCAGTC     29866       AC   TAGTG
                                ATGTTGCT  GCC    GGTC
                                ||||||||  |||    ||||
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                                TACAACGA  CGG    TCAG
                                    CA  _____
GAM1151  DKFZP727G051 3'  TGCTGTGTGGTGTCTGGTGGGT 29867      CTACGC__  A
            CT                    TGTTG       CT GTGGGTCT
                                  |||||       || ||||||||
                                  ACGAC       GA CACCCAGA
                                     ACACCACA  C
GAM1151  ICK      3'  TATGTTGCTACAGTATGGT   29868          GCCT   _
                                  TATGTTGCTAC    AGTG GGT
                                  ||||||||||    |||| |||
                                  ATACAACGATG    TCAT CCA
                                        ____   A
GAM1151  KIAA1024  3'  TATGTTGCTATTTCCCTTAGT  29869         CG_   AGTG
                                  TATGTTGCTA   CCT    GGT
                                  |||||||||   |||    |||
                                  ATACAACGAT   GGG    TCA
                                       AAA   AA__
GAM1151  LOC128209 3'  TGTTGTTGGCCTGTGGGTCT   29870      CTAC    A
                                  TGTTG    GCCT GTGGGTCT
                                  |||||    |||| ||||||||
                                  ACAAC    CGGA CACCCAGA
                                     AAC_   _
GAM1151  LOC170217 5'  ACCAATGCCTGGTGGGTCT    29871      C_    A
                                  GCTA  GCCT GTGGGTCT
                                  ||||  |||| ||||||||
                                  TGGT  CGGA CACCCAGA
                                    TA    C
GAM1151  LOC170218 5'  ACCAATGCCTGGTGGGTCT    29871      C_    A
                                  GCTA  GCCT GTGGGTCT
                                  ||||  |||| ||||||||
                                  TGGT  CGGA CACCCAGA
                                    TA    C
GAM1151  LOC220573 5'  TGTTGCTAAGCAGTGGGTCT   29872         C  CT
                                  TGTTGCTA GC  AGTGGGTCT
                                  |||||||| ||  |||||||||
                                  ACAACGAT CG  TCACCCAGA
                                       T  __
GAM1151  LOC255000 3'  TGTTCTACGCCTGCACGTCT   29873      G       A   G
                                  TGTT CTACGCCT GTG GTCT
                                  |||| |||||||| ||| ||||
                                  ACAA GATGCGGA CGT CAGA
                                    _       _  G
GAM1152  EPS15    3'  TCAGAATAACTACAGAACA    29876      TACT
                                  TTAG    GCTACAGAACA
                                  ||||    ||||||||||||
                                  AGTC    TGATGTCTTGT
                                    TTAT
GAM1152  HLCS     3'  TTAATAAAAACACAGAACA    29877        CT_  T
                                  TTAGTA   GC ACAGAACA
                                  ||||||   || ||||||||
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                                AATTAT   TG TGTCTTGT
                                   TTT  _
GAM1152 HMGCR    3' TTAGTAATTGTACAAAACA   29878       C_  C
                                TTAGTA  TG TACAGAACA
                                ||||||  || |||||||||
                                AATCAT  AC ATGTTTTGT
                                   TA  _
GAM1152 LBR      3' TTAGCACTGATAAAACA     29879         CTAC
                                TTAGTACTG    AGAACA
                                |||||||||    ||||||
                                AATCGTGAC    TTTTGT
                                     TA__
GAM1152 MYO6     3' TTAGTACCTCTTATCACAGAA 29880         G ____
                                TTAGTACT CT    ACAGAA
                                |||||||| ||    ||||||
                                AATCATGG GA    TGTCTT
                                     A  ATAG
GAM1152 NAPB     3' TAGTCACAGCACAGAACA    29881      _  T  T
                                TAGT AC GC ACAGAACA
                                |||| || || ||||||||
                                ATCA TG CG TGTCTTGT
                                  G  T  _
GAM1152 PKP2     3' TCAACACTGCAGAACA      29882          TAC
                                TTAGTACTGC   AGAACA
                                ||||||||||   ||||||
                                AGTTGTGACG   TCTTGT
                                      ___
GAM1152 PTPRJ    3' TTAGTTCTCACAAAACAGAACA 29883       A  _  T__
                                TTAGT CT GC   ACAGAACA
                                ||||| || ||   ||||||||
                                AATCA GA TG   TGTCTTGT
                                   A  G  TTT
GAM1152 SP110    3' TCAGTCTTTACAGAACA     29884       A  GC
                                TTAGT CT  TACAGAACA
                                ||||| ||  |||||||||
                                AGTCA GA  ATGTCTTGT
                                   _  A_
GAM1152 SP110    3' TCAGTCTTTACAGAACA     29884       A  GC
                                TTAGT CT  TACAGAACA
                                ||||| ||  |||||||||
                                AGTCA GA  ATGTCTTGT
                                   _  A_
GAM1152 ABCA8    3' TCAGTATTATACAGAACA    29885       C  C
                                TTAGTA TG TACAGAACA
                                |||||| || |||||||||
                                AGTCAT AT ATGTCTTGT
                                   A  _
GAM1152 ARNTL2   3' TAGCACCATATAGAACA     29886         C  C
                                TAGTACTG TA AGAACA
                                |||||||| || ||||||
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                                ATCGTGGT AT TCTTGT
                                     _ A
GAM1152  DKFZp434E2220 3'  TTAGTACTAATTAACGGAACA  29887        CT__  A
                                TTAGTACTG   AC GAACA
                                |||||||||   || |||||
                                AATCATGAT   TG CTTGT
                                     TAAT  C
GAM1152  ELF2     3'  TCAGTACTGCCACTAACA    29888          AG
                                TTAGTACTGCTAC  AACA
                                ||||||||||||  ||||
                                AGTCATGACGGTG  TTGT
                                       A_
GAM1152  FIGN     3'  TTAATACTGCAGAACA      29889         TAC
                                TTAGTACTGC   AGAACA
                                ||||||||||   ||||||
                                AATTATGACG   TCTTGT
                                     ___
GAM1152  KIAA1946 3'  TCAGTTAACACAGAACA     29890      ACT  T
                                TTAGT   GC ACAGAACA
                                |||||   || ||||||||
                                AGTCA   TG TGTCTTGT
                                   AT_ _
GAM1152  MGC10500 3'  GTACAAACGCTACAGAAC    29891     ___
                                GTAC   TGCTACAGAAC
                                ||||   ||||||||||
                                CATG   GCGATGTCTTG
                                  TTT
GAM1152  MGC13033 3'  CTAGTGCTGCCACCCACA    29892      A     AGA
                                TTAGT CTGCTAC   ACA
                                ||||| |||||||   |||
                                GATCA GACGGTG   TGT
                                   C      GG_
GAM1152  MGC14817 3'  TTAATACCTGACAGAAC     29893        GCT
                                TTAGTACT   ACAGAAC
                                ||||||||   |||||||
                                AATTATGG   TGTCTTG
                                     AC_
GAM1152  SEMA3E   3'  TCAGTACTGCCATAAACA    29894          CA
                                TTAGTACTGCTA  GAACA
                                ||||||||||||  |||||
                                AGTCATGACGGT  TTTGT
                                       A_
GAM1152  LOC146784 5'  TCAGTACTGAGAAAACA     29895        CTAC
                                TTAGTACTG   AGAACA
                                |||||||||   ||||||
                                AGTCATGAC   TTTTGT
                                     TC__
GAM1152  LOC151273 3'  TCAGTACTGCCACTAACA    29888          AG
                                TTAGTACTGCTAC  AACA
                                ||||||||||||  ||||
```

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                                AGTCATGACGGTG  TTGT
                                      A_
GAM1152  LOC220926 5'  TTAGCATCACAACAGAACA   29896       CT  T
                                TTAGTA  GC ACAGAACA
                                ||||||  || ||||||||
                                AATCGT  TG TGTCTTGT
                                   AG  T
GAM1153  BBOX1     3'  CTTTATTTGCAAAAGAGTGG   29899       C       TTA
                                CTTTGT TGCAGAGG   TGG
                                |||||| ||||||||   |||
                                GAAATA ACGTTTTC   ACC
                                   A       TC_
GAM1153  C20orf162 5'  CCTTGTCTGCAGAGTTCTG   29900            GTTA
                                CTTTGTCTGCAGAG    TG
                                ||||||||||||||    ||
                                GGAACAGACGTCTC    AC
                                      AAG_
GAM1153  DKFZP434K028 3'  TACTTTGTCCGCAGGCAGGC   29901             __
                                TACTTTGTCTGCAG  AGGT
                                |||||||||||||  ||||
                                ATGAAACAGGCGTC  TCCG
                                      CG
GAM1153  FLJ20457  3'  TACTTTGTTTCAGAGGGGAAGG 29902        CTG     TTAT
            C                    TACTTTGT   CAGAGG    GGC
                                ||||||||   ||||||    |||
                                ATGAAACA   GTCTCC    CCG
                                     AA_     CCTT
GAM1153  KIAA0876  3'  CTTTGTCTGCAAGGAAG     29903          G   TTAT
                                CTTTGTCTGCA AGG    GG
                                |||||||||| |||    ||
                                GAAACAGACGT TCC    TC
                                      _   T___
GAM1153  NMT1      3'  CTTTGTCTCAGAATGCAGGC   29904        G    GTTAT
                                CTTTGTCT CAGAG    GGC
                                |||||||| |||||    |||
                                GAAACAGA GTCTT    CCG
                                     _    ACGT_
GAM1153  OS4       3'  TTTGTCTGCAGCAGCTGGC   29905          A   TA
                                TTTGTCTGCAG GGT  TGGC
                                |||||||||| |||  ||||
                                AAACAGACGTC TCG  ACCG
                                      G  __
GAM1153  RNAC      3'  CTTTGTCTGTAGGCACTGG    29906        CAG    TA
                                CTTTGTCTG   AGGT  TGG
                                |||||||||   ||||  |||
                                GAAACAGAC   TCCG  ACC
                                     A__    TG
GAM1153  STAF65(gamma) 3'  TTTATCTGTGAAGGGTGGC   29907        CA    TTA
                                TTTGTCTG  GAGG   TGGC
                                ||||||||  ||||   ||||
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                                AAATAGAC  TTCC   ACCG
                                    AC    C__
GAM1153  TRIM2     3'  TACTTTGTTTGCTGATACAAGG 29908        C   A  GGT  T
                                TACTTTGT TGC GA   TA GG
                                |||||||| ||| ||   || ||
                                ATGAAACA ACG CT   GT CC
                                    A   A  AT_  T
GAM1153  LOC120534 5'  TTTGTCTGGAGGTTTAGG    29909        CA     AT
                                TTTGTCTG  GAGGTT  GG
                                ||||||||  ||||||  ||
                                AAACAGAC  CTCCAA  CC
                                   __      AT
GAM1153  LOC150218 5'  TTTGTCTGGGAGAGGAGG    29910        C_    TTAT
                                TTTGTCTG  AGAGG   GG
                                ||||||||  |||||   ||
                                AAACAGAC  TCTCC   CC
                                    CC    T___
GAM1153  LOC150848 5'  TTTGTCTGCAAGGTGG      29911         G    TAT
                                TTTGTCTGCA AGGT   GG
                                |||||||||| ||||   ||
                                AAACAGACGT TCCA   CC
                                   _   ___
GAM1153  LOC154084 5'  TTTGGTTGCAAAGATGTGG   29912      TC       TA
                                TTTG  TGCAGAGGT  TGG
                                ||||  |||||||||  |||
                                AAAC  ACGTTTCTA  ACC
                                  CA       C_
GAM1153  LOC166341 3'  CTTTGTCTGCAGTCTGGC    29913          AGGTTA
                                CTTTGTCTGCAG     TGGC
                                ||||||||||||     ||||
                                GAAACAGACGTC     ACCG
                                      AG____
GAM1153  LOC197342 3'  CCTTGTCTGTGGGGTGGGGC  29914        CAGA   TAT
                                CTTTGTCTG   GGT   GGC
                                |||||||||   |||   |||
                                GGAACAGAC   CCA   CCG
                                    ACC_   CC_
GAM1153  LOC253461 3'  TACTTTGTTGCAGTAATGG   29915        C    AGGTT
                                TACTTTGT TGCAG    ATGG
                                |||||||| |||||    ||||
                                ATGAAACA ACGTC    TACC
                                   _    AT___
GAM1153  LOC256158 5'  CTTTGTCTGCGGAGAGGT    29916         __
                                CTTTGTCTGC  AGAGGT
                                ||||||||||  ||||||
                                GAAACAGACG  TCTCCA
                                      CC
GAM1154  IL6R      3'  AGGTGTTGAGGGGTGGGCT   29919        C   AATCTAA
                                AGGTGTTG AGG      GGCT
                                |||||||| |||      ||||
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                                TCCACAAC TCC      CCGA
                                     _  CCAC___
GAM1154  SLC30A3   3'  AGATGCTGAGAGTCTGGGGCTG 29920        CA  A  AA
                                AGGTGTTG  GGA TCT  GGCTG
                                ||||||||  ||| |||  |||||
                                TCTACGAC  TCT AGA  CCGAC
                                     __  C  CC
GAM1154  KIAA0140  3'  GGTTTGTGGGCAAGGCT    29921    G  CA  AATC
                                GGT TTG  GG   TAAGGCT
                                ||| |||  ||   |||||||
                                CCA AAC  CC   GTTCCGA
                                  _  AC  ____
GAM1154  LOC196955 3'  GGTGTTGCGGGAGCTGAGGCTG 29922        A  AT  A
                                GGTGTTGC GGA  CT AGGCTG
                                |||||||| |||  || ||||||
                                CCACAACG CCT  GA TCCGAC
                                     C  C_  C
GAM1154  LOC197408 5'  AGGCAGCAGGAATTTAGGG   29923     GTT      C  A
                                AGGT   GCAGGAAT TA GG
                                ||||   |||||||| || ||
                                TCCG   CGTCCTTA AT CC
                                  T__      A  C
GAM1155  CD53    3'  CAGAGGGTTGTGACAATGGT   29926    C    CATA
                                CA AGGGT    ACAATGGT
                                || |||||    ||||||||
                                GT TCCCA    TGTTACCA
                                 C    ACAC
GAM1155  CLTC    3'  CATGGTCATATGCCAGTGTTT  29927    G     ACAA
                                CA GGTCATA    TGGTGTTT
                                || |||||||    ||||||||
                                GT CCAGTAT    GTCACAAA
                                 A      ACG_
GAM1155  GJB1    3'  CACAGGGTTAAGATTAGT    29928        CA  CAA
                                CACAGGGT  TAA   TGGT
                                ||||||||  |||   ||||
                                GTGTCCCA  ATT   ATCA
                                     __  CTA
GAM1155  WNT5A   3'  CACAGGATCATAACAGTGAT   29929            A
                                CACAGGGTCATAACA TGGT
                                |||||||||||||| ||||
                                GTGTCCTAGTATTGT ACTA
                                          C
GAM1155  Apg4B   3'  CACAGGGTCAGGCGGTGGTG   29930         TAACAA
                                CACAGGGTCA     TGGTG
                                ||||||||||     |||||
                                GTGTCCCAGT     ACCAC
                                     CCGCC_
GAM1155  ARNTL2   3'  CAGGGTCAAAATAATGCTT   29931        TAAC
                                CAGGGTCA    AATGGTGTTT
                                ||||||||    ||||||||||
```

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                                GTCCCAGT    TTATTACGAA
                                     T___
GAM1155  C9orf14   5'  CAAGGTCATAGGTGTT      29932          ACAAT
                                CAGGGTCATA    GGTGTT
                                ||||||||||    ||||||
                                GTTCCAGTAT    CCACAA
                                      _____
GAM1155  FLJ10971  3'  CACAGGGTCATACCAATAAC   29933           A   GG
                                CACAGGGTCATA CAAT  T
                                |||||||||||| ||||  |
                                GTGTCCCAGTAT GTTA  G
                                       G   TT
GAM1155  KIAA1233  3'  ACACCTTAACAGTGGTGTTT   29934    GGG  A    A
                                ACA   TC TAACA TGGTGTTT
                                |||   || ||||| ||||||||
                                TGT   GG ATTGT ACCACAAA
                                  ___ A    C
GAM1155  MESDC2    3'  CACAGGGTCTTAGCTCAGACTG 29935         A  ACAAT  _
             TTT                  CACAGGGTC TA    GG TGTTT
                                |||||||| ||    || |||||
                                GTGTCCCAG AT    CT ACAAA
                                     A  CGAGT  G
GAM1155  MGC13053  3'  ACAGGAGTCGTAATGTCT    29936      _  ATAACAA
                                ACAGG GTC      TGGTGTTT
                                ||||| |||      ||||||||
                                TGTCC CAG      ATTACAGA
                                   T  C_______
GAM1155  MSTP028   3'  CACAGGGTCAGATGGCCTT   29937         TAACA    G
                                CACAGGGTCA    ATGGT TT
                                ||||||||||    ||||| ||
                                GTGTCCCAGT    TACCG AA
                                     C____    G
GAM1155  LOC154739 5'  GGGTCATAATGTATTATGTTT  29938         CAATG_
                                GGGTCATAA     GTGTTT
                                |||||||||     ||||||
                                CCCAGTATT     TACAAA
                                     ACATAA
GAM1155  LOC157506 3'  CACAGGTCATGGCATT      29939       G   TAACAA
                                CACAGG TCA     TGGTGTT
                                ||||||  |||    |||||||
                                GTGTCC AGT     ACCGTAA
                                     _  _______
GAM1155  LOC161734 3'  CACAGGGCTCATGGGTGCAGGT 29940        _   AACAAT_
             GTTT                  CACAGGG TCAT      GGTGTTT
                                ||||||| ||||      |||||||
                                GTGTCCC AGTA      CCACAAA
                                    G   CCCACGT
GAM1155  LOC197408 5'  GTGCACACGATGGTGTTT    29941    _   ACA
                                GT CATA   ATGGTGTTT
                                || ||||   |||||||||
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                                CA GTGT   TACCACAAA
                                 C   GC_
GAM1155  LOC221922 5'  CACAGGGTCATGGTGT      29942          TAACAA
                                CACAGGGTCA     TGGTGT
                                ||||||||||     ||||||
                                GTGTCCCAGT     ACCACA
                                       _______
GAM1155  LOC222182 3'  CACAGGGTCAGAGCAGTGC    29943          TAACAAT
                                CACAGGGTCA      GGTGT
                                ||||||||||      |||||
                                GTGTCCCAGT      TCACG
                                     CTCG___
GAM1156  FKBP9     3'  TGATGTGCGTGTGCGTGTGCG  29946     C_   CCGG  C
                                TGAT  GCG    GT CGTGTGCG
                                ||||  |||    || ||||||||
                                ACTA  CGC    CA GCACACGC
                                  CA   A___  C
GAM1156  LGI3      5'  TGACCGCGCCGGGTGGATGCG  29947            CC
                                TGATCGCGCCGGGT  GTGTG
                                ||||||||||||||  |||||
                                ACTGGCGCGGCCCA  TACGC
                                       CC
GAM1156  LOC147054 5'  TGATCACGTGTGTGTGTG    29948        CCGG  CC
                                TGATCGCG    GT  GTGTG
                                ||||||||    ||  |||||
                                ACTAGTGC    CA  CACAC
                                    ACA_  __
GAM1156  LOC220522 3'  TGATGGTGCCGGGTCTCCAGCG 29949   CGC      _________  TGTG
              CACACG                   GCCGGGTC       CG    CG
                                ||||||||       ||    ||
                                CGGCCCAG       GC    GC
                                CCA       AGGTCIII  GTGT
GAM1157  FLJ23053  3'  TCGTCTTGACTCTGCCAGCC   29952     _   C
                                TCG CTT GACTCTGCCGGTC
                                ||| ||| ||||||||||||
                                AGC GAA CTGAGACGGTCGG
                                  A  _
GAM1157  SCAMP-4   3'  GCTCTCTGCCGGTTTGCT     29953     TCGA        CC
                                GCT    CTCTGCCGGT  GCT
                                |||    ||||||||||  |||
                                CGA    GAGACGGCCA  CGA
                                  _____         AA
GAM1158  ADRA1A    3'  GGAGAGAATGTGTGTGTGTGT  29956     _  T   A
                                GGA AG AAT TGTGTGTGTGT
                                ||| || ||| ||||||||||
                                CCT TC TTA ACACACACACA
                                  C  _   C
GAM1158  ANK1      3'  GGAGGCGAGTGGTGTGTGTGTG 29957     A  AATA__
              T                   GGA GT      TGTGTGTGTGT
                                ||| ||      ||||||||||
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                                CCT CG     ACACACACACA
                                  C  CTCACC
GAM1158  ANK1     3'  GGAGGCGAGTGGTGTGTGTGTG 29957     A  AATA__
                T                  GGA GT     TGTGTGTGTGT
                                   ||| ||     ||||||||||
                                   CCT CG     ACACACACACA
                                     C  CTCACC
GAM1158  ATP8B2   3'  AGGAATTGATATGTGTGTGTGT 29958      GTA
                                   AGGAA   ATATGTGTGTGTGT
                                   |||||   ||||||||||||||
                                   TCCTT   TATACACACACACA
                                      AAC
GAM1158  CCND1    3'  AGAAGGTTTGTGTGTGTGTGT  29959      TAATA
                                   GGAAG    TGTGTGTGTGT
                                   |||||    ||||||||||
                                   TCTTC    ACACACACACA
                                      CAAAC
GAM1158  CD22     3'  AGTGAGTGTGTGTGTGTGT    29960    GA   AATA
                                   AG  AGT    TGTGTGTGTGT
                                   ||  |||    ||||||||||
                                   TC  TCA    ACACACACACA
                                    AC   C___
GAM1158  CDH12    3'  AGAAAGAGTGTGTGTGTGTGT  29961       TAATA
                                   AGGAAG    TGTGTGTGTGT
                                   ||||||    ||||||||||
                                   TCTTTC    ACACACACACA
                                       TCAC_
GAM1158  CDKN2B   3'  AGCATGTGTGTGTGTGT     29962     ATA
                                   AGTA   TGTGTGTGTGT
                                   ||||   ||||||||||
                                   TCGT   ACACACACACA
                                     AC_
GAM1158  CENTD2   5'  GTGTGTATGTGTGTGTGTAT   29963    AA_
                                   GT   TATGTGTGTGTGTAT
                                   ||   ||||||||||||||
                                   CA   ATACACACACACATA
                                    CAC
GAM1158  CRHBP    3'  GTGTGTATGTGTGTGTGT    29964    AA_
                                   GT   TATGTGTGTGTGT
                                   ||   ||||||||||||
                                   CA   ATACACACACACA
                                    CAC
GAM1158  CSPG3    3'  AGAAAAATGTGTGTGTGTGT   29965      T   A
                                   GGAAG AAT TGTGTGTGTGT
                                   ||||| ||| ||||||||||
                                   TCTTT TTA ACACACACACA
                                      _   C
GAM1158  DGKG     3'  AGAAGAGTGTGTATGTGTGTGT 29966      TAA___
                GT                   GGAAG     TATGTGTGTGTGT
                                     |||||     ||||||||||||
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                          TCTTC    ATACACACACACA
                            TCACAC
GAM1158 DMD    3' GTGTGTATGTGTGTGTGT   29964   AA_
                          GT  TATGTGTGTGTGT
                          ||  |||||||||||||
                          CA  ATACACACACACA
                           CAC
GAM1158 DMD    3' GTGTGTATGTGTGTGTGT   29964   AA_
                          GT  TATGTGTGTGTGT
                          ||  |||||||||||||
                          CA  ATACACACACACA
                           CAC
GAM1158 DMD    3' GTGTGTATGTGTGTGTGT   29964   AA_
                          GT  TATGTGTGTGTGT
                          ||  |||||||||||||
                          CA  ATACACACACACA
                           CAC
GAM1158 DMD    3' GTGTGTATGTGTGTGTGT   29964   AA_
                          GT  TATGTGTGTGTGT
                          ||  |||||||||||||
                          CA  ATACACACACACA
                           CAC
GAM1158 DMD    3' GTGTGTATGTGTGTGTGT   29964   AA_
                          GT  TATGTGTGTGTGT
                          ||  |||||||||||||
                          CA  ATACACACACACA
                           CAC
GAM1158 DMD    3' GTGTGTATGTGTGTGTGT   29964   AA_
                          GT  TATGTGTGTGTGT
                          ||  |||||||||||||
                          CA  ATACACACACACA
                           CAC
GAM1158 DMD    3' GTGTGTATGTGTGTGTGT   29964   AA_
                          GT  TATGTGTGTGTGT
                          ||  |||||||||||||
                          CA  ATACACACACACA
                           CAC
GAM1158 DMD    3' GTGTGTATGTGTGTGTGT   29964   AA_
                          GT  TATGTGTGTGTGT
                          ||  |||||||||||||
                          CA  ATACACACACACA
                           CAC
GAM1158 DMD    3' GTGTGTATGTGTGTGTGT   29964   AA_
                          GT  TATGTGTGTGTGT
                          ||  |||||||||||||
                          CA  ATACACACACACA
                           CAC
GAM1158 DMD    3' GTGTGTATGTGTGTGTGT   29964   AA_
                          GT  TATGTGTGTGTGT
                          ||  |||||||||||||
                          CA  ATACACACACACA
                           CAC
GAM1158 DMD    3' GTGTGTATGTGTGTGTGT   29964   AA_
                          GT  TATGTGTGTGTGT
                          ||  |||||||||||||
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                                CA  ATACACACACACA
                                 CAC
GAM1158 DMD     3' GTGTGTATGTGTGTGTGT   29964   AA_
                                GT  TATGTGTGTGTGT
                                ||  |||||||||||||
                                CA  ATACACACACACA
                                 CAC
GAM1158 DMD     3' GTGTGTATGTGTGTGTGT   29964   AA_
                                GT  TATGTGTGTGTGT
                                ||  |||||||||||||
                                CA  ATACACACACACA
                                 CAC
GAM1158 DMD     3' GTGTGTATGTGTGTGTGT   29964   AA_
                                GT  TATGTGTGTGTGT
                                ||  |||||||||||||
                                CA  ATACACACACACA
                                 CAC
GAM1158 EFNB1   3' AGGAAGGGATTTTTGTGTGTGT 29967      TA  A__
            GT                   AGGAAG  AT  TGTGTGTGTGT
                                |||||| ||  ||||||||||||
                                TCCTTC  TA  ACACACACACA
                                   CC  AAA
GAM1158 EHD2    3' AGGAATTAGTGTGTGTTTGC  29968     GTAATA     G
                                AGGAA    TGTGTGT TGT
                                |||||    ||||||| |||
                                TCCTT    ACACACA ACG
                                   AATC__     A
GAM1158 EN2     3' GGCGCGCCTGGTGTGTGTGTGT 29969   AA_  AATA
                                GG  GT   TGTGTGTGTGT
                                ||  ||   ||||||||||||
                                CC  CG   ACACACACACA
                                 GCG  GACC
GAM1158 ERBB3   5' GGGAGGGGTGTGTGTGTGT   29970   A  TAATA
                                GG AG    TGTGTGTGTGT
                                || ||    ||||||||||||
                                CC TC    ACACACACACA
                                 C  CCC__
GAM1158 FGFRL1  3' AGCATATCCGTGTGTGTGT   29971     ATA_
                                AGTA   TGTGTGTGTGT
                                ||||   ||||||||||||
                                TCGT   GCACACACACA
                                  ATAG
GAM1158 FMR2    3' AGGGTGAGTTTGTGTGTGTGT  29973    A__  AATA
                                AGG  AGT   TGTGTGTGTGT
                                |||  |||   ||||||||||||
                                TCC  TCA   ACACACACACA
                                 CAC  A___
GAM1158 FMR2    3' AAGTGTATGTGTGTGTGT    29972     AA
                                AAGT  TATGTGTGTGTGT
                                ||||  ||||||||||||||
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                              TTCA  ATACACACACACA
                                C_
GAM1158 GLP1R    3' GAAAGCAGGATGTATGTGTGTG 29974       A____
            TGT                 GGAAGTA    TATGTGTGTGTGT
                              |||||||    ||||||||||||
                              CTTTCGT    ATACACACACACA
                                 CCTAC
GAM1158 GRLF1    3' AAGTTTTGTGTGTGTGTGT   29976     AATA
                              AAGT   TGTGTGTGTGT
                              ||||   ||||||||||
                              TTCA   ACACACACACA
                                AAAC
GAM1158 GRLF1    3' GAAGTTTTGTGTGTGTGTGT  29975      AATA
                              GAAGT   TGTGTGTGTGT
                              |||||   ||||||||||
                              CTTCA   ACACACACACA
                                 AAAC
GAM1158 GTF2H1   3' GTACATATATGTGTGTGTGT  29977    ___
                              GTA   ATATGTGTGTGTGT
                              |||   ||||||||||||
                              CAT   TATACACACACACA
                                GTA
GAM1158 HRASLS   5' GGAGGCAGCTGTGTGTGT    29978    A   ATA
                              GGA GTA   TGTGTGTGT
                              ||| |||   |||||||||
                              CCT CGT   ACACACACA
                                C   CG_
GAM1158 IGF1     3' AGGGTGAATGTGTGTGTGT   29979    AA  AAT
                              AGG  GT   ATGTGTGTGTGT
                              |||  ||   ||||||||||||
                              TCC  CA   TACACACACACA
                                __  CT_
GAM1158 ITGA11   3' GGAGGCAGTGTGTGTGTGTGT 29980    A   ATA
                              GGA GTA   TGTGTGTGTGT
                              ||| |||   ||||||||||
                              CCT CGT   ACACACACACA
                                C   CAC
GAM1158 JMJ      3' AAGTTTCGTGTGTGTGTGT   29981     AATA
                              AAGT   TGTGTGTGTGT
                              ||||   ||||||||||
                              TTCA   ACACACACACA
                                AAGC
GAM1158 KCNJ16   3' AGCAAAAACTGTGTGTGTGT  29982      TA__
                              AGTAA   TGTGTGTGTGT
                              |||||   ||||||||||
                              TCGTT   ACACACACACA
                                 TTTG
GAM1158 LILRB4   3' AAGTTTGTGTGTGTGTGT    29983     AATA
                              AAGT   TGTGTGTGTGT
                              ||||   ||||||||||
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                                TTCA   ACACACACACA
                                  AAC_
GAM1158 NR2E1   3' GGTGTGTGTGTGTGTGT    29984   AA AATA
                                GG GT   TGTGTGTGTGT
                                || ||   ||||||||||
                                CC CA   ACACACACACA
                                 A_ C___
GAM1158 NR2E1   3' AGGACGGTGTGTGTGTGTGT 29985     AGTAATA
                                AGGA     TGTGTGTGTGT
                                ||||     ||||||||||
                                TCCT     ACACACACACA
                                  GCCACAC
GAM1158 NR4A2   3' GTGTGTATGTGTGTGTGT   29964   AA_
                                GT   TATGTGTGTGTGT
                                ||   ||||||||||||
                                CA   ATACACACACACA
                                 CAC
GAM1158 PLAG1   3' AAGTATGTATGTGTGTGTGTAT 29986     A_
                                AAGTA  TATGTGTGTGTGTAT
                                |||||  ||||||||||||||
                                TTCAT  ATACACACACACATA
                                   AC
GAM1158 PLAG1   3' GTGTGCATGTGTGTGTGT   29987   AA_
                                GT   TATGTGTGTGTGT
                                ||   ||||||||||||
                                CA   GTACACACACACA
                                 CAC
GAM1158 PURA    3' GGCTGTGTGTGTGTGTGTAT  29988   AA AATA
                                GG GT   TGTGTGTGTGTAT
                                || ||   ||||||||||||
                                CC CA   ACACACACACATA
                                 GA C___
GAM1158 RCV1    3' GGATGTGTGTGTGTGTGT   29989    A AATA
                                GGA GT   TGTGTGTGTGT
                                ||| ||   ||||||||||
                                CCT CA   ACACACACACA
                                  A C___
GAM1158 SLC1A4  3' AGATATACATATGTGTGTGTGT 29990    A  _
                                GGA GTA ATATGTGTGTGTGT
                                ||| ||| ||||||||||||||
                                TCT TAT TATACACACACACA
                                  A  G
GAM1158 SLC31A1 3' AGCAGGGGTGTGTGTGTGT   29991    ATA_
                                AGTA   TGTGTGTGTGT
                                ||||   ||||||||||
                                TCGT   ACACACACACA
                                  CCCC
GAM1158 SNAI2   3' GGGTGTGTGTGTGTGTGT   29992   AA AATA
                                GG GT   TGTGTGTGTGT
                                || ||   ||||||||||
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                                CC  CA    ACACACACACA
                                 CA  C___
GAM1158  SNX2     3'  AGAGTGTGTGTGTGTGTGT   29993    A   AATA
                                GG AGT    TGTGTGTGTGT
                                || |||    ||||||||||
                                TC TCA    ACACACACACA
                                 _   CAC_
GAM1158  SRGAP2   3'  AGAAAAACATATGTGTGTGTGT 29994       TA
                                AGGAAG  ATATGTGTGTGTGT
                                ||||||  ||||||||||||||
                                TCTTTT  TATACACACACACA
                                   TG
GAM1158  TFAP4    5'  GGTGCGTGTGTATGTGTGTGTG 29995    AA_  AA_
              T                  GG   GT   TATGTGTGTGTGT
                                 ||   ||   ||||||||||||
                                 CC   CA   ATACACACACACA
                                  ACG  CAC
GAM1158  TRAF5    3'  AGGTGTATATGTATGTGTGTGT 29996     AA   A___
              GTAT                 AGG  GTA    TATGTGTGTGTGTAT
                                   |||  |||    |||||||||||||||
                                   TCC  CAT    ATACACACACACATA
                                    A_   ATAC
GAM1158  VSNL1    3'  AGCAATATTTGTGTGTGTGT   29997        __
                                   AGTAATA  TGTGTGTGTGT
                                   |||||||  ||||||||||
                                   TCGTTAT  ACACACACACA
                                      AA
GAM1158  ARFGAP3  3'  AGGAAGTGTGTGTGGT      29998       AATAT      T
                                   AGGAAGT    GTGTGTG GT
                                   |||||||    ||||||| ||
                                   TCCTTCA    CACACAC CA
                                      _____     _
GAM1158  ARHGEF9  3'  AGGGTCTCTGTGTGTGTGT   29999     AA  AATA
                                   AGG  GT    TGTGTGTGTGT
                                   |||  ||    ||||||||||
                                   TCC  CA    ACACACACACA
                                     __  GAG_
GAM1158  BLOV1    3'  GTATATGTATGTGTGTGTGTAT 30000     A___
                                   GTA    TATGTGTGTGTGTAT
                                   |||    |||||||||||||||
                                   CAT    ATACACACACACATA
                                     ATAC
GAM1158  BM045    5'  GAGAGCCTGTGTGTGTGTGT   30001    GA   AATA
                                   G  AGT    TGTGTGTGTGT
                                   |  |||    ||||||||||
                                   C  TCG    ACACACACACA
                                    TC   GAC_
GAM1158  C8orf13  3'  GGGGGTGTGTGTGTGTGTGT   30002     AA  AATA
                                   GG  GT    TGTGTGTGTGT
                                   ||  ||    ||||||||||
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                                CC  CA   ACACACACACA
                                 CC  CAC_
GAM1158 C8orf13  3' GGGGGTGTGTGTGTGTGT   30003   AA  AATA
                                GG  GT   TGTGTGTGTGT
                                ||  ||   ||||||||||
                                CC  CA   ACACACACACA
                                 CC  C___
GAM1158 CACNA1I  3' GTCTGTCTATGTGTGTGTGTAT 30004   AA___
                                GT   TATGTGTGTGTGTAT
                                ||   ||||||||||||||
                                CA   ATACACACACACATA
                                 GACAG
GAM1158 CHSY1    3' AGGGTGTATGTGTGTGTGT   30005    AA  ATA
                                AGG  GTA  TGTGTGTGTGT
                                |||  |||  ||||||||||
                                TCC  CAT  ACACACACACA
                                  CA  ___
GAM1158 CLIC6    3' GAAATTGTGTGTGTGTGTGT   30006     AATA
                                GAAGT   TGTGTGTGTGT
                                |||||   ||||||||||
                                CTTTA   ACACACACACA
                                   ACAC
GAM1158 CNOT3    5' AGAAGGGCGTGTGTGTGTGT   30007     TAATA
                                GGAAG    TGTGTGTGTGT
                                |||||    ||||||||||
                                TCTTC    ACACACACACA
                                   CCGC_
GAM1158 CRMP5    3' AGGAAGCCATGCGTGTGTGT   30008      AA
                                AGGAAGT  TATGTGTGTGTGT
                                |||||||  ||||||||||||
                                TCCTTCG  GTACGCACACACA
                                      __
GAM1158 CSEN     3' GGCTGTGTGTGTGTGTGT    30009    AA  AATA
                                GG  GT   TGTGTGTGTGT
                                ||  ||   ||||||||||
                                CC  CA   ACACACACACA
                                 GA  C___
GAM1158 dA141H5.1 3' GGACGTGCGTGTGTGTGTGT   30010    A  AATA
                                GGA GT   TGTGTGTGTGT
                                ||| ||   ||||||||||
                                CCT CA   ACACACACACA
                                  G  CGC_
GAM1158 DKFZP761I2123 3' AGGGGCGTGAGATGTGTGTGT  30011    AA_  AAT
                                AGG   GT   ATGTGTGTGT
                                |||   ||   ||||||||||
                                TCC   CA   TACACACACA
                                  CCG  CTC
GAM1158 DKFZp761O132 3' GGACACAGGTGTGTGTGTGT   30012    AG  ATA
                                GGA  TA   TGTGTGTGTGT
                                |||  ||   ||||||||||
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                                CCT  GT   ACACACACACA
                                  GT  CC_
GAM1158  DNAJC6   3'  GCGTGCATGTGTGTGTGT    30013    AA_
                                GT   TATGTGTGTGTGT
                                ||   |||||||||||||
                                CG   GTACACACACACA
                                 CAC
GAM1158  DRIL2    3'  GGGAGATGGGGTATGTGTGTGT 30014    A  TAA___
              GT                  GG AG     TATGTGTGTGTGT
                                || ||     |||||||||||||
                                CC TC     ATACACACACACA
                                 C  TACCCC
GAM1158  ERO1L    3'  AGGAAAAATTTGTGTGTGTGT  30015       T   A
                                AGGAAG AAT TGTGTGTGTGT
                                |||||| ||| ||||||||||
                                TCCTTT TTA ACACACACACA
                                   _   A
GAM1158  FLJ13693 3'  AGTAGACACCTGTGTGTGT   30016     _    G
                                AGTA ATAT TGTGTGTGT
                                |||| |||| |||||||||
                                TCAT TGTG ACACACACA
                                  C   G
GAM1158  FLJ14871 3'  GGGGGCAGTGTGTGTGTA    30017    AA   ATAT
                                GG  GTA   GTGTGTGTGTA
                                ||  |||   ||||||||||
                                CC  CGT   CACACACACAT
                                 CC  _____
GAM1158  FLJ14950 3'  AGGGGCGTGTGTGTGTGTGT   30018    AA_  AATA
                                AGG   GT   TGTGTGTGTGT
                                |||   ||   ||||||||||
                                TCC   CA   ACACACACACA
                                  CCG  C___
GAM1158  FLJ20043 3'  AGGAAATACGTGTGTGTAT    30019     GTA
                                AGGAA   ATATGTGTGTGTGT
                                |||||   ||||||||||||||
                                TCCTT   TATGCACACACATA
                                   ___
GAM1158  FLJ20511 3'  GGGGGTGTGTGTGTGTGTGT   30002    AA  AATA
                                GG  GT   TGTGTGTGTGT
                                ||  ||   ||||||||||
                                CC  CA   ACACACACACA
                                 CC  CAC_
GAM1158  FLJ21477 3'  AGAAAGTGTGTGTGTGTGT    30020       AATA
                                AGGAAGT   TGTGTGTGTGT
                                |||||||   ||||||||||
                                TCTTTCA   ACACACACACA
                                    C___
GAM1158  FLJ23120 3'  GCGTGCATGTGTGTGTGT    30013    AA_
                                GT   TATGTGTGTGTGT
                                ||   |||||||||||||
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                                CG   GTACACACACACA
                                 CAC
GAM1158 FLNC     3' GGCACATTTGTGTGTGTGT   30021    AAGTA  A
                                GG    AT TGTGTGTGTGT
                                ||    || ||||||||||
                                CC    TA ACACACACACA
                                 GTG__  A
GAM1158 HLA-DOA  3' AGCAAGAATGTGTGTGTGTGT  30022    G   T   A
                                AG AAG AAT TGTGTGTGTGT
                                || ||| ||| ||||||||||
                                TC TTC TTA ACACACACACA
                                 G   _   C
GAM1158 HSPC111  3' GGGAGTGTGCACGTGTGTGTGT 30023    A   AA_
                                GG AGT   TATGTGTGTGTGT
                                || |||   ||||||||||||
                                CC TCA   GTGCACACACACA
                                 C   CAC
GAM1158 KIAA0084 3' AGAAGTAATGTGGTTTGTA    30024       AT    T  G
                                GGAAGTA  ATGTG GT TGTA
                                |||||||  ||||| || ||||
                                TCTTCAT  TACAC CA ACAT
                                    __    _ A
GAM1158 KIAA0143 3' AGGAAATATGTGTGTGTGT    30025      GTA
                                AGGAA   ATATGTGTGTGTGT
                                |||||   ||||||||||||||
                                TCCTT   TATACACACACACA
                                   ___
GAM1158 KIAA0293 3' GGTTTGTGTATGTGTGTGTGT  30026    AAGTAA
                                GG     TATGTGTGTGTGT
                                ||     ||||||||||||
                                CC     ATACACACACACA
                                 AAACAC
GAM1158 KIAA0431 3' AGGAGCATGTCGTGTGTGTGT  30027     A   ATA
                                AGGA GTA   TGTGTGTGTGT
                                |||| |||   ||||||||||
                                TCCT CGT   GCACACACACA
                                  _   ACA
GAM1158 KIAA0471 5' GAGAGTGTGTGTGTGTGT    30028   GA   AATA
                                G  AGT    TGTGTGTGTGT
                                |  |||    ||||||||||
                                C  TCA    ACACACACACA
                                 TC   C___
GAM1158 KIAA0544 3' AGGAGTATGTGCGTGTGTGTAT 30029     A   ATA
                                AGGA GTA   TGTGTGTGTGTAT
                                |||| |||   |||||||||||||
                                TCCT CAT   ACGCACACACATA
                                  _   AC_
GAM1158 KIAA0574 3' AGAAGCATGTGTGTGT      30030       AAT
                                GGAAGT   ATGTGTGTGT
                                ||||||   ||||||||||
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                              TCTTCG   TACACACACA
                                 ___
GAM1158 KIAA0596 3' AGGTAGGTGTGTGTGTGT    30031     A  TAATA
                              AGG AG    TGTGTGTGTGT
                              ||| ||    ||||||||||
                              TCC TC    ACACACACACA
                                A  C____
GAM1158 KIAA1219 3' GAGTATGCGAGTGTGTGTGT   30032    A   ATAT_
                              GA GTA    GTGTGTGTGT
                              || |||    ||||||||||
                              CT CAT    CACACACACA
                               _  ACGCT
GAM1158 KIAA1260 3' GACTAATGTGTGTGTGTGT   30034    AG   A
                              GA  TAAT TGTGTGTGTGT
                              ||  |||| ||||||||||
                              CT  ATTA ACACACACACA
                               G_   C
GAM1158 KIAA1260 3' AGGTGATATGACTAATGTGTGT 30033     AA   AT____
           GTGT                  AGG  GTA     ATGTGTGTGTGT
                              |||  |||     ||||||||||||
                              TCC  TAT     TACACACACACA
                                AC   ACTGAT
GAM1158 KIAA1354 3' AGGGGGTTGTGTGTGTGTAT   30035     AA  AATA
                              AGG  GT   TGTGTGTGTGTAT
                              |||  ||   ||||||||||||
                              TCC  CA   ACACACACACATA
                                CC  _____
GAM1158 KIAA1399 3' AGGGGTGTGTGTGTGTGT    30036     AA  AATA
                              AGG  GT   TGTGTGTGTGT
                              |||  ||   ||||||||||
                              TCC  CA   ACACACACACA
                                C_  C___
GAM1158 KIAA1545 3' AGCAGTGATTTTGTGTGTGTGT 30037    A   AATA_
                              GG AGT    TGTGTGTGTGT
                              || |||    ||||||||||
                              TC TCA    ACACACACACA
                               G   CTAAA
GAM1158 KIAA1550 3' GACTGCATGTGTGTGTGTAT   30039    AGTAA
                              GA    TATGTGTGTGTGTAT
                              ||    ||||||||||||||
                              CT    GTACACACACACATA
                               GAC__
GAM1158 KIAA1550 3' AGGGAGTGTATGTGAGTGTGT  30038     A   AA    T
                              AGG AGT  TATGTG GTGTGT
                              ||| |||  |||||| ||||||
                              TCC TCA  ATACAC CACACA
                                C   C_     T
GAM1158 KIAA1615 3' GTATATAGTGTGTGTGTGT   30040     _   _
                              GTA ATA TGTGTGTGTGT
                              ||| ||| ||||||||||
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                                CAT TAT ACACACACACA
                                  A   C
GAM1158 KIAA1655 3' AGGAGACAGCCGTGTGTGTGT 30041     AG  ATA
                                AGGA  TA   TGTGTGTGTGT
                                ||||  ||   ||||||||||||
                                TCCT  GT   GCACACACACA
                                  CT  CG_
GAM1158 KIAA1671 3' GTCTCTGTGTGTGTGTGTAT  30042    AATA_
                                GT    TGTGTGTGTGTAT
                                ||    ||||||||||||||
                                CA    ACACACACACATA
                                 GAGAC
GAM1158 KIAA1854 3' AGAAGCGTGTGTGTGTGTGT  30043      AATA
                                GGAAGT    TGTGTGTGTGT
                                ||||||    ||||||||||||
                                TCTTCG    ACACACACACA
                                   CAC_
GAM1158 KIAA1870 3' GGGAGGGTGTGTGTGTGT    30044    A  TAATA
                                GG AG     TGTGTGTGTGT
                                || ||     ||||||||||||
                                CC TC     ACACACACACA
                                 C  CC___
GAM1158 KIAA1879 5' GAGCCCTCTGTGTGTGTGT   30045    A  AATA
                                GA GT    TGTGTGTGTGT
                                || ||    ||||||||||||
                                CT CG    ACACACACACA
                                 _  GGAG
GAM1158 KIAA1900 5' GAAAGTGTGTGTGTGTGT    30046      AATA
                                GGAAGT    TGTGTGTGTGT
                                ||||||    ||||||||||||
                                CTTTCA    ACACACACACA
                                   C___
GAM1158 KIAA1918 3' AGGTAGAATTGCATGTGTGTGT 30047     A  TAA__
            GT                    AGG AG     TATGTGTGTGTGT
                                ||| ||     ||||||||||||||
                                TCC TC     GTACACACACACA
                                  A  TTAAC
GAM1158 KLF12    3' GTGTGTATGTGTGTGTGT    29964    AA_
                                GT   TATGTGTGTGTGT
                                ||   ||||||||||||||
                                CA   ATACACACACACA
                                 CAC
GAM1158 MGC11386 3' GTGTATGTGTGTGTGTA     30048    AA
                                GT  TATGTGTGTGTGTA
                                ||  ||||||||||||||
                                CA  ATACACACACACAT
                                 C_
GAM1158 MGC12679 3' AGAGAGAGATTGTGTGTGTGT 30049    GA  TA  A
                                AG  AG  AT TGTGTGTGTGT
                                ||  ||  || ||||||||||
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                              TC  TC  TA ACACACACACA
                               TC  TC  _
GAM1158 MGC12679 3' AGGAGTGAGTGTGTGTGTGT  30050     A  AATA
                              AGGA GT   TGTGTGTGTGT
                              |||| ||   ||||||||||
                              TCCT CA   ACACACACACA
                                _ CTC_
GAM1158 MGC15882 3' GGTCGTGTGTGTGTGTGT    30051    AA  AATA
                              GG  GT   TGTGTGTGTGT
                              ||  ||   ||||||||||
                              CC  CA   ACACACACACA
                               AG  C___
GAM1158 MGC34923 3' AGAGAGACTCTGTGTGTGTGT 30052    GA  TAATA
                              AG  AG    TGTGTGTGTGT
                              ||  ||    ||||||||||
                              TC  TC    ACACACACACA
                               TC  TGAG_
GAM1158 NAC1     3' GGCAGGTGTGTGTGTGTGT   30053    A  TAATA
                              GG AG    TGTGTGTGTGT
                              || ||    ||||||||||
                              CC TC    ACACACACACA
                               G  CAC__
GAM1158 NFAT5    3' GTATGTATGTGTGTGTGT    30054     A_
                              GTA  TATGTGTGTGTGT
                              |||  ||||||||||||
                              CAT  ATACACACACACA
                                AC
GAM1158 OSBPL9   3' GTATATATATGTGTGTGTGT  30055     ___
                              GTA   ATATGTGTGTGTGT
                              |||   ||||||||||||||
                              CAT   TATACACACACACA
                                ATA
GAM1158 PAPSS2   3' GTATATGTGTGTGTGTA     30056     A
                              GTA TATGTGTGTGTGTA
                              ||| |||||||||||||
                              CAT ATACACACACACAT
                                _
GAM1158 POU4F2   3' AGAGGTGTGTGTGTGTGT    30057     A  AATA
                              GGA GT    TGTGTGTGTGT
                              ||| ||    ||||||||||
                              TCT CA    ACACACACACA
                                C  C___
GAM1158 PPP1R16B 3' AGCTTGTGTGTGTGTGTA    30058     AATA
                              AGT    TGTGTGTGTGTA
                              |||    ||||||||||||
                              TCG    ACACACACACAT
                                AAC_
GAM1158 PRO0365  5' GAAAGGTGTGTGTGTGTGTGT 30059      TAATA
                              GGAAG     TGTGTGTGTGT
                              |||||     ||||||||||
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                                CTTTC    ACACACACACA
                                   CACAC
GAM1158 PRO2214  3' AAGAAATTATGTGTGTGTGTAT 30060       AA
                                AGGAAGT  TATGTGTGTGTGTAT
                                |||||||  |||||||||||||||
                                TTCTTTA  ATACACACACACATA
                                      __
GAM1158 RNF24    5' GGGAGAGTGTGTGTGTGT    30061    A  TAATA
                                GG AG    TGTGTGTGTGT
                                || ||    ||||||||||
                                CC TC    ACACACACACA
                                 C  TC___
GAM1158 RPH3A    3' GAAAGGGTGTGTGTGTGTGT   30062      TAATA
                                GGAAG    TGTGTGTGTGT
                                |||||    ||||||||||
                                CTTTC    ACACACACACA
                                   CCAC_
GAM1158 SEPT3    3' GGGGGTTTGTGTGTGTGT    30063    AA  AATA
                                GG  GT   TGTGTGTGTGT
                                ||  ||   ||||||||||
                                CC  CA   ACACACACACA
                                 CC  A___
GAM1158 SIAT8C   5' GGCGTGTATATATGTGTGTGTG 30064    AA_  _
           T                     GG   GTA ATATGTGTGTGTGT
                                ||   ||| |||||||||||||
                                CC   CAT TATACACACACACA
                                 GCA   A
GAM1158 SNAP29   3' AGAGTGTGTGTGTGTGT     30065     A  AATA
                                GGA GT   TGTGTGTGTGT
                                |||  ||   ||||||||||
                                TCT CA   ACACACACACA
                                  _  C___
GAM1158 SP192    3' GGGTGTGTATGTGTGTGTGT   30066    AA  AA
                                GG  GT  TATGTGTGTGTGT
                                ||  ||  ||||||||||||
                                CC  CA  ATACACACACACA
                                 CA  C_
GAM1158 SPRY4    3' GGGGTAGGGGTGTGTGTGTGT  30067    AA   ATA_
                                GG  GTA   TGTGTGTGTGT
                                ||  |||   ||||||||||
                                CC  CAT   ACACACACACA
                                 C_   CCCC
GAM1158 SR-BP1   3' GAAAACTGTGATATGTGTGTGT 30068      ___  A
           GT                     GGAA   GT ATATGTGTGTGTGT
                                ||||   || ||||||||||||||
                                CTTT   CA TATACACACACACA
                                  TGA  C
GAM1158 TIX1     3' GTATATGTGTGTGTGTA     30056     A
                                GTA TATGTGTGTGTGTA
                                ||| |||||||||||||
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                                CAT ATACACACACACAT
                                  _
GAM1158  TRIM2    3'  AGCTATATATATGTGTGTGTGT 30069    AA  _
              AT                   GG  GTA ATATGTGTGTGTGTAT
                                  ||  ||| ||||||||||||||||
                                  TC  TAT TATACACACACACATA
                                   GA   A
GAM1158  UGT2B10  3'  AGGAAGGGAACTCTTGTGTGTA 30070       TAAT  GTG
              T                    AGGAAG   AT   TGTGTGTAT
                                  ||||||   ||  |||||||||
                                  TCCTTC   TG   ACACACATA
                                     CCT_  AGA
GAM1158  ZNF387   3'  GGATGAGTCTGTGTGTGTGTGT 30071     __  AATA
                                  GGA  AGT   TGTGTGTGTGT
                                  |||  |||   ||||||||||
                                  CCT  TCA   ACACACACACA
                                    AC   GAC_
GAM1158  LOC121506 3'  AAGCTCTGTGTGTGTGT     30073     AATA
                                  AAGT   TGTGTGTGTGT
                                  ||||   ||||||||||
                                  TTCG   ACACACACACA
                                    AG__
GAM1158  LOC121506 3'  GAAGCTCTGTGTGTGTGT    30072      AATA
                                  GAAGT   TGTGTGTGTGT
                                  |||||   ||||||||||
                                  CTTCG   ACACACACACA
                                     AG__
GAM1158  LOC126917 3'  AGGAGTGCGAGTGTGTGTGTGT 30074     A  AATA_
                                  AGGA GT    TGTGTGTGTGT
                                  |||| ||    ||||||||||
                                  TCCT CA    ACACACACACA
                                    _  CGCTC
GAM1158  LOC127435 3'  AGGGTGTGATGTGTGTGCATGT 30075     AA  A  A
                                  AGG  GT AT TGTGTGTGTGT
                                  |||  || || ||||||||||
                                  TCC  CA TA ACACACGTACA
                                    CA  C  C
GAM1158  LOC130813 5'  GCAAGTGTGTGTGTGTGT    30076     TA_
                                  GTAA   TGTGTGTGTGT
                                  ||||   ||||||||||
                                  CGTT   ACACACACACA
                                     CAC
GAM1158  LOC131583 3'  AGGAAGGGTGTGTGTGT     30077       TAATAT
                                  AGGAAG     GTGTGTGTGT
                                  ||||||     ||||||||||
                                  TCCTTC     CACACACACA
                                     C_____
GAM1158  LOC145135 5'  GGATTGCAGTGCGTGTGTGTGT 30078     A_  ATA
                                  GGA  GTA   TGTGTGTGTGT
                                  |||  |||   ||||||||||
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                                CCT  CGT   GCACACACACA
                                  AA   CAC
GAM1158  LOC145719 5'  GTATATATGTGTGTGTGT    30079     _
                                GTA ATATGTGTGTGTGT
                                ||| |||||||||||||
                                CAT TATACACACACACA
                                  A
GAM1158  LOC145720 5'  GTATATATGTGTGTGTGT    30079     _
                                GTA ATATGTGTGTGTGT
                                ||| |||||||||||||
                                CAT TATACACACACACA
                                  A
GAM1158  LOC146733 5'  GGGTCTGTGTGTGTGTGT    30080    AA  AATA
                                GG  GT    TGTGTGTGTGT
                                ||  ||    ||||||||||
                                CC  CA    ACACACACACA
                                 __  GAC_
GAM1158  LOC147042 5'  GGAGGGTAAGGGCTGTGTGTGT 30081     A_    TA__
                                GGA  GTAA    TGTGTGTGT
                                |||  ||||    |||||||||
                                CCT  CATT    ACACACACA
                                  CC    CCCG
GAM1158  LOC148603 3'  GTGTGTATGTGTGTGTGT    29964    AA_
                                GT   TATGTGTGTGTGT
                                ||   |||||||||||||
                                CA   ATACACACACACA
                                 CAC
GAM1158  LOC150577 3'  AGGGAGTGTGTGTGTGTGTGT  30082     A   AATA
                                AGG AGT    TGTGTGTGTGT
                                ||| |||    ||||||||||
                                TCC TCA    ACACACACACA
                                  C   CAC_
GAM1158  LOC150577 3'  AGGGAGTGTGTGTGTGTGT    30083     A   AATA
                                AGG AGT    TGTGTGTGTGT
                                ||| |||    ||||||||||
                                TCC TCA    ACACACACACA
                                  C   C___
GAM1158  LOC150759 3'  AAGTTTGTGTGTGTGTGT    29983     AATA
                                AAGT    TGTGTGTGTGT
                                ||||    ||||||||||
                                TTCA    ACACACACACA
                                   AAC_
GAM1158  LOC151878 5'  AGGAAGTGTGTGTGT       30084       AATAT
                                AGGAAGT    GTGTGTGT
                                |||||||    ||||||||
                                TCCTTCA    CACACACA
                                     _____
GAM1158  LOC197114 5'  GTATATATGTGTGTGTGT    30079     _
                                GTA ATATGTGTGTGTGT
                                ||| |||||||||||||
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                                CAT TATACACACACACA
                                  A
GAM1158  LOC199906 3'  AGGGTGTGTGAGTGTGTGTGT  30085     AA  AATAT
                                AGG  GT    GTGTGTGTGT
                                |||  ||    ||||||||||
                                TCC  CA    CACACACACA
                                  CA  CACT_
GAM1158  LOC199923 3'  AGAAGATGTGTGTGTGT     30086      TAAT
                                GGAAG    ATGTGTGTGTGT
                                |||||    ||||||||||||
                                TCTTC    TACACACACACA
                                   ____
GAM1158  LOC200399 5'  GAAGAGTGTGTGTGTGTGT   30087      TAATA
                                GAAG     TGTGTGTGTGT
                                ||||     ||||||||||
                                CTTC     ACACACACACA
                                  TCAC_
GAM1158  LOC200844 5'  GGGAGTGATTGTGTGTGT    30088    A   A  A
                                GG AGT AT TGTGTGTGT
                                || ||| || |||||||||
                                CC TCA TA ACACACACA
                                 C   C  _
GAM1158  LOC200918 3'  GAGCAGGTGTGTGTGTGT    30089    A   ATA
                                GA GTA   TGTGTGTGTGT
                                || |||   ||||||||||
                                CT CGT   ACACACACACA
                                 _   CC_
GAM1158  LOC201911 3'  GGGGCATTGTGTGTGTGTGT   30090    AA   ATA
                                GG  GTA   TGTGTGTGTGT
                                ||  |||   ||||||||||
                                CC  CGT   ACACACACACA
                                 C_   AAC
GAM1158  LOC203536 3'  AAGTAGGTGTGTGTGTGT    30091      ATA
                                AAGTA   TGTGTGTGTGT
                                |||||   ||||||||||
                                TTCAT   ACACACACACA
                                   CC_
GAM1158  LOC204301 3'  AGGAAGTAAATGAATTGTGT   30092        T   TG_
                                AGGAAGTAA ATG   TGTGT
                                ||||||||| |||   |||||
                                TCCTTCATT TAC   ACACA
                                     _   TTA
GAM1158  LOC219649 3'  AGCAGTGCTTGTGTGTGTGT   30093    A   AATA
                                GG AGT    TGTGTGTGTGT
                                || |||    ||||||||||
                                TC TCA    ACACACACACA
                                 G   CGA_
GAM1158  LOC219988 3'  GTATCTATGTGTGTGTGTAT   30095     A_
                                GTA  TATGTGTGTGTGTAT
                                |||  ||||||||||||||
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                                CAT  ATACACACACACATA
                                  AG
GAM1158  LOC219988 3'  GGGGTGTGTGTGTGTGTAT   30094    AA  AATA
                                GG  GT    TGTGTGTGTGTAT
                                ||  ||    |||||||||||||
                                CC  CA    ACACACACACATA
                                 C_  C___
GAM1158  LOC221543 3'  GTATGTATGTGTGTGTGTAT  30096     A_
                                GTA  TATGTGTGTGTGTAT
                                |||  ||||||||||||||
                                CAT  ATACACACACACATA
                                  AC
GAM1158  LOC221981 3'  GGGTGTGTGTGTGTGTGT    29992    AA  AATA
                                GG  GT    TGTGTGTGTGT
                                ||  ||    ||||||||||
                                CC  CA    ACACACACACA
                                 CA  C___
GAM1158  LOC222662 3'  GTATATATATGTGTGTGTGTAT 30097     ___
                                GTA   ATATGTGTGTGTGTAT
                                |||   ||||||||||||||||
                                CAT   TATACACACACACATA
                                  ATA
GAM1158  LOC222662 3'  GTATGTATGTGTGTGTGT    30054     A_
                                GTA  TATGTGTGTGTGT
                                |||  |||||||||||||
                                CAT  ATACACACACACA
                                  AC
GAM1158  LOC222662 3'  GTATATATATGTGTGTGTGTAT 30097     ___
                                GTA   ATATGTGTGTGTGTAT
                                |||   ||||||||||||||||
                                CAT   TATACACACACACATA
                                  ATA
GAM1158  LOC253150 3'  GTGTGTATGTGTGTGTGT    29964    AA_
                                GT   TATGTGTGTGTGT
                                ||   |||||||||||||
                                CA   ATACACACACACA
                                 CAC
GAM1158  LOC253982 3'  GAGAGTATGTGTGTGTGT    30098   GA   ATA
                                G  AGTA   TGTGTGTGTGT
                                |  ||||   ||||||||||
                                C  TCAT   ACACACACACA
                                 TC   ___
GAM1158  LOC254358 3'  AGGAAGTAAATGAATTGTGT   30092        T   TG_
                                AGGAAGTAA ATG   TGTGT
                                ||||||||| |||   |||||
                                TCCTTCATT TAC   ACACA
                                      _  TTA
GAM1158  LOC256520 3'  GGGTGTGTGTGTGTGTGT    29992    AA  AATA
                                GG  GT    TGTGTGTGTGT
                                ||  ||    ||||||||||
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                                CC  CA    ACACACACACA
                                 CA  C___
GAM1158  LOC257596 3'  GTATGTATGTGTGTGTGTAT   30096     A_
                                GTA  TATGTGTGTGTGTAT
                                |||  ||||||||||||||
                                CAT  ATACACACACACATA
                                  AC
GAM1158  LOC51141  3'  AGTAATATGTGTGTGTGTAT   30099
                                AGTAATATGTGTGTGTGTAT
                                ||||||||||||||||||
                                TCATTATACACACACACATA

GAM1158  LOC64744  3'  GGAAGGGATGTGTGTCTGTGT  30100      TA  A    G
                                GGAAG  AT TGTGT TGTGT
                                |||||  || ||||| |||||
                                CCTTC  TA ACACA ACACA
                                   CC  C    G
GAM1158  LOC90139  3'  GGAATGTGATGTGCACCTCTGT 30101     GTAAT     _______
            GTGT                   GGAA    ATGTGT     GTGTGT
                                ||||    ||||||     ||||||
                                CCTT    TACACG     CACACA
                                  ACAC_     TGGAGA
GAM1158  LOC93166  5'  AGTGAGTGAGTGTGTGTGTGT  30102    GA   AATA
                                AG  AGT    TGTGTGTGTGT
                                ||  |||    ||||||||||
                                TC  TCA    ACACACACACA
                                 AC   CTC_
GAM1158  LOC93463  3'  GGAAATTAGTGGTGTGTGTGTG 30103       AATA__
            T                   GGAAGT     TGTGTGTGTGT
                                ||||||     ||||||||||
                                CCTTTA     ACACACACACA
                                   ATCACC
GAM1159  ABAT     5'  GCCCCGAGTTCCGGCAGCG   30106        CGTC    T   A
                                GCCCCGAG    TCTG GCA CG
                                ||||||||    |||| ||| ||
                                CGGGGCTC    AGGC CGT GC
                                     A___    _   C
GAM1159  B3GAT1    5'  CCGGAGCGTCTCCGGTGC    30107    C         _
                                CC GAGCGTCTCTG TGC
                                || ||||||||||| |||
                                GG CTCGCAGAGGC ACG
                                 C          C
GAM1159  B3GAT1    5'  CCGGAGCGTCTCCGGTGC    30107    C         _
                                CC GAGCGTCTCTG TGC
                                || ||||||||||| |||
                                GG CTCGCAGAGGC ACG
                                 C          C
GAM1159  B4GALT2   3'  GCACCCACACAAGTTTCTGTGC 30108    _    A   TC__
            AA                    GC CCCG GCG    TCTGTGCAA
                                || |||| |||    |||||||||
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                                CG GGGT TGT    AGACACGTT
                                 T   G   TCAA
GAM1159 B4GALT2  3'  GCACCCACACAAGTTTCTGTGC 30108    _   A   TC__
             AA                   GC CCCG GCG    TCTGTGCAA
                                || |||| |||    |||||||||
                                CG GGGT TGT    AGACACGTT
                                 T   G   TCAA
GAM1159 CYP4A11  3'  GCCCCGAGCTCTGGAAGTGC   30109        G   CT__
                                GCCCCGAGC TCT    GTGC
                                ||||||||| |||    ||||
                                CGGGGCTCG AGA    CACG
                                      _  CCTT
GAM1159 F2R     5'  CCCGGGCTCTGCGCGGCGC   30110     A  GTC      AA
                                CCCG GC   TCTGTGC  CGC
                                |||| ||   |||||||  |||
                                GGGC CG   AGACGCG  GCG
                                  C ___      CC
GAM1159 FBP1    5'  GCCCCGAGTGTCCGCAGCGC   30111        C    CT_
                                GCCCCGAG GTCT   GTGC
                                |||||||| ||||   ||||
                                CGGGGCTC CAGG   CGCG
                                    A   CGT
GAM1159 RPS5    5'  GCCTGAGCGTCTCTGTCACTCG 30112     CC         G  AC__
             GC                   GCC  GAGCGTCTCTGT CA    GC
                                |||  ||||||||||| ||    ||
                                CGG  CTCGCAGAGACA GT    CG
                                  A_          _  GAGC
GAM1159 WNT14    3'  GCCCATTCATGCTCTGTGCAAT 30113      CGAG  _        C
             GC                   GCCC    CGT CTCTGTGCAA GC
                                ||||    ||| ||||||||||| ||
                                CGGG    GTA GAGACACGTT CG
                                  TAA_   C        A
GAM1159 ZNFN2A1  3'  GCCCCGAGTGCCTTTCATATG  30114        C    C___
                                GCCCCGAG GTCT    TGTG
                                |||||||| ||||    ||||
                                CGGGGCTC CGGA    ATAC
                                    A    AAGT
GAM1159 DKFZp762M136 3'  AGAATTTCTGTGCAACGC    30115    C  C
                                AG GT TCTGTGCAACGC
                                || || ||||||||||||
                                TC TA AGACACGTTGCG
                                 T  A
GAM1159 FBP17    3'  GCCTCAGCGTCTCTGCGC    30116     C G
                                GCC C AGCGTCTCTGTGC
                                ||| | ||||||||||||
                                CGG G TCGCAGAGACGCG
                                  A _
GAM1159 FLJ10748 5'  GCCCCAGTGTCTCCGCGC    30117      G  C
                                GCCCC AG GTCTCTGTGC
                                ||||| || ||||||||||
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                                CGGGG TC CAGAGGCGCG
                                  _ A
GAM1159 FLJ20190 5' GCCTGGGGCGTCTCTGCCTAGC 30118    CCGA       ___
                                GCC   GCGTCTCTGT  GC
                                |||   ||||||||||  ||
                                CGG   CGCAGAGACG  CG
                                  ACCC        GAT
GAM1159 FLJ22501 3' GCCCTGAGTGTTCTGATGC   30119    C  C C   _
                                GCCC GAG GT TCTG TGC
                                |||| ||| || |||| |||
                                CGGG CTC CA AGAC ACG
                                  A  A _   T
GAM1159 GTF3C1   5' GCCCCGGGGGTGCGCAACG   30120      AGCGTCTC
                                GCCCCG      TGTGCAACG
                                ||||||      |||||||||
                                CGGGGC      ACGCGTTGC
                                   CCCC____
GAM1159 HAAO    5' CCCGGGCGCCTCCTCGCAGCGC 30121    A      G   A
                                CCCG GCGTCTCT TGCA CGC
                                |||| |||||||| |||| |||
                                GGGC CGCGGAGG GCGT GCG
                                  C       A   C
GAM1159 HUMAGCGB 5' CCCGGGCGCCTCCGGCA    30122    A       T
                                CCCG GCGTCTCTG GCA
                                |||| ||||||||| |||
                                GGGC CGCGGAGGC CGT
                                  C       _
GAM1159 KIAA0447 3' GCCCTTGAGTGCCGTGCAATGC 30123    C_  C  TCT    C
                                GCCC  GAG GTC  GTGCAA GC
                                ||||  ||| |||  |||||| ||
                                CGGG  CTC CGG  CACGTT CG
                                  AA  A  ___     A
GAM1159 KIAA1209 5' GCCTTTGCTAGTCTGTGCAGCG 30124    CCGA  GTC      A
            C                    GCC   GC  TCTGTGCA CGC
                                |||   ||  |||||||| |||
                                CGG   CG  AGACACGT GCG
                                  AAA_ ATC      C
GAM1159 LLGL2   5' GCCTCGGCGTCCCTCGGCGC  30125    C A     __
                                GCC CG GCGTCTCT  GTGC
                                ||| || ||||||||  ||||
                                CGG GC CGCAGGGA  CGCG
                                  A _      GC
GAM1159 MGC10485 5' GCCTCCGGCGGTGCAACG   30126    _  A  TCTCT
                                GCC CCG GCG    GTGCAACG
                                ||| ||| |||    ||||||||
                                CGG GGC CGC    CACGTTGC
                                  A  _  _____
GAM1159 RNPC2   5' GCCTTCGGGCGCCTGTGGTGC  30127    C_  A    CT_
                                GCC  CG GCGTCT   GTGC
                                |||  || ||||||   ||||
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                                CGG  GC CGCGGA   CACG
                                  AA  C     CAC
GAM1159  STK23    3'  GCTCCAGCGTCTCTCTGC    30128    C  G       G
                                GC CC AGCGTCTCT TGC
                                || || ||||||||| |||
                                CG GG TCGCAGAGA ACG
                                 A  _       G
GAM1159  ZNF185   3'  GCTCTGTAGCGTTCTGCGCAAT 30129    CCCG_    C       C
              GC                  GC    AGCGT TCTGTGCAA GC
                                ||    ||||| ||||||||| ||
                                CG    TCGCA AGACGCGTT CG
                                 AGACA    _       A
GAM1159  ZNF226   5'  GCCTCCTCCTCTGTGCAGTGC  30130    _ GAGCG        AC
                                GCC CC    TCTCTGTGCA  GC
                                ||| ||    ||||||||||  ||
                                CGG GG    GGAGACACGT  CG
                                  A  A____        CA
GAM1159  LOC124446 5'  GCCCCGAACGATTGCAACG   30131         TCTCTG
                                GCCCCGAGCG     TGCAACG
                                ||||||||||     |||||||
                                CGGGGCTTGC     ACGTTGC
                                      TA____
GAM1159  LOC125061 3'  GCTCCGGGCATCTCTGAGC   30132    C   A       T
                                GC CCG GCGTCTCTG GC
                                || ||| ||||||||| ||
                                CG GGC CGTAGAGAC CG
                                 A   C       T
GAM1159  LOC130574 5'  GCCCCCAGAGTGTGCAAG    30133      G  C  CTCT     C
                                GCCCC AG GT    GTGCAA G
                                ||||| || ||    |||||| |
                                CGGGG TC CA    CACGTT C
                                   G  T  ____     A
GAM1159  LOC135570 5'  CCCCGGCGTCTGATGC      30134       A     CT
                                CCCCG GCGTCT  GTGC
                                ||||| ||||||  ||||
                                GGGGC CGCAGA  TACG
                                   _     C_
GAM1159  LOC145566 5'  GCCCCATGCATCTGTGTG    30135       A     C
                                GCCCCG GCGTCT TGTG
                                |||||| |||||| ||||
                                CGGGGT CGTAGA ACAC
                                    A     C
GAM1159  LOC151176 5'  CCCCGAGCGCCACGTGCAGCG  30136          TC     A
                                CCCCGAGCGTC  TGTGCA CG
                                ||||||||||  |||||| ||
                                GGGGCTCGCGG  GCACGT GC
                                      T_     C
GAM1159  LOC157660 5'  CCCGAGCGCCGTCGCAGCGC   30137          TCTG    A
                                CCCGAGCGTC    TGCA CGC
                                ||||||||||    |||| |||
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                                GGGCTCGCGG   GCGT GCG
                                     CA__   C
GAM1159  LOC165257 5'  GCCCCGAGGGTCCGGCGC   30138       C   CT
                                GCCCCGAG GTCT  GTGC
                                |||||||| ||||  ||||
                                CGGGGCTC CAGG  CGCG
                                    C   C_
GAM1159  LOC201507 3'  CCCCGGGCGTCCCCGGC    30139      A       T
                                CCCCG GCGTCTCTG GC
                                ||||| ||||||||| ||
                                GGGGC CGCAGGGGC CG
                                  C       _
GAM1159  LOC201965 5'  GCCCCGAGCCTCGGCAGCGC  30140        G  TCT_
                                GCCCCGAGC TC   GTGC
                                ||||||||| ||   ||||
                                CGGGGCTCG AG   CGCG
                                     G  CCGT
GAM1159  LOC245744 3'  GCCCCGGGCCTCTCTGCG    30141      A  G
                                GCCCCG GC TCTCTGTG
                                |||||| || ||||||||
                                CGGGGC CG AGAGACGC
                                   C  G
GAM1159  LOC83690  5'  GCACCGAGCGTCCGGGGGCGAC 30142    C       CTGT  A
           G                     GC CCGAGCGTCT   GC ACG
                                || ||||||||||   || |||
                                CG GGCTCGCAGG   CG TGC
                                 T        CCCC  C
GAM1160  COL9A2   3'  GCATAGACCTCAGTATTG    30145      GT   _
                                GCATAG  TTTA TATTG
                                ||||||  |||| |||||
                                CGTATC  GAGT ATAAC
                                   TG   C
GAM1160  PAWR     3'  CAGCATAGGAATATTG      30146        TTTT
                                TAGCATAGG   ATATTG
                                |||||||||   ||||||
                                GTCGTATCC   TATAAC
                                     T___
GAM1160  LOC149194 3'  CAGCACTGGTTTTATGTTG   30147      A      A
                                TAGCAT GGTTTTAT TTG
                                |||||| |||||||| |||
                                GTCGTG CCAAAATA AAC
                                   A      C
GAM1161  FLJ21415  3'  TGGTATAAACTGTTCACAT   30150    A      A_
                                TG TATAAACT  TCACAT
                                || ||||||||  ||||||
                                AC ATATTTGA  AGTGTA
                                 C       CA
GAM1161  LOC122773 3'  ATATAAACTAGACAAACT    30151         TCAC
                                ATATAAACTA   ATAAACT
                                ||||||||||   |||||||
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                                TATATTTGAT   TGTTTGA
                                     C___
GAM1161 LOC56965 5' TGATATGATCATATCCATAAAC 30152      AAAC_   A
             TA                   TGATAT    TATC CATAAACTA
                                |||||||    |||| |||||||||
                                ACTATA    ATAG GTATTTGAT
                                   CTAGT   _
GAM1162 SNCG    3' CATGTCACTCAAGGCG     30155     G      TAC
                                CATG CACTCGAG   GCG
                                |||| ||||||||   |||
                                GTAC GTGAGTTC   CGC
                                  A      ___
GAM1162 FLJ12389 3' CATGACACAGACACACG     30156       TC  G
                                CATGGCAC  GA TACGCG
                                ||||||||  || ||||||
                                GTACTGTG  CT GTGTGC
                                     T_ _
GAM1162 HSU79266 3' CATGGCACTGCACAGCG     30157       CGA   _
                                CATGGCACT   GTAC GCG
                                |||||||||   |||| |||
                                GTACCGTGA   CGTG CGC
                                     ___   T
GAM1162 KIAA0087 3' ATGGGCTAAAATACGCG     30158     CA  C
                                ATGG  CT GAGTACGCG
                                ||||  || |||||||||
                                TACC  GA TTTATGCGC
                                  C_  T
GAM1162 LOC90639 3' CATGGCACGTGGCCACACCGCG 30159       _____  AGTA
                                CATGGCAC   TCG   CGCG
                                ||||||||   |||   ||||
                                GTACCGTG   GGT   GCGC
                                    CACC   GTG_
GAM1163 FBXW1B   3' GAATACTGCAGGAAGGG     30162       TTC
                                GAATACTGCG   AAGGG
                                ||||||||||   |||||
                                CTTATGACGT   TTCCC
                                     CC_
GAM1163 FBXW1B   3' GAATACTGCAGGAAGGG     30162       TTC
                                GAATACTGCG   AAGGG
                                ||||||||||   |||||
                                CTTATGACGT   TTCCC
                                     CC_
GAM1163 FBXW1B   3' GAATACTGCAGGAAGGG     30162       TTC
                                GAATACTGCG   AAGGG
                                ||||||||||   |||||
                                CTTATGACGT   TTCCC
                                     CC_
GAM1163 INPP5D   3' TATGACGAATGTTCGTAAAG  30163       ACTG  TC
                                TATGACGAAT   CGT  AAGG
                                ||||||||||   |||  ||||
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                                ATACTGCTTA   GCA  TTTC
                                     CAA_  __
GAM1163  SIX2     3'  TATGACGAGGCGGCGTTTAGGG 30164       ATACT    CA
                                TATGACGA    GCGTT  AGGG
                                ||||||||    |||||  ||||
                                ATACTGCT    CGCAA  TCCC
                                     CCGC_    A_
GAM1163  LOC121506 5'  TATGACAATACATATTAAGGG  30165       ATAC    TC_
                                TATGACGA   TGCGT   AAGGG
                                ||||||||   |||||  |||||
                                ATACTGTT   ATGTA   TTCCC
                                     _____    TAA
GAM1163  LOC130902 3'  TGGCAAATACCAGACAAGGG   30166    A       CGTT
                                TG CGAATACTG    CAAGGG
                                || |||||||||    ||||||
                                AC GTTTATGGT    GTTCCC
                                  C       CT__
GAM1163  LOC51117  3'  TATGATAAATGTTGTCCAAGGG 30167      CG   ACTGC
                                TATGA  AAT    GTTCAAGGG
                                |||||  |||    |||||||||
                                ATACT  TTA    CAGGTTCCC
                                   AT   CAA__
GAM1164  LOXL1    3'  TTTATTCAGCCCAGACC     30170         G   GA
                                TTTATTCAG CCCA  GACC
                                ||||||||| ||||  ||||
                                AAATAAGTC GGGT  CTGG
                                          _   __
GAM1164  NEBL     3'  TTCAGCCCAGAGGTCATT    30171      G      AC
                                TTCAG CCCAGAG  CATT
                                ||||| |||||||  ||||
                                AAGTC GGGTCTC  GTAA
                                   _      CA
GAM1164  POR      3'  CTTTATTCCAAGGGCCAGAG   30172        __  C
                                CTTTATTC  AGG CCAGAG
                                ||||||||  ||| ||||||
                                GAAATAAG  TCC GGTCTC
                                     GT   C
GAM1164  PAK2     3'  TTCATTCAGGTTATGCAGACCA 30173         CCCAG_
              TT                  TTTATTCAGG     AGACCATT
                                  ||||||||||     ||||||||
                                  AAGTAAGTCC     TCTGGTAA
                                       AATACG
GAM1164  LOC146224 5'  TTTGTTCAGGCCTGAAGCC   30174     A      CA   A
                                TTT TTCAGGCC  GAG CC
                                ||| ||||||||  ||| ||
                                AAA AAGTCCGG  TTC GG
                                  C       AC   _
GAM1164  LOC152220 3'  TTCATTCAGGTTATGCAGACCA 30173         CCCAG_
              TT                  TTTATTCAGG     AGACCATT
                                  ||||||||||     ||||||||
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                                AAGTAAGTCC     TCTGGTAA
                                     AATACG
GAM1165 C1orf34   3'  TCTCCAGGGATGTACAGGGGCT 30177        _     CATCGA
             AT                   TCTCCAGG ATGTAC     CTAT
                                  |||||||| ||||||     ||||
                                  AGAGGTCC TACATG     GATA
                                       C     TCCCC_
GAM1165 FLJ10656 3'  CAAGATGTTTTATTGACTAT   30178        ACC  C
                                  CAGGATGT   AT GACTAT
                                  ||||||||   || ||||||
                                  GTTCTACA   TA CTGATA
                                       AAA  A
GAM1165 FLJ10916  5'  TCTCCAGGAAGTACTGCAGGAA 30179         T   __ TC
             CT                   TCTCCAGGA GTAC  CA  GACT
                                  ||||||||| ||||  ||  ||||
                                  AGAGGTCCT CATG  GT  TTGA
                                       T    AC  CC
GAM1165 LOC151242 3'  TCCAGGATGTGCATAGCTACT  30180         AC   CG__
                                  TCCAGGATGT  CAT    ACT
                                  ||||||||||  |||    |||
                                  AGGTCCTACA  GTA    TGA
                                       C_   TCGA
GAM1165 LOC196264 3'  TCTCCAGGATTGTCCATCGCTA 30181          _ A     A
             T                    TCTCCAGGAT GT CCATCG CTAT
                                  |||||||||| || |||||| ||||
                                  AGAGGTCCTA CA GGTAGC GATA
                                       A  _     _
GAM1166 ADAMTS3   3'  TCTTTGGTGATTTCTTCCAATG 30184        _______  TC
             A                    TCTTTGGTG     TCC  TGA
                                  |||||||||     |||  |||
                                  AGAAACCAC     AGG  ACT
                                       TAAAGA   TT
GAM1166 AK1       3'  TCTTTGATGTTCTTCTTTCA   30185         _ C   GAGG
                                  TCTTTGGTGT C TCT    CA
                                  |||||||||| | |||    ||
                                  AGAAACTACA G AGA    GT
                                       A A   AA__
GAM1166 ARHGAP6   3'  TCTTTGGCACTGAGG       30186         TCCT
                                  TCTTTGGTG    CTGAGG
                                  |||||||||    ||||||
                                  AGAAACCGT    GACTCC
                                               ____
GAM1166 CACNA1C   5'  TCTCTGGTGTCTGGCA      30187          CTCTGA
                                  TCTTTGGTGTC     GGCA
                                  ||||||||||      ||||
                                  AGAGACCACAG     CCGT
                                       A_____
GAM1166 CASP2     3'  TCGTTTGGTGTTCCGCA     30188    _      _  TCTGAG
                                  TC TTTGGTGT CC     GCA
                                  || ||||||| ||      |||
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                                AG AAACCACA GG     CGT
                                 C       A _______
GAM1166  CASP2    3'  TCGTTTGGTGTTCCGCA     30188    _      _  TCTGAG
                                TC TTTGGTGT CC     GCA
                                || |||||||| ||     |||
                                AG AAACCACA GG     CGT
                                 C       A _______
GAM1166  CASP2    3'  TCGTTTGGTGTTCCGCA     30188    _      _  TCTGAG
                                TC TTTGGTGT CC     GCA
                                || |||||||| ||     |||
                                AG AAACCACA GG     CGT
                                 C       A _______
GAM1166  CBFA2T2  3'  TCTTTGGTCTTCTCTGGTCCCT 30189        GTC    AG____
              GCA                   TCTTTGGT   CTCTG     GCA
                                |||||||   |||||     |||
                                AGAAACCA   GAGAC     CGT
                                     GAA     CAGGGA
GAM1166  CLCN5    5'  TCTGTGGTGTAGGCAC      30190     T     CCTCTG
                                TCT TGGTGT     AGGCAC
                                ||| ||||||     ||||||
                                AGA ACCACA     TCCGTG
                                 C     _______
GAM1166  CLOCK    3'  TCTTTGGTTGTTTTCTTTTTCA 30191        _  CC   GAGG
                                TCTTTGGT GT  TCT    CA
                                |||||||| ||  |||    ||
                                AGAAACCA CA  AGA    GT
                                     A  AA   AAAA
GAM1166  CYP3A4   3'  TCTCTGGTGTTCTCAGGCACA  30192         CC   G
                                TCTTTGGTGT  TCT AGGCACA
                                ||||||||||  ||| |||||||
                                AGAGACCACA  AGA TCCGTGT
                                      __   G
GAM1166  CYP3A5   3'  TCTCTGGTGTTCTGGGGCACA  30193         CC    A
                                TCTTTGGTGT  TCTG GGCACA
                                ||||||||||  |||| ||||||
                                AGAGACCACA  AGAC CCGTGT
                                      __    C
GAM1166  FBXL2    3'  TCTTTGGTGTCTCATGG     30194          C  TGA
                                TCTTTGGTGTC TC   GG
                                |||||||||| ||   ||
                                AGAAACCACAG AG   CC
                                      _  TA_
GAM1166  GJA1     3'  TCTTTGTGTTTTCTAAG     30195       G   CC
                                TCTTTG TGT  TCTGAG
                                |||||| |||  ||||||
                                AGAAAC ACA  AGATTC
                                    _   AA
GAM1166  GRIA2    5'  TCTTTGGCTGTTTTCCTCTG  30196        G____
                                TCTTTGGT    TCCTCTG
                                ||||||||    |||||||
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                                AGAAACCG    AGGAGAC
                                    ACAAA
GAM1166 HMGA2    3' TCTTTGGTGTTCTAAACA    30197        CC     G
                                TCTTTGGTGT  TCTGAG CA
                                ||||||||||  ||||||  ||
                                AGAAACCACA  AGATTT GT
                                    __     _
GAM1166 KCNN4    5' CTTTTGCTCTGAGGCACA    30198     GGTGTC
                                CTTT     CTCTGAGGCACA
                                ||||     ||||||||||||
                                GAAA     GAGACTCCGTGT
                                  AC____
GAM1166 MMP16    3' TTTGGTGTTTTCGAATGCA   30199       CC  T  _
                                TTTGGTGT  TC GAG GCA
                                ||||||||  || ||| |||
                                AAACCACA  AG CTT CGT
                                    AA  _   A
GAM1166 MYO5A    3' TCTTTGGTGCCTTCCTAACA  30200         C   GA
                                TCTTTGGTGTC TCT  GGCA
                                ||||||||||| |||  ||||
                                AGAAACCACGG AGG  TTGT
                                     A  A_
GAM1166 ONECUT1  3' TCTTTGGTTTCTTTGGAC    30201       GTC  C  A
                                TCTTTGGT   CT TG GGC
                                ||||||||   || || |||
                                AGAAACCA   GA AC CTG
                                    AA_  A  _
GAM1166 PCDH9    5' TCTTTGGTGCCCTCATAG    30202          TG
                                TCTTTGGTGTCCTC  AG
                                ||||||||||||||  ||
                                AGAAACCACGGGAG  TC
                                       TA
GAM1166 TCF8     3' CTTTGGTGTTTTCTCTGCGG  30203       C__    A
                                CTTTGGTGT   CTCTG GG
                                |||||||||   ||||| ||
                                GAAACCACA   GAGAC CC
                                    AAA     G
GAM1166 XYLB     3' TCTCTGGTGTTCTTTTATATCC 30204        C  CTGAGG__
          ACAA                   TCTTTGGTGT CT       CACAA
                                ||||||||||  ||       |||||
                                AGAGACCACA GA       GTGTT
                                     A  AAATATAG
GAM1166 ZNF219   5' TCTTTGGTTCTGGGAAGTGCA 30205       GTCC   ___  _
                                TCTTTGGT    TCTG   AG GCA
                                ||||||||    ||||   || |||
                                AGAAACCA    AGAC   TC CGT
                                    _____   CCT  A
GAM1166 C21orf100 3' TCTTTGGTGTTCCTTGGC    30206         _   CTGA
                                TCTTTGGTGT CCT    GGC
                                ||||||||||  |||    |||
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                                AGAAACCACA GGA   CCG
                                      A  A___
GAM1166 CYP3A7   3' TCTCTGGTGTTCTGGGGCACA 30193        CC   A
                                TCTTTGGTGT  TCTG GGCACA
                                |||||||||  |||| ||||||
                                AGAGACCACA  AGAC CCGTGT
                                      __   C
GAM1166 FLJ32940 5' TCTTTGGCTTATGGGGCACAA 30207      GTCCTC  A
                                TCTTTGGT     TG GGCACAA
                                ||||||||     || |||||||
                                AGAAACCG     AC CCGTGTT
                                     AAT___  C
GAM1166 KIAA0174 3' TCTTTGGTGGTCTTCCCACA  30208       _  C   GAGG
                                TCTTTGGTG TC TCT    CACA
                                ||||||||| || |||    ||||
                                AGAAACCAC AG AGG    GTGT
                                      C  A  _____
GAM1166 KIAA1202 3' TCTTTGGTGTCCTAGTACAA  30209         CTG  GC
                                TCTTTGGTGTCCT   AG  ACAA
                                ||||||||||||   ||  ||||
                                AGAAACCACAGGA   TC  TGTT
                                       ___  A_
GAM1166 KIAA1937 3' CTCTTAACTCTCTGAGGCGCA 30210     GGT TC       A
                                CTTT   G  CTCTGAGGC CA
                                ||||   |  ||||||||| ||
                                GAGA   T  GAGACTCCG GT
                                  AT_ GA       C
GAM1166 MGC20460 5' TCTTTGATGTCCTTTTGA    30211          C_
                                TCTTTGGTGTCCT  TGA
                                ||||||||||||  |||
                                AGAAACTACAGGA  ACT
                                       AA
GAM1166 NMU2R    3' TCTCTGAAGTTTTGAGGCA   30212       T  CCTC
                                TCTTTGG GT    TGAGGCA
                                |||||||  ||    |||||||
                                AGAGACT CA    ACTCCGT
                                     T  AA__
GAM1166 RASGRF2  3' TCTGGAATCCTCTGGGGCACA 30213     T      A
                                TTTGG GTCCTCTG GGCACA
                                |||||  ||||||||  ||||||
                                AGACC TAGGAGAC CCGTGT
                                   T       C
GAM1166 ShrmL    5' TCTTTGGTATTTTCAGTGA   30214        CC  __
                                TCTTTGGTGT  TC  TGA
                                ||||||||||  ||  |||
                                AGAAACCATA  AG  ACT
                                      AA  TC
GAM1166 SPTLC2   3' TCCTTGGTGTTTGAAGAGGCA 30215        CCTCT
                                TCTTTGGTGT    GAGGCA
                                ||||||||||    ||||||
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                                AGGAACCACA    CTCCGT
                                     AACTT
GAM1166 TUBGCP2  5' TTTAGCTCTGAGGCAC     30216      TGTC
                                TTTGG   CTCTGAGGCAC
                                |||||   ||||||||||
                                AAATC   GAGACTCCGTG
                                  ____
GAM1166 ZDHHC5   3' CCTTTGGTGTAGGCC      30217         CCTCTG   A
                                TCTTTGGTGT     AGGC C
                                ||||||||||     |||| |
                                GGAAACCACA     TCCG G
                                     _______   C
GAM1166 LOC154141 5' TCTGCTGCCTTTCTGAGGCA  30218      G   C_
                                TTTG TGTC  TCTGAGGCA
                                |||| ||||  |||||||||
                                AGAC ACGG  AGACTCCGT
                                  G   AA
GAM1166 LOC159121 5' TCTGGTGGGAGGCACA     30219       TCCTCT
                                TTTGGTG     GAGGCACA
                                |||||||     ||||||||
                                AGACCAC     CTCCGTGT
                                    C_____
GAM1166 LOC161978 5' TCTTTGTGTCCTCTGAA     30220       G
                                TCTTTG TGTCCTCTGAG
                                |||||| ||||||||||
                                AGAAAC ACAGGAGACTT
                                  _
GAM1166 LOC197423 5' TCTTTGGTGGCTAAAGCACAA  30221         TCCT
                                TCTTTGGTG   CTGAGGCACAA
                                |||||||||   ||||||||||
                                AGAAACCAC   GATTTCGTGTT
                                    C___
GAM1166 LOC200627 5' TCCTTGGTGTTCAAGGAGTGAG 30222          _ CTC___    C
           GTACA                TCTTTGGTGT C     TGAGG ACA
                                |||||||||| |     ||||| |||
                                AGGAACCACA G     ACTCC TGT
                                     A TTCCTC    A
GAM1166 LOC220565 5' TCTTTGGTGGCTAAAGCAC   30223        TCCT
                                TCTTTGGTG   CTGAGGCAC
                                |||||||||   |||||||||
                                AGAAACCAC   GATTTCGTG
                                    C___
GAM1166 LOC51326 3' CTTTGGTGTTACCTGGCA   30224        CC   GA
                                CTTTGGTGT  TCT  GGCA
                                |||||||||  |||  ||||
                                GAAACCACA  GGA  CCGT
                                     AT   __
GAM1166 LOC90288 3' TCTTTGGCGTTTTCTTGTCA  30225        CC   GAGG
                                TCTTTGGTGT  TCT   CA
                                ||||||||||  |||   ||
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                                AGAAACCGCA AGA   GT
                                     AA  ACA_
GAM1166 LOC90317 3' TCTTTGGTGTTTGCTGAG   30226       CCT
                                TCTTTGGTGT  CTGAG
                                ||||||||||  |||||
                                AGAAACCACA  GACTC
                                     AAC
GAM1166 LOC90342 5' TCTTTGGTGTCCTGTGGG   30227         C A
                                TCTTTGGTGTCCT TG GG
                                |||||||||||| || ||
                                AGAAACCACAGGA AC CC
                                       C _
GAM1166 LOC92283 3' TCTTTGATGTTGAATAAGG  30228       CCTC
                                TCTTTGGTGT   TGAGG
                                ||||||||||   |||||
                                AGAAACTACA   ATTCC
                                     ACTT
GAM1166 LOC92283 3' TCTCTGATGTCTTTTGAGG  30229       CTC
                                TCTTTGGTGTC  TGAGG
                                ||||||||||   |||||
                                AGAGACTACAG  ACTCC
                                      AAA
GAM1167 ATP11A   3' TATGTGCATATGTATTGT   30232         C
                                TATGTGTATATGTA TGT
                                |||||||||||||| |||
                                ATACACGTATACAT ACA
                                       A
GAM1167 ATP7A    3' TATGTGTATGTACATATATA  30233      TA   TGT
                                TATGTGTA  TGTAC  TATATA
                                ||||||||  |||||  ||||||
                                ATACACAT  ACATG  ATATAT
                                    __    T__
GAM1167 CXCR6    3' TATGTGTGTATGTGTGT    30234      A   AC
                                TATGTGT TATGT  TGT
                                ||||||| |||||  |||
                                ATACACA ATACA  ACA
                                    C    C_
GAM1167 DSG2     3' ATGTGTATGTGTCTCTGT   30235       A  A_
                                ATGTGTAT TGT  CTGT
                                |||||||| |||  ||||
                                TACACATA ACA  GACA
                                    C  GA
GAM1167 EGR3     3' TGTATATATGTACACTCACAT 30236         TG
                                TGTGTATATGTAC  TTATAT
                                ||||||||||||  ||||||
                                ACATATATACATG  AGTGTA
                                       TG
GAM1167 EPHA1    3' TATATGTGTATGTATGT    30237      A    C
                                TATGTGT TATGTA TGT
                                ||||||| |||||| |||
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                                ATATACA ATACAT ACA
                                    C     _
GAM1167  EXTL3    3'  TGTGTGCATGTATTTATAT   30238      A     CTG
                                TGTGT TATGTA   TTATAT
                                ||||| ||||||   ||||||
                                ACACA GTACAT   AATATA
                                   C     A__
GAM1167  F9       3'  TATGTGTGTATGCGTGT     30239       A     AC
                                TATGTGT TATGT  TGT
                                ||||||| |||||  |||
                                ATACACA ATACG  ACA
                                    C     C_
GAM1167  GABRB3   3'  TATGTATATATGTGTGT     30241           AC
                                TATGTGTATATGT  TGT
                                ||||||||||||  |||
                                ATACATATATACA  ACA
                                       C_
GAM1167  GABRB3   3'  TATGTATATATGTGTGT     30241           AC
                                TATGTGTATATGT  TGT
                                ||||||||||||  |||
                                ATACATATATACA  ACA
                                       C_
GAM1167  GABRB3   3'  TATGTGTGTGTCTGCT      30240       ATA   A
                                TATGTGT   TGT CTGTT
                                |||||||   ||| |||||
                                ATACACA   ACA GACGA
                                    C__   _
GAM1167  GABRB3   3'  TATGTGTGTGTCTGCT      30240       ATA   A
                                TATGTGT   TGT CTGTT
                                |||||||   ||| |||||
                                ATACACA   ACA GACGA
                                    C__   _
GAM1167  GFRA2    3'  TATATGTATATGGATGT     30242           TAC
                                TATGTGTATATG   TGT
                                ||||||||||||   |||
                                ATATACATATAC   ACA
                                       CT_
GAM1167  KCNJ3    3'  TATGTATGTATGTATGT     30244       A     C
                                TATGTGT TATGTA TGT
                                ||||||| |||||| |||
                                ATACATA ATACAT ACA
                                    C     _
GAM1167  KCNJ3    3'  TATGTATGTATGTATGT     30244       A     C
                                TATGTGT TATGTA TGT
                                ||||||| |||||| |||
                                ATACATA ATACAT ACA
                                    C     _
GAM1167  KCNJ3    3'  TATATGTATATGTGTGT     30243           AC
                                TATGTGTATATGT  TGT
                                ||||||||||||  |||
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                                ATATACATATACA  ACA
                                      C_
GAM1167  MORC     3'  TATGTGTAATATGTATACATA  30245        _     CTGT
                                TATGTGTA TATGTA    TATATA
                                |||||||| ||||||    ||||||
                                ATACACAT ATACAT    ATGTAT
                                     T     _____
GAM1167  MS4A1    3'  TATGTGTGTGTGACTGT     30246        ATA  _
                                TATGTGT   TGT ACTGT
                                |||||||   ||| |||||
                                ATACACA   ACA TGACA
                                    C__   C
GAM1167  NR4A2    3'  TATGTGTGTGTGTGTTACAT   30247        ATA   AC
                                TATGTGT   TGT  TGTTATAT
                                |||||||   |||  ||||||||
                                ATACACA   ACA  ACAATGTA
                                    C__   C_
GAM1167  NRF1     3'  TATGTATATATATACTTTATAT 30248             G
              A                  TATGTGTATATGTACT TTATATA
                                 ||||||||||||||| |||||||
                                 ATACATATATATATGA AATATAT
                                                 _
GAM1167  PODXL    3'  TATGTGTATATGTATCAGTT   30249           CT_
                                TATGTGTATATGTA   GTT
                                ||||||||||||||   |||
                                ATACACATATACAT   CAA
                                       AGT
GAM1167  PPAT     3'  TATGTGTATGTGTACATGT    30250         A    _
                                TATGTGTAT TGTAC TGT
                                ||||||||| ||||| |||
                                ATACACATA ACATG ACA
                                     C    T
GAM1167  RBBP9    3'  TATGTGTATGTGTGTGT     30251         A   AC
                                TATGTGTAT TGT  TGT
                                ||||||||| |||  |||
                                ATACACATA ACA  ACA
                                     C   C_
GAM1167  SLC6A6   3'  GTGTATATATACTTATAT    30252           GT
                                GTGTATATGTACT  TATAT
                                ||||||||||||  |||||
                                CACATATATATGA  ATATA
                                              __
GAM1167  TCF3     3'  TGCTACAGTGCTGTTATATA   30253     G    T  A
                                TGT TATA GT CTGTTATATA
                                ||| |||| || ||||||||||
                                ACG ATGT CA GACAATATAT
                                  _   _ C
GAM1167  VENTX2   3'  TATGTATATATATATTTATATA 30254           CTG
                                TATGTGTATATGTA   TTATATA
                                ||||||||||||||   |||||||
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                                ATACATATATATAT   AATATAT
                                      A__
GAM1167 API5     3' TATGTATGTATGTATATTATA 30255       A     C
                                TATGTGT TATGTA TGTTATA
                                ||||||| |||||| |||||||
                                ATACATA ATACAT ATAATAT
                                   C     _
GAM1167 BCMP1    3' TGTGTATATCTATATCTATA  30256        G  CTG
                                TGTGTATAT TA   TTATA
                                ||||||||| ||   |||||
                                ACACATATA AT   GATAT
                                     G  ATA
GAM1167 caspr5   3' TGTGTATATATACTCACATATA 30257            GT
                                TGTGTATATGTACT  TATATA
                                |||||||||||||  ||||||
                                ACACATATATATGA  GTATAT
                                      GT
GAM1167 CSR1     3' TATGTGTGCATGCATGT     30258       A     C
                                TATGTGT TATGTA TGT
                                ||||||| |||||| |||
                                ATACACA GTACGT ACA
                                   C     _
GAM1167 CSR1     3' TATGTGTGCATGCATGT     30258       A     C
                                TATGTGT TATGTA TGT
                                ||||||| |||||| |||
                                ATACACA GTACGT ACA
                                   C     _
GAM1167 CSR1     3' TATGTGTGCATGCATGT     30258       A     C
                                TATGTGT TATGTA TGT
                                ||||||| |||||| |||
                                ATACACA GTACGT ACA
                                   C     _
GAM1167 DIO2     3' TATGTATGTATGTATGT     30244       A     C
                                TATGTGT TATGTA TGT
                                ||||||| |||||| |||
                                ATACATA ATACAT ACA
                                   C     _
GAM1167 DIO2     3' TATGTATGTATGTATGT     30244       A     C
                                TATGTGT TATGTA TGT
                                ||||||| |||||| |||
                                ATACATA ATACAT ACA
                                   C     _
GAM1167 DKFZP547E1010 3' TATGGTATATGTGCTGTCA   30259      T       A
                                TATG GTATATGT CTGTTA
                                |||| |||||||| ||||||
                                ATAC CATATACA GACAGT
                                  _       C
GAM1167 DKFZP547E1010 3' TATGGTATATGTGCTGTCA   30259      T       A
                                TATG GTATATGT CTGTTA
                                |||| |||||||| ||||||
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                                ATAC CATATACA GACAGT
                                  _      C
GAM1167  DKFZP761L0424 3'  TATGTCTATGTATATTTATATA 30260      A     CTG
                                TGTGT TATGTA   TTATATA
                                ||||| ||||||   |||||||
                                ATACA ATACAT   AATATAT
                                   G     ATA
GAM1167  ELL2     3'  TATGTGTATGTGAATCTAT    30261         A  TA_
                                TATGTGTAT TG   CTGT
                                ||||||||| ||   ||||
                                ATACACATA AC   GATA
                                     C  TTA
GAM1167  FLJ11149  3'  TATGTGTAAATGTGTTCAC    30262        T    ACTG
                                TATGTGTA ATGT    TTAT
                                |||||||| ||||    ||||
                                ATACACAT TACA    AGTG
                                     T    CA__
GAM1167  FLJ11175  3'  TGTGTGTATGTCTGTGCAC    30263      A    A   _
                                TGTGT TATGT CTGT TAT
                                ||||| ||||| |||| |||
                                ACACA ATACA GACA GTG
                                   C    _   C
GAM1167  FLJ12987  3'  TATGTGTATATATATCCATATA 30264           CTG
                                TATGTGTATATGTA   TTATATA
                                ||||||||||||||   |||||||
                                ATACACATATATAT   GGTATAT
                                      A__
GAM1167  FLJ23259  3'  TGTATATATGTATATTACATA  30265          C
                                TGTGTATATGTA TGTTATATA
                                |||||||||||| |||||||||
                                ACATATATACAT ATAATGTAT
                                      _
GAM1167  KIAA0189  3'  TGTATATATATACACACATATA 30266           TGT
                                TGTGTATATGTAC   TATATA
                                ||||||||||||   ||||||
                                ACATATATATATG   GTATAT
                                      TGT
GAM1167  KIAA0562  3'  CATGTGTATATGTGTGT     30267           AC
                                TATGTGTATATGT  TGT
                                ||||||||||||  |||
                                GTACACATATACA  ACA
                                      C_
GAM1167  KIAA0970  3'  TATATGTATGTGTATACCCTTA 30269        A__     G
            TA                   TATGTGTAT   TGTACT TTATA
                                ||||||||   |||||| ||||||
                                ATATACATA   ATATGG AATAT
                                     CAC     G
GAM1167  KIAA0970  3'  TATGTGTATATGTGTACACTTG 30268          ____   _
            TTATAT                ATGTGTATATGT    ACT GTTATAT
                                ||||||||||||    ||| |||||||
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                                TACACATATACA    TGA CAATATA
                                      CATG   A
GAM1167  KIAA1354  3'  TATGTGTGCATGCATGT     30258        A     C
                                TATGTGT TATGTA TGT
                                ||||||| |||||| |||
                                ATACACA GTACGT ACA
                                    C     _
GAM1167  KIAA1354  3'  TATGTGTGCATGCATGT     30258        A     C
                                TATGTGT TATGTA TGT
                                ||||||| |||||| |||
                                ATACACA GTACGT ACA
                                    C     _
GAM1167  KIAA1361  3'  TATGTGTATGTGTGTGT     30251         A   AC
                                TATGTGTAT TGT  TGT
                                ||||||||| |||  |||
                                ATACACATA ACA  ACA
                                      C   C_
GAM1167  KIAA1546  3'  TGTATATATGTACATATATA   30270           TGT
                                TGTGTATATGTAC   TATATA
                                ||||||||||||   ||||||
                                ACATATATACATG   ATATAT
                                        T__
GAM1167  KIAA1577  3'  TATATGTATACATAAGTTGTAT 30271            CT   A
           A                     TATGTGTATATGTA  GTT TATA
                                ||||||||||||||  ||| ||||
                                ATATACATATGTAT  CAA ATAT
                                      T_   C
GAM1167  KIAA1615  3'  TATGTGATATGTATAGT     30272       T      CT
                                TATGTG ATATGTA  GT
                                |||||| |||||||  ||
                                ATACAC TATACAT  CA
                                   _      AT
GAM1167  KIAA1906  3'  TATGTATATGCGTTTATATA   30273          ACTG
                                TGTGTATATGT    TTATATA
                                ||||||||||    |||||||
                                ATACATATACG    AATATAT
                                      CA__
GAM1167  KLHL6     3'  TATGTGTATATGTGTGTT    30274           AC
                                TATGTGTATATGT  TGTT
                                ||||||||||||  ||||
                                ATACACATATACA  ACAA
                                        C_
GAM1167  LAIR2     3'  TATTTGTATATGTATGT     30275     G        C
                                TAT TGTATATGTA TGT
                                ||| |||||||||| |||
                                ATA ACATATACAT ACA
                                  A        _
GAM1167  LAIR2     3'  TATTTGTATATGTATGT     30275     G        C
                                TAT TGTATATGTA TGT
                                ||| |||||||||| |||
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                                ATA ACATATACAT ACA
                                  A       _
GAM1167  MAN1     3'  TGTATATATATACATCTATATA 30276          TG
                                TGTGTATATGTAC  TTATATA
                                ||||||||||||  |||||||
                                ACATATATATATG  GATATAT
                                      TA
GAM1167  MBLL39   3'  TATGTGTATATATAATAT    30277          C
                                TATGTGTATATGTA TGT
                                |||||||||||||| |||
                                ATACACATATATAT ATA
                                      T
GAM1167  MGC10540 3'  CATGTGTGTATGTACTTACAT  30278       A      GT
                                TATGTGT TATGTACT  TATAT
                                ||||||| ||||||||  |||||
                                GTACACA ATACATGA  ATGTA
                                    C      __
GAM1167  PLP1     3'  TATGTGTATGTATGCATGT   30279        __     C
                                TATGTGTA  TATGTA TGT
                                ||||||||  |||||| |||
                                ATACACAT  ATACGT ACA
                                     AC     _
GAM1167  PRO0365  5'  TATGTGTATATATATATTTATA 30280          CTG
                                TATGTGTATATGTA   TTATA
                                ||||||||||||||   |||||
                                ATACACATATATAT   AATAT
                                      ATA
GAM1167  RAI1     3'  TATATGTATATGTATACATATA 30281          CTGT
                                TATGTGTATATGTA    TATATA
                                ||||||||||||||    ||||||
                                ATATACATATACAT    GTATAT
                                      AT__
GAM1167  SEMA3E   3'  TATGTGTGTGTATAATTATAT  30282       ATA   CT
                                TATGTGT   TGTA  GTTATAT
                                |||||||   ||||  |||||||
                                ATACACA   ACAT  TAATATA
                                    C__    AT
GAM1167  SLK      3'  TATATGTATATATATTTATATA 30283          CTG
                                TATGTGTATATGTA   TTATATA
                                ||||||||||||||   |||||||
                                ATATACATATATAT   AATATAT
                                      A__
GAM1167  SPIN     3'  TGTGTATATATTATATA     30284         ACTGT
                                TGTGTATATGT    TATATA
                                ||||||||||    ||||||
                                ACACATATATA    ATATAT
                                       _____
GAM1167  SSBP2    3'  TATGTGTATATGTCTGT     30285          A
                                TATGTGTATATGT CTGT
                                |||||||||||| ||||
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                                ATACACATATACA GACA
                                          _
GAM1167  TSPAN-2   3'  TATGTATATGTGTATGT     30286         A    C
                                TATGTGTAT TGTA TGT
                                ||||||||| |||| |||
                                ATACATATA ACAT ACA
                                    C    _
GAM1167  LOC121536 3'  TGTATATATGTATACAT      30287           CTGT
                                TGTGTATATGTA    TATAT
                                ||||||||||||    |||||
                                ACATATATACAT    ATGTA
                                          _____
GAM1167  LOC124045 3'  TATGTGTGTATATACTACATA  30288        A       GTT
                                TATGTGT TATGTACT   ATATA
                                ||||||| ||||||||   |||||
                                ATACACA ATATATGA   TGTAT
                                    C       ___
GAM1167  LOC143465 5'  TATGTGCATGTGTATACAT    30289         A    CTGT
                                TATGTGTAT TGTA    TATAT
                                ||||||||| ||||    |||||
                                ATACACGTA ACAT    ATGTA
                                    C    _____
GAM1167  LOC144766 3'  TACGTGTGTATGTGTCTTTATA 30290         A     ACTG
                                TATGTGT TATGT    TTATA
                                ||||||| |||||    |||||
                                ATGCACA ATACA    AATAT
                                    C    CAGA
GAM1167  LOC145719 5'  TATGTATATATGTGTGT      30241           AC
                                TATGTGTATATGT  TGT
                                ||||||||||||  |||
                                ATACATATATACA  ACA
                                      C_
GAM1167  LOC145720 5'  TATGTATATATGTGTGT      30241           AC
                                TATGTGTATATGT  TGT
                                ||||||||||||  |||
                                ATACATATATACA  ACA
                                      C_
GAM1167  LOC146520 5'  TGTGTATATGCATAAACATATA 30291           CTGT
                                TGTGTATATGTA    TATATA
                                ||||||||||||    ||||||
                                ACACATATACGT    GTATAT
                                      ATTT
GAM1167  LOC151127 3'  TATGTGTGTATGTGTGT      30234        A    AC
                                TATGTGT TATGT  TGT
                                ||||||| |||||  |||
                                ATACACA ATACA  ACA
                                    C    C_
GAM1167  LOC151273 3'  TGTATATATGCATATAT      30292           CTGT
                                TGTGTATATGTA    TATAT
                                ||||||||||||    |||||
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                                ACATATATACGT    ATATA
                                      ____
GAM1167  LOC153711 5'  TATGTGTGTATGTATGT     30293        A     C
                                TATGTGT TATGTA TGT
                                ||||||| |||||| |||
                                ATACACA ATACAT ACA
                                   C     _
GAM1167  LOC153711 5'  TATGTATATGTGTATGT     30286         A   C
                                TATGTGTAT TGTA TGT
                                ||||||||| |||| |||
                                ATACATATA ACAT ACA
                                     C   _
GAM1167  LOC157285 3'  TATGGTATATGTATTTTCTATA 30294      T       CTG_
              TA                  TATG GTATATGTA    TTATATA
                                ||||| |||||||||    |||||||
                                ATAC CATATACAT    GATATAT
                                  _       AAAA
GAM1167  LOC158434 3'  TGTGTTATATGTATTATATA   30295      _     ACT
                                TGTGT ATATGT   GTTATATA
                                ||||| ||||||   ||||||||
                                ACACA TATACA   TAATATAT
                                   A     ___
GAM1167  LOC196411 3'  TGTATATATGTATACATATA   30296          CTGT
                                TGTGTATATGTA    TATATA
                                ||||||||||||    ||||||
                                ACATATATACAT    GTATAT
                                       AT__
GAM1167  LOC196411 3'  TGTATATATGTATACATATA   30296          CTGT
                                TGTGTATATGTA    TATATA
                                ||||||||||||    ||||||
                                ACATATATACAT    GTATAT
                                       AT__
GAM1167  LOC197114 5'  TATGTATATATGTGTGT     30241           AC
                                TATGTGTATATGT  TGT
                                ||||||||||||  |||
                                ATACATATATACA  ACA
                                       C_
GAM1167  LOC197117 3'  TATATGTATATGTGTGT     30243           AC
                                TATGTGTATATGT  TGT
                                ||||||||||||  |||
                                ATATACATATACA  ACA
                                       C_
GAM1167  LOC197287 5'  TATGTGCATATGTATTGT    30232           C
                                TATGTGTATATGTA TGT
                                ||||||||||||| |||
                                ATACACGTATACAT ACA
                                       A
GAM1167  LOC201595 3'  TGTGTTATGCTTGTTATATA   30297      A    AC
                                TGTGT TATGT  TGTTATATA
                                ||||| |||||  |||||||||
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                                ACACA ATACG  ACAATATAT
                                  _    A_
GAM1167  LOC219397 3'  GTGATATATTGTTATAT    30298    T    AC
                                GTG ATATGT  TGTTATAT
                                ||| ||||||  ||||||||
                                CAC TATATA  ACAATATA
                                  _    __
GAM1167  LOC257358 3'  GTGCAGCACTGTTATATA    30299     TAT
                                GTGTA  GTACTGTTATATA
                                |||||  ||||||||||||
                                CACGT  CGTGACAATATAT
                                  ___
GAM1168  CDH11    3'  GCACTACATATAGAGTGTCCAG 30302          AATA_
            A                    GCACTACATGTA    TCCAGA
                                ||||||||||||    ||||||
                                CGTGATGTATAT    AGGTCT
                                      CTCAC
GAM1168  IKBKB    3'  TGGCACTAGTAATGATCCAG   30303       CAT   AT
                                TGGCACTA   GTAA  ATCCAG
                                ||||||||   ||||  ||||||
                                ACCGTGAT   CATT  TAGGTC
                                    ___    AC
GAM1168  ITGB1    3'  TGGCCTGTATGTAAATA     30304     A  AC
                                TGGC CT  ATGTAAATA
                                |||| ||  |||||||||
                                ACCG GA  TACATTTAT
                                  _ CA
GAM1168  NXF5     3'  TGGTACCACATGTCCACCAG   30305    C       AAATAT
                                TGG ACTACATGT     CCAG
                                ||| |||||||||     ||||
                                ACC TGGTGTACA     GGTC
                                  A       GGT___
GAM1168  PGM1     3'  TGGGTTACATGTAAACA     30306     CAC
                                TGG   TACATGTAAATA
                                |||   ||||||||||||
                                ACC   ATGTACATTTGT
                                  CA_
GAM1168  CCT4     3'  TGGTGCTAGTCAGTTATCCAGA 30307    CA   CAT  AAA_
                                TGG  CTA   GT    TATCCAGA
                                |||  |||   ||   ||||||||
                                ACC  GAT   CA    ATAGGTCT
                                  AC   ___  GTCA
GAM1168  CDC14A   3'  TGGTACTCGTGGCATCCAG   30308    C   ACA   AAA
                                TGG ACT   TGT   TATCCAG
                                ||| |||   |||   |||||||
                                ACC TGA   GCA   GTAGGTC
                                  A  ____  CC_
GAM1168  DKFZP761C169 5'  TGGCCACTTAAAATATCCAG   30309     ACTA  GT_
                                TGGC   CAT   AAATATCCAG
                                ||||   |||   ||||||||||
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                                ACCG   GTG  TTTATAGGTC
                                  ____  AAT
GAM1168 FLJ20360 3' TGGCATCATCCATATCCAG   30310     CTA  GTAA
                                TGGCA  CAT   ATATCCAG
                                |||||  |||   ||||||||
                                ACCGT  GTA   TATAGGTC
                                  A__  GG__
GAM1168 FLJ20967 3' GCACTATAGAGTATATCCAG  30311     CAT_  AA
                                GCACTA   GTA  TATCCAG
                                ||||||   |||  |||||||
                                CGTGAT   CAT  ATAGGTC
                                   ATCT  __
GAM1168 NRBF-2   3' TGGCACATATAGTTTCATCTAG 30312     TACAT  AAA   C
            A                    TGGCAC    GT   TATC AGA
                                ||||||    ||   |||| |||
                                ACCGTG    CA   GTAG TCT
                                   TATAT  AA_   A
GAM1168 UBE1C    3' TGGCACTACAAGTAAACA    30313       T
                                TGGCACTACA GTAAATA
                                |||||||||| |||||||
                                ACCGTGATGT CATTTGT
                                      T
GAM1168 LOC149535 3' GGCACTGTGGGGATATCCAGA  30314     ACA  TAA
                                GGCACT   TG   ATATCCAGA
                                ||||||   ||   |||||||||
                                CCGTGA   AC   TATAGGTCT
                                   C__  CCC
GAM1168 LOC220758 3' TGGCACACATGTAAGCAG    30315      T      ATATC
                                TGGCAC ACATGTAA    CAG
                                |||||| ||||||||    |||
                                ACCGTG TGTACATT    GTC
                                   _      C____
GAM1168 LOC254249 5' TGGTATAAAAGCAATATCCAGA 30316    CACTACAT   A
                                TGG       GTAA TATCCAGA
                                |||       |||| ||||||||
                                ACC       CGTT ATAGGTCT
                                  ATATTTT_   _
GAM1168 LOC57147  3' TGTACTACATGTGGAACAGTCA 30317    GC       A_   TC
            G                    TG  ACTACATGT  AATA  CAG
                                ||  |||||||||  ||||  |||
                                AC  TGATGTACA  TTGT  GTC
                                 A_       CC    CA
GAM1169 PRG4     5' GTTTTCAGGTACCGAAT     30320     A     AC
                                GTTT TCAGGT  GCCGAGT
                                |||| ||||||  |||||||
                                CAAA AGTCCA  TGGCTTA
                                   _     __
GAM1169 ZNF278   5' GTCTCGCAGGTGCGCCGAGT   30321     AT    A
                                GTTT  CAGGT CGCCGAGT
                                ||||  ||||| ||||||||
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                                CAGA  GTCCA GCGGCTCA
                                  GC    C
GAM1169  ZNF278   5'  GTCTCGCAGGTGCGCCGAGT  30321     AT    A
                                GTTT  CAGGT CGCCGAGT
                                ||||  ||||| ||||||||
                                CAGA  GTCCA GCGGCTCA
                                  GC    C
GAM1169  ZNF278   5'  GTCTCGCAGGTGCGCCGAGT  30321     AT    A
                                GTTT  CAGGT CGCCGAGT
                                ||||  ||||| ||||||||
                                CAGA  GTCCA GCGGCTCA
                                  GC    C
GAM1169  ZNF278   5'  GTCTCGCAGGTGCGCCGAGT  30321     AT    A
                                GTTT  CAGGT CGCCGAGT
                                ||||  ||||| ||||||||
                                CAGA  GTCCA GCGGCTCA
                                  GC    C
GAM1169  PLU-1    3'  CACCGTTTACAGGCTGGCTTGA 30322       T    AC  C_
           GT                    CACCGTTTA CAGGT  GC  GAGT
                                |||||||||| |||||  ||  ||||
                                GTGGCAAAT GTCCG  CG  CTCA
                                     _    AC  AA
GAM1169  PLU-1    3'  CACCGTTTACAGGCTGGCTTGA 30322       T    AC  C_
           GT                    CACCGTTTA CAGGT  GC  GAGT
                                |||||||||| |||||  ||  ||||
                                GTGGCAAAT GTCCG  CG  CTCA
                                     _    AC  AA
GAM1170  DMXL1    3'  CACCTTTAACACTATGACA   30325         AGAC
                                TACCTTTAACA   GACA
                                ||||||||||    ||||
                                GTGGAAATTGT   CTGT
                                      GATA
GAM1170  ITGB2    3'  CACCTTTAATCAGACTGA    30326        CA   _
                                TACCTTTAA  AGAC GA
                                |||||||||  |||| ||
                                GTGGAAATT  TCTG CT
                                     AG   A
GAM1170  DKFZP564O0463 3'  ACCTAAACAGACGACA     30327     TT   A
                                ACCT  AACA GACGACA
                                ||||  |||| |||||||
                                TGGA  TTGT CTGCTGT
                                  T_   _
GAM1170  FLJ20094  3'  TACCTTTACAGAGACA     30328        A  A  C
                                TACCTTTA CA GA GACA
                                |||||||| || || ||||
                                ATGGAAAT GT CT CTGT
                                     _ _ _
GAM1170  KIAA0319  3'  TACCTTCAACCTGCACGGCA  30329         AAG_  A
                                TACCTTTAAC   ACG CA
                                ||||||||||   ||| ||
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                                ATGGAAGTTG    TGC GT
                                      GACG   C
GAM1170  KIAA1549  3'  TACCTTTAAAAAAGAGAC    30330        C_   C
                                TACCTTTAA  AAGA GAC
                                |||||||||  |||| |||
                                ATGGAAATT  TTCT CTG
                                     TT   _
GAM1170  MGC5306   3'  TACCTTTAACTCCAGACA    30331        A__
                                TACCTTTAAC   AGACG
                                ||||||||||   |||||
                                ATGGAAATTG   TCTGT
                                      AGG
GAM1170  LOC143308 5'  TACCAACAAGACGACA      30332     TTT
                                TACC   AACAAGACGACA
                                ||||   ||||||||||||
                                ATGG   TTGTTCTGCTGT
                                  ___
GAM1170  LOC255739 3'  TACCCTTAATAGAGGACA    30333        CA   C
                                TACCTTTAA  AGA GACA
                                |||||||||  ||| ||||
                                ATGGGAATT  TCT CTGT
                                      A_   C
GAM1170  LOC93273  3'  CACCTTTAATGAGAGTTGACA  30334        CA   C__
                                TACCTTTAA  AGA   GACA
                                |||||||||  |||   ||||
                                GTGGAAATT  TCT   CTGT
                                      AC   CAA
GAM1171  COL4A3    3'  TTAATCTGTAATATTAATC    30337          GTCGAT
                                TTAGTCTGTAATAT     ATC
                                ||||||||||||||     |||
                                AATTAGACATTATA     TAG
                                       AT____
GAM1171  COL4A3    3'  TTAATCTGTAATATTAATC    30337          GTCGAT
                                TTAGTCTGTAATAT     ATC
                                ||||||||||||||     |||
                                AATTAGACATTATA     TAG
                                       AT____
GAM1171  COL4A3    3'  TTAATCTGTAATATTAATC    30337          GTCGAT
                                TTAGTCTGTAATAT     ATC
                                ||||||||||||||     |||
                                AATTAGACATTATA     TAG
                                       AT____
GAM1171  GPM6B     3'  TTAGTCTGGAGTGTCAGTGATA 30338        TAATA   ___
           T                    TTAGTCTG    TGTC   GATAT
                                ||||||||    ||||   |||||
                                AATCAGAC    ACAG   CTATA
                                     CTC__    TCA
GAM1171  NRXN2     3'  GTCTGTAATATATATC      30339          CGAT
                                GTCTGTAATATGT    ATC
                                ||||||||||||    |||
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                                CAGACATTATATA   TAG
                                        ____
GAM1171 NRXN2    3' GTCTGTAATATATATC     30339          CGAT
                                GTCTGTAATATGT   ATC
                                ||||||||||||   |||
                                CAGACATTATATA   TAG
                                        ____
GAM1171 NRXN2    3' GTCTGTAATATATATC     30339          CGAT
                                GTCTGTAATATGT   ATC
                                ||||||||||||   |||
                                CAGACATTATATA   TAG
                                        ____
GAM1171 TSG      3' AGTCTGTAATATAAATAT   30340          TC
                                AGTCTGTAATATG  GATAT
                                ||||||||||||  |||||
                                TCAGACATTATAT  TTATA
                                        __
GAM1171 FLJ13456 3' TTAGTCTGTGAAAATTTATC  30341        ___  A
                                TTAGTCTGT   AAT TGTC
                                |||||||||   ||| ||||
                                AATCAGACA   TTA ATAG
                                      CTT   A
GAM1171 H2BFQ    3' TCAGTCTGTGATAATGTC    30342        A  _
                                TTAGTCTGT ATA TGTC
                                |||||||||  ||| ||||
                                AGTCAGACA TAT ACAG
                                      C   T
GAM1171 KIAA1423 3' GTATGTAATATGTCGGTAT   30343   C        A
                                GT TGTAATATGTCG TAT
                                ||  ||||||||||||  |||
                                CA ACATTATACAGC ATA
                                 T         C
GAM1172 ACCN2    3' CAGAGGGATGTGTGACACAACG 30346       __________    GTT
          TG                     CAGAGGG       GACAC   GTG
                                |||||||        |||||   |||
                                GTCTCCC        CTGTG   CAC
                                    TACACAIII    TTG
GAM1172 ADAM15   3' CCAGAGGGCACGCCCGCCTC  30347        GA    _ G
                                CCAGAGGG  CACGTT GT TC
                                ||||||||  ||||||  ||  ||
                                GGTCTCCC  GTGCGG CG AG
                                    __     G  G
GAM1172 ADAM19   3' GAGGGGACGTGGCTTGTC    30348        AC_  G
                                GAGGGGAC   GTT TGTC
                                ||||||||   ||| ||||
                                CTCCCCTG   CGA ACAG
                                    CAC   _
GAM1172 ANKRD3   3' GAGGGGACACTCCGGTC     30349         G   T
                                GAGGGGACAC TTG GTC
                                ||||||||||  ||| |||
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                                CTCCCCTGTG GGC CAG
                                     A  _
GAM1172 B3GALT5  3' CAGAAGGGATGTCCTGC    30350       CAC  G
                                CAGAGGGGA  GTT TGT
                                |||||||||  ||| |||
                                GTCTTCCCT  CAG ACG
                                     A__  G
GAM1172 B3GALT5  3' CAGAAGGGATGTCCTGC    30350       CAC  G
                                CAGAGGGGA  GTT TGT
                                |||||||||  ||| |||
                                GTCTTCCCT  CAG ACG
                                     A__  G
GAM1172 B3GALT5  3' CAGAAGGGATGTCCTGC    30350       CAC  G
                                CAGAGGGGA  GTT TGT
                                |||||||||  ||| |||
                                GTCTTCCCT  CAG ACG
                                     A__  G
GAM1172 B3GALT5  3' CAGAAGGGATGTCCTGC    30350       CAC  G
                                CAGAGGGGA  GTT TGT
                                |||||||||  ||| |||
                                GTCTTCCCT  CAG ACG
                                     A__  G
GAM1172 B3GALT5  3' CAGAAGGGATGTCCTGC    30350       CAC  G
                                CAGAGGGGA  GTT TGT
                                |||||||||  ||| |||
                                GTCTTCCCT  CAG ACG
                                     A__  G
GAM1172 CA12     3' CAGAGGGAGATGCCCCGTC   30351      _ CAC  G
                                CAGAGGG GA  GTT TGTC
                                |||||||  ||  ||| ||||
                                GTCTCCC CT  CGG GCAG
                                    T A__  G
GAM1172 CACNG1   3' CCAGAGAGGGTGTGT      30352       ACAC  T
                                CCAGAGGGG   GT GTGT
                                |||||||||   || ||||
                                GGTCTCTCC   CA CACA
                                     ____ _
GAM1172 CAPN1    3' CAGAGGGGGCGTTGGC     30353       ACA   T
                                CAGAGGGG  CGTTG GT
                                ||||||||  ||||| ||
                                GTCTCCCC  GCAAC CG
                                     C__   _
GAM1172 CD4      3' CCAGAGGGGCTGTTGACACAAC 30354      _________   GTT
          GTG                    CAGAGGG       GACAC  GTG
                                |||||||       |||||  |||
                                GTCTCCC       CTGTG  CAC
                                   CGACAAIII   TTG
GAM1172 CDH23    3' CCGGAGGGAACATCAGTC   30355   A      _ _
                                CC GAGGGGACA C GTT
                                || |||||||| | |||
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                                GG CTCCCTTGT G CAG
                                 C        A T
GAM1172  CDK10    3'  TGAGAGGGGATACGAAGGTC  30356   C       C   TTGT
                                C AGAGGGGA ACG    GTC
                                | |||||||| |||    |||
                                A TCTCCCCT TGC    CAG
                                 C       A   TTC_
GAM1172  CDK10    3'  TGAGAGGGGATACGAAGGTC  30356   C       C   TTGT
                                C AGAGGGGA ACG    GTC
                                | |||||||| |||    |||
                                A TCTCCCCT TGC    CAG
                                 C       A   TTC_
GAM1172  CDK10    3'  TGAGAGGGGATACGAAGGTC  30356   C       C   TTGT
                                C AGAGGGGA ACG    GTC
                                | |||||||| |||    |||
                                A TCTCCCCT TGC    CAG
                                 C       A   TTC_
GAM1172  CSPG3    3'  CCAGAGGAGGCATGGGAAAGGT 30357         A  CGTT____
              GT                  CCAGAGGGG CA       GTGT
                                |||||||||  ||       ||||
                                GGTCTCCTC GT       CACA
                                     C  ACCCTTTC
GAM1172  D1S155E  5'  CAGATCAAGTGTTGTGTC   30358     G_   ACAC
                                CAGA  GGG    GTTGTGTC
                                ||||  |||    ||||||||
                                GTCT  TTC    CAACACAG
                                  AG   A___
GAM1172  DAG1     3'  CCAGAGAGGGCGGGCTTGTC  30359         ACAC   G
                                CCAGAGGGG    GTT TGTC
                                |||||||||    ||| ||||
                                GGTCTCTCC    CGA ACAG
                                     CGCC   _
GAM1172  DPH2L1   3'  TGAGAGGGGATGACTTTGT   30360   C       C_  G
                                C AGAGGGGA  AC TTGT
                                | ||||||||  || ||||
                                A TCTCCCCT  TG AACA
                                 C       AC  A
GAM1172  DUSP2    3'  CCAGAGGGGAGCCCACCAGTC  30361         CA_  TT T
                                CCAGAGGGGA   CG  G GTC
                                ||||||||||   ||  | |||
                                GGTCTCCCCT   GT  T CAG
                                     CGG  GG _
GAM1172  EGFL4    3'  CAGAGGGACATGCGACACAACG 30362         __________    GTT
              TG                  CAGAGGG       GACAC   GTG
                                |||||||        |||||  |||
                                GTCTCCC       CTGTG   CAC
                                   TGTACGIII    TTG
GAM1172  EVA1     3'  CCAGAGGGGTGTTGCTTGTC  30363         ACAC    __
                                CCAGAGGGG    GTTGT  GTC
                                |||||||||    |||||  |||
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                                GGTCTCCCC   CAACG  CAG
                                    A___    AA
GAM1172  FANCC    3'  CCAGAGGGACAGTCGACACAAC 30364       _________   GTT
             GTG                  CAGAGGG       GACAC   GTG
                                  |||||||       |||||  |||
                                  GTCTCCC       CTGTG   CAC
                                     TGTCAGIII    TTG
GAM1172  FNTB     3'  CAGAGGGGGTTTTGACACAACG 30365       _________   GTT
             TG                   CAGAGGG       GACAC   GTG
                                  |||||||       |||||  |||
                                  GTCTCCC       CTGTG   CAC
                                     CCAAAAIII    TTG
GAM1172  FOXE3    3'  CAAAGGGGACGCTTCTGTC   30366         ACG  G
                                  CAGAGGGGAC   TT TGTC
                                  ||||||||||   || ||||
                                  GTTTCCCCTG   AA ACAG
                                        CG_  G
GAM1172  G6PT1    5'  CCAAGGGGACCCAGTGTC    30367    G     ACGTT
                                  CCA AGGGGAC    GTGTC
                                  ||| |||||||    |||||
                                  GGT TCCCCTG    CACAG
                                    _     GGT__
GAM1172  HPCA     3'  CCAGGGGGACCGTGT      30368     A     ACGT
                                  CCAG GGGGAC    TGTGT
                                  |||| ||||||    |||||
                                  GGTC CCCCTG    GCACA
                                    _    _____
GAM1172  INHBB    3'  GAGGGGACACCCCCCATC    30369         G  G
                                  GAGGGGACAC TT TGTC
                                  |||||||||| || ||||
                                  CTCCCCTGTG GG GTAG
                                        G  G
GAM1172  KCNJ5    3'  CAGAGGGGCTGTCGACACAACG 30370       _________   GTT
             TG                   CAGAGGG       GACAC   GTG
                                  |||||||       |||||  |||
                                  GTCTCCC       CTGTG   CAC
                                     CGACAGIII    TTG
GAM1172  KLHL2    5'  CCGGAGGGGGCGCCGCGC    30371    A     ACA
                                  CC GAGGGG   CGTTGTGT
                                  || ||||||   ||||||||
                                  GG CTCCCC   GCGGCGCG
                                   C     C__
GAM1172  LFG      3'  GAGGGGGTACACTGTGTC    30372       AC
                                  GAGGGG  ACGTTGTGTC
                                  ||||||  ||||||||||
                                  CTCCCC  TGTGACACAG
                                     CA
GAM1172  MAN2A2   3'  CCAGAGGGTACAGTAACGTC  30373        G   C  TG
                                  CCAGAGGG ACA GT  TGTC
                                  |||||||| ||| ||  ||||
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                                GGTCTCCC TGT CA  GCAG
                                    A   _ TT
GAM1172  NR1I2    5'  CCAGAGGGGAGCTGAAGAGTC  30374         CAC    T___
                                CCAGAGGGGA  GTTG   GTC
                                ||||||||||  ||||   |||
                                GGTCTCCCCT  CGAC   CAG
                                    ____   TTCT
GAM1172  ODF2     5'  CCAGAGGGGCAGGCTTGTC   30375         A  C   G
                                CCAGAGGGG CA GTT TGTC
                                ||||||||| || ||| ||||
                                GGTCTCCCC GT CGA ACAG
                                    _ C  _
GAM1172  PDGFRB   5'  CCAGAGGGGCCGCCCTG    30376         ACA    G
                                CCAGAGGGG  CGTT TG
                                |||||||||  |||| ||
                                GGTCTCCCC  GCGG AC
                                    G__   G
GAM1172  PML      3'  CCAGGGGGAACACCTGC     30377      A       G
                                CCAG GGGGACAC TTGT
                                |||| |||||||| ||||
                                GGTC CCCTTGTG GACG
                                  C      _
GAM1172  PPT2     3'  CCAGGGGGGTACTCGACACAAC 30378     A  __________    GTT
           GTG                    CAG GGG       GACAC   GTG
                                ||| |||       |||||  |||
                                GTC CCC       CTGTG   CAC
                                  C  CATGAGIII    TTG
GAM1172  PPT2     3'  CCAGGGGGGTACTCGACACAAC 30378     A  __________    GTT
           GTG                    CAG GGG       GACAC   GTG
                                ||| |||       |||||  |||
                                GTC CCC       CTGTG   CAC
                                  C  CATGAGIII    TTG
GAM1172  PRKRA    3'  CCAGAGGGGAACTTGACACAAC 30379       __________    GTT
           GTG                    CAGAGGG       GACAC   GTG
                                |||||||       |||||  |||
                                GTCTCCC       CTGTG   CAC
                                    CTTGAAIII    TTG
GAM1172  PXF      3'  CAGAGAGGAAAACGTGTTGTGT 30380        C_   __
                                CAGAGGGGA  ACGT  TGTGT
                                |||||||||  ||||  |||||
                                GTCTCTCCT  TGCA  ACACA
                                    TT   CA
GAM1172  PYCS     3'  CACGGGGGACACAGCATC    30381    GA      TT
                                CA  GGGGACACG  GTGTC
                                ||  |||||||||  |||||
                                GT  CCCCTGTGT  CGTAG
                                 GC       __
GAM1172  RAB36    3'  CCAGAGGAGGGCAGTGCCATGT 30382       _  A  C_  TG
                                CCAGAGG GG CA  GT  TGT
                                |||||||  ||  ||  ||  |||
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                                GGTCTCC CC GT  CG  ACA
                                    T  C  CA  GT
GAM1172 RANBP2L1 5' CCAGTGGCCAGTTGTGTC    30383     AG  GA  C
                                CCAG  GG  CA GTTGTGTC
                                ||||  ||  || ||||||||
                                GGTC  CC  GT CAACACAG
                                  A_  G_  _
GAM1172 RAP1GA1  3' CCAGAGGGATGCTCGACACAAC 30385       __________    GTT
           GTG                   CAGAGGG       GACAC   GTG
                                |||||||       |||||  |||
                                GTCTCCC       CTGTG   CAC
                                    TACGAGIII    TTG
GAM1172 RAP1GA1  3' CAGAGGGGGTGGCGACACAACG 30384       __________    GTT
           TG                    CAGAGGG       GACAC   GTG
                                |||||||       |||||  |||
                                GTCTCCC       CTGTG   CAC
                                    CCACCGIII    TTG
GAM1172 S100A6   5' GAGGGGATGGGCTATGTC    30386       CAC
                                GAGGGGA   GTTGTGTC
                                |||||||   ||||||||
                                CTCCCCT   CGATACAG
                                    ACC
GAM1172 SHANK2   3' CCAGAGGAGACGCTGT     30387         AC
                                CCAGAGGGGAC  GTTGT
                                ||||||||||  |||||
                                GGTCTCCTCTG  CGACA
                                          __
GAM1172 SKI      3' CCAGAGGGGGTTTCGACACAAC 30388       __________    GTT
           GTG                   CAGAGGG       GACAC   GTG
                                |||||||       |||||  |||
                                GTCTCCC       CTGTG   CAC
                                    CCAAAGIII    TTG
GAM1172 SLC7A8   5' CCAGGGGAGACATACATT    30389     A    __
                                CCAG GGGGAC  ACGTT
                                ||||  ||||||  |||||
                                GGTC CCTCTG  TGTAA
                                  C     TA
GAM1172 SORCS2   3' CAGAGGGGGTGGTGCC      30390       ACAC  T
                                CAGAGGGG   GT GTGTC
                                ||||||||   || |||||
                                GTCTCCCC   CA CACGG
                                     ____  C
GAM1172 SOST     5' CCAGAGGAGGGCACGCCAC   30391       _  A   TG
                                CCAGAGG GG CACGT  T
                                ||||||| || |||||  |
                                GGTCTCC CC GTGCG  G
                                    T  C    GT
GAM1172 STX1A    3' CCAGAGGGACACCTGGGGTC  30392       G   G   T_
                                CCAGAGGG ACAC TTG  GTC
                                |||||||| |||| |||  |||
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                                GGTCTCCC TGTG GAC  CAG
                                    _   _  CC
GAM1172  THOP1    3'  CCAGAGAGGAGACGTGT     30393          C   T
                                CCAGAGGGGA ACGT GT
                                |||||||||| |||| ||
                                GGTCTCTCCT TGCA CA
                                     C   _
GAM1172  ACTR1A   3'  CCAGAGGGGGCCTTGACACAAC 30394        _________    GTT
              GTG                  CAGAGGG       GACAC   GTG
                                |||||||       |||||  |||
                                GTCTCCC       CTGTG   CAC
                                   CCGGAAIII    TTG
GAM1172  AKAP5    5'  CCAGAGGGGAGCAGTTGT    30395          _ C
                                CCAGAGGGGA CA GTTGT
                                |||||||||| || |||||
                                GGTCTCCCCT GT CAACA
                                     C  _
GAM1172  APOL4    3'  CCAGGGGAGACATCACACATC  30396      A     CGT  TG
                                CCAG GGGGACA   TG  TC
                                |||| |||||||   ||  ||
                                GGTC CCTCTGT   GT  AG
                                  C      AGT  GT
GAM1172  BOP      5'  CAGAGGGACACAGCAGGTC   30397       G   _  TGT
                                CAGAGGG ACAC GT   GTC
                                ||||||| |||| ||   |||
                                GTCTCCC TGTG CG   CAG
                                    _   T  TC_
GAM1172  BTN2A1   3'  CCAGAGGGGAGGAGGGCGTGTC 30398          CACGT_
                                CCAGAGGGGA     TGTGTC
                                ||||||||||     ||||||
                                GGTCTCCCCT     GCACAG
                                     CCTCCC
GAM1172  BTN2A2   3'  CCAGAGGGGAGGAGGGCGTGTC 30398          CACGT_
                                CCAGAGGGGA     TGTGTC
                                ||||||||||     ||||||
                                GGTCTCCCCT     GCACAG
                                     CCTCCC
GAM1172  C(27)-3BETA-HSD 3'  CCAGAGGGGAATTCGACACAAC 30399        _________    GTT
              GTG                  CAGAGGG       GACAC   GTG
                                |||||||       |||||  |||
                                GTCTCCC       CTGTG   CAC
                                   CTTAAGIII    TTG
GAM1172  C1orf33  3'  CCAGAGGGGCGGCAGCAGTC   30400         ACAC  T  _
                                CCAGAGGGG    GT GT GTC
                                |||||||||    || || |||
                                GGTCTCCCC    CG CG CAG
                                     GC__  T  T
GAM1172  C6orf9   3'  CCAGAGGGGAATTATAT     30401          CAC
                                CCAGAGGGGA   GTTGTGT
                                ||||||||||   |||||||
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                                GGTCTCCCCT   TAATATA
                                    ___
GAM1172  CLSTN1    3'  CCAGAGAGGACGTGT      30402          ACGTT
                                CCAGAGGGGAC    GTGT
                                ||||||||||    ||||
                                GGTCTCTCCTG    CACA
                                    _____
GAM1172  CRELD1    5'  CCAGAGGGGTTGTCGACACAAC 30403        _________    GTT
              GTG                   CAGAGGG       GACAC   GTG
                                |||||||       |||||  |||
                                GTCTCCC       CTGTG   CAC
                                    CAACAGIII    TTG
GAM1172  DKFZP434H204 5'  CACAGGGGACACCGGTGTC   30404    G       GTT
                                CA AGGGGACAC   GTGTC
                                || |||||||||   |||||
                                GT TCCCCTGTG   CACAG
                                 G       GC_
GAM1172  DKFZP762D096 5'  CAGAGGGACAGTTGACACAACG 30405       _________    GTT
              TG                    CAGAGGG       GACAC   GTG
                                |||||||       |||||  |||
                                GTCTCCC       CTGTG   CAC
                                    TGTCAAIII    TTG
GAM1172  DKFZp762L0311 3'  CAGGGGGGACACACCCAATC   30406    A       TTGT
                                CAG GGGGACACG    GTC
                                ||| |||||||||    |||
                                GTC CCCCTGTGT    TAG
                                  C       GGGT
GAM1172  DPM3      5'  CCAGAGGGGAATCGCCGATC   30407         CA    T
                                CCAGAGGGGA  CGTTG GTC
                                ||||||||||  ||||| |||
                                GGTCTCCCCT  GCGGC TAG
                                      TA    _
GAM1172  EPS8R3    3'  CCAGAAGGGACACTGT      30408          GT
                                CCAGAGGGGACAC  TGT
                                ||||||||||||  |||
                                GGTCTTCCCTGTG  ACA
                                    __
GAM1172  EPS8R3    3'  CCAGAAGGGACACTGT      30408          GT
                                CCAGAGGGGACAC  TGT
                                ||||||||||||  |||
                                GGTCTTCCCTGTG  ACA
                                    __
GAM1172  FLJ10103  5'  AGAGGGGACCGTGGGT      30409        A  T T
                                AGAGGGGAC CGT G GT
                                ||||||||| ||| | ||
                                TCTCCCCTG GCA C CA
                                      _  _ C
GAM1172  FLJ14775  5'  CAGAGGGGGTTGTGT       30410        ACAC
                                CAGAGGGG   GTTGTGT
                                ||||||||   |||||||
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                                GTCTCCCC    CAACACA
                                        ____
GAM1172  FLJ20422  3'  CAGAGGGGGCAGGCTAGTGTC  30411        A  C  _
                                CAGAGGGG CA GTT GTGTC
                                |||||||| || ||| |||||
                                GTCTCCCC GT CGA CACAG
                                     C  C   T
GAM1172  FLJ20552  3'  CCAGAGGGGACCATGT      30412          A   T
                                CCAGAGGGGAC CGT GT
                                |||||||||||| ||| ||
                                GGTCTCCCCTG GTA CA
                                          _  _
GAM1172  FLJ21125  3'  CCAAGGGGGGTGTTGACACAAC 30413     A  __________    GTT
              GTG                  CAG GGG       GACAC   GTG
                                ||| |||       |||||   |||
                                GTT CCC       CTGTG   CAC
                                  C   CCACAAIII    TTG
GAM1172  FLJ21977  3'  CCAGAGGGGGCCTCGACACAAC 30414        __________    GTT
              GTG                  CAGAGGG       GACAC   GTG
                                |||||||       |||||   |||
                                GTCTCCC       CTGTG   CAC
                                    CCGGAGIII    TTG
GAM1172  FLJ23309  3'  CCAGAGGGGTATGTGACACAAC 30415        __________    GTT
              GTG                  CAGAGGG       GACAC   GTG
                                |||||||       |||||   |||
                                GTCTCCC       CTGTG   CAC
                                    CATACAIII    TTG
GAM1172  FLJ23519  3'  GAGGGGACCCAAGCTGTGTC   30416        AC__
                                GAGGGGAC    GTTGTGTC
                                ||||||||    ||||||||
                                CTCCCCTG    CGACACAG
                                    GGTT
GAM1172  FLJ23537  3'  CAGAGGGGGGTGCCGACTGTC  30417        ACAC   __
                                CAGAGGGG    GTTG  TGTC
                                ||||||||    ||||  ||||
                                GTCTCCCC    CGGC  ACAG
                                    CCA_    TG
GAM1172  FLJ23537  3'  CAGAGGGGGGTGCCGACTGTC  30417        ACAC   __
                                CAGAGGGG    GTTG  TGTC
                                ||||||||    ||||  ||||
                                GTCTCCCC    CGGC  ACAG
                                    CCA_    TG
GAM1172  FLJ32356  3'  CCAGAGGGCATAGAGCTTGTGT 30418        GACACG__
              C                   CCAGAGGG       TTGTGTC
                                ||||||||       |||||||
                                GGTCTCCC       AACACAG
                                    GTATCTCG
GAM1172  FREQ     3'  CCAGGGGGCGCGCCGCGC    30419     A   ACA
                                CCAG GGGG   CGTTGTGT
                                |||| ||||   ||||||||
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                              GGTC CCCC   GCGGCGCG
                                _   GC_
GAM1172 HPCAL4   3' CCAGAGGGCACAAGATGTGTC 30420       G   CGT
                              CCAGAGGG ACA   TGTGTC
                              |||||||| |||   ||||||
                              GGTCTCCC TGT   ACACAG
                                   G   TCT
GAM1172 HSPC117  3' CAGAGAGGGTTGGTGGTGTC  30421       ACAC  T
                              CAGAGGGG    GT GTGTC
                              ||||||||    || |||||
                              GTCTCTCC    CA CACAG
                                   CAAC  C
GAM1172 HYPC     5' GAGGGGACAGCCTTGTC     30422        C  TG
                              GAGGGGACA GT  TGTC
                              ||||||||| ||  ||||
                              CTCCCCTGT CG  ACAG
                                   _ GA
GAM1172 KEAP1    3' CCAGAGGGGGCCTCGACACAAC 30414       __________    GTT
             GTG                 CAGAGGG       GACAC   GTG
                              |||||||       |||||  |||
                              GTCTCCC       CTGTG   CAC
                                 CCGGAGIII    TTG
GAM1172 KIAA0174 3' CCAGAGGGAGTGTTGACACAAC 30423       __________    GTT
             GTG                 CAGAGGG       GACAC   GTG
                              |||||||       |||||  |||
                              GTCTCCC       CTGTG   CAC
                                 TCACAAIII    TTG
GAM1172 KIAA0211 3' CCAGAGGGACTGTGT      30424        ACACG
                              CCAGAGGGG    TTGTGT
                              |||||||||    ||||||
                              GGTCTCCCT    GACACA
                                   _____
GAM1172 KIAA0415 3' CCGCGGGGGACACCAGCCGT  30425    AGA      __
                              CC   GGGGACAC  GTTGT
                              ||   ||||||||  |||||
                              GG   CCCCTGTG  CGGCA
                               CGC       GT
GAM1172 KIAA0418 3' CCAGAGGGGGTGGCTGGC    30426        ACAC   T
                              CCAGAGGGG    GTTG GT
                              |||||||||    |||| ||
                              GGTCTCCCC    CGAC CG
                                   CAC_   _
GAM1172 KIAA0436 5' CAGAGGGGAGCAGGTGTC    30427        CAC  T_
                              CAGAGGGGA   GT  GTGTC
                              |||||||||   ||  |||||
                              GTCTCCCCT   CG  CACAG
                                   ___ TC
GAM1172 KIAA1061 3' CCAGAGGGGCTCGTGT      30428        ACACG
                              CCAGAGGGG    TTGTGT
                              |||||||||    ||||||
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                                GGTCTCCCC    AGCACA
                                     G____
GAM1172 KIAA1486 5' CCAGAAGGTGACTTGTGTC   30429       _  ACG
                                CCAGAGGG GAC   TTGTGTC
                                |||||||| |||   |||||||
                                GGTCTTCC CTG   AACACAG
                                    A   ___
GAM1172 KIAA1862 5' CCAGAGGGGACAGCCTAGCTGT 30430          C____
                                CCAGAGGGGACA    GTTGT
                                ||||||||||||    |||||
                                GGTCTCCCCTGT    CGACA
                                      CGGAT
GAM1172 KIAA1870 5' CCAGTGGGGACTGGTACGTGTC 30431     A    AC  _
                                CCAG GGGGAC  GT TGTGTC
                                |||| ||||||  || ||||||
                                GGTC CCCCTG  CA GCACAG
                                  A     AC  T
GAM1172 KIAA1884 3' CCAGGGGGGTGCCGTGTC    30432     A   ACAC
                                CCAG GGGG   GTTGTGTC
                                |||| ||||   ||||||||
                                GGTC CCCC   CGGCACAG
                                  _   CA__
GAM1172 KIAA1938 3' CAGAGGGGACTGTGTGTC    30433         ACGT
                                CAGAGGGGAC   TGTGTC
                                ||||||||||   ||||||
                                GTCTCCCCTG   ACACAG
                                     AC__
GAM1172 KIF1C    5' CCAGGGGGGCTGTAT      30434     A   ACAC
                                CCAG GGGG   GTTGTGT
                                |||| ||||   |||||||
                                GGTC CCCC   CGACATA
                                  _   _____
GAM1172 LCHN     3' CCACAGGGGACAGGTGGT    30435    G      C  T
                                CCA AGGGGACA GT GT
                                ||| |||||||| || ||
                                GGT TCCCCTGT CA CA
                                  G      C  C
GAM1172 LIECG3   3' CCAGGCGGGGCGCTGCGTC   30436    A_   ACA
                                CCAG  GGGG  CGTTGTGTC
                                ||||  ||||  |||||||||
                                GGTC  CCCC  GCGACGCAG
                                  CG   ___
GAM1172 MAP3K3   3' CCAGAGGGCACACACAGT    30437       G    TT
                                CCAGAGGG ACACG  GT
                                |||||||| |||||  ||
                                GGTCTCCC TGTGT  CA
                                     G    GT
GAM1172 MGC13114 3' CCAGGAGGGCTGTGT      30438     A   ACAC
                                CCAG GGGG   GTTGTGT
                                |||| ||||   |||||||
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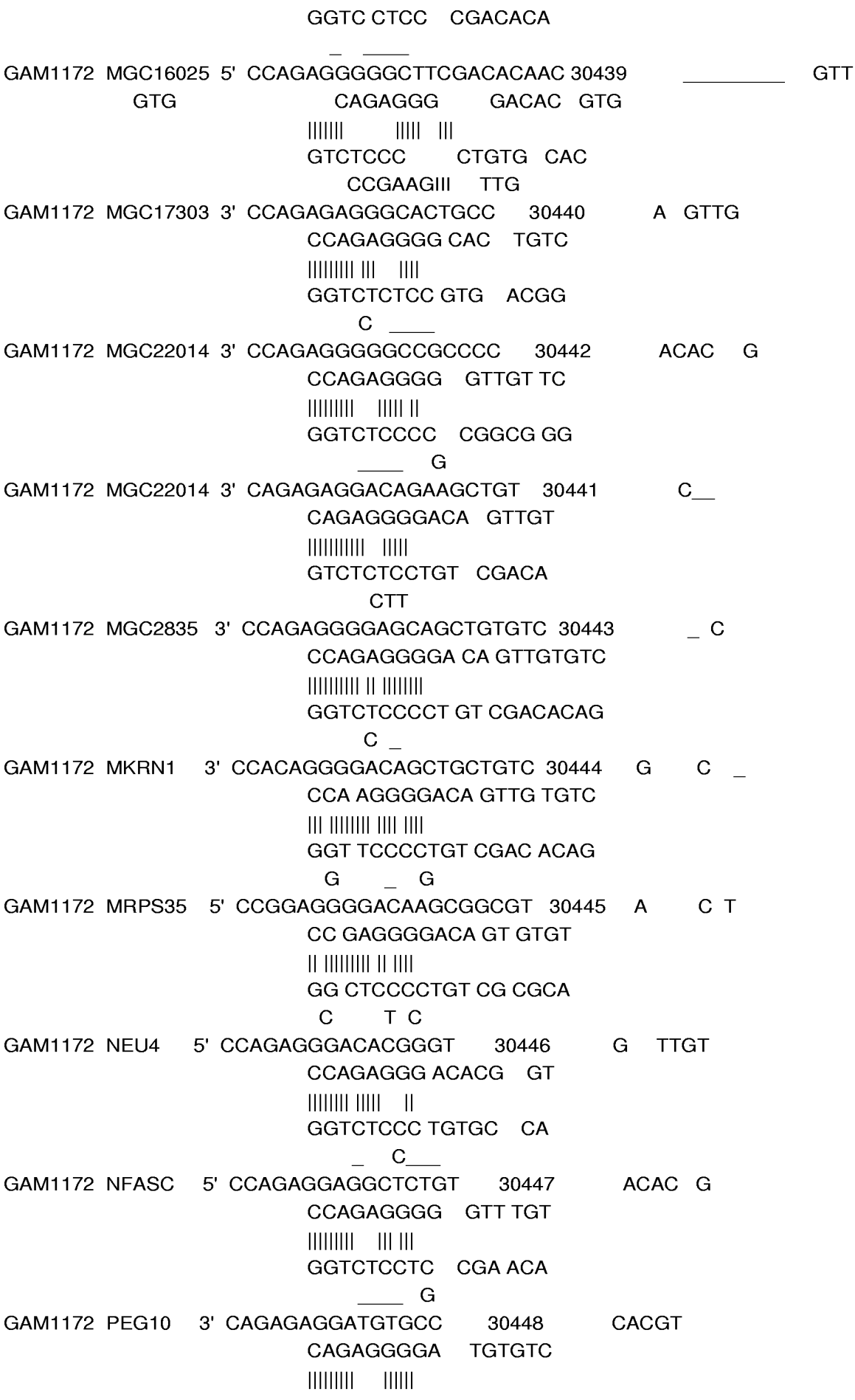
GGTC CTCC CGACACA
GAM1172 MGC16025 5' CCAGAGGGGGCTTCGACACAAC 30439 GTT
GTG CAGAGGG GACAC GTG
GTCTCCC CTGTG CAC
CCGAAG TTG
GAM1172 MGC17303 3' CCAGAGAGGGCACTGCC 30440 A GTTG
CCAGAGGGG CAC TGTC
GGTCTCTCC GTG ACGG
C
GAM1172 MGC22014 3' CCAGAGGGGGCCGCCCC 30442 ACAC G
CCAGAGGGG GTTGT TC
GGTCTCCCC CGGCG GG
G
GAM1172 MGC22014 3' CAGAGAGGACAGAAGCTGT 30441 C
CAGAGGGGACA GTTGT
GTCTCTCCTGT CGACA
CTT
GAM1172 MGC2835 3' CCAGAGGGGAGCAGCTGTGTC 30443 C
CCAGAGGGGA CA GTTGTGTC
GGTCTCCCCT GT CGACACAG
C
GAM1172 MKRN1 3' CCACAGGGGACAGCTGCTGTC 30444 G C
CCA AGGGGACA GTTG TGTC
GGT TCCCCTGT CGAC ACAG
G G
GAM1172 MRPS35 5' CCGGAGGGGACAAGCGGCGT 30445 A C T
CC GAGGGGACA GT GTGT
GG CTCCCCTGT CG CGCA
C T C
GAM1172 NEU4 5' CCAGAGGGACACGGGT 30446 G TTGT
CCAGAGGG ACACG GT
GGTCTCCC TGTGC CA
C
GAM1172 NFASC 5' CCAGAGGAGGCTCTGT 30447 ACAC G
CCAGAGGGG GTT TGT
GGTCTCCTC CGA ACA
G
GAM1172 PEG10 3' CAGAGAGGATGTGCC 30448 CACGT
CAGAGGGGA TGTGTC

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                                GTCTCTCCT    ACACGG
                                      _____
GAM1172 phospho1 5' GAGGGGACGCGGTGTC     30449        A  TT
                                GAGGGGAC CG  GTGTC
                                |||||||| ||  |||||
                                CTCCCCTG GC  CACAG
                                     C  __
GAM1172 PMF1     3' AAAGGGGGTGTATGTC     30450        ACAC  _
                                AGAGGGG   GT TGTGTC
                                |||||||   || ||||||
                                TTTCCCC   CA ATACAG
                                    ____ C
GAM1172 PMPCB    3' CAGAGGGGTAGTCGACACAACG 30451        __________    GTT
             TG                   CAGAGGG       GACAC   GTG
                                |||||||       |||||  |||
                                GTCTCCC       CTGTG   CAC
                                    CATCAGIII    TTG
GAM1172 R32184_3 3' CCCAGGGGAGTTGTGT     30452    AG     CAC
                                CC  AGGGGA   GTTGTGT
                                ||  ||||||   |||||||
                                GG  TCCCCT   CAACACA
                                 G_     ___
GAM1172 RAB40C   3' CCAGAGGGAGCACCGGCCCTGT 30453        GA   __   G
             C                   CCAGAGGG  CAC  GTT TGTC
                                |||||||  |||  ||| ||||
                                GGTCTCCC  GTG  CGG ACAG
                                     TC   GC   G
GAM1172 RALGPS1A 3' CCAGAGAGGGCGTGTG     30454        ACA   T
                                CCAGAGGGG   CGT GTG
                                |||||||||   ||| |||
                                GGTCTCTCC   GCA CAC
                                     C__   _
GAM1172 SEMA5A   3' GAGGGAACGCCATGAGTC    30455        A_   T T
                                GAGGGGAC  CGT G GTC
                                ||||||||  ||| | |||
                                CTCCCTTG  GTA C CAG
                                     CG   _ T
GAM1172 THTPA    5' GAGGGGCACACTGTGTC     30456       A
                                GAGGGG CACGTTGTGTC
                                |||||| ||||||||||
                                CTCCCC GTGTGACACAG
                                   _
GAM1172 TM4SF11  3' CCAGAGGGGGCCGTG      30457        ACAC
                                CCAGAGGGG    GTTGTG
                                |||||||||    ||||||
                                GGTCTCCCC    CGGCAC
                                     _____
GAM1172 TTTY9    3' CCAGAGAGGACAAATACAGTGT 30458          CGTT__
             C                   CCAGAGGGGACA     GTGTC
                                ||||||||||||     |||||
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                                GGTCTCTCCTGT     CACAG
                                      TTATGT
GAM1172 UST      3' CCAGAGGAGATACCCTGGTC  30459         C  G   T
                                CCAGAGGGGA AC TTG GTC
                                |||||||||| || ||| |||
                                GGTCTCCTCT TG GAC CAG
                                     A  G  _
GAM1172 WNT10A   3' CCAAGAGGACAAGTGTTGTGTC 30460     G      C__
                                CCA AGGGGACA   GTTGTGTC
                                ||| ||||||||   ||||||||
                                GGT TCTCCTGT   CAACACAG
                                  _      TCA
GAM1172 LOC115219 3' CCAGAGGGTGTGTCGACACAAC 30461        __________    GTT
             GTG                   CAGAGGG       GACAC   GTG
                                |||||||       |||||   |||
                                GTCTCCC       CTGTG   CAC
                                    ACACAGIII    TTG
GAM1172 LOC124044 3' CCAGAGGGGCTGTCGACACAAC 30462        __________    GTT
             GTG                   CAGAGGG       GACAC   GTG
                                |||||||       |||||   |||
                                GTCTCCC       CTGTG   CAC
                                    CGACAGIII    TTG
GAM1172 LOC127534 3' CAGAGGGGACTCACCTATC   30463         A  TTG
                                CAGAGGGGAC CG   TGTC
                                |||||||||| ||   ||||
                                GTCTCCCCTG GT   ATAG
                                     A  GG_
GAM1172 LOC134111 3' CCAGAGGGCGCACCTGGTGTC  30464        GA   GTT
                                CCAGAGGG  CAC   GTGTC
                                ||||||||  |||   |||||
                                GGTCTCCC  GTG   CACAG
                                    GC   GAC
GAM1172 LOC144395 5' CCAGAGGGGGCTTTGACACAAC 30465        __________    GTT
             GTG                   CAGAGGG       GACAC   GTG
                                |||||||       |||||   |||
                                GTCTCCC       CTGTG   CAC
                                    CCGAAAIII    TTG
GAM1172 LOC146445 3' CCGAGGGGACCGGGTGTGT   30466    A      A  T_
                                CC GAGGGGAC CG  TGTGT
                                || ||||||||  ||  |||||
                                GG CTCCCCTG GC  ACACA
                                  _      _ CC
GAM1172 LOC146485 5' CCTGAGGGGACTGCTGTGT   30467    A      AC
                                CC GAGGGGAC  GTTGTGT
                                || ||||||||  |||||||
                                GG CTCCCCTG  CGACACA
                                 A       A_
GAM1172 LOC146669 5' CAGAAGGGGACGATGTC     30468     _     ACGTT
                                CAGA GGGGAC    GTGTC
                                ||||  ||||||    |||||
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                                GTCT CCCCTG     TACAG
                                  T     C____
GAM1172  LOC146669 5'  CAGAAGGGGACGATGTC     30468      _     ACGTT
                                CAGA GGGGAC     GTGTC
                                |||| ||||||     |||||
                                GTCT CCCCTG     TACAG
                                  T     C____
GAM1172  LOC146669 5'  CAGAAGGGGACGATGTC     30468      _     ACGTT
                                CAGA GGGGAC     GTGTC
                                |||| ||||||     |||||
                                GTCT CCCCTG     TACAG
                                  T     C____
GAM1172  LOC146895 5'  CCAGAGGGCGTGGTGT      30469         GACA   T
                                CCAGAGGG    CGT GTGT
                                ||||||||    ||| ||||
                                GGTCTCCC    GCA CACA
                                     ____   C
GAM1172  LOC148183 5'  CAGAGGGGTGTGTGTGT     30470         ACAC  _
                                CAGAGGGG    GT TGTGT
                                ||||||||    || |||||
                                GTCTCCCC    CA ACACA
                                     A___   C
GAM1172  LOC148753 3'  CCAGCAGGGGGGCGCTGGT    30471      _     ACA     T
                                CCAG AGGGG   CGTTG GT
                                |||| |||||   ||||| ||
                                GGTC TCCCC   GCGAC CA
                                  G     C__    _
GAM1172  LOC148979 5'  CAGAGGGGGGCTCGACACAACG 30472          __________     GTT
            TG                    CAGAGGG        GACAC   GTG
                                |||||||         |||||   |||
                                GTCTCCC        CTGTG   CAC
                                    CCCGAGIII     TTG
GAM1172  LOC151429 3'  CAGAGGAGGTCACAGTGT     30473       _ A    TT
                                CAGAGG GG CACG  GTGT
                                |||||| || ||||  ||||
                                GTCTCC CC GTGT  CACA
                                    T  A    __
GAM1172  LOC152633 5'  CAGAGGGGAGCCAGGTC      30474         CAC    T
                                CAGAGGGGA   GTTG GTC
                                |||||||||   |||| |||
                                GTCTCCCCT   CGGT CAG
                                     ___    C
GAM1172  LOC153077 3'  CAGAGGGGGTTTCACTGTGT   30475         ACA_
                                CAGAGGGG    CGTTGTGT
                                ||||||||    ||||||||
                                GTCTCCCC    GTGACACA
                                     CAAA
GAM1172  LOC153338 5'  AGAGGGGAGCACTGTC      30476         _  GTTG
                                AGAGGGGA CAC    TGTC
                                |||||||| |||    ||||
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                                TCTCCCCT GTG   ACAG
                                    C  ____
GAM1172  LOC163682 5'  CCAGAGGGGAGGCCCAGC   30477        CAC  GT
                                CCAGAGGGGA  GTT  GT
                                ||||||||||  |||  ||
                                GGTCTCCCCT  CGG  CG
                                     C__  GT
GAM1172  LOC164714 5'  CCAGAGGAGGTACGGCATC   30478       AC  TT
                                CCAGAGGGG  ACG  GTGTC
                                |||||||||  |||  |||||
                                GGTCTCCTC  TGC  CGTAG
                                     CA  __
GAM1172  LOC197136 3'  CCAGAGGGGCTGTCGACACAAC 30462      __________   GTT
           GTG                   CAGAGGG       GACAC  GTG
                                 |||||||       |||||  |||
                                 GTCTCCC       CTGTG  CAC
                                    CGACAGIII    TTG
GAM1172  LOC199704 3'  CAGGGGGCACACCACTGTC   30479    A   A   TT _
                                CAG GGGG CACG  G TGTC
                                ||| |||| ||||  | ||||
                                GTC CCCC GTGT  T ACAG
                                  _   _   GG G
GAM1172  LOC200860 3'  AAGGACCCTGCGTTGTGTC   30480      A___
                                GGGGAC   CGTTGTGTC
                                ||||||   |||||||||
                                TTCCTG   GCAACACAG
                                   GGAC
GAM1172  LOC201514 3'  CCAGAGGTGGGTCATGTC    30481      _ ACAC  TG
                                CCAGAGG GG   GT  TGTC
                                ||||||| ||   ||  ||||
                                GGTCTCC CC   CA  ACAG
                                    A  ____  GT
GAM1172  LOC202986 5'  CAAAGGGGACGCGACTGGT   30482        A  _  T
                                CAGAGGGGAC CG TTG GT
                                |||||||||| || ||| ||
                                GTTTCCCCTG GC GAC CA
                                     C  T  _
GAM1172  LOC219914 5'  CAGAGGGGAACTCGACACAACG 30483      __________   GTT
           TG                    CAGAGGG       GACAC  GTG
                                 |||||||       |||||  |||
                                 GTCTCCC       CTGTG  CAC
                                    CTTGAGIII    TTG
GAM1172  LOC220549 5'  CAAAGGGGACGAAGGTGTC   30484        ACGTT
                                CAGAGGGGAC    GTGTC
                                ||||||||||    |||||
                                GTTTCCCCTG    CACAG
                                     CTTC_
GAM1172  LOC220980 5'  CCAGAGGGGCAGCAGT     30485        A  C  T
                                CCAGAGGGG CA GT GT
                                ||||||||| || || ||
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                                GGTCTCCCC GT CG CA
                                     _ _  T
GAM1172  LOC254946 5'  CCAGAAGGGGCACAGGGT    30486         A    TT
                                CCAGAGGGG CACG  GT
                                ||||||||| ||||  ||
                                GGTCTTCCC GTGT  CA
                                    C    CC
GAM1172  LOC255031 5'  CCAGGGAGGCTGTGT       30487      A    ACAC
                                CCAG GGGG    GTTGTGT
                                |||| ||||    |||||||
                                GGTC CCTC    CGACACA
                                  _   _____
GAM1172  LOC255269 5'  GAGGGGATGGGCTGTGTC    30488        CAC
                                GAGGGGA   GTTGTGTC
                                |||||||   ||||||||
                                CTCCCCT   CGACACAG
                                    ACC
GAM1172  LOC255552 5'  CCAGAGGGGGCTTTGACACAAC 30465        __________    GTT
           GTG                    CAGAGGG        GACAC   GTG
                                |||||||        |||||   |||
                                GTCTCCC        CTGTG   CAC
                                   CCGAAAIII    TTG
GAM1172  LOC257407 5'  CCAGGGGAGACACTGT      30489      A       GT
                                CCAG GGGGACAC  TGT
                                |||| ||||||||  |||
                                GGTC CCTCTGTG  ACA
                                  C       __
GAM1172  LOC90408  5'  CCAGAGGGGAACTGT       30490          C  GTTG
                                CCAGAGGGGA AC    TGT
                                |||||||||| ||    |||
                                GGTCTCCCCT TG    ACA
                                     _ _____
GAM1172  LOC91547  5'  CCAGAGGCGGTGACCGCGTC   30491        _  ACAC TT
                                CCAGAGG GG    G  GTGTC
                                ||||||| ||    |  |||||
                                GGTCTCC CC    T  CGCAG
                                   G  AC__ GG
GAM1172  LOC91748  3'  CAGAGGGGTGGTCGACACAACG 30492        __________    GTT
           TG                     CAGAGGG        GACAC   GTG
                                |||||||        |||||   |||
                                GTCTCCC        CTGTG   CAC
                                   CACCAGIII    TTG
GAM1172  LOC91813  5'  GAAGGGACCAGGTGTC      30493        A  TT
                                GAGGGGAC CG  GTGTC
                                |||||||| ||  |||||
                                CTTCCCTG GT  CACAG
                                    _ C_
GAM1173  FGFR2     3'  GTGGATACTGAGGAAGGC    30496        _    TC
                                GTGGATAC GAGGA  GT
                                |||||||| |||||  ||
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                                CACCTATG CTCCT  CG
                                     A    TC
GAM1173  LOC204593 5'  TACGTGGACACAGTCTCGTTTG 30497          G  GA
              C                   TACGTGGATAC AG  TCGTTTGC
                                  |||||||||||  ||  ||||||||
                                  ATGCACCTGTG TC  AGCAAACG
                                       _  AG
GAM1174  BICD2    3'  TATTATTTTTTTGTTTGGGTCT 30500          _  A  TTC
              GTG                   TATTATTTTTT GT TG   CTGTG
                                  ||||||||||| || ||   |||||
                                  ATAATAAAAAA CA AC   GACAC
                                       A  A  CCA
GAM1174  KLHL6    3'  TTTTTTGTTTGTTTTTCCTG   30501        A  ___
                                  TTTTTTGT TGT   TCCTG
                                  ||||||||  |||   |||||
                                  AAAAAACA ACA   AGGAC
                                       A   AAA
GAM1174  LOC116437 3'  TATTTTTTTTCCTGT       30502        GTATG
                                  TATTTTTT    TTCCTGT
                                  ||||||||    |||||||
                                  ATAAAAAA    AAGGACA
                                       _____
GAM1175  ADCY9     3'  CGAGGCCGAGGCCAGCCCTGAA 30505         C  _  AC__
              GGC                   CGAGGCCGA GC GG    GAAGGC
                                  |||||||||  || ||    ||||||
                                  GCTCCGGCT CG TC    CTTCCG
                                       C  G  GGGA
GAM1175  APPL      3'  CGAGGCGGGCGGATCATGAGG  30506       CGAC    _  A_
                                  CGAGGC    GCGGA CG  AGG
                                  ||||||    ||||| ||  |||
                                  GCTCCG    CGCCT GT  TCC
                                     CC__     A  AC
GAM1175  ARNT2     3'  CGGGCTGAAGAACGAAGGC    30507    A   C  CGC
                                  CG GGC GA   GGACGAAGGC
                                  || ||| ||   ||||||||||
                                  GC CCG CT   CTTGCTTCCG
                                   _   A  T__
GAM1175  AVP       3'  CGAGGCCGTGCATTGGCGGAGG 30508         AC  ___  A  A
                                  CGAGGCCG  GC   GG CG AGG
                                  ||||||||  ||   || || |||
                                  GCTCCGGC  CG   CC GC TCC
                                       A_  TAA  _  C
GAM1175  CACNG8    5'  GAGGCCGAAGGCGGCGAAGGC  30509         C_   A
                                  GAGGCCGA  GCGG CGAAGGC
                                  ||||||||  ||||  |||||||
                                  CTCCGGCT  CGCC GCTTCCG
                                       TC   _
GAM1175  CTNS      3'  GGCCCGGACGAAGGC       30510      GACG
                                  GGCC    CGGACGAAGGC
                                  ||||    ||||||||||
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                                CCGG   GCCTGCTTCCG
                                  ____
GAM1175  DSC3    3'  CGAGGCAGGCGGATCACGAGG  30511      CGAC   ___  A
                                CGAGGC   GCGGA  CGA GG
                                ||||||   |||||  ||| ||
                                GCTCCG   CGCCT  GCT CC
                                   TC__    AGT  _
GAM1175  DSC3    3'  CGAGGCAGGCGGATCACGAGG  30511      CGAC   ___  A
                                CGAGGC   GCGGA  CGA GG
                                ||||||   |||||  ||| ||
                                GCTCCG   CGCCT  GCT CC
                                   TC__    AGT  _
GAM1175  ELMO3   5'  CGAGGCCAGCGGAACAAGGC  30512       AC   CG
                                CGAGGCCG  GCGGA  AAGGC
                                ||||||||  |||||  |||||
                                GCTCCGGT  CGCCT  TTCCG
                                    __    TG
GAM1175  FOXF2   5'  CGAGGCCGGGCCGCGAGGGC  30513       AC  GGA  A
                                CGAGGCCG  GC   CGA GGC
                                ||||||||  ||   ||| |||
                                GCTCCGGC  CG   GCT CCG
                                    C_  GC_   C
GAM1175  FOXO1A  5'  CGAAGCCGGTGCGGCGA    30514       AC   A
                                CGAGGCCG  GCGG CGA
                                ||||||||  |||| |||
                                GCTTCGGC  CGCC GCT
                                    CA   _
GAM1175  GAD1    5'  CGAGGCCGTTGCTCGCGGGGGC 30515       A____    ACGAA
                                CGAGGCCG    CGCGG    GGC
                                ||||||||    |||||    |||
                                GCTCCGGC    GCGCC    CCG
                                    AACGA    C____
GAM1175  GNA14   5'  CGGGGCGACGCGGCCCCGGGC  30516   A  C     ACGAA
                                CG GGC GACGCGG    GGC
                                || ||| |||||||    |||
                                GC CCG CTGCGCC    CCG
                                 C  _     GGGGC
GAM1175  GPR44   3'  CCAGGCCGACAGGGAGG    30517   G      C  CGAA
                                C AGGCCGACG GGA   GG
                                | |||||||| |||   ||
                                G TCCGGCTGT CCT   CC
                                 G       C  ____
GAM1175  HCN2    3'  CGAGGCCGCCGCCGGGGGC   30518       A  GGA  AA
                                CGAGGCCG CGC   CG  GGC
                                |||||||| |||   ||  |||
                                GCTCCGGC GCG   GC  CCG
                                    G   ___  CC
GAM1175  HCN2    3'  GACGCGCGCGGACGGGGGC   30519    _  A      AA
                                GGC CG CGCGGACG  GGC
                                ||| || ||||||||  |||
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                                CTG GC GCGCCTGC  CCG
                                  C _       CC
GAM1175  HDGF     5'  CGGGGCGGGCGCGGATCGGGGC 30520    A   CGA     _ AA
                                CG GGC   CGCGGA CG  GGC
                                || |||   |||||| ||  |||
                                GC CCG   GCGCCT GC  CCG
                                 C  CCC     A  C_
GAM1175  HRB      5'  GGCTCGACGCGGCCCGGGC   30521     _      A_  AA
                                GGC CGACGCGG  CG  GGC
                                ||| ||||||||  ||  |||
                                CCG GCTGCGCC  GC  CCG
                                  A       GG  __
GAM1175  KCNS2    5'  CGAGGCCGGCGGGAAA      30522         AC    AC
                                CGAGGCCG  GCGG  GAAG
                                ||||||||  ||||  ||||
                                GCTCCGGC  CGCC  CTTT
                                    __    __
GAM1175  MDM2     3'  CGAGGTGGGCGGATCACGAGG  30523      CCGAC    ___  A
                                CGAGG    GCGGA   CGA GG
                                |||||    |||||   ||| ||
                                GCTCC    CGCCT   GCT CC
                                   ACC__     AGT   _
GAM1175  MDM2     3'  CGAGGTGGGCGGATCACGAGG  30523      CCGAC    ___  A
                                CGAGG    GCGGA   CGA GG
                                |||||    |||||   ||| ||
                                GCTCC    CGCCT   GCT CC
                                   ACC__     AGT   _
GAM1175  MDM2     3'  CGAGGTGGGCGGATCACGAGG  30523      CCGAC    ___  A
                                CGAGG    GCGGA   CGA GG
                                |||||    |||||   ||| ||
                                GCTCC    CGCCT   GCT CC
                                   ACC__     AGT   _
GAM1175  MDM2     3'  CGAGGTGGGCGGATCACGAGG  30523      CCGAC    ___  A
                                CGAGG    GCGGA   CGA GG
                                |||||    |||||   ||| ||
                                GCTCC    CGCCT   GCT CC
                                   ACC__     AGT   _
GAM1175  MDM2     3'  CGAGGTGGGCGGATCACGAGG  30523      CCGAC    ___  A
                                CGAGG    GCGGA   CGA GG
                                |||||    |||||   ||| ||
                                GCTCC    CGCCT   GCT CC
                                   ACC__     AGT   _
GAM1175  MXI1     5'  CGGGCCGACAGGAGG       30524    A      C   CGAA
                                CG GGCCGACG GGA    GG
                                || |||||||| |||    ||
                                GC CCGGCTGT CCT    CC
                                  _      _  ____
GAM1175  MYO1D    5'  CGAGGCCGCGCCGCGAGGC   30525        A   GGA   A
                                CGAGGCCG CGC   CGA GGC
                                |||||||| |||   ||| |||
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                                GCTCCGGC GCG  GCT CCG
                                    _  GC_  _
GAM1175 P4HB    3' CGAGGCCGCAGGCTTCGGAGGC 30526       AC_ GGA A
                                CGAGGCCG  GC  CG AGGC
                                ||||||||  ||  || ||||
                                GCTCCGGC  CG  GC TCCG
                                    GTC AA_ C
GAM1175 PDGFB   5' CGAGGCCGGCTACCTGGGC  30527       AC GG GAA
                                CGAGGCCG GC AC  GGC
                                ||||||||  || ||  |||
                                GCTCCGGC CG TG  CCG
                                    __ A_ GAC
GAM1175 PPFIA3  3' CGAGAGTCGGGGGCGAGGGC  30528     CCGA C A  A
                                CGAGG  CG GG CGA GGC
                                |||||  || || ||| |||
                                GCTCT  GC CC GCT CCG
                                   CA__ C C  C
GAM1175 PRKCSH  5' CGAGGCCGGAGCAAAGG    30529       ACGC GA
                                CGAGGCCG  G CGAAGG
                                ||||||||  | ||||||
                                GCTCCGGC  C GTTTCC
                                    ____ TC
GAM1175 PTN     5' CGGGCCAGGAGGACGAAGGC 30530   A   ACGC
                                CG GGCCG  GGACGAAGGC
                                || |||||  ||||||||||
                                GC CCGGT  CCTGCTTCCG
                                 _   CCT_
GAM1175 PTPN13  5' GAGCGCCGGGCGAGGGC    30531   _   ACGC A  A
                                GAG GCCG  GG CGA GGC
                                ||| ||||  || ||| |||
                                CTC CGGC  CC GCT CCG
                                  G  ____ _  C
GAM1175 PTPN13  5' GAGCGCCGGGCGAGGGC    30531   _   ACGC A  A
                                GAG GCCG  GG CGA GGC
                                ||| ||||  || ||| |||
                                CTC CGGC  CC GCT CCG
                                  G  ____ _  C
GAM1175 PTPN13  5' GAGCGCCGGGCGAGGGC    30531   _   ACGC A  A
                                GAG GCCG  GG CGA GGC
                                ||| ||||  || ||| |||
                                CTC CGGC  CC GCT CCG
                                  G  ____ _  C
GAM1175 RABL2A  3' CGAGGCGGGCGGATCACGAGG 30532     CGAC  ___  A
                                CGAGGC  GCGGA  CGA GG
                                ||||||  |||||  ||| ||
                                GCTCCG  CGCCT  GCT CC
                                   CC__   AGT  _
GAM1175 RABL2B  3' CGAGGCGGGCGGATCACGAGG 30532     CGAC  ___  A
                                CGAGGC  GCGGA  CGA GG
                                ||||||  |||||  ||| ||
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                                GCTCCG   CGCCT   GCT CC
                                   CC__    AGT  _
GAM1175 SH3GL3   5' CGAGGCAGGCGGATCACGAGG 30511      CGAC   ___  A
                                CGAGGC   GCGGA  CGA GG
                                ||||||   |||||  ||| ||
                                GCTCCG   CGCCT  GCT CC
                                   TC__    AGT  _
GAM1175 SPON2    5' CGAGGCCGGCGCCCCGGGC   30533       A  GGA  AA
                                CGAGGCCG CGC  CG  GGC
                                |||||||| |||  ||  |||
                                GCTCCGGC GCG  GC  CCG
                                    C  GG_ __
GAM1175 STK11    3' CGAGGCCACGGGCGGGG    30534       G  C  A  AA
                                CGAGGCC ACG GG CG  GG
                                ||||||| ||| || ||  ||
                                GCTCCGG TGC CC GC  CC
                                   _  _ _ C_
GAM1175 TNFAIP2  3' GAGGCCGACTGTGGAGGGGC  30535       GC_  CGAA
                                GAGGCCGAC  GGA   GGC
                                |||||||||  |||   |||
                                CTCCGGCTG  CCT   CCG
                                    ACA  CC__
GAM1175 TP53BP2  5' CGAGGCAGGCGGATCACAAGG 30536      CGAC   _ _
                                CGAGGC   GCGGA CG AAGG
                                ||||||   ||||| || ||||
                                GCTCCG   CGCCT GT TTCC
                                   TC__    A  G
GAM1175 TRIM9    5' CAAGGCCGGTGGATCAAGAGGC 30537       ACGC  _  _
                                CGAGGCCG   GGA CGA AGGC
                                ||||||||   ||| ||| ||||
                                GTTCCGGC   CCT GTT TCCG
                                    CA__   A  C
GAM1175 VENTX2   3' CGAGGCGGGCGGATCACAGG  30538      CGAC   _ A
                                CGAGGC   GCGGA CG AGG
                                ||||||   ||||| || |||
                                GCTCCG   CGCCT GT TCC
                                   CC__    A  G
GAM1175 WDR1     5' CGAGGCCGGGGCTCAGAGGC  30539       AC  GGA  A
                                CGAGGCCG  GC   CG AGGC
                                ||||||||  ||   || ||||
                                GCTCCGGC  CG   GT TCCG
                                    CC  A__  C
GAM1175 WDR1     5' CGAGGCCGGGGCTCAGAGGC  30539       AC  GGA  A
                                CGAGGCCG  GC   CG AGGC
                                ||||||||  ||   || ||||
                                GCTCCGGC  CG   GT TCCG
                                    CC  A__  C
GAM1175 WHSC1L1  5' GAGGCCGAGGGACGGGGG   30540       CGC   AA
                                GAGGCCGA  GGACG  GG
                                ||||||||  |||||  ||
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                                CTCCGGCT  CCTGC  CC
                                    C__    CC
GAM1175  WHSC1L1  5'  GAGGCCGAGGGACGGGGG   30540       CGC   AA
                                GAGGCCGA  GGACG  GG
                                ||||||||  |||||  ||
                                CTCCGGCT  CCTGC  CC
                                    C__    CC
GAM1175  AGS3     5'  CGAGGCCGTCATCGAGGGC   30541       ACG  GA  A
                                CGAGGCCG  CG  CGA GGC
                                ||||||||  ||  ||| |||
                                GCTCCGGC  GT  GCT CCG
                                    A__ A_  C
GAM1175  BRD2     5'  AGGCCGGGACGAAGG      30542       ACGC
                                AGGCCG   GGACGAAGG
                                ||||||   |||||||||
                                TCCGGC   CCTGCTTCC
                                   ____
GAM1175  C1orf17  3'  CGAGGCTGGCGTCTGGTGGAAG 30543      CGAC  GAC____
           GC                   CGAGGC   GCG     GAAGGC
                                ||||||   |||     ||||||
                                GCTCCG   CGC     CTTCCG
                                   AC__  AGACCAC
GAM1175  C6orf5   3'  CGAGGTGGGCGGATCACAAGG  30544      CCGAC   _ _
                                CGAGG    GCGGA CG AAGG
                                |||||    ||||| || ||||
                                GCTCC    CGCCT GT TTCC
                                  ACC__    A  G
GAM1175  C7orf13  5'  CGAAGCCGGCGCGGGG     30545       A    ACGAA
                                CGAGGCCG CGCGG    GG
                                |||||||| |||||    ||
                                GCTTCGGC GCGCC    CC
                                    C   _____
GAM1175  CARD9    3'  CAAGGCCGACCCTCAGTGAGGG 30546        G__  AC  A
           C                    CGAGGCCGAC  CGG  GA GGC
                                ||||||||||  |||  || |||
                                GTTCCGGCTG  GTC  CT CCG
                                     GGA  A_  C
GAM1175  DKFZP434B205 3'  CGAGGCCGTGGGCGAGG    30547       ACGC  A  A
                                CGAGGCCG   GG CGA GG
                                ||||||||   || ||| ||
                                GCTCCGGC   CC GCT CC
                                    AC__  _  _
GAM1175  ELF4     5'  GAGGCCGAGTGGCTCACGGGC  30548       C__  GG  AA
                                GAGGCCGA  GC  ACG  GGC
                                ||||||||  ||  |||  |||
                                CTCCGGCT  CG  TGC  CCG
                                    CAC  AG  __
GAM1175  FKBP9    3'  CGAGGTGGGCGGATCACGAGG  30523      CCGAC   ___  A
                                CGAGG    GCGGA  CGA GG
                                |||||    |||||  ||| ||
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                                GCTCC    CGCCT   GCT CC
                                  ACC__    AGT   _
GAM1175  FLJ00060  5' CGAGGCGGGCGGATCATGAGG  30506      CGAC    _ A_
                                CGAGGC   GCGGA CG  AGG
                                ||||||   ||||| ||  |||
                                GCTCCG   CGCCT GT  TCC
                                   CC__    A  AC
GAM1175  FLJ10099  5' CGGGGCCGACGCGAAGA    30549    A         C
                                CG GGCCGACGCGGA GA
                                || ||||||||||| ||
                                GC CCGGCTGCGCTT CT
                                 C         _
GAM1175  FLJ10846  3' CGAGGTCGGCGGATCACGAGG  30550      C  AC    ___   A
                                CGAGG CG  GCGGA   CGA GG
                                ||||| ||  |||||   ||| ||
                                GCTCC GC  CGCCT   GCT CC
                                   A  __    AGT   _
GAM1175  FLJ12581  3' CGAGGCGGGCGGATCACAAGG  30551      CGAC    _ _
                                CGAGGC   GCGGA CG AAGG
                                ||||||   ||||| || ||||
                                GCTCCG   CGCCT GT TTCC
                                   CC__    A  G
GAM1175  FLJ12704  3' GAGGTCAGTGAGGACGAAGG   30552     C  ACGC
                                GAGG CG   GGACGAAGG
                                |||| ||   |||||||||
                                CTCC GT   CCTGCTTCC
                                  A  CACT
GAM1175  FLJ13621  5' CGGGGCCGACACGGAGGAGGC  30553    A         C  A
                                CG GGCCGACGCGGA GA GGC
                                || |||||||||||| || |||
                                GC CCGGCTGTGCCT CT CCG
                                 C         C  _
GAM1175  FLJ20097  3' CGAGGCGGGCGGATCACGAGG  30532      CGAC    ___   A
                                CGAGGC   GCGGA   CGA GG
                                ||||||   |||||   ||| ||
                                GCTCCG   CGCCT   GCT CC
                                   CC__    AGT   _
GAM1175  FLJ20294  3' CGAAGCCGCCCATGGAGGC   30554       A_  C   CGAA
                                CGAGGCCG  CG GGA   GGC
                                ||||||||  || |||   |||
                                GCTTCGGC  GT CCT   CCG
                                    GG  A  ____
GAM1175  FLJ20625  3' GAGGCCAACGGAGAGGG    30555       AC    C  A
                                GAGGCCG  GCGGA GA GG
                                |||||||  ||||| || ||
                                CTCCGGT  TGCCT CT CC
                                   __    _ C
GAM1175  FLJ20897  5' CGAGGCGGGCGGATCACAGG   30538      CGAC    _ A
                                CGAGGC   GCGGA CG AGG
                                ||||||   ||||| || |||
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                                GCTCCG   CGCCT GT TCC
                                   CC__    A  G
GAM1175  FLJ21939  5'  CGGGCCGACGCGGGAGAAGGC  30556   A        AC
                                CG GGCCGACGCGG  GAAGGC
                                || ||||||||||  ||||||
                                GC CCGGCTGCGCC  CTTCCG
                                 _         CT
GAM1175  FLJ22167  5'  CGAGGCGGGCGGATCACGAGG  30532      CGAC    ___   A
                                CGAGGC   GCGGA   CGA GG
                                ||||||   |||||   ||| ||
                                GCTCCG   CGCCT   GCT CC
                                   CC__    AGT   _
GAM1175  FLJ23519  3'  CGAGGCAGGCGGATCACGAGG  30511      CGAC    ___   A
                                CGAGGC   GCGGA   CGA GG
                                ||||||   |||||   ||| ||
                                GCTCCG   CGCCT   GCT CC
                                   TC__    AGT   _
GAM1175  FRAT1    5'  CGGGGCGGACGCGGAAG    30557    A  C      CGAA
                                CG GGC GACGCGGA    GG
                                || ||| ||||||||    ||
                                GC CCG CTGCGCCT    TC
                                 C   C      _____
GAM1175  GPS2     5'  GAGGCCGAGGCGGAGG      30558        C    CGAA
                                GAGGCCGA GCGGA    GG
                                |||||||| |||||    ||
                                CTCCGGCT CGCCT    CC
                                    C     _____
GAM1175  GREB1    3'  CGAGGCGGGCGGATCACGAGG  30532      CGAC    ___   A
                                CGAGGC   GCGGA   CGA GG
                                ||||||   |||||   ||| ||
                                GCTCCG   CGCCT   GCT CC
                                   CC__    AGT   _
GAM1175  HT002    3'  CGAGGTGGGCGGATCACGAGG  30523     CCGAC    ___   A
                                CGAGG    GCGGA   CGA GG
                                |||||    |||||   ||| ||
                                GCTCC    CGCCT   GCT CC
                                  ACC__    AGT   _
GAM1175  KIAA0418 3'  GAGGCCGACCACCCAGGC    30559        G  GA GA
                                GAGGCCGAC CG  C  AGGC
                                ||||||||| ||  |  ||||
                                CTCCGGCTG GT  G  TCCG
                                     _ GG __
GAM1175  KIAA0545 3'  CGAGGCTGCTGGTCAGGGC   30560      CGAC  _  A  AA
                                CGAGGC   GC GG CG  GGC
                                ||||||   || || ||  |||
                                GCTCCG   CG CC GT  CCG
                                   A___  A  A  C_
GAM1175  KIAA0594 3'  CGAGGCGGGTGGATCACAAGG  30561      CGACGC  _  _
                                CGAGGC     GGA CG AAGG
                                ||||||     ||| || ||||
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                                GCTCCG     CCT GT TTCC
                                   CCCA__   A  G
GAM1175 KIAA0638 3' CGAGGCCAGACAGCTGGAGGC 30562       _  _ _  CGAA
                                CGAGGCC GAC GC GGA    GGC
                                ||||||| ||| || |||    |||
                                GCTCCGG CTG CG CCT    CCG
                                    T  T A  ____
GAM1175 KIAA1285 5' CGAGGCCGGGAGGCGCGCGGGC 30563     A_______    A A   III
           GGAGGCG                CCG      CGCGG CG AGGC   G
                                |||      ||||| || ||||  |
                                GGC      GCGCC GC TCCG   C
                                  CCTCCGC    C  C    III
GAM1175 KIAA1530 5' CGAGGCCGGGGCGGAGG     30564        AC    CGAA
                                CGAGGCCG  GCGGA   GG
                                ||||||||  |||||   ||
                                GCTCCGGC  CGCCT   CC
                                    CC    ____
GAM1175 KIAA1643 5' CGGGGCGGACGCGGAGG     30565    A  C      CGAA
                                CG GGC GACGCGGA   GG
                                || ||| ||||||||   ||
                                GC CCG CTGCGCCT   CC
                                 C  C      ____
GAM1175 KIAA1950 3' GAGGCCGAGTTAGGAAAGGC  30566        CGC_  CG
                                GAGGCCGA   GGA  AAGGC
                                ||||||||   |||  |||||
                                CTCCGGCT   CCT  TTCCG
                                    CAAT  __
GAM1175 MAP2K5   5' CGAGGCCGCGCGGACCGGC   30567        A     GAA
                                CGAGGCCG CGCGGAC   GGC
                                |||||||| |||||||   |||
                                GCTCCGGC GCGCCTG   CCG
                                    _      G__
GAM1175 MAPK8IP3 3' CGAGGCCGCGTGGAACAGC   30568        A  C   CGAA
                                CGAGGCCG CG GGA    GGC
                                |||||||| || |||    |||
                                GCTCCGGC GC CCT    TCG
                                    _  A   TG__
GAM1175 NIFU     5' CGGGGCCGACAGCTCCGGGC  30569    A     _ GGA  AA
                                CG GGCCGAC GC   CG  GGC
                                || |||||| ||   ||  |||
                                GC CCGGCTG CG   GC  CCG
                                 C      T  AG_  __
GAM1175 NUDE1    3' CGAGGCCGAGGGGAAGG     30570         CGC  AC
                                CGAGGCCGA   GG  GAAGG
                                |||||||||   ||  |||||
                                GCTCCGGCT   CC  CTTCC
                                     ___  C_
GAM1175 PP1665   5' GAGGCCAAAGGTGAAGG     30571        CGC  AC
                                GAGGCCGA   GG  GAAGG
                                ||||||||   ||  |||||
```

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                                CTCCGGTT  CC  CTTCC
                                    T__  A_
GAM1175 PRDM12   5' CGGGCCGACGGGGGAGG    30572    A      C  AC  A
                                CG GGCCGACG GG  GA GG
                                || |||||||| ||  || ||
                                GC CCGGCTGC CC  CT CC
                                 _      _ C_ _
GAM1175 PYPAF4   3' GAGACCGAGAGACCATGAAGGC 30573        CGC  ___
                                GAGGCCGA  GGAC  GAAGGC
                                ||||||||  ||||  ||||||
                                CTCTGGCT  TCTG  CTTCCG
                                    C__   GTA
GAM1175 QKI     5' CGAGGCCGGCGGGCGGG    30574        AC   A  AA
                                CGAGGCCG  GCGG CG  GG
                                ||||||||  |||| ||  ||
                                GCTCCGGC  CGCC GC  CC
                                    __   C  __
GAM1175 RAB21    3' CGAGGCGGGCGGATCACAAGG  30551      CGAC   _ _
                                CGAGGC   GCGGA CG AAGG
                                ||||||   ||||| || ||||
                                GCTCCG   CGCCT GT TTCC
                                   CC__    A  G
GAM1175 RCD-8    3' CGAGGCCATGCAGCATGAGGC  30575       AC   ACGA
                                CGAGGCCG  GCGG   AGGC
                                ||||||||  ||||   ||||
                                GCTCCGGT  CGTC   TCCG
                                    A_   GTAC
GAM1175 RHOBTB3  5' CGGGGCCGACGCAGAGCGGGGC 30576    A        _ AA
                                CG GGCCGACGCGGA CG  GGC
                                || ||||||||||| ||  |||
                                GC CCGGCTGCGTCT GC  CCG
                                 C         C  C_
GAM1175 RIS1     5' CGAGGCCGGCGGCGGTTGC   30577       AC   A  AAG
                                CGAGGCCG  GCGG CG   GC
                                ||||||||  |||| ||   ||
                                GCTCCGGC  CGCC GC   CG
                                    __   _ CAA
GAM1175 SLC16A10 5' CGAGGCCGAGGCGAGGG    30578       CGC  A   A
                                CGAGGCCGA   GG CGA GG
                                |||||||||   || ||| ||
                                GCTCCGGCT   CC GCT CC
                                    ___ _   C
GAM1175 SNRK     5' CGAGGCCGCGCCCGGG     30579       A   GGA  AA
                                CGAGGCCG CGC   CG  GG
                                |||||||| |||   ||  ||
                                GCTCCGGC GCG   GC  CC
                                    _  G__  __
GAM1175 SYT12    5' CGAGCCCGACGCAGGG     30580     G       ACGAA
                                CGAG CCGACGCGG    GG
                                |||| |||||||||    ||
```

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                                GCTC GGCTGCGTC    CC
                                  G      _____
GAM1175  TCL6    3'  CGAGGTAGGCGGATCACGAGG  30581     CCGAC   ___  A
                                CGAGG    GCGGA   CGA GG
                                |||||    |||||   ||| ||
                                GCTCC    CGCCT   GCT CC
                                   ATC__    AGT   _
GAM1175  TCL6    3'  CGAGGTAGGCGGATCACGAGG  30581     CCGAC   ___  A
                                CGAGG    GCGGA   CGA GG
                                |||||    |||||   ||| ||
                                GCTCC    CGCCT   GCT CC
                                   ATC__    AGT   _
GAM1175  YAP     3'  GAGGCCGAAGTGAAGG     30582       CGC  AC
                                GAGGCCGA   GG  GAAGG
                                ||||||||   ||  |||||
                                CTCCGGCT   TC  CTTCC
                                    ___  A_
GAM1175  YAP     3'  GAGGCCGAAGTGAAGG     30582       CGC  AC
                                GAGGCCGA   GG  GAAGG
                                ||||||||   ||  |||||
                                CTCCGGCT   TC  CTTCC
                                    ___  A_
GAM1175  YAP     3'  GAGGCCGAAGTGAAGG     30582       CGC  AC
                                GAGGCCGA   GG  GAAGG
                                ||||||||   ||  |||||
                                CTCCGGCT   TC  CTTCC
                                    ___  A_
GAM1175  YAP     3'  GAGGCCGAAGTGAAGG     30582       CGC  AC
                                GAGGCCGA   GG  GAAGG
                                ||||||||   ||  |||||
                                CTCCGGCT   TC  CTTCC
                                    ___  A_
GAM1175  YAP     3'  GAGGCCGAAGTGAAGG     30582       CGC  AC
                                GAGGCCGA   GG  GAAGG
                                ||||||||   ||  |||||
                                CTCCGGCT   TC  CTTCC
                                    ___  A_
GAM1175  LOC115219 5'  CGAGGCCAGGCAGGGAGGC   30583       AC   AC  A
                                CGAGGCCG  GCGG  GA GGC
                                ||||||||  ||||  || |||
                                GCTCCGGT  CGTC  CT CCG
                                    C_   C_  _
GAM1175  LOC143287 3'  CGAGGCCACCACCAGGGGGC  30584       A  __  ACGAA
                                CGAGGCCG CGC  GG    GGC
                                |||||||| |||  ||    |||
                                GCTCCGGT GTG  CC    CCG
                                    G  GT  C____
GAM1175  LOC146229 3'  CGAGGCGGGCGGATCACGAGGG 30585      CGAC    ___  A
            C                    CGAGGC    GCGGA   CGA GGC
                                ||||||    |||||   ||| |||
```

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                                GCTCCG   CGCCT   GCT CCG
                                   CC__    AGT   C
GAM1175  LOC146603 5'  CGAGGCAGGCGGATCATGAGG  30586      CGAC    _  A_
                                CGAGGC   GCGGA CG  AGG
                                ||||||   ||||| ||  |||
                                GCTCCG   CGCCT GT  TCC
                                   TC__    A  AC
GAM1175  LOC147080 5'  CGAGGCGGGCGGATCACAAGG  30551      CGAC    _ _
                                CGAGGC   GCGGA CG AAGG
                                ||||||   ||||| || ||||
                                GCTCCG   CGCCT GT TTCC
                                   CC__    A  G
GAM1175  LOC148479 5'  CGAGGCCGCGCGAGCGGGGG  30587       A   GA  AA
                                CGAGGCCG CGCG  CG  GG
                                |||||||| ||||  ||  ||
                                GCTCCGGC GCGC  GC  CC
                                     _   TC  CC
GAM1175  LOC149577 3'  CGAGGCGGGCGGCAAGG    30588      CGAC   A G
                                CGAGGC   GCGG C AAGG
                                ||||||   |||| | ||||
                                GCTCCG   CGCC G TTCC
                                   CC__   _ _
GAM1175  LOC151534 5'  GAGGCCGAGCAGCGCGGAAGGC 30589       C   AC__
                                GAGGCCGA GCGG   GAAGGC
                                |||||||| ||||   ||||||
                                CTCCGGCT CGTC   CTTCCG
                                     _   GCGC
GAM1175  LOC152719 5'  CGAGGCGGGCGGATCACGAGG  30532      CGAC    ___  A
                                CGAGGC   GCGGA   CGA GG
                                ||||||   |||||   ||| ||
                                GCTCCG   CGCCT   GCT CC
                                   CC__    AGT   _
GAM1175  LOC159199 5'  CGAGGCCGAGCTTGAGG    30590       C  GGAC  A
                                CGAGGCCGA GC   GA GG
                                |||||||||| ||   || ||
                                GCTCCGGCT CG   CT CC
                                     _  AA__  _
GAM1175  LOC160292 3'  CAAGGCCGGTGACAGCAAGGC  30591       AC_   A G
                                CGAGGCCG   GCGG C AAGGC
                                ||||||||   |||| | |||||
                                GTTCCGGC   TGTC G TTCCG
                                     CAC   _ _
GAM1175  LOC164714 5'  CGAGGCCGAGGCCTTGAGG   30592       C  GGAC  A
                                CGAGGCCGA GC   GA GG
                                |||||||||| ||   || ||
                                GCTCCGGCT CG   CT CC
                                     C  GAA_  _
GAM1175  LOC197342 3'  CGAGGCCAGGAACCTGAAGG  30593       ACGC   __
                                CGAGGCCG   GGAC  GAAGG
                                ||||||||   ||||  |||||
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                                GCTCCGGT   CTTG  CTTCC
                                    C___   GA
GAM1175  LOC200310 3'  CGAGGCCATGCAGGAGAGGC  30594       AC  _  C  A
                                CGAGGCCG  GC GGA GA GGC
                                ||||||||  || ||| || |||
                                GCTCCGGT  CG CCT CT CCG
                                    A_  T  _ _
GAM1175  LOC200316 5'  CGAGGCGGGCGGATCACGAGG  30532      CGAC   ___  A
                                CGAGGC   GCGGA  CGA GG
                                ||||||   |||||  ||| ||
                                GCTCCG   CGCCT  GCT CC
                                   CC__   AGT  _
GAM1175  LOC201245 5'  CGAGGCAGACGAGAAGG    30595      C   CGGAC
                                CGAGGC GACG   GAAGG
                                |||||| ||||   |||||
                                GCTCCG CTGC   CTTCC
                                   T   T____
GAM1175  LOC201595 5'  CGAGGCCGGCGGACTGGGG   30596      AC    GAA
                                CGAGGCCG  GCGGAC  GG
                                ||||||||  ||||||  ||
                                GCTCCGGC  CGCCTG  CC
                                    __    ACC
GAM1175  LOC202460 5'  CGAGGCAGGCGGATCACAAGG  30536      CGAC   _ _
                                CGAGGC   GCGGA CG AAGG
                                ||||||   ||||| || ||||
                                GCTCCG   CGCCT GT TTCC
                                   TC__   A  G
GAM1175  LOC220082 3'  CGAGGACGACAAAGGAAGGC  30597     C    C  AC
                                CGAGG CGACG GG  GAAGGC
                                ||||| ||||| ||  ||||||
                                GCTCC GCTGT TC  CTTCCG
                                  T    T __
GAM1175  LOC220776 3'  AGGCCGACTGGACGAAGGC   30598       GC
                                AGGCCGAC  GGACGAAGGC
                                ||||||||  ||||||||||
                                TCCGGCTG  CCTGCTTCCG
                                    A_
GAM1175  LOC220930 5'  CGAGGTGACAGCAGGTGAGGGC 30599     CC  _   AC  A
                                CGAGG  GAC GCGG  GA GGC
                                |||||  ||| ||||  || |||
                                GCTCC  CTG CGTC  CT CCG
                                  A_   T   CA  C
GAM1175  LOC221496 5'  CGAGGCCGGCTGGGAGAGC   30600       AC  _  AC  AG
                                CGAGGCCG  GC GG  GA  GC
                                ||||||||  || ||  ||  ||
                                GCTCCGGC  CG CC  CT  CG
                                    __  A  __  CT
GAM1175  LOC222832 5'  CGAGGCCGCCGCGTCCCCGGGC 30601       A   GA__  AA
                                CGAGGCCG CGCG   CG  GGC
                                |||||||| ||||   ||  |||
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                                GCTCCGGC GCGC   GC  CCG
                                    G   AGGG __
GAM1175  LOC253822 5'  CGAGGCCGACGGGCGGGGC   30602          C  A  AA
                                CGAGGCCGACG GG CG  GGC
                                |||||||||| || ||  |||
                                GCTCCGGCTGC CC GC  CCG
                                      _ _  C_
GAM1175  LOC253842 5'  CGAGGCAGGCGGATCACGAGG  30511       CGAC   ___  A
                                CGAGGC   GCGGA  CGA GG
                                ||||||   |||||  ||| ||
                                GCTCCG   CGCCT  GCT CC
                                   TC__    AGT  _
GAM1175  LOC255975 5'  GAGGCCGACGGGAGG       30603          C  CGAA
                                GAGGCCGACG GGA   GG
                                |||||||||| |||   ||
                                CTCCGGCTGC CCT   CC
                                      _  _____
GAM1175  LOC255987 5'  GAGGCCGACGGGAGG       30603          C  CGAA
                                GAGGCCGACG GGA   GG
                                |||||||||| |||   ||
                                CTCCGGCTGC CCT   CC
                                      _  _____
GAM1175  LOC256019 3'  GAGGCCGAGGCCGAGG      30604         CGC  A  A
                                GAGGCCGA  GG CGA GG
                                ||||||||  || ||| ||
                                CTCCGGCT  CC GCT CC
                                    ___  G  _
GAM1175  LOC256158 5'  CCAGGCCGACCACAAAGCGGGG 30605   G      _   _ AA
            GC                    C AGGCCGAC GCGGA CG  GGC
                                | ||||||| ||||| ||  |||
                                G TCCGGCTG TGTTT GC  CCG
                                 G       G    C  CC
GAM1175  LOC56181  5'  CGAGGTGGGCGGATCACGAGG  30523      CCGAC   ___  A
                                CGAGG    GCGGA  CGA GG
                                |||||    |||||  ||| ||
                                GCTCC    CGCCT  GCT CC
                                   ACC__    AGT  _
GAM1175  LOC91115  3'  CGAGGTGGGCGGATCACAAGG  30544      CCGAC   _ _
                                CGAGG    GCGGA CG AAGG
                                |||||    ||||| || ||||
                                GCTCC    CGCCT GT TTCC
                                   ACC__    A  G
GAM1175  LOC91319  3'  CGGGGCCTGGGGGGGACGAAGG  30606   A   GACGC
                                CG GGCC    GGACGAAGG
                                || ||||    |||||||||
                                GC CCGG    CCTGCTTCC
                                 C   ACCCC
GAM1176  ALS2CR3   3'  TCATCTTTCATTAAAAATAT  30609     AGG
                                TTAT   TTCATTAAAAATAT
                                ||||   ||||||||||||||
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                                AGTA   AAGTAATTTTTATA
                                  GA_
GAM1176 ARHGEF9   3'  TCTTATAGATCCATTAGAAATA 30610             A
              TA                   TTTTATAGGTTCATTA AAATATA
                                   |||||||||||||||| |||||||
                                   AGAATATCTAGGTAAT TTTATAT
                                         C
GAM1176 FLJ31101  3'  TTTCATAGGTTTCATGAAA   30611          _  T
                                   TTTTATAGGTT CAT AAA
                                   |||||||||| ||| |||
                                   AAAGTATCCAA GTA TTT
                                         A  C
GAM1176 KIAA0672  3'  TTTTATAGATTCAGAAATATA  30612          TTAA
                                   TTTTATAGGTTCA   AAATATA
                                   ||||||||||||   |||||||
                                   AAAATATCTAAGT   TTTATAT
                                         C___
GAM1177 PHB       5'  GCTGGACCCTCTCACACCTGC  30615   _       CG
                                   GC GGACCCTCTC  ACGCCTGC
                                   || ||||||||||  ||||||||
                                   CG CCTGGGAGAG  TGTGGACG
                                    A       __
GAM1177 C20orf151 3'  GGTGTGCCCTCTCCAGGCTG   30616   A___      AC  C
                                   GG   CCCTCTCCG  GC TG
                                   ||   |||||||||  || ||
                                   CC   GGGAGAGGT  CG AC
                                    ACAC       C_ _
GAM1177 ERMAP     3'  TAGCGAACTCTTTTCCCTGAAC 30617       C  C__   GAC
              CTG                    TAGCGGAC CT   TCC   GCCTG
                                   ||||||||  ||   |||   |||||
                                   ATCGCTTG GA   GGG   TGGAC
                                        A  AAA   ACT
GAM1177 KCNV1     5'  GCGCACCCTCTCCACCCGC   30618    G       GAC
                                   GCG ACCCTCTCC   GCCTGC
                                   ||| |||||||||   ||||||
                                   CGC TGGGAGAGG   TGGGCG
                                     G       ____
GAM1177 MGC15416  3'  GGGTCCTCTCCACGTACTGC   30619    AC      G   C_
                                   GG  CCTCTCC ACG  CTGC
                                   ||  ||||||| |||  ||||
                                   CC  GGAGAGG TGC  GACG
                                    CA      _   AT
GAM1177 MGC15416  3'  GGGTCCTCTCCACGTACTGC   30619    AC      G   C_
                                   GG  CCTCTCC ACG  CTGC
                                   ||  ||||||| |||  ||||
                                   CC  GGAGAGG TGC  GACG
                                    CA      _   AT
GAM1177 LOC144017 5'  CGGATGGCCGACGCCTGC    30620      CCCTCT
                                   CGGA     CCGACGCCTGC
                                   ||||     ||||||||||
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                                GCCT     GGCTGCGGACG
                                  ACC___
GAM1177  LOC151007 3'  TAGCGGACTCTCTCTGTCTTCT 30621        C    CGACGC__
             CTGC                   TAGCGGAC CTCTC       CTGC
                                ||||||||  |||||       ||||
                                ATCGCCTG GAGAG       GACG
                                    A    ACAGAAGA
GAM1177  LOC92095  3'  GCGGACCCTCTGCCC      30622          CCGAC
                                GCGGACCCTCT    GCCT
                                ||||||||||    ||||
                                CGCCTGGGAGA    CGGG
                                      _____
GAM1177  LOC92096  3'  GCGGACCCTCTGCCC      30622          CCGAC
                                GCGGACCCTCT    GCCT
                                ||||||||||    ||||
                                CGCCTGGGAGA    CGGG
                                      _____
GAM1178  AQP5     5'  GCGGCGGTGTAGACCGGCC   30625       CACG
                                GCGGCG   AGATCGGCC
                                ||||||   |||||||||
                                CGCCGC   TCTGGCCGG
                                   CACA
GAM1178  CALCA    5'  TGGCAGCGGCGGCGGCGGC   30626         CA  AGAT
                                TGGCAGCGGCG  CG   CGGC
                                ||||||||||  ||   ||||
                                ACCGTCGCCGC  GC   GCCG
                                      C_  C___
GAM1178  CSK      3'  TGGCAGCGGCACACGAAATC  30627
                                TGGCAGCGGCGCACGAGATC
                                ||||||||||||||||||||
                                ACCGTCGCCGTGTGCTTTAG

GAM1178  CTSB     3'  TGGCAGCGGTGGCTCACATGGC 30628        C_  A  AG  C
             C                   TGGCAGCGG  GC CG  AT GGCC
                                |||||||||  || ||  || ||||
                                ACCGTCGCC  CG GT  TA CCGG
                                     AC  A  G_  _
GAM1178  GRM3     5'  TGGCAGCGGCGGCGGTGAGCC  30629         CA  AGATC
                                TGGCAGCGGCG  CG    GGCC
                                ||||||||||  ||    ||||
                                ACCGTCGCCGC  GC    TCGG
                                      C_  CAC__
GAM1178  HMGN2    5'  GCAGCGGCGCGCGGGC      30630         A  AGATC
                                GCAGCGGCGC CG    GGC
                                |||||||||| ||    |||
                                CGTCGCCGCG GC    CCG
                                      C  _____
GAM1178  LMO4     5'  TGGCAGCGGCGGCTCGGC    30631          CACGAGA
                                TGGCAGCGGCG     TCGGC
                                ||||||||||      |||||
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                                ACCGTCGCCGC      AGCCG
                                      CG_____
GAM1178 MBD3    3' TGGCAGCGGCTGGAGTTTGG  30632        GCAC  ATC
                                TGGCAGCGGC  GAG  GG
                                ||||||||||  |||  ||
                                ACCGTCGCCG  CTC  CC
                                      AC__  AAA
GAM1178 NAV2    5' TGGCAGCGGCGGCGGGGGC  30633         CA  AGATC
                                TGGCAGCGGCG  CG   GGC
                                ||||||||||  ||   |||
                                ACCGTCGCCGC  GC   CCG
                                      C_  CC___
GAM1178 OXTR    5' GGCAGCGGTGCGCCCCGGCC  30634       C  ACGAGA
                                GGCAGCGG GC    TCGGCC
                                ||||||| ||     ||||||
                                CCGTCGCC CG    GGCCGG
                                     A  CGG___
GAM1178 PLXNA1  3' TGGCAGCGGTGCAGCGGGC  30635        C  _  AGATC
                                TGGCAGCGG GCA CG   GGC
                                ||||||||| ||| ||   |||
                                ACCGTCGCC CGT GC   CCG
                                     A  C  _____
GAM1178 PTPRJ   5' TGGCAGCGGCGGCGGCGGC  30626         CA  AGAT
                                TGGCAGCGGCG  CG   CGGC
                                ||||||||||  ||   ||||
                                ACCGTCGCCGC  GC   GCCG
                                      C_  C___
GAM1178 TBL1X   5' TGGCGGCGCCGCGCGCCCGGCC 30636    A  G  A  AGA
                                TGGC GCG CGC CG  TCGGCC
                                |||| ||| ||| ||  ||||||
                                ACCG CGC GCG GC  GGCCGG
                                  C  G  C  G__
GAM1178 TRPC1   5' TGGTGGCGGCGCATGCGCGGCC 30637    CA     CGAGAT
                                TGG  GCGGCGCA    CGGCC
                                |||  ||||||||    |||||
                                ACC  CGCCGCGT    GCCGG
                                  AC      ACGC__
GAM1178 APOF    3' GCAGCGGCGCGATCTCGGC  30638        AC  GA
                                GCAGCGGCGC  GA  TCGGC
                                ||||||||||  ||  |||||
                                CGTCGCCGCG  CT  AGCCG
                                     __  AG
GAM1178 COTL1   5' TGGCGGCGGTGGCGACGGC  30639    A  C_  ACGA  T
                                TGGC GCGG  GC   GA CGGC
                                |||| ||||  ||   || ||||
                                ACCG CGCC  CG   CT GCCG
                                  C  AC  _____  _
GAM1178 KIAA1853 5' TGGCAGCGGCTTGCGGGC  30640        GCA  AGATC
                                TGGCAGCGGC  CG   GGC
                                |||||||||  ||   |||
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                                ACCGTCGCCG  GC    CCG
                                     AAC  _____
GAM1178 NSE1     3' GCAGCGGCGCCCTTTCGGCC  30641        ACGAGA
                                GCAGCGGCGC    TCGGCC
                                ||||||||||    ||||||
                                CGTCGCCGCG    AGCCGG
                                     GGAA__
GAM1178 PRO2015  3' GCAGCGGCGCGATCTCGGC   30638        AC  GA
                                GCAGCGGCGC  GA  TCGGC
                                ||||||||||  ||  |||||
                                CGTCGCCGCG  CT  AGCCG
                                     __  AG
GAM1178 SLC16A10 5' TGGCAGCGCGCAGGCGGC    30642       G   CGAGAT
                                TGGCAGCG CGCA    CGGC
                                |||||||| ||||    ||||
                                ACCGTCGC GCGT    GCCG
                                     _   CC____
GAM1178 TBL1Y    5' TGGCGGCGGCGCGTACCTGGCC 30643     A     ACGAG  _
                                TGGC GCGGCGC    ATC GGCC
                                |||| |||||||    ||| ||||
                                ACCG CGCCGCG    TGG CCGG
                                  C      CA___   A
GAM1178 TBL1Y    5' TGGCGGCGGCGCGTACCTGGCC 30643     A     ACGAG  _
                                TGGC GCGGCGC    ATC GGCC
                                |||| |||||||    ||| ||||
                                ACCG CGCCGCG    TGG CCGG
                                  C      CA___   A
GAM1178 TBL1Y    5' TGGCGGCGGCGCGTACCTGGCC 30643     A     ACGAG  _
                                TGGC GCGGCGC    ATC GGCC
                                |||| |||||||    ||| ||||
                                ACCG CGCCGCG    TGG CCGG
                                  C      CA___   A
GAM1178 LOC115294 5' GGCAGCGGCGCGCAGGC    30644         A  AGATC
                                GGCAGCGGCGC CG    GGC
                                |||||||||| ||    |||
                                CCGTCGCCGCG GT    CCG
                                     C  _____
GAM1178 LOC153474 5' GGCGGCGGCGCGCGCGAGGCC  30645    A     A  A  TC
                                GGC GCGGCGC CG GA  GGCC
                                ||| ||||||| || ||  ||||
                                CCG CGCCGCG GC CT  CCGG
                                  C      C  G  __
GAM1178 LOC153546 5' GCAGCGGCGCACCGAGGC    30646         GA  TC
                                GCAGCGGCGCAC  GA  GGC
                                ||||||||||||  ||  |||
                                CGTCGCCGCGTG  CT  CCG
                                     G_  __
GAM1178 LOC202781 3' GCAGCGGCGCGATCTCGGC   30638        AC  GA
                                GCAGCGGCGC  GA  TCGGC
                                |||||||||  ||  |||||
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                                CGTCGCCGCG  CT  AGCCG
                                     __  AG
GAM1178  LOC220662 3'  TGTAGCGGCGCAATCTTGGC  30647   GC      CGAG  __
                                TG  AGCGGCGCA   ATC  GGC
                                ||  |||||||||   |||  |||
                                AC  TCGCCGCGT   TAG  CCG
                                 A_       ____   AA
GAM1178  LOC253216 3'  TGGCAGCGGCGGGCAGGC   30648        CA  AGATC
                                TGGCAGCGGCG  CG   GGC
                                ||||||||||  ||    |||
                                ACCGTCGCCGC  GT   CCG
                                     CC  _____
GAM1178  LOC254986 5'  GGCAGCGGCGCGCAGGC    30644        A  AGATC
                                GGCAGCGGCGC CG    GGC
                                ||||||||||| ||    |||
                                CCGTCGCCGCG GT    CCG
                                     C  _____
GAM1178  LOC91035  5'  TGGCAGCGGGGGCAGTTGGC  30649       C_  CGAGATC
                                TGGCAGCGG  GCA     GGC
                                |||||||||  |||     |||
                                ACCGTCGCC  CGT     CCG
                                     CC   CAA____
GAM1178  LOC95702  3'  TGGCAGCGGCGGGCAGGC   30648        CA  AGATC
                                TGGCAGCGGCG  CG   GGC
                                ||||||||||  ||    |||
                                ACCGTCGCCGC  GT   CCG
                                     CC  _____
GAM1179  GALE     3'  TGCTGCTTTTCCTGGTCCTT  30652        C   ACGAA
                                TGTTGCTTT CCTG    CCTT
                                |||||||||  ||||    ||||
                                ACGACGAAA GGAC    GGAA
                                     A   CA___
GAM1179  LY64     3'  TTGCTTTCTCTGGAAACCTTC  30653       C   AC
                                TTGCTTTC CTG  GAACCTTC
                                ||||||||  |||  ||||||||
                                AACGAAAG GAC  TTTGGAAG
                                     A   C_
GAM1179  PABPN1   5'  TGTTGTTTCCTTCCACTCTTC  30654      C    C GA  AAC
                                TGTTG TTTCC T  CG   CTTC
                                |||||  |||||  |  ||   ||||
                                ACAAC AAAGG A  GT   GAAG
                                  _    _ AG  GA_
GAM1179  PCSK2    3'  TGTGCTTTCCTCACAGAGGTCT 30655    T      C G  _  AC_
            TC                    TGT GCTTTCC T AC GA   CTTC
                                |||  |||||||  |  ||  ||   ||||
                                ACA CGAAAGG A TG CT   GAAG
                                  _      _ G  T  CCA
GAM1179  SLC22A12  3'  TTGCTTTCCTCCTGCCTT    30656         _  GACGAA
                                TTGCTTTCC CT     CCTT
                                |||||||||  ||     ||||
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                                AACGAAAGG GG     GGAA
                                     A  AC____
GAM1179  TIRAP    3'  TGTTGCTTTCTCCTGATGCCCA 30657          _    CGAA  _
             TTC                   TGTTGCTTTC CCTGA   CC TTC
                                   |||||||||| |||||   || |||
                                   ACAACGAAAG GGACT   GG AAG
                                        A    ACG_  T
GAM1179  KIAA0417 3'  TGTCGCTTTCTTGCAA     30658         CC  A
                                   TGTTGCTTTC  TG CGA
                                   |||||||||  || |||
                                   ACAGCGAAAG  AC GTT
                                        A_  _
GAM1179  KIAA1095 3'  TTGCTTTCTGCTAAAACCTT  30659       C_   CG
                                   TTGCTTTC  CTGA  AACCTT
                                   ||||||||  ||||  ||||||
                                   AACGAAAG  GATT  TTGGAA
                                        AC   __
GAM1179  KIAA1271 3'  TGTTGCCTTTTTGAGATACTT  30660        CCC   C  AC
                                   TGTTGCTTT   TGA GA  CTT
                                   |||||||||   ||| ||  |||
                                   ACAACGGAA   ACT CT  GAA
                                        AA_   _  AT
GAM1179  MGC15396 3'  TGTGCTTTCCCGAGTCTT    30661     T      TGAC  AC
                                   TGT GCTTTCCC    GA  CTT
                                   ||| ||||||||    ||  |||
                                   ACA CGAAAGGG    CT  GAA
                                     _       _____  CA
GAM1179  RIL      3'  TGTTCTTTTCTTTCTAAACCTT 30662      G   CC  GAC_
             C                      TGTT CTTT  CT    GAACCTTC
                                   |||| ||||  ||    ||||||||
                                   ACAA GAAA  GA    TTTGGAAG
                                     _    A_  AAGA
GAM1179  RNPS1    3'  TTGCTTTCCTACTGGTCTTC   30663        CTG  GAAC
                                   TTGCTTTCC   AC    CTTC
                                   |||||||||   ||    ||||
                                   AACGAAAGG   TG    GAAG
                                        A__  ACCA
GAM1179  RNPS1    3'  TTGCTTTCCTACTGGTCTTC   30663        CTG  GAAC
                                   TTGCTTTCC   AC    CTTC
                                   |||||||||   ||    ||||
                                   AACGAAAGG   TG    GAAG
                                        A__  ACCA
GAM1179  LOC132720 3'  TGTTATTTTCCCTGTTCACTTT 30664      C       ACGA  C
             C                      TGTTG TTTCCCTG    AC TTC
                                   ||||| ||||||||    || |||
                                   ACAAT AAAGGGAC    TG AAG
                                     A       AAG_  A
GAM1179  LOC143188 5'  TGTTGCTTTTGTTCCTTATGAT 30665         _____  C__   C
             GA                     TGTTGCTT    TCC   TGA GA
                                   ||||||||    |||   ||| ||
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                                ACAACGAA   AGG   ACT CT
                                    AACA   AAT   A
GAM1179  LOC144455 3'  TGTTGCCTTTCCTGAAATCTCT 30666        C    CGAAC
             TC                   TGTTGCTTT CCTGA    CTTC
                                  ||||||||| |||||    ||||
                                  ACAACGGAA GGACT    GAAG
                                      A    TTAGA
GAM1179  LOC145945 5'  TGTTACTTTTCCTATTGTCTTC 30667        C   ACGAAC
                                  TGTTGCTTT CCTG     CTTC
                                  ||||||||| ||||     ||||
                                  ACAATGAAA GGAT     GAAG
                                      A   AACA__
GAM1179  LOC147741 3'  TGTTACTTTCTCCTGTGAA   30668         _   AC
                                  TGTTGCTTTC CCTG  GAA
                                  |||||||||| ||||  |||
                                  ACAATGAAAG GGAC  CTT
                                      A   A_
GAM1179  LOC153910 3'  TGTTGTATTCCCTGATGGAA   30669      CT      C_
                                  TGTTG  TTCCCTGA  GAA
                                  |||||  ||||||||  |||
                                  ACAAC  AAGGGACT  CTT
                                     AT       AC
GAM1179  LOC201382 5'  TGTGCTTTCCTGGGGTCTT   30670     T     C  ACGAAC
                                  TGT GCTTTCC TG     CTT
                                  ||| ||||||| ||     |||
                                  ACA CGAAAGG AC     GAA
                                    _     _ CCCA__
GAM1179  LOC222136 3'  TGCTGCTTTCTCTGACTGCATC 30671        C    GAAC_
             TTC                  TGTTGCTTTC CTGAC    CTTC
                                  |||||||||| |||||    ||||
                                  ACGACGAAAG GACTG    GAAG
                                      A    ACGTA
GAM1179  LOC257415 3'  TGTTGCTTTTTCTCGTTCTTC  30672        CC  GA  AAC
                                  TGTTGCTTT  CT  CG   CTTC
                                  |||||||||  ||  ||   ||||
                                  ACAACGAAA  GA  GC   GAAG
                                      AA  __  AA_
GAM1179  LOC91947  3'  TGTTGCTTTTCTAGATGGAAC  30673        CC  _  C_
                                  TGTTGCTTT  CT GA  GAAC
                                  |||||||||  || ||  ||||
                                  ACAACGAAA  GA CT  CTTG
                                      A_  T  AC
GAM1180  CLECSF5   3'  GGAGTTAGGAGGGGCAT    30676        AAAAA  A_
                                  GGGGTTAG    GAG  GCGT
                                  ||||||||    |||  ||||
                                  CCTCAATC    CTC  CGTA
                                      _____  CC
GAM1180  COX10    5'  CGGGCTCCGAAAGGAGAGCGT  30677     G  A   AA
                                  CGGG TT GAAA  GAGAGCGT
                                  |||| || ||||  ||||||||
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                                GCCC AG CTTT  CTCTCGCA
                                  G G   C_
GAM1180  ESPN     3'  CACGGGGCTGGGGAGAGC    30678        AGAAAAA
                                CACGGGGTT     GAGAGC
                                |||||||||     ||||||
                                GTGCCCCGA     CTCTCG
                                    CCC____
GAM1180  LIMK1    3'  CACGGGGTGGGAGAAGGCA   30679       TA  AAAA  A
                                CACGGGGT  GA   GAG GCG
                                ||||||||  ||   ||| |||
                                GTGCCCCA  CT   TTC CGT
                                    CC  C___  _
GAM1180  LIMK1    3'  CACGGGGTGGGAGAAGGCA   30679       TA  AAAA  A
                                CACGGGGT  GA   GAG GCG
                                ||||||||  ||   ||| |||
                                GTGCCCCA  CT   TTC CGT
                                    CC  C___  _
GAM1180  MX1      3'  ACGGGGCTGGACAGAGG     30680       A  AAAAG   C
                                ACGGGGTT GA    AGAG G
                                |||||||| ||    |||| |
                                TGCCCCGA CT    TCTC C
                                    C  G____   A
GAM1180  MYO3A    3'  CGGGAGTTCCGAGAGAGAGCGT 30681     _  A_  AAA
                                CGGG GTT  GA  AGAGAGCGT
                                |||| |||  ||  |||||||||
                                GCCC CAA  CT  TCTCTCGCA
                                  T  GG  C__
GAM1180  PAX2     3'  CGGCGGTCCCGGGAGAGCGT  30682    _   AGAAAAA
                                CGG GGTT     GAGAGCGT
                                ||| ||||     ||||||||
                                GCC CCAG     CTCTCGCA
                                  G   GGCC___
GAM1180  PAX2     3'  CGGCGGTCCCGGGAGAGCGT  30682    _   AGAAAAA
                                CGG GGTT     GAGAGCGT
                                ||| ||||     ||||||||
                                GCC CCAG     CTCTCGCA
                                  G   GGCC___
GAM1180  BICD2    3'  ACGGGAGAAAAGAGAGCG    30683     GTT    A
                                ACGGG  AGAAAA GAGAGCG
                                |||||  |||||| |||||||
                                TGCCC  TCTTTT CTCTCGC
                                   ___    _
GAM1180  FLJ10101 3'  GGGGTTAGGAGGGAGACCCGT 30684       AAAAA   G_
                                GGGGTTAG    GAGA  CGT
                                ||||||||    ||||  |||
                                CCCCAATC    CTCT  GCA
                                    CTCC_   GG
GAM1180  FLJ11726 3'  GGGACCAGAAAAGAGAGTGT  30685    GT     A    C
                                GGG  TAGAAAA GAGAG GT
                                |||  ||||||| ||||| ||
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                                CCC  GTCTTTT CTCTC CA
                                  TG     _    A
GAM1180  FLJ32499  5'  CGGGAGCCGAGGGGAGAGCGT  30686     _  A  AAAA
                                CGGG GTT GA   GAGAGCGT
                                |||| ||| ||   ||||||||
                                GCCC CGG CT   CTCTCGCA
                                  T  _ CCC_
GAM1180  HSJ1      3'  CGGGGTGACAGGAGAGAGCGT  30687      TA  AAA_
                                CGGGGT  GA   AGAGAGCGT
                                ||||||  ||   |||||||||
                                GCCCCA  CT   TCTCTCGCA
                                   __ GTCC
GAM1180  HTR3A     3'  GGGGTTAGAGAAGCCTCGT   30688        AA   AGAG
                                GGGGTTAGA  AAG   CGT
                                |||||||||  |||   |||
                                CCCCAATCT  TTC   GCA
                                     C_  GGA_
GAM1180  KIAA0447  3'  CAGGGCCATGGAGGAGGGCGT  30689       GAAAAA  A
                                CGGGGTTA    GAG GCGT
                                ||||||||    ||| ||||
                                GTCCCGGT    CTC CGCA
                                    ACCTC_  C
GAM1180  MGC15429  3'  GGGAGAGAAGAGAGAGCGT   30690    TT   AA
                                GGG  AGAA  AGAGAGCGT
                                |||  ||||  |||||||||
                                CCC  TCTT  TCTCTCGCA
                                  TC   C_
GAM1180  RPH3A     3'  CGGAAAGAGGAGAGCG     30691      TT   AAAA
                                CGGGG  AGA   GAGAGCG
                                |||||  |||   |||||||
                                GCCTT  TCT   CTCTCGC
                                   __  C___
GAM1180  SMOC2     3'  GGGGTTAGAGAAAGC      30692        AAAA
                                GGGGTTAGA   GAGAGC
                                |||||||||   ||||||
                                CCCCAATCT   CTTTCG
                                     ____
GAM1180  SYT12     3'  CACTGGGTTAGAGAAAG    30693    G      AAAA
                                CAC GGGTTAGA   GAGAG
                                ||| ||||||||   |||||
                                GTG CCCAATCT   CTTTC
                                  A      ____
GAM1180  THEG      3'  CACAGGGTTAGGGTGCCTGAGG 30694          AAAAAGA  C
            GT                   CACGGGGTTAG     GAG GT
                                ||||||||||      ||| ||
                                GTGTCCCAATC     CTC CA
                                      CCACGGA  C
GAM1180  LOC129446 3'  CACGGTGTTAGAAAAGAAAAAG 30695      G       _    C
            TGT                   CACGG GTTAGAAAA AGAGAG GT
                                ||||| |||||||| |||||| ||
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                                GTGCC CAATCTTTT TTTTTC CA
                                   A       C     A
GAM1180  LOC144747 5'  CACGGGGCTTAGAGAGAA    30696         _  AAAA
                                CACGGGGTT AGA    GAGAG
                                ||||||||| |||    |||||
                                GTGCCCCGA TCT    CTCTT
                                    A  _____
GAM1180  LOC150135 3'  GGGATCAGGGGAGGAGAGTGT  30697        AAAAA    C
                                GGGGTTAG    GAGAG GT
                                ||||||||    ||||| ||
                                CCCTAGTC    CTCTC CA
                                    CCCTC    A
GAM1180  LOC170221 3'  GGGGATGGAAAGAAAATGAGGC 30698     TT____     A  A
            GT                    GGGG     AGAAAA GAG GCGT
                                ||||     |||||| ||| ||||
                                CCCC     TCTTTT CTC CGCA
                                  TACCTT     A  _
GAM1180  LOC200169 3'  CGGGGTTATTATGGAGAGTGT  30699        GAAAAA    C
                                CGGGGTTA     GAGAG GT
                                ||||||||     ||||| ||
                                GCCCCAAT     CTCTC CA
                                    AATAC_    A
GAM1180  LOC200720 5'  CACAGGGTTGGAGAGGCA    30700        A  AAAA  A
                                CACGGGGTT GA   GAG GCG
                                ||||||||| ||   ||| |||
                                GTGTCCCAA CT   CTC CGT
                                    C  _____  _
GAM1180  LOC253291 3'  GGAGCCAGGAAGAGAGTGT   30701        AAA      C
                                GGGGTTAG   AAGAGAG GT
                                ||||||||   ||||||| ||
                                CCTCGGTC   TTCTCTC CA
                                    C__      A
GAM1180  LOC91461  3'  CACAGGGTTGGAGAGGCA    30700        A  AAAA  A
                                CACGGGGTT GA   GAG GCG
                                ||||||||| ||   ||| |||
                                GTGTCCCAA CT   CTC CGT
                                    C  _____  _
GAM1181  D10S170   3'  TAGTATTTTCTAATGGTATT   30704          AATTT
                                TAGTATTTTCTAA    GTATT
                                ||||||||||||    |||||
                                ATCATAAAAGATT    CATAA
                                      AC___
GAM1181  PLA2R1    3'  TAGTATTTTCCAAATCCTGC   30705           A
                                TAGTATTTTCTAAA TTTGT
                                |||||||||||||| |||||
                                ATCATAAAAGGTTT GGACG
                                      A
GAM1181  COLEC10   3'  TAGCATTTTCTAGCTATGT   30706          AAATT
                                TAGTATTTTCTA    TGT
                                ||||||||||||    |||
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                                ATCGTAAAAGAT    ACA
                                      CGAT_
GAM1181  ENAH    3'  TAGTATTTTCTGCATAACTGT  30707         AAAAT_
                                TAGTATTTTCT     TTGT
                                ||||||||||     ||||
                                ATCATAAAAGA     GACA
                                      CGTATT
GAM1181  JDD1    3'  TAGTATTTCCTAGAAAGCACT  30708         AAATTT
                                TAGTATTTTCTA    GTATT
                                ||||||||||||    |||||
                                ATCATAAAGGAT    CGTGA
                                      CTTT__
GAM1181  PMFBP1  5'  TAGTATTTTCTGAGCTTTGT  30709         AAAA
                                TAGTATTTTCT   TTTGT
                                ||||||||||   |||||
                                ATCATAAAAGA   AAACA
                                      CTCG
GAM1181  ZFD25   3'  GTATTTTCTAAGCTGTA    30710         AAT
                                GTATTTTCTAA   TTGTA
                                ||||||||||   |||||
                                CATAAAAGATT   GACAT
                                      C__
GAM1181  LOC197273 3'  ATATTTTCTAATTCCTGT    30711         AA
                                GTATTTTCTAA  TTTGT
                                ||||||||||  |||||
                                TATAAAAGATT  GGACA
                                      AA
GAM1181  LOC50999  3'  TAGTATTTTTAAAATTTG    30712        C
                                TAGTATTTT TAAAATTTG
                                ||||||||| |||||||||
                                ATCATAAAA ATTTTAAAC
                                          _
GAM1182  ADCY6   3'  AAGCTGTCAGAGGTCCCTTTGT 30715        T    AAGGG
           T                     AAGCTGTC GAGGTT    TGTT
                                ||||||||| ||||||    ||||
                                TTCGACAG CTCCAG    ACAA
                                     T     GGAA_
GAM1182  ADCY6   3'  AAGCTGTCAGAGGTCCCTTTGT 30715        T    AAGGG
           T                     AAGCTGTC GAGGTT    TGTT
                                ||||||||| ||||||    ||||
                                TTCGACAG CTCCAG    ACAA
                                     T     GGAA_
GAM1182  ICOS    3'  AAGCTGGTTGCAAGAGGGTGTT 30716       TC  _  TTA
                                AAGCTG  TG AGG   AGGGTGTT
                                ||||||  || |||   ||||||||
                                TTCGAC  AC TTC   TCCCACAA
                                   CA  G  ___
GAM1182  TRIM9   3'  GCTGTCTAGGTCCTTTGTT   30717        G    AAGGG
                                GCTGTCT AGGTT    TGTT
                                |||||||  |||||    ||||
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                                CGACAGA TCCAG    ACAA
                                   _    GAA__
GAM1182  FLJ31951  3'  AAGTTGCTGAGGTTGAAT   30718    C  T      AA
                                AAG TG CTGAGGTT  GGGT
                                ||| || ||||||||  ||||
                                TTC AC GACTCCAA  CTTA
                                  A  _       __
GAM1182  KIAA0889  3'  AAGCTGCTGAGGTTGTCAGGT  30719       T      AA_
                                AAGCTG CTGAGGTT   GGGT
                                ||||||| ||||||||   ||||
                                TTCGAC GACTCCAA   TCCA
                                   _       CAG
GAM1182  KIAA1870  5'  GCTGTCTGGGGCTAGGC    30720        A    AA
                                GCTGTCTG GGTT  GGGT
                                |||||||| ||||  ||||
                                CGACAGAC CCGA  TCCG
                                     C   __
GAM1182  SMARCF1   3'  AGCTGACTGAGGTTGAAGGT   30721      T      A
                                AGCTG CTGAGGTT AGGGT
                                ||||| |||||||| |||||
                                TCGAC GACTCCAA TTCCA
                                   T       C
GAM1182  LOC145368 5'  AAGCTGTCTATCTTGGGTGTT  30722        GAG   AA
                                AAGCTGTCT   GTT  GGGTGTT
                                |||||||||   |||  |||||||
                                TTCGACAGA   TAG  CCCACAA
                                      ___   AA
GAM1182  LOC146923 3'  AGCTTGTCTGGGGTTAGGG   30723     _    A    A
                                AGCT GTCTG GGTTA GGG
                                |||| ||||| ||||| |||
                                TCGA CAGAC CCAAT CCC
                                  A    C    _
GAM1182  LOC149460 3'  AGTGTCTGGGGTTGGAGC    30724    C     A    AA
                                AG TGTCTG GGTT  GGGT
                                || |||||| ||||  ||||
                                TC ACAGAC CCAA  CTCG
                                 _     C   C_
GAM1182  LOC150423 5'  AAGCTGTCTACCTTGGGTGTT  30725         AGGTTAA
                                AAGCTGTCTG      GGGTGTT
                                ||||||||||      |||||||
                                TTCGACAGAT      CCCACAA
                                     GGAA___
GAM1182  LOC157273 3'  AGCTATCTGGGGTTCTGT    30726        A   AAGG
                                AGCTGTCTG GGTT   GT
                                ||||||||| ||||   ||
                                TCGATAGAC CCAA   CA
                                     C   GA__
GAM1182  LOC54466  5'  AGCTGTCTGGGGTTAGGA    30727         A    A
                                AGCTGTCTG GGTTA GGG
                                ||||||||| ||||| |||
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                                TCGACAGAC CCAAT CCT
                                    C    _
GAM1182 LOC90072 3' AAGCTGCTGAGGTTGTCAGGT 30719      T      AA_
                                AAGCTG CTGAGGTT   GGGT
                                |||||| ||||||||   ||||
                                TTCGAC GACTCCAA   TCCA
                                   _      CAG
GAM1183 ABCA2    3' TCTGTGCGCTATGTACAG    30730        A   C
                                TCTGTGCGT GTGT CAG
                                ||||||||| |||| |||
                                AGACACGCG TACA GTC
                                    A   T
GAM1183 ABCA2    3' TCTGTGCGCTATGTACAG    30730        A   C
                                TCTGTGCGT GTGT CAG
                                ||||||||| |||| |||
                                AGACACGCG TACA GTC
                                    A   T
GAM1183 ABCC5    3' TCTGTGCAGTGGCCAG      30731       GT   T
                                TCTGTGC  AGTG CCAG
                                |||||||  |||| ||||
                                AGACACG  TCAC GGTC
                                   __   C
GAM1183 ADAM19   3' CCTCTGCAGTGTCCAG      30732     G  GT
                                TCT TGC  AGTGTCCAG
                                ||| |||  |||||||||
                                GGA ACG  TCACAGGTC
                                  G  __
GAM1183 ALDOC    5' CCTGTGCGCAGCCAG       30733         TGT
                                TCTGTGCGTAG   CCAG
                                ||||||||||   ||||
                                GGACACGCGTC   GGTC
                                      ___
GAM1183 ALPP     3' TCTATGCCCAGTGTCCAG    30734       G
                                TCTGTGC TAGTGTCCAG
                                ||||||| ||||||||||
                                AGATACG GTCACAGGTC
                                    G
GAM1183 DLX2     3' TCTGTGTCCAAGTCCAG     30735      CG  T
                                TCTGTG  TAG GTCCAG
                                ||||||  ||| ||||||
                                AGACAC  GTT CAGGTC
                                   AG  _
GAM1183 EBAF     3' TCTATGCACACGTTCAG     30736        G  C
                                TCTGTGCGTA TGT CAG
                                |||||||||| ||| |||
                                AGATACGTGT GCA GTC
                                      _  A
GAM1183 EFNB1    3' CTGTCCATCAGTGTCCAG    30737     G  _
                                CTGT CGT AGTGTCCAG
                                |||| ||| |||||||||
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                                GACA GTA TCACAGGTC
                                  G   G
GAM1183  EPHB6    3'  TCTCGGACCAGTGTCCAG    30738    _ TG G
                                TCT G  C TAGTGTCCAG
                                ||| |  | ||||||||||
                                AGA C  G GTCACAGGTC
                                  G CT _
GAM1183  FGFRL1   3'  TCTGTGTGTGTGTCCAG     30740       C  A
                                TCTGTG GT GTGTCCAG
                                |||||| || ||||||||
                                AGACAC CA CACAGGTC
                                   A  _
GAM1183  FGFRL1   3'  CTGTGTGTGTGTGTCCAG    30739      C  A_
                                CTGTG GT  GTGTCCAG
                                ||||| ||  ||||||||
                                GACAC CA  CACAGGTC
                                   A  CA
GAM1183  FMN2     5'  TCTGTAGTAATTCCAG      30741       C    G
                                TCTGTG GTAGT TCCAG
                                |||||| ||||| |||||
                                AGACAT CATTA AGGTC
                                   _    _
GAM1183  FTSJ2    3'  TCTGTGCGTGGTGCTCTCAG   30742         A  _ _
                                TCTGTGCGT GTG TC CAG
                                ||||||||| ||| || |||
                                AGACACGCA CAC AG GTC
                                     C   G  A
GAM1183  HF1      5'  TCTGTTCACAACGTCCAG    30743      G
                                TCTGT CGTAGTGTCCAG
                                ||||| ||||||||||||
                                AGACA GTGTTGCAGGTC
                                   A
GAM1183  INSRR    5'  TCTGAGCGAATATCCAG     30744      T   T
                                TCTG GCG AGTGTCCAG
                                |||| ||| |||||||||
                                AGAC CGC TTATAGGTC
                                  T   _
GAM1183  IRS1     3'  TCTGCTGTGATGTCCAG     30745      GC  A
                                TCTGT  GT GTGTCCAG
                                |||||  || ||||||||
                                AGACG  CA TACAGGTC
                                   A_  C
GAM1183  LPP      5'  TCTGATGAGCGTCCAG      30746     _  CGT
                                TCTG TG   AGTGTCCAG
                                |||| ||   |||||||||
                                AGAC AC   TCGCAGGTC
                                  T  ____
GAM1183  LRPAP1   3'  TCTGTGCATGGTATTTCC    30747         A  __
                                TCTGTGCGT GTG  TCC
                                ||||||||| |||  |||
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                                AGACACGTA CAT  AGG
                                     C   AA
GAM1183  MEL     3'  TCTTGGCCATGTCCAG      30748     G  C  A
                                TCT TG GT GTGTCCAG
                                ||| || || ||||||||
                                AGA AC CG TACAGGTC
                                  _ _  G
GAM1183  MSR1    3'  TCCGTGCATGAGAGGTGTCCAG 30749          A____
                                TCTGTGCGT    GTGTCCAG
                                |||||||||    ||||||||
                                AGGCACGTA    CACAGGTC
                                     CTCTC
GAM1183  MYLK2   3'  CTGTGTGGCTGCGTCCAG    30750       C_  A
                                CTGTG  GT GTGTCCAG
                                |||||  || ||||||||
                                GACAC  CG CGCAGGTC
                                   AC  A
GAM1183  NRIP1   3'  TCTATACATTTGTCCAG     30751         AG
                                TCTGTGCGT  TGTCCAG
                                |||||||||  |||||||
                                AGATATGTA  ACAGGTC
                                     A_
GAM1183  NUMA1   5'  TCTGTGCAGATACCAG      30752         TA   T
                                TCTGTGCG  GTG CCAG
                                ||||||||  ||| ||||
                                AGACACGT  TAT GGTC
                                     C_   _
GAM1183  OCA2    3'  TCTGTAGCATCTCCAG      30753        C   G G
                                TCTGTG GTA T TCCAG
                                |||||| ||| | |||||
                                AGACAT CGT A AGGTC
                                   _   _ G
GAM1183  PML     3'  CTGTCAGCAGGTGTCCAG    30754       GC   _
                                CTGT  GTAG TGTCCAG
                                ||||  |||| |||||||
                                GACA  CGTC ACAGGTC
                                  GT    C
GAM1183  SLC12A7 3'  TCTGGCCACGTCCAG       30755      T  G  G
                                TCTG GC TA TGTCCAG
                                |||| || || |||||||
                                AGAC CG GT GCAGGTC
                                   _ _ _
GAM1183  TNFRSF8 3'  TCTGGCCAATGTCCAG      30756      T  G
                                TCTG GC TAGTGTCCAG
                                |||| || ||||||||||
                                AGAC CG GTTACAGGTC
                                   _ _
GAM1183  UBE2G2  3'  CCTGTGCGAGGCCAG       30757         T  T T
                                TCTGTGCG AG G CCAG
                                |||||||| || | ||||
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                                GGACACGC TC C GGTC
                                   _ _ _
GAM1183 ZNF26    5' TCTGTGTAGAATCCAG      30758      GC   T
                                TCTGT  GTAG GTCCAG
                                |||||  |||| ||||||
                                AGACA  CATC TAGGTC
                                   __    T
GAM1183 C1orf9   3' TCTGTGCATATGTATGCAG   30759         _   C
                                TCTGTGCGTA GTGT CAG
                                |||||||||| |||| |||
                                AGACACGTAT CATA GTC
                                      A    C
GAM1183 C6orf32  5' TCTGGTAGTACATCCAG     30760     TGC    __
                                TCTG   GTAGT  GTCCAG
                                ||||   |||||  ||||||
                                AGAC   CATCA  TAGGTC
                                   ___     TG
GAM1183 CLDN1    3' TGTGCGTAGGTTTTGTTCAG  30761         ____   C
                                TGTGCGTAG    TGT CAG
                                |||||||||    ||| |||
                                ACACGCATC    ACA GTC
                                      CAAA   A
GAM1183 CLIPR-59 3' TCTTTGTCAGGTGTCCAG    30762     G _ TA
                                TCT TG CG  GTGTCCAG
                                ||| || ||  ||||||||
                                AGA AC GT  CACAGGTC
                                  A  A  C_
GAM1183 COL21A1  5' CCTGGCGCAGTGTCCAG     30763      T
                                TCTG GCGTAGTGTCCAG
                                |||| ||||||||||||
                                GGAC CGCGTCACAGGTC
                                   _
GAM1183 CSR1     3' TCTGTGAGTGTCCAG       30764       CGT
                                TCTGTG   AGTGTCCAG
                                ||||||   |||||||||
                                AGACAC   TCACAGGTC
                                   ___
GAM1183 CTPS2    3' TCTGTGGCTGAGTTCCAG    30765       C __   G
                                TCTGTG GT  AGT TCCAG
                                |||||| ||  ||| |||||
                                AGACAC CG  TCA AGGTC
                                   _ AC  _
GAM1183 CYP2S1   3' TCTGTGCATAATCGCAG     30766         GT  _
                                TCTGTGCGTA  GTC CAG
                                ||||||||||  ||| |||
                                AGACACGTAT  TAG GTC
                                      __   C
GAM1183 DKFZP547L112 5' TCTAGTGCAGGTGTCCAG    30767     _    TA
                                TCT GTGCG  GTGTCCAG
                                ||| |||||  ||||||||
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                                AGA CACGT  CACAGGTC
                                  T    C_
GAM1183  DKFZP667O116 5'  TCCGTGTGTACATCCAG     30768       C   G
                                TCTGTG GTA TGTCCAG
                                ||||||| ||| |||||||
                                AGGCAC CAT GTAGGTC
                                   A   _
GAM1183  FLJ11117  3'  TCCGCCATGTGTCCAG      30769      G   A
                                TCTGT CGT GTGTCCAG
                                ||||| ||| ||||||||
                                AGGCG GTA CACAGGTC
                                  _   _
GAM1183  FLJ12592  5'  TCTGTGGTAGTACAG       30770       C     TC
                                TCTGTG GTAGTG  CAG
                                |||||| ||||||  |||
                                AGACAC CATCAT  GTC
                                  _     ___
GAM1183  FLJ13909  5'  CTGTGCGCAGGCGTCCAG    30771          _
                                CTGTGCGTAG TGTCCAG
                                |||||||||| |||||||
                                GACACGCGTC GCAGGTC
                                     C
GAM1183  FLJ14166  3'  TCAGTGGTCTGTGTCCAG    30772    T   C  A_
                                TC GTG GT  GTGTCCAG
                                || ||| ||  ||||||||
                                AG CAC CA  CACAGGTC
                                 T   _  GA
GAM1183  FLJ20294  3'  TCTGGGCGTAGTATGCAG    30773     T       C
                                TCTG GCGTAGTGT CAG
                                |||| ||||||||| |||
                                AGAC CGCATCATA GTC
                                  C        C
GAM1183  HCBP6     3'  CCTGTGCACCATCCAG      30774        TAG
                                TCTGTGCG   TGTCCAG
                                ||||||||   |||||||
                                GGACACGT   GTAGGTC
                                     G___
GAM1183  HEMK      3'  TCTGGGCTCAACGTCCAG    30775     T  G
                                TCTG GC TAGTGTCCAG
                                |||| || ||||||||||
                                AGAC CG GTTGCAGGTC
                                  C  A
GAM1183  IKKE      5'  TCTGTGGCACGTCCAG      30776       C   G
                                TCTGTG GTA TGTCCAG
                                |||||| ||| |||||||
                                AGACAC CGT GCAGGTC
                                  _   _
GAM1183  KCNT1     3'  CCCGGCGTGGTGTCCAG     30777      T    A
                                TCTG GCGT GTGTCCAG
                                |||| |||| ||||||||
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                                GGGC CGCA CACAGGTC
                                  _   C
GAM1183 KIAA0218 3' TCCGAGATAGGTGTCCAG   30778     TGC   _
                                TCTG  GTAG TGTCCAG
                                ||||  |||| |||||||
                                AGGC  TATC ACAGGTC
                                  TC_   C
GAM1183 KIAA0493 5' TCTGTGATATATCCAG     30779      C   G
                                TCTGTG GTA TGTCCAG
                                |||||| ||| |||||||
                                AGACAC TAT ATAGGTC
                                  _  _
GAM1183 KIAA0556 3' TCTGGTAGTATCCAG      30780     TGC
                                TCTG  GTAGTGTCCAG
                                ||||  ||||||||||
                                AGAC  CATCATAGGTC
                                  ___
GAM1183 KIAA0705 3' TCTATGCGTGTGACAG     30781       A   TC
                                TCTGTGCGT GTG  CAG
                                ||||||||| |||  |||
                                AGATACGCA CAC  GTC
                                     _  T_
GAM1183 KIAA0884 5' TCTGTGTGTTCATCCAG    30782      C  AG
                                TCTGTG GT  TGTCCAG
                                |||||| ||  |||||||
                                AGACAC CA  GTAGGTC
                                   A  A_
GAM1183 KIAA1118 3' TCTGGGCCCACGTCCAG    30783     T  G  G
                                TCTG GC TA TGTCCAG
                                |||| || || |||||||
                                AGAC CG GT GCAGGTC
                                  C  G  _
GAM1183 KIAA1357 3' TCTGTGCATTAAGAACCAG  30784        __ TGT
                                TCTGTGCGT  AG   CCAG
                                |||||||||  ||   ||||
                                AGACACGTA  TC   GGTC
                                     AT  TT_
GAM1183 KIAA1399 3' TCTGTGCATGTGCCAA     30785       A   T
                                TCTGTGCGT GTG CCAG
                                ||||||||| ||| ||||
                                AGACACGTA CAC GGTT
                                     _  _
GAM1183 KIAA1466 3' TGTGCGTAGACTGACCAG   30786       __  T
                                TGTGCGTAG  TG CCAG
                                |||||||||  || ||||
                                ACACGCATC  AC GGTC
                                     TG  T
GAM1183 KIAA1582 5' TCTTGGTATGTCCAG      30787    G  C   G
                                TCT TG GTA TGTCCAG
                                ||| || ||| |||||||
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                                AGA AC CAT ACAGGTC
                                  _ _  _
GAM1183  MGC15737  5'  TCTGCGCGGGCGCCAG     30788        TA   T
                                TCTGTGCG  GTG CCAG
                                ||||||||  ||| ||||
                                AGACGCGC  CGC GGTC
                                    C_  _
GAM1183  MGC3222   5'  CTGGAGCGTGGTGTCCAG    30789     T_   A
                                CTG  GCGT GTGTCCAG
                                |||  |||| ||||||||
                                GAC  CGCA CACAGGTC
                                  CT   C
GAM1183  MGC4737   5'  TCTGCTGTCTGTGTCCAG    30790      GC  A_
                                TCTGT  GT  GTGTCCAG
                                |||||  ||  ||||||||
                                AGACG  CA  CACAGGTC
                                   A_  GA
GAM1183  NETO1     5'  TCTGTGCGTTACACCAG     30791        AG  T
                                TCTGTGCGT  TG CCAG
                                |||||||||  || ||||
                                AGACACGCA  GT GGTC
                                     AT  _
GAM1183  NIR3      3'  TCAGTGCGTGTGCCCAG     30792    T     A
                                TC GTGCGT GTGTCCAG
                                || |||||| ||||||||
                                AG CACGCA CACGGGTC
                                 T     _
GAM1183  NXPH3     3'  CCTGCCCGGTGTCCAG      30793      G  TA
                                TCTGT CG  GTGTCCAG
                                ||||| ||  ||||||||
                                GGACG GC  CACAGGTC
                                   G  __
GAM1183  PRO1163   5'  TCTATACAACATGGTGTCCAG  30794        TA___
                                TCTGTGCG    GTGTCCAG
                                ||||||||    ||||||||
                                AGATATGT    CACAGGTC
                                     TGTAC
GAM1183  RAB34     3'  TCAGTGCAAATGTCCAG     30795    T    T
                                TC GTGCG AGTGTCCAG
                                || ||||| |||||||||
                                AG CACGT TTACAGGTC
                                 T    _
GAM1183  TXI1      5'  TCTGTGCCCAGGTCCAG     30796       G   T
                                TCTGTGC TAG GTCCAG
                                ||||||| ||| ||||||
                                AGACACG GTC CAGGTC
                                    G  _
GAM1183  LOC118672 5'  TCCGTGCGGCCCCAG       30797        TA  G
                                TCTGTGCG  GT TCCAG
                                ||||||||  || |||||
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                                AGGCACGC  CG GGGTC
                                   __  _
GAM1183  LOC122970 5'  TCTGTACGTCCCGCTTCAG   30798        AG   C_
                                TCTGTGCGT  TGT  CAG
                                |||||||||  |||  |||
                                AGACATGCA  GCG  GTC
                                     GG   AA
GAM1183  LOC125268 3'  CCTGTGCGAGGCCAG      30757        T  T T
                                TCTGTGCG AG G CCAG
                                |||||||| || | ||||
                                GGACACGC TC C GGTC
                                   _ _ _
GAM1183  LOC131583 5'  TCCGAGGCGGTGTCCAG    30799     T_   TA
                                TCTG  GCG  GTGTCCAG
                                ||||  |||  ||||||||
                                AGGC  CGC  CACAGGTC
                                  TC  __
GAM1183  LOC133688 5'  TCTGTGCGCGCCTCAG     30800        AGT  _
                                TCTGTGCGT   GTC CAG
                                |||||||||   ||| |||
                                AGACACGCG   CGG GTC
                                     ___  A
GAM1183  LOC146957 5'  TCTCTGCAGCATCCAG     30801     G   GT
                                TCT TGC  AGTGTCCAG
                                ||| |||  |||||||||
                                AGA ACG  TCGTAGGTC
                                  G  __
GAM1183  LOC150372 5'  TCTGTGCCCAGTCCAG     30802       G  GT
                                TCTGTGC TA  GTCCAG
                                |||||||  ||  ||||||
                                AGACACG GT  CAGGTC
                                    G  __
GAM1183  LOC150696 3'  CTGGAACGCAGTGTCCAG    30803     T_
                                CTG  GCGTAGTGTCCAG
                                |||  ||||||||||||
                                GAC  TGCGTCACAGGTC
                                  CT
GAM1183  LOC150998 3'  TCTGTGCAGCCTCCAG     30804       GT   G
                                TCTGTGC  AGT TCCAG
                                |||||||  ||| |||||
                                AGACACG  TCG AGGTC
                                   __  G
GAM1183  LOC151171 5'  CCTGCCCGGTGTCCAG     30793      G  TA
                                TCTGT CG  GTGTCCAG
                                |||||  ||  ||||||||
                                GGACG GC  CACAGGTC
                                   G  __
GAM1183  LOC151647 5'  TCGGTGCGCCCCGTCCAG    30805    T     AG
                                TC GTGCGT  TGTCCAG
                                ||  ||||||  |||||||
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                                AG CACGCG  GCAGGTC
                                 C     GG
GAM1183  LOC153785 5'  TCTGTGCGCTGACCAG      30806         AG  T
                                TCTGTGCGT  TG CCAG
                                |||||||||  || ||||
                                AGACACGCG  AC GGTC
                                     __  T
GAM1183  LOC158236 5'  TCTGAGCACCCATCCAG     30807      T    AG
                                TCTG GCGT  TGTCCAG
                                |||| ||||  |||||||
                                AGAC CGTG  GTAGGTC
                                  T   G_
GAM1183  LOC158314 3'  TCCCACTAGTGTCCAG      30808     G   G
                                TCT TGC TAGTGTCCAG
                                ||| ||| ||||||||||
                                AGG GTG ATCACAGGTC
                                 _  _
GAM1183  LOC163255 5'  CCTCTGGGTAGTGTCCAG    30809     G  C
                                TCT TG GTAGTGTCCAG
                                ||| ||  ||||||||||||
                                GGA AC CATCACAGGTC
                                  G  C
GAM1183  LOC164714 5'  TCTTTGCGTAGTGGTTCAG   30810     G        TC_
                                TCT TGCGTAGTG   CAG
                                ||| |||||||||   |||
                                AGA ACGCATCAC   GTC
                                  A        CAA
GAM1183  LOC201227 5'  TCTGGGACCCGGGTGTCCAG  30811      ___ G  TA
                                TCTG   T CG  GTGTCCAG
                                ||||   | ||  ||||||||
                                AGAC   G GC  CACAGGTC
                                   CCT G  C_
GAM1183  LOC204845 5'  TCTGTGCAGTGTCCAG      30812        GT
                                TCTGTGC  AGTGTCCAG
                                |||||||  |||||||||
                                AGACACG  TCACAGGTC
                                     __
GAM1183  LOC219513 5'  TCTGTCCGTGTGCCCAG     30813      G   A
                                TCTGT CGT GTGTCCAG
                                ||||| ||| ||||||||
                                AGACA GCA CACGGGTC
                                   G   _
GAM1183  LOC220739 3'  TCTGTGCAGAGCCCCAG     30814         T   G
                                TCTGTGCG AGT TCCAG
                                |||||||| ||| |||||
                                AGACACGT TCG GGGTC
                                     C   _
GAM1183  LOC220980 3'  TCTGGGCAGCGTCCAG      30815      TGC
                                TCTG   GTAGTGTCCAG
                                ||||   ||||||||||
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                                AGAC   CGTCGCAGGTC
                                  C__
GAM1183  LOC254531 5'  CCCAGCTGGTGGTGTCCAG   30816      T  __  A
                                TCTG GC  GT GTGTCCAG
                                |||| ||  || ||||||||
                                GGGT CG  CA CACAGGTC
                                  _  AC  C
GAM1183  LOC254532 3'  CCTGTGCGGGCCCCAG      30817        TA  G
                                TCTGTGCG  GT TCCAG
                                ||||||||  || |||||
                                GGACACGC  CG GGGTC
                                     C_  _
GAM1183  LOC254557 5'  TCTCTATAGTGTCCAG      30818     G GC
                                TCT T  GTAGTGTCCAG
                                ||| |  ||||||||||
                                AGA A  TATCACAGGTC
                                  G __
GAM1183  LOC255104 3'  TCTGTTAGTGGTGTCCAG    30819      GC  A
                                TCTGT  GT GTGTCCAG
                                |||||  || ||||||||
                                AGACA  CA CACAGGTC
                                   AT  C
GAM1183  LOC255397 5'  TCTGTGCGCAGTGAGCAG    30820           TC
                                TCTGTGCGTAGTG  CAG
                                ||||||||||||  |||
                                AGACACGCGTCAC  GTC
                                        TC
GAM1183  LOC91133  3'  TCTGTGCAGGTGAGCGTC    30821        __  _
                                TCTGTGC  GT AGTGTC
                                |||||||  || ||||||
                                AGACACG  CA TCGCAG
                                     TC  C
GAM1183  LOC91301  5'  TCTGTGCGACCGTCTCCAG   30822        TA_  G
                                TCTGTGCG   GT TCCAG
                                ||||||||   || |||||
                                AGACACGC   CA AGGTC
                                     TGG  G
GAM1183  LOC93052  5'  CCTGGCTAGTGTCCAG      30823      T  G
                                TCTG GC TAGTGTCCAG
                                |||| || ||||||||||
                                GGAC CG ATCACAGGTC
                                  _  _
GAM1184  FOXG1B    5'  ACCGGTGGGTGCCGAACG    30826      A        TTTG
                                GCCG TGGGTGCCGG    GCG
                                |||| ||||||||||    |||
                                TGGC ACCCACGGCT    TGC
                                  C        ____
GAM1184  SIAT8C    5'  GCTGAGGGTGCCGGCGAGG   30827    C  T        TT
                                GC GA GGGTGCCGGT  GG
                                || || ||||||||||  ||
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                                CG CT CCCACGGCCG  CC
                                 A  _        CT
GAM1184  ZNF342    3'  CAATGGGTGTTGGCAGCGG   30828        CC   TT
                                CGATGGGTG  GGT  GGCGG
                                |||||||||  |||  |||||
                                GTTACCCAC  CCG  TCGCC
                                     AA   __
GAM1184  LOC116173 3'  GCTGGGGTGGGGTTTGGCGG  30829    CGAT    CC
                                GC   GGGTG  GGTTTGGCGG
                                ||   |||||  ||||||||||
                                CG   CCCAC  CCAAACCGCC
                                 AC__    C_
GAM1184  LOC146823 3'  TGGTGTGGAGGTTTGGTGG   30830     _  CC      C
                                TGG GTG  GGTTTGG GG
                                ||| |||  ||||||| ||
                                ACC CAC  CCAAACC CC
                                  A  CT      A
GAM1184  LOC147111 3'  GCCGGTGGGTGCTGTCTG    30831      A      CG
                                GCCG TGGGTGC  GTTTG
                                |||| |||||||  |||||
                                CGGC ACCCACG  CAGAC
                                  C      A_
GAM1184  LOC201191 5'  GCCGATGGTGGGGCTGGCGG   30832        G  CC    T
                                GCCGATGG TG  GGTT GGCGG
                                |||||||| ||  |||| |||||
                                CGGCTACC AC  CCGA CCGCC
                                     _  C_   _
GAM1184  LOC254211 3'  CGATGGGTGTCTGAGTGG    30833        GCCG    _ C
                                CGATGGGT    GTTTG G GG
                                ||||||||    ||||| | ||
                                GCTACCCA    CAGAC C CC
                                     _____     T A
GAM1184  LOC254587 5'  AGCTGCTGGGCTTTGGCG    30834     CGA    GCCGG
                                AGC   TGGGT    TTTGGCG
                                |||   |||||    |||||||
                                TCG   ACCCG    AAACCGC
                                  ACG    ______
GAM1185  TNFRSF6B  5'  GCTCCCGGCGGAAACTGTT   30837         CC_  _
                                GCTCTCGGCG   GC GTT
                                ||||||||||   || |||
                                CGAGGGCCGC   TG CAA
                                      CTT  A
GAM1185  FLJ13964  5'  GCTCTCGGCCCGCCCCGTT   30838         __  G
                                GCTCTCGGC  GCC CGTT
                                |||||||||  ||| ||||
                                CGAGAGCCG  CGG GCAA
                                     GG   G
GAM1185  KIAA0596  5'  GCCCTCGGGCATCGCGTT    30839        C  __
                                GCTCTCGG GC  CGCGTT
                                |||||||| ||  ||||||
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                                CGGGAGCC CG  GCGCAA
                                     _ TA
GAM1185 KIAA1819 5' GCTCTCGGCCTACCTCGTT   30840        __  G
                                GCTCTCGGC  GCC CGTT
                                |||||||||  ||| ||||
                                CGAGAGCCG  TGG GCAA
                                     GA   A
GAM1185 LOC147841 5' TCTCGGCACCGTCTTGCGTTA 30841         _____   III
                                TCTCGGCGCC    GCGTT   A
                                ||||||||||    |||||  |
                                AGAGCCGTGG    CGCAA   T
                                      CAGAA    III
GAM1186 BAT1    5' TAGGTGAAAACAAGGGGT    30844       CACTG    A
                                TAGGTGAA    GACAA GGGT
                                ||||||||    ||||| ||||
                                ATCCACTT    TTGTT CCCA
                                     _____   C
GAM1186 CDS2    3' GGTGTTCAGGCAAAGGGT    30845     AA  CT  A
                                GGTG  CA  GG CAAAGGGT
                                ||||  ||  || ||||||||
                                CCAC  GT  CC GTTTCCCA
                                  AA  __  _
GAM1186 PPP2R5A  3' GGTGAGACAAAGAGAAGGGTA 30846      _  CT   CA
                                GGTGA ACA  GGA  AAGGGTA
                                ||||| |||  |||  |||||||
                                CCACT TGT  TCT  TTCCCAT
                                   C   T_   C_
GAM1186 C21orf51  3' GGTAGGGGGAGACAAAGGGT   30847     AACACT
                                GGTG     GGACAAAGGGT
                                ||||     ||||||||||
                                CCAT     TCTGTTTCCCA
                                  CCCCC_
GAM1186 FLJ14082  3' GGGAAGATGCAAAGGGT     30848    T   CAC  GA
                                GG GAA   TG  CAAAGGGT
                                || |||   ||  ||||||||
                                CC CTT   AC  GTTTCCCA
                                 _   CT_  __
GAM1186 KIAA1649  5' GGGGAACAAAATAAGGGGTA   30849    T    CT   C  A
                                GG GAACA  GGA AA GGGTA
                                || |||||  ||| || |||||
                                CC CTTGT  TTT TT CCCAT
                                 C     __   A  C
GAM1186 NYD-SP18  3' GGTGAGCATCTCTCAGGGGT   30850      A  _  GGA  AA
                                GGTGA CA CT   CA  GGGT
                                ||||| || ||   ||  ||||
                                CCACT GT GA   GT  CCCA
                                   C  A  GA_  C_
GAM1186 LOC120425 5' TAGGTGAAGGCAGTAAGGGTA  30851        CACT  A  __
                                TAGGTGAA   GG CA  AAGGGTA
                                ||||||||   || ||  |||||||
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                                ATCCACTT   CC GT  TTCCCAT
                                    ____  _  CA
GAM1186  LOC126964 3'  TAGATGAGGAAAAGACAGGGGG 30852       ACACT    AA
            TA                    TAGGTGA    GGACA  GGGTA
                                  |||||||    |||||  |||||
                                  ATCTACT    TCTGT  CCCAT
                                     CCTTT    CC
GAM1186  LOC145241 5'  TAGGTGAACACTGGGAGGT   30853           ACAAA
                                  TAGGTGAACACTGG    GGGT
                                  ||||||||||||||    ||||
                                  ATCCACTTGTGACC    TCCA
                                           C____
GAM1186  LOC150135 3'  TAGGTGGTATTTCAAAGGGTA  30854       AACACTGGA
                                  TAGGTG       CAAAGGGTA
                                  ||||||       |||||||||
                                  ATCCAC       GTTTCCCAT
                                     CATAAA___
GAM1187  PKNOX1    3'  CTAGAAATTTTATCCTCAATAT 30857       C    TGA_
            AG                    CTAGAA ATTTT   TTAATATAG
                                  |||||| |||||   |||||||||
                                  GATCTT TAAAA   AGTTATATC
                                     _    TAGG
GAM1187  ABCC13    3'  CTAGAACAGTTTTGGCATGCAT 30858        T    ATTAA
            AG                    CTAGAACA TTTTG    TATAG
                                  |||||||| |||||    |||||
                                  GATCTTGT AAAAC    GTATC
                                       C    CGTAC
GAM1187  KIAA0408  3'  CTAGAACTTCTGTAATATA   30859       AT    AT
                                  CTAGAAC  TTTTG  TAATATA
                                  |||||||  |||||  |||||||
                                  GATCTTG  AAGAC  ATTATAT
                                     __    __
GAM1187  PTDSS1    3'  CTGGAACATCTTTGATTAAC   30860    A
                                  CT GAACATTTTTGATTAAT
                                  || ||||||||||||||||
                                  GA CTTGTAGAAACTAATTG
                                   C
GAM1187  RAB40A    5'  TAAAACATTGCCATTAATATAG 30861        T  G
                                  TAGAACATT TT ATTAATATAG
                                  |||||||||  || ||||||||||
                                  ATTTTGTAA GG TAATTATATC
                                        C  _
GAM1187  LOC158629 5'  TAGAATATTTTAGATTAATAT  30862      C    T
                                  TAGAA ATTTT GATTAATAT
                                  ||||| ||||| |||||||||
                                  ATCTT TAAAA CTAATTATA
                                     A    T
GAM1188  RANBP3    5'  GCACCTGTTTTTCAAAACAGCC 30865      ____      T  C
                                  GTACT    TTTCAAA AC GCC
                                  |||||    ||||||| || |||
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                                CGTGG    AAAGTTT TG CGG
                                  ACAA      _ T
GAM1188 C20orf82 5' CATGTACTTCTTTAAGAACTCG 30866    C       CAAAT_ _
            C                    CA GTACTTTT     AC CGC
                                 || ||||||||     || |||
                                 GT CATGAAGA     TG GCG
                                  A       AATTCT  A
GAM1188 STAM2    3' ACTGAGCTTTCAAATACTGC   30867    GTAC         C
                                 AC    TTTTCAAATAC GC
                                 ||    |||||||||||| ||
                                 TG    GAAAGTTTATG CG
                                  ACTC         A
GAM1188 LOC147353 3' TACACTGTAGGAGTAATACCGC 30868      _   CTTTTCA
            C                    TACAC GTA      AATACCGCC
                                 ||||| |||      |||||||||
                                 ATGTG CAT      TTATGGCGG
                                    A   CCTCA__
GAM1188 LOC201931 3' TACAGGTACTTTTCAAGTGACC 30869      C         AT_
                                 TACA GTACTTTTCAA   ACC
                                 |||| ||||||||||   |||
                                 ATGT CATGAAAAGTT   TGG
                                   C         CAC
GAM1189 UNC13    3' TGATTGGTATGTATGTGT    30872     CT_
                                 TGA   GTATGTATGTGT
                                 |||   ||||||||||||
                                 ACT   CATACATACACA
                                   AAC
GAM1189 FLJ10300 5' TGACTGTATGGCCCAGAGATGT 30873          TAT  G  ___
            TT                    TGACTGTATG   GT TA   ATGTTT
                                  ||||||||||   || ||   ||||||
                                  ACTGACATAC   CG GT   TACAAA
                                        ___  G  CTC
GAM1189 FLJ22644 3' TGCTTGTATGTGTATGTT    30874     A        A
                                 TGT TGTATGTGTA TGTT
                                 ||| |||||||||| ||||
                                 ACG ACATACACAT ACAA
                                   A        _
GAM1189 IDI1     3' TGACTGTAAGTATCAACATGTT 30875         T    GTGTA
            T                     TGACTGTA GTAT     ATGTTT
                                  |||||||| ||||    ||||||
                                  ACTGACAT CATA     TACAAA
                                       T    GTTG_
GAM1189 KIAA1323 3' TGTTGTATGTGTATGT      30876     A        A
                                 TGT TGTATGTGTA TGT
                                 ||| |||||||||| |||
                                 ACA ACATACACAT ACA
                                   _        _
GAM1189 KIAA1795 3' TGACTGATCTCAAGTGTAATGT 30877       TATG  T
            TT                    TGACTG    TA GTGTAATGTTT
                                  ||||||    || ||||||||||
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                                ACTGAC   GT CACATTACAAA
                                   TAGA  T
GAM1189  P101-PI3K 3'  TGCATGCCATGTGTGTGT    30878       _    AA
                                TGTATGT ATGTGT  TGT
                                ||||||| ||||||  |||
                                ACGTACG TACACA  ACA
                                    G     C_
GAM1189  TRPV5    5'  TGGCTGTGGTGTATGTGT    30879    A   A_
                                TG CTGT  TGTATGTGT
                                || ||||  |||||||||
                                AC GACA  ACATACACA
                                 C   CC
GAM1189  LOC203427 3'  TGAGTGTATGTGTGTGTA    30880     C      A
                                TGA TGTATGT TGTGTA
                                ||| ||||||| ||||||
                                ACT ACATACA ACACAT
                                  C      C
GAM1189  LOC92360  5'  TGTTGTGTGTGTAATGT     30882     A  A
                                TGT TGT TGTGTAATGT
                                ||| ||| ||||||||||
                                ACA ACA ACACATTACA
                                  _  C
GAM1189  LOC92360  5'  TGTTGTGTGTGTAATGT     30882     A  A
                                TGT TGT TGTGTAATGT
                                ||| ||| ||||||||||
                                ACA ACA ACACATTACA
                                  _  C
GAM1189  LOC92360  5'  TGATGTGTGTGTAATGT     30883    T   A
                                TG ATGT TGTGTAATGT
                                || |||| ||||||||||
                                AC TACA ACACATTACA
                                  _   C
GAM1189  LOC92360  5'  TGTTGTGTGTGTGTAATGTT   30881     A_  A
                                TGT  TGT TGTGTAATGTT
                                |||  ||| ||||||||||
                                ACA  ACA ACACATTACAA
                                  AC   C
GAM1190  ABCD1    3'  TGGGGGAGAGGATGCAGGT    30886     CA   A TTTTTA
                                TGG  GGA G     ATGCAGGT
                                |||  ||| |     ||||||||
                                ACC  CCT C     TACGTCCA
                                  C_   _ TCC___
GAM1190  ALDH3A2   5'  GGCGGGAAGCATGCAGG     30887     A     TTTTA
                                GGC GGAAGT    ATGCAGG
                                ||| ||||||    |||||||
                                CCG CCTTCG    TACGTCC
                                  C     _____
GAM1190  NRL      3'  TGGCAGGAGCACCCTGTGCAGG 30888         A  T   AA
              T                  TGGCAGGA GT TTT  TGCAGGT
                                 |||||||| || |||  |||||||
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                                ACCGTCCT CG GGG  ACGTCCA
                                    _ T   AC
GAM1190  PATE     3'  TGGCAGGGAAGCTGGATGCAGG 30889       _    TTTA
              T                  TGGCAGG AAGTT   ATGCAGGT
                                 ||||||| |||||   ||||||||
                                 ACCGTCC TTCGA   TACGTCCA
                                     C    CC__
GAM1190  CILP     5'  TGGCAAGAGGTAGATGTGGGT  30890        A  TTTTA  CA
                                 TGGCAGGA GT    ATG  GGT
                                 |||||||| ||    |||  |||
                                 ACCGTTCT CA    TAC  CCA
                                     C  TC___   AC
GAM1190  RAP2B    3'  TGGTGGGAAGTTCACAGG    30891     CA      TTAAT
                                 TGG  GGAAGTTT    GCAGG
                                 |||  ||||||||    |||||
                                 ACC  CCTTCAAG    TGTCC
                                   AC       _____
GAM1191  ARF5     3'  TAGCACCACCCGAAGCC     30894        G
                                 TGGCACCA CTCGAAGCC
                                 |||||||| |||||||||
                                 ATCGTGGT GGGCTTCGG
                                     _
GAM1191  B4GALT7  3'  TGGCCCAGCCCAAGCC      30895     A     G
                                 TGGC CCAGCTC AAGCC
                                 |||| ||||||| |||||
                                 ACCG GGTCGGG TTCGG
                                     _     _
GAM1191  BCLG     3'  TGGCCCATCAAAGCC       30896     A   GC
                                 TGGC CCA  TCGAAGCC
                                 |||| |||  ||||||||
                                 ACCG GGT  AGTTTCGG
                                     _  __
GAM1191  CDC25B   5'  GGCACCAGCCAGGGAAGCC   30897         C__
                                 GGCACCAGCT   GAAGCC
                                 ||||||||||   ||||||
                                 CCGTGGTCGG   CTTCGG
                                       TCC
GAM1191  CDC25B   5'  GGCACCAGCCAGGGAAGCC   30897         C__
                                 GGCACCAGCT   GAAGCC
                                 ||||||||||   ||||||
                                 CCGTGGTCGG   CTTCGG
                                       TCC
GAM1191  CNP      5'  TGGCACAACCCGAGCC      30898       C     A
                                 TGGCAC AGCTCGA GCC
                                 |||||| ||||||| |||
                                 ACCGTG TTGGGCT CGG
                                     _     _
GAM1191  CNP      5'  GGCACCAGCGCTCCGGGGCC   30899         ___   AA
                                 GGCACCAGC   TCG  GCC
                                 |||||||||   |||  |||
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                                CCGTGGTCG  GGC  CGG
                                     CGA   CC
GAM1191  CYP4F3   3'  TGGCACCACCCCAGCC     30900       G   GA
                                TGGCACCA CTC  AGCC
                                |||||||| |||  ||||
                                ACCGTGGT GGG  TCGG
                                     G   __
GAM1191  DUSP7    3'  TGGACGCCCAAAGCC      30901     C  CA
                                TGG AC  GCTCGAAGCC
                                ||| ||  ||||||||||
                                ACC TG  CGGGTTTCGG
                                  _ __
GAM1191  EGFL3    3'  TAGCACCAAAAAGCC      30902        CTC
                                TGGCACCAG   GAAGCC
                                |||||||||   ||||||
                                ATCGTGGTT   TTTCGG
                                     ___
GAM1191  HSPG2    3'  GGCACCAGCCCACAAGCC    30903          _
                                GGCACCAGCTCG AAGCC
                                |||||||||||| |||||
                                CCGTGGTCGGGT TTCGG
                                       G
GAM1191  MCM3     3'  TGGAACCACCCAAAGCC     30904     C   G
                                TGG ACCA CTCGAAGCC
                                ||| |||| |||||||||
                                ACC TGGT GGGTTTCGG
                                  T   _
GAM1191  MLC1     3'  TGGCACTACCCAAAGCC     30905      CA
                                TGGCAC  GCTCGAAGCC
                                ||||||  ||||||||||
                                ACCGTG  TGGGTTTCGG
                                   A_
GAM1191  MLC1     3'  TGGCACTACCCAAAGCC     30905      CA
                                TGGCAC  GCTCGAAGCC
                                ||||||  ||||||||||
                                ACCGTG  TGGGTTTCGG
                                   A_
GAM1191  MPP2     3'  TGGCACCACCACCCGGGCC   30906        __    AA
                                TGGCACCA  GCTCG  GCC
                                ||||||||  |||||  |||
                                ACCGTGGT  TGGGC  CGG
                                     GG    C_
GAM1191  MYOG     5'  TGCCACCAGCCCCCAAGC    30907    G      _ G
                                TG CACCAGCT C AAGC
                                || |||||||| | ||||
                                AC GTGGTCGG G TTCG
                                  G       G G
GAM1191  PAX2     3'  TGACGCCCCCAAAGCC      30908     A  AG
                                TGGC CC  CTCGAAGCC
                                |||| ||  |||||||||
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                                ACTG GG  GGGTTTCGG
                                  C __
GAM1191  PAX2     3'  TGACGCCCCCAAAGCC      30908      A  AG
                                TGGC CC  CTCGAAGCC
                                |||| ||  |||||||||
                                ACTG GG  GGGTTTCGG
                                  C __
GAM1191  PCMT1    3'  TGACACCACATCAAAAGC     30909        GC    _
                                TGGCACCA  TCGAA GC
                                ||||||||  ||||| ||
                                ACTGTGGT  AGTTT CG
                                     GT    T
GAM1191  PIP5K1A  5'  TGGACCAGCTCAAGGCC     30910     C        A
                                TGG ACCAGCTCGA GCC
                                ||| ||||||||| |||
                                ACC TGGTCGAGTT CGG
                                  _        C
GAM1191  PPP2R4   3'  GGCACCAGCCAGGACAGC    30911          C_ _
                                GGCACCAGCT  GA AGC
                                ||||||||||  || |||
                                CCGTGGTCGG  CT TCG
                                      TC  G
GAM1191  RPA2     5'  TGGCACCACAAACGCC      30912        GCT   _
                                TGGCACCA   CGAA GCC
                                ||||||||   |||| |||
                                ACCGTGGT   GTTT CGG
                                     ____   G
GAM1191  TNFRSF6B 3'  TGGCACCACTCACAGGCC    30913        G   AA_
                                TGGCACCA CTCG   GCC
                                |||||||| ||||   |||
                                ACCGTGGT GAGT   CGG
                                     _   GTC
GAM1191  TNFRSF6B 3'  TGGCACCACTCACAGGCC    30913        G   AA_
                                TGGCACCA CTCG   GCC
                                |||||||| ||||   |||
                                ACCGTGGT GAGT   CGG
                                     _   GTC
GAM1191  WNT1     3'  TGACACCATCAGGAGCC     30914        GC  A_
                                TGGCACCA  TCG  AGCC
                                ||||||||  |||  ||||
                                ACTGTGGT  AGT  TCGG
                                     __  CC
GAM1191  C1orf34  3'  TGGCCACCCCAAAGCC      30915      AC  G
                                TGGC  CA CTCGAAGCC
                                ||||  || |||||||||
                                ACCG  GT GGGTTTCGG
                                  __ G
GAM1191  C20orf39 5'  TGGCCCAGACCAGGGAGGCC  30916      A   _ C__  A
                                TGGC CCAG CT   GA GCC
                                |||| |||| ||   || |||
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                                ACCG GGTC GG   CT CGG
                                  _   T  TCC  C
GAM1191  CEGP1    3'  TGATGCCACTCAAAGCC     30917     CA   G
                                TGG  CCA CTCGAAGCC
                                |||  ||| |||||||||
                                ACT  GGT GAGTTTCGG
                                  AC  _
GAM1191  CRMP5    3'  TGGCACCAGCCTCGAGCC    30918          _   A
                                TGGCACCAGC TCGA GCC
                                |||||||||| |||| |||
                                ACCGTGGTCG AGCT CGG
                                      G   _
GAM1191  CSEN     3'  TGACACCAGCTGGGAGGGC   30919          C_  A_
                                TGGCACCAGCT  GA  GC
                                ||||||||||  ||  ||
                                ACTGTGGTCGA  CT  CG
                                       CC  CC
GAM1191  CTDP1    3'  TGGGACCCCCAAAGCC      30920     C   AG
                                TGG ACC  CTCGAAGCC
                                ||| |||  |||||||||
                                ACC TGG  GGGTTTCGG
                                  C  __
GAM1191  CX46.6   3'  TGGCCCAGCTCGCAAGCC    30921      A      _
                                TGGC CCAGCTCG AAGCC
                                |||| |||||||| |||||
                                ACCG GGTCGAGC TTCGG
                                  _       G
GAM1191  DKFZP434C171 3'  TGGCACCAAGACTGAAGGGCC  30922         __  C  __
                                TGGCACCA  GCT GAA  GCC
                                ||||||||  ||| |||  |||
                                ACCGTGGT  TGA CTT  CGG
                                     TC   _   CC
GAM1191  DKFZp564A176 3'  TAGCACCAACGTGAGCC     30923          TC  A
                                TGGCACCAGC  GA GCC
                                ||||||||||  || |||
                                ATCGTGGTTG  CT CGG
                                      CA  _
GAM1191  DKFZP586J1624 5'  TGGTCCAGCCCAAAGGCC    30924     CA        _
                                TGG  CCAGCTCGAAG CC
                                |||  |||||||||| ||
                                ACC  GGTCGGGTTTC GG
                                  A_         C
GAM1191  DKFZp762E1511 3'  GGCACCAGCAGAGGGAAGCC   30925         TC___
                                GGCACCAGC    GAAGCC
                                |||||||||    ||||||
                                CCGTGGTCG    CTTCGG
                                      TCTCC
GAM1191  EDG1     3'  TGGCAGCAGTCGAAGCC     30926      C   C
                                TGGCA CAG TCGAAGCC
                                ||||| ||| ||||||||
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                                ACCGT GTC AGCTTCGG
                                  C  _
GAM1191  ERp44    3'  TAGCACCAACCCAGGCC     30927          AA
                                TGGCACCAGCTCG  GCC
                                ||||||||||||  |||
                                ATCGTGGTTGGGT  CGG
                                      C_
GAM1191  FLJ10901 3'  TGGACCAGCCCCCAGCC     30928     C      GA
                                TGG ACCAGCTC  AGCC
                                ||| ||||||||  ||||
                                ACC TGGTCGGG  TCGG
                                  _      GG
GAM1191  FLJ12572 3'  TAGCACCAGCCTGCAGCC    30929          CGA
                                TGGCACCAGCT   AGCC
                                ||||||||||   ||||
                                ATCGTGGTCGG   TCGG
                                      ACG
GAM1191  FLJ21324 5'  TGACACCAGGCACGAGAGGCC  30930        _ T   A__
                                TGGCACCAG C CGA   GCC
                                |||||||||  | |||   |||
                                ACTGTGGTC G GCT   CGG
                                     C T   CTC
GAM1191  FLJ22693 3'  TGGCACCACACAGCAGCC    30931        G T  A_
                                TGGCACCA C CG  AGCC
                                ||||||||  | ||  ||||
                                ACCGTGGT G GT  TCGG
                                     _ T  CG
GAM1191  HAND1    3'  TAGCACCAGTCGCCGGAGCC   30932        C__   A
                                TGGCACCAG   TCG AGCC
                                |||||||||   ||| ||||
                                ATCGTGGTC   GGC TCGG
                                     AGC   C
GAM1191  KIAA0140 3'  TGACACCAAGGCAGAGCC    30933        CT  A
                                TGGCACCAG  CG AGCC
                                |||||||||  ||  ||||
                                ACTGTGGTT  GT TCGG
                                     CC  C
GAM1191  KIAA0420 3'  TGACACCACCCACAGGCC    30934        G    AA_
                                TGGCACCA CTCG   GCC
                                ||||||||  ||||   |||
                                ACTGTGGT GGGT   CGG
                                     _   GTC
GAM1191  KIAA0544 3'  TGGCACCAGGACTGATGGCC   30935         __  C  A_
                                TGGCACCAG  CT GA  GCC
                                |||||||||  ||  ||  |||
                                ACCGTGGTC  GA CT  CGG
                                     CT  _  AC
GAM1191  KIAA0876 3'  TGGCACCAGACCATCAAAGCC  30936         _ __
                                TGGCACCAG C  TCGAAGCC
                                |||||||||  |  ||||||||
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                                ACCGTGGTC G  AGTTTCGG
                                     T GT
GAM1191  KIAA1030  3'  TGGCCCGGCCGAAGCC     30937     A  A  T
                                TGGC CC GC CGAAGCC
                                |||| || || |||||||
                                ACCG GG CG GCTTCGG
                                  _  C  _
GAM1191  KIAA1582  5'  TAGCACCAGGAAGGCC     30938        CTC   _
                                TGGCACCAG   GAAG CC
                                |||||||||   |||| ||
                                ATCGTGGTC   CTTC GG
                                     ___    C
GAM1191  KIAA1655  3'  TGGCACCATGCCTCTAGGAGCC 30939        _  _  GA__
                                TGGCACCA GC TC    AGCC
                                |||||||| || ||    ||||
                                ACCGTGGT CG AG    TCGG
                                     A  G  ATCC
GAM1191  LIMK2     3'  TGGCCCAGCTCAGGGAGC    30940     A      A__
                                TGGC CCAGCTCG   AGC
                                |||| ||||||||   |||
                                ACCG GGTCGAGT   TCG
                                  _       CCC
GAM1191  LIMK2     3'  TGGCCCAGCTCAGGGAGC    30940     A      A__
                                TGGC CCAGCTCG   AGC
                                |||| ||||||||   |||
                                ACCG GGTCGAGT   TCG
                                  _       CCC
GAM1191  MGC14161  3'  TGGCACCAGCAGGAAAAGC   30941        TC__
                                TGGCACCAGC    GAAGC
                                ||||||||||    |||||
                                ACCGTGGTCG    TTTCG
                                      TCCT
GAM1191  MGC14258  5'  TGACACCACATCAAAGCC    30942        GC
                                TGGCACCA  TCGAAGCC
                                ||||||||  ||||||||
                                ACTGTGGT  AGTTTCGG
                                     GT
GAM1191  SRCRB4D   5'  GGCACCAGCTGGAGCGGCC   30943        C  A__
                                GGCACCAGCT GA   GCC
                                |||||||||| ||   |||
                                CCGTGGTCGA CT   CGG
                                      C  CGC
GAM1191  TNFAIP3   3'  TGACTGACAGCTCGAGGCC   30944     AC_      A
                                TGGC   CAGCTCGA GCC
                                ||||   |||||||| |||
                                ACTG   GTCGAGCT CGG
                                  ACT       C
GAM1191  ZAK       3'  TGACACCACACCCAGCC     30945        _   GA
                                TGGCACCA GCTC  AGCC
                                |||||||| ||||  ||||
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                                ACTGTGGT TGGG  TCGG
                                    G   __
GAM1191  LOC129526 3'  TGGACGCTCAAAAGGCC    30946    C  CA     __
                                TGG AC  GCTCGAA  GCC
                                ||| ||  |||||||  |||
                                ACC TG  CGAGTTT  CGG
                                  _ __      TC
GAM1191  LOC130502 5'  TGGCACCACAAAGCC      30947       GCT
                                TGGCACCA   CGAAGCC
                                ||||||||   |||||||
                                ACCGTGGT   GTTTCGG
                                    ___
GAM1191  LOC145693 3'  TGGTGTCAGCTCGAAACC    30948    CAC
                                TGG   CAGCTCGAAGCC
                                |||   ||||||||||||
                                ACC   GTCGAGCTTTGG
                                  ACA
GAM1191  LOC151996 5'  TGGCACCAGGCACAGCAGGCC  30949        _ T  AA__
                                TGGCACCAG C CG    GCC
                                |||||||||  | ||    |||
                                ACCGTGGTC G GT    CGG
                                     C T  CGTC
GAM1191  LOC196549 3'  GGCACCAGCTTGGAGGCC    30950         C_  A
                                GGCACCAGCT  GA GCC
                                ||||||||||  || |||
                                CCGTGGTCGA  CT CGG
                                      AC  C
GAM1191  LOC199780 5'  TGGCACCACGAAGGCC      30951       GCT    _
                                TGGCACCA   CGAAG CC
                                ||||||||   ||||| ||
                                ACCGTGGT   GCTTC GG
                                    ___    C
GAM1191  LOC200531 5'  TGGCACCAACTGTGTAGCC   30952         CGA_
                                TGGCACCAGCT    AGCC
                                ||||||||||    ||||
                                ACCGTGGTTGA    TCGG
                                      CACA
GAM1191  LOC204161 5'  TGGCCCCAGCTCGAGTGC    30953     A       A_
                                TGGC CCAGCTCGA  GC
                                |||| |||||||||  ||
                                ACCG GGTCGAGCT  CG
                                  G       CA
GAM1191  LOC206426 5'  TGGACCAGCTCAAGGCC     30910    C       A
                                TGG ACCAGCTCGA GCC
                                ||| ||||||||| |||
                                ACC TGGTCGAGTT CGG
                                  _       C
GAM1191  LOC221336 3'  TGACACCAAGCGAGAAGCC   30954       _  TC
                                TGGCACCA GC  GAAGCC
                                |||||||| ||  ||||||
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                                ACTGTGGT CG  CTTCGG
                                     T  CT
GAM1191  LOC256306 5'  TGGCCCCAGCTCACTGAGC   30955      A       A__
                                TGGC CCAGCTCG   AGC
                                |||| ||||||||   |||
                                ACCG GGTCGAGT   TCG
                                   G       GAC
GAM1191  LOC256789 3'  TAGCACCACACACCGGGCC   30956         _ _   AA
                                TGGCACCA GC TCG  GCC
                                |||||||| || |||  |||
                                ATCGTGGT TG GGC  CGG
                                     G  T   C_
GAM1191  LOC257354 3'  TGACACCACCCACAGGCC    30934         G    AA_
                                TGGCACCA CTCG   GCC
                                |||||||| ||||   |||
                                ACTGTGGT GGGT   CGG
                                     _    GTC
GAM1191  LOC90092  5'  TGGCCCCGCCCAAAGCC     30957      A  A
                                TGGC CC GCTCGAAGCC
                                |||| || ||||||||||
                                ACCG GG CGGGTTTCGG
                                   _ G
GAM1191  LOC91012  3'  TGGCACCATTGCTGGAGC    30958         __   C  A
                                TGGCACCA  GCT GA GC
                                ||||||||  ||| || ||
                                ACCGTGGT  CGA CT CG
                                     AA   C  _
GAM1191  LOC92078  3'  TAGCACCAGAACCGTGGGGCC 30959         C_   AA__
                                TGGCACCAG  TCG    GCC
                                |||||||||  |||    |||
                                ATCGTGGTC  GGC    CGG
                                      TT   ACCC
GAM1191  LOC92973  5'  TGGCACTGCCCAAAGCC     30960       CA
                                TGGCAC  GCTCGAAGCC
                                ||||||  ||||||||||
                                ACCGTG  CGGGTTTCGG
                                   A_
GAM1192  LNK       3'  CACAGGATGTCAGATGTG    30963        ATCTAAA
                                TACAGGA      TCAGATGTG
                                |||||||      |||||||||
                                GTGTCCT      AGTCTACAC
                                     AC_____
GAM1192  M11S1     3'  TGAGGAATCTGAGTATCATGTG 30964   C       AA__   GA
              C                  A AGGAATCT    ATCA  TGTGC
                                | ||||||||    ||||  |||||
                                A TCCTTAGA    TAGT  ACACG
                                 C       CTCA   __
GAM1192  ARL8      3'  TACAGGAGTACTAAGTATG   30965        AT_  AATC  A
                                TACAGGA   CTA    AG TGTG
                                |||||||   |||    || ||||
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                                ATGTCCT  GAT   TC ATAC
                                   CAT  ____ _
GAM1192 D4ST-1   3' CAGTCTTTAGATCAGATGTG  30966    GAATC  A
                                CAG    TA ATCAGATGTG
                                |||    || ||||||||||
                                GTC    AT TAGTCTACAC
                                  AGAA_  C
GAM1192 FLJ10290 3' TACAGCAGTAACCAGATGTG  30967     GAATCTA
                                TACAG     AATCAGATGTG
                                |||||     ||||||||||
                                ATGTC     TTGGTCTACAC
                                   GTCA___
GAM1192 FLJ22282 3' TACAGGGACAGGCAGATGTGC 30968      A  CTAAAT
                                TACAGG AT     CAGATGTGC
                                |||||| ||     |||||||||
                                ATGTCC TG     GTCTACACG
                                   C  TCC___
GAM1192 KIAA0417 3' AGAATCTAAAACAGTGC     30969         T   A
                                GGAATCTAAA CAG TGT
                                |||||||||| ||| |||
                                TCTTAGATTT GTC ACG
                                      T  _
GAM1192 MG61     3' AGGGTCCACAGATGTGC     30970     AA   AAT
                                AGG  TCTA   CAGATGTGC
                                |||  ||||   |||||||||
                                TCC  AGGT   GTCTACACG
                                  C_   ___
GAM1192 LOC143154 3' AGTGAGTCTAAATCAAAT    30971    _  A
                                AG GA TCTAAATCAGAT
                                || || ||||||||||||
                                TC CT AGATTTAGTTTA
                                 A  C
GAM1192 LOC144317 3' TACAGCAATCTAAACATTGTG 30972      G      T  GA
                                TACAG AATCTAAA CA  TGTG
                                ||||| |||||||| ||  ||||
                                ATGTC TTAGATTT GT  ACAC
                                   G      _  A_
GAM1192 LOC145098 5' GGGTTCACAAAATCAGATGTG 30973    AA  T__
                                GG  TC   AAATCAGATGTG
                                ||  ||   ||||||||||||
                                CC  AG   TTTAGTCTACAC
                                 CA  TGT
GAM1192 LOC145314 3' GAAATCTGAGAGATGTGC    30974       AAATC
                                GGAATCT    AGATGTGC
                                |||||||    ||||||||
                                CTTTAGA    TCTACACG
                                    CTC__
GAM1192 LOC152582 5' AAGAGCAGATCAGATGTG    30975     ATC  A
                                AGGA   TA ATCAGATGTG
                                ||||   || ||||||||||
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                                TTCT   GT TAGTCTACAC
                                  C__  C
GAM1192  LOC219294 3'  AGTGAGTCTAAATCAAAT    30971    _  A
                                AG GA TCTAAATCAGAT
                                || || ||||||||||||
                                TC CT AGATTTAGTTTA
                                 A  C
GAM1193  FLJ13263  3'  GCTCCGTTTTCGGGAGCG    30978    A  C      A
                                GCT TCG TTTCGGGA CG
                                ||| ||| |||||||| ||
                                CGA GGC AAAGCCCT GC
                                  _  A      C
GAM1193  LOC147429 3'  TAAGTGCTATGCAGGA      30979         C  TTTC
                                TAAGTGCTAT GC    GGGA
                                |||||||||| ||    ||||
                                ATTCACGATA CG    TCCT
                                          _ _____
GAM1194  C1orf6    3'  AGGAAAATTACCACCT      30982      CTATG
                                AGGA     AAATTACCACCT
                                ||||     ||||||||||||
                                TCCT     TTTAATGGTGGA
                                          ______
GAM1194  IQGAP2    3'  GGACTATGCTCACTATCTA    30983        AAA    CAC
                                GGACTATG   TTAC   CTA
                                ||||||||   ||||   |||
                                CCTGATAC   AGTG   GAT
                                     G__    ATA
GAM1194  TPM4      3'  AGGATCAATTAATTACCATCTA 30984      C  TGA      C
                                AGGA TA   AATTACCA CTA
                                |||| ||   |||||||| |||
                                TCCT GT   TTAATGGT GAT
                                  A  TAA       A
GAM1194  LOC126669 3'  TAGGACAATTTCCCACCACCT  30985       T  GAAA
                                TAGGAC AT    TTACCACCT
                                |||||| ||    |||||||||
                                ATCCTG TA    GGTGGTGGA
                                   T  AAG_
GAM1194  LOC152106 3'  AGGATCTATTAATTACCATCTA 30986      _   GA      C
                                AGGA CTAT  AATTACCA CTA
                                |||| ||||  |||||||| |||
                                TCCT GATA  TTAATGGT GAT
                                  A   A_       A
GAM1195  PIK4CB    3'  GTTTCCTGGTTTGGGGTT    30989       AA  CAAC
                                GTTTTT  TG    TTGGGGTT
                                ||||||  ||    ||||||||
                                CAAAGG  AC    AACCCCAA
                                   __ CA__
GAM1195  PMP22     3'  GCTTTTGGACATTTGGGGTT  30990       AAT   AC
                                GTTTTT   GCA  TTGGGGTT
                                ||||||   |||  ||||||||
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                                CGAAAA  TGT  AACCCCAA
                                   CC_  A_
GAM1195  POLR2E   3'  AAGTTTTTAATCGGGTGT    30991        TGCAAC    _
                                AAGTTTTTAA     TTGGG GT
                                ||||||||||     ||||| ||
                                TTCAAAAATT     AGCCC CA
                                       _______    A
GAM1195  XT3      3'  AGACTTCTAATGTGGTTTGGGG 30992    _      CAAC
           TT                    AG TTTTTAATG    TTGGGGTT
                                 || |||||||||    ||||||||
                                 TC GAAGATTAC    AACCCCAA
                                  T       ACCA
GAM1195  ASB10    3'  ATTTTTAATGCACATACAGGGT 30993          ACT_
           T                     GTTTTTAATGCA    TGGGGTT
                                 ||||||||||||    |||||||
                                 TAAAAATTACGT    GTCCCAA
                                       GTAT
GAM1195  KIAA0935 3'  AAGTTTTTAATTCATTGG    30994         G  AC
                                AAGTTTTTAAT CA  TTGG
                                ||||||||||| ||  ||||
                                TTCAAAAATTA GT  AACC
                                      A  __
GAM1195  LHFPL2   3'  AGTTTTTAGTGGTTTGGGGTT  30995        A  CAAC
                                AGTTTTTA TG    TTGGGGTT
                                ||||||||  ||    ||||||||
                                TCAAAAAT AC    AACCCCAA
                                   C  CA__
GAM1195  NIBAN    5'  AAGTTTTTGATGGCAGCCTCAG 30996        A  _  A_  TG
                                AAGTTTTT ATG CA  CT  G
                                |||||||| ||| ||  ||  |
                                TTCAAAAA TAC GT  GA  C
                                   C   C  CG  GT
GAM1195  LOC254549 5'  AAGTTTTTAGTGCATACT    30997         A   _
                                AAGTTTTTA TGCA ACT
                                ||||||||| |||| |||
                                TTCAAAAAT ACGT TGA
                                   C    A
GAM1195  LOC255030 5'  GTTTTTTGTTTTTTGGGGTT   30998       AA  CAAC
                                GTTTTT  TG    TTGGGGTT
                                ||||||  ||    ||||||||
                                CAAAAA  AC    AACCCCAA
                                   __  AAAA
GAM1196  AGTR1    5'  TGGGTCGAATTTGTTGCAAAC  31001     CATA    TTA
                                TGGG   AGTTT   TTGCAAAC
                                ||||   |||||   ||||||||
                                ACCC   TTAAA   AACGTTTG
                                  AGC_    C__
GAM1196  AGTR1    5'  TGGGTCGAATTTGTTGCAAAC  31001     CATA    TTA
                                TGGG   AGTTT   TTGCAAAC
                                ||||   |||||   ||||||||
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                                ACCC   TTAAA  AACGTTTG
                                  AGC_   C__
GAM1196 AGTR1   5' TGGGTCGAATTTGTTGCAAAC 31001    CATA   TTA
                                TGGG   AGTTT  TTGCAAAC
                                ||||   |||||  ||||||||
                                ACCC   TTAAA  AACGTTTG
                                  AGC_   C__
GAM1196 AGTR1   5' TGGGTCGAATTTGTTGCAAAC 31001    CATA   TTA
                                TGGG   AGTTT  TTGCAAAC
                                ||||   |||||  ||||||||
                                ACCC   TTAAA  AACGTTTG
                                  AGC_   C__
GAM1196 AGTR1   5' TGGGTCGAATTTGTTGCAAAC 31001    CATA   TTA
                                TGGG   AGTTT  TTGCAAAC
                                ||||   |||||  ||||||||
                                ACCC   TTAAA  AACGTTTG
                                  AGC_   C__
GAM1196 MGAT5   5' TGAGCATAGGTTGCAA     31002       A  TTTTAT
                                TGGGCATA GT    TGCAA
                                |||||||| ||    |||||
                                ACTCGTAT CA    ACGTT
                                    C _______
GAM1196 RANBP2L1 3' TGGGATAGGTTTTTATT    31003    C  A
                                TGGG ATA GTTTTTATT
                                |||| ||| |||||||||
                                ACCC TAT CAAAAATAA
                                  _  C
GAM1196 CBARA1  3' TGGGGATGTTTATTGCAAA   31004    CATAA  T
                                TGGG   GT TTTATTGCAAA
                                ||||   || ||||||||||
                                ACCC   TA AAATAACGTTT
                                  C____  C
GAM1196 DCTN3   3' TGGGTGTTGCAAATTGCAAAC 31005    CATAA  TTTT
                                TGGG   GT   ATTGCAAAC
                                ||||   ||   |||||||||
                                ACCC   CG   TAACGTTTG
                                  ACAA_  TT__
GAM1196 DCTN3   3' TGGGTGTTGCAAATTGCAAAC 31005    CATAA  TTTT
                                TGGG   GT   ATTGCAAAC
                                ||||   ||   |||||||||
                                ACCC   CG   TAACGTTTG
                                  ACAA_  TT__
GAM1196 FLJ20086 3' GGGCAGATTTTTATTGCAAA  31006    TAA
                                GGGCA  GTTTTTATTGCAAA
                                |||||  ||||||||||||||
                                CCCGT  TAAAAATAACGTTT
                                  C__
GAM1196 KIAA1908 3' GCATACAGAGTTTTTATTGCA 31007     ___
                                GCATA  AGTTTTTATTGCA
                                |||||  |||||||||||||
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                                CGTAT   TCAAAAATAACGT
                                  GTC
GAM1196  LOC146268 3'  TGGGCGAAAGCCACATTTGCAA 31008      AT    TTTA
           AC                    TGGGC  AAGTT   TTGCAAAC
                                 |||||  |||||   ||||||||
                                 ACCCG  TTCGG   AACGTTTG
                                   CT    TGTA
GAM1196  LOC220692 3'  TGGGATAGGTTTTTATT     31003     C   A
                                 TGGG ATA GTTTTTATT
                                 |||| ||| |||||||||
                                 ACCC TAT CAAAAATAA
                                   _  C
GAM1197  TTK      3'  AACAGTCCAATATATTTTA   31011     CA
                                 AGCG  CCAATATATTTTA
                                 ||||  ||||||||||||
                                 TTGT  GGTTATATAAAAT
                                   CA
GAM1198  TRIM37   3'  TGAATGAATCTTTAAATGTGT  31014          ACTTTTAC
                                 TGAATGAGTCTT      GTGT
                                 ||||||||||||      ||||
                                 ACTTACTTAGAA      CACA
                                       ATTTA___
GAM1198  FLJ23462  3'  TGAATGAGCTAATATGTG    31015        T  TACTTT  C
                                 TGAATGAG CT     TA GTG
                                 |||||||| ||     || |||
                                 ACTTACTC GA     AT CAC
                                     _ TT____  A
GAM1198  LOC257465 3'  TGAATGAGTTTATTTAACACAT 31016         CTTACTTT
           GT                    TGAATGAGT      TACGTGT
                                 |||||||||      |||||||
                                 ACTTACTCA      GTGTACA
                                      AATAAATT
GAM1199  ACK1     3'  TTCTGCCCGACACCCCAG    31019        A  T
                                 TTTTGCCC AT TCCCAG
                                 |||||||| || ||||||
                                 AAGACGGG TG GGGGTC
                                     C  T
GAM1199  ALS2     3'  TTTTGCTTATTTCCCAG     31020       CCA
                                 TTTTGC   ATTTCCCAG
                                 ||||||   |||||||||
                                 AAAACG   TAAAGGGTC
                                    AA_
GAM1199  AQP6     5'  TCTTGGCCTTTCCCAG      31021      C  AA
                                 TTTTG CC  TTTCCCAG
                                 ||||| ||  ||||||||
                                 AGAAC GG  AAAGGGTC
                                   C  __
GAM1199  ATP5B    5'  TTCTGCCCAAAGTCTCAG    31022         TT  C
                                 TTTTGCCCAA  TC CAG
                                 ||||||||||  || |||
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                                AAGACGGGTT  AG GTC
                                      TC  A
GAM1199  BARX2    3'  TTTTCCCTTCTCCCCAG     31023      G   AA
                                TTTT CCC  TTTCCCAG
                                |||| |||  ||||||||
                                AAAA GGG  GAGGGGTC
                                  _   AA
GAM1199  C1orf1   3'  TTTTGCCATGTTTCCCAG    31024        CAA
                                TTTTGCC   TTTCCCAG
                                |||||||   ||||||||
                                AAAACGG   AAAGGGTC
                                    TAC
GAM1199  CD5L     3'  TCTTGACCTTTTCCCAG     31025      C  AA
                                TTTTG CC  TTTCCCAG
                                |||||  ||  ||||||||
                                AGAAC GG  AAAGGGTC
                                   T  A_
GAM1199  CDH1     3'  TTCTGCATTTCCCAG       31026       CCA
                                TTTTGC   ATTTCCCAG
                                ||||||   |||||||||
                                AAGACG   TAAAGGGTC
                                  ___
GAM1199  CRP      3'  TTTTGGACCGTTTCCCAG    31027       C_  AA
                                TTTTG  CC  TTTCCCAG
                                |||||  ||  ||||||||
                                AAAAC  GG  AAAGGGTC
                                   CT  C_
GAM1199  DGKI     3'  CTTTGCCCGAATACCAG     31028         _   TTC
                                TTTTGCCC AAT   CCAG
                                |||||||| |||   ||||
                                GAAACGGG TTA   GGTC
                                     C   T__
GAM1199  DLG4     3'  TTTTCCCCAAAAAAATTCCCAG 31029      G    T____
                                TTTT CCCAA     TTCCCAG
                                |||| |||||     |||||||
                                AAAA GGGTT     AAGGGTC
                                  G     TTTTT
GAM1199  FEN1     3'  TTCTGCCCATCTTCTCTCAG   31030         A__   C
                                TTTTGCCCA   TTTC CAG
                                |||||||||   |||| |||
                                AAGACGGGT   AGAG GTC
                                     AGA    A
GAM1199  FMR2     3'  TTTGCCCAGATTTCATTCC    31031         _    ___
                                TTTGCCCA ATTTC   CC
                                |||||||| |||||   ||
                                AAACGGGT TAAAG   GG
                                     C     TAA
GAM1199  H4F2     3'  TTTTCCCCGGTTTCCCAG    31032      G   AA
                                TTTT CCC  TTTCCCAG
                                |||| |||  ||||||||
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                                AAAA GGG  AAAGGGTC
                                  G   CC
GAM1199  HP      3'  CTTTGCCCTCTTCCAG     31033       AA   C
                                TTTTGCCC  TTT CCAG
                                ||||||||  ||| ||||
                                GAAACGGG  AGA GGTC
                                    __    A
GAM1199  IRF1    3'  TTTTCCCAAGCCCCTCAG    31034     G    T   _
                                TTTT CCCAA TTCC CAG
                                |||| ||||| |||| |||
                                AAAA GGGTT GGGG GTC
                                  _    C    A
GAM1199  KCNK3   3'  TCTTGCCCTGTCACCCAG    31035       AA  T
                                TTTTGCCC  TT CCCAG
                                ||||||||  || |||||
                                AGAACGGG  AG GGGTC
                                    AC  T
GAM1199  KLRG1   3'  TCTTGCTCTATCTCCCAG    31036      CCA
                                TTTTGC   ATTTCCCAG
                                ||||||   |||||||||
                                AGAACG   TAGAGGGTC
                                   AGA
GAM1199  LFG     3'  TTCTGCCCGGCTTCCCCAG   31037       AA_
                                TTTTGCCC  TTTCCCAG
                                ||||||||  ||||||||
                                AAGACGGG  AAGGGGTC
                                    CCG
GAM1199  MAPK4   3'  TTTTACCCACAGACCCCAG   31038        ATT_
                                TTTTGCCCA   TCCCAG
                                |||||||||   ||||||
                                AAAATGGGT   GGGGTC
                                     GTCT
GAM1199  MGAM    3'  CTTTGCCCATCATCCCAG    31039       ATT
                                TTTTGCCCA  TCCCAG
                                |||||||||  ||||||
                                GAAACGGGT  AGGGTC
                                    AGT
GAM1199  MTMR8   3'  TCTTGCCCTTTCGCCCAG    31040       AA  T
                                TTTTGCCC  TT CCCAG
                                ||||||||  || |||||
                                AGAACGGG  AG GGGTC
                                    AA  C
GAM1199  P2RY1   3'  TTCTGCCCACCCCAG      31041       ATT
                                TTTTGCCCA  TCCCAG
                                |||||||||  ||||||
                                AAGACGGGT  GGGGTC
                                    ___
GAM1199  PHLDA3  3'  TTCTGCCCTCCTCCCAG    31042       AA
                                TTTTGCCC  TTTCCCAG
                                ||||||||  ||||||||
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                                AAGACGGG  GGAGGGTC
                                   A_
GAM1199  PPARA    5'  TCTTGAACTTCCCAG      31043      CCC
                                TTTTG   AATTTCCCAG
                                |||||   ||||||||||
                                AGAAC   TTGAAGGGTC
                                  ___
GAM1199  SCN3A    5'  CTTTGCTCCTTTCCCAG     31044       _  AA
                                TTTTGC CC  TTTCCCAG
                                ||||||  ||  ||||||||
                                GAAACG GG  AAAGGGTC
                                   A  __
GAM1199  SELP     5'  TTCTGCCCAACCCAG       31045         TTT
                                TTTTGCCCAA   CCCAG
                                ||||||||||   |||||
                                AAGACGGGTT   GGGTC
                                     ___
GAM1199  SH3BP2   3'  TTTTCCCAAGCCCCAG      31046      G    TT
                                TTTT CCCAA  TCCCAG
                                ||||  |||||  ||||||
                                AAAA GGGTT  GGGGTC
                                  _    C_
GAM1199  SLC9A1   3'  TTCTGCCCAATCCACCAG    31047           TC
                                TTTTGCCCAATT  CCAG
                                ||||||||||||  ||||
                                AAGACGGGTTAG  GGTC
                                      GT
GAM1199  TNS      3'  TTTTCCCAACTGTCCAG     31048      G      TC
                                TTTT CCCAATT  CCAG
                                ||||  |||||||  ||||
                                AAAA GGGTTGA  GGTC
                                  _      CA
GAM1199  VAT1     3'  TTTTGCCCTGCCTCCCCAG   31049        AA_
                                TTTTGCCC   TTTCCCAG
                                ||||||||   ||||||||
                                AAAACGGG   GAGGGGTC
                                     ACG
GAM1199  ZIC3     3'  TCTTGCCCAAAACCTTCC    31050          ___
                                TTTTGCCCAA   TTTCC
                                ||||||||||   |||||
                                AGAACGGGTT   GAAGG
                                      TTG
GAM1199  ZNF24    3'  TTTTACATTTCCCAG       31051       CCA
                                TTTTGC   ATTTCCCAG
                                ||||||   |||||||||
                                AAAATG   TAAAGGGTC
                                   ___
GAM1199  ZNF264   3'  TTTTGCCCAACTGCAG      31052           TCC
                                TTTTGCCCAATT   CAG
                                ||||||||||||   |||
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                                AAAACGGGTTGA  GTC
                                      C__
GAM1199 ZNF268   3' TTTTGCCGTACTTCCCAG   31053       CA
                                TTTTGCC ATTTCCCAG
                                ||||||| |||||||||
                                AAAACGG TGAAGGGTC
                                    CA
GAM1199 BACH     3' TTCTGCCCAACGCCTCCC    31054         __
                                TTTTGCCCAAT TTCCC
                                |||||||||||  |||||
                                AAGACGGGTTG GAGGG
                                      CG
GAM1199 CNR2     5' TTCTGTCCTCTCCCAG      31055      C AA
                                TTTTG CC TTTCCCAG
                                ||||| ||  ||||||||
                                AAGAC GG AGAGGGTC
                                   A __
GAM1199 DKFZp547I094 3' TCCTGAAATTTCCCAG      31056      CCC
                                TTTTG  AATTTCCCAG
                                |||||  ||||||||||
                                AGGAC  TTAAAGGGTC
                                   T__
GAM1199 DKFZp761O17121 3' TTTTGTCCAATCCCAG      31057      C   TT
                                TTTTG CCAA TCCCAG
                                ||||| ||||  ||||||
                                AAAAC GGTT AGGGTC
                                   A  __
GAM1199 DNAJC5   3' TTTTGCCAATTCCACAG     31058       C    C
                                TTTTGCC AATTTC CAG
                                ||||||| |||||| |||
                                AAAACGG TTAAGG GTC
                                    _    T
GAM1199 EIF2S1   3' TCTTGCCCTGTCACCCAG    31035       AA  T
                                TTTTGCCC TT CCCAG
                                |||||||| || |||||
                                AGAACGGG AG GGGTC
                                     AC  T
GAM1199 FLJ11259 3' TTTTGCCATGTTTCCCAG    31024       CAA
                                TTTTGCC  TTTCCCAG
                                |||||||  ||||||||
                                AAAACGG  AAAGGGTC
                                     TAC
GAM1199 FLJ12934 3' TTTTCCCACTCCTCCCAG    31059     G   A_
                                TTTT CCCA TTTCCCAG
                                |||| ||||  ||||||||
                                AAAA GGGT GGAGGGTC
                                   _   GA
GAM1199 FLJ14166 3' CTTTGCACCTCCCAG       31060       CCA
                                TTTTGC  ATTTCCCAG
                                ||||||  |||||||||
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                                GAAACG   TGGAGGGTC
                                   ___
GAM1199  FLJ14641  5'  TTTTGCCCAAGCGCTCCC    31061          T__
                                TTTTGCCCAA   TTCCC
                                ||||||||||   |||||
                                AAAACGGGTT   GAGGG
                                     CGC
GAM1199  FLJ20275  3'  TCTTGCCCATTTCCTCAG    31062         A    _
                                TTTTGCCCA TTTCC CAG
                                ||||||||| ||||| |||
                                AGAACGGGT AAAGG GTC
                                     _    A
GAM1199  FLJ20337  3'  TTCTGTCCTCTCCCAG      31055       C  AA
                                TTTTG CC  TTTCCCAG
                                ||||| ||  ||||||||
                                AAGAC GG  AGAGGGTC
                                   A  __
GAM1199  FLJ30213  3'  TTTTACTATTTCCCAG      31063       CCA
                                TTTTGC   ATTTCCCAG
                                ||||||   |||||||||
                                AAAATG   TAAAGGGTC
                                   A__
GAM1199  GDAP2     5'  TTTTCCCAAAATCCTCAG    31064      G    TT  _
                                TTTT CCCAA  TCC CAG
                                |||| |||||  ||| |||
                                AAAA GGGTT  AGG GTC
                                  _    TT   A
GAM1199  HSA250839 3'  TTTTACACCCTTCCCAG     31065       _ AA
                                TTTTGC CC  TTTCCCAG
                                |||||| ||  ||||||||
                                AAAATG GG  GAAGGGTC
                                   T  __
GAM1199  HSPC065   3'  TTTTCCCCAACTTTTCAG    31066      G       CC
                                TTTT CCCAATTT  CAG
                                |||| ||||||||  |||
                                AAAA GGGTTGAA  GTC
                                  G       AA
GAM1199  KIAA0193  5'  TTTTCCCAAATACCACCAG   31067      G    TT_ _
                                TTTT CCCAA   TC CCAG
                                |||| |||||   || ||||
                                AAAA GGGTT   GG GGTC
                                  _    TAT  T
GAM1199  KIAA0252  5'  TCTTGCCCGCCTGCCAG     31068        AA   C
                                TTTTGCCC  TTT CCAG
                                ||||||||  ||| ||||
                                AGAACGGG  GGA GGTC
                                     C_   C
GAM1199  KIAA0319  3'  TTCTGCCTTTCCCCAG      31069        CAA
                                TTTTGCC   TTTCCCAG
                                |||||||   ||||||||
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                                AAGACGG  AAGGGGTC
                                   A__
GAM1199 KIAA0415 3' CTTTGCCCTTTTCCCAG    31070       AA
                                TTTTGCCC TTTCCCAG
                                |||||||| ||||||||
                                GAAACGGG AAAGGGTC
                                   A_
GAM1199 KIAA0676 3' TTCTGCCCATGTTCCTCAG  31071       AT  _
                                TTTTGCCCA TTCC CAG
                                ||||||||| |||| |||
                                AAGACGGGT AAGG GTC
                                   AC   A
GAM1199 KIAA0737 3' TCTTGGACACTTTCCCAG   31072     CC  A
                                TTTTG CA TTTCCCAG
                                ||||| || ||||||||
                                AGAAC GT AAAGGGTC
                                  CT  G
GAM1199 KIAA0759 3' TTCTGCCTCTCCCAG      31073      CAA
                                TTTTGCC  TTTCCCAG
                                |||||||  ||||||||
                                AAGACGG  AGAGGGTC
                                   ___
GAM1199 KIAA1554 5' CTTTGCATCTCCCAG      31074      CCA
                                TTTTGC  ATTTCCCAG
                                ||||||  |||||||||
                                GAAACG  TAGAGGGTC
                                   ___
GAM1199 KIAA1582 5' CTTTGTCCATCTCCCCAG   31075     C  A
                                TTTTG CCA TTTCCCAG
                                ||||| ||| ||||||||
                                GAAAC GGT GAGGGGTC
                                  A  A
GAM1199 KIAA1718 3' TTCTGCCCCACCCCCAG    31076      AAT
                                TTTTGCCC  TTCCCAG
                                ||||||||  |||||||
                                AAGACGGG  GGGGGTC
                                   GT_
GAM1199 KIAA1719 3' CTTTGCCCAACTAACCAG   31077        TC
                                TTTTGCCCAATT  CCAG
                                ||||||||||||  ||||
                                GAAACGGGTTGA  GGTC
                                     TT
GAM1199 KIAA1853 5' TTCTGCCCTTCCTCAG     31078      AAT  _
                                TTTTGCCC  TTCC CAG
                                ||||||||  |||| |||
                                AAGACGGG  AAGG GTC
                                   ___  A
GAM1199 KIAA1904 3' TTTTCCCAGACCTACCCAG  31079    G  _  _
                                TTTT CCCA ATTT CCCAG
                                |||| |||| |||| |||||
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                                AAAA GGGT TGGA GGGTC
                                  _   C   T
GAM1199  MEP50    3'  TTTTGCCCATATTCCTTCAG  31080        AT   __
                                TTTTGCCCA  TTCC  CAG
                                |||||||||  ||||  |||
                                AAAACGGGT  AAGG  GTC
                                     AT   AA
GAM1199  NAF1     3'  TTTTCCCAGTCACTCCCAG   31081     G   AT__
                                TTTT CCCA   TTCCCAG
                                |||| ||||   |||||||
                                AAAA GGGT   GAGGGTC
                                  _   CAGT
GAM1199  NUDT11   3'  TTTTGCCCTCTCTCAG     31082       AA   C
                                TTTTGCCC  TTTC CAG
                                ||||||||  |||| |||
                                AAAACGGG  AGAG GTC
                                     __   A
GAM1199  PEG10    3'  TTCTGCCCAGGTCTTTCCAG  31083        A__  C
                                TTTTGCCCA   TTT CCAG
                                |||||||||   ||| ||||
                                AAGACGGGT   GAA GGTC
                                     CCA  A
GAM1199  RBAK     3'  TTTTACCTTTTCCCAG     31084       CAA
                                TTTTGCC   TTTCCCAG
                                |||||||   ||||||||
                                AAAATGG   AAAGGGTC
                                    A__
GAM1199  WIRE     5'  TCTTGCCCTGCTCCCAG    31085       AAT
                                TTTTGCCC   TTCCCAG
                                ||||||||   |||||||
                                AGAACGGG   GAGGGTC
                                     AC_
GAM1199  LOC113523 3'  TCTTGCCCTGTCGCCCAG   31086       AA  T
                                TTTTGCCC  TT CCCAG
                                ||||||||  || |||||
                                AGAACGGG  AG GGGTC
                                     AC  C
GAM1199  LOC144473 5'  TCTTGTTCCATTTCCCAG   31087      C_   A
                                TTTTG  CCA TTTCCCAG
                                |||||  ||| ||||||||
                                AGAAC  GGT AAAGGGTC
                                   AA   _
GAM1199  LOC146243 5'  TTCTGCCCATCTTCCCAG   31088        A
                                TTTTGCCCA TTTCCCAG
                                ||||||||| ||||||||
                                AAGACGGGT GAAGGGTC
                                     A
GAM1199  LOC149069 3'  TTCAACACAGTTTCCCAG   31089     T  C  A
                                TTT GC CA TTTCCCAG
                                ||| || || ||||||||
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                                AAG TG GT AAAGGGTC
                                  T  T  C
GAM1199  LOC149460 5'  TTCTGCCCAAGAGCCCCAG   31090          TT_
                                TTTTGCCCAA   TCCCAG
                                ||||||||||   ||||||
                                AAGACGGGTT   GGGGTC
                                     CTC
GAM1199  LOC152200 3'  TTTTCCCCAAGTCTTTTCCAG  31091      G    ___   C
                                TTTT CCCAA   TTT CCAG
                                |||| |||||   ||| ||||
                                AAAA GGGTT   AAA GGTC
                                  G    CAG   A
GAM1199  LOC152453 3'  TTTTGCCATGCTTCCCAG    31092        CAA
                                TTTTGCC   TTTCCCAG
                                |||||||   ||||||||
                                AAAACGG   GAAGGGTC
                                    TAC
GAM1199  LOC153577 5'  TTCTGCCCCTCTCCAG      31093        AAT  _
                                TTTTGCCC   TTC CCAG
                                ||||||||   ||| ||||
                                AAGACGGG   GAG GGTC
                                    ___   A
GAM1199  LOC154739 5'  TTTTGCCCTTCCCAG       31094        AAT
                                TTTTGCCC   TTCCCAG
                                ||||||||   |||||||
                                AAAACGGG   AAGGGTC
                                    ___
GAM1199  LOC157660 3'  TCTTGCCCAACCACAG      31095         TTT  _
                                TTTTGCCCAA   CC CAG
                                ||||||||||   || |||
                                AGAACGGGTT   GG GTC
                                     ___  T
GAM1199  LOC167147 5'  TTTTCCCCCTCCCCAG      31096      G   AA
                                TTTT CCC  TTTCCCAG
                                |||| |||  ||||||||
                                AAAA GGG  GAGGGGTC
                                  G   __
GAM1199  LOC199907 3'  TCCTGAAAATTTCCCAG     31097      CCC
                                TTTTG   AATTTCCCAG
                                |||||   ||||||||||
                                AGGAC   TTAAAGGGTC
                                   TT_
GAM1199  LOC201868 3'  CTTTGCCTTTCCCAG       31098        CAA
                                TTTTGCC   TTTCCCAG
                                |||||||   ||||||||
                                GAAACGG   AAAGGGTC
                                    ___
GAM1199  LOC203276 3'  TTTTGCCCTTCCCAG       31094        AAT
                                TTTTGCCC   TTCCCAG
                                ||||||||   |||||||
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                                AAAACGGG   AAGGGTC
                                           ___
GAM1199  LOC203305 3'  TTTTGCCCTTCCCAG      31094        AAT
                                TTTTGCCC   TTCCCAG
                                ||||||||   |||||||
                                AAAACGGG   AAGGGTC
                                           ___
GAM1199  LOC220021 3'  TTCTCCCTTTCCCAG      31099     G   AA
                                TTTT CCC  TTTCCCAG
                                |||| |||  ||||||||
                                AAGA GGG  AAAGGGTC
                                  _  __
GAM1199  LOC221415 5'  TCTTGTCCCCTTTCCCAG    31100      _   AA
                                TTTTG CCC  TTTCCCAG
                                ||||| |||  ||||||||
                                AGAAC GGG  AAAGGGTC
                                   A   G_
GAM1199  LOC221431 3'  TTTTGCCCAGCTTTCTCA    31101        A_    C
                                TTTTGCCCA  TTTC CA
                                |||||||||  |||| ||
                                AAAACGGGT  AAAG GT
                                     CG    A
GAM1199  LOC253634 3'  TCTTGCCCCGACCTCCCAG   31102        A_
                                TTTTGCCC  ATTTCCCAG
                                ||||||||  |||||||||
                                AGAACGGG  TGGAGGGTC
                                     GC
GAM1199  LOC254243 3'  TTTTGCCCTTCCCAG      31094        AAT
                                TTTTGCCC   TTCCCAG
                                ||||||||   |||||||
                                AAAACGGG   AAGGGTC
                                           ___
GAM1199  LOC254531 5'  TTTTCCCAGTTCCCAG     31103     G    AT
                                TTTT CCCA  TTCCCAG
                                |||| ||||  |||||||
                                AAAA GGGT  AAGGGTC
                                  _    C_
GAM1199  LOC255057 3'  TTTTCCCAGCCTCCCAG    31104     G    A
                                TTTT CCCA TTTCCCAG
                                |||| |||| ||||||||
                                AAAA GGGT GGAGGGTC
                                  _    C
GAM1199  LOC255654 5'  TTCTGCCATTCTCCCAG    31105       CAA
                                TTTTGCC   TTTCCCAG
                                |||||||   ||||||||
                                AAGACGG   AGAGGGTC
                                    TA_
GAM1199  LOC63923  3'  TCTTGCCCTAATCCAG     31106        _   TTC
                                TTTTGCCC AAT   CCAG
                                |||||||| |||   ||||
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                                AGAACGGG TTA   GGTC
                                    A  ___
GAM1199  LOC90038  3'  TTTTGCCCTTCCCAG      31094        AAT
                                TTTTGCCC   TTCCCAG
                                ||||||||   |||||||
                                AAAACGGG   AAGGGTC
                                    ___
GAM1199  LOC92539  5'  TTTGCTCAAGTCTCCCAG    31107      C  _
                                TTTGC CAA TTTCCCAG
                                ||||| ||| ||||||||
                                AAACG GTT AGAGGGTC
                                   A  C
GAM1199  LOC93624  5'  TCTTGTCCTTCCCCAG      31108      C  AA
                                TTTTG CC  TTTCCCAG
                                ||||| ||  ||||||||
                                AGAAC GG  AAGGGGTC
                                   A  __
GAM1200  FLJ12455  3'  TTCGTGGGGACACCTTCAGAGT 31111      CGA       C_
                                TTCG   GGGACACC  CAGAGT
                                ||||   ||||||||  ||||||
                                AAGC   CCCTGTGG  GTCTCA
                                  AC_      AA
GAM1200  LOC203392 5'  TCCGTGGGGGACACCTAGC    31112      CGA       CCAG
                                TTCG   GGGACACC    AGT
                                ||||   ||||||||    |||
                                AGGC   CCCTGTGG    TCG
                                  ACC      A___
GAM1201  ARHGDIA   3'  AGAGGCTAGTGAGGCCCC    31115        AC   ACGGC
                                AGAGGCTA  GAG    GTCCC
                                ||||||||  |||    |||||
                                TCTCCGAT  CTC    CGGGG
                                    CA  _____
GAM1201  DPP6      3'  AGAGGCTAGTGTGGGCGGGTCT 31116        ACGAGA_  C  C
           CA                    AGAGGCTA      CGG GTC CA
                                ||||||||      ||| ||| ||
                                TCTCCGAT      GCC CAG GT
                                    CACACCC  _  A
GAM1201  FGF4      5'  AGAGCTGCGCCTGTGGCGTCCC 31117      G  AA  AGAC_
                                AGAG CT  CG    GGCGTCCC
                                |||| ||  ||    ||||||||
                                TCTC GA  GC    CCGCAGGG
                                  _  C_  GGACA
GAM1201  PCTK1     5'  GAGGCGGAGGCGGCGTCCC   31118      TAAC   A
                                GAGGC   GAG CGGCGTCCC
                                |||||   ||| |||||||||
                                CTCCG   CTC GCCGCAGGG
                                  C___   C
GAM1201  PCTK1     5'  GAGGCGGAGGCGGCGTCCC   31118      TAAC   A
                                GAGGC   GAG CGGCGTCCC
                                |||||   ||| |||||||||
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                                CTCCG   CTC GCCGCAGGG
                                  C___  C
GAM1201  PFKM     3'  AAAGGCTGATGGCGTCCC    31119       AACGA  C
                                AGAGGCT    GA GGCGTCCC
                                |||||||    || ||||||||
                                TTTCCGA    CT CCGCAGGG
                                   _____ A
GAM1201  PPT2     3'  AGAGGCTACTGAGGCCCCCC  31120        A GA  C   G
                                AGAGGCTA C  GA GGC TCCC
                                |||||||| |  || ||| ||||
                                TCTCCGAT G  CT CCG GGGG
                                    _ A_ _   G
GAM1201  TPMT     3'  AGAGGCTGACAAGACATATC  31121       A       GC
                                AGAGGCT ACGAGACG  GTC
                                ||||||| ||||||||  |||
                                TCTCCGA TGTTCTGT  TAG
                                    C       A_
GAM1201  ARP3BETA 3'  GAGGCTGGCAGACAGCGGTC  31122       AA G      _
                                GAGGCT  C AGACGGCG TC
                                ||||||  | ||||||||  ||
                                CTCCGA  G TCTGTCGC AG
                                   CC _       C
GAM1201  CASKIN1  3'  AGCGGCTGGCCGGGCGTCCC  31123    A   AA_  AGAC
                                AG GGCT   CG    GGCGTCCC
                                || ||||   ||    ||||||||
                                TC CCGA   GC    CCGCAGGG
                                 G   CCG  _____
GAM1201  FLJ23112 5'  AGAGGCAGAGGGTGGCGTCCCA 31124       TAAC   AC_
                                AGAGGC   GAG   GGCGTCCCA
                                ||||||   |||   |||||||||
                                TCTCCG   CTC   CCGCAGGGT
                                   T___   CCA
GAM1201  KIAA0599 3'  AGAGGCTAGTGACAACCTC   31125        ACGA     G
                                AGAGGCTA    GACGGC TC
                                ||||||||    |||||| ||
                                TCTCCGAT    CTGTTG AG
                                    CA__     G
GAM1201  KIAA0700 3'  AGCCACGGGGGCGGCGTCC   31126      A  AGA_
                                GGCTA CG    CGGCGTCC
                                ||||| ||    ||||||||
                                TCGGT GC    GCCGCAGG
                                  _ CCCC
GAM1201  KIAA1332 3'  AGAGGCTACATGGGACGCAGGC 31127        ACGA_   G  TC
           C                     AGAGGCTA    GACG CG  CC
                                ||||||||    |||| ||  ||
                                TCTCCGAT    CTGC GT  GG
                                    GTACC    _  CC
GAM1201  MIG      3'  AGAGGCTAACTGGGCACC    31128         GAGAC    T
                                AGAGGCTAAC    GGCG CC
                                ||||||||||    |||| ||
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                                TCTCCGATTG    CCGT GG
                                      AC___   _
GAM1201  MKRN4    3'  AGGGGTTGACAAGACAGGCCC  31129    A  CTA       C
                                AG GG   ACGAGACGG GTCC
                                || ||   ||||||||| ||||
                                TC CC   TGTTCTGTC CGGG
                                 C  AAC       _
GAM1201  Rab11-FIP3 5'  AGAGGCTAGTGGTGCGGAGGGC 31130        A_____  A  C
           G                     AGAGGCTA     CG GA GGCG
                                |||||||||     || || ||||
                                TCTCCGAT     GC CT CCGC
                                     CACCAC  _  C
GAM1201  STX3A    5'  GAGGCAGGTAGCGCGTCCCA   31131      TAACG  A  G
                                GAGGC    AG CG CGTCCCA
                                |||||    || || |||||||
                                CTCCG    TC GC GCAGGGT
                                   TCCA_  _  _
GAM1201  LOC124739 3'  GGCTGACCAGACATCCC     31132     A  G   GGC
                                GGCT AC AGAC   GTCCC
                                |||| || ||||   |||||
                                CCGA TG TCTG   TAGGG
                                  C  G   ___
GAM1201  LOC150035 5'  GAGGCTAAGAGGTCC       31133        C   ACGGC
                                GAGGCTAA GAG    GTCC
                                |||||||| |||    ||||
                                CTCCGATT CTC    CAGG
                                     _  ______
GAM1201  LOC151979 5'  AGAGGCCAGGCGCGGTGTCTCA 31134        A_  AGA   C   C
                                AGAGGCTA  CG   CGG GTC CA
                                ||||||||  ||   ||| ||| ||
                                TCTCCGGT  GC   GCC CAG GT
                                     CC  ___   A   A
GAM1201  LOC196483 5'  AAGGCAGAGGGTGGCGTCCCA  31135      TAAC   AC_
                                GAGGC   GAG   GGCGTCCCA
                                |||||   |||   |||||||||
                                TTCCG   CTC   CCGCAGGGT
                                   T___   CCA
GAM1201  LOC200862 5'  AGAGGCTAATAGATGTGCCCA  31136        CG   CGGC  _
                                AGAGGCTAA  AGA    GT CCCA
                                |||||||||  |||    || ||||
                                TCTCCGATT  TCT    CA GGGT
                                     A_   A___  C
GAM1201  LOC200953 5'  GGCTAACGGAGAGCCC      31137        A  C  C T
                                GGCTAACG GA GG G CCC
                                |||||||| || || | |||
                                CCGATTGC CT CT C GGG
                                     _  _  _ _
GAM1201  LOC219988 3'  AGAGGTAATGAGACAAC     31138      C   C
                                AGAGG TAA GAGACGGC
                                ||||| ||| ||||||||
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                                TCTCC ATT CTCTGTTG
                                  _  A
GAM1201  LOC221288 3'  AGAGGCTAACGGACTTCCCC  31139          A  GGCG
                                AGAGGCTAACG GAC   TCCC
                                |||||||||||| |||   ||||
                                TCTCCGATTGC CTG   GGGG
                                      _  AA__
GAM1201  LOC51236  3'  AGAGGCCAATGAGAGCACCCA  31140        C   CG  T
                                AGAGGCTAA GAGA  GCG CCCA
                                ||||||||| ||||  ||| ||||
                                TCTCCGGTT CTCT  CGT GGGT
                                      A   __  _
GAM1201  LOC56930  5'  AGAGGCTAACCAGGCAGGCCTC 31141         G  A _  G
            C                    AGAGGCTAAC AG C GGC TCC
                                ||||||||||| || | ||| |||
                                TCTCCGATTG TC G CCG AGG
                                      G  C T  G
GAM1202  CLDN3   5'  CGGCAAGGCCCGCTCCACC   31144   A  TAA
                                CG CAA  CCCGCTCCGCC
                                || |||  ||||||||||
                                GC GTT  GGGCGAGGTGG
                                 C  CC_
GAM1202  TMEPAI   5'  CGCGGGACCGCGCTCCGCTGCG 31145   ACAATA  _     CA
                                CG    ACC CGCTCCGC  CG
                                ||    ||| ||||||||  ||
                                GC    TGG GCGAGGCG  GC
                                 GCCC__  C      AC
GAM1202  ZNF26   5'  GACAATAATCCCCAGCACG   31146       CCCG   C
                                GACAATAA   CTCCG CACG
                                ||||||||   ||||| ||||
                                CTGTTATT   GGGGT GTGC
                                     A___    C
GAM1202  KIAA0596  5'  CGGCAATTTCAGCTCCGCCGCG 31147   A   AACCC     A
                                CG CAAT    GCTCCGCC CG
                                || ||||    |||||||| ||
                                GC GTTA    CGAGGCGG GC
                                 C   AAGT_     C
GAM1203  ANK1    3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  ANK1    3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  ANK1    3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  ANK1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  ANK1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  ANK1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  ANK1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  ANK1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  ANK1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  ANK1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  APBA1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  APBA1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  ASTN    3' TGTGCACACGTGTGTGTGTGT  31151     TT
                                TGTGC  TGCGTGTGTGTGT
                                |||||  ||||||||||||||
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                                ACACG  GTGCACACACACACA
                                  T_
GAM1203 ASTN     3'  TGTGCACACGTGTGTGTGTGT  31151      TT
                                TGTGC  TGCGTGTGTGTGTGT
                                |||||  ||||||||||||||||
                                ACACG  GTGCACACACACACA
                                  T_
GAM1203 CACNA2D2 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 CACNA2D2 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 CACNA2D2 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 CACNA2D2 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 CACNG3   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 CACNG3   5'  TCTGTGTGAGTGTGTGTGTGTG 31152       CTT_  C
           TGT                    TTTGTG    TG GTGTGTGTGTGT
                                ||||||    || ||||||||||||
                                AGACAC    AC CACACACACACA
                                   ACTC  A
GAM1203 CARPX    3'  TTGTAAGAGTGTGTGTGTGTGT 31153       CTTTGC
                                TTGTG     GTGTGTGTGTGT
                                |||||     ||||||||||||
                                AACAT     CACACACACACA
                                  TCTCA_
GAM1203 CBFA2T1  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 CBFA2T1  3'  TGTGCGTGTGTGTGTGTGTGT  31155      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||||
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                                ACACG  AC CACACACACACA
                                  C_  A
GAM1203  CBFA2T1  3'  TATGTGCGTGTGTGTGTGT   31154    CTT
                                TGTG  TGCGTGTGTGTGTGT
                                ||||  ||||||||||||||
                                ATAC  ACGCACACACACACA
                                  ___
GAM1203  CBFA2T1  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

```
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CBFA2T1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CCND1     3'  TTTGTGTGTGTGTGTGTGTG 31156       CTT  C
           T                     TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM1203  CCND1     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CCND1     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CCND1     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CD22      3'  TGTGCGTGTGTGTGTGTGTGT 31155      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||||
```

```
                                ACACG  AC CACACACACACA
                                  C_  A
GAM1203  CD22     3'  TGTGTGTGCGTGTGTGTGTGT  31157     CTT
                                TGTG  TGCGTGTGTGTGTGT
                                ||||  ||||||||||||||
                                ACAC  ACGCACACACACACA
                                  AC_
GAM1203  CDH12    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CDH12    3'  TGTGTTTGTGTGTGTGTGTGTA 31158     C   C         III
                                TGTG TTTG GTGTGTGTGTGT  A
                                |||| |||| ||||||||||||  |
                                ACAC AAAC CACACACACACA  T
                                  _   A          III
GAM1203  CDH12    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CDKN2B   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CDKN2B   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CDKN2B   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CDKN2B   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CDKN2B   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CDKN2B   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CDKN2B   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 CDKN2B  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 CENTD2  5' TCTGTGTGTATGTGTGTGTGT 31159     CTT CG
                                TTTGTG  TG TGTGTGTGTGT
                                ||||||  || ||||||||||
                                AGACAC  AC ACACACACACA
                                   ___ AT
GAM1203 CHES1   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 CHES1   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 CHES1   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 CHES1   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 CHES1   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 CHES1   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 CHES1   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 CHES1   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 CHES1   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CHES1    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CHES1    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CHES1    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  COLQ     5'  TGTGTTTGTGTGTGTGTGTGT  31160      C    C
                                TGTG TTTG GTGTGTGTGTGT
                                |||| |||| ||||||||||||
                                ACAC AAAC CACACACACACA
                                  _    A
GAM1203  COLQ     5'  TGTGTTTGTGTGTGTGTGTGT  31160      C    C
                                TGTG TTTG GTGTGTGTGTGT
                                |||| |||| ||||||||||||
                                ACAC AAAC CACACACACACA
                                  _    A
GAM1203  COLQ     5'  TGTGTTTGTGTGTGTGTGTGT  31160      C    C
                                TGTG TTTG GTGTGTGTGTGT
                                |||| |||| ||||||||||||
                                ACAC AAAC CACACACACACA
                                  _    A
GAM1203  COLQ     5'  TGTGTTTGTGTGTGTGTGTGT  31160      C    C
                                TGTG TTTG GTGTGTGTGTGT
                                |||| |||| ||||||||||||
                                ACAC AAAC CACACACACACA
                                  _    A
GAM1203  COLQ     5'  TGTGTTTGTGTGTGTGTGTGT  31160      C    C
                                TGTG TTTG GTGTGTGTGTGT
                                |||| |||| ||||||||||||
                                ACAC AAAC CACACACACACA
                                  _    A
GAM1203  CRHBP    3'  TGTGTATGTGTGTGTGTGTGT  31161      CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  AT_  A
GAM1203  CRTL1    5'  TGTGAGAGTGTGTGTGTGTGTG 31162      CTT_ C
              T                  TGTG    TG GTGTGTGTGTGT
                                 ||||    || ||||||||||||
```

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                                ACAC    AC CACACACACACA
                                  TCTC  A
GAM1203  CRTL1    5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CRTL1    5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CSF2RB   3'  TGTGCATGTACGTGTGTGTGTG 31164      TT_
           T                     TGTGC   TGCGTGTGTGTGTGT
                                |||||   ||||||||||||||
                                ACACG   ATGCACACACACACA
                                  TAC
GAM1203  CSF2RB   3'  TGTACGTGTGTGTGTGTGTGT  31163      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||||
                                ACATG  AC CACACACACACA
                                  C_  A
GAM1203  DGKA     3'  TGTGTTTTGGGGTGTGTGT   31165     C   CGT
                                TGTG TTTG   GTGTGTGT
                                |||| ||||   ||||||||
                                ACAC AAAC   CACACACA
                                  A   CC_
GAM1203  DGKG     3'  TGTGTATGTGTGTGTGTGTGT  31161     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  AT_  A
GAM1203  DMD      3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  DMD      3'  TGTGTATGTGTGTGTGTGTGT  31161     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  AT_  A
GAM1203  DMD      3'  TGTGTATGTGTGTGTGTGTGT  31161     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  AT_  A
GAM1203  DMD      3'  TGTGTATGTGTGTGTGTGTGT  31161     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
```

```
                          ACAC  AC CACACACACACA
                            AT_ A
GAM1203 DMD    3' TGTGTATGTGTGTGTGTGTGT 31161    CTT C
                          TGTG  TG GTGTGTGTGTGT
                          ||||  || ||||||||||||
                          ACAC  AC CACACACACACA
                            AT_ A
GAM1203 DMD    3' TGTGTATGTGTGTGTGTGTGT 31161    CTT C
                          TGTG  TG GTGTGTGTGTGT
                          ||||  || ||||||||||||
                          ACAC  AC CACACACACACA
                            AT_ A
GAM1203 DMD    3' TATGTGTGTGTGTGTGTG   31166    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ATAC  AC CACACACACAC
                            ___ A
GAM1203 DMD    3' TATGTGTGTGTGTGTGTG   31166    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ATAC  AC CACACACACAC
                            ___ A
GAM1203 DMD    3' TGTGTATGTGTGTGTGTGTGT 31161    CTT C
                          TGTG  TG GTGTGTGTGTGT
                          ||||  || ||||||||||||
                          ACAC  AC CACACACACACA
                            AT_ A
GAM1203 DMD    3' TATGTGTGTGTGTGTGTG   31166    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ATAC  AC CACACACACAC
                            ___ A
GAM1203 DMD    3' TATGTGTGTGTGTGTGTG   31166    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ATAC  AC CACACACACAC
                            ___ A
GAM1203 DMD    3' TGTGTATGTGTGTGTGTGTGT 31161    CTT C
                          TGTG  TG GTGTGTGTGTGT
                          ||||  || ||||||||||||
                          ACAC  AC CACACACACACA
                            AT_ A
GAM1203 DMD    3' TGTGTATGTGTGTGTGTGTGT 31161    CTT C
                          TGTG  TG GTGTGTGTGTGT
                          ||||  || ||||||||||||
                          ACAC  AC CACACACACACA
                            AT_ A
GAM1203 DMD    3' TATGTGTGTGTGTGTGTG   31166    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
```

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                              ATAC  AC CACACACACAC
                                ___ A
GAM1203  DMD    3' TGTGTATGTGTGTGTGTGTGT 31161    CTT C
                              TGTG  TG GTGTGTGTGTGT
                              ||||  || ||||||||||||
                              ACAC  AC CACACACACACA
                                AT_ A
GAM1203  DMD    3' TATGTGTGTGTGTGTGTG   31166    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || |||||||||||
                              ATAC  AC CACACACACAC
                                ___ A
GAM1203  DMD    3' TATGTGTGTGTGTGTGTG   31166    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || |||||||||||
                              ATAC  AC CACACACACAC
                                ___ A
GAM1203  DMD    3' TATGTGTGTGTGTGTGTG   31166    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || |||||||||||
                              ATAC  AC CACACACACAC
                                ___ A
GAM1203  DMD    3' TATGTGTGTGTGTGTGTG   31166    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || |||||||||||
                              ATAC  AC CACACACACAC
                                ___ A
GAM1203  DMD    3' TATGTGTGTGTGTGTGTG   31166    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || |||||||||||
                              ATAC  AC CACACACACAC
                                ___ A
GAM1203  DMD    3' TGTGTATGTGTGTGTGTGTGT 31161    CTT C
                              TGTG  TG GTGTGTGTGTGT
                              ||||  || ||||||||||||
                              ACAC  AC CACACACACACA
                                AT_ A
GAM1203  DMD    3' TGTGTATGTGTGTGTGTGTGT 31161    CTT C
                              TGTG  TG GTGTGTGTGTGT
                              ||||  || ||||||||||||
                              ACAC  AC CACACACACACA
                                AT_ A
GAM1203  DMD    3' TGTGTATGTGTGTGTGTGTGT 31161    CTT C
                              TGTG  TG GTGTGTGTGTGT
                              ||||  || ||||||||||||
                              ACAC  AC CACACACACACA
                                AT_ A
GAM1203  DMD    3' TGTGTATGTGTGTGTGTGTGT 31161    CTT C
                              TGTG  TG GTGTGTGTGTGT
                              ||||  || ||||||||||||
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                                ACAC   AC CACACACACACA
                                  AT_  A
GAM1203  DMD     3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  DMD     3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  EFNB1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  EFNB1   3'  TTTGTGTGTGTGTGTGTGTG 31156       CTT  C
           T                     TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM1203  EFNB1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  EFNB1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  EFNB1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  EHD3    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  EHD3    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  EHD3    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  EHD3    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  EHD3    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  EHD3    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  EHD3    3'  TGTGCATGTTTGTGTGTGTGTG 31167     ___    C          III
            TGTA                  TGC   TTTG GTGTGTGTGTGT   A
                              |||   |||| ||||||||||||  |
                              ACG   AAAC CACACACACACA   T
                                TAC    A          III
GAM1203  EHD3    3'  TTTGTGTGTGTGTGTGTGTGTG 31156       CTT  C
            T                  TTTGTG   TG GTGTGTGTGTGT
                              ||||||   || ||||||||||||
                              AAACAC   AC CACACACACACA
                                 AC_  A
GAM1203  EN2     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  EN2     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  EN2     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  EN2     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  EN2     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  EN2     3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  F7      3'  TGTGCATTGGCGTGTGTGTGTG 31168      _  T
           T                     TGTGC TT GCGTGTGTGTGTGT
                                 |||||  || ||||||||||||||
                                 ACACG AA CGCACACACACACA
                                    T  C
GAM1203  F7      3'  TGTGCATTGGCGTGTGTGTGTG 31168      _  T
           T                     TGTGC TT GCGTGTGTGTGTGT
                                 |||||  || ||||||||||||||
                                 ACACG AA CGCACACACACACA
                                    T  C
GAM1203  FGFR2   3'  TTTGTGCTCTGTAAGTGTGT  31169         CGT
                                TTTGTGCTTTG  GTGTGT
                                ||||||||||   ||||||
                                AAACACGAGAC  CACACA
                                      ATT
GAM1203  FGFR2   3'  TTTGTGCTCTGTAAGTGTGT  31169         CGT
                                TTTGTGCTTTG  GTGTGT
                                ||||||||||   ||||||
                                AAACACGAGAC  CACACA
                                      ATT
GAM1203  FGFR2   3'  TTTGTGCTCTGTAAGTGTGT  31169         CGT
                                TTTGTGCTTTG  GTGTGT
                                ||||||||||   ||||||
                                AAACACGAGAC  CACACA
                                      ATT
GAM1203  FGFR2   3'  TTTGTGCTCTGTAAGTGTGT  31169         CGT
                                TTTGTGCTTTG  GTGTGT
                                ||||||||||   ||||||
                                AAACACGAGAC  CACACA
                                      ATT
GAM1203  FGFR2   3'  TTTGTGCTCTGTAAGTGTGT  31169         CGT
                                TTTGTGCTTTG  GTGTGT
                                ||||||||||   ||||||
                                AAACACGAGAC  CACACA
                                      ATT
GAM1203  FGFR2   3'  TTTGTGCTCTGTAAGTGTGT  31169         CGT
                                TTTGTGCTTTG  GTGTGT
                                ||||||||||   ||||||
                                AAACACGAGAC  CACACA
                                      ATT
GAM1203  FGFRL1  3'  TCTGTGCACGCGTGTGTGTGTG 31171        TT
           T                     TTTGTGC  TGCGTGTGTGTGTGT
                                 |||||||  ||||||||||||||
```

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                                AGACACG  GCGCACACACACACA
                                   T_
GAM1203  FGFRL1   3'  CCGTGTGTGTGTGTGTGT    31172    T  C
                                CT TG GTGTGTGTGTGT
                                || || ||||||||||||
                                GG AC CACACACACACA
                                 C  A
GAM1203  FGFRL1   3'  TGTGTCTGTGTGTGTGTGT   31170     C    C
                                TGTG TTTG GTGTGTGTGT
                                |||| |||| ||||||||||
                                ACAC AGAC CACACACACA
                                  _    A
GAM1203  FLRT2    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLRT2    3'  TGTTTGTGTGTGTGTGTG    31173    C    C
                                TG TTTG GTGTGTGTGTG
                                || |||| ||||||||||
                                AC AAAC CACACACACAC
                                 _    A
GAM1203  FLRT2    3'  TTTGTGTGTGTGTGTGTGTG 31156       CTT  C
           T                     TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM1203  FMR2     3'  TGTGAGTGTGTGTGTGTGTGT  31175     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  TC_  A
GAM1203  FMR2     3'  TGTGTGTGAGTGTGTGTGTGT  31174     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  AC_  T
GAM1203  GFRA2    3'  TTTGCAAGGTGTGTGTGTGT   31176      ___
                                TTTGC   GTGTGTGTGTGT
                                |||||   ||||||||||||
                                AAACG   CACACACACACA
                                   TTC
GAM1203  GLP1R    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  GLP1R    3'  TGTATGTGTGTGTGTGTG    31177     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAT  AC CACACACACAC
                                  ___ A
GAM1203  GLP1R   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  GLP1R   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  GLP1R   3'  TATGTGTGTGTGTGTGTG   31166    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ATAC  AC CACACACACAC
                                  ___ A
GAM1203  GLP1R   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  GLP1R   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  GLP1R   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  GLP1R   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  GLP1R   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  GLP1R   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  GLS     3'  TTTGTGTGCATGTGTGTGTGT  31178     CTT
                                TTTGTG  TGCGTGTGTGTGTGT
                                ||||||  ||||||||||||||
```

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                                AAACAC   ACGTACACACACACA
                                   ___
GAM1203  GNAZ    3'  TGTGTGTGCATGTGTGTGTGT  31179     CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   ||||||||||||||
                                ACAC   ACGTACACACACACA
                                  AC_
GAM1203  GRLF1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  GRLF1   3'  TTTGTGTGTGTGTGTGTGTG 31156       CTT  C
           T                     TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM1203  GRLF1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  GRLF1   3'  TGTGAAGTTTTGTGTGTGTGTG 31180     C___   C
           TGT                    TGTG   TTTG GTGTGTGTGTGT
                                ||||   |||| ||||||||||||
                                ACAC   AAAC CACACACACACA
                                  TTCA   A
GAM1203  GRLF1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  GRLF1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  GRLF1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  GYPA    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  GYPA    3'  TGTGTTTGTGTGTGTGTGTGT  31160     C   C
                                TGTG TTTG GTGTGTGTGTGT
                                |||| |||| ||||||||||||
```

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                                ACAC AAAC CACACACACACA
                                  _   A
GAM1203  GYPA    3'  TTTGTGTGTGTGTGTGTGTGTG 31156       CTT  C
             T                   TTTGTG   TG GTGTGTGTGTGT
                                 ||||||   || ||||||||||||
                                 AAACAC   AC CACACACACACA
                                    AC_  A
GAM1203  HCN4    3'  TTTGTTTTTCTGGTGTGTGT   31181      GC_   C
                                 TTTGT   TTTG GTGTGTGT
                                 |||||   |||| ||||||||
                                 AAACA   AGAC CACACACA
                                   AAA   _
GAM1203  HPS3    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  HPS3    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  HPS3    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  HPS3    3'  TATGTGTGTGTGTGTGTGTG    31166     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ATAC   AC CACACACACAC
                                   ___  A
GAM1203  HPS3    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  HPS3    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  HPS3    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  HPS3    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  HPS3     3'  TTTGTATCATATATGTGTGTGT 31182       CTT____  C
                GTGTGT                  TTGTG      TG GTGTGTGTGTGT
                                |||||      || ||||||||||||
                                AACAT      AC CACACACACACA
                                   AGTATAT  A
GAM1203  HPS3     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  HPS3     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  HPS3     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  IGF1     3'  GTGAATGTGTGTGTGTGTGT    31183     CTT  C
                              GTG   TG GTGTGTGTGTGT
                              |||   || ||||||||||
                              CAC   AC CACACACACACA
                                TT_  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  IGF1     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  ITGA11   3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  ITGA11   3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  ITGA11   3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  ITGA11   3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  ITGA11   3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  ITGA11   3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KCNJ5    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KCNJ5    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KCNJ5    5'  CTCTGTGTGTGTGTGTGT     31184      C
                                CTTTG GTGTGTGTGTGT
                                ||||| ||||||||||||
                                GAGAC CACACACACACA
                                   A
GAM1203  KCNJ5    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KCNJ5    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KCNJ5    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIF1B    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIF1B    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIF1B    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIF1B    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIF1B    3'  TTTGTGTTTTTGTCTGTGT    31185      C   GC  G
                                TTTGTG TTT  GT TGTGT
                                |||||| |||  || |||||
                                AAACAC AAA  CA ACACA
                                   A   A_  G
GAM1203  KIF1B    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIF1B    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIF1B    3'  TCTGTGTATGTGTGTGTGTGTG 31186       CTT  C
              T                  TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AGACAC   AC CACACACACACA
                                   AT_   A
GAM1203  KIF1B    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIF1B    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIF1B    3'  TATGTGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                              ATAC   AC CACACACACAC
                                ___  A
GAM1203  KLF7    3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ATAC   AC CACACACACAC
                                ___  A
GAM1203  KLF7    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KLF7    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KLF7    3'  TGTGTATATGTGTGTGTGTGTG 31187     CTT_  C
               T                 TGTG    TG GTGTGTGTGTGT
                              ||||    || ||||||||||||
                              ACAC    AC CACACACACACA
                                ATAT  A
GAM1203  KLF7    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LDHB    5'  TGAATTTGTGTGTGTGTGTGT  31188    TGC   C
                              TG   TTTG GTGTGTGTGTGT
                              ||   |||| ||||||||||||
                              AC   AAAC CACACACACACA
                               TT_   A
GAM1203  LILRB4   3'  TATGCAAGTTTGTGTGTGTGTG 31189      ___   C
               TGT                TGTGC   TTTG GTGTGTGTGTGT
                              |||||   |||| ||||||||||||
                              ATACG   AAAC CACACACACACA
                                 TTC   A
GAM1203  MAPK10   3'  TGTGTCTGCGTGTGTGTGTGT  31191     C
                              TGTG TTTGCGTGTGTGTGTGT
                              |||| ||||||||||||||||
                              ACAC AGACGCACACACACACA
                                _
GAM1203  MAPK10   3'  TGTGTCTGCATTTGTGTGTGTG 31190     C   ____
               TGT                TGTG TTTGC   GTGTGTGTGTGT
                              |||| |||||   ||||||||||||
                              ACAC AGACG   CACACACACACA
                                _   TAAA
GAM1203  MAPK10   3'  TGTGTCTGCGTGTGTGTGTGT  31191     C
                              TGTG TTTGCGTGTGTGTGTGT
                              |||| ||||||||||||||||
```

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                                ACAC AGACGCACACACACACA
                                  _
GAM1203  MAPK10   3' TGTGTCTGCATTTGTGTGTGTG 31190     C     ____
             TGT                  TGTG TTTGC   GTGTGTGTGTGT
                                  |||| |||||   ||||||||||||
                                  ACAC AGACG   CACACACACACA
                                    _   TAAA
GAM1203  MNT      3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                                  TGTG  TG GTGTGTGTGTG
                                  ||||  || ||||||||||
                                  ACAC  AC CACACACACAC
                                    ___ A
GAM1203  MNT      3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                                  TGTG  TG GTGTGTGTGTG
                                  ||||  || ||||||||||
                                  ACAC  AC CACACACACAC
                                    ___ A
GAM1203  MNT      3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                                  TGTG  TG GTGTGTGTGTG
                                  ||||  || ||||||||||
                                  ACAC  AC CACACACACAC
                                    ___ A
GAM1203  MNT      3' TGTGCGTGCGTGTGTGTGTGT  31192      TT
                                  TGTGC  TGCGTGTGTGTGT
                                  |||||  ||||||||||||||
                                  ACACG  ACGCACACACACACA
                                    C_
GAM1203  MNT      3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                                  TGTG  TG GTGTGTGTGTG
                                  ||||  || ||||||||||
                                  ACAC  AC CACACACACAC
                                    ___ A
GAM1203  MNT      3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                                  TGTG  TG GTGTGTGTGTG
                                  ||||  || ||||||||||
                                  ACAC  AC CACACACACAC
                                    ___ A
GAM1203  MNT      3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                                  TGTG  TG GTGTGTGTGTG
                                  ||||  || ||||||||||
                                  ACAC  AC CACACACACAC
                                    ___ A
GAM1203  MNT      3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                                  TGTG  TG GTGTGTGTGTG
                                  ||||  || ||||||||||
                                  ACAC  AC CACACACACAC
                                    ___ A
GAM1203  MNT      3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                                  TGTG  TG GTGTGTGTGTG
                                  ||||  || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MNT     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MNT     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MUC4    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MUC4    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  NAPB    3'  CTTGTGATATGTGTGTGTGTGT 31193       CTT  C
                                TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                GAACAC   AT CACACACACACA
                                   T__   A
GAM1203  NLGN3   3'  TGTGTCTGCGTGTGTGTGTGT  31191      C
                                TGTG TTTGCGTGTGTGTGTGT
                                |||| ||||||||||||||||
                                ACAC AGACGCACACACACACA
                                  _
GAM1203  NLGN3   3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  NLGN3   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  NLGN3   3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  NR2E1   3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  NR2E1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  NR2E1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  NR2E1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  NR2E1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  NR2E1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  NR2E1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  NR2E1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  NR2E1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  NR2E1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  NR2E1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  NR2E1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  NR2E1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  NR2E1    3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  NR2E1    3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  NR2E1    3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  NR2E1    3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  NR2E1    3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  NR2E1    3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  NR4A2    3' TGTGTGTGTATGTGTGTGTGT  31194      CTT  CG
                                TGTG   TG  TGTGTGTGTGT
                                ||||   ||  ||||||||||
                                ACAC   AC  ACACACACACA
                                  AC_  AT
GAM1203  NR4A2    3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  NR4A2    3' TGTGTCTCTGTGTGTGTGTGTG 31195     _    C
             T                   TGTG CTTTG GTGTGTGTGTGT
                                 |||| ||||| ||||||||||||
                                 ACAC GAGAC CACACACACACA
                                   A    A
GAM1203  NRXN1    3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  NRXN1   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  NRXN1   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  NRXN1   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  NRXN1   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  NRXN1   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  NRXN1   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  NRXN1   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  NRXN1   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  NRXN1   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  NRXN1   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  OLR1    3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  OLR1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  OLR1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  OLR1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  OLR1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  OLR1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  OLR1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  OLR1    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  OXTR    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  OXTR    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  OXTR    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  OXTR     3'  TGTGCGTGTGTGTGTGTGTGT  31155      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||||
                                ACACG  AC CACACACACACA
                                  C_  A
GAM1203  OXTR     3'  TGTGTGCGTGTGTGTGTG    31196     CTT
                                TGTG   TGCGTGTGTGTGTG
                                ||||   ||||||||||||||
                                ACAC   ACGCACACACACAC
                                  ___
GAM1203  PACSIN3  3'  TTTGGTTTTGTGTGTGGGTGTG 31197     TGC   C    T
           T                     TTTG   TTTG GTGTG GTGTGT
                                ||||   |||| ||||| ||||||
                                AAAC   AAAC CACAC CACACA
                                  CA_   A    C
GAM1203  PATE     3'  TCTGTAGTGTGTGTGTGTGTGT 31198       CTT  C
                                TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AGACAT   AC CACACACACACA
                                   C__  A
GAM1203  PATE     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PCDH11X  3'  TGTGCACGTGTGTGTGTGT   31199      TTT
                                TGTGC   GCGTGTGTGTGTGT
                                |||||   ||||||||||||||
                                ACACG   TGCACACACACACA
                                  ___
GAM1203  PCDH11X  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PCDH11X  3'  TGTGCACGTGTGTGTGTGT   31199      TTT
                                TGTGC   GCGTGTGTGTGTGT
                                |||||   ||||||||||||||
                                ACACG   TGCACACACACACA
                                  ___
GAM1203  PCDH11X  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PCDH11X  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 PCDH11X  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 PCDH11X  3' TGTGCACGTGTGTGTGTGT  31199    TTT
                          TGTGC  GCGTGTGTGTGTGT
                          |||||  ||||||||||||
                          ACACG  TGCACACACACACA
                             ___
GAM1203 PCDH11X  3' TGTGCACGTGTGTGTGTGT  31199    TTT
                          TGTGC  GCGTGTGTGTGTGT
                          |||||  ||||||||||||
                          ACACG  TGCACACACACACA
                             ___
GAM1203 PCDH11X  3' TGTGCACGTGTGTGTGTGT  31199    TTT
                          TGTGC  GCGTGTGTGTGTGT
                          |||||  ||||||||||||
                          ACACG  TGCACACACACACA
                             ___
GAM1203 PCDH11X  3' TGTGCACGTGTGTGTGTGT  31199    TTT
                          TGTGC  GCGTGTGTGTGTGT
                          |||||  ||||||||||||
                          ACACG  TGCACACACACACA
                             ___
GAM1203 PCDH11Y  3' TGTGCACGTGTGTGTGTGT  31199    TTT
                          TGTGC  GCGTGTGTGTGTGT
                          |||||  ||||||||||||
                          ACACG  TGCACACACACACA
                             ___
GAM1203 PCDH11Y  3' TGTGCACGTGTGTGTGTGT  31199    TTT
                          TGTGC  GCGTGTGTGTGTGT
                          |||||  ||||||||||||
                          ACACG  TGCACACACACACA
                             ___
GAM1203 PCDH11Y  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 PCDH11Y  3' TGTGTGTGTATGTGTGTGTGT 31194    CTT CG
                          TGTG  TG  TGTGTGTGTGT
                          ||||  ||  ||||||||||
                          ACAC  AC  ACACACACACA
                            AC_ AT
GAM1203 PCDH11Y  3' TGTGCACGTGTGTGTGTGT  31199    TTT
                          TGTGC  GCGTGTGTGTGTGT
                          |||||  ||||||||||||
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                                ACACG  TGCACACACACACA
                                  ___
GAM1203 PCDHB16 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 PCDHB16 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 PCDHB16 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 PCDHB16 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 PCDHB16 5' TATGTGTGTGTGTGTGTG   31166    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ATAC  AC CACACACACAC
                                  ___ A
GAM1203 PCDHB16 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 PCDHB16 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 PCDHB16 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 PCDHB16 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 PCDHB16 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PCDHB16  5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PIM1     3'  TTTGTGCATTTTTTGTGTGTGT 31200       _  GCG
                                TTTGTGC TTT   TGTGTGTGT
                                ||||||| |||   |||||||||
                                AAACACG AAA   ACACACACA
                                    T  AA_
GAM1203  PLAG1    3'  TGTGCATGTGTGTGTGTGTGT  31201      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||||
                                ACACG  AC CACACACACACA
                                   T_  A
GAM1203  PURA     3'  TGTGGCTGTGTGTGTGTGTGT  31202     CT   C
                                TGTG  TTG GTGTGTGTGTGT
                                ||||  ||| ||||||||||||
                                ACAC  GAC CACACACACACA
                                  C_   A
GAM1203  PURA     3'  TGTGTATGCATGTGTGTGTGT  31203     CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   |||||||||||||||
                                ACAC   ACGTACACACACACA
                                  AT_
GAM1203  RAB33A   5'  TGTGCGCGCGTGTGTGTGTGT  31204      TT
                                TGTGC  TGCGTGTGTGTGTGT
                                |||||  |||||||||||||||
                                ACACG  GCGCACACACACACA
                                   C_
GAM1203  RBBP9    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  RBBP9    3'  TGTGTATGTGTGTGTGTGTGT  31161     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  AT_  A
GAM1203  RBBP9    3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  RCV1     3'  TGTGTGTGCATGTGTGTGTGT  31179     CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   |||||||||||||||
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                                ACAC   ACGTACACACACACA
                                  AC_
GAM1203  SCN8A    3'  TGTGAGTGTGTGTGTGTG    31205     CTTTGC
                                TGTG     GTGTGTGTGTG
                                ||||     ||||||||||
                                ACAC     CACACACACAC
                                  TCA___
GAM1203  SLC31A1  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SLC31A1  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SLC31A1  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SLC31A1  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SLC31A1  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SLC31A1  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SLC31A1  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SLC31A1  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SLC31A1  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SLC31A1  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SLC31A1  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SNAI2    3'  TGTGTGTGCATATGTGTGTGT  31207     CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   ||||||||||||||
                                ACAC   ACGTATACACACACA
                                  AC_
GAM1203  SNAI2    3'  TCTGTGGGTGTGTGTGTGTGTG 31206       CTT  C
           T                     TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AGACAC   AC CACACACACACA
                                   CC_  A
GAM1203  SNAP25   3'  CTGTTGTTTTGTGTGTGTGTGT 31208     GC_   C          III
           GTA                    TGT   TTTG GTGTGTGTGTGT   A
                                |||   |||| ||||||||||||  |
                                ACA   AAAC CACACACACACA   T
                                  ACA    A          III
GAM1203  SNAP25   3'  CTGTTGTTTTGTGTGTGTGTGT 31208     GC_   C          III
           GTA                    TGT   TTTG GTGTGTGTGTGT   A
                                |||   |||| ||||||||||||  |
                                ACA   AAAC CACACACACACA   T
                                  ACA    A          III
GAM1203  SNX2     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SNX2     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SNX2     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SNX2     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SNX2     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SNX2     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SNX2     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SRGAP2  3' TATGTGTGTGTGTGTGTGTG   31166    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ATAC  AC CACACACACAC
                                  ___ A
GAM1203 SRGAP2  3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SRGAP2  3' TGTGTAAAATGTGTGTGTGTGT 31209    CTTTGC
                                TGTG    GTGTGTGTGTGT
                                ||||    ||||||||||||
                                ACAC    CACACACACACA
                                  ATTTTA
GAM1203 SRGAP2  3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SRGAP2  3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SRGAP2  3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

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                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 SSX2    3' TTTGTGTGCGTGTGTGTGT   31210     CTT
                              TTTGTG  TGCGTGTGTGTGT
                              ||||||  ||||||||||||
                              AAACAC  ACGCACACACACA
                                ___
GAM1203 SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
```

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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  SSX2    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  SSX3    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  SSX3    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  SSX3    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  SSX3    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  SSX3    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  SSX3    3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  SSX3    3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  TFAP4   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  TFAP4   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  TFAP4   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  TFAP4   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  TFAP4   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  TFAP4   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  TFAP4   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  TFAP4   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  TFAP4   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  TFAP4   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

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                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TFAP4   5'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TFAP4   5'  TATGTGTGTGTGTGTGTG   31166    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ATAC  AC CACACACACAC
                                ___ A
GAM1203  TFAP4   5'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TFAP4   5'  TGTGTATGTGTGTGTGTGTGT 31161    CTT  C
                              TGTG  TG GTGTGTGTGTGT
                              ||||  || ||||||||||||
                              ACAC  AC CACACACACACA
                                AT_ A
GAM1203  TFAP4   5'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TFAP4   5'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
```

```
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
```

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                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  TNFSF5  3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  TTC1    3'  TGCTGGGCTGTGTGTGTGT   31211     TT  G
                                TGCT  GC TGTGTGTGTGT
                                ||||  || ||||||||||
                                ACGA  CG ACACACACACA
                                  CC  _
GAM1203  VSNL1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  VSNL1   3'  TTTGTGTGTGTGTGTGTGTGTG 31156       CTT  C
           T                     TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM1203  VSNL1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  VSNL1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  VSNL1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  VSNL1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  VSNL1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  VSNL1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  VSNL1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 VSNL1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 VSNL1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 VSNL1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 VSNL1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 VSNL1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 VSNL1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 VSNL1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 XRCC1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 XRCC1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 XRCC1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 XRCC1   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 XRCC1    3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 XRCC1    3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 XRCC1    3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 XRCC1    3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 ABCC13   3' TATGTTTGTGTGTGTGT   31212     C  C
                                TGTG TTTG GTGTGTGTGT
                                |||| |||| |||||||||
                                ATAC AAAC CACACACACA
                                  _  A
GAM1203 ALOX15B  3' TCTGTTTTTGTGTGTGTGT  31213     GC  C
                                TTTGT  TTTG GTGTGTGT
                                |||||  |||| ||||||||
                                AGACA  AAAC CACACACA
                                   A_  A
GAM1203 ARHGEF9  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 ARHGEF9  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 ARHGEF9  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 ARHGEF9  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 ARHGEF9  3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 ARHGEF9  3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 ARHGEF9  3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 ARHGEF9  3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 ARHGEF9  3' CTCTGTGTGTGTGTGTGT    31184      C
                                CTTTG GTGTGTGTGTGT
                                ||||| ||||||||||
                                GAGAC CACACACACACA
                                   A
GAM1203 ARHGEF9  3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 ARHGEF9  3' TGTGTCTGTGTGTGTGTGTGT 31214     C   C
                                TGTG TTTG GTGTGTGTGTGT
                                |||| |||| ||||||||||
                                ACAC AGAC CACACACACACA
                                  _   A
GAM1203 BM045    5' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 BM045    5' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 BM045    5' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

```
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  BM045    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  BM045    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  BM045    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  BM045    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  BM045    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  BM045    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  BM045    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C1QR1    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C1QR1    3'  TGTCTCTGTGTGTGTGTGTGT  31215     G    C
                                TGT CTTTG GTGTGTGTGTGT
                                ||| ||||| ||||||||||||
                                ACA GAGAC CACACACACACA
                                  _    A
GAM1203  C1QR1    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C1QR1     3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C1QR1     3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C1QR1     3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C1QR1     3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C1QR1     3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C1QR1     3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  C20orf154 3'  TGACTGTGTGTGTGTGTGT    31216    CT   C
                                TG  TTG GTGTGTGTGTGT
                                ||  ||| ||||||||||||
```

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                                AC  GAC CACACACACACA
                                 T_  A
GAM1203  C20orf154 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C8orf13   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C8orf13   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C8orf13   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C8orf13   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C8orf13   3'  TGTGGGGGTGTGTGTGTGTGTG 31218     CTT_  C
            T                    TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  CCCC  A
GAM1203  C8orf13   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C8orf13   3'  TGTGGGGGTGTGTGTGTGTGT  31217     CTTTGC
                                TGTG    GTGTGTGTGTGT
                                ||||    ||||||||||||
                                ACAC    CACACACACACA
                                  CCCCA_
GAM1203  C8orf13   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  C8orf13   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CAMTA1   3'  TGTGTGTACGTGTGTGTGTGT  31219     CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   ||||||||||||||
                                ACAC   ATGCACACACACACA
                                  AC_
GAM1203  caspr5   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  caspr5   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  caspr5   3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  caspr5   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CBX1     3'  TTTGTGTGTGTATGTGTGTGT  31220      CTT  C
                                TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CATACACACACA
                                   ___  A
GAM1203  CLIC6    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CLIC6    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CLIC6    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  CLIC6    3'  ATGAAATTGTGTGTGTGTGT 31222     CT_  C
                                GTG   TTG GTGTGTGTGTGT
                                |||   ||| ||||||||||||
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                                TAC   AAC CACACACACACA
                                  TTT   A
GAM1203  CLIC6    3'  TTGTGTGTGTGTGTGTGTGTGT 31221      CTT  C
                                TTGTG   TG GTGTGTGTGTGT
                                |||||   || ||||||||||||
                                AACAC   AC CACACACACACA
                                   AC_   A
GAM1203  CLIC6    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___   A
GAM1203  CLIC6    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___   A
GAM1203  CLIC6    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___   A
GAM1203  CLIC6    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___   A
GAM1203  CLIC6    3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___   A
GAM1203  CNOT3    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___   A
GAM1203  CNOT3    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___   A
GAM1203  CNOT3    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___   A
GAM1203  CNOT3    5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CNOT3   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CNOT3   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CNOT3   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CNOT3   5' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CRMP5   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CRMP5   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CRMP5   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CRMP5   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CRMP5   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CRMP5   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CRMP5   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CRMP5   3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CSEN    3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CSEN    3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CSEN    3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CSEN    3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CSEN    3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CSEN    3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CSEN    3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CSEN    3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CSEN    3' TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

```
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CSEN    3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CSEN    3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CSEN    3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CYLC2   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CYLC2   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CYLC2   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CYLC2   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CYLC2   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CYLC2   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  CYLC2   3'  TGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

```
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  CYLC2   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  CYLC2   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  CYLC2   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  CYLC2   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  CYLC2   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  CYLC2   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  CYLC2   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  CYLC2   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  CYLC2   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  CYLC2   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  CYLC2   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  CYLC2   3' TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  dA141H5.1 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  dA141H5.1 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  dA141H5.1 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  dA141H5.1 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  dA141H5.1 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  dA141H5.1 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  dA141H5.1 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  dA141H5.1 3'  TGTGGACGTGCGTGTGTGTGTG 31223     CTT_
                T                TGTG   TGCGTGTGTGTGTGT
                                ||||   ||||||||||||||
                                ACAC   ACGCACACACACACA
                                  CTGC
GAM1203  dA141H5.1 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  dA141H5.1 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  DKFZP434C1715 3'  CTTGTGCTTTGTGTGTGGT   31224          C    T
                                TTTGTGCTTTG GTGTG GT
                                |||||||||| ||||| ||
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                                GAACACGAAAC CACAC CA
                                      A    _
GAM1203  DKFZp762A227 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  DKFZp762A227 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  DKFZp762A227 3'  TTTGTGTGTGTGTGTGTGTG 31156       CTT  C
              T                  TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM1203  DKFZp762A227 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  DKFZp762A227 3'  TGTGTCTTTATTTTGTGTGTGT 31225     _    C___
              GTGT                TGTG CTTTG   GTGTGTGTGTGT
                                |||| |||||   ||||||||||||
                                ACAC GAAAT   CACACACACACA
                                  A    AAAA
GAM1203  DNAJC6   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  DNAJC6   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  DNAJC6   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  DNAJC6   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  DNAJC6   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  DNAJC6   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 DNAJC6  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 DNAJC6  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 DNAJC6  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 DNAJC6  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 DNAJC6  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 DNAJC6  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 DNAJC6  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 DNAJC6  3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 DNAJC6  3' TGTGCGTGCATGTGTGTGTGT 31226     TT
                              TGTGC TGCGTGTGTGTGTGT
                              |||||  ||||||||||||||
                              ACACG ACGTACACACACACA
                                C_
GAM1203 DRIL2   3' TATGTGTGTGTGTGTGTG   31166    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ATAC  AC CACACACACAC
                                ___ A
GAM1203 ERO1L   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
```

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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

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                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ10210 5' TGTACAGCTGTGTGTGTGTGTG 31227     T_  C
             T             TGTGC  TTG GTGTGTGTGTGT
                          |||||  ||| ||||||||||||
                          ACATG  GAC CACACACACACA
                             TC  A
GAM1203 FLJ10210 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ10210  5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ10597  3'  TGTGTAAATGTGTGTGTGTGT  31228      CTTTGC
                                TGTG    GTGTGTGTGTGT
                                ||||    ||||||||||||
                                ACAC    CACACACACACA
                                  ATTTA_
GAM1203  FLJ10718  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ10718  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ10718  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ10718  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ10718  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ10718  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ10718  3'  TTGTGTGTGTGTGTGTGTGTGT 31221      CTT  C
                                TTGTG   TG GTGTGTGTGTGT
                                |||||   || ||||||||||||
                                AACAC   AC CACACACACACA
                                  AC_  A
GAM1203  FLJ10898  3'  CTTGTATTGTGTGTGTGTGTGT 31229      CT   C
                                TTTGTG  TTG GTGTGTGTGTGT
                                ||||||  ||| ||||||||||||
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                                GAACAT  AAC CACACACACACA
                                   __   A
GAM1203  FLJ12078  3'  TGTGTTTGTGTATGTGTGTGT  31230      C    C
                                TGTG TTTG GTGTGTGTGTGT
                                |||| |||| ||||||||||||
                                ACAC AAAC CATACACACACA
                                  _    A
GAM1203  FLJ13352  3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  FLJ13352  3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  FLJ13352  3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  FLJ13352  3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  FLJ13352  3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  FLJ13352  3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  FLJ13352  3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  FLJ13352  3'  CTTTGTGTGTGTGTGTGT    31231      C
                                CTTTG GTGTGTGTGTGT
                                ||||| ||||||||||||
                                GAAAC CACACACACACA
                                   A
GAM1203  FLJ13352  3'  TTTGTGTGTGTGTGTGTGTGTG 31156       CTT  C
            T                    TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM1203  FLJ13352  3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ13352 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ13352 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

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                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ13693 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
```

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                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ13693  3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ14686  3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ14686  3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ14686  3' TTTGTGTGTGTGTGTGTGTGTG 31156       CTT  C
                T              TTTGTG   TG GTGTGTGTGTGT
                              ||||||   || ||||||||||||
                              AAACAC   AC CACACACACACA
                                 AC_  A
GAM1203  FLJ14686  3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ14686  3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ14950  3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ14950  3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ14950  3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ14950  3' TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
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                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ14950 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ14950 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ14950 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ14950 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ14950 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ14950 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ14950 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ14950 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ14950 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ14950 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ14950 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                            ___ A
GAM1203 FLJ14950 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ14950  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ20043  3'  TGTGTGTGCGTGTGTGTGTGT  31157     CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   ||||||||||||||
                                ACAC   ACGCACACACACACA
                                  AC_
GAM1203  FLJ20043  3'  TTGCACACTGTGTGTGTGTGTG 31233     TG T   C
           T                     TTG  C TTG GTGTGTGTGTGT
                                |||  | ||| ||||||||||||
                                AAC  G GAC CACACACACACA
                                  GT T   A
GAM1203  FLJ20043  3'  TGTGCGTGTGTGTGTGTGTGT  31155      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||||
                                ACACG  AC CACACACACACA
                                   C_  A
GAM1203  FLJ20043  3'  TGTGTATGTGCGTGTGTGTGTG 31232     CTT_
           T                     TGTG   TGCGTGTGTGTGTGT
                                ||||   ||||||||||||||
                                ACAC   ACGCACACACACACA
                                  ATAC
GAM1203  FLJ20043  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ20043  3'  TGTGCGTGTGTGTGTGTGTGT  31155      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||||
                                ACACG  AC CACACACACACA
                                   C_  A
GAM1203  FLJ20511  3'  TGTGGGGGTGTGTGTGTGTGTG 31218     CTT_  C
           T                     TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  CCCC  A
GAM1203  FLJ20511  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ20689  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 FLJ20689 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 FLJ20689 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 FLJ20689 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 FLJ20689 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 FLJ20689 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 FLJ20689 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 FLJ20689 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 FLJ20689 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 FLJ20689 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 FLJ20689 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 FLJ20689 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 FLJ20689 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
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                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ21290  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ21290  3'  TGTGTGCATGTGTGTGTGT    31234     CTT
                              TGTG   TGCGTGTGTGTGTGT
                              ||||   ||||||||||||||
                              ACAC   ACGTACACACACACA
                                ___
GAM1203  FLJ21290  3'  TGTGCTTGTGTGTGTGTGTA 31235       T C          III
                              TGTGCTT G GTGTGTGTGTGT   A
                              ||||||| | ||||||||||||   |
                              ACACGAA C CACACACACACA   T
                                  _ A          III
GAM1203  FLJ22601  3'  TGTGCACGTGCGTGTGTGTG 31236      TT_
           T                   TGTGC   TGCGTGTGTGTGTGT
                              |||||   ||||||||||||||
                              ACACG   ACGCACACACACACA
                                 TGC
GAM1203  FLJ22601  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ22601  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ22601  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ22601  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ23120  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  FLJ23120  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
```

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                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  FLJ23120  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  FLJ23120  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  FLJ23120  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  FLJ23120  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  FLJ23120  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  FLJ23120  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  FLJ23120  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  FLJ23120  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203  FLJ23120  3'  TGTGCGTGCATGTGTGTGTGT  31226     TT
                              TGTGC  TGCGTGTGTGTGTGT
                              |||||  ||||||||||||||
                              ACACG  ACGTACACACACACA
                                C_
GAM1203  FLJ23120  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                              TGTG  TG GTGTGTGTGTG
                              ||||  || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ23311  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ23311  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ23311  3'  TATGTGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ23311  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ23311  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ23311  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ23311  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ23311  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLJ32783  3'  TTTGTGTTTGTGTGTGT     31237       C   C
                                TTTGTG TTTG GTGTGT
                                |||||| |||| ||||||
                                AAACAC AAAC CACACA
                                  _    A
GAM1203  FLNC      3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  FLNC     3'  TTTGTGTGTGTGTGTGTGTGTG 31156       CTT  C
                T                  TTTGTG   TG GTGTGTGTGTGT
                                   ||||||   || ||||||||||||
                                   AAACAC   AC CACACACACACA
                                      AC_  A
GAM1203  FLNC     3'  GCACATTTGTGTGTGTGTGTGT 31238    TG _    C
                                   G  C TTTG GTGTGTGTGTGT
                                   |  | |||| ||||||||||||
                                   C  G AAAC CACACACACACA
                                    GT T    A
GAM1203  HH114    3'  TTTGTATAAAGTGTGTGTGTGT 31239       CTTTGC
                GT                   TTTGTG     GTGTGTGTGTGT
                                   ||||||     ||||||||||||
                                   AAACAT     CACACACACACA
                                      ATTTCA
GAM1203  HH114    3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  HH114    3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  HRIHFB2122 3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  HRIHFB2122 3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  HRIHFB2122 3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  HRIHFB2122 3'  TATGCAGTGTGTGTGTGTGTGT 31240       TT  C
                                   TGTGC  TG GTGTGTGTGTGT
                                   |||||  || ||||||||||||
                                   ATACG  AC CACACACACACA
                                      TC  A
GAM1203  HRIHFB2122 3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  HRIHFB2122 3'  TCTGTGTGTCTGTGTGTGTGTG 31241       C_   C
                TGT                  TTTGTG  TTTG GTGTGTGTGTGT
                                |||||| ||||  ||||||||||||
                                AGACAC  AGAC CACACACACACA
                                   AC    A
GAM1203  HRIHFB2122 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  HRIHFB2122 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  HRIHFB2122 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  HRIHFB2122 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  HRIHFB2122 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  HRIHFB2122 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KCND1    3'  TTTGTGCTATCTGAGTGTGTGT 31242        __  C
                                TTTGTGCT  TTG GTGTGTGT
                                |||||||  ||| ||||||||
                                AAACACGA  GAC CACACACA
                                     TA   T
GAM1203  KIAA0087  3'  TGTGTGTTTGTGTGTGTG    31243     CTT  CG
                                TGTG   TG  TGTGTGTGTG
                                ||||   ||  ||||||||||
                                ACAC   AC  ACACACACAC
                                  ___  AA
GAM1203  KIAA0222  3'  TGTGTTTGTGTGTGTGTGTGTA 31158     C   C         III
                                TGTG TTTG GTGTGTGTGTGT   A
                                |||| |||| ||||||||||||   |
                                ACAC AAAC CACACACACACA   T
                                  _   A          III
GAM1203  KIAA0293  3'  TTTGTGTATGTGTGTGTGTGT  31244       CTT  C
                                TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
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                                AAACAC  AT CACACACACACA
                                   ___  A
GAM1203 KIAA0416 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                   ___  A
GAM1203 KIAA0416 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                   ___  A
GAM1203 KIAA0416 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                   ___  A
GAM1203 KIAA0416 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                   ___  A
GAM1203 KIAA0416 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                   ___  A
GAM1203 KIAA0416 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                   ___  A
GAM1203 KIAA0416 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                   ___  A
GAM1203 KIAA0431 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                   ___  A
GAM1203 KIAA0431 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                   ___  A
GAM1203 KIAA0431 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA0431  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA0431  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA0431  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA0431  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA0431  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA0431  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA0471  5'  TGTGAGAGTGTGTGTGTGTGT  31245      CTTTGC
                                TGTG     GTGTGTGTGTGT
                                ||||     ||||||||||||
                                ACAC     CACACACACACA
                                  TCTCA_
GAM1203  KIAA0471  5'  TGTGAGAGTGTGTGTGTGTGTG 31162      CTT_  C
           T                     TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  TCTC  A
GAM1203  KIAA0471  5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA0471  5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0471 5' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0544 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0544 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0544 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0544 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0544 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0544 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA0607 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0607  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0607  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0607  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3'  TATGGAGTGTGTGTGTGTGTGT 31246      CTT  C
                              TGTG   TG GTGTGTGTGTGT
                              ||||   || ||||||||||||
                              ATAC   AC CACACACACACA
                                CTC  A
GAM1203  KIAA0848  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
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                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0848  3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA0869  3' TCTGTTTTTGTGTGTGTGTGTG 31247     GC   C          III
            TA                  TTGT  TTTG GTGTGTGTGTGT   A
                              ||||  |||| ||||||||||||  |
                              GACA  AAAC CACACACACACA   T
                                A_   A          III
GAM1203  KIAA1029  3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA1029  3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  KIAA1029  3' TGTGTGTGTGTGTGTGTGTG   31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
```

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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1029 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1029 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1029 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1029 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1029 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1029 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1029 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1029 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1029 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1029 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1029 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1029 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1029  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1029  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1219  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1219  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1219  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1219  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1219  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1219  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1219  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1219  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1219  3'  TATGCGAGTGTGTGTGTGTGTG 31248      TT_  C
                  T              TGTGC   TG GTGTGTGTGTGT
                                 |||||   || ||||||||||||
```

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                                ATACG   AC CACACACACACA
                                   CTC  A
GAM1203  KIAA1219  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  KIAA1260  3'  TATGACTAATGTGTGTGTGTGT 31249     _  T_  C
             GT                   TGTG CT  TG GTGTGTGTGTGT
                                ||||  ||  || ||||||||||||
                                ATAC GA  AC CACACACACACA
                                   T  TT  A
GAM1203  KIAA1399  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  KIAA1399  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  KIAA1399  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  KIAA1399  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  KIAA1399  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  KIAA1399  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  KIAA1399  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  KIAA1399  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                   ___  A
GAM1203  KIAA1399  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1399  3' CTCTAGGGGTGTGTGTGTGT  31250      C__
                                CTTTG   GTGTGTGTGTGT
                                |||||   ||||||||||||
                                GAGAT   CACACACACACA
                                   CCC
GAM1203  KIAA1399  3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1399  3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1399  3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1545  3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1545  3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1545  3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1545  3' GTGATTTTGTGTGTGTGTGT 31251     C_   C
                                GTG  TTTG GTGTGTGTGTGT
                                |||  |||| ||||||||||||
                                CAC  AAAC CACACACACACA
                                  TA   A
GAM1203  KIAA1545  3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1545  3' TTTGTGTGTGTGTGTGTGTG 31156       CTT  C
            T                    TTTGTG   TG GTGTGTGTGTGT
                                 ||||||   || ||||||||||||
```

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                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM1203  KIAA1545  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1545  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1545  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1545  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1545  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1577  3'  TTGTTGGTGGTGTGTGTGTGT  31252     GCTT  C
                                TTGT    TG GTGTGTGTGTGT
                                ||||    || ||||||||||||
                                AACA    AC CACACACACACA
                                  ACC_  _
GAM1203  KIAA1594  3'  TGTGTGTGTCTGTGTGTGTGT  31253     CTT  CG
                                TGTG   TG  TGTGTGTGTGT
                                ||||   ||  ||||||||||
                                ACAC   AC  ACACACACACA
                                  AC_  AG
GAM1203  KIAA1615  3'  TGTATATAGTGTGTGTGTGTGT 31254     CTT__  C
            GT                    TGTG    TG GTGTGTGTGTGT
                                ||||    || ||||||||||||
                                ACAT    AC CACACACACACA
                                  ATATC  A
GAM1203  KIAA1615  3'  ATATATTGTGTGTGTGTGTGT  31255     CT   C
                                GTG  TTG GTGTGTGTGTGT
                                |||  ||| ||||||||||||
                                TAT  AAC CACACACACACA
                                  AT   A
GAM1203  KIAA1615  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1615  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1615  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1623  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1623  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1623  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1623  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1623  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1623  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1623  3'  TGTTCTGTGTGTGTGTGTG   31256    C   C
                                TG TTTG GTGTGTGTGTG
                                || |||| ||||||||||
                                AC AGAC CACACACACAC
                                 A   A
GAM1203  KIAA1623  3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1623  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1671  3'  TGTGTCTCTGTGTGTGTGTGT  31258      _    C
                                TGTG CTTTG GTGTGTGTGT
                                |||| ||||| ||||||||||
                                ACAC GAGAC CACACACACA
                                  A    A
GAM1203  KIAA1671  3'  TATACTTGTGTGTGTGTGTGT  31257       T C
                                TGTGCTT G GTGTGTGTGTGT
                                ||||||| | ||||||||||||
                                ATATGAA C CACACACACACA
                                   _ A
GAM1203  KIAA1828  5'  TGTGTTTGTGTGTGTGTGTGT  31160     C   C
                                TGTG TTTG GTGTGTGTGTGT
                                |||| |||| ||||||||||||
                                ACAC AAAC CACACACACACA
                                  _   A
GAM1203  KIAA1854  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1854  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1854  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1854  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1854  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1854  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  KIAA1854  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1854 3' TGTGTGTGTGTGTGTGTGTG  31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1854 3' TGTGTGTGTGTGTGTGTGTG  31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1854 3' TGTGTGTGTGTGTGTGTGTG  31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1854 3' TGTGTGTGTGTGTGTGTGTG  31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1854 3' TGTGTGTGTGTGTGTGTGTG  31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1900 5' TGTGTGTGTGTGTGTGTGTG  31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1900 5' TGTGTGTGTGTGTGTGTGTG  31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1900 5' TGTGTGTGTGTGTGTGTGTG  31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1900 5' TGTGTGTGTGTGTGTGTGTG  31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 KIAA1900 5' TGTGCGAAAGTGTGTGTGTGT 31259     TTTGC
                                TGTGC   GTGTGTGTGTGT
                                |||||   ||||||||||||
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                                ACACG    CACACACACACA
                                  CTTT_
GAM1203 KIAA1900 5' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 KIAA1900 5' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 KIAA1900 5' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 KIAA1900 5' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 KIAA1904 3' TTTGTGCTTTGTTTGATGT   31260         CG  T
                                TTTGTGCTTTG  TG GTGT
                                ||||||||||  || ||||
                                AAACACGAAAC  AC TACA
                                     AA  _
GAM1203 KIAA1972 3' TATTTTTTGTGTGTGTGTGTGT 31261     GC   C
                                TGT  TTTG GTGTGTGTGTGT
                                |||  |||| ||||||||||||
                                ATA  AAAC CACACACACACA
                                  AA   A
GAM1203 KIAA1972 3' TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203 KLF12    3' TCTGTGTGTATGTGTGTGTGTG 31262      CTT  C
           T                     TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AGACAC   AT CACACACACACA
                                   AC_  A
GAM1203 LGI4     5' TATGTGAGTGTGTGTGTG    31263     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  T
GAM1203 LHFP     3' TTTGTTGTGTGTGTGTGTGT   31264      GCTT  C
                                TTTGT    TG GTGTGTGTGTGT
                                |||||    || ||||||||||||
```

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                                AAACA   AC CACACACACACA
                                  ____  A
GAM1203  LHFP    3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  LHFP    3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  LHFP    3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  LHFP    3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  LHFP    3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  LHFP    3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  LHFP    3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  LHFP    3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  LHFP    3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  LHFP    3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  LHFP    3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203  LHFP    3'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LHFP     3'  TTGTGTGTGTGTGTGTGTGTGT 31221      CTT  C
                                TTGTG   TG GTGTGTGTGTGT
                                |||||   || ||||||||||||
                                AACAC   AC CACACACACACA
                                   AC_  A
GAM1203  MAP3K2   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MAP3K2   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MAP3K2   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MAWBP    3'  TTTGTGTGTGTGTGTGTGTGTG 31156       CTT  C
            T                    TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM1203  MG61     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MG61     3'  TGTGATTTTGTGTGTGTGTGTG 31265     C_   C
            T                    TGTG  TTTG GTGTGTGTGTGT
                                ||||  |||| ||||||||||||
                                ACAC  AAAC CACACACACACA
                                  TA   A
GAM1203  MG61     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MG61     3'  TTTGTGTGTGTGTGTGTGTGTG 31156       CTT  C
            T                    TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM1203  MGC10067 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  MGC10067  3'  TTTGTGTGTGTGTGTGTGTGTG 31156       CTT  C
             T                   TTTGTG   TG GTGTGTGTGTGT
                                 ||||||   || ||||||||||||
                                 AAACAC   AC CACACACACACA
                                    AC_  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MGC10067  3'  TCTCCACTTTGTGTGTGTGTGT 31266     G      C
            GT                    TTT TGCTTTG GTGTGTGTGTGT
                                ||| ||||||| ||||||||||||
                                AGA GTGAAAC CACACACACACA
                                  G      A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MGC10067  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MGC12679  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MGC12679  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MGC12679  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MGC20481  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  MGC20481  3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

```
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 MGC20481 3' TGTGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 MUC13   3' TTTGTGTGTGTGGTTGTGTGTG 31267      CTT_ CG
           TGT                TTTGTG   TG TGTGTGTGTGT
                              |||||| ||  ||||||||||
                              AAACAC   AC  ACACACACACA
                                 ACAC  CA
GAM1203 N-PAC   3' TGTGTGTGTGTGTGTGTGTG   31150     CTT C
                              TGTG  TG GTGTGTGTGTG
                              |||| || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 N-PAC   3' TGTGTGTGTGTGTGTGTGTG   31150     CTT C
                              TGTG  TG GTGTGTGTGTG
                              |||| || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 N-PAC   3' TGTGTGTGTGTGTGTGTGTG   31150     CTT C
                              TGTG  TG GTGTGTGTGTG
                              |||| || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 N-PAC   3' TGTGTGTGTGTGTGTGTGTG   31150     CTT C
                              TGTG  TG GTGTGTGTGTG
                              |||| || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 N-PAC   3' TGTGTGTGTGTGTGTGTGTG   31150     CTT C
                              TGTG  TG GTGTGTGTGTG
                              |||| || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 N-PAC   3' TGTGTGTGTGTGTGTGTGTG   31150     CTT C
                              TGTG  TG GTGTGTGTGTG
                              |||| || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 N-PAC   3' TGTGTGTGTGTGTGTGTGTG   31150     CTT C
                              TGTG  TG GTGTGTGTGTG
                              |||| || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 N-PAC   3' TGTGTGTGTGTGTGTGTGTG   31150     CTT C
                              TGTG  TG GTGTGTGTGTG
                              |||| || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 N-PAC   3' TGTGTGTGTGTGTGTGTGTG   31150     CTT C
                              TGTG  TG GTGTGTGTGTG
                              |||| || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 N-PAC   3' TGTGTGTGTGTGTGTGTGTG   31150     CTT C
                              TGTG  TG GTGTGTGTGTG
                              |||| || ||||||||||
                              ACAC  AC CACACACACAC
                                ___ A
GAM1203 N-PAC   3' TGTGTGTGTGTGTGTGTGTG   31150     CTT C
                              TGTG  TG GTGTGTGTGTG
                              |||| || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  N-PAC    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  OSBPL9   3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  POU4F2   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  POU4F2   3'  TGTTAGAGGTGTGTGTGTGTGT 31268     GCTT__  C
           GT                     TGT     TG GTGTGTGTGTGT
                                |||     || ||||||||||||
                                ACA     AC CACACACACACA
                                  ATCTCC  A
GAM1203  POU4F2   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  POU4F2   3'  TCTGTTAGAGGTGTGTGTGTGT 31269      GCTTTGC
           GT                     TTTGT      GTGTGTGTGTGT
                                |||||      ||||||||||||
                                AGACA      CACACACACACA
                                   ATCTCCA
GAM1203  POU4F2   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  POU4F2   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  POU4F2   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PPP1R16B 3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  PPP1R16B  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PPP1R16B  3'  TGTGTATATGTGTGTGTGTGTG 31187     CTT_  C
           T                     TGTG   TG GTGTGTGTGTGT
                                 ||||   || ||||||||||||
                                 ACAC   AC CACACACACACA
                                   ATAT  A
GAM1203  PRO0365   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PRO0611   5'  TTTGTTTTTGTGTGTGC     31270      GC   C
                                TTTGT  TTTG GTGTGT
                                |||||  |||| ||||||
                                AAACA  AAAC CACACG
                                   A_   A
GAM1203  PRO1386   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PRO1386   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PRO1386   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PRO1386   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PRO1386   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  PRO1386   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 PRO1386 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 PRO1386 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 PRO1386 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 PRO1386 5' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 RPH3A   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 RPH3A   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 RPH3A   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 RPH3A   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 RPH3A   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 RPH3A   3' TGTGTGTGTGTGTGTGTG   31150    CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SEMA3E   3'  TGTGAGGGGTGTGTGTGTGTGT 31271      CTTTGC
                                TGTG     GTGTGTGTGTGT
                                ||||     ||||||||||||
                                ACAC     CACACACACACA
                                  TCCCCA
GAM1203  SEMA5B   3'  TGTGAGTGTGTGTGTGTGTGT  31175     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  TC_  A
GAM1203  SIAT8C   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SIAT8C   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SIAT8C   5'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  SIAT8C   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SIAT8C   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SIAT8C   5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SNAP29   3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SNAP29   3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNAP29  3' TGTGTGTGTGTGTGTGTG  31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNAP29  3' TGTGTGTGTGTGTGTGTG  31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNAP29  3' TGTGTGTGTGTGTGTGTG  31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNAP29  3' TGTGTGTGTGTGTGTGTG  31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNAP29  3' TGTGTGTGTGTGTGTGTG  31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNAP29  3' TGTGTGTGTGTGTGTGTG  31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNAP29  3' TGTGTGTGTGTGTGTGTG  31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNAP29  3' TGTGTGTGTGTGTGTGTG  31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNAP29  3' TGTGTGTGTGTGTGTGTG  31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SNAP29  3' TGTGTGTGTGTGTGTGTG  31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 SP192   3' TGTGTATGTGTGTGTGTGT 31161    CTT C
                                TGTG  TG GTGTGTGTGTGT
                                ||||  || ||||||||||||
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                                ACAC   AC CACACACACACA
                                  AT_  A
GAM1203  SPIN    3'  TGTGTGGTGTGTGTGT     31272     CTT  C
                                TGTG   TG GTGTGTGTGT
                                ||||   || ||||||||||
                                ACAC   AC CACACACACA
                                  ___  _
GAM1203  SPRY4   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SPRY4   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SPRY4   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SPRY4   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SPRY4   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SPRY4   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SPRY4   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SPRY4   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SPRY4   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SPRY4   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
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                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  SPRY4    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  SPRY4    3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  SR-BP1   3'  TGTGATATGTGTGTGTGTGT 31273      CTT  C
                              TGTG   TG GTGTGTGTGTGT
                              ||||   || ||||||||||||
                              ACAC   AC CACACACACACA
                                TAT  A
GAM1203  SR-BP1   3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  SR-BP1   3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ATAC   AC CACACACACAC
                                ___  A
GAM1203  SSX5     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  SSX5     3'  TCTGTGTGGCATGTGTGTGTGT 31274       CTTT
                              TTTGTG   GCGTGTGTGTGTGT
                              ||||||   ||||||||||||||
                              AGACAC   CGTACACACACACA
                                 AC__
GAM1203  SSX5     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  SSX5     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  SSX5     3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SSX5     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SSX5     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SSX5     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  SSX5     3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  ZNF387   3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  ZNF387   3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  ZNF387   3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC121133 5'  TGTGTTTGTGTTTGTGTGTGT  31275      C   C  G
                                TGTG TTTG GT TGTGTGTGT
                                |||| |||| || |||||||||
                                ACAC AAAC CA ACACACACA
                                  _   A  A
GAM1203  LOC121506 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC126917 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC126917 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC126917 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC126917 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC126917 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC126917 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC126917 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC127435 3'  CTTGTGCATGTGTGTGTGTGT  31276       TTTGC
                                TTTGTGC    GTGTGTGTGTGT
                                |||||||    ||||||||||||
                                GAACACG    CACACACACACA
                                   TA___
GAM1203  LOC128989 3'  TGTGCACCTGTGTGTGTGTGT  31277      T  GC
                                TGTGC TT  GTGTGTGTGTGT
                                ||||| ||  ||||||||||||
                                ACACG GG  CACACACACACA
                                  T  A_
GAM1203  LOC132235 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC132235 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC132235 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC132235 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC132235 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC132235 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC132235 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC143286 3'  TATGAATGTGTGTGTGTGTGT  31278      CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ATAC   AC CACACACACACA
                                  TT_  A
GAM1203  LOC143381 3'  TTGTGTGTGTGTGTGTGTGTGT 31221       CTT  C
                                TTGTG   TG GTGTGTGTGTGT
                                |||||   || ||||||||||||
                                AACAC   AC CACACACACACA
                                   AC_  A
GAM1203  LOC143381 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC143381 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC143381 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC143381 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC143381 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC143381 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC143381 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC143381 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145135 5'  TGCAGTGCGTGTGTGTGTGT  31279      TT
                                TGC  TGCGTGTGTGTGTGT
                                |||  ||||||||||||||
                                ACG  ACGCACACACACACA
                                  TC
GAM1203  LOC145135 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145135 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145719 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145719 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145719 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145719 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145719 5'  TGTATATATGTGTGTGTGTGTG 31280     CTT_  C
                T                TGTG    TG GTGTGTGTGTGT
                                ||||    || ||||||||||||
                                ACAT    AC CACACACACACA
                                  ATAT  A
GAM1203  LOC145719 5'  TATGTGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145719 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145719 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145719 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145719 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145720 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145720 5'  TGTATATATGTGTGTGTGTGTG 31280     CTT_  C
                T                TGTG    TG GTGTGTGTGTGT
                                ||||    || ||||||||||||
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                                ACAT    AC CACACACACACA
                                  ATAT  A
GAM1203  LOC145720 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145720 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145720 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145720 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145720 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145720 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145720 5'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC145720 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC146856 3'  TGCTTGTGTGTGTGTGTGT   31281      T C
                                TGCTT G GTGTGTGTGTGT
                                ||||| | ||||||||||||
                                ACGAA C CACACACACACA
                                  _ A
GAM1203  LOC146988 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC146988 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC146988 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC147054 5'  TGTGTGTGCGTGTGTGTGTGT  31157     CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   |||||||||||||||
                                ACAC   ACGCACACACACACA
                                  AC_
GAM1203  LOC147054 5'  TGTGCATGTTTGTGTGTGTGTG 31167     ___   C          III
           TGTA                   TGC   TTTG GTGTGTGTGTGT   A
                                |||   |||| ||||||||||||  |
                                ACG   AAAC CACACACACACA   T
                                  TAC    A          III
GAM1203  LOC147054 5'  TGATCACGTGTGTGTGTGT    31282    CT TG
                                TG  T  CGTGTGTGTGTGT
                                ||  |  ||||||||||||
                                AC  A  GCACACACACACA
                                 T_ GT
GAM1203  LOC148203 3'  TTTGTGTGTGTGTGTGTGTGTG 31156       CTT  C
           T                    TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM1203  LOC148603 3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC148603 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC148603 3'  TGTGTATGTGTGTGTGTGTGT  31161     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  AT_  A
GAM1203  LOC148753 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC148753 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC148753 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC148753 3'  GTTACTGTGTGTGTGTGTG    31283    GCT   C
                                GT   TTG GTGTGTGTGTG
                                ||   ||| ||||||||||
                                CA   GAC CACACACACAC
                                 AT_   A
GAM1203  LOC148753 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC148753 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC148753 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC148753 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC148753 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC148753 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC148753 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC148753 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149267 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149267 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149301 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149301 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149301 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149301 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149301 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149301 3'  CCTAGGCTTTGTGTGTGTGTGT 31284     T     C          III
            GTA                   TTG GCTTTG GTGTGTGTGTGT   A
                                ||| |||||| ||||||||||||   |
                                GAT CGAAAC CACACACACACA   T
                                  C     A          III
GAM1203  LOC149301 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149301 3'  TTTGTGTGTGTGTGTGTGTGTG 31156       CTT  C
            T                    TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
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                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM1203  LOC149301 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149301 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149422 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149422 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149422 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149422 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149422 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149422 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149422 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149422 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149422 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149422 3'  TATACCGTGTGTGTGTGTGTGT 31285       T  C
                                TGTGCT TG GTGTGTGTGTGT
                                |||||| || ||||||||||||
                                ATATGG AC CACACACACACA
                                   C  A
GAM1203  LOC149422 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149422 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149422 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC149711 3'  TGTGTGCATGTGTGTGTG    31286     CTT
                                TGTG   TGCGTGTGTGTGTG
                                ||||   ||||||||||||||
                                ACAC   ACGTACACACACAC
                                  ___
GAM1203  LOC150112 3'  TGTGTGTTGTGTGTGTGTGTGT 31288      CT   C
                                TGTG  TTG GTGTGTGTGTGT
                                ||||  ||| ||||||||||||
                                ACAC  AAC CACACACACACA
                                  AC   A
GAM1203  LOC150112 3'  TGTGAGTGTGCGTGTGTGTGTG 31287      CTT_
           T                     TGTG   TGCGTGTGTGTGTGT
                                ||||   |||||||||||||||
                                ACAC   ACGCACACACACACA
                                  TCAC
GAM1203  LOC150577 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC150577 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC150577 3'  TTTATGAAGGGAGTGTGTGTGT 31289       CTTTGC
                GT                TTTGTG     GTGTGTGTGTGT
                                  ||||||     ||||||||||||
                                  AAATAC     CACACACACACA
                                     TTCCCT
GAM1203  LOC150759 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                  TGTG   TG GTGTGTGTGTG
                                  ||||   || ||||||||||
                                  ACAC   AC CACACACACAC
                                    ___  A
GAM1203  LOC150759 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                  TGTG   TG GTGTGTGTGTG
                                  ||||   || ||||||||||
                                  ACAC   AC CACACACACAC
                                    ___  A
GAM1203  LOC150759 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                  TGTG   TG GTGTGTGTGTG
                                  ||||   || ||||||||||
                                  ACAC   AC CACACACACAC
                                    ___  A
GAM1203  LOC150759 3'  TGAAGTTTGTGTGTGTGTGT 31290    TGC    C
                                  TG   TTTG GTGTGTGTGTGT
                                  ||   |||| ||||||||||||
                                  AC   AAAC CACACACACACA
                                   TTC    A
GAM1203  LOC150759 3'  TTTGTGTGTGTGTGTGTGTG 31156       CTT  C
                T                  TTTGTG   TG GTGTGTGTGTGT
                                   ||||||   || ||||||||||||
                                   AAACAC   AC CACACACACACA
                                      AC_  A
GAM1203  LOC150759 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                  TGTG   TG GTGTGTGTGTG
                                  ||||   || ||||||||||
                                  ACAC   AC CACACACACAC
                                    ___  A
GAM1203  LOC150759 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                  TGTG   TG GTGTGTGTGTG
                                  ||||   || ||||||||||
                                  ACAC   AC CACACACACAC
                                    ___  A
GAM1203  LOC150759 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                  TGTG   TG GTGTGTGTGTG
                                  ||||   || ||||||||||
                                  ACAC   AC CACACACACAC
                                    ___  A
GAM1203  LOC150759 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                  TGTG   TG GTGTGTGTGTG
                                  ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC150759 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC150759 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC150759 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC151196 3'  TCTGCCTCTGTGTGTGTGTGTG 31291       G    C
                 T             TTTGT CTTTG GTGTGTGTGTGT
                              ||||| ||||| ||||||||||||
                              AGACG GAGAC CACACACACACA
                                _    A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC151196 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152441 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152441 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152441 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC152765 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC153218 5'  TGTGGGTGTGTGTGTGTGTGT  31292      CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  CC_  A
GAM1203  LOC153218 5'  TGTGCGTGTGGGTGTGTGTGTG 31293       TT_  C
           T                     TGTGC   TG GTGTGTGTGTGT
                                 |||||   || ||||||||||||
                                 ACACG   AC CACACACACACA
                                    CAC  C
GAM1203  LOC153387 5'  TGTGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC153387 5'  TGTGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC153387 5'  TGTGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC153387 5'  TGTGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC153387 5'  TGTGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC153387 5'  TATGTGTGTGTGTGTGTG    31166      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC154215 3'  TGTGTGTGTGTGTGTGTG    31150      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC157570 3'  TGTGTGTGCGTGTGTGTGTGT  31157      CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   ||||||||||||||
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                                ACAC   ACGCACACACACACA
                                  AC_
GAM1203  LOC157570 3'  TGTGCGTGTGTGTGTGTGTGT  31155      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||||
                                ACACG  AC CACACACACACA
                                   C_  A
GAM1203  LOC158263 3'  TTTGTGTTTGTATGTGTGT   31294       C   CG
                                TTTGTG TTTG  TGTGTGT
                                |||||| ||||  |||||||
                                AAACAC AAAC  ACACACA
                                   _   AT
GAM1203  LOC196955 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC196955 5'  TGTGTAGGTGTGTGTGTGTG 31295      CTT_  C
           T                     TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  ATCC  A
GAM1203  LOC196955 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC196955 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC196955 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC197114 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC197114 5'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC197114 5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC197114 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC197114 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC197114 5'  TGTATATATGTGTGTGTGTGTG 31280      CTT_  C
                T                TGTG    TG GTGTGTGTGTGT
                                ||||    || ||||||||||||
                                ACAT    AC CACACACACACA
                                  ATAT  A
GAM1203  LOC197117 3'  TGTATATGTGTGTGTGTGTGT  31296     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAT   AC CACACACACACA
                                  AT_  A
GAM1203  LOC197117 3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC197117 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC197117 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC197117 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC199923 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC199923 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG   31150    CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200399 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200918 3'  TTGAGCAGGTGTGTGTGTGTGT 31297      T  TTTGC
                                TTG GC    GTGTGTGTGTGT
                                ||| ||    ||||||||||||
                                AAC CG    CACACACACACA
                                  T  TCCA_
GAM1203  LOC200918 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200918 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200918 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200918 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200918 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200918 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200918 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC200918 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC201911 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC201911 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC201911 3'  TTGTGTGTGTGTGTGTGTGTGT 31221       CTT  C
                                TTGTG   TG GTGTGTGTGTGT
                                |||||   || ||||||||||||
                                AACAC   AC CACACACACACA
                                  AC_  A
GAM1203  LOC201911 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC201911 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC201911 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC203536 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC203536 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC219649 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC219649 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC219649 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC219649 3'  GTGCTTGTGTGTGTGTGTG    31298       T C
                                GTGCTT G GTGTGTGTGTG
                                |||||| | ||||||||||
                                CACGAA C CACACACACAC
                                   _ A
GAM1203  LOC219649 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC219649 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC219649 3'  CTTGTGTGTGTGTGTGTGTGTG 31299       CTT  C
                T                  TTTGTG   TG GTGTGTGTGTGT
                                   ||||||   || ||||||||||||
                                   GAACAC   AC CACACACACACA
                                     AC_  A
GAM1203  LOC221042 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  LOC221042 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  LOC221042 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  LOC221042 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  LOC221042 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  LOC221042 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  LOC221042 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  LOC221042 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  LOC221042 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
                                   ACAC   AC CACACACACAC
                                     ___  A
GAM1203  LOC221042 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                   TGTG   TG GTGTGTGTGTG
                                   ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221042 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221042 5'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221463 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC221981 3'  TATGGGTGTGTGTGTGTGTGT  31300      CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ATAC   AC CACACACACACA
                                  CC_  A
GAM1203  LOC221981 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222008 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222008 3'  TGTGTGTGCGTGTGTGTGTGT  31157     CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   ||||||||||||||
                                ACAC   ACGCACACACACACA
                                  AC_
GAM1203  LOC222008 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222008 3'  TGTGCGTGTGTGTGTGTGTGT  31155      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||||
                                ACACG  AC CACACACACACA
                                   C_  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTATGTATGTGTGTGTGTG 31301     CTT___  C
            TGT                   TGTG     TG GTGTGTGTGTGT
                                ||||     || ||||||||||||
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                                ACAC     AC CACACACACACA
                                  ATACAT  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222662 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222865 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222865 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222865 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222865 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222865 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222865 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222865 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC222865 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC253150 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC253150 3'  TATGTGTGTGTGTGTGTG    31166     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ATAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC253150 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC253150 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC253150 3'  TGTGTATGTGTGTGTGTGTGT  31161      CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || |||||||||||
                                ACAC   AC CACACACACACA
                                  AT_  A
GAM1203  LOC253150 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC253150 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC253982 3'  TGTGAGAGTATGTGTGTGTGTG 31302      CTT___  C
                    TGT           TGTG     TG GTGTGTGTGTGT
                                ||||     || ||||||||||||
                                ACAC     AC CACACACACACA
                                  TCTCAT  A
GAM1203  LOC256520 3'  TCTGCGGGTGTGTGTGTGTGTG 31303       CTT  C
                    T          TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AGACGC   AC CACACACACACA
                                   CC_  A
GAM1203  LOC257453 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC257453 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC257453 3'  TGTGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC257453 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC257453 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC257453 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC257453 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC257453 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC257453 3'  TTTGTGTGCGTGTGTGTGT   31210       CTT
                                TTTGTG   TGCGTGTGTGTGT
                                ||||||   ||||||||||||
                                AAACAC   ACGCACACACACA
                                   ___
GAM1203  LOC257453 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC257453 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC257453 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC257453 3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC257464 3'  CTTGTCTGTGTGTGTGTG    31304      G  TTGC
                                TTTGT CT    GTGTGTGTGTG
                                ||||| ||    ||||||||||
                                GAACA GA    CACACACACAC
                                  _  ____
GAM1203  LOC51701  3'  TTTGTGTGTGTGTGTGTGTGTG 31156       CTT  C
           T                     TTTGTG   TG GTGTGTGTGTGT
                                 ||||||   || ||||||||||||
                                 AAACAC   AC CACACACACACA
                                    AC_  A
GAM1203  LOC51701  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC51701  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC51701  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC51701  3'  TTTGTGTTTGTGTGTGTGTGTG 31305       C    C
           T                     TTTGTG TTTG GTGTGTGTGTGT
                                 |||||| |||| ||||||||||||
                                 AAACAC AAAC CACACACACACA
                                    _    A
GAM1203  LOC51701  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC51701  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC57795  3'  TGTGCCAGTGTGTGTGTGTGTG 31306       T_  C
           T                     TGTGCT  TG GTGTGTGTGTGT
                                 ||||||  || ||||||||||||
                                 ACACGG  AC CACACACACACA
                                    TC  A
GAM1203  LOC57795  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||||
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                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC90632  5'  TGTGCGTGCGTGTGTGTGTGT  31192      TT
                              TGTGC  TGCGTGTGTGTGTGT
                              |||||  ||||||||||||||
                              ACACG  ACGCACACACACACA
                                C_
GAM1203  LOC90632  5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC92299  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC93097  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC93097  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC93097  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC93097  3'  TTGTGTGTGTGTGTGTGTGT  31221      CTT  C
                              TTGTG   TG GTGTGTGTGTGT
                              |||||   || ||||||||||||
                              AACAC   AC CACACACACACA
                                 AC_  A
GAM1203  LOC93097  3'  TGAGATTGTGTGTGTGTGT   31307    TGCT   C
                              TG    TTG GTGTGTGTGTGT
                              ||    ||| ||||||||||||
                              AC    AAC CACACACACACA
                               TCT_   A
GAM1203  LOC93097  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
                              ACAC   AC CACACACACAC
                                ___  A
GAM1203  LOC93097  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                              TGTG   TG GTGTGTGTGTG
                              ||||   || ||||||||||
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                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 LOC93097 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 LOC93097 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 LOC93097 3' TGTGTGTGTGTGTGTGTG   31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 LOC93166 5' TGTGTGTGTGTGTGTGTG   31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 LOC93166 5' TGTGTGTGTGTGTGTGTG   31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 LOC93166 5' TGTGTGTGTGTGTGTGTG   31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 LOC93166 5' TGTGTGTGTGTGTGTGTG   31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 LOC93166 5' TGTGTGTGTGTGTGTGTG   31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 LOC93166 5' TGTGTGTGTGTGTGTGTG   31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM1203 LOC93166 5' TGTGTGTGTGTGTGTGTG   31150   CTT C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC93166  5'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC93463  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC93463  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC93463  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC93463  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC93463  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1203  LOC93463  3'  GTGGTGTGTGTGTGTGTGT   31308     CTT  C
                                GTG   TG GTGTGTGTGTGT
                                |||   || ||||||||||||
                                CAC   AC CACACACACACA
                                  C__  A
GAM1203  LOC93463  3'  TGTGTGTGTGTGTGTGTG    31150     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM1204  ADAR      3'  GGGGGTGAGTGGGGGT      31311     AT  A  AT  T
                                GGG  GGT GGG  TGG GGGT
                                |||  ||| |||  ||| ||||
                                CCC  CCA CTC  ACC CCCA
                                  __  _  __  _
GAM1204  ADAR      3'  GGGGGTGAGTGGGGGT      31311     AT  A  AT  T
                                GGG  GGT GGG  TGG GGGT
                                |||  ||| |||  ||| ||||
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                                CCC  CCA CTC  ACC CCCA
                                  __  _  __  _
GAM1204  ADAR     3'  GGGGGTGAGTGGGGGT     31311     AT   A   AT   T
                                GGG  GGT GGG  TGG GGGT
                                |||  ||| |||  ||| ||||
                                CCC  CCA CTC  ACC CCCA
                                  __  _  __  _
GAM1204  ASNS     5'  GGGGACTGGTGGGGATGGCGGG 31312       _   A    T
                                GGGGA TGGT GGGAT GGTGGG
                                ||||| |||| ||||| ||||||
                                CCCCT ACCA CCCTA CCGCCC
                                   G   C    _
GAM1204  GAP43    3'  GGGGAGGGTGGGGATGTG    31313      T   A    TG
                                GGGGA GGT GGGAT  GTG
                                ||||| ||| |||||  |||
                                CCCCT CCA CCCTA  CAC
                                   C   C    __
GAM1204  GAS7     3'  GGGGTGGTGCGGGGGCAGGTG  31314     A   A_  ATT  TG
                                GGGG TGGT  GGG   GG  GGTG
                                |||| ||||  |||   ||  ||||
                                CCCC ACCA  CCC   CC  CCAC
                                  _   CG   ___  GT
GAM1204  HCN2     3'  GGGGTGTGGGGGTTAATG    31315     A  GTA   A
                                GGGG TG   GGG TTGGTG
                                |||| ||   ||| ||||||
                                CCCC AC   CCC AATTAC
                                  _ AC_   C
GAM1204  JAM2     5'  GGGGTGGGGGGATTGGGT    31316     A   TA    TGG
                                GGGG TGG  GGGAT   TGGGT
                                |||| |||  |||||   |||||
                                CCCC ACC  CCCTA   ACCCA
                                  _   C_    ___
GAM1204  KCNK3    3'  GGGGTGCTGGGGGAGAGTGGTG 31317      A__   TA   T
                                GGGG   TGG  GGGA TGGTG
                                ||||   |||  |||| |||||
                                CCCC   ACC  CTCT ACCAC
                                  ACG   CC   C
GAM1204  KLK10    3'  GGGGATAGGTGGGGGAATGAGG 31318       _   A_   T  GT
            TG                    GGGGAT GGT  GGGA TG  GGGTG
                                ||||||  |||  |||| ||  |||||
                                CCCCTA CCA  CCCT AC  TCCAC
                                   T   CC    T  __
GAM1204  LCN1     3'  GGGGTGGTAGGAAGGGGTG   31319      A       TT
                                GGGG TGGTAGGGA  GGTG
                                |||| |||||||||  ||||
                                CCCC ACCATCCTT  CCAC
                                  _        CC
GAM1204  LCN1     3'  GGGGTGGTAGGAAGGGGTG   31319      A       TT
                                GGGG TGGTAGGGA  GGTG
                                |||| |||||||||  ||||
```

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                                CCCC ACCATCCTT  CCAC
                                  _       CC
GAM1204  LHX5     5'  GGGGTGGTGGGGGGCGGGTG  31320     A   A  ATT
                                GGGG TGGT GGG   GGTGGGTG
                                |||| |||| |||   ||||||||
                                CCCC ACCA CCC   CCGCCCAC
                                  _   C  ___
GAM1204  MSR1     3'  GGGGTGATAGGGGAGAGAGGTG 31321     A      ATT GT
                                GGGG TGGTAGGG   G  GGGTG
                                |||| ||||||||   |  |||||
                                CCCC ACTATCCC   C  TCCAC
                                  _      CT_ TC
GAM1204  RPA1     3'  GGGGATGGGGGGGGGGG     31322        TA   ATT  T
                                GGGGATGG  GGG   GG GGG
                                ||||||||  |||   || |||
                                CCCCTACC  CCC   CC CCC
                                    __  ___ _
GAM1204  SHOX     3'  GGGGTGGTGGTGGCAGGT    31323     A   A  GAT   TG
                                GGGG TGGT GG   TGG  GGT
                                |||| |||| ||   |||  |||
                                CCCC ACCA CC   ACC  CCA
                                  _   _ ___   GT
GAM1204  SYNGR1   3'  GGGGATGGGGGGGATGGTG    31325        TA    T
                                GGGGATGG  GGGAT GGTG
                                ||||||||  ||||| ||||
                                CCCCTACC  CCCTA CCAC
                                    C_   _
GAM1204  SYNGR1   3'  GGGGATGGTAGGAGGTGGGTG  31324           ATT
                                GGGGATGGTAGGG   GGTGGGTG
                                ||||||||||||   ||||||||
                                CCCCTACCATCCT   CCACCCAC
                                      ___
GAM1204  TBX6     3'  GGGGGGTGGGGATTGA      31326      AT   A
                                GGGG  GGT GGGATTGG
                                ||||  ||| ||||||||
                                CCCC  CCA CCCTAACT
                                  __  C
GAM1204  C8orf13  5'  GGGGAGGCTTGGTGGGT     31327       T  AGGGA
                                GGGGA GGT    TTGGTGGGT
                                |||||  |||    |||||||||
                                CCCCT CCG    AACCACCCA
                                  _  _____
GAM1204  CBX8     3'  GGGGCTGGTGGGGTGGGGGTG  31328     A   A  AT   T
                                GGGG TGGT GGG  TGG GGGTG
                                |||| |||| |||  ||| |||||
                                CCCC ACCA CCC  ACC CCCAC
                                  G   C  __  _
GAM1204  DJ159A19.3 3'  GGGGGTGTAGGGGGCAGGGTG  31329     ATG    ATT  _
                                GGGG   GTAGGG   GGT GGGTG
                                ||||   ||||||   ||| |||||
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                                CCCC   CATCCC   CCG CCCAC
                                  CA_     ___   T
GAM1204  DOCK3    3'  GGGGTGGTAGGGCTTGG     31330      A      A
                                GGGG TGGTAGGG TTGG
                                |||| |||||||| ||||
                                CCCC ACCATCCC AACC
                                  _       G
GAM1204  FLJ10748 3'  GGGGTGGGGGGAGGTG      31331      A  TA   TT
                                GGGG TGG  GGGA  GGTG
                                |||| |||  ||||  ||||
                                CCCC ACC  CCCT  CCAC
                                  _  C_   __
GAM1204  FLJ14950 3'  GGGGTGGGGTGGGGGTGGGTG  31332      A  TA_  ATT
                                GGGG TGG   GGG   GGTGGGTG
                                |||| |||   |||   ||||||||
                                CCCC ACC   CCC   CCACCCAC
                                  _  CCA  ___
GAM1204  FLJ23590 5'  GGGGTGGTGAGGAAGCGGGTG  31333      A   AG   TT
                                GGGG TGGT  GGA  GGTGGGTG
                                |||| ||||  |||  ||||||||
                                CCCC ACCA  CCT  TCGCCCAC
                                  _   CT   __
GAM1204  IMP13    3'  GGGGATGGGGGGGGTTGATG   31334        TA   A
                                GGGGATGG  GGG TTGGTG
                                ||||||||  ||| ||||||
                                CCCCTACC  CCC AACTAC
                                    CC  _
GAM1204  KIAA0140 3'  GGGGAGGTGGGGAGGTG     31335      T   A    TT
                                GGGGA GGT GGGA  GGTG
                                ||||| ||| ||||  ||||
                                CCCCT CCA CCCT  CCAC
                                  _  C    __
GAM1204  KIAA0256 3'  GGGGTGGTGGGGAGTTGGATG  31336      A   A    TTGG
                                GGGG TGGT GGGA    TGGGTG
                                |||| |||| ||||    ||||||
                                CCCC ACCA CCCT    ACCTAC
                                  _   C    CA__
GAM1204  KIAA0339 3'  GGGGTGGTGGGCAGGGGT    31337      A   A   ATT  T
                                GGGG TGGT GGG   GG GGGT
                                |||| |||| |||   || ||||
                                CCCC ACCA CCC   TC CCCA
                                  _   _   G__  _
GAM1204  KIAA0481 3'  GGGGATAGTGGGGCTGGGT   31338        A   ATTGG
                                GGGGATGGT GGG    TGGGT
                                |||||||||  |||    |||||
                                CCCCTATCA CCC    ACCCA
                                    C   G____
GAM1204  KIAA1328 3'  GGGGTGGGGGGGGTGGG      31339      A   TA   ATT
                                GGGG TGG  GGG   GGTGGG
                                |||| |||  |||   ||||||
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                                CCCC ACC  CCC   CCACCC
                                  _  __  ___
GAM1204  KIAA1866  3'  GGGGATGGGAGTGGTGGGT   31340      GGTA   T
                                GGGGAT   GGGA TGGTGGGT
                                ||||||   |||| ||||||||
                                CCCCTA   CCCT ACCACCCA
                                   ____   C
GAM1204  MAP       3'  GGGGTGGGGGGGAGCAGGT   31341     A   TA   TTG TG
                                GGGG TGG  GGGA   G  GGT
                                |||| |||  ||||  |  |||
                                CCCC ACC  CCCT   C  CCA
                                  _  C_   ___ GT
GAM1204  MGC13138  3'  GGGAGTGGTGGGGATGGGT   31342    GA   A   ATT
                                GGG  TGGT GGG   GGTGGGT
                                |||  |||| |||   |||||||
                                CCC  ACCA CCC   CTACCCA
                                  TC   _  ___
GAM1204  MGC14386  5'  GGGGATGGGGGGGAGCGGGGTG  31343       TA   T   TG
                                GGGGATGG  GGGA TGG  GGTG
                                ||||||||  |||| |||  ||||
                                CCCCTACC  CCCT GCC  CCAC
                                    C_   C  __
GAM1204  PURB      3'  GGGGATGGTGGTTGGG      31344         AGGGATT  _
                                GGGGATGGT      GGT GGG
                                |||||||||      ||| |||
                                CCCCTACCA      CCA CCC
                                    ________  A
GAM1204  UBP1      3'  GGGGTGGGGGGGTTAGGGT    31345     A   TA   A   GT
                                GGGG TGG  GGG TTG  GGGT
                                |||| |||  ||| |||  ||||
                                CCCC ACC  CCC AAT  CCCA
                                  _  __   C  __
GAM1204  LOC115098 3'  GGGGATGGGAGGGGATGGGGTG 31346        T   AT   TG
                                GGGGATGG AGGG  TGG  GGTG
                                |||||||| ||||  |||  ||||
                                CCCCTACC TCCC  ACC  CCAC
                                    C   CT  __
GAM1204  LOC145608 5'  GGGGTGGGGGGGAGGTG     31331     A   TA   TT
                                GGGG TGG  GGGA  GGTG
                                |||| |||  ||||  ||||
                                CCCC ACC  CCCT  CCAC
                                  _  C_   __
GAM1204  LOC147160 5'  GGGGGGGGTGGACGTGGGT   31347     AT   AG   TG
                                GGGG  GGT  GGAT  GTGGGT
                                ||||  |||  ||||  ||||||
                                CCCC  CCA  CCTG  CACCCA
                                  CC  __   __
GAM1204  LOC149692 3'  GGGGTGGTAGAGAGGGT     31348      A       TTGGT
                                GGGG TGGTAGGGA    GGGT
                                |||| |||||||||    ||||
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                                CCCC ACCATCTCT    CCCA
                                  _     _____
GAM1204  LOC150381 3'  GGGGTGGCAGGGGGCGG    31349     A      ATT
                                GGGG TGGTAGGG  GGTGG
                                |||| ||||||||  |||||
                                CCCC ACCGTCCC  CCGCC
                                  _     ___
GAM1204  LOC158515 5'  GGGGATGGTGGTGATAGTG   31350       A _  T
                                GGGGATGGT GG GAT GGTG
                                ||||||||| || ||| ||||
                                CCCCTACCA CC CTA TCAC
                                     _ A  _
GAM1204  LOC163944 5'  GGGGATGATGAGGTGGGT    31351       A  GATT
                                GGGGATGGT GG   GGTGGGT
                                ||||||||| ||   |||||||
                                CCCCTACTA CT   CCACCCA
                                  _ ____
GAM1204  LOC221749 3'  GGGAATGGTGGGGAGTCAGGGT 31352       A   TTGGT
           G                     GGGGATGGT GGGA    GGGTG
                                ||||||||| ||||    |||||
                                CCCTTACCA CCCT    CCCAC
                                     C   CAGT_
GAM1204  LOC255473 5'  GGGGATGGTGGTGGAGGT    31353       A  GAT  T
                                GGGGATGGT GG  TGG GGGT
                                ||||||||| ||  ||| ||||
                                CCCCTACCA CC  ACC TCCA
                                  _ ___  _
GAM1204  LOC256073 5'  GGGGATGGAAGGTTGTATGGGT 31354       T   A  _
           G                     GGGGATGG AGGG TTG GTGGGTG
                                |||||||| |||| ||| |||||||
                                CCCCTACC TTCC AAC TACCCAC
                                     _   _  A
GAM1204  LOC257095 5'  GGGGGTGGGGAGGTGGGT    31355    AT  A   TT
                                GGG  GGT GGGA  GGTGGGT
                                |||  ||| ||||  |||||||
                                CCC  CCA CCCT  CCACCCA
                                  __  C   __
GAM1204  LOC257200 3'  GGCGGTGGTGATGGTGGGT   31356   A   A _  T
                                GG TGGT GG GAT GGTGGGT
                                || |||| || ||| |||||||
                                CC GCCA CC CTA CCACCCA
                                  _   _ A  _
GAM1205  ANGPT1   3'  TGGAGTTCTAAAAATATTTTT  31359      CG
                                TGGAGT  TAAAAATATTTTT
                                ||||||  |||||||||||||
                                ACCTCA  ATTTTTATAAAAA
                                   AG
GAM1205  DAAM2    3'  TGATGGAGTTTTAGAAAAATTT 7469        CG  A  T
           T                     TGATGGAGT  TA AAA ATTTT
                                |||||||||  || ||| |||||
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                                ACTACCTCA  AT TTT TAAAA
                                     AA  C   T
GAM1205  NKTR     3'  TGTGGCATAAAAATATTTT   31360    A   AGT
                                TG TGG   CGTAAAAATATTTT
                                || |||   ||||||||||||||
                                AC ACC   GTATTTTTATAAAA
                                 _  ____
GAM1205  NUP153   3'  TGCTGGATCATAAAATATTTTT 31361    A   G       A
                                TG TGGA TCGTAAAA TATTTTT
                                || |||| |||||||| |||||||
                                AC ACCT AGTATTTT ATAAAAA
                                 G   _       _
GAM1205  FLJ13920 3'  TGAAGGAGCTCAAAATATTTTT 31362     T    CGTA
                                TGA GGAGT    AAAATATTTTT
                                ||| |||||    ||||||||||
                                ACT CCTCG    TTTTATAAAAA
                                  T    AG__
GAM1205  LOC157753 3'  TGGGTCATTAGAAATATTTTT  31363     A    AA_
                                TGG GTCGT   AAATATTTTT
                                ||| |||||   ||||||||||
                                ACC CAGTA   TTTATAAAAA
                                  _    ATC
GAM1206  ANXA6    3'  GGCAGAAGTGCCCGCCAAA   31366    __     TA   A
                                GG  GGAGTG  CCC CCAAA
                                ||  ||||||  ||| |||||
                                CC  CTTCAC  GGG GGTTT
                                 GT     __   C
GAM1206  EFNB2    3'  CAGGGAGCGTGTGTGTTCACCA 31367       A_   ACC__
             A                   CAGGGG  GTGT    CACCAA
                                ||||||  ||||    ||||||
                                GTCCCT  CACA    GTGGTT
                                   CG    CACAA
GAM1206  IGFBP4   3'  TACAGGGAGCGAGCCAC     31368       G    TAC
                                TACAGGG AGTG   CCAC
                                ||||||| ||||   ||||
                                ATGTCCC TCGC   GGTG
                                    _   TC_
GAM1206  MCL1     3'  AAGGAATACTTACCAAA     31369      GT   CC
                                GGGGA  GTAC  ACCAAA
                                |||||  ||||  ||||||
                                TTCCT  TATG  TGGTTT
                                   __    AA
GAM1206  RNH      5'  CACAGCTCAGGTACCCGCCA  31370      GGG  T     A
                                TACAG   AG GTACCC CCA
                                |||||   || |||||| |||
                                GTGTC   TC CATGGG GGT
                                   GAG  _     C
GAM1206  RNH      5'  CACAGCTCAGGTACCCGCCA  31370      GGG  T     A
                                TACAG   AG GTACCC CCA
                                |||||   || |||||| |||
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                                GTGTC   TC CATGGG GGT
                                   GAG _     C
GAM1206  TEAD3    3'  TAAGGGAACAGTGCCCACCAA  31371   C     GT  A
                                A AGGGGA  GT CCCACCAA
                                | ||||||  || ||||||||
                                A TCCCTT  CA GGGTGGTT
                                 T     GT  C
GAM1206  BFAR     3'  TACAGGGGTGAGGTATCACCAA 31372        __  T   CC
              AA                  TACAGGGG  AG GTA  CACCAAAA
                                ||||||||  || |||  ||||||||
                                ATGTCCCC  TC CAT  GTGGTTTT
                                     AC  _   A_
GAM1206  C9orf5   3'  AGGGGAATATCACCAAA     31373          ACC
                                AGGGGAGTGT   CACCAAA
                                ||||||||||   |||||||
                                TCCCCTTATA   GTGGTTT
                                      ___
GAM1206  FLJ10038 3'  TACAGTGGAGTGTTCCA     31374      G      AC
                                TACAG GGAGTGT  CCA
                                ||||| |||||||  |||
                                ATGTC CCTCACA  GGT
                                   A      A_
GAM1206  FLJ10415 3'  CAGGAGAGTAAAGCCACC    31375         TAC
                                CAGGGGAGTG   CCACC
                                ||||||||||   |||||
                                GTCCTCTCAT   GGTGG
                                      TTC
GAM1206  FLJ10829 3'  AGGCAGCCAGTACCCACC    31376     G   __
                                GGG AGT  GTACCCACC
                                ||| |||  |||||||||
                                TCC TCG  CATGGGTGG
                                  G   GT
GAM1206  FLJ23519 5'  CACAGCTCAGGTACCCGCCA  31370       GGG  T     A
                                TACAG   AG GTACCC CCA
                                |||||   || |||||| |||
                                GTGTC   TC CATGGG GGT
                                   GAG _     C
GAM1206  FLJ23519 5'  CACAGCTCAGGTACCCGCCA  31370       GGG  T     A
                                TACAG   AG GTACCC CCA
                                |||||   || |||||| |||
                                GTGTC   TC CATGGG GGT
                                   GAG _     C
GAM1206  GL009    3'  CAGAGGAGACCACAGCCTGCCA 31377         TG   __  A_
              A                   CAGGGGAG  TAC  CC  CCAA
                                ||||||||  |||  ||  ||||
                                GTCTCCTC  GTG  GG  GGTT
                                     TG   TC  AC
GAM1206  HTR3A    5'  CAGGGCGAGGCCCACCAA    31378       _   T TA
                                CAGGG GAG G  CCCACCAA
                                ||||| ||| |  ||||||||
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                                GTCCC CTC C  GGGTGGTT
                                   G  _ __
GAM1206  KIAA0892  3'  CACAGGAAAGTACTTATCAAAA 31379       GG    TACCCAC
                                TACAGG  AGTG      CAAAA
                                ||||||  ||||      |||||
                                GTGTCC  TCAT      GTTTT
                                   TT    GAATA__
GAM1206  PRRG1     3'  GGGGAGTGGTCAACCAAAA    31380        TACCC
                                GGGGAGTG    ACCAAAA
                                ||||||||    |||||||
                                CCCCTCAC    TGGTTTT
                                     CAGT_
GAM1206  SAMHD1    3'  CACAGGGGCACTGCCCCACCAA 31381         AG_   A
                                TACAGGGG   TGT CCCACCAA
                                ||||||||   ||| ||||||||
                                GTGTCCCC   ACG GGGTGGTT
                                     GTG  _
GAM1206  SIMRP7    3'  CAGGATGCTGCCCACCAA    31382      GA  GTA
                                CAGGG  GT   CCCACCAA
                                |||||  ||   ||||||||
                                GTCCT  CG   GGGTGGTT
                                   A_  AC_
GAM1206  SNX10     3'  CAGGGGAGGTATCCACAAAA   31383        T   C    C
                                CAGGGGAG GTA CCAC AAAA
                                |||||||| ||| |||| ||||
                                GTCCCCTC CAT GGTG TTTT
                                     _   A    _
GAM1206  SUCLG2    3'  AGGATTAGATGCCCACCAAAA  31384      GAGT  A
                                AGGG    GT CCCACCAAAA
                                ||||    || ||||||||||
                                TCCT    TA GGGTGGTTTT
                                  AATC  C
GAM1206  TUCAN     3'  TAAGAGAATCTGTACCTATCA  31385    C     G_     CAC
                                A AGGGGA  TGTACC   CA
                                | ||||||  ||||||   ||
                                A TCTCTT  ACATGG   GT
                                 T     AG     ATA
GAM1206  ZNF297    3'  GGGCTTCAGTGTACCCATCA   31386     G___         C
                                GGG    AGTGTACCCA CA
                                |||    |||||||||| ||
                                CCC    TCACATGGGT GT
                                  GAAG         A
GAM1206  LOC124538 3'  ACAGGAAACTGTCCACCAA    31387      GG G   AC
                                ACAGG  A TGT  CCACCAA
                                |||||  | |||  |||||||
                                TGTCC  T ACA  GGTGGTT
                                   TT G  __
GAM1206  LOC139483 5'  TACAGGGAGTGTTTCCA     31388        G     AC
                                TACAGGG AGTGT  CCA
                                |||||||  |||||  |||
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                                ATGTCCC TCACA  GGT
                                   _    AA
GAM1206  LOC162083 5'  TACAGGGGGTCCCACCA     31389        A  GTA
                                TACAGGGG GT   CCCACCA
                                |||||||| ||   |||||||
                                ATGTCCCC CA   GGGTGGT
                                   _ ____
GAM1206  LOC170261 3'  AGGGAAATATCACTCATCAAA  31390          _  C  C
                                AGGGGAGTGT AC CA CAAA
                                |||||||||| || || ||||
                                TCCCTTTATA TG GT GTTT
                                     G  A  A
GAM1206  LOC201952 3'  GGGATTTTTACCCACTAAAA   31391      GTG_      C
                                GGGA    TACCCAC AAAA
                                ||||    ||||||| ||||
                                CCCT    ATGGGTG TTTT
                                  AAAA       A
GAM1206  LOC219972 3'  AAGGGAGTGTTCATCAA      31392          ACC  C
                                AGGGGAGTGT   CA CAA
                                ||||||||||   || |||
                                TTCCCTCACA   GT GTT
                                     A__  A
GAM1206  LOC257051 3'  AGGGAAATATCACTCATCAAA  31390          _  C  C
                                AGGGGAGTGT AC CA CAAA
                                |||||||||| || || ||||
                                TCCCTTTATA TG GT GTTT
                                     G  A  A
GAM1206  LOC257489 3'  AGGATTAGATGCCCACCAAAA  31384      GAGT  A
                                AGGG    GT CCCACCAAAA
                                ||||    || ||||||||||
                                TCCT    TA GGGTGGTTTT
                                  AATC  C
GAM1206  LOC51291  3'  GGGGAGTGACCACAACCAAA   31393        T  _  _
                                GGGGAGTG ACC CA CCAAA
                                |||||||| ||| || |||||
                                CCCCTCAC TGG GT GGTTT
                                     _  T  T
GAM1207  ADCY6     3'  TCTTTGTACAAAATATTGTACA 31396       G       TTCAC
            A                    TCTTTG TACAAAAT     ACAA
                                |||||| ||||||||     ||||
                                AGAAAC ATGTTTTA     TGTT
                                   _       TAACA
GAM1207  ADCY6     3'  TCTTTGTACAAAATATTGTACA 31396       G       TTCAC
            A                    TCTTTG TACAAAAT     ACAA
                                |||||| ||||||||     ||||
                                AGAAAC ATGTTTTA     TGTT
                                   _       TAACA
GAM1207  APBB2     5'  TCTTTGGTACAAAGCTCA    31397           AT
                                TCTTTGGTACAAA  TTCA
                                ||||||||||||  ||||
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                                AGAAACCATGTTT GAGT
                                      C_
GAM1207 ATP8B2   3' TCTTTGGTATAAAAATCA   31398       C   TT
                                TCTTTGGTA AAAA TCA
                                ||||||||| |||| |||
                                AGAAACCAT TTTT AGT
                                    A   T_
GAM1207 CEACAM1  3' TCTTTGCTAGTTCACACA   31399      G CAAAAT
                                TCTTTG TA    TTCACACA
                                |||||| ||    ||||||||
                                AGAAAC AT    AAGTGTGT
                                   G C_____
GAM1207 CHST1    3' TTTGGCACAAAGAAATATCACA 31400         ___ T
                                TTTGGTACAAA  AT TCACA
                                |||||||||||  || |||||
                                AAACCGTGTTT  TA AGTGT
                                      CTT T
GAM1207 FBXL7    3' TCTTTGGTGGAAAACACGCA  31401       AC   TTT  A
                                TCTTTGGT AAAA  CAC CA
                                |||||||| ||||  ||| ||
                                AGAAACCA TTTT  GTG GT
                                     CC   ___  C
GAM1207 HOXC9    3' GTACAAAATCTGCACGCA    31402         _  A
                                GTACAAAATTT CAC CA
                                |||||||||| ||| ||
                                CATGTTTTAGA GTG GT
                                      C  C
GAM1207 IGF1     3' TTTGGTACAAATGCCACA    31403         ATT
                                TTTGGTACAAA  TCACA
                                ||||||||||  |||||
                                AAACCATGTTT  GGTGT
                                      AC_
GAM1207 ITGAL    3' TTTGGACAGAATTTCACA    31404      T  A
                                TTTGG ACA AATTTCACA
                                ||||| ||| |||||||||
                                AAACC TGT TTAAAGTGT
                                   _  C
GAM1207 LBR      3' TCCTTGGTGCAATCCAGTACA 31405       A  AAT  C_
                                TCTTTGGT CAA  TTCA ACA
                                |||||||| |||  |||| |||
                                AGGAACCA GTT  AGGT TGT
                                     C  ___  CA
GAM1207 MIP      3' CTTGAAAGATTTCACACA    31406      TACAAA
                                TTTGG    ATTTCACACA
                                |||||    ||||||||||
                                GAACT    TAAAGTGTGT
                                   TTC___
GAM1207 RLN2     3' TTTGGTACAACCAACA      31407        AATT  C
                                TTTGGTACAA   TCA ACA
                                |||||||||   ||| |||
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                                AAACCATGTT   GGT TGT
                                     ____  _
GAM1207 SART2   3' TCTTTGGTATGAAAATCA   31408       CA  TT
                                TCTTTGGTA  AAA  TCA
                                |||||||||  |||  |||
                                AGAAACCAT  TTT  AGT
                                     AC   T_
GAM1207 TPK1    3' TCTTTGGTAGCAAAATTT   31409       _
                                TCTTTGGTA CAAAATTT
                                |||||||||  ||||||||
                                AGAAACCAT GTTTTAAA
                                     C
GAM1207 TRIP12  3' CCTTTTTTAAATTTCACACA  31410     GGTACA
                                TCTTT     AAATTTCACACA
                                |||||     ||||||||||||
                                GGAAA     TTTAAAGTGTGT
                                   AAA___
GAM1207 BRD3    3' TCTTCGGTACGAATCTCACAC 31411       AA
                                TCTTTGGTAC  AATTTCACAC
                                ||||||||||  ||||||||||
                                AGAAGCCATG  TTAGAGTGTG
                                     C_
GAM1207 FLJ13397 3' TTTGCTAGTAAATTTCACAC  31412     G  CA
                                TTTG TA  AAATTTCACAC
                                ||||  ||  ||||||||||||
                                AAAC AT  TTTAAAGTGTG
                                  G  CA
GAM1207 FLJ22202 3' TTTGGTACAAAATGATACA   31413         TTC
                                TTTGGTACAAAAT   ACA
                                ||||||||||||||  |||
                                AAACCATGTTTTA   TGT
                                       CTA
GAM1207 GROS1   3' TCTTTGGTTGTCTACACA    31414       ACAAAATT  _
                                TCTTTGGT       TC ACACA
                                ||||||||       ||  |||||
                                AGAAACCA       AG TGTGT
                                     AC_______  A
GAM1207 KIAA0981 3' TCCTTGGCAGTTTTACACA   31415       CAAAA   C
                                TCTTTGGTA    TTT ACACA
                                |||||||||    |||  |||||
                                AGGAACCGT    AAA TGTGT
                                     C_____   A
GAM1207 KIAA1243 3' TCTTTGGTCATGTCACA     31416       A  AAATT
                                TCTTTGGT CA    TCACA
                                ||||||||  ||    |||||
                                AGAAACCA GT    AGTGT
                                     _  AC___
GAM1207 KIAA1462 3' TCTTTGGGTTCCTCTCACACAA 31417       TACAAAA
                                TCTTTGG      TTTCACACAA
                                |||||||      ||||||||||
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                                AGAAACC      AGAGTGTGTT
                                   CAAGG__
GAM1207  MGC1136   3'  TCTATGCTAGGGGTTTCACACA 31418     T  G  CAAAA
              A                    TCT TG TA     TTTCACACAA
                                   ||| || ||     ||||||||||
                                   AGA AC AT     AAAGTGTGTT
                                     T  G  CCCC_
GAM1207  MSTP043   3'  TCTTTGGTAAAAATAAAGACA  31419         C     TTC_
                                   TCTTTGGTA AAAAT    ACA
                                   ||||||||| |||||    |||
                                   AGAAACCAT TTTTA    TGT
                                         _    TTTC
GAM1207  Nup43     3'  TCTGATACTAAAATTTTGCACA 31420         _      CA
                                   TTTGGTAC AAAATTT  CACA
                                   |||||||| |||||||  ||||
                                   AGACTATG TTTTAAA  GTGT
                                        A      AC
GAM1207  RPS6KA4   3'  TCTTTGGTGGACGTAATTGCAC 31421         __ AA    T
              A                    TCTTTGGT  AC  AATT CACA
                                   ||||||||  ||  |||| ||||
                                   AGAAACCA  TG  TTAA GTGT
                                        CC  CA    C
GAM1207  SLC17A6   3'  TCTGTGGCACAAGTTTCA    31422     T       AA
                                   TCT TGGTACAA  TTTCA
                                   ||| ||||||||  |||||
                                   AGA ACCGTGTT  AAAGT
                                     C       C_
GAM1207  TERA      3'  CTTTGGTACTATTCATACA    31423          AAAAT    C
                                   CTTTGGTAC     TTCA ACA
                                   |||||||||     |||| |||
                                   GAAACCATG     AAGT TGT
                                        AT___    A
GAM1207  VAV3      3'  TCTTTGGTATTAGAACTCTACA 31424         CAA_    TC
              CAA                    TCTTTGGTA    AATT  ACACAA
                                   |||||||||    ||||  ||||||
                                   AGAAACCAT    TTGA  TGTGTT
                                        AATC    GA
GAM1207  LOC120892 3'  TCTTTGGTAAAAAAAATTGCA  31425         C__     T
                                   TCTTTGGTA   AAAATT CA
                                   |||||||||   |||||| ||
                                   AGAAACCAT   TTTTAA GT
                                        TTT     C
GAM1207  LOC155434 3'  TTTGGTACGAAATCACACAA   31426         A   TT
                                   TTTGGTAC AAA  TCACACAA
                                   |||||||| |||  ||||||||
                                   AAACCATG TTT  AGTGTGTT
                                        C   __
GAM1207  LOC169966 3'  TCTTTGGTAAAGGCAAAAT    31427          ____
                                   TCTTTGGTA    CAAAAT
                                   |||||||||    ||||||
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                                AGAAACCAT   GTTTTA
                                     TTCC
GAM1207 LOC221272 3' TCTCTGGTACAGAGCAGACA  31428          AAATTT C
                                TCTTTGGTACA     CA ACA
                                ||||||||||      || |||
                                AGAGACCATGT     GT TGT
                                      CTC___  C
GAM1207 LOC221968 3' TTCGACAAAATTTCACACAA  31429      GT
                                TTTG  ACAAAATTTCACACAA
                                ||||  ||||||||||||||||
                                AAGC  TGTTTTAAAGTGTGTT
                                  __
GAM1207 LOC86651  5' TCCTTGGTATGAAACATCTTTC 31430        CA   ____
             ACACAA                 CTTTGGTA  AAAT   TTCACACAA
                                ||||||||  ||||   |||||||||
                                GGAACCAT  TTTG   AAGTGTGTT
                                     AC   TAGA
GAM1207 LOC90322  3' TCTTTAGTATGGAATCTC    31431         CAA
                                TCTTTGGTA   AATTTC
                                |||||||||   ||||||
                                AGAAATCAT   TTAGAG
                                     ACC
GAM1208 CDH19    3' TATTTTTACTCTTTCC      31434         TT
                                TATTTTTA  CTCTTTCT
                                ||||||||  ||||||||
                                ATAAAAAT  GAGAAAGG
                                  __
GAM1208 CLTC     3' AATATTTTGTTTGAATTTCTCT 31435         TATTCTC
             CT                   AATATTTT      TTTCTCTCT
                                ||||||||      |||||||||
                                TTATAAAA      AAAGAGAGA
                                     CAAACTT
GAM1208 CRH      5' TTCCCACTCTCTTTTTCT    31436            C
                                TTTTTATTCTCTTT TCT
                                |||||||||||||| |||
                                AAGGGTGAGAGAAA AGA
                                       A
GAM1208 DYRK2    3' GGATTTTCAACCCTCTTTCT  31437   T     _
                                A ATTTTTA TTCTCTTTCT
                                | |||||||| ||||||||||
                                C TAAAAGT GGGAGAAAGA
                                 C      T
GAM1208 DYRK2    3' GGATTTTCAACCCTCTTTCT  31437   T     _
                                A ATTTTTA TTCTCTTTCT
                                | |||||||| ||||||||||
                                C TAAAAGT GGGAGAAAGA
                                 C      T
GAM1208 MEIS2    5' ATATTTCTTCTTTTTCTCT   31438       TA   C
                                ATATTTT  TTCT TTTCTCT
                                |||||||  |||| |||||||
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                                TATAAAG  AAGA AAAGAGA
                                   __    A
GAM1208  NOTCH2   3'  AATATTTTAATTCTCAGACTCT 31439        T     TTT
              CT                    AATATTTT ATTCTC   CTCTCT
                                    |||||||| ||||||   ||||||
                                    TTATAAAA TAAGAG   GAGAGA
                                       T     TCT
GAM1208  PTP4A2   3'  ATTCCTTTTCTCTTTCTCT   31440       A
                                    ATTTTT TTCTCTTTCTCT
                                    |||||| ||||||||||||
                                    TAAGGA AAGAGAAAGAGA
                                       A
GAM1208  PTP4A2   3'  ATTCCTTTTCTCTTTCTCT   31440       A
                                    ATTTTT TTCTCTTTCTCT
                                    |||||| ||||||||||||
                                    TAAGGA AAGAGAAAGAGA
                                       A
GAM1208  RTN3     3'  TTCTTTCATTTTCTCTCT    31441     A   TC
                                    TTT TTC  TTTCTCTCT
                                    ||| |||  |||||||||
                                    AAG AAG  AAAGAGAGA
                                      A   TA
GAM1208  ALDH5A1  3'  CTTTTACTTTCTCTC       31442       TTCT
                                    TTTTTA    CTTTCTCTC
                                    ||||||    |||||||||
                                    GAAAAT    GAAAGAGAG
                                              ____
GAM1208  C21orf41 3'  TTTTTATTTTATTTTTCTCTCT 31443         CTC__
                                    TTTTTATT     TTTCTCTCT
                                    ||||||||     |||||||||
                                    AAAAATAA     AAAGAGAGA
                                         AATAA
GAM1208  C6orf37  3'  ATATTTTTTTCTCCCGTGGTCT 31444         A     ____
              CTCT                     ATATTTTT TTCTCTT    TCTCTCT
                                       |||||||| |||||||    |||||||
                                       TATAAAAA AAGAGGG    AGAGAGA
                                          _       CACC
GAM1208  FLJ11710 5'  TTTTCTTTCTTTTTCTCTCT   31445       A   C
                                    TTTTT TTCT TTTCTCTCT
                                    ||||| |||| |||||||||
                                    AAAAG AAGA AAAGAGAGA
                                       A    A
GAM1208  FLJ14007 3'  TATTTCATCTCTTTCTCTCT   31446       TAT
                                    TATTTT   TCTCTTTCTCTCT
                                    ||||||   ||||||||||||||
                                    ATAAAG   AGAGAAAGAGAGA
                                       T__
GAM1208  FLJ21791 3'  AATATTGTTATTCTCTACATCT 31447        T       TTC
                                    AATATT TTATTCTCT   TCT
                                    |||||| |||||||||   |||
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                                TTATAA AATAAGAGA   AGA
                                   C        TGT
GAM1208 KIAA0303 5' ACATATCCATTTCTTTCTCTCT 31448      T     C
                                ATAT TTTATT TCTTTCTCTCT
                                |||| |||||| ||||||||||
                                TGTA AGGTAA AGAAAGAGAGA
                                  T     _
GAM1208 NIFU     5' AATATGTCTATTTTTCTCTCT  31449       T     CTC
                                AATAT TTTATT   TTTCTCTCT
                                ||||| ||||||   |||||||||
                                TTATA AGATAA   AAAGAGAGA
                                  C     ___
GAM1208 PTD012   3' ATATTTTTGTTCCCAATCTCT  31450         A     TT
                                ATATTTTT TTCTC  TCTCT
                                |||||||| |||||  |||||
                                TATAAAAA AAGGG  AGAGA
                                     C     TT
GAM1208 SAMHD1   3' ATATTTCTTTCTCTTTCTTTCT 31451         A         C
                                ATATTTTT TTCTCTTTCT TCT
                                |||||||| |||||||||| |||
                                TATAAAGA AAGAGAAAGA AGA
                                     _         A
GAM1208 SMBP     3' AATATTTTCTAATTCTCTC   31452        TTAT   CT
                                AATATTT    TCT  TTCTCTC
                                |||||||    |||  |||||||
                                TTATAAA    AGA  AAGAGAG
                                     _____   TT
GAM1208 SRP9     3' AATATTTTATTTACTGATCTCT 31453         T   CT  T_
             CT                    AATATTTT ATT  CT  TCTCTCT
                                |||||||| |||  ||  |||||||
                                TTATAAAA TAA  GA  AGAGAGA
                                     _   AT  CT
GAM1208 SRPUL    5' TATTTTGTGCCCTTTTTCTCTC 31454        TA_    C
             T                     TATTTT   TTCT TTTCTCTCT
                                ||||||   |||| |||||||||
                                ATAAAA   GGGA AAAGAGAGA
                                   CAC    A
GAM1208 UBAP     3' ATTTTTATTAGTAGTTCTCTCT 31455          CTCT_
                                ATTTTTATT     TTCTCTCT
                                |||||||||     ||||||||
                                TAAAAATAA     AAGAGAGA
                                     TCATC
GAM1208 LOC146723 3' TATTTTCTTTTCTTTCTCT    31456        A  C
                                TATTTTT TT TCTTTCTCT
                                ||||||| || |||||||||
                                ATAAAAG AA AGAAAGAGA
                                     A  _
GAM1208 LOC146952 5' CATTTTTGTCCTCTCTCT     31457        A
                                TATTTTT TTCTCTTTCT
                                ||||||| ||||||||||
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                                GTAAAAA AGGAGAGAGA
                                    C
GAM1208  LOC152992 3'  TTTTTATTCTCTGTAACTCT   31458          TTCT
                                TTTTTATTCTCT    CTCT
                                ||||||||||||   ||||
                                AAAAATAAGAGA    GAGA
                                      CATT
GAM1208  LOC199837 5'  TATTTTCAGTCTTGTTTTTCTC 31459        T   C___
           T                    TATTTTTA TCT    TTTCTCT
                                |||||||| |||    |||||||
                                ATAAAAGT AGA    AAAGAGA
                                    C   ACAA
GAM1208  LOC222166 3'  CATTCCTTTCTCTTTCTTTCT  31460        A        C
                                TATTTTT TTCTCTTTCT TCT
                                ||||||| |||||||||| |||
                                GTAAGGA AAGAGAAAGA AGA
                                   _        A
GAM1209  LTB4R    5'  TCAGATTGGAGGCTACAA    31463        TTA  CA
                                TCAGATTG   GA  GCTACAA
                                ||||||||   ||  |||||||
                                AGTCTAAC   CT  CGATGTT
                                    ____  C_
GAM1209  SAFB     3'  TCACATTGTATTGAGCTACAA  31464     G    TAGAC
                                TCA ATTGT     AGCTACAA
                                ||| |||||     ||||||||
                                AGT TAACA     TCGATGTT
                                  G     TAAC_
GAM1209  ASAH     3'  GAAGGTCAGACAGCTGCA    31465    TT         A
                                GA  GTTAGACAGCT CA
                                ||  ||||||||||| ||
                                CT  CAGTCTGTCGA GT
                                  TC          C
GAM1209  C21orf59  5'  CCGGATCGCCAGCAGCT     31466    A        A
                                TC GATTGTTAG CAGCT
                                || |||||||| |||||
                                GG CTAGCGGTC GTCGA
                                  C        _
GAM1209  C21orf59  5'  CCGGATCGCCAGCAGCT     31466    A        A
                                TC GATTGTTAG CAGCT
                                || |||||||| |||||
                                GG CTAGCGGTC GTCGA
                                  C        _
GAM1209  DKFZP566J091 3'  TCAGATGGCTCTTAGCTACAA  31467       T   AGAC
                                TCAGAT GTT    AGCTACAA
                                |||||| |||    ||||||||
                                AGTCTA CGA    TCGATGTT
                                    C   GAA_
GAM1209  DKFZP761D0211 3'  CAGCCAGTAGACAGCTGCAACA 31468     ATT  T       A
                                CAG   GT AGACAGCT CAACA
                                |||   || |||||||| |||||
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                                GTC   CA TCTGTCGA GTTGT
                                  GGT  _       C
GAM1209  KIAA0138  3'  TCACATTGTATTGAGCTACAAC 31469     G    TAGAC
             A                    TCA ATTGT    AGCTACAACA
                                  ||| |||||    ||||||||||
                                  AGT TAACA    TCGATGTTGT
                                    G    TAAC_
GAM1209  MGC20533  3'  TCACATAAAAAATAGCTACA   31470     G  TGTT   C
                                  TCA AT    AGA AGCTACA
                                  ||| ||    ||| |||||||
                                  AGT TA    TTT TCGATGT
                                    G  TTT_   A
GAM1209  RAB33B   3'  AGTTGTTAGATAGCTATCA    31471    A      C    _
                                  AG TTGTTAGA AGCTA CA
                                  || |||||||| ||||| ||
                                  TC AACAATCT TCGAT GT
                                   _       A    A
GAM1209  SEF      5'  AGATTGTCCGGCTGTAACA    31472        AGACA   AC
                                  AGATTGTT    GCT  AACA
                                  ||||||||    |||  ||||
                                  TCTAACAG    CGA  TTGT
                                       GC___   CA
GAM1209  UST      3'  TCAGATTGTGAGATTGCACA   31473         T   CA  T
                                  TCAGATTGT AGA  GC ACA
                                  ||||||||| |||  || |||
                                  AGTCTAACA TCT  CG TGT
                                        C   AA  _
GAM1209  ZNF262   3'  TCAGGCTGTGAGACAGCTGCAA 31474      AT   T      A
                                  TCAG  TGT AGACAGCT CAA
                                  ||||  ||| |||||||| |||
                                  AGTC  ACA TCTGTCGA GTT
                                    CG   C       C
GAM1209  LOC150940 5'  TCAGGATGTTAGAAGCAGC    31475      AT     __
                                  TCAG  TGTTAGA  CAGC
                                  ||||  |||||||  ||||
                                  AGTC  ACAATCT  GTCG
                                    CT      TC
GAM1209  LOC202451 3'  TCAAATCATTATGGCTATAACA 31476       TG   GACA   C
                                  TCAGAT  TTA    GCTA AACA
                                  ||||||  |||    |||| ||||
                                  AGTTTA  AAT    CGAT TTGT
                                     GT   AC__    A
GAM1209  LOC253263 3'  TCAAGAGTTCAGACAGCT    31477     _ TTG
                                  TCA GA   TTAGACAGCT
                                  ||| ||   ||||||||||
                                  AGT CT   AGTCTGTCGA
                                    T  CA_
GAM1209  LOC253890 5'  TCGGATTGTCACACCTA     31478    A      AG   G
                                  TC GATTGTT  ACA CTA
                                  || |||||||  ||| |||
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                                AG CTAACAG  TGT GAT
                                 C      __  G
GAM1210 ARHI    3' CATTTTGTTCTCCTCTTC    31481       A    TTTCT
                                TATTTT TTCTC    CTCTTC
                                |||||| |||||    ||||||
                                GTAAAA AAGAG    GAGAAG
                                   C    _____
GAM1210 CBFA2T1  3' TATTCTCTGCTCTCTTTTCA  31482        _    C
                                TATTCTCT TTCTCT TTCA
                                |||||||| |||||| ||||
                                ATAAGAGA GAGAGA AAGT
                                     C     A
GAM1210 CDH18   5' TTCTGTTCTTGCTCCTCTTCA 31483     A   CT  T
                                TTTT TTCT  TTC CTCTTCA
                                |||| ||||  ||| |||||||
                                AAGA AAGA  GAG GAGAAGT
                                  C   AC  _
GAM1210 CREBL2   3' TATTTTCCCCCTTTTCTTTCTT 31484       A      _ C
                                TATTTT TTCTCTTT CT TCTT
                                |||||| |||||||| || ||||
                                ATAAAA GGGGGAAA GA AGAA
                                   _       A  A
GAM1210 ENC1    3' TCTTTTCCTTTTTTTCTCTTCA 31485     A   C  C
                                TTTT TTCT TTT TCTCTTCA
                                |||| |||| ||| ||||||||
                                AGAA AGGA AAA AGAGAAGT
                                  A   A  A
GAM1210 GOLGA4   5' TTTTGTTCAGCTTTTCTCTTCA 31486     A  T_   C
                                TTTT TTC  CTTT TCTCTTCA
                                |||| |||  |||| ||||||||
                                AAAA AAG  GAAA AGAGAAGT
                                  C  TC   _
GAM1210 IL6R    3' TATTTTTTCTCTTCCTCCTTTT 31487       A         C__
            TCA                   TATTTT TTCTCTTTCTCT   TTCA
                                |||||| ||||||||||||   ||||
                                ATAAAA AAGAGAAGGAGG   AAGT
                                   _          AAA
GAM1210 KERA    3' TATTTTATTTTCTCATTTTCTT 31488         C   TCTC
            CA                   TATTTTATT TCTT    TCTTCA
                                |||||||| ||||    ||||||
                                ATAAAATAA AGAG    AGAAGT
                                     A    TAAA
GAM1210 POH1    5' TATTTTATTTTTTCTTTCTCTC 31489         C__
            CT                   TATTTTATT   TCTTTCTCTCTT
                                |||||||||   ||||||||||||
                                ATAAAATAA   AGAAAGAGAGGA
                                     AAA
GAM1210 PURA    3' TTTTATTTTCTCTCTTTCTT   31490       C      C
                                TTTTATT TCTTTCT TCTT
                                ||||||| ||||||| ||||
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                                AAAATAA AGAGAGA AGAA
                                   A      A
GAM1210  TPD52L2   3'  TATTTTATGCTTAGAACTCTTC 31491        T  CTTTCT
             A                   TATTTTAT CT     CTCTTCA
                                 |||||||| ||     |||||||
                                 ATAAAATA GA     GAGAAGT
                                    C  ATCTT_
GAM1210  VIP       3'  CTTTATTTTCTCTCTT      31492        CTCT
                                 TTTTATT    TTCTCTCTT
                                 |||||||    |||||||||
                                 GAAATAA    AAGAGAGAA
                                      ____
GAM1210  ANGPTL1   5'  ATTTTATTAGTAGCTTTTCTCT 31493        CT___    C
             TCA                   ATTTTATT    CTTT TCTCTTCA
                                 ||||||||    |||| ||||||||
                                 TAAAATAA    GAAA AGAGAAGT
                                    TCATC   _
GAM1210  C6orf37   3'  TATTTTTTTCTCCCGTGGTCTC 31494       A     ____
             TCTT                  TATTTT TTCTCTT    TCTCTCTT
                                 |||||| |||||||    ||||||||
                                 ATAAAA AAGAGGG    AGAGAGAA
                                    A      CACC
GAM1210  DCOHM     3'  TACTTTTGTGACTTCTCTCTT  31495       ATTCTC
                                 TATTTT     TTTCTCTCTT
                                 ||||||     ||||||||||
                                 ATGAAA     GAAGAGAGAA
                                    ACACT_
GAM1210  DKFZP434G072 5'  TTTATTTTCCCCTCTTCA    31496       CTC
                                 TTTATT   TTTCTCTCTTCA
                                 ||||||   ||||||||||||
                                 AAATAA   AAGGGGAGAAGT
                                      ___
GAM1210  FLJ21126  5'  TTTATCCTACTTTTTTCTTCA  31497         _   CTC
                                 TTTATTCT CTTT   TCTTCA
                                 |||||||| ||||   ||||||
                                 AAATAGGA GAAA   AGAAGT
                                    T    AA_
GAM1210  FLJ22595  5'  TTTCTTTCTTTCTTTCTCTCTT 31498      A  __
             C                    TTTT TTC  TCTTTCTCTCTTC
                                 |||| |||  ||||||||||||||
                                 AAAG AAG  AGAAAGAGAGAAG
                                   A   AA
GAM1210  FLJ22794  5'  ATTTTTTCACTTTCTCTTTTCA 31499       A   T       C
                                 ATTTT TTC CTTTCTCT TTCA
                                 ||||| ||| |||||||| ||||
                                 TAAAA AAG GAAAGAGA AAGT
                                   _  T       A
GAM1210  KIAA0303  5'  TCCATTTCTTTCTCTCTTCA   31500       C
                                 TTTATT TCTTTCTCTCTTCA
                                 |||||| ||||||||||||||
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                                AGGTAA AGAAAGAGAGAAGT
                                   _
GAM1210 KIAA1363 3' CATTTTATTTTCTTTTTCTTC 31501         C    CTC
                                TATTTTATT TCTTT   TCTTC
                                ||||||||| |||||   |||||
                                GTAAAATAA AGAAA   AGAAG
                                     A    A__
GAM1210 KIAA1384 3' TATTTTATCTTTCTCCTT    31502       TTC      T
                                TATTTTA   TCTTTCTC CTT
                                |||||||   |||||||| |||
                                ATAAAAT   AGAAAGAG GAA
                                   ___     _
GAM1210 SIAT9    3' TTTTATTCTTTTTCATCTT   31503        C   TC
                                TTTTATTCT TTTC  TCTT
                                ||||||||| ||||  ||||
                                AAAATAAGA AAAG  AGAA
                                     A   T_
GAM1210 TCL6     5' TATTTTATTTTCTCTC     31504        CTCT
                                TATTTTATT   TTCTCTC
                                |||||||||   |||||||
                                ATAAAATAA   AAGAGAG
                                   ____
GAM1210 TCL6     5' TATTTTATTTTCTCTC     31504        CTCT
                                TATTTTATT   TTCTCTC
                                |||||||||   |||||||
                                ATAAAATAA   AAGAGAG
                                   ____
GAM1210 TCL6     5' TATTTTATTTTCTCTC     31504        CTCT
                                TATTTTATT   TTCTCTC
                                |||||||||   |||||||
                                ATAAAATAA   AAGAGAG
                                   ____
GAM1210 TCL6     5' TATTTTATTTTCTCTC     31504        CTCT
                                TATTTTATT   TTCTCTC
                                |||||||||   |||||||
                                ATAAAATAA   AAGAGAG
                                   ____
GAM1210 ZAK      3' TTTTATCCTCTTTGCTCCTT  31505          _  T
                                TTTTATTCTCTTT CTC CTT
                                |||||||||||| ||| |||
                                AAAATAGGAGAAA GAG GAA
                                     C  _
GAM1210 LOC123876 3' CTTCTTTCTCTTTCTCTCTT  31506     A
                                TTTT TTCTCTTTCTCTCTT
                                |||| ||||||||||||||
                                GAAG AAGAGAAAGAGAGAA
                                  A
GAM1210 LOC145826 5' TATTTTATTCTCTCATTC    31507           TC
                                TATTTTATTCTCTT  TC
                                ||||||||||||  ||
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                                ATAAAATAAGAGAG  AG
                                       TA
GAM1210  LOC146723 3'  TATTTTCTTTTCTTTCTCTTTC 31508       A  C       C
                                TATTTT TT TCTTTCTCT TTC
                                |||||| || ||||||||| |||
                                ATAAAA AA AGAAAGAGA AAG
                                   G  A       _
GAM1210  LOC151174 5'  TATTTCTGTTCTTTCTCT    31509       ATTC
                                TATTTT    TCTTTCTCT
                                ||||||    |||||||||
                                ATAAAG    AGAAAGAGA
                                   ACA_
GAM1210  LOC51313  3'  CTTGACTCTCTTTCTTTTTTCA 31510     T         CTC
                                TTT ATTCTCTTTCT   TTCA
                                ||| ||||||||||   ||||
                                GAA TGAGAGAAAGA   AAGT
                                  C         AAA
GAM1210  LOC91263  3'  TATTTTATTTCCTTTCTCC    31511         CT
                                TATTTTATT  CTTTCTCT
                                |||||||||  ||||||||
                                ATAAAATAA  GAAAGAGG
                                     AG
GAM1211  ARHGEF12  3'  TCATAAAAGAGCTATTTTACAA 31514         A  ___
            A                    TCATAAAA AGT   TTTACAAA
                                ||||||||| |||   ||||||||
                                AGTATTTT TCG   AAATGTTT
                                     C   ATA
GAM1211  IL12A     3'  TCATTTCAAAGTTTTATAAAAA 31515      AAA       C
            T                    TCAT   AAAGTTTTA AAAAAT
                                ||||   ||||||||| ||||||
                                AGTA   TTTCAAAAT TTTTTA
                                  AAG        A
GAM1211  MADH2     3'  TAAAAAAGACACACAAAAATA  31516         TTT
                                TAAAAAAG   TACAAAAATA
                                ||||||||   ||||||||||
                                ATTTTTTC   GTGTTTTTAT
                                     TGT
GAM1211  MPHOSPH1  3'  ATAAAAAAGCCTTATAAAAATA 31517            C
                                ATAAAAAAGTTTTA AAAAATA
                                |||||||||||||| |||||||
                                TATTTTTTCGGAAT TTTTTAT
                                       A
GAM1211  MYH8      3'  TCATAAAGCAAGTGACCAAAAA 31518       A_   TTTA
            TA                    TCATAAA  AAGT    CAAAAATA
                                |||||||  ||||   ||||||||
                                AGTATTT  TTCA    GTTTTTAT
                                   CG   CTG_
GAM1211  PMP2      3'  AAAAAGTCTTGTACAAAAATA  31519         __
                                AAAAAGTTT  TACAAAAATA
                                |||||||||  ||||||||||
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                                TTTTTCAGA  ATGTTTTTAT
                                     AC
GAM1211  PROML1   3'  TAAAAAAGTAAAAAACAAAAAT 31520        TTT__
            A                   TAAAAAAGT    ACAAAAATA
                                |||||||||    |||||||||
                                ATTTTTTCA    TGTTTTTAT
                                     TTTTT
GAM1211  CDH9     3'  TCATAAAAATACAAAAAT    31521        AGTTT
                                TCATAAAAA    TACAAAAAT
                                |||||||||    |||||||||
                                AGTATTTTT    ATGTTTTTA
                                     _____
GAM1211  EVI5     3'  TCATGAAACAGTTTTACCAAAA 31522     A  A     A
            TA                    TCAT AAA AGTTTTAC AAAATA
                                |||| ||| |||||||| |||||||
                                AGTA TTT TCAAAATG TTTTAT
                                  C  G      G
GAM1211  FLJ31101 3'  TCACAAATACATTTTACAAAAA 31523       AAA
            TA                    TCATAAA   GTTTTACAAAAATA
                                |||||||   ||||||||||||||
                                AGTGTTT   TAAAATGTTTTTAT
                                    ATG
GAM1211  SGKL     3'  TCATTAAACTTTTACAAAAAT  31524     AAA  G
                                TCAT   AAA TTTTACAAAAAT
                                ||||   ||| ||||||||||||
                                AGTA   TTT AAAATGTTTTTA
                                  A__  G
GAM1211  ZAK      3'  CCATAAAAAGACCCACCAAAAA 31525        AG  TA
            TA                    TCATAAAAA  TTT  CAAAAATA
                                |||||||||  |||  ||||||||
                                GGTATTTTT  GGG  GTTTTTAT
                                     CT   TG
GAM1211  LOC150245 3'  TCACAAAAAAGTCACAAA    31526          TT
                                TCATAAAAAAGTT  ACAAA
                                ||||||||||||  |||||
                                AGTGTTTTTTCAG  TGTTT
                                     __
GAM1212  CDH19    3'  TATTTTTACTCTTTCC      31434        TT
                                TATTTTTA  CTCTTTCT
                                ||||||||  ||||||||
                                ATAAAAAT  GAGAAAGG
                                     __
GAM1212  CLTC     3'  AATATTTTGTTTGAATTTCTCT 31435        TATTCTC
            CT                    AATATTTT      TTTCTCTCT
                                ||||||||      |||||||||
                                TTATAAAA      AAAGAGAGA
                                    CAAACTT
GAM1212  CRH      5'  TTCCCACTCTCTTTTTCT    31436           C
                                TTTTTATTCTCTTT TCT
                                |||||||||||||| |||
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                                AAGGGTGAGAGAAA AGA
                                       A
GAM1212  DYRK2    3'  GGATTTTCAACCCTCTTTCT  31437   T     _
                                A ATTTTTA TTCTCTTTCT
                                | ||||||| ||||||||||
                                C TAAAAGT GGGAGAAAGA
                                 C      T
GAM1212  DYRK2    3'  GGATTTTCAACCCTCTTTCT  31437   T     _
                                A ATTTTTA TTCTCTTTCT
                                | ||||||| ||||||||||
                                C TAAAAGT GGGAGAAAGA
                                 C      T
GAM1212  MEIS2    5'  ATATTTCTTCTTTTTCTCT   31438       TA   C
                                ATATTTT  TTCT TTTCTCT
                                |||||||  |||| |||||||
                                TATAAAG  AAGA AAAGAGA
                                    __   A
GAM1212  NOTCH2   3'  AATATTTTAATTCTCAGACTCT 31439       T    TTT
              CT                  AATATTTT ATTCTC  CTCTCT
                                |||||||| ||||||  ||||||
                                TTATAAAA TAAGAG  GAGAGA
                                    T     TCT
GAM1212  PTP4A2   3'  ATTCCTTTTCTCTTTCTCT   31440       A
                                ATTTTT TTCTCTTTCTCT
                                |||||| ||||||||||||
                                TAAGGA AAGAGAAAGAGA
                                   A
GAM1212  PTP4A2   3'  ATTCCTTTTCTCTTTCTCT   31440       A
                                ATTTTT TTCTCTTTCTCT
                                |||||| ||||||||||||
                                TAAGGA AAGAGAAAGAGA
                                   A
GAM1212  RTN3     3'  TTCTTTCATTTTCTCTCT    31441     A   TC
                                TTT TTC  TTTCTCTCT
                                ||| |||  |||||||||
                                AAG AAG  AAAGAGAGA
                                  A   TA
GAM1212  ALDH5A1  3'  CTTTTACTTTCTCTC      31442       TTCT
                                TTTTTA   CTTTCTCTC
                                ||||||   |||||||||
                                GAAAAT   GAAAGAGAG
                                   ____
GAM1212  C21orf41 3'  TTTTTATTTTATTTTTCTCTCT 31443        CTC__
                                TTTTTATT    TTTCTCTCT
                                ||||||||    |||||||||
                                AAAAATAA    AAAGAGAGA
                                    AATAA
GAM1212  C6orf37  3'  ATATTTTTTTCTCCCGTGGTCT 31444        A    ____
              CTCT                 ATATTTTT TTCTCTT   TCTCTCT
                                |||||||| |||||||   |||||||
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                                TATAAAAA AAGAGGG   AGAGAGA
                                   _     CACC
GAM1212 FLJ11710 5' TTTTCTTTCTTTTTCTCTCT  31445      A   C
                                TTTTT TTCT TTTCTCTCT
                                ||||| |||| |||||||||
                                AAAAG AAGA AAAGAGAGA
                                   A   A
GAM1212 FLJ14007 3' TATTTCATCTCTTTCTCTCT  31446      TAT
                                TATTTT  TCTCTTTCTCTCT
                                ||||||  ||||||||||||
                                ATAAAG  AGAGAAAGAGAGA
                                   T__
GAM1212 FLJ21791 3' AATATTGTTATTCTCTACATCT 31447      T       TTC
                                AATATT TTATTCTCT  TCT
                                |||||| |||||||||  |||
                                TTATAA AATAAGAGA  AGA
                                   C       TGT
GAM1212 KIAA0303 5' ACATATCCATTTCTTTCTCTCT 31448     T     C
                                ATAT TTTATT TCTTTCTCTCT
                                |||| |||||| ||||||||||
                                TGTA AGGTAA AGAAAGAGAGA
                                  T    _
GAM1212 NIFU     5' AATATGTCTATTTTTCTCTCT  31449      T     CTC
                                AATAT TTTATT  TTTCTCTCT
                                ||||| ||||||  |||||||||
                                TTATA AGATAA  AAAGAGAGA
                                  C    ___
GAM1212 PTD012   3' ATATTTTTGTTCCCAATCTCT  31450       A     TT
                                ATATTTTT TTCTC  TCTCT
                                |||||||| |||||  |||||
                                TATAAAAA AAGGG  AGAGA
                                    C    TT
GAM1212 SAMHD1   3' ATATTTCTTTCTCTTTCTTTCT 31451       A       C
                                ATATTTTT TTCTCTTTCT TCT
                                |||||||| |||||||||| |||
                                TATAAAGA AAGAGAAAGA AGA
                                   _       A
GAM1212 SMBP     3' AATATTTTCTAATTCTCTC   31452       TTAT  CT
                                AATATTT   TCT  TTCTCTC
                                |||||||   |||  |||||||
                                TTATAAA   AGA  AAGAGAG
                                   ____  TT
GAM1212 SRP9     3' AATATTTTATTTACTGATCTCT 31453       T  CT  T_
            CT                   AATATTTT ATT  CT  TCTCTCT
                                |||||||| |||  ||  |||||||
                                TTATAAAA TAA  GA  AGAGAGA
                                   _  AT  CT
GAM1212 SRPUL    5' TATTTTGTGCCCTTTTTCTCTC 31454       TA_   C
            T                    TATTTT   TTCT TTTCTCTCT
                                ||||||  |||| |||||||||
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                                ATAAAA   GGGA AAAGAGAGA
                                   CAC    A
GAM1212  UBAP     3'  ATTTTTATTAGTAGTTCTCTCT 31455         CTCT_
                                ATTTTTATT     TTCTCTCT
                                |||||||||     ||||||||
                                TAAAAATAA     AAGAGAGA
                                   TCATC
GAM1212  LOC146723 3'  TATTTTCTTTTCTTTCTCT    31456        A  C
                                TATTTTT TT TCTTTCTCT
                                ||||||| || |||||||||
                                ATAAAAG AA AGAAAGAGA
                                   A  _
GAM1212  LOC146952 5'  CATTTTTGTCCTCTCTCT     31457        A
                                TATTTTT TTCTCTTTCT
                                ||||||| ||||||||||
                                GTAAAAA AGGAGAGAGA
                                   C
GAM1212  LOC152992 3'  TTTTTATTCTCTGTAACTCT   31458           TTCT
                                TTTTTATTCTCT    CTCT
                                ||||||||||||    ||||
                                AAAAATAAGAGA    GAGA
                                      CATT
GAM1212  LOC199837 5'  TATTTTCAGTCTTGTTTTTCTC 31459         T   C___
            T                    TATTTTTA TCT    TTTCTCT
                                ||||||||| |||    |||||||
                                ATAAAAGT AGA    AAAGAGA
                                   C   ACAA
GAM1212  LOC222166 3'  CATTCCTTTCTCTTTCTTTCT  31460        A         C
                                TATTTTT TTCTCTTTCT TCT
                                ||||||| |||||||||| |||
                                GTAAGGA AAGAGAAAGA AGA
                                   _         A
GAM1213  CDH10    3'  TAATGTACAGAACAGGATA    31530         T    TG
                                TAATGTACAG ACAG  TA
                                |||||||||| ||||  ||
                                ATTACATGTC TGTC  AT
                                      T    CT
GAM1213  HRB      3'  ATGTACAGTACTGCAGCATA   31531          AG    A
                                ATGTACAGTAC  TGTA CATA
                                |||||||||||  |||| ||||
                                TACATGTCATG  ACGT GTAT
                                      __    C
GAM1213  KLHL1    3'  TAATGTACAGATCAATGTA    31532         TA
                                TAATGTACAG  CAGTGTA
                                ||||||||||  |||||||
                                ATTACATGTC  GTTACAT
                                      TA
GAM1213  LDHA     3'  TAATGTACACTACTGATATA   31533         G   A_
                                TAATGTACA TAC  GTGTA
                                ||||||||| |||  |||||
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                                ATTACATGT ATG  TATAT
                                     G   AC
GAM1213  SUV39H2   3'  TAATGTACATTACAGTAT    31534         G
                                TAATGTACA TACAGTGT
                                ||||||||| ||||||||
                                ATTACATGT ATGTCATA
                                     A
GAM1213  TRHDE     3'  TACATGTGCAGTGTACAACATA 31535     _  A      __
                                TACA GT CAGTGTA  ACATA
                                |||| || |||||||  |||||
                                ATGT CA GTCACAT  TGTAT
                                  A  C      GT
GAM1213  BNIP2     3'  TAATTTACAGTATTGTCAAACA 31536     G      CA  GT
              T                  TAAT TACAGTA  GT  AACAT
                                |||| |||||||  ||  |||||
                                ATTA ATGTCAT  CA  TTGTA
                                  A      AA  GT
GAM1213  CAMKK2    3'  TAATGTACATGAAAGCATA   31537         GTAC
                                TAATGTACA    AGTGTA
                                |||||||||    ||||||
                                ATTACATGT    TCGTAT
                                     ACTT
GAM1213  FLJ11342  3'  TAATGTGCAGTTTATATAACAT 31538       A    ACA
              A                  TAATGT CAGT   GTGTAACATA
                                |||||| ||||   ||||||||||
                                ATTACA GTCA   TATATTGTAT
                                   C    AA_
GAM1213  KIAA0630  3'  TAATGTACATATAATGTA    31539         GTAC
                                TAATGTACA    AGTGTA
                                |||||||||    ||||||
                                ATTACATGT    TTACAT
                                     ATA_
GAM1213  KIAA1301  3'  GTGCAGGAGTGTAACAT     31540     A   TAC
                                GT CAG   AGTGTAACAT
                                || |||   ||||||||||
                                CA GTC   TCACATTGTA
                                 C   C__
GAM1213  KIAA1322  3'  ATGTACAGTAAGAAAATATA   31541          C___
                                ATGTACAGTA    AGTGTA
                                |||||||||    ||||||
                                TACATGTCAT    TTATAT
                                      TCTT
GAM1213  KIAA1409  3'  AATGTACAGTACCAATAT    31542           _
                                AATGTACAGTAC AGTGT
                                |||||||||||| |||||
                                TTACATGTCATG TTATA
                                       G
GAM1213  MGC5306   3'  TGTACAGTGAGTGAACAT    31543         AC    T
                                TGTACAGT  AGTG AACAT
                                ||||||||  |||| |||||
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                                ACATGTCA  TCAC TTGTA
                                    C_   _
GAM1213  PB1      3'  TAATGTACAGTTTTGAAAGTGT 31544          AC____
             A                   TAATGTACAGT     AGTGTA
                                 ||||||||||      ||||||
                                 ATTACATGTCA     TCACAT
                                      AAACTT
GAM1213  SFRS4    3'  AATGTACAGCAGTGACAT    31545        TA    TA
                                 AATGTACAG  CAGTG  ACAT
                                 |||||||||  |||||  ||||
                                 TTACATGTC  GTCAC  TGTA
                                     __    __
GAM1213  SMARCF1  3'  TGTACAGTACAGTACAT     31546          GTA
                                 TGTACAGTACAGT   ACAT
                                 ||||||||||||   ||||
                                 ACATGTCATGTCA   TGTA
                                     ___
GAM1213  SMARCF1  3'  TGTACAGTACAGTACAT     31546          GTA
                                 TGTACAGTACAGT   ACAT
                                 ||||||||||||   ||||
                                 ACATGTCATGTCA   TGTA
                                     ___
GAM1213  SMARCF1  3'  TGTACAGTACAGTACAT     31546          GTA
                                 TGTACAGTACAGT   ACAT
                                 ||||||||||||   ||||
                                 ACATGTCATGTCA   TGTA
                                     ___
GAM1213  SPARCL1  3'  CAATGTACAGTATTTTGCA   31547          CAG
                                 TAATGTACAGTA   TGTA
                                 ||||||||||||   ||||
                                 GTTACATGTCAT   ACGT
                                      AAA
GAM1213  LOC132720 3'  ATGTACAGTACTGACAGTATA  31548         ____
                                 ATGTACAGT    ACAGTGTA
                                 |||||||||    ||||||||
                                 TACATGTCA    TGTCATAT
                                     TGAC
GAM1213  LOC145945 3'  TAATATACAGTCAAGATGATGT 31549          A _____
                                 TAATGTACAGT CA     GTGT
                                 ||||||||||| ||     ||||
                                 ATTATATGTCA GT     TACA
                                      _ TCTAC
GAM1213  LOC91549  3'  TAATTTACAGCATCAGTAACAT 31550      G     _    TA
             A                   TAAT TACAGTA CAGTG  ACATA
                                 |||| ||||||| |||||  |||||
                                 ATTA ATGTCGT GTCAT  TGTAT
                                   A      A   __
GAM1214  CDH19    3'  TATTTTTACTCTTTCC     31434         TT
                                 TATTTTTA  CTCTTTCT
                                 ||||||||  ||||||||
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                                ATAAAAAT  GAGAAAGG
                                   __
GAM1214  SHOX2    3'  AATATTTTCTCTTTTCTTGCT  31553       TTAT     _  C
                                AATATTT    TCTCTTT CT GCT
                                |||||||    ||||||| || |||
                                TTATAAA    AGAGAAA GA CGA
                                   ____      A  A
GAM1214  SHOX2    3'  AATATTTTCTCTTTTCTTGCT  31553       TTAT     _  C
                                AATATTT    TCTCTTT CT GCT
                                |||||||    ||||||| || |||
                                TTATAAA    AGAGAAA GA CGA
                                   ____      A  A
GAM1214  TRPS1    3'  AATATTTTCATTTCCTTCT    31554          C
                                AATATTTTTATT TCTTTCT
                                |||||||||||| |||||||
                                TTATAAAAGTAA AGGAAGA
                                   _
GAM1214  BTBD1    3'  TTTTATTCGGTTTCTTGCT    31555        TC    C
                                TTTTATTC  TTTCT GCT
                                ||||||||  ||||| |||
                                AAAATAAG  AAAGA CGA
                                     CC    A
GAM1214  FLJ21791 3'  AATATTGTTATTCTCTACATC  31556       T       TTC
                                AATATT TTATTCTCT   TC
                                |||||| |||||||||   ||
                                TTATAA AATAAGAGA   AG
                                   C        TGT
GAM1214  ICAM4    3'  ATATTCCTCTTTTTCTCGCT   31557       TTA    C
                                ATATTT   TTCT TTTCTCGCT
                                ||||||   |||| |||||||||
                                TATAAG   GAGA AAAGAGCGA
                                   ___    A
GAM1214  ICAM4    3'  ATATTCCTCTTTTTCTCGCT   31557       TTA    C
                                ATATTT   TTCT TTTCTCGCT
                                ||||||   |||| |||||||||
                                TATAAG   GAGA AAAGAGCGA
                                   ___    A
GAM1214  LOC253981 3'  AACATTTTTATTTTTAACTCCG 31558          CTCT_   T
            CT                    AATATTTTTATT     TTC CGCT
                                |||||||||||     ||| ||||
                                TTGTAAAAATAA     GAG GCGA
                                      AAATT   _
GAM1215  ATF5     3'  TCATGATTTGGACGAGA     31561     G     CC
                                TC ATGAT  GGACGAGG
                                || |||||  ||||||||
                                AG TACTA  CCTGCTCT
                                 _    AA
GAM1215  ITPR2    3'  GATGATCCTGGATTTTATAGGA 31562       _  CG_______  GTTC
            ACCT                   TGATCC GGA        AG    CT
                                ||||||  |||        ||    ||
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                                ACTAGG CCT       TC   GA
                                   A  AAAATIIIA  CTTG
GAM1215  RAD50    3'  GATGATTACTTAAGGTTCCT  31563      CCGGAC
                                GATGAT    GAGGTTCCT
                                ||||||    |||||||||
                                CTACTA    TTCCAAGGA
                                   ATGAA_
GAM1215  RAD50    3'  GATGATTACTTAAGGTTCCT  31563      CCGGAC
                                GATGAT    GAGGTTCCT
                                ||||||    |||||||||
                                CTACTA    TTCCAAGGA
                                   ATGAA_
GAM1215  LOC144278 3'  TCGGAGATCTGGGGTCTCCT  31564    AT   C  ACGA  _
                                TCG  GATC GG   GGT TCCT
                                |||  |||| ||   ||| ||||
                                AGC  CTAG CC   CCA AGGA
                                  CT   A ____  G
GAM1216  B4GALT1  3'  GTCATCTCATCCCAGGTGGC  31567    CCA        C
                                GTC  CTCATCCCAGG GGC
                                |||  ||||||||||| |||
                                CAG  GAGTAGGGTCC CCG
                                  TA_        A
GAM1216  FGFR1    5'  TCGGTCCCGTCCGGACG    31568      ACTCA  CA
                                TCGGTCCC   TCC  GGCG
                                ||||||||   |||  ||||
                                AGCCAGGG   AGG  CTGC
                                   C____  C_
GAM1216  FGFR1    5'  TCGGTCCCGTCCGGACG    31568      ACTCA  CA
                                TCGGTCCC   TCC  GGCG
                                ||||||||   |||  ||||
                                AGCCAGGG   AGG  CTGC
                                   C____  C_
GAM1216  FGFR1    5'  TCGGTCCCGTCCGGACG    31568      ACTCA  CA
                                TCGGTCCC   TCC  GGCG
                                ||||||||   |||  ||||
                                AGCCAGGG   AGG  CTGC
                                   C____  C_
GAM1216  FGFR1    5'  TCGGTCCCGTCCGGACG    31568      ACTCA  CA
                                TCGGTCCC   TCC  GGCG
                                ||||||||   |||  ||||
                                AGCCAGGG   AGG  CTGC
                                   C____  C_
GAM1216  FGFR1    5'  TCGGTCCCGTCCGGACG    31568      ACTCA  CA
                                TCGGTCCC   TCC  GGCG
                                ||||||||   |||  ||||
                                AGCCAGGG   AGG  CTGC
                                   C____  C_
GAM1216  FGFR1    5'  TCGGTCCCGTCCGGACG    31568      ACTCA  CA
                                TCGGTCCC   TCC  GGCG
                                ||||||||   |||  ||||
                                AGCCAGGG   AGG  CTGC
                                   C____  C_
GAM1216  FGFR1    5'  TCGGTCCCGTCCGGACG    31568      ACTCA  CA
                                TCGGTCCC   TCC  GGCG
                                ||||||||   |||  ||||
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                                AGCCAGGG    AGG  CTGC
                                    C____   C_
GAM1216 HNRPM    5' GGCCCCACTCGCCCGCGGC   31569         AT   AG
                                GGTCCCACTC  CCC  GCGGC
                                ||||||||||  |||  |||||
                                CCGGGGTGAG  GGG  CGCCG
                                    C_   __
GAM1216 IER3     3' TCGGTCCCGCCTCAAGCACCGG 31570        A_   TC__  A  C
            GTGGC                   TCGGTCCC  CTCA    CC GG GGC
                                ||||||||  ||||   || || |||
                                AGCCAGGG  GAGT    GG CC CCG
                                    CG    TCGT  C  A
GAM1216 IER3     3' TCGGTCCCGCCTCAAGCACCGG 31570        A_   TC__  A  C
            GTGGC                   TCGGTCCC  CTCA    CC GG GGC
                                ||||||||  ||||   || || |||
                                AGCCAGGG  GAGT    GG CC CCG
                                    CG    TCGT  C  A
GAM1216 KIAA0481 3' TCGGTCCCACTTCTCCCAG   31571          CA
                                TCGGTCCCACT  TCCCAG
                                ||||||||||  ||||||
                                AGCCAGGGTGA  AGGGTC
                                     AG
GAM1216 P24B     5' TCGGTCCCGTCTCGAGGGCCGC 31572        A_   ATC__  AG
            GGC                   TCGGTCCC  CTC    CC  GCGGC
                                ||||||||  |||    ||  |||||
                                AGCCAGGG  GAG    GG  CGCCG
                                    CA   CTCCC  __
GAM1216 PCCX2    3' TCGGCTCACTCATCCCCCAAAC 31573      CC        __
            GG                    TCGGT  CACTCATCCC  AGGCGG
                                |||||  ||||||||||  ||||||
                                AGCCG  GTGAGTAGGG  TTTGCC
                                   A_        GG
GAM1216 PPFIA4   3' TCGGTTCCATCATCCCA     31574      C   C
                                TCGGT CCA TCATCCCA
                                ||||| ||| ||||||||
                                AGCCA GGT AGTAGGGT
                                   A  _
GAM1216 YEA      5' TCGGTCCCATTCATCCGAGGGG 31575        C     C   C
            GC                    TCGGTCCCA TCATCC AGG GGC
                                |||||||| |||||| ||| |||
                                AGCCAGGGT AGTAGG TCC CCG
                                     A     C   C
GAM1216 LOC146520 5'  TCGGCCCCATTCATCTCCCTGG 31576         C    _ A_
                                TCGGTCCCA TCATC CC  GG
                                |||||||| ||||| ||  ||
                                AGCCGGGGT AGTAG GG  CC
                                     A    A  GA
GAM1216 LOC158056 5'  CGGTCTCGGACCCAGGCGG   31577      CCAC  AT_
                                CGGTC   TC   CCCAGGCGG
                                |||||   ||   |||||||||
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                              GCCAG   AG   GGGTCCGCC
                                ____ CCT
GAM1217  CALD1    3'  TGAGCTCGTCCTGCGTCTTGAG 31580          ___ AA_   C
            CTTG                  TGAGCTCGTCT   GT   GAGC TG
                                  ||||||||||   ||   |||| ||
                                  ACTCGAGCAGG   CA   CTCG AC
                                       ACG  GAA    A
GAM1217  CALD1    3'  TGAGCTCGTCCTGCGTCTTGAG 31580          ___ AA_   C
            CTTG                  TGAGCTCGTCT   GT   GAGC TG
                                  ||||||||||   ||   |||| ||
                                  ACTCGAGCAGG   CA   CTCG AC
                                       ACG  GAA    A
GAM1217  CALD1    3'  TGAGCTCGTCCTGCGTCTTGAG 31580          ___ AA_   C
            CTTG                  TGAGCTCGTCT   GT   GAGC TG
                                  ||||||||||   ||   |||| ||
                                  ACTCGAGCAGG   CA   CTCG AC
                                       ACG  GAA    A
GAM1217  DHFR     3'  AGCTACTTGGGAGCCTGA    31581      C TC  TAA
                                  AGCT G  TG   GAGCCTGA
                                  |||| |  ||   ||||||||
                                  TCGA T  AC   CTCGGACT
                                    _ GA  C__
GAM1217  OLFM1    3'  TGGCTCTCAAAGAGCCTG    31582    A   G  TGT
                                  TG GCTC TC   AAGAGCCTG
                                  || |||| ||   |||||||||
                                  AC CGAG AG   TTCTCGGAC
                                   _   _  T__
GAM1217  PHEMX    3'  TGACTTGTCAACAGCCTGA   31583     G  C   TGT  G
                                  TGA CT GTC   AA AGCCTGA
                                  ||| || |||   || |||||||
                                  ACT GA CAG   TT TCGGACT
                                    _  A   ___  G
GAM1217  PHEMX    3'  TGACTTGTCAACAGCCTGA   31583     G  C   TGT  G
                                  TGA CT GTC   AA AGCCTGA
                                  ||| || |||   || |||||||
                                  ACT GA CAG   TT TCGGACT
                                    _  A   ___  G
GAM1217  PHEMX    3'  TGACTTGTCAACAGCCTGA   31583     G  C   TGT  G
                                  TGA CT GTC   AA AGCCTGA
                                  ||| || |||   || |||||||
                                  ACT GA CAG   TT TCGGACT
                                    _  A   ___  G
GAM1217  PHEMX    3'  TGACTTGTCAACAGCCTGA   31583     G  C   TGT  G
                                  TGA CT GTC   AA AGCCTGA
                                  ||| || |||   || |||||||
                                  ACT GA CAG   TT TCGGACT
                                    _  A   ___  G
GAM1217  T        3'  TCATCTGTAAGCCACCTG    31584          A_
                                  TCGTCTGTAAG  GCCTG
                                  ||||||||||  |||||
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                                AGTAGACATTC  TGGAC
                                      GG
GAM1217  TACC1    3'  TGAGTCCAGTAAGAGCTTGA   31585     CT  TCT      C
                                TGAG  CG   GTAAGAGC TGA
                                |||| ||   |||||||| |||
                                ACTC  GT   CATTCTCG ACT
                                  AG  ___      A
GAM1217  CLDN6    3'  GAGCCTAAGTGAGAGTCTGA   31586      CGTCT  A    C
                                GAGCT    GT AGAG CTGA
                                |||||    || |||| ||||
                                CTCGG    CA TCTC GACT
                                   ATT__  C    A
GAM1217  DKFZp434D177 5'  TGGCTGGTGAGAGCCTG     31587    A   CGTCT  A
                                TG GCT    GT AGAGCCTG
                                || |||    || ||||||||
                                AC CGA    CA TCTCGGAC
                                 _   C_____  C
GAM1217  DKFZP434O125 3'  TGAGCTATGTCATTTCAGCCTG 31588       C_   TGTAAG
             AA                   TGAGCT  GTC     AGCCTGAA
                                ||||||  |||     ||||||||
                                ACTCGA  CAG     TCGGACTT
                                   TA   TAAAG_
GAM1217  E2IG5    3'  TGAGTTCGCCTGTGGAGAG    31589      C       A_
                                TGAG TCGTCTGT  AGAG
                                |||| ||||||||  ||||
                                ACTC AGCGGACA  TCTC
                                  A       CC
GAM1217  FLJ13949  5'  TGAGTCGTCTGTGGGTACGCTG 31590      C       AAGA  _
                                TGAG TCGTCTGT    GC CTG
                                |||| ||||||||    || |||
                                ACTC AGCAGACA    TG GAC
                                  _       CCCA  C
GAM1217  GG2-1    3'  TGAGTTCATCTGTAGAATGAA  31591      C       A   CC
                                TGAG TCGTCTGTA GAG  TGAA
                                |||| |||||||| |||  ||||
                                ACTC AGTAGACAT CTT  ACTT
                                  A       _  __
GAM1217  KIAA0555  3'  TGGGCTTGCTGTAAGAG     31592    A   C T
                                TG GCT G CTGTAAGAG
                                || ||| | |||||||||
                                AC CGA C GACATTCTC
                                 C   A _
GAM1217  KIAA0774  3'  TGAGCTTTTTGTAACTAACCTG 31593       CGTC    G_
             AA                   TGAGCT   TGTAA  AGCCTGAA
                                ||||||   |||||  ||||||||
                                ACTCGA   ACATT  TTGGACTT
                                   AAA_    GA
GAM1217  KIAA1001  3'  TGGACTCGTCTGCTCTGA    31594    AG       AAGAGC
                                TG  CTCGTCTGT     CTGA
                                ||  |||||||||     ||||
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                                AC  GAGCAGACG     GACT
                                 CT       A_____
GAM1217  MGC5601   5'  TGGCTCGTCTGTGGCTG     31595    A        AAGA  C
                                TG GCTCGTCTGT    GC TG
                                || ||||||||||    || ||
                                AC CGAGCAGACA    CG AC
                                 _        C___  _
GAM1217  MSP       3'  TGGGCTAGTCTGTAAGTGA   31596    A  C       AGCC
                                TG GCT GTCTGTAAG    TGA
                                || ||| |||||||||    |||
                                AC CGA CAGACATTC    ACT
                                 C  T       _____
GAM1217  TINF2     5'  TGGCTCGGGCTGGAGGAGCCTG 31597    A    T_   TAA
              A                  TG GCTCG  CTG   GAGCCTGA
                                || |||||  |||   ||||||||
                                AC CGAGC  GAC   CTCGGACT
                                 _    CC   CTC
GAM1217  LOC125144 3'  TGAGCCCAGGAGCCTG      31598        TCTGTAA
                                TGAGCTCG      GAGCCTG
                                ||||||||      |||||||
                                ACTCGGGT      CTCGGAC
                                     C_______
GAM1217  LOC145693 5'  GAGCTCAGAGAGCCTG      31599        TCTGTA
                                GAGCTCG     AGAGCCTG
                                |||||||     ||||||||
                                CTCGAGT     TCTCGGAC
                                     C______
GAM1217  LOC253891 3'  TGAGGCTCACAGGAGCCTGA   31600     _   TCTG  A
                                TGAG CTCG    TA GAGCCTGA
                                |||| ||||    || ||||||||
                                ACTC GAGT    GT CTCGGACT
                                  C    _____ C
GAM1217  LOC57151  5'  TGATCTTCTCTGAGAGCCTG   31601    G  CG    TA
                                TGA CT  TCTG  AGAGCCTG
                                ||| ||  ||||  ||||||||
                                ACT GA  AGAC  TCTCGGAC
                                  A  AG   __
GAM1217  LOC92270  5'  TGGCTCGTCTGTAAGGTCC    31602    A         AG
                                TG GCTCGTCTGTAAG  CC
                                || ||||||||||||  ||
                                AC CGAGCAGACATTC  GG
                                 _           CA
GAM1218  BCR       5'  TCTGGCCACGGCCCGCGCGCTC 31605       G   C   __
              CT                   TCTGGC CAC GGT  GCGCGCTCCT
                                |||||| ||| |||  ||||||||||
                                AGACCG GTG CCG  CGCGCGAGGA
                                   _  _  GG
GAM1218  BCR       5'  TCTGGCCACGGCCCGCGCGCTC 31605       G   C   __
              CT                   TCTGGC CAC GGT  GCGCGCTCCT
                                |||||| ||| |||  ||||||||||
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                                AGACCG GTG CCG  CGCGCGAGGA
                                   _  _  GG
GAM1218 EGR3    3' TCTGCGCTTTGGTGCGCTCCT 31606     G  ACC    GC
                                TCTG CGC  GGTGC  GCTCCT
                                |||| |||  |||||  ||||||
                                AGAC GCG  CCACG  CGAGGA
                                  _  AAA   __
GAM1218 TSG     3' TCTGCGCACCTGCTTCT    31607     G    GG  GCG
                                TCTG CGCACC  TGC  CT
                                |||| ||||||  |||  ||
                                AGAC GCGTGG  ACG  GA
                                  _    __  AA_
GAM1218 KIAA0461 3' TGTGCACACCCCTGTGCGCTTC 31608   _     GG  C    C
           T                     TG GCGCACC  TG GCGCT CT
                                || |||||||  || ||||| ||
                                AC CGTGTGG  AC CGCGA GA
                                 A      GG  A    A
GAM1218 MGC2477  5' CTGGCGTGGGCTACGCGCTCCT 31609      CACC  _
                                CTGGCG   GG TGCGCGCTCCT
                                ||||||   || ||||||||||
                                GACCGC   CC ATGCGCGAGGA
                                   AC__  G
GAM1218 OSBPL1A  5' CTGGCGCGCTCCACCCTGCGCT 31610       A__  GTGC
           CCT                   CTGGCGC  CCG   GCGCTCCT
                                |||||||  |||   ||||||||
                                GACCGCG  GGT   CGCGAGGA
                                    CGA  GGGA
GAM1219 FBXW1B   3' TGTTTTTTATTAAGCACATTC  31613          A AGAT
                                TGTTTTTTATTAA G   CATTC
                                |||||||||||| |   |||||
                                ACAAAAAATAATT C   GTAAG
                                       _ GT__
GAM1219 FBXW1B   3' TGTTTTTTATTAAGCACATTC  31613          A AGAT
                                TGTTTTTTATTAA G   CATTC
                                |||||||||||| |   |||||
                                ACAAAAAATAATT C   GTAAG
                                       _ GT__
GAM1219 FBXW1B   3' TGTTTTTTATTAAGCACATTC  31613          A AGAT
                                TGTTTTTTATTAA G   CATTC
                                |||||||||||| |   |||||
                                ACAAAAAATAATT C   GTAAG
                                       _ GT__
GAM1219 PLAG1    3' TGTTTTTTTTTAAAGAGAT   31614        A
                                TGTTTTTT TTAAAGAGAT
                                |||||||| ||||||||||
                                ACAAAAAA AATTTCTCTA
                                    A
GAM1219 TACC2    3' TGTCTTTTATTAGAGAATC   31615          AA   _
                                TGTTTTTTATT  AGAGA TC
                                |||||||||| |||||  ||
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                                ACAGAAAATAA  TCTCT AG
                                       __    T
GAM1219  FLJ10853  3'  TGTATTTTACAGATCATT    31616    T    TAAAG
                                TGT TTTTAT    AGATCATT
                                ||| ||||||    ||||||||
                                ACA AAAATG    TCTAGTAA
                                  T    _____
GAM1219  KIAA1086  3'  TGTTTTTTACTAGAGAC    31617         AA
                                TGTTTTTTATT  AGAGAT
                                ||||||||||  ||||||
                                ACAAAAAATGA  TCTCTG
                                       __
GAM1219  USP29    3'  TGTTTTTCATTGAGAT     31618         AAA
                                TGTTTTTTATT   GAGAT
                                ||||||||||   |||||
                                ACAAAAAGTAA   CTCTA
                                       ___
GAM1219  LOC150279 3'  TGTTTTTTAATAGCCAGAGAT  31619        TTAA__
                                TGTTTTTTA     AGAGAT
                                |||||||||     ||||||
                                ACAAAAAAT     TCTCTA
                                     TATCGG
GAM1219  LOC150378 3'  TGTTTATTATTAAAGTGAT   31620      T       A
                                TGTTT TTATTAAAG GAT
                                ||||| ||||||||| |||
                                ACAAA AATAATTTC CTA
                                   T       A
GAM1220  DKFZp434G179 3'  TTCTTGAGAGTATGTTGACAGT 31623    A       A__  TC
           CTG                    TTC TGAGAGTATG   GC  GTCTG
                                ||| ||||||||||   ||  |||||
                                AAG ACTCTCATAC   TG  CAGAC
                                  A         AAC  T_
GAM1220  KIAA0711  3'  TTCATGAGGAGTGTGGACAGCT 31624        _   A  ___
                                TTCATGAG AGT TG   AGCT
                                |||||||| ||| ||   ||||
                                AAGTACTC TCA AC   TCGA
                                     C   C  CTG
GAM1220  KRTAP17-1 3'  TTCATCAGAGTATGGCTC    31625      G       A
                                TTCAT AGAGTATG GCTC
                                ||||| |||||||| ||||
                                AAGTA TCTCATAC CGAG
                                   G       _
GAM1220  SE57-1    3'  TTCATGGAAGTATGAGCT    31626       AG
                                TTCATG  AGTATGAGCT
                                ||||||  ||||||||||
                                AAGTAC  TCATACTCGA
                                   CT
GAM1220  LOC148085 5'  TTCATGAGAGTAGGCT      31627          TGA
                                TTCATGAGAGTA   GCT
                                ||||||||||||   |||
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                                AAGTACTCTCAT   CGA
                                      C__
GAM1220  LOC148343 5'  TTCAGGAGGGACTCGTCT    31628     T   AGTATGA
                                TTCA GAG      GCTCGTCT
                                |||| |||      ||||||||
                                AAGT CTC      TGAGCAGA
                                  C   CC_____
GAM1221  CAPZA1    5'  TTCCAACCCCGGGGGG      31631      ACGGAC      A
                                TTTCA     GCCCCGGG GG
                                |||||     |||||||| ||
                                AAGGT     TGGGGCCC CC
                                  _______       C
GAM1221  DDEF1     3'  TTTCAACGGTTGCTGGAG    31632        AC  CCCG
                                TTTCAACGG  GC   GGAG
                                |||||||||  ||   ||||
                                AAAGTTGCC  CG   CCTC
                                     AA  A___
GAM1221  FECH      3'  CAAGGTCCCGGGAGGA      31633     C  ACGC
                                CAA GG   CCCGGGAGGA
                                ||| ||   ||||||||||
                                GTT CC   GGGCCCTCCT
                                  _ A___
GAM1221  PK428     5'  TTTCAACGGATTCCGGG      31634         CGCC
                                TTTCAACGGA   CCGGG
                                |||||||||    |||||
                                AAAGTTGCCT   GGCCC
                                     AA__
GAM1221  CYP4F2    3'  TTTCACCATCCCGGGAGGAA   31635      ACGGACGC
                                TTTCA       CCCGGGAGGAA
                                |||||       ||||||||||
                                AAAGT       GGGCCCTCCTT
                                   GGTA____
GAM1221  FLJ32384  5'  TTTCAGCAGACGCCTGGAA    31636      A       CC
                                TTTCA CGGACGCC  GGGA
                                ||||| ||||||||  ||||
                                AAAGT GTCTGCGG  CCTT
                                   C       A_
GAM1221  HCNGP     3'  TTTCAACCCCGGGGGGA     31637      ACGGAC      A
                                TTTCA     GCCCCGGG GGA
                                |||||     |||||||| |||
                                AAAGT     TGGGGCCC CCT
                                  _______       C
GAM1221  KCNS1     3'  TCTCACATCAGCCCTGGGAGGA 31638      A  GAC   C
              A                  TTTCA CG   GCCC GGGAGGAA
                                 ||||| ||   |||| ||||||||
                                 AGAGT GT   CGGG CCCTCCTT
                                   _ AGT    A
GAM1221  KIAA0674  5'  TTTCACCGGGTTGCGGGGAGGA 31639      A   AC_  CCC
              A                  TTTCA CGG   GC   GGGAGGAA
                                 ||||| |||   ||   ||||||||
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                                AAAGT GCC   CG   CCCTCCTT
                                   G   CAA  C__
GAM1221  KIAA0774  5'  TTCAACTCTCCTGGGAGGAA  31640      GGACG  CC
                                TTCAAC    CC  GGGAGGAA
                                ||||||    ||  ||||||||
                                AAGTTG    GG  CCCTCCTT
                                   AGA__  A_
GAM1221  KIAA1402  5'  TCTCCCGGCGTCCCGGGAGG  31641     AA   A  C
                                TTTC  CGG CG CCCGGGAGG
                                ||||  ||| || |||||||||
                                AGAG  GCC GC GGGCCCTCC
                                  G_   _  A
GAM1221  LOC129138 3'  TTTCAATGACTGGGAGGA    31642      CG   GCCCC
                                TTTCAA  GAC    GGGAGGA
                                ||||||  |||    |||||||
                                AAAGTT  CTG    CCCTCCT
                                   A_   A____
GAM1221  LOC57795  5'  CTTCAACGACTGGGAGGA    31643        ACGCCCC
                                TTTCAACGG      GGGAGGA
                                |||||||||      |||||||
                                GAAGTTGCT      CCCTCCT
                                     GA_____
GAM1222  C18orf1   3'  CATTCTTCCGTCATTATT    31646       A TA
                                CATTCTT T  TCATTATT
                                ||||||| |  ||||||||
                                GTAAGAA G  AGTAATAA
                                    _ GC
GAM1222  KIAA0280  3'  ATTATTATTATCATTATT    31647     C
                                ATT TTATTATCATTATT
                                ||| ||||||||||||||
                                TAA AATAATAGTAATAA
                                  T
GAM1222  KLK14     3'  CCATTTTTATTGTCATTATT   31648      C     A
                                TCATT TTATT TCATTATT
                                ||||| ||||| ||||||||
                                GGTAA AATAA AGTAATAA
                                   A    C
GAM1222  LOC123688 3'  TGTTCATTCTTACAGTTTATTC 31649    A        TATCA
                                TG TCATTCTTAT     TTATTC
                                || ||||||||||     ||||||
                                AC AGTAAGAATG     AATAAG
                                 A         TCA__
GAM1223  LHX2      5'  CTAATGATACATGCTACA    31652          CA
                                TTAATGATACA  CTACA
                                ||||||||||  |||||
                                GATTACTATGT  GATGT
                                       AC
GAM1223  MS4A1     3'  TTAATGATACAATACTGC    31653          CACTAC
                                TTAATGATACA     ACTGT
                                ||||||||||      |||||
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                                AATTACTATGT     TGACG
                                      TA____
GAM1223  CST9L    3'  TTAATGATCTACACTACA    31654        AC
                                TTAATGAT  ACACTACA
                                ||||||||  ||||||||
                                AATTACTA  TGTGATGT
                                    GA
GAM1223  EHM2     3'  TTAATGATATCACTGCACCG  31655        CA   A
                                TTAATGATA  CACT CACTG
                                |||||||||  |||| |||||
                                AATTACTAT  GTGA GTGGC
                                     A_   C
GAM1223  VDAC3    3'  TAACATGACGCTACACTGTCG 31656      C_  A
                                TGATA  AC CTACACTGTCG
                                |||||  || ||||||||||
                                ATTGT  TG GATGTGACAGC
                                   AC  C
GAM1223  ZNF333   3'  TAATAGTGCACACTGCCA    31657      CACAC
                                TGATA    TACACTGTCG
                                |||||    ||||||||||
                                ATTAT    GTGTGACGGT
                                   CAC__
GAM1224  AGL      3'  TTTTATTTTCTTAACACACA  31660      GACCC
                                TTTTAT    TAACACACA
                                ||||||    |||||||||
                                AAAATA    ATTGTGTGT
                                   AAAGA
GAM1224  AGL      3'  TTTTATTTTCTTAACACACA  31660      GACCC
                                TTTTAT    TAACACACA
                                ||||||    |||||||||
                                AAAATA    ATTGTGTGT
                                   AAAGA
GAM1224  AGL      3'  TTTTATTTTCTTAACACACA  31660      GACCC
                                TTTTAT    TAACACACA
                                ||||||    |||||||||
                                AAAATA    ATTGTGTGT
                                   AAAGA
GAM1224  AGL      3'  TTTTATTTTCTTAACACACA  31660      GACCC
                                TTTTAT    TAACACACA
                                ||||||    |||||||||
                                AAAATA    ATTGTGTGT
                                   AAAGA
GAM1224  AGL      3'  TTTTATTTTCTTAACACACA  31660      GACCC
                                TTTTAT    TAACACACA
                                ||||||    |||||||||
                                AAAATA    ATTGTGTGT
                                   AAAGA
GAM1224  AGL      3'  TTTTATTTTCTTAACACACA  31660      GACCC
                                TTTTAT    TAACACACA
                                ||||||    |||||||||
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                                AAAATA    ATTGTGTGT
                                   AAAGA
GAM1224 APLP2    3' ACTTTTATGGAGACACACA   31661        ACCCTA
                                ACTTTTATG     ACACACA
                                |||||||||     |||||||
                                TGAAAATAC     TGTGTGT
                                     CTC___
GAM1224 CLECSF2  3' CTTTTATGTGTAGCCTGACAC 31662        AC___  A
                                CTTTTATG    CCT ACAC
                                ||||||||    ||| ||||
                                GAAAATAC    GGA TGTG
                                     ACATC  C
GAM1224 CUL3     3' TAACCTTTATGACCTAA     31663           C
                                TAACTTTTATGACC TAA
                                |||||||||||||| |||
                                ATTGGAAATACTGG ATT
                                                _
GAM1224 JRK      3' CTTTTATAATCTTCACACA   31664        CC  AA
                                CTTTTATGA  CT  CACACA
                                |||||||||  ||  ||||||
                                GAAAATATT  GA  GTGTGT
                                     A_  A_
GAM1224 MFI2     3' TTTTATGACCTTAAGACA    31665        C   C
                                TTTTATGACC TAA ACA
                                |||||||||| ||| |||
                                AAAATACTGG ATT TGT
                                     A   C
GAM1224 NT5C2    3' TTTTAATACCCTAACATACA  31666      TG       C
                                TTTTA  ACCCTAACA ACA
                                |||||  ||||||||| |||
                                AAAAT  TGGGATTGT TGT
                                   TA        A
GAM1224 PCDHB13  3' TTTTACACATTAACACACA   31667      G  CC
                                TTTTAT AC  TAACACACA
                                ||||||  ||  |||||||||
                                AAAATG TG  ATTGTGTGT
                                   _  TA
GAM1224 PLOD2    3' TTTTATAATTTTCTAACACA  31668       CC__
                                TTTTATGA   CTAACACA
                                ||||||||   ||||||||
                                AAAATATT   GATTGTGT
                                     AAAA
GAM1224 RFXAP    3' TAACTTTATGACTTCCACA   31669       T    CCTAA
                                TAACTTT ATGAC    CACA
                                ||||||| |||||    ||||
                                ATTGAAA TACTG    GTGT
                                   _    AAG__
GAM1224 SCN1A    3' TAACATTTATGACTCCAAACA 31670     T      _  T
                                TAAC TTTATGAC CC AACA
                                |||| |||||||| || ||||
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                                ATTG AAATACTG GG TTGT
                                  T       A  T
GAM1224  FER1L3    3'  ACTTTTATGACATCCATACA   31671          __  TA
                                ACTTTTATGAC  CC  ACA
                                ||||||||||  ||  |||
                                TGAAAATACTG  GG  TGT
                                      TA  TA
GAM1224  HERPUD1   3'  ACTTCTATGTACAAACACACA  31672         _  CCT
                                ACTTTTATG AC   AACACACA
                                |||||||| ||   ||||||||
                                TGAAGATAC TG   TTGTGTGT
                                     A  T__
GAM1224  KIAA0265  3'  ACTTTTATGAAAATAAAACACA 31673          CCCT__
              CA                  ACTTTTATGA     AACACACA
                                ||||||||||     ||||||||
                                TGAAAATACT     TTGTGTGT
                                      TTTATT
GAM1224  KIAA0268  3'  ACTTTTATGGCCATGACACA   31674         A  CTA
                                ACTTTTATG CC   ACACA
                                |||||||| ||   |||||
                                TGAAAATAC GG   TGTGT
                                     C  TAC
GAM1224  KIAA1155  3'  CAACTTTCCTCTCTAACAC    31675         ATGACC
                                TAACTTTT     CTAACAC
                                ||||||||     |||||||
                                GTTGAAAG     GATTGTG
                                     GAGA__
GAM1224  KIAA1671  3'  CTTTTGTGTTTTAACACAC    31676       A  ACCC
                                CTTTT TG    TAACACAC
                                ||||| ||    ||||||||
                                GAAAA AC    ATTGTGTG
                                   C  AAA_
GAM1224  KIAA1918  3'  ACTTAGCAACTTTAACACACA  31677      TTA    CC
                                ACTT   TGAC  TAACACACA
                                ||||   ||||  ||||||||||
                                TGAA   GTTG  ATTGTGTGT
                                   TC_    AA
GAM1224  MAP2K1IP1 3'  TAAATTTTATGAAGAACACACA 31678      C       CCCT
                                TAA TTTTATGA    AACACACA
                                ||| ||||||||    ||||||||
                                ATT AAAATACT    TTGTGTGT
                                  T       TC__
GAM1224  MGC26651  3'  ACTTCTACTACTTTAACATACA 31679         G  CC    C
                                ACTTTTAT AC  TAACA ACA
                                |||||||| ||  ||||| |||
                                TGAAGATG TG  ATTGT TGT
                                     A  AA    A
GAM1224  PRO0943   5'  TTTTATGAACCATTTTAACAC  31680         C  ____
                                TTTTATGA CC    TAACAC
                                |||||||| ||    ||||||
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                                AAAATACT GG   ATTGTG
                                    T  TAAA
GAM1224  VEZATIN   3'  TTTTATGACACCTCACA     31681         _   AA
                                TTTTATGAC CCT  CACA
                                ||||||||| |||  ||||
                                AAAATACTG GGA  GTGT
                                    T  __
GAM1224  LOC114932 3'  CTTTTATTAACACACA      31682        GACCC
                                CTTTTAT    TAACACACA
                                |||||||    |||||||||
                                GAAAATA    ATTGTGTGT
                                    _____
GAM1224  LOC132671 3'  AACTTTTATATATAACACA   31683          ACCC
                                AACTTTTATG   TAACACA
                                ||||||||||   |||||||
                                TTGAAAATAT   ATTGTGT
                                    AT__
GAM1224  LOC146754 3'  ACTTTTATGGCTAACACA    31684          ACC
                                ACTTTTATG   CTAACACA
                                |||||||||   ||||||||
                                TGAAAATAC   GATTGTGT
                                    C__
GAM1224  LOC149761 3'  CAACTTTTTTCTCTCCTGACAC 31685         ATGAC_   A
           ACA                    TAACTTTT     CCT ACACACA
                                |||||||      ||| |||||||
                                GTTGAAAA     GGA TGTGTGT
                                    AAGAGA   C
GAM1224  LOC157273 3'  ACCTCCTAATCCTAACACA   31686        A   C
                                ACTTTT TGA CCTAACACA
                                |||||| ||| |||||||||
                                TGGAGG ATT GGATTGTGT
                                   _   A
GAM1224  LOC157867 5'  TAACTTTTCATGGCCCATTTAC 31687         _    A   TAAC
           A                     TAACTTT TATG CCC    ACA
                                ||||||| |||| |||    |||
                                ATTGAAA GTAC GGG    TGT
                                    A   C   TAAA
GAM1224  LOC200232 3'  CAACTTTTTTCTCTCCTGACAC 31685         ATGAC_   A
           ACA                    TAACTTTT     CCT ACACACA
                                |||||||      ||| |||||||
                                GTTGAAAA     GGA TGTGTGT
                                    AAGAGA   C
GAM1224  LOC51014  3'  CTTCCTCCCTAACACA      31688       ATGA
                                CTTTT    CCCTAACACA
                                |||||    ||||||||||
                                GAAGG    GGGATTGTGT
                                   A___
GAM1224  LOC81537  3'  ACTTTTATGCCTGTCACCCTGA 31689      _______    A   C   III
           CATACAT                  TATG     ACCCT ACA ACA   T
                                ||||     ||||| ||| |||   |
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                                ATAC     TGGGA TGT TGT   A
                                  GGACAG    C  A  III
GAM1225 GTF2I    3' GCTACCATGTCATATAAT    31692       CAC
                                GTTACTA   CATATAAT
                                |||||||   ||||||||
                                CGATGGT   GTATATTA
                                    ACA
GAM1225 GTF2I    3' GCTACCATGTCATATAAT    31692       CAC
                                GTTACTA   CATATAAT
                                |||||||   ||||||||
                                CGATGGT   GTATATTA
                                    ACA
GAM1225 HOXD4    3' CAGTAGCTCCTGCCATATAAT 31693     TA  ACA_
                                CAGT  CT    CCATATAAT
                                ||||  ||    |||||||||
                                GTCA  GA    GGTATATTA
                                  TC  GGAC
GAM1225 USP9Y    3' TCCACATCAACCATATAA    31694      G   CTAC
                                TCCACA TTA    ACCATATAA
                                ||||||| |||    |||||||||
                                AGGTGT AGT    TGGTATATT
                                  _  ____
GAM1225 FLJ14743 3' TCCGCAATTACTTCTGGATATA 31695     A       ACACC
          AT                      TCC CAGTTACT    ATATAAT
                                ||| ||||||||    |||||||
                                AGG GTTAATGA    TATATTA
                                  C       AGACC
GAM1225 HSPC067  3' AGTTACTACTACAAATAAT   31696        AC  T
                                AGTTACTAC  CA ATAAT
                                |||||||||  || |||||
                                TCAATGATG  GT TATTA
                                     AT  T
GAM1225 PABPC5   3' CACAGTTCTCATATAA      31697       A  ACAC
                                CACAGTT CT    CATATAA
                                ||||||| ||    |||||||
                                GTGTCAA GA    GTATATT
                                  _  ____
GAM1225 PRRG1    3' TCCACAGTTATTGGATCACAT  31698         CTACAC
                                TCCACAGTTA     CATAT
                                ||||||||||     |||||
                                AGGTGTCAAT     GTGTA
                                     AACCTA
GAM1225 RPIA     3' TCCACAGTTTTATACACC    31699        AC_
                                TCCACAGTT   TACACC
                                |||||||||   ||||||
                                AGGTGTCAA   ATGTGG
                                     AAT
GAM1225 LOC128710 5' TCCACAGTAACTACAGACC   31700        T    __
                                TCCACAGT ACTAC  ACC
                                |||||||| |||||  |||
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                                AGGTGTCA TGATG  TGG
                                     T    TC
GAM1225  LOC203428 3'  AGTTACTACTACAAATAAT   31696        AC  T
                                AGTTACTAC  CA ATAAT
                                |||||||||  || |||||
                                TCAATGATG  GT TATTA
                                     AT  T
GAM1225  LOC92285  5'  CCACAGTTATTGCATTCATAT  31701        CTA  C_
                                CCACAGTTA   CA  CATAT
                                |||||||||   ||  |||||
                                GGTGTCAAT   GT  GTATA
                                     AAC  AA
GAM1226  CHRNA10   5'  TGCAAGAGCGGGGGCAGG    31704      A      __
                                TGCAA AGCGGGGG  GG
                                ||||| ||||||||  ||
                                ACGTT TCGCCCCC  CC
                                   C       GT
GAM1226  DGCR2     3'  GCAGAAGGCGGGCTGTGGT   31705     AAA C   G   A   C
                                GCA   G GGG GGG CTG GGT
                                |||   | ||| ||| ||| |||
                                CGT   C TCC CCC GAC CCA
                                  ___ T   G   _   A
GAM1226  GRLF1     3'  AGCGGGAGTGGGGGCAGC    31706        _  ACT
                                AGCGGGGG GG   GCGGT
                                |||||||| ||   |||||
                                TCGCCCTC CC   CGTCG
                                     A  CC_
GAM1226  ITM2B     5'  GCAGAGGCGGCTACTGCGGT   31707        _  __
                                GCGGGGG GG  ACTGCGGT
                                ||||||| ||  ||||||||
                                CGTCTCC CC  TGACGCCA
                                     G  GA
GAM1226  PACE      3'  TGCAAGAGAGGGGAGGGTGGT  31708      A  C      ACTGC
                                TGCAA AG GGGGGGG    GGT
                                ||||| || |||||||    |||
                                ACGTT TC CCCCTCC    CCA
                                   C  T      CA___
GAM1226  PRDM2     5'  TGTAAGAGTGGAGGGAAGG   31709    C  A  C      CTGC
                                TG AA AG GGGGGGGA   GG
                                || || || ||||||||   ||
                                AC TT TC CCTCCCTT   CC
                                 A  C  A      _____
GAM1226  PRDM2     5'  TGTAAGAGTGGAGGGAAGG   31709    C  A  C      CTGC
                                TG AA AG GGGGGGGA   GG
                                || || || ||||||||   ||
                                AC TT TC CCTCCCTT   CC
                                 A  C  A      _____
GAM1226  SCN8A     5'  TGCGGCGGGCGGGACTGCGGT  31710    AAAA    G
                                TGC   GCGGG GGGACTGCGGT
                                |||   ||||| ||||||||||
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                                ACG    CGCCC CCCTGACGCCA
                                  C___    G
GAM1226 KIAA0495  5'  AGCGGGGAGCTGCGGT     31711         GA
                                AGCGGGGGGG  CTGCGGT
                                |||||||||  |||||||
                                TCGCCCCTC  GACGCCA
                                     __
GAM1226 KLK14     3'  GCAAGGGTGGGGGCTTGG    31712     AA  C  _    A  GC
                                GCA  AG GG GGGGG CT  GG
                                |||  || || ||||| ||  ||
                                CGT  TC CC CCCCC GA  CC
                                  __  _ A    _ A_
GAM1226 MGC10960  3'  CAAAAGCACAAAGGCTGTGGT  31713        G    A   C
                                CAAAAGCG GGGGG CTG GGT
                                |||||||| ||||| ||| |||
                                GTTTTCGT TTTCC GAC CCA
                                     G    _  A
GAM1226 OR7C1     3'  TACAAAAGTGAACAAATTGTGG 31714        CG   G   C  C
              T                  TGCAAAAG  GGG GGA TG GGT
                                |||||||||  ||| ||| || |||
                                ATGTTTTC  CTT TTT AC CCA
                                     A_   G   A  A
GAM1226 PEPP3     3'  TGCAGGGGCAGGGGGCCAGGGT 31715      AAA       GA   C
                                TGCA   GCGGGGGG  CTG GGT
                                ||||   ||||||||  ||| |||
                                ACGT   CGTCCCCC  GGT CCA
                                  CCC        __   C
GAM1226 LOC143286 5'  AGCAGAAGGAAATGGAT     31716          C  C
                                AGCGGGGGGGA TG GGT
                                ||||||||||| || |||
                                TCGTCTTCCTT AC CTA
                                       T  _
GAM1226 LOC146940 5'  GCGATCTTGGGGACTGTGGT   31717     G___       C
                                GCGG    GGGGACTG GGT
                                ||||    |||||||| |||
                                CGCT    CCCCTGAC CCA
                                  AGAA       A
GAM1226 LOC147645 5'  GCGGAAGCGGAGGCTGCGGT   31718    AA       GGA
                                GC  AAGCGGGGG   CTGCGGT
                                ||  |||||||||   |||||||
                                CG  TTCGCCTCC   GACGCCA
                                 CC        ___
GAM1226 LOC150685 5'  AAGCGGGGGCTGCTGCTGTGGT 31719         GGA   ___
                                AAGCGGGGG   CTGC   GGT
                                |||||||||   ||||   |||
                                TTCGCCCCC   GACG   CCA
                                     GAC    ACA
GAM1227 CHL1      3'  CGTTGCTTACATATGTTG    31722          TT
                                CGTTGCTTATA  TATGTTG
                                ||||||||||  |||||||
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                                GCAACGAATGT  ATACAAC
                                           __
GAM1227  FLJ10283  3'  GTTGCTTATATGGATGTTG   31723          TT
                                GTTGCTTATAT  ATGTTG
                                ||||||||||  ||||||
                                CAACGAATATA  TACAAC
                                      CC
GAM1227  KIAA1116  3'  ACTTTAATATTTATGTTGTTG  31724     __
                                GCTT  ATATTTATGTTGTTG
                                ||||  ||||||||||||||
                                TGAA  TATAAATACAACAAC
                                  AT
GAM1227  KIAA1383  3'  ATTGCTTATATTTTTATTG   31725          A
                                GTTGCTTATATTT TGTTG
                                ||||||||||||| |||||
                                TAACGAATATAAA ATAAC
                                        A
GAM1227  LOC137362 3'  TGATGTAATTTATGTTGTTG  31726   CTTAT
                                TG    ATTTATGTTGTTG
                                ||    ||||||||||||
                                AC    TAAATACAACAAC
                                 TACAT
GAM1227  LOC154075 3'  GTTGATTATATTCACATTGTTG 31727     C
                                GTTG TTATATTTATGTTGTTG
                                |||| ||||||||||||||||
                                CAAC AATATAAGTGTAACAAC
                                  T
GAM1227  LOC203025 3'  TGATGTAATTTATGTTGTTG  31726   CTTAT
                                TG    ATTTATGTTGTTG
                                ||    ||||||||||||
                                AC    TAAATACAACAAC
                                 TACAT
GAM1228  BDKRB2   3'  CAGCACTGTGATCCTCTG   31730   A   CTA
                                CA CACTG   ATCCTCTG
                                || |||||   ||||||||
                                GT GTGAC   TAGGAGAC
                                 C    AC_
GAM1228  CKN1     3'  CCTCCACTTGCTGATCCTCTG  31731   ACAA   _  A
                                CC   CACT GCT ATCCTCTG
                                ||   |||| ||| ||||||||
                                GG   GTGA CGA TAGGAGAC
                                 AG__   A  C
GAM1228  FBXL3A   3'  AACACTGCCTCCCTTCTG   31732        AA   _
                                AACACTGCT  TCCT CTG
                                |||||||||  |||| |||
                                TTGTGACGG  GGGA GAC
                                      A_   A
GAM1228  HSD17B8  3'  AACCATACACTGCCACCCCT  31733     CA       AT
                                AACCA  ACACTGCTA  CCTCT
                                |||||  |||||||||  |||||
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                                TTGGT  TGTGACGGT  GGGGA
                                  A_       __
GAM1228  PDE4D    3'  CATCACAGTACTAACCCTCTG  31734    CA   C
                                CA  ACA TGCTAATCCTCTG
                                ||  ||| |||||||||||||
                                GT  TGT ATGATTGGGAGAC
                                 AG   C
GAM1228  PRKAB1   3'  CCAGGGCTGCAGATCCTCTG   31735    CAACA   TA
                                CCA    CTGC  ATCCTCTG
                                |||    ||||  ||||||||
                                GGT    GACG  TAGGAGAC
                                  CCC__   TC
GAM1228  TAF12    3'  AACCACAAATAAAATCTTCTCT 31736       CACTGCT   __
           G                     AACCACAA     AATC  CTCTG
                                ||||||||     ||||  |||||
                                TTGGTGTT     TTAG  GAGAC
                                     TATT___   AA
GAM1228  TRPC5    3'  AACCACAAGCTGACAATTCT   31737       CA   C   CC
                                AACCACAA  CTG TAAT  TCT
                                ||||||||  ||| ||||  |||
                                TTGGTGTT  GAC GTTA  AGA
                                     C_   T   __
GAM1228  WBSCR5   3'  CACAACACTGTTTAATCAGCTC 31738        C_    __
           TG                    CACAACACTG  TAATC  CTCTG
                                ||||||||||  |||||  |||||
                                GTGTTGTGAC  ATTAG  GAGAC
                                     AA    TC
GAM1228  WBSCR5   3'  CACAACACTGTTTAATCAGCTC 31738        C_    __
           TG                    CACAACACTG  TAATC  CTCTG
                                ||||||||||  |||||  |||||
                                GTGTTGTGAC  ATTAG  GAGAC
                                     AA    TC
GAM1228  WBSCR5   3'  CACAACACTGTTTAATCAGCTC 31738        C_    __
           TG                    CACAACACTG  TAATC  CTCTG
                                ||||||||||  |||||  |||||
                                GTGTTGTGAC  ATTAG  GAGAC
                                     AA    TC
GAM1228  YES1     3'  AACCACTAATGCTGCTATTCAA 31739       _ CA     A  C__
           ATCTG                   AACCAC AA  CTGCTA TC   TCTG
                                ||||||  ||  ||||||  ||   ||||
                                TTGGTG TT  GACGAT AG   AGAC
                                   A  AC     A  TTT
GAM1228  C19orf7  3'  AACCACAACACTGCCACACTG  31740             ATCCT
                                AACCACAACACTGCTA    CTG
                                ||||||||||||||||    |||
                                TTGGTGTTGTGACGGT    GAC
                                         GT___
GAM1228  DDX17    5'  ACGGTGCACATAATCCTCTG   31741    AC   ___
                                AC  TGC   TAATCCTCTG
                                ||  |||   ||||||||||
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                                TG  ACG   ATTAGGAGAC
                                 CC   TGT
GAM1228  LAMB4    3'  CACATGACTGACATCCTCTG  31742     AC    CTA
                                CACA  ACTG   ATCCTCTG
                                ||||  ||||   ||||||||
                                GTGT  TGAC   TAGGAGAC
                                  AC    TG_
GAM1228  MCAM     3'  CAGCAACACTGCAGCTGCTTCT 31743    _       TAATCC_
           G                     CA CAACACTGC      TCTG
                                || |||||||||      ||||
                                GT GTTGTGACG      AGAC
                                 C        TCGACGA
GAM1228  MGC10870 5'  ACCCAGCGCCCATCCTCT    31744     A  ACAC    A
                                ACC CA    TGCT ATCCTCT
                                ||| ||    |||| |||||||
                                TGG GT    GCGG TAGGAGA
                                  _ C___    G
GAM1228  MGC13198 3'  ACTGCAACACTGATTTCTCTG  31745    CA      CTAATC
                                AC  CAACACTG     CTCTG
                                ||  ||||||||     |||||
                                TG  GTTGTGAC     GAGAC
                                 AC       TAAA__
GAM1228  RAB24    3'  CCACACTGACGTAATCCTCTG  31746     AAC   _ _
                                CCAC   ACTG C TAATCCTCTG
                                ||||   |||| | ||||||||||
                                GGTG   TGAC G ATTAGGAGAC
                                   ___    T C
GAM1228  RASGRF2  3'  CACTGTCTGGAATCCTCTG   31747      _ __
                                CACTG CT  AATCCTCTG
                                ||||| ||  |||||||||
                                GTGAC GA  TTAGGAGAC
                                   A  CC
GAM1228  TEX27    3'  CAGCTGCTGAAATCCTCTG   31748    _    __
                                CA CTGCT  AATCCTCTG
                                || |||||  |||||||||
                                GT GACGA  TTAGGAGAC
                                 C     CT
GAM1228  TXN2     3'  CAGCAGCACCACCATCCTCTG  31749    _ A   TG   A
                                CA CA CAC  CTA TCCTCTG
                                || || |||  ||| |||||||
                                GT GT GTG  GGT AGGAGAC
                                 C  C   GT  _
GAM1228  LOC149464 3'  ACCACAACACCCAGCTAAT   31750          __
                                ACCACAACACT  GCTAAT
                                ||||||||||  ||||||
                                TGGTGTTGTGG  CGATTA
                                       GT
GAM1228  LOC150933 5'  ACCTGGCCAAACAATCCTCTG  31751     ACAA  CT  T
                                ACC    CA  GC AATCCTCTG
                                |||    ||  || |||||||||
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                                TGG    GT  TG TTAGGAGAC
                                  ACCG  T_  _
GAM1228  LOC151304 3'  CCCAATCCAATCCTCT      31752     A   CACTG
                                CC CAA     CTAATCCTCT
                                || |||     ||||||||||
                                GG GTT     GGTTAGGAGA
                                 _   A_____
GAM1228  LOC157798 5'  ACACTGCTGGATCAAGTCTG   31753         A_   C__
                                ACACTGCT  ATC   TCTG
                                ||||||||  |||   ||||
                                TGTGACGA  TAG   AGAC
                                     CC   TTC
GAM1228  LOC158714 5'  AACCATAGAGGACACATCCTCT 31754      CA____    TGCTA
              G                  ACCA     ACAC     ATCCTCTG
                                ||||     ||||     ||||||||
                                TGGT     TGTG     TAGGAGAC
                                  ATCTCC   ______
GAM1228  LOC162239 3'  AACTTCAACACTGTCTTCT    31755     CA       CTAA  C
                                AAC  CAACACTG    TC TCT
                                |||  ||||||||    || |||
                                TTG  GTTGTGAC    AG AGA
                                  AA       _____  A
GAM1228  LOC197201 3'  AACCACAACTTTGCTTCTCTG  31756          AC    AATC
                                AACCACAAC  TGCT    CTCTG
                                |||||||||  ||||    |||||
                                TTGGTGTTG  ACGA    GAGAC
                                     AA    A___
GAM1228  LOC221540 3'  CCACCAACAGACTGCTAATTCT 31757      _   __        C
              CTG                   CCAC AAC  ACTGCTAAT CTCTG
                                |||| |||  ||||||||| |||||
                                GGTG TTG  TGACGATTA GAGAC
                                  G   TC        A
GAM1228  LOC255645 3'  ACCAATACCTACCTTCTCTG   31758      CA  A    AATC
                                ACCA  AC CTGCT    CTCTG
                                ||||  || |||||    |||||
                                TGGT  TG GATGG    GAGAC
                                  TA  _     AA__
GAM1228  LOC257545 3'  CCACCAACAGACTGCTAATTCT 31757      _   __        C
              CTG                   CCAC AAC  ACTGCTAAT CTCTG
                                |||| |||  ||||||||| |||||
                                GGTG TTG  TGACGATTA GAGAC
                                  G   TC        A
GAM1228  LOC257598 3'  CCACCAACAGACTGCTAATTCT 31757      _   __        C
              CTG                   CCAC AAC  ACTGCTAAT CTCTG
                                |||| |||  ||||||||| |||||
                                GGTG TTG  TGACGATTA GAGAC
                                  G   TC        A
GAM1229  CELSR3    3'  TACTGTAAACAAAGTGTA    31761     CC        A
                                TAC  GTAAACGGGG TGTA
                                |||  |||||||||| ||||
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                                ATG  CATTTGTTTC ACAT
                                  A_        _
GAM1229  KIF5B    3'  CACCTGTGGGTATGTATAA   31762      C  AAAC   G
                                TACC GT    GGG ATGTATAA
                                |||| ||    ||| ||||||||
                                GTGG CA    CCC TACATATT
                                  A _____   A
GAM1229  KIAA0565 3'  TACCCCTAAAATGTATAA    31763      G   ACGGG
                                TACCC TAA     GATGTATAA
                                ||||| |||     |||||||||
                                ATGGG ATT     TTACATATT
                                   G  ______
GAM1229  LOC255520 3'  GTAGAGAGGTGTATAAA     31764     AAC    A
                                GTA   GGGG TGTATAAA
                                |||   |||| ||||||||
                                CAT   CTCC ACATATTT
                                  CT_   _
GAM1230  PCDHB16   5'  TGCATCCGCCATCACAATTT   31767      A_   GC
                                TGCAT  GTTG  CACAATTT
                                |||||  ||||  ||||||||
                                ACGTA  CGGT  GTGTTAAA
                                   GG    A_
GAM1230  RBMX      3'  TTACATAGGCATGTGATTTCAG 31768       GTT   CACA_
                                TTGCATA   GGC    ATTTCAG
                                |||||||   |||    |||||||
                                AATGTAT   CCG    TAAAGTC
                                    ___   TACAC
GAM1230  SNAI1     3'  TTGCATAGTTAGTCACACCTC  31769          C    A
                                TTGCATAGTTGG CACA TTTC
                                |||||||||||| |||| ||||
                                AACGTATCAATC GTGT GGAG
                                       A    _
GAM1230  CLLD8     3'  TTGCATGGCTTTAATTTCA    31770      TAGT    CAC
                                TTGCA    TGGC   AATTTCA
                                |||||    ||||   |||||||
                                AACGT    ACCG   TTAAAGT
                                   _____    AAA
GAM1230  KIAA1729  3'  TTGCATGTACAATTTCA     31771       A  TGGCC
                                TTGCAT GT     ACAATTTCA
                                ||||||  ||    |||||||||
                                AACGTA CA     TGTTAAAGT
                                   _  ______
GAM1230  LOC165693 5'  TTGAATAGTTATAGAATTTCAG 31772     C      GCCAC
                                TTG ATAGTTG     AATTTCAG
                                |||  |||||||    ||||||||
                                AAC TATCAAT     TTAAAGTC
                                  T      ATC__
GAM1231  BMP1      3'  GCCTGTGCTGTCTTGCA     31775     AA  AT
                                GCC  GT  CTGTCTTGCA
                                |||  ||  ||||||||||
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                                CGG  CA  GACAGAACGT
                                  A_  C_
GAM1231  CALCR    3'  AAGCCGCTTTGTCTTGCA    31776      AA  ATC
                                AAGCC  GT   TGTCTTGCA
                                |||||  ||   |||||||||
                                TTCGG  CG   ACAGAACGT
                                  ___  AA_
GAM1231  GRM7     5'  AGCCAAGTGTTTGCCCCATAA  31777        ATC     GC
                                AGCCAAGT   TGTCTT  AA
                                ||||||||   ||||||  ||
                                TCGGTTCA   ACGGGG  TT
                                    CAA     TA
GAM1231  HLCS     3'  AGCTGCACAGTCTTGCA     31778     CAA    CT
                                AGC   GTAT  GTCTTGCA
                                |||   ||||  ||||||||
                                TCG   CGTG  CAGAACGT
                                  A__    T_
GAM1231  LAD1     3'  AGCTGGCTGAGTCTTGCAAA  31779     CAA  ATCT
                                AGC   GT    GTCTTGCAAA
                                |||   ||    ||||||||||
                                TCG   CG    CAGAACGTTT
                                  AC_  ACT_
GAM1231  PITPN    3'  TGACCACTGTCTTGCA      31780   A    AGTAT
                                A GCCA     CTGTCTTGCA
                                | ||||     ||||||||||
                                A TGGT     GACAGAACGT
                                 C   _____
GAM1231  PRX      3'  CAAGTATCTTGTTCCCCAAA  31781         _  CT G
                                CAAGTATCT GT  T CAAA
                                ||||||||| ||  | ||||
                                GTTCATAGA CA  G GTTT
                                     A  AG G
GAM1231  PTGFRN   3'  AAGTCAGTCAGTCTTGCAA   31782     CCA   ATCT
                                AAG   AGT    GTCTTGCAA
                                |||   |||    |||||||||
                                TTC   TCA    CAGAACGTT
                                  AG_   GT__
GAM1231  SCGB2A2  3'  AGCCAAAGGTCTTGCA      31783       TATCT
                                AGCCAAG     GTCTTGCA
                                |||||||     ||||||||
                                TCGGTTT     CAGAACGT
                                   C_____
GAM1231  WHSC1    3'  TAAGTTAATATCTGCTCCCCAA 31784      CCA      TC  G
           A                     TAAG   AGTATCTG  TT CAAA
                                 ||||   ||||||||  || ||||
                                 ATTC   TTATAGAC  GG GTTT
                                   AA_       GA  G
GAM1231  WHSC1    3'  TAAGTTAATATCTGCTCCCCAA 31784      CCA      TC  G
           A                     TAAG   AGTATCTG  TT CAAA
                                 ||||   ||||||||  || ||||
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                                ATTC   TTATAGAC  GG GTTT
                                  AA_       GA  G
GAM1231  WHSC1    3'  TAAGTTAATATCTGCTCCCCAA 31784      CCA       TC  G
             A                   TAAG   AGTATCTG  TT CAAA
                                 ||||   ||||||||  || ||||
                                ATTC   TTATAGAC  GG GTTT
                                  AA_       GA  G
GAM1231  ZNF215   5'  TAAGCCAAGTTATTTCAC    31785          ATC   C TG
                                TAAGCCAAGT   TGT T  C
                                ||||||||||   ||| |  |
                                ATTCGGTTCA   ATA A  G
                                      ___   A GT
GAM1231  C20orf60  3'  GCTGCGCGCTCTGTCTTGCAAA 31786    CAA  A_
                                GC   GT  TCTGTCTTGCAAA
                                ||   ||  ||||||||||||
                                CG   CG  AGACAGAACGTTT
                                 ACG  CG
GAM1231  DKFZP434C1715 3'  AGCAAGTATCTGAACTG     31787     C       TC
                                AGC AAGTATCTG  TTG
                                ||| |||||||||  |||
                                TCG TTCATAGAC  GAC
                                  _       TT
GAM1231  FLJ13397  3'  TGACCAAGTATCTGAATGCAAA 31788    A         TCT
                                A GCCAAGTATCTG   TGCAAA
                                | ||||||||||||   ||||||
                                A TGGTTCATAGAC   ACGTTT
                                 C          TT_
GAM1231  KIAA1940  3'  TAAGCCAAGTGGCTCCAGC    31789          ATCTG   T
                                TAAGCCAAGT    TCT GC
                                ||||||||||    ||| ||
                                ATTCGGTTCA    AGG CG
                                      CCG__   T
GAM1231  MAP3K2    3'  TAAGTTGAGTACCTACCCTA   31790     CCA     GT
                                TAAG   AGTATCT  CTTG
                                ||||   |||||||  ||||
                                ATTC   TCATGGA  GGAT
                                  AAC      TG
GAM1231  MGC3079   3'  GCTGAGCCTGTCTTGCA     31791    CA   AT
                                GC  AGT  CTGTCTTGCA
                                ||  |||  ||||||||||
                                CG  TCG  GACAGAACGT
                                 AC  __
GAM1231  MGC5149   5'  AGCCAAGTGTCTTCAA      31792        ATCT    G
                                AGCCAAGT    GTCTT CAA
                                ||||||||    ||||| |||
                                TCGGTTCA    CAGAA GTT
                                      ____    _
GAM1231  PRO1777   3'  AAGTCATATCCACTGTCTTG   31793     C  A  AT_
                                AAG CA GT   CTGTCTTG
                                ||| || ||   ||||||||
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                                TTC GT TA   GACAGAAC
                                  A  A  GGT
GAM1231  ZNF185    3'  TAAGTCAATAATGGCTCTTGCA 31794      C   GTATCTG
              A                    TAAG CAA      TCTTGCAA
                                   |||| |||      ||||||||
                                   ATTC GTT      AGAACGTT
                                     A   ATTACCG
GAM1231  LOC143188 5'  AGCAAGCAGGTCTTGCAA    31795     C     TCT
                                   AGC AAGTA   GTCTTGCAA
                                   ||| |||||   |||||||||
                                   TCG TTCGT   CAGAACGTT
                                     _     C__
GAM1231  LOC151196 3'  TAAGCTAAGTACCTGCTCA    31796       C        T
                                   TAAGC AAGTATCTG CTTG
                                   ||||| ||||||||| ||||
                                   ATTCG TTCATGGAC GAGT
                                      A       _
GAM1231  LOC221178 3'  TAAGCCAAGATATTTTGT     31797          _   C_
                                   TAAGCCAAG TAT  TGT
                                   ||||||||| |||  |||
                                   ATTCGGTTC ATA  ACA
                                         T   AA
GAM1231  LOC222031 5'  GCCAAGACTTATCTTGCAA    31798       T TC
                                   GCCAAG A  TGTCTTGCAA
                                   |||||| |  ||||||||||
                                   CGGTTC T  ATAGAACGTT
                                      _ GA
GAM1231  LOC222258 5'  CAAGCCAGGCATGGTTTTGCAA 31799         A    CT  C
              A                     TAAGCCA GTAT  GT TTGCAAA
                                   ||||||| ||||  || |||||||
                                   GTTCGGT CGTA  CA AACGTTT
                                       C    C_  A
GAM1231  LOC254532 3'  AGCCAGCTATCTGCCCTG     31800       AG
                                   AGCCA  TATCTGTCTTG
                                   |||||  ||||||||||
                                   TCGGT  ATAGACGGGAC
                                      CG
GAM1232  NELL2     3'  CTTCTACATGGTGATGT      31803          TATTAT
                                   CTTCTATAT     TGATGT
                                   |||||||||     ||||||
                                   GAAGATGTA     ACTACA
                                         CC_____
GAM1232  TRIM9     3'  CCCTTCTATTTGTTATTCTTG  31804          A__    A
                                   CCCTTCTAT   TTATT TTG
                                   |||||||||   ||||| |||
                                   GGGAAGATA   AATAA AAC
                                         AAC    G
GAM1232  KLHL4     3'  CCTTTTATATTATCAGCTG    31805      C        _
                                   CCTT TATATTATTA TTG
                                   |||| |||||||||| |||
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                                GGAA ATATAATAGT GAC
                                  A        C
GAM1232 LANO     3' CCCTTATGTATTATTATTA   31806      CTA
                                CCCTT   TATTATTATTG
                                |||||   ||||||||||
                                GGGAA   ATAATAATAAT
                                   TAC
GAM1232 TBC1D2   5' CCTTTCTCTCCCATTGATGTA 31807    C   ATATTA
                                CC TTCT     TTATTGATGTA
                                || ||||     ||||||||||
                                GG AAGA     GGTAACTACAT
                                 A   GAG___
GAM1232 VDAC3    3' CCCTTCTTCACATTGATGT   31808       ATA   T
                                CCCTTCT   TTAT ATTGATGT
                                |||||||   |||| ||||||||
                                GGGAAGA   AGTG TAACTACA

                                   ___   _
GAM1232 LOC158046 3' CCATCTATATTATTGCAAATG 31809    T        ATT
                                CC TCTATATTATT   GATG
                                || ||||||||||   ||||
                                GG AGATATAATAA   TTAC
                                 T         CGT
GAM1233 FBXL5    3' TTCTATAATCCTAAAGAA    31812           CC
                                TTCTATAATCCTGA  AGGA
                                ||||||||||||  ||||
                                AAGATATTAGGATT  TCTT

                                   __
GAM1233 FBXL5    3' TTCTATAATCCTAAAGAA    31812           CC
                                TTCTATAATCCTGA  AGGA
                                ||||||||||||  ||||
                                AAGATATTAGGATT  TCTT

                                   __
GAM1233 RNMT     3' TTTCTATGATCCTGACCAA   31813       A
                                TTTCTAT ATCCTGACCAG
                                ||||||| ||||||||||
                                AAAGATA TAGGACTGGTT
                                    C
GAM1233 AP4E1    3' TCTTTCTTGACCAGG       31814       ATAATCC
                                TCTTTCT      TGACCAGG
                                |||||||      ||||||||
                                AGAAAGA      ACTGGTCC

                                   _______
GAM1233 DKFZP586I2223 3' TCATTCTGCAGTGACCAGGA  31815    T   A  ATCC
                                TC TTCT TA    TGACCAGGA
                                || |||| ||    |||||||||
                                AG AAGA GT    ACTGGTCCT
                                 T   C  C___
GAM1233 DKFZP586I2223 3' TCATTCTGCAGTGACCAGGA  31815    T   A  ATCC
                                TC TTCT TA    TGACCAGGA
                                || |||| ||    |||||||||
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                                AG AAGA GT    ACTGGTCCT
                                 T    C  C___
GAM1233  DKFZP586I2223 3'  TCATTCTGCAGTGACCAGGA   31815    T    A  ATCC
                                TC TTCT TA    TGACCAGGA
                                || |||| ||    |||||||||
                                AG AAGA GT    ACTGGTCCT
                                 T    C  C___
GAM1233  FLJ10326  3'  TCTTCTATAATTCTGATTTTGA 31817      T      C    CCAG
                                TCTT CTATAAT CTGA    GA
                                |||| ||||||| ||||    ||
                                AGAA GATATTA GACT    CT
                                  _      A    AAAA
GAM1233  FLJ10326  3'  TCTTTCTATAGTTACAGGA    31816          ATCCTGAC
                                TCTTTCTATA       CAGGA
                                ||||||||||       |||||
                                AGAAAGATAT       GTCCT
                                      CAAT_____
GAM1233  FLJ12876  5'  TTTCTGTAAGACCAGGA     31818       A   TCCT
                                TTTCT TAA    GACCAGGA
                                ||||| |||    ||||||||
                                AAAGA ATT    CTGGTCCT
                                   C   _____
GAM1233  KIAA1257  3'  TCTTTCTAGAATCTTACTGGG  31819         T   CTG  CA
                                TCTTTCTA AATC   AC  GG
                                |||||||| ||||   ||  ||
                                AGAAAGAT TTAG   TG  CC
                                     C    AA_  AC
GAM1233  LEAP-2    5'  TCTTCCTATGACCTGGGA    31820         AAT    ACCA
                                TCTTTCTAT   CCTG    GGA
                                |||||||||   ||||    |||
                                AGAAGGATA   GGAC    CCT
                                     CT_    _____
GAM1233  MGC27434  3'  TCTCTCTGTGGGACCAGGA   31821        ATAATCCT
                                TCTTTCT       GACCAGGA
                                |||||||       ||||||||
                                AGAGAGA       CTGGTCCT
                                    CACC_____
GAM1233  OS4       3'  TCTTTCTAAATGAGGCCTCAGG 31822         TAAT___   GAC
              AA                  TCTTTCTA      CCT   CAGGAA
                                |||||||||      |||   ||||||
                                AGAAAGAT      GGA   GTCCTT
                                     TTACTCC   ___
GAM1234  CLCN4     3'  TATGATTCAGTAACATAG    31825       CA
                                TATGA  CAGTAACATAG
                                |||||  ||||||||||
                                ATACT  GTCATTGTATC
                                   AA
GAM1234  D8S2298E  3'  ATGGCACAGTCCACAGATTATT 31826     A     AA
                                ATG CACAGT  CATAGATTATT
                                ||| ||||||  ||||||||||
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                                TAC GTGTCA  GTGTCTAATAA
                                  C     G_
GAM1234  RFXAP    3'  TATGTTCTACAGGCATAGATTA 31827     AC__   TAA
                TT                  TATG   ACAG   CATAGATTATT
                                    ||||   ||||  ||||||||||
                                    ATAC   TGTC   GTATCTAATAA
                                      AAGA   C__
GAM1234  C9orf5   3'  TATAATATAGTAACATAGAT   31828      CAC
                                    TATGA   AGTAACATAGAT
                                    |||||   ||||||||||||
                                    ATATT   TCATTGTATCTA
                                       ATA
GAM1234  DKFZP586F1318 3'  TATGACACAGTAAGTGTGAT   31829          CATA
                                    TATGACACAGTAA    GAT
                                    ||||||||||||    |||
                                    ATACTGTGTCATT    CTA
                                            CACA
GAM1234  HSPC177  3'  GACACAGTAACGACT      31830          ATA
                                    GACACAGTAAC   GATT
                                    ||||||||||   ||||
                                    CTGTGTCATTG   CTGA
                                                ___
GAM1234  KIAA0630  3'  TATGACACTAGTGACAGAAATT 31831        _  A   T
                                    TATGACAC AGT ACA AGATT
                                    |||||||| ||| ||| |||||
                                    ATACTGTG TCA TGT TTTAA
                                         A   C   C
GAM1234  KIAA1265  3'  TATGACTAGTAATACAAATTAT 31832       AC    C
                T                    TATGAC  AGTAA ATAGATTATT
                                     ||||||  ||||| ||||||||||
                                     ATACTG  TCATT TGTTTAATAA
                                        A_    A
GAM1234  MAP4K3   3'  TATGAGGTAGTAACTAAATTAT 31833      CAC     A
                T                    TATGA   AGTAAC TAGATTATT
                                     |||||   ||||||  |||||||||
                                     ATACT   TCATTG ATTTAATAA
                                        CCA     _
GAM1235  CA7     3'  AGGTGGCTTTGGTGACTGGGTG 31836     A   CCCTC
                                     AGGT GCT    GACTGGGTG
                                     ||||  |||    |||||||||
                                     TCCA CGA    CTGACCCAC
                                       C   AACCA
GAM1235  MBP     3'  AGGTGGCCCCCTCTCTG     31837      A      GA
                                     AGGT GCTCCCTC  CTG
                                     ||||  ||||||||  |||
                                     TCCA CGGGGGAG  GAC
                                       C       A_
GAM1235  ALTE    3'  AGGTAGTTCCTTTGCCCTCTG  31838       C  ____   GA
                                     AGGTAG TCC    CTC  CTG
                                     ||||||  |||    |||  |||
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                                TCCATC AGG   GGG  GAC
                                   A  AAAC  A_
GAM1235  LOC196047 3'  AAAGGTAGTTTTTATTCTGGGT 31839       CTCCCTCGA
             G                   GAAGGTAG       CTGGGTG
                                 ||||||||       |||||||
                                 TTTCCATC       GACCCAC
                                    AAAAATAA_
GAM1235  LOC205095 3'  GGTGGTCCCAACTGGGTG   31840    AGC   TC
                                 GGT  TCCC  GACTGGGTG
                                 |||  ||||  |||||||||
                                 CCA  AGGG  TTGACCCAC
                                   CC_   __
GAM1236  GFPT2    3'  TGGGCCACACACGAGAA    31843     ATCT
                                 TGGGC   TGCACGAGAA
                                 |||||   ||||||||||
                                 ACCCG   GTGTGCTCTT
                                    GT__
GAM1236  NT5E     3'  GCACATGGGTGTTGCAAGAGA  31844       CATC   C
                                 GTACATGGG   TTGCA GAGA
                                 |||||||||   ||||| ||||
                                 CGTGTACCC   AACGT CTCT
                                      AC__    T
GAM1236  RNMT     3'  GTACATGGCATCAGATGGTGAG 31845       G   TTGCAC_
             AA                    GTACATGG CATC      GAGAA
                                 |||||||| ||||      |||||
                                 CATGTACC GTAG      CTCTT
                                    _   TCTACCA
GAM1236  SHC1     3'  GTACATAGGCATGCAACATGGG 31846         CTT  C__
             AG                    GTACATGGGCAT  GCA  GAG
                                 ||||||||||||  |||  |||
                                 CATGTATCCGTA  TGT  CTC
                                       CGT  ACC
GAM1236  C6orf9   5'  ATGGGCATTTCTTGGAG     31847       __    CAC
                                 ATGGGCA  TCTTG  GAG
                                 |||||||  |||||  |||
                                 TACCCGT  AGAAC  CTC
                                    AA    ___
GAM1236  EFNA2    3'  GTACATGGTCAACGGCGAG   31848       G  TCTT  A_
                                 GTACATGG CA   GC  CGAG
                                 |||||||| ||   ||  ||||
                                 CATGTACC GT   TG  GCTC
                                    A  _____  CC
GAM1236  EREG     5'  GTGCACGGGCAGGGCGGGAG  31849   A      TCTT  AC
                                 GT CATGGGCA   GC  GAG
                                 || ||||||||   ||  |||
                                 CA GTGCCCGT   CG  CTC
                                   C      CC__  CC
GAM1236  FLJ20073 3'  GTACATTGGCATCTTCTGGATG 31850       G      GCAC__
             AG                    GTACAT GGCATCTT     GAG
                                 ||||||  ||||||||     |||
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                                CATGTA CCGTAGAA     CTC
                                   A       GACCTA
GAM1236  FLJ25410  3'  GTACATAGGTGTGTGTTGAGA  31851         CATCT  CAC
                                GTACATGGG    TG   GAGA
                                |||||||||    ||   ||||
                                CATGTATCC    AC   CTCT
                                     ACAC_  AA_
GAM1236  HCGIV.9   3'  GTGCATGAGCACTGGTGAG   31852    A       CT  CAC
                                GT CATGGGCAT  TG   GAG
                                || |||||||||  ||   |||
                                CA GTACTCGTG  AC   CTC
                                 C        __  CA_
GAM1236  IL14      5'  GTACATAGGGCATTTTGCA   31853       _     C
                                GTACAT GGGCAT TTGCA
                                |||||| |||||| |||||
                                CATGTA CCCGTA AACGT
                                   T     A
GAM1236  KIAA1045  3'  GCACATGGGAAGGGCATGAG  31854         CATCTT  C
                                GTACATGGG     GCA GAG
                                |||||||||     ||| |||
                                CGTGTACCC     CGT CTC
                                     TTCC__   A
GAM1236  KIAA1437  5'  GTACATGGCATCTGGAGA    31855         G    TGCAC
                                GTACATGG CATCT    GAGA
                                |||||||| |||||    ||||
                                CATGTACC GTAGA    CTCT
                                   _    C_____
GAM1236  KIAA1550  3'  GTGCATGGGCACTTGTCTGAG  31856    A       T    CAC
                                GT CATGGGCA CTTG   GAG
                                || |||||||| ||||   |||
                                CA GTACCCGT GAAC   CTC
                                 C       _    AGA
GAM1236  LEAP-2    5'  ACATGGGCATTTTAAGTTTGAG 31857          C   CAC__
                                ACATGGGCAT TTG    GAG
                                |||||||||| |||    |||
                                TGTACCCGTA AAT    CTC
                                     A   TCAAA
GAM1236  PRKAG3    3'  ACATGGGCTCACTGCGAGA    31858         A _    AC
                                ACATGGGC TC TTGC  GAGA
                                |||||||| || ||||  ||||
                                TGTACCCG AG GACG  CTCT
                                   _ T    __
GAM1236  TReP-132  5'  GTGCATGGGCAATCCGACGAGA 31859    A       TC   C
            A                    GT CATGGGCA  TTG ACGAGAA
                                || ||||||||  ||| |||||||
                                CA GTACCCGT  GGC TGCTCTT
                                 C       TA  _
GAM1236  TReP-132  5'  GTGCATGGGCAATCCGACGAGA 31859    A       TC   C
            A                    GT CATGGGCA  TTG ACGAGAA
                                || ||||||||  ||| |||||||
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                                CA GTACCCGT  GGC TGCTCTT
                                 C       TA  _
GAM1236  TReP-132  5'  GTGCATGGGCAATCCGACGAGA 31859    A       TC   C
                A                GT CATGGGCA  TTG ACGAGAA
                                 || ||||||||  ||| |||||||
                                CA GTACCCGT  GGC TGCTCTT
                                 C       TA  _
GAM1236  LOC129138 3'  ACATGGGCATCTTGGGAG    31860            CAC
                                ACATGGGCATCTTG   GAG
                                ||||||||||||||   |||
                                TGTACCCGTAGAAC   CTC
                                        C__
GAM1236  LOC150406 3'  TACATGGGTGTCATATTTGAGA 31861        CA  TTGCAC
                A                TACATGGG  TC     GAGAA
                                 ||||||||  ||     |||||
                                ATGTACCC  AG     CTCTT
                                     AC  TATAAA
GAM1236  LOC222031 3'  CATGGGCATCTCAGAGA     31862           CAC
                                CATGGGCATCTTG   GAGA
                                ||||||||||||   ||||
                                GTACCCGTAGAGT   CTCT
                                        ___
GAM1236  LOC253974 3'  ATGGGCATGAACCATGAGAA   31863        CTT  AC_
                                ATGGGCAT   GC   GAGAA
                                ||||||||   ||   |||||
                                TACCCGTA   TG   CTCTT
                                     CT_  GTA
GAM1236  LOC254387 3'  TGGGCATCTCCCACGGAA    31864         G    A
                                TGGGCATCTT CACG GAA
                                |||||||||| |||| |||
                                ACCCGTAGAG GTGC CTT
                                      G   _
GAM1237  DNMT2    3'  TTATGCCTGTTATGACACT    31867          TT   G
                                TTATGTCTGTTA  TGA ATT
                                ||||||||||||  ||| |||
                                AATACGGACAAT  ACT TGA
                                        __  G
GAM1237  HEM1     5'  TATCAACTTGTTTGAGATTC   31868      TG_  A
                                TGTC   TT TTTGAGATTC
                                ||||   || ||||||||||
                                ATAG   AA AAACTCTAAG
                                  TTG  C
GAM1237  FLJ10204  3'  TTATGGGCATTTGAGATTC    31869       TCT  T
                                TTATG   GT ATTTGAGATTC
                                |||||   || ||||||||||
                                AATAC   CG TAAACTCTAAG
                                  C__  _
GAM1237  INE1     5'  TATTGTGTCTATTGTTTG    31870      A       A
                                TATT TGTCTGTT TTTG
                                |||| |||||||| ||||
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                                ATAA ACAGATAA AAAC
                                  C       C
GAM1237  MRPL35    3'  TGTCCCACTTGAGATTC     31871      GT
                                TGTCT  TATTTGAGATTC
                                |||||  ||||||||||||
                                ACAGG  GTGAACTCTAAG
                                  __
GAM1237  LOC129831 3'  CATTATGTTTGTGAGATT    31872        C   TATTT
                                TATTATGT TGT    GAGATT
                                |||||||| |||    ||||||
                                GTAATACA ACA    CTCTAA
                                    A  _____
GAM1237  LOC145945 5'  TGTTTGTTTTTGAGATTC    31873     C    A
                                TGT TGTT TTTGAGATTC
                                ||| |||| ||||||||||
                                ACA ACAA AAACTCTAAG
                                  A   _
GAM1237  LOC254101 5'  TGAGGAGTTATTTGAGATT    31874    TCT_
                                TG   GTTATTTGAGATT
                                ||   ||||||||||||
                                AC   CAATAAACTCTAA
                                 TCCT
GAM1237  LOC256809 3'  TATGTCTGTACAAAGATT    31875         TATTT
                                TATGTCTGT    GAGATT
                                |||||||||    ||||||
                                ATACAGACA    TTCTAA
                                     TGT__
GAM1237  LOC57826  3'  TGTACTTGTTATTTGAGATT   31876     _ _
                                TGT CT GTTATTTGAGATT
                                ||| || ||||||||||||
                                ACA GA CAATAAACTCTAA
                                  T  A
GAM1238  DNASE1L1  3'  ATACAACATCTTCATTCCTC   31879       CAAGCC
                                GTACAAT     CATTCCTC
                                |||||||     ||||||||
                                TATGTTG     GTAAGGAG
                                    TAGAA_
GAM1238  HOXA7     3'  AGTACAATCAAGTCATCCCTC  31880          CC
                                AGTACAATCAAG  CATTCCTC
                                ||||||||||||  ||||||||
                                TCATGTTAGTTC  GTAGGGAG
                                      A_
GAM1238  LDB3      3'  TCAGTACAGTCAGCAACCTCCT 31881        A   A  CCA
                                TCAGTACA TCA GC   TTCCT
                                |||||||| ||| ||   |||||
                                AGTCATGT AGT CG   GAGGA
                                    C   _ TTG
GAM1238  MAP7      3'  TCATGCCTAGTCAGCCCATTTC 31882     _ ACAA   A      C
             T                   TCA GT    TCA GCCCATT CT
                                ||| ||    ||| ||||||| ||
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                                AGT CG    AGT CGGGTAA GA
                                  A  GATC  _      A
GAM1238  C21orf25  3'  TCAATACAGCCCATTTCT    31883        ATCAA      C
                                TCAGTACA    GCCCATT CT
                                ||||||||    ||||||| ||
                                AGTTATGT    CGGGTAA GA
                                     _____      A
GAM1238  ChGn      3'  AGTACAAACCATTCCT      31884        TCAAGC
                                AGTACAA     CCATTCCT
                                |||||||     ||||||||
                                TCATGTT     GGTAAGGA
                                    T_____
GAM1238  FLJ21478  3'  TCAGCTATGCCCATTCCT    31885       ACAATCAA
                                TCAGT       GCCCATTCCT
                                |||||       ||||||||||
                                AGTCG       CGGGTAAGGA
                                   ATA_____
GAM1238  KIAA0256  3'  TCAGCACAATTAGAACAACTTT 31886         CA_   CCA  C
            CTC                   TCAGTACAAT   AGC   TT CTC
                                ||||||||||   |||   || |||
                                AGTCGTGTTA   TTG   AA GAG
                                     ATC   TTG  A
GAM1238  NY-REN-25 3'  TCAGCACAGATTACCCATTTCT 31887        ATCAA      C
                                TCAGTACA    GCCCATT CT
                                ||||||||    ||||||| ||
                                AGTCGTGT    TGGGTAA GA
                                     CTAA_      A
GAM1238  NYD-SP11  5'  TCAGCACAATCAGGCAGTTC   31888          A  CCA
                                TCAGTACAATCA GC   TTC
                                ||||||||||||| ||   |||
                                AGTCGTGTTAGT CG   AAG
                                      C  TC_
GAM1238  PRO2086   5'  TCAGTACATACAAATCAAGCTC 31889    _____      CCA   C  III
            GTTCTTCG                CA    ATCAAGC   TTC TC   G
                                ||    |||||||   ||| ||   |
                                GT    TAGTTCG   AAG AG   C
                                 ATGTT      AGC   A  III
GAM1238  SMAP1     3'  TCAGTACAGCAGCCTTTC    31890        ATCA    CA
                                TCAGTACA    AGCC  TTC
                                ||||||||    ||||  |||
                                AGTCATGT    TCGG  AAG
                                     CG__    A_
GAM1238  LOC146174 3'  TCAAATCCTCGAGTCCATTCCT 31891      TACAA  A  C
                                TCAG     TC AG CCATTCCT
                                ||||     || || ||||||||
                                AGTT     AG TC GGTAAGGA
                                   TAGG_  C  A
GAM1238  LOC147976 3'  CAGCTTTCAAGCCCATTCCTC  31892      ACAA
                                CAGT    TCAAGCCCATTCCTC
                                ||||    ||||||||||||||
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                                GTCG   AGTTCGGGTAAGGAG
                                  AA__
GAM1238  LOC158337 3'  CAATCAAGTGCAAATCCTC   31893       CC  T_
                                CAATCAAG  CA  TCCTC
                                ||||||||  ||  |||||
                                GTTAGTTC  GT  AGGAG
                                    AC  TT
GAM1238  LOC159199 5'  TCAGTACAGACAGCACTTCCTC 31894       AT  A  CCA
                                TCAGTACA  CA GC   TTCCTC
                                ||||||||  || ||   ||||||
                                AGTCATGT  GT CG   AAGGAG
                                    CT  _  TG_
GAM1238  LOC57117  5'  TCAGTACAACTTGGCAATTC  31895        CAA  CC
                                TCAGTACAAT   GC  ATTC
                                ||||||||||   ||  ||||
                                AGTCATGTTG   CG  TAAG
                                     AAC  T_
GAM1238  LOC84570  3'  CAGTACAGCCTTCTTCATTCCT 31896       AT AAGCC
           C                     CAGTACA  C    CATTCCTC
                                |||||||  |    ||||||||
                                GTCATGT  G    GTAAGGAG
                                   CG AAGAA
GAM1239  DKK1     3'  AATAGGCAGTGCAGCACCT   31899       A  ___  A
                                AATAGG CA   CA CACCT
                                ||||||  ||   ||  |||||
                                TTATCC GT   GT GTGGA
                                   _  CAC  C
GAM1239  EGLN1    5'  AATAGAACACTTGCAACAC   31900         ____
                                AATAGGACAC    AACAC
                                ||||||||||    |||||
                                TTATCTTGTG    TTGTG
                                     AACG
GAM1239  KPNB2    3'  CAGTGACGGCAACACCTC    31901     _   A_
                                TAG GAC  CAACACCTC
                                |||  |||  |||||||||
                                GTC CTG  GTTGTGGAG
                                  A   CC
GAM1239  MCM6     3'  CAATAGGACAGCACATACCT   31902         _  AC_
                                TAATAGGACA CA   ACCT
                                ||||||||||  ||   ||||
                                GTTATCCTGT GT   TGGA
                                     C  GTA
GAM1239  SMN1     3'  TAAGACACTCTAACACTTC    31903        ___    C
                                TAGGACAC   AACAC TC
                                ||||||||   |||||  ||
                                ATTCTGTG   TTGTG AG
                                     AGA    A
GAM1239  SMN1     3'  TAAGACACTCTAACACTTC    31903        ___    C
                                TAGGACAC   AACAC TC
                                ||||||||   |||||  ||
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                                ATTCTGTG  TTGTG AG
                                    AGA    A
GAM1239 SP4     5' TAACAGGACAAACCCTC    31904        C  A
                                TAATAGGACA AAC CCTC
                                |||||||||| ||| ||||
                                ATTGTCCTGT TTG GGAG
                                      _  _
GAM1239 C1orf22  3' CAATGAAAGGCAACACCTC   31905    AG  CA
                                TAAT  GA  CAACACCTC
                                ||||  ||  |||||||||
                                GTTA  TT  GTTGTGGAG
                                  CT  CC
GAM1239 FLJ14451 3' TAAGAGGACACAGCCCCTC   31906    T      ACA
                                TAA AGGACACA   CCTC
                                ||| ||||||||   ||||
                                ATT TCCTGTGT   GGAG
                                  C       CGG
GAM1239 KIAA0321 3' TAACAGGACCAAAACTTC    31907        A  C  C
                                TAATAGGAC CAA AC TC
                                ||||||||| ||| || ||
                                ATTGTCCTG GTT TG AG
                                     _  T  A
GAM1239 KIAA0893 3' TAACACCACCCAACACCTC   31908     GG  A
                                TAATA  AC CAACACCTC
                                |||||  || |||||||||
                                ATTGT  TG GTTGTGGAG
                                   GG  G
GAM1239 KIAA1102 3' TAAAACAGCAAACACCTC    31909       _  _
                                TAGGACA CAA CACCTC
                                ||||||| ||| ||||||
                                ATTTTGT GTT GTGGAG
                                    C  T
GAM1239 KIAA1712 3' AACAAAACACAACACCTC    31910
                                AATAGGACACAACACCTC
                                ||||||||||||||||||
                                TTGTTTTGTGTTGTGGAG

GAM1239 MGC3184  3' AATACAACACAACACTTC    31911     G        C
                                AATA GACACAACAC TC
                                |||| ||||||||||  ||
                                TTAT TTGTGTTGTG AG
                                  G        A
GAM1239 PDZD2    5' TAGAGACACAAGCATCTC    31912    _     _ C
                                TAG GACACAA CA CTC
                                ||| ||||||| || |||
                                ATC CTGTGTT GT GAG
                                  T      C  A
GAM1239 LOC124961 3' TAATAAGATACAATGCCTC   31913        C   CA
                                TAATAGGA ACAA  CCTC
                                ||||||||  ||||  ||||
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                                ATTATTCT TGTT  GGAG
                                    A    AC
GAM1239  LOC158062 5'  TAGAGTCACCAAACACCTC   31914     _ A   __
                                TAG G CAC  AACACCTC
                                ||| | |||  ||||||||
                                ATC C GTG  TTGTGGAG
                                  T A   GT
GAM1239  LOC222662 5'  TAATAGGACAAGGACAACCT   31915          CA_   _
                                TAATAGGACA   ACA CCT
                                ||||||||||   ||| |||
                                ATTATCCTGT   TGT GGA
                                     TCC   T
GAM1240  CDH11    5'  AACTGTACGGTGGTCTTGCTGA 31918        ATTAGC     A
           GG                    AATTGTAT     CTTGCT AGG
                                ||||||||     |||||| |||
                                TTGACATG     GAACGA TCC
                                   CCACCA     C
GAM1240  KIAA1577  3'  ATTGTATATTCTTAATGCTAAG 31919          AGCCT
           G                     ATTGTATATT    TGCTAAGG
                                ||||||||||    ||||||||
                                TAACATATAA    ACGATTCC
                                     GAATT
GAM1240  LOC131870 3'  ATTGTATATTTGCATGCCTGGG 31920          A  CT   AA
                                ATTGTATATT GC  TGCT  GG
                                |||||||||| ||  ||||  ||
                                TAACATATAA CG  ACGG  CC
                                     A  T_   AC
GAM1241  CYP3A43   5'  TTTTCAGCTCTGTCTTCT    31923         CA   C
                                TTTTCAGTTC  GTC TCT
                                ||||||||||  ||| |||
                                AAAAGTCGAG  CAG AGA
                                     A_   A
GAM1241  CYP3A43   5'  TTTTCAGCTCTGTCTTCT    31923         CA   C
                                TTTTCAGTTC  GTC TCT
                                ||||||||||  ||| |||
                                AAAAGTCGAG  CAG AGA
                                     A_   A
GAM1241  CYP3A43   5'  TTTTCAGCTCTGTCTTCT    31923         CA   C
                                TTTTCAGTTC  GTC TCT
                                ||||||||||  ||| |||
                                AAAAGTCGAG  CAG AGA
                                     A_   A
GAM1241  DAG1     3'  GTCCCTTGGTCTTCTCTAAG   31924       A__   C
                                GTTCC   GTC TCTCTAAG
                                |||||   ||| ||||||||
                                CAGGG   CAG AGAGATTC
                                   AAC   A
GAM1241  GALNT7   5'  TTTCACCCCAAGTCCTCTCT   31925       G   C
                                TTTCA TTC AGTCCTCTCT
                                ||||| ||| ||||||||||
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                                AAAGT GGG TCAGGAGAGA
                                  G   T
GAM1241  HLA-DRA   3'  TCTTCAGTGATCTTCTCTCTAA 31926        TCCA  __
           G                    TTTTCAGT   GTC  CTCTCTAAG
                                ||||||||   |||  |||||||||
                                AGAAGTCA   TAG  GAGAGATTC
                                    C___   AA
GAM1241  HLA-DRA   3'  TCTTCAGTGATCTTCTCTCTAA 31926        TCCA  __
           G                    TTTTCAGT   GTC  CTCTCTAAG
                                ||||||||   |||  |||||||||
                                AGAAGTCA   TAG  GAGAGATTC
                                    C___   AA
GAM1241  PPP1R2    3'  TTTTCAGTCTAATCAGTCTCTA 31927        CC   C_
           AG                   TTTTCAGTT  AGTC  TCTCTAAG
                                |||||||||  ||||  ||||||||
                                AAAAGTCAG  TTAG  AGAGATTC
                                    A_   TC
GAM1241  DKFZp761H039 5'  TTTTCAGTTGCTATCCTCTTTA 31928         CCA     C
           AG                   TTTTCAGTT   GTCCTCT TAAG
                                |||||||||   ||||||| ||||
                                AAAAGTCAA   TAGGAGA ATTC
                                    CGA     A
GAM1241  FLJ14442  3'  TTCTCAGTTCCACATTCTAAG  31929          GTCCTC
                                TTTTCAGTTCCA     TCTAAG
                                ||||||||||||    ||||||
                                AAGAGTCAAGGT     AGATTC
                                    GTA___
GAM1241  FLJ22301  5'  TTTCAGGGTTCTTCTCTAAG   31930       TTCCAG  C
                                TTTCAG     TC TCTCTAAG
                                ||||||     || ||||||||
                                AAAGTC     AG AGAGATTC
                                   CCA___  A
GAM1241  HSA404617 3'  TTTTCAGTTTTCCATCTGCTTC 31931         __   GTCCTC
           T                    TTTTCAGT  TCCA     TCT
                                ||||||||  ||||     |||
                                AAAAGTCA  AGGT     AGA
                                    AA    AGACGA
GAM1241  KIAA0268  3'  TCTTCAGTTCTGGGAGCCT   31932          C___  T
                                TTTTCAGTTC    AG CCT
                                |||||||||    || |||
                                AGAAGTCAAG    TC GGA
                                    ACCC  _
GAM1241  KIAA0420  3'  TTTTTAATTCCAGTCCTCCC   31933      C
                                TTTT AGTTCCAGTCCTCTC
                                ||||  ||||||||||||||
                                AAAA TTAAGGTCAGGAGGG
                                  A
GAM1241  MGC4832   3'  TTTTCAGTTCTCAGTCCTCT   31934          _
                                TTTTCAGTTC CAGTCCTCT
                                |||||||||| |||||||||
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                                AAAAGTCAAG GTCAGGAGA
                                     A
GAM1241  PARVA     3'  TTTCAGTTTCCACTATCTCT  31935        _  GTCC
                                TTTCAGTT CCA    TCTCT
                                |||||||| |||    |||||
                                AAAGTCAA GGT    AGAGA
                                     A   GAT_
GAM1241  LOC152822 3'  CTTTCAGCATGTCCTCTTTAAG 31936        TCCA      C
                                TTTTCAGT    GTCCTCT TAAG
                                ||||||||    ||||||| ||||
                                GAAAGTCG    CAGGAGA ATTC
                                     TA__       A
GAM1241  LOC153743 3'  TTTTCAGTCTAATTAGTCTCTA 31937         CCAGTCC
              AG                   TTTTCAGTT      TCTCTAAG
                                |||||||||      ||||||||
                                AAAAGTCAG      AGAGATTC
                                     ATTAATC
GAM1241  LOC257354 3'  TTTTTAATTCCAGTCCTCCC   31933      C
                                TTTT AGTTCCAGTCCTCTC
                                |||| ||||||||||||||
                                AAAA TTAAGGTCAGGAGGG
                                  A
GAM1241  LOC91351  3'  TTTCCAGTTTTTCAGCCTTCT  31938         C__     C
                                TTTTCAGTT   CAGTC TCT
                                |||||||||   ||||| |||
                                AAAGGTCAA   GTCGG AGA
                                     AAA     A
GAM1242  CKM       3'  GAGTGTGCTGGGAGCTCTCCA  31941     CA  AC  C  _  AC
                                GAG  TG  GG GA CT  CTCCA
                                |||  ||  || || ||  |||||
                                CTC  AC  CC CT GA  GAGGT
                                  AC  GA  _  C  __
GAM1242  DTR       3'  GACCATGACAGCATACCTTCA  31942    G        AC     C
                                GA CATGACGGCG  TACCT CA
                                || ||||||||||  ||||| ||
                                CT GTACTGTCGT  ATGGA GT
                                 G         __     A
GAM1242  MN1       5'  GCATGACAGCCGGCTCTCC    31943          _ A  AC
                                GCATGACGGC G CT  CTCC
                                |||||||||| | ||  ||||
                                CGTACTGTCG C GA  GAGG
                                     G C  __
GAM1242  COLEC10   3'  GAGCATGATGATGGAGGCTCCA 31944         C  CGACTAC
                                GAGCATGA GG      CTCCA
                                |||||||| ||      |||||
                                CTCGTACT CT      GAGGT
                                     A  ACCTCC_
GAM1242  DD5       3'  ATGACAGCATTAACTTCCA   31945          ACT  C
                                ATGACGGCG   AC TCCA
                                |||||||||   || ||||
```

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                                TACTGTCGT   TG AGGT
                                     AAT  A
GAM1242  FLJ00058  5'  GCGTGGTGGCTCCACCTCCAC  31946    A  AC   GA
                                GC TG  GGC  CTACCTCCAC
                                || ||  |||  ||||||||||
                                CG AC  CCG  GGTGGAGGTG
                                 C  CA   A_
GAM1242  FLJ13273  5'  GAGCGTGTCGGCGACCTGGGCC 31947      A  A       ACCT
                                GAGC TG CGGCGACT    CC
                                |||| || ||||||||    ||
                                CTCG AC GCCGCTGG    GG
                                  C  A       ACCC
GAM1242  KIAA0356  3'  GCAAGACGGCGACCCTCCA   31948     T       TA
                                GCA GACGGCGAC  CCTCCA
                                ||| |||||||||  ||||||
                                CGT CTGCCGCTG  GGAGGT
                                  T       __
GAM1242  KIAA1389  3'  GAGCCTGCAGCTACCTCCA   31949     A  A   GAC
                                GAGC TG CGGC   TACCTCCA
                                |||| || ||||   ||||||||
                                CTCG AC GTCG   ATGGAGGT
                                  G  _   ____
GAM1242  PHYHIP    3'  GAGCATGAGGCGGCCCAC    31950        C   A_
                                GAGCATGA GGCG  CTAC
                                |||||||| ||||  ||||
                                CTCGTACT CCGC  GGTG
                                     _   CG
GAM1242  LOC146958 5'  GAGCACGATGCAGCTTCCAC   31951         __   GA
                                GAGCATGA  CGGC  CTAC
                                ||||||||  ||||  ||||
                                CTCGTGCT  GTCG  GGTG
                                     AC    AA
GAM1242  LOC201242 5'  GCATAACGGCTGCCCTTCAC   31952          GACTA   C
                                GCATGACGGC    CCT CAC
                                ||||||||||    ||| |||
                                CGTATTGCCG    GGA GTG
                                      ACG__   A
GAM1242  LOC56267  3'  GAACCTCCTGACTACCTCCAC  31953     ATGACGGC
                                GAGC       GACTACCTCCAC
                                ||||       ||||||||||||
                                CTTG       CTGATGGAGGTG
                                  GAGGA___
GAM1242  LOC65243  5'  AGCATGACGGCGTCC       31954          ACTACC
                                AGCATGACGGCG     TCC
                                ||||||||||||     |||
                                TCGTACTGCCGC     AGG
                                                 _______
GAM1242  LOC92465  5'  GAGGATGACGCCACCTCCA   31955     C     GCGA
                                GAG ATGACG    CTACCTCCA
                                ||| ||||||    |||||||||
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                                CTC TACTGC    GGTGGAGGT
                                  C     ____
GAM1243  SLC22A1LS 5'  GTGGGGGTTTCATGCTG     31958     CA     C   T
                                GTG  GGGGTT CAT CTG
                                |||  |||||| ||| |||
                                CAC  CCCCAA GTA GAC
                                  __      A   C
GAM1243  SLC22A2   3'  GTGCAGGGATTTCTACT     31959          CCAT
                                GTGCAGGGGTT    TCTGTT
                                ||||||||||    ||||||
                                CACGTCCCTAA    AGATGA
                                       ____
GAM1243  THBD      3'  ATGTAGGGGTTCTGTCTG     31960     C       CAT
                                GTG AGGGGTTC   TCTG
                                ||| ||||||||   ||||
                                TAC TCCCCAAG   AGAC
                                  A       AC_
GAM1243  TRIM39    3'  GTGCAGGGGTTTCTGTTTCCTC 31961          _ CA__    G
            CTCTG                   GTGCAGGGGTT C    TTCT TTCTG
                                ||||||||||| |    |||| |||||
                                CACGTCCCCAA G    AGGA GAGAC
                                      A ACAA    G
GAM1243  KIAA1001  3'  GTAAGGCCATTCTGTT      31962     C   GGTT
                                GTG AGG    CCATTCTGTT
                                ||| |||    ||||||||||
                                CAT TCC    GGTAAGACAA
                                  _  _____
GAM1243  KIAA1908  3'  GTGCAGGGGTGCTGGTTTCTG  31963          TCCA__
                                GTGCAGGGGT     TTCTG
                                ||||||||||     |||||
                                CACGTCCCCA     AAGAC
                                      CGACCA
GAM1243  STK3      3'  GTGCAAGGGTTCCATTGATTTC 31964              CTG
            T                    GTGCAGGGGTTCCATT   TTCT
                                ||||||||||||||||   ||||
                                CACGTTCCCAAGGTAA   AAGA
                                          CTA
GAM1243  WWP1      3'  GCAGGGGTTCTTCATTCTG    31965          __
                                GCAGGGGTTC  CATTCTG
                                ||||||||||  |||||||
                                CGTCCCCAAG  GTAAGAC
                                      AA
GAM1243  LOC142820 3'  GAATCCTCTGTTCTG       31966       CAT
                                GGGTTC   TCTGTTCTG
                                ||||||   |||||||||
                                CTTAGG   AGACAAGAC
                                   ___
GAM1243  LOC90750  3'  ATGCGAAGCCCATTCTGTT    31967      A    T
                                GTGC GGGGT CCATTCTGTT
                                |||| ||||| ||||||||||
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                                TACG CTTCG GGTAAGACAA
                                  _    _
GAM1244  ADD2     3'  GCCGCTGGTGACCGAC      31970        C    TTGAG
                                GCCGTTGG GACC     GAC
                                |||||||| ||||     |||
                                CGGCGACC CTGG     CTG
                                   A   ______
GAM1244  EFNA4    3'  GCCCCCACGTGGCCTTGAGGA  31971     G  G   A__
                                GCC TT GCG   CCTTGAGGA
                                ||| || |||   |||||||||
                                CGG GG TGC   GGAACTCCT
                                  _ G   ACC
GAM1244  EGFL4    3'  AGCCGTTGGCGCCGGGC     31972          A  TT A  A
                                AGCCGTTGGCG CC  G GG C
                                |||||||||| ||  | || |
                                TCGGCAACCGC GG  C CC G
                                      _  __ _  _
GAM1244  FXYD2    3'  AGGCGTTGGCGATGCCACCTGG 31973    C       C____    A
              GG                  AG CGTTGGCGA     CTTG GG
                                || |||||||||     |||| ||
                                TC GCAACCGCT     GGAC CC
                                 C        ACGGT    C
GAM1244  FXYD2    3'  AGGCGTTGGCGATGCCACCTGG 31973    C       C____    A
              GG                  AG CGTTGGCGA     CTTG GG
                                || |||||||||     |||| ||
                                TC GCAACCGCT     GGAC CC
                                 C        ACGGT    C
GAM1244  MUC4     3'  AGCCGTTGCGGCTCAGGAGGAC 31974        G  AC  __
                                AGCCGTTG CG  CTT  GAGGAC
                                |||||||| ||  |||  ||||||
                                TCGGCAAC GC  GAG  CTCCTG
                                     _ C_   TC
GAM1244  PGF      3'  GCCGTGGCGGCCCCAGCAGGA  31975      T   A_   TG_
                                GCCGT GGCG  CCT   AGGA
                                ||||| ||||  |||   ||||
                                CGGCA CCGC  GGG   TCCT
                                   _   CG   TCG
GAM1244  SORCS2   5'  GTTGGGCGTGAGGACC      31976      _ ACCT
                                GTTGG CG    TGAGGACC
                                ||||| ||    ||||||||
                                CAACC GC    ACTCCTGG
                                   C  ____
GAM1244  TRIM37   5'  GCCGCTGGCGACCCGCAGG    31977           TG
                                GCCGTTGGCGACCT  AGG
                                ||||||||||||||  |||
                                CGGCGACCGCTGGG  TCC
                                          CG
GAM1244  CUGBP2   3'  AACTCGTTACGCCTTTGAGGAC 31978     _    G  A   _
                                AGC CGTTG CG CCTT GAGGAC
                                ||| ||||| || |||| ||||||
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                                TTG GCAAT GC GGAA CTCCTG
                                  A    _ _   A
GAM1244  DKFZP566M114 5'  GCTCCGGCGGCTTTGAGGACC  31979    CG     ACC
                                GC  TTGGCG   TTGAGGACC
                                ||  ||||||   |||||||||
                                CG  GGCCGC   AACTCCTGG
                                 A_     CGA
GAM1244  FLJ11160  3'  AGCCTTGGGCCTGAGGAC    31980     G    CGAC
                                AGCC TTGG    CTTGAGGAC
                                |||| ||||    |||||||||
                                TCGG AACC    GGACTCCTG
                                  _    C___
GAM1244  FLJ20671  3'  AAGCCATCAAATTCTTGAGGAC 31981        TG CGAC
                                AAGCCGT  G    CTTGAGGAC
                                |||||||  |    |||||||||
                                TTCGGTA  T    GAACTCCTG
                                    GT TAA_
GAM1244  FLJ22559  5'  AGCCGCTGGCGGCGACGACC   31982          ACCT   G
                                AGCCGTTGGCG    TGA GACC
                                ||||||||||    ||| ||||
                                TCGGCGACCGC    GCT CTGG
                                      C___   G
GAM1244  HSJ001348 5'  GCCGTCTCCTTGAGGACC    31983       GGCGA
                                GCCGTT    CCTTGAGGACC
                                ||||||    ||||||||||
                                CGGCAG    GGAACTCCTGG
                                   A____
GAM1244  KIAA0125  5'  GCCGTTGGCAGAGGCTGGGGA  31984         _  CC   A
                                GCCGTTGGC GA  TTG GGA
                                ||||||||| ||  ||| |||
                                CGGCAACCG CT  GAC CCT
                                      T  CC   C
GAM1244  KIAA0710  3'  AAGCAGTTGGTGACTTG     31985      C    C   C
                                AAGC GTTGG GAC TTG
                                |||| ||||| ||| |||
                                TTCG CAACC CTG AAC
                                  T    A   _
GAM1244  LHFPL2    5'  AAGCCGCTGGCGATCTCG    31986           C
                                AAGCCGTTGGCGA CTTG
                                |||||||||||| ||||
                                TTCGGCGACCGCT GAGC
                                       A
GAM1244  MGC2452   5'  GCTGTTAGGTCTCTGAGGAC   31987    C    CGACC
                                GC GTTGG    TTGAGGAC
                                || |||||    ||||||||
                                CG CAATC    GACTCCTG
                                 A    CAGA_
GAM1244  SLI       3'  CCTTGGCGACGTAGGCC     31988    G      CTTG   A
                                CC TTGGCGAC    AGG CC
                                || ||||||||    ||| ||
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                                GG AACCGCTG    TCC GG
                                 _       CA__   _
GAM1244  STK22D    3'  AGCCGTTGCGGCCAGTGGGGAC 31989        G  A  T_  A
              C                  AGCCGTTG CG CC  TG GGACC
                                 |||||||| || ||  || |||||
                                 TCGGCAAC GC GG  AC CCTGG
                                     _ C  TC  C
GAM1244  LOC144017 5'  GCCGTTGGCGCGGGAC      31990          ACCT  A
                                 GCCGTTGGCG    TG GGAC
                                 ||||||||||    || ||||
                                 CGGCAACCGC    GC CCTG
                                       _____  _
GAM1244  LOC154789 5'  GCCATTGGGTGAGGAC      31991         CGACCT
                                 GCCGTTGG      TGAGGAC
                                 ||||||||      |||||||
                                 CGGTAACC      ACTCCTG
                                     C_____
GAM1244  LOC159121 5'  GCTGGTGACCTTGAGGAC    31992       C
                                 GTTGG GACCTTGAGGAC
                                 ||||| ||||||||||||
                                 CGACC CTGGAACTCCTG
                                    A
GAM1244  LOC163033 5'  GCCGGGTCGAGGCCTTGAGGA  31993      TT  _  __
                                 GCCG  GG CGA  CCTTGAGGA
                                 ||||  || |||  |||||||||
                                 CGGC  CC GCT  GGAACTCCT
                                   __ A   CC
GAM1244  LOC200853 5'  AGCTATATACACTTTGAGGACC 31994     CGTTG  G  C
                                 AGC     GC AC TTGAGGACC
                                 |||     || || |||||||||
                                 TCG     TG TG AACTCCTGG
                                   ATATA  _  A
GAM1244  LOC205272 5'  AAGCCGTTGATCTTGGGGAC   31995          CGAC    A
                                 AAGCCGTTGG    CTTG GGAC
                                 ||||||||||    |||| ||||
                                 TTCGGCAACT    GAAC CCTG
                                       A___    C
GAM1244  LOC220370 3'  CCTTGGCTTTGAGGACC     31996    G    GACC
                                 CC TTGGC    TTGAGGACC
                                 || |||||    |||||||||
                                 GG AACCG    AACTCCTGG
                                  _    A___
GAM1244  LOC257364 3'  GCCTTGGCCTCGAGG       31997     G    GAC
                                 GCC TTGGC   CTTGAGG
                                 ||| |||||   |||||||
                                 CGG AACCG   GAGCTCC
                                   _    ____
GAM1244  LOC91149  5'  AAGCTTTTGGTGACCTTGAAA  31998      CG    C
                                 AAGC  TTGG GACCTTGAGG
                                 ||||  |||| ||||||||||
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                                TTCG  AACC CTGGAACTTT
                                  AA   A
GAM1245  ARIX    5'  GCGGGGGCCGGGCCAGGC    32001    CCTC    A
                                GC   GGGCC GGCCAGGC
                                ||   ||||| ||||||||
                                CG   CCCGG CCGGTCCG
                                 CC__    C
GAM1245  ARIX    5'  GCCGGGCCAGGCCGGG     32002    CTC       A
                                GCC  GGGCCAGGCC GG
                                |||  |||||||||| ||
                                CGG  CCCGGTCCGG CC
                                  ___       C
GAM1245  CST     5'  TGAGACCCTCGGGCTGTGGC  32003    AG       CA_
                                TGA  CCCTCGGGC  GGC
                                |||  |||||||||  |||
                                ACT  GGGAGCCCG  CCG
                                  CT       ACA
GAM1245  DNM2    3'  TGGCAGCCGAGGCTGGGCCAGG 32004    A_   CTC   CA
             C                   TG  AGCC  GGGC  GGCCAGGC
                                 ||  ||||  ||||  ||||||||
                                 AC  TCGG  TCCG  CCGGTCCG
                                  CG   C__   AC
GAM1245  FBLN1   3'  GAGGCCAGATCAGGCCAGGC  32005    A  CTC  GC
                                GA GCC  GG  CAGGCCAGGC
                                || |||  ||  ||||||||||
                                CT CGG  TC  GTCCGGTCCG
                                 C  ___  TA
GAM1245  FUT3    3'  TGAGGTTCCCGGCAGCCCAGGC 32006    AG__  TCG  C  G
                                TGA   CCC  GGC AG CCAGGC
                                |||   |||  ||| || ||||||
                                ACT   GGG  CCG TC GGTCCG
                                  CCAA  ___  _ G
GAM1245  GYPC    5'  GCCAGGCCGGGCCAGGCCGGGC 32007    C__       A
                                GCC  TCGGGCCAGGCC GGC
                                |||  |||||||||||| |||
                                CGG  GGCCCGGTCCGG CCG
                                  TCC         C
GAM1245  GYPC    5'  GCCAGGCCGGGCCAGGCCGGGC 32007    C__       A
                                GCC  TCGGGCCAGGCC GGC
                                |||  |||||||||||| |||
                                CGG  GGCCCGGTCCGG CCG
                                  TCC         C
GAM1245  KCNJ5   3'  TGAGATTCTTGGGCCAAAAAGC 32008    AGCC  C     CC
                                TGA   CT GGGCCAGG  AGGC
                                |||   || ||||||||  ||||
                                ACT   GA CCCGGTTT  TTCG
                                  CTAA  A      __
GAM1245  LU      3'  CGGAGCCTTGTCCCAGGCTGGG 32009    A   CTCGGG    CA
             C                   TG AGCC    CCAGGC  GGC
                                 || ||||    ||||||  |||
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                                GC TCGG     GGTCCG  CCG
                                 C    AACAG_     AC
GAM1245  MARK3    5'  TGAGGCCCTCGGATCGGC    32010     A       CCA
                                TGA GCCCTCGGG   GGC
                                ||| |||||||||   |||
                                ACT CGGGAGCCT   CCG
                                  C        AG_
GAM1245  MSF      3'  TGAGCCCTCGGGGAGCCAGGC  32011     A       CCA
                                TGA GCCCTCGGG   GGCCAGGC
                                ||| |||||||||   ||||||||
                                ACT CGGGAGCCC   TCGGTCCG
                                  _       C__
GAM1245  MYO1D    3'  GCCGGGCTCCGGGCCAGGC   32012     ___  _
                                GCC   CTC GGGCCAGGC
                                |||   ||| |||||||||
                                CGG   GAG CCCGGTCCG
                                  CCC   G
GAM1245  NUP62    3'  TGAGCCTGGGCCAGGC     32013     A   CTC
                                TGA GCC   GGGCCAGGC
                                ||| |||   |||||||||
                                ACT CGG   CCCGGTCCG
                                  _  A__
GAM1245  PDE6D    5'  TGGAGACCTCGGGCTAGC    32014    A  C      CA
                                TG AG CCTCGGGC  GGC
                                || || ||||||||  |||
                                AC TC GGAGCCCG  TCG
                                 C  T       A_
GAM1245  PDGFRB   3'  GAAGCCCGGTCAGGCCAGGC   32015       TC  GC
                                GAAGCCC  GG  CAGGCCAGGC
                                |||||||  ||  ||||||||||
                                CTTCGGG  CC  GTCCGGTCCG
                                    __  A_
GAM1245  PIM2     3'  GCCAGGCCAGGCCAGGC     32016     CTC
                                GCC   GGGCCAGGCCAGGC
                                |||   ||||||||||||||
                                CGG   TCCGGTCCGGTCCG
                                  ____
GAM1245  PPP3R1   5'  TGCGGCCCTCGGGTCGCCGGC  32017    AA       CCAG   A
                                TG  GCCCTCGGG   GCC GGC
                                ||  |||||||||   ||| |||
                                AC  CGGGAGCCC   CGG CCG
                                 GC       AG__  _
GAM1245  PSCD4    3'  ACTCCTCCTCCAGGCCAGGC   32018    _   GGG
                                GC CCTC   CCAGGCCAGGC
                                || ||||   ||||||||||
                                TG GGAG   GGTCCGGTCCG
                                 A   GA_
GAM1245  RBM3     5'  GAGGTCCTCTCCGGGCCAGGC  32019    AG_ _  _
                                GA   CC CTC GGGCCAGGC
                                ||   || ||| |||||||||
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                                CT   GG GAG CCCGGTCCG
                                 CCA  A   G
GAM1245  REST     5'  TGGGGCCCCGGGCCTCGGC   32020    AA   T     A_
                                TG  GCCC CGGGCC  GGC
                                ||  |||| ||||||  |||
                                AC  CGGG GCCCGG  CCG
                                 CC    _     AG
GAM1245  SH3BP2   3'  TGAGGCCCTCGGCCTAGAACAG 32021     A       G  _  GC
                                TGA GCCCTCGG CC AG  CAG
                                ||| |||||||| || ||  |||
                                ACT CGGGAGCC GG TC  GTC
                                  C       _  A  TT
GAM1245  SIAT1    3'  TGACAGGACAGGGTCAGGCCAG 32022     AGCCCTC   C
              GC                   TGA      GGG CAGGCCAGGC
                                |||      ||| ||||||||||
                                ACT      CCC GTCCGGTCCG
                                  GTCCTGT   A
GAM1245  SLC6A8   3'  GAAGCCTGAGCAGGCCAGG    32023       CTC    C
                                GAAGCC   GGGC AGGCCAGG
                                ||||||   |||| ||||||||
                                CTTCGG   CTCG TCCGGTCC
                                   A__   _
GAM1245  SLC7A7   3'  TGAAGCTGCCTAGGCCAGGC   32024       __   C
                                TGAAGC  CCT GGGCCAGGC
                                ||||||  ||| |||||||||
                                ACTTCG  GGA TCCGGTCCG
                                   AC  _
GAM1245  SYNGR2   3'  TGAAGCCCTCTGGGCACAGGC  32025          _    _
                                TGAAGCCCTC GGGC CAGGC
                                |||||||||| |||| |||||
                                ACTTCGGGAG CCCG GTCCG
                                     A   T
GAM1245  TP53BP1  5'  TGGAGACCTCGGGCAGGACCCA 32026    A  C       C   __
              GGC                    TG AG CCTCGGGC AGG  CCAGGC
                                || || ||||||||  |||  ||||||
                                AC TC GGAGCCCG TCC  GGTCCG
                                 C  T       _   TG
GAM1245  UNC119   3'  GAGGCCCAGCCAGGCCGGGC   32027    A    TCG       A
                                GA GCCC   GGCCAGGCC GGC
                                || ||||   ||||||||| |||
                                CT CGGG   TCGGTCCGG CCG
                                 C   ____        C
GAM1245  ZAP70    5'  TGAGGCCCACGGTGGGCCAGGC 32028     A    T   GCCA
                                TGA GCCC CGG    GGCCAGGC
                                ||| |||| |||    ||||||||
                                ACT CGGG GCC    CCGGTCCG
                                  C    T   AC__
GAM1245  CAMKK2   3'  AGCCACCAGGCCAGGC      32029      CTCGG
                                AGCC    GCCAGGCCAGGC
                                ||||    ||||||||||||
```

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                                TCGG    TGGTCCGGTCCG
                                  _____
GAM1245 CASKIN1  3' TGGAGCCCCCGGCCAGGC   32030   A      G
                                TG AGCCCTCGG CCAGGC
                                || ||||||||| ||||||
                                AC TCGGGGGCC GGTCCG
                                 C       _
GAM1245 CNNM1    3' TGAGCCTCAGGCCAGGCCAGGC 32031    A  C
                                TGA GCC TCGGGCCAGGCCAGGC
                                ||| ||| ||||||||||||||||
                                ACT CGG AGTCCGGTCCGGTCCG
                                  _  _
GAM1245 CXYorf1  5' TGGGTCCCCACTAAGCCAGGCC 32032    AAG   C__       A
           GGGC                   TG   CCCT   GGGCCAGGCC GGC
                                ||   ||||   |||||||||| |||
                                AC   GGGG   TTCGGTCCGG CCG
                                 CCA   TGA        C
GAM1245 DDX8     3' GCAGGCTCTTGCCAAAGCCAGG 32033    C__   GG    _
                                GC   CTC  GCCAG GCCAGG
                                ||   |||  ||||| ||||||
                                CG   GAG  CGGTT CGGTCC
                                 TCC   AA    T
GAM1245 DECR2    3' TGGCAGCTCCACGGGCCAGGC  32034    A_  _ T
                                TG  AGC CC CGGGCCAGGC
                                ||  ||| || ||||||||||
                                AC  TCG GG GCCCGGTCCG
                                 CG   A  T
GAM1245 DEFCAP   5' TGGAGCCCCGGGCTGCTGG   32035   A    T    CAG  CA
                                TG AGCCC CGGGC   GC  GG
                                || ||||| |||||   ||  ||
                                AC TCGGG GCCCG   CG  CC
                                 C    _    A__  A_
GAM1245 DEFCAP   5' TGGAGCCCCGGGCTGCTGG   32035   A    T    CAG  CA
                                TG AGCCC CGGGC   GC  GG
                                || ||||| |||||   ||  ||
                                AC TCGGG GCCCG   CG  CC
                                 C    _    A__  A_
GAM1245 DKFZP434B044 5' GCTCCTCGGGCAGAGCTGGGC  32036    _      CA   CA
                                GC CCTCGGGC  GGC  GGC
                                || ||||||||  |||  |||
                                CG GGAGCCCG  TCG  CCG
                                 A       TC   AC
GAM1245 FLJ10142 5' TGAGCCGAGCCAGGCTGGG   32037    A  CTC       CA
                                TGA GCC   GGGCCAGGC  GG
                                ||| |||   |||||||||  ||
                                ACT CGG   CTCGGTCCG  CC
                                  _  ____        AC
GAM1245 FLJ20330 5' TGGAGCCCCGGCTCAGGC    32038    A    CG  _
                                TG AGCCCT  GGC CAGGC
                                || ||||||  ||| |||||
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                                AC TCGGGG  CCG GTCCG
                                 C     __   A
GAM1245  FLJ20506  5'  TGGAGCCCCGGGCGCTAGG   32039    A    T    CAG  C
                                TG AGCCC CGGGC   GC AGG
                                || ||||| |||||   || |||
                                AC TCGGG GCCCG   CG TCC
                                 C    _    ___  A
GAM1245  FLJ21240  3'  TGAAGCCCTAATTAAGGGCTGG 32040        C_____   CA  CC
           GTTAGG                 GAAGCCCT     GGGC  GG  AGG
                                ||||||||     ||||  ||  |||
                                CTTCGGGA     CCCG  CC  TCC
                                     TTAATT    AC  AA
GAM1245  FLJ22593  5'  GCCCTGGGCCAGGCTGGG    32041      C       CA
                                GCCCT GGGCCAGGC  GG
                                ||||| |||||||||  ||
                                CGGGA CCCGGTCCG  CC
                                   _       AC
GAM1245  FLJ22800  3'  TGAAATTACCTTCAGGCCAGG  32042     ___   C
                                TGAA   GCC TCGGGCCAGG
                                ||||   ||| ||||||||||
                                ACTT   TGG AGTCCGGTCC
                                  TAA   A
GAM1245  FLJ22865  5'  GCGGGCGGGCCAGGTCAGGC   32043    CCT       C
                                GC   CGGGCCAGG CAGGC
                                ||   ||||||||| |||||
                                CG   GCCCGGTCC GTCCG
                                 CCC        A
GAM1245  FLJ23093  5'  TGAGGCCCTCGGGCACC     32044     A        CAG
                                TGA GCCCTCGGGC   GCC
                                ||| ||||||||||   |||
                                ACT CGGGAGCCCG   TGG
                                  C        ___
GAM1245  GMPPB     5'  TGAACCCAGAGCCAGGCTGGGC 32045      G   TC       CA
                                TGAA CCC  GGGCCAGGC  GGC
                                |||| |||  |||||||||  |||
                                ACTT GGG  CTCGGTCCG  CCG
                                   _   T_        AC
GAM1245  HRH3      3'  TGGGACCCTCGGGCCCAGCCGG 32046    AA        A   A
             GC                   TG  GCCCTCGGGCC GGCC GGC
                                ||  ||||||||||| |||| |||
                                AC  TGGGAGCCCGG TCGG CCG
                                 CC          G   C
GAM1245  KIAA0140  3'  TGACGCGGCCAGGCCAGG    32047     A  CCTCG
                                TGA GC    GGCCAGGCCAGG
                                ||| ||    ||||||||||||
                                ACT CG    CCGGTCCGGTCC
                                  G _____
GAM1245  KIAA0450  3'  TGCGGCCCAGGCCCAGGCTGGG 32048    AA   TC  G    CA
             C                    TG  GCCC  GG CCAGGC  GGC
                                ||  ||||  || ||||||  |||
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                                AC  CGGG  CC GGTCCG  CCG
                                 GC    T_ G     AC
GAM1245  KIAA0478  3'  AGCCAGGCTGCCAGGTCAGGC  32049      CTCGG     C
                                AGCC     GCCAGG CAGGC
                                ||||     |||||| |||||
                                TCGG     CGGTCC GTCCG
                                  TCCGA      A
GAM1245  KIAA0662  3'  AAGTCCTCGGGCCGCCTGGC   32050     C        AG   A
                                AAG CCTCGGGCC  GCC GGC
                                ||| |||||||||  ||| |||
                                TTC GGAGCCCGG  CGG CCG
                                  A        __   A
GAM1245  KIAA1202  3'  TGAAGCCCTGGGGTAGGC    32051          C   CC
                                TGAAGCCCT GGG  AGGC
                                |||||||||| |||  ||||
                                ACTTCGGGA CCC  TCCG
                                      _   CA
GAM1245  KIAA1977  5'  GCGAGGCTAGGCCAGGC     32052    CCTC    C
                                GC    GGGC AGGCCAGGC
                                ||    |||| |||||||||
                                CG    TCCG TCCGGTCCG
                                 C___    A
GAM1245  KIAA1985  3'  TGAAATGAGGGGGCTAGGCCAG 32053       CCCTC    C
             G                   TGAAG     GGGC AGGCCAGG
                                |||||     |||| ||||||||
                                ACTTT     CCCG TCCGGTCC
                                   ACTCC    A
GAM1245  KLF12    3'  TGAGCTCCCAGGCCGGG     32054     A  C       A
                                TGA GC CTCGGGCC GG
                                ||| || |||||||| ||
                                ACT CG GGGTCCGG CC
                                  _ A       C
GAM1245  MAN1C1   5'  GAAGCCCTCGGAGTCCAGGC   32055           _ _
                                GAAGCCCTCGG G CCAGGC
                                |||||||||||  | ||||||
                                CTTCGGGAGCC C GGTCCG
                                       T A
GAM1245  MGC10500  3'  GCTCCCTGGCGGCCAGGCCGGG 32056   AAG    CG_       A
             C                   G   CCCT   GGCCAGGCC GGC
                                |   ||||   ||||||||| |||
                                C   GGGA   CCGGTCCGG CCG
                                 GA_    CCG        C
GAM1245  MGC16332  5'  GCCCCACCCGGGCCAGGC    32057      ___
                                GCCCT   CGGGCCAGGC
                                |||||   ||||||||||
                                CGGGG   GCCCGGTCCG
                                   TGG
GAM1245  MGC2752   5'  GAAGCTCTCGGGCTAGGC    32058       C      C
                                GAAGC CTCGGGC AGGC
                                ||||| ||||||| ||||
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                                CTTCG GAGCCCG TCCG
                                  A      A
GAM1245 MGC4172  3' TGAAATCCACTGGGCCAGGC  32059      _ _ C
                                TGAAG CC CT GGGCCAGGC
                                ||||| || || |||||||||
                                ACTTT GG GA CCCGGTCCG
                                  A  T  _
GAM1245 NPD002   3' GAGGCTCTCCCAGGCCAGGC  32060    A  C   GGG
                                GA GC CTC   CCAGGCCAGGC
                                || || |||   ||||||||||
                                CT CG GAG   GGTCCGGTCCG
                                 C  A  ___
GAM1245 PCDH16   5' GCTCCAGCTCCAGGCCAGGC  32061    C T   G_
                                GC C CGG  CCAGGCCAGGC
                                || | |||  ||||||||||
                                CG G GTC  GGTCCGGTCCG
                                 A _  GA
GAM1245 PIP5K1C  3' TGGGGCCCCCGGGGCTCAGG  32062    AA       CCAG  _
                                TG  GCCCTCGGG   GC CAGG
                                ||  |||||||||   || ||||
                                AC  CGGGGGCCC   CG GTCC
                                 CC       _____ A
GAM1245 PPM1A    5' TGCAGCGGCGGGCCAGGTCAGG 32063    A   CCT       C
            C                    TG AGC   CGGGCCAGG CAGGC
                                || |||   ||||||||| |||||
                                AC TCG   GCCCGGTCC GTCCG
                                 G  CC_       A
GAM1245 PPP1R16A 5' AGCTTGGGGGCCAGGCTGGGC 32064    CCTC       CA
                                AGC   GGGCCAGGC  GGC
                                |||   |||||||||  |||
                                TCG   CCCGGTCCG  CCG
                                  AACC       AC
GAM1245 PTPRT    3' GAAGCCCCATGCAGGTTAGG  32065       CGG  C   CC
                                GAAGCCCT   GC AGG  AGG
                                ||||||||   || |||  |||
                                CTTCGGGG   CG TCC  TCC
                                     TA_  _   AA
GAM1245 RALGPS1A 5' GCCGGGGCCGGGCCAGGC    32066    CTC    A
                                GCC   GGGCC GGCCAGGC
                                |||   ||||| ||||||||
                                CGG   CCCGG CCGGTCCG
                                  C__    C
GAM1245 SCYA28   3' TAAAGCCTAATACGTAGGCCAG 32067       CTCGG  C_
            G                    TGAAGCC    GC  AGGCCAGG
                                |||||||    ||  ||||||||
                                ATTTCGG    TG  TCCGGTCC
                                    ATTA_  CA
GAM1245 SLC25A18 5' TGAGGCACTCACGGGCCAGGC  32068    A  C  __
                                TGA GC CTC  GGGCCAGGC
                                ||| || |||  |||||||||
```

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                                ACT CG GAG  CCCGGTCCG
                                  C  T   TG
GAM1245  TIP-1    3'  GAAGGAAGGCCAGGCCAGGC   32069      CCCTC
                                GAAG    GGGCCAGGCCAGGC
                                ||||    ||||||||||||||
                                CTTC    TCCGGTCCGGTCCG
                                  CT___
GAM1245  TOLLIP   3'  TGGGTCCCTCGGGCCCCCACAC 32070    AAG        AGG   G
                                TG   CCCTCGGGCC   CCA GC
                                ||   ||||||||||   ||| ||
                                AC   GGGAGCCCGG   GGT TG
                                 CCA        G__   G
GAM1245  LOC126526 3'  AGTCCTGGAGCAGGCCAGGC   32071    C   C  GC
                                AG CCT GG  CAGGCCAGGC
                                || ||| ||  ||||||||||
                                TC GGA CC  GTCCGGTCCG
                                 A   _  TC
GAM1245  LOC127435 3'  AGCAGGGTGGGCCAGGCCAGGC 32072     CCTC_
                                AGC    GGGCCAGGCCAGGC
                                |||    ||||||||||||||
                                TCG    CCCGGTCCGGTCCG
                                  TCCCA
GAM1245  LOC131377 3'  TGGAGCCCCCACAAGGCCAGGC 32073    A      GG  C
                                TG AGCCCTC  GC AGGCCAGGC
                                || |||||||  || |||||||||
                                AC TCGGGGG  TG TCCGGTCCG
                                 C       __  T
GAM1245  LOC144512 3'  TGAAGCCCCTGGGGCACAGG   32074         C_   _
                                TGAAGCCCT  GGGC CAGG
                                |||||||||  |||| ||||
                                ACTTCGGGG  CCCG GTCC
                                      AC    T
GAM1245  LOC146488 3'  GAAGCCTGAGCAGGCCAGG    32023       CTC    C
                                GAAGCC   GGGC AGGCCAGG
                                ||||||   |||| ||||||||
                                CTTCGG   CTCG TCCGGTCC
                                   A__   _
GAM1245  LOC148132 3'  TGAACCATAGCCAGGCTGGGC  32075      G  CTCG       CA
                                TGAA CC    GGCCAGGC  GGC
                                |||| ||    ||||||||  |||
                                ACTT GG    TCGGTCCG  CCG
                                  _  TA__        AC
GAM1245  LOC148137 3'  GCCCCAGGCTCTTAGGCTGGGC 32076      T    C___    CA
                                GCCC CGGGC    AGGC  GGC
                                |||| |||||    ||||  |||
                                CGGG GTCCG    TCCG  CCG
                                  _     AGAA    AC
GAM1245  LOC148223 3'  TGGGGCCCTCAGGTCACGC    32077    AA       C  G
                                TG  GCCCTCGGG CA GC
                                ||  ||||||||| || ||
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                                AC  CGGGAGTCC GT CG
                                 CC        A  G
GAM1245  LOC148979 5'  CGATGCAGGGCCAGGCCGGGC  32078     A  CCTC        A
                                TGA GC    GGGCCAGGCC GGC
                                ||| ||    |||||||||| |||
                                GCT CG    CCCGGTCCGG CCG
                                  A  T___         C
GAM1245  LOC149460 3'  TGCAGCACCGGCCAGGCCAGGC 32079    A  _  TCG
                                TG AGC CC   GGCCAGGCCAGGC
                                || ||| ||   ||||||||||||
                                AC TCG GG   CCGGTCCGGTCCG
                                 G   T  ___
GAM1245  LOC152582 5'  TGAGCTCCTGCCATGGGCCAGG 32080     A  _  CGG   __
              C                   TGA GC CCT   GCCA  GGCCAGGC
                                ||| || |||   ||||  ||||||||
                                ACT CG GGA   CGGT  CCGGTCCG
                                  _  A   ___    AC
GAM1245  LOC152849 3'  CGGAGCTCTTGGGCCAGAAGGC 32081    A   C  C       CC
                                TG AGC CT GGGCCAGG  AGGC
                                || ||| || ||||||||  ||||
                                GC TCG GA CCCGGTCT  TCCG
                                 C   A  A       __
GAM1245  LOC196878 5'  GAGGCCGCCGGGCCAGGC    32082    A   C
                                GA GCC TCGGGCCAGGC
                                || ||| ||||||||||
                                CT CGG GGCCCGGTCCG
                                 C   C
GAM1245  LOC200093 5'  TGGGTCCCCACTAAGCCAGGCC 32032    AAG    C__        A
              GGGC                   TG   CCCT   GGGCCAGGCC GGC
                                ||   ||||   |||||||||| |||
                                AC   GGGG   TTCGGTCCGG CCG
                                 CCA    TGA        C
GAM1245  LOC203427 5'  TGGGGCTCTCCGGCCACGGGC  32083    AA  C   G    __
                                TG  GC CTC GGCCA  GGC
                                ||  || ||| |||||  |||
                                AC  CG GAG CCGGT  CCG
                                 CC  A   G    GC
GAM1245  LOC220003 3'  GCCCTCGGCCCCCTGGGC    32084        G  AGG  A_
                                GCCCTCGG CC   CC  GGC
                                |||||||| ||   ||  |||
                                CGGGAGCC GG   GG  CCG
                                     G  ___  AC
GAM1245  LOC220073 5'  TGGAGCCGGGTGGGCCAGGC   32085    A   CTC_
                                TG AGCC    GGGCCAGGC
                                || ||||    |||||||||
                                AC TCGG    CCCGGTCCG
                                 C    CCCA
GAM1245  LOC221543 3'  TGAAGCTTTGAAGCCAGGC    32086       CCTC
                                TGAAGC    GGGCCAGGC
                                ||||||    |||||||||
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                                ACTTCG   TTCGGTCCG
                                   AAAC
GAM1245  LOC254143 3'  TGAAGCCCCTGGGGCACAGG  32074        C_   _
                                TGAAGCCCT  GGGC CAGG
                                |||||||||  |||| ||||
                                ACTTCGGGG  CCCG GTCC
                                     AC   T
GAM1245  LOC254423 3'  TGGAGCTCCGGGCCAGATGGC  32087    A  C T      CCA
                                TG AGC C CGGGCCAGG  GGC
                                || ||| | |||||||||  |||
                                AC TCG G GCCCGGTCT  CCG
                                 C  A _      A__
GAM1245  LOC254647 5'  TGGGGCCCTGGTGGGAGGCCAG 32088    AA   C__  CC
            G                    TG  GCCCT  GGG  AGGCCAGG
                                || |||||  |||  ||||||||
                                AC  CGGGA  CCC  TCCGGTCC
                                 CC    CCA  __
GAM1245  LOC254848 3'  TGGCAGCCCTGGGCCAGGC   32089    A_    C
                                TG  AGCCCT GGGCCAGGC
                                ||  |||||| |||||||||
                                AC  TCGGGA CCCGGTCCG
                                 CG    _
GAM1245  LOC255082 5'  AGCCGCCGGCCGGGCCAGGC  32090     C   G  A
                                AGCC TCGG CC GGCCAGGC
                                |||| |||| || ||||||||
                                TCGG GGCC GG CCGGTCCG
                                  C   _ C
GAM1245  LOC256306 5'  TGGAGACCTTGGGCCAGGC   32091    A  C   C
                                TG AG CCT GGGCCAGGC
                                || || ||| |||||||||
                                AC TC GGA CCCGGTCCG
                                 C  T   A
GAM1245  LOC256980 3'  TGAGCTCCAGGCCAGGCCGGG  32092    A  C T       A
                                TGA GC C CGGGCCAGGCC GG
                                ||| || | |||||||||| ||
                                ACT CG G GTCCGGTCCGG CC
                                  _  A _        C
GAM1245  LOC257596 3'  TGAAGCTTTGAAGCCAGGC   32086      CCTC
                                TGAAGC   GGGCCAGGC
                                ||||||   |||||||||
                                ACTTCG   TTCGGTCCG
                                   AAAC
GAM1245  LOC58512  3'  GCCCGGGCCGGGCTGGGC   32093     TC   A  CA
                                GCCC  GGGCC GGC  GGC
                                ||||  ||||| |||  |||
                                CGGG  CCCGG CCG  CCG
                                  __    C  AC
GAM1245  LOC91040  5'  TGGGTCCCCACTAAGCCAGGCC 32032   AAG   C__       A
            GGGC                  TG   CCCT   GGGCCAGGCC GGC
                                ||   ||||   |||||||||| |||
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                                AC   GGGG   TTCGGTCCGG CCG
                                 CCA    TGA         C
GAM1245  LOC92170  3'  CCCTGGAGCTGGCCAGGC    32094      C    CA
                                CCCT GGGC  GGCCAGGC
                                |||| ||||  ||||||||
                                GGGA CTCG  CCGGTCCG
                                  C    A_
GAM1245  LOC92840  3'  TGGAGCCTCCTAGCAGGCCAGG 32095    A    CT G   C
                                TG AGCC  C GGC AGGCCAGG
                                || ||||  | ||| ||||||||
                                AC TCGG  G TCG TCCGGTCC
                                 C    AG A   _
GAM1245  LOC96652  3'  TGGGACCCTGGGAGGCCAGGC  32096    AA    C   CC
                                TG  GCCCT GGG  AGGCCAGGC
                                ||  ||||| |||  |||||||||
                                AC  TGGGA CCC  TCCGGTCCG
                                 CC    _  __
GAM1246  FLJ20856  3'  TGAGAAACTTGGGGCTCCG    32099          AAAGTAGA
                                TGAGAAACTT       CTCCG
                                ||||||||||       |||||
                                ACTCTTTGAA       GAGGC
                                      CCCC____
GAM1246  GRIN3A    3'  GAGAAGCTTAAGGTAAACCCGA 32100      A    A     T
                                GAGAA CTTAA GTAGAC CCGA
                                ||||| ||||| |||||| ||||
                                CTCTT GAATT CATTTG GGCT
                                   C    C     _
GAM1246  KIAA0061  3'  TGGAAACTTAAAGTAGA     32101    A
                                TG GAAACTTAAAGTAGA
                                || ||||||||||||||
                                AC CTTTGAATTTCATCT
                                 _
GAM1246  KIAA0729  3'  TGAGGGACTTAAAAGTAGA    32102      AA      _
                                TGAG  ACTTAAA GTAGA
                                ||||  ||||||| |||||
                                ACTC  TGAATTT CATCT
                                  CC      T
GAM1246  KIAA1198  3'  TGGAAACTTAAAAGGCAGATTC 32103    A        __    C
                                TG GAAACTTAAA  GTAGA TC
                                || ||||||||||  |||||  ||
                                AC CTTTGAATTT  CGTCT AG
                                 _         TC    A
GAM1246  PASK      3'  TGAGAAACTAAACTC       32104          TAAAGT    C
                                TGAGAAACT      AGACT C
                                |||||||||      |||||  |
                                ACTCTTTGA      TTTGA G
                                      _______    A
GAM1246  LOC128954 5'  TGAGAAAGTTAAAACTCCA    32105        C    AGTA
                                TGAGAAA TTAA    GACTCCG
                                |||||||  ||||    |||||||
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                                ACTCTTT AATT    TTGAGGT
                                   C   ____
GAM1246  LOC149301 5'  AACTTAAAAAACTCCGA     32106         TA
                                AACTTAAAG  GACTCCGA
                                |||||||||  ||||||||
                                TTGAATTTT  TTGAGGCT
                                    __
GAM1246  LOC220705 3'  TGAGAAACTTAAGAGTAGA    32107          _
                                TGAGAAACTTAA AGTAGA
                                |||||||||||| ||||||
                                ACTCTTTGAATT TCATCT
                                      C
GAM1246  LOC220954 3'  TGAGAAACATGGATTGATCTCT 32108        TTAAA  A  _   C
            GA                    TGAGAAAC    GT GA CTC GA
                                |||||||||    || || ||| ||
                                ACTCTTTG     TA CT GAG CT
                                     TACC_  A  A   A
GAM1246  LOC256642 3'  AGAAACTTAAGAAAACTTCGA  32109          A T     C
                                AGAAACTTAA G AGACT CGA
                                |||||||||| | ||||| |||
                                TCTTTGAATT C TTTGA GCT
                                     _ T    A
GAM1246  LOC257438 3'  TGAGGAAAGTAGACTC      32110      AAACTT
                                TGAG     AAAGTAGACTC
                                ||||     ||||||||||
                                ACTC     TTTCATCTGAG
                                  C_____
GAM1246  LOC51301  3'  GAGAACTTAAAGATACCGA    32111       A      TAGACT
                                GAGAA CTTAAAG     CCGA
                                ||||| |||||||     ||||
                                CTCTT GAATTTC     GGCT
                                   _      TAT___
GAM1247  MAP3K7IP1 3'  TGGAATGTTTACAACAGA     32114     A
                                TG AATGTTTACAATAGA
                                || ||||||||||||||
                                AC TTACAAATGTTGTCT
                                 C
GAM1247  PPP1R3C   3'  TGAAATATTTACAGTAGAAA   32115           A
                                TGAAATGTTTACA TAGAAA
                                |||||||||||| ||||||
                                ACTTTATAAATGT ATCTTT
                                      C
GAM1247  DKFZP564I1171 3'  TGAAATGTTTTTAATAGAA    32116          AC
                                TGAAATGTTT  AATAGAA
                                |||||||||  |||||||
                                ACTTTACAAA  TTATCTT
                                     AA
GAM1247  POU4F2    3'  TGAAATATTTACAGTAGA     32117           A
                                TGAAATGTTTACA TAGA
                                |||||||||||| ||||
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                                ACTTTATAAATGT ATCT
                                       C
GAM1248 IL17     3'  AAGAGGAGGAAATACTATATCC 32120      CACA
              G                  AAGA   GAAATACTATATCCG
                                 ||||   ||||||||||||||
                                 TTCT   CTTTATGATATAGGC
                                   CCTC
GAM1248 LIPA     3'  TAAGACACAAAATGAATCC   23777           ATACTAT
                                 TAAGACACAGAA      ATCC
                                 ||||||||||||      ||||
                                 ATTCTGTGTTTT      TAGG
                                        ACT____
GAM1248 MAP3K9   3'  GACACAGAAAAGCTCCTATCTC 23778          TA  A_   _
              G                  GACACAGAAA  CT  TATC CG
                                 ||||||||||  ||  |||| ||
                                 CTGTGTCTTT  GA  ATAG GC
                                       TC  GG   A
GAM1248 OLFM1    3'  TAAGACACAGGCATAGCC    23779          AA  _
                                 TAAGACACAG  ATA CT
                                 ||||||||||  ||| ||
                                 ATTCTGTGTC  TAT GG
                                       CG   C
GAM1248 DDX31    3'  GACACAGAACTGACAT      23783         AAT  _
                                 GACACAGA   ACT ATAT
                                 ||||||||   ||| ||||
                                 CTGTGTCT   TGA TGTA
                                      ___   C
GAM1248 DORFIN   3'  TGAACACAGAAAATGTATC   23786   A        TACTA
                                 A GACACAGAAA     TATC
                                 | ||||||||||     ||||
                                 A TTGTGTCTTT     ATAG
                                  C         TAC__
GAM1248 FLJ12704 3'  AGTGCACAGGAATACCAT    23787    A_    A
                                 AG  CACAG AATACTAT
                                 ||  ||||| ||||||||
                                 TC  GTGTC TTATGGTA
                                   AC    C
GAM1248 KIAA1143 3'  TAAGCCACAGAAATAGCCACAT 23790      A        _
                                 TAAG CACAGAAATA CTATAT
                                 |||| |||||||||| ||||||
                                 ATTC GTGTCTTTAT GGTGTA
                                    G         C
GAM1248 Rpo1-2   3'  TAAGGCACAGAAACAGTAT   32121      A        C
                                 TAAG CACAGAAATA TAT
                                 |||| |||||||||| |||
                                 ATTC GTGTCTTTGT ATA
                                    C         C
GAM1248 LOC158402 5' AAGACACAGGGCCTCGTATC   23796          AAATA  A_
                                 AAGACACAG     CT  TATC
                                 |||||||||     ||  ||||
```

```
                                TTCTGTGTC    GA  ATAG
                                     CCG__  GC
GAM1248  LOC205313 5'  TAAGCACAGAAAACATATC   23797     A      T  T
                                TAAG CACAGAAA AC ATATC
                                |||| |||||||| || |||||
                                ATTC GTGTCTTT TG TATAG
                                  _       _ _
GAM1248  LOC56181  3'  TAAGAGGCAGAAACATCT    32122      CA      _
                                TAAGA  CAGAAATA CT
                                |||||  |||||||| ||
                                ATTCT  GTCTTTGT GA
                                   CC       A
GAM1249  IGFBP7    3'  TTGATGTGTGATCTTTATTTTG 32125       GTAAG   TC
                                TTGATG    GAT  TTATTTTG
                                ||||||    |||  ||||||||
                                AACTAC    CTA  AATAAAAC
                                    ACA__   GA
GAM1249  POPX1     3'  TGGTGGTATCTTACTTTG    32126     AA  AT
                                TGGT  GG  TCTTATTTTG
                                ||||  ||  ||||||||||
                                ACCA  CC  AGAATGAAAC
                                   __ AT
GAM1250  CDH6      3'  TGGATGGATTTTACATTACTTT 32129     _  AC__
                                TGGA GGA    ACATTACTTT
                                |||| |||    ||||||||||
                                ACCT CCT    TGTAATGAAA
                                  A   AAAA
GAM1250  CNTNAP2   3'  TTACAGGAAGTGTATTACTTT  32130      T    AACAC
                                TTACA GGAGG    ATTACTTT
                                |||||| |||||    ||||||||
                                AATGT CCTTC    TAATGAAA
                                   _    ACA__
GAM1250  SOX11     3'  TTACATGGAGACGGTTACTTT  32131          AACACA
                                TTACATGGAGG     TTACTTT
                                ||||||||||     |||||||
                                AATGTACCTCT     AATGAAA
                                      GCC___
GAM1250  TEGT      3'  GGAAAGGGAACACATTACTTT  32132     ___
                                GGA   GGAACACATTACTTT
                                |||   ||||||||||||||||
                                CCT   CCTTGTGTAATGAAA
                                  TTC
GAM1250  APOBEC3G  3'  CTACTTGGTCAGGAGTGCATTG 32133     A  __   ACA   A
            CTTT                   TTAC TGG  AGGA   CATT CTTT
                                |||| |||  ||||  |||| ||||
                                GATG ACC  TCCT   GTAA GAAA
                                  A  AG   CAC   C
GAM1250  FLJ12661  3'  TTACATAGGGGAGTGTTCACAC 32134        A  A____
            T                   TTACATGG GGA    CACATT
                                |||||||| |||    ||||||
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                                AATGTATC CCT    GTGTGA
                                    C   CACAA
GAM1250  KIAA0256  3'  ATGTATAACACACATTACTTT  32135    GAGGA_
                                ATG     ACACATTACTTT
                                |||     ||||||||||||
                                TAC     TGTGTAATGAAA
                                  ATATTG
GAM1250  WSB1      3'  TTACTGTGGGGGAAATTACTTT 32136     A_  A   CAC
                                TTAC  TGG GGAA   ATTACTTT
                                ||||  ||| ||||   ||||||||
                                AATG  ACC CCTT   TAATGAAA
                                  AC   C   ___
GAM1251  COL1A2    3'  TGGGAAAGTGTTTTGAG    32139    CA       C
                                TGG  AAAGTGTTT GAG
                                |||  ||||||||| |||
                                ACC  TTTCACAAA CTC
                                  C_       A
GAM1251  DNAJB9    3'  TGGTAAGAATGCAGTAGAAATT 32140    C  A    TTCG
             A                   TGG AA AGTGT    AGAAATTA
                                 ||| || |||||    ||||||||
                                 ACC TT TTACG    TCTTTAAT
                                   A  C    TCA_
GAM1251  PAG       3'  TGGCACTTTTGAGAAATT    32141      AAAGTG   C
                                TGGCA     TTT GAGAAATT
                                |||||     ||| ||||||||
                                ACCGT     AAA CTCTTTAA
                                   GA____   _
GAM1251  RFXAP     3'  TGTTAAAAGTGTTTTGAA    32142    GC       C
                                TG  AAAAGTGTTT GAG
                                ||  |||||||||| |||
                                AC  TTTTCACAAA CTT
                                  AA        A
GAM1251  FLJ11413  3'  TGGTAAAAGTGCTTTCAATCCC 32143    C       _   GAA_
             ATTA                   TGG AAAAGTGTTT CGA    ATTA
                                    ||| |||||||||| |||    ||||
                                    ACC TTTTCACGAA GTT    TAAT
                                      A        A   AGGG
GAM1251  FLJ20432  5'  TGGTGAAAGGTCTGAAGAAATT 32144     CA   T   C
                                TGG  AAAG GTTT GAGAAATT
                                |||  |||| |||| ||||||||
                                ACC  TTTC CAGA TTCTTTAA
                                  AC   _   C
GAM1251  FLJ21313  3'  TGCCAAAAAGGAATTGAGAAAT 32145    G     TGTTTC
             TA                   TG CAAAAG     GAGAAATTA
                                  || ||||||     |||||||||
                                  AC GTTTTT     CTCTTTAAT
                                    G     CCTTAA
GAM1251  KIAA0257  3'  TGGCGCATAATATTGAGAAATT 32146     AAA_     TC
             A                    TGGC    AGTGTT  GAGAAATTA
                                  ||||    ||||||  |||||||||
```

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                                ACCG    TTATAA  CTCTTTAAT
                                  CGTA      __
GAM1251  PCDH20    3'  GCTAAAAGTGAGAAAGAAATTA 32147    _      TTTC
                                GC AAAAGTG    GAGAAATTA
                                || |||||||    |||||||||
                                CG TTTTCAC    TTCTTTAAT
                                 A      TCT_
GAM1251  RASAL2    3'  TGACAGGAGTTCAATAGAAATT 32148      AA   GTTTCG
           A                     TGGCA  AGT     AGAAATTA
                                |||||  |||     ||||||||
                                ACTGT  TCA     TCTTTAAT
                                  CC   AGTTA_
GAM1251  LOC123047 5'  GGTGAAAAGTAAGTGAGAAATT 32149    C_      TTTC
           A                     GG  AAAAGTG    GAGAAATTA
                                ||  |||||||    |||||||||
                                CC  TTTTCAT    CTCTTTAAT
                                 AC      TCA_
GAM1251  LOC132235 5'  TGCCAAAAGATGAGTGAGAGAT 32150    G     _  TTTC    A
           T                     TG CAAAAG TG    GAGA ATT
                                || ||||||| ||    |||| |||
                                AC GTTTTC AC    CTCT TAA
                                 G     T  TCA_    C
GAM1251  LOC143286 5'  GCTAAAGCTGAGAAATT     32151    A    GTTTC
                                GC AAAGT     GAGAAATT
                                || |||||     ||||||||
                                CG TTTCG     CTCTTTAA
                                 A    A_____
GAM1251  LOC148195 5'  GCAAAAACTTGAGAAATTA    32152        TG   C
                                GCAAAAG  TTT GAGAAATTA
                                |||||||  ||| |||||||||
                                CGTTTTT  GAA CTCTTTAAT
                                   __   _
GAM1251  LOC221301 3'  TGGCAAAATTTCAAAA      32153        AGT
                                TGGCAAA   GTTTCGAGA
                                |||||||   |||||||||
                                ACCGTTT   TAAAGTTTT
                                   ____
GAM1251  LOC221981 3'  GGTAAAAGTGTCAATAGAGAA  32154    C       TC__
                                GG AAAAGTGTT    GAGAA
                                || |||||||||    |||||
                                CC TTTTCACAG    CTCTT
                                 A        TTAT
GAM1251  LOC90309  5'  GCAGAAGTGAGAGAAATT    32155     A    TTTC
                                GCA AAGTG    GAGAAATT
                                ||| |||||    ||||||||
                                CGT TTCAC    CTCTTTAA
                                  C    T____
GAM1252  ACADM     5'  ACTCCTCTGGTCCCGCCCACT  32158    _  A  AA_
                                GC CC CT   CCCGCCCACT
                                || || ||   ||||||||||
```

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                                TG GG GA   GGGCGGGTGA
                                 A  A  CCA
GAM1252  ACTN4    5'  CGCCCACCAGCCTGTCCGCT   32159        A  CGC  A
                                CGCCCACTA CC   CC CT
                                |||||||||  ||   || ||
                                GCGGGTGGT GG   GG GA
                                     C  ACA  C
GAM1252  ASCL2    5'  CGCCTGCATCCACCCGCCCGCT 32160     __ _  A     A
                                CGCC  CA CTA CCCGCCC CT
                                ||||  || ||| ||||||| ||
                                GCGG  GT GGT GGGCGGG GA
                                  AC  A  _     C
GAM1252  ASCL2    5'  CGCCTGCATCCACCCGCCCGCT 32160     __ _  A     A
                                CGCC  CA CTA CCCGCCC CT
                                ||||  || ||| ||||||| ||
                                GCGG  GT GGT GGGCGGG GA
                                  AC  A  _     C
GAM1252  DDB2     3'  CCCTCTGCTACCACCCACT   32161    GCCCA  AC
                                CCC    CTA  CCGCCCACT
                                |||    |||  |||||||||
                                GGG    GAT  GGTGGGTGA
                                 AGAC_  __
GAM1252  EZH1     3'  CGCCTCTAACCCAGACCACT  32162     CA      C_
                                CGCC  CTAACCCG  CCACT
                                ||||  ||||||||  |||||
                                GCGG  GATTGGGT  GGTGA
                                  A_      CT
GAM1252  GSTM4    5'  ACCCGCCCCCTCGGCCCCGC  32163       A  AA__
                                ACCCGCCC CT   CCCGC
                                ||||||||  ||   |||||
                                TGGGCGGG GA   GGGCG
                                    G  GCCG
GAM1252  PHLDA1   5'  CCGCCTCTCGCCGCCCACT   32164     CA  AAC
                                CCGCC  CT   CCGCCCACT
                                |||||  ||   |||||||||
                                GGCGG  GA   GGCGGGTGA
                                  A_  GC_
GAM1252  RANBP2L1 5'  CCGCCCACGGAGGCCCACT   32165       TAACCC
                                CCGCCCAC     GCCCACT
                                ||||||||     |||||||
                                GGCGGGTG     CGGGTGA
                                    CCTC__
GAM1252  RARG     5'  ACCCGCCCTGCCTGGCCTGCCC 32166       A__  AA  C
           ACT                    ACCCGCCC   CT  CC GCCCACT
                                ||||||||   ||  || |||||||
                                TGGGCGGG   GA  GG CGGGTGA
                                    ACG  CC  A
GAM1252  C5orf3   5'  AACCCGCCCACAGGTTAACAGC 32167          ____   CC
                                AACCCGCCCAC   TAAC  GC
                                ||||||||||    ||||  ||
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                                TTGGGCGGGTG   ATTG  CG
                                      TCCA   T_
GAM1252  DKFZP434N014 3'  ACCCACTTGTCCTGGGCGCCTA 32168       AA_ ____   C
            CT                   GCCCACT   CC   CGCC ACT
                                 |||||||  ||   |||| |||
                                 TGGGTGA   GG   GCGG TGA
                                    ACA  ACCC   A
GAM1252  DMWD     5'  CCTCACCCACCGCCCACT    32169    _    CTAAC
                                 CC CGCCCA    CCGCCCACT
                                 || ||||||    |||||||||
                                 GG GTGGGT    GGCGGGTGA
                                  A    _____
GAM1252  FLJ20006  5'  AACCACGTCCGCCGCCCAC   32170     _ C  ACTAAC
                                 AACC CG CC     CCGCCCAC
                                 |||| || ||     ||||||||
                                 TTGG GC GG     GGCGGGTG
                                   T  A  C_____
GAM1252  FLJ20758  5'  AACCCGCCCGCCGACCCG    32171        A TA
                                 AACCCGCCC C  ACCCG
                                 |||||||||  |  |||||
                                 TTGGGCGGG G  TGGGC
                                      C GC
GAM1252  FLJ32940  5'  CCCGCCCAGCATCCGCTCACT  32172       CTAAC   C
                                 CCCGCCCA    CCGC CACT
                                 ||||||||    |||| ||||
                                 GGGCGGGT    GGCG GTGA
                                      CGTA_   A
GAM1252  HN1L     3'  AACCCTCTTCCCACCCCGCTCA 32173      G___    TAA    C
                                 AACCC   CCCAC   CCCGC CA
                                 |||||   |||||   ||||| ||
                                 TTGGG   GGGTG   GGGCG GT
                                    AGAA    ___    A
GAM1252  KIAA0356  3'  CCTGCCCACCAGCCACCCGCT  32174    C       AC     A
                                 CC GCCCACTA  CCGCCC CT
                                 || ||||||||  |||||| ||
                                 GG CGGGTGGT  GGTGGG GA
                                  A       C_     C
GAM1252  KIAA1674  5'  ACCTGCCGCGTCCCCGCCCACT 32175    C   CACTAA
                                 ACC GCC     CCCGCCCACT
                                 ||| |||     ||||||||||
                                 TGG CGG     GGGCGGGTGA
                                   A  CGCAG_
GAM1252  KIAA1796  5'  ACCCACTCTGAAGCCCGCCTGC 32176       AA____     CA
            T                    GCCCACT     CCCGCC  CT
                                 |||||||     ||||||  ||
                                 TGGGTGA     GGGCGG  GA
                                     GACTTC     AC
GAM1252  MGC13251  3'  CCCGCCCACCGCTCAC      32177        CTAAC   C
                                 CCCGCCCA    CCGC CAC
                                 ||||||||    |||| |||
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                                GGGCGGGT    GGCG GTG
                                   _____    A
GAM1252  NEDD5    3'  ACCTGCCCACTAGCCTATGC   32178    C      A  C__
                                ACC GCCCACTA CC   GC
                                ||| |||||||| ||   ||
                                TGG CGGGTGAT GG   CG
                                  A       C  ATA
GAM1252  LOC125929 3'  CCACTAACTACAACCACT    32179       C_  C
                                CCACTAAC  CG CCACT
                                ||||||||  || |||||
                                GGTGATTG  GT GGTGA
                                     AT  T
GAM1252  LOC145501 3'  AACCTTCTCACTAACCCCACT  32180     CGCC       GCC
                                AACC   CACTAACCC   CACT
                                ||||   |||||||||   ||||
                                TTGG   GTGATTGGG   GTGA
                                  AAGA       ___
GAM1252  LOC146223 3'  ACCCGCCCACTGGGCCAC    32181          AAC
                                ACCCGCCCACT   CCGC
                                ||||||||||   ||||
                                TGGGCGGGTGA   GGTG
                                      CCC
GAM1252  LOC146517 5'  AACTTCCCACTAAAATACTCGC 32182    CCG      ____  C
                                AAC   CCCACTA    AC CGC
                                |||   |||||||    || |||
                                TTG   GGGTGAT    TG GCG
                                  AA_      TTTA  A
GAM1252  LOC221954 5'  TGACCTCAGGTGATCCGCCCAC 32183   C   _  CTAAC_
            T                    C GCC CA     CCGCCCACT
                                | ||| ||     |||||||||
                                A TGG GT     GGCGGGTGA
                                 C   A  CCACTA
GAM1252  LOC51112  5'  ACCCTGCCACCCGCCCAC    32184     _   CACTA
                                ACCC GCC    ACCCGCCCAC
                                |||| |||    ||||||||||
                                TGGG CGG    TGGGCGGGTG
                                  A  _____
GAM1253  CNGB3    3'  CTGGGTGTTAGCAATGGGAT   32187      ___      C
                                CTGG   TTAGCAA GGGAT
                                ||||   ||||||| |||||
                                GACC   AATCGTT CCCTA
                                  CAC      A
GAM1253  DPYSL2   3'  GCAGGTGGTTAGCACCAG    32188     C       A
                                GCAG TGGTTAGCA CGG
                                |||| ||||||||| |||
                                CGTC ACCAATCGT GTC
                                  C       G
GAM1253  TRPV1    3'  CAGCAGCCCCCCGTGGCAACGG 32189        GG  A__
            G                    CAGCAGCT  TT   GCAACGGG
                                ||||||||  ||   ||||||||
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                                GTCGTCGG GG  CGTTGCCC
                                    GG CAC
GAM1253 TRPV1    3' CAGCAGCCCCCCGTGGCAACGG 32189      GG A__
           G                    CAGCAGCT TT  GCAACGGG
                                |||||||| ||  ||||||||
                                GTCGTCGG GG  CGTTGCCC
                                    GG CAC
GAM1253 TRPV1    3' CAGCAGCCCCCCGTGGCAACGG 32189      GG A__
           G                    CAGCAGCT TT  GCAACGGG
                                |||||||| ||  ||||||||
                                GTCGTCGG GG  CGTTGCCC
                                    GG CAC
GAM1253 TRPV1    3' CAGCAGCCCCCCGTGGCAACGG 32189      GG A__
           G                    CAGCAGCT TT  GCAACGGG
                                |||||||| ||  ||||||||
                                GTCGTCGG GG  CGTTGCCC
                                    GG CAC
GAM1253 B3GNT6   3' CAGAGAGGTAACGGGA    32190    C CT  TAGC
                                CAG AG GGT   AACGGGA
                                ||| || |||   |||||||
                                GTC TC CCA   TTGCCCT
                                  _ T_ ____
GAM1253 CRA      3' CAGCAATTTCAGTGGGAT   32191     CTGG  CAAC
                                CAGCAG  TTAG  GGGAT
                                ||||||  ||||  |||||
                                GTCGTT  AGTC  CCCTA
                                   AA__  A___
GAM1253 DKFZP434L0117 3' GCAGCTGGAGAGTGGGATC  32192      TT CAAC
                                GCAGCTGG AG  GGGATC
                                |||||||| ||  ||||||
                                CGTCGACC TC  CCCTAG
                                    TC A___
GAM1253 DKFZP566G1424 5' CAGTGGCTGGTTAGGGA    32193    CA     GCAAC
                                CAG GCTGGTTA   GGGA
                                ||| ||||||||   ||||
                                GTC CGACCAAT   CCCT
                                  AC     _____
GAM1253 FLJ11722 3' CAGCAGCTGGTGGTACAAAAT 32194        TAGCA
                                CAGCAGCTGGT   ACGGGAT
                                ||||||||||   |||||||
                                GTCGTCGACCA   TGTTTTA
                                     CCA__
GAM1253 FLJ21918 3' CAGGAGCTGGTTAGCCCCA  32195    C       AA
                                CAG AGCTGGTTAGC CG
                                ||| |||||||||| ||
                                GTC TCGACCAATCG GT
                                  C       GG
GAM1253 HEY1     3' CAGCAGCTGGTCAGATGGAT  32196         CAACG
                                CAGCAGCTGGTTAG   GGAT
                                ||||||||||||   ||||
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                                GTCGTCGACCAGTC    CCTA
                                      TA___
GAM1253  KIAA0152  3'  CAGTCAGCTGGGCTCAGTGGGA 32197    _     TTAG  AC
           TC                   CAG CAGCTGG   CA  GGGATC
                                ||| |||||||   ||  ||||||
                                GTC GTCGACC   GT  CCCTAG
                                  A     CGA_  CA
GAM1253  KIAA1884  3'  GCAGCTGGTGTAGTGGAC    32198        _  CAACG
                                GCAGCTGGT TAG    GGAT
                                ||||||||| |||    ||||
                                CGTCGACCA ATC    CCTG
                                     C   A____
GAM1253  MGC16175  3'  GCAGCTGGGTGGCAGGAC    32199       TTA   ACG
                                GCAGCTGG   GCA   GGAT
                                ||||||||   |||   ||||
                                CGTCGACC   CGT   CCTG
                                     CAC   ___
GAM1253  MGC26651  3'  ACAGTTTTATCCAACGGGAT   32200     CTGG   G_
                                GCAG   TTA  CAACGGGAT
                                ||||   |||  |||||||||
                                TGTC   AAT  GTTGCCCTA
                                  AA__   AG
GAM1253  OS4       3'  CAGCAGCTGGCTGGAGAAGGAT 32201          AGCAAC
                                CAGCAGCTGGTT     GGGAT
                                ||||||||||||     |||||
                                GTCGTCGACCGA     TCCTA
                                      CCTCT_
GAM1253  UBE2G1    3'  ACTATTGTTAGTGACGGGATC  32202     __    CA
                                GCTG  GTTAG  ACGGGATC
                                ||||  |||||  ||||||||
                                TGAT  CAATC  TGCCCTAG
                                  AA    AC
GAM1253  LOC134288 3'  GCAGCTGAGTTGTTTGGGAT   32203       _  AGCAAC
                                GCAGCTG GTT     GGGAT
                                ||||||| |||     |||||
                                CGTCGAC CAA     CCCTA
                                    T   CAAA__
GAM1253  LOC146669 5'  CAGCAGCTGGTTGGG       32204          AGCAAC
                                CAGCAGCTGGTT     GGG
                                ||||||||||||     |||
                                GTCGTCGACCAA     CCC
                                      _______
GAM1253  LOC153469 3'  GCTGGTTAGTACAGTAATC    32205        CA   _
                                GCTGGTTAG  ACGG GATC
                                |||||||||  |||| ||||
                                CGACCAATC  TGTC TTAG
                                     A_    A
GAM1253  LOC158490 3'  CAGCAGCTCCGATGGGAT    32206        __   TAGCAAC
                                CAGCAGCT  GGT     GGGAT
                                ||||||||  |||     |||||
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                                GTCGTCGA  CTA      CCCTA
                                    GG  _______
GAM1253  LOC203871 5'  GCAGCTGGCTCAGCGGG     32207          AG  A
                                GCAGCTGGTT  CA CGGG
                                ||||||||||  || ||||
                                CGTCGACCGA  GT GCCC
                                     __  C
GAM1253  LOC220827 3'  CAGCAGCTGGTGGAAT      32208          TAGCAAC
                                CAGCAGCTGGT      GGGAT
                                ||||||||||       |||||
                                GTCGTCGACCA      CCTTA
                                         _______
GAM1253  LOC253461 3'  CAGCAGCTGGTTGTGGAC    32209           AGCAACG
                                CAGCAGCTGGTT      GGAT
                                ||||||||||||      ||||
                                GTCGTCGACCAA      CCTG
                                      CA_____
GAM1253  LOC255196 5'  CAGTACTGATCAGTAGTGGGAT 32210     CA       CAAC
                                CAG  GCTGGTTAG    GGGAT
                                |||  |||||||||    |||||
                                GTC  TGACTAGTC    CCCTA
                                  A_       ATCA
GAM1254  PDK4     3'  TAGCATAAAGACAAAAACA   32213      C   AT
                                TAGCA AAA  CAAAAACA
                                ||||| |||  ||||||||
                                ATCGT TTT  GTTTTTGT
                                   A   CT
GAM1254  SORBS1   3'  GCACAGGCATTGAAAACAAAT  32214      AA_  CA
                                GCACA   AT  AAAACAAAT
                                |||||   ||  |||||||||
                                CGTGT   TA  TTTTGTTTA
                                   CCG  AC
GAM1254  C6orf33  3'  GCACAAAACCCACAAATCT   32215          AAAA
                                GCACAAAATC    ACAAATCT
                                ||||||||||    ||||||||
                                CGTGTTTTGG    TGTTTAGA
                                      G___
GAM1254  FLJ10188 3'  GCACCATACAAAAACAAAT   32216     AAAAT
                                GCAC    CAAAAACAAAT
                                ||||    ||||||||||||
                                CGTG    GTTTTTGTTTA
                                  GTAT_
GAM1254  FLJ23445 3'  GCATTTTAATAAAAACAAATCT 32217     CAAAATC
                                GCA      AAAAACAAATCT
                                |||      ||||||||||||
                                CGT      TTTTTGTTTAGA
                                  AAAATTA
GAM1254  KIAA1238 3'  TAGTACAACAAAAACAAATCT  32218     C    AAT
                                TAG ACAA   CAAAAACAAATCT
                                ||| ||||   ||||||||||||
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                                ATC TGTT   GTTTTTGTTTAGA
                                  A   ___
GAM1254  OR7C1     3'  GCACATCATAAAAACAAGTCT  32219      AA  C      A
                                GCACA  AT AAAAACAA TCT
                                |||||  || |||||||| |||
                                CGTGT  TA TTTTTGTT AGA
                                   AG  _      C
GAM1254  RIL       3'  TAGCACAAAATTGAAAACA   32220          CA
                                TAGCACAAAAT  AAAACA
                                ||||||||||  ||||||
                                ATCGTGTTTTA  TTTTGT
                                      AC
GAM1254  LOC149113 3'  GCATCAAACACCACAAATCT   32221    _   AT  AAA
                                GCA CAAA  CA   ACAAATCT
                                ||| ||||  ||   ||||||||
                                CGT GTTT  GT   TGTTTAGA
                                  A   __  GG_
GAM1254  LOC152790 5'  GCACATGCCGAAGACAAATCT  32222      AAA  A  A
                                GCACA   TC AA ACAAATCT
                                |||||   || || ||||||||
                                CGTGT   GG TT TGTTTAGA
                                   AC_  C  C
GAM1254  LOC154403 3'  GCATCAAACACCACAAATCT   32221    _   AT  AAA
                                GCA CAAA  CA   ACAAATCT
                                ||| ||||  ||   ||||||||
                                CGT GTTT  GT   TGTTTAGA
                                  A   __  GG_
GAM1254  LOC200170 3'  AGCACAAAATCACTGGGGATCT 32223          AAAACAA
                                AGCACAAAATCA      ATCT
                                ||||||||||||      ||||
                                TCGTGTTTTAGT      TAGA
                                      GACCCC_
GAM1254  LOC201868 3'  GCATCAAACACCACAAATCT   32221    _   AT  AAA
                                GCA CAAA  CA   ACAAATCT
                                ||| ||||  ||   ||||||||
                                CGT GTTT  GT   TGTTTAGA
                                  A   __  GG_
GAM1255  CYP2B6    3'  TCGATAATCTCACTCCT    32226    A   C
                                TC ATAA TCTCACTTTT
                                || |||| ||||||||||
                                AG TATT AGAGTGAGGA
                                 C   _
GAM1255  HMGCR     3'  TCAATAACTCTGCTGACCCCCT 32227          CA  TT   G
                                TCAATAACTCT  CT  TTT CT
                                ||||||||||  ||  ||| ||
                                AGTTATTGAGA  GA  GGG GA
                                      C_  CT   G
GAM1255  SORCS1    3'  TCAGTAACTCTCCTCCTTTA   32228    A      A
                                TCA TAACTCTC CTTTTTTG
                                ||| |||||||| ||||||||
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                                AGT ATTGAGAG GAGGAAAT
                                  C       _
GAM1255  TACC1    3'  TCAGAACTTTCACTCCCACTA  32229     AT    C     TT TG
                                TCA  AACT TCACTT  T  CTA
                                |||  |||| ||||||  |  |||
                                AGT  TTGA AGTGAG  G  GAT
                                  C_    A      __ GT
GAM1255  C4ST     3'  AATAATTCTCACTATGCT    32230       C      TTTT
                                AATAA TCTCACT    TGCT
                                ||||| |||||||    ||||
                                TTATT AGAGTGA    ACGA
                                   A      T___
GAM1255  FLJ11127 3'  TCAATAACTGTCATTTGCT    32231         C   CTTT
                                TCAATAACT TCA    TTTGCT
                                ||||||||| |||    ||||||
                                AGTTATTGA AGT    AAACGA
                                     C  ____
GAM1255  FLJ20152 3'  TCAGTAACTCTTCTCCCTT    32232     A      CA
                                TCA TAACTCT  CTTTTTT
                                ||| |||||||  |||||||
                                AGT ATTGAGA  GAGGGAA
                                  C      A_
GAM1255  HSPF2    5'  TCAGTGACCCTCACTCAGGCC  32233     ATA        TTTT
                                TCA   ACTCTCACTT    GCT
                                |||   ||||||||||    |||
                                AGT   TGGGAGTGAG    CGG
                                  CAC         TC__
GAM1255  KIAA0217 3'  ATAACTCTCATTTTCTTCT    32234         C     G
                                ATAACTCTCA TTTTTT CT
                                |||||||||| |||||| ||
                                TATTGAGAGT AAAGAA GA
                                     A     _
GAM1255  KIAA0417 3'  TCAGTAACTCTTCACTATCTG  32235     A      _    TT
                                TCA TAACTCT CACT  TTTG
                                ||| ||||||| ||||  ||||
                                AGT ATTGAGA GTGA  AGAC
                                  C      A    T_
GAM1255  KIAA0451 3'  TCAGTAGCTCTCTCTCTCT    32236     A  A    A
                                TCA TA CTCTC CTTTTT
                                ||| || ||||| ||||||
                                AGT AT GAGAG GAGAGA
                                  C  C     A
GAM1255  KIAA1317 3'  ATAACTCCACTCAAACTA    32237        T    TTTT
                                ATAACTC CACTT    GCTA
                                ||||||| |||||    ||||
                                TATTGAG GTGAG    TGAT
                                     _     TT__
GAM1255  MGC13033 3'  ACTCTCCAACTTTTTGCTA    32238       AC_
                                ACTCTC   TTTTTTGCTA
                                ||||||   ||||||||||
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                                TGAGAG   GAAAAACGAT
                                   GTT
GAM1255  PADI1    3'  TCAGTGACCTCACTCCGGGCTA 32239     ATA  T       TTT
                                TCA   AC CTCACTTT   GCTA
                                |||   || ||||||||   ||||
                                AGT   TG GAGTGAGG   CGAT
                                  CAC  _       CC_
GAM1255  SAMHD1   3'  TCAGTAACTCTCTAGAGGCTA  32240     A       ACTTTTTT
                                TCA TAACTCTC       GCTA
                                ||| ||||||||       ||||
                                AGT ATTGAGAG       CGAT
                                  C       ATCTC___
GAM1255  LOC143915 3'  CCAATAATTCTCACTATCTTGC 32241        C       T
              T                    TCAATAA TCTCACT TTTTGCT
                                |||||||  |||||||  |||||||
                                GGTTATT AGAGTGA AGAACGA
                                     A      T
GAM1255  LOC147123 3'  TCCACACATTACTTTTTTGCT  32242    AATA  TCTC
                                TC    AC    ACTTTTTTGCT
                                ||    ||    ||||||||||
                                AG    TG    TGAAAAAACGA
                                 GTG_  TAA_
GAM1255  LOC148255 3'  AATAACTCTGAGCCTGCTA    32243         CACTTT
                                AATAACTCT      TTTGCTA
                                |||||||||      |||||||
                                TTATTGAGA      GGACGAT
                                     CTC___
GAM1255  LOC150848 5'  TCAACAACTCTCACTTCCCTG  32244
                                TCAATAACTCTCACTTTTTTG
                                |||||||||||||||||||
                                AGTTGTTGAGAGTGAAGGGAC

GAM1256  FLJ23563  3'  TATCAGCAAAACTGGT      32247        AATTTA
                                TATTAG     CAAAACTGGT
                                ||||||     ||||||||||
                                ATAGTC     GTTTTGACCA
                                   _______
GAM1256  HCA127    3'  TACTAGAATTTGCAAAGACTAG 32248           A   _
                                TATTAGAATTT CAAA ACTGG
                                |||||||||| |||| |||||
                                ATGATCTTAAA GTTT TGATC
                                      C   C
GAM1256  KIAA0893  3'  TTAGAATCTACAAAGCTG    32249            A
                                TTAGAATTTACAAA CTG
                                |||||||||||||| |||
                                AATCTTAGATGTTT GAC
                                        C
GAM1256  KIAA1323  3'  TATCAGTCACCTTGAAACTGGT 32250       A_   ACA
              AA                   TATTAG  ATTT   AAACTGGTAA
                                ||||||  ||||   ||||||||||
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                                ATAGTC  TGGA   TTTGACCATT
                                   AG    AC_
GAM1256 KIAA1576 3' ATTGAAATTTACAGAATTGGTA 32251     AG       A  C
             A                   ATT  AATTTACA AA TGGTAA
                                 |||  |||||||| || ||||||
                                 TAA  TTAAATGT TT ACCATT
                                   CT       C  A
GAM1256 PRO2533  3' TATCAGTACGGAACTGGTAA  32252       AATT   AA
                                 TATTAG    TAC  AACTGGTAA
                                 ||||||    |||  ||||||||||
                                 ATAGTC    ATG  TTGACCATT
                                    ____   CC
GAM1256 LOC196559 5' GATTACAAAATTGGTA      32253     AT       C
                                 GA  TTACAAAA TGGTA
                                 ||  |||||||| |||||
                                 CT  AATGTTTT ACCAT
                                   __       A
GAM1256 LOC96810  3' TATTAGAATAACTGGT      32254         TTACAA
                                 TATTAGAAT     AACTGGT
                                 |||||||||     |||||||
                                 ATAATCTTA     TTGACCA
                                      _______
GAM1257 ADAM19   3' TCTCCACAGCAAGGATGAC   32257      T      T_
                                 TCTC CACAGCA  GATGAC
                                 |||| |||||||  ||||||
                                 AGAG GTGTCGT  CTACTG
                                   _      TC
GAM1257 DLG5     5' TCTCCCACAGCAAGGGAC    32258          TGAT
                                 TCTCTCACAGCA    GAC
                                 ||||||||||||    |||
                                 AGAGGGTGTCGT    CTG
                                        TCC_
GAM1257 GJA1     3' TCTCTCACATTAATGAC     32259         GCA
                                 TCTCTCACA   TGATGAC
                                 |||||||||   |||||||
                                 AGAGAGTGT   ATTACTG
                                      A__
GAM1257 NFE2     5' TCTTTCCAAGATGATGAC    32260     C  A   C
                                 TCT TC CAG ATGATGAC
                                 ||| || ||| ||||||||
                                 AGA AG GTT TACTACTG
                                   A  _   C
GAM1257 P23      3' CCTCTCACAGGCTGGGGTGA  32261         CA  A__
                                 TCTCTCACAG  TG   TGA
                                 ||||||||||  ||   |||
                                 GGAGAGTGTC  AC   ACT
                                       CG  CCC
GAM1257 PFC      5' TCTCTAACATAATGAC      32262       CAC
                                 TCTCT   AGCATGATGAC
                                 |||||   ||||||||||
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                                AGAGA   TTGTATTACTG
                                  ___
GAM1257  PLGL     3'  TCCCTCACAGACACAGAC    32263          _  _
                                TCTCTCACAG CAT GAT
                                |||||||||| ||| |||
                                AGGGAGTGTC GTG CTG
                                      T   T
GAM1257  RARB     5'  TCCCTCACAGGCGCTGAC    32264          _ A_
                                TCTCTCACAG C  TGAT
                                |||||||||| |  ||||
                                AGGGAGTGTC G  ACTG
                                      C CG
GAM1257  RP42     3'  TCTCTCACAGACACAGAC    32265          _  _
                                TCTCTCACAG CAT GAT
                                |||||||||| ||| |||
                                AGAGAGTGTC GTG CTG
                                      T   T
GAM1257  STXBP1   3'  CTCTTACAAACACGATGA    32266      C   _
                                CTCT ACAG CATGATGA
                                |||| |||| ||||||||
                                GAGA TGTT GTGCTACT
                                  A   T
GAM1257  ADPRTL3  3'  TCTTGTACAGCATGGTGAC   32267     CTC       A
                                TCT   ACAGCATG TGAC
                                |||   |||||||| ||||
                                AGA   TGTCGTAC ACTG
                                  ACA       C
GAM1257  AK5      3'  TCTCTTAGCCATAATGAC    32268      CAC   _
                                TCTCT   AGC ATGATGAC
                                |||||   ||| ||||||||
                                AGAGA   TCG TATTACTG
                                   A__   G
GAM1257  BAGE     3'  TCTTCACAGCATTTGA      32269     C       GA
                                TCT TCACAGCAT  TGA
                                ||| |||||||||  |||
                                AGA AGTGTCGTA  ACT
                                  _       A_
GAM1257  C20orf82 3'  TCTCTCACAGACGTGA      32270          C   A
                                TCTCTCACAG ATG TGA
                                |||||||||| ||| |||
                                AGAGAGTGTC TGC ACT
                                      _  _
GAM1257  CHK      3'  TCTCCCACAAGAATGATGA    32271          C_
                                TCTCTCACAG  ATGATGA
                                ||||||||||  |||||||
                                AGAGGGTGTT  TACTACT
                                      CT
GAM1257  DKFZP434A236 3'  TCTCCACAGCAATGAC      32272      T      TG
                                TCTC CACAGCA  ATGAC
                                |||| |||||||  |||||
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                                AGAG GTGTCGT  TACTG
                                  _     __
GAM1257  DKFZp566H0824 5'  TCTCTCACTCAGCTGTGAC   32273        __  A  A
                                TCTCTCAC  AGC TG TGAC
                                ||||||||  ||| || ||||
                                AGAGAGTG  TCG AC ACTG
                                    AG  _ _
GAM1257  DRCTNNB1A 3'  TCTCTCACTCTGAATGATGAC  32274        AGC__
                                TCTCTCAC    ATGATGAC
                                ||||||||    ||||||||
                                AGAGAGTG    TACTACTG
                                    AGACT
GAM1257  ELKS     3'  TCTCCACTGCTGATGAC     32275     T  A  A
                                TCTC CAC GC TGATGAC
                                |||| ||| || |||||||
                                AGAG GTG CG ACTACTG
                                  _  A  _
GAM1257  FLJ10420  3'  TCTCTCACATCAAGAGGAC   32276        G  T  T
                                TCTCTCACA CA GA GAC
                                ||||||||| || || |||
                                AGAGAGTGT GT CT CTG
                                    A  T  C
GAM1257  FLJ11004  3'  TCTCCCCAGATGATGAC     32277       A   C
                                TCTCTC CAG ATGATGAC
                                |||||| ||| ||||||||
                                AGAGGG GTC TACTACTG
                                  _  _
GAM1257  FLJ12577  3'  TCTTCCCAAGAATGATGAC   32278     _   C  C
                                TCT CTCA AG ATGATGAC
                                ||| |||| || ||||||||
                                AGA GGGT TC TACTACTG
                                  A   _ T
GAM1257  FLJ13639  3'  TCTCACAGGACCTTGATGAC  32279        CA___
                                TCTCACAG    TGATGAC
                                ||||||||    |||||||
                                AGAGTGTC    ACTACTG
                                    CTGGA
GAM1257  FLJ22215  3'  CCTCTCACAGCAAGAAGA    32280          T  T
                                TCTCTCACAGCA GA GA
                                |||||||||||| || ||
                                GGAGAGTGTCGT CT CT
                                      T  T
GAM1257  FLJ22215  5'  CCTCTCACAGCAAGAAGA    32280          T  T
                                TCTCTCACAGCA GA GA
                                |||||||||||| || ||
                                GGAGAGTGTCGT CT CT
                                      T  T
GAM1257  GMPPB    5'  CCCCTCACATGATGA       32281         GCA
                                TCTCTCACA   TGATGA
                                |||||||||   ||||||
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                                GGGGAGTGT   ACTACT
                                    ___
GAM1257  KIAA0565  3'  TCATTCACATATGATGAC    32282    TC    GC
                                TC  TCACA  ATGATGAC
                                ||  |||||  ||||||||
                                AG  AGTGT  TACTACTG
                                 TA    A_
GAM1257  KIAA0596  3'  CCTCTCACAGCACCAAGATGAC 32283          ___
                                TCTCTCACAGCAT   GATGAC
                                ||||||||||||   ||||||
                                GGAGAGTGTCGTG   CTACTG
                                       GTT
GAM1257  MGC17299  5'  CCTCTCACAGTCCAGGAT    32284         __ T
                                TCTCTCACAG  CA GAT
                                ||||||||||  || |||
                                GGAGAGTGTC  GT CTA
                                      AG  C
GAM1257  PFTK1     3'  TCTTCCCAGAATGATGAC    32285     CT A   C
                                TCT  C CAG ATGATGAC
                                |||  | ||| ||||||||
                                AGA  G GTC TACTACTG
                                  AG _   T
GAM1257  PIGQ      3'  TCTGCTCACTCCCAATGAC   32286     _    AGCA
                                TCT CTCAC    TGATGAC
                                ||| |||||    |||||||
                                AGA GAGTG    GTTACTG
                                  C    AGG_
GAM1257  PP3501    3'  TCTCTCACTGAGCGTGAC    32287        __  A
                                TCTCTCAC  AGC TGAT
                                ||||||||  ||| ||||
                                AGAGAGTG  TCG ACTG
                                     AC   C
GAM1257  TTTY2     5'  CCTCTCACAGGTGCAGAT    32288        ___  T
                                TCTCTCACA   GCA GAT
                                |||||||||   ||| |||
                                GGAGAGTGT   CGT CTA
                                     CCA  _
GAM1257  TTTY2     5'  TCTCTCACTCATGTAGATGA   32289       AG  ___
                                TCTCTCAC  CAT   GATGA
                                ||||||||  |||   |||||
                                AGAGAGTG  GTA   CTACT
                                     A_   CAT
GAM1257  LOC118472 3'  TCCCTCACAGCTTCTGATGAC  32290         A__
                                TCTCTCACAGC   TGATGAC
                                ||||||||||   |||||||
                                AGGGAGTGTCG   ACTACTG
                                       AAG
GAM1257  LOC145387 3'  TCTCTCACAGATGCAATGAC   32291         C  __
                                TCTCTCACAG ATG  ATGAC
                                |||||||||| |||  |||||
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                                AGAGAGTGTC TAC  TACTG
                                      _  GT
GAM1257  LOC145945 5'  TCTCTCACAATATATGTGTGAT 32292         CA_____
              G                  TCTCTCACAG       TGATG
                                 ||||||||||       |||||
                                 AGAGAGTGTT       ACTAC
                                       ATATACAC
GAM1257  LOC158382 5'  TCTCTCACCATGTGA       32293        AG   A
                                 TCTCTCAC  CATG TGA
                                 ||||||||  |||| |||
                                 AGAGAGTG  GTAC ACT
                                    __   _
GAM1257  LOC159148 5'  CCTCTCACAGGTGCAGAT    32288        ___  T
                                 TCTCTCACA   GCA GAT
                                 |||||||||   ||| |||
                                 GGAGAGTGT   CGT CTA
                                       CCA  _
GAM1257  LOC159148 5'  TCTCTCACTCATGTAGATGA   32289       AG  ___
                                 TCTCTCAC  CAT   GATGA
                                 ||||||||  |||   |||||
                                 AGAGAGTG  GTA   CTACT
                                      A_   CAT
GAM1257  LOC159371 5'  TCTCTACAGCATGGAC      32294      C      AT
                                 TCTCT ACAGCATG  GAC
                                 ||||| ||||||||  |||
                                 AGAGA TGTCGTAC  CTG
                                    _      __
GAM1257  LOC197285 3'  TCTCCCACAGCGCTGTGA    32295         A_  A
                                 TCTCTCACAGC  TG TGA
                                 ||||||||||  ||  |||
                                 AGAGGGTGTCG  AC ACT
                                       CG  _
GAM1257  LOC203292 3'  CCTCTCACAGGCTGGGGTGA  32261         CA  A__
                                 TCTCTCACAG  TG   TGA
                                 ||||||||||  ||   |||
                                 GGAGAGTGTC  AC   ACT
                                       CG  CCC
GAM1257  LOC221632 3'  TCTTCACCATGATGA       32296     C   AG
                                 TCT TCAC  CATGATGA
                                 ||| ||||  ||||||||
                                 AGA AGTG  GTACTACT
                                   _   __
GAM1257  LOC255187 3'  TCTCTGCAGTCATCTTGAC   32297      CA  _  GA
                                 TCTCT  CAG CAT  TGAC
                                 |||||  ||| |||  ||||
                                 AGAGA  GTC GTA  ACTG
                                    C_   A   GA
GAM1257  LOC256207 3'  TCATTCACATATGATGAC    32282    TC    GC
                                 TC  TCACA  ATGATGAC
                                 ||  |||||  ||||||||
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                                AG  AGTGT  TACTACTG
                                 TA    A_
GAM1257  LOC257282 5'  TCCCTCACAGGCAATGAC    32298         CAT
                                TCTCTCACAG   GATGAC
                                ||||||||||   ||||||
                                AGGGAGTGTC   TTACTG
                                     CG_
GAM1257  LOC51716  3'  CTCTCCAGATGATGAC      32299      A   C
                                CTCTC CAG ATGATGAC
                                ||||| ||| ||||||||
                                GAGAG GTC TACTACTG
                                  _  _
GAM1257  LOC59346  3'  TCTCCCACAGTCCAAGAC    32300         CA   T
                                TCTCTCACAG  TGA GAC
                                ||||||||||  ||| |||
                                AGAGGGTGTC  GTT CTG
                                     AG  _
GAM1257  LOC90784  5'  TCTGTCATGGCACGATGAC    32301     C   CA
                                TCT TCA  GCATGATGAC
                                ||| |||  ||||||||||
                                AGA AGT  CGTGCTACTG
                                  C   AC
GAM1257  LOC91801  3'  TCCCTCACGGAACACATG     32302         __    G
                                TCTCTCAC  AGCAT ATG
                                ||||||||  ||||| |||
                                AGGGAGTG  TTGTG TAC
                                     CC    _
GAM1258  POU2AF1   3'  ATTAAAATTAAACCTAATG    32305       CTAC
                                ATTAGA    AAACCTAATG
                                ||||||    ||||||||||
                                TAATTT    TTTGGATTAC
                                   TAA_
GAM1258  C20orf21  3'  CTAAATACAAGTCTAATGATA  32306      C    AC
                                TTAGA TACAA  CTAATGATA
                                ||||| |||||  |||||||||
                                GATTT ATGTT  GATTACTAT
                                   _    CA
GAM1258  FLJ10813  3'  TATCAGACTACAAACACCA    32307           _
                                TATTAGACTACAAAC CTA
                                |||||||||||||| |||
                                ATAGTCTGATGTTTG GGT
                                          T
GAM1258  KIAA0608  3'  TTAGACTAGAACCAGAATG    32308         CA   T_
                                TTAGACTA  AACC  AATG
                                ||||||||  ||||  ||||
                                AATCTGAT  TTGG  TTAC
                                     C_   TC
GAM1258  SLC21A8   5'  TATTAAACTACAGATACC     32309          A__
                                TATTAGACTACA   ACC
                                ||||||||||||   |||
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                                ATAATTTGATGT   TGG
                                       CTA
GAM1258  SLC26A7   3'  TATTAGACTACATGAT     32310          AACCTAA
                                TATTAGACTACA      TGAT
                                ||||||||||||      ||||
                                ATAATCTGATGT      ACTA
                                          _______
GAM1259  HSA275986 3'  CCATGATGAAGCCTATTTG   32313    T   CA  A
                                CC TGA  AA CCTATTTG
                                || |||  || ||||||||
                                GG ACT  TT GGATAAAC
                                 T   AC  C
GAM1259  KIAA0451  3'  CTTGGCAAGGCCTACCTG    32314     A   AA
                                CTTG CAA  CCTATTTG
                                |||| |||  ||||||||
                                GAAC GTT  GGATGGAC
                                  C   CC
GAM1259  MEGF11    3'  CTGACCATGAACCTATTTG    32315     AA__
                                TTGAC    AACCTATTTG
                                |||||    ||||||||||
                                GACTG    TTGGATAAAC
                                   GTAC
GAM1259  LOC146243 3'  AACCTTGACAGAACAGCCCTG  32316         A   CTA
                                AACCTTGACA AAC   TTTG
                                |||||||||| |||   ||||
                                TTGGAACTGT TTG   GGAC
                                      C   TCG
GAM1259  LOC146839 5'  TCAAATCTTAACAAAGCTATCT 32317      C       AC
                                TCAAA CTTGACAAA  CTATTT
                                ||||| |||||||||  ||||||
                                AGTTT GAATTGTTT  GATAGA
                                   A       C_
GAM1259  LOC148764 3'  TCGAACCCTGACATTTTTATTA 32318    A       AAACC__
            TTTG                   TC AACCTTGACA      TATTTG
                                || ||||||||||      ||||||
                                AG TTGGGACTGT      ATAAAC
                                 C         AAAAATA
GAM1259  LOC200107 3'  TCAAACCTGACGAAAAGGTACT 32319        T   _   CC
            TG                     TCAAACCT GAC AAAA  TATTTG
                                ||||||| ||| ||||  ||||||
                                AGTTTGGA CTG TTTT  ATGAAC
                                     _  C   CC
GAM1259  LOC256730 3'  TCAGATCTTGGAAAACCCACT  32320    AAC   AC
                                TCA   CTTG  AAAACCTATT
                                |||   ||||  ||||||||||
                                AGT   GAAC  TTTTGGGTGA
                                  CTA   C_
GAM1260  PMP2      3'  TGTATTCAGTTTTGTCAATGG  32323        A  C   TTCA
                                TGTATTCAG TT GTT    GG
                                ||||||||| || |||    ||
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                                ACATAAGTC AA CAG    CC
                                     A  A   TTA_
GAM1260  EST-YD1   3'  AATGTATTTAATTCTTCCAGG  32324        CA    GT
                                AATGTATT  GATTC  TTTCAGG
                                ||||||||  |||||  |||||||
                                TTACATAA  TTAAG  AAGGTCC
                                    A_    __
GAM1260  FLJ10716  3'  AATGTATTCAGGCTCCAG    32325          ATTC    T
                                AATGTATTCAG    GTTT CAG
                                ||||||||||    |||| |||
                                TTACATAAGTC    CGAG GTC
                                      ____   _
GAM1260  KIAA0410  3'  AATGTCTTCAGTTTTTCAG   32326       A    ATTCG
                                AATGT TTCAG    TTTTCAG
                                |||||  |||||    |||||||
                                TTACA AAGTC    AAAAGTC
                                   G    A____
GAM1260  KRT20     3'  AATGTATTGCAATTTTCAG   32327         _ GATTC
                                AATGTATT CA    GTTTTCAG
                                ||||||||  ||    ||||||||
                                TTACATAA GT    TAAAAGTC
                                    C  _____
GAM1260  NFX1      3'  ATGTTTCAGGCATTTTCAGG  32328      A    ATT
                                ATGT TTCAG   CGTTTTCAGG
                                ||||  |||||  ||||||||||
                                TACA AAGTC   GTAAAAGTCC
                                  _    C__
GAM1260  PRO1866   5'  AATGTGTTAGTCCATTTTCAGG 32329      A  C  A
                                AATGT TT AG TTCGTTTTCAGG
                                |||||  ||  ||  ||||||||||||
                                TTACA AA TC AGGTAAAAGTCC
                                   C  _  _
GAM1260  PRO2405   3'  GTATTCAGGTTCTTCCGGG   32330        A   GT    A
                                GTATTCAG TTC  TTTC GG
                                ||||||||  |||  ||||  ||
                                CATAAGTC AAG  AAGG CC
                                    C   __    C
GAM1260  LOC145453 3'  AATGTGCTCAGATTACAG    32331       A       CGTTTT
                                AATGT TTCAGATT      CAG
                                |||||  ||||||||      |||
                                TTACA GAGTCTAA      GTC
                                   C       T_____
GAM1260  LOC92912  3'  AATGTATTCAAGATTTAGCCTT 32332          _   C_    C
            AGG                    AATGTATTCA GATT  GTTTT AGG
                                ||||||||||  ||||  |||||  |||
                                TTACATAAGT CTAA  CGGAA TCC
                                     T    AT    _
GAM1261  DPYSL2    3'  TCTGCGGTTCCACGTGTGA   32335       AA   __    C
                                TCTGC  TTCC  GTGT GA
                                |||||  ||||  ||||  ||
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                                AGACG  AAGG  CACA CT
                                  CC    TG   _
GAM1261  HNRPK    5'  TCTGCAATGCTGTCGCCTG   32336       TCCG    A_
                                TCTGCAAT   TGTCG  TG
                                ||||||||   |||||  ||
                                AGACGTTA   ACAGC  AC
                                    CG__    GG
GAM1261  LENG4    3'  TCTGCAATATTGGTGCGATGA  32337       TCC_  T
                                TCTGCAAT   GTG CGATGA
                                ||||||||   ||| ||||||
                                AGACGTTA   CAC GCTACT
                                    TAAC  _
GAM1261  MMP1     3'  TGCAACTCTGGCCTATATGA  32338       CGT  G__
                                TGCAATTC   GTC  ATGA
                                ||||||||   |||  ||||
                                ACGTTGAG   CGG  TACT
                                    AC_  ATA
GAM1261  TBL2     3'  GCAATGCCAATGTCGATGA   32339      T  _
                                GCAAT CCG TGTCGATGA
                                ||||| ||| |||||||||
                                CGTTA GGT ACAGCTACT
                                  C  T
GAM1261  DKFZp547J036 3'  TGCAATTCTCAGTTCCGATG  32340       _ _ GT
                                TGCAATTC C GT  CGATG
                                |||||||| | ||  |||||
                                ACGTTAAG G CA  GCTAC
                                    A T  AG
GAM1261  FLJ10052  3'  TCTGCAATGTCGATG      32341      ATTCC
                                TCTGCA    GTGTCGATG
                                ||||||    |||||||||
                                AGACGT    TACAGCTAC
                                   _____
GAM1261  FLJ23293  3'  TACAATTCCTATGAGATG    32342        _  TC
                                TGCAATTCC GTG  GATG
                                ||||||||| |||  ||||
                                ATGTTAAGG TAC  CTAC
                                    A  T_
GAM1261  KIAA0202  3'  TCTCCAGTTCCATGCCCTG   32343    G  A      GA
                                TCT CA TTCCGTGTC  TG
                                ||| || |||||||||  ||
                                AGA GT AAGGTACGG  AC
                                  G  C       G_
GAM1261  KIAA0265  3'  TCTACAATTCCCCATG     32344         GTGT G
                                TCTGCAATTCC   C ATG
                                ||||||||||   | |||
                                AGATGTTAAGG   G TAC
                                      ____ G
GAM1261  KIAA0712  5'  TCTGCATTCCGTACAA     32345      A     T
                                TCTGCA TTCCGTG CGA
                                |||||| ||||||| |||
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                                AGACGT AAGGCAT GTT
                                      _     _
GAM1261  UNC5D     3'  TCTGCAATGTTTCATG      32346        TCC  G  G
                                TCTGCAAT   GT TC ATG
                                ||||||||   || || |||
                                AGACGTTA   CA AG TAC
                                     ____  A  _
GAM1261  LOC151963 3'  TGCAATTCTGACAATG      32347        CG  T
                                TGCAATTC  TG CGATG
                                ||||||||  || |||||
                                ACGTTAAG  AC GTTAC
                                     __  T
GAM1261  LOC201931 3'  TCTGCAATTGCTGTCATGA   32348         CCG   G
                                TCTGCAATT   TGTC ATGA
                                |||||||||   |||| ||||
                                AGACGTTAA   ACAG TACT
                                      CG_   _
GAM1261  LOC221272 3'  TCTGCAATTTGGTGTGA     32349        CC   C
                                TCTGCAATT  GTGT GA
                                |||||||||  |||| ||
                                AGACGTTAA  CACA CT
                                      AC   _
GAM1261  LOC256471 3'  TCTGCAATATCTGTAGTC    32350        _  C  _
                                TCTGCAAT TC GT GTC
                                |||||||| || || |||
                                AGACGTTA AG CA CAG
                                      T  A  T
GAM1261  LOC57805  3'  TCTTCAATTCCGTTCACTGA  32351    G       G  A
                                TCT CAATTCCGT TCG TGA
                                ||| |||||||||| ||| |||
                                AGA GTTAAGGCA AGT ACT
                                  A        _  G
GAM1261  LOC58525  5'  CCCGCAGCGTGTCGATG     32352      ATTC
                                TCTGCA   CGTGTCGATG
                                ||||||   ||||||||||
                                GGGCGT   GCACAGCTAC
                                   C___
GAM1261  LOC89953  5'  TCTGCAATCTGCCGGTG     32353        CCG    A
                                TCTGCAATT   TGTCG TG
                                |||||||||   ||||| ||
                                AGACGTTAG   ACGGC AC
                                     ___    C
GAM1262  CDY1      3'  AATTGTGTGTCTCTGA      32356        A   GTTAC
                                AATTGTGTG TCTC    TGA
                                ||||||||| ||||    |||
                                TTAACACAC AGAG    ACT
                                     _   _____
GAM1262  CDY1      3'  AATTGTGTGTCTCTGA      32356        A   GTTAC
                                AATTGTGTG TCTC    TGA
                                ||||||||| ||||    |||
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                                TTAACACAC AGAG    ACT
                                      _  _____
GAM1262  DMXL1    3'  TGTGAAGAAATTACTGAAA   32357      TCTC
                                TGTGA   GTTACTGAAA
                                |||||   ||||||||||
                                ACACT   TAATGACTTT
                                   TCTT
GAM1262  DNMT2    3'  TGTGATTGTTTACTGAAA    32358      CTCG
                                TGTGAT   TTACTGAAA
                                ||||||   |||||||||
                                ACACTA   AATGACTTT
                                   ACA_
GAM1262  ZFHX1B   3'  AATTGTGTGGTTACT      32359       ATCTC
                                AATTGTGTG    GTTACT
                                |||||||||    ||||||
                                TTAACACAC    CAATGA
                                      _____
GAM1262  BLCAP    3'  TTGCCAACACTTGTTACTGAA  32360     GTGAT  C
                                TTGT    CT GTTACTGAA
                                ||||    || |||||||||
                                AACG    GA CAATGACTT
                                  GTTGT  A
GAM1262  CALN1    3'  TGTGTGACGTGCTGAA     32361      TCT   TA
                                TGTGTGA   CGT  CTGAA
                                |||||||   |||  |||||
                                ACACACT   GCA  GACTT
                                   ___   C_
GAM1262  FLJ14251 3'  GTGTGATCTCAGCTCGCTGAAA 32362         _   A_
                                GTGTGATCTC GTT  CTGAAA
                                |||||||||| |||  ||||||
                                CACACTAGAG CGA  GACTTT
                                      T   GC
GAM1262  KIAA0368 3'  TGTGTGATCTTGTCCTAA    32363         C   A
                                TGTGTGATCT GTT CTGA
                                |||||||||| ||| ||||
                                ACACACTAGA CAG GATT
                                      A   _
GAM1262  PRO1768  3'  AATTATGTGATTGTACTTGA  32364         CTC  T   _
                                AATTGTGTGAT   GT ACT GA
                                ||||||||||   || ||| ||
                                TTAATACACTA   CA TGA CT
                                      A__  _   A
GAM1262  LOC158332 3'  AACTGTGTGGTTCCTTCTG   32365        ATC  G  A
                                AATTGTGTG   TC TT CTG
                                |||||||||   || || |||
                                TTGACACAC   AG AA GAC
                                      CA_  G  _
GAM1262  LOC221810 3'  TTGTGTAAATTACTGAA     32366        TCTC
                                TTGTGTGA    GTTACTGAA
                                ||||||||    |||||||||
```

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                                AACACATT   TAATGACTT
                                    ____
GAM1262  LOC222681 3'  AATTGTGTGGTCTTCTCATT  32367       A___
                                AATTGTGTG   TCTCGTT
                                |||||||||   |||||||
                                TTAACACAC   AGAGTAA
                                     CAGA
GAM1262  LOC257507 3'  AATTGTGTGGTCTTCTCATT  32367       A___
                                AATTGTGTG   TCTCGTT
                                |||||||||   |||||||
                                TTAACACAC   AGAGTAA
                                     CAGA
GAM1262  LOC257625 3'  AATTGTGTGGTCTTCTCATT  32367       A___
                                AATTGTGTG   TCTCGTT
                                |||||||||   |||||||
                                TTAACACAC   AGAGTAA
                                     CAGA
GAM1263  COP     3'  GAAAGCAAAGCTTGATT    32370    TCTA
                                GAA   CGAAGCTTGATT
                                |||   ||||||||||||
                                CTT   GTTTCGAACTAA
                                  TC__
GAM1263  KIAA0694  3'  CATGAATCTATCTTGAT    32371        CGAAG
                                CATGAATCTA    CTTGAT
                                ||||||||||    ||||||
                                GTACTTAGAT    GAACTA
                                     A_____
GAM1263  SMOC2    3'  TCTGTGGCTCCAAAGGCTTGAT 32372    CA  AA   C  A
            T                    TC  TG  TCTA GA GCTTGATT
                                 ||  ||  |||| || ||||||||
                                 AG  AC  AGGT TT CGAACTAA
                                  AC  CG   _  C
GAM1263  LOC144871 3'  CATGAATCAGCGAAACAACAGA 32373       TA    TT__
            TT                    CATGAATC  CGAAGC   GATT
                                  ||||||||  ||||||   ||||
                                  GTACTTAG  GCTTTG   CTAA
                                       TC     TTGT
GAM1263  LOC151325 3'  CAGGAACACAGAGGCTTGATT  32374    T   C  C  A
                                  CA GAAT TA GA GCTTGATT
                                  || |||| || || ||||||||
                                  GT CTTG GT CT CGAACTAA
                                   C   T  _  C
GAM1263  LOC220930 3'  TCCATAGTCTATGACCTGATT  32375      AA   C AA
                                  TCCATG  TCTA G  GCTTGATT
                                  ||||||  |||| |  ||||||||
                                  AGGTAT  AGAT C  TGGACTAA
                                     C_   A __
GAM1264  ABCC3    3'  AGGGAGCGAGGGAGGCGGC   32378       C  A   AGTCCT
                                  AGGGAGCG GG AGG     GC
                                  |||||||| || |||     ||
```

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                                TCCCTCGC CC TCC     CG
                                    T C   GC____
GAM1264  ACP2    3'  AGGGAGCGTGGAGGAGGCAAAT 32379        C   A   _____
            CCTG                  AGGGAGCG GGA GGAG    TCCTG
                                |||||||| ||| ||||    |||||
                                TCCCTCGC CCT CCTC    AGGAC
                                    A   _   CGTTT
GAM1264  ARIH1   5'  AGGGAGCGAGGGGGCCGCTTGC 32380        C  AA  A   _ _
            T                   AGGGAGCG GG  GG GTC CT GCT
                                |||||||| ||  || ||| || |||
                                TCCCTCGC CC  CC CGG GA CGA
                                    T __  _   C  A
GAM1264  BMP1    3'  AGGGATGGCGATGGGGTCCTGC 32381      GC    AA  A
            T                   AGGGA  GCGG  GG GTCCTGCT
                                |||||  ||||  || ||||||||
                                TCCCT  CGCT  CC CAGGACGA
                                   AC    AC  _
GAM1264  ENG     3'  GGCGAGCGCGGGGGGCCGGGGC 32382    _      AA  A   CT_
            T                   GG GAGCGCGG  GG GTC   GCT
                                || ||||||||  || |||   |||
                                CC CTCGCGCC  CC CGG   CGA
                                 G       C_ _   CCC
GAM1264  EPB49   3'  AGGGAGGCGGAAGGCCCAGCT  32383       C       AG   T
                                AGGGAG GCGGAAGG  TCC GCT
                                |||||| ||||||||  ||| |||
                                TCCCTC CGCCTTCC  GGG CGA
                                   _       __   T
GAM1264  GAB2    3'  AGGGGGCTGGAAGGAAGCCT   32384     A  GC      T
                                AGGG GC  GGAAGGAG CCT
                                |||| ||  |||||||| |||
                                TCCC CG  CCTTCCTT GGA
                                  C  A_       C
GAM1264  GAB2    3'  AGGGGGCTGGAAGGAAGCCT   32384     A  GC      T
                                AGGG GC  GGAAGGAG CCT
                                |||| ||  |||||||| |||
                                TCCC CG  CCTTCCTT GGA
                                  C  A_       C
GAM1264  GAB2    3'  AGGGGGCTGGAAGGAAGCCT   32384     A  GC      T
                                AGGG GC  GGAAGGAG CCT
                                |||| ||  |||||||| |||
                                TCCC CG  CCTTCCTT GGA
                                  C  A_       C
GAM1264  GAB2    3'  AGGGGGCTGGAAGGAAGCCT   32384     A  GC      T
                                AGGG GC  GGAAGGAG CCT
                                |||| ||  |||||||| |||
                                TCCC CG  CCTTCCTT GGA
                                  C  A_       C
GAM1264  VWF     5'  AGGGGCTGTGGAGTCCCCACTG 32385     A  GCGGAA      ____
            CT                    GGG GC     GGAGTCCT    GCT
                                ||| ||     ||||||||    |||
```

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                                CCC CG     CCTCAGGG   CGA
                                  _ ACA___       GTGA
GAM1264 CXorf12  5' AGGAAGGCAGGAGTCCTGC   32386       C  GGA
                                AGGGAG GC   AGGAGTCCTGC
                                ||||||| ||   ||||||||||
                                TCCTTC CG   TCCTCAGGACG
                                  _ ____
GAM1264 DNAJA1   5' AGGGAGCGGGAAGGAGCGCCGA 32387         C       _ T_
            GCT                    AGGGAGCG GGAAGGAGT CC  GCT
                                ||||||||| ||||||||| ||  |||
                                TCCCTCGC CCTTCCTCG GG  CGA
                                  _       C  CT
GAM1264 FLJ21324 5' AGGCGGCGTGGAAGGAAAAGGC 32388     GA   C       TCCT
            T                   AGG  GCG GGAAGGAG    GCT
                                |||  ||| ||||||||    |||
                                TCC  CGC CCTTCCTT    CGA
                                  GC   A       TTC_
GAM1264 FLJ23191 5' AGGGAGCGTGCGGGGGC     32389        __    AA  A
                                AGGGAGC  GCGG  GG GT
                                |||||||  ||||  || ||
                                TCCCTCG  CGCC  CC CG
                                   CA   __ _
GAM1264 KIAA0774 5' GGGTGGTGTGGAGAGAATCCTG 32390     AGCGC_   AG
            CT                    GGG     GGA  GAGTCCTGCT
                                |||     |||  ||||||||||
                                CCC     CCT  CTTAGGACGA
                                  ACCACA   CT
GAM1264 MESDC1   5' AGGAGCGCGGGAGGCAGC    32391          A   _
                                GGGAGCGCGG AGG AGT
                                |||||||||| ||| |||
                                TCCTCGCGCC TCC TCG
                                     C   G
GAM1264 moblak   3' AGGGAGAGAAGAGTCCTGC   32392       CGC    G
                                AGGGAG   GGAAG AGTCCTGC
                                ||||||   ||||| ||||||||
                                TCCCTC   TCTTC TCAGGACG
                                  ___    _
GAM1264 MOST2    3' AGGAGGTGAGAGTCCTGC    32393      GCGC  AA
                                GGGA   GG  GGAGTCCTGC
                                ||||   ||  ||||||||||
                                TCCT   CC  TCTCAGGACG
                                  _____ AC
GAM1264 PRO2015  3' AGGGAAGGAGGGGTCCTG    32394       CGC   A  A
                                AGGGAG   GGA GG GTCCTG
                                ||||||   ||| || ||||||
                                TCCCTT   CCT CC CAGGAC
                                   ___   C  _
GAM1264 SV2      3' AGGGAGCATGGGAGGGCAGCT  32395        C  A   A  CCT
                                AGGGAGCG GG AGG GT   GCT
                                |||||||| || ||| ||   |||
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                                TCCCTCGT CC TCC CG   CGA
                                     A  C   _  T__
GAM1264  LOC143677 3'  GGGTGAGGATGGGAGTCCTGCT 32396     AGCGC   A_
                                GGG    GGA  GGAGTCCTGCT
                                |||    |||  ||||||||||
                                CCC    CCT  CCTCAGGACGA
                                  ACT__   AC
GAM1264  LOC152274 5'  AGGGAGTTTGGGATGCCCTGCT 32397       CGCGGAA  _
                                AGGGAG      GGA GTCCTGCT
                                ||||||      ||| ||||||||
                                TCCCTC      CCT CGGGACGA
                                   AAAC___   A
GAM1264  LOC204285 3'  AGGGAGCGTGGGGGAAGAGACC 32398        C  A__    T
                                AGGGAGCG GG   AGGAG CC
                                |||||||| ||   ||||| ||
                                TCCCTCGC CC   TTCTC GG
                                     A  CCC    T
GAM1264  LOC205418 5'  AGGGGGCTGCCAGGTCCTGCT  32399     A  _  GGAA  A
                                AGGG GC GC    GG GTCCTGCT
                                |||| || ||    || ||||||||
                                TCCC CG CG    TC CAGGACGA
                                  C  A  G___  _
GAM1264  LOC58489  5'  GGCGAGCGCGGAGGGCGGC    32400    _       A  A  CCT
                                GG GAGCGCGGA GG GT   GC
                                || |||||||| || ||   ||
                                CC CTCGCGCCT CC CG   CG
                                 G        _  _  C__
GAM1265  DPYD     3'  CCATTAAAAGAGGATGAGTT   32403      A      TT  T
                                CCAT AAAAGAG  AT AGTT
                                |||| |||||||  || ||||
                                GGTA TTTTCTC  TA TCAA
                                  A      C_  C
GAM1265  IDS      3'  TACCACAGAAAGGGTTATT    32404        A    A
                                TACCATA AAAG GTTATT
                                ||||||| |||| ||||||
                                ATGGTGT TTTC CAATAA
                                     C    C
GAM1265  MTMR8    3'  TACCATAAGAAAGTTAT     32405         AA
                                TACCATAA  AGAGTTAT
                                ||||||||  ||||||||
                                ATGGTATT  TTTCAATA
                                     C_
GAM1265  QDPR     3'  TACCACAAAAGGAGTTAAGGCA 32406          A     T__
              GTT                    TACCATAAAA GAGTTA   TAGTT
                                ||||||||||| ||||||   |||||
                                ATGGTGTTTT CTCAAT   GTCAA
                                      C     TCC
GAM1265  FLJ20793  3'  CATGGAAAAAGTTATTAGTTC  32407     AA
                                CAT  AAAGAGTTATTAGTTC
                                |||  ||||||||||||||||
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                                GTA  TTTTTCAATAATCAAG
                                  CC
GAM1265  KIAA1016  5'  TACCAAGGAAAGATCTACTAGT 32408      TAA    G
              TC                  TACCA   AAAGA TTATTAGTTC
                                  |||||   ||||| ||||||||||
                                  ATGGT   TTTCT GATGATCAAG
                                    TCC    A
GAM1265  KIAA1918  3'  CCATAAAAAAGAGTGAGTT    32409           TATT
                                  CCATAAAAAAGAGT    AGTT
                                  ||||||||||||||    ||||
                                  GGTATTTTTCTCA    TCAA
                                          C___
GAM1265  SBBI31    3'  ACCATGATGTAGTTATTAGTT  32410      AAAAAG
                                  ACCAT     AGTTATTAGTT
                                  |||||     ||||||||||
                                  TGGTA     TCAATAATCAA
                                    CTACA_
GAM1265  ZNF340    3'  CATAAAAAAATATTTATTAGTT 32411         G__
                                  CATAAAAAAGA   TTATTAGTT
                                  ||||||||||   |||||||||
                                  GTATTTTTTT   AATAATCAA
                                       ATA
GAM1266  C14orf1   3'  TCAGCTCAAATCCCACCTCTT  32414     C  _   CAC
                                  TCA GC CAA   GTCCCACCTCTT
                                  ||| || |||   ||||||||||||
                                  AGT CG GTT   TAGGGTGGAGAA
                                    _  A   ____
GAM1266  CARD4     5'  CGCCGCCACAATCTCCACCTCT 32415      AA    _  _
              T                    CGCC  CACG TC CCACCTCTT
                                   ||||  |||| || |||||||||
                                   GCGG  GTGT AG GGTGGAGAA
                                     CG    T  A
GAM1266  OSM       3'  GCCCAGCTCCCACCTCTT    32416     AA  CG
                                   GCC  CA  TCCCACCTCTT
                                   |||  ||  ||||||||||||
                                   CGG  GT  AGGGTGGAGAA
                                     __  CG
GAM1266  PCDH15    5'  TCATTCACATGTTCCACCTCTT 32417     CGCCA   C  C
                                   TCA     ACA GT CCACCTCTT
                                   |||     ||| || |||||||||
                                   AGT     TGT CA GGTGGAGAA
                                     AAG__   A  A
GAM1266  RAG1      3'  ACTCCAACCTACCACCTCTT   32418    G    ACGTC
                                   AC CCAAC     CCACCTCTT
                                   || |||||     |||||||||
                                   TG GGTTG     GGTGGAGAA
                                    A    GAT__
GAM1266  ASPSCR1   3'  TCAGGCTGGCAGCTCTCACCTC 32419     C  CAA  CG  C
              TT                   TCA GC   CA  TC CACCTCTT
                                   ||| ||   ||  || ||||||||
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                                AGT CG   GT  AG GTGGAGAA
                                  C  ACC  CG  A
GAM1266 CNNM1    3'  CGCCAACATGGCTGAGTCCCAC 32420      C_______      C    III
              TTCTTA                  AACA      GTCCCAC TCTT   A
                                ||||      ||||||| ||||  |
                                TTGT      CAGGGTG AGAA   T
                                  ACCGACT      A    III
GAM1266 GNG11    5'  TCACGCCAGCGTGCCCCAGCT  32421         ACAC     C
                                TCACGCCA    GTCCCA CT
                                ||||||||    |||||| ||
                                AGTGCGGT    CGGGGT GA
                                     CGCA     C
GAM1266 KIAA1260  3'  TCAGGCTGGCAAAACACCTCTT 32422     C  CAA  CGTCC
                                TCA GC   CA    CACCTCTT
                                ||| ||   ||    ||||||||
                                AGT CG   GT    GTGGAGAA
                                  C  ACC  TTT__
GAM1266 KLF12    3'  GCCTGGGCAGCCCCACCTCTT  32423     AA__  C
                                GCC    CA GTCCCACCTCTT
                                |||    || ||||||||||||
                                CGG    GT CGGGGTGGAGAA
                                  ACCC  _
GAM1266 LEAP-2    5'  CACCCTAATCTGCACCTCTT   32424      AACAC   C_
                                CGCC    GTC  CACCTCTT
                                ||||    |||  ||||||||
                                GTGG    TAG  GTGGAGAA
                                  GAT__   AC
GAM1266 NTN4     5'  TCCGCTTTTCCCACCTCT    32425    A   CAACACG
                                TC CGC      TCCCACCTCT
                                || |||      ||||||||||
                                AG GCG      AGGGTGGAGA
                                 _   AAA____
GAM1266 LOC151571 5'  CACCCACATTCACCTCT     32426      AA    CC
                                CGCC  CACGT  CACCTCT
                                ||||  |||||  |||||||
                                GTGG  GTGTA  GTGGAGA
                                  __     A_
GAM1266 LOC153684 5'  GCCAGCAATCCCACCTCTT    32427      A  C
                                GCCA CA GTCCCACCTCTT
                                |||| || ||||||||||||
                                CGGT GT TAGGGTGGAGAA
                                  C  _
GAM1266 LOC221312 3'  TCACGTCAAAATTTCACACCTC 32428       C   CACG  C
              TT                  TCACG CAA    TC CACCTCTT
                                ||||| |||    || ||||||||
                                AGTGC GTT    AG GTGGAGAA
                                  A   TTAA  T
GAM1266 LOC256453 5'  TCACACCATTTCCCCATCTCTT 32429         ACACG    C
                                TCACGCCA     TCCCA CTCTT
                                ||||||||     ||||| |||||
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                                AGTGTGGT    GGGGT GAGAA
                                    AAA__    A
GAM1267 LHX2    5' CTAATGATACATGCTACA   31652         CA
                                TTAATGATACA  CTATA
                                ||||||||||  |||||
                                GATTACTATGT  GATGT
                                   AC
GAM1267 MS4A1   3' TTAATGATACAATACTGC   31653         CACT
                                TTAATGATACA   ATACTGT
                                ||||||||||   |||||||
                                AATTACTATGT   TATGACG
                                    ____
GAM1267 TRHDE   3' TGGTACCACTATACTGT    32432   A  A
                                TG TAC CACTATACTGT
                                || ||| ||||||||||
                                AC ATG GTGATATGACA
                                 C  _
GAM1267 CST9L   3' TTAATGATCTACACTACA   31654       AC
                                TTAATGAT  ACACTATA
                                ||||||||  ||||||||
                                AATTACTA  TGTGATGT
                                    GA
GAM1267 EHM2    3' TTAATGATATCACTGCACCG  31655       CA   A
                                TTAATGATA  CACT TACTG
                                |||||||||  |||| |||||
                                AATTACTAT  GTGA GTGGC
                                    A_   C
GAM1267 KIAA0757 3' TTAATATACACACTGTAC   32433      A      A
                                TTAATG TACACACT TAC
                                |||||| |||||||| |||
                                AATTAT ATGTGTGA ATG
                                   _      C
GAM1267 PCDH19  3' TTAATGAGACATACTGTACT  32434      T  C  A
                                TTAATGA ACA ACT TACT
                                ||||||| ||| ||| ||||
                                AATTACT TGT TGA ATGA
                                    C  A  C
GAM1267 PRO0800 3' TTAATGATAAACATTACTG   32435       C  CTA
                                TTAATGATA ACA   TACTG
                                |||||||||  |||   |||||
                                AATTACTAT TGT   ATGAC
                                    T  A__
GAM1268 ACCN2   5' CCCGGCCCCGCTCGGCTCC   32438   G      CCCCCAC _
                                CC CGGCCCCGC      GC CC
                                || |||||||||      || ||
                                GG GCCGGGGCG      CG GG
                                 _       AGC_____ A
GAM1268 ACK1    3' CCTTGGCCTTGCTCCATCCCCG 32439   GC   CC  CCC   CG
                                CC  GGCC  GC   CCA  CCCG
                                ||  ||||  ||   |||  ||||
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                              GG  CCGG  CG   GGT  GGGC
                               AA    AA  A__   AG
GAM1268  ALDH3A2   5'  CCGCGACCTCCACGCC     32440        CCGCCCC
                              CCGCGGCC      CCACGCC
                              ||||||||      |||||||
                              GGCGCTGG      GGTGCGG
                                  A_______
GAM1268  ASK       5'  CCGCCTCGCGCTCGCCCCTCGT 32441      G__  CC_     CCAC
             GCC                   CCGC   GC   CGCCCC   GCC
                              ||||   ||   ||||||   |||
                              GGCG   CG   GCGGGG   CGG
                                GAG  CGA     AGCA
GAM1268  ASK       5'  CCGTGCCCCGCCTCGCGCTCG  32442    CG      CCCCA   C
                              CCG  GCCCCGCC    CGC CG
                              |||  ||||||||    ||| ||
                              GGC  CGGGGCGG    GCG GC
                                A_       AGC__   A
GAM1268  ASL       5'  CGGCGTCCTCCACGCCCG    32443     CCCG  CC
                              CGGC    CC  CCACGCCCG
                              ||||    ||  |||||||||
                              GCCG    GG  GGTGCGGGC
                                CA__  A_
GAM1268  ATF4      5'  CCGCGCCCCGCCCACCGCCCG  32444      G      CCCA
                              CCGCG CCCCGCCC    CGCCCG
                              ||||| ||||||||    ||||||
                              GGCGC GGGGCGGG    GCGGGC
                                 _       TG__
GAM1268  ATP11A    3'  CCGCGGCCCTTCCCAGCTGGCT 32445        CG   CCCAC  C
             CG                    CCGCGGCCC  CCC    GC CG
                              |||||||||  |||    || ||
                              GGCGCCGGG  GGG    CG GC
                                   AA   TCGAC  A
GAM1268  CAPNS1    5'  CCGCGGCCCTCGTGTCGCCCG  32446        _  CCCCCCA
                              CCGCGGCCC CG      CGCCCG
                              ||||||||| ||      ||||||
                              GGCGCCGGG GC      GCGGGC
                                   A  ACA_____
GAM1268  CAV2      5'  CCCGGCCCCGCCCCCCCTCG   32447    G          A_
                              CC CGGCCCCGCCCCCC  CG
                              || ||||||||||||||  ||
                              GG GCCGGGGCGGGGGG  GC
                                _           GA
GAM1268  CDR2      5'  CCGCCGTCCCGCCTCAGCC    32448     _ GC     CCC  C
                              CCGC G  CCCGCC   CA GCC
                              |||| |  ||||||   || |||
                              GGCG C  GGGCGG   GT CGG
                                G A_     A__  _
GAM1268  CHRNA4    5'  CGCGGCCCCCGCCCGGCCC    32449          CCCAC
                              CGCGGCCCCCGCCC    GCCC
                              ||||||||||||    ||||
```

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                                GCGCCGGGGCGGG    CGGG
                                      C____
GAM1268 CKAP1    5' CGTGGCCCCGCCCTGCCC    32450    C       CCCAC
                                CG GGCCCCGCCC    GCCC
                                || ||||||||||    ||||
                                GC CCGGGGCGGG    CGGG
                                 A        A____
GAM1268 CRHR1    5' CCGCGGCCCGGCCCGGCCC   32451        C   CCCAC
                                CCGCGGCCC GCCC    GCCC
                                ||||||||| ||||    ||||
                                GGCGCCGGG CGGG    CGGG
                                     C   C____
GAM1268 CRMP1    5' CGGCCCCGCTCCCAGC      32452        CC   C
                                CGGCCCCGC  CCCA GC
                                |||||||||  |||| ||
                                GCCGGGGCG  GGGT CG
                                     A_   _
GAM1268 CSNK1D   5' CCCGGCTCCGCCCCCCTCAC  32453    G   C       A
                                CC CGGC CCGCCCCCC CGC
                                || |||| ||||||||| |||
                                GG GCCG GGCGGGGGG GTG
                                 _   A       A
GAM1268 CSNK1D   5' CACGGCCCCGCTTTCACC    32454         CCCCCA
                                CGCGGCCCCGC     CGCC
                                ||||||||||      ||||
                                GTGCCGGGGCG     GTGG
                                      AAA___
GAM1268 CSNK1D   5' CACGGCCCCGCTTTCACC    32454         CCCCCA
                                CGCGGCCCCGC     CGCC
                                ||||||||||      ||||
                                GTGCCGGGGCG     GTGG
                                      AAA___
GAM1268 CSNK1D   5' CCCGGCTCCGCCCCCCTCAC  32453    G   C       A
                                CC CGGC CCGCCCCCC CGC
                                || |||| ||||||||| |||
                                GG GCCG GGCGGGGGG GTG
                                 _   A       A
GAM1268 CYFIP2   5' CGGCCCCGCCCCGGCCC     32455          CCAC
                                CGGCCCCGCCCC    GCCC
                                ||||||||||||    ||||
                                GCCGGGGCGGGG    CGGG
                                      C___
GAM1268 DBN1     5' CCGCGCCTCCGGGCCGCGTCCG 32456      G _  CCCC  A  C
                                CCGCG CC CCG    CC CG CCG
                                ||||| || |||    || || |||
                                GGCGC GG GGC    GG GC GGC
                                   _ A  CC__  C  A
GAM1268 DDX38    3' GCAGCCCCGCTCCCGCCATGCC 32457          _  _  C
                                GCGGCCCCGC CCC CCA GCC
                                |||||||||| ||| ||| |||
```

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                                CGTCGGGGCG GGG GGT CGG
                                     A   C   A
GAM1268  DPP6     3'  CCCGGCCCCGCCCCGCCC    32458    G         CCAC
                                CC CGGCCCCGCCCC   GCCC
                                || ||||||||||||   ||||
                                GG GCCGGGGCGGGG   CGGG
                                 _         _____
GAM1268  DSCAM    5'  CCGCGCTCCGCCCGGCCC    32459      G C     CCCAC
                                CCGCG C CCGCCC    GCCC
                                ||||| | ||||||    ||||
                                GGCGC G GGCGGG    CGGG
                                   _ A     C_____
GAM1268  DVL1     5'  GCGCCCCGCCCGGCCC      32460     G       CCCAC
                                GCG CCCCGCCC    GCCC
                                ||| ||||||||    ||||
                                CGC GGGGCGGG    CGGG
                                  _       C_____
GAM1268  DVL3     5'  CCGCGCTTCCGCTCCCCACTCT 32461      GCC   C     G__
              CCCG                  CCGCG   CCGC CCCCAC   CCCG
                                ||||||   |||| ||||||   ||||
                                GGCGC   GGCG GGGGTG   GGGC
                                   GAA    A     AGA
GAM1268  FANCC    3'  CCGCGTCCCCGCCCAGCA    32462      G       CC
                                CCGCG CCCCGCCC  CA
                                ||||| ||||||||  ||
                                GGCGC GGGGCGGG  GT
                                   A       TC
GAM1268  FBXL3A   5'  CCGCGCTCCGCCCGCATCC    32463      G C     CCCA  C
                                CCGCG C CCGCCC    CG CC
                                ||||| | ||||||    || ||
                                GGCGC G GGCGGG    GT GG
                                   _ A     C___  A
GAM1268  FBXL5    5'  CCGCGGCCGCCGCCTCTCCA   32464        _    CC_
                                CCGCGGCC CCGCC   CCA
                                |||||||| |||||   |||
                                GGCGCCGG GGCGG   GGT
                                     C     AGA
GAM1268  FBXL5    5'  CCGCGGCCGCCGCCTCTCCA   32464        _    CC_
                                CCGCGGCC CCGCC   CCA
                                |||||||| |||||   |||
                                GGCGCCGG GGCGG   GGT
                                     C     AGA
GAM1268  FHL2     5'  CCGTGCCCCCGCCCCGGGC   32465     CG    _    CCAC
                                CCG  GCCCC GCCCC    GC
                                |||  ||||| |||||    ||
                                GGC  CGGGG CGGGG    CG
                                  A_     G     CC__
GAM1268  FZD10    5'  CGGGCCCCCGCCCATGCCCG   32466    C     _    CCCAC
                                CG GGCCCC GCCC    GCCCG
                                || |||||| ||||    |||||
```

```
                                GC CCGGGG CGGG    CGGGC
                                 _    G   TA___
GAM1268 G6PD    5' CCCGGCCCCGCCCCTACTGTCC 32467   G        CC  GC_
            G                    CC CGGCCCCGCCCC  AC   CCG
                                 || |||||||||||  ||   |||
                                 GG GCCGGGGCGGGG  TG   GGC
                                 _         A_  ACA
GAM1268 GAK     3' CCGGGGCTCCAGAGGCCACGCC 32468    C   C   CCCC
            CG                    CCG GGC CCG    CCACGCCCG
                                 ||| ||| |||    |||||||||
                                 GGC CCG GGT    GGTGCGGGC
                                   C   A   CTCC
GAM1268 GNB1    5' CCCGGCCCCGCTCCCCAC    32469    G       C
                                 CC CGGCCCCGC CCCCAC
                                 || |||||||| ||||||
                                 GG GCCGGGGCG GGGGTG
                                 _       A
GAM1268 GPRC5B  5' CCGCGGCCCCCGCTCCACGCAC 32470          _ _  CC_
            GCCCG                   CCGCGGCCCC GC CC   CACGCCCG
                                 |||||||||| || ||   ||||||||
                                 GGCGCCGGGG CG GG   GTGCGGGC
                                       G  A  TGC
GAM1268 GPT     5' GGCCCCGCCCCACCC       32471          CCAC
                                 GGCCCCGCCCC    GCCC
                                 ||||||||||    ||||
                                 CCGGGGCGGGG    TGGG
                                              ____
GAM1268 GRB10   5' CCGCGGCCCCGCCGCGC     32472           CCCCA
                                 CCGCGGCCCCGCC    CGC
                                 ||||||||||||     |||
                                 GGCGCCGGGGCGG    GCG
                                        C____
GAM1268 GSTM4   5' CCTCGGCCCCGCTGCGCCC   32473    G       CCCCCA
                                 CC CGGCCCCGC     CGCCC
                                 || |||||||||     |||||
                                 GG GCCGGGGCG     GCGGG
                                  A        AC____
GAM1268 HCN2    3' CCGCCGGCCCTGCCCGTCC   32474     _    C   C_
                                 CCGC GGCCC GCCC  CC
                                 |||| ||||| ||||  ||
                                 GGCG CCGGG CGGG  GG
                                   G    A   CA
GAM1268 HRB     5' CCGCGGCCGCCGCCCTCC    32475        _    C
                                 CCGCGGCC CCGCCC CC
                                 |||||||| |||||| ||
                                 GGCGCCGG GGCGGG GG
                                      C     A
GAM1268 HUNK    5' CGCGGCTCCTGCTCGTCTCCCG 32476   _ C  CC____   A   C  III
            CGCTCGC                 C CC GC     CCC CGC CG   C
                                 | || ||     ||| ||| ||   |
```

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                                G GG CG     GGG GCG GC   G
                                 A  A  AGCAGA   C   A  III
GAM1268  IFNGR2   5'  CCGCGCCCCCGCCCCCGCCC   32477      G        CAC
                                CCGCG CCCCGCCCCC   GCCC
                                |||||| ||||||||||   ||||
                                GGCGC GGGGCGGGGG   CGGG
                                   G         ____
GAM1268  IL6R     5'  CCTCGGCCCCGCGCCGCGCTCG 32478    G       CCC  A   C
                                CC CGGCCCCGC   CC CGC CG
                                || |||||||||   || ||| ||
                                GG GCCGGGGCG   GG GCG GC
                                 A        C__  C   A
GAM1268  IQGAP2   5'  GCGCCCCGCCGGCGCGCTCG   32479     G      CCCCA   C
                                GCG CCCCGCC     CGC CG
                                ||| |||||||     ||| ||
                                CGC GGGGCGG     GCG GC
                                  _      CCGC_   A
GAM1268  JAG2     5'  CCGCCGCCGCCCCGCGCCC    32480    _     C   A
                                CC CCGCC CCC CGCCC
                                || ||||| ||| |||||
                                GG GGCGG GGG GCGGG
                                 C     C   C
GAM1268  JUND     5'  CCGCGGCCTCCCGGGGGGCCCG 32481         CCG   CCCAC
                                CCGCGGCC   CCC    GCCCG
                                ||||||||   |||    |||||
                                GGCGCCGG   GGG    CGGGC
                                     A__   CCCCC
GAM1268  LAMC1    5'  CCGCGCCCCGCCTCCGCG    32482      G      CC  A
                                CCGCG CCCCGCC  CC CG
                                ||||| |||||||  || ||
                                GGCGC GGGGCGG  GG GC
                                   _      A_  C
GAM1268  MAF      5'  CCCTGCCCGCGCCCCCCGCGCC 32483    GCG   _       A
              CG                    CC   GCCC CGCCCCCC CGCCCG
                                ||   |||| |||||||| ||||||
                                GG   CGGG GCGGGGGG GCGGGC
                                 GA_    C       C
GAM1268  MAPK3    5'  GCGGCCCCGCCCGAGGCCC   32484           CCCAC
                                GCGGCCCCGCCC    GCCC
                                ||||||||||||    ||||
                                CGCCGGGGCGGG    CGGG
                                       CTC__
GAM1268  MIF      5'  CCGCGGCCGCCGCTGAGCTACG 32485         _   CCCCC_   C_
              TGCC                   CCGCGGCC CCGC     ACG  CC
                                ||||||||| ||||     |||  ||
                                GGCGCCGG GGCG     TGC  GG
                                     C    ACTCGA   AC
GAM1268  MLLT1    5'  CCGGGCCCCGCGTCGCC     32486     C       CCCCCA   C
                                CCG GGCCCCGC     CGC C
                                ||| ||||||||     ||| |
```

```
                                GGC CCGGGGCG     GCG G
                                  _       CA____   A
GAM1268 MLLT2    5' CCAGCGGGCCCCCACGCC    32487    _   CCCC     C   C
                                CC GCGG    GCCCCC ACGC C
                                || ||||    |||||| |||| |
                                GG CGCC    CGGGGG TGCG G
                                 T   _____     _   A
GAM1268 MSF      5' GCGCCCCCGCCCCGCCCCCG   32488     G       _ ACG
                                GCG CCCCGCCCC CC   CCCG
                                ||| ||||||||| ||   ||||
                                CGC GGGGCGGGG GG   GGGC
                                  G       C ___
GAM1268 MTL5     5' CCGCGAGCTTCGCCTTGACCCC 32489      _ CC   _____
                                CCGCG GC  CGCC    CCCC
                                ||||| ||  ||||    ||||
                                GGCGC CG  GCGG    GGGG
                                   T  AA    AACT
GAM1268 MUCDHL   3' CCGCGCCCTCGCCCTCATCG   32490      G  _    CC  _
                                CCGCG CCC CGCCC  CA CG
                                ||||| ||| |||||  || ||
                                GGCGC GGG GCGGG  GT GC
                                   _  A    A_ A
GAM1268 NOC4     5' CCCGGCCCCGTTTGGGCCTCG  32491    G      CCCCCCAC  _
                                CC CGGCCCCG       GCC CG
                                || ||||||||       ||| ||
                                GG GCCGGGGC       CGG GC
                                  _       AAACC___   A
GAM1268 NPAS2    5' CCGCGGCCGCCGCTCCTGGGCC 32492        _   C  CCAC
                                CCGCGGCC CCGC CC    GCC
                                |||||||| |||| ||    |||
                                GGCGCCGG GGCG GG    CGG
                                     C    A  ACC_
GAM1268 NRXN2    5' CCCCGGCCCCGCCCGGCCC    32493    G        CCCAC
                                CC CGGCCCCGCCC    GCCC
                                || ||||||||||     ||||
                                GG GCCGGGGCGGG     CGGG
                                 G         C____
GAM1268 NRXN2    5' CCCCGGCCCCGCCCGGCCC    32493    G        CCCAC
                                CC CGGCCCCGCCC    GCCC
                                || ||||||||||     ||||
                                GG GCCGGGGCGGG     CGGG
                                 G         C____
GAM1268 NTRK2    5' CCGGGCTCCGGCGCCTCACGCC 32494     C  _ C  C  C
              CG                   CCG GGC CC GC CC CACGCCCG
                                ||| ||| || || || ||||||||
                                GGC CCG GG CG GG GTGCGGGC
                                  _  A  C  C  A
GAM1268 OCLN     5' CGCGGTCCTGCTTCCCACACCC 32495      C  C  CC
                                CGCGG CC GC  CCCACGCCC
                                ||||| || ||  |||||||||
```

```
                                GCGCC GG CG  GGGTGTGGG
                                  A  A  AA
GAM1268  OLFM1    5'  CCTGGCTCGTGTCCCCACGCC  32496    GC   CC  CC_
                                CC  GGC  CG   CCCCACGCC
                                ||  |||  ||   |||||||||
                                GG  CCG  GC   GGGGTGCGG
                                 A_   A_  ACA
GAM1268  OLFM1    5'  CCTGGCTCGTGTCCCCACGCC  32496    GC   CC  CC_
                                CC  GGC  CG   CCCCACGCC
                                ||  |||  ||   |||||||||
                                GG  CCG  GC   GGGGTGCGG
                                 A_   A_  ACA
GAM1268  OLFM1    5'  CCTGGCTCGTGTCCCCACGCC  32496    GC   CC  CC_
                                CC  GGC  CG   CCCCACGCC
                                ||  |||  ||   |||||||||
                                GG  CCG  GC   GGGGTGCGG
                                 A_   A_  ACA
GAM1268  OPHN1    5'  GCGCCCCGCCCCAGCGAAGCCC 32497     G        CCAC__
              G                  GCG CCCCGCCCC      GCCCG
                                 ||| |||||||||      |||||
                                 CGC GGGGCGGGG      CGGGC
                                  _        TCGCTT
GAM1268  P3       5'  CCGCGGCCCCGCCAGGCCTCG  32498            CCCCAC  _
                                 CCGCGGCCCCGCC      GCC CG
                                 ||||||||||||       ||| ||
                                 GGCGCCGGGGCGG      CGG GC
                                          TC_____   A
GAM1268  PAX2     3'  CCGCGGCTCCACCCGTCC    32499        C     C_
                                 CCGCGGC CCGCCC  CC
                                 |||||||  ||||||  ||
                                 GGCGCCG GGTGGG  GG
                                     A      CA
GAM1268  PAX2     3'  CCGCGGCTCCACCCGTCC    32499        C     C_
                                 CCGCGGC CCGCCC  CC
                                 |||||||  ||||||  ||
                                 GGCGCCG GGTGGG  GG
                                     A      CA
GAM1268  PIAS1    5'  CCTGGCCCCGCCCCGGCCC   32500    GC         CCAC
                                 CC  GGCCCCGCCCC    GCCC
                                 ||  ||||||||||    ||||
                                 GG  CCGGGGCGGGG    CGGG
                                  A_          C___
GAM1268  PITX1    3'  CCGGGGCCCCGCGTGCGTCCTC 32501       _______  C  A      III
              CGCGCCCGC                  CCCGC      CC CC CGCCCG   C
                                 |||||      || || ||||||   |
                                 GGGCG      GG GG GCGGGC   G
                                    CACGCA  A  C      III
GAM1268  POU3F2   3'  CCGCGCTCTGCCCCTCCCCCAG 32502      _____    GC     C  C
              CTCG                   CGCG    GCCCC  CCCCCA GC CG
                                 ||||    |||||  |||||| || ||
```

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                                GCGC   CGGGG  GGGGGT CG GC
                                  GAGA    A_     _ A
GAM1268 PPP2R5D  5' GCGGCCCCGCTCCGGCTCCG  32503         C  CCAC _
                                GCGGCCCCGC CC   GC CCG
                                |||||||||| ||   || |||
                                CGCCGGGGCG GG   CG GGC
                                     A  C___  A
GAM1268 PPP3CC   5' CCGCGGCCGCCGCCTTCTCCTC 32504        _    CC__  A
           G                     CCGCGGCC CCGCC   CC CG
                                |||||||| |||||   || ||
                                GGCGCCGG GGCGG   GG GC
                                     C    AAGA  A
GAM1268 PRDM16   3' CCGGGGCCCCGCCCGCCTCCG  32505    C        _ CA
                                CCG GGCCCCGCCC CC  CG
                                ||| |||||||||| ||  ||
                                GGC CCGGGGCGGG GG  GC
                                  C         C  AG
GAM1268 PTPN2    5' CCGCGCCCCGCCCCCACG    32506      G        C
                                CCGCG CCCCGCCCCC ACG
                                ||||| |||||||||| |||
                                GGCGC GGGGCGGGGG TGC
                                   _         _
GAM1268 PTPRJ    5' CGGGCCCCGCCGTGCGCCCG   32507    C       CCCCA
                                CG GGCCCCGCC    CGCCCG
                                || |||||||||    ||||||
                                GC CCGGGGCGG    GCGGGC
                                 _        CAC__
GAM1268 RASGRP1  5' CCGCGGCCCGCGCTCCCGGTGC 32508         _  C  CAC
           C                     CCGCGGCCC CGC CCC   GCC
                                ||||||||| ||| |||   |||
                                GGCGCCGGG GCG GGG   CGG
                                     C   A   CCA
GAM1268 RDBP     5' CCACGGTCTCCGGCCGCGCCCG 32509       CC_  CCCC  A
                                CCGCGG   CCG    CC CGCCCG
                                ||||||   |||    || ||||||
                                GGTGCC   GGC    GG GCGGGC
                                    AGA   C___  C
GAM1268 RRM2B    5' CCCGGCCCCGCCTCCCCCG   32510    G        _   A
                                CC CGGCCCCGCC CCCC CG
                                || |||||||||| |||| ||
                                GG GCCGGGGCGG GGGG GC
                                 _         A   _
GAM1268 SIX2     5' GCGTCCCCGCCCGCCC      32511     G      CCCAC
                                GCG CCCCGCCC    GCCC
                                ||| ||||||||    ||||
                                CGC GGGGCGGG    CGGG
                                  A       _____
GAM1268 SLC12A7  3' GCTGCCCACGCCGTCCTCCGTG 32512    G   _   __ _ AC
           CC                     GC GCCC CGCC  CC CC  GCC
                                || |||| ||||  || ||  |||
```

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                                CG CGGG GCGG  GG GG  CGG
                                 A    T    CA  A  CA
GAM1268  SLC22A12  5'  CCGTGGCTCCTGCCTCCACTCA 32513     C   _  C   CC    __
              CC                  CCG GGC CC GCC  CCAC  GCC
                                ||| ||| || |||  ||||  |||
                                GGC CCG GG CGG  GGTG  TGG
                                  A   A  A   A_    AG
GAM1268  SMARCC2   5'  CGGGCCCCGCCGCCGCCC    32514    C       CCCCA
                                CG GGCCCCGCC    CGCCC
                                || |||||||||    |||||
                                GC CCGGGGCGG    GCGGG
                                 _       CG___
GAM1268  SMARCC2   5'  CGGGCCCCGCCGCCGCCC    32514    C       CCCCA
                                CG GGCCCCGCC    CGCCC
                                || |||||||||    |||||
                                GC CCGGGGCGG    GCGGG
                                 _       CG___
GAM1268  SNX6     5'  CCGCGCCCGCCCCGCGCCC   32515      GC      CCA
                                CCGCG  CCCGCCCC   CGCCC
                                |||||  ||||||||   |||||
                                GGCGC  GGGCGGGG   GCGGG
                                   __       C__
GAM1268  SOX12    5'  CCGCGGCTCGGCCCGGCCCCC  32516        ____    C
                                CCGCGGC    CCCG CCCCC
                                |||||||    |||| |||||
                                GGCGCCG    GGGC GGGGG
                                    AGCC    C
GAM1268  SP3      5'  CCGCCGCCAGCCCACGCC    32517    _    C_
                                CC CCGCC  CCCACGCC
                                || |||||  ||||||||
                                GG GGCGG  GGGTGCGG
                                 C    TC
GAM1268  SPTAN1   5'  CCGCGGCCTCCGCTCCACACC  32518        _   CCC
                                CCGCGGCC CCGC   CCACGCC
                                |||||||| ||||   |||||||
                                GGCGCCGG GGCG   GGTGTGG
                                    A    A__
GAM1268  SWAP70   5'  CCGCGGCCCTGCTGCCCC    32519         C  C_
                                CCGCGGCCC GC  CCCC
                                ||||||||| ||  ||||
                                GGCGCCGGG CG  GGGG
                                     A  AC
GAM1268  TFG      5'  CCGCGGCCGCCGCCTCTCC    32520        _    CC_
                                CCGCGGCC CCGCC   CC
                                |||||||| |||||   ||
                                GGCGCCGG GGCGG   GG
                                    C    AGA
GAM1268  TFRC     5'  CGCGGCCCCGCTCCATCCCG   32521          C  CCACG
                                CGCGGCCCCGC CC    CCCG
                                |||||||||| ||    ||||
```

```
                                GCGCCGGGGCG GG    GGGC
                                      A  TA___
GAM1268  TMOD     3'  CCTGGCCCCGCCTCCAGTTACC 32522    GC       _  CCAC
              C                    CC  GGCCCCGCC CC    GCCC
                                   ||  |||||||| ||    ||||
                                   GG  CCGGGGCGG GG    TGGG
                                    A_        A  TCAA
GAM1268  UGCG     5'  CCGCGGCCCCCGCGCTCCG    32523          CCCCCAC  _
                                   CCGCGGCCCCCGC      GC CCG
                                   ||||||||||||       || |||
                                   GGCGCCGGGGCG      CG GGC
                                          ________  A
GAM1268  WNT2     5'  CCGCGCCCCCCGCCCCCCCGCTCG 32524      G         AC  C
                                   CCGCG CCCCGCCCCCC  GC CG
                                   |||||| ||||||||||  || ||
                                   GGCGC GGGGCGGGGGG  CG GC
                                      G          __  A
GAM1268  ZNF26    5'  GGCCCCGTCCACGCCC      32525        CCCC
                                   GGCCCCG    CCACGCCC
                                   |||||||    ||||||||
                                   CCGGGGC    GGTGCGGG
                                       A___
GAM1268  54TM     5'  CCGCCGGTCTCGGCCACCATGT 32526      _  CCC  C  C   CGC
              CCG                    CCGC GG   CG CC CCA   CCG
                                   |||| ||   || || |||   |||
                                   GGCG CC   GC GG GGT   GGC
                                     G  AGA  C  T   ACA
GAM1268  ALS2CR2  5'  CGCGGCCCCCGCCTCCCTCCCCG 32527           C   ACG
                                   CGCGGCCCCCGCC CCC   CCCG
                                   |||||||||||| |||   ||||
                                   GCGCCGGGGCGG GGG   GGGC
                                         A   AG_
GAM1268  BIKE     5'  CCGCGGCTCCGCTGCAGC    32528        C    CCCC  C
                                   CCGCGGC CCGC    CA GC
                                   ||||||| ||||    || ||
                                   GGCGCCG GGCG    GT CG
                                       A    AC__  _
GAM1268  CDC14B   5'  CCATGGCCCCCGCGCGCCC    32529     C       CCCCCA
                                   CCG GGCCCCCGC     CGCCC
                                   ||| ||||||||      |||||
                                   GGT CCGGGGCG      GCGGG
                                     A       C_____
GAM1268  CDC14B   5'  CCATGGCCCCCGCGCGCCC    32529     C       CCCCCA
                                   CCG GGCCCCCGC     CGCCC
                                   ||| ||||||||      |||||
                                   GGT CCGGGGCG      GCGGG
                                     A       C_____
GAM1268  CDC14B   5'  CCATGGCCCCCGCGCGCCC    32529     C       CCCCCA
                                   CCG GGCCCCCGC     CGCCC
                                   ||| ||||||||      |||||
```

```
                                GGT CCGGGGCG     GCGGG
                                  A       C_____
GAM1268 cerk     3' CCACGGCCCCGCTCCTTACA  32530          C  CC
                                CCGCGGCCCCGC CC  ACG
                                |||||||||||| ||  |||
                                GGTGCCGGGGCG GG  TGT
                                    A  AA
GAM1268 CHDH     5' CCGCGGCCCGGCCCCTGCCC  32531         C    CCAC
                                CCGCGGCCC GCCCC   GCCC
                                ||||||||| |||||   ||||
                                GGCGCCGGG CGGGG   CGGG
                                     C    A___
GAM1268 CHST3    5' CCGCGGCCCCGGCGCC      32532          CCCCCCA
                                CCGCGGCCCCG      CGCC
                                ||||||||||       ||||
                                GGCGCCGGGGC      GCGG
                                    C_______
GAM1268 CHSY1    5' CGCGGCCCCCGAGCCGCCCG  32533        GCCCCCCA
                                CGCGGCCCC       CGCCCG
                                |||||||||       ||||||
                                GCGCCGGGG       GCGGGC
                                    GCTCG___
GAM1268 CSRP2BP  5' CCGCGGCCTCTCTCTCCCGCCC 32534        CCGCCCC  A
              G                  CCGCGGCC      CC CGCCCG
                                 ||||||||      || ||||||
                                 GGCGCCGG      GG GCGGGC
                                    AGAGAGA  _
GAM1268 CTCF     5' CCGCGGCGCCCGCTCCGCC   32535       _    C  _
                                CCGCGGC CCCGC CC CC
                                ||||||| ||||| || ||
                                GGCGCCG GGGCG GG GG
                                   C    A  C
GAM1268 DJ1042K10.2 3' CCGCGGCCCCGGCCAGGGC   32536          C  CCCAC
                                CCGCGGCCCCG CC    GC
                                |||||||||| ||    ||
                                GGCGCCGGGGC GG    CG
                                     C  TCC__
GAM1268 DKFZP434J154 5' CGCGGCCCCGCCCCCGC    32537            CAC
                                CGCGGCCCCGCCCCC   GC
                                ||||||||||||||   ||
                                GCGCCGGGGCGGGGG   CG
                                                 ___
GAM1268 DKFZp547A023 5' GGCTCCGCCCCCTCAGCCGCCC 32538     C       _ __
              G                  GGC CCGCCCCC CA  CGCCCG
                                 ||| ||||||| ||  ||||||
                                 CCG GGCGGGGG GT  GCGGGC
                                   A       A  CG
GAM1268 DNAL4    3' CCGCTGCCCCGTCCACACCC  32539     G     CCCC
                                CCGC GCCCCG   CCACGCCC
                                |||| ||||||   ||||||||
```

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                                GGCG CGGGGC   GGTGTGGG
                                  A    A___
GAM1268 DXS1357E 5' CCCCGGCCCCGCCCCTCATACC 32540   G        C  CG
                                CC CGGCCCCGCCCC CA  CC
                                || |||||||||||| ||  ||
                                GG GCCGGGGCGGGG GT  GG
                                 G         A  AT
GAM1268 ECE2    5' CCGCGGCCCCGGTCCCCTGCCC 32541         CC   AC
          G                      CCGCGGCCCCG  CCCC  GCCCG
                                |||||||||||  ||||  |||||
                                GGCGCCGGGGC  GGGG  CGGGC
                                      CA   A_
GAM1268 ELL2    5' CCGCGCCCCGCCCCGGGCTCG  32542     G      CCAC  C
                                CCGCG CCCCGCCCC   GC CG
                                ||||| |||||||||   || ||
                                GGCGC GGGGCGGGG   CG GC
                                  _       CC__  A
GAM1268 FAPP2   5' CCGCGGCCACTCGGCCCACGCC 32543       CCGCCC
          CG                     CCGCGGCC    CCCACGCCCG
                                |||||||     ||||||||||
                                GGCGCCGG    GGGTGCGGGC
                                    TGAGCC
GAM1268 FLJ10350 5' CCGCGGCGCATCACGCCC   32544       CCC  CCCC
                                CCGCGGC  GC   CACGCCC
                                |||||||  ||   |||||||
                                GGCGCCG  CG   GTGCGGG
                                   ___  TA__
GAM1268 FLJ11712 5' CCGCGGCCTCTCCCTCGCGGCT 32545       CCG  CCCAC _
          CCG                    CCGCGGCC  CCC    GC CCG
                                |||||||  |||    || |||
                                GGCGCCGG  GGG    CG GGC
                                    AGA   AGCGC  A
GAM1268 FLJ12132 5' GCGCCCCGCCCCTATATCCCG  32546    G      CCACG
                                GCG CCCCGCCCC    CCCG
                                ||| |||||||||    ||||
                                CGC GGGGCGGGG    GGGC
                                  _       ATATA
GAM1268 FLJ12697 3' CCCGGCCCCAGCCACGCTCG  32547   G     CCCC    C
                                CC CGGCCCCG   CCACGC CG
                                || ||||||||   |||||| ||
                                GG GCCGGGGT   GGTGCG GC
                                  _      C___     A
GAM1268 FLJ13052 3' CCACGGCCTCCACACACCTGTG 32548       _   CC_ CAC
          CCCG                   CCGCGGCC CCGC  CC  GCCCG
                                |||||||| ||||  ||  |||||
                                GGTGCCGG GGTG  GG  CGGGC
                                    A   TGT  ACA
GAM1268 FLJ13063 5' CCGTGCCCCGCCCCCGGC   32549    CG       CAC
                                CCG  GCCCCGCCCCC  GC
                                |||  ||||||||||  ||
```

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                                GGC  CGGGGCGGGGG   CG
                                  A_         C__
GAM1268  FLJ13881  5'  GCGGCCCCGCTCCAGCC     32550          CCC   C
                                GCGGCCCCGC   CCA GCC
                                ||||||||||   ||| |||
                                CGCCGGGGCG   GGT CGG
                                     A__   _
GAM1268  FLJ20277  5'  CCGCGGCCTCCGCCTCCTCCAT 32552         _    _ _  C
                  GCC                  CCGCGGCC CCGCC CC CCA GCC
                                ||||||||| ||||| || ||| |||
                                GGCGCCGG GGCGG GG GGT CGG
                                     A    A A  A
GAM1268  FLJ20277  5'  CCGGGCCCCGCTCGGGCCC   32551    C      CCCCCAC
                                CCG GGCCCCGC      GCCC
                                ||| ||||||||      ||||
                                GGC CCGGGGCG      CGGG
                                  _      AGCC____
GAM1268  FLJ22004  5'  CCCCGGCCCCGCCCCCGGC   32553   G          CAC
                                CC CGGCCCCGCCCCC   GC
                                || ||||||||||||   ||
                                GG GCCGGGGCGGGGG   CG
                                 G          C__
GAM1268  FLJ22393  5'  CCGCGGCCCCGGCGCCGGCGCC 32554          _ C  CCA
                                CCGCGGCCCCG C CC   CGCC
                                |||||||||| | ||   ||||
                                GGCGCCGGGGC G GG   GCGG
                                      C C  CC_
GAM1268  FLJ22940  5'  CCGCGGCCTCCGTCTCCTCCA  32555        _  CC_ _
                                CCGCGGCC CCG   CC CCA
                                |||||||| |||   || |||
                                GGCGCCGG GGC   GG GGT
                                     A   AGA  A
GAM1268  FLJ31890  5'  GCGGCCCAGCCCAGACCCG   32556       C   CCCAC
                                GCGGCCC GCCC    GCCCG
                                ||||||| ||||    |||||
                                CGCCGGG CGGG    TGGGC
                                    T   TC___
GAM1268  FLJ32780  5'  CGCGGCCCTGGCCCTGACG   32557        C_   CCC
                                CGCGGCCC  GCCC   ACG
                                ||||||||  ||||  |||
                                GCGCCGGG  CGGG   TGC
                                     AC   AC_
GAM1268  FREQ     5'  CCGCGGCCCCCGCCCCCCCG   32558          _     A
                                CCGCGGCCCC GCCCCCC CG
                                |||||||||| ||||||| ||
                                GGCGCCGGGG CGGGGGG GC
                                      G      _
GAM1268  GBTS1    5'  CCGCGGCCGCTGCTCCTGCCCG 32559        CC_  C  CCAC
                                CCGCGGCC   GC CC   GCCCG
                                ||||||||   || ||   |||||
```

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                                GGCGCCGG  CG GG   CGGGC
                                    CGA  A  A___
GAM1268  GDBR1    5'  CCGCCGCCCCCGCCCCGGCTCCC 32560     G       CCACG
              G                  CCGC GCCCCGCCCC    CCCG
                                 |||| ||||||||||    ||||
                                 GGCG CGGGGCGGGG    GGGC
                                   G        CCGA_
GAM1268  GTPBP1   5'  CCGCGGCCCTGGCCGCCCCC  32561        ____
                                 CCGCGGCCC   CGCCCCC
                                 |||||||||   |||||||
                                 GGCGCCGGG   GCGGGGG
                                     ACCG
GAM1268  HDAC10   5'  GGTCCCGCCCCGCGCCC    32562   C      CCA
                                 GG CCCGCCCC  CGCCC
                                 || ||||||||  |||||
                                 CC GGGCGGGG  GCGGG
                                  A       C__
GAM1268  HSPBP1   5'  CCGGGCCCCGCCTCCAAGC   32564    C       CC  C
                                 CCG GGCCCCGCC  CCA GC
                                 ||| |||||||||  ||| ||
                                 GGC CCGGGGCGG  GGT CG
                                   _       A_  T
GAM1268  HSPBP1   5'  CGGCCCCGCCCCTCCCATCCG  32563          _  A  C
                                 CGGCCCCGCCCC CC CG CCG
                                 |||||||||||| || || |||
                                 GCCGGGGCGGGG GG GT GGC
                                        A  _  A
GAM1268  HSSEXGENE 5'  CCACGGCCTCGCCCCGCGCCC  32566       C     CCA
                                 CCGCGGCC CGCCCC  CGCCC
                                 |||||||| ||||||  |||||
                                 GGTGCCGG GCGGGG  GCGGG
                                     A     C__
GAM1268  HSSEXGENE 5'  CCGCGGCCCCGCTCGCACG   32565          CCCC
                                 CCGCGGCCCCGC   CACG
                                 ||||||||||||   ||||
                                 GGCGCCGGGGCG   GTGC
                                        AGC_
GAM1268  KIAA0265  5'  CCCGGTCCCGTCAGCGCC   32567   G  C   CCCCC  _
                                 CC CGG CCCG    CA CGCC
                                 || ||| ||||    || ||||
                                 GG GCC GGGC    GT GCGG
                                   _  A   A____  C
GAM1268  KIAA0354  5'  CGGGCTCCGCCCCCCTCCTCCT 32568   C  C       ACG_  _
              CG                   CG GGC CCGCCCCCC   CC CG
                                 || ||| |||||||||   || ||
                                 GC CCG GGCGGGGGG   GG GC
                                   _  A       AGGA  A
GAM1268  KIAA0534  5'  CGCGGCCCCGCCTCGCCCG   32569          CCCCA
                                 CGCGGCCCCGCC    CGCCCG
                                 ||||||||||||    ||||||
```

```
                                GCGCCGGGGCGG    GCGGGC
                                      A____
GAM1268 KIAA0552 5' CGCGGCCCCAAGGATCCTGCGC 32570         CCC__ CA
              C                  CGCGGCCCCG    CC CGCC
                                 ||||||||||    || ||||
                                 GCGCCGGGGT    GG GCGG
                                       TCCTA AC
GAM1268 KIAA0664 3' GGCCCCGCTTCCCCCAGCCTCG 32571        __    C _
                                 GGCCCCGC CCCCCA GCC CG
                                 |||||||| |||||| ||| ||
                                 CCGGGGCG GGGGGT CGG GC
                                     AA    _ A
GAM1268 KIAA0783 5' CCCCGGCCTCGCCTGGCCC  32572   G   C  CCCCAC
                                 CC CGGCC CGCC     GCCC
                                 || ||||| ||||     ||||
                                 GG GCCGG GCGG     CGGG
                                  G   A  AC_____
GAM1268 KIAA0995 5' CCGCGGCCCGGCCCCCGCCACC 32573        C     CA
              CG                  CCGCGGCCC GCCCCC CGCCCG
                                  ||||||||| ||||||  ||||||
                                  GGCGCCGGG CGGGGG GTGGGC
                                      C     CG
GAM1268 KIAA1026 5' CCGCGGCCCGGCTTCGCCC  32574        C CCCCCA
                                 CCGCGGCCC GC     CGCCC
                                 ||||||||| ||     |||||
                                 GGCGCCGGG CG     GCGGG
                                      C AA_____
GAM1268 KIAA1026 5' CCCGGCTTCGCCCGCGCCC  32575   G  CC   CCCA
                                 CC CGGC CGCCC   CGCCC
                                 || ||||  |||||   |||||
                                 GG GCCG GCGGG   GCGGG
                                  _   AA   C___
GAM1268 KIAA1157 5' CCTTCCCCGCCCCCTGCGCTCG 32576   GCGG       CA  C
                                 CC   CCCCGCCCCC CGC CG
                                 ||   |||||||||| ||| ||
                                 GG   GGGGCGGGGG GCG GC
                                  AA__        AC  A
GAM1268 KIAA1247 5' CCCGGCCCTGCCTGTCCCC  32577   G    C ___
                                 CC CGGCCC GCC  CCCC
                                 || |||||| |||  ||||
                                 GG GCCGGG CGG  GGGG
                                  _    A  ACA
GAM1268 KIAA1494 5' GCGGCCCCACCGCGCC     32578         CCCCA  C
                                 GCGGCCCCGCC    CGC C
                                 ||||||||||     ||| |
                                 CGCCGGGGTGG    GCG G
                                       C____  A
GAM1268 KIAA1533 5' CCGCGGCCGCCGCCCCCACCCG 32579        _      CAC
                                 CCGCGGCC CCGCCCCC  GCCCG
                                 |||||||| ||||||||  |||||
```

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                                GGCGCCGG GGCGGGGG  TGGGC
                                    C      ___
GAM1268 KIAA1634 5' CGGCCCCGTCTCAGCCCG   32580       CCCCC  C
                                CGGCCCCG   CA GCCCG
                                ||||||||   || |||||
                                GCCGGGGC   GT CGGGC
                                    AGA__  _
GAM1268 KIAA1668 5' CCGCGGCCCGCCCGGCTCC  32581        C   CCCAC  _
                                CCGCGGCCC GCCC   GC CC
                                ||||||||| ||||   || ||
                                GGCGCCGGG CGGG   CG GG
                                    _   C____  A
GAM1268 KIAA1950 3' GACCCCGCCCTCGTCACTCCG 32582        CCCA  _
                                GGCCCCGCCC   CGC CCG
                                ||||||||||   ||| |||
                                CTGGGGCGGG   GTG GGC
                                     AGCA  A
GAM1268 KIAA1981 3' CCGCGGCCTCGCACTTCCCCA 32583       C  C___
                                CCGCGGCC CGC   CCCCA
                                |||||||| |||   |||||
                                GGCGCCGG GCG   GGGGT
                                    A  TGAA
GAM1268 LGI3     5' CCGCGGCCCCCCGCCCCACC   32584        _   _
                                CCGCGGCCCC GCCCC CC
                                |||||||||| ||||| ||
                                GGCGCCGGGG CGGGG GG
                                     G   T
GAM1268 LIV-1    5' CCGCGGCCTCGTTGTCCCACGG 32585       C  CCC_    _
            CCCG                  CCGCGGCC CG   CCCACG CCCG
                                |||||||| ||   |||||| ||||
                                GGCGCCGG GC   GGGTGC GGGC
                                    A  AACA    C
GAM1268 MAPK11   5' CCGCGCCCCGCGCCCGCGCCCG 32586     G    CC  A
                                CCGCG CCCCGC  CCC CGCCCG
                                ||||| ||||||  ||| ||||||
                                GGCGC GGGGCG  GGG GCGGGC
                                  _    C_  C
GAM1268 MAPK11   5' CCGCGCCCCGCGCCCGCGCCCG 32586     G    CC  A
                                CCGCG CCCCGC  CCC CGCCCG
                                ||||| ||||||  ||| ||||||
                                GGCGC GGGGCG  GGG GCGGGC
                                  _    C_  C
GAM1268 MGC10818 5' CCGCGGCCGCGCGAGGCGCGCT 32587       C  CCCCCA  C
            CG                  CCGCGGCC CGC    CGC CG
                                |||||||| |||    ||| ||
                                GGCGCCGG GCG    GCG GC
                                    C  CTCCGC  A
GAM1268 MGC11257 3' GCGGCCCCGCCCCGCGC    32588          CCA
                                GCGGCCCCGCCCC  CGC
                                ||||||||||||  |||
```

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                                CGCCGGGGCGGGG  GCG
                                      C__
GAM1268 MGC15827 3' CCTGGCCCCGCCTCCGCC   32589   GC      C CAC
                                CC GGCCCCGCC CC  GCC
                                || ||||||||| ||  |||
                                GG CCGGGGCGG GG  CGG
                                 A_       A ___
GAM1268 MGC15875 5' CGGCCCCGCCCCGAAGCGCCCG 32590         CCA_
                                CGGCCCCGCCCC  CGCCCG
                                ||||||||||||  ||||||
                                GCCGGGGCGGGG  GCGGGC
                                      CTTC
GAM1268 MGC16037 5' GCAGCCCCGCCCCCGCCC   32591          CAC
                                GCGGCCCCGCCCCC  GCCC
                                ||||||||||||||  ||||
                                CGTCGGGGCGGGGG  CGGG
                                      ___
GAM1268 MGC2555  5' CGCGGCCCCGCGCCGGCGC  32592        C CCA
                                CGCGGCCCCGC CC  CGC
                                |||||||||| ||  |||
                                GCGCCGGGGCG GG  GCG
                                      C CC_
GAM1268 MGC4399  5' CCGCGGCCCGTCGCCGCCC  32593       __  CCCCAC
                                CCGCGGCCC CGCC   GCCC
                                |||||||| ||||   ||||
                                GGCGCCGGG GCGG   CGGG
                                     CA  _______
GAM1268 MGC4607  5' CCGCGGCCCGCCCGGCCC   32594       C  CCCAC
                                CCGCGGCCC GCCC   GCCC
                                |||||||| ||||   ||||
                                GGCGCCGGG CGGG   CGGG
                                     _  C_____
GAM1268 N4BP1    5' CCGCGCCCCGCCGCC     32595     G    CCCCAC
                                CCGCG CCCCGCC    GCC
                                ||||| |||||||    |||
                                GGCGC GGGGCGG    CGG
                                     _    _______
GAM1268 NIR1     5' CCGCGCCCCCGCCCCGCC   32596     G     CCAC C
                                CCGCG CCCCGCCCC  GC C
                                ||||| |||||||||  || |
                                GGCGC GGGGCGGGG  CG G
                                   G       _____ A
GAM1268 NPEPL1   5' CCCCGGCCCTGCCCGGCCC  32597   G    C  CCCAC
                                CC CGGCCC GCCC   GCCC
                                || |||||| ||||   ||||
                                GG GCCGGG CGGG   CGGG
                                 G    A  C_____
GAM1268 NR5A1    3' GCGGCCCCGCCCAGGCCC   32598         CCCAC
                                GCGGCCCCGCCC   GCCC
                                ||||||||||||   ||||
```

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                                CGCCGGGGCGGG    CGGG
                                      TC___
GAM1268 NXPH3    3' CCCGGCCCCGCCCCACCCGTGC 32599    G        _ AC_
             CCG                   CC CGGCCCCGCCCC CC   GCCCG
                                || ||||||||||| ||   |||||
                                GG GCCGGGGCGGGG GG   CGGGC
                                 _         T  GCA
GAM1268 OSBPL2   5' GCCGCCCCGCCCCCGCCC    32600    G        CAC
                                GC GCCCCGCCCCC   GCCC
                                || ||||||||||   ||||
                                CG CGGGGCGGGGG   CGGG
                                 G        ___
GAM1268 OSBPL2   5' GCCGCCCCGCCCCCGCCC    32600    G        CAC
                                GC GCCCCGCCCCC   GCCC
                                || ||||||||||   ||||
                                CG CGGGGCGGGGG   CGGG
                                 G        ___
GAM1268 P5326    5' CCCGGCTCCGCTCCTGCC    32601    G   C    C  CCAC
                                CC CGGC CCGC CC    GCC
                                || |||| |||| ||    |||
                                GG GCCG GGCG GG    CGG
                                 _   A    A  A___
GAM1268 PANX1    5' GCGGTTCCACCCCGCACGCCCG 32602      CC      C
                                GCGG  CCGCCCC CACGCCCG
                                ||||  ||||||| ||||||||
                                CGCC  GGTGGGG GTGCGGGC
                                  AA      C
GAM1268 PCF11    5' CCGCGGCCCCCCTCCGAGGTCC 32603          G  C  CACGC
             G                    CCGCGGCCCC CC CC    CCG
                                |||||||||| || ||    |||
                                GGCGCCGGGG GG GG    GGC
                                      _  A  CTCCA
GAM1268 PIP5K2A  5' CCGCGCTCCGCTCCGCCC    32604      G C    C  CCAC
                                CCGCG C CCGC CC    GCCC
                                ||||| | |||| ||    ||||
                                GGCGC G GGCG GG    CGGG
                                  _ A    A _____
GAM1268 PM5      5' CCGGGTCCCGCCCCTCACAC   32605    C  C       C
                                CCG GG CCCGCCCC CACGC
                                ||| || |||||||| |||||
                                GGC CC GGGCGGGG GTGTG
                                  _  A       A
GAM1268 PPP1R1B  5' CGGGGCTCGCCCCCCGCGCTCG 32606    C   CC      A   C
                                CG GGC  CGCCCCCC CGC CG
                                || |||  |||||||| ||| ||
                                GC CCG  GCGGGGGG GCG GC
                                 C  A_       C   A
GAM1268 PTR4     5' CCGCGGCCGCCGCCGCCC    32607         _    CCCCAC
                                CCGCGGCC CCGCC     GCCC
                                |||||||| |||||     ||||
```

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                                GGCGCCGG GGCGG     CGGG
                                    C    _______
GAM1268 RASD2    3' CCTGGCCTGCCCACCCCACGC 32608    GC   CC   __
                                CC  GGCC  GCCC  CCCACGC
                                ||  ||||  ||||  |||||||
                                GG  CCGG  CGGG  GGGTGCG
                                 A_   A_   TG
GAM1268 REV1L    5' CCACGCTCCCCCACGCC     32609    _  _      C
                                CC CGC CCCCCACGC C
                                || ||| |||||||| |
                                GG GCG GGGGGTGCG G
                                 T  A       A
GAM1268 RHOBTB2  3' CCTGGCTCTGCCCCTCCTCCG 32610    GC   CCC    _ ACGC
                                CC  GGC   GCCCC CC    CCG
                                ||  |||   ||||| ||    |||
                                GG  CCG   CGGGG GG    GGC
                                 A_   AGA    A  A___
GAM1268 SDS3     5' CCGCGGCCACCCGCGCC     32611        CC   CCCA   C
                                CCGCGGCC  GCCC    CGC C
                                ||||||||  ||||    ||| |
                                GGCGCCGG  TGGG    GCG G
                                     __    C___   A
GAM1268 SMARCE1  5' CGCTCGCCCCGCCCCTCGCGTC 32612     G_        CCA   __
             CG                   CGC  GCCCCGCCCC   CGC  CCG
                                  |||  ||||||||||   |||  |||
                                  GCG  CGGGGCGGGG   GCG  GGC
                                    AG        A__   CA
GAM1268 SNAP91   5' CCGGGCCCCGCTCCTCAGCTCC 32613     C      C  C  C  _
             G                    CCG GGCCCCGC CC CA GC CCG
                                  ||| ||||||| || || || |||
                                  GGC CCGGGGCG GG GT CG GGC
                                    _       A  A  _  A
GAM1268 SRF      5' CCGGGGCCCCTGCACGCCC   32614     C     GCCCCC
                                  CCG GGCCCC     CACGCCC
                                  ||| ||||||     |||||||
                                  GGC CCGGGG     GTGCGGG
                                    C     AC____
GAM1268 SSB-3    3' CGGCCCCGCCCCCACCC      32615          CCAC
                                  CGGCCCCGCCCC    GCCC
                                  ||||||||||||    ||||
                                  GCCGGGGCGGGG    TGGG
                                                 _____
GAM1268 STK17B   5' CCGCTGTCCCGCCCCACGCC   32616     GGC      CC
                                  CCGC   CCCGCCCC  ACGCC
                                  ||||   ||||||||  |||||
                                  GGCG   GGGCGGGG  TGCGG
                                    ACA       __
GAM1268 TIGD5    5' GCCCCGGGGTCCCCTGCGCCCG 32617       C___   CA
                                  GCCCCG    CCCC  CGCCCG
                                  ||||||    ||||  ||||||
```

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                                CGGGGC   GGGG  GCGGGC
                                   CCCA   AC
GAM1268 TLN1    5' GCGCCCCGCCCGCCGGCCCG  32618    G      C  AC
                                GCG CCCCGCCC CC  GCCCG
                                ||| |||||||| ||  |||||
                                CGC GGGGCGGG GG  CGGGC
                                  _      C  C_
GAM1268 TOB2    5' CCTGGCCCCGCGTCGCCC    32619    GC      CCCCCA
                                CC  GGCCCCGC     CGCCC
                                ||  ||||||||     |||||
                                GG  CCGGGGCG     GCGGG
                                 A_      CA____
GAM1268 TRAP-1  5' GGCCCCGCCCACGCGTCCG   32620         CCC   __
                                GGCCCCGCCC   ACGC  CCG
                                ||||||||||   ||||  |||
                                CCGGGGCGGG   TGCG  GGC
                                     ___   CA
GAM1268 TUBGCP3 5' CCGCGGCCCGCGCCCTTCC   32621         _    C_
                                CCGCGGCCC CGCCC  CC
                                ||||||||| |||||  ||
                                GGCGCCGGG GCGGG  GG
                                     C    AA
GAM1268 UHRF2   5' CCGCGCCCCGCCCGGCCC    32622      G      CCCAC
                                CCGCG CCCCGCCC    GCCC
                                ||||| ||||||||    ||||
                                GGCGC GGGGCGGG    CGGG
                                  _      C_____
GAM1268 ULK2    5' CCGCGGCCCCGCGCTTCCCC  32623          C___
                                CCGCGGCCCCGC   CCCC
                                ||||||||||||   ||||
                                GGCGCCGGGGCG   GGGG
                                       CGAA
GAM1268 YAP1    5' CCGCGGCCCCGCATCCCCC   32624          __
                                CCGCGGCCCCGC  CCCCC
                                ||||||||||||  |||||
                                GGCGCCGGGGCG  GGGGG
                                       TA
GAM1268 ZDHHC2  5' GCGCTCCGCCCCCGCC      32625     G C      CAC
                                GCG C CCGCCCCC   GCC
                                ||| | ||||||||   |||
                                CGC G GGCGGGGG   CGG
                                  _ A      ___
GAM1268 ZDHHC5  5' CGCGGCCCCCGCACGCTCCACG 32626         _ CCC__
            CCCG                   CGCGGCCCC GC    CCACGCCCG
                                ||||||||| ||    |||||||||
                                GCGCCGGGG CG    GGTGCGGGC
                                     G  TGCGA
GAM1268 LOC115110 3' CCACGGCCACCTTTCCCTGCG 32627        _ GCC   CA
                                CCGCGGCC CC   CCC  CG
                                |||||||| ||   |||  ||
```

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                                GGTGCCGG GG   GGG  GC
                                    T  AAA   AC
GAM1268  LOC124093 5'  CCGGTGCTGCCTCCACGCCCG  32628    CG  CCC   CC
                                CCG  GC   GCC  CCACGCCCG
                                |||  ||   |||  |||||||||
                                GGC  CG   CGG  GGTGCGGGC
                                  CA  A__   A_
GAM1268  LOC126969 5'  CCGCGGCCCGCGTCTCCCCC   32629        _  C__
                                CCGCGGCCC CG   CCCCC
                                |||||||||  ||   |||||
                                GGCGCCGGG GC   GGGGG
                                     C  AGA
GAM1268  LOC138128 5'  CCGAGGTCCGGGCCACGCCCG  32630    C  CC   CCCC
                                CCG GG  CCG    CCACGCCCG
                                ||| ||  |||    |||||||||
                                GGC CC  GGC    GGTGCGGGC
                                  T  A_   CC__
GAM1268  LOC145371 5'  CGCGGCCCGCGCCCGCCC    32631        _    CCCAC
                                CGCGGCCC CGCCC    GCCC
                                ||||||| |||||     ||||
                                GCGCCGGG GCGGG    CGGG
                                    C    _____
GAM1268  LOC145980 5'  CCGCAGCCCCGGGTGCGCGCTC 32632          CCCCCCA   C
           G                    CCGCGGCCCCG      CGC CG
                                ||||||||||       ||| ||
                                GGCGTCGGGGC      GCG GC
                                      CCACGC_   A
GAM1268  LOC145990 5'  CCGCCGCCCCGCCTCCTCCACC 32633     G      C  CA
                                CCGC GCCCCGCC CC  CGCC
                                |||| |||||||| ||  ||||
                                GGCG CGGGGCGG GG  GTGG
                                  G       A  AG
GAM1268  LOC146108 5'  CCCGGCCCCGGGCGCCC     32634    G      CCCCCCA
                                CC CGGCCCCG      CGCCC
                                || ||||||||      |||||
                                GG GCCGGGGC      GCGGG
                                 _       CC_____
GAM1268  LOC146733 3'  CCGGGCCCCGCCCCTCCCC    32635    C        CCACG
                                CCG GGCCCCGCCCC    CCC
                                ||| ||||||||||     |||
                                GGC CCGGGGCGGGG    GGG
                                  _         AG___
GAM1268  LOC147965 5'  CCGCGGCCCCCTCCCACG    32636         GCCC
                                CCGCGGCCCC    CCCACG
                                ||||||||||    ||||||
                                GGCGCCGGGG    GGGTGC
                                      GA__
GAM1268  LOC148753 5'  CCGCGGCCTCCCCGGCGCTCCG 32637        CCGC    CA  _
                                CCGCGGCC    CCCC  CGC CCG
                                ||||||||    ||||  ||| |||
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                                GGCGCCGG   GGGG  GCG GGC
                                    A___   CC   A
GAM1268  LOC149297 5'  CCCGGCCCCGCCCCGTAGCC  32638   G        CCAC
                                CC CGGCCCCGCCCC   GCC
                                || ||||||||||||   |||
                                GG GCCGGGGCGGGG   CGG
                                 _         CAT_
GAM1268  LOC150465 5'  CCGCGGCCCGGCCCCCGCCGCC 32639        C     CA
           CG                    CCGCGGCCC GCCCCC  CGCCCG
                                |||||||||| ||||||  ||||||
                                GGCGCCGGG CGGGGG  GCGGGC
                                    C     CG
GAM1268  LOC152137 5'  GCTCCCGCCCCCGGGCCC   32640   _      CAC
                                GC CCCGCCCCC   GCCC
                                || |||||||||   ||||
                                CG GGGCGGGGG   CGGG
                                 A       CC_
GAM1268  LOC155064 5'  CCATGGCCCCGCTTTCGGAGGC 32641    C      CCCCCAC_
           CCG                    CCG GGCCCCGC       GCCCG
                                ||| ||||||||       |||||
                                GGT CCGGGGCG       CGGGC
                                 A       AAAGCCTC
GAM1268  LOC155382 5'  CGGCCCCGCCCGCGCCGCCCG  32642         CCCA
                                CGGCCCCGCCC   CGCCCG
                                ||||||||||   ||||||
                                GCCGGGGCGGG   GCGGGC
                                      CGCG
GAM1268  LOC158856 5'  CCGCGGCCCAGCTTTCCTTCAT 32643        C ___ CC  C
           GCC                    CCGCGGCCC GC   CC  CA GCC
                                ||||||||| ||   ||  || |||
                                GGCGCCGGG CG   GG  GT CGG
                                     T  AAA  AA  A
GAM1268  LOC163682 5'  GGCCTGGCCTCCCCTCAGCCC  32644     CC  _   A _
                                GGCC  GCC CCCC C GCCC
                                ||||  ||| |||| | ||||
                                CCGG  CGG GGGG G CGGG
                                  AC   A    A T
GAM1268  LOC165257 5'  GCGGCCCCGCTCCCCGCGCTCG 32645         C   A   C
                                GCGGCCCCGC CCCC CGC CG
                                |||||||||| |||| ||| ||
                                CGCCGGGGCG GGGG GCG GC
                                     A   C   A
GAM1268  LOC196411 5'  CCGCCGGCTCCGCTCCCGCC   32646     _  C   C   CAC
                                CCGC GGC CCGC CCC   GCC
                                |||| ||| |||| |||   |||
                                GGCG CCG GGCG GGG   CGG
                                  G   A   A   ___
GAM1268  LOC196489 3'  CCCGGGCCCCCCCACGCCC    32647    G   CCCC
                                CC CGG   GCCCCCCCACGCCC
                                || |||   ||||||||||||
```

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                                GG GCC    CGGGGGGTGCGGG
                                 _  _____
GAM1268  LOC197273 5'  CGGGCCGCTTCACGCCC     32648    C    CC  CCCC
                                CG GGCC  GC    CACGCCC
                                || ||||  ||    |||||||
                                GC CCGG  CG    GTGCGGG
                                 _   __  AA__
GAM1268  LOC197287 3'  CCGCGGCCCTTCCCAGCTGGCT 32445         CG   CCCAC  C
                  CG                    CCGCGGCCC  CCC     GC CG
                                |||||||||  |||     || ||
                                GGCGCCGGG  GGG     CG GC
                                     AA   TCGAC  A
GAM1268  LOC199923 3'  CCGCGGCCCCCCGTTCCCCATCG 32649          _ CC     _
                                CCGCGGCCCC G  CCCCA CG
                                |||||||||| |  ||||| ||
                                GGCGCCGGGG C  GGGGT GC
                                      G AA     A
GAM1268  LOC199988 5'  GCGGTCCCCACCCACGCC     32650      _       CCC
                                GCGG CCCCGCCC   ACGCC
                                |||| ||||||||   |||||
                                CGCC GGGGTGGG   TGCGG
                                  A       ____
GAM1268  LOC202020 5'  CCGCGGCCCCTCCCCTGCGC   32651          GC    CA
                                CCGCGGCCCC  CCCC  CGC
                                |||||||||  ||||  |||
                                GGCGCCGGGG  GGGG  GCG
                                      A_    AC
GAM1268  LOC206962 5'  CCCCGGCCCCGCCCCGCC     32652    G          _
                                CC CGGCCCCGCCCC CC
                                || ||||||||||| ||
                                GG GCCGGGGCGGGG GG
                                 G          C
GAM1268  LOC219654 5'  CGCGGCCCCCCTCCGCAGC    32653          G  C  _  C
                                CGCGGCCCC CC CC CA GC
                                |||||||| || || || ||
                                GCGCCGGGG GG GG GT CG
                                     _  A  C  _
GAM1268  LOC220107 5'  CCACGCCCCCGCCCCGCTCCTC 32654          ____  A__      III
                  GCGCCCGC                CCCCGCCCC   CC   CGCCCG   C
                                |||||||||   ||   ||||||   |
                                GGGGCGGGG   GG   GCGGGC   G
                                     CGA  AGC      III
GAM1268  LOC253358 5'  CGCAGCCGCCGCCCTCCACGCC 32655        _     C
                  CG                    CGCGGCC CCGCCC CCACGCCCG
                                ||||||| |||||| |||||||||
                                GCGTCGG GGCGGG GGTGCGGGC
                                    C     A
GAM1268  LOC255082 5'  CGAGGCCCCGCCCCTTCACG   32656    C         C_
                                CG GGCCCCGCCCC  CACG
                                || ||||||||||  ||||
```

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                                GC CCGGGGCGGGG  GTGC
                                 T          AA
GAM1268  LOC255251 5'  CGGCCCCGCCCCGAAGCGCCCG 32590           CCA_
                                CGGCCCCGCCCC    CGCCCG
                                ||||||||||||   ||||||
                                GCCGGGGCGGGG    GCGGGC
                                      CTTC
GAM1268  LOC255251 5'  CCGGGCCCCGCCCCTGCC    32657     C         CCAC
                                CCG GGCCCCGCCCC    GCC
                                ||| ||||||||||||   |||
                                GGC CCGGGGCGGGG    CGG
                                  _         A___
GAM1268  LOC255718 5'  CCGCGGCGTCGCCCTTGACAGC 32658        CC    CCC  _
                                CCGCGGC  CGCCC   AC GC
                                |||||||  |||||   || ||
                                GGCGCCG  GCGGG   TG CG
                                    CA    AAC  T
GAM1268  LOC256520 5'  CGCGGCCCCGCCTCCGCCGCTC 32659           C  CA   C
            G                    CGCGGCCCCGCC CC  CGC CG
                                ||||||||||| ||  ||| ||
                                GCGCCGGGGCGG GG  GCG GC
                                      A  CG   A
GAM1268  LOC256536 3'  CGGCCGCCCCACGCCC      32660       CCGCC
                                CGGCC    CCCCACGCCC
                                |||||    ||||||||||
                                GCCGG    GGGGTGCGGG
                                  C_____
GAM1268  LOC256664 5'  CCGCGCCCCGCCCCGCCC    32661       G       CCAC
                                CCGCG CCCCGCCCC    GCCC
                                ||||| |||||||||    ||||
                                GGCGC GGGGCGGGG    CGGG
                                  _       _____
GAM1268  LOC256789 5'  CGTGGCCCCGCATCCTGCGCC  32662    C       CC  CA
                                CG GGCCCCGC  CC  CGCC
                                || ||||||||  ||  ||||
                                GC CCGGGGCG  GG  GCGG
                                 A       TA  AC
GAM1268  LOC257471 5'  CCGCCGCCAGCCCACGCC    32517    _    C_
                                CC CCGCC  CCCACGCC
                                || |||||  ||||||||
                                GG GGCGG  GGGTGCGG
                                 C    TC
GAM1268  LOC51029  5'  CCGCCGCCTCGTCCTCAAGCC  32663     G   C  CC  C  C
                                CCGC GCC CG  CC CA GCC
                                |||| ||| ||  || || |||
                                GGCG CGG GC  GG GT CGG
                                  G   A  A_  A  T
GAM1268  LOC92267  5'  CGCGGCCCCCAGCCCACG     32664          CCC
                                CGCGGCCCCG   CCCACG
                                ||||||||||   ||||||
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                                GCGCCGGGGT  GGGTGC
                                     C__
GAM1269 ASK     5' CCTCGTGCCTGCCTTCTCGC  32668     CCC  CCC  C_
                                CCTCG  CCT  GCC  CTCGC
                                |||||  |||  |||  |||||
                                GGAGC  GGA  CGG  GAGCG
                                  AC_  ___  AA
GAM1269 ASK     5' CCTCGCGCTCGCCCCTCG   32667     CCC  CC
                                CCTCGC  CTC  GCCCCTCG
                                ||||||  |||  ||||||||
                                GGAGCG  GAG  CGGGGAGC
                                   C__  __
GAM1269 BAX     5' CCCGCCGCCGCCTCTCG    32669     CCCTC   C
                                CTCGCC   CCGCC CTCG
                                ||||||   ||||| ||||
                                GGGCGG   GGCGG GAGC
                                   C____   A
GAM1269 BAX     5' CCCGCCGCCGCCTCTCG    32669     CCCTC   C
                                CTCGCC   CCGCC CTCG
                                ||||||   ||||| ||||
                                GGGCGG   GGCGG GAGC
                                   C____   A
GAM1269 BAX     5' CCCGCCGCCGCCTCTCG    32669     CCCTC   C
                                CTCGCC   CCGCC CTCG
                                ||||||   ||||| ||||
                                GGGCGG   GGCGG GAGC
                                   C____   A
GAM1269 BAX     5' CCCGCCGCCGCCTCTCG    32669     CCCTC   C
                                CTCGCC   CCGCC CTCG
                                ||||||   ||||| ||||
                                GGGCGG   GGCGG GAGC
                                   C____   A
GAM1269 BAX     5' CCCGCCGCCGCCTCTCG    32669     CCCTC   C
                                CTCGCC   CCGCC CTCG
                                ||||||   ||||| ||||
                                GGGCGG   GGCGG GAGC
                                   C____   A
GAM1269 BCL9    3' CTCCCCCCTCCCCCCACCCCTC 32670   G  __
           GC                    CTC CCCC  CTCCCGCCCCTCGC
                                 ||| ||||  ||||||||||||||
                                 GAG GGGG  GGGGGTGGGGAGCG
                                   G   AG
GAM1269 CACNG8  5' CTCGCACCAGAGGCCCCGCTCT 32671     _ CC___    CCC
           TCG                   CTCGC CC   TCCCGC  TCG
                                 ||||| ||   ||||||  |||
                                 GAGCG GG   GGGGCG  AGC
                                   T  TCTCC    AGA
GAM1269 CCND1   5' CCTCGCGCTCTTCTGCCCCTCG 32672     CCC  CC__
           C                     CCTCGC  CTC   GCCCCTCGC
                                 ||||||  |||   |||||||||
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                                GGAGCG  GAG   CGGGGAGCG
                                   C__  AAGA
GAM1269 CD63    5' CTGCGCCCCCCGGCCCCTCG  32673   _     CCC
                                CT CGCCCCCT  GCCCCTCG
                                || ||||||||  ||||||||
                                GA GCGGGGGG  CGGGGAGC
                                 C      C__
GAM1269 CDC2L2  5' CCTGCGGGCCTCCCGCTCCTTG 32674    C CC_     C  C
            C                    CCT GC  CCTCCCGC CCT GC
                                ||| ||  |||||||| ||| ||
                                GGA CG  GGAGGGCG GGA CG
                                  _ CCC      A  A
GAM1269 CHES1   5' CCTGCCCCCCCCGCTGCTTCTCG 32675    C      CC_ CC
            C                    CCT GCCCCCTC  GC  CTCGC
                                ||| ||||||||  ||  |||||
                                GGA CGGGGGGG  CG  GAGCG
                                  _      CGA  AA
GAM1269 CHRNB2  3' CCTGCCCTTCCACCCCT    32676    C   CCTC
                                CCT GCCC   CCGCCCCT
                                ||| ||||   ||||||||
                                GGA CGGG   GGTGGGGA
                                  _   AA__
GAM1269 DDX26   5' CCTCCGCCTCCTCCTGCC    32677    _  C   C
                                CCTC GCC CCTCC GCC
                                |||| ||| ||||| |||
                                GGAG CGG GGAGG CGG
                                  G  A    A
GAM1269 DLC1    5' CTCGCCGCTCCCTGCCCCTCG  32678      CC   _
                                CTCGCC  CTCCC GCCCCTCG
                                ||||||  ||||| ||||||||
                                GAGCGG  GAGGG CGGGGAGC
                                   C_    A
GAM1269 DYRK2   5' CCTCCCGGCCGCCCCTCG   32679   _  TC
                                CC CCC  CCGCCCCTCG
                                || |||  ||||||||||
                                GG GGG  GGCGGGGAGC
                                 A  CC
GAM1269 DYRK2   5' CCTCCCGGCCGCCCCTCG   32679   _  TC
                                CC CCC  CCGCCCCTCG
                                || |||  ||||||||||
                                GG GGG  GGCGGGGAGC
                                 A  CC
GAM1269 G6PD    3' CTCGCCCCTTTCCTCCCCCT  32680      C_  CG
                                CTCGCCCC  TCC  CCCCT
                                ||||||||  |||  |||||
                                GAGCGGGG  AGG  GGGGA
                                     AA  AG
GAM1269 GCS1    5' CCTCTCCGGCTCCCGCCTCTCG 32681    G  CC      C
            C                    CCTC CC  CTCCCGCC CTCGC
                                |||| ||  |||||||| |||||
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                                GGAG GG  GAGGGCGG GAGCG
                                  A  CC       A
GAM1269  GPR2     3'  CCTGCCCCCTCCTCTAGATTCG 32682     C       CGCCCC_
               C                   CCT GCCCCCTCC      TCGC
                                   ||| |||||||||      ||||
                                   GGA CGGGGGAGG      AGCG
                                    _       AGATCTA
GAM1269  HHEX     5'  CGCGCTCCGGCCCCTCG     32683     CCC    C
                                   CGC   CTCC GCCCCTCG
                                   |||   |||| ||||||||
                                   GCG   GAGG CGGGGAGC
                                     C__    C
GAM1269  HLF      5'  CCTGCCTCGAACCCCTCG    32684     C   CCC  CC
                                   CCT GCC   TC  GCCCCTCG
                                   ||| |||   ||  ||||||||
                                   GGA CGG   AG  TGGGGAGC
                                     _  ___  CT
GAM1269  HNRPD    5'  CCTTCGCCTCCCACTCTCGC   32685     _   CCC     CC
                                   CCT CGCC   TCCCGC  CTCGC
                                   ||| ||||   ||||||  |||||
                                   GGA GCGG   AGGGTG  GAGCG
                                     A   ___     A_
GAM1269  HNRPD    5'  CCTTCGCCTCCCACTCTCGC   32685     _   CCC     CC
                                   CCT CGCC   TCCCGC  CTCGC
                                   ||| ||||   ||||||  |||||
                                   GGA GCGG   AGGGTG  GAGCG
                                     A   ___     A_
GAM1269  INHBB    5'  CCTCGCCCTCACTGCCTCGC   32686        CCTCC   C_
                                   CCTCGCCC    CGC  CCTCGC
                                   ||||||||    |||  ||||||
                                   GGAGCGGG    GTG  GGAGCG
                                       A____   AC
GAM1269  JJAZ1    5'  CCTGCCTCCTCCCCCC      32687     C   C     G
                                   CCT GCC CCTCCC CCC
                                   ||| ||| |||||| |||
                                   GGA CGG GGAGGG GGG
                                     _  A     _
GAM1269  KCNK10   5'  CCTTACCCCCTCCCCACG    32688     CG     CCCG    T
                                   CCT  CCCCCT    CCCC CG
                                   |||  ||||||    |||| ||
                                   GGA  GGGGGA    GGGG GC
                                     AT     _____    T
GAM1269  KCNQ3    5'  CCTCGCCCCCGCCGGCCGCTTC 32689          T  C   C  _
               GC                    CCTCGCCCCC CC GCC CT CGC
                                     |||||||||| || ||| || |||
                                     GGAGCGGGGG GG CGG GA GCG
                                           C  C   C  A
GAM1269  LYPLA1   5'  CCGCCCTGCCCTGCCCCTCGC  32690       CCT   _
                                   TCGCCC   CCC GCCCCTCGC
                                   ||||||   ||| |||||||||
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                                GGCGGG  GGG CGGGGAGCG
                                   AC_  A
GAM1269 MAF     5' CCTTGCGCTCGCCTCCTTGC  32691    C CCC  CC  _  C
                                CCT GC  CTC  GCC CCT GC
                                ||| ||  |||  ||| ||| ||
                                GGA CG  GAG  CGG GGA CG
                                  A C__  __  A  A
GAM1269 MAP1B   5' CCTCCGCCCTCTCCCAGC   32692     _   C   _
                                CCTC GCCC CTCCC GC
                                |||| |||| ||||| ||
                                GGAG CGGG GAGGG CG
                                  G   A   T
GAM1269 MAPRE3  3' CCATGCCCCCAAGCCCCCCTCG 32693   TC    TC_  G
             C                   CC  GCCCCC  CC CCCCTCGC
                                 ||  ||||||  || ||||||||
                                 GG  CGGGGG  GG GGGGAGCG
                                  TA    TTC  _
GAM1269 MGEA5   5' CCTTCCCCCTCCTTCTCG   32694    CG     CGCCC
                                CCT  CCCCCTCC   CTCG
                                |||  ||||||||   ||||
                                GGA  GGGGGAGG   GAGC
                                  A_     AA___
GAM1269 MMP25   3' CCTTGTCCTCCCCGCCCCTC  32695    CGCC  CT
                                CCT   CC  CCCGCCCCTC
                                |||   ||  ||||||||||
                                GGA   GG  GGGCGGGGAG
                                  ACA_  AG
GAM1269 MNT     3' CTCTGTCCCCTCCCCGGGCCCC 32696    GC_     ___   _
             CTCGC                 CTC  CCCCTCCC  GCCCC TCGC
                                |||  ||||||||  ||||| ||||
                                GAG  GGGGAGGG  CGGGG AGCG
                                  ACA      GCC    G
GAM1269 NCKAP1  5' CCTCCTCCCCTCCCGCCC   32697     GC
                                CCTC  CCCCTCCCGCCC
                                ||||  ||||||||||||
                                GGAG  GGGGAGGGCGGG
                                   GA
GAM1269 NEUD4   3' CCTCTCCCCCTCCCCCTG   32698     G      GCC  C
                                CCTC CCCCCTCCC  CCT G
                                |||| |||||||||  ||| |
                                GGAG GGGGGAGGG  GGA C
                                  A      ___  _
GAM1269 PAPPA   5' CCCCGCCCCCCCCTTCGC   32699          __
                                CCTCGCCCCCTCC  CGC
                                ||||||||||||  |||
                                GGGGCGGGGGGGG  GCG
                                       AA
GAM1269 PGF     3' CCTGTCCTTCCCTGCCCCTCG 32700    CGCC  C   _
                                CCT   CC TCCC GCCCCTCG
                                |||   || |||| ||||||||
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                                GGA   GG AGGG CGGGGAGC
                                  CA__  A   A
GAM1269  PRDM16   3'  CCCCGCCCGCCTCCGTCCTTCG 32701        _    C C  C
                                CCTCGCCC CCTCC G CC TCG
                                |||||||| ||||| | || |||
                                GGGGCGGG GGAGG C GG AGC
                                     C    _ A  A
GAM1269  PTPN11   5'  CCTCCTCCGCCCCCGCCCTTCG 32702     GC  C       C
           C                     CCTC  CC CTCCCGCCC TCGC
                                ||||  || |||||||| ||||
                                GGAG  GG GGGGGCGGG AGCG
                                  GA  C       A
GAM1269  PTPN11   5'  CCTCCTCCGCCCCCGCCCTTCG 32702     GC  C       C
           C                     CCTC  CC CTCCCGCCC TCGC
                                ||||  || |||||||| ||||
                                GGAG  GG GGGGGCGGG AGCG
                                  GA  C       A
GAM1269  PTTG1IP  5'  CCTCGCCATCTGCCCCGCCCCT 32704       CC  __
           CGC                     CCTCGCC  CT  CCCGCCCCTCGC
                                |||||||  ||  ||||||||||||
                                GGAGCGG  GA  GGGCGGGGAGCG
                                   TA  CG
GAM1269  PTTG1IP  5'  CTCGCCCCGCTCCCTCG     32703        CTCCC  _
                                CTCGCCCC    GC CCCTCG
                                ||||||||    || ||||||
                                GAGCGGGG    CG GGGAGC
                                     _____  A
GAM1269  RIMS1    5'  CCCGCCCCCTCTGCTCG     32705         CC  CCC
                                CTCGCCCCCTC  GC   TCG
                                ||||||||||  ||   |||
                                GGGCGGGGGAG  CG   AGC
                                      A_  ___
GAM1269  ROBO1    5'  TCGCCCTCGGCCCCTCGC    32706       CC  CC
                                TCGCCC  TC  GCCCCTCGC
                                ||||||  ||  |||||||||
                                AGCGGG  AG  CGGGGAGCG
                                   __  C_
GAM1269  RPS6KA1  5'  CCGCGCCCCCCCCGAGCCCCTCG 32707    T       CC
           C                     CC CGCCCCCTC  GCCCCTCGC
                                || |||||||||  |||||||||
                                GG GCGGGGGGGG  CGGGGAGCG
                                 C       CT
GAM1269  S100B    5'  CTCACCCCTTCCTGGTCTCCTT 32708        C   CGCC__   C
           GC                     CTCGCCCC TCC     CCT GC
                                |||||||| |||     ||| ||
                                GAGTGGGG AGG     GGA CG
                                     A   ACCAGA   A
GAM1269  SET7     5'  CCTTCGCCCACTTGCCCCTCGC 32709     _    C  CCC
                                CCT CGCCC CT   GCCCCTCGC
                                ||| ||||| ||   |||||||||
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                                GGA GCGGG GA   CGGGGAGCG
                                  A    T A__
GAM1269 SLC18A3  5' CTGCGCTCCCCTCCCCTCGC  32710   _ _    CCCG
                                CT CGC CCCCT   CCCCTCGC
                                || ||| |||||   ||||||||
                                GA GCG GGGGA   GGGGAGCG
                                 C  A   ____
GAM1269 SLC6A8   5' CCTCGCCCTCTCCTTCCC   32711       C   CG
                                CCTCGCCC CTCC  CCC
                                |||||||| ||||  |||
                                GGAGCGGG GAGG  GGG
                                    A   AA
GAM1269 SOX2    3' GCACCCCTCCCATTTCCCTCG 32712   _      C__
                                GC CCCCTCCCG   CCCTCG
                                || |||||||||   ||||||
                                CG GGGGAGGGT   GGGAGC
                                 T       AAA
GAM1269 TGIF    5' CCTCCCCTCTCCGCTCCT   32713    CGC    _   C
                                CCT   CCCCTC CCGC CCT
                                |||   |||||| |||| |||
                                GGA   GGGGAG GGCG GGA
                                  ___    A   A
GAM1269 TMPRSS3  5' CCTTTCCCCCTCCCCTC    32714    CG    CCCG
                                CCT  CCCCCT   CCCCTC
                                |||  ||||||   ||||||
                                GGA  GGGGGA   GGGGAG
                                  AA    ____
GAM1269 TNFRSF12 3' TCACCCCCTCTCGACATTCG  32715       C  CCCC
                                TCGCCCCCTC CG   TCG
                                ||||||||||  ||   |||
                                AGTGGGGGAG GC   AGC
                                     A  TGTA
GAM1269 ZNF205   3' CCTCGCCCTCCCCCATCG    32716       C    CCCC
                                CCTCGCCC CTCCCG   TCG
                                |||||||| ||||||   |||
                                GGAGCGGG GGGGGT   AGC
                                    A    ____
GAM1269 ARHGEF11 5' CCTCTTCCCCTCCCCCGC    32717    G_   _
                                CCTC  CCCC CTCCCGC
                                ||||  |||| |||||||
                                GGAG  GGGG GGGGGCG
                                  AA   A
GAM1269 ATP6V1B2 5' CCTCGCCCCGCCCCCTTCGC  32718       CTCCC   __
                                CCTCGCCCC   GCCCC  TCGC
                                |||||||||   |||||  ||||
                                GGAGCGGGG   CGGGG  AGCG
                                     _____   GA
GAM1269 BNIP2   5' GCCCCCTCGTCCTCTTCGC   32720       CCG  C  _
                                GCCCCCTC   CC CT CGC
                                ||||||||   || || |||
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                                CGGGGGAG  GG GA GCG
                                    CA_  A  A
GAM1269 BNIP2    5' CCTCGTCCTCTTCGCCCCTC  32719      CCC   C_
                                CCTCG  CCTC  CGCCCCTC
                                |||||  ||||  ||||||||
                                GGAGC  GGAG  GCGGGGAG
                                  A__   AA
GAM1269 C1orf21  5' CCCCGCCCCTGTCCTCCTCG  32721        CTCCCG _
                                CCTCGCCCC    CC CCTCG
                                |||||||||    || |||||
                                GGGGCGGGG    GG GGAGC
                                    ACA___  A
GAM1269 C20orf126 3' CCTCCCTCCCTCCTTCCTTGC 32722     G _    CGCC  C
                                CCTC CC CCCTCC   CCT GC
                                |||| || ||||||   ||| ||
                                GGAG GG GGGAGG   GGA CG
                                  _ A    AA__  A
GAM1269 C20orf67 5' CCTCGCCCTCCCCAGCGC   32723       _   C_
                                CCTCGCCC CCTC  CGC
                                |||||||| ||||  |||
                                GGAGCGGG GGGG  GCG
                                    A   TC
GAM1269 C5orf3   5' CCTCGCACCCCTCCTGCCTCG  32724      _    C  CC
                                CCTCGC CCCCTCC GCC  TCG
                                |||||| ||||||| |||  |||
                                GGAGCG GGGGAGG CGG  AGC
                                   T     A  __
GAM1269 CENTG2   3' CCTCGCCTCCCCTCCCCCTCGC 32725       __     GCC
                                CCTCGCC  CCCTCCC  CCTCGC
                                |||||||  |||||||  ||||||
                                GGAGCGG  GGGAGGG  GGAGCG
                                   AG     ___
GAM1269 CGI-57   5' CCTCGCCCTCGCCCTCG    32726       CCTCC   C
                                CCTCGCCC   CGCCC TCG
                                ||||||||   ||||| |||
                                GGAGCGGG   GCGGG AGC
                                   A____   _
GAM1269 CSE-C    5' CTCGCCCCTTCTCGGCCGC  32727       __  __
                                CTCGCCCC  CTC  CCGC
                                ||||||||  |||  ||||
                                GAGCGGGG  GAG  GGCG
                                   AA  CC
GAM1269 DAZAP1   3' CCTCGCGCCCTCCCCCC    32728      C     G
                                CCTCGC CCCTCCC CCC
                                |||||| ||||||| |||
                                GGAGCG GGGAGGG GGG
                                   C     _
GAM1269 DKFZp434E2220 5' CCTCGCCCTCGCCCGGCG   32729       CCTCC   CT
                                CCTCGCCC   CGCCC  CG
                                ||||||||   |||||  ||
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                                GGAGCGGG    GCGGG  GC
                                    A____    CC
GAM1269  DKFZP564C196 3'  CCTCACCCTGGCCTCCTCGC   32730        CCTCCC  _
                                CCTCGCCC     GCC CCTCGC
                                ||||||||     ||| ||||||
                                GGAGTGGG     CGG GGAGCG
                                    AC____   A
GAM1269  EIF2S1   5'  CCCCCTCACCGGCCGCCCCTCG 32731        _____
                                CCCCCTC    CCGCCCCTCG
                                |||||||    ||||||||||
                                GGGGGAG    GGCGGGGAGC
                                    TGGCC
GAM1269  FDPS     3'  CCTCCTCTCCCCGCCCTTGC   32732    _ _    _   CTC
                                CC CC CTCCC GCCC   GC
                                || || ||||| ||||   ||
                                GG GG GAGGG CGGG   CG
                                 A A    G    AA_
GAM1269  FLJ10540  5'  CCTCGCCACCCTCCGCGGTCGC 32733        _     C  CCC
                                CCTCGCC CCCTCC GC   TCGC
                                ||||||| |||||| ||   ||||
                                GGAGCGG GGGAGG CG   AGCG
                                    T     _ CC_
GAM1269  FLJ10724  3'  CTGGCCCCCTCCCATCTC    32734    C        CCC
                                CT GCCCCCTCCCG   CTC
                                || ||||||||||   |||
                                GA CGGGGGAGGGT   GAG
                                 C         A__
GAM1269  FLJ11526  5'  TCGCTCCCCCCGCCCTTCGC   32735     C   T     C
                                TCGC CCC CCCGCCC TCGC
                                |||| ||| ||||||| ||||
                                AGCG GGG GGGCGGG AGCG
                                  A   _      A
GAM1269  FLJ12455  3'  CCTTTCCCCCTTTCTGGCCTTC 32736     CG     CCC__   CC
            G                    CCT  CCCCCT    GCC  TCG
                                |||  ||||||    |||  |||
                                GGA  GGGGGA    CGG  AGC
                                  AA     AAGAC   A_
GAM1269  FLJ12700  3'  CCTCTTCCTTGCCCCTCG    32737     GCCC   CCC
                                CCTC    CCT   GCCCCTCG
                                ||||    |||   ||||||||
                                GGAG    GGA   CGGGGAGC
                                  AA__   A__
GAM1269  FLJ13057  5'  CCTCGCCCCCTCGCTTTCGC   32738          CC  CCC
                                CCTCGCCCCCTC  GC   TCGC
                                ||||||||||||  ||   ||||
                                GGAGCGGGGGAG  CG   AGCG
                                       __  AA_
GAM1269  FLJ13491  3'  CCTGCTTCCCTGACTCCCTCGC 32739     C  C_   CCC  _
                                CCT GC  CCCT   GC CCCTCGC
                                ||| ||  ||||   || |||||||
```

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                                GGA CG  GGGA   TG GGGAGCG
                                  _ AA    C__  A
GAM1269  FLJ14547  5'  CCTCCTTTCCTCCGCCCCTTGC 32740     GCCC    C     C
                                CCTC    CCTCC GCCCCT GC
                                ||||    ||||| |||||| ||
                                GGAG    GGAGG CGGGGA CG
                                  GAAA    _     A
GAM1269  FLJ14564  3'  CCTCGCCCCGGCACTCCTCG   32741         CTCC   C
                                CCTCGCCCC    CGC CCTCG
                                |||||||||    ||| |||||
                                GGAGCGGGG    GTG GGAGC
                                     CC__   A
GAM1269  FLJ14708  5'  CCTCCCTCTCTCCCTTTCTCCC 32742   CC_    G_____      III
            CCTCGCG                 C   CTCCC     CCCCTCGC   G
                                |   |||||     ||||||||   |
                                G   GAGGG     GGGGAGCG   C
                                 AGA     AAAGAG       III
GAM1269  FLJ20257  5'  CCCGCCCCCTCCCCGGCGC   32743           GCCCCT
                                CTCGCCCCCTCCC     CGC
                                ||||||||||||      |||
                                GGGCGGGGGAGGG     GCG
                                      GCC___
GAM1269  FLJ21511  5'  CCTGCGTCCGCGCCCCTCG   32744     C  CCCC   _
                                CCT GC    TCC CGCCCCTCG
                                ||| ||    ||| |||||||||
                                GGA CG    AGG GCGGGGAGC
                                  _ C___   C
GAM1269  GPS2     5'  CCTCGCCCTCGTCATCCTCCTC 32745        CC_  CCG  _
            GC                    CCTCGCCC   TC   CC CCTCGC
                                |||||||   ||   || ||||||
                                GGAGCGGG   AG   GG GGAGCG
                                     AGC  TA_  A
GAM1269  GTPBP5   3'  CCTCGGCCCCACCCCTG     32746      C    TCCC     C
                                CCTCG CCCC    GCCCCT G
                                ||||| ||||    |||||| |
                                GGAGC GGGG    TGGGGA C
                                   C    _____      A
GAM1269  HAND2    3'  TCTCCCCTCGCCCTCGC     32747    GC     CC    C
                                TC  CCCCTC  GCCC TCGC
                                ||  ||||||  |||| ||||
                                AG  GGGGAG  CGGG AGCG
                                 A_     __    _
GAM1269  HRK      5'  CCGCGCTCGGGCCGCCCCTCGC 32750    T   CCCCTC
                                CC CGC     CCGCCCCTCGC
                                || |||     ||||||||||
                                GG GCG     GGCGGGGAGCG
                                 C  AGCCC_
GAM1269  HRK      5'  CCTCGCTCCCGCCCC      32748       CCCC
                                CCTCGC    TCCCGCCCC
                                ||||||    |||||||||
```

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                                GGAGCG   AGGGCGGGG
                                   ____
GAM1269 HRK     5' CCTCGCCTCCTCTCCCTCC   32749       _ _   G
                                CCTCGCC CC CTCCC CC
                                ||||||| || ||||| ||
                                GGAGCGG GG GAGGG GG
                                    A A    A
GAM1269 HSPBAP1  5' CCCCGGCGACTCCCGCCCCTCG 32751      CCCC
                                CCTCG   CTCCCGCCCCTCG
                                |||||   |||||||||||||
                                GGGGC   GAGGGCGGGGAGC
                                  CGCT
GAM1269 KATII   5' CCGCGCCCCCTCCCGCCCC   32752   T
                                CC CGCCCCCTCCCGCCCC
                                || ||||||||||||||||
                                GG GCGGGGGAGGGCGGGG
                                 C
GAM1269 KIAA0215 5' CCCGCCCTCGGCCCTCG    32754       CCTCC  C
                                CTCGCCC    CG CCCTCG
                                |||||||    || ||||||
                                GGGCGGG    GC GGGAGC
                                    A____  C
GAM1269 KIAA0215 5' CCTCGCCCCCGCCCCCCG   32753         TCCC
                                CCTCGCCCCC   GCCCCTCG
                                |||||||||   ||||||||
                                GGAGCGGGGG   CGGGGGGC
                                   ____
GAM1269 KIAA0258 3' CCTCGCCCCTCCTGCCTCCTTG 32755        C  C  _  C
            C                    CCTCGCCCC TCC GCC CCT GC
                                ||||||||| ||| ||| ||| ||
                                GGAGCGGGG AGG CGG GGA CG
                                     _  A  A  A
GAM1269 KIAA0293 3' CCTTGCCCCCTCACCCTG   32756    C      CCGC   C
                                CCT GCCCCCTC   CCCT G
                                ||| ||||||||   |||| |
                                GGA CGGGGGAG   GGGA C
                                  A      T___   _
GAM1269 KIAA0354 5' CCGCCCCCCTCCTCCTCGC   32757       TC  GCC
                                TCGCCCCC  CC   CCTCGC
                                ||||||||  ||   ||||||
                                GGCGGGGG  GG   GGAGCG
                                    GA  A__
GAM1269 KIAA0455 5' CCCCGCCTTCTCCCCGCCCCT  32758       CC   _
                                CCTCGCC  CTCCC GCCCCT
                                |||||||  ||||| ||||||
                                GGGGCGG  GAGGG CGGGGA
                                    AA    G
GAM1269 KIAA0616 5' CCTCGCCCCCCCCACTCG    32759         CCGCCC
                                CCTCGCCCCCTC    CTCG
                                ||||||||||||    ||||
```

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                                GGAGCGGGGGGG     GAGC
                                       T_____
GAM1269  KIAA0664  3'  CTCGCCCCCTTCTCCCGC    32760         ___
                                CTCGCCCCC   TCCCGC
                                |||||||||   ||||||
                                GAGCGGGGG   AGGGCG
                                     AAG
GAM1269  KIAA0913  5'  CCTCGGCCTTCTCTTCCTCGC  32761      _ CC   CCGCC
                                CCTCG CC  CTC    CCTCGC
                                ||||| ||  |||    ||||||
                                GGAGC GG  GAG    GGAGCG
                                   C  AA   AA___
GAM1269  KIAA0923  5'  CCCGCCTTCCCCGCCCCTTGC  32762       CC T       C
                                CTCGCC  C CCCGCCCCT GC
                                ||||||  | |||||||||  ||
                                GGGCGG  G GGGCGGGGA CG
                                    AA _       A
GAM1269  KIAA1259  3'  CCTGCCCCCTCTCTCCGC    32763     C      ___
                                CCT GCCCCCTC   CCGC
                                ||| ||||||||   ||||
                                GGA CGGGGGAG   GGCG
                                  _       AGA
GAM1269  KIAA1272  3'  CTCTGCCCCCTCCCTGAAAGCG 32764     _        GCCCCT
             C                   CTC GCCCCCTCCC      CGC
                                ||| ||||||||||      |||
                                GAG CGGGGGAGGG      GCG
                                  A         ACTTTC
GAM1269  KIAA1649  3'  CCTGCCCCGCCCCCTCG     32765     C    CTCCCG
                                CCT GCCCC     CCCCTCG
                                ||| |||||     |||||||
                                GGA CGGGG     GGGGAGC
                                  _    CG____
GAM1269  KIAA1821  3'  CCTTGCCTCCTCCCACTTCC   32766     C  C      C_
                                CCT GCC CCTCCCGC  CC
                                ||| ||| ||||||||  ||
                                GGA CGG GGAGGGTG  GG
                                  A  A       AA
GAM1269  KIAA1872  5'  CTGCGCCCCCTCTCATCG    32767    _      C  CCCC
                                CT CGCCCCCTC CG    TCG
                                || |||||||| ||    |||
                                GA GCGGGGGAG GT    AGC
                                 C        A  ____
GAM1269  LAGY      5'  CCGCGCCCCCCGGGACCCCTTG 32768    T       CCC     C
             C                   CC CGCCCCCT   GCCCCT GC
                                || ||||||||   |||||| ||
                                GG GCGGGGGGG   TGGGGA CG
                                 C       CCC     A
GAM1269  MAD4      3'  CCCGCCCTTCACAGACCCCT   32769       CC  CC__
                                CTCGCCC  TC    GCCCCT
                                |||||||  ||    ||||||
```

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                              GGGCGGG AG   TGGGGA
                                 A_ TGTC
GAM1269 MGC12992 5' CCTCACCTCCTCCCGCCTCGC 32770       C       CC
                              CCTCGCC CCTCCCGCC TCGC
                              ||||||| ||||||||| ||||
                              GGAGTGG GGAGGGCGG AGCG
                                 A       __
GAM1269 MGC15396 5' CCGCTCCCTCCCGCGGGCCGC 32771     C       CCC
                              TCGC CCCTCCCGC  TCGC
                              |||| ||||||||  ||||
                              GGCG GGGAGGGCG  GGCG
                                A       CCC
GAM1269 MGC15437 5' CCTCCGCCCCCTTCCCTCTCCT 32772     _     _  GCC
           CGC                  CCTC GCCCCCT CCC  CCTCGC
                              |||| ||||||| |||  ||||||
                              GGAG CGGGGGA GGG  GGAGCG
                                G      A  AGA
GAM1269 MGC16385 5' CCGCGCCCCTGCCCCTCG    32773    T    CTCCC
                              CC CGCCCC    GCCCCTCG
                              || ||||||    ||||||||
                              GG GCGGGG    CGGGGAGC
                               C     A____
GAM1269 MGC20486 5' CCTCCGCCCCTACGCCGCCCCT 32774     _    CTC_
           CG                   CCTC GCCCC   CCGCCCCTCG
                              |||| |||||   ||||||||||
                              GGAG CGGGG   GGCGGGGAGC
                                G    ATGC
GAM1269 MGC20533 5' TCGCCTGTCCTCCCCTCGC   32775     CCC  CG
                              TCGCC  TCC  CCCCTCGC
                              |||||  |||  ||||||||
                              AGCGG  AGG  GGGGAGCG
                                 AC_  A_
GAM1269 MGC2555  3' CCTCCCCCTCTCCCTCCTCTCC 32776    G  _   GC____
           CTCGC                 CTC CCCC CTCCC    CCCTCGC
                              ||| |||| |||||    |||||||
                              GAG GGGG GAGGG    GGGAGCG
                                _   A    AGGAGA
GAM1269 MGC3262  3' CCCTGCTCGGCTGCCCCTCGC 32777    C_  CC__
                              CCC  CTC   GCCCCTCGC
                              |||  |||   |||||||||
                              GGG  GAG   CGGGGAGCG
                                AC  CCGA
GAM1269 MGC4701  5' CCCCGCCCCAGCTCCTCG    32778       CTCCC  C
                              CCTCGCCCC    GC CCTCG
                              |||||||||    || |||||
                              GGGGCGGGG    CG GGAGC
                                    T____  A
GAM1269 MKP-7    5' TCTCCCCTCGGGCCCCCCTCGC 32780    GC    ___  G
                              TC  CCCCTC   CC CCCCTCGC
                              ||  ||||||   || ||||||||
```

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                                AG  GGGGAG   GG GGGGAGCG
                                 A_     CCC  _
GAM1269  MKP-7    5'  CCTCGCCTCCCGGACTG     32779        CCC    CCC  C
                                CCTCGCC   TCCCG   CT G
                                |||||||   |||||   || |
                                GGAGCGG   AGGGC   GA C
                                    ___    CT_  A
GAM1269  NDUFB2   5'  CCTCGCCCCTGCCTACTTCGC  32781         CT  CG CCC
                                CCTCGCCCC  CC  C   TCGC
                                |||||||||  ||  |  ||||
                                GGAGCGGGG  GG  G   AGCG
                                     AC  AT A__
GAM1269  NXPH3    5'  CCTCCGCTCTCGTCCCCTCGC  32782    _  _  C  _
                                CC CC CTC CG CCCCTCGC
                                || || ||| || ||||||||
                                GG GG GAG GC GGGGAGCG
                                 A  C   A  A
GAM1269  P114-RHO-GEF 3'  CCCCGCCCCCTCCTGAGC    32783           C__
                                CCTCGCCCCCTCC   GC
                                ||||||||||||   ||
                                GGGGCGGGGGAGG   CG
                                       ACT
GAM1269  p47      5'  CCGCGTTCCGCTTGCCCCTCG  32784    T  CC  _  CCC
                                CC CG  CC CT   GCCCCTCG
                                || ||  || ||   ||||||||
                                GG GC  GG GA   CGGGGAGC
                                 C  AA  C  A__
GAM1269  PTRF     5'  CCTCGCCCAGCTCCTCG     32785        CCTCCC  C
                                CCTCGCCC     GC CCTCG
                                ||||||||     || |||||
                                GGAGCGGG     CG GGAGC
                                    T_____  A
GAM1269  RAB40C   3'  CCGCGCCCCCTCCTCCC     32786    T        CG
                                CC CGCCCCCTCC  CCC
                                || ||||||||||  |||
                                GG GCGGGGGGAGG  GGG
                                 C         A_
GAM1269  RC3      5'  TCGCCTTCCCTCCGCCTCG   32787      CCC   G  _
                                TCGCC   TCCC CC CCTCG
                                |||||   |||| || |||||
                                AGCGG   AGGG GG GGAGC
                                   A__    A  C
GAM1269  RTN4IP1  5'  TCACCCCCTCCACTTCCTCG   32788          C  C_
                                TCGCCCCCTCC GC  CCTCG
                                |||||||||| ||  |||||
                                AGTGGGGGAGG TG  GGAGC
                                       _  AA
GAM1269  SEMA4G   5'  TCTTCCCTCCCAGGTCTCCCTT 32789    GCC       C____    C
             GC                   TC   CCCTCCCG    CCCT GC
                                ||   ||||||||    |||| ||
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                                AG  GGGAGGGT   GGGA CG
                                 AA_      CCAGA   A
GAM1269  SERF2    5'  CCTTTCCTCCCCGCCCCTTCGC 32790    CG  CCC       _
                                CCT  CC   TCCCGCCCCT CGC
                                |||  ||   |||||||||| |||
                                GGA  GG   GGGGCGGGGA GCG
                                  AA  A__        A
GAM1269  SMARCE1  5'  CTCGCCCCGCCCCTCGC     32791        CTCCC
                                CTCGCCCC    GCCCCTCGC
                                ||||||||    |||||||||
                                GAGCGGGG    CGGGGAGCG
                                      _____
GAM1269  SRCRB4D  3'  GCCCCTCCCCCAGTCCCCT   32792      _     __
                                GCCCC CTCCCG  CCCCT
                                ||||| ||||||  |||||
                                CGGGG GGGGGT  GGGGA
                                   A     CA
GAM1269  SSH-3    3'  CCTCGCCCTCCTCTCCAC    32793        _   _
                                CCTCGCCC CCTC CCGC
                                |||||||| |||| ||||
                                GGAGCGGG GGAG GGTG
                                    A   A
GAM1269  SYPL     5'  CCGCGCCCCCTTCCCTGC    32794    T      _  _
                                CC CGCCCCCT CCC GC
                                || |||||||| ||| ||
                                GG GCGGGGGA GGG CG
                                 C       A   A
GAM1269  TADA3L   5'  CCCCGCCCCCTCTACCTCCTCG 32795          CC  _
            C                    CCTCGCCCCCTC  GCC CCTCGC
                                 ||||||||||||  ||| ||||||
                                 GGGGCGGGGGAG  TGG GGAGCG
                                       A_   A
GAM1269  TADA3L   5'  CCCCGCCCCCTCTACCTCCTCG 32795          CC  _
            C                    CCTCGCCCCCTC  GCC CCTCGC
                                 ||||||||||||  ||| ||||||
                                 GGGGCGGGGGAG  TGG GGAGCG
                                       A_   A
GAM1269  TADA3L   5'  CCCCGCCCCCTCTACCTCCTCG 32795          CC  _
            C                    CCTCGCCCCCTC  GCC CCTCGC
                                 ||||||||||||  ||| ||||||
                                 GGGGCGGGGGAG  TGG GGAGCG
                                       A_   A
GAM1269  TNKS2    5'  CCGCGCCCACGCGCGCCCCTCG 32796    T    CCTCC
            C                    CC CGCCC    CGCCCCTCGC
                                 || |||||    ||||||||||
                                 GG GCGGG    GCGGGGAGCG
                                  C    TGCGC
GAM1269  VI       5'  CCGCGCTCCTCAGGCCCCTCG  32797    T  CC   CC
                                CC CGC  CCTC  GCCCCTCG
                                || |||  ||||  ||||||||
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                                GG GCG  GGAG  CGGGGAGC
                                 C  A_   TC
GAM1269  WNT16    5'  CCTCGCCCTCTTCCTCCTTGC  32798       _____    C_
                                CCTCGCCC   CCTCC  GC
                                ||||||||   |||||  ||
                                GGAGCGGG   GGAGG  CG
                                    AGAA    AA
GAM1269  LOC115219 5'  CCCCGCCCTGCTCCCCTCGC   32799       CCTCCCG
                                CCTCGCCC     CCCCTCGC
                                ||||||||     ||||||||
                                GGGGCGGG     GGGGAGCG
                                    ACGA___
GAM1269  LOC116150 5'  CCTCGCCCCCGCCGCCACCTCG 32800         TC   _
                                CCTCGCCCCC  CCGCC CCTCG
                                ||||||||||  ||||| |||||
                                GGAGCGGGGG  GGCGG GGAGC
                                      C_    T
GAM1269  LOC123096 5'  CCTCCCCCTGAGGCCCCTCGC  32801    CG    CCC
                                CCT  CCCCCT   GCCCCTCGC
                                |||  ||||||   |||||||||
                                GGA  GGGGGA   CGGGGAGCG
                                  __     CTC
GAM1269  LOC124446 5'  CCTCGTCCCCTCCCGGTCTCGC 32802     C       CCC
                                CCTCG CCCCTCCCG   CTCGC
                                ||||| |||||||||   |||||
                                GGAGC GGGGAGGGC   GAGCG
                                   A       CA_
GAM1269  LOC132299 5'  CTCTTGCTCCGCCCCCTCGC   32803    GCCCC   C    _
                                CTC    CTCC GCCCC TCGC
                                |||    |||| ||||| ||||
                                GAG    GAGG CGGGG AGCG
                                  AAC__   _    G
GAM1269  LOC149464 5'  CCTCTTCCCCTCCCTGGGCTTC 32804     GC      ___  CC
            T                    CCTC  CCCCTCCC   GC  CT
                                ||||  ||||||||  ||  ||
                                GGAG  GGGGAGGG   CG  GA
                                  AA       ACC  AA
GAM1269  LOC151556 5'  CCCGCCCCCAGCCCTCTTCGC  32805       TCCC   _ _
                                CTCGCCCCC    GCCC CT CGC
                                |||||||||    |||| || |||
                                GGGCGGGGG    CGGG GA GCG
                                     T___    A  A
GAM1269  LOC153243 3'  CCTCGCCCTCCAGCAGCT    32806       CC   C  CC
                                CCTCGCCC  TCC GC  CT
                                ||||||||  ||| ||  ||
                                GGAGCGGG  AGG CG  GA
                                     __   T  TC
GAM1269  LOC158158 3'  CCTCGCCCTGCTTCGGCTCGC  32807       CCTCC  CCC
                                CCTCGCCC    CG   CTCGC
                                ||||||||    ||   |||||
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                                GGAGCGGG    GC   GAGCG
                                    ACGAA  C__
GAM1269  LOC197136 3'  CCTGCCCCCTCCCTCG      32808     C        GCCCC
                                CCT GCCCCCTCCC    TCG
                                ||| ||||||||||    |||
                                GGA CGGGGGAGGG    AGC
                                  _       _____
GAM1269  LOC201158 3'  CCTTCCCTCTTCGTCCTCGC   32809     CGCC    C_ CC
                                CCT   CCCTC  CG  CCTCGC
                                |||   |||||  ||  ||||||
                                GGA   GGGAG  GC  GGAGCG
                                  A___    AA  A_
GAM1269  LOC219908 5'  CTGCGCCCCCTCGGCGCCCTC  32810    _       CC  _
                                CT CGCCCCCTC  GC CCCTC
                                || |||||||||  || |||||
                                GA GCGGGGGAG  CG GGGAG
                                 C        C_  C
GAM1269  LOC220018 5'  CCTCCCTCCCTCCCTCG     32811    _      GC     _
                                CC CCCTCCC  CCCTC G
                                || |||||||  ||||| |
                                GG GGGAGGG  GGGAG C
                                 A      A_    A
GAM1269  LOC220107 5'  CCACGCCCCCGCCCCGCTCCTC 32812    T      _     C
              GC                  CC CGCCCCC TCCCGC CCTCGC
                                || ||||||| |||||| ||||||
                                GG GCGGGGG GGGGCG GGAGCG
                                 T      C     A
GAM1269  LOC221496 5'  CCTCCTCCCGCAGCCGCTCCTC 32813     G_   CCTC    C
              G                   CCTC  CCC    CCGC CCTCG
                                ||||  |||    |||| |||||
                                GGAG  GGG    GGCG GGAGC
                                  GA   CGTC    A
GAM1269  LOC221749 5'  CCGCGCCTCCTCCCTCG     32814    T    C     GCCCC
                                CC CGCC CCTCCC    TCG
                                || |||| ||||||    |||
                                GG GCGG GGAGGG    AGC
                                 C    A     _____
GAM1269  LOC221922 5'  CCTTGCTCTCTCACCCCTGC   32816     C  CCC   C      C
                                CCT GC   CTC CGCCCCT GC
                                ||| ||   ||| ||||||| ||
                                GGA CG   GAG GTGGGGA CG
                                  A  A__   A      _
GAM1269  LOC221922 5'  CCTCACCCCTGCCCTCTTGC   32815         CTCCC   _  C
                                CCTCGCCCC    GCCC CT GC
                                |||||||||    |||| || ||
                                GGAGTGGGG    CGGG GA CG
                                     A____    A  A
GAM1269  LOC221935 3'  CCTCTCCCTGGGGCCCCTCG  32817     GCC    CCC
                                CCTC   CCCT   GCCCCTCG
                                ||||   ||||   ||||||||
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                                GGAG  GGGA  CGGGGAGC
                                  A__   CCC
GAM1269 LOC253767 3' CCCCGTTCCCTCTCAGAGCGC 32818     CC    C CCCCT
                                CCTCG CCCTC CG    CGC
                                ||||| ||||| ||    |||
                                GGGGC GGGAG GT    GCG
                                   AA    A CTC__
GAM1269 LOC254124 3' CCGCGCCCGGCCGCCCCTTGC 32819   T    CCTC      C
                                CC CGCCC   CCGCCCCT GC
                                || |||||   |||||||| ||
                                GG GCGGG   GGCGGGGA CG
                                 C    CC__      A
GAM1269 LOC254263 5' CCTCGCCCGCGGCTCCCTCGC 32820       CCTCCC _
                                CCTCGCCC    GC CCCTCGC
                                ||||||||    || |||||||
                                GGAGCGGG    CG GGGAGCG
                                     CGC___ A
GAM1269 LOC255812 5' CCTCAGGACCTGCCCCTCG   32821     CCC   CCC
                                CCTCG  CCT  GCCCCTCG
                                |||||  |||  ||||||||
                                GGAGT  GGA  CGGGGAGC
                                   CCT  ___
GAM1269 LOC256812 5' CCGCGCCCCGCCCCTCG    32822    T    CTCCC
                                CC CGCCCC   GCCCCTCG
                                || ||||||   ||||||||
                                GG GCGGGG   CGGGGAGC
                                 C    _____
GAM1269 LOC58509  5' CCTCGCCCTCGCCCTCG    32726       CCTCC    C
                                CCTCGCCC    CGCCC TCG
                                ||||||||    ||||| |||
                                GGAGCGGG    GCGGG AGC
                                    A____    _
GAM1269 LOC90673  5' CCGCTTCTGCAGCCCCTCGC  32823     CCC  CCC
                                TCGC  CT  GCCCCTCGC
                                ||||  ||  |||||||||
                                GGCG  GA  CGGGGAGCG
                                  AA_ CGT
GAM1270 AK3     3' TATGGAGCGTGGATGTAGAA  32826      A  GTAC
                                TATGGA CG   TGGATGTAGAA
                                |||||| ||   ||||||||||
                                ATACCT GC   ACCTACATCTT
                                   C ____
GAM1270 CYP3A4  3' ATGGAATGCAAGAGGTGTAG  32827      CG  CT_ A
                                ATGGAA  GTA  GG TGTAG
                                ||||||  |||  || |||||
                                TACCTT  CGT  CC ACATC
                                   A_  TCT  _
GAM1270 EMX2    3' TGGGATGGGGCTAGATATGGAA 32828    AAC  TA      A
                                TGG  GG  CTGGATGT GAA
                                |||  ||  |||||||| |||
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                                ACC  CC  GATCTATA CTT
                                  CTA  CC      C
GAM1270 GCK     3' TATGGGAGCTGAAGATGTAG  32829     AAC  ACT
                                TATGG  GGT  GGATGTAG
                                |||||  |||  ||||||||
                                ATACC  TCG  TCTACATC
                                   C__  ACT
GAM1270 GCK     3' TATGGGAGCTGAAGATGTAG  32829     AAC  ACT
                                TATGG  GGT  GGATGTAG
                                |||||  |||  ||||||||
                                ATACC  TCG  TCTACATC
                                   C__  ACT
GAM1270 GCK     3' TATGGGAGCTGAAGATGTAG  32829     AAC  ACT
                                TATGG  GGT  GGATGTAG
                                |||||  |||  ||||||||
                                ATACC  TCG  TCTACATC
                                   C__  ACT
GAM1270 TNFRSF6B 3' TGGGGTGCCAAGGATGTAGAA 32830    AAC  A __
                                TGG  GGT CT  GGATGTAGAA
                                |||  ||| ||  ||||||||||
                                ACC  CCA GG  CCTACATCTT
                                  ___  C  TT
GAM1270 TNFRSF6B 3' TGGGGTGCCAAGGATGTAGAA 32830    AAC  A __
                                TGG  GGT CT  GGATGTAGAA
                                |||  ||| ||  ||||||||||
                                ACC  CCA GG  CCTACATCTT
                                  ___  C  TT
GAM1270 TNFRSF6B 3' TGGGGTGCCAAGGATGTAGAA 32830    AAC  A __
                                TGG  GGT CT  GGATGTAGAA
                                |||  ||| ||  ||||||||||
                                ACC  CCA GG  CCTACATCTT
                                  ___  C  TT
GAM1270 DKFZP434K028 3' TGTGTATAAACTGGATGTAGAA 32831    GAACGGT
                                TG     ACTGGATGTAGAA
                                ||     ||||||||||||
                                AC     TGACCTACATCTT
                                 ACATATT
GAM1270 SIMRP7   3' GGAACACTGGGATGTAGA    32832     GGT   _
                                GGAAC  ACTGG ATGTAGA
                                |||||  ||||| |||||||
                                CCTTG  TGACC TACATCT
                                   ___   C
GAM1270 LOC145566 5' CGGGGTGCCCTGATGTAGA   32833    AAC  A_ G
                                TGG  GGT  CT GATGTAGA
                                |||  |||  || ||||||||
                                GCC  CCA  GG CTACATCT
                                  ___  CG  A
GAM1270 LOC146445 3' GGAGCGGTACTGTCAGA    32834    A      GATG
                                GGA CGGTACTG   TAGA
                                ||| ||||||||   ||||
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                                CCT GCCATGAC    GTCT
                                  C       A___
GAM1271  LOC158156 3'  TCTAAGATAAAAACATTAAATA 32837       T
                                TCTAA ATAAGGACGTTAAATA
                                ||||| ||||||||||||||||
                                AGATT TATTTTTGTAATTTAT
                                   C
GAM1271  LOC256273 3'  CCTGATATAAGGAGTCA     32838     A       C
                                TCT ATATAAGGA GTTA
                                ||| ||||||||| ||||
                                GGA TATATTCCT CAGT
                                  C       _
GAM1272  BID      3'  TTCAAGTATATTAATGTA    32841           CAACA
                                TTCAGGTATAT    AATGTA
                                ||||||||||     ||||||
                                AAGTTCATATA    TTACAT
                                       A____
GAM1272  RDX      3'  AGTTACCAACAAATGTATA   32842     A
                                GGT TATCAACAAATGTATA
                                ||| ||||||||||||||||
                                TCA ATGGTTGTTTACATAT
                                  _
GAM1272  DKFZP564I0422 3'  AGGTAGACAAATGTAT      32843       TATCA
                                AGGTA    ACAAATGTAT
                                |||||    ||||||||||
                                TCCAT    TGTTTACATA
                                   C____
GAM1272  KIAA1016  5'  TTCAGGTAAGTCAGCATCTG   32844        TA   A  AA
                                TTCAGGTA  TCA CA  TG
                                ||||||||  ||| ||  ||
                                AAGTCCAT  AGT GT  AC
                                     TC   C  AG
GAM1272  MGC11034  3'  TTCAGGTATAATCAACTAACAT 32845          _    A
                                TTCAGGTATA TCAAC AATGT
                                |||||||||| ||||| |||||
                                AAGTCCATAT AGTTG TTGTA
                                       T    A
GAM1272  NTT5     3'  TTCAGGTATGTCTGTAT     32846         A  AACAAA
                                TTCAGGTAT TC     TGTAT
                                ||||||||| ||     |||||
                                AAGTCCATA AG     ACATA
                                     C _______
GAM1272  LOC257042 3'  TTCAGGTATGGTCAACAAA   32847         A_
                                TTCAGGTAT  TCAACAAA
                                |||||||||  ||||||||
                                AAGTCCATA  AGTTGTTT
                                     CC
GAM1272  LOC92303  3'  TTCAGGTAATCAGCAAATA   32848        T   A
                                TTCAGGTA ATCA CAAATG
                                |||||||| |||| ||||||
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                                AAGTCCAT TAGT GTTTAT
                                    _   C
GAM1272 LOC92606 3' TTCAGGTAATCAATTTGCAT  32849       T    CAAA
                                TTCAGGTA ATCAA   TGTAT
                                |||||||| |||||   |||||
                                AAGTCCAT TAGTT   ACGTA
                                    _    AA__
GAM1273 PSMD9    3' TCCTGTTACTGTTCCCCAG   32852       AGCTC  G
                                TCCTGTTACT    TTC CCGG
                                ||||||||||    ||| ||||
                                AGGACAATGA    AAG GGTC
                                     C____  G
GAM1273 DCAMKL1  5' CTCCTGGTGCTGTCCTCGCCGG 32853      TTA  AGC
                                CTCCTG  CT  TCTTCGCCGG
                                ||||||  ||  ||||||||||
                                GAGGAC  GA  AGGAGCGGCC
                                   CAC  C__
GAM1273 FLJ20232 3' TCCTGTTACTATCGTG     32854        GCTCT  CC
                                TCCTGTTACTA    TCG  G
                                ||||||||||    |||  |
                                AGGACAATGAT    AGC  C
                                      _____  AA
GAM1273 FLJ23375 5' CTCCTGTTGCTAGGACGAGAGC 32855       A   CTCTTC_  C
           TGG                   CTCCTGTT CTAG      GC GG
                                ||||||||| ||||      || ||
                                GAGGACAA GATC      CG CC
                                    C   CTGCTCT  A
GAM1273 LOC150174 3' CTCCTGCTGCTGTTTGCCG  32856       ACTA  C  C
                                CTCCTGTT   GCT TT GCCG
                                ||||||||   ||| || ||||
                                GAGGACGA   CGA AA CGGC
                                    ____  C  A
GAM1273 LOC150213 3' CTCCTGCTGCTGTTTGCCG  32856       ACTA  C  C
                                CTCCTGTT   GCT TT GCCG
                                ||||||||   ||| || ||||
                                GAGGACGA   CGA AA CGGC
                                    ____  C  A
GAM1273 LOC150236 5' CTCCTGCTGCTGTTCGCCG  32857       ACTA  C
                                CTCCTGTT   GCT TTCGCCG
                                ||||||||   ||| |||||||
                                GAGGACGA   CGA AAGCGGC
                                    ____  C
GAM1273 LOC161527 5' TCTTGGTACTGGCTCTCCA  32858    C  T   A
                                TC TG TACT GCTCTTCG
                                || || |||| ||||||||
                                AG AC ATGA CGAGAGGT
                                 A  C   C
GAM1273 LOC200014 5' CTCCTGTTGGCTGGTTCCTGG 32859       ACTA  CTTCG  _
                                CTCCTGTT   GCT    CC GG
                                ||||||||   |||    || ||
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                                GAGGACAA   CGA    GG CC
                                    C___   CCAA_  A
GAM1273  LOC257447 5'  TCTTGGTACTGGCTCTCCA   32858    C  T   A
                                TC TG TACT GCTCTTCG
                                || || |||| ||||||||
                                AG AC ATGA CGAGAGGT
                                 A  C   C
GAM1274  RGL      3'  TATTTTACATTGCAGTATATAA 32862        ____
              ATCTA                 TATTTTAT   CGGTATATAAATCTA
                                ||||||||   ||||||||||||||||
                                ATAAAATG   GTCATATATTTAGAT
                                    TAAC
GAM1274  KLHL4    3'  TATTTTACTGGTAACAAATCTA 32863        C   T
              A                   TATTTTAT GGTA ATAAATCTAA
                                |||||||| |||| ||||||||||
                                ATAAAATG CCAT TGTTTAGATT
                                    A  _
GAM1274  LOC203080 3'  TATTTTATCTGGTTACCAGTCT 32864        _  A  AAA
              AA                   TATTTTATC GGT TAT   TCTAA
                                ||||||||| ||| |||   |||||
                                ATAAAATAG CCA ATG   AGATT
                                    A  _  GTC
GAM1275  GEM      3'  ATTCTGATTTTAAAAATATTTT 32867        GTT___
              TAT                  ATTCTGGT     AATATTTTTAT
                                ||||||||     ||||||||||
                                TAAGACTA     TTATAAAAATA
                                    AAATTT
GAM1275  PTGFRN   3'  TTCTGGGGCTATTTTTAT    32868       T  TAA
                                TTCTGG GT   TATTTTTAT
                                ||||||  ||   |||||||||
                                AAGACC CG   ATAAAAATA
                                   C  ___
GAM1275  SCML2    3'  ATTCTGATAAAATATTTTTAT  32869         TT
                                ATTCTGGTG  AATATTTTTAT
                                |||||||||  ||||||||||
                                TAAGACTAT  TTATAAAAATA
                                    T_
GAM1275  XYLB     3'  CTCTGGTGTTCTTTTATA    32870         AATA
                                TTCTGGTGTT    TTTTTATA
                                ||||||||||    ||||||||
                                GAGACCACAA    GAAAATAT
                                              ____
GAM1275  DKFZP564D0462 3'  TCTGACATGATAATATTTTTAT 32871       TG __
              A                   TCTGG  T  TAATATTTTTATA
                                |||||  |  ||||||||||||
                                AGACT  A  ATTATAAAAATAT
                                   GT CT
GAM1275  MGC10981  3'  TGGTGTTAGTCCTCAT      32872         ATA
                                TGGTGTTA   TTTTTAT
                                ||||||||   |||||||
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                                ACCACAAT   AGGAGTA
                                    C__
GAM1275  LOC133022 3'  TGATTTTAATATTTTTATA   32873      G
                                TGGT TTAATATTTTTATA
                                |||| ||||||||||||||
                                ACTA AATTATAAAAATAT
                                  A
GAM1275  LOC196477 3'  ATTCTGGAAAACTATTTTTAT  32874        TGTTAA
                                ATTCTGG     TATTTTTAT
                                |||||||     |||||||||
                                TAAGACC     ATAAAAATA
                                    TTTTG_
GAM1276  FLJ20725  3'  TGGATCACTAAAATATAACAA  32877
                                TGGATCACTAAAATATAATAA
                                ||||||||||||||||||||
                                ACCTAGTGATTTTATATTGTT

GAM1276  MIG-6    3'  TAGTTCATACTAAAATATAATA 32878     A __
              A                  TGG TC  ACTAAAATATAATAA
                                ||| ||  ||||||||||||||||
                                ATC AG  TGATTTTATATTATT
                                  A  TA
GAM1276  LOC221687 3'  TAATAGAACCAAAAATATAATA 32879        TC      _
                                TAATGGA  ACTAAAA TATAATA
                                |||||||  ||||||| |||||||
                                ATTATCT  TGGTTTT ATATTAT
                                    __      T
GAM1277  XRCC3     3'  CACTACTAGAGACAAGGC     32882          C  T_
                                TACTACTAGG GC  GGC
                                |||||||||| ||  |||
                                GTGATGATCT TG  CCG
                                      C  TT
GAM1277  MGC33182  3'  TACTACTAGATCAGCTGGC    32883          _ _
                                TACTACTAGG C GCTGGC
                                |||||||||| | ||||||
                                ATGATGATCT G CGACCG
                                      A T
GAM1277  MRPL42    3'  TACTACTAACAATGCTTGGC   32884         GC__  _
                                TACTACTAG    GCT GGC
                                |||||||||    ||| |||
                                ATGATGATT    CGA CCG
                                     GTTA   A
GAM1277  WBSCR20A  5'  TACACTAGCACCCTTGGC     32885     T    _ G  _
                                TAC ACTAG GC CT GGC
                                ||| ||||| || || |||
                                ATG TGATC TG GA CCG
                                  _    G  G  A
GAM1278  ADAM12    3'  TCTTTGTCCAATATCTACGAAT 32888       T       GTGT
              A                  TCTTT GTCCAATA    CGAATA
                                ||||| ||||||||    ||||||
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                                AGAAA CAGGTTAT   GCTTAT
                                  _      AGAT
GAM1278 EFG2    3' TCTTTTATCTAGTTCTCTGAAT 32889        CAA   G_ _
                                TCTTTTGTC  TAGT  TC GAAT
                                |||||||||  ||||  || ||||
                                AGAAAATAG  ATCA  AG CTTA
                                     ___   AG  A
GAM1278 LUZP1   3' CTTTTGTCCAGTGTTAA    32890         ATA   CG
                                CTTTTGTCCA  GTGT  A
                                ||||||||||  ||||  |
                                GAAAACAGGT  CACA  T
                                     ___   AT
GAM1278 ALLC    5' TCTTTTTGTCCAGTACCGAATA 32891       _    ATA  GT
                                TCTTTT GTCCA  GT  CGAATA
                                ||||||| |||||  ||  ||||||
                                AGAAAA CAGGT  CA  GCTTAT
                                   A    ___ TG
GAM1278 FLJ13386 5' TCTTTTGCCTAATAAAAAAGAA 32892        C    TGTC
            TA                   TCTTTTGTC AATAG   GAATA
                                |||||||||| |||||   |||||
                                AGAAAACGG TTATT   CTTAT
                                     A    TTTT
GAM1278 KIAA0318 3' TCTTTTGTTCAAATGCCAA   32893       C   TA
                                TCTTTTGT CAA  GTGTCGA
                                |||||||| |||  |||||||
                                AGAAAACA GTT  TACGGTT
                                     A  __
GAM1278 MAPK6   5' TCTTTTGTTAGTGATCA    32894        CCAA   _
                                TCTTTTGT   TAGTG TCG
                                ||||||||   ||||| |||
                                AGAAAACA   ATCAC AGT
                                     _____   T
GAM1278 SMAP1   3' TTTTGTACAGTGCCGA     32895       CCA
                                TTTTGT  ATAGTGTCGA
                                ||||||  ||||||||||
                                AAAACA  TGTCACGGCT
                                     ___
GAM1278 LOC133088 3' TCTTTGTCCAATTCCCTTGAAT 32896      T     AGTGTC
            A                    TCTTT GTCCAAT     GAATA
                                ||||| |||||||     |||||
                                AGAAA CAGGTTA     CTTAT
                                  _      AGGGAA
GAM1278 LOC145497 5' CCTTTTGTCCAGTGGTGA   32897         ATA  TC
                                TCTTTTGTCCA  GTG  GA
                                ||||||||||  |||  ||
                                GGAAAACAGGT  CAC  CT
                                     ___  CA
GAM1278 LOC148304 3' TCTTTTATCCAGTGAAAAT  32898         ATA  TC
                                TCTTTTGTCCA  GTG  GAAT
                                ||||||||||  |||  ||||
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                                AGAAAATAGGT  CAC  TTTA
                                     ___  T_
GAM1278 LOC200488 5'  TTCTGTCCAGTGGAA      32899        ATA  TC
                                TTTTGTCCA  GTG  GAA
                                |||||||||  |||  |||
                                AAGACAGGT  CAC  CTT
                                     ___  __
GAM1278 LOC220082 3'  TCTTTTGCCCAGTGTTCG    32900         ATA  _
                                TCTTTTGTCCA  GTGT CG
                                ||||||||||  ||||  ||
                                AGAAAACGGGT  CACA GC
                                     ___  A
GAM1278 LOC51580  3'  TCTTTTGTCTGTGGTATGAGAA 32901        CAATA  C_
          T                      TCTTTTGTC    GTGT  GAAT
                                |||||||||    ||||  ||||
                                AGAAAACAG    CATA  CTTA
                                     ACAC_   CT
GAM1279 CIT     3'  ATAGTGTGTTTGGTGTTTT   32904     _   C
                                ATGG GTGTT GGTGTTTT
                                |||| ||||| ||||||||
                                TATC CACAA CCACAAAA
                                  A    A
GAM1279 SOX9    3'  TTTTAAGGCTCAAGGTGTTTT  32905     T   GTTC
                                TTTTA GGGT   GGTGTTTT
                                ||||| ||||   ||||||||
                                AAAAT TCCG   CCACAAAA
                                  _   AGTT
GAM1279 SPF30   3'  TTTTAGCAGGTTGGTGTTTT  32906     _   GTTC
                                TTTTA TGGGT   GGTGTTTT
                                ||||| |||||   ||||||||
                                AAAAT GTCCA   CCACAAAA
                                  C    A___
GAM1279 C20orf183 3'  TTTTATGGGTGGTTTATTTT  32907         TTCGG
                                TTTTATGGGTG    TGTTTT
                                ||||||||||    ||||||
                                AAAATACCCAC    ATAAAA
                                     CAA__
GAM1279 DKFZP564B1162 3'  TTTTATGGGAGTAGTATTTT  32908        T  TC
                                TTTTATGGG GT  GGTGTTTT
                                |||||||| ||  ||||||||
                                AAAATACCC CA  TCATAAAA
                                     T  __
GAM1279 FBXO9   3'  TTTTGTAGAGACGGTGTTTT  32909     A   TGTT
                                TTTT TGGG   CGGTGTTTT
                                |||| ||||   |||||||||
                                AAAA ATCT   GCCACAAAA
                                  C   CT__
GAM1279 KIAA0319  3'  CTTTGTGGGTGGGAATGTTTT  32910     A    TTC
                                TTTT TGGGTG  GGTGTTTT
                                |||| ||||||  ||||||||
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                                GAAA ACCCAC   TTACAAAA
                                  C     CC_
GAM1279 KIAA1423 3' TTTTATGAGGGTCTGTGTTTT 32911        T   CG
                                TTTTATGGG GTT  GTGTTTT
                                ||||||||| |||  |||||||
                                AAAATACTC CAG  CACAAAA
                                     C   A_
GAM1279 PLAC3    5' TCTTGTGGGTTCCAAGTGTTTT 32912     A    G   _
                                TTTT TGGGT TTCG GTGTTTT
                                |||| ||||| |||| |||||||
                                AGAA ACCCA AGGT CACAAAA
                                  C     _   T
GAM1279 SNAPC3   3' CTTTTTGAAGTTTGGTGTTTT  32913     A   T   C
                                TTTT TGGG GTT GGTGTTTT
                                |||| |||| ||| ||||||||
                                GAAA ACTT CAA CCACAAAA
                                  A   _  A
GAM1279 LOC91266 5' CTTTGTGGGTGTTTTGTATTTT 32914     A       CG
                                TTTT TGGGTGTT  GTGTTTT
                                |||| ||||||||  |||||||
                                GAAA ACCCACAA  CATAAAA
                                  C       AA
GAM1280 BLAME    3' AAACTGCAGGGTCTGGGG    32917        AGTTC    CC
                                AAGCTGCAG    GTCT  GG
                                |||||||||    ||||  ||
                                TTTGACGTC    CAGA  CC
                                     C____    CC
GAM1280 CDKN2C   5' GCTCGGCGCGCGTCTCCGGAG  32918    GCAGA  T
                                GCT    GT CGTCTCCGGAG
                                |||    || ||||||||||
                                CGA    CG GCAGAGGCCTC
                                  GCCG_  C
GAM1280 EDARADD  5' GCTGGCAGGCCTCCGG      32919     _  AGTTC
                                GCTG CAG    GTCTCCGG
                                |||| |||    ||||||||
                                CGAC GTC    CGGAGGCC
                                  C  _____
GAM1280 GCN5L2   3' AGCTGCAGGATCGGGTCCGGAG 32920        AGT   TC
                                AGCTGCAG   TCG  TCCGGAG
                                ||||||||   |||  |||||||
                                TCGACGTC   AGC  AGGCCTC
                                     CT_   CC
GAM1280 GNAI2    3' AAGCTGGGGGTCCAGGCTGGAG 32921      CAGA    TCTCC
                                AAGCTG   GTTCG    GGAG
                                ||||||   |||||    ||||
                                TTCGAC   CAGGT    CCTC
                                   CCC_    CCGA_
GAM1280 HSF4     5' AGCTGCAGAGTCCGCAGAG   32922           CTCC
                                AGCTGCAGAGTTCGT   GGAG
                                ||||||||||||||   ||||
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                                TCGACGTCTCAGGCG   TCTC
                                          ____
GAM1280 MYCL2    3' AGCTGCAGAGTCCAGCTGGGG 32923          T  CC
                                AGCTGCAGAGTTCG CT  GG
                                |||||||||||||| ||  ||
                                TCGACGTCTCAGGT GA  CC
                                        C  CC
GAM1280 NESH     3' GCTGCAGAGGGGTGTCTGGGG 32924       TTC_   CC
                                GCTGCAGAG   GTCT  GG
                                |||||||||   ||||  ||
                                CGACGTCTC   CAGA  CC
                                     CCCA   CC
GAM1280 PA2G4    3' ACTTGCAGAACTCTGGA    32925    _    TTCGT   C
                                GCT GCAGAG    CTC GGA
                                ||| ||||||    ||| |||
                                TGA CGTCTT    GAG CCT
                                  A     _____  A
GAM1280 REQ      3' GCCGCAGAGAGCCACTCTGGAG 32926       T_  T   C
                                GCTGCAGAG  TCG CTC GGAG
                                |||||||||  ||| ||| ||||
                                CGGCGTCTC  GGT GAG CCTC
                                     TC   _   A
GAM1280 SLC21A2  3' AGGTGCAGAGTCAGTCTGGGG  32927    C       C   CC
                                AG TGCAGAGTT GTCT  GG
                                || |||||||| ||||  ||
                                TC ACGTCTCAG CAGA  CC
                                 C       T   CC
GAM1280 ZNF80    5' AAGCTGCAGACGTTTGCGG   32928        GTT   CTC
                                AAGCTGCAGA   CGT   CGG
                                ||||||||||   |||   |||
                                TTCGACGTCT   GCA   GCC
                                     ___   AAC
GAM1280 AGTRL2   5' AAGTTGCAGGGGCCTCTGGAG  32929    C    AGTTC    C
                                AAG TGCAG    GTCTC GGAG
                                ||| |||||    ||||| ||||
                                TTC ACGTC    CGGAG CCTC
                                  A    CC___    A
GAM1280 APCL     3' AGCTGTGCTGTTTCTGGA    32930      CAGA   C  C  C
                                AGCTG    GTT GT TC GGA
                                |||||    ||| || || |||
                                TCGAC    CGA CA AG CCT
                                   A___   _  A  A
GAM1280 CBCIP2   3' AAGCTGCACAGGCTCCGG    32931        G  TTC T
                                AAGCTGCA AG   G CTCCGG
                                |||||||| ||   | ||||||
                                TTCGACGT TC   C GAGGCC
                                     G  ___ _
GAM1280 CILP     3' AAGCTGCAGAGTTTTACCAG   32932           CGTCT
                                AAGCTGCAGAGTT    CCGG
                                ||||||||||||    ||||
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                                TTCGACGTCTCAA    GGTC
                                      AAT__
GAM1280  CSR1     3'  AAGCTGCAGGGTCAGCCCTGGG 32933        A  C   CC
                                AAGCTGCAG GTT GTCT  GG
                                ||||||||| ||| ||||  ||
                                TTCGACGTC CAG CGGG  CC
                                    C  T   AC
GAM1280  DKFZP564O0463 3'  AAGTTCAGAGAAAGATCTGGAG 32934    CTG    TTC_   CC
                                AAG   CAGAG   GTCT  GGAG
                                |||   |||||   ||||  ||||
                                TTC   GTCTC   TAGA  CCTC
                                  AA_    TTTC   __
GAM1280  FLJ20446  3'  AAGCGCAGGGTTTCTGATTGGA 32935    T   A   CG   CC__
            G                    AAGC GCAG GTT  TCT   GGAG
                                |||| |||| |||  |||   ||||
                                TTCG CGTC CAA  AGA   CCTC
                                  _   C   __  CTAA
GAM1280  FLJ20464  5'  TGCAGAAGCAGCTCCGGAG   32936      TT  T
                                TGCAGAG  CG CTCCGGAG
                                |||||||  || ||||||||
                                ACGTCTT  GT GAGGCCTC
                                    C_  C
GAM1280  FLJ20507  3'  AGCTGCAGAGTTGAGGGA    32937         CGTCTCC
                                AGCTGCAGAGTT      GGA
                                ||||||||||||      |||
                                TCGACGTCTCAA      CCT
                                      CTC_____
GAM1280  FLJ20507  3'  AGCTGCAGAGTTGAGGGA    32937         CGTCTCC
                                AGCTGCAGAGTT      GGA
                                ||||||||||||      |||
                                TCGACGTCTCAA      CCT
                                      CTC_____
GAM1280  FLJ21865  3'  GCTGCTGAAAACGCTCCGGAG  32938      A   TT  T
                                GCTGC GAG  CG CTCCGGAG
                                ||||| |||  || ||||||||
                                CGACG CTT  GC GAGGCCTC
                                   A   TT  _
GAM1280  KIAA0097  3'  AAGCTGCAGGGTGCCGG     32939        A  TCGTCT
                                AAGCTGCAG GT     CCGG
                                ||||||||| ||     ||||
                                TTCGACGTC CA     GGCC
                                    C  C_____
GAM1280  KIAA0202  3'  AAGTTGCAGAGTTTCGTCT   32940     C       _
                                AAG TGCAGAGTT CGTCT
                                ||| ||||||||| |||||
                                TTC ACGTCTCAA GCAGA
                                  A        A
GAM1280  KIAA0449  5'  AGCTGCAGAGTCGAAGGA    32941         T  TCTCC
                                AGCTGCAGAGT CG    GGA
                                |||||||||| ||    |||
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                                TCGACGTCTCA GC     CCT
                                      _ TT___
GAM1280 KIAA1053 3' GCTGCAAAGTATCTTGGAG   32942         TC    CC
                                GCTGCAGAGT  GTCT  GGAG
                                ||||||||||  ||||  ||||
                                CGACGTTTCA  TAGA  CCTC
                                     __    A_
GAM1280 KIAA1272 3' AAGTTGCAGCGTGAGGCTTTTG 32943     C     A  TC_  CTCC
             GAG                   AAG TGCAG GT   GT    GGAG
                                ||| ||||| ||   ||    ||||
                                TTC ACGTC CA   CG    CCTC
                                  A    G  CTC  AAAA
GAM1280 KIAA1533 5' AGCTGCAGCCGTTTCCGGAG  32944         AGT    C
                                AGCTGCAG   TCGT TCCGGAG
                                ||||||||   |||| |||||||
                                TCGACGTC   GGCA AGGCCTC
                                     ___    A
GAM1280 KIAA1655 5' AGCTGCGTGCGAGAGCTCCGGA 32945       A___   TTCGT
             G                   AGCTGC    GAG    CTCCGGAG
                                ||||||    |||    ||||||||
                                TCGACG    CTC    GAGGCCTC
                                   CACG   TC___
GAM1280 MGC11242 3' GCTCCAGGACTCATCTCTGGAG 32946     G   AG       C
                                GCT CAG  TTCGTCTC GGAG
                                ||| |||  |||||||| ||||
                                CGA GTC  GAGTAGAG CCTC
                                  G   CT       A
GAM1280 MGC14839 3' AAGCTCAGAATGCTTTTCCGGA 32947      G     TCGTC
             G                   AAGCT CAGAGT     TCCGGAG
                                |||||  ||||||     |||||||
                                TTCGA GTCTTA     AGGCCTC
                                  _     CGAAA
GAM1280 MGC2452  5' AGCTGCAGGGTCGCTGGGG   32948         A  T  T  CC
                                AGCTGCAG GT CG CT  GG
                                |||||||| || || ||  ||
                                TCGACGTC CA GC GA  CC
                                     C  _  _  CC
GAM1280 PLSCR3   3' CAGAGGCCTCCTTTGGAG    32949       TTC     ___
                                CAGAG   GTCTCC   GGAG
                                |||||   ||||||   ||||
                                GTCTC   CGGAGG   CCTC
                                   ___     AAA
GAM1280 PLSCR3   3' CAGAGGCCTCCTTTGGAG    32949       TTC     ___
                                CAGAG   GTCTCC   GGAG
                                |||||   ||||||   ||||
                                GTCTC   CGGAGG   CCTC
                                   ___     AAA
GAM1280 LOC144184 5' AGCTGCAGGGTCCCTATCCCGG 32950         A   __   T
                                AGCTGCAG GTTC  GTC CCGG
                                |||||||| ||||  ||| ||||
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                                TCGACGTC CAGG  TAG GGCC
                                    C    GA  _
GAM1280  LOC146268 3'  AAGCTGCAGGTCTGGGG     32951         AGTTC    CC
                                AAGCTGCAG     GTCT  GG
                                |||||||||     ||||  ||
                                TTCGACGTC     CAGA  CC
                                     _____    CC
GAM1280  LOC148932 3'  AAGCTGCCAGGCCACTCTGGAG 32952        AG  TT  T   C
                                AAGCTGC  AG  CG CTC GGAG
                                |||||||  ||  || ||| ||||
                                TTCGACG  TC  GT GAG CCTC
                                   G_  CG  _   A
GAM1280  LOC149345 3'  AGCTGCAGGGTTGTAGACTGG  32953        A   C  CTCC_
                                AGCTGCAG GTT GT     GG
                                |||||||| ||| ||     ||
                                TCGACGTC CAA CA     CC
                                    C   _  TCTGA
GAM1280  LOC149422 3'  AAGCTGCAAAGTGCTGGA     32954          TC  CTCC
                                AAGCTGCAGAGT  GT    GGA
                                ||||||||||||  ||    |||
                                TTCGACGTTTCA  CG    CCT
                                      __  A___
GAM1280  LOC158056 5'  GCGCAGAGTCCCAATCTGGGG  32955    T       __    CC
                                GC GCAGAGTTC  GTCT  GG
                                || |||||||||  ||||  ||
                                CG CGTCTCAGG  TAGA  CC
                                 _        GT    CC
GAM1280  LOC203636 3'  CTGCAGAGCCTTCTGGGG     32956         CG   CC
                                CTGCAGAGTT  TCT  GG
                                ||||||||||  |||  ||
                                GACGTCTCGG  AGA  CC
                                     A_   CC
GAM1280  LOC219376 5'  AAGCTCAGGTCTCTGG      32957      G   AGTTC    C
                                AAGCT CAG     GTCTC GG
                                ||||| |||     ||||| ||
                                TTCGA GTC     CAGAG CC
                                  _  ______     A
GAM1280  LOC253767 3'  AGCTGCAGAGTCCGCAGAG    32922            CTCC
                                AGCTGCAGAGTTCGT    GGAG
                                ||||||||||||||    ||||
                                TCGACGTCTCAGGCG    TCTC
                                                  ____
GAM1281  ACN      5'  CCATCCGCCCTGCAGCGCCCCT 32960         GATTAA_
                                CCATCCGCCC      CCCCT
                                ||||||||||      |||||
                                GGTAGGCGGG      GGGGA
                                     ACGTCGC
GAM1281  ADRA2A   3'  CCCCCATCCATTAACC      32961         GCCCG
                                TCCCCATCC    ATTAACC
                                |||||||||    |||||||
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                              GGGGGTAGG    TAATTGG
                                    _____
GAM1281 AP2B1    3' TCCCCATCTCTACTCAAATTCC 32962       C__ C  TTAA
                              TCCCCATC  GC CGA   CC
                              ||||||||  || |||   ||
                              AGGGGTAG  TG GTT   GG
                                   AGA  A  TAA_
GAM1281 AQP6     3' TCCTCACCCGCCCCCGCCT   32963    C      GATTAA _
                              TCC CATCCGCCC    CC CCT
                              ||| |||||||||    || |||
                              AGG GTGGGCGGG    GG GGA
                                A       _______ C
GAM1281 ARHGEF5  3' TCTCCATCCACAGAAGGCCTCT 32965   C      CC  TTAA  C
                              TC CCATCCGC  GA   CC CT
                              || ||||||||  ||   || ||
                              AG GGTAGGTG  CT   GG GA
                               A       T_  TCC_  A
GAM1281 ARHGEF5  3' CCCATCTGATGTGTTAACCCCT 32964      CGCCCGA
                              CCCATC      TTAACCCCT
                              ||||||      |||||||||
                              GGGTAG      AATTGGGGA
                                  ACTACAC
GAM1281 ARHGEF6  3' TCCCCATCTGGCCAAATT    32966       C_  C
                              TCCCCATC  GCC GATT
                              ||||||||  ||| ||||
                              AGGGGTAG  CGG TTAA
                                   AC   T
GAM1281 CCNT2    5' TCCTCCTCCGCCCGCTCC    32967    _ A      ATTAA
                              TCC CC TCCGCCCG    CC
                              ||| || ||||||||    ||
                              AGG GG AGGCGGGC    GG
                                A  _       GA___
GAM1281 DAAM2    3' TCCCCATCTCCCCAGTTTCCCT 32968       CG   A  AAC
                              TCCCCATC  CCCG TT   CCCT
                              ||||||||  |||| ||   ||||
                              AGGGGTAG  GGGT AA   GGGA
                                   AG   C  A__
GAM1281 ERBB2IP  3' TCCCCATTCTTTGCTTCCAGAT 32969       _ C__  __  _
           T                   TCCCCAT C   GC  CC GATT
                              |||||||  |   ||  || ||||
                              AGGGGTA G   CG  GG CTAA
                                   A AAA  AA  T
GAM1281 GSTM5    3' TCCCCATCAGCCTAGCCCC   32970       C  CGAT  A
                              TCCCCATC GCC    TA CCCC
                              |||||||| |||    || ||||
                              AGGGGTAG CGG    AT GGGG
                                   T  _____ C
GAM1281 HRMT1L2  3' TCCCCATCCCCCCCAGCCCAGGC 32971       G   A_  A_
           CCCT                    TCCCCATCC CCCG  TTA  CCCCT
                              |||||||||  ||||  |||  |||||
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                                AGGGGTAGG GGGT  GGT  GGGGA
                                     G   CG   CC
GAM1281 JUP     3'  TCCCCATCTCCCCTGGACGGTC 32972        CG  __  TAAC
            CCT                   TCCCCATC  CCC  GAT   CCCT
                                ||||||||  |||  |||   ||||
                                AGGGGTAG  GGG  CTG   GGGA
                                     AG   AC   CCA_
GAM1281 LARGE   3'  TCCCCATCGCTATAGCCCC   32973        C  CCGAT  A
                                TCCCCATC GC    TA CCCC
                                |||||||| ||    || ||||
                                AGGGGTAG CG    AT GGGG
                                     _ AT___  C
GAM1281 LARGE   3'  TCCCCATCGCTATAGCCCC   32973        C  CCGAT  A
                                TCCCCATC GC    TA CCCC
                                |||||||| ||    || ||||
                                AGGGGTAG CG    AT GGGG
                                     _ AT___  C
GAM1281 MAB21L1  3'  TCTCCATCCGCTTCCCCT   32974    C      CCGATTAA
                                TC CCATCCGC      CCCCT
                                || ||||||||      |||||
                                AG GGTAGGCG      GGGGA
                                 A       AA_______
GAM1281 NDRG1   3'  CCCATCCGTACTCAGCCTCT   32975        CCCGA   A  C
                                CCCATCCG    TTA CC CT
                                ||||||||    ||| || ||
                                GGGTAGGC    AGT GG GA
                                     ATG__   C  A
GAM1281 OPA3    3'  CCACCACGCCCGGTTAAC    32976      _     A
                                CCATC CGCCCG TTAAC
                                ||||| |||||| |||||
                                GGTGG GCGGGC AATTG
                                   T     C
GAM1281 P2RX3   5'  TCCCCATTCCTCCAACCCC   32977        _  G  CGATT
                                TCCCCAT CC CC    AACCCC
                                ||||||| || ||    ||||||
                                AGGGGTA GG GG    TTGGGG
                                     A  A  _____
GAM1281 S100A12  5'  CCCAGCCTAATGTTAACCCCT  32978     TCC   CG  __
                                CCCA   GCC  AT  TAACCCCT
                                ||||   |||  ||  ||||||||
                                GGGT   CGG  TA  ATTGGGGA
                                   ___   AT  CA
GAM1281 ZNF278   5'  TCTCCGCCCGCCCGCCTCCCCT 32979    C  AT     ATTAA
                                TC CC  CCGCCCG    CCCCT
                                || ||  |||||||    |||||
                                AG GG  GGCGGGC    GGGGA
                                 A  CG      GGA__
GAM1281 ZNF278   5'  TCTCCGCCCGCCCGCCTCCCCT 32979    C  AT     ATTAA
                                TC CC  CCGCCCG    CCCCT
                                || ||  |||||||    |||||
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                                AG GG  GGCGGGC    GGGGA
                                 A  CG      GGA__
GAM1281  ZNF278   5'  TCTCCGCCCGCCCGCCTCCCCT 32979    C  AT     ATTAA
                                TC CC  CCGCCCG    CCCCT
                                || ||  |||||||    |||||
                                AG GG  GGCGGGC    GGGGA
                                 A  CG      GGA__
GAM1281  ZNF278   5'  TCTCCGCCCGCCCGCCTCCCCT 32979    C  AT     ATTAA
                                TC CC  CCGCCCG    CCCCT
                                || ||  |||||||    |||||
                                AG GG  GGCGGGC    GGGGA
                                 A  CG      GGA__
GAM1281  A4GALT   3'  TCCCCATCCCCTTAGCACCGGC 32980        G  CGATTA  __
            CT                   TCCCCATCC CC     ACC  CCT
                                |||||||||  ||     |||  |||
                                AGGGGTAGG GG     TGG  GGA
                                     _  AATCG_   CC
GAM1281  APOL2    3'  CCATCTGCATTAACCCCT    32981      C  CCG
                                CCATC GC   ATTAACCCCT
                                |||||  ||   ||||||||||
                                GGTAG CG   TAATTGGGGA
                                   A  ___
GAM1281  APOL3    3'  CCATCTGCATTAACCCCT    32981      C  CCG
                                CCATC GC   ATTAACCCCT
                                |||||  ||   ||||||||||
                                GGTAG CG   TAATTGGGGA
                                   A  ___
GAM1281  C1orf16  3'  TCCCCATCCTGTCACCACCAAC 32982         GC___  G      C
            CTCT                    TCCCCATCC     CC ATTAACC CT
                                |||||||||     || |||||| ||
                                AGGGGTAGG     GG TGGTTGG GA
                                     ACAGT  _      A
GAM1281  DKFZP434P0721 3'  TCCCCATCCCCCACCAAACCC  32983         G    ATT
                                TCCCCATCC CCCG   AACCC
                                |||||||||  ||||   |||||
                                AGGGGTAGG GGGT   TTGGG
                                     _    GGT
GAM1281  DKFZP761E2110 5'  TCCTCCTCCGCCCGGGACCTCT 32984     _  A       ATTA   C
                                TCC CC TCCGCCCG    ACC CT
                                ||| || ||||||||    ||| ||
                                AGG GG AGGCGGGC    TGG GA
                                  A  _       CC__   A
GAM1281  EHM2     3'  TCCTACATCATATTAACCCCT  32985     C_   CGCCCG
                                TCC  CATC     ATTAACCCCT
                                |||  ||||     ||||||||||
                                AGG  GTAG     TAATTGGGGA
                                  AT   TA_____
GAM1281  FLJ12190 3'  TCCCCACCGAACTGTTGGCCT  32986       T   CCC    AACC_
                                TCCCCA CCG   GATT    CCT
                                ||||||  |||   ||||    |||
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                                AGGGGT GGC   TTGA    GGA
                                  _  ___    CAACC
GAM1281  FLJ12650  3'  CCCCCATCTGCCCCTTCAGAAC 32987       C   GA  __ C
              TCCT                  TCCCCATC GCCC  TTA  AC CCT
                                    |||||||| ||||  |||  || |||
                                    GGGGGTAG CGGG  AGT  TG GGA
                                       A   GA   CT  A
GAM1281  FLJ12700  3'  TCCCCTCATTAACCC      32988      A  CGCCCG
                                    TCCCC TC     ATTAACCC
                                    ||||| ||     ||||||||
                                    AGGGG AG     TAATTGGG
                                      _ _______
GAM1281  FLJ23550  3'  TCCCCATCCGACTTCAAATA   32989         _ C_   T
                                    TCCCCATCCG C  CGA TA
                                    ||||||||||  |  ||| ||
                                    AGGGGTAGGC G  GTT AT
                                          T AA   T
GAM1281  GMPPB     5'  CCTCGTCCGCCCGGTCGCCCT  32990    CCA      A  AAC
                                    CC   TCCGCCCG TT   CCCT
                                    ||   |||||||| ||   ||||
                                    GG   AGGCGGGC AG   GGGA
                                     AGC       C  C__
GAM1281  GMPPB     5'  CCTCGTCCGCCCGGTCGCCCT  32990    CCA      A  AAC
                                    CC   TCCGCCCG TT   CCCT
                                    ||   |||||||| ||   ||||
                                    GG   AGGCGGGC AG   GGGA
                                     AGC       C  C__
GAM1281  GMPPB     5'  CCTCGTCCGCCCGGTCGCCCT  32990    CCA      A  AAC
                                    CC   TCCGCCCG TT   CCCT
                                    ||   |||||||| ||   ||||
                                    GG   AGGCGGGC AG   GGGA
                                     AGC       C  C__
GAM1281  KIAA0721  3'  CCCAACCTAGATTAACCTCT   32991     T  GCCC      C
                                    CCCA CC    GATTAACC CT
                                    |||| ||    |||||||| ||
                                    GGGT GG    CTAATTGG GA
                                      T  AT__       A
GAM1281  KIAA0721  3'  CCCAACCTAGATTAACCTCT   32991     T  GCCC      C
                                    CCCA CC    GATTAACC CT
                                    |||| ||    |||||||| ||
                                    GGGT GG    CTAATTGG GA
                                      T  AT__       A
GAM1281  KIAA0774  5'  CCCACTGCCCAACCGCCT    32992      CC    ATTA  _
                                    CCCAT  GCCCG    ACC CCT
                                    |||||  |||||    ||| |||
                                    GGGTG  CGGGT    TGG GGA
                                      A_     _____   C
GAM1281  KIAA1100  3'  TCCCCATCCTCCTGGGACTTCC 32993        G  C__   AACC
              T                     TCCCCATCC CC   GATT    CCT
                                    |||||||| ||   ||||    |||
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                                AGGGGTAGG GG   CTGA    GGA
                                     A  ACC    A___
GAM1281  KIAA1437  3'  TCCCCATTCCCGACCAGCCTCT 32994       CCG      A  C
                                TCCCCAT   CCCGATTA CC CT
                                |||||||   |||||||| || ||
                                AGGGGTA   GGGCTGGT GG GA
                                    A__       C  A
GAM1281  KIAA1867  3'  TCCCCACCCGCCCACCC     32995          GATTA   C
                                TCCCCATCCGCCC    ACC C
                                ||||||||||||     ||| |
                                AGGGGTGGGCGGG    TGG G
                                       _____  A
GAM1281  MGC20470  3'  TCCCCATCCGGGGATTGTAGCC 32996         CCC    AACC
           T                     TCCCCATCCG   GATT    CCT
                                ||||||||||   ||||    |||
                                AGGGGTAGGC   CTAA    GGA
                                      CC_    CATC
GAM1281  PRO1770   5'  TCCCCATCTTCCCACTTAA   32997        CG    A
                                TCCCCATC  CCCG TTAA
                                ||||||||  |||| ||||
                                AGGGGTAG  GGGT AATT
                                     AA    G
GAM1281  SLC26A9   3'  CCTCCGCCCGACACCCCCT   32998    A       TAA
                                CC TCCGCCCGAT   CCCCT
                                || ||||||||||   |||||
                                GG AGGCGGGCTG   GGGGA
                                 _        TG_
GAM1281  SLC6A13   3'  CATCTGTTCAACAACCCCT   32999     CGCC    T
                                CATC    CGAT AACCCCT
                                ||||    |||| |||||||
                                GTAG    GTTG TTGGGGA
                                  ACAA    _
GAM1281  SPTLC2    3'  TCCCCATTCACAACCC      33000       C   CCGATT
                                TCCCCAT CGC     AACCC
                                ||||||| |||     |||||
                                AGGGGTA GTG     TTGGG
                                    A  _______
GAM1281  TSCOT     3'  TCCCCATCCACCAGGGATCCCT 33001          C__   TAAC
                                TCCCCATCCGCC   GAT    CCCT
                                ||||||||||||   |||    ||||
                                AGGGGTAGGTGG   CTA    GGGA
                                       TCC   _____
GAM1281  LOC145497 5'  TCCCCACCCGCCTGTGACT    33002          C__
                                TCCCCATCCGCC   GATT
                                ||||||||||||   ||||
                                AGGGGTGGGCGG   CTGA
                                       ACA
GAM1281  LOC146733 5'  TCCCCATCAGCCCGGTCACC   33003        C    ATTA
                                TCCCCATC GCCCG    ACC
                                ||||||||  |||||    |||
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                                AGGGGTAG CGGGC   TGG
                                    T    CAG_
GAM1281  LOC146823 3'  TCCCCATCCTTCGATTCCC   33004       GCC    AAC
                                TCCCCATCC  CGATT  CCC
                                |||||||||  |||||  |||
                                AGGGGTAGG  GCTAA  GGG
                                    AA_    ___
GAM1281  LOC151477 5'  TCCCCATCTTCTACCTCC    33005       CGCCCGA  A  _
                                TCCCCATC     TT ACC CC
                                ||||||||     || ||| ||
                                AGGGGTAG     AG TGG GG
                                    A_______ A  A
GAM1281  LOC153688 3'  TCCTTATCCTTAGACAACCCCT 33006    CC   GCCC  T
                                TCC  ATCC   GAT AACCCCT
                                |||  ||||   ||| |||||||
                                AGG  TAGG   CTG TTGGGGA
                                  AA   AAT_  _
GAM1281  LOC255328 3'  TCCCCATCCGGAATAACC    33007       CCC  T
                                TCCCCATCCG  GA TAACC
                                ||||||||||  || |||||
                                AGGGGTAGGC  CT ATTGG
                                      ___  T
GAM1281  LOC255786 5'  TCCCTGTCCGCCCACAGAAACT 33008     CA      ATT_  C
            CCT                   TCCC  TCCGCCCG   AAC CCT
                                |||| ||||||||   ||| |||
                                AGGG  AGGCGGGT   TTG GGA
                                  AC      GTCT  A
GAM1281  LOC257408 5'  TCCCCACCGCTCTTCACTCCT  33009      T   CCGATTA  C
                                TCCCCA CCGC     AC CCT
                                ||||||| ||||     || |||
                                AGGGGT GGCG     TG GGA
                                   _   AGAAG__  A
GAM1281  LOC90381  3'  CCTACCCGCCCCCCACT    33010    C      GATTAA  _
                                CC ATCCGCCC     CCC CT
                                || ||||||||     ||| ||
                                GG TGGGCGGG     GGG GA
                                 A      _______  T
GAM1281  LOC93190  3'  CATCATCCGTCAACCCC     33011     CGC  A
                                CATC  CCG TTAACCCC
                                ||||  ||| ||||||||
                                GTAG  GGC AGTTGGGG
                                  TA_  _
GAM1282  AGR2      3'  TGGTGTGGTGAGATGATAAC  33014     CA    C   G
                                TGG  TGGTGA ATGA TGAT
                                |||  |||||| |||| ||||
                                ACC  ACCACT TACT ATTG
                                  AC    C   _
GAM1282  APM1      3'  TGGCATGGTGGTAGGCACCTGT 33015        A____  GA
            G                    TGGCATGGTG    CAT  GTG
                                ||||||||||    |||  |||
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                                ACCGTACCAC    GTG  CAC
                                      CATCC   GA
GAM1282 CLECSF12 3' TGGCATGGTGGCATGCACCTG 33016         A   AGTGA
                                TGGCATGGTG CATG    TG
                                |||||||||| ||||    ||
                                ACCGTACCAC GTAC    AC
                                      C   GTGG_
GAM1282 DNASE1L1 3' TGGCAGGTGGCATGAGT    33017      T   A
                                TGGCA GGTG CATGAGT
                                ||||| |||| |||||||
                                ACCGT CCAC GTACTCA
                                   _   C
GAM1282 EPB72    3' GGCATGGTGGCATGAGCCTG  33018        A     GA
                                GGCATGGTG CATGAGT  TG
                                ||||||||| |||||||  ||
                                CCGTACCAC GTACTCG  AC
                                      C      G_
GAM1282 GNA14    3' TGGCATGGGACTGGCTCTG   33019       T  A  A  GA
                                TGGCATGG GAC TG GT  TG
                                |||||||| ||| || ||  ||
                                ACCGTACC CTG AC CG  AC
                                      _  _ _ AG
GAM1282 HLA-DRA  3' GCATGGTGATAATAAAATGAT 33020        CAT__
                                GCATGGTGA    GAGTGAT
                                |||||||||    |||||||
                                CGTACCACT    TTTACTA
                                      ATTAT
GAM1282 HLA-DRA  3' GCATGGTGATAATAAAATGAT 33020        CAT__
                                GCATGGTGA    GAGTGAT
                                |||||||||    |||||||
                                CGTACCACT    TTTACTA
                                      ATTAT
GAM1282 SOX10    3' TGGCATAGGTGGCATGGGCA  33021      _   A   A
                                TGGCAT GGTG CATG GTG
                                |||||| |||| |||| |||
                                ACCGTA CCAC GTAC CGT
                                   T   C   C
GAM1282 AMOT     5' TGGTGATGGTGATGA      33022      CA  A
                                TGGTGA  TG GTGATGA
                                ||||||  || |||||||
                                ACCACT  AC CACTACT
                                      __ _
GAM1282 BOP      5' TGGCTGGGAGTGATG      33023     A  TGACAT
                                TGGC TGG     GAGTGATG
                                |||| |||     ||||||||
                                ACCG ACC     CTCACTAC
                                   _  _______
GAM1282 FLJ25449 5' TGGTGATGGTGATGATAGCGAT 33024     C_     CATG
            G                    TGG  ATGGTGA   AGTGATG
                                |||  |||||||   |||||||
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                                ACC  TACCACT    TCGCTAC
                                  AC      ACTA
GAM1282  KIAA0295  3'  TGGTGATGGTGGTAATGATG   33025     C_     ACATG
                                TGG  ATGGTG    AGTGATG
                                |||  ||||||    |||||||
                                ACC  TACCAC    TTACTAC
                                  AC     CA___
GAM1282  KIAA0446  5'  GGCATGGTGGCATGCACCTGTG 33026         A    A____
                                GGCATGGTG CATG    GTG
                                ||||||||| ||||    |||
                                CCGTACCAC GTAC    CAC
                                     C    GTGGA
GAM1282  KIAA0527  3'  GACATTGACATGAGTGATGAT  33027      GG
                                GGCAT  TGACATGAGTGATGAT
                                |||||  ||||||||||||||||
                                CTGTA  ACTGTACTCACTACTA

                                  __
GAM1282  KIAA1040  3'  TGGCATGGTGGCATGTCTG    33028         A    AG
                                TGGCATGGTG CATG  TG
                                |||||||||| ||||  ||
                                ACCGTACCAC GTAC  AC
                                     C    AG
GAM1282  KIAA1257  3'  TGGCATGGTGGCATGCGCCTG  33029         A    A  GA
                                TGGCATGGTG CATG GT  TG
                                |||||||||| |||| ||  ||
                                ACCGTACCAC GTAC CG  AC
                                     C    G  G_
GAM1282  TCL6      5'  TGGCATGGTGGTGGGCACCTG  33030         ACA  A   A_
                                TGGCATGGTG   TG GTG  TG
                                ||||||||||   || |||  ||
                                ACCGTACCAC   AC CGT  AC
                                     C__  C   GG
GAM1282  TCL6      5'  TGGCATGGTGGTGGGCACCTG  33030         ACA  A   A_
                                TGGCATGGTG   TG GTG  TG
                                ||||||||||   || |||  ||
                                ACCGTACCAC   AC CGT  AC
                                     C__  C   GG
GAM1282  TCL6      5'  TGGCATGGTGGTGGGCACCTG  33030         ACA  A   A_
                                TGGCATGGTG   TG GTG  TG
                                ||||||||||   || |||  ||
                                ACCGTACCAC   AC CGT  AC
                                     C__  C   GG
GAM1282  TCL6      5'  TGGCATGGTGGTGGGCACCTG  33030         ACA  A   A_
                                TGGCATGGTG   TG GTG  TG
                                ||||||||||   || |||  ||
                                ACCGTACCAC   AC CGT  AC
                                     C__  C   GG
GAM1282  LOC155434 3'  TGGCATGGTGAGGTGAT     33031         CATGA
                                TGGCATGGTGA    GTGAT
                                ||||||||||     |||||
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                                ACCGTACCACT    CACTA
                                      C____
GAM1282 LOC201456 3' GGCATTGAGAGTGATG     33032      GG   CAT
                                GGCAT  TGA   GAGTGATG
                                |||||  |||   ||||||||
                                CCGTA  ACT   CTCACTAC
                                  __   ___
GAM1283 P2RY1    3' TAGTGTTTTGTTATATACCA   33035      CTCA
                                TGGTGT    TTATATACTA
                                ||||||    ||||||||||
                                ATCACA    AATATATGGT
                                   AAAC
GAM1283 LOC221954 5' TGGTGTCTTGTTCCTCTAGTGT 33036        CA  ATATA    C
                                TGGTGTCT  TT    CTAG GT
                                ||||||||  ||    |||| ||
                                ACCACAGA  AA    GATC CA
                                     AC  GGA__    A
GAM1284 FANCC    5' TTAAATCGGGTGGTCCTCGC   33039         AAAT   AAA_
                                TTAAATCGGGT   GGT   GC
                                ||||||||||    |||   ||
                                AATTTAGCCCA   CCA   CG
                                      ____  GGAG
GAM1284 GABRA2   3' TTAAATCAGGTCCTAGGGTA   33040         AAAT_
                                TTAAATCGGGT    GGTA
                                ||||||||||    ||||
                                AATTTAGTCCA    CCAT
                                      GGATC
GAM1284 FLJ23598 3' TCAGATCTTCGATGGTAAAG   33041       AA___
                                TCGGGT    ATGGTAAAG
                                ||||||    |||||||||
                                AGTCTA    TACCATTTC
                                   GAAGC
GAM1284 LOC92154 3' TTAAATCGGGGAGGATGGT   33042         TAA_
                                TTAAATCGGG   ATGGT
                                ||||||||||   |||||
                                AATTTAGCCC   TACCA
                                      CTCC
GAM1285 CRABP1   3' AGCACTAGGGATACAAGAGG   33045       TA  TA  T
                                AGCACTAG  GG  AC AAGAGG
                                ||||||||  ||  || ||||||
                                TCGTGATC  CC  TG TTCTCC
                                     __  TA  _
GAM1285 ELAC2    3' GCACCAGTCCTAAGAG      33046        AGGTAA
                                GCACTAGT     CTAAGAG
                                ||||||||     |||||||
                                CGTGGTCA     GATTCTC
                                     G_____
GAM1285 HAP1     3' AAGCAATAGGAGATTGAGAGG 33047      CTA    TAACTA
                                AAGCA  GTAGG     AGAGG
                                |||||  |||||     |||||
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                                TTCGT   TATCC     TCTCC
                                  ___     TCTAAC
GAM1285  KRT5     5'  GCACTAGTGGGTTGGGAGG   33048         A   AACTAA
                                GCACTAGT GGT      GAGG
                                |||||||| |||      ||||
                                CGTGATCA CCA      CTCC
                                    C   ACC___
GAM1285  MMP25    3'  AAGCACTAGGGGGTCACTGAGG 33049          TA   A   AA
                                AAGCACTAG  GGT ACT  GAGG
                                |||||||||  ||| |||  ||||
                                TTCGTGATC  CCA TGA  CTCC
                                    CC   G   __
GAM1285  PACSIN1  3'  GCAGCTAGAGTGCTAAGAGG   33050     _    T  GTAA
                                GCA CTAG AG    CTAAGAGG
                                ||| |||| ||    ||||||||
                                CGT GATC TC    GATTCTCC
                                  C    _  AC__
GAM1285  PODXL    3'  GCACTAGTGGGTTATTTTACAA 33051         A   AAC_____
            GAGG                    GCACTAGT GGT       TAAGAGG
                                |||||||| |||       |||||||
                                CGTGATCA CCA       GTTCTCC
                                    C   ATAAAAT
GAM1285  TYRP1    3'  ACATTAGTAGGTGAAATGTAAG 33052     C       AACTAA_
            G                    GCA TAGTAGGT      GAGG
                                ||| ||||||||      ||||
                                TGT ATCATCCA      TTCC
                                  A       CTTTACA
GAM1285  ARG99    3'  AAGCACTAGTAAAACTCTTAGG 33053           GT    AA___
            AGG                     AAGCACTAGTAG  AACT    GAGG
                                ||||||||||||  ||||    ||||
                                TTCGTGATCATT  TTGA    CTCC
                                      __    GAATC
GAM1285  BACH     3'  GCACCAGTGGCAGGAG      33054         A    ACTAA
                                GCACTAGT GGTA     GAG
                                |||||||| ||||     |||
                                CGTGGTCA CCGT     CTC
                                    _    C_____
GAM1285  DKFZP434F0318 3'  AAGACTAGTAGGACTTGGAGAG 33055     C       TAACTA
            G                    AAG ACTAGTAGG      AGAGG
                                ||| |||||||||      |||||
                                TTC TGATCATCC      TCTCC
                                  _        TGAACC
GAM1285  FLJ12526 5'  AGCACTAGCGGCGTGAGG    33056         A   AACTAA
                                AGCACTAGT GGT     GAGG
                                |||||||||| |||      ||||
                                TCGTGATCG CCG     CTCC
                                    _  CA_____
GAM1285  FLJ13848 3'  ACTGTTGGCCACTGAGAG    33057     A  A   A   A
                                ACT GT GGT ACT AGAG
                                ||| || ||| ||| ||||
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                                TGA CA CCG TGA TCTC
                                  _ A  G  C
GAM1285 KIAA0476 3' GCACCAGTTCTTCCTAAGGG  33058       AGGTAA   A
                                GCACTAGT    CTAAG GG
                                ||||||||    ||||| ||
                                CGTGGTCA    GATTC CC
                                    AGAAG_   _
GAM1285 KIAA0638 3' GCACCAGTGGAAGGGAGAGG  33059       A  TAACTA
                                GCACTAGT GG    AGAGG
                                |||||||| ||    |||||
                                CGTGGTCA CC    TCTCC
                                    _ TTCCC_
GAM1285 KIAA1025 3' ACACCAGTAACTAAGAGG   33060       GGTA
                                GCACTAGTA   ACTAAGAGG
                                |||||||||   |||||||||
                                TGTGGTCAT   TGATTCTCC
                                     ____
GAM1285 KIAA1189 3' AGCACAGAGCTAAGA      33061      T  T  GTAA
                                AGCAC AG AG   CTAAGA
                                ||||| || ||   ||||||
                                TCGTG TC TC   GATTCT
                                  _ _ ____
GAM1285 MGC14859 3' AGCGCTAGTAGGCAGGCACAGG 33062    A       AC  AG
                                AGC CTAGTAGGTA  TA  AGG
                                ||| ||||||||||  ||  |||
                                TCG GATCATCCGT  GT  TCC
                                  C        CC  G_
GAM1285 RBMS1    5' TAGTAGGTGGCGTACTGAGG  33063       A____   AA
                                TAGTAGGT    ACT  GAGG
                                ||||||||    |||  ||||
                                ATCATCCA    TGA  CTCC
                                    CCGCA  __
GAM1285 LOC129526 3' CTGGCAAGGGACTAAGAGG   33064    A    TA
                                CT GTAGG  ACTAAGAGG
                                || |||||  |||||||||
                                GA CGTTC  TGATTCTCC
                                 C    CC
GAM1285 LOC147807 5' GCACTGGAGCCAGCTAAGAGG  33065      AGT  G  A
                                GCACT   AG TA CTAAGAGG
                                |||||   || || ||||||||
                                CGTGA   TC GT GATTCTCC
                                   CC_  G  C
GAM1285 LOC219997 3' AGCACTAGCCCAGGGACTGGGA 33066        A_  TA   AA
          GG                    AGCACTAGT  GG  ACT  GAGG
                                |||||||||  ||  |||  ||||
                                TCGTGATCG  TC  TGA  CTCC
                                     GG  CC   CC
GAM1286 CD28     3' TGCGTAGTGGGTTTAAATTT   33069      CTT   C_
                                TGTGTA   GTGG  TTAAATTT
                                ||||||   ||||  ||||||||
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                                ACGCAT   CACC  AATTTAAA
                                   ___    CA
GAM1286  CD80     3'  TGGGTAAAACAGCTTAAATTT  33070    T   CTT TG
                                TG GTA   G  GCTTAAATTT
                                || |||   |  ||||||||||
                                AC CAT   T  CGAATTTAAA
                                 C   TT_ GT
GAM1286  SLC15A1  3'  TGTGTACGTGTGGCTTAAAT   33071        T
                                TGTGTAC TGTGGCTTAAAT
                                ||||||| ||||||||||||
                                ACACATG ACACCGAATTTA
                                    C
GAM1286  FLJ20059 3'  TATGTACTTGGTCCCTCTTAGA 33072          TGG___    A
            TTTAT                  TGTGTACTTG     CTTA ATTTAT
                                ||||||||||      |||| ||||||
                                ATACATGAAC     GAAT TAAATA
                                      CAGGGA    C
GAM1287  ADRBK1   5'  GCGCTCGGCCGCGCCCGA    33075         _    GA
                                GCGCTCGGC GCGCC  GA
                                ||||||||| |||||  ||
                                CGCGAGCCG CGCGG  CT
                                     G    G_
GAM1287  C21orf2  3'  CGCTCGGCGGAGGATG      33076         CGCC  _
                                CGCTCGGCG   GAG ATG
                                |||||||||   ||| |||
                                GCGAGCCGC   CTC TAC
                                     _____  C
GAM1287  ETS2     5'  GCTGCTCGGTGCGCGCCG    33077    _    ___
                                GC GCTCG  GCGCGCCG
                                || |||||  ||||||||
                                CG CGAGC  CGCGCGGC
                                 A    CA
GAM1287  HSF2BP   5'  GCGTCGGCGCGCCCTCTGA   33078    C        GAGA
                                GCG TCGGCGCGCC   TGA
                                ||| ||||||||||   |||
                                CGC AGCCGCGCGG   ACT
                                  _        GAG_
GAM1287  KCNQ4    5'  GCGCTCGGGGCGCTCAGA    33079        C   CG
                                GCGCTCGG GCGC  AGA
                                |||||||| ||||  |||
                                CGCGAGCC CGCG  TCT
                                     C   AG
GAM1287  NAV2     5'  GCGCCTTTGGGGTGCCGGGATG 33080      C__  CGC   A
                                GCGCT   GG   GCCG GATG
                                |||||   ||   |||| ||||
                                CGCGG   CC   CGGC CTAC
                                   AAA  CCA   C
GAM1287  PTPRG    5'  GCGCTCGGCGGCCCGA      33081         C   GA
                                GCGCTCGGCG GCC  GA
                                |||||||||| |||  ||
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                              CGCGAGCCGC CGG  CT
                                    _  G_
GAM1287 ASB16   5' GCCTCAGGGCCGAGATG    33082    G    CGC
                              GC CTCGG  GCCGAGATG
                              || |||||  |||||||||
                              CG GAGTC  CGGCTCTAC
                               _    C__
GAM1287 CYP4F12  3' GCCCTCGGCGCGCATG     33083    G       CGAG
                              GC CTCGGCGCGC   ATG
                              || ||||||||||   |||
                              CG GAGCCGCGCG   TAC
                               G       _____
GAM1287 FLJ10811 3' GCGCTCAGCAGAAAGGTG    33084         CGCC  A
                              GCGCTCGGCG   GAG TG
                              ||||||||||   ||| ||
                              CGCGAGTCGT   TTC AC
                                    CT__  C
GAM1287 FLJ10829 3' GCCTTGGCACAGCAGATG    33085    G C    _ CG
                              GC CT GGCGC GC  AGATG
                              || || ||||| ||  |||||
                              CG GA CCGTG CG  TCTAC
                               _ A    T __
GAM1287 FLJ11099 3' CTCGGCCAGAGATGA      33086      G  CC
                              CTCGGC CG  GAGATGA
                              |||||| ||  |||||||
                              GAGCCG GT  CTCTACT
                                 _ __
GAM1287 FLJ12903 3' GCACTTTAGGAGGCCGAGGTG  33087     C__  CGC    A
                              GCGCT  GG  GCCGAG TG
                              |||||  ||  |||||| ||
                              CGTGA  CC  CGGCTC AC
                                 AAT  TC_    C
GAM1287 FLJ20291 3' GCACTCCCACCGAGATG    33088      GGCG
                              GCGCTC   CGCCGAGATG
                              ||||||   ||||||||||
                              CGTGAG   GTGGCTCTAC
                                 G___
GAM1287 KIAA0205 3' GCACTTTAGGAAGCCGAGGTG  33089     C__  CGC    A
                              GCGCT  GG  GCCGAG TG
                              |||||  ||  |||||| ||
                              CGTGA  CC  CGGCTC AC
                                 AAT  TT_    C
GAM1287 KIAA0924 3' GCACTTTCGGAGGCTGAGGTG  33090     __   CGC  C  A
                              GCGC  TCGG  GC GAG TG
                              ||||  ||||  || ||| ||
                              CGTG  AGCC  CG CTC AC
                                AA   TC_  A  C
GAM1287 KIAA0997 5' GCGCTCGGCGCTCGGGCTG   33091         GC  AGA
                              GCGCTCGGCGC  CG  TG
                              ||||||||||  ||  ||
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                                CGCGAGCCGCG  GC   AC
                                      A_  CCG
GAM1287  KIAA1274  5'  GCGCCCGGCGCGCGCTCTG   33092          C AGA
                                GCGCTCGGCGCGC G   TG
                                |||||||||||| |   ||
                                CGCGGGCCGCGCG C   AC
                                       _ GAG
GAM1287  KIAA1405  5'  CGTCCACCAGCGCCGAGATGA  33093    CT  G _
                                CG  CG C GCGCCGAGATGA
                                ||  || | ||||||||||||
                                GC  GT G CGCGGCTCTACT
                                 AG  G T
GAM1287  KIAA1484  5'  GCGCACGGCGGCGATG     33094     T    C  CGA
                                GCGC CGGCG GC   GATG
                                |||| ||||| ||   ||||
                                CGCG GCCGC CG   CTAC
                                  T    _  ___
GAM1287  KIAA1508  3'  GCGCCCGGCCGGATG      33095        G  CCGA
                                GCGCTCGGC CG    GATG
                                |||||||| ||    ||||
                                CGCGGGCCG GC    CTAC
                                      _  ____
GAM1287  MGC2655   5'  GCCTTCGGCGCGAAGGTG    33096    GC      CC   A
                                GC  TCGGCGCG  GAG TG
                                ||  ||||||||  ||| ||
                                CG  AGCCGCGC  TTC AC
                                 GA       __  C
GAM1287  MGC5149   3'  GCGCTTTGGGAGACCGAGGTG  33097      C_  CGC     A
                                GCGCT  GG   GCCGAG TG
                                |||||  ||   |||||| ||
                                CGCGA  CC   TGGCTC AC
                                   AA  CTC     C
GAM1287  MRPS7     5'  GCCCTCGGCGCGCCTGA     33098    G        GA
                                GC CTCGGCGCGCC  GA
                                || ||||||||||  ||
                                CG GAGCCGCGCGG  CT
                                 G         A_
GAM1287  OCT11     3'  GCACTTCGGGACGCTGAGGTG  33099      _  C   C  A
                                GCGCT CGG GCGC GAG TG
                                ||||| ||| |||| ||| ||
                                CGTGA GCC TGCG CTC AC
                                   A   C    A   C
GAM1287  YAP1      5'  GCTCCACGGGCCGAGGTG    33100     G  C     A
                                GCTC GCG GCCGAG TG
                                |||| ||| |||||| ||
                                CGAG TGC CGGCTC AC
                                  G   C     C
GAM1287  ZDHHC1    3'  GCACTCGGTGCGGCAAGGATG  33101        C   C   _
                                GCGCTCGG GCG CGAG ATG
                                |||||||| ||| |||| |||
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                                CGTGAGCC CGC GTTC TAC
                                    A   C    C
GAM1287  LOC124944 5'  CGCTCGGCGCGCCCAGTCGA  33102          G  A
                                CGCTCGGCGCGCC AG TGA
                                |||||||||||| || |||
                                GCGAGCCGCGCGG TC GCT
                                    G  A
GAM1287  LOC126669 3'  GCACTCGGGGAGACTGAGGTG  33103       CGC_  C   A
                                GCGCTCGG    GC GAG TG
                                ||||||||    || ||| ||
                                CGTGAGCC    TG CTC AC
                                    CCTC  A   C
GAM1287  LOC130639 5'  GCACTCGGGGAGGCTGAGGTG  33104       CGC_  C   A
                                GCGCTCGG    GC GAG TG
                                ||||||||    || ||| ||
                                CGTGAGCC    CG CTC AC
                                    CCTC  A   C
GAM1287  LOC133383 5'  GCGCTCGGCCGCCTTCCCCTG  33105       G   GAGA__
                                GCGCTCGGC CGCC     TG
                                ||||||||| ||||     ||
                                CGCGAGCCG GCGG     AC
                                    _   AAGGGG
GAM1287  LOC149194 3'  GCACTTTTGGAGGCCGAGGTGA 33106     C__  CGC     A
                                GCGCT   GG   GCCGAG TGA
                                |||||   ||   |||||| |||
                                CGTGA   CC   CGGCTC ACT
                                   AAA  TC_     C
GAM1287  LOC149711 3'  GCACTTTCGGAGGCTGAGGTG  33090     __   CGC  C   A
                                GCGC  TCGG   GC GAG TG
                                ||||  ||||   || ||| ||
                                CGTG  AGCC   CG CTC AC
                                  AA    TC_  A   C
GAM1287  LOC151057 3'  GCACTTTAGGAGGCCGAGGTG  33087     C__  CGC     A
                                GCGCT   GG   GCCGAG TG
                                |||||   ||   |||||| ||
                                CGTGA   CC   CGGCTC AC
                                   AAT  TC_     C
GAM1287  LOC151534 5'  GCGCTCAGGCCGGAT      33107        CGC    A
                                GCGCTCGG   GCCG GAT
                                ||||||||   |||| |||
                                CGCGAGTC   CGGC CTA
                                    ____   _
GAM1287  LOC153572 5'  GCGCGTTGGCGAACCAGGTG  33108     TC_   C   G  A
                                GCGC   GGCG GCC AG TG
                                ||||   |||| ||| || ||
                                CGCG   CCGC TGG TC AC
                                  CAA    T   _  C
GAM1287  LOC158158 5'  GCGCCCAAGCGCCGAGGTG   33109       C       A
                                GCGCTCGG GCGCCGAG TG
                                |||||||| |||||||| ||
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                                CGCGGGTT CGCGGCTC AC
                                   _       C
GAM1287  LOC199688 5'  GCGCTAGGTTGGCGAGATGA  33110      C  CGC  C
                                GCGCT GG   GC GAGATGA
                                ||||| ||   || |||||||
                                CGCGA CC   CG CTCTACT
                                   T  AAC  _
GAM1287  LOC253767 5'  GCTCGGCGGACCAGATG     33111        C   G
                                GCTCGGCG GCC AGATG
                                |||||||| ||| |||||
                                CGAGCCGC TGG TCTAC
                                     C   _
GAM1287  LOC256514 5'  GCGCTCGGCACGCTGGGA    33112           CGA
                                GCGCTCGGCGCGC   GA
                                ||||||||||||   ||
                                CGCGAGCCGTGCG   CT
                                       ACC
GAM1287  LOC257473 3'  GCACTCGGTGCGGCAAGGATG  33101        C   C   _
                                GCGCTCGG GCG CGAG ATG
                                |||||||| ||| |||| |||
                                CGTGAGCC CGC GTTC TAC
                                     A   C   C
GAM1287  LOC90231  3'  GCCTCCGAACGCCGAGATG   33113    G   GGC
                                GC CTC   GCGCCGAGATG
                                || |||   ||||||||||
                                CG GAG   TGCGGCTCTAC
                                 _  GCT
GAM1287  LOC91115  3'  GCACTTTAGGATGCCGAGGTG  33114      C__  CGC     A
                                GCGCT   GG   GCCGAG TG
                                |||||   ||   |||||| ||
                                CGTGA   CC   CGGCTC AC
                                   AAT  TA_     C
GAM1288  APM1      3'  GTGGATCACAAAGTCAGGAG   33117     A   C G
                                GTG ATC C AGAGTCAGGAG
                                ||| ||| | ||||||||||
                                CAC TAG G TTTCAGTCCTC
                                  C   T _
GAM1288  APPL      3'  GCGTGAACCTGGGAGGCGGAG  33118         CC_   A  CA
                                GCGTGAATC   GAG GT  GGAG
                                |||||||||   ||| ||  ||||
                                CGCACTTGG   CTC CG  CCTC
                                     ACC  _ ___
GAM1288  BAZ2B     5'  AGGTGGATCACAAGGTCAGGAG 33119    C   A   C   A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GTTC CAGTCCTC
                                 _  C   T   _
GAM1288  CASP2     3'  GCGTGAACCCGGGAGTTGGAG  33121       T   A   CA
                                GCGTGAA CCCG GAGT  GGAG
                                ||||||| |||| ||||  ||||
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                                CGCACTT GGGC CTCA  CCTC
                                   _   C   A_
GAM1288  CASP2   3' GTGGATCATGAGGTCAGGAG  33120    A  CC  A
                                GTG ATC  GAG GTCAGGAG
                                ||| |||  ||| ||||||||
                                CAC TAG  CTC CAGTCCTC
                                  C  TA  _
GAM1288  CASP2   3' GTGGATCATGAGGTCAGGAG  33120    A  CC  A
                                GTG ATC  GAG GTCAGGAG
                                ||| |||  ||| ||||||||
                                CAC TAG  CTC CAGTCCTC
                                  C  TA  _
GAM1288  CASP2   3' GTGGATCATGAGGTCAGGAG  33120    A  CC  A
                                GTG ATC  GAG GTCAGGAG
                                ||| |||  ||| ||||||||
                                CAC TAG  CTC CAGTCCTC
                                  C  TA  _
GAM1288  CASP2   3' GCGTGAACCCGGGAGTTGGAG 33121      T  A  CA
                                GCGTGAA CCCG GAGT  GGAG
                                ||||||| |||| ||||  ||||
                                CGCACTT GGGC CTCA  CCTC
                                   _   C   A_
GAM1288  CASP2   3' GCGTGAACCCGGGAGTTGGAG 33121      T  A  CA
                                GCGTGAA CCCG GAGT  GGAG
                                ||||||| |||| ||||  ||||
                                CGCACTT GGGC CTCA  CCTC
                                   _   C   A_
GAM1288  CASP2   3' GTGGATCATGAGGTCAGGAG  33120    A  CC  A
                                GTG ATC  GAG GTCAGGAG
                                ||| |||  ||| ||||||||
                                CAC TAG  CTC CAGTCCTC
                                  C  TA  _
GAM1288  CASP2   3' GCGTGAACCCGGGAGTTGGAG 33121      T  A  CA
                                GCGTGAA CCCG GAGT  GGAG
                                ||||||| |||| ||||  ||||
                                CGCACTT GGGC CTCA  CCTC
                                   _   C   A_
GAM1288  CASP8   3' GTGGATCACGAGGTCAGGAG  33122    A  C  A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288  CASP8   3' GTGGATCACGAGGTCAGGAG  33122    A  C  A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288  CASP8   3' GTGGATCACGAGGTCAGGAG  33122    A  C  A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
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                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288 CASP8   3' GCGTGAACCCGGGAGGCGGAG 33123      T   A  TCA
                                GCGTGAA CCCG GAG  GGAG
                                ||||||| |||| |||  ||||
                                CGCACTT GGGC CTC  CCTC
                                   _  C  CG_
GAM1288 CASP8   3' GCGTGAACCCGGGAGGCGGAG 33123      T   A  TCA
                                GCGTGAA CCCG GAG  GGAG
                                ||||||| |||| |||  ||||
                                CGCACTT GGGC CTC  CCTC
                                   _  C  CG_
GAM1288 CASP8   3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288 CASP8   3' GCGTGAACCCGGGAGGCGGAG 33123      T   A  TCA
                                GCGTGAA CCCG GAG  GGAG
                                ||||||| |||| |||  ||||
                                CGCACTT GGGC CTC  CCTC
                                   _  C  CG_
GAM1288 CDC6    3' GCAGATCACTTGAGGGTCAGGA 33124   GA  CC__  A
          G                  GT  ATC   GAG GTCAGGAG
                             ||  |||   ||| ||||||||
                             CG  TAG   CTC CAGTCCTC
                              TC  TGAA  C
GAM1288 CGB     5' GTGGGGTCCTGGGAGCCAGGAG 33125    AA_  CGA
                                GTG  TCC  GAGTCAGGAG
                                |||  |||  ||||||||||
                                CAC  AGG  CTCGGTCCTC
                                  CCC  ACC
GAM1288 CR1     3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288 DSCR3   3' GTGGGTCACGAGGTCAGGAG  33126    AA C   A
                                GTG  TC CGAG GTCAGGAG
                                |||  || |||| ||||||||
                                CAC  AG GCTC CAGTCCTC
                                  CC  T   _
GAM1288 GHR     3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288 HCS     3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
```

```
                                CAC TAG GCTC CAGTCCTC
                                  C   T   _
GAM1288 HLCS     5' AGGTGGATCACGAGGTCAGGAG 33127    C   A   C    A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GCTC CAGTCCTC
                                 _   C   T   _
GAM1288 INMT     3' GTGGATCACCAGGTCAGGAG   33128     A   _   G   A
                                GTG ATC CC AG GTCAGGAG
                                ||| ||| || || ||||||||
                                CAC TAG GG TC CAGTCCTC
                                  C   T   _ _
GAM1288 INMT     3' GCGTGAACCCGGGAGGCGGAG  33123        T    A   TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
                                CGCACTT GGGC CTC   CCTC
                                    _   C   CG_
GAM1288 KCNA6    3' AGCTGGAGAGTCAGG      33129     G  AATCCC
                                AGC TG     GAGAGTCAGG
                                ||| ||     ||||||||||
                                TCG AC     CTCTCAGTCC
                                 _ _______
GAM1288 LYZ      3' GTGGATCACAAGGTCAGGAG   33131     A   C    A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GTTC CAGTCCTC
                                  C   T   _
GAM1288 LYZ      3' GCGTGAACCCGGGAGGTGGAG  33130        T    A   TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
                                CGCACTT GGGC CTC   CCTC
                                    _   C   CA_
GAM1288 PMCHL1   3' AGGTGGATCACGAGGTCAGGAG 33127    C   A   C    A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GCTC CAGTCCTC
                                 _   C   T   _
GAM1288 PODXL    3' AGCGATGGAGAGTCAGGA    33132      _  AATCCC
                                AGCG TG     GAGAGTCAGGA
                                |||| ||     ||||||||||||
                                TCGC AC     CTCTCAGTCCT
                                  T _______
GAM1288 PPFIA3   3' GCCGACCGAGAGTCGGG     33133    G   ATC       A
                                GC TGA   CCGAGAGTC GG
                                || |||   ||||||||| ||
                                CG GCT   GGCTCTCAG CC
                                 _  ____       C
GAM1288 PPID     3' GTGGATCACAAGGTCAGGAG   33131     A   C    A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
```

```
                                CAC TAG GTTC CAGTCCTC
                                  C  T   _
GAM1288 RP2     5' GCGTGAACCCTGGGAACCCCGG 33134         CGA  GT A_
                                GCGTGAATCC  GA  C  GG
                                ||||||||||  ||  |  ||
                                CGCACTTGGG  CT  G  CC
                                      ACC  TG GG
GAM1288 SEDL    3' GTGGATCAACTGAGGTCAGGAG 33135    A  CC__  A
                                GTG ATC   GAG GTCAGGAG
                                ||| |||   ||| ||||||||
                                CAC TAG   CTC CAGTCCTC
                                  C  TTGA  _
GAM1288 SEDL    3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288 SERPINB9 3' GCGTGAACCCGGGAGGCGGAG 33123       T   A  TCA
                                GCGTGAA CCCG GAG  GGAG
                                ||||||| |||| |||  ||||
                                CGCACTT GGGC CTC  CCTC
                                    _   C  CG_
GAM1288 SERPINB9 3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288 TAPBP   3' GCGTGAACCCGAGAGGCGGAG 33136       T      TCA
                                GCGTGAA CCCGAGAG  GGAG
                                ||||||| ||||||||  ||||
                                CGCACTT GGGCTCTC  CCTC
                                    _      CG_
GAM1288 TAZ     5' GTGAGTCCCGAGATTGCGGAG 33137     A      GTCA
                                GTGA TCCCGAGA   GGAG
                                |||| ||||||||   ||||
                                CACT AGGGCTCT   CCTC
                                  C      AACG
GAM1288 TERF1   3' GTGGATCATGAAGTCAGGAG  33138    A  CCGA
                                GTG ATC   GAGTCAGGAG
                                ||| |||   ||||||||||
                                CAC TAG   TTCAGTCCTC
                                  C  TAC_
GAM1288 TERF2   3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288 UGDH    3' GCGTGAACCTGGGAAGCAGA  33139       CCGA  T
                                GCGTGAATC   GAG CAGG
                                |||||||||   ||| ||||
```

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                                CGCACTTGG    TTC GTCT
                                     ACCC  _
GAM1288 VENTX2   3' GCGGATCACAGGGTCAGGAG  33140    T  A  C G  A
                                GCG GA TC C AG GTCAGGAG
                                ||| || || | || ||||||||
                                CGC CT AG G TC CAGTCCTC
                                  _ _ T _ C
GAM1288 VHL      3' GTGGATCACAAGGTCAGGAG  33131    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GTTC CAGTCCTC
                                  C  T   _
GAM1288 VIPR2    3' GCGTGAACCCGGGAGGCGGAG 33123      T   A  TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
                                CGCACTT GGGC CTC   CCTC
                                    _   C  CG_
GAM1288 WHSC1    3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288 APOL2    3' GTGAACCCGGGAGGCGGAG   33141     T   A  TCA
                                GTGAA CCCG GAG   GGAG
                                ||||| |||| |||   ||||
                                CACTT GGGC CTC   CCTC
                                   _   C  CG_
GAM1288 ARHF     3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288 ASE-1    3' AGGTGGATCACGAGGTCAGGAG 33127   C  A  C   A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GCTC CAGTCCTC
                                 _  C  T   _
GAM1288 ASE-1    3' GCGTGAACCCGGGAGGCGGAG 33123      T   A  TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
                                CGCACTT GGGC CTC   CCTC
                                    _   C  CG_
GAM1288 C13orf1  3' AGGTGGATCATGAGGTCAGGAG 33142   C  A  CC  A
                                AG GTG ATC  GAG GTCAGGAG
                                || ||| |||  ||| ||||||||
                                TC CAC TAG  CTC CAGTCCTC
                                 _  C  TA  _
GAM1288 C20orf162 5' GCTTGAGTCCTTAATCAGGAG 33143   G  A  CGAG
                                GC TGA TCC    AGTCAGGAG
                                || ||| |||    |||||||||
```

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                                CG ACT AGG    TTAGTCCTC
                                 A  C  AA__
GAM1288 C9orf9   3' GCGTGAACCTGGGAGGCGGAG 33118        CC_  A  CA
                                GCGTGAATC  GAG GT  GGAG
                                |||||||||  ||| ||  ||||
                                CGCACTTGG  CTC CG  CCTC
                                     ACC  _ __
GAM1288 CGB5     5' GTGGGGTCCTGGGAGCCAGGAG 33125    AA_  CGA
                                GTG  TCC  GAGTCAGGAG
                                |||  |||  ||||||||||
                                CAC  AGG  CTCGGTCCTC
                                  CCC  ACC
GAM1288 CGB8     5' GTGGGGTCCTGGGAGCCAGGAG 33125    AA_  CGA
                                GTG  TCC  GAGTCAGGAG
                                |||  |||  ||||||||||
                                CAC  AGG  CTCGGTCCTC
                                  CCC  ACC
GAM1288 CNNM4    3' AGCTGAGTCCCGACTCACCAGG 33144    G  A    GA_
             AG                   AGC TGA TCCCGA  GTCAGGAG
                                |||  ||| ||||||  ||||||||
                                TCG ACT AGGGCT  TGGTCCTC
                                  _  C    GAG
GAM1288 DKFZP434C212 3' GTGGATCACGAGGTCAGGAG  33122    A  C  A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T  _
GAM1288 FLJ10298 3' AGGGTGGATCACTAGGTCAGGA 33145   C  A  CCG  A
             G                    AG GTG ATC  AG GTCAGGAG
                                || ||| |||  || ||||||||
                                TC CAC TAG  TC CAGTCCTC
                                 C  C  TGA  _
GAM1288 FLJ10560 3' GCGTGAACCCGGGAGGCAGA  33146       T  A  T
                                GCGTGAA CCCG GAG CAGG
                                ||||||| |||| ||| ||||
                                CGCACTT GGGC CTC GTCT
                                    _  C  C
GAM1288 FLJ12581 3' GCGTGAACCCGGGAGGCGGAG 33123       T  A  TCA
                                GCGTGAA CCCG GAG  GGAG
                                ||||||| |||| |||  ||||
                                CGCACTT GGGC CTC  CCTC
                                    _  C  CG_
GAM1288 FLJ12668 3' GTGGATCCCCTGAGGTCAGGAG 33147    A   __  A
                                GTG ATCCC  GAG GTCAGGAG
                                ||| |||||  ||| ||||||||
                                CAC TAGGG  CTC CAGTCCTC
                                  C   GA  _
GAM1288 FLJ14486 3' AGCGAGAGTCCCGAGGCCCAG  33148    T A    AG
                                AGCG GA TCCCGAG  TCAG
                                |||| || |||||||  ||||
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                                TCGC CT AGGGCTC  GGTC
                                  T C      CG
GAM1288  FLJ20045  3'  GTGGATCACGAGGTCAGGAG   33122     A   C    A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C   T   _
GAM1288  FLJ20813  3'  GCGTGAACCCGGGAGGTGGAG  33130       T    A   TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
                                CGCACTT GGGC CTC   CCTC
                                    _   C   CA_
GAM1288  FLJ20813  3'  GTGGATCATGAGGTCAGGAG   33120     A   CC   A
                                GTG ATC  GAG GTCAGGAG
                                ||| |||  ||| ||||||||
                                CAC TAG  CTC CAGTCCTC
                                  C   TA  _
GAM1288  FLJ22167  5'  GCGTGAACCTGGGAGGCAGA   33149        CCGA   T
                                GCGTGAATC    GAG CAGG
                                |||||||||    ||| ||||
                                CGCACTTGG    CTC GTCT
                                     ACC_   C
GAM1288  FLJ22794  3'  AGGTGGATCACGAGGTCAGGAG 33127    C   A   C    A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GCTC CAGTCCTC
                                 _   C   T    _
GAM1288  FLJ23074  3'  ATGAACCCCCTGGGAGTTGGG  33150        GA__    CA
                                GTGAATCCC    GAGT  GG
                                |||||||||    ||||  ||
                                TACTTGGGG    CTCA  CC
                                     GACC    AC
GAM1288  FLJ23322  3'  AGCTGGAAGATGAGTCAGG    33151     GT   TCCC  _
                                AGC  GAA    GA GAGTCAGG
                                |||  |||    || ||||||||
                                TCG  CTT    CT CTCAGTCC
                                  AC   ____  A
GAM1288  FLJ23392  3'  GTGGATCACGAGGTCAGGAG   33122     A   C    A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C   T   _
GAM1288  FLJ25193  3'  ATGACTTGAGGGTCAGGAG    33152     ATCCC   A
                                GTGA     GAG GTCAGGAG
                                ||||     ||| ||||||||
                                TACT     CTC CAGTCCTC
                                   GAA__   C
GAM1288  FLJ31101  3'  GTGGATCATGAGGTCAGGAG   33120     A   CC   A
                                GTG ATC  GAG GTCAGGAG
                                ||| |||  ||| ||||||||
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                                CAC TAG  CTC CAGTCCTC
                                  C   TA  _
GAM1288 FLJ32894 3' GTGGATCCCGAGGTCAGGAG  33153    A      A
                                GTG ATCCCGAG GTCAGGAG
                                ||| |||||||| ||||||||
                                CAC TAGGGCTC CAGTCCTC
                                  C       _
GAM1288 GNG4    3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C   T   _
GAM1288 GTF2E1  3' GTGGATCATGAGGTCAGGAG  33120    A  CC  A
                                GTG ATC  GAG GTCAGGAG
                                ||| |||  ||| ||||||||
                                CAC TAG  CTC CAGTCCTC
                                  C   TA  _
GAM1288 HSPC065  3' GTGGATCATGAGGTCAGGAG  33120    A  CC  A
                                GTG ATC  GAG GTCAGGAG
                                ||| |||  ||| ||||||||
                                CAC TAG  CTC CAGTCCTC
                                  C   TA  _
GAM1288 ICK     3' AGGGTGGATCACGAGGTCAGGA 33154    C  A  C   A
             G                   AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GCTC CAGTCCTC
                                 C   C   T   _
GAM1288 KIAA0469 3' GCGTGAACCTGGGAGATGGAG  33155        CC_   GTCA
                                GCGTGAATC   GAGA   GGAG
                                |||||||||   ||||   ||||
                                CGCACTTGG   CTCT   CCTC
                                     ACC   A___
GAM1288 KIAA0475 3' AGGTGGATCACCTGGGGTCAGG 33156    C  A  _  GAGA
             AG                   AG GTG ATC CC    GTCAGGAG
                                || ||| ||| ||    ||||||||
                                TC CAC TAG GG    CAGTCCTC
                                 _  C   T  ACCC
GAM1288 KIAA0562 3' GTGGATCACAAGGTCAGGAG  33131    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GTTC CAGTCCTC
                                  C   T   _
GAM1288 KIAA0594 3' GTGGATCACAAGGTCAGGAG  33131    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GTTC CAGTCCTC
                                  C   T   _
GAM1288 KIAA0923 3' AGGTGGATCTTTATCAGGA   33157    C  A  CCGAGA
                                AG GTG ATC     GTCAGGA
                                || ||| |||     |||||||
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                                TC CAC TAG     TAGTCCT
                                 _  C  AAA___
GAM1288 KIAA1143 3' AGGTGGATCATGAGGTCAGGAG 33142   C  A  CC  A
                                AG GTG ATC  GAG GTCAGGAG
                                || ||| |||  ||| ||||||||
                                TC CAC TAG  CTC CAGTCCTC
                                 _  C  TA  _
GAM1288 KIAA1198 3' GTGGATCACAAGGTCAGGAG  33131    A  C  A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GTTC CAGTCCTC
                                  C  T  _
GAM1288 KIAA1210 3' GCGTGAACCCGGGAGGCGGAG 33123      T  A  TCA
                                GCGTGAA CCCG GAG  GGAG
                                ||||||| |||| |||  ||||
                                CGCACTT GGGC CTC  CCTC
                                    _  C  CG_
GAM1288 KIAA1297 3' GTGAGGTAGGAGAGTCAGGAG 33158    ATCCC
                                GTGA   GAGAGTCAGGAG
                                ||||   ||||||||||||
                                CACT   CTCTCAGTCCTC
                                  CCATC
GAM1288 KIAA1456 3' GCGTGAACCCGGGAGGCGGAG 33123      T  A  TCA
                                GCGTGAA CCCG GAG  GGAG
                                ||||||| |||| |||  ||||
                                CGCACTT GGGC CTC  CCTC
                                    _  C  CG_
GAM1288 KIAA1668 3' GTGGATCACAAGGTCAGGAG  33131    A  C  A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GTTC CAGTCCTC
                                  C  T  _
GAM1288 KIAA1971 3' AGGTGGATCACGAGGTCAGGAG 33127   C  A  C  A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GCTC CAGTCCTC
                                 _  C  T  _
GAM1288 MEF-2   3' GTGGATCACGAGGTCAGGAG  33122    A  C  A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T  _
GAM1288 MGC10200 3' GCGTGAACCTGGGAGGCAGA  33149      CCGA  T
                                GCGTGAATC   GAG CAGG
                                |||||||||   ||| ||||
                                CGCACTTGG   CTC GTCT
                                     ACC_  C
GAM1288 MGC2477  5' GCGTGAACCCGGGAGGCAGA  33146     T  A  T
                                GCGTGAA CCCG GAG CAGG
                                ||||||| |||| ||| ||||
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                                CGCACTT GGGC CTC GTCT
                                   _   C  C
GAM1288 MGC35558 3' AGCGTGGGTTCTGAAGTCAGG 33159      AA_ CC G
                                AGCGTG  TC  GA AGTCAGG
                                ||||||  ||  || |||||||
                                TCGCAC  AG  CT TCAGTCC
                                   CCA  A_  _
GAM1288 moblak  3' GCGTGAATCTGGGAGGCGGAG 33160       CC_  A CA
                                GCGTGAATC  GAG GT  GGAG
                                |||||||||  ||| ||  ||||
                                CGCACTTAG  CTC CG  CCTC
                                     ACC  _ __
GAM1288 OCT11   3' GTGGATCAGGAGGTCAGGAG  33161    A  CC  A
                                GTG ATC  GAG GTCAGGAG
                                ||| |||  ||| ||||||||
                                CAC TAG  CTC CAGTCCTC
                                  C  TC  _
GAM1288 OR51E2  3' GTGGATCACAAGGTCAGGAG  33131    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GTTC CAGTCCTC
                                  C  T   _
GAM1288 PRO0365  5' AGGTGGATCATGAGGTCAGGAG 33142   C  A  CC  A
                                AG GTG ATC  GAG GTCAGGAG
                                || ||| |||  ||| ||||||||
                                TC CAC TAG  CTC CAGTCCTC
                                 _  C  TA  _
GAM1288 PSPH    3' GCGTGAACCTGGGAGGCAGA  33149       CCGA  T
                                GCGTGAATC   GAG CAGG
                                |||||||||   ||| ||||
                                CGCACTTGG   CTC GTCT
                                     ACC_  C
GAM1288 R32184_3 3' GCTGGCCGGCAGAGTCAGG  33162   G AATC  __
                                GC TG   CCG  AGAGTCAGG
                                || ||   |||  |||||||||
                                CG AC   GGC  TCTCAGTCC
                                 _ C___  CG
GAM1288 RAB21   3' GCGTGAACCTGGGAGGTGGAG 33163       CC_  A CA
                                GCGTGAATC  GAG GT  GGAG
                                |||||||||  ||| ||  ||||
                                CGCACTTGG  CTC CA  CCTC
                                     ACC  _ __
GAM1288 RASSF2  3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288 SERF1B  3' GTGAATCACGAGGTCAGGAG  33164      C   A
                                GTGAATC CGAG GTCAGGAG
                                ||||||| |||| ||||||||
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```
                                CACTTAG GCTC CAGTCCTC
                                   T   _
GAM1288 SLC12A8  3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288 SREC     3' GCGTGAACCCGGGAGGCAGA  33146      T   A  T
                                GCGTGAA CCCG GAG CAGG
                                ||||||| |||| ||| ||||
                                CGCACTT GGGC CTC GTCT
                                   _   C  C
GAM1288 SREC     3' AGGTGGATCACGAGGTCAGGAG 33127   C  A  C   A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GCTC CAGTCCTC
                                 _  C  T   _
GAM1288 TADA3L   3' GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288 TCL6     5' AGGTGGATCACTTGGTCAGGAG 33165   C  A  CCGAGA
                                AG GTG ATC     GTCAGGAG
                                || ||| |||     ||||||||
                                TC CAC TAG     CAGTCCTC
                                 _  C  TGAAC_
GAM1288 TCL6     5' AGGTGGATCACTTGGTCAGGAG 33165   C  A  CCGAGA
                                AG GTG ATC     GTCAGGAG
                                || ||| |||     ||||||||
                                TC CAC TAG     CAGTCCTC
                                 _  C  TGAAC_
GAM1288 TCL6     5' AGGTGGATCACTTGGTCAGGAG 33165   C  A  CCGAGA
                                AG GTG ATC     GTCAGGAG
                                || ||| |||     ||||||||
                                TC CAC TAG     CAGTCCTC
                                 _  C  TGAAC_
GAM1288 TCL6     5' AGGTGGATCACTTGGTCAGGAG 33165   C  A  CCGAGA
                                AG GTG ATC     GTCAGGAG
                                || ||| |||     ||||||||
                                TC CAC TAG     CAGTCCTC
                                 _  C  TGAAC_
GAM1288 TUCAN    3' GTGGATCATGAGGTCAGGAG  33120    A  CC  A
                                GTG ATC  GAG GTCAGGAG
                                ||| |||  ||| ||||||||
                                CAC TAG  CTC CAGTCCTC
                                  C  TA  _
GAM1288 UBN1     3' GCTGTACCCTGGGAGTCAGGAG 33166   G  AAT  GA_
                                GC TG   CCC   GAGTCAGGAG
                                || ||   |||   ||||||||||
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                                CG AC   GGG   CTCAGTCCTC
                                 _ AT_   ACC
GAM1288  ZNF221    3'  GCGTGAACTTGGGAGGCGGAG  33167        CCC_   A  CA
                                GCGTGAAT    GAG GT  GGAG
                                ||||||||    ||| ||  ||||
                                CGCACTTG    CTC CG  CCTC
                                     AACC   _ __
GAM1288  LOC113523 5'  GTGAATCACGAGGTCAGGAG   33164        C    A
                                GTGAATC CGAG GTCAGGAG
                                ||||||| |||| ||||||||
                                CACTTAG GCTC CAGTCCTC
                                     T    _
GAM1288  LOC118976 5'  GCGTGAACCTCGGGGCGAG    33168         C  AGA  C
                                GCGTGAATC CG   GT AG
                                ||||||||| ||   || ||
                                CGCACTTGG GC   CG TC
                                      A  CC_  C
GAM1288  LOC120114 3'  AGGTGGATTACGAGGTCAGGAG 33169    C   A  CC    A
                                AG GTG AT  CGAG GTCAGGAG
                                || ||| ||  |||| ||||||||
                                TC CAC TA  GCTC CAGTCCTC
                                 _   C  AT   _
GAM1288  LOC128077 3'  AGGTGGATCACGAGGTCAGGAG 33127    C   A   C    A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GCTC CAGTCCTC
                                 _   C   T    _
GAM1288  LOC128989 3'  AGGTGGATCACCACGTCAGGAG 33170    C   A   _  GAGA
                                AG GTG ATC CC    GTCAGGAG
                                || ||| ||| ||    ||||||||
                                TC CAC TAG GG    CAGTCCTC
                                 _   C   T  TG__
GAM1288  LOC135154 3'  AGGTGGATCAACTGAGGTCAGG 33171    C   A   CC__   A
           AG                    AG GTG ATC    GAG GTCAGGAG
                                || ||| |||    ||| ||||||||
                                TC CAC TAG    CTC CAGTCCTC
                                 _   C   TTGA   _
GAM1288  LOC138050 5'  GTGAACCCGGGAGGCAGA    33172       T    A   T
                                GTGAA CCCG GAG CAGG
                                ||||| |||| ||| ||||
                                CACTT GGGC CTC GTCT
                                   _    C   C
GAM1288  LOC145009 3'  GTGGATCACGAGGTCAGGAG   33122     A   C    A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C   T    _
GAM1288  LOC145757 5'  GCGTGAACCCGGGAGGCGGAG  33123        T    A   TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
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                                CGCACTT GGGC CTC   CCTC
                                   _   C  CG_
GAM1288  LOC146229 3'  GCGTGAACCTGGGAGCCGGAG  33173        CCGA    A
                                GCGTGAATC   GAGTC GGAG
                                |||||||||   ||||| ||||
                                CGCACTTGG   CTCGG CCTC
                                   ACC_    _
GAM1288  LOC148137 3'  GTGGATCACGAGGTCAGGAG  33122    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1288  LOC149421 3'  GTGAATCACGAGGTCAGGAG  33164       C   A
                                GTGAATC CGAG GTCAGGAG
                                ||||||| |||| ||||||||
                                CACTTAG GCTC CAGTCCTC
                                   T   _
GAM1288  LOC149821 5'  GCGTGAACCTGGGAGGCGGAG  33118        CC_  A  CA
                                GCGTGAATC   GAG GT  GGAG
                                |||||||||   ||| ||  ||||
                                CGCACTTGG   CTC CG  CCTC
                                   ACC  _ __
GAM1288  LOC152445 3'  AGGTGGATCACGAGGTCAGGAG 33127   C  A  C   A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GCTC CAGTCCTC
                                  _  C  T   _
GAM1288  LOC152719 5'  GCGTGAACCCGGGAGGCGGAG  33123       T   A  TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
                                CGCACTT GGGC CTC   CCTC
                                   _   C  CG_
GAM1288  LOC154877 3'  GTGAACCCGGAAGGCGGAG   33174      T   AG  TCA
                                GTGAA CCCG  AG   GGAG
                                ||||| ||||  ||   ||||
                                CACTT GGGC  TC   CCTC
                                   _   CT  CG_
GAM1288  LOC158549 5'  AGGTGGATCACCAGGTCAGGAG 33175   C  A  _  G  A
                                AG GTG ATC CC AG GTCAGGAG
                                || ||| ||| || || ||||||||
                                TC CAC TAG GG TC CAGTCCTC
                                  _  C  T  _  _
GAM1288  LOC158668 3'  GTGGATCATGAAGTCAGGAG  33138    A  CCGA
                                GTG ATC   GAGTCAGGAG
                                ||| |||   ||||||||||
                                CAC TAG   TTCAGTCCTC
                                  C  TAC_
GAM1288  LOC167989 5'  AGCGTGAATCTCGGCAGCACAG 33176        C  AG  _
                                AGCGTGAATC CG  AGT CAG
                                |||||||||| ||  ||| |||
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                                TCGCACTTAG GC  TCG GTC
                                      A  CG   T
GAM1288  LOC200014 3'  GTGGATCATGAGGTCAGGAG  33120     A   CC   A
                                GTG ATC  GAG GTCAGGAG
                                ||| |||  ||| ||||||||
                                CAC TAG  CTC CAGTCCTC
                                  C   TA  _
GAM1288  LOC200301 5'  GCGTGAACCCGGGAGGCGGAG  33123        T   A   TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
                                CGCACTT GGGC CTC   CCTC
                                    _   C   CG_
GAM1288  LOC203350 3'  AGGTGGATCACAAGGTCAGGAG 33119    C   A   C    A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GTTC CAGTCCTC
                                 _   C   T    _
GAM1288  LOC219735 3'  GTGGATCACGAGGTCAGGAG   33122     A   C    A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C   T    _
GAM1288  LOC219894 3'  GCGTGAACCCGGGAGGTGGAG  33130        T   A   TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
                                CGCACTT GGGC CTC   CCTC
                                    _   C   CA_
GAM1288  LOC220074 3'  GCGTGAACCTGGAAGGCGGAG  33177         CC   A  CA
                                GCGTGAATC  GAG GT  GGAG
                                |||||||||  ||| ||  ||||
                                CGCACTTGG  CTT CG  CCTC
                                     AC   C  __
GAM1288  LOC220074 3'  GTGGATCACAAGGTCAGGAG   33131     A   C    A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GTTC CAGTCCTC
                                  C   T    _
GAM1288  LOC222068 3'  AGGTGGATCAACTGAGGTCAGG 33171    C   A   CC__   A
           AG                     AG GTG ATC    GAG GTCAGGAG
                                || ||| |||    ||| ||||||||
                                TC CAC TAG    CTC CAGTCCTC
                                 _   C   TTGA   _
GAM1288  LOC253981 3'  GTGGATCACGAGGTCAGGAG   33122     A   C    A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C   T    _
GAM1288  LOC254672 3'  AGGTGGATCACAGGGTCAGGAG 33178    C   A   C G  A
                                AG GTG ATC C AG GTCAGGAG
                                || ||| ||| | || ||||||||
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                                TC CAC TAG G TC CAGTCCTC
                                 _  C  T _  C
GAM1288  LOC256905 5'  AGCTGTGGCCTGAGAGTCAGG  33179     _  AAT  C
                                AGC GTG  CC GAGAGTCAGG
                                ||| |||  || ||||||||||
                                TCG CAC  GG CTCTCAGTCC
                                  A  C__  A
GAM1288  LOC257465 3'  GTGGATCACCAAGGTCAGGAG  33180     A  _   A
                                GTG ATC CCGAG GTCAGGAG
                                ||| ||| ||||| ||||||||
                                CAC TAG GGTTC CAGTCCTC
                                  C  T   _
GAM1288  LOC257486 3'  GCGTGAACCCGGGAGGCGGAG  33123       T  A  TCA
                                GCGTGAA CCCG GAG  GGAG
                                ||||||| |||| |||  ||||
                                CGCACTT GGGC CTC  CCTC
                                   _  C  CG_
GAM1288  LOC81034  3'  GCGTGAACCCGGGAGGTGGAG  33130       T  A  TCA
                                GCGTGAA CCCG GAG  GGAG
                                ||||||| |||| |||  ||||
                                CGCACTT GGGC CTC  CCTC
                                   _  C  CA_
GAM1288  LOC91373  3'  GTGGATCACGAGGTCAGGAG  33122     A  C  A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T  _
GAM1288  LOC92661  5'  GTGAACCCGGGAGGTGGAG  33181      T  A  TCA
                                GTGAA CCCG GAG  GGAG
                                ||||| |||| |||  ||||
                                CACTT GGGC CTC  CCTC
                                   _  C  CA_
GAM1289  CASP8     3'  GAACTGAGATGTCAGCTCAT  33184     AACC  AC
                                GAA  GGA  GTCAGCTCAT
                                |||  |||  ||||||||||
                                CTT  TCT  CAGTCGAGTA
                                  GAC_  A_
GAM1289  CDH1      3'  TGGAGGCTGGGCACAGCAGCTC 33185     AAACC  A  T
            AT                   TGGA   GG ACG CAGCTCAT
                                ||||   || ||| ||||||||
                                ACCT   CC TGT GTCGAGTA
                                  CCGAC  G  C
GAM1289  PCLO      3'  TGGAAAACTGGCAGCCAC   33186       C  AACGT  T
                                TGGAAAAC GG   CAGC CAT
                                |||||||| ||   |||| |||
                                ACCTTTTG CC   GTCG GTG
                                   A _____  _
GAM1289  SLC4A5    5'  TGGAAACATCCATCAGCTCAT  33187      ACCGGAA
                                TGGAAA     CGTCAGCTCAT
                                ||||||     ||||||||||
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                                ACCTTT      GTAGTCGAGTA
                                   GTAG___
GAM1289 SLC4A5   5' TGGAAACATCCATCAGCTCAT 33187      ACCGGAA
                                TGGAAA      CGTCAGCTCAT
                                ||||||      ||||||||||
                                ACCTTT      GTAGTCGAGTA
                                   GTAG___
GAM1289 SLC4A5   5' TGGAAACATCCATCAGCTCAT 33187      ACCGGAA
                                TGGAAA      CGTCAGCTCAT
                                ||||||      ||||||||||
                                ACCTTT      GTAGTCGAGTA
                                   GTAG___
GAM1289 SLC9A6   3' TGGAAAATCTGAACATCA    33188       CCG
                                TGGAAAA   GAACGTCA
                                |||||||   ||||||||
                                ACCTTTT   CTTGTAGT
                                    AGA
GAM1289 C8orf2   3' TGGGGGGTGGGGGTCAGCTCAT 33189    AAAACC  AAC
                                TGG     GG   GTCAGCTCAT
                                |||     ||   ||||||||||
                                ACC     CC   CAGTCGAGTA
                                  CCCCA_  CC_
GAM1289 MGC4737  5' TGGAAGCCGATCAGCTCA    33190     AA   GAAC
                                TGGAA  CCG   GTCAGCTCA
                                |||||  |||   |||||||||
                                ACCTT  GGC   TAGTCGAGT
                                   C_   _____
GAM1289 LOC64744 3' GGAGGCGGAACACACACTCAT 33191    AAAC      TCA
                                GGA   CGGAACG   GCTCAT
                                |||   |||||||   ||||||
                                CCT   GCCTTGT   TGAGTA
                                  CC__      GTG
GAM1290 SIAT8C   5' TTAATCCATTTTCAGTCAT   33194        CGA   TAA
                                TTAGTCCATT   TAG   TCAT
                                ||||||||||   |||   ||||
                                AATTAGGTAA   GTC   AGTA
                                     AA_   ___
GAM1291 AQP6     5' GAGATTGGGGAAAGTAAGG   33197      A  ACA    A
                                GAGAT GG   GGAAA GTAAGG
                                ||||| ||   ||||| ||||||
                                CTCTA CC   CCTTT CATTCC
                                   A ___    _
GAM1291 B4GALT1  3' TGAGGTGGAACAGGAGGCTTTA 33198     ATA      AAAGTA
             GG                   TGAG   GGACAGGA     AGG
                                ||||   ||||||||     |||
                                ACTC   CTTGTCCT     TCC
                                  CAC       CCGAAA
GAM1291 C18orf1  3' TGAGGCAGGTAGAGAAGTAAGG 33199     A    ACA   A
                                TGAG TAGG   GGA AAGTAAGG
                                |||| ||||   ||| ||||||||
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                                ACTC GTCC   TCT TTCATTCC
                                  C    A__   C
GAM1291  CACNA1C   3'  GAAAACAGGAAAGGTGAGG    33200    TA        A  A
                                GA  GGACAGGAAA GT AGG
                                ||  |||||||||| || |||
                                CT  TTTGTCCTTT CA TCC
                                 __         C  C
GAM1291  DDX11     3'  TGGGACAGGATAGGGAGCAGGG 33201    A      C   AAA    A
                                TG GATAGGA AGG   AGTA GG
                                || ||||||| |||   |||| ||
                                AC CTGTCCT TCC   TCGT CC
                                 C      A  C__    C
GAM1291  DISC1     3'  AGATCACAGGAGAAGTAAGG   33202      AGG     A
                                AGAT   ACAGGA AAGTAAGG
                                ||||   |||||| ||||||||
                                TCTA   TGTCCT TTCATTCC
                                  G__     C
GAM1291  EIF2C1    3'  CAGGGAGGAGAAGTAAG     33203      AC    A
                                TAGG  AGGA AAGTAAG
                                ||||  |||| |||||||
                                GTCC  TCCT TTCATTC
                                  C_   C
GAM1291  FHL1      3'  TGGTATAGGGCAGAAAGTAAGG 33204    AG    A    AA
                                TG  ATAGG CAGGA  AGTAAGG
                                ||  ||||| |||||  |||||||
                                AC  TATCC GTCTT  TCATTCC
                                 CA    C    __
GAM1291  GUCY1B2   3'  TGAGAGGAAGGAAAAGTGAGG  33205      TA  C       A
                                TGAGA  GGA AGGAAAAGT AGG
                                |||||  ||| |||||||||| |||
                                ACTCT  CCT TCCTTTTCA TCC
                                   __  _       C
GAM1291  IKBKB     3'  TGAGAGAGGACAGGGAGCAGGG 33206      T      AAA    A
                                TGAGA AGGACAGG   AGTA GG
                                ||||| ||||||||   |||| ||
                                ACTCT TCCTGTCC   TCGT CC
                                   C       C__    C
GAM1291  MAPT      3'  TGGGAAGGACAGGGGGCTCGG  33207    A  T      AAAA  AA
                                TG GA AGGACAGG    GT  GG
                                || || ||||||||    ||  ||
                                AC CT TCCTGTCC    CG  CC
                                 C  _       CC__  AG
GAM1291  MAPT      3'  TGGGAAGGACAGGGGGCTCGG  33207    A  T      AAAA  AA
                                TG GA AGGACAGG    GT  GG
                                || || ||||||||    ||  ||
                                AC CT TCCTGTCC    CG  CC
                                 C  _       CC__  AG
GAM1291  MAPT      3'  TGGGAAGGACAGGGGGCTCGG  33207    A  T      AAAA  AA
                                TG GA AGGACAGG    GT  GG
                                || || ||||||||    ||  ||
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```
                                AC CT TCCTGTCC    CG  CC
                                 C  _      CC__  AG
GAM1291  MAPT     3'  TGGGAAGGACAGGGGGCTCGG  33207    A  T      AAAA  AA
                                TG GA AGGACAGG    GT  GG
                                || || ||||||||    ||  ||
                                AC CT TCCTGTCC    CG  CC
                                 C  _      CC__  AG
GAM1291  MTMR8    3'  TGAGGGAGCACAAAAAAGTGAG 33208      AT  G    G     A
            G                    TGAG  AG ACAG AAAAGT AGG
                                ||||  || |||| |||||| |||
                                ACTC  TC TGTT TTTTCA TCC
                                  CC  G    _     C
GAM1291  NGFB     3'  TGAGGTAGGGAGGGGCCCAGG  33209      A   AC   AAAA  A_
                                TGAG TAGG  AGG    GT  AGG
                                |||| ||||  |||    ||  |||
                                ACTC ATCC  TCC    CG  TCC
                                  C   C_   C___  GG
GAM1291  PDGFRB   3'  GATCCCAGGGAAGTAAGG    33210     AGGA    AA
                                GAT    CAGG  AAGTAAGG
                                |||    ||||  ||||||||
                                CTA    GTCC  TTCATTCC
                                 GG__    C_
GAM1291  PPP2R5A  3'  TGAGACAAAGAGAAGGGTAAGG 33211         ACA    AA
                                TGAGATAGG   GGAA  GTAAGG
                                |||||||||   ||||  ||||||
                                ACTCTGTTT   TCTT  CATTCC
                                     C__    CC
GAM1291  ABT1     3'  TGAGGTAGACAGGAAGCA    33212      ATA       AA
                                TGAG   GGACAGGA  AGTA
                                ||||   ||||||||  ||||
                                ACTC   TCTGTCCT  TCGT
                                  CA_       __
GAM1291  FLJ10700 3'  GAGACAAGAGGAAAGGTAAGG  33213         CA    A
                                GAGATAGGA  GGAAA GTAAGG
                                |||||||||  ||||| ||||||
                                CTCTGTTCT  CCTTT CATTCC
                                     __     C
GAM1291  FLJ12389 3'  TGAGATGGGAAGGGAAGAAAGG 33214       A   C   AA   T
                                TGAGAT GGA AGG  AAG AAGG
                                |||||| ||| |||  ||| ||||
                                ACTCTA CCT TCC  TTC TTCC
                                   C   _   C_   T
GAM1291  FLJ14800 3'  TGGGACGGGGCAGGAAAAG   33215    A  TA  A
                                TG GA  GG CAGGAAAAG
                                || ||  || |||||||||
                                AC CT  CC GTCCTTTTC
                                 C  GC  C
GAM1291  FLJ22301 3'  TGAGATAGGACAAGAGAAG   33216             A
                                TGAGATAGGACAGGA AAG
                                |||||||||||||| |||
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                                ACTCTATCCTGTTCT TTC
                                        C
GAM1291  FLJ22679  3'  TGAGGAAGGACAGGGGTAGGG  33217     AT      AAAA   A
                                TGAG  AGGACAGG    GTA GG
                                ||||  ||||||||    ||| ||
                                ACTC  TCCTGTCC    CAT CC
                                  CT       C___   C
GAM1291  FLJ22679  3'  TGAGGAAGGACAGGGGTAGGG  33217     AT      AAAA   A
                                TGAG  AGGACAGG    GTA GG
                                ||||  ||||||||    ||| ||
                                ACTC  TCCTGTCC    CAT CC
                                  CT       C___   C
GAM1291  KIAA0522  3'  AGACCTCCAGGGAAAAGTGGGG 33218     AGGA   _     AA
                                AGAT    CAGG AAAAGT  GG
                                ||||    |||| ||||||  ||
                                TCTG    GTCC TTTTCA  CC
                                  GAG_    C     CC
GAM1291  KIAA1958  3'  GATAGACAGAAAGTAGGG    33219      G     AA    A
                                GATAG ACAGGA  AGTA GG
                                ||||| ||||||  |||| ||
                                CTATC TGTCTT  TCAT CC
                                  _     __    C
GAM1291  NSG-X    5'  TGAGCAAATGGGAAAAGTAAGG 33220      A    ACA
                                TGAG TAGG   GGAAAAGTAAGG
                                |||| ||||   ||||||||||||
                                ACTC GTTT   CCTTTTCATTCC
                                  _    AC_
GAM1291  SEMA4G   3'  TGAGGTAGGACAGGGGTAG    33221     A       AAAA   A
                                TGAG TAGGACAGG    GTA G
                                |||| |||||||||    ||| |
                                ACTC ATCCTGTCC    CAT C
                                  C        C___   _
GAM1291  SEMA4G   3'  TGAGGTAGGACAGGGGTAG    33221     A       AAAA   A
                                TGAG TAGGACAGG    GTA G
                                |||| |||||||||    ||| |
                                ACTC ATCCTGTCC    CAT C
                                  C        C___   _
GAM1291  SSH-3    3'  TGGGAGAGGACAGGAGGTGCAG 33222    A  T       AAA   A
            GG                    TG GA AGGACAGGA   GTA GG
                                || || |||||||||   ||| ||
                                AC CT TCCTGTCCT   CGT CC
                                 C  C        CCA   C
GAM1291  SSH-3    3'  TGGGAGAGGACAGGAGGTGCAG 33222    A  T       AAA   A
            GG                    TG GA AGGACAGGA   GTA GG
                                || || |||||||||   ||| ||
                                AC CT TCCTGTCCT   CGT CC
                                 C  C        CCA   C
GAM1291  TNFSF13  3'  GAAAAGGGAAAAGTGAG     33223     T   ACA       A
                                GA AGG   GGAAAAGT AG
                                || |||   |||||||| ||
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                                CT TTC   CCTTTTCA TC
                                 T  ___       C
GAM1291  LOC144667 3'  GAGGGGCCCCAGGAAAAGTGAG 33224     ATAGGA        A
                  G                GAG      CAGGAAAAGT AGG
                                   |||      |||||||||| |||
                                   CTC      GTCCTTTTCA TCC
                                     CCCGGG         C
GAM1291  LOC256306 5'  GACCGGACAGGAGGGGTGAGG  33225     A       AAA  A
                                   GAT GGACAGGA   GT AGG
                                   ||| ||||||||   || |||
                                   CTG CCTGTCCT   CA TCC
                                     G       CCC  C
GAM1291  LOC257203 3'  TGAATTCGGAGGAAAAGTAGGG 33226      ATA   CA       A
                                   TGAG   GGA  GGAAAAGTA GG
                                   ||||   |||  |||||||||  ||
                                   ACTT   CCT  CCTTTTCAT CC
                                     AAG   __        C
GAM1291  LOC90573  3'  AGATGGGAGAGGGTAAG     33227      A   C   AAAA
                                   AGAT GGA AGG    GTAAG
                                   |||| ||| |||    |||||
                                   TCTA CCT TCC    CATTC
                                     C   C   _____
GAM1291  LOC93259  5'  GAGGGCCCCAGGAAAAGTGAGG 33228     ATAGGA        A
                                   GAG      CAGGAAAAGT AGG
                                   |||      |||||||||| |||
                                   CTC      GTCCTTTTCA TCC
                                     CCGGG_         C
GAM1292  BCDO     5'  GCCGTTTCTGCCTTTGCTT    33231        ACTC   GTC
                                   GCCGTTTT    GCC   GCTT
                                   ||||||||    |||   ||||
                                   CGGCAAAG    CGG   CGAA
                                        A___    AAA
GAM1292  CNOT7    5'  CACCGTGCTGCGCCGTCGCTT  33232       TTTA  _
                                   CGCCGT    CT CGCCGTCGCTT
                                   ||||||    || ||||||||||
                                   GTGGCA    GA GCGGCAGCGAA
                                      C___  C
GAM1292  DAMS     3'  CCGTGCCGCCGTCGCT      33233      TTTAC
                                   CCGT     TCGCCGTCGCT
                                   ||||     ||||||||||
                                   GGCA     GGCGGCAGCGA
                                     C_____
GAM1292  FLJ14827  3'  ACGCCGTTTATTCGCACT    33234         TAC    CGTC
                                   ACGCCGTTT   TCGC    GCT
                                   |||||||||   ||||    |||
                                   TGCGGCAAA   AGCG    TGA
                                        TA_    _____
GAM1292  LOC254876 5'  GCGACACTCGCCGTCGCTT    33235     TT
                                   GT  TACTCGCCGTCGCTT
                                   ||  ||||||||||||||
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                                CG  GTGAGCGGCAGCGAA
                                 CT
GAM1293  EPHB6    5'  TCACAATGAAGACAAACAG   33238            TTT
                                TCATAATGAAGACA   TAG
                                |||||||||||||   |||
                                AGTGTTACTTCTGT   GTC
                                       TT_
GAM1293  GAS7     3'  TATTATAATAAAGAATCCCAGA 33239     C        C
           G                    TAT ATAATGAAGA ATTTTAGAG
                                ||| |||||||||| |||||||||
                                ATA TATTATTTCT TAGGGTCTC
                                  A        _
GAM1293  PUM2     3'  CATTGCCAGAGACATTTTAG   33240     AA_ GA
                                CAT   T  AGACATTTTAG
                                |||   |  ||||||||||
                                GTA   G  TCTGTAAAATC
                                  ACG TC
GAM1293  GGH      3'  CATAATGAAGAATCAGA     33241           CATT
                                CATAATGAAGA    TTAGA
                                ||||||||||    |||||
                                GTATTACTTCT    AGTCT
                                       T___
GAM1293  KIAA0620  3'  TATTATAAAGAAGATTCCAGAG 33242     C    T    CA
                                TAT ATAA GAAGA  TTTTAGAG
                                ||| |||| |||||  ||||||||
                                ATA TATT CTTCT  AAGGTCTC
                                  A   T    __
GAM1293  LOC142927 3'  TATTATAAAGAAGACATCCATG 33243     C    T        TA
           AG                     TAT ATAA GAAGACATTT  GAG
                                ||| |||| ||||||||||  |||
                                ATA TATT CTTCTGTAGG  CTC
                                  A   T        TA
GAM1293  LOC221302 3'  TAACACAGGCATTTTAGAG   33244       A  A
                                TAATG AG CATTTTAGAG
                                ||||| || ||||||||||
                                ATTGT TC GTAAAATCTC
                                   G  C
GAM1294  PFN2     3'  GTTGGGATACCTAATGTC    33247           CGTC
                                GTTGGGATGCT    GATGTC
                                ||||||||||    ||||||
                                CAACCCTATGG    TTACAG
                                       A___
GAM1294  PFN2     3'  GTTGGGATACCTAATGTC    33247           CGTC
                                GTTGGGATGCT    GATGTC
                                ||||||||||    ||||||
                                CAACCCTATGG    TTACAG
                                       A___
GAM1294  PLS1     3'  TTGGGATGTTCTAGCCAATGT  33248         C  __
                                TTGGGATG TC  GTCGATGT
                                |||||||| ||  ||||||||
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                                AACCCTAC AG  CGGTTACA
                                    A  AT
GAM1294  C1orf24   3'  GTTGAGATCTGATGT      33249        G  CGTC
                                GTTGGGAT CT   GATGT
                                |||||||| ||   |||||
                                CAACTCTA GA   CTACA
                                   _  ____
GAM1294  KIAA0620  3'  GTGGTCTGTCTTGTCGATGTC  33250    T  GA  _  C
                                GT GG  TG CT GTCGATGTC
                                || ||  || || |||||||||
                                CA CC  AC GA CAGCTACAG
                                 _  AG  A  A
GAM1295  IL8RA     3'  TGGAAAGCATTTGGGGAGGGAC 33253     TTT  ____
                                TGGA   CA    GGGAGGGAC
                                ||||   ||    |||||||||
                                ACCT   GT    CCCTCCCTG
                                  TTC  AAAC
GAM1295  PYCR1     3'  AATGGAGGGCAGGGAGGGGCCG 33254       TTT       A
                                AATGGA   CAGGGAGGG CCG
                                ||||||   ||||||||| |||
                                TTACCT   GTCCCTCCC GGC
                                   CCC        C
GAM1295  GCN2      5'  TAAATTGATTTCAGGGGG    33255      G        A
                                TAAAT GATTTCAGGG GG
                                ||||| |||||||||| ||
                                ATTTA CTAAAGTCCC CC
                                  A        _
GAM1295  MGC10200  3'  TAAATGCATTTCAGGTAAG   33256       G       G
                                TAAATG ATTTCAGG AGG
                                |||||| |||||||| |||
                                ATTTAC TAAAGTCC TTC
                                   G       A
GAM1295  MGC2817   3'  AAATGGATTTCAGGAACCA   33257           GAGG
                                AAATGGATTTCAGG   GACCG
                                ||||||||||||||   |||||
                                TTTACCTAAAGTCC   TTGGT
                                          ____
GAM1295  P2RXL1    3'  TGGGAGTCAGGGGAGGGAC   33258     ATT     _
                                TGG   TCAGGG AGGGAC
                                |||   |||||| ||||||
                                ACC   AGTCCC TCCCTG
                                  CTC     C
GAM1295  LOC146853 3'  AATGGTTTCAGGGAAAG     33259      A
                                AATGG TTTCAGGGAGGG
                                ||||| ||||||||||||
                                TTACC AAAGTCCCTTTC
                                   _
GAM1296  ARNT2     3'  TATGTCCCACGGCACAG     33262         ATCA  TCT
                                TATGTCCCAC   GGT   CAG
                                ||||||||||   |||  |||
```

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                                ATACAGGGTG   CCG  GTC
                                     _____  T__
GAM1296 DIAPH2   3' TGTTTCACTGGTTCTCAGA   33263    CC  ATCA
                                TGT  CAC   GGTTCTCAGA
                                |||  |||   ||||||||||
                                ACA  GTG   CCAAGAGTCT
                                  AA   A___
GAM1296 FOXE1    3' GTCTCAAGTTCTCAG      33264    CCACA
                                GTC    TCAGGTTCTCAG
                                |||    ||||||||||||
                                CAG    AGTTCAAGAGTC
                                 ______
GAM1296 HIP12    3' TATGTCTCACCTCACTCCCCAG 33265      C  A  GG
            A                    TATGTC CAC TCA  TTCTCAGA
                                |||||| ||| |||  ||||||||
                                ATACAG GTG AGT  AGGGGTCT
                                   A  G  G_
GAM1296 RAI3     3' TGTCTTGTACAGTTTTCTCAGA 33266     CCACAT  G_
                                TGTC     CAG  TTCTCAGA
                                ||||     |||  ||||||||
                                ACAG     GTC  AAGAGTCT
                                  AACAT_   AA
GAM1296 DKFZp434H2226 3' GTCCCACAAACTTTTTCAGA   33267        TCAGG  C
                                GTCCCACA     TT TCAGA
                                ||||||||     || |||||
                                CAGGGTGT     AA AGTCT
                                     TTGA_  A
GAM1296 DOC2B    3' TGTCTCATTCACCCCCAG    33268     C  CA   GG
                                TGTC CA  TCA  TTCTCAG
                                |||| ||  |||  |||||||
                                ACAG GT  AGT  GGGGGTC
                                  A  A_  ___
GAM1296 FLJ20758 3' TATATCTCAGTTCTCA      33269       CCACA   G
                                TATGTC    TCAG TTCTCA
                                ||||||    |||| ||||||
                                ATATAG    AGTC AAGAGT
                                  ______   _
GAM1296 FLJ23590 3' TATGTCTCCCATTTCATCCTCA 33270       _  A  CAG
            GA                    TATGTC CC CAT   GTTCTCAGA
                                |||||| || |||   |||||||||
                                ATACAG GG GTA   TAGGAGTCT
                                   A  _   AAG
GAM1296 FLJ30567 3' TATGTCCCACAGTCAGACT   33271          _   GT
                                TATGTCCCACA TCAG  T
                                |||||||||||| ||||  |
                                ATACAGGGTGT AGTC  A
                                      C   TG
GAM1296 KIAA1377 3' TGTCTTTCATGGTATTCTCAGA 33272     CCA   CAG
                                TGTC   CAT   GTTCTCAGA
                                ||||   |||   |||||||||
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                                ACAG  GTA  TAAGAGTCT
                                  AAA  CCA
GAM1296 KIAA1673 3' TATGTCCCATGCTAAATTC  33273       CATC
                                TATGTCCCA   AGGTTC
                                |||||||||   ||||||
                                ATACAGGGT   TTTAAG
                                     ACGA
GAM1296 LHX6    3' TGTCTGACCTCTGTTCTCAG  33274    CC  A  AG
                                TGTC  AC TC  GTTCTCAG
                                ||||  || ||  ||||||||
                                ACAG  TG AG  CAAGAGTC
                                  AC  G  A_
GAM1296 PRSC    3' TGTCTTTTATCAGTTCTCAGA 33275    CCAC    G
                                TGTC   ATCAG TTCTCAGA
                                ||||   ||||| ||||||||
                                ACAG   TAGTC AAGAGTCT
                                  AAAA   _
GAM1296 SDS3    3' TATATTTTACATTCACCTCTCA 33276     CCC   _ GG
            GA                    TATGT   ACAT CA  TTCTCAGA
                                |||||   |||| ||  ||||||||
                                ATATA   TGTA GT  GAGAGTCT
                                  AAA   A  G_
GAM1296 STRN    3' TGTTTTAACCAGATTTCTCAG  33277    CCCAC      _
                                TGT    ATCAGGTT CTCAG
                                |||    |||||||| |||||
                                ACA    TGGTCTAA GAGTC
                                 AAAT_      A
GAM1296 LOC147353 3' TATGTATCATATCAGGTT   33278     CC  C
                                TATGT  CA ATCAGGTT
                                |||||  || ||||||||
                                ATACA  GT TAGTCCAA
                                   TA  A
GAM1296 LOC151457 5' TATGTCCCAAAGGTTTCAG  33279       CATC    C
                                TATGTCCCA   AGGTT TCAG
                                |||||||||   ||||| ||||
                                ATACAGGGT   TCCAA AGTC
                                     T___   _
GAM1296 LOC51308  3' TGTCTCCCATGTCATCCTCAGA 33280    _ A  CAG
                                TGTC CC CAT   GTTCTCAGA
                                |||| || |||   |||||||||
                                ACAG GG GTA   TAGGAGTCT
                                  A  _  CAG
GAM1297 ADM     5' TGGCAAGGCTTGAGCTGTTCTA 33283       GCCCATTG
                                TGGCAAGGC      GTTCTA
                                |||||||||      ||||||
                                ACCGTTCCG      CAAGAT
                                     AACTCGA_
GAM1297 FUT9    3' TGGTAGGTTTATTTGGTTCTA  33284    CA  CGCCCA
                                TGG  AGG    TTGGTTCTA
                                |||  |||    |||||||||
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                                ACC  TCC     AACCAAGAT
                                  A_   AAATA_
GAM1297 LYL1     5' TGGTGAGTGCCCTGGCTCT   33285    CA  GC    AT
                                TGG  AG  GCCC  TGGTTCT
                                |||  ||  ||||  |||||||
                                ACC  TC  CGGG  ACCGAGA
                                  AC  A_   __
GAM1297 ARGBP2   3' TGGCAGGCGCCCTCT      33286      A      ATTGGT
                                TGGCA GGCGCCC     TCT
                                |||||| |||||||     |||
                                ACCGT CCGCGGG     AGA
                                   _     _______
GAM1297 DKFZP434B0335 5' TGGTGGGGCACTCGGCTCC   33287     CAA    CCA
                                TGG   GGCGC   TTGGTTCT
                                |||   |||||   ||||||||
                                ACC   CCGTG   AGCCGAGG
                                  ACC    ___
GAM1297 DKFZp762L0311 3' TGGTGAGGTGGCTGGTTCT   33288     CA   C_  CCAT
                                TGG  AGG  GC   TGGTTCT
                                |||  |||  ||   |||||||
                                ACC  TCC  CG   ACCAAGA
                                  AC   AC  _____
GAM1297 FLJ10997  3' TGGCAAGGTGTTGTGTTCT   33289        CGCCCA  _
                                TGGCAAGG     TTG GTTCT
                                ||||||||     ||| |||||
                                ACCGTTCC     AAC CAAGA
                                     AC_____  A
GAM1297 GDAP2    3' TGGTTAGCATACATTGGTTCT  33290     CAA   CC
                                TGG   GGCG  CATTGGTTCT
                                |||   ||||  ||||||||||
                                ACC   TCGT  GTAACCAAGA
                                  AA_   AT
GAM1297 IRO039700 5' TGGCAAGGGCCTGGGCT     33291        C   CATT
                                TGGCAAGG GCC    GGTT
                                |||||||| |||    ||||
                                ACCGTTCC CGG    CCGA
                                     _   AC__
GAM1297 KIAA0143  3' TAGCAAGGTGCCTATCCCAGCT 33292        C   CA__ TG
                                TGGCAAGG GCC    T  GTT
                                |||||||| |||    |  |||
                                ATCGTTCC CGG    G  CGA
                                     A   ATAG GT
GAM1297 KIAA0323  3' TGGCAAGGGCCTGAGGCC    33293        C   CATT
                                TGGCAAGG GCC    GGTT
                                |||||||| |||    ||||
                                ACCGTTCC CGG    CCGG
                                     _   ACT_
GAM1297 OLIG1    3'  GGCAAGGCGCCCTAAGTTCTAC 33294           ATT
                                GGCAAGGCGCCC   GGTTCTAC
                                ||||||||||||   ||||||||
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                                CCGTTCCGCGGG  TCAAGATG
                                      AT_
GAM1297  TU12B1-TY 3'  TGGCAAGGAGCCCATGG    33295       C    T
                                TGGCAAGG GCCCAT GG
                                |||||||| |||||| ||
                                ACCGTTCC CGGGTA CC
                                    T    _
GAM1297  LOC124783 3'  TGGAGGCTTTATTGGTTCT   33296    CA   GCCC
                                TGG  AGGC   ATTGGTTCT
                                |||  ||||   |||||||||
                                ACC  TCCG   TAACCAAGA
                                  __   AAA_
GAM1297  LOC126133 5'  TGGCAAGGCACTGAATTTCT  33297         CCATTGG
                                TGGCAAGGCGC     TTCT
                                ||||||||||      ||||
                                ACCGTTCCGTG     AAGA
                                      ACTTA__
GAM1297  LOC203871 3'  TGGAGGGGCTGGTTCT    33298    CA  C  CCAT
                                TGG  AGG GC   TGGTTCT
                                |||  ||| ||   |||||||
                                ACC  TCC CG   ACCAAGA
                                  __  C  ____
GAM1297  LOC219654 3'  TGGCAAGGGTGTCCACAGCC  33299       CGC_   T
                                TGGCAAGG   CCAT GGTT
                                ||||||||   |||| ||||
                                ACCGTTCC   GGTG TCGG
                                    CACA   _
GAM1298  ABCA4   3'  AGGCCAAAGCTGCTAGTGGG  33302      CT       A
                                GGGCTG  GGGCTGCTAGT GG
                                ||||||  |||||||||| ||
                                TCCGGT  TTCGACGATCA CC
                                  __        C
GAM1298  CACNB1   3'  CAGGGTTGCTGGGCTACAG   33303      C        T
                                TAGGG TGCTGGGCTGC AG
                                ||||| |||||||||| ||
                                GTCCC ACGACCCGATG TC
                                  A        _
GAM1298  CAPN10   3'  GGGCTGCTGGACAGTGGG    33304         TGCT   A
                                GGGCTGCTGGGC   AGT GG
                                ||||||||||   ||| ||
                                CCCGACGACCTG   TCA CC
                                      ____  C
GAM1298  PCTK3    3'  TAGGGCTGATGGAAAGAGTGGG 33305       C   CTGCT   A
                                TAGGGCTG TGGG    AGT GG
                                |||||||| ||||    ||| ||
                                ATCCCGAC ACCT    TCA CC
                                    T   TTC__   C
GAM1298  TEM6     5'  GGGCTGTCGGGCTAGTCGG   33306      C    GCT   A
                                GGGCTG TGGGCT   AGT GG
                                |||||| ||||||   ||| ||
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                                CCCGAC GCCCGA   TCA CC
                                   A     ___  G
GAM1298 FASTK    3' GGGCTCTGGGCTGCAG     33307      G       T
                                GGGCT CTGGGCTGC AG
                                ||||| ||||||||| ||
                                CCCGA GACCCGACG TC
                                  _       _
GAM1298 FLJ12150 3' TAGGGCTAGCAGCTGGTG    33308       _ TG    CTA  A
                                TAGGGCT GC  GGCTG   GT G
                                ||||||| ||  |||||   || |
                                ATCCCGA CG  TCGAC   CA C
                                   T __    ___  C
GAM1298 FLJ12505 5' GGGCTGCTGGGGCTTGCTGG  33309          CT   A  A
                                GGGCTGCTGGG  GCT GT GG
                                ||||||||||  ||| || ||
                                CCCGACGACCC  CGA CG CC
                                      __   A  A
GAM1298 FLJ13693 3' AGGCTGCTGGGTCCCCTGTGGG 33310          _  G  A  A
                                GGGCTGCTGGG CT CT GT GG
                                |||||||||| || || || ||
                                TCCGACGACCC GG GA CA CC
                                      A  G  _  C
GAM1298 FYCO1    3' GGCTGCTGGTGTGTGGTGGG   33311         GC  CTA  A
                                GGCTGCTGG  TG   GT GG
                                |||||||||  ||   || ||
                                CCGACGACC  AC   CA CC
                                     AC  AC_  C
GAM1298 ILF3     3' TAGGACTGCTGCTGGCCCTGGT 33312          __   G  A  A
           GGG                    TAGGGCTGCTG  GGCT CT GT GG
                                ||||||||||  |||| || || ||
                                ATCCTGACGAC  CCGG GA CA CC
                                      GA   _  C  C
GAM1298 KIAA0481 3' TAGGGCTGCTTGGGGATAGTGG 33313         _  CTGC   A
           G                     TAGGGCTGCT GGG   TAGT GG
                                |||||||||| |||   |||| ||
                                ATCCCGACGA CCC   ATCA CC
                                      A  CT__   C
GAM1298 KIAA1243 3' AGGCTTGTTGGGTGTGTTAGG  33314      GC_   C  CTAG
                                GGGCT   TGGG TG   TAGG
                                |||||   |||| ||   ||||
                                TCCGA   ACCC AC   ATCC
                                   ACA   _  ACA_
GAM1298 MGC15435 3' GGGCTGCTGGGTGTATAGG   33315         C  CTA
                                GGGCTGCTGGG TG   GTAGG
                                |||||||||| ||   |||||
                                CCCGACGACCC AC   TATCC
                                      _  A__
GAM1298 PPP1R16B 3' CAGGGCTGTTGGGCTGGCC   33316        C     _
                                TAGGGCTG TGGGCTG CT
                                |||||||| ||||||| ||
```

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                                GTCCCGAC ACCCGAC GG
                                    A      C
GAM1298  PRKWNK2   3'  AGCCGTGGGCTGCTGGTAGG  33317      C       A
                                GGCTG TGGGCTGCT GTAGG
                                ||||| ||||||||| |||||
                                TCGGC ACCCGACGA CATCC
                                  _       C
GAM1298  UBCE7IP5  3'  GGGTGTCAAGCTGCTGGTGGG 33318    C  CT      A  A
                                GGG TG  GGGCTGCT GT GG
                                ||| ||  |||||||| || ||
                                CCC AC  TTCGACGA CA CC
                                  _ AG       C  C
GAM1298  LOC123242 3'  GGGCTACTGGGCCCTCTAG   33319          G_
                                GGGCTGCTGGGCT  CTAG
                                ||||||||||||  ||||
                                CCCGATGACCCGG  GATC
                                       GA
GAM1298  LOC150685 5'  GGGCTGCTGCTGTGGTGGG   33320       GG   CTA  A
                                GGGCTGCT  GCTG   GT GG
                                ||||||||  ||||   || ||
                                CCCGACGA  CGAC   CA CC
                                    __    AC_  C
GAM1298  LOC152048 5'  GGGTCAGGCTGCTGGTAG    33321    CTGC       A
                                GGG    TGGGCTGCT GTAG
                                |||    ||||||||| ||||
                                CCC    GTCCGACGA CATC
                                  A___        C
GAM1298  LOC152282 3'  GGGCTGCTGGAGCTGCTA    33322         _
                                GGGCTGCTGG GCTGCTA
                                |||||||||| |||||||
                                CCCGACGACC CGACGAT
                                      T
GAM1298  LOC152282 3'  GGGCTGCTGGAGCTGCTA    33322         _
                                GGGCTGCTGG GCTGCTA
                                |||||||||| |||||||
                                CCCGACGACC CGACGAT
                                      T
GAM1298  LOC152457 3'  GGGCTGCTTGCTCGGTAGG   33323       GG   GCTA
                                GGGCTGCT  GCT    GTAGG
                                ||||||||  |||    |||||
                                CCCGACGA  CGA    CATCC
                                    A_   GC__
GAM1298  LOC219700 5'  TAGAGGCTGCTGGGCTGAG   33324    _         CTAGT
                                TAG GGCTGCTGGGCTG    AG
                                ||| ||||||||||||    ||
                                ATC CCGACGACCCGAC    TC
                                  T          _____
GAM1298  LOC253001 3'  GGGCTACTGGGCCCTCTAG   33319          G_
                                GGGCTGCTGGGCT  CTAG
                                ||||||||||||  ||||
```

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                                CCCGATGACCCGG  GATC
                                       GA
GAM1298 LOC93589 3' TAGGGCTATTTGCTGGTAG   33325       CTGG   CTA
                                TAGGGCTG   GCTG  GTAG
                                ||||||||   ||||  ||||
                                ATCCCGAT   CGAC  CATC
                                    AAA_   ___
GAM1299 BIN3    3' TGGCATGCTGGGCTGCC    33328     T   AGTA
                                TGGC TGCT   GGGCTGCT
                                |||| ||||   ||||||||
                                ACCG ACGA   CCCGACGG
                                  T   _____
GAM1299 BLAME   3' TGGCTGCCCAGGCTGC     33329     T  AGTA
                                TGGCT GCT   GGGCTGC
                                ||||| |||   |||||||
                                ACCGA CGG   TCCGACG
                                  _  G___
GAM1299 CA7     3' GCTCGGGGTGGGGCTGCT   33330     CTA  A
                                GCTTG  GT GGGCTGCT
                                |||||  || ||||||||
                                CGAGC  CA CCCGACGA
                                   CC_  C
GAM1299 CDK10   3' GGTTGTTGTAGGGCTGCT   33331   C  CTA
                                GG TTG  GTAGGGCTGCT
                                || |||  ||||||||||
                                CC AAC  CATCCCGACGA
                                 _  AA_
GAM1299 CKMT2   5' TGGCCTGCTGGCTATGCT   33332       AGTAG  __
                                TGGCTTGCT   GGCT  GCT
                                |||||||||   ||||  |||
                                ACCGGACGA   CCGA  CGA
                                     _____   TA
GAM1299 COL4A2  5' CGGCTTCAGGGCTGC      33333     GCTAG
                                TGGCTT   TAGGGCTGC
                                ||||||   |||||||||
                                GCCGAA   GTCCCGACG
                                     _____
GAM1299 KIR3DL2 3' TGGTTTTGAGACAGGGCTG  33334   C  GCT  _
                                TGG TT  AG TAGGGCTG
                                ||| ||  || ||||||||
                                ACC AA  TC GTCCCGAC
                                  A  AC_  T
GAM1299 LZTS1   3' TGGCTGTCCAGAGGCTGCT  33335     TG   TA
                                TGGCT  CTAG  GGGCTGCT
                                |||||  ||||  ||||||||
                                ACCGA  GGTC  TCCGACGA
                                   CA   __
GAM1299 MSN     3' TGGCATGACTCCAGGGCTGCT 33336    T  _  AG
                                TGGC TG CT  TAGGGCTGCT
                                |||| || ||  ||||||||||
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                                ACCG AC GA  GTCCCGACGA
                                  T  T  G_
GAM1299 MTNR1B   3'  TGGCGTTGATGGGCTGCT    33337     _  CTA  A
                                TGGC TTG   GT GGGCTGCT
                                |||| |||   || ||||||||
                                ACCG AAC   TA CCCGACGA
                                  C  ___  _
GAM1299 NSEP1    5'  GGCGGCGGTGGGGCTGCT    33338    TT  TA  A
                                GGC  GC  GT GGGCTGCT
                                |||  ||  || ||||||||
                                CCG  CG  CA CCCGACGA
                                 C_  C_  C
GAM1299 PCDH12   3'  GCTTACAAGGGGCTGCT     33339      T  TA
                                GCTTGC AG  GGGCTGCT
                                ||||||  ||  ||||||||
                                CGAATG TC  CCCGACGA
                                   T  __
GAM1299 PGLS     3'  AGCCCCGGGTAGGGCTGCT   33340     GCTA
                                GGCTT   GTAGGGCTGCT
                                |||||   ||||||||||||
                                TCGGG   CATCCCGACGA
                                  GCC_
GAM1299 RENT1    3'  TGGGTTTGTCAAGGCTGCT   33341    C  GCTAG
                                TGG TT    TAGGGCTGCT
                                ||| ||    ||||||||||
                                ACC AA    GTTCCGACGA
                                 C  ACA__
GAM1299 SLC10A2  3'  GCTTGCTGCAGCTGC      33342       A  AG
                                GCTTGCT GT  GGCTGC
                                |||||||  ||  ||||||
                                CGAACGA CG  TCGACG
                                    _  __
GAM1299 SURF4    3'  TGGCTTGCAGGGTGCTGCT   33343       T  TA  _
                                TGGCTTGC AG  GG GCTGCT
                                ||||||||  ||  ||  ||||||
                                ACCGAACG TC  CC CGACGA
                                    _  __  A
GAM1299 TLL2     5'  TGGTTACACAGGGCTGCT    33344    C   TAG
                                TGG TTGC   TAGGGCTGCT
                                |||  ||||   ||||||||||
                                ACC AATG   GTCCCGACGA
                                  _   T__
GAM1299 UC28     3'  TGGCTTACTAATTGC       33345          AGGGC
                                TGGCTTGCTAGT    TGC
                                ||||||||||||    |||
                                ACCGAATGATTA    ACG
                                      _____
GAM1299 VENTX2   3'  TGTTTTGTCCCGAGGCTGCT  33346    GC  _  AGTA
                                TG  TTG CT    GGGCTGCT
                                ||  |||  ||   ||||||||
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                                AC  AAC GG    TCCGACGA
                                 AA   A  GC__
GAM1299  WARS     3'  GGCTCCACTGTGGGGCTGCT   33347     _ TG  A  A
                                GGC T  CT GT GGGCTGCT
                                ||| |  || || ||||||||
                                CCG G  GA CA CCCGACGA
                                  A GT  _  C
GAM1299  B3GNT7   3'  TGGCTTGCTCATACTGCT    33348         AGTAGG
                                TGGCTTGCT     GCTGCT
                                |||||||||     ||||||
                                ACCGAACGA     TGACGA
                                     GTA___
GAM1299  BIVM     5'  TAGCTTGCCCAGGCTG      33349          AGTA
                                TGGCTTGCT    GGGCTG
                                |||||||||    ||||||
                                ATCGAACGG    TCCGAC
                                     G___
GAM1299  C1orf29  3'  TGGTTTGCAGTAGGACC     33350     C    T
                                TGG TTGC AGTAGGGCT
                                ||| |||| |||||||||
                                ACC AACG TCATCCTGG
                                  A   _
GAM1299  C20orf54 3'  GGCTTGCTTGATGCGGGCTGCT 33351         AGTA__
                                GGCTTGCT     GGGCTGCT
                                ||||||||     ||||||||
                                CCGAACGA     CCCGACGA
                                     ACTACG
GAM1299  CCNE2    5'  TGGCTGGGCTGGGGCTGCT    33352      T_  AGTA
                                TGGCT  GCT    GGGCTGCT
                                |||||  |||    ||||||||
                                ACCGA  CGA    CCCGACGA
                                   CC   C___
GAM1299  CGI-142  3'  TGGTTTCCCATAGGGCTG     33353     C  G   G
                                TGG TT CTA TAGGGCTG
                                ||| || ||| ||||||||
                                ACC AA GGT ATCCCGAC
                                  A  G   _
GAM1299  DKFZp434M0331 3'  TGGCTTGTCAGTAGCCCCAAGC 33354         C     GG  __
            T                    TGGCTTG TAGTAG  CT  GCT
                                |||||||  ||||||  ||  |||
                                ACCGAAC GTCATC  GG  CGA
                                     A     GG  TT
GAM1299  DKFZP434P211 5'  TGGCTTGCTGTGGTACC     33355          A  A  _
                                TGGCTTGCT GT GG GCT
                                ||||||||| || || |||
                                ACCGAACGA CA CC TGG
                                     _  _  A
GAM1299  DKFZp761D0614 3'  TGGCTTGCTTGTGTGGACT    33356          A  A_
                                TGGCTTGCT GT  GGGCT
                                ||||||||| ||  |||||
```

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                                ACCGAACGA CA  CCTGA
                                     A  CA
GAM1299  FLJ10157  5'  TGGTTGGTTCAGGGGGCTGCT  33357    C   C__   TA
                                TGG TTG   TAG  GGGCTGCT
                                ||| |||   |||  ||||||||
                                ACC AAC   GTC  CCCGACGA
                                  _   CAA   C_
GAM1299  FLJ10597  3'  TGGGGGCAGGTGGGGCTGCT   33358    CTT  TA  A
                                TGG   GC  GT GGGCTGCT
                                |||   ||  || ||||||||
                                ACC   CG  CA CCCGACGA
                                  CC_  TC  C
GAM1299  FLJ10997  3'  TGATTTGCTAGTAGAAACT   33359    GC         _
                                TG  TTGCTAGTAGGG CT
                                ||  ||||||||||||  ||
                                AC  AACGATCATCTT GA
                                 TA          T
GAM1299  FLJ13397  3'  TGGCTTACAGGGCTG      33360        TAGT
                                TGGCTTGC    AGGGCTG
                                ||||||||    |||||||
                                ACCGAATG    TCCCGAC
                                      _____
GAM1299  FLJ13693  3'  TGGGCTGTGGGGCTGC     33361     CTT   A  A
                                TGG   GCT GT GGGCTGC
                                |||   ||| || |||||||
                                ACC   CGA CA CCCGACG
                                  ___   _  C
GAM1299  FLJ20225  3'  TGGCTTGCAAGTCCCGCT    33362        T   AGGG
                                TGGCTTGC AGT    CTGCT
                                |||||||| |||    |||||
                                ACCGAACG TCA    GGCGA
                                     T   G___
GAM1299  FLJ25193  3'  GGCTTCTCTGGGGTGGGGCTGC 33363      G_  A__  A
            T                    GGCTT  CT   GT GGGCTGCT
                                |||||  ||   || ||||||||
                                CCGAA  GA   CA CCCGACGA
                                   GA  CCC  C
GAM1299  FLJ32884  5'  TGACTTGCTGTCCTCCTGCT   33364        A  AGGG
                                TGGCTTGCT GT    CTGCT
                                |||||||| ||    |||||
                                ACTGAACGA CA    GACGA
                                     _  GGAG
GAM1299  HS6ST     3'  TGGCTTTTGGTAGGGCCA    33365      GCTA
                                TGGCTT    GTAGGGCTG
                                ||||||    |||||||||
                                ACCGAA    CATCCCGGT
                                   AAC_
GAM1299  HSU24186  3'  TAGCTTGCTAGTAAATCC    33366            G
                                TGGCTTGCTAGTAGG CT
                                ||||||||||||||  ||
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                                ATCGAACGATCATTT GG
                                        A
GAM1299 INPP5E   3' TGGCTTGCGGTGGTCAGGCT  33367       TA__ A
                                TGGCTTGC   GT GGGCT
                                ||||||||   || |||||
                                ACCGAACG   CA TCCGA
                                     CCAC  G
GAM1299 KIAA0391 3' GCCTCCTGTAGGGCTGCT    33368     G  A
                                GCTT CT GTAGGGCTGCT
                                |||| || ||||||||||
                                CGGA GA CATCCCGACGA
                                  G  _
GAM1299 KIAA0542 3' GCTTGCCGTCGGGGGCTGCT  33369       A  A__
                                GCTTGCT GT   GGGCTGCT
                                ||||||| ||   ||||||||
                                CGAACGG CA   CCCGACGA
                                    _  GCC
GAM1299 KIAA0556 3' GGCACTGAGTGGGGCTGCT   33370     TT  _  A
                                GGC  GCT AGT GGGCTGCT
                                |||  ||| ||| ||||||||
                                CCG  TGA TCA CCCGACGA
                                  __   C  C
GAM1299 KIAA0574 3' TGGCTGCTAGTGGCCC      33371      T     A  G
                                TGGCT GCTAGT GG CT
                                ||||| |||||| || ||
                                ACCGA CGATCA CC GG
                                  _     _  G
GAM1299 KIAA0939 3' TGTCTTGAAGGGGCTGCT    33372    G   CT  TA
                                TG CTTG  AG  GGGCTGCT
                                || ||||  ||  ||||||||
                                AC GAAC  TC  CCCGACGA
                                 A   T_  __
GAM1299 KIAA1030 3' GCTATGCCTGGGGCTGCT    33373     _   AGTA
                                GCT TGCT   GGGCTGCT
                                ||| ||||   ||||||||
                                CGA ACGG   CCCGACGA
                                  T   AC__
GAM1299 KIAA1320 3' TGGGTTGCATTTAGGCTGCT  33374     C   TAGTA
                                TGG TTGC    GGGCTGCT
                                ||| ||||    ||||||||
                                ACC AACG    TCCGACGA
                                  C   TAAA_
GAM1299 KIAA1550 3' TGGCTTGCTGTGAAGTCT    33375       A  AG  _
                                TGGCTTGCT GT  GG CT
                                ||||||||| ||  || ||
                                ACCGAACGA CA  TC GA
                                      _  CT  A
GAM1299 KIAA1819 5' TGGGGGCGGTGGGGCTGCT   33376     CTT  TA  A
                                TGG   GC  GT GGGCTGCT
                                |||   ||  || ||||||||
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                                ACC   CG  CA CCCGACGA
                                  CC_  C_  C
GAM1299 KIAA1870 5' GGCTTCCGGGGGCTGCT     33377      G  AGTA
                                GGCTT CT    GGGCTGCT
                                ||||| ||    ||||||||
                                CCGAA GG    CCCGACGA
                                   _  CC__
GAM1299 MGC29643 5' TGGCTGCCGAGGCTGC      33378      T   AGTA
                                TGGCT GCT    GGGCTGC
                                ||||| |||    |||||||
                                ACCGA CGG    TCCGACG
                                   _  C___
GAM1299 MGC32104 3' TGGTTTACTAGTATTTTGCT   33379     C       GGGC
                                TGG TTGCTAGTA    TGCT
                                ||| |||||||||    ||||
                                ACC AATGATCAT    ACGA
                                  A        AAA_
GAM1299 PPP1R16A 5' GCTTGCCCACAGGGCTGCT    33380       AG
                                GCTTGCT  TAGGGCTGCT
                                |||||||  ||||||||||
                                CGAACGG  GTCCCGACGA
                                    GT
GAM1299 PRO0386  5' GGTTTGCTAATCCCTGCT     33381     C      AGGG
                                GG TTGCTAGT    CTGCT
                                || ||||||||    |||||
                                CC AACGATTA    GACGA
                                 A       GG__
GAM1299 RNF24    3' TGGCTCAAGGGCTGC       33382       CTAGT
                                TGGCTTG    AGGGCTGC
                                |||||||    ||||||||
                                ACCGAGT    TCCCGACG
                                    _____
GAM1299 SB52     3' TGGCTTGCTAGGTATAAAGCT  33383         ___
                                TGGCTTGCTAG   TAGGGCT
                                ||||||||||   |||||||
                                ACCGAACGATC   ATTTCGA
                                      CAT
GAM1299 SLC1A7   3' GGCTTGGCCCTGGGCTGCT    33384       _  AGTA
                                GGCTTG CT    GGGCTGCT
                                |||||| ||    ||||||||
                                CCGAAC GG    CCCGACGA
                                   C  GA__
GAM1299 SLC26A1  3' TGGCTTGCAGACGTCTGCT    33385        T  TAGGG
                                TGGCTTGC AG    CTGCT
                                |||||||| ||    |||||
                                ACCGAACG TC    GACGA
                                    _ TGCA_
GAM1299 SOX30    3' TGACTTGCTGGATGC       33386         AGTA   C
                                TGGCTTGCT    GGG TGC
                                |||||||||    ||| |||
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                                ACTGAACGA   CCT ACG
                                     ____  _
GAM1299  SRPK1    3'  TGGCTTGCTAGCAGAGCC    33387
                                TGGCTTGCTAGTAGGGCT
                                ||||||||||||||||||
                                ACCGAACGATCGTCTCGG

GAM1299  TIEG     5'  TGGCTGCTAGGCTGC      33388      T  AGTA
                                TGGCT GCT   GGGCTGC
                                ||||| |||   |||||||
                                ACCGA CGA   TCCGACG
                                  _  _____
GAM1299  TREX1    5'  TGGCCTGCTGGTGGCAC    33389       A  AG  T
                                TGGCTTGCT GT  GGC GC
                                |||||||| ||  ||| ||
                                ACCGGACGA CA  CCG TG
                                     C  __  _
GAM1299  TREX1    5'  TGGCCTGCTGGTGGCAC    33389       A  AG  T
                                TGGCTTGCT GT  GGC GC
                                |||||||| ||  ||| ||
                                ACCGGACGA CA  CCG TG
                                     C  __  _
GAM1299  TREX1    5'  TGGCCTGCTGGTGGCAC    33389       A  AG  T
                                TGGCTTGCT GT  GGC GC
                                |||||||| ||  ||| ||
                                ACCGGACGA CA  CCG TG
                                     C  __  _
GAM1299  TRIM38   3'  TGGCTTACTGCAGCTGCT   33390       A  AG
                                TGGCTTGCT GT  GGCTGCT
                                |||||||| ||  |||||||
                                ACCGAATGA CG  TCGACGA
                                     _  __
GAM1299  LOC115051 3'  TGGCTTTTAGTAGGGCCA   33391      GC
                                TGGCTT  TAGTAGGGCTG
                                ||||||  ||||||||||
                                ACCGAA  ATCATCCCGGT
                                   A_
GAM1299  LOC123855 3'  TGACTTCTGGGGCTGC     33392      G  AGTA
                                TGGCTT CT   GGGCTGC
                                ||||||  ||  |||||||
                                ACTGAA GA   CCCGACG
                                   _  C___
GAM1299  LOC125268 3'  TGGCTGTAATTGGGGTTGCT  33393      T C   A_  C
                                TGGCT G TAGT  GGG TGCT
                                ||||| | ||||  ||| ||||
                                ACCGA C ATTA  CCC ACGA
                                   _ _   AC  A
GAM1299  LOC143153 3'  TGGCCTGCTGGCTGC      33394       AGTAG
                                TGGCTTGCT   GGCTGC
                                |||||||||   ||||||
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                                ACCGGACGA    CCGACG
                                         _____
GAM1299  LOC143154 3'  TGGCCTGCTGGCTGC      33394        AGTAG
                                TGGCTTGCT    GGCTGC
                                |||||||||    ||||||
                                ACCGGACGA    CCGACG
                                         _____
GAM1299  LOC145216 3'  TGGCTTGCTGGGAGCAGAG   33395        ___
                                TGGCTTGCT   AGTAGGG
                                |||||||||   |||||||
                                ACCGAACGA   TCGTCTC
                                      CCC
GAM1299  LOC146346 5'  TGGTTTGCTAATGACT     33396    C      AG
                                TGG TTGCTAGT  GGCT
                                ||| ||||||||  ||||
                                ACC AACGATTA  CTGA
                                  A       __
GAM1299  LOC148166 5'  TGGTTTCTCCAAGGCTGCT   33397    C  G  AG
                                TGG TT CT  TAGGGCTGCT
                                ||| || ||  ||||||||||
                                ACC AA GA  GTTCCGACGA
                                  A  _  G_
GAM1299  LOC148223 3'  TGGCTGGGTCTCAGGGCTGCT  33398      TGCTAG
                                TGGCT     TAGGGCTGCT
                                |||||     |||||||||
                                ACCGA     GTCCCGACGA
                                   CCCAGA
GAM1299  LOC148426 3'  GGCTTGGCCGGGGGCTGCT   33399      _  AGTA
                                GGCTTG CT    GGGCTGCT
                                ||||||  ||   ||||||||
                                CCGAAC GG    CCCGACGA
                                   C  CC__
GAM1299  LOC149013 3'  CGGCTTAGTAAGGGCTGCT   33400      TGC    _
                                TGGCT   TAGTA GGGCTGCT
                                |||||   ||||| ||||||||
                                GCCGA   ATCAT CCCGACGA
                                   ____     T
GAM1299  LOC149670 3'  GGTCTTGGGTGGGGCTGCT   33401    _   CTA  A
                                GG CTTG   GT GGGCTGCT
                                ||  ||||   ||  ||||||||
                                CC GAAC   CA CCCGACGA
                                 A    C__  C
GAM1299  LOC149722 5'  TGGGTTGCTAGTAGCATGGCT  33402     C        ___
                                TGG TTGCTAGTAG   GGCT
                                ||| ||||||||||   ||||
                                ACC AACGATCATC   CCGA
                                  C         GTA
GAM1299  LOC150174 5'  TGGCTTGCTGTGGTACC     33355        A  A  _
                                TGGCTTGCT GT GG GCT
                                ||||||||| || || |||
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                                ACCGAACGA CA CC TGG
                                     _ _  A
GAM1299  LOC150213 5'  TGGCTTGCTGTGGTACC     33355         A  A  _
                                TGGCTTGCT GT GG GCT
                                ||||||||| || || |||
                                ACCGAACGA CA CC TGG
                                     _ _  A
GAM1299  LOC150343 5'  TGGCTTGCTAATGATGTCACTG 33403           A  ____
           CT                     TGGCTTGCTAGT GG    GCTGCT
                                ||||||||||||| ||    ||||||
                                ACCGAACGATTA CT    TGACGA
                                      _ ACAG
GAM1299  LOC152009 3'  TGGTGTGATCAGGGCTGCT   33404     CT  CTAG
                                TGG  TG    TAGGGCTGCT
                                |||  ||    ||||||||||
                                ACC  AC    GTCCCGACGA
                                  AC  TA__
GAM1299  LOC152286 5'  TGGCTTCTGGTGCCTGCT    33405       G  AGTA  _  _
                                TGGCTT CT    GG GC TGCT
                                |||||| ||    || || ||||
                                ACCGAA GA    CC CG ACGA
                                   _ _____ A  G
GAM1299  LOC161482 5'  TGGCTTGCTGCTTTTCTGCT   33406         A  AGGG
                                TGGCTTGCT GT    CTGCT
                                ||||||||| ||    |||||
                                ACCGAACGA CG    GACGA
                                     _ AAAA
GAM1299  LOC166983 5'  TGGCCTGCTCCAGGGCTGCT   33407         AG
                                TGGCTTGCT  TAGGGCTGCT
                                |||||||||  ||||||||||
                                ACCGGACGA  GTCCCGACGA
                                     G_
GAM1299  LOC168742 5'  GGCTTGCTGTCTTCTGCT    33408         A  AGGG
                                GGCTTGCT GT    CTGCT
                                |||||||| ||    |||||
                                CCGAACGA CA    GACGA
                                     _ GAA_
GAM1299  LOC170127 3'  TGGTTTCTTCCCAGGGCTGCT  33409     ___   G  AGT
                                TGG   CTT CT   AGGGCTGCT
                                |||   ||| ||   |||||||||
                                ACC   GAA GG   TCCCGACGA
                                  AAA   G  ___
GAM1299  LOC200081 3'  TGGCTTCAGCAATGGGCTGCT  33410       GC    __
                                TGGCTT  TAGTA  GGGCTGCT
                                ||||||  |||||  ||||||||
                                ACCGAA  GTCGT  CCCGACGA
                                   __    TA
GAM1299  LOC200940 5'  TGGCCTGCTGGATGC       33411         AGTA   C
                                TGGCTTGCT    GGG TGC
                                |||||||||    ||| |||
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                                ACCGGACGA   CCT ACG
                                     ____  _
GAM1299  LOC201771 5'  TGGTTGCTAGTGCAGATCT   33412    C      A_  _
                                TGG TTGCTAGT  GGG CT
                                ||| ||||||||  ||| ||
                                ACC AACGATCA  TCT GA
                                  _      CG   A
GAM1299  LOC219731 5'  TGGTTGCTTGAGCTGC     33413    C    AGTA
                                TGG TTGCT    GGGCTGC
                                ||| |||||    |||||||
                                ACC AACGA    CTCGACG
                                  _    A___
GAM1299  LOC220002 3'  TGGCTCCCAGGGCTGC     33414      G  AGT
                                TGGCTT CT   AGGGCTGC
                                |||||| ||   ||||||||
                                ACCGAG GG   TCCCGACG
                                   _ ____
GAM1299  LOC257319 3'  GCTTGTAATAGGCTGCT    33415     C     G
                                GCTTG TAGTAGG CTGCT
                                ||||| ||||||| |||||
                                CGAAC ATTATCC GACGA
                                   _     _
GAM1299  LOC93613  5'  TGGCTTGCTAGGTGGAAGCT  33416         TA  CT
                                TGGCTTGCTAG  GGG  GCT
                                ||||||||||  |||  |||
                                ACCGAACGATC  CCT  CGA
                                      CA   T_
GAM1300  BF      5'  TCCTGGCTTGCTTTGCTTG   33419   G   C   _
                                TC CTGGC TGCTT GCTTG
                                || ||||| ||||| |||||
                                AG GACCG ACGAA CGAAC
                                 _    A    A
GAM1300  GRIA1    5'  CCTTCCTTGCTTGCTTGC   33420   GG  _
                                CT  CCT GCTTGCTTGC
                                ||  ||| ||||||||||
                                GG  GGA CGAACGAACG
                                 AA   A
GAM1300  LRP1     3'  TCGCTTGCCGGCTTGCTCGC  33421     G  T
                                TCGCT GCC GCTTGCTTGC
                                ||||| ||| ||||||||||
                                AGCGA CGG CGAACGAGCG
                                   A   C
GAM1300  PSME3    5'  GCTGGCTTACTCACTGCTCGC 33422      C   TG  T
                                GCTGGC TGCT  CT GCTCGC
                                |||||| ||||  || ||||||
                                CGACCG ATGA  GA CGAGCG
                                   A   GT  _
GAM1300  SLC16A1  5'  TCGCTCGCTGCCTCGTTTGCT  33423     G  C   _ C
                                TCGCT GC TGCTT G TTGCT
                                ||||| || ||||| | |||||
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                                AGCGA CG ACGGA C AACGA
                                  G _    G A
GAM1300 SLC25A15 3' TAGCCTGCTTGCACTCA     33424          TT
                                TGGCCTGCTTGC GCTCG
                                |||||||||||| ||||||
                                ATCGGACGAACG TGAGT
                                          __
GAM1300 TRIM9    5' GCTTGCTTTCTTGCTTGCTTGC 33425     G C____         C
          TTGC                    GCT GC     TGCTTGCTTGCT GC
                                ||| ||     |||||||||||| ||
                                CGA CG     ACGAACGAACGA CG
                                  A AAAGA          A
GAM1300 TRIM9    5' GCTTGCTTTCTTGCTTGCTTGC 33429     G CTG        C
                                GCT GC   CTTGCTTGCT GC
                                ||| ||   |||||||||| ||
                                CGA CG   GAACGAACGA CG
                                  A AAA         A
GAM1300 TRIM9    5' TCGCTCGCTTGCTTGCTTGC   33426      G C
                                TCGCT GC TGCTTGCTTGC
                                ||||| || ||||||||||
                                AGCGA CG ACGAACGAACG
                                   G A
GAM1300 TRIM9    5' TCGCTTGCTTGCTTGCT     33427      GGCC
                                TCGCT    TGCTTGCTTGCT
                                |||||    ||||||||||||
                                AGCGA    ACGAACGAACGA
                                         _____
GAM1300 TRIM9    5' GCTTGCTTTCTTGCTTGCTTGC 33428   G C____         C III
          TTGCG                    GC     TGCTTGCTTGCT GC   G
                                 ||     |||||||||||| ||   |
                                 CG     ACGAACGAACGA CG   C
                                A AAAGA          A III
GAM1300 KIAA1084 3' CTGGCTTGCTTTTCTGGCTTGC 33430      C    _____
                                CTGGC TGCTT     GCTTGC
                                ||||| |||||     ||||||
                                GACCG ACGAA     CGAACG
                                   A     AAGAC
GAM1300 KIAA1550 3' GCCTGGCCTGCTTGCTTG    33431    _
                                GC TGGCCTGCTTGCTTG
                                || ||||||||||||||
                                CG ACCGGACGAACGAAC
                                 G
GAM1300 LOC122773 5' TCGCTGGCCCGCCGCTTGC    33432          T
                                TCGCTGGCCTGCT GCTTGC
                                |||||||||||| ||||||
                                AGCGACCGGGCGG CGAACG
                                          _
GAM1300 LOC123096 3' CCGCTGGCCTGTTTGCTC     33433          C
                                TCGCTGGCCTG TTGCTT
                                |||||||||| ||||||
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                                GGCGACCGGAC AACGAG
                                      A
GAM1300  LOC146455 5'  GCTGGCCTGTTGCCCATTTGC  33434        C    ____
                                GCTGGCCTG TTGCT   TGC
                                ||||||||| |||||   |||
                                CGACCGGAC AACGG   ACG
                                     _    GTAA
GAM1300  LOC146506 3'  TCACTGGTTTGACTGCTTGC  33435       CC  C
                                TCGCTGG  TG TTGCTTGC
                                |||||||  || ||||||||
                                AGTGACC  AC GACGAACG
                                    AA  T
GAM1300  LOC165552 3'  GCTGCTTGCTACTTGC     33436     G C   T
                                GCTG C TGCT GCTTGC
                                |||| | |||| ||||||
                                CGAC G ACGA TGAACG
                                  _ A   _
GAM1300  LOC219879 3'  CCTGTCCTTGCTTGCTCG    33437     __
                                CCTG  CTTGCTTGCTCG
                                ||||  ||||||||||||
                                GGAC  GAACGAACGAGC
                                  AG
GAM1301  CYLN2    3'  CTGGTGTGGACTGGGCTGCT  33440    A  AG  CT
                                CT GT  GG  GCTGGGCTGCT
                                || ||  ||  ||||||||||
                                GA CA  CC  TGACCCGACGA
                                 C  CA  __
GAM1301  CYP3A5   5'  TGCTGCTGTTTGCTGGGCTG  33441     A  AGGGC
                                TGCT GT    TGCTGGGCTG
                                |||| ||    ||||||||||
                                ACGA CG    ACGACCCGAC
                                  _  ACAA_
GAM1301  STK13    5'  GCTGCTGGGCTGCTGGGCTG  33443    A  A
                                GCT GT GGGCTGCTGGGCTG
                                ||| || ||||||||||||||
                                CGA CG CCCGACGACCCGAC
                                  _  A
GAM1301  STK13    5'  GTGGGCTGCTGGGCTGC    33442    A
                                GT GGGCTGCTGGGCTGC
                                || |||||||||||||||
                                CA CCCGACGACCCGACG
                                 _
GAM1301  ARHGEF4  3'  TGCTGCTGGGGCCGGTTGC  33444     A  A  CT   GC
                                TGCT GT GGG  GCTGG  TGC
                                |||| || |||  |||||  |||
                                ACGA CG CCC  CGGCC  ACG
                                  _ A   __    A_
GAM1301  BRAG     5'  TGCCAGTGCCCTGGGCTGC   33445       AGG  G
                                TGCTAGT   GCT CTGGGCTGC
                                |||||||   ||| |||||||||
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                                ACGGTCA   CGG GACCCGACG
                                    ___   _
GAM1301  C21orf41  3'  GTTGGCTGGGGCTGCT     33446    AG    CT
                                GT  GGCTG  GGGCTGCT
                                ||  |||||  ||||||||
                                CA  CCGAC  CCCGACGA
                                 A_    __
GAM1301  DKFZp566D133 3'  TGCTGATCACTGCTGGGCTGCT 33447      A  AGG
                                TGCT GT   GCTGCTGGGCTGCT
                                |||| ||   ||||||||||||||
                                ACGA TA   TGACGACCCGACGA
                                  C  G__
GAM1301  DKFZP586J1624 3'  GTGGGCTGCTGGGCTGC     33442    A
                                GT GGGCTGCTGGGCTGC
                                || ||||||||||||||
                                CA CCCGACGACCCGACG
                                _
GAM1301  KIAA1755  5'  TGTGAGTAGGGAGCACAGGCTG 33448    CT      CT  _
              CT                  TG  AGTAGGG  GC TGGGCTGCT
                                ||  |||||||  || |||||||||
                                AC  TCATCCC  CG GTCCGACGA
                                 AC      T_  T
GAM1301  PP1628   3'  TGCTGGTGGGGGAAGGCTG   33449     A  A   CTGCT
                                TGCT GT GGG    GGGCTG
                                |||| || |||    ||||||
                                ACGA CA CCC    TCCGAC
                                  C  C   CT___
GAM1301  UBCE7IP5  3'  TGCTGGTGGGAAGCAGGCTG   33450     A  A   CT  T
                                TGCT GT GGG  GC GGGCTG
                                |||| || |||  || ||||||
                                ACGA CA CCC  CG TCCGAC
                                  C  _   TT  _
GAM1301  LOC144121 5'  TGCTAGTCGGGCTGCGTG    33451       A     _
                                TGCTAGT GGGCTGC TG
                                ||||||| ||||||| ||
                                ACGATCA CCCGACG AC
                                    G      C
GAM1301  LOC149722 5'  TGCTGGAACTGCTGGGTTGCT  33452      AGTA        C
                                TGCT    GGGCTGCTGGG TGCT
                                ||||    |||||||||||| ||||
                                ACGA    CTTGACGACCC ACGA
                                  C___         A
GAM1301  LOC151201 3'  TGCTAATAGGGCAGTGCTG    3163           __
                                TGCTAGTAGGGC  TGCTG
                                ||||||||||||  |||||
                                ACGATTATCCCG  ACGAC
                                       TC
GAM1301  LOC152282 3'  TGCTACTGGGGCTGCTGGAGCT 33454       GTA       _
              GCT                   TGCTA   GGGCTGCTGG GCTGCT
                                |||||   |||||||||| ||||||
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                              ACGAT   CCCGACGACC CGACGA
                                 GAC        T
GAM1301  LOC152282 3'  TGCTACTGGGGCTGCTGGAGCT 33454      GTA       _
            GCT                  TGCTA   GGGCTGCTGG GCTGCT
                              |||||   |||||||||| ||||||
                              ACGAT   CCCGACGACC CGACGA
                                 GAC        T
GAM1301  LOC152282 3'  TGCTACTGGGGCTGCTGCCGCT 33455      GTA       G_
            GCT                  TGCTA   GGGCTGCTG  GCTGCT
                              |||||   |||||||||  ||||||
                              ACGAT   CCCGACGAC  CGACGA
                                 GAC        GG
GAM1301  LOC152282 3'  TGCTACTGGGGCTGCTGGTGGA 33453     GTA       ____
            GCTGCT               GCTA   GGGCTGCTGG   GCTGCT
                              ||||   ||||||||||   ||||||
                              CGAT   CCCGACGACC   CGACGA
                                 GAC        ACCT
GAM1301  LOC157349 5'  TGCGGGTGGGGGCAGGGGCTGC 33456     TA  A_   TGCT
            T                    TGC  GT  GGGC   GGGCTGCT
                              |||  ||  ||||   ||||||||
                              ACG  CA  CCCG   CCCGACGA
                                CC  CC   TC__
GAM1301  LOC165480 5'  TGCTGGAGGGGCTGAACTGCT  33457     AGT   CT
                              TGCT   AGGG  GCTGGGCTGCT
                              ||||   ||||  ||||||||||
                              ACGA   TCCC  CGACTTGACGA
                                CC_   __
GAM1301  LOC220558 3'  GTAAGGCTGTGGCCTGCT    33458        C   G
                              GTAGGGCTG TGG CTGCT
                              ||||||||| ||| |||||
                              CATTCCGAC ACC GACGA
                                    _  G
GAM1301  LOC221100 5'  TGCTGGTGGAGGGATTGGCTG  33459     A  __   CTGCTG
                              TGCT GT  AGGG     GGCTG
                              |||| ||  ||||     |||||
                              ACGA CA  TCCC     CCGAC
                                C  CC   TAA___
GAM1301  LOC253959 3'  TGCTGATCACTGCTGGGCTGCT 33447     A  AGG
                              TGCT GT   GCTGCTGGGCTGCT
                              |||| ||   ||||||||||||||
                              ACGA TA   TGACGACCCGACGA
                                C  G__
GAM1301  LOC254617 5'  GTGGGCTGCTGGGCTGC     33442    A
                              GT GGGCTGCTGGGCTGC
                              || ||||||||||||||
                              CA CCCGACGACCCGACG
                               _
GAM1301  LOC256492 5'  TGCTGTGGGGCTGCTGTACT   33460      A  A       GG
                              TGCT GT GGGCTGCTG  CT
                              |||| || |||||||||  ||
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                                ACGA CA CCCGACGAC  GA
                                  _ C       AT
GAM1302  DKFZP434J037 3'  GCCACGGAGGTCCATTAG    33463        A   AATC
                                GCCACGGA GTC    TTAG
                                |||||||| |||    ||||
                                CGGTGCCT CAG    AATC
                                    C   GT__
GAM1302  LOC51170  3'  GCCACAAATAATCTTGGA    33464        AGTC     A
                                GCCACGGA    AATCTT GA
                                ||||||||    |||||| ||
                                CGGTGTTT    TTAGAA CT
                                    A___     C
GAM1303  DLG5     5'  TCTGGGAGGTTTTGGGGGG    12266      C__
                                TTTGG   GTTTTGGGGG
                                |||||   ||||||||||
                                AGACC   CAAAACCCCC
                                   CTC
GAM1303  JAM2     5'  CTGTTCTGTTTTGGGGG     33467      GGC
                                CTGTTT   GTTTTGGGGG
                                ||||||   ||||||||||
                                GACAAG   CAAAACCCCC
                                   A__
GAM1303  CLIPR-59  3'  TACTCTTTTGCTTTGGGGG   33468     G   GGC
                                TACT TTT   GTTTTGGGGG
                                |||| |||   ||||||||||
                                ATGA AAA   CGAAACCCCC
                                  G   A__
GAM1303  FLJ22332  5'  TATTTGGCAAAGGGGTGC    33469        TTTT   _
                                TGTTTGGCG    GGGG GC
                                |||||||||    |||| ||
                                ATAAACCGT    CCCC CG
                                     TT__    A
GAM1303  ILF3     3'  CTTCCCAGCGTGTTTTGGGGGC 33470    G  TG   __
             AC                   CT TT  GCGT  TTTGGGGGCAC
                                || ||  ||||  ||||||||||
                                GA GG  CGCA  AAACCCCCGTG
                                 A  GT    CA
GAM1303  KIAA0451  3'  CTGTTAGGCTGGGGGC     33471      T   GTTT
                                CTGTT GGC    TGGGGGC
                                |||||| |||    |||||||
                                GACAA CCG    ACCCCCG
                                   T  _____
GAM1303  KIAA1328  3'  TGTTTGTGATGGCAGGGGCAC  33472      GC  TT
                                TGTTTG  GT  TGGGGGCAC
                                ||||||  ||  |||||||||
                                ACAAAC  TA  GTCCCCGTG
                                   AC  CC
GAM1303  KIAA1361  3'  TACTGTTTGGGGTCTTGGG   33473         C
                                TACTGTTTGG GTTTTGGG
                                |||||||||| ||||||||
```

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                                ATGACAAACC CAGAACCC
                                      C
GAM1303 SLC21A11 3' CTGTCTGGCTCCAGGGGG   33474        G  TT
                                CTGTTTGGC TT  GGGGG
                                ||||||||| ||  |||||
                                GACAGACCG AG  CCCCC
                                     _ GT
GAM1303 LOC255971 3' TACTGTTTGTGTTTCTTCTGCA 33475        GC    GGGG
                                TACTGTTTG  GTTTT   GCA
                                |||||||||  |||||   |||
                                ATGACAAAC  CAAAG   CGT
                                     A_    AAGA
GAM1304 PLCB4   3' AGTAAATTTTTGTGGATTTG  33478    C  CC       C
                                GGT AGT  TTTGTGGAT TG
                                ||| |||  ||||||||| ||
                                TCA TTA  AAACACCTA AC
                                  T  A_       A
GAM1304 SHOC2   3' GTTAGTTTTGTGGATCTGCA  33479   C  CC
                                GT AGT  TTTGTGGATCTGCA
                                || |||  ||||||||||||||
                                CA TCA  AAACACCTAGACGT
                                 A  __
GAM1304 ZNF268   5' CGGTCAGTTTTGTGTGCCT   33480       CC     GA
                                CGGTCAGT  TTTGTG  TCT
                                ||||||||  ||||||  |||
                                GCCAGTCA  AAACAC  GGA
                                     __     AC
GAM1304 DKFZP564C1940 5' GGGCAGTCCTCCTCATCTG   33481    T       GTGG
                                GG CAGTCCTTT   ATCTG
                                || |||||||||   |||||
                                CC GTCAGGAGG   TAGAC
                                 C       AG__
GAM1304 PDE4DIP  3' GGTCAGGTGTGGATCTG    33482       TCCTT
                                GGTCAG    TGTGGATCTG
                                ||||||    ||||||||||
                                CCAGTC    ACACCTAGAC
                                   C____
GAM1305 KIAA1735 3' CATTAATATACTCGTAAT   33485   C  C
                                CA TGA ATACTCGTAAT
                                || ||| ||||||||||
                                GT ATT TATGAGCATTA
                                 A  A
GAM1305 NRF     3' CATAGACATACTCAACTGTCA 33486   CT       TAATC
                                CA  GACATACTCG    GTCA
                                ||  ||||||||||    ||||
                                GT  CTGTATGAGT    CAGT
                                 AT        TGA__
GAM1305 TPD52   3' CCACTGACTACTTGGCTCTCA 33487        A   CGTAA  G
                                CCACTGAC TACT    TC TCA
                                |||||||| ||||    || |||
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                              GGTGACTG ATGA    AG AGT
                                  _   ACCG_ _
GAM1306 ATP1A2   3' TGCCACCTCTAGCAAT     33490      GGGA
                              TGCCAC   TTTAGCAAT
                              ||||||   |||||||||
                              ACGGTG   AGATCGTTA
                                 G___
GAM1306 BCL11B   3' TGCCACGCTTAGCAAT     33491       GGA
                              TGCCACG   TTTAGCAAT
                              |||||||  |||||||||
                              ACGGTGC   GAATCGTTA
                                   ___
GAM1306 CLCA3    3' TGTCACAGTTAGCAAT     33492    C    GAT
                              TG CACGG   TTAGCAAT
                              || |||||  ||||||||
                              AC GTGTC   AATCGTTA
                               A    ___
GAM1306 COL19A1  3' TGACGAGATGTTTAGCAAT   33493   C     __
                              C ACGGGAT  TTAGCAAT
                              | |||||||  ||||||||
                              A TGCTCTA  AATCGTTA
                               C      CA
GAM1306 DDOST    3' TGCCACTTTTAGCAAT     33494      GGGA
                              TGCCAC   TTTAGCAAT
                              ||||||   |||||||||
                              ACGGTG   AAATCGTTA
                                 A___
GAM1306 EFNA4    3' TGCCCTGGTCCAGCAAT    33495     ACG  A
                              TGCC   GG TTTAGCAAT
                              ||||   || |||||||||
                              ACGG   CC AGGTCGTTA
                                GA_  _
GAM1306 MDFI     3' TGTCAGGTCCTCAGCAAT    33496    C  C  GA
                              TG CA GG  TTTAGCAAT
                              || || ||  |||||||||
                              AC GT CC  GAGTCGTTA
                               A  _  AG
GAM1306 MEN1     5' TGCTGGGCAGTTTAGCAAT   33497    CAC   A__
                              TGC   GGG   TTTAGCAAT
                              |||   |||   |||||||||
                              ACG   CCC   AAATCGTTA
                                A__   GTC
GAM1306 PIP5K1A  3' TGCCAAGTCCAGCAAT     33498      CG  A
                              TGCCA  GG TTTAGCAAT
                              |||||  || |||||||||
                              ACGGT  TC AGGTCGTTA
                                   __  _
GAM1306 PPARGC1  3' TACCACGGCATGAAGGCAAT  33499        G  TTA_
                              TGCCACGG AT   GCAAT
                              |||||||| ||   |||||
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                                ATGGTGCC TA   CGTTA
                                    G  CTTC
GAM1306  TACC1    3'  GCAAAAAGATTTAGCAAT    33500    CAC
                                GC   GGGATTTAGCAAT
                                ||   ||||||||||||
                                CG   TTCTAAATCGTTA
                                 TTT
GAM1306  WNT15    3'  TGCCACAGGAGGTCCTGGCA   33501         ___   A
                                TGCCACGGGA   TTT GCA
                                ||||||||||   ||| |||
                                ACGGTGTCCT   GGA CGT
                                     CCA   C
GAM1306  FLJ14050 5'  GCCACGGGGCCTAGAGCAAT   33502        A_  T_
                                GCCACGGG  TT  AGCAAT
                                ||||||||  ||  ||||||
                                CGGTGCCC  GA  TCGTTA
                                    CG  TC
GAM1306  GMPPA    5'  TGCCACAGGAAACAAT      33503         TTT
                                TGCCACGGGA   AGCAAT
                                ||||||||||   ||||||
                                ACGGTGTCCT   TTGTTA
                                    ___
GAM1306  GTF3C4   3'  TGCCACGGACCAAGCAAT    33504         ATTT
                                TGCCACGGG    AGCAAT
                                |||||||||    ||||||
                                ACGGTGCCT    TCGTTA
                                     GGT_
GAM1306  HPCAL4   3'  TGCCCCGGGCTCAGCAAT    33505     A   A
                                TGCC CGGG TTTAGCAAT
                                |||| |||| |||||||||
                                ACGG GCCC GAGTCGTTA
                                  G   _
GAM1306  KIAA0534 3'  GCCACAGAGTTAGCAAT     33507        AT
                                GCCACGGG  TTAGCAAT
                                ||||||||  ||||||||
                                CGGTGTCT  AATCGTTA
                                    C_
GAM1306  KIAA0534 3'  TGCCTGAACCCAAGCAAT    33506     ACG     _
                                TGCC   GGATTTA GCAAT
                                ||||   ||||||| |||||
                                ACGG   CTTGGGT CGTTA
                                  A__      T
GAM1306  KIAA1069 3'  TGGCACGACTAGCAAT      33508    C    GAT
                                TG CACGG   TTAGCAAT
                                || |||||   ||||||||
                                AC GTGCT   GATCGTTA
                                 C    ___
GAM1306  KIAA1297 3'  TGCCACAGCTCTCAGCAAT   33509        GA
                                TGCCACGG  TTTAGCAAT
                                ||||||||  |||||||||
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                                ACGGTGTC  GAGTCGTTA
                                     GA
GAM1306 KIAA1365 3' TGCCATTGGTCCAGCAAT    33510      CG  A
                                TGCCA  GG TTTAGCAAT
                                |||||  || |||||||||
                                ACGGT  CC AGGTCGTTA
                                   AA  _
GAM1306 KIAA1729 3' TGCCACAGGAGTACAAT     33511          TTTA
                                TGCCACGGGA   GCAAT
                                ||||||||||   |||||
                                ACGGTGTCCT   TGTTA
                                      CA__
GAM1306 KIAA1906 3' TGTCACGAGATGACTAACAAT 33512    C       __
                                TG CACGGGAT  TTAGCAAT
                                || ||||||||  ||||||||
                                AC GTGCTCTA  GATTGTTA
                                 A       CT
GAM1306 LHX6     3' TGCCATTGATTAGCAAT     33513      CGG    T
                                TGCCA   GATT AGCAAT
                                |||||   |||| ||||||
                                ACGGT   CTAA TCGTTA
                                   AA_   _
GAM1306 PTRF     5' TGCGCGGGACTCCTCAAT    33514     CA       AG
                                TGC  CGGGATTT  CAAT
                                |||  ||||||||  ||||
                                ACG  GCCCTGAG  GTTA
                                  C_       GA
GAM1306 RAP140   3' TACCAGAATTTTAGCAAT    33515      C   A
                                TGCCA GGG TTTAGCAAT
                                ||||| ||| |||||||||
                                ATGGT CTT AAATCGTTA
                                   _  A
GAM1306 TCL6     3' TGCGAGGATTAGCAAT      33516     CAC     T
                                TGC   GGGATT AGCAAT
                                |||   |||||| ||||||
                                ACG   TCCTAA TCGTTA
                                  C__     _
GAM1306 TCL6     3' TGCGAGGATTAGCAAT      33516     CAC     T
                                TGC   GGGATT AGCAAT
                                |||   |||||| ||||||
                                ACG   TCCTAA TCGTTA
                                  C__     _
GAM1306 TFEC     5' TGCTGGGACCAGCAAT      33517     CAC     T
                                TGC   GGGATT AGCAAT
                                |||   |||||| ||||||
                                ACG   CCCTGG TCGTTA
                                  A__     _
GAM1306 TRIP10   3' GCCACGGGGTCAGAAAT     33518        AT   C
                                GCCACGGG  TTAG AAT
                                ||||||||  |||| |||
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                                CGGTGCCC  AGTC TTA
                                    C_    T
GAM1306  LOC115110 3'  TGCTGGAACCCCAGCAAT    33519     CAC      _
                                TGC   GGGATTT AGCAAT
                                |||   ||||||| ||||||
                                ACG   CCTTGGG TCGTTA
                                  A__      G
GAM1306  LOC145098 5'  TGTCACGGAATAACAAT     33520    C      TT
                                TG CACGGGA  TAGCAAT
                                || |||||||  |||||||
                                AC GTGCCTT  ATTGTTA
                                 A      __
GAM1306  LOC149992 5'  TGACACGACTAGCAAT      33521    C    GAT
                                TG CACGG   TTAGCAAT
                                || |||||   ||||||||
                                AC GTGCT   GATCGTTA
                                 T    ____
GAM1306  LOC151121 5'  TGCTGGGCCCAGCAAT      33522     CAC   A
                                TGC   GGG TTTAGCAAT
                                |||   ||| |||||||||
                                ACG   CCC GGGTCGTTA
                                  A__   _
GAM1306  LOC151121 5'  TGCTGGGCCCAGCAAT      33522     CAC   A
                                TGC   GGG TTTAGCAAT
                                |||   ||| |||||||||
                                ACG   CCC GGGTCGTTA
                                  A__   _
GAM1306  LOC152059 5'  TGCCACAGGACCAGCAA     33523           T
                                TGCCACGGGATT AGCAA
                                |||||||||||| |||||
                                ACGGTGTCCTGG TCGTT
                                        _
GAM1306  LOC200609 5'  TACCATATGGTTTAGCAAT    33524       CG_  A
                                TGCCA   GG TTTAGCAAT
                                |||||   || |||||||||
                                ATGGT   CC AAATCGTTA
                                   ATA  _
GAM1306  LOC203350 3'  TGCCTGGAATCCCAGCAAT    33525      AC      _
                                TGCC  GGGATTT AGCAAT
                                ||||  ||||||| ||||||
                                ACGG  CCTTAGG TCGTTA
                                  A_      G
GAM1306  LOC245757 3'  TGCACGGGATGGCAAT      33526     C      TTA
                                TGC ACGGGAT   GCAAT
                                ||| |||||||   |||||
                                ACG TGCCCTA   CGTTA
                                  _      C__
GAM1306  LOC254504 5'  TGCGTGGGATTTACAAT     33527     CAC       G
                                TGC   GGGATTTA CAAT
                                |||   |||||||| ||||
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                                ACG   CCCTAAAT GTTA
                                  CA_       _
GAM1306 LOC90520 3' TGCGTGGGATTTACAAT     33527     CAC       G
                                TGC   GGGATTTA CAAT
                                |||   |||||||| ||||
                                ACG   CCCTAAAT GTTA
                                  CA_       _
GAM1307 ABCC2    3' TGACATTTATTTTCTTAAC   33530     TG    C
                                TGG  TTTA TTTCTTAAC
                                |||  |||| |||||||||
                                ACT  AAAT AAAGAATTG
                                  GT    A
GAM1307 BGN      3' TTGCACGGTGTTTCTTT     33531            A
                                TTGCATGGTGTTT CTTT
                                |||||||||||| ||||
                                AACGTGCCACAAA GAAA
                                                _
GAM1307 CSPG3    3' GCATGGTGTCTACTTCTTA   33532              T
                                GCATGGTGTTTACTT CTTA
                                |||||||||||||| ||||
                                CGTACCACAGATGAA GAAT
                                                _
GAM1307 HIP1     3' TGTTTAAGTGCTTTCTTAAC  33533       ____
                                TGTTTA    CTTTCTTAAC
                                ||||||    ||||||||||
                                ACAAAT    GAAAGAATTG
                                    TCAC
GAM1307 PTEN     3' CATGGTGTTTTATCCCTCTT  33534         A__
                                CATGGTGTTT   CTTTCTT
                                ||||||||||   |||||||
                                GTACCACAAA   GGGAGAA
                                      ATA
GAM1307 TEM7R    3' TTGCATGGGCTGTTTTTCTTA 33535         T   TAC
                                TTGCATGG GTT   TTTCTTA
                                |||||||| |||   |||||||
                                AACGTACC CGA   AAAGAAT
                                     _  CAA
GAM1307 FBXO30   3' TGCAATTCTTACTTTCTT    33536      TGGTG
                                TGCA    TTTACTTTCTT
                                ||||    ||||||||||
                                ACGT    GAATGAAAGAA
                                  TAA__
GAM1307 KIAA0430 3' TTCCATGGTGTTCTGTCTT   33537    G       TA  T
                                TT CATGGTGTT  CT TCTT
                                || |||||||||  || ||||
                                AA GTACCACAA  GA AGAA
                                 G        __  C
GAM1307 KLHL6    3' TGCTCAGGTGTTTACTTTTTTA 33538     AT_         C
            A                    TGC   GGTGTTTACTTT TTAA
                                |||   |||||||||||| ||||
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                                ACG   CCACAAATGAAA AATT
                                  AGT          A
GAM1307  NRF      3'  CTGCATGTTTACTTGTTTTCTT 33539      TGG       ____
                                TTGCA  TGTTTACTT   TCTT
                                |||||  |||||||||   ||||
                                GACGT  ACAAATGAA   AGAA
                                   ___       CAAA
GAM1307  LOC150095 5'  TTACATACTTACTTTCTT    33540       GTG
                                TTGCATG  TTTACTTTCTT
                                |||||||  ||||||||||
                                AATGTAT  GAATGAAAGAA
                                   ___
GAM1308  CLN6     3'  TTGCTCAACAGCCACAGTAG  33543     G____
                                TTGT    AGCCACAGTAG
                                ||||    ||||||||||
                                AACG    TCGGTGTCATC
                                  AGTTG
GAM1308  STAT6    3'  TTCAGATTGTGTACAGTAGA  33544     T     AGCC
                                TTCA ATTGTG   ACAGTAGA
                                |||| ||||||   ||||||||
                                AAGT TAACAC   TGTCATCT
                                  C     A___
GAM1308  FLJ20094  3'  TTCATATATATGCAGTAGA   33545       _   AGCCA
                                TTCATAT TGTG    CAGTAGA
                                |||||||  ||||    |||||||
                                AAGTATA ATAC    GTCATCT
                                    T  _____
GAM1308  FLJ21272  3'  TTCATATTGTGATCCCACGAGA 33546          G_   AGT
                                TTCATATTGTGA  CCAC   AGA
                                ||||||||||||  ||||   |||
                                AAGTATAACACT  GGTG   TCT
                                       AG    C__
GAM1309  CPLX1    3'  TGTAAGGTCATGAAGGTCAATG 33549          _   ATA
                                TGTAAGGTTAT AAG   TAATG
                                ||||||||||| |||   |||||
                                ACATTCCAGTA TTC   GTTAC
                                       C   CA_
GAM1309  FLJ21934  3'  TAAGGTTATAGAAGTAATG   33550         A  TA
                                TAAGGTTATA GA  TAATG
                                |||||||||| ||  |||||
                                ATTCCAATAT CT  ATTAC
                                      _  TC
GAM1309  HHLA3    3'  TGCAGGTCACAGGGGATATGAT 33551      A      A__     A
              G                   TGTA GGTTATA   GATAT ATG
                                  ||||  |||||||   |||||  |||
                                  ACGT  CCAGTGT   CTATA TAC
                                    _       CCC     C
GAM1309  KIAA0748  3'  TGCAGGTCACAGGGGATATGAT 33551      A      A__     A
              G                   TGTA GGTTATA   GATAT ATG
                                  ||||  |||||||   |||||  |||
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                                ACGT CCAGTGT   CTATA TAC
                                  _     CCC    C
GAM1309  PDE11A   3'  TGTAAGGTTAAAACAT     33552          TA
                                TGTAAGGTTA  AGATAT
                                ||||||||||  ||||||
                                ACATTCCAAT  TTTGTA
                                      __
GAM1309  LOC253716 3'  TGCAGGTCACAGGGGATATGAT 33551      A      A__    A
            G                    TGTA GGTTATA   GATAT ATG
                                ||||| |||||||   ||||| |||
                                ACGT CCAGTGT   CTATA TAC
                                  _     CCC    C
GAM1310  CTPS     3'  TGAGAAACAAGGTGACC     33555        T   AA
                                TGAGGAGC GAG  GTGACC
                                ||||||||| |||  ||||||
                                ACTCTTTG TTC  CACTGG
                                    _  __
GAM1310  DCC      3'  TAACTGAGTGGTCCTGATGGGT 33556        GAG__   GAA
            GACC                   TAACTGAG    CTGA   GTGACC
                                |||||||||    ||||  ||||||
                                ATTGACTC    GACT   CACTGG
                                     ACCAG    ACC
GAM1310  FEN1     3'  AACTGCCTGAGAAGTG      33557       AGGAG
                                AACTG    CTGAGAAGTG
                                |||||    ||||||||||
                                TTGAC    GACTCTTCAC
                                  G____
GAM1310  GALE     5'  ACTGAGGACTGGAGAGT     33558        G  _  A
                                ACTGAGGA CTG AGA GT
                                |||||||| ||| ||| ||
                                TGACTCCT GAC TCT CA
                                     _  C  _
GAM1310  GPR65    5'  ACTGAGGAGCTTGATAAAT   33559          _ G
                                ACTGAGGAGCT GA AAGT
                                |||||||||| || ||||
                                TGACTCCTCGA CT TTTA
                                       A  A
GAM1310  GRB10    3'  ACTGAGGAGCAGAGAAATG   33560          T
                                ACTGAGGAGC GAGAAGTG
                                |||||||||| ||||||||
                                TGACTCCTCG CTCTTTAC
                                       T
GAM1310  KCNN4    3'  TAACTGAGAGCTGGAGGT    33561        G    A  A
                                TAACTGAG AGCTG GA GT
                                |||||||| ||||| || ||
                                ATTGACTC TCGAC CT CA
                                     _    _  C
GAM1310  NOS1     3'  AACTGAGGACAAGTGAC     33562         G TGAG
                                AACTGAGGA C    AAGTGAC
                                ||||||||| |    |||||||
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                              TTGACTCCT G   TTCACTG
                                  _ _____
GAM1310 SELL    3' CAACTGAAAAAGAGAGGTG   33563        CT   A
                              TAACTGAGGAG  GAGA GTG
                              ||||||||||  |||| |||
                              GTTGACTTTTT  CTCT CAC
                                    __   C
GAM1310 SLC6A6  3' GACTGAGCTTGGAAGTGAC   33564   G_   GA
                              GA  GAGCT  GAAGTGAC
                              ||  |||||  ||||||||
                              CT  CTCGA  CTTCACTG
                               GA    AC
GAM1310 SP100   3' TGATGGAGGAATAAAGTGAC  33565    _   CTGA
                              TGA GGAG   GAAGTGAC
                              ||| ||||   ||||||||
                              ACT CCTC   TTTCACTG
                                A   CTTA
GAM1310 ST7     3' CTGAAGAGCAGTGAC       33566        TGAGA
                              CTGAGGAGC    AGTGAC
                              |||||||||    ||||||
                              GACTTCTCG    TCACTG
                                  _____
GAM1310 TRAF1   3' TGAGGAGCTGGGAGGAC     33567         A  A T
                              TGAGGAGCTG GA G GAC
                              |||||||||| || | |||
                              ACTCCTCGAC CT C CTG
                                    C  _ _
GAM1310 TRIM8   3' AAGCTGCTTGAGAAGTGC    33568    GA  _      A
                              GAG  GCT GAGAAGTG C
                              |||  ||| |||||||| |
                              TTC  CGA CTCTTCAC G
                                GA  A      C
GAM1310 YES1    3' ACTTGGGGAAAAAAAAGTG   33569    GA_   CT
                              ACT   GGAG  GAGAAGTG
                              |||   ||||  ||||||||
                              TGA   CCTT  TTTTTCAC
                                ACC   T_
GAM1310 DLGAP1  3' AACTGAGGACGGCGGGTGACC 33570        __ TGAGAA
                              AACTGAGGA  GC     GTGACC
                              |||||||||  ||     ||||||
                              TTGACTCCT  CG     CACTGG
                                   GC  CC_____
GAM1310 DLGAP1  3' AACTGAGGACGGCGGGTGACC 33570        __ TGAGAA
                              AACTGAGGA  GC     GTGACC
                              |||||||||  ||     ||||||
                              TTGACTCCT  CG     CACTGG
                                   GC  CC_____
GAM1310 E1B-AP5 3' CTGAGGGGCTGGAGCA      33571       A   A  A
                              CTGAGG GCTG GA GTG
                              |||||| |||| || |||
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                                GACTCC CGAC CT CGT
                                   C   _ _
GAM1310 E1B-AP5  3' CTGAGGGGCTGGAGCA     33571       A   A A
                                CTGAGG GCTG GA GTG
                                |||||| |||| || |||
                                GACTCC CGAC CT CGT
                                   C   _ _
GAM1310 HRD1     3' CTGCCAGTTGAGAAGTGGCC  33572     AGG  C       A
                                CTG  AG TGAGAAGTG CC
                                |||  || |||||||| ||
                                GAC  TC ACTCTTCAC GG
                                  GG_ A       C
GAM1310 KIAA0255 3' CTGAGGAAAGGGCTGGGGAGTG 33573        ____   AGA
             A                   CTGAGGA   GCTG   AGTGA
                                |||||||   ||||  |||||
                                GACTCCT   CGAC   TCACT
                                    TTCC   CCC
GAM1310 KIAA0700 3' ACTGAGGGCCTGAACAC    33574       A  GA  GTG
                                ACTGAGG GCT  GAA  AC
                                ||||||| |||  |||  ||
                                TGACTCC CGG  CTT  TG
                                   _  A_  G__
GAM1310 KIAA1695 3' TAACTGTGACAGAAGTGA   33575      AG  GCTG
                                TAACTG  GA   AGAAGTGA
                                ||||||  ||   ||||||||
                                ATTGAC  CT   TCTTCACT
                                   A_  G___
GAM1310 MGC2628  3' CTGAGGGGCTGGGAGAGC   33576      A   A _
                                CTGAGG GCTG GA AGT
                                |||||| |||| || |||
                                GACTCC CGAC CT TCG
                                   C   C  C
GAM1310 NUP133   3' AACTGAGGCCTAGAAGTGA  33577       AG  G
                                AACTGAGG  CT AGAAGTGA
                                ||||||||  || ||||||||
                                TTGACTCC  GA TCTTCACT
                                    G_  _
GAM1310 OR51E2   5' AACTGAGGAGGGGTGAC    33578        CTGAGAA
                                AACTGAGGAG      GTGAC
                                ||||||||||      |||||
                                TTGACTCCTC      CACTG
                                    CC_____
GAM1310 PEG10    3' ACTTGAGGTAAACAGAAGTGAC 33579    _   AGCTG
                                ACT GAGG    AGAAGTGAC
                                ||| ||||    |||||||||
                                TGA CTCC    TCTTCACTG
                                  A   ATTTG
GAM1310 PPP2R3A  3' CTGAGGATGTAAAGTGAC   33580       GC  A
                                CTGAGGA  TG GAAGTGAC
                                |||||||  || ||||||||
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                                GACTCCT  AC TTTCACTG
                                   __ A
GAM1310  RAB34    3'  CTGGGGGCAGGAAGTGAC    33581     A  A  TGA
                                CTG GG GC   GAAGTGAC
                                ||| || ||   ||||||||
                                GAC CC CG   CTTCACTG
                                  _  C  TC_
GAM1310  SYT12    5'  CTGAAGCAACAGAGGTG     33582       _   T   AA
                                CTGAGG AGC GAG  GTG
                                |||||| ||| |||  |||
                                GACTTC TTG CTC  CAC
                                   G   T  __
GAM1310  LOC138429 3'  TAACTGATGAGAAAAGTGAC   33583       G  GCT
                                TAACTGA GA   GAGAAGTGAC
                                ||||||| ||   ||||||||||
                                ATTGACT CT   CTTTTCACTG
                                    A  ___
GAM1310  LOC146515 3'  TGAGGAGCTGCCATGAC     33584         AGAA
                                TGAGGAGCTG    GTGAC
                                ||||||||||    |||||
                                ACTCCTCGAC    TACTG
                                      GG__
GAM1310  LOC148089 3'  AACTGAGGGGGACTTAGTG   33585        A__   GAGA
                                AACTGAGG   GCT    AGTG
                                ||||||||   |||   ||||
                                TTGACTCC   TGA    TCAC
                                     CCC   A___
GAM1310  LOC150244 3'  TAACTGAGGGCTGAGGGGT   33586         A     AA
                                TAACTGAGG GCTGAG  GT
                                ||||||||| ||||||  ||
                                ATTGACTCC CGACTC  CA
                                      _     CC
GAM1310  LOC158295 5'  ACTGAGGAGCTGAAAGAACC   33587             A T
                                ACTGAGGAGCTGAGA G GACC
                                |||||||||||||| | ||||
                                TGACTCCTCGACTTT C TTGG
                                                _ _
GAM1310  LOC55954  3'  ACTGATGAGAAAAGTGACC    33588      G  GCT
                                ACTGA GA   GAGAAGTGACC
                                |||||  ||   ||||||||||
                                TGACT CT   CTTTTCACTGG
                                   A  ___
GAM1310  LOC91464  5'  ACTGGGAGCTGACAGT      33589      A       GA
                                ACTG GGAGCTGA  AGT
                                ||||  ||||||||  |||
                                TGAC CCTCGACT  TCA
                                  _       G_
GAM1310  LOC91517  3'  CTGAGAGAAGGGAAGTGAC    33590       _   CTGA
                                CTGAG GAG    GAAGTGAC
                                |||||  |||    ||||||||
```

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                                GACTC CTT   CTTCACTG
                                  T  CC__
GAM1311 PCDHGC3  5' TTTCAGCGGGTTAGCGCT   33593       T  CC  CATC
                                TTTCAGCG GG  AGC   GCT
                                |||||||| ||  |||   |||
                                AAAGTCGC CC  TCG   CGA
                                    _ AA  ____
GAM1311 PCDHGC3  5' TTTCAGCGGGTTAGCGCT   33593       T  CC  CATC
                                TTTCAGCG GG  AGC   GCT
                                |||||||| ||  |||   |||
                                AAAGTCGC CC  TCG   CGA
                                    _ AA  ____
GAM1311 PCDHGC3  5' TTTCAGCGGGTTAGCGCT   33593       T  CC  CATC
                                TTTCAGCG GG  AGC   GCT
                                |||||||| ||  |||   |||
                                AAAGTCGC CC  TCG   CGA
                                    _ AA  ____
GAM1312 ABCD2    3' TTGATACATTTTAGCCAT    33596       AAGG
                                TTGATATA   TGGCCAT
                                ||||||||   |||||||
                                AACTATGT   ATCGGTA
                                    AAA_
GAM1312 CAT      3' TTAATATAATAGGCCAT     33597       AGGT
                                TTGATATAA   GGCCAT
                                |||||||||   ||||||
                                AATTATATT   CCGGTA
                                    AT__
GAM1312 CD83     3' CTGAAAAGGTGGCCAT      33598     TAT
                                TTGA  AAAGGTGGCCAT
                                ||||  ||||||||||||
                                GACT  TTTCCACCGGTA
                                  ___
GAM1312 ETV3     3' CTTGATACTGAATAGCC     33599       AAA
                                CTTGATAT  GGTGGCC
                                ||||||||  |||||||
                                GAACTATG  TTATCGG
                                    AC_
GAM1312 KCNK2    3' CTTGATGATAGATGACCAT   33600      ATAA
                                CTTGAT   AGGTGGCCAT
                                ||||||   ||||||||||
                                GAACTA   TCTACTGGTA
                                   CTA_
GAM1312 KIF5C    3' TTGATATAAACCACCAT     33601       GG G
                                TTGATATAAA  T GCCAT
                                ||||||||||  | |||||
                                AACTATATTT  G TGGTA
                                    __ G
GAM1312 MTRF1    3' CTTGATATAGGTCCA       33602       AA   GG
                                CTTGATAT  AGGT  CCA
                                ||||||||  ||||  |||
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                                GAACTATA  TCCA  GGT
                                   __   __
GAM1312 NFE2L2   3'  TTAATATAAAAAATGCCAT   33603          TG
                                TTGATATAAAGG  GCCAT
                                ||||||||||||  |||||
                                AATTATATTTTT  CGGTA
                                      TA
GAM1312 PLAB     5'  CTCGATATGAGGACACCAT   33604        AA   TG
                                CTTGATAT  AGG  GCCAT
                                ||||||||  |||  |||||
                                GAGCTATA  TCC  TGGTA
                                     C_   TG
GAM1312 RASGRP1  3'  CTTGATACTGTTTAGCCAT   33605        AAAGG
                                CTTGATAT    TGGCCAT
                                ||||||||    |||||||
                                GAACTATG    ATCGGTA
                                     ACAA_
GAM1312 SLC7A6   3'  CTGGATAGTAATGGCCAT    33606    T   TAAA
                                CT GATA    GGTGGCCAT
                                || ||||    |||||||||
                                GA CTAT    TTACCGGTA
                                 C    CA__
GAM1312 SRGAP1   5'  AACATGAAAGGTGGTCAT    33607      _      C
                                GATAT AAAGGTGG CAT
                                ||||| |||||||| |||
                                TTGTA TTTCCACC GTA
                                   C       A
GAM1312 TMPRSS4  3'  TTAATAATAGTGGCCAT     33608       TAAA
                                TTGATA    GGTGGCCAT
                                ||||||    |||||||||
                                AATTAT    TCACCGGTA
                                    TA__
GAM1312 CAGE     5'  CTTGATATGCATCCAGAGTGGC 33609         AA____ _
                                CTTGATAT     AG GTGGC
                                ||||||||     || |||||
                                GAACTATA     TC CACCG
                                     CGTAGG  T
GAM1312 DKFZP564I0422 3'  TTGGTACAAAGATGAACCAT   33610     A        _
                                TTG TATAAAGGTGG CCAT
                                ||| ||||||||||| ||||
                                AAC ATGTTTCTACT GGTA
                                  C          T
GAM1312 DKFZp564I1922 3'  TTCATATAAAATGGTAGC    33611    G     __
                                TT ATATAAA  GGTGGC
                                || |||||||  ||||||
                                AA TATATTT  CCATCG
                                 G      TA
GAM1312 EIF5     3'  CCTGCACTCAGGTGGCCAT   33612      A   AA
                                CTTG TAT  AGGTGGCCAT
                                |||| |||  ||||||||||
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                                GGAC GTG  TCCACCGGTA
                                  _  AG
GAM1312  FLJ13639  3'  TTGAAATAAAAGTTCCCAT   33613     T      GG
                                TTGA ATAAAGGT  CCAT
                                |||| ||||||||  ||||
                                AACT TATTTTCA  GGTA
                                  T       AG
GAM1312  HSPC019   3'  CTTGGTATAAAAATAATCCAT  33614     A        _
                                CTTG TATAAAGGTGG CCAT
                                |||| |||||||||| ||||
                                GAAC ATATTTTTATT GGTA
                                  C         A
GAM1312  KIAA0391  3'  TTGATATAAAAGAGGTCAT   33615          T  C
                                TTGATATAAAGG GG CAT
                                |||||||||||| || |||
                                AACTATATTTTC CC GTA
                                       T  A
GAM1312  KIAA0882  3'  TTGATGGAAAGATGGTCAT   33616      AT       C
                                TTGAT  AAAGGTGG CAT
                                |||||  |||||||| |||
                                AACTA  TTTCTACC GTA
                                   CC       A
GAM1312  KIAA1613  3'  CTGATATAAGAGAGGCCAT   33617         AG T
                                TTGATATAA  G GGCCAT
                                |||||||||  | ||||||
                                GACTATATT  C CCGGTA
                                     CT T
GAM1312  KIAA1656  3'  CTGGATATAAGGCAGCCAT   33618    T     A  TG
                                CT GATATAA GG  GCCAT
                                || ||||||| ||  |||||
                                GA CTATATT CC  CGGTA
                                 C      _  GT
GAM1312  KLK11     3'  CTTGATATATGGCCA      33619        AAAG
                                CTTGATAT   GTGGCCA
                                ||||||||   |||||||
                                GAACTATA   TACCGGT
                                     ____
GAM1312  MGC2594   3'  CTTGATACAGGTTACAGC    33620        AA   ___
                                CTTGATAT  AGGT   GGC
                                ||||||||  ||||  |||
                                GAACTATG  TCCA   TCG
                                     __   ATG
GAM1312  MRPS31    3'  TTGAAATAAAAATTTCCAT   33621     T      GG
                                TTGA ATAAAGGT  CCAT
                                |||| ||||||||  ||||
                                AACT TATTTTTA  GGTA
                                  T       AA
GAM1312  SIAT8D    5'  CTTGATATAAAGGCTCC     33622           GG
                                CTTGATATAAAGGT  CC
                                ||||||||||||||  ||
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                                GAACTATATTTCCG  GG
                                       A_
GAM1312  ZAK      3'  CTTGATATGGAAAGGACC    33623        A_   T
                                CTTGATAT  AAGG GGCC
                                ||||||||  |||| ||||
                                GAACTATA  TTTC CTGG
                                     CC   _
GAM1312  LOC115219 5'  TGATGTAGCCACGATGGCCAT  33624      A  AA___
                                TGAT TA    GGTGGCCAT
                                |||| ||    |||||||||
                                ACTA AT    CTACCGGTA
                                  C  CGGTG
GAM1312  LOC123792 3'  CTCCCACAGGGTGGCCAT    33625     GA    AA
                                CTT  TATA  GGTGGCCAT
                                |||  ||||  |||||||||
                                GAG  GTGT  CCACCGGTA
                                  G_   C_
GAM1312  LOC131308 3'  CTTGGTAAAGCGGCTCAT    33626      ATATA       _
                                CTTG    AAGGTGGC CAT
                                ||||    |||||||| |||
                                GAAC    TTTCGCCG GTA
                                  CA___       A
GAM1312  LOC143920 5'  CCTGATACGCCATGGTGGCC   33627         AAA__
                                CTTGATAT    GGTGGCC
                                ||||||||    |||||||
                                GGACTATG    CCACCGG
                                     CGGTA
GAM1312  LOC154789 5'  CTTGATGGTGACCAT       33628        ATAAA
                                CTTGAT    GGTGGCCAT
                                ||||||    |||||||||
                                GAACTA    CCACTGGTA
                                   _____
GAM1312  LOC221692 3'  CTTGAATAAAAGCCCAT     33629       T       GG
                                CTTGA ATAAAGGT  CCAT
                                ||||| ||||||||  ||||
                                GAACT TATTTTCG  GGTA
                                   _     __
GAM1312  LOC253970 3'  CTTAATATAAAGCAAAAGC    33630           GT__
                                CTTGATATAAAG    GGC
                                ||||||||||||    |||
                                GAATTATATTTC    TCG
                                      GTTT
GAM1312  LOC257428 3'  TTGGTGAAAGATAACCAT    33631     ATAT
                                TTG    AAAGGTGGCCAT
                                |||    ||||||||||||
                                AAC    TTTCTATTGGTA
                                  CAC_
GAM1312  LOC90643  3'  CTTGATAGAAAATAACC     33632        TA
                                CTTGATA  AAGGTGGCC
                                |||||||  |||||||||
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                                GAACTAT  TTTTATTGG
                                   C_
GAM1312 LOC91960 3' CTGGACATGGGGTGGCCAT   33633    T    AAA
                                CT GATAT   GGTGGCCAT
                                || |||||   |||||||||
                                GA CTGTA   CCACCGGTA
                                 C    CC_
GAM1313 CAMLG    3' TATGGCAGTTACTGAGTTAGTT 33636    C      CAA
             A                   TAT GCAGTTAT   GGTTAGTTA
                                ||| ||||||||   |||||||||
                                ATA CGTCAATG   TCAATCAAT
                                  C       AC_
GAM1313 IL17BR   3' GCATTATCAAAATGGTTA    33637    G     ___
                                GCA TTATCAA   GGTTA
                                ||| |||||||   |||||
                                CGT AATAGTT   CCAAT
                                  _      TTA
GAM1313 FLJ14936 3' ACAGTCAAGGTTAGTT      33638     TTA
                                GCAG   TCAAGGTTAGTT
                                ||||   ||||||||||||
                                TGTC   AGTTCCAATCAA
                                  ___
GAM1313 FLJ14936 3' ACAGTCAAGGTTAGTT      33638     TTA
                                GCAG   TCAAGGTTAGTT
                                ||||   ||||||||||||
                                TGTC   AGTTCCAATCAA
                                  ___
GAM1314 CYP2E    3' TGATGATTTATTTATATTCTGG 33641         GAATTG   C
                                TGATGATTTAT     ATTC GG
                                ||||||||||      |||| ||
                                ACTACTAAATA     TAAG CC
                                      AATA__    A
GAM1314 KIAA0987 3' TGATGATTCATATGTGAT    33642          AAT
                                TGATGATTTATG   TGAT
                                ||||||||||||   ||||
                                ACTACTAAGTAT   ACTA
                                      AC_
GAM1315 ASTN     3' TGGGAGCTGGGAGAGTGTTGGT 33645    A   T    C  _  CA
             G                   TGG AGCT GGGGG AG GT  GTG
                                ||| |||| ||||| || ||  |||
                                ACC TCGA CCCTC TC CA  CAC
                                  C    _    _ A  AC
GAM1315 CALB2    3' TGGAAGTTTGGGGTGGGTGGTG 33646      C     GCA   CA
                                TGGAAG TTGGGG   GGT  GTG
                                |||||| ||||||   |||  |||
                                ACCTTC AACCCC   CCA  CAC
                                   A     AC_   C_
GAM1315 CASP10   3' GAAGTTTGGGGGGACAAGT   33647     C      __
                                GAAG TTGGGGG  CAGGT
                                |||| |||||||  |||||
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                                CTTC AACCCCC  GTTCA
                                  A      CT
GAM1315 CD7     3'  TGGGGGTTGGGGGCCTGCTGGT 33648     AAGC       AG  CA
              G                   TGG    TTGGGGGC  GT  GTG
                                  |||    ||||||||  ||  |||
                                  ACC    AACCCCCG  CG  CAC
                                    CCC_       GA  AC
GAM1315 CRHR1    3'  TGGAGGCCTGGGGGGGT     33649      A        CA
                                  TGGA GCTTGGGGG  GGT
                                  |||| |||||||||  |||
                                  ACCT CGGACCCCC  CCA
                                    C       __
GAM1315 CRHR1    3'  TGGACATGGGCAGGTCAGT    33650      AGCTTGG
                                  TGGA      GGGCAGGTCAGT
                                  ||||      ||||||||||||
                                  ACCT      CCCGTCCAGTCA
                                    GTA_____
GAM1315 CTGF     3'  TGGGGCTACAGGCAGGTCAGTG 33651     AA   T G
                                  TGG  GCT G GGGCAGGTCAGTG
                                  |||  ||| | ||||||||||||
                                  ACC  CGA T TCCGTCCAGTCAC
                                    C_   _ G
GAM1315 DNMT3L   5'  TGGGGTTTGGGGACCTCAGTG  33652     AAGC       AGG
                                  TGG    TTGGGGGC   TCAGTG
                                  |||    ||||||||   ||||||
                                  ACC    AACCCCTG   AGTCAC
                                    CCA_       G__
GAM1315 FACL4    3'  TGGGAGTTGGGGGGCAGAT    33653     A  C
                                  TGG AG TTGGGGGGCAGGT
                                  ||| || ||||||||||||
                                  ACC TC AACCCCCGTCTA
                                    C  _
GAM1315 FACL4    3'  TGGGAGTTGGGGGGCAGAT    33653     A  C
                                  TGG AG TTGGGGGGCAGGT
                                  ||| || ||||||||||||
                                  ACC TC AACCCCCGTCTA
                                    C  _
GAM1315 JUP      3'  TGGGGGCTTAGGGCAGTTGGTC 33654     AA       G  ___    A
              GGTG                  TGG  GCTTGGGG CA   GGTC GTG
                                  |||  |||||||| ||   |||| |||
                                  ACC  CGAATCCC GT   CCAG CAC
                                    CC       _ CAA    C
GAM1315 MMP19    5'  TGGGAGCCTTGGGGGAGCAGTG 33655     A  _      CA  T
                                  TGG AGC TTGGGGG  GG CAGTG
                                  ||| ||| |||||||  || |||||
                                  ACC TCG AACCCCC  TC GTCAC
                                    C  G      __ _
GAM1315 RANBP3   3'  TGGGGGCTGGGGGCAGG     33656     AA   T
                                  TGG  GCT GGGGGCAGG
                                  |||  ||| |||||||||
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                                ACC  CGA CCCCCGTCC
                                  CC  _
GAM1315 TSC      3' GGAGGTGGCGGTGGGTCAGTG 33657     AGCT  G  CA
                                GGA   TGG GG  GGTCAGTG
                                |||   ||| ||  ||||||||
                                CCT   ACC CC  CCAGTCAC
                                  CC__  G  AC
GAM1315 WDR3     3' GGGGCGTAGGGGTGGGTCAGTG 33658    AA  T     CA
                                GG  GC TGGGGG  GGTCAGTG
                                ||  || ||||||  ||||||||
                                CC  CG ATCCCC  CCAGTCAC
                                 C_  C     AC
GAM1315 DEPP     5'  GGAAGCTTGGGGGCCGAAGGGT 33659           A  TCA
             G                   GGAAGCTTGGGGGC GG   GTG
                                ||||||||||||| ||   |||
                                CCTTCGAACCCCCG CT   CAC
                                        G  TCC
GAM1315 FLJ20254 3'  TGGAGGCTGGGGGCCATGT   33660     A   T     AG_
                                TGGA GCT GGGGGC   GT
                                |||| ||| ||||||   ||
                                ACCT CGA CCCCCG   CA
                                  C   _     GTA
GAM1315 HYPC     5'  TGGAAGCATTGGGGGCAGG   33661       _
                                TGGAAGC TTGGGGGCAGG
                                ||||||| ||||||||||
                                ACCTTCG AACCCCCGTCC
                                    T
GAM1315 KIAA0767 3'  CCTGGGGGGTGGGTCAGTG    33662       CA
                                CTTGGGGG  GGTCAGTG
                                ||||||||  ||||||||
                                GGACCCCC  CCAGTCAC
                                     AC
GAM1315 KIAA1509 3'  TGGAGGCTGGGGGCAAAT    33663     A   T
                                TGGA GCT GGGGGCAGGT
                                |||| ||| ||||||||||
                                ACCT CGA CCCCCGTTTA
                                  C   _
GAM1315 MGC1203  5'  TGGAGGTTTGGGGTCTCGAGTG 33664      AGC     GCAGG  _
                                TGGA   TTGGGG     TC AGTG
                                ||||   ||||||     || ||||
                                ACCT   AACCCC     AG TCAC
                                  CCA     AG___  C
GAM1315 MGC4655  3'  GGAGCTTGGGGCTGTAGTG   33665     A       GCAG  C
                                GGA GCTTGGGG    GT AGTG
                                ||| ||||||||    || ||||
                                CCT CGAACCCC    CA TCAC
                                  _       GA__  _
GAM1315 TAPBP-R  3'  TGGGGGCTTGGGGAAGGGT   33666     AA       CA
                                TGG  GCTTGGGGGG  GGT
                                |||  |||||||||  |||
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                                ACC  CGAACCCCT  CCA
                                  CC        TC
GAM1315  LOC149076 3'  TGGGGGCTGGGGGGCAGGGTC   33667     AA   T       _
                                TGG  GCT GGGGGGCAGG TC
                                |||  ||| |||||||||| ||
                                ACC  CGA CCCCCGTCC AG
                                  CC   _        C
GAM1315  LOC164714 3'  TGGGAGCCTGGGCCTCAGT    33668     A       GGCAGG
                                TGG AGCTTGGG      TCAGT
                                ||| ||||||||      |||||
                                ACC TCGGACCC      AGTCA
                                  C       GG____
GAM1315  LOC196707 3'  TGGAAGCCTGGGGCTGGT     33669            G A
                                TGGAAGCTTGGGG C GGT
                                |||||||||||| | |||
                                ACCTTCGGACCCC G CCA
                                        _ A
GAM1315  LOC254057 3'  TGGGATAGGGGCAGGTTGGTG  33670     AAGCT         CA
                                TGG    TGGGGGCAGGT  GTG
                                |||    ||||||||||  |||
                                ACC    ATCCCCGTCCA  CAC
                                  CT___          AC
GAM1315  LOC255520 5'  GAAGTACCCGCAGGTCAGTG   33671     CTTGGGG
                                GAAG      GCAGGTCAGTG
                                ||||      ||||||||||
                                CTTC      CGTCCAGTCAC
                                   ATGGG__
GAM1315  LOC90371  3'  TGGGAGCTGTGGGGCTTCAGTG 33672     A   TG    AGG
                                TGG AGCT  GGGGC   TCAGTG
                                ||| ||||  |||||   ||||||
                                ACC TCGA  CCCCG   AGTCAC
                                  C   CA    A__
GAM1315  LOC92095  5'  TGGGAGCTTGGGGGAGGGT    33673     A        CA
                                TGG AGCTTGGGGG  GGT
                                ||| ||||||||||  |||
                                ACC TCGAACCCCC  CCA
                                  C         TC
GAM1315  LOC92096  5'  TGGGAGCTTGGGGGAGGGT    33673     A        CA
                                TGG AGCTTGGGGG  GGT
                                ||| ||||||||||  |||
                                ACC TCGAACCCCC  CCA
                                  C         TC
GAM1315  LOC92719  3'  TGGAACCTTCAGGTCAGT     33674      G   GGGGG
                                TGGAA CTT     CAGGTCAGT
                                ||||| |||     |||||||||
                                ACCTT GAA     GTCCAGTCA
                                   G  _____
GAM1316  BDP1      3'  GCCTGGGCAACAGAAC      33677     GAG   TAAA
                                GCT   TGG    CAACAGAAC
                                |||   |||    |||||||||
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                                CGG  ACC   GTTGTCTTG
                                 ___  C___
GAM1316 CORO2B   5' CCAGCTTGGGCAACAGAA   33678   _  GAG  TAAA
                                CC GCT  TGG   CAACAGAA
                                || |||  |||   ||||||||
                                GG CGA  ACC   GTTGTCTT
                                 T  ___  C___
GAM1316 EFNB2    3' GCAGAGCCCTGGGTAACAGAAC 33679   T  ____  AACA
                                GC GAGT   GGTA   ACAGAAC
                                || ||||   ||||   |||||||
                                CG CTCG   CCAT   TGTCTTG
                                 T  GGAC  ____
GAM1316 GCGR     5' GCTGAGTGGCAGAGCAGCAGA 33680        AA_ A
                                GCTGAGTGGTA  CA CAGA
                                ||||||||||  || ||||
                                CGACTCACCGT  GT GTCT
                                       CTC  C
GAM1316 HMOX1    3' CCCTGCTATAAAAACAACAGAA 33681   G  AGTGGT
             C                   CC CTG    AAACAACAGAAC
                                || |||    ||||||||||||
                                GG GAC    TTTGTTGTCTTG
                                 _  GATATT
GAM1316 HS3ST2   3' GCTGTGTTCATAGCAACAGAAC 33682    A  GGTAAA
                                GCTG GT    CAACAGAAC
                                |||| ||    |||||||||
                                CGAC CA    GTTGTCTTG
                                  A  AGTATC
GAM1316 PIM2     3' CCTTGGGGTAACAACAG    33683   GC  AGT   A
                                CC  TG  GGTAA CAACAG
                                ||  ||  ||||| ||||||
                                GG  AC  CCATT GTTGTC
                                 A_  C__   _
GAM1316 PIP5K1B  5' GCTTAGTAGCAACAGA     33684    G   TAAA
                                GCT AGTGG   CAACAGA
                                ||| |||||   |||||||
                                CGA TCATC   GTTGTCT
                                  A   ____
GAM1316 RBM3     3' CTGTATGAGACACAACAGAA  33685    A   TAA
                                CTG GTGG  ACAACAGAA
                                ||| ||||  |||||||||
                                GAC TACT  TGTTGTCTT
                                  A   CTG
GAM1316 SMAC     3' CCACTGAGTGGGGAGACAG   33686        TAAACA
                                CCGCTGAGTGG    ACAG
                                ||||||||||    ||||
                                GGTGACTCACC    TGTC
                                       CCTC__
GAM1316 SMAC     3' CCACTGAGTGGGGAGACAG   33686        TAAACA
                                CCGCTGAGTGG    ACAG
                                ||||||||||    ||||
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                                GGTGACTCACC     TGTC
                                      CCTC__
GAM1316 SMAC     3' CCACTGAGTGGGGAGACAG   33686          TAAACA
                                CCGCTGAGTGG     ACAG
                                ||||||||||     ||||
                                GGTGACTCACC     TGTC
                                      CCTC__
GAM1316 SOST     3' CCGTGAGTGGTGGGCAGAA   33687    C      AAACAA
                                CCG TGAGTGGT     CAGAA
                                ||| ||||||||     |||||
                                GGC ACTCACCA     GTCTT
                                  _      CCC___
GAM1316 ZNF10    5' CCTTGAGTGACAGCAGA     33688    GC     GTAA   A
                                CC  TGAGTG    ACA CAGA
                                ||  ||||||    ||| ||||
                                GG  ACTCAC    TGT GTCT
                                 A_     _____  C
GAM1316 ABCA10   5' TGAGTAACTAACAGAA      33689       GTAA  _
                                TGAGTG    AC AACAGAA
                                ||||||    || |||||||
                                ACTCAT    TG TTGTCTT
                                    _____ A
GAM1316 H2AFJ    3' CCACAGAGTAAATAGCAGAAC  33690     T     TAAACAA
                                CCGC GAGTGG      CAGAAC
                                |||| ||||||      ||||||
                                GGTG CTCATT      GTCTTG
                                  T     TATC___
GAM1316 HSH2     3' GCTTTTAGACAACAGAAC    33691     GAG   TAA
                                GCT   TGG   ACAACAGAAC
                                |||   |||   ||||||||||
                                CGA   ATC   TGTTGTCTTG
                                 AA_   ___
GAM1316 KIAA1024 3' CCCCTTAATGGTGAACAACAGA 33692    G  G     A
            A                    CC CT AGTGGT AACAACAGAA
                                || || |||||| ||||||||||
                                GG GA TTACCA TTGTTGTCTT
                                 G  A     C
GAM1316 KIAA1399 3' TGACTGATTGGAAATAGCAGAA 33693   C    G   T   CAA
            C                    C GCTGA TGG AAA   CAGAAC
                                | ||||| ||| |||   ||||||
                                A TGACT ACC TTT   GTCTTG
                                 C    A   _   ATC
GAM1316 MIC2L1   3' CCGTGAGCCTCTGACAACAGA  33694     C    GGTAA
                                CCG TGAGT    ACAACAGA
                                ||| |||||    ||||||||
                                GGC ACTCG    TGTTGTCT
                                  _    GAGAC
GAM1316 RASGRF2  3' CCCTGAGTTCTAACAGAA    33695    G     GGTAAAC
                                CC CTGAGT      AACAGAA
                                || ||||||      |||||||
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                                GG GACTCA      TTGTCTT
                                 _     AGA____
GAM1316  TJP2     3'  CCACTGAAGCAAGTAACAG   33696       GT    AC
                                CCGCTGA  GGTAA  AACAG
                                |||||||  |||||  |||||
                                GGTGACT  TCGTT  TTGTC
                                   __    CA
GAM1316  LOC145945 5'  GCAAGTAAGTAACAGAA     33697    T    _  AACA
                                GC GAGTG GTA    ACAGAA
                                || ||||| |||    ||||||
                                CG TTCAT CAT    TGTCTT
                                 _    T  _____
GAM1316  LOC202020 3'  GCTGCCTTAGGCAACAGAA   33698     AG_  TAAA
                                GCTG   TGG    CAACAGAA
                                ||||   |||   ||||||||
                                CGAC   ATC    GTTGTCTT
                                  GGA   C___
GAM1316  LOC220766 5'  CCTCTGAGTGGTGAAATCCAGA 33699    G       AAACAA
                                CC CTGAGTGGT     CAGA
                                || |||||||||     ||||
                                GG GACTCACCA     GTCT
                                 A        CTTTAG
GAM1316  LOC256277 3'  CACTGCTGAACAACAG      33700      AG   TAA
                                CGCTG  TGG   ACAACAG
                                |||||  |||   |||||||
                                GTGAC  ACT   TGTTGTC
                                   G_   ___
GAM1316  LOC256337 3'  CACTGCTGAACAACAG      33700      AG   TAA
                                CGCTG  TGG   ACAACAG
                                |||||  |||   |||||||
                                GTGAC  ACT   TGTTGTC
                                   G_   ___
GAM1317  ATP6V1A1  3'  ATAAAATGATTTTTTTTCATG  33703     TC    C
                                ATAA  TGAT TTTTTTCATG
                                ||||  |||| ||||||||||
                                TATT  ACTA AAAAAAGTAC
                                  TT    A
GAM1317  SMARCA3   3'  ATAATCCCTAATTTTTTCATG  33704       GATC
                                ATAATCT    TTTTTTCATG
                                |||||||    ||||||||||
                                TATTAGG    AAAAAAGTAC
                                   GATT
GAM1317  TGFA     3'  TAAATGACTGGTCCCCCTTTCA 33705      AAT   A_
            TG                   TAAAT   CTG  TCTTTTTTCATG
                                |||||   |||  ||||||||||||
                                ATTTA   GAC  GGGGGAAAGTAC
                                   CT_   CA
GAM1317  TA-KRP    3'  AATCTGATTCCTTCATG     33706        CT
                                AATCTGAT  TTTTTCATG
                                ||||||||  |||||||||
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                                TTAGACTA  AGGAAGTAC
                                    __
GAM1317  LOC122481 3'  ATAGTCTGATTTTCTTCATG   33707     A     C
                                ATA TCTGAT TTTTTTCATG
                                ||| |||||| ||||||||||
                                TAT AGACTA AAAGAAGTAC
                                  C     _
GAM1318  AKAP11    3'  AGAAAGCTATATTTACTTG    33710     C    CC
                                AGA AAGC  TATATTTACTTG
                                ||| ||||  ||||||||||||
                                TCT TTCG  ATATAAATGAAC
                                  _   __
GAM1318  CPXCR1    3'  TAAGACAGTGAAAACATTTACT 33711        AGCCCT
              TG                  TAAGACA     ATATTTACTTG
                                |||||||     ||||||||||
                                ATTCTGT     TGTAAATGAAC
                                    CACTTT
GAM1318  EREG      3'  GACCATATATATTTACTTG    33712     AAGCCC
                                GAC     TATATTTACTTG
                                |||     ||||||||||||
                                CTG     ATATAAATGAAC
                                  GTAT__
GAM1318  SEMA4B    3'  AGGCAGGCCCCCATATTT     33713     A  A    _
                                AG CA GCCCT ATATTT
                                || || ||||| ||||||
                                TC GT CGGGG TATAAA
                                 C  C    G
GAM1318  TNFRSF19L 3'  GACAAGCCCCATGGGGGCCTTG 33714           ATTTA_
                                GACAAGCCCTAT     CTTG
                                ||||||||||||     ||||
                                CTGTTCGGGGTA     GAAC
                                      CCCCCG
GAM1318  LOC201705 5'  AGACAGCCCTACTCCCACTTG  33715       A      A
                                AGACA GCCCTAT TTTACTTG
                                ||||| ||||||| ||||||||
                                TCTGT CGGGATG GGGTGAAC
                                  _      A
GAM1319  CEP1      3'  TATAAAAACATTGGCATTAATG 33718         TTA  _____
              GT                  TATAAAAAC   GGT    ATGGT
                                |||||||||   |||    |||||
                                ATATTTTTG   CCG    TACCA
                                     TAA   TAAT
GAM1319  FAT       3'  TATAAAAACTGTGTCATGGT   33719         TAGG
                                TATAAAAACT    TATGGT
                                ||||||||||    ||||||
                                ATATTTTTGA    GTACCA
                                      CACA
GAM1319  HDAC4     3'  TATAAAAACTCATTAGGT     33720           GGTAT
                                TATAAAAACTTA    GGT
                                ||||||||||||    |||
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                                ATATTTTTGAGT    CCA
                                      AAT__
GAM1319  IFNAR2   3'  TACAAAAATTTGCTAGGCATGG 33721       C___
                T                TATAAAAA   TTAGGTATGGT
                                 ||||||||   ||||||||||
                                 ATGTTTTT   GATCCGTACCA
                                     AAAC
GAM1319  PTGES    3'  TACAAAAATTAGCTGGGTATGG 33722       C  ____
                T                TATAAAAA TTA   GGTATGGT
                                 |||||||| |||   ||||||||
                                 ATGTTTTT AAT   CCATACCA
                                     _  CGAC
GAM1319  RAB23    3'  TATAAAAATTAGGTATGAT   33723       C
                                 TATAAAAA TTAGGTATGGT
                                 |||||||| ||||||||||
                                 ATATTTTT AATCCATACTA
                                     _
GAM1319  SEDL     3'  TACAAAAATTAGCCAGGTGTGG 33724       C___     A
                T                TATAAAAA   TTAGGT TGGT
                                 ||||||||   |||||| ||||
                                 ATGTTTTT   GGTCCA ACCA
                                     AATC     C
GAM1319  TRAF5    3'  TACAAAAATTACCTGGGTGTGG 33725       ___   A   A
                T                TATAAAA   ACTT GGT TGGT
                                 |||||||   |||| ||| ||||
                                 ATGTTTT   TGGA CCA ACCA
                                     TAA   C   C
GAM1319  WDR1     3'  TAAAAACTTGGACACGGT    33726       A  _
                                 TAAAAACTT GG TATGGT
                                 ||||||||| || ||||||
                                 ATTTTTGAA CC GTGCCA
                                     _  T
GAM1319  WDR1     3'  TAAAAACTTGGACACGGT    33726       A  _
                                 TAAAAACTT GG TATGGT
                                 ||||||||| || ||||||
                                 ATTTTTGAA CC GTGCCA
                                     _  T
GAM1319  AAK1     3'  TATAAAAATTAGCCAGGCATGG 33727       C___
                T                TATAAAAA   TTAGGTATGGT
                                 ||||||||   ||||||||||
                                 ATATTTTT   GGTCCGTACCA
                                     AATC
GAM1319  CXorf1   3'  ATAAAAACTTAGCCACAGGT  33728         G  _
                                 ATAAAAACTTAG TAT GGT
                                 |||||||||||| ||| |||
                                 TATTTTTGAATC GTG CCA
                                       G   T
GAM1319  CXorf15  3'  TAAGAAAATACAGATATGGT  33729    TA   CT
                                 TA  AAAA  TAGGTATGGT
                                 ||  ||||  ||||||||||
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                                AT  TTTT  GTCTATACCA
                                 TC    AT
GAM1319  DKFZp434A2417 3'  TAAAAACTCAGTCTGGT     33730          GTA
                                TAAAAACTTAG   TGGT
                                ||||||||||   ||||
                                ATTTTTGAGTC   ACCA
                                      AG_
GAM1319  DKFZP564I0422 3'  TATAAAATAGATATGGT     33731        ACT
                                TATAAAA   TAGGTATGGT
                                |||||||   ||||||||||
                                ATATTTT   ATCTATACCA
                                   ___
GAM1319  DNAM-1    3'  AAACAATATTAGGTATGGT    33732      _____
                                AAAC    TTAGGTATGGT
                                ||||    ||||||||||
                                TTTG    AATCCATACCA
                                  TTAT
GAM1319  FLJ10298  3'  TACAAAAATCACCCAGGTGTGG 33733        ___       A
            T                    TATAAAA   ACTTAGGT TGGT
                                ||||||||   |||||||| ||||
                                ATGTTTT   TGGGTCCA ACCA
                                     TAG       C
GAM1319  FLJ10956  3'  TACAAAAATTAGCCAGGTGTGG 33724        C___      A
            T                    TATAAAAA    TTAGGT TGGT
                                ||||||||    |||||| ||||
                                ATGTTTTT    GGTCCA ACCA
                                     AATC      C
GAM1319  FLJ12610  3'  TACAAAAATTAGCTAGGTGTGG 33734        C___      A
            T                    TATAAAAA    TTAGGT TGGT
                                ||||||||    |||||| ||||
                                ATGTTTTT    GATCCA ACCA
                                     AATC      C
GAM1319  FLJ12960  3'  TATAAAAAATTAGCCAGGCATG 33735        C____
            GT                    TATAAAAA     TTAGGTATGGT
                                |||||||     ||||||||||
                                ATATTTTT     GGTCCGTACCA
                                     TAATC
GAM1319  FLJ14351  3'  TATAAAAATTAGCTGGGTATGG 33736        C  ____
            T                    TATAAAAA TTA    GGTATGGT
                                ||||||| |||    ||||||||
                                ATATTTTT AAT    CCATACCA
                                     _   CGAC
GAM1319  FLJ31153  3'  TACAAAAACTACTCCGGTGTGG 33737          TA___   A
            T                    TATAAAAACT     GGT TGGT
                                ||||||||||     ||| ||||
                                ATGTTTTTGA     CCA ACCA
                                      TGAGG   C
GAM1319  FLJ32452  3'  TATAAAAACTCAGGCCAAGT   33738            AT
                                TATAAAAACTTAGGT  GGT
                                ||||||||||||||  |||
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                                ATATTTTTGAGTCCG  TCA
                                      GT
GAM1319 GAL3ST-4  3' TATAAAAATTAGCCGGGTATGG 33739       C___ TA
           T                   TATAAAAA   T  GGTATGGT
                               ||||||||   |  ||||||||
                               ATATTTTT   G  CCATACCA
                                   AATC GC
GAM1319 HTATIP2   3' TATATAAGCTTAGGTATA    33740     A  A
                               TATA AA CTTAGGTATG
                               |||| || ||||||||||
                               ATAT TT GAATCCATAT
                                 A  C
GAM1319 KIAA0555  3' TACAAAAATTAGCCAGGTGTGG 33724       C___     A
           T                   TATAAAAA   TTAGGT TGGT
                               ||||||||   |||||| ||||
                               ATGTTTTT   GGTCCA ACCA
                                   AATC     C
GAM1319 KIAA1024  3' CATAAAAATGCCAGAGTATGGT 33741       __  TA
                               TATAAAAA  CT  GGTATGGT
                               ||||||||  ||  ||||||||
                               GTATTTTT  GG  TCATACCA
                                   AC  TC
GAM1319 KIAA1571  3' ATAAAAACTGATATGGT     33743       TA
                               ATAAAAACT  GGTATGGT
                               |||||||||  ||||||||
                               TATTTTTGA  CTATACCA
                                    __
GAM1319 KIAA1571  3' TAAAAACTGATATGGT      33742       TA
                               TAAAAACT  GGTATGGT
                               ||||||||  ||||||||
                               ATTTTTGA  CTATACCA
                                    __
GAM1319 KIAA1735  3' TATAAAAATAGACATGGT    33744       CT  GT
                               TATAAAAA  TAG  ATGGT
                               ||||||||  |||  |||||
                               ATATTTTT  ATC  TACCA
                                   __  TG
GAM1319 KIAA1829  3' TACAAAAATTAGCCAGGTATGG 33745       C___
           T                   TATAAAAA   TTAGGTATGGT
                               ||||||||   ||||||||||
                               ATGTTTTT   GGTCCATACCA
                                   AATC
GAM1319 LIECG3    3' TACAAAAATTAGCCAGGTGTGG 33724       C___     A
           T                   TATAAAAA   TTAGGT TGGT
                               ||||||||   |||||| ||||
                               ATGTTTTT   GGTCCA ACCA
                                   AATC     C
GAM1319 MRPL44    3' TACAAAAATTAGCCAGGTATGG 33745       C___
           T                   TATAAAAA   TTAGGTATGGT
                               ||||||||   ||||||||||
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                                ATGTTTTT   GGTCCATACCA
                                    AATC
GAM1319  SCYA16   3'  TACAAAAATTAGCCAGGTGTGG 33724       C___    A
            T                    TATAAAAA   TTAGGT TGGT
                                 ||||||||   |||||| ||||
                                 ATGTTTTT   GGTCCA ACCA
                                    AATC    C
GAM1319  WBSCR23  3'  TACAAAAACTAGCCAGGTGTGG 33746         ___    A
            T                    TATAAAAACT  TAGGT TGGT
                                 ||||||||||  ||||| ||||
                                 ATGTTTTTGA  GTCCA ACCA
                                      TCG    C
GAM1319  LOC126964 3'  TAAAAACTTCAGTAGGT    33747        A   T
                                 TAAAAACTT GGTA GGT
                                 ||||||||| |||| |||
                                 ATTTTTGAA TCAT CCA
                                      G  _
GAM1319  LOC143425 3'  TAAACACTGGTATGGT     33748     A  TA
                                 TAAA ACT  GGTATGGT
                                 |||| |||  ||||||||
                                 ATTT TGA  CCATACCA
                                   G  __
GAM1319  LOC143916 3'  TACAAAAATTTGCCGGGCATGG 33749       C___ TA
            T                    TATAAAAA   T  GGTATGGT
                                 ||||||||   |  ||||||||
                                 ATGTTTTT   G  CCGTACCA
                                    AAAC GC
GAM1319  LOC145899 5'  TAAAAAGCAGGTATGGT    33750      CT
                                 TAAAAA  TAGGTATGGT
                                 ||||||  ||||||||||
                                 ATTTTT  GTCCATACCA
                                    C_
GAM1319  LOC146894 3'  TACAAAAATTAGCCAGGTGTGG 33724       C___    A
            T                    TATAAAAA   TTAGGT TGGT
                                 ||||||||   |||||| ||||
                                 ATGTTTTT   GGTCCA ACCA
                                    AATC    C
GAM1319  LOC147817 3'  TACAAAAATTAGTCAGGTGTGG 33751       C___    A
            T                    TATAAAAA   TTAGGT TGGT
                                 ||||||||   |||||| ||||
                                 ATGTTTTT   AGTCCA ACCA
                                    AATC    C
GAM1319  LOC148887 5'  TACAAAAATTAGCCAGGTGTGG 33724       C___    A
            T                    TATAAAAA   TTAGGT TGGT
                                 ||||||||   |||||| ||||
                                 ATGTTTTT   GGTCCA ACCA
                                    AATC    C
GAM1319  LOC151050 5'  TATAAAAATTAGCCGGGCATGG 33752       C___ TA
            T                    TATAAAAA   T  GGTATGGT
                                 ||||||||   |  ||||||||
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                                ATATTTTT   G  CCGTACCA
                                    AATC GC
GAM1319  LOC151201 3'  TACAAAAATTAGCCAGGTGTGG 33724       C___    A
             T                   TATAAAAA   TTAGGT TGGT
                                 |||||||    |||||| ||||
                                ATGTTTTT   GGTCCA ACCA
                                    AATC    C
GAM1319  LOC151877 3'  TACAAAAATTAGCCAGGTGTGG 33724       C___    A
             T                   TATAAAAA   TTAGGT TGGT
                                 |||||||    |||||| ||||
                                ATGTTTTT   GGTCCA ACCA
                                    AATC    C
GAM1319  LOC153883 5'  CATAAAAATTAGTTAGGTGTGG 33753       C___    A
             T                   TATAAAAA   TTAGGT TGGT
                                 |||||||    |||||| ||||
                                GTATTTTT   AATCCA ACCA
                                    AATC    C
GAM1319  LOC157623 3'  TACAAAAATTAGCCAGGTGTGG 33724       C___    A
             T                   TATAAAAA   TTAGGT TGGT
                                 |||||||    |||||| ||||
                                ATGTTTTT   GGTCCA ACCA
                                    AATC    C
GAM1319  LOC158865 5'  TATAAAAACTAGCCAGGTGTGG 33754        ___    A
             T                   TATAAAAACT   TAGGT TGGT
                                 ||||||||||   ||||| ||||
                                ATATTTTTGA   GTCCA ACCA
                                     TCG    C
GAM1319  LOC199678 3'  TATAAAAACTCTGAAAATGGT  33755        A  T_
                                TATAAAAACTT GG  ATGGT
                                ||||||||||| ||  |||||
                                ATATTTTTGAG CT  TACCA
                                     A  TT
GAM1319  LOC200316 5'  TACAAAAATTAGCCAGGTGTGG 33724       C___    A
             T                   TATAAAAA   TTAGGT TGGT
                                 |||||||    |||||| ||||
                                ATGTTTTT   GGTCCA ACCA
                                    AATC    C
GAM1319  LOC222070 5'  TGAAAGACCAGAGTATGGT   33756   T   A   TA
                                A AAA ACT  GGTATGGT
                                | ||| |||  ||||||||
                                A TTT TGG  TCATACCA
                                 C   C   TC
GAM1319  LOC51193  3'  TAAAAACTTAGCGGGCATGGT  33757        ___
                                TAAAAACTTA   GGTATGGT
                                ||||||||||   ||||||||
                                ATTTTTGAAT   CCGTACCA
                                     CGC
GAM1319  LOC51580  3'  TATAAAAAAAGGTATGGT    33758        CTT
                                TATAAAAA   AGGTATGGT
                                ||||||||   |||||||||
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                                ATATTTTT  TCCATACCA
                                    T__
GAM1320 AGL     3' TCAATATTATAATAAATGA  33761          TAAAT
                                TCAATATTATGATA   ATGA
                                ||||||||||||||  ||||
                                AGTTATAATATTAT   TACT
                                      T____
GAM1320 AGL     3' TCAATATTATAATAAATGA  33761          TAAAT
                                TCAATATTATGATA   ATGA
                                ||||||||||||||  ||||
                                AGTTATAATATTAT   TACT
                                      T____
GAM1320 AGL     3' TCAATATTATAATAAATGA  33761          TAAAT
                                TCAATATTATGATA   ATGA
                                ||||||||||||||  ||||
                                AGTTATAATATTAT   TACT
                                      T____
GAM1320 AGL     3' TCAATATTATAATAAATGA  33761          TAAAT
                                TCAATATTATGATA   ATGA
                                ||||||||||||||  ||||
                                AGTTATAATATTAT   TACT
                                      T____
GAM1320 AGL     3' TCAATATTATAATAAATGA  33761          TAAAT
                                TCAATATTATGATA   ATGA
                                ||||||||||||||  ||||
                                AGTTATAATATTAT   TACT
                                      T____
GAM1320 AGL     3' TCAATATTATAATAAATGA  33761          TAAAT
                                TCAATATTATGATA   ATGA
                                ||||||||||||||  ||||
                                AGTTATAATATTAT   TACT
                                      T____
GAM1320 RAB27A   3' TCAACATTATAAATATGA   33762         TATAA
                                TCAATATTATGA   ATATGA
                                ||||||||||||  ||||||
                                AGTTGTAATATT   TATACT
                                      _____
GAM1320 SEL1L    3' TCAACATTATGAGTTTTATGA 33763         TATAAA
                                TCAATATTATGA    TATGA
                                ||||||||||||    |||||
                                AGTTGTAATACT    ATACT
                                      CAAA__
GAM1320 KIAA1999 3' TCTATATCCATCATAAATATGA 33764   A   ATGA
                                TC ATATT   TATAAATATGA
                                || |||||   ||||||||||||
                                AG TATAG   GTATTTATACT
                                  A   GTA_
GAM1320 LOC121838 5' TCAATATTATGGGATAAAATGA 33765        AT   T
             A                   TCAATATTATG  ATAAA ATGAA
                                ||||||||||  ||||| |||||
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                                AGTTATAATAC  TATTT TACTT
                                      CC    _
GAM1320  LOC157807 3'  TCAATTTACTACAATAAATATG 33766      A   GAT_
           AA                   TCAAT TTAT    ATAAATATGAA
                                ||||| ||||   ||||||||||
                                AGTTA AATG    TATTTATACTT
                                  _   ATGT
GAM1321  LOC90936  3'  CTCTTGAGGGACGGGTTGT   33769     GTC  C      C
                                CTC   GG GGACGGGT GT
                                |||   || |||||||| ||
                                GAG   TC CCTGCCCA CA
                                  AAC  _       A
GAM1322  CHEK1     3'  TTTCAAATTCAGATACTAA    33772            _
                                TTTCAAATTCAGAT TTAA
                                |||||||||||||| ||||
                                AAAGTTTAAGTCTA GATT
                                       T
GAM1322  FLJ20699  3'  TTCGGAATCACATTTAAAATTA 33773     AAAT   G
           A                    TTC    TCA ATTTAAAATTAA
                                |||    ||| ||||||||||||
                                AAG    AGT TAAATTTTAATT
                                  CCTT   G
GAM1322  KIAA1350  3'  TTTCAAATTCAGATAAAAT    33774           TT
                                TTTCAAATTCAGA  TAAAAT
                                ||||||||||||  ||||||
                                AAAGTTTAAGTCT  ATTTTA
                                       __
GAM1323  AP1M1     5'  GCGGCAGCGACGGTGGG     33777    T        A   A
                                G CGGCGGCGACG TGG G
                                | ||||||||||| ||| |
                                C GCCGTCGCTGC ACC C
                                _         C   C
GAM1323  BAALC     5'  AGGAGGCGGCGGCGGCGA     33778      T       A
                                AGGAG CGGCGGCG CGA
                                ||||| |||||||| |||
                                TCCTC GCCGCCGC GCT
                                   C       C
GAM1323  BMP3      5'  AGGAGCCGGCGGCGGAGCCGAG 33779            A___   T
           G                    AGGAGTCGGCGGCG    CGA GG
                                ||||||||||||||    ||| ||
                                TCCTCGGCCGCCGC    GCT CC
                                       CTCG  _
GAM1323  CPNE3     5'  GAAGTCGAGCGACGGTGGAGA  33780        GC      A
                                GGAGTCG  GGCGACG TGGAGA
                                |||||||  ||||||| ||||||
                                CTTCAGC  TCGCTGC ACCTCT
                                   __      C
GAM1323  EGR1      3'  AGGGGTCAGGCATATGATGGAG 33781     A  _   GCGAC
           A                    AGG GTC GGCG     GATGGAGA
                                ||| ||| ||||     ||||||||
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                                TCC CAG CCGT    CTACCTCT
                                  C  T   ATA__
GAM1323 ELAVL1   5' GGAGGCGGCGGCGGCGCGG   33782     T      A A
                                GGAG CGGCGGCG CG TGG
                                |||| |||||||| || |||
                                CCTC GCCGCCGC GC GCC
                                  C      C _
GAM1323 GARS     5' GGAGGCGGCGGCGGGCAAGGAG 33783     T      A_  T
            A                    GGAG CGGCGGCG  CGA GGAGA
                                |||| ||||||||  ||| |||||
                                CCTC GCCGCCGC  GTT CCTCT
                                  C      CC  _
GAM1323 IL12RB2  5' GGAGCTGGCGGCGAGTGAG   33784      C      CGATG
                                GGAGT GGCGGCGA    GAG
                                ||||| ||||||||    |||
                                CCTCG CCGCCGCT    CTC
                                   A       CA___
GAM1323 KCNMB4   5' GGAGTGGGCGGCGAGGGG    33785      C      CGAT
                                GGAGT GGCGGCGA   GG
                                ||||| ||||||||   ||
                                CCTCA CCGCCGCT   CC
                                   C       CC__
GAM1323 MADH7    5' AGGAGCGGCGGCGGCCCGAGG  33786      T      A__  T
                                AGGAG CGGCGGCG   CGA GG
                                ||||| ||||||||  ||| ||
                                TCCTC GCCGCCGC   GCT CC
                                  _       CGG  _
GAM1323 MAGEA9   5' AGGAGCTGGGCGATGGAG    33787      CGGC    CGA
                                AGGAGT   GGCGA   TGGAG
                                ||||||   |||||  |||||
                                TCCTCG   CCGCT   ACCTC
                                   AC__    ____
GAM1323 NFIC     3' GGATTCCTGGGACGATGGAGA  33788    G  GGC  C
                                GGA TC   GG GACGATGGAGA
                                ||| ||   || ||||||||||
                                CCT AG   CC CTGCTACCTCT
                                  A  GA_  _
GAM1323 PABPC4   5' GGAGTCGGCGGGCTTGGAGA   33789          CGACGA
                                GGAGTCGGCGG     TGGAGA
                                ||||||||||      ||||||
                                CCTCAGCCGCC     ACCTCT
                                      CGA___
GAM1323 PLCG1    5' GGGGCGGCGGCGGCACAGG    33790    A T      A  AT
                                GG G CGGCGGCG CG  GG
                                || | |||||||| ||  ||
                                CC C GCCGCCGC GT  CC
                                 C _       C  GT
GAM1323 PLXNA1   3' GGAGTCGGTGGCAACGGG    33791        C      AT
                                GGAGTCGG GGCGACG  GG
                                |||||||| |||||||  ||
```

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                                CCTCAGCC CCGTTGC  CC
                                   A      __
GAM1323  PRX      3'  AGGGTTGGCAGGTGGAG     33792     A  C     CGACGA
                                AGG GT GGCGG     TGGAG
                                ||| || |||||     |||||
                                TCC CA CCGTC     ACCTC
                                  _ A    C_____
GAM1323  PRX      3'  AGGAGCGGCGGCGGCCAGCCGG 33793      T      A_  A_
                                AGGAG CGGCGGCG  CG  TGG
                                ||||| ||||||||  ||  |||
                                TCCTC GCCGCCGC  GT  GCC
                                   _       CG  CG
GAM1323  SLC9A3R2 5'  GGGGCGGCGGCGGCGCTGG   33794    A T      A  A
                                GG G CGGCGGCG CG TGG
                                || | |||||||| || |||
                                CC C GCCGCCGC GC ACC
                                 C _       C  G
GAM1323  SMG1     5'  AGGAGGCGGCGGCGGA      33795      T      GACGAT
                                AGGAG CGGCGGC     GGA
                                ||||| |||||||     |||
                                TCCTC GCCGCCG     CCT
                                   C      _______
GAM1323  UMPK     3'  AGGGGCTGGGGTCCGATGGAGA 33796     A  C  C  CGA
                                AGG GT GG GG   CGATGGAGA
                                ||| || || ||   |||||||||
                                TCC CG CC CC   GCTACCTCT
                                  C  A  _  AG_
GAM1323  USP14    5'  GGAGGCGGCGGCGCAGGAGA   33797     T      ACGAT
                                GGAG CGGCGGCG     GGAGA
                                |||| ||||||||     |||||
                                CCTC GCCGCCGC     CCTCT
                                   C       GT___
GAM1323  YWHAH    3'  AAGAATCGGTGATGATGG     33798         CGGC  C
                                AGGAGTCGG    GA GATGG
                                |||||||||    || |||||
                                TTCTTAGCC    CT CTACC
                                      A___  A
GAM1323  20D7-FC4 3'  GGGGTTGGGGCTGAATGGAGA  33799    A  C  C   GAC
                                GG GT GG GGC   GATGGAGA
                                || || || |||   ||||||||
                                CC CA CC CCG   TTACCTCT
                                 C  A  _   AC_
GAM1323  C21orf93 3'  GGAGTCAGCGGCTGCTTGGGGA 33800           GACGA   A
                                GGAGTCGGCGGC     TGG GA
                                ||||||||||||     ||| ||
                                CCTCAGTCGCCG     ACC CT
                                       ACGA_   C
GAM1323  CACNG4   3'  GGAGGTGGCGGATGGAG     33801      TC     CGACG
                                GGAG  GGCGG     ATGGAG
                                ||||  |||||     ||||||
```

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                                CCTC  CCGCC    TACCTC
                                  CA   _____
GAM1323 CECR2    5' GGGGCGGCGGCGCGGGGG   33802   A T      A  AT
                                GG G CGGCGGCG CG  GG
                                || | |||||||| ||  ||
                                CC C GCCGCCGC GC  CC
                                 C _      _ CC
GAM1323 FASTK    5' AGGAGGCGGCGGCGGCACAGA  33803      T      A G
                                AGGAG CGGCGGCG C ATGGA
                                ||||| |||||||| | |||||
                                TCCTC GCCGCCGC G TGTCT
                                  C       C _
GAM1323 FLJ10201 3' GGAGTCAGGTGGTGAAATCTCG 33804       _  C  C  CGA__
             GA                   GGAGTC GG GG GA    TGGA
                                |||||| || || ||    ||||
                                CCTCAG CC CC CT    GCCT
                                   T  A  A  TTAGA
GAM1323 FLJ14154 5' GGAGCCGGCGGCCGCTGG    33805          GA  A
                                GGAGTCGGCGGC  CG TGG
                                ||||||||||||  || |||
                                CCTCGGCCGCCG  GC ACC
                                       __ G
GAM1323 FLJ14681 5' GGAGTTGGCGGCGAGACGTAGA 33806      C      C   G
                                GGAGT GGCGGCGA GATG AGA
                                ||||| |||||||| |||| |||
                                CCTCA CCGCCGCT CTGC TCT
                                  A       _   A
GAM1323 FLJ21156 3' GGAGTCAGGCTGGAGGTGATGG 33807       _  _ CGAC
             AGA                   GGAGTC GGC GG   GATGGAGA
                                |||||| ||| ||   ||||||||
                                CCTCAG CCG CC   CTACCTCT
                                   T  A  TCCA
GAM1323 GSA7     3' AGCAGTCCTGCTCTGGCGATGG 33808    G   G_ GGCGA
             AGA                   AG AGTC  GC    CGATGGAGA
                                || ||||  ||    |||||||||
                                TC TCAG  CG    GCTACCTCT
                                 G   GA  AGACC
GAM1323 KIAA0258 3' GGGGTCGGCTGTGACTCACCAG 33809    A    GGC   GA__
             A                    GG GTCGGC   GAC    TGGA
                                || ||||||   |||   ||||
                                CC CAGCCG   CTG   GTCT
                                 C     ACA   AGTG
GAM1323 LR8      5' GGAGGTCGGCGGTGGCGGGGA  33810     _     CGA  AT
                                GGAG TCGGCGG   CG  GGA
                                |||| |||||||   ||  |||
                                CCTC AGCCGCC   GC  CCT
                                  C      ACC  C_
GAM1323 MGC10772 5' GGAGGCGGCGGCGGCCCGG   33811     T      ACGA
                                GGAG CGGCGGCG    TGG
                                |||| ||||||||    |||
```

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                                CCTC GCCGCCGC    GCC
                                  C       CGG_
GAM1323 MGC10940 5' AGGAGGTGGCGGCGACAGCGG 33812       TC        A
                                AGGAG  GGCGGCGACG TGG
                                |||||  |||||||||| |||
                                TCCTC  CCGCCGCTGT GCC
                                   CA        C
GAM1323 MGC15437 5' AGGAGGCGGCGGCAGCGGAG   33813      T      ACGA
                                AGGAG CGGCGGCG    TGGAG
                                ||||| ||||||||    |||||
                                TCCTC GCCGCCGT    GCCTC
                                  C       C___
GAM1323 MGC21675 5' GGAGAGTGACGATGGG      33814      TCGGC  C      A
                                GGAG     GG GACGATGG G
                                ||||     || |||||||| |
                                CCTC     TC CTGCTACC C
                                  _____  A       C
GAM1323 MGC2817  5' AGGAGGCGGCGGCAGAGGAG   33815      T      AC  T
                                AGGAG CGGCGGCG  GA GGAG
                                ||||| ||||||||  || ||||
                                TCCTC GCCGCCGT  CT CCTC
                                  C       __  _
GAM1323 MGC2817  5' AGGAGGCGGCGGCGACTGAGG  33816      T        GAT
                                AGGAG CGGCGGCGAC   GG
                                ||||| ||||||||||   ||
                                TCCTC GCCGCCGCTG   CC
                                  C         ACT
GAM1323 NCX      3' GGAGCCGGCCGGTGGTGGAG   33817         _  CGACGA
                                GGAGTCGGC GG      TGGAG
                                |||||||||  ||     |||||
                                CCTCGGCCG CC      ACCTC
                                     G  ACC___
GAM1323 OSBPL3   5' AGGAGTCGGGGGGCGGGGA    33818         C    ACGAT
                                AGGAGTCGG GGCG     GGA
                                |||||||||  ||||     |||
                                TCCTCAGCC CCGC     CCT
                                     C    C____
GAM1323 PEG10    3' GGAGGCGGCGGCGGTGGTGGTG 33819     T      ACGA_______
            GTGGAG                  GAG CGGCGGCG         TGGAG
                                ||| ||||||||         |||||
                                CTC GCCGCCGC         ACCTC
                                  C       CACCACCACC
GAM1323 PTPN4    5' AGGAGCGGCGGCGGCAGCAACA 33820       __       A
            G                    AGGAGT  CGGCGGCG CGATGG
                                ||||||  |||||||| ||||||
                                TCCTCG  GCCGCCGT GTTGTC
                                   CC       C
GAM1323 RNF10    5' GGGGTCGGCGGCGGCAGCGG   33821    A        A  A
                                GG GTCGGCGGCG CG TGG
                                || |||||||||| || |||
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                                CC CAGCCGCCGC GT GCC
                                 C         C  C
GAM1323 SLC12A8   5' AAGTTGATGGTGACGATGG   33822     C GC  C
                                GAGT G  GG GACGATGG
                                |||| |  || ||||||||
                                TTCA C  CC CTGCTACC
                                  A TA  A
GAM1323 SLC2A10   5' GGACTCGGCGGCGTGCTGG   33823     G       ACGA
                                GGA TCGGCGGCG    TGG
                                ||| |||||||||    |||
                                CCT AGCCGCCGC    ACC
                                  G       ACG_
GAM1323 SMARCF1   5' AGGAGGCGGCGGCGGCGGCCGA 33824      T      A  ATG
             G                   AGGAG CGGCGGCG CG   GAG
                                ||||| |||||||| ||   |||
                                TCCTC GCCGCCGC GC   CTC
                                   C       C  CGG
GAM1323 SMARCF1   5' AGGAGGCGGCGGCGGCGGCCGA 33824      T      A  ATG
             G                   AGGAG CGGCGGCG CG   GAG
                                ||||| |||||||| ||   |||
                                TCCTC GCCGCCGC GC   CTC
                                   C       C  CGG
GAM1323 SMARCF1   5' AGGAGGCGGCGGCGGCGGCCGA 33824      T      A  ATG
             G                   AGGAG CGGCGGCG CG   GAG
                                ||||| |||||||| ||   |||
                                TCCTC GCCGCCGC GC   CTC
                                   C       C  CGG
GAM1323 USP22     5' GGGGCGGCGGCGAGGGAG    33825    A T       CGAT
                                GG G CGGCGGCGA    GGAG
                                || | |||||||||    ||||
                                CC C GCCGCCGCT    CCTC
                                 C _       C___
GAM1323 VELI1     5' GGGTTGGTAGCCAGATGGAGA  33826    A  C  CG  GAC
                                GG GT GG  GC   GATGGAGA
                                || || ||  ||   ||||||||
                                CC CA CC  CG   CTACCTCT
                                 _  A  AT  GT_
GAM1323 LOC143158 5' GGAGTCGATGGAATGGAG    33827       GC  CGAC
                                GGAGTCG  GG    GATGGAG
                                |||||||  ||    |||||||
                                CCTCAGC  CC    TTACCTC
                                    TA  _____
GAM1323 LOC148479 5' GGGGCGGCGGCGGCTGCGAGA  33828    A T       ACGA  _
                                GG G CGGCGGCG    TG GAGA
                                || | ||||||||    || ||||
                                CC C GCCGCCGC    AC CTCT
                                 C _       CG__  G
GAM1323 LOC149386 5' AGGAGTCGGTGGCCGGCAGGAG 33829          C   GA  AT_
                                AGGAGTCGG GGC  CG   GGAG
                                ||||||||| |||  ||   ||||
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                                TCCTCAGCC CCG  GC   CCTC
                                     A   __  CGT
GAM1323  LOC151127 5'  GGTAGCAGCGGCGGCGGTGGAG 33830    _ T      A  A
                                GG AG CGGCGGCG CG TGGAG
                                || || |||||||| || |||||
                                CC TC GTCGCCGC GC ACCTC
                                 A  _       C  C
GAM1323  LOC152485 5'  AGGAGCTGGCCGGTGGAG    33831       C   GGCGA  A
                                AGGAGT GGC    CG TGGAG
                                |||||| |||    || |||||
                                TCCTCG CCG    GC ACCTC
                                   A  _____  C
GAM1323  LOC153546 5'  GGGGCGGCGGCGCGGGG     33832    A T      A  AT
                                GG G CGGCGGCG CG  GG
                                || | ||||||||  ||  ||
                                CC C GCCGCCGC GC  CC
                                 C _       _  C_
GAM1323  LOC158373 5'  GGTGTCGGCGGCGCTGAGG    33833    A        AC  T
                                GG GTCGGCGGCG  GA GG
                                || ||||||||||  || ||
                                CC CAGCCGCCGC  CT CC
                                 A         GA  _
GAM1323  LOC197423 5'  AGGAGGCGGCGGCGGGCGGGGG 33834       T       A_  AT
                                AGGAG CGGCGGCG  CG  GG
                                ||||| ||||||||  ||  ||
                                TCCTC GCCGCCGC  GC  CC
                                   C       CC  CC
GAM1323  LOC220565 5'  AGGAGGCGGCGGCGGA      33795       T      GACGAT
                                AGGAG CGGCGGC     GGA
                                ||||| |||||||     |||
                                TCCTC GCCGCCG     CCT
                                   C      _______
GAM1323  LOC221184 5'  GGAGCCGGTGGCGGTGG     33835         C    ACGA
                                GGAGTCGG GGCG    TGG
                                |||||||| ||||    |||
                                CCTCGGCC CCGC    ACC
                                     A   C___
GAM1323  LOC221250 5'  GGCGGCGGCGGCGGCGGTGGAG 33836     AGT       A  A
                                GG   CGGCGGCG CG TGGAG
                                ||   |||||||| || |||||
                                CC   GCCGCCGC GC ACCTC
                                 GCC       C  C
GAM1323  LOC222133 3'  AGGGGTTGGGGTGAAGTGGGGA 33837     A  C  C  C  CGA   A
                                AGG GT GG GG GA   TGG GA
                                ||| || || || ||   ||| ||
                                TCC CA CC CC CT   ACC CT
                                  C  A  _  A  TC_   C
GAM1323  LOC51161  3'  AGCGGACAGTGACGGTGGAGA  33838     C    C    A
                                AGT GGCGG GACG TGGAGA
                                ||| ||||| |||| ||||||
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                                TCG CTGTC CTGC ACCTCT
                                  C    A   C
GAM1323  LOC91272  5'  GGGGCGGCGGCGGCGAAGG   33839    A T      A   T
                                GG G CGGCGGCG CGA GG
                                || | |||||||| ||| ||
                                CC C GCCGCCGC GCT CC
                                 C _      C   T
GAM1324  C20orf67  5'  GCTCGACCGCCCGTTTTG    33842     CT
                                GCTT  TCGCCCGTTTTG
                                ||||  ||||||||||||
                                CGAG  GGCGGGCAAAAC
                                  CT
GAM1324  LOC122726 5'  TGTTGCTTGTTCCCATTTTG   33843    C   CTTCG
                                TGT GCTT    CCCGTTTTG
                                ||| ||||    |||||||||
                                ACA CGAA    GGGTAAAAC
                                  A   CAA__
GAM1325  DKK1      3'  AATAGGCAGTGCAGCACCT   31899      A ___ A
                                AATAGG CA   CA CACCT
                                |||||| ||   || |||||
                                TTATCC GT   GT GTGGA
                                   _ CAC  C
GAM1325  EGLN1     5'  AATAGAACACTTGCAACAC   31900        ____
                                AATAGGACAC    AACAC
                                ||||||||||    |||||
                                TTATCTTGTG    TTGTG
                                      AACG
GAM1325  KPNB2     3'  CAGTGACGGCAACACCTC    31901    _  A_
                                TAG GAC  CAACACCTC
                                ||| |||  |||||||||
                                GTC CTG  GTTGTGGAG
                                  A   CC
GAM1325  MCM6      3'  CAATAGGACAGCACATACCT  31902        _ AC_
                                TAATAGGACA CA   ACCT
                                |||||||||| ||   ||||
                                GTTATCCTGT GT   TGGA
                                      C  GTA
GAM1325  SMN1      3'  TAAGACACTCTAACACTTC   31903        ___    C
                                TAGGACAC   AACAC TC
                                ||||||||   ||||| ||
                                ATTCTGTG   TTGTG AG
                                     AGA     A
GAM1325  SMN1      3'  TAAGACACTCTAACACTTC   31903       ___    C
                                TAGGACAC   AACAC TC
                                ||||||||   ||||| ||
                                ATTCTGTG   TTGTG AG
                                     AGA     A
GAM1325  SP4       5'  TAACAGGACAAACCCTC     31904        C   A
                                TAATAGGACA AAC CCTC
                                |||||||||| ||| ||||
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                                ATTGTCCTGT TTG GGAG
                                      _  _
GAM1325 C1orf22  3' CAATGAAAGGCAACACCTC  31905    AG  CA
                                TAAT  GA  CAACACCTC
                                ||||  ||  |||||||||
                                GTTA  TT  GTTGTGGAG
                                  CT  CC
GAM1325 FLJ14451 3' TAAGAGGACACAGCCCCTC  31906    T      ACA
                                TAA AGGACACA   CCTC
                                ||| ||||||||   ||||
                                ATT TCCTGTGT   GGAG
                                  C       CGG
GAM1325 KIAA0321 3' TAACAGGACCAAAACTTC   31907        A  C  C
                                TAATAGGAC CAA AC TC
                                ||||||||| ||| || ||
                                ATTGTCCTG GTT TG AG
                                      _  T  A
GAM1325 KIAA0893 3' TAACACCACCCAACACCTC  31908     GG  A
                                TAATA  AC CAACACCTC
                                |||||  || |||||||||
                                ATTGT  TG GTTGTGGAG
                                   GG  G
GAM1325 KIAA1102 3' TAAAACAGCAAACACCTC   31909       _  _
                                TAGGACA CAA CACCTC
                                ||||||| ||| ||||||
                                ATTTTGT GTT GTGGAG
                                    C  T
GAM1325 KIAA1712 3' AACAAAACACAACACCTC   31910
                                AATAGGACACAACACCTC
                                ||||||||||||||||||
                                TTGTTTTGTGTTGTGGAG

GAM1325 MGC3184  3' AATACAACACAACACTTC   31911     G        C
                                AATA GACACAACAC TC
                                |||| ||||||||||  ||
                                TTAT TTGTGTTGTG AG
                                  G        A
GAM1325 PDZD2    5' TAGAGACACAAGCATCTC   31912    _     _ C
                                TAG GACACAA CA CTC
                                ||| ||||||| || |||
                                ATC CTGTGTT GT GAG
                                  T      C  A
GAM1325 LOC124961 3' TAATAAGATACAATGCCTC  31913        C   CA
                                TAATAGGA ACAA  CCTC
                                ||||||||  ||||  ||||
                                ATTATTCT TGTT  GGAG
                                     A   AC
GAM1325 LOC158062 5' TAGAGTCACCAAACACCTC  31914    _ A  __
                                TAG G CAC  AACACCTC
                                ||| | |||  ||||||||
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                                ATC C GTG  TTGTGGAG
                                  T A   GT
GAM1325  LOC222662 5'  TAATAGGACAAGGACAACCT   31915          CA_  _
                                TAATAGGACA   ACA CCT
                                ||||||||||   ||| |||
                                ATTATCCTGT   TGT GGA
                                     TCC   T
GAM1326  BLK      3'  CCAGTCTGGCTTCTGTAGC   33847     CACCA      C
                                CCAG    GCTTCTGT GGT
                                ||||    |||||||| |||
                                GGTC    CGAAGACA TCG
                                  AGAC_      _
GAM1326  COL17A1  3'  CCAGCATCAGGTTTTCTGT   33848      C   C__
                                CCAGCA CAG   TTCTGT
                                |||||| |||   ||||||
                                GGTCGT GTC   AAGACA
                                   A   CAA
GAM1326  COL17A1  3'  CCAGCATCAGGTTTTCTGT   33848      C   C__
                                CCAGCA CAG   TTCTGT
                                |||||| |||   ||||||
                                GGTCGT GTC   AAGACA
                                   A   CAA
GAM1326  CYP4A11  3'  CAGCACAGAGCTTGGTGT    33849      C_    CTGTC
                                CAGCAC  AGCTT    GGTGT
                                ||||||  |||||    |||||
                                GTCGTG  TCGAA    CCACA
                                   TC    _____
GAM1326  DAPP1    3'  CAGCATCTGCTTCTGATTTGT  33850      CCA      TCGG
                                CAGCA   GCTTCTG    TGT
                                |||||   |||||||    |||
                                GTCGT   CGAAGAC    ACA
                                  AGA      TAA_
GAM1326  FSTL3    3'  CCAGCACCTGGCTGGTGT    33851        A_   TCTGTC
                                CCAGCACC  GCT     GGTGT
                                ||||||||  |||     |||||
                                GGTCGTGG  CGA     CCACA
                                     AC  _______
GAM1326  FUS1     3'  GCACCAGCCTTAGGGTGT    33852         CTGTC
                                GCACCAGCTT    GGTGT
                                ||||||||||    |||||
                                CGTGGTCGGA    CCACA
                                      ATC__
GAM1326  HOXD4    5'  CCAGCGCCGGCTGCTTCTAGTC 33853       A  A___    _
                                CCAGC CC    GCTTCT GTC
                                ||||| ||    |||||| |||
                                GGTCG GG    CGAAGA CAG
                                  C  CCGA     T
GAM1326  IHPK1    3'  GCAATGGCTGAAATCGGTGTC  33854     CCA   TCT
                                GCA   GCT   GTCGGTGTC
                                |||   |||   |||||||||
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                                CGT  CGA  TAGCCACAG
                                  TAC  CTT
GAM1326 KCNA7   5' CCAGCCCGGTGTCCGGTGT  33855      C_  _
                                CCAGCTT  TGTC GGTGT
                                |||||||  |||| |||||
                                GGTCGGG  ACAG CCACA
                                    CC   G
GAM1326 RBM3    5' CCAGTGCCTGCTCGTCGGTGT 33856    CA A   CT
                                CCAG  CC GCTT  GTCGGTGT
                                ||||  || ||||  ||||||||
                                GGTC  GG CGAG  CAGCCACA
                                  AC A   __
GAM1326 RGS2    3' ACCAGCTTCTCCTAGTC    33857        G  GGT
                                ACCAGCTTCT TC   GTC
                                |||||||||| ||   |||
                                TGGTCGAAGA GG   CAG
                                      _ AT_
GAM1326 VANGL2  5' CAGCACCGGCTTCTTTAGGC  33858      A    GTC
                                CAGCACC GCTTCT   GGT
                                ||||||| ||||||   |||
                                GTCGTGG CGAAGA   CCG
                                    C     AAT
GAM1326 VEGF    3' CCAGGGCTGGGTTTGTCGGTGT 33859    CACCA  TC___
                                CCAG    GCT    TGTCGGTGT
                                ||||    |||    |||||||||
                                GGTC    CGA    ACAGCCACA
                                  C____  CCCAA
GAM1326 ZNF195  3' CAGTGTCATTTCTGAACGTGTC 33860    CAC  GC    TCG
                                CAG   CA  TTCTG   GTGTC
                                |||   ||  |||||   |||||
                                GTC   GT  AAGAC   CACAG
                                  ACA  A_    TTG
GAM1326 FLJ10738 3' GCTCCAGCTTCCCACTTGTC  33861    A       GTCGG
                                GC CCAGCTTCT    TGTC
                                || |||||||||    ||||
                                CG GGTCGAAGG    ACAG
                                 A       GTGA_
GAM1326 FLJ14001 5' GCGCCCGGTTCGCTCCGGTGTC 33862    A  AGC   TG_
                                GC CC   TTC   TCGGTGTC
                                || ||   |||   ||||||||
                                CG GG   AAG   GGCCACAG
                                 C  GCC   CGA
GAM1326 FLJ20308 3' CCAGCATCAGCCTCTGTC    33863      C
                                CCAGCA CAGCTTCTGTC
                                |||||| ||||||||||
                                GGTCGT GTCGGAGACAG
                                   A
GAM1326 FLJ21432 3' GCTACTTCTGTTGGTGT    33864    ACCA      C
                                GC   GCTTCTGT GGTGT
                                ||   |||||||| |||||
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                                CG    TGAAGACA CCACA
                                 A___       A
GAM1326  FLJ22393  3'  CCGCGCTGGCTTCTGTGAGGC  33865    A_  ACCA      C_
                                CC  GC    GCTTCTGT  GGT
                                ||  ||    ||||||||  |||
                                GG  CG    CGAAGACA  CCG
                                 CG  AC__       CT
GAM1326  KIAA0290  5'  CCAGTGCCTGTCTGGTGT    33866     CT     _
                                CCAG  TCTGTC GGTGT
                                ||||  |||||| |||||
                                GGTC  GGACAG CCACA
                                  AC     A
GAM1326  KIAA0295  3'  CCAGCACCAGCTTGCTCCCAGT 33867            _  G
              GTC                   CCAGCACCAGCTT CT TCGGTGTC
                                ||||||||||||| || ||||||||
                                GGTCGTGGTCGAA GA GGTCACAG
                                       C  G
GAM1326  KIAA1096  3'  CCAGCACCAGTTATCTTCAGT  33868          CT_  G
                                CCAGCACCAG   TCT TCGGT
                                ||||||||||   ||| |||||
                                GGTCGTGGTC   AGA AGTCA
                                      AAT  _
GAM1326  KIAA1115  3'  CCAGCCCAGTTCGGTG      33869       A   CTTCTG
                                CCAGC CCAG     TCGGTG
                                ||||| ||||     ||||||
                                GGTCG GGTC     AGCCAC
                                  _    A_____
GAM1326  KIAA1644  3'  AGCACCAGCTGTTGGC      33870          TCT  C
                                AGCACCAGCT   GT GGT
                                ||||||||||   || |||
                                TCGTGGTCGA   CA CCG
                                      ___  A
GAM1326  MGC13033  5'  CAGCACCAGATTCTCCAGT    33871         C    G
                                CAGCACCAG TTCT TCGGT
                                ||||||||| |||| |||||
                                GTCGTGGTC AAGA GGTCA
                                      T   _
GAM1326  NMP200    5'  CCGGGACTAGCTTCTGAGCCTC 33872    AGC  C       TC   G
                                CC   AC AGCTTCTG  GGT TC
                                ||   || ||||||||  ||| ||
                                GG   TG TCGAAGAC  TCG AG
                                 CCC  A       __   G
GAM1326  NUP54     5'  CCAGTACTAGTTCCCGTTGT   33873     C  C  C     CG
                                CCAG AC AG TTCTGT  GT
                                |||| || || ||||||  ||
                                GGTC TG TC AGGGCA  CA
                                  A  A  A     A_
GAM1326  SIMRP7    3'  CCAGCTCCAGCTGGCTGGTGTC 33874       A     TCT  C
                                CCAGC CCAGCT   GT GGTGTC
                                ||||| ||||||   || ||||||
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                                GGTCG GGTCGA   CG CCACAG
                                  A     C__  A
GAM1326  SMT3H2   3'  GCATCAGTATCAGTCTGTC   33875    C   CT  T   GG
                                GCA CAG  TC GTC  TGTC
                                ||| |||  || |||  ||||
                                CGT GTC  AG CAG  ACAG
                                 A   AT  T   __
GAM1326  Spir-1   5'  ACCGTCAGCTTCCACCGTGT   33876    AC_     TG   G
                                GC   CAGCTTC  TCG TGT
                                ||   |||||||  ||| |||
                                TG   GTCGAAG  GGC ACA
                                 GCA      GT   _
GAM1326  SSAT2    3'  CAGCATCAGTGTCTGTGG    33877      C   CT    C
                                CAGCA CAG  TCTGT GG
                                ||||| |||  ||||| ||
                                GTCGT GTC  AGACA CC
                                  A   AC    _
GAM1326  LOC118742 3'  CCAGCATCCGCTTTTTCTTGTC 33878       _ A    CTG  GG
                                CCAGCA CC GCTT   TC  TGTC
                                |||||| || ||||   ||  ||||
                                GGTCGT GG CGAA   AG  ACAG
                                  A  _    AA_  A_
GAM1326  LOC124997 3'  CCAGGCCAGCTTCCCTGTC   33879      CA       __
                                CCAG  CCAGCTTCT  GTC
                                ||||  |||||||||  |||
                                GGTC  GGTCGAAGG  CAG
                                  C_       GA
GAM1326  LOC129676 5'  CCAGCGCCGGCTTATGCGGC   33880      A  A    C  T
                                CCAGC CC GCTT TG CGGT
                                ||||| || |||| || ||||
                                GGTCG GG CGAA AC GCCG
                                  C  C    T  _
GAM1326  LOC144347 3'  CAGTGCTGGCTTCTGGGGTGT  33881     CACCA      TC
                                CAG    GCTTCTG  GGTGT
                                |||    |||||||  |||||
                                GTC    CGAAGAC  CCACA
                                 ACGAC      C_
GAM1326  LOC145693 5'  CCAGTGCCAGCCTTTGCC    33882      CA      C
                                CCAG  CCAGCTT TGTC
                                ||||  ||||||| ||||
                                GGTC  GGTCGGA ACGG
                                  AC      A
GAM1326  LOC147063 3'  GCCCAGCTTCTCAGCAC     33883    A       TG    TG
                                GC CCAGCTTC  TCGG  T
                                || ||||||||  ||||  |
                                CG GGTCGAAG  AGTC  G
                                 _       __    GT
GAM1326  LOC148413 3'  CCAGCCTCAGCTTCCCTATGTC 33884       AC       GTCG
                                CCAGC  CAGCTTCT    GTGTC
                                |||||  ||||||||    |||||
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                                GGTCG  GTCGAAGG    TACAG
                                  GA       GA__
GAM1326  LOC151325 3'  CAGTCTAGCTTCTGTGGAAGTC 33885     CACC        C  T_
                                CAG    AGCTTCTGT GG  GTC
                                |||    ||||||||| ||  |||
                                GTC    TCGAAGACA CC  CAG
                                  AGA_        _  TT
GAM1326  LOC151475 5'  CCAGCACCAGTTTTTGAGT    33886          C  C  TC
                                CCAGCACCAG TT TG  GGT
                                |||||||||| || ||  |||
                                GGTCGTGGTC AA AC  TCA
                                      A  A  __
GAM1326  LOC158056 5'  CCAGCGCCAGTGTGTG      33887       A    CTTC   CG
                                CCAGC CCAG    TGT  GTG
                                ||||| ||||    |||  |||
                                GGTCG GGTC    ACA  CAC
                                  C   _____  __
GAM1326  LOC196485 3'  CCGGCACCGGCCTCTGAGT    33888    A    A      TC
                                CC GCACC GCTTCTG  GGT
                                || ||||| |||||||  |||
                                GG CGTGG CGGAGAC  TCA
                                 C    C      __
GAM1326  LOC219653 3'  CCAGCATCATTTTCTGAGGAT  33889       C  GC     TC
                                CCAGCA CA  TTCTG  GGT
                                |||||| ||  |||||  |||
                                GGTCGT GT  AAGAC  CTA
                                    A  AA    TC
GAM1326  LOC219731 5'  CAGCACCGGCGAAGTTGGTGTC 33890        A  TTCT  C
                                CAGCACC GC    GT GGTGTC
                                ||||||| ||    || ||||||
                                GTCGTGG CG    CA CCACAG
                                    C  CTT_  A
GAM1326  LOC219894 3'  TAAGCACCAGTTGGTTTGGTGT 33891    C       CTTCTGTC
            C                    C AGCACCAG       GGTGTC
                                | ||||||||       ||||||
                                A TCGTGGTC       CCACAG
                                 T       AACCAAA_
GAM1326  LOC221354 3'  CCGGCACCGGCCTCTGAGT    33888    A    A      TC
                                CC GCACC GCTTCTG  GGT
                                || ||||| |||||||  |||
                                GG CGTGG CGGAGAC  TCA
                                 C    C      __
GAM1326  LOC254228 3'  CCAGTACTGCTTTGGACAGTGT 33892      C  CA    CTGT
            C                    CCAG AC  GCTT    CGGTGTC
                                |||| ||  ||||   |||||||
                                GGTC TG  CGAA    GTCACAG
                                  A  A_    ACCT
GAM1326  LOC257476 3'  GCAATGGCTGAAATCGGTGTC  33854     CCA   TCT
                                GCA   GCT   GTCGGTGTC
                                |||   |||   |||||||||
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                                CGT   CGA   TAGCCACAG
                                  TAC   CTT
GAM1326 LOC90826 3' ACCAGCTTTTAAATGT     33893        C  TC
                                ACCAGCTT TG  GGTGT
                                |||||||| ||  |||||
                                TGGTCGAA AT  TTACA
                                    A  __
GAM1326 LOC90906 5' AGCACCAGCTGTAACCAAGTGT 33894          TCTG  _
             C                   AGCACCAGCT    TCG GTGTC
                                ||||||||||    ||| |||||
                                TCGTGGTCGA    GGT CACAG
                                      CATT   T
GAM1327 C11orf25 5' AGGGGTGGGCGTTGAGCGG   33897    A  AT   CGT   T
                                AGG GT  GCGT   TGGG CGG
                                ||| ||  ||||   |||| |||
                                TCC CA  CGCA   ACTC GCC
                                  C  CC   ___   _
GAM1327 FLJ10661 3' AGGGGTTGTTTTTGGGTCGG  33898    A  ATGC  CG
                                AGG GT    GT  TTGGGTCGG
                                ||| ||    ||  |||||||||
                                TCC CA    CA  AACCCAGCC
                                  C  A___  AA
GAM1327 FLJ23375 3' AGGGGTAGTGAGGGTCGG    33899    A   TGC  CGTT
                                AGG GTA   GT    GGGTCGG
                                ||| |||   ||    |||||||
                                TCC CAT   CA    CCCAGCC
                                  C   ___  CT__
GAM1327 KIAA0469 3' AGGGGTGTGCGCCGCGTGGG  33900     A  A      _
                                AGG GT TGCGTCGT TGGG
                                ||| || |||||||| ||||
                                TCC CA ACGCGGCG ACCC
                                  C  C       C
GAM1327 KIAA0892 3' AGTGGTGTGCAGGGGTCGG   33901    GA  A   TCGTT
                                AG  GT TGCG    GGGTCGG
                                ||  || ||||    |||||||
                                TC  CA ACGT    CCCAGCC
                                 AC  C   C____
GAM1327 MGC16279 3' GGAGGGGTTGTTGTTGGGTCGG 33902      TATGC  C
                                GGAG    GT GTTGGGTCGG
                                ||||    || ||||||||||
                                CCTC    CA CAACCCAGCC
                                  CCCAA  A
GAM1327 P2RX1    3' AGGGTGTGTGGGGTCG      33903     A  ATGC  C  T
                                AGG GT    GT GT GGGTCG
                                ||| ||    || || ||||||
                                TCC CA    CA CA CCCAGC
                                  _  _____  _  C
GAM1327 PRDM12   3' GGAGTGTGTGTGTTGGA     33904      A  C  C
                                GGAGT TG GT GTTGGG
                                ||||| || || ||||||
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                                CCTCA AC CA CAACCT
                                  C  A  _
GAM1327  SLC5A7   5'  GGAGGGTGCGGGGTGGGTCGG  33905     TA   TC  T
                                GGAG  TGCG  GT GGGTCGG
                                ||||  ||||  || |||||||
                                CCTC  ACGC  CA CCCAGCC
                                  CC   CC  _
GAM1327  LOC146745 5'  AGGAGTACTGCGTGGGTCGG  33906       _   CGTT
                                AGGAGTA TGCGT   GGGTCGG
                                ||||||| |||||   |||||||
                                TCCTCAT ACGCA   CCCAGCC
                                   G   ____
GAM1327  LOC148753 3'  GGGTGTGTGTGCGGGTCGG   33907   A  A  C  C  T
                                GG GT TG GT GT GGGTCGG
                                || || || || || |||||||
                                CC CA AC CA CG CCCAGCC
                                 _  C  A  _  _
GAM1327  LOC149721 3'  GGAGCATGCGTTTGAATTTGGA 33908         CG    C_
                                GGAGTATGCGT  TTGGGT  GGA
                                ||||||||||  ||||||  |||
                                CCTCGTACGCA  AACTTA  CCT
                                      __    AA
GAM1327  LOC157450 3'  GGAGGGGTTGTTGTTGGGTCGG 33902     TATGC  C
                                GGAG    GT GTTGGGTCGG
                                ||||    || ||||||||||
                                CCTC    CA CAACCCAGCC
                                  CCCAA  A
GAM1327  LOC196484 5'  GGAGGGGTTGTTGTTGGGTCGG 33902     TATGC  C
                                GGAG    GT GTTGGGTCGG
                                ||||    || ||||||||||
                                CCTC    CA CAACCCAGCC
                                  CCCAA  A
GAM1327  LOC201243 5'  AGGAGTACTGCGTGGGTCGG  33906       _   CGTT
                                AGGAGTA TGCGT   GGGTCGG
                                ||||||| |||||   |||||||
                                TCCTCAT ACGCA   CCCAGCC
                                   G   ____
GAM1327  LOC220073 5'  GGAGGGGTTGTTGTTGGGTCGG 33902     TATGC  C
                                GGAG    GT GTTGGGTCGG
                                ||||    || ||||||||||
                                CCTC    CA CAACCCAGCC
                                  CCCAA  A
GAM1327  LOC91069  3'  GGAGGGGTTGTTGTTGGGTCGG 33902     TATGC  C
                                GGAG    GT GTTGGGTCGG
                                ||||    || ||||||||||
                                CCTC    CA CAACCCAGCC
                                  CCCAA  A
GAM1328  ATSV     3'  CCGACCGACCAGGATACC    33911    _     AA
                                CTG CCGGCCA  ATACC
                                ||| |||||||  |||||
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                                GGC GGCTGGT  TATGG
                                  T      CC
GAM1328  EPHB2    3'  CCTGTGACCAAAATACC     33912      CC
                                TCTG  GGCCAAAATACC
                                ||||  ||||||||||||
                                GGAC  CTGGTTTTATGG
                                  A_
GAM1328  EPHB2    3'  CCTGTGACCAAAATACC     33912      CC
                                TCTG  GGCCAAAATACC
                                ||||  ||||||||||||
                                GGAC  CTGGTTTTATGG
                                  A_
GAM1328  FZD3     3'  TCTATTAGCTAAAATACC    33913      CC  C
                                TCTG  GGC AAAATACC
                                ||||  ||| ||||||||
                                AGAT  TCG TTTTATGG
                                  AA  A
GAM1328  JRK      3'  TCTGAGCCAAAATGCC      33914      CC       A
                                TCTG  GGCCAAAAT CC
                                ||||  ||||||||| ||
                                AGAC  TCGGTTTTA GG
                                  __       C
GAM1328  JRK      3'  GCCAAAATGCCAAAATACC   33915      _____
                                GCCG   GCCAAAATACC
                                ||||   ||||||||||
                                CGGT   CGGTTTTATGG
                                  TTTA
GAM1328  NR2C2    3'  TGCACATACCAAAATACC    33916      _ _
                                TGC CG GCCAAAATACC
                                ||| || ||||||||||
                                ACG GT TGGTTTTATGG
                                  T  A
GAM1328  ACTR2    3'  CCTGCCAAATCAAAGTAC    33917        C_   A
                                TCTGCCGG  CAAA TAC
                                ||||||||  |||| |||
                                GGACGGTT  GTTT ATG
                                     TA   C
GAM1328  CBCIP2   3'  TCTGCCAGCCACGCATGCC   33918          AA_  A
                                TCTGCCGGCCA   AT CC
                                ||||||||||   || ||
                                AGACGGTCGGT   TA GG
                                      GCG  C
GAM1328  FLJ23563 3'  TCTGTGCTCAAAATACC     33919      CCG  _
                                TCTG   GC CAAAATACC
                                ||||   || |||||||||
                                AGAC   CG GTTTTATGG
                                  A__  A
GAM1328  KIAA1909 5'  TCTACCAACAGCAAGATAC   33920          __   A
                                TCTGCCGGC  CAA ATAC
                                |||||||||  ||| ||||
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                                AGATGGTTG  GTT TATG
                                     TC   C
GAM1328  LPAAT-delta 3'  CCTGCAGCCTAAAATACC    33921      C   _
                                TCTGC GGCC AAAATACC
                                ||||| |||| ||||||||
                                GGACG TCGG TTTTATGG
                                  _   A
GAM1328  PSR      3'  TCTACCAGCAATACC       33922         CAA
                                TCTGCCGGC   AATACC
                                |||||||||   ||||||
                                AGATGGTCG   TTATGG
                                    ___
GAM1328  LOC144266 5'  TCTGCCAGCCACACC       33923          AAA
                                TCTGCCGGCCA   TACC
                                ||||||||||   ||||
                                AGACGGTCGGT   GTGG
                                    ___
GAM1328  LOC151248 5'  CCTACAGGTTAAAATACC    33924      C  CC
                                TCTGC GG  AAAATACC
                                ||||| ||  ||||||||
                                GGATG CC  TTTTATGG
                                   T  AA
GAM1328  LOC157507 3'  CTGACAAGCTAAAATACC    33925     _ C   C
                                CTG C GGC AAAATACC
                                ||| | ||| ||||||||
                                GAC G TCG TTTTATGG
                                  T T   A
GAM1328  LOC200010 3'  TCTGCCCAAAATACC       33926       GGC
                                TCTGCC   CAAAATACC
                                ||||||   |||||||||
                                AGACGG   GTTTTATGG
                                   ___
GAM1328  LOC91355  5'  TCTCCTGGCCACACACC     33927     G _    AA
                                TCT CC GGCCA  ATACC
                                ||| || |||||  |||||
                                AGA GG CCGGT  TGTGG
                                  _ A    G_
GAM1329  DNMT3B    3'  TGCCGGGTAAAAGACATATACA 33930         T  _    G
                                TGCCGGGT AAA ACATA ACA
                                |||||||| ||| ||||| |||
                                ACGGCCCA TTT TGTAT TGT
                                     T  C    A
GAM1329  LANCL1    3'  AGCTAAAAGCATAGGCACA   33931         _    A
                                GGTTAAAA CATAG CACA
                                |||||||| ||||| ||||
                                TCGATTTT GTATC GTGT
                                     C    C
GAM1329  NMI       3'  CCGGGTTAAAAAGCTATAG   33932          C___
                                CCGGGTTAAAA    ATAG
                                ||||||||||    ||||
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                                GGCCCAATTTT   TATC
                                      TCGA
GAM1329 UTY      3' TGCAGGGTTAAAATACAA    33933    C       C
                                TGC GGGTTAAAA ATAG
                                ||| ||||||||| ||||
                                ACG CCCAATTTT TGTT
                                  T       A
GAM1329 FLJ10079 3' TGCCGGGCTGCAGGCAC     33934        AAAACA  A
                                TGCCGGGTT     TAG CAC
                                |||||||||     ||| |||
                                ACGGCCCGA     GTC GTG
                                      C_____  C
GAM1329 FLJ10700 3' GGATCAATATAGACACAA    33935       AAC
                                GGGTTAA   ATAGACACAA
                                |||||||   ||||||||||
                                CCTAGTT   TATCTGTGTT
                                    A__
GAM1329 FLJ21240 3' GCTGGGTTAGGTAAACACA   33936    C    AAACA
                                GC GGGTTA     TAGACACA
                                || ||||||     ||||||||
                                CG CCCAAT     ATTTGTGT
                                 A     CC___
GAM1329 NFAT5    3' AGCTAAAAACATAGATGCAA   33937        _     CA
                                GGTTAAAA CATAGA  CAA
                                |||||||| ||||||  |||
                                TCGATTTT GTATCT  GTT
                                     T     AC
GAM1329 VPS35    3' TGCTGGGTAAAACACATCACA  33938    C   T      GA
                                TGC GGGT AAAACATA  CACA
                                ||| |||| ||||||||  ||||
                                ACG CCCA TTTTGTGT  GTGT
                                  A   _       A_
GAM1329 LOC144584 3' TGCTGGGTAAAACACATCACA  33938    C   T      GA
                                TGC GGGT AAAACATA  CACA
                                ||| |||| ||||||||  ||||
                                ACG CCCA TTTTGTGT  GTGT
                                  A   _       A_
GAM1329 LOC221683 5' CCGGGTTACAGGCACA     33939       AAAAC   A
                                CCGGGTT     ATAG CACA
                                |||||||     |||| ||||
                                GGCCCAA     TGTC GTGT
                                      _____    C
GAM1330 FLJ13611  3' TTCATTAATTATTACTCAATTT 33942        CAA_
             T                   TTCATTAAT    GCTTAATTTT
                                 |||||||||    ||||||||||
                                 AAGTAATTA    TGAGTTAAAA
                                      ATAA
GAM1330 PRO0097   3' ACTTCACTAGCAATTTTAATTT 33943        AT   GC
             T                   ACTTCATTA  CAA  TTAATTTT
                                 |||||||||  |||  ||||||||
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                                TGAAGTGAT  GTT  AATTAAAA
                                    C_   AA
GAM1330  RBBP1    3'  ACTTATTAATCAGCTTA     33944      C       A
                                ACTT ATTAATCA GCTTA
                                |||| |||||||| |||||
                                TGAA TAATTAGT CGAAT
                                  _       _
GAM1330  RBBP1    3'  ACTTATTAATCAGCTTA     33944      C       A
                                ACTT ATTAATCA GCTTA
                                |||| |||||||| |||||
                                TGAA TAATTAGT CGAAT
                                  _       _
GAM1331  CENTD1   5'  AAGTTTCTTAAAATGTTATTTT 33947            ACAA
                                AAGTTTCTTAAAA    TATTTT
                                ||||||||||||    ||||||
                                TTCAAAGAATTTT    ATAAAA
                                      ACA_
GAM1331  DSC3     3'  CAAGTTTCTTTAAAAGCAA   33948          A   _
                                CAAGTTTCTT AAAA CAA
                                |||||||||| ||||| |||
                                GTTCAAAGAA TTTT GTT
                                      A   C
GAM1331  DSC3     3'  CAAGTTTCTTTAAAAGCAA   33948          A   _
                                CAAGTTTCTT AAAA CAA
                                |||||||||| ||||| |||
                                GTTCAAAGAA TTTT GTT
                                      A   C
GAM1331  PTPRB    3'  CAAGTTTTTAAAAACAA     33949        C
                                CAAGTTT TTAAAAACAA
                                |||||||| ||||||||||
                                GTTCAAA AATTTTTGTT
                                  _
GAM1331  ZNF217   3'  AGTTTCTTAATAAAATATTTT  33950          A  C
                                AGTTTCTTAA AA AATATTTT
                                |||||||||| || ||||||||
                                TCAAAGAATT TT TTATAAAA
                                      A  _
GAM1331  MUF1     5'  CAAGTCTCTTAGGAGCTACTAT 33951           AAAACAA_
            TTT                   CAAGTTTCTTA       TATTTT
                                ||||||||||        ||||||
                                GTTCAGAGAAT       ATAAAA
                                      CCTCGATG
GAM1332  EGFL5    3'  GAGTATTGCTTTAATGGTCAAT 33954     C       TAAA_
            TT                    GAG ATTGCTTTA    CAATTT
                                |||  |||||||||    ||||||
                                CTC TAACGAAAT    GTTAAA
                                  A        TACCA
GAM1332  FLJ12788 3'  GCCTAAACCATAAACAATTTT  33955    A   CT
                                GC TTG  TTATAAACAATTTT
                                ||  |||  ||||||||||||||
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                                CG GAT  GGTATTTGTTAAAA
                                 _  TT
GAM1332  LAT1-3TM  3'  GAGCATTGCTTGATAAACA   33956          T
                                GAGCATTGCTT ATAAACA
                                |||||||||||  |||||||
                                CTCGTAACGAA TATTTGT
                                      C
GAM1332  LOC196424 3'  AAGCATTTAAACAATT      33957        GCTTTA
                                GAGCATT     TAAACAATT
                                |||||||     |||||||||
                                TTCGTAA     ATTTGTTAA
                                      _____
GAM1333  HMGB3     3'  TATGTACAACTTTGATACAGTT 33960      T       A  T
           T                     TATGT CAACTTTGA AT GTTT
                                |||||  |||||||||  ||  ||||
                                ATACA GTTGAAACT TG CAAA
                                   T       A  T
GAM1333  DKFZP761C169 3'  GTTCAGGAAATTGTTT      33961      ACTTT
                                GTTCA    GAAATTGTTT
                                |||||    ||||||||||
                                CAAGT    CTTTAACAAA
                                  C____
GAM1333  FLJ10381  3'  TATGTTCAAAATAAAGTTGTTT 33962        CTT    A
           T                     TATGTTCAA   TGAA TTGTTTT
                                |||||||||   ||||  |||||||
                                ATACAAGTT   ATTT AACAAAA
                                     TT_   C
GAM1333  MGC22014  3'  GTTCAACTTCCTGTTT      33963         GAAA
                                GTTCAACTTT    TTGTTT
                                ||||||||||    ||||||
                                CAAGTTGAAG    GACAAA
                                      ____
GAM1334  TERF2     3'  TACAGATTACCAGGGATTTAAA 33966      TTG    AA
           T                     TATA   TACCA  GATTTAAAT
                                ||||   |||||  |||||||||
                                ATGT   ATGGT  CTAAATTTA
                                  CTA    CC
GAM1334  STK3      3'  TTGTACCAAACATCAAAAATC  33967         G   T_
                                TTGTACCAAA ATT  AAATC
                                ||||||||||  |||  |||||
                                AACATGGTTT TAG  TTTAG
                                     G   TT
GAM1334  LOC92935  3'  TATATTGTATTAAAGATC    33968         CC
                                TATATTGTA  AAAGATT
                                |||||||||  |||||||
                                ATATAACAT  TTTCTAG
                                     AA
GAM1335  ACCN1     3'  TGATTGTGCAGTTCTGATTCCA 33971      T       AC___
           G                     TGATT TGCAGTTC    CCAG
                                |||||  ||||||||    ||||
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                                ACTAA ACGTCAAG    GGTC
                                  C       ACTAA
GAM1335  CARD4    5'  CCTGACTTACAATCAC      33972        T    T
                                CCTGATTT GCAGT CAC
                                |||||||| ||||| |||
                                GGACTGAA TGTTA GTG
                                        _    _
GAM1335  CLCN4    3'  CCCCTGATGTTGGTTCA     33973        T   CA
                                CCCCTGAT TTG  GTTCA
                                |||||||| |||  |||||
                                GGGGACTA AAC  CAAGT
                                    C  __
GAM1335  CPD      3'  CCCCTGATTTAGTATAAGTTCA 33974          TGC___
                                CCCCTGATTT     AGTTCA
                                ||||||||||     ||||||
                                GGGGACTAAA     TCAAGT
                                     TCATAT
GAM1335  CYP3A43  3'  CTAATTATTCACCCA      33975       TTGCA
                                CTGATT    GTTCACCCA
                                ||||||    |||||||||
                                GATTAA    TAAGTGGGT
                                      _____
GAM1335  CYP3A43  3'  CTAATTATTCACCCA      33975       TTGCA
                                CTGATT    GTTCACCCA
                                ||||||    |||||||||
                                GATTAA    TAAGTGGGT
                                      _____
GAM1335  CYP3A43  3'  CTAATTATTCACCCA      33975       TTGCA
                                CTGATT    GTTCACCCA
                                ||||||    |||||||||
                                GATTAA    TAAGTGGGT
                                      _____
GAM1335  DAPK1    3'  CCCTTGGTTCTGCAGTCCAAAC 33976     C  A         CC
           AG                     CCC TG TTTTGCAGTTCA  CAG
                                ||| || ||||||||||||  |||
                                GGG AC AAGACGTCAGGT  GTC
                                  A  C          TT
GAM1335  DLX4     3'  CTGATTTTGCACCCA       33977          AGTTC
                                CTGATTTTGC    ACCCA
                                ||||||||||    |||||
                                GACTAAAACG    TGGGT
                                      _____
GAM1335  DLX4     3'  CTGATTTTGCACCCA       33977          AGTTC
                                CTGATTTTGC    ACCCA
                                ||||||||||    |||||
                                GACTAAAACG    TGGGT
                                      _____
GAM1335  F13A1    3'  CTGATTTTGCCCCCA       33978          AGTT A
                                CTGATTTTGC    C CCCA
                                ||||||||||    | ||||
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                                GACTAAAACG   G GGGT
                                     _____ _
GAM1335 MKI67    3' CCGCTGATTTCTGCATTCATTC 33979   _    _   G   CC
            AG                    CC CTGATT TTGCA TTCA  CAG
                                  || |||||| ||||| ||||  |||
                                  GG GACTAA GACGT AAGT  GTC
                                   C     A    _   AA
GAM1335 POP4     3' CCTCTGACTTCTTCAC      33980   _      GCAG
                                  CC CTGATTTT    TTCAC
                                  || ||||||||    ||||||
                                  GG GACTGAAG    AAGTG
                                   A       _____
GAM1335 RNMT     3' CCTCTATTTTGCAGACCC    33981    G_       TTC
                                  CCT  ATTTTGCAG   ACCC
                                  |||  |||||||||   ||||
                                  GGA  TAAAACGTC   TGGG
                                    GA        ___
GAM1335 SLC35A1  3' CTGTATTAGCAGTTCACTCAG  33982    _  TT       C
                                  CTG ATT  GCAGTTCAC CAG
                                  ||| |||  ||||||||| |||
                                  GAC TAA  CGTCAAGTG GTC
                                    A  T_       A
GAM1335 SORBS1   3' CCTGACTTCATCACTCA     33983          CAGT   C
                                  CCTGATTTTG    TCAC CA
                                  ||||||||||    |||| ||
                                  GGACTGAAGT    AGTG GT
                                        _____   A
GAM1335 SPAG9    3' ATTTGTGCACTTCACCCAG   33984     _   G
                                  ATTT TGCA TTCACCCAG
                                  |||| |||| |||||||||
                                  TAAA ACGT AAGTGGGTC
                                    C   G
GAM1335 C1orf8   5' CCTTGATTTTGAAGAAGTAGCC 33985    C       C  TTCA__
              CAG                   CC TGATTTTG AG     CCCAG
                                  || |||||||| ||     |||||
                                  GG ACTAAAAC TC     GGGTC
                                   A       T  TTCATC
GAM1335 CDCA4    3' CCTGATTTTCACCCA       33986         TGCAGT
                                  CCTGATTT     TCACCCA
                                  ||||||||     |||||||
                                  GGACTAAA     AGTGGGT
                                        _______
GAM1335 CDIPT    3' CCCTGATTTGAGGCCC      33987          T C  TTCA
                                  CCCTGATTT G AG    CCC
                                  ||||||||| | ||    |||
                                  GGGACTAAA C TC    GGG
                                       _ _  C___
GAM1335 KIAA0674 3' CCTCACCCTGTGGTTCGCC   33988     G     CA    A
                                  CCT ATTTTG  GTTC CC
                                  ||| ||||||  ||||| ||
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                                GGA TGGGAC  CAAG GG
                                  G     AC    C
GAM1335  KIAA1580  5'  TGATTTCAGCCACCC      33989       TG    T
                                TGATTT  CAGT CACCC
                                ||||||  |||| |||||
                                ACTAAA  GTCG GTGGG
                                   __   _
GAM1335  KIAA1649  3'  CTGATTTTGCAGAGCTCCCAG  33990          TTCA
                                CTGATTTTGCAG   CCCAG
                                ||||||||||||   |||||
                                GACTAAAACGTC   GGGTC
                                       TCGA
GAM1335  KIAA1649  3'  CTGATTTTGCAGAGCTCCCAG  33990          TTCA
                                CTGATTTTGCAG   CCCAG
                                ||||||||||||   |||||
                                GACTAAAACGTC   GGGTC
                                       TCGA
GAM1335  KIAA1789  5'  CCTTGTTTCTGAGTTCACCCAG 33991    C  A    C
                                CC TG TTTTG AGTTCACCCAG
                                || || ||||| ||||||||||
                                GG AC AAGAC TCAAGTGGGTC
                                 A  A    _
GAM1335  TCL6      5'  CCCTGATTTCTGCAAGACCAG  33992        _     TTCAC
                                CCCTGATT TTGCAG    CCAG
                                |||||||| ||||||    ||||
                                GGGACTAA GACGTT    GGTC
                                     A     CT___
GAM1335  TCL6      5'  CCCTGATTTCTGCAAGACCAG  33992        _     TTCAC
                                CCCTGATT TTGCAG    CCAG
                                |||||||| ||||||    ||||
                                GGGACTAA GACGTT    GGTC
                                     A     CT___
GAM1335  TCL6      5'  CCCTGATTTCTGCAAGACCAG  33992        _     TTCAC
                                CCCTGATT TTGCAG    CCAG
                                |||||||| ||||||    ||||
                                GGGACTAA GACGTT    GGTC
                                     A     CT___
GAM1335  TCL6      5'  CCCTGATTTCTGCAAGACCAG  33992        _     TTCAC
                                CCCTGATT TTGCAG    CCAG
                                |||||||| ||||||    ||||
                                GGGACTAA GACGTT    GGTC
                                     A     CT___
GAM1335  LOC115939 3'  CTAGATTTTCTCGTCACCCAG  33993    _     GCA  T
                                CT GATTTT   GT CACCCAG
                                || ||||||   || |||||||
                                GA CTAAAA   CA GTGGGTC
                                 T     GAG  _
GAM1335  LOC138693 5'  CTGATTTCATCATCCA      33994         CAGT   C
                                CTGATTTTG    TCA CCA
                                |||||||||    ||| |||
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                                GACTAAAGT    AGT GGT
                                     _____  A
GAM1335  LOC144465 3'  CCTCTAATTTTGTAAACTGCCC 33995    _       C  TTCA
              AG                    CC CTGATTTTG AG    CCCAG
                                    || |||||||| ||    |||||
                                    GG GATTAAAAC TT    GGGTC
                                     A        A  TGAC
GAM1335  LOC150382 5'  CCTTGGGTTTACAGCTACCCAG 33996    C  AT       C
                                    CC TG  TTTGCAGTT ACCCAG
                                    || ||  |||||||| ||||||
                                    GG AC  AAATGTCGA TGGGTC
                                     A  CC       _
GAM1335  LOC152845 5'  CCTGATTTGCATCTTGAATCCA 33997        T   GTTCAC__
              G                     CCTGATTT GCA       CCAG
                                    |||||||| |||       ||||
                                    GGACTAAA CGT       GGTC
                                         _  AGAACTTA
GAM1335  LOC169611 3'  CCTGATTTTGAAACC       33998          C  TTC
                                    CCTGATTTTG AG   ACC
                                    |||||||||| ||   |||
                                    GGACTAAAAC TT   TGG
                                         _ ___
GAM1335  LOC199957 5'  CTGGAAATTGCAGTTCATCC   33999     _ TT        C
                                    CTG A  TTGCAGTTCA CC
                                    ||| |  |||||||||| ||
                                    GAC T  AACGTCAAGT GG
                                      C TT         A
GAM1335  LOC96573  3'  TGTTTTTGTAGCCCCCATCCAG 34000    A    C    AC__
                                    TG TTTTG AGTTC    CCAG
                                    || ||||| |||||    ||||
                                    AC AAAAC TCGGG    GGTC
                                     A    A    GGTA
GAM1336  NR3C2     3'  TGTATATATTTTTTTATTATTT 34003   T      _______       III
              TTTTGTGC                  ATTTTTTT     TTTTTGTG   C
                                     ||||||||     ||||||||  |
                                     TAAAAAAA     AAAAACAC   G
                                    _       TAATAA       III
GAM1336  LOC136288 3'  TGTATATTATTTTTATTCAATG 34004            T   TT
                                    TGTATATTATTTTT TTT  TG
                                    |||||||||||||| |||  ||
                                    ACATATAATAAAAA AAG  AC
                                              T   TT
GAM1336  LOC196411 3'  TGTATATATACATTTTTTTTTG 34005        TATTT
              TG                     TGTATAT    TTTTTTTTTGTG
                                    |||||||    ||||||||||||
                                    ACATATA    AAAAAAAAACAC
                                         TATGT
GAM1337  ADAM19    3'  TAGAGTAAGGAGGAAGA     34008      ACAAA
                                    TAGA     AAGGAGGAAGA
                                    ||||     ||||||||||
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                                ATCT    TTCCTCCTTCT
                                  CA___
GAM1337 ANGPT1   3' TCTAGACAAAAAAAAAAGAA  34009      AC
                                TCTAGA  AAAAAGGAGGAA
                                ||||||  ||||||||||||
                                AGATCT  TTTTTTTTTCTT
                                   GT
GAM1337 ARHGDIB  5' TAGAACAGGAAGGAAG     34010      AAAA
                                TAGAACA   GGAGGAAG
                                |||||||   ||||||||
                                ATCTTGT   CTTCCTTC
                                   C___
GAM1337 ASB2     3' TCCAGAACAAGTGGAGG     34011        AAA
                                TCTAGAACAA  GGAGG
                                ||||||||||  |||||
                                AGGTCTTGTT  CCTCC
                                      CA_
GAM1337 BBS4     3' TCAAGAACAAAATACAGGGAGG 34012   T      A____
                                TC AGAACAAAA    GGAGG
                                || |||||||||    |||||
                                AG TCTTGTTTT    CCTCC
                                 T       ATGTC
GAM1337 CACNA1B  3' TCTAGAGTAAAAGAGGGGAGGA 34013      AC   A___
                                TCTAGA  AAAA   GGAGGA
                                ||||||  ||||   ||||||
                                AGATCT  TTTT   CCTCCT
                                   CA   CTCC
GAM1337 CALM1    3' TCTAGAGGGGGGAAAAAGGAG  34014      AC____
                                TCTAGA     AAAAAGGAG
                                ||||||     |||||||||
                                AGATCT     TTTTTCCTC
                                   CCCCCC
GAM1337 CASP2    3' TCTAGGACAAAAAGGGCGGAGG 34015      A      A_  A
           A                     TCTAG ACAAAAAGG  GGA GA
                                |||||  |||||||||  ||| ||
                                AGATC TGTTTTTCC  CCT CT
                                   C       CG   C
GAM1337 CASP2    3' TCTAGGACAAAAAGGGCGGAGG 34015      A      A_  A
           A                     TCTAG ACAAAAAGG  GGA GA
                                |||||  |||||||||  ||| ||
                                AGATC TGTTTTTCC  CCT CT
                                   C       CG   C
GAM1337 CASP2    3' TCTAGGACAAAAAGGGCGGAGG 34015      A      A_  A
           A                     TCTAG ACAAAAAGG  GGA GA
                                |||||  |||||||||  ||| ||
                                AGATC TGTTTTTCC  CCT CT
                                   C       CG   C
GAM1337 CASP2    3' TCTAGGACAAAAAGGGCGGAGG 34015      A      A_  A
           A                     TCTAG ACAAAAAGG  GGA GA
                                |||||  |||||||||  ||| ||
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                                AGATC TGTTTTTCC  CCT CT
                                  C       CG   C
GAM1337  CST1     3'  TAGAAGCAAGAAGGAAG     34016      CAAA
                                TAGAA    AAGGAGGAAG
                                |||||    ||||||||||
                                ATCTT    TTCTTCCTTC
                                  CG__
GAM1337  CST4     3'  TAGAAGCAAGAAGGAAG     34016      CAAA
                                TAGAA    AAGGAGGAAG
                                |||||    ||||||||||
                                ATCTT    TTCTTCCTTC
                                  CG__
GAM1337  DDB1     3'  TCTAAATAAAAAGAGGA     34017       ACA
                                TCTAGA   AAAAGGAGGA
                                ||||||   ||||||||||
                                AGATTT   TTTTTCTCCT
                                   A__
GAM1337  EPB42    3'  TAGAACAAGGGTTGGCAGGAGA 34018        AAA__ _   A
                                TAGAACAA     GG AGGA GA
                                ||||||||     || |||| ||
                                ATCTTGTT     CC TCCT CT
                                     CCCAA  G   _
GAM1337  ESRRG    3'  TAGAAAAAAGGGGAAG      34019      CA     A
                                TAGAA  AAAAGG GGAAG
                                |||||  ||||||  |||||
                                ATCTT  TTTTCC CCTTC
                                  __     _
GAM1337  FBN2     3'  TCTAAGACAGGGAGGAAAGAA  34020     GA   AAAA      _
                                TCTA  ACA    GGAGGAA GAA
                                ||||  |||    ||||||| |||
                                AGAT  TGT    CCTCCTT CTT
                                  TC   C___      T
GAM1337  GABRA3   5'  TCTGAGCGGAAAGGAGAGAAG  34021     A  ACAA      _
                                TCT GA    AAAGGAG GAAG
                                ||| ||    ||||||| ||||
                                AGA CT    TTTCCTC CTTC
                                  _  CGCC      T
GAM1337  GNAS     5'  TCTGAGCAAGAAGAAGG     34022     A  A   A
                                TCT GA CAA AAGGAGG
                                ||| || ||| |||||||
                                AGA CT GTT TTCTTCC
                                  _  C   C
GAM1337  IL1R1    3'  CCTAGGCAAAGGAGGAGGAAG  34023       AA    A_
                                TCTAG  CAAA  AGGAGGAAG
                                |||||  ||||  |||||||||
                                GGATC  GTTT  TCCTCCTTC
                                  C_    CC
GAM1337  KMO      3'  TCTAGAATGAAAAAGAAA    34024        CA
                                TCTAGAA  AAAAGGAGG
                                |||||||  |||||||||
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                                AGATCTT  TTTTTCTTT
                                    AC
GAM1337 LILRB4   3' TCTTGAGCAAAGGGAAGAAG  34025    A A   AA
                                TCT GA CAAA  GGAGGAAG
                                ||| || ||||  ||||||||
                                AGA CT GTTT  CCTTCTTC
                                  A C   C_
GAM1337 LRP4     3' TCTAGGAGGAGGAAGAA     34026      AACAAAA
                                TCTAG      AGGAGGAAGAA
                                |||||      ||||||||||
                                AGATC      TCCTCCTTCTT
                                   C_______
GAM1337 MAOB     3' TCTAAAACAGAAGGTGAGGA  34027        A AG_
                                TCTAGAACA AA   GAGGA
                                ||||||||| ||   |||||
                                AGATTTTGT TT   CTCCT
                                      C CCA
GAM1337 MN1      3' TCTAGAGGAAAAAGGCTTAAG 34028      AC      AGG
                                TCTAGA  AAAAAGG   AAG
                                ||||||  |||||||   |||
                                AGATCT  TTTTTCC   TTC
                                    CC      GAA
GAM1337 MTMR2    3' CCTAGAATGGAGAAAG      34029       CAAAAA
                                TCTAGAA     GGAGGAAG
                                |||||||     ||||||||
                                GGATCTT     CCTCTTTC
                                    A_____
GAM1337 NDUFV3   5' TCTAGAGGAAAGGATGAA    34030      ACAA     G
                                TCTAGA    AAAGGA GAA
                                ||||||    |||||| |||
                                AGATCT    TTTCCT CTT
                                    CC__     A
GAM1337 NPAT     3' TAAAACAAAGAGAACAGA    34031       AAA     _
                                TAGAACAA   GGAGGA AGA
                                ||||||||   |||||| |||
                                ATTTTGTT   TCTCTT TCT
                                     ___      G
GAM1337 NR3C2    3' TCTAGAGGAAAAGGGAAA    34032      ACA     A
                                TCTAGA   AAAAGG GGAA
                                ||||||   |||||| ||||
                                AGATCT   TTTTCC CTTT
                                    CC_     _
GAM1337 OAS2     3' CTGGAAGGAAAAAGGAGGA   34033    A   C_
                                CT GAA  AAAAAGGAGGA
                                || |||  ||||||||||
                                GA CTT  TTTTTCCTCCT
                                 C   CC
GAM1337 PAFAH1B1 3' TCCAGAGGAAAAGAGGGAGGA 34034       AC    A__
                                TCTAGA  AAAA   GGAGGA
                                ||||||  ||||   ||||||
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                                AGGTCT  TTTT   CCTCCT
                                   CC    CTC
GAM1337  PCDH11Y   5'  TCTGGATAAAAGGAGGCAAG   34035     A  ACA       _
                                TCT GA   AAAAGGAGG AAG
                                ||| ||   ||||||||| |||
                                AGA CT   TTTTCCTCC TTC
                                  C  A__       G
GAM1337  PCDH11Y   5'  TCTGGATAAAAGGAGGCAAG   34035     A  ACA       _
                                TCT GA   AAAAGGAGG AAG
                                ||| ||   ||||||||| |||
                                AGA CT   TTTTCCTCC TTC
                                  C  A__       G
GAM1337  PCDHB13   3'  TAAAACAAAGGGAGAAAGAAC  34036         AA
                                TAGAACAAA  GGAGGAAGAAC
                                |||||||||  ||||||||||
                                ATTTTGTTT  CCTCTTTCTTG
                                     C_
GAM1337  PLCB4     5'  CTAGGGTAAAAGGAAGAGGA   34037      AACA        A
                                CTAG    AAAAGGAGGA GA
                                ||||    |||||||||| ||
                                GATC    TTTTCCTTCT CT
                                  CCA_        C
GAM1337  PLD2      3'  TCAAGGGCAGGAAGAGGAAG   34038    T  AA  AAA
                                TC AG  CA   AGGAGGAAG
                                || ||  ||   |||||||||
                                AG TC  GT   TTCTCCTTC
                                 T  CC  CC_
GAM1337  PML       3'  TCTGGGATGAAAGGAGAAGGGA 34039     A_  ACAA       A_
            AC                    TCT  GA    AAAGGAGGA  GAAC
                                ||| ||   |||||||||  ||||
                                AGA  CT    TTTCCTCTT  CTTG
                                  CC  AC__       CC
GAM1337  POMZP3    5'  TCTGAACGAAGGAGGA      34040     A    AAA
                                TCT GAAC   AAGGAGGA
                                ||| ||||   ||||||||
                                AGA CTTG   TTCCTCCT
                                  _   C__
GAM1337  POU3F4    3'  CTAGAATGAAAGGAAAGAGA   34041       CAA      GA
                                CTAGAA   AAAGGAG  AGA
                                ||||||   |||||||  |||
                                GATCTT   TTTCCTT  TCT
                                   AC_      TC
GAM1337  PPARGC1   3'  TCCAGGGCAAAAAGGAGAA    34042       AA
                                TCTAG  CAAAAAGGAGGA
                                |||||  ||||||||||||
                                AGGTC  GTTTTTCCTCTT
                                   CC
GAM1337  PPT1      3'  TCGAGAATGGAATAGGAAGAAC 34043     T    CAAAAAGG
                                TC AGAA       AGGAAGAAC
                                || ||||       |||||||||
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                                AG TCTT       TCCTTCTTG
                                 C   ACCTTA__
GAM1337  PRKR    3'  TAGAACAAAGAGATGAGG    34044         A  __
                                TAGAACAAA AG  GAGG
                                ||||||||| ||  ||||
                                ATCTTGTTT TC  CTCC
                                     C  TA
GAM1337  PSMB9   3'  CCTGGGACAAAAGAAGAAAGA  34045     AGA     A
                                TCT   ACAAAA GGAGGAAGA
                                |||   |||||| |||||||||
                                GGA   TGTTTT CTTCTTTCT
                                  CCC     _
GAM1337  PSMD9   3'  AAAATAAAAGGGAGGAAGAA   34046     C    A
                                AGAA AAAA GGAGGAAGAA
                                |||| |||| ||||||||||
                                TTTT TTTT CCTCCTTCTT
                                  A    C
GAM1337  PTPN7   3'  TCTCAGATTCAAGGAGGAGGAA 34047     _  ACAAA       A
                                TCT AGA     AAGGAGGA GAA
                                ||| |||     |||||||| |||
                                AGA TCT     TTCCTCCT CTT
                                  G   AAG__       C
GAM1337  PTPN7   3'  TCTCAGATTCAAGGAGGAGGAA 34047     _  ACAAA       A
                                TCT AGA     AAGGAGGA GAA
                                ||| |||     |||||||| |||
                                AGA TCT     TTCCTCCT CTT
                                  G   AAG__       C
GAM1337  PTPN7   5'  TCTAGGACGGAAGGGAGAAAG  34048      A  AA  A
                                TCTAG AC  AA GGAGGAAG
                                ||||| ||  || ||||||||
                                AGATC TG  TT CCTCTTTC
                                   C  CC  C
GAM1337  PTPN7   3'  TCTCAGATTCAAGGAGGAGGAA 34047     _  ACAAA       A
                                TCT AGA     AAGGAGGA GAA
                                ||| |||     |||||||| |||
                                AGA TCT     TTCCTCCT CTT
                                  G   AAG__       C
GAM1337  PTPRO   3'  TCTGGAAGCAAGGGAGGA    34049     A  _  AAA
                                TCT GAA CAA   GGAGGA
                                ||| ||| |||   ||||||
                                AGA CTT GTT   CCTCCT
                                  C   C   C__
GAM1337  PTPRO   3'  TCTGGAAGCAAGGGAGGA    34049     A  _  AAA
                                TCT GAA CAA   GGAGGA
                                ||| ||| |||   ||||||
                                AGA CTT GTT   CCTCCT
                                  C   C   C__
GAM1337  PTPRO   3'  TCTGGAAGCAAGGGAGGA    34049     A  _  AAA
                                TCT GAA CAA   GGAGGA
                                ||| ||| |||   ||||||
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                                AGA CTT GTT   CCTCCT
                                  C   C   C__
GAM1337  PTPRO    3'  TCTGGAAGCAAGGGAGGA    34049     A  _  AAA
                                TCT GAA CAA   GGAGGA
                                ||| ||| |||   ||||||
                                AGA CTT GTT   CCTCCT
                                  C   C   C__
GAM1337  PTPRO    3'  TCTGGAAGCAAGGGAGGA    34049     A  _  AAA
                                TCT GAA CAA   GGAGGA
                                ||| ||| |||   ||||||
                                AGA CTT GTT   CCTCCT
                                  C   C   C__
GAM1337  PYCS     3'  TCTCAAAAAAGGGGGAAGAA  34050     AGAAC      A
                                TCT     AAAAAGG GGAAGAA
                                |||     ||||||| |||||||
                                AGA     TTTTTCC CCTTCTT
                                  GT___       C
GAM1337  RABIF    3'  TCTAGAGCAAGAAAAAGCGGGA 34051       A  __    A  A
              G                   TCTAGA CAA  AAAGG GG AG
                                ||||||| |||  ||||| || ||
                                AGATCT GTT  TTTTC CC TC
                                    C   CT    G  C
GAM1337  SALL2    3'  TCTGGAGCAGGGGGGAGGAAGAA 34052     A  A  AAAA
                                TCT GA CA    GGAGGAAGAA
                                ||| || ||    ||||||||||
                                AGA CT GT    CCTCCTTCTT
                                  C  C  CCC_
GAM1337  SDC4     3'  TCTAGAACCAAGGAAGAA     34053         AAA
                                TCTAGAAC   AAGGAGGAA
                                ||||||||   |||||||||
                                AGATCTTG   TTCCTTCTT
                                     G__
GAM1337  SDHC     3'  TCTAAACAAATAAGGAGAA    34054       A   _
                                TCTAGA CAAA AAGGAGGA
                                |||||| |||| ||||||||
                                AGATTT GTTT TTCCTCTT
                                    _   A
GAM1337  SMARCC1  3'  TCCAGAACAAAAACAAAAGGA  34055             __
                                TCTAGAACAAAAA  GGAGGA
                                ||||||||||||  ||||||
                                AGGTCTTGTTTTT  TTTCCT
                                       GT
GAM1337  SRRM1    3'  ACAAAAGAAGGAGGGGGAAC   34056       __     AA
                                ACAAAA  AGGAGG  GAAC
                                ||||||  ||||||  ||||
                                TGTTTT  TCCTCC  CTTG
                                    CT     CC
GAM1337  STAC     3'  CCTAGAACAGCAGGAAGGA    34057         AAA   _
                                TCTAGAACA   AGGA GGA
                                |||||||||   |||| |||
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                                GGATCTTGT   TCCT CCT
                                     CG_    T
GAM1337  TNFRSF11A 3'  TCTAGAATAAGAAGAA      34058        CAAA
                                TCTAGAA    AAGGAGGA
                                |||||||    ||||||||
                                AGATCTT    TTCTTCTT
                                   A___
GAM1337  TOP2A    3'  TAGAAAAGGAGGAAGA      34059       CAAA
                                TAGAA    AAGGAGGAAGA
                                |||||    ||||||||||
                                ATCTT    TTCCTCCTTCT
                                  ____
GAM1337  UBE2L3   3'  TAAAACAAAGAGAGCAGAAC   34060         AA   GA
                                TAGAACAAA  GGAG  AGAAC
                                |||||||||  ||||  |||||
                                ATTTTGTTT  TCTC  TCTTG
                                     C_    G_
GAM1337  ZNF189   3'  CCTAGAACAAGAAATAAGGA   34061          _   G
                                TCTAGAACAA AAA GAGGA
                                |||||||||| ||| |||||
                                GGATCTTGTT TTT TTCCT
                                      C   A
GAM1337  ZNF83    5'  TAGAAAAAATACCTGAGGAAGA 34062       C   AAG__
            AC                    TAGAA AAA    GAGGAAGAAC
                                |||||  |||    ||||||||||
                                ATCTT TTT    CTCCTTCTTG
                                   T   ATGGA
GAM1337  AMOT     3'  CAGAACAAGGGTACAAAAGGAA 34063        AA____
                                TAGAACAA     AGGAGGAA
                                ||||||||     ||||||||
                                GTCTTGTT     TTTTCCTT
                                     CCCATG
GAM1337  ARFGAP1  3'  CAAATGGAAGGAGGAGGAAC   34064     ___       A
                                CAAA   AAGGAGGA GAAC
                                ||||   |||||||| ||||
                                GTTT   TTCCTCCT CTTG
                                   ACC       C
GAM1337  BRAG     3'  TCTAGGGGGAAAAAAAGGGAAC 34065      AACA        AA
                                TCTAG    AAAAGGAGG  GAAC
                                |||||    |||||||||  ||||
                                AGATC    TTTTTTTCC  CTTG
                                   CCCC        __
GAM1337  CNNM4    3'  TCTGGAACCAAAAGGAAGAA   34066     A   A
                                TCT GAAC AAAAGGAGGAA
                                ||| |||| ||||||||||
                                AGA CTTG TTTTCCTTCTT
                                  C   G
GAM1337  CNOT3    5'  TAGAACAAGAAGCCCATAAAGG 34067         A   _______
            A                     TAGAACAA AAG      GAGGA
                                ||||||||  |||      |||||
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                                ATCTTGTT TTC     TTCCT
                                     C   GGGTAT
GAM1337  DKFZP586C1324 3'  TCCAGAACAGGGAGGAGA    34068         AAAA     A
                                TCTAGAACA    GGAGGA GA
                                |||||||||    |||||| ||
                                AGGTCTTGT    CCTCCT CT
                                     C___     _
GAM1337  DKFZP586M0622 3'  TCTAGAAAAAGAGGA      34069        CAAA
                                TCTAGAA    AAGGAGGA
                                |||||||    ||||||||
                                AGATCTT    TTTCTCCT
                                     ____
GAM1337  EPB41L1   3'  CAGAACAAGGAAGAGA      34070        AAA      A
                                TAGAACA   AGGAGGA GA
                                |||||||   ||||||| ||
                                GTCTTGT   TCCTTCT CT
                                     ___     _
GAM1337  EPSIN     5'  TCCAGGGCGGCAGGAAGAA   34071      AACAAAAA _
                                TCTAG       GG AGGAAGAA
                                |||||       || ||||||||
                                AGGTC       CC TCCTTCTT
                                   CCG_____  G
GAM1337  FLJ10314  5'  TCTAGGAAAGGAAGAA      34072       AACAA
                                TCTAG     AAAGGAGGAA
                                |||||     ||||||||||
                                AGATC     TTTCCTTCTT
                                   C____
GAM1337  FLJ11110  3'  TCTAGAAAAGAAGAGA      34073        CAAAA      A
                                TCTAGAA     AGGAGGA GA
                                |||||||     ||||||| ||
                                AGATCTT     TTCTTCT CT
                                     _____     _
GAM1337  FLJ12132  3'  TCTAGAACAGAAATACAAGGGG 34074         AA_____    A
                                TCTAGAACA      AAGG GG
                                |||||||||      |||| ||
                                AGATCTTGT      TTCC CC
                                     CTTTATG   _
GAM1337  FLJ12484  3'  TCTAGAACAAAGTTCTGGAG   34075          AA___
                                TCTAGAACAAA     GGAG
                                ||||||||||     ||||
                                AGATCTTGTTT     CCTC
                                      CAAGA
GAM1337  FLJ14735  3'  TAGAGGGGAAAAGAAAAAGAA  34076      ACAA
                                TAGA    AAAGGAGGAAGAA
                                ||||    ||||||||||||
                                ATCT    TTTTCTTTTTCTT
                                   CCCC
GAM1337  FLJ20498  3'  TCTAGAGCATGAAGGAAAAA   34077       A  AAAA
                                TCTAGA CA    GGAGGAAGAA
                                ||||||  ||    ||||||||||
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                                AGATCT GT    CTTCCTTTTT
                                   C  A___
GAM1337  FLJ20699  3'  TCTAGAATATAAAGAAAAGAA  34078       CAAA     G
                                TCTAGAA    AAGGAG AAGAA
                                |||||||    |||||| |||||
                                AGATCTT    TTTCTT TTCTT
                                    ATA_     _
GAM1337  FLJ21069  3'  CAAAGGAGGGAGGAAGAAC    34079      AA__
                                CAAA    GGAGGAAGAAC
                                ||||    ||||||||||
                                GTTT    CCTCCTTCTTG
                                  CCTC
GAM1337  GLCCI1    3'  TCTGGAACAAAACACAGGA    34080     A       AGG
                                TCT GAACAAAA   AGGA
                                ||| ||||||||   ||||
                                AGA CTTGTTTT   TCCT
                                  C       GTG
GAM1337  HRIHFB2122 3'  GAAAAAAAGGAAAAAAA     34081     C
                                GAA AAAAAGGAGGAAGA
                                ||| ||||||||||||||
                                CTT TTTTTCCTTTTTTT
                                  _
GAM1337  HSPC133   3'  TCTAGAAGAAAAGATTGGA    34082       CAA     __
                                TCTAGAA   AAAGGA  GGA
                                |||||||   ||||||  |||
                                AGATCTT   TTTTCT  CCT
                                    C__     AA
GAM1337  KIAA0182  3'  CTAGGACAAGGAGGAAGA    34083      A   AAA
                                CTAG ACA   AGGAGGAAGA
                                |||| |||   ||||||||||
                                GATC TGT   TCCTCCTTCT
                                  C   ___
GAM1337  KIAA0459  3'  TCTACAACAGAAGGGAAGAAAA 34084      G    A  A
                                TCTA AACA AA GGAGGAAGA
                                |||| |||| || |||||||||
                                AGAT TTGT TT CCTTCTTTT
                                  G    C  C
GAM1337  KIAA0513  3'  TCTAGGAAAGAGAAAG      34085       AACAAA
                                TCTAG     AAGGAGGAAG
                                |||||     ||||||||||
                                AGATC     TTTCTCTTTC
                                  C_____
GAM1337  KIAA0534  3'  TCTGGAATGTAGGGGGAAAAAC 34086     A   CAAAA   A
                                TCT GAA     AGG GGAAGAAC
                                ||| |||     ||| ||||||||
                                AGA CTT     TCC CCTTTTTG
                                  C   ACA__   C
GAM1337  KIAA0564  3'  TCTAGCAGCAAGGAGAAGA    34087      AACAAA     G
                                TCTAG     AAGGAG AAGA
                                |||||     |||||| ||||
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                                AGATC     TTCCTC TTCT
                                  GTCG__    _
GAM1337  KIAA0711  3'  TCTAGAGGAAAAGGCAGGA   34088      ACA    _
                                TCTAGA   AAAAGG AGGA
                                ||||||   |||||| ||||
                                AGATCT   TTTTCC TCCT
                                   CC_     G
GAM1337  KIAA0721  3'  CAGAGTGAAAGGGAAGAAAA  34089     ACA   A
                                TAGA   AAA GGAGGAAGA
                                ||||   ||| |||||||||
                                GTCT   TTT CCTTCTTTT
                                  CAC   C
GAM1337  KIAA0721  3'  CAGAGTGAAAGGGAAGAAAA  34089     ACA   A
                                TAGA   AAA GGAGGAAGA
                                ||||   ||| |||||||||
                                GTCT   TTT CCTTCTTTT
                                  CAC   C
GAM1337  KIAA0843  3'  TCCAGGGCAGAAGGAGGA    34090     AA  AA
                                TCTAG  CA  AAGGAGGA
                                |||||  ||  ||||||||
                                AGGTC  GT  TTCCTCCT
                                   CC  C_
GAM1337  KIAA0894  3'  TAGAGGAAAGGGAGAAAGAA  34091     ACA   A
                                TAGA   AAA GGAGGAAGAA
                                ||||   ||| ||||||||||
                                ATCT   TTT CCTCTTTCTT
                                  CC_   C
GAM1337  KIAA1032  3'  TCTGGAAAAGGAAGAAG     34092     A   CAAA
                                TCT GAA    AAGGAGGAAG
                                ||| |||    ||||||||||
                                AGA CTT    TTCCTTCTTC
                                  C  _____
GAM1337  KIAA1042  3'  TCTGAAACAAGAAGGAAAA   34093     AG    AAA
                                TCT  AACA   AGGAGGAAGA
                                |||  ||||   ||||||||||
                                AGA  TTGT   TCTTCCTTTT
                                  CT   ___
GAM1337  KIAA1265  3'  TCATAGAGTAGGAGGAAAGAA  34094    _   ACAAAA      _
                                TC TAGA      AGGAGGAA GAA
                                || ||||      |||||||| |||
                                AG ATCT      TCCTCCTT CTT
                                  T    CA____       T
GAM1337  KIAA1349  5'  TCTGGGGCAAAAAAGAGAAAAA 34095     AGAA
                                TCT    CAAAAAGGAGGAAGA
                                |||    ||||||||||||||
                                AGA    GTTTTTTCTCTTTTT
                                  CCCC
GAM1337  KIAA1391  3'  TAGAACAAAAAAGAAAGAAC   34096          AG
                                TAGAACAAAA  GAGGAAGAAC
                                ||||||||||  ||||||||||
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                                ATCTTGTTTT  TTCTTTCTTG
                                   __
GAM1337 KIAA1546 3' TAGAACAAAAAGGTTGAAG   34097          AG
                                TAGAACAAAAAGG  GAAG
                                |||||||||||||  ||||
                                ATCTTGTTTTTCC  CTTC
                                      AA
GAM1337 KIAA1549 3' CCAGAAGAAGGAGGAAGAA   34098      CAAA
                                CTAGAA   AAGGAGGAAGAA
                                ||||||   ||||||||||||
                                GGTCTT   TTCCTCCTTCTT
                                   C___
GAM1337 KIAA1649 5' TAGAACAGAGGAAACGGAA   34099      AAA     AA
                                TAGAACA  AGGAGG  GAA
                                |||||||  ||||||  |||
                                ATCTTGT  TCCTTT  CTT
                                    C__    GC
GAM1337 KIAA1750 3' AAACAAAATAAAAAAGAA    34100       AG
                                GAACAAAA  GAGGAAGAA
                                ||||||||  |||||||||
                                TTTGTTTT  TTTTTTCTT
                                    A_
GAM1337 KIAA1765 3' TCTGGAAGGGAAAGGAAAGAAG 34101    A  CAA     _
                                TCT GAA  AAAGGAG GAAG
                                ||| |||  ||||||| ||||
                                AGA CTT  TTTCCTT CTTC
                                  C  CCC     T
GAM1337 LEPROTL1 3' TCCAGAACAGAAAATAGGGAAG 34102        A   GA_
                                TCTAGAACA AAAG  GGAAG
                                |||||||| ||||  |||||
                                AGGTCTTGT TTTT  CCTTC
                                     C   ATC
GAM1337 LSR7    5' TAAAACCCAGGAGGAAG    34103      AAAA
                                TAGAAC   AGGAGGAAG
                                ||||||   |||||||||
                                ATTTTG   TCCTCCTTC
                                   GG__
GAM1337 MGC12518 3' TCTATAACAAAAATGGAA    34104     G      _
                                TCTA AACAAAAA GGAG
                                |||| |||||||| ||||
                                AGAT TTGTTTTT CCTT
                                  A      A
GAM1337 MGC27277 5' TCTGAACAAAACTATAAAGGAA 34105    A      AG___
                                TCT GAACAAAA    GAGGAA
                                ||| ||||||||    ||||||
                                AGA CTTGTTTT    TTCCTT
                                  _      GATAT
GAM1337 MGC35558 3' TAAAACAAAAGCAAAAAGA   34106         A G
                                TAGAACAAAA G AGGAAGA
                                |||||||||| | |||||||
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                                ATTTTGTTTT C TTTTTCT
                                      _ G
GAM1337  MGC4730   3'  CTAGAACAAAAAACTGACAAGA 34107          GA  _
             AC                   CTAGAACAAAAAG  GG AAGAAC
                                  ||||||||||||  || ||||||
                                  GATCTTGTTTTTT  CT TTCTTG
                                        GA  G
GAM1337  MGC5391   3'  CTAGAACAGAAATTTAGGGGA  34108       _  ___  A
                                  CTAGAACA AAA   AGG GGA
                                  |||||||| |||   ||| |||
                                  GATCTTGT TTT   TCC CCT
                                       C   AAA  _
GAM1337  MGC5395   3'  TAGAACAATGCTCCAAAGAAC  34109       AAAGGAG
                                  TAGAACAA      GAAGAAC
                                  ||||||||      |||||||
                                  ATCTTGTT      TTTCTTG
                                       ACGAGG_
GAM1337  NR6A1     3'  TCTGGAGAGAAAAGGAGAA   34110     A  ACA
                                  TCT GA   AAAAGGAGGA
                                  ||| ||   ||||||||||
                                  AGA CT   TTTTCCTCTT
                                    C  CTC
GAM1337  NR6A1     3'  TCTGGAGAGAAAAGGAGAA   34110     A  ACA
                                  TCT GA   AAAAGGAGGA
                                  ||| ||   ||||||||||
                                  AGA CT   TTTTCCTCTT
                                    C  CTC
GAM1337  NR6A1     3'  TCTGGAGAGAAAAGGAGAA   34110     A  ACA
                                  TCT GA   AAAAGGAGGA
                                  ||| ||   ||||||||||
                                  AGA CT   TTTTCCTCTT
                                    C  CTC
GAM1337  PASK      5'  TCTGGAAAAAGGGGAAG     34111     A  CAA    A
                                  TCT GAA   AAAGG GGAAG
                                  ||| |||   ||||| |||||
                                  AGA CTT   TTTCC CCTTC
                                    C  ___    _
GAM1337  PLSCR3    3'  CCTAGGGCAAGGGAAGGAAG  34112      AA  AAA
                                  TCTAG  CAA   GGAGGAAG
                                  |||||  |||   ||||||||
                                  GGATC  GTT   CTTCCTTC
                                     CC   CC_
GAM1337  PLSCR3    3'  CCTAGGGCAAGGGAAGGAAG  34112      AA  AAA
                                  TCTAG  CAA   GGAGGAAG
                                  |||||  |||   ||||||||
                                  GGATC  GTT   CTTCCTTC
                                     CC   CC_
GAM1337  PP1201    3'  TCCAGGACAGAAAGGAAA    34113      A  A
                                  TCTAG ACA AAAGGAGG
                                  ||||| ||| ||||||||
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                                AGGTC TGT TTTCCTTT
                                  C   C
GAM1337  PRO1489   5'  TAAAACAAGAAGAGAA      34114        AAAA      A
                                TAGAACA    GGAGGA GAA
                                |||||||    |||||| |||
                                ATTTTGT    TCTTCT CTT
                                   _____     _
GAM1337  PRO1598   5'  TCTAGAGGCAAAAAGGATTCCA 34115        A_        GGA_
            GAA                   TCTAGA  CAAAAAGGA    AGAA
                                |||||||  |||||||||    ||||
                                AGATCT  GTTTTTCCT    TCTT
                                   CC        AAGG
GAM1337  PRO1914   3'  TCTAGCAATAAAAGGAATGAA  34116       AACA       _
                                TCTAG    AAAAGGAG GAA
                                |||||    |||||||| |||
                                AGATC    TTTTCCTT CTT
                                   GTTA       A
GAM1337  PTDSS1    3'  TCTAGAAGGAAGGGGAA     34117        CAAA    A
                                TCTAGAA    AAGG GGAA
                                |||||||    |||| ||||
                                AGATCTT    TTCC CCTT
                                    CC__    _
GAM1337  RNF13     3'  GAACAGAAAGGGAAAAAAC    34118       A     A
                                GAACA AAAGG GGAAGAAC
                                ||||| ||||| ||||||||
                                CTTGT TTTCC CTTTTTTG
                                   C    _
GAM1337  Rpo1-2    3'  TCAGGAACATAAGGAAGA    34119     TA     AA
                                TC  GAACA  AAGGAGGA
                                ||  |||||  ||||||||
                                AG  CTTGT  TTCCTTCT
                                  TC     A_
GAM1337  SAD1      3'  TCTAGAAAAAAATGATCAAAGA 34120        C     G  G_
            AC                    TCTAGAA AAAAA GA  GAAGAAC
                                |||||||  |||||  ||  |||||||
                                AGATCTT  TTTTT CT  TTTCTTG
                                    _     A  AG
GAM1337  SYNJ2     3'  TCTGGAACGAAGAGAAAA    34121     A    AAAA
                                TCT GAAC    AGGAGGAAG
                                |||  ||||    |||||||||
                                AGA CTTG    TTCTCTTTT
                                  C    C___
GAM1337  SYTL4     3'  TCTAGAACTGGAAAAAG     34122         AAAAA
                                TCTAGAAC     GGAGGAAG
                                ||||||||     ||||||||
                                AGATCTTG     CCTTTTTC
                                    A_____
GAM1337  TAF2      3'  TAGAGCAAAAGGAAAAA     34123       ACA
                                TAGA   AAAAGGAGGAA
                                ||||   ||||||||||
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                                ATCT   TTTTCCTTTTT
                                  CG_
GAM1337  UHRF1    3'  TAGAAAGAAGGAACGAA     34124      CAAAA      _
                                TAGAA     AGGAGGAA GAA
                                |||||     |||||||| |||
                                ATCTT     TCTTCCTT CTT
                                  _____       G
GAM1337  VCY2     3'  TCCAGAATAAAGAGGAGA    34125       C   A
                                TCTAGAA AAA AGGAGG
                                ||||||| ||| ||||||
                                AGGTCTT TTT TCCTCT
                                    A   C
GAM1337  VCY2     3'  TCCAGAATAAAGAGGAGA    34125       C   A
                                TCTAGAA AAA AGGAGG
                                ||||||| ||| ||||||
                                AGGTCTT TTT TCCTCT
                                    A   C
GAM1337  ZNF238   3'  TAGAACAAAGGAAGAA      34126       AA
                                TAGAACAA  AGGAGGAA
                                ||||||||  ||||||||
                                ATCTTGTT  TCCTTCTT
                                  __
GAM1337  ZNF313   3'  TCTAGAACAAGAATGTAGG   34127         A  GG_
                                TCTAGAACAA AA   AGG
                                |||||||||| ||   |||
                                AGATCTTGTT TT   TCC
                                    C  ACA
GAM1337  LOC119467 5'  TCTAGGACAAAAAAAGGAA   34128      A      G
                                TCTAG ACAAAAAG AGGAA
                                ||||| |||||||| |||||
                                AGATC TGTTTTTT TCCTT
                                  C      _
GAM1337  LOC133688 3'  TCTAAACAAGGAGGATGAA   34129      A  AAA     A
                                TCTAGA CA   AGGAGGA GAA
                                |||||| ||   ||||||| |||
                                AGATTT GT   TCCTCCT CTT
                                  _ ____       A
GAM1337  LOC138389 3'  TCTAGAGCACAGAAAGAA    34130      A  AAA
                                TCTAGA CA   AGGAGGAA
                                |||||| ||   ||||||||
                                AGATCT GT   TCTTTCTT
                                    C  G__
GAM1337  LOC145623 3'  TCTAGACTGGAAAGGAAGAAG  34131       ACAA
                                TCTAGA    AAAGGAGGAAG
                                ||||||    ||||||||||
                                AGATCT    TTTCCTTCTTC
                                    GACC
GAM1337  LOC145824 5'  TCTGGAACAAAAGCTAGGAG   34132     A      ___
                                TCT GAACAAAA   AGGAG
                                ||| ||||||||   |||||
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                                AGA CTTGTTTT   TCCTC
                                  C       CGA
GAM1337  LOC146050 3'  TCTAGATCAGGAAAAACAAGGA 34133       A ___   G
              A                   TCTAGA CA   AAAA GAGGAA
                                  |||||| ||   |||| ||||||
                                  AGATCT GT   TTTT TTCCTT
                                     A  CCT    G
GAM1337  LOC146229 3'  CCTAGAATGGAGAAAA      34134        CAAAAA
                                  TCTAGAA     GGAGGAAG
                                  ||||||| |||||||| |
                                  GGATCTT     CCTCTTTT
                                     A_____
GAM1337  LOC146237 3'  TCTAGAGAAAGAGGGCAGA   34135       ACAAA      A_
                                  TCTAGA    AAGGAGG  AGA
                                  ||||||    ||||||| |||
                                  AGATCT    TTTCTCC  TCT
                                     C____      CG
GAM1337  LOC146845 3'  TCAAGAACAAAAACAGAG    34136    T        _
                                  TC AGAACAAAAA GGAG
                                  || |||||||||| ||||
                                  AG TCTTGTTTTT TCTC
                                    T         G
GAM1337  LOC147081 5'  CTAGAACAAAAGAGGA      34137          AA
                                  CTAGAACAAA  GGAGGA
                                  |||||||||  ||||||
                                  GATCTTGTTT  TCTCCT
                                             __
GAM1337  LOC147093 3'  TCTAAACAAAGGAGG       34138       A   AA
                                  TCTAGA CAA  AGGAGG
                                  |||||| |||  ||||||
                                  AGATTT GTT  TCCTCC
                                     _  __
GAM1337  LOC149478 3'  TCTGGAATGAAAGAAGGA    34139     A   CAA
                                  TCT GAA   AAAGGAGGA
                                  ||| |||   |||||||||
                                  AGA CTT   TTTCTTCCT
                                    C   AC_
GAM1337  LOC150147 3'  TCTGGAACAAAAGGGCAG    34140     A       A  _
                                  TCT GAACAAAA GG AG
                                  ||| ||||||| || ||
                                  AGA CTTGTTTT CC TC
                                    C       C  G
GAM1337  LOC150848 5'  TCTAAAACAGAAAAATAAGGA  34141          __   G
                                  TCTAGAACA  AAAA GAGGA
                                  |||||||||  |||| |||||
                                  AGATTTTGT  TTTT TTCCT
                                        CT    A
GAM1337  LOC151040 3'  TCTAAGCAATGAGGAAGA    34142       AA   AAAG
                                  TCTAG  CAA    GAGGAAGA
                                  |||||  |||    ||||||||
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                                AGATT  GTT    CTCCTTCT
                                  C_   A___
GAM1337  LOC151429 3'  TAGAACAAAATAGATGGAA    34143          A   _
                                TAGAACAAAA GGA GGAA
                                |||||||||| ||| ||||
                                ATCTTGTTTT TCT CCTT
                                     A   A
GAM1337  LOC151996 3'  TCTAAATTCTAAGGAGGAAGAA 34144       ACAAA
              C                  TCTAGA     AAGGAGGAAGAAC
                                 ||||||     ||||||||||||
                                 AGATTT     TTCCTCCTTCTTG
                                    AAGA_
GAM1337  LOC154215 3'  TAGAACAAAATTTCCTAGGAG  34145          _______
                                TAGAACAAAA      AGGAG
                                ||||||||||      |||||
                                ATCTTGTTTT      TCCTC
                                     AAAGGA
GAM1337  LOC158819 5'  TAGGGACAGGGGAGGAAAGA   34146     A_   AAAA      _
                                TAG  ACA    GGAGGAA GA
                                |||  |||    ||||||| ||
                                ATC  TGT    CCTCCTT CT
                                  CC   CC__       T
GAM1337  LOC161829 5'  TCTAGAACTAAAAGAAGA     34147         A
                                TCTAGAAC AAAAGGAGG
                                |||||||| |||||||||
                                AGATCTTG TTTTCTTCT
                                     A
GAM1337  LOC199923 3'  CAGAACAAAAAGGCCTGTGGGA 34148             AGGAA__
              AC                   TAGAACAAAAAGG       GAAC
                                   ||||||||||||       ||||
                                   GTCTTGTTTTTCC      CTTG
                                         GGACACC
GAM1337  LOC219590 3'  TCTGGAACAAGAAAGATGA    34149     A     AAA      A
                                TCT GAACA   AGGAGGA GA
                                ||| |||||   ||||||| ||
                                AGA CTTGT   TCTTTCT CT
                                  C    ___       A
GAM1337  LOC220930 3'  TCTTAAAAAAAGGGAGGAAGAA 34150     A   C    A
              C                   TCT GAA AAAA GGAGGAAGAAC
                                  ||| ||| |||| ||||||||||||
                                  AGA TTT TTTT CCTCCTTCTTG
                                    A   _    C
GAM1337  LOC221448 3'  TCTGGGACAAAAAGGGAAAAGA 34151     AGA        AG
              A                   TCT   ACAAAAAGG  GAAGAA
                                  |||   |||||||||  ||||||
                                  AGA   TGTTTTTCC  TTTCTT
                                    CCC        CT
GAM1337  LOC221466 3'  TCTAGGGCAGGAAGAA      34152       AACAAAAA  _
                                TCTAG       GG AGGAAGAA
                                |||||       || ||||||||
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                                AGATC       CC TCCTTCTT
                                  _________ G
GAM1337  LOC221683 5'  TCTATAGCAAGAAGGACTAGAA 34153      GAACAAA       __
                                TCTA      AAGGAGGA  AGAA
                                ||||      ||||||||  ||||
                                AGAT      TTCTTCCT  TCTT
                                  ATCG___       GA
GAM1337  LOC221692 3'  TAAAACAAACTATTGGAGGA   34154         AA___
                                TAGAACAAA     GGAGGA
                                |||||||||     ||||||
                                ATTTTGTTT     CCTCCT
                                      GATAA
GAM1337  LOC255520 3'  CTGGAACAAAAGTGAAGA    34155    A       AG
                                CT GAACAAAA  GAGGA
                                || ||||||||  |||||
                                GA CTTGTTTT  CTTCT
                                 C       CA
GAM1337  LOC257106 5'  TCTAGGAAGGAGAAGGA     34156      AACAAA       A
                                TCTAG     AAGGAGGA GA
                                |||||     |||||||| ||
                                AGATC     TTCCTCTT CT
                                  C_____       C
GAM1337  LOC51107  3'  TCTGGGACCAAGGAGAAAG   34157     A_  ACAAA
                                TCT  GA    AAGGAGGAAG
                                |||  ||    ||||||||||
                                AGA  CT    TTCCTCTTTC
                                 CC  GG___
GAM1337  LOC51605  3'  TAGAACAAAGAATAAGA     34158        AA    GG
                                TAGAACAA  AGGA  AAGA
                                ||||||||  ||||  ||||
                                ATCTTGTT  TCTT  TTCT
                                     __    A_
GAM1337  LOC51652  3'  TCTAGAAAAGGAAGA       34159        CAAAAAG
                                TCTAGAA      GAGGAAGA
                                |||||||      ||||||||
                                AGATCTT      TTCCTTCT
                                  ________
GAM1337  LOC55885  3'  GAGCAAAAAAGATAAAAGAA   34160    A       _
                                GA CAAAAAGGA GGAAGAA
                                || |||||||| |||||||
                                CT GTTTTTTCT TTTTCTT
                                 C       A
GAM1337  LOC90288  3'  AACAAAAAGGCACAAAGA    34161          AG_
                                AACAAAAAGG   GAAGA
                                ||||||||||   |||||
                                TTGTTTTTCC   TTTCT
                                      GTG
GAM1337  LOC92249  3'  TAGTATAAAAAGGAAAAAG    34162     AAC
                                TAG   AAAAAGGAGGAAG
                                |||   |||||||||||||
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                                ATC  TTTTTCCTTTTTC
                                  ATA
GAM1338 ZNF185   3' TTGCGCACATTAGTGTGGA  34165       CTTT  CC
                                TTGCGCACG   TTA GTGGA
                                |||||||||   ||| |||||
                                AACGCGTGT   AAT CACCT
                                     ____  CA
GAM1339 KLHL3    3' TTTGATGCTGCAAATGCC    34168       _  TC
                                TTTGATGTT TAA GCC
                                ||||||||| ||| |||
                                AAACTACGA GTT CGG
                                     C  TA
GAM1339 FLJ20079 5' CTTGATGCCAAGATCGCC    34169       TA_
                                TTTGATGTT  ATCGCC
                                |||||||||  ||||||
                                GAACTACGG  TAGCGG
                                     TTC
GAM1339 MGC12335 3' TTTGATGTTTATACCTGCC   34170         _  _
                                TTTGATGTTTA ATC GCC
                                |||||||||||| ||| |||
                                AAACTACAAAT TGG CGG
                                      A  A
GAM1340 CNTNAP2  3' GTTACTTAATACTTTATCCAC 34173      _  TT
                                GTTACT AAT  CTTTATCCAC
                                |||||| |||  ||||||||||
                                CAATGA TTA  GAAATAGGTG
                                   A  T_
GAM1340 DSC3     3' TTTATTACTAAAATATCC    34174       TTTCTT
                                TTTGTTACTAA     TATCC
                                ||||||||||      |||||
                                AAATAATGATT     ATAGG
                                      TT____
GAM1340 DSC3     3' TTTATTACTAAAATATCC    34174       TTTCTT
                                TTTGTTACTAA     TATCC
                                ||||||||||      |||||
                                AAATAATGATT     ATAGG
                                      TT____
GAM1340 FSTL1    3' TCACTTTAATTTCTTTATTCA 34175      __       C
                                TTACT  AATTTCTTTAT CA
                                |||||  |||||||||||  ||
                                AGTGA  TTAAAGAAATA GT
                                   AA         A
GAM1340 VRK1     3' TTTGTCAAACATTTTTATCCAC 34176      CTA   CT
                                TTTGTTA   ATTT  TTATCCAC
                                |||||||   ||||  ||||||||
                                AAACAGT   TAAA  AATAGGTG
                                     TTG   __
GAM1340 DKFZp761K1423 3' TTTGTCACTAATTACTTT   34177         T
                                TTTGTTACTAATT CTTT
                                |||||||||||| ||||
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                                AAACAGTGATTAA GAAA
                                       T
GAM1340  DMTF1    3'  TTTGTTACTATGCTTATCCA  34178          ATTTC
                                TTTGTTACTA    TTTATCCA
                                ||||||||||    ||||||||
                                AAACAATGAT    GAATAGGT
                                      AC___
GAM1340  FLJ13187 3'  TTTGTTACTGGTGTCTTAACCA 34179         AATT   TAT
                                TTTGTTACT   TCTT  CCA
                                |||||||||   ||||  |||
                                AAACAATGA   AGAA  GGT
                                      CCAC   TT_
GAM1340  FLJ13215 3'  TTTCTTATCTTCTTCTTTATCC 34180    G  _ AA
              AC                  TTT TTA CT  TTTCTTTATCCAC
                                ||| ||| ||  ||||||||||||
                                AAA AAT GA  GAAGAAATAGGTG
                                  G  A  A_
GAM1340  LOC146420 3'  TTTGCTACTGATTTCTTC    34181          A
                                TTTGTTACT ATTTCTTT
                                ||||||||| ||||||||
                                AAACGATGA TAAAGAAG
                                      C
GAM1340  LOC152804 3'  TTTGTTACTGATTTCCTCCTC  34182         A       A
                                TTTGTTACT ATTTCTTT TC
                                ||||||||| |||||||| ||
                                AAACAATGA TAAAGGAG AG
                                      C       G
GAM1341  ADCY8    5'  GGAGGCCCGAGGCCGCG     34185        ACAG   A
                                GGAGGCC    CGA GGCCGCG
                                |||||||    ||| |||||||
                                CCTCCGG    GCT CCGGCGC
                                     _____   _
GAM1341  F8A      3'  GGAGGCAGGAGGCTGCG     34186        CAC  C  A   C
                                GGAGGC   AG GA GGC GCG
                                ||||||   || || ||| |||
                                CCTCCG   TC CT CCG CGC
                                   ___  _  _   A
GAM1341  FMNL     3'  GGCGGGCCACAGCGGAGG    34187    A_        A
                                GG  GGCCACAGCG AGG
                                ||  ||||||||||| |||
                                CC  CCGGTGTCGC TCC
                                  GC         C
GAM1341  GNA11    5'  AGGGGGCTGCGGTGTGGGGGCG 34188    A   CACA   AA_____  C
              CGT                   GG GGC    GCG     GG CGCGT
                                || |||    |||     || |||||
                                CC CCG    CGC     CC GCGCA
                                 C   A___   CACACC  C
GAM1341  GNPI     3'  AGGAGCCACAGTGAGGCC    34189       G     C  A
                                AGGAG CCACAG GA GGCC
                                ||||| |||||| || ||||
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                                TCCTC GGTGTC CT CCGG
                                  _     A  _
GAM1341 HUNK     3' GGAGGCCAAGGTGGGCAGATCG 34190       C  CGAA  CG__
             T                   GGAGGCCA AG   GGC   CGT
                                 |||||||| ||   |||   |||
                                 CCTCCGGT TC   CCG   GCA
                                    _ CAC_   TCTA
GAM1341 LGALS3BP 3' GGGAGCCTGCAGTGAGGGCGT 34191   AG  A_  C A CC
                                 GG  GCC  CAG GA GG  GCGT
                                 ||  |||  ||| || ||  ||||
                                 CC  CGG  GTC CT CC  CGCA
                                  CT  AC  A  _ __
GAM1341 RERE     5' GGAGGCCGCGCGGAGGCTGCG 34192       ACA  A   C
                                 GGAGGCC   GCG AGGC GCG
                                 |||||||   ||| |||| |||
                                 CCTCCGG   CGC TCCG CGC
                                     CG_   C   A
GAM1341 SPG4     5' GGGGGCCACAGACCCCCGT   34193    A      CGAAGG  G
                                 GG GGCCACAG     CC CGT
                                 || ||||||||     || |||
                                 CC CCGGTGTC     GG GCA
                                  C       TG____  G
GAM1341 C20orf39 3' GGCAGGCTGCAGAGAGCCGCGT 34194    _   CA  C  AG
                                 GG AGGC  CAG GA  GCCGCGT
                                 || ||||  ||| ||  |||||||
                                 CC TCCG  GTC CT  CGGCGCA
                                  G   AC   T __
GAM1341 DKFZp762K222 5' GGAGGCCACGGCGAGC      34195        A   AG
                                 GGAGGCCAC GCGA  GC
                                 ||||||||| ||||  ||
                                 CCTCCGGTG CGCT  CG
                                       C   __
GAM1341 FLJ21478 3' AGGAGGCCACAGAGGGAAAAGG 34196          C____
                                 AGGAGGCCACAG    GAAGG
                                 ||||||||||||    |||||
                                 TCCTCCGGTGTC    TTTCC
                                        TCCCT
GAM1341 KIAA0298 3' GGAGGCCACGGGAAGCCC    34197        AGC   G
                                 GGAGGCCAC   GAAG CC
                                 |||||||||   |||| ||
                                 CCTCCGGTG   CTTC GG
                                       CC_   G
GAM1341 KIAA0953 3' AGGAGGCCACTAGTGAGGAGG  34198        _  C  __
                                 AGGAGGCCAC AG GA  AGG
                                 |||||||||| || ||  |||
                                 TCCTCCGGTG TC CT  TCC
                                        A  A  CC
GAM1341 KIAA1169 5' AGGAGGCCACTGTGGAAGA   34199        AGC_
                                 AGGAGGCCAC    GAAGG
                                 ||||||||||    |||||
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                                TCCTCCGGTG   CTTCT
                                     ACAC
GAM1341 KIAA1784 3' GGAGGCCGCAGCAGGC     34200       A   GA
                                GGAGGCC CAGC  AGGC
                                ||||||| ||||  ||||
                                CCTCCGG GTCG  TCCG
                                   C   __
GAM1341 KIAA1908 5' GGAGGCCACGGCAGAC     34201        A  GA
                                GGAGGCCAC GC  AGGC
                                ||||||||| ||  ||||
                                CCTCCGGTG CG  TCTG
                                     C  __
GAM1341 KIAA1981 3' AGGGCGCCATAGTGAGCCGCGT 34202    AG   C  C  AG
                                AGG  GCCA AG GA  GCCGCGT
                                |||  |||| || ||  |||||||
                                TCC  CGGT TC CT  CGGCGCA
                                  CG   A  A  __
GAM1341 NYD-SP15 3' AGGAAGCCCAGTGAGGCCGTGT 34203       A   C  A    C
                                AGGAGGCC CAG GA GGCCG GT
                                |||||||| ||| || ||||| ||
                                TCCTTCGG GTC CT CCGGC CA
                                     _  A  _    A
GAM1341 PALM     3' GGCAGGCTGGCCTGGGCCGCGT 34204    _   CACA  GAA
                                GG AGGC   GC   GGCCGCGT
                                || ||||   ||   ||||||||
                                CC TCCG   CG   CCGGCGCA
                                 G   AC__  GAC
GAM1341 Rab11-FIP3 3' AGGAGGCCACAGCAGGGC    34205           AA
                                AGGAGGCCACAGCG  GGC
                                ||||||||||||||  |||
                                TCCTCCGGTGTCGT  CCG
                                       C_
GAM1341 RALGPS1A 3' GAGGCCACAGGCCGG      34206        GCGAA    C
                                GAGGCCACA    GGCCG G
                                |||||||||    ||||| |
                                CTCCGGTGT    CCGGC C
                                     _____    A
GAM1341 RGS19    3' AGGAGGCCCCAGCGAGGC    34207       A     A
                                AGGAGGCC CAGCGA GGC
                                |||||||| |||||| |||
                                TCCTCCGG GTCGCT CCG
                                     G    _
GAM1341 SLC12A8  5' AGGAAGTCATAGCGAAGGGCC  34208      C  C      _
                                AGGAGG CA AGCGAAGG CC
                                |||||| || |||||||| ||
                                TCCTTC GT TCGCTTCC GG
                                   A  A       C
GAM1341 LOC120448 5' GGAGGCCACAGGCTGCG     34209         GCGAA   C
                                GGAGGCCACA    GGC GCG
                                ||||||||||    ||| |||
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                                CCTCCGGTGT    CCG CGC
                                      _____   A
GAM1341  LOC144017 5'  AGGAGGCCGTGGCGAGGC    34210       ACA   A
                                AGGAGGCC   GCGA GGC
                                ||||||||   |||| |||
                                TCCTCCGG   CGCT CCG
                                    CAC    _
GAM1341  LOC147495 5'  AGGAGGCCTGGCGGAGGC    34211       ACA   A
                                AGGAGGCC   GCG AGGC
                                ||||||||   ||| ||||
                                TCCTCCGG   CGC TCCG
                                    AC_    C
GAM1341  LOC147639 5'  AGGAGGCCACAGAGGAAGG    34212         C_
                                AGGAGGCCACAG  GAAGG
                                ||||||||||||  |||||
                                TCCTCCGGTGTC  CTTCC
                                       TC
GAM1341  LOC148171 3'  GGAGGCCGCAGTGAGGC     34213       A   C  A
                                GGAGGCC CAG GA GGC
                                ||||||| ||| || |||
                                CCTCCGG GTC CT CCG
                                    C   A  _
GAM1341  LOC149684 5'  AGGAGCCCATCTCTGGCCGCGT 34214      G   CAGCGAA
                                AGGAG CCA      GGCCGCGT
                                ||||| |||      ||||||||
                                TCCTC GGT      CCGGCGCA
                                   G   AGAGA__
GAM1341  LOC154215 3'  AGGAGGCCACTGCGAAAA    34215         A
                                AGGAGGCCAC GCGAAGG
                                |||||||||| |||||||
                                TCCTCCGGTG CGCTTTT
                                      A
GAM1341  LOC165140 5'  GGAGGTCCAGGGCCGCG     34216      CCA   CGAA
                                GGAGG   CAG    GGCCGCG
                                |||||   |||    |||||||
                                CCTCC   GTC    CCGGCGC
                                   AG_   _____
GAM1341  LOC197285 3'  AGGGGTCACAGCGAGGAGG    34217     A  C      __
                                AGG GG CACAGCGA  AGG
                                ||| || ||||||||  |||
                                TCC CC GTGTCGCT  TCC
                                  _  A       CC
GAM1341  LOC199990 3'  AGGAGTCGGTGTGAGGCCGCGT 34218       GCCACAGC  A
                                AGGAG       GA GGCCGCGT
                                |||||       || ||||||||
                                TCCTC       CT CCGGCGCA
                                   AGCCACA_  _
GAM1341  LOC221683 5'  GGAGGCAGGAAGGCCGCGT    34219       CAC  C
                                GGAGGC   AG GAAGGCCGCGT
                                ||||||   || ||||||||||
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                                CCTCCG   TC CTTCCGGCGCA
                                   ___  _
GAM1341  LOC222057 3'  GGAGGCCGCAGTGAGGC     34213        A   C  A
                                GGAGGCC CAG GA GGC
                                ||||||| ||| || |||
                                CCTCCGG GTC CT CCG
                                    C   A  _
GAM1341  LOC222057 3'  AGGAGGCCAGGGTGAGGAAGA  34220         C____  C
                                AGGAGGCCA     AG GAAGG
                                |||||||||     || |||||
                                TCCTCCGGT     TC CTTCT
                                     CCCAC  _
GAM1341  LOC253891 5'  AGGAGGCCGCATGAGCCG    34221         ACA   AA
                                AGGAGGCC   GCG  GGCCG
                                ||||||||   |||  |||||
                                TCCTCCGG   CGT  TCGGC
                                   ___   AC
GAM1341  LOC255316 3'  AGGGGGCCACATGAAGG     34222     A      GC
                                AGG GGCCACA  GAAGG
                                ||| |||||||  |||||
                                TCC CCGGTGT  CTTCC
                                  C      A_
GAM1341  LOC255975 3'  GGAGGCCGCAGTGAGGC     34213        A   C  A
                                GGAGGCC CAG GA GGC
                                ||||||| ||| || |||
                                CCTCCGG GTC CT CCG
                                    C   A  _
GAM1341  LOC256019 3'  GGAGGCCACAGTGAGGC     34223          C  A
                                GGAGGCCACAG GA GGC
                                |||||||||||| || |||
                                CCTCCGGTGTC CT CCG
                                     A  _
GAM1341  LOC256019 5'  GGAGGCCGCAGTGAGGC     34213        A   C  A
                                GGAGGCC CAG GA GGC
                                ||||||| ||| || |||
                                CCTCCGG GTC CT CCG
                                    C   A  _
GAM1342  CAV2      3'  CATCTTAATAGTTTTCTT     34226      A
                                TATT TAATAGTTTTCTT
                                |||| ||||||||||||
                                GTAG ATTATCAAAAGAA
                                  A
GAM1342  DSCAM     3'  TTAATATATTTTGGCAATTTTC 34227          ATAA
                TT                  TTAATATATT    TAGTTTTCTT
                                    ||||||||||    ||||||||||
                                    AATTATATAA    GTTAAAAGAA
                                         AACC
GAM1342  FLJ11099  3'  AATATATTCATCAAAATAGTTT 34228         AT____
                TCTT                  AATATATT     AATAGTTTTCTT
                                      ||||||||     ||||||||||||
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                                TTATATAA     TTATCAAAAGAA
                                     GTAGTT
GAM1342  GOLGA1   3'  ATATATTTGCTAGTTTTCTT  34229       ATAA
                                ATATATT    TAGTTTTCTT
                                |||||||    ||||||||||
                                TATATAA    ATCAAAAGAA
                                    ACG_
GAM1343  CPA3     3'  TGCCCCACTGTATATCAC    34232        A   C
                                TGTCCCACT TATA CAC
                                ||||||||| |||| |||
                                ACGGGGTGA ATAT GTG
                                     C   A
GAM1343  GRM1     3'  CTGCTGTCCCATCATCCCA   34233    A      C   ATA
                                CT CTGTCCCA TAT   CCA
                                || |||||||| |||   |||
                                GA GACAGGGT GTA   GGT
                                 C       A   G__
GAM1343  HCS      3'  CACTGTCCCTGAATACCAC   34234        ACTAT
                                TACTGTCCC    ATACCAC
                                |||||||||    |||||||
                                GTGACAGGG    TATGGTG
                                     ACT__
GAM1343  NAPB     3'  CACTGTCCTACATCCA      34235       CAC    A
                                TACTGTCC   TATAT CCA
                                ||||||||   ||||| |||
                                GTGACAGG   ATGTA GGT
                                     ___    _
GAM1343  NFIA     3'  TGACTGTCCCGTTATATA    34236   T      AC
                                C ACTGTCCC  TATATA
                                | ||||||||  ||||||
                                A TGACAGGG  ATATAT
                                 C       CA
GAM1343  SYCP1    5'  CTGTCCCATTAAATTCCA    34237       C  T  A
                                CTGTCCCA TA AT CCA
                                |||||||| || || |||
                                GACAGGGT AT TA GGT
                                     A  T  A
GAM1343  SYT4     3'  CACTGTCTCACACACCA     34238       C   TAT
                                TACTGTC CAC   ATACCA
                                ||||||| |||   ||||||
                                GTGACAG GTG   TGTGGT
                                     A  ___
GAM1343  YES1     3'  CACTGTCCTTCATTACCA    34239       CAC   A
                                TACTGTCC   TAT TACCA
                                ||||||||   ||| |||||
                                GTGACAGG   GTA ATGGT
                                     AA_  _
GAM1343  ZNF180   3'  CACTTTTCACTATATATCA   34240     GTCC       C
                                TACT    CACTATATA CA
                                ||||    ||||||||| ||
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                                GTGA   GTGATATAT GT
                                  AAA_       A
GAM1343 ASAH     3' TACTGTCCCGTTACTCAC   34241        AC  A
                                TACTGTCCC  TAT TAC
                                |||||||||  ||| |||
                                ATGACAGGG  ATG GTG
                                     CA   A
GAM1343 B7-H1    3' TACTGTCCCGTTCCAACAC   34242        A__  T
                                TACTGTCCC   CTA ATAC
                                |||||||||   ||| ||||
                                ATGACAGGG   GGT TGTG
                                     CAA  _
GAM1343 C20orf142 3' CACTGTTCAGTCTATACCAC  34243      CC  CTA
                                TACTGT  CA   TATACCAC
                                ||||||  ||   ||||||||
                                GTGACA  GT   ATATGGTG
                                   A_  CAG
GAM1343 CBX1     3' CTACTGTCTTACCTCCTCTACC 34244        ___  A  ATA
             AC                   CTACTGTC   CC CT   TACCAC
                                |||||||   || ||   ||||||
                                GATGACAG   GG GG   ATGGTG
                                     AAT  A  AG_
GAM1343 DCLRE1A  5' CTGCTATTCCATTTATACCAC  34245    A   C   CTA
                                CT CTGT CCA   TATACCAC
                                || |||| |||   ||||||||
                                GA GATA GGT   ATATGGTG
                                 C   A   AA_
GAM1343 DKFZP434B103 5' CCACTGTCCCAGGACCTGTCAC 34246          CT  ATAC
                                CTACTGTCCCA  AT    CAC
                                ||||||||||  ||    |||
                                GGTGACAGGGT  TG    GTG
                                      CC  GACA
GAM1343 DKFZp761J139 5' CTATATCACTATATGTCAC   34247     CC      AC
                                CTGT  CACTATAT  CAC
                                ||||  ||||||||  |||
                                GATA  GTGATATA  GTG
                                  TA       CA
GAM1343 FLJ11116  3' CTACTGGAAACCTATATACCA  34248      TCCCA
                                CTACTG    CTATATACCA
                                ||||||    ||||||||||
                                GATGAC    GATATATGGT
                                   CTTTG
GAM1343 FLJ20034  3' CACTGTCCCAGCCTGACCAC   34249        _  ATAT
                                TACTGTCCCA CT    ACCAC
                                |||||||||| ||    |||||
                                GTGACAGGGT GG    TGGTG
                                      C  AC__
GAM1343 FLJ21302  3' CCACTGTCCCATTCCAC     34250          CTATATA
                                CTACTGTCCCA      CCAC
                                ||||||||||       ||||
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                                GGTGACAGGGT      GGTG
                                      AA_____
GAM1343  KIAA0295  3'  TACTGTCCCCTATTTCCCA   34251        A   ATA
                                TACTGTCCC CTAT   CCA
                                ||||||||| ||||   |||
                                ATGACAGGG GATA   GGT
                                      _   AAG
GAM1343  KIAA1130  3'  CCACTGTCCCATCTCCA     34252         _ ATATA
                                CTACTGTCCCA CT    CCA
                                |||||||||| ||    |||
                                GGTGACAGGGT GA    GGT
                                      A _____
GAM1343  KIAA1243  3'  CTACAGTCCCACTGATAT    34253     T      _
                                CTAC GTCCCACT ATAT
                                |||| |||||||| ||||
                                GATG CAGGGTGA TATA
                                  T       C
GAM1343  KIAA1944  5'  CTACTGTCTTCACTCCCA    34254       C_   ATATA
                                CTACTGTC  CACT    CCA
                                ||||||||  ||||    |||
                                GATGACAG  GTGA    GGT
                                     AA   G____
GAM1343  MY014     5'  CCATGTAAACATTATATACCAC 34255    C   CC_  C
                                CTA TGT   CA TATATACCAC
                                ||| |||   || ||||||||||
                                GGT ACA   GT ATATATGGTG
                                  _   TTT  A
GAM1343  PB1       3'  CTACTGTCTGCCATCCTAT   34256       __   __
                                CTACTGTC  CCA  CTAT
                                ||||||||  |||  ||||
                                GATGACAG  GGT  GATA
                                     AC   AG
GAM1343  PRO2012   3'  TAACTGTGGCATATACCAC   34257   T    CCCAC
                                C ACTGT    TATATACCAC
                                | |||||    ||||||||||
                                A TGACA    GTATATGGTG
                                 T    CC___
GAM1343  RINZF     3'  CTACTATCCAGCATGTACCA  34258       CAC   A
                                CTACTGTCC   TAT TACCA
                                |||||||||   ||| |||||
                                GATGATAGG   GTA ATGGT
                                      TC_   C
GAM1343  SEMA5B    3'  CCACTGTCCCATCTCCA     34252         _ ATATA
                                CTACTGTCCCA CT    CCA
                                |||||||||| ||    |||
                                GGTGACAGGGT GA    GGT
                                      A _____
GAM1343  SSR3      3'  CTACTTTTCCATATACCAC   34259      GTCCCA
                                CTACT     CTATATACCAC
                                |||||     ||||||||||
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                                GATGA     GGTATATGGTG
                                  AAA___
GAM1343  TTTY8    5'  CACTGTCCTGTGTATCCCAC   34260        CACTA   A
                                TACTGTCC     TAT CCAC
                                ||||||||     ||| ||||
                                GTGACAGG     ATA GGTG
                                   ACAC_   G
GAM1343  ULK2     3'  CACTGTTTCACACACACCA   34261       CC   T
                                TACTGT  CAC ATATACCA
                                ||||||  ||| ||||||||
                                GTGACA  GTG TGTGTGGT
                                  AA   _
GAM1343  LOC115708 3'  CTGCTGTCCCACTCTGGCCAC  34262     A        ATATA
                                CT CTGTCCCACT     CCAC
                                || ||||||||||     ||||
                                GA GACAGGGTGA     GGTG
                                 C         GACC_
GAM1343  LOC138399 5'  CTGCTGCTCCCACAGCCAC    34263    A   _     TATATA
                                CT CTG TCCCAC     CCAC
                                || ||| ||||||      ||||
                                GA GAC AGGGTG     GGTG
                                 C   G     TC_____
GAM1343  LOC145483 3'  CTACTGTCTACACCCA      34264        CCAC     A
                                CTACTGTC    TATAT CCA
                                ||||||||    ||||| |||
                                GATGACAG    ATGTG GGT
                                    _____    _
GAM1343  LOC150159 3'  CTACTGTCATCACATCC     34265        CCAC     A
                                CTACTGTC    TATAT CC
                                ||||||||    ||||| ||
                                GATGACAG    GTGTA GG
                                   TA__     _
GAM1343  LOC150212 3'  CCACTGTATGGATATACCAC   34266       CCCACT
                                CTACTGT     ATATACCAC
                                |||||||     |||||||||
                                GGTGACA     TATATGGTG
                                   TACC__
GAM1343  LOC152313 3'  CCACTGTCCCAGTACTTACTAC 34267          C   A   C
                                CTACTGTCCCA TAT TAC AC
                                |||||||||||| ||| ||| ||
                                GGTGACAGGGT ATG ATG TG
                                     C   A   A
GAM1343  LOC161734 3'  CTACTGTCCCCCCTCCCAC    34269         A  ATATA
                                CTACTGTCCC CT     CCAC
                                |||||||||| ||     ||||
                                GATGACAGGG GG     GGTG
                                   _  GAG__
GAM1343  LOC161734 3'  CCACTGTCCTGCACCCAC     34268         __   TATATA
                                CTACTGTCC  CAC     CCAC
                                |||||||||  |||     ||||
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                                GGTGACAGG GTG    GGTG
                                     AC  ______
GAM1343 LOC165186 3' CTACTTCAAAATATACCA   34270     GTCC CT
                                CTACT   CA ATATACCA
                                |||||   || ||||||||
                                GATGA   GT TATATGGT
                                   A___ TT
GAM1343 LOC221421 3' CTGTCCCACCCCACCAC    34271        ATA
                                CTGTCCCACT  TACCAC
                                ||||||||||  ||||||
                                GACAGGGTGG  GTGGTG
                                     G__
GAM1344 CASP10   3' TGTAGTTCTATTTCTAAATAA 34274   _    GCAAGC
                                TG AGTTCTA    TCTAAATAA
                                || |||||||    |||||||||
                                AC TCAAGAT    AGATTTATT
                                 A     AA____
GAM1344 CHN2     3' TGAGTTCTATTGCTAAAATAA 34275       GCAA  CT
                                TGAGTTCTA   GCT AAATAA
                                |||||||||   ||| ||||||
                                ACTCAAGAT   CGA TTTATT
                                     AA__  T_
GAM1344 KITLG    3' AGCTGCAAGTTCTAAAT    34276    CTA   C
                                AGTT  GCAAG TCTAAAT
                                ||||  ||||| |||||||
                                TCGA  CGTTC AGATTTA
                                  ___   A
GAM1344 KITLG    3' AGCTGCAAGTTCTAAAT    34276    CTA   C
                                AGTT  GCAAG TCTAAAT
                                ||||  ||||| |||||||
                                TCGA  CGTTC AGATTTA
                                  ___   A
GAM1344 SOX11    3' TGAGTTCTAACAGGTTTTAAAT 34277         AGCTC
                                TGAGTTCTAGCA    TAAAT
                                ||||||||||||    |||||
                                ACTCAAGATTGT    ATTTA
                                       CCAAA
GAM1344 C17orf26 3' TGAGTTCTAGCAGTTTGCT   34278         A___
                                TGAGTTCTAGCA   GCT
                                ||||||||||||   |||
                                ACTCAAGATCGT   CGA
                                       CAAA
GAM1344 DKFZP761E2110 3' TGGGTTTTAACAAGCCTTCCAA 34279   A  C     __
                                TG GTT TAGCAAGC  TCTAA
                                || ||| ||||||||  |||||
                                AC CAA ATTGTTCG  AGGTT
                                 C  A      GA
GAM1344 LOC123036 3' TGAGTTCTAATAAGTACT   34280        C  CT
                                TGAGTTCTAG AAG  CT
                                |||||||||| |||  ||
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                                ACTCAAGATT TTC  GA
                                      A   AT
GAM1344  LOC158819 5'  TGGGTTTTAACAAGCCCC    34281    A   C
                                TG GTT TAGCAAGCTCT
                                || ||| ||||||||||
                                AC CAA ATTGTTCGGGG
                                 C   A
GAM1344  LOC256080 5'  TGGGTTCTAGCAGGGCTCT   34282    A       A_
                                TG GTTCTAGCA  GCTCT
                                || |||||||||  |||||
                                AC CAAGATCGT  CGAGA
                                 C        CC
GAM1344  LOC91263  5'  TGAGTTCTGTGAGCCACTCTA  34283        ___   AA
                                TGAGTTCT   AGC  GCTCTA
                                ||||||||   |||  ||||||
                                ACTCAAGA   TCG  TGAGAT
                                     CAC   G_
GAM1345  DKFZP547N043 3'  TTTATTATAATGTTTTAAAC   34286      A
                                TTTAT ATAATGTTTTAGAT
                                ||||| ||||||||||||||
                                AAATA TATTACAAAATTTG
                                   A
GAM1345  ZNF297B   3'  TTTATAATAAAGTTTTAAAT   34287         T
                                TTTATAATAA GTTTTAGAT
                                |||||||||| |||||||||
                                AAATATTATT CAAAATTTA
                                      T
GAM1345  ZNF333    3'  TTTATAAATGTGTAGATGGTT  34288       TA    TT
                                TTTATAA  ATGT  TAGATGGTT
                                |||||||  ||||  |||||||||
                                AAATATT  TACA  ATCTACCAA
                                    __   C_
GAM1345  LOC158014 5'  TTTATAATATGCAGATAATGGT 34289         A   TTTA
            T                    TTTATAATA TGT    GATGGTT
                                |||||||||| |||    |||||||
                                AAATATTAT ACG    TTACCAA
                                      _  TCTA
GAM1346  ARHGEF7   3'  TGTCTGGATTCATCAGTCA    34292     CA   C      GGT
                                TGTC  GGA TCATCGG   TCA
                                ||||  ||| |||||||   |||
                                ACAG  CCT AGTAGTC   AGT
                                  A_   A      ___
GAM1346  ENTPD6    3'  GTCCAGGACAGGAGGGTT    34293         TCATC
                                GTCCAGGAC     GGGGTT
                                |||||||||     ||||||
                                CAGGTCCTG     TCCCAA
                                      TCC__
GAM1346  CAPN6     3'  TGTCTAGGACTCATTGAA    34294      C        C
                                TGTC AGGACTCAT GGG
                                |||| ||||||||| |||
```

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                                ACAG TCCTGAGTA CTT
                                  A       A
GAM1346 E       5' TGCCGGGGCTCATCGCCGGGT 34295     CA A     __
                                TGTC  GG CTCATCG  GGGT
                                ||||  || |||||||  ||||
                                ACGG  CC GAGTAGC  CCCA
                                  CC  _     GG
GAM1346 H2BFQ   3' TGTCTAGAGCTCATTTGGATTC 34296     C  GA    CG
             AT                   TGTC AG  CTCAT  GGGTTCAT
                                ||||  ||  |||||  ||||||||
                                ACAG TC  GAGTA  CCTAAGTA
                                  A  TC    AA
GAM1346 IGF2AS  3' TGTCTGTGGGGAGGGGGTTCAT 34297     CA_  ACTCATC
                                TGTC   GG      GGGGTTCAT
                                ||||   ||      |||||||||
                                ACAG   CC      CCCCAAGTA
                                  ACA  CCTC___
GAM1346 KIAA0652 3' GTCTAGGGCTCATTCCTTTCAT 34298    C   A    CGGGG
                                GTC AGG CTCAT     TTCAT
                                ||| ||| |||||     |||||
                                CAG TCC GAGTA     AAGTA
                                  A   C    AGGA_
GAM1346 KIAA1762 5' TGGCCAGGGCTTCCTGAGGGTT 34299    T    A  _ ATC
                                TG CCAGG CT C   GGGGTT
                                || ||||| || |   ||||||
                                AC GGTCC GA G   TCCCAA
                                 C    C  A GAC
GAM1346 KLF12   3' TCCAGGGTTCATGTCTATTCAT 34300       AC   CGGG
                                TCCAGG  TCAT    GTTCAT
                                ||||||  ||||    ||||||
                                AGGTCC  AGTA    TAAGTA
                                   CA    CAGA
GAM1346 MGC2628  3' TGTCTGGGTCTCATCGGCAGGC 34301     CA  A      __
             T                   TGTC  GG CTCATCGG  GGTT
                                ||||  || ||||||||  ||||
                                ACAG  CC GAGTAGCC  CCGA
                                  AC  A       GT
GAM1346 PIGQ    3' TGCCTGGGACTGGAGGGTTCAT 34302     CA    CATC
                                TGTC  GGACT    GGGGTTCAT
                                ||||  |||||    |||||||||
                                ACGG  CCTGA    TCCCAAGTA
                                  AC    CC__
GAM1346 SLC25A18 3' TGCTAGGACTCATAAGTT    34303     CC       CG
                                TGT  AGGACTCAT  GGGTT
                                |||  |||||||||  |||||
                                ACG  TCCTGAGTA  TTCAA
                                  A_        __
GAM1346 LOC133995 5' CGTCCAGGGCTCGTTGGGTT   34304        A   ATCG
                                TGTCCAGG CTC    GGGTT
                                |||||||| |||    |||||
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                                GCAGGTCC GAG   CCCAA
                                    C  CAA_
GAM1346  LOC148756 3'  TGTCCAGAGTTTATTCAAGTTC 34305       ACTC  CG
             AT                  TGTCCAGG   AT  GGGTTCAT
                                 ||||||||   ||  ||||||||
                                 ACAGGTCT   TA  TTCAAGTA
                                    CAAA  AG
GAM1346  LOC148758 5'  TGTCCAGGACTTCTCCCTGCC  34306         CA  GGG
                                 TGTCCAGGACT  TC  GTT
                                 ||||||||||  ||  |||
                                 ACAGGTCCTGA  AG  CGG
                                       AG  GGA
GAM1346  LOC149117 3'  TGATCAGGGTCGGGGTTCAT  34307   TC   ACTCA
                                 TG  CAGG   TCGGGGTTCAT
                                 ||  ||||   ||||||||||
                                 AC  GTCC   AGCCCCAAGTA
                                  TA   C____
GAM1346  LOC149117 3'  CAGGGTCGGGGTTCAT     34308     ACTCA
                                 CAGG   TCGGGGTTCAT
                                 ||||   ||||||||||
                                 GTCC   AGCCCCAAGTA
                                   C____
GAM1346  LOC149117 3'  TGATCAGGGTCGGGGTTCAT  34307   TC   ACTCA
                                 TG  CAGG   TCGGGGTTCAT
                                 ||  ||||   ||||||||||
                                 AC  GTCC   AGCCCCAAGTA
                                  TA   C____
GAM1346  LOC197319 3'  TGTCTGGGGCTCATGGAACC  34309     CA  A   C  GG
                                 TGTC  GG CTCAT GG  TT
                                 ||||  || ||||| ||  ||
                                 ACAG  CC GAGTA CC  GG
                                   AC  C    _  TT
GAM1346  LOC202551 3'  TGTTGAGGGCTCATCTGCTTCT 34310    CC   A    GGGG_
             C                   TGT  AGG CTCATC    TTC
                                 |||  ||| ||||||    |||
                                 ACA  TCC GAGTAG    GAG
                                   AC   C    ACGAA
GAM1346  LOC203286 5'  TGTCCAGGGTCATCCAATGAGT 34311        AC   G___
             TCAT                  TGTCCAGG  TCATC   GGGTTCAT
                                 ||||||||  |||||   ||||||||
                                 ACAGGTCC  AGTAG   CTCAAGTA
                                    C_    GTTA
GAM1346  LOC207089 3'  TGTCCGGGTACTTGAGTTCAT  34312      A  _   CATCG
                                 TGTCC GG ACT    GGGTTCAT
                                 ||||| || |||    ||||||||
                                 ACAGG CC TGA    CTCAAGTA
                                   C  A  A____
GAM1346  LOC220538 3'  TGTCCAGGCTCACTTC      34313        A    CGGGG
                                 TGTCCAGG CTCAT    TTC
                                 |||||||| |||||    |||
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                                ACAGGTCC GAGTG     AAG
                                  _    _____
GAM1346  LOC222070 5'  TGTCTGGACTCAGAAAATTCAT 34314      CA      TC
                                TGTC  GGACTCA  GGGGTTCAT
                                ||||  |||||||  |||||||||
                                ACAG  CCTGAGT  TTTTAAGTA
                                  A_      C_
GAM1346  LOC254670 5'  TGTCTAGGACTCAGCGTGC   34315      C       T  GG
                                TGTC AGGACTCA CG  GT
                                |||| |||||||| ||  ||
                                ACAG TCCTGAGT GC  CG
                                  A       C  A_
GAM1346  LOC92973  5'  GTCCAGGGCTCATTCTAGGC   34316        A    _ G
                                GTCCAGG CTCAT C GGGT
                                ||||||| ||||| | ||||
                                CAGGTCC GAGTA G TCCG
                                    C     A A
GAM1347  DGKB     3'  GCTTATTGTCTGTCTGTG    34319        A
                                GCTTATT TCTGTTTGTG
                                ||||||| ||||||||||
                                CGAATAA AGACAGACAC
                                    C
GAM1347  ECH1     3'  GCTTTATTGTTTGTG       34320      AT   C
                                GCTT  TAT TGTTTGTG
                                ||||  ||| ||||||||
                                CGAA  ATA ACAAACAC
                                  __  _
GAM1347  MOG      3'  TAGCTTGTTTGTTTGTGTCT   34321       A  ATC       _
                                TAGCTT TT   TGTTTGTG CT
                                |||||| ||   |||||||| ||
                                ATCGAA AA   ACAAACAC GA
                                   C  ___       A
GAM1347  SACM1L   3'  TAGCTTATTACTGAACT     34322          T   TTTGT
                                TAGCTTATTA CTG     GCT
                                |||||||||| |||     |||
                                ATCGAATAAT GAC     TGA
                                     _   T____
GAM1347  VCAM1    3'  GCTTATTATTTGTCTATA    34323          C
                                GCTTATTAT TGTTTGTG
                                ||||||||| ||||||||
                                CGAATAATA ACAGATAT
                                     A
GAM1347  VCAM1    3'  GCTTATTATTTGTCTATA    34323          C
                                GCTTATTAT TGTTTGTG
                                ||||||||| ||||||||
                                CGAATAATA ACAGATAT
                                     A
GAM1347  CDC14B   3'  TTATTATCTGAGTACTAA    34324          TTT
                                TTATTATCTG   GTGCTAA
                                ||||||||||   |||||||
```

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                                AATAATAGAC   CATGATT
                                     T__
GAM1347  FLJ00060  3'  GCTAGTTGTCTGTTCAGCAGTG 34325     TA  A     ____
              CT                   GCT  TT TCTGTTT    GTGCT
                                   |||  || |||||||    |||||
                                   CGA  AA AGACAAG    CACGA
                                     TC  C      TCGT
GAM1347  KIAA0419  3'  GCTTATTATTTCTGTCTATA   34326        __
                                   GCTTATTA  TCTGTTTGTG
                                   ||||||||  ||||||||||
                                   CGAATAAT  AGACAGATAT
                                        AA
GAM1347  KIAA0701  3'  TAGTTTATTGATCTGCTTG   34327     C    _
                                   TAG TTATT ATCTGTTTG
                                   ||| ||||| |||||||||
                                   ATC AATAA TAGACGAAC
                                     A    C
GAM1347  LHFPL2   3'  TAGCTTGTTTCTGTGCTGCT   34328       A  A    TTG
                                   TAGCTT TT TCTGT   TGCT
                                   ||||||| || |||||   ||||
                                   ATCGAA AA AGACA   ACGA
                                      C  _    CG_
GAM1347  SCYA27   3'  GCTTTATTATTTGGCTA     34329      AT   C     T
                                   GCTT  TAT TGTTTG GCTA
                                   ||||  ||| ||||||| ||||
                                   CGAA  ATA ATAAAC CGAT
                                     __  _     _
GAM1347  TEB4     3'  TAGCTTATGTTTGGCT      34330        TTATC     T
                                   TAGCTTA    TGTTTG GCT
                                   |||||||    ||||||| |||
                                   ATCGAAT    ACAAAC CGA
                                      _____     _
GAM1347  LOC256683 5'  TAGCTTATAATCTGTTGTCT   34331         T      T  G
                                   TAGCTTAT ATCTGTT GT CT
                                   |||||||| ||||||| || ||
                                   ATCGAATA TAGACAA CA GA
                                        T      _ _
GAM1348  ABCB4    5'  TGACAGTTTCTTCAGTCTCTGC 34334    T      C    ACC
                                   TG ACAGTTTC TTAGT   CTGC
                                   || |||||||| |||||   ||||
                                   AC TGTCAAAG AGTCA   GACG
                                    _       A    GA_
GAM1348  ABCB4    5'  TGACAGTTTCTTCAGTCTCTGC 34334    T      C    ACC
                                   TG ACAGTTTC TTAGT   CTGC
                                   || |||||||| |||||   ||||
                                   AC TGTCAAAG AGTCA   GACG
                                    _       A    GA_
GAM1348  CDK3     3'  TGCTGAATTCCTTAGTGCTTTG 34335     ACAGT       ACCC
              C                    TGT    TTCCTTAGT    TGC
                                   |||    |||||||||    |||
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                                ACG    AAGGAATCA   ACG
                                  ACTT_       CGAA
GAM1348 EVC     5' TGTGCAGTCTCCCGACTCCTGC 34336    A       TAGT _
                                TGT CAGTTTCCT   AC CCTGC
                                ||| |||||||||   || |||||
                                ACA GTCAGAGGG   TG GGACG
                                  C       C___  A
GAM1348 MLLT2   3' TGTAGGGTTTCCCTCCTG   34337     CA      AGTAC
                                TGTA  GTTTCCTT    CCTG
                                ||||  ||||||||    ||||
                                ACAT  CAAAGGGA    GGAC
                                  CC      _____
GAM1348 PIGH    3' TGTCAGTTTCCCATTGTTTTGC 34338    A       TAGTACCC
                                TGT CAGTTTCCT       TGC
                                ||| |||||||||       |||
                                ACA GTCAAAGGG       ACG
                                  _       TAACAAA_
GAM1348 RNTRE   3' TACAGTTTTTTCAGTACTTTG  34339       CC      CC
                                TACAGTTT  TTAGTAC  TG
                                ||||||||  |||||||  ||
                                ATGTCAAA  AGTCATG  AC
                                     AA      AA
GAM1348 WNT11   3' TGTCGGTTTCCTTTGATGTCCT 34340    ACA       AGTAC_
                  GC                  TGT   GTTTCCTT     CCTGC
                                ||| |||||||     |||||
                                ACA   CAAAGGAA     GGACG
                                  GC_       ACTACA
GAM1348 C20orf110 3' TGCACACTCCCTTGGTGCCCTG 34341       G      A  A
                  C                  TGTACA TTTCCTT GT CCCTGC
                                |||||| ||||||| || ||||||
                                ACGTGT GAGGGAA CA GGGACG
                                     _      C  C
GAM1348 DKFZP434P0721 3' TGTACAGTTGCTTTAAAAAACT 34342         TCC    TACC
                  G                  TGTACAGTT   TTAG    CTG
                                |||||||||   ||||    |||
                                ACATGTCAA   AATT    GAC
                                     CGA    TTTT
GAM1348 DKFZp761D221 3' TACAGTTTTTATTATACCTTGC 34343        CCTTA    C
                                TACAGTTT    GTACC TGC
                                ||||||||    ||||| |||
                                ATGTCAAA    TATGG ACG
                                     AATAA    A
GAM1348 DNCI2   3' TGTAAGTTTCCTTGCT     34344     C       A TACC
                                TGTA AGTTTCCTT G    CT
                                |||| ||||||||| |    ||
                                ACAT TCAAAGGAA C    GA
                                  _       _ _____
GAM1348 FLJ11715 3' TGTGCAGTTTCCTTTCTG    34345    A       AGTACC
                                TGT CAGTTTCCTT     CTG
                                ||| ||||||||||     |||
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                                ACA GTCAAAGGAA     GAC
                                  C        A_____
GAM1348  FLJ12171  3'  TACAGTTTCCCCACCTTG    34346          TAG    C
                                TACAGTTTCCT   TACC TG
                                ||||||||||   |||| ||
                                ATGTCAAAGGG   GTGG AC
                                      ___    A
GAM1348  FLJ20281  5'  TGTACAGCTTCTCGCTGAGCTC 34347          ___  T   ACC
           TG                    TGTACAGTTTC   CT AGT   CTG
                                ||||||||||   || |||   |||
                                ACATGTCGAAG   GA TCG   GAC
                                      AGC  C   A__
GAM1348  GP       5'  GTGCAGTTTCCCCTCTG     34348    A       TTAGTA  _
                                GT CAGTTTCC     CC CTG
                                || ||||||||     || |||
                                CA GTCAAAGG     GG GAC
                                 C       _______  A
GAM1348  IL1RAPL1  3'  TCTCTTCTTAGTACTCTG    34349     __       C
                                TTTC  CTTAGTAC CTG
                                ||||  |||||||| |||
                                AGAG  GAATCATG GAC
                                  AA       A
GAM1348  KIAA1979  3'  TGTAAAGTTTCCCTCT      34350      C        AGTACC
                                TGTA AGTTTCCTT     CT
                                |||| |||||||||     ||
                                ACAT TCAAAGGGA     GA
                                  T       _______
GAM1348  PRO0365   5'  AGTTTCCTAAGACCTTG     34351        T  T   C
                                AGTTTCCT AG ACC TG
                                |||||||| || ||| ||
                                TCAAAGGA TC TGG AC
                                     T  _   A
GAM1348  TU12B1-TY 3'  TACAGTTTCTAGTTTTTG    34352         CT    ACCC
                                TACAGTTTC  TAGT    TG
                                |||||||||  ||||    ||
                                ATGTCAAAG  ATCA    AC
                                      __    AAA_
GAM1348  LOC150819 5'  TGTGTGGCTTCCTTCCACTGC  34353     ACA       AGTA  _
                                TGT   GTTTCCTT    CC CTGC
                                |||   ||||||||    || ||||
                                ACA   CGAAGGAA    GG GACG
                                  CAC       _____  T
GAM1348  LOC200860 3'  TGTTAGTTTCCCAGCCTCTGC  34354     AC       T   ACC
                                TGT  AGTTTCCT AGT   CTGC
                                |||  |||||||| |||   ||||
                                ACA  TCAAAGGG TCG   GACG
                                  A_       _   GA_
GAM1348  LOC254549 5'  TGTACAGTGTCACTTTGT    34355         T  _   A
                                TGTACAGT TC CTT GT
                                |||||||| || ||| ||
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                                ACATGTCA AG GAA CA
                                     C T   A
GAM1348 LOC90639 3' TGTAGTTTCCTGTGTCCCTGC 34356     AC       TA  A
                                TGT  AGTTTCCT  GT CCCTGC
                                |||  ||||||||  || ||||||
                                ACA  TCAAAGGA  CA GGGACG
                                  __       CA  _
GAM1348 LOC91445 3' TGACAGTTTCTCTCTTTCTGC 34357    T      _   AGTACC
                                TG ACAGTTTC CTT     CTGC
                                || |||||||| |||     ||||
                                AC TGTCAAAG GAG     GACG
                                 _       A   AAA___
GAM1348 LOC92340 3' TGTACAATTTCTGAACCTTG  34358          CTTAGT   C
                                TGTACAGTTTC     ACC TG
                                ||||||||||      ||| ||
                                ACATGTTAAAG     TGG AC
                                       ACT___   A
GAM1349 BRIP1    3' TAATAACATTTACATTTCT   34361        C
                                TAATAACA TTACGTTTTT
                                |||||||| ||||||||||
                                ATTATTGT AATGTAAAGA
                                     A
GAM1349 FLJ11726 3' TAATAACACTTGTGTTTC    34362          AC
                                TAATAACACTT  GTTTT
                                ||||||||||  |||||
                                ATTATTGTGAA  CAAAG
                                       CA
GAM1349 KIAA1136 3' ACACTTACAGCTTTATTGA   34363        T     C
                                ACACTTACG TTTTAT GA
                                ||||||||| ||||||  ||
                                TGTGAATGT GAAATA CT
                                     C     A
GAM1349 LOC145801 3' TAACAACACTTACAATTTT   34364           T
                                TAATAACACTTACG TTTT
                                |||||||||||||| ||||
                                ATTGTTGTGAATGT AAAA
                                       T
GAM1349 LOC257295 3' TAACAACACTTACAATTTT   34364           T
                                TAATAACACTTACG TTTT
                                |||||||||||||| ||||
                                ATTGTTGTGAATGT AAAA
                                       T
GAM1350 KIAA0993 3' TGATTCTGTTGATTTCTGC   34367        A   CA   C
                                TGATTCTG TGA  TCT GC
                                |||||||| |||  ||| ||
                                ACTAAGAC ACT  AGA CG
                                     A   AA  _
GAM1350 LOC133418 3' TAAGTGATTCTGCTGATATCT  34368     A       A   C
                                TAA TGATTCTG TGA ATCT
                                ||| |||||||| ||| ||||
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                                ATT ACTAAGAC ACT TAGA
                                  C       G   A
GAM1350  LOC255098 3'  TAAGTGATTCTGCTGATATCT  34368     A       A   C
                                TAA TGATTCTG TGA ATCT
                                ||| |||||||| ||| ||||
                                ATT ACTAAGAC ACT TAGA
                                  C       G   A
GAM1351  ATSV     3'  TCTCTGCCCTGGGAACAAAGAG 34371      A_   CA   CTA
              AG                  TCTC  CCC  GGA   AAAGAGAG
                                ||||  |||  |||   ||||||||
                                AGAG  GGG  CCT   TTTCTCTC
                                  AC   AC   TG_
GAM1351  BRAF     3'  TCCACCTTAAAAAAAAAGAGAG 34372    T    CC    CT
                                TC CACC  AGGA  AAAAGAGAG
                                || ||||  ||||  |||||||||
                                AG GTGG  TTTT  TTTTCTCTC
                                 _    AA    T_
GAM1351  CDKN1A   3'  CCTCACCCCCACAGCTAGAGGA 34373         A__  A   AAA
              G                   TCTCACCCC   GG CTA   GAG
                                |||||||||   || |||   |||
                                GGAGTGGGG   TC GAT   CTC
                                     GTG  _   CTC
GAM1351  CELSR3   3'  CCACCCCAGGAAGGAGAGAG   34374          CTAAA
                                TCACCCCAGGA    AGAGAG
                                ||||||||||    ||||||
                                GGTGGGGTCCT    TCTCTC
                                      TCC__
GAM1351  COL4A2   3'  TCCCACCCCGAGAAGGGA    34375         AG  CTAAA  A
                                TCTCACCCC  GA    AG GA
                                |||||||||  ||    || ||
                                AGGGTGGGG  CT    TC CT
                                     CT _____  C
GAM1351  EGLN2    5'  CCTTGCCCTGGAAAGAGA    34376     CA   CA   CTAA
                                TCT  CCC  GGA   AAGAGA
                                |||  |||  |||   ||||||
                                GGA  GGG  CCT   TTCTCT
                                  AC   A_  ____
GAM1351  FTSJ2    3'  TCTCTTTTTGGTTAAAAAGAGA 34377      ACCCCA  ACT
              G                   TCTC     GG   AAAAGAGAG
                                ||||     ||   |||||||||
                                AGAG     CC   TTTTCTCTC
                                  AAAAA_  AAT
GAM1351  IKBKG    3'  TCTACCCCAAAAGAG      34378     C     GGACTA
                                TCT ACCCCA     AAAGAG
                                ||| ||||||     ||||||
                                AGA TGGGGT     TTTCTC
                                  _    _______
GAM1351  IKBKG    3'  TCTACCCCAAAAGAG      34378     C     GGACTA
                                TCT ACCCCA     AAAGAG
                                ||| ||||||     ||||||
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                                AGA TGGGGT     TTTCTC
                                  _    _______
GAM1351  MAPRE2   3'  TCACACCAGGATAAAAAGAG  34379     C     CT
                                TCAC CCAGGA  AAAAGAG
                                |||| ||||||  |||||||
                                AGTG GGTCCT  TTTTCTC
                                  T     AT
GAM1351  NPR1     5'  CTCACCCCGGGGCTCGAG    34380       A  A  AAAA
                                CTCACCCC GG CT   GAG
                                |||||||| || ||   |||
                                GAGTGGGG CC GA   CTC
                                    C  C  G___
GAM1351  PML      3'  TCTCGTCCAGGACCCTGAG   34381     ACC      AAAA
                                TCTC   CCAGGACT   GAG
                                ||||   ||||||||   |||
                                AGAG   GGTCCTGG   CTC
                                  CA_      GA__
GAM1351  SNL      3'  CTCACCCCAGGGCTCCCGGAG  34382         A  AAAA
                                CTCACCCCAGG CT   GAG
                                |||||||||| ||   |||
                                GAGTGGGGTCC GA   CTC
                                      C  GGGC
GAM1351  SOD3     5'  TCTCTCCTGAAAAGAGA     34383     A  CCAG  CTA
                                TCTC CC   GA   AAAGAGA
                                |||| ||   ||   |||||||
                                AGAG GG   CT   TTTCTCT
                                  A  A___  ___
GAM1351  TEM8     3'  TCTCAACTTTGGTAAAAGAGAG 34384      CCCCA  AC
                                TCTCA    GG  TAAAAGAGAG
                                |||||    ||  ||||||||||
                                AGAGT    CC  ATTTTCTCTC
                                  TGAAA  __
GAM1351  TK1      3'  CCTCACCCCAAGGAGA      34385          ACTAAAA
                                TCTCACCCCAGG      GAGA
                                ||||||||||||      ||||
                                GGAGTGGGGTTC      CTCT
                                          _______
GAM1351  TRAF1    3'  TCTGACCCTGGAGAAAAAGAGA 34386     C   CA   CT
           G                     TCT ACCC  GGA  AAAAGAGAG
                                ||| ||||  |||  |||||||||
                                AGA TGGG  CCT  TTTTCTCTC
                                  C   A_   CT
GAM1351  TRPV1    5'  TCTCACCCCAGAGGCCTCAGAG 34387          _ A  AAA
                                TCTCACCCCAG G CT   AGAG
                                |||||||||| | ||   ||||
                                AGAGTGGGGTC C GG   TCTC
                                      T C  AG_
GAM1351  C9orf5   3'  TCTCTCTCAGAAAAGAGA    34388     ACCC    CTAA
                                TCTC   CAGGA   AAGAGA
                                ||||   |||||   ||||||
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                                AGAG   GTCTT   TTCTCT
                                  AGA_   ____
GAM1351 CEACAM7  3' TCATTCCAGCCAAAGAGAG   34389    CC   GACTA
                                TCA  CCAG    AAAGAGAG
                                |||  ||||    ||||||||
                                AGT  GGTC    TTTCTCTC
                                  AA   GG___
GAM1351 DDX18    3' CCCAGAAATAAAAGAGAG    34390       C
                                CCCAGGA TAAAAGAGAG
                                ||||||| |||||||||
                                GGGTCTT ATTTTCTCTC
                                    T
GAM1351 DKFZP434P0721 3' CCACCCCATCTCAAAGAGAG   34391        GGACTA
                                TCACCCCA     AAAGAGAG
                                ||||||||     ||||||||
                                GGTGGGGT     TTTCTCTC
                                    AGAG__
GAM1351 FLJ10246 3' TCTCCTAAACTCTAAAAGAGAG 34392     ACCCCAGGA
                                TCTC       CTAAAAGAGAG
                                ||||       ||||||||||
                                AGAG       GATTTTCTCTC
                                  GATTTGA__
GAM1351 FLJ20170 5' TCTCACCCTGTGGCTGACTGGA 34393        CAG____   AAAA
           G                     TCTCACCC      GACT   GAG
                                ||||||||      ||||   |||
                                AGAGTGGG      CTGA   CTC
                                    ACACCGA   C___
GAM1351 FLJ20413 3' TCCCACCCCAGGGATCCAGGAA 34394          ACTAAA  AG
           G                     TCTCACCCCAGG     AG  AG
                                ||||||||||||     ||  ||
                                AGGGTGGGGTCC     TC  TC
                                      CTAGG_  CT
GAM1351 GMPPB    3' TCCCACCCCCTTGGGAAGGGGA 34395        A___   CTAAAA
           G                     TCTCACCCC    GGA     GAG
                                |||||||||    |||     |||
                                AGGGTGGGG    CCT     CTC
                                    GAAC   TCCC__
GAM1351 HSPC055  5' TCTTTCCTCAGGACTATGAG   34396    CA  C      AAA
                                TCT  CC CAGGACTA   GAG
                                |||  || ||||||||   |||
                                AGA  GG GTCCTGAT   CTC
                                  AA  A       A__
GAM1351 KIAA0783 3' TCACACTAGGACTAATAAG   34397     CCC      _
                                TCAC   AGGACTAA AAG
                                ||||   |||||||| |||
                                AGTG   TCCTGATT TTC
                                  TGA       A
GAM1351 KIAA1724 3' CCTCACCCTGAAAAAAGAAGAG 34398        CA   CT  _
           AG                     TCTCACCC  GGA  AA AAGAGAG
                                ||||||||  |||  || |||||||
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                                GGAGTGGG  CTT  TT TTCTCTC
                                    A_   TT  C
GAM1351  MGC29898  5'  TCTACCCCAGGAAAGGA     34399     C       CTAA   A
                                TCT ACCCCAGGA    AAG GA
                                ||| |||||||||    ||| ||
                                AGA TGGGGTCCT    TTC CT
                                  _       _____   _
GAM1351  OS4       3'  TCCCACCCCAGGAGGAGGGAG  34400           CTAAAA
                                TCTCACCCCAGGA     GAG
                                ||||||||||||      |||
                                AGGGTGGGGTCCT     CTC
                                       CCTCC_
GAM1351  OSBPL10   5'  CCACCTCGGGACCTGGAGGGAG 34401      CCA    AAA  A
                                TCACC   GGACT   AG GAG
                                |||||   |||||   || |||
                                GGTGG   CCTGG   TC CTC
                                   AGC    ACC  C
GAM1351  SDC3      3'  TCTCACCCAGCTAGAGAGA   34402        CA  A   AA
                                TCTCACCC  GG CTA  AGAGA
                                ||||||||  || |||  |||||
                                AGAGTGGG  TC GAT  TCTCT
                                    __  _   C_
GAM1351  LOC116113 3'  TCCCACCCCAGCAGCAGAG   34403          GACTAAA
                                TCTCACCCCAG      AGAG
                                ||||||||||       ||||
                                AGGGTGGGGTC      TCTC
                                      GTCG___
GAM1351  LOC129566 5'  TCTGCCCCCAAGAGGAGA    34404     CA       CTAAAA
                                TCT  CCCCAGGA     GAGA
                                |||  ||||||||     ||||
                                AGA  GGGGTTCT     CTCT
                                  CG       C_____
GAM1351  LOC153196 5'  TCTTCCCCAGAACGGGAG    34405     CA       TAAAA
                                TCT  CCCCAGGAC    GAG
                                |||  |||||||||    |||
                                AGA  GGGGTCTTG    CTC
                                  A_       CC___
GAM1351  LOC157421 5'  TCTCGCCTCAGGACCATAAG   34406      A  C       A
                                TCTC CC CAGGACTA AAG
                                |||| || |||||||| |||
                                AGAG GG GTCCTGGT TTC
                                  C  A       A
GAM1351  LOC159090 5'  TCTCACTGCAGGACTGAG    34407       CC      AAAA
                                TCTCAC  CAGGACT    GAG
                                ||||||  |||||||    |||
                                AGAGTG  GTCCTGA    CTC
                                   AC      _____
GAM1351  LOC200059 3'  TCTCATATTGAACAAAAAGAGA 34408       CCCCA    T
            G                   TCTCA    GGAC AAAAGAGAG
                                |||||    |||| |||||||||
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                                AGAGT    CTTG TTTTCTCTC
                                   ATAA_   T
GAM1351  LOC201109 3'  CCACCCCAGGCCTGGGGGAG  34409         A  AAAA
                                TCACCCCAGG CT    GAG
                                |||||||||| ||    |||
                                GGTGGGGTCC GA    CTC
                                     G  CCCC
GAM1351  LOC253187 5'  TCTCAATCCAGGACTGAG    34410      CC      AAAA
                                TCTCA  CCAGGACT    GAG
                                |||||  ||||||||    |||
                                AGAGT  GGTCCTGA    CTC
                                   TA      _____
GAM1351  LOC253983 3'  TCTCTCCCAGGACAAAGAG   34411     AC      TA
                                TCTC  CCCAGGAC  AAAGAG
                                ||||  ||||||||  ||||||
                                AGAG  GGGTCCTG  TTTCTC
                                  A_      __
GAM1351  LOC255480 3'  TCTCTCCCCAAAAGAG     34412     A    GGACTA
                                TCTC CCCCA     AAAGAG
                                |||| |||||     ||||||
                                AGAG GGGGT     TTTCTC
                                  A    _______
GAM1352  B3GALT3   3'  ACTACCACCATCTGTCTTAA   34415      ATAG     A
                                ACTAC    TTATCT TCTTAA
                                |||||    |||||| ||||||
                                TGATG    GGTAGA AGAATT
                                   GT__     C
GAM1352  C20orf80  3'  TACATGTTATCTATTTTAA    34416      A       C
                                TACAT GTTATCTAT TTAA
                                ||||| ||||||||| ||||
                                ATGTA CAATAGATA AATT
                                   _       A
GAM1352  CBX3     3'  TTACTACAAAGTTGTTCTTCCT 34417        T    A_   A
                                TTACTACA AGTT  TCT TCTT
                                |||||||| ||||  ||| ||||
                                AATGATGT TCAA  AGA AGGA
                                     T    CA   _
GAM1352  CBX3     3'  TTACTACAAAGTTGTTCTTCCT 34417        T    A_   A
                                TTACTACA AGTT  TCT TCTT
                                |||||||| ||||  ||| ||||
                                AATGATGT TCAA  AGA AGGA
                                     T    CA   _
GAM1352  FLJ10261  3'  TTACCATTTTGCATCTATCTTA 34418       CATA  T
            A                    TTACTA    GT ATCTATCTTAA
                                ||||||    || ||||||||||
                                AATGGT    CG TAGATAGAATT
                                   AAAA  _
GAM1352  FLJ20519  3'  TACATAGTTCAGTCTTA     34419        TA  TA
                                TACATAGT  TC  TCTTA
                                ||||||||  ||  |||||
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                                ATGTATCA  AG  AGAAT
                                    __  TC
GAM1352  KIAA0426  3'  TTACTATGTGTTATCTAT    34420       CATA
                                TTACTA   GTTATCTAT
                                ||||||   |||||||||
                                AATGAT   CAATAGATA
                                   ACA_
GAM1352  LOC257048 3'  TTACCACAGGACTCTATCTTA  34421        TAGTTA
                                TTACTACA    TCTATCTTA
                                ||||||||    |||||||||
                                AATGGTGT    AGATAGAAT
                                    CCTG__
GAM1352  LOC51133  3'  TTACTACATAGTGGTATCT   34422          __
                                TTACTACATAGT  TATCT
                                ||||||||||||  |||||
                                AATGATGTATCA  ATAGA
                                      CC
GAM1353  ABCD1     3'  GGGTGGTGCCCGGCCCGAGG   34425     T  _  A__    AA
                                GGGT GG GC   GCCC  AGG
                                |||| || ||   ||||  |||
                                CCCA CC CG   CGGG  TCC
                                  _ A  GGC    C_
GAM1353  CACNG1    3'  GAGCCTGCGGCAGCCCAGAGG  34426      _ _       A
                                GGGT TG GGCAGCCCA AGG
                                |||| || |||||||| |||
                                CTCG AC CCGTCGGGT TCC
                                  G  G        C
GAM1353  FBXO7     5'  CGGGCAGGCGGCCTAAAGG    34427      T    A   C
                                CGGGT GGGC GCC AAAGG
                                ||||| |||| ||| |||||
                                GCCCG TCCG CGG TTTCC
                                  _    C   A
GAM1353  GAS7      3'  GGGCCAGGGCAGCCCAAAGG   34428      _
                                GGGTT GGGCAGCCCAAAGG
                                ||||| ||||||||||||||
                                CCCGG CCCGTCGGGTTTCC
                                   T
GAM1353  GAS7      3'  GGGCCAGGGCAGCCCAAAGG   34428      _
                                GGGTT GGGCAGCCCAAAGG
                                ||||| ||||||||||||||
                                CCCGG CCCGTCGGGTTTCC
                                   T
GAM1353  GRB7      3'  GGGCGGCGGGCAGCCTGAAGG  34429      __       CA
                                GGGT  TGGGCAGCC  AAGG
                                ||||  |||||||||  ||||
                                CCCG  GCCCGTCGG  TTCC
                                  CC        AC
GAM1353  LASS2     5'  CGCGAGCAGCCCAAG       34430    GGT         A
                                CG   TGGGCAGCCCAA G
                                ||   ||||||||||||
```

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                                GC   GCTCGTCGGGTT C
                                 ___          C
GAM1353  LZTFL1   5'  CAGCGGCGGCAGCCTAAAGG  34431    A   GTTG      C
                                CA CGG    GGCAGCC AAAGG
                                || |||    ||||||| |||||
                                GT GCC    CCGTCGG TTTCC
                                 C   G___      A
GAM1353  NCOA6    5'  GGGTAATCCAGCCCAAAGG   34432     TGGG
                                GGGT    CAGCCCAAAGG
                                ||||    ||||||||||
                                CCCA    GTCGGGTTTCC
                                  TTAG
GAM1353  PIK3CD   3'  ACAGCAGGTTCCCAAA     34433     A     GGGCAG
                                ACA CGGGTT     CCCAAA
                                ||| ||||||     ||||||
                                TGT GTCCAA     GGGTTT
                                 C     _______
GAM1353  PLTP     5'  GGGATGGCGGGCAGCTCAGGGG 34434     T___       C  AA
                                GGG    TGGGCAGC CA  GG
                                |||    |||||||| ||  ||
                                CCC    GCCCGTCG GT  CC
                                  TACC       A  CC
GAM1353  PTPN11   5'  ACATCGGGCTGGCCCGAG    34435     A      GGCA    AA
                                ACA CGGGTTG    GCCC  AG
                                ||| |||||||    ||||  ||
                                TGT GCCCGAC    CGGG  TC
                                  A      _____    C_
GAM1353  PTPN11   5'  ACATCGGGCTGGCCCGAG    34435     A      GGCA    AA
                                ACA CGGGTTG    GCCC  AG
                                ||| |||||||    ||||  ||
                                TGT GCCCGAC    CGGG  TC
                                  A      _____    C_
GAM1353  PVT1     3'  ACGTGCCAAGCAGCTCAAAGG  34436     G  TG     C
                                ACG GT  GGCAGC CAAAGG
                                ||| ||  |||||| ||||||
                                TGC CG  TCGTCG GTTTCC
                                  A  GT     A
GAM1353  RAB36    3'  ACGGGCCTACAGCTTGAGG    34437        GG     CCAA
                                ACGGGTT  GCAGC    AGG
                                |||||||  |||||    |||
                                TGCCCGG  TGTCG    TCC
                                    A_     AAC_
GAM1353  SLC6A1   5'  ACAGCAGTTTTGCGGCTCAAGG 34438     A   G  GG  A  C   A
              G                  ACA CGG TT  GC GC CAA GG
                                 ||| ||| ||  || || ||| ||
                                 TGT GTC AA  CG CG GTT CC
                                   C   _  AA  C  A   C
GAM1353  SLC9A5   3'  GGTGACATGGCAGCCCAGAGG  34439     TG___       A
                                GGT     GGCAGCCCA AGG
                                |||     ||||||||| |||
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                                CCA    CCGTCGGGT TCC
                                  CTGTA       C
GAM1353 SLC9A5   3' GGTGACATGGCAGCCCAGAGG 34439    TG___       A
                                GGT    GGCAGCCCA AGG
                                |||    ||||||||| |||
                                CCA    CCGTCGGGT TCC
                                  CTGTA       C
GAM1353 SORCS3   3' CGGGTTGGTCAGCTCTGAGG  34440       G   CCAA
                                CGGGTTGG CAGC   AGG
                                |||||||| ||||   |||
                                GCCCAACC GTCG   TCC
                                     A   AGAC
GAM1353 SOX9     3' ACAATATAAGGCAGCCCAAAGG 34441     GTT_
                                ACGG   GGGCAGCCCAAAGG
                                ||||   ||||||||||||||
                                TGTT   TCCGTCGGGTTTCC
                                  ATAT
GAM1353 ST7      3' CAACGGGGTGGATGGCGGAGG  34442       T   CA  CCAA
                                CAACGGG TGGG  GC   AGG
                                ||||||| ||||  ||   |||
                                GTTGCCC ACCT  CG   TCC
                                    C   AC  CC__
GAM1353 SYNGR2   3' ACCACGGGAGGCAGCCCAGAGG 34443    A    TT       A
                                AC ACGGG  GGGCAGCCCA AGG
                                || |||||  |||||||||| |||
                                TG TGCCC  TCCGTCGGGT TCC
                                 G    __        C
GAM1353 TCF19    5' AACTGGTTGAACCTCCGAGG   34444    G      AG  CAA
                                AAC GGTTGGGC  CC   AGG
                                ||| ||||||||  ||   |||
                                TTG CCAACTTG  GG   TCC
                                  A       GA  C__
GAM1353 TCF19    5' AACTGGTTGAACCTCCGAGG   34444    G      AG  CAA
                                AAC GGTTGGGC  CC   AGG
                                ||| ||||||||  ||   |||
                                TTG CCAACTTG  GG   TCC
                                  A       GA  C__
GAM1353 TEGT     3' ACCAGCATGGGCAGCTCAGAGG 34445    G  _      C  A
                                AC GGT TGGGCAGC CA AGG
                                || ||| |||||||| || |||
                                TG TCG ACCCGTCG GT TCC
                                 G  T       A  C
GAM1353 WISP1    5' GACCGAGCAGCCCAGAGG    34446   GT        A
                                G  TGGGCAGCCCA AGG
                                |  |||||||||| |||
                                C  GCTCGTCGGGT TCC
                                 TG         C
GAM1353 WISP1    5' GACCGAGCAGCCCAGAGG    34446   GT        A
                                G  TGGGCAGCCCA AGG
                                |  |||||||||| |||
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                                C  GCTCGTCGGGT TCC
                                 TG         C
GAM1353  WNT15    3'  GGCTGGGCAGCTTGAAGG    34447          CCA
                                GGTTGGGCAGC   AAGG
                                ||||||||||   ||||
                                CCGACCCGTCG   TTCC
                                      AAC
GAM1353  WNT3A    3'  CAGCAGCTCTGGGCAGCC    5533     A   G_
                                CA CGG  TTGGGCAGCC
                                || |||  ||||||||||
                                GT GTC  GACCCGTCGG
                                 C   GA
GAM1353  ZNF257   3'  GGGTTGAGAACTTTTAAAGG   34448        C   CC__
                                GGGTTGGG AGC    AAAGG
                                ||||||||| |||    |||||
                                CCCAACTC TTG    TTTCC
                                     _   AAAA
GAM1353  C20orf59 3'  GCTGGGCAGGGCCCAAGGG    34449         __     A
                                GTTGGGCA  GCCCAA GG
                                ||||||||  ||||||  ||
                                CGACCCGT  CGGGTT CC
                                     CC     C
GAM1353  CKAP2    3'  CAACAGGCAGTCCAAG      34450      GGGTT     C    A
                                CAAC    GGGCAG CCAA G
                                ||||    |||||| |||| |
                                GTTG    TCCGTC GGTT C
                                  ______     A    C
GAM1353  CRA      5'  GGGTTGGACACAAGGG      34451          GCC   A
                                GGGTTGGGCA   CAA GG
                                ||||||||||   ||| ||
                                CCCAACCTGT   GTT CC
                                      ___   C
GAM1353  DKFZP586J1624 5'  GGCTGGTCCAGCCCAAAGG    34452       G_
                                GGTTGG  CAGCCCAAAGG
                                ||||||  ||||||||||
                                CCGACC  GTCGGGTTTCC
                                   AG
GAM1353  DKFZP761C169 5'  ACAACGGGGTGGGGGAAG    34453         T    CAGCCCA
                                ACAACGGG TGGG      AAG
                                ||||||||  ||||      |||
                                TGTTGCCC ACCC      TTC
                                     C    CC_____
GAM1353  DLGAP1   3'  ACGGCGGGTGACCTAAAG    34454      GT    CA   C
                                ACGG  TGGG  GCC AAAG
                                ||||  ||||  ||| ||||
                                TGCC  GCCC  TGG TTTC
                                  __    AC   A
GAM1353  DLGAP1   3'  ACGGCGGGTGACCTAAAG    34454      GT    CA   C
                                ACGG  TGGG  GCC AAAG
                                ||||  ||||  ||| ||||
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                                TGCC  GCCC  TGG TTTC
                                  __   AC   A
GAM1353  FLJ10647  3'  GGGCCGAGGCAGTCCGAAGG  34455      _    C  A
                                GGGTTG GGCAG CC AAGG
                                |||||| ||||| || ||||
                                CCCGGC CCGTC GG TTCC
                                   T    A  C
GAM1353  FLJ12057  3'  CATGGAGGCTGGTCCAAAGG  34456   AC_     GCAGC
                                CA  GGGTTGG    CCAAAGG
                                ||  |||||||    |||||||
                                GT  TCCGACC    GGTTTCC
                                 ACC     A____
GAM1353  FLJ20584  3'  CGGGAGGACAGCCCAGAGG   34457     TT        A
                                CGGG  GGGCAGCCCA AGG
                                ||||  |||||||||| |||
                                GCCC  CCTGTCGGGT TCC
                                  T_        C
GAM1353  FLJ21687  3'  GGGGGCACGGCCCAAAGG    34458    TT    __
                                GG  GGGCA  GCCCAAAGG
                                ||  |||||  |||||||||
                                CC  CCCGT  CGGGTTTCC
                                 __    GC
GAM1353  KIAA0010  3'  ACAAGTGGGCGCAGCCCAGGGG 34459       T  _      AA
                                ACGGGT GG GCAGCCCA  GG
                                |||||| || ||||||||  ||
                                TGTTCA CC CGTCGGGT  CC
                                   C  G       CC
GAM1353  KIAA0226  3'  CAACAGGTGTGACCCGGCCCGG 34460        TG   A__    AA
           AGG                   CAACGGGT  GGC   GCCC  AGG
                                ||||||||  |||   ||||  |||
                                GTTGTCCA  CTG   CGGG  TCC
                                    CA   GGC    CC
GAM1353  KIAA0444  3'  CAGGGGGCCCAGGCCCAAAGG  34461     TT   A___
                                CGGG  GGGC   GCCCAAAGG
                                ||||  ||||   |||||||||
                                GTCC  CCCG   CGGGTTTCC
                                  __   GGTC
GAM1353  KIAA0544  3'  CGGGGAGACAGCCCGGAGG   34462     TT       AA
                                CGGG  GGGCAGCCC  AGG
                                ||||  |||||||||  |||
                                GCCC  TCTGTCGGG  TCC
                                  C_       CC
GAM1353  KIAA0545  3'  ACCACAGCTGGGCAGCTTGGAG 34463    A   G       CCAA
           G                    AC ACGG TTGGGCAGC    AGG
                                || |||| |||||||||   |||
                                TG TGTC GACCCGTCG    TCC
                                 G   _       AACC
GAM1353  KIAA0690  3'  GGACCACAGGGCAGCCCAGGGG 34464    GT ___       AA
                                GG  T   GGGCAGCCCA  GG
                                ||  |   ||||||||||  ||
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                                CC  G   CCCGTCGGGT  CC
                                 TG TGT        CC
GAM1353  KIAA1372  5'  GGGTGAGGGCAGCCCAGGGG   34465     T_        AA
                                GGGT  GGGCAGCCCA  GG
                                ||||  ||||||||||  ||
                                CCCA  CCCGTCGGGT  CC
                                  CT        CC
GAM1353  KIAA1691  3'  GGCGGGTCAAGCCCAGAGG    34466     T  _ _    A
                                GGT GGG CA GCCCA AGG
                                ||| ||| || ||||| |||
                                CCG CCC GT CGGGT TCC
                                  _  A  T    C
GAM1353  LLGL2     3'  CGGGAAGGGCAGCCCAGGGG   34467     TT        AA
                                CGGG  GGGCAGCCCA  GG
                                ||||  ||||||||||  ||
                                GCCC  CCCGTCGGGT  CC
                                  TT        CC
GAM1353  MAPK8IP3  3'  GGGCGCGAGAGGCAGCCCGGAG 34468      T____        AA
              G                  GGGT    GGGCAGCCC  AGG
                                ||||    |||||||||  |||
                                CCCG    TCCGTCGGG  TCC
                                  CGCTC       CC
GAM1353  MGC10966  5'  GGTTGGGCAACCGAAGG     34469          CA
                                GGTTGGGCAGCC  AAGG
                                ||||||||||||  ||||
                                CCAACCCGTTGG  TTCC
                                       C_
GAM1353  MGC17303  5'  CGGGTTGGCAGCGCCGAGG    34470        G   _  AA
                                CGGGTTGG CAGC CC  AGG
                                |||||||| |||| ||  |||
                                GCCCAACC GTCG GG  TCC
                                     _   C  C_
GAM1353  MGC4796   3'  ACGCACGGGCAGCAGCCTGGAG 34471    A_     TG      CAA
              G                  AC  ACGGGT  GGCAGCC   AGG
                                ||  ||||||  |||||||   |||
                                TG  TGCCCG  TCGTCGG   TCC
                                 CG      __       ACC
GAM1353  MGC861    3'  GAGAAGGGGCAGCCCAGGGG   34472     TT_        AA
                                GGG   GGGCAGCCCA  GG
                                |||   ||||||||||  ||
                                CTC   CCCGTCGGGT  CC
                                  TTC        CC
GAM1353  OSBPL3    5'  AACATTTTGGGTGGCCCAAAGG 34473      GG     CA
                                AACG  TTGGG  GCCCAAAGG
                                ||||  |||||  |||||||||
                                TTGT  AACCC  CGGGTTTCC
                                  AA    AC
GAM1353  PTK6      5'  ACAAGCCTCGCAGCCTGAGG   34474        GG     CAA
                                ACGGGTT  GCAGCC   AGG
                                |||||||  ||||||   |||
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                                TGTTCGG  CGTCGG   TCC
                                   AG     AC_
GAM1353  RES4-25   3'  CAGCGGGTGGGGGGGAGCTGGAG 34475    A    T_   C   CCAA
              G                     CA CGGGT  GGG AGC    AGG
                                || |||||  ||| |||    |||
                                GT GCCCA  CCC TCG    TCC
                                 C     CC   C   ACC_
GAM1353  THG-1     5'  GGGTTGGGGCTCCTTGAAGG   34476        CA  _  A__
                                GGGTTGGG  GC CC   AAGG
                                ||||||||  || ||   ||||
                                CCCAACCC  CG GG   TTCC
                                     __  A  AAC
GAM1353  TIX1      5'  ACAATGAGTTGGGTAGCAG   34477      C       C   CCAA
                                ACAA GGGTTGGG AGC    AG
                                |||| |||||||| |||    ||
                                TGTT CTCAACCC TCG    TC
                                  A       A  _____
GAM1353  LOC115207 3'  AGACGAAGCAGCCCAGAG    34478     TT        A
                                GGG  GGGCAGCCCA AG
                                |||  |||||||||| ||
                                TCT  TTCGTCGGGT TC
                                  GC         C
GAM1353  LOC133634 5'  CAAGGGGTTGGGATCATCCAGA 34479     C       __  GC   A
              GG                    CAA GGGTTGGG  CA  CCA AGG
                                ||| ||||||||  ||  ||| |||
                                GTT CCCAACCC  GT  GGT TCC
                                  C       TA  A_   C
GAM1353  LOC147160 5'  ACGGGCAGCAGCCTGAAGG    34480       TG      CA
                                ACGGGT  GGCAGCC  AAGG
                                ||||||  |||||||  ||||
                                TGCCCG  TCGTCGG  TTCC
                                   __      AC
GAM1353  LOC151827 5'  GGTTAAAGGCAGCCTGAGG    34481      __       CAA
                                GGTT  GGGCAGCC   AGG
                                ||||  ||||||||   |||
                                CCAA  TCCGTCGG   TCC
                                  TT       AC_
GAM1353  LOC163231 3'  ACGGATTGGGTGACAAGG     34482         CA  CCA
                                ACGGGTTGGG  GC   AAGG
                                ||||||||||  ||   ||||
                                TGCCTAACCC  TG   TTCC
                                     AC  ___
GAM1353  LOC196743 5'  CGGTCCGGGCAGTCCGAGG    34483     GT      C  AA
                                CGG  TGGGCAG CC  AGG
                                |||  ||||||| ||  |||
                                GCC  GCCCGTC GG  TCC
                                  AG      A  C_
GAM1353  LOC196759 3'  CAACAGTACAGCTCAGAG     34484       GTTGG     C  A
                                CAACGG     GCAGC CA AG
                                ||||||     ||||| || ||
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                                GTTGTC    TGTCG GT TC
                                   A____    A  C
GAM1353  LOC199864 3'  CAACAGTACAGCTCAGAG    34484       GTTGG    C  A
                                CAACGG    GCAGC CA AG
                                ||||||    ||||| || ||
                                GTTGTC    TGTCG GT TC
                                   A____    A  C
GAM1353  LOC200269 3'  ACAGCAGGAAGAATAGCCCAAA 34485     A    TT   C
            GG                    ACA CGGG  GGG AGCCCAAAGG
                                ||| ||||  ||| ||||||||||
                                TGT GTCC  CTT TCGGGTTTCC
                                  C    TT   A
GAM1353  LOC201965 5'  AGGCAGCGGCCCAGAGG     34486      TG   A    A
                                GGGT  GGC GCCCA AGG
                                ||||  ||| ||||| |||
                                TCCG  TCG CGGGT TCC
                                  __   C    C
GAM1353  LOC204804 3'  GGGCGGGGCTAAGCTCAAAGG  34487      T   __   C
                                GGGT GGGC  AGC CAAAGG
                                |||| ||||  ||| ||||||
                                CCCG CCCG  TCG GTTTCC
                                  C    AT   A
GAM1353  LOC219397 3'  CGATGGTGGCACCAGGCCCAAG 34488     GTTG   ____     A
            GG                    CGG    GGCA    GCCCAA GG
                                |||    ||||    |||||| ||
                                GCT    CCGT    CGGGTT CC
                                  ACCA    GGTC     C
GAM1353  LOC222178 3'  GGGCGGGAGCTAGCCTGAAGG  34489      T  _  _   CA
                                GGGT GG GC AGCC  AAGG
                                |||| || || ||||  ||||
                                CCCG CC CG TCGG  TTCC
                                  C  T  A    AC
GAM1353  LOC253150 3'  GGGTTAGGGAGAGAAAGG    34490        C  CCC
                                GGGTTGGG AG   AAAGG
                                |||||||| ||   |||||
                                CCCAATCC TC   TTTCC
                                     C  TC_
GAM1353  LOC256050 5'  CAGCGGGCTGGGTGCCAGG    34491    A       CA   CAA
                                CA CGGGTTGGG  GCC   AGG
                                || |||||||||  |||   |||
                                GT GCCCGACCC  CGG   TCC
                                 C       A_  ___
GAM1353  LOC91035  5'  GGGCAGCAGGTGGCCCAAGGG  34492      __   CA     A
                                GGGT  TGGG  GCCCAA GG
                                ||||  ||||  |||||| ||
                                CCCG  GTCC  CGGGTT CC
                                  TC    AC     C
GAM1354  BAALC    3'  AGTAAGGATTAGTTTCTG    34495        ATC   CTG
                                AGTAAGGA   AGT   TTCTG
                                ||||||||   |||   |||||
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                                TCATTCCT  TCA  AAGAC
                                    AA_  ___
GAM1354 CKM     3' AGTGAGGGAGCAGGACTCTGGT 34496    A  AAT  TCTG
                                AGT AGG  CAG   TTCTGGT
                                ||| |||  |||   |||||||
                                TCA TCC  GTC   GAGACCA
                                  C  CTC  CT__
GAM1354 DUSP4    5' GTAAGGAAATCGGCTCTCTGGT 34497       _ A T  G
                                GTAAGGAA TC G CT TTCTGGT
                                |||||||| || | || |||||||
                                CATTCCTT AG C GA GAGACCA
                                    T  C _  _
GAM1354 EDNRA    3' AGTGAAGAATCGTAAGTTCTGG 34498    A     A  CT
             T                   AGT AGGAATC GT  GTTCTGGT
                                ||| ||||||| ||  ||||||||
                                TCA TTCTTAG CA  CAAGACCA
                                  C     _ TT
GAM1354 ENO2     3' AGTGAGAGGTTGCTCTGG    34499    A  GAATC  TC
                                AGT AG    AG  TGTTCTGG
                                ||| ||    ||  ||||||||
                                TCA TC    TC  ACGAGACC
                                  C  _____  CA
GAM1354 FLJ20079 3' GTAAGGGTTATTCTG       34500       AATCA  C
                                GTAAGG    GT TGTTCTG
                                ||||||    || |||||||
                                CATTCC    CA ATAAGAC
                                    _____  _
GAM1354 PRO1617  5' AGCAAGGAATTGTTTTGG    34501         CAGTC   C
                                AGTAAGGAAT    TGTT TGG
                                ||||||||||    |||| |||
                                TCGTTCCTTA    ACAA ACC
                                     _____   A
GAM1354 ZFPL1    5' GTAGGAAGTCAGGTTCTGGT   34502    A   _   TCT
                                GTA GGAA TCAG   GTTCTGGT
                                ||| |||| ||||   ||||||||
                                CAT CCTT AGTC   CAAGACCA
                                  _   C   ___
GAM1354 LOC120376 5' GTAGGAATCAAAGATCTGGT   34503    A      TCTGT
                                GTA GGAATCAG    TCTGGT
                                ||| ||||||||    ||||||
                                CAT CCTTAGTT    AGACCA
                                  _      TCT__
GAM1354 LOC136337 5' GTGAGGAACCAGCGGTTGGT   34504    A       CT  TC
                                GT AGGAATCAGT  GT  TGGT
                                || ||||||||||  ||  ||||
                                CA TCCTTGGTCG  CA  ACCA
                                 C        C_ __
GAM1354 LOC150848 5' AATGAGGAATCAGTCTTAGAGA 34505    A         GTTCT_
             GGT                   AGT AGGAATCAGTCT    GGT
                                ||| ||||||||||||    |||
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                                TTA TCCTTAGTCAGA     CCA
                                  C          ATCTCT
GAM1354  LOC219347 5'  AGCGAGGCAGTCTGTTCTGGT  34506    TA   AAT
                                AG  AGG   CAGTCTGTTCTGGT
                                ||  |||   ||||||||||||||
                                TC  TCC   GTCAGACAAGACCA
                                 GC  ___
GAM1354  LOC219735 3'  AGTAAGGAATTAGATGTGAGTG 34507         C  TC   TC_
           GT                    AGTAAGGAAT AG  TGT   TGGT
                                ||||||||||  ||  |||   ||||
                                TCATTCCTTA TC  ACA   ACCA
                                      A  T_   CTC
GAM1354  LOC255106 5'  AGAGAGGAATCCTGGCTTCTGG 34508    TA      AGT   __
           T                     AG  AGGAATC   CTG  TTCTGGT
                                ||  |||||||   |||  |||||||
                                TC  TCCTTAG   GAC  AAGACCA
                                 TC      ___   CG
GAM1355  CRMP1    3'  GTTGTTAAGTAAAAATGGGAG  34511          C  __
                                GTTGTTAAGTA GA  GGGAG
                                ||||||||||| ||  |||||
                                CAACAATTCAT TT  CCCTC
                                       T  TA
GAM1355  PCDHB16   5'  TGATGTTGTACAGGGAGGAG   34512    T   AA   G
                                TG TGTT  GTAC AGGGAGGAG
                                || ||||  |||| |||||||||
                                AC ACAA  CATG TCCCTCCTC
                                 T   __   _
GAM1355  PLP2     3'  TGTTGTTGGGGTGGGGAGGAG  34513       AAGTACGA
                                TGTTGTT      GGGAGGAG
                                |||||||      ||||||||
                                ACAACAA      CCCTCCTC
                                    CCCCAC__
GAM1355  PPP5C    3'  TGCTTGAGTGGGGGAGGAG   34514     GTTA   ACGA
                                TGTT   AGT   GGGAGGAG
                                ||||   |||   ||||||||
                                ACGA   TCA   CCCTCCTC
                                  AC__   CC__
GAM1355  C20orf18  3'  TGTTGTGGTGGGAGGA     34515      TAA  ACGA
                                TGTTGT   GT   GGGAGGA
                                ||||||   ||   |||||||
                                ACAACA   CA   CCCTCCT
                                   C__   ____
GAM1355  C20orf18  3'  TGTTGTGGTGGGAGGA     34515      TAA  ACGA
                                TGTTGT   GT   GGGAGGA
                                ||||||   ||   |||||||
                                ACAACA   CA   CCCTCCT
                                   C__   ____
GAM1355  FLJ22615  3'  TGTTGTGCAGGGGGAGGAG   34516      TAA   CGA
                                TGTTGT   GTA   GGGAGGAG
                                ||||||   |||   ||||||||
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                                ACAACA  CGT  CCCTCCTC
                                   ___  CC_
GAM1355 KIAA1954 5' TGGTGTTGAACAAGGGAGGAGC 34517   T   AAGT
                                TG TGTT   ACGAGGGAGGAGC
                                || ||||   ||||||||||||
                                AC ACAA   TGTTCCCTCCTCG
                                 C   CT__
GAM1355 LOC145842 5' TGTTGTTAGTATCACAGGAG  34518       A  _  A
                                TGTTGTTA GTA CG GGGAG
                                |||||||| ||| || |||||
                                ACAACAAT CAT GT TCCTC
                                     _  A  G
GAM1355 LOC149072 5' TGCTGTTGTGGGGAGGAG   34519       AA  ACGA
                                TGTTGTT  GT   GGGAGGAG
                                |||||||  ||   ||||||||
                                ACGACAA  CA   CCCTCCTC
                                   __ C___
GAM1355 LOC169225 5' TGTGTTAAGTGTGAACAGGAGC 34520    T     AC  G G
                                TGT GTTAAGT  GA G AGGAGC
                                ||| |||||||  || | ||||||
                                ACA CAATTCA  CT T TCCTCG
                                  _     CA  _ G
GAM1355 LOC253917 5' TGTTGATAGGGTCTGGAGGAGC 34521      T  A_  ACGAG
                                TGTTG TA  GT    GGAGGAGC
                                ||||| ||  ||    ||||||||
                                ACAAC AT  CA    CCTCCTCG
                                   T  CC  GA___
GAM1356 MX1     3'  TGTGATGTTCAGCATGTGTCAG 34524    C       ___  _  C
            T                    TG GATGTTCAGC   TG CA GT
                                || ||||||||||   || || ||
                                AC CTACAAGTCG   AC GT CA
                                 A        TAC  A  _
GAM1356 DKFZP564K0822 3'  TGCGGTGAGAGCTGCACGTGCT 34525     A  TTC       A
                                TGCG TG   AGCTGCACGT CT
                                |||| ||   |||||||||| ||
                                ACGC AC   TCGACGTGCA GA
                                  C  TC_        C
GAM1356 GIT2    3'  TGTGAGTTCAGCTGTCTACT   34526    C  T      CACG
                                TG GA GTTCAGCTG    TACT
                                || || |||||||||    ||||
                                AC CT CAAGTCGAC    ATGA
                                 A  _       AG__
GAM1356 KIAA1762  3'  TGCGCGTGTGCACGTAC     34527     A   TCAGC
                                TGCG TGT    TGCACGTAC
                                |||| |||    |||||||||
                                ACGC GCA    ACGTGCATG
                                  _  C_____
GAM1356 MGC27434  3'  TGCAGTCTTGCTGCACGTA   34528     AT   CA
                                TGCG  GTT  GCTGCACGTA
                                ||||  |||  ||||||||||
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                                ACGT  CAG  CGACGTGCAT
                                  __   AA
GAM1356  MR       3'  TGCTTTGCTGCACGTGCT    34529      CA       A
                                TGTT  GCTGCACGT CT
                                ||||  ||||||||| ||
                                ACGA  CGACGTGCA GA
                                  AA        C
GAM1357  DACH     3'  TGGTATTGGACTGGTACA    34532      T        A
                                TGGT TTGGACTGGTG CA
                                |||| |||||||||| ||
                                ACCA AACCTGACCAT GT
                                  T         _
GAM1357  IL6R     3'  TGGTTTTGGGCTAAACAAA   34533          A   GT
                                TGGTTTTGG CTG  GACAAA
                                ||||||||| |||  ||||||
                                ACCAAAACC GAT  TTGTTT
                                     C  __
GAM1357  MSF      3'  TGGTTTTGGCAAAAACATGGCA 34534          _____ _   TG
              A                  TGGTTTTGG    AC TGG  A
                                 |||||||||    || |||  |
                                 ACCAAAACC    TG ACC  T
                                      GTTTT  T   GT
GAM1357  RUNX3    3'  TGGTTCTGGCCGTTGTGACA   34535          A  __
                                TGGTTTTGG CTG  GTGACA
                                ||||||||| |||  ||||||
                                ACCAAGACC GGC  CACTGT
                                     _   AA
GAM1357  TBX5     5'  TGGTTTGTGGTCTCCGACAAAT 34536        _   A  GG
                                TGGTTT TGG CT  TGACAAAT
                                |||||| ||| ||  ||||||||
                                ACCAAA ACC GA  GCTGTTTA
                                   C   A  G_
GAM1357  TBX5     5'  TGGTTTGTGGTCTCCGACAAAT 34536        _   A  GG
                                TGGTTT TGG CT  TGACAAAT
                                |||||| ||| ||  ||||||||
                                ACCAAA ACC GA  GCTGTTTA
                                   C   A  G_
GAM1357  DKFZP564F0522 3'  GTTTTGGATGGATGCAGGTCA  34537          C   _  A  AA
                                GTTTTGGA TGG TG CA  TCA
                                |||||||| ||| || ||  |||
                                CAAAACCT ACC AC GT  AGT
                                     _   T  _  CC
GAM1357  FLJ10352 3'  TGGTTTGGAGGTCAAAC     34538        T   CT   GA
                                TGGTTT GGA  GGT  CAAAT
                                |||||| |||  |||  |||||
                                ACCAAA CCT  CCA  GTTTG
                                     _   __   __
GAM1357  FLJ21034 3'  TGGTTTTGGGCTGGTAAACATC 34539          A      CAA
              A                  TGGTTTTGG CTGGTGA   ATCA
                                 |||||||||  |||||||   ||||
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                                ACCAAAACC GACCATT   TAGT
                                     C      TG_
GAM1357  KIAA1468  3'  TGGCTTTGCCTATGGCAAAT   34540       GA   G  A
                                TGGTTTTG  CTG TG CAAAT
                                |||||||  ||| || |||||
                                ACCGAAAC  GAT AC GTTTA
                                     G_  _ C
GAM1357  TTY7      5'  TGGTTTTGGCTGGAAGCA    34541        A    TGA
                                TGGTTTTGG CTGG   CA
                                |||||||| ||||   ||
                                ACCAAAACC GACC   GT
                                      _   TTC
GAM1357  LOC143308 5'  TGGCTTTGGATTGGACA     34542         C   TG
                                TGGTTTTGGA TGG  ACA
                                |||||||||| |||  |||
                                ACCGAAACCT ACC  TGT
                                     A  __
GAM1357  LOC154981 5'  GTTTTGGGTGACAAAT      34543       ACTG
                                GTTTTGG   GTGACAAAT
                                |||||||   |||||||||
                                CAAAACC   CACTGTTTA
                                    ____
GAM1357  LOC200399 5'  TAGTTTTGTTTATGTGATGAAT 34544       GACTG   CA
           CA                     TGGTTTTG    GTGA  AATCA
                                |||||||    ||||  |||||
                                ATCAAAAC    CACT  TTAGT
                                     AAATA   AC
GAM1357  LOC221895 3'  TGGTTTTGAACATATGTGA   34545        TG__
                                TGGTTTTGGAC   GTGA
                                ||||||||||    ||||
                                ACCAAAACTTG   CACT
                                      TATA
GAM1358  AQP6      3'  TTTCACACACTCTCCATCT   34548         G  _
                                TTTCACACACTC TCC TCT
                                |||||||||||| ||| |||
                                AAAGTGTGTGAG AGG AGA
                                      _  T
GAM1358  COL4A6    3'  ACGCACCCACCCCTCTACTTC  34549    A    GT  _    C
                                AC CACTC  CC TCTAC TC
                                || |||||  || ||||| ||
                                TG GTGGG  GG AGATG AG
                                 C    TG  G    A
GAM1358  COL9A2    3'  CACCCATCAGTGCTCTACCTC  34550       ____
                                CACTCGTC   CTCTACCTC
                                ||||||||   |||||||||
                                GTGGGTAG   GAGATGGAG
                                     TCAC
GAM1358  SRGAP1    5'  TTTCAACAGCACTCTACCT   34551      C   CTC TC
                                TTTCA ACA   G  CTCTACCT
                                ||||| |||   |  ||||||||
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                                AAAGT TGT   C  GAGATGGA
                                  _  ___ GT
GAM1358  C12orf4   3'  TTTCACACACATGTATCT    34552         TC  CC
                                TTTCACACAC  GT  TCT
                                ||||||||||  ||  |||
                                AAAGTGTGTG  CA  AGA
                                     TA  T_
GAM1358  HSPC063   5'  CACACCCATCTTTTACTTC   34553         CTC   C
                                CACACTCGTC   TAC TC
                                ||||||||||   ||| ||
                                GTGTGGGTAG   ATG AG
                                     AAA   A
GAM1358  MGC10955  5'  TCTCACACTCCTTTGCCT    34554        ACTCG    CTA
                                TTTCACAC    TCCT   CCT
                                ||||||||    ||||  |||
                                AGAGTGTG    AGGA   GGA
                                    _____   AAC
GAM1358  P24B      3'  TTTCCCACAGTTTTCTACCTC  34555     A    CTC  CC
                                TTTC CACA   GT  TCTACCTC
                                |||| ||||   ||  ||||||||
                                AAAG GTGT   CA  AGATGGAG
                                  G    ___  AA
GAM1358  TACR3     3'  TCTCACACTAATCTTTTACCTC 34556    A     C   CTC
                                TC CACACT GTC   TACCTC
                                || |||||| |||   ||||||
                                AG GTGTGA TAG   ATGGAG
                                 A     T   AAA
GAM1358  TCF17     3'  TTTCACACATACAAATCTAC   34557         CT  TCC
                                TTTCACACA  CG   TCTAC
                                |||||||||  ||   |||||
                                AAAGTGTGT  GT   AGATG
                                     AT  TT_
GAM1358  ZER6      3'  CATTCTGTCTTCTACCTC    34558    C  _   C
                                CA TC GTC TCTACCTC
                                || || ||| ||||||||
                                GT AG CAG AGATGGAG
                                 A  A   A
GAM1358  LOC120856 3'  TTTCACTATTTTTCCTCTACCT 34559       ACACTCG
                                TTTCAC      TCCTCTACCT
                                ||||||      ||||||||||
                                AAAGTG      AGGAGATGGA
                                   ATAAAA_
GAM1358  LOC154007 3'  TTTCGGCATCATCCTCTGCCT  34560      ACA  C       A
                                TTTC   CA TCGTCCTCT CCT
                                ||||   || |||||||| |||
                                AAAG   GT AGTAGGAGA GGA
                                  CC_  _        C
GAM1358  LOC221773 3'  TCTCACGTCCCCTCTACT    34561       ACAC  G      C
                                TTTCAC    TC TCCTCTAC T
                                ||||||    || |||||||| |
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                                AGAGTG    AG GGGAGATG A
                                   C___ _       A
GAM1358  LOC254128 3'  TTTCAAATCACATACCTCTACC 34562      CA_   TCGT
              T                    TTTCA   CAC    CCTCTACCT
                                   |||||   |||    |||||||||
                                   AAAGT   GTG    GGAGATGGA
                                     TTA   TAT_
GAM1359  STK38    3'  CCTGGGCTCTCCTCGTTA    34565    GT_ A   TAC
                                   CC   GC TTT   CCTCGTTA
                                   ||   || |||   ||||||||
                                   GG   CG AGA   GGAGCAAT
                                    ACC  _   ___
GAM1359  BDG-29    5'  CCCGTGCGGCCCTCGTTAA    34566        ATTTTA
                                   CCCGTGC     CCCTCGTTAA
                                   |||||||     ||||||||||
                                   GGGCACG     GGGAGCAATT
                                       CC____
GAM1359  C3orf1    5'  CCGTGCATTTGACCCAGGTTAA 34567          T    TC
                                   CCGTGCATTT ACCC  GTTAA
                                   |||||||||| ||||  |||||
                                   GGCACGTAAA TGGG  CAATT
                                         C    TC
GAM1359  DKFZP761F241 3'  CCTTGCATTTTATCCATTTA   34568    G        C  TCG
                                   CC TGCATTTTA CC   TTA
                                   || |||||||| ||   |||
                                   GG ACGTAAAAT GG   AAT
                                    A        A  TA_
GAM1359  RASSF2    3'  GTGCATCTTGTGCTCAGTTAA  34569         ACC  _
                                   GTGCATTTT   CTC GTTAA
                                   |||||||||   ||| |||||
                                   CACGTAGAA   GAG CAATT
                                         CAC   T
GAM1359  X123      3'  ACCTGTGCATTTACTCCT     34570     C       T  _
                                   ACC GTGCATTT AC CCT
                                   ||| |||||||| || |||
                                   TGG CACGTAAA TG GGA
                                     A       _ A
GAM1359  LOC152245 3'  CCCAGAGACTTTATCCTCGTTA 34571      TGC     C
              A                     CCCG   ATTTTA CCTCGTTAA
                                   ||||   |||||| |||||||||
                                   GGGT   TGAAAT GGAGCAATT
                                     CTC     A
GAM1360  ACE       3'  GCCCTTGGGCAGGGCC      34574        A  GT
                                   GCCCTTG GC  GGGGCC
                                   |||||||  ||  ||||||
                                   CGGGAAC CG  TCCCGG
                                       C  __
GAM1360  BIG1      3'  TGCCAAAAACGTGGGGC     34575      CTT
                                   TGCC   GAGCGTGGGGC
                                   ||||   ||||||||||
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                                ACGG  TTTGCACCCCG
                                  TT_
GAM1360 BSN     3' TGCCCTTGCGTGGTGCC    34576      GA    G
                                TGCCCTT GCGTGG GCC
                                ||||||| |||||| |||
                                ACGGGAA CGCACC CGG
                                   __    A
GAM1360 CDKN2C  5' TGCCCTGGAGCAGAGCC    34577      T   GT
                                TGCCCT GAGC GGGGCC
                                |||||| |||| ||||||
                                ACGGGA CTCG TCTCGG
                                   C  __
GAM1360 CENPB   5' TGCCCTTGACCGGCAGGCC  34578       G TG
                                TGCCCTTGA CG GGGCC
                                ||||||||| || |||||
                                ACGGGAACT GC TCCGG
                                     G CG
GAM1360 CHST6   3' GCCCTTGAGTAGGAGCC    34579       CGT
                                GCCCTTGAG  GGGGCC
                                ||||||||  ||||||
                                CGGGAACTC  CCTCGG
                                     AT_
GAM1360 CLCN6   3' TGCCTTTGCATGGGGCC    34580    C GA
                                TGCC TT GCGTGGGGCC
                                |||| || ||||||||||
                                ACGG AA CGTACCCCGG
                                  _ A_
GAM1360 CLCN6   3' TGCCTTTGCATGGGGCC    34580    C GA
                                TGCC TT GCGTGGGGCC
                                |||| || ||||||||||
                                ACGG AA CGTACCCCGG
                                  _ A_
GAM1360 CLCN6   3' TGCCTTTGCATGGGGCC    34580    C GA
                                TGCC TT GCGTGGGGCC
                                |||| || ||||||||||
                                ACGG AA CGTACCCCGG
                                  _ A_
GAM1360 COPS3   5' TGCCCTTGAGCTGAGAGC   34581       GT
                                TGCCCTTGAGC GGGGC
                                |||||||||| |||||
                                ACGGGAACTCG TCTCG
                                     AC
GAM1360 DRD2    3' TGCCCCTGAGCTGGGGGGCC 34582       GT_
                                TGCCCTTGAGC  GGGGCC
                                |||||||||| ||||||
                                ACGGGGACTCG  CCCCGG
                                     ACC
GAM1360 EGLN2   5' TGTCCTTGACGCAGATGCC  34583   C   G TG _
                                TG CCTTGA CG GG GCC
                                || |||||| ||  || |||
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                                AC GGAACT GC  CT CGG
                                 A     _ GT  A
GAM1360  EPOR     3'  TGCTCCTGAGAGAGGCC     34584     C     CGT
                                TGC CTTGAG   GGGGCC
                                ||| ||||||   ||||||
                                ACG GGACTC   CTCCGG
                                  A     T__
GAM1360  EYA1     5'  TGCCCATGGAGCCTCGGGGC   34585      TT_   G_
                                TGCCC   GAGC  TGGGGC
                                |||||   ||||  ||||||
                                ACGGG   CTCG  GCCCCG
                                   TAC    GA
GAM1360  FBLN1    3'  GCCTCCCCGTGGGGCC      34586     _  GAG
                                GCC CTT   CGTGGGGCC
                                ||| |||   |||||||||
                                CGG GGG   GCACCCCGG
                                  A  ____
GAM1360  FER      5'  TGCTCTTCAGTGATGGCC    34587     C   G GC   _
                                TGC CTT A  GTGG GGCC
                                ||| ||| |  |||| ||||
                                ACG GAA T  CACT CCGG
                                  A   G __    A
GAM1360  FKRP     3'  TGCCCTAGAGCGCAGGGC    34588       T     TG
                                TGCCCT GAGCG  GGGC
                                ||||||| |||||  ||||
                                ACGGGA CTCGC  CCCG
                                    T     GT
GAM1360  GNA15    3'  TGCCCCAGGTGGGGCC      34589       TG  C
                                TGCCCT  AG GTGGGGCC
                                ||||||  || ||||||||
                                ACGGGG  TC CACCCCGG
                                    __  _
GAM1360  HDAC1    3'  TGCCCTGAGCTCGGGGCC    34590       T    G
                                TGCCCT GAGC TGGGGCC
                                |||||| |||| |||||||
                                ACGGGA CTCG GCCCCGG
                                    _    A
GAM1360  HOXD4    3'  TGCCCTCGGGCAGGATGC    34591        A   T   _
                                TGCCCTTG GCG GGG GC
                                |||||||| ||| ||| ||
                                ACGGGAGC CGT CCT CG
                                     C   _   A
GAM1360  IHPK3    3'  TGCCCTTGGAGCGAGC      34592         _   TGG
                                TGCCCTTG AGCG   GGC
                                |||||||| ||||   |||
                                ACGGGAAC TCGC   TCG
                                     C    ____
GAM1360  IMPDH1   3'  TGCCCCTGGGGTGGGGGCC   34593         AGC     _
                                TGCCCTTG   GTGGGG CC
                                ||||||||   |||||| ||
```

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                                ACGGGGAC   CACCCC GG
                                    CC_     C
GAM1360  ITGA7    3'  TGCCCCTGAGGAAGCC      34594         CGT
                                TGCCCTTGAG   GGGGCC
                                ||||||||||   ||||||
                                ACGGGGACTC   CTTCGG
                                    ____
GAM1360  IVD      5'  TGCCCTTGGACCGCACC      34595        _ G   GGG
                                TGCCCTTG A CGT   GCC
                                |||||||| | |||   |||
                                ACGGGAAC T GCG   TGG
                                    C G   ____
GAM1360  KCNH2    3'  TGCCCCTCTCACTGGGGCC    34596        GA_ G
                                TGCCCTT   GC TGGGGCC
                                |||||||   || |||||||
                                ACGGGGA   TG ACCCCGG
                                    GAG  _
GAM1360  KCNH3    3'  TGCCCTGAGCCAGCGGGCC    34597        T   __    G
                                TGCCCT GAGC  GTGGG CC
                                ||||||| ||||  ||||| ||
                                ACGGGA CTCG  CGCCC GG
                                    _   GT    _
GAM1360  KCNK5    3'  GCCCTTGACATCATGGCC     34598        G   GG_
                                GCCCTTGA CGT   GGCC
                                |||||||| |||   ||||
                                CGGGAACT GTA   CCGG
                                    _  GTA
GAM1360  LRP1     3'  TGCCCCTGGAGTTGGGGC     34599        _ CG
                                TGCCCTTG AG  TGGGGC
                                |||||||| ||  ||||||
                                ACGGGGAC TC  ACCCCG
                                    C  A_
GAM1360  LRRC2    3'  TGTCCTTAAGCACAAGCC     34600    C       TG  G
                                TG CCTTGAGCG  GG CC
                                || |||||||||  || ||
                                AC GGAATTCGT  TC GG
                                 A        GT  _
GAM1360  MADH3    3'  TGCCCTTCAAAGTGGGGCC    34601        G  C
                                TGCCCTT AG GTGGGGCC
                                ||||||| || ||||||||
                                ACGGGAA TT CACCCCGG
                                    G  T
GAM1360  MAN2A2   3'  GCCCTTGGCCTAGGCC      34602        A  G   G
                                GCCCTTG GC TGGG CC
                                ||||||| || |||| ||
                                CGGGAAC CG ATCC GG
                                    _  G   _
GAM1360  MAP3K12  3'  TGCCCTTAGCCACAGC      34603        G  G  G
                                TGCCCTT AGC TG GGC
                                ||||||| ||| || |||
```

```
                                ACGGGAA TCG GT TCG
                                    _  _  G
GAM1360  MMP15    3'  TGCCCCTGGGTGGAAGGC    34604        AGC   __
                                TGCCCTTG  GTGG  GGC
                                ||||||||  ||||  |||
                                ACGGGGAC  CACC  CCG
                                    C__   TT
GAM1360  PABPN1   3'  TACCCTTGAGCAGGCC     34605         GTG
                                TGCCCTTGAGC  GGGCC
                                ||||||||||  |||||
                                ATGGGAACTCG  TCCGG
                                     ___
GAM1360  PCLO     3'  TGCTTTGAACAGGGCC     34606     CC     GT
                                TGC  TTGAGC  GGGGCC
                                |||  ||||||  ||||||
                                ACG  AACTTG  TCCCGG
                                  A_    __
GAM1360  PLXNB2   3'  TGACCTTTGACGTGGGGCC   34607    C    GA
                                TG CCTT  GCGTGGGGCC
                                || ||||  ||||||||||
                                AC GGAA  TGCACCCCGG
                                 T   AC
GAM1360  PPP1R8   5'  TGCCCTTGTGGATGCGCC    34608       GAGC    ___
                                TGCCCTT   GTGGG  GCC
                                |||||||   |||||  |||
                                ACGGGAA   CACCT  CGG
                                    _____   ACG
GAM1360  PPP2R5B  3'  TGCCCTTGCCCAAGGCC     34609       GA  G
                                TGCCCTT  GC TGGGGCC
                                |||||||  ||  |||||||
                                ACGGGAA  CG GTTCCGG
                                    __  G
GAM1360  PPP5C    3'  TGCCCTGGGGCGGGGCC     34610       T AGC
                                TGCCCT G  GTGGGGCC
                                ||||||  |  ||||||||
                                ACGGGA C  CGCCCCGG
                                    _ CC_
GAM1360  PRKACA   3'  TGCCCTTAGCAAGTGGGGCC  34611        G   __
                                TGCCCTT AGC  GTGGGGCC
                                |||||||  |||  ||||||||
                                ACGGGAA TCG  CACCCCGG
                                    _  TT
GAM1360  SIT      3'  TGCCCCTGCTACGGGGGGC   34612        A_  T
                                TGCCCTTG  GCG GGGGC
                                ||||||||  |||  |||||
                                ACGGGGAC  TGC CCCCG
                                     GA  C
GAM1360  SMOH     3'  TGTCCCTGGGGTGAGGCC    34613    C    AGC
                                TG CCTTG  GTGGGGCC
                                || |||||  ||||||||
```

```
                                AC GGGAC   CACTCCGG
                                 A    CC_
GAM1360  SOX9     3'  TGCCTTCCACATGGGGCC    34614      C  GA
                                TGCC TT  GCGTGGGGCC
                                |||| ||  ||||||||||
                                ACGG AA  TGTACCCCGG
                                  _  GG
GAM1360  TBX1     3'  TGCCCTTGGGGCAGGGTGGCC  34615         A_   T  _
                                TGCCCTTG  GCG GG GGCC
                                ||||||||  ||| || ||||
                                ACGGGAAC  CGT CC CCGG
                                     CC   C  A
GAM1360  TCF3     3'  TGCATCTACCATGGGGCC    34616     CC   AG
                                TGC  TTG  CGTGGGGCC
                                |||  |||  |||||||||
                                ACG  GAT  GTACCCCGG
                                  TA   G_
GAM1360  TFE3     3'  TACCCTCCATGGGGCC      34617       GAG
                                TGCCCTT   CGTGGGGCC
                                |||||||   |||||||||
                                ATGGGAG   GTACCCCGG
                                     ___
GAM1360  XRCC3    3'  TGCCGAGGTGGGGCC       34618      CTT   C
                                TGCC   GAG GTGGGGCC
                                ||||   ||| ||||||||
                                ACGG   CTC CACCCCGG
                                     ___  _
GAM1360  ALDH9    3'  TGCCTCTGTAAACAGGGCC   34619      _ _    GT
                                TGCC CT TGAGC  GGGGCC
                                |||| || |||||  ||||||
                                ACGG GA ATTTG  TCCCGG
                                  A  C    __
GAM1360  C20orf150 3'  TGCCCTGAGCCTTCTGTGGGGC 34620       T   _____
              C                  TGCCCT GAGC     GTGGGGCC
                                 ||||||| ||||    ||||||||
                                 ACGGGA CTCG     CACCCCGG
                                    _   GAAGA
GAM1360  C21orf108 3'  TGCCCCTGGAGTCACGGCC   34621         _ CG  G
                                TGCCCTTG AG  TG GGCC
                                |||||||| ||  || ||||
                                ACGGGGAC TC  GT CCGG
                                     C  A_  G
GAM1360  C2F      5'  TGCCCCTAGTCGGGGCC     34622        AGCG
                                TGCCCTTG   TGGGGCC
                                ||||||||   |||||||
                                ACGGGGAT   GCCCCGG
                                     CA__
GAM1360  C9orf7   3'  TGCCCCTGCCACCCTGGGGC  34623        A_  G_
                                TGCCCTTG  GC  TGGGGC
                                ||||||||  ||  ||||||
```

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                                ACGGGGAC  TG  ACCCCG
                                    GG  GG
GAM1360  CILP     3'  TGTCCTGTGGAGCAAGGCC   34624    C   T__    TG
                                TG CCT   GAGCG  GGGCC
                                || |||   |||||  |||||
                                AC GGA   CTCGT  TCCGG
                                 A   CAC    __
GAM1360  DKFZP434C128 3'  TGCTATGTGCTGTGGGGCC   34625     CCT  A  _
                                TGC   TG GC GTGGGGCC
                                |||   || || ||||||||
                                ACG   AC CG CACCCCGG
                                  AT_  A  A
GAM1360  DKFZp434J0226 5'  TGCATCTTCCGTGGGGCC    34626     C_   GAG
                                TGC  CTT   CGTGGGGCC
                                |||  |||   |||||||||
                                ACG  GAA   GCACCCCGG
                                  TA   G__
GAM1360  DKFZp586H0623 3'  TGCTCCCTGTGGGGCC      34627     _    GAGC
                                TGC CCTT    GTGGGGCC
                                ||| ||||    ||||||||
                                ACG GGGA    CACCCCGG
                                  A   _____
GAM1360  DKFZp761J1523 3'  TGCCCCTGGCTTGGGGCC    34628         A  G
                                TGCCCTTG GC TGGGGCC
                                |||||||| || |||||||
                                ACGGGGAC CG ACCCCGG
                                     _  A
GAM1360  DKFZp762M136 3'  TGCCCTGGGCAGAGCC      34629       T A  GT
                                TGCCCT G GC  GGGGCC
                                |||||| | ||  ||||||
                                ACGGGA C CG  TCTCGG
                                   _ C  __
GAM1360  DMRTB1    3'  TGTCCTAGAGTGGGGCC     34630    C   TG  C
                                TG CCT  AG GTGGGGCC
                                || |||  || ||||||||
                                AC GGA  TC CACCCCGG
                                 A   __  T
GAM1360  DOC2B     3'  TGTCCTCTCAGCCGGGGC    34631    C    G_   G
                                TG CCTT  AGC TGGGGC
                                || ||||  ||| ||||||
                                AC GGAG  TCG GCCCCG
                                 A    AG  _
GAM1360  EDR2      3'  TGCCCTTGAAGTAACC      34632          C   GG
                                TGCCCTTGAG GTG  GCC
                                |||||||||| |||  |||
                                ACGGGAACTT CAT  TGG
                                      _  __
GAM1360  FLJ10044  3'  TGCGCTTAGTGGGGCC      34633     C    AGC
                                TGC CTTG   GTGGGGCC
                                ||| ||||   ||||||||
```

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                              ACG GAAT   CACCCCGG
                                C   ___
GAM1360  FLJ10156  3'  TGCTCTTGAACAGGGC     34634     C      GT
                              TGC CTTGAGC  GGGGC
                              ||| |||||||  |||||
                              ACG GAACTTG  TCCCG
                                A     __
GAM1360  FLJ10521  3'  TGCCCATTGAGTGAGACC    34635      _    GC
                              TGCCC TTGA  GTGGGGCC
                              ||||| ||||  ||||||||
                              ACGGG AACT  CACTCTGG
                                 T   __
GAM1360  FLJ10815  3'  TGTCCAGAGGTGTGGGGCC   34636    C  TT   C_
                              TG CC  GAG  GTGGGGCC
                              || ||  |||  ||||||||
                              AC GG  CTC  CACCCCGG
                               A  T_   CA
GAM1360  FLJ11099  3'  TGCCCTTGAAGGGGC       34637          CGT
                              TGCCCTTGAG   GGGGC
                              ||||||||||   |||||
                              ACGGGAACTT   CCCCG
                                           ___
GAM1360  FLJ11259  3'  TGCCCTTGGCATGTGCC     34638         A    GG
                              TGCCCTTG GCGTG  GCC
                              |||||||| |||||  |||
                              ACGGGAAC CGTAC  CGG
                                   _    A_
GAM1360  FLJ12190  3'  TGCCCTGAGCACAGCC      34639       T    TGG
                              TGCCCT GAGCG   GGCC
                              |||||| |||||   ||||
                              ACGGGA CTCGT   TCGG
                                 _    G__
GAM1360  FLJ12681  3'  TGGCCTGGATGTGGGGCC    34640    C   T  GC
                              TG CCT GA  GTGGGGCC
                              || ||| ||  ||||||||
                              AC GGA CT  CACCCCGG
                               C   C  A_
GAM1360  FLJ12800  3'  TGTCCTGCATGGGGCC      34641    C   TGA
                              TG CCT   GCGTGGGGCC
                              || |||   ||||||||||
                              AC GGA   CGTACCCCGG
                               A  ___
GAM1360  FLJ13241  3'  TGCCCTTGGGAACAGAGGG    34642        __    T
                              TGCCCTT  GAGCG GGGG
                              |||||||  ||||| ||||
                              ACGGGAA  CTTGT TCCC
                                   CC    C
GAM1360  FLJ13902  3'  TGCCCCTGCGCCGGGC      34643        GA   G
                              TGCCCTT  GCGT GGGC
                              |||||||  |||| ||||
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                                ACGGGGA  CGCG CCCG
                                   __    G
GAM1360  FLJ13902  3'  TGCCCTTGTGACCCAGCC    34644        A_  G GG
                                TGCCCTTG  GC T  GGCC
                                ||||||||  || |  ||||
                                ACGGGAAC  TG G  TCGG
                                    AC  G __
GAM1360  FLJ14107  5'  TGCCTTGAGCCAAAAACC    34645      C     GT
                                TGCC TTGAGC  GGGGCC
                                |||| ||||||  ||||||
                                ACGG AACTCG  TTTTGG
                                  _     GT
GAM1360  FLJ14124  3'  GCCCTCACATGGGGCC      34646       GA
                                GCCCTT  GCGTGGGGCC
                                ||||||  ||||||||||
                                CGGGAG  TGTACCCCGG
                                   __
GAM1360  FLJ14564  3'  TGTCCCTGAGCTGCAGC     34647    C      G  G
                                TG CCTTGAGC TG GGC
                                || ||||||||  || |||
                                AC GGGACTCG AC TCG
                                 A       _ G
GAM1360  FLJ14594  3'  TGCCCCTGTGTAGGTGGGG    34648        ___  C
                                TGCCCTTG   AG GTGGGG
                                ||||||||   || ||||||
                                ACGGGGAC   TC CACCCC
                                    ACA  _
GAM1360  FLJ14708  3'  TGCCCATGGCAGGGCC      34649      T  A  GT
                                TGCCC TG GC  GGGGCC
                                |||||  || ||  ||||||
                                ACGGG AC CG  TCCCGG
                                  T  _  __
GAM1360  FLJ20184  3'  CCTTGAACTACGTGGGGCC    34650       ___
                                CCTTGA   GCGTGGGGCC
                                ||||||   ||||||||||
                                GGAACT   TGCACCCCGG
                                   TGA
GAM1360  FLJ20296  3'  TGCCCTTGGCTGGAATGCC    34651        A  G   __
                                TGCCCTTG GC TGGG  GCC
                                |||||||| || ||||  |||
                                ACGGGAAC CG ACCT  CGG
                                    _ _   TA
GAM1360  FLJ21736  3'  TGCTCTGAGTGGGGCC      34652     CC   GC
                                TGC  TTGA  GTGGGGCC
                                |||  ||||  ||||||||
                                ACG  GACT  CACCCCGG
                                 A_   __
GAM1360  FLJ22408  5'  GCCCTTGGCCTGGGGCC     34653        A  G
                                GCCCTTG GC TGGGGCC
                                ||||||| || |||||||
```

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                                CGGGAAC CG ACCCCGG
                                    _ G
GAM1360  FLJ23058  3'  TGCTGCTTGCACCTGGGGCC  34654    C_   A  G
                                TGC  CTTG GC TGGGGCC
                                |||  |||| || |||||||
                                ACG  GAAC TG ACCCCGG
                                  AC   G  G
GAM1360  FLJ23093  3'  TGCCCTTAGCCCGGGCC    34655      G  G   G
                                TGCCCTT AGC TGGG CC
                                ||||||| ||| |||| ||
                                ACGGGAA TCG GCCC GG
                                    _  G   _
GAM1360  FLJ23168  3'  TGCCCATGAGCGCAGCC    34656     T     GG
                                TGCCC TGAGCGT  GGCC
                                ||||| |||||||  ||||
                                ACGGG ACTCGCG  TCGG
                                   T     __
GAM1360  FLJ23392  3'  TGCCCTTGGAGAGAGC     34657       _ CGT
                                TGCCCTTG AG   GGGGC
                                |||||||| ||   |||||
                                ACGGGAAC TC   TCTCG
                                    C  ___
GAM1360  FLJ32784  3'  TGCCCTCGGCTCCAGGCC   34659       A  GTG
                                TGCCCTTG GC   GGGCC
                                |||||||| ||   |||||
                                ACGGGAGC CG   TCCGG
                                    _ AGG
GAM1360  FLJ32784  3'  TGCCCTTGGCCAGAGGC    34658       A  GT
                                TGCCCTTG GC  GGGGC
                                |||||||| ||  |||||
                                ACGGGAAC CG  CTCCG
                                    _ GT
GAM1360  FLNC      5'  TGCACCTTGGTGGGGCC    34661    _    AGC
                                TGC CCTTG   GTGGGGCC
                                |||  |||||   ||||||||
                                ACG GGAAC   CACCCCGG
                                  T   ___
GAM1360  FLNC      3'  TGCCCCTGAGCCTGGCC    34660         GTGG
                                TGCCCTTGAGC   GGCC
                                ||||||||||    ||||
                                ACGGGGACTCG   CCGG
                                     GA__
GAM1360  HCNGP     3'  TGCCCTTGGCCAATGAGGGGCC 34662       A  GT____
                                TGCCCTTG GC     GGGGCC
                                |||||||| ||     ||||||
                                ACGGGAAC CG     CCCCGG
                                    _ GTTACT
GAM1360  HSPB7     3'  TGCTCGCTGGCGTGGGGC    34663    CC_  A
                                TGC   TTG GCGTGGGGC
                                |||   ||| |||||||||
```

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                                ACG   GAC CGCACCCCG
                                  AGC   _
GAM1360 JM11     3' TGCCCCTCCTGTGGGGCC    34664       GAGC
                                TGCCCTT   GTGGGGCC
                                |||||||   ||||||||
                                ACGGGGA   CACCCCGG
                                   GGA_
GAM1360 JM11     3' TGCCCCTCCTGTGGGGCC    34664       GAGC
                                TGCCCTT   GTGGGGCC
                                |||||||   ||||||||
                                ACGGGGA   CACCCCGG
                                   GGA_
GAM1360 KCNT1    3' GCTCTGAGGTCGTGGGGC    34665    CC    __
                                GC  TTGAG  CGTGGGGC
                                ||  |||||  ||||||||
                                CG  GACTC  GCACCCCG
                                 A_    CA
GAM1360 KIAA0323 3' TGCCCTTGAAGCAAACC     34666         C TG  G
                                TGCCCTTGAG G  GG CC
                                ||||||||||  |  || ||
                                ACGGGAACTT C  TT GG
                                      _ GT  _
GAM1360 KIAA0514 3' GCCCAGCTGTGTGGGGCC    34667     TTG  ___
                                GCCC   AGC   GTGGGGCC
                                ||||   |||   ||||||||
                                CGGG   TCG   CACCCCGG
                                  ___   ACA
GAM1360 KIAA0522 3' TGCCCCACGTGGGGCC      34668       TGA
                                TGCCCT   GCGTGGGGCC
                                ||||||   ||||||||||
                                ACGGGG   TGCACCCCGG
                                   ___
GAM1360 KIAA0769 3' TGCCCTGGAATGAGGCC     34669       T  GC
                                TGCCCT GA  GTGGGGCC
                                |||||| ||  ||||||||
                                ACGGGA CT  TACTCCGG
                                   C  __
GAM1360 KIAA1089 3' GCCCTAGGTGGGGCC       34670      TG  C
                                GCCCT  AG GTGGGGCC
                                |||||  || ||||||||
                                CGGGA  TC CACCCCGG
                                   __  _
GAM1360 KIAA1372 5' TGCCCCTGGGCCAGAAGC    34671         A  GT
                                TGCCCTTG GC  GGGGC
                                ||||||||  ||  |||||
                                ACGGGGAC CG  CTTCG
                                     C  GT
GAM1360 KIAA1465 5' TACTCTTGAGCACGGTGGGC  34672     C       TG__
                                TGC CTTGAGCG   GGGC
                                ||| ||||||||   ||||
```

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                                ATG GAACTCGT   CCCG
                                  A       GCCA
GAM1360  KIAA1486  3'  TACCCTTGAGAGAAGCC     34673          CGT
                                TGCCCTTGAG   GGGGCC
                                ||||||||||   ||||||
                                ATGGGAACTC   CTTCGG
                                      T__
GAM1360  KIAA1656  3'  TGCTCTGGGCAATGGGGCC   34674     CC   A  _
                                TGC  TTG GCG TGGGGCC
                                |||  ||| ||| |||||||
                                ACG  GAC CGT ACCCCGG
                                  A_   C   T
GAM1360  KIAA1719  3'  GCCTCCCCAGTGGGGCC     34675     _   G GC
                                GCC CTT A  GTGGGGCC
                                ||| ||| |  ||||||||
                                CGG GGG T  CACCCCGG
                                  A   G __
GAM1360  KIAA1765  3'  TGTCCTTGAGCAGAAC      34676    C       GT
                                TG CCTTGAGC  GGGGC
                                || ||||||||  |||||
                                AC GGAACTCG  TCTTG
                                 A       __
GAM1360  KIAA1822  3'  TGCCCCTCCAGTGGGGCC    34677        GAGC
                                TGCCCTT    GTGGGGCC
                                |||||||    ||||||||
                                ACGGGGA    CACCCCGG
                                    GGT_
GAM1360  KIAA1856  3'  CCCTTGAAGGCTTGGGGCC   34678         __  G
                                CCCTTGA  GC TGGGGCC
                                |||||||  ||  |||||||
                                GGGAACT  CG ACCCCGG
                                    TC  A
GAM1360  KIAA1881  5'  TGCCAAGCGTGGGGC       34679      CTT
                                TGCC   GAGCGTGGGGC
                                ||||   ||||||||||
                                ACGG   TTCGCACCCCG
                                   ___
GAM1360  KIAA1924  3'  TGCCCTTGGCAGAGTGGGG   34680         A  ___
                                TGCCCTTG GC   GTGGGG
                                |||||||| ||   ||||||
                                ACGGGAAC CG   CACCCC
                                    _  TCT
GAM1360  MAP2K7    3'  TGCCCCTGGCCCCCTGTGGGGC 34681         A  _____
                                TGCCCTTG GC    GTGGGGC
                                |||||||| ||    |||||||
                                ACGGGGAC CG    CACCCCG
                                    _  GGGGA
GAM1360  MAPKAPK2  3'  TGACCTTGAGCAGACTGCC   34682    C       T  G_
                                TG CCTTGAGCG GG  GCC
                                || |||||||| ||  |||
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                                AC GGAACTCGT CT  CGG
                                 T       _  GA
GAM1360  MGC13053  3'  TGTCCTTAGCAGAGCC     34683    C   G  GT
                                TG CCTT AGC  GGGGCC
                                || |||| |||  ||||||
                                AC GGAA TCG  TCTCGG
                                 A   _  __
GAM1360  MGC16063  3'  TGCCTCACCTGTGGGGCC    34684     C  AGC
                                TGCC TTG   GTGGGGCC
                                |||| |||   ||||||||
                                ACGG AGT   CACCCCGG
                                  _  GGA
GAM1360  MGC2721   3'  TGTCCCTGAGCCCAGCC     34685    C      G GG
                                TG CCTTGAGC T  GGCC
                                || ||||||||  |  ||||
                                AC GGGACTCG G  TCGG
                                 A       G __
GAM1360  moblak    3'  TGCCCTTGAGAGACAGGCC   34686         CGTG
                                TGCCCTTGAG    GGGCC
                                ||||||||||    |||||
                                ACGGGAACTC    TCCGG
                                      TCTG
GAM1360  MRPL10    3'  TGACCTTGAGCAAGCC      34687    C       TGG
                                TG CCTTGAGCG   GGCC
                                || |||||||||   ||||
                                AC GGAACTCGT   TCGG
                                 T       ____
GAM1360  MSE55     3'  TGCACCTAGGTGGGGCC     34688    _  TG  C
                                TGC CCT  AG GTGGGGCC
                                ||| |||  || ||||||||
                                ACG GGA  TC CACCCCGG
                                  T  __ _
GAM1360  NKX2C     3'  TGCCCTGAGCGCACGCGGCC  34689      T    __ G
                                TGCCCT GAGCGT  G GGCC
                                |||||| ||||||  | ||||
                                ACGGGA CTCGCG  C CCGG
                                   _     TG G
GAM1360  NPTXR     3'  TGCCCTTGACTGGCAGC     34690        G G  _
                                TGCCCTTGA C TGG GGC
                                |||||||||  | ||| |||
                                ACGGGAACT G ACC TCG
                                      _ _  G
GAM1360  NPTXR     3'  TGCCCTTGACTGGCAGC     34690        G G  _
                                TGCCCTTGA C TGG GGC
                                |||||||||  | ||| |||
                                ACGGGAACT G ACC TCG
                                      _ _  G
GAM1360  NUDEL     3'  GCTCCTGCCACGTGGGGC    34691    C   A_
                                GC CTTG  GCGTGGGGC
                                || ||||  |||||||||
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                                CG GGAC  TGCACCCCG
                                 A   GG
GAM1360 OSBPL5   3' TGCCCCTGAGAGGGGCC    34692        CGT
                                TGCCCTTGAG  GGGGCC
                                ||||||||||  ||||||
                                ACGGGGACTC  CCCCGG
                                      T__
GAM1360 p25      3' TGCCCTTGGCACAGAGC    34693       A  TG
                                TGCCCTTG GCG  GGGC
                                |||||||| |||  ||||
                                ACGGGAAC CGT  CTCG
                                     _  GT
GAM1360 PARVA    3' GCACTTAGTGTGGGGCC    34694    C  G  C
                                GC CTT AG GTGGGGCC
                                || ||| || ||||||||
                                CG GAA TC CACCCCGG
                                 T  _  A
GAM1360 PIG11    3' TGCCCTGTGGGGTGAGGCC  34695      _  AGC
                                TGCCCT TG  GTGGGGCC
                                |||||| ||  ||||||||
                                ACGGGA AC  CACTCCGG
                                   C  CC_
GAM1360 PKMYT1   5' TGTCCCTGAGCTAAGGCC   34696    C      G
                                TG CCTTGAGC TGGGGCC
                                || |||||||| |||||||
                                AC GGGACTCG ATTCCGG
                                 A      _
GAM1360 PRAM-1   3' TGCCCTTGGGGCTGGGGC   34697       A_  G
                                TGCCCTTG  GC TGGGGC
                                ||||||||  || ||||||
                                ACGGGAAC  CG ACCCCG
                                     CC  _
GAM1360 PRIC285  5' TGCCCCTGAGCACAGCC    34698         TGG
                                TGCCCTTGAGCG  GGCC
                                ||||||||||||  ||||
                                ACGGGGACTCGT  TCGG
                                       G__
GAM1360 PRO1770  3' TGCCTTTGATAAGGCC     34699     C   GCG
                                TGCC TTGA  TGGGGCC
                                |||| ||||  |||||||
                                ACGG AACT  ATTCCGG
                                  A  ____
GAM1360 PRSS22   3' TGCCTTGGAGGCGGGGCC   34700     CTT  C
                                TGCC  GAG GTGGGGCC
                                ||||  ||| ||||||||
                                ACGG  CTC CGCCCCGG
                                  AAC  _
GAM1360 PSK      5' GCCCTGAGAGTGGGGCC    34701      T  C
                                GCCCT GAG GTGGGGCC
                                ||||| ||| ||||||||
```

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                                CGGGA CTC CACCCCGG
                                  _  T
GAM1360  RHOBTB3   3'  GCCTTGAACCAAGTGTGGGG  34702    C    _____
                                GCC TTGAGC    GTGGGG
                                ||| ||||||    ||||||
                                CGG AACTTG    CACCCC
                                  _    GTTCA
GAM1360  SEMA4G    5'  TGCGCTTGAGCAGCAGGGGCC 34703    C    _ _
                                TGC CTTGAGC GT GGGGCC
                                ||| ||||||| || ||||||
                                ACG GAACTCG CG CCCCGG
                                  C      T  T
GAM1360  SMCR7     3'  TGCTCTCCAGTGGGGCC    34704    C   G GC
                                TGC CTT A  GTGGGGCC
                                ||| ||| |  ||||||||
                                ACG GAG T  CACCCCGG
                                  A  G __
GAM1360  SMOC2     3'  TGCCCTGAGCTCTGGGGCC   34705      T   G_
                                TGCCCT GAGC  TGGGGCC
                                |||||| ||||  |||||||
                                ACGGGA CTCG  ACCCCGG
                                   _   AG
GAM1360  SSH2      3'  TGCCCCTGGCTGAGGCC    34706       A  G
                                TGCCCTTG GC TGGGGCC
                                |||||||| || |||||||
                                ACGGGGAC CG ACTCCGG
                                     _ _
GAM1360  TAO1      5'  GCCCTGAGAGTGGGGCC    34701      T   C
                                GCCCT GAG GTGGGGCC
                                ||||| ||| ||||||||
                                CGGGA CTC CACCCCGG
                                   _  T
GAM1360  LOC124044 3'  GCCCTTGACCTGGGGCC    34707       G G
                                GCCCTTGA C TGGGGCC
                                |||||||| | |||||||
                                CGGGAACT G ACCCCGG
                                     _ G
GAM1360  LOC124222 3'  GCCCTTGAAAGCTGGGGCC  19080       __  G
                                GCCCTTGA  GC TGGGGCC
                                ||||||||  || |||||||
                                CGGGAACT  CG ACCCCGG
                                     TT  _
GAM1360  LOC126669 3'  TGCCCTTGAAGGTGCC     34708       GCGT  _
                                TGCCCTTGA   GGG GCC
                                |||||||||   ||| |||
                                ACGGGAACT   TCC CGG
                                     ____  A
GAM1360  LOC133584 3'  TGTCCCTTGGACAAGGCC   34709   _    AG  TG
                                TG CCCTTG  CG  GGGCC
                                || ||||||  ||  |||||
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                                AC GGGAAC  GT  TCCGG
                                 A     CT  __
GAM1360  LOC144308 3'  GCCTGGAGCTGTGGGGCC    34710     CTT   _
                                GCC   GAGC GTGGGGCC
                                |||   |||| ||||||||
                                CGG   CTCG CACCCCGG
                                  AC_   A
GAM1360  LOC145601 3'  TGCCTTGCACAGGGGGC     34711     C   A   T
                                TGCC TTG GCG GGGGC
                                |||| ||| ||| |||||
                                ACGG AAC TGT CCCCG
                                   _  G   C
GAM1360  LOC146159 5'  TGCCCTGGCAATGGGGC     34712       T A   _
                                TGCCCT G GCG TGGGGC
                                |||||| | ||| ||||||
                                ACGGGA C CGT ACCCCG
                                   _ _   T
GAM1360  LOC146445 3'  GCCCTAGGTGGGGCC       34670      TG  C
                                GCCCT  AG GTGGGGCC
                                |||||  || ||||||||
                                CGGGA  TC CACCCCGG
                                   __ _
GAM1360  LOC146909 3'  GCCATCACCGTGGGGCC     34713     C   AG
                                GCC TTG  CGTGGGGCC
                                ||| |||  |||||||||
                                CGG AGT  GCACCCCGG
                                  T   G_
GAM1360  LOC147136 3'  TGCCCTGAACTGGGGC      34714       T    G
                                TGCCCT GAGC TGGGGC
                                |||||| |||| ||||||
                                ACGGGA CTTG ACCCCG
                                   _   _
GAM1360  LOC148753 3'  TGCCCTTAGAAGGGGGCC    34715        _   CGT
                                TGCCCTT GAG   GGGGCC
                                ||||||| |||   ||||||
                                ACGGGAA CTT   CCCCGG
                                    T   C__
GAM1360  LOC149668 5'  TGCCTTTCTGACTGGGGC    34716     C__   G G
                                TGCC   TTGA C TGGGGC
                                ||||   |||| | ||||||
                                ACGG   GACT G ACCCCG
                                  AAA   _ _
GAM1360  LOC150421 3'  TGCCCCTGGCATCCTGGCC   34717        A   GG_
                                TGCCCTTG GCGT   GGCC
                                |||||||| ||||   ||||
                                ACGGGGAC CGTA   CCGG
                                    _   GGA
GAM1360  LOC151176 5'  TGCCCCTGAGAGGAAGGGCC  34718          CGT_
                                TGCCCTTGAG    GGGGCC
                                ||||||||||    ||||||
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                                ACGGGGACTC   TCCCGG
                                     TCCT
GAM1360  LOC151429 3'  TGCCCTGAGCACGAGGGCC   34719      T    _
                                TGCCCT GAGCGTG GGGCC
                                |||||| ||||||| |||||
                                ACGGGA CTCGTGC CCCGG
                                   _     T
GAM1360  LOC152762 3'  TGCCCTGAGCTGTGCC     34720      T   G  GG
                                TGCCCT GAGC TG  GCC
                                |||||| |||| ||  |||
                                ACGGGA CTCG AC  CGG
                                   _   _ A_
GAM1360  LOC155061 3'  TGCCCTTGGGACGGGTACC   34721       A_   T  GG
                                TGCCCTTG  GCG GG  CC
                                ||||||||  ||| ||  ||
                                ACGGGAAC  TGC CC  GG
                                     CC   _  AT
GAM1360  LOC162137 3'  TGCCCTTAGTGGTGAAGGCC  34722       AGC   _
                                TGCCCTTG   GTGG GGCC
                                ||||||||   |||| ||||
                                ACGGGAAT   CACT CCGG
                                     CAC    T
GAM1360  LOC163598 5'  TGTCCATGAGTGGAACC    34723    C  T   GC
                                TG CC TGA  GTGGGGCC
                                || || |||  ||||||||
                                AC GG ACT  CACCTTGG
                                 A  T  __
GAM1360  LOC196047 5'  TGCCCTTCAGTGCAGAGCC   34724       G  C TG
                                TGCCCTT AG G  GGGCC
                                ||||||| || |  |||||
                                ACGGGAA TC C  CTCGG
                                    G  A GT
GAM1360  LOC199990 3'  TGCCTCTGAGTGAGGCC    34725     C    GC
                                TGCC TTGA  GTGGGGCC
                                |||| ||||  ||||||||
                                ACGG GACT  CACTCCGG
                                  A   __
GAM1360  LOC200317 3'  TGCCCTTGAGTGGAAC     34726        GC
                                TGCCCTTGA  GTGGGGC
                                |||||||||  |||||||
                                ACGGGAACT  CACCTTG
                                     __
GAM1360  LOC200473 5'  TGCTCCTGAGCGGGTGAGGCC 34727     C     __
                                TGC CTTGAGC  GTGGGGCC
                                ||| |||||||  ||||||||
                                ACG GGACTCG  CACTCCGG
                                  A      CC
GAM1360  LOC200860 3'  TGCCCCTGCAGTGGGGCC    34728        AGC
                                TGCCCTTG   GTGGGGCC
                                ||||||||   ||||||||
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                                ACGGGGAC   CACCCCGG
                                     GT_
GAM1360  LOC201229 5'  TGCTCCTGGCAGCGGGGCC   34729     C    A  _
                                TGC CTTG GC GTGGGGCC
                                ||| |||| || ||||||||
                                ACG GGAC CG CGCCCCGG
                                  A    _  T
GAM1360  LOC201689 5'  TGCCCCTGCTACAGTGGGGC   34730        A_  _
                                TGCCCTTG  GC GTGGGGC
                                ||||||||  || |||||||
                                ACGGGGAC  TG CACCCCG
                                     GA  T
GAM1360  LOC203248 3'  TGCCCTGAGCCCCAGGGC    34731       T    GT_
                                TGCCCT GAGC   GGGGC
                                |||||| ||||   |||||
                                ACGGGA CTCG   TCCCG
                                   _    GGG
GAM1360  LOC204084 5'  TGCCCTTGGGGCATTGGG    34732        A_    G
                                TGCCCTTG  GCGT GGG
                                ||||||||  |||| |||
                                ACGGGAAC  CGTA CCC
                                     CC    A
GAM1360  LOC204820 5'  TGCTCTTGAATAAAACC     34733     C     GC
                                TGC CTTGA  GTGGGGCC
                                ||| |||||  ||||||||
                                ACG GAACT  TATTTTGG
                                  A    __
GAM1360  LOC220595 5'  TGCCCCTGGGATGGGGC     34734        AGC
                                TGCCCTTG   GTGGGGC
                                ||||||||   |||||||
                                ACGGGGAC   TACCCCG
                                     CC_
GAM1360  LOC221143 3'  TGCCCTCGAGACCCAGCC    34735          _ G GG
                                TGCCCTTGAG C T  GGCC
                                |||||||||| | |  ||||
                                ACGGGAGCTC G G  TCGG
                                      T G __
GAM1360  LOC221474 5'  TGCCCTTGGTGTGGAAGGGC   34736        AGC   ____
                                TGCCCTTG   GTGG   GGC
                                ||||||||   ||||   |||
                                ACGGGAAC   CACC   CCG
                                     CA_    TTC
GAM1360  LOC221943 5'  GCCATCGAGGTGTGGGGCC   34737     C     C_
                                GCC TTGAG  GTGGGGCC
                                ||| |||||  ||||||||
                                CGG AGCTC  CACCCCGG
                                  T     CA
GAM1360  LOC221955 3'  TGCCCTTGGTGACGCC      34738        AGC    G
                                TGCCCTTG   GTGG GCC
                                ||||||||   |||| |||
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                                ACGGGAAC   CACT CGG
                                    ___    G
GAM1360  LOC253815 3'  TGCCCCTGGGCTGTGGC     34739        A  G  G
                                TGCCCTTG GC TG GGC
                                |||||||| || || |||
                                ACGGGGAC CG AC CCG
                                     C  _  A
GAM1360  LOC253980 3'  GCTCTGAGTGGTGGGGCC    34740    CC    C_
                                GC  TTGAG  GTGGGGCC
                                ||  |||||  ||||||||
                                CG  GACTC  CACCCCGG
                                 A_    AC
GAM1360  LOC254387 3'  TGCCCCTGGCCCATGTGGGGCC 34741        A  _____
                                TGCCCTTG GC    GTGGGGCC
                                |||||||| ||    ||||||||
                                ACGGGGAC CG    CACCCCGG
                                     _  GGTA
GAM1360  LOC254556 3'  TGCCCCTGAGCGAACC      34742          TGG
                                TGCCCTTGAGCG   GGCC
                                ||||||||||||   ||||
                                ACGGGGACTCGC   TTGG
                                       ___
GAM1360  LOC254685 5'  TGCCCTTGAGAAGAGC      34743         CGT
                                TGCCCTTGAG   GGGGC
                                ||||||||||   |||||
                                ACGGGAACTC   TCTCG
                                      T__
GAM1360  LOC256529 5'  TGCGCCTGGGTGTGGGGCC   34744    C    AGC
                                TGC CTTG   GTGGGGCC
                                ||| ||||   ||||||||
                                ACG GGAC   CACCCCGG
                                  C    CCA
GAM1360  LOC51312  3'  TGCCCTTAAGCTGGGGCC    34745          G
                                TGCCCTTGAGC TGGGGCC
                                |||||||||| |||||||
                                ACGGGAATTCG ACCCCGG
                                       _
GAM1360  LOC56912  3'  TGCCCCTGAGCCAAGC      34746          GTG
                                TGCCCTTGAGC   GGGC
                                ||||||||||   ||||
                                ACGGGGACTCG   TTCG
                                      G__
GAM1360  LOC88745  3'  TGCCCTTGAACGGAAACC    34747          T GG
                                TGCCCTTGAGCG G  GCC
                                |||||||||||| |  |||
                                ACGGGAACTTGC C  TGG
                                      _ TT
GAM1360  LOC90639  5'  TGCCCTTGTCCGGGGGCC    34748        AG  T
                                TGCCCTTG  CG GGGGCC
                                ||||||||  || ||||||
```

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                                ACGGGAAC  GC CCCCGG
                                    AG  _
GAM1361  CDH23    5'  CGCGCCTGCAGCCCGC      34751         GCTT   G
                                CGCGCTTGC    GGC CGC
                                |||||||||    ||| |||
                                GCGCGGACG    TCG GCG
                                     ____   G
GAM1361  CDH23    5'  CGCGCCTGCAGCCCGC      34751         GCTT   G
                                CGCGCTTGC    GGC CGC
                                |||||||||    ||| |||
                                GCGCGGACG    TCG GCG
                                     ____   G
GAM1361  DYT1     5'  CACCCTGCTTGTTCTCGCGCC  34752      GC    CG  TGG
                                CACC  GCTTG  CT   CGCGCC
                                ||||  |||||  ||   ||||||
                                GTGG  CGAAC  GA   GCGCGG
                                  GA    AA  ___
GAM1361  LHX5     3'  CACCGCGTCTGCGTCGGGCG   34753        CT    C    C
                                CACCGCG  TGCG TTGG GCG
                                |||||||  |||| |||| |||
                                GTGGCGC  ACGC AGCC CGC
                                    AG   _   _
GAM1361  MAF      5'  CGCGCTGCTGGCGCGC      34754        T  GCT
                                CGCGCT GC   TGGCGCGC
                                ||||||  ||   ||||||||
                                GCGCGA CG   ACCGCGCG
                                  _  ___
GAM1361  NGFR     5'  GCGCTGCGCTCCAGCGCC    34755       T     GGC
                                GCGCT GCGCTT   GCGCC
                                |||||  ||||||   |||||
                                CGCGA CGCGAG   CGCGG
                                  _     GT_
GAM1361  NOX4     5'  CGCTGCGCTCTGTGCCCGC   34756      T    _ _  G
                                CGCT GCGCT TG GC CGC
                                |||| ||||| || || |||
                                GCGA CGCGA AC CG GCG
                                  _    G  A  G
GAM1361  NOX4     5'  CCGCGCTGCGCTCTGTGCC   34757        T     GGCGC
                                CCGCGCT GCGCTT    GCC
                                |||||||  ||||||    |||
                                GGCGCGA CGCGAG    CGG
                                  _     ACA__
GAM1361  P2RY2    5'  CACTGCGCTGCGCTTCTGG   34758     C    T    T_____
                                CAC GCGCT GCGCT     GG
                                |||  |||||  |||||     ||
                                GTG CGCGA CGCGA     CC
                                  A    _    AGAIII
GAM1361  PKD2     5'  CCGCGCTCGGCGCTGTGCGCC  34759         _   T GC
                                CCGCGCTTG CGCT G  GCGCC
                                |||||||||  ||||  |  |||||
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                                GGCGCGAGC GCGA C  CGCGG
                                     C    _ A_
GAM1361  SGT     5'  GCGCTTGCGCACCGCGGTGCC  34760         TTG  C_
                                GCGCTTGCGC   GCG  GCC
                                ||||||||||   |||  |||
                                CGCGAACGCG   CGC  CGG
                                      TGG   CA
GAM1361  C14orf4  5'  CCCGCTTCAGCTGGCGCGC   34761    G    GC   T
                                CC CGCTT  GCT GGCGCGC
                                || |||||  ||| |||||||
                                GG GCGAA  CGA CCGCGCG
                                 _    GT  _
GAM1361  CARD9    3'  CACCTGCTTGCGCAGCGCG   34762     GC      TT
                                CACC  GCTTGCGC  GGCGCG
                                ||||  ||||||||  ||||||
                                GTGG  CGAACGCG  TCGCGC
                                  A_      __
GAM1361  CCNE1    5'  CACCGCGCTGGCGGCCGCGCC  34763         T  GCTT  _
                                CACCGCGCT GC    GGC GCGCC
                                |||||||||  ||    |||  |||||
                                GTGGCGCGA CG    CCG CGCGG
                                     C  _____   G
GAM1361  FLJ13194  5'  CCGCCGCGCTTGTGCCGC    34764     GCT      _  G
                                CCGC   TGCGCTTG GC CGC
                                ||||   ||||||||  ||  |||
                                GGCG   GCGCGAAC CG GCG
                                  ___       A  _
GAM1361  FLJ20531  5'  CACTGCGCCTGCGCCTGCGC   34765     C          G
                                CAC GCGCTTGCGCTTG CGC
                                |||  ||||||||||||  |||
                                GTG CGCGGACGCGGAC GCG
                                  A           _
GAM1361  FLJ21438  5'  CCGTGCGTGCCAGCAGCGCGCC 34766     C  T   __  TT
                                CCG GC TGC  GC  GGCGCGCC
                                |||  ||  |||  ||  ||||||||
                                GGC CG ACG  CG  TCGCGCGG
                                  A  C   GT  __
GAM1361  HSPC065   3'  CACTGTGCTGTGCTCAGCACG  34767     CGC   T C   TG
                                CAC   GCT G GCT  GCGCG
                                |||   |||  |  |||  |||||
                                GTG   CGA C CGA  CGTGC
                                  ACA   _ A   GT
GAM1361  KIAA0247  5'  CCGCCGCTTGCGCGCGC     34768      _       TTGGC
                                CCGC GCTTGCGC    GCGC
                                ||||  ||||||||     ||||
                                GGCG CGAACGCG    CGCG
                                  G       _____
GAM1361  KIAA0252  5'  CACTGCGCTTTCGCTTTGC   34769     C     G    G
                                CAC GCGCTT CGCTT GC
                                |||  ||||||  |||||  ||
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                                GTG CGCGAA GCGAA CG
                                  A     A    A
GAM1361  KIAA0711  5'  GCGCTGCGCCCGCGCGCC    34770      T     G
                                GCGCT GCGCTTG CGCGCC
                                ||||| ||||||| ||||||
                                CGCGA CGCGGGC GCGCGG
                                  _     _
GAM1361  KIAA0789  5'  CCGCGTCCCGCTTGGCGCGCC  34771      C  G
                                CCGCG TT CGCTTGGCGCGCC
                                ||||| || ||||||||||||
                                GGCGC AG GCGAACCGCGCGG
                                   _ G
GAM1361  KIAA1014  5'  CGCGCTTGCGCAAGCGC     34772          TT
                                CGCGCTTGCGC  GGCGC
                                ||||||||||  |||||
                                GCGCGAACGCG  TCGCG
                                      T_
GAM1361  KIAA1465  3'  CCGCGCTTGTGCTGCGC     34773        C   TG
                                CCGCGCTTG GCT  GCGC
                                |||||||| |||  ||||
                                GGCGCGAAC CGA  CGCG
                                    A  __
GAM1361  NIFU      5'  CCGGCTTGCGCCTGCGC     34774     C        G
                                CCG GCTTGCGCTTG CGC
                                ||| ||||||||||| |||
                                GGC CGAACGCGGAC GCG
                                  _        _
GAM1361  PRDM8     3'  CGCTGCGCTTCGCCTCGC    34775      T     G  G_
                                CGCT GCGCTT GC  CGC
                                |||| |||||| ||  |||
                                GCGA CGCGAA CG  GCG
                                   _     G  GA
GAM1361  STK29     3'  CACTCCGCTTGGCGGGC     34776      G       C
                                CGCTT CGCTTGGCG GC
                                ||||| |||||||| ||
                                GTGAG GCGAACCGC CG
                                   _       C
GAM1361  STRBP     5'  CCGCGCTCTGCCCGCGC     34777        GC   TGG
                                CCGCGCTT  GCT   CGCGC
                                ||||||||  |||   |||||
                                GGCGCGAG  CGG   GCGCG
                                    A_  ____
GAM1361  Tenr      5'  CCGCGCTTGCGCCAGCG     34778           T
                                CCGCGCTTGCGCT GGCG
                                |||||||||||| ||||
                                GGCGCGAACGCGG TCGC
                                                _
GAM1362  ACRC      3'  TGTGAAAAATATGGAACTCAAG 34781          C__   A   T_
              TAAGA                  TGTGAAAAAT   GAA TCG  TAAGA
                                |||||||||   ||| |||  |||||
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                                ACACTTTTTA  CTT AGT  ATTCT
                                      TAC  G  TC
GAM1362  LOC147353 3'  TGTGAAAAATCAAAACATACAG 34782            T  TA
           A                    TGTGAAAAATCGAAA CGT  AGA
                                |||||||||||||| |||  |||
                                ACACTTTTTAGTTTT GTA  TCT
                                       _  TG
GAM1362  LOC220692 5'  TGTGAAAAATCAGTGCAAG   34783          AAATC  _
                                TGTGAAAAATCG    GT TAAG
                                ||||||||||||    || ||||
                                ACACTTTTTAGT    CA GTTC
                                       _____ C
GAM1363  APOBEC2   3'  TAAAAAAATACCCAACTTAACA 34786          ___
           T                    TAAAAAAATA  AACTTAACAT
                                ||||||||||  ||||||||||
                                ATTTTTTTAT  TTGAATTGTA
                                      GGG
GAM1363  PLAG1    3'  CTTGTAAAAAAATAAACC    34787
                                TTTGTAAAAAAATAAACT
                                ||||||||||||||||||
                                GAACATTTTTTTATTTGG

GAM1363  RAG1     3'  TTTGTAAGAAAATAAACT    34788       A
                                TTTGTAA AAAATAAACT
                                ||||||| ||||||||||
                                AAACATT TTTTATTTGA
                                    C
GAM1363  ST7      3'  TTTGTAAAAACAAACCATTTAA 34789         AA     ___
           CAT                    TTTGTAAAA  ATAAACT  TAACAT
                                ||||||||| |||||||  ||||||
                                AAACATTTT  TGTTTGG  ATTGTA
                                      __     TAA
GAM1363  LOC221830 3'  TTTGCAGAAAAATAAACT    34790       A
                                TTTGTA AAAAATAAACT
                                |||||| ||||||||||
                                AAACGT TTTTTATTTGA
                                    C
GAM1363  LOC257319 3'  TTTGTAGAAAATAAACTTAAC  34791       AA
                                TTTGTA  AAAATAAACTTAAC
                                ||||||  ||||||||||||||
                                AAACAT  TTTTATTTGAATTG
                                    C_
GAM1364  RRM2B    3'  TTCCTCTATGTATAAAT     34794         C
                                TTCCTCTAT GTATAAAT
                                ||||||||| ||||||||
                                AAGGAGATA CATATTTA
                                       _
GAM1364  AD-017   5'  TTCTTCTGTCATATAAATATTA 34795     C  A        A
           G                    TTC TCT TCGTATAAATA TTAG
                                ||| ||| |||||||||| ||||
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                                AAG AGA AGTATATTTAT AATC
                                  A   C         _
GAM1364  FLJ10961  5'  TTCCTCAGTGATCAAATAATTA 34796       TATCGTA
                 G                 TTCCTC      TAAATAATTAG
                                   ||||||      ||||||||||
                                   AAGGAG      GTTTATTAATC
                                     TCACTA_
GAM1364  FLJ23040  3'  CTCTACAAATAAAATAATTAG  34797       CGTAT
                                   CTCTAT    AAATAATTAG
                                   ||||||    ||||||||||
                                   GAGATG    TTTATTAATC
                                     TTTAT
GAM1364  LOC144866 5'  TTCCTCTATTGTTATAAATA   34798        CG_
                                   TTCCTCTAT   TATAAATA
                                   |||||||||   ||||||||
                                   AAGGAGATA   ATATTTAT
                                         ACA
GAM1365  ABCC3     3'  GTGAAGGTGGTTGTGG      34801          CA  A
                                   GTGGAGGTGGT  TG GG
                                   ||||||||||  || ||
                                   CACTTCCACCA  AC CC
                                         __ A
GAM1365  ADARB1    3'  GTGGAGGTGGTCCACACAGGG  34802          ATG__
                                   GTGGAGGTGGTC    AGGG
                                   ||||||||||||    ||||
                                   CACCTCCACCAG    TCCC
                                         GTGTG
GAM1365  ADARB1    3'  GTGGAGGTGGTCCACACAGGG  34802          ATG__
                                   GTGGAGGTGGTC    AGGG
                                   ||||||||||||    ||||
                                   CACCTCCACCAG    TCCC
                                         GTGTG
GAM1365  ANPEP     3'  GCGGGGTTGGCATGAGGG    34803      A  _  T
                                   GTGG GGT GG CATGAGGG
                                   |||| ||| || ||||||||
                                   CGCC CCA CC GTACTCCC
                                     _  A  _
GAM1365  AP1S1     3'  GTGGAGGTAGGTTATGGGAC  34804         TCA  A
                                   GTGGAGGTGG   TG GGGAC
                                   |||||||||   || |||||
                                   CACCTCCATC   AT CCCTG
                                         CA_  A
GAM1365  AQP6      5'  GGACTCAAGCATGAGGGAC   34805     GG   T
                                   GGA  TGG CATGAGGGAC
                                   |||  ||| ||||||||||
                                   CCT  GTT GTACTCCCTG
                                     GA   C
GAM1365  ARF1      3'  GTGGGGTGCTCCCGAGGG    34806      A   G  A
                                   GTGG GGTG TC TGAGGG
                                   |||| |||| || ||||||
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                                CACC CCAC AG GCTCCC
                                  _   G  G
GAM1365 ARL2    3' GTGAAGGTTGAGGGA      34807        GGTCA
                                GTGGAGGT    TGAGGGA
                                ||||||||    |||||||
                                CACTTCCA    ACTCCCT

                                _____
GAM1365 ATSV    3' GTGGAGGTGGTTGGGG     34808          CA  A
                                GTGGAGGTGGT  TG GGG
                                ||||||||||  || |||
                                CACCTCCACCA  AC CCC

                                __ _
GAM1365 B3GALT5  3' GTGGGAGTGGTTCAAGTCAGGG 34809     AG    _  TG__
                                GTGG  GTGGT CA    AGGG
                                ||||  ||||| ||    ||||
                                CACC  CACCA GT    TCCC
                                  CT    A  TCAG
GAM1365 B3GALT5  3' GTGGGAGTGGTTCAAGTCAGGG 34809     AG    _  TG__
                                GTGG  GTGGT CA    AGGG
                                ||||  ||||| ||    ||||
                                CACC  CACCA GT    TCCC
                                  CT    A  TCAG
GAM1365 B3GALT5  3' GTGGGAGTGGTTCAAGTCAGGG 34809     AG    _  TG__
                                GTGG  GTGGT CA    AGGG
                                ||||  ||||| ||    ||||
                                CACC  CACCA GT    TCCC
                                  CT    A  TCAG
GAM1365 B3GALT5  3' GTGGGAGTGGTTCAAGTCAGGG 34809     AG    _  TG__
                                GTGG  GTGGT CA    AGGG
                                ||||  ||||| ||    ||||
                                CACC  CACCA GT    TCCC
                                  CT    A  TCAG
GAM1365 B3GALT5  3' GTGGGAGTGGTTCAAGTCAGGG 34809     AG    _  TG__
                                GTGG  GTGGT CA    AGGG
                                ||||  ||||| ||    ||||
                                CACC  CACCA GT    TCCC
                                  CT    A  TCAG
GAM1365 BAK1    5' ATGGAGGTCCCGAGGG      34810        GG  A
                                GTGGAGGT  TC TGAGGG
                                ||||||||  || ||||||
                                TACCTCCA  GG GCTCCC

                                __ _
GAM1365 BRF1    3' GTGGGGGTGTCTGCCTCGGAC  34811      A   G  A  AG__
                                GTGG GGTG TC TG    GGAC
                                |||| |||| || ||    ||||
                                CACC CCAC AG AC    CCTG
                                  C    _  _  GGAG
GAM1365 BRPF1    3' GTAGAGGTGGTGGGA      34812          CATGA
                                GTGGAGGTGGT    GGGA
                                ||||||||||     ||||
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                                CATCTCCACCA    CCCT
                                      _____
GAM1365 CA3      5' GCGGAGGTGGGCGAAGGG   34813        TCAT
                                GTGGAGGTGG   GAGGG
                                ||||||||||   |||||
                                CGCCTCCACC   TTCCC
                                     CGC_
GAM1365 CACNA2D2 3' GTGGAGGTGGGGTGGGG    34814        TCA  A
                                GTGGAGGTGG  TG GGG
                                ||||||||||  || |||
                                CACCTCCACC  AC CCC
                                     CC_ _
GAM1365 CDK9     3' GTGGGTGGGTGAGGGA     34815     AG   TCA
                                GTGG  GTGG  TGAGGGA
                                ||||  ||||  |||||||
                                CACC  CACC  ACTCCCT
                                  __   C__
GAM1365 EGFL4    5' GTGAGGGTGAGTGGGGGAC  34816    GA   TCA  A
                                GTG  GGTGG  TG GGGAC
                                |||  |||||  || |||||
                                CAC  CCACT  AC CCCTG
                                  TC    C__  C
GAM1365 EGFL4    3' GTGGAGGTGGTGGGG      34817         CAT A
                                GTGGAGGTGGT  G GGG
                                ||||||||||  | |||
                                CACCTCCACCA  C CCC
                                     ___ _
GAM1365 FGD1     3' GTGGTAGGGTATTGAGGGA  34818     A  T  CA
                                GTGG GG GGT  TGAGGGA
                                |||| || |||  |||||||
                                CACC TC CCA  ACTCCCT
                                  A  _  TA
GAM1365 GARP     3' GTGGGGCTGGGCAGGGAC   34819     A  __  CATG
                                GTGG GGT  GGT   AGGGAC
                                |||| |||  |||   ||||||
                                CACC CCG  CCG   TCCCTG
                                  _  AC  _____
GAM1365 HOXC13   3' GTGGAGGCTGGGGATGGGA  34820       _  TCAT  _
                                GTGGAGG TGG   GA GGGA
                                ||||||| |||   || ||||
                                CACCTCC ACC   CT CCCT
                                   G  C___  A
GAM1365 HSPG2    3' GTGGAGGTGGGTGGGG     34821        TCA  A
                                GTGGAGGTGG  TG GGG
                                ||||||||||  || |||
                                CACCTCCACC  AC CCC
                                     C__  _
GAM1365 HTR6     5' GGAGGTGAGTGGGGGGAC   34822       TCA  A_
                                GGAGGTGG  TG  GGGAC
                                ||||||||  ||  |||||
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                                CCTCCACT   AC  CCCTG
                                    C__  CC
GAM1365  HYOU1    3'  GTGGGGGTGGGGTGAGGG    34823      A    TCA
                                GTGG GGTGG   TGAGGG
                                |||| |||||   ||||||
                                CACC CCACC   ACTCCC
                                  C    CC_
GAM1365  IGFBP5   5'  GTGGAGATGGCGTTGGGG    34824          CA  A
                                GTGGAGGTGGT  TG GGG
                                ||||||||||  || |||
                                CACCTCTACCG  AC CCC
                                     CA  _
GAM1365  ITGB3    3'  GTGGAGGTGCTATGGATGAGGG 34825         GTC___
              AC                  GTGGAGGTG     ATGAGGGAC
                                |||||||||     |||||||||
                                CACCTCCAC     TACTCCCTG
                                    GATACC
GAM1365  KCNK3    3'  GGAGAGTGGTGAGGGA      34826      _    CAT
                                GGAG GTGGT   GAGGGA
                                |||| |||||   ||||||
                                CCTC CACCA   CTCCCT
                                  T    ____
GAM1365  KRT15    3'  GTGGGGAGTGGCAAGGGAC   34827      A_     CAT
                                GTGG  GGTGGT   GAGGGAC
                                ||||  ||||||   |||||||
                                CACC  TCACCG   TTCCCTG
                                  CC     ____
GAM1365  LASS1    3'  GGAGGTGGTGGCCGCAGGGAC 34828         CA_ _
                                GGAGGTGGT   TG AGGGAC
                                |||||||||   || ||||||
                                CCTCCACCA   GC TCCCTG
                                    CCG  G
GAM1365  MEOX1    3'  GTGAAGGTGGGATTGGGG    34829          TCA  A
                                GTGGAGGTGG   TG GGG
                                ||||||||||   || |||
                                CACTTCCACC   AC CCC
                                     CTA  _
GAM1365  MEOX1    3'  GTGAAGGTGGGATTGGGG    34829          TCA  A
                                GTGGAGGTGG   TG GGG
                                ||||||||||   || |||
                                CACTTCCACC   AC CCC
                                     CTA  _
GAM1365  MLC1     3'  GTGGGGGTGGCCTGCAGAC   34830      A      A  AG
                                GTGG GGTGGTC TG  GGAC
                                |||| ||||||| ||  ||||
                                CACC CCACCGG AC  TCTG
                                  C       _  G_
GAM1365  MLC1     3'  GTGGGGGTGGCCTGCAGAC   34830      A      A  AG
                                GTGG GGTGGTC TG  GGAC
                                |||| ||||||| ||  ||||
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                                CACC CCACCGG AC  TCTG
                                  C      _ G_
GAM1365 MPHOSPH1 3' GTGGGGATGGTTAATGGG    34831     A     CA  _
                                GTGG GGTGGT  TGA GGG
                                |||| ||||||  ||| |||
                                CACC CTACCA  ATT CCC
                                  C     __   A
GAM1365 NDUFB3   5' GTAGAGACTACATGAGGGAC  34832       TG T
                                GTGGAGG  G CATGAGGGAC
                                |||||||  | ||||||||||
                                CATCTCT  T GTACTCCCTG
                                    GA _
GAM1365 OPHN1    3' ATGGAGGTGCTGTGGGG     34833        G CA  A
                                GTGGAGGTG T  TG GGG
                                |||||||||  |  || |||
                                TACCTCCAC G  AC CCC
                                     _ AC  _
GAM1365 PDE4A    5' GTGGAGGCGGTGGGGG      34834         CAT A
                                GTGGAGGTGGT   G GGG
                                ||||||||||   | |||
                                CACCTCCGCCA   C CCC
                                      ___ C
GAM1365 POU2AF1  5' GTGAAGGTGGTGTGGGG     34835         CA  A
                                GTGGAGGTGGT  TG GGG
                                ||||||||||  || |||
                                CACTTCCACCA  AC CCC
                                      C_  _
GAM1365 RASGRP2  5' GTGGAGGTCGGGGGCGTGGGGA 34836        _____  CA  A
           C                     GTGGAGGT    GGT  TG GGGAC
                                ||||||||    |||  || |||||
                                CACCTCCA    CCG  AC CCCTG
                                     GCCC   C_  _
GAM1365 RET      3' GTGGGGGTGCGTCCTCCCAGGG 34837      A   _   ATG__
                                GTGG GGTG GTC     AGGG
                                |||| |||| |||     ||||
                                CACC CCAC CAG     TCCC
                                  C   G   GAGGG
GAM1365 SCA2     5' GCGGAGGTGCGGATAGGGAC  34838        GTCATG
                                GTGGAGGTG     AGGGAC
                                |||||||||     ||||||
                                CGCCTCCAC     TCCCTG
                                     GCCTA_
GAM1365 SETDB1   3' TGGAGGTGGAGAAGGGA     34839        TCAT
                                TGGAGGTGG    GAGGGA
                                |||||||||    ||||||
                                ACCTCCACC    TTCCCT
                                     TC__
GAM1365 SLC22A3  3' GGAGGTGGACGGGAGGGAC   34840        TCAT
                                GGAGGTGG    GAGGGAC
                                ||||||||    |||||||
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                                CCTCCACC   CTCCCTG
                                    TGCC
GAM1365  SPTB     3'  GGAGGTGGCTGCAGGGA    34841       CA  _
                                GGAGGTGGT  TG AGGGA
                                |||||||||  || |||||
                                CCTCCACCG  AC TCCCT
                                    __  G
GAM1365  TAGLN    3'  GTAGAGGTGATGGGG      34842       GTC  A
                                GTGGAGGTG  ATG GGG
                                |||||||||  ||| |||
                                CATCTCCAC  TAC CCC
                                    ___  _
GAM1365  TGFBR2   5'  GTGGAGGTGGACATTTGA   34843        T  GAGG
                                GTGGAGGTGG CAT   GA
                                |||||||||| |||   ||
                                CACCTCCACC GTA   CT
                                    T  AA__
GAM1365  TRIM34   3'  ATGGGGGTGGTTCCTATGGAC  34844    A    _ ATGAG
                                GTGG GGTGGT C    GGAC
                                |||| ||||||  |    ||||
                                TACC CCACCA G    CCTG
                                  C    A GATA_
GAM1365  TRIM34   3'  ATGGGGGTGGTTCCTATGGAC  34844    A    _ ATGAG
                                GTGG GGTGGT C    GGAC
                                |||| ||||||  |    ||||
                                TACC CCACCA G    CCTG
                                  C    A GATA_
GAM1365  ZNF175   3'  GTGGAGATGGAAAGGG     34845       TCAT
                                GTGGAGGTGG   GAGGG
                                ||||||||||   |||||
                                CACCTCTACC   TTCCC
                                    T___
GAM1365  ZNF274   5'  GGAGGCCTCTGGTGAGGGAC  34846     ____  CAT
                                GGAGGT   GGT  GAGGGAC
                                ||||||   |||  |||||||
                                CCTCCG   CCA  CTCCCTG
                                   GAGA  ___
GAM1365  ZNF274   5'  GGAGGCCTCTGGTGAGGGAC  34846     ____  CAT
                                GGAGGT   GGT  GAGGGAC
                                ||||||   |||  |||||||
                                CCTCCG   CCA  CTCCCTG
                                   GAGA  ___
GAM1365  AIF1     5'  GTGGGGTTGGGGAGTTGAGGG 34847    A  _  TCA__
                                GTGG GGT GG    TGAGGG
                                |||| ||| ||    ||||||
                                CACC CCA CC    ACTCCC
                                  _  A  CCTCA
GAM1365  ALS2CR8  5'  GCGGGACGGCGTGAGGGAC   34848    A GT  CA
                                GTGG G  GGT  TGAGGGAC
                                |||| |  |||  ||||||||
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                                CGCC C  CCG  ACTCCCTG
                                  _ TG   C_
GAM1365 APCL     3'  TGGGGCGACCTATGGGGGAC  34849     A   GT _  A
                                TGG GGTG  C ATG GGGAC
                                ||| ||||  | ||| |||||
                                ACC CCGC  G TAC CCCTG
                                  _   TG A   C
GAM1365 ARHF     3'  GTGGAGATGGGAGGG       34850          TCAT
                                GTGGAGGTGG   GAGGG
                                ||||||||||   |||||
                                CACCTCTACC   CTCCC
                                             _____
GAM1365 BCL2L1   5'  GGAGGTGGCTGCGGGGA     34851         CA  A
                                GGAGGTGGT  TG GGGA
                                |||||||||  || ||||
                                CCTCCACCG  GC CCCT
                                     AC  _
GAM1365 BMF      3'  GTGGAGGTCGGGGGGGAGGG  34852         _  TCAT
                                GTGGAGGT GG   GAGGG
                                |||||||| ||   |||||
                                CACCTCCA CC   CTCCC
                                    G  CCCC
GAM1365 BRPF3    3'  GTGAAGGTGGGGAGGG      34853         TCAT
                                GTGGAGGTGG   GAGGG
                                ||||||||||   |||||
                                CACTTCCACC   CTCCC
                                     C___
GAM1365 C1QTNF6  3'  GTGAGAGGGGCATGAGGG    34854     _   T  T
                                GTG GAGG GG CATGAGGG
                                ||| |||| || ||||||||
                                CAC CTCC CC GTACTCCC
                                  T   _ _
GAM1365 C20orf36 3'  GTGCATGTTGCATGAGGGAC  34855     GAG  G T
                                GTG   GT G CATGAGGGAC
                                |||   || | ||||||||||
                                CAC   CA C GTACTCCCTG
                                  GTA  A _
GAM1365 C7orf13  3'  ATGGAGTGTGAGGGA       34856       G  GTCA
                                GTGGAG TG    TGAGGGA
                                |||||| ||    |||||||
                                TACCTC AC    ACTCCCT
                                  _ _____
GAM1365 CACNG4   3'  GTGGAGGTGGTGACAGGG    34857          C  G
                                GTGGAGGTGGT AT AGGG
                                |||||||||| || ||||
                                CACCTCCACCA TG TCCC
                                     C  _
GAM1365 CDC37    3'  GTGGCGGTGGTAGCTGGGG   34858      A     CA_  A
                                GTGG GGTGGT   TG GGG
                                |||| ||||||   || |||
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                                CACC CCACCA   AC CCC
                                  G     TCG  _
GAM1365 CGRP-RCP  3' GTGGGGTGGTCAGAAAGG    34859      A       T
                                GTGG GGTGGTCA GAGGG
                                |||| |||||||| |||||
                                CACC CCACCAGT TTTCC
                                  _       C
GAM1365 CSEN      3' GTGGAGGTGGCTGTGG      34860          CA  A
                                GTGGAGGTGGT  TG GG
                                ||||||||||  || ||
                                CACCTCCACCG  AC CC
                                      __ A
GAM1365 DDA3      3' GTGGGGGTGGATAAAGAC    34861      A    TCATG
                                GTGG GGTGG    AGGGAC
                                |||| |||||    ||||||
                                CACC CCACC    TTTCTG
                                  C    TA___
GAM1365 DEPP      3' GTGGAAGTGGTGTAGGG     34862          CATG
                                GTGGAGGTGGT   AGGG
                                ||||||||||   ||||
                                CACCTTCACCA   TCCC
                                      CA__
GAM1365 DKFZp434G171 3' GTGGAGGTGGTCTGTGAA    34863          A_
                                GTGGAGGTGGTC  TGAG
                                ||||||||||||  ||||
                                CACCTCCACCAG  ACTT
                                       AC
GAM1365 DKFZp434J1015 3' GTGGAGGCGGGTGGGGG    34864          TCA  A
                                GTGGAGGTGG   TG GGG
                                |||||||||   || |||
                                CACCTCCGCC   AC CCC
                                      C__  C
GAM1365 DKFZP434O047 5' GTGGGGCTGGGCCAAGGGAC  34865      A  __    TG
                                GTGG GGT  GGTCA  AGGGAC
                                |||| |||  |||||  ||||||
                                CACC CCG  CCGGT  TCCCTG
                                  _  AC    __
GAM1365 DKFZP566J091 3' GGGAGGTGGGGAGGGA      34866   T      TCAT
                                G GGAGGTGG    GAGGGA
                                | ||||||||    ||||||
                                C CCTCCACC    CTCCCT
                                 _       C___
GAM1365 DKFZP727C091 3' GGGGGTGGTCATCTAAGA    34867    A       GA
                                GG GGTGGTCAT  GGGA
                                || |||||||||  ||||
                                CC CCACCAGTA  TTCT
                                  C        GA
GAM1365 DLGAP1    3' GTGGGGGGCTGAGGG      34868      A  T   CA
                                GTGG GG GGT  TGAGGG
                                |||| || |||  ||||||
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                              CACC CC CCG  ACTCCC
                                _ _  __
GAM1365 DLGAP1   3' GTGGGGGGCTGAGGG      34868     A T  CA
                              GTGG GG GGT  TGAGGG
                              |||| || |||  ||||||
                              CACC CC CCG  ACTCCC
                                _ _  __
GAM1365 FBH1     5' GTGGAGATGGCCCAGGG     34869          ATG
                              GTGGAGGTGGTC  AGGG
                              ||||||||||||  ||||
                              CACCTCTACCGG  TCCC
                                    G__
GAM1365 FENS-1   3' GTGGAGCTGCGTGAGAGGGAC 34870      G _ CAT
                              GTGGAG TG GT  GAGGGAC
                              |||||| || ||  |||||||
                              CACCTC AC CA  CTCCCTG
                                 G  G  CT_
GAM1365 FGD3     5' GTGGAGGCTGGCCAGGGG    34871       _    TGA
                              GTGGAGG TGGTCA  GGG
                              ||||||| ||||||  |||
                              CACCTCC ACCGGT  CCC
                                 G    C__
GAM1365 FLJ00024 3' GTGAAGGTGGGTCAGGGGG   34872         _  TGA
                              GTGGAGGTGG TCA  GGG
                              |||||||||| |||  |||
                              CACTTCCACC AGT  CCC
                                    C  CC_
GAM1365 FLJ00060 5' GTGGAGGTAGGGGAGGG     34873         TCAT
                              GTGGAGGTGG   GAGGG
                              ||||||||||   |||||
                              CACCTCCATC   CTCCC
                                    CC__
GAM1365 FLJ10101 3' GTGGAGGGGCTCCTGGGAC   34874       T  CATGA
                              GTGGAGG GGT    GGGAC
                              ||||||| |||    |||||
                              CACCTCC CCG    CCCTG
                                 _  AGGA_
GAM1365 FLJ10737 3' GGAGGTGGTCATGGGAA     34875          A
                              GGAGGTGGTCATG GGGA
                              |||||||||||| ||||
                              CCTCCACCAGTAC CCTT
                                        _
GAM1365 FLJ10871 3' GTGAGGGCAGCCAGTGAGGGAC 34876     GA TG  _
                              GTG  GG  GTCA TGAGGGAC
                              |||  ||  |||| ||||||||
                              CAC  CC  CGGT ACTCCCTG
                                TC  GT   C
GAM1365 FLJ12221 3' TGGAGGTGGCATAATGGG    34877        T   _
                              TGGAGGTGG CATGA GGG
                              ||||||||| ||||| |||
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                                ACCTCCACC GTATT CCC
                                      _    A
GAM1365  FLJ12389  3' GAGGGCTCACCCATGAGGGAC  34878     ___  G
                                GAGG  TG TCATGAGGGAC
                                ||||  || ||||||||||
                                CTCC  GT GGTACTCCCTG
                                  CGA  G
GAM1365  FLJ12529  3' GTGGGGATGGGGTTGGGGGAC  34879     A    TCA  A
                                GTGG GGTGG  TG GGGAC
                                |||| |||||  || |||||
                                CACC CTACC  AC CCCTG
                                  C    CCA  C
GAM1365  FLJ12529  3' GTGGAGGTGGGGATGGGG    34880         TC   A
                                GTGGAGGTGG  ATG GGG
                                ||||||||||  ||| |||
                                CACCTCCACC  TAC CCC
                                      CC  _
GAM1365  FLJ12587  3' GGAGGTGCTGGTGAGGGAC   34881       GTCA
                                GGAGGTG   TGAGGGAC
                                |||||||   ||||||||
                                CCTCCAC   ACTCCCTG
                                    GACC
GAM1365  FLJ12650  3' GTGGAGGTGATGGGGA     34882        GTC  A
                                GTGGAGGTG  ATG GGGA
                                |||||||||  ||| ||||
                                CACCTCCAC  TAC CCCT
                                     ___  _
GAM1365  FLJ12681  3' GCGGGGGTGGAGATGAGGGA  34883     A    TC
                                GTGG GGTGG  ATGAGGGA
                                |||| |||||  ||||||||
                                CGCC CCACC  TACTCCCT
                                  C    TC
GAM1365  FLJ13769  3' GTGGAGGGGTGTGGGG     34884       T  CA  A
                                GTGGAGG GGT  TG GGG
                                ||||||| |||  || |||
                                CACCTCC CCA  AC CCC
                                    _  C_  _
GAM1365  FLJ14525  3' TGGAGATGATGAGGG      34885       GTC
                                TGGAGGTG  ATGAGGG
                                ||||||||  |||||||
                                ACCTCTAC  TACTCCC
                                     ___
GAM1365  FLJ14549  3' GTGGGGTGTGGTGGGAAGGGAC 34886     AG_   CAT
                                GTGG  GTGGT  GAGGGAC
                                ||||  |||||  |||||||
                                CACC  CACCA  TTCCCTG
                                  CCA   CCC
GAM1365  FLJ14642  3' GGAGGTGGGGCGGGGAC    34887       TCA  A
                                GGAGGTGG  TG GGGAC
                                ||||||||  || |||||
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                                CCTCCACC   GC CCCTG
                                     CC_  _
GAM1365  FLJ14743  5'  GCGGAGGTGGCGGGG      34888         CAT A
                                GTGGAGGTGGT   G GGG
                                ||||||||||   | |||
                                CGCCTCCACCG   C CCC
                                      ___ _
GAM1365  FLJ22021  3'  GTGGAGGTGACGGGG      34889        GTC   A
                                GTGGAGGTG   ATG GGG
                                |||||||||   ||| |||
                                CACCTCCAC   TGC CCC
                                      ___   _
GAM1365  FLJ22215  3'  GTGGAGGAGACGCGGGGAC   34890       T  TCA  A
                                GTGGAGG GG   TG GGGAC
                                ||||||| ||   || |||||
                                CACCTCC CT   GC CCCTG
                                     T  GC_  _
GAM1365  FLJ32356  3'  GTGGAGGTGTCCTCAGGG    34891        G  ATG
                                GTGGAGGTG TC   AGGG
                                ||||||||| ||   ||||
                                CACCTCCAC AG   TCCC
                                     _  GAG
GAM1365  FLJ32934  3'  GGAGGTGAGAGAGGGAC     34892        TCAT
                                GGAGGTGG    GAGGGAC
                                ||||||||    |||||||
                                CCTCCACT    CTCCCTG
                                     CT__
GAM1365  GPS1      3'  GTGGAGGTGGGGAGGG      34893        TCAT
                                GTGGAGGTGG    GAGGG
                                ||||||||||    |||||
                                CACCTCCACC    CTCCC
                                      C___
GAM1365  GRIN3A    3'  GTGGGTGTGAGGATGGGGGA  34894     AG   TC   A
                                GTGG  GTGG  ATG GGGA
                                ||||  ||||  ||| ||||
                                CACC  CACT  TAC CCCT
                                   CA   CC   C
GAM1365  GSK3A     3'  TGGAGGTGGGGACAGGGAC   34895        TC  G
                                TGGAGGTGG  AT AGGGAC
                                |||||||||  || ||||||
                                ACCTCCACC  TG TCCCTG
                                     CC  _
GAM1365  HCA4      3'  GTGAAGGTGGAGGGA       34896         TCATG
                                GTGGAGGTGG    AGGGA
                                ||||||||||    |||||
                                CACTTCCACC    TCCCT
                                      _____
GAM1365  HU-K4     3'  GTGGGGGTGGGCCAGGGGG   34897     A    _  TGA
                                GTGG GGTGG TCA   GGG
                                |||| ||||| |||   |||
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                                CACC CCACC GGT   CCC
                                  C    C   CC_
GAM1365  KATNB1   3' GTAGAGGTGGCCAGGGAC    34898          TGA
                                GTGGAGGTGGTCA   GGGAC
                                ||||||||||||   |||||
                                CATCTCCACCGGT   CCCTG
                                       ___
GAM1365  KIAA0284 3' GTGGGGGTGGCCATGGGG    34899     A        A
                                GTGG GGTGGTCATG GGG
                                |||| |||||||||| |||
                                CACC CCACCGGTAC CCC
                                  C        _
GAM1365  KIAA0620 3' ATGGAGGTGCCCAGGG      34900        G   TGA
                                GTGGAGGTG TCA   GGG
                                |||||||| |||   |||
                                TACCTCCAC GGT   CCC
                                     G  ___
GAM1365  KIAA0669 5' GTGGCGGCGGCGTGAGGG    34901     A     CA
                                GTGG GGTGGT  TGAGGG
                                |||| ||||||  ||||||
                                CACC CCGCCG  ACTCCC
                                  G     C_
GAM1365  KIAA0729 3' TGGGGGTTGGGGGGTGAGGGAC 34902     A  _  TCA
                                TGG GGT GG   TGAGGGAC
                                ||| ||| ||   ||||||||
                                ACC CCA CC   ACTCCCTG
                                  C   A  CCC
GAM1365  KIAA0788 3' GTGGAGGTAGGCGGGGAC    34903         TCA  A
                                GTGGAGGTGG   TG GGGAC
                                ||||||||||   || |||||
                                CACCTCCATC   GC CCCTG
                                     C__  _
GAM1365  KIAA0789 3' GTGGAGATGAGAAGGG      34904         TCAT
                                GTGGAGGTGG    GAGGG
                                ||||||||||    |||||
                                CACCTCTACT    TTCCC
                                     C___
GAM1365  KIAA0937 3' GGGAGGGATGAGGGA       34905   T    T GTC
                                G GGAGG G   ATGAGGGA
                                | ||||| |   ||||||||
                                C CCTCC C   TACTCCCT
                                _    _ ___
GAM1365  KIAA1086 3' GTGGAGGTGGGTGGGGG     34906         TCA  A
                                GTGGAGGTGG   TG GGG
                                ||||||||||   || |||
                                CACCTCCACC   AC CCC
                                     C__  C
GAM1365  KIAA1297 3' GTGGAGGTAGTCCAGG      34909          ATG
                                GTGGAGGTGGTC   AGG
                                ||||||||||||   |||
```

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                                CACCTCCATCAG  TCC
                                      G__
GAM1365 KIAA1297 3' GTGGAGGCTGGGATCGGGG  34908      _  TCA A
                                GTGGAGG TGG  TG GGG
                                ||||||| |||  || |||
                                CACCTCC ACC  GC CCC
                                   G  CTA _
GAM1365 KIAA1297 5' GTGGGAATGTCTGTGAGGGAC 34907    AG  GTCA
                                GTGG GTG   TGAGGGAC
                                |||| |||   ||||||||
                                CACC TAC   ACTCCCTG
                                  CT  AGAC
GAM1365 KIAA1535 3' GTGAGGGTGGTAAAGGAC   34910    GA    CAT
                                GTG GGTGGT  GAGGGAC
                                ||| ||||||  |||||||
                                CAC CCACCA  TTTCCTG
                                  TC    ___
GAM1365 KIAA1602 3' GTGGGGTGTGCCAGGGAC   34911    A  _  TGA
                                GTGG GGTG GTCA  GGGAC
                                |||| |||| ||||  |||||
                                CACC CCAC CGGT  CCCTG
                                  _  A  ___
GAM1365 KIAA1854 3' GTGGAGGTGGTTGGGG     34808       CA A
                                GTGGAGGTGGT TG GGG
                                |||||||||| || |||
                                CACCTCCACCA AC CCC
                                      __ _
GAM1365 KIAA1957 3' GTGGAGGGGCAAAGGGGGAC 34912      T  CATGA
                                GTGGAGG GGT   GGGAC
                                ||||||| |||   |||||
                                CACCTCC CCG   CCCTG
                                   _  TTTCC
GAM1365 LY6G5C   3' GAGGGCTGGTATGAGGGAC  34913    __  C
                                GAGG TGGT ATGAGGGAC
                                |||| |||| |||||||||
                                CTCC ACCA TACTCCCTG
                                  CG  _
GAM1365 MCRS1    3' GTGAAGGTGGCAATGGGGG  34914       C  A
                                GTGGAGGTGGT ATG GGG
                                |||||||||| ||| |||
                                CACTTCCACCG TAC CCC
                                      T  C
GAM1365 MEP50    3' GTGGACACTCATGGGGGAC  34915    G TGG   A
                                GTGGA G  TCATG GGGAC
                                ||||| |  ||||| |||||
                                CACCT T  AGTAC CCCTG
                                  G G__   C
GAM1365 MGC11335 3' GAGGGTCCCTGAGGGAC   34916    TG  A_
                                GAGG GTC TGAGGGAC
                                |||| ||| ||||||||
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                              CTCC  CAG  ACTCCCTG
                                __  GG
GAM1365 MGC13064 3' GTGGAAGCCAGTATGGGGG  34917       _  C  A
                              GTGGAGGT GGT ATG GGG
                              |||||||| ||| ||| |||
                              CACCTTCG TCA TAC CCC
                                 G  _  C
GAM1365 MGC14126 5' GTGGGGGCCGGCTGGGGGAC  34918    A  _  CA  A
                              GTGG GGT GGT  TG GGGAC
                              |||| ||| |||  || |||||
                              CACC CCG CCG  AC CCCTG
                                C  G  __ C
GAM1365 MGC15854 5' GTGGAGTGGGGCCAAAGGG  34919     GT_   T
                              GTGGAG  GGTCA GAGGG
                              ||||||  ||||| |||||
                              CACCTC  CCGGT TTCCC
                                 ACC   _
GAM1365 MGC16491 5' GTGGGGGTGGTTAAGG     34920    A    CA
                              GTGG GGTGGT  TGAGG
                              |||| ||||||  |||||
                              CACC CCACCA  ATTCC
                                C    __
GAM1365 MGC20255 3' GTGGGGGTTGTCTGAGA    34921    A  G  A
                              GTGG GGT GTC TGAGG
                              |||| ||| ||| |||||
                              CACC CCA CAG ACTCT
                                C  A  _
GAM1365 MGC2647  3' GTGGAAGTGGGGCCGGGG   34922       TCA  A
                              GTGGAGGTGG  TG GGG
                              ||||||||||  || |||
                              CACCTTCACC  GC CCC
                                   CCG  _
GAM1365 MGC29761 3' GTGGGTGATGAGGGA     34923    AG  GTC
                              GTGG  GTG  ATGAGGGA
                              ||||  |||  ||||||||
                              CACC  CAC  TACTCCCT
                                __  ___
GAM1365 MGC3101  3' GTGGAAGTGTGGCCAGGGAC  34924     _ _    TGA
                              GTGGA G GTGGTCA  GGGAC
                              ||||| | |||||||  |||||
                              CACCT C CACCGGT  CCCTG
                                 T A    ___
GAM1365 MGC3771  5' GCGGAGGTAGGAGAGGGAC  34925       TCAT
                              GTGGAGGTGG   GAGGGAC
                              ||||||||||   |||||||
                              CGCCTCCATC   CTCCCTG
                                   CT__
GAM1365 MGC4171  5' GTGAAGGTCAGCGGGGG    34926       _  CAT A
                              GTGGAGGT GGT  G GGG
                              |||||||| |||  | |||
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                                CACTTCCA TCG   C CCC
                                    G  ___ C
GAM1365 MGC5457  3' GTGGAGGTGGCAGGG      34927          CATG
                                GTGGAGGTGGT   AGGG
                                ||||||||||   ||||
                                CACCTCCACCG   TCCC
                                          ____
GAM1365 MOT8     3' GTGGTAGGTGCGGGGA      34928     _    GTCA  A
                                GTGG AGGTG   TG GGGA
                                |||| |||||   || ||||
                                CACC TCCAC   GC CCCT
                                  A   ____ _
GAM1365 PDZ-GEF1 3' GTGGAGGGGTCATTTCAG    34929       T     GA_
                                GTGGAGG GGTCAT   GG
                                |||||| ||||||   ||
                                CACCTCC CCAGTA   TC
                                   _     AAG
GAM1365 PPP1R16B 3' ATGGAGGTGGAAGGG       34930         TCAT
                                GTGGAGGTGG   GAGGG
                                ||||||||||   |||||
                                TACCTCCACC   TTCCC
                                          _____
GAM1365 PTPNS1   3' GTGGAGGTGGTGGAGG      34931          CAT
                                GTGGAGGTGGT   GAGG
                                ||||||||||   ||||
                                CACCTCCACCA   CTCC
                                      C__
GAM1365 RAB40A   5' ATGGGGGCAGGATGAGGGAC  34932     A  TG TC
                                GTGG GG  G  ATGAGGGAC
                                |||| ||  |  |||||||||
                                TACC CC  C  TACTCCCTG
                                  C  GT C_
GAM1365 RAI17    3' TGGAGGTGGAGCCTCAGGGAC 34933        TCATG_
                                TGGAGGTGG     AGGGAC
                                |||||||||     ||||||
                                ACCTCCACC     TCCCTG
                                     TCGGAG
GAM1365 RICH1    3' GTGGAAGTGGTGGAGGG     34934          CAT
                                GTGGAGGTGGT   GAGGG
                                ||||||||||   |||||
                                CACCTTCACCA   CTCCC
                                      C__
GAM1365 RIN3     3' ATGGGGTGGGTGTGGGGGAC  34935     A    TCA  A
                                GTGG GGTGG   TG GGGAC
                                |||| |||||   || |||||
                                TACC CCACC   AC CCCTG
                                  _    CAC  C
GAM1365 SDCCAG43 3' GTGGAGGAGGCTGGGG      34936       T   CA  A
                                GTGGAGG GGT  TG GGG
                                ||||||| |||  || |||
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                                CACCTCC CCG  AC CCC
                                   T  __ _
GAM1365  SDF1     3'  GTGGAGGTGCTCGGGA      34937         G  ATGA
                                GTGGAGGTG TC    GGGA
                                ||||||||| ||    ||||
                                CACCTCCAC AG    CCCT
                                   G  _____
GAM1365  SEPT1    3'  GCGGAGGTCCCGGGGGG      34938         GG  A  A
                                GTGGAGGT  TC TG GGG
                                ||||||||  || || |||
                                CGCCTCCA  GG GC CCC
                                   __  _  C
GAM1365  SHAPY    3'  GGAGAGGTTTGTGAGGGAC    34939       T   CA_
                                GGAGG GGT   TGAGGGAC
                                ||||| |||   ||||||||
                                CCTCT CCA   ACTCCCTG
                                  _   AAC
GAM1365  SRF      5'  GTGGAGGGGGCCGGGA      34940         T    ATGA
                                GTGGAGG GGTC    GGGA
                                ||||||| ||||    ||||
                                CACCTCC CCGG    CCCT
                                   C    _____
GAM1365  STK29    3'  GTGGAGGCGGTGGACGGGG    34941           C_   A
                                GTGGAGGTGGT  ATG GGG
                                ||||||||||  ||| |||
                                CACCTCCGCCA  TGC CCC
                                      CC  _
GAM1365  SV2      3'  GTGGGGAGTGAGGGA       34942      A  T   CAT
                                GTGG GG GGT   GAGGGA
                                |||| || |||   ||||||
                                CACC CC TCA   CTCCCT
                                  _  _  ___
GAM1365  TUBB5    3'  ATGGGATTCATGGGGG       34943      A  GG    A
                                GTGG GGT  TCATG GGG
                                |||| |||  ||||| |||
                                TACC CTA  AGTAC CCC
                                  _  __    C
GAM1365  UBP1     3'  GTGGGGGTGGTCAGAGA      34944      A      T
                                GTGG GGTGGTCA GAGG
                                |||| ||||||| ||||
                                CACC CCACCAGT CTCT
                                  C      _
GAM1365  LOC126364 3'  GGAGCGGCATGAGGGAC     34945      G   T
                                GGAG TGG CATGAGGGAC
                                |||| ||| ||||||||||
                                CCTC GCC GTACTCCCTG
                                  _  _
GAM1365  LOC126961 3'  GTGGAGGTGGCGCGGGGAC   34946           CA  A
                                GTGGAGGTGGT  TG GGGAC
                                ||||||||||  || |||||
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                                CACCTCCACCG  GC CCCTG
                                      C_  _
GAM1365  LOC127534 3'  GTGGGGTGTGAGGGAC      34947      A    GTCA
                                GTGG GGTG    TGAGGGAC
                                |||| ||||    ||||||||
                                CACC CCAC    ACTCCCTG
                                  _   _____
GAM1365  LOC127943 3'  GTGGAGGTGGTGTTCCGGAC   34948           CATGAG
                                GTGGAGGTGGT     GGAC
                                ||||||||||      ||||
                                CACCTCCACCA     CCTG
                                      CAAGG_
GAM1365  LOC134637 3'  ATGGAGGTGAACTGGGGAC    34949          TCA  A
                                GTGGAGGTGG   TG GGGAC
                                |||||||||   || |||||
                                TACCTCCACT   AC CCCTG
                                      TG_  _
GAM1365  LOC143677 5'  GTGGAGGTGGCTGGGG      34950          CA  A
                                GTGGAGGTGGT  TG GGG
                                ||||||||||  || |||
                                CACCTCCACCG  AC CCC
                                      __  _
GAM1365  LOC144079 5'  GTGGGGGTGGATGAGA      34951      A     TC
                                GTGG GGTGG  ATGAGG
                                |||| |||||  ||||||
                                CACC CCACC  TACTCT
                                  C     __
GAM1365  LOC145135 5'  GTGGAGATGCAAGGG       34952         GTCA
                                GTGGAGGTG    TGAGGG
                                |||||||||    ||||||
                                CACCTCTAC    GTTCCC
                                      _____
GAM1365  LOC145693 5'  GTGGAGGTGGGCGTGGGG    34953          TCA  A
                                GTGGAGGTGG   TG GGG
                                |||||||||   || |||
                                CACCTCCACC   AC CCC
                                      CGC  _
GAM1365  LOC145813 5'  GAGGAGGAAAATGAGGGAC    34954      T  TC_
                                GAGG GG   ATGAGGGAC
                                |||| ||   |||||||||
                                CTCC CC   TACTCCCTG
                                  T  TTT
GAM1365  LOC146332 3'  GTGGAGGTTGTCCAAGGG    34955        G   A
                                GTGGAGGT GTC TGAGGG
                                |||||||| ||| ||||||
                                CACCTCCA CAG GTTCCC
                                     A   _
GAM1365  LOC146957 3'  GTGGAGGTGGGCAATGGGG    34956          T  _  A
                                GTGGAGGTGG CA TG GGG
                                |||||||||| || || |||
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                                CACCTCCACC GT AC CCC
                                      C  T  _
GAM1365  LOC147645 3'  GGGGGTGACCACGGGGAC    34957    A   GT   A
                                GG GGTG  CATG GGGAC
                                || ||||  |||| |||||
                                CC CCAC  GTGC CCCTG
                                 C   TG   _
GAM1365  LOC148137 3'  GTGGAGGCTGGAGGTGCAGGG  34958       _  TCA  _
                                GTGGAGG TGG   TG AGGG
                                ||||||| |||   || ||||
                                CACCTCC ACC   AC TCCC
                                    G   TCC  G
GAM1365  LOC150197 5'  GTGGAGGTGTTTGCCCTGGGGG 34959        ___  A  A
                                GTGGAGGTG   GTC TG GGG
                                |||||||||   ||| || |||
                                CACCTCCAC   CGG AC CCC
                                      AAA   G  C
GAM1365  LOC150319 5'  GTGGAGGTGGCATAGA      34960         T   GAG
                                GTGGAGGTGG CAT   GGA
                                |||||||||| |||   |||
                                CACCTCCACC GTA   TCT
                                      _  ___
GAM1365  LOC151429 3'  GGAGGTGGGGTGGGGAC     34961        TCA  A
                                GGAGGTGG   TG GGGAC
                                ||||||||   || |||||
                                CCTCCACC   AC CCCTG
                                     CC_  _
GAM1365  LOC152190 5'  GTGGAGGTGTTTGTCCGA    34962        ___  A
                                GTGGAGGTG   GTC TGA
                                |||||||||   ||| |||
                                CACCTCCAC   CAG GCT
                                      AAA  _
GAM1365  LOC153480 5'  GCGGAGGCTGTGAGGGAC    34963        GGTCA
                                GTGGAGGT    TGAGGGAC
                                ||||||||    ||||||||
                                CGCCTCCG    ACTCCCTG
                                     AC___
GAM1365  LOC154222 3'  GAGGTGATTAGGTCATGGGGG  34964      _____     A
                                GAGGT    GGTCATG GGG
                                |||||    ||||||| |||
                                CTCCA    CCAGTAC CCC
                                   CTAAT      C
GAM1365  LOC162137 3'  GCGGAGGTGGCGGGG       34888         CAT A
                                GTGGAGGTGGT   G GGG
                                ||||||||||   | |||
                                CGCCTCCACCG   C CCC
                                     ___ _
GAM1365  LOC170396 3'  GTGGGACAAAACATGAGGG   34965     A  TG T_
                                GTGG GG  G  CATGAGGG
                                |||| ||  |  ||||||||
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                                CACC CT  T  GTACTCCC
                                  _  GT TT
GAM1365  LOC195977 3'  GTGGAGGTGGTGGAGG      34931          CAT
                                GTGGAGGTGGT   GAGG
                                ||||||||||   ||||
                                CACCTCCACCA   CTCC
                                      C__
GAM1365  LOC199927 3'  GTGGAGGTCGGTGTGGGGA   34966        _  CA  A
                                GTGGAGGT GGT  TG GGGA
                                |||||||| |||  || ||||
                                CACCTCCA CCA  AC CCCT
                                    G   C_ _
GAM1365  LOC201522 3'  GTGGCGAGCAGCATGAGGG   34967     A_  TG T
                                GTGG  GG  G CATGAGGG
                                ||||  ||  | ||||||||
                                CACC  TC  C GTACTCCC
                                  GC  GT _
GAM1365  LOC205327 5'  GTGGAGGGTGGCGGAGGG    34968        _   CAT
                                GTGGAGG TGGT   GAGGG
                                |||||||| ||||   |||||
                                CACCTCC ACCG   CTCCC
                                    C    C__
GAM1365  LOC221263 3'  GTGAAGGTGGTGGGG       34969          CAT A
                                GTGGAGGTGGT   G GGG
                                ||||||||||   | |||
                                CACTTCCACCA   C CCC
                                       ___ _
GAM1365  LOC221712 5'  GTGGAGGTTGGGGCAGGTGGGG 34970         ___  CA_  A
            GA                    GTGGAGGT   GGT   TG GGGA
                                ||||||||   |||   || ||||
                                CACCTCCA   CCG   AC CCCT
                                    ACC   TCC  C
GAM1365  LOC222031 3'  ATGGAGGCATCTGAGGG     34971          G  A
                                GTGGAGGTG TC TGAGGG
                                ||||||||| || ||||||
                                TACCTCCGT AG ACTCCC
                                      _  _
GAM1365  LOC254182 3'  TGGAGGCCTGGGTGAGGGAC   34972        __  TCA
                                TGGAGGT  GG   TGAGGGAC
                                |||||||  ||   ||||||||
                                ACCTCCG  CC   ACTCCCTG
                                    GA  C__
GAM1365  LOC254191 3'  GTGAGGGTGGGGGTGAGGGA   34973     GA    TCA
                                GTG  GGTGG   TGAGGGA
                                |||  |||||   |||||||
                                CAC  CCACC   ACTCCCT
                                  TC    CCC
GAM1365  LOC254428 3'  GTGGGGTGGAGGAGGGAC    34974      A    TCAT
                                GTGG GGTGG    GAGGGAC
                                |||| |||||    |||||||
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                                CACC CCACC    CTCCCTG
                                  _    TC__
GAM1365  LOC254753 3'  GTGGAGAGTTGGGGGTGAGGG  34975       _ _  TCA
                                GTGGAG GT GG   TGAGGG
                                |||||| || ||   ||||||
                                CACCTC CA CC   ACTCCC
                                   T  A  CCC
GAM1365  LOC255650 3'  GTGGGGAATCTTGAGGGAC    34976     A  T   A
                                GTGG GG GGTC TGAGGGAC
                                |||| || |||| ||||||||
                                CACC CC TTAG ACTCCCTG
                                  _ _   A
GAM1365  LOC257395 3'  GTGGAGGTGGCGCGGGGAC    34946          CA  A
                                GTGGAGGTGGT  TG GGGAC
                                ||||||||||  || |||||
                                CACCTCCACCG  GC CCCTG
                                      C_ _
GAM1365  LOC257463 3'  GGAGGTGGAGCACAGGGGA    34977        T_  GA
                                GGAGGTGG  CAT  GGGA
                                ||||||||  |||  ||||
                                CCTCCACC  GTG  CCCT
                                    TC   TC
GAM1365  LOC257490 5'  GTGGAGGCTGAGGGA       34978        GGTCA
                                GTGGAGGT    TGAGGGA
                                ||||||||    |||||||
                                CACCTCCG    ACTCCCT
                                          _____
GAM1365  LOC51162  3'  GTGGGGGTAGCCAGGG      34979      A       TGA
                                GTGG GGTGGTCA   GGG
                                |||| ||||||||   |||
                                CACC CCATCGGT   CCC
                                  C      ___
GAM1365  LOC51162  3'  GTGGGGGTAGCCAGGG      34979      A       TGA
                                GTGG GGTGGTCA   GGG
                                |||| ||||||||   |||
                                CACC CCATCGGT   CCC
                                  C      ___
GAM1365  LOC51315  5'  GTGGAGGTGGCGGAGAGG    34980          CAT
                                GTGGAGGTGGT   GAGG
                                ||||||||||   ||||
                                CACCTCCACCG   CTCC
                                      CCT
GAM1365  LOC55924  3'  GTGGAGATGTCAGAGGGA    34981         G   T
                                GTGGAGGTG TCA GAGGGA
                                ||||||||| ||| ||||||
                                CACCTCTAC AGT CTCCCT
                                          _  _
GAM1365  LOC57019  3'  GTGGGATGTGAGGGA       34982      A   GTCA
                                GTGG GGTG    TGAGGGA
                                |||| ||||    |||||||
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                                CACC CTAC    ACTCCCT
                                  _   _____
GAM1365 LOC58525 5' GTGAAGGTCCGAGGG      34983      GGT    A
                                GTGGA   GGTC TGAGGG
                                |||||   |||| ||||||
                                CACTT   CCAG GCTCCC
                                  ____   _
GAM1365 LOC91272 5' GTAGAGGTGGTGAAGGG     34984          CAT
                                GTGGAGGTGGT   GAGGG
                                ||||||||||   |||||
                                CATCTCCACCA   TTCCC
                                      C__
GAM1365 LOC91748 3' GTGGGGATGATGAGGG      34985      A    GTC
                                GTGG GGTG   ATGAGGG
                                |||| ||||   |||||||
                                CACC CTAC   TACTCCC
                                  C   ____
GAM1365 LOC92558 3' TGGGGCCCTAGCATGAGGG   34986     A   ___  T
                                TGG GGT   GG CATGAGGG
                                ||| |||   || ||||||||
                                ACC CCG   TC GTACTCCC
                                  _   GGA  _
GAM1365 LOC93259 5' GTGGTGGTGGCTACGGGG    34987      A     TC   A
                                GTGG GGTGG  ATG GGG
                                |||| |||||  ||| |||
                                CACC CCACC  TGC CCC
                                  A     GA  _
GAM1365 LOC94976 3' GTGGAGGCTGGATGGGAC    34988        _   TCATGA
                                GTGGAGG TGG      GGGAC
                                |||||||  |||      |||||
                                CACCTCC ACC      CCCTG
                                    G   TA____
GAM1366 ADAMTS5   3'  AGAGAGAAAGTAGTTGTGAAAA 34991          _  AATA_
              TA                  AGAGAGAAAG AG     AAAATA
                                ||||||||||  ||     ||||||
                                TCTCTCTTTC TC     TTTTAT
                                      A  AACAC
GAM1366 ADAT1    3'  GAAGAAAGAAAGGCTGGGAATA 34992           A____
                                GAAGAGAGAAAG     GAATA
                                ||||||||||||     |||||
                                CTTCTTTCTTTC     CTTAT
                                      CGACC
GAM1366 ADCY2    3'  GAAGACAGGAAAATAAAA    34993       G  AAA
                                GAAGA AG   GAGAATAAAA
                                |||||  ||   ||||||||||
                                CTTCT TC   CTTTTATTTT
                                  G  ___
GAM1366 AHR      3'  GAAGAGAGTAACAAAAAT    34994         _  A
                                GAAGAGAG AA GAGAAT
                                ||||||||  ||  ||||||
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                                CTTCTCTC TT TTTTTA
                                     A  G
GAM1366  BSN     3'  AGAGAGAAACAAAAGAAAAAT  34995        G   T
                                AGAGAGAAA AGAA AAAAAT
                                ||||||||| |||| ||||||
                                TCTCTCTTT TTTT TTTTTA
                                     G   C
GAM1366  BSN     3'  GAAGAGAGAAAGGGGGAGA   34996         ____
                                GAAGAGAGAAA   GAGA
                                ||||||||||   ||||
                                CTTCTCTCTTT   CTCT
                                      CCCC
GAM1366  C7      3'  AAAGAGAAATAAGGAATA    34997         _  A
                                GAAGAGAGA AAG GAATA
                                ||||||||| ||| |||||
                                TTTCTCTTT TTC CTTAT
                                     A  _
GAM1366  CFTR    3'  GAGGAGAGAAAAAGGAATA   34998    A       _
                                GA GAGAGAAAGAG AATA
                                || ||||||||||| ||||
                                CT CTCTCTTTTTC TTAT
                                 C         C
GAM1366  CHD2    3'  GAAGAGAGAGTGGGGGATCAGA 34999     AA____  GAAT_     III
           AAAAATAT               AGA     GA    AAAAATA   T
                                |||     ||    |||||||  |
                                TCT     CT    TTTTTAT   A
                                  CACCCC  AGTCT      III
GAM1366  CKN1    3'  GAAGAAAGAATAAAATA     35000         AG
                                GAAGAGAGAA  AGAATA
                                ||||||||||  ||||||
                                CTTCTTTCTT  TTTTAT
                                     A_
GAM1366  CTH     5'  GAAGAGAGGAAAAGAACA    35001        A
                                GAAGAGAG AAGAGAATA
                                |||||||| |||||||||
                                CTTCTCTC TTTTCTTGT
                                     C
GAM1366  EVA1    3'  GAGAGACATAAAAATAAAAAT  35002       AA_
                                GAGAGA   GAGAATAAAAAT
                                ||||||   ||||||||||||
                                CTCTCT   TTTTTATTTTTA
                                   GTA
GAM1366  FBXL11  3'  AAAGAGAGAGGGGGAACAA   35003         AAGA
                                GAAGAGAGA   GAATAA
                                |||||||||   ||||||
                                TTTCTCTCT   CTTGTT
                                      CCCC
GAM1366  GATA3   3'  GAGAGAGAAGGAAAATA     35004    A      A
                                GA GAGAGAA GAGAATA
                                || ||||||| |||||||
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                                CT CTCTCTT CTTTTAT
                                 _      C
GAM1366  GDI2     5'  AAGAGAAAGAGAGGAAAA    35005          AT
                                GAGAGAAAGAGA  AAAA
                                ||||||||||||  ||||
                                TTCTCTTTCTCT  TTTT
                                      CC
GAM1366  HD       3'  AAAGAGAGAAGGGAGAAT    35006         A_
                                GAAGAGAGAA  GAGAAT
                                ||||||||||  ||||||
                                TTTCTCTCTT  CTCTTA
                                      CC
GAM1366  HTR2C    3'  GAAGGGAGGGAGAGCAAAAATA 35007     A  AAA   A
                                GAAG GAG   GAGA TAAAAATA
                                |||| |||   |||| ||||||||
                                CTTC CTC   CTCT GTTTTTAT
                                  C  C__   C
GAM1366  LGR6     3'  GAAGAGAGGGGAAGAGAA    35008        A__
                                GAAGAGAG   AAGAGAA
                                ||||||||   |||||||
                                CTTCTCTC   TTCTCTT
                                     CCC
GAM1366  LRP8     3'  GAAAAGAGAAATAAGAGA    35009         ___
                                GAAGAGAGAA   AGAGA
                                ||||||||||   |||||
                                CTTTTCTCTT   TCTCT
                                      TAT
GAM1366  LRP8     3'  GAAAAGAGAAATAAGAGA    35009         ___
                                GAAGAGAGAA   AGAGA
                                ||||||||||   |||||
                                CTTTTCTCTT   TCTCT
                                      TAT
GAM1366  MEF2C    5'  GAGAGAGAGAGAGAGAAAAAAA 35010   _     A     T
            A                    GA AGAGAGA AGAGAA AAAAA
                                || ||||||| |||||| |||||
                                CT TCTCTCT TCTCTT TTTTT
                                 C      C     T
GAM1366  MSR1     3'  AGAGAGAAACCAAAAATA    35011         __
                                AGAGAGAAA  GAGAATA
                                |||||||||  |||||||
                                TCTCTCTTT  TTTTTAT
                                     GG
GAM1366  PCDH11X  3'  AGAGAGAAAATGTGAAAATA  35012        ____
                                AGAGAGAAA   GAGAATA
                                |||||||||   |||||||
                                TCTCTCTTT   CTTTTAT
                                      TACA
GAM1366  PCDH11X  3'  AGAGAGAAAATGTGAAAATA  35012        ____
                                AGAGAGAAA   GAGAATA
                                |||||||||   |||||||
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                                TCTCTCTTT   CTTTTAT
                                     TACA
GAM1366  PCDH11Y  3'  AGAGAGAAAATGTGAAAATA  35012        ____
                                AGAGAGAAA   GAGAATA
                                |||||||||   |||||||
                                TCTCTCTTT   CTTTTAT
                                     TACA
GAM1366  PCMT1    3'  GAAGAAAGAGCAGAAGATA   35013        A_  GA
                                GAAGAGAGA  AGA  ATA
                                |||||||||  |||  |||
                                CTTCTTTCT  TCT  TAT
                                     CG   TC
GAM1366  PCNA     3'  GAATAGAGAAAAAAAATA    35014     G
                                GAA AGAGAAAGAGAATA
                                ||| ||||||||||||||
                                CTT TCTCTTTTTTTTAT
                                  A
GAM1366  PRELP    3'  GAGAGAGAGAAAACGAAT    35015    _       A
                                GA AGAGAGAAAG GAAT
                                || ||||||||||| ||||
                                CT TCTCTCTTTT CTTA
                                 C        G
GAM1366  PTMS     3'  AGGGAGAAAGAGAGCAAA    35016    A       A
                                AG GAGAAAGAGA TAAA
                                || ||||||||||| ||||
                                TC CTCTTTCTCT GTTT
                                 C        C
GAM1366  SLC4A4   3'  AAAGACTTAAGAGAATAAAAAT 35017      GAGA
            A                    GAAGA   AAGAGAATAAAAATA
                                |||||   ||||||||||||||||
                                TTTCT   TTCTCTTATTTTTAT
                                  GAA_
GAM1366  STC1     3'  AAAGAGAGAAATTTGCTAGGAA 35018        _______  A
            TA                    GAAGAGAGAA      AG GAATA
                                ||||||||||      || |||||
                                TTTCTCTCTT      TC CTTAT
                                     TAAACGA  _
GAM1366  TRPS1    5'  AGAGAGAAAGAGAAAGGAAATA 35019           TAA
                                AGAGAGAAAGAGAA   AAATA
                                ||||||||||||||  |||||
                                TCTCTCTTTCTCTT   TTTAT
                                       TCC
GAM1366  ARS2     5'  GAAGAGAGGCGAACAAAA    35020       AAAGA
                                GAAGAGAG    GAATAAAA
                                ||||||||    ||||||||
                                CTTCTCTC    CTTGTTTT
                                    CG___
GAM1366  BRD4     3'  GAAGAGAGAATTAAAAATA   35021        A_
                                GAAGAGAGAA  GAGAATA
                                ||||||||||  |||||||
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                                CTTCTCTCTT  TTTTTAT
                                     AA
GAM1366  CAPN13    3'  GAAGAGAGGCAGGTAAAATA  35022        AA  __
                                GAAGAGAG  AG  AGAATA
                                ||||||||  ||  ||||||
                                CTTCTCTC  TC  TTTTAT
                                     CG  CA
GAM1366  CECR6     3'  GAAGAGAGGAGAGGGTAA    35023        AA   AA
                                GAAGAGAG  AGAG  TAA
                                ||||||||  ||||  |||
                                CTTCTCTC  TCTC  ATT
                                     C_   CC
GAM1366  DKFZP434I0714 5'  GAAGAGGGGGAAAAACAAAAA  35024       AGAAA
                                GAAGAG    GAGAATAAAAA
                                ||||||    ||||||||||
                                CTTCTC    TTTTTGTTTTT
                                   CCCC_
GAM1366  DKFZP564G092 5'  GAAAAGAAAGAGGAATA     35025         A  A
                                GAAGAGAGA AG GAATA
                                |||||||| || |||||
                                CTTTTCTTT TC CTTAT
                                     C  _
GAM1366  DKFZp564K142 3'  GAAGAGAAGGTTAAGAGGATA  35026        A___    A
                                GAAGAGAG   AAGAG ATA
                                ||||||||   ||||| |||
                                CTTCTCTT   TTCTC TAT
                                     CCAA    C
GAM1366  DKFZp566D234 3'  GACAGAGAAAAAAAATA    35027    AG
                                GA  AGAGAAAGAGAATA
                                ||  ||||||||||||||
                                CT  TCTCTTTTTTTTAT
                                 G_
GAM1366  DKFZP566I1024 3'  GAGAGAATAGATTTTAAAA   35028       _  GAA
                                GAGAGAA AGA   TAAAA
                                ||||||| |||   |||||
                                CTCTCTT TCT   ATTTT
                                     A   AAA
GAM1366  EPI64     3'  GAAGAGAGAGAGATGTCAAAAT 35029         A  GAATA
            A                    GAAGAGAGA AGA    AAAATA
                                |||||||| |||    ||||||
                                CTTCTCTCT TCT    TTTTAT
                                     C   ACAG_
GAM1366  FLJ00012  3'  AGGAGATAGAGATAAAAATA  35030    A   A    A
                                AG GAGA AGAGA TAAAAATA
                                || |||| ||||| ||||||||
                                TC CTCT TCTCT ATTTTTAT
                                 _   A    _
GAM1366  FLJ10460  3'  GAAAGGTAGAATAAAAAT    35031      AAAG
                                GAGAG   AGAATAAAAAT
                                |||||   ||||||||||
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                                CTTTC   TCTTATTTTTA
                                  CA__
GAM1366  FLJ10687  3'  GAGGAGAGAAATGAATAAA   35032    A      GA
                                GA GAGAGAAA  GAATAAA
                                || ||||||||  |||||||
                                CT CTCTCTTT  CTTATTT
                                 C       A_
GAM1366  FLJ10738  3'  GAAGAGGGAGAGTAAAAATA  35033      AGAAA   A
                                GAAGAG    GAGA TAAAAATA
                                ||||||    |||| ||||||||
                                CTTCTC    CTCT ATTTTTAT
                                   C____   C
GAM1366  FLJ13154  3'  AAAGAGAGAGAGAGAATA    35034        A
                                GAAGAGAGA AGAGAATA
                                ||||||||| ||||||||
                                TTTCTCTCT TCTCTTAT
                                      C
GAM1366  FLJ13158  3'  GAAGAGAAAGGGAGAGAA    35035        A__
                                GAAGAGAGA   AGAGAA
                                |||||||||   ||||||
                                CTTCTCTTT   TCTCTT
                                      CCC
GAM1366  FLJ20294  5'  AAAGAGGAGACAGGAATA    35036      _  A  A
                                GAAGAG AGA AG GAATA
                                |||||| ||| || |||||
                                TTTCTC TCT TC CTTAT
                                   C   G  _
GAM1366  FLJ21657  3'  GAAGAGAGAAGTAGAATA    35037        AG
                                GAAGAGAGAA  AGAATA
                                ||||||||||  ||||||
                                CTTCTCTCTT  TCTTAT
                                      CA
GAM1366  FLJ21945  3'  AAGGAGAGAAAATAAAAAT   35038    A   AA
                                AAG GAGA  GAGAATAAAAAT
                                ||| ||||  ||||||||||||
                                TTC CTCT  CTTTTATTTTTA
                                  _   __
GAM1366  GT650    3'  GAAGAGAGGGAGAATCAGAAAT 35039       AAA     AA_
           A                     GAAGAGAG   GAGAAT   AAATA
                                |||||||   ||||||   |||||
                                CTTCTCTC   CTCTTA   TTTAT
                                     C__     GTC
GAM1366  HEY2     3'  GAGAAAAAAAAGAGAATA    35040    AG
                                GA  AGAGAAAGAGAATA
                                ||  ||||||||||||||
                                CT  TTTTTTTCTCTTAT
                                 CT
GAM1366  HIC2     3'  GAAAAGAGAGAGAAAAAAAAAT 35041        A     T
                                GAAGAGAGA AGAGAA AAAAAT
                                ||||||||| |||||| ||||||
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                                CTTTTCTCT TCTTTT TTTTTA
                                      C     _
GAM1366  HOOK3     3'  AGAGAGAAAAAGTCCTCAAAAT 35042           AATA_
                                AGAGAGAAAGAG     AAAAT
                                ||||||||||||     |||||
                                TCTCTCTTTTTC     TTTTA
                                      AGGAG
GAM1366  IL1RAPL1  5'  AAAGAGAGGGGAAAATAAGAAT 35043        AAA       A
           A                     GAAGAGAG   GAGAATAA AATA
                                ||||||||   |||||||| ||||
                                TTTCTCTC   CTTTTATT TTAT
                                     CC_       C
GAM1366  KALI      3'  GAGAGGGACAAGAACAAAA    35044       AAA_
                                GAGAG    GAGAATAAAA
                                |||||    ||||||||||
                                CTCTC    TTCTTGTTTT
                                   CCTG
GAM1366  KIAA0077  3'  AAAGGGAGAGAGAATAAAA    35045      A    AA
                                GAAG GAGA  GAGAATAAAA
                                |||| ||||  ||||||||||
                                TTTC CTCT  CTCTTATTTT
                                  C    __
GAM1366  KIAA0089  3'  GAAGAGAAAAGAGGCTAAAAAT 35046          A   AA
                                GAAGAGAGAA GAG  TAAAAAT
                                |||||||||| |||  |||||||
                                CTTCTCTTTT CTC  ATTTTTA
                                      _  CG
GAM1366  KIAA0286  3'  GAAAAGAGGGTGAAAATA     35047         AAA
                                GAAGAGAG   GAGAATA
                                ||||||||   |||||||
                                CTTTTCTC   CTTTTAT
                                     CCA
GAM1366  KIAA0295  3'  AGAGAGAAAGGGAAAAAA     35048          A   T
                                AGAGAGAAAG GAA AAA
                                |||||||||| ||| |||
                                TCTCTCTTTC CTT TTT
                                      C   T
GAM1366  KIAA0342  3'  AAAGAGAAGTAATGAGAATA   35049        _ _  A
                                GAAGAGA G AA GAGAATA
                                ||||||| | || |||||||
                                TTTCTCT C TT CTCTTAT
                                    T A  A
GAM1366  KIAA0564  3'  GAGCAGGGAGAAAATAAAAATA 35050     _  AA
                                GAG AG  AGAGAATAAAAATA
                                ||| ||  ||||||||||||||
                                CTC TC  TCTTTTATTTTTAT
                                  G  CC
GAM1366  KIAA0630  3'  AGAGAGAAAGACTTTTAAAAAA 35051          GAAT__
           TA                    AGAGAGAAAGA     AAAAATA
                                ||||||||||      |||||||
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                                TCTCTCTTTCT     TTTTTAT
                                      GAAAAT
GAM1366  KIAA0662  3'  AAAGAGAGAGAGAGAACA    35052        A
                                GAAGAGAGA AGAGAATA
                                ||||||||| ||||||||
                                TTTCTCTCT TCTCTTGT
                                     C
GAM1366  KIAA0830  3'  AGGAGAAAGAGAAGCAAA    35053    A       _
                                AG GAGAAAGAGAA TAAA
                                || |||||||||| ||||
                                TC CTCTTTCTCTT GTTT
                                 _        C
GAM1366  KIAA0964  3'  GAAAAGAGAAAAACATAAGAAT 35054          GA   A
                                GAAGAGAGAAAGA  ATAA AAT
                                ||||||||||||  |||| |||
                                CTTTTCTCTTTTT  TATT TTA
                                      G_   C
GAM1366  KIAA1076  3'  GAGAGAAAGCAAAAAATA    35055        AGAAT
                                GAGAGAAAG    AAAAATA
                                |||||||||    |||||||
                                CTCTCTTTC    TTTTTAT
                                     GT___
GAM1366  KIAA1181  3'  GAAGAGAGGAAGAGGAAT    35056        A    _
                                GAAGAGAG AAGAG AAT
                                |||||||| ||||| |||
                                CTTCTCTC TTCTC TTA
                                     C    C
GAM1366  KIAA1319  3'  GAAAGGAAGAAGACAAAAATA  35057      A   GA
                                GAGAG AAGA  ATAAAAATA
                                ||||| ||||  |||||||||
                                CTTTC TTCT  TGTTTTTAT
                                   C   TC
GAM1366  KIAA1522  3'  AGAGAGAAAGGTCAGAGAAT   35058       _____
                                AGAGAGAA    AGAGAAT
                                ||||||||    |||||||
                                TCTCTCTT    TCTCTTA
                                     TCCAG
GAM1366  KIAA1906  3'  AAGCAGAGAATAAAAAT     35059     AA
                                GAG  AGAGAATAAAAAT
                                |||  |||||||||||||
                                TTC  TCTCTTATTTTTA
                                  G_
GAM1366  MAPK6    5'  AAAGGGAGAAGAAAAATA     35060     A    AG
                                GAAG GAGAA  AGAATA
                                |||| |||||  ||||||
                                TTTC CTCTT  TTTTAT
                                  C    CT
GAM1366  MGC13138  3'  GAGGGTCACAAGAATAAAAATA 35061     AGAAA_
                                GAG     GAGAATAAAAATA
                                |||     |||||||||||||
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                                CTC     TTCTTATTTTTAT
                                  CCAGTG
GAM1366  MGC2742   5'  GAAGAGAGAAAAGAAATA    35062          AG
                                GAAGAGAGAAAG  AATA
                                ||||||||||||  ||||
                                CTTCTCTCTTTT  TTAT
                                      CT
GAM1366  MGC32043  3'  AAAGAGAAAACAGGAATA    35063         _  A
                                GAAGAGAGAA AG GAATA
                                |||||||||| || |||||
                                TTTCTCTTTT TC CTTAT
                                      G  _
GAM1366  MGC5338   3'  GAAGGGGGAGAGAGAAAATA  35064     A__   A
                                GAAG   GAGA AGAGAATA
                                ||||   |||| ||||||||
                                CTTC   CTCT TCTTTTAT
                                   CCC    C
GAM1366  NFAT5     3'  GAAGAGAAAAAGGGAATA    35065          A
                                GAAGAGAGAAAG GAATA
                                |||||||||||| |||||
                                CTTCTCTTTTTC CTTAT
                                      C
GAM1366  OSBPL8    3'  GAAGAGAGGAGGATAATAAAAA 35066        AAA  G
                                GAAGAGAG   GA AATAAAAA
                                ||||||||   || ||||||||
                                CTTCTCTC   CT TTATTTTT
                                     CTC  A
GAM1366  RAB10     3'  GAGGAGGAAAAGCAGAACA   35067    A   AG   _
                                GA GAG  AAAG AGAATA
                                || |||  |||| ||||||
                                CT CTC  TTTC TCTTGT
                                 C  CT   G
GAM1366  RANBP1    3'  AAAGAGAGGAAAAGAAAATA  35068        __
                                GAAGAGAG  AAAGAGAATA
                                ||||||||  ||||||||||
                                TTTCTCTC  TTTCTTTTAT
                                     CT
GAM1366  RASSF2    3'  GAAGAGAGGATTGTGAAAATA  35069        AAA___
                                GAAGAGAG     GAGAATA
                                ||||||||     |||||||
                                CTTCTCTC     CTTTTAT
                                     CTAACA
GAM1366  STK22D    3'  AGAGAGAAGAAGCTGATGAAAA 35070        AG  AATA__
            TA                   AGAGAGAA  AG     AAAATA
                                ||||||||  ||     ||||||
                                TCTCTCTT  TC     TTTTAT
                                     CT  GACTAC
GAM1366  SYNJ2     3'  GAAGAGAAAACCTAAAAAT   35071          AGAGAA
                                GAAGAGAGAA     TAAAAAT
                                ||||||||||     |||||||
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                                CTTCTCTTTT     ATTTTTA
                                     GG____
GAM1366  TBLR1    3'  GAAGGGAAAAAAAGAATA    35072      A
                                GAAG GAGAAAGAGAATA
                                |||| ||||||||||||
                                CTTC CTTTTTTTCTTAT
                                  C
GAM1366  TM9SF1   3'  GAAGAAAGGGAGAGAACAGCAA 35073        AA       AA
             TA                   GAAGAGAG  AGAGAATA  AATA
                                |||||||||  ||||||||  ||||
                                CTTCTTTC  TCTCTTGT  TTAT
                                     CC       CG
GAM1366  ULK2     3'  GAAGAGGAGAGGATAGAATA   35074       _   AAG_
                                GAAGAG AGA    AGAATA
                                |||||| |||    ||||||
                                CTTCTC TCT    TCTTAT
                                    C   CCTA
GAM1366  UNC5D    3'  GAAGAGGAAGAAAGAATAA    35075       A   _
                                GAAGAG GAA AGAGAATAA
                                |||||| ||| |||||||||
                                CTTCTC CTT TTTCTTATT
                                    _   C
GAM1366  LOC121219 5'  AAAGAGAGAAGGAGTTAATAA  35076          A   __
                                GAAGAGAGAA GAG  AATAA
                                |||||||||| |||  |||||
                                TTTCTCTCTT CTC  TTATT
                                     C   AA
GAM1366  LOC128077 3'  GAGGAAAGAAAGAGAAAACAAA 35077    A          TAA
             T                    GA GAGAGAAAGAGAA   AAAT
                                || ||||||||||||   ||||
                                CT CTTTCTTTCTCTT   TTTA
                                 C           TTG
GAM1366  LOC143451 3'  GAAGAGAGAAGGAGAGAA    35078          __
                                GAAGAGAGAA  AGAGAA
                                ||||||||||  ||||||
                                CTTCTCTCTT  TCTCTT
                                     CC
GAM1366  LOC145125 3'  GAAGAGAGAAGGAGAGAA    35078          __
                                GAAGAGAGAA  AGAGAA
                                ||||||||||  ||||||
                                CTTCTCTCTT  TCTCTT
                                     CC
GAM1366  LOC149351 3'  AAAGAGAAAGATCTGAAAAAT  35079          GAAT
                                AGAGAGAAAGA    AAAAAT
                                ||||||||||    ||||||
                                TTTCTCTTTCT    TTTTTA
                                      AGAC
GAM1366  LOC149722 5'  GAAGAGAAAGAAAGAATA    35080          A
                                GAAGAGAGA AGAGAATA
                                ||||||||| ||||||||
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                                CTTCTCTTT TTTCTTAT
                                     C
GAM1366  LOC149837 5'  AGAGAGAAAGACAGGAATA   35081          ___
                                AGAGAGAAAGA   GAATA
                                ||||||||||   |||||
                                TCTCTCTTTCT   CTTAT
                                      GTC
GAM1366  LOC150054 3'  GAGGAGAAAGACAGAATA    35082    _     __
                                GAG AGAAAGA  GAATA
                                ||| |||||||  |||||
                                CTC TCTTTCT  CTTAT
                                  C      GT
GAM1366  LOC150150 5'  GAAGAAAGAGAGGCACAAAA  35083         AA  A_
                                GAAGAGAGA  GAG  ATAAAA
                                |||||||||  |||  ||||||
                                CTTCTTTCT  CTC  TGTTTT
                                     __  CG
GAM1366  LOC150225 3'  GAAGAGGGAAACAAAATA    35084       A   G
                                GAAGAG GAAA AGAATA
                                |||||| |||| ||||||
                                CTTCTC CTTT TTTTAT
                                   C   G
GAM1366  LOC152816 3'  AAGAGGTTGAGGATAAAAATA 35085      AAA  A
                                GAGAG   GAG ATAAAAATA
                                |||||   ||| |||||||||
                                TTCTC   CTC TATTTTTAT
                                  CAA   C
GAM1366  LOC155038 3'  GAAGGAGAAAGAGAAACGCAAT 35086     A        TAAA
                                GAAG GAGAAAGAGAA    AAT
                                |||| ||||||||||    |||
                                CTTC CTCTTTCTCTT    TTA
                                  _         TGCG
GAM1366  LOC158629 3'  GAGAGGGAAAGAAAATA    35087    A  A
                                GA GAG GAAAGAGAATA
                                || ||| ||||||||||
                                CT CTC CTTTCTTTTAT
                                 _  C
GAM1366  LOC158943 3'  AAAGAGAGGAAAAGAAAATA  35068        __
                                GAAGAGAG  AAAGAGAATA
                                ||||||||  ||||||||||
                                TTTCTCTC  TTTCTTTTAT
                                     CT
GAM1366  LOC170082 3'  GAAAAGAGAGGGGAAAAGAAT  35088        ____
                                GAAGAGAGA   AAGAGAAT
                                |||||||||   ||||||||
                                CTTTTCTCT   TTTTCTTA
                                      CCCC
GAM1366  LOC199920 5'  GAAGAATCAAAGAATAAAAATA 35089      AGAA
                                GAAGAG   AGAGAATAAAAATA
                                ||||||   ||||||||||||||
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                                CTTCTT    TTTCTTATTTTTAT
                                   AG__
GAM1366  LOC219667 3'  GAAGAGAGATAACAAAAAT    35090          AAGAG
                                GAAGAGAGA     AATAAAAAT
                                |||||||||     |||||||||
                                CTTCTCTCT     TTGTTTTTA
                                     A____
GAM1366  LOC220279 5'  GAAGAGAGGTAGGGGAAGAAAA 35091          A_______
              TA                  GAAGAGAG      AAGAGAATA
                                |||||||||      |||||||||
                                CTTCTCTC      TTCTTTTAT
                                     CATCCCC
GAM1366  LOC221830 3'  GAAGAAAGAAAAGAAAATA    35092           _
                                GAAGAGAGAAA GAGAATA
                                |||||||||||| |||||||
                                CTTCTTTCTTT CTTTTAT
                                      T
GAM1366  LOC222166 3'  AAAGAGAGAAGGTAAAAT     35093          AG_
                                GAAGAGAGAA   AGAAT
                                ||||||||||   |||||
                                TTTCTCTCTT   TTTTA
                                     CCA
GAM1366  LOC254440 3'  GAAGAGAGAAGGAGAGAA     35078          __
                                GAAGAGAGAA  AGAGAA
                                ||||||||||  ||||||
                                CTTCTCTCTT  TCTCTT
                                     CC
GAM1366  LOC51123  3'  AAGAGGGAACAGCATAAAAAT  35094      A   AG  A
                                AAGAG GAA  AG ATAAAAAT
                                ||||| |||  || ||||||||
                                TTCTC CTT  TC TATTTTTA
                                   C   G_  G
GAM1366  LOC51596  5'  GAGAGAGAAACTTGGAAAATA  35095     A       ____
                                GA GAGAGAAA    GAGAATA
                                || ||||||||    |||||||
                                CT CTCTCTTT    CTTTTAT
                                 _       GAAC
GAM1366  LOC84570  5'  GAAGAGAGAGGAAAACGAAA   35096          AA    TA
                                GAAGAGAGA  GAGAA  AAA
                                |||||||||  |||||  |||
                                CTTCTCTCT  CTTTT  TTT
                                     C_     GC
GAM1366  LOC92710  5'  GAGACAGAGGCATAAAAATA   35097      A   A_
                                GAGA AGAG  ATAAAAATA
                                |||| ||||  |||||||||
                                CTCT TCTC  TATTTTTAT
                                  G    CG
GAM1367  GATM      3'  TAAGTCTTTCTCTCCTTTA    35100          CTCA    C
                                TAAGTTTTTT    TCTCC TTA
                                ||||||||||    ||||| |||
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                                ATTCAGAAAG    AGAGG AAT
                                      _____     A
GAM1367  IL1RAP    3'  ATGTTTCCCCATTTCCCTT    35101    T       C
                                GT TTTTCTCAT TCCCTT
                                || ||||||||| ||||||
                                TA AAAGGGGTA AGGGAA
                                 C        A
GAM1367  LPIN2     3'  TAAGTTTTTTCTTTTTCC     35102           CATC
                                TAAGTTTTTTCT    TCC
                                ||||||||||||    |||
                                ATTCAAAAAAGA    AGG
                                       AAA_
GAM1367  MTAP      3'  GTTTTTTTTTTCCCCCTTAA   35103        CTCA
                                GTTTTTT    TCTCCCTTAA
                                |||||||    ||||||||||
                                CAAAAAA    AGGGGGAATT
                                    AAA_
GAM1367  NR5A2     3'  AAGTTTGTAGTCATTTCCCTTA 35104       TTTC    C
                A                AAGTTT    TCAT TCCCTTAA
                                |||||||    |||| ||||||||
                                TTCAAA    AGTA AGGGAATT
                                   CATC    A
GAM1367  UCP3      3'  AGTTTTTTCTCTTGTTCCTT   35105          ATCTC
                                AGTTTTTTCTC     CCTT
                                ||||||||||     ||||
                                TCAAAAAAGAG     GGAA
                                       AACAA
GAM1367  YWHAG     3'  TAAGTTTTCTTTTCATCT    35106          C_
                                TAAGTTTTTT  TCATCT
                                ||||||||||  ||||||
                                ATTCAAAAGA  AGTAGA
                                       AA
GAM1367  DKFZP434B044 3'  AAGTTTCAAGTCTCCCTT    35107        TTCTCA
                                AAGTTTT     TCTCCCTT
                                |||||||     ||||||||
                                TTCAAAG     AGAGGGAA
                                    TTC___
GAM1367  EREG      3'  TAAGTTTTTTCCCATTTCC    35108             C
                                TAAGTTTTTTCTCAT TCC
                                |||||||||||||| |||
                                ATTCAAAAAAGGGTA AGG
                                          A
GAM1367  KIAA0280  3'  TTTTTCCCTCCCTTA      35109        CAT
                                TTTTTCT   CTCCCTTA
                                |||||||   ||||||||
                                AAAAAGG   GAGGGAAT
                                    ___
GAM1367  KIAA0773  3'  GTCTTTTCCCAGATCCTTA    35110          TCTC
                                GTTTTTTCTCA    CCTTA
                                ||||||||||    |||||
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                                CAGAAAAGGGT   GGAAT
                                      CTA_
GAM1367  NFAT5    3'  TAACCTTTTTCTCATTTCC   35111    G        C
                                TAA TTTTTTCTCAT TCC
                                ||| |||||||||| |||
                                ATT GAAAAAGAGTA AGG
                                  G         A
GAM1367  RBMS2    3'  AAGTTTTTTTGATCTCC    35112        CTC
                                AAGTTTTTT   ATCTCC
                                |||||||||   ||||||
                                TTCAAAAAA   TAGAGG
                                     AC_
GAM1367  TTYH2    3'  GCTTTTTTCTCCTCTTA    35113       CTCA    _
                                GTTTTTT   TCTCC CTTA
                                |||||||   ||||| ||||
                                CGAAAAA   AGAGG GAAT
                                    ____    A
GAM1367  LOC122786 3'  GTTTTTTCTTTATCTTTCTT   35114        C_   CC
                                GTTTTTTCT  ATCT  CTT
                                |||||||||  ||||  |||
                                CAAAAAAGA  TAGA  GAA
                                     AA   AA
GAM1367  LOC150159 3'  TAAGTTTTTTCTGGTCTTCACT 35115          CA   _ C
           T                     TAAGTTTTTTCT  TCT C CTT
                                ||||||||||||  ||| | |||
                                ATTCAAAAAAGA  AGA G GAA
                                      CC   A T
GAM1367  LOC200310 3'  CAAGTTTTTTCTAAAAACTCTT 35116          CA____   C
           CCTTA                   TAAGTTTTTTCT     TCT CCTTA
                                ||||||||||||     ||| |||||
                                GTTCAAAAAAGA     AGA GGAAT
                                      TTTTTG   A
GAM1368  CCR9     3'  CACTGGCAAGACCTGCAG    35119     CG   C_
                                CAC  GGC  GACCTGCAG
                                |||  |||  |||||||||
                                GTG  CCG  CTGGACGTC
                                  A_   TT
GAM1368  CCR9     3'  CACTGGCAAGACCTGCAG    35119     CG   C_
                                CAC  GGC  GACCTGCAG
                                |||  |||  |||||||||
                                GTG  CCG  CTGGACGTC
                                  A_   TT
GAM1368  EMS1     3'  CACAGGGCCGACCTGAG     35120     C        C
                                CAC GGGCCGACCTG AG
                                ||| |||||||||| ||
                                GTG CCCGGCTGGAC TC
                                  T        _
GAM1368  EMS1     3'  CACAGGGCCGACCTGAG     35120     C        C
                                CAC GGGCCGACCTG AG
                                ||| |||||||||| ||
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                                GTG CCCGGCTGGAC TC
                                  T        _
GAM1368 FOXD2    5' CACCGGGCCGAAGCGCAG    35121          CC
                                CACCGGGCCGA TGCAG
                                |||||||||| |||||
                                GTGGCCCGGCT GCGTC
                                     TC
GAM1368 KLHL2    3' CATCAAAAACCTGCAG      35122    C    CC
                                CA CGGG GACCTGCAG
                                || |||| |||||||||
                                GT GTTT TTGGACGTC
                                 A   __
GAM1368 LYPLA1   5' CACCGGGCGCACGCTCAG    35123        _ G _ G
                                CACCGGGC C AC CT CAG
                                |||||||| | || || |||
                                GTGGCCCG G TG GA GTC
                                     C _ C _
GAM1368 MSL3L1   5' CACCAGGCAACCTGCAG     35124        C
                                CACCGGGC GACCTGCAG
                                |||||||| |||||||||
                                GTGGTCCG TTGGACGTC
                                     _
GAM1368 OVOL1    3' CACTGGGGACCTGCAG      35125     C  CC
                                CAC GGG GACCTGCAG
                                ||| ||| |||||||||
                                GTG CCC CTGGACGTC
                                  A  __
GAM1368 PHKA1    5' CACCAGGCCCCGCAG       35126        GAC
                                CACCGGGCC  CTGCAG
                                |||||||||  ||||||
                                GTGGTCCGG  GGCGTC
                                     ____
GAM1368 TNFRSF8  3' CACCAGACCCCTGCAG      35127        GA
                                CACCGGGCC CCTGCAG
                                |||||||||  |||||||
                                GTGGTCTGG GGACGTC
                                     __
GAM1368 TSSC4    3' CACCGGTGCCACCTGCAG    35128      _  G
                                CACCGG GCC ACCTGCAG
                                |||||| ||| ||||||||
                                GTGGCC CGG TGGACGTC
                                   A  _
GAM1368 ALTE     5' CACTGGCCGACCGCAG      35129    CG      T
                                CAC GGCCGACC GCAG
                                |||  |||||||| ||||
                                GTG CCGGCTGG CGTC
                                  A_      _
GAM1368 B3GNT6   3' CACCCATGGAACCTGCAG    35130     G__  CC
                                CACC  GG GACCTGCAG
                                ||||  ||  |||||||||
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                                GTGG  CC  TTGGACGTC
                                  GTA  __
GAM1368  C20orf161 3'  CCTGGGCCAGACCTGCAG    35131    _    _
                                CC GGGCC GACCTGCAG
                                || ||||| |||||||||
                                GG CCCGG CTGGACGTC
                                 A    T
GAM1368  C3IP1    5'  CACCGGGCCCGTCCCCAGCC   35132        GAC  G   III
                                CACCGGGCC   CT CAG   CC
                                |||||||||   || |||   ||
                                GTGGCCCGG   GG GTC   GG
                                     GCA  G   ___
GAM1368  DCTD     3'  CACCAGGCCACCACAG      35133        G   T
                                CACCGGGCC ACC GCAG
                                ||||||||| ||| ||||
                                GTGGTCCGG TGG TGTC
                                          _   _
GAM1368  DKFZP564O0423 3'  CACTGAGTCACCTGCAG     35134     C   C G
                                CAC GGG C ACCTGCAG
                                ||| ||| | ||||||||
                                GTG CTC G TGGACGTC
                                  A   A _
GAM1368  DKFZP761F241 3'  CACCAGGCCCTGCAG       35135         GAC
                                CACCGGGCC   CTGCAG
                                |||||||||   ||||||
                                GTGGTCCGG   GACGTC
                                          ___
GAM1368  FLJ20695  3'  CACCAGGCCAAGAGCAG     35136          CCT
                                CACCGGGCCGA   GCAG
                                ||||||||||   ||||
                                GTGGTCCGGTT   CGTC
                                      CT_
GAM1368  FLJ23360  3'  CACCAGGCCCCTCAG       35137         GA   G
                                CACCGGGCC  CCT CAG
                                |||||||||  ||| |||
                                GTGGTCCGG  GGA GTC
                                          __   _
GAM1368  FLJ23416  3'  CACCAGGCCTCCAACTGCAG   35138         GAC__
                                CACCGGGCC    CTGCAG
                                |||||||||    ||||||
                                GTGGTCCGG    GACGTC
                                     AGGTT
GAM1368  FOXD4    5'  CACCGGGCCACCTGCAG     35139         G
                                CACCGGGCC ACCTGCAG
                                ||||||||| ||||||||
                                GTGGCCCGG TGGACGTC
                                          _
GAM1368  GPS1     3'  CACAGGGTCGAGCCCTGCAG  35140     C   C   __
                                CAC GGG CGA  CCTGCAG
                                ||| ||| |||  |||||||
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                                GTG CCC GCT  GGACGTC
                                  T   A   CG
GAM1368 HSPC047   3' CACCAGGCCATACAG       35141          ACC
                                CACCGGGCCG   TGCAG
                                ||||||||||   |||||
                                GTGGTCCGGT   ATGTC
                                     ____
GAM1368 HT021     5' CACTGGACCGACACAG      35142     C       CT
                                CAC GGGCCGAC  GCAG
                                ||| ||||||||  ||||
                                GTG CCTGGCTG  TGTC
                                  A       __
GAM1368 HTMP10    3' CACCAGGCTGACCTCAG     35143         C     G
                                CACCGGGC GACCT CAG
                                |||||||| ||||| |||
                                GTGGTCCG CTGGA GTC
                                    A    _
GAM1368 KIAA0544  3' CACCCACAGCAGATCTGCAG  35144      G__   C  C
                                CACC   GGC GA CTGCAG
                                ||||   ||| || ||||||
                                GTGG   TCG CT GACGTC
                                  GTG   T  A
GAM1368 KIAA1514  5' CACCAGGCCGCTGATCTGCAG 35145          AC___
                                CACCGGGCCG    CTGCAG
                                ||||||||||    ||||||
                                GTGGTCCGGC    GACGTC
                                     GACTA
GAM1368 KIAA1535  3' ACCGGGCAGAACCTGCAG    35146        C_
                                ACCGGGC  GACCTGCAG
                                |||||||  |||||||||
                                TGGCCCG  TTGGACGTC
                                   TC
GAM1368 KIAA1872  3' CACAGGAACCTGCAG       35147     C   CC
                                CAC GGG  GACCTGCAG
                                ||| |||  |||||||||
                                GTG TCC  TTGGACGTC
                                  _  __
GAM1368 KIAA1887  5' CACCAGGCTGGATCTGAG    35148        C_  C   C
                                CACCGGGC  GA CTG AG
                                ||||||||  || ||| ||
                                GTGGTCCG  CT GAC TC
                                    AC  A   _
GAM1368 LGALS12   5' CACCTGCGACCTGCAG      35149      GG  C
                                CACC  GC GACCTGCAG
                                ||||  || |||||||||
                                GTGG  CG CTGGACGTC
                                  A_  _
GAM1368 MGC15716  3' CACCGGACCCCGCAG       35150          GAC
                                CACCGGGCC   CTGCAG
                                |||||||||   ||||||
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                              GTGGCCTGG  GGCGTC
                                  ___
GAM1368 MGC17998 3' CACCAGCACCTGCAG      35151      G CG
                              CACCGG C  ACCTGCAG
                              ||||||  |  ||||||||
                              GTGGTC G  TGGACGTC
                                 _ __
GAM1368 MGC3020  5' ACCGTCCAGTACCTGCAG   35152     GG  __
                              ACCG  CCG  ACCTGCAG
                              ||||  |||  ||||||||
                              TGGC  GGT  TGGACGTC
                                A_  CA
GAM1368 NEIL2    3' CACCGGGCACCCCAG      35153       CG   G
                              CACCGGGC  ACCT CAG
                              ||||||||  |||| |||
                              GTGGCCCG  TGGG GTC
                                  __  _
GAM1368 PP1044   5' CACCCCTAACCTGCAG     35154     GGG  _
                              CACC   CC GACCTGCAG
                              ||||   || |||||||||
                              GTGG   GG TTGGACGTC
                                ___ A
GAM1368 SIMRP7   3' CACCAGGCCCGAGAGCAG   35155        _ CCT
                              CACCGGGCC GA   GCAG
                              |||||||||  ||   ||||
                              GTGGTCCGG CT   CGTC
                                   G  CT_
GAM1368 SLC5A6   5' CACCGGGCTGAGGGAGTCTGCA 35156       C  C_____     III
           GC                   CACCGGGC GA     CTGCAG   C
                              ||||||||  ||     ||||||   |
                              GTGGCCCG CT     GACGTC   G
                                   A  CCCTCA     III
GAM1368 SPTLC2   5' CACCAGGCGCAAGGCAG    35157       _  CCT
                              CACCGGGC CGA   GCAG
                              ||||||||  |||   ||||
                              GTGGTCCG GTT   CGTC
                                   C   C__
GAM1368 UQCR     3' CACCAGGCACCAGAGCAG   35158       CG   T__
                              CACCGGGC  ACC   GCAG
                              ||||||||  |||   ||||
                              GTGGTCCG  TGG   CGTC
                                   __   TCT
GAM1368 LOC125704 3' CACAGATGACCTGCAG    35159     C   CC
                              CAC GGG  GACCTGCAG
                              ||| |||  |||||||||
                              GTG TCT  CTGGACGTC
                                _  A_
GAM1368 LOC126282 3' CACCAGGCTGAAGTGCAG  35160       C  CC
                              CACCGGGC GA  TGCAG
                              ||||||||  ||  |||||
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                                GTGGTCCG CT  ACGTC
                                     A  TC
GAM1368  LOC149483 5'  ACCAGCCAAGACCTGCAG    35161      G  __
                                ACCGG CC  GACCTGCAG
                                ||||| ||  |||||||||
                                TGGTC GG  CTGGACGTC
                                  _  TT
GAM1368  LOC149650 3'  CACCAGGCCAGGTCCTGCAG  35162         A__
                                CACCGGGCCG  CCTGCAG
                                ||||||||||  |||||||
                                GTGGTCCGGT  GGACGTC
                                     CCA
GAM1368  LOC150538 3'  CCGGGCCGGACCGCGCAG    35163        _  _
                                CCGGGCCG ACC TGCAG
                                |||||||| ||| |||||
                                GGCCCGGC TGG GCGTC
                                     C   C
GAM1368  LOC151512 5'  CACCGAGCGGGCGCGTCTGCAG 35164        ___  AC_
                                CACCGGGC   CG   CTGCAG
                                ||||||||   ||   ||||||
                                GTGGCTCG   GC   GACGTC
                                     CCC  GCA
GAM1368  LOC158308 3'  CACCCCGACACCTGCAG     35165     GGG   __
                                CACC   CCGA  CCTGCAG
                                ||||   ||||  |||||||
                                GTGG   GGCT  GGACGTC
                                  ___    GT
GAM1368  LOC161441 5'  CCGGGCCAGGAGGCCTGCAG  35166        A____
                                CCGGGCCG    CCTGCAG
                                ||||||||    |||||||
                                GGCCCGGT    GGACGTC
                                     CCTCC
GAM1368  LOC205366 5'  ACCAAACCCTGGCCTGCAG   35167        GA__
                                ACCGGGCC    CCTGCAG
                                ||||||||    |||||||
                                TGGTTTGG    GGACGTC
                                     GACC
GAM1368  LOC221486 3'  CACCAGGACCTGCAG       35168        CCG
                                CACCGGG   ACCTGCAG
                                |||||||   ||||||||
                                GTGGTCC   TGGACGTC
                                    ___
GAM1368  LOC221955 3'  CACTGGCCGACCCCAG      35169     CG       G
                                CAC  GGCCGACCT CAG
                                |||  ||||||||| |||
                                GTG  CCGGCTGGG GTC
                                  A_       _
GAM1368  LOC256158 5'  CACCCAGGACCTGCAG      35170      G  CC
                                CACC GG  GACCTGCAG
                                |||| ||  |||||||||
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                                GTGG TC  CTGGACGTC
                                  G __
GAM1368 LOC256846 5' ACCAGCCAAGACCTGCAG    35161      G __
                                ACCGG CC  GACCTGCAG
                                ||||| ||  |||||||||
                                TGGTC GG  CTGGACGTC
                                  _ TT
GAM1368 LOC91149 3' CAGGTTCCTGACCTGCAG    35171     __ _
                                CGGG  CC GACCTGCAG
                                ||||  || |||||||||
                                GTCC  GG CTGGACGTC
                                  AA  A
GAM1368 LOC91409 3' CACCGAGCGATGCAG      35172       C  CC
                                CACCGGGC GA  TGCAG
                                |||||||| ||  |||||
                                GTGGCTCG CT  ACGTC

                                  _ __
GAM1368 LOC92715 3' CACAGGCACCTGCAG      35173    C   CG
                                CAC GGGC  ACCTGCAG
                                ||| ||||  ||||||||
                                GTG TCCG  TGGACGTC

                                  _  __
GAM1369 MME     3' TATTTCTGTAACTTTTTTT   7335         AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA

                                  __
GAM1369 MME     3' TATTTCTGTAACTTTTTTT   7335         AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA

                                  __
GAM1369 MME     3' TATTTCTGTAACTTTTTTT   7335         AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA

                                  __
GAM1369 MME     3' TATTTCTGTAACTTTTTTT   7335         AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA

                                  __
GAM1369 DKFZP434C212 3' AATATTTCTGTGTACTTTTT  7336          AAA
                                AATATTTTTGT   ACTTTTT
                                ||||||||||   |||||||
                                TTATAAAGACA   TGAAAAA
                                    CA_
GAM1369 FLJ11275 3' AATATTTTTATAAATCCCATTT 7337            A  TT
          TA                    AATATTTTTGTAAA CT  TTTTA
                                ||||||||||||| ||  |||||
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                                TTATAAAAATATTT GG  AAAAT
                                      A  GT
GAM1369  GOLPH3    3'  AATATGGCAGTAAAACTTTTTT 7338       TTTT
           TA                   AATAT   GTAAAACTTTTTTTA
                                |||||   ||||||||||||||
                                TTATA   CATTTTGAAAAAAAT
                                  CCGT
GAM1369  KIAA0563  5'  ATACTTTTGCTCCTTTTTTTA  7339         AAAA
                                ATATTTTTGT   CTTTTTTTA
                                ||||||||||   |||||||||
                                TATGAAAACG   GAAAAAAAT
                                      AG__
GAM1369  TAF2      3'  TATTTTTGTCAAACTTTCT   7340         A
                                TATTTTTGT AAACTTTTT
                                ||||||||| |||||||||
                                ATAAAAACA TTTGAAAGA
                                      G
GAM1369  LOC147071 5'  ATACTTTTGCTCCTTTTTTTA  7339         AAAA
                                ATATTTTTGT   CTTTTTTTA
                                ||||||||||   |||||||||
                                TATGAAAACG   GAAAAAAAT
                                      AG__
GAM1369  LOC147639 5'  AATATTTTTGCAGCACTTTT   7341          AA
                                AATATTTTTGTA  ACTTTT
                                ||||||||||| ||||||
                                TTATAAAAACGT  TGAAAA
                                       CG
GAM1369  LOC201173 5'  ATACTTTTGCTCCTTTTTTTA  7339         AAAA
                                ATATTTTTGT   CTTTTTTTA
                                ||||||||||   |||||||||
                                TATGAAAACG   GAAAAAAAT
                                      AG__
GAM1369  LOC201220 5'  ATACTTTTGCTCCTTTTTTTA  7339         AAAA
                                ATATTTTTGT   CTTTTTTTA
                                ||||||||||   |||||||||
                                TATGAAAACG   GAAAAAAAT
                                      AG__
GAM1370  MME       3'  TATTTCTGTAACTTTTTTT   7335         AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA
                                       __
GAM1370  MME       3'  TATTTCTGTAACTTTTTTT   7335         AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA
                                       __
GAM1370  MME       3'  TATTTCTGTAACTTTTTTT   7335         AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
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                                ATAAAGACAT  TGAAAAAAA
                                          __
GAM1370  MME      3'  TATTTCTGTAACTTTTTTT   7335          AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA
                                          __
GAM1370  DKFZP434C212 3'  AATATTTCTGTGTACTTTTT   7336           AAA
                                AATATTTTTGT   ACTTTTT
                                ||||||||||||  |||||||
                                TTATAAAGACA   TGAAAAA
                                      CA_
GAM1370  FLJ11275  3'  AATATTTTTATAAATCCCATTT 7337             A  TT
              TA                  AATATTTTTGTAAA CT  TTTTA
                                ||||||||||||||| ||  |||||
                                TTATAAAAATATTT GG  AAAAT
                                      A  GT
GAM1370  GOLPH3    3'  AATATGGCAGTAAAACTTTTTT 7338       TTTT
              TA                  AATAT   GTAAAACTTTTTTTA
                                |||||   ||||||||||||||||
                                TTATA   CATTTTGAAAAAAAT
                                  CCGT
GAM1370  KIAA0563  5'  ATACTTTTGCTCCTTTTTTTA  7339          AAAA
                                ATATTTTTGT   CTTTTTTTA
                                |||||||||   |||||||||
                                TATGAAAACG   GAAAAAAAT
                                      AG__
GAM1370  TAF2      3'  TATTTTTGTCAAACTTTCT   7340          A
                                TATTTTTGT AAACTTTTT
                                ||||||||| |||||||||
                                ATAAAAACA TTTGAAAGA
                                      G
GAM1370  LOC147071 5'  ATACTTTTGCTCCTTTTTTTA  7339          AAAA
                                ATATTTTTGT   CTTTTTTTA
                                |||||||||   |||||||||
                                TATGAAAACG   GAAAAAAAT
                                      AG__
GAM1370  LOC147639 5'  AATATTTTTGCAGCACTTTT   7341           AA
                                AATATTTTTGTA  ACTTTT
                                ||||||||||||  ||||||
                                TTATAAAAACGT  TGAAAA
                                      CG
GAM1370  LOC201173 5'  ATACTTTTGCTCCTTTTTTTA  7339          AAAA
                                ATATTTTTGT   CTTTTTTTA
                                |||||||||   |||||||||
                                TATGAAAACG   GAAAAAAAT
                                      AG__
GAM1370  LOC201220 5'  ATACTTTTGCTCCTTTTTTTA  7339          AAAA
                                ATATTTTTGT   CTTTTTTTA
                                |||||||||   |||||||||
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                                TATGAAAACG   GAAAAAAAT
                                     AG__
GAM1371 AGPAT2   3' TGAGACCAGTGACAGAA     35178        T  AG
                                TGAGACCA TGA  AGAG
                                |||||||| |||  ||||
                                ACTCTGGT ACT  TCTT
                                     C  G_
GAM1371 ARHGEF6  3' GAGAAAGAGAAGAGAGAGGGAG 35180      CCATT       AA
                                GAGA    GAAGAGAGA  GAG
                                ||||    |||||||||  |||
                                CTCT    CTTCTCTCT  CTC
                                  TTCT_       CC
GAM1371 ARHGEF6  3' GAGAGAGGGAGAGAGAGAGAG  35179      CCATT  A     A
                                GAGA    GA GAGAGA AGAG
                                ||||    || |||||| ||||
                                CTCT    CT CTCTCT TCTC
                                  CTCC_ _     C
GAM1371 ATP8A2   3' TGAGGCCTGGGAGAAAGA    35181      A  AT  AAGA
                                TGAG CC  TG    GAGAAAGA
                                |||| ||  ||    ||||||||
                                ACTC GG  AC    CTCTTTCT
                                  C  __  C___
GAM1371 BSN      3' TGAGCCAAGAGAAGAGAGAAAG 35182      A   TT_
                                TGAG CCA   GAAGAGAGAAAG
                                |||| |||   ||||||||||||
                                ACTC GGT   CTTCTCTCTTTC
                                  _   TCT
GAM1371 DPYSL2   5' GAGAGAGAGAGAGAGAAGGAG  35183      CCATT  _      A
                                GAGA    GA AGAGAGAA GAG
                                ||||    || |||||||| |||
                                CTCT    CT TCTCTCTT CTC
                                  CT___  C       C
GAM1371 ENO2     3' TGAGGGAAGAGAGAAAGA    35184      ACCATT
                                TGAG     GAAGAGAGAAAGA
                                ||||     ||||||||||||
                                ACTC     CTTCTCTCTTTCT
                                  C_____
GAM1371 EYA3     3' GAGAGGGAGAGAGAGAAAGAG  35186      CCATT  A
                                GAGA    GA GAGAGAAAGAG
                                ||||    || ||||||||||
                                CTCT    CT CTCTCTTTCTC
                                  CCCT_ _
GAM1371 EYA3     3' GAGAGAGAAAGAGAGAAAGAG  35185      CCATT
                                GAGA    GAAGAGAGAAAGAG
                                ||||    ||||||||||||||
                                CTCT    TTTCTCTCTTTCTC
                                  CTC__
GAM1371 FTSJ2    3' GAGAGAGAAAGAGAGAGAGAG  35187      CCATT       A
                                GAGA    GAAGAGAGA AGAG
                                ||||    ||||||||| ||||
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                                CTCT    TTTCTCTCT TCTC
                                  CTC__       C
GAM1371  FTSJ2    3'  GAGAGAGAGAGAAAG      35188     CCATT  A
                                GAGA    GA GAGAGAAAG
                                ||||    || |||||||||
                                CTCT    CT CTCTCTTTC
                                  _____  _
GAM1371  GAC1     3'  TGAGACTGTACAGAGAAAGAG  35189      CAT  AAG
                                TGAGAC   TG   AGAGAAAGAG
                                ||||||   ||   ||||||||||
                                ACTCTG   AC   TCTCTTTCTC
                                   ___ ATG
GAM1371  GLUD1    3'  TGAGTCAGGAGAGAAAG     35190     AC  TTGAA
                                TGAG  CA    GAGAGAAAG
                                ||||  ||    |||||||||
                                ACTC  GT    CTCTCTTTC
                                  A_  C____
GAM1371  HCN4     3'  TGAGACCAGAGATGGGGAGAGA 35191       TT  A___
                                TGAGACCA  GA    GAGAGA
                                ||||||||  ||    ||||||
                                ACTCTGGT  CT    CTCTCT
                                    CT  ACCC
GAM1371  HMGA2    3'  GAGAGAGGGAGAGGGAGAG    35192     CCATT  A_    AA
                                GAGA    GA  GAGAG  AGAG
                                ||||    ||  |||||  ||||
                                CTCT    CT  CTCTC  TCTC
                                  _____ CC    CC
GAM1371  HMGA2    3'  GAGAGGGAGAGAGAGAGAG   35193     CCATT  A     A
                                GAGA    GA GAGAGA AGAG
                                ||||    || |||||| ||||
                                CTCT    CT CTCTCT TCTC
                                  CC___  _     C
GAM1371  IGF1R    3'  GAGAGGAGAGAGAAAG      35194     CCATT  A
                                GAGA    GA GAGAGAAAG
                                ||||    || |||||||||
                                CTCT    CT CTCTCTTTC
                                  C____  _
GAM1371  KIF3B    3'  GAGAGAGGAGAGAAAG      35195     CCATT  A
                                GAGA    GA GAGAGAAAG
                                ||||    || |||||||||
                                CTCT    CT CTCTCTTTC
                                  _____ C
GAM1371  LPL      3'  TGAGACAAAAAAGAAGGGGGAG 35196      CATT__  ____
           AGA                    TGAGAC     GAA    GAGAGA
                                ||||||     |||    ||||||
                                ACTCTG     CTT    CTCTCT
                                   TTTTTT   CCCC
GAM1371  MEIS1    3'  GAGGAAAAGAGAGAGAAAGAG  35197     ACCATT  A
                                GAG     GA GAGAGAAAGAG
                                |||     || ||||||||||
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                                CTC     CT CTCTCTTTCTC
                                  CTTTT_ _
GAM1371  NFIA    5'  GAGAGGAGAAAGAGGGAGAGAG 35198     CCATT     A  A
                                GAGA    GAAGAG GA AGAG
                                ||||    |||||| || ||||
                                CTCT    TTTCTC CT TCTC
                                  CCTC_     C  C
GAM1371  NFIA    5'  GAGAGAGGAAGAGAGAGAGAG  35199     CCATT       A
                                GAGA    GAAGAGAGA AGAG
                                ||||    ||||||||| ||||
                                CTCT    CTTCTCTCT TCTC
                                  CTC__       C
GAM1371  NPR1    5'  GAGAGAGAGAGAGAGAAAG   35200     CCATT  _
                                GAGA    GA AGAGAGAAAG
                                ||||    || ||||||||||
                                CTCT    CT TCTCTCTTTC
                                  CT___  C
GAM1371  NTRK2   3'  GAGATGGAAAGAGAGAAAGAG  35201     CCATT
                                GAGA    GAAGAGAGAAAGAG
                                ||||    ||||||||||||||
                                CTCT    TTTCTCTCTTTCTC
                                  ACC__
GAM1371  PAX5    3'  GAGGAAGAGAGGAAGA     35202     ACCATT      A
                                GAG     GAAGAGAG AAGA
                                |||     |||||||| ||||
                                CTC     CTTCTCTC TTCT
                                  _______       C
GAM1371  PCDHA1  3'  AGAAAAGAGAGAGAGA     35204     CCATT       A
                                AGA     GAAGAGAGA AGA
                                |||     ||||||||| |||
                                TCT     TTTCTCTCT TCT
                                  ______       C
GAM1371  PCDHA1  3'  AGAAAAGAGAGAGAGA     35204     CCATT       A
                                AGA     GAAGAGAGA AGA
                                |||     ||||||||| |||
                                TCT     TTTCTCTCT TCT
                                  ______       C
GAM1371  PCDHA1  3'  GAGAGAGAGAGAGAGAAAGAG  35203     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHA1  3'  GAGAGAGAGAGAGAGAAAGAG  35203     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHA10 3'  GAGAGAGAGAGAGAGAAAGAG  35203     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
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                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHA10  3'  GAGAGAGAGAGAGAGAAAGAG  35203     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHA10  3'  AGAAAAGAGAGAGAGA     35204     CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                  _____       C
GAM1371  PCDHA10  3'  AGAAAAGAGAGAGAGA     35204     CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                  _____       C
GAM1371  PCDHA11  3'  GAGAGAGAGAGAGAGAAAGAG  35203     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHA11  3'  AGAAAAGAGAGAGAGA     35204     CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                  _____       C
GAM1371  PCDHA12  3'  GAGAGAGAGAGAGAGAAAGAG  35203     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHA12  3'  AGAAAAGAGAGAGAGA     35204     CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                  _____       C
GAM1371  PCDHA13  3'  GAGAGAGAGAGAGAGAAAGAG  35203     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHA13  3'  AGAAAAGAGAGAGAGA     35204     CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                  _____       C
GAM1371  PCDHA2   3'  GAGAGAGAGAGAGAGAAAGAG  35203     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
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                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHA2   3' AGAAAAGAGAGAGAGA     35204    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1371  PCDHA3   3' GAGAGAGAGAGAGAGAAAGAG 35203     CCATT _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHA3   3' AGAAAAGAGAGAGAGA     35204    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1371  PCDHA4   3' AGAAAAGAGAGAGAGA     35204    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1371  PCDHA4   3' GAGAGAGAGAGAGAGAAAGAG 35203     CCATT _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHA5   3' AGAAAAGAGAGAGAGA     35204    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1371  PCDHA5   3' GAGAGAGAGAGAGAGAAAGAG 35203     CCATT _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHA6   3' AGAAAAGAGAGAGAGA     35204    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1371  PCDHA6   3' GAGAGAGAGAGAGAGAAAGAG 35203     CCATT _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHA6   3' GAGAGAGAGAGAGAGAAAGAG 35203     CCATT _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
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                              CTCT    CT TCTCTCTTTCTC
                                CT___  C
GAM1371  PCDHA6   3'  AGAAAAGAGAGAGAGA     35204    CCATT       A
                              AGA    GAAGAGAGA AGA
                              |||    ||||||||| |||
                              TCT    TTTCTCTCT TCT
                                _____       C
GAM1371  PCDHA7   3'  GAGAGAGAGAGAGAGAAAGAG 35203     CCATT _
                              GAGA    GA AGAGAGAAAGAG
                              ||||    || ||||||||||||
                              CTCT    CT TCTCTCTTTCTC
                                CT___  C
GAM1371  PCDHA7   3'  AGAAAAGAGAGAGAGA     35204    CCATT       A
                              AGA    GAAGAGAGA AGA
                              |||    ||||||||| |||
                              TCT    TTTCTCTCT TCT
                                _____       C
GAM1371  PCDHA8   3'  GAGAGAGAGAGAGAGAAAGAG 35203     CCATT _
                              GAGA    GA AGAGAGAAAGAG
                              ||||    || ||||||||||||
                              CTCT    CT TCTCTCTTTCTC
                                CT___  C
GAM1371  PCDHA8   3'  AGAAAAGAGAGAGAGA     35204    CCATT       A
                              AGA    GAAGAGAGA AGA
                              |||    ||||||||| |||
                              TCT    TTTCTCTCT TCT
                                _____       C
GAM1371  PCDHA9   3'  GAGAGAGAGAGAGAGAAAGAG 35203     CCATT _
                              GAGA    GA AGAGAGAAAGAG
                              ||||    || ||||||||||||
                              CTCT    CT TCTCTCTTTCTC
                                CT___  C
GAM1371  PCDHA9   3'  AGAAAAGAGAGAGAGA     35204    CCATT       A
                              AGA    GAAGAGAGA AGA
                              |||    ||||||||| |||
                              TCT    TTTCTCTCT TCT
                                _____       C
GAM1371  PCDHAC1  3'  AGAAAAGAGAGAGAGA     35204    CCATT       A
                              AGA    GAAGAGAGA AGA
                              |||    ||||||||| |||
                              TCT    TTTCTCTCT TCT
                                _____       C
GAM1371  PCDHAC1  3'  GAGAGAGAGAGAGAGAAAGAG 35203     CCATT _
                              GAGA    GA AGAGAGAAAGAG
                              ||||    || ||||||||||||
                              CTCT    CT TCTCTCTTTCTC
                                CT___  C
GAM1371  PCDHAC2  3'  GAGAGAGAGAGAGAGAAAGAG 35203     CCATT _
                              GAGA    GA AGAGAGAAAGAG
                              ||||    || ||||||||||||
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                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  PCDHAC2  3'  AGAAAAGAGAGAGAGA     35204    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1371  PCTK1    3'  CGGGACTGCAGGAGAGAAAGAG 35205    A   CAT  AA_
                                TG GAC   TG   GAGAGAAAGAG
                                || |||   ||   ||||||||||
                                GC CTG   AC   CTCTCTTTCTC
                                 C   ___  GTC
GAM1371  PCTK1    3'  CGGGACTGCAGGAGAGAAAGAG 35205    A   CAT  AA_
                                TG GAC   TG   GAGAGAAAGAG
                                || |||   ||   ||||||||||
                                GC CTG   AC   CTCTCTTTCTC
                                 C   ___  GTC
GAM1371  PCTK1    3'  CGGGACTGCAGGAGAGAAAGAG 35205    A   CAT  AA_
                                TG GAC   TG   GAGAGAAAGAG
                                || |||   ||   ||||||||||
                                GC CTG   AC   CTCTCTTTCTC
                                 C   ___  GTC
GAM1371  PPOX     5'  TGAGAGAAAATGAGGGAGAAGG 35206      CCAT_   A A    A
           AG                     TGAGA    TGA G GAGAA GAG
                                |||||    ||| | ||||| |||
                                ACTCT    ACT C CTCTT CTC
                                   CTTTT   _ C    C
GAM1371  PPT2     3'  TGAAAATAAAGAGAGAGAGAG  35207      CCAT        A
                                TGAGA    TGAAGAGAGA AGAG
                                |||||    |||||||||| ||||
                                ACTTT    ATTTCTCTCT TCTC
                                   T___         C
GAM1371  PRELP    3'  GAGAAAGAAGGGGAGAGAGAG  35208     CCATT    A_   A
                                GAGA    GAAG  GAGA AGAG
                                ||||    ||||  |||| ||||
                                CTCT    CTTC  CTCT TCTC
                                  TT___    CC    C
GAM1371  PTK2B    3'  TGAGGGCCGAAGAGGAA     35209      A_  ATT     A
                                TGAG  CC   GAAGAG GAA
                                ||||  ||   |||||| |||
                                ACTC  GG   CTTCTC CTT
                                  CC  ___     _
GAM1371  RUNX3    3'  TGAGACCACCTAGGGGAAAG   35210          GA  AGA
                                TGAGACCATT  AG   GAAAG
                                ||||||||||  ||   |||||
                                ACTCTGGTGG  TC   CTTTC
                                      A_  CC_
GAM1371  SH3BP5   3'  TGAGGGTGAGAAGAGAAAGAG  35211     ACCAT   AG
                                TGAG    TGA  AGAGAAAGAG
                                ||||    |||  ||||||||||
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                                ACTC    ACT  TCTCTTTCTC
                                  CC___   CT
GAM1371  SIX2     3'  GAGAAGGAGAGAGAAAG     35212      CCATT  A
                                GAGA    GA GAGAGAAAG
                                ||||    || |||||||||
                                CTCT    CT CTCTCTTTC
                                  TC___  _
GAM1371  SLC18A3  3'  TGGACAAGAGAGAAAG      35213    A   CATTG
                                TG GAC    AAGAGAGAAAG
                                || |||    ||||||||||
                                AC CTG    TTCTCTCTTTC
                                 _  _____
GAM1371  SLC7A6   3'  TGAAACCACAAGGGAGGGGGAG 35214         TG   A   AAA
                                TGAGACCAT  AAG GAG   GAG
                                |||||||||  ||| |||   |||
                                ACTTTGGTG  TTC CTC   CTC
                                     __   C   CCC
GAM1371  TBL1X    3'  GAGAGAGAGAGAGAAAGAG    35215      CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  _____  C
GAM1371  TCN1     3'  GAACATGTAGAGAGAGAAG    35216    C   T A      _
                                GA CAT G AGAGAGA AAG
                                || ||| | ||||||| |||
                                CT GTA C TCTCTCT TTC
                                 T   _ A      C
GAM1371  TGFBR2   3'  TGAGACTTTTGATATAAAAAGA 35217       CA    AGAG
           G                     TGAGAC  TTGA    AGAAAGAG
                                ||||||  ||||    ||||||||
                                ACTCTG  AACT    TTTTTCTC
                                   AA    ATA_
GAM1371  TNFSF5   3'  GAGATGGAGAGAGAGAG     35218      CCAT  A      A
                                GAGA    TG AGAGAGA AG
                                ||||    || ||||||| ||
                                CTCT    AC TCTCTCT TC
                                  ____  C      C
GAM1371  TRPS1    5'  GAGAGAGAGAGAGAGAAAGAG  35203      CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  ACTR1A   3'  GAGGAAAAGGGAGAAAGA    35219     ACCATT    A
                                GAG     GAAG GAGAAAGA
                                |||     |||| ||||||||
                                CTC     TTTC CTCTTTCT
                                 CT____    C
GAM1371  BCL2L1   3'  GAGCAGAAGAGAGAGGGAG    35220     ACCATT       AA
                                GAG     GAAGAGAGA  GAG
                                |||     |||||||||  |||
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                                CTC     CTTCTCTCT  CTC
                                  GT____        CC
GAM1371  BIRC5    3'  TGAGCCCCCAAAAAAGAGAGAG 35221     A__   TT       A
             AGAG                    TGAG   CCA  GAAGAGAGA AGAG
                                |||||   |||  ||||||||| ||||
                                ACTC   GGT  TTTCTCTCT TCTC
                                  GGG   TT       C
GAM1371  C1QR1    3'  GAGAGAGAGAGAGAGAAAGAG  35203     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  C20orf139 3'  TGAGACAGAGAGAAAG      35222       CATTGA
                                TGAGAC     AGAGAGAAAG
                                ||||||     ||||||||||
                                ACTCTG     TCTCTCTTTC

                                  _______
GAM1371  C6orf9   3'  TGAGACCAGTGGCAAGGAA   35223        T  AA   A
                                TGAGACCA TG  GAG GAA
                                |||||||| ||  ||| |||
                                ACTCTGGT AC  TTC CTT
                                     C  CG   _
GAM1371  CRK7     3'  GAGAGAGAGAGAGAGAAAGAG  35203     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  CRK7     3'  GAGAGAGAAAGAGAGAGAGAG  35187     CCATT       A
                                GAGA    GAAGAGAGA AGAG
                                ||||    ||||||||| ||||
                                CTCT    TTTCTCTCT TCTC
                                  CTC__        C
GAM1371  dA141H5.1 3'  GAGAGAGAGAGAGAGAAGGAG  35183     CCATT  _      A
                                GAGA    GA AGAGAGAA GAG
                                ||||    || |||||||| |||
                                CTCT    CT TCTCTCTT CTC
                                  CT___  C       C
GAM1371  DCTD     3'  TGAGATTAAAGAGAA      35224      CCA
                                TGAGA   TTGAAGAGAG
                                |||||   ||||||||||
                                ACTCT   AATTTCTCTT

                                  ___
GAM1371  DKFZp564B0769 3'  TGAGTTTATTAAAGAGAGAGAG 35225      ACC          A
                                TGAG   ATTGAAGAGAGA AG
                                ||||   |||||||||||| ||
                                ACTC   TAATTTCTCTCT TC
                                  AAA          C
GAM1371  FLJ12572  3'  TGAACTGTTGAAGAGAA     35226      A CA
                                TGAG C  TTGAAGAGAG
                                |||| |  ||||||||||
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                                ACTT G  AACTTCTCTT
                                  _ AC
GAM1371  FLJ13154  3'  GAGAGAGAGGAGAGGAAGAG   35227     CCATT  A    A
                                GAGA    GA GAGAG AAGAG
                                ||||    || ||||| |||||
                                CTCT    CT CTCTC TTCTC
                                  CT___  C    C
GAM1371  FLJ13154  3'  GAGACAGAGGAGAGAAAGAG   35230      CATT  A
                                GAGAC   GA GAGAGAAAGAG
                                |||||   || ||||||||||
                                CTCTG   CT CTCTCTTTCTC
                                   T___  C
GAM1371  FLJ13154  3'  GAGAGAGAGAGGAGAGGAAGAG 35231     CCATT  A    A
                                GAGA    GA GAGAG AAGAG
                                ||||    || ||||| |||||
                                CTCT    CT CTCTC TTCTC
                                  CTCT_  C    C
GAM1371  FLJ13154  3'  GAGGAAGAGAGGAGAGGAAGAG 35228     ACCATT  A    A
                                GAG     GA GAGAG AAGAG
                                |||     || ||||| |||||
                                CTC     CT CTCTC TTCTC
                                 CTTCT_  C    C
GAM1371  FLJ13154  3'  GAGAGGAAGAGAGAGGAG    35229     CCATT       AA
                                GAGA    GAAGAGAGA  GAG
                                ||||    |||||||||  |||
                                CTCT    CTTCTCTCT  CTC
                                  C_____        C_
GAM1371  FLJ13154  3'  GAGAGAGAGGAGAGGAAGAG   35227     CCATT  A    A
                                GAGA    GA GAGAG AAGAG
                                ||||    || ||||| |||||
                                CTCT    CT CTCTC TTCTC
                                  CT___  C    C
GAM1371  FLJ13154  3'  GAGAGAAGAGAGGAAGA     35233     CCATT       A
                                GAGA    GAAGAGAG AAGA
                                ||||    |||||||| ||||
                                CTCT    CTTCTCTC TTCT
                                  ______       C
GAM1371  FLJ13154  3'  GAGAGAGGAGAGGAAGA     35232     CCATT  A    A
                                GAGA    GA GAGAG AAGA
                                ||||    || ||||| ||||
                                CTCT    CT CTCTC TTCT
                                  ______ C    C
GAM1371  FLJ13154  3'  GAGAGAGAGGAGAGGAAGAG   35227     CCATT  A    A
                                GAGA    GA GAGAG AAGAG
                                ||||    || ||||| |||||
                                CTCT    CT CTCTC TTCTC
                                  CT___  C    C
GAM1371  FLJ14594  3'  GAGGCGGGAGGGAGAAAGAG   35234     ACCATT  A A
                                GAG     GA G GAGAAAGAG
                                |||     || | |||||||||
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                                CTC      CT C CTCTTTCTC
                                  CGCC__  _ C
GAM1371  FLJ22671  3'  GAGAGCAAAAGGAGAGGGGGAG 35235      C  TT  A    AAA
                                GAGA CA  GA GAGAG   GAG
                                |||| ||  || |||||   |||
                                CTCT GT  TT CTCTC   CTC
                                  C  T_  C    CCC
GAM1371  FLJ22679  3'  TGAGGAGAGAGAGAGAAAGAG  35236      ACCATT  _
                                TGAG     GA AGAGAGAAAGAG
                                ||||     || ||||||||||||
                                ACTC     CT TCTCTCTTTCTC
                                  CT_____  C
GAM1371  FLJ23263  5'  GATCCGCTGAAGAGGGAAGGAG 35237    _ A       A   A
                                GA CC TTGAAGAG GAA GAG
                                || || |||||||| ||| |||
                                CT GG GACTTCTC CTT CTC
                                 A  C       C   C
GAM1371  FLJ30574  3'  GAGAAAAAAAAGAGAGAGAGAG 35238      CCATT        A
                                GAGA     GAAGAGAGA AGAG
                                ||||     ||||||||| ||||
                                CTCT     TTTCTCTCT TCTC
                                  TTTT_        C
GAM1371  HAND1     3'  GACAAGAGAGAAAGAG      35239      CATTG
                                GAC     AAGAGAGAAAGAG
                                |||     ||||||||||||
                                CTG     TTCTCTCTTTCTC
                                  _____
GAM1371  HSPC065   3'  GAGAAAGAAAGAGAGAAAGAG  35240      CCATT
                                GAGA     GAAGAGAGAAAGAG
                                ||||     ||||||||||||||
                                CTCT     TTTCTCTCTTTCTC
                                  TTC__
GAM1371  HTATSF1   5'  GAGCTGAGCAGAGAAAG     35241     ACCA    AG
                                GAG    TTGA  AGAGAAAG
                                |||    ||||  ||||||||
                                CTC    GACT  TCTCTTTC
                                  ____   CG
GAM1371  JIK       3'  TAAGAGTAAGAGAGAGAGA    35242       CCATTG       A
                                TGAGA     AAGAGAGA AGA
                                |||||     |||||||| |||
                                ATTCT     TTCTCTCT TCT
                                   CA____       C
GAM1371  KIAA0159  5'  TGAGGCACAGAGAAAG      35243      AC   TGAAG
                                TGAG  CAT     AGAGAAAG
                                ||||  |||     ||||||||
                                ACTC  GTG     TCTCTTTC
                                  C_  _____
GAM1371  KIAA0210  5'  TGAAACCATGAGGGAGAG     35244          T  A_
                                TGAGACCAT GA  GAGAG
                                |||||||| ||  |||||
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                                ACTTTGGTA CT  CTCTC
                                      _ CC
GAM1371  KIAA0450  3'  GAGAAGCAGAAGAGAGAGAG  35245     CCATT       A
                                GAGA    GAAGAGAGA AG
                                ||||    ||||||||| ||
                                CTCT    CTTCTCTCT TC
                                  TCGT_       C
GAM1371  KIAA0721  3'  GAGGAGGAGGGAGAGAAAGAG  35246    ACCATT  A_
                                GAG     GA  GAGAGAAAGAG
                                |||     ||  ||||||||||
                                CTC     CT  CTCTCTTTCTC
                                  CTC___  CC
GAM1371  KIAA0721  3'  GAGGAGGAGGGAGAGAAAGAG  35246    ACCATT  A_
                                GAG     GA  GAGAGAAAGAG
                                |||     ||  ||||||||||
                                CTC     CT  CTCTCTTTCTC
                                  CTC___  CC
GAM1371  KIAA1029  3'  GAGAGAGAGAGAGAGAAAGAG  35203     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  KIAA1029  3'  TGAGAGAGAGAGAGAG     35247      CCATT  A     A
                                TGAGA    GA GAGAGA AG
                                |||||    || |||||| ||
                                ACTCT    CT CTCTCT TC
                                  _____  _     C
GAM1371  KIAA1076  3'  GAGACAGAGAAGAGAGAGAG  35248      CATT       A
                                GAGAC    GAAGAGAGA AG
                                |||||    ||||||||| ||
                                CTCTG    CTTCTCTCT TC
                                  TCT_       C
GAM1371  KIAA1181  3'  GAGGAGAAGAGAGGAAGA    35249     ACCATT       A
                                GAG     GAAGAGAG AAGA
                                |||     |||||||| ||||
                                CTC     CTTCTCTC TTCT
                                  CT____       C
GAM1371  KIAA1384  5'  GAGAAAAGAGAGAAAGAG    35250     CCATT
                                GAGA    GAAGAGAGAAAGAG
                                ||||    ||||||||||||||
                                CTCT    TTTCTCTCTTTCTC
                                  _____
GAM1371  KIAA1384  5'  GAGAGAGGGAGAGAGAGAG   35251     CCATT  A_    A
                                GAGA    GA  GAGAGA AGAG
                                ||||    ||  |||||| ||||
                                CTCT    CT  CTCTCT TCTC
                                  _____  CC     C
GAM1371  MGC10765  3'  GAGGGACAGGGAGAGGGAAAGA 35252     AC_  TT  A   A
            G                    GAG   CA  GA GAG GAAAGAG
                                |||   ||  || ||| |||||||
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                                CTC   GT  CT CTC CTTTCTC
                                  CCT  CC  _   C
GAM1371  MGC10812  3'  GAGGCACAGCGGGGAGAAAGAG 35253     AC   TGAAGA
                                GAG  CAT     GAGAAAGAG
                                |||  |||     |||||||||
                                CTC  GTG     CTCTTTCTC
                                  C_   TCGCCC
GAM1371  MGC11115  3'  GAGGGTAAAGAGAGAGGGAG   35255     ACCAT        AA
                                GAG    TGAAGAGAGA  GAG
                                |||    ||||||||||  |||
                                CTC    ATTTCTCTCT  CTC
                                  CC___         CC
GAM1371  MGC11115  3'  GAGAGAGGGAGAGAGAGGGAG  35254      CCATT  A     AA
                                GAGA    GA GAGAGA  GAG
                                ||||    || ||||||  |||
                                CTCT    CT CTCTCT  CTC
                                   CTCC_ _     CC
GAM1371  MGC13053  3'  GAGAGAGAAAGAGAGAGAGAG  35187      CCATT        A
                                GAGA    GAAGAGAGA AGAG
                                ||||    ||||||||| ||||
                                CTCT    TTTCTCTCT TCTC
                                   CTC__        C
GAM1371  MGC13053  3'  GAGAGAGAGAGAGAAAGA    35257      CCATT  _
                                GAGA    GA AGAGAGAAAGA
                                ||||    || ||||||||||
                                CTCT    CT TCTCTCTTTCT
                                  _____  C
GAM1371  MGC13053  3'  GAGACGAGAGAGAGAGAG    35256       CATT  A     A
                                GAGAC    GA GAGAGA AGAG
                                |||||    || |||||| ||||
                                CTCTG    CT CTCTCT TCTC
                                   ____ _     C
GAM1371  MGC14798  3'  TGGAGCAAGAAAGAGAGAAGGA 35258     A  C  TT        A
            G                    TG GA CA  GAAGAGAGAA GAG
                                || || ||  |||||||||| |||
                                AC CT GT  TTTCTCTCTT CTC
                                 _  C  TC         C
GAM1371  MGC15827  3'  TGAAACCGTTGAAGAGAA     35259        A
                                TGAGACC TTGAAGAGAG
                                ||||||| ||||||||||
                                ACTTTGG AACTTCTCTT
                                    C
GAM1371  MGC4796   3'  TGAGACGGGAGAGAAAGA     35260       CATTGAA
                                TGAGAC      GAGAGAAAGA
                                ||||||      ||||||||||
                                ACTCTG      CTCTCTTTCT
                                   CC_____
GAM1371  MOST2     5'  TGAGACCTGAAGAGGGAGAG   35261        AT      A  A
                                TGAGACC  TGAAGAG GA AG
                                |||||||  ||||||| || ||
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                                ACTCTGG  ACTTCTC CT TC
                                   __      C  C
GAM1371  NAG73    3'  GAGAAGGAGGAGAGAAAG    35262      CCATT  A
                                GAGA    GA GAGAGAAAG
                                ||||    || |||||||||
                                CTCT    CT CTCTCTTTC
                                  TC___  C
GAM1371  NFAT5    3'  GAGAGAGAGAGAGAGAAAGAG  35203      CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1371  NFAT5    3'  GAGAAAGGAAGGGGAGAGGGAG 35263      CCATT   A_   AA
                                GAGA    GAAG  GAGA  GAG
                                ||||    ||||  ||||  |||
                                CTCT    CTTC  CTCT  CTC
                                  TTC__   CC   CC
GAM1371  NKG7     5'  GAATCTCAGAGAGAAGGA    35264    CC   GA      A
                                GA  ATT  AGAGAGAA GA
                                ||  |||  |||||||| ||
                                CT  TAG  TCTCTCTT CT
                                 __  AG       C
GAM1371  NPD009   5'  TGAGCAAAAGAGAGGAAGA    35265     ACCATT      A
                                TGAG     GAAGAGAG AAGA
                                ||||     |||||||| ||||
                                ACTC     TTTCTCTC TTCT
                                  GT____       C
GAM1371  NRN1     5'  GAGGGAGGAGAGAAAGA     35266     ACCATT  A
                                GAG     GA GAGAGAAAGA
                                |||     || ||||||||||
                                CTC     CT CTCTCTTTCT
                                 C_____  C
GAM1371  OR7C1    5'  GAGAGAGAGAGAGAAAGAG    35215     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  _____  C
GAM1371  PFTK1    3'  GAGACAGAGAGAGAGAGA    35268      CATT  A     A
                                GAGAC   GA GAGAGA AGA
                                |||||   || |||||| |||
                                CTCTG   CT CTCTCT TCT
                                  T___  _     C
GAM1371  PFTK1    3'  GAGGGGTTTGGGGGGAGAAAGA 35267     ACCA   AAGA
            G                    GAG   TTG   GAGAAAGAG
                                |||   |||   |||||||||
                                CTC   AAC   CTCTTTCTC
                                 CCCA  CCCC
GAM1371  PROL2    5'  CAACGAAGAGAGAAGGAG    35269    T        A
                                CA TGAAGAGAGAA GAG
                                || ||||||||||| |||
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                                GT GCTTCTCTCTT CTC
                                 T         C
GAM1371  RFX3     5'  GAGAGAGGGAGAGAGAGAGAG  35179      CCATT  A     A
                                GAGA     GA GAGAGA AGAG
                                ||||     || |||||| ||||
                                CTCT     CT CTCTCT TCTC
                                  CTCC_ _     C
GAM1371  RFX3     5'  GAGAGAGGGAGAGAGAGAGAG  35179      CCATT  A     A
                                GAGA     GA GAGAGA AGAG
                                ||||     || |||||| ||||
                                CTCT     CT CTCTCT TCTC
                                  CTCC_ _     C
GAM1371  RGS7     3'  TGAGAGAGAGAGAGAG      35247       CCATT  A     A
                                TGAGA     GA GAGAGA AG
                                |||||     || |||||| ||
                                ACTCT     CT CTCTCT TC
                                  _____ _     C
GAM1371  SEC14L1  3'  TGAGACACAGAGAAAG      35270       C  TGAAG
                                TGAGAC AT     AGAGAAAG
                                |||||| ||     ||||||||
                                ACTCTG TG     TCTCTTTC
                                  _ _____
GAM1371  SSH2     3'  GAGAGAGAGAGGAGAGAGAGAG 35271      CCATT  A     A
                                GAGA     GA GAGAGA AGAG
                                ||||     || |||||| ||||
                                CTCT     CT CTCTCT TCTC
                                  CTCT_ C     C
GAM1371  TRIM15   5'  GAGACAGAGAGAGAGAAAGAG  35272      CATT  A
                                GAGAC    GA GAGAGAAAGAG
                                |||||    || ||||||||||
                                CTCTG    CT CTCTCTTTCTC
                                   TCT_ _
GAM1371  TRIM15   5'  GAGAGAGAAAGAGAGAGAGAG  35187      CCATT       A
                                GAGA     GAAGAGAGA AGAG
                                ||||     ||||||||| ||||
                                CTCT     TTTCTCTCT TCTC
                                  CTC__        C
GAM1371  UPLC1    3'  TGAGTTGACCAAGAGAAAGAG  35273      ACCA   A_
                                TGAG    TTGA  GAGAGAAAGAG
                                ||||    ||||  ||||||||||
                                ACTC    AACT  TTCTCTTTCTC
                                  ____    GG
GAM1371  LOC112868 3'  GAGAAAGAGAGGAGAGAGAGAG 35276      CCATT  A     A
                                GAGA     GA GAGAGA AGAG
                                ||||     || |||||| ||||
                                CTCT     CT CTCTCT TCTC
                                  TTCT_ C     C
GAM1371  LOC112868 3'  GAGAGGGAGAGAGAGAAAGAG  35186      CCATT  A
                                GAGA     GA GAGAGAAAGAG
                                ||||     || ||||||||||
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                                CTCT    CT CTCTCTTTCTC
                                  CCCT_ _
GAM1371  LOC112868 3'  GAGAGGAGAGAGAGAGA    35275     CCATT  A     A
                                GAGA    GA GAGAGA AGA
                                ||||    || |||||| |||
                                CTCT    CT CTCTCT TCT
                                  C____ _     C
GAM1371  LOC112868 3'  GAGGAGAGAGAGAGAGA    35274     ACCATT  _     A
                                GAG     GA AGAGAGA AGA
                                |||     || ||||||| |||
                                CTC     CT TCTCTCT TCT
                                  ______ C      C
GAM1371  LOC113612 3'  GAGAGAGAGAGAGAAAG    35277     CCATT  _
                                GAGA    GA AGAGAGAAAG
                                ||||    || ||||||||||
                                CTCT    CT TCTCTCTTTC
                                  _____ C
GAM1371  LOC113612 3'  GAGGATGAAAGAGAGAGAGAG  35278     ACC  T       A
                                GAG   AT GAAGAGAGA AGAG
                                |||   || |||||||| ||||
                                CTC   TA TTTCTCTCT TCTC
                                  C__  C        C
GAM1371  LOC116411 5'  CACTAAGGAGAGAGAAAG    35279       __
                                CATTGA  AGAGAGAAAG
                                ||||||  ||||||||||
                                GTGATT  TCTCTCTTTC
                                    CC
GAM1371  LOC123775 3'  GACGGGGAGGAGAGAAAGAG   35280     CATT  A
                                GAC    GA GAGAGAAAGAG
                                |||    || ||||||||||
                                CTG    CT CTCTCTTTCTC
                                  CCC_  C
GAM1371  LOC129285 3'  GAGAGAAAGAAGAGAGAGAGAG 35281      CCATT       A
                                GAGA    GAAGAGAGA AGAG
                                ||||    ||||||||| ||||
                                CTCT    CTTCTCTCT TCTC
                                  CTTT_        C
GAM1371  LOC131034 5'  TGAGAAAAGAGGGAGGGA    35282      CCATT     A  AA
                                TGAGA    GAAGAG GA  GA
                                |||||    |||||| ||  ||
                                ACTCT    TTTCTC CT  CT
                                  _____     C  CC
GAM1371  LOC144231 5'  GAGCAGAAGGGAGAAAGAG    35283     ACCATT    A
                                GAG     GAAG GAGAAAGAG
                                |||     |||| |||||||||
                                CTC     CTTC CTCTTTCTC
                                  GT____    C
GAM1371  LOC144262 5'  TAAGACTATGAGAGAGAAAG   35284       CAT   A
                                TGAGAC   TGA GAGAGAAAG
                                ||||||   ||| |||||||||
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                                ATTCTG   ACT CTCTCTTTC
                                   AT_   _
GAM1371  LOC145439 3'  GAGGCTCAAAGAGAGAAAGAG  35285     ACCA TG
                                GAG    T  AAGAGAGAAAGAG
                                |||    |  |||||||||||||
                                CTC    A  TTCTCTCTTTCTC
                                  CG__ GT
GAM1371  LOC145645 3'  GAGAAGGGGAGGAGAGAAAGAG 35286      CCATT  A
                                GAGA     GA GAGAGAAAGAG
                                ||||     ||  ||||||||||
                                CTCT     CT CTCTCTTTCTC
                                   TCCC_  C
GAM1371  LOC145645 3'  AAGACAGAAAGAGAGAA     35287       CATT
                                GAGAC    GAAGAGAGAA
                                |||||    ||||||||||
                                TTCTG    TTTCTCTCTT
                                   TC__
GAM1371  LOC146839 5'  GAGGAAAAAGAGAGAAAGAG   35288     ACCATT
                                GAG      GAAGAGAGAAAGAG
                                |||      |||||||||||||
                                CTC      TTTCTCTCTTTCTC
                                  CTT___
GAM1371  LOC148137 3'  GAGAGAGAGAGAAAGA      35289      CCATT  A
                                GAGA     GA GAGAGAAAGA
                                ||||     ||  ||||||||||
                                CTCT     CT CTCTCTTTCT
                                   _____  _
GAM1371  LOC150577 3'  GAGAGAGAGAGAGAGAAAGAG  35203      CCATT  _
                                GAGA     GA AGAGAGAAAGAG
                                ||||     ||  ||||||||||||
                                CTCT     CT TCTCTCTTTCTC
                                   CT___  C
GAM1371  LOC151742 3'  TAAGACCACCAGGGAG      35290          GA  A
                                TGAGACCATT  AG GAG
                                ||||||||||  ||  |||
                                ATTCTGGTGG  TC CTC
                                      __  C
GAM1371  LOC154761 3'  TGAGCTTTGGTGGAGAGAAAGA 35291      ACCA   AA_
            G                    TGAG    TTG   GAGAGAAAGAG
                                ||||    |||   ||||||||||||
                                ACTC    AAC   CTCTCTTTCTC
                                   GA__   CAC
GAM1371  LOC157638 3'  GAGGAAGAGAGGGAGAA     35292     ACCATT       AA
                                GAG      GAAGAGAG  AGAG
                                |||      ||||||||  ||||
                                CTC      CTTCTCTC  TCTT
                                  _______       CC
GAM1371  LOC196752 3'  GAGGATCTGAGGGAGAAAGAG  35293     ACCA    A A
                                GAG    TTGA G GAGAAAGAG
                                |||    |||| | |||||||||
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                                CTC    GACT C CTCTTTCTC
                                  CTA_   _ C
GAM1371  LOC200734 3'  TGAACCAAGAGAAAG       35294      A   TTGAAG
                                TGAG CCA      AGAGAAAG
                                |||| |||      ||||||||
                                ACTT GGT      TCTCTTTC
                                  _   _______
GAM1371  LOC201617 5'  TGAGGCAGAGAAAGAGAGAGAG 35295      ACCATT        A
                                TGAG      GAAGAGAGA AG
                                ||||      ||||||||| ||
                                ACTC      TTTCTCTCT TC
                                   CGTCTC        C
GAM1371  LOC201799 3'  GATACCTAAAGAGAGAAAG    35296    G   AT
                                GA ACC  TGAAGAGAGAAAG
                                || |||  ||||||||||||
                                CT TGG  ATTTCTCTCTTTC
                                 A   __
GAM1371  LOC221477 3'  TGAGACCCACAGAGAAAGA    35297        ATTGAAG
                                TGAGACC       AGAGAAAGA
                                |||||||       |||||||||
                                ACTCTGG       TCTCTTTCT
                                    GTG____
GAM1371  LOC221662 3'  TGGAAAATTGGGAGGGAAAGAG 35298    A  CC    AA   A
                                TG GA  ATTG  GAG GAAAGAG
                                || ||  ||||  ||| |||||||
                                AC CT  TAAC  CTC CTTTCTC
                                 _  TT    C_   C
GAM1371  LOC253847 5'  TGGGACCACTGCAGCTGGGGGA 35299    A       A  AGAGAAA
            G                    TG GACCATTG AG       GAG
                                || ||||||||  ||       |||
                                AC CTGGTGAC TC       CTC
                                 C       G  GACCCC_
GAM1371  LOC254945 5'  TGAGGTAGACAGAGAGAAGGAG 35300      ACCATTGA       A
                                TGAG       AGAGAGAA GAG
                                ||||       |||||||| |||
                                ACTC       TCTCTCTT CTC
                                   CATCTG__       C
GAM1371  LOC51008  5'  TGAATCATCAAAGAGAAGGAG  35301      AC   TG      AAA
                                TGAG  CAT  AAGAGAG   GAG
                                ||||  |||  |||||||   |||
                                ACTT  GTA  TTCTCTT   CTC
                                   A_   GT      C__
GAM1371  LOC56930  5'  GAATGAAAGAGAGGAAGA    35302    CC  T       A
                                GA  AT GAAGAGAG AAGA
                                ||  || |||||||| ||||
                                CT  TA TTTCTCTC TTCT
                                 __  C       C
GAM1371  LOC91812  5'  GACACTGAAAAGGGAGAGAG   35303     C        A  A
                                GAC ATTGAAGAG GA AGAG
                                ||| ||||||||| || ||||
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                                CTG TGACTTTTC CT TCTC
                                  _       C  C
GAM1371 LOC91813 5' GACACTGAAAAGGGAGAGAG  35303     C       A  A
                                GAC ATTGAAGAG GA AGAG
                                ||| ||||||||| || ||||
                                CTG TGACTTTTC CT TCTC
                                  _       C  C
GAM1372 CA3      3' TGTGAAATTTTAGATAACAGAA 35306          TACCAA
             AA                   TGTGAAATTTTG     AGAAAA
                                ||||||||||||     ||||||
                                ACACTTTAAAAT     TCTTTT
                                       CTATTG
GAM1372 FZD1     3' TGTGGAGTTCTGTACCTTAAGA 35307      AAA       A_
                                TGTG   TTTTGTACC  AAGA
                                ||||   |||||||||  ||||
                                ACAC   AAGACATGG  TTCT
                                  CTC        AA
GAM1372 IGFBP4   3' TGTGTAACACCAAAGA      35308      A   TTTGT
                                TGTG AAT    ACCAAAGA
                                |||| |||    ||||||||
                                ACAC TTG    TGGTTTCT
                                  A  _____
GAM1372 MTMR7    3' TGTGAAATATTTGTATTGCACT 35309        _     C__  AA
             GAA                   TGTGAAAT TTTGTA   CA  GAA
                                ||||||||| ||||||   ||  |||
                                ACACTTTA AAACAT   GT  CTT
                                     T     AAC  GA
GAM1372 NPPB     3' TGGAAATTTTGTGCTCAAAG   35310    T       AC_
                                TG GAAATTTTGT   CAAAG
                                || ||||||||||   |||||
                                AC CTTTAAAACA   GTTTC
                                  _        CGA
GAM1372 PODXL    3' TGGAAATGGAAGCCCAAAGAA  35311    T    TTTGTA
                                TG GAAAT     CCAAAGAA
                                || |||||     ||||||||
                                AC CTTTA     GGTTTCTT
                                  _    CCTTCG
GAM1372 PRKAR1A  3' TGTGAAATTTTGTTTAAAAAA  35312          ACC
                                TGTGAAATTTTGT   AAAGAA
                                ||||||||||||   ||||||
                                ACACTTTAAAACA   TTTTTT
                                       AA_
GAM1372 RPL30    3' GTGAAATTTTGTAGGTGAAAA  35313          CCAAA
                                GTGAAATTTTGTA    GAAAA
                                ||||||||||||    |||||
                                CACTTTAAAACAT    CTTTT
                                       CCA__
GAM1372 TAPBP    3' TGTGAGATTTTATAACAAAA   35314      A       C
                                TGTGA ATTTTGTA CAAAG
                                ||||| |||||||| |||||
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                                ACACT TAAAATAT GTTTT
                                  C       T
GAM1372  TGM4     3'  GTGGATGGAATACCAAAGAAA  35315     AAATTTT
                                GTG      GTACCAAAGAAA
                                |||      ||||||||||||
                                CAC      TATGGTTTCTTT
                                  CTACCT_
GAM1372  TNFSF15  3'  TGTGAAATTTTGGCCCCAAA   35316          TA_
                                TGTGAAATTTTG   CCAAA
                                ||||||||||||   |||||
                                ACACTTTAAAAC   GGTTT
                                       CGG
GAM1372  TP53BP2  3'  TGTGAAATTTTTGCCAAAA    35317          GTA
                                TGTGAAATTTT   CCAAAG
                                ||||||||||   ||||||
                                ACACTTTAAAA   GGTTTT
                                       AC_
GAM1372  TRPM8    3'  TGTAAAATTTTGAAAGA     35318          TACC
                                TGTGAAATTTTG    AAAGA
                                ||||||||||||    |||||
                                ACATTTTAAAAC    TTTCT
                                          ____
GAM1372  WNT11    3'  TGAGAAGTGCCACCCCAAAGAA 35319    T   ATT TG A
           AA                     TG GAA   T  T CCAAAGAAAA
                                || |||   |  | ||||||||||
                                AC CTT   G  G GGTTTCTTTT
                                 T   CAC GT G
GAM1372  BIRC3    5'  TGTGAAATTTAGTGGCCAGGAA 35320         T  A_   AA
           AA                     TGTGAAATTT GT  CCA  GAAAA
                                ||||||||||  ||  |||  |||||
                                ACACTTTAAA CA  GGT  CTTTT
                                       T  CC   C_
GAM1372  BIVM     3'  TGTGAAATTTTCTGTCCA    35321         __    A
                                TGTGAAAT  TTTGT CCA
                                ||||||||  ||||| |||
                                ACACTTTA  AGACA GGT
                                     AA    _
GAM1372  FAM8A1   3'  TATGAAATTTTGTACTAAAA   35322            C
                                TGTGAAATTTTGTAC AAAG
                                ||||||||||||||| ||||
                                ATACTTTAAAACATG TTTT
                                          A
GAM1372  FLJ13305 3'  TGTGAAATGCACTGCAGAGAAA 35323        TTT    __  A
           A                     TGTGAAA   TGTAC  CA AGAAAA
                                |||||||   |||||  || ||||||
                                ACACTTT   ACGTG  GT TCTTTT
                                     ___    AC  C
GAM1372  FLJ20010 3'  TGGAACCTTTGCCAAAGAAA  35324    T   A    TA
                                TG GAA TTTTG  CCAAAGAAA
                                || ||| |||||  |||||||||
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                                AC CTT GAAAC  GGTTTCTTT
                                 _  G    __
GAM1372  FLJ22031  3'  TGTGAAATATTGTGGTCAAG  35325       T   ACCA
                                TGTGAAAT TTGT   AAG
                                |||||||| ||||   |||
                                ACACTTTA AACA   TTC
                                     T   CCAG
GAM1372  KIAA0057  3'  TGTGAAATAAACGTGCCAGGGA 35326       TT_  A  AA
                                TGTGAAAT  TGT CCA  GA
                                ||||||||  ||| |||  ||
                                ACACTTTA  GCA GGT  CT
                                     TTT  C  CC
GAM1372  KIAA0992  3'  TGAAGAAAACCAAAGAAAA   35327     ATTTTGT
                                TGAA      ACCAAAGAAAA
                                ||||      ||||||||||
                                ACTT      TGGTTTCTTTT
                                  CTTT___
GAM1372  KIAA1233  3'  TATGAAATTTTGTTAATAAGAA 35328          ACCA
              AA                  TGTGAAATTTTGT   AAGAAAA
                                |||||||||||||   |||||||
                                ATACTTTAAAACA   TTCTTTT
                                       ATTA
GAM1372  LOC115073 3'  TGTGAAATCTTGTAAGAA    35329          CCAA
                                TGTGAAATTTTGTA   AGAA
                                |||||||||||||   ||||
                                ACACTTTAGAACAT   TCTT
                                          _____
GAM1372  LOC139793 3'  TGTGAAACTTTATTGAGAGAA  35330          ACCAA
                                TGTGAAATTTTGT    AGAA
                                |||||||||||||    ||||
                                ACACTTTGAAATA    TCTT
                                       ACTC_
GAM1372  LOC145288 5'  TGCGGAATGACCAAAGAAA   35331     AAATTT  T
                                TGTG     TG ACCAAAGAAA
                                ||||     || ||||||||||
                                ACGC     AC TGGTTTCTTT
                                  CTT___  _
GAM1372  LOC150397 3'  TGTGGAACTTTGTACTTTTAGA 35332     A       CAA_
              A                  TGTG AATTTTGTAC   AGAA
                                |||| ||||||||||   ||||
                                ACAC TTGAAACATG   TCTT
                                  C        AAAA
GAM1372  LOC220963 3'  TGTGAAATTTTGCTATGAGAAA 35333          ACCAA
              A                  TGTGAAATTTTGT    AGAAAA
                                |||||||||||||    ||||||
                                ACACTTTAAAACG    TCTTTT
                                       ATAC_
GAM1372  LOC90038  3'  TGTAAAATTTTGTAATGGGAGA 35334          CCAA_
                                TGTGAAATTTTGTA    AGA
                                |||||||||||||    |||
```

```
                                ACATTTTAAAACAT    TCT
                                      TACCC
GAM1373 ACVRL1   5' ACGGCGGGCTGGGGTCCGGCGC 35337    A  AC  GC____
            GG                  ACG GCG  GC    CCGGCGCGG
                                ||| |||  ||    |||||||||
                                TGC CGC  CG    GGCCGCGCC
                                 _  C_  ACCCCA
GAM1373 ARNTL    5' CGGCGGCGGTGAGTCCGGCGCG 35338   A  A  ACGCGC
            G                   CG CG GCG    CCGGCGCGG
                                || || |||    |||||||||
                                GC GC CGC    GGCCGCGCC
                                 C  _  CACTCA
GAM1373 ATP11A   3' CGGCGGGCGGAGCTGCAGTGCG 35339   A  A  AC  GCC  C
            G                   CG CG GCG  GC  CGG GCGG
                                || || |||  ||  ||| ||||
                                GC GC CGC  CG  GTC CGCC
                                 C  C  CT  AC_  A
GAM1373 BACE     5' CGGCGGGCGGCGGCGCG    35340   A  AC  CC
                                CG GCG  GCG  CGGCGCG
                                || |||  |||  |||||||
                                GC CGC  CGC  GCCGCGC
                                 _  C_  C_
GAM1373 BACE     5' CGGCGGGCGGCGGCGCG    35340   A  AC  CC
                                CG GCG  GCG  CGGCGCG
                                || |||  |||  |||||||
                                GC CGC  CGC  GCCGCGC
                                 _  C_  C_
GAM1373 BSG      3' CGGCGGCGGCGCAGACGCG   35342   A  A  AC   CC
                                CG CG GCG  GCGC  GGCGCG
                                || || |||  ||||  ||||||
                                GC GC CGC  CGCG  CTGCGC
                                 C  _  __   T_
GAM1373 BSG      3' CGGCGGCGGCGCAGACGG    35341   A  A  AC   CC   C
                                CG CG GCG  GCGC  GGCG G
                                || || |||  ||||  |||| |
                                GC GC CGC  CGCG  CTGC C
                                 C  _  __   T_   A
GAM1373 DSCAM    5' CGCGAGCGACGCGCCGG    35343   A         C
                                CG CGAGCGACGCGCC GG
                                || ||||||||||||| ||
                                GC GCTCGCTGCGCGG CC
                                 _         _
GAM1373 DVL3     5' CGGCGGCGGCGCGCGGCGCGG  35344   A  A  A   CC
                                CG CG GCG CGCGC  GGCGCGG
                                || || ||| |||||  |||||||
                                GC GC CGC GCGCG  CCGCGCC
                                 C  _  C    __
GAM1373 E2F1     5' GACAGGCGGCGGCGGCGGCGCG 35345    A  A C  C_
            G                   GACG GCG CG GC  CGGCGCGG
                                |||| ||| || ||  ||||||||
```

```
                                CTGT CGC GC CG  GCCGCGCC
                                  C   C  _  CC
GAM1373  ELK4     5'  GAGCGACGCCGCGCGCGG    35346         _  CCG
                                GAGCGACGC GC   GCGCGG
                                ||||||||| ||   ||||||
                                CTCGCTGCG CG   CGCGCC
                                    G  ____
GAM1373  ELK4     5'  GAGCGACGCCGCGCGCGG    35346         _  CCG
                                GAGCGACGC GC   GCGCGG
                                ||||||||| ||   ||||||
                                CTCGCTGCG CG   CGCGCC
                                    G  ____
GAM1373  EN2      5'  CGCCGGCCGCGCTCGGCGCGG  35347    A  A  GA    C
                                CG CG GC  CGCGC CGGCGCGG
                                || || ||  ||||| ||||||||
                                GC GC CG  GCGCG GCCGCGCC
                                 G  _  __    A
GAM1373  FKBP1A   5'  CGGGCGGCGCGACGGGCGG   35348    A   A    CC   C
                                CG GCG CGCG  CGG GCGG
                                || ||| ||||  ||| ||||
                                GC CGC GCGC  GCC CGCC
                                 C   C    T_  _
GAM1373  FKBP1A   5'  CGGGCGGCGCGACGGGCGG   35348    A   A    CC   C
                                CG GCG CGCG  CGG GCGG
                                || ||| ||||  ||| ||||
                                GC CGC GCGC  GCC CGCC
                                 C   C    T_  _
GAM1373  FOXG1B   5'  CGGCGGCGGCGCGGGAGCG   35349    A  A   A    CCC  C
                                CG CG GCG CGCG   GG GCG
                                || || ||| ||||   || |||
                                GC GC CGC GCGC   CC CGC
                                 C  _   C    ___  T
GAM1373  FOXG1B   5'  CGGCGCGCGGGCGGCGCG    35350    A   A    CC
                                CG GCG CGCG  CGGCGCG
                                || ||| ||||  |||||||
                                GC CGC GCGC  GCCGCGC
                                 _   _    CC
GAM1373  GNB2     5'  CGGCGGCGGCGGCGGCGGCGCG 35351    A  A   A  C  C_
           G                     CG CG GCG CG GC  CGGCGCGG
                                || || ||| || ||  ||||||||
                                GC GC CGC GC CG  GCCGCGCC
                                 C  _   C  _  CC
GAM1373  GPC1     5'  CGGCGGCGGCGGCGGCGCG   35353    A   A  C  C_
                                CG GCG CG GC  CGGCGCG
                                || ||| || ||  |||||||
                                GC CGC GC CG  GCCGCGC
                                 _   C  _  CC
GAM1373  GPC1     5'  CGGCGGCGGCGCGGGGCGCG  35352    A  A   A   CCC
                                CG CG GCG CGCG   GGCGCG
                                || || ||| ||||   ||||||
```

```
                                GC GC CGC GCGC   CCGCGC
                                 C  _  C   C__
GAM1373 HDAC4    5' CGGCGGCGGCGGCGGCGCG   35353    A  A  C  C_
                                CG GCG CG GC  CGGCGCG
                                || ||| || ||  |||||||
                                GC CGC GC CG  GCCGCGC
                                 _  C  _  CC
GAM1373 HK2      5' CGGCGAGGGTGCGCCCGGCTGG 35354    A   C___      GC
                                CG GCGA   GCGCCCGGC  GG
                                || ||||   |||||||||  ||
                                GC CGCT   CGCGGGCCG  CC
                                 _   CCCA       A_
GAM1373 IGFBP2   5' CGGCAGCGCGGCGCGG     35355    A  AC   CC
                                CG GCG  GCGC  GGCGCGG
                                || |||  ||||  |||||||
                                GC CGT  CGCG  CCGCGCC
                                 _  __   __
GAM1373 ISL1     5' CGGCGGCGGCAGACTCGGCGCG 35356    A  A   A  C  C
             G                   CG CG GCG CG GC CGGCGCGG
                                || || ||| || || ||||||||
                                GC GC CGC GT TG GCCGCGCC
                                 C  _  C  C  A
GAM1373 JAG2     5' CGGCGGCGGCGGCGGCGCG   35353    A  A  C  C_
                                CG GCG CG GC  CGGCGCG
                                || ||| || ||  |||||||
                                GC CGC GC CG  GCCGCGC
                                 _  C  _  CC
GAM1373 KCNN2    5' CGACAGCGGCGAGGAGGTGCGG 35357     G   AC   CCC_  C
                                CGAC AGCG  GCG   GG GCGG
                                |||| ||||  |||   || ||||
                                GCTG TCGC  CGC   CC CGCC
                                  _   __  TCCT  A
GAM1373 KLF4     5' CGGCGGCGCAGGGCGCGG   35358    A  AC   CC
                                CG GCG  GCGC  GGCGCGG
                                || |||  ||||  |||||||
                                GC CGC  CGCG  CCGCGCC
                                 _  __   TC
GAM1373 MSI1     5' CGCGGGCGGCGCGGGCAGCGG  35359    A  A   A   CCC  _
                                CG CG GCG CGCG   GGC GCGG
                                || || ||| ||||   ||| ||||
                                GC GC CGC GCGC   CCG CGCC
                                 _ C  C   ___   T
GAM1373 NR2C2    5' CGGCGGGCGGCCCCCGGCGCGG 35360    A  A   AC  G
                                CG CG GCG  GC CCCGGCGCGG
                                || || |||  || ||||||||||
                                GC GC CGC  CG GGGCCGCGCC
                                 C  C  __  G
GAM1373 PRKY     5' GCGGCGCGGCAGCCGCGG    35361     A   CC   _
                                GCG CGCG  CGGC GCGG
                                ||| ||||  |||| ||||
```

```
                                CGC GCGC  GTCG CGCC
                                  C   C_   G
GAM1373 PSD     3' CGGACACCGCGTCCGGCGCGG 35362    AG A   C
                                CG  CG CGCG CCGGCGCGG
                                ||  || |||| |||||||||
                                GC  GT GCGC GGCCGCGCC
                                 CT  G   A
GAM1373 PTGS2   5' CGGCGGGCAGGGCGCGGCGCGG 35363    A A   AC   CC
                                CG CG GCG  GCGC  GGCGCGG
                                || || |||  ||||  |||||||
                                GC GC CGT  CGCG  CCGCGCC
                                 C  C   CC   __
GAM1373 RNTRE   5' CGGCCGAGCAGATCCGGCGCGG 35364    A_     ACGCGC
                                CG  CGAGCG     CCGGCGCGG
                                ||  ||||||     |||||||||
                                GC  GCTCGT     GGCCGCGCC
                                 CG     CTA___
GAM1373 RPL36A  5' GCGTGAGCGCTATCGGCGCGG  35365    AC_   C__
                                GCG   GCGC   CGGCGCGG
                                |||   ||||   ||||||||
                                CGC   CGCG   GCCGCGCC
                                  ACT    ATA
GAM1373 SMT3H1  5' CGCGAGCGGCGCGGGGAGGCGG 35366     A   CC____      III
           CGCGGC                AGCG CGCG     CGGCGCGG   C
                                |||| ||||     ||||||||   |
                                TCGC GCGC     GCCGCGCC   G
                                  C    CCCTCC       III
GAM1373 SNX9    5' CGGCTGGGCCCCGGCGCG    35367    A  GAC  G
                                CG GC   GC CCCGGCGCG
                                || ||   || |||||||||
                                GC CG   CG GGGCCGCGC
                                 _  ACC  _
GAM1373 SRM     5' CGGGCGGGCGGGCGGCGCGG   35368    A   AC   CC
                                CG GCG  GCG  CGGCGCGG
                                || |||  |||  ||||||||
                                GC CGC  CGC  GCCGCGCC
                                 C   C_   CC
GAM1373 SRM     5' CGGGCGGCGCGGGGCGCGG    35369    A   A    CCC
                                CG GCG CGCG   GGCGCGG
                                || ||| ||||   |||||||
                                GC CGC GCGC   CCGCGCC
                                 C   C    C__
GAM1373 TMEPAI  5' CGGCGCGGCGGCGCGGCGCGG  35370    A_   A  C  C
                                CG  GCG CG GC CGGCGCGG
                                ||  ||| || || ||||||||
                                GC  CGC GC CG GCCGCGCC
                                 CG   C  _  C
GAM1373 TMEPAI  5' CGGCGGCGCGGCGCGGGGCGCG 35371    A  A   AC   CC
           G                     CG CG GCG  GCGC  GGCGCGG
                                || || |||  ||||  |||||||
```

```
                                GC GC CGC  CGCG  CCGCGCC
                                 C  _  GC   CC
GAM1373 TSLP    5' CGAGCGACGCGCAGCCGGCG  35372          __
                                CGAGCGACGCGC  CCGGCG
                                ||||||||||||  ||||||
                                GCTCGCTGCGCG  GGCCGC
                                       TC
GAM1373 VAMP1   5' CGGCGAGGGACGCTGCGGCCGC 35373   A   C   _ _____  GCG
           GC                    G CGAG GACGC GC    CCG  C
                                | |||| ||||| ||    |||  |
                                C GCTC CTGCG CG    GGC  G
                                 C   C    A  CCIII  GCG
GAM1373 VAMP1   5' CGGCGAGGGACGCTGCGGCCGC 35373   A   C   _ _____  GCG
           GC                    G CGAG GACGC GC    CCG  C
                                | |||| ||||| ||    |||  |
                                C GCTC CTGCG CG    GGC  G
                                 C   C    A  CCIII  GCG
GAM1373 WEE1    5' GCGGCAGCGGCGGCGCGG   35374    A _  CC
                                GCG C GCG  CGGCGCGG
                                ||| | |||  ||||||||
                                CGC G CGC  GCCGCGCC
                                  C T  C_
GAM1373 ZNF219  5' CGGCGGGCCGGCGGCGCG   35375   A  ACGC  __
                                CG GCG   GCC  CGGCGCG
                                || |||   |||  |||||||
                                GC CGC   CGG  GCCGCGC
                                 _  C___  CC
GAM1373 A4GALT  5' CGGGCGGCGCGCCCACG    35376   A  A     G
                                CG GCG CGCGCCCG CG
                                || ||| ||||||| ||
                                GC CGC GCGCGGGT GC
                                 C  C      _
GAM1373 calmin  5' CGCGGGCGGCGGGCGC     35377   A  A  AC  CCC
                                CG CG GCG  GCG  GGCGC
                                || || |||  |||  |||||
                                GC GC CGC  CGC  CCGCG
                                 _ C  __  ___
GAM1373 CHK     5' CGACAGGCGGCCGAGGAGGCGC 35378    A  ACGC  C____
           GG                    GACG GCG   GCC    GGCGCGG
                                ||||  |||   |||    |||||||
                                CTGT CGC   CGG    CCGCGCC
                                  C  ____  CTCCT
GAM1373 DC-TM4F2 5' CGGCGGCGGCAGCGGCGGCGCG 35379   A  A  A _  CC
           G                     CG CG GCG C GCG  CGGCGCGG
                                || || ||| | |||  ||||||||
                                GC GC CGC G CGC  GCCGCGCC
                                 C  _  C T  C_
GAM1373 DKFZp434F054 5' GAGCGGCGCAGTGGCGCGG  35380     AC   CC_
                                GAGCG  GCGC  GGCGCGG
                                |||||  ||||  |||||||
```

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                                CTCGC  CGCG   CCGCGCC
                                  __    TCA
GAM1373  DKFZp547C176 5'  CGGCGAGCGACGCGCTCGGTCC 35381    A         C   CG_
            CGG                    CG CGAGCGACGCGC CGG   CGG
                                || ||||||||||| |||   |||
                                GC GCTCGCTGCGCG GCC   GCC
                                 C          A   AGG
GAM1373  GABARAP   5'  CGGCGGCGACGCGCGGGCG   35382    A  A       CC  C
                                CG CG GCGACGCGC  GG GCG
                                || || |||||||||  || |||
                                GC GC CGCTGCGCG  CC CGC
                                 C  _       __  _
GAM1373  H3F3A    5'  GAGAGCGACGGCGGCGCGG   35384    C       C  CC
                                GA GAGCGACG GC  GGCGCGG
                                || |||||||| ||  |||||||
                                CT CTCGCTGC CG  CCGCGCC

                                 _      _  __
GAM1373  H3F3A    5'  CGACGGCGGCGCGGCG      35383      A   AC    CC
                                CGACG GCG  GCGC  GGCG
                                ||||| |||  ||||  ||||
                                GCTGC CGC  CGCG  CCGC

                                   _  __    __
GAM1373  KIAA0215  5'  CGGCGGCGGCTGAGGCGGCGCG 35385    A   A  C  C____
            G                    CG GCG CG GC    CGGCGCGG
                                || ||| || ||    ||||||||
                                GC CGC GC CG    GCCGCGCC
                                 _  C  _  ACTCC
GAM1373  KIAA0637  5'  CGACGGCGGCGCGGGC      35386      A   AC    CC  C
                                CGACG GCG  GCGC  GG GC
                                ||||| |||  ||||  || ||
                                GCTGC CGC  CGCG  CC CG

                                   _  __    __  _
GAM1373  MGC15730  5'  CGGGCAGCGCGGAGAGCCGCGG 35387    A   A    CCC   _
                                CG GCG CGCG   GGC GCGG
                                || ||| ||||   ||| ||||
                                GC CGT GCGC   TCG CGCC
                                 C   C    CTC   G
GAM1373  MGC2817   5'  CGGCGCGGCCCGGCGC      35388    A   A  C
                                CG GCG CG GCCCGGCGC
                                || ||| || |||||||||
                                GC CGC GC CGGGCCGCG

                                   _   _  _
GAM1373  MGC4415   3'  GAGACGGCGCGTCCGGCGCGG  35389     _  A    C
                                GAG CG CGCG CCGGCGCGG
                                ||| || |||| |||||||||
                                CTC GC GCGC GGCCGCGCC
                                  T  C    A
GAM1373  RIS1      5'  GACGGCGGCTGGCTCGGCGCGG 35390      A   AC  __  C
                                GACG GCG  GC  GC CGGCGCGG
                                |||| |||  ||  || ||||||||
```

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                                CTGC CGC  CG  CG GCCGCGCC
                                  _  __ AC  A
GAM1373  SAST     5'  CGGCGGCGGCGGCGGCGCG   35353    A  A  C  C_
                                CG GCG CG GC  CGGCGCG
                                || ||| || ||  |||||||
                                GC CGC GC CG  GCCGCGC
                                 _  C  _  CC
GAM1373  SEC61A1  5'  CGGCAAGCGGCGCGGCGCG   35391    A    AC   CC
                                CG CGAGCG  GCGC  GGCGCG
                                || ||||||  ||||  ||||||
                                GC GTTCGC  CGCG  CCGCGC
                                 C     __   __
GAM1373  STK29    3'  GACGGGCGGCGCGGCCGCGG  35392     A  AC   CC  _
                                GACG GCG  GCGC  GGC GCGG
                                |||| |||  ||||  ||| ||||
                                CTGC CGC  CGCG  CCG CGCC
                                  C  __   __  G
GAM1373  TOB2     5'  CGGCGACGACGCGGGGATGGCG 35393    A    _  CC  C__
              G                  CG GCGACG CGC  GG   GCGG
                                || |||||| |||  ||   ||||
                                GC CGCTGC GCG  CC   CGCC
                                 _     T  CC  TAC
GAM1373  TOLLIP   5'  CGACAGTGACGCGCCGG     35394     G  C      C
                                CGAC AG GACGCGCC GG
                                |||| || |||||||| ||
                                GCTG TC CTGCGCGG CC
                                  _ A       _
GAM1373  LOC115219 5'  ACGATGGCCATGCTCGGCGCGG 35395     GCGA  C  C
                                ACGA   CG GC CGGCGCGG
                                ||||   || || ||||||||
                                TGCT   GT CG GCCGCGCC
                                  ACCG  A  A
GAM1373  LOC132617 5'  CGGCCGGCAGCCCGGCGCG   35396    A  GAC  _
                                CG GC   GC GCCCGGCGCG
                                || ||   || ||||||||||
                                GC CG   CG CGGGCCGCGC
                                 _  GC_  T
GAM1373  LOC149345 5'  GAGCGGCGCGGCCCGGCG    35397      A   _
                                GAGCG CGCG CCCGGCG
                                ||||| |||| |||||||
                                CTCGC GCGC GGGCCGC
                                   C   C
GAM1373  LOC151127 5'  CGACAGCTCGGCCCGGCGCGG  35398     G   GA  C
                                CGAC AGC  CG GCCCGGCGCGG
                                |||| |||  || ||||||||||
                                GCTG TCG  GC CGGGCCGCGCC
                                  _  A_  _
GAM1373  LOC151571 5'  CGGCCCGCGCGCGCCCGGCGTG 35399    ACGA  A        C
              G                  CG   GCG CGCGCCCGGCG GG
                                ||   ||| |||||||||| ||
```

```
                                GC    CGC GCGCGGGCCGC CC
                                 CGGG  _         A
GAM1373  LOC162022 5'  CGGTGAGGCCCGGCGCG     35400    AC   CGACGC
                                CG  GAG     GCCCGGCGCG
                                ||  |||     ||||||||||
                                GC  CTC     CGGGCCGCGC
                                 CA  _______
GAM1373  LOC196500 5'  CGCGGCGGCGCGACGACTGCGG 35401    A  A   A    CC   _
                                CG CG GCG CGCG  CGGC GCGG
                                || || ||| ||||  |||| ||||
                                GC GC CGC GCGC  GCTG CGCC
                                 _ _  C    T_   A
GAM1373  LOC57118  5'  CGACGAGCGCGGCGC       35402          ACGCGCC
                                CGACGAGCG      CGGCGC
                                |||||||||      ||||||
                                GCTGCTCGC      GCCGCG
                                               _______
GAM1373  LOC92405  5'  CGCGGGCGACGCGACGG     35403    A  A       CC
                                CG CG GCGACGCG  CGG
                                || || ||||||||  |||
                                GC GC CGCTGCGC  GCC
                                 _ C       T_
GAM1373  LOC93550  5'  CGGCCGGCGGCGGCAGCGCGG  35404    A_  A   AC   CC
                                CG  CG GCG  GCG  CGGCGCGG
                                ||  || |||  |||  ||||||||
                                GC  GC CGC  CGC  GTCGCGCC
                                 CG  _  ___  C_
GAM1374  FLJ20605  3'  TAAAAACATTTTTGCAGCTTTT 35407              AAA
                                TAAAAATATTTTTGTA   CTTTT
                                ||||||||||||||||   |||||
                                ATTTTTGTAAAAACGT   GAAAA
                                          C__
GAM1374  SGP28     3'  AAAAATATTTTTGTAAAA    35408
                                AAAAATATTTTTGTAAAA
                                ||||||||||||||||||
                                TTTTTTATAAAAACATTTT

GAM1374  LOC147639 5'  AAAATATTTTTGCAGCACTTTT 35409            AA
                                AAAATATTTTTGTA  ACTTTT
                                ||||||||||||||  ||||||
                                TTTTATAAAAACGT  TGAAAA
                                          CG
GAM1375  ADCY2     3'  GAGCAGATGCGGTTGGCG    35412          CC_
                                GAGCAGATGCG   GGCG
                                ||||||||||||  ||||
                                CTCGTCTACGC   CCGC
                                       CAA
GAM1375  ADRBK1    3'  GAGGGTGCGCCAACCCA     35414     CAGA      GCGC
                                GAG    TGCGCCG    ACCCA
                                |||    |||||||    |||||
```

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                                CTC   ACGCGGT   TGGGT
                                  CC__     _____
GAM1375 ADRBK1   3' GGGCAGATGGGGTCGCACCCAG 35413   A     CGCC _
                                G GCAGATG   GG CGCACCCAG
                                | |||||||   || |||||||||
                                C CGTCTAC   CC GCGTGGGTC
                                 C      C___  A
GAM1375 ADRBK2   3' GCAGATGCTGCTGGGACCAG  35415       _ C  CGCAC
                                GCAGATGC GC GG    CCAG
                                |||||||| || ||    ||||
                                CGTCTACG CG CC    GGTC
                                     A  A  CT___
GAM1375 CDK5R2   5' GAGCGGGGCCGGCGCCCA   35416    AGATGC      AC
                                GAGC    GCCGGCGC  CCA
                                ||||    ||||||||  |||
                                CTCG    CGGCCGCG  GGT
                                  CCC___      __
GAM1375 CHST1    5' GAGCAGCTGCAGCGCCCA   35417      A  GCC    AC
                                GAGCAG TGC   GGCGC  CCA
                                |||||| |||   |||||  |||
                                CTCGTC ACG   TCGCG  GGT
                                   G  ___    __
GAM1375 CYP19    3' GAGCAGATGACCAATAGCACC  35418       C    C_
                                GAGCAGATG GCCGG  GCACC
                                ||||||||| |||||  |||||
                                CTCGTCTAC TGGTT  CGTGG
                                     _    AT
GAM1375 CYP19    3' GAGCAGATGACCAATAGCACC  35418       C    C_
                                GAGCAGATG GCCGG  GCACC
                                ||||||||| |||||  |||||
                                CTCGTCTAC TGGTT  CGTGG
                                     _    AT
GAM1375 CYP21A2  3' GAGCAGATGGGACATCCGG   35419       ___ _
                                GAGCAGATG   CG CCGG
                                |||||||||   || ||||
                                CTCGTCTAC   GT GGCC
                                     CCT  A
GAM1375 EN1      3' GAGCAGATGCTTTCTCCCCCAG 35420       GCCGGCGCA
                                GAGCAGATGC       CCCAG
                                ||||||||||       |||||
                                CTCGTCTACG       GGGTC
                                     AAAGAGG__
GAM1375 FXYD6    3' GAGCAGATGGCCATGTGGCTCA 35421       C  ____  G
                                GAGCAGATG GCC    GGC CA
                                ||||||||| |||    ||| ||
                                CTCGTCTAC CGG    CCG GT
                                     _  TACA   A
GAM1375 HMG20A   3' AGCAGATGTCAGCATCC     35422       CGC    CA
                                AGCAGATG   CGGCG  CC
                                ||||||||   |||||  ||
```

```
                                TCGTCTAC  GTCGT  GG
                                    A__    A_
GAM1375 LMO4     5' GGCAGGCAGGCGCACCCA   35423   A   ATGC  C
                                G GCAG   GC GGCGCACCCA
                                | ||||   || ||||||||||
                                C CGTC   CG CCGCGTGGGT
                                _   ____  T
GAM1375 SIX1     5' AACGGCCGGCGCACTCA    35424     C       C
                                GATG GCCGGCGCAC CA
                                |||| |||||||||| ||
                                TTGC CGGCCGCGTG GT
                                  _       A
GAM1375 ZNF219   5' AGATGCGCCGGGCCCC     35425         C  A
                                AGATGCGCCGG GC CCC
                                |||||||||| || |||
                                TCTACGCGGCC CG GGG
                                      _ _
GAM1375 ZNF38    5' GCAATGCTCCTGCACCCAG   35426    A   G  GGC
                                GCAG TGC CC   GCACCCAG
                                |||| ||| ||   ||||||||
                                CGTT ACG GG   CGTGGGTC
                                  _   A  A__
GAM1375 ARHGAP8  5' GCAGATGCCTCCACTCACCCAG 35427       G_   G G
                                GCAGATGC  CCG C CACCCAG
                                ||||||||  ||| | |||||||
                                CGTCTACG  GGT G GTGGGTC
                                    GA   _ A
GAM1375 C20orf36 3' GCAGGTGCGTCACACCCAG   35428    A   CCGG
                                GCAG TGCG   CGCACCCAG
                                |||| ||||   |||||||||
                                CGTC ACGC   GTGTGGGTC
                                  C   A___
GAM1375 DKFZP566B183 3' GATGGAGCTGCACCCAG    35429     CGCC  _
                                GATG   GGC GCACCCAG
                                ||||   ||| ||||||||
                                CTAC   TCG CGTGGGTC
                                  C___   A
GAM1375 DUSP14   3' GAGCAGATGCCGGCCCC    35430       GC    GCA
                                GAGCAGAT  GCCGGC   CCC
                                ||||||||  ||||||   |||
                                CTCGTCTA  CGGCCG   GGG
                                     __    ___
GAM1375 FLJ23506 3' GAGCAGATGGCTCCTGCCCCAG 35431       C  CGGC  A
                                GAGCAGATG GC   GC CCCAG
                                ||||||||| ||   || |||||
                                CTCGTCTAC CG   CG GGGTC
                                     _ AGGA  _
GAM1375 KIAA0544 3' ACAGTGGCTCTGGCGCACC   35432    A  C  C__
                                GCAG TG GC   GGCGCACC
                                |||| || ||   ||||||||
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                                TGTC AC CG   CCGCGTGG
                                  _ _ AGA
GAM1375 KIAA1522 3' GCAGGTGCAGCGTACACCCAG 35433     A   C  GC
                                GCAG TGCG CG  GCACCCAG
                                |||| |||| ||  ||||||||
                                CGTC ACGT GC  TGTGGGTC
                                  C   C  A_
GAM1375 MGC5139  5' AGCAGATACAGTGTGCCCAG  35434         CCGGCGCA
                                AGCAGATGCG       CCCAG
                                ||||||||||       |||||
                                TCGTCTATGT       GGGTC
                                     CACAC___
GAM1375 P24B     3' GAGCAGATCTGCAAAGTCACCC 35435        GC  CGGCG
            AG                    GAGCAGAT  GC    CACCCAG
                                |||||||  ||    |||||||
                                CTCGTCTA  CG    GTGGGTC
                                    GA  TTTCA
GAM1375 p25      3' GAGCAGGAGCGCCGGCTTCTCC 35436       AT      GCA__
            CCAG                   GAGCAG  GCGCCGGC    CCCAG
                                ||||||  ||||||||    |||||
                                CTCGTC  CGCGGCCG    GGGTC
                                   CT       AAGAG
GAM1375 PDZ-GEF1  3' GAGCAGATGGTTGCTACAC   35437         CGCCG  _
                                GAGCAGATG    GC GCAC
                                |||||||||    || ||||
                                CTCGTCTAC    CG TGTG
                                     CAA__  A
GAM1375 RALGPS1A  5' GAGCGGAGCCGGTGCCCA    35438     A  TGC    C  AC
                                GAGC GA   GCCGG GC  CCA
                                |||| ||   ||||| ||  |||
                                CTCG CT   CGGCC CG  GGT
                                  C ____    A __
GAM1375 SMAP1    5' GCAGAGTGAACGCACC      35439      _  CGCC
                                GCAGA TG    GGCGCACC
                                ||||| ||    ||||||||
                                CGTCT AC    TTGCGTGG
                                  C _____
GAM1375 TPD52L1   5' GAGCAGATGGCAGCTGCGCCCA 35440         C  C   _  A
            G                    GAGCAGATG GC GGC GC CCCAG
                                |||||||| || ||| || |||||
                                CTCGTCTAC CG TCG CG GGGTC
                                     _ _   A  C
GAM1375 LOC122728 3'  AGCAGATGGGCTGTGCGTTCAG 35441         C  CG_   CACC
                                AGCAGATG GC   GCG    CAG
                                |||||||| ||   |||    |||
                                TCGTCTAC CG   CGC    GTC
                                    C  ACA   AA__
GAM1375 LOC124944 5'  GACCGCTCGGCGCGCCCA    35442     G  _     A
                                GAT CGC CGGCGC CCCA
                                ||| ||| |||||| ||||
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                                CTG GCG GCCGCG GGGT
                                  _  A     C
GAM1375  LOC145368 3'  AGCAGATGGGCTGTGCGTTCAG 35441        C  CG_   CACC
                                AGCAGATG GC   GCG    CAG
                                |||||||| ||   |||    |||
                                TCGTCTAC CG   CGC    GTC
                                    C  ACA   AA__
GAM1375  LOC151571 5'  GAGGACCTGCTGGCGCACC   35443     CA   GC  C
                                GAG  GAT  GC GGCGCACC
                                |||  |||  || ||||||||
                                CTC  CTG  CG CCGCGTGG
                                  __   GA  A
GAM1375  LOC163682 5'  GAGCAGATGGGCCAGTGTCC   35444         C     CGCA
                                GAGCAGATG GCCGG    CC
                                ||||||||| |||||    ||
                                CTCGTCTAC CGGTC    GG
                                     C     ACA_
GAM1375  LOC165904 3'  GAGCAGATGGCTGGGAACACTC 35445         C  C  C_    C
            AG                    GAGCAGATG GC GG  GCAC CAG
                                |||||||| || ||  |||| |||
                                CTCGTCTAC CG CC  TGTG GTC
                                     _ A  CT    A
GAM1375  LOC168283 5'  GAGCAGATCGCCTCCCCA    35446        G    GGCGCA
                                GAGCAGAT CGCC     CCCA
                                |||||||| ||||     ||||
                                CTCGTCTA GCGG     GGGT
                                     _    AG_____
GAM1375  LOC220045 5'  GGCTGCACAGTTGCACCCAG   35447    A  AGA    CGGC
                                G GC   TGCGC    GCACCCAG
                                | ||   |||||    ||||||||
                                C CG   ACGTG    CGTGGGTC
                                 _ ____     TCAA
GAM1375  LOC221931 3'  GCAGGTGCGTCACCCCA     35448      A    CCGG   A
                                GCAG TGCG    CGC CCCA
                                |||| ||||    ||| ||||
                                CGTC ACGC    GTG GGGT
                                  C    A___   _
GAM1375  LOC253350 5'  GAGCAAATGCAGGGCAC     35449           CC
                                GAGCAGATGCG  GGCGC
                                ||||||||||  |||||
                                CTCGTTTACGT  CCGTG
                                      C_
GAM1375  LOC253936 5'  GAGCAGACGCGCAGCGACCCAG 35450            C    C
                                GAGCAGATGCGC GGCG ACCCAG
                                |||||||||||| |||| ||||||
                                CTCGTCTGCGCG TCGC TGGGTC
                                      _    _
GAM1375  LOC255271 5'  GCAGACGCGCCGAGGAGCGCCC 35451            C__  A
            AG                    GCAGATGCGCCGG   GC CCCAG
                                |||||||||||||   || |||||
```

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                                CGTCTGCGCGGCT  CG GGGTC
                                       CCT  C
GAM1376  AMPD3    5'  CGCCCGGGCCGCGGCGCCAAC  35454         _  A
                                CGCCCGGGCC CG CGCCGAT
                                |||||||||| || |||||||
                                GCGGGCCCGG GC GCGGTTG
                                      C  C
GAM1376  EBAG9    5'  CGCCTGGCGCCCGGCGTGAC  35455     C  _    A  CC
                                CGCC GG GCCCG CG  GAT
                                |||| || ||||| ||  |||
                                GCGG CC CGGGC GC  CTG
                                  A  G    C  A_
GAM1376  FBN1     5'  CGCCCGGGGCTCGGTCTG    35456        CCCGAC  _  A
                                CGCCCGGG     GC CG TCTG
                                ||||||||     || || ||||
                                GCGGGCCC     CG GC AGAC
                                     _______  A  C
GAM1376  GAMT     5'  CGCCCGGGCCCGCTCCCTG   35457          ACG  GAT
                                CGCCCGGGCCCG  CC  CTG
                                ||||||||||||  ||  |||
                                GCGGGCCCGGGC  GG  GAC
                                      GA_  ___
GAM1376  GAMT     5'  CGCCCGGGCCCGCTCCCTG   35457          ACG  GAT
                                CGCCCGGGCCCG  CC  CTG
                                ||||||||||||  ||  |||
                                GCGGGCCCGGGC  GG  GAC
                                      GA_  ___
GAM1376  HSF4     5'  CGCTCGGGCCCGGCCGCTG   35458    C      AC   AT
                                CGC CGGGCCCG  GCCG  CTG
                                ||| ||||||||  ||||  |||
                                GCG GCCCGGGC  CGGC  GAC
                                  A       __   __
GAM1376  INSM1    5'  GCCCGGGCGCGGCGGCTG    35459        C  A  CCGAT
                                GCCCGGGC CG CG    CTG
                                |||||||| || ||    |||
                                CGGGCCCG GC GC    GAC
                                     C  C  C____
GAM1376  ITGB1    5'  CGTTCGGGCCCGGTCCCCCGC  35460    CC      ACG  GA
                                CG  CGGGCCCG   CC  TCTGC
                                ||  ||||||||   ||  |||||
                                GC  GCCCGGGC   GG  GGGCG
                                  AA       CA_  __
GAM1376  KCNK1    5'  CGCCCGGGCCTGGCTCCCG   35461         CGAC  CGA
                                CGCCCGGGCC   GC   TCTG
                                ||||||||||   ||   ||||
                                GCGGGCCCGG   CG   GGGC
                                      AC__  A__
GAM1376  C20orf163 5'  CGCCCGGGCTACGATCTG   35462         CCGACGC
                                CGCCCGGGC      CGATCTG
                                |||||||||      |||||||
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                                GCGGGCCCG      GCTAGAC
                                     AT_____
GAM1376 C20orf29 5' CGTCCGGGCCCGCGGACTG   35463    C       A  CC  T
                                CG CCGGGCCCG CG  GA CTG
                                || ||||||||| ||  || |||
                                GC GGCCCGGGC GC  CT GAC
                                 A       _ __  _
GAM1376 DGS-A    3' GCCCAGGCCTGGGCCTCTGC  35464         CGAC   GA
                                GCCCGGGCC   GCC  TCTGC
                                |||||||||   |||  |||||
                                CGGGTCCGG   CGG  AGACG
                                     ACC_  __
GAM1376 JIK      5' CCCCCGGGCCCGGCGCCG    35465   G       A
                                C CCCGGGCCCG CGCCG
                                | ||||||||| |||||
                                G GGGCCCGGGC GCGGC
                                 G        C
GAM1376 KIAA0449 3' GCCTGGGCCTGTCAAGTCTGC 35466    C    CGACGC  _
                                GCC GGGCC     CGA TCTGC
                                ||| |||||     ||| |||||
                                CGG CCCGG     GTT AGACG
                                  A    ACA___   C
GAM1376 KIAA1643 5' CGCCCGGGCCCGGCTGA     35467          AC  C
                                CGCCCGGGCCCG  GC GA
                                ||||||||||||  || ||
                                GCGGGCCCGGGC  CG CT
                                     __  A
GAM1376 KIAA1691 3' CCCTTGGGCTGCCTGTCGGTCT 35468    __   __ GACGC  A
             G                   CCC  GGGC  CC    CG TCTG
                                ||| ||||  ||    || ||||
                                GGG  CCCG  GG    GC AGAC
                                  AA    AC  ACA__  C
GAM1376 KIAA1870 3' CCTGGGCTCAAGCGATCTGC  35469   C   C   C  C
                                CC GGGC CGA GC GATCTGC
                                || |||| ||| || |||||||
                                GG CCCG GTT CG CTAGACG
                                 A   A  _  _
GAM1376 MR       5' CGCCCGGGCCCTGCCGCCTGC  35470         GAC   A
                                CGCCCGGGCCC   GCCG TCTGC
                                ||||||||||   |||| |||||
                                GCGGGCCCGGG   CGGC GGACG
                                     A__   _
GAM1376 NCX      3' CCGGGCCCGGCGCTCCC     35471        A  CGA  TG
                                CCGGGCCCG CGC   TC  C
                                ||||||||| |||   ||  |
                                GGCCCGGGC GCG   AG  G
                                     C   ___  GT
GAM1376 OSBPL1A  5' CGCTCGAGCCCGCGTAACGTCT 35472    C       A  C__  A
             G                   CGC CGGGCCCG CG   CG TCTG
                                ||| |||||||| ||   || ||||
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                                GCG GCTCGGGC GC   GC AGAC
                                  A       _ ATT  _
GAM1376 OSBPL1A   5'  CGCTCGAGCCCGCGTAACGTCT 35472     C       A  C__  A
              G                    CGC CGGGCCCG CG   CG TCTG
                                |||  |||||||| ||   || ||||
                                GCG GCTCGGGC GC   GC AGAC
                                  A       _ ATT  _
GAM1376 OSBPL1A   5'  CGCCCGGGCCGCAGAGGTCTGC 35473          CGAC  C  __
                                CGCCCGGGCC    GC GA  TCTGC
                                ||||||||||    || ||  |||||
                                GCGGGCCCGG    CG CT  AGACG
                                      _____  T  CC
GAM1376 Rab11-FIP3 5'  CGCTCGGGCCCTGCTCTG    35474     C      GAC  CGA
                                CGC CGGGCCC   GC   TCTG
                                |||  |||||||   ||   ||||
                                GCG GCCCGGG   CG   AGAC
                                  A      A__  ___
GAM1376 SPIB      3'  GCTCAGGCCCGGCGGACTGC   35475    C      AC  C  T
                                GC CGGGCCCG  GC GA CTGC
                                ||  ||||||||  || || ||||
                                CG GTCCGGGC  CG CT GACG
                                 A       __  C  _
GAM1376 SPUVE     5'  CGCCCGGGCCGCGGCTCGCTGC 35476          _  AC  _  AT
                                CGCCCGGGCC CG  GC CG  CTGC
                                ||||||||||  ||  ||  ||  ||||
                                GCGGGCCCGG GC  CG GC  GACG
                                      C  __  A  __
GAM1376 LOC145981 5'  CCCGGGCCCGGCGCCCTG    35477          A   GAT
                                CCCGGGCCCG CGCC   CTG
                                ||||||||||  ||||   |||
                                GGGCCCGGGC GCGG   GAC
                                      C   ___
GAM1376 LOC201522 5'  CCCGGGCCCCGGATTTG     35478         GA  CC   C
                                CCCGGGCCC  CG  GAT TG
                                |||||||||  ||  ||| ||
                                GGGCCCGGG  GC  CTA AC
                                     __  __   A
GAM1376 LOC221787 5'  CCCGGGCCTGACCCGAGGTCTG 35479         C   G   __
                                CCCGGGCC GAC CCGA  TCTG
                                ||||||||  ||| ||||  ||||
                                GGGCCCGG CTG GGCT  AGAC
                                    A   _   CC
GAM1376 LOC254158 5'  GCCCGGGCGCGACGCGCTGC   35480         C     CGAT
                                GCCCGGGC CGACGC   CTGC
                                ||||||||  ||||||   ||||
                                CGGGCCCG GCTGCG   GACG
                                    C     C___
GAM1376 LOC255463 3'  CCTGGGCTCAGGCGATCTGC   35481    C   C  AC  C
                                CC GGGC CG  GC GATCTGC
                                ||  ||||  ||  ||  |||||||
```

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                                GG CCCG GT  CG CTAGACG
                                 A   A C_ _
GAM1376 LOC57109 5' CCCGGGCCCGGCGCCCTG   35477        A   GAT
                                CCCGGGCCCG CGCC  CTG
                                |||||||||| ||||  |||
                                GGGCCCGGGC GCGG  GAC
                                     C  ___
GAM1376 LOC90529 3' CCCCCGGGCCCGGCCACTG  35482  G      AC  AT
                                C CCCGGGCCCG  GCCG  CTG
                                | |||||||||  ||||  |||
                                G GGGCCCGGGC  CGGT  GAC
                                 G       __  __
GAM1376 LOC91050 5' CGCCCGGGCCCCGCGCG    35483        GA  _
                                CGCCCGGGCCC  CGC CG
                                ||||||||||  ||| ||
                                GCGGGCCCGGG  GCG GC
                                      __  C
GAM1376 LOC92095 3' GCCCGGGCTCGGGCTCTG   35484      C  AC  CGA
                                GCCCGGGC CG  GC  TCTG
                                |||||||| ||  ||  ||||
                                CGGGCCCG GC  CG  AGAC
                                     A  C_  ___
GAM1376 LOC92096 3' GCCCGGGCTCGGGCTCTG   35484      C  AC  CGA
                                GCCCGGGC CG  GC  TCTG
                                |||||||| ||  ||  ||||
                                CGGGCCCG GC  CG  AGAC
                                     A  C_  ___
GAM1376 LOC92181 5' CGTCCGGGCCCGCCGCCG   35485  C      A
                                CG CCGGGCCCG CGCCG
                                || |||||||| |||||
                                GC GGCCCGGGC GCGGC
                                 A       G
GAM1377 NQO1    3' GTATAGATCAGAAATAAAGTAT 35488       _   TC_
                                GTATAGAT AGGG  GAGTAT
                                |||||||| ||||  ||||||
                                CATATCTA TCTT  TTCATA
                                     G   TAT
GAM1377 MGC16332 3' GTAGAGATAGGGGGCAGGT  35489    T      T_  A
                                GTA AGATAGGG  CG GT
                                ||| ||||||||  || ||
                                CAT TCTATCCC  GT CA
                                  C       CC  C
GAM1377 LOC90750 3' ATATAGATGGGGAAAAATCC  35490       A  TC  T
                                GTATAGAT GGG  GAG ATCC
                                |||||||| |||  ||| ||||
                                TATATCTA CCC  TTT TAGG
                                     _  CT  _
GAM1378 DGKE    3' TTACGTGTCTGAATAA      35493         T  C
                                TTACGTGTCT GA GTAG
                                |||||||||| || ||||
```

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                                AATGCACAGA CT TATT
                                      _ _
GAM1378 HYAL4    5' TTACGTATCTTCTGCTTTAGTG 35494          __ ACG
                                TTACGTGTCT TG  TAGTG
                                |||||||||| ||  |||||
                                AATGCATAGA AC  ATCAC
                                     AG GAA
GAM1378 PKIG     3' TTACAGTGTCTTGAAAGTG  35495    _      CGT
                                TTAC GTGTCTTGA  AGTG
                                |||| |||||||||  ||||
                                AATG CACAGAACT  TCAC
                                  T       T__
GAM1378 SYT4     3' TTACATGTTTAATACAGTG  35496       C  CG
                                TTACGTGT TTGA  TAGTG
                                |||||||| ||||  |||||
                                AATGTACA AATT  GTCAC
                                     _  AT
GAM1378 LOC221715 3' CGCTGTCTTGATGTAGTG  35497   _     C
                                CG TGTCTTGA GTAGTG
                                || |||||||| ||||||
                                GC ACAGAACT CATCAC
                                 G      A
GAM1379 CD34     3' GCTTTCCCCCGTCACACGTTT 35500   CC  A  C
                                GC  TCCC CCG CGCGCGTTT
                                ||  |||| ||| |||||||||
                                CG  AGGG GGC GTGTGCAAA
                                 AA   _  A
GAM1379 FOLH1    5' CAGTTTCTCCACCACAGCAGT 35501    CCC _    C  C
                                CAG  TC CCACCGC GCG GT
                                |||  || ||||||| ||| ||
                                GTC  AG GGTGGTG CGT CA
                                 AA_ A     T  _
GAM1379 KLF7     3' CAGCCCCCTGCCTCATGGCGTT 35502       CCACC  GC___
           T                     CAGCCCTC   GCC   GCGTTT
                                ||||||||   |||   ||||||
                                GTCGGGGGG   CGG   CGCAAA
                                     A____  AGTAC
GAM1379 LRRC2    5' GCCTGCCCGCCGCGGCTGTTT 35503    CT  A  C GC
                                GCC  CCC CCGC GC  GTTT
                                |||  ||| |||| ||  ||||
                                CGG  GGG GGCG CG  CAAA
                                 AC  C   C  A_
GAM1379 PRKY     3' GCTTCTCACTGCACACATTT  35504   CC C  C  C
                                GC  TC CAC GC GCGCGTTT
                                ||  || ||| || ||||||||
                                CG  AG GTG CG TGTGTAAA
                                 A_  A  A  _
GAM1379 RLF      3' AGCCCTCCCACCCTGGGACC  35505         _____
                                AGCCCTCCCACC    GCC
                                ||||||||||||    |||
```

```
                                TCGGGAGGGTGG    TGG
                                      GACCC
GAM1379 SOX4     5' GCTCTCTCACCGCGCTGCAGTT 35506   C  C    C _ _
             T                    GC CTC CACCGC GC GC GTTT
                                  || ||| |||||| || || ||||
                                  CG GAG GTGGCG CG CG CAAA
                                   A  A    _ A  T
GAM1379 AWP1     5' GCCCCTCCGTCCGCTGTTT   35507     CCCA  _   GC
                                  GCCCT   CCG CCGC  GTTT
                                  |||||   ||| ||||  ||||
                                  CGGGG   GGC GGCG  CAAA
                                     A___   A   A_
GAM1379 FLJ10110 5' CAGCCCTCGCCGCCGCCG    35508        _ A
                                  CAGCCCTC CC CCGCCG
                                  |||||||| || ||||||
                                  GTCGGGAG GG GGCGGC
                                       C  C
GAM1379 KIAA0087 3' CAGCCCTTCCAGCTGTCGT   35509       C   CC  CGCG
                                  CAGCCCT CCA  GC   CGT
                                  ||||||| |||  ||   |||
                                  GTCGGGA GGT  CG   GCA
                                      A  __  ACA_
GAM1379 KIAA1387 5' GCTCTCCCGCCGCCGCGGT   35510   C    A      C
                                  GC CTCCC CCGCCGCG GT
                                  || ||||| |||||||| ||
                                  CG GAGGG GGCGGCGC CA
                                   A    C      _
GAM1379 TTYH2    3' CAGCCCCCCACTGCAGAGC   35511       T    C  CGC
                                  CAGCCC CCCAC GC   GC
                                  |||||| ||||| ||   ||
                                  GTCGGG GGGTG CG   CG
                                     _    A  TCT
GAM1379 LOC145694 5' CAGCCGTCCCGCATGCGCGTTT 35512      C   ACC  C_
                                  CAGCC TCCC   GC  GCGCGTTT
                                  ||||| ||||   ||  ||||||||
                                  GTCGG AGGG   CG  CGCGCAAA
                                     C   ___  TA
GAM1379 LOC158288 5' AGCGCTTCTTGCCTGACACGTT 35513    C  CCCACC  __
             T                    AGC CT     GCC  GCGCGTTT
                                  ||| ||     |||  ||||||||
                                  TCG GA     CGG  TGTGCAAA
                                    C  AGAA__   AC
GAM1379 LOC222112 5' GCCCCTCCCACTGCTGCG    35514     _    C  C
                                  GCCC TCCCAC GC GCG
                                  |||| |||||| || |||
                                  CGGG AGGGTG CG CGC
                                    G     A  A
GAM1379 LOC255037 3' CAGTCCTCCCACTCTGCGTGTT 35515    C      CGCC   C
                                  CAG CCTCCCAC    GCG GTT
                                  ||| ||||||||    ||| |||
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                                GTC GGAGGGTG   CGC CAA
                                  A      AGA_  A
GAM1379  LOC255736 5'  CAGCCTTTCCACCGCCGC    35516      CTC
                                CAGCC  CCACCGCCGC
                                |||||  ||||||||||
                                GTCGG  GGTGGCGGCG
                                   AAA
GAM1380  ADAR    3'  TAGCAAACACAAAGGGAAAGGA 35519       T   A_   A
           AA                    TGGCAAAT TAGA  GAAA GAAA
                                |||||||| ||||  |||| ||||
                                ATCGTTTG GTTT  CTTT CTTT
                                     T   CC   C
GAM1380  ADAR    3'  TAGCAAACACAAAGGGAAAGGA 35519       T   A_   A
           AA                    TGGCAAAT TAGA  GAAA GAAA
                                |||||||| ||||  |||| ||||
                                ATCGTTTG GTTT  CTTT CTTT
                                     T   CC   C
GAM1380  ADAR    3'  TAGCAAACACAAAGGGAAAGGA 35519       T   A_   A
           AA                    TGGCAAAT TAGA  GAAA GAAA
                                |||||||| ||||  |||| ||||
                                ATCGTTTG GTTT  CTTT CTTT
                                     T   CC   C
GAM1380  AKAP2   5'  GGCAGGGGAAAGAGGAAAGAAA 35520     AATTT_  A   A
           A                     GGCA     AGA GAAA GAAAA
                                ||||     ||| |||| |||||
                                CCGT     TCT CTTT CTTTT
                                  CCCCTT  C   _
GAM1380  AP1S1   3'  TGGCAAGGTTAGAAAAAA    35521      AT
                                TGGCAA  TTAGAAGAAA
                                ||||||  ||||||||||
                                ACCGTT  AATCTTTTTT
                                   CC
GAM1380  BACE    3'  GCAAATTTAGAAATTGAAAA   35522          AAAA
                                GCAAATTTAGAAG   GAAAA
                                ||||||||||||   |||||
                                CGTTTAAATCTTT   CTTTT
                                       AA__
GAM1380  BACE    3'  GCAAATTTAGAAATTGAAAA   35522          AAAA
                                GCAAATTTAGAAG   GAAAA
                                ||||||||||||   |||||
                                CGTTTAAATCTTT   CTTTT
                                       AA__
GAM1380  BAZ2A   3'  TAGCAAATAAAACAGAAAAGAA 35523       TTAGA
           AA                    TGGCAAAT    AGAAAAGAAAA
                                ||||||||    ||||||||||
                                ATCGTTTA    TCTTTTCTTTT
                                     TTTTG
GAM1380  BCL7B   3'  GCAGATTTCAAAGAAAAG    35524     A   A
                                GCA ATTT GAAGAAAAG
                                ||| |||| |||||||||
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                                CGT TAAA TTTCTTTTC
                                  C   G
GAM1380 CD69     3' TGGCAAATTTCTCTAAAAAGA 35525         AGAA
                                TGGCAAATTT   GAAAAGA
                                ||||||||||   |||||||
                                ACCGTTTAAA   TTTTTCT
                                     GAGA
GAM1380 COL3A1   5' TGTGCAAAAAGGAGAAAAGAAA 35526   _   TTT  A
             A                   TG GCAAA   AG AGAAAAGAAAA
                                 || |||||   || ||||||||||
                                 AC CGTTT   TC TCTTTTCTTTT
                                  A    T__  C
GAM1380 CORO1C   3' TGGCAACATTAAAAAAGAAA  35527       ATTTAGA
                                TGGCAA      AGAAAAGAAA
                                ||||||      ||||||||||
                                ACCGTT      TTTTTTCTTT
                                    GTAA___
GAM1380 CTNNA2   3' TGGCACAACTAGAAGAGGAAA 35528      AAT      AAA
                                TGGCA   TTAGAAGA   GAAA
                                |||||   ||||||||   ||||
                                ACCGT   GATCTTCT   CTTT
                                   GTT      C__
GAM1380 GRIK3    3' TGGCAGCTTTAGAAACCCACAG 35529      AA      AAA__
             AA                   TGGCA  TTTAGAAG    AGAA
                                  |||||  ||||||||    ||||
                                  ACCGT  AAATCTTT    TCTT
                                     CG       GGGTG
GAM1380 HELLS    3' GCATTACTAGAAGAAAGGA   35530    AAT       A
                                GCA   TTAGAAGAAA GA
                                |||   |||||||||| ||
                                CGT   GATCTTCTTT CT
                                  AAT        C
GAM1380 HPSE     3' TGGAGACTCAGAAGGGAAGA  35531    CAA       AA
                                TGG   ATTTAGAAG  AAGA
                                |||   |||||||||  ||||
                                ACC   TGAGTCTTC  TTCT
                                  TC_        CC
GAM1380 HYAL3    3' TGGCAGCAGGGAAAAGAA    35532     AATT   AA
                                TGGCA    TAG  GAAAAGAA
                                |||||    |||  ||||||||
                                ACCGT    GTC  CTTTTCTT
                                   C____   C_
GAM1380 KIT      3' GCAAGTTGAAAGAAAAGAAAA 35533     AT  AG
                                GCAA  TT  AAGAAAAGAAAA
                                ||||  ||  ||||||||||||
                                CGTT  AA  TTCTTTTCTTTT
                                  C_  CT
GAM1380 KPNA1    3' TGGCGCCAATAGAGGAAAGAAA 35534     AAATT    A   A
             A                    TGGC     TAGA GAAA GAAAA
                                  ||||     |||| |||| |||||
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                                ACCG    ATCT CTTT CTTTT
                                  CGGTT   C   _
GAM1380  KRT1    3'  TGGGAAACAGCAGAAAAGAAA  35535    C   TT  A
                                TGG AAAT  AG AGAAAAGAAA
                                ||| ||||  || ||||||||||
                                ACC TTTG  TC TCTTTTCTTT
                                  C   __  G
GAM1380  MAPK10  5'  GGCAAAGGAGAAGAAAA    35536      TTT
                                GGCAAA   AGAAGAAAA
                                ||||||   |||||||||
                                CCGTTT   TCTTCTTTT
                                   CC_
GAM1380  MPDZ    3'  GCAAGAAGAAAAGAA      35537    AATTT
                                GCA    AGAAGAAAAGAA
                                |||    ||||||||||||
                                CGT    TCTTCTTTTCTT
                                 _____
GAM1380  MTAP    3'  GCAAATTTAATAGGGGGAGAA  35538         A  AAA_
                                GCAAATTTAG AG    AGAA
                                |||||||||| ||    ||||
                                CGTTTAAATT TC    TCTT
                                      A  CCCC
GAM1380  MXI1    3'  AGCAAACTAGAAAAGA     35539        TAGA
                                GGCAAATT    AGAAAAGA
                                ||||||||    ||||||||
                                TCGTTTGA    TCTTTTCT
                                  ____
GAM1380  MXI1    3'  AGCAAACTAGAAAAGA     35539        TAGA
                                GGCAAATT    AGAAAAGA
                                ||||||||    ||||||||
                                TCGTTTGA    TCTTTTCT
                                  ____
GAM1380  NFRKB   5'  TGACTTCAGAAGAAGAG    35540     AAA       A
                                TGGC   TTTAGAAGAA AG
                                ||||   |||||||||| ||
                                ACTG   AAGTCTTCTT TC
                                  ___        C
GAM1380  PACE    3'  TGGCTAGGGTAGAAAAGAAAA  35541     AAATT   A__
                                TGGC    TAG   AGAAAAGAAAA
                                ||||    |||   ||||||||||||
                                ACCG    ATC   TCTTTTCTTTT
                                  _____  CCA
GAM1380  PCSK2   3'  GCCAATATGGGAGAAAAGAAA  35542    A   TTAGA
                                GC AAT    AGAAAAGAAA
                                || |||    ||||||||||
                                CG TTA    TCTTTTCTTT
                                 G   TACCC
GAM1380  PLCG2   3'  TGGCAGGCTTGAAGAAAA    35543      AA   A
                                TGGCA  TTT GAAGAAAA
                                |||||  ||| ||||||||
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                                ACCGT  GAA CTTCTTTT
                                  CC  _
GAM1380  PMX1     5'  GGCAAACAGAAGAAGAGA    35544        TT      A
                                GGCAAAT  AGAAGAA AGA
                                ||||||| ||||||| |||
                                CCGTTTG  TCTTCTT TCT
                                   __      C
GAM1380  PMX1     5'  GGCAAACAGAAGAAGAGA    35544        TT      A
                                GGCAAAT  AGAAGAA AGA
                                ||||||| ||||||| |||
                                CCGTTTG  TCTTCTT TCT
                                   __      C
GAM1380  PTGS2    3'  TGGCTAAAAGAAGAAAAGAAAA 35545      AAATTT
                                TGGC     AGAAGAAAAGAAAA
                                ||||     ||||||||||||||
                                ACCG     TCTTCTTTTCTTTT
                                  ATTT__
GAM1380  PTK2B    3'  GCAAACACATGAGAAAAGAA   35546       T  GA
                                GCAAAT TA  AGAAAAGAA
                                |||||| ||  |||||||||
                                CGTTTG GT  TCTTTTCTT
                                    T  AC
GAM1380  REGL     3'  GCAAATTTAGCAGAGGAGA    35547          A   AA
                                GCAAATTTAG AGA  AGA
                                |||||||||| |||  |||
                                CGTTTAAATC TCT  TCT
                                      G   CC
GAM1380  RFX5     3'  GCAAGACTGAGGAGAAAAGAAA 35548      _  T  A
                                GCAA ATT AG AGAAAAGAAA
                                |||| ||| || ||||||||||
                                CGTT TGA TC TCTTTTCTTT
                                  C   C  C
GAM1380  SHANK2   3'  TGACATTAAGAAGAAAGGAA   35549      AATTT       A
                                TGGCA    AGAAGAAA GAA
                                |||||    |||||||| |||
                                ACTGT    TCTTCTTT CTT
                                   AAT__       C
GAM1380  SSR4     5'  GCCTAGAGGAAAAGAAA     35550    AAAT    A
                                GC    TTAGA GAAAAGAAA
                                ||    ||||| |||||||||
                                CG    GATCT CTTTTCTTT
                                  _____     C
GAM1380  TCF3     3'  TGGCTTTAGAAGAATAAG     35551      AAA         _
                                TGGC   TTTAGAAGAA AAG
                                ||||   |||||||||| |||
                                ACCG   AAATCTTCTT TTC
                                  ___         A
GAM1380  TCIRG1   5'  GGCAGGACCAGAAGAGGAGA   35552      AAT       AA
                                GGCA   TTAGAAGA  AGA
                                ||||   |||||||  |||
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                                CCGT   GGTCTTCT  TCT
                                  CCT      CC
GAM1380  TDGF1    5'  TGGCAATTTAAGAAGAAAA   35553       A  T
                                TGGCAA TT AGAAGAAAA
                                |||||| || |||||||||
                                ACCGTT AA TCTTCTTTT
                                   A  T
GAM1380  TNC      5'  TGGGGATTTAGAAGCACAGA  35554    CAA       AAA
                                TGG   ATTTAGAAG   AGA
                                |||   |||||||||   |||
                                ACC   TAAATCTTC   TCT
                                  CC_       GTG
GAM1380  TRIM9    5'  TGGGGAAAAAGAAGAAAAGAAA 35555    CA  TTT
            A                    TGG  AA   AGAAGAAAAGAAAA
                                |||  ||   ||||||||||||||
                                ACC  TT   TCTTCTTTTCTTTT
                                  CC  TT_
GAM1380  UNRIP    5'  GGCAACAGGAAAAGAA     35556      ATT   AA
                                GGCAA   TAG  GAAAAGAA
                                ||||||   |||  ||||||||
                                CCGTT   GTC  CTTTTCTT
                                   ___   __
GAM1380  WNT5A    3'  TGGCATATTTGAGAAAAAGAAA 35557      A   A  AG
            A                    TGGCA ATTT GA  AAAAGAAAA
                                ||||| |||| ||  |||||||||
                                ACCGT TAAA CT  TTTTCTTTT
                                   A   _  CT
GAM1380  C5orf7   3'  GGCACAAGAGGAAAAGAAAA  35558     AATTT   A
                                GGCA    AGA GAAAAGAAAA
                                ||||    ||| ||||||||||
                                CCGT    TCT CTTTTCTTTT
                                  GT___   C
GAM1380  CHST3    3'  TAGCAAAAGAAAAGAA     35559      AATTTA
                                TGGCA    GAAGAAAAGAA
                                |||||    ||||||||||
                                ATCGT    TTTCTTTTCTT
                                   _______
GAM1380  CLL-1    3'  TGGCAAATCTTGGCCAGAAG  35560        _____
                                TGGCAAATT    TAGAAG
                                |||||||||    ||||||
                                ACCGTTTAG    GTCTTC
                                     AACCG
GAM1380  DKFZP434L1717 3'  TGGCCACAAGGAAAAGAAA   35561     AAATTTA  A
                                TGGC      GA GAAAAGAAA
                                ||||      || |||||||||
                                ACCG      TT CTTTTCTTT
                                  GTG____  C
GAM1380  DKFZP566J091 3'  GGCAAGAAAAGAAAAGAAAA  35562      ATTT
                                GGCAA   AGAAGAAAAGAAAA
                                |||||   ||||||||||||||
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                                CCGTT   TTTTCTTTTCTTTT
                                  C___
GAM1380 DNAJA2   3' GGCAAATGTGGAAAGAAAA   35563       TTA_
                                GGCAAAT   GAAGAAAA
                                |||||||   ||||||||
                                CCGTTTA   TTTCTTTT
                                   CACC
GAM1380 FLJ10687 3' GCCGAATTGTTCAAAGAAAAGA 35564   A_   TA__
          AAA                     GC  AATT   GAAGAAAAGAAAA
                                || ||||   ||||||||||||
                                CG  TTAA   TTTCTTTTCTTTT
                                 GC   CAAG
GAM1380 FLJ20085 3' GGCAAAGAGAGAAAGGAA   35565      TTT  A   A
                                GGCAAA  AGA GAAA GAA
                                ||||||  ||| |||| |||
                                CCGTTT  TCT CTTT CTT
                                   C__  _   C
GAM1380 FLJ22390 3' GGCTTGAGAAGAAAAG     35566    AAA  T
                                GGC  TT AGAAGAAAAG
                                |||  || ||||||||||
                                CCG  AA TCTTCTTTTC
                                  ___ C
GAM1380 FLJ22471 3' TGGCAGGTTTAGAAAATAAAG  35567      AA       _
                                TGGCA  TTTAGAAGA AAAG
                                |||||  ||||||||| ||||
                                ACCGT  AAATCTTTT TTTC
                                   CC       A
GAM1380 GW112    3' TGGACAATGAGAGAAAAGAAAA 35568    _  ATTT  A
                                TGG CAA   AGA GAAAAGAAAA
                                ||| |||   ||| ||||||||||
                                ACC GTT   TCT CTTTTCTTTT
                                  T  AC__  _
GAM1380 H_GS165L15.1 3' TGGAAATGGAGAAGAAAA   35569    C   TT
                                TGG AAAT  AGAAGAAAA
                                ||| ||||  |||||||||
                                ACC TTTA  TCTTCTTTT
                                  _   CC
GAM1380 HSA243666 3' TGGTAAGTTCAGAAGAAA   35570    C  A
                                TGG AA TTTAGAAGAAA
                                ||| || ||||||||||
                                ACC TT AAGTCTTCTTT
                                  A  C
GAM1380 HT010    3' TGGCAAAAAAGAAAAG     35571       TTTA
                                TGGCAAA   GAAGAAAAG
                                |||||||   |||||||||
                                ACCGTTT   TTTCTTTTC
                                   ____
GAM1380 KIAA0164 3' TGACAAACAGGGAAGGAAGA  35572       TTA   AA
                                TGGCAAAT  GAAG  AAGA
                                ||||||||  ||||  ||||
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                                ACTGTTTG  CTTC  TTCT
                                     TCC   C_
GAM1380  KIAA0455  3'  GCAAATTTACTCACTAAGAAAA 35573        GAAGAA
                                GCAAATTTA     AAGAAAA
                                |||||||||     |||||||
                                CGTTTAAAT     TTCTTTT
                                     GAGTGA
GAM1380  KIAA0478  3'  TGGCATGGAAGGAAAAGAA   35574      AATTTA   _
                                TGGCA     GAAG AAAAGAA
                                |||||     |||| |||||||
                                ACCGT     CTTC TTTTCTT
                                   AC____   C
GAM1380  KIAA0997  3'  TGCCAAGTTCAGAAGAAAA   35575   G   A
                                TG CAA TTTAGAAGAAAA
                                || ||| ||||||||||||
                                AC GTT AAGTCTTCTTTT
                                 G   C
GAM1380  KIAA1155  3'  GGCAAATTTATAGAGAAA    35576         GA_
                                GGCAAATTTA   AGAAA
                                ||||||||||   |||||
                                CCGTTTAAAT   TCTTT
                                      ATC
GAM1380  KIAA1243  3'  GCAAGCAAGAAAAGAAA    35577    AATTT  _
                                GCA    AG AAGAAAAGAAA
                                |||    || ||||||||||
                                CGT    TC TTCTTTTCTTT
                                  _____  G
GAM1380  KIAA1332  3'  TGACAAGGTGAAAGAAAGGAAA 35578       ATTTA      A
                                TGGCAA    GAAGAAA GAAA
                                ||||||    ||||||| ||||
                                ACTGTT    TTTCTTT CTTT
                                   CCAC_      C
GAM1380  KIAA1580  5'  TGGGAAATTCAAAAAGAAAAGA 35579    C        _
            AAA                   TGG AAATTTAGAA GAAAAGAAAA
                                ||| |||||||||| ||||||||||
                                ACC TTTAAGTTTT CTTTTCTTTT
                                  C         T
GAM1380  KIAA1906  3'  TGGCAAATCCCAGGGAAGAAAA 35580          A___
                                TGGCAAATTT    GAAGAAAA
                                ||||||||||    ||||||||
                                ACCGTTTAGG    CTTCTTTT
                                      GTCC
GAM1380  KSP37    3'  GCAAACTCCAGAAAGGAAG   35581        _    AA
                                GCAAATTT AGAAG  AAG
                                |||||||| |||||  |||
                                CGTTTGAG TCTTT  TTC
                                     G    CC
GAM1380  MGC2827  3'  TGGGGAAAAAGAGGAAAAGAAA 35582     CA  TTT   A
                                TGG  AA   AGA GAAAAGAAA
                                |||  ||   ||| |||||||||
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                                ACC  TT   TCT CTTTTCTTT
                                  CC  TT_   C
GAM1380  MGC5139   5'  GGCAGGAAAAAAAGGGAAGAAA 35583      AATTT    AA
             A                    GGCA    AGAAG  AAGAAAA
                                  ||||    |||||  |||||||
                                  CCGT    TTTTC  TTCTTTT
                                    CCTTT    CC
GAM1380  OLFM3     3'  TGTAAATTTAGAAGTTAAGA   35584    GC        AA
                                  TG  AAATTTAGAAG  AAGA
                                  ||  ||||||||||  ||||
                                  AC  TTTAAATCTTC  TTCT
                                   A_         AA
GAM1380  PALM2     5'  GGCAGGGGAAAGAGGAAAGAAA 35520      AATTT_   A    A
             A                    GGCA     AGA GAAA GAAAA
                                  ||||     ||| |||| |||||
                                  CCGT     TCT CTTT CTTTT
                                    CCCCTT   C   _
GAM1380  PCDH10    5'  TGGCAAATCCCAAAGAGGAAA  35585        TA    AAA
                                  TGGCAAATT  GAAGA   GAAA
                                  |||||||||  |||||   ||||
                                  ACCGTTTAG  TTTCT   CTTT
                                       GG    C__
GAM1380  PCDH10    5'  TGGCAAATCCCAAAGAGGAAA  35585        TA    AAA
                                  TGGCAAATT  GAAGA   GAAA
                                  |||||||||  |||||   ||||
                                  ACCGTTTAG  TTTCT   CTTT
                                       GG    C__
GAM1380  PRO0767   5'  GGCAGGAAGAAAAGAAA     35586      AATTTA
                                  GGCA     GAAGAAAAGAAA
                                  ||||     ||||||||||||
                                  CCGT     CTTCTTTTCTTT
                                    C_____
GAM1380  STRN3     3'  GGCAAAAGAAGGAAAGAAA   35587       TTT    A
                                  GGCAAA   AGAAG AAAGAAA
                                  ||||||   ||||| |||||||
                                  CCGTTT   TCTTC TTTCTTT
                                     ___     C
GAM1380  TRIP-Br2  3'  ACCATTGGAAGAAAAGAAAA   35588    AAAT  A
                                  GC    TT GAAGAAAAGAAAA
                                  ||    || ||||||||||||
                                  TG    AA CTTCTTTTCTTTT
                                   GT__  C
GAM1380  YAP1      3'  TAGCACTAGGAGGAAAAGAAAA 35589      AATTTA  A
                                  TGGCA     GA GAAAAGAAAA
                                  |||||     || ||||||||||
                                  ATCGT     CT CTTTTCTTTT
                                     GATC__  C
GAM1380  LOC112687 3'  GGCTTCAGGGAAGAAAAGAAAA 35590     AAATTTA
                                  GGC      GAAGAAAAGAAAA
                                  |||      ||||||||||||
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                                CCG      CTTCTTTTCTTTT
                                  AAGTCC_
GAM1380  LOC115648 3'  TGGGGAACACAAGAAAAGAA   35591     CAAATT  G
                                TGG     TA AAGAAAAGAA
                                |||     || ||||||||||
                                ACC     GT TTCTTTTCTT
                                  CCTT__  G
GAM1380  LOC118487 3'  GGCAAATCAGGAAGGAAAG   35592        TA   A
                                GGCAAATT  GAAG AAAG
                                ||||||||  |||| ||||
                                CCGTTTAG  CTTC TTTC
                                     TC   C
GAM1380  LOC119587 3'  TGGGAACAAAGAAAAGAAA   35593     CAAATTTA
                                TGG       GAAGAAAAGAAA
                                |||       ||||||||||||
                                ACC       TTTCTTTTCTTT
                                  CTTG____
GAM1380  LOC130355 5'  GGCAAGATTTAAGGAAAGAAAA 35594       _    GA  A
                                GGCAA ATTTA  AG AAAGAAAA
                                ||||| |||||  || ||||||||
                                CCGTT TAAAT  TC TTTCTTTT
                                   C    __ C
GAM1380  LOC145226 3'  TGGCAAATATTTTTAAAAAGAA 35595        TTAGAA
           A                     TGGCAAAT     GAAAAGAAA
                                |||||||     |||||||||
                                ACCGTTTA     TTTTTCTTT
                                     TAAAAA
GAM1380  LOC145314 3'  GCAAATTTAGAAAGTTGAAGA  35596           AA__
                                GCAAATTTAGAAG    AAGA
                                ||||||||||||    ||||
                                CGTTTAAATCTTT    TTCT
                                       CAAC
GAM1380  LOC145581 3'  TGGCAAATTTTTTCAGGAGAGA 35597        ____   A   AA
           GA                     TGGCAAAT    TTAG AGA  AGA
                                |||||||    |||| |||  |||
                                ACCGTTTA    AGTC TCT  TCT
                                     AAAA    C   C_
GAM1380  LOC146488 5'  TGGCATAAGAAAAGAA      35598       AATTTAG
                                TGGCA      AAGAAAAGAA
                                |||||      ||||||||||
                                ACCGT      TTCTTTTCTT
                                  A_______
GAM1380  LOC151094 3'  TGGCAAATCAGAAAAG      35599         TAGA
                                TGGCAAATT    AGAAAAG
                                |||||||||    |||||||
                                ACCGTTTAG    TCTTTTC
                                       ____
GAM1380  LOC169026 3'  TGGCAATTTAGAAACCAGAGAA 35600       A       AAA_
           A                     TGGCAA TTTAGAAG    AGAAA
                                ||||||| ||||||||    |||||
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                                ACCGTT AAATCTTT    TCTTT
                                   _       GGTC
GAM1380  LOC220513 3'  GCATTACTAGAAGAAAGGA    35530     AAT         A
                                GCA   TTAGAAGAAA GA
                                |||   |||||||||| ||
                                CGT   GATCTTCTTT CT
                                  AAT         C
GAM1380  LOC221975 5'  TGGCCTTTCGGAAGAAAAGA   35601      AAA  TA
                                TGGC   TT  GAAGAAAAGA
                                ||||   ||  ||||||||||
                                ACCG   AA  CTTCTTTTCT
                                  GA_  GC
GAM1380  LOC253981 3'  TGGCAAATTTGGAAGCCTGCCA 35602           A    AAA___
            GA                    TGGCAAATTT GAAG      AGA
                                |||||||||| ||||      |||
                                ACCGTTTAAA CTTC      TCT
                                      C    GGACGG
GAM1380  LOC254065 5'  GGCAAAATCCAGGGAAAGAA   35603        _    AA    A
                                GGCAAA TTTAG  GAAA GAA
                                |||||| |||||  |||| |||
                                CCGTTT AGGTC  CTTT CTT
                                   T    C_   _
GAM1380  LOC255360 5'  GGCAGAAGAAAGAGAAA     35604      AATTTA      _
                                GGCA      GAAGAAA AGAAA
                                ||||      ||||||| |||||
                                CCGT      CTTCTTT TCTTT
                                  _______       C
GAM1380  LOC90371  5'  TGATGAGGGAAGAAGAAAAGAA 35605     CAAATTT
                                TGG       AGAAGAAAAGAA
                                |||       ||||||||||||
                                ACT       TCTTCTTTTCTT
                                  ACTCCCT
GAM1380  LOC90957  3'  TGGCGACAGGAAAAGAAA    35606      AAATT   AA
                                TGGC     TAG  GAAAAGAAA
                                ||||     |||  |||||||||
                                ACCG     GTC  CTTTTCTTT
                                  CT___   __
GAM1381  CENPF     5'  TCTCGGGGACGGGAAAACGAC  35609    G    A   C C
                                TC CGGG GAC G GGAAAACGAC
                                || |||| ||| | ||||||||||
                                AG GCCC CTG C CCTTTTGCTG
                                 A   _  _ _
GAM1381  DFFA      5'  TCGCGGGAGGCCGGAGCGG    35610         A ___
                                TCGCGGGAG CC   GCGG
                                |||||||| ||   ||||
                                AGCGCCCTC GG   CGCC
                                      C  CCT
GAM1381  IRS2      3'  TCGAGGGAGCAGAAAACG     35611     C    GACC
                                TCG GGGA    GCGGAAAACG
                                ||| ||||    ||||||||||
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                                AGC CCCT   CGTCTTTTGC
                                  T  ____
GAM1381 KIAA1735 5' TCGCGGGAGAAAGCGGGAACG 35612        CC   AA
                                TCGCGGGAGA GCGG AACG
                                |||||||||| |||| ||||
                                AGCGCCCTCT CGCC TTGC
                                     TT   C_
GAM1381 NIP30   5' CGCGGGAGGCGAGACGA    35613       ACC   AAA
                                CGCGGGAG  GCGG  ACGA
                                |||||||| |||| ||||
                                GCGCCCTC  CGCT  TGCT
                                    ___   C__
GAM1381 NKX2C   3' TCGCGGAGGCCGCGGAAA   35614      G  A
                                TCGCGG AG CCGCGGAAA
                                |||||| || |||||||||
                                AGCGCC TC GGCGCCTTT
                                   _ C
GAM1381 LOC139046 5' CCGCGGGAGGATGTGCGGGGGG 35615       ACC__   AAAA
            CG                   TCGCGGGAG   GCGG   CG
                                |||||||||   ||||  ||
                                GGCGCCCTC   CGCC  GC
                                     CTACA  CCCC
GAM1382 EGLN2   5' TTACCTAGTACTGCC      35618         GGTA
                                TTACCTAGTAC   TGCT
                                ||||||||||   ||||
                                AATGGATCATG   ACGG
                                      ____
GAM1382 MAT2A   3' GCCTACCTGGGAATGCT    35619       AGTAC  T
                                GCTTACCT   GG ATGCT
                                ||||||||   || |||||
                                CGGATGGA   CC TACGA
                                    C____  T
GAM1382 PTP4A2  3' TAGCTTAGCAGGTATGCT   35620     TACC   C
                                TAGCT   TAGTA GGTATGCT
                                |||||   ||||| ||||||||
                                ATCGA   ATCGT CCATACGA
                                   ____   _
GAM1382 SYNGR1  3' AGCTTACCTGGTACCCT    35621       AGTAC   G
                                AGCTTACCT   GGTAT CT
                                |||||||||   ||||| ||
                                TCGAATGGA   CCATG GA
                                     _____   G
GAM1382 LGP1    3' TAGCTTGCCCAGTGCAC    35622      A    ACG
                                TAGCTT CCTAGT  GTAT
                                |||||| ||||||  ||||
                                ATCGAA GGGTCA  CGTG
                                   C   ___
GAM1382 LOC151201 3' TAGTGTACCTAGTCTGCT   35623    CT     ACGGTA
                                TAG  TACCTAGT    TGCT
                                |||  ||||||||    ||||
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                                ATC  ATGGATCA     ACGA
                                  AC       G_____
GAM1383  ADRB3    3'  AGCAGTAATAAGGGAACCAGA  35626          AA    CA
                                GGCAGTAATA  AGGGG  TAGA
                                ||||||||||  |||||  ||||
                                TCGTCATTAT  TCCCT  GTCT
                                      __     TG
GAM1383  AFP      5'  GGCAGTGGTGGAAGCACAA   35627       AATAAAA
                                GGCAGT      GGGGCATAG
                                ||||||      |||||||||
                                CCGTCA      CTTCGTGTT
                                   CCAC___
GAM1383  BTG2     3'  AGGCAGTAATAAAGGACCTGGA 35628           AA    ATA
                                AGGCAGTAATAA  GGGGC   GA
                                ||||||||||||  |||||   ||
                                TCCGTCATTATT  TCCTG   CT
                                      __     GAC
GAM1383  CYP4A11  3'  AGCAGTAATAGGAAACTAATAT 35629          AAA GG  ____
             AG                   GGCAGTAATA   G  GC    ATAG
                                ||||||||||   |  ||    ||||
                                TCGTCATTAT   C  TG    TATC
                                     C__ TT  ATTA
GAM1383  DRD2     3'  GGCAGTGAGGAGCATG      35630       AATAAA       A
                                GGCAGT      AGGGGCAT G
                                ||||||      |||||||| |
                                CCGTCA      TCCTCGTA C
                                   C_____       C
GAM1383  FBXL11   3'  AGGCAGAATGAAGACACATGGA 35631       T   AA    G    A
                                AGGCAG AAT  AAGG GCAT GA
                                |||||| |||  |||| |||| ||
                                TCCGTC TTA  TTCT TGTA CT
                                   _  C_   G    C
GAM1383  FBXL11   3'  GGCAGTCAGTGGGAGGCAAAAG 35632       AATAAAA     T_
             A                   GGCAGT      GGGGCA  AGA
                                ||||||      ||||||  |||
                                CCGTCA      CTCCGT  TCT
                                   GTCACC_     TT
GAM1383  IL1RN    3'  AGGCAGTGGCAAGAGGAG    35633        AA   A
                                AGGCAGT  TAA AGGGG
                                |||||||  ||| |||||
                                TCCGTCA  GTT TCCTC
                                    CC   C
GAM1383  KCNJ5    3'  AGGAAGTGACCCAGGGCATGGA 35634     C   A  AAAA      A
                                AGG AGT AT    GGGGCAT GA
                                ||| ||| ||    ||||||| ||
                                TCC TCA TG    TCCCGTA CT
                                  T   C  GG__      C
GAM1383  LANCL1   3'  AGGCAGTAATAGAAAGAGTAGA 35635           A     CA
                                AGGCAGTAATA AAGGGG  TAGA
                                |||||||||| ||||||  ||||
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                                TCCGTCATTAT TTTCTC  ATCT
                                      C     __
GAM1383  LOH11CR2A 3'  AGGCAGTGGAAGAAAAGACAT  35636       AATAA
                                AGGCAGT    AAGGGGCAT
                                |||||||    |||||||||
                                TCCGTCA    TTTTCTGTA
                                    CCTTC
GAM1383  MECP2    3'  AGGCAGAAATGGAAGGGG    35637      T   AA
                                AGGCAG AAT  AAGGGG
                                |||||| |||  ||||||
                                TCCGTC TTA  TTCCCC
                                   T   CC
GAM1383  PTBP1    3'  GGCGGTAGAAAGAGCACAGA   35638    A   ATAA
                                GGC GTA    AAGGGGCATAGA
                                ||| |||    ||||||||||||
                                CCG CAT    TTTCTCGTGTCT
                                  C   C___
GAM1383  PTBP1    3'  GGCGGTAGAAAGAGCACAGA   35638    A   ATAA
                                GGC GTA    AAGGGGCATAGA
                                ||| |||    ||||||||||||
                                CCG CAT    TTTCTCGTGTCT
                                  C   C___
GAM1383  PTEN     5'  AGGCAGTAGAAGGGGA      35639        ATAA     CAT
                                AGGCAGTA    AAGGGG   A
                                ||||||||    ||||||   |
                                TCCGTCAT    TTCCCC   T
                                    C___     ___
GAM1383  SLC7A8   3'  AGGTAGGATAAAAGGGG     35640     C  TA
                                AGG AG  ATAAAAGGGG
                                ||| ||  ||||||||||
                                TCC TC  TATTTTCCCC
                                  A  C_
GAM1383  SOX10    3'  AGACAGTAATGAGTTACAT    35641         AAA  GG
                                AGGCAGTAAT   AG  GCAT
                                ||||||||||   ||  ||||
                                TCTGTCATTA   TC  TGTA
                                      C__  AA
GAM1383  STK24    3'  AGGTGTACCAAAAGGGGCGTAG 35642     CA   A       A
                                AGG  GTA TAAAAGGGGC TAG
                                |||  ||| ||||||||||| |||
                                TCC  CAT GTTTTCCCCG ATC
                                  A_   G        C
GAM1383  TNF      3'  AGGGGGTAATAAAGGGA     35643     CA      A
                                AGG  GTAATAAA GGGG
                                |||  |||||||| ||||
                                TCC  CATTATTT CCCT
                                  CC       _
GAM1383  VAT1     3'  AGGCAGAGGTGAAAGCACATGG 35644       TAATAA   G   A
             A                   AGGCAG     AAGG GCAT GA
                                ||||||     |||| |||| ||
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                                TCCGTC     TTTC TGTA CT
                                   TCCAC_   G   C
GAM1383 ATP6V0A2 3' AGGCAGTAATGAAGATGG    35645         AA   _
                                AGGCAGTAAT  AAGG GG
                                ||||||||||  |||| ||
                                TCCGTCATTA  TTCT CC
                                     C_   A
GAM1383 C21orf45 3' GGCAGAATGGAGGACACAGA  35646      T   AAAA
                                GGCAG AAT   GGGGCATAGA
                                ||||| |||   ||||||||||
                                CCGTC TTA   TCCTGTGTCT
                                   _  CC__
GAM1383 DKFZP547E1010 5' AGGTGGTAACAAGAGCACAGA 35647     CA     AAA
                                AGG  GTAATA   GGGGCATAGA
                                |||  ||||||   ||||||||||
                                TCC  CATTGT   TCTCGTGTCT
                                  AC     ___
GAM1383 DKFZP547E1010 5' AGGTGGTAACAAGAGCACAGA 35647     CA     AAA
                                AGG  GTAATA   GGGGCATAGA
                                |||  ||||||   ||||||||||
                                TCC  CATTGT   TCTCGTGTCT
                                  AC     ___
GAM1383 DKFZp547I094 3' AGACAGTGGTAAGAGCAC    35648        AATAAA
                                AGGCAGT     AGGGGCAT
                                |||||||     ||||||||
                                TCTGTCA     TTCTCGTG
                                    CCA___
GAM1383 FLJ10922 3' AGCAGCAAGGAGGGGCGTAG   35649        TAAA     A
                                GGCAGTAA    AGGGGC TAG
                                ||||||||    |||||| |||
                                TCGTCGTT    TCCCCG ATC
                                    CC__     C
GAM1383 FLJ11078 3' AGGCAGTAGAGAAGTGAGATGG 35650        ATAA  _  C  A
          A                      AGGCAGTA    AAG GGG AT GA
                                ||||||||    ||| ||| || ||
                                TCCGTCAT    TTC CTC TA CT
                                    CTC_   A   _  C
GAM1383 FLJ12899 3' GGTAATAATAAGGCAT      35651    C      AAAG
                                GG AGTAATA    GGGCAT
                                || |||||||    ||||||
                                CC TTATTAT    TCCGTA
                                  A     _____
GAM1383 FLJ13456 3' AGGCAATGATAAAGGAA     35652        A    A
                                AGGCAGT ATAAA GGGG
                                ||||||| ||||| ||||
                                TCCGTTA TATTT CCTT
                                    C    _
GAM1383 KIAA0022 3' AGTCAGTAATGGACCACA    35653    G      AAAA   G
                                AG CAGTAAT    GGG CATA
                                || |||||||    ||| ||||
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                                TC GTCATTA   CCT GTGT
                                 A      ____  G
GAM1383  KIAA0171  3'  GGTAGTAAAAGGAACA     35654    C    TAA
                                GG AGTAA   AAGGGGCA
                                || |||||   ||||||||
                                CC TCATT   TTCCTTGT
                                 A    ___
GAM1383  KIAA1205  3'  GGCAGTGGGTGGGGGCCAGA  35655       AATAAAA    A
                                GGCAGT      GGGGC TAGA
                                ||||||      ||||| ||||
                                CCGTCA      CCCCG GTCT
                                   CCCAC__    _
GAM1383  MGC13138  3'  GGCAGTAAAAAGACA      35656        TAAA
                                GGCAGTAA    AGGGGCA
                                ||||||||    |||||||
                                CCGTCATT    TTTCTGT
                                   _____
GAM1383  MRPL20    3'  GCAGTAATGAGGCGGCAC    35657        AAA  _
                                GCAGTAAT   AGG GGCAT
                                ||||||||   ||| |||||
                                CGTCATTA   TCC CCGTG
                                     C__   G
GAM1383  PRKRIR    3'  AGGCAGTATATAAGAGTCATGG 35658        A A    G   A
              A                  AGGCAGTA TA AAGGG CAT GA
                                 |||||||| || ||||| ||| ||
                                 TCCGTCAT AT TTCTC GTA CT
                                      _ A    A   C
GAM1383  RAP140    3'  AGGCAGTAGTTAGGAATAG    35659        ATAAAAG   C
                                AGGCAGTA      GGG ATAG
                                ||||||||      ||| ||||
                                TCCGTCAT      TCC TATC
                                     CAA_____   T
GAM1383  LOC112868 3'  GGCAGTGTGGGGGACACAG    35660       AATAAAA
                                GGCAGT      GGGGCATAG
                                ||||||      |||||||||
                                CCGTCA      CCCTGTGTC
                                   CACC___
GAM1383  LOC123628 5'  AGGAGGAAGTAAAAGGGGTATG 35661     C  T  _       C  A
              GA                  AGG AG AA TAAAAGGGG AT GA
                                  ||| || || ||||||||| || ||
                                  TCC TC TT ATTTTCCCC TA CT
                                    _  C  C        A  C
GAM1383  LOC142927 5'  GTGGTAAAAGGAGCAAGCAGA  35662    AA         __
                                GT  TAAAAGGGGCA  TAGA
                                ||  ||||||||||  ||||
                                CA  ATTTTCCTCGT  GTCT
                                 CC          TC
GAM1383  LOC149706 5'  AGGCAGTAGCGGGGACAG     35663        ATAAAA   C
                                AGGCAGTA     GGGG ATAG
                                ||||||||     |||| ||||
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                                TCCGTCAT     CCCC TGTC
                                    CG____   _
GAM1383  LOC155435 3'  GGCAGTAAGAAAGAAC      35664        TAA
                                GGCAGTAA   AAGGGGC
                                ||||||||   |||||||
                                CCGTCATT   TTTCTTG
                                    C__
GAM1383  LOC164397 5'  GGCAGTAATCAAAGCAAAGA   35665        AAAAG    T
                                GGCAGTAAT    GGGCA AGA
                                |||||||||    ||||| |||
                                CCGTCATTA    TTCGT TCT
                                     GT___    T
GAM1383  LOC199704 3'  AGGTGTAATAAAAGTATCA    35666     CA        GGG
                                AGG  GTAATAAAAG   CA
                                |||  ||||||||||   ||
                                TCC  CATTATTTTC   GT
                                  A_         ATA
GAM1383  LOC199777 3'  AGATAGTAATAAAAACAGAATG 35667    GC         G  C  A
            GA                    AG  AGTAATAAAAG GG AT GA
                                ||  ||||||||||| || || ||
                                TC  TCATTATTTTT TC TA CT
                                 TA         G  T  C
GAM1383  LOC200933 3'  AGGCAGTTGTAAAATGGG     35668        AA    _
                                AGGCAGT  TAAAA GGG
                                |||||||  ||||| |||
                                TCCGTCA  ATTTT CCC
                                    AC    A
GAM1383  LOC204804 3'  GGGGGTGATAAGAGACACAG   35669    CA  A   AA
                                GG  GT ATA  AGGGGCATAG
                                ||  || |||  ||||||||||
                                CC  CA TAT  TCTCTGTGTC
                                 CC  C  __
GAM1383  LOC220846 3'  AGCAGTAATAAGGGAACCAGA  35626         AA    CA
                                GGCAGTAATA  AGGGG  TAGA
                                ||||||||||  |||||  ||||
                                TCGTCATTAT  TCCCT  GTCT
                                      __     TG
GAM1383  LOC257551 3'  AGGGGGTAATAAAGGGA     35643     CA       A
                                AGG  GTAATAAA GGGG
                                |||  |||||||| ||||
                                TCC  CATTATTT CCCT
                                  CC       _
GAM1383  LOC257601 3'  AGGGGGTAATAAAGGGA     35643     CA       A
                                AGG  GTAATAAA GGGG
                                |||  |||||||| ||||
                                TCC  CATTATTT CCCT
                                  CC       _
GAM1383  LOC55971  3'  GGCTGTAATAAAGGGGCCAG   35670     A       A    A
                                GGC GTAATAAA GGGGC TAG
                                |||  |||||||| ||||| |||
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                                CCG CATTATTT CCCCG GTC
                                  A      _   _
GAM1383 LOC92689 3' AGGCAGTAATGCAAGCTCTGGG 35671          AA  _____
                                AGGCAGTAAT  AAG   GGG
                                ||||||||||  |||   |||
                                TCCGTCATTA  TTC   CCC
                                     CG   GAGA
GAM1384 CIT      3' ATGAGACACACAATATACA   35674      CCAT   G
                                ATGAG   ATA ACAATATACA
                                |||||   ||| ||||||||||
                                TACTC   TGT TGTTATATGT
                                   _____  G
GAM1384 GAS1     3' GAGCAGAGGCAATATACAT   35675     CATAT  A
                                GAGC    AG CAATATACAT
                                ||||    || ||||||||||
                                CTCG    TC GTTATATGTA
                                  TC___  C
GAM1384 SIRT1    3' ATGAGCCAATATAGACATTACT 35676        _      ATA_
             ACAT                  ATGAGCCA TATAGACA   TACAT
                                ||||||||| ||||||||   |||||
                                TACTCGGT ATATCTGT   ATGTA
                                     T       AATG
GAM1384 FLJ12987 3' ATGTGCCATATATATAATACAT 35677     A       GACAAT
                                ATG GCCATATA     ATACAT
                                ||| ||||||||     ||||||
                                TAC CGGTATAT     TATGTA
                                  A       ATAT__
GAM1384 SPBPBP   5' ATGAGCCTGTAACAATAT    35678       ATATA
                                ATGAGCC    GACAATAT
                                |||||||    ||||||||
                                TACTCGG    TTGTTATA
                                    ACA__
GAM1385 CAPN7    5' GCCGGGCTGGGGTCCACCG   35681        AAC   A
                                GCCGGGCT   GGGG TCACCG
                                ||||||||   |||| ||||||
                                CGGCCCGA   CCCC GGTGGC
                                     ___    A
GAM1385 SIM2     3' GCCGGGCTCGGTGGCGCCG   35682        AA  _  ATCA
                                GCCGGGCT  CGG GG   CCG
                                ||||||||  ||| ||   |||
                                CGGCCCGA  GCC CC   GGC
                                     __   A  GC__
GAM1385 TMEPAI   5' TCGCCGGGCTCGGGTCGCC   35683         AA   GA  A
                                TCGCCGGGCT  CGGG  TC CC
                                ||||||||||  ||||  || ||
                                AGCGGCCCGA  GCCC  AG GG
                                     __   __ C
GAM1385 CHPT1    5' GCCGGGCTGGACTCACC     35684        AACG  GA
                                GCCGGGCT    GG  TCACC
                                ||||||||    ||  |||||
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                                CGGCCCGA   CC  AGTGG
                                     ____  TG
GAM1385  DCAMKL1   5'  TCGCCGGGCTGGGCGCGGCCG  35685        AA_  G  ATCA
                                TCGCCGGGCT   CG GG   CCG
                                ||||||||||   || ||   |||
                                AGCGGCCCGA   GC CC   GGC
                                     CCC  G  ____
GAM1385  DKFZP564C1940 5'  GCCAGGCTGGCAATGCC    35686       AAC  G   CA
                                GCCGGGCT   GG GAT  CC
                                ||||||||   || |||  ||
                                CGGTCCGA   CC TTA  GG
                                     ___  G   C_
GAM1385  FLJ12697  3'  TCGCCAGGGCTGAGCCTGTCGC 35687      _    AAC   GA__  A
           CG                     TCGCC GGGCT   GGG    TC CCG
                                |||||  |||||   |||    || |||
                                AGCGG CCCGA   CTC    AG GGC
                                   T    ___   GGAC  C
GAM1385  H2AFA    3'  TCTGGGACTCGGGATCAC    35688    GCC    AACG
                                TC   GGGCT   GGGATCAC
                                ||   |||||   ||||||||
                                AG   CCTGA   CCCTAGTG
                                 AC_    G___
GAM1385  KIAA1204  5'  TCCCGGGCTAGATCAC     35689    G     AACGG
                                TC CCGGGCT    GGATCAC
                                || |||||||    |||||||
                                AG GGCCCGA    TCTAGTG
                                 _     _____
GAM1385  MGC15523  5'  TCGCCGGGCTGCGGCCGCGGTG 35690       AA  ________  ATCA
           AC                     GCCGGGCT  CGG      GG   C
                                ||||||||  |||      ||   |
                                CGGCCCGA  GCC      CC   G
                                    C_   GGCIIIG  ACTA
GAM1385  LOC112885 3'  CAGGCTCTGGCGGGGATCAC   35691       AA__
                                CGGGCT   CGGGGATCAC
                                ||||||   ||||||||||
                                GTCCGA   GCCCCTAGTG
                                   GACC
GAM1385  LOC123096 5'  TCGCCGGGCTGGGCGCCG    35692        AACG   ATCA
                                TCGCCGGGCT   GGG   CCG
                                ||||||||||   |||   |||
                                AGCGGCCCGA   CCC   GGC
                                     _____  GC__
GAM1386  CA14     3'  TGATCAAAAATATACAACTTC  35695    T       _   A
                                TG ATCAAAAATAT CAAT TC
                                || |||||||||| |||| ||
                                AC TAGTTTTTATA GTTG AG
                                 _        T   A
GAM1386  IRTA1    3'  TGTATCATGAAATATCCATAC  35696       A_     A
                                TGTATCA  AAATATC ATAT
                                |||||||  ||||||| ||||
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                                ACATAGT  TTTATAG TATG
                                   AC      G
GAM1386 SOX11    3' TGTATCAAAAATGTTTCAA   35697          A__
                                TGTATCAAAAAT   TCAA
                                ||||||||||||  ||||
                                ACATAGTTTTTA   AGTT
                                     CAA
GAM1386 VAPB     3' TGTACCAAGGCCTACCAAT   35698        AAA_
                                TGTATCAA   TATCAAT
                                ||||||||   |||||||
                                ACATGGTT   ATGGTTA
                                    CCGG
GAM1386 XRCC4    3' TGTATCAAAAATTTTATTATC 35699          ATCAA
                                TGTATCAAAAAT    TATC
                                ||||||||||||    ||||
                                ACATAGTTTTTA    ATAG
                                      AAATA
GAM1386 XRCC4    3' TGTATCAAAAATTTTATTATC 35699          ATCAA
                                TGTATCAAAAAT    TATC
                                ||||||||||||    ||||
                                ACATAGTTTTTA    ATAG
                                      AAATA
GAM1386 XRCC4    3' TGTATCAAAAATTTTATTATC 35699          ATCAA
                                TGTATCAAAAAT    TATC
                                ||||||||||||    ||||
                                ACATAGTTTTTA    ATAG
                                      AAATA
GAM1386 DCLRE1A  3' GTATCATCAATATCC      35700       AAAATA
                                GTATCA     TCAATATCC
                                ||||||     |||||||||
                                CATAGT     AGTTATAGG

                                _______
GAM1386 EREG     3' TGTATAAAAATATCAAT     35701       C
                                TGTAT AAAAATATCAAT
                                ||||| ||||||||||||
                                ACATA TTTTTATAGTTA

                                _
GAM1386 FLJ23560 3' TATATCAAAGGTGAAAATCTAT 35702         AATATCAA__
            CCAA                  TGTATCAAA        TATCCAA
                                ||||||||||        |||||||
                                ATATAGTTT        ATAGGTT
                                     CCACTTTTAG
GAM1386 HE3-BETA 3' TGTATCAAGAGAGTCAATATC  35703        AAATA
                                TGTATCAA    TCAATATC
                                ||||||||    ||||||||
                                ACATAGTT    AGTTATAG
                                    CTCTC
GAM1386 ST13     3' TGCATCAGGAACCACATATCCA 35704        AA   ATCA
            A                   TGTATCA  AAT    ATATCCAA
                                |||||||  |||    ||||||||
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                                ACGTAGT  TTG   TATAGGTT
                                   CC  GTG_
GAM1386 STXBP3   3' TATCAAAAATGACAAATCCA  35705        AT  T
                                TATCAAAAAT  CAA ATCCA
                                ||||||||||  ||| |||||
                                ATAGTTTTTA  GTT TAGGT
                                     CT  _
GAM1387 ADK      3' AATAAACATCATTTTTTAGATT 35708      G  AT
                                AGTAAA AT  TTTTTTAGATT
                                ||||||| ||  ||||||||||
                                TTATTT TA  AAAAAATCTAA
                                   G  GT
GAM1387 ADK      3' AATAAACATCATTTTTTAGATT 35708      G  AT
                                AGTAAA AT  TTTTTTAGATT
                                ||||||| ||  ||||||||||
                                TTATTT TA  AAAAAATCTAA
                                   G  GT
GAM1387 LOC150848 5' AGTGGAGATATTTTTCTAG   35709    AA
                                AGT  AGATATTTTTTTAG
                                |||  ||||||||||||||
                                TCA  TCTATAAAAAGATC
                                  CC
GAM1387 LOC221584 3' AGTAAAGGTATTTTTTTAA   35710       A
                                AGTAAAG TATTTTTTTAG
                                ||||||| ||||||||||
                                TCATTTC ATAAAAAAATT
                                    C
GAM1387 LOC91138  3' AGTAAGAATATTTTTCTA    35711      AG
                                AGTAA  ATATTTTTTTA
                                |||||  ||||||||||
                                TCATT  TATAAAAAGAT
                                   CT
GAM1388 CD3E     3' TTAGGGGGTTGGTAGGGA    35714    A  A   A  C
                                TTA GGG TTGG TAG GA
                                ||| ||| |||| ||| ||
                                AAT CCC AACC ATC CT
                                  C  C   _  C
GAM1388 NCOA3    3' TTAAGAGATTGAAAAGAGCGAG 35715          T__    AA
            GCAT                   TTAAGGGATTGGA  AGCGA  CAT
                                ||||||||||||  |||||  |||
                                AATTCTCTAACTT  TCGCT  GTA
                                       TTC    CC
GAM1388 OPA1     3' AGGGATCACAACGAAGCAT   35716       GG      A
                                AGGGATT  ATAGCGAA CAT
                                |||||||  |||||||| |||
                                TCCCTAG  TGTTGCTT GTA
                                    __       C
GAM1388 OPA1     3' AGGGATCACAACGAAGCAT   35716       GG      A
                                AGGGATT  ATAGCGAA CAT
                                |||||||  |||||||| |||
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                                TCCCTAG  TGTTGCTT GTA
                                   __       C
GAM1388  OPA1     3'  AGGGATCACAACGAAGCAT   35716       GG       A
                                AGGGATT  ATAGCGAA CAT
                                |||||||  |||||||| |||
                                TCCCTAG  TGTTGCTT GTA
                                   __       C
GAM1388  OPA1     3'  AGGGATCACAACGAAGCAT   35716       GG       A
                                AGGGATT  ATAGCGAA CAT
                                |||||||  |||||||| |||
                                TCCCTAG  TGTTGCTT GTA
                                   __       C
GAM1388  OPA1     3'  AGGGATCACAACGAAGCAT   35716       GG       A
                                AGGGATT  ATAGCGAA CAT
                                |||||||  |||||||| |||
                                TCCCTAG  TGTTGCTT GTA
                                   __       C
GAM1388  FLJ21551 3'  TTAAGGGATTGGGTATAAATTA 35717           A_______
              GCG                  TTAAGGGATTGG       TAGCG
                                |||||||||||        |||||
                                AATTCCCTAACC       ATCGC
                                      CATATTTA
GAM1388  TLK2     5'  TAAGGGATTGGATAAGGAA   35718             C
                                TAAGGGATTGGATAG GAA
                                |||||||||||||| |||
                                ATTCCCTAACCTATT CTT
                                      C
GAM1388  LOC152457 3'  CTAAGGGATCAACAGGTGA   35719          G   C_
                                TTAAGGGATTG ATAG  GA
                                |||||||||| ||||  ||
                                GATTCCCTAGT TGTC  CT
                                      _   CA
GAM1388  LOC253281 5'  GGGATTGGCAAAAACAT     35720        ATAGC
                                GGGATTGG    GAAACAT
                                ||||||||    |||||||
                                CCCTAACC    TTTTGTA
                                     GT___
GAM1389  ATP7B    3'  TCTAATATTGCATGAAATGTTT 35723        C_  ATT
              TT                   TCTAATGT  CA   AATGTTTTT
                                |||||||  ||   |||||||||
                                AGATTATA  GT   TTACAAAAA
                                     AC  ACT
GAM1389  BCL11B   3'  AATGTCCAATTTATTTTTA   35724          AA
                                AATGTCCAATT  TGTTTTTA
                                ||||||||||  ||||||||
                                TTACAGGTTAA  ATAAAAAT
                                      __
GAM1389  CYP24    3'  TCTAGTTTCCCAATAATGTTTT 35725      ATG   AAT
              TA                   TCTA   TCC   TAATGTTTTTA
                                ||||   |||   ||||||||||
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                                AGAT   AGG   ATTACAAAAAT
                                  CAA   GTT
GAM1389  EGFL5    5'  CTAATGTCTAATTAGATTAATG 35726        CA_____
             TTTTT                  CTAATGTC      ATTAATGTTTTT
                                ||||||||      ||||||||||||
                                GATTACAG      TAATTACAAAAA
                                    ATTAATC
GAM1389  ZNF137   3'  TCTAATGTCAATTAAAGCTTT  35727         C     T
                                TCTAATGTC AATTAA GTTTT
                                ||||||||| |||||| |||||
                                AGATTACAG TTAATT CGAAA
                                      _     T
GAM1389  C20orf139 3'  CTAATGTCCTGTTTT       35728          AATTAA
                                CTAATGTCC     TGTTTT
                                |||||||||     ||||||
                                GATTACAGG     ACAAAA
                                              _______
GAM1389  CYYR1    3'  TCCAATGTTCAATATACAATTT 35729         C    TAAT_
             TTA                   TCTAATGT CAAT     GTTTTTA
                                |||||||| ||||     |||||||
                                AGGTTACA GTTA     TAAAAAT
                                    A    TATGT
GAM1389  FLJ11184  3'  CCTAATACTGCATTAATGTTTT 35730        TCCA
             TA                    TCTAATG    ATTAATGTTTTTA
                                |||||||    ||||||||||||||
                                GGATTAT    TAATTACAAAAAT
                                    GACG
GAM1389  FLJ14260  5'  TCTGATGTCCAATAAGATG    35731     A       TA_
                                TCT ATGTCCAAT   ATG
                                ||| |||||||||   |||
                                AGA TACAGGTTA   TAC
                                  C        TTC
GAM1389  FLJ20073  3'  TCTAATGTCTAAATGCCATT   35732         CAATT     TT
                                TCTAATGTC     AATGT  TT
                                |||||||||     |||||  ||
                                AGATTACAG     TTACG  AA
                                      AT___     GT
GAM1389  KIAA0022  3'  TCTAATATCCAATGTCAAGTTT 35733           TAAT_
             T                     TCTAATGTCCAAT     GTTTT
                                ||||||||||||||     |||||
                                AGATTATAGGTTA     CAAAA
                                      CAGTT
GAM1389  KIAA0103  3'  TCTAATGTCAAAGAGTTTTT   35734         C  TTAAT
                                TCTAATGTC AA     GTTTTT
                                ||||||||| ||     ||||||
                                AGATTACAG TT     CAAAAA
                                      _ TCT__
GAM1389  KIAA1979  3'  TAATGTCAATTAAGGCTT     35735         C     T
                                TAATGTC AATTAA GTTT
                                ||||||| |||||| ||||
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                                ATTACAG TTAATT CGAA
                                   _     C
GAM1389  MDN1     3'  TAATGTCCAGTTGCTTT     35736         ATTAA
                                TAATGTCCA    TGTTTT
                                |||||||||    ||||||
                                ATTACAGGT    ACGAAA
                                     CA___
GAM1389  ZNF33A   3'  ATGTCCAATTCCTTTTTA    35737          AATG
                                ATGTCCAATT    TTTTTA
                                ||||||||||    ||||||
                                TACAGGTTAA    AAAAAT
                                     GG__
GAM1389  LOC132321 3'  TGCTCAACTTAATGTTTTT    35738    TC    _
                                TG  CAATT AATGTTTTT
                                ||  ||||| |||||||||
                                AC  GTTGA TTACAAAAA
                                 GA    A
GAM1389  LOC149157 3'  CAATGTCCCCTTGGTGTTTTTA 35739        AA  AA
                                TAATGTCC  TT  TGTTTTTA
                                ||||||||  ||  ||||||||
                                GTTACAGG  AA  ACAAAAAT
                                     GG  CC
GAM1389  LOC151438 5'  TCTGGTGTCCGCTTCTATGCTT 35740     AA    AA  A_
            TTA                   TCT  TGTCC  TT  ATGTTTTTA
                                |||  |||||  ||  |||||||||
                                AGA  ACAGG  AA  TACGAAAAT
                                  CC    CG  GA
GAM1389  LOC90333  3'  TCTAATGTCAATTAATGCTT   35741         C
                                TCTAATGTC AATTAATGTTT
                                ||||||||| ||||||||||
                                AGATTACAG TTAATTACGAA
                                     _
GAM1389  LOC91664  3'  TAATGTCAATTAATGCTT    35742        C
                                TAATGTC AATTAATGTTT
                                ||||||| ||||||||||
                                ATTACAG TTAATTACGAA
                                   _
GAM1389  LOC91664  3'  TCTAATGCCAATTAATGCTT   35743        T
                                TCTAATG CCAATTAATGTTT
                                ||||||| ||||||||||||
                                AGATTAC GGTTAATTACGAA
                                   _
GAM1390  RPL15     3'  CTAGTCTCCTGGAAGACATGGT 35746      CATG   A      A
                                TTAG    TTCT GAAGACAT GT
                                ||||    |||| |||||||| ||
                                GATC    AGGA CTTCTGTA CA
                                  AG__    C       C
GAM1390  TPX1      3'  TTAGCATGTTTCAGGAAATAC  35747          _ TA   _
                                TTAGCATGTT C  GAAG AC
                                |||||||||| |  |||| ||
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                                AATCGTACAA G  CTTT TG
                                     A TC    A
GAM1390  ZNF268    3'  TGTACTAAGAAGACATAGT    35748     T  _
                                TGT CTA GAAGACATAGT
                                ||| ||| ||||||||||
                                ACA GAT CTTCTGTATCA
                                  T   T
GAM1390  KALI      3'  TTAGCATGTTTTGGCCTGAAG  35749          ____  A
                                TTAGCATGTT    CT GAAG
                                ||||||||||    || ||||
                                AATCGTACAA    GG CTTC
                                     AACC  A
GAM1390  LOC155006 3'  GCGTGTTCTAGGGGAAGGCAGT 35750     A       AA  CA_
                                GC TGTTCTAG  GA   TAGT
                                || ||||||||  ||   ||||
                                CG ACAAGATC  CT   GTCA
                                 C       CC  TCC
GAM1390  LOC222166 3'  TTAGCATGTTTTGAAACAG    35751          CTA   GAC
                                TTAGCATGTT   GAA   ATAG
                                ||||||||||   |||   ||||
                                AATCGTACAA   CTT   TGTC
                                     AA_   ___
GAM1390  LOC255096 3'  TGCCCCAGGAGATGTAGT     35752         A   CA
                                TGTTCTAG AGA  TAGT
                                ||||||||| |||  ||||
                                ACGGGGTC TCT  ATCA
                                     C   AC
GAM1391  PDK4      3'  TATATCAAAAATATATCT     35755            TCAA
                                TGTATCAAAAATA    TATCT
                                ||||||||||||    |||||
                                ATATAGTTTTTAT    ATAGA
                                          ____
GAM1391  SDC1      3'  TGTGCAAAAACAAGTCGATATC 35756     AT       __  A
              TA                  TGT  CAAAAATA  TC ATATCTA
                                ||| ||||||||  || |||||||
                                ACA  GTTTTTGT  AG TATAGAT
                                  C_       TC  C
GAM1391  VAPB      3'  TGTACCAAGGCCTACCAAT    35698         AAA_
                                TGTATCAA    TATCAAT
                                ||||||||    |||||||
                                ACATGGTT    ATGGTTA
                                     CCGG
GAM1391  EREG      3'  TGTATAAAAATATCAATTTTCT 35757       C          A_
                                TGTAT AAAAATATCAAT  TCT
                                ||||| ||||||||||||  |||
                                ACATA TTTTTATAGTTA  AGA
                                   _          AA
GAM1392  TBR1      3'  TCAACATCCTATGGTTAAT    35760         A   TCCAA
                                TCAATATCC ATG    TTAAT
                                ||||||||| |||    |||||
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                                AGTTGTAGG TAC     AATTA
                                     A   C____
GAM1392  DKFZP564D1378 3'  TCAATACCTTTCTTTCTAATTA 35761         CAATG_  C
            ATG                      TCAATATC      TC AATTAATG
                                     ||||||||      || ||||||||
                                     AGTTATGG      AG TTAATTAC
                                          AAAGAA  A
GAM1392  FLJ22104  3'  TCAATATCACAGTCCTTTAATG 35762          _  AT    AA
                                     TCAATATC CA  GTCC  TTAATG
                                     |||||||| ||  ||||  ||||||
                                     AGTTATAG GT  CAGG  AATTAC
                                          T  __   A_
GAM1393  CYP1A1   3'  CAATGCAGGCTAGAATAGAA   35765      A         TAT
                                     CAAT CAGGCTAGAAT   GAA
                                     |||| ||||||||||   |||
                                     GTTA GTCCGATCTTA   CTT
                                       C         T__
GAM1393  GNRH1    3'  CAACACAGCACTTTATTATG   35766         _   AGA
                                     CAATACAG GCT   ATTATG
                                     |||||||| |||   ||||||
                                     GTTGTGTC TGA   TAATAC
                                          G   AA_
GAM1393  KCNMB3   5'  CAGTCCACTCAGAATTATGAA  35767     ___   _
                                     CAG   GCT AGAATTATGAA
                                     |||   ||| ||||||||||
                                     GTC   TGA TCTTAATACTT
                                       AGG   G
GAM1393  PARK2    3'  CAATACAGGTAGAACAAAAGA  35768         C     TAT_
                                     CAATACAGG TAGAAT    GA
                                     |||||||| ||||||    ||
                                     GTTATGTCC ATCTTG    CT
                                          _     TTTT
GAM1393  PARK2    3'  CAATACAGGTAGAACAAAAGA  35768         C     TAT_
                                     CAATACAGG TAGAAT    GA
                                     |||||||| ||||||    ||
                                     GTTATGTCC ATCTTG    CT
                                          _     TTTT
GAM1393  PARK2    3'  CAATACAGGTAGAACAAAAGA  35768         C     TAT_
                                     CAATACAGG TAGAAT    GA
                                     |||||||| ||||||    ||
                                     GTTATGTCC ATCTTG    CT
                                          _     TTTT
GAM1393  CBLNL1   3'  ACAGGCTAGAATCCTTAGAA   35769           AT__
                                     ACAGGCTAGAATT    GAA
                                     ||||||||||||    |||
                                     TGTCCGATCTTAG    CTT
                                             GAAT
GAM1393  GMFB     3'  TAAAAACTGGAATTATGAAAT  35770    C    A
                                     TA AGGCT GAATTATGAAAT
                                     || ||||| ||||||||||||
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                                AT TTTGA CTTAATACTTTA
                                 T    C
GAM1393  HSPBAP1   3'  TGACACAGGCTAAAAGTATG  35771   A          T
                                C ATACAGGCTAGAA TATG
                                | ||||||||||||| ||||
                                A TGTGTCCGATTTT ATAC
                                 C           C
GAM1393  MSTP028   3'  GGCTGGAGGATTATGAAAT   35772     A  __
                                GGCT GA  ATTATGAAAT
                                |||| ||  ||||||||||
                                CCGA CT  TAATACTTTA
                                  C  CC
GAM1393  ZNF340    5'  ATACAGGCTAGAAAAAGA    35773           TTAT
                                ATACAGGCTAGAA    GA
                                ||||||||||||    ||
                                TATGTCCGATCTT    CT
                                        TTT_
GAM1393  LOC144231 5'  CAATAGAGGCTAGAAATG    35774      C       TT
                                CAATA AGGCTAGAA  ATG
                                ||||| |||||||||  |||
                                GTTAT TCCGATCTT  TAC
                                   C       __
GAM1393  LOC150933 3'  AATATAAGCTAGATATAAAATG 35775     C       ATT___
            AAAT                   AATA AGGCTAGA     ATGAAAT
                                |||| ||||||||     |||||||
                                TTAT TTCGATCT     TACTTTA
                                  A       ATATTT
GAM1393  LOC221718 3'  CAGTAGAGGCTAGAACTGGAA  35776    A  C         AT
                                CA TA AGGCTAGAATT  GAA
                                || || ||||||||||  |||
                                GT AT TCCGATCTTGA  CTT
                                 C  C         C_
GAM1393  LOC254100 3'  ATACAGGCTGGAGTCCAAGA   35777         A  A  AT_
                                ATACAGGCT GA TT   GA
                                ||||||||| || ||   ||
                                TATGTCCGA CT AG   CT
                                      C  C  GTT
GAM1394  PKNOX1    3'  TCGCTGCTGGGACTCCA     35780          C   CAAC
                                TCGCTGCTGG GAC    TTCA
                                |||||||||| |||    ||||
                                AGCGACGACC CTG    AGGT
                                          _  ____
GAM1394  RERE      3'  TCGCTGCTGTGACCAGGCCTC  35781         GC    A_
                                TCGCTGCTG  GACCA  CTTC
                                |||||||||  |||||  ||||
                                AGCGACGAC  CTGGT  GGAG
                                      A_    CC
GAM1394  CDC14B    3'  CCGCTGCTGAGAGGCTTCAAT  35782          C  CCAA
                                TCGCTGCTGG GA    CTTCAAT
                                |||||||||| ||    |||||||
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                                GGCGACGACT CT   GAAGTTA
                                      _ CC__
GAM1394 DGS-A    3' TCCTTGCTGGCGATCCTGCCTT 35783    GC      _ AA_
           CAAT                  TC TGCTGGCGA CC  CTTCAAT
                                || |||||||| ||  |||||||
                                AG ACGACCGCT GG  GAAGTTA
                                 GA       A ACG
GAM1394 KIAA0475 3' GCTGCTGGCCACTTCCAAT   35784        G CAAC
                                GCTGCTGGC AC   TTCAAT
                                ||||||||| ||   ||||||
                                CGACGACCG TG   AGGTTA
                                     G A___
GAM1394 LOC203504 5' GCTGCTAGCCGATTTCA    35785        _ CCAAC
                                GCTGCTGGC GA    TTCA
                                ||||||||| ||    ||||
                                CGACGATCG CT    AAGT
                                     G A____
GAM1395 RNGTT    3' AGTTGTTTAATATAGTACA   35788        _ C
                                AGTTGTTTA TA AGTACA
                                ||||||||| || ||||||
                                TCAACAAAT AT TCATGT
                                     T A
GAM1395 DKFZp547O146 3' GTCTATATACAGTATGTGATTG 35789    GTT      CAC
                                GTT  TATACAGTA  GATTG
                                |||  |||||||||  |||||
                                CAG  ATATGTCAT  CTAAC
                                  AT_       ACA
GAM1395 LNX      3' AGTTTTTATACAGTTACTAACG 35790     G       _ __
           ATTG                   AGTT TTTATACAGT AC  ACGATTG
                                |||| |||||||||| ||  |||||||
                                TCAA AAATATGTCA TG  TGCTAAC
                                  _       A  AT
GAM1395 OS-9     3' AGTTGTTTATTTAGAAACCTGA 35791         AC  T_  AC
           TTG                   AGTTGTTTAT  AG  AC  GATTG
                                ||||||||||  ||  ||  |||||
                                TCAACAAATA  TC  TG  CTAAC
                                     AA  TT  GA
GAM1396 GAS11    3' TGAGTGCGGGGCACTCTGAGAA 35794   T        GGTT_
           GG                    A AGTGCGGGGCAC    GAAGG
                                | ||||||||||||    |||||
                                A TCACGCCCCGTG    CTTCC
                                 C          AGACT
GAM1396 ATP6V0A1 3' TAGTGCAGGGCATGAACGG   35795         CGGT   _
                                TAGTGCGGGGCA   TGAA GG
                                ||||||||||||   |||| ||
                                ATCACGTCCCGT   ACTT CC
                                       ____   G
GAM1396 CHERP    3' GTGCGGGGAGCTGGAG     35796       CAC    A
                                GTGCGGGG  GGTTG AG
                                ||||||||  ||||| ||
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                                CACGCCCC   TCGAC TC
                                    ___     C
GAM1396  DKFZP547L112 5'  TAGTCCGGGGCACGGCAAGG   35797     G        TG
                                TAGT CGGGGCACGGT  AAGG
                                |||| ||||||||||  ||||
                                ATCA GCCCCGTGCCG  TTCC
                                  G         __
GAM1396  KIAA0121  3'  GTGCGGGGCAAGGAGAAGG   35798         C  TT
                                GTGCGGGGCA GG  GAAGG
                                ||||||||| ||  |||||
                                CACGCCCCGT CC  CTTCC
                                      T  T_
GAM1396  KIAA1941  3'  CACAACCAGGGGTATGGTTGGG 35799      TGC   CAC    AA
            GG                    TATAG   GGGG   GGTTG  GG
                                |||||   ||||   |||||  ||
                                GTGTT   CCCC   CCAAC  CC
                                   GGT    ATA    CC
GAM1396  RAI17    3'  GTGCGGGGCGGTCTGAGG    35800        AC    GA
                                GTGCGGGGC  GGTT  AGG
                                |||||||||  ||||  |||
                                CACGCCCCG  CCAG  TCC
                                     __    AC
GAM1396  LOC157918 3'  GTGTGGGGCAGATGAAGG    35801     C     C   T
                                GTG GGGGCA GGT GAAGG
                                ||| |||||| ||| |||||
                                CAC CCCCGT CTA CTTCC
                                  A     _   _
GAM1397  ACTN2    3'  CAAAAAGCATGGGAACCTGGAA 35804          A  A
                                TAAAAAGCATGG AA TTGGAA
                                |||||||||||| || ||||||
                                GTTTTTCGTACC TT GACCTT
                                      C  G
GAM1397  ADAMTS5  3'  AAAAGCATGGAATAGTGG    35805          AAT
                                AAAAGCATGGAA   TGG
                                ||||||||||||   |||
                                TTTTCGTACCTT   ACC
                                      ATC
GAM1397  DSS1     5'  AAGCAGAAAAGTTGGAAC    35806      T    A
                                AAGCA GGAAA TTGGAAC
                                ||||| ||||| |||||||
                                TTCGT CTTTT AACCTTG
                                   _    C
GAM1397  DYRK1A   3'  TAAAAAGCAGGAAGGGA     35807        T   AATT
                                TAAAAAGCA GGAA    GGA
                                |||||||||  ||||    |||
                                ATTTTTCGT CCTT    CCT
                                      _   C___
GAM1397  DYRK1A   3'  TAAAAAGCAGGAAGGGA     35807        T   AATT
                                TAAAAAGCA GGAA    GGA
                                |||||||||  ||||    |||
```

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                                ATTTTTCGT CCTT    CCT
                                      _   C___
GAM1397  DYRK1A   3'  TAAAAAGCAGGAAGGGA     35807         T    AATT
                                TAAAAAGCA GGAA    GGA
                                ||||||||| ||||    |||
                                ATTTTTCGT CCTT    CCT
                                      _   C___
GAM1397  GPR85    3'  AAAAAGTAAACTCTAATTGGAA 35808       CATGGAA_
              CC                  AAAAAG       AATTGGAACC
                                  ||||||       ||||||||||
                                  TTTTTC       TTAACCTTGG
                                     ATTTGAGA
GAM1397  LANGERIN 3'  AGCAGGGCAATTGGAAC     35809      T  AA
                                AGCA GG  AATTGGAAC
                                |||| ||  |||||||||
                                TCGT CC  TTAACCTTG
                                  _  CG
GAM1397  MIR16    3'  TAAAAAGCCTGGAAAAGTGCAA 35810        A      T  G
              C                   TAAAAAGC TGGAAAA TG AAC
                                  |||||||| ||||||| || |||
                                  ATTTTTCG ACCTTTT AC TTG
                                       G      C  G
GAM1397  PHTF1    3'  AAAAGCATGAAAATACAGG    35811           _  T
                                AAAAGCATGGAAA AT GG
                                |||||||||||| || ||
                                TTTTCGTACTTTT TG CC
                                       A  T
GAM1397  PKHD1    3'  CAAAAAGCATGGAGAAATGG   35812           A  T
                                TAAAAAGCATGGA AA TGG
                                |||||||||||| || |||
                                GTTTTTCGTACCT TT ACC
                                       C  T
GAM1397  RAB1A    3'  TGAAAGCATGGAAGAAAAAC   35813    A         AATT
                                A AAAGCATGGAA    GGAAC
                                | ||||||||||    |||||
                                A TTTCGTACCTT    TTTTG
                                 C          CT__
GAM1397  RAG1     3'  TAAAAAGCAAGGAAAACT     35814         T
                                TAAAAAGCA GGAAAATT
                                ||||||||| ||||||||
                                ATTTTTCGT CCTTTTGA
                                      T
GAM1397  RBMX     3'  TAAAAATTATGGAGGGGAAC   35815       GC    AAATT
                                TAAAAA  ATGGA    GGAAC
                                ||||||  |||||    |||||
                                ATTTTT  TACCT    CCTTG
                                   AA    CC___
GAM1397  RPS15A   5'  GCAGACGGATGAAATTGGA    35816     __   __
                                GCA  TGGA  AAATTGGA
                                |||  ||||  ||||||||
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                                CGT  GCCT  TTTAACCT
                                  CT    AC
GAM1397  SLC21A9   3'  TAAAAAGGGAATTGGAAC    35817       CAT   AA
                                TAAAAAG   GGA  ATTGGAAC
                                |||||||   |||  ||||||||
                                ATTTTTC   CCT  TAACCTTG
                                     ___   __
GAM1397  SLC4A7    3'  AAAAGCCATAAAAATTGGAAC  35818       ATG
                                AAAAGC   GAAAATTGGAAC
                                ||||||   ||||||||||||
                                TTTTCG   TTTTTAACCTTG
                                   GTA
GAM1397  TNFSF11   3'  AAGAGCATGGATACTGA     35819    A      AA
                                AA AGCATGGA  ATTGG
                                || ||||||||  |||||
                                TT TCGTACCT  TGACT
                                 C       A_
GAM1397  TNFSF11   3'  AAGAGCATGGATACTGA     35819    A      AA
                                AA AGCATGGA  ATTGG
                                || ||||||||  |||||
                                TT TCGTACCT  TGACT
                                 C       A_
GAM1397  ACTR1A    3'  AAAGCGAGGTCCTGGAACC    35820      AT  AAAA
                                AAAGC  GG    TTGGAACC
                                |||||  ||    ||||||||
                                TTTCG  CC    GACCTTGG
                                   CT  AG__
GAM1397  AGMAT     3'  TGAAAACATGGAAACATG     35821    A        AT
                                A AAAGCATGGAAA  TG
                                | ||||||||||||  ||
                                A TTTTGTACCTTT  AC
                                 C          GT
GAM1397  C20orf106 3'  TAAAAAGCAAGGGAACAGTGAA 35822         T_   AAT
                                TAAAAAGCA  GGAA   TGGA
                                |||||||||  ||||   ||||
                                ATTTTTCGT  CCTT   ACTT
                                      TC    GTC
GAM1397  C20orf126 3'  AAAAAGTGCAAAATTGGA     35823       CA  G
                                AAAAAG  TG AAAATTGGA
                                ||||||  || |||||||||
                                TTTTTC  AC TTTTAACCT
                                   __  G
GAM1397  CREG      3'  TAAAAAGCTGTGGAGAGTGG   35824        A_   AAAT
                                TAAAAAGC  TGGA    TGG
                                ||||||||  ||||    |||
                                ATTTTTCG  ACCT    ACC
                                     AC    CTC_
GAM1397  DDX34     3'  TAAAAAGCAGGAGGGA      35825         T   AAATT
                                TAAAAAGCA GGA     GGA
                                |||||||||  |||    |||
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                                ATTTTTCGT CCT    CCT
                                      _  C____
GAM1397  DKFZP564K0822 3'  AAAAGCATGGACACCAAA    35826          AA  TG
                                AAAAGCATGGA  AT  GA
                                ||||||||||  ||  ||
                                TTTTCGTACCT  TG  TT
                                     G_  GT
GAM1397  DKFZp761G2113 3'  AAGGATGGGAATTGAAACC   35827    C    AA
                                AAG ATGG  AATTGGAACC
                                ||| ||||  ||||||||||
                                TTC TACC  TTAACTTTGG
                                  C   C_
GAM1397  DNAJC6   3'  CAAAAAGCAATTGGAA      35828         TGGAAA
                                TAAAAAGCA     ATTGGAA
                                |||||||||     |||||||
                                GTTTTTCGT     TAACCTT

                                      _______
GAM1397  FLJ11939  3'  AAAAAGCCAGAGTTGGAACC   35829       A    AAA
                                AAAAAGC TGGA   TTGGAACC
                                ||||||| ||||   ||||||||
                                TTTTTCG GTCT   AACCTTGG
                                    _   C__
GAM1397  HSU79266  3'  AAACCATGGAAAAAGAAACC   35830     G       TT
                                AAA CATGGAAAA  GGAACC
                                ||| |||||||||  ||||||
                                TTT GTACCTTTT  CTTTGG
                                  G        T_
GAM1397  IF2      3'  TGAACAGGCACATTGGAAC    35831    A    T  AAA
                                A AGCA GG   ATTGGAAC
                                | |||| ||   ||||||||
                                A TTGT CC   TAACCTTG
                                 C    _  GTG
GAM1397  KIAA0440  5'  AAAGCACTGAAAAATTGGAAC  35832       _
                                AAAGCA TGGAAAATTGGAAC
                                ||||||| ||||||||||||||
                                TTTCGT ACTTTTTAACCTTG
                                    G
GAM1397  KIAA0451  5'  AAAAAGCATGGGAAAAGA     35833          A   TT
                                AAAAAGCATGG AAA  GGA
                                |||||||||||  |||  |||
                                TTTTTCGTACC TTT  TCT
                                      C   __
GAM1397  KIAA0628  3'  AGCATGGAAAATGACAAGA    35834           T___
                                AGCATGGAAAAT    GGA
                                ||||||||||||    |||
                                TCGTACCTTTTA    TCT
                                      CTGT
GAM1397  KIAA1432  3'  TAAAAAGCAAGGAGAGAGGACC 35835         T   AAATT   A
                                TAAAAAGCA GGA    GGA CC
                                |||||||||  |||    ||| ||
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                                ATTTTTCGT CCT    CCT GG
                                     T  CTCT_  _
GAM1397 LRG     3' AAGCATGGATGGATGAAAC  35836       AAAT
                                AAGCATGGA   TGGAAC
                                |||||||||   ||||||
                                TTCGTACCT   ACTTTG
                                     ACCT
GAM1397 SHAPY   3' AAAGGCCATGGAAAGAAACC  35837    __     ATT
                                AAAG  CATGGAAA  GGAACC
                                ||||  ||||||||  ||||||
                                TTTC  GTACCTTT  CTTTGG
                                  CG      ___
GAM1397 SMC1L1  3' TAAAAAGTGGGACCAGAAC  35839      CA  AAA  TG
                                TAAAAAG  TGG  AT  GAAC
                                |||||||  |||  ||  ||||
                                ATTTTTC  ACC  TG  CTTG
                                    __  C__  GT
GAM1397 SMC1L1  3' TAAAAAGCAATATACAGATTGG 35838       TGGAAA__
             AA                   TAAAAAGCA      ATTGGAA
                                |||||||||      |||||||
                                ATTTTTCGT      TAACCTT
                                     TATATGTC
GAM1397 SOX6    3' ACAAATGGAAAATTGGAA   35840    __
                                GCA  TGGAAAATTGGAA
                                |||  ||||||||||||
                                TGT  ACCTTTTAACCTT
                                  TT
GAM1397 TRAF6   3' AAAAAGCATGGAACGTGTGGA  35841          AAT_
                                AAAAAGCATGGAA   TGGA
                                ||||||||||||   ||||
                                TTTTTCGTACCTT   ACCT
                                       GCAC
GAM1397 XLKD1   3' TAAGGAGCATGAAAGAAAC   35842    AA      AATT
                                TAA  AGCATGGAA   GGAAC
                                |||  |||||||||   |||||
                                ATT  TCGTACTTT   CTTTG
                                  CC       _____
GAM1397 LOC127702 3' AACAGGAAATTGGAACC    35843    T   A
                                AGCA GGAAA TTGGAACC
                                |||| ||||| ||||||||
                                TTGT CCTTT AACCTTGG
                                  _    _
GAM1397 LOC143154 3' TAAGAAGCATGAGAAAAGGAA  35844    A    _   TT
                                TAA AAGCATG GAAAA  GGAA
                                ||| ||||||| |||||  ||||
                                ATT TTCGTAC CTTTT  CCTT
                                  C      T   __
GAM1397 LOC143383 5' TGAACACAAAGATTGGAAC   35845   A   TG  AA
                                A AGCA  GA  ATTGGAAC
                                | ||||  ||  ||||||||
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                                A TTGT  TT  TAACCTTG
                                 C    GT  C_
GAM1397  LOC144317 5'  AAAAAAAAAAAAAAAATTGGAGC 35846       CAT         A
                C                 AAAAAG   GGAAAATTGGA CC
                                  ||||||   |||||||||||  ||
                                  TTTTTT   TTTTTTAACCT GG
                                     TTT         C
GAM1397  LOC148549 5'  TGAACACGAAGATTGGAAC    35847    A       AA
                                  A AGCATGGA  ATTGGAAC
                                  | ||||||||  ||||||||
                                  A TTGTGCTT  TAACCTTG
                                   C       C_
GAM1397  LOC149711 5'  AAGCATGGATAGAAC       35848          AAAT
                                  AAGCATGGA    TGGAAC
                                  |||||||||    ||||||
                                  TTCGTACCT    ATCTTG
                                               ____
GAM1397  LOC163590 3'  AAAGATATAGCCAATTGGAA   35849      C_    AA
                                  AAAG  ATGG  AATTGGAA
                                  ||||  ||||  ||||||||
                                  TTTC  TATC  TTAACCTT
                                    TA    GG
GAM1397  LOC196264 3'  TAAAAAGCAAGGGACTAG     35850          T  AAA
                                  TAAAAAGCA GG   ATTGG
                                  |||||||||  ||   |||||
                                  ATTTTTCGT CC   TGATC
                                        T  C__
GAM1397  LOC219294 3'  TAAGAAGCATGAGAAAAGGAA  35844     A      _     TT
                                  TAA AAGCATG GAAAA  GGAA
                                  |||  |||||||  |||||  ||||
                                  ATT TTCGTAC CTTTT  CCTT
                                    C      T    __
GAM1397  LOC219621 3'  AGATAGCAAAATTGGGACC    35851    C    _       A
                                  AG ATGG AAAATTGG ACC
                                  ||  ||||  ||||||||  |||
                                  TC TATC TTTTAACC TGG
                                   _   G       C
GAM1397  LOC220534 3'  TAAAAAGCATGGCAGCCTG    35852           AAAA
                                  TAAAAAGCATGG    TTG
                                  ||||||||||||    |||
                                  ATTTTTCGTACC    GAC
                                         GTCG
GAM1397  LOC90736  3'  ACAAGGAATTGGAATTGGGACC 35853     T    ____      A
                                  GCA GGAA    AATTGG ACC
                                  |||  ||||    ||||||  |||
                                  TGT CCTT    TTAACC TGG
                                    T    AACC     C
GAM1398  ATP2B4    5'  GTCCAGGGTAGGTAGGTTCC   35856        TCCGCA
                                  GTTCAGG     TAGGTTCC
                                  |||||||     ||||||||
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                                CAGGTCC     ATCCAAGG
                                    CATCC_
GAM1398 CDH5     3' GTTTGGGTCCCCAGGCCCA   35857     CA    G  TA  TT
                                GTT  GGTCC CA  GG  CCCA
                                |||  ||||| ||  ||  ||||
                                CAA  CCAGG GT  CC  GGGT
                                  AC    G  __  __
GAM1398 DFFB     3' GTTCAGATCCGCGTGTTTCCTT 35858          ATAGG  __
             CCAG                  GTTCAGGTCCGC    TTC  CCAG
                                |||||||||||    |||  ||||
                                CAAGTCTAGGCG    AGG  GGTC
                                      CACAA   AA
GAM1398 GFRA1    5' GTTCAGGTCCGACCCAA     35859          CATAGGTT
                                GTTCAGGTCCG      CCCAG
                                ||||||||||       |||||
                                CAAGTCCAGGC      GGGTT
                                      T________
GAM1398 FLJ10101 3' GTTCAGGTCCCCAGACCCA   35860         G  TAGGTT
                                GTTCAGGTCC CA     CCCA
                                |||||||||| ||     ||||
                                CAAGTCCAGG GT     GGGT
                                     G  CT_____
GAM1398 FLJ10101 3' GTTCAGGTCCCCAGACCCA   35860         G  TAGGTT
                                GTTCAGGTCC CA     CCCA
                                |||||||||| ||     ||||
                                CAAGTCCAGG GT     GGGT
                                     G  CT_____
GAM1398 FLJ10101 3' GTTCAGGTCCCCAGACCCA   35860         G  TAGGTT
                                GTTCAGGTCC CA     CCCA
                                |||||||||| ||     ||||
                                CAAGTCCAGG GT     GGGT
                                     G  CT_____
GAM1398 FLJ10101 3' GTTCAGGTCCCCAGACCCA   35860         G  TAGGTT
                                GTTCAGGTCC CA     CCCA
                                |||||||||| ||     ||||
                                CAAGTCCAGG GT     GGGT
                                     G  CT_____
GAM1398 FLJ10101 3' GTTCAGGTCCCCAGACCCA   35860         G  TAGGTT
                                GTTCAGGTCC CA     CCCA
                                |||||||||| ||     ||||
                                CAAGTCCAGG GT     GGGT
                                     G  CT_____
GAM1398 FLJ10751 3' GTTCAGGTTCCCACCAGTCCAG 35861         _  G   A   TC
                                GTTCAGGT CC CAT GGT  CCAG
                                |||||||| || ||| |||  ||||
                                CAAGTCCA GG GTG TCA  GGTC
                                     A  _   G   __
GAM1398 FLJ10751 3' GTTCAGGTTCCCACCAGTCCAG 35861         _  G   A   TC
                                GTTCAGGT CC CAT GGT  CCAG
                                |||||||| || ||| |||  ||||
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                                CAAGTCCA GG GTG TCA  GGTC
                                    A  _   G   __
GAM1398  FLJ25059  5'  GTTCAGGTCTGAAATTCC    35862         CGCAT
                                GTTCAGGTC    AGGTTCC
                                |||||||||    |||||||
                                CAAGTCCAG    TTTAAGG
                                    AC___
GAM1398  KIAA1691  3'  GTTCAGGCCTCAGTTCC     35863        T  GCATA
                                GTTCAGG CC    GGTTCC
                                ||||||| ||    ||||||
                                CAAGTCC GG    TCAAGG
                                   _  AG___
GAM1398  KIAA1706  3'  GCTCAGGTCTGTGGCATCCAG  35864         CGCATA   TC
                                GTTCAGGTC     GGT  CCAG
                                |||||||||     |||  ||||
                                CGAGTCCAG     CCG  GGTC
                                    ACA___   TA
GAM1398  MGC15875  5'  GCTCAGGTTCGCACTCGG    35865        C    A_
                                GTTCAGGT CGCAT  GG
                                |||||||| |||||  ||
                                CGAGTCCA GCGTG  CC
                                    A    AG
GAM1398  MGC20235  5'  GTTCAGGTCTGGGATCCCA    35866         CGCATA  T
                                GTTCAGGTC     GG TCCCA
                                |||||||||     || |||||
                                CAAGTCCAG     CC AGGGT
                                    AC____  T
GAM1398  SSI-1    3'  GTTCAGGTCCTGGCTCC     35867          GCATA
                                GTTCAGGTCC    GGTTCC
                                ||||||||||    ||||||
                                CAAGTCCAGG    CCGAGG
                                    A____
GAM1398  STK17A   5'  GTTCAGGCCCGCTTCTTTCC   35868          ATAGG
                                GTTCAGGTCCGC    TTCC
                                ||||||||||||    ||||
                                CAAGTCCGGGCG    AAGG
                                      AAGA_
GAM1398  TTC4     3'  ATTCAGGTGTGCTAGGTTCCCA 35869         CC  A
            G                    GTTCAGGT  GC TAGGTTCCCAG
                                ||||||||  || ||||||||||
                                TAAGTCCA  CG ATCCAAGGGTC
                                    CA  _
GAM1398  ZFD25    3'  ATTCAGGTTTGTAAAGTTTTCA 35870        CCGCAT    CC
            G                    GTTCAGGT     AGGTT  CAG
                                ||||||||     |||||  |||
                                TAAGTCCA     TTCAA  GTC
                                    AACAT_    AA
GAM1398  LOC145858 5'  GTCTGGGTCAGTGGTTCCCAG  35871     CA   CGCATA
                                GTT  GGTC     GGTTCCCAG
                                |||  ||||     |||||||||
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                                CAG  CCAG     CCAAGGGTC
                                  AC    TCA___
GAM1398  LOC152849 3'  GTTCAGGTCCGCGGCCCCC   35872          ATA
                                GTTCAGGTCCGC   GGTTCCC
                                ||||||||||||   |||||||
                                CAAGTCCAGGCG   CCGGGGG
                                       ___
GAM1398  LOC165552 3'  GTTTAGGTCCTCATAAGCC   35873     C     G
                                GTT AGGTCC CATAGGTT
                                ||| |||||| ||||||||
                                CAA TCCAGG GTATTCGG
                                  A     A
GAM1398  LOC201227 3'  GTTCGGGTCCCACAGGCCCAG  35874     A    G     TT
                                GTTC GGTCC CATAGG  CCCAG
                                |||| ||||| ||||||  |||||
                                CAAG CCAGG GTGTCC  GGGTC
                                  C    _     __
GAM1398  LOC202546 3'  GTTCAGGTCCTGCTCC      35875          GCATAG
                                GTTCAGGTCC     GTTCC
                                ||||||||||     |||||
                                CAAGTCCAGG     CGAGG
                                     A_____
GAM1398  LOC255251 5'  GCTCAGGTTCGCACTCGG    35865        C    A_
                                GTTCAGGT CGCAT  GG
                                |||||||| |||||  ||
                                CGAGTCCA GCGTG  CC
                                     A     AG
GAM1398  LOC257460 5'  GTTCAGGTCCTGCTCC      35875          GCATAG
                                GTTCAGGTCC     GTTCC
                                ||||||||||     |||||
                                CAAGTCCAGG     CGAGG
                                     A_____
GAM1398  LOC91960  3'  TTCAGGAAGAGGTGGGTTCCCA 35876       TCCGCATA
            G                    TTCAGG       GGTTCCCAG
                                ||||||       |||||||||
                                AAGTCC       CCAAGGGTC
                                   TTCTCCAC
GAM1399  CDH12    3'  AATTTAGTAACTTACTAGA   35879          AGA  G
                                AATTTAGTAAC   TA TAGA
                                ||||||||||   || ||||
                                TTAAATCATTG   AT ATCT
                                     A__  G
GAM1399  DSC3     3'  ATGAATTTGGTAGTGCAGTAG  35880        A   ACAGA
                                ATGAATTT GTA     TAGTAG
                                ||||||||| |||    ||||||
                                TACTTAAA CAT     GTCATC
                                     C   CAC__
GAM1399  DSC3     3'  ATGAATTTGGTAGTGCAGTAG  35880        A   ACAGA
                                ATGAATTT GTA     TAGTAG
                                ||||||||| |||    ||||||
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                                TACTTAAA CAT    GTCATC
                                    C   CAC__
GAM1399  TRHDE    3'  ATGAATTCAGTGGTGATAG   35881          AACA
                                ATGAATTTAGT   GATAG
                                ||||||||||   |||||
                                TACTTAAGTCA   CTATC
                                     CCA_
GAM1399  FLJ10324 5'  TGAATAGCAGCAGGTAGTAGA 35882     TT    A  A
                                TGAA  TAGTA CAG TAGTAGA
                                ||||  ||||| ||| |||||||
                                ACTT  ATCGT GTC ATCATCT
                                  __    C  C
GAM1399  FLJ20986 5'  ATGACATTTAGTACATAGTAGA 35883     _      A  GA
                                ATGA ATTTAGTA CA  TAGTAGA
                                |||| |||||||| ||  |||||||
                                TACT TAAATCAT GT  ATCATCT
                                  G      _ __
GAM1399  PGGT1B   5'  ATGGATTTTGTAACAGAATCCC 35884    A   A      TAG__
           TAGA                   ATG ATTT GTAACAGA    TAGA
                                ||| |||| ||||||||    ||||
                                TAC TAAA CATTGTCT    ATCT
                                  C   A      TAGGG
GAM1399  LOC200269 3'  ATGGATTTAGTAATAAATAG   35885    A       C
                                ATG ATTTAGTAA AGATAG
                                ||| |||||||| ||||||
                                TAC TAAATCATT TTTATC
                                  C       A
GAM1399  LOC219899 3'  TGAGTTAGTAACATACAAAGA  35886    AT      G   T
                                TGA  TTAGTAACA ATAG AGA
                                |||  ||||||||| |||| |||
                                ACT  AATCATTGT TGTT TCT
                                  C_       A   _
GAM1399  LOC253971 3'  TGGATTTAGTATCAGACCACAG 35887    A      A    AG
           A                     TG ATTTAGTA CAGAT  TAGA
                                || |||||||| |||||  ||||
                                AC TAAATCAT GTCTG  GTCT
                                 C       A    GT
GAM1399  LOC63875  3'  ATGAATTTACTATCTCAGGTAG 35888        G  A__  ATA
           A                     ATGAATTTA TA   CAG   GTAGA
                                |||||||| ||   |||   |||||
                                TACTTAAAT AT   GTC   CATCT
                                     G  AGA   ___
GAM1400  ABCC11   3'  AAGTAGCCTATTCCAGGGT   35891    C    CC   AA
                                AAG AGCCTA  CCG  GGT
                                ||| ||||||  |||  |||
                                TTC TCGGAT  GGT  CCA
                                  A     AA  C_
GAM1400  ATP1A2   3'  ACAGCCTTTGGGAGGTGGTT   35892       ACCCC  A
                                GCAGCCT    GA GGTGGTT
                                |||||||    || |||||||
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                                TGTCGGA    CT CCACCAA
                                   AACC_  _
GAM1400 BTG1    5' AGCAGCCACCCCGGGC     35893       T    AA
                                AGCAGCC ACCCCG  GGT
                                ||||||| ||||||  |||
                                TCGTCGG TGGGGC  CCG
                                   _    __
GAM1400 LIMD1   3' AAGCAGTGTACCTTATCCTGGT 35894      CC   CCGAAGG
           T                     AAGCAG  TACC      TGGTT
                                ||||||  ||||      |||||
                                TTCGTC  ATGG      ACCAA
                                   AC    AATAGG_
GAM1400 LPO     3' GCAGCCACCCTGGGGC     35895       T   CGAA  T
                                GCAGCC ACCC    GG GGT
                                |||||| ||||    || |||
                                CGTCGG TGGG    CC CCG
                                   _    A___  _
GAM1400 MYO1D   3' AAGCGGCCGACCCTGAGGGC   35896     A   T    C  A
                                AAGC GCC ACCC GA GGT
                                |||| ||| |||| || |||
                                TTCG CGG TGGG CT CCG
                                  C   C    A  C
GAM1400 RFNG    3' GCAGCCCTGGGTCGGGGTGGTT 35897       ACCC_  AA
                                GCAGCCT    CG  GGTGGTT
                                |||||||    ||  |||||||
                                CGTCGGG    GC  CCACCAA
                                   ACCCA  C_
GAM1400 SFN     3' AAGTAGCCTGGTCCTGGGGT   35898     C    ACC  GAA  T
                                AAG AGCCT   CC   GG GGT
                                ||| |||||   ||   || |||
                                TTC TCGGA   GG   CC CCA
                                  A    CCA  A__  _
GAM1400 WNT3A   3' AGCAGCCTACCCCAGAGCCG   35899           A  G
                                AGCAGCCTACCCCG AG TG
                                |||||||||||||| || ||
                                TCGTCGGATGGGGT TC GC
                                        C  G
GAM1400 ZNF76   3' AGCTGGCCTCCAGGGAGGTGGT 35900     A_   A  CCGA
           T                     AGC  GCCT CC    AGGTGGTT
                                |||  |||| ||   ||||||||
                                TCG  CGGA GG    TCCACCAA
                                  AC    _  TCCC
GAM1400 C21orf55 5' AGCCGGCTGCGAAGGTGGTT   35901     TACCC
                                AGCC    CGAAGGTGGTT
                                ||||    ||||||||||
                                TCGG    GCTTCCACCAA
                                  CCGAC
GAM1400 DKFZP434I2117 3' AGCTGGCCTACCCTGGAGA   35902     A_      CGAA  T
                                AGC  GCCTACCC    GG GG
                                |||  ||||||||    || ||
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                              TCG  CGGATGGG   CC CT
                                AC       A___  T
GAM1400  FKBP5    3'  GCAGCCTAAAAGGTGGT    35903        CCCC
                              GCAGCCTA   GAAGGTGGT
                              ||||||||   |||||||||
                              CGTCGGAT   TTTCCACCA
                                         ____
GAM1400  FLJ10704 3'  AAGCAGCCGTGTCCCGAGG   35904        TAC_   A
                              AAGCAGCC   CCCGA GG
                              ||||||||   ||||| ||
                              TTCGTCGG   GGGCT CC
                                  CACA   _
GAM1400  FLJ12568 3'  AAGCAGTCAATTTCCTGGTGGT 35905       CCTACC_ GAA
           T                   AAGCAG     CC   GGTGGTT
                              ||||||     ||   |||||||
                              TTCGTC     GG   CCACCAA
                                 AGTTAAA  A__
GAM1400  FLJ22479 5'  GCAGCCTGCTGCGGAGGGGTT  35906       ACCC  A   T
                              GCAGCCT   CG AGG GGTT
                              |||||||   || ||| ||||
                              CGTCGGA   GC TCC CCAA
                                  CGAC  C   _
GAM1400  H2-ALPHA 3'  AAGCAGCCATCCCGGGGGT   35907        TAC   AA  T
                              AAGCAGCC   CCCG  GG GGT
                              ||||||||   ||||  || |||
                              TTCGTCGG   GGGC  CC CCA
                                  TA_    __  _
GAM1400  KIAA0847 3'  AAGCAGTCTACTCTGGTCAGTT 35908       C   CCCGAA  _
                              AAGCAG CTAC     GGT GGTT
                              |||||| ||||     ||| ||||
                              TTCGTC GATG     CCA TCAA
                                 A   AGA___   G
GAM1400  KIAA1706 3'  GCAGCTCTGCCCTGAAGCGT   35909      _  A   C   _
                              GCAGC CT CCC GAAG GT
                              ||||| || ||| |||| ||
                              CGTCG GA GGG CTTC CA
                                 A  C   A   G
GAM1400  KIAA1822 5'  AAGCAGCTGGCCCCCGTTGTGG 35910       CTA_   AAG
           TT                  AAGCAGC   CCCCG   GTGGTT
                              |||||||   |||||   ||||||
                              TTCGTCG   GGGGC   CACCAA
                                 ACCG    AA_
GAM1400  NICN1    3'  AGCAGCCTGCATCACTTAATGG 35911        ACCC  AA_
           TT                  AGCAGCCT   CG   GGTGGTT
                              ||||||||   ||   |||||||
                              TCGTCGGA   GT   TTACCAA
                                  CGTA  GAA
GAM1400  NUDT11   5'  GCAGCCTCCTCGAGGC     35912        A  C   A
                              GCAGCCT CC CGA GGT
                              ||||||| || ||| |||
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                                CGTCGGA GG GCT CCG
                                   _ A  _
GAM1400 POLR3K   3' AAGCATCTACCCCGAGGG   35913     GC      A
                                AAGCA  CTACCCCGA GG
                                |||||  ||||||||| ||
                                TTCGT  GATGGGGCT CC
                                  A_       C
GAM1400 PRO0611  3' AGCTCACCCACTCAGTGGTT  35914    C    CGAA
                                AGC TACCC   GGTGGTT
                                ||| |||||   |||||||
                                TCG GTGGG   TCACCAA
                                 A    TGAG
GAM1400 PTPRT    3' AAGCAGCTGTTCCCTATGGTT 35915      CTAC  GAAG
                                AAGCAGC   CCC   GTGGTT
                                |||||||   |||   ||||||
                                TTCGTCG   GGG   TACCAA
                                    ACAA  A___
GAM1400 RFX4     3' AGTAGCTTACTAGAAGTGGTT 35916   C  C  CCC   G
                                AG AGC TAC  GAAG TGGTT
                                || ||| |||  |||| |||||
                                TC TCG ATG  CTTC ACCAA
                                 A  A  AT_  _
GAM1400 RLUCL    3' AGCAGCCCATCCTGGAGG    35917       C  CGAA  T
                                AGCAGCCTA CC   GG GG
                                ||||||||| ||   || ||
                                TCGTCGGGT GG   CC CC
                                     A  A___  T
GAM1400 TOM1     3' AGCCAGCCTGTCCTGGGGCC  35918    _   AC  CGAA  T
                                AGC AGCCT  CC   GG GGTT
                                ||| |||||  ||   || ||||
                                TCG TCGGA  GG   CC CCGG
                                  G    CA  A___  _
GAM1400 LOC121506 5' GCAGCCTACTCTGTAGCTGATT 35919       CCCGA  G
                                GCAGCCTAC    AG TGGTT
                                |||||||||    || |||||
                                CGTCGGATG    TC ACTAA
                                     AGACA  G
GAM1400 LOC145135 5' AGGAGCCTGCTCCGAAGGT   35920   C    ACC
                                AG AGCCT   CCGAAGGT
                                || |||||   ||||||||
                                TC TCGGA   GGCTTCCA
                                 C    CGA
GAM1400 LOC145678 3' AAGCAGCCTACTTGAACAT   35921       CCC   G
                                AAGCAGCCTAC   GAA GT
                                ||||||||||   ||| ||
                                TTCGTCGGATG   CTT TA
                                      AA_   G
GAM1400 LOC146774 3' AAGCGGCCTCACCTCGAA    35922     A   _  C
                                AAGC GCCT ACC CGAA
                                |||| |||| ||| ||||
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                                TTCG CGGA TGG GCTT
                                  C   G   A
GAM1400  LOC150157 5'  GCAGTCGTCCCCTTGATGGTT  35923     CCTA   GAA
                                GCAG   CCCC   GGTGGTT
                                ||||   ||||   |||||||
                                CGTC   GGGG   CTACCAA
                                  AGCA   AA_
GAM1400  LOC151188 3'  AAGCAGTTTGACTACTTAATGG 35924      C____   CCCGAA
           TT                    AGCAG    CTAC     GGTGGTT
                                |||||    ||||     |||||||
                                TCGTC    GATG     TTACCAA
                                  AAACT   AA____
GAM1400  LOC196890 5'  GCAGTCGTCCCCTTGATGGTT  35923     CCTA   GAA
                                GCAG   CCCC   GGTGGTT
                                ||||   ||||   |||||||
                                CGTC   GGGG   CTACCAA
                                  AGCA   AA_
GAM1400  LOC51644  3'  AGCAGTTTATGAAGGTGGTT   35925     CCTACCCC
                                AGCAG       GAAGGTGGTT
                                |||||       ||||||||||
                                TCGTC       CTTCCACCAA
                                  AAATA___
GAM1401  GALK1     5'  CCCCGTCGGCGCGGGATGCTC  35928          ACGC
                                CCCCGTTGGCGCG   GCTT
                                ||||||||||||   ||||
                                GGGGCAGCCGCGC   CGAG
                                      CCTA
GAM1401  NMB       5'  CGTTCGGGCGCGCTTC      35929     _  C  GAC
                                CGTT GG GC   GCGCTTC
                                |||| || ||   |||||||
                                GCAA CC CG   CGCGAAG
                                  G  _  ___
GAM1401  FLJ20551  5'  CGCTAGCCAGGCGACGCGCTT  35930       ___
                                CGTTGGC   GCGACGCGCTT
                                |||||||   ||||||||||
                                GCGATCG   CGCTGCGCGAA
                                    GTC
GAM1401  KIAA1580  5'  CCCGTTGGCGCAGACCTTC    35931         _  GCG
                                CCCGTTGGCGC GAC   CTTC
                                |||||||||| |||   ||||
                                GGGCAACCGCG CTG   GAAG
                                      T  ___
GAM1401  LOC138389 5'  CCCCGTTGGCCGGCGGGGC    35932         __  AC
                                CCCCGTTGGC  GCG  GC
                                ||||||||||  |||  ||
                                GGGGCAACCG  CGC  CG
                                      GC   CC
GAM1402  ADARB1    5'  GCCGCTTGGCCGCCGCTG    35935      C    AC  _
                                GCCGC TGGCC  GTC CTG
                                ||||| |||||  ||| |||
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                                CGGCG ACCGG  CGG GAC
                                  A    __  C
GAM1402  ADARB1   5'  GCCGCTTGGCCGCCGCTG   35935     C    AC  _
                                GCCGC TGGCC  GTC CTG
                                ||||| |||||  ||| |||
                                CGGCG ACCGG  CGG GAC
                                  A    __  C
GAM1402  ALPL     3'  GCTTCCTGGGACCCTGGTG   35936   CG    CCACG
                                GC  CCTGG    TCCTGGTG
                                ||  |||||    ||||||||
                                CG  GGACC    GGGACCAC
                                 AA    CT___
GAM1402  AMN      3'  CAGCCTCTGGCCGCCCAGGTG  35937     GC    AC   T
                                CAGCC  CTGGCC  GTCC GGTG
                                |||||  ||||||  |||| ||||
                                GTCGG  GACCGG  CGGG CCAC
                                  A_     __   T
GAM1402  MMP2     3'  GCCACCTGGCCATGCCCTG   35938          C
                                GCCGCCTGGCCA GTCCTG
                                |||||||||||| ||||||
                                CGGTGGACCGGT CGGGAC
                                       A
GAM1402  NCOR2    3'  GCCGCCCTGGCCGCCTG     9949       _    AC T
                                GCCGCC TGGCC  G CCTG
                                |||||| |||||  | ||||
                                CGGCGG ACCGG  C GGAC
                                   G    __ _
GAM1402  NFKB2    5'  CAGCCGCCTGTCCGGG      35939        GGCCAC   T
                                CAGCCGCCT     GTCC GG
                                |||||||||     |||| ||
                                GTCGGCGGA     CAGG CC
                                      _______   C
GAM1402  PAX5     3'  GCTCTCTGCCATCCTGGTG   35940   _ G_   CG
                                GC CT  GCCA  TCCTGGTG
                                || ||  ||||  ||||||||
                                CG GA  CGGT  AGGACCAC
                                 A  GA   __
GAM1402  PITX1    5'  GCCGCCTGGCTGCGACCTG   35941         CA  T
                                GCCGCCTGGC  CG CCTG
                                ||||||||||  || ||||
                                CGGCGGACCG  GC GGAC
                                      AC  T
GAM1402  SORCS2   3'  CAGCCGCCGGCTTTGCTGGTG  35942        T   CACGTC
                                CAGCCGCC GGC     CTGGTG
                                |||||||| |||     ||||||
                                GTCGGCGG CCG     GACCAC
                                     _  AAAC__
GAM1402  TNFRSF6B 3'  CAGCTCCTGGTACCCTGGT   35943     CG    CCACG
                                CAGC  CCTGG    TCCTGGT
                                ||||  |||||    |||||||
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                                GTCG  GGACC    GGGACCA
                                  A_    AT___
GAM1402  C21orf25  3'  CACACTGGCTGCGTCCTGGTG  35944    _    CA
                                CGC CTGGC  CGTCCTGGTG
                                ||| |||||  ||||||||||
                                GTG GACCG  GCAGGACCAC
                                  T    AC
GAM1402  FLJ23042  3'  GCCTGCCTGGCCAGAGGT    35945    _      CGTCCT
                                GCC GCCTGGCCA    GGT
                                ||| |||||||||     |||
                                CGG CGGACCGGT    CCA
                                  A       CT____
GAM1402  GBTS1    3'  CAGCCTCCTCTGGTCCTGGTG  35946     G   GGCCAC
                                CAGCC CCT    GTCCTGGTG
                                ||||| |||    |||||||||
                                GTCGG GGA    CAGGACCAC
                                   A   GAC___
GAM1402  HEYL     3'  CAGCCTGCCTTGGGTCCTGGTG 35947     _   _ CCAC
                                CAGCC GCCT GG   GTCCTGGTG
                                ||||| |||| ||   |||||||||
                                GTCGG CGGA CC   CAGGACCAC
                                   A   A ____
GAM1402  HMT-1    3'  CAGCTTCTGGCCACTGGGAGGT 35948    CGC      GTCCT
            G                    CAGC   CTGGCCAC    GGTG
                                ||||   ||||||||    ||||
                                GTCG   GACCGGTG    CCAC
                                  AA_      ACCCT
GAM1402  KIAA0140  3'  CAGCCCCTGGCAGTTTGGT   35949     G    CAC  CC
                                CAGCC CCTGGC   GT  TGGT
                                ||||| ||||||   ||  ||||
                                GTCGG GGACCG   CA  ACCA
                                  _     T__  A_
GAM1402  KIAA1941  3'  CCGCCTGGCCATGTTTCTCTG  35950         CG__  _
                                CCGCCTGGCCA    TC CTG
                                ||||||||||    || |||
                                GGCGGACCGGT    AG GAC
                                      ACAA  A
GAM1402  LIECG3   5'  GCTCCTGGGCCCTGGT     35951    CG    CCAC
                                GC  CCTGG    GTCCTGGT
                                ||  |||||    ||||||||
                                CG  GGACC    CGGGACCA
                                 A_    _____
GAM1402  MAP4K4   3'  CAGCTGTCCTGGTTGCCCTCGG 35952     CG_    CCAC    _
            TG                    CAGC   CCTGG    GTCCT GGTG
                                ||||   |||||    ||||| ||||
                                GTCG   GGACC    CGGGA CCAC
                                  ACA    AA__     G
GAM1402  MGC26655  3'  CAGTCTCTGGCCACTAAGGTG  35953    CCGC      GTCCT
                                CAG    CTGGCCAC    GGTG
                                |||    ||||||||    ||||
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                                GTC   GACCGGTG    CCAC
                                  AGA_      ATT__
GAM1402 NLI-IF   3' ACCGCCTGGTGGGGCTGGTG  35954        CCACGTC
                                GCCGCCTGG     CTGGTG
                                |||||||||     ||||||
                                TGGCGGACC     GACCAC
                                     ACCCC__
GAM1402 PRO0529  3' GCCACCTGGTCCCATTGGTG  35955        _ A  CC
                                GCCGCCTGG CC CGT  TGGTG
                                ||||||||| || |||  |||||
                                CGGTGGACC GG GTA  ACCAC
                                     A  _  __
GAM1402 TIX1     3' CAGCTGCCTAGTGCACTGGTG 35956     C     CCAC TC
                                CAGC GCCTGG   G  CTGGTG
                                |||| ||||||   |  ||||||
                                GTCG CGGATC   C  GACCAC
                                  A     A___ GT
GAM1402 UPLC1    3' CAGCTGTGTTGGCCATTGGTG 35957     CGCC_     CGTCC
                                CAGC    TGGCCA    TGGTG
                                ||||    ||||||    |||||
                                GTCG    ACCGGT    ACCAC
                                  ACACA     A_____
GAM1402 ZDHHC5   3' GCCACCTGGGGCCCTTTGGTG 35958        CCAC    __
                                GCCGCCTGG   GTCCT  GGTG
                                |||||||||   |||||  ||||
                                CGGTGGACC   CGGGA  CCAC
                                     C___     AA
GAM1402 LOC144810 5' GCCGCCTGGCGTGCTTGGTG  35959        CAC  CC
                                GCCGCCTGGC   GT  TGGTG
                                ||||||||||   ||  |||||
                                CGGCGGACCG   CG  ACCAC
                                     CA_  A_
GAM1402 LOC153565 5' GCGGCCTTTAGTCCTGGTG   35960    C   GGCCAC
                                GC GCCT     GTCCTGGTG
                                || ||||     |||||||||
                                CG CGGA     CAGGACCAC
                                 C   AAT___
GAM1402 LOC202860 3' CAGCCTCTCTTGTGTCTTGGTG 35961      GC  GGCCAC   C
                                CAGCC  CT     GTC TGGTG
                                |||||  ||     ||| |||||
                                GTCGG  GA     CAG ACCAC
                                   A_  GAACA_   A
GAM1402 LOC204994 5' TGACCGCCTGGTGCTGGT    35962    A       CCACGTC
                                C GCCGCCTGG      CTGGT
                                | |||||||||      |||||
                                A TGGCGGACC      GACCA
                                 C        AC_____
GAM1402 LOC255452 5' CAGTCGCATGCTCCTGGT    35963     C   CTG  CACG
                                CAG CGC   GC    TCCTGGT
                                ||| |||   ||    |||||||
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                                GTC GCG   CG    AGGACCA
                                  A   TA_  _____
GAM1402  LOC256032 5'  CAGCAGTCTGGAGATCCTGGTG 35964      CGC    CCAC
                                CAGC   CTGG    GTCCTGGTG
                                ||||   ||||    |||||||||
                                GTCG   GACC    TAGGACCAC
                                  TCA    TC__
GAM1402  LOC55565  5'  AGCCGCCTGGCTGTTCACCTG  35965          CACGT_
                                AGCCGCCTGGC     CCTG
                                ||||||||||     ||||
                                TCGGCGGACCG     GGAC
                                      ACAAGT
GAM1402  LOC58509  5'  GCCGCAGCACGTCCTGGTG   35966      CT   C
                                GCCGC  GGC ACGTCCTGGTG
                                |||||  ||| ||||||||||
                                CGGCG  TCG TGCAGGACCAC

                                  __   _
GAM1402  LOC91316  3'  AGCTGCTGGCCACGTACT    35967     C  C       C
                                AGC GC TGGCCACGT CT
                                ||| || |||||||| ||
                                TCG CG ACCGGTGCA GA
                                  A  _        T
GAM1403  B4GALT1   3'  GTGCCCTGGCTGTGCCTTGGG  35970        A  ACGG   C_
                                GTGCCCTG GT    GCT  GGG
                                |||||||| ||    |||  |||
                                CACGGGAC CG    CGG  CCC
                                     _  ACA_   AA
GAM1403  EPHB3    3'  GCCCTGAGGGGCTTGGG     35971         TAC    C
                                GCCCTGAG   GGGCT GGG
                                ||||||||   ||||| |||
                                CGGGACTC   CCCGA CCC
                                     ___     A
GAM1403  FAAH     3'  GTGCCCTGACTAGGCTGGG    35972         G AC    C
                                GTGCCCTGA T  GGGCT GGG
                                ||||||||| |  ||||| |||
                                CACGGGACT A  TCCGA CCC
                                     G __    _
GAM1403  HM13     3'  GCCCTGAGAGGCTCGG      35973         TAC
                                GCCCTGAG   GGGCTCGG
                                ||||||||   ||||||||
                                CGGGACTC   TCCGAGCC
                                     ___
GAM1403  LAMA4    5'  GTGCTCTTCCAGGGCTCGGG   35974      C  GAGTAC
                                GTGC CT     GGGCTCGGG
                                ||||  ||     |||||||||
                                CACG GA     CCCGAGCCC
                                  A  AGGT__
GAM1403  LRP3     5'  GCTCTGGCTGCGGCTCGGG    35975    C   A  ACG
                                GC CTG GT   GGCTCGGG
                                ||  ||| ||   ||||||||
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                                CG GAC CG   CCGAGCCC
                                 A   _  ACG
GAM1403  MASP1    3'  GTCCCTGAGTATTCAGCCTGGG 35976    G       CG_  TC
                                GT CCCTGAGTA   GGC  GGG
                                || |||||||||   |||  |||
                                CA GGGACTCAT   TCG  CCC
                                 _       AAG   GA
GAM1403  MYLK2    3'  GCCCTGAGGCAAGCTCGGG   35977        TA
                                GCCCTGAG  CGGGCTCGGG
                                ||||||||  ||||||||||
                                CGGGACTC  GTTCGAGCCC
                                     C_
GAM1403  PPOX     5'  CGGCCCTCGCAGGGCTCGGG  35978    T    GA   C
                                CG GCCCT  GTA GGGCTCGGG
                                || |||||  ||| |||||||||
                                GC CGGGA  CGT CCCGAGCCC
                                 _    G_  _
GAM1403  SLC4A2   5'  CGTGCCCCGGGGGTCTCGGG  35979        AGTAC  _
                                CGTGCCCTG    GGG CTCGGG
                                |||||||||    ||| ||||||
                                GCACGGGGC    CCC GAGCCC
                                     C____  A
GAM1403  C5orf6   3'  GTGCCCTGGGGCTTTGG     35980        AGTAC    C_
                                GTGCCCTG    GGGCT  GG
                                ||||||||    |||||  ||
                                CACGGGAC    CCCGA  CC
                                     _____    AA
GAM1403  FBXO32   5'  CCGGCCTGGTGGGCTCGG    35981    T   C  A  AC
                                CCG GCC TG GT  GGGCTCGG
                                ||| ||| || ||  ||||||||
                                GGC CGG AC CA  CCCGAGCC
                                 _  _  _  __
GAM1403  LSR7     5'  CCTGCAACAGGGCTCGGG    35982     AGT  _
                                CCTG   AC GGGCTCGGG
                                ||||   || |||||||||
                                GGAC   TG CCCGAGCCC
                                  GT_  T
GAM1403  PRKWNK2  5'  CGTGCCCACGGGCTCGG     35983       TGAGT
                                CGTGCCC    ACGGGCTCGG
                                |||||||    ||||||||||
                                GCACGGG    TGCCCGAGCC
                                     _____
GAM1403  SHANK3   3'  GTGCGCTGGGTGGGCTGGG   35984     C   A  AC    C
                                GTGC CTG GT  GGGCT GGG
                                |||| ||| ||  ||||| |||
                                CACG GAC CA  CCCGA CCC
                                  C   C  __    _
GAM1403  SMARCF1  5'  CCGGCTCTGTAGGCTCGG    35985    T  C   AGTAC
                                CCG GC CTG    GGGCTCGG
                                ||| || |||    ||||||||
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                                GGC CG GAC    TCCGAGCC
                                  _ A  A____
GAM1403  SMARCF1   5' CCGGCTCTGTAGGCTCGG   35985    T  C  AGTAC
                                CCG GC CTG    GGGCTCGG
                                ||| || |||    ||||||||
                                GGC CG GAC    TCCGAGCC
                                  _ A  A____
GAM1403  SMARCF1   5' CCGGCTCTGTAGGCTCGG   35985    T  C  AGTAC
                                CCG GC CTG    GGGCTCGG
                                ||| || |||    ||||||||
                                GGC CG GAC    TCCGAGCC
                                  _ A  A____
GAM1403  LOC145945 5' CGTGCCCTGTTGCCCGTACGGG 35986     A_____      C  III
            CTTGGGC                 CCTG    GTACGGGCT GGG  C
                                ||||    ||||||||| |||  |
                                GGAC    CATGCCCGA CCC  G
                                  AACGGG       A  III
GAM1403  LOC147958 5' GTGCCCTGGGAGCTCTGGG   35987       AGTAC    _
                                GTGCCCTG    GGGCTC GGG
                                ||||||||    |||||| |||
                                CACGGGAC    CTCGAG CCC
                                    C____    A
GAM1403  LOC149506 5' GTGCTCTGGGGCTCGG     35988     C  AGTAC
                                GTGC CTG    GGGCTCGG
                                |||| |||    ||||||||
                                CACG GAC    CCCGAGCC
                                  A  _____
GAM1403  LOC253394 5' GTGCCCTGAGATGGCTGG   35989       TACG   C
                                GTGCCCTGAG   GGCT GG
                                ||||||||||   |||| ||
                                CACGGGACTC   CCGA CC
                                     TA__   _
GAM1404  ELMO1     3'  TCTGGTGGGCAAGTTTTTGGG  35992    CGAC      C
                                TCT   GGCAAGTT TTGGG
                                |||   |||||||| |||||
                                AGA   CCGTTCAA AACCC
                                  CCAC      A
GAM1404  ITGAM     3'  CTCTCTCGGTGGTGCAGTGG   35993       AC  CAA  TCT
                                CTCTCTCG  GG   GT   TGG
                                ||||||||  ||   ||   |||
                                GAGAGAGC  CC   CG   ACC
                                    CA  A__  TC_
GAM1404  SLC2A6    5'  CTCTCTCGGGGCGAGCGGAGGG 35994       AC   A   TCTT
                                CTCTCTCG  GGC AGT   GGG
                                ||||||||  ||| |||   |||
                                GAGAGAGC  CCG TCG   CCC
                                    C_   C   CCT_
GAM1404  C20orf39  3'  CTTTCTTGAGGAGTCTTGG   35995   C  C  C  CA   T
                                CT TCT GA GG  AGT CTTGG
                                || ||| || ||  ||| |||||
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                                GA AGA CT CC  TCA GAACC
                                 A  A  _ __  _
GAM1404  FLJ10697  3'  CTCTTTTGACAGCAAAGG    35996     CTC       TTCTT
                                CTCT  GACGGCAAG    GG
                                ||||  |||||||||    ||
                                GAGA  CTGTCGTTT    CC
                                  AAA       _____
GAM1404  FLJ13912  3'  CTCCTTGGCCATGGGTTCTTGG 35997     CGAC   AA___
            G                    CTCT   GGC    GTTCTTGGG
                                ||||   |||    |||||||||
                                GAGG   CCG    CAAGAACCC
                                  AA__  GTACC
GAM1404  KIAA1163  3'  CTCTCCTGGCCCCTTTCTTGGG 35998      CGAC   AAG_
                                CTCTCT   GGC   TTCTTGGG
                                ||||||   |||   ||||||||
                                GAGAGG   CCG   AAGAACCC
                                   A___  GGGA
GAM1404  KIAA1465  5'  TCTCTCGATGGCGAGGGTTTGG 35999       C   A  TTC
            G                    TCTCTCGA GGC AG   TTGGG
                                ||||||||| ||| ||   |||||
                                AGAGAGCT CCG TC   AACCC
                                    A   C  CCA
GAM1404  POLD4    3'  CTGTCCTGAGGTTCTTGGG   36000    C  TC  C  CAAG
                                CT TC  GA GG   TTCTTGGG
                                || ||  || ||   ||||||||
                                GA AG  CT CC   AAGAACCC
                                 C  GA  _  _____
GAM1404  LOC131744 5'  TCTCACTTTGTTCTTGGG    36001     G  GGCAA
                                TCTC AC    GTTCTTGGG
                                |||| ||    |||||||||
                                AGAG TG    CAAGAACCC
                                  _  AAA__
GAM1404  LOC158056 5'  CTCTCTCGGTGGTCACTGTGGG 36002        AC  _  AGTTCT
                                CTCTCTCG  GG CA     TGGG
                                ||||||||  || ||     ||||
                                GAGAGAGC  CC GT     ACCC
                                    CA  A  GAC___
GAM1404  LOC158318 3'  CTCTCTGGACGGTGTTGGTGGG 36003       C    CAA   CT
                                CTCTCT GACGG   GTT  TGGG
                                |||||| |||||   |||  ||||
                                GAGAGA CTGCC   CAA  ACCC
                                   C    A__   CC
GAM1404  LOC165693 5'  TCTTGGATTGCTTCTTGGG   36004    CTC  CG  AAG
                                TCT   GA  GC   TTCTTGGG
                                |||   ||  ||   ||||||||
                                AGA   CT  CG   AAGAACCC
                                  AC_  AA  ___
GAM1404  LOC91517  3'  TCTCTTGAGGTAGTTTTTGGG  36005      C  C  CA   C
                                TCTCT GA GG  AGTT TTGGG
                                ||||| || ||  |||| |||||
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                                AGAGA CT CC  TCAA AACCC
                                  A  _ A_   A
GAM1405 CABC1    5' GGGCCCTCGCTGTGGGCATG  36008   A GCG  CC
                                GG CC  TGC  GTGGGCATG
                                || ||  |||  |||||||||
                                CC GG  GCG  CACCCGTAC
                                 C  GA_  A_
GAM1405 PLAB     5' ACGGGTCCTGGCCTGGGCATG 36009    A_ GCGT  CG
                                ACGG  CC   GCC  TGGGCATG
                                ||||  ||   |||  ||||||||
                                TGCC  GG   CGG  ACCCGTAC
                                  CA  AC__  __
GAM1405 ZNF144   5' GGGCTGCAGTGGGCAT     36010   ACC  G  CC
                                GG  GC TGC  GTGGGCAT
                                ||  || |||  ||||||||
                                CC  CG ACG  CACCCGTA
                                 ___  _  T_
GAM1405 C20orf130 3' GGACTGTTGCTTGTGGGCAC  36011    CGCG  CC
                                GGAC   TGC  GTGGGCAT
                                ||||   |||  ||||||||
                                CCTG   ACG  CACCCGTG
                                  ACA_  AA
GAM1405 CINP     3' GGCCGCGGGTTGTGGGCATG  36012   A   TGCCC
                                GG CCGCG   GTGGGCATG
                                || |||||   |||||||||
                                CC GGCGC   CACCCGTAC
                                 _   CCAA_
GAM1405 FLJ14249 3' GCAGAACCCGTGGGCATG   36013   T_
                                GCG  GCCCGTGGGCATG
                                |||  ||||||||||||
                                CGT  TGGGCACCCGTAC
                                  CT
GAM1405 FLJ14249 3' GCAGAACCCGTGGGCATG   36013   T_
                                GCG  GCCCGTGGGCATG
                                |||  ||||||||||||
                                CGT  TGGGCACCCGTAC
                                  CT
GAM1405 FLJ14957 3' GGGCCTGGCCTGTGGGCATG  36014   A GCGT  C
                                GG CC   GCC GTGGGCATG
                                || ||   ||| |||||||||
                                CC GG   CGG CACCCGTAC
                                 C  AC__  A
GAM1405 KIAA0450 5' GGGGTGCGGCCTGGGCATG  36015   ACC  T  CG
                                GG  GCG GCC  TGGGCATG
                                ||  ||| |||  ||||||||
                                CC  CGC CGG  ACCCGTAC
                                 CCA  _  __
GAM1405 SIMRP7   3' GGATCCGGCCCGTGGG     36016    _  CGT
                                GGA CCG  GCCCGTGGG
                                ||| |||  |||||||||
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                                CCT GGC   CGGGCACCC
                                  A  ___
GAM1405  LOC148055 5'  CGGACCGCGAGCGCGAGC    36017        T  CC
                                CGGACCGCG GC  GTGGGC
                                ||||||||| ||  ||||||
                                GCCTGGCGC CG  CGCTCG
                                     T  __
GAM1405  LOC159199 5'  CAGACTGTGCTGGGCAT     36018      CGC   CCG
                                CGGAC   GTGC   TGGGCAT
                                |||||   ||||   |||||||
                                GTCTG   CACG   ACCCGTA
                                  A__    ___
GAM1405  LOC164532 5'  ACGGGCTGGTGCTCGTAG    36019     ACC  __   C
                                ACGG   GC  GTGC CGTGG
                                ||||   ||  |||| |||||
                                TGCC   CG  CACG GCATC
                                  ___  AC   A
GAM1405  LOC164584 5'  GGACCGCGTCCTCGTTAGC    36020        G  _  G
                                GGACCGCGT CC CGT GGC
                                ||||||||| || ||| |||
                                CCTGGCGCA GG GCA TCG
                                     _ A  A
GAM1405  LOC253296 5'  CGGACCGCGGTCGAGGCATG   36021         TGCC  T
                                CGGACCGCG    CG GGGCATG
                                |||||||||    || |||||||
                                GCCTGGCGC    GC TCCGTAC
                                     CA__  _
GAM1405  LOC257570 5'  CGGACCGCGGTCGAGGCATG   36021         TGCC  T
                                CGGACCGCG    CG GGGCATG
                                |||||||||    || |||||||
                                GCCTGGCGC    GC TCCGTAC
                                     CA__  _
GAM1406  ARHGEF7   5'  GAGCGCCGTGGCCGGCA     36024        CC  AGTA  A
                                GAGCGCCG  GG    CC GCA
                                ||||||||  ||    || |||
                                CTCGCGGC  CC    GG CGT
                                    A_  _____  C
GAM1406  CD1D     5'  GCGCCGCCGCTCACTTCAG    36025         GAG   CAG
                                GCGCCGCCG   TAC   CAG
                                |||||||||   |||   |||
                                CGCGGCGGC   GTG   GTC
                                     GA_   AA_
GAM1406  HDAC4    5'  CGGCGCCGCCGGGGGCCCAG   36026    A        AGTA
                                CG GCGCCGCCGG    CCAG
                                || ||||||||||    ||||
                                GC CGCGGCGGCC    GGTC
                                  _        CCCG
GAM1406  LY6E     5'  CGGACGCAGGTACCAGCA    36027    AG   CGCC  A
                                CG  CGC    GG GTACCAGCA
                                ||  |||    || |||||||||
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                                GC  GCG    TC CATGGTCGT
                                 CT  ____  _
GAM1406  MARK1    5'  CGGCGCCGCCGGGGTATGC   36028    A       A   CCA
                                CG GCGCCGCCGG GTA   GC
                                || |||||||||| |||   ||
                                GC CGCGGCGGCC CAT   CG
                                 _        C   A__
GAM1406  PHF1     5'  GCCGCCGGGAGCCGGGCAG   36029        _   ACCA
                                GCCGCCGG AGT    GCAG
                                |||||||| |||    ||||
                                CGGCGGCC TCG    CGTC
                                     C   GCC_
GAM1406  PHF1     5'  GCCGCCGGGAGCCGGGCAG   36029        _   ACCA
                                GCCGCCGG AGT    GCAG
                                |||||||| |||    ||||
                                CGGCGGCC TCG    CGTC
                                     C   GCC_
GAM1406  PPP3CB   5'  CGGCGCCGCCGGGGAACATGGC 36030    A       AGT  CA_
                                CG GCGCCGCCGG   AC   GC
                                || ||||||||||   ||   ||
                                GC CGCGGCGGCC   TG   CG
                                 _        CCT  TAC
GAM1406  PTK7     5'  CGGGCGCCGCAGCAGC      36031    A     C  AGTAC
                                CG GCGCCGC GG     CAGC
                                || ||||||| ||     ||||
                                GC CGCGGCG TC     GTCG
                                 C      _ ______
GAM1406  ROBO1    5'  CGAGCGCCGCTGCGAGGGCAG  36032          CG_   TACCA
                                CGAGCGCCGC   GAG    GCAG
                                ||||||||||   |||    ||||
                                GCTCGCGGCG   CTC    CGTC
                                      ACG   C_____
GAM1406  SECTM1   3'  CGGGCGCCGCCGCGTCCTGC   36033    A       GA  A  A
                                CG GCGCCGCCG  GT CC GC
                                || |||||||||  || || ||
                                GC CGCGGCGGC  CA GG CG
                                 C        G_  _  A
GAM1406  UBE3A    5'  CGAGCGCGCCGGGTCGGCA    36034       C    A  ACCA
                                CGAGCGC GCCGG GT    GCA
                                ||||||| ||||| ||    |||
                                GCTCGCG CGGCC CA    CGT
                                    _    _ GC__
GAM1406  ZNF148   5'  CGGGCGCGGCCGAAGTCGTCAG 36035    A   C       AC_
              C                  CG GCGC GCCGGAGT   CAGC
                                 || |||| ||||||||   ||||
                                 GC CGCG CGGCTTCA   GTCG
                                  C   C       GCA
GAM1406  C20orf97 5'  CGGGCGCCGCCGGGGCTCAG   36036    A        A  AC
                                CG GCGCCGCCGG GT  CAG
                                || |||||||||| ||  |||
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                                GC CGCGGCGGCC CG  GTC
                                 C        C  A_
GAM1406  COASTER   5'  GAGCGCCGACGCCACCGGC   36037        C  GAG   A
                                GAGCGCCG CG   TACC GC
                                |||||||| ||   |||| ||
                                CTCGCGGC GC   GTGG CG
                                     T  G__   C
GAM1406  DKFZP564D172 3'  CGACGCCGCCGGACCCGCA   36038     G        GTA  A
                                CGA CGCCGCCGGA   CC GCA
                                ||| ||||||||||   || |||
                                GCT GCGGCGGCCT   GG CGT
                                  _        ___ G
GAM1406  FBXW2    5'  CGAGCGCCCCGGGGCCC     36039        G    A  A
                                CGAGCGCC CCGG GT CC
                                |||||||| |||| || ||
                                GCTCGCGG GGCC CG GG
                                     _   C  _
GAM1406  FLJ00024  3'  GAGCACCGTGCCAGCCGGCAG  36040        __    AGTA  A
                                GAGCGCC  GCCGG    CC GCAG
                                |||||||  |||||    || ||||
                                CTCGTGG  CGGTC    GG CGTC
                                    CA    _____  C
GAM1406  HYPH     5'  CGAGCCCCGCCGGAGGCGACGC 36041      G        TACCA
                                CGAGC CCGCCGGAG     GC
                                ||||| |||||||||     ||
                                GCTCG GGCGGCCTC     CG
                                   G        CGCTG
GAM1406  KIAA1545  3'  CGGCGCCGCCCCAGGATCGGC  36042    A       ___  GTACCA
                                CG GCGCCGCC   GGA     GC
                                || ||||||||   |||     ||
                                GC CGCGGCGG   CCT     CG
                                 _       GGT   AGC___
GAM1406  KIAA1814  3'  GCGTGCCGCCGATTCACAG   36043    __       AG   C
                                GC  GCCGCCGG  TAC AG
                                ||  ||||||||  ||| ||
                                CG  CGGCGGCT  GTG TC
                                 CA       AA  _
GAM1406  KIAA1941  3'  GCGGGCGTGAAGTACCAG    36044     CC  C_
                                GCG  GC  GGAGTACCAG
                                |||  ||  ||||||||||
                                CGC  CG  CTTCATGGTC
                                  C_  CA
GAM1406  MAP2K3   5'  CGGGCGGCGCCGGAGACA    36045    A   C       TACCA
                                CG GCG CGCCGGAG     GCA
                                || ||| ||||||||     |||
                                GC CGC GCGGCCTC     TGT
                                 C   C       ______
GAM1406  MGC9753   5'  CCAGCGCCGCTGCCCCAGC   36046   G       CGGA TA
                                C AGCGCCGC    G  CCAGC
                                | ||||||||    |  |||||
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                                G TCGCGGCG    C  GGTCG
                                 G       A___ GG
GAM1406  NETO1    5'  AGCGCCGCGCAGCCAGCAG   36047        _  AGTA
                                AGCGCCGC CGG    CCAGCAG
                                |||||||| |||    |||||||
                                TCGCGGCG GTC    GGTCGTC
                                     C  _____
GAM1406  OSMR     5'  CGAGCGCCGTCCGAGCGCA   36048        _  G   ACCA
                                CGAGCGCCG CCG AGT    GCA
                                ||||||||| ||| |||    |||
                                GCTCGCGGC GGC TCG    CGT
                                     A  _  _____
GAM1406  PEX16    3'  GACGCTGCCGGAGTCAG     36049    G   C       AC
                                GA CGC GCCGGAGT  CAG
                                || ||| ||||||||  |||
                                CT GCG CGGCCTCA  GTC
                                 _  A       __
GAM1406  PNMA1    5'  CGAGAGCCGCCGGGGTGTGTCG 36050      C       A  ACCA_
              C                  CGAG GCCGCCGG GT     GC
                                |||| |||||||| ||     ||
                                GCTC CGGCGGCC CA     CG
                                  T       C  CACAG
GAM1406  RNF13    5'  CACAGCCCGGAGTACTAGCAG  36051     C  _      C
                                CGC GCC GGAGTAC AGCAG
                                ||| ||| ||||||| |||||
                                GTG CGG CCTCATG TCGTC
                                  T  G      A
GAM1406  SMAP1    5'  GCGCCGCCGGGACCGC      36052          AGT   A
                                GCGCCGCCGG   ACC GC
                                ||||||||||   ||| ||
                                CGCGGCGGCC   TGG CG
                                     C__   _
GAM1406  STIM2    5'  CCAGCGCCGCCGCCGCAGCAG  36053    G        GA TAC
                                C AGCGCCGCCG  G   CAGCAG
                                | ||||||||||  |   ||||||
                                G TCGCGGCGGC  C   GTCGTC
                                 G        GG ___
GAM1406  LOC196411 5'  CGAGCGCCCGACCGCCAGCAG  36054         __   GAGTA
                                CGAGCGCC  GCCG    CCAGCAG
                                ||||||||  ||||    |||||||
                                GCTCGCGG  TGGC    GGTCGTC
                                     GC   ______
GAM1406  LOC201595 5'  AGCGCCGCGAGGCCGGC     36055        CG   TA  A
                                AGCGCCGC  GAG  CC GC
                                ||||||||  |||  || ||
                                TCGCGGCG  CTC  GG CG
                                     __   C_  C
GAM1406  LOC201917 5'  CGGGCGCTGACCTCAACCAGCA 36056    A   C_   GGAGT
              G                   CG GCGC  GCC    ACCAGCAG
                                || ||||  |||    ||||||||
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                                GC CGCG  TGG    TGGTCGTC
                                 C   AC  AGT__
GAM1406  LOC206480 5'  CGAGTGCCGCCAGCAGCA    36057     C      AGTAC
                                CGAG GCCGCCGG    CAGCA
                                |||| ||||||||    |||||
                                GCTC CGGCGGTC    GTCGT
                                  A      _____
GAM1406  LOC221271 5'  CGGGCGCCACCTCCCAGC    36058    A      GGAGTA
                                CG GCGCCGCC     CCAGC
                                || ||||||||     |||||
                                GC CGCGGTGG     GGTCG
                                 C      AG____
GAM1406  LOC256219 5'  CGAGCGCCCTCGGAAGATGGGC 36059       GC    TA____  A
            CGGCAG                  GAGCGCC  CGGAG     CC GCAG
                                |||||||  |||||     || ||||
                                CTCGCGG  GCCTT     GG CGTC
                                    GA    CTACCC  C
GAM1406  LOC56926  5'  CGGGCGCCGCGCGGGGCA    36060    A     _  A
                                CG GCGCCGC CGG GTA
                                || ||||||| ||| |||
                                GC CGCGGCG GCC CGT
                                 C      C   C
GAM1406  LOC90525  3'  CGGGCGCGGCTGTGCCCGGCAG 36061    A   C  CGGA  A_  A
                                CG GCGC GC    GT  CC GCAG
                                || |||| ||    ||  || ||||
                                GC CGCG CG    CA  GG CGTC
                                 C    C  A___  CG  C
GAM1407  CD164    3'  AGCTTACCTTTCACTGTCTT   36064       ___   __
                                AGCTTACC   CGC  TCTT
                                ||||||||   |||  ||||
                                TCGAATGG   GTG  AGAA
                                    AAA   AC
GAM1407  EIF2C1   3'  AAGCTTGCTGCCAACACC    36065      ACCC   C TG
                                AAGCTT    GCT T  GCACT
                                ||||||    ||| |  |||||
                                TTCGAA    CGA G  TGTGG
                                   _____   C GT
GAM1407  GAB2     3'  GCCTACCTCAGGCACTC     36066      CGC  TT
                                GCTTACC   TC  GGCACTC
                                |||||||   ||  |||||||
                                CGGATGG   AG  CCGTGAG
                                   ___  T_
GAM1407  GAB2     3'  GCCTACCTCAGGCACTC     36066      CGC  TT
                                GCTTACC   TC  GGCACTC
                                |||||||   ||  |||||||
                                CGGATGG   AG  CCGTGAG
                                   ___  T_
GAM1407  IL15RA   3'  AGCTTGCTCCTGGAGCCC    36067      ACCC      CA
                                AGCTT    GCTCTTGG  CTC
                                |||||    ||||||||  |||
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                                TCGAA   CGAGGACC  GGG
                                  ____      TC
GAM1407  MYO10    3'  GCTGCCCGCAGCACTC     36068    TA    TCTT
                                GCT  CCCGC   GGCACTC
                                |||  |||||   |||||||
                                CGA  GGGCG   TCGTGAG
                                  C_   ____
GAM1407  PSMD5    3'  AAGCTTGTCTGCTCTTAATGCA 36069      ACCC     __  C
             TTCC                 AAGCTT   GCTCTTG  GCA TCC
                                |||||||  |||||||  ||| |||
                                TTCGAA   CGAGAAT  CGT AGG
                                   CAGA     TA  A
GAM1407  REQ      3'  AGCTTGCTCGCTCCCAGCTCC  36070     ACC    TG  AC
                                AGCTT   CGCTCT  GC  TCC
                                |||||   ||||||  ||  |||
                                TCGAA   GCGAGG  CG  AGG
                                   CGA     GT  __
GAM1407  C20orf64 3'  AAGCTAGCTCCTGGTACT    36071      TACCC      C
                                AAGCT    GCTCTTGG ACT
                                |||||    |||||||| |||
                                TTCGA    CGAGGACC TGA
                                   T____      A
GAM1407  FAM8A1   3'  GCTTACCCAGCTCTTGGCTCC  36072        _       AC
                                GCTTACCC GCTCTTGGC  TCC
                                |||||||| |||||||||  |||
                                CGAATGGG CGAGAACCG  AGG
                                     T       __
GAM1407  FLJ10726 3'  AACTTACCTGCTCTGGGCCTCC 36073        C    T   A
                                AGCTTACC GCTCT GGC CTCC
                                |||||||| ||||| ||| ||||
                                TTGAATGG CGAGA CCG GAGG
                                     A    C   _
GAM1407  FLJ12484 3'  AAGCTTACCTGCCTTCCCTCC  36074        C  T   GGCA
                                AAGCTTACC GC CTT    CTCC
                                |||||||||  || |||    ||||
                                TTCGAATGG CG GAA    GAGG
                                     A  _   GG__
GAM1407  FLJ12892 3'  AGCTTATCTGTTAGCACT    36075       CCCG  C
                                AGCTTA    CT TTGGCACT
                                ||||||    || ||||||||
                                TCGAAT    GA AATCGTGA
                                   A___  C
GAM1407  KIAA0876 3'  GCTTGCTCCTGCGTAACACTC  36076     ACCC      ____
                                GCTT    GCTCTTG    GCACTC
                                ||||    |||||||    ||||||
                                CGAA    CGAGGAC    TGTGAG
                                  ____       GCAT
GAM1407  MYT1     3'  GCTGCCTGCGGCCAGCACTCC  36077     TA  C  TC TG
                                GCT  CC GC  T  GCACTCC
                                |||  || ||  |  |||||||
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                                CGA  GG CG  G  CGTGAGG
                                  C_  A  CC GT
GAM1407  OPRL1    3'  AAGCTGCCTGCTGCACT     36078      TA  C   CTTG
                                AAGCT  CC GCT    GCACT
                                |||||  || |||    |||||
                                TTCGA  GG CGA    CGTGA
                                  C_  A  _____
GAM1407  SNFT     5'  GCTTCCCGCTCTCCCCGCTACT 36079      A       G__  _
              CC                  GCTT CCCGCTCTT   GC ACTCC
                                |||| |||||||||   || |||||
                                CGAA GGGCGAGAG   CG TGAGG
                                  _       GGG  A
GAM1407  LOC124460 3'  AAGCTAGCCTGCTCCTGGACT  36080       TA  C       C
                                AAGCT  CC GCTCTTGG ACT
                                |||||  || |||||||| |||
                                TTCGA  GG CGAGGACC TGA
                                  TC  A       _
GAM1407  LOC127294 3'  GCTCATGGCCCTTGGCACT    36081       CCC
                                GCTTA   GCTCTTGGCACT
                                |||||   ||||||||||||
                                CGAGT   CGGGAACCGTGA
                                  AC_
GAM1407  LOC145317 3'  GCCTTCTGCTCTTGGCGCTCC  36082      ACCC        A
                                GCTT    GCTCTTGGC CTCC
                                ||||    ||||||||| ||||
                                CGGA    CGAGAACCG GAGG
                                  AGA_       C
GAM1407  LOC148534 3'  GCTTATCGGTAGCACTC     36083       CC  CTCT
                                GCTTA  CG    TGGCACTC
                                |||||  ||    ||||||||
                                CGAAT  GC    ATCGTGAG
                                  A_  C___
GAM1407  LOC153727 5'  GCTTCCCGCTCCCATTC     36084      A       TGG  C
                                GCTT CCCGCTCT   CA TC
                                |||| ||||||||   || ||
                                CGAA GGGCGAGG   GT AG
                                  _       ___  A
GAM1408  WHSC1L1   3'  TGCCAATAATGATGATTGGCGA 36087          AAATT   C
              A                   TGCCAATAAT     TTG GCGAA
                                ||||||||||     ||| |||||
                                ACGGTTATTA     AAC CGCTT
                                     CTACT   _
GAM1408  B3GNT1    3'  TGGCAATAATAAATTCTG    36088    C
                                TG CAATAATAAATTTTG
                                || ||||||||||||||
                                AC GTTATTATTTAAGAC
                                 C
GAM1408  BANK      3'  TGCCAATAACAAATTCTG    36089
                                TGCCAATAATAAATTTTG
                                ||||||||||||||||||
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                                ACGGTTATTGTTTAAGAC

GAM1408  LOC149332 5'  ATAATATTGTGCGCGAA     36090       AA  T
                                ATAATA  TT TGCGCGAA
                                ||||||  || ||||||||
                                TATTAT  AA ACGCGCTT
                                   __  C
GAM1409  APM1      3'  CATGTATATATCTAATAAT    36093     _          III
                                TATG ATATATCTAATAA   T
                                |||| ||||||||||||   |
                                GTAC TATATAGATTATT   A
                                  A          III
GAM1410  TRPM6     3'  TAGTACCCCTGAGCTTTA     36096         AAA
                                TAGTACCCCT   CTTTA
                                ||||||||||   |||||
                                ATCATGGGGA   GAAAT
                                      CTC
GAM1410  COL21A1   3'  TAGTACTTCCAAACTTACA    36097       CC       T
                                TAGTAC  CTAAACTT ATA
                                ||||||  |||||||| |||
                                ATCATG  GGTTTGAA TGT
                                   AA       _
GAM1410  FLJ20695  3'  TAGCGCCCCTAAATTTAAAG   36098     TA       C    T
                                TAG  CCCCTAAA TTTA AG
                                |||  |||||||| |||| ||
                                ATC  GGGGATTT AAAT TC
                                  GC       _   T
GAM1410  KIAA0161  3'  GTGCCCTAAACTGGTTTTATGG 36099     AC        ____    A
            AAT                   GT  CCCTAAACT    TTAT GAAT
                                ||  |||||||||    |||| ||||
                                CA  GGGATTTGA    AATA CTTA
                                 C_       CCAA    C
GAM1410  PLCL1     3'  TAGTACCCCTAAAATTACA    36100           CT
                                TAGTACCCCTAAA  TTATA
                                ||||||||||||  |||||
                                ATCATGGGGATTT  AATGT
                                       T_
GAM1411  C1QG      3'  GGAGGAGAAGTCCATCTGGTGG 36103         _   GCG   AC
            GG                    GGAGGAGA GTCT   TTG  GGGG
                                ||||||||  ||||   |||  ||||
                                CCTCCTCT CAGG   GAC  CCCC
                                     T   TA_   CA
GAM1411  FOXF1     3'  GGAGGAGACTTCGGAGGTGGGG 36104         GT  G  TTGAC
                                GGAGGAGA  CT CG     GGGG
                                ||||||||  || ||     ||||
                                CCTCCTCT  GA GC     CCCC
                                   __  A  CTCCA
GAM1411  KCNC3     3'  GGTGGGGTCTGCAAGGGG     36105    A  AGA      TTGAC
                                GG GG   GTCTGCG     GGGG
                                || ||   |||||||     ||||
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                                CC CC   CAGACGT    CCCC
                                 A  C__      T____
GAM1411  SCAP1    3'  GAGAGGAGTCCAAGGCGTTGGT 36106     GA     ___     AC
            GGGG                   GAG  GAGTCT   GCGTTG  GGGG
                                ||| ||||||  ||||||  ||||
                                CTC  CTCAGG   CGCAAC  CCCC
                                  TC     TTC     CA
GAM1411  SYNGR3   3'  GGGGCCTGCGTTGGTGGG    36107    AGA       AC
                                GG   GTCTGCGTTG  GGG
                                ||   ||||||||||  |||
                                CC   CGGACGCAAC  CCC
                                 C__        CA
GAM1411  ZIC3     5'  GGAGGGGGTGTTGGCGGG    36108      AGA  CTGC    A
                                GGAGG   GT    GTTG CGGG
                                |||||   ||    |||| ||||
                                CCTCC   CA    CAAC GCCC
                                   CC_ _____    C
GAM1411  BMF      3'  GGTGGAGAGTCTGCCAAAAGGG 36109    A        GTT  C
            G                   GG GGAGAGTCTGC   GA GGGG
                                || ||||||||||   || ||||
                                CC CCTCTCAGACG   TT CCCC
                                 A         GT_  T
GAM1411  FLJ20378 3'  GGAGGAGAGTCTGTGTGAGG   36110          C  T  C
                                GGAGGAGAGTCTG GT GA GG
                                |||||||||||| || || ||
                                CCTCCTCTCAGAC CA CT CC
                                      A  _  _
GAM1411  KIAA0057 3'  AGAGGAGAGTTTTCGAAGTGGG 36111         CTG  TTGAC
            G                   GGAGGAGAGT   CG    GGGG
                                ||||||||||   ||    ||||
                                TCTCCTCTCA   GC    CCCC
                                     AAA  TTCA_
GAM1411  KIAA0121 5'  GGGGAGAGACTCTAGAGACGGG 36112    A     T  GCGTT
            G                   GG GGAGAG CT    GACGGGG
                                || |||||| ||    |||||||
                                CC CCTCTC GA    CTGCCCC
                                 _     T  GATCT
GAM1411  SP2      3'  GGAGGAGAGGTTGTGGCGGGG  36113        TC  CGT  A
                                GGAGGAGAG  TG   TG CGGGG
                                |||||||||  ||   || |||||
                                CCTCCTCTC  AC   AC GCCCC
                                     CA  ___  C
GAM1411  TLK1     5'  GGGGAGAGTCAAGGGGATGGGG 36114    A      TGCGTT  C
                                GG GGAGAGTC     GA GGGG
                                || ||||||||     || ||||
                                CC CCTCTCAG     CT CCCC
                                 _       TTCCC_  A
GAM1411  LOC166206 3'  GGAGGAGACTCTGGGTGGTGGG 36115        G    C  T AC
            G                   GGAGGAGA TCTG GT G  GGGG
                                |||||||| |||| || |  ||||
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                                CCTCCTCT AGAC CA C  CCCC
                                     G    C  _ CA
GAM1411  LOC219927 3'  GGAGGACAGTCTGCGGG     36116       G       TTGAC
                                GGAGGA AGTCTGCG     GG
                                |||||| ||||||||     ||
                                CCTCCT TCAGACGC     CC
                                   G       _____
GAM1412  LIMD1     3'  GAGGGAACATTTGGGTATAG   36119     TAT  C
                                GAG   AT TTTGGGTATAG
                                |||   || ||||||||||
                                CTC   TG AAACCCATATC
                                  CCT  T
GAM1412  MAGEL2    3'  AAAGTATATTTATATATATAGA 36120         CTTTGG
                T                AGAGTATAT     GTATAGAT
                                |||||||||     ||||||||
                                TTTCATATA     TATATCTA
                                      AATATA
GAM1412  ZFP36L1   3'  AAGAATATATTCTATGGAT    36121          _  T
                                AAGAGTATAT CT TGGGT
                                |||||||||| || |||||
                                TTCTTATATA GA ACCTA
                                      A  T
GAM1412  ZNF10     3'  AAGAGGGTATCTTTGGAC     36122       TA
                                AAGAG  TATCTTTGGGT
                                |||||  ||||||||||
                                TTCTC  ATAGAAACCTG
                                   CC
GAM1412  DKFZP566D1346 3'  GAGTGTTTTAGATATAGAT    36123      ATATC
                                GAGT    TTTGGGTATAGAT
                                ||||    ||||||||||||
                                CTCA    AAATCTATATCTA
                                  CA___
GAM1412  FLJ10097  3'  AAGAGTATTTTTCCTAAAATAG 36124         A__   ____
                GT                 AAGAGTAT   TCTT    TGGGT
                                |||||||   ||||   |||||
                                TTCTCATA   AGGA    ATCCA
                                     AAA    TTTT
GAM1412  FLJ10188  3'  AAGGGTATTTTTTTGTGTACAG 36125     A   ATC   G
                AT                 AAG GTAT   TTTG GTATAGAT
                                ||| ||||   |||| ||||||||
                                TTC CATA   AAAC CATGTCTA
                                  C    AAA    A
GAM1412  KIAA0493  3'  AAGAGTATGTCTTCAAAGTA   36126         A   TG _
                                AAGAGTAT TCTT  G GTA
                                |||||||| ||||  | |||
                                TTCTCATA AGAA  T CAT
                                     C    GT T
GAM1412  KIAA0853  5'  GAGAATGTCTTTGAATAGAT   36127     T  A      GT
                                GAG AT TCTTTGG  ATAGAT
                                ||| || |||||||  ||||||
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                                CTC TA AGAAACT  TATCTA
                                  T  C      __
GAM1412  PLP1     3'  AGAATATATTTGGCCCCTATAG 36128         CT    G___
                AT                  AGAGTATAT  TTGG    TATAGAT
                                    |||||||||  ||||    |||||||
                                    TCTTATATA  AACC    ATATCTA
                                         __    GGGG
GAM1412  LOC143188 5'  AAGAGTGAGTCTTATGGAT    36129       ATA    _
                                    AAGAGT   TCTT TGGGT
                                    ||||||   |||| |||||
                                    TTCTCA   AGAA ACCTA
                                       CTC    T
GAM1412  LOC145824 3'  AAGAGTAGTCTTTAAGT     36130        TA
                                    AAGAGTA  TCTTTGGGT
                                    |||||||  |||||||||
                                    TTCTCAT  AGAAATTCA
                                       C_
GAM1413  CSTB     3'  AGGAAGAGAAATGCAAAAGCAG 36133       AA_       TTCC_
                C                    AGGAA   AAATGCAA    GC
                                     |||||   ||||||||    ||
                                     TCCTT   TTTACGTT    CG
                                       CTC       TTCGT
GAM1413  D1S155E   3'  AAGGAAAAGAATGCAACT    36134         A
                                    AAGGAAAA AATGCAATT
                                    ||||||||  |||||||||
                                    TTCCTTTT TTACGTTGA
                                       C
GAM1413  EIF4EBP2  3'  AAGGAAAAAAATGCAGTTC    36135              A
                                    AAGGAAAAAAATGCA TTC
                                    ||||||||||||||  |||
                                    TTCCTTTTTTTACGT AAG
                                              C
GAM1413  FGA      3'  AAGAAGGAAATGCAAGGGGCC  36136       AA       TTCC
                                    AGGAA  AAATGCAA    GCC
                                    |||||  ||||||||    |||
                                    TTCTT  TTTACGTT    CGG
                                       CC       CCC_
GAM1413  FZD7     3'  CAAGGGGAAAAATGCATTCC   36137       AA        A
                                    TAAGG  AAAAATGCA TTCC
                                    |||||  |||||||||  ||||
                                    GTTCC  TTTTTACGT AAGG
                                       CC        _
GAM1413  GALNT1   3'  AGGAAAAGAAATGCAAGC    36138        _       TTCC
                                    AGGAAAA AAATGCAA    GC
                                    |||||||  ||||||||    ||
                                    TCCTTTT TTTACGTT    CG
                                       C       _____
GAM1413  GRB10    3'  AAGGAAGAAAATGCAATT    36139        A
                                    AAGGAA AAAATGCAATT
                                    ||||||  ||||||||||
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                                TTCCTT TTTTACGTTAA
                                   C
GAM1413 HLA-F    3' AGGCACAAGTGCAATTCTGC  36140     AAAA A      C
                                AGG   AA TGCAATTC GC
                                |||   || |||||||| ||
                                TCC   TT ACGTTAAG CG
                                  GTG_ C      A
GAM1413 IL5      3' TAAGAAAAAAGTATATCAATTT 36141          A_  _    CC
             TGCC                  TAAGGAAAAA  ATG CAATT  GCC
                                |||||||||  ||| |||||  |||
                                ATTCTTTTTT  TAT GTTAA  CGG
                                      CA  A    AA
GAM1413 SIM1     3' TAAGGAAAATAAACATTTTGCC 36142         AAAT   A  CC
                                TAAGGAAAA   GCA TT  GCC
                                |||||||||   ||| ||  |||
                                ATTCCTTTT   TGT AA  CGG
                                      ATT_  A  A_
GAM1413 ZNF32    3' AAGGAAAAAAAATCAGTTTGCC  36143          G  A  CC
                                AAGGAAAAAAAT CA TT  GCC
                                ||||||||||||| || ||  |||
                                TTCCTTTTTTTA GT AA  CGG
                                      _ C  A_
GAM1413 C4orf6   3' GGAAAAAAATCTGCAGCC    36144         __   ATTCC
                                GGAAAAAAA  TGCA    GCC
                                |||||||||  ||||    |||
                                CCTTTTTTT  ACGT    CGG
                                      AG   _____
GAM1413 C5orf6   3' AAGAGAAAAATGCCCTTCTTGC 36145     A      AA   C_
             C                   AGGA AAAAATGC  TTC  GCC
                                |||| ||||||||  |||  |||
                                TTCT TTTTTACG  AAG  CGG
                                  C       GG   AA
GAM1413 ERMAP    3' GGAAAAAAAAGCTTCTAC    36146        T  AA   CG
                                GGAAAAAAA GC  TTC  C
                                |||||||||  ||  |||  |
                                CCTTTTTTT CG  AAG  G
                                      T  __   AT
GAM1413 FLJ12704 5' AGGACATAAAATGCAGTTTTGC 36147     AA_      A  CC
                                AGGA   AAAATGCA TT  GC
                                ||||   |||||||| ||  ||
                                TCCT   TTTTACGT AA  CG
                                  GTA       C  AA
GAM1413 FLJ13119 3' TAAGGAAAAGAATCCA      36148         A  TGCAAT
                                TAAGGAAAA AA     TCCG
                                |||||||||  ||     ||||
                                ATTCCTTTT TT     AGGT
                                      C  _______
GAM1413 FLJ23033 3' AGGAAAAAAATGAATTGC    36149          C   CC
                                AGGAAAAAAATG AATT  GC
                                ||||||||||||  ||||  ||
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                                TCCTTTTTTTAC TTAA  CG
                                          _   __
GAM1413  FLJ23323  5'  TAAGCAAAGAAATGCAACC   36150     G   A      TT
                                TAAG AAA AAATGCAA  CC
                                |||| ||| ||||||||  ||
                                ATTC TTT TTTACGTT  GG
                                  G   C      __
GAM1413  KIAA0626  3'  GGAAAAAAAATGAATTAATTGC  36151          C   CC__
                                GGAAAAAAATG AATT   GC
                                |||||||||| ||||   ||
                                CCTTTTTTTAC TTAA   CG
                                       _   TTAA
GAM1413  KIAA0648  3'  TAAGGAAATGGAGTGAGCACAT 36152        AAAAT___  _   C
            TCTGC                  TAAGGAAA       GCA ATTC GC
                                |||||||       ||| |||| ||
                                ATTCCTTT       CGT TAAG CG
                                     ACCTCACT   G   A
GAM1413  KIAA1155  3'  AAGGGGGGAAAATGCAATTTCC 36153      AAA_        _
                                AAGG   AAAATGCAATT CC
                                ||||   |||||||||| ||
                                TTCC   TTTTACGTTAA GG
                                  CCCC         A
GAM1413  KIAA1622  3'  AAGAGATGCAATTCTGCC    36154      AAAAA       C
                                AGGA    ATGCAATTC GCC
                                ||||    |||||||| |||
                                TTCT    TACGTTAAG CGG
                                  C____        A
GAM1413  LIM       3'  CAAGGGAAAAAATGGAATTTGC 36155      A      C   CC
            C                   TAAGG AAAAAATG AATT  GCC
                                ||||| |||||||| ||||  |||
                                GTTCC TTTTTTAC TTAA  CGG
                                  C       C   A_
GAM1413  MGC14376  3'  TAAGGGAAAAATGCTTCCAGC  36156      AA      AA   _
                                TAAGG  AAAAATGC  TTCC GC
                                |||||  ||||||||  |||| ||
                                ATTCC  TTTTTACG  AAGG CG
                                  C_       __    T
GAM1413  MGC14836  3'  TAAGGAAAAAAGCTTTGC    36157          AT  AATTCC
                                TAAGGAAAAAA  GC     GC
                                ||||||||||  ||     ||
                                ATTCCTTTTTT  CG     CG
                                      __  AAA___
GAM1413  LOC148078 3'  CAAGGAAAAAAATGCAAAAGC  36158              TTCC
                                TAAGGAAAAAAATGCAA   GC
                                ||||||||||||||||   ||
                                GTTCCTTTTTTTACGTT   CG
                                      TT__
GAM1413  LOC158235 5'  CAAGGGGAAAAATGCTTAGTGC 36159      AA       AATTCC
            C                   TAAGG  AAAAATGC     GCC
                                |||||  ||||||||     |||
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                                GTTCC  TTTTTACG     CGG
                                   CC       AATCA_
GAM1413  LOC196549 5'  TAAGGAAAGGGTGTGTTTCCG  36160        AAAA  CAA
                                TAAGGAAA    TG   TTCCG
                                ||||||||    ||   |||||
                                ATTCCTTT    AC   AAGGC
                                     CCC_  ACA
GAM1413  LOC221312 3'  TAAGGAAAAAGAGCATCACG   36161         AAT   A TC
                                TAAGGAAAAA   GCA T  CG
                                ||||||||||   ||| |  ||
                                ATTCCTTTTT   CGT A  GC
                                      CT_   _ GT
GAM1413  LOC91170  5'  AGGAAAATGCACCCTGC     36162       AAA    AT   _
                                AGGAAA   ATGCA  TCC GC
                                ||||||   |||||  ||| ||
                                TCCTTT   TACGT  GGG CG
                                   ___    __  A
GAM1414  FMN2     3'  AAATGCTGTGATGTGG      36165           ATT
                                AAATGCTGTGGTG   TGG
                                ||||||||||||   |||
                                TTTACGACACTAC   ACC
                                          ___
GAM1414  GPR30    5'  GCACCTGTGGTGGTTTG     36166      AAATG       A
                                GCAC    CTGTGGTG TTTG
                                ||||    |||||||| ||||
                                CGTG    GACACCAC AAAC
                                  _____       C
GAM1414  LDB3     3'  TGCAGCGAGTGCTGTTTG    36167     CAAAT  T_   G  A
                                TGCA    GC  GTG TG TTTG
                                ||||    ||  ||| || ||||
                                ACGT    CG  CAC AC AAAC
                                  _____  CT   G  _
GAM1414  WFS1     3'  TACACAGATGCTTATTTG    36168       A    GTGGTG
                                TGCACA ATGCT     ATTTG
                                |||||| |||||     |||||
                                ATGTGT TACGA     TAAAC
                                   C    A_____
GAM1414  FIGN     3'  GCACAAATGCTGATGTCTTTGG 36169           _  GTGA
                                GCACAAATGCTG TG    TTTGG
                                ||||||||||| ||    |||||
                                CGTGTTTACGAC AC    AAACC
                                       T  AG__
GAM1414  KIAA0918  3'  TGTACAAATGCAACTGGGTTTG 36170    C       TG_   TGA
            G                    TG ACAAATGC   TGG   TTTGG
                                || ||||||||   |||   |||||
                                AC TGTTTACG   ACC   AAACC
                                 A       TTG   C__
GAM1414  MGC16025  3'  TGCCAGGTGCTGTGGGAACGG  36171     A  AA       T  TT
                                TGC CA  TGCTGTGG GA  TGG
                                ||| ||  |||||||| ||  |||
```

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                                ACG GT  ACGACACC CT  GCC
                                  _ CC       _ T_
GAM1414  MGC3123   3'  GCAGGTGCTGTGAAGAATTGG  36172     CAAA       T  T
                                GCA    TGCTGTGG GA TTGG
                                |||    |||||||| || ||||
                                CGT    ACGACACT CT AACC
                                  CC__       T  T
GAM1414  PEPP3     3'  TGACAAGTGCTGTCCTTG    36173    C    A     GGTGA
                                TG ACAA TGCTGT     TTTG
                                || |||| ||||||     ||||
                                AC TGTT ACGACA     GAAC
                                 _   C     G____
GAM1414  LOC115827 3'  ACAAATGCTGTTTGTTGG    36174          GG  AT
                                ACAAATGCTGT  TG  TTGG
                                ||||||||||  ||  ||||
                                TGTTTACGACA  AC  AACC
                                       A_ __
GAM1414  LOC127435 3'  TGACAGAGACTGTGGTGGTTTG 36175    C   AAT        A
              G                  TG ACA   GCTGTGGTG TTTGG
                                || |||   ||||||||| |||||
                                AC TGT   TGACACCAC AAACC
                                 _  CTC        C
GAM1414  LOC145748 3'  TGCACAGTGCTGTGGATGAGTG 36176       AA       _  TT
              G                  TGCACA  TGCTGTGG TGA  TGG
                                ||||||  |||||||| |||  |||
                                ACGTGT  ACGACACC ACT  ACC
                                   C_       T  C_
GAM1414  LOC150622 3'  TGCACAAAGAACTCTGATTTGG 36177        T_  GTGG
                                TGCACAAA  GCT    TGATTTGG
                                ||||||||  |||    ||||||||
                                ACGTGTTT  TGA    ACTAAACC
                                     CT   G___
GAM1414  LOC158263 3'  TGGACAGGTGCTATGGATTTGG 36178    C   AA       TG
                                TG ACA  TGCTGTGG  ATTTGG
                                || |||  ||||||||  ||||||
                                AC TGT  ACGATACC  TAAACC
                                 C   CC       __
GAM1414  LOC255232 3'  TGCTAGATGCTGTGTGATGTGG 36179     ACAA       G    T
                                TGC    ATGCTGTG TGAT TGG
                                |||    |||||||| |||| |||
                                ACG    TACGACAC ACTA ACC
                                  ATC_       _    C
GAM1415  LOC199957 3'  TTTGTATATCTATTAATG    36182       A
                                TTTGTA GTTTATTAATG
                                |||||| ||||||||||
                                AAACAT TAGATAATTAC
                                   A
GAM1416  CD48      3'  AAGATCTTCTGGCCTTGAAGT  36185         CGACG   ____
                                AAGGTCTTC    TGGC    AAGT
                                |||||||||    ||||    ||||
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                                TTCTAGAAG    ACCG   TTCA
                                     _____   GAAC
GAM1416 EFNB1   5' GGTCTTCCCGCAGAGGTCT   36186       GA  TG CAA
                                GGTCTTCC  CG  G   GTCT
                                ||||||||  ||  |   ||||
                                CCAGAAGG  GC  C   CAGA
                                    __  GT TC_
GAM1416 GLO1    3' AAGGTCTTCCACTAGAGTC   36187        G  G   CA
                                AAGGTCTTCC AC TGG  AGTC
                                |||||||||| || |||  ||||
                                TTCCAGAAGG TG ATC  TCAG
                                      _  _  __
GAM1416 HNRPH2  5' GGCTCTTGGTGGCAAGT    36188   _   CCGAC
                                GG TCTT    GTGGCAAGT
                                || ||||    |||||||||
                                CC AGAA    CACCGTTCA
                                 G   C____
GAM1416 HRH1    3' AGGTCTTCTGAACAATGG    36189       C_   _
                                AGGTCTTC  GACG TGG
                                ||||||||  |||| |||
                                TCCAGAAG  TTGT ACC
                                    AC    T
GAM1416 MLPH    3' AAGGTCTTCGGTGTGTC     36190       CGAC   GCAA
                                AAGGTCTTC   GTG   GTC
                                |||||||||   |||   |||
                                TTCCAGAAG   CAC   CAG
                                    C___   A___
GAM1416 NFYC    3' GGCAGAACAACGTGGCAAGTCT 36191     CTTC
                                GGT   CGACGTGGCAAGTCT
                                |||   ||||||||||||||
                                CCG   GTTGCACCGTTCAGA
                                  TCTT
GAM1416 PCK1    5' GGCTCTTCCCGCCAGCAAGT  36192   _    GA  _
                                GG TCTTCC  CGT GGCAAGT
                                || ||||||  ||| |||||||
                                CC AGAAGG  GCG TCGTTCA
                                 G    __  G
GAM1416 SPAP1   3' AAGGTTTTATAGCAAGTC    36193     C  CCGAC
                                AAGGT TT    GTGGCAAGTC
                                ||||| ||    ||||||||||
                                TTCCA AA    TATCGTTCAG
                                  A _____
GAM1416 SPAP1   3' AAGGTTTTATAGCAAGTC    36193     C  CCGAC
                                AAGGT TT    GTGGCAAGTC
                                ||||| ||    ||||||||||
                                TTCCA AA    TATCGTTCAG
                                  A _____
GAM1416 TCF7L2  5' AGATCTTCTGCACGCGTGAGT  36194       CG_   GCA
                                AGGTCTTC   ACGTG   AGT
                                ||||||||   |||||   |||
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                                TCTAGAAG  TGCGC  TCA
                                    ACG    AC_
GAM1416  C21orf108 3'  AAGGTCTTCTGGATGTGAC   36195        C_  C
                                AAGGTCTTC  GA GTGGC
                                |||||||||  || |||||
                                TTCCAGAAG  CT CACTG
                                    AC  A
GAM1416  KIAA0321  3'  AAGGTTTTCAGAGTGGCAAGTC 36196      C  C  C
           T                     AAGGT TTC GA GTGGCAAGTCT
                                |||||  ||| ||  ||||||||||
                                TTCCA AAG CT CACCGTTCAGA
                                  A  T  _
GAM1416  NXPH3    3'  AAGGTCCTTTGAGTGGGTC   36197       CC  C   CAA
                                AAGGTCTT  GA GTGG  GTC
                                ||||||||  || ||||  |||
                                TTCCAGGA  CT CACC  CAG
                                    AA  _  ___
GAM1416  TCL6     3'  AAGGTCTTTGTGACGTGTATCT 36198       CC_    GCAA
                                AAGGTCTT  GACGTG  GTCT
                                ||||||||  ||||||  ||||
                                TTCCAGAA  CTGCAC  TAGA
                                    ACA    A___
GAM1416  TCL6     3'  AAGGTCTTTGTGACGTGTATCT 36198       CC_    GCAA
                                AAGGTCTT  GACGTG  GTCT
                                ||||||||  ||||||  ||||
                                TTCCAGAA  CTGCAC  TAGA
                                    ACA    A___
GAM1416  TLR8     5'  AAGGTCTCCTGGGATGGGTCT  36199       CGAC   CAA
                                AAGGTCTTC   GTGG  GTCT
                                |||||||||   ||||  ||||
                                TTCCAGAGG   TACC  CAGA
                                    ACCC   ___
GAM1416  LOC146520 5'  AGGTTTTCCGAGTGGCAAGT   36200     C     C
                                AGGT TTCCGA GTGGCAAGT
                                |||| |||||| |||||||||
                                TCCA AAGGCT CACCGTTCA
                                  A    _
GAM1416  LOC148018 3'  AAGGCCTTCTGACCTCCTCCGG 36201       C  G_____  CAA
             GTCT                 GGTCTTC GAC    TGG  GTCT
                                |||||||  |||     |||  ||||
                                CCGGAAG CTG     GCC  CAGA
                                    A  GAGGAG  ___
GAM1416  LOC164397 5'  GTCCTCCGTGTGGTAGGTCT   36202       AC   CAA
                                GTCTTCCG  GTGG  GTCT
                                ||||||||  ||||  ||||
                                CAGGAGGC  CACC  CAGA
                                    A_   ATC
GAM1416  LOC197003 3'  AAGGTCTCTTGACTTCAAG   36203       CC  GTGG
                                AAGGTCTT  GAC   CAAG
                                ||||||||  |||   ||||
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                                TTCCAGAG CTG   GTTC
                                    AA  AA__
GAM1417 PBX3    3' ATGCACTTATCAAGGCATGTA 36206     T      TT CCC
                                ATGCA CTTATCAA GC  GTA
                                ||||| |||||||| ||  |||
                                TACGT GAATAGTT CG  CAT
                                  _      C_ TA_
GAM1417 TRPM8   3' GCATTTCAATTGCCTTGT   36207     CTTA       CC
                                GCAT   TCAATTGCC GT
                                ||||   ||||||||| ||
                                CGTA   AGTTAACGG CA
                                  A___       AA
GAM1417 C9orf7  3' TGCACCTTAGGAGCCCTGT   36208        TCAATT   C
                                TGCATCTTA    GCCC GT
                                |||||||||    |||| ||
                                ACGTGGAAT    CGGG CA
                                     CCT___   A
GAM1417 KIAA0557 3' ATGTGTCCTGCTGTCTGCCCCG 36209    CA   ATCAA
             T                   ATG TCTT   TTGCCCCGT
                                ||| ||||   |||||||||
                                TAC AGGA   GACGGGGCA
                                  AC   CGACA
GAM1417 PPAP2A  3' ATGCATCCTCTTGCCTTGT   36210       TATCAA   CC
                                ATGCATCT    TTGCC GT
                                ||||||||    ||||| ||
                                TACGTAGG    AACGG CA
                                    AG____    AA
GAM1417 LOC124470 3' TGCATCCTGACTCCTGCCTCGT 36211       ATCAA   C
                                TGCATCTT   TTGCC CGT
                                ||||||||   ||||| |||
                                ACGTAGGA   GACGG GCA
                                    CTGAG   A
GAM1417 LOC159036 3' ATGCATCTCGTTATGATAACCC 36212       ATCAAT_ C
             GT                   ATGCATCTT     TG CCCGT
                                |||||||||     || |||||
                                TACGTAGAG     AT GGGCA
                                     CAATACT  T
GAM1417 LOC256295 3' GCATCTTATTGGGCTCCGT   36213       CAATT  C
                                GCATCTTAT    GC CCGT
                                |||||||||    || ||||
                                CGTAGAATA    CG GGCA
                                     ACC__  A
GAM1418 ST13    3' TATGGTAATATTTGCAAT    36216          AT
                                TATGGTAATATTT  CAAT
                                |||||||||||||  ||||
                                ATACCATTATAAA  GTTA
                                       C_
GAM1419 PPP1R12B 3' TATGGTAGGCTGGGCGTGG   36219       CT   CCGA   C
                                TATGGTAG  CTG   GCG GG
                                ||||||||  |||   ||| ||
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                                ATACCATC  GAC   CGC CC
                                    C_  C___  A
GAM1420  CASP10   3'  TTCATGCCTGTAGTCCCAGA  36222       CGCCTC
                                TTCATGCC    GTTCCAGA
                                ||||||||    ||||||||
                                AAGTACGG    CAGGGTCT
                                    ACAT__
GAM1420  CASP10   3'  TTCATGCCTGTAGTCCCAGA  36222       CGCCTC
                                TTCATGCC    GTTCCAGA
                                ||||||||    ||||||||
                                AAGTACGG    CAGGGTCT
                                    ACAT__
GAM1420  FBXL7    5'  CGTCATGCCCGCCGTCTCCC  36223    T       _  G
                                CGT CATGCCCGCC TC TTCC
                                ||| |||||||||| || ||||
                                GCA GTACGGGCGG AG AGGG
                                  _       C  _
GAM1420  MLC1     3'  CGTTCATGTCTTCTCA     36224       CCCGCC  G  _
                                CGTTCATG    TC TTC CA
                                ||||||||    || ||| ||
                                GCAAGTAC    AG AAG GT
                                    _______ _  A
GAM1420  MLC1     3'  CGTTCATGTCTTCTCA     36224       CCCGCC  G  _
                                CGTTCATG    TC TTC CA
                                ||||||||    || ||| ||
                                GCAAGTAC    AG AAG GT
                                    _______ _  A
GAM1420  PIGN     3'  TTCATGCCTGCAAAACCTAGA  36225       C  CTCGTT  _
                                TTCATGCC GC    CC AGA
                                |||||||| ||    || |||
                                AAGTACGG CG    GG TCT
                                    A  TTTT__  A
GAM1420  SHANK2   3'  GTTCATTCTAGAGCTGTTCCAG 36226      GCCC__  CTC
            A                    GTTCAT    GC  GTTCCAGA
                                ||||||    ||  ||||||||
                                CAAGTA    CG  CAAGGTCT
                                   AGATCT  A__
GAM1420  TNFSF4   3'  GTTCATGCTGGTGCCTGGTTTT 36227       CC__   C  CC
            AGA                   GTTCATGC   GCCT GTT  AGA
                                ||||||||   |||| |||  |||
                                CAAGTACG   CGGA CAA  TCT
                                    ACCA   C   AA
GAM1420  FLJ00058 5'  CGTTTATGTCCCCAGAGGCCAG 36228     C  C  G  TCGTT
            A                    CGTT ATG CC CC    CCAGA
                                |||| ||| || ||    |||||
                                GCAA TAC GG GG    GGTCT
                                  A  A  _  TCTCC
GAM1420  FLJ12960 3'  GTTCAAGCCCCACATTCCAG  36229     T   GCCT
                                GTTCA GCCC   CGTTCCAG
                                ||||| ||||   ||||||||
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                                CAAGT CGGG   GTAAGGTC
                                  T   GT__
GAM1420  FLJ22672  3'  ATTTGTACCTGCCTTGTTCCAG 36230    CA   C   C
            A                    GTT  TGCC GCCT GTTCCAGA
                                 |||  |||| |||| ||||||||
                                 TAA  ATGG CGGA CAAGGTCT
                                   AC   A   A
GAM1420  FUT10    3'  GTTCATGCTCGGCTGCAG    36231       C  CCTC   C
                                 GTTCATGC CG   GTT CAG
                                 |||||||| ||   ||| |||
                                 CAAGTACG GC   CGA GTC
                                     A ____  C
GAM1420  KIAA0280  3'  GTTCGTGCCCCACCCCCAGA   36232     A   _   CGTT
                                 GTTC TGCCC GCCT   CCAGA
                                 |||| ||||| ||||   |||||
                                 CAAG ACGGG TGGG   GGTCT
                                   C   G   ____
GAM1420  KIAA0469  3'  GCTCATGTCCCACTGTTC    36233       _    CTC
                                 GTTCATG CCCGC   GTTC
                                 ||||||| |||||   ||||
                                 CGAGTAC GGGTG   CAAG
                                     A   A__
GAM1420  TOB2     3'  GTCCATGCTTGCCTGGCCTCCT 36234        CC   C  _  _
            AGA                    GTTCATGC  GCCT GT TCC AGA
                                 ||||||||  |||| || ||| |||
                                 CAGGTACG  CGGA CG AGG TCT
                                     AA   C  G   A
GAM1420  LOC116236 3'  GTTCAGTCCGCCCCATCTTTCC 36235      TGC       ___
            AG                    GTTCA   CCGCCTCGT   TCCAG
                                 |||||   |||||||||   |||||
                                 CAAGT   GGCGGGGTA   AGGTC
                                   CA_       GAA
GAM1420  LOC166236 5'  GTGCATGCCCGCCGAACAGA   36236    T        TCGTTC
                                 GT CATGCCCGCC     CAGA
                                 || ||||||||||     ||||
                                 CA GTACGGGCGG     GTCT
                                  C        CTT___
GAM1420  LOC220758 3'  CGTTCATATTTGCCCCGTC    36237        CCC
                                 CGTTCATG   GCCTCGTT
                                 ||||||||   ||||||||
                                 GCAAGTAT   CGGGGCAG
                                     AAA
GAM1420  LOC254013 5'  CGCTCATGCTTTACATTTCC   36238         CC_  CTCG
                                 CGTTCATGC   GC    TTCC
                                 |||||||||   ||    ||||
                                 GCGAGTACG   TG    AAGG
                                      AAA  TA__
GAM1420  LOC91300  5'  GTTCATGAAATCGTTCCAGA   36239       CCCGCC
                                 GTTCATG     TCGTTCCAGA
                                 |||||||     ||||||||||
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                                CAAGTAC     AGCAAGGTCT
                                    TTT___
GAM1420 LOC91300 5' GTTCATGAAATCGTTCCAGA  36239       CCCGCC
                                GTTCATG     TCGTTCCAGA
                                |||||||     ||||||||||
                                CAAGTAC     AGCAAGGTCT
                                    TTT___
GAM1421 CENTD1   5' TCCAGGTCTCAATTCATTGTT 36242     AGCAC  _   _
                                TCCA    GTC CGGT CATTGTT
                                ||||    ||| |||| |||||||
                                AGGT    CAG GTTA GTAACAA
                                  C____  A   A
GAM1421 INPP5B   3' TCCAAGCAGTCCCTGATATGTT 36243       C   GGTCAT
             C                   TCCAAGCA GTCC     TGTTC
                                ||||||||| ||||     |||||
                                AGGTTCGT CAGG     ACAAG
                                    _   GACTAT
GAM1421 LRRC2    3' CAATCACATCAGTCATTGTTC 36244     G     C
                                CAA CACGTC GGTCATTGTTC
                                ||| |||||| ||||||||||
                                GTT GTGTAG TCAGTAACAAG
                                  A     _
GAM1421 NET1     3' AACACATTTCATTGTT      36245       CCGG
                                AGCACGT    TCATTGTT
                                |||||||    ||||||||
                                TTGTGTA    AGTAACAA
                                    A___
GAM1421 FEM-2    3' CCAAGCAATACTTGGTCATTGT 36246       CGTCC_
             T                   CCAAGCA     GGTCATTGTT
                                |||||||     ||||||||||
                                GGTTCGT     CCAGTAACAA
                                    TATGAA
GAM1421 FLJ11053 5' TCCAGGCACTGTTCCCTGTTC 36247     A   GTCCGG  A
                                TCCA GCAC     TC TTGTTC
                                |||| ||||     || ||||||
                                AGGT CGTG     AG GACAAG
                                  C   ACA___  G
GAM1421 GP5      3' TCCAAGTGTTCTCATTGTTC  36248      CACG  CGG
                                TCCAAG   TC   TCATTGTTC
                                ||||||   ||   |||||||||
                                AGGTTC   AG   AGTAACAAG
                                   ACA_  ___
GAM1421 MIC2L1   3' TCCAGGCATGTCCAGTCAC   36249     A  C
                                TCCA GCA GTCCGGTCAT
                                |||| ||| ||||||||||
                                AGGT CGT CAGGTCAGTG
                                  C  A
GAM1421 SSH2     3' CAAACATGTCACTGTT      36250       CGTCCG
                                CAAGCA     GTCATTGTT
                                ||||||     |||||||||
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                                GTTTGT     CAGTGACAA
                                   A_____
GAM1421  LOC128989 3'  TCCAAGCACGCCTGTGTT    36251         T  GGTCAT
                                TCCAAGCACG CC     TGTT
                                |||||||||| ||     ||||
                                AGGTTCGTGC GG     ACAA
                                      _  AC____
GAM1421  LOC130733 3'  AAGCACGTTTGATCTGTT    36252        CC    AT
                                AAGCACGT  GGTC  TGTT
                                ||||||||  ||||  ||||
                                TTCGTGCA  CTAG  ACAA
                                     AA   __
GAM1421  LOC145384 3'  TCCAAGTGTTCTCATTGTTC  36248       CACG  CGG
                                TCCAAG   TC   TCATTGTTC
                                ||||||   ||   |||||||||
                                AGGTTC   AG   AGTAACAAG
                                   ACA_  ___
GAM1421  LOC145945 5'  AAGCACATCCCAGTGTTC    36253         GGT  T
                                AAGCACGTCC   CA TGTTC
                                ||||||||||   || |||||
                                TTCGTGTAGG   GT ACAAG
                                      ___  C
GAM1421  LOC147063 3'  TCTCAGCACGTCTCTGTT    36254    CA      CGG  AT
                                TC  AGCACGTC   TC  TGTT
                                ||  ||||||||   ||  ||||
                                AG  TCGTGCAG   AG  ACAA
                                 AG       ___  __
GAM1421  LOC149010 5'  TCTAAGCATATTCCTCACTGTT 36255    C    CG_   GG
                                TC AAGCA   TCC  TCATTGTT
                                || |||||   |||  ||||||||
                                AG TTCGT   AGG  AGTGACAA
                                 A    ATA   __
GAM1421  LOC150299 3'  GCCATGTGGTCATTGTTC    36256    A   CC
                                GC CGT  GGTCATTGTTC
                                || |||  ||||||||||
                                CG GTA  CCAGTAACAAG
                                 _   CA
GAM1422  RPL15    3'  CTAGTCTCCTGGAAGACATGGT 35746     CATG    A      A
                                TTAG    TTCT GAAGACAT GT
                                ||||    |||| |||||||| ||
                                GATC    AGGA CTTCTGTA CA
                                   AG__    C       C
GAM1422  TPX1     3'  TTAGCATGTTTCAGGAAATAC  35747         _ TA   _
                                TTAGCATGTT C  GAAG AC
                                |||||||||| |  |||| ||
                                AATCGTACAA G  CTTT TG
                                      A TC    A
GAM1422  ZNF268   3'  TGTACTAAGAAGACATAGT    35748     T   _
                                TGT CTA GAAGACATAGT
                                ||| ||| ||||||||||
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                                ACA GAT CTTCTGTATCA
                                  T   T
GAM1422  KALI     3'  TTAGCATGTTTTGGCCTGAAG  35749          ____  A
                                TTAGCATGTT    CT GAAG
                                ||||||||||    || ||||
                                AATCGTACAA    GG CTTC
                                      AACC  A
GAM1422  LOC155006 3'  GCGTGTTCTAGGGGAAGGCAGT 35750    A       AA  CA_
                                GC TGTTCTAG  GA   TAGT
                                || ||||||||  ||   ||||
                                CG ACAAGATC  CT   GTCA
                                 C       CC  TCC
GAM1422  LOC222166 3'  TTAGCATGTTTTGAAACAG   35751          CTA   GAC
                                TTAGCATGTT   GAA   ATAG
                                ||||||||||   |||   ||||
                                AATCGTACAA   CTT   TGTC
                                      AA_   ___
GAM1422  LOC255096 3'  TGCCCCAGGAGATGTAGT    35752        A   CA
                                TGTTCTAG AGA  TAGT
                                ||||||||| |||  ||||
                                ACGGGGTC TCT  ATCA
                                     C   AC
GAM1423  CREBL2   3'  TGTTTACTCAGAAAGCAAGG   36260     G  TA  A
                                TGT TG  TA AAAGCAAGG
                                ||| ||  || |||||||||
                                ACA AT  GT TTTCGTTCC
                                  A  GA  C
GAM1423  MADH6    3'  ATATATATATAAAAAGTAAGG  36261            C
                                ATGTGTGTATAAAAAG AAGG
                                |||||||||||||||| ||||
                                TATATATATATTTTTC TTCC
                                          A
GAM1423  PFN1     3'  TGTGTGTATGGGGAGGAAAGG  36262        AAAA  C_
                                TGTGTGTAT    AG  AAGG
                                |||||||||    ||  ||||
                                ACACACATA    TC  TTCC
                                      CCCC  CT
GAM1423  PPP1R12B  3'  TCCAAGTGAGAAAAGCAAG   36263     T   TGTATA
                                TCCA GTG     AAAAGCAAG
                                |||| |||     |||||||||
                                AGGT CAC     TTTTCGTTC
                                  T   TC____
GAM1423  PPP3R1   3'  TGTGTGAAATAAAAGTAAGG   36264       TATA    C
                                TGTGTG    AAAAG AAGG
                                ||||||    ||||| ||||
                                ACACAC    TTTTC TTCC
                                    TTTA    A
GAM1423  RAG1     3'  TGCATATAAAAAGCAAGG    36265
                                TGTGTATAAAAAGCAAGG
                                ||||||||||||||||||
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                                ACGTATATTTTTCGTTCC

GAM1423 SIM1     3' TCCTTGTCTAACTGAAAAGCAA 36266     A   G  TATA
              GG                  TCC TGT TG    AAAAGCAAGG
                                  ||| ||| ||    ||||||||||
                                  AGG ACA AT    TTTTCGTTCC
                                    A   G  TGAC
GAM1423 SLC2A2   3' TGTTCATGTCAAAAAGCAGGG  36267     __   A       A
                                  TGT  GTGT TAAAAAGCA GG
                                  |||  |||| ||||||||| ||
                                  ACA  TACA GTTTTTCGT CC
                                    AG   _       C
GAM1423 SYBL1    3' CAGGTGTGTATAAGAAAGG   36268    T       AAA  C
                                  CA GTGTGTATA   AG AAGG
                                  || |||||||||   || ||||
                                  GT CACACATAT   TC TTCC
                                   C        ___  T
GAM1423 WIG1     5' TCCAGTGGGTGATGAGAAGCAA 36269      _  T   TATAAA
              GG                  TCCA TG GTG     AAGCAAGG
                                  |||| || |||     ||||||||
                                  AGGT AC CAC     TTCGTTCC
                                    C  C   TACTC_
GAM1423 CNOT3    5' TCTACGTGTGCAGGGCAG    36270    C       TAAAAA   A
                                  TC ATGTGTGTA     GCA G
                                  || |||||||||     ||| |
                                  AG TGCACACGT     CGT C
                                   A        CC____   C
GAM1423 DKFZp547G183 3' CATGTGTGTATCCTTTAAGG   36271          AAAAAGC
                                  CATGTGTGTAT      AAGG
                                  ||||||||||      ||||
                                  GTACACACATA      TTCC
                                        GGAAA__
GAM1423 EVI5     3' TATGTTGTCAAAAAAGCAGGG  36272      _  AT       A
                                  TGTGT GT  AAAAAGCA GG
                                  ||||| ||  |||||||| ||
                                  ATACA CA  TTTTTCGT CC
                                     A  GT       C
GAM1423 FLJ13848 3' TCCAAGTGTGTATGTGTCAGGG 36273     T      AAAAAG  A
                                  TCCA GTGTGTAT     CA GG
                                  |||| ||||||||     || ||
                                  AGGT CACACATA     GT CC
                                    T       CACA__  C
GAM1423 FLJ14810 3' CATGTGTGCACACAAGG     36274          AAAAA
                                  CATGTGTGTAT    GCAAGG
                                  ||||||||||    ||||||
                                  GTACACACGTG    TGTTCC
                                                 _____
GAM1423 GRIN3A   3' TCCTGTGCCAGAAAAGCAAGG  36275     ATG    ATA
                                  TCC   TGTGT   AAAAGCAAGG
                                  |||   |||||   ||||||||||
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                                AGG   ACACG   TTTTCGTTCC
                                  ___    GTC
GAM1423  KIAA1233  3'  TCCATGGGTGTTCTAAAAGCAA 36276      T   ATA
              GG                   TCCATG GTGT   AAAAGCAAGG
                                |||||| ||||  ||||||||||
                                AGGTAC CACA   TTTTCGTTCC
                                   C   AGA
GAM1423  NYD-SP17  5'  CATGGTGAAACAAGAGGCAAGG 36277     T  T_   AAA
                                CATG GTG  ATAA   GCAAGG
                                |||| |||  ||||  ||||||
                                GTAC CAC  TGTT   CGTTCC
                                  _  TT   CTC
GAM1423  OSBPL8   3'  TGTGTGTATATGGCACAAGG  36278        AAAA
                                TGTGTGTATA   GCAAGG
                                ||||||||||   ||||||
                                ACACACATAT   TGTTCC
                                     ACCG
GAM1423  P101-PI3K 3'  CCATGTGTGTGTGGTGTTTGCA 36279        ATAAAAA__  A
              GGG                  CCATGTGTGT       GCA GG
                                |||||||||        ||| ||
                                GGTACACACA       CGT CC
                                     CACCACAAA   C
GAM1423  PDZD2    5'  CATGTGTGTGGGTGTCGAGCAG 36280        ATAAAA__   A
              GG                   CATGTGTGT       AGCA GG
                                |||||||||       |||| ||
                                GTACACACA       TCGT CC
                                     CCCACAGC    C
GAM1423  RASGRP4   3'  TCCAAGTGGTCGAAAAGCAAGG 36281     T   T  ATA
                                TCCA GTG GT   AAAAGCAAGG
                                |||| ||| ||   ||||||||||
                                AGGT CAC CA   TTTTCGTTCC
                                  T   _  GC_
GAM1423  TA-PP2C   3'  CATGCTCTATAGAAAGCAAGG  36282      GTG    A
                                CATGT   TATA AAAGCAAGG
                                |||||   |||| |||||||||
                                GTACG   ATAT TTTCGTTCC
                                   AG_    C
GAM1423  ZNF220    3'  TCCATGTGGTATGTAAAGAAAG 36283        T    AA    C
                                TCCATGTG GTAT  AAAG AAG
                                |||||||| ||||  |||| |||
                                AGGTACAC CATA  TTTC TTC
                                     _    CA    T
GAM1423  LOC122614 3'  CACATGTGTCTGGAGCAGGG   36284        ATAAAA    A
                                CATGTGTGT      AGCA GG
                                |||||||||      |||| ||
                                GTGTACACA      TCGT CC
                                     GACC__    C
GAM1423  LOC149657 3'  CATGTGTGACACAGGCAAGG   36285        T   AAAA
                                CATGTGTG ATA    GCAAGG
                                |||||||| |||    ||||||
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                                GTACACAC TGT    CGTTCC
                                     _  GTC_
GAM1423  LOC150967 5'  TCCACTCATAAAAAGCAG    36286      GTGTG        A
                                TCCAT    TATAAAAAGCA G
                                |||||    |||||||||||  |
                                AGGTG    GTATTTTTCGT C
                                   A____         C
GAM1423  LOC196264 3'  CAGTCATTTAAAAAGCAAGG   36287    T  G   A
                                CA GT TGT TAAAAAGCAAGG
                                || || ||| ||||||||||||
                                GT CA GTA ATTTTTCGTTCC
                                 _ _  A
GAM1423  LOC253003 3'  ATGTGCTCCCTTAAAAAGCAGG 36288       GTA__       A
            G                    ATGTGT    TAAAAAGCA GG
                                ||||||    ||||||||| ||
                                TACACG    ATTTTTCGT CC
                                    AGGGA        C
GAM1423  LOC253091 3'  GTGTGTATAAAATACCAG    36289          A  A
                                GTGTGTATAAAA GC AG
                                |||||||||||| || ||
                                CACACATATTTT TG TC
                                       A  G
GAM1423  LOC253675 3'  TCCATGTGTGATAAAAAG    36290         T
                                TCCATGTGTG ATAAAAAG
                                |||||||||| ||||||||
                                AGGTACACAC TATTTTTC
                                      _
GAM1423  LOC253907 3'  GTGTGTATAAAATACCAG    36289          A  A
                                GTGTGTATAAAA GC AG
                                |||||||||||| || ||
                                CACACATATTTT TG TC
                                       A  G
GAM1424  DXYS155E  3'  CGGGCTCGTGCTGCGCCGGCG  36293    T  __  C
                                TGG CTC  GC GCGCCGGCG
                                ||| |||  || |||||||||
                                GCC GAG  CG CGCGGCCGC
                                  C   CA  A
GAM1424  CES2     5'  CTCGCTGGTCTCGGTTCGCTGC 36294     A      C__  _
            CGGCG                  CTCG TGGTCTCG   CGC GCCGGCG
                                |||| ||||||||   ||| |||||||
                                GAGC ACCAGAGC   GCG CGGCCGC
                                  G       CAA   A
GAM1424  KRTAP1-3  3'  TCCATGGTCTCGTCGGC     36295    G       CCGCGC
                                TC ATGGTCTCG     CGGC
                                || |||||||||     ||||
                                AG TACCAGAGC     GCCG
                                 G       A_____
GAM1424  LOC126402 3'  TCGGTGACCTCGCGCTGGCG   36296    A  GT    CGC  C
                                TCG TG  CTCGC   GC GGCG
                                ||| ||  |||||   || ||||
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                                AGC AC  GAGCG   CG CCGC
                                  C TG    ___  A
GAM1424  LOC146227 5'  CGGTGTCGACGCCGGC     36297     C   CC
                                TGGT TCG  GCGCCGGC
                                |||| |||  ||||||||
                                GCCA AGC  TGCGGCCG
                                  C  __
GAM1424  LOC151009 5'  CTCATGGCTGCGTCGG      36298    G   T  CGCC   C
                                CTC ATGG CT    GCG CGG
                                ||| |||| ||    ||| |||
                                GAG TACC GA    CGC GCC
                                  _   _ ____  A
GAM1424  LOC91966  5'  GATGGTCTGCTGCTTCCG    36299       C  C  G_
                                GATGGTCT GC GC  CCG
                                |||||||| || ||  |||
                                CTACCAGA CG CG  GGC
                                    _ A  AA
GAM1425  FGFR2     5'  CAGGCTTGCGTTGCCTCC    36302     G       GGTGTG
                                CAGG TTGCGTTGC     CC
                                |||| |||||||||      ||
                                GTCC AACGCAACG     GG
                                  G       GA____
GAM1425  FGFR2     5'  CAGGCTTGCGTTGCCTCC    36302     G       GGTGTG
                                CAGG TTGCGTTGC     CC
                                |||| |||||||||      ||
                                GTCC AACGCAACG     GG
                                  G       GA____
GAM1425  MUCDHL    3'  GGGTCTGTGCTGTGCCC     36303     GC  T  GG
                                GGGTT  GT GC  TGTGCCC
                                |||||  || ||  |||||||
                                CCCAG  CA CG  ACACGGG
                                  A_  _  __
GAM1425  MUCDHL    3'  GGGTCTGTGCTGTGCCC     36303     GC  T  GG
                                GGGTT  GT GC  TGTGCCC
                                |||||  || ||  |||||||
                                CCCAG  CA CG  ACACGGG
                                  A_  _  __
GAM1425  MUCDHL    3'  GGGTCTGTGCTGTGCCC     36303     GC  T  GG
                                GGGTT  GT GC  TGTGCCC
                                |||||  || ||  |||||||
                                CCCAG  CA CG  ACACGGG
                                  A_  _  __
GAM1425  MUCDHL    3'  GGGTCTGTGCTGTGCCC     36303     GC  T  GG
                                GGGTT  GT GC  TGTGCCC
                                |||||  || ||  |||||||
                                CCCAG  CA CG  ACACGGG
                                  A_  _  __
GAM1425  MUCDHL    3'  GGGTCTGTGCTGTGCCC     36303     GC  T  GG
                                GGGTT  GT GC  TGTGCCC
                                |||||  || ||  |||||||
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                                CCCAG  CA CG  ACACGGG
                                  A_  _ __
GAM1425  POP4     3'  CAGTGTTAACCCCGGTGTGC  36304    G   CGT G
                                CAG GTTG  T CGGTGTGC
                                ||| ||||  | ||||||||
                                GTC CAAT  G GCCACACG
                                  A   TG_ G
GAM1425  ZNF265   3'  CAGGGTTGTTTAGTGT     36305      GC  GC
                                CAGGGTT  GTT  GGTGT
                                |||||||  |||  |||||
                                GTCCCAA  CAA  TCACA
                                   __  A_
GAM1425  ZNF42    5'  GGGTTTGGATGTGCC      36306     GCGT  C
                                GGGTT   TG GGTGTGCC
                                |||||   || ||||||||
                                CCCAA   AC CTACACGG

                                 _____  _
GAM1425  AKAP8    3'  TGAGGTTGCGGTGGGTGTG   36307   A     T  C
                                C GGGTTGCG TG GGTGTG
                                | |||||||| || ||||||
                                A TCCAACGC AC CCACAC
                                 C       C  _
GAM1425  DKFZP434H132 3'  AGGTTGCGTTGTCCC      36308       TGCGG  G
                                GGGTTGCGT    TGT CCC
                                |||||||||    ||| |||
                                TCCAACGCA    ACA GGG

                                  ______  _
GAM1425  DKFZP434H132 3'  AGGTTGCGTTGTCCC      36308       TGCGG  G
                                GGGTTGCGT    TGT CCC
                                |||||||||    ||| |||
                                TCCAACGCA    ACA GGG

                                  ______  _
GAM1425  FLJ14621  3'  CAGTGGCCAGTGTGGTGTGC  36309    _    C  T C
                                CAG GGTTG GT G GGTGTGC
                                ||| ||||| || | |||||||
                                GTC CCGGT CA C CCACACG
                                  A    _ _ A
GAM1425  KIAA1434  3'  CAGGGGTGGGTGGTGTGCC  36310     T  C  TGC
                                CAGGG TG GT  GGTGTGCC
                                ||||| || ||  ||||||||
                                GTCCC AC CA  CCACACGG
                                   C  C  ___
GAM1425  MGC2494   5'  GGGCTGGCGGTGTGCCC    36311      CGTT
                                GGGTTG   GCGGTGTGCCC
                                ||||||   ||||||||||
                                CCCGAC   CGCCACACGGG

                                  ____
GAM1425  PRO1163   5'  TGAGGTATGGTGGTGTGCC  36312   A   _  C  TGC
                                C GGGT TG GT  GGTGTGCC
                                | |||| || ||  ||||||||
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                                A TCCA AC CA   CCACACGG
                                 C   T  _ ___
GAM1425  SV2      3'  CAGGGTTGTGTGTGCATCC   36313        C  TGCG   GC
                                CAGGGTTG GT   GTGT  CC
                                |||||||| ||   ||||  ||
                                GTCCCAAC CA   CACG  GG
                                    A  ____   TA
GAM1425  LOC130245 5'  CAGGGTGGCGGTGTGC     36314       T CGTT
                                CAGGGT G   GCGGTGTGC
                                |||||| |   |||||||||
                                GTCCCA C   CGCCACACG
                                  _ ____
GAM1425  LOC158852 5'  GGGAGTTGTGGGAAATGTGCCC 36315    TTGC   C ____
              C                  GGG   GTTG GG   TGTGCCCC
                                 |||   |||| ||   ||||||||
                                 CCC   CAAC CC   ACACGGGG
                                   T___   A  CTTT
GAM1425  LOC201696 3'  CAGGGTTGTGCTGCGCAACTCC 36316        C     GTGT  _
                                CAGGGTTG GTTGCG   GC CC
                                |||||||| ||||||   || ||
                                GTCCCAAC CGACGC   TG GG
                                    A     GT__  A
GAM1425  LOC202266 3'  CAGGGTTGGTTTAATGT     36317        C   GC
                                CAGGGTTG GTT  GGTGT
                                |||||||| |||  |||||
                                GTCCCAAC CAA  TTACA
                                   _   A_
GAM1425  LOC220073 3'  GGGTTGCGTTTACTTGTTCC   36318         _  GG   G
                                GGGTTGCGTT GC  TGT CC
                                |||||||||| ||  ||| ||
                                CCCAACGCAA TG  ACA GG
                                    A  A_   A
GAM1425  LOC254423 5'  CAGGGCTGTGCCATTGTGCTCC 36319        CGT   G  _   _
                                CAGGGTTG   TGC GT GTGC CC
                                ||||||||   ||| || |||| ||
                                GTCCCGAC   ACG TA CACG GG
                                    ___   G  A   A
GAM1425  LOC257122 5'  GGGAGTTGTGGGAAATGTGCCC 36315    TTGC   C ____
              C                  GGG   GTTG GG   TGTGCCCC
                                 |||   |||| ||   ||||||||
                                 CCC   CAAC CC   ACACGGGG
                                   T___   A  CTTT
GAM1426  EHD3     5'  CTCAGCCGCACCATGGCCC   36322     AG  _   A
                                CTCA  TGC CCAT GCCC
                                ||||  ||| |||| ||||
                                GAGT  GCG GGTA CGGG
                                  CG   T   C
GAM1426  KCNS2    3'  TGATTCAGTGCCCAGTTGCC   36323    C   A     TA_
                                TGA TCA GTGCCCA   GCC
                                ||| ||| |||||||   |||
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                                ACT AGT CACGGGT   CGG
                                  A  _      CAA
GAM1426  OPCML    3'  TGCTCAAGTGCCCTCAGC    36324    A         A
                                TG CTCAAGTGCCC TAGC
                                || |||||||||| ||||
                                AC GAGTTCACGGG GTCG
                                  _         A
GAM1426  POLK     3'  TGATTCAAGTGCTTATTCATAA 36325     C       C____
                                TGA TCAAGTGC    CATAG
                                ||| ||||||||    |||||
                                ACT AGTTCACG    GTATT
                                  A       AATAA
GAM1426  PTK2B    3'  ACCCTGTGTCCATAGCCCA   36326     AA   C
                                ACTC  GTG CCATAGCCCA
                                ||||  ||| ||||||||||
                                TGGG  CAC GGTATCGGGT
                                  A_  A
GAM1426  ZNF261   3'  TGACTCAAGGTCCCATAG    36327        TG
                                TGACTCAAG  CCCATAG
                                |||||||||  |||||||
                                ACTGAGTTC  GGGTATC
                                     CA
GAM1426  FHOD2    3'  TGGATCAAGTGCCCTGCC    36328    AC        ATA
                                TG  TCAAGTGCCC   GCC
                                ||  ||||||||||   |||
                                AC  AGTTCACGGG   CGG
                                 CT        A__
GAM1426  FLJ11413 3'  GACGAGGCCCATAGCC      36329     TCA  T
                                GAC   AG GCCCATAGCC
                                |||   || ||||||||||
                                CTG   TC CGGGTATCGG
                                  C__  _
GAM1426  FLJ20605 3'  ACTCAAGTACAGCCCA      36330          CCAT
                                ACTCAAGTGC    AGCCCA
                                ||||||||||    ||||||
                                TGAGTTCATG    TCGGGT
                                      _____
GAM1426  FLJ22389 3'  TGAGTCAAGTGCTAGCTTTCAA 36331     C       CCA    C__
            A                    TGA TCAAGTGC   TAGC   CAAA
                                ||| ||||||||   ||||   ||||
                                ACT AGTTCACG   ATCG   GTTT
                                  C       ___    AAA
GAM1426  HCNGP    3'  TGCTCAAGTGCACTCA      36332    A       CCATA  C
                                TG CTCAAGTGC    GC CA
                                || |||||||||    || ||
                                AC GAGTTCACG    TG GT
                                  _       _____  A
GAM1426  KIAA0247 3'  TGACTCAAGAGCTCTCACACC  36333         T  C__    G
                                TGACTCAAG GC   CATA CC
                                ||||||||| ||   |||| ||
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                                ACTGAGTTC CG   GTGT GG
                                     T  AGA   _
GAM1426  KIAA0913  3'  CCCAAGCTATAGCCCAA     36334        GCCC
                                CTCAAGT    ATAGCCCAA
                                |||||||    |||||||||
                                GGGTTCG    TATCGGGTT
                                   A___
GAM1426  KIAA1184  3'  TGACTCAAGGTACACCTGCC   36335         _  _ ATA
                                TGACTCAAG TGC CC   GCC
                                ||||||||| ||| ||   |||
                                ACTGAGTTC ATG GG   CGG
                                     C   T  A__
GAM1426  LOC130074 3'  TGACCAGGTGCCCACCCCAA   36336      T  A       AG
                                TGAC CA GTGCCCAT  CCCAA
                                |||| || ||||||||  |||||
                                ACTG GT CACGGGTG  GGGTT
                                  _  C       __
GAM1426  LOC134875 5'  TGATTCCAGTGCCCATACTCTC 36337     C  A        G___
            CCAA                    TGA TC AGTGCCCATA    CCCAA
                                ||| || ||||||||||    |||||
                                ACT AG TCACGGGTAT    GGGTT
                                  A  G         GAGA
GAM1426  LOC146713 3'  CGGCTCAGGTCTAGCCCA    36338    A    A  GCCCA
                                TG CTCA GT     TAGCCCA
                                || |||| ||     |||||||
                                GC GAGT CA     ATCGGGT
                                 C    C  G____
GAM1426  LOC149127 3'  AGTGCCCATGGCTCCAAA    36339         A  _
                                AGTGCCCAT GC CCAAA
                                ||||||||| || |||||
                                TCACGGGTA CG GGTTT
                                     C  A
GAM1426  LOC153811 3'  CTCTTAACCATAGCCCA     36340     AAG  C
                                CTC   TG CCATAGCCCA
                                |||   || ||||||||||
                                GAG   AT GGTATCGGGT
                                  A__  T
GAM1426  LOC221424 3'  TCAAGTGCCCCCCAA       36341          ATAG
                                TCAAGTGCCC    CCCAA
                                ||||||||||    |||||
                                AGTTCACGGG    GGGTT
                                      _____
GAM1426  LOC256228 5'  TGACCACAAGTCTCATAGCCCA 36342       _    GCC
                                TGACT CAAGT   CATAGCCCA
                                ||||| |||||   |||||||||
                                ACTGG GTTCA   GTATCGGGT
                                   T     GA_
GAM1426  LOC90785  3'  TGGCTGGAGTGCCCAAGC    36343    A  CA       T
                                TG CT  AGTGCCCA AGC
                                || ||  |||||||| |||
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                                AC GA  TCACGGGT TCG
                                 C  CC       _
GAM1426 LOC91445 3' TGACTCAATGCCAAGGCC    36344        G    C TA
                                TGACTCAA TGCC A  GCC
                                |||||||| |||| |  |||
                                ACTGAGTT ACGG T  CGG
                                     _   _ TC
GAM1426 LOC92231 3' TGCTCAAGTGTGGCCCAA    36345    A      CCCATA
                                TG CTCAAGTG     GCCCAA
                                || ||||||||     ||||||
                                AC GAGTTCAC     CGGGTT
                                 _      AC____
GAM1427 ACPT     3' TGAGTACATGACCATC      36348        CA   AT
                                TGAGTACA  GAC  TATC
                                ||||||||  |||  ||||
                                ACTCATGT  CTG  GTAG
                                     A_  __
GAM1427 ACPT     3' TGAGTACATGACCATC      36348        CA   AT
                                TGAGTACA  GAC  TATC
                                ||||||||  |||  ||||
                                ACTCATGT  CTG  GTAG
                                     A_  __
GAM1427 AGTR1    5' TGGGCACACAGATCCTAT    36349    A       CA
                                TG GTACACAGA  TTAT
                                || |||||||||  ||||
                                AC CGTGTGTCT  GATA
                                 C        AG
GAM1427 PML      3' TGGGTACACAGACTTCACCA   36350    A       A
                                TG GTACACAGAC TTATCG
                                || ||||||||||  ||||||
                                AC CATGTGTCTG AGTGGT
                                 C         A
GAM1427 FLJ14082 3' TGAGTACACACACTTAGGCTCG 36351          G  ATTA__
                                TGAGTACACA AC      TCG
                                ||||||||||  ||     |||
                                ACTCATGTGT TG      AGC
                                      G  AATCCG
GAM1427 FLJ20397 5' TGGCTGCACAGACACTTCCG   36352    A  A_       A
                                TG GT  CACAGACATT TCG
                                || ||  ||||||||||  |||
                                AC CG  GTGTCTGTGA GGC
                                 _  AC         A
GAM1427 HTCD37   3' TGAATACATGGAGACCATCG   36353        CA  C
                                TGAGTACA  GA ATTATCG
                                ||||||||  ||  |||||||
                                ACTTATGT  CT TGGTAGC
                                     AC  C
GAM1427 KIAA0352 3' TAAGTACACAGACCACC     36354           AT
                                TGAGTACACAGAC  TATC
                                ||||||||||||  ||||
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                                ATTCATGTGTCTG GTGG
                                      __
GAM1427 LOC147463 3' TGAGTTACAGGACACCAT    36355      AC   _
                                TGAGT ACAG ACATTAT
                                ||||| |||| |||||||
                                ACTCA TGTC TGTGGTA
                                   A_   C
GAM1427 LOC253461 5' TGAGTACAGGGACAATC     36356       CA   TT
                                TGAGTACA GACA ATC
                                |||||||| |||| |||
                                ACTCATGT CTGT TAG
                                     CC   __
GAM1428 AMFR    3' TTATTGAAATAAATTATCT   36359       ACA
                                TTATTGGAA AAGTTGTCT
                                ||||||||| |||||||||
                                AATAACTTT TTTAATAGA
                                     A__
GAM1428 AMFR    3' TTATTGAAATAAATTATCT   36359       ACA
                                TTATTGGAA AAGTTGTCT
                                ||||||||| |||||||||
                                AATAACTTT TTTAATAGA
                                     A__
GAM1428 GLO1    3' TTGTGAAAAAAGTTGTTTCTG 36360    _  C     C
                                TTG GAAA AAAGTTGT TCTG
                                ||| |||| |||||||| ||||
                                AAC CTTT TTTCAACA AGAC
                                  A  _      A
GAM1428 MAPRE1  3' TTATTGGAAAAGGAGTGAAACG 36361        CAA  ____
           TCT                  TTATTGGAAA  AGT   TGTCT
                                |||||||||| |||   |||||
                                AATAACCTTT  TCA   GCAGA
                                     TCC  CTTT
GAM1428 MYL2    3' TTATTGGAACATGGCCTCT   36362       A  AAGTT
                                TTATTGGAA CA    GTCTCT
                                ||||||||| ||    ||||||
                                AATAACCTT GT    CGGAGA
                                     _ AC___
GAM1428 TIMM17A 3' TATTGGAAGCAAGTTGTTTCTG 36363       ACA     C
                                TATTGGAA  AAGTTGT TCTG
                                |||||||  ||||||| ||||
                                ATAACCTT  TTCAACA AGAC
                                     CG_     A
GAM1428 TNKS    3' TTATTAGAAACAATCCTCT   36364         AGTTG
                                TTATTGGAAACAA    TCTCT
                                ||||||||||||    |||||
                                AATAATCTTTGTT    GGAGA
                                       A____
GAM1428 FLJ10139 3' GGAAAAAAGTTGTCTCTG   36365     C
                                GGAAA AAAGTTGTCTCTG
                                ||||| ||||||||||||
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                                CCTTT TTTCAACAGAGAC
                                  _
GAM1428 FLJ14397 3' TTAGTGGAAACAGGGTTTCACC 36366     T      AA  G  T
             G                   TTA TGGAAACA  GTT TC CTG
                                 ||| ||||||||  ||| || |||
                                 AAT ACCTTTGT  CAA AG GGC
                                   C       CC  _ T
GAM1428 KNSL5    3' TTGAATACTAGTTGTCT     36367      A  AA
                                 TTGGA AC  AGTTGTCT
                                 ||||| ||  ||||||||
                                 AACTT TG  TCAACAGA
                                    A  A_
GAM1428 KNSL5    3' TTGAATACTAGTTGTCT     36367      A  AA
                                 TTGGA AC  AGTTGTCT
                                 ||||| ||  ||||||||
                                 AACTT TG  TCAACAGA
                                    A  A_
GAM1428 MGC13010 3' TTATTGGAGACTAGGCCTCTTC 36368        A  AAA  TG__
             TCTG                   TTATTGGA AC   GT    TCTCTG
                                 |||||||| ||   ||   ||||||
                                 AATAACCT TG   CG    AGAGAC
                                      C  ATC  GAGA
GAM1428 My015    3' TTATTGGAAACCAAAATCT   36369          AAAGTT
                                 TTATTGGAAAC     GTCT
                                 ||||||||||      ||||
                                 AATAACCTTTG     TAGA
                                       GTTT__
GAM1428 STK36    3' TTATTGGAGAAAAGGCCCCTG  36370        AAC    TT
                                 TTATTGGA   AAAG  GTCTCTG
                                 ||||||||   ||||  |||||||
                                 AATAACCT   TTTC  CGGGGAC
                                      CT_   __
GAM1428 LOC149650 3' TTGGAAACAGAGTCCAGTCCTG 36371         A   __  T
                                 TTGGAAACA AGTT  GTC CTG
                                 ||||||||| ||||  ||| |||
                                 AACCTTTGT TCAG  CAG GAC
                                      C    GT  _
GAM1428 LOC92370 3' TTATTGGAAGAAAGTGCCT   36372         AC    T
                                 TTATTGGAA  AAAGT GTCT
                                 |||||||||  ||||| ||||
                                 AATAACCTT  TTTCA CGGA
                                      C_    _
GAM1429 ABL1     3' AGGGAGTGCAGGCAGAGGGCCT 36375       C   A   CT_  A
                                 GGGGAG GCA GGC   GG GCCT
                                 |||||| ||| |||   || ||||
                                 TCCCTC CGT CCG   CC CGGA
                                    A   _   TCT  _
GAM1429 ABL1     3' AGGGAGTGCAGGCAGAGGGCCT 36375       C   A   CT_  A
                                 GGGGAG GCA GGC   GG GCCT
                                 |||||| ||| |||   || ||||
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                                TCCCTC CGT CCG   CC CGGA
                                   A   _   TCT  _
GAM1429  ALDH3B1   3'  GGGGTGCCCTGGAGCC      36376      A  GCAAGG
                                GGGG GC     CCTGGAGCC
                                |||| ||     |||||||||
                                CCCC CG     GGACCTCGG
                                  A _______
GAM1429  ALPP      3'  GGGGAGGCAGGGGAGC      36377       C   A  CCT    C
                                GGGGAG GCA GG   GGAG C
                                |||||| ||| ||   |||| |
                                CCCCTC CGT CC   CCTC G
                                   _   _ ___    A
GAM1429  BLVRB     5'  GGGGGTGCAAGGCCTCAGAGTC 36378      AGC        _    C
             T                   GGGG   GCAAGGCCT GGAG CT
                                ||||   ||||||||| |||| ||
                                CCCC   CGTTCCGGA TCTC GA
                                  CA_       G    A
GAM1429  BTG3      5'  AGGGAGCGCAGCGAGCC     36379          AG  CTG
                                GGGGAGCGCA  GC   GAGCC
                                ||||||||||  ||   |||||
                                TCCCTCGCGT  CG   CTCGG
                                          __  ___
GAM1429  CCND3     5'  GGAGAGCGCGGGGCGCGG    36380         AA   C
                                GGGGAGCGC  GGC TGG
                                |||||||||  ||| |||
                                CCTCTCGCG  CCG GCC
                                     CC   C
GAM1429  CDX1      3'  GAGGAGGTGGGGCCTGGAGCCT 36381       CGCAA
                                GGGGAG    GGCCTGGAGCCT
                                ||||||    ||||||||||||
                                CTCCTC    CCGGACCTCGGA
                                   CACC_
GAM1429  CTGF      5'  GGGGAGCGCGGGGCCTGGAGCG 36382         AA        _
             CT                   GGGGAGCGC  GGCCTGGAGC CT
                                |||||||||  |||||||||| ||
                                CCCCTCGCG  CCGGACCTCG GA
                                     CC        C
GAM1429  DAG1      5'  GGGGCGCGCGGCCGGAGCCT   36383     A   AA   T
                                GGGG GCGC  GGCC GGAGCCT
                                |||| ||||  |||| |||||||
                                CCCC CGCG  CCGG CCTCGGA
                                  G   __   _
GAM1429  DLST      3'  GGAGAGCGTGAGGGCAGGCCT  36384        CA   CCT  A
                                GGGGAGCG  AGG   GG GCCT
                                ||||||||  |||   || ||||
                                CCTCTCGC  TCC   TC CGGA
                                     AC   CG_  _
GAM1429  EGLN1     5'  GGGGAGCGCAAGACCGGCCCCC 36385             T  AG
                                GGGGAGCGCAAGGCC GG  CCT
                                |||||||||||||| ||  |||
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                                CCCCTCGCGTTCTGG CC  GGG
                                        _ GG
GAM1429  FXYD2    5'  GAGGTGCTGCTTGCCTGGGGCC 36386     A _ AAG     A
                T                GGGG GC GC   GCCTGG GCCT
                                 |||| || ||   |||||| |||||
                                 CTCC CG CG   CGGACC CGGA
                                   A  A  AA_     C
GAM1429  GALR1    5'  GGAGAGTGCGAGTTTAGGAGTC 36387       C  A  GCCT    C
                T                GGGGAG GC AG   GGAG CT
                                 |||||| || ||   |||| ||
                                 CCTCTC CG TC   CCTC GA
                                    A  C  AAAT   A
GAM1429  GGT2     3'  GGGAGGCCACCTGGAGCC    36388      C  AAG
                                 GGGAG GC   GCCTGGAGCC
                                 ||||| ||   ||||||||||
                                 CCCTC CG   TGGACCTCGG
                                   _ G__
GAM1429  HSD11B2  5'  GGGGAGCGGGGAGAGAGAGC  36389       CAA  CCT_
                                 GGGGAGCG   GG   GGAGC
                                 ||||||||   ||   |||||
                                 CCCCTCGC   CC   TCTCG
                                      C__  TCTC
GAM1429  JUN      3'  GGGGAGCGTGGAGTATGAAGCC 36390       CAA  CC
                T                GGGGAGCG   GG  TGGAGCCT
                                 ||||||||   ||  ||||||||
                                 CCCCTCGC   TC  ACTTCGGA
                                      ACC  AT
GAM1429  MYD88    5'  GGCGGGCGGTCCTGGAGCCT  36391    _ A  CAAGG
                                 GG GG GCG    CCTGGAGCCT
                                 || || |||    ||||||||||
                                 CC CC CGC    GGACCTCGGA
                                  G  _  CA___
GAM1429  ODC1     5'  GGGAAGCGCAGACGCCGGAGCC 36392         A  _
                T                GGGGAGCGCA GGC CTGGAGCCT
                                 |||||||||| ||| |||||||||
                                 CCCTTCGCGT CTG GGCCTCGGA
                                       _  C
GAM1429  P2RX3    3'  GGGGAGGCCTGGAGCC     36393      GCGCAA
                                 GGGGA     GGCCTGGAGCC
                                 |||||     ||||||||||
                                 CCCCT     CCGGACCTCGG
                                      _______
GAM1429  PBP      3'  GGGGAACATGGCTTGGGGCCT 36394       CAA  C  A
                                 GGGGAGCG   GGC TGG GCCT
                                 ||||||||   ||| ||| ||||
                                 CCCCTTGT   CCG ACC CGGA
                                      A__   A  C
GAM1429  PTPRF    3'  GGGAGCGCAACAGAGAGC    36395       AG  CT
                                 GGGAGCGCA  GC  GGAGC
                                 |||||||||  ||  |||||
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                                CCCTCGCGT  TG  TCTCG
                                     __ TC
GAM1429 PTPRF    3' GGGAGCGCAACAGAGAGC    36395        AG  CT
                                GGGAGCGCA  GC  GGAGC
                                |||||||||  ||  |||||
                                CCCTCGCGT  TG  TCTCG
                                     __ TC
GAM1429 RAP1GA1  3' GGGGAGGCAAGGCCTGGACTCT 36396       C         GC
                                GGGGAG GCAAGGCCTGGA  CT
                                ||||||| ||||||||||||  ||
                                CCCCTC CGTTCCGGACCT  GA
                                   _         GA
GAM1429 S100A11  5' GGCGTGCGGGTCTGGAGCCT  36397    GGA  CAA  C
                                GG  GCG  GG CTGGAGCCT
                                ||  |||  || |||||||||
                                CC  CGC  CC GACCTCGGA
                                 GCA  ___ A
GAM1429 SLC22A5  5' GGGGAACGCGGCGGGC     36398        AA  CT  A
                                GGGGAGCGC  GGC  GG GC
                                |||||||||  |||  || ||
                                CCCCTTGCG  CCG  CC CG
                                     __  __ _
GAM1429 TACSTD1  5' GGGCAGCGCGAGGCCTGGGGC 36399    G    A      A
                                GGG AGCGC AGGCCTGG GC
                                ||| ||||| |||||||| ||
                                CCC TCGCG TCCGGACC CG
                                  G    C      C
GAM1429 ALOX15B  3' GGGCACTTTGAGGCTTGGAGCC 36400    A   A___    C
            T                    GG GCGC    AGGC TGGAGCCT
                                || ||||    |||| ||||||||
                                CC CGTG    TCCG ACCTCGGA
                                 _   AAAC   A
GAM1429 C20orf97 3' GGGGAGAGGCCTGGAGCCT   36401      CGCA
                                GGGGAG   AGGCCTGGAGCCT
                                ||||||   ||||||||||||
                                CCCCTC   TCCGGACCTCGGA
                                     _____
GAM1429 C2F      3' GGGGTGCAAGGCCCTGCCT   36402     AGC       GGA
                                GGGG  GCAAGGCCT  GCCT
                                ||||  |||||||||  ||||
                                CCCC  CGTTCCGGG  CGGA
                                  A__       A__
GAM1429 DKFZP564O0423 3' GGGAGTCGATGCTTGGAGCCT  36403      _  CAAG  C
                                GGGAG CG   GC TGGAGCCT
                                ||||| ||   || ||||||||
                                CCCTC GC   CG ACCTCGGA
                                   A  TA__  A
GAM1429 DKFZP586C1619 3' GGGGAGTGCATGGCTGCCC   36404       C   A   CTGGA
                                GGGGAG GCA GGC    GCCT
                                |||||| ||| |||    ||||
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                                CCCCTC CGT CCG    CGGG
                                   A  A  A____
GAM1429  DOC2A    3'  GAGGAGCGCGGGGCCTGG    36405        AA
                                GGGGAGCGC  GGCCTGG
                                |||||||||  |||||||
                                CTCCTCGCG  CCGGACC
                                     CC
GAM1429  FASTK    3'  AGGCCCAGGGCCTGGAGC    36406    A  G  A
                                GG GC CA GGCCTGGAGC
                                || || || ||||||||||
                                TC CG GT CCGGACCTCG
                                 _  G  C
GAM1429  FASTK    3'  AGGCCCAGGGCCTGGAGC    36406    A  G  A
                                GG GC CA GGCCTGGAGC
                                || || || ||||||||||
                                TC CG GT CCGGACCTCG
                                 _  G  C
GAM1429  FLJ11618 3'  GGGGAGGCAGGCCCAGGGCCT  36407      C   A   TG A
                                GGGGAG GCA GGCC  G GCCT
                                |||||| ||| ||||  | ||||
                                CCCCTC CGT CCGG  C CGGA
                                   _  _   GT C
GAM1429  FLJ13848 3'  GAGGAGTGCAGGCAGAGGGGCC 36408      C   A   CT_  A
           T                     GGGGAG GCA GGC   GG GCCT
                                |||||| ||| |||   || ||||
                                CTCCTC CGT CCG   CC CGGA
                                   A  _  TCT  C
GAM1429  FLJ14100 5'  GGGGAGCACAGGGTCTCACCT  36409        A  C  GGA
                                GGGGAGCGCA GG CT   GCCT
                                |||||||||| || ||   ||||
                                CCCCTCGTGT CC GA   TGGA
                                     C  A  G__
GAM1429  FLJ20093 5'  GGAGAGCGCGGGGCTCGCTGGC 36410        AA  ___  GA
           CT                    GGGGAGCGC  GGC   CTG  GCCT
                                |||||||||  |||  |||  ||||
                                CCTCTCGCG  CCG   GAC  CGGA
                                     CC   AGC  __
GAM1429  FLJ20898 3'  GGAGCGCAGGGCAGCC     36411        A  CTGG
                                GGAGCGCA GGC   AGCC
                                |||||||| |||   ||||
                                CCTCGCGT CCG   TCGG
                                     C  ____
GAM1429  FLJ21839 3'  GGGGATGTGGGGCCTGAAGAGC 36412      GCGCAA    __
           CT                    GGGGA    GGCCTG  GAGCCT
                                |||||    ||||||  ||||||
                                CCCCT    CCGGAC  CTCGGA
                                   ACACC_    TT
GAM1429  FLJ22283 5'  GGGAGCGCGGTTGGGCC    36413        AA  CC   A
                                GGGAGCGC  GG  TGG GCC
                                ||||||||  ||  ||| |||
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                                CCCTCGCG  CC  ACC CGG
                                    __  A_  _
GAM1429  GGTLA4   3' GGGAGGCCACCTGGAGCC    36388      C  AAG
                                GGGAG GC   GCCTGGAGCC
                                ||||| ||   ||||||||||
                                CCCTC CG   TGGACCTCGG
                                  _ G__
GAM1429  KIAA0125 3' GGGAGGGTGTCCTTGGAGCCT  36414      CGCAAGG  _
                                GGGAG      CCT GGAGCCT
                                |||||      ||| |||||||
                                CCCTC      GGA CCTCGGA
                                   CCACA__   A
GAM1429  KIAA0420 3' GGGAAGTGGGCTGGAGCC    36415      CGCAA   C
                                GGGGAG     GGC TGGAGCC
                                ||||||     ||| |||||||
                                CCCTTC     CCG ACCTCGG
                                    AC___  _
GAM1429  KIAA0710 5' GGGGAGCGCAAGCGCTGTCAGC 36416          _  C  G_
                                GGGGAGCGCAAG GC TG  AGC
                                |||||||||||| || ||  |||
                                CCCCTCGCGTTC CG AC  TCG
                                      G  _  AG
GAM1429  KIAA0711 3' AGGGAGCACCTGGGGC      36417       GCAAG     A
                                GGGGAGC    GCCTGG GC
                                |||||||    |||||| ||
                                TCCCTCG    TGGACC CG
                                   _____     C
GAM1429  KIAA0830 3' GCTTTGTCAGGGCCTGGAGTCT 36418    G____  A       C
                                GC    CA GGCCTGGAG CT
                                ||    || ||||||||| ||
                                CG    GT CCGGACCTC GA
                                 AAACA  C        A
GAM1429  KIAA1266 5' GGGGCCGGCCTGGAGCC     36419     AGCGCAA
                                GGGG      GGCCTGGAGCC
                                ||||      ||||||||||
                                CCCC      CCGGACCTCGG
                                  GG_____
GAM1429  KIAA1655 5' GGGGAGAGCACACCTGGAG   36420       C   AG
                                GGGGAG GCA  GCCTGGAG
                                |||||| |||  ||||||||
                                CCCCTC CGT  TGGACCTC
                                   T   G_
GAM1429  KIAA1966 5' GGGCGGCGCTAAAATGGAGCCT 36421     GA   _   CC
                                GGG  GCGC AAGG  TGGAGCCT
                                |||  |||| ||||  ||||||||
                                CCC  CGCG TTTT  ACCTCGGA
                                 GC   A   __
GAM1429  LGP2     3' AGGAGGGGCCTGGAGC      36422       CGCAA       C
                                GGGAG    GGCCTGGAG C
                                |||||    ||||||||| |
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                                TCCTC    CCGGACCTC G
                                  C____       A
GAM1429  MGC16169  5'  GAGGAGCGCAAGCCTGGCCT  36423          G   GA
                                GGGGAGCGCAAG CCTG  GCCT
                                |||||||||||| ||||  ||||
                                CTCCTCGCGTTC GGAC  CGGA
                                          _   __
GAM1429  SMCR7     3'  GGGGTGCAGCACAGAGCCT   36424     A  GCAA   C
                                GGGG GC   GGC TGGAGCCT
                                |||| ||   ||| ||||||||
                                CCCC CG   TCG GTCTCGGA
                                  A ____  T
GAM1429  UBP1      5'  GGAGGGCGCGGGTGAAGCCT  36425     A   AA  CC
                                GGGG GCGC  GG  TGGAGCCT
                                |||| ||||  ||  ||||||||
                                CCTC CGCG  CC  ACTTCGGA
                                  C   C_  __
GAM1429  LOC132332 3'  GGGGAGCAGTGCTGCTTGGAGC 36426        CAAG_  C
                                GGGGAGCG    GC TGGAGC
                                ||||||||    || ||||||
                                CCCCTCGT    CG ACCTCG
                                     CACGA  A
GAM1429  LOC133957 5'  GGGGAGCGCGGGACCTCAGC  36427        AA    GG
                                GGGGAGCGC  GGCCT  AGC
                                |||||||||  |||||  |||
                                CCCCTCGCG  CTGGA  TCG
                                     CC    G_
GAM1429  LOC143920 5'  GGGGTGCCGCTGCAGAGCCT  36428     A  _  AAG  CT
                                GGGG GC GC   GC  GGAGCCT
                                |||| || ||   ||  |||||||
                                CCCC CG CG   CG  TCTCGGA
                                  A  G  A__  __
GAM1429  LOC145719 3'  GGAGAAGTGGGTCTGGAGTCT  36429      CGCAA  C     C
                                GGGGAG    GG CTGGAG CT
                                ||||||    || |||||| ||
                                CCTCTT    CC GACCTC GA
                                   CAC__  A     A
GAM1429  LOC145720 3'  GGAGAAGTGGGTCTGGAGTCT  36429      CGCAA  C     C
                                GGGGAG    GG CTGGAG CT
                                ||||||    || |||||| ||
                                CCTCTT    CC GACCTC GA
                                   CAC__  A     A
GAM1429  LOC146657 5'  GGGGTGCCGCTGCAGAGCCT  36428     A  _  AAG  CT
                                GGGG GC GC   GC  GGAGCCT
                                |||| || ||   ||  |||||||
                                CCCC CG CG   CG  TCTCGGA
                                  A  G  A__  __
GAM1429  LOC149351 5'  GGGGAGCGGAGCCCCAGCCT  36430       CAA    GG
                                GGGGAGCG   GGCCT  AGCCT
                                ||||||||   |||||  |||||
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                                CCCCTCGC  TCGGG  TCGGA
                                   C__    G_
GAM1429  LOC149657 3'  GGGGGCGCAGGCTGGGCCT  36431     A   A  C  A
                                GGGG GCGCA GGC TGG GCCT
                                |||| ||||| ||| ||| ||||
                                CCCC CGCGT CCG ACC CGGA
                                  _   _  _  _
GAM1429  LOC149657 3'  GGGGGCGCAGGCTGGGCCT  36431     A   A  C  A
                                GGGG GCGCA GGC TGG GCCT
                                |||| ||||| ||| ||| ||||
                                CCCC CGCGT CCG ACC CGGA
                                  _   _  _  _
GAM1429  LOC149657 3'  GGGGGCGCAGGCTGGGCCT  36431     A   A  C  A
                                GGGG GCGCA GGC TGG GCCT
                                |||| ||||| ||| ||| ||||
                                CCCC CGCGT CCG ACC CGGA
                                  _   _  _  _
GAM1429  LOC149657 3'  GGGGGCGCAGGCTGGGCCT  36431     A   A  C  A
                                GGGG GCGCA GGC TGG GCCT
                                |||| ||||| ||| ||| ||||
                                CCCC CGCGT CCG ACC CGGA
                                  _   _  _  _
GAM1429  LOC150378 5'  GGGGAGCGTAGGCTGA     36432       CA  C
                                GGGGAGCG  AGGC TGG
                                ||||||||  |||| |||
                                CCCCTCGC  TCCG ACT
                                   A_   _
GAM1429  LOC150445 3'  GGGGAACATGGCTTGGGGCCT 36394       CAA  C  A
                                GGGGAGCG   GGC TGG GCCT
                                ||||||||   ||| ||| ||||
                                CCCCTTGT   CCG ACC CGGA
                                   A__   A  C
GAM1429  LOC197114 3'  GGAGAAGTGGGTCTGGAGTCT  36429     CGCAA  C    C
                                GGGGAG    GG CTGGAG CT
                                ||||||    || |||||| ||
                                CCTCTT    CC GACCTC GA
                                   CAC__  A    A
GAM1429  LOC197117 3'  GGAGAAGTGGGTCTGGAGTCT  36429     CGCAA  C    C
                                GGGGAG    GG CTGGAG CT
                                ||||||    || |||||| ||
                                CCTCTT    CC GACCTC GA
                                   CAC__  A    A
GAM1429  LOC199964 5'  GGGGAGCGCGGGACCCGGGCCT 36433       AA    A
                                GGGGAGCGC  GGCCTGG GCCT
                                |||||||||  ||||||| ||||
                                CCCCTCGCG  CTGGGCC CGGA
                                   CC     _
GAM1429  LOC200316 3'  GGGGAGGTGGATGGAGAGCCT  36434     CGCAA_  CCT
                                GGGGAG    GG  GGAGCCT
                                ||||||    ||  |||||||
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                                CCCCTC     CC   TCTCGGA
                                   CACCTA  ___
GAM1429  LOC200860 5'  GAGGAGTGGGCAGCCTGGAGC  36435       CGCAA
                                GGGGAG    GGCCTGGAGC
                                ||||||    ||||||||||
                                CTCCTC    TCGGACCTCG
                                   ACCCG
GAM1429  LOC202024 5'  GGAGAGTGTGACGGAGCC    36436       CGCAA   CT
                                GGGGAG    GGC  GGAGCC
                                ||||||    |||  ||||||
                                CCTCTC    CTG  CCTCGG
                                   ACA__   __
GAM1429  LOC220549 5'  GGGGAGGCGAGGCCTAAGTGCC 36437       C  A      _ A
             T                   GGGGAG GC AGGCCTG G GCCT
                                ||||||| || ||||||| | ||||
                                CCCCTC CG TCCGGAT C CGGA
                                   _  C      T A
GAM1429  LOC221975 5'  GGGTGGCGAGAATCTGGAGCCT 36438     GA   CA  GC
                                GGG  GCG  AG  CTGGAGCCT
                                |||  |||  ||  |||||||||
                                CCC  CGC  TT  GACCTCGGA
                                  AC   TC  A_
GAM1429  LOC253502 3'  GGGGAGCGCAGGACGCCG    36439          A  _
                                GGGGAGCGCA GGC CTG
                                |||||||||| ||| |||
                                CCCCTCGCGT CTG GGC
                                      C   C
GAM1429  LOC253805 3'  GGGAGGAGCCTGGAGTCT    36440      CGCAA       C
                                GGGAG    GGCCTGGAG CT
                                |||||    ||||||||| ||
                                CCCTC    TCGGACCTC GA
                                   C_____       A
GAM1429  LOC255189 5'  GGGGAGCGGGGGTCCTCAGCCT 36441        CAA  _   GG
                                GGGGAGCG   GG CCT  AGCCT
                                ||||||||   || |||  |||||
                                CCCCTCGC   CC GGA  TCGGA
                                     CC_  A   G_
GAM1429  LOC256158 5'  GGGGAGCCTGAGGCCTGG    36442       GCA
                                GGGGAGC   AGGCCTGG
                                |||||||   ||||||||
                                CCCCTCG   TCCGGACC
                                   GAC
GAM1429  LOC257354 3'  GGGAAGTGGGCTGGAGCC    36415       CGCAA   C
                                GGGGAG    GGC TGGAGCC
                                ||||||    ||| |||||||
                                CCCTTC    CCG ACCTCGG
                                   AC___   _
GAM1429  LOC51014  5'  GGGGGTGAAGGGGCGGAGCCT  36443     AGCGC   CC
                                GGGG    AAGG  TGGAGCCT
                                ||||    ||||  ||||||||
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                                CCCC    TTCC  GCCTCGGA
                                  CAC__   CC
GAM1429  LOC92080  5'  GGGGAACCCTCTGGAGCC    36444       GCAAGGC
                                GGGGAGC     CTGGAGCC
                                |||||||     ||||||||
                                CCCCTTG     GACCTCGG
                                   GGA____
GAM1429  LOC92405  5'  GGGGGCGTGGCCTCTGGAGCCT 36445     A  CAA   __
                                GGGG GCG   GGCCT  GGAGCCT
                                |||| |||   |||||  |||||||
                                CCCC CGC   CCGGA  CCTCGGA
                                  _  A__    GA
GAM1429  LOC92973  3'  GGGCTTATGGGCCTGGAGCCT  36446    AGCGCAA
                                GGG     GGCCTGGAGCCT
                                |||     ||||||||||||
                                CCC     CCGGACCTCGGA
                                 GAATAC_
GAM1430  IFNA2     3'  TTACTTATATCTTGAATATA   36449       AAACA
                                TTACTTA    CTTGAATATA
                                |||||||    ||||||||||
                                AATGAAT    GAACTTATAT
                                   ATA__
GAM1430  FLJ10242  3'  ACCTGCTTAAAACTGAAAATAT 36450     A       ACTT
           A                     ACTT CTTAAAAC    GAATATA
                                |||| ||||||||    |||||||
                                TGGA GAATTTTG    TTTATAT
                                  C       ACT_
GAM1430  FLJ11715  3'  ACTTACTGAAAACACTGA    36451       T       T
                                ACTTACT AAAACACT GA
                                ||||||| |||||||| ||
                                TGAATGA TTTTGTGA CT
                                   C       _
GAM1430  KIAA1344  3'  ACTCACTTAAAATATAAATA   36452          CACT
                                ACTTACTTAAAA    TGAATA
                                ||||||||||||    ||||||
                                TGAGTGAATTTT    ATTTAT
                                      AT__
GAM1430  MRPL32    3'  TTACTTAAAACCTTGTATA    36453          A   A
                                TTACTTAAAAC CTTG ATA
                                |||||||||| |||| |||
                                AATGAATTTTG GAAC TAT
                                      _   A
GAM1430  LOC221399 5'  ACTTACTCAAAATGTGAAT    36454          CACT
                                ACTTACTTAAAA    TGAAT
                                ||||||||||||    |||||
                                TGAATGAGTTTT    ACTTA
                                      AC__
GAM1431  B4GALT4   5'  GGTCACACCCACTGCCTT    36457     GA       C
                                GGT  CATACCCAC GCCTT
                                |||  ||||||||| |||||
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                                CCA  GTGTGGGTG CGGAA
                                  __       A
GAM1431  FGFR1    3'  TCCAGGTGGCATAACGGACCTT 36458        A   CCCACC
                                TCCAGGTG CATA     GCCTT
                                |||||||| ||||     |||||
                                AGGTCCAC GTAT     TGGAA
                                    C   TGCC__
GAM1431  FGFR2    3'  TCCAGGTGACATACCTCC    36459            CA
                                TCCAGGTGACATACC  CC
                                ||||||||||||||  ||
                                AGGTCCACTGTATGG  GG
                                       A_
GAM1431  GCNT1    5'  TCCAGGTGACATCCTGCC    36460          A  CACC
                                TCCAGGTGACAT CC   GCC
                                ||||||||||| ||   |||
                                AGGTCCACTGTA GG   CGG
                                      _  A___
GAM1431  PRELP    5'  TCCAGGTGATGCACCTGC    36461        CATACC   _
                                TCCAGGTGA     CACC GC
                                |||||||||     |||| ||
                                AGGTCCACT     GTGG CG
                                     AC____    A
GAM1431  SUFU     3'  TCCAGGCTGATATGCCT     36462       _  C  ACCCACC
                                TCCAGG TGA AT      GCCT
                                |||||| ||| ||      ||||
                                AGGTCC ACT TA      CGGA
                                   G   A ________
GAM1431  FLJ30567 3'  AGTTGACATACCTCTGGCCCT  36463    G       CACC
                                AG TGACATACC    GCCTT
                                || |||||||||    |||||
                                TC ACTGTATGG    CGGGA
                                 A        AGAC
GAM1431  KIAA0218 3'  TCCAGGTGATCTATCCACC    36464        CA  C
                                TCCAGGTGA  TA CCACC
                                |||||||||  || |||||
                                AGGTCCACT  AT GGTGG
                                     AG  A
GAM1431  LOC131873 5'  CCCAGGTAGCCTTCACTGCCTT 36465        ACATA  __   C
                                TCCAGGTG    CC  CAC GCCTT
                                ||||||||    ||  ||| |||||
                                GGGTCCAT    GG  GTG CGGAA
                                     C____  AA   A
GAM1431  LOC143311 5'  TCTGGGTCGCATTGACCGCCTT 36466    CA   GA   ACCC
                                TC  GGT  CAT    ACCGCCTT
                                ||  |||  |||    ||||||||
                                AG  CCA  GTA    TGGCGGAA
                                 AC   GC   AC__
GAM1431  LOC167555 5'  CCAGGTGATCTCAGCACCGTCT 36467        CATACC    C
            T                   CCAGGTGA     CACCG CTT
                                ||||||||     ||||| |||
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                                GGTCCACT     GTGGC GAA
                                    AGAGTC     A
GAM1432  FMR1     3'  ACTAATGTTTGACAGGGTTTG  36470        CTCGT  G    C
                                ACTGATGT     GC AGGG TTG
                                ||||||||     || |||| |||
                                TGATTACA     TG TCCC AAC
                                    AAC__  _    A
GAM1432  PLAG1    3'  ACTGATGCTTTGTGTTTAGGGT 36471        CTC   CG_    C
           TTG                    ACTGATGT   GTG   AGGG TTG
                                ||||||||   |||   |||| |||
                                TGACTACG   CAC   TCCC AAC
                                    AAA   AAA    A
GAM1432  SOX11    5'  CTGGGTCTCGTGCGGAG     36472     AT        A
                                CTG  GTCTCGTGCG GGG
                                |||  |||||||||| |||
                                GAC  CAGAGCACGC CTC
                                  C_         _
GAM1432  FLJ11560 5'  ACTGATGCCTCGTGCCCCTAGC 36473             GAG_
           TTG                    ACTGATGTCTCGTGC    GGCTTG
                                |||||||||||||||    ||||||
                                TGACTACGGAGCACG    TCGAAC
                                        GGGA
GAM1432  TUSP     3'  ACTGGGTTTTGTCATCAGGGCT 36474     A____    TCGTG G
           TG                     CTG     TGTC     C AGGGCTTG
                                |||     ||||     | ||||||||
                                GAC     ACAG     G TCCCGAAC
                                  CCAAA    TA___ _
GAM1432  LOC204084 5'  CTGATCTCTTGGTCAGGGCTTG 36475      G   CGTG G
                                CTGAT TCT    C AGGGCTTG
                                ||||| |||    | ||||||||
                                GACTA AGA    G TCCCGAAC
                                   G   ACCA _
GAM1432  LOC256112 3'  CTGATGTCTTGTGTGGGCT    36476         C   CGA
                                CTGATGTCT GTG   GGGCT
                                ||||||||| |||   |||||
                                GACTACAGA CAC   CCCGA
                                     A   A__
GAM1432  LOC51629  5'  CTGGTGCTCGTGCGGC      36477     A  T      GAG
                                CTG TG CTCGTGC   GGC
                                ||| || |||||||   |||
                                GAC AC GAGCACG   CCG
                                  C  _      ___
GAM1433  FLJ23142  3'  TGAGATATTTTTCATGA     36480        C  CCGGCA
                                TGAGATA TT     TTCATGA
                                |||||||  ||     |||||||
                                ACTCTAT AA     AAGTACT
                                    A  _______
GAM1433  IL17D    3'  TGAGACTGTTTATGTATTCATG 36481        ACTTCCGGC
           AC                     TGAGAT       ATTCATGAC
                                ||||||        |||||||||
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                                ACTCTG       TAAGTACTG
                                   ACAAATACA
GAM1433  VAV3     3'  GATGACTGGCATTCATG     36482     _  TCC
                                GAT ACT   GGCATTCATG
                                ||| |||   ||||||||||
                                CTA TGA   CCGTAAGTAC
                                  C  ____
GAM1433  LOC160336 5'  TGGATACTGGACATTCATG    36483    A     TCC
                                TG GATACT   GGCATTCATG
                                || ||||||   ||||||||||
                                AC CTATGA   CTGTAAGTAC
                                  _     C__
GAM1433  LOC219347 5'  TGAGATACTCTCGGCCCTCTTG 36484         TC    A   A
                                TGAGATACT  CGGC TTC TG
                                |||||||||  |||| ||| ||
                                ACTCTATGA  GCCG GAG AC
                                      GA   G   A
GAM1433  LOC220763 5'  TGAGATACTCTGGTATCA    36485         CC  CAT
                                TGAGATACTT  GG   TCA
                                ||||||||||  ||   |||
                                ACTCTATGAG  CC   AGT
                                      A_  AT_
GAM1434  CLASP2    3'  AAAGCTTTAAGCATTCC     36488           CGGA
                                AAAGTTTTAAGTA    CC
                                ||||||||||||    ||
                                TTTCGAAATTCGT    GG
                                       AA__
GAM1434  PER2      3'  TCCACAGTTTTAAGTCG     36489      A        A
                                TCCA AGTTTTAAGT CG
                                |||| |||||||||| ||
                                AGGT TCAAAATTCA GC
                                  G        _
GAM1434  SRGAP2    3'  CCTAAGAACGGTACGGACTGC  36490    A   TTTTAA      C
                                CC AAG     GTACGGAC GC
                                || |||     |||||||| ||
                                GG TTC     CATGCCTG CG
                                 A   TTGC__       A
GAM1434  CLSTN1    3'  GTTCTGAGTACGGATCGC    36491      A       C
                                GTTTT AGTACGGA CGC
                                ||||| |||||||| |||
                                CAAGA TCATGCCT GCG
                                   C       A
GAM1434  FLJ11273  3'  CAAAATTTTAGGTATGGA    36492          A   C
                                CAAAGTTTTA GTA GGA
                                |||||||||| ||| |||
                                GTTTTAAAAT CAT CCT
                                      C   A
GAM1434  FLJ20241  5'  TCCAGTGTTTTAAGCCCCCG   36493      AA       ACGGA
                                TCCA  GTTTTAAGT    CCG
                                ||||  |||||||||    |||
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                                AGGT  CAAAATTCG    GGC
                                  CA       GG___
GAM1434  KIAA1328  3'  TCCAGAGTTTTAAGGACA    36494      A       T
                                TCCA AGTTTTAAG ACG
                                |||| ||||||||| |||
                                AGGT TCAAAATTC TGT
                                  C       C
GAM1434  SLK       3'  TCCAAAGTTTTCAAATTAACTG 36495          AAGTACG   C
              C                   TCCAAAGTTTT      GAC GC
                                |||||||||||      ||| ||
                                AGGTTTCAAAA      TTG CG
                                      GTTTAA_   A
GAM1434  LOC154792 5'  TCCGAAGTTTAAGTACTAACGC 36496     A     T     G   C
                                TCC AAGTTT AAGTAC GAC GC
                                ||| |||||| |||||| ||| ||
                                AGG TTCAAA TTCATG TTG CG
                                  C     _     A   _
GAM1434  LOC201952 5'  TCCAAGGTTTTAAGACAA    36497      A       T
                                TCCAA GTTTTAAG ACGG
                                ||||| |||||||| ||||
                                AGGTT CAAAATTC TGTT
                                   C       _
GAM1434  LOC220776 3'  TCCAAATTTTTGGAGGTACCGC 36498       G    AAGTAC  _
                                TCCAAA TTTT      GG ACCGC
                                |||||| ||||      || |||||
                                AGGTTT AAAA      CC TGGCG
                                    A    CCT___  A
GAM1434  LOC257444 5'  TCCAGAGTTTCAACACCAC    36499      A       GTACGG
                                TCCA AGTTTTAA      ACCGC
                                |||| ||||||||      |||||
                                AGGT TCAAAGTT      TGGTG
                                  C       G_____
GAM1434  LOC57821  3'  TCCAAAATTTTGATAGCAGCTG 36500          AA  _  ACC
              C                   TCCAAAGTTTT  GTA CGG   GC
                                ||||||||||  ||| |||   ||
                                AGGTTTTAAAA  TAT GTC   CG
                                      C_   C   GA_
GAM1435  DPYSL3    3'  TTGGGGGGCAGGCCAAGGG    36503       A   CTG
                                TTGGGG GCA   GGCCAAGGG
                                |||||| |||   |||||||||
                                AACCCC CGT   CCGGTTCCC
                                   C   ___
GAM1435  ELAVL3    3'  CACCAGGGGGCACTGGGCCGGG 36504     TG   A       AA
              GG                    TAT  GGG GCACTGGGCC  GGG
                                |||  ||| ||||||||||  |||
                                GTG  CCC CGTGACCCGG  CCC
                                  GT   C        CC
GAM1435  F2RL3     3'  TTGGGGAGCAGAGTTGGGGG   36505         C___    CCAA
                                TTGGGGAGCA    TGGG    GG
                                ||||||||||    ||||    ||
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                                AACCCCTCGT   ACCC   CC
                                     CTCA   ____
GAM1435 GAS11   3' TGGGGAGGCTGGGCCAAGGG  36506       CA
                                TGGGGAG CTGGGCCAAGGG
                                ||||||| ||||||||||||
                                ACCCCTC GACCCGGTTCCC
                                   C_
GAM1435 IL10    3' TTGGGGAATGAGGTTAGGG   36507       CAC   CCA
                                TTGGGGAG  TGGG  AGGG
                                ||||||||  ||||  ||||
                                AACCCCTT  ACTC  TCCC
                                     ___   CAA
GAM1435 MAFG    5' TATTGGGGGTCGTCATAACCCG 36508       AGCACTG_   AA
           GGG                   TATTGGGG      GGCC  GGG
                                ||||||||      ||||  |||
                                ATAACCCC      TTGG  CCC
                                     CAGCAGTA   GC
GAM1435 SLC35A2  3' TTGGTCCCAGCTGGGCCAAGGG 36509     GGAG  _
                                TTGG   CA CTGGGCCAAGGG
                                ||||   || ||||||||||||
                                AACC   GT GACCCGGTTCCC
                                  AGG_  C
GAM1435 TEM8    3' TTGGGGAGAGGCTGGGGG    36510       CA_   CCAA
                                TTGGGGAG  CTGGG   GG
                                ||||||||  |||||   ||
                                AACCCCTC  GACCC   CC
                                     TCC   ____
GAM1435 VDR     3' TTGGTGGGCACTGAAGG     36511     _ A     GCCA
                                TTGG GG GCACTGG   AGG
                                |||| || |||||||   |||
                                AACC CC CGTGACT   TCC
                                  A _     _____
GAM1435 C20orf44 3' TTGGGGAGTGTGTGCTGGGGG 36512       CA____   CCAA
                                TTGGGGAG    CTGGG   GG
                                ||||||||    |||||   ||
                                AACCCCTC    GACCC   CC
                                     ACACAC    ____
GAM1435 DKFZP434I2117 3' TGGGGAGCCCTGGGGG     36513       A    CCAA
                                TGGGGAGC CTGGG   GG
                                |||||||| |||||   ||
                                ACCCCTCG GACCC   CC
                                     G    _____
GAM1435 EPI64   3' GGAAGCCTGGGTCGAGGG    36514      A    CCA
                                GGGAGC CTGGG  AGGG
                                |||||| |||||  ||||
                                CCTTCG GACCC  TCCC
                                   _    AGC
GAM1435 FLJ10404 3' TGGGGAGCACAGAGG      36515         T  GCCA
                                TGGGGAGCAC GG   AGG
                                |||||||||| ||   |||
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                                ACCCCTCGTG TC    TCC
                                    _ _____
GAM1435 FLJ10432 3' TTGGGGAGCCCGGGG      36516        A    CCAA
                                TTGGGGAGC CTGGG    G
                                ||||||||| |||||    |
                                AACCCCTCG GGCCC    C
                                    _    _____
GAM1435 FLJ13262 3' TATTGGAGAGTGAGTGAGG   36517         CAC    CCA
                                TATTGGGGAG   TGGG   AGG
                                ||||||||||   ||||   |||
                                ATAACCTCTC   ACTC   TCC
                                     ____   AC_
GAM1435 FXYD3    3' TATTGGGGAGTCTCAAGG    36518        CA  GGGC
                                TATTGGGGAG  CT    CAAGG
                                ||||||||||  ||    |||||
                                ATAACCCCTC  GA    GTTCC
                                     A_ _____
GAM1435 FXYD3    3' TATTGGGGAGTCTCAAGG    36518        CA  GGGC
                                TATTGGGGAG  CT    CAAGG
                                ||||||||||  ||    |||||
                                ATAACCCCTC  GA    GTTCC
                                     A_ _____
GAM1435 GABBR1   5' TTGGGGAGCGTTAGGAGCTCAG 36519         ACT_ _  CA
          GG                    TTGGGGAGC    GG GC  AGGG
                                |||||||||    || ||  ||||
                                AACCCCTCG    CC CG  TCCC
                                     CAAT  T  AG
GAM1435 GPR64    3' TACTGGGGATGCGGTCAGGG   36520         _ ACT  GCCA
                                TATTGGGGA GC   GG    AGGG
                                ||||||||| ||   ||    ||||
                                ATGACCCCT CG   CC    TCCC
                                     A  ____  AG__
GAM1435 HSPC152  3' TTGGTGTCATTGGGTCAAGGG  36521     GGAG  C    C
                                TTGG    CA TGGG CAAGGG
                                ||||    || |||| ||||||
                                AACC    GT ACCC GTTCCC
                                  ACA_  A    A
GAM1435 HSPC152  3' TTGGTGTCATTGGGTCAAGGG  36521     GGAG  C    C
                                TTGG    CA TGGG CAAGGG
                                ||||    || |||| ||||||
                                AACC    GT ACCC GTTCCC
                                  ACA_  A    A
GAM1435 HUMZD58C02 3' TATTGGGACGGCCAAG     36522       GA  ACTG
                                TATTGGG  GC    GGCCAAG
                                |||||||  ||    |||||||
                                ATAACCC  TG    CCGGTTC
                                     __ _____
GAM1435 KIAA1465 3' TTGGGGAGTAGTAAGG      36523        CAC   GCC
                                TTGGGGAG   TGG   AAGG
                                ||||||||   |||   ||||
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                                AACCCCTC  ATC  TTCC
                                   ___  A__
GAM1435 KIAA1949 5' TTGGGGAGGCAAGGAGG    36524       _ CT  CCA
                                TTGGGGAG CA  GGG  AGG
                                |||||||| ||  |||  |||
                                AACCCCTC GT  TCC  TCC
                                   C __  ___
GAM1435 KIAA1949 5' TTGGGGAGGCAAGGAGG    36524       _ CT  CCA
                                TTGGGGAG CA  GGG  AGG
                                |||||||| ||  |||  |||
                                AACCCCTC GT  TCC  TCC
                                   C __  ___
GAM1435 KIAA1949 5' TTGGGGAGGCAAGGAGG    36524       _ CT  CCA
                                TTGGGGAG CA  GGG  AGG
                                |||||||| ||  |||  |||
                                AACCCCTC GT  TCC  TCC
                                   C __  ___
GAM1435 MGC2780  5' ATTGGGGAGTGAGGTGGGGG 36525       CAC  CCAA
                                ATTGGGGAG  TGGG  GGG
                                |||||||||  ||||  |||
                                TAACCCCTC  ACTC  CCC
                                   ___  CACC
GAM1435 MGC4294  5' GGGGAGCACGCAGTCCCAGGG 36526       _  G A
                                GGGGAGCAC TGG CC AGGG
                                ||||||||| ||| || ||||
                                CCCCTCGTG GTC GG TCCC
                                   C  A G
GAM1435 STAB2    3' TGTCAGGCACTGGGCTAGGG  36527   G_ A      CA
                                TG  GG GCACTGGGC  AGGG
                                ||  || |||||||||  ||||
                                AC  TC CGTGACCCG  TCCC
                                 AG  _      A_
GAM1435 ZNF304   3' CTGGGGAGTACGTGACAGTTAA 36528       C  TG  C___
          GGG                   TTGGGGAG AC  GGC   AAGGG
                                |||||||| ||  |||   |||||
                                GACCCCTC TG  CTG   TTCCC
                                   A  CA  TCAA
GAM1435 LOC142893 5' TGGGGAGCACTTGGGGG   36529         _  CCAA
                                TGGGGAGCACT GGG   GG
                                |||||||||| |||   ||
                                ACCCCTCGTGA CCC   CC
                                   A  ____
GAM1435 LOC150299 3' TATTGGGAAGTACTGGGTAAG 36530        C    CC
                                TATTGGGGAG ACTGGG  AAG
                                |||||||||| ||||||  |||
                                ATAACCCTTC TGACCC  TTC
                                   A    A_
GAM1435 LOC152274 3' AGGCACTGGGCTAAGGG    36531   A      C
                                GG GCACTGGGC AAGGG
                                || ||||||||| |||||
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                                TC CGTGACCCG TTCCC
                                 _       A
GAM1435 LOC196410 3' TGGGGAGAGAGGGTCAGGGG  36532       CACT  C  A
                                TGGGGAG   GGG CA GGG
                                |||||||   ||| || |||
                                ACCCCTC   CCC GT CCC
                                    TCT_  A  C
GAM1435 LOC199992 3' CTGGGGCTGGGCCAGGG    36533      AGCA      A
                                TTGGGG   CTGGGCCA GG
                                ||||||   |||||||| ||
                                GACCCC   GACCCGGT CC
                                   ____      C
GAM1435 LOC201952 5' TACTGGGGAAGTGGTTGAGGG 36534         CAC  GCCA
                                TATTGGGGAG  TGG   AGGG
                                ||||||||||  |||   ||||
                                ATGACCCCTT  ACC   TCCC
                                      C__  AAC_
GAM1435 LOC51207  3' TGGGGTTGGGCCAAGG     36535     AGCAC
                                TGGGG   TGGGCCAAGG
                                |||||   ||||||||||
                                ACCCC   ACCCGGTTCC
                                  A____
GAM1435 LOC58525  5' TTGGGGAGGCCGGCCGGGGG  36536       CA   G  AA
                                TTGGGGAG  CTGG CC  GGG
                                ||||||||  |||| ||  |||
                                AACCCCTC  GGCC GG  CCC
                                    C_   _ CC
GAM1435 LOC91179  3' TATTGGGACGGCCAAG     36522       GA  ACTG
                                TATTGGG  GC   GGCCAAG
                                |||||||  ||   |||||||
                                ATAACCC  TG   CCGGTTC
                                   __ ____
GAM1436 CYP11B1   3' GTGGGAGAGAAGAGGGGTGG  36539    T      CTT  CGA
                                GT GGAGAGAAG  GG  TGG
                                || |||||||||  ||  |||
                                CA CCTCTCTTC  CC  ACC
                                 C       T__  CC_
GAM1436 GRM7      5' CGCTGGAGGGAACGGTGGTGG 36540       A  GCT  CGA
                                CGTTGGAG GAA  TGG  TGG
                                |||||||| |||  |||  |||
                                GCGACCTC CTT  ACC  ACC
                                    C  GCC  ___
GAM1436 HIVEP3    5' GTTGGAGGGAGGCCTTCG    36541       A  A   GG
                                GTTGGAG GA GCTT  CG
                                ||||||| || ||||  ||
                                CAACCTC CT CGGA  GC
                                    C  C   A_
GAM1436 SYNGR1    3' GTGGAGAGAGGGGACAGATGG 36542    T     A CTT  _
                                GT GGAGAGA G   GGC GATGG
                                || ||||||| |   ||| |||||
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                                CA CCTCTCT C   CTG CTACC
                                 _      _ CC_   T
GAM1436 CACNG4   3' TTGGAGAGAGGGAGAGATGG  36543        A CTT  C
                                TTGGAGAGA G   GG GATGG
                                ||||||||| |   || |||||
                                AACCTCTCT C   TC CTACC
                                      _ CC_  T
GAM1436 CHST8    5' GTTGGGAGAGAGGCTGCTATGG 36544      _    A   TG  G
                                GTTGG AGAGA GCT  GC ATGG
                                ||||| ||||| |||  || ||||
                                CAACC TCTCT CGA  CG TACC
                                   C    C  __ A
GAM1436 FLJ11726 3' TTGGAGGAAGGTGGCGATGG  36545      A    CT
                                TTGGAG GAAG  TGGCGATGG
                                |||||| ||||  |||||||||
                                AACCTC CTTC  ACCGCTACC
                                   _   C_
GAM1436 FLJ12443 3' GCTGGAGAGAGGCCTGATGG  36546        A   GGC
                                GTTGGAGAGA GCTT   GATGG
                                |||||||||| ||||   |||||
                                CGACCTCTCT CGGA   CTACC
                                      C   ___
GAM1436 FXYD5    5' CGTGGAGAGAGGGACGCGGCGG 36547    T     A__  T    A
           TGG                   CGT GGAGAGA   GC TGGCG TGG
                                ||| |||||||   || ||||| |||
                                GCA CCTCTCT   TG GCCGC ACC
                                  _     CCC  C    C
GAM1436 HSA9947  3' GCTGGAGAGGGGTCCAGTTGGT 36548        AAG_ ___   CGA
           GG                    GTTGGAGAG   CT   TGG   TGG
                                |||||||||   ||   |||   |||
                                CGACCTCTC   GG   ACC   ACC
                                     CCCA  TCA  ___
GAM1436 KIAA1674 3' GCTGGAGAGGAGCAGGATGG  36549        A   TT  C
                                GTTGGAGAG AGC  GG GATGG
                                ||||||||| |||  || |||||
                                CGACCTCTC TCG  TC CTACC
                                     C  __ _
GAM1436 KIAA1674 3' GCTGGAGAGGAGCAGGATGG  36549        A   TT  C
                                GTTGGAGAG AGC  GG GATGG
                                ||||||||| |||  || |||||
                                CGACCTCTC TCG  TC CTACC
                                     C  __ _
GAM1436 KIAA1710 5' CCTTGGAGAGGGAAGTGATGG 36550   G      AAGCTT  C
                                C TTGGAGAG     GG GATGG
                                | ||||||||     || |||||
                                G AACCTCTC     TC CTACC
                                 G       CCT___  A
GAM1436 MCAM     3' CGTGGAGGAGATGGTGGTG   36551    T   _  AGCT   CGA
                                CGT GGAG AGA    TGG   TG
                                ||| |||| |||    |||   ||
```

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                                GCA CCTC TCT   ACC  AC
                                  _   C  ____  ACC
GAM1436  MGC4707   3'  GCTGGAGAGGAGGCTGGGTGG  36552        A  C   CGA
                                GTTGGAGAG AG TTGG  TGG
                                ||||||||| || ||||  |||
                                CGACCTCTC TC GACC  ACC
                                     C  C   C__
GAM1436  LOC151719 5'  CATTGGAGGGGCAGTGG    36553       AGAAGCTT   A
                                CGTTGGAG      GGCG TGG
                                ||||||||      |||| |||
                                GTAACCTC      CCGT ACC
                                     C_______  C
GAM1436  LOC164714 5'  CGCTGGAGAGCTGGTGATG  36554        AAGC   C
                                CGTTGGAGAG   TTGG GATG
                                ||||||||||   |||| ||||
                                GCGACCTCTC   GACC CTAC
                                      ____  A
GAM1436  LOC170395 5'  GCTGGAGAGGAGCAGGATGG  36549       A  TT  C
                                GTTGGAGAG AGC  GG GATGG
                                ||||||||| |||  || |||||
                                CGACCTCTC TCG  TC CTACC
                                     C  __ _
GAM1436  LOC256158 5'  GTTGGAGGGGCTGGGGGCGATG 36555      AGAA  T__
           G                     GTTGGAG   GCT  GGCGATGG
                                 |||||||   |||  ||||||||
                                 CAACCTC   CGA  CCGCTACC
                                    CC__  CCC
GAM1437  EHHADH   3'  TTTGTTGGTTTTTTGTTT   36558         AATGAG
                                TTTGTTGGTTT    TTGTTT
                                ||||||||||    ||||||
                                AAACAACCAAA    AACAAA
                                      A_____
GAM1437  MEN1     5'  TTTGTTAGTTTGTCTGTTT   36559         AATGAG
                                TTTGTTGGTTT    TTGTTT
                                ||||||||||    ||||||
                                AAACAATCAAA    GACAAA
                                      CA____
GAM1437  NOTCH2   3'  TTTGTTGGTTCAATAAATT   36560
                                TTTGTTGGTTTAATGAGTT
                                |||||||||||||||||||
                                AAACAACCAAGTTATTTAA

GAM1437  RABIF    3'  TTTGTTGTTACTGTTGTTGTTT 36561       GTTTAA  A_
           G                    TTTGTTG    TG  GTTGTTTG
                                |||||||    ||  ||||||||
                                AAACAAC    AC  CAACAAAC
                                    AATG__  AA
GAM1437  RPP30    3'  TTTGTTGTTTTAATGGATTG  36562       G     AG
                                TTTGTTG TTTAATG  TTG
                                ||||||| |||||||  |||
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                                AAACAAC AAATTAC  AAC
                                    A      CT
GAM1437  DKFZP434P211 3'  TTTGTTGGTTTGAGAGC     36563          AAT
                                TTTGTTGGTTT   GAGT
                                ||||||||||   ||||
                                AAACAACCAAA   CTCG
                                      CT_
GAM1437  IMP-2    3'  GTTGGTTTGGTGGGTTCCT   36564        AA  A   G
                                GTTGGTTT  TG GTT TT
                                ||||||||  || ||| ||
                                CAACCAAA  AC CAA GA
                                    CC  C   G
GAM1437  KIAA1854  3'  TTTGTTGGTTGATTTAATTTG  36565        TTAA   GTT_
                                TTTGTTGGT    TGA    GTTTG
                                |||||||||    |||    |||||
                                AAACAACCA    ACT    TAAAC
                                     _____   AAAT
GAM1437  PRO0611   5'  TTTCTTGGTTTAGAGTT     36566     G      AT
                                TTT TTGGTTTA  GAGTT
                                ||| ||||||||  |||||
                                AAA AACCAAAT  CTCAA
                                  G       __
GAM1437  LOC150174 3'  TTTGTTGGTTTGAGAGC     36563          AAT
                                TTTGTTGGTTT   GAGT
                                ||||||||||   ||||
                                AAACAACCAAA   CTCG
                                      CT_
GAM1437  LOC150213 3'  TTTGTTGGTTTGAGAGC     36563          AAT
                                TTTGTTGGTTT   GAGT
                                ||||||||||   ||||
                                AAACAACCAAA   CTCG
                                      CT_
GAM1437  LOC150236 3'  TTTGTTGGTTTGAGAGC     36563          AAT
                                TTTGTTGGTTT   GAGT
                                ||||||||||   ||||
                                AAACAACCAAA   CTCG
                                      CT_
GAM1437  LOC166206 5'  TTTGCTGGTTTGGTGGGC    36567          AA  A
                                TTTGTTGGTTT  TG GT
                                ||||||||||  || ||
                                AAACGACCAAA  AC CG
                                      CC  C
GAM1438  AF1Q     3'  TAAAGTGAGTAGGTGT      36570           CCA
                                TAAAGTGAGTAG   TGT
                                ||||||||||||  |||
                                ATTTCACTCATC   ACA
                                      C__
GAM1438  AHCY     3'  TATAAAGTGGTGGCAG      36571         A  AGCCAT
                                TATAAAGTG GT     GTAG
                                |||||||| ||     ||||
```

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                                ATATTTCAC CA     CGTC
                                     _ C_____
GAM1438  EMS1     3'  TACAAAGTGAGTGGCCACA   36572          A
                                TATAAAGTGAGT GCCATG
                                |||||||||||| ||||||
                                ATGTTTCACTCA CGGTGT
                                       C
GAM1438  EMS1     3'  TACAAAGTGAGTGGCCACA   36572          A
                                TATAAAGTGAGT GCCATG
                                |||||||||||| ||||||
                                ATGTTTCACTCA CGGTGT
                                       C
GAM1438  FETUB    3'  AAGTGAGTGGCTGAAGAC    36573       A  CA  T
                                AAGTGAGT GC  TG AGAT
                                |||||||| ||  || ||||
                                TTCACTCA CG  AC TCTG
                                     C  __  T
GAM1438  MBL2     3'  AAAGTGAGTATATAG       36574         GCCA
                                AAAGTGAGTA   TGTAG
                                ||||||||||   |||||
                                TTTCACTCAT   ATATC
                                      _____
GAM1438  DKFZp434D177 3'  TAAGGTGAGCAGCTTAGGAAAG 36575     A       CATGT__
           AT                     TAA GTGAGTAGC      AGAT
                                ||| |||||||||      ||||
                                ATT CACTCGTCG      TCTA
                                  C        AATCCTT
GAM1438  PIP5K2A  3'  TAAAGCGAGTAGCCCCCAAAT  36576           ATG
                                TAAAGTGAGTAGCC   TAGAT
                                ||||||||||||||   |||||
                                ATTTCGCTCATCGG   GTTTA
                                       GG_
GAM1438  TSC22    3'  GTAGCAGTTTTTATGTAGAT   36577    G    CC___
                                GT AGTAG    ATGTAGAT
                                || |||||    ||||||||
                                CA TCGTC    TACATCTA
                                 _    AAAAA
GAM1438  LOC200609 5'  AAGTGAGTCTCTTGTAGAT   36578        AGCCA
                                AAGTGAGT    TGTAGAT
                                ||||||||    |||||||
                                TTCACTCA    ACATCTA
                                     GAGA_
GAM1438  LOC257441 3'  TAAGGTGAGCAGCTTAGGAAAG 36575     A       CATGT__
           AT                     TAA GTGAGTAGC      AGAT
                                ||| |||||||||      ||||
                                ATT CACTCGTCG      TCTA
                                  C        AATCCTT
GAM1438  LOC92283  3'  AAAGTGAGTGGCTACAGA    36579        A  CA
                                AAAGTGAGT GC  TGTAGA
                                ||||||||| ||  ||||||
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                                TTTCACTCA CG  ATGTCT
                                      C  __
GAM1439  ARHGEF12  3'  TTCATTTTAGTTGGCAAAA   36582        C    A
                                TTCATTTT AGTTG CGGAG
                                |||||||| ||||| |||||
                                AAGTAAAA TCAAC GTTTT
                                     _    C
GAM1439  SNAI2     3'  TTCTTTTCAGTTGAAATGA   36583     A        CG_
                                TTC TTTTCAGTTGA  GA
                                ||| ||||||||||  ||
                                AAG AAAAGTCAACT  CT
                                  _        TTA
GAM1439  SS18      3'  TTCATTTTCAGTTATTGC    36584            ACGGA
                                TTCATTTTCAGTTG    GC
                                ||||||||||||||    ||
                                AAGTAAAAGTCAAT    CG
                                          AA___
GAM1439  FLJ11088  3'  TTCGTTTTCAGTAGACCAA   36585     A      T  G
                                TTC TTTTCAGT GAC GA
                                ||| |||||||| ||| ||
                                AAG AAAAGTCA CTG TT
                                  C       T  G
GAM1439  KR18      3'  TTCATGTTCAGTTGATAGA   36586      T       CG
                                TTCAT TTCAGTTGA  GA
                                ||||| |||||||||  ||
                                AAGTA AAGTCAACT  CT
                                   C        AT
GAM1439  MAPK6     3'  TTCATTTTCAGTTGCTGC    36587            ACGGA
                                TTCATTTTCAGTTG    GC
                                ||||||||||||||    ||
                                AAGTAAAAGTCAAC    CG
                                          GA___
GAM1439  SDOS      3'  TTTTGCAGCTGCGGAGCGAC  36588     _     A
                                TTTT CAGTTG CGGAGCGAC
                                |||| |||||| |||||||||
                                AAAA GTCGAC GCCTCGCTG
                                  C     _
GAM1439  SSH2      3'  TTTTCAGTTGGGAGGAC     36589          AC   C
                                TTTTCAGTTG  GGAG GAC
                                |||||||||  |||| |||
                                AAAAGTCAAC  CCTC CTG
                                          __   _
GAM1439  LOC153454 3'  TTCAATTTCAGTTGAGG     36590      T        C
                                TTCA TTTCAGTTGA GG
                                |||| |||||||||| ||
                                AAGT AAAGTCAACT CC
                                  T        _
GAM1439  LOC170372 3'  TTCATTTTCAGTTGCTGC    36587            ACGGA
                                TTCATTTTCAGTTG    GC
                                ||||||||||||||    ||
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                                AAGTAAAAGTCAAC     CG
                                       GA___
GAM1439  LOC256239 5'  TTCACTTTTCAGTTGACTTTAG 36591         _       GG_
                                TTCATTTT CAGTTGAC   AG
                                |||||||| ||||||||   ||
                                AAGTGAAA GTCAACTG   TC
                                     A       AAA
GAM1440  MGAT3     3'  GGCTTTTTCCCGGCCTGGCCA  36594    ATC         CTA
                                GG   TTTCCCGGCCT   CCA
                                ||   ||||||||||   |||
                                CC   AAAGGGCCGGA   GGT
                                 GAA         CC_
GAM1440  SMOH      3'  TAGGCTCTTTCCCACAGTCCTG 36595      A       __  _  _
              CT                   TAGG TCTTTCCC  GG CCT CT
                                |||| ||||||||  || ||| ||
                                ATCC AGAAAGGG  TC GGA GA
                                  G       TG  A   C
GAM1440  SNAPAP    3'  TAGGATCTTTGCATGTCT    36596         CCCG  C__
                                TAGGATCTTT    GC   TCT
                                ||||||||||    ||   |||
                                ATCCTAGAAA    CG   AGA
                                      _____  TAC
GAM1440  FLJ10716  3'  TAGGATCTTTTCAGGAACACCA 36597          CC   CCTC
                                TAGGATCTTT  CGG    TACCA
                                ||||||||||  |||    |||||
                                ATCCTAGAAA  GTC    GTGGT
                                      A_   CTT_
GAM1440  KIAA0599  3'  TAGGATGTTTCCTGGGGACC   36598       C     C  CCTCT
                                TAGGAT TTTCC GG     ACC
                                ||||||  ||||| ||     |||
                                ATCCTA AAAGG CC     TGG
                                   C     A  CC___
GAM1440  MGC29761  3'  TAGCATCTTTCCCATGTACT   36599     G         GCCT
                                TAG ATCTTTCCCG    CT
                                |||  ||||||||||    ||
                                ATC TAGAAAGGGT    GA
                                  G         ACAT
GAM1440  SIAT4B    5'  TAGGTCTTGGCCCTTCTGCC   36600      A    TCCC    __   A
                                TAGG TCTT    GGCC  TCT CC
                                ||||  ||||    ||||  |||  ||
                                ATCC AGAA    CCGG  AGA GG
                                  _    _____    GA   C
GAM1440  SYNCOILIN 3'  TAGGCTTTGAAGGCCTCTATCA 36601      AT    CCC       C
                                TAGG  CTTT   GGCCTCTA CA
                                ||||  ||||   |||||||| ||
                                ATCC  GAAA   CCGGAGAT GT
                                   __   CTT       A
GAM1440  ZWINT     3'  TAGGATCTTTCTCCATGC     36602           _   _
                                TAGGATCTTTC CCG GC
                                |||||||||| ||| ||
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```
                                ATCCTAGAAAG GGT CG
                                      A   A
GAM1440  ZWINT     3'  TAGGATCTTTCTCCATGC    36602          _  _
                                TAGGATCTTTC CCG GC
                                |||||||||||| ||| ||
                                ATCCTAGAAAG GGT CG
                                      A   A
GAM1440  LOC196415 5'  TAGGCATCTTTCCCAGCACTGC 36603     _         _ _
               T                 TAGG ATCTTTCCCGGC CT CT
                                 |||| |||||||||||| || ||
                                 ATCC TAGAAAGGGTCG GA GA
                                   G          T  C
GAM1440  LOC92080  5'  TAAGATCTTTCCTCTGCC    36604          CG_
                                TAGGATCTTTCC   GCC
                                ||||||||||||   |||
                                ATTCTAGAAAGG   CGG
                                       AGA
GAM1441  ABCB1     5'  CTGGTTGCTTCCTGAAGT    36607    A       CATATT
                                CT GTTGTTTCC     TGGAGT
                                || |||||||||     ||||||
                                GA CAACGAAGG     ACTTCA
                                 C       _______
GAM1441  COL15A1   3'  CTAGTTTCAGATTATTTGGAGT 36608       GTTTCCCA
                                CTAGTT       TATTTGGAGT
                                ||||||       ||||||||||
                                GATCAA       ATAAACCTCA
                                    AGTCTA__
GAM1441  OTX1      3'  TAGTGGTTTTGATTTGGAGT   36609     T   CCCAT
                                TAGT GTTT    ATTTGGAGT
                                |||| ||||    |||||||||
                                ATCA CAAA    TAAACCTCA
                                  C   AC___
GAM1441  C5orf4    3'  GTTCAGCATATTTGGAGT    36610     CC
                                GTTT  CATATTTGGAGT
                                ||||  ||||||||||||
                                CAAG  GTATAAACCTCA
                                  TC
GAM1441  C5orf4    5'  GTTCAGCATATTTGGAGT    36610     CC
                                GTTT  CATATTTGGAGT
                                ||||  ||||||||||||
                                CAAG  GTATAAACCTCA
                                  TC
GAM1441  KIAA1871  3'  GTTAGTTTTTAATCTGGAGT  36611    _   CCCAT
                                GTT GTTT    ATTTGGAGT
                                ||| ||||    |||||||||
                                CAA CAAA    TAGACCTCA
                                  T   AAT__
GAM1441  PROL3     3'  CAGTTGTTCATATTTGGG    36612       TCC       A
                                TAGTTGTT   CATATTTGG G
                                ||||||||   ||||||||| |
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                                GTCAACAA  GTATAAACC C
                                   ___       C
GAM1441  LOC152579 3'  GTTGTGGAGGAGTATTTGGAGT 36613      TTCCCA_
                                GTTGT      TATTTGGAGT
                                |||||      ||||||||||
                                CAACA      ATAAACCTCA
                                   CCTCCTC
GAM1442  DISC1    3'  TTGCAGACTCCTCAGTT     36616      A  A
                                TTGCA AC TCCTCAGTT
                                ||||| || |||||||||
                                AACGT TG AGGAGTCAA
                                   C  _
GAM1442  GADD45G  3'  TTGCAGAGTCCTCAGCTCG   36617      AACA
                                TTGCA   TCCTCAGTTCG
                                |||||   ||||||||||
                                AACGT   AGGAGTCGAGC
                                   CTC_
GAM1442  MSH2     3'  TTGCAAACAGTCCTCAGTTACA 36618        _      _
                                TTGCAAACA TCCTCAGTT CG
                                ||||||||| ||||||||| ||
                                AACGTTTGT AGGAGTCAA GT
                                     C       T
GAM1442  UBE2V1   3'  TTACAAGTATCTTCATGC    36619      AC  CTCAG
                                TTGCAA  ATC    TTCGTGC
                                ||||||  |||    |||||||
                                AATGTT  TAG    AAGTACG
                                   CA  _____
GAM1442  UBE2V1   3'  TTACAAGTATCTTCATGC    36619      AC  CTCAG
                                TTGCAA  ATC    TTCGTGC
                                ||||||  |||    |||||||
                                AATGTT  TAG    AAGTACG
                                   CA  _____
GAM1442  UBE2V1   3'  TTACAAGTATCTTCATGC    36619      AC  CTCAG
                                TTGCAA  ATC    TTCGTGC
                                ||||||  |||    |||||||
                                AATGTT  TAG    AAGTACG
                                   CA  _____
GAM1442  PREI3    3'  TTGCAAATAATCTCACACGTG  36620      CATC   GTT
                                TTGCAAA   CTCA  CGTG
                                |||||||   ||||  ||||
                                AACGTTT   GAGT  GCAC
                                    ATTA   GT_
GAM1442  SPTLC2   3'  TTGCGCACATCCTCAGACTGTG 36621     AA       TTC
                                TTGC  ACATCCTCAG  GTG
                                ||||  ||||||||||  |||
                                AACG  TGTAGGAGTC  CAC
                                  CG       TGA
GAM1442  LOC145828 5'  TTGCAAACATTCATATCCACTG 36622        CC  _   _
                                TTGCAAACAT  TCA GTTCG TG
                                ||||||||||  ||| ||||| ||
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                                AACGTTTGTA  AGT TAGGT AC
                                      __  A    G
GAM1442  LOC254944 3'  TTGCAGGCATAACTCGTGC   36623      AA   CCTC GT
                                TTGCA  CAT    A  TCGTGC
                                |||||  |||    |  ||||||
                                AACGT  GTA    T  AGCACG
                                   CC  _____ TG
GAM1443  AKAP2    3'  TATATATATATATGTGTGTGTG 36626       _
            T                    TATATAT TATATGTGTGTGTGT
                                 ||||||| ||||||||||||||
                                 ATATATA ATATACACACACACA
                                     T
GAM1443  LAMP2    3'  TATATGTCTGTGTGTGTGT   36627      TATA
                                 TATAT    TGTGTGTGTGT
                                 |||||    ||||||||||
                                 ATATA    ACACACACACA
                                    CAG_
GAM1443  ROCK2    3'  TATATATATATATGTGTGTGTG 36628      _            III
            TTTA                    TATAT TATATGTGTGTGTGTTT   A
                                 ||||| ||||||||||||||||   |
                                 ATATA ATATACACACACACAAA   T
                                    T             III
GAM1443  SHOC2    3'  CATATATAGATTGTGTGTGTTT 36629       TATATG
                                 TATATAT     TGTGTGTGTTT
                                 |||||||     ||||||||||
                                 GTATATA     ACACACACAAA
                                     TCTA__
GAM1443  VAPB     3'  TATATTTGTGTGTGTGT     36630       ATA
                                 TATATT   TGTGTGTGTGT
                                 ||||||   ||||||||||
                                 ATATAA   ACACACACACA
                                    ___
GAM1443  VNN1     3'  TATATTATCTGGTGTGTGTGTG 36631        A___
            TTT                   TATATTAT    TGTGTGTGTGTTT
                                 ||||||||    ||||||||||||
                                 ATATAATA    ACACACACACAAA
                                      GACC
GAM1443  caspr5   3'  TATATATATGTGTGTGTGT    36632      T
                                 TATAT ATATGTGTGTGTGT
                                 ||||| ||||||||||||||
                                 ATATA TATACACACACACA
                                    _
GAM1443  caspr5   3'  TATATATATATATGTGTGTGTG 36626       _
            T                    TATATAT TATATGTGTGTGTGT
                                 ||||||| ||||||||||||||
                                 ATATATA ATATACACACACACA
                                     T
GAM1443  CHODL    3'  TATATTTGTGTGTGTGT     36630       ATA
                                 TATATT   TGTGTGTGTGT
                                 ||||||   ||||||||||
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                              ATATAA  ACACACACACA
                                    ___
GAM1443 CMG2     3' TATATTTGTGTGTGTGT    36630      ATA
                              TATATT  TGTGTGTGTGT
                              ||||||  ||||||||||
                              ATATAA  ACACACACACA
                                    ___
GAM1443 FLJ11218 3' TATATATTTGTGTGTGTGT  36633       ATA
                              TATATATT  TGTGTGTGTGT
                              ||||||||  ||||||||||
                              ATATATAA  ACACACACACA
                                    ___
GAM1443 FLJ11598 3' TATATTTGTGTGTGTGT    36630      ATA
                              TATATT  TGTGTGTGTGT
                              ||||||  ||||||||||
                              ATATAA  ACACACACACA
                                    ___
GAM1443 FLJ12078 3' TACTAGTGTGTGTGTGTGTTT 36634     TA_
                              TATTA  TGTGTGTGTGTTT
                              |||||  ||||||||||||
                              ATGAT  ACACACACACAAA
                                 CAC
GAM1443 KIAA0628 3' TATATATTACATGTATGT   36635
                              TATATATTATATGTGTGT
                              ||||||||||||||||||
                              ATATATAATGTACATACA

GAM1443 KIAA1613 3' TATATTGTAGCCCATGTGTGTT 36636     A  T  __
           T                   TATATT TA GT  GTGTGTGTTT
                              |||||| || ||  ||||||||||
                              ATATAA AT CG  TACACACAAA
                                 C  _  GG
GAM1443 KIAA1615 3' TATATAGTGTGTGTGTGTGT  36637     TATA
                              TATAT   TGTGTGTGTGT
                              |||||   ||||||||||
                              ATATA   ACACACACACA
                                 TCAC
GAM1443 KIAA1615 3' CATATATTGTGTGTGTGTGT  36638      ATA
                              TATATATT  TGTGTGTGTGT
                              ||||||||  ||||||||||
                              GTATATAA  ACACACACACA
                                   C__
GAM1443 LIN-7-C  3' TATATATTATGTGTGTGT    36639      TA
                              TATATAT  TATGTGTGTGT
                              |||||||  ||||||||||
                              ATATATA  ATACACACACA
                                    __
GAM1443 OSBPL9   3' TATATATATGTATGTGTGT   36640      T
                              TATAT ATATGTGTGTGTGT
                              ||||| ||||||||||||||
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                                ATATA TATACATACACACA
                                  _
GAM1443  OSBPL9   3'  TATATATATGTGTGTGTGT   36632      T
                                TATAT ATATGTGTGTGTGT
                                ||||| ||||||||||||||
                                ATATA TATACACACACACA
                                  _
GAM1443  OSBPL9   3'  TATATATATGTGTGTGTGT   36632      T
                                TATAT ATATGTGTGTGTGT
                                ||||| ||||||||||||||
                                ATATA TATACACACACACA
                                  _
GAM1443  SCDGF-B  3'  ATATATTTCTGTGTGTGT    36641       ATA
                                ATATATT   TGTGTGTGT
                                |||||||   |||||||||
                                TATATAA   ACACACACA
                                    AG_
GAM1443  SCDGF-B  3'  ATATATTTCTGTGTGTGT    36641       ATA
                                ATATATT   TGTGTGTGT
                                |||||||   |||||||||
                                TATATAA   ACACACACA
                                    AG_
GAM1443  SSX5     3'  CATGTGTGTGTGTTTA      36642            III
                                TATGTGTGTGTGTTT   A
                                ||||||||||||||   |
                                GTACACACACACAAA   T
                                        III
GAM1443  TSPAN-2  3'  TATATATTATATGTGTGTCTAT 36643              G
            TT                   TATATATTATATGTGTGT TGTTT
                                ||||||||||||||||| |||||
                                ATATATAATATACACACA ATAAA
                                        G
GAM1443  ZNF237   3'  TACATATTATGCTTCGTGTGTT 36644          ATGTG
            T                    TATATATTAT    TGTGTGTTT
                                ||||||||||    |||||||||
                                ATGTATAATA    GCACACAAA
                                    CGAA_
GAM1443  LOC115123 3'  TATATATATATATGTGTGTGTG 36645        _
            TTT                    TATATAT TATATGTGTGTGTGTTT
                                ||||||| ||||||||||||||||
                                ATATATA ATATACACACACACAAA
                                    T
GAM1443  LOC145719 5'  TATATGTATATATGTGTGTGTG 36646      AT_
            T                    TATAT   TATATGTGTGTGTGT
                                |||||   ||||||||||||||
                                ATATA   ATATACACACACACA
                                  CAT
GAM1443  LOC145720 5'  TATATGTATATATGTGTGTGTG 36646      AT_
            T                    TATAT   TATATGTGTGTGTGT
                                |||||   ||||||||||||||
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```
                                ATATA   ATATACACACACACA
                                   CAT
GAM1443  LOC145868 5'  TATATATAGTATATATACTGTG 36647        TA      _
                TTT                  TATATAT  TATGTGTG TGTGTTT
                                |||||||  ||||||||  |||||||
                                ATATATA  ATATATAT ACACAAA
                                   TC       G
GAM1443  LOC148645 3'  CATCTCCGTGTGTGTGTTT    36648      ATA
                                TATT   TGTGTGTGTGTTT
                                ||||   ||||||||||||
                                GTAG   GCACACACACAAA
                                  AG_
GAM1443  LOC149267 3'  TATATATAATGTGTGTGT     36649        TAT
                                TATATAT   ATGTGTGTGT
                                |||||||   ||||||||||
                                ATATATA   TACACACACA
                                   T__
GAM1443  LOC152903 3'  TACCAAGGTGTGTGTGTTT    36650       TAT
                                TATTA   GTGTGTGTGTTT
                                |||||   ||||||||||||
                                ATGGT   CACACACACAAA
                                   TC_
GAM1443  LOC153387 5'  TATATATATATATGTGTGTGTG 36626         _
                T                   TATATAT TATATGTGTGTGTGT
                                |||||||  ||||||||||||||
                                ATATATA ATATACACACACACA
                                   T
GAM1443  LOC153387 5'  TATATATATGTGTGTGTGT    36632       T
                                TATAT ATATGTGTGTGTGT
                                |||||  ||||||||||||||
                                ATATA TATACACACACACA
                                  _
GAM1443  LOC153387 5'  TATATATATATATGTGTGT    36651        T
                                TATATAT ATATGTGTGTGT
                                |||||||  ||||||||||||
                                ATATATA TATATACACACA
                                  _
GAM1443  LOC168667 3'  TATATACTCTGTGTGTGTGTGT 36652         ATA
                TT                   TATATATT   TGTGTGTGTGTTT
                                |||||||||   ||||||||||||||
                                ATATATGA   ACACACACACAAA
                                     GAC
GAM1443  LOC197114 5'  TATATGTATATATGTGTGTGTG 36646       AT_
                T                   TATAT   TATATGTGTGTGTGT
                                |||||   ||||||||||||||||
                                ATATA   ATATACACACACACA
                                   CAT
GAM1443  LOC197117 3'  TATATATGTATATGTGTGTGTG 36653         _
                T                   TATATAT TATATGTGTGTGTGT
                                |||||||  ||||||||||||||||
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                                ATATATA ATATACACACACACA
                                    C
GAM1443  LOC221747 5'  TATATATTATATGTAGTA    36654            T
                                TATATATTATATGTG GTG
                                ||||||||||||||| |||
                                ATATATAATATACAT CAT
                                                _
GAM1443  LOC221814 5'  TATATATGTATGTGTGTGTGT  36655       TA
                                TATATAT  TATGTGTGTGTGT
                                |||||||  ||||||||||||
                                ATATATA  ATACACACACACA
                                    C_
GAM1443  LOC222224 3'  TATTATATGGTAAATGTTT   36656        T  T
                                TATTATATG GTG GTGTTT
                                ||||||||| ||| ||||||
                                ATAATATAC CAT TACAAA
                                     _  T
GAM1443  LOC222662 3'  TATATATATGTGTGTGTGT   36632      T
                                TATAT ATATGTGTGTGTGT
                                ||||| ||||||||||||||
                                ATATA TATACACACACACA
                                  _
GAM1443  LOC222662 3'  TATATATATGTGTGTGTGT   36632      T
                                TATAT ATATGTGTGTGTGT
                                ||||| ||||||||||||||
                                ATATA TATACACACACACA
                                  _
GAM1443  LOC92344  3'  TATATATAAGTGTGTGTGTTT  36657       TATAT
                                TATATAT    GTGTGTGTGTTT
                                |||||||    ||||||||||||
                                ATATATA    CACACACACAAA
                                    TT___
GAM1444  PCDHB13   5'  TGGGAGGACGGTTCTGTGG   36660     T  T  TTT
                                TGGG AGG TG   GTTCTGTGG
                                |||| ||| ||   |||||||||
                                ACCC TCC GC   CAAGACACC
                                  _  T  ___
GAM1444  PCDHB8    5'  TGGGAGGACGGTTCTGTGG   36660     T  T  TTT
                                TGGG AGG TG   GTTCTGTGG
                                |||| ||| ||   |||||||||
                                ACCC TCC GC   CAAGACACC
                                  _  T  ___
GAM1444  SEPN1     3'  GGCTGGGTTGTGCTTCTGTGGA 36661     A_     TTG
                                GGT  GGTTGT   TTCTGTGGA
                                |||  ||||||   |||||||||
                                CCG  CCAACA   AAGACACCT
                                  AC     CG_
GAM1444  DKFZP564O0423 3'  TGGGTGGCCTTCTGTTCTGTGG 36662       A   TG
            A                    TGGGT GGT  TTTGTTCTGTGGA
                                |||||  |||  ||||||||||||
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                                ACCCA CCG  AGACAAGACACCT
                                  _  GA
GAM1444  KIAA0992  3'  TGGGTGGTTTGGATGCTTTCTG 36663      A   _ TT  __
             TGGA                  TGGGT GGTT G  TGT  TCTGTGGA
                                |||||  ||||  |  |||  ||||||||
                                ACCCA CCAA C  ACG  AGACACCT
                                  _   A CT   AA
GAM1444  MGC2721   3'  GGGTGGGGGGGTTCTGTGG    36664     A  TTGTTT
                                GGGT GG     GTTCTGTGG
                                ||||  ||     |||||||||
                                CCCA CC     CAAGACACC
                                  C  CC_____
GAM1444  PME-1    3'  TGGGAGGTTGTTGAGTGG    36665     T      TGTTCT
                                TGGG AGGTTGTT     GTGG
                                ||||  ||||||||     ||||
                                ACCC TCCAACAA     CACC
                                  _       CT_____
GAM1444  PPP1R14C  3'  GGTAGGTGGGTTTCTGTGG   36666       TGTTTG
                                GGTAGGT     TTCTGTGG
                                |||||||     ||||||||
                                CCATCCA     AAGACACC
                                    CCCA__
GAM1444  RAB14    3'  TGGGTGGTTTGTTTGTTTTG   36667      A   _     C
                                TGGGT GGTT GTTTGTT TG
                                |||||  ||||  |||||||  ||
                                ACCCA CCAA CAAACAA AC
                                  _   A      A
GAM1445  ALDH3A2   5'  TGTAGGGGGTGGAGTGAGC   36670    CA   AT   CT  CA
                                TGT  AGG  GTGG  TG  AGC
                                |||  |||  ||||  ||  |||
                                ACA  TCC  CACC  AC  TCG
                                  __  CC   TC  __
GAM1445  ARG2     3'  TGTTAGGGATGTGGATAGAATA 36671     CAA      CTTGC__
             AGCA                  TGT   GGATGTGG      AAGCA
                                |||   ||||||||      |||||
                                ACA   CCTACACC      TTCGT
                                  ATC       TATCTTA
GAM1445  GPR48    3'  TGTCAAGGATGGCAAG      36672          TGGCTT
                                TGTCAAGGATG     GCAAG
                                ||||||||||     |||||
                                ACAGTTCCTAC     CGTTC
                                              _______
GAM1445  SFTPA2   3'  TGTCAAGGTGTGTGGCACA   36673        A_     TT
                                TGTCAAGG  TGTGGC  GCA
                                ||||||||  ||||||  |||
                                ACAGTTCC  ACACCG  TGT
                                    AC     __
GAM1445  MGC13170  3'  TGTCAGGGTGTGGCTAGC    36674      A  A      T
                                TGTCA GG TGTGGCT GC
                                |||||  ||  |||||||  ||
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                                ACAGT CC ACACCGA CG
                                  C _     T
GAM1445 LOC151174 5' TGTCAAGGGGTAACAAG    36675       ATGT  CTT
                                TGTCAAGG   GG  GCAAG
                                ||||||||   ||  |||||
                                ACAGTTCC   CC  TGTTC
                                     _____ AT_
GAM1445 LOC199782 3' TGCAAGGATGTGAACAAG    36676    T       CTT
                                TG CAAGGATGTGG  GCAAG
                                || ||||||||||  |||||
                                AC GTTCCTACACT  TGTTC
                                 _       ___
GAM1445 LOC221914 3' TGTGAAGGATGTGGGTGGCA  36677    C       CTT
                                TGT AAGGATGTGG  GCA
                                ||| ||||||||||  |||
                                ACA TTCCTACACC  CGT
                                  C       CAC
GAM1445 LOC51068  3' TCAAGGATGTGGGAAGCA    36678         CTT
                                TCAAGGATGTGG  GCA
                                ||||||||||||  |||
                                AGTTCCTACACC  CGT
                                      CTT
GAM1445 LOC93166  3' TGTTGAGGGTGGTGGCCCCGGC 36679    CA  AT_    __
          A                      TGT  AGG  GTGGCTT  GCA
                                ||| |||  |||||||  |||
                                ACA  TCC  CACCGGG  CGT
                                  AC  CAC     GC
GAM1446 SLC2A2   3' GTAAAGGCAGATAGATAGTG  36682     C  ATA
                                GTAAA GCG  ATAGATAGTG
                                ||||| |||  ||||||||||
                                CATTT CGT  TATCTATCAC
                                  C  C__
GAM1446 KIAA1322  3' AAACGTGACACATGATAGTGC  36683     C   ATA
                                AAACG GATA  GATAGTGC
                                ||||| ||||  ||||||||
                                TTTGC CTGT  CTATCACG
                                  A   GTA
GAM1446 WS-3     5' GTAGAGCGATAATTCCACATGC 36684    AAC      AGATA
                                GTA  GCGATAAT   GTGC
                                |||  ||||||||   ||||
                                CAT  CGCTATTA   TACG
                                  CT_      AGGTG
GAM1446 LOC201696 3' GTAGGTGCTCAATAGATGGTG  36685    AAC  GA      A
                                GTA  GC  TAATAGAT GTG
                                |||  ||  |||||||| |||
                                CAT  CG  GTTATCTA CAC
                                  CCA  A_      C
GAM1447 NPHP1    3' CATGGTATCTTTACTGGGAA  36688     A       AA
                                TATG TATCTTTACT  GAA
                                |||| ||||||||||  |||
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                                GTAC ATAGAAATGA  CTT
                                  C        CC
GAM1447  TEX15    3'  ATGATGATTATTACTAAGAGAG 36689      _ CT       A
                TT                  ATGAT AT  TTACTAAGA AGTT
                                    ||||| ||  |||||||||| ||||
                                    TACTA TA  AATGATTCT TCAA
                                      C  AT       C
GAM1447  CL24751  5'  TGGTATCTTCTACAGAAAGTT  36690    A     ACTA
                                    TG TATCTTT   AGAAAGTT
                                    || |||||||   ||||||||
                                    AC ATAGAAG   TCTTTCAA
                                     C      ATG_
GAM1448  CRLF1    5'  GCACGTCGCTGGGCGCGCT   36693    GAC      A
                                    GCA   CGCTGGGC TGTT
                                    |||   |||||||| ||||
                                    CGT   GCGACCCG GCGA
                                      GCA       C
GAM1448  FMOD     3'  ACAGGTTGCTGGGCAGATGCT  36694     ACC      __
                                    GCAG   GCTGGGCA  TGTT
                                    ||||   ||||||||  ||||
                                    TGTC   CGACCCGT  ACGA
                                      CAA       CT
GAM1448  S100A10  5'  GCGGACGCTGGGCGAGCT    36695    A  C     AT
                                    GC GAC GCTGGGC  GTT
                                    || ||| |||||||  |||
                                    CG CTG CGACCCG  CGA
                                     C  _      CT
GAM1448  SFRS2IP  3'  GCAACTGATATGTTCTA     36696    GACC    GC
                                    GCA   GCTGG  ATGTTCTA
                                    |||   |||||  ||||||||
                                    CGT   TGACT  TACAAGAT
                                      _____    A_
GAM1448  CAC-1    5'  GCGGGCCGCCGGGGGACCCTGC 36697    AGA      CAT TT  A
                T                    GC   CCGCTGGG   G  CT CT
                                    ||   ||||||||  |  || ||
                                    CG   GGCGGCCC   T  GA GA
                                     CCC       CC_ GG  C
GAM1448  CLIC4    3'  GCATGTTGCTGGGTCGTCCT  36698    GACC    CA
                                    GCA   GCTGGG  TGTTCT
                                    |||   ||||||  ||||||
                                    CGT   CGACCC  GCAGGA
                                      ACAA     A_
GAM1448  DKFZp434L0850 3'  GACCCTGGGCATGAGAACC   36699     G       TTCT
                                    GACC CTGGGCATG    ACT
                                    |||| |||||||||    |||
                                    CTGG GACCCGTAC    TGG
                                      _       TCT_
GAM1448  FLJ10297 3'  GCAGCTTGCTGGGCAGTT    36700     ACC      T
                                    GCAG   GCTGGGCA GTT
                                    ||||   |||||||| |||
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                                CGTC   CGACCCGT CAA
                                  GAA       _
GAM1448  FLJ20419  3'  ACAGACCAAACGTGTT      36701         CTG   A
                                GCAGACCG   GGC TGTT
                                ||||||||   ||| ||||
                                TGTCTGGT   TTG ACAA
                                     ____   C
GAM1448  GP5       3'  GCAGGCCGCTGGGCTAAGTC   36702      A        AT_
                                GCAG CCGCTGGGC   GTT
                                |||| |||||||||   |||
                                CGTC GGCGACCCG   CAG
                                  C        ATT
GAM1448  MGC4771   3'  GCGACCGCTGGGCAGC      36703    A          T
                                GC GACCGCTGGGCA GT
                                || ||||||||||| ||
                                CG CTGGCGACCCGT CG

                                 _          _
GAM1448  LOC127435 5'  GCAGGCCACTGGGCACGCGCT  36704      A          T
                                GCAG CCGCTGGGCATGT CT
                                |||| |||||||||||| ||
                                CGTC GGTGACCCGTGCG GA
                                  C          C
GAM1448  LOC150095 5'  GCAGGCGCTGGGCAGC      36705      AC        T
                                GCAG  CGCTGGGCA GT
                                ||||  ||||||||| ||
                                CGTC  GCGACCCGT CG
                                  C_        _
GAM1448  LOC151283 3'  GAACCGAACAATGTTCT     36706    CC        _
                                GA  GCTGGGCA TGTTCT
                                ||  |||||||| ||||||
                                CT  TGGCTTGT ACAAGA
                                 __        T
GAM1448  LOC91450  5'  GCAAGTTGCTGGGCAAGCT    36707      ACC       T
                                GCAG   GCTGGGCA GTT
                                ||||   |||||||| |||
                                CGTT   CGACCCGT CGA
                                  CAA       T
GAM1449  FGF2      3'  TAGCAGCATAATTTCTAATATT 36710         CA    AAA
           A                     TAGCAGCA  AATT   GGTATTA
                                |||||||  ||||   |||||||
                                ATCGTCGT  TTAA   TTATAAT
                                    A_    AGA
GAM1449  PPIG      3'  TAGCAGTACAAATTATCCAGAT 36711       C       A__
                                TAGCAG ACAAATTA   AGGT
                                |||||| ||||||||   ||||
                                ATCGTC TGTTTAAT   TCTA
                                   A       AGG
GAM1449  DKFZP566G1424 5'  TAGCAGCACTGGTAGGTATT   36712          AAATTAA
                                TAGCAGCAC      AGGTATT
                                |||||||||      |||||||
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                                ATCGTCGTG      TCCATAA
                                     ACCA___
GAM1449 ELAC1    3' TAGTAGCACAAAATAAGAT   36713    C      TTA
                                TAG AGCACAAA   AAGGT
                                ||| ||||||||   |||||
                                ATC TCGTGTTT   TTCTA
                                  A       TA_
GAM1449 FLJ10970 3' TAGCAGCAATAAGTATT     36714        CAAATTAA
                                TAGCAGCA       AGGTATT
                                ||||||||       |||||||
                                ATCGTCGT       TTCATAA
                                     TA______
GAM1449 FLJ13158 3' GCAGCACAAAGCAGTATTA   36715         TTAAA
                                GCAGCACAAA     GGTATTA
                                ||||||||||     |||||||
                                CGTCGTGTTT     TCATAAT
                                     CG___
GAM1449 KIAA1949 5' GCAGCACAGGGTTAATGCGTAT 36716        AA_   AG_
           TA                     GCAGCACA   TTAA   GTATTA
                                ||||||||   ||||   ||||||
                                CGTCGTGT   AATT   CATAAT
                                     CCC    ACG
GAM1449 KIAA1949 5' GCAGCACAGGGTTAATGCGTAT 36716        AA_   AG_
           TA                     GCAGCACA   TTAA   GTATTA
                                ||||||||   ||||   ||||||
                                CGTCGTGT   AATT   CATAAT
                                     CCC    ACG
GAM1449 KIAA1949 5' GCAGCACAGGGTTAATGCGTAT 36716        AA_   AG_
           TA                     GCAGCACA   TTAA   GTATTA
                                ||||||||   ||||   ||||||
                                CGTCGTGT   AATT   CATAAT
                                     CCC    ACG
GAM1449 LIN-7-C  3' AGCTAGTGAGGTTAAAGGTATT 36717     _  CACAAA
           A                     AGC AG     TTAAAGGTATTA
                                ||| ||     ||||||||||||
                                TCG TC     AATTTCCATAAT
                                  A  ACTCC_
GAM1449 SETBP1   3' ACAGCACAGGTTAAGGATTA   36718        AA    A  T
                                GCAGCACA  TTAA GG ATTA
                                ||||||||  |||| || ||||
                                TGTCGTGT  AATT CC TAAT
                                     CC    _  _
GAM1449 LOC113523 3' ACAGCACTAAGGTATT      36719        AAATTA
                                GCAGCAC     AAGGTATT
                                |||||||     ||||||||
                                TGTCGTG     TTCCATAA
                                     A_____
GAM1449 LOC220963 5' TAGCAACATAAAGATACAAGGT 36720         C   TTA__
           ATTA                     TAGCAGCA AAA     AAGGTATTA
                                ||||||||| |||    |||||||||
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                                ATCGTTGT TTT    TTCCATAAT
                                    A  CTATG
GAM1449  LOC256158 5'  TAGCAGCACAAGTGTAGAT   36721         ATTAA
                                TAGCAGCACAA    AGGT
                                ||||||||||    ||||
                                ATCGTCGTGTT    TCTA
                                     CACA_
GAM1450  FLJ11151  3'  TTCCTGCCAGGATTTGGAG   36724        A_   A
                                TTCCTGCCG  ATTT GAG
                                |||||||||  |||| |||
                                AAGGACGGT  TAAA CTC
                                     CC   C
GAM1450  KIAA1813  5'  CTCCTGCCTCCCAGAGGTGGAT 36725       GAAT    A
                                TTCCTGCC   TTAGAG TGGAT
                                ||||||||   |||||| |||||
                                GAGGACGG   GGTCTC ACCTA
                                    AG__    C
GAM1450  KIAA1913  5'  CTGCTCGGCTCCAGATGGAT   36726    _ AA  AG
                                CTGC CG  TTT  AGATGGAT
                                |||| ||  |||  ||||||||
                                GACG GC  AGG  TCTACCTA
                                  A  CG  __
GAM1450  LOC130633 5'  CTGTCGAATCAGATGGAT    36727    C    TAG
                                CTG CGAATT   AGATGGAT
                                ||| ||||||   ||||||||
                                GAC GCTTAG   TCTACCTA
                                  A    ___
GAM1450  LOC149830 3'  TCCTGCCTTAGAGATGG     36728       GAAT
                                TCCTGCC   TTAGAGATGG
                                |||||||   ||||||||||
                                AGGACGG   AATCTCTACC
                                    _____
GAM1451  ADCY2    3'  AAACATTAGCTTATACACGA   36731        CCTG
                                AAACATTAGC   ATGCACGA
                                ||||||||||   ||||||||
                                TTTGTAATCG   TATGTGCT
                                     AA__
GAM1451  JDD1     3'  AAACAATAGCCCTGGTCAGC   36732      T      AT__
                                AAACA TAGCCCTG   GC
                                |||||| ||||||||   ||
                                TTTGT ATCGGGAC   CG
                                   T       CAGT
GAM1451  KIAA0217  3'  AAACACTAGCCCTGTGGC    36733          AT
                                AAACATTAGCCCTG  GC
                                ||||||||||||||  ||
                                TTTGTGATCGGGAC  CG
                                      AC
GAM1451  KIAA0626  3'  ATCAGCCCTGGTACTGGTGACT 36734         A  AC__
                                ATTAGCCCTG TGC   GACT
                                |||||||||| |||   ||||
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                                TAGTCGGGAC ATG   CTGA
                                     C   ACCA
GAM1451  KIAA1615  3'  AACATTAGCACTGATGGTAACT 36735        C     CAC
                                AACATTAGC CTGATG   GACT
                                ||||||||| ||||||   ||||
                                TTGTAATCG GACTAC   TTGA
                                     T     CA_
GAM1451  NAPG      5'  AAACATTAGCCTGGGAGCCG   36736         C  AT_  A
                                AAACATTAGCC TG   GC CG
                                |||||||||||  ||   || ||
                                TTTGTAATCGG AC   CG GC
                                     _  CCT  _
GAM1451  SCYB5     3'  ATTAGCCCTCATAGAACT    36737         G   CAC
                                ATTAGCCCT ATG   GACT
                                ||||||||| |||   ||||
                                TAATCGGGA TAT   TTGA
                                     G   C__
GAM1451  TUSP      3'  AAACATTAGCCTGGC       36738          C  AT
                                AAACATTAGCC TG  GC
                                ||||||||||| ||  ||
                                TTTGTAATCGG AC  CG
                                     _  __
GAM1451  LOC145678 5'  AAACATTAACCCTCTAATGAC  36739           __   C
                                AAACATTAGCCCT  GATG AC
                                ||||||||||||  |||| ||
                                TTTGTAATTGGGA  TTAC TG
                                      GA   _
GAM1451  LOC201229 3'  AAACACTAGTTCATCCCTGTGG 36740         _____    AT
              C                  AAACATTAG    CCCTG  GC
                                 |||||||||    |||||  ||
                                 TTTGTGATC    GGGAC  CG
                                      AAGTA    AC
GAM1451  LOC254659 5'  TTAGCAAAGGCACGACT     36741      CCT  T
                                TTAGC   GA GCACGACT
                                |||||   || ||||||||
                                AATCG   TT CGTGCTGA
                                   T__  C
GAM1451  LOC57146  3'  GGACATAAGCCCTGAGGC    36742   A   T      T
                                A ACAT AGCCCTGA GC
                                | |||| |||||||| ||
                                C TGTA TCGGGACT CG
                                 C   T       C
GAM1452  CDH8      5'  TGCGCTGGCGAATGTCAA    36745       A   CGGAA
                                TGCGTTG CGA    GTGTCAA
                                ||||||| |||    |||||||
                                ACGCGAC GCT    TACAGTT
                                    C  _____
GAM1452  KIAA1750  3'  TGCGTTATTAACAGGGTGTCAA 36746       AC    AA
              A                  TGCGTTG  GACGG  GTGTCAAA
                                 |||||||  |||||  ||||||||
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                                ACGCAAT  TTGTC  CACAGTTT
                                    AA    C_
GAM1452  ZNF323   3'  GTTGATGATTCATGTCAAA   36747      C  CGGAA
                                GTTGA GA    GTGTCAAA
                                |||||| ||    ||||||||
                                CAACT CT    TACAGTTT
                                   A  AAG__
GAM1453  AF1Q     3'  TTAAAATGGGAAAGGAGTGGAA 36750       ATTT__
           A                     TTAAAAT     GGAGTGGAAA
                                |||||||     ||||||||||
                                AATTTTA     CCTCACCTTT
                                    CCCTTT
GAM1453  ASPH     3'  ATATTTGGAATTCAAAAA    36751          GG
                                ATATTTGGAGT  AAAAA
                                ||||||||||  ||||||
                                TATAAACCTTA  TTTTT
                                      AG
GAM1453  BARX1    3'  TAAAATATTTTATTGGAAAAAA 36752          GGAG
                                TAAAATATTT   TGGAAAAAA
                                ||||||||||   |||||||||
                                ATTTTATAAA   ACCTTTTTT
                                     ATA_
GAM1453  DNCI1    3'  TTAGAATACTTGGAGCAAA   36753     A        TG
                                TTA AATATTTGGAG  GA
                                ||| ||||||||||  ||
                                AAT TTATGAACCTC  TT
                                  C         GT
GAM1453  ELK4     3'  TCAAAATATTTTTAAAGGAGAA 36754          __    TG
           AA                     TTAAAATATT  TGGAG  GAAAA
                                ||||||||||  |||||  |||||
                                AGTTTTATAA  ATTTC  CTTTT
                                     AA    CT
GAM1453  FANCC    3'  AAATACAGAGTGGAAA      36755       TT
                                AAATAT  GGAGTGGAAA
                                ||||||  ||||||||||
                                TTTATG  TCTCACCTTT
                                  __
GAM1453  FLRT2    5'  TAAAATACAATGTGGTGGGAAA 36756        T_  GA   _
           AA                     TAAAATAT  TG  GTGG AAAAA
                                ||||||||  ||  |||| |||||
                                ATTTTATG  AC  CACC TTTTT
                                    TT  AC   C
GAM1453  GIF      3'  TTAAAATGAAGTGGAAAAAA  36757       TATT
                                TTAAAA   TGGAGTGGAAAAAA
                                ||||||   ||||||||||||||
                                AATTTT   ACTTCACCTTTTTT
                                  ____
GAM1453  GNB1     3'  AAATACAAAAGGTGGAAA    36758       TT_  A
                                AAATAT   GG GTGGAAA
                                ||||||   || |||||||
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                                TTTATG   TC CACCTTT
                                   TTT  _
GAM1453  HNF3A    3'  CTAGAATGTCTGGAGGGGA   36759     A   A      T
                                TTA AAT TTTGGAG GGA
                                ||| ||| ||||||| |||
                                GAT TTA AGACCTC CCT
                                  C   C       C
GAM1453  KCNJ15   3'  AAATATTTTGAATGGAAA    36760         G
                                AAATATTT GAGTGGAAA
                                |||||||| |||||||||
                                TTTATAAA CTTACCTTT
                                     A
GAM1453  LPIN2    3'  TTAAAATGATGCAATGGAA   36761        ATT  G
                                TTAAAAT   TG AGTGGAA
                                |||||||   || |||||||
                                AATTTTA   AC TTACCTT
                                     CT_  G
GAM1453  MLLT2    3'  TAAAATATTTGTAGCAGAAAA  36762          G  TG
                                TAAAATATTTG AG  GAAAA
                                |||||||||||  ||  |||||
                                ATTTTATAAAC TC  CTTTT
                                       A  GT
GAM1453  MS4A1    3'  TAAAATATTTGCATAGGAA   36763          GAGT
                                TAAAATATTTG    GGAA
                                ||||||||||    ||||
                                ATTTTATAAAC    CCTT
                                       GTAT
GAM1453  PTBP1    3'  TTAGAATATTTGGTCAACTGGA 36764     A       ___ G
                AA                TTA AATATTTGG   A TGGAAA
                                ||| |||||||||   | ||||||
                                AAT TTATAAACC   T ACCTTT
                                  C        AGT G
GAM1453  PTBP1    3'  TTAGAATATTTGGTCAACTGGA 36764     A       ___ G
                AA                TTA AATATTTGG   A TGGAAA
                                ||| |||||||||   | ||||||
                                AAT TTATAAACC   T ACCTTT
                                  C        AGT G
GAM1453  SCA1     3'  TAAAATATGTTGGAGAGAA   36765        _     T
                                TAAAATAT TTGGAG GGAA
                                |||||||| |||||| ||||
                                ATTTTATA AACCTC TCTT
                                     C     _
GAM1453  STMN1    3'  CTAAAATATTTGTCAGGAGGGA 36766          ____   T
                A                 TTAAAATATTT    GGAG GGAA
                                ||||||||||    |||| ||||
                                GATTTTATAAA    CCTC CCTT
                                       CAGT   _
GAM1453  TXNIP    3'  AAAATATTTGCAGTAGGA    36767          G  _
                                AAAATATTTG AGT GGA
                                ||||||||| ||| |||
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                                TTTTATAAAC TCA CCT
                                     G   T
GAM1453 AMOT     3' TTAAATTATTTGGATAGAAA  36768      A      G
                                TTAAA TATTTGGA TGGAAA
                                ||||| |||||||| ||||||
                                AATTT ATAAACCT ATCTTT
                                   A      _
GAM1453 ATP6V1D  3' AATACATGGAGTGGGAAAAA  36769      T      _
                                AATAT TGGAGTGG AAAAA
                                ||||| |||||||| |||||
                                TTATG ACCTCACC TTTTT
                                   T       C
GAM1453 BZW1     3' TTAGGATATCTGGAGTTAAAAA 36770     AA         G
                                TTA  ATATTTGGAGT GAAAA
                                |||  |||||||||||| |||||
                                AAT  TATAGACCTCA TTTTT
                                  CC          A
GAM1453 FLJ13194 3' TTAACATATTTGGAAATGA   36771      A        _
                                TTAA ATATTTGGAG TGG
                                |||| |||||||||| |||
                                AATT TATAAACCTT ACT
                                   G         T
GAM1453 FLJ20758 5' AAAATATTTGGGGTATGAA   36772          A  _
                                AAAATATTTGG GTG GAA
                                |||||||||||| ||| |||
                                TTTTATAAACC CAT CTT
                                      C   A
GAM1453 G4       3' TTAAAAAGTGGAGGTGGAAAAA 36773       TATT    _
             A                   TTAAAA    TGGAG TGGAAAAAA
                                ||||||    ||||| |||||||||
                                AATTTT    ACCTC ACCTTTTTT
                                   TC__     C
GAM1453 GL009    3' TTAAAATGCTTTGCAGAGGA  36774       A_   G  T
                                TTAAAAT  TTTG AG GGA
                                |||||||  |||| || |||
                                AATTTTA  AAAC TC CCT
                                     CG    G  T
GAM1453 HABP4    3' TCAAAATATTCCAGGAGAGAA  36775          __   T
                                TTAAAATATTT  GGAG GGAA
                                ||||||||||  |||| ||||
                                AGTTTTATAAG  CCTC TCTT
                                      GT   _
GAM1453 KIAA0007 3' AAAATATTTTCTTTGGAAAAAA 36776         GGAG
                                AAAATATTT    TGGAAAAAA
                                |||||||||    |||||||||
                                TTTTATAAA    ACCTTTTTT
                                      AGAA
GAM1453 KIAA0036 3' AAAATATTTATTTAGAAAAAA  36777          GAG
                                AAAATATTTG   TGGAAAAAA
                                ||||||||||   |||||||||
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                                TTTTATAAAT  ATCTTTTTT
                                     AA_
GAM1453  KIAA0408  3'  TAAAATATTTAAAAAGAGAAAA 36778           T_
                                TAAAATATTTGGAG  GGAAAA
                                |||||||||||||  ||||||
                                ATTTTATAAATTTT  TCTTTT
                                      TC
GAM1453  KIAA1320  5'  TTAAAATATTTCAAGGAAA   36779         G  T
                                TTAAAATATTT GAG GGAA
                                |||||||||| ||| ||||
                                AATTTTATAAA TTC CTTT
                                     G  _
GAM1453  KIAA1805  3'  TTAAAGCTATTTGGAGGAG   36780      A_      TG
                                TTAAA  TATTTGGAG  G
                                |||||  |||||||||  |
                                AATTT  ATAAACCTC  C
                                   CG       CT
GAM1453  LIPG      3'  TAAAATATTTCAAAGAGGAAA  36781       _ TG  T
                                TAAAATAT T  GAG GGAAA
                                ||||||||  |  ||| |||||
                                ATTTTATA A  TTC CCTTT
                                     A GT  T
GAM1453  OCT11     3'  CTAAAATATTTGGAACTAGAA  36782           _
                                TTAAAATATTTGGAG TGGAA
                                |||||||||||||| |||||
                                GATTTTATAAACCTT ATCTT
                                      G
GAM1453  PFTK1     3'  CTAAAATATGCTGCTGTGGGAA 36783        _  GA   A
            AA                    TTAAAATAT TTG  GTGG AAAA
                                |||||||||  |||  |||| ||||
                                GATTTTATA GAC  CACC TTTT
                                     C  GA   C
GAM1453  PRO2964   3'  TTAAAATACTTGGGTTGAAA   36784           AG
                                TTAAAATATTTGG  TGGAA
                                ||||||||||||  |||||
                                AATTTTATGAACC  ACTTT
                                      CA
GAM1453  SLC2A13   3'  TTAAAATATTGTTCCTTGTGGA 36785         TGGA___
            AAAAA                   TTAAAATATT      GTGGAAAAAA
                                ||||||||||      ||||||||||
                                AATTTTATAA      CACCTTTTTT
                                     CAAGGAA
GAM1453  SNAPC1    3'  TTAAAATGTCTGGAACAA    36786       A      TG
                                TTAAAAT TTTGGAG  G
                                |||||||  |||||||  |
                                AATTTTA AGACCTT  T
                                     C      GT
GAM1453  LOC121504 3'  TCAAAATATGCTTGGAAAAGA  36787         __     T
                                TTAAAATAT  TTGGAG GGA
                                |||||||||  ||||||  |||
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                                AGTTTTATA  AACCTT TCT
                                     CG     T
GAM1453  LOC123036 3'  TAAAATATTTGAGGGAA     36788          G  T
                                TAAAATATTTG AG GGAA
                                |||||||||| || ||||
                                ATTTTATAAAC TC CCTT
                                      _ _
GAM1453  LOC151579 3'  TTAGGATATCTGGAGTTAAAAA 36770     AA         G
                                TTA  ATATTTGGAGT GAAAA
                                |||  |||||||||| |||||
                                AAT  TATAGACCTCA TTTTT
                                  CC         A
GAM1453  LOC199907 3'  TTAAAATACTTGGTGGCCAA   36789           AG   AA
                                TTAAAATATTTGG  TGG  AA
                                ||||||||||||  |||  ||
                                AATTTTATGAACC  ACC  TT
                                       __  GG
GAM1453  LOC221405 5'  CTAAAATATTTGGAGATGGAA  36790             _
                                TTAAAATATTTGGAG TGGAA
                                |||||||||||||| |||||
                                GATTTTATAAACCTC ACCTT
                                         T
GAM1453  LOC257554 3'  TTAAAAAGTGGAGGTGGAAAAA 36773       TATT    _
           A                     TTAAAA    TGGAG TGGAAAAAA
                                ||||||    ||||| |||||||||
                                AATTTT    ACCTC ACCTTTTTT
                                   TC__    C
GAM1453  LOC50999  3'  TCAAAATATTTTGGAGAAGA   36791          _   T
                                TTAAAATATTT GGAG GGA
                                |||||||||| |||| |||
                                AGTTTTATAAA CCTC TCT
                                       A   T
GAM1454  ADCY2    3'  ATCAGCTTCGATAAGTGCCTTT 36794       TC   GC   CA
                                ATCAGCT  TCG  GAG  CCTTT
                                |||||||  |||  |||  |||||
                                TAGTCGA  AGC  TTC  GGAAA
                                   __  TA   AC
GAM1454  AHSG     3'  AGCTTAGCAAGAGCACCTTT   36795      CT   C
                                AGCTT  CGG GAGCACCTTT
                                |||||  ||| ||||||||||
                                TCGAA  GTT CTCGTGGAAA
                                  TC  _
GAM1454  EXTL3    5'  CCAGCTTCTTATGATGCCTTT  36796        CGGC  GCA
                                TCAGCTTCT   GA   CCTTT
                                |||||||||   ||   |||||
                                GGTCGAAGA   CT   GGAAA
                                      ATA_  AC_
GAM1454  NFKB1    3'  CCGGCTCTCTGAGCACCTTT   36797    A   T   GGC
                                TC GCT CTC   GAGCACCTTT
                                || ||| |||   ||||||||||
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                                GG CGA GAG   CTCGTGGAAA
                                 C   _   A__
GAM1454  FLJ20312  5'  TCAGCTTCTTTGTCACCTTT   36798        CGGCGAG
                                TCAGCTTCT      CACCTTT
                                |||||||||      |||||||
                                AGTCGAAGA      GTGGAAA
                                     AACA___
GAM1454  FLJ20666  3'  GCTTCCAAAAGCACCTTT    36799      T   C
                                GCTTC CGG GAGCACCTTT
                                ||||| ||| ||||||||||
                                CGAAG GTT TTCGTGGAAA
                                  _   _
GAM1454  KIAA1253  5'  CAGCTTCTTTCTCGCCTTT   36800        CGG_  AGCA
                                CAGCTTCT   CG   CCTTT
                                ||||||||   ||   |||||
                                GTCGAAGA   GC   GGAAA
                                     AAGA  ____
GAM1454  LOC150378 3'  TCAGCTTCCCCACCT       36801         GGCGAG
                                TCAGCTTCTC     CACCT
                                ||||||||||     |||||
                                AGTCGAAGGG     GTGGA
                                       ______
GAM1454  LOC253350 5'  ACCAGCTCGAGCGCCT      36802        TCTCGG    A
                                ATCAGCT     CGAGC CCT
                                |||||||     ||||| |||
                                TGGTCGA     GCTCG GGA
                                   ______   C
GAM1455  DDX3     5'  TTCGTTTTTTTTGTTTTT    36805          C
                                TTCGTTTTTTT GTTTTT
                                |||||||||| ||||||
                                AAGCAAAAAAA CAAAAA
                                      A
GAM1455  DDX3     5'  TTCGTTTTTTTTGTTTTT    36805          C
                                TTCGTTTTTTT GTTTTT
                                |||||||||| ||||||
                                AAGCAAAAAAA CAAAAA
                                      A
GAM1455  DLC1     3'  TTTTTTTTTTTTTTTTCGCA   36806        CG
                                TTTTTTT  TTTTTTTCGCA
                                |||||||  ||||||||||
                                AAAAAAA  AAAAAAAGCGT
                                    AA
GAM1455  EN1      5'  GTTTTTTTTTTTTTTTCA    36807         CG
                                GTTTTTTT  TTTTTTTCG
                                ||||||||  |||||||||
                                CAAAAAAA  AAAAAAAGT
                                    AA
GAM1455  IL13RA2  3'  TTTTTTTTTTTTTTTTCGCA   36806        CG
                                TTTTTTT  TTTTTTTCGCA
                                |||||||  ||||||||||
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                                AAAAAAA  AAAAAAAGCGT
                                    AA
GAM1455  MMP19    3'  TTCGTTTTTATTTTTTTGCA  36808        TTC      C
                                TTCGTTTTT  GTTTTTTT GCA
                                |||||||||  |||||||| |||
                                AAGCAAAAA  TAAAAAAA CGT
                                    ___     _
GAM1455  MMP19    3'  TTCGTTTTTATTTTTTTGCA  36808        TTC      C
                                TTCGTTTTT  GTTTTTTT GCA
                                |||||||||  |||||||| |||
                                AAGCAAAAA  TAAAAAAA CGT
                                    ___     _
GAM1455  VIL2     3'  TTTTTTTCGTGCCTTTGCA   36809         T    C
                                TTTTTTTCGT TTTTT GCA
                                |||||||||| ||||| |||
                                AAAAAAAGCA GGAAA CGT
                                      C   _
GAM1455  C9orf7   3'  TTTTTTTTTTTTTTTTCGC   36810       CG
                                TTTTTTT  TTTTTTTCGC
                                |||||||  ||||||||||
                                AAAAAAA  AAAAAAAGCG
                                    AA
GAM1455  DPCR1    3'  TCCGTTTTTTTTGTTTTTT   36811         C
                                TTCGTTTTTTT GTTTTTT
                                |||||||||| |||||||
                                AGGCAAAAAAA CAAAAAA
                                      A
GAM1455  GPR51    3'  GTTTTTTTTTTTTTTTTGCA  36812       CG     C
                                GTTTTTTT  TTTTTTT GCA
                                ||||||||  ||||||| |||
                                CAAAAAAA  AAAAAAA CGT
                                    AA     _
GAM1455  KIAA1223 3'  TTCATTTTTTTTGTTTTTTC  36813         C
                                TTCGTTTTTTT GTTTTTTT
                                |||||||||| ||||||||
                                AAGTAAAAAAA CAAAAAAG
                                      A
GAM1455  KIAA1560 3'  TTCGTTTTTTTGTTTTTT    36814         C
                                TTCGTTTTTTT GTTTTTT
                                |||||||||| |||||||
                                AAGCAAAAAAA CAAAAAA
                                      _
GAM1455  MGC22793 3'  TTTTTTTTTTTTTTTTCGCA  36806       CG
                                TTTTTTT  TTTTTTTCGCA
                                |||||||  ||||||||||
                                AAAAAAA  AAAAAAAGCGT
                                    AA
GAM1455  MGC4734  3'  TTCGTTTTTTTGTTTTTTT   36815         C
                                TTCGTTTTTTT GTTTTTTT
                                |||||||||| ||||||||
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                                AAGCAAAAAAA CAAAAAAA
                                        _
GAM1455  ODZ2     3'  TTCGTTTGTTTTGTTTTCCTCG 36816       T   C
                                TTCGTTT TTT GTTTTTTTCG
                                ||||||| ||| ||||||||||
                                AAGCAAA AAA CAAAAGGAGC
                                    C   A
GAM1455  SBBI54   3'  TTTTTTTTTTTTTTTTCGCA  36806       CG
                                TTTTTTT  TTTTTTTCGCA
                                |||||||  ||||||||||
                                AAAAAAA  AAAAAAAGCGT
                                    AA
GAM1455  SNRPG    3'  TTTTTTTTTTTTTTTTCGCA  36806       CG
                                TTTTTTT  TTTTTTTCGCA
                                |||||||  ||||||||||
                                AAAAAAA  AAAAAAAGCGT
                                    AA
GAM1455  LOC115416 3'  TTTTTTTTTTTTTTTTCGCA  36806       CG
                                TTTTTTT  TTTTTTTCGCA
                                |||||||  ||||||||||
                                AAAAAAA  AAAAAAAGCGT
                                    AA
GAM1455  LOC146520 3'  TTCGTTTTCTTTGTTTCT    36817         C
                                TTCGTTTTTTT GTTTTT
                                |||||||||| ||||||
                                AAGCAAAAGAA CAAAGA
                                     A
GAM1455  LOC153320 3'  GTTTTTTTTGCTTTTTCCA   36818       C
                                GTTTTTTT GTTTTTTTCG
                                |||||||| ||||||||||
                                CAAAAAAA CGAAAAAGGT
                                    A
GAM1455  LOC90678  3'  TTTTTTTTTTTTTTTTCGCA  36806       CG
                                TTTTTTT  TTTTTTTCGCA
                                |||||||  ||||||||||
                                AAAAAAA  AAAAAAAGCGT
                                    AA
GAM1456  ACAD8    3'  TCCAAAATCCAGTTAAGTG   36821       T   A   T
                                TCCAAAAT CCA TTAA TG
                                |||||||| ||| |||| ||
                                AGGTTTTA GGT AATT AC
                                    _  C   C
GAM1456  EIF1AY   3'  CAAAATATCCAATTACTTG   36822       _     A
                                CAAAAT TCCAATTA TTG
                                |||||| |||||||| |||
                                GTTTTA AGGTTAAT AAC
                                   T      G
GAM1456  HTR2C    3'  TCCAAAATTTATCCACAGTTGT 36823        ___   ATTAA
                                TCCAAAAT  TCCA   TTGT
                                ||||||||  ||||   ||||
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                                AGGTTTTA  AGGT    AACA
                                    AAT   GTC__
GAM1456 SLC25A4  3' AATTCTTCAGTTAATTGTACA 36824      __ A
                                AATTC  CA TTAATTGTACA
                                |||||  || ||||||||||
                                TTAAG  GT AATTAACATGT
                                   AA  C
GAM1456 DKFZP566K0524 3' TCCAAAATATCACTATTAATTG 36825        TC __
          TAC                    TCCAAAAT  CA  ATTAATTGTAC
                                |||||||  ||  ||||||||||
                                AGGTTTTA  GT  TAATTAACATG
                                    TA  GA
GAM1456 FLJ10803 3' TCCAAATTCCAATTAAT    36826       A
                                TCCAAA TTCCAATTAAT
                                |||||| ||||||||||
                                AGGTTT AAGGTTAATTA
                                   _
GAM1456 FLJ12876 3' TCCAAAATTTGACATTTGTACA 36827         CCAAT  A
                                TCCAAAATT    TA TTGTACA
                                |||||||||    || |||||||
                                AGGTTTTAA    GT AACATGT
                                    ACT__  A
GAM1456 FLJ12910 3' AAAATTCCAATATAAATGTA  36828          _  T
                                AAAATTCCAAT TAA TGTA
                                |||||||||| ||| ||||
                                TTTTAAGGTTA ATT ACAT
                                     T  T
GAM1456 FLJ22794 5' CAAAGCTGTCATTAATTGTACA 36829     ATTCCA
                                CAAA     ATTAATTGTACA
                                ||||     ||||||||||||
                                GTTT     TAATTAACATGT
                                  CGACAG
GAM1456 KIAA0009 3' TCCAAAATTCAATACTGATACA 36830         C  TA  _
                                TCCAAAATTC AAT  ATTG TACA
                                |||||||||| |||  |||| ||||
                                AGGTTTTAAG TTA  TGAC ATGT
                                    _  __   T
GAM1456 KIAA0254 3' TCCACAAACCACTTTAATTGT  36831     AAATT  A_
                                TCCA    CCA  TTAATTGT
                                ||||    |||  ||||||||
                                AGGT    GGT  AATTAACA
                                  GTTT_  GA
GAM1456 KIAA1240 3' AAAATCTTAATTAATTGTACA  36832      CC
                                AAAATT  AATTAATTGTACA
                                ||||||  ||||||||||||
                                TTTTAG  TTAATTAACATGT
                                   AA
GAM1456 KIAA1546 3' CCAAAATGTAATTGTAC     36833       TCCAAT
                                CCAAAAT     TAATTGTAC
                                |||||||     |||||||||
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                                GGTTTTA     ATTAACATG
                                   C_____
GAM1456 KIAA1906 3' CCAGAATTCCAAATTCAGTGCA 36834     A       TTAAT_
                                CCA AATTCCAA     TGTA
                                ||| ||||||||     ||||
                                GGT TTAAGGTT     ACGT
                                  C       TAAGTC
GAM1456 MacGAP   3' AAAATTCCATTTAGAAGAGTAC 36835         A   ATT__
             A                   AAAATTCCA TTA     GTACA
                                 ||||||||| |||     |||||
                                 TTTTAAGGT AAT     CATGT
                                       A   CTTCT
GAM1456 MGC17330 3' CCCAAAGTTCTGACTTCTGTAC 36836       A   CA   AA
             A                   TCCAAA TTC  ATT  TTGTACA
                                 |||||| |||  |||  |||||||
                                 GGGTTT AAG  TGA  GACATGT
                                    C   AC   A_
GAM1456 MLL3     3' CAAAATTCCAATGGTGT     36837           TAAT
                                 CAAAATTCCAAT    TGT
                                 ||||||||||||    |||
                                 GTTTTAAGGTTA    ACA
                                       CC__
GAM1456 RBM5     3' TCCAAAATTCTGTACA      36838          CAATTAAT
                                 TCCAAAATTC       TGTACA
                                 ||||||||||       ||||||
                                 AGGTTTTAAG       ACATGT
                                          _________
GAM1456 SFRS12   3' TCCAAAATTTTAATGTAC    36839         CCAA    T
                                 TCCAAAATT    TTAAT GTAC
                                 |||||||||    ||||| ||||
                                 AGGTTTTAA    AATTA CATG
                                          ____    _
GAM1456 LOC153727 5' TCCTGAATTCCAATTAACTAC  36840     AA          TG
                                 TCC  AATTCCAATTAAT  TAC
                                 |||  ||||||||||||||  |||
                                 AGG  TTAAGGTTAATTG  ATG
                                   AC           __
GAM1456 LOC255937 3' CAAACATTCCAATTATTACA   36841      _        ATTG
                                 CAAA ATTCCAATTA    TACA
                                 |||| ||||||||||    ||||
                                 GTTT TAAGGTTAAT    ATGT
                                   G         A___
GAM1457 CA11     5' CACCTCCTCTCCGTTCTCT   36844       AGA      ATC
                                 TACCT   CCTCTCC   CTCT
                                 |||||   |||||||   ||||
                                 GTGGA   GGAGAGG   GAGA
                                    ___       CAA
GAM1457 CA14     3' AGCCTGGGTCCATTCCTCTCT  36845    A   C__     _
                                 AG CCT   TCCAT CCTCTCT
                                 || |||   ||||| |||||||
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                                TC GGA   AGGTA GGAGAGA
                                 _  CCC    A
GAM1457  CDY1    5'  CCTGAACCTCTCCATACT    36846    AG       C
                                CCT  ACCTCTCCAT CT
                                |||  |||||||||| ||
                                GGA  TGGAGAGGTA GA
                                  CT        T
GAM1457  CDY1    5'  CCTGAACCTCTCCATACT    36846    AG       C
                                CCT  ACCTCTCCAT CT
                                |||  |||||||||| ||
                                GGA  TGGAGAGGTA GA
                                  CT        T
GAM1457  DDC     5'  GACTTGCTCTCTGTCCTCTCT  36847    ___    CA
                                GAC   CTCTC  TCCTCTCT
                                |||   |||||  ||||||||
                                CTG   GAGAG  AGGAGAGA
                                  AAC    AC
GAM1457  EPB49   5'  CCTGGCCCTCTCTCCCTTTCT  36848    AGA    CA   C
                                CCT   CCTCTC  TCCT TCT
                                |||   ||||||  |||| |||
                                GGA   GGAGAG  GGGA AGA
                                  CCG     A_   A
GAM1457  FCGR2B  3'  TACCAGATCTTCCCTCTC    36849    T   CC   CCA
                                TACC AGA  TCT   TCCTCTC
                                |||| |||  |||   |||||||
                                ATGG TCT  AGA   GGGAGAG
                                  _  __   A__
GAM1457  SART2   3'  TAGACTCTCCATCTTCT     36850      C      C
                                TAGAC TCTCCATC TCT
                                |||||  |||||||| |||
                                ATCTG AGAGGTAG AGA
                                   _       A
GAM1457  WT1     3'  CCTGGACCATCCCCTATTTTCT 36851    A   _    _ CC
                                CCT GACC TCTCC AT  TCT
                                |||  |||| |||||  ||  |||
                                GGA CTGG AGGGG TA  AGA
                                  C    T    A  AA
GAM1457  WT1     3'  CCTGGACCATCCCCTATTTTCT 36851    A   _    _ CC
                                CCT GACC TCTCC AT  TCT
                                |||  |||| |||||  ||  |||
                                GGA CTGG AGGGG TA  AGA
                                  C    T    A  AA
GAM1457  WT1     3'  CCTGGACCATCCCCTATTTTCT 36851    A   _    _ CC
                                CCT GACC TCTCC AT  TCT
                                |||  |||| |||||  ||  |||
                                GGA CTGG AGGGG TA  AGA
                                  C    T    A  AA
GAM1457  WT1     3'  CCTGGACCATCCCCTATTTTCT 36851    A   _    _ CC
                                CCT GACC TCTCC AT  TCT
                                |||  |||| |||||  ||  |||
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                                GGA CTGG AGGGG TA  AGA
                                  C    T    A  AA
GAM1457 ZNF174   3' CCCAGACCTGCCTTCTC    36852        CT  ATCC
                                CCTAGACCT  CC    TCTC
                                |||||||||  ||    ||||
                                GGGTCTGGA  GG    AGAG
                                     C_  A___
GAM1457 ADAMTS10 5' CACCTGGGCCTCCCTCTC    36853      AGA    TCCAT
                                TACCT   CCTC    CCTCTC
                                |||||   ||||    ||||||
                                GTGGA   GGAG    GGAGAG
                                  CCC   _____
GAM1457 BC008967 5' CTGGATTAGCTCATCCTCTCT 36854    A  CCT_   C
                                CT GA    CTC ATCCTCTCT
                                || ||    ||| |||||||||
                                GA CT    GAG TAGGAGAGA
                                 C  AATC  _
GAM1457 C11orf16 3'  TACCTAGATCCTCAGGGCTCT 36855        _    TCCATC
                                TACCTAGA CCTC     CTCT
                                |||||||| ||||     ||||
                                ATGGATCT GGAG     GAGA
                                     A    TCCC__
GAM1457 DNAM-1   3'  TACTTAAGCCATTCCATCCTTT 36856    C  GA  TC      C
           CT                    TAC TA  CC  TCCATCCT TCT
                                |||  ||  ||  |||||||| |||
                                ATG AT  GG  AGGTAGGA AGA
                                  A  TC  TA       A
GAM1457 FLJ11017 5' TAGAGGTTCTGTCCTCTCT   36857     CC_  CCA
                                TAGA   TCT   TCCTCTCT
                                ||||   |||   ||||||||
                                ATCT   AGA   AGGAGAGA
                                  CCA   C__
GAM1457 FLJ12650 3' CTGAGACCTGATCCTCTCT   36858    _     CTCC
                                CT AGACCT    ATCCTCTCT
                                || ||||||    |||||||||
                                GA TCTGGA    TAGGAGAGA
                                 C     C___
GAM1457 FLJ13955 3' TAGACCTCTTTCTTCTCT    36859        CCA  C
                                TAGACCTCT   TC TCTCT
                                |||||||||   || |||||
                                ATCTGGAGA   AG AGAGA
                                     A__  A
GAM1457 FLJ20249 3' TACCAGACCTTTAGTCTCTCT 36860     T     CTCCATC
                                TACC AGACCT      CTCTCT
                                |||| ||||||      ||||||
                                ATGG TCTGGA      GAGAGA
                                  _     AATCA__
GAM1457 IL-17RE  3' CCTAGGTCCAGAGTCCTCTCT 36861      ACCTC   ___
                                CCTAG    TCCA   TCCTCTCT
                                |||||    ||||   ||||||||
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                                GGATC    AGGT   AGGAGAGA
                                  C_____   CTC
GAM1457 KIAA0285 3' CCTGTCTCTTCCATCCTTTCT 36862    AGAC   _     C
                                CCT    CTCT CCATCCT TCT
                                |||    |||| ||||||| |||
                                GGA    GAGA GGTAGGA AGA
                                  CA__   A      A
GAM1457 KIAA0298 3' CTAAACCTCTCTCCCTTCT   36863         CA   TC
                                CTAGACCTCTC  TCC  TCT
                                ||||||||||  |||  |||
                                GATTTGGAGAG  AGG  AGA
                                       __  GA
GAM1457 KIAA1458 3' TAGATTTTTTTCCCCCTCTCT 36864     CCTC__   A
                                TAGA     TCC TCCTCTCT
                                ||||     ||| ||||||||
                                ATCT     AGG GGGAGAGA
                                  AAAAAA  _
GAM1457 MAFB    3' TACTGGGACCTCTCGGTTCTCT 36865    CTA      CATC
             CT                   TAC   GACCTCTC   CTCTCT
                                |||   ||||||||   ||||||
                                ATG   CTGGAGAG   GAGAGA
                                  ACC       CCAA
GAM1457 MGC2776  5' TACCTAGGCCCTTTCCTCTCT  36866       A  T  CCA
                                TACCTAG CC CT   TCCTCTCT
                                ||||||| || ||   ||||||||
                                ATGGATC GG GA   AGGAGAGA
                                    C  _  A__
GAM1457 PINK1   3' CCTTGGCCTGGATCCTCTCT   36867    AGA   CTCC
                                CCT   CCT    ATCCTCTCT
                                |||   |||    |||||||||
                                GGA   GGA    TAGGAGAGA
                                  ACC   CC__
GAM1457 POLD3   3' CTCTCCCTCTCCATCCTCTCT  36868    AGA
                                CT   CCTCTCCATCCTCTCT
                                ||   ||||||||||||||||
                                GA   GGAGAGGTAGGAGAGA
                                 GAG
GAM1457 PRO1331  3' TACTTGGAACCTCCTCCCTTCT 36869    CTA_     _  ATCC
             CT                   TAC    GACCTC TCC    TCTCT
                                |||    |||||| |||    |||||
                                ATG    TTGGAG AGG    AGAGA
                                  AACC     G   GA__
GAM1457 SEEK1   5' CTAGATGCCATCCTCTC     36870      CCTCT
                                CTAGA    CCATCCTCTC
                                |||||    ||||||||||
                                GATCT    GGTAGGAGAG
                                  AC___
GAM1457 WIRE    3' TACCTAGACTGGGGACCTCCAT 36871    C_____      CC    III
             TTTCTCTA               GAC     TCTCCAT  TCTCT   A
                                |||     |||||||  |||||  |
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                                CTG     GGAGGTA  AGAGA   T
                                  ACCCCT      AA    III
GAM1457  LOC145439 5'  CCTCAGGTCTGCGACCCTCTCT 36872     AGACC   CC_
                                CCT     TCT   ATCCTCTCT
                                |||     |||   |||||||||
                                GGA     AGA   TGGGAGAGA
                                  GTCC_   CGC
GAM1457  LOC148645 3'  TAGATCTGCTTCCTCTCC     36873      C  _  CCA
                                TAGA CT CT   TCCTCTCT
                                |||| || ||   ||||||||
                                ATCT GA GA   AGGAGAGG
                                  A  C  ___
GAM1457  LOC148887 3'  CTGGACCTCCGGGCCCTCTCT  36874     A      CCA
                                CT GACCTCT   TCCTCTCT
                                || |||||||   ||||||||
                                GA CTGGAGG   GGGAGAGA
                                 C      CCC
GAM1457  LOC149153 5'  CTAGGGCCTTTCACCCTCT    36875      A_   CTC
                                CTAG  CCT   CATCCTCT
                                ||||  |||   ||||||||
                                GATC  GGA   GTGGGAGA
                                  CC   AA_
GAM1457  LOC159184 3'  CCTTGGGCCACCTCCTCTCT   36876     AGACC  T  A
                                CCT     TC CC TCCTCTCT
                                |||     || || ||||||||
                                GGA     GG GG AGGAGAGA
                                  ACCC_  T  _
GAM1457  LOC200563 5'  CAGACCTCTCTCTACATTCTCT 36877           _____   C
                                TAGACCTCTC    CAT CTCT
                                ||||||||||    ||| ||||
                                GTCTGGAGAG    GTA GAGA
                                      AGAT   A
GAM1457  LOC200942 3'  CCCACATCCTCTCTATTCTCTC 36878      GA_     C  C
            T                    CCTA   CCTCTC AT CTCTCT
                                ||||   |||||| || ||||||
                                GGGT   GGAGAG TA GAGAGA
                                  GTA     A  A
GAM1457  LOC257443 3'  TAGATTTTTTTCCCCCTCTCT  36864     CCTC__   A
                                TAGA     TCC TCCTCTCT
                                ||||     ||| ||||||||
                                ATCT     AGG GGGAGAGA
                                  AAAAAA  _
GAM1457  LOC90538  3'  CTAGATTCCTCCTCTC      36879      CCTC   A
                                CTAGA    TCC TCCTCTC
                                |||||    ||| |||||||
                                GATCT    AGG AGGAGAG
                                  A___   _
GAM1458  CXCL16    5'  GCCCGCGCCATGCCAGCCTCT  36882     GAT  A
                                GCC   TG CTATGCCAGCCTCT
                                |||   || ||||||||||||||
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                                CGG   GC GGTACGGTCGGAGA
                                  GC_  _
GAM1458  DPH2L1   3'  ACCATGGTGCCAGCCTCT    36883      AT  ACTA
                                GCCG  TG    TGCCAGCCTCT
                                ||||  ||    ||||||||||
                                TGGT  AC    ACGGTCGGAGA
                                  __  C___
GAM1458  DYRK1A   3'  CCAGCTATGCCAGTCTCT    36884     ATTGA       C
                                CCG     CTATGCCAG CTCT
                                |||     ||||||||| ||||
                                GGT     GATACGGTC GAGA
                                  C____        A
GAM1458  NPTX1    3'  GACTGAACCTCATGCCAGCCTC 36885       _  __
              T                  GATTGA CT  ATGCCAGCCTCT
                                ||||||  ||  ||||||||||||
                                CTGACT GG  TACGGTCGGAGA
                                    T  AG
GAM1458  PBP      3'  AGCCTCAATGCCAGCCTCT    36886      GATTGACT
                                AGCC       ATGCCAGCCTCT
                                ||||       ||||||||||||
                                TCGG       TACGGTCGGAGA
                                  AGT_____
GAM1458  FLJ21324 5'  AGCTGATGTGGGGACTCAGCCT 36887    C   T____    ATGC
              CT                  GC GAT     GACT    CAGCCTCT
                                || |||     ||||    ||||||||
                                CG CTA     CTGA    GTCGGAGA
                                 A   CACCC   _____
GAM1458  ICK      3'  GATTGACTGTGTTAACCT    36888         A  CC
                                GATTGACT TG  AGCCT
                                ||||||||  ||  |||||
                                CTAACTGA AC  TTGGA
                                     C  AA
GAM1458  KIAA0152 3'  CGATTGAGCAGCCTC       36889        CTAT  C
                                CGATTGA    GC AGCCTC
                                |||||||    ||  ||||||
                                GCTAACT    CG TCGGAG
                                     _____  _
GAM1458  KIAA1163 3'  ACCGATTGAGGTCTCAGCCT   36890          CTATGC
                                GCCGATTGA      CAGCCT
                                |||||||||      ||||||
                                TGGCTAACT      GTCGGA
                                     CCAGA_
GAM1458  MGC2628  3'  ATTGGTCCTTGTCAGCCTC    36891      A_  A  C
                                ATTG  CT TG CAGCCTC
                                ||||  ||  ||  |||||||
                                TAAC  GG AC GTCGGAG
                                  CA  A  A
GAM1458  OVCA2    3'  ACCATCGTGCCAGCCTCT    36892     G    ACTA
                                GCC ATTG    TGCCAGCCTCT
                                |||  ||||    ||||||||||
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                                TGG TAGC   ACGGTCGGAGA
                                  _  ____
GAM1458 RNF38    3' AGCTGATTATTATGCCAA    36893    C    AC
                                AGC GATTG  TATGCCAG
                                ||| |||||  ||||||||
                                TCG CTAAT  ATACGGTT
                                  A    A_
GAM1458 LOC150445 3' AGCCTCAATGCCAGCCTCT   36886     GATTGACT
                                AGCC       ATGCCAGCCTCT
                                ||||       ||||||||||||
                                TCGG       TACGGTCGGAGA
                                  AGT_____
GAM1458 LOC154877 3' GATTGGTTGCACCAGCCTCT  36894      ACTAT
                                GATTG    GCCAGCCTCT
                                |||||    ||||||||||
                                CTAAC    TGGTCGGAGA
                                   CAACG
GAM1458 LOC163412 5' GCTGGGGAGATGCCAGCTTCT 36895    CGATT CT      C
                                GC    GA  ATGCCAGC TCT
                                ||    ||  |||||||| |||
                                CG    CT  TACGGTCG AGA
                                 ACCC_ C_      A
GAM1458 LOC200916 5' AGCCGATTAATTGCAGTGGCCT 36896         CTA   CA__
             CT                   AGCCGATTGA   TGC    GCCTCT
                                  ||||||||||   |||    ||||||
                                  TCGGCTAATT   ACG    CGGAGA
                                       A__   TCAC
GAM1458 LOC221410 3' AGCTGCTTGGCCTCCAGCCTCT 36897     CGA   A  ATG
                                AGC   TTG CT   CCAGCCTCT
                                |||   ||| ||   |||||||||
                                TCG   AAC GG   GGTCGGAGA
                                  ACG   C  A__
GAM1458 LOC221931 5' GCCACTCCATGCCAGCCTCT   36898     ATTGA
                                GCCG    CTATGCCAGCCTCT
                                ||||    ||||||||||||||
                                CGGT    GGTACGGTCGGAGA
                                  GA___
GAM1458 LOC90841  5' GCATGAAAGGTGCCAGCCTCT  36899    CGAT   CTA_
                                GC    TGA    TGCCAGCCTCT
                                ||    |||    ||||||||||
                                CG    ACT    ACGGTCGGAGA
                                 T___   TTCC
GAM1458 LOC91097  3' AGCTGATGTGGGGACTCAGCCT 36887    C   T____    ATGC
             CT                   GC GAT    GACT    CAGCCTCT
                                  || |||    ||||    ||||||||
                                  CG CTA    CTGA    GTCGGAGA
                                   A  CACCC   ____
GAM1459 ADAMTS5   3' TGACAAGGGGGAGACAGT    36902        A  T    T
                                TGACAAGG GG GATG GT
                                |||||||| || |||| ||
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                                ACTGTTCC CC CTGT CA
                                    C  T   _
GAM1459 BACE    3' TGATAGGGAGGTAATGAACT  36903    CAA       TGT
                                TGA  GGAGGTGATG  GACT
                                |||  ||||||||||  ||||
                                ACT  CCTCCATTAC  TTGA
                                  ATC       ___
GAM1459 BACE    3' TGATAGGGAGGTAATGAACT  36903    CAA       TGT
                                TGA  GGAGGTGATG  GACT
                                |||  ||||||||||  ||||
                                ACT  CCTCCATTAC  TTGA
                                  ATC       ___
GAM1459 CBFB    3' AAGGAGGTGCCAAATGACT   36904       ATGT
                                AAGGAGGTG   GTGACT
                                |||||||||   ||||||
                                TTCCTCCAC   TACTGA
                                     GGTT
GAM1459 CBFB    3' AAGGAGGTGCCAAATGACT   36904       ATGT
                                AAGGAGGTG   GTGACT
                                |||||||||   ||||||
                                TTCCTCCAC   TACTGA
                                     GGTT
GAM1459 CHST6   3' TGCAGGGAGGATGTGACT    36905    A A    TGAT
                                TG CA GGAGG   GTGTGACT
                                || || |||||   ||||||||
                                AC GT CCTCC   TACACTGA
                                 _ C    ____
GAM1459 CPT2    3' TGATGAGGAAGTGATGGTAGCT 36906    CA        T  A
                                TGA  AGGAGGTGATG GTG CT
                                |||  |||||||||| ||| ||
                                ACT  TCCTTCACTAC CAT GA
                                  AC         _  C
GAM1459 PYCR1   5' TGAAGGGGATGATGTGTGGCT  36907   C   A       A
                                A AAGG GGTGATGTGTG CT
                                | |||| |||||||||| ||
                                A TTCC CTACTACACAC GA
                                 C   C         C
GAM1459 C11orf21 3' GGCAGTGTGTGTGACTC    36908    A   A
                                GG GGTG TGTGTGACTC
                                || |||| ||||||||||
                                CC TCAC ACACACTGAG
                                 G   _
GAM1459 COLEC12  3' TGATGAGAAGGTGATGCA    36909    CA
                                TGA  AGGAGGTGATGTG
                                |||  ||||||||||||
                                ACT  TCTTCCACTACGT
                                  AC
GAM1459 COLEC12  3' TGATGAGAAGGTGATGCA    36909    CA
                                TGA  AGGAGGTGATGTG
                                |||  ||||||||||||
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                                ACT  TCTTCCACTACGT
                                  AC
GAM1459  FBXO2     3'  GGAGGAGGATGTGTGGCT    36910      T_      A
                                GGAGG  GATGTGTG CT
                                |||||  |||||||| ||
                                CCTCC  CTACACAC GA
                                   TC       C
GAM1459  FLJ10241  3'  TGACAAGGTGAGTGTGGCT    36911      AGG     T    A
                                TGACA   AGGTGA GTGTG CT
                                |||||   |||||| ||||| ||
                                ACTGT   TCCACT CACAC GA
                                   ____     _    C
GAM1459  FLJ10743  3'  ACAAGGAGGGAGGTGACT    36912        T  TGT
                                ACAAGGAGG GA   GTGACT
                                |||||||||| ||   ||||||
                                TGTTCCTCC CT   CACTGA
                                     _ C__
GAM1459  FLJ10829  3'  GAAAGGAGGTGACGTCACTC   36913    C          GTG
                                GA AAGGAGGTGATGT   ACTC
                                || ||||||||||||   ||||
                                CT TTCCTCCACTGCA   TGAG
                                 _          G__
GAM1459  FLJ12816  3'  GACAGGGAGGTAAGAGTGACTC 36914      A       TGT
                                GACA GGAGGTGA   GTGACTC
                                |||| ||||||||   |||||||
                                CTGT CCTCCATT   CACTGAG
                                  C       CT_
GAM1459  FLJ21777  3'  TGACAGGTGGGCGCAGTGACTC 36915      A  A_    ATGT
                                TGACA GG  GGTG    GTGACTC
                                ||||| ||  ||||    |||||||
                                ACTGT CC  CCGC    CACTGAG
                                   _ AC    GT__
GAM1459  HTMP10    3'  GGTCAGGGAATGTGTGGCTC   36916    __   TG      A
                                GG  AGG  ATGTGTG CTC
                                ||  |||  ||||||| |||
                                CC  TCC  TACACAC GAG
                                 AG   CT      C
GAM1459  KIAA0140  3'  GGAGGTGGCTGTGACTC     36917       ATG
                                GGAGGTG   TGTGACTC
                                |||||||   ||||||||
                                CCTCCAC   ACACTGAG
                                    CG_
GAM1459  KIAA1613  3'  GGAGGTGATTTATCAACT    36918        G  _
                                GGAGGTGAT TGT GACT
                                ||||||||| ||| ||||
                                CCTCCACTA ATA TTGA
                                     A  G
GAM1459  MRPL3     3'  TGACAAAGATGACATGTGTGA  36919        GGTG
                                TGACAAGGA    ATGTGTGA
                                |||||||||    ||||||||
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                                ACTGTTTCT   TACACACT
                                     ACTG
GAM1459 SAST     5' TGATAAGGAGGCTGTA     36920    C      GA
                                TGA AAGGAGGT  TGTG
                                ||| ||||||||  ||||
                                ACT TTCCTCCG  ACAT
                                  A       __
GAM1459 SC4MOL   3' GACAAGGAGACAGAGTGTGGCT 36921         GT AT    A
                                GACAAGGAG  G  GTGTG CT
                                |||||||||  |  ||||| ||
                                CTGTTCCTC  T  CACAC GA
                                     TG CT    C
GAM1459 SLC34A1  3' TGGCAAGGAGGTGTGCA    36922    A        A
                                TG CAAGGAGGTG TGTG
                                || ||||||||| ||||
                                AC GTTCCTCCAC ACGT
                                 C        _
GAM1459 STHM     3' TGACAAGGTGGTGATACAT   36923        A      TG
                                TGACAAGG GGTGATG  T
                                |||||||| |||||||  |
                                ACTGTTCC CCACTAT  A
                                     A      GT
GAM1459 STX12    5' TGACGAGGAGCTGAGACCTGCT 36924     A    G   TG G  A
           C                     TGAC AGGAG TGA  T TG CTC
                                |||| ||||| |||  | || |||
                                ACTG TCCTC ACT  G AC GAG
                                  C    G   CT G  _
GAM1459 LOC112687 3' CAAGGAGGTGAGCCACTC    36925          TGT  G
                                CAAGGAGGTGA   GT ACTC
                                ||||||||||   || ||||
                                GTTCCTCCACT   CG TGAG
                                       ___  G
GAM1459 LOC124538 3' TGAAAAGGAAGGTGTG      36926    C      TGAT
                                TGA AAGGAGG    GTGTG
                                ||| |||||||    |||||
                                ACT TTCCTTC    CACAC
                                  T      _____
GAM1459 LOC134266 3' TGACAAGGAGGCTGAAAATAA  36927          _   TGT
                                TGACAAGGAGG TGA   GTGA
                                ||||||||||| |||   ||||
                                ACTGTTCCTCC ACT   TATT
                                       G   TT_
GAM1459 LOC144519 5' TGAAAGGAGGTTTTATTGGCT  36928    C      GA   G  A
                                TGA AAGGAGGT  TGT TG CT
                                ||| ||||||||  ||| || ||
                                ACT TTCCTCCA  ATA AC GA
                                  _       AA   _  C
GAM1459 LOC146227 3' TGGCAGGGTGGTGATGTTGTGG 36929    A  A  A      _   A
           CTC                    TG CA GG GGTGATGT GTG CTC
                                || || || |||||||| ||| |||
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                                AC GT CC CCACTACA CAC GAG
                                 C  C  A       A   C
GAM1459  LOC163081 5'  TGACGAATGAGGTGTGACT   36930     AAG   G   T
                                TGAC   GAG TGA GTGTGACT
                                ||||   ||| ||| ||||||||
                                ACTG   CTT ACT CACACTGA
                                  ___   _   C
GAM1459  LOC256942 3'  GGCAGGGAGATGTGTGGCTC   36931    _   T_      A
                                GG AGG  GATGTGTG CTC
                                || |||  |||||||| |||
                                CC TCC  CTACACAC GAG
                                 G   CT       C
GAM1460  ARVCF     3'  TCAGTGTTTTTCTTCTG     36934      A     GATCA
                                TCAG TGTTTT    CTTCTG
                                |||| ||||||    ||||||
                                AGTC ACAAAA    GAAGAC
                                  _     A____
GAM1460  M6PR      3'  GATGTCCCACTTCTGC      36935       TTGA
                                GATGTT    TCACTTCTGC
                                ||||||    ||||||||||
                                CTACAG    GGTGAAGACG
                                    ____
GAM1460  ORC3L     3'  CAGGTGTTTTGATACATGCC   36936     A       C  TTC
                                CAG TGTTTTGAT AC   TGCC
                                ||| |||||||| ||   ||||
                                GTC ACAAAACTA TG   ACGG
                                  C        _ T__
GAM1460  BANP      5'  AAATGTATCATCATTTCTG    36937       T  G    C
                                AGATGT TT ATCA TTCTG
                                |||||| || |||| |||||
                                TTTACA AG TAGT AAGAC
                                   T  _    A
GAM1460  C20orf108 3'  AGATGTTTTATTCTGC      36938          ATCAC
                                AGATGTTTTG    TTCTGC
                                ||||||||||    ||||||
                                TCTACAAAAT    AAGACG
                                    _____
GAM1460  C2F       3'  AGATAAAATCACTTCTG     36939       TTTT
                                AGATG   GATCACTTCTG
                                |||||   ||||||||||
                                TCTAT   TTAGTGAAGAC
                                   T___
GAM1460  CHAF1B    3'  TCAGTACACATGTCACTTCTG  36940     _ TG TT  A
                                TCAG A  T  TG TCACTTCTG
                                |||| |  |  || |||||||||
                                AGTC T  G  AC AGTGAAGAC
                                  A GT T_  _
GAM1460  FADS1     3'  TCCCAATTTGGTCACTTCTGC  36941    AGATGT    A
                                TC     TTTG TCACTTCTGC
                                ||     |||| ||||||||||
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                                AG     AAAC AGTGAAGACG
                                 GGTT__   C
GAM1460  FLJ12921  3'  CCAGTGGTCACTTCTG     36942     ATGTTT  A
                                TCAG     TG TCACTTCTG
                                ||||     || |||||||||
                                GGTC     AC AGTGAAGAC
                                  _______  C
GAM1460  FLJ14280  3'  CAGGTGAGGGCTCACTTCTGCC 36943     A  TTTTGA
                                CAG TG     TCACTTCTGCC
                                ||| ||     ||||||||||
                                GTC AC     AGTGAAGACGG
                                  C  TCCCG_
GAM1460  KIAA0220  5'  AAATGTATCATCATTTCTG   36937       T  G   C
                                AGATGT TT ATCA TTCTG
                                |||||| || |||| |||||
                                TTTACA AG TAGT AAGAC
                                   T  _   A
GAM1460  KIAA0603  3'  TCAGATGTTTGTCATCTG    36944         T A   CT
                                TCAGATGTTT G TCA  TCTG
                                |||||||||| | |||  ||||
                                AGTCTACAAA C AGT  AGAC
                                      _ _  __
GAM1460  MGC26610  3'  AATGTCTTTTATTTCTGCC   36945        GATCAC
                                GATGTTTT     TTCTGCC
                                ||||||||     |||||||
                                TTACAGAA     AAGACGG
                                     AATA__
GAM1460  PDCD5     3'  TCAGATCTTAACTTCTG     36946       G  TTGATC
                                TCAGAT TT     ACTTCTG
                                |||||| ||     |||||||
                                AGTCTA AA     TGAAGAC
                                   G  T_____
GAM1460  TCL6      3'  CCAGAGATCACTTTTG      36947       TGTTTT       C
                                TCAGA     GATCACTT TG
                                |||||     |||||||| ||
                                GGTCT     CTAGTGAA AC
                                  _______       A
GAM1460  TCL6      3'  CCAGAGATCACTTTTG      36947       TGTTTT       C
                                TCAGA     GATCACTT TG
                                |||||     |||||||| ||
                                GGTCT     CTAGTGAA AC
                                  _______       A
GAM1460  VELI1     3'  TCGGATGTTTGATCAAGTAGC  36948    A      T    CTTCT
                                TC GATGTTT GATCA     GC
                                || ||||||| |||||     ||
                                AG CTACAAA CTAGT     CG
                                 C       _     TCAT_
GAM1460  LOC124302 5'  AAATGTATCATCATTTCTG   36937       T  G   C
                                AGATGT TT ATCA TTCTG
                                |||||| || |||| |||||
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                                TTTACA AG TAGT AAGAC
                                   T _   A
GAM1460  LOC146667 3'  TCGGATGTTTTGAGTCACC   36949    A       _
                                TC GATGTTTTGA TCACT
                                || |||||||||| |||||
                                AG CTACAAAACT AGTGG
                                 C        C
GAM1460  LOC152502 3'  TCAGATATTAAATTCTACTTTT 36950        TTGA _   C
           GCC                    TCAGATGTT   TC ACTT TGCC
                                |||||||||   || |||| ||||
                                AGTCTATAA   AG TGAA ACGG
                                     TTTA  A   A
GAM1460  LOC197358 3'  TCAATTCTGTCACTTCTG    36951    GAT    A
                                TCA  GTTTTG TCACTTCTG
                                |||  |||||| |||||||||
                                AGT  TAAGAC AGTGAAGAC
                                 ___    _
GAM1460  LOC219972 3'  GTCCCAGAATCACTTTTGC    36952     __     C
                                GTTTT  GATCACTT TGC
                                |||||  |||||||| |||
                                CAGGG  TTAGTGAA ACG
                                   TC      A
GAM1460  LOC90190  3'  TCAGCTGAGGTCTTGCTTCTGC 36953    AT___    ATCA
           C                    TCAG    GTTTTG   CTTCTGCC
                                ||||    ||||||   ||||||||
                                AGTC    CAGAAC   GAAGACGG
                                  GACTC    ____
GAM1461  ABCD3    3'  TCACTGAAGCAGGTATAG    36956          GAT
                                TCACTGAAGCGGG  TGG
                                ||||||||||||  |||
                                AGTGACTTCGTCC  ATC
                                       AT_
GAM1461  FLJ13848  3'  CCTCACTGAGGCAGCGAGGGGC 36957        A   G  TT
                                CCTCACTGA GCGG GA  GGC
                                ||||||||| |||| ||  |||
                                GGAGTGACT CGTC CT  CCG
                                     C   G  CC
GAM1461  KIAA0255  3'  ACCTCACTGAAGCTCTGG    36958          GGGGAT
                                ACCTCACTGAAGC     TGG
                                ||||||||||||     |||
                                TGGAGTGACTTCG     ACC
                                       AG____
GAM1461  KIAA1163  3'  TACCACACTGAGAATTGG    36959    T    AGCGG
                                TACC CACTGA    GGATTGG
                                |||| ||||||    |||||||
                                ATGG GTGACT    CTTAACC
                                  T    _____
GAM1461  PDE10A   3'  CCTCACAGAAGAGATTGGC   36960      T  AGC
                                CCTCAC GA   GGGGATTGGC
                                |||||| ||  ||||||||||
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                                GGAGTG CT   TCTCTAACCG
                                   T ___
GAM1461  TEX27    3'  CCTCACTGAGGATGGC      36961        AGCGG   T
                                CCTCACTGA    GGAT GGC
                                |||||||||    |||| |||
                                GGAGTGACT    CCTA CCG
                                     _____   _
GAM1461  LOC146895 5'  TACCTCACTGGGCCTTGG    36962        GAAGC   GA
                                TACCTCACT    GGG  TTGG
                                |||||||||    |||  ||||
                                ATGGAGTGA    CCC  AACC
                                     _____  GG
GAM1461  LOC149734 3'  CTTACTAAGTGAATTGGC    36963    C    AGCGG
                                CT ACTGA     GGATTGGC
                                || |||||    ||||||||
                                GA TGATT     CTTAACCG
                                 A    CA___
GAM1461  LOC157292 3'  TCACTGAAGAAATGTTGG    36964        C   GA
                                TCACTGAAG GGG  TTGG
                                ||||||||| |||  ||||
                                AGTGACTTC TTT  AACC
                                     _  AC
GAM1461  LOC203378 3'  TCACTGAAGAGTTGG       36965        AGC   A
                                TCACTGA   GGGG TTGG
                                |||||||   |||| ||||
                                AGTGACT   TCTC AACC
                                     ___   _
GAM1461  LOC205355 5'  CCTCACTGGTGGTGATTATGGC 36966        AAGCG _  __
                                CCTCACTG     GG GAT  TGGC
                                ||||||||     || |||  ||||
                                GGAGTGAC     CC CTA  ACCG
                                     CA___  A   AT
GAM1461  LOC222484 3'  CCTCACTGTGACTTAAATTGG  36967        AA  GG
                                CCTCACTG  GC  GGATTGG
                                ||||||||  ||  |||||||
                                GGAGTGAC  TG  TTTAACC
                                     AC  AA
GAM1462  RAD54B   3'  TCGAAGTTCGTGGATAAC     36970          CC
                                TCGAAGTTCGTGG  AAC
                                ||||||||||||  |||
                                AGCTTCAAGCACC  TTG
                                      TA
GAM1462  FLJ21687  3'  CGAAGCTCGTCAGCGATTAC  36971         GGC  A   C
                                CGAAGTTCGT   CA CGA TAC
                                ||||||||||   || ||| |||
                                GCTTCGAGCA   GT GCT ATG
                                     ___  C   A
GAM1462  LOC144108 3'  TCGAAGTTCATGTGGACT    36972          GCCAAC
                                TCGAAGTTCGTG     GACT
                                ||||||||||||     ||||
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                                AGCTTCAAGTAC     CTGA
                                      AC____
GAM1462  LOC204823 3'  TCAAAGGGAAGTGTTGACGACT 36973       TTC_   GCCA
              AC                  TCGAAG   GTG   ACGACTAC
                                  ||||||   |||   ||||||||
                                  AGTTTC   CAC   TGCTGATG
                                     CCTT   AAC_
GAM1462  LOC254268 3'  TCAAAGTCACCAACGA      36974        CGTG
                                  TCGAAGTT   GCCAACGA
                                  ||||||||   ||||||||
                                  AGTTTCAG   TGGTTGCT
                                       ____
GAM1462  LOC92305  5'  TCGAAATTCATGGGGCGACT   36975           CCAA
                                  TCGAAGTTCGTGG   CGACT
                                  ||||||||||||   |||||
                                  AGCTTTAAGTACC   GCTGA
                                        CC__
GAM1463  KIAA1254  3'  CGGTAACCTTACAAGA     36978    A   CCCA
                                  CG GTA   ACCTTACAAGA
                                  || |||   ||||||||||
                                  GC CAT   TGGAATGTTCT
                                   _  ____
GAM1463  LOC152739 5'  GAGTACCTGATCCCACAAG   36979        CAAC
                                  GAGTACC   CTTACAAG
                                  |||||||   ||||||||
                                  CTCATGG   GGGTGTTC
                                      ACTA
GAM1464  PKIG     3'  GAATTGATTGTCAGCTCTCT   36982      A___  C
                                  GAGT   TG TCAGCTCTCT
                                  ||||   || ||||||||||
                                  CTTA   AC AGTCGAGAGA
                                    ACTA  _
GAM1464  TFAP2A   5'  GAACGGATATGCCCCTCT    36983      AG     AG
                                  GAACG  TATGCTC  CTCT
                                  |||||  |||||||  ||||
                                  CTTGC  ATACGGG  GAGA
                                     CT      __
GAM1464  THY1     3'  GCTGGAGATGCTCAGTTCTCT  36984    GAAC   T      C
                                  GC   GAG ATGCTCAG TCTCT
                                  ||   ||| ||||||| |||||
                                  CG   CTC TACGAGTC AGAGA
                                   AC__  _      A
GAM1464  UQCRC2   3'  GAGAACGTTCAGCTCTCT    36985     T   C
                                  GAG ATG TCAGCTCTCT
                                  ||| ||| ||||||||||
                                  CTC TGC AGTCGAGAGA
                                    T   A
GAM1464  ALOXE3   5'  GAGGATGGGCCCAGCTCTC   36986     T  __
                                  GAG AT  GCTCAGCTCTC
                                  ||| ||  ||||||||||
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                                CTC TA  CGGGTCGAGAG
                                  C  CC
GAM1464  C14orf4   5'  GCGGACGGGTTCAGCCCTCT   36987     A   A  ATGC
                                GCG ACG GT    TCAGCTCTCT
                                ||| ||| ||    ||||||||||
                                CGC TGC CA    AGTCGGGAGA
                                  C   C  ____
GAM1464  DNAJC6    3'  GCAGGTGAGTGCAGCTCTC    36988     AAC    ATGCT
                                GCG   GAGT    CAGCTCTC
                                |||   ||||    ||||||||
                                CGT   CTCA    GTCGAGAG
                                  CCA    C____
GAM1464  SYT12     3'  GCGACATGCTCAGTTCT     36989      ACGAG       C
                                GCGA     TATGCTCAG TCT
                                ||||     ||||||||| |||
                                CGCT     GTACGAGTC AGA
                                  _____         A
GAM1464  LOC253842 3'  GAACCACAGCTCAGCTTTCT   36990      GAGTAT      C
                                GAAC     GCTCAGCT TCT
                                ||||     |||||||| |||
                                CTTG     CGAGTCGA AGA
                                  GTGT__       A
GAM1464  LOC256520 3'  GCAATGGCGCGATCTCAGCTCT 36991      ACGA  ATG
            CT                    GCGA    GT   CTCAGCTCTCT
                                ||||    ||   ||||||||||||
                                CGTT    CG   GAGTCGAGAGA
                                  ACCG  CTA
GAM1464  LOC58525  3'  GCAGGTGAGTTCCAGCTCTCT  36992     AAC    ATGC
                                GCG   GAGT    TCAGCTCTCT
                                |||   ||||    ||||||||||
                                CGT   CTCA    GGTCGAGAGA
                                  CCA    A___
GAM1465  AP1G1     3'  TTCTTGGTAACAAACATAC    36995          AT
                                TTCTTGGTGA  AACATAC
                                ||||||||||  |||||||
                                AAGAACCATT  TTGTATG
                                      GT
GAM1465  CRY2      3'  TTTCTAGTGAAGGTGACATAC  36996       T     TA__
                                TTTCT GGTGAA    ACATAC
                                ||||| ||||||    ||||||
                                AAAGA TCACTT    TGTATG
                                  _     CCAC
GAM1465  CSNK1G3   3'  TTTCTTGCTGTCTAACATAC   36997        G  AA
                                TTTCTTG TG  TAACATAC
                                ||||||| ||  ||||||||
                                AAAGAAC AC  ATTGTATG
                                    G  AG
GAM1465  CYB561    3'  TTTCTTGGAGAACCATA     36998         T   AA
                                TTTCTTGG GAAT  CATA
                                |||||||| ||||  ||||
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                                AAAGAACC CTTG  GTAT
                                     T   __
GAM1465  FBXL3A   3'  CTTCTTGGATATTATAACATA  36999        TGA__
                                TTTCTTGG    ATAACATA
                                ||||||||    ||||||||
                                GAAGAACC    TATTGTAT
                                     TATAA
GAM1465  HGF      3'  TTTCTTGATGCCAGCACATA  37000        AATA_
                                TTTCTTGGTG    ACATA
                                ||||||||||    |||||
                                AAAGAACTAC    TGTAT
                                      GGTCG
GAM1465  NEBL     3'  TTCCTTGAATATAACATA    37001        TGA
                                TTTCTTGG   ATAACATA
                                ||||||||   ||||||||
                                AAGGAACT   TATTGTAT
                                     TA_
GAM1465  SCD      3'  TTTCTTGGAGAACCATA     36998        T   AA
                                TTTCTTGG GAAT  CATA
                                |||||||| ||||  ||||
                                AAAGAACC CTTG  GTAT
                                     T   __
GAM1465  SLC6A3   3'  TTTCCTGGTGAGACATAC    37002         ATA
                                TTTCTTGGTGA   ACATAC
                                ||||||||||   ||||||
                                AAAGGACCACT   TGTATG
                                      C__
GAM1465  AKR1D1   3'  TTTCTTGTGAACAAAATA    37003       G     C
                                TTTCTTG TGAATAA ATA
                                ||||||| ||||||| |||
                                AAAGAAC ACTTGTT TAT
                                    _      T
GAM1465  CYP2C18  3'  TTTCTAGTGATAACATAC    37004      T    A
                                TTTCT GGTGA TAACATAC
                                ||||| ||||| ||||||||
                                AAAGA TCACT ATTGTATG
                                    _    _
GAM1465  DKFZP434I0714 5'  TTTCTTGATGACAACGTAC   37005          A   A
                                TTTCTTGGTGA TAAC TAC
                                |||||||||| |||| |||
                                AAAGAACTACT GTTG ATG
                                      _   C
GAM1465  FLJ11040 3'  TCTCTGTAGATAACATAC    37006     G  A
                                TCTT GTG ATAACATAC
                                |||| ||| |||||||||
                                AGAG CAT TATTGTATG
                                  A  C
GAM1465  FLJ11795 3'  TTTCCTACTGATAACATA    37007       G  A
                                TTTCTTG TGA TAACATA
                                ||||||| ||| |||||||
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                                AAAGGAT ACT ATTGTAT
                                   G  _
GAM1465  FLJ13194  3'  TTCCTCCTTAAATAACAT    37008       GG
                                TTTCTT  TGAATAACAT
                                ||||||  ||||||||||
                                AAGGAG  ATTTATTGTA
                                   GA
GAM1465  HSD17B12  3'  TTTCTTGGTGAGTTCTCCATAC 37009          ATAA__
                                TTTCTTGGTGA     CATAC
                                ||||||||||      |||||
                                AAAGAACCACT     GTATG
                                      CAAGAG
GAM1465  POT1      3'  TCTTTGGCAAATAACATAC   37010      _  TG
                                TCTT GG  AATAACATAC
                                ||||  ||  ||||||||||
                                AGAA CC  TTATTGTATG
                                  A  GT
GAM1465  PRO0159   5'  TTCTCAAAAAATAACATA    37011      TG T
                                TTCT  G GAATAACATA
                                ||||  | ||||||||||
                                AAGA  T TTTATTGTAT
                                  GT T
GAM1465  PSIP1     3'  TTTCTAGATGAATAATGTAC  37012       T       CA
                                TTTCT GGTGAATAA  TAC
                                |||||  |||||||||  |||
                                AAAGA CTACTTATT  ATG
                                   T        AC
GAM1465  RAI       5'  TTCCTTGGGCTGTGAATAATAT 37013         ____       C
              AC                  TTTCTTGG    TGAATAA ATAC
                                ||||||||    ||||||| ||||
                                AAGGAACC    ACTTATT TATG
                                     CGAC      A
GAM1465  LOC124470 3'  TCTCTTGGACAACATAC     37014         TGA
                                TTTCTTGG   ATAACATAC
                                ||||||||   |||||||||
                                AGAGAACC   TGTTGTATG
                                           ___
GAM1465  LOC149132 5'  TTCCCACCTGAATAACAT    37015       TGG
                                TTTCT   TGAATAACAT
                                |||||   ||||||||||
                                AAGGG   ACTTATTGTA
                                   TGG
GAM1465  LOC197387 3'  TTTCTTGGAGAAAGTCTGACAT 37016         T   TA____
                                TTTCTTGG GAA      ACAT
                                |||||||| |||      ||||
                                AAAGAACC CTT      TGTA
                                     T   TCAGAC
GAM1465  LOC201283 3'  TTTCTTGGGAGACCTAAACATA 37017         T_  AT__
                                TTTCTTGG  GA    AACATA
                                ||||||||  ||    ||||||
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                                AAAGAACC CT   TTGTAT
                                    CT GGAT
GAM1465 LOC221399 5' TTTCTTGGTAATAGCAC    37018        A A
                                TTTCTTGGTGA TA CAT
                                |||||||||| || |||
                                AAAGAACCATT AT GTG
                                      _ C
GAM1465 LOC90410 5' TTTCTTGAGTGCCTACTACAT 37019      _ AA __
                                TTTCTTG GTG TA ACAT
                                ||||||| ||| || ||||
                                AAAGAAC CAC AT TGTA
                                    T GG GA
GAM1466 FAAH    3' CAGTACAAATCACAAGGT   37022    C     _
                                CAG ACAAATCA AAGGT
                                ||| |||||||| |||||
                                GTC TGTTTAGT TTCCA
                                  A      G
GAM1466 GOCAP1  3' AACACAAATTAAAGCTAT   37023       C  G
                                AGCACAAAT AAAG TAT
                                ||||||||| ||||| |||
                                TTGTGTTTA TTTC ATA
                                    A  G
GAM1466 IL13RA1 3' AGCACAAACCAAAGACAC   11624         GT
                                AGCACAAATCAAAG AT
                                |||||||||||||| ||
                                TCGTGTTTGGTTTC TG
                                      TG
GAM1466 IMPA1   3' CAGCACAATCAAATCAGTA  11625      A  __
                                CAGCACAA TCAAA GGTA
                                |||||||| ||||| ||||
                                GTCGTGTT AGTTT TCAT
                                    _  AG
GAM1466 KLHL3   3' CAGCACAAACTAGAAAATA  11627       CA_
                                CAGCACAAAT  AAGGTA
                                |||||||||| ||||||
                                GTCGTGTTTG  TTTTAT
                                     ATC
GAM1466 MMP10   3' CAGTGCAATTCAAAAGCA   11628    CA A
                                CAG CAA TCAAAGGTA
                                ||| ||| |||||||||
                                GTC GTT AGTTTTCGT
                                  AC A
GAM1466 MPL     3' CAGCGAGATCAAAGGAACT  37024    ACAA     T
                                CAGC  ATCAAAGG ATT
                                ||||  |||||||| |||
                                GTCG  TAGTTTCC TGA
                                  CTC_     T
GAM1466 NOTCH2  3' CAGACAAATCAGGTA      37025    C      AA
                                CAG ACAAATCA GGTA
                                ||| |||||||| ||||
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                                GTC TGTTTAGT  CCAT
                                  _     __
GAM1466 PRKG1    3' CAGCATCGATCAAAGGCATCA 37026      CAA
                                CAGCA  ATCAAAGGTATTA
                                |||||  ||||||||||||
                                GTCGT  TAGTTTCCGTAGT
                                   AGC
GAM1466 SCAP2    3' ACACAAATCAAATGGGTA    37027         __
                                GCACAAATCAAA  GGTA
                                ||||||||||||  ||||
                                TGTGTTTAGTTT  CCAT
                                      AC
GAM1466 SLC14A2  5' CAGTAAAATCAAAAGCA     11630     CAC
                                CAG  AAATCAAAGGTA
                                |||  ||||||||||||
                                GTC  TTTAGTTTTCGT
                                  AT_
GAM1466 USP6     3' AACACAAATCACACAACATTA 37028         AA_
                                AGCACAAATCA  GGTATTA
                                ||||||||||  |||||||
                                TTGTGTTTAGT  TTGTAAT
                                      GTG
GAM1466 AFAP     3' CAGCACAAATAATTAATTAATA 11631        CAAAGGT
                                CAGCACAAAT     ATTAATA
                                |||||||||      |||||||
                                GTCGTGTTTA     TAATTAT
                                     TTAAT__
GAM1466 C20orf27 3' CAGCACAAATGAAGGCA     37029        CA
                                CAGCACAAAT  AAGGTA
                                |||||||||  ||||||
                                GTCGTGTTTA  TTCCGT
                                     C_
GAM1466 HSPC228  3' CAGCACAAATGCAGGTA     37030        CAA
                                CAGCACAAAT  AGGTA
                                |||||||||  |||||
                                GTCGTGTTTA  TCCAT
                                     CG_
GAM1466 KIAA0240 3' GCACAAATAAGGAAAAAAT   37031        CA   TATT
                                GCACAAAT  AAGG   AAT
                                ||||||||  ||||   |||
                                CGTGTTTA  TTCC   TTA
                                    __   TTTT
GAM1466 KIAA0438 3' AGCAAAATCAAAGGGACTA   37032     C       T
                                AGCA AAATCAAAGG ATTA
                                ||||  |||||||||| ||||
                                TCGT TTTAGTTTCC TGAT
                                  _       C
GAM1466 KIAA0820 3' AACACAAATCAAGTAGTA    11635         A_
                                AGCACAAATCAA  GGTA
                                ||||||||||||  ||||
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                                TTGTGTTTAGTT  TCAT
                                      CA
GAM1466  KIAA1054  3'  CAGCACAAATGCAATAAT    11636          _  AG
                                CAGCACAAAT CAA  GT
                                |||||||||| |||  ||
                                GTCGTGTTTA GTT  TA
                                     C   AT
GAM1466  KIAA1530  3'  CAGCACTGATCAAGGCACT   37033       AA    A
                                CAGCAC  ATCAA GGTATT
                                ||||||  ||||| ||||||
                                GTCGTG  TAGTT CCGTGA
                                   AC    _
GAM1466  MDN1      3'  AGCACAGCATCAACTAGTA   11637       A_    A_
                                AGCACA  ATCAA  GGTA
                                ||||||  |||||  ||||
                                TCGTGT  TAGTT  TCAT
                                   CG    GA
GAM1466  RINZF     3'  CAGCACAAAATCGAGAAATAAT 11638         TCAA   TAT
              A                  CAGCACAAA   AGG   TAATA
                                 |||||||||   |||  |||||
                                 GTCGTGTTT   TCT   ATTAT
                                      TAGC   TT_
GAM1466  LOC134111 3'  AGCACAAATGAGGTCTAAAT   37034         CAA   ATT
                                AGCACAAAT   AGGT   AAT
                                |||||||||  ||||  |||
                                TCGTGTTTA   TCCA   TTA
                                     C__    GAT
GAM1466  LOC219376 3'  AGCACAGAATTAAAGATA    37035       _  C
                                AGCACA AAT AAAGGTA
                                |||||| ||| |||||||
                                TCGTGT TTA TTTCTAT
                                   C   A
GAM1466  LOC222223 5'  CAGCATAGATCAAAGACACC   37036      CAA      GT
                                CAGCA   ATCAAAG  ATT
                                |||||   |||||||  |||
                                GTCGT   TAGTTTC  TGG
                                   ATC      TG
GAM1467  CIT       3'  TGAGCTGCGGCTGCTTTCTCAA 37039     A  ACAT    A
              A                  TGA CT    GTTGT TTCTCAAA
                                 ||| ||    ||||| ||||||||
                                 ACT GA    CGACG AAGAGTTT
                                   C  CGC_    A
GAM1467  CYB561    3'  TGTTTATGTATTCTCAAA    37040     ___
                                TGT   TGTATTCTCAAA
                                |||   ||||||||||||
                                ACA   ACATAAGAGTTT
                                  AAT
GAM1467  MBNL      3'  TGACACTACATGTAATTC    37041     _       TGT
                                TGA ACTACATGT   ATTC
                                ||| |||||||||   ||||
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                                ACT TGATGTACA   TAAG
                                  G       T__
GAM1467  MDM2    3'  TGAGCTACATATTCAAGTCAAA 37042    A       G  TTC
                                TGA CTACATGTT TA   TCAAA
                                ||| ||||||||| ||   |||||
                                ACT GATGTATAA GT   AGTTT
                                  C       _ TC_
GAM1467  MDM2    3'  TGAGCTACATATTCAAGTCAAA 37042    A       G  TTC
                                TGA CTACATGTT TA   TCAAA
                                ||| ||||||||| ||   |||||
                                ACT GATGTATAA GT   AGTTT
                                  C       _ TC_
GAM1467  MDM2    3'  TGAGCTACATATTCAAGTCAAA 37042    A       G  TTC
                                TGA CTACATGTT TA   TCAAA
                                ||| ||||||||| ||   |||||
                                ACT GATGTATAA GT   AGTTT
                                  C       _ TC_
GAM1467  MDM2    3'  TGAGCTACATATTCAAGTCAAA 37042    A       G  TTC
                                TGA CTACATGTT TA   TCAAA
                                ||| ||||||||| ||   |||||
                                ACT GATGTATAA GT   AGTTT
                                  C       _ TC_
GAM1467  MDM2    3'  TGAGCTACATATTCAAGTCAAA 37042    A       G  TTC
                                TGA CTACATGTT TA   TCAAA
                                ||| ||||||||| ||   |||||
                                ACT GATGTATAA GT   AGTTT
                                  C       _ TC_
GAM1467  MEN1    5'  TGAACTACCATGTCAACATATT 37043       _   ___
                                TGAACTAC ATGTT   GTATT
                                |||||||| |||||   |||||
                                ACTTGATG TACAG   TATAA
                                    G    TTG
GAM1467  PCDHGA8  5'  TGAATTACATGTCGATAATATT 37044    C      ____   C
           TTCAAA                GAA TACATGTTG    TATT TCAAA
                                ||| |||||||||    |||| |||||
                                CTT ATGTACAGC    ATAA AGTTT
                                  A       TATT    A
GAM1467  PCDHGA8  5'  TGAATTACATGTCGATAATATT 37044    C      ____   C
           TTCAAA                GAA TACATGTTG    TATT TCAAA
                                ||| |||||||||    |||| |||||
                                CTT ATGTACAGC    ATAA AGTTT
                                  A       TATT    A
GAM1467  PLA2G4C  3'  TGAGCACTTGTTGTATTCTCA  37045    AC   A
                                TGA  TAC TGTTGTATTCTCA
                                |||  ||| ||||||||||||||
                                ACT  GTG ACAACATAAGAGT
                                  C_   A
GAM1467  PON1    3'  TGATTTGATAGTGTATTCTCAA 37046    ACTAC   T
           A                    TGA    ATG TGTATTCTCAAA
                                |||    ||| ||||||||||||
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                                ACT     TAT ACATAAGAGTTT
                                  AAAC_   C
GAM1467  PWP2H     3'  TGGGCTACATGTGTGCAC     37047     AA       _
                                TG  CTACATGT TGTAT
                                ||  |||||||| |||||
                                AC  GATGTACA ACGTG
                                 CC       C
GAM1467  SCD       3'  TGTTTATGTATTCTCAAA     37040     ___
                                TGT   TGTATTCTCAAA
                                |||   ||||||||||||
                                ACA   ACATAAGAGTTT
                                  AAT
GAM1467  DKFZP434F2021 3'  GAATTACATCTGCTTCTCAA   37048     C    G    A
                                GAA TACAT TTGT TTCTCAA
                                ||| ||||| |||| |||||||
                                CTT ATGTA GACG AAGAGTT
                                  A    _   _
GAM1467  KIAA1715  3'  TGAATTACATGTTCGTATT    37049      C       _
                                TGAA TACATGTT GTATT
                                |||| |||||||| |||||
                                ACTT ATGTACAA CATAA
                                   A       G
GAM1467  KRTHB3    3'  TGAGCCGATGGTGTATTCTCA  37050     A  AC   T
                                TGA CT  ATG TGTATTCTCA
                                ||| ||  ||| ||||||||||
                                ACT GG  TAC ACATAAGAGT
                                  C  C_   C
GAM1467  PRO1596   5'  TACATATTTGTATTTTCAAA   37051         _    C
                                TACATGTT GTATT TCAAA
                                |||||||| ||||| |||||
                                ATGTATAA CATAA AGTTT
                                     A     A
GAM1467  LOC143785 3'  TGACCTTAGATGTATTCTCAAA 37052     A  ACATGT
                                TGA CT      TGTATTCTCAAA
                                ||| ||      ||||||||||||
                                ACT GA      ACATAAGAGTTT
                                  G  ATCT__
GAM1467  LOC51652  3'  TGAACTCCTATTCTCA      37053        ACATGT G
                                TGAACT      T TATTCTCA
                                ||||||      | ||||||||
                                ACTTGA      G ATAAGAGT
                                   _______ G
GAM1467  LOC91263  5'  GAGCTACAGTGATTCTCAAA   37054    A     T  T T
                                GA CTACA GT G ATTCTCAAA
                                || ||||| || | |||||||||
                                CT GATGT CA C TAAGAGTTT
                                 C     _ _ _
GAM1468  ANGPTL1   5'  TGATTCAGTGAATCCAGAAACT 37057      _    AA GC
              T                  TGAT TAGT  G  TTTAGAAACTT
                                ||||  ||||  |  ||||||||||
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                                ACTA GTCA  C  AGGTCTTTGAA
                                  A   __ TT
GAM1468 ATP6V1B2 3' GTAAACACTTTAGAAACTT   37058      _
                                GTAAG GCTTTAGAAACTT
                                ||||| ||||||||||||
                                CATTT TGAAATCTTTGAA
                                   G
GAM1468 FLJ12409 3' TGACTAGTGGGGTTTTAAA   37059        AA  C
                                TGATTAGT  GG TTTAGA
                                |||||||| || ||||||
                                ACTGATCA  CC AAATTT
                                     CC  A
GAM1468 KIAA0008 5' TGATTGGAGGGGCTTTAACCAA 37060      AGTAA     ___
            AACTT                 TGATT    GGCTTTA   GAAACTT
                                |||||    |||||||  |||||||
                                ACTAA    CCGAAAT   TTTTGAA
                                   CCTCC      TGG
GAM1468 PIP3-E   3' TGATTAGTAAGGGAAGA     37061          CTTT
                                TGATTAGTAAGG   AGA
                                ||||||||||||   |||
                                ACTAATCATTCC   TCT
                                      CT__
GAM1469 ATP6V1G2 3' TGAGCAGGATATTTATAAG   37064       TTT
                                TGAGTAG   TGTTTATAAG
                                |||||||  ||||||||||
                                ACTCGTC   ATAAATATTC
                                     CT_
GAM1469 ATP6V1G2 3' TGAGCAGGATATTTATAAG   37064       TTT
                                TGAGTAG   TGTTTATAAG
                                |||||||  ||||||||||
                                ACTCGTC   ATAAATATTC
                                     CT_
GAM1469 TRHDE    3' TGAATTGTTTGTTTATAAG   37065      A   T
                                TGAGT GTTT GTTTATAAG
                                ||||| |||| |||||||||
                                ACTTA CAAA CAAATATTC
                                   A   _
GAM1469 ARHGEF9  3' TGAGCAGTTTTGTCACA     37066          T
                                TGAGTAGTTTTGTT ATA
                                |||||||||||||| |||
                                ACTCGTCAAAACAG TGT
                                                _
GAM1469 CHRAC1   3' TGAATCGAGCTGTTTATAAG  37067      AGTT
                                TGAGT   TTGTTTATAAG
                                |||||   ||||||||||
                                ACTTA   GACAAATATTC
                                   GCTC
GAM1469 EBF2     3' TAAGTAGTTTTGTGCTATAAG 37068          _
                                TGAGTAGTTTTGT TTATAAG
                                |||||||||||| |||||||
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                                ATTCATCAAAACA GATATTC
                                       C
GAM1469 EVI5     3' TGAATAGTTCTGATTATAAG  37069          T
                                TGAGTAGTTTTG TTATAAG
                                |||||||||||| |||||||
                                ACTTATCAAGAC AATATTC
                                       T
GAM1469 FBXO22   3' TGAGAAGTTTTGCCATAAAG  37070     T       TAT
                                TGAG AGTTTTGTT   AAG
                                |||| |||||||||   |||
                                ACTC TCAAAACGG   TTC
                                   T       TAT
GAM1469 FLJ21162 3' TGAGTAGCTGGGTTTATA    37071        TT
                                TGAGTAGTT  GTTTATA
                                |||||||||  |||||||
                                ACTCATCGA  CAAATAT
                                      CC
GAM1469 KIAA0367 3' TGAGTAGTTTTCCATA      37072         TG
                                TGAGTAGTTT  TTTATA
                                ||||||||||  ||||||
                                ACTCATCAAA  AGGTAT
                                      __
GAM1469 KIAA0551 3' TGAGTAAGAGTTTATAAG    37073       TTTT
                                TGAGTAG    GTTTATAAG
                                |||||||    |||||||||
                                ACTCATT    CAAATATTC
                                    CT__
GAM1469 KIAA1726 3' TGAGTAGTTTTTACAA      37074         GTT
                                TGAGTAGTTTT   TATAA
                                ||||||||||   |||||
                                ACTCATCAAAA   ATGTT
                                      ___
GAM1469 KIAA1728 3' TGAGAGCTAATTTATAAG    37075     T   TT
                                TGAG AGTT  GTTTATAAG
                                |||| ||||  |||||||||
                                ACTC TCGA  TAAATATTC
                                   _   T_
GAM1469 TTLL1    3' TGAGTAGTTTTGATAAG     37076          TTT
                                TGAGTAGTTTTG   ATAAG
                                ||||||||||||   |||||
                                ACTCATCAAAAC   TATTC
                                      ___
GAM1469 ZFP106   5' AATAAGTTTGTTTATAAG    37077      T
                                AGTAG TTTGTTTATAAG
                                ||||| ||||||||||||
                                TTATT AAACAAATATTC
                                   C
GAM1469 LOC144195 3' TGAGTAGCTTTATTAAATA  37078           T_
                                TGAGTAGTTTTGTT  ATA
                                ||||||||||||||  |||
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                                ACTCATCGAAATAA  TAT
                                       TT
GAM1469  LOC153397 3'  TGGTAATCTTGTTTATA     37079    A
                                TG GTAGTTTTGTTTATA
                                || ||||||||||||||
                                AC CATTAGAACAAATAT
                                 _
GAM1469  LOC221787 3'  AAGTAGAGGTTTATAAG     37080       TTTT
                                GAGTAG   GTTTATAAG
                                ||||||   |||||||||
                                TTCATC   CAAATATTC
                                   TC__
GAM1470  CCNF     3'  CACATACGAACGCCTCTGG   37083       A    GTA
                                TACATAC AACGC   TGG
                                ||||||| |||||   |||
                                GTGTATG TTGCG   ACC
                                    C    GAG
GAM1470  DIRC1    3'  TGAGTACAAACGAATAAAGG   37084       TACA   C   T_
                                TGAGTACA   AACG GTA  GG
                                ||||||||   |||| |||  ||
                                ACTCATGT   TTGC TAT  CC
                                     ____   T   TT
GAM1470  KIAA0022  3'  TGAGTACATAAAAATGTTACTG 37085        C   CGCGTA
            GA                   TGAGTACATA AAA     TGGA
                                ||||||||||| |||     ||||
                                ACTCATGTAT TTT     ACCT
                                      T   ACAATG
GAM1470  KIAA0265  3'  TGAGTACATGTGCATGTAATGG 37086        ACAAAC   ___
                                TGAGTACAT     GCGT   ATGG
                                |||||||||     ||||   ||||
                                ACTCATGTA     CGTA   TACC
                                     CA____    CAT
GAM1470  KIAA0352  3'  TGAGTACATACCAAGAAAATGG 37087         AAACGCGT
                                TGAGTACATAC       ATGG
                                ||||||||||       ||||
                                ACTCATGTATG       TACC
                                      GTTCTTT_
GAM1470  KIAA1040  3'  TGATACATACAAATTTAAGGA  37088    G        CGCG  T
                                TGA TACATACAAA    TA GGA
                                ||| ||||||||||    || |||
                                ACT ATGTATGTTT    AT CCT
                                  _        AA__  T
GAM1470  KIAA1093  5'  TGAGGCATACAAGGTAGAAATG 37089     TA      ACGCGT_
            GA                   TGAG  CATACAA      ATGGA
                                ||||  |||||||      |||||
                                ACTC  GTATGTT      TACCT
                                  C_      CCATCTT
GAM1470  PFTK1    3'  TGAGTATCATATAGACGCA   37090       _   CAA
                                TGAGTA CATA   ACGCG
                                ||||||| ||||   |||||
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                                ACTCAT GTAT   TGCGT
                                   A   ATC
GAM1470  LOC145195 3'  TGAGTACATAGTAGG      37091         CAAACGC   T
                                TGAGTACATA     GTA GG
                                ||||||||||     ||| ||
                                ACTCATGTAT     CAT CC
                                       _______  _
GAM1470  LOC150468 5'  TGAGGTATACAAACTTGGCTGG 37092     TAC      GCGTA
           A                     TGAG   ATACAAAC    TGGA
                                ||||   ||||||||    ||||
                                ACTC   TATGTTTG    ACCT
                                  CA_      AACCG
GAM1470  LOC158314 3'  TGAGTACATAAGTAATGTGGA  37093         CAAACGC  A
                                TGAGTACATA     GT TGGA
                                ||||||||||     || ||||
                                ACTCATGTAT     TA ACCT
                                      TCAT___  C
GAM1471  DLG5     5'  TTCAAGGCGTTGGTGTGCT   37096         ATACA  _  _
                                TTCAAGGCGTT    GG GT CT
                                ||||||||||    || || ||
                                AAGTTCCGCAA    CC CA GA
                                      _____ A  C
GAM1471  BIRC1    3'  AGACAGACAGGGTCTT     37097      TTAT
                                AGGCG   ACAGGGTCTT
                                |||||   ||||||||||
                                TCTGT   TGTCCCAGAA
                                  C___
GAM1471  CHFR     3'  CTCAGGCTCTGTAGGGTCTT  37098     A   GTTATAC
                                TTCA GGC      AGGGTCTT
                                |||| |||     ||||||||
                                GAGT CCG      TCCCAGAA
                                  _  AGACA__
GAM1471  DKFZP547L112 5'  CAAGGCGGGTCAGGGGTCTTA  37099       TTATA    _
                                CAAGGCG    CAGGG TCTTA
                                |||||||    ||||| |||||
                                GTTCCGC    GTCCC AGAAT
                                    CCA__    C
GAM1471  DKFZP547L112 5'  TTCAGGCGAGGGTCT      37100     A   TTATAC
                                TTCA GGCG     AGGGTCT
                                |||| ||||     |||||||
                                AAGT CCGC     TCCCAGA
                                  _   _______
GAM1471  FLJ23447  3'  TTCAAGAGACAGGGTCTT    37101       CGTTAT
                                TTCAAGG     ACAGGGTCTT
                                |||||||     ||||||||||
                                AAGTTCT     TGTCCCAGAA
                                    C_____
GAM1471  KIAA0633  3'  TTCAAGCCGTTATACAGG    37102       G
                                TTCAAG CGTTATACAGG
                                ||||||||||||||||||
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                                AAGTTC GCAATATGTCC
                                   G
GAM1471  KIAA1879  3'  TTCAAAGAGGCAGGGTCTT   37103       CGTTATA
                                TTCAAGG      CAGGGTCTT
                                |||||||      |||||||||
                                AAGTTTC      GTCCCAGAA
                                   TCC____
GAM1471  LOC200138 5'  TTCAAGGCGTTTGTGGCC    37104          ATACAG
                                TTCAAGGCGTT     GGTC
                                ||||||||||     ||||
                                AAGTTCCGCAA     CCGG
                                      ACA___
GAM1472  GDF8      3'  TAACAAAATCCCAATTTAC    37107          AAACA
                                TAACAAAATCC     TTAC
                                ||||||||||     ||||
                                ATTGTTTTAGG     AATG
                                      GTTA_
GAM1472  PPARBP    3'  TAAGAAACAGACACCAAACATT 37108     AT    AAAT
              AC                  TAA  AACA    CCAAACATTAC
                                |||  ||||    ||||||||||
                                ATT  TTGT    GGTTTGTAATG
                                  CT    CTGT
GAM1472  ARL8      3'  CAAATAACAACTTAAACATTA  37109         AATCC
                                TAAATAACAA     AAACATTA
                                |||||||||     ||||||||
                                GTTTATTGTT     TTTGTAAT
                                      GAA__
GAM1472  ULK2      3'  TAAATTACAAAATCCAATAC   37110       A         _
                                TAAAT ACAAAATCCAA AC
                                ||||| |||||||||| ||
                                ATTTA TGTTTTAGGTT TG
                                   A          A
GAM1472  ZF        3'  CAAATAACAAAATAAAACAT   37111           CC
                                TAAATAACAAAAT  AAACAT
                                ||||||||||||  ||||||
                                GTTTATTGTTTTA  TTTGTA
                                      T_
GAM1473  MAP1A     3'  CACAAGGTGGGCTCA       37114         AATAT  T
                                TACAAGGTG    GG CTTA
                                |||||||||    || ||||
                                GTGTTCCAC    CC GAGT
                                     _____  _
GAM1473  RGS5      3'  TACAAGCTGAAGATATCTTAAT 37115       G    TATG
              T                   TACAAG TGAA    GTCTTAATT
                                ||||||| ||||    |||||||||
                                ATGTTC ACTT    TAGAATTAA
                                   G    CTA_
GAM1473  KIAA1349  5'  AATGAATATATGGTTTTAATT  37116       __      C
                                GGTGA  ATATGGT TTAATT
                                |||||  ||||||| ||||||
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                                TTACT  TATACCA AATTAA
                                   TA      A
GAM1473  LOC133121 3'  TACAATGTGCATGGTCTT    37117      G   AA
                                TACAA GTG  TATGGTCTT
                                ||||| |||  |||||||||
                                ATGTT CAC  GTACCAGAA
                                   A  __
GAM1473  LOC151742 3'  GGTGGATGATCCTAATT     37118      AAT
                                GGTG   ATGGTCTTAATT
                                ||||   ||||||||||||
                                CCAC   TACTAGGATTAA
                                  C__
GAM1473  LOC163231 5'  TACAGTGGTGAATATGTC    37119      A_        G
                                TACA  GGTGAATATG TC
                                ||||  |||||||||| ||
                                ATGT  CCACTTATAC AG
                                   CA         _
GAM1474  DDX6      3'  TCTGCCAGCAATTTACAGTGC  37122     A         AC__
                                TCT CCAGCAATTTG   GC
                                ||| ||||||||||    ||
                                AGA GGTCGTTAAAT   CG
                                  C         GTCA
GAM1474  OPA1      3'  TCTACCAGCGCATCTGTGC   37123        A_    AC
                                TCTACCAGC  ATTTG  GC
                                |||||||||  |||||  ||
                                AGATGGTCG  TAGAC  CG
                                     CG    A_
GAM1474  OPA1      3'  TCTACCAGCGCATCTGTGC   37123        A_    AC
                                TCTACCAGC  ATTTG  GC
                                |||||||||  |||||  ||
                                AGATGGTCG  TAGAC  CG
                                     CG    A_
GAM1474  OPA1      3'  TCTACCAGCGCATCTGTGC   37123        A_    AC
                                TCTACCAGC  ATTTG  GC
                                |||||||||  |||||  ||
                                AGATGGTCG  TAGAC  CG
                                     CG    A_
GAM1474  OPA1      3'  TCTACCAGCGCATCTGTGC   37123        A_    AC
                                TCTACCAGC  ATTTG  GC
                                |||||||||  |||||  ||
                                AGATGGTCG  TAGAC  CG
                                     CG    A_
GAM1474  OPA1      3'  TCTACCAGCGCATCTGTGC   37123        A_    AC
                                TCTACCAGC  ATTTG  GC
                                |||||||||  |||||  ||
                                AGATGGTCG  TAGAC  CG
                                     CG    A_
GAM1474  TRIM14    3'  TCTGCAAGCAATTTGCCATA  37124     ACC       GAC
                                TCT   AGCAATTT   GCCATA
                                |||   ||||||||   ||||||
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                              AGA  TCGTTAAA  CGGTAT
                                CGT     ___
GAM1474 TRIM14   3' TCTGCAAGCAATTTGCCATA  37124    ACC     GAC
                              TCT  AGCAATTT  GCCATA
                              |||  ||||||||  ||||||
                              AGA  TCGTTAAA  CGGTAT
                                CGT     ___
GAM1474 LOC92597 5' TCTACCAGCAACTAACA    37125         T
                              TCTACCAGCAATT GACG
                              |||||||||||| ||||
                              AGATGGTCGTTGA TTGT
                                           _
GAM1475 CASP10   3' GAACCTTAAAATGCACCT   37128  T  GC
                              A ACC  AAAATGCACCT
                              | |||  ||||||||||
                              C TGG  TTTTACGTGGA
                               T  AA
GAM1475 CASP10   3' GAACCTTAAAATGCACCT   37128  T  GC
                              A ACC  AAAATGCACCT
                              | |||  ||||||||||
                              C TGG  TTTTACGTGGA
                               T  AA
GAM1475 DDX11    3' CCACAGGCCTGGATGCACCT  37129     CC  AAA_
                              CCATA  GC   ATGCACCT
                              |||||  ||   ||||||||
                              GGTGT  CG   TACGTGGA
                                 C_  GACC
GAM1475 XPA      3' ACCTACCACTTCTGCACCTA  37130    A    AAAA
                              ACC TACCGC   TGCACCTA
                              ||| ||||||   ||||||||
                              TGG ATGGTG   ACGTGGAT
                                _    AAG_
GAM1475 DDX12    3' CCACAGGCCTGGATGCACCT  37129     CC  AAA_
                              CCATA  GC   ATGCACCT
                              |||||  ||   ||||||||
                              GGTGT  CG   TACGTGGA
                                 C_  GACC
GAM1475 FLJ10520 5' CCACGTGGAAATGCACCTA   37131    A___
                              CCGC   AAATGCACCTA
                              ||||   ||||||||||
                              GGTG   TTTACGTGGAT
                                CACC
GAM1475 FLJ10980 5' CCAGAGTGCTGTGAAATGCACC 37132    TACC  A___
           T                   CCA   GC   AAATGCACCT
                              |||   ||   ||||||||||
                              GGT   CG   TTTACGTGGA
                                CTCA  ACAC
GAM1475 KIAA1096 3' TAACCATATCCGAAGAACA   37133       _  C  AAT
                              TAACCATA CCG AA  GCA
                              |||||||| ||| ||  |||
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                                ATTGGTAT GGC TT   TGT
                                    A   _ CT_
GAM1475  LOC147172 3'  TAACAATATTGATTCTGCACCT 37134     C   CCGCAAAA
             A                   TAAC ATA       TGCACCTA
                                 |||| |||       ||||||||
                                 ATTG TAT       ACGTGGAT
                                   T   AACTAAG_
GAM1475  LOC203292 5'  ACCATACCCAGCCCCACACCT  37135        __  AAAA
                                 ACCATACC  GC    TGCACCT
                                 ||||||||  ||    |||||||
                                 TGGTATGG  CG    GTGTGGA
                                     GT  GG__
GAM1476  ABCA8    3'  TTAAACAGAATTTGTTTATC   37138          ___
                                 TTAAGCAGAA   GTTTATT
                                 ||||||||||   |||||||
                                 AATTTGTCTT   CAAATAG
                                      AAA
GAM1476  CDC2L5   3'  TTAAGCAAAGGTTTTTTTTGTC 37139         A   A__
                                 TTAAGCAGA GTTT   TTGTC
                                 ||||||||| ||||   |||||
                                 AATTCGTTT CAAA   AACAG
                                     C    AAA
GAM1476  CDC2L5   3'  TTAAGCAAAGGTTTTTTTTGTC 37139         A   A__
                                 TTAAGCAGA GTTT   TTGTC
                                 ||||||||| ||||   |||||
                                 AATTCGTTT CAAA   AACAG
                                     C    AAA
GAM1476  CLIC4    3'  TTAGGCAAAAGTAAAAATCTAT 37140     A       TTATT
             C                    TTA GCAGAAGT     GTCTATC
                                  ||| ||||||||     |||||||
                                  AAT CGTTTTCA     TAGATAG
                                    C       TTTT_
GAM1476  ERN1     3'  TTAAGCAGGAATTTAAAAAGTC 37141         A     TT__
                                 TTAAGCAG AGTTTA    GTC
                                 |||||||| ||||||    |||
                                 AATTCGTC TTAAAT    CAG
                                     C     TTTT
GAM1476  KIAA0391  3'  TCAAGCAGAAGTTAGGGTTTTG 37142           TA____
             T                    TTAAGCAGAAGTT     TTGT
                                  ||||||||||||      ||||
                                  AGTTCGTCTTCAA     AACA
                                       TCCCAA
GAM1476  KIAA1634  3'  TTAAGCAGATGTTTAGTC    37143         A    TT
                                 TTAAGCAGA GTTTA  GTC
                                 ||||||||| |||||  |||
                                 AATTCGTCT CAAAT  CAG
                                     A    __
GAM1476  LC27     3'  TTAGGCAGAAGTATATCAAATA 37144     A       T    TC
             T                    TTA GCAGAAGT TATTG  TAT
                                  ||| |||||||| |||||  |||
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                                AAT CGTCTTCA ATAGT  ATA
                                  C       T    TT
GAM1476  LY75     3'  TAAGCATGTCTTATTGTTTAT  37145       GAAG       C
                                TAAGCA    TTTATTGT TAT
                                ||||||    |||||||| |||
                                ATTCGT    GAATAACA ATA
                                   ACA_       A
GAM1476  MARCKS   3'  TTAAGCAGGAGTTTAATAGC   37146        A     TT_
                                TTAAGCAG AGTTTA   GT
                                |||||||| ||||||   ||
                                AATTCGTC TCAAAT   CG
                                     C     TAT
GAM1476  MIL1     3'  AGCAGAAGTCCCCAATTATC   37147          ___
                                AGCAGAAGTTT   ATTGTC
                                ||||||||||   ||||||
                                TCGTCTTCAGG   TAATAG
                                      GGT
GAM1476  PLSCR4   3'  TTAAGCAGCGGTGGAATTTGTC 37148        AA  TTA__
                                TTAAGCAG  GT    TTGTC
                                ||||||||  ||    |||||
                                AATTCGTC  CA    AACAG
                                     GC  CCTTA
GAM1476  LOC153196 5'  TTAGGCAGAAGTGAAGCTGTC  37149     A       TTA_
                                TTA GCAGAAGT    TTGTC
                                ||| ||||||||    |||||
                                AAT CGTCTTCA    GACAG
                                  C       CTTC
GAM1476  LOC200488 5'  TTAAGCAGGTAGACGTCTAT   37150        AA  TTAT
                                TTAAGCAG  GT    TGTCTAT
                                ||||||||  ||    |||||||
                                AATTCGTC  CA    GCAGATA
                                     __  TCT_
GAM1476  LOC220074 3'  TTAAGCAGAAGATTCTTTTTAT 37151          _   A__
              C                  TTAAGCAGAAG TTT   TTGTC
                                ||||||||||| |||   |||||
                                AATTCGTCTTC AAG   AATAG
                                      T   AAA
GAM1476  LOC257048 3'  TTAAGCAGAAGATACAAGT    37152          TT   T_
                                TTAAGCAGAAG  TAT  GT
                                ||||||||||  |||  ||
                                AATTCGTCTTC  ATG  CA
                                      T_   TT
GAM1476  LOC64744  3'  TTAAGCAAAGTTTTCTTGTC   37153        A    A_
                                TTAAGCAGA GTTT  TTGTC
                                |||||||| ||||  |||||
                                AATTCGTTT CAAA  AACAG
                                     _    AG
GAM1477  CACNG7    3'  TGGAGAACGAGGGAGGAG    37156      A       _
                                TGGA AACGAGGG GGAG
                                |||| |||||||| ||||
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                                ACCT TTGCTCCC CCTC
                                  C       T
GAM1477  DDX24    3'  TGGAAGAGAGGGAGACTTT   37157      AAC       G
                                TGGAA   GAGGGGGAG ACTTT
                                |||||   ||||||||| |||||
                                ACCTT   CTCTCCCTC TGAAA
                                  ____       _
GAM1477  HRC      3'  TGGAAGGCAGGGGGAGG     37158      AA G
                                TGGAA  C AGGGGGAGG
                                |||||  | |||||||||
                                ACCTT  G TCCCCCTCC
                                   CC _
GAM1477  MEN1     5'  TGGTAAGATTACTGAGGACTTT 37159     AAAAC    GG___
              T                  TGG    GAGG    GAGGACTTTT
                                |||    ||||    ||||||||||
                                ACC    TTCT    CTCCTGAAAA
                                  A____    AATGA
GAM1477  NEFH     3'  TGGAAAGGAGGGGGGCAG    37160       AC      A_
                                TGGAAA  GAGGGGG  GG
                                ||||||  |||||||  ||
                                ACCTTT  CTCCCCC  TC
                                   C_      CG
GAM1477  NYX      3'  TGGAAGATGAGGGGAAGG    37161       AAC
                                TGGAA   GAGGGGGAGG
                                |||||   ||||||||||
                                ACCTT   CTCCCCTTCC
                                   CTA
GAM1477  PRX      3'  TGGAAGAGGGCTTGACTTT   37162     AAACG     AG_
                                TGGA    AGGGGG   GACTTT
                                ||||    ||||||   ||||||
                                ACCT    TCTCCC   CTGAAA
                                  _____     GAA
GAM1477  RORA     5'  TGGAGAATGATGGGGAGGA   37163      A  C  G
                                TGGA AA GA GGGGAGGA
                                |||| || || ||||||||
                                ACCT TT CT CCCCTCCT
                                  C  A  A
GAM1477  RORA     5'  TGGAGAATGATGGGGAGGA   37163      A  C  G
                                TGGA AA GA GGGGAGGA
                                |||| || || ||||||||
                                ACCT TT CT CCCCTCCT
                                  C  A  A
GAM1477  CGB1     3'  TGGAAGGCTGGGGGGAGGGGCC 37164      AACGA      A_
              TTT                 TGGAA    GGGGGAGG  CTTTT
                                |||||    ||||||||  |||||
                                ACCTT    CCCCCTCC  GGAAA
                                   CCGAC       CC
GAM1477  CGB2     3'  TGGAAGGCTGGGGGGAGGGGCC 37164      AACGA      A_
              TTT                 TGGAA    GGGGGAGG  CTTTT
                                |||||    ||||||||  |||||
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                                ACCTT    CCCCCTCC  GGAAA
                                   CCGAC       CC
GAM1477  FLJ13189  3'  TAGAAAGTTATTAGGGGACTTT 37165       ACGAGG   A
              T                    TGGAAA      GGG GGACTTTT
                                   ||||||      ||| ||||||||
                                   ATCTTT      TCC CCTGAAAA
                                      CAATAA  _
GAM1477  HAPIP     3'  TGGAAACTGGAGGACTTT     37166       ACGAGGG
                                   TGGAAA      GGAGGACTTT
                                   ||||||      ||||||||||
                                   ACCTTT      CCTCCTGAAA
                                      GA_____
GAM1477  ORMDL3    3'  GGAAGCGAGGGGGGAA      37167      AA       A
                                   GGAA  CGAGGGGG GGA
                                   ||||  |||||||| |||
                                   CCTT  GCTCCCCC CTT
                                     C_       _
GAM1477  PLSCR4    5'  GGAGACGGAGAGGATTTTT    37168     AAAC  G       C
                                   GGA    GA GGGGAGGA TTTT
                                   |||    || |||||||| ||||
                                   CCT    CT CCTCTCCT AAAA
                                     _____ G       A
GAM1477  PRKCBP1   5'  GAGGGCTGGGGAACTTTC     37169       __  A
                                   GAGGG  GG GGACTTTT
                                   |||||  || ||||||||
                                   CTCCC  CC CTTGAAAG
                                      GA  C
GAM1477  RAB39     3'  TGGAGGCCGAGGGGGGCGAA   37170      AAA       A_
                                   TGGA   CGAGGGGG  GGA
                                   ||||   ||||||||  |||
                                   ACCT   GCTCCCCC  CTT
                                     CCG       CG
GAM1477  SLC38A4   3'  TGGAAGACGAGAGGGAGA     37171       A
                                   TGGAA ACGAGGGGGAGG
                                   ||||| ||||||||||||
                                   ACCTT TGCTCTCCCTCT
                                      C
GAM1477  LOC121441 5'  TGGAGACGAGGCAAACTTTT   37172      AAAC  G    AG
                                   TGGA    GA GGGG  GACTTTT
                                   ||||    || ||||  |||||||
                                   ACCT    CT CTCC  TTGAAAA
                                     _____ G    GT
GAM1477  LOC125268 3'  TGGAAGGCGAGGGAGGGGA    37173       AA       A
                                   TGGAA  CGAGGGGG GGA
                                   |||||  |||||||| |||
                                   ACCTT  GCTCCCTC CCT
                                      CC       C
GAM1477  LOC133482 5'  TGGAAACTGAGGACTTGGCTTT 37174       AC     GGA  A
              T                    TGGAAA  GAGGG   GG CTTTT
                                   ||||||  |||||   || |||||
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                                ACCTTT  CTCCT   CC GAAAA
                                   GA    GAA  _
GAM1477  LOC144558 5'  TGGAAAGCGGGGGGAGG     37175       A  A
                                TGGAAA CG GGGGGAGG
                                |||||| || ||||||||
                                ACCTTT GC CCCCCTCC
                                   C  _
GAM1477  LOC146268 3'  GGAGGTGAGGGGAAGCACT    37176     AAAC       G
                                GGA    GAGGGGGAG ACT
                                |||    ||||||||| |||
                                CCT    CTCCCCTTC TGA
                                  CCA_        G
GAM1477  LOC151361 5'  TGGAGAGTGAGGGAGGCTT    37177      AAAC  _ _     A
                                TGGA    GAG G GGGAGG CTT
                                ||||    ||| | |||||| |||
                                ACCT    CTC C CCCTCC GAA
                                  _____   A T     _
GAM1477  LOC151623 5'  TGGAAAGCGGGGGGAGG     37175       A  A
                                TGGAAA CG GGGGGAGG
                                |||||| || ||||||||
                                ACCTTT GC CCCCCTCC
                                   C  _
GAM1477  LOC199678 3'  TGGAAAACTGATAAGGGCTTTT 37178         GA  GG    A
                                TGGAAAAC  GG  GAGG CTTTT
                                ||||||||  ||  |||| |||||
                                ACCTTTTG  CT  TTCC GAAAA
                                     A_  A_   C
GAM1477  LOC199918 5'  GGGTGAGAGAAGCAGGACTTTT 37179    AAAAC     G
                                GG     GAGGGG AGGACTTTT
                                ||     |||||| |||||||||
                                CC     CTCTTC TCCTGAAAA
                                 CACT_     G
GAM1477  LOC255516 5'  TGGAAAGCGGGGGGAGG     37175       A  A
                                TGGAAA CG GGGGGAGG
                                |||||| || ||||||||
                                ACCTTT GC CCCCCTCC
                                   C  _
GAM1478  ITGA1    3'  GGATCGGACAATCAGCA     37182       TGTT       A
                                GGATT    GACAATCA CA
                                |||||    |||||||| ||
                                CCTAG    CTGTTAGT GT
                                   C___       C
GAM1478  MSL3L1   3'  GGGGTGACACAATCAACAAG   37183    ATT  TTG
                                GG   TG   ACAATCAACAAG
                                ||   ||   ||||||||||||
                                CC   AC   TGTTAGTTGTTC
                                 CC_  TG_
GAM1478  FLJ20637 3'  GGATTTATTGGAGCACAAG    37184          ACAATCA
                                GGATTTGTTG      ACAAG
                                ||||||||||      |||||
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                                CCTAAATAAC      TGTTC
                                     CTCG___
GAM1478 KIAA0152 3' GATTTGTTGTGGTAACAAG   37185         ACAATC
                                GATTTGTTG     AACAAG
                                |||||||||     ||||||
                                CTAAACAAC     TTGTTC
                                     ACCA__
GAM1478 LOC115207 3' GGATTTATAATCAACAA     37186        TGAC
                                GGATTTGT    AATCAACAA
                                ||||||||    |||||||||
                                CCTAAATA    TTAGTTGTT
                                     _____
GAM1479 HNF3B    3' GGTATCTGTGTGGCCCT     37189        C    AT
                                GGTATCTG GTGG  TCCT
                                |||||||| ||||  ||||
                                CCATAGAC CACC  GGGA
                                     A   __
GAM1479 MYOG     3' AGTGGCATCTGTGGCCAGCT   37190    C      GC    ATTC
                                AG GGTATCT  GTGG    CT
                                || |||||||  ||||    ||
                                TC CCGTAGA  CACC    GA
                                 A      __   GGTC
GAM1479 PTPRE    5' CAGAGGCCGTGGGTTCCT    37191     C   ATCTG     A
                                CAG GGT     CGTGG TTCCT
                                ||| |||     ||||| |||||
                                GTC CCG     GCACC AAGGA
                                  T  ______    C
GAM1479 RAB11A   5' CAGTGGTATCTGTGGGACC   37192     C       CGT
                                CAG GGTATCTG   GGATT
                                ||| ||||||||   |||||
                                GTC CCATAGAC   CCTGG
                                  A       AC_
GAM1479 KIAA1546 3' CAGATGGTATTTTAAGATTCCT 37193     C_    CTGCGT
              G                  CAG  GGTAT     GGATTCCTG
                                |||  |||||     |||||||||
                                GTC  CCATA     TCTAAGGAC
                                  TA    AAAT__
GAM1479 PELI2    3' GGTATCTGTTACACTCCTG    37194        CG  G
                                GGTATCTG  TG ATTCCTG
                                ||||||||  || |||||||
                                CCATAGAC  AT TGAGGAC
                                     A_  G
GAM1479 SPTLC2   3' CAGGGTATCTGTAGGTTC    37195     C       CGT  A
                                CAG GGTATCTG   GG TTC
                                ||| ||||||||   || |||
                                GTC CCATAGAC   CC AAG
                                  _       AT_  _
GAM1479 LOC140214 5' CAGGGTGAGTGGATTC      37196     C   ATCT C
                                CAG GGT    G GTGGATTC
                                ||| |||    | ||||||||
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                                GTC CCA    C CACCTAAG
                                  _  ____ T
GAM1480  ADAMTS5  3'  GGCTTTGCAGTGTTTCAC    37199      C  AG
                                GGCT TG  AGTGTTTCAC
                                |||| ||  ||||||||||
                                CCGA AC  TCACAAAGTG
                                  A  G_
GAM1480  ANXA2    3'  AGGCAAAGTGTTTCA       37200      TCTG
                                AGGC    AGAGTGTTTCA
                                ||||    ||||||||||
                                TCCG    TTTCACAAAGT
                                  ____
GAM1480  ATP7B    3'  CAGGCTCTGAGGCCCTCAC    37201           A  G
                                CAGGCTCTGAG GT TTTCAC
                                |||||||||| || ||||||
                                GTCCGAGACTC CG GGAGTG
                                    _ _
GAM1480  AXUD1    3'  CAGACTCTGGGGAGCCCC    37202         A_   G
                                CAGGCTCTG  GAGT TT
                                |||||||||  |||| ||
                                GTCTGAGAC  CTCG GG
                                     CC    G
GAM1480  BCRP2    3'  CAGGCCCTGGTTTCA       37203         AGAGT
                                CAGGCTCTG    GTTTCA
                                |||||||||    ||||||
                                GTCCGGGAC    CAAAGT
                                  _____
GAM1480  BMPR2    3'  AGGCTTGAAAACATTTCAC    37204      C     TG
                                AGGCT TGAGAG  TTTCAC
                                ||||| ||||||  ||||||
                                TCCGA ACTTTT  AAAGTG
                                  _     GT
GAM1480  C9       3'  CAGTTCTGGCGTATTTCAC    37205     GC    AGA
                                CAG  TCTG   GTGTTTCAC
                                |||  ||||   |||||||||
                                GTC  AGAC   CATAAAGTG
                                  A_   CG_
GAM1480  CDS2     5'  GGCTCTGAGCGGCTCAC      37206         AGT   T
                                GGCTCTGAG   GTT CAC
                                |||||||||   ||| |||
                                CCGAGACTC   CGA GTG
                                     GC_  _
GAM1480  CREBL2   3'  CAGGTCTGAATGTTT       37207      C    GA
                                CAGG TCTGA  GTGTTT
                                |||| |||||  ||||||
                                GTCC AGACT  TACAAA
                                  _    __
GAM1480  DDAH2    3'  GGTTCTGAGAGGGAGGATTCAC 37208     C       TGT___
                                GG TCTGAGAG     TTCAC
                                || ||||||||     |||||
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                                CC AGACTCTC     AAGTG
                                 A       CCTCCT
GAM1480  DDX3    3'  CAGTGTTTTGAAGTGTTTCA  37209    GCTC_  G
                                CAG    TGA AGTGTTTCA
                                |||    ||| |||||||||
                                GTC    ACT TCACAAAGT
                                  ACAAA  _
GAM1480  DLG5    5'  CAGGCTCTGCAGGTCCGAC   37210        AG  T   TC
                                CAGGCTCTG  AG GTT  AC
                                |||||||||  || |||  ||
                                GTCCGAGAC  TC CAG  TG
                                     G_ _   GC
GAM1480  DMBT1   3'  GGGTCTGAGAGCGACCAC   37211   C        TT
                                GG TCTGAGAGTG  TCAC
                                || ||||||||||  ||||
                                CC AGACTCTCGC  GGTG
                                 C        T_
GAM1480  DTR     3'  CAGGCTTGTGGTATTTCAC   37212      C  AGA
                                CAGGCT TG   GTGTTTCAC
                                ||||||  ||   |||||||||
                                GTCCGA AC   CATAAAGTG
                                   _  AC_
GAM1480  E2F1    3'  CAGATTCTGGGAGCAGGCAC  37213    GC    A    TTT
                                CAG  TCTG GAGTG   CAC
                                |||  |||| |||||   |||
                                GTC  AGAC CTCGT   GTG
                                  TA   C    CC_
GAM1480  FOS     3'  AGCCTGGTGTGTTTCAC    37214    T   AGA
                                GGC CTG   GTGTTTCAC
                                ||| |||   |||||||||
                                TCG GAC   CACAAAGTG
                                  _   CA_
GAM1480  HLCS    3'  AAGTTCTTTTAATGTTTCA   37215    C   GAG
                                AGG TCT   AGTGTTTCA
                                ||| |||   |||||||||
                                TTC AGA   TTACAAAGT
                                  A   AAA
GAM1480  ITGA11  3'  CAGGCTCCGGGAGTCCTT   37216        A   G
                                CAGGCTCTG GAGT TTT
                                ||||||||| |||| |||
                                GTCCGAGGC CTCA GAA
                                     C   G
GAM1480  ITGB3   3'  CAGGCCTGAGAACCATGTGAAA 37217     T    A_________   TTT
            CA                    AGGC CTGAG       GTG   CA
                                ||||  |||||       |||   ||
                                TCCG GACTC       CAC   GT
                                  _    TTGGTAIII   TTT
GAM1480  JAM3    3'  GGCAAAGTGTTTCAC      37218    TCTG
                                GGC    AGAGTGTTTCAC
                                |||    ||||||||||||
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                              CCG   TTTCACAAAGTG
                                ____
GAM1480 KIF2    3' AGACAAAAGAGTGTTTCAC  37219     TCT
                              AGGC  GAGAGTGTTTCAC
                              ||||  ||||||||||||
                              TCTG  TTCTCACAAAGTG
                                TT_
GAM1480 MECP2   3' CAGTTTCTATGATGTTTCAC 37220    GC   A  G
                              CAG  TCTG GA TGTTTCAC
                              |||  |||| || ||||||||
                              GTC  AGAT CT ACAAAGTG
                                AA   A  _
GAM1480 MGAM    3' CAGTTCTGGAAATATTCAC  37221    GC   AG    T
                              CAG  TCTG  AGTGTT CAC
                              |||  ||||  |||||| |||
                              GTC  AGAC  TTATAA GTG
                                A_   CT    _
GAM1480 MHC2TA  3' AGGCTCTGACCTCATTTCA  37222       GAG
                              AGGCTCTGA  TGTTTCA
                              |||||||||  |||||||
                              TCCGAGACT  GTAAAGT
                                   GGA
GAM1480 NCOA4   3' GGCTAAAATGTTTCA      37223     CTG
                              GGCT  AGAGTGTTTCA
                              ||||  ||||||||||
                              CCGA  TTTTACAAAGT
                                ___
GAM1480 POLA    3' CAGGCTCTGAGAAGCTC    37224          T
                              CAGGCTCTGAGAG GTTT
                              |||||||||||| ||||
                              GTCCGAGACTCTT CGAG
                                     _
GAM1480 PON1    3' CAGTGCTTTGATGCTTCA   37225    _  C  GAG
                              CAG GCT TGA  TGTTTCA
                              ||| ||| |||  |||||||
                              GTC CGA ACT  ACGAAGT
                                A  A  ___
GAM1480 PREB    3' CAGGCTCTTGGGCATCTTCAC 37226       GAGA    _
                              CAGGCTCT   GTGTTT CAC
                              ||||||||   |||||| |||
                              GTCCGAGA   CGTAGA GTG
                                   ACC_    A
GAM1480 SLC4A4  3' GGCTCTAAAAGTTTCAC    37227         GT
                              GGCTCTGAGAGT  TTCAC
                              ||||||||||||  |||||
                              CCGAGATTTTCA  AAGTG
                                     __
GAM1480 STAT1   3' GGCTTTGAACTATTTCAC   37228    C   AG
                              GGCT TGAG  TGTTTCAC
                              |||| ||||  ||||||||
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                                CCGA ACTT  ATAAAGTG
                                  A   G_
GAM1480  TCL1A    3'  CAGGCCCTGGGTAGAGCTCA  37229        ___    GTT
                                CAGGCTCTG  AGAGT  TCA
                                |||||||||  |||||  |||
                                GTCCGGGAC  TCTCG  AGT
                                    CCA   ___
GAM1480  UBE2H    3'  CAGGTCTGGATTTCA     37230     C   A  GTG
                                CAGG TCTG GA  TTTCA
                                |||| |||| ||  |||||
                                GTCC AGAC CT  AAAGT
                                  _   _ ___
GAM1480  VIPR2    3'  CAGGCTCTGCGGCTCCCAC   37231        AGA  G TT
                                CAGGCTCTG  GT T  CAC
                                |||||||||  || |  |||
                                GTCCGAGAC  CG A  GTG
                                    GC_  _ GG
GAM1480  WASF3    3'  CAGGCTCATGAATATTT    37232       TGA
                                CAGGCTC  GAGTGTTT
                                |||||||  ||||||||
                                GTCCGAG  CTTATAAA
                                   TA_
GAM1480  WNT5A    3'  CAGAGCTCCTAATGTTTCA   37233    _   GAGA
                                CAG GCTCT   GTGTTTCA
                                ||| |||||   ||||||||
                                GTC CGAGG   TACAAAGT
                                  T    AT__
GAM1480  ZFH4     5'  AGGATCGACATGTGTTTCAC  37234    C  T  GA_
                                AGG TC GA  GTGTTTCAC
                                ||| || ||  |||||||||
                                TCC AG CT  CACAAAGTG
                                  T  _  GTA
GAM1480  APCL     3'  AGCTCTGGGAGTTCCCCAC   37235      A   G TT
                                GGCTCTG GAGT T  CAC
                                ||||||| |||| |  |||
                                TCGAGAC CTCA G  GTG
                                    C   A GG
GAM1480  BMP10    5'  GGCTCTAAGTGGCAGTTT    37236       A_  _
                                GGCTCTGAG  GT GTTT
                                |||||||||  || ||||
                                CCGAGATTC  CG CAAA
                                    AC  T
GAM1480  C21orf100 3'  AGGCTCTGAGGGAGAATGTTTC 37237       ____
           A                    AGGCTCTGA   GAGTGTTTCA
                                |||||||||   ||||||||||
                                TCCGAGACT   CTTACAAAGT
                                    CCCT
GAM1480  C6orf37  3'  AGCTCTGACAGAATTCAC   37238       G  TGT
                                GGCTCTGA AG  TTCAC
                                |||||||| ||  |||||
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                                TCGAGACT TC   AAGTG
                                     G  TT_
GAM1480  C9orf7    3'  CAGGCCCTGGGGCTCCAC    37239         AGAGT
                                CAGGCTCTG    GTTTCAC
                                |||||||||    |||||||
                                GTCCGGGAC    CGAGGTG
                                     CC___
GAM1480  CCNB3     3'  CAGGCCCTGAGCCTCA      37240         GAGT
                                CAGGCTCTGA   GTTTCA
                                ||||||||||   ||||||
                                GTCCGGGACT   CGGAGT
                                     _____
GAM1480  CD36L1    3'  GGGACTGCAGTGTTTCAC    37241    CT   AG
                                GG  CTG  AGTGTTTCAC
                                ||  |||  ||||||||||
                                CC  GAC  TCACAAAGTG
                                 CT   G_
GAM1480  CNNM4     3'  CAGGCTCTGGGATCCCAC    37242         A  GTG TT
                                CAGGCTCTG GA   T  CAC
                                ||||||||| ||   |  |||
                                GTCCGAGAC CT   A  GTG
                                     C  ___ GG
GAM1480  CYP4F8    3'  AGACTCTGGGAGATCCCAC   37243         A   T  TT
                                AGGCTCTG GAG GT  CAC
                                |||||||| ||| ||  |||
                                TCTGAGAC CTC TA  GTG
                                     C   _  GG
GAM1480  DDX31     5'  CAGGCTCTGGAGCTCA      37244         A    GTT
                                CAGGCTCTG GAGT   TCA
                                ||||||||| ||||   |||
                                GTCCGAGAC CTCG   AGT
                                     _   ____
GAM1480  DDX31     5'  CAGGCTCTGGAGCTCA      37244         A    GTT
                                CAGGCTCTG GAGT   TCA
                                ||||||||| ||||   |||
                                GTCCGAGAC CTCG   AGT
                                     _   ____
GAM1480  DKFZP434I092 3'  CAGGCACTGAAGTATTT     37245       T    G
                                CAGGC CTGA AGTGTTT
                                ||||| |||| |||||||
                                GTCCG GACT TCATAAA
                                   T   _
GAM1480  DKFZp434N127 3'  AGGCCTTGAGTGTTTTCAC   37246      T  GA      _
                                AGGC CT  GAGTGTTT CAC
                                |||| ||  |||||||| |||
                                TCCG GA  CTCACAAA GTG
                                  _ A_       A
GAM1480  DKFZp434O0320 3'  CAGGCTCTGGGTGAAGTGC   37247         A___
                                CAGGCTCTG    GAGTGT
                                |||||||||    ||||||
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                                GTCCGAGAC    TTCACG
                                     CCAC
GAM1480  DKFZP564A2416 5'  AGGCCCTGGGAATCCAC     37248         A    GTT
                                AGGCTCTG GAGT   TCAC
                                |||||||| ||||   ||||
                                TCCGGGAC CTTA   GGTG
                                     C    ___
GAM1480  DKFZP586M1019 3'  CAGGCTCTGGGAGTGGACA    37249         A     TTT
                                CAGGCTCTG GAGTG   CA
                                ||||||||| |||||   ||
                                GTCCGAGAC CTCAC   GT
                                     C     CT_
GAM1480  DKFZp761B1514 3'  CAGGGTTTTGAAGTGTTTCA   37250      CTC_   G
                                CAGG    TGA AGTGTTTCA
                                ||||    ||| |||||||||
                                GTCC    ACT TCACAAAGT
                                  CAAA   _
GAM1480  FEM-2     3'  GACTCTGAATGCCTTCA     37251          A  G
                                GGCTCTGAG GT TTTCA
                                ||||||||| || |||||
                                CTGAGACTT CG GAAGT
                                     A  _
GAM1480  FER1L4    3'  AGACTCTGGGGTAGCTCAC    37252         AGA   T
                                AGGCTCTG   GTG TTCAC
                                ||||||||   ||| |||||
                                TCTGAGAC   CAT GAGTG
                                     CC_   C
GAM1480  FLJ00001  3'  CAGGCTCTGGAGGGCCCTCA  37253         A   T   _
                                CAGGCTCTG GAG GTT TCA
                                ||||||||| ||| ||| |||
                                GTCCGAGAC CTC CGG AGT
                                     _  C   G
GAM1480  FLJ10043  3'  CAGGTTCTGAGAAGCCTTT   37254      C      _  G
                                CAGG TCTGAGA GT TTT
                                |||| ||||||| || |||
                                GTCC AGACTCT CG AAA
                                  A      T  G
GAM1480  FLJ10520  3'  CAGGTCAGAAGTGTTT      37255      C  T  G
                                CAGG TC GA AGTGTTT
                                |||| || || |||||||
                                GTCC AG CT TCACAAA
                                  _  T  _
GAM1480  FLJ10607  3'  AGCTTTGTTGCGTTTCAC    37256      C  AGA
                                GGCT TG   GTGTTTCAC
                                |||| ||   |||||||||
                                TCGA AC   CGCAAAGTG
                                  A  AA_
GAM1480  FLJ10916  3'  CAGGCCCTGAAACTTTCAC   37257           GTG
                                CAGGCTCTGAGA   TTTCAC
                                ||||||||||||   ||||||
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                                GTCCGGGACTTT  AAAGTG
                                      G__
GAM1480  FLJ11700  3' CAGGCTCTGGTGACAC     37258        AGA  TTT
                                CAGGCTCTG  GTG  CAC
                                |||||||||  |||  |||
                                GTCCGAGAC  CAC  GTG
                                     ___  T__
GAM1480  FLJ12439  3' CAGGCTGATGTTTCA      37259      CTGA  G
                                CAGGCT   GA TGTTTCA
                                ||||||   || |||||||
                                GTCCGA   CT ACAAAGT
                                    ____ _
GAM1480  FLJ14054  3' CAGGATCTGAGTGCTT     37260     C    GA
                                CAGG TCTGA  GTGTTT
                                |||| |||||  ||||||
                                GTCC AGACT  CACGAA
                                  T    __
GAM1480  FLJ14346  3' GGCTCTGAGTGTGATCA    37261        A  TT
                                GGCTCTGAG GTG  TCA
                                ||||||||| |||  |||
                                CCGAGACTC CAC  AGT
                                     A  T_
GAM1480  FLJ14351  5' CAAGCTCTGGGAGAAGGTCA  37262        A  TGTT
                                CAGGCTCTG GAG   TCA
                                ||||||||| |||   |||
                                GTTCGAGAC CTC   AGT
                                     C  TTCC
GAM1480  FLJ14397  3' CAGGCTATTGAGGCAGCT   37263      C_   A  _
                                CAGGCT  TGAG GT GTT
                                ||||||  |||| || |||
                                GTCCGA  ACTC CG CGA
                                   TA   _ T
GAM1480  FLJ14594  3' CAGGTTACAAAGTGTTTCAC  37264     CTCTG
                                CAGG    AGAGTGTTTCAC
                                ||||    ||||||||||||
                                GTCC    TTTCACAAAGTG
                                  AATG_
GAM1480  FLJ14957  3' GGCTCTGAGAGTGAGCAC   37265          TTT
                                GGCTCTGAGAGTG  CAC
                                ||||||||||||  |||
                                CCGAGACTCTCAC  GTG
                                       TC_
GAM1480  FLJ20595  5' CAGGCTCTCAGGTAAGACAC  37266       G  A  TTT
                                CAGGCTCT AG GTG  CAC
                                |||||||| || |||  |||
                                GTCCGAGA TC CAT  GTG
                                     G  _  TCT
GAM1480  FLJ21276  3' GGCTTCTGAGAGACCAC    37267     _     TGTT
                                GGCT CTGAGAG   TCAC
                                |||| |||||||   ||||
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                                CCGA GACTCTC    GGTG
                                  A      T___
GAM1480  FLJ22378  3'  GGCTCAGACGGTGTTTCA    37268      T  GA
                                GGCTC GA  GTGTTTCA
                                ||||| ||  ||||||||
                                CCGAG CT  CACAAAGT
                                   T  GC
GAM1480  FLJ31168  3'  CAGGTGCTGAGAACAGACCAC  37269     CT     GT TT
                                CAGG  CTGAGA  G  TCAC
                                ||||  ||||||  |  ||||
                                GTCC  GACTCT  T  GGTG
                                  AC     TG CT
GAM1480  FUT10     3'  AGGCTCTAGTCTGTTTCA    37270       G  AG
                                AGGCTCT AG  TGTTTCA
                                ||||||| ||  |||||||
                                TCCGAGA TC  ACAAAGT
                                   _  AG
GAM1480  FYCO1     3'  CAGGCTCTGTGATTTCA     37271        A  GTG
                                CAGGCTCTG GA   TTTCA
                                ||||||||| ||   |||||
                                GTCCGAGAC CT   AAAGT
                                     A  ___
GAM1480  GAB3      3'  CAAGCTTCCCTGTTTCAC    37272       _  GAGAG
                                CAGGCT CT    TGTTTCAC
                                |||||| ||    ||||||||
                                GTTCGA GG    ACAAAGTG
                                   A  G____
GAM1480  GMEB2     3'  CAGGCTCTGGGCTCCA      37273        AGAGT
                                CAGGCTCTG    GTTTCA
                                |||||||||    ||||||
                                GTCCGAGAC    CGAGGT
                                     C____
GAM1480  GPS2      5'  AGGCTCTGAGACGGTGTTT   37274          __
                                AGGCTCTGAGA  GTGTTT
                                ||||||||||  ||||||
                                TCCGAGACTCT  CACAAA
                                      GC
GAM1480  H326      5'  AGGCTCTGTAGATTCAC     37275        _  GTGT
                                AGGCTCTG AGA    TTCAC
                                |||||||| |||   |||||
                                TCCGAGAC TCT    AAGTG
                                     A  _____
GAM1480  HCA4      3'  GGCCTCTGATGTTTCA      37276    _    GAG
                                GGC TCTGA   TGTTTCA
                                ||| |||||   |||||||
                                CCG AGACT   ACAAAGT
                                  G    ___
GAM1480  HE3-ALPHA 5'  GACTCTGAGTTCAGGTCAC   37277         AG  TT
                                GGCTCTGAG  TG  TCAC
                                |||||||||  ||  ||||
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                                CTGAGACTC  GT  AGTG
                                     AA  CC
GAM1480 HIG2     3' CAGGCTTTGGCATCCCAC    37278      C  AGA   TT
                                CAGGCT TG   GTGT  CAC
                                |||||| ||   ||||  |||
                                GTCCGA AC   CGTA  GTG
                                   A ___    GG
GAM1480 HRMT1L3  5' AGCGGGAGGAGTGTTTCA    37279    TCT  _
                                GGC   GAG AGTGTTTCA
                                |||   ||| |||||||||
                                TCG   CTC TCACAAAGT
                                  CC_  C
GAM1480 HSA243666 3' GGCCTCTGTCATTTCAC     37280    _   AGAG
                                GGC TCTG    TGTTTCAC
                                ||| ||||    ||||||||
                                CCG AGAC    GTAAAGTG
                                  G   A___
GAM1480 IMAP1    5' CAGGCTCTGAAGTTGGCCAC   37281        G   GTT
                                CAGGCTCTGA AGT   TCAC
                                |||||||||| |||   ||||
                                GTCCGAGACT TCA   GGTG
                                     _  ACC
GAM1480 IRAK3    3' AGGCTCTGAGGACTCAC     37282        AGTGT
                                AGGCTCTGAG    TTCAC
                                |||||||||     |||||
                                TCCGAGACTC    GAGTG
                                     CT___
GAM1480 KIAA0016 3' CAAGCTCTACTAGGTTT     37283        AG  T
                                CAGGCTCTG  AG GTTT
                                |||||||||  || ||||
                                GTTCGAGAT  TC CAAA
                                     GA  _
GAM1480 KIAA0101 5' CAGCCGAGGGTGTTTCAC    37284    GCT    A
                                CAG   CTGAG GTGTTTCAC
                                |||   ||||| |||||||||
                                GTC   GGCTC CACAAAGTG
                                  ___    C
GAM1480 KIAA0186 5' GGCTCTCGGCGCCTCAC     37285      GAGA
                                GGCTCT    GTGTTTCAC
                                ||||||    |||||||||
                                CCGAGA    CGCGGAGTG
                                   GC__
GAM1480 KIAA0377 3' GGCTCTGAGGGTTTGGATCAC 37286        AG__  TT
                                GGCTCTGAG    TG  TCAC
                                |||||||||    ||  ||||
                                CCGAGACTC    AC  AGTG
                                     CCAA  CT
GAM1480 KIAA0513 3' CAGGCTCTGACTGTTT      37287        GAG
                                CAGGCTCTGA   TGTTT
                                |||||||||   |||||
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                                GTCCGAGACT   ACAAA
                                     G__
GAM1480  KIAA0680  3'  CAGACTCTAGGTGTGTTT    37288         AGA
                                CAGGCTCTG   GTGTTT
                                |||||||||   ||||||
                                GTCTGAGAT   CACAAA
                                     CCA
GAM1480  KIAA0934  3'  TGAGCTCTGAGAAGGTGT    37289   A       __
                                C GGCTCTGAGA  GTGT
                                | ||||||||||  ||||
                                A TCGAGACTCT  CACA
                                 C         TC
GAM1480  KIAA1005  3'  CAGGCTTTGAATGTTCAC    37290       CTGA     T
                                CAGGCT    GAGTGTT CAC
                                ||||||    ||||||| |||
                                GTCCGA    CTTACAA GTG
                                   AA__     _
GAM1480  KIAA1497  5'  CAAGCTCTGAATTCA       37291          AGTGT
                                CAGGCTCTGAG     TTCA
                                ||||||||||     ||||
                                GTTCGAGACTT     AAGT
                                      _____
GAM1480  KIAA1554  5'  CAGGCCCTGAGGCAGCGC    37292          __
                                CAGGCTCTGAG  AGTGT
                                ||||||||||  |||||
                                GTCCGGGACTC  TCGCG
                                      CG
GAM1480  KIAA1808  3'  CAGACTTTGGTGTTTCA     37293       C  AGA
                                CAGGCT TG   GTGTTTCA
                                |||||| ||   ||||||||
                                GTCTGA AC   CACAAAGT
                                   A  ___
GAM1480  KIAA1862  3'  CAGGCCTCTGGATGCTTCAC  37294      _   A  G
                                CAGGC TCTG GA TGTTTCAC
                                ||||| |||| || ||||||||
                                GTCCG AGAC CT ACGAAGTG
                                   G   _ _
GAM1480  KIAA1950  3'  CAGGCTCCGGCTTTCA      37295         AGA  G
                                CAGGCTCTG   GT TTTCA
                                |||||||||   || |||||
                                GTCCGAGGC   CG AAAGT
                                      ___ _
GAM1480  MAPK8IP3  3'  GCTCTGAGGTGCACTCAC    37296         A   _
                                GCTCTGAG GTGT TTCAC
                                |||||||| |||| |||||
                                CGAGACTC CACG GAGTG
                                     _   T
GAM1480  MASA      3'  CAGTCTTTGAAATATTTCA   37297     G  C    G
                                CAG CT TGAGA TGTTTCA
                                ||| || ||||| |||||||
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                                GTC GA ACTTT ATAAAGT
                                  A A    _
GAM1480 MGC14161 5' GGATCTCAATTGTTTCAC    37298    C   G  AG
                                GG TCT AG  TGTTTCAC
                                || ||| ||  ||||||||
                                CC AGA TT  ACAAAGTG
                                 T   G  A_
GAM1480 MGC14859 3' CAGGTCCCCGTGTTTCAC    37299     _    GAGA
                                CAGG CTCT    GTGTTTCAC
                                |||| ||||    |||||||||
                                GTCC GGGG    CACAAAGTG
                                  A    _____
GAM1480 MGC15906 3' CAGGCCCTGAGGGGGGTGC   37300          A___
                                CAGGCTCTGAG    GTGT
                                ||||||||||    ||||
                                GTCCGGGACTC    CACG
                                       CCCC
GAM1480 MGC16179 5' CAGGCCCTGAGGATCCTC    37301          AG G
                                CAGGCTCTGAG  T TTT
                                ||||||||||  | |||
                                GTCCGGGACTC  A GAG
                                       CT G
GAM1480 MGC4368  3' AGGCCCTGGATGTTCAC     37302        A  G    T
                                AGGCTCTG GA TGTT CAC
                                |||||||| || |||| |||
                                TCCGGGAC CT ACAA GTG
                                      _ _   _
GAM1480 MRPL50   3' CAGTTCTGGTAGTATTTCAC  37303     GC    AG
                                CAG  TCTG  AGTGTTTCAC
                                |||  ||||  ||||||||||
                                GTC  AGAC  TCATAAAGTG
                                  A_   CA
GAM1480 OSBPL6   3' CAGGTTCTGAGAAGCATCAC  37304      C       T  T
                                CAGG TCTGAGAG GT TCAC
                                |||| |||||||| || ||||
                                GTCC AGACTCTT CG AGTG
                                  A       _ T
GAM1480 PEG10    3' CAGGCCTGAGATGTTTCA    37305      T     G
                                CAGGC CTGAGA TGTTTCA
                                ||||| |||||| |||||||
                                GTCCG GACTCT ACAAAGT
                                    _     _
GAM1480 PIF1     3' AGGCTCTGAAGGGTGTTT    37306          A_
                                AGGCTCTGAG  GTGTTT
                                ||||||||||  ||||||
                                TCCGAGACTT  CACAAA
                                      CC
GAM1480 PRO0255  3' AGCTCTGAGATATGATTCA   37307          _   T
                                GGCTCTGAGA GTG TTCA
                                |||||||||| ||| ||||
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                                TCGAGACTCT TAC AAGT
                                     A   T
GAM1480  RASGRP4   3'  CAGGCTCTTGGGACAACGC   37308        ___  G
                                CAGGCTCT   GA AGTGT
                                ||||||||   || |||||
                                GTCCGAGA   CT TTGCG
                                    ACC  G
GAM1480  RBPMS     5'  CAGGCTCTGGGAAGTCC     37309         A   T
                                CAGGCTCTG GAG GTTT
                                ||||||||| ||| ||||
                                GTCCGAGAC CTT CAGG
                                     C  _
GAM1480  RNF38     5'  CAGGCTCTGAAGTCTCAC    37310          AGT
                                CAGGCTCTGAG   GTTTCAC
                                ||||||||||   |||||||
                                GTCCGAGACTT   CAGAGTG
                                      ___
GAM1480  RNP24     3'  CAGTTTTGAAGTGTTTCAC   37311     GCTC   G
                                CAG    TGA AGTGTTTCAC
                                |||    ||| ||||||||||
                                GTC    ACT TCACAAAGTG
                                  AAA_  _
GAM1480  RoXaN     3'  CAGGGCCGAGAGTGTTT     37312      CT
                                CAGG  CTGAGAGTGTTT
                                ||||  ||||||||||||
                                GTCC  GGCTCTCACAAA
                                  C_
GAM1480  SAD1      5'  CAGGCTCCGAGTCCTCA     37313          AGTG
                                CAGGCTCTGAG    TTTCA
                                ||||||||||    |||||
                                GTCCGAGGCTC    GGAGT
                                     A___
GAM1480  SCIN      5'  AAGTTCTGAGGGTTCAC     37314     C     A  GTT
                                AGG TCTGAG GT   TCAC
                                ||| |||||| ||   ||||
                                TTC AGACTC CA   AGTG
                                  A     C  ___
GAM1480  SFRS9     3'  CAGTTTAAAATGTTTCAC    37315     GCTCTG
                                CAG     AGAGTGTTTCAC
                                |||     ||||||||||||
                                GTC     TTTTACAAAGTG
                                  AAA___
GAM1480  SOX30     3'  CAGACTCTAGTTTCA       37316         AGAGT
                                CAGGCTCTG    GTTTCA
                                |||||||||    ||||||
                                GTCTGAGAT    CAAAGT
                                      _____
GAM1480  TA-NFKBH  3'  AGGGGTGCAGGGTGTTTCAC  37317     CTC  _  A
                                AGG   TG AG GTGTTTCAC
                                |||   || || |||||||||
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                                TCC   AC TC CACAAAGTG
                                  CC_  G  C
GAM1480  TSPAN-1   3'  AGGCTCTGCTGATTTCAC    37318        AGAGT
                                AGGCTCTG    GTTTCAC
                                ||||||||    |||||||
                                TCCGAGAC    TAAAGTG
                                    GAC__
GAM1480  WBSCR20A  5'  CAGGTCTTGAGAGTGTTCAC  37319     C  _       T
                                CAGG TCT GAGAGTGTT CAC
                                |||| ||| ||||||||| |||
                                GTCC AGA CTCTCACAA GTG
                                  _  A       _
GAM1480  ZFP95     3'  CAAGGTAGAGTGTTTCAC    37320     CTCTG
                                CAGG    AGAGTGTTTCAC
                                ||||    ||||||||||||
                                GTTC    TCTCACAAAGTG
                                  CA___
GAM1480  ZFP95     3'  CAAGGTAGAGTGTTTCAC    37320     CTCTG
                                CAGG    AGAGTGTTTCAC
                                ||||    ||||||||||||
                                GTTC    TCTCACAAAGTG
                                  CA___
GAM1480  ZNF271    3'  TGAGCTCTGAGTTAACCTTTCA 37321    A       AG__ G
                                C GGCTCTGAG    T TTTCA
                                | |||||||||    | |||||
                                A TCGAGACTC    G AAAGT
                                 C        AATT G
GAM1480  LOC112885 3'  CAGGCTCTGGCGGGGATCAC  35691        AGA   TT__
                                CAGGCTCTG   GTG    TCAC
                                |||||||||   |||    ||||
                                GTCCGAGAC   CGC    AGTG
                                    ___   CCCT
GAM1480  LOC123872 5'  CAGGCTCCGAGGGCTCA     37322          A  GTT
                                CAGGCTCTGAG GT   TCA
                                |||||||||||| ||   |||
                                GTCCGAGGCTC CG   AGT
                                      C  ___
GAM1480  LOC126755 3'  CAGGCTCTGTTCAGTTCAC   37323        AG_   GTT
                                CAGGCTCTG   AGT   TCAC
                                |||||||||   |||   ||||
                                GTCCGAGAC   TCA   AGTG
                                    AAG   ___
GAM1480  LOC127687 3'  AGGCTCTACTGAAGGTGTTT  37324       ____   A
                                AGGCTCT    GAG GTGTTT
                                |||||||    ||| ||||||
                                TCCGAGA    TTC CACAAA
                                   TGAC   _
GAM1480  LOC131870 3'  CAGGCTCTGAGAACCTGC    37325           __
                                CAGGCTCTGAGAG  TGT
                                ||||||||||||  |||
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                                GTCCGAGACTCTT  ACG
                                      GG
GAM1480  LOC138639 3'  AGGTCTGAAATATTCAC     37326     C      GTGT
                                AGG TCTGAGA    TTCAC
                                ||| |||||||    |||||
                                TCC AGACTTT    AAGTG
                                  _      AT__
GAM1480  LOC143631 3'  CAGGTGCTGAGTGCTTTCA    37327      CT    A  G
                                CAGG  CTGAG GT TTTCA
                                ||||  ||||| || |||||
                                GTCC  GACTC CG AAAGT
                                   AC     A  _
GAM1480  LOC145317 3'  CAGGCTCTGCAGTCCCTC     37328         AG   G
                                CAGGCTCTG  AGT TTTC
                                |||||||||  ||| ||||
                                GTCCGAGAC  TCA GGAG
                                      G_   G
GAM1480  LOC147711 3'  GACTCTGAGATGAACAC      37329         G  TTT
                                GGCTCTGAGA TG   CAC
                                |||||||||| ||   |||
                                CTGAGACTCT AC   GTG
                                      _  TT_
GAM1480  LOC148003 3'  CAGGCTCTAGGAATCCCA     37330         A  GT  TT
                                CAGGCTCTG GA  GT  CA
                                |||||||| ||  ||  ||
                                GTCCGAGAT CT  TA  GT
                                      C  __  GG
GAM1480  LOC148137 3'  CAGGCTCTTAGGCTGGGCAC   37331        G  A  GTTT
                                CAGGCTCT AG GT    CAC
                                |||||||| || ||    |||
                                GTCCGAGA TC CG    GTG
                                     A  _  ACCC
GAM1480  LOC150157 5'  CAGGCTCTGGGAGCAGCT     37332         A    _
                                CAGGCTCTG GAGT GTT
                                ||||||||| |||| |||
                                GTCCGAGAC CTCG CGA
                                      C    T
GAM1480  LOC150319 3'  CAGGCTCCTGAGATCTCAC    37333        GA   T
                                CAGGCTCT  GAG GTTTCAC
                                ||||||||  ||| |||||||
                                GTCCGAGG  CTC TAGAGTG
                                     A_   _
GAM1480  LOC150368 3'  CAGGCTCTGGTGACCCA      37334         AGA   T
                                CAGGCTCTG   GTG TTCA
                                |||||||||   ||| ||||
                                GTCCGAGAC   CAC GGGT
                                      ____   T
GAM1480  LOC150407 3'  CAGGCTCTGGGAATTTAACCA  37335         A    GTT_
                                CAGGCTCTG GAGT    TCA
                                ||||||||| ||||    |||
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                                GTCCGAGAC CTTA    GGT
                                     C    AATT
GAM1480  LOC150605 5'  CAGGCCCTGGGCCCTTCAC    37336         AGA  G
                                CAGGCTCTG   GT TTTCAC
                                |||||||||   || ||||||
                                GTCCGGGAC   CG GAAGTG
                                     C__  G
GAM1480  LOC151176 3'  CAGGCCTGAGCGCCCTT     37337       T    A  G
                                CAGGC CTGAG GT TTT
                                ||||| ||||| || |||
                                GTCCG GACTC CG GAA
                                   _    G  G
GAM1480  LOC151658 5'  CAGGCTCTGTGAATAGCCAC   37338         A    TT
                                CAGGCTCTG GAGTG  TCAC
                                ||||||||| |||||  ||||
                                GTCCGAGAC CTTAT  GGTG
                                     A    C_
GAM1480  LOC151827 5'  GGCCCTGAGGCCTCAC      37339         AGT
                                GGCTCTGAG   GTTTCAC
                                |||||||||   |||||||
                                CCGGGACTC   CGGAGTG
                                      ___
GAM1480  LOC152018 3'  GGCCCTAGTGTTTCAC      37340       GAG
                                GGCTCT   AGTGTTTCAC
                                ||||||   ||||||||||
                                CCGGGA   TCACAAAGTG
                                     ___
GAM1480  LOC152225 5'  CAGACTCTGAGAAGTCT     37341           T
                                CAGGCTCTGAGAG GTTT
                                |||||||||||| ||||
                                GTCTGAGACTCTT CAGA
                                      _
GAM1480  LOC153146 5'  AGGCTCTGGCAGCTCAC     37342         AG   GTT
                                AGGCTCTG  AGT   TCAC
                                ||||||||  |||   ||||
                                TCCGAGAC  TCG   AGTG
                                     CG   ___
GAM1480  LOC153346 3'  CAGTTCTGAAGTATTT      37343     GC    G
                                CAG  TCTGA AGTGTTT
                                |||  ||||| |||||||
                                GTC  AGACT TCATAAA
                                  A_    _
GAM1480  LOC154214 5'  CAGGCTCTAAATTCA       37344          AGTGT
                                CAGGCTCTGAG    TTCA
                                ||||||||||    ||||
                                GTCCGAGATTT    AAGT
                                      _____
GAM1480  LOC165246 3'  CAGGCCCTGGGGATCCAC    37345         A_  GTGT
                                CAGGCTCTG  GA    TTCAC
                                |||||||||  ||    |||||
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                                GTCCGGGAC CT   AGGTG
                                     CC ____
GAM1480 LOC169225 5' CAGGCTCTGAGGACAGTGT  37346        ___
                                CAGGCTCTGAG  AGTGT
                                ||||||||||  |||||
                                GTCCGAGACTC  TCACA
                                      CTG
GAM1480 LOC196385 3' CAGGCTCCGAATTCA     37347         AGTGT
                                CAGGCTCTGAG   TTCA
                                ||||||||||   ||||
                                GTCCGAGGCTT   AAGT
                                     _____
GAM1480 LOC196890 5' CAGGCTCTGGGAGCAGCT   37332        A  _
                                CAGGCTCTG GAGT GTT
                                ||||||||| |||| |||
                                GTCCGAGAC CTCG CGA
                                     C   T
GAM1480 LOC201595 3' AGCACTAAAGAGTGTTTCA  37348    T  _
                                GGC CTGA GAGTGTTTCA
                                ||| |||| ||||||||||
                                TCG GATT CTCACAAAGT
                                  T   T
GAM1480 LOC202915 3' GGCTCCGAGGGCCTCAC    37349        AGT
                                GGCTCTGAG  GTTTCAC
                                |||||||||  |||||||
                                CCGAGGCTC  CGGAGTG
                                     C__
GAM1480 LOC219940 3' GACTCTGAGACTCCAC     37350        GTG
                                GGCTCTGAGA  TTTCAC
                                ||||||||||  ||||||
                                CTGAGACTCT  GAGGTG
                                     ___
GAM1480 LOC220980 5' CAGGCTCTGCAGGGCCTCAC 37351        AG  T
                                CAGGCTCTG  AG GTTTCAC
                                |||||||||  || |||||||
                                GTCCGAGAC  TC CGGAGTG
                                     G_  C
GAM1480 LOC221025 3' AGGCAAAGTGTTTCA      37200     TCTG
                                AGGC   AGAGTGTTTCA
                                ||||   ||||||||||
                                TCCG   TTTCACAAAGT
                                    ____
GAM1480 LOC221903 3' CAGACTTGGAAGTGTTT    37352      C  AG
                                CAGGCT TG  AGTGTTT
                                ||||||  ||  |||||||
                                GTCTGA AC  TCACAAA
                                    _  CT
GAM1480 LOC221935 3' AGCTCTGAGATCTCA      37353        GTG
                                GGCTCTGAGA  TTTCA
                                |||||||||  |||||
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                                TCGAGACTCT   AGAGT
                                     ___
GAM1480  LOC222803 5'  CAAGCTCTGAGCTTTCAC    37354          AGTG
                                CAGGCTCTGAG    TTTCAC
                                ||||||||||    ||||||
                                GTTCGAGACTC    AAAGTG
                                      G___
GAM1480  LOC222933 5'  CAGTGCTCTGAGAAGTAT    37355    _       _
                                CAG GCTCTGAGA GTGT
                                ||| ||||||||| ||||
                                GTC CGAGACTCT CATA
                                  A        T
GAM1480  LOC54466  3'  AAGTTCTGAGAGCCCCAC    37356    C       GT
                                AGG TCTGAGAGT  TTCAC
                                ||| |||||||||  |||||
                                TTC AGACTCTCG  GGGTG
                                  A       __
GAM1480  LOC90170  5'  CAGGCTCTGAGGGCTCA     37357          A  GTT
                                CAGGCTCTGAG GT   TCA
                                |||||||||| ||   |||
                                GTCCGAGACTC CG   AGT
                                      C ___
GAM1480  LOC90620  3'  GACTCTGAGGTGCATTCAC    37358         A   _
                                GGCTCTGAG GTGT TTCAC
                                ||||||||| |||| |||||
                                CTGAGACTC CACG AAGTG
                                     _   T
GAM1480  LOC90826  5'  GACTCTGAAATTTCAC      37359         AGT
                                GGCTCTGAG   GTTTCAC
                                |||||||||   |||||||
                                CTGAGACTT   TAAAGTG
                                     ___
GAM1480  LOC90925  3'  CAGGTTCTAAAATATTT     37360      C      G
                                CAGG TCTGAGA TGTTT
                                |||| ||||||| |||||
                                GTCC AGATTTT ATAAA
                                  A      _
GAM1480  LOC92249  3'  AGGCTCTGGTATTAGAC     37361        AGA    TC
                                AGGCTCTG   GTGTT  AC
                                ||||||||   |||||  ||
                                TCCGAGAC   CATAA  TG
                                     ___     TC
GAM1480  LOC92573  5'  GGTTCCCAGTGTTTCAC     37362    C   GAG
                                GG TCT   AGTGTTTCAC
                                || |||   ||||||||||
                                CC AGG   TCACAAAGTG
                                 A  G__
GAM1480  LOC92689  3'  CAAGCTCTGGGGAGCAGCT   37363         A_   _
                                CAGGCTCTG  GAGT GTT
                                |||||||||  |||| |||
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                                GTTCGAGAC  CTCG CGA
                                     CC    T
GAM1480  LOC92710  3'  CAAGCTCTTTGTTTCA     37364        GAGAG
                                CAGGCTCT    TGTTTCA
                                ||||||||    |||||||
                                GTTCGAGA    ACAAAGT
                                    A____
GAM1481  CLCA3     3'  CAAAAATTGCCAAACTGATT   37367       GATC
                                CAAGGAT    GCCAAACTGATT
                                |||||||    ||||||||||||
                                GTTTTTA    CGGTTTGACTAA
                                    A___
GAM1481  DNM1      3'  ACAAGGATAGCACAGTGACTGA 37368        AT   CAA_
              TT                  ACAAGGATG  CGC    ACTGATT
                                |||||||||  |||   |||||||
                                TGTTCCTAT  GTG    TGACTAA
                                     C_   TCAC
GAM1481  DPYD      3'  ACAGAGAGTAGTCAAACTGATT 37369     AG  TGATCGC
                                ACA  GA      CAAACTGATT
                                |||  ||      ||||||||||
                                TGT  CT      GTTTGACTAA
                                  CT  CATCA__
GAM1481  KCNC3     5'  AGGAACCAAACTGAT      37370      TGATC
                                AGGA    GCCAAACTGAT
                                ||||    ||||||||||
                                TCCT    TGGTTTGACTA
                                  _____
GAM1481  ARHGEF9   3'  ACCAGGACACTGAACTGAT   37371    A   TGAT   CA
                                AC AGGA    CGC  AACTGAT
                                || ||||    |||  |||||||
                                TG TCCT    GTG  TTGACTA
                                 G   _____   AC
GAM1481  ITGA10    3'  CAAGGGCTGGCAAACTGATT   37372      A_  ATC  C
                                CAAGG  TG   GC AAACTGATT
                                |||||  ||   || |||||||||
                                GTTCC  AC   CG TTTGACTAA
                                   CG  ___  _
GAM1481  KIAA0433  3'  CAAGGATAATAAATTGAT    37373         CGCC   C
                                CAAGGATGAT    AAA TGAT
                                ||||||||||    ||| ||||
                                GTTCCTATTA    TTT ACTA
                                     _____   A
GAM1481  KIAA0779  3'  ACCAGGATGATGGAACTG    37374    A      CGCCA
                                AC AGGATGAT     AACTG
                                || ||||||||     |||||
                                TG TCCTACTA     TTGAC
                                 G       CC___
GAM1481  NFX1      3'  GGGGGACGGCCAAACTGATT   37375    AT   C
                                GG  GAT GCCAAACTGATT
                                ||  ||| ||||||||||||
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                                CC  CTG CGGTTTGACTAA
                                 CC   C
GAM1481  LOC150111 5'  ACAAGGACTGATCAGTCACTGA 37376       _     CCAA
                TT                  ACAAGGA TGATCG    ACTGATT
                                    ||||||| ||||||    |||||||
                                    TGTTCCT ACTAGT    TGACTAA
                                       G     CAG_
GAM1481  LOC154089 3'  CAAGGTCGGTTAAACTGATT   37377      ATGA   CC_
                                    CAAGG   TCG   AAACTGATT
                                    ||||||   |||   |||||||||
                                    GTTCC   AGC   TTTGACTAA
                                       _____  CAA
GAM1482  AIM1     3'  ACAAAATCACCCAAAA      37380         AT  TG
                                    GCAAAATCA  CC  CAAAA
                                    |||||||||  ||  |||||
                                    TGTTTTAGT  GG  GTTTT
                                          __  __
GAM1482  CRYGA    5'  GCAAAAACAACACAAAAG    37381       T    CCT
                                    GCAAAA CAAT   GCAAAAG
                                    |||||| ||||   |||||||
                                    CGTTTT GTTG   TGTTTTC
                                       T   ___
GAM1482  CRYGA    5'  GCAAAAACAACACAAAAG    37381       T    CCT
                                    GCAAAA CAAT   GCAAAAG
                                    |||||| ||||   |||||||
                                    CGTTTT GTTG   TGTTTTC
                                       T   ___
GAM1482  LANCL1   3'  GCAAAATCAGTTGCAAA     37382         ATCC
                                    GCAAAATCA    TGCAAA
                                    |||||||||    ||||||
                                    CGTTTTAGT    ACGTTT
                                         CA__
GAM1482  NUFIP1   3'  TTAGCTGAATCAATCCTTTTAA 37383       AA        GC_
                AAG                    TTAGC  AATCAATCCT   AAAAG
                                    |||||  ||||||||||   |||||
                                    AATCG  TTAGTTAGGA   TTTTC
                                       AC        AAA
GAM1482  P23      3'  CTAGCAAAACCCTGCA      37384         ATCA
                                    TTAGCAAA    ATCCTGCA
                                    ||||||||    ||||||||
                                    GATCGTTT    TGGGACGT
                                          _____
GAM1482  PCDHB16  3'  GCAAAATCTCATCGCTGCAAAA 37385         A_  _
                G                   GCAAAATC  ATC CTGCAAAAG
                                    |||||||||  ||| |||||||||
                                    CGTTTTAG  TAG GACGTTTTC
                                         AG   C
GAM1482  PIM2     3'  GCAAGAATCTGCAAAA      37386      AATC    C
                                    GCAA    AATC TGCAAAA
                                    ||||    |||| |||||||
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                                CGTT    TTAG ACGTTTT
                                  C___   _
GAM1482 RLN2     3' TCAGCAAAATCTAGCAA     37387          AATCCT
                                TTAGCAAAATC     GCAA
                                ||||||||||     ||||
                                AGTCGTTTTAG     CGTT
                                      AT____
GAM1482 FLJ10520 3' TTAGTGGAATCAATCAGCA   37388     CAA      CT
                                TTAG   AATCAATC  GCA
                                ||||   ||||||||  |||
                                AATC   TTAGTTAG  CGT
                                  ACC       T_
GAM1482 FLJ20716 3' CAGCAAATGTTTTGCAAAAG  37389       ATCAATCC
                                TAGCAAA       TGCAAAAG
                                |||||||       ||||||||
                                GTCGTTT       ACGTTTTC
                                    ACAAA___
GAM1482 FLJ20793 3' AGCACCAAATTCTGCAAAAG  37390     AAA    TC_
                                AGCA   TCAA   CTGCAAAAG
                                ||||   ||||   |||||||||
                                TCGT   GGTT   GACGTTTTC
                                  ___    TAA
GAM1482 FLJ22282 3' TTAGCAAGTCAGCCTGCAAA  37391       AA   AT
                                TTAGCAA  TCA  CCTGCAAA
                                |||||||  |||  ||||||||
                                AATCGTT  AGT  GGACGTTT
                                    C_   C_
GAM1482 KIAA0757 3' TTAGCAAAATGAATCTGAAC  37392         C    CT_
                                TTAGCAAAAT AATC   GC
                                |||||||||| ||||   ||
                                AATCGTTTTA TTAG   TG
                                      C    ACT
GAM1482 KIAA1136 3' CTAGCAGGATCAATCCTG    37393       AA
                                TTAGCA  ATCAATCCTG
                                ||||||  ||||||||||
                                GATCGT  TAGTTAGGAC
                                    CC
GAM1482 KIAA1205 3' TTAGCAAAGATCTTGGCCTGCA 37394        _   AAT_
                                TTAGCAAA ATC    CCTGCA
                                |||||||| |||    ||||||
                                AATCGTTT TAG    GGACGT
                                     C   AACC
GAM1482 KIAA1497 3' CTAGCAAAGTCAAAAATACAAA 37395        A    TCC
             AG                   TTAGCAAA TCAA   TGCAAAAG
                                |||||||| ||||   ||||||||
                                GATCGTTT AGTT   ATGTTTTC
                                     C    TTT
GAM1482 MGC26641 3' GCAAAATCAATCTTAAGCTTTT 37396          _________  GCAAA
             GA                   CAAAATCAATC       CT     A
                                ||||||||||       ||    |
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                                GTTTTAGTTAG      GA    T
                                      AATTCIII  AAACG
GAM1482  MGC27171  3'  TTAGCAAAATTACAAAA    37397         CAATCC
                                TTAGCAAAAT    TGCAAAA
                                ||||||||||    |||||||
                                AATCGTTTTA    ATGTTTT
                                      _______
GAM1482  MRPL42    3'  TTAGCAAAATTATCTAACA   37398         CA  CT
                                TTAGCAAAAT  ATC  GCA
                                ||||||||||  |||  |||
                                AATCGTTTTA  TAG  TGT
                                      A_   AT
GAM1482  LOC143719 5'  TTAGGAGCTCCTCCTGCAAAAG 37399      CAAAA  AA
                                TTAG    TC  TCCTGCAAAAG
                                ||||    ||  ||||||||||||
                                AATC    AG  AGGACGTTTTC
                                  CTCG_  G_
GAM1482  LOC149483 3'  TCAGCAAAGCCAACTGC    37400         AT  TC
                                TTAGCAAA  CAA  CTGC
                                ||||||||  |||  ||||
                                AGTCGTTT  GTT  GACG
                                     CG   __
GAM1482  LOC158177 3'  CTAGCAAAACCCTGC      37401         ATCA
                                TTAGCAAA   ATCCTGC
                                ||||||||   |||||||
                                GATCGTTT   TGGGACG
                                      _____
GAM1482  LOC203292 3'  CTAGCAAAACCCTGCA     37384         ATCA
                                TTAGCAAA   ATCCTGCA
                                ||||||||   ||||||||
                                GATCGTTT   TGGGACGT
                                      _____
GAM1482  LOC221981 3'  TCAGCAAAATATGACCTGCAAA 37402          CAAT
                                TTAGCAAAAT   CCTGCAAA
                                ||||||||||   ||||||||
                                AGTCGTTTTA   GGACGTTT
                                      TACT
GAM1482  LOC253649 3'  CTAGCAAAACCCTGC      37401         ATCA
                                TTAGCAAA   ATCCTGC
                                ||||||||   |||||||
                                GATCGTTT   TGGGACG
                                      _____
GAM1482  LOC56906  3'  CTAGCAAATGTCAAGTCCTG  37403         A_   _
                                TTAGCAAA  TCAA TCCTG
                                ||||||||  |||| |||||
                                GATCGTTT  AGTT AGGAC
                                     AC   C
GAM1482  LOC90499  3'  CTAGCAAAACCCTGCA     37384         ATCA
                                TTAGCAAA   ATCCTGCA
                                ||||||||   ||||||||
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                                GATCGTTT   TGGGACGT
                                       ____
GAM1482 LOC91907 3' CTAGCAAAGTCAAAAATACAAA 37395       A   TCC
             AG                  TTAGCAAA TCAA  TGCAAAAG
                                 |||||||| ||||  ||||||||
                                 GATCGTTT AGTT  ATGTTTTC
                                     C   TTT
GAM1483 C7      3' TGATAGGCCTGAATGGAGCATT 37406    CAA    CGA
             CA                  TGA  GCCTGA  GAGCGTTCA
                                 |||  ||||||  |||||||||
                                 ACT  CGGACT  CTCGTAAGT
                                  ATC    TAC
GAM1483 DUSP5   3' TGCAAGCCTGGTGACCACTCA 37407   A      ACGA  G
                                 TG CAAGCCTG   GA CGTTCA
                                 || ||||||||   || ||||||
                                 AC GTTCGGAC   CT GTGAGT
                                  _      CA__  G
GAM1483 ATP6V1F  3' TGGCAAGCCTGGGGAGAG   37408   A      AC
                                 TG CAAGCCTG  GAGAG
                                 || ||||||||  |||||
                                 AC GTTCGGAC  CTCTC
                                  C      CC
GAM1483 DKFZP564C103 3' TGATGGCCTGACGCTCTCTTCA 37409    CAA      AGAGCG
                                 TGA  GCCTGACG    TTCA
                                 |||  ||||||||    ||||
                                 ACT  CGGACTGC    AAGT
                                   AC_      GAGAG_
GAM1483 KIAA0561 5' GATGAGCTTGACGAGAGGGT  37410   CA  C      C
                                 GA  AGC TGACGAGAG GT
                                 ||  ||| |||||||||| ||
                                 CT  TCG ACTGCTCTC CA
                                  AC  A       C
GAM1483 KIAA0935 3' TGGCAAGCCTGGCAGGGC   37411   A      A G  A
                                 TG CAAGCCTG C AG GC
                                 || |||||||| | || ||
                                 AC GTTCGGAC G TC CG
                                  C      C _  C
GAM1483 MIC2L1   3' GACAAGCCTGACAAAGTTCA  37412           AGC
                                 GACAAGCCTGACGAG  GTTCA
                                 ||||||||||||||   |||||
                                 CTGTTCGGACTGTTT  CAAGT
                                       ___
GAM1483 PPP4R1L  5' TGACAAGTCTGATGAAGAGCG 37413       C   C_
                                 TGACAAG CTGA  GAGAGCG
                                 ||||||| ||||  |||||||
                                 ACTGTTC GACT  TTCTCGC
                                     A   AC
GAM1483 ZAK     3' TGACAAGCCAGATCAGTTC   37414        TGACG  GC_
                                 TGACAAGCC    AGA  GTTC
                                 |||||||||    |||  ||||
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                                ACTGTTCGG    TCT   CAAG
                                      _____  AGT
GAM1483  LOC149566 3'  TGACAAGTTGGGTGAACGTT  37415       CC  ACGA
                                TGACAAG  TG   GAGCGTT
                                |||||||  ||   |||||||
                                ACTGTTC  AC   CTTGCAA
                                   A_  CCA_
GAM1483  LOC150368 3'  TGGCAAGCCTGTGACAGTCTC 37416    A      AC  G  CG
                                TG CAAGCCTG  GA AG  TTC
                                || ||||||||  || ||  |||
                                AC GTTCGGAC  CT TC  GAG
                                 C       A_  G  A_
GAM1483  LOC255718 5'  TGACAGGCCTGAGGGTCC    37417      A     CGAGA C
                                TGACA GCCTGA    G GTTC
                                ||||| ||||||    | ||||
                                ACTGT CGGACT    C CAGG
                                   C     _____ C
GAM1484  ABCB1    3'  TGATGATGTCTCTCACTC    37420    C       AC
                                TGA GATGTCTTT  CATTC
                                ||| |||||||||  |||||
                                ACT CTACAGAGA  GTGAG
                                  A       __
GAM1484  BSND     3'  TGTGTATTTCTTTACCATTC  37421     ACGATG
                                TGTG     TCTTTACCATTC
                                ||||     ||||||||||||
                                ACAC     AGAAATGGTAAG
                                  ATAA__
GAM1484  FLJ13962  3'  TGGACGATGTCTTCCATC    37422    T        TA
                                TG GACGATGTCTT  CCATT
                                || ||||||||||  |||||
                                AC CTGCTACAGAA  GGTAG
                                 _        __
GAM1484  NY-REN-60 3'  TGTGACCATTAACCATTC    37423       G  GTCTTT
                                TGTGAC AT     ACCATTC
                                |||||| ||     |||||||
                                ACACTG TA     TGGTAAG
                                   G  AT____
GAM1484  PRO1489   5'  TGAGGAAATCTTTTACCATT  37424    C  T    _
                                TGA GA GTCTTT ACCATT
                                ||| || |||||| ||||||
                                ACT CT TAGAAA TGGTAA
                                  C  T     A
GAM1484  LOC146512 3'  TGTGGGATGTCTTCTTC     37425     AC       ACCA
                                TGTG  GATGTCTTT    TTC
                                ||||  |||||||||    |||
                                ACAC  CTACAGAAG    AAG
                                  C_       _____
GAM1484  LOC152925 3'  TGTGATATGTCCCTGAGTCATT 37426      CG       AC__
                                TGTGA  ATGTCTTT    CATT
                                |||||  ||||||||    ||||
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                                ACACT  TACAGGGA   GTAA
                                  A_       CTCA
GAM1484  LOC256221 3'  GTGATGATGTCTACCATT    37427     C      TT
                                GTGA GATGTCT  ACCATT
                                |||| |||||||  ||||||
                                CACT CTACAGA  TGGTAA
                                  A      __
GAM1484  LOC92017  3'  TGTACGATCCACCATTC     37428     A   TGTC
                                TGTG CGA    TTTACCATTC
                                |||| |||    ||||||||||
                                ACAT GCT    AGGTGGTAAG
                                  _  ____
GAM1485  CCNT2     3'  CACAGTGTATATGACCATC    37431      TTA
                                TACGGT   TATATGACCATC
                                ||||||   ||||||||||||
                                GTGTCA   ATATACTGGTAG
                                   C__
GAM1485  FAAH      3'  GGTTTATAAATAAGACCGTCC  37432       TAT__   A
                                GGTTTATA     GACC TCC
                                ||||||||     |||| |||
                                CCAAATAT     CTGG AGG
                                     TTATT    C
GAM1485  ING1      3'  ACACGGTTTATTTTGTCC     37433         ATA  A
                                ATACGGTTTAT   TG CC
                                ||||||||||   || ||
                                TGTGCCAAATA   AC GG
                                      AA_  A
GAM1485  C6.1A     3'  CATACAGTATGTGACCAT     37434       TTAT  A
                                CATACGGT    AT TGACCAT
                                ||||||||    || |||||||
                                GTATGTCA    TA ACTGGTA
                                     ____  C
GAM1485  CHRNA9    3'  CACACTAATATATATATGAC   37435      GGTT_
                                CATAC     TATATATGAC
                                |||||     ||||||||||
                                GTGTG     ATATATACTG
                                   ATTAT
GAM1485  DCOHM     3'  TACAACAAGTATATATGACCAT 37436      TT__
                                TACGG    TATATATGACCAT
                                |||||    ||||||||||||
                                ATGTT    ATATATACTGGTA
                                   GTTC
GAM1485  IMPACT    3'  ATACAGTTTAATACCAT     37437         TATATG
                                ATACGGTTTA     ACCAT
                                ||||||||||     |||||
                                TATGTCAAAT     TGGTA
                                      TA____
GAM1485  KIAA0789  3'  CACATGGCATGTGACCATC   37438     C   TTAT  A
                                CATA GGT    AT TGACCATC
                                |||| |||    || ||||||||
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                                GTGT CCG    TA ACTGGTAG
                                  A  ____  C
GAM1485  KIAA1170  3'  ACATGGTTTATATATTAAC   37439     C         _
                                ATA GGTTTATATAT GAC
                                ||| |||||||||| |||
                                TGT CCAAATATATA TTG
                                  A          A
GAM1485  MGC5560   3'  CATAGGTTTATATAAACTAATC 37440      C         T   C_
              C                  CATA GGTTTATATA GAC  ATCC
                                |||| |||||||||| |||  ||||
                                GTAT CCAAATATAT TTG  TAGG
                                  _         _  AT
GAM1485  PELI2     3'  ACATGGTAAATGTGACCATCC  37441     C   TTAT  A
                                ATA GGT    AT TGACCATCC
                                ||| |||    || |||||||||
                                TGT CCA    TA ACTGGTAGG
                                  A   TT__  C
GAM1485  LOC113386 5'  CACACGGTTTGTCCAT      37442          TATATA  A
                                CATACGGTT      TG CCAT
                                |||||||||      || ||||
                                GTGTGCCAA      AC GGTA
                                     _______ A
GAM1485  LOC148709 5'  GGTTTATACATCATC       37443           GAC
                                GGTTTATATAT   CATC
                                ||||||||||   ||||
                                CCAAATATGTA   GTAG
                                     ___
GAM1485  LOC154007 3'  ATACATAACAATATATGGCCAT 37444       GTTT_      A
                                ATACG     ATATATG CCAT
                                |||||     ||||||| ||||
                                TATGT     TATATAC GGTA
                                   ATTGT      C
GAM1485  LOC51696  3'  CAAGTTCTATATATATGATCAT 37445    C     ___       C
              CC                  A GGTTT   ATATATGA CATCC
                                | |||||   |||||||| |||||
                                G TCAAG   TATATACT GTAGG
                                 T     ATA       A
GAM1485  LOC91496  5'  GGTTTATCAAACCATCC     37446        ATAT
                                GGTTTAT    GACCATCC
                                |||||||    ||||||||
                                CCAAATA    TTGGTAGG
                                    GT__
GAM1486  CARD15    3'  TGGAGTGTGGTCATA       37449     T       AGCTAA
                                TG GAGTGTGG      TCATA
                                || ||||||||      |||||
                                AC CTCACACC      AGTAT
                                 _      _______
GAM1486  KIAA1550  3'  TGTGAGTGTGCATAT       37450           GAGCTAAT
                                TGTGAGTGTG       CATAT
                                ||||||||||       |||||
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                                ACACTCACAC       GTATA
                                          ________
GAM1486  LOC128102 5'  TGTGGGTATGGAGCGTACCAT  37451      A        TA
                                TGTG GTGTGGAGC  ATCAT
                                |||| |||||||||  |||||
                                ACAC CATACCTCG  TGGTA
                                  C        CA
GAM1487  ATP7A    3'  TTTGCCAACAGATAAACGC    37454      TA       GTCTT
                                TTTG  CCAACAGG    ACGC
                                ||||  ||||||||    ||||
                                AAAC  GGTTGTCT    TGCG
                                  __       ATT__
GAM1487  IHPK3    5'  CTTTGTACTGTGGGGTGAACCG 37455        CAACA    CTTA
              C                  CTTTGTAC    GGGT    CGC
                                |||||||     ||||   |||
                                GAAACATG    CCCA    GCG
                                     ACAC_    CTTG
GAM1487  NLGN1    3'  CTTTATACTGACAGCACTTA   37456        CA    G T
                                CTTTGTAC  ACAG G CTTA
                                |||||||  |||| | ||||
                                GAAATATG  TGTC T GAAT
                                     AC    G _
GAM1487  PCDH9    5'  CTTTGTATTGACAGGATC    37457       CCA
                                CTTTGTA   ACAGGGTC
                                |||||||   ||||||||
                                GAAACAT   TGTCCTAG
                                     AAC
GAM1487  DKFZp761K1423 5'  CTTTGCATCTTAAGGTCTTA   37458        CCAAC
                                CTTTGTA    AGGGTCTTA
                                |||||||    |||||||||
                                GAAACGT    TTCCAGAAT
                                     AGAA_
GAM1487  HN1L     3'  CTTTGGTTGACAAAGCCTTGTG 37459       TACCA        AC
              C                  CTTTG    ACAGGGTCTT  GC
                                |||||    ||||||||||  ||
                                GAAAC    TGTTTCGGAA  CG
                                   CAAC_        CA
GAM1487  KIAA1679  3'  CTTTGTACAAACAGGATC    37460        C
                                CTTTGTAC AACAGGGTC
                                |||||||| |||||||||
                                GAAACATG TTGTCCTAG
                                     T
GAM1487  LOC147649 5'  CTTTGCACTGACAGCAGT    37461        CA   _
                                CTTTGTAC  ACAG GGT
                                |||||||  |||| |||
                                GAAACGTG  TGTC TCA
                                     AC    G
GAM1488  COX15    3'  TCGCCAGTGTTACTGTCTCCAT 37464    A     CCA  GA
                                TC CTAGTG   AC  GTCTCCAT
                                || ||||||   ||  ||||||||
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                                AG GGTCAC   TG  CAGAGGTA
                                 C     AA_  A_
GAM1488  WRN      3'  CTAGTGCAATTGGTCTCCAT   37465       CAACGA
                                CTAGTGC     GTCTCCAT
                                |||||||     ||||||||
                                GATCACG     CAGAGGTA
                                    TTAAC_
GAM1488  ZNF180   3'  CCACTAGTGTTAGCATTCCAT  37466        CCAACG   C_
                                TCACTAGTG     AGT  TCCAT
                                |||||||||     |||  |||||
                                GGTGATCAC     TCG  AGGTA
                                     AA____   TA
GAM1488  CLST11240 5'  CCATTAGTGCCATTTCTCC    37467     C       ACGAG
                                TCA TAGTGCCA     TCTCC
                                ||| ||||||||     |||||
                                GGT ATCACGGT     AGAGG
                                  A       AA___
GAM1488  MGC2941   3'  TCACTGGAGCTGGCATCTCCAT 37468       AGT  CAACGA
                                TCACT   GC     GTCTCCAT
                                |||||   ||     ||||||||
                                AGTGA   CG     TAGAGGTA
                                   CCT  ACCG__
GAM1488  SYTL2     3'  TCACTGATGTCTGTCTCCA    37469       A   CCAACGA
                                TCACT GTG      GTCTCCA
                                ||||| |||      |||||||
                                AGTGA TAC      CAGAGGT
                                   C   AGA____
GAM1488  SYTL2     3'  TCACTGATGTCTGTCTCCA    37469       A   CCAACGA
                                TCACT GTG      GTCTCCA
                                ||||| |||      |||||||
                                AGTGA TAC      CAGAGGT
                                   C   AGA____
GAM1488  TP53TG3   3'  CACTGGTGGGAAAGTCTCC    37470      A   CCAAC
                                CACT GTG     GAGTCTCC
                                |||| |||     ||||||||
                                GTGA CAC     TTCAGAGG
                                   C   CCT__
GAM1488  ZNF185    3'  CCAGCCATCCAACGAGTTTCCA 37471       G__        C
            T                    CTAGT   CCAACGAGT TCCAT
                                |||||   ||||||||| |||||
                                GGTCG   GGTTGCTCA AGGTA
                                   GTA        A
GAM1488  LOC146435 3'  TAGTGCCAAGCTCCA       37472        ACG  T
                                TAGTGCCA   AG CTCCA
                                ||||||||   || |||||
                                ATCACGGT   TC GAGGT
                                     ___  _
GAM1488  LOC163115 5'  TCACTAGTGTGAGTTCTC     37473         CCAAC   _
                                TCACTAGTG     GAGT CTC
                                |||||||||     |||| |||
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                                AGTGATCAC    CTCA GAG
                                     A____   A
GAM1488 LOC90459 3' TCACTAGTGGCCAATGAA    37474        _   C
                                TCACTAGTG CCAA GAG
                                ||||||||| |||| |||
                                AGTGATCAC GGTT CTT
                                     C   A
GAM1489 AMN     3' GGCTGGACGAGGAGGTG    37477        TA  A
                                GGCTGGAC  GAG AGGTG
                                ||||||||  ||| |||||
                                CCGACCTG  CTC TCCAC
                                     __  C
GAM1489 MS4A1   3' TTAAGGCTGGATGAAAAGGTG 37478     T     CTA
                                TTAA GGCTGGA   GAGAAGGTG
                                |||| |||||||   |||||||||
                                AATT CCGACCT   CTTTTCCAC
                                  _     A__
GAM1489 CACNA1H  3' TGGCTGGAAGGGGAGGGTG   37479       CTA_  AA
                                TGGCTGGA   GAG  GGTG
                                ||||||||   |||  ||||
                                ACCGACCT   CTC  CCAC
                                     TCCC  __
GAM1489 KIAA0703 3' CGAGATGATTAGGGAAGGTG  37480    CTG C   A
                                TGG   GA TAG GAAGGTG
                                |||   || ||| |||||||
                                GCT   CT ATC CTTCCAC
                                  CTA  A   C
GAM1489 KRTAP4-7 3' TGGCTGGATCTGAGGGTG    37481       _ A   AA
                                TGGCTGGA CT GAG  GGTG
                                |||||||| || |||  ||||
                                ACCGACCT GA CTC  CCAC
                                     A  _  __
GAM1489 LOC153876 5' TTAAGGGCTCCAAAGAGAAGGT 37482     T   GGACT
           G                     TTAA GGCT    AGAGAAGGTG
                                |||| ||||    ||||||||||
                                AATT CCGA    TCTCTTCCAC
                                  C   GGTT_
GAM1489 LOC222865 3' AATGGCTGGGGTCAGGGGTG  37483       AC_  AGAA
                                AATGGCTGG   TAG   GGTG
                                |||||||||   |||   ||||
                                TTACCGACC   GTC   CCAC
                                     CCA   C___
GAM1489 LOC257109 3' TTAATGGCTGAATAGG     37484          CTAGAGA
                                TTAATGGCTGGA      AGG
                                ||||||||||||      |||
                                AATTACCGACTT      TCC
                                     A_______
GAM1490 B4GALT6  3' TGGAAATAATAAAAGTGC    37487        C   C
                                TGGAAATAA AAAA TGT
                                ||||||||| |||| |||
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                                ACCTTTATT TTTT ACG
                                     A   C
GAM1490 DDX26    3' TGGAATAACAAAAGTGC    37488      A      C
                                TGGAA TAACAAAA TGT
                                ||||| |||||||| |||
                                ACCTT ATTGTTTT ACG
                                   _      C
GAM1490 SUV39H2  3' TAGCAAAAACAGAACTGTAGA 37489    AAAT   A
                                TGG   AACA AACTGTAGA
                                |||   |||| |||||||||
                                ATC   TTGT TTGACATCT
                                  GTTT   C
GAM1490 APMCF1   3' TGGAAATAGTGCAACTGGAAA 37490       ACAA    T
                                TGGAAATA   AACTG AGA
                                ||||||||   ||||| |||
                                ACCTTTAT   TTGAC TTT
                                     CACG   C
GAM1490 DEFB118  3' TGGAAATAGTGAAAATTTTAGA 37491       AC_   CTG
             CTT                  TGGAAATA   AAAA   TAGACTT
                                |||||||||  ||||  |||||||
                                ACCTTTAT   TTTT   ATCTGAA
                                     CAC   AAA
GAM1490 KIAA0792 5' TGGGGTACCAAACTGTAGACTT 37492    AAATA  A
                                TGG    AC AAACTGTAGACTT
                                |||    || ||||||||||||
                                ACC    TG TTTGACATCTGAA
                                  CCA__  G
GAM1490 KIAA1399 3' TGGAAATAGCAGAACTGC    37493       A  A
                                TGGAAATA CA AACTGT
                                |||||||| || ||||||
                                ACCTTTAT GT TTGACG
                                     C  C
GAM1490 KIAA1649 5' GGAAATAACAAAGCAAACC   37494         ACT
                                GGAAATAACAAA   GTAGACT
                                ||||||||||||   |||||||
                                CCTTTATTGTTT   CGTTTGG
                                              ___
GAM1490 MGC13198 3' TGGAAATACCAACAGCAA    37495       ACAA   T
                                TGGAAATA   AAC GTAG
                                ||||||||   ||| ||||
                                ACCTTTAT   TTG CGTT
                                     GG__   T
GAM1490 P66      3' TGGATAGTAACAAGTAGACTT  37496     AA_    AACT
                                TGGA   TAACAA   GTAGACTT
                                ||||   ||||||   ||||||||
                                ACCT   ATTGTT   CATCTGAA
                                  ATC    _____
GAM1490 PRO1580  5' GGAAATAATAAAATTATAGTCT 37497       C   C    A
             T                   GGAAATAA AAAA TGTAG CTT
                                |||||||| |||| ||||| |||
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                                CCTTTATT TTTT ATATC GAA
                                     A   A    A
GAM1491  AMPD3    3'  CATCACAGTAGATAAGGGAGAA 37500       C  C   AAAA
                                CATCACAG AG ATAA   AGAA
                                |||||||| || ||||   ||||
                                GTAGTGTC TC TATT   TCTT
                                     A  _   CCC_
GAM1491  C9       3'  CATCACAGGAGTTTAAGGAAGA 37501       C  CA  AAA
            A                    CATCACAG AG  TAA  AAGAA
                                |||||||| ||  |||  |||||
                                GTAGTGTC TC  ATT  TTCTT
                                     C  AA  CC_
GAM1491  CCND1    3'  CATCACAGGCGCAGGGAAGA  37502       CA  TAAAAA
                                CATCACAG  GCA    AAGA
                                ||||||||  |||    ||||
                                GTAGTGTC  CGT    TTCT
                                     CG  CCC___
GAM1491  FOXO1A   3'  CATCACAGTATTACAAAAAGA  37503       CAGCATAA
                                CATCACAG       AAAAAGA
                                ||||||||       |||||||
                                GTAGTGTC       TTTTTCT
                                     ATAATG__
GAM1491  GABRE    5'  CACCACAGCCAAGAAAAAGAA  37504       AG  TAA
                                CATCACAGC  CA  AAAAAGAA
                                |||||||||  ||  ||||||||
                                GTGGTGTCG  GT  TTTTTCTT
                                     __  TC_
GAM1491  HS2ST1   3'  TCACAGCAATTAGAAAAGA   37505       CATAAA
                                TCACAGCAG     AAAAGA
                                |||||||||     ||||||
                                AGTGTCGTT     TTTTCT
                                     AATC__
GAM1491  MAP3K7IP1 3'  TCACAGCACCAGAAGGAAGAA  37506       G  T  AAA
                                TCACAGCA CA AA   AAGAA
                                |||||||| || ||   |||||
                                AGTGTCGT GT TT   TTCTT
                                     G  C  CC_
GAM1491  NEK6     3'  CCACAACAGTATAAAGAAAG  37507       C    A
                                TCACAGCAG ATAAA AAAG
                                ||||||||| ||||| ||||
                                GGTGTTGTC TATTT TTTC
                                     A    C
GAM1491  RANBP7   3'  CACAGCAGGAAAGAAAGA   37508       CAT  A
                                CACAGCAG   AAA AAAGA
                                ||||||||   ||| |||||
                                GTGTCGTC   TTT TTTCT
                                     C__   C
GAM1491  SLC9A6   3'  TCACAGCAAGCGGGGGAAAAG  37509       _  ATAAA
                                TCACAGCA GC    AAAAG
                                |||||||| ||    |||||
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                                AGTGTCGT CG    TTTTC
                                    T  CCCCC
GAM1491  SOX13    3'  ACAGTCATAAAAAAAGAA    37510     _
                                GCAG CATAAAAAAAGAA
                                |||| ||||||||||||
                                TGTC GTATTTTTTTCTT
                                  A
GAM1491  SOX4     3'  CATCACGCGTTTAAAAAAAG  37511      A  AGCA
                                CATCAC GC   TAAAAAAAG
                                |||||| ||   |||||||||
                                GTAGTG CG   ATTTTTTTC
                                   _ CAA_
GAM1491  SS18     3'  ATCAACCAACATAAAAAA    37512     CAG
                                ATCA  CAGCATAAAAAA
                                ||||  ||||||||||||
                                TAGT  GTTGTATTTTTT
                                  TG_
GAM1491  BRAG     5'  CACCACAGCACTAGAGAAAGA 37513         GCATAAAA
                                CATCACAGCA      AAAGA
                                ||||||||||      |||||
                                GTGGTGTCGT      TTTCT
                                     GATCTC__
GAM1491  C11orf15 3'  CATCACAGTACATGAAGA    37514        CA   AAAAA
                                CATCACAG  GCAT    AAGA
                                ||||||||  ||||    ||||
                                GTAGTGTC  TGTA    TTCT
                                    A_   C____
GAM1491  DKFZP434A043 3'  TCACACAAAATAAGAAAAGAA  37515      G  C   A
                                TCACA CAG ATAA AAAAGAA
                                ||||| ||| |||| |||||||
                                AGTGT GTT TATT TTTTCTT
                                   _  T   C
GAM1491  DKFZp434N035 3'  ACAGTAGCCACAAAAAAAG   37516     C  _
                                ACAG AGC ATAAAAAAAG
                                |||| ||| ||||||||||
                                TGTC TCG TGTTTTTTTC
                                  A  G
GAM1491  DKFZp566H0824 5'  CATCAACAGCAGAAAAGA    37517      _    CATAAA
                                CATCA CAGCAG     AAAAGA
                                ||||| ||||||     ||||||
                                GTAGT GTCGTC     TTTTCT
                                   T    _______
GAM1491  FLJ10769  3'  CATCACAGGGTATCACTCAAGA 37518        CAG__  AAAAA
                                CATCACAG    CAT    AAGA
                                ||||||||    |||    ||||
                                GTAGTGTC    GTG    TTCT
                                     CCATA   AG___
GAM1491  FLJ10901  3'  CATCACAGAGCACATTAGAAAA 37519        C     AA__
            G                    CATCACAG AGCATA    AAAAG
                                ||||||||| ||||||    |||||
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                                GTAGTGTC TCGTGT    TTTTC
                                    _     AATC
GAM1491  FLJ20984  3'  TCACAAAATTAAAAAAAGAA  37520       CAGCA
                                TCACAG    TAAAAAAAGAA
                                ||||||    ||||||||||
                                AGTGTT    ATTTTTTTCTT
                                   TTA__
GAM1491  FLJ21125  3'  CAGCACAGCAGCAGGGAAGA  37521    T        TAAAAA
                                CA CACAGCAGCA     AAGA
                                || ||||||||||     ||||
                                GT GTGTCGTCGT     TTCT
                                 C        CCC___
GAM1491  HAK       3'  CATCACAGCAGGATGTGTCTAG 37522          CATAAAAAA
            AA                   CATCACAGCAG        AGAA
                                ||||||||||         ||||
                                GTAGTGTCGTC        TCTT
                                      CTACACAGA
GAM1491  KIAA0182  3'  CATGGCAACACAAGAAAGAA  37523    CA        AA
                                CA  GCAGCATAA  AAAGAA
                                ||  |||||||||  ||||||
                                GT  CGTTGTGTT  TTTCTT
                                 AC        C_
GAM1491  KIAA0186  3'  ACAACATTAAAAAAAGAA    37524        _
                                GCAGCAT AAAAAAAGAA
                                ||||||| ||||||||||
                                TGTTGTA TTTTTTTCTT
                                    A
GAM1491  KIAA0240  3'  CATCACAGGCCAATCTGGAAAA 37525         _ AGCATAAA
            GAA                    CATCACAG C       AAAAGAA
                                ||||||||| |       |||||||
                                GTAGTGTC G       TTTTCTT
                                    C GTTAGACC
GAM1491  KIAA0335  3'  CACAGTCACTTAGAAAAAGAA  37526      CA  A  A
                                CACAG  GC TA AAAAAGAA
                                |||||  || || ||||||||
                                GTGTC  TG AT TTTTTCTT
                                   AG  A  C
GAM1491  KIAA0470  3'  CAGCATGGCTTAAAAAAAAGAA 37527      __  AT_
                                CAGCA  GC   AAAAAAAGAA
                                |||||  ||   ||||||||||
                                GTCGT  CG   TTTTTTTCTT
                                   AC  AAT
GAM1491  KIAA0494  3'  CAGCAACCATAAAGAAAG    37528        _    A
                                CAGCAGC ATAAA AAAG
                                ||||||| ||||| ||||
                                GTCGTTG TATTT TTTC
                                    G    C
GAM1491  KIAA0527  3'  CATCACAACATTAAAAG     37529          GCATAAA
                                CATCACAGCA      AAAAG
                                ||||||||||      |||||
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                                GTAGTGTTGT      TTTTC
                                     AA_____
GAM1491  KIAA1030  3'  CCACAGCAGTGAAAGGAGA   37530         CATA   AA
                                TCACAGCAG    AAA  AGA
                                |||||||||    |||  |||
                                GGTGTCGTC    TTT  TCT
                                     AC__   CC
GAM1491  KIAA1155  3'  CAGCACAGTAGCAATCAGAAAG 37531    T    C    TAAAA
              AA                   CA CACAG AGCA     AAAGAA
                                || ||||| ||||     ||||||
                                GT GTGTC TCGT     TTTCTT
                                 C    A   TAGTC
GAM1491  KIAA1203  3'  CACAGCAATACTGAAAAG    37532         C  AAA
                                CACAGCAG AT   AAAAG
                                |||||||| ||   |||||
                                GTGTCGTT TG   TTTTC
                                     A  AC_
GAM1491  KIAA1765  3'  CATCCAGCAGCACCCCAAG    37533      A       AAAAA
                                CATC CAGCAGCAT     AAG
                                |||| |||||||||     |||
                                GTAG GTCGTCGTG     TTC
                                  _       GGG__
GAM1491  LRPPRC    3'  CACAGCAGCAGCATTGAAGAA  37534          TAAAAA
                                CACAGCAGCA     AAGAA
                                ||||||||||     |||||
                                GTGTCGTCGT     TTCTT
                                     CGTAAC
GAM1491  MGC14258  5'  CATCACAGGTGACCCCAGAAAG 37535         CA_  ATAAAA
              AA                   CATCACAG   GC     AAAGAA
                                |||||||   ||     ||||||
                                GTAGTGTC   TG     TTTCTT
                                     CAC  GGGTC_
GAM1491  MGC15606  3'  ATCACAGCTCAAAAAGAAAAGA 37536         AG  T   _
                                ATCACAGC  CA AAA AAAAGA
                                |||||||  || ||| ||||||
                                TAGTGTCG  GT TTT TTTTCT
                                     A_  T   C
GAM1491  MGC2668   3'  CACCACAGCTGCTGGAAAAG   37537         A  ATAAA
                                CATCACAGC GC     AAAAG
                                |||||||| ||     |||||
                                GTGGTGTCG CG     TTTTC
                                     A  ACC__
GAM1491  N4BP3     3'  ACAGCAGCACAGAAAGA     37538          AAA
                                ACAGCAGCATA   AAAGA
                                ||||||||||   |||||
                                TGTCGTCGTGT   TTTCT
                                      C__
GAM1491  PELI2     3'  GCAAGACATAAAAAAAGAA   37539     __
                                GCA  GCATAAAAAAAGAA
                                |||  ||||||||||||||
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                                CGT  TGTATTTTTTTCTT
                                  TC
GAM1491  PP1665   5'  ATAACAGCAGCCCTGGAAGAA  37540    C       ATAAAAA
                                AT ACAGCAGC      AAGAA
                                || ||||||||      |||||
                                TA TGTCGTCG      TTCTT
                                 T       GGACC__
GAM1491  PTBP2    3'  CAGCATGGAAAAAAAAAAGAA  37541      GCAT__
                                CAGCA     AAAAAAAGAA
                                |||||     ||||||||||
                                GTCGT     TTTTTTTCTT
                                   ACCTTT
GAM1491  TRAP150  3'  ACATATGCCTAAAAAAAGAA   37542     GCA  A
                                ACA   GC TAAAAAAAGAA
                                |||   || ||||||||||
                                TGT   CG ATTTTTTTCTT
                                  ATA  G
GAM1491  TRIM4    3'  GCAGCCATAAAAAAAGAA     37543      _
                                GCAGC ATAAAAAAAGAA
                                ||||| ||||||||||||
                                CGTCG TATTTTTTTCTT
                                   G
GAM1491  ZD52F10  3'  CACCACAGTGCAGTGGGAAGAA 37544        CA   TAAAAA
                                CATCACAG  GCA     AAGAA
                                ||||||||  |||     |||||
                                GTGGTGTC  CGT     TTCTT
                                     A_   CACCC_
GAM1491  LOC122786 3'  CATCACAAATATTATAAAGAAA 37545        CAGC_    A
            GA                    CATCACAG     ATAAA AAAGA
                                |||||||     ||||| |||||
                                GTAGTGTT     TATTT TTTCT
                                     TATAA    C
GAM1491  LOC133418 3'  TCACAGCAATAAAAAAGAA    37546         CATA
                                TCACAGCAG    AAAAAAGAA
                                |||||||||    |||||||||
                                AGTGTCGTT    TTTTTTCTT
                                      A___
GAM1491  LOC137964 3'  CATCAGCAGCAGCATAAAA    37547       _
                                CATCA CAGCAGCATAAAA
                                ||||| ||||||||||||
                                GTAGT GTCGTCGTATTTT
                                   C
GAM1491  LOC147524 5'  ATCAAGCAGCATGATGCCAGA  37548      C       AAAAAA
                                ATCA AGCAGCAT      AGA
                                |||| ||||||||      |||
                                TAGT TCGTCGTA      TCT
                                   _       CTACGG
GAM1491  LOC148823 3'  ATCCAGTACATAGAAAAAGAA  37549     A   CA    A
                                ATC CAG  GCATA AAAAAGAA
                                ||| |||  ||||| ||||||||
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                                TAG GTC  TGTAT TTTTTCTT
                                  _  A_    C
GAM1491  LOC151094 3'  ATCACAGCAGCCGGAAGA    37550          ATAAAAA
                                ATCACAGCAGC      AAGA
                                ||||||||||       ||||
                                TAGTGTCGTCG      TTCT
                                     GCC_____
GAM1491  LOC153020 3'  CAACACAGCACATACTAAG   37551    T     G    AAAA
                                CA CACAGCA CATA    AAG
                                || ||||||| ||||    |||
                                GT GTGTCGT GTAT    TTC
                                 T      _    GA__
GAM1491  LOC153817 3'  CACAGCACATTAAAAAGAA   37552       G   AA
                                CACAGCA CAT  AAAAAGAA
                                ||||||| |||  ||||||||
                                GTGTCGT GTA  TTTTTCTT
                                   _  A_
GAM1491  LOC200933 3'  CATCACAACCTGAAAAAGA   37553        AGCATAA
                                CATCACAGC      AAAAAGA
                                |||||||||      |||||||
                                GTAGTGTTG      TTTTTCT
                                     GAC_____
GAM1491  LOC220766 3'  CAGCATGGCTTAAAAAAAAGAA 37527      __  AT_
                                CAGCA  GC   AAAAAAAGAA
                                |||||  ||   ||||||||||
                                GTCGT  CG   TTTTTTTCTT
                                   AC  AAT
GAM1491  LOC245771 5'  CATCACAGAGCACATTAGAAAG 37554        C     AAA_
                                CATCACAG AGCATA    AAAG
                                |||||||| ||||||    ||||
                                GTAGTGTC TCGTGT    TTTC
                                     _     AATC
GAM1491  LOC253897 3'  CATCAGCAGCAGCATAAAA   37547      _
                                CATCA CAGCAGCATAAAA
                                ||||| ||||||||||||
                                GTAGT GTCGTCGTATTTT
                                   C
GAM1491  LOC254756 3'  GCAGCGCTAGAAAAAGAA    37555      A_  A
                                GCAGC  TA AAAAAGAA
                                |||||  || ||||||||
                                CGTCG  AT TTTTTCTT
                                   CG  C
GAM1491  LOC91115  3'  CATCACACACGCAAAAAAAG  37556       G  _   TA
                                CATCACA CA GCA  AAAAAAG
                                ||||||| || |||  |||||||
                                GTAGTGT GT CGT  TTTTTTC
                                     _  G   __
GAM1491  LOC91380  3'  CACAGCTGAAGAAAAAAGAA  37557       AGCATA
                                CACAGC     AAAAAAGAA
                                ||||||     |||||||||
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                                GTGTCG     TTTTTTCTT
                                   ACTTC_
GAM1492  CNN2     3'  TGGAGGTGCAGTGAGCCAA   37560    AT      AGT
                                TG  GGTGCAGT   AGTTAA
                                ||  ||||||||   ||||||
                                AC  CCACGTCA   TCGGTT
                                 CT       C__
GAM1492  DSC3     3'  TGGTAGTGCAGTAGGGGT    37561    A        TA
                                TG TGGTGCAGTAG  GT
                                || ||||||||||  ||
                                AC ATCACGTCATC  CA
                                 C         CC
GAM1492  DSC3     3'  TGGTAGTGCAGTAGGGGT    37561    A        TA
                                TG TGGTGCAGTAG  GT
                                || ||||||||||  ||
                                AC ATCACGTCATC  CA
                                 C         CC
GAM1492  GGPS1    3'  TGATGGTAGTAGGATAGAGTTG 37562        CA___   T   AA
              GTG                  TGATGGTG    GTAG AGTT  TG
                                ||||||||    |||| ||||  ||
                                ACTACCAT    TATC TCAA  AC
                                     CATCC   _   CC
GAM1492  HEM1     5'  TGACTGGTAGTAGTTGGTGA   37563     GGTGCA       AA
                                TGAT     GTAGTAGTT  TGA
                                ||||     |||||||||  |||
                                ACTG     CATCATCAA  ACT
                                  AC____        CC
GAM1492  KIAA1829 3'  TGATGGTGTAGCTGTCAGGAAT 37564        C   A  AGTT
              GA                   TGATGGTG AGT GT    AATGA
                                ||||||||  ||| ||    |||||
                                ACTACCAC TCG CA    TTACT
                                     A   A  GTCC
GAM1492  NPD009   5'  GATGGTGCAGCTATTTAATGA  37565          AGTAG
                                GATGGTGCAGT    TTAATGA
                                ||||||||||    |||||||
                                CTACCACGTCG    AATTACT
                                       ATA__
GAM1492  PPFIBP2  3'  TGAGGTGCAGTTATATGGTGA  37566    T       A   GTTAA
                                TGA GGTGCAGT GTA    TGA
                                ||| ||||||| |||    |||
                                ACT CCACGTCA TAT    ACT
                                  _       A   ACC__
GAM1492  SMC1L1   3'  TGATGGTGTATGTGAATG    37567        CAGTA  A  T
                                TGATGGTG    GT GT AATG
                                ||||||||    || || ||||
                                ACTACCAC    TA CA TTAC
                                     A____  _  C
GAM1492  LOC151103 3'  TGTGGTGCAGTGGTGC     37568    A       A  A
                                TG TGGTGCAGT GT GT
                                || |||||||| || ||
```

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                                AC ACCACGTCA CA CG
                                 _       C  _
GAM1492  LOC151719 5'  TGATGGTGGTGGTAGTAG    37569        CA_
                                TGATGGTG   GTAGTAG
                                ||||||||   |||||||
                                ACTACCAC   CATCATC
                                     CAC
GAM1492  LOC163682 5'  TGATGGTGTGGTATGGCAG    37570        CA  __
                                TGATGGTG  GTA  GTAG
                                ||||||||  |||  ||||
                                ACTACCAC  CAT  CGTC
                                     AC   AC
GAM1493  MGC13061  3'  TAGGGATTGATCACATTGGCAT 37573      A       CTCG__
           GCTT                    TAGG ATTGATTAC     ATGCTT
                                ||||  |||||||||      ||||||
                                ATCC TAACTAGTG     TACGAA
                                  C        TAACCG
GAM1493  MGC4771   3'  AGGGGGAAGCCTCGATGCTT   37574     AATT  TTA
                                AGG    GA   CCTCGATGCTT
                                |||    ||   ||||||||||||
                                TCC    CT   GGAGCTACGAA
                                  CC__  TC_
GAM1493  LOC152348 5'  AGGAATTGGTGGTGACTGATGC 37575        ATTAC__  C
           TT                     AGGAATTG      CT GATGCTT
                                ||||||||      || |||||||
                                TCCTTAAC      GA CTACGAA
                                     CACCACT  _
GAM1494  NBEA      3'  ATGGAGCCCAAATTCAACCCTT 37578      TAAA_   C
                                ATGG     GAAT CAACCCTT
                                ||||     |||| ||||||||
                                TACC     TTTA GTTGGGAA
                                  TCGGG    A
GAM1494  PIR51     3'  GACATGGTAATGGATTCC    37579          A_  A
                                GACATGGTAA  GA TCC
                                ||||||||||  || |||
                                CTGTACCATT  CT AGG
                                      AC  A
GAM1494  SERPINA5  3'  CACAGCAAGAATCTGATCCTT  37580        A    CAAC
                                CATGGTAA GAATC    CCTT
                                |||||||| |||||    ||||
                                GTGTCGTT CTTAG    GGAA
                                     _    ACTA
GAM1494  FLJ20273  3'  ACATGGTAACACCATCAACCCT 37581         AGA_   C
           T                     ACATGGTAA    ATC AACCCTT
                                |||||||||    ||| |||||||
                                TGTACCATT    TAG TTGGGAA
                                     GTGG  _
GAM1494  KIAA0630  3'  GACATGGTAAGCAATACAAC   37582         AG   C
                                GACATGGTAA  AAT CAAC
                                ||||||||||  ||| ||||
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                                CTGTACCATT  TTA GTTG
                                      CG   T
GAM1494  LOC145858 5'  AACATGGTAGACAGGCCT    37583        AA  ATC  AC
                                GACATGGT  AGA   CA  CCT
                                ||||||||  |||   ||  |||
                                TTGTACCA  TCT   GT  GGA
                                    __   ___  CC
GAM1494  LOC149722 5'  ATGGTAAAGCTGTCAATTCTT  37584         AATC   CC
                                ATGGTAAAG    CAA  CTT
                                |||||||||    |||  |||
                                TACCATTTC    GTT  GAA
                                     GACA   AA
GAM1494  LOC151162 5'  ATGGCAGAATCCAGCCCTT   37585      AA       A
                                ATGGT  AGAATCCA CCCTT
                                |||||  |||||||| |||||
                                TACCG  TCTTAGGT GGGAA
                                  __       C
GAM1494  LOC199745 3'  TGGTAGAACCCAGGCCCTT   37586     AA       A_
                                TGGT  AGAATCCA  CCCTT
                                ||||  ||||||||  |||||
                                ACCA  TCTTGGGT  GGGAA
                                  __       CC
GAM1494  LOC203377 5'  ATGGCAGAATCCAGCCCTT   37585      AA       A
                                ATGGT  AGAATCCA CCCTT
                                |||||  |||||||| |||||
                                TACCG  TCTTAGGT GGGAA
                                  __       C
GAM1495  ACTN2    3'  TGGAAAAACAGGGGGGAATTA  37589     C        TT_
                                TGG AAAACAGGGG   ATTA
                                ||| ||||||||||   ||||
                                ACC TTTTGTCCCC   TAAT
                                  T        CCT
GAM1495  ISL1     3'  TGGCAAAATAGAGGTAACC   37590        C     T
                                TGGCAAAA AGGGGT ATT
                                |||||||| |||||| |||
                                ACCGTTTT TCTCCA TGG
                                     A     T
GAM1495  SLC24A1  3'  TAGCGAGGCAATTAAT      37591      AAAACA    T
                                TGGC     GGGGT ATTAAT
                                ||||     ||||| ||||||
                                ATCG     CTCCG TAATTA
                                  _______    T
GAM1495  AKAP11   3'  CAGACTAGTTATTAATTA    37592      __
                                CAGG  GGTTATTAATTA
                                ||||  ||||||||||||
                                GTCT  TCAATAATTAAT
                                  GA
GAM1495  GMFB     3'  TGCCAAAAACATGTTATTAATT 37593    G    CAGGG
             A                   TG CAAAA    GTTATTAATTA
                                 || |||||    ||||||||||
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                                AC GTTTT    CAATAATTAAT
                                 G    TGTA_
GAM1495 HSP105B  3' TGGCAAAAATATTTTATTAATT 37594       CAGGGG
                                TGGCAAAA     TTATTAATT
                                ||||||||     |||||||||
                                ACCGTTTT     AATAATTAA
                                    TATAA_
GAM1495 KIAA0475 3' TGGCAAAAGGGGAAAAAATTA 37595       AC    TTATT
                                TGGCAAA  AGGGG    AATTA
                                |||||||  |||||    |||||
                                ACCGTTT  TCCCC    TTAAT
                                   __    TTTT_
GAM1495 ZNF33A   3' TGGAAGGTTATTAAT      37596     CAAAACA
                                TGG      GGGGTTATTAAT
                                |||      ||||||||||||
                                ACC      TTCCAATAATTA
                                 ________
GAM1495 LOC154525 5' TGGCAAAACATGGGAATATTA 37597         _  GT
                                TGGCAAAACA GGG  TATTA
                                |||||||||| |||  |||||
                                ACCGTTTTGT CCC  ATAAT
                                     A   TT
GAM1495 LOC161829 3' TGACAAAACAGGTTTATT    37598          GG
                                TGGCAAAACAGG  TTATT
                                ||||||||||||  |||||
                                ACTGTTTTGTCC  AATAA
                                      A_
GAM1496 GLUD1    3' ACAATACATGAATGATAAGCTA 37601       CAT
                                ACAATATG   ATGATAAGCTA
                                ||||||||   ||||||||||
                                TGTTATGT   TACTATTCGAT
                                    ACT
GAM1496 MADH5    3' ATATGCCCTCTTATAAGCTAC  37602      ATATG_
                                ATATGC     ATAAGCTAC
                                ||||||     |||||||||
                                TATACG     TATTCGATG
                                   GGAGAA
GAM1496 NCAM2    3' TATGTATATGTGTACAAGCTA  37603     C    ___
                                TATG ATATG   ATAAGCTA
                                |||| |||||   ||||||||
                                ATAC TATAC   TGTTCGAT
                                  A    ACA
GAM1496 CCNG2    3' AAAATGTTTAAGATAAGCTAC  37604    T   CA  T
                                AA ATG  TA GATAAGCTAC
                                || |||  || ||||||||||
                                TT TAC  AT CTATTCGATG
                                 T   AA  T
GAM1496 KIAA0625 3' TACAATATGCTGTGGCT     37605         ATA  ATAA
                                TACAATATGC   TG    GCT
                                ||||||||||   ||    |||
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                                ATGTTATACG  AC   CGA
                                     AC_  ____
GAM1496 KIAA1463 3' CAACATGCATGTAATTGC   37606        A   AA
                                CAATATGCAT TGAT  GC
                                |||||||||| ||||  ||
                                GTTGTACGTA ATTA  CG
                                     C   A_
GAM1496 TSLRP    3' AATATGCATATGGTCTCTAC  37607         ATAAG
                                AATATGCATATG    CTAC
                                ||||||||||||    ||||
                                TTATACGTATAC    GATG
                                      CAGA_
GAM1496 LOC144874 5' TACAATGTGCATATATTA   37608      A      A
                                TACAAT TGCATATG TA
                                |||||| |||||||| ||
                                ATGTTA ACGTATAT AT
                                   C       A
GAM1496 LOC158722 3' TACATATGCATATGCATA   37609     A       _
                                TACA TATGCATATG ATA
                                |||| |||||||||| |||
                                ATGT ATACGTATAC TAT
                                  _       G
GAM1496 LOC200933 3' CAACATGCATATGTCAACT   37610          ATA
                                CAATATGCATATG   AGCT
                                ||||||||||||   ||||
                                GTTGTACGTATAC   TTGA
                                      AG_
GAM1496 LOC221301 3' TACAATGTGCAGATGACAAA  37611      A   T
                                TACAAT TGCA ATGATAAG
                                |||||| |||| ||||||||
                                ATGTTA ACGT TACTGTTT
                                   C   C
GAM1496 LOC221405 3' TACAATATGTGCATGGAAAGC 37612       CA   AT
                                TACAATATG  TATG  AAGC
                                |||||||||  ||||  ||||
                                ATGTTATAC  GTAC  TTCG
                                     AC    CT
GAM1496 LOC91628  3' TACAATATGGATATGTCCTAC 37613       C    ATAAG
                                TACAATATG ATATG    CTAC
                                |||||||||| |||||    ||||
                                ATGTTATAC TATAC    GATG
                                     C    AG___
GAM1497 CYP2J2   3' AGACACCAGTGGTTTCAGAACA 37616       ACAAC_  TCC
            C                    AGGCACCA     TCA  GACAT
                                 ||||||||     |||  |||||
                                 TCTGTGGT     AGT  TTGTG
                                     CACCAA  C__
GAM1497 B3GALT6  3' AGGCACCAAGTTCTGACA   37617        CAACTCA  C
                                AGGCACCAA      TC GACA
                                |||||||||      || ||||
```

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                                TCCGTGGTT      AG CTGT
                                     CA_____  A
GAM1497  FLJ20847  5'  AGACACCAACAGCTGCAT    37618          A  _
                                AGGCACCAACA CT CAT
                                |||||||||||  || |||
                                TCTGTGGTTGT GA GTA
                                      C  C
GAM1497  FLJ21657  3'  AGGCACCAATCACTAACA    37619         CAAC    CC
                                AGGCACCAA    TCAT  GACA
                                |||||||||    ||||  ||||
                                TCCGTGGTT    AGTG  TTGT
                                     _____    A_
GAM1497  FLJ21924  3'  AAGCACCAACAGCTTCAAAACA 37620          A  _  TCC
              T                  AGGCACCAACA CT CA   GACAT
                                 ||||||||||| || ||   |||||
                                 TTCGTGGTTGT GA GT   TTGTA
                                       C  A  T__
GAM1497  MGC2452   5'  AGGCACCAGCAGCCGTCAGCCC 37621         A  A __  _
              G                   AGGCACCA CA C  TCA TCCG
                                  |||||||| || |  ||| ||||
                                  TCCGTGGT GT G  AGT GGGC
                                       C  C GC   C
GAM1497  PLPL     3'  AGGACCAACAAATAATACTGAC 37622     C       CTCATCC_
              AT                   AGG ACCAACAA       GACAT
                                   ||| ||||||||       |||||
                                   TCC TGGTTGTT       CTGTA
                                     _       TATTATGA
GAM1497  LOC145226 3'  AGGTGTCCACAACTCATGCCA  37623     CA_   A       _
                                AGG   CCA CAACTCAT CCG
                                |||   ||| |||||||| |||
                                TCC   GGT GTTGAGTA GGT
                                  ACA   _       C
GAM1497  LOC51754  5'  AGGTACTGACACTCATCC    37624     C  CA   A
                                AGG AC  ACA CTCATCC
                                ||| ||  ||| |||||||
                                TCC TG  TGT GAGTAGG
                                  A  AC   _
GAM1497  LOC89932  3'  AGGTCCAACATCTCGAC     37625     CA     A   ATCC
                                AGG  CCAACA CTC    GAC
                                |||  |||||| |||    |||
                                TCC  GGTTGT GAG    CTG
                                  A_     A   _____
GAM1498  ETS2     5'  CCGGGCGGCTCCGGGAGCTCTG 37628      A  _ C   CT_  GC
                                CCGG CG C CCG   GC  CTG
                                |||| || | |||   ||  |||
                                GGCC GC G GGC   CG  GAC
                                  C  C A   CCT  A_
GAM1498  HBQ1     5'  CGCCCTGCGACCCCGCTGCGCC 37629    A  GGA  _
              TG                   CG CC   CG CCCCGCTGCGCCTG
                                   || ||   || ||||||||||||||
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                                GC GG   GC GGGGCGACGCGGAC
                                 G  AC_  T
GAM1498  IFNGR2    5'  CGGCCGGGGCCCCGCTCG    37630    A   AC      G
                                CG CCGG  GCCCCGCT CG
                                || ||||  |||||||| ||
                                GC GGCC  CGGGGCGA GC
                                 C    C_      _
GAM1498  RFP       5'  CCGGGCCGATGCCTGCGCCTG  37631     AC   CC_ _
                                CCGG  GCC   GC TGCGCCTG
                                ||||  |||   || ||||||||
                                GGCC  CGG   CG ACGCGGAC
                                  __   CTA  G
GAM1498  RNH       5'  CGCCTGGGCGCCCGGCCT    37632    A  _  A    CGCT C
                                CG CC GG CGCCC    G GCCT
                                || || || |||||    | ||||
                                GC GG CC GCGGG    C CGGA
                                 _  A  C    _____ _
GAM1498  RNH       5'  CGCCTGGGCGCCCGGCCT    37632    A  _  A    CGCT C
                                CG CC GG CGCCC    G GCCT
                                || || || |||||    | ||||
                                GC GG CC GCGGG    C CGGA
                                 _  A  C    _____ _
GAM1498  FLJ12387  5'  CGCCGGGCCTGCGCC      37633    A   AC   CCGC
                                CG CCGG  GCC    TGCGCC
                                || ||||  |||    ||||||
                                GC GGCC  CGG    ACGCGG
                                 _    __   _____
GAM1498  FLJ23519  5'  CGCCTGGGCGCCCGGCCT    37632    A  _  A    CGCT C
                                CG CC GG CGCCC    G GCCT
                                || || || |||||    | ||||
                                GC GG CC GCGGG    C CGGA
                                 _  A  C    _____ _
GAM1498  HOMER-3   5'  CCGGGCGCCCCGCTCGCTCCCT 37634      A       _  G_
              G                  CCGG CGCCCCGCT GC  CCTG
                                ||||  |||||||| ||  ||||
                                GGCC GCGGGGCGA CG  GGAC
                                  C        G  AG
GAM1498  IMAGE:4907098 5'  CGGCCGGGTGGCTGCGCCTG   37635    A   ACGCCCC
                                CG CCGG      GCTGCGCCTG
                                || ||||      ||||||||||
                                GC GGCC      CGACGCGGAC
                                 C    CAC_____
GAM1498  KIAA0427  3'  CCATCTCCCCCGCTGCGCCTG  37636     GACG
                                CCG    CCCCGCTGCGCCTG
                                |||    ||||||||||||||
                                GGT    GGGGCGACGCGGAC
                                  AGAG
GAM1498  KIAA0819  3'  GACTGGACGCCCCCATCCTG   37637     C       GCTGCG
                                GAC GGACGCCCC     CCTG
                                ||| |||||||||     ||||
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                                CTG CCTGCGGGG     GGAC
                                  A       GTA___
GAM1498 KIAA1729 5' GACTGGCCGTTTCGCACCTG  37638    C  ACGCC   C__
                                GAC GG    CCG   TGCGCCTG
                                ||| ||    |||   ||||||||
                                CTG CC    GGC   GCGTGGAC
                                  A _____   AAA
GAM1498 MGC2508  5' GGCTGCCTTTCGCTGCGCCTG 37639    AC   C__
                                GG  GCC   CGCTGCGCCTG
                                ||  |||   ||||||||||
                                CC  CGG   GCGACGCGGAC
                                 GA   AAA
GAM1498 PACSIN2  5' CGGCCGGGCTCCCGCTAC    37640    A    AC  _
                                CG CCGG  GC CCCGCTGC
                                || ||||  || ||||||||
                                GC GGCC  CG GGGCGATG
                                 C   __  A
GAM1498 PRSS21   5' CGGCCTGACGCCCCCTCTG   37641    A  G      G_
                                CG CC GACGCCCC  CTG
                                || || ||||||||  |||
                                GC GG CTGCGGGG  GAC
                                 C  A       GA
GAM1498 PRSS21   5' CGGCCTGACGCCCCCTCTG   37641    A  G      G_
                                CG CC GACGCCCC  CTG
                                || || ||||||||  |||
                                GC GG CTGCGGGG  GAC
                                 C  A       GA
GAM1498 SS18L2   5' GATTGGATTCCCGCTGCGCCTG 37642    CC   CGC
                                GA  GGA   CCCGCTGCGCCTG
                                ||  |||   ||||||||||||
                                CT  CCT   GGGCGACGCGGAC
                                 AA   AA_
GAM1498 LOC162048 5' CAGCTCCCCGCTGCGCCT    37643    ACG
                                CGG   CCCCGCTGCGCCT
                                |||   ||||||||||||
                                GTC   GGGGCGACGCGGA
                                  GA_
GAM1498 LOC162083 5' CCGGACGCTCTGACGGCTG   37644        CCCG   _  C
                                CCGGACGC    CTG CG CTG
                                ||||||||    ||| || |||
                                GGCCTGCG    GAC GC GAC
                                     A___   T  C
GAM1498 LOC219513 5' CGACTAGGGCCTGCGCCT    37645     CG AC   CCGC
                                CGAC  G  GCC    TGCGCCT
                                ||||  |  |||    |||||||
                                GCTG  C  CGG    ACGCGGA
                                  AT C_  _____
GAM1498 LOC91828  5' CAGCCCGCCCCGCTGTGCCTG 37646     A_        C
                                CGG  CGCCCCGCTG GCCTG
                                |||  |||||||||| |||||
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                                GTC  GCGGGGCGAC CGGAC
                                  GG         A
GAM1499  CTGF     3'  TGTTTTGACGGACTGTCA    37649         TACTTCT  C
                                TGTTTTGAC      GC GTCA
                                |||||||||      || ||||
                                ACAAAACTG      TG CAGT
                                     CC_____  A
GAM1499  HAP1     3'  TGTTTTGACTGCTGCTGCC    37650          A  T
                                TGTTTTGACT CT CTGCC
                                |||||||||| || |||||
                                ACAAAACTGA GA GACGG
                                     C  C
GAM1499  SELE     3'  TGTTTTGACTGTTGGCTTTGTC 37651          ACTT_ GCC
                                TGTTTTGACT    CT   GTC
                                ||||||||||    ||   |||
                                ACAAAACTGA    GA   CAG
                                     CAACC  AA_
GAM1499  SON      3'  TGTTTTGACACTTGGC      37652          T   CT
                                TGTTTTGAC ACTT  GC
                                ||||||||| ||||  ||
                                ACAAAACTG TGAA  CG
                                     _   C_
GAM1499  DNAM-1   3'  TGCTTTGACTGTTGGTGATGTC 37653          ACTTC  CC
           AT                     TGTTTTGACT    TG  GTCAT
                                ||||||||||    ||  |||||
                                ACGAAACTGA    AC  CAGTA
                                     CAACC  TA
GAM1499  FLJ11126 3'  GTTTCTCTCTACTTCTGCCGT  37654      GA_
                                GTTTT   CTACTTCTGCCGT
                                |||||   ||||||||||||||
                                CAAAG   GATGAAGACGGCA
                                   AGA
GAM1499  KIAA1229 3'  TGTTCTGACTAAGTTGTCA    37655          CTTCTGCC
                                TGTTTTGACTA       GTCA
                                ||||||||||       ||||
                                ACAAGACTGAT       CAGT
                                     TCAA____
GAM1499  VILL     3'  GTTGTTGACTTCTGCTGT    37656     _     ACT    C
                                GTT TTGACT   TCTGC GT
                                ||| ||||||   ||||| ||
                                CAA AACTGA   AGACG CA
                                  C     ___     A
GAM1499  LOC145981 3'  TGGTTTGACTACTTGTCA    37657    T         CTGCC
                                TG TTTGACTACTT    GTCA
                                || ||||||||||    ||||
                                AC AAACTGATGAA    CAGT
                                 C         _____
GAM1500  ARF5     3'  CACGCAGGAGCTTCC       37660          CTCGC
                                CACGCAGGA    GCTTCC
                                |||||||||    ||||||
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                                GTGCGTCCT    CGAAGG
                                             _____
GAM1500 CDKN1A   3' AGGCCCTCGCGCTTCCAG    37661     A_
                                AGG  CTCGCGCTTCCAG
                                |||  ||||||||||||||
                                TCC  GAGCGCGAAGGTC
                                  GG
GAM1500 CYP11B1  3' CCCTGCAGGACCCTATTCCAG 37662    AC       GCGC
                                CC  GCAGGACTC    TTCCAG
                                ||  |||||||||    ||||||
                                GG  CGTCCTGGG    AAGGTC
                                 GA        AT__
GAM1500 DHCR24   3' CCACGGGGACATGTCTTCCAGA 37663      CA    TCGCG
                                CCACG  GGAC     CTTCCAGA
                                |||||  ||||    ||||||||
                                GGTGC  CCTG     GAAGGTCT
                                   C_    TACA_
GAM1500 ETFDH    5' CACCAGGACTCTCGGTC     37664     G      G  C
                                CAC CAGGACTC CG TT
                                ||| |||||||| || ||
                                GTG GTCCTGAG GC AG
                                  _       A  C
GAM1500 GPC1     3' CCACTCAGGGCTGCCCCTTCCA 37665      G    A  C  G _
              GA                  CCAC CAGG CT GC C TTCCAGA
                                |||| |||| || || | |||||||
                                GGTG GTCC GA CG G AAGGTCT
                                  A   C  _  G G
GAM1500 GPR17    3' CCACCAGGACTCCCA       37666      G       GCGCTT
                                CCAC CAGGACTC      CCA
                                |||| ||||||||      |||
                                GGTG GTCCTGAG      GGT
                                  _       _______
GAM1500 IMMP2L   5' CACGCAGGACTCGCGGCC    37667             _
                                CACGCAGGACTCGCG CT
                                |||||||||||||||| ||
                                GTGCGTCCTGAGCGC GG
                                         C
GAM1500 ITGA4    5' CGCAGGACTCGCGTCTGGCCC  37668           _ ___
                                CGCAGGACTCGCG CT  TCC
                                |||||||||||| ||  |||
                                GCGTCCTGAGCGC GA  GGG
                                        A  CC
GAM1500 LAMB1    5' GCGGGGCTGGGGCGCTTCCAG  37669    A  A  C__
                                GC GG CT   GCGCTTCCAG
                                || || ||   ||||||||||
                                CG CC GA   CGCGAAGGTC
                                 C  C  CCC
GAM1500 NTSR1    3' CACGCAGGGCCAGCTTCC    37670        A T  C
                                CACGCAGG C CG GCTTCC
                                |||||||| | || ||||||
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                                GTGCGTCC G GT CGAAGG
                                     C _ _
GAM1500 PRKAR1A  3' CAGCAGGATAGCCTTTCAGA  37671   C    CTC  G  C
                                CA GCAGGA  GC CTT CAGA
                                || ||||||  || ||| ||||
                                GT CGTCCT  CG GAA GTCT
                                 _    AT_ _  A
GAM1500 PRSS8   5' CCACGCAGGGTCCTCCCAG  37672       AC  GCG
                                CCACGCAGG  TC  CTTCCAG
                                |||||||||  ||  |||||||
                                GGTGCGTCC  AG  GAGGGTC
                                     C_ ___
GAM1500 SURF1   5' CCCGCGGGCGCTTCC     37673   A  A  ACTC
                                CC CGC GG   GCGCTTCC
                                || ||| ||   ||||||||
                                GG GCG CC   CGCGAAGG
                                 _  _ ____
GAM1500 TRPM4   5' CGCCGGCTCTGCTTCCAG   37674    A  A  GC
                                CGC GG CTC  GCTTCCAG
                                ||| || |||  ||||||||
                                GCG CC GAG  CGAAGGTC
                                  G  _  A_
GAM1500 UBE3A   5' CATGCGGGACCCGCGCTTCC  37675   C  A
                                CA GC GGACTCGCGCTTCC
                                || || ||||||||||||||
                                GT CG CCTGGGCGCGAAGG
                                 A  C
GAM1500 VAV1    3' CCACGCCGGGCTCAGAGCCT  37676     A  A   C_
                                CCACGC GG CTCG  GCTT
                                |||||| || ||||  ||||
                                GGTGCG CC GAGT  CGGA
                                   G  C   CT
GAM1500 A       5' CCATGCTGGGACTTCCAG   37677    C  A_   CGCGCT
                                CCA GC  GGACT    TCCAG
                                ||| ||  |||||    |||||
                                GGT CG  CCTGA    AGGTC
                                  A  AC   _______
GAM1500 A       5' CCATGCTGGGACTTCCAG   37677    C  A_   CGCGCT
                                CCA GC  GGACT    TCCAG
                                ||| ||  |||||    |||||
                                GGT CG  CCTGA    AGGTC
                                  A  AC   _______
GAM1500 ARHGEF4  3' CCACACAGGACTTGCTCCTGGA 37678         CGC   CA
                                CCACGCAGGACT  GCTTC  GA
                                ||||||||||||  |||||  ||
                                GGTGTGTCCTGA  CGAGG  CT
                                       A__    AC
GAM1500 C20orf21 3' CAGGACTCCATTCAG     37679       G  C  C
                                CAGGACTC CG TTC AG
                                |||||||| || ||| ||
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                                GTCCTGAG GT AAG TC
                                    _ _  _
GAM1500 C20orf97 5' CGCCGGGGCTCAGAGCCTCCAG 37680    A_ A   C_
                                CGC  GG CTCG  GCTTCCAG
                                |||  || ||||  ||||||||
                                GCG  CC GAGT  CGGAGGTC
                                  GC  C   CT
GAM1500 C7orf13  5' CCACGCAGGGCTCACCC    37681        A    G
                                CCACGCAGG CTCGC CT
                                ||||||||| ||||| ||
                                GGTGCGTCC GAGTG GG
                                     C    _
GAM1500 CSMD1    5' CCATGCAGAACTCCTTTCAG  37682    C       GCG  C
                                CCA GCAGGACTC   CTT CAG
                                ||| |||||||||   ||| |||
                                GGT CGTCTTGAG   GAA GTC
                                  A       ___  A
GAM1500 DDX33    3' CCATCAGGCCACAGCTTCCAGA 37683    CG   A T  _
                                CCA  CAGG C CGC GCTTCCAGA
                                |||  |||| | ||| |||||||||
                                GGT  GTCC G GTG CGAAGGTCT
                                  A_   _ _  T
GAM1500 DKFZp762E1312 5' CACCAGGACTCTTTCCG    37684    G      GCGC   A
                                CAC CAGGACTC   TTCC G
                                ||| ||||||||   |||| |
                                GTG GTCCTGAG   AAGG C
                                  _      A___   C
GAM1500 FLJ10607 5' CACGCAGGGCCGCGCGCAG   37685        A T    TTC
                                CACGCAGG C CGCGC   CAG
                                |||||||| | |||||   |||
                                GTGCGTCC G GCGCG   GTC
                                    C _    C__
GAM1500 FLJ12057 5' CATCCAGGGCTCTGCTTCCAGA 37686   CG   A   GC
                                CA  CAGG CTC  GCTTCCAGA
                                ||  |||| |||  |||||||||
                                GT  GTCC GAG  CGAAGGTCT
                                 AG   C  A_
GAM1500 FLJ20555 5' CCTGCGCGAGCGCTTCC    37687    A_  A  ACTC
                                CC  CGC GG   GCGCTTCC
                                ||  ||| ||   ||||||||
                                GG  GCG CT   CGCGAAGG
                                 AC  _ _____
GAM1500 FLJ21709 3' CAGGTCAAGCTTCCGGA    37688     AC  C    A
                                CAGG  TCG GCTTCC GA
                                ||||  ||| ||||||  ||
                                GTCC  AGT CGAAGG CT
                                  __  T    C
GAM1500 FLJ22578 5' CCGCGCTGGACTTGCTGACT  37689    A  A    C  __
                                CC CGC GGACT GC  GCT
                                || ||| ||||| ||  |||
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                                GG GCG CCTGA CG  TGA
                                 C  A    A  AC
GAM1500  FLJ22670  3'  GCAGGACTTATGCCCAGA    37690        CGC  TT
                                GCAGGACT   GC  CCAGA
                                ||||||||   ||  |||||
                                CGTCCTGA   CG  GGTCT
                                    ATA  __
GAM1500  GTPBP1    3'  CCAGGCAGGGGTTCTTCCAGA  37691     C    ACTCGCG
                                CCA GCAGG      CTTCCAGA
                                ||| |||||      ||||||||
                                GGT CGTCC      GAAGGTCT
                                  C    CCAA___
GAM1500  HSPC159   3'  GCTAGGACACTTCTTCCAGA   37692    _    TCGCG
                                GC AGGAC    CTTCCAGA
                                || |||||    ||||||||
                                CG TCCTG    GAAGGTCT
                                 A    TGAA_
GAM1500  KIAA0596  3'  CACTTGGGACAGGCTTCCAGA  37693     GCA   TCGC
                                CAC   GGAC   GCTTCCAGA
                                |||   ||||   |||||||||
                                GTG   CCTG   CGAAGGTCT
                                  AAC   TC__
GAM1500  KIAA0876  5'  GCGGGAAGCACACTTCTGGA   37694    A  CT      CA
                                GC GGA  CGCGCTTC  GA
                                || |||  ||||||||  ||
                                CG CCT  GTGTGAAG  CT
                                 C  TC       AC
GAM1500  KIAA1322  3'  CCACGTGGGCCCTGCTTCCAGA 37695      CA  A   GC
                                CCACG  GG CTC  GCTTCCAGA
                                |||||  || |||  |||||||||
                                GGTGC  CC GGG  CGAAGGTCT
                                   AC  _   A_
GAM1500  KIAA1328  3'  CCACGCAGACTCGCTGCATGCA 37696        G     _  TTC
            G                    CCACGCAG ACTCGC GC   CAG
                                ||||||||  ||||||  ||   |||
                                GGTGCGTC TGAGCG CG   GTC
                                     _     A  TAC
GAM1500  KIAA1430  5'  CCGCGCGCCCGCGCTTCCGGA  37697    A   AGGA        A
                                CC CGC    CTCGCGCTTCC GA
                                || |||    |||||||||||  ||
                                GG GCG    GGGCGCGAAGG CT
                                 C   C___          C
GAM1500  KIAA1866  3'  CCACGGGGGTCCCTTCCAG    37698      CA  A  CGCG
                                CCACG  GG CT    CTTCCAG
                                |||||  || ||    |||||||
                                GGTGC  CC GG    GAAGGTC
                                   CC  A  _____
GAM1500  MFN2      3'  CCACGCAGACTCCGCCTCAG   37699        G   G     C
                                CCACGCAG ACTC CGCTTC AG
                                |||||||| |||| |||||| ||
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                                GGTGCGTC TGAG GCGGAG TC
                                      _   _    _
GAM1500  PANX2    3'  CCACGCAGGGCTGGTGTCCA  37700        ACTC  GCT__
                                CCACGCAGG   GC    TCCA
                                |||||||||   ||    ||||
                                GGTGCGTCC   CG    AGGT
                                     _____  ACCAC
GAM1500  PP1057   3'  CCGGGCAGGGCCACCTTCCAGA 37701    AC    A T   G
                                CC  GCAGG C CGC CTTCCAGA
                                ||  ||||| | ||| ||||||||
                                GG  CGTCC G GTG GAAGGTCT
                                 CC    C _  _
GAM1500  TIP120A  5'  CGCGGCGGCTCCCGCTTCCAG  37702    A__  A   G
                                CGC   GG CTC CGCTTCCAG
                                |||   || ||| |||||||||
                                GCG   CC GAG GCGAAGGTC
                                  CCG  _   G
GAM1500  TM4SF11  3'  CCACGCAGGGCTCCCCAGCTTC 37703        A   GC__    C
           AG                     CCACGCAGG CTC    GCTTC AG
                                |||||||||  |||    ||||| ||
                                GGTGCGTCC GAG    CGAAG TC
                                     C   GGGT    _
GAM1500  TNFRSF19L 5'  CCACGCAGGGCCGGCCC     37704         A T  C
                                CCACGCAGG C CG GCTT
                                |||||||||  | || ||||
                                GGTGCGTCC G GC CGGG
                                     C _  _
GAM1500  TNRC9    5'  CGCGTGGGACTCGCGGCCGGA  37705     A__       CTT  A
                                CGC   GGACTCGCG   CC GA
                                |||   |||||||||   || ||
                                GCG   CCTGAGCGC   GG CT
                                  CAC        C__  C
GAM1500  WFDC3    3'  GCCAGGAAAAGCTTCCAGA   37706    _    CTCGC
                                GC AGGA    GCTTCCAGA
                                || ||||    |||||||||
                                CG TCCT    CGAAGGTCT
                                 G   TTT__
GAM1500  ZNF333   3'  GCAGGAACCTTCCAG       37707       CTC  G
                                GCAGGA   GC CTTCCAG
                                ||||||   || |||||||
                                CGTCCT   TG GAAGGTC
                                     ___  _
GAM1500  LOC123443 5'  GCAGATCTGCTTCCAG      37708       AC  GC
                                GCAGG  TC  GCTTCCAG
                                |||||  ||  ||||||||
                                CGTCT  AG  CGAAGGTC
                                   __  A_
GAM1500  LOC124222 3'  GCAGGACTTGAACTCTCAGA   37709        CGC   TC
                                GCAGGACT   GCT  CAGA
                                ||||||||   |||  ||||
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                                CGTCCTGA  TGA  GTCT
                                    ACT  GA
GAM1500  LOC153768 5'  CACGCAGGGTGCTATCCTAGA  37710       ACTC  GCT  _
                                CACGCAGG   GC   TCC AGA
                                ||||||||   ||   ||| |||
                                GTGCGTCC   CG   AGG TCT
                                    CA__  AT_  A
GAM1500  LOC166983 3'  CCCTGCAGGGACTTCCAG   37711   AC   ACTCGC
                                CC  GCAGG    GCTTCCAG
                                ||  |||||    ||||||||
                                GG  CGTCC    TGAAGGTC
                                 GA   C_____
GAM1500  LOC201158 5'  ACGCCAGCCCTGCTTCCAG   37712     A  A  GC
                                ACGC GG CTC  GCTTCCAG
                                |||| || |||  ||||||||
                                TGCG TC GGG  CGAAGGTC
                                  G  _  A_
GAM1500  LOC203504 3'  CCAGTAGGGAAGCAGCTTCCAG 37713    CGCA  CTC  _
           A                     CCA   GGA  GC GCTTCCAGA
                                |||   |||  || |||||||||
                                GGT   CCT  CG CGAAGGTCT
                                  CATC  T__  T
GAM1500  LOC219401 5'  CCAGCGCTCCCTGCGCTTCCGG 37714    _  AGGA TC      A
           A                     CCA CGC   C  GCGCTTCC GA
                                ||| |||   |  |||||||| ||
                                GGT GCG   G  CGCGAAGG CT
                                  C  AG__ GA      C
GAM1500  LOC221477 5'  CATGCGGGGCTCGCGCCCC   37715   C  A  A
                                CA GC GG CTCGCGCTTC
                                || || || ||||||||||
                                GT CG CC GAGCGCGGGG
                                 A  C  C
GAM1500  LOC253181 5'  CCATGTGGGACCCCCAGCCAGA 37716    CGCA    G  CTT
                                CCA   GGACTC CG   CCAGA
                                |||   |||||| ||   |||||
                                GGT   CCTGGG GT   GGTCT
                                  ACAC    G  C__
GAM1500  LOC254228 3'  GCAGCCCTGCTTCCAG     37717     GA  GC
                                GCAG  CTC  GCTTCCAG
                                ||||  |||  ||||||||
                                CGTC  GGG  CGAAGGTC
                                  __  A_
GAM1500  LOC254636 5'  CCACGGCTCAGCGCTTCCAG  37718     GCA  A  _
                                CCAC   GG CTC GCGCTTCCAG
                                ||||   || ||| ||||||||||
                                GGTG   CC GAG CGCGAAGGTC
                                  ___  _  T
GAM1500  LOC91917  5'  CGCTGGGATCCGCACTTCCGGA 37719    A_  CT      A
                                CGC  GGA  CGCGCTTCC GA
                                |||  |||  ||||||||| ||
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                                GCG  CCT  GCGTGAAGG CT
                                  AC   AG       C
GAM1501  CRLF1    5'  GCGCGCTGGGCGCGGACGCG   37722    _       A_ _
                                GC CGCTGGGCG  GA GCG
                                || |||||||||  || |||
                                CG GCGACCCGC  CT CGC
                                 C        GC  G
GAM1501  DLK1     5'  GCTTCTGGTTGCGGACGCGA   37723    CG   __   A _
                                GC  CTGG  GCG GA GCGA
                                ||  ||||  ||| || ||||
                                CG  GACC  CGC CT CGCT
                                 AA   AA   _  G
GAM1501  KCNN2    5'  GCCGCCGGGCGAGGAGGTGCG  37724           A____
                                GCCGCTGGGCGAG    GCG
                                ||||||||||||    |||
                                CGGCGGCCCGCTC    CGC
                                       CTCCA
GAM1501  MADH7    5'  GCCTGCTAAGGAGCGAACATGA 37725    _    CGA       C
                                GCC GCTGGG   GAGCGAACA GA
                                ||| ||||||   |||||||||  ||
                                CGG CGATTC   CTCGCTTGT CT
                                  A     ___       A
GAM1501  NTRK3    5'  GCCGCCGGGTGGGAGCCGCGA  37726        C__   A_
                                GCCGCTGGG   GAG  GCGA
                                |||||||||   |||  ||||
                                CGGCGGCCC   CTC  CGCT
                                     ACC   GG
GAM1501  TARBP2   5'  GCCGCTGGGTAGGGAGGCG   37727        C___   A
                                GCCGCTGGG    GAG GCG
                                |||||||||    ||| |||
                                CGGCGACCC    CTC CGC
                                     ATCC   _
GAM1501  TARBP2   5'  GCCGCTGGGTAGGGAGGCG   37727        C___   A
                                GCCGCTGGG    GAG GCG
                                |||||||||    ||| |||
                                CGGCGACCC    CTC CGC
                                     ATCC   _
GAM1501  TERF2    5'  GCCGCTGGGTCACGCACG    37728        CGAGA   AA
                                GCCGCTGGG    GCG  CACG
                                |||||||||    |||  ||||
                                CGGCGACCC    TGC  GTGC
                                     AG___   __
GAM1501  TFG      5'  CCGCTGAATGGGCGGACGCGA  37729      _____    A _
                                CCGCT    GGGCG GA GCGA
                                |||||    ||||| || ||||
                                GGCGA    CCCGC CT CGCT
                                   CTTA    _  G
GAM1501  WEE1     5'  GCCACTGGGGCGTAGTGGGCG  37730         _ _  A__
                                GCCGCTGGG CG AG   GCG
                                ||||||||| || ||   |||
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                                CGGTGACCC GC TC   CGC
                                     C  A  ACC
GAM1501  ABHD3    5'  GCGGGCGAGAGCGGACGCG   37731    T        A  A
                                GC GGGCGAGAGCG AC CG
                                || |||||||||| || ||
                                CG CCCGCTCTCGC TG GC
                                 _        C  C
GAM1501  APCL     3'  GCTGCTGGGCAAGGCGTCACG  37732    C        A   AA
                                GC GCTGGGCGAG GCG  CACG
                                || |||||||||| |||  ||||
                                CG CGACCCGTTC CGC  GTGC
                                 A        _  A_
GAM1501  C22orf5  5'  CGCTGGGCGAGGCTGCTGCG   37733          A  GAACA
                                CGCTGGGCGAG GC    CG
                                |||||||||| ||    ||
                                GCGACCCGCTC CG    GC
                                      _ ACGAC
GAM1501  CARD9    3'  GCCGCTGGGCGCGGAGGC    37734          A_ _
                                GCCGCTGGGCG  GA GC
                                ||||||||||  || ||
                                CGGCGACCCGC  CT CG
                                      GC  C
GAM1501  FLJ10618 5'  GCCGCTGAGGCGGGACGCG   37735       _   A _
                                GCCGCTG GGCG GA GCG
                                ||||||| |||| || |||
                                CGGCGAC CCGC CT CGC
                                    T   C  G
GAM1501  FLJ12666 5'  GCCAGGGACCGGGAGCGGACGC 37736     CT  G  A    A  A
            G                    GCCG  GG CG GAGCG AC CG
                                ||||  || || ||||| || ||
                                CGGT  CT GC CTCGC TG GC
                                  CC  G  C    C  C
GAM1501  FLJ13102 3'  GCTGCTGGGCGACGACGACGA  37737    C       GA    ACA
                                GC GCTGGGCGA  GCGA   CGA
                                || |||||||||  ||||   |||
                                CG CGACCCGCT  TGCT   GCT
                                 A        GC   ___
GAM1501  HSA250839 5'  GCCGCTGGGATGCCGGATGCG  37738         ____  A  _
                                GCCGCTGGG    CG GA GCG
                                |||||||||    || || |||
                                CGGCGACCC    GC CT CGC
                                      TACG  _  A
GAM1501  KIAA1813  3'  GCCTCTGGGTAACAGTGAACAC 37739     G    CG G  C
            G                    GCC CTGGG  A AG GAACACG
                                ||| |||||  | || |||||||
                                CGG GACCC  T TC CTTGTGC
                                  A    AT G  A
GAM1501  MCAM     3'  GCCGCTGGGGTGCTCTCCGGAG 37740          _________  A
            CG                    GCCGCTGGG       CG GAGCG
                                |||||||||       || |||||
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                                CGGCGACCC       GC CTCGC
                                     CACGAGAG  _
GAM1501  OLIG1     3'  GCTGGGTGAGAGCGAGCAC   37741       C       A
                                GCTGGG GAGAGCGA CAC
                                |||||| |||||||| |||
                                CGACCC CTCTCGCT GTG
                                   A       C
GAM1501  LOC122553 5'  GCCGCTGGGCGGGGGCGA    37742          AGA
                                GCCGCTGGGCG   GCGA
                                ||||||||||   ||||
                                CGGCGACCCGC   CGCT
                                      CCC
GAM1501  LOC126520 5'  ACCACCTTGAGGGCGAACACG  37743       GGGC   A
                                GCCGCT    GAG GCGAACACG
                                ||||||    ||| |||||||||
                                TGGTGG    CTC CGCTTGTGC
                                   AA__   C
GAM1501  LOC148113 5'  GCCGCTGGGTGGAGGGCG    37744         C_   A
                                GCCGCTGGG  GAG GCG
                                |||||||||  ||| |||
                                CGGCGACCC  CTC CGC
                                     AC   C
GAM1501  LOC157280 3'  GCCGCTGGGTGATGGGACA    37745         C  GAGC  A
                                GCCGCTGGG GA    GA CA
                                ||||||||| ||    || ||
                                CGGCGACCC CT    CT GT
                                     A  ACC_  _
GAM1501  LOC221477 5'  GCCGCCGGGCGAGGAGGA    37746           _  C
                                GCCGCTGGGCGAG AG GA
                                |||||||||||| || ||
                                CGGCGGCCCGCTC TC CT
                                       C  _
GAM1501  LOC253216 3'  GCTGGGCGGAGAGCACGA    37747         _    GAAC
                                GCTGGGCG AGAGC    ACGA
                                |||||||| |||||    ||||
                                CGACCCGC TCTCG    TGCT
                                     C    _____
GAM1501  LOC255448 3'  GCCGCTGGGTGATGGGACA    37745         C  GAGC  A
                                GCCGCTGGG GA    GA CA
                                ||||||||| ||    || ||
                                CGGCGACCC CT    CT GT
                                     A  ACC_  _
GAM1501  LOC90591  3'  GCCGCTGGAGTGCAGTGGCGCG 37748         ___   AGA__
            A                    GCCGCTGG   GCG     GCGA
                                ||||||||   |||    ||||
                                CGGCGACC   CGT    CGCT
                                     TCA   CACCG
GAM1502  EDAR      3'  CTGCCTAAGACTGAAGTGGAAG 37751      G ___       A
                                CTGC T   GCTGAAGTG AAG
                                |||| |   ||||||||| |||
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                                GACG A   TGACTTCAC TTC
                                  G TTC        C
GAM1502  PTHLH    3'  CTCCCTTGAAGTGAAA      37752      G  GCGTGC
                                TTCC CT     TGAAGTGAAA
                                |||| ||     ||||||||||
                                GAGG GA     ACTTCACTTT
                                  _ _______
GAM1502  SLC19A2  5'  CTCCGCCAACTGGAGTGA    37753         CGT    A
                                TTCCGCTG   GCTG AGTGA
                                ||||||||   |||| |||||
                                GAGGCGGT   TGAC TCACT
                                     ___    C
GAM1502  SUPT5H   5'  TTCCGCTGCTGCTGGGAAA   37754         G     AAGT
                                TTCCGCTGC TGCTG    GAAA
                                ||||||||| |||||    ||||
                                AAGGCGACG ACGAC    CTTT
                                     _    C___
GAM1502  AKAP8    3'  TTCTGTTGCGTGCTAACCTTG  37755     CGC        AG_
                                TTC   TGCGTGCTGA   TG
                                |||   ||||||||||   ||
                                AAG   ACGCACGATT   AC
                                  ACA         GGA
GAM1502  KIAA0854 5'  TTCCTTGTGTGCTGAAG     37756      GC  C
                                TTCC  TG GTGCTGAAG
                                ||||  || |||||||||
                                AAGG  AC CACGACTTC
                                  A_  A
GAM1502  SEMA4G   5'  TTCCACTGTGTGCTCAGCGTGA 37757         C     GAA_
            A                    TTCCGCTG GTGCT    GTGAA
                                ||||||||| |||||    |||||
                                AAGGTGAC CACGA    CACTT
                                     A     GTCG
GAM1502  LOC158147 3'  TTCTGCTGTGTTCTGAGTA   37758     C    C  G    A
                                TTC GCTG GT CTGA GTG
                                ||| |||| || |||| |||
                                AAG CGAC CA GACT CAT
                                  A    A  A    _
GAM1503  TNP1     3'  TGTGAAGCGCACCAGG      37761      C        TGCGAC
                                TGTG AAGCGCACC      GG
                                |||| |||||||||      ||
                                ACAC TTCGCGTGG      CC
                                  _        T_____
GAM1503  DKFZP434C128 3'  TGTGCAAATGCATCTGACTGGC 37762         C   C  GC   G
                                TGTGCAAG GCA CT  GAC GGC
                                |||||||| ||| ||  ||| |||
                                ACACGTTT CGT GA  CTG CCG
                                     A   A  __   A
GAM1503  KIAA0040  3'  TGTGCAAGGCACTTGCCTGAGC 37763         C    C   GAC
                                TGTGCAAG GCAC TGC   GGGC
                                |||||||| |||| |||   ||||
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                                ACACGTTC CGTG ACG   CTCG
                                    _   A  GA_
GAM1503 RIS1    5' TGGCGAGCGGGCGACGGG   37764   T A   CACCT
                                TG GC AGCG    GCGACGGG
                                || || ||||    ||||||||
                                AC CG TCGC    CGCTGCCC
                                 _ C   C____
GAM1503 LOC149117 3' TGTGTAACTGCACCTGCTCCGG 37765     CA  _     GA
                                TGTG  AGC GCACCTGC  CGG
                                ||||  ||| ||||||||  |||
                                ACAC  TTG CGTGGACG  GCC
                                  A_  A      AG
GAM1504 LNK     5' CAGGCAGGAAACCCGGGCTCGG 37768     AC   ____  A
                                CAGG  CAGG   TCG GCTCGG
                                ||||  ||||   ||| ||||||
                                GTCC  GTCC   GGC CGAGCC
                                  __   TTTG  C
GAM1504 WNT10B  5' TCGATCAGGACCTCCAG    37769    _     AGG  G
                                TCGA CAGGACC   TC AG
                                |||| |||||||   || ||
                                AGCT GTCCTGG   AG TC
                                  A      ___  G
GAM1504 ZNF180  5' GAAGGGCCGAGCTGCTCGG   37770   C  A  AG  CGA
                                GA AGG CC  GT   GCTCGG
                                || ||| ||  ||   ||||||
                                CT TCC GG  CG   CGAGCC
                                 _  C  CT  A__
GAM1504 HEAB    5' TCGAGGGACCAGGCTTCG   37771    CA      CGAGC
                                TCGA  GGACCAGGT   TCG
                                ||||  |||||||||    |||
                                AGCT  CCTGGTCCG   AGC
                                  C_       A____
GAM1505 BCRP2   3' CAAGAGAAGAGTTAAC     37774      TAG
                                TAAGA   GAAGAGTTAAC
                                |||||   ||||||||||
                                GTTCT   CTTCTCAATTG
                                  ___
GAM1505 COX11   3' TAAGTATGAAGAGTTAA    37775     A  G
                                TAAG TA GAAGAGTTAA
                                |||| ||  ||||||||||
                                ATTC AT CTTCTCAATT
                                  _ A
GAM1505 GAN     3' TAAAATGGAGAGTTAA     37776      A  A
                                TAAGAT GGA GAGTTAA
                                |||||| ||| |||||||
                                ATTTTA CCT CTCAATT
                                  _  _
GAM1505 MADH4   3' TAACATAGGTGAATTAAC   37777    G   AA
                                TAA ATAGG  GAGTTAAC
                                ||| |||||  ||||||||
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                                ATT TATCC  CTTAATTG
                                  G    A_
GAM1505  PIN4     3'  TAAAAAGAAAGGAGTTAAC   37778      T    _
                                TAAGA AGGAAG AGTTAAC
                                ||||| |||||| |||||||
                                ATTTT TCTTTC TCAATTG
                                   _    C
GAM1505  PTGS1    3'  TAAGACAGGAGACTTAAC    37779         A  G
                                TAAGATAGGA GA TTAAC
                                |||||||||| || |||||
                                ATTCTGTCCT CT AATTG
                                      _ G
GAM1505  PTGS1    3'  TAAGACAGGAGACTTAAC    37779         A  G
                                TAAGATAGGA GA TTAAC
                                |||||||||| || |||||
                                ATTCTGTCCT CT AATTG
                                      _ G
GAM1505  WRB      3'  TAAGCTAGGAAGAGGAAA    37780      A       TT
                                TAAG TAGGAAGAG  AA
                                |||| |||||||||  ||
                                ATTC ATCCTTCTC  TT
                                  G        CT
GAM1505  ZHX1     3'  GATACGGCAAGAGTTAAC    37781      _ _
                                GATA GG AAGAGTTAAC
                                |||| || ||||||||||
                                CTAT CC TTCTCAATTG
                                  G  G
GAM1505  DKFZP434F0318 3'  TAAGATAGCTAAACAGTTAA  37782        __  G
                                TAAGATAG  GAA AGTTAA
                                ||||||||  ||| ||||||
                                ATTCTATC  TTT TCAATT
                                     GA   G
GAM1505  DORFIN   3'  TAAGATAGAACATTTTAAC   37783          AGAG
                                TAAGATAGGA    TTAAC
                                ||||||||||    |||||
                                ATTCTATCTT    AATTG
                                      GTAA
GAM1505  EDR2     3'  GACAACGGAAGAGTTAAC    37784      __
                                GATA  GGAAGAGTTAAC
                                ||||  ||||||||||||
                                CTGT  CCTTCTCAATTG
                                  TG
GAM1505  FLJ11078 3'  TAAGATAGGAGGTTAA      37785          A A
                                TAAGATAGGA G GTTAA
                                |||||||||| | |||||
                                ATTCTATCCT C CAATT
                                      _ _
GAM1505  FLJ14437 5'  AGAGAGTGAGGAGTTAAC    37786     T  _  A
                                AGA AG GA GAGTTAAC
                                ||| || || ||||||||
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                                TCT TC CT CTCAATTG
                                  C  A  C
GAM1505  GRASP1    3'  TAAGACAGGATCATTAAC    37787          AGA
                                TAAGATAGGA   GTTAAC
                                ||||||||||   ||||||
                                ATTCTGTCCT   TAATTG
                                     AG_
GAM1505  KIAA0451  5'  TAAGATAAGGAAAAAGAGC   37788        _  ___
                                TAAGATA GGA   AGAGT
                                ||||||| |||   |||||
                                ATTCTAT CCT   TCTCG
                                    T   TTT
GAM1505  KIAA0650  3'  AAGATAGATAGGTTAAC     37789        A  A
                                AAGATAGG AG GTTAAC
                                |||||||| || ||||||
                                TTCTATCT TC CAATTG
                                     A  _
GAM1505  KIAA0993  3'  CAAGAAAAGAGAGTTAA     37790      T    A
                                TAAGA AGGA GAGTTAA
                                ||||| |||| |||||||
                                GTTCT TTCT CTCAATT
                                   T    _
GAM1505  KIAA1724  3'  TAAAATAGGCTTAGAGTTA    37791        A__
                                TAAGATAGG   AGAGTTA
                                |||||||||   |||||||
                                ATTTTATCC   TCTCAAT
                                     GAA
GAM1505  KIAA1737  3'  CAAGATGGCAGCAGAGTTAAC  37792       A  A___
                                TAAGAT GG    AGAGTTAAC
                                |||||| ||    |||||||||
                                GTTCTA CC    TCTCAATTG
                                   _ GTCG
GAM1505  MRPL35    3'  AGAGAGAATGGAGTTAAC    37793     T    A_
                                AGA AGGA  GAGTTAAC
                                ||| ||||  ||||||||
                                TCT TCTT  CTCAATTG
                                  C    AC
GAM1505  PEX11B    3'  TAAGGGAGGAAGAGGAAAC    37794     AT       TT
                                TAAG  AGGAAGAG  AAC
                                ||||  ||||||||  |||
                                ATTC  TCCTTCTC  TTG
                                   CC       CT
GAM1505  LOC255520 3'  AAGAGAAGCAAGAGTTAAC    37795      T_  G
                                AAGA  AG AAGAGTTAAC
                                ||||  || ||||||||||
                                TTCT  TC TTCTCAATTG
                                  CT  G
GAM1505  LOC257415 3'  CAAGAGTGAGGAGTTAAC     37796       TAG  A
                                TAAGA   GA GAGTTAAC
                                |||||   || ||||||||
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                                GTTCT   CT CTCAATTG
                                   CA_  C
GAM1505 LOC51652 3'  TAACATAGGAACAGGAAAC   37797     G      G  TT
                                TAA ATAGGAA AG  AAC
                                ||| ||||||| ||  |||
                                ATT TATCCTT TC  TTG
                                  G      G  CT
GAM1506 ASPA     3'  TATGATATCTTTAAAGATATAT 37800          ACAAA
             TA                   TATGATATCTT    ATATATTA
                                ||||||||||     ||||||||
                                ATACTATAGAA    TATATAAT
                                      ATTTC
GAM1506 NCOA6IP  3'  TATATTACAAAATATATT    37801     C
                                TAT TTACAAAATATATT
                                ||| ||||||||||||||
                                ATA AATGTTTTATATAA
                                  T
GAM1506 FLJ23441 3'  TATGATATCTTATGGCACAACA 37802          ___  A
                                TATGATATCTTA   CA AATA
                                ||||||||||||   || ||||
                                ATACTATAGAAT   GT TTGT
                                      ACC  G
GAM1507 LOC220906 5'  TTTCCTTGTCATGTAATCTTTG 37805       CG  ATCA
             C                    TTTCTT  GT    TAATCTTTGC
                                ||||||  ||    ||||||||||
                                AAAGGA  CA    ATTAGAAACG
                                   A_  GTAC
GAM1508 dA141H5.1 3'  TGGTAAATTTTATTGATGTGA  37808          TTATT   C
                                TGGTAAATTTT    ATG GA
                                ||||||||||     ||| ||
                                ACCATTTAAAA    TAC CT
                                      TAAC_   A
GAM1508 KIAA1323  3'  TATGGTAAATTTTATGTTATG  37809           TTA
                                TATGGTAAATTTT   TTATG
                                ||||||||||||   |||||
                                ATACCATTTAAAA   AATAC
                                      TAC
GAM1509 KAL1     3'  ATTAGCAGCTTATTTCAT    37812        TT    AA
                                ATTAGCAG  CTTAT  CAT
                                ||||||||  |||||  |||
                                TAATCGTC  GAATA  GTA
                                   __     AA
GAM1509 NRXN1    3'  TTAGCAACACTTATAACAT   37813       TT
                                TTAGCAG  CTTATAACAT
                                |||||||  ||||||||||
                                AATCGTT  GAATATTGTA
                                   GT
GAM1509 NRXN1    3'  TTAGCAACACTTATAACAT   37813       TT
                                TTAGCAG  CTTATAACAT
                                |||||||  ||||||||||
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                                AATCGTT  GAATATTGTA
                                    GT
GAM1509  AP4E1    3'  ATTAGCAGTTTATAACAT    37814         CT
                                ATTAGCAGTT  TATAACAT
                                ||||||||||  ||||||||
                                TAATCGTCAA  ATATTGTA
                                          __
GAM1509  Rab11-FIP2 3'  ATTAGCAATATTTTTATAACAT 37815         TC__
                                ATTAGCAGT    TTATAACAT
                                |||||||||    |||||||||
                                TAATCGTTA    AATATTGTA
                                     TAAA
GAM1509  ZNF363    3'  ATTAGCAGTTATTACATCA    37816         TCT   A
                                ATTAGCAGT   TAT ACATCA
                                |||||||||   ||| ||||||
                                TAATCGTCA   ATA TGTAGT
                                     ___   A
GAM1509  LOC142955 5'  CAATTAGCAGTTACTGATTAAC 37817           _  TA_
            ATCA                    TAATTAGCAGTT CT   TAACATCA
                                ||||||||||||| ||   ||||||||
                                GTTAATCGTCAA GA   ATTGTAGT
                                      T  CTA
GAM1509  LOC200583 5'  GCTTGCCCTTTATAACATCA   37818    A_     _
                                GC  GTTCTT ATAACATCA
                                ||  |||||| |||||||||
                                CG  CGGGAA TATTGTAGT
                                 AA     A
GAM1510  RNF14    3'  GTATTAAAACATATATTTATAT 37821           _  C
                                GTATTAAAACAT TAT TATAT
                                |||||||||||| ||| |||||
                                CATAATTTTGTA ATA ATATA
                                      T   A
GAM1510  DKFZP566A1524 3'  CAAGTATTAACATCAATCT    37822         AA    _
                                TAAGTATTA  ACATTA TCT
                                |||||||||  |||||| |||
                                GTTCATAAT  TGTAGT AGA
                                     __     T
GAM1511  KIF5C    3'  TTATATATTTTAGTTCCCAGAC 37825           A    T_
            ATA                   TTATATGTTTTA TTTTT  GCATA
                                ||||||||||| |||||  |||||
                                AATATATAAAAT AAGGG  TGTAT
                                      C    TC
GAM1511  RNTRE    3'  TATATATATATTTTTTGCATA  37826       TTTA
                                TATATGT    ATTTTTTGCATA
                                |||||||    ||||||||||||
                                ATATATA    TAAAAAACGTAT
                                    TA__
GAM1511  KIAA0748  3'  TTATATATTTTAATACACACAT 37827           TTTT
            A                    TTATATGTTTTAAT    TGCATA
                                ||||||||||||||    ||||||
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                                AATATATAAAATTA   GTGTAT
                                       TGT_
GAM1511  KIAA1677  3'  TTATATGTTTTAATTAATTA  37828           TT
                                TTATATGTTTTAATT  TTG
                                |||||||||||||||  |||
                                AATATACAAAATTAA  AAT
                                       TT
GAM1511  LOC125434 3'  TGTTTTCCTTTTTGCATA   37829      AA
                                TGTTTT  TTTTTTGCATA
                                ||||||  ||||||||||
                                ACAAAA  GAAAAACGTAT
                                   G_
GAM1511  LOC126917 3'  TGTTTTGTTTTTTGCATA   37830      AA
                                TGTTTT  TTTTTTGCATA
                                ||||||  ||||||||||
                                ACAAAA  AAAAAACGTAT
                                   C_
GAM1512  MGC4268   5'  CGGGTTTTAAAATTTTCTA   37833   ATA
                                CG   TTTTAAAATTTTCTA
                                ||   ||||||||||||||
                                GC   AAAATTTTAAAAGAT
                                 CC_
GAM1513  CHAC      3'  CAATACAAAGCTATAAAATATA 37836        A_   C
            T                    CAATACAAA  TGTAG ATATAT
                                 |||||||||  ||||| ||||||
                                 GTTATGTTT  ATATT TATATA
                                      CG    T
GAM1513  PIGA      3'  TACAAACAAAACACAAATATAT 37837      T    TG  C
                                TACAA ACAAAA  TAG ATATAT
                                ||||| ||||||  ||| ||||||
                                ATGTT TGTTTT  GTT TATATA
                                   _     GT   _
GAM1513  PIGA      3'  TACAAACAAAACACAAATATAT 37837      T    TG  C
                                TACAA ACAAAA  TAG ATATAT
                                ||||| ||||||  ||| ||||||
                                ATGTT TGTTTT  GTT TATATA
                                   _     GT   _
GAM1513  PIGA      3'  TACAAACAAAACACAAATATAT 37837      T    TG  C
                                TACAA ACAAAA  TAG ATATAT
                                ||||| ||||||  ||| ||||||
                                ATGTT TGTTTT  GTT TATATA
                                   _     GT   _
GAM1513  SLC10A2   3'  TACATATATAAAACATATACAT 37838     _  C      _
            ATAT                    TACA ATA AAAATGTA GCATATAT
                                    |||| ||| |||||||| ||||||||
                                    ATGT TAT TTTTGTAT TGTATATA
                                      A  A       A
GAM1513  BY55      3'  TACAAAAACGCATATAT     37839        TGTA
                                TACAAAA    GCATATAT
                                |||||||    ||||||||
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                                ATGTTTT   CGTATATA
                                    TG__
GAM1513  COL21A1   3'  TACAATGAAAATTAACATATAT 37840      AC    G
                                TACAAT  AAAAT TAGCATATAT
                                ||||||  ||||| ||||||||||
                                ATGTTA  TTTTA ATTGTATATA
                                   C_    _
GAM1513  KIAA1622  3'  TACAATCTAAAATGTAAACA  37841      AC      _
                                TACAAT  AAAATGTAG CA
                                ||||||  ||||||||| ||
                                ATGTTA  TTTTACATT GT
                                   GA       T
GAM1513  PBEF      3'  TACAATACAACAACCAAGATAT 37842         AATGT_  C
              AT                  TACAATACAA     AG ATATAT
                                ||||||||||     || ||||||
                                ATGTTATGTT     TC TATATA
                                     GTTGGT  _
GAM1513  PRO0082   3'  AATACAAATGTAGCATATATA  37843        A         III
                                AATACAAA TGTAGCATATAT   A
                                |||||||| ||||||||||||   |
                                TTATGTTT ACATCGTATATA   T
                                    _         III
GAM1513  ST7L      3'  CAAAATGCTTTAGCATATAT   37844       ___
                                CAAAATGT   AGCATATAT
                                ||||||||   |||||||||
                                GTTTTACG   TCGTATATA
                                    AAA
GAM1513  ST7L      3'  CAAAATGCTTTAGCATATAT   37844       ___
                                CAAAATGT   AGCATATAT
                                ||||||||   |||||||||
                                GTTTTACG   TCGTATATA
                                    AAA
GAM1513  ST7L      3'  CAAAATGCTTTAGCATATAT   37844       ___
                                CAAAATGT   AGCATATAT
                                ||||||||   |||||||||
                                GTTTTACG   TCGTATATA
                                    AAA
GAM1513  LOC144519 3'  TACATATACGGGCAGCACATAT 37845     _   AAAAT
                                TACA ATAC     GTAGCATATAT
                                ||||  ||||     ||||||||||||
                                ATGT TATG     CGTCGTGTATA
                                  A   CC___
GAM1513  LOC154739 5'  CACTACAAAATCCAGAATAT   37846    A      G   C
                                CA TACAAAAT TAG ATAT
                                ||  |||||||| ||| ||||
                                GT ATGTTTTA GTC TATA
                                 G       G   T
GAM1513  LOC158629 5'  TACATATACAAAAAACATATAT 37847     _      TGT
                                TACA ATACAAAA   AGCATATAT
                                ||||  ||||||||   |||||||||
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                                ATGT TATGTTTT   TTGTATATA
                                  A      ___
GAM1513  LOC254065 5'  TACAATACAAGGGGTAGGCAC  37848         AAT   _
                                TACAATACAA   GTAG CAT
                                ||||||||||   |||| |||
                                ATGTTATGTT   CATC GTG
                                     CCC    C
GAM1514  CHRNB2   3'  CCACTGTGGGGCCCACCCAG   37851     GA_  TT
                                CCGC   GG  TCCACCCAG
                                ||||   ||  |||||||||
                                GGTG   CC  GGGTGGGTC
                                  ACA  CC
GAM1514  DDEF2    5'  CTACCCGCCACCCAG      37852      G  AGGTTT
                                CTACC CG     CCACCCAG
                                ||||| ||     ||||||||
                                GATGG GC     GGTGGGTC
                                  _ _______
GAM1514  DDX3     5'  CTGTCGCGGCGACTTCTGCCCG 37853    AC   A_ GT   CA   A
            GC                    CT  CGCG  G  TTC  CCC GC
                                ||  ||||  |  |||  ||| ||
                                GA  GCGC  C  AAG  GGG CG
                                 CA    CG TG   AC   C
GAM1514  DDX3     5'  CTGTCGCGGCGACTTCTGCCCG 37853    AC   A_ GT   CA   A
            GC                    CT  CGCG  G  TTC  CCC GC
                                ||  ||||  |  |||  ||| ||
                                GA  GCGC  C  AAG  GGG CG
                                 CA    CG TG   AC   C
GAM1514  EIF2C1   5'  CCACTGCGAGCGCCCGGC    37854      C    _ TTTCCA   A
                                CTAC GCGAG G     CCC GC
                                |||| ||||| |     ||| ||
                                GGTG CGCTC C     GGG CG
                                  A    G _______   C
GAM1514  FCN2     3'  TGACCGCCTCTGCCCAGC    37855   T    GAGGT   CA
                                C ACCGC    TTC  CCCAGC
                                | |||||    |||  ||||||
                                A TGGCG    GAG  GGGTCG
                                 C    ______  AC
GAM1514  FXYD7    3'  CCACCGCCTCCACCC       37856        GAGGT
                                CTACCGC    TTCCACCC
                                |||||||    ||||||||
                                GGTGGCG    GAGGTGGG
                                     ______
GAM1514  GPR30    3'  CGTGAGGTTTCCTAAGCAGCC  37857    C       ACC_
                                CG GAGGTTTCC    CAGCC
                                || |||||||||    |||||
                                GC CTCCAAAGG    GTCGG
                                 A        ATTC
GAM1514  KCNA6    5'  CCACCGCGGGGCTGGGTCCGGC 37858         A    TCCAC  A
            C                     CTACCGCG GGTT     CC GCC
                                |||||||| ||||     || |||
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                                GGTGGCGC CCGA    GG CGG
                                    C   CCCA_ C
GAM1514 N33     5' CTACCGCGCACCACGCCTGCC 37859       AGGTTT  _ A
                                CTACCGCG    CCAC CC GCC
                                ||||||||    |||| || |||
                                GATGGCGC    GGTG GG CGG
                                    GT____  C A
GAM1514 PGF     5' CTGCCCCGAGGCCCCGGC   37860   A G    TTCCA  A
                                CT CC CGAGGT    CCC GC
                                || || ||||||    ||| ||
                                GA GG GCTCCG    GGG CG
                                 C G    _____  C
GAM1514 PTN     5' CTACCGCTGAGTCCAGGTACCC 37861      GA   CC__   A
             GGC                   CTACCGC  GGTTT   ACCC GC
                                |||||||  |||||   |||| ||
                                GATGGCG  TCAGG   TGGG CG
                                    AC   TCCA   C
GAM1514 SORCS2  3' CCAGCTTGGTTTCCACCC   37862   _ GA
                                CC GC  GGTTTCCACCC
                                || ||  ||||||||||
                                GG CG  CCAAAGGTGGG
                                 T  AA
GAM1514 DKFZP727G051 5' GCGAGGTCCCCGCCCGCC   37863      TT  A  A
                                GCGAGGT  CC CCC GCC
                                |||||||  || ||| |||
                                CGCTCCA  GG GGG CGG
                                    GG  C  _
GAM1514 FLJ20079 3' CTGCCCCGGACACCCAGC   37864   A  G  A  TTTC
                                CT CC CG GG   CACCCAGC
                                || || || ||   ||||||||
                                GA GG GC CT   GTGGGTCG
                                 C  G  _ _____
GAM1514 FLJ20445 5' CCGCGAACCCGTCACCCAGC  37865      G  TC
                                CCGCGAG TT  CACCCAGC
                                |||||||  ||  ||||||||
                                GGCGCTT GG  GTGGGTCG
                                    G  CA
GAM1514 HSJ1    3' CTACTGCCACCTCCCACCCGGC 37866    C  GAGG      A
             C                   CTAC GC   TTTCCACCC GCC
                                ||||  ||   ||||||||| |||
                                GATG CG   GAGGGTGGG CGG
                                  A  GTG_      C
GAM1514 KIAA0218 5' CTGCCGTAGGTTTCCAAGC   37867   A  CG      CCC
                                CT CCG  AGGTTTCCA   AGC
                                || |||  |||||||||   |||
                                GA GGC  TCCAAAGGT   TCG
                                 C  A_      ____
GAM1514 KIAA0711 5' TACTCCGGGGTTTCCAGCC   37868    CG  A     C
                                TAC  CG GGTTTCCA CC
                                |||  || |||||||| ||
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                                ATG  GC CCAAAGGT GG
                                  AG  C       C
GAM1514  LIPG     3'  CCGCGAGGAGTCCCAGCC    37869        TTTCCA
                                CCGCGAGG     CCCAGCC
                                ||||||||     |||||||
                                GGCGCTCC     GGGTCGG
                                    TCA___
GAM1514  MGC10870  5'  GCCAGTGACCACACCCAGCC   37870    G  GTT  _
                                GC AG   TC CACCCAGCC
                                || ||   || |||||||||
                                CG TC   GG GTGGGTCGG
                                 G  ACT  T
GAM1514  MGC18079  5'  CTATCGCTGGGTTTCCAGCC   37871     C   GA      C
                                CTA CGC  GGTTTCCA CC
                                ||| |||  |||||||| ||
                                GAT GCG  CCAAAGGT GG
                                  A   AC       C
GAM1514  MGC23940  5'  GCGCGGACCGCACCCAGC    37872     A  TT  _
                                GCG GG  TC CACCCAGC
                                ||| ||  || ||||||||
                                CGC CC  GG GTGGGTCG
                                  G  T_  C
GAM1514  PDE11A    5'  CTGCCCCGAGGCCTCTAGC    37873    A  G       CACCC
                                CT CC CGAGGTTTC     AGC
                                || || |||||||||     |||
                                GA GG GCTCCGGAG     TCG
                                 C  G        A_____
GAM1514  PRO0386   3'  TACTGCTGAAGATTTTGCCCAG 37874     C  __      CCA
              C                  TAC GC  GAGGTTT   CCCAGC
                                ||| ||  |||||||   ||||||
                                ATG CG  TTCTAAA   GGGTCG
                                  A  AC      AC_
GAM1514  STRAIT11499 5'  TGACCGCGAGTAACACTCGCCC 37875    T       GT___   CA   A
              GGCC                  C ACCGCGAG     TTC  CCC GCC
                                | ||||||||     |||  ||| |||
                                A TGGCGCTC     GAG  GGG CGG
                                 C       ATTGT   C_   C
GAM1514  TNKS2     5'  CCTGCCAGCTCCGTCCAGCC   37876     _  G  GT    AC
                                CC GC AG  TTCC  CCAGCC
                                || || ||  ||||  ||||||
                                GG CG TC  GAGG  GGTCGG
                                 A  G  __    CA
GAM1514  LOC125875 5'  CTACCCCGAGGCCCCCAGC    37877       G    TTT  A
                                CTACC CGAGG   CC CCCAGC
                                ||||| |||||   || ||||||
                                GATGG GCTCC   GG GGGTCG
                                   G    ____ _
GAM1514  LOC132949 5'  CTATCGCAGGTTTCCCC     37878     C   G       A
                                CTA CGC AGGTTTCC CC
                                ||| ||| |||||||| ||
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                                GAT GCG TCCAAAGG GG
                                  A  _      _
GAM1514  LOC145135 5'  CCGCGAGGCCACGTGCTCAGCC 37879        TTT   C____
                                CCGCGAGG  CCAC    CAGCC
                                ||||||||  ||||    |||||
                                GGCGCTCC  GGTG    GTCGG
                                     ___   CACGA
GAM1514  LOC146253 5'  CCGTGGTGCCCACCCAGC    37880     CGA   T
                                CCG  GGT TCCACCCAGC
                                |||  ||| ||||||||||
                                GGC  CCA GGGTGGGTCG
                                  A__  C
GAM1514  LOC152048 3'  CCATCGCAAAACTTCATCCAG  37881     C    GG    CAC
                                CTA CGCGA  TTTC  CCAG
                                ||| |||||  ||||  ||||
                                GGT GCGTT  GAAG  GGTC
                                  A    TT   TA_
GAM1514  LOC157740 5'  CCGCGCCCACCCAGC       37882       AGGTT
                                CCGCG    TCCACCCAGC
                                |||||    ||||||||||
                                GGCGC    GGGTGGGTCG
                                   _____
GAM1514  LOC200138 3'  GCCAGGTCTCCCAGCC      37883    G     CCA
                                GC AGGTTT  CCCAGCC
                                || ||||||  |||||||
                                CG TCCAGA  GGGTCGG
                                 G    ___
GAM1514  LOC219920 5'  CTACCGGAGTCCACCCAGC   37884       C   GTT
                                CTACCG GAG  TCCACCCAGC
                                |||||| |||  ||||||||||
                                GATGGC CTC  AGGTGGGTCG
                                   _  ___
GAM1514  LOC51117  3'  CCTGTGAGGACACCCAGCC   37885    GC_   TTTC
                                CC  GAGG   CACCCAGCC
                                ||  ||||   |||||||||
                                GG  CTCC   GTGGGTCGG
                                 ACA   T___
GAM1515  CCND2     3'  TGGAAAGTTACAGACTGTAAA  37888       TCAATA  T
                                TGGAAA     GC GACTGTAAA
                                ||||||     || |||||||||
                                ACCTTT     TG CTGACATTT
                                   CAA___  T
GAM1515  DIBD1     3'  TGGAATCAATAGTTAAC     37889       A     C
                                TGGAA TCAATAG TGAC
                                ||||| ||||||| ||||
                                ACCTT AGTTATC ATTG
                                  _     A
GAM1515  HCCS      5'  TGGAAACAGTGTTGACTGTAAA 37890        CAATAGC
                                TGGAAAT      TGACTGTAAA
                                |||||||      ||||||||||
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                                ACCTTTG      ACTGACATTT
                                    TCACA__
GAM1515 SLC4A7   3' TGGAAATCAAGGCATCTA    37891         TA  TGA
                                TGGAAATCAA  GC   CTG
                                ||||||||||  ||   |||
                                ACCTTTAGTT  CG   GAT
                                     C_  TA_
GAM1515 UBE3A    3' TGGAAATCAGTAATGTAA    37892        A   CTGAC
                                TGGAAATCA TAG    TGTAA
                                ||||||||| |||    |||||
                                ACCTTTAGT ATT    ACATT
                                     C  _____
GAM1515 UBE3A    3' TGGAAATCAGTAATGTAA    37892        A   CTGAC
                                TGGAAATCA TAG    TGTAA
                                ||||||||| |||    |||||
                                ACCTTTAGT ATT    ACATT
                                     C  _____
GAM1515 UBE3A    3' TGGAAATCAGTAATGTAA    37892        A   CTGAC
                                TGGAAATCA TAG    TGTAA
                                ||||||||| |||    |||||
                                ACCTTTAGT ATT    ACATT
                                     C  _____
GAM1515 FLJ12838 3' TGGAATTCAGCACTGTAA    37893      A   ATA  TG
                                TGGAA TCA   GC  ACTGTAA
                                ||||| |||   ||  |||||||
                                ACCTT AGT   CG  TGACATT
                                   A  ___  __
GAM1515 KIAA0332 3' TGGAAATCATATTGCTTCTGT  37894         _  A   GA
                                TGGAAATCA AT GCT  CTGT
                                ||||||||| || |||  ||||
                                ACCTTTAGT TA CGA  GACA
                                     A  A   A_
GAM1515 KIAA1006 3' TGAAAATTTCAGATTGACTGTA 37895        CAA   C_
           AA                     TGGAAAT   TAG  TGACTGTAAA
                                ||||||||   |||  ||||||||||
                                ACTTTTA   GTC  ACTGACATTT
                                    AA_   TA
GAM1515 MGC12921 3' TGGGGGTTAATAGCTGTTCCCC 37896     AAATC      A_  G
           AA                     TGG     AATAGCTG  CT TAA
                                |||     ||||||||  || |||
                                ACC     TTATCGAC  GG GTT
                                  CCCAA       AA  G
GAM1515 MGC5139  5' GAAATCAATACTGTA      37897         AGCTG
                                GAAATCAAT     ACTGTA
                                |||||||||     ||||||
                                CTTTAGTTA     TGACAT
                                              _____
GAM1515 PEG10    3' TGAAGATCAATTGACAACTGTA 37898      A     A_  T
           AA                     TGGA ATCAAT  GC GACTGTAAA
                                |||| ||||||  || |||||||||
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                                ACTT TAGTTA  TG TTGACATTT
                                  C     AC  _
GAM1515  LOC132671 3'  TGTAAATCAGGGCAAGACTGTA 37899    G     ATA  T_
             A                    TG AAATCA   GC  GACTGTAA
                                  || ||||||   ||  ||||||||
                                  AC TTTAGT   CG  CTGACATT
                                   A     CC_  TT
GAM1515  LOC150372 5'  GAAAGTAGCTGACTGT      37900      TCAA
                                  GAAA    TAGCTGACTGT
                                  ||||    ||||||||||
                                  CTTT    ATCGACTGACA
                                    C___
GAM1515  LOC158230 3'  TGGGAACAGCTACGCTGT    37901     AAATC       A_
                                  TGG     AATAGCTG  CTGT
                                  |||     ||||||||  ||||
                                  ACC     TTGTCGAT  GACA
                                    C____       GC
GAM1515  LOC221981 3'  GGAAATGTAATGACTGTAAA   37902       CAA   C
                                  GGAAAT   TAG TGACTGTAAA
                                  ||||||   ||| ||||||||||
                                  CCTTTA   ATT ACTGACATTT
                                     C__   _
GAM1515  LOC253502 3'  GGACAGGAGCTGACTGT     37903     AAT  AT
                                  GGA   CA  AGCTGACTGT
                                  |||   ||  ||||||||||
                                  CCT   GT  TCGACTGACA
                                    ___  CC
GAM1516  ATP6V0E   3'  GCACTGTAGAGCATGTCTTC   37906        T GA  C
                                  GTATTGT G  CA GTCTTC
                                  ||||||| |  || ||||||
                                  CGTGACA C  GT CAGAAG
                                      T TC  A
GAM1516  CRP       3'  GTATTGCTGGGCTTC       37907          ACAC T
                                  GTATTGTTGG    G CTTC
                                  ||||||||||    | ||||
                                  CATAACGACC    C GAAG
                                               _____ _
GAM1516  EGFL5     3'  GAAGTATTGTTGCTTTAGTTTT 37908    C        GACAC  C
             C                     A AGTATTGTTG     GT TTC
                                   | ||||||||||     || |||
                                   C TCATAACAAC     CA AAG
                                    T         GAAAT  A
GAM1516  SUV39H2   3'  ACAGTATTGTTAGGTACAGC   37909          _ _   C
                                  ACAGTATTGTT GG ACA GT
                                  |||||||||||| || ||| ||
                                  TGTCATAACAA CC TGT CG
                                         T  A   _
GAM1516  XRCC2     3'  AGGATTGTTGGCCACAGATGTC 37910    T       A  _____
             TTC                     AG ATTGTTGG CAC    GTCTTC
                                   || |||||||| |||    ||||||
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                                TC TAACAACC GTG    CAGAAG
                                 C       G   TCTA
GAM1516 COLEC12  3' ACAGTACTGTCTCCCTGTCTT 37911          GGACAC
                                ACAGTATTGTT     GTCTT
                                ||||||||||      |||||
                                TGTCATGACAG     CAGAA
                                      AGGGA_
GAM1516 DPP8     3' GTATTGCTGGGTCTC      37912          ACAC
                                GTATTGTTGG    GTCTT
                                ||||||||||    |||||
                                CATAACGACC    CAGAG
                                      _____
GAM1516 KIAA0323 3' ACAGGGTTGGAATGTCTTC   37913     TATT     CAC
                                ACAG    GTTGGA   GTCTTC
                                ||||    ||||||   ||||||
                                TGTC    CAACCT   CAGAAG
                                  C___      TA_
GAM1516 KIAA0542 3' CACTGCAGATGGTGCGTCTTCC 37914       ___   ACA
                                TATTGT   TGG   CGTCTTCC
                                ||||||   |||   ||||||||
                                GTGACG   ACC   GCAGAAGG
                                   TCT   AC_
GAM1516 KIAA1194 3' CAATATTCTTACACGTCTTCC  37915       G  GG
                                CAGTATT TT  ACACGTCTTCC
                                ||||||| ||  ||||||||||
                                GTTATAA AA  TGTGCAGAAGG
                                    G  __
GAM1516 LOC129892 5' CAGTATTGTTGTGTTTCTTC  37916          GACACG
                                CAGTATTGTTG     TCTTC
                                ||||||||||      |||||
                                GTCATAACAAC     AGAAG
                                      ACAA__
GAM1517 B4GALT7  3' TTCGAAAAATCAGAAGATC   37919        A     ATT
                                TTTGAAAAA TCAGAA   GGTC
                                ||||||||| ||||||   ||||
                                AAGCTTTTT AGTCTT   CTAG
                                      _    ____
GAM1517 B4GALT7  3' AAAAAATCAGAAGATATCA   37920          ATTG
                                AAAAAATCAGAA    GTCA
                                ||||||||||||    ||||
                                TTTTTTAGTCTT    TAGT
                                      CTA_
GAM1517 MTMR8    3' TTTGAAAAACATTTCTATGGTC 37921        ATCAGAAAT
             A                   TTTGAAAAA       TGGTCA
                                 |||||||||       ||||||
                                 AAACTTTTT       ACCAGT
                                     GTAAAGAT_
GAM1517 PCMT1    3' TTTGAAGAATCAGAAACC    37922       AA
                                TTTGAA  AATCAGAAATT
                                ||||||  ||||||||||
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                                AAACTT  TTAGTCTTTGG
                                   C_
GAM1517 RFX5     3'  TCTGAAAAGGTCAGAGGC    37923        AA    AATT
                                TTTGAAAA  TCAGA   GGT
                                ||||||||  |||||   |||
                                AGACTTTT  AGTCT   CCG
                                    CC    ____
GAM1517 SHMT1    3'  TTTGAAATATAAAAATTGGT  37924        AAATC
                                TTTGAAA    AGAAATTGGT
                                |||||||    ||||||||||
                                AAACTTT    TTTTTAACCA
                                   ATA__
GAM1517 STAU2    3'  TTTGAAAGAATCAGAAGGGT  37925        A      ATT
                                TTTGAAA AATCAGAA   GGT
                                ||||||| ||||||||   |||
                                AAACTTT TTAGTCTT   CCA
                                   C      C__
GAM1517 DKFZp434G179 3'  TTTGAAGACATCAGAAAAGT  37926       AAA      TT
                                TTTGAA   ATCAGAAA  GGT
                                ||||||   ||||||||  |||
                                AAACTT   TAGTCTTT  TCA
                                   CTG      __
GAM1517 FLJ20508  3'  TTTAAAAAAATTTGTGAATTGG 37927          CAGA_
          TCA                    TTTGAAAAAAT    AATTGGTCA
                                ||||||||||    |||||||||
                                AAATTTTTTTA    TTAACCAGT
                                     AACAC
GAM1517 FLJ21034  3'  GAAAAAATCAGAGGC      37928          AATT
                                GAAAAAATCAGA   GGT
                                ||||||||||||   |||
                                CTTTTTTAGTCT   CCG
                                     ____
GAM1517 KIAA1463  3'  TTTGGCAACCCAGATTGGTCA  37929     AAA  AT   AA
                                TTTG   AA  CAGA  TTGGTCA
                                ||||   ||  ||||  |||||||
                                AAAC   TT  GTCT  AACCAGT
                                  CG_  GG   __
GAM1517 KIAA1500  3'  TTGGAGAAATCAGAAATT    37930    AAA
                                TTG   AAATCAGAAATT
                                |||   ||||||||||||
                                AAC   TTTAGTCTTTAA
                                  CTC
GAM1517 KIAA1718  3'  TTTGAAAAAGGCAGAAAGAATC 37931         AT     TT
                                TTTGAAAAA  CAGAAA  GGTC
                                |||||||||  ||||||  ||||
                                AAACTTTTT  GTCTTT  TTAG
                                     CC     C_
GAM1517 MGC13168  3'  TTTGGAAATCAAAGTTGGTCA  37932     AAA      AA
                                TTTG   AAATCAGA  TTGGTCA
                                ||||   ||||||||  |||||||
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                                AAAC   TTTAGTTT  AACCAGT
                                  C__      C_
GAM1517 SRPK1    3'  TCTGAGAAAATCAGAAAGGC   37933      A         TT
                                TTTGA AAAATCAGAAA  GGT
                                ||||| ||||||||||  |||
                                AGACT TTTTAGTCTTT  CCG
                                  C         __
GAM1517 LOC256965 3'  TTTGAAAAATTGTAAATTGGTC 37934         ATCAG
              A                  TTTGAAAAA    AAATTGGTCA
                                |||||||||    ||||||||||
                                AAACTTTTT    TTTAACCAGT
                                     AACA_
GAM1517 LOC90410  3'  TCTGAAAAATAAATTGGTCA   37935         ATCAG
                                TTTGAAAAA    AAATTGGTCA
                                |||||||||    ||||||||||
                                AGACTTTTT    TTTAACCAGT
                                     A____
GAM1518 C18orf1   3'  TGAAGGAAGACATTGCTTTCT  37938      A      _   CC
                                TGAA GAGGACAT GCT  TCT
                                |||| |||||||| |||  |||
                                ACTT CTTCTGTA CGA  AGA
                                  C       A  A_
GAM1518 EXTL3     3'  GAGGAGGGCGTGCCCCTCAG   37939      CAT  T__
                                GAGGA   GC   CCTCTCAG
                                |||||   ||   ||||||||
                                CTCCT   CG   GGGGAGTC
                                   CC_  CAC
GAM1518 FEZ1      3'  TGAAAGAGTACTTTTCTCA    37940        GACA    CC
                                TGAAAGAG    TGCT  TCTCA
                                ||||||||    ||||  |||||
                                ACTTTCTC    ATGA  AGAGT
                                     _____    AA
GAM1518 GJA5      3'  GAGAGAGGACAACAGCTTCT   37941    A      T__   C
                                GA AGAGGACA   GCT CT
                                || ||||||||   ||| ||
                                CT TCTCCTGT   CGA GA
                                 C       TGT   A
GAM1518 MAP3K7IP2 3'  AAGGCATTGTTCCTCTCAG    37942      A   GC_
                                GAGG CAT   TCCTCTCAG
                                |||| |||   |||||||||
                                TTCC GTA   AGGAGAGTC
                                  _   ACA
GAM1518 SH3BP5    3'  TGAAAGAGGGTTGCTTTTTTCT 37943         ACA    CC__
                                TGAAAGAGG   TGCT    TCT
                                |||||||||   ||||    |||
                                ACTTTCTCC   ACGA    AGA
                                     CA_    AAAA
GAM1518 UFD1L     5'  AGACTCCGCTCCTCTCAG    37944      A_
                                GGAC  TGCTCCTCTCAG
                                ||||  ||||||||||||
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                                TCTG  GCGAGGAGAGTC
                                  AG
GAM1518  FLJ10139  3'  GAAAGGTATTCATGCTTTTCTC 37945      AGGA_     CC
              AG                   GAAAG    CATGCT  TCTCAG
                                |||||    ||||||  ||||||
                                CTTTC    GTACGA  AGAGTC
                                   CATAA     AA
GAM1518  MGC13007  5'  AGTCACATGCTTCTCTCA    37946    G_      C
                                AG  ACATGCT CTCTCA
                                ||  ||||||| ||||||
                                TC  TGTACGA GAGAGT
                                 AG      A
GAM1518  MGC16279  5'  TGAGAAGGACATTCCCTC    37947     AA       GC
                                TGA  GAGGACAT  TCCTC
                                |||  ||||||||  |||||
                                ACT  TTCCTGTA  GGGAG
                                  C_       A_
GAM1518  TM4-B     3'  AGGGACAGCTCCTCTCA     37948    A     T
                                AG GGACA GCTCCTCTCA
                                || ||||| ||||||||||
                                TC CCTGT CGAGGAGAGT
                                 _    _
GAM1518  VI        3'  TGGGAAAGGACATGTCCT    37949    AA        C
                                TG  AGAGGACATG TCCT
                                ||  |||||||||| ||||
                                AC  TTTCCTGTAC AGGA
                                 CC         _
GAM1518  ZNF306    3'  TGGGAGAGAACAAACAGTTTCA 37950    AA       T  TCCTC
              G                   TG  AGAGGACA GC    TCAG
                                ||  |||||||| ||     ||||
                                AC  TCTCTTGT TG    AGTC
                                 CC       T  TCAA_
GAM1518  LOC130612 3'  GAGGGGGCTTTCCTCTCAG   37951      ACAT  __
                                GAGG    GC  TCCTCTCAG
                                ||||    ||  |||||||||
                                CTCC    CG  AGGAGAGTC
                                  CC__  AA
GAM1518  LOC148195 5'  TGAGAGAGACATGCATCA    37952    A   _      TCCTC
                                A AGAG GACATGC     TCA
                                | |||| |||||||     |||
                                A TCTC CTGTACG     AGT
                                 C   T      T_____
GAM1518  LOC149073 5'  GAAAAAATGTTCCTCTCAG    37953       C   C
                                GAGGA ATG TCCTCTCAG
                                ||||| ||| |||||||||
                                CTTTT TAC AGGAGAGTC
                                   T   A
GAM1518  LOC150383 3'  TGAAGGAGGTCATCCCTCTCAG 37954       A    A   G T
                                TGAA GAGG CAT C CCTCTCAG
                                |||| |||| ||| | ||||||||
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                                ACTT CTCC GTA G GGAGAGTC
                                  C    A  _ _
GAM1518  LOC153937 5'  AAAGACTTGATGCTCCTTTC   37955       ___       C
                                GAGGAC   ATGCTCCT TC
                                ||||||   |||||||| ||
                                TTTCTG   TACGAGGA AG
                                   AAC       A
GAM1518  LOC196337 5'  GAAGTAAGGGCTCCTCTC    37956     A_    ACAT
                                GAA  GAGG    GCTCCTCTC
                                |||  ||||    |||||||||
                                CTT  TTCC    CGAGGAGAG
                                  CA   _____
GAM1518  LOC199676 5'  AGAGGCCTGGGTTCCTCTCAG  37957       ACA  C__
                                AGAGG   TG   TCCTCTCAG
                                |||||   ||   |||||||||
                                TCTCC   AC   AGGAGAGTC
                                   GG_  CCA
GAM1518  LOC200138 3'  GAGCTCGATGCTCCTTTCAG   37958     GAC_       C
                                GAG    ATGCTCCT TCAG
                                |||    |||||||| ||||
                                CTC    TACGAGGA AGTC
                                  GAGC       A
GAM1518  LOC221391 5'  TGGAAGAGGACTTAACCT    37959     A       A  CT
                                TG AAGAGGAC TG  CCT
                                || |||||||| ||  |||
                                AC TTCTCCTG AT  GGA
                                 C       A  T_
GAM1518  LOC254042 3'  GAAAGAGAAAACCGTGCTTCTC 37960         __   A_    C
            T                    GAAAGAG  GAC  TGCT CTCT
                                |||||||  |||  |||| ||||
                                CTTTCTC  TTG  ACGA GAGA
                                    TT   GC    A
GAM1518  LOC57805  3'  TGGAAGAGGACAGGAGAAAGTC 37961     A        TGCTCCTC
            AG                     TG AAGAGGACA       TCAG
                                || |||||||||       ||||
                                AC TTCTCCTGT       AGTC
                                 C        CCTCTTTC
GAM1518  LOC91351  3'  TGAGAGGGAACTGTCCTCTCAG 37962     A  A   CA  C
                                TGA AG GGA  TG TCCTCTCAG
                                ||| || |||  || |||||||||
                                ACT TC CCT  AC AGGAGAGTC
                                  C  _   TG  _
GAM1518  LOC91963  5'  GAAAGGGGCCCCTCT       37963       A  ACAT
                                GAAAG GG    GCTCCTCT
                                ||||| ||    ||||||||
                                CTTTC CC    CGGGGAGA
                                   _  _____
GAM1519  FACL4     3'  TAACTATGGTTCAAGTGTGAAT 37966      A___     A
            A                     TAGC    GTTCAA TGTGAATA
                                ||||    |||||| ||||||||
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                                ATTG    CAAGTT ACACTTAT
                                  ATAC     C
GAM1519  FACL4    3'  TAACTATGGTTCAAGTGTGAAT 37966      A___     A
              A                    TAGC    GTTCAA TGTGAATA
                                   ||||    |||||| ||||||||
                                ATTG    CAAGTT ACACTTAT
                                  ATAC     C
GAM1519  RNTRE    3'  TAGCTCTGTGTTCAAATGTG   37967      A____
                                TAGC    GTTCAAATGTG
                                ||||    ||||||||||
                                ATCG    CAAGTTTACAC
                                  AGACA
GAM1519  SALL1    3'  CAAATAGCAGTTCAAAATG    37968             T
                                TAAATAGCAGTTCAAA GTG
                                |||||||||||||||| |||
                                GTTTATCGTCAAGTTT TAC
                                                _
GAM1519  SPF30    3'  AATAGCAGTTATCAAATG     37969          __
                                AATAGCAGT  TCAAATG
                                |||||||||  |||||||
                                TTATCGTCA  AGTTTAC
                                     AT
GAM1519  TIAL1    3'  AGCACCCTTATGTGAATA     37970      G   AA
                                AGCA TTC  ATGTGAATA
                                |||| |||  |||||||||
                                TCGT GGG  TACACTTAT
                                  _  AA
GAM1519  TIMM17A  3'  CAAATGCAATTCAAGTGTGAAT 37971       A        A
              A                    TAAAT GCAGTTCAA TGTGAATA
                                   ||||| ||||||||| ||||||||
                                GTTTA CGTTAAGTT ACACTTAT
                                  _       C
GAM1519  C6orf37  3'  AAATGGCAGTTCAATATA     37972      A        A
                                AAAT GCAGTTCAA TGTG
                                |||| ||||||||| ||||
                                TTTA CGTCAAGTT ATAT
                                  C       _
GAM1519  FLJ12994 3'  ATAGTCAATCAATGTGAATA   37973      _    CA
                                ATAG CAGTT  AATGTGAATA
                                |||| |||||  ||||||||||
                                TATC GTTAG  TTACACTTAT
                                  A    __
GAM1519  FLJ12994 3'  ATAGTCAATCAATGTGAATA   37973      _    CA
                                ATAG CAGTT  AATGTGAATA
                                |||| |||||  ||||||||||
                                TATC GTTAG  TTACACTTAT
                                  A    __
GAM1519  KIAA0152 3'  TAAGGAGCAGTTCAAATA     37974     AT
                                TAA  AGCAGTTCAAATG
                                |||  ||||||||||||
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                                ATT  TCGTCAAGTTTAT
                                  CC
GAM1519  KIAA0967  3'  TAAGCAGCAGTTTATTTGAATA 37975     A       CAAATG
                                TAA TAGCAGTT     TGAATA
                                ||| ||||||||     ||||||
                                ATT GTCGTCAA     ACTTAT
                                  C       ATAA__
GAM1519  KIAA1198  3'  AGAAATTCAGATGTGAAT    37976    C     A
                                AG AGTTCA ATGTGAAT
                                || |||||| ||||||||
                                TC TTAAGT TACACTTA
                                 T     C
GAM1519  NLI-IF    3'  AAATAGCAGTTTAAAAAATG   37977          C   T_
                                AAATAGCAGTT AAA  GTG
                                |||||||||||| |||  |||
                                TTTATCGTCAA TTT  TAC
                                       A   TT
GAM1519  LOC149157 3'  AACAGCAGTTTTCAGAATG    37978         __  _
                                AATAGCAGT  TCA AATG
                                |||||||||  ||| ||||
                                TTGTCGTCA  AGT TTAC
                                     AA   C
GAM1519  LOC254655 3'  AGTATCACAATGTGAATA    37979     _  _
                                AGT TCA AATGTGAATA
                                ||| ||| ||||||||||
                                TCA AGT TTACACTTAT
                                  T   G
GAM1520  ATP11B    3'  TAATATGCTAATAGTATCTAA  37982             GG
                                TAATATGCTAATAGTA  TAA
                                ||||||||||||||||  |||
                                ATTATACGATTATCAT  ATT
                                          AG
GAM1520  DISC1     3'  TAATATGCTAATGTGCA     37983           A  AG
                                TAATATGCTAAT GT  GTA
                                |||||||||||| ||  |||
                                ATTATACGATTA CA  CGT
                                          _  __
GAM1520  FGF5      3'  TAATATGCTAATCAAATCAAAC 37984           AGTAGG
               C                 TAATATGCTAAT     TAAACC
                                 ||||||||||||     ||||||
                                 ATTATACGATTA     GTTTGG
                                       GTTTA_
GAM1520  FGF5      3'  TAATATGCTAATCAAATCAAAC 37984           AGTAGG
               C                 TAATATGCTAAT     TAAACC
                                 ||||||||||||     ||||||
                                 ATTATACGATTA     GTTTGG
                                       GTTTA_
GAM1520  GAS1      3'  AATATGCTAATAGACAGC    37985           TA
                                AATATGCTAATAG  GGT
                                |||||||||||||  |||
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                                TTATACGATTATC  TCG
                                      TG
GAM1520  HGF      3'  TAATATGCAATAATAAA     37986         T
                                TAATATGC AATAGTAGG
                                |||||||| |||||||||
                                ATTATACG TTATTATTT
                                       _
GAM1520  IL12B    3'  TAATATACTAATAAATACATAA 37987             _  G
              A                  TAATATGCTAATAG TA GTAAA
                                |||||||||||||| || |||||
                                ATTATATGATTATT AT TATTT
                                      T  G
GAM1520  ING1     5'  TAATATGCTAATGAAGT     37988           AGT
                                TAATATGCTAAT   AGGT
                                ||||||||||||   ||||
                                ATTATACGATTA   TTCA
                                      C__
GAM1520  KMO      3'  TAACATGCTAGTTAAGT     37989          ATAG
                                TAATATGCTA    TAGGT
                                ||||||||||    |||||
                                ATTGTACGAT    ATTCA
                                     CA__
GAM1520  PHLDA3   3'  ATGCTAATGGCCAAACC     37990         AGTA  _
                                ATGCTAAT    GGT AAACC
                                ||||||||    ||| |||||
                                TACGATTA    CCG TTTGG
                                     _____  G
GAM1520  ATP6V1D  3'  TAATATGCTTGGTAAGCAGAT 37991          AAT__
                                TAATATGCT    AGTAGGT
                                |||||||||    |||||||
                                ATTATACGA    TCGTCTA
                                     ACCAT
GAM1520  FLJ10483 3'  TATACTAATAGTGCAACC    37992           AG   A
                                TATGCTAATAGT  GTAA CC
                                ||||||||||||  |||| ||
                                ATATGATTATCA  CGTT GG
                                      __   _
GAM1520  IDI1     3'  TAATCTGCTAATATGAAAGT   37993      A      GT_
                                TAAT TGCTAATA   AGGT
                                |||| ||||||||   ||||
                                ATTA ACGATTAT   TTCA
                                  G       ACT
GAM1520  KIAA0451 5'  TAATATGCTGAAAGTAAAC   37994         AATAGT
                                TAATATGCT     AGGTAAAC
                                |||||||||     ||||||||
                                ATTATACGA     TTCATTTG
                                     CT_____
GAM1520  MGC8974  3'  TATGCTAATGCCATAGGTAAA 37995          A__
                                TATGCTAAT   GTAGGTAAA
                                |||||||||   |||||||||
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                                ATACGATTA   TATCCATTT
                                     CGG
GAM1520  NUDC     3'  TAATGTGTAACAGTAGGC    37996      A  C
                                TAAT TG TAATAGTAGGT
                                |||| || ||||||||||
                                ATTA AC ATTGTCATCCG
                                  C  _
GAM1520  pcnp     3'  TAATGTGCTAATAGTTGTGT   37997      A        AG_
                                TAAT TGCTAATAGT   GT
                                |||| ||||||||||   ||
                                ATTA ACGATTATCA   CA
                                  C         ACA
GAM1520  TCL6     3'  ATATGCTAAACAAGGGGT    37998          _   TA
                                ATATGCTAA TAG  GGT
                                ||||||||| |||  |||
                                TATACGATT GTT  CCA
                                     T   CC
GAM1520  TCL6     3'  ATATGCTAAACAAGGGGT    37998          _   TA
                                ATATGCTAA TAG  GGT
                                ||||||||| |||  |||
                                TATACGATT GTT  CCA
                                     T   CC
GAM1520  ZNF17    3'  TAATATGCTATACAAGT     37999          A  G
                                TAATATGCTA TA TAGGT
                                |||||||||| || |||||
                                ATTATACGAT AT GTTCA
                                          _  _
GAM1520  LOC121536 3'  TGTTAACAGTATCAAACC    38000    C       GG
                                TG TAATAGTA  TAAACC
                                || ||||||||  ||||||
                                AC ATTGTCAT  GTTTGG
                                 A       A_
GAM1520  LOC151201 3'  TAATATGCTAAGAAAAGT    38001           TAGT
                                TAATATGCTAA    AGGT
                                ||||||||||    ||||
                                ATTATACGATT    TTCA
                                       CTT_
GAM1520  LOC220827 3'  ATATGCTAAACAAAGGGTA    27905          _   TA
                                ATATGCTAA TAG  GGTA
                                ||||||||| |||  ||||
                                TATACGATT GTT  CCAT
                                     T   TC
GAM1520  LOC221337 3'  TAATATGCAATAGTCTAAC    38002         T     AGGTA
                                TAATATGC AATAGT     AAC
                                |||||||| ||||||     |||
                                ATTATACG TTATCA     TTG
                                     _     GA___
GAM1520  LOC256112 3'  TAATATTGCTAATTGAGTGGGT 38003        _     __   A
                                TAATAT GCTAAT  AGT GGT
                                |||||| ||||||  ||| |||
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                                ATTATA CGATTA  TCA CCA
                                   A     AC   C
GAM1520  LOC91689  3'  TATGCTAACAAGCAGAGC    38004          _   _
                                TATGCTAATA GTAG GT
                                |||||||||| |||| ||
                                ATACGATTGT CGTC CG
                                      T    T
GAM1520  LOC92405  3'  TAACATGCTAATGTATGG    38005           A  _
                                TAATATGCTAAT GTA GG
                                |||||||||||| ||| ||
                                ATTGTACGATTA CAT CC
                                       _  A
GAM1521  FANCC     3'  TCTTTATCAGGAATTTCCAATT 38008     A_  T    C
              C                  TCT  GTT GGAAT TCCAATTC
                                ||| ||| ||||| ||||||||
                                AGA  TAG CCTTA AGGTTAAG
                                  AA  T    A
GAM1521  LAMA4     3'  TGTTTATTTGGAATCCC     38009     CTA
                                TGT   GTTTGGAATCTC
                                |||   ||||||||||||
                                ACA   TAAACCTTAGGG
                                  AA_
GAM1521  MIA       5'  GTGCTGGGGTCTCCAATT    38010    _   AA
                                GT TTGG  TCTCCAATT
                                || ||||  |||||||||
                                CA GACC  AGAGGTTAA
                                 C   CC
GAM1521  ZNF18     3'  TCTAAAACTGGATCTCCAATT  38011      T_    A
                                TCTAG  TTGGA TCTCCAATT
                                |||||  ||||| |||||||||
                                AGATT  GACCT AGAGGTTAA
                                   TT    _
GAM1521  ADAMDEC1  5'  TGTCCAGTTTTATCTTCTCCAA 38012          GGAA_
              TT                   TGTCTAGTTT    TCTCCAATT
                                ||||||||||    |||||||||
                                ACAGGTCAAA    AGAGGTTAA
                                      ATAGA
GAM1521  FLJ20401  5'  TCTGGCTGACGGTCTCCAATT  38013     A  __  AA
                                TCT GTT  TGG  TCTCCAATT
                                ||| |||  |||  |||||||||
                                AGA CGA  GCC  AGAGGTTAA
                                  C  CT  __
GAM1521  Rabip4R   3'  ATTTAGTGCTTTCTCCAATT   38014       AA___
                                GTTTGG    TCTCCAATT
                                ||||||    |||||||||
                                TAAATC    AGAGGTTAA
                                   ACGAA
GAM1521  RBSK      3'  GTTGTGGAATCTTTAATT    38015    _      CC
                                GTT TGGAATCT  AATT
                                ||| ||||||||  ||||
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                                CAA ACCTTAGA  TTAA
                                  C       AA
GAM1521  YAP1     3'  TCTGGTTTGCTCCTTTCCAATT 38016     A    GAATC_
                C                  TCT GTTTG     TCCAATTC
                                   ||| |||||     ||||||||
                                   AGA CAAAC     AGGTTAAG
                                     C    GAGGAA
GAM1521  LOC145845 3'  TCTAGTTCTTCCAATT      38017        GGAATC
                                   TCTAGTTT     TCCAATT
                                   ||||||||     |||||||
                                   AGATCAAG     AGGTTAA
                                        A_____
GAM1521  LOC222681 5'  TGTTGTTCTGGAATCTTCA    38018     CTAG        C
                                   TGT    TTTGGAATCT CA
                                   |||    |||||||||| ||
                                   ACA    AGACCTTAGA GT
                                     ACA_         A
GAM1521  LOC257507 5'  TGTTGTTCTGGAATCTTCA    38018     CTAG        C
                                   TGT    TTTGGAATCT CA
                                   |||    |||||||||| ||
                                   ACA    AGACCTTAGA GT
                                     ACA_         A
GAM1521  LOC257625 5'  TGTTGTTCTGGAATCTTCA    38018     CTAG        C
                                   TGT    TTTGGAATCT CA
                                   |||    |||||||||| ||
                                   ACA    AGACCTTAGA GT
                                     ACA_         A
GAM1521  LOC91574  3'  TGTCAGTTGGAATCTCTAATTC 38019      T    T       C
                                   TGTC AGTT GGAATCTC AATTC
                                   |||| |||| |||||||| |||||
                                   ACAG TCAA CCTTAGAG TTAAG
                                     _   _       A
GAM1522  TLR9     3'  TGAGTGCCTGCTCTGTGT     38022       T       A
                                   TGAGT CCTGCTCT TGT
                                   ||||| |||||||| |||
                                   ACTCA GGACGAGA ACA
                                      C       C
GAM1522  FLJ10140  3'  TGGGTCCTGCTCTCCAGGT    38023     A  T       ATGTTC
                                   TG GT CCTGCTCT     GGT
                                   || || ||||||||     |||
                                   AC CA GGACGAGA     CCA
                                    C  _       GGT___
GAM1522  FLJ12572  5'  TGGTTCCTGCTTTATCAGT    38024     A       C  TGT
                                   TG GTTCCTGCT TA   TCGGT
                                   || |||||||| ||   |||||
                                   AC CAAGGACGA AT   AGTCA
                                    _        A  ___
GAM1522  LOC196527 3'  TGAGTATTTGCTCTAATGTT   38025       TCC      _
                                   TGAGT   TGCTCTA TGTT
                                   |||||   ||||||| ||||
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                                ACTCA   ACGAGAT ACAA
                                   TAA      T
GAM1522  LOC197320 3'  TGAGTTCCTGCCTGCCGGGTT  38026          CTA   TC
                                TGAGTTCCTGCT   TGT  GGTT
                                ||||||||||||   |||  ||||
                                ACTCAAGGACGG   ACG  CCAA
                                      ____   GC
GAM1522  LOC199906 3'  TGAGTTCCTGTTTATAAACA   38027         CTC    TT
                                TGAGTTCCTG   TATG  CG
                                ||||||||||   ||||  ||
                                ACTCAAGGAC   ATAT  GT
                                      AA_    TT
GAM1522  LOC257464 3'  TGAGTTCTTGTCTGTGT     38028        C  C   A
                                TGAGTTC TG TCT TGT
                                ||||||| || ||| |||
                                ACTCAAG AC AGA ACA
                                     A  _   C
GAM1522  LOC257464 3'  TGGGTCCCCGCATGTGTTTGGT 38029    A       TCTA    C
            T                    TG GTTCCTGC    TGTT GGTT
                                || |||||||||    ||||  ||||
                                AC CAGGGGCG    ACAA CCAA
                                 C       TAC_    A
GAM1523  ABCA1    3'  TGGCTTAGTGAATGAGGATGTG 38032      CAAATA    AA
                                TGGC     TGAG  AGGATGTG
                                ||||     ||||  |||||||||
                                ACCG     ACTT  TCCTACAC
                                  AATC__    AC
GAM1523  HOXB5    5'  GGCCAAATATGGGGGGGGGGT  38033          AGAAA  AT
                                GGCCAAATATG    GG  GT
                                ||||||||||||    ||  ||
                                CCGGTTTATAC    CC  CA
                                      CCCC_  CC
GAM1523  IFNA14   3'  TGGCTAAATATGAAGAACATA  38034      C       GAA
                                TGGC AAATATGA   AGGATGTG
                                |||| ||||||||   |||||||||
                                ACCG TTTATACT   TCTTGTAT
                                  A       ____
GAM1523  PNN      3'  TGGTTAAAATATGAGAAA    38035     CC_
                                TGG   AAATATGAGAAA
                                |||   ||||||||||||
                                ACC   TTTATACTCTTT
                                  AAT
GAM1523  AOP2     3'  TGGCTGTGATGACACCAGGATG 38036      CAAAT    GAA_
            TG                    TGGC    ATGA    AGGATGTG
                                ||||    ||||    |||||||||
                                ACCG    TACT    TCCTACAC
                                  ACAC_    GTGG
GAM1523  FLJ12587 3'  GGCCAGGAGGGAAAGGATGTG  38037      AATATGA
                                GGCCA      GAAAGGATGTG
                                |||||      ||||||||||
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                                CCGGT      CTTTCCTACAC
                                   CCTCC__
GAM1523  FLJ12671  5'  TGGATGAAAAGAGGATGT    38038     CCAAAT      _
                                TGG      ATGAGAA AGGATGT
                                |||      ||||||| |||||||
                                ACC      TACTTTT TCCTACA
                                  _______      C
GAM1523  FLJ32940  5'  GGCCAAATGTGGGGGACA    38039         A  AGAAA
                                GGCCAAAT TG     GGATG
                                |||||||| ||     |||||
                                CCGGTTTA AC     CCTGT
                                     C  CC___
GAM1523  FRAG1     3'  GGCCAAGAGAGGATG       38040       ATAT    AA
                                GGCCAA    GAGA  GGATG
                                ||||||    ||||  |||||
                                CCGGTT    CTCT  CCTAC
                                   ____    __
GAM1523  KIAA0417  3'  TGACTGTTTGGGAAGGATGTG  38041      CAAATA  A   A
                                TGGC      TG GAA GGATGTG
                                ||||      || ||| |||||||
                                ACTG      AC CTT CCTACAC
                                   ACAA__  C   _
GAM1523  KIAA0514  3'  TGGCCATGGGAAAAAGGGGTGT 38042       AATAT       A_
           G                     TGGCCA    GAGAAAGG  TGTG
                                ||||||    ||||||||  ||||
                                ACCGGT    CTTTTTCC  ACAC
                                   ACC__       CC
GAM1523  KIAA1025  3'  TGGTCTGAAGAAAAGGATGTG  38043     CCAAATA  __
                                TGG      TGA  GAAAGGATGTG
                                |||      |||  ||||||||||||
                                ACC      ACT  TTTTCCTACAC
                                  AG_____   TC
GAM1523  MRPL44    3'  TAGCCAGGTATGGTGGTGT    38044       AA    AGAAA  A
                                TGGCCA  TATG     GG TGT
                                ||||||  ||||     || |||
                                ATCGGT  ATAC     CC ACA
                                   CC    CA___  _
GAM1523  PEG10     3'  TAGCCGTTTCAGAGAGGATGTG 38045      AAATAT    AA
                                TGGCC     GAGA  GGATGTG
                                |||||     ||||  |||||||
                                ATCGG     CTCT  CCTACAC
                                   CAAAGT   __
GAM1523  LOC128499 3'  GGCCAGTGGAGAGGATGT    38046      AATA  A  A
                                GGCCA    TG GA AGGATGT
                                |||||    || || |||||||
                                CCGGT    AC CT TCCTACA
                                   C___  _  C
GAM1523  LOC154792 3'  TGGCTAATGTATGAGGAAGATG 38047      CAAA_     AA
                                TGGC     TATGAG  AGGATG
                                ||||     ||||||  ||||||
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                                ACCG    ATACTC  TTCTAC
                                  ATTAC     C_
GAM1523  LOC221143 3'  GGCTGAATATGAGGACAAAGTG 38048     CA       AAA   T
                                GGC  AATATGAG   GGA GTG
                                |||  ||||||||   ||| |||
                                CCG  TTATACTC   TTT CAC
                                  AC       CTG  _
GAM1523  LOC222493 5'  TGGCCAAAGTGAGAGG      38049        TA    AA
                                TGGCCAAA  TGAGA  GG
                                ||||||||  |||||  ||
                                ACCGGTTT  ACTCT  CC
                                     C_    __
GAM1523  LOC90190  3'  TGGCCAAATGTGAGGGGAC   38050         A   AAA
                                TGGCCAAAT TGAG   GGAT
                                |||||||||| ||||   ||||
                                ACCGGTTTA ACTC   CCTG
                                      C   C__
GAM1524  LOC152445 3'  GTGCAACTGCATGGGGCGC   38053       C    AGA
                                GTGCAGC GCATG   CGT
                                |||||||  |||||   |||
                                CACGTTG CGTAC   GCG
                                    A    CCC
GAM1524  LOC196485 5'  CGTGCAGCTGCAGATGACCATG 38054        C   T  _  _
                                CGTGCAGC GCA GA GAC GTG
                                |||||||| ||| || ||| |||
                                GCACGTCG CGT CT CTG TAC
                                     A   _  A   G
GAM1525  ATP2B2   3'  CGTTGATATAGATACAAAG   38057         ATCTTT
                                CGTTGATATA     CAAAG
                                ||||||||||     |||||
                                GCAACTATAT     GTTTC
                                      CTAT__
GAM1525  GRAF     5'  CGTCGATCTCATCTTTCA    38058        ATA
                                CGTTGAT   ATCTTTCA
                                |||||||   ||||||||
                                GCAGCTA   TAGAAAGT
                                    GAG
GAM1525  DOCK3    3'  GTTGATGTAATCTTTATCAAAG 38059       A      __
                                GTTGAT TAATCTT  TCAAAG
                                |||||| |||||||  ||||||
                                CAACTA ATTAGAA  AGTTTC
                                   C      AT
GAM1525  FLJ13263 3'  CATAGTTCATAATCTTTCA   38060     C   GA
                                CAT GTT  TATAATCTTTCA
                                ||| |||  ||||||||||||
                                GTA CAA  GTATTAGAAAGT
                                  T  __
GAM1525  FLJ14124 3'  GTTGATATAATTCCAAA     38061          CT
                                GTTGATATAAT  TTCAAA
                                ||||||||||  ||||||
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                                CAACTATATTA  AGGTTT
                                           __
GAM1525  FLJ20054  5'  CATTGTTGATATGACCTC    38062     C       A
                                CAT GTTGATAT ATCTT
                                ||| |||||||| |||||
                                GTA CAACTATA TGGAG
                                  A       C
GAM1525  HSPC055   5'  CATTTACCATAGTCTTTCAAAG 38063      GA_    A
                                CGTT   TATA TCTTTCAAAG
                                ||||   |||| ||||||||||
                                GTAA   GTAT AGAAAGTTTC
                                  ATG    C
GAM1525  KIAA0461  3'  CACTGTTGGTATAATCTT    38064     C    A
                                CAT GTTG TATAATCTT
                                ||| |||| |||||||||
                                GTG CAAC ATATTAGAA
                                  A   C
GAM1525  KIAA1610  3'  CTGTAAAAATCTTTCAAAG   38065     ATAT
                                TTG    AATCTTTCAAAG
                                |||    ||||||||||||
                                GAC    TTAGAAAGTTTC
                                  ATTT
GAM1525  OLFM3     3'  CATCCTTATCTTTCAA      38066      G  GATATA
                                CATC TT      ATCTTTCAA
                                |||| ||      |||||||||
                                GTAG AA      TAGAAAGTT
                                  G _______
GAM1525  LOC158402 5'  CATCTTGATATGATTTCCCAAA 38067      G      A  C TT
            A                    CATC TTGATAT AT T  CAAAG
                                |||| ||||||| || |  |||||
                                GTAG AACTATA TA A  GTTTT
                                  _      C  A GG
GAM1525  LOC91796  3'  CATCGCTGATGTAATTCTT    38068          A   _
                                CATCGTTGAT TAAT CTT
                                |||||||||| |||| |||
                                GTAGCGACTA ATTA GAA
                                      C    A
GAM1526  CKTSF1B1  3'  CGTTTGTATACATGCATC    38071      CA  C
                                CGTT  TG TGTATGCATC
                                ||||  || ||||||||||
                                GCAA  AT ATGTACGTAG
                                  AC  _
GAM1526  EIF4E     3'  GCTAGAAAACTGTATGCATCAT 38072     CAT__
                                GTT    GCTGTATGCATCAT
                                |||    ||||||||||||||
                                CGA    TGACATACGTAGTA
                                  TCTTT
GAM1526  HIVEP2    3'  GTTTTGCTTTACATCAT     38073     CA   GTA
                                GTT  TGCT   TGCATCAT
                                |||  ||||   ||||||||
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                                CAA  ACGA   ATGTAGTA
                                  A_   A__
GAM1526  MAN1A1   3'  CCCTTCAGTATATGCATC    38074    G    TGC
                                CC TTCA   TGTATGCATC
                                || ||||   ||||||||||
                                GG AAGT   ATATACGTAG
                                 G   C__
GAM1526  SFRS12   5'  ACCGTTCGTGTTGGCTGCATCA 38075        A  C  TA
           T                     ACCGTTC TG TG  TGCATCAT
                                ||||||| || ||  ||||||||
                                TGGCAAG AC AC  ACGTAGTA
                                    C  A  CG
GAM1526  LOC221474 5'  TACTGTCTATGACCTTGCATCA 38076     C  TC   _  GTA
           T                     TAC GT  ATG CT   TGCATCAT
                                ||| ||  ||| ||   ||||||||
                                ATG CA  TAC GG   ACGTAGTA
                                  A  GA   T  A__
GAM1527  SLC6A12  5'  AGGGCCAAAGCCTTAGTT    38079    A         AAA
                                AG GGCCAAAGTTT   TAGTT
                                || ||||||||||   |||||
                                TC CCGGTTTCGGA   ATCAA
                                 _         ____
GAM1527  KIAA1954  3'  AAGAAGTTGCTTTAAATAGTTT 38080       CCAAAG
                                AAGAGG     TTTAAATAGTTT
                                ||||||     ||||||||||||
                                TTCTTC     AAATTTATCAAA
                                   AACG__
GAM1527  MGC20255  3'  AGAGGCCAGACAGCCAAGTGGT 38081         A__    TAAATA
           TT                    AGAGGCCA   AGTT     GTTT
                                ||||||||   ||||     ||||
                                TCTCCGGT   TCGG     CAAA
                                    CTG    TTCAC_
GAM1527  PELI2    3'  AGAGGCTGAACTTTAAACA   38082       CA  G
                                AGAGGC  AA TTTAAATA
                                ||||||  || ||||||||
                                TCTCCG  TT AAATTTGT
                                   AC  G
GAM1527  PRDM5    3'  AGGAGCCCTTCTGAATAGTTT  38083    AG   AAAG   A
                                AG  GCC    TTT AATAGTTT
                                ||  |||    ||| ||||||||
                                TC  CGG    AGA TTATCAAA
                                 CT   GA__   C
GAM1527  PRO0650  3'  GAAGCCAAAGATAGTT      38084          TTTAA
                                GAGGCCAAAG    ATAGTT
                                ||||||||||    ||||||
                                CTTCGGTTTC    TATCAA
                                      _____
GAM1527  LOC221477 3'  AGAGGCCAAAGTGTAGTT    38085           TTAAA
                                AGAGGCCAAAGT    TAGTT
                                ||||||||||||    |||||
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                                TCTCCGGTTTCA    ATCAA
                                      C____
GAM1527  LOC221833 3'  AAAGGCCAAAGTTAGTCGAGTT 38086          TAAAT
             T                  AGAGGCCAAAGTT    AGTTT
                                ||||||||||||    |||||
                                TTTCCGGTTTCAA    TCAAA
                                      TCAGC
GAM1528  ADCY9    3'  GAACGGATGACCCAGA     38089        CAG
                                GGACGGATG   TCCAGA
                                |||||||||   ||||||
                                CTTGCCTAC   GGGTCT
                                     T__
GAM1528  ADM      3'  CCGGACGGTGCCTCCCGGA   38090       A   AG   A
                                CCGGACGG TGC  TCC GA
                                |||||||| |||  ||| ||
                                GGCCTGCC ACG  GGG CT
                                     _  GA   C
GAM1528  AP3B1    3'  CCAGATTCTAAAGTCCAGA   38091      CGGA  C
                                CCGGA    TG AGTCCAGA
                                |||||    || ||||||||
                                GGTCT    AT TCAGGTCT
                                   AAG_  T
GAM1528  BIRC7    3'  CCAGAACACAGTCCAGA     38092      CGG
                                CCGGA   ATGCAGTCCAGA
                                |||||   ||||||||||||
                                GGTCT   TGTGTCAGGTCT
                                   ___
GAM1528  BIRC7    3'  CCAGAACACAGTCCAGA     38092      CGG
                                CCGGA   ATGCAGTCCAGA
                                |||||   ||||||||||||
                                GGTCT   TGTGTCAGGTCT
                                   ___
GAM1528  CARPX    5'  GACGGATGTGCGCCCCAGA   38093       CA_   _
                                GACGGATG   GTCC AGA
                                ||||||||   |||| |||
                                CTGCCTAC   CGGG TCT
                                     ACG    G
GAM1528  CDA      3'  GGGGAAGCAGTCCAGA      38094    AC   T
                                GG  GGA GCAGTCCAGA
                                ||  ||| ||||||||||
                                CC  CCT CGTCAGGTCT
                                 __   T
GAM1528  CDKN1A   3'  CCGAGAGAAAACAGTCCAG   38095    _ C   T
                                CCG GA GGA GCAGTCCAG
                                ||| || ||| |||||||||
                                GGC CT CTT TGTCAGGTC
                                  T  _   T
GAM1528  DLEC1    3'  CCAGGCGGATGTCACAG     38096     A    GCA  _
                                CCGG CGGAT   GTC CAG
                                |||| |||||   ||| |||
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                                GGTC GCCTA   CAG GTC
                                  C    ___   T
GAM1528  DLEC1    3'  CCAGGCGGATGTCACAG     38096      A    GCA  _
                                CCGG CGGAT   GTC CAG
                                |||| |||||   ||| |||
                                GGTC GCCTA   CAG GTC
                                  C    ___   T
GAM1528  DMD      5'  ACGGATGCTTTTAGTTCAGA   38097        ____  C
                                ACGGATGC    AGT CAGA
                                ||||||||    ||| ||||
                                TGCCTACG    TCA GTCT
                                     AAAA   A
GAM1528  DMD      5'  ACGGATGCTTTTAGTTCAGA   38097        ____  C
                                ACGGATGC    AGT CAGA
                                ||||||||    ||| ||||
                                TGCCTACG    TCA GTCT
                                     AAAA   A
GAM1528  DMD      5'  ACGGATGCTTTTAGTTCAGA   38097        ____  C
                                ACGGATGC    AGT CAGA
                                ||||||||    ||| ||||
                                TGCCTACG    TCA GTCT
                                     AAAA   A
GAM1528  EIF2C1   3'  CAGAGGACAGTCCAG       38098      C  AT
                                CGGA GG  GCAGTCCAG
                                |||| ||  |||||||||
                                GTCT CC  TGTCAGGTC
                                  _  __
GAM1528  GPT      3'  CCTGAGCACACAGTCCAG    38099    G  CGG
                                CC GA   ATGCAGTCCAG
                                || ||   ||||||||||
                                GG CT   TGTGTCAGGTC
                                 A  CG_
GAM1528  GRB7     5'  CGGACAGAGAAGTCAGA     38100        TGC    C
                                CGGACGGA   AGTC AGA
                                ||||||||   |||| |||
                                GCCTGTCT   TCAG TCT
                                     CT_   _
GAM1528  HAO2     3'  CCGGACAGAATGGGGTCCAG  38101         _  CA
                                CCGGACGGA TG  GTCCAG
                                ||||||||| ||  ||||||
                                GGCCTGTCT AC  CAGGTC
                                      T  CC
GAM1528  HTR4     3'  CGGACGGAAAGCCTCAG     38102        TGC   _
                                CGGACGGA   AGTC CAG
                                ||||||||   |||| |||
                                GCCTGCCT   TCGG GTC
                                     T__    A
GAM1528  ID3      5'  GGGGAGTGAGTCCAGA      38103    AC  _  C
                                GG  GGA TG AGTCCAGA
                                ||  ||| || ||||||||
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                                CC  CCT AC TCAGGTCT
                                 __   C  _
GAM1528 IL1RN    3' GGACAGAGGAGTCCAGA     38104        TGC
                                GGACGGA   AGTCCAGA
                                |||||||   ||||||||
                                CCTGTCT   TCAGGTCT
                                    CC_
GAM1528 IRF2     5' CCTGAGAACAGTCCAGA     38105    GGAC   T
                                CC    GGA GCAGTCCAGA
                                ||    ||| ||||||||||
                                GG    TCT TGTCAGGTCT
                                 AC__   _
GAM1528 LILRA1   3' GGCAGACAGTCCAGA       38106    A   AT
                                GG CGG  GCAGTCCAGA
                                || |||  ||||||||||
                                CC GTC  TGTCAGGTCT
                                 _   __
GAM1528 MAD2L2   3' CCGGCGGAACCCCAG       38107     A    T  AG
                                CCGG CGGA GC  TCCAG
                                |||| |||| ||  |||||
                                GGCC GCCT TG  GGGTC
                                  _    _ __
GAM1528 MAP3K8   5' GGCGCGCAGTCCAGA       38108    A  GA
                                GG CG  TGCAGTCCAGA
                                || ||  ||||||||||||
                                CC GC  GCGTCAGGTCT
                                 _  __
GAM1528 MERTK    5' CCGGACGGATGGACAGA     38109          CAGTC
                                CCGGACGGATG    CAGA
                                ||||||||||     ||||
                                GGCCTGCCTAC    GTCT
                                      CT___
GAM1528 NKX2H    3' CGGACGGAGAGCGTTCCAG   38110        T_  AG
                                CGGACGGA  GC  TCCAG
                                ||||||||  ||  |||||
                                GCCTGCCT  CG  AGGTC
                                     CT  CA
GAM1528 PMM2     3' GGAGGTGGAAGTCCAGA     38111     C  A  C_
                                GGA GG TG  AGTCCAGA
                                ||| || ||  ||||||||
                                CCT CC AC  TCAGGTCT
                                  _  _  CT
GAM1528 PUM2     3' AGACAAACTGGTCCAGA     38112        GCA
                                GGACGGAT   GTCCAGA
                                ||||||||   |||||||
                                TCTGTTTG   CAGGTCT
                                     AC_
GAM1528 RUNX3    3' GGACAGATGTCCTAGA      38113        GCA   _
                                GGACGGAT   GTCC AGA
                                ||||||||   |||| |||
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                                CCTGTCTA  CAGG TCT
                                   ___   A
GAM1528 SPAG11   3' CCGAGAGGCAGTCCAG     38114    GAC  T
                                CCG  GGA GCAGTCCAG
                                |||  ||| |||||||||
                                GGC  TCT CGTCAGGTC
                                  ___  C
GAM1528 SPAG11   3' CCGAGAGGCAGTCCAG     38114    GAC  T
                                CCG  GGA GCAGTCCAG
                                |||  ||| |||||||||
                                GGC  TCT CGTCAGGTC
                                  ___  C
GAM1528 TAL1     5' CCCGACCAACCAGTCCAG    38115    G  G  G
                                CC GAC GAT CAGTCCAG
                                || ||| ||| ||||||||
                                GG CTG TTG GTCAGGTC
                                 G  G  _
GAM1528 TGM2     3' GGTACGGGATGCAGTCTAG   38116    _  _     C
                                GG ACGG ATGCAGTC AG
                                || |||| |||||||| ||
                                CC TGCC TACGTCAG TC
                                 A  C      A
GAM1528 WISP1    3' CCAGACAGGCCAGTCCAGA   38117       ATG
                                CCGGACGG  CAGTCCAGA
                                ||||||||  |||||||||
                                GGTCTGTC  GTCAGGTCT
                                    CG_
GAM1528 C20orf162 5' GGAGGGATGCAGTTGCTCAG  38118    C      C___
                                GGA GGATGCAGT   CAG
                                ||| |||||||||   |||
                                CCT CCTACGTCA   GTC
                                  C       ACGA
GAM1528 C22orf4  3' CGGGAACCAGTCCAG      38119    AC   G
                                CGG  GGAT CAGTCCAG
                                |||  |||| ||||||||
                                GCC  CTTG GTCAGGTC
                                  __   _
GAM1528 D21S2056E 3' GGAACCGGATGCAGTCCAG   38120    __
                                GGA  CGGATGCAGTCCAG
                                |||  ||||||||||||||
                                CCT  GCCTACGTCAGGTC
                                  TG
GAM1528 FLJ10377 3' CAGATGTACACAGTCCAG    38121     CGG
                                CGGA  ATGCAGTCCAG
                                ||||  ||||||||||
                                GTCT  TGTGTCAGGTC
                                  ACA
GAM1528 FLJ12425 3' CCGGACAGATATCCGGA     38122        GCA  A
                                CCGGACGGAT  GTCC GA
                                ||||||||||  |||| ||
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                                GGCCTGTCTA   TAGG CT
                                     ____    C
GAM1528  FLJ20152  3'  GGCAAAACTCAGTCCAGA    38123    A    TG_
                                GG CGGA   CAGTCCAGA
                                || ||||   |||||||||
                                CC GTTT   GTCAGGTCT
                                  _    TGA
GAM1528  FLJ21736  3'  CCCGACGGATGCCCTGGTCCAG 38124    G       A___
              A                  CC GACGGATGC    GTCCAGA
                                 || |||||||||    |||||||
                                 GG CTGCCTACG    CAGGTCT
                                   G       GGAC
GAM1528  FLJ22479  3'  CCAGACGGGACTCCAGA     38125        AT  AG
                                 CCGGACGG  GC  TCCAGA
                                 ||||||||  ||  ||||||
                                 GGTCTGCC  TG  AGGTCT
                                      C_  __
GAM1528  FLJ31300  3'  CCAGGGTGCCAGGGTCCAGA   38126     AC  A   A___
                                 CCGG  GG TGC    GTCCAGA
                                 ||||  || |||    |||||||
                                 GGTC  CC ACG    CAGGTCT
                                   __  _   GTCC
GAM1528  GFRA4     3'  GGAGGATGCAGTGTTAGA    38127     C       CC_
                                 GGA GGATGCAGT   AGA
                                 ||| |||||||||   |||
                                 CCT CCTACGTCA   TCT
                                   _       CAA
GAM1528  GREB1     3'  GGACTGCAGAGTCCAGA     38128     GGA   __
                                 GGAC   TGCA  GTCCAGA
                                 ||||   ||||  |||||||
                                 CCTG   ACGT  CAGGTCT
                                   ____    CT
GAM1528  HSPC047   3'  CCGGACGGGGCCACCAGA    38129        AT  AGT
                                 CCGGACGG  GC   CCAGA
                                 ||||||||  ||   |||||
                                 GGCCTGCC  CG   GGTCT
                                      C_  GT_
GAM1528  KIAA0226  3'  GGAAACGCAGTTCAGA      38130     CG      C
                                 GGA  GATGCAGT CAGA
                                 |||  |||||||| ||||
                                 CCT  TTGCGTCA GTCT
                                   __       A
GAM1528  KIAA0286  3'  CAGACTTGAGTCCAGA      38131      GGA  C
                                 CGGAC   TG AGTCCAGA
                                 |||||   || ||||||||
                                 GTCTG   AC TCAGGTCT
                                    A__  _
GAM1528  KIAA1026  3'  CCAGACGGGCTCCAG       38132        AT  AG
                                 CCGGACGG  GC  TCCAG
                                 ||||||||  ||  |||||
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                                GGTCTGCC  CG  AGGTC
                                   __  __
GAM1528 KIAA1546 3' GGATGAGCAAAATCCAGA    38133    CG  T  __
                                GGA  GA GCA  GTCCAGA
                                |||  || |||  |||||||
                                CCT  CT CGT  TAGGTCT
                                  A_  _   TT
GAM1528 KIAA1553 3' CCTGACGACAGTCCAGA     38134    G   GAT
                                CC GACG   GCAGTCCAGA
                                ||  ||||   ||||||||||
                                GG CTGC   TGTCAGGTCT
                                 A   ____
GAM1528 KIAA1755 3' GGAGGCTGAGTCCAGA      38135    C  A  C
                                GGA GG TG AGTCCAGA
                                |||  ||  ||  ||||||||
                                CCT CC AC TCAGGTCT
                                  _  G  _
GAM1528 KIAA1904 3' GGATGAGCAGCCCAGA      38136    CG  T
                                GGA  GA GCAGTCCAGA
                                |||  ||  ||||||||||
                                CCT  CT CGTCGGGTCT
                                  A_  _
GAM1528 MGC13186 5' CAGGGGAGCAGTCCAG      38137     AC   T
                                CGG  GGA GCAGTCCAG
                                |||  |||  |||||||||
                                GTC  CCT CGTCAGGTC
                                  C_   _
GAM1528 MGC4606  3' CAGAAAATTCAGTCCAG     38138     C    G
                                CGGA GGAT CAGTCCAG
                                ||||  ||||  ||||||||
                                GTCT TTTA GTCAGGTC
                                   _    A
GAM1528 My015    3' GGACAATAAAGTCCAGA     38139      G   C
                                GGACG ATG AGTCCAGA
                                |||||  |||  ||||||||
                                CCTGT TAT TCAGGTCT
                                   _   T
GAM1528 PRIC285  3' CCGAACACTCAGTCCAG     38140       GATG
                                CCGGACG    CAGTCCAG
                                |||||||    ||||||||
                                GGCTTGT    GTCAGGTC
                                    GA__
GAM1528 REC8     5' CCGGGCCGGAATCCAGA     38141     A_   TGCA
                                CCGG  CGGA   GTCCAGA
                                ||||  ||||   |||||||
                                GGCC  GCCT   TAGGTCT
                                  CG   _____
GAM1528 RLUCL    5' CCGGGCCGTGCAGTCCAG    38142     A_  GA
                                CCGG  CG  TGCAGTCCAG
                                ||||  ||  ||||||||||
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                                GGCC  GC  ACGTCAGGTC
                                  CG  __
GAM1528  RTVP1    5'  GGAGGCTGCAGTCCAGA     38143     C  A
                                GGA GG TGCAGTCCAGA
                                ||| || ||||||||||
                                CCT CC ACGTCAGGTCT
                                  _  G
GAM1528  SHANK3   3'  GGATGGAGCTTAGTCCAGA   38144     C   T  __
                                GGA GGA GC  AGTCCAGA
                                ||| ||| ||  ||||||||
                                CCT CCT CG  TCAGGTCT
                                  A  _  AA
GAM1528  TAGAP    5'  CGGACGGAGCCAGCCAGA    38145        T  _  T
                                CGGACGGA GC AG CCAGA
                                |||||||| || || |||||
                                GCCTGCCT CG TC GGTCT
                                     _  G  _
GAM1528  LOC112817 3'  CCAGAGACACAGTTTAG     38146      CG       CC
                                CCGGA  GATGCAGT  AG
                                |||||  ||||||||  ||
                                GGTCT  CTGTGTCA  TC
                                   __       AA
GAM1528  LOC126961 3'  GGACAGAAAATCCAGA      38147       TGC
                                GGACGGA   AGTCCAGA
                                |||||||   ||||||||
                                CCTGTCT   TTAGGTCT
                                    T__
GAM1528  LOC145468 3'  CCGATGGTGAGTCCAGA     38148     AC  A  C
                                CCGG  GG TG AGTCCAGA
                                ||||  || || ||||||||
                                GGCT  CC AC TCAGGTCT
                                  A_  _  _
GAM1528  LOC149421 5'  CCAGGCCCGTGAGTCCAGA   38149    _  A_  GA  C
                                CC GG  CG  TG AGTCCAGA
                                || ||  ||  || ||||||||
                                GG CC  GC  AC TCAGGTCT
                                 T  GG  __  _
GAM1528  LOC152316 5'  CGGATGGATGGGTCAACCAGA  38150      C    ___   T
                                CGGA GGATG   CAG CCAGA
                                |||| |||||   ||| |||||
                                GCCT CCTAC   GTT GGTCT
                                  A    CCA  _
GAM1528  LOC154789 5'  CCAGACGGGCCAGTCAGA    38151        ATG    C
                                CCGGACGG   CAGTC AGA
                                ||||||||   ||||| |||
                                GGTCTGCC   GTCAG TCT
                                    CG_    _
GAM1528  LOC158297 5'  CCGGCCTCCGCAGTCCAGA   38152      ACGGA
                                CCGG    TGCAGTCCAGA
                                ||||    ||||||||||
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                                GGCC    GCGTCAGGTCT
                                  GGAG_
GAM1528  LOC163682 3'  CCAGAATGCAGTCTGGA     38153      CGG      CA
                                CCGGA   ATGCAGTC  GA
                                |||||   ||||||||  ||
                                GGTCT   TACGTCAG  CT
                                  ___       AC
GAM1528  LOC221975 5'  CCGGACGAACAGTCCAG     38154        AT
                                CCGGACGG  GCAGTCCAG
                                ||||||||  |||||||||
                                GGCCTGCT  TGTCAGGTC
                                    __
GAM1528  LOC253832 3'  GGAAAATACAGTTTAGA     38155     C       CC
                                GGA GGATGCAGT  AGA
                                ||| |||||||||  |||
                                CCT TTTATGTCA  TCT
                                  _       AA
GAM1528  LOC254532 3'  CCAGAACGCAGTCTGGA     38156      CGG      CA
                                CCGGA   ATGCAGTC  GA
                                |||||   ||||||||  ||
                                GGTCT   TGCGTCAG  CT
                                  ___       AC
GAM1528  LOC255290 5'  GGACAGATGGACAAACAG    38157         __  TC
                                GGACGGATG  CAG  CAG
                                |||||||||  |||  |||
                                CCTGTCTAC  GTT  GTC
                                     CT   T_
GAM1528  LOC257395 3'  GGACAGAAAATCCAGA      38147       TGC
                                GGACGGA   AGTCCAGA
                                |||||||   ||||||||
                                CCTGTCT   TTAGGTCT
                                   T__
GAM1528  LOC90268  3'  CCAGACGGGTTACACAGA    38158        A_   GTC
                                CCGGACGG  TGCA   CAGA
                                ||||||||  ||||   ||||
                                GGTCTGCC  ATGT   GTCT
                                     CA   ___
GAM1528  LOC91250  5'  GGACAGAAAATCCAGA      38147       TGC
                                GGACGGA   AGTCCAGA
                                |||||||   ||||||||
                                CCTGTCT   TTAGGTCT
                                   T__
GAM1529  PBP      3'  TTAATAATTTGATGACCCCATC 38161      A       A  A
                                TTAA AATTTGAT ACT CCATT
                                |||| |||||||| ||| |||||
                                AATT TTAAACTA TGG GGTAG
                                  A       C  _
GAM1529  RGR      3'  TTAAAAATAGAGCTACCATT   38162        TT  TAA
                                TTAAAAAT  GA   CTACCATT
                                ||||||||  ||   ||||||||
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                                AATTTTTA  CT   GATGGTAA
                                    T_  C__
GAM1529  SRR      3'  TTAAGAATCTGATAACTA    38163      A
                                TTAA AATTTGATAACTA
                                |||| ||||||||||||
                                AATT TTAGACTATTGAT
                                  C
GAM1529  DKFZP434A0225 3'  AAAAAATGAAGCTACCATTC   38164      TT   TAA
                                AAAA  TGA   CTACCATTC
                                ||||  |||   |||||||||
                                TTTT  ACT   GATGGTAAG
                                  TT   TC_
GAM1529  HSA250839 3'  TTAAAAATGAGGAAACTGCCAT 38165        TTGAT    A
            TC                    TTAAAAAT     AACT CCATTC
                                ||||||||     |||| ||||||
                                AATTTTTA     TTGA GGTAAG
                                    CTCCT    C
GAM1529  PPIL4    3'  TCAAAAATGAAGACTACCATT  38166       TT   TA
                                TTAAAAA  TGA  ACTACCATT
                                |||||||  |||  |||||||||
                                AGTTTTT  ACT  TGATGGTAA
                                   __   TC
GAM1529  STARD7   3'  AAAACTTGATCCCTATTATTC  38167         AA   CC
                                AAAATTTGAT  CTA  ATTC
                                ||||||||||  |||  ||||
                                TTTTGAACTA  GAT  TAAG
                                     GG   AA
GAM1529  STARD7   3'  AAAACTTGATCCCTATTATTC  38167         AA   CC
                                AAAATTTGAT  CTA  ATTC
                                ||||||||||  |||  ||||
                                TTTTGAACTA  GAT  TAAG
                                     GG   AA
GAM1529  LOC150445 3'  TTAACAATTTGATGACCCCATC 38168      A       A   A
                                TTAA AATTTGAT ACT CCATT
                                |||| |||||||| ||| |||||
                                AATT TTAAACTA TGG GGTAG
                                  G       C  _
GAM1529  LOC169966 3'  TCAAAAATAGTTGGTAACTACT 38169         __   A      C
            ATTC                    TTAAAAAT  TTG TAACTAC ATTC
                                ||||||||  ||| ||||||| ||||
                                AGTTTTTA  AAC ATTGATG TAAG
                                    TC   C      A
GAM1530  FLJ11703  3'  TAATTACTTTTACATTAAAAAG 38172      A       AAT___
            TCAT                    TAAT TACTTTTA     AAAGTCAT
                                ||||  ||||||||     ||||||||
                                ATTA ATGAAAAT     TTTCAGTA
                                  _       GTAATT
GAM1530  KIAA0820  3'  TAATATACTTTAGAATAAAGT  38173          TA
                                TAATATACTTT  AATAAAGT
                                ||||||||||  ||||||||
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                                ATTATATGAAA  TTATTTCA
                                      TC
GAM1530  LOC151162 5'  TAAAATACTTTTAAATAAA   38174    T
                                TAA ATACTTTTAAATAAA
                                ||| ||||||||||||||
                                ATT TATGAAAATTTATTT
                                  T
GAM1530  LOC168433 3'  TAATACACTTCCTCAAAAGTCA 38175          AAAT
            T                    TAATATACTTTT   AAAGTCAT
                                ||||||||||||   ||||||||
                                ATTATGTGAAGG   TTTCAGTA
                                      AGT_
GAM1530  LOC203377 5'  TAAAATACTTTTAAATAAA   38174    T
                                TAA ATACTTTTAAATAAA
                                ||| ||||||||||||||
                                ATT TATGAAAATTTATTT
                                  T
GAM1531  TIAL1    3'  TACTTTCATGTCTTCAGAGTGT 38178    CTCA      TAT  C
                                TAC   ATGTCTTC  GGG GT
                                |||   ||||||||  ||| ||
                                ATG   TACAGAAG  CTC CA
                                  AAAG      T__  A
GAM1531  TIAL1    3'  TACTTTCATGTCTTCAGAGTGT 38178    CTCA      TAT  C
                                TAC   ATGTCTTC  GGG GT
                                |||   ||||||||  ||| ||
                                ATG   TACAGAAG  CTC CA
                                  AAAG      T__  A
GAM1531  CCR6     3'  CTTAATGTCTCCTGAGAGTGT  38179   C       AT  C
                                CT AATGTCTTCT  GGG GT
                                || ||||||||||  ||| ||
                                GA TTACAGAGGA  CTC CA
                                  A        CT  A
GAM1531  CCR6     3'  CTTAATGTCTCCTGAGAGTGT  38179   C       AT  C
                                CT AATGTCTTCT  GGG GT
                                || ||||||||||  ||| ||
                                GA TTACAGAGGA  CTC CA
                                  A        CT  A
GAM1531  FLJ14871  3'  TACCACAGACCGCTGTGGGTGT 38180     T ATGT  T A   C
                                TACC CA   CT CT TGGG GT
                                ||||  ||   || ||  |||| ||
                                ATGG GT   GG GA ACCC CA
                                   T  CT__  C  C   A
GAM1531  FLJ21126  3'  TCAATGTCTTCTTCATAG    38181          __
                                TCAATGTCTTCT  ATGG
                                ||||||||||||  ||||
                                AGTTACAGAAGA  TATC
                                      AG
GAM1531  FLJ21596  3'  AATGTCTTCTATGATGT     38182          GC
                                AATGTCTTCTATGG  GT
                                ||||||||||||||  ||
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                                TTACAGAAGATACT  CA
                                       A_
GAM1531  KIAA1524  5'  CTCAATGTCTTTATGTGCGT   38183          C   G
                                CTCAATGTCTT TATG GCGT
                                |||||||||| |||| ||||
                                GAGTTACAGAA ATAC CGCA
                                      _   A
GAM1531  LAT1-3TM  5'  TCCATGTCTTCTAGAAAC    38184    A       TG
                                TC ATGTCTTCTA  GGC
                                || ||||||||||  |||
                                AG TACAGAAGAT  TTG
                                 G         CT
GAM1531  LAT1-3TM  3'  TCCATGTCTTCTAGAAAC    38184    A       TG
                                TC ATGTCTTCTA  GGC
                                || ||||||||||  |||
                                AG TACAGAAGAT  TTG
                                 G         CT
GAM1531  MGC2541   5'  CCTTAATGTCTTCTCCACGT   38185    C       ATGG
                                CCT AATGTCTTCT   GCGT
                                ||| ||||||||||   ||||
                                GGA TTACAGAAGA   TGCA
                                  A         GG__
GAM1531  PRO0038   3'  CCTTAGTCTCCCAGGGTGT   38186    CAAT      T   C
                                CCT   GTCTTCTA GGG GT
                                |||   |||||||| ||| ||
                                GGA   CAGAGGGT CCC CA
                                  AT__       _  A
GAM1531  RI58      3'  ACCTTGGTAATCTATGGGTGT  38187    CAAT  CT      C
                                ACCT   GT  TCTATGGG GT
                                ||||   ||  |||||||| ||
                                TGGA   CA  AGATACCC CA
                                  AC__  TT       A
GAM1531  LOC126066 5'  TACAGACACGTCTGTGGGTGT  38188    CTCA    TCTA   C
                                TAC   ATGTCT   TGGG GT
                                |||   ||||||   |||| ||
                                ATG   TGCAGA   ACCC CA
                                  TCTG    C___   A
GAM1531  LOC163231 5'  TACTTTGACGTCTTCTCCTAG  38189    CTCA       A_
                                TAC   ATGTCTTCT  TGG
                                |||   |||||||||  |||
                                ATG   TGCAGAAGA  ATC
                                  AAAC        GG
GAM1531  LOC197423 5'  TCCATGTCTTCTAGAAAC    38184    A       TG
                                TC ATGTCTTCTA  GGC
                                || ||||||||||  |||
                                AG TACAGAAGAT  TTG
                                 G         CT
GAM1531  LOC220565 5'  TCCATGTCTTCTAGAAAC    38184    A       TG
                                TC ATGTCTTCTA  GGC
                                || ||||||||||  |||
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                                AG TACAGAAGAT  TTG
                                 G         CT
GAM1531 LOC91813 5' TACTTCCATGTCTTCTGAC   38190     C  A       ATG
                                TAC TC ATGTCTTCT   GGC
                                ||| || |||||||||   |||
                                ATG AG TACAGAAGA   CTG
                                  A  G        ___
GAM1531 LOC91974 5' CCTTCAATGTCTTTTCGG    38191     _       CTA
                                CCT CAATGTCTT   TGG
                                ||| |||||||||   |||
                                GGA GTTACAGAA   GCC
                                  A        AA_
GAM1532 NAP1L3   3' TTTAATATTTATTTATTTT   38194
                                TTTAATATTTATTTATTTT
                                ||||||||||||||||||
                                AAATTATAAATAAATAAAA

GAM1532 LOC157867 3'  TTTAATATTTATTAAAACTTTT 38195           T__
              TTA                  TTTAATATTTATT   ATTTTTTTA
                                ||||||||||||   |||||||||
                                AAATTATAAATAA   TGAAAAAAT
                                       TTT
GAM1532 LOC51020 3' TTTAATATTTATTTATTT    38196
                                TTTAATATTTATTTATTT
                                ||||||||||||||||||
                                AAATTATAAATAAATAAA

GAM1533 ALOX15   3' CAGCCTAGGCAACATA      38199      G    ATGTTT
                                CAGCC AGGCA     ACATA
                                ||||| |||||     |||||
                                GTCGG TCCGT     TGTAT
                                   A    _______
GAM1533 CD1D     3' GAGGTGTCCCACATAGT     38200      CAA    _
                                GAGG   TGTTT ACATAGT
                                ||||   ||||| |||||||
                                CTCC   ACAGG TGTATCA
                                   ___     G
GAM1533 FLJ11743 5' GCTGGCGCCGTTTACATGGT   38201    CGA   AA       A
                                GC   GGC  TGTTTACAT GT
                                ||   |||  ||||||||| ||
                                CG   CCG  GCAAATGTA CA
                                 A__   CG        C
GAM1533 FLJ13769 5' CAGCCTAGGCAACATA      38199      G    ATGTTT
                                CAGCC AGGCA     ACATA
                                ||||| |||||     |||||
                                GTCGG TCCGT     TGTAT
                                   A    _______
GAM1533 RNF8     3' CAGCCTAGGCAACATA      38199      G    ATGTTT
                                CAGCC AGGCA     ACATA
                                ||||| |||||     |||||
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                                GTCGG TCCGT     TGTAT
                                  A   _______
GAM1533  SPTLC2    3'  AGCTGAGGCAATGTCTTTCAC  38202     C         A_
                                AGC GAGGCAATGTTT  CAT
                                ||| ||||||||||||  |||
                                TCG CTCCGTTACAGA  GTG
                                  A          AA
GAM1533  LOC148089 3'  AGCCGAGGACGGATATAG    38203        CA   TT  CA
                                AGCCGAGG  ATG  TA  TAG
                                ||||||||  |||  ||  |||
                                TCGGCTCC  TGC  AT  ATC
                                    __  CT  __
GAM1533  LOC219673 3'  CAGCCTAGGCAACATA      38199       G    ATGTTT
                                CAGCC AGGCA     ACATA
                                ||||| |||||     |||||
                                GTCGG TCCGT     TGTAT
                                  A   _______
GAM1534  FBXW1B    3'  TCAACAGGGCCTTCTTATT   38206      _    CC
                                TCAAC GGGCC  CTTATT
                                ||||| |||||  ||||||
                                AGTTG CCCGG  GAATAA
                                  T    AA
GAM1534  FBXW1B    3'  TCAACAGGGCCTTCTTATT   38206      _    CC
                                TCAAC GGGCC  CTTATT
                                ||||| |||||  ||||||
                                AGTTG CCCGG  GAATAA
                                  T    AA
GAM1534  FBXW1B    3'  TCAACAGGGCCTTCTTATT   38206      _    CC
                                TCAAC GGGCC  CTTATT
                                ||||| |||||  ||||||
                                AGTTG CCCGG  GAATAA
                                  T    AA
GAM1534  PTCRA     3'  TCAAGGGGCCCCCTTTTGGA  38207     C        A  T
                                TCAA GGGCCCCCTT TTG GA
                                |||| |||||||||| ||| ||
                                AGTT CCCGGGGGAA AAC CT
                                  C        _  _
GAM1534  RAB7L1    3'  CAATGGGCCTCCTTACTG    38208    C    C
                                CAA GGGCC CCTTATTG
                                ||| ||||| ||||||||
                                GTT CCCGG GGAATGAC
                                  A    A
GAM1534  RBP3      3'  TCAGCAGGCCCCTTTGC     38209     A      CTTA
                                TCA CGGGCCCC   TTGT
                                ||| ||||||||   ||||
                                AGT GTCCGGGG   AACG
                                  C       A___
GAM1534  C11orf11  5'  TCAGCAGGCCCCCTGGCG    38210     A       TATT
                                TCA CGGGCCCCCT   GTG
                                ||| ||||||||||   |||
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                                AGT GTCCGGGGGA   CGC
                                  C       C___
GAM1534 C14orf4   5' CCGACGGGCCCCCTGGGGCG  38211   A       TATT
                                TC ACGGGCCCCCT   GTG
                                || ||||||||||   |||
                                GG TGCCCGGGGGA   CGC
                                 C        CCC_
GAM1534 FLJ23499  3' TCAACAGGTTTCCTTAGTG  38212      CCC    TT
                                TCAACGGG  CCTTA  GTG
                                ||||||||  |||||  |||
                                AGTTGTCC  GGAAT  CAC
                                    AAA   __
GAM1534 LOC145663 5' CCAACGGGCCTTCTTGCGACG 38213        CCCTTA
                                TCAACGGGCC    TTGTGACG
                                ||||||||||    ||||||||
                                GGTTGCCCGG    AACGCTGC
                                     AAG___
GAM1534 LOC163231 5' TCAGCAGGTTCCCATTGTG  38215   A  CC  TT
                                TCA CGGG  CCC  ATTGTG
                                ||| ||||  |||  ||||||
                                AGT GTCC  GGG  TAACAC
                                  C   AA  __
GAM1534 LOC163231 5' AACGGGTTTCCACTATGA   38214     CCC  TT
                                AACGGG  CC  ATTGTGA
                                ||||||  ||  |||||||
                                TTGCCC  GG  TGATACT
                                   AAA  __
GAM1534 LOC163231 5' AACGGGTTTCCACTGTGA   38217     CCC  TT
                                AACGGG  CC  ATTGTGA
                                ||||||  ||  |||||||
                                TTGCCC  GG  TGACACT
                                   AAA  __
GAM1534 LOC163231 5' AACAGGTTCCCACTGTG    38216     CC   TT
                                AACGGG  CCC  ATTGTG
                                ||||||  |||  ||||||
                                TTGTCC  GGG  TGACAC
                                   AA  __
GAM1534 LOC164714 5' TCAGGGGGTTCCAGTCCGTGAC 38218    AC   CC  CTTA
           G                     TCA  GGG  CC   TTGTGACG
                                ||| ||| ||  ||||||||
                                AGT  CCC  GG   GGCACTGC
                                  CC   AA  TCA_
GAM1535 AGR2    3'  TCACACATGTACACTTGAAACC 38221       CAGGAAG
           A                     TCACACAT     TTGAAACCA
                                ||||||||     |||||||||
                                AGTGTGTA     AACTTTGGT
                                    CATGTG_
GAM1535 CCR2    3'  TCACACATCTGTGAAGCCA   38222       AG_
                                TCACACATC   GAAGTTG
                                |||||||||  |||||||
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                                AGTGTGTAG  CTTCGGT
                                     ACA
GAM1535 CERD4    3' TCCACATCAGGTGTGGGCTG  38223   A      AA___
                                TC CACATCAGG    GTTG
                                || |||||||||    ||||
                                AG GTGTAGTCC    CGAC
                                 _       ACACC
GAM1535 COL4A1   3' TCACACATCAGTGCATTG    38224         GAA
                                TCACACATCAG  GTTG
                                ||||||||||  ||||
                                AGTGTGTAGTC  TAAC
                                      ACG
GAM1535 CYP27B1  3' TCACACATTGGTCAGGGCCG  38225       ____   AA
                                TCACACA   TCAGG  GTTG
                                |||||||   |||||  ||||
                                AGTGTGT   AGTCC  CGGC
                                    AACC   __
GAM1535 FGF2     3' CACATCAGAGTAAAAA     38226        GA  T
                                CACATCAG  AGT GAAA
                                ||||||||  ||| ||||
                                GTGTAGTC  TCA TTTT
                                    __  T
GAM1535 IFNG     5' CCAAAGAAGTTGAAATCA    38227     _       C
                                TCAG GAAGTTGAAA CA
                                |||| ||||||||| ||
                                GGTT CTTCAACTTT GT
                                  T        A
GAM1535 IL1RN    3' TCACACATTAGAAAGACC    38228       C    TTGAA
                                TCACACAT AGGAAG    ACC
                                |||||||| ||||||    |||
                                AGTGTGTA TCTTTC    TGG
                                    A    _____
GAM1535 KNS2     3' ACACATGGGAAGGGAGCC    38229      CA    TT  AA
                                ACACAT  GGAAG  GA  CC
                                ||||||  |||||  ||  ||
                                TGTGTA  CCTTC  CT  GG
                                   C_    C_  C_
GAM1535 LTB4R    5' ACACACAAAGTTGAGGCC    38230      CAG      AA
                                ACACAT   GAAGTTGA  CC
                                ||||||   ||||||||  ||
                                TGTGTG   TTTCAACT  GG
                                   ___       CC
GAM1535 M11S1    3' ACCATCAGAACTGAAAC     38231    A      AG
                                AC CATCAGGA  TTGAAAC
                                || ||||||||  |||||||
                                TG GTAGTCTT  GACTTTG
                                 _      __
GAM1535 MLLT2    3' TCACTTTCAGAGTTGAAAC   38232     ACA   GA
                                TCAC   TCAG  AGTTGAAAC
                                ||||   ||||  |||||||||
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                                AGTG  AGTC  TCAACTTTG
                                  AA_   __
GAM1535 PDE4D    3' TCATGTATCAGGAAGACTTGAA 38233    CAC       __
             A                   TCA  ATCAGGAAG  TTGAAA
                                 |||  |||||||||  ||||||
                                 AGT  TAGTCCTTC  AACTTT
                                   ACA       TG
GAM1535 PPP4R1   3' TCACACACAGGGCTG      38234       T   AA
                                 TCACACA CAGG  GTTG
                                 |||||||  ||||  ||||
                                 AGTGTGT GTCC  CGAC
                                    _   __
GAM1535 RAF1     3' TCCACATCAGGGCTG      38235    A       AA
                                 TC CACATCAGG  GTTG
                                 || |||||||||  ||||
                                 AG GTGTAGTCC  CGAC
                                  _       __
GAM1535 TMPRSS2  3' TCATGCACGGGGAAGCAAAACC 38236    CA  CA    T
             A                   TCA  CAT  GGAAGT GAAACCA
                                 |||  |||  |||||| |||||||
                                 AGT  GTG  CCTTCG TTTTGGT
                                   AC   CC    _
GAM1535 TXNIP    3' TCCTACATTAGGAAGTCAGA  38237    AC   C      _
                                 TC  ACAT AGGAAGTT GA
                                 ||  |||| |||||||| ||
                                 AG  TGTA TCCTTCAG CT
                                  GA   A       T
GAM1535 AIF1     3' TCATACATCAGGATCCTG    38238    C       AG
                                 TCA ACATCAGGA  TTG
                                 ||| |||||||||  |||
                                 AGT TGTAGTCCT  GAC
                                   A       AG
GAM1535 CARD11   5' TCACACACAGGGGCTG      38239       T   AA
                                 TCACACA CAGG  GTTG
                                 |||||||  ||||  ||||
                                 AGTGTGT GTCC  CGAC
                                    _   C_
GAM1535 CRELD1   3' TCACACATTGTGAAGCCTGCCA 38240        CAG     GAAA
                                 TCACACAT   GAAGTT   CCA
                                 ||||||||   ||||||   |||
                                 AGTGTGTA   CTTCGG   GGT
                                      ACA     AC__
GAM1535 FLJ10081 3' TCACACCTCAGGAAGTCA    38241       A
                                 TCACAC TCAGGAAGTTG
                                 ||||||  ||||||||||
                                 AGTGTG AGTCCTTCAGT
                                    G
GAM1535 FLJ10547 3' CCACACATTAGTTTTTTGAGAC 38242        C  GAAG   A
             C                   TCACACAT AG    TTGA ACC
                                 ||||||||  ||    |||| |||
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                                GGTGTGTA TC    AACT TGG
                                     A  AAAA    C
GAM1535  FLJ10726  3'  ACACATCAGGAAAGTAAGGCCA 38243           T   AA
                                ACACATCAGGAAG TGA  CCA
                                |||||||||||| |||  |||
                                TGTGTAGTCCTTT ATT  GGT
                                      C   CC
GAM1535  FLJ20730  3'  TCATACATCAGTTAAAAGTCA  38244     C      ___
                                TCA ACATCAG   GAAGTTG
                                ||| |||||||   |||||||
                                AGT TGTAGTC   TTTCAGT
                                  A      AAT
GAM1535  FLJ21432  3'  TCCCACATCAATGGAACC    38245    A      GAAGT  A
                                TC CACATCAG    TG AACC
                                || ||||||||    || ||||
                                AG GTGTAGTT    AC TTGG
                                 G       _____  C
GAM1535  FLJ22283  5'  CACGTCGGGAGAAACCA     38246     A  A   AGTT
                                CAC TC GGA    GAAACCA
                                ||| || |||    |||||||
                                GTG AG CCT    CTTTGGT
                                  C  C  ____
GAM1535  GGA2      3'  TCAGGCATCAGGAAGCCA    38247     CA
                                TCA  CATCAGGAAGTTG
                                |||  ||||||||||||
                                AGT  GTAGTCCTTCGGT
                                  CC
GAM1535  GGA2      3'  TCAGGCATCAGGAAGCCA    38247     CA
                                TCA  CATCAGGAAGTTG
                                |||  ||||||||||||
                                AGT  GTAGTCCTTCGGT
                                  CC
GAM1535  HH114     3'  CCACACATGTTGGGACC     38248        CAGGAA   AA
                                TCACACAT     GTTG  ACC
                                ||||||||     ||||  |||
                                GGTGTGTA     CAAC  TGG
                                     _______   CC
GAM1535  KIAA0298  3'  TCAACATCAGGAAAGTGA    38249     C         T
                                TCA ACATCAGGAAG TGA
                                ||| ||||||||||| |||
                                AGT TGTAGTCCTTT ACT
                                  _         C
GAM1535  KIAA0419  5'  TCACACACTATCTGAAATTA   38250         CAG__
                                TCACACAT    GAAGTTG
                                ||||||||    |||||||
                                AGTGTGTG    CTTTAAT
                                     ATAGA
GAM1535  KIAA0680  3'  TCCACATCAGGAGGTTA     38251    A        A
                                TC CACATCAGGA GTTG
                                || ||||||||| ||||
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                                AG GTGTAGTCCT CAAT
                                 _        C
GAM1535 KIAA1322 3' TCAACATCAGAAATGAGA    38252    C        GTT
                                TCA ACATCAGGAA   GA
                                ||| ||||||||||   ||
                                AGT TGTAGTCTTT   CT
                                  _        ACT
GAM1535 KIAA1393 3' TCACACATTGGGAAGCCG    38253        CA
                                TCACACAT  GGAAGTTG
                                ||||||||  ||||||||
                                AGTGTGTA  CCTTCGGC
                                     AC
GAM1535 MAWBP    3' CACATCAGGAGAAACACA    38254         AGTT    _
                                CACATCAGGA    GAAAC CA
                                ||||||||||    ||||| ||
                                GTGTAGTCCT    CTTTG GT
                                     ____     T
GAM1535 MCF2L    3' ACACATCAGAGGAAAAGCTG   38255         ____
                                ACACATCAG    GAAGTTG
                                |||||||||    |||||||
                                TGTGTAGTC    TTTCGAC
                                     TCCT
GAM1535 MGC32043 3' TCACCATCCTTGAAAC      38256     A   AGGAAG
                                TCAC CATC     TTGAAAC
                                |||| ||||     |||||||
                                AGTG GTAG     AACTTTG
                                  _   G_____
GAM1535 MKP-7    3' CACATTTGGCTTGAAACC    38257      CA  AAG
                                CACAT  GG   TTGAAACC
                                |||||  ||   ||||||||
                                GTGTA  CC   AACTTTGG
                                   AA  G__
GAM1535 PCDH19   3' TCATACATCAGACAATTG    38258     C      GA
                                TCA ACATCAG  AGTTG
                                ||| |||||||  |||||
                                AGT TGTAGTC  TTAAC
                                  A      TG
GAM1535 SPRY4    3' ACATCAGGACTGAAACCA     38259         AG
                                ACATCAGGA  TTGAAACCA
                                |||||||||  |||||||||
                                TGTAGTCCT  GACTTTGGT
                                     __
GAM1535 SV2      3' TCACACACAGTCCTGCGGAGCT 38260         CA_______  A
           G                     TCACACAT       GGA GTTG
                                 ||||||||       ||| ||||
                                 AGTGTGTG       CCT CGAC
                                      TCAGGACG  _
GAM1535 TBL1Y    3' TCACACATTTTGGAGCTG     38261         CA_  A
                                TCACACAT   GGA GTTG
                                ||||||||   ||| ||||
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                                AGTGTGTA  CCT CGAC
                                    AAA  _
GAM1535  TBL1Y    3'  TCACACATTTTGGAGCTG    38261       CA_  A
                                TCACACAT  GGA GTTG
                                ||||||||  ||| ||||
                                AGTGTGTA  CCT CGAC
                                    AAA  _
GAM1535  TBL1Y    3'  TCACACATTTTGGAGCTG    38261       CA_  A
                                TCACACAT  GGA GTTG
                                ||||||||  ||| ||||
                                AGTGTGTA  CCT CGAC
                                    AAA  _
GAM1535  LOC143425 3'  TCACACATCAGCGAGACT    38262         _ AG
                                TCACACATCAG GA  TT
                                |||||||||| ||  ||
                                AGTGTGTAGTC CT  GA
                                      G  CT
GAM1535  LOC144742 3'  TCACACATCTGGGACAACTGA  38263       A_  AG_
                                TCACACATC  GGA  TTGA
                                |||||||||  |||  ||||
                                AGTGTGTAG  CCT  GACT
                                     AC  GTT
GAM1535  LOC147004 5'  CATCGGCAAGAAGTTGAA    38264     ___
                                CATC  AGGAAGTTGAA
                                ||||  ||||||||||
                                GTAG  TTCTTCAACTT
                                  CCG
GAM1535  LOC147669 5'  TCACACACTGGGGAGTCCAGGA 38265       CA  A  ___
            AACCA                   TCACACAT  GG AGTT  GAAACCA
                                ||||||||  || ||||  |||||||
                                AGTGTGTG  CC TCAG  CTTTGGT
                                    AC  C   GTC
GAM1535  LOC147976 3'  CACACAGGTAGTTGAAACCA  38266     T   A
                                CACA CAGG AGTTGAAACCA
                                |||| |||| ||||||||||
                                GTGT GTCC TCAACTTTGGT
                                  _   A
GAM1535  LOC148195 5'  CATGCATCAGGACAGCCA    38267    CA     _
                                CA  CATCAGGA AGTTG
                                ||  |||||||| |||||
                                GT  GTAGTCCT TCGGT
                                 AC       G
GAM1535  LOC149911 3'  TCACACATCAGAGGGAGAGTTA 38268         ___  _
                                TCACACATCA  GGA AGTTG
                                ||||||||||  ||| |||||
                                AGTGTGTAGT  CCT TCAAT
                                      CTC  C
GAM1535  LOC155061 3'  TCACACACTAGGGGACACC   38269       C  AAGTT  A
                                TCACACAT AGG    GA ACC
                                |||||||| |||    || |||
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                                AGTGTGTG TCC     CT TGG
                                     A   C____  G
GAM1535  LOC158055 3'  TCCACATCAGGCTACAAAC   38270    A        AAGTTG
                                TC CACATCAGG      AAAC
                                || |||||||||      ||||
                                AG GTGTAGTCC      TTTG
                                 _        GATG__
GAM1535  LOC200269 3'  TCACGTGTCAGAAAGCCA    38271      ACA
                                TCAC   TCAGGAAGTTG
                                ||||   ||||||||||
                                AGTG   AGTCTTTCGGT
                                  CAC
GAM1535  LOC219942 3'  TCCACATCAGGAAACTG     38272    A          GT
                                TC CACATCAGGAA  TG
                                || ||||||||||  ||
                                AG GTGTAGTCCTT  AC
                                 _         TG
GAM1535  LOC90170  5'  TCACACATCAAGATCTGAGACC 38273             AG    A
             A                   TCACACATCAGGA  TTGA ACCA
                                ||||||||||||  |||| ||||
                                AGTGTGTAGTTCT  GACT TGGT
                                        A_   C
GAM1536  DKFZP566B183 3'  CTATTGGAATTTTAACAT    38276       AT
                                TTATTG  ATTTTAACAT
                                ||||||  ||||||||||
                                GATAAC  TAAAATTGTA
                                    CT
GAM1536  GPR64    3'  ACATTTTTGATTTTAACATAT  38277       A     AT
                                ACATT TTGAT  TTTAACATAT
                                ||||| |||||  ||||||||||
                                TGTAA AACTA  AAATTGTATA
                                  A    __
GAM1536  HSU79252  5'  TTACCATATTTTAACATA    38278       G
                                TTATT ATATTTTAACATA
                                ||||| ||||||||||||
                                AATGG TATAAAATTGTAT
                                  _
GAM1536  KLHL4    3'  TACAAAATGATATTTTGGCATA 38279      TTAT        AA
             T                   TACA   TGATATTTT  CATAT
                                ||||   |||||||||  |||||
                                ATGT   ACTATAAAA  GTATA
                                  TTT_        CC
GAM1536  LOC90550  3'  CTAATGATATTTTAGCATAT   38280     T         A
                                TTA TGATATTTTA CATAT
                                ||| |||||||||| |||||
                                GAT ACTATAAAAT GTATA
                                  T         C
GAM1537  ATRN     3'  AGGTGAAACTCAGACATTGT   38283     A  TCA__
                                AGG TG     TAGACATTGT
                                ||| ||     ||||||||||
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                                TCC AC    GTCTGTAACA
                                  _ TTTGA
GAM1537 F8       3' TCAAGAAGACATTGT      38284       ATGTCAT
                                TCAAGG      AGACATTGT
                                ||||||      |||||||||
                                AGTTCT      TCTGTAACA
                                  ________
GAM1537 C20orf97 3' TCAAGGATGCCAGTTTGTC   38285          TAGACA
                                TCAAGGATGTCA     TTGTC
                                ||||||||||||     |||||
                                AGTTCCTACGGT     AACAG
                                       CA____
GAM1537 CSMD1    5' AAGGGTGTCATAGCCTCG    38286     A       ACA
                                AAGG TGTCATAG   TTG
                                |||| ||||||||   |||
                                TTCC ACAGTATC   AGC
                                  C       GG_
GAM1537 FLJ23563 3' TCAAGGATTCATAGAGATT   38287       G      C
                                TCAAGGAT TCATAGA ATT
                                |||||||| ||||||| |||
                                AGTTCCTA AGTATCT TAA
                                     _      C
GAM1537 LIMR     5' GGAGTAGGTAGACATTGT    38288     T  CA_
                                GGA GT   TAGACATTGT
                                ||| ||   ||||||||||
                                CCT CA   ATCTGTAACA
                                  _ TCC
GAM1537 STIP-1   3' GGATGGAGTAGACATTGT    38289      TCA
                                GGATG   TAGACATTGT
                                |||||   ||||||||||
                                CCTAC   ATCTGTAACA
                                   CTC
GAM1537 TNRC9    3' AGTGGTCATAGATATTGT    38290    GAT       C
                                AG   GTCATAGA ATTGT
                                ||   |||||||| |||||
                                TC   CAGTATCT TAACA
                                 AC_       A
GAM1537 ZFP100   3' TCAAGATGTCACTTGT      38291      G      AGACA
                                TCAAG ATGTCAT    TTGT
                                ||||| |||||||    ||||
                                AGTTC TACAGTG    AACA
                                  _     ______
GAM1537 LOC145820 3' TCAAGGATGTTATGGTATGACA 38292        CATA________  ATT
           ATGT                   AAGGATGT         GAC   GT
                                ||||||||         |||   ||
                                TTCCTACA         CTG   CA
                                     ATACCATIIIA   TTA
GAM1537 LOC149603 3' AAGGATAAATGGACATTGT   38293        TCATA
                                AAGGATG    GACATTGT
                                |||||||    ||||||||
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                                TTCCTAT    CTGTAACA
                                    TTAC_
GAM1538  CHAC     3'  TATAAAATATATAAAAGCA   38296            _
                                TATAAAATATATAAAA CA
                                |||||||||||||||| ||
                                ATATTTTATATATTTT GT
                                          C
GAM1538  JRKL     3'  TATAAAATATACAAAACAT   38297
                                TATAAAATATATAAAACAT
                                ||||||||||||||||||
                                ATATTTTATATGTTTTGTA

GAM1538  TSG      3'  TATAAAATACAATAAACATAAA 38298          TA
              CT                  TATAAAATATA  AAACATAAACT
                                ||||||||||  ||||||||||
                                ATATTTTATGT  TTTGTATTTGA
                                       TA
GAM1538  RIS1     3'  TATTAAATATATAAAACA    38299     A
                                TAT AAATATATAAAACA
                                ||| ||||||||||||||
                                ATA TTTATATATTTTGT
                                  A
GAM1538  LOC154792 5'  TATAAAATATTTAAAACACA   38300          A
                                TATAAAATAT TAAAACATA
                                |||||||||| |||||||||
                                ATATTTTATA ATTTTGTGT
                                       A
GAM1539  LOC154215 3'  TTGAATTAGATATAAAA     38303      T
                                TTGA ATTAGATATAAAA
                                |||| ||||||||||||
                                AACT TAATCTATATTTT
                                  _
GAM1540  ACADL    3'  TATTCTGTGTTCTCAGAT    38306         ATA
                                TATTTTGTG   TCAGAT
                                |||||||||   ||||||
                                ATAAGACAC   AGTCTA
                                      AAG
GAM1540  KLRC4    3'  TATTTTGTGATAAAAACAT   38307           TC
                                TATTTTGTGATA  AGATAT
                                ||||||||||||  ||||||
                                ATAAAACACTAT  TTTGTA
                                       T_
GAM1540  PLS1     3'  CTTAATGTATCAGATAT     38308     T  A
                                TTT GTG TATCAGATAT
                                ||| ||| ||||||||||
                                GAA TAC ATAGTCTATA
                                  T  _
GAM1540  RELN     3'  TATTTCCTGATATCAGAT    38309       G
                                TATTTT TGATATCAGAT
                                |||||| ||||||||||
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                                ATAAAG ACTATAGTCTA
                                   G
GAM1540  SMP1     3'  TTTTGGACCTCAGATAT     38310      T  A
                                TTTTG GAT TCAGATAT
                                ||||| ||| ||||||||
                                AAAAC CTG AGTCTATA
                                  _  G
GAM1540  C21orf109 3'  TTTTGTGAATCTGATAT     38311        T  A
                                TTTTGTGA ATC GATAT
                                |||||||| ||| |||||
                                AAAACACT TAG CTATA
                                    _  A
GAM1540  C8orf4    3'  TATTTTGAACACTCAGATAT   38312       T  _
                                TATTTTG GATA TCAGATAT
                                ||||||| |||| ||||||||
                                ATAAAAC TTGT AGTCTATA
                                   _   G
GAM1540  CEP3     3'  ATTTTGCAATATAGATAT    38313      TG   C
                                ATTTTG  ATAT AGATAT
                                ||||||  |||| ||||||
                                TAAAAC  TATA TCTATA
                                   GT   _
GAM1540  COQ3     3'  TTTGAAAACATCAGATAT    38314     T_
                                TTTG  GATATCAGATAT
                                ||||  ||||||||||||
                                AAAC  TTGTAGTCTATA
                                  TT
GAM1540  FLJ12604  3'  TTTTGTGGGCATCAGATAT   38315       A_
                                TTTTGTG  TATCAGATAT
                                |||||||  ||||||||||
                                AAAACAC  GTAGTCTATA
                                    CC
GAM1540  FLJ20272  3'  TATCTTGCATTTCAGATAT   38316       G  A
                                TATTTTGT AT TCAGATAT
                                |||||||| || ||||||||
                                ATAGAACG TA AGTCTATA
                                    _ A
GAM1540  GGA2     3'  TGTAAAAATATCAGATAT    38317    ___
                                TGT   GATATCAGATAT
                                |||   ||||||||||||
                                ACA   TTATAGTCTATA
                                  TTT
GAM1540  GGA2     3'  TGTAAAAATATCAGATAT    38317    ___
                                TGT   GATATCAGATAT
                                |||   ||||||||||||
                                ACA   TTATAGTCTATA
                                  TTT
GAM1540  KIAA1012  3'  TATTTTGCAGGGATCAGATAT  38318        AT_
                                TATTTTGTG   ATCAGATAT
                                |||||||||   |||||||||
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                                ATAAAACGT   TAGTCTATA
                                     CCC
GAM1540 KIAA1497 5' TATTTTATGATTCCACATAT  38319         A  G
                                TATTTTGTGAT TCA ATAT
                                |||||||||| ||| ||||
                                ATAAAATACTA GGT TATA
                                      A  G
GAM1540 KIAA1571 3' TATTTTGTGACATAAAT    38320          C
                                TATTTTGTGATAT AGAT
                                |||||||||||| ||||
                                ATAAAACACTGTA TTTA
                                          _
GAM1540 KIAA1676 3' TACTTTGCACCAGATAT    38321        GAT
                                TATTTTGT  ATCAGATAT
                                ||||||||  |||||||||
                                ATGAAACG  TGGTCTATA
                                          ___
GAM1540 KLHL8    3' TTTTGTACCTATCAGATAT   38322       A_
                                TTTTGTG  TATCAGATAT
                                |||||||  ||||||||||
                                AAAACAT  ATAGTCTATA
                                    GG
GAM1540 PRO1430  3' TATTTTGAACACTCAGATAT  38312       T  _
                                TATTTTG GATA TCAGATAT
                                ||||||| |||| ||||||||
                                ATAAAAC TTGT AGTCTATA
                                   _  G
GAM1540 PRSS12   3' TATATTGTGACAGGCAGAT   38323    T     T_
                                TAT TTGTGATA  CAGAT
                                ||| ||||||||  |||||
                                ATA AACACTGT  GTCTA
                                  T      CC
GAM1540 SCYB11   3' CATTTTGTATTTCAGAT     38324        ATA
                                TATTTTGTG  TCAGAT
                                |||||||||  ||||||
                                GTAAAACAT  AGTCTA
                                     AA_
GAM1540 LOC54557 3' TTTCACACATCAGATAT     38325    TG G
                                TTT  T ATATCAGATAT
                                |||  | ||||||||||||
                                AAA  G TGTAGTCTATA
                                  GT _
GAM1540 LOC81537 3' TATAATATATATCAGATAT   38326    TT  A
                                TAT  TGTG TATCAGATAT
                                |||  |||| ||||||||||
                                ATA  ATAT ATAGTCTATA
                                  TT  _
GAM1541 MLLT7    3' TATTTATTGTCTGTAGTG    38329         A  GCGAC
                                TGTTTATTGTC TG    AGTG
                                ||||||||||| ||    ||||
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                                ATAAATAACAG AC    TCAC
                                      _ A____
GAM1541  DKFZp761O17121 3'  TGTTTATCCTTGCTGGTGGCAG 38330       GTCA_  CGA
           TGT                  TGTTTATT    TGG  CAGTGT
                                ||||||||    |||  ||||||
                                ACAAATAG    ACC  GTCACA
                                    GAACG   ACC
GAM1541  KIAA0555  3'  TGTTTATTATCAGGACTAGTGT 38331          T  GAC
                                TGTTTATTGTCA GGC  AGTGT
                                ||||||||||| |||  |||||
                                ACAAATAATAGT CTG  TCACA
                                      C  A__
GAM1541  KIAA1161  5'  TGTTTATTGGTAGTTGTCAGTG 38332       TCA  CGA_
           T                   TGTTTATTG   TGG   CAGTGT
                               |||||||||  |||   ||||||
                               ACAAATAAC  ATC   GTCACA
                                    C__   AACA
GAM1541  LOC149566 3'  TATTTATTGTTACAGT     38333        CATGGCG
                               TGTTTATTGT     ACAGT
                               ||||||||||     |||||
                               ATAAATAACA     TGTCA
                                    A_______
GAM1542  GYS1     3'  CTGGAGTGCAGGAACTG     38336     TA  ATC      C
                               TTGGA  GT   GCAGGAACT G
                               |||||  ||   ||||||||| |
                               GACCT  CA   CGTCCTTGA C
                                  __  ___       A
GAM1542  UBE2L3   3'  TTGGATAGCTGACAGAA     38337       ATC
                               TTGGATAGT   GCAGGA
                               |||||||||   ||||||
                               AACCTATCG   TGTCTT
                                    AC_
GAM1542  ARF6     5'  TGGATCCTCGCGGGAACTCGG  38338      AGTA   A
                               TGGAT    TCGC GGAACTCGG
                               |||||    |||| |||||||||
                               ACCTA    AGCG CCTTGAGCC
                                  GG__    C
GAM1543  SLA      3'  TTACATTCATTTCTCATACG   38341        C  G  CC
                               TTATATTCAT TC CA  ACG
                               |||||||||| || ||  |||
                               AATGTAAGTA AG GT  TGC
                                    A  A  A_
GAM1544  ADORA1   3'  TATGGCCTGGGGTCCA     38344     T   TTT  T
                               TATG CCTG   GG GTCCA
                               |||| ||||   || |||||
                               ATAC GGAC   CC CAGGT
                                 C   ___  _
GAM1544  EHF      3'  TGTTTTGGTTTGTGTCCAAA  38345     CCT_   G
                               TGT   GTTTG TGTCCAAA
                               |||   ||||| ||||||||
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                                ACA   CAAAC ACAGGTTT
                                  AAAC    _
GAM1544  MGAT2    3'  TATGTCCTGTTTGGACAAA   38346          TGTC
                                TATGTCCTGTTTGG   CAAA
                                |||||||||||||   ||||
                                ATACAGGACAAACC   GTTT
                                       T___
GAM1544  SELPLG   3'  TGTCCTGTTTGGGTGGCCA   38347         _ T
                                TGTCCTGTTTGG TG CCA
                                |||||||||||| || |||
                                ACAGGACAAACC AC GGT
                                       C  C
GAM1544  FIBL-6   3'  TATGTCCTGTTAGATGTTCA  38348         T    C
                                TATGTCCTGTT GGTGT CA
                                |||||||||| ||||| ||
                                ATACAGGACAA CTACA GT
                                       T    A
GAM1544  KIAA0416 3'  TGTCTTGTTTATCTCCAAAAT 38349     C     G G
                                TGTC TGTTTG T TCCAAAAT
                                |||| |||||| | ||||||||
                                ACAG ACAAAT A AGGTTTTA
                                  A     _ G
GAM1544  KIAA1775 3'  ATGTCCTGCTGTTCAA      38350        TTGG   C
                                ATGTCCTGT   TGT CAA
                                |||||||||   ||| |||
                                TACAGGACG   ACA GTT
                                      ____  A
GAM1544  LCHN     3'  TGTTTGTGAGGGGTCCAAAAT 38351    CC   TT  T
                                TGT  TGT  GG GTCCAAAAT
                                |||  |||  || |||||||||
                                ACA  ACA  CC CAGGTTTTA
                                 A_   CT  C
GAM1544  NEDD5    3'  TATGTTTTATTTGGTTAACA  38352      CC      GTC
                                TATGT  TGTTTGGT   CA
                                |||||  ||||||||   ||
                                ATACA  ATAAACCA   GT
                                   AA       ATT
GAM1544  OASIS    3'  TGTCTGTTTGGGTGCA     38353     C      T  C
                                TGTC TGTTTGG GT CA
                                |||| ||||||| || ||
                                ACAG ACAAACC CA GT
                                  _      _ C
GAM1544  LOC116236 3'  TATGTCCTGTTGCCAAAA    38354         TTGG  T
                                TATGTCCTGT    TG CCAAAA
                                ||||||||||    || ||||||
                                ATACAGGACA    AC GGTTTT
                                      ____  _
GAM1544  LOC118851 5'  TATGTTGTATGTCCAAAA    38355      CC   TTG
                                TATGT  TGT   GTGTCCAAAA
                                |||||  |||   ||||||||||
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                                ATACA  ACA   TACAGGTTTT
                                  __  ___
GAM1544  LOC152559 3'  TGTCTTTTGTTTGGCCAAAAT  38356     C__      TGT
                                TGTC   TGTTTGG   CCAAAAT
                                ||||   |||||||   |||||||
                                ACAG   ACAAACC   GGTTTTA
                                  AAA      ___
GAM1544  LOC154792 5'  TATGGCCTGTTTGCAAAA    38357     T      GTGTC
                                TATG CCTGTTTG    CAAAA
                                |||| ||||||||    |||||
                                ATAC GGACAAAC    GTTTT
                                  C      _____
GAM1544  LOC158438 3'  TCCATCATTGGTGTCTGAAAT  38358    TGT_      CA
                                TCC    TTGGTGTC  AAAT
                                |||    ||||||||  ||||
                                AGG    AACCACAG  TTTA
                                  TAGT       AC
GAM1544  LOC202865 3'  TGTCTGCTGGTGTTCAAA    38359     C    T    C
                                TGTC TGTT GGTGT CAAA
                                |||| |||| ||||| ||||
                                ACAG ACGA CCACA GTTT
                                  _    _     A
GAM1544  LOC221583 5'  TGTCCTGTTTCTCCAA      38360         GGTG
                                TGTCCTGTTT    TCCAA
                                ||||||||||    |||||
                                ACAGGACAAA    AGGTT
                                     G___
GAM1545  ABCA1    5'  TGGCTCGGGAGCCCTGG     38363         ATTG
                                TGGCTTGGGA    CTTGG
                                ||||||||||    |||||
                                ACCGAGCCCT    GGACC
                                     CG__
GAM1545  ABCD2    3'  GGTTGAGACATTGTTTGG    38364    C     _   C
                                GG TTGGGA ATTG TTGG
                                || |||||| |||| ||||
                                CC AACTCT TAAC AACC
                                 _     G   A
GAM1545  AMBP     3'  TGGACCCAGGTTGCTTGG    38365     _ TG  AA
                                TGG CT  GG  TTGCTTGG
                                ||| ||  ||  ||||||||
                                ACC GG  CC  AACGAACC
                                  T  GT  __
GAM1545  CHRNA2   5'  TGGCTTGGAGATTCTGG     38366        GA   G  T
                                TGGCTTGG  ATT CT GG
                                ||||||||  ||| || ||
                                ACCGAACC  TAA GA CC
                                     TC  _ _
GAM1545  CRP      3'  TGGCCTGGGTATATTGG     38367         AAT  C
                                TGGCTTGGG   TG TTGG
                                |||||||||   || ||||
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                                ACCGGACCC  AT AACC
                                     AT_ _
GAM1545 DPEP1   5' GGCTTGGGGGTTGTTTCTGG  38368       AA  C__
                                GGCTTGGG  TTG  TTGG
                                ||||||||  |||  ||||
                                CCGAACCC  AAC  GACC
                                     CC  AAA
GAM1545 DPH2L1  5' TGGCCTGGGCTTGTTGG    38369       AA  C
                                TGGCTTGGG  TTG TTGG
                                |||||||||  ||| ||||
                                ACCGGACCC  AAC AACC
                                     G_  _
GAM1545 DRD2    3' TGGCTTGGGAATCTCTGG   38370         GC
                                TGGCTTGGGAATT  TTGG
                                ||||||||||||  ||||
                                ACCGAACCCTTAG  GACC
                                       A_
GAM1545 DTR     3' TGGCCTGGGGCCATGG     38371       AATT  _
                                TGGCTTGGG   GCT TGG
                                |||||||||   ||| |||
                                ACCGGACCC   CGG ACC
                                     ____  T
GAM1545 EML1    3' TGACTTGGTCTACTTGG    38372       GAAT
                                TGGCTTGG   TGCTTGG
                                ||||||||   |||||||
                                ACTGAACC   ATGAACC
                                     AG__
GAM1545 EPHB2   3' TGGCTGGCACCGCTTGG    38373     T  GA
                                TGGCT GG  ATTGCTTGG
                                |||||  ||  |||||||||
                                ACCGA CC  TGGCGAACC
                                   _  G_
GAM1545 FBXL11  3' TGGCTGGGAGGCAGGTTGG  38375     T   ATT  ___
                                TGGCT GGGA  GC  TTGG
                                |||||  ||||  ||  ||||
                                ACCGA CCCT  CG  AACC
                                   _   C__  TCC
GAM1545 FBXL11  3' TGGCTTGGAAATTTCTGTGG 38374         G  _
                                TGGCTTGGGAATT CT TGG
                                |||||||||||||  || |||
                                ACCGAACCTTTAA GA ACC
                                       A  C
GAM1545 FLNA    3' GGCTTGGGGGCTGCCGG    38376       AA   T
                                GGCTTGGG  TTGCT GG
                                ||||||||  |||||  ||
                                CCGAACCC  GACGG CC
                                     CC   _
GAM1545 HGF     3' TGGTAGGGAATTGTTTGG   38377    CTT     C
                                TGG  GGGAATTG TTGG
                                |||  |||||||| ||||
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                                ACC   CCCTTAAC AACC
                                  AT_       A
GAM1545  HOXB1    3'  TGGGTTGGGAGAGCCTGG    38378     C     ATT
                                TGG TTGGGA   GCTTGG
                                ||| ||||||   ||||||
                                ACC AACCCT   CGGACC
                                  C     CT_
GAM1545  ITGA11   3'  TGACTTGGGAGCCAATGG    38379         ATT  __
                                TGGCTTGGGA   GCT  TGG
                                ||||||||||   |||  |||
                                ACTGAACCCT   CGG  ACC
                                      ____  TT
GAM1545  LY64     5'  GGCTAGGATTGCTTGG      38380     T   A
                                GGCT GGGA TTGCTTGG
                                |||| |||| ||||||||
                                CCGA TCCT AACGAACC
                                  _   _
GAM1545  MAK      3'  TGGCTTGGGGGAACCAGCTGG  38381       __      _  T
                                TGGCTT  GGGAATT GCT GG
                                ||||||  ||||||| ||| ||
                                ACCGAA  CCCTTGG CGA CC
                                   CC      T  _
GAM1545  NR4A1    3'  GGCTTGGGGGTGCTCTGG    38382        AAT   _
                                GGCTTGGG   TGCT TGG
                                ||||||||   |||| |||
                                CCGAACCC   ACGA ACC
                                     CC_   G
GAM1545  ODF2     3'  TGGCTTGGCAACTCTGG     38383        G   G  T
                                TGGCTTGG AATT CT GG
                                |||||||| |||| || ||
                                ACCGAACC TTGA GA CC
                                     G   _ _
GAM1545  PIK3R2   5'  TGGCTTGGGGTGCTGG      38384         AAT   T
                                TGGCTTGGG   TGCT GG
                                |||||||||   |||| ||
                                ACCGAACCC   ACGA CC
                                     C__   _
GAM1545  PPARBP   3'  TGACTAATTTGCTTGG      38385      TGG  A
                                TGGCT   GA TTGCTTGG
                                |||||   || ||||||||
                                ACTGA   TT AACGAACC
                                   ____ A
GAM1545  PRKACA   3'  TGGCTTGGGGGGGACTTGG    38386         AATT
                                TGGCTTGGG   GCTTGG
                                |||||||||   ||||||
                                ACCGAACCC   TGAACC
                                     CCC_
GAM1545  RGS3     5'  TGGCTTGGGGCAGCTGCAGG   38387         AA__   TT
                                TGGCTTGGG   TTGC  GG
                                |||||||||   ||||  ||
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                                ACCGAACCC   GACG  CC
                                     CGTC   T_
GAM1545  SLC1A5   5'  TGGCTGGGAGCGCTTGG    38388      T   AT
                                TGGCT GGGA  TGCTTGG
                                ||||| ||||  |||||||
                                ACCGA CCCT  GCGAACC
                                   _   C_
GAM1545  SLC1A5   5'  TGGCTGGGAGCGCTTGG    38388      T   AT
                                TGGCT GGGA  TGCTTGG
                                ||||| ||||  |||||||
                                ACCGA CCCT  GCGAACC
                                   _   C_
GAM1545  SLC7A6   3'  GGTTGGGATTGCTTGG     38389    C     A
                                GG TTGGGA TTGCTTGG
                                || |||||| ||||||||
                                CC AACCCT AACGAACC
                                 _     _
GAM1545  SYN3     3'  TGGCTTGGAGGCCTGG      38390        AATT
                                TGGCTTGGG   GCTTGG
                                |||||||||   ||||||
                                ACCGAACCT   CGGACC
                                     C___
GAM1545  TAF1C    3'  TGGCTCCAAATTGCTTGG    38391      G G
                                TGGCTT G AATTGCTTGG
                                |||||| | ||||||||||
                                ACCGAG T TTAACGAACC
                                   G _
GAM1545  TCIRG1   5'  GGCTTGGGACTGTGG       38392        A   CT
                                GGCTTGGGA TTG  TGG
                                ||||||||| |||  |||
                                CCGAACCCT GAC  ACC
                                      _  __
GAM1545  TRPM2    3'  GGCTTGGGGACGATGCTGG   38393        _ AT_   T
                                GGCTTGGG A   TGCT GG
                                |||||||| |   |||| ||
                                CCGAACCC T   ACGA CC
                                     C GCT   _
GAM1545  ZNF35    3'  GGCTTGAGTTGTTTGG      38394        AA   C
                                GGCTTGGG  TTG TTGG
                                ||||||||  ||| ||||
                                CCGAACTC  AAC AACC
                                     __   A
GAM1545  AD-020   3'  TGACTTGGGTGCTTTGG     38395        AAT    _
                                TGGCTTGGG   TGCTT GG
                                |||||||||   ||||| ||
                                ACTGAACCC   ACGAA CC
                                     ____    A
GAM1545  AD-020   3'  TGACTTGGGTGCTTTGG     38395        AAT    _
                                TGGCTTGGG   TGCTT GG
                                |||||||||   ||||| ||
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                                ACTGAACCC  ACGAA CC
                                    ___    A
GAM1545 ATIP1    3' TGGCTCTGGGGCTCTGG    38396     _   AATT  _
                                TGGCT TGGG   GCT TGG
                                ||||| ||||   ||| |||
                                ACCGA ACCC   CGA ACC
                                   G   ____  G
GAM1545 BP75     3' TGGTTGCTGAAATTGCTTGG  38397    C  __
                                TGG TTG  GGAATTGCTTGG
                                ||| |||  ||||||||||||
                                ACC AAC  CTTTAACGAACC
                                  _  GA
GAM1545 C1orf34  3' GGTGGGAAGATTGCTTGG   38398    CT   __
                                GG  TGGGA  ATTGCTTGG
                                ||  |||||  |||||||||
                                CC  ACCCT  TAACGAACC
                                 __    TC
GAM1545 C21orf69 3' TGGCTTGGGGAGGTGCTGG  38399        AAT_   T
                                TGGCTTGGG   TGCT GG
                                |||||||||   |||| ||
                                ACCGAACCC   ACGA CC
                                     CTCC   _
GAM1545 CSAGE    3' TGTCTTGGGAACCTCTTTGG  38400    G       TG  _
                                TG CTTGGGAAT  CTT GG
                                || |||||||||  ||| ||
                                AC GAACCCTTG  GAA CC
                                 A       GA   A
GAM1545 CSEN     3' TGGCCTGGGAAGGGCTGG    38401         TT   T
                                TGGCTTGGGAA  GCT GG
                                ||||||||||  ||| ||
                                ACCGGACCCTT  CGA CC
                                      CC   _
GAM1545 CXYorf1  5' GGCTAGGATTGCTTGG     38380     T   A
                                GGCT GGGA TTGCTTGG
                                |||| |||| ||||||||
                                CCGA TCCT AACGAACC
                                  _   _
GAM1545 DJ159A19.3 5' TGGCTTGGGGATGAACTTGG  38402        AATT_
                                TGGCTTGGG    GCTTGG
                                |||||||||    ||||||
                                ACCGAACCC    TGAACC
                                     CTACT
GAM1545 DKFZp434O0320 3' TGGCTTCGGGGCCTGG     38403      _  AATT
                                TGGCTT GGG   GCTTGG
                                |||||| |||   ||||||
                                ACCGAA CCC   CGGACC
                                   G  ____
GAM1545 DKFZP434P0721 3' TGGCTTGAGAACTCTGG    38404          G  T
                                TGGCTTGGGAATT CT GG
                                |||||||||||| || ||
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                                ACCGAACTCTTGA GA CC
                                      _ _
GAM1545  DKFZP547E2110 3'  TGGCTTGGAAAATTGG     38405          TTGC
                                TGGCTTGGGAA   TTGG
                                ||||||||||   ||||
                                ACCGAACCTTT   AACC
                                      T___
GAM1545  DKFZP566I1024 3'  GGTGGGAGAATTGCTTGG   38406    CTT
                                GG  GGGAATTGCTTGG
                                ||  ||||||||||||
                                CC  CTCTTAACGAACC
                                 ACC
GAM1545  DKFZp761J1523 3'  TGGCTTGGGGCCTCCTTGG   38407        AA  G
                                TGGCTTGGG  TT CTTGG
                                |||||||||  || |||||
                                ACCGAACCC  GA GAACC
                                     CG  G
GAM1545  EFA6R    3'  TGGCCTGGGAGACAAGATGG  38408         _ TGCT
                                TGGCTTGGGA AT   TGG
                                ||||||||||  ||   |||
                                ACCGGACCCT TG   ACC
                                     C  TTCT
GAM1545  ERN1     3'  TGGTTTGGGAAGCCTGG    38409    C     TT
                                TGG TTGGGAA  GCTTGG
                                |||  |||||||  ||||||
                                ACC AACCCTT  CGGACC
                                 A     __
GAM1545  FLJ10803  5'  GGCTTGGGAAAGCACGG    38410         TT  T
                                GGCTTGGGAA  GC TGG
                                ||||||||||  ||  |||
                                CCGAACCCTT  CG GCC
                                     T_  T
GAM1545  FLJ10853  3'  TGGCTTGGGTTACTTGG    38411        AA
                                TGGCTTGGG  TTGCTTGG
                                |||||||||  ||||||||
                                ACCGAACCC  AATGAACC
                                      __
GAM1545  FLJ12975  3'  GGTGGGAGGATTGCTTGG   38412    CT    __
                                GG  TGGGA  ATTGCTTGG
                                ||  |||||  |||||||||
                                CC  ACCCT  TAACGAACC
                                 __    CC
GAM1545  FLJ14107  5'  TGGCTAGGAACCTTGG     38413     T     TG
                                TGGCT GGGAAT  CTTGG
                                |||||  ||||||  |||||
                                ACCGA TCCTTG  GAACC
                                   _    __
GAM1545  FLJ14107  3'  TGGCTGGGGACTGCTTGG   38414      T   A
                                TGGCT GGGA TTGCTTGG
                                |||||  ||||  ||||||||
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                                ACCGA CCCT GACGAACC
                                  C   _
GAM1545  FLJ14442  3'  TGGCCTGGGAAAGATTTGG   38415          TTGC
                                TGGCTTGGGAA   TTGG
                                ||||||||||   ||||
                                ACCGGACCCTT   AACC
                                    TCTA
GAM1545  FLJ14816  3'  TGGCTTGGGGTGTTGG     38416        AAT  C
                                TGGCTTGGG  TG TTGG
                                |||||||||  || ||||
                                ACCGAACCC  AC AACC
                                    C__  _
GAM1545  FLJ21103  3'  TGGGTTGGGAGCTGCATTTGG  38417    C     A   __
                                TGG TTGGGA TTGC  TTGG
                                ||| |||||| ||||  ||||
                                ACC AACCCT GACG  AACC
                                  C     C    TA
GAM1545  FLJ22615  3'  GGCTTGGGAGCTCTGG     38418        ATT   _
                                GGCTTGGGA   GCT TGG
                                |||||||||  ||| |||
                                CCGAACCCT   CGA ACC
                                    ___  G
GAM1545  FLJ23420  3'  TGGCCTGGACCCACTTGG    38419         AA TG
                                TGGCTTGGG  T  CTTGG
                                |||||||||  |  |||||
                                ACCGGACCT  G  GAACC
                                    G_ GT
GAM1545  GEMIN7    3'  TGGCTCGGGAACATTGG     38420          TGC
                                TGGCTTGGGAAT   TTGG
                                ||||||||||||  ||||
                                ACCGAGCCCTTG   AACC
                                    T__
GAM1545  HGC6.1.1  5'  TGGCCTGGGCCACATTGG    38421         AA TG _
                                TGGCTTGGG  T  C TTGG
                                |||||||||  |  | ||||
                                ACCGGACCC  G  G AACC
                                    __ GT T
GAM1545  HTMP10    5'  TGGCCTGAGAGCTTGG     38422         ATT
                                TGGCTTGGGA   GCTTGG
                                |||||||||   ||||||
                                ACCGGACTCT   CGAACC
                                    ___
GAM1545  KIAA0057  3'  TGGCTTGGCACTTTGG     38423        GA   GC
                                TGGCTTGG  ATT  TTGG
                                ||||||||  |||  ||||
                                ACCGAACC  TGA  AACC
                                    G_  __
GAM1545  KIAA0255  3'  TGGCTTGGGAAATACTTGG   38424          T
                                TGGCTTGGGAA TGCTTGG
                                |||||||||| |||||||
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                                ACCGAACCCTT ATGAACC
                                       T
GAM1545 KIAA0318 3' GGCTTCAAGCTTGCTTGG    38425      G  AA
                                GGCTT GG  TTGCTTGG
                                ||||| ||  ||||||||
                                CCGAA TT  AACGAACC
                                   G  CG
GAM1545 KIAA0356 3' TGGCTTAGGAGGCATTGG    38426         ATT  _
                                TGGCTTGGGA   GC TTGG
                                ||||||||||   || ||||
                                ACCGAATCCT   CG AACC
                                      C__  T
GAM1545 KIAA0420 3' GGCTTGGGGCTGCTGG      38427        AA    T
                                GGCTTGGG  TTGCT GG
                                ||||||||  ||||| ||
                                CCGAACCC  GACGA CC
                                     C_    _
GAM1545 KIAA0450 5' GGCTTGGGAAGCTGCTGG    38428          _    T
                                GGCTTGGGAA TTGCT GG
                                |||||||||| ||||| ||
                                CCGAACCCTT GACGA CC
                                      C    _
GAM1545 KIAA0779 5' TGGCCTGGGAGAAGCTGG    38429         ATT   T
                                TGGCTTGGGA   GCT GG
                                ||||||||||   ||| ||
                                ACCGGACCCT   CGA CC
                                      CTT  _
GAM1545 KIAA0924 3' TGGCTTGGGTACCTGG      38430        AAT
                                TGGCTTGGG   TGCTTGG
                                |||||||||   |||||||
                                ACCGAACCC   ATGGACC
                                     ____
GAM1545 KIAA0953 3' TGGCTGGGAATGCCAGG     38431      T     T  T
                                TGGCT GGGAAT GCT GG
                                ||||| |||||| ||| ||
                                ACCGA CCCTTA CGG CC
                                   _     _  T
GAM1545 KIAA0961 3' TGGTTGGGAAACCAGG      38432     C      TT  T
                                TGG TTGGGAA  GCT GG
                                ||| |||||||  ||| ||
                                ACC AACCCTT  TGG CC
                                  _      __  T
GAM1545 KIAA1029 3' TGGCTTGGGAACTGCCGG    38433            T
                                TGGCTTGGGAATTGCT GG
                                ||||||||||||||| ||
                                ACCGAACCCTTGACGG CC
                                        _
GAM1545 KIAA1297 5' TGGCTGGGGATGAACTTGG   38434      T   ATT
                                TGGCT GGGA   GCTTGG
                                ||||| ||||   ||||||
```

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                                ACCGA CCCT   TGAACC
                                   C    ACT
GAM1545 KIAA1535 3' GGCTTGGATACCTTGG     38435        A  TG
                                GGCTTGGG AT  CTTGG
                                |||||||| ||  |||||
                                CCGAACCT TG  GAACC
                                    A  __
GAM1545 KIAA1813 5' TGGCTTGAGGGCCCATTGG   38436         AATT  ___
                                TGGCTTGGG   GCT   TGG
                                |||||||||   |||   |||
                                ACCGAACTC   CGG   ACC
                                     C___   GTA
GAM1545 KLF12    3' GCCTAGTCTATTGCTTGG    38437      GA_
                                GCTTGG   ATTGCTTGG
                                ||||||   |||||||||
                                CGGATC   TAACGAACC
                                   AGA
GAM1545 KRTAP1-1 5' GGTTGGGTTGCTTGG      38438    C    AA
                                GG TTGGG  TTGCTTGG
                                || |||||  ||||||||
                                CC AACCC  AACGAACC
                                 _    __
GAM1545 MGC10924 5' GGCTTGGGAGCGCTGG     38439        AT    T
                                GGCTTGGGA  TGCT GG
                                |||||||||  |||| ||
                                CCGAACCCT  GCGA CC
                                     C_   _
GAM1545 MGC16386 3' TGGCTATGGTACTTTGG    38440      _  GAAT    _
                                TGGCT TGG    TGCTT GG
                                ||||| |||    ||||| ||
                                ACCGA ACC    ATGAA CC
                                   T  _____    A
GAM1545 MGC20460 5' TGGCTCGGGAATCTTGG    38441          TG
                                TGGCTTGGGAAT  CTTGG
                                ||||||||||||  |||||
                                ACCGAGCCCTTA  GAACC
                                      __
GAM1545 MGC4796  3' TGGCCTGGGCCACTTGG    38442        AA TG
                                TGGCTTGGG  T  CTTGG
                                |||||||||  |  |||||
                                ACCGGACCC  G  GAACC
                                     __ GT
GAM1545 MRPS2    3' TGGCTGTGGTTTGCTTTGG   38443      _  GAA    _
                                TGGCT TGG   TTGCTT GG
                                ||||| |||   |||||| ||
                                ACCGA ACC   AACGAA CC
                                   C  A__     A
GAM1545 NFASC    3' TGGCTTGGTGGCTACTGG    38444        GAA    T
                                TGGCTTGG   TTGCT GG
                                ||||||||   ||||| ||
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                                ACCGAACC   GATGA CC
                                    ACC    _
GAM1545  P2RX1    3'  TGGCCTGGCACACTTGG     38445        GAAT
                                TGGCTTGG    TGCTTGG
                                ||||||||    |||||||
                                ACCGGACC    GTGAACC
                                    GT__
GAM1545  PPP2R3A  3'  TGGATATTAAGTTGCTTGG   38446     C__    AA
                                TGG   TTGGG  TTGCTTGG
                                |||   |||||  ||||||||
                                ACC   AATTC  AACGAACC
                                  TAT    __
GAM1545  PRKAG3   3'  TGGCTTGGGATTGAGG      38447         A   CTT
                                TGGCTTGGGA TTG   GG
                                |||||||||| |||   ||
                                ACCGAACCCT AAC   CC
                                    _   T__
GAM1545  PRO0899  5'  AGCAGGAGGATTGCTTGG    38448     TT   A
                                GGC  GGG ATTGCTTGG
                                |||  ||| |||||||||
                                TCG  CTC TAACGAACC
                                  TC   C
GAM1545  Rab11-FIP3 3'  TGGCCTGGGAAGTGCGTGG   38449          T   T
                                TGGCTTGGGAA TGC TGG
                                |||||||||| ||| |||
                                ACCGGACCCTT ACG ACC
                                     C   C
GAM1545  REC8     5'  TGGCTTGGGCGGCCGCGG     38450         AATT   _
                                TGGCTTGGG    GCT TGG
                                |||||||||    ||| |||
                                ACCGAACCC    CGG GCC
                                    GC__   C
GAM1545  SARM     3'  TGGTTGGGGAATCGATCCTTGG 38451     CTT      ___
                                TGG   GGGAATTG   CTTGG
                                |||   ||||||||   |||||
                                ACC   CCCTTAGC   GAACC
                                  AAC       TAG
GAM1545  SFRS5    3'  TGGTTTGGGAATTTTTG     38452     C       GC
                                TGG TTGGGAATT  TTG
                                ||| |||||||||  |||
                                ACC AACCCTTAA  AAC
                                  A        A_
GAM1545  SPIB     3'  GGCTTGGGGATTATGG      38453         A   CT
                                GGCTTGGG ATTG  TGG
                                |||||||| ||||  |||
                                CCGAACCC TAAT  ACC
                                    C    __
GAM1545  SUI1     3'  TGACGGTATTGCTTGG      38454      TTG  A
                                TGGC   GG ATTGCTTGG
                                ||||   || |||||||||
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                                ACTG   CC TAACGAACC
                                  ___  A
GAM1545  TAPBP-R   3'  TGGCTTGGTTGTTGTTTGG   38455        GAA   C
                                TGGCTTGG   TTG TTGG
                                ||||||||   ||| ||||
                                ACCGAACC   AAC AACC
                                    AAC   A
GAM1545  TIX1      3'  TGGCTTGGCACTCTGG      38456        GA   G  T
                                TGGCTTGG  ATT CT GG
                                ||||||||  ||| || ||
                                ACCGAACC  TGA GA CC
                                    G_  _ _
GAM1545  TTYH2     3'  TGGCCTGGGACACTGG      38457         AT    T
                                TGGCTTGGGA  TGCT GG
                                ||||||||||  |||| ||
                                ACCGGACCCT  GTGA CC

                                    __   _
GAM1545  UBN1      3'  TGACTTGGGACCCTGG      38458         ATTG
                                TGGCTTGGGA   CTTGG
                                ||||||||||   |||||
                                ACTGAACCCT   GGACC
                                    G___
GAM1545  ZIN       3'  TGGCCTGGAAGCCTTGG     38459         ATTG
                                TGGCTTGGGA   CTTGG
                                ||||||||||   |||||
                                ACCGGACCTT   GAACC
                                    CG__
GAM1545  LOC113230 5'  GGCTTGGGGACCTCGG      38460         A  TG
                                GGCTTGGG AT  CTTGG
                                ||||||||  ||  |||||
                                CCGAACCC TG  GAGCC
                                    C  __
GAM1545  LOC118611 5'  TAGCCAGAGATTGCTTGG    38461       T    A
                                TGGCT GGGA TTGCTTGG
                                ||||| |||| ||||||||
                                ATCGG CTCT AACGAACC
                                   T   _
GAM1545  LOC129526 3'  TGCCTTGGGAAGCCACTGG   38462    G      _ TG  T
                                TG CTTGGGAA T  CT GG
                                || ||||||||  |  || ||
                                AC GAACCCTT G  GA CC
                                 G       C GT  _
GAM1545  LOC134266 3'  GGCAGGATTGCTTGG       38463     TT    A
                                GGC  GGGA TTGCTTGG
                                |||  |||| ||||||||
                                CCG  TCCT AACGAACC
                                  __   _
GAM1545  LOC138515 5'  TGACAGGATTGCTTGG      38464      TT    A
                                TGGC  GGGA TTGCTTGG
                                ||||  |||| ||||||||
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                                ACTG  TCCT AACGAACC
                                  __   _
GAM1545  LOC144563 5'  TGGCTGAGGTTGCTTGG     38465      T   AA
                                TGGCT GGG  TTGCTTGG
                                ||||| |||  ||||||||
                                ACCGA TCC  AACGAACC
                                   C  __
GAM1545  LOC144587 5'  TGGCTCGGGGTTGCCTTGG   38466        AA   _
                                TGGCTTGGG  TTGC TTGG
                                |||||||||  |||| ||||
                                ACCGAGCCC  AACG AACC
                                     C_   G
GAM1545  LOC148171 5'  TGGCTTGAGGAAGCTGTGG   38467       _   TT  _
                                TGGCTTG GGAA  GCT TGG
                                ||||||| ||||  ||| |||
                                ACCGAAC CCTT  CGA ACC
                                    T   __  C
GAM1545  LOC148181 3'  TGGCTTAGGGAAGTTGTGG   38468      _   _  CT
                                TGGCTT GGGAA TTG  TGG
                                |||||| ||||| |||  |||
                                ACCGAA CCCTT AAC  ACC
                                   T    C  __
GAM1545  LOC148397 3'  TGGCTCTGGCTTGCTTGG    38469      G  AA
                                TGGCTT GG  TTGCTTGG
                                |||||| ||  ||||||||
                                ACCGAG CC  AACGAACC
                                   A  G_
GAM1545  LOC148918 5'  TGGCTTGGGTACAGCAGG    38470        A  T  TT
                                TGGCTTGGG AT GC  GG
                                ||||||||| || ||  ||
                                ACCGAACCC TG CG  CC
                                     A  T  T_
GAM1545  LOC148932 3'  GGCTTGGGAACCAGCATGG   38471          _  T
                                GGCTTGGGAATT GC TGG
                                |||||||||||| || |||
                                CCGAACCCTTGG CG ACC
                                       T  T
GAM1545  LOC148936 5'  TGTCTTGGGAATTAGCATTTGG 38472    G       _  __
                                TG CTTGGGAATT GC  TTGG
                                || ||||||||| ||  ||||
                                AC GAACCCTTAA CG  AACC
                                 A        T  TA
GAM1545  LOC148938 5'  TGTCTTGGGAATTAGCATTTGG 38472    G       _  __
                                TG CTTGGGAATT GC  TTGG
                                || ||||||||| ||  ||||
                                AC GAACCCTTAA CG  AACC
                                 A        T  TA
GAM1545  LOC149124 5'  TGGCTTGAGGAAGCTGTGG   38467       _   TT  _
                                TGGCTTG GGAA  GCT TGG
                                ||||||| ||||  ||| |||
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                                ACCGAAC CCTT  CGA ACC
                                    T   __  C
GAM1545  LOC149134 5'  TGGCTTGGGGACAACATGG   38473        A  T  T
                                TGGCTTGGG AT GC TGG
                                ||||||||| || || |||
                                ACCGAACCC TG TG ACC
                                    C  T  T
GAM1545  LOC149650 5'  TGGCTTGGGGGGGACCCGG   38474        AATT
                                TGGCTTGGG   GCTTGG
                                |||||||||   ||||||
                                ACCGAACCC   TGGGCC
                                    CCC_
GAM1545  LOC150481 5'  TGGCCTGGGGAAATGTTGG   38475        _  T  C
                                TGGCTTGGG AA TG TTGG
                                ||||||||| || || ||||
                                ACCGGACCC TT AC AACC
                                    C  T  _
GAM1545  LOC151632 5'  TGGCTGAGGTTGCTTGG     38465      T   AA
                                TGGCT GGG  TTGCTTGG
                                ||||| |||  ||||||||
                                ACCGA TCC  AACGAACC
                                   C  __
GAM1545  LOC152275 3'  TGACTTGGATCAGACTTGG   38476        AATT
                                TGGCTTGGG   GCTTGG
                                |||||||||   ||||||
                                ACTGAACCT   TGAACC
                                    AGTC
GAM1545  LOC155036 5'  GGCTCCTGAAATTGCTTGG   38477      G_
                                GGCTT  GGAATTGCTTGG
                                |||||  ||||||||||||
                                CCGAG  CTTTAACGAACC
                                   GA
GAM1545  LOC155438 3'  TGGCCTGGGGTGCTGG     38478        AAT   T
                                TGGCTTGGG   TGCT GG
                                |||||||||   |||| ||
                                ACCGGACCC   ACGA CC
                                    C__   _
GAM1545  LOC157254 3'  TGTTTGGGAACACGCAGG    38479    GC      _   TT
                                TG  TTGGGAAT TGC  GG
                                ||  |||||||| |||  ||
                                AC  AACCCTTG GCG  CC
                                 A_      T   T_
GAM1545  LOC158125 5'  TGGCCTGGCTGCTTGG     38480        GAA
                                TGGCTTGG   TTGCTTGG
                                ||||||||   ||||||||
                                ACCGGACC   GACGAACC
                                    ___
GAM1545  LOC158191 3'  TGGCCTGGGGAAATGTTGG   38475        _  T  C
                                TGGCTTGGG AA TG TTGG
                                ||||||||| || || ||||
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                                ACCGGACCC TT AC AACC
                                     C  T  _
GAM1545  LOC158814 3'  TGGCTTAGTGATTTTGG     38481        GA   GC
                                TGGCTTGG  ATT  TTGG
                                ||||||||  |||  ||||
                                ACCGAATC  TAA  AACC
                                     AC  __
GAM1545  LOC158927 3'  TGGCTTTGGATCTAATGG    38482       G   A   CT
                                TGGCTT GGA TTG  TGG
                                ||||||| ||| |||  |||
                                ACCGAA CCT GAT  ACC
                                   A   A   T_
GAM1545  LOC200093 5'  GGCTAGGATTGCTTGG      38380      T    A
                                GGCT GGGA TTGCTTGG
                                |||| |||| ||||||||
                                CCGA TCCT AACGAACC
                                  _   _
GAM1545  LOC200904 5'  TGGCTGAGGTTGCTTGG     38465      T   AA
                                TGGCT GGG  TTGCTTGG
                                ||||| |||  ||||||||
                                ACCGA TCC  AACGAACC
                                   C  __
GAM1545  LOC203052 3'  AGCGAGGATTGCTTGG      38483     TT    A
                                GGC  GGGA TTGCTTGG
                                |||  |||| ||||||||
                                TCG  TCCT AACGAACC
                                  C_   _
GAM1545  LOC203232 3'  TGGCCTGGGAAGCGCAGG    38484          T   TT
                                TGGCTTGGGAA TGC  GG
                                |||||||||||| |||  ||
                                ACCGGACCCTT GCG  CC
                                       C   T_
GAM1545  LOC203413 5'  TGGATTTGGGAAACTTTGG   38485     C_      TT   _
                                TGG  TTGGGAA  GCTT GG
                                |||  |||||||  |||| ||
                                ACC  AACCCTT  TGAA CC
                                  TA      __   A
GAM1545  LOC219914 5'  TGGCCTCGATTTGCTTGG    38486       G  AA
                                TGGCTT GG  TTGCTTGG
                                ||||||  ||  ||||||||
                                ACCGGA CT  AACGAACC
                                   G  A_
GAM1545  LOC219919 5'  TGGCTGAGGTTGCTTGG     38465      T   AA
                                TGGCT GGG  TTGCTTGG
                                ||||| |||  ||||||||
                                ACCGA TCC  AACGAACC
                                   C  __
GAM1545  LOC220753 3'  TGGCCTGGGACCACATGG    38487          A TG T
                                TGGCTTGGGA T  C TGG
                                |||||||||| |  | |||
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                                ACCGGACCCT G  G ACC
                                      _ GT T
GAM1545  LOC221491 5'  TGGCCTGGGGGGCATTGG    38488        AATT  _
                                TGGCTTGGG   GC TTGG
                                |||||||||   || ||||
                                ACCGGACCC   CG AACC
                                     CC__  T
GAM1545  LOC221795 5'  TGGCTGAGGTTGCTTGG     38465      T   AA
                                TGGCT GGG  TTGCTTGG
                                ||||| |||  ||||||||
                                ACCGA TCC  AACGAACC
                                   C  __
GAM1545  LOC221876 5'  TGGCCTGGGAACCCGG      38489         ATT
                                TGGCTTGGGA   GCTTGG
                                ||||||||||   ||||||
                                ACCGGACCCT   TGGGCC
                                      ____
GAM1545  LOC222252 5'  TGGCTTAGGATTGACTTGG   38490         A  _
                                TGGCTTGGGA TTG CTTGG
                                |||||||||| ||| |||||
                                ACCGAATCCT AAC GAACC
                                      _  T
GAM1545  LOC256515 5'  TGGCTGAGGTTGCTTGG     38465      T   AA
                                TGGCT GGG  TTGCTTGG
                                ||||| |||  ||||||||
                                ACCGA TCC  AACGAACC
                                   C  __
GAM1545  LOC256594 5'  TGGCTGAGGTTGCTTGG     38465      T   AA
                                TGGCT GGG  TTGCTTGG
                                ||||| |||  ||||||||
                                ACCGA TCC  AACGAACC
                                   C  __
GAM1545  LOC256667 5'  TGGCTTAGGTCGTTTTGG    38491         AA   C_
                                TGGCTTGGG  TTG  TTGG
                                |||||||||  |||  ||||
                                ACCGAATCC  AGC  AACC
                                     __  AA
GAM1545  LOC257101 5'  TGGCTTGGGTCTCTGG      38492         AA  GC
                                TGGCTTGGG  TT  TTGG
                                |||||||||  ||  ||||
                                ACCGAACCC  AG  GACC
                                     __  A_
GAM1545  LOC257354 3'  GGCTTGGGGCTGCTGG      38427         AA    T
                                GGCTTGGG  TTGCT GG
                                ||||||||  ||||| ||
                                CCGAACCC  GACGA CC
                                     C_    _
GAM1545  LOC57086  3'  TGTTTTGGGAATTGTATGG   38493    GC         CT
                                TG  TTGGGAATTG  TGG
                                ||  ||||||||||  |||
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                                AC  AACCCTTAAC  ACC
                                 AA         AT
GAM1545  LOC90141  3'  TGGCTGATTGCTTGG       38494      TGG  A
                                TGGCT   GA TTGCTTGG
                                |||||   || ||||||||
                                ACCGA   CT AACGAACC
                                  ____  _
GAM1545  LOC90342  5'  GGCTTGGCTTGCTTGG      38495       GAA
                                GGCTTGG   TTGCTTGG
                                |||||||   ||||||||
                                CCGAACC   AACGAACC
                                   G__
GAM1545  LOC90632  5'  GGCTTGGGGCACTCTGG     38496        AAT   _
                                GGCTTGGG   TGCT TGG
                                ||||||||   |||| |||
                                CCGAACCC   GTGA ACC
                                    C__    G
GAM1545  LOC90982  5'  GGCTTGGGGTACTTGG      38497        AAT
                                GGCTTGGG   TGCTTGG
                                ||||||||   |||||||
                                CCGAACCC   ATGAACC
                                    C__
GAM1545  LOC91040  5'  GGCTAGGATTGCTTGG      38380     T   A
                                GGCT GGGA TTGCTTGG
                                |||| |||| ||||||||
                                CCGA TCCT AACGAACC
                                  _   _
GAM1545  LOC91301  5'  TGGCCTGGGAGTTAATGG    38498         A   CT
                                TGGCTTGGGA TTG  TGG
                                |||||||||| |||  |||
                                ACCGGACCCT AAT  ACC
                                     C   T_
GAM1545  LOC91974  5'  TGGCTTGGAGAAATTGG     38499        _   TTGC
                                TGGCTTGG GAA    TTGG
                                |||||||| |||    ||||
                                ACCGAACC CTT    AACC
                                    T   T___
GAM1545  LOC93070  3'  TGGCTGGGAATACAGG      38500      T     T  TT
                                TGGCT GGGAAT GC  GG
                                ||||| |||||| ||  ||
                                ACCGA CCCTTA TG  CC
                                  _     _ T_
GAM1545  LOC93259  5'  TGGTTTAGACGCTTGG      38501     C     AAT
                                TGG TTGGG   TGCTTGG
                                ||| |||||   |||||||
                                ACC AATCT   GCGAACC
                                  A    ___
GAM1546  ABCD2     5'  TGAAAATGAGGAGAGAGC    38504         AC   CC
                                TGAAAATGAG  AGA  GT
                                ||||||||||  |||  ||
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                                ACTTTTACTC  TCT  CG
                                      C_   CT
GAM1546  PLAU     3'  TGAAACTGAGACAGTGC     38505      A      GACC
                                TGAAA TGAGACA    GTGT
                                ||||| |||||||    ||||
                                ACTTT ACTCTGT    CACG
                                   G      ____
GAM1546  PUM1     3'  TGGAAATGTACACCGTGTA    38506    A    AG  AG
                                TG AAATG  AC  ACCGTGTA
                                || |||||  ||  ||||||||
                                AC TTTAC  TG  TGGCACAT
                                 C    A_  __
GAM1546  SLC26A4  3'  TGAAAATGAGGCAGCATTATAA 38507          A   ACCG
                                TGAAAATGAG CAG    TGTAA
                                |||||||||| |||    |||||
                                ACTTTTACTC GTC    ATATT
                                      C   GTA_
GAM1546  STAC     3'  TGAAAATGGAGACTTTTTGTG  38508         _    AGACC
                                TGAAAATG AGAC     GTG
                                |||||||| ||||     |||
                                ACTTTTAC TCTG     CAC
                                     C    AAAAA
GAM1546  UBE2V1   3'  GAGACCCCAGGCCGTGTAA    38509       ___  A
                                GAGAC   AG CCGTGTAA
                                |||||   || ||||||||
                                CTCTG   TC GGCACATT
                                   GGG  C
GAM1546  UBE2V1   3'  GAGACCCCAGGCCGTGTAA    38509       ___  A
                                GAGAC   AG CCGTGTAA
                                |||||   || ||||||||
                                CTCTG   TC GGCACATT
                                   GGG  C
GAM1546  UBE2V1   3'  GAGACCCCAGGCCGTGTAA    38509       ___  A
                                GAGAC   AG CCGTGTAA
                                |||||   || ||||||||
                                CTCTG   TC GGCACATT
                                   GGG  C
GAM1546  ZNF42    5'  TGATAATGAGACAGAACC     38510     A        _
                                TGA AATGAGACAGA CC
                                ||| |||||||||| ||
                                ACT TTACTCTGTCT GG
                                  A         T
GAM1546  BS69     5'  TGAAAATGACATATCTGTGTAA 38511         GA   GACC_
                                TGAAAAT  GACA     GTGTAA
                                |||||||  ||||     ||||||
                                ACTTTTA  CTGT     CACATT
                                     __    ATAGA
GAM1546  DKFZp586H0623 3'  TGCAAATGAGACTACAGTTGT  38512    A       AG  CG_
                                TG AAATGAGAC  AC   TGT
                                || |||||||||  ||   |||
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                                AC TTTACTCTG  TG   ACA
                                 G        A_  TCA
GAM1546  DVS27     3'  TGAAAAGAGACAGATGT     38513       T       CCG
                                TGAAAA GAGACAGA   TGT
                                |||||| ||||||||   |||
                                ACTTTT CTCTGTCT   ACA
                                   _       ___
GAM1546  GABARAPL1 3'  TGAAAATGTGATGACGGTGT   38514         A  CA   C
                                TGAAAATG GA  GAC GTGT
                                |||||||| ||  ||| ||||
                                ACTTTTAC CT  CTG CACA
                                     A  A_   C
GAM1546  HAND1     5'  TGAAAATGAGACGCGCA     38515           AGACC
                                TGAAAATGAGAC    GTGTA
                                ||||||||||||    |||||
                                ACTTTTACTCTG    CGCGT
                                      ______
GAM1546  HNRPC     3'  TGAAAATGGGACTAGGCGCG   38516         A  _  AC
                                TGAAAATG GAC AG  CGTG
                                |||||||| ||| ||  ||||
                                ACTTTTAC CTG TC  GCGC
                                     C   A  C_
GAM1546  HT002     3'  TGAAAATGAGCAGGCCTGT    38517          A   A  G
                                TGAAAATGAG CAG CC TGT
                                |||||||||| ||| || |||
                                ACTTTTACTC GTC GG ACA
                                     _   C  _
GAM1546  USP24     3'  TGAAAATAAGGCAGGACCTGTA 38518          A   _   G
              AC                  TGAAAATGAG CAG ACC TGTAAC
                                |||||||||| ||| ||| ||||||
                                ACTTTTATTC GTC TGG ACATTG
                                      C   C   _
GAM1546  LOC164295 5'  GAGAATGAGACAGCATG     38519     A        AC
                                GA AATGAGACAG  CGTG
                                || ||||||||||  ||||
                                CT TTACTCTGTC  GTAC
                                 C         __
GAM1546  LOC256283 3'  TGAAGATGAAACAGGTAT     38520      A        ACC
                                TGAA ATGAGACAG   GTGT
                                |||| |||||||||   ||||
                                ACTT TACTTTGTC   CATA
                                  C        ____
GAM1546  LOC93268  3'  TGAAAATGGGGAGCAGGCTGTA 38521         A_  _   ACCG
              AC                  TGAAAATG  GA CAG    TGTAAC
                                ||||||||  || |||    ||||||
                                ACTTTTAC  CT GTC    ACATTG
                                     CC  C   CG__
GAM1547  ACP2      3'  TCTGAGCTATTTGCC       38524          CCTCAT    A
                                TCTGGGCTA     TTTG CC
                                |||||||||     |||| ||
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                                AGACTCGAT     AAAC GG
                                        _______   _
GAM1547  APOBEC1   3'  TGGGGTACCTTGTGAACATTTC 38525     C    _______
                                TGGG TACCT     CATTTT
                                |||| |||||     ||||||
                                ACCC ATGGA     GTAAAG
                                  C    ACACTT
GAM1547  APOBEC1   3'  TGGGGTACCTTGTGAACATTTC 38525     C    _______
                                TGGG TACCT     CATTTT
                                |||| |||||     ||||||
                                ACCC ATGGA     GTAAAG
                                  C    ACACTT
GAM1547  CYLN2     3'  TCTGAGCTGCCTCTGCCC    38526       A   ATTT  A
                                TCTGGGCT CCTC    TG CCC
                                |||||||| ||||    || |||
                                AGACTCGA GGAG    AC GGG
                                     C   ____  _
GAM1547  DISC1     5'  CCTGGGCTGCCTCCTGCTCC   38527       A   ATT   AC
                                TCTGGGCT CCTC   TTG  CC
                                |||||||| ||||   |||  ||
                                GGACCCGA GGAG   GAC  GG
                                     C    ___   GA
GAM1547  DYRK1A    3'  TCTAGGCTTCTTTTGATCC    38528       ACC  A     C
                                TCTGGGCT   TC TTTTGA CC
                                ||||||||   || |||||| ||
                                AGATCCGA   AG AAAACT GG
                                     ___  _     A
GAM1547  DYRK1A    3'  TCTAGGCTTCTTTTGATCC    38528       ACC  A     C
                                TCTGGGCT   TC TTTTGA CC
                                ||||||||   || |||||| ||
                                AGATCCGA   AG AAAACT GG
                                     ___  _     A
GAM1547  DYRK1A    3'  TCTAGGCTTCTTTTGATCC    38528       ACC  A     C
                                TCTGGGCT   TC TTTTGA CC
                                ||||||||   || |||||| ||
                                AGATCCGA   AG AAAACT GG
                                     ___  _     A
GAM1547  EPB42     5'  TCTGGGCTCCTTCTG       38529       A   CAT
                                TCTGGGCT CCT   TTTG
                                |||||||| |||   ||||
                                AGACCCGA GGA   AGAC
                                     _   ___
GAM1547  FZD7      3'  TCTGGGCTCCAGTTTGGCCCC  38530       A  TCAT   A
                                TCTGGGCT CC    TTTG CCCC
                                |||||||| ||    |||| ||||
                                AGACCCGA GG    AAAC GGGG
                                     _ TC__    C
GAM1547  GPR23     5'  TCTGGGCTGCCGCAGCTT     38531       A  T  T
                                TCTGGGCT CC CA TTT
                                |||||||| || || |||
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                                AGACCCGA GG GT GAA
                                     C  C  C
GAM1547  HOXD4    5'  TGGGTACCTTTGCACC      38532      C     CATT  _
                                TGGG TACCT    TTG ACC
                                |||| |||||    ||| |||
                                ACCC ATGGA    AAC TGG
                                  _    ____  G
GAM1547  KCNA5    3'  TCTGGGCTATTTAGAGTCATTT 38533         CC_____
              T                  TCTGGGCTA      TCATTTT
                                |||||||||      |||||||
                                AGACCCGAT      AGTAAAA
                                     AAATCTC
GAM1547  KLHL3    3'  TCTCGGCTGCTTCTAACC    38534     G   ACCTCA
                                TCT GGCT     TTTTGACC
                                ||| ||||     ||||||||
                                AGA CCGA     AAGATTGG
                                  G   CG____
GAM1547  L1CAM    3'  TCTGGGCTCTCCAGATGGCC   38535        AC   ATTT  A
                                TCTGGGCT  CTC    TG CC
                                ||||||||  |||    || ||
                                AGACCCGA  GAG    AC GG
                                     __   GTCT  C
GAM1547  L1CAM    3'  TCTGGGCTCTCCAGATGGCC   38535        AC   ATTT  A
                                TCTGGGCT  CTC    TG CC
                                ||||||||  |||    || ||
                                AGACCCGA  GAG    AC GG
                                     __   GTCT  C
GAM1547  LNK      3'  TCTGGGCTTCCTGATGATCCC  38536        A   CATTT  _
                                TCTGGGCT CCT    TGA CCC
                                |||||||| |||    ||| |||
                                AGACCCGA GGA    ACT GGG
                                     A   CT___   A
GAM1547  LZTR1    3'  TCTGGGCACCCTGACC      38537        T   CATTT
                                TCTGGGC ACCT    TGACC
                                ||||||| ||||    |||||
                                AGACCCG TGGG    ACTGG
                                  _   ______
GAM1547  NINJ1    3'  TCTGGGCTATTGTGCCAGCCCC 38538         CCTCATT  GA
                                TCTGGGCTA      TT  CCCC
                                |||||||||      ||  ||||
                                AGACCCGAT      GG  GGGG
                                     AACAC__   TC
GAM1547  TNC      3'  TCTGGGCCGCCTTATTCC    38539        TA   C
                                TCTGGGC  CCT ATTTT
                                |||||||  ||| |||||
                                AGACCCG  GGA TAAGG
                                     GC   A
GAM1547  TRIM34   5'  TCTGGGCTCAACTTGACC    38540        TACC   T
                                TCTGGGC    TCA TTTGACC
                                |||||||    ||| |||||||
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                                AGACCCG   AGT GAACTGG
                                    ____  T
GAM1547 VENTX2   3' TCTGGGCACTTCCAGACC   38541       T  C  ATTTT
                                TCTGGGC AC TC   GACC
                                ||||||| || ||   ||||
                                AGACCCG TG AG   CTGG
                                   _ A  GT___
GAM1547 CDV-1    5' TCTGAGCTGTCTCAACCC   38542       AC   TTTTG
                                TCTGGGCT  CTCA   ACCC
                                ||||||||  ||||   ||||
                                AGACTCGA  GAGT   TGGG
                                    CA  _____
GAM1547 DKFZP434P0721 3' TCTGGGCTTCCTTATTCT   38543       A   C
                                TCTGGGCT CCT ATTTT
                                |||||||| ||| |||||
                                AGACCCGA GGA TAAGA
                                    A   A
GAM1547 DKFZp566H0824 5' CCTGGGCTGCCTCGCCACGA   38544       A   A TT
                                TCTGGGCT CCTC T  TGA
                                |||||||| |||| |  |||
                                GGACCCGA GGAG G  GCT
                                    C   C GT
GAM1547 FBXL9    3' TCTGGGCTGCCCTGGATTGGCC 38545       A   CATT   A
          CC                  TCTGGGCT CCT   TTG CCCC
                              |||||||| |||   ||| ||||
                              AGACCCGA GGG   AAC GGGG
                                  C   ACCT   C
GAM1547 FLJ12921 3' TGGGTCTTTATTTTGACC   38546    _ ACCTC
                              TGGG CT   ATTTTGACC
                              |||| ||   |||||||||
                              ACCC GA   TAAAACTGG
                                A  AA___
GAM1547 FLJ14594 3' TCTGGGCTTCTGAGGTCC   38547       ACCTCAT   C__
                              TCTGGGCT     TTTGA   CC
                              ||||||||     |||||   ||
                              AGACCCGA     AGACT   GG
                                  ________   CCA
GAM1547 FLJ20034 3' TCTGGGCTTAGCCTTGGCCC  38548       A__   CATTT  A
                              TCTGGGCT   CCT    TG CCC
                              ||||||||   |||    || |||
                              AGACCCGA   GGA    AC GGG
                                  ATC   _____  C
GAM1547 FLJ20189 3' TCTGAGTTACCTCACCTT   38549      C
                              TCTGGG TACCTCATTTT
                              |||||| ||||||||||
                              AGACTC ATGGAGTGGAA
                                 A
GAM1547 FOXJ1    3' TGGCACCACCTCATTTTG   38550    _
                              TGG GCTACCTCATTTTG
                              ||| ||||||||||||||
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                                ACC TGGTGGAGTAAAAC
                                  G
GAM1547 HSJ1     3' CCTGGGCTGCCGCATGGCC   38551        A  T  TTT  A
                                TCTGGGCT CC CA   TG CC
                                |||||||| || ||   || ||
                                GGACCCGA GG GT   AC GG
                                     C  C  ___  C
GAM1547 KIAA0800 3' TCTGGGCTACCTATCTT     38552           C
                                TCTGGGCTACCT ATTTT
                                |||||||||||| |||||
                                AGACCCGATGGA TAGAA
                                           _
GAM1547 KIAA1110 3' AGCTTCCCTCATTTTGATTCC 38553     A_        CC
                                GGCT  CCTCATTTTGA  CC
                                ||||  ||||||||||  ||
                                TCGA  GGAGTAAAACT  GG
                                  AG         AA
GAM1547 KIAA1229 3' TCTTAATACTCTCATTTTGA   38554     GGGC  _
                                TCT    TAC CTCATTTTGA
                                |||    ||| ||||||||||
                                AGA    ATG GAGTAAAACT
                                  ATT_  A
GAM1547 KIAA1266 3' TCTGGGTTGCCCCTCACTCC   38555       CTA__
                                TCTGGG    CCTCATTTT
                                ||||||    |||||||||
                                AGACCC    GGAGTGAGG
                                    AACGG
GAM1547 KIAA1649 3' TCTGGCTGCCTCACTCC     38556      G  A
                                TCTGG CT CCTCATTTT
                                ||||| || |||||||||
                                AGACC GA GGAGTGAGG
                                   _  C
GAM1547 KIAA1649 5' TCTGGCTGCCTCACTCC     38556      G  A
                                TCTGG CT CCTCATTTT
                                ||||| || |||||||||
                                AGACC GA GGAGTGAGG
                                   _  C
GAM1547 KIAA1940 3' TCTGAGCTGCCTTGTGGAGCCC 38557        A   CATTTT  _
             C                   TCTGGGCT CCT     GA CCCC
                                ||||||||| |||     || ||||
                                AGACTCGA GGA     CT GGGG
                                     C   ACAC__  C
GAM1547 MGC11296 5' TCTGAGCTATCTCCATCCT   38558        C  _
                                TCTGGGCTA CTC ATTTT
                                ||||||||| ||| |||||
                                AGACTCGAT GAG TAGGA
                                      A  G
GAM1547 NEU4     3' CCTGGGCTACCTGCGGTCCC   38559          CATTTTGA
                                TCTGGGCTACCT       CCC
                                ||||||||||||       |||
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                                GGACCCGATGGA      GGG
                                      CGCCA___
GAM1547 NYD-SP11 3' GGCTATGCTTTTTGACCCC  38560     CCTCA
                                GGCTA    TTTTGACCCC
                                |||||    ||||||||||
                                CCGAT    AAAACTGGGG
                                  ACGA_
GAM1547 POPX1    3' TCTGGGCTCACTTTAGAC    38561      TACC     _
                                TCTGGGC   TCATTTT GAC
                                |||||||   ||||||| |||
                                AGACCCG   AGTGAAA CTG
                                    ____      T
GAM1547 SCYD1    3' TCTGAGCTGCCAGAGTGACCCC 38562       A  TCATTT
                                TCTGGGCT CC     TGACCCC
                                |||||||| ||     |||||||
                                AGACTCGA GG     ACTGGGG
                                     C  TCTC__
GAM1547 SMOC2    5' TCCGGGCTGTCTCTGTGCC   38563       AC   ATTT  A
                                TCTGGGCT  CTC    TG CC
                                |||||||  |||    || ||
                                AGGCCCGA  GAG    AC GG
                                     CA   AC__  _
GAM1547 SNAP29   3' TCTGGGCTTTTTGCC      38564       ACCTCA    A
                                TCTGGGCT     TTTTG CC
                                |||||||      ||||| ||
                                AGACCCGA     AAAAC GG
                                     _______    _
GAM1547 SRCRB4D  5' TCTGGGCTCTTTCTGTCCC   38565       ACCTCA    A
                                TCTGGGCT     TTTTG CCC
                                |||||||      ||||| |||
                                AGACCCGA     AAGAC GGG
                                     GA____     A
GAM1547 LOC120526 3' TCTTCAACCTCATTTTGA   38566    GGGCT
                                TCT    ACCTCATTTTGA
                                |||    ||||||||||||
                                AGA    TGGAGTAAAACT
                                  AGT__
GAM1547 LOC123242 3' CCTGGGCTACCTCCAGCTGGTC 38567          ATT   AC
          CC                      TCTGGGCTACCTC   TTG  CCC
                                |||||||||||||   |||  |||
                                GGACCCGATGGAG   GAC  GGG
                                      GTC   CA
GAM1547 LOC126364 5' TCTAGGCTGTCTGACC     38568       ACCTCAT    _
                                TCTGGGCT      TTTGAC C
                                ||||||||      |||||| |
                                AGATCCGA      AGACTG G
                                     C_______     A
GAM1547 LOC138389 5' CCTGGGTTACTTCATCC    38569      C   C    TTTGA
                                TCTGGG TAC TCAT    CC
                                |||||| ||| ||||    ||
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                                GGACCC ATG AGTA     GG
                                   A   A   _____
GAM1547  LOC147136 3'  TCTGGGCTGCCCTGCC      38570        A   CATTT  A
                                TCTGGGCT CCT     TG CC
                                |||||||| |||     || ||
                                AGACCCGA GGG     AC GG
                                    C   _____  _
GAM1547  LOC148223 3'  TCTGGGCCGCCTTGCCC     38571        TA   CATTT  A
                                TCTGGGC  CCT     TG CCC
                                |||||||  |||     || |||
                                AGACCCG  GGA     AC GGG
                                    GC   _____  _
GAM1547  LOC149127 5'  TCTGGCTTACATTTTGAC     38572       G  ACCT
                                TCTGG CT    CATTTTGAC
                                ||||| ||    |||||||||
                                AGACC GA    GTAAAACTG
                                   _  AT__
GAM1547  LOC149722 5'  TCTGGGTACCTCATTCT      38573       C
                                TCTGGG TACCTCATTTT
                                |||||| ||||||||||
                                AGACCC ATGGAGTAAGA
                                   _
GAM1547  LOC150630 5'  TCTGGGCTCATCTCACAGCCGC 38574         AC_    T_   A
            CCC                    TCTGGGCT   CTCAT  TTG CCCC
                                |||||||   |||||  ||| ||||
                                AGACCCGA   GAGTG  GGC GGGG
                                    GTA     TC   _
GAM1547  LOC151996 5'  TCTGGGCTCACTTCCTGTTG   38575         _  C  ATT
                                TCTGGGCT AC TC   TTG
                                |||||||| || ||   |||
                                AGACCCGA TG AG   AAC
                                    G  A  GAC
GAM1547  LOC153453 5'  TCTGGCTTTCATTTTG      38576       G  ACC
                                TCTGG CT   TCATTTTG
                                ||||| ||   ||||||||
                                AGACC GA   AGTAAAAC
                                   _  A__
GAM1547  LOC157695 5'  TCCGGGCTATCTGTCAGGTGGC 38577         C  CATTT_  A
            C                    TCTGGGCTA CT     TG CC
                                |||||||||  ||     || ||
                                AGGCCCGAT GA     AC GG
                                    A  CAGTCC  C
GAM1547  LOC158226 3'  TCTGGGCATCACTTTGA     38578        TACC
                                TCTGGGC    TCATTTTGA
                                |||||||    |||||||||
                                AGACCCG    AGTGAAACT
                                    T___
GAM1547  LOC196074 3'  TCTGAGCTGTCTTCAGTCCC   38579         ACC  A   TGA
                                TCTGGGCT   TC TTT   CCC
                                ||||||||   || |||   |||
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                                AGACTCGA  AG AAG  GGG
                                   C__  _  TCA
GAM1547  LOC200488 5'  TCTGGGCTCCTTTTG     38580       A  CAT
                                TCTGGGCT CCT  TTTG
                                |||||||| |||  ||||
                                AGACCCGA GGA  AAAC
                                   _  ___
GAM1547  LOC221300 3'  TCTGGGCTGCCTTGTAGGCCGC 38581       A  CATT__  A
            CC                   TCTGGGCT CCT    TTG CCC
                                |||||||| |||    ||| |||
                                AGACCCGA GGA    GGC GGG
                                   C  ACATCC  _
GAM1547  LOC221496 3'  TCTGGGCTATCACCCTG    38582       CC
                                TCTGGGCTA  TCATTTTG
                                |||||||||  ||||||||
                                AGACCCGAT  AGTGGGAC
                                   __
GAM1547  LOC253001 3'  CCTGGGCTACCTCCAGCTGGTC 38567          ATT  AC
            CC                   TCTGGGCTACCTC  TTG  CCC
                                ||||||||||||  |||  |||
                                GGACCCGATGGAG  GAC  GGG
                                      GTC  CA
GAM1547  LOC253650 3'  TCTGAGCTGCCTCCTGGCCCC  38583       A  ATT  A
                                TCTGGGCT CCTC  TTG CCCC
                                |||||||| ||||  ||| ||||
                                AGACTCGA GGAG  GAC GGGG
                                   C  ___  C
GAM1547  LOC255520 5'  TCTGGGCGTCTCTGCGCCGACC 38584       TAC  ATT_
            CC                   TCTGGGC  CTC  TTGACCCC
                                |||||||  |||  ||||||||
                                AGACCCG  GAG  GGCTGGGG
                                   CA_  ACGC
GAM1547  LOC51231  5'  TCTGGGCTTCTGCAGCCTGACC 38585       AC  _  T
            C                    TCTGGGCT  CT CA TTTGACCC
                                ||||||||  || || ||||||||
                                AGACCCGA  GA GT GGACTGGG
                                   A_  C  C
GAM1547  LOC91496  5'  TGGGTTACTCTGACCC     38586     C  CTCAT
                                TGGG TAC    TTTGACCC
                                |||| |||    ||||||||
                                ACCC ATG    AGACTGGG
                                  A  _____
GAM1547  LOC91516  5'  TCTGAGCTGCCTTTCAGCCC  38587       A  CAT  GA
                                TCTGGGCT CCT  TTT  CCC
                                |||||||| |||  |||  |||
                                AGACTCGA GGA  AAG  GGG
                                   C  ___  TC
GAM1547  LOC91523  5'  CTGGGTGTAGCTTATTTTGAC  38588     C_  C  C
                                CTGGG  TA CT ATTTTGAC
                                |||||  || || ||||||||
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                                GACCC  AT GA TAAAACTG
                                  AC  C  A
GAM1547 LOC91812 5' TCTGGGCTTCTCGCC      38589       ACCTCA    A
                                TCTGGGCT     TTTTG CC
                                ||||||||     ||||| ||
                                AGACCCGA     AGAGC GG
                                  _______    _
GAM1547 LOC91813 5' TCTGGGCTTCTCGCC      38589       ACCTCA    A
                                TCTGGGCT     TTTTG CC
                                ||||||||     ||||| ||
                                AGACCCGA     AGAGC GG
                                  _______    _
GAM1548 ARNT2    3' GGACAGGGCCACACATTTTGG 38592       AA   GC
                                GGACAGG  TCG  CATTTTGG
                                |||||||  |||  ||||||||
                                CCTGTCC  GGT  GTAAAACC
                                   C_   GT
GAM1548 TNNC1    3' GGAGGGAGTCGGGGGATTTGG 38593     CA   A    CCAT
                                GGA  GGA TCGG    TTTGG
                                |||  ||| ||||    |||||
                                CCT  CCT AGCC    AAACC
                                  C_   C    CCCT
GAM1548 DKFZP564D172 3' AGACAGTTCGAAGTCATTTTGG 38594       GAATC  C
                                GGACAG     GG CATTTTGG
                                ||||||     || ||||||||
                                TCTGTC     TC GTAAAACC
                                   AAGCT  A
GAM1548 HPRP8BP  3' GGACAGAAGTGGTTTTTGG   38595       ATC  CCA
                                GGACAGGA   GG   TTTTGG
                                ||||||||   ||   ||||||
                                CCTGTCTT   CC   AAAACC
                                    CA_  A__
GAM1548 KIAA0564 3' GGATAGGAGCATTTTG     38596     C   ATCG  C
                                GGA AGGA    GC ATTTTG
                                ||| ||||    || ||||||
                                CCT TCCT    CG TAAAAC
                                  A   _____  _
GAM1548 KIAA0828 3' CAGGATGGGAAGGTTTTG    38597      CA   TC  CCA
                                TAGGA  GGAA  GG   TTTTG
                                |||||  ||||  ||   |||||
                                GTCCT  CCTT  CC   AAAAC
                                   AC    __  ____
GAM1548 MGC12921 3' TAGGTTGGGGGCATTTTG    38598     ACA  AATC   C
                                TAGG   GG    GGC ATTTTG
                                ||||   ||    ||| ||||||
                                ATCC   CC    CCG TAAAAC
                                  AA_  C___   _
GAM1548 MGC3248  3' TAGGACAGCTAAGGTCATTTTG 38599        GAATC  C
            G                    TAGGACAG    GG CATTTTGG
                                ||||||||    || ||||||||
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                                ATCCTGTC    CC GTAAAACC
                                    GATT_  A
GAM1548  TBLR1    3'  GGTCAGGGACAGTCATTTTGG  38600    A   AAT   C
                                GG CAGG   CGG CATTTTGG
                                || ||||   ||| ||||||||
                                CC GTCC   GTC GTAAAACC
                                 A   CT_  A
GAM1548  LOC147178 3'  GGGGAGGAATCAGCTTTGG   38601    AC       CAT
                                GG  AGGAATCGGC   TTTGG
                                ||  ||||||||||   |||||
                                CC  TCCTTAGTCG   AAACC
                                 CC        ___
GAM1548  LOC150280 3'  AGGCAGGGCACATTTTG     38602    A   AATCG  _
                                AGG CAGG    GC CATTTTG
                                ||| ||||    || |||||||
                                TCC GTCC    CG GTAAAAC
                                 _   _____  T
GAM1549  FANCE    3'  TTGATGAGGAGTGTGCCTGG   38605       CTA  CCA
                                TTGATGGGG   TG   CCTGG
                                |||||||||   ||   |||||
                                AACTACTCC   AC   GGACC
                                     TC_  AC_
GAM1549  GCK      3'  TGATGGGGTTGTCCCTTGG    38606       CTA  _  ACC
                                TGATGGGG   TG CC   TGG
                                ||||||||   || ||   |||
                                ACTACCCC   AC GG   ACC
                                    A__  A  GA_
GAM1549  GCK      3'  TGATGGGGTTGTCCCTTGG    38606       CTA  _  ACC
                                TGATGGGG   TG CC   TGG
                                ||||||||   || ||   |||
                                ACTACCCC   AC GG   ACC
                                    A__  A  GA_
GAM1549  GCK      3'  TGATGGGGTTGTCCCTTGG    38606       CTA  _  ACC
                                TGATGGGG   TG CC   TGG
                                ||||||||   || ||   |||
                                ACTACCCC   AC GG   ACC
                                    A__  A  GA_
GAM1549  ITGA11   3'  TCGGTGGGGCCACAGGCCTGG  38607     A       CCA
                                TTG TGGGGCTATG   CCTGG
                                ||| ||||||||||   |||||
                                AGC ACCCCGGTGT   GGACC
                                  C        CC_
GAM1549  MGAT5    5'  TGGTGGGGCTGTTCCAGCCTGG 38608    A     ATG  _
                                TG TGGGGCT   CCA CCTGG
                                || |||||||   ||| |||||
                                AC ACCCCGA   GGT GGACC
                                 C      CAA  C
GAM1549  NR5A2    3'  TTGGTGGAGCTACCACTGG   38609    A     AT    C
                                TTG TGGGGCT  GCCAC TGG
                                ||| |||||||  ||||| |||
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                                AAC ACCTCGA  TGGTG ACC
                                  C      __    _
GAM1549 SALL2    3' CTGGTGGGGCCAGGCTTGG   38610    A      T  CACC
                                TTG TGGGGCTA GC    TGG
                                ||| |||||||| ||    |||
                                GAC ACCCCGGT CG    ACC
                                  C       C  A___
GAM1549 SON      3' TTAATGGGGTTGTTTTGACACT 38611         CTA___  C   C
             TGG                   TTGATGGGG     TG CAC TGG
                                |||||||||     || ||| |||
                                AATTACCCC     AC GTG ACC
                                     AACAAA  T   A
GAM1549 A        5' TTGATGGGGCAGGCAAGCTGG  38612         TAT  CAC
                                TTGATGGGGC   GC   CTGG
                                ||||||||||   ||   ||||
                                AACTACCCCG   CG   GACC
                                      TC_  TTC
GAM1549 A        5' TTGATGGGGCAGGCAAGCTGG  38612         TAT  CAC
                                TTGATGGGGC   GC   CTGG
                                ||||||||||   ||   ||||
                                AACTACCCCG   CG   GACC
                                      TC_  TTC
GAM1549 C20orf139 5'  TCGATGGGGGGCACGCTGTCTG 38613         C_    CAC
             G                   TTGATGGGG  TATGC   CTGG
                                |||||||||  |||||   ||||
                                AGCTACCCC  GTGCG   GACC
                                     CC    ACA
GAM1549 DKFZp761G2113 3'  TTGCCAGGCTATGCCACCTGG  38614     ATG
                                TTG   GGGCTATGCCACCTGG
                                |||   ||||||||||||||||
                                AAC   TCCGATACGGTGGACC
                                  GG_
GAM1549 DKFZp762E1511 3'  CTGGTGGGGCTGTGGATTGG   38615     A      A  CCACC
                                TTG TGGGGCT TG     TGG
                                ||| ||||||| ||     |||
                                GAC ACCCCGA AC     ACC
                                  C      C  CTA__
GAM1549 DOCK3    3'  TTCATGGGGCTGTGCCGGTGG  38616    G      A    ACC
                                TT ATGGGGCT TGCC   TGG
                                || |||||||| ||||   |||
                                AA TACCCCGA ACGG   ACC
                                  G      C    CC_
GAM1549 FLJ13449 3'  TTGATGGGCTGGCACTG     38617        G  AT  CAC
                                TTGATGGG CT  GC   CTG
                                |||||||| ||  ||   |||
                                AACTACCC GA  CG   GAC
                                     _ C_  T__
GAM1549 FREQ     3'  TTGATGGGATTGCCTG      38618         CTA    ACC
                                TTGATGGGG   TGCC   TG
                                |||||||||   ||||   ||
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                                AACTACCCT  ACGG  AC
                                    A__  ____
GAM1549 KIAA0680 3' TTGTTGGAGCCATCTG     38619    A      GCCAC
                                TTG TGGGGCTAT    CTG
                                ||| |||||||||    |||
                                AAC ACCTCGGTA    GAC
                                  A      ______
GAM1549 KIAA1203 3' CTGATGGGGCTGTGATGTGCTG 38620         A  CCAC_
             G                   TTGATGGGGCT TG    CTGG
                                ||||||||||| ||    ||||
                                GACTACCCCGA AC    GACC
                                      C  TACAC
GAM1549 KIAA1243 3' TGAAGAAAGCTATGCTGCCTGG 38621    T_       CA
                                TGA  GGGGCTATGC  CCTGG
                                |||  ||||||||||  |||||
                                ACT  TTTCGATACG  GGACC
                                  TC        AC
GAM1549 KIAA1706 3' CTGGTGGGGTACGCGCCTGG   38622    A    C    CA
                                TTG TGGGG TATGC  CCTGG
                                ||| ||||| |||||  |||||
                                GAC ACCCC ATGCG  GGACC
                                  C    _    C_
GAM1549 KIAA1870 5' TTGTGGGGCTAGTCCTTTGG   38623    A      TG  ACC
                                TTG TGGGGCTA  CC   TGG
                                ||| ||||||||  ||   |||
                                AAC ACCCCGAT  GG   ACC
                                  _      CA  AA_
GAM1549 OSBPL6   5' TTGCTGGGGCTATCTG     38624    A      GCCAC
                                TTG TGGGGCTAT    CTG
                                ||| |||||||||    |||
                                AAC ACCCCGATA    GAC
                                  G      ______
GAM1549 SUPT4H1  3' TTGATGGGGTTACTGAGCCTCT 38625        C  ___  AC
             GG                   TTGATGGGG TAT   GCC  CTGG
                                ||||||||| |||   |||  ||||
                                AACTACCCC ATG   CGG  GACC
                                      A   ACT   A_
GAM1549 LOC142955 3' ATGTGATTGTGCCACCTGG   38626    _  GCTA
                                ATG GG    TGCCACCTGG
                                ||| ||    ||||||||||
                                TAC CT    ACGGTGGACC
                                  A  AAC_
GAM1549 LOC146795 5' ATGGGGCTGCCTCTGG     38627       AT   AC
                                ATGGGGCT  GCC  CTGG
                                ||||||||  |||  ||||
                                TACCCCGA  CGG  GACC
                                     __   A_
GAM1549 LOC151871 3' GATGGGGCTGTGTCACTAG   38628        A  C   C
                                GATGGGGCT TG CAC TGG
                                ||||||||| || ||| |||
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                                CTACCCCGA AC GTG ATC
                                     C  A  _
GAM1549  LOC158490 3'  TGATGGCAGTAGTGCCACCTGG 38629      _  CTA
                                TGATGG GG   TGCCACCTGG
                                |||||| ||   ||||||||||
                                ACTACC TC   ACGGTGGACC
                                   G  ATC
GAM1549  LOC164582 5'  CTGATGGGGCACCAGATCTGG  38630        TAT   C__
                                TTGATGGGGC   GCCA   CTGG
                                ||||||||||   ||||   ||||
                                GACTACCCCG   TGGT   GACC
                                     ___   CTA
GAM1549  LOC197414 3'  CTGATGGGGCTGCTTCTGG   38631         AT  CAC
                                TTGATGGGGCT  GC   CTGG
                                ||||||||||  ||   ||||
                                GACTACCCCGA  CG   GACC
                                     __  AA_
GAM1549  LOC253187 5'  TTGATGGGCTGGCTCCTGG   38632       G  AT  CA
                                TTGATGGG CT  GC  CCTGG
                                |||||||| ||  ||  |||||
                                AACTACCC GA  CG  GGACC
                                    _ C_  A_
GAM1549  LOC91049  5'  TTGATGAGGCTGTGCTGTGG  38633         A   CACC
                                TTGATGGGGCT TGC   TGG
                                |||||||||| |||   |||
                                AACTACTCCGA ACG   ACC
                                     C   AC__
GAM1549  LOC92336  3'  CTGATGGGGCTGCCTTTTGCCA 38634       A_____       III
            CCTGGC                 TGGGGCT    TGCCACCTGG  C
                                |||||||    ||||||||||  |
                                ACCCCGA    ACGGTGGACC  G
                                   CGGAAA       III
GAM1550  SCN1A    3'  TATGTTATCCACTTAAAATGTA 38637      _     AATT
                                TATGT ATCCACT   GATGTA
                                ||||| |||||||   ||||||
                                ATACA TAGGTGA   TTACAT
                                   A     ATT_
GAM1550  FLJ20281  3'  TATATGTATTTACGTGACGC  38638       CC  TAAT
                                TATATGTAT  AC   TGATGT
                                |||||||||  ||   ||||||
                                ATATACATA  TG   ACTGCG
                                     AA  C___
GAM1550  FLJ20445  3'  ATATGTGTCCATTTAATGTA  38639      A   CTAA
                                ATATGT TCCA   TTGATGTA
                                |||||| ||||   ||||||||
                                TATACA AGGT   AATTACAT
                                   C   A___
GAM1550  LOC153642 3'  TATATGTATCTCTAGAACACTA 38640        ________
                                TATATGTATC     CACTA
                                ||||||||||     |||||
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                                ATATACATAG      GTGAT
                                     AGATCTT
GAM1550  LOC219401 3'  TATGTGTATCCTTTGATGTA   38641     A      ACTAA
                                TAT TGTATCC    TTGATGTA
                                ||| |||||||    ||||||||
                                ATA ACATAGG    AACTACAT
                                  C      A____
GAM1551  BMPR1A    3'  TTGGCGAATCTTGGTCAGATAT 38644      TA    CCA  T
           T                     TTGG  AATC   GT CGGGTATT
                                ||||  ||||   || ||||||||
                                AACC  TTAG   CA GTCTATAA
                                  GC    AAC  _
GAM1551  C8orf13   3'  TTGGGAATCCCAGTTCA     38645      TA
                                TTGG  AATCCCAGTTCG
                                ||||  ||||||||||||
                                AACC  TTAGGGTCAAGT
                                  C_
GAM1551  HSU15552  3'  TTGGTAAATCTTAATTGCGAA  38646          CC   _
                                TTGGTAAATC  AGTT CGGG
                                ||||||||||  |||| ||||
                                AACCATTTAG  TTAA GCTT
                                     AA    C
GAM1551  KIAA0416  3'  TTGGTAAATTTTAGCTCG    38647         CCC
                                TTGGTAAAT   AGTTCG
                                |||||||||   ||||||
                                AACCATTTA   TCGAGC
                                     AAA
GAM1551  T54       3'  TTGGTAAATATTGGGT      38648         CCCA   C
                                TTGGTAAAT    GTT GGGT
                                |||||||||    ||| ||||
                                AACCATTTA    TAA CCCA
                                     ____   _
GAM1552  GDF10     3'  TAAACAGAGTTCTTTCCGT    38651        AAA
                                TAAACA   TTTTTTCCGT
                                ||||||   ||||||||||
                                ATTTGT   AAGAAAGGCA
                                   CTC
GAM1552  KLF12     3'  TCTAAGAAAGTTTTTTTCCCCT 38652       ACAAAA       G
           GG                     TCTAA     TTTTTTCC TTGG
                                |||||      |||||||| ||||
                                AGATT      AAAAAAGG GACC
                                   CTTTCA       G
GAM1552  MYLE      3'  CAAACAGGAACCTCTCTGTTGG 38653       AAAT     C
                                TAAACA    TTTTTC GTTGG
                                ||||||    |||||| |||||
                                GTTTGT    GGAGAG CAACC
                                   CCTT     A
GAM1553  FLJ10379  3'  TTGGAAAATATTTCTGATATT  38656      CC   C  C
                                TTGG  AAT AT TCTGATATT
                                ||||  ||| || |||||||||
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                                AACC  TTA TA AGACTATAA
                                  TT   _  A
GAM1553  FLJ21324  5'  TATTGACCAGTCATCTAAAC   38657        A     CT
                                TATTGGCCA TCATCT  GAT
                                ||||||||| ||||||  |||
                                ATAACTGGT AGTAGA  TTG
                                     C     T_
GAM1553  PEG10     3'  TATTGGCCAGTCCTTGAT    38658        ATCA  TC
                                TATTGGCCA   TC  TGAT
                                |||||||||   ||  ||||
                                ATAACCGGT   AG  ACTA
                                     C___  GA
GAM1553  VANGL1    3'  TACTGGTCAATCATCTGCCA   38659       C       _
                                TATTGG CAATCATCT CTG
                                |||||| ||||||||| |||
                                ATGACC GTTAGTAGA GGT
                                   A       C
GAM1553  LOC145739 3'  TATTGAATCTCTGAT       38660       CCAATC
                                TATTGG     ATCTCTGAT
                                ||||||     |||||||||
                                ATAACT     TAGAGACTA
                                  _______
GAM1553  LOC200310 3'  TACTGGCCAGTCGTCTAAAC   38661         A  A   CT
                                TATTGGCCA TC TCT  GAT
                                ||||||||| || |||  |||
                                ATGACCGGT AG AGA  TTG
                                     C  C   T_
GAM1554  CYBA      3'  TATTGCAGGTGGGTGCACCTG  38664       TA      TG A
                                TATTGC  GTGGGTG  C CTG
                                ||||||  |||||||  | |||
                                ATAACG  CACCCAC  G GAC
                                   TC      GT _
GAM1554  FGFR2     3'  TGCTCTGTAAGTGTGTGCTGAC 38665      A_       CA
                                TGCT  GTGGGTGTG  CTGAC
                                ||||  |||||||||  |||||
                                ACGA  CATTCACAC  GACTG
                                  GA        AC
GAM1554  FGFR2     3'  TGCTCTGTAAGTGTGTGCTGAC 38665      A_       CA
                                TGCT  GTGGGTGTG  CTGAC
                                ||||  |||||||||  |||||
                                ACGA  CATTCACAC  GACTG
                                  GA        AC
GAM1554  FGFR2     3'  TGCTCTGTAAGTGTGTGCTGAC 38665      A_       CA
                                TGCT  GTGGGTGTG  CTGAC
                                ||||  |||||||||  |||||
                                ACGA  CATTCACAC  GACTG
                                  GA        AC
GAM1554  FGFR2     3'  TGCTCTGTAAGTGTGTGCTGAC 38665      A_       CA
                                TGCT  GTGGGTGTG  CTGAC
                                ||||  |||||||||  |||||
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                                ACGA  CATTCACAC  GACTG
                                  GA        AC
GAM1554  FGFR2    3'  TGCTCTGTAAGTGTGTGCTGAC 38665      A_        CA
                                TGCT  GTGGGTGTG  CTGAC
                                ||||  |||||||||  |||||
                                ACGA  CATTCACAC  GACTG
                                  GA        AC
GAM1554  FGFR2    3'  TGCTCTGTAAGTGTGTGCTGAC 38665      A_        CA
                                TGCT  GTGGGTGTG  CTGAC
                                ||||  |||||||||  |||||
                                ACGA  CATTCACAC  GACTG
                                  GA        AC
GAM1554  SCG3     3'  TATTGCTAGCTACAGAGCGCTG 38666          GGGTGT  A
             A                   TATTGCTAGT     GC CTGA
                                ||||||||||      || ||||
                                ATAACGATCG     CG GACT
                                      ATGTCT  C
GAM1554  BDG-29   3'  TATTGCGAGTGTTGAGTGT    38667       T   ___
                                TATTGC AGTG   GGTGT
                                |||||| ||||   |||||
                                ATAACG TCAC   TCACA
                                   C    AAC
GAM1554  C20orf108 3'  TGTTAGTGGAGATAACTGAC   38668    C     GT   C
                                TG TAGTGG  GTG ACTGAC
                                || ||||||  ||| ||||||
                                AC ATCACC  TAT TGACTG
                                 A     TC  _
GAM1554  KIAA1058  3'  TGCTAGTGGGCCAGCATTGAC  38669          GT   C
                                TGCTAGTGGGT  GCA TGAC
                                ||||||||||  ||| ||||
                                ACGATCACCCG  CGT ACTG
                                      GT   A
GAM1554  LOC145195 3'  TATTGCTGTGTCCCCACTG    38670        A   GGTGTG
                                TATTGCT GTG     CACTG
                                ||||||| |||     |||||
                                ATAACGA CAC     GTGAC
                                   _  AGGG__
GAM1554  LOC91947  3'  TATTTTTGGTGAACATGCTGA  38671     GCTA   GG    AC
                                TATT   GTG  TGTGC  TGA
                                ||||   |||  |||||  |||
                                ATAA   CAC  GTACG  ACT
                                  AAAC   TT    __
GAM1555  AMPD3    3'  TCCTAGTTCGGAATCTTG    38674     C      G
                                TCC AGTTCGG AATTTTG
                                ||| ||||||| |||||||
                                AGG TCAAGCC TTAGAAC
                                 A      _
GAM1555  C12orf22  3'  GTAAATCCTGGAGATTTT    38675        CAGTTC  GA
                                GTAAATCC     GG  ATTTT
                                ||||||||     ||  |||||
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                                CATTTAGG     CC  TAAAA
                                   A_____  TC
GAM1555  MGC3101   3'  AAATCAAGGTGGGAATTTTG  38676      CCA  TC
                                AAATC   GT  GGGAATTTTG
                                |||||   ||  ||||||||||
                                TTTAG   CA  CCCTTAAAAC
                                  TTC  __
GAM1555  LOC149013 3'  AAATCCCTGAGGAATTTT    38677       AGTTC
                                AAATCCC    GGGAATTTT
                                |||||||    |||||||||
                                TTTAGGG    TCCTTAAAA
                                   AC___
GAM1555  LOC149317 3'  AAATCCCTGAGGAATTTT    38677       AGTTC
                                AAATCCC    GGGAATTTT
                                |||||||    |||||||||
                                TTTAGGG    TCCTTAAAA
                                   AC___
GAM1555  LOC151040 3'  TAGATCCCTGAGGAATTTTG  38678    A    AGTTC
                                TA ATCCC    GGGAATTTTG
                                || |||||    ||||||||||
                                AT TAGGG    TCCTTAAAAC
                                 C    AC___
GAM1555  LOC257031 3'  AAATCCCTGAGGAATTTT    38677       AGTTC
                                AAATCCC    GGGAATTTT
                                |||||||    |||||||||
                                TTTAGGG    TCCTTAAAA
                                   AC___
GAM1556  ADSL      3'  AGGAAAGCACCATGGGAAGAA  38681       A   AAGAATA
                                GGGAAA CAT      GGAAGAA
                                |||||| |||      |||||||
                                TCCTTT GTG      CCTTCTT
                                   C   GTAC___
GAM1556  ATP6V1G2  3'  GGGAAATAGGAAAGGAGGAA   38682      AAC   A   T   A
                                GGGAA   ATA GAA AGGA GAA
                                |||||   ||| ||| |||| |||
                                CCCTT   TAT CTT TCCT CTT
                                   ___   C   _    C
GAM1556  ATP6V1G2  3'  GGGAAATAGGAAAGGAGGAA   38682      AAC   A   T   A
                                GGGAA   ATA GAA AGGA GAA
                                |||||   ||| ||| |||| |||
                                CCCTT   TAT CTT TCCT CTT
                                   ___   C   _    C
GAM1556  BLTR2     5'  GGGTAAGACAAGAATGGGGAG  38683     AAAAC       A  A
                                GGG     ATAAGAAT GG AG
                                |||     |||||||| || ||
                                CCC     TGTTCTTA CC TC
                                  ATTC_       C  C
GAM1556  CARD4     3'  GGGAAAGTGCTGAGAAGGAAGA 38684       ACATAA  AT
            A                   GGGAAA     GA  AGGAAGAA
                                ||||||     ||  ||||||||
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                                CCCTTT     CT  TCCTTCTT
                                   CACGA_  CT
GAM1556  CARKL    3'  GGGAAAACTTGGGAACTGTTTG 38685        ATAA    AG___
             AAGAA                 GGGAAAAC    GAAT     GAAGAA
                                ||||||||    ||||    ||||||
                                CCCTTTTG    CTTG    CTTCTT
                                     AACC    ACAAA
GAM1556  CD3G     3'  GGGAACTGAATAGGAGGA    38686      AACATAA      A
                                GGGAA      GAATAGGA GA
                                |||||      |||||||| ||
                                CCCTT      CTTATCCT CT
                                   GA_____       C
GAM1556  CD83     3'  GGAAAACATGAGAAATGGA    38687         A    TA
                                GGAAAACAT AGAA  GGA
                                |||||||| ||||  |||
                                CCTTTTGTA TCTT  CCT
                                     C    TA
GAM1556  GNB3     3'  GAGAAAGCATGAATAAGAAGA  38688       A   AA
                                GGGAAA CAT  GAATAGGAAGA
                                |||||| |||  ||||||||||
                                CTCTTT GTA  CTTATTCTTCT
                                   C   __
GAM1556  GRINL1A  3'  GGGAAGACAGAAAAAGGAGAA  38689      A  T   AT   A
                                GGGAA ACA AAGA  AGGA GAA
                                ||||| ||| ||||  |||| |||
                                CCCTT TGT TTTT  TCCT CTT
                                   C  C   __   _
GAM1556  KLHL3    3'  GGGAAAGCACAAGAAAAAGAA  38690       A       T
                                GGGAAA CATAAGAA AGGAA
                                |||||| |||||||| |||||
                                CCCTTT GTGTTCTT TTCTT
                                   C       T
GAM1556  LOH11CR2A 5'  GGAAAGCATGCCTCATAGGAAG 38691       A   AAGA_
             A                    GGAAA CAT     ATAGGAAGA
                                |||||  |||    |||||||||
                                CCTTT GTA     TATCCTTCT
                                   C   CGGAG
GAM1556  MAML1    3'  GGGAGACATAATACTCCAGGA  38692      AA     GAA__
                                GGGA  ACATAA     TAGGA
                                ||||  ||||||    |||||
                                CCCT  TGTATT    GTCCT
                                   C_     ATGAG
GAM1556  MID1     3'  GGGAGCGGGAAATAGGAGAA   38693      AAACATAA      A
                                GGGA       GAATAGGA GAA
                                ||||       |||||||| |||
                                CCCT       TTTATCCT CTT
                                   CGCCC___       _
GAM1556  MID1     3'  GGGAGCGGGAAATAGGAGAA   38693      AAACATAA      A
                                GGGA       GAATAGGA GAA
                                ||||       |||||||| |||
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                                CCCT       TTTATCCT CTT
                                  CGCCC___       _
GAM1556  PAX4     3'  GGGAAAACATGATGGACAACAG 38694          AAG____
                AA                  GGGAAAACAT      AATAGGA
                                    ||||||||||      |||||||
                                    CCCTTTTGTA      TTGTCTT
                                         CTACCTG
GAM1556  PKD2L1   5'  GGGAGAGGGGAGAATAGGAGGA 38695      AAACATA       A
                                    GGGA      AGAATAGGA GA
                                    ||||      ||||||||| ||
                                    CCCT      TCTTATCCT CT
                                      CTCCCC_       C
GAM1556  PLA2G2D  3'  GGGAAAACAGGGGAAACAGA   38696         TAA_
                                    GGGAAAACA    GAATAGG
                                    |||||||||    |||||||
                                    CCCTTTTGT    TTTGTCT
                                         CCCC
GAM1556  POLE2    5'  GGGAAAACAGACGGAG      38697         TAA  ATA   A
                                    GGGAAAACA   GA   GGA G
                                    |||||||||   ||   ||| |
                                    CCCTTTTGT   CT   CCT C
                                         ___ G__  _
GAM1556  PPT1     3'  GAGAATGGAATAGGAAGA    38698       AACATAA
                                    GGGAA      GAATAGGAAGA
                                    |||||      ||||||||||
                                    CTCTT      CTTATCCTTCT
                                      AC_____
GAM1556  PXN      3'  GGGAGGAATAAGGATAAAAAGA 38699      AAAC     A
                                    GGGA    ATAAG ATAGGAAGA
                                    ||||    ||||| |||||||||
                                    CCCT    TATTC TATTTTTCT
                                      CCT_    C
GAM1556  RNH      3'  GGGAGAGCAGCAGCAGGAAGA  38700      AAA  TA  AA
                                    GGGA   CA  AG  TAGGAAGA
                                    ||||   ||  ||  ||||||||
                                    CCCT   GT  TC  GTCCTTCT
                                      CTC  CG  __
GAM1556  RNH      3'  GGGAGAGCAGCAGCAGGAAGA  38700      AAA  TA  AA
                                    GGGA   CA  AG  TAGGAAGA
                                    ||||   ||  ||  ||||||||
                                    CCCT   GT  TC  GTCCTTCT
                                      CTC  CG  __
GAM1556  RPS6KA1  3'  GGGAAAACTAAGGCTCAGG   38701         A   AA_
                                    GGGAAAAC TAAG   TAGG
                                    |||||||| ||||   ||||
                                    CCCTTTTG ATTC   GTCC
                                         _   CGA
GAM1556  SEPN1    3'  GGGAAAACAGGCAGGGAGA   38702         TAAGAA   A
                                    GGGAAAACA     TAGG AGA
                                    |||||||||     |||| |||
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                                CCCTTTTGT     GTCC TCT
                                     CC____    C
GAM1556 SGK     3' GGGAAAATAAAGAACTGAA   38703       CAT     A
                                GGGAAAA   AAGAAT GGA
                                ||||||| ||||||| |||
                                CCCTTTT   TTCTTG CTT
                                    AT_     A
GAM1556 SLC1A4  3' GGGAAAACAAGGGAGTGAAGGA 38704         TAA  AT__
                                GGGAAAACA   GA    AGGA
                                ||||||||| ||    ||||
                                CCCTTTTGT   CT    TCCT
                                     TCC  CACT
GAM1556 SLC2A8  3' GGGAGCATGACAGGAAG    38705     AAA   AA  A
                                GGGA   CAT  GA TAGGAAG
                                ||||  |||  || |||||||
                                CCCT   GTA  CT GTCCTTC
                                  C__   __  _
GAM1556 WBSCR1  3' GGGAAAACAAGGAGCAGGAGAA 38706         TAA  A    A
                                GGGAAAACA   GA TAGGA GAA
                                ||||||||| ||  ||||| |||
                                CCCTTTTGT   CT GTCCT CTT
                                     TC_  C    _
GAM1556 WBSCR1  3' GGGAAAACAAGGAGCAGGAGAA 38706         TAA  A    A
                                GGGAAAACA   GA TAGGA GAA
                                ||||||||| ||  ||||| |||
                                CCCTTTTGT   CT GTCCT CTT
                                     TC_  C    _
GAM1556 ZNF45   5' GAGAAAACATGAGGGAAG    38707         A  AATA
                                GGGAAAACAT AG    GGAAG
                                |||||||||| ||    |||||
                                CTCTTTTGTA TC    CCTTC
                                     C  _____
GAM1556 AGPAT1  3' GAGAAGACCACATAGGAAGA   38708      A  ATAAGA
                                GGGAA AC     ATAGGAAGA
                                ||||| ||     |||||||||
                                CTCTT TG     TATCCTTCT
                                   C  GTG___
GAM1556 AGPAT1  3' GAGAAGACCACATAGGAAGA   38708      A  ATAAGA
                                GGGAA AC     ATAGGAAGA
                                ||||| ||     |||||||||
                                CTCTT TG     TATCCTTCT
                                   C  GTG___
GAM1556 AKR1D1  3' GGGAAAACATAATTTTTGAAGA 38709          GAATAG
            A                    GGGAAAACATAA     GAAGAA
                                ||||||||||||     ||||||
                                CCCTTTTGTATT     CTTCTT
                                       AAAAA_
GAM1556 APOL6   5' GGAGAAAGACGGATAGGAAGA  38710     AAACAT   ___
                                GGA     AAGA   ATAGGAAGA
                                |||     ||||   |||||||||
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                                CCT     TTCT   TATCCTTCT
                                  CT____    GCC
GAM1556  BZW1     3'  AGGAAGATGTAAGAACCAGGA  38711       AACA      _
                                GGGAA    TAAGAAT AGGA
                                |||||    ||||||| ||||
                                TCCTT    ATTCTTG TCCT
                                   CTAC      G
GAM1556  CG012    5'  GGGAAAACATGAGTTGAGGA   38712          A  AAT
                                GGGAAAACAT AG   AGGA
                                |||||||||| ||   ||||
                                CCCTTTTGTA TC   TCCT
                                      C  AAC
GAM1556  CHL1     3'  GGGAACACGAAGTGTAGGAAGA 38713      AA   _   AA
                                GGGA  ACAT AAG  TAGGAAGA
                                ||||  |||| |||  ||||||||
                                CCCT  TGTG TTC  ATCCTTCT
                                  __    C   AC
GAM1556  DGKD     3'  GGGAAAACAATGAGAGGTGGAA 38714         TA_   ATA
                                GGGAAAACA   AGA   GGAA
                                |||||||||   |||   ||||
                                CCCTTTTGT   TCT   CCTT
                                     TAC   CCA
GAM1556  DIS3     3'  GGGAGAATAAGAATGTGGGAGA 38715      AAAC       A_  A
            A                    GGGA    ATAAGAAT  GG AGAA
                                ||||    ||||||||  || ||||
                                CCCT    TATTCTTA  CC TCTT
                                  CT__       CA  C
GAM1556  DKFZP434F1017 3'  GGGAAGGCAAAGACAAGAA    38716       AA  T    A
                                GGGAA  CA AAGA TAGGAA
                                |||||  || |||| ||||||
                                CCCTT  GT TTCT GTTCTT
                                   CC  _    _
GAM1556  DKFZP434L0117 3'  GGGAGAACAAGAGCCCTGAGGA 38717      A    TA  AAT__
            AGAA                   GGGA AACA  AG     AGGAAGAA
                                |||| ||||  ||    ||||||||
                                CCCT TTGT  TC     TCCTTCTT
                                   C    TC  GGGAC
GAM1556  DKFZP564G092 5'  GGGAAAGGGTGATAGGAAG    38718       ACATAA  A
                                GGGAAA     GA TAGGAAG
                                ||||||     || |||||||
                                CCCTTT     CT ATCCTTC
                                    CCCA__  _
GAM1556  DKFZP564O0463 3'  GGGAAACATAAGGAAGGA    38719       A     AAT
                                GGGAAA CATAAG   AGGA
                                |||||| ||||||   ||||
                                CCCTTT GTATTC   TCCT
                                    _     CT_
GAM1556  E1B-AP5  3'  AGGAAGAAGGTAGGAAGA    38720      AAACATA   __
                                GGGA      AGAA  TAGGAAGA
                                ||||      ||||  ||||||||
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                                TCCT      TCTT  ATCCTTCT
                                  _______   CC
GAM1556 E1B-AP5  3' AGGAAGAAGGTAGGAAGA    38720     AAACATA   __
                                GGGA      AGAA  TAGGAAGA
                                ||||      ||||  ||||||||
                                TCCT      TCTT  ATCCTTCT
                                  _______   CC
GAM1556 EPSIN    5' GGGAAGACAGGGAGGCAGGA   38721      A   TAA  A_
                                GGGAA ACA   GA  TAGGA
                                ||||| |||   ||  |||||
                                CCCTT TGT   CT  GTCCT
                                   C   CC_  CC
GAM1556 FADS1    3' GGCAAAGAATAGGAATAGGAAG 38722    G   AC   A
                                GG AAA  ATA GAATAGGAAG
                                || |||  ||| ||||||||||
                                CC TTT  TAT CTTATCCTTC
                                 G   CT   C
GAM1556 FBXO30   3' GGGACAAATGTAGGAAGA    38723     AAACA    AA
                                GGGA    TAAG  TAGGAAGA
                                ||||    ||||  ||||||||
                                CCCT    GTTT  ATCCTTCT
                                  _____   AC
GAM1556 FLJ12644 3' GGGAAAGCAGAAAAAGAAGAA  38724       ACATA    T
                                GGGAAA    AGAA AGGAAGAA
                                ||||||    |||| ||||||||
                                CCCTTT    TCTT TTCTTCTT
                                   CG___    T
GAM1556 FLJ20113 3' GGGGGGTCATGTGACAGGAAGA 38725     AAAA   AA  A
             A                   GGG    CAT  GA TAGGAAGAA
                                |||    |||  || |||||||||
                                CCC    GTA  CT GTCCTTCTT
                                  CCCA   CA  _
GAM1556 FLJ20257 3' GGGCTAGAGAATAGGAGGAA   38726     AAAACATA       A
                                GGG       AGAATAGGA GAA
                                |||       ||||||||| |||
                                CCC       TCTTATCCT CTT
                                  GATC____        C
GAM1556 FLJ23153 3' GGGAAAATAAGAGTCAGG    38727       AC     A_
                                GGGAAA  ATAAGA  TAGG
                                ||||||  ||||||  ||||
                                CCCTTT  TATTCT  GTCC
                                   __      CA
GAM1556 FLJ23519 3' GGGAGAGCAGCAGCAGGAAGA  38700     AAA  TA  AA
                                GGGA   CA  AG  TAGGAAGA
                                ||||   ||  ||  ||||||||
                                CCCT   GT  TC  GTCCTTCT
                                  CTC  CG  __
GAM1556 FLJ31978 3' GGGAAAACACAAGGGGTGCGA  38728           AATA  AA_
                                GGGAAAACATAAG   GG   GA
                                ||||||||||||   ||   ||
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                                CCCTTTTGTGTTC   CC  CT
                                      C___  ACG
GAM1556 FLJ32332 3' GGGAAAACAAAGCAAGG    38729        T  AAT
                                GGGAAAACA AAG  AGG
                                ||||||||| |||  |||
                                CCCTTTTGT TTC  TCC
                                     _  GT_
GAM1556 FREQ    3' GGAAAAAGCAGATAGGAAG   38730       CATA  A
                                GGGAAAA   AGA TAGGAAG
                                |||||||   ||| |||||||
                                CCTTTTT   TCT ATCCTTC
                                    CG__  _
GAM1556 H2BFQ   3' GGGAGAGTAAGAAAAGGAGAA 38731     AAACA    T  A
                                GGGA    TAAGAA AGGA GAA
                                ||||    |||||| |||| |||
                                CCCT    ATTCTT TCCT CTT
                                  CTC__     T   _
GAM1556 IL-23R  3' GGGAAAATAAAGAGGAA    38732       CAT   ATA
                                GGGAAAA  AAGA  GGAA
                                |||||||  ||||  ||||
                                CCCTTTT  TTCT  CCTT
                                    AT_  ____
GAM1556 IL1RAPL1 5' GGGAAAATAAGAATAA    38733       AC
                                GGGAAA  ATAAGAATAG
                                ||||||  ||||||||||
                                CCCTTT  TATTCTTATT
                                     __
GAM1556 JM11    3' GGGAAGACAAGAAGAAGA   38734      AAC    ATA
                                GGGAA  ATAAGA  GGAAGA
                                |||||  ||||||  ||||||
                                CCCTT  TGTTCT  TCTTCT
                                  C__    ____
GAM1556 KIAA0014 3' GGGAAAACAGAAGACAGGAA  38735        T   A
                                GGGAAAACA AAGA TAGGAA
                                ||||||||| |||| ||||||
                                CCCTTTTGT TTCT GTCCTT
                                     C   _
GAM1556 KIAA0286 3' GGGTAAGGAAGAATGGGAAGA 38736    AAAACAT    A
                                GGG      AAGAAT GGAAGA
                                |||      |||||| ||||||
                                CCC      TTCTTA CCTTCT
                                  ATTCC__     C
GAM1556 KIAA0295 3' GGGAGAACAGGAAAA      38737     AAACATAA
                                GGGA      GAATAGGAAGA
                                ||||      ||||||||||
                                CCCT      CTTGTCCTTTT
                                  ________
GAM1556 KIAA0323 3' GGGAAACAGAAACCAGGAGGA 38738      A  T  AA   A
                                GGGAAA CA AAG  TAGGA GA
                                |||||| || |||  ||||| ||
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                                CCCTTT GT TTT  GTCCT CT
                                   _ C  G_    C
GAM1556 KIAA1193 3' GGGAGAACACAAGGTCAAGA  38739     A       AA
                                GGGA AACATAAG  TAGGA
                                |||| ||||||||  |||||
                                CCCT TTGTGTTC  GTTCT
                                  C       CA
GAM1556 KIAA1462 3' GGGAGGACAGAAGGAAG    38740     AA   TAA  AT
                                GGGA  ACA   GA  AGGAAG
                                ||||  |||   ||  ||||||
                                CCCT  TGT   CT  TCCTTC
                                  CC  ___  __
GAM1556 KIAA1467 3' GGGAAAGAATAAGGAG     38741      AACATA      A
                                GGGAA     AGAATAGG AG
                                |||||     |||||||| ||
                                CCCTT     TCTTATTC TC
                                  _______       C
GAM1556 KIAA1644 3' GGGAAAAATAGGAAG      38742      AACATAA
                                GGGAA     GAATAGGAAG
                                |||||     ||||||||||
                                CCCTT     TTTATCCTTC
                                  ________
GAM1556 KIAA1786 3' GGGAGACAAGAAGGGGAGGA  38743     AAAC     TA   A
                                GGGA   ATAAGAA  GGA GA
                                ||||   |||||||  ||| ||
                                CCCT   TGTTCTT  CCT CT
                                  C___      CC   C
GAM1556 KIAA1970 3' GAGAAAGCCACAAAATAGGAAG 38744       A_     A
                                GGGAAA  CATAAGA TAGGAAG
                                ||||||  ||||||| |||||||
                                CTCTTT  GTGTTTT ATCCTTC
                                   CG     _
GAM1556 LIM      3' GGGAAGAAATAAGAAAAGAA  38745      AAC      T
                                GGGAA   ATAAGAA AGGA
                                |||||   ||||||| ||||
                                CCCTT   TATTCTT TCTT
                                  CTT      T
GAM1556 MGC3035  5' GAGACGCTGAGTAGGAAGAA  38746     AAACATAA  A
                                GGGA       GA TAGGAAGAA
                                ||||       || |||||||||
                                CTCT       CT ATCCTTCTT
                                  GCGA____  C
GAM1556 NCOA2    3' GGGAAAACAAAGCAAGAA    38747         T   AA
                                GGGAAAACA AAG  TAGGAA
                                ||||||||| |||  ||||||
                                CCCTTTTGT TTC  GTTCTT
                                     _  __
GAM1556 RNF34    3' GGGAAATAAGAGAACAGGA   38748       ACATA
                                GGGAAA    AGAATAGGA
                                ||||||    |||||||||
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                                CCCTTT    TCTTGTCCT
                                   ATTC_
GAM1556 SIAT9    3' GGAAAAAAAAAGTGGGAAGA  38749       CAT   AATA
                                GGGAAAA  AAG   GGAAGA
                                |||||||  |||   ||||||
                                CCTTTTT  TTC   CCTTCT
                                    TT_  AC__
GAM1556 SMT3H2   3' GGGAAATGAAAGAATAGAGAA 38750      ACAT      _
                                GGGAAA   AAGAATAG GAA
                                ||||||   |||||||| |||
                                CCCTTT   TTCTTATC CTT
                                   ACT_      T
GAM1556 SUPT4H1  3' GGGAGAACAAGGAACTTAGG  38751     A   TAA   __
                                GGGA AACA  GAAT  AGG
                                |||| ||||  ||||  |||
                                CCCT TTGT  CTTG  TCC
                                  C   TC_   AA
GAM1556 UBAP     3' GGGAAAAAATAAAACCCTGGAA 38752       C     ATA_
            GAA                   GGGAAAA ATAAGA   GGAAGAA
                                |||||||  ||||||   |||||||
                                CCCTTTT TATTTT   CCTTCTT
                                    T     GGGA
GAM1556 USP24    3' GGGAAACAGTAGGACAGGAA  38753       A  TA  A
                                GGGAAA CA  AG ATAGGAA
                                ||||||  ||  || |||||||
                                CCCTTT GT  TC TGTCCTT
                                   _  CA  C
GAM1556 VPS4A    3' GAGAGGAGGAAGTAGGAAGA  38754     AAACAT   AA
                                GGGA     AAG  TAGGAAGA
                                ||||     |||  ||||||||
                                CTCT     TTC  ATCCTTCT
                                  CCTCC_  __
GAM1556 LOC124538 3' GGGAAAACAAAGCCAAAGA   38755        T   AAT
                                GGGAAAACA AAG   AGGA
                                |||||||||  |||   ||||
                                CCCTTTTGT TTC   TTCT
                                     _  GGT
GAM1556 LOC126526 3' GGGAATGTAGGAGAGGAAGAA  38756      AACATA   ATA
                                GGGAA     AGA   GGAAGAA
                                |||||     |||   |||||||
                                CCCTT     TCT   CCTTCTT
                                   ACATCC  ____
GAM1556 LOC146611 3' GGGAAACATAAAAATAA     38757       A
                                GGGAAA CATAAGAATAG
                                ||||||  ||||||||||
                                CCCTTT GTATTTTTATT
                                   _
GAM1556 LOC146723 3' GGAAAATATAAAACAGGAGA   38758       C     A    A
                                GGAAAA ATAAGA TAGGA GA
                                ||||||  |||||  ||||| ||
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                                CCTTTT TATTTT GTCCT CT
                                   A     _    _
GAM1556  LOC146856 5'  AGGAAGAAAGTAGGAAG     38759       AACAT   AA
                                GGGAA     AAG  TAGGAAG
                                |||||     |||  |||||||
                                TCCTT     TTC  ATCCTTC
                                  CT___   __
GAM1556  LOC148183 3'  GGGAAAAATAAGTCTTGGGAAG 38760        C     AATA_
            AA                    GGGAAAA ATAAG     GGAAGAA
                                |||||||  |||||     |||||||
                                CCCTTTT TATTC     CCTTCTT
                                   _     AGAAC
GAM1556  LOC150606 3'  GGGAAAACATGAGCAGCTCTAG 38761          A  AA____
            AA                    GGGAAAACAT AG      TAGGA
                                ||||||||||  ||      |||||
                                CCCTTTTGTA TC      ATCTT
                                     C  GTCGAG
GAM1556  LOC151579 3'  AGGAAGATGTAAGAACCAGGA  38711       AACA      _
                                GGGAA    TAAGAAT AGGA
                                |||||    |||||||  ||||
                                TCCTT    ATTCTTG TCCT
                                  CTAC       G
GAM1556  LOC153077 3'  GGGAAAAATAGGTACAGGGAG  38762        C   AGA     A
                                GGGAAAA ATA   ATAGG AG
                                |||||||  |||   |||||  ||
                                CCCTTTT TAT   TGTCC TC
                                   _  CCA     C
GAM1556  LOC154547 3'  GGGAAATGAAAGAATAGAGAA  38750       ACAT       _
                                GGGAAA    AAGAATAG GAA
                                ||||||    ||||||||  |||
                                CCCTTT    TTCTTATC CTT
                                   ACT_       T
GAM1556  LOC158997 3'  GGGAAATGAAAGAATAGAGAA  38750       ACAT       _
                                GGGAAA    AAGAATAG GAA
                                ||||||    ||||||||  |||
                                CCCTTT    TTCTTATC CTT
                                   ACT_       T
GAM1556  LOC164118 3'  GGGATGGGCATAAGAAGCGGA  38763      AAA_       TA
                                GGGA    CATAAGAA  GGA
                                ||||    ||||||||  |||
                                CCCT    GTATTCTT  CCT
                                  ACCC       CG
GAM1556  LOC200269 3'  GGGAAAACATGGCTGTCAAGA  38764          AAGAA_
                                GGGAAAACAT      TAGGA
                                ||||||||||      |||||
                                CCCTTTTGTA      GTTCT
                                     CCGACA
GAM1556  LOC202134 5'  GGGAAAGATAGGAAG       38765       AACATA   A
                                GGGAA      AGA TAGGAAG
                                |||||      |||  |||||||
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                                CCCTT     TCT ATCCTTC
                                  _______  _
GAM1556  LOC219649 3'  GGGAGGCATCTCCAGGAAGA  38766     AAA  AAGAA
                                GGGA  CAT    TAGGAAGA
                                ||||  |||    ||||||||
                                CCCT  GTA    GTCCTTCT
                                  CC_  GAG__
GAM1556  LOC221550 5'  GGGAAAATAAGAGAAG     38767       AC     ATAG
                                GGGAAA  ATAAGA   GAAG
                                ||||||  ||||||   ||||
                                CCCTTT  TATTCT   CTTC
                                  __    _____
GAM1556  LOC221561 3'  GGGAAATGAAAGAATAGAGAA  38750       ACAT       _
                                GGGAAA   AAGAATAG GAA
                                ||||||   |||||||| |||
                                CCCTTT   TTCTTATC CTT
                                   ACT_       T
GAM1556  LOC221692 3'  GGGAAAAATAAGAACCTATGGG 38769       C       A____
            AA                    GGGAAAA ATAAGAAT    GGAA
                                ||||||| ||||||||    ||||
                                CCCTTTT TATTCTTG    CCTT
                                   _       GATAC
GAM1556  LOC221692 3'  GGGAAAACGGATGGAAGA    38768        ATAA  ATA
                                GGGAAAAC   GA   GGAAGA
                                ||||||||   ||   ||||||
                                CCCTTTTG   CT   CCTTCT
                                    C___  A__
GAM1556  LOC222031 3'  GGGAAAGTGAGGAAGCAGGAAG 38770       ACATAA  _
            A                     GGGAAA     GAA TAGGAAGA
                                ||||||     ||| ||||||||
                                CCCTTT     CTT GTCCTTCT
                                   CACTC_  C
GAM1556  LOC222159 5'  GGTAAAACATAAGTAGGAA   38771    G        AA
                                GG AAAACATAAG  TAGGAA
                                || ||||||||||  ||||||
                                CC TTTTGTATTC  ATCCTT
                                 A        __
GAM1556  LOC254158 5'  GGGAAAAAATAAGGTCAGA   38772       C    AA
                                GGGAAAA ATAAG  TAGG
                                ||||||| |||||  ||||
                                CCCTTTT TATTC  GTCT
                                    T    CA
GAM1556  LOC255196 5'  GGAAAGGAGAAATAGGAAG   38773      ACATAA
                                GGAAA     GAATAGGAAG
                                |||||     ||||||||||
                                CCTTT     TTTATCCTTC
                                  CCTC__
GAM1556  LOC255316 3'  GGGAAAACCTGAAGCTGGAAGA 38774        AT_   AATA
            A                     GGGAAAAC   AAG   GGAAGAA
                                ||||||||   |||   |||||||
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                                CCCTTTTG  TTC   CCTTCTT
                                    GAC  GA__
GAM1556  LOC256112 5'  GGGAAAGAATAAGGAG     38741      AACATA      A
                                GGGAA     AGAATAGG AG
                                |||||     |||||||| ||
                                CCCTT     TCTTATTC TC
                                  _______       C
GAM1556  LOC257495 5'  GGGAAAATAAGAGAAG     38767      AC     ATAG
                                GGGAAA  ATAAGA   GAAG
                                ||||||  ||||||   ||||
                                CCCTTT  TATTCT   CTTC
                                  __    _____
GAM1556  LOC257576 5'  GGGAAAATAAGAGAAG     38767      AC     ATAG
                                GGGAAA  ATAAGA   GAAG
                                ||||||  ||||||   ||||
                                CCCTTT  TATTCT   CTTC
                                  __    _____
GAM1556  LOC257591 3'  GGGAAATGAAAGAATAGAGAA  38750      ACAT      _
                                GGGAAA   AAGAATAG GAA
                                ||||||   |||||||| |||
                                CCCTTT   TTCTTATC CTT
                                   ACT_      T
GAM1556  LOC51024  3'  GGGAGAACAGGGAAAGGA    38775     A   TAA   T
                                GGGA AACA   GAA AGGA
                                |||| ||||   ||| ||||
                                CCCT TTGT   CTT TCCT
                                  C   CC_  _
GAM1556  LOC89932  5'  GGGAGAAACAGAAGTTAGG   38776     _    T   AA
                                GGGA AAACA AAG  TAGG
                                |||| ||||| |||  ||||
                                CCCT TTTGT TTC  ATCC
                                  C    C   A_
GAM1557  FLJ20288  5'  TGATGTTGTTTTAAGCA     38779         A   T
                                TGATGTTGTT TTGA CG
                                |||||||||| |||| ||
                                ACTACAACAA AATT GT
                                     _   C
GAM1557  TRF4-2    3'  TGATGTTGTTTGTTTGTCA   38780         A__  A
                                TGATGTTGTT   TTG TCG
                                ||||||||||   ||| |||
                                ACTACAACAA   AAC AGT
                                     ACA  _
GAM1558  EP300     5'  GAGAACTCGCGGCTCTAGAGG  38783        G T   CC
                                GAGAACTCG C GCTC  AGAGG
                                ||||||||| | ||||  |||||
                                CTCTTGAGC G CGAG  TCTCC
                                     _ C   A_
GAM1558  HMOX1     3'  TGAAACTCAGGGCTTTTGGAGG 38784      A    CT   CCCA
                                TGAGA CTCGG  GCT   GAGG
                                |||||  |||||  |||   ||||
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                                ACTTT GAGTC  CGA   CTCC
                                  _    C_  AAAC
GAM1558 RXRA    3' GGCTGTCCTTCCCAGAGG   38785     _ __
                                GGCTG C  TCCCAGAGG
                                ||||| |  |||||||||
                                CCGAC G  AGGGTCTCC
                                   A GA
GAM1558 SLC2A6  3' AGCTGCCTGTTCCCAGAGG   38786      ____
                                GGCTGC   TCCCAGAGG
                                ||||||   |||||||||
                                TCGACG   AGGGTCTCC
                                   GACA
GAM1558 TNFSF15  3' GAACTCGGTGGCAGAG     38787       C  CTCC
                                GAACTCGG TG   CAGAG
                                |||||||| ||   |||||
                                CTTGAGCC AC   GTCTC
                                     _ C___
GAM1558 TPR     5' TGGGAACCCGAGCTCAGAG   38788   A     CT   CC
                                TG GAACTCGG  GCTC  AGAG
                                || |||||||  ||||  ||||
                                AC CTTGGGCT  CGAG  TCTC
                                 C      __   __
GAM1558 VAT1    3' TGGGAACTGGTCAAGCCCAGAG 38789   A    C  CT CT
             G                   TG GAACT GG  G  CCCAGAGG
                                || ||||| ||  |  ||||||||
                                AC CTTGA CC  T  GGGTCTCC
                                 C    _ AG TC
GAM1558 CABP4   3' GAACTCCCTACCTCCCAGAGG  38790      GG   _
                                GAACTC  CTGC TCCCAGAGG
                                ||||||  |||| |||||||||
                                CTTGAG  GATG AGGGTCTCC
                                   G_   G
GAM1558 DGKZ    3' ACCCGGCCGAAGACCAGGG   38791        CTC_   A
                                ACTCGGCTG   CCAG GG
                                |||||||||   |||| ||
                                TGGGCCGGC   GGTC CC
                                     TTCT   _
GAM1558 DKFZP434F0318 3' AGGACTTGGAGAGGACCCAGAG 38792   A   C  CTGCT_
             G                   AG ACT GG    CCCAGAGG
                                || ||| ||    ||||||||
                                TC TGA CC    GGGTCTCC
                                 C   A  TCTCCT
GAM1558 DKFZP434P0111 3' TGAGAGCCCATCCCAGAG   38793      A   GCTGC
                                TGAGA CTCG    TCCCAGAG
                                ||||| ||||   ||||||||
                                ACTCT GGGT    AGGGTCTC
                                   C   _____
GAM1558 ERN1    5' GAGGACTCGGCCCTGGCTCC  38794    A     ___
                                GAG ACTCGGCT   GCTCC
                                ||| ||||||||  |||||
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                                CTC TGAGCCGG   CGAGG
                                  C       GAC
GAM1558  FLJ20034  3'  TGAAAATGAGGCTCTTGGAGG  38795       CTC    G  CCCA
                                TGAGAA   GGCT CT    GAGG
                                ||||||   |||| ||    ||||
                                ACTTTT   CCGA GA    CTCC
                                   ACT    _  AC__
GAM1558  FLJ20188  3'  TGGGAACTAGGCTTCCCAGAGG 38796    A     C    GC
                                TG GAACT GGCT  TCCCAGAGG
                                || ||||| ||||  |||||||||
                                AC CTTGA CCGA  AGGGTCTCC
                                 C    T   __
GAM1558  GOLGA3   3'  AGAACTCGGTTGTGGGCCTCTG 38797        C _________  CCA
            GGA                    GAACTCGG TG       CTC   GA
                                |||||||| ||       |||   ||
                                CTTGAGCC AC       GAG   CT
                                     A  ACCCIIIG   ACC
GAM1558  KIAA1317  5'  GAGCCGGTGCGAGCCAGAGG   38798     AAC    C   TC_
                                GAG   TCGG TGC   CCAGAGG
                                |||   |||| |||   |||||||
                                CTC   GGCC ACG   GGTCTCC
                                  ___   _  CTC
GAM1558  KIAA1813  5'  CTCCTGCCTCCCAGAGG     38799     GG   _
                                CTC  CTGC TCCCAGAGG
                                |||  |||| |||||||||
                                GAG  GACG AGGGTCTCC
                                  __   G
GAM1558  KRTAP1-5  3'  TGAGAACTTGTTAGTGGTCCAG 38800        C___  C  CTC
            AGG                    TGAGAACT    GG TG   CCAGAGG
                                ||||||||    || ||   |||||||
                                ACTCTTGA    TC AC   GGTCTCC
                                     ACAA  _  CA_
GAM1558  MAGE-E1   3'  GGCTCGCAGGCCCCAGAGG   38801      _  ___
                                GGCT GC   TCCCAGAGG
                                ||||  ||   |||||||||
                                CCGA CG   GGGGTCTCC
                                  G  TCC
GAM1558  moblak   3'  TGAGGGCTCGGCTGGGAG    38802      AA       CTCCCA
                                TGAG  CTCGGCTG     GAG
                                ||||  ||||||||     |||
                                ACTC  GAGCCGAC     CTC
                                  CC       C_____
GAM1558  MYH10    3'  TGAGGGCCCGGCTGGCGATGG  38803      AA       CTCCCA  _
                                TGAG  CTCGGCTG     GA GG
                                ||||  ||||||||     || ||
                                ACTC  GGGCCGAC     CT CC
                                  CC       CG____  A
GAM1558  TBC1D2   5'  AGAAGGGCCTCTGCTCCCAGGG 38804      CTC    ___       A
                                AGAA   GGCT   GCTCCCAG GG
                                ||||   ||||   |||||||| ||
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                                TCTT   CCGG   CGAGGGTC CC
                                  C__    AGA       _
GAM1558  TNK1     3'  TGAGAACTGGGCTGGAGCAGGG 38805        C    CTCC   A
                                TGAGAACT GGCTG    CAG GG
                                |||||||| |||||    ||| ||
                                ACTCTTGA CCGAC    GTC CC
                                     C    CTC_  _
GAM1558  LOC126767 3'  TGAAGACTCTGATCCCAGAGG  38806     GA    GGC  C
                                TGA  ACTC   TG TCCCAGAGG
                                |||  ||||   || |||||||||
                                ACT  TGAG   AC AGGGTCTCC
                                  TC    ___  T
GAM1558  LOC146774 3'  GAGGACTCGGCCCTGGCTCC   38794     A       ___
                                GAG ACTCGGCT   GCTCC
                                ||| ||||||||   |||||
                                CTC TGAGCCGG   CGAGG
                                  C       GAC
GAM1558  LOC150223 3'  TGAGGACCTGAGCCCAGAG    38807     A  TCGG   CT
                                TGAG AC    CTG  CCCAGAG
                                |||| ||    |||  |||||||
                                ACTC TG    GAC  GGGTCTC
                                  C _____   TC
GAM1558  LOC150290 3'  TGAGGACACTGATGCTCCCAGG 38808      A  TC_  C       A
            G                    TGAG AC   GG TGCTCCCAG GG
                                |||| ||   || |||||||| ||
                                ACTC TG   CT ACGAGGGTC CC
                                  C  TGA  _       _
GAM1558  LOC155064 5'  ACCCAGGCTCCCGGAGG     38809       CT     A
                                ACTCGG  GCTCCC GAGG
                                ||||||  |||||| ||||
                                TGGGTC  CGAGGG CTCC
                                   __      C
GAM1558  LOC253587 3'  GAAGCTTCAGTTTTCCCAGAGG 38810     _ _  CTGC
                                GAA CT CGG    TCCCAGAGG
                                ||| || |||    |||||||||
                                CTT GA GTC    AGGGTCTCC
                                  C  A   AAA_
GAM1558  LOC256477 5'  TGAGAACTCGGTGCGGGGAGG  38811          C   TCCCA
                                TGAGAACTCGG TGC     GAGG
                                ||||||||||| |||     ||||
                                ACTCTTGAGCC ACG     CTCC
                                       _   CCC__
GAM1558  LOC256526 5'  TGAGAGCTGTGGCTCCCAGAGG 38812       ACTCG   ___
                                TGAGA    GCT   GCTCCCAGAGG
                                |||||    |||   ||||||||||||
                                ACTCT    CGA   CGAGGGTCTCC
                                   ______  CAC
GAM1558  LOC257465 3'  TGAAACACTGCTCCTAGG    38813       A TCG       C  A
                                TGAGA C   GCTGCTCC AG G
                                ||||| |   |||||||| || |
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                                ACTTT G   TGACGAGG TC C
                                  _ ___       A  _
GAM1559  BPAG1    3'  GGTGTGTTTGTCTTTTT     38816      A  AC
                                GGTG TG  TGTCTTTTT
                                |||| ||  |||||||||
                                CCAC AC  ACAGAAAAA
                                  _  AA
GAM1559  CASPR3   3'  TGGAATGAATTGTCTTTTT    38817     T    C_
                                TGG GATGA  TGTCTTTTT
                                ||| |||||  |||||||||
                                ACC TTACT  ACAGAAAAA
                                  _    TA
GAM1559  DKFZP434L0718 3'  AGATGGTGGTGGTTAACTTTTT 38818         A  AC  T
                                AGATGGTG TG  TG CTTTTT
                                |||||||| ||  || ||||||
                                TCTACCAC AC  AT GAAAAA
                                     C  CA  T
GAM1559  E2IG3    3'  GAGATGAATTGTCTTTTT    38819    T    TGAC
                                GA GGTGA    TGTCTTTTT
                                || |||||    |||||||||
                                CT CTACT    ACAGAAAAA
                                 _    TA__
GAM1559  FLJ30927  3'  GATAATCTGGCTGTTTTTTTA  38820       GA  A    C
                                GATGGT  TG CTGT TTTTTA
                                ||||||  || |||| ||||||
                                CTATTA  AC GACA AAAAAT
                                   G_  C    A
GAM1559  FLJ31709  3'  GAAGGTGATGACAAGGCCTTTT 38821    T       T__
                                GA GGTGATGAC   GTCTTTT
                                || |||||||||   |||||||
                                CT CCACTACTG   CGGAAAA
                                 T        TTC
GAM1559  HYPH     3'  TAGAGGTTTGTCTTTT      38822      T   GATGAC
                                TAGA GGT     TGTCTTTT
                                |||| |||     ||||||||
                                ATCT CCA     ACAGAAAA
                                  _  A_____
GAM1559  KLHL6    3'  TAGGGGCGCTGTCTTTTT    38823     AT    ATGA
                                TAG  GGTG   CTGTCTTTTT
                                |||  ||||   ||||||||||
                                ATC  CCGC   GACAGAAAAA
                                  C_   ____
GAM1560  CD69     3'  TACACGATCATCCCA       38826          TAAATT
                                TACACGATC     ATCCCA
                                |||||||||     ||||||
                                ATGTGCTAG     TAGGGT
                                              _____
GAM1560  MOCS2    3'  CACATTTAAATTATTCCAT    38827      ATC       C
                                CACG   TAAATTAT CCAT
                                ||||   |||||||| ||||
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                                GTGT   ATTTAATA GGTA
                                  AA_       A
GAM1560 KIAA0514 5' ACACTGCAAATTATCTCATC   38828      GATC        C
                                ACAC    TAAATTATC CATC
                                ||||    ||||||||| ||||
                                TGTG    GTTTAATAG GTAG
                                  AC__        A
GAM1560 LOC152313 3' GATACAATTATCCCATC     38829     CTA
                                GAT   AATTATCCCATC
                                |||   ||||||||||||
                                CTA   TTAATAGGGTAG
                                  TG_
GAM1561 FANCF    3' CAAGATGGCCTTCATGGATTA  38832      TAAAC  C
                                CAAG     CC TCATGGATTA
                                ||||     || ||||||||||
                                GTTC     GG AGTACCTAAT
                                  TACC_  A
GAM1561 FLJ10895 3' TTCTGAGTATAAATCATGGATT 38833     A_    AACCCC
                                TTC  AGTA     TCATGGATT
                                |||  ||||     |||||||||
                                AAG  TCAT     AGTACCTAA
                                  AC    ATTT__
GAM1561 GPT2     3' TTCAAGGGAACCCCTCAT    38834       TA
                                TTCAAG  AACCCCTCAT
                                ||||||  ||||||||||
                                AAGTTC  TTGGGGAGTA
                                    CC
GAM1561 KIAA1676 3' AAACACCTCTCATGGATTA   38835      _ _
                                AAAC CC CTCATGGATTA
                                |||| || ||||||||||
                                TTTG GG GAGTACCTAAT
                                  T  A
GAM1561 LOC200609 5' AAGTATATTCATGGATTA    38836      AACCCC
                                AAGTA     TCATGGATTA
                                |||||     ||||||||||
                                TTCAT     AGTACCTAAT
                                  ATA____
GAM1562 SYT4     3' TGGCTAATCAGACAAACAATTA 38839    A     T    TGT
                                TG CTAATC AGATA   TAATTA
                                || |||||| |||||   ||||||
                                AC GATTAG TCTGT   GTTAAT
                                 C     _     TT_
GAM1562 LOC149606 3' TGACTAATTTAGAGGTGC    38840        C    TA
                                TGACTAAT TAGA  TGT
                                |||||||| ||||  |||
                                ACTGATTA ATCT  ACG
                                     A    CC
GAM1563 BMPR1B   5' CAGGCTTGTAAGTTTAACTTTT 38843     AAA__
             T                   CAG     TAAGTTTAACTTTTT
                                 |||     ||||||||||||||
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                                GTC    ATTCAAATTGAAAAA
                                  CGAAC
GAM1563  GPR85    3'  AAACAAAAATAATAACTTTTT  38844          GTT
                                AAACAGAAATAA  TAACTTTTT
                                ||||||||||||  |||||||||
                                TTTGTTTTTATT  ATTGAAAAA
                                      ____
GAM1563  ZNF265   3'  ACAACATAGTTTAACTTTT   38845     AAATA
                                ACAG    AGTTTAACTTTT
                                ||||    ||||||||||||
                                TGTT    TCAAATTGAAAA
                                  GTA__
GAM1563  FLJ20580 3'  CAGAAATAAAGTTTAATTTTT  38846        _    C
                                CAGAAATAA GTTTAA TTTTT
                                ||||||||| |||||| |||||
                                GTCTTTATT CAAATT AAAAA
                                     T    _
GAM1563  TA-KRP   3'  AGAAATAAGTTACCTTT    38847         TA
                                AGAAATAAGTT  ACTTTT
                                ||||||||||  ||||||
                                TCTTTATTCAA  TGGAAA
                                      __
GAM1563  TRIP-Br2 3'  AAAAGAAGTCCAACTTTT   38848     T
                                GAAA AAGTTTAACTTTT
                                |||| ||||||||||||
                                TTTT TTCAGGTTGAAAA
                                  C
GAM1563  ZNF291   3'  AAACAGAATAAGTTACTTTT  38849       A    TA
                                AAACAGAA TAAGTT  ACTTTT
                                |||||||| ||||||  ||||||
                                TTTGTCTT ATTCAA  TGAAAA
                                    _    __
GAM1563  LOC138046 3' CAGAAATATAACTTTTT    38850       AGTT
                                CAGAAATA   TAACTTTTT
                                ||||||||   |||||||||
                                GTCTTTAT   ATTGAAAAA
                                     _____
GAM1563  LOC91308 3'  AACAAAAATAAGTATACTTTTT 38851          TTA
                                AACAGAAATAAGT   ACTTTTT
                                ||||||||||||   |||||||
                                TTGTTTTTATTCA   TGAAAAA
                                     TA_
GAM1563  LOC93166 3'  AAAATAAGTCCTCAACTTTTT  38852        __
                                GAAATAAGTT  TAACTTTTT
                                ||||||||||  |||||||||
                                TTTTATTCAG  GTTGAAAAA
                                     GA
GAM1564  EML1     3'  AGTTCATAGAAAAGTTACT   38855    C   TC
                                AGT CATA  GGAGTTACT
                                ||| ||||  |||||||||
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                                TCA GTAT  TTTCAATGA
                                  A    CT
GAM1564  SRD5A2    3'  AGTCCATATCTCAGCACT    38856         GG   T
                                AGTCCATATC  AGT ACT
                                ||||||||||  ||| |||
                                TCAGGTATAG  TCG TGA
                                     AG  _
GAM1564  KIAA1165  3'  TATAAGGTCCATATAGCT    38857       A       CGG
                                TATAA GTCCATAT   AGTT
                                ||||| ||||||||   ||||
                                ATATT CAGGTATA   TCGA
                                   C       ___
GAM1564  KIAA1257  3'  TATAAAGTCCAGTTCATAAATT 38858           TA  _
                                TATAAAGTCCA  TCG GAGTT
                                ||||||||||  ||| |||||
                                ATATTTCAGGT  AGT TTTAA
                                     CA   A
GAM1564  LOC115106 3'  TAAAGTCCTATTCAATTTACT  38859         A   CG  G
                                TAAAGTCC TAT  GA TTACT
                                ||||||||| |||  || |||||
                                ATTTCAGG ATA  TT AATGA
                                     _  AG  A
GAM1564  LOC144747 5'  TATGGAGTCCATAGCATCAGGG 38860     AA       ___    A
           CT                     TAT  AGTCCATA   TCGG GTT
                                |||  ||||||||   |||| |||
                                ATA  TCAGGTAT   AGTC CGA
                                  CC       CGT    C
GAM1564  LOC222008 3'  TATAAAGTCTATATTTGA    38861         C    CG
                                TATAAAGTC ATAT  GA
                                |||||||||  ||||  ||
                                ATATTTCAG TATA  CT
                                     A    AA
GAM1564  LOC253461 3'  TATAAAGTTTATACGGA     38862         CC   T
                                TATAAAGT  ATA CGGA
                                ||||||||  ||| ||||
                                ATATTTCA  TAT GCCT
                                     AA  _
GAM1565  GIF       3'  AGATGTTGAGACTCCAGT    38865     C        GG
                                AGA GTTGAGACTC  AGT
                                ||| ||||||||||  |||
                                TCT CAACTCTGAG  TCA
                                  A         G_
GAM1565  KIAA1954  3'  AAGATGTTGAAACTTGA     38866      C       CG
                                AAGA GTTGAGACT  GA
                                |||| |||||||||  ||
                                TTCT CAACTTTGA  CT
                                  A        A_
GAM1565  LOC221931 3'  GACGTTGAGGCCTAAAGT    38867         A  CG
                                GACGTTGAG CT  GAGT
                                |||||||||  ||  ||||
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                                CTGCAACTC GG  TTCA
                                     C  AT
GAM1566 SLC22A11 3' CTGGCAGCTCTCTCAGC     38870      CCAG   C
                                TTGGT    AGC CTCTCAGC
                                |||||    ||| ||||||||
                                GACCG    TCG GAGAGTCG
                                   _____  A
GAM1566 BOP      5' TCTTGGTAAGAGCCCT      38871    A    CC
                                TC TTGGT  AGAGCCCT
                                || |||||  ||||||||
                                AG AACCA  TCTCGGGA
                                 _    T_
GAM1566 CENTG3   3' TCCTTGGCTTCGTCCTCTCAGC 38872    A    CCAGAGC
                                TC TTGGT      CCTCTCAGC
                                || |||||      |||||||||
                                AG AACCG      GGAGAGTCG
                                 G    AAGCA__
GAM1566 DKFZP434H204 5' TCATTGGTGCAGAGGACATTTC 38873        C    CCCTC_ A
             GGC                   TCATTGGT CAGAG     TC GC
                                |||||||| |||||     || ||
                                AGTAACCA GTCTC     AG CG
                                     C    CTGTAA  C
GAM1566 HSPC072  3' CATTGGTCCAGAGAAAGCAGC  38874           CCCTCT
                                CATTGGTCCAGAG     CAGC
                                ||||||||||||     ||||
                                GTAACCAGGTCTC     GTCG
                                       TTTC__
GAM1566 HSPC111  3' TCACTGGTCCGGGGGACGCCTC 38875        A___ _  CTC
             AGC                   CATTGGTCC    GA GCC   TCAGC
                                |||||||||   || |||  |||||
                                GTGACCAGG   CT CGG   AGTCG
                                     CCCC  G  ___
GAM1566 ICT1     3' TGGTGTGAAAGTCCTCTCAGC  38876     CC_   C
                                TGGT   AGAG CCTCTCAGC
                                ||||   |||| |||||||||
                                ACCA   TTTC GGAGAGTCG
                                  CAC    A
GAM1566 KIAA0349 3' TCTATTGGTCCTCCTCTCAGC  38877    _      AGAGC
                                TC ATTGGTCC    CCTCTCAGC
                                || ||||||||    |||||||||
                                AG TAACCAGG    GGAGAGTCG
                                 A      A____
GAM1566 MGC16824 5' TTGGTCCAAGGCTCAA      38878        A  CCTC
                                TTGGTCCAG GC    TCAG
                                ||||||||| ||    ||||
                                AACCAGGTT CG    AGTT
                                     C  ____
GAM1566 NLI-IF   3' TTGGTAGGGGCCCTCTCAG   38879      CC  A_
                                TTGGT  AG  GCCCTCTCAG
                                |||||  ||  ||||||||||
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                                AACCA  TC  CGGGAGAGTC
                                  __  CC
GAM1566  TBDN100   3'  TCATTGGCCAGTTCTTCAG   38880       T   AGCC  C
                                TCATTGG CCAG   CT TCAG
                                ||||||| ||||   || ||||
                                AGTAACC GGTC   GA AGTC
                                   _   AA__  _
GAM1566  LOC157464 5'  TCATTGTCCAGAGCTACCAAG  38881       G       CCT  C
                                TCATTG TCCAGAGC   CT AG
                                |||||| ||||||||   || ||
                                AGTAAC AGGTCTCG   GG TC
                                   _       AT_  T
GAM1566  LOC201500 5'  TCATTGGCCATGTTCTCAG   38882       T   GAGCCC
                                TCATTGG CCA     TCTCAG
                                ||||||| |||     ||||||
                                AGTAACC GGT     AGAGTC
                                   _   ACA___
GAM1566  LOC221760 3'  TCATTGGTTTCTCTGCCTCTTA 38883        CCAGAGC    C
             G                   TCATTGGT      CCTCT AG
                                 ||||||||      ||||| ||
                                 AGTAACCA      GGAGA TC
                                     AAGAGAC    A
GAM1566  LOC253170 3'  TCTTGGTAAGAGCCCT      38871    A    CC
                                TC TTGGT  AGAGCCCT
                                || |||||  ||||||||
                                AG AACCA  TCTCGGGA
                                  _    T_
GAM1566  LOC85479  5'  TCCTGTCGGAGTTCTCTCAGC  38884    ATTG   CA   CC
                                TC   GTC  GAG  CTCTCAGC
                                ||   |||  |||  ||||||||
                                AG   CAG  CTC  GAGAGTCG
                                 GA__   C_   AA
GAM1567  C11orf9   3'  TGGGAATCGTAAAATTCCTATG 38887     A       TACCAG
             T                   TGG AATCGTAA     TTATGT
                                 ||| ||||||||     ||||||
                                 ACC TTAGCATT     GATACA
                                   C       TTAAG_
GAM1567  KIAA1841  3'  TGGTAACACTACCAGTTGTGT  38888     A   CGTAA      A
                                TGG AAT     TACCAGTT TGT
                                ||| |||     |||||||| |||
                                ACC TTG     ATGGTCAA ACA
                                  A   TG___       C
GAM1568  ATP1B4    3'  TACTGTGTCAATAAGACT    38891            _
                                TACTGTGTTAATAA ACT
                                |||||||||||||| |||
                                ATGACACAGTTATT TGA
                                          C
GAM1568  DKFZP434J193 3'  CTGTGTTAATAGGACACTTT   38892          AAC
                                CTGTGTTAATA   TACTTT
                                ||||||||||   ||||||
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                                GACACAATTAT  GTGAAA
                                     CCT
GAM1568 FLJ14824 3' TGTGTTAATAACTGCTT    38893          A  A
                                TGTGTTAATAA CT CTT
                                |||||||||||  || |||
                                ACACAATTATT GA GAA
                                      _  C
GAM1568 FLJ23537 3' TACTGCAGTAAACTACTTTTT 38894        TTAA
                                TACTGTG   TAAACTACTTTTT
                                |||||||   ||||||||||||
                                ATGACGT   ATTTGATGAAAAA
                                    C___
GAM1568 OSMR     3' TACTGTGTCAGTGAACTA    38895         ATA
                                TACTGTGTTA  AACTA
                                ||||||||||  |||||
                                ATGACACAGT  TTGAT
                                      CAC
GAM1568 LOC221981 3' TACTGTGTCAAACTTT     38896          TAAACT
                                TACTGTGTTAA    ACTTT
                                ||||||||||     |||||
                                ATGACACAGTT    TGAAA
                                      _______
GAM1569 ADH4     3' CAAAACGTGGAGAGAAAAGTAT 38899       AACT
              AA                  TAAAAC   AGAGAAAAGTATAA
                                |||||   ||||||||||||||
                                GTTTTG   TCTCTTTTCATATT
                                   CACC
GAM1569 BLTR2    5' AACCTCTGAGAAAAGTATA   38900     AA  A
                                AAC  CT GAGAAAAGTATA
                                |||  || ||||||||||||
                                TTG  GA CTCTTTTCATAT
                                  GA  _
GAM1569 CSNK2A1  3' TGAACTAAAAATAAAAGTATAA 38901   C       __
                                A AACTAGAGA  AAAGTATAA
                                | |||||||||  |||||||||
                                A TTGATTTTT  TTTCATATT
                                 C        AT
GAM1569 DKFZP434F0318 3' TAAAACACTAGAGAAAA     38902        A
                                TAAAACA CTAGAGAAAA
                                ||||||| ||||||||||
                                ATTTTGT GATCTCTTTT
                                      _
GAM1569 ESDN     3' TGAACTAAAAAGAAGTATA   38903   C       A
                                A AACTAGAGA AAGTATA
                                | |||||||||  |||||||
                                A TTGATTTTT TTCATAT
                                 C        C
GAM1569 FLJ20273 3' TAAGGCAACTAGAAGCATA   38904     AA       GAAA
                                TAA  CAACTAGA    AGTATA
                                |||  ||||||||    ||||||
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                                ATT  GTTGATCT    TCGTAT
                                  CC       ____
GAM1569  KIAA0534  3'  TAAAACAACTGGTAGAAAA   38905          AG_
                                TAAAACAACT   AGAAAA
                                ||||||||||   ||||||
                                ATTTTGTTGA   TCTTTT
                                     CCA
GAM1569  METAP2    3'  AACACCAGAGGGTATA      38906      A     AAAA
                                AACA CTAGAG    GTATA
                                ||||  ||||||    |||||
                                TTGT GGTCTC    CATAT
                                  _     C___
GAM1569  RBPMS     3'  AACAGCTAGAGAACAGTA     38907      A       A
                                AACA CTAGAGAA AGTA
                                ||||  |||||||| ||||
                                TTGT GATCTCTT TCAT
                                  C       G
GAM1569  SET07     3'  AAAACAACTAGAATATA      38908           GAAAA
                                AAAACAACTAGA    GTATA
                                ||||||||||||    |||||
                                TTTTGTTGATCT    TATAT
                                                _____
GAM1569  SPUF      3'  CAAGCACAGAAAAGTATA     38909     C  G
                                CAA TA AGAAAAGTATA
                                |||  ||  ||||||||||
                                GTT GT TCTTTTCATAT
                                  C  G
GAM1569  TTYH2     3'  TAAAACACTGGAGAAAA      38910        A  A
                                TAAAACA CT GAGAAAA
                                |||||||  ||  |||||||
                                ATTTTGT GA CTCTTTT
                                     _  C
GAM1569  ZNF262    3'  TAAAACAACGGGAGAAAA     38911          TA
                                TAAAACAAC  GAGAAAA
                                |||||||||  |||||||
                                ATTTTGTTG  CTCTTTT
                                      CC
GAM1569  ZNF282    3'  AAAACACTTAAAAAAGTATAA  38912        ACTAG
                                AAAACA    AGAAAAGTATAA
                                ||||||    ||||||||||||
                                TTTTGT    TTTTTTCATATT
                                   GAA__
GAM1569  LOC146540 3'  TAAAACAAATAGAGAAAA     38913         C
                                TAAAACAA TAGAGAAAA
                                ||||||||  |||||||||
                                ATTTTGTT ATCTCTTTT
                                      T
GAM1569  LOC168667 3'  ACAACTAATTGTAAAGTATAA  38914          AGA_
                                ACAACTAG    AAAGTATAA
                                ||||||||    |||||||||
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                                TGTTGATT    TTTCATATT
                                     AACA
GAM1569  LOC201965 3'  CAAATCAAGAGAAAAGTATAA  38915      A  ACT
                                TAAA CA   AGAGAAAAGTATAA
                                |||| ||   ||||||||||||||
                                GTTT GT   TCTCTTTTCATATT
                                  A  ___
GAM1569  LOC219686 3'  CAACAGAGAAGTATA       38916      T    AA
                                CAAC AGAGA  AGTATA
                                |||| |||||  ||||||
                                GTTG TCTCT  TCATAT
                                  _    __
GAM1569  LOC219848 3'  TAAAACAACTGTGGGAGAA   38917          A___
                                TAAAACAACT    GAGAA
                                ||||||||||    |||||
                                ATTTTGTTGA    CTCTT
                                      CACC
GAM1569  LOC253295 3'  AAACAAATAGAGAAAAGTA   38918       C
                                AAACAA TAGAGAAAAGTA
                                |||||| ||||||||||||
                                TTTGTT ATCTCTTTTCAT
                                   T
GAM1570  ACHE     3'  TGAGGAGGAAGGGAGCACTAGG 38921          AA    AA_
                                TGAGGAGGAG  GGAG   TGGG
                                ||||||||||  ||||   ||||
                                ACTCCTCCTT  CCTC   ATCC
                                      C_    GTG
GAM1570  ALMS1     5'  GAGGAGGAGGGGGGGAGGGA   38924         AA  A  ATG
                                GAGGAGGAG  GG GA   GGGA
                                |||||||||  || ||   ||||
                                CTCCTCCTC  CC CT   CCCT
                                      CC  C  ___
GAM1570  ALMS1     5'  GAGGAGGAGGAGGAGGGGG    38923         A    AAT
                                GAGGAGGAG AGGAG   GGGG
                                |||||||||| |||||   ||||
                                CTCCTCCTC TCCTC   CCCC
                                      C    ___
GAM1570  ALMS1     5'  GGAGGAGGAGGAGGGGG     38922        A    AAT
                                GGAGGAG AGGAG   GGG
                                ||||||| |||||   |||
                                CCTCCTC TCCTC   CCC
                                    C    C__
GAM1570  AMFR      3'  GAGGGGAGGGGACCCATGGGG  38925      A   AA  GA_
                                GAGG GGAG  GGA   ATGGGG
                                |||| ||||  |||   ||||||
                                CTCC CCTC  CCT   TACCCC
                                  _   C_   GGG
GAM1570  AMFR      3'  GAGGGGAGGGGACCCATGGGG  38925      A   AA  GA_
                                GAGG GGAG  GGA   ATGGGG
                                |||| ||||  |||   ||||||
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                              CTCC CCTC  CCT   TACCCC
                                _   C_  GGG
GAM1570 AR      5'  GAGGGGGGGAAGGCAGGGTGGG 38926     A  A    _  AA
             G                 GAGG GG GAAGG AG  TGGGG
                               |||| || ||||| ||  |||||
                               CTCC CC CTTCC TC  ACCCC
                                 C  C    G  CC
GAM1570 ARD1    3'  TGAGGAGGGGATGGGG     38927        AGAA   GAA
                               TGAGGAGG   GGA   TGGGG
                               ||||||||   |||   |||||
                               ACTCCTCC   CCT   ACCCC
                                    _____  ___
GAM1570 ATP2B4   5'  GAGGAGGAAGAGGATGGGG   38928        GA   GAA
                               GAGGAGGA  AGGA   TGGGG
                               ||||||||  ||||   |||||
                               CTCCTCCT  TCCT   ACCCC
                                    TC   ___
GAM1570 AXL     5'  TGAGGAGGGGGAAGGGGA    38929        AGAA  A   T
                               TGAGGAGG   GG GAA GGGGA
                               ||||||||   || ||| |||||
                               ACTCCTCC   CC CTT CCCCT
                                    _____ _  _
GAM1570 AXL     5'  TGAGGAGGGGGAAGGGGA    38929        AGAA  A   T
                               TGAGGAGG   GG GAA GGGGA
                               ||||||||   || ||| |||||
                               ACTCCTCC   CC CTT CCCCT
                                    _____ _  _
GAM1570 BAK1    3'  GAGGAGCATGGAGGGTGGGG  38930       AA_   AA
                               GAGGAG  GGAG  TGGGG
                               ||||||  ||||  |||||
                               CTCCTC  CCTC  ACCCC
                                  GTA   CC
GAM1570 BCAS1    3'  TGGGGAGGAGATGGAGTAAGGA 38931    A      A   AA
                               TG GGAGGAGA GGAG  TGGGGA
                               || |||||||| ||||  ||||||
                               AC CCTCCTCT CCTC  ATTCCT
                                C      A   __
GAM1570 BTG2    3'  TGGGGAGGAGAACCTGGGG   38932    A      GGAGAA
                               TG GGAGGAGAA     TGGGG
                               || |||||||||     |||||
                               AC CCTCCTCTT     ACCCC
                                C       GG____
GAM1570 C1orf6   5'  GAGGAGGAGGAGGGGCGGG   38933        A  AGAA
                               GAGGAGGAG AGG   TGGG
                               ||||||||| |||   ||||
                               CTCCTCCTC TCC   GCCC
                                    C  CC__
GAM1570 CACNA1D  5'  TGAGGCGGGGGCGGAATGGGGA 38934      A  AGAA  A_
                               TGAGG GG   GG  GAATGGGGA
                               ||||| ||   ||  |||||||||
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                                ACTCC CC   CC  CTTACCCCT
                                   G  C___  GC
GAM1570  CACNG7   3'  GAGGAGGAGGAGGAGGCAGGGG 38935         A    AAT
                                GAGGAGGAG AGGAG   GGGG
                                ||||||||| |||||   ||||
                                CTCCTCCTC TCCTC   CCCC
                                     C    CGT
GAM1570  CALU     3'  GAGGAGGAGGAATGGGG     38936         AAGGA
                                GAGGAGGAG    GAATGGGG
                                |||||||||    ||||||||
                                CTCCTCCTC    CTTACCCC
                                             _____
GAM1570  CAPN1    3'  TGGGAGGAGAGGGGACAGGA   38937    A      A  A  A
                                TG GGAGGAGA GG GA TGGGG
                                || |||||||| || || |||||
                                AC CCTCCTCT CC CT GTCCT
                                 _      C  _  _
GAM1570  CD34     3'  GGGGAGGGGGAGGTGGGA    38938    A   AA   AA
                                GG GGAG  GGAG  TGGGG
                                || ||||  ||||  |||||
                                CC CCTC  CCTC  ACCCT
                                 _   CC   C_
GAM1570  CDK4     3'  TGGGAAGGAGAAGGAGAA    38939    A
                                TG GGAGGAGAAGGAGAA
                                || ||||||||||||||
                                AC CTTCCTCTTCCTCTT
                                 C
GAM1570  CDK4     3'  TGGGAAGGAGAAGGAGAA    38939    A
                                TG GGAGGAGAAGGAGAA
                                || ||||||||||||||
                                AC CTTCCTCTTCCTCTT
                                 C
GAM1570  CDS1     5'  GAGGAGGAGAAGGGGCGGGGA  38940           AGAA
                                GAGGAGGAGAAGG   TGGGGA
                                ||||||||||||   ||||||
                                CTCCTCCTCTTCC   GCCCCT
                                       CC__
GAM1570  CELSR2   3'  GAGGAGAGGGGAGGAGAGGTGG 38941       ____    A_
            GGA                  GAGGAGA   AGGAGA  TGGGGA
                                |||||||   ||||||  ||||||
                                CTCCTCT   TCCTCT  ACCCCT
                                    CCCC    CC
GAM1570  CELSR2   3'  TGAGGGGAGAAGACAGGGG   38942      A      AGAAT
                                TGAGG GGAGAAGG    GGGG
                                ||||| ||||||||    ||||
                                ACTCC CCTCTTCT    CCCC
                                   _      GT___
GAM1570  CHAD     3'  AGAGGAGCTGGAGGGTGGGGA  38943       AA   AA
                                GGAGGAG  GGAG  TGGGGA
                                |||||||  ||||  ||||||
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                                TCTCCTC  CCTC  ACCCCT
                                    GA   CC
GAM1570  CKTSF1B1  3'  TGAGGAGGAGGAGGAAAGGA  38944        A    AATG
                                TGAGGAGGAG AGGAG   GGGA
                                |||||||||| |||||   ||||
                                ACTCCTCCTC TCCTT   TCCT
                                     C    _____
GAM1570  CLTC      5'  GAGGAGGAGAAGGGGAGGGG  38945          A  AT
                                GAGGAGGAGAAGG GA  GGGG
                                |||||||||||| ||  ||||
                                CTCCTCCTCTTCC CT  CCCC
                                      C  __
GAM1570  COL5A3    3'  TGAGGAGGCAGGCATTGGGG  38946       AGA  AGAA
                                TGAGGAGG  AGG   TGGGG
                                ||||||||  |||   |||||
                                ACTCCTCC  TCC   ACCCC
                                    G__  GTA_
GAM1570  CRY2      3'  TGAGGAGGGAGGGAAGGA   38947       A  A  A  T
                                TGAGGAGG GA GG GAA GGG
                                |||||||| || || ||| |||
                                ACTCCTCC CT CC CTT CCT
                                    _  _  _  _
GAM1570  CSF3R     3'  TGGGAGGAGAGGGAGATGCTGG 38948    A      A    A  G_
                                TG GGAGGAGA GGAGA TG  GG
                                || |||||||| ||||| ||  ||
                                AC CCTCCTCT CCTCT AC  CC
                                 _      C    _ GA
GAM1570  CX3CR1    3'  TGGGAAGGAGGAGGCAATGGGG 38949    A     A  AG
            A                    TG GGAGGAG AGG  AATGGGGA
                                || ||||||| |||  ||||||||
                                AC CTTCCTC TCC  TTACCCCT
                                 C      C  G_
GAM1570  DMPK      3'  TGAGGAGGGGGGCGCGGGA   38950       AGAA  AGAA
                                TGAGGAGG   GG   TGGGG
                                ||||||||   ||   |||||
                                ACTCCTCC   CC   GCCCT
                                    CC__  GC__
GAM1570  DNM2      3'  GAGGAGGAGGAGGAGAGGA   38951        A    AT
                                GAGGAGGAG AGGAGA  GGG
                                ||||||||| ||||||  |||
                                CTCCTCCTC TCCTCT  CCT
                                     C    __
GAM1570  ESRRA     3'  GGAGGAGAGGGCGTGGGG    38952       A  AGAA
                                GGAGGAGA GG   TGGGG
                                |||||||| ||   |||||
                                CCTCCTCT CC   ACCCC
                                    C  GC__
GAM1570  FGFRL1    3'  AGGGGGAGAATGCAGTGGGGA  38953    A    GGAGAA
                                AGG GGAGAA     TGGGGA
                                ||| ||||||     ||||||
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                                TCC CCTCTT     ACCCCT
                                  C     ACGTC_
GAM1570  FOXD1    5'  TGAGGAGGGGGTGGCGGGG   38954        AGAA  AGAA
                                TGAGGAGG   GG   TGGGG
                                ||||||||   ||   |||||
                                ACTCCTCC   CC   GCCCC
                                     CCCA  ____
GAM1570  FOXF2    3'  TGAGGAGGGGAGAGGAGA    38955        A  _
                                TGAGGAGG GA AGGAGA
                                |||||||| || ||||||
                                ACTCCTCC CT TCCTCT
                                     C  C
GAM1570  GAB2     3'  TGGGAGCTGAAAGGGGAATGGG 38956    A   GA_    A
              G                   TG GGAG   GAAGG GAATGGGG
                                || ||||   ||||| ||||||||
                                AC CCTC   TTTCC CTTACCCC
                                 _   GAC    C
GAM1570  GAB2     3'  TGGGAGCTGAAAGGGGAATGGG 38956    A   GA_    A
              G                   TG GGAG   GAAGG GAATGGGG
                                || ||||   ||||| ||||||||
                                AC CCTC   TTTCC CTTACCCC
                                 _   GAC    C
GAM1570  GRB14    5'  GAGGAGGAGGGTGGG       38958         AA  AGAA
                                GAGGAGGAG  GG   TGGG
                                |||||||||  ||   ||||
                                CTCCTCCTC  CC   ACCC
                                       __  _____
GAM1570  GRB14    5'  GGGGAGAGGGGAGGAG      38957    A    A  A  AT
                                GG GGAGA GG GA  GGGG
                                || ||||| || ||  ||||
                                CC CCTCT CC CT  CCTC
                                 _    C  _  __
GAM1570  HDAC2    5'  TGGGAGGAGAGGAGGGG     38959    A      A   AAT
                                TG GGAGGAGA GGAG   GGG
                                || |||||||| ||||   |||
                                AC CCTCCTCT CCTC   CCC
                                 _      _   ____
GAM1570  HHIP     5'  GAGGAGGAGAAGGAGTTGGA   38960            AA
                                GAGGAGGAGAAGGAG  TGGG
                                ||||||||||||||  ||||
                                CTCCTCCTCTTCCTC  ACCT
                                         A_
GAM1570  HMGA2    5'  GAGGAGGAGGAGGAGAGGA   38951         A     AT
                                GAGGAGGAG AGGAGA  GGG
                                |||||||||  ||||||  |||
                                CTCCTCCTC TCCTCT  CCT
                                     C     __
GAM1570  HOXA3    3'  GGGGGAAGGAGAGGA       38961    A  A      AT
                                GG GG GAAGGAGA  GGG
                                || || ||||||||  |||
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                                CC CC CTTCCTCT  CCT
                                 _ _     __
GAM1570 HOXB5    3' TGAGGAGGGAGGAGGAGG    38962       A A   AAT
                                TGAGGAGG GA GGAG   GGGG
                                |||||||| || ||||   ||||
                                ACTCCTCC CT CCTC   CTCC
                                   _ _   ___
GAM1570 IL13RA1  3' TGAGGAGAGAAATGGGGTGGGG 38963       _   A AGAA
                                TGAGGAG GAGA GG    TGGGG
                                ||||||| |||| ||    |||||
                                ACTCCTC CTTT CC    ACCCC
                                    T   A CC__
GAM1570 JJAZ1    5' GGAGGAGAGGGGAAGGGA    38964       A A   T
                                GGAGGAGA GG GAA GGGG
                                |||||||| || ||| ||||
                                CCTCCTCT CC CTT CCCT
                                     C _  _
GAM1570 KCNJ16   3' TGAGGGGGAGGAGGGAA    38965      A   A  A
                                TGAGG GGAG AGG GAA
                                ||||| |||| ||| |||
                                ACTCC CCTC TCC CTT
                                   C   C  _
GAM1570 KCNK7    3' TGGGGAGGAGAAGGTGCTGGGG 38966    A        AGAA
                                TG GGAGGAGAAGG   TGGGG
                                || ||||||||||   |||||
                                AC CCTCCTCTTCC   ACCCC
                                 C         ACG_
GAM1570 KLHL3    3' TGAGGGGAGGGGAGGATGGGG  38967     A   AA   A
                                TGAGG GGAG  GGAG ATGGGG
                                ||||| ||||  |||| ||||||
                                ACTCC CCTC  CCTC TACCCC
                                   _   C_   C
GAM1570 LAG3     5' TGAGGAGGTGGGGGCGGGG   38968       AGAA  AGAA
                                TGAGGAGG   GG   TGGGG
                                ||||||||   ||   |||||
                                ACTCCTCC   CC   GCCCC
                                     ACCC  ____
GAM1570 LIMK1    3' TGAGGAGGGGCAGGGAGCCTTG 38969       AGAA_   AA_
            GGG                    TGAGGAGG    GGAG   TGGGG
                                ||||||||    ||||  |||||
                                ACTCCTCC    CCTC   ACCCC
                                     CCGTC   GGA
GAM1570 LIMK1    3' TGAGGAGGGGCAGGGAGCCTTG 38969       AGAA_   AA_
            GGG                    TGAGGAGG    GGAG   TGGGG
                                ||||||||    ||||  |||||
                                ACTCCTCC    CCTC   ACCCC
                                     CCGTC   GGA
GAM1570 LPL      5' TGAGGAGGAGGAAGAGGGG   38970        AA    AT
                                TGAGGAGGAG  GGAGA  GGGG
                                ||||||||||  |||||  ||||
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                                ACTCCTCCTC  CTTCT  CCCC
                                      __    __
GAM1570 LTF     3'  GGGGAGAAGAGCTGGGG     38971    A      AGAA
                                GG GGAGAAGG    TGGGG
                                || ||||||||    |||||
                                CC CCTCTTCT    ACCCC
                                 _       CG__
GAM1570 LY9     3'  TGAGAAGGAGGGGGAGGGG   38972          AA   GAAT
                                TGAGGAGGAG  GGA   GGGG
                                ||||||||||  |||   ||||
                                ACTCTTCCTC  CCT   CCCC
                                      CC  _____
GAM1570 MGAT5    5'  TGGGGAGGAGAGAGGGG    38973    A      AG   AAT
                                TG GGAGGAGA  GAG   GGG
                                || ||||||||  |||   |||
                                AC CCTCCTCT  CTC   CCC
                                 C       __   ____
GAM1570 MLLT7    3'  TGGGGTGGAGAAGGAGCCCCAG 38974    A  A        AA_
              A                  TG GG GGAGAAGGAG   TGGG
                                || || ||||||||||   ||||
                                AC CC CCTCTTCCTC   GTCT
                                 C  A         GGG
GAM1570 MN1     5'  TGGGGAGGGAAGGGGGTTGGGA 38976    A    A    AGAA
                                TG GGAGG GAAGG    TGGGG
                                || ||||| |||||    |||||
                                AC CCTCC CTTCC    ACCCT
                                 C     _    CCCA
GAM1570 MN1     5'  TAAGTGGGGGGAATGGGG    38975     GA  AGAA  A
                                TGAG  GG    GG GAATGGGG
                                ||||  ||    || ||||||||
                                ATTC  CC    CC CTTACCCC
                                  AC  _____  _
GAM1570 MUC3B    3'  TGAGGAGGAGGGAGACTGAGGG 38977          AA    AT__
              G                  TGAGGAGGAG  GGAGA   GGGG
                                ||||||||||  |||||   ||||
                                ACTCCTCCTC  CCTCT   CCCC
                                      __    GACT
GAM1570 MUC4    5'  TGGGAGGAGACATGGG     38978    A      AGGAGA
                                TG GGAGGAGA     ATGGG
                                || ||||||||     |||||
                                AC CCTCCTCT     TACCC
                                 _       G_____
GAM1570 MUC4    5'  TGGGAGGAGACATGGG     38978    A      AGGAGA
                                TG GGAGGAGA     ATGGG
                                || ||||||||     |||||
                                AC CCTCCTCT     TACCC
                                 _       G_____
GAM1570 NCALD    3'  TGGGAAGGAGAAGGAGAA    38939    A
                                TG GGAGGAGAAGGAGAA
                                || ||||||||||||||
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                                AC CTTCCTCTTCCTCTT
                                 C
GAM1570  NCALD    3'  TGGGGAAGAGAGGGGAGTGGG  38979    A      A  A  A
                                TG GGAGGAGA GG GA TGGG
                                || |||||||| || || ||||
                                AC CCTTCTCT CC CT ACCC
                                 C       C  _  C
GAM1570  NEDD4    5'  GAGGAGGAGGAGGAGAAGCGGG 38980          A      _
            A                    GAGGAGGAG AGGAGAA TGGGG
                                ||||||||| ||||||| |||||
                                CTCCTCCTC TCCTCTT GCCCT
                                      C      C
GAM1570  NKX2H    5'  GAGGAGGGGAAGGAGGCGGGG  38981        A      AA
                                GAGGAGG GAAGGAG  TGGGG
                                ||||||| |||||||  |||||
                                CTCCTCC CTTCCTC  GCCCC
                                    C      C_
GAM1570  NPDC1    5'  GAGGAGGAGGAGGAAGAGGA   38982          A    AAT
                                GAGGAGGAG AGGAG   GGGGA
                                ||||||||| |||||   |||||
                                CTCCTCCTC TCCTT   CTCCT
                                      C    ___
GAM1570  NPR1     3'  TGGGGAGGGGAGGGGATCAGGA 38983    A    A  A  A  A G
                                TG GGAGG GA GG GA T GGGA
                                || ||||| || || || | ||||
                                AC CCTCC CT CC CT A TCCT
                                 C    C  C  _  _ G
GAM1570  NRXN2    3'  GAAGTAGGGAAGGAGGGTGGGG 38984     _  A      AA
            A                    GAGG AGG GAAGGAG  TGGGGA
                                |||| ||| |||||||  ||||||
                                CTTC TCC CTTCCTC  ACCCCT
                                  A  _      CC
GAM1570  NRXN2    3'  GAAGTAGGGAAGGAGGGTGGGG 38984     _  A      AA
            A                    GAGG AGG GAAGGAG  TGGGGA
                                |||| ||| |||||||  ||||||
                                CTTC TCC CTTCCTC  ACCCCT
                                  A  _      CC
GAM1570  NRXN2    3'  GAAGTAGGGAAGGAGGGTGGGG 38984     _  A      AA
            A                    GAGG AGG GAAGGAG  TGGGGA
                                |||| ||| |||||||  ||||||
                                CTTC TCC CTTCCTC  ACCCCT
                                  A  _      CC
GAM1570  ODF2     5'  TGAGGGGAGAAGGGTGGA    38985      A      AGAA
                                TGAGG GGAGAAGG    TGGG
                                ||||| ||||||||    ||||
                                ACTCC CCTCTTCC    ACCT
                                   _      C___
GAM1570  OGDH     3'  GGGGAGGGAGTCCAAGA     38986    A   AA   AA
                                GG GGAG  GGAG  TGGGG
                                || ||||  ||||  |||||
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                                CC CCTC  CCTC  GTTCT
                                 _  __   AG
GAM1570 PCDH12   5' TGAGGAGGATGAGGCCGGGG  38987       GA  AGAA
                                TGAGGAGGA AGG   TGGGG
                                ||||||||| |||   |||||
                                ACTCCTCCT TCC   GCCCC
                                    AC  G___
GAM1570 PCDHGA1  3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGA10 3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGA11 3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGA11 3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGA12 3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGA2  3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGA3  3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGA4  3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGA5  3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
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                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGA6  3' TGAGGAGGAGGTGGGGGA   38988      AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGA7  3' TGAGGAGGAGGTGGGGGA   38988      AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGA8  3' TGAGGAGGAGGTGGGGGA   38988      AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGA9  3' TGAGGAGGAGGTGGGGGA   38988      AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGB1  3' TGAGGAGGAGGTGGGGGA   38988      AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGB2  3' TGAGGAGGAGGTGGGGGA   38988      AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGB3  3' TGAGGAGGAGGTGGGGGA   38988      AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGB4  3' TGAGGAGGAGGTGGGGGA   38988      AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGB5  3' TGAGGAGGAGGTGGGGGA   38988      AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1570 PCDHGB6  3' TGAGGAGGAGGTGGGGGA   38988      AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
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                                ACTCCTCCTC CC    CCCT
                                     CA _____
GAM1570 PCDHGB7  3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG    GGGG
                                |||||||||| ||    ||||
                                ACTCCTCCTC CC    CCCT
                                     CA _____
GAM1570 PCDHGC3  3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG    GGGG
                                |||||||||| ||    ||||
                                ACTCCTCCTC CC    CCCT
                                     CA _____
GAM1570 PCDHGC3  3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG    GGGG
                                |||||||||| ||    ||||
                                ACTCCTCCTC CC    CCCT
                                     CA _____
GAM1570 PCDHGC4  3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG    GGGG
                                |||||||||| ||    ||||
                                ACTCCTCCTC CC    CCCT
                                     CA _____
GAM1570 PCDHGC5  3' TGAGGAGGAGGTGGGGGA   38988       AA AGAAT
                                TGAGGAGGAG GG    GGGG
                                |||||||||| ||    ||||
                                ACTCCTCCTC CC    CCCT
                                     CA _____
GAM1570 PCOLN3   3' TGAGGAGGGGAGGGCAGGA   38989      AGAA   AA
                                TGAGGAGG   GGAG TGGGG
                                ||||||||   |||| |||||
                                ACTCCTCC   CCTC GTCCT
                                     _____  CC
GAM1570 PCTK1    5' TGAGGAGGAGGAGGCGGCGG  38990       A  AGAA  _
                                TGAGGAGGAG AGG   TGG GG
                                |||||||||| |||   ||| ||
                                ACTCCTCCTC TCC   GCC CC
                                     C  _____  G
GAM1570 PCTK1    5' TGAGGAGGAGGAGGCGGCGG  38990       A  AGAA  _
                                TGAGGAGGAG AGG   TGG GG
                                |||||||||| |||   ||| ||
                                ACTCCTCCTC TCC   GCC CC
                                     C  _____  G
GAM1570 PIK3C2B  3' TGGGGAGTGATGGATGGGG   38991   A   GA A  GAA
                                TG GGAG  GA GGA   TGGGG
                                || ||||  || |||   |||||
                                AC CCTC  CT CCT   ACCCC
                                 C   A_ A  ___
GAM1570 PLAT     3' GAGAGCCAGGGAGTGGGG    38992    G A_  A A
                                GAG AG  AGG GA TGGGG
                                ||| ||  ||| || |||||
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                                CTC TC  TCC CT ACCCC
                                  _ GG  _ C
GAM1570 PLAT    3' GAGAGCCAGGGAGTGGGG   38992    G A_  A A
                                GAG AG  AGG GA TGGGG
                                ||| ||  ||| || |||||
                                CTC TC  TCC CT ACCCC
                                  _ GG  _ C
GAM1570 PLXNB3  3' GGGGAGAGGGGGAAGGA    38993   A   A A  T
                                GG GGAGA GG GAA GGG
                                || ||||| || ||| |||
                                CC CCTCT CC CTT CCT
                                 _   C C  _
GAM1570 POU2F2  3' GGAGGAGGAGGAGGATGAGGA 38994      A   A
                                GGAGGAG AGGAG ATGGGGA
                                ||||||| ||||| |||||||
                                CCTCCTC TCCTC TACTCCT
                                    C   C
GAM1570 PPP2R2B 5' TGAGGAGGAGACGGGG     38995        AGGAGAA
                                TGAGGAGGAGA     TGGGG
                                ||||||||||      |||||
                                ACTCCTCCTCT     GCCCC
                                          ________
GAM1570 PREB    3' TGAGGGGAGGAGGAGAA    38996     A  A
                                TGAGG GGAG AGGAGAA
                                ||||| |||| |||||||
                                ACTCC CCTC TCCTCTT
                                   _  C
GAM1570 PRKCM   5' GGAGGAGGAGGAGGGCGAGGA 38997      A   AA
                                GGAGGAG AGGAG  TGGGGA
                                ||||||| |||||  ||||||
                                CCTCCTC TCCTC  GCTCCT
                                    C   CC
GAM1570 PRKCM   5' GAGGAGGAGGAGGAGGG    38998       A  GAAT
                                GAGGAGGAG AGGA   GGG
                                ||||||||| ||||   |||
                                CTCCTCCTC TCCT   CCC
                                     C  _____
GAM1570 PSD     3' GGGGAGGAAGGAGGGGA    38999   A  _    AAT
                                GG GGAG AAGGAG  GGGG
                                || |||| ||||||  ||||
                                CC CCTC TTCCTC  CCCT
                                 _  C    ___
GAM1570 RAD51L1 3' TGGGAGGAGGGGGGAAATAGGA 39000   A    AA AG
                                TG GGAGGAG  GG  AATGGGG
                                || |||||||  ||  |||||||
                                AC CCTCCTC  CC  TTATCCT
                                 _     C_ CT
GAM1570 RARA    3' TGAGGAGGAGAACTGGGG   39001        GGAGAA
                                TGAGGAGGAGAA    TGGGG
                                ||||||||||||    |||||
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                                ACTCCTCCTCTT     ACCCC
                                      G_____
GAM1570  RORA     5'  TGATGGGGAGGAGTATGGGG   39002     _ A   GAA    A
                                TGA GG GGA   GGAG ATGGGG
                                ||| || |||   |||| ||||||
                                ACT CC CCT   CCTC TACCCC
                                  A _  ___    A
GAM1570  RORA     5'  TGATGGGGAGGAGTATGGGG   39002     _ A   GAA    A
                                TGA GG GGA   GGAG ATGGGG
                                ||| || |||   |||| ||||||
                                ACT CC CCT   CCTC TACCCC
                                  A _  ___    A
GAM1570  RORB     5'  TGAGGAGGAGGAGGAAGGG   39003         A   GAAT
                                TGAGGAGGAG AGGA    GGGG
                                |||||||||| ||||    ||||
                                ACTCCTCCTC TCCT    TCCC
                                      C   _____
GAM1570  SET7     5'  GAGGAGGAGGAGGAAGAGGA  38982         A    AAT
                                GAGGAGGAG AGGAG   GGGGA
                                ||||||||| |||||   |||||
                                CTCCTCCTC TCCTT   CTCCT
                                     C    ___
GAM1570  SIX3     3'  GAGGAGGAGAAGGAAGAGGA  39006           AAT
                                GAGGAGGAGAAGGAG   GGGGA
                                |||||||||||||||   |||||
                                CTCCTCCTCTTCCTT   CTCCT
                                                  ___
GAM1570  SIX3     5'  GAGGAGGAGAAGGAAAGG    39005           AATG
                                GAGGAGGAGAAGGAG    GGG
                                ||||||||||||||    |||
                                CTCCTCCTCTTCCTT    TCC
                                                  _____
GAM1570  SIX3     3'  GAGGAGGGGAAGGAGAGGGA  39004       A       ATG
                                GAGGAGG GAAGGAGA   GGGA
                                ||||||| ||||||||   ||||
                                CTCCTCC CTTCCTCT   CCCT
                                    C       ____
GAM1570  SLC2A4   3'  TGGGGAGGAAAGGGGATGGGG  39007    A       A  A  A
                                TG GGAGGAGA GG GA TGGGG
                                || |||||||| || || |||||
                                AC CCTCCTTT CC CT ACCCC
                                  C       C  _  _
GAM1570  SLC5A1   3'  TGGGGAGGAGGACGGACAGGA  39008    A      AA_   GAA
                                TG GGAGGAG   GGA   TGGGG
                                || |||||||   |||   |||||
                                AC CCTCCTC   CCT   GTCCT
                                  C      CTG   ____
GAM1570  SLC9A1   3'  TGAGGAGGAGGATGAGG     39009          AAGGA  A
                                TGAGGAGGAG    GA TGGGG
                                ||||||||||    || |||||
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                                ACTCCTCCTC    CT ACTCC
                                      _____ _
GAM1570  SMARCD1  3'  TGAGGAGGGGGTGGGGAAGCAG 39010       AGAA__   AAT
           GGG                  TGAGGAGG    GGAG  GGGG
                                ||||||||    ||||  ||||
                                ACTCCTCC    CCTT  CCCC
                                   CCCACC   CGT
GAM1570  SMARCD1  3'  TGAGGAGGGGGTGGGGAAGCAG 39010       AGAA__   AAT
           GGG                  TGAGGAGG    GGAG  GGGG
                                ||||||||    ||||  ||||
                                ACTCCTCC    CCTT  CCCC
                                   CCCACC   CGT
GAM1570  SMCX     3'  AAAGAGGGGAGGAGAGTGGGG 39011       A A   A
                                GAGGAGG GA GGAGA TGGGG
                                ||||||| || ||||| |||||
                                TTTCTCC CT CCTCT ACCCC
                                   C _   C
GAM1570  SOX9     5'  GAGGAGGAGGAGGGGAGG   39012       A  AGAAT
                                GAGGAGGAG AGG   GGGG
                                ||||||||| |||   ||||
                                CTCCTCCTC TCC   CTCC
                                   C  C____
GAM1570  STAU     5'  GAGGAGGGGAAGGAAGAAGGA 39013       A   _  T
                                GAGGAGG GAAGGA GAA GGG
                                ||||||| |||||| ||| |||
                                CTCCTCC CTTCCT CTT CCT
                                   C    T  _
GAM1570  STAU     5'  GAGGAGGGGAAGGAAGAAGGA 39013       A   _  T
                                GAGGAGG GAAGGA GAA GGG
                                ||||||| |||||| ||| |||
                                CTCCTCC CTTCCT CTT CCT
                                   C    T  _
GAM1570  STAU     5'  GAGGAGGGGAAGGAAGAAGGA 39013       A   _  T
                                GAGGAGG GAAGGA GAA GGG
                                ||||||| |||||| ||| |||
                                CTCCTCC CTTCCT CTT CCT
                                   C    T  _
GAM1570  STAU     5'  GAGGAGGGGAAGGAAGAAGGA 39013       A   _  T
                                GAGGAGG GAAGGA GAA GGG
                                ||||||| |||||| ||| |||
                                CTCCTCC CTTCCT CTT CCT
                                   C    T  _
GAM1570  TAF1C    3'  TGAGAAGGGGAGGGAG    39014       AGAA  AAT
                                TGAGGAGG   GGAG  GGG
                                ||||||||   ||||  |||
                                ACTCTTCC   CCTC  CTC
                                     _____  C__
GAM1570  TAF4     3'  TGGGAGGGGAAGGGAAGGA  39015   A   A   A  T
                                TG GGAGG GAAGG GAA GGG
                                || ||||| ||||| ||| |||
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                                AC CCTCC CTTCC CTT CCT
                                 _    C    _  _
GAM1570  TBL1X    3'  GGAGGAGAGGGTGGGA     39016        A  AGAA
                                GGAGGAGA GG    TGGGG
                                |||||||| ||    |||||
                                CCTCCTCT CC    ACCCT
                                     C ____
GAM1570  TBR1     3'  GGGGAGGCGGAGCTGGGG    39017    A   AA   AA
                                GG GGAG  GGAG  TGGGG
                                || ||||  ||||  |||||
                                CC CCTC  CCTC  ACCCC
                                 _   CG   G_
GAM1570  TCF7L2   5'  GAGGAGGGGAGGGGAAGGGGG  39018       A  A  A   T
                                GAGGAGG GA GG GAA GGGG
                                ||||||| || || ||| ||||
                                CTCCTCC CT CC CTT CCCC
                                     C  C  _  C
GAM1570  TEGT     3'  TGAGGGGTGGAAGGAGAGGA   39019      A  A_      AT
                                TGAGG GG  GAAGGAGA  GGG
                                ||||| ||  ||||||||  |||
                                ACTCC CC  CTTCCTCT  CCT
                                   _ AC      __
GAM1570  TNXB     5'  GGAGGAGAAGGGGAGG      39020          AGAAT
                                GGAGGAGAAGG    GGGG
                                ||||||||||    ||||
                                CCTCCTCTTCC    CTCC
                                       C____
GAM1570  TRIM8    3'  TGGTGAGGAGAAGGAAGCAGGA 39021    AG         AAT
                                TG  GAGGAGAAGGAG   GGGG
                                ||  ||||||||||||   ||||
                                AC  CTCCTCTTCCTT   TCCT
                                 CA          CG_
GAM1570  TTC3     3'  TGGGGTGGGGAAGGAGAATGGT 39022    A  A  A         _
            GG                    TG GG GG GAAGGAGAATGG GG
                                || || || |||||||||||| ||
                                AC CC CC CTTCCTCTTACC CC
                                 C  A  C          A
GAM1570  UBE2V1   3'  GGGGGAGAGAAGATATGGGGA  39023    A    A    _
                                GG GGAGA GGAGA ATGGGGA
                                || ||||| ||||| |||||||
                                CC CCTCT CTTCT TACCCCT
                                 C    _    A
GAM1570  UGCG     5'  GAGGAAAGGGCGGAGGGGGGTG 39024        AGAA   AA___
            GGGA                   GAGGAGG   GGAG    TGGGGA
                                |||||||   ||||    ||||||
                                CTCCTTT   CCTC    ACCCCT
                                    CCCG   CCCCC
GAM1570  VAT1     3'  GGAGGAGAAGGAGGTGGGA   39025          AA
                                GGAGGAGAAGGAG  TGGGG
                                ||||||||||||  |||||
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                                CCTCCTCTTCCTC  ACCCT
                                      C_
GAM1570 VTN      5' TGAGGAAGGGAGGGAGAGG   39026       A  A    AT
                                TGAGGAGG GA GGAGA  GG
                                |||||||| || |||||  ||
                                ACTCCTTC CT CCTCT  CC
                                     C  C    __
GAM1570 ZNF278   5' CGGGGAGGAGAAGGAGGGG   39027    A        GAAT
                                TG GGAGGAGAAGGA   GGGG
                                || ||||||||||||   ||||
                                GC CCTCCTCTTCCT   CCCC
                                 C        _____
GAM1570 ZNF278   5' CGGGGAGGAGAAGGAGGGG   39027    A        GAAT
                                TG GGAGGAGAAGGA   GGGG
                                || ||||||||||||   ||||
                                GC CCTCCTCTTCCT   CCCC
                                 C        _____
GAM1570 ZNF278   5' CGGGGAGGAGAAGGAGGGG   39027    A        GAAT
                                TG GGAGGAGAAGGA   GGGG
                                || ||||||||||||   ||||
                                GC CCTCCTCTTCCT   CCCC
                                 C        _____
GAM1570 ZNF278   5' CGGGGAGGAGAAGGAGGGG   39027    A        GAAT
                                TG GGAGGAGAAGGA   GGGG
                                || ||||||||||||   ||||
                                GC CCTCCTCTTCCT   CCCC
                                 C        _____
GAM1570 20D7-FC4 3' TGAGGGAGAGGATGGG     39028      AG   A  GAA
                                TGAGG  GAGA GGA   TGGG
                                |||||  |||| |||   ||||
                                ACTCC  CTCT CCT   ACCC
                                   __   _  ___
GAM1570 ABCC13   3' TGGGGAGCAGAAAAACAGTGGG 39029    A   G     GAA
           GA                    TG GGAG AGAAGGA   TGGGGA
                                || |||| |||||||   ||||||
                                AC CCTC TCTTTTT   ACCCCT
                                 C   G      GTC
GAM1570 ABLIM    5' TGAGAAATGGGGAGTGGGG   39030       GAGAA   AA
                                TGAGGAG    GGAG  TGGGG
                                |||||||    ||||  |||||
                                ACTCTTT    CCTC  ACCCC
                                    ACC__   __
GAM1570 ADPRTL3  3' TGGGAGGAGAGGGACTGGG   39031    A      A  A  A
                                TG GGAGGAGA GG GA TGGG
                                || |||||||| || || ||||
                                AC CCTCCTCT CC CT ACCC
                                 _      _ _ G
GAM1570 ALOXE3   3' TGGGGAGGATGAGGGAGAA   39032    A     _ A
                                TG GGAGGA GA GGAGAA
                                || |||||| || ||||||
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                                AC CCTCCT CT CCTCTT
                                 C     A  C
GAM1570 AMOTL1   3' AGAGGCAAGGAGAATGGGG   39033      AG
                                GGAGG  AAGGAGAATGGGG
                                |||||  ||||||||||||
                                TCTCC  TTCCTCTTACCCC
                                  G_
GAM1570 ARP3BETA 3' GGAGGAGGAGGAGGAGGG    39034       A    AAT
                                GGAGGAG AGGAG   GGGG
                                |||||||| |||||   ||||
                                CCTCCTC TCCTC   TCCC
                                    C    C__
GAM1570 B3GNT7   3' TGAGGGGAGGGAAGGGAGG   39035      A   AA   AAT
                                TGAGG GGAG  GGAG   GGGG
                                ||||| ||||  ||||   ||||
                                ACTCC CCTC  CCTT   CTCC
                                  _   __    CC_
GAM1570 C19orf7  3' TGAGGAGGAGGGAAGGGG    39036        AA   AAT
                                TGAGGAGGAG  GGAG   GGGG
                                ||||||||||  ||||   ||||
                                ACTCCTCCTC  CCTT   CCCC
                                      __    ____
GAM1570 C1orf34  3' TGAGGAGGGGGTGTGGGG    39037       AGAA  AGAA
                                TGAGGAGG   GG   TGGGG
                                ||||||||   ||   |||||
                                ACTCCTCC   CC   ACCCC
                                     _____  CAC_
GAM1570 C21orf57 5' TGGGGAGAGAAGGGGCTGGAAT 39038    A  AG     A____
            GGGG                   TG GG  GAGAAGG    GAATGGGG
                                || ||  |||||||    ||||||||
                                AC CC  CTCTTCC    CTTACCCC
                                 _ CT      CCGAC
GAM1570 C22orf5  3' TAAGGAGGAGGAGGGGATGGA  39039         A  A  A
                                TGAGGAGGAG AGG GA TGGG
                                |||||||||| ||| || ||||
                                ATTCCTCCTC TCC CT ACCT
                                      C   C  _
GAM1570 CBX6     3' TGAGGAGGGCAGGGGGGTGGGG 39040        AGA   AGAA
                                TGAGGAGG   AGG   TGGGG
                                ||||||||   |||   |||||
                                ACTCCTCC   TCC   ACCCC
                                     CG_   CCCC
GAM1570 CDON     3' GAGGGGGAGGAAGGAATGGGGA 39041     A   A   A
                                GAGG GGAG AGG GAATGGGGA
                                |||| |||| ||| |||||||||
                                CTCC CCTC TTC CTTACCCCT
                                  C   C   _
GAM1570 CL24751  5' GAGGAGGAGGAGGAGGGG    39042        A   GAAT
                                GAGGAGGAG AGGA   GGGG
                                |||||||| ||||   ||||
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                                CTCCTCCTC TCCT   CCCC
                                    C   ____
GAM1570  CL24751   5'  GGAGGAGGAGGAGGGG     39043       A   GAAT
                                GGAGGAG AGGA   GGGG
                                ||||||| ||||   ||||
                                CCTCCTC TCCT   CCCC
                                   C   ____
GAM1570  CL25084   5'  GAGGAGGAGGAGGAGGTGGA  39044        A   AA
                                GAGGAGGAG AGGAG  TGGG
                                ||||||||| |||||  ||||
                                CTCCTCCTC TCCTC  ACCT
                                    C   C_
GAM1570  CLSTN1    3'  TGGGGAGGAGAGAGGAGA   39045   A      _
                                TG GGAGGAGA AGGAGA
                                || |||||||| ||||||
                                AC CCTCCTCT TCCTCT
                                 C       C
GAM1570  CLSTN2    3'  TGAGGAGGAGTGAAGGATGGGG 39046         AA   A
            A                    TGAGGAGGAG  GGAG ATGGGGA
                                ||||||||||  |||| |||||||
                                ACTCCTCCTC  CTTC TACCCCT
                                    A_   C
GAM1570  CNNM4     3'  GAGGAGGAGGAGGAAGGG    39047        A   GAAT
                                GAGGAGGAG AGGA   GGGG
                                ||||||||| ||||   ||||
                                CTCCTCCTC TCCT   TCCC
                                    C   ____
GAM1570  CORO1A    5'  GAGGAGGAGGAGGAAGAGGA  38982        A   AAT
                                GAGGAGGAG AGGAG  GGGGA
                                ||||||||| |||||  |||||
                                CTCCTCCTC TCCTT  CTCCT
                                    C   ___
GAM1570  CRMP5     3'  GGAGGGGAAGGGGAAAGGG   39048      A   A  T
                                GGAGG GAAGG GAA GGG
                                ||||| ||||| ||| |||
                                CCTCC CTTCC CTT CCC
                                   C   C  T
GAM1570  dA141H5.1 3'  TGAGGAGGGAGGATGGGG    39049       A  A  GAA
                                TGAGGAGG GA GGA  TGGGG
                                |||||||| || |||  |||||
                                ACTCCTCC CT CCT  ACCCC
                                    _ _  ___
GAM1570  DKFZP434L1435 3'  TGAGAGGGAGGAAAACTGATGG 39050     GA  _  AGA
            GGA                   TGAG  GGAG AAGG  ATGGGGA
                                ||||  |||| ||||  |||||||
                                ACTC  CCTC TTTT  TACCCCT
                                  TC   C   GAC
GAM1570  DKFZP434L1435 3'  TGAGAGGGAGGAAAACTGATGG 39050     GA  _  AGA
            GGA                   TGAG  GGAG AAGG  ATGGGGA
                                ||||  |||| ||||  |||||||
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                                ACTC  CCTC TTTT   TACCCCT
                                  TC    C    GAC
GAM1570  DKFZP434L1435 3'  TGAGAGGGAGGAAAACTGATGG 39050      GA   _    AGA
            GGA                   TGAG  GGAG AAGG   ATGGGGA
                                |||| |||| ||||   |||||||
                                ACTC  CCTC TTTT   TACCCCT
                                  TC    C    GAC
GAM1570  DKFZp547M072 3'  GAGGAGGAGGAGGAAGAGGA   38982         A    AAT
                                GAGGAGGAG AGGAG   GGGGA
                                ||||||||| |||||   |||||
                                CTCCTCCTC TCCTT   CTCCT
                                     C    ___
GAM1570  DPCR1    3'  TGGGAGGAGAGAGAATGGGGA  39051    A      AG
                                TG GGAGGAGA  GAGAATGGGGA
                                || ||||||||  ||||||||||
                                AC CCTCCTCT  CTCTTACCCCT
                                 _      __
GAM1570  EPB41L1   3'  GAGGCCCAAGAGGGGGAATGGG 39052      AG_   A  A
            GA                    GAGG   GAGA GG GAATGGGGA
                                ||||   |||| || |||||||||
                                CTCC   TTCT CC CTTACCCCT
                                  GGG    C  C
GAM1570  FEM-2    3'  TGAGGGAGAGAAGGACAAGGA  39053      AG       G  T
                                TGAGG  GAGAAGGA AA GGG
                                |||||  |||||||| || |||
                                ACTCC  CTCTTCCT TT CCT
                                   CT       G  _
GAM1570  FLJ10074  5'  TGGGGAGGGGAGGGACCGGGGA 39054    A    A  A  A  A
                                TG GGAGG GA GG GA TGGGGA
                                || ||||| || || || ||||||
                                AC CCTCC CT CC CT GCCCCT
                                 C    C  _  _  G
GAM1570  FLJ10210  5'  AGGAGGAGGGGGGGATGGGA   39055        AA  A  A
                                AGGAGGAG  GG GA TGGGG
                                ||||||||  || || |||||
                                TCCTCCTC  CC CT ACCCT
                                     CC  _  _
GAM1570  FLJ10468  3'  GAGGAGGAGGAGGAAGAGGA   38982         A    AAT
                                GAGGAGGAG AGGAG   GGGGA
                                ||||||||| |||||   |||||
                                CTCCTCCTC TCCTT   CTCCT
                                     C    ___
GAM1570  FLJ10597  3'  TGGGAGGGGGAGGGG      39056    A    AGAA  A  AT
                                TG GGAGG    GG GA  GGGG
                                || |||||    || ||  ||||
                                AC CCTCC    CC CT  CCCC
                                 _    _____  _  __
GAM1570  FLJ10613  3'  GAGGGGGAGAAGACACACAGTG 39057      A       AGAA___
            GGGA                    GAGG GGAGAAGG      TGGGGA
                                |||| ||||||||      ||||||
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                                CTCC CCTCTTCT      ACCCCT
                                  C       GTGTGTC
GAM1570  FLJ12587  3'  TGAGGAGGGGAGGGGAGGGG  39058        A  A  A  AT
                                TGAGGAGG GA GG GA  GGGG
                                |||||||| || || ||  ||||
                                ACTCCTCC CT CC CT  CCCC
                                     C  C  _  __
GAM1570  FLJ12910  5'  GGAGGAGCTGAGAATGGGG   39059        AAG
                                GGAGGAG   GAGAATGGGG
                                |||||||   ||||||||||
                                CCTCCTC   CTCTTACCCC
                                    GA_
GAM1570  FLJ13055  3'  TGAGGAGGGGGCAGGAAAGGGG 39060        AGA_     AT
                                TGAGGAGG    AGGAGA  GGGG
                                ||||||||    ||||||  ||||
                                ACTCCTCC    TCCTTT  CCCC
                                     CCCG     __
GAM1570  FLJ13158  3'  TGAGTAGGGGAGATGGGG    39061      G   AGAA    A
                                TGAG AGG    GGAGA TGGGG
                                |||| |||    ||||| |||||
                                ACTC TCC    CCTCT ACCCC
                                  A  _____    _
GAM1570  FLJ13194  3'  GGGGGAGGAATCAATGGG    39062    A  A  A   __
                                GG GG GA GGAG  AATGGG
                                || || || ||||  ||||||
                                CC CC CT CCTT  TTACCC
                                 _  _  _   AG
GAM1570  FLJ14126  3'  TGGGAGGAGAGGGGGCTGGGGA 39063    A       A  AGAA
                                TG GGAGGAGA GG    TGGGGA
                                || |||||||| ||    ||||||
                                AC CCTCCTCT CC    ACCCCT
                                 _       C  CCG_
GAM1570  FLJ14280  3'  TGGGGAGGAGGAAGGAGGG   39064    A     _    GAATG
                                TG GGAGGAG AAGGA     GGG
                                || ||||||| |||||     |||
                                AC CCTCCTC TTCCT     CCC
                                 C      C    _____
GAM1570  FLJ14442  3'  TGAGGAGGGAGGAGGAGGG   39065        A  A   AAT
                                TGAGGAGG GA GGAG   GGGG
                                |||||||| || ||||   ||||
                                ACTCCTCC CT CCTC   TCCC
                                     _  _   C__
GAM1570  FLJ20294  3'  TGAGGAAGAGGAGGAGGTGGA  39066         A    AA
                                TGAGGAGGAG AGGAG  TGGG
                                |||||||||| |||||  ||||
                                ACTCCTTCTC TCCTC  ACCT
                                      C    C_
GAM1570  FLJ22246  5'  AGGGGACCTGGAGAATGGGGA  39067     A   GAA
                                AGG GGA   GGAGAATGGGGA
                                ||| |||   ||||||||||||
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                                TCC CCT   CCTCTTACCCCT
                                  _  GGA
GAM1570  FLJ23416  3'  GGAGGAGAGGGAGTAGGA    39068        A    AA
                                GGAGGAGA GGAG  TGGGG
                                |||||||| ||||  |||||
                                CCTCCTCT CCTC  ATCCT
                                     C   __
GAM1570  FLJ31300  3'  TGCGGAGTGCAGGGAGGGTGGG 39069    A   GAGAA   AA
           GA                    TG GGAG    GGAG  TGGGGA
                                || ||||    ||||  ||||||
                                AC CCTC    CCTC  ACCCCT
                                 G   ACGTC   CC
GAM1570  GP5      3'  TGGGGAGGGGAGGGAGAGCAAG 39070    A    A A    AT
           A                     TG GGAGG GA GGAGA  GGGG
                                || ||||| || |||||  ||||
                                AC CCTCC CT CCTCT  TTCT
                                 C    C  C    CG
GAM1570  GTF2A1    5'  GAGGAGGAGGAGGGGG      39071         A   AGAAT
                                GAGGAGGAG AGG    GGG
                                |||||||||| |||    |||
                                CTCCTCCTC TCC    CCC
                                     C  _____
GAM1570  H17      3'  TGAGAGGAGAGGACACTGGGGA 39072      G     A   GAA
                                TGAG AGGAGA GGA   TGGGGA
                                |||| |||||| |||   ||||||
                                ACTC TCCTCT CCT   ACCCCT
                                  _    _  GTG
GAM1570  H17      3'  GAGGGGGAGAAGGCCTGG    39073      A       AGAA
                                GAGG GGAGAAGG   TGG
                                |||| ||||||||   |||
                                CTCC CCTCTTCC   ACC
                                  C       GG__
GAM1570  HARS2    3'  TGAGGAGGTGGAAGGGAAGGG  39074        A_    A   T
                                TGAGGAGG  GAAGG GAA GGG
                                ||||||||  ||||| ||| |||
                                ACTCCTCC  CTTCC CTT CCC
                                     AC    _  _
GAM1570  HERC1    3'  TGAGGGAGAGAAGGGAGGG   39075      AG      A  AT
                                TGAGG  GAGAAGG GA  GGG
                                |||||  ||||||| ||  |||
                                ACTCC  CTCTTCC CT  CCC
                                   CT      _ __
GAM1570  HIC2     3'  GAGGGGCCCTGGGAATGGGGA  39076     A  AGAA  A
                                GAGG GG   GG GAATGGGGA
                                |||| ||   || |||||||||
                                CTCC CC   CC CTTACCCCT
                                  _ GGGA  _
GAM1570  HSU47926  5'  TGAGGAGGCGAAGGGAGG    39077        A    AGAAT
                                TGAGGAGG GAAGG    GGGG
                                |||||||| |||||    ||||
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                                ACTCCTCC CTTCC    CTCC
                                    G   _____
GAM1570 HZFW1    3' TGAGGAGGAGAGAGGG     39078         A  AGAAT
                                TGAGGAGGAGA GG    GGG
                                |||||||||| ||    |||
                                ACTCCTCCTCT CT    CCC
                                      _ _____
GAM1570 ILF3     5' GAGGAGGAGGAGGAGTCCGGA 39079        A    AA
                                GAGGAGGAG AGGAG  TGGG
                                ||||||||| |||||  ||||
                                CTCCTCCTC TCCTC  GCCT
                                     C    AG
GAM1570 IMP-2    3' AGGGGAGGGGAGGGAGGGG   39080    A   AA   AAT
                                AGG GGAG  GGAG   GGGG
                                ||| ||||  ||||   ||||
                                TCC CCTC  CCTC   CCCC
                                  _   C_   CCT
GAM1570 KHDRBS1  3' GGGGAGAAGAAGGGGA     39081    A       GAAT
                                GG GGAGAAGGA    GGGGA
                                || |||||||||    |||||
                                CC CCTCTTCTT    CCCCT
                                  _       ____
GAM1570 KIAA0057 3' TGAGGGGGAGAAAGAGAA    39082      A
                                TGAGG GGAGAAGGAGAA
                                ||||| ||||||||||||
                                ACTCC CCTCTTTCTCTT
                                   C
GAM1570 KIAA0082 3' TGAGTGGGGGAAGGAGACAAGA 39083     GA  A     A TG
                                TGAG  GG GAAGGAG A  GGG
                                ||||  || |||||||  |  |||
                                ACTC  CC CTTCCTC T  TCT
                                  AC  C      _ GT
GAM1570 KIAA0144 3' GGGGGAGAGGGAAATGGGG   39084    A    A  AG
                                GG GGAGA GG  AATGGGG
                                || ||||| ||  |||||||
                                CC CCTCT CC  TTACCCC
                                 C    _  CT
GAM1570 KIAA0161 3' TGAAGGGGGGACGGTGGGG   39085      A  A  A  AGAA
                                TGAGG GG GA GG    TGGGG
                                ||||| || || ||    |||||
                                ACTTC CC CT CC    ACCCC
                                   C  C  G  ____
GAM1570 KIAA0212 3' GGGGAGAAGGGGAAAGGGGA  39086    A      A   T
                                GG GGAGAAGG GAA GGGGA
                                || |||||||| ||| |||||
                                CC CCTCTTCC CTT CCCCT
                                 _      C   T
GAM1570 KIAA0280 3' TGAGGAGGAGAGAGGGG     39087          A  AGAAT
                                TGAGGAGGAGA GG    GGGG
                                |||||||||| ||    ||||
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                                ACTCCTCCTCT CT    CCCC
                                    _ _____
GAM1570 KIAA0427 3' TGAGGAAGGGGAGGGCCAGGG 3529       AGAA   AA_
                                TGAGGAGG   GGAG  TGGGG
                                ||||||||   ||||  |||||
                                ACTCCTTC   CCTC  GTCCC
                                    C___   CCG
GAM1570 KIAA0451 3' TGAGGAGGAGAGGAGGGGAGGG 39088        A____   AA
          TGGGGA                GAGGAGGAGA   GGAG  TGGGGA
                                ||||||||||   ||||  ||||||
                                CTCCTCCTCT   CCTC  ACCCCT
                                     CCTCC   CC
GAM1570 KIAA0451 3' AGGGAAGAGGAGGATGGGG  39089    A   A   A
                                AGG GGAGA GGAG ATGGGG
                                ||| ||||| |||| ||||||
                                TCC CTTCT CCTC TACCCC
                                 _   _   C
GAM1570 KIAA0451 3' TGAGGAGGGTGGGGAGAGTGGG 39090       AGAA   A
          GA                   TGAGGAGG   GGAGA TGGGGA
                               ||||||||   ||||| ||||||
                               ACTCCTCC   CCTCT ACCCCT
                                    CACC   C
GAM1570 KIAA0451 3' GAGGAGGATGGGGAGGGTGGGG 39092       GAA   AA
          A                    GAGGAGGA   GGAG  TGGGGA
                               ||||||||   ||||  ||||||
                               CTCCTCCT   CCTC  ACCCCT
                                    ACC   CC
GAM1570 KIAA0451 3' GGGGAGGGTGGGGATGGGGA  39091   A   AA_  A  A
                               GG GGAG   GG GA TGGGGA
                               || ||||   || || ||||||
                               CC CCTC   CC CT ACCCCT
                                _   CCA  C  _
GAM1570 KIAA0552 3' GAGGGGAGGGGACACTGGGGA  39093    A   AA   GAA
                               GAGG GGAG  GGA   TGGGGA
                               |||| ||||  |||   ||||||
                               CTCC CCTC  CCT   ACCCCT
                                 _   C_   GTG
GAM1570 KIAA0561 3' TGGGGAGGGGAATGAGACCAGG 39094   A   A  G   AT
                               TG GGAGG GAA GAGA  GGG
                               || ||||| ||| ||||  |||
                               AC CCTCC CTT CTCT  TCC
                                C    C  A   GG
GAM1570 KIAA0618 3' GAGGAGGAGGAGGACATGGGG  39095       A   GA
                               GAGGAGGAG AGGA  ATGGGG
                               ||||||||| ||||  ||||||
                               CTCCTCCTC TCCT  TACCCC
                                    C   G_
GAM1570 KIAA0669 5' GAGGAGGAGGAGGAGGCGG   39096       A    AA
                               GAGGAGGAG AGGAG  TGG
                               ||||||||| |||||  |||
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                                CTCCTCCTC TCCTC  GCC
                                      C    C_
GAM1570 KIAA0705 5' TGAGGATGGAGGAGCAAGGGG 39097      _  GAA   AAT
                                TGAGGA GGA   GGAG   GGGG
                                |||||| |||   ||||   ||||
                                ACTCCT CCT   CCTC   CCCC
                                   A   ___   GTT
GAM1570 KIAA0721 3' TGGGAGGGAGAGGGGGAGGGA 39098   A   _  A A ATG
                                TG GGAGG AGA GG GA   GGGA
                                || ||||| ||| || ||   ||||
                                AC CCTCC TCT CC CT   CCCT
                                 _    C  C C ___
GAM1570 KIAA0721 3' TGGGAGGGAGAGGGGGAGGGA 39098   A   _  A A ATG
                                TG GGAGG AGA GG GA   GGGA
                                || ||||| ||| || ||   ||||
                                AC CCTCC TCT CC CT   CCCT
                                 _    C  C C ___
GAM1570 KIAA0769 5' GGAGGAGGAGGAGGGCCGGA  39099      A   AA_
                                GGAGGAG AGGAG  TGGG
                                ||||||| |||||  ||||
                                CCTCCTC TCCTC  GCCT
                                    C   CCG
GAM1570 KIAA0937 3' TGGGGAGGAGATAGGGTCTTGG 39101   A     _  AGAA
           GA                    TG GGAGGAGA AGG   TGGGG
                                || |||||||| |||   |||||
                                AC CCTCCTCT TCC   ACCCT
                                 C      A  CAGA
GAM1570 KIAA0937 3' TGAGGAGGAGAGGAGGG    39100        A  GAAT
                                TGAGGAGGAGA GGA   GGG
                                |||||||||| |||   |||
                                ACTCCTCCTCT CCT   CCC
                                      _  _____
GAM1570 KIAA0984 3' GGCGAGGAGAAGGGGA     39102   A A    T
                                GG GA GGAGAA GGGGA
                                || || |||||| |||||
                                CC CT CCTCTT CCCCT
                                 G _    _
GAM1570 KIAA1130 3' TGAGGAGGGTGAGCAGGGG  39103      AGAAG  AAT
                                TGAGGAGG   GAG  GGGG
                                ||||||||   |||  ||||
                                ACTCCTCC   CTC  CCCC
                                    CA___  GT_
GAM1570 KIAA1183 3' AGGGGAGGGGAGGGCGGGG  39104   A  AA  AA
                                AGG GGAG  GGAG  TGGGG
                                ||| ||||  ||||  |||||
                                TCC CCTC  CCTC  GCCCC
                                  _   C_   CC
GAM1570 KIAA1196 3' TGAAGAGGCGGGGGTGGGG  39105      AGAA  AGAA
                                TGAGGAGG   GG   TGGGG
                                ||||||||   ||   |||||
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                              ACTTCTCC   CC   ACCCC
                                   GCCC ____
GAM1570 KIAA1200 3' TGGGGAGGAGAGAGGGTGGGG 39106   A     AG  AA
                              TG GGAGGAGA  GAG  TGGGG
                              || ||||||||  |||  |||||
                              AC CCTCCTCT  CTC  ACCCC
                               C      __  CC
GAM1570 KIAA1238 5' GAGGAGGGGGAGGGGG     39107      AGAA   AAT
                              GAGGAGG   GGAG   GGGG
                              |||||||   ||||  ||||
                              CTCCTCC   CCTC   CCCC
                                  C___   ___
GAM1570 KIAA1643 3' TGAGGGGTGAGGGCTGGGG   39108     A  A  A  AGAA
                              TGAGG GG GA GG   TGGGG
                              ||||| || || ||   |||||
                              ACTCC CC CT CC   ACCCC
                                 _ A _ CG__
GAM1570 KIAA1904 3' TGAGGAAGGGAGGGAGGGAGGG 39109       A  A   AAT
            A                  TGAGGAGG GA GGAG  GGGGA
                              |||||||| || ||||  |||||
                              ACTCCTTC CT CCTC  TCCCT
                                   C  C   CC_
GAM1570 KIAA1938 3' GGGGAGGGAGAACGA     39110   A   AA
                              GG GGAG  GGAGAATGG
                              || ||||  |||||||||
                              CC CCTC  CCTCTTGCT
                               _   __
GAM1570 LAP1B   5' GAGGAGGAGAAGGGG      39111          AGAATG
                              GAGGAGGAGAAGG    GG
                              ||||||||||||     ||
                              CTCCTCCTCTTCC    CC
                                       _______
GAM1570 LGP1    3' TGGGGAAGAGAGGGAAGGGA  39112   A     A  A  T
                              TG GGAGGAGA GG GAA GGGG
                              || |||||||| || ||| ||||
                              AC CCTTCTCT CC CTT CCCT
                               C      _ _  _
GAM1570 LIMK2   5' GGGGAGGAGGAGGCGGGG   39113   A   A   AA
                              GG GGAG AGGAG  TGGGG
                              || |||| |||||  |||||
                              CC CCTC TCCTC  GCCCC
                               _   C    C_
GAM1570 MAB21L2  5' TGAGGAAGGAGAAGGAGAGGGA 39114      _       ATG
                              TGAGGA GGAGAAGGAGA   GGGA
                              |||||| ||||||||||   ||||
                              ACTCCT CCTCTTCCTCT   CCCT
                                  T        ___
GAM1570 MGC12217 3' GGGGGGAAGGAGGTGGGA   39115   A A     AA
                              GG GG GAAGGAG  TGGGG
                              || || |||||||  |||||
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                                CC CC CTTCCTC  ACCCT
                                 _ C      C_
GAM1570  MGC16824  5'  GGAGGAGGAGGAGGACGTGGA  39116       A    A  G
                                GGAGGAG AGGAG ATG GGA
                                ||||||| ||||| ||| |||
                                CCTCCTC TCCTC TGC CCT
                                    C    C  A
GAM1570  MGC2452   5'  TGAAGAGGAGAGGGGGTGCTGG 39117          A  AGAA_
            GG                    TGAGGAGGAGA GG    TGGGG
                                ||||||||||| ||    |||||
                                ACTTCTCCTCT CC    ACCCC
                                      C  CCACG
GAM1570  MGC2817   5'  GAGGAGGAGGAGGAAGGG    39047        A   GAAT
                                GAGGAGGAG AGGA   GGGG
                                ||||||||| ||||   ||||
                                CTCCTCCTC TCCT   TCCC
                                     C   ____
GAM1570  MGC3222   3'  TGAAGAGGAGAGGGAGTGCAGA 39118          A   AA  G
                                TGAGGAGGAGA GGAG  TG GGA
                                |||||||||| ||||  || |||
                                ACTTCTCCTCT CCTC  AC TCT
                                      C   __  G
GAM1570  MKRN4     5'  GGAGGGGAAGGAGACTGA    39119      A      A
                                GGAGG GAAGGAGA TGG
                                ||||| |||||||| |||
                                CCTCC CTTCCTCT ACT
                                   C       G
GAM1570  NOVA2     3'  GAGGAGGAGAGGGAAGAGGA   39120         A  A   T
                                GAGGAGGAGA GG GAA GGGGA
                                |||||||||| || ||| |||||
                                CTCCTCCTCT CC CTT CTCCT
                                          _  _  _
GAM1570  NPAS3     3'  AGAGGGGGTGGAATGGGG    39121      AGAA  A_
                                GGAGG   GG  GAATGGGG
                                |||||   ||  ||||||||
                                TCTCC   CC  CTTACCCC
                                   C___  AC
GAM1570  P66       3'  TGAGGAAGGAGGAGGGAAGGGA 39122       _   A  A  T
                                TGAGGA GGAG AGG GAA GGGG
                                |||||| |||| ||| ||| ||||
                                ACTCCT CCTC TCC CTT CCCT
                                    T   C  _  _
GAM1570  POLM      3'  TGAGAAGGGGAGGGAGTTGG  39123        A  A   AA
                                TGAGGAGG GA GGAG  TGG
                                |||||||| || ||||  |||
                                ACTCTTCC CT CCTC  ACC
                                     C  C   A_
GAM1570  PRO2214   3'  GAAGGAGAGGAAATGGGGA   39124        A    A
                                GGAGGAGA GGAGA TGGGGA
                                |||||||| ||||| ||||||
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                                CTTCCTCT CCTTT ACCCCT
                                      _    _
GAM1570  PSK-1    3'  TGAGGAGGGGAGGGGCGTCCTG 39125        A  A_  AGAA_
                GG                  TGAGGAGG GA  GG    TGGG
                                    |||||||| ||  ||    ||||
                                    ACTCCTCC CT  CC    ACCC
                                        C  CC  GCAGG
GAM1570  QSCN6    3'  TGGGAGGGGAGGGAATGGGG   39126    A    A  A  A
                                    TG GGAGG GA GG GAATGGGG
                                    || ||||| || || ||||||||
                                    AC CCTCC CT CC CTTACCCC
                                     _    C  _ _
GAM1570  R3HDM    5'  TGAGGAGGAGGAGGCGGTTGGA 39127          A   AGAA
                                    TGAGGAGGAG AGG    TGGG
                                    |||||||||| |||    ||||
                                    ACTCCTCCTC TCC    ACCT
                                          C   GCCA
GAM1570  RAB3IL1  3'  TGGGGAAGAGAGGGGGGG     39128    A      A  AGAAT
                                    TG GGAGGAGA GG     GGGG
                                    || ||||||||  ||     ||||
                                    AC CCTTCTCT CC     CCCC
                                     C       _ _____
GAM1570  RBAF600  3'  TGAGAGAGGGGAGGGCGGGG   39129     _   AGAA   AA
                                    TGAG GAGG    GGAG  TGGGG
                                    |||| ||||    ||||  |||||
                                    ACTC CTCC    CCTC  GCCCC
                                      T   _____   CC
GAM1570  RBPMS    5'  GAGGAGGAGGAGGAGCGGGG   39130        A    AA
                                    GAGGAGGAG AGGAG  TGGGG
                                    |||||||||  |||||  |||||
                                    CTCCTCCTC TCCTC  GCCCC
                                          C    __
GAM1570  RBPMS    5'  GAGGAGGAGGAGGAAGAGGA   38982        A    AAT
                                    GAGGAGGAG AGGAG   GGGGA
                                    |||||||||  |||||   |||||
                                    CTCCTCCTC TCCTT   CTCCT
                                          C    ___
GAM1570  RELB     3'  TGAGGAAGGGCCAAGGGGATGG 39131       __  AG   A  A
                GG                  TGAGGA  GG  AAGG GA TGGGG
                                    ||||||  ||  |||| || |||||
                                    ACTCCT  CC  TTCC CT ACCCC
                                       TC  GG   C  _
GAM1570  RFX3     5'  GAGGAGGAGGAGGAGAGGA    38951         A     AT
                                    GAGGAGGAG AGGAGA  GGG
                                    |||||||||  ||||||  |||
                                    CTCCTCCTC TCCTCT  CCT
                                          C    __
GAM1570  RFX3     5'  GAGGAGGAGGAGGAAGAGGA   38982         A    AAT
                                    GAGGAGGAG AGGAG   GGGGA
                                    |||||||||  |||||   |||||
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                                CTCCTCCTC TCCTT  CTCCT
                                     C    ___
GAM1570  RFX3    5'  GAGGAGGAGGAGGAGAGGA  38951       A    AT
                                GAGGAGGAG AGGAGA  GGG
                                ||||||||| ||||||  |||
                                CTCCTCCTC TCCTCT  CCT
                                     C    __
GAM1570  RFX3    5'  GAGGAGGAGGAGGAAGAGGA  38982       A    AAT
                                GAGGAGGAG AGGAG  GGGGA
                                ||||||||| |||||  |||||
                                CTCCTCCTC TCCTT  CTCCT
                                     C    ___
GAM1570  RNF40   3'  GGGGAGGAGATGGGG     39132    A  GAA    A
                                GG GGA  GGAGA TGGGG
                                || |||  ||||| |||||
                                CC CCT  CCTCT ACCCC
                                 _  ___   _
GAM1570  SAST    5'  AGGAGGAGGGGGAGCGCCCGGG 39133       AA   AA__
            G                    AGGAGGAG  GGAG   TGGGG
                                ||||||||  ||||   |||||
                                TCCTCCTC  CCTC   GCCCC
                                     CC   GCGG
GAM1570  SDC3    5'  GGGGAGTAGGGGATGGGG   39134    A   A  A  A
                                GG GGAG AGG GA TGGGG
                                || |||| ||| || |||||
                                CC CCTC TCC CT ACCCC
                                 _   A  C  _
GAM1570  SEPT3   3'  AGGAGGAGAGGGAATTAGGGA  39135       A  A   _
                                AGGAGGAGA GG GAAT GGGGA
                                ||||||||| || |||| |||||
                                TCCTCCTCT CC CTTA TCCCT
                                     _ _   A
GAM1570  SRF     3'  TGGGAGGAGAGGGGG     39136    A      A  AGAAT
                                TG GGAGGAGA GG    GGG
                                || |||||||| ||    |||
                                AC CCTCCTCT CC    CCC
                                 _     _ _____
GAM1570  STIM2   3'  GGGGAGTGGAGGGTGGGG   39137    A   AA   AA
                                GG GGAG  GGAG  TGGGG
                                || ||||  ||||  |||||
                                CC CCTC  CCTC  ACCCC
                                 _   A_   CC
GAM1570  SV2     3'  TGAGGAGGGAAGGAGATGGG  39138       A      A
                                TGAGGAGG GAAGGAGA TGGG
                                |||||||| |||||||| ||||
                                ACTCCTCC CTTCCTCT ACCC
                                     _      _
GAM1570  TRIAD3  3'  GAGGAGGGTGAGTGGGG    39139       AGAAG   AA
                                GAGGAGG    GAG  TGGGG
                                |||||||    |||  |||||
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                                CTCCTCC    CTC  ACCCC
                                   CA___   __
GAM1570  ZDHHC3    3'  TGGGGAAGAGAGGGAGATGGGG 39140    A      A    A
                                TG GGAGGAGA GGAGA TGGGG
                                || |||||||| ||||| |||||
                                AC CCTTCTCT CCTCT ACCCC
                                 C       C    _
GAM1570  ZF5128    3'  GAGGAGGGATAATGGGG     39141       AA   G
                                GAGGAG  GGA AATGGGG
                                ||||||  ||| |||||||
                                CTCCTC  CCT TTACCCC
                                   __  A
GAM1570  LOC115273 5'  TGAGGAGGGGCATGGG      39142        AGAA  AGA
                                TGAGGAGG   GG   ATGGG
                                ||||||||   ||   |||||
                                ACTCCTCC   CC   TACCC
                                    _____  G__
GAM1570  LOC121036 3'  TGAGGAGGGCAGGGACAGGA   39143        AGA   A  A
                                TGAGGAGG   AGG GA TGGGG
                                ||||||||   ||| || |||||
                                ACTCCTCC   TCC CT GTCCT
                                    CG_   _ _
GAM1570  LOC121133 5'  GAGGAGAGGAGGGGG       39144        A    AAT
                                GAGGAGA GGAG   GGGG
                                ||||||| ||||   ||||
                                CTCCTCT CCTC   CCCC
                                   _   ___
GAM1570  LOC123775 3'  GAGGAGAGAAAGAGAGAGTGGG 39145       GA   _   A
            G                    GAGGAG  GAAG GAGA TGGGG
                                ||||||  |||| |||| |||||
                                CTCCTC  TTTC CTCT ACCCC
                                   TC   T   C
GAM1570  LOC145678 5'  AGGAGGAGAGGCCTGGGG    39146         A  AGAA
                                AGGAGGAGA GG   TGGGG
                                ||||||||| ||   |||||
                                TCCTCCTCT CC   ACCCC
                                    _ GG__
GAM1570  LOC146733 5'  TGAGGAGAGGAAGGGAAGGA  39147        GA    A   T
                                TGAGGAG  GAAGG GAA GGG
                                |||||||  ||||| ||| |||
                                ACTCCTC  CTTCC CTT CCT
                                    TC    _  _
GAM1570  LOC146756 3'  GAGGAGAGGGACTGGGG     39148        A  A  A
                                GAGGAGA GG GA TGGGG
                                ||||||| || || |||||
                                CTCCTCT CC CT ACCCC
                                    _ _  G
GAM1570  LOC146894 3'  TGGGGAGGGTGGGGAGAGCCCT 39149    A    AGAA    ATGG_
            GGA                   TG GGAGG   GGAGA    GGA
                                || |||||   |||||    |||
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                                AC CCTCC    CCTCT     CCT
                                 C     CACC     CGGGA
GAM1570  LOC146894 3'  AGAGGAGAACCTGGGGAGGGTG 39150          _____    AA
                GGGA                    GGAGGAGAA     GGAG  TGGGGA
                                |||||||||     ||||  ||||||
                                TCTCCTCTT     CCTC  ACCCCT
                                     GGACC    CC
GAM1570  LOC147299 3'  TGAGGAGAGGAAGGCATTGGGA 39151         GA     AGAA
                                TGAGGAG  GAAGG    TGGGG
                                |||||||  |||||    |||||
                                ACTCCTC  CTTCC    ACCCT
                                    TC     GTA_
GAM1570  LOC147632 5'  GAGGAGGAGGAGGAGAAGGA   39152          A      T
                                GAGGAGGAG AGGAGAA GGG
                                ||||||||| ||||||| |||
                                CTCCTCCTC TCCTCTT CCT
                                     C      _
GAM1570  LOC149153 3'  TGAGGAGGAGGGGGGGACAATGG 39153          AA_   G
                G                    TGAGGAGGAG   GGA AATGGG
                                ||||||||||   ||| ||||||
                                ACTCCTCCTC   CCT TTACCC
                                      CCC   G
GAM1570  LOC149271 3'  GAGGAGGAGAGGGAGGCTG    39154          A    AA
                                GAGGAGGAGA GGAG  TG
                                |||||||||| ||||  ||
                                CTCCTCCTCT CCTC  AC
                                      C    CG
GAM1570  LOC149478 5'  GGAGGAGGGAGCCTGGGA     39155        AA    AA
                                GGAGGAG  GGAG  TGGGG
                                |||||||  ||||  |||||
                                CCTCCTC  CCTC  ACCCT
                                    __    GG
GAM1570  LOC149506 3'  TGGGGTGGAGAAAAATGGGG   39156    A  A     GGA
                                TG GG GGAGAA   GAATGGGG
                                || || ||||||   ||||||||
                                AC CC CCTCTT   TTTACCCC
                                 C  A     ___
GAM1570  LOC149670 3'  GGAGGAGGAGGAACTGGGG    39157        A    AA
                                GGAGGAG AGGAG  TGGGG
                                |||||||  |||||  |||||
                                CCTCCTC TCCTT  ACCCC
                                    C    G_
GAM1570  LOC150498 3'  TGGGAGGGGGAAGGAGAA     39158    A    A_
                                TG GGAGG  GAAGGAGAA
                                || |||||  |||||||||
                                AC CCTCC  CTTCCTCTT
                                 _    CC
GAM1570  LOC150498 3'  GAGGGGAAGGAGGTAGTGGGA  39159      A      AATG_
                                GAGG GAAGGAG     GGGA
                                ||||  |||||||     ||||
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                                CTCC CTTCCTC    CCCT
                                  C      CATCA
GAM1570  LOC151429 3'  TGAGGGGGGAAGGGGA     39160      A  A    AGAAT
                                TGAGG GG GAAGG    GGG
                                ||||| || |||||    |||
                                ACTCC CC CTTCC    CCT
                                  _ C    _____
GAM1570  LOC151534 3'  TGAGGAGGAGAGGGAGCTGA  39161          A   AA
                                TGAGGAGGAGA GGAG  TGG
                                |||||||||| ||||  |||
                                ACTCCTCCTCT CCTC  ACT
                                      C   G_
GAM1570  LOC151877 3'  TGAGAAGGAGAAGGAGTAGA  39162             AA
                                TGAGGAGGAGAAGGAG  TGGG
                                |||||||||||||||  ||||
                                ACTCTTCCTCTTCCTC  ATCT
                                                __
GAM1570  LOC152286 3'  GAGGGGGTGATGGGAATGGGG  39163     A  A  A  A
                                GAGG GG GA GG GAATGGGG
                                |||| || || || ||||||||
                                CTCC CC CT CC CTTACCCC
                                  C  A  A  _
GAM1570  LOC154321 5'  TGACGGGGGAGAAGGGGCTGAG 39164     _ A       AGAA  _
           GGA                    TGA GG GGAGAAGG    TG GGGA
                                ||| || ||||||||    || ||||
                                ACT CC CCTCTTCC    AC CCCT
                                  G  C       CCG_  T
GAM1570  LOC165721 5'  TGAGAGGAGAGGGAACGTGGA  39165     G     A  A    G
                                TGAG AGGAGA GG GAATG GGA
                                |||| |||||| || ||||| |||
                                ACTC TCCTCT CC CTTGC CCT
                                  _     _ _    A
GAM1570  LOC196812 3'  TGAGGAGGGGGTGGGG      39166        AGAA  AGAA
                                TGAGGAGG    GG    TGGGG
                                ||||||||    ||    |||||
                                ACTCCTCC    CC    ACCCC
                                     C___  _____
GAM1570  LOC196996 3'  GAGGAGGAGGGATCTGGA    39167         AA   GAA
                                GAGGAGGAG  GGA   TGGG
                                |||||||||  |||   ||||
                                CTCCTCCTC  CCT   ACCT
                                     __   AG_
GAM1570  LOC197350 3'  TGAGGAAACCGGGGGGATGGGG 39168         AGAA  A  A
                                TGAGGAGG    GG GA TGGGG
                                ||||||||    || || |||||
                                ACTCCTTT    CC CT ACCCC
                                     GGCC  C  _
GAM1570  LOC197423 5'  GAGGAGGAGGAGGAGGCGG    39096         A    AA
                                GAGGAGGAG AGGAG  TGG
                                |||||||||  |||||  |||
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                                CTCCTCCTC TCCTC  GCC
                                     C    C_
GAM1570  LOC200205 3'  TGAGGAGGAACAGAGGTGGGGA 39169         AA   AA
                                TGAGGAGGAG  GGAG  TGGGGA
                                ||||||||||  ||||  ||||||
                                ACTCCTCCTT  TCTC  ACCCCT
                                     G_   C_
GAM1570  LOC200301 3'  TGAGGAGGGGCAGGTTTGGGG  39170        AGA  AGAA
                                TGAGGAGG  AGG   TGGGG
                                ||||||||  |||   |||||
                                ACTCCTCC  TCC   ACCCC
                                    CCG   AA__
GAM1570  LOC200314 3'  TGAGGGGCCAGGGTGGGG    39171      A AGA  AGAA
                                TGAGG GG  AGG   TGGGG
                                ||||| ||  |||   |||||
                                ACTCC CC  TCC   ACCCC
                                   _ GG_  C___
GAM1570  LOC202546 3'  GAGGAGAAGAAGGCAGTGGGG  39172           AGAA
                                GAGGAGGAGAAGG   TGGGG
                                ||||||||||||   |||||
                                CTCCTCTTCTTCC   ACCCC
                                      GTC_
GAM1570  LOC203504 3'  GGGGAGGGGAGGTAGAG     39173    A   AA   AA
                                GG GGAG  GGAG  TGGGG
                                || ||||  ||||  |||||
                                CC CCTC  CCTC  ATCTC
                                 _   C_   C_
GAM1570  LOC219688 5'  GAGGAGGAGGAGGGAGAGGA  39174        A  A  AT
                                GAGGAGGAG AGG GA  GGGGA
                                |||||||||| ||| ||  |||||
                                CTCCTCCTC TCC CT  CTCCT
                                     C  _ __
GAM1570  LOC219688 5'  GAGGAGGAGGAGGAAGAGGA  38982        A    AAT
                                GAGGAGGAG AGGAG   GGGGA
                                |||||||||| |||||  |||||
                                CTCCTCCTC TCCTT   CTCCT
                                     C    ___
GAM1570  LOC219688 5'  GAGGAGGAGGAGGGGG      39071        A  AGAAT
                                GAGGAGGAG AGG    GGG
                                |||||||||| |||    |||
                                CTCCTCCTC TCC    CCC
                                     C  _____
GAM1570  LOC219688 5'  GAGGAGGAGGGGGGGCAGCGGGG 39175        AA  AGAA
                                GAGGAGGAG  GG   TGGGG
                                |||||||||  ||   |||||
                                CTCCTCCTC  CC   GCCCC
                                     CC  CGTC
GAM1570  LOC220565 5'  GAGGAGGAGGAGGAGGCGG   39096        A    AA
                                GAGGAGGAG AGGAG  TGG
                                |||||||||| |||||  |||
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                                CTCCTCCTC TCCTC  GCC
                                      C    C_
GAM1570  LOC221477 3'  AGGGGAGGGGGTGCAGTGGGGA 39176    A   AA  AGAA_
                                AGG GGAG  GG    TGGGGA
                                ||| ||||  ||    ||||||
                                TCC CCTC  CC    ACCCCT
                                  _   CC  ACGTC
GAM1570  LOC254428 3'  TGGGGTGGAGGAGGGACAGGG  39177    A A   A  A A
                                TG GG GGAG AGG GA TGGGG
                                || || |||| ||| || |||||
                                AC CC CCTC TCC CT GTCCC
                                 C A   C  _ _
GAM1570  LOC254873 3'  TGGGGAGGAAAGGGGATGGGG  39007    A      A A  A
                                TG GGAGGAGA GG GA TGGGG
                                || ||||||| || || |||||
                                AC CCTCCTTT CC CT ACCCC
                                 C      C  _ _
GAM1570  LOC255271 3'  GGAGAAGGGAGAGTGGGG    39178       AA    A
                                GGAGGAG  GGAGA TGGGG
                                |||||||  ||||| |||||
                                CCTCTTC  CCTCT ACCCC
                                    __    C
GAM1570  LOC256369 5'  TGGGGAGAGAAGGTGAGGGG  39179    A AG     A AT
                                TG GG  GAGAAGG GA  GGGG
                                || ||  ||||||| ||  ||||
                                AC CC  CTCTTCC CT  CCCC
                                 _ CT      A __
GAM1570  LOC51337  3'  GAGGAGGAGGAGGAGGCAAGG  39180        A    AAT
                                GAGGAGGAG AGGAG   GGG
                                ||||||||| |||||   |||
                                CTCCTCCTC TCCTC   TCC
                                      C    CGT
GAM1570  LOC55971  5'  CGGGGAGGAGAAGGAACAGGGG 39181    A         AAT
           A                     TG GGAGGAGAAGGAG   GGGGA
                                || ||||||||||||   |||||
                                GC CCTCCTCTTCCTT   CCCCT
                                 C          GT_
GAM1570  LOC90110  5'  TGAGGAGGGGAGTGAGAA    39182       A AG
                                TGAGGAGG GA  GAGAA
                                |||||||| ||  |||||
                                ACTCCTCC CT  CTCTT
                                    C  CA
GAM1570  LOC91828  5'  CGGGGGGAGAAGGGTGGG    39183    A A     AGAA
                                TG GG GGAGAAGG    TGGG
                                || || ||||||||    ||||
                                GC CC CCTCTTCC    ACCC
                                 _ C      C___
GAM1570  LOC92973  3'  GGAGGGGAGGGAACAGGA    39184      A A A
                                GGAGG GA GG GAATGGGG
                                ||||| || || ||||||||
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                                CCTCC CT CC CTTGTCCT
                                  C  _  _
GAM1571 B4GALT4  5' AGGAAGTGTTGCGTGG     39187       G    CATGCG
                                AGGAAGTG TTGCG     GG
                                |||||||| |||||     ||
                                TCCTTCAC AACGC     CC
                                    _    A_____
GAM1571 GFPT2    3' AGAAGTGGAGGGATGTGGGCC 39188       TTGCGC  C
                                GGAAGTGG     ATG GGGCC
                                ||||||||     ||| |||||
                                TCTTCACC     TAC CCCGG
                                     TCCC__  A
GAM1571 SERPINH2 5' AGGAAGTGGTTTGCGTGCACC 39189         GC  A  GG
                                AGGAAGTGGTT  GC TGC  GCC
                                ||||||||||  || |||  |||
                                TCCTTCACCAA  CG ACG  TGG
                                      A_  C  __
GAM1571 SLC1A5   5' GGAGGGTGGGATGCGGGC    39190    A_   TTGCGC
                                GGA  GTGG     ATGCGGGC
                                |||  ||||     ||||||||
                                CCT  CACC     TACGCCCG
                                  CC   C_____
GAM1571 SLC1A5   5' GGAGGGTGGGATGCGGGC    39190    A_   TTGCGC
                                GGA  GTGG     ATGCGGGC
                                |||  ||||     ||||||||
                                CCT  CACC     TACGCCCG
                                  CC   C_____
GAM1571 CDC42BPB 3' AGGAAGTGGTGTTGGCAGGGCC 39191         __  C   TGC
                                AGGAAGTGGT  TG GCA   GGGCC
                                ||||||||||  || |||   |||||
                                TCCTTCACCA  AC CGT   CCCGG
                                     CA  _  ___
GAM1571 FLJ10650 5' GGAAGTGGTTTTGGGG      39192        GCGCA  C
                                GGAAGTGGTT    TG GGG
                                ||||||||||    || |||
                                CCTTCACCAA    AC CCC
                                     A____  _
GAM1571 HAPIP    3' AGGAAGTGGTTGTTGCCAG   39193         CGCA   G
                                AGGAAGTGGTTG   TGC GG
                                ||||||||||||   ||| ||
                                TCCTTCACCAAC   ACG TC
                                      A___   G
GAM1571 KCNT1    3' AGGAAGTGGTGGTCGGGC    39194        TGCGCATG
                                AGGAAGTGGT      CGGGC
                                ||||||||||      |||||
                                TCCTTCACCA      GCCCG
                                     CCA_____
GAM1571 KIAA0258 3' AGCAGGCACGCATGCGGGC   39195    TG TT
                                AG  G  GCGCATGCGGGC
                                ||  |  ||||||||||||
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                                TC  C  TGCGTACGCCCG
                                 GT CG
GAM1571  KIAA0514  3'  AGGAAGTGGGATGTGGGC    39196        TTGCGC   C
                                AGGAAGTGG     ATG GGGC
                                |||||||||     ||| ||||
                                TCCTTCACC     TAC CCCG
                                    C_____   A
GAM1571  KIAA1987  3'  AGGAAGTGGTGGCGTGC     39197         T   CA
                                AGGAAGTGGT GCG  TGC
                                |||||||||| |||  |||
                                TCCTTCACCA CGC  ACG
                                     C  __
GAM1571  MGC15854  5'  GGAAGTGGTTGTCGTGGAGTGG 39198          _  CA___  C
            GGCC                   GGAAGTGGTTG CG     TG GGGCC
                                |||||||||| ||     || |||||
                                CCTTCACCAAC GC     AC CCCGG
                                      A  ACCTC  _
GAM1571  MGC16279  5'  AGGAGGTGGTTACCTGCGGGCC 39199      A       GCA
                                AGGA GTGGTTGC   TGCGGGCC
                                |||| ||||||||   ||||||||
                                TCCT CACCAATG   ACGCCCGG
                                  C       G__
GAM1571  MGC16279  5'  AGGAGGTGGTTACCCGCGGGCC 39200      A       GCA
                                AGGA GTGGTTGC   TGCGGGCC
                                |||| ||||||||   ||||||||
                                TCCT CACCAATG   GCGCCCGG
                                  C       G__
GAM1571  MYT1     5'  GGAAGCCTGCGTGCGGG     39201       GG     CA
                                GGAAGT  TTGCG  TGCGGG
                                ||||||  |||||  ||||||
                                CCTTCG  GACGC  ACGCCC
                                    __    __
GAM1571  NY-REN-25 3'  AGTGAGTCTAGGGCATGCGGGC 39202      _  GC__
                                AGTG GTT    GCATGCGGGC
                                |||| |||    ||||||||||
                                TCAC CAG    CGTACGCCCG
                                  T   ATCC
GAM1571  PLAGL2    3'  AGGAGGTGGCTGCGTAC     39203      A       CA
                                AGGA GTGGTTGCG  TGC
                                |||| |||||||||  |||
                                TCCT CACCGACGC  ATG
                                  C       __
GAM1571  PRO0902   3'  GGAAGTGGTTGCTGTTGGCCCG 39204          _________  ATGCGG
            CAG                   AAGTGGTTGC       GC     G
                                ||||||||||       ||     |
                                TTCACCAACG       CG     C
                                     ACAAIIIC  GGCGTA
GAM1571  SFXN2     3'  GGAAGTGGCTGTGCATTGC    39205          C   _
                                GGAAGTGGTTG GCAT GC
                                |||||||||| |||| ||
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                                CCTTCACCGAC CGTA CG
                                      A   A
GAM1571 Ubc6p    3' AGAAAGATGAGCGCGTGCGGGC 39206      _  TT   A
                                AGGAAG TGG  GCGC TGCGGGC
                                |||||| |||  |||| |||||||
                                TCTTTC ACT  CGCG ACGCCCG
                                   T  __   C
GAM1571 LOC196374 3' AGGAGGTGGCTGCTGGG    39207     A      GCATGC
                                AGGA GTGGTTGC     GGG
                                |||| ||||||||     |||
                                TCCT CACCGACG     CCC
                                  C       A_____
GAM1571 LOC51336 5' AGGATGGTGGTTGCCAGGGGC 39208     A_      G TGC
                                AGGA  GTGGTTGC CA   GGGC
                                ||||  |||||||| ||   ||||
                                TCCT  CACCAACG GT   CCCG
                                  AC       _ C__
GAM1571 LOC90120 5' AGGCAGGTGGTGTGCGGGC   39209    AA_    T CGCA
                                AGG   GTGGT G    TGCGGGC
                                |||   ||||| |    |||||||
                                TCC   CACCA C    ACGCCCG
                                 GTC    _ ____
GAM1571 LOC91409 3' AGGAAGTGGTTTAGGGGC    39210          GCGCATGC
                                AGGAAGTGGTT       GGGC
                                ||||||||||       ||||
                                TCCTTCACCAA       CCCG
                                      ATC_____
GAM1572 ACVRL1   5' TCTGCGGGTGGCGGGG     39213    C    AGTA
                                TC GTGG    GTGGCGGGG
                                || ||||    |||||||||
                                AG CGCC    CACCGCCCC
                                 A   ____
GAM1572 AF5Q31   5' TCCGGGAGGCGGCGGGG     39214     T    TA
                                TCCG GGAG  GTGGCGGGG
                                |||| ||||  |||||||||
                                AGGC CCTC  CGCCGCCCC
                                  _   __
GAM1572 APG5L    5' TCCGGTGGGGCGGCGGGG    39215     _  AGTA
                                TCCG TGG    GTGGCGGGG
                                |||| |||    |||||||||
                                AGGC ACC    CGCCGCCCC
                                  C   C___
GAM1572 BIN3     3' TCCGTGGAGGGCAGCAGG    39216        TA TG
                                TCCGTGGAG  G  GCGGG
                                |||||||||  |  |||||
                                AGGCACCTC  C  CGTCC
                                     C_ GT
GAM1572 CDK2AP1  5' TCCGCGGAGCCGGCGGGG    39217          AG
                                TCCGTGGAGT  TGGCGGGG
                                |||||||||  ||||||||
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                                AGGCGCCTCG  GCCGCCCC
                                          __
GAM1572 CKMT1    5' TCCTGGAGTAGGCGCTGG    39218    G      TG  G
                                TCC TGGAGTAG  GC GG
                                ||| ||||||||  || ||
                                AGG ACCTCATC  CG CC
                                  _      CG  A
GAM1572 DIAPH2   3' TCCTGGAGTAATCTGGG     39219    G      GGC
                                TCC TGGAGTAGT   GGG
                                ||| |||||||||   |||
                                AGG ACCTCATTA   CCC
                                  _       GA_
GAM1572 DNCI1    5' TCCCGAAGGTGGCGGGG     39220    G    TA
                                TCC TGGAG  GTGGCGGGG
                                ||| |||||  |||||||||
                                AGG GCTTC  CACCGCCCC
                                  _    __
GAM1572 EGFL4    3' CCCAGCAGTGGTGGCGGGG   39221     TGG   A
                                TCCG   AGT GTGGCGGGG
                                ||||   ||| |||||||||
                                GGGT   TCA CACCGCCCC
                                   CG_   C
GAM1572 ENTPD6   3' TCCATGGAGGAGGTGGGG    39222        TAGT  C
                                TCCGTGGAG    GG GGGG
                                |||||||||    || ||||
                                AGGTACCTC    CC CCCC
                                      CT__  A
GAM1572 GNG5     5' CCGTGGGTCGGCGGGG      39223       A  AG
                                CCGTGG GT  TGGCGGGG
                                ||||||  ||  ||||||||
                                GGCACC CA  GCCGCCCC
                                   _  __
GAM1572 LILRB1   3' TCCATGGAGTGTGGGG      39224         A   C
                                TCCGTGGAGT GTGG GG
                                |||||||||| |||| ||
                                AGGTACCTCA CACC CC
                                      _   _
GAM1572 MYC      5' TCCTGGCAGCGGCGGGG     39225    G   AG
                                TCC TGG  TAGTGGCGGGG
                                ||| |||  ||||||||||
                                AGG ACC  GTCGCCGCCCC
                                   _  __
GAM1572 NONO     3' TCCTGGAGGAGCTGGGG     39226    G    T  GGC
                                TCC TGGAG AGT   GGGG
                                ||| ||||| |||   ||||
                                AGG ACCTC TCG   CCCC
                                  _    C   A__
GAM1572 PITX1    3' TCCGCGGAGTGGGCCTCCGGGG 39227         AGT  ____
                                TCCGTGGAGT   GGC   GGGG
                                |||||||||   |||   ||||
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                                AGGCGCCTCA  CCG   CCCC
                                      C__  GAGG
GAM1572 RERE    5' TCCGGGGAAAGTGGCGGGG  39228    T  T
                                TCCG GGAG AGTGGCGGGG
                                |||| |||| ||||||||||
                                AGGC CCTT TCACCGCCCC
                                  C  _
GAM1572 RFX2    3' TCCGTGGAGCGGGACGCAGG  39229       AGTG_
                                TCCGTGGAGT   GCGGG
                                ||||||||||   |||||
                                AGGCACCTCG   CGTCC
                                      CCCTG
GAM1572 ROR2    3' CCTGTGGGGTCTCGGCGGGG  39230   _  A  AG
                                CC GTGG GT  TGGCGGGG
                                || |||| ||  ||||||||
                                GG CACC CA  GCCGCCCC
                                 A   C  GA
GAM1572 SCA1    3' TCCGTGTGGTGACAGGG    39231     GAGTA
                                TCCGTG   GTGGCGGGG
                                ||||||   |||||||||
                                AGGCAC   CACTGTCCC
                                   AC___
GAM1572 SELPLG  3' CCCGTGGAGGTGGGG      39232       TA  C
                                TCCGTGGAG  GTGG GG
                                |||||||||  |||| ||
                                GGGCACCTC  CACC CC
                                      __  _
GAM1572 SEZ6L   5' TCCGTGGAGGAGGAGAGG   39233       TAGT  C
                                TCCGTGGAG   GG GGGG
                                |||||||||   || ||||
                                AGGCACCTC   CC CTCC
                                      CT__  T
GAM1572 SLC17A7 3' TCCCTGGAATGGCGGGG    39234    G  GTA
                                TCC TGGA  GTGGCGGGG
                                ||| ||||  |||||||||
                                AGG ACCT  TACCGCCCC
                                  G  ___
GAM1572 SLC6A9  3' CGTGGAGCACGGGTGGGG   39235       GT  C
                                CGTGGAGTA  GG GGGG
                                |||||||||  || ||||
                                GCACCTCGT  CC CCCC
                                      GC  A
GAM1572 TBR1    3' TCCGGGCCGCGGCGGGG    39236    T  AGTA
                                TCCG GG   GTGGCGGGG
                                |||| ||   |||||||||
                                AGGC CC   CGCCGCCCC
                                  _ GG__
GAM1572 TGFB1   5' TCCTCCCCGCAGTGGCGGGG  39237    GTGGA
                                TCC   GTAGTGGCGGGG
                                |||   ||||||||||||
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                                AGG    CGTCACCGCCCC
                                  AGGGG
GAM1572 TIRAP    5' GTGGAGCAGAGCCTGTGGGG  39238        T  _____
                                GTGGAGTAG GGC   GGGG
                                ||||||||| |||   ||||
                                CACCTCGTC TCG   CCCC
                                     _  GACA
GAM1572 VIPR2    3' CCTGTGGAGTTGGGTGGGG   39239   _     AGT  C
                                CC GTGGAGT   GG GGGG
                                || |||||||   || ||||
                                GG CACCTCA   CC CCCC
                                 A      AC_  A
GAM1572 ALTE     5' TCCGGGGCCTGGCGGGG     39240     T  A  AG
                                TCCG GG GT  TGGCGGGG
                                |||| || ||  ||||||||
                                AGGC CC CG  ACCGCCCC
                                  _ _  G_
GAM1572 AP1GBP1  3' CCGTGGGGATGACGGGG     39241      AGTA
                                CCGTGG   GTGGCGGGG
                                ||||||   |||||||||
                                GGCACC   TACTGCCCC
                                   CC__
GAM1572 AP1GBP1  3' CCGTGGGGATGACGGGG     39241      AGTA
                                CCGTGG   GTGGCGGGG
                                ||||||   |||||||||
                                GGCACC   TACTGCCCC
                                   CC__
GAM1572 CARD14   5' TCCGTGCAGCAGGGTGGGG   39242      G    T  C
                                TCCGTG AGTAG GG GGGG
                                |||||| ||||| || ||||
                                AGGCAC TCGTC CC CCCC
                                   G    _  A
GAM1572 CSEN     3' TCAGTGGAGTAGCAGGGG    39243    C       TG C
                                TC GTGGAGTAG  G GGG
                                || |||||||||  | |||
                                AG CACCTCATC  C CCC
                                 T       GT _
GAM1572 DKFZP434B205 3' GTGTGAGCGTGTGGCGGGG   39244    _   A_
                                GTG GAGT  GTGGCGGGG
                                ||| ||||  |||||||||
                                CAC CTCG  CACCGCCCC
                                  A   CA
GAM1572 DKFZP434P0111 3' CCTGGATGTGGTGGCGGGG   39245   G   _  A
                                CC TGGA GT GTGGCGGGG
                                || |||| || |||||||||
                                GG ACCT CA CACCGCCCC
                                 _   A  C
GAM1572 FLJ10719 3' CCCGTGGAGCTTCATCGGGG  39246        AGTGG
                                TCCGTGGAGT    CGGGG
                                ||||||||||    |||||
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                                GGGCACCTCG    GCCCC
                                     AAGTA
GAM1572  FLJ11017  5'  TCCGGAGCTTGGCGGGG    39247    GT    AG
                                TCC  GGAGT  TGGCGGGG
                                |||  |||||  ||||||||
                                AGG  CCTCG  ACCGCCCC
                                  __    A_
GAM1572  FLJ12586  3'  CCATGGAGGTAGTGGTGGGG  39248       _    C
                                CCGTGGAG TAGTGG GGGG
                                |||||||| |||||| ||||
                                GGTACCTC ATCACC CCCC
                                     C     A
GAM1572  FLJ12895  5'  TCCTGGACGCACAGCGGGG   39249    G   _  G
                                TCC TGGA GTA TGGCGGGG
                                ||| |||| ||| ||||||||
                                AGG ACCT CGT GTCGCCCC
                                  _   G  _
GAM1572  FLJ20174  3'  TCTGTGGAGTGACAGGG    39250    C     AGT
                                TC GTGGAGT   GGCGGGG
                                || |||||||   |||||||
                                AG CACCTCA   CTGTCCC
                                 A     ___
GAM1572  FLJ20257  5'  CCCGTGGAGTAAGGG      39251          TGGC
                                TCCGTGGAGTAG   GGG
                                ||||||||||||   |||
                                GGGCACCTCATT   CCC
                                          _____
GAM1572  FLJ20509  5'  TCCGCGGAGGCCTGGGG    39252       GTAGT  __
                                TCCGTGGA    GGC  GGGG
                                ||||||||    |||  ||||
                                AGGCGCCT    CCG  CCCC
                                     ______  GA
GAM1572  FLJ23168  3'  TCCATGGAGTGGGTGAGGG  39253        A_   C
                                TCCGTGGAGT  GTGG GGG
                                ||||||||||  |||| |||
                                AGGTACCTCA  CACT CCC
                                      CC   _
GAM1572  GPS1     3'  TCCGTGGAGGTGGGG      39254        TA   C
                                TCCGTGGAG  GTGG GG
                                |||||||||  |||| ||
                                AGGCACCTC  CACC CC
                                          __   _
GAM1572  HCGIV.9   5'  TCCTGGCGAGGGCGGGG    39255    G  AGT  T
                                TCC TGG   AG GGCGGGG
                                ||| |||   || |||||||
                                AGG ACC   TC CCGCCCC
                                  _   GC_  _
GAM1572  IMP13     5'  TCCGTGGAGTTGAGGGG    39256         AG   C
                                TCCGTGGAGT  TGG GGGG
                                ||||||||||  ||| ||||
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                                AGGCACCTCA  ACT CCCC
                                   __  _
GAM1572 KIAA0153 3' CCTGTGGGTGCAGTGTGGGG  39257   _   A_    GC
                                CC GTGG  GTAGTG  GGGG
                                || ||||  ||||||  ||||
                                GG CACC  CGTCAC  CCCC
                                 A   CA    A_
GAM1572 KIAA0237 3' TCCTCAACAGTGGCGGGG   39258    GTG  G
                                TCC   GA TAGTGGCGGGG
                                |||   || ||||||||||
                                AGG   TT GTCACCGCCCC
                                  AG_  _
GAM1572 KIAA0254 3' CGTGGAGTAGAGGTGGGG   39259         T  C
                                CGTGGAGTAG GG GGGG
                                |||||||||| || ||||
                                GCACCTCATC CC CCCC
                                      T  A
GAM1572 KIAA0427 3' CCCGTGGAGGGTGGCGGGG   39260         TA
                                TCCGTGGAG  GTGGCGGGG
                                |||||||||  |||||||||
                                GGGCACCTC  CACCGCCCC
                                     C_
GAM1572 KIAA0700 3' TCCCTGGAGTGGCCGCGTGGG 39261    G     A  G   _
                                TCC TGGAGT GT GCG GGG
                                ||| |||||| || ||| |||
                                AGG ACCTCA CG CGC CCC
                                  G     C  G   A
GAM1572 KIAA1691 3' CCCGTGGAGTTTGGGG      39262          AG   C
                                TCCGTGGAGT  TGG GG
                                ||||||||||  ||| ||
                                GGGCACCTCA  ACC CC
                                     A_  _
GAM1572 KIAA1775 3' TCCGAGCAGCAGGGTGGTGGGG 39263     T  _   __   C
                                TCCG GG AGTA  GTGG GGGG
                                |||| || ||||  |||| ||||
                                AGGC TC TCGT  CACC CCCC
                                  _ G   CC   A
GAM1572 KIAA1784 3' TCCCTGCAAATGGCGGGG    39264    G  G  TA
                                TCC TG AG  GTGGCGGGG
                                ||| || ||  |||||||||
                                AGG AC TT  TACCGCCCC
                                  G  G  __
GAM1572 KIAA1819 5' CCGTGGAGAAGTTGTGGGG   39265        T   GGC
                                CCGTGGAG AGT   GGGG
                                |||||||| |||   ||||
                                GGCACCTC TCA   CCCC
                                     T   ACA
GAM1572 KIAA1912 5' TCCGCGGGGTGGCAGG      39266        AGTA
                                TCCGTGG   GTGGCGGG
                                |||||||   ||||||||
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                                AGGCGCC   CACCGTCC
                                   C___
GAM1572 LYPLA3   3' TCCATGGAGCACCCTGGGG   39267         GTGGC
                                TCCGTGGAGTA    GGGG
                                ||||||||||    ||||
                                AGGTACCTCGT    CCCC
                                      GGGA_
GAM1572 MGC26847 5' TCCGAGGCGCTTGGCGGGG   39268     T  A  AG
                                TCCG GG GT  TGGCGGGG
                                |||| || ||  ||||||||
                                AGGC CC CG  ACCGCCCC
                                  T  G  A_
GAM1572 MGC2721  3' TCCTGGGCTCAGCGGGG    39269     G   A  AG
                                TCC TGG GT  TGGCGGGG
                                ||| ||| ||  ||||||||
                                AGG ACC CG  GTCGCCCC
                                  _  _  A_
GAM1572 MGC3101  3' TCCGTGGAGTAGAAGAAGGGG 39270          T_  C
                                TCCGTGGAGTAG  GG GGGG
                                ||||||||||||  || ||||
                                AGGCACCTCATC  CT CCCC
                                      TT  T
GAM1572 MRPL4    3' TCCGTGGAATGAAGGGG     39271       GTA   C
                                TCCGTGGA   GTGG GGGG
                                ||||||||   |||| ||||
                                AGGCACCT   TACT CCCC
                                   ____    T
GAM1572 PCQAP    3' CCCAGCTGGTGGCGGGG     39272     GTGG   A_
                                TCC    AGT  GTGGCGGGG
                                |||    |||  |||||||||
                                GGG    TCG  CACCGCCCC
                                  _____   AC
GAM1572 PPP1R14C 3' TCTGTGGGAGTCAGCGGGG   39273    C    _   AG
                                TC GTGG AGT  TGGCGGGG
                                || |||| |||  ||||||||
                                AG CACC TCA  GTCGCCCC
                                 A    C   __
GAM1572 PPY2     3' CCCGTGGAGTGGTAGGGG    39274         A   C
                                TCCGTGGAGT GTGG GGG
                                |||||||||| |||| |||
                                GGGCACCTCA CATC CCC
                                      C    _
GAM1572 PRDM14   5' TCCTGGACGCTGCGGGG     39275     G   GTA  G
                                TCC TGGA   GT GCGGGG
                                ||| ||||   || ||||||
                                AGG ACCT   CG CGCCCC
                                  _    G__  A
GAM1572 PRO2900  3' CCCGTGGAGCTGGGG       39276         AG   C
                                TCCGTGGAGT  TGG GG
                                ||||||||||  ||| ||
```

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                                GGGCACCTCG  ACC CC
                                          __  _
GAM1572 RSHL1    5' CCCGTGGAGGGCGCGGGG    39277        TA  G
                                TCCGTGGAG  GTG CGGGG
                                |||||||||  ||| |||||
                                GGGCACCTC  CGC GCCCC
                                     C_  _
GAM1572 SLC37A1  5' TCCGTGGAGCGGCTGCCGG   39278        TA  G  G
                                TCCGTGGAG  GT GC GG
                                |||||||||  || || ||
                                AGGCACCTC  CG CG CC
                                     GC  A  G
GAM1572 STMN3    3' TCCGTGGAGAAGTGGGG     39279        T    C
                                TCCGTGGAG AGTGG GG
                                ||||||||| ||||| ||
                                AGGCACCTC TCACC CC
                                     T    _
GAM1572 TETRAN   3' TCCCTGGACTGGCGGGG     39280     G   GTAG
                                TCC TGGA   TGGCGGGG
                                ||| ||||   ||||||||
                                AGG ACCT   ACCGCCCC
                                  G   G___
GAM1572 TNKS1BP1 3' GTGGGGTACCTGGCGGGG    39281     A   G_
                                GTGG GTA  TGGCGGGG
                                |||| |||  ||||||||
                                CACC CAT  ACCGCCCC
                                  C   GG
GAM1572 ZDHHC2   5' TCCTGGGCGGCGGCGGGG    39282     G   A TA
                                TCC TGG G  GTGGCGGGG
                                ||| ||| |  |||||||||
                                AGG ACC C  CGCCGCCCC
                                  _  _ GC
GAM1572 LOC116411 5' CCGTGGAAAGAGCGGGG    39283        T  T
                                CCGTGGAG AG GGCGGGG
                                |||||||| || |||||||
                                GGCACCTT TC TCGCCCC
                                          _  _
GAM1572 LOC144245 5' TCCTGGAGTGACGGG      39284     G     AGT
                                TCC TGGAGT   GGCGGG
                                ||| ||||||   ||||||
                                AGG ACCTCA   CTGCCC
                                  _     ____
GAM1572 LOC147700 3' CGTGGAGTAGCTAGTGGGG  39285          _  C
                                CGTGGAGTAG TGG GGGG
                                |||||||||| ||| ||||
                                GCACCTCATC ATC CCCC
                                     G   A
GAM1572 LOC150236 5' TCCTGGGAGCAGTGGGG    39286     GT        C
                                TCC  GGAGTAGTGG GG
                                |||  |||||||||| ||
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                                AGG  CCTCGTCACC CC
                                  AC        _
GAM1572  LOC153603 5'  TCCTGGGGTGCAGCGGGG    39287     G   A  A TG
                                TCC TGG GT G  GCGGGG
                                ||| ||| || |  ||||||
                                AGG ACC CA C  CGCCCC
                                  _   C  _ GT
GAM1572  LOC155060 3'  TCTTCAGATGGTGGCGGGG   39288    CG    GTA
                                TC  TGGA   GTGGCGGGG
                                ||  ||||   |||||||||
                                AG  GTCT   CACCGCCCC
                                 AA    AC_
GAM1572  LOC160646 3'  TCCGTAGAGTGCCTCGGGG   39289          A  GG
                                TCCGTGGAGT GT  CGGGG
                                |||||||||| ||  |||||
                                AGGCATCTCA CG  GCCCC
                                      _  GA
GAM1572  LOC163033 5'  CGCGGACGGTGGTGGCGGGG   39290       __  A
                                CGTGGA  GT GTGGCGGGG
                                ||||||  || |||||||||
                                GCGCCT  CA CACCGCCCC
                                   GC  C
GAM1572  LOC196500 3'  TCCTTGGAGTAGGATGGGG   39291     G       T GC
                                TCC TGGAGTAG G  GGGG
                                ||| ||||||| |  ||||
                                AGG ACCTCATC C  CCCC
                                  A       _ TA
GAM1572  LOC201484 5'  TCCGAGTCCTGGCGGGG     39292     GTG    AG
                                TCC   GAGT  TGGCGGGG
                                |||   ||||  ||||||||
                                AGG   CTCA  ACCGCCCC
                                  ____   GG
GAM1572  LOC221178 3'  TCCGTGGAGGTAGGTGGG    39293         TA   CG
                                TCCGTGGAG  GTGG  GGG
                                |||||||||  ||||  |||
                                AGGCACCTC  CATC  CCC
                                     __   CA
GAM1572  LOC221416 3'  TCCGTGTCTGTGGCGGGG    39294       GAGTA
                                TCCGTG    GTGGCGGGG
                                ||||||    |||||||||
                                AGGCAC    CACCGCCCC
                                   AGA__
GAM1572  LOC245806 3'  TCCATGGAGACAGTTGGGG   39295         _   GGC
                                TCCGTGGAG TAGT   GGGG
                                ||||||||| ||||   ||||
                                AGGTACCTC GTCA   CCCC
                                     T   A__
GAM1572  LOC253664 5'  CCTGGAGGTGGCGGG       39296    G    TA
                                CC TGGAG  GTGGCGGG
                                || |||||  ||||||||
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                                GG ACCTC  CACCGCCC
                                 _    __
GAM1572  LOC254479 5'  TCCATGTCCACTGGCGGGG   39297      GAG  G
                                TCCGTG   TA TGGCGGGG
                                ||||||   || ||||||||
                                AGGTAC   GT ACCGCCCC
                                   AG_  G
GAM1572  LOC255386 5'  TCCTGGAGTAGGCGCTGG    39218    G      TG  G
                                TCC TGGAGTAG  GC GG
                                ||| ||||||||  || ||
                                AGG ACCTCATC  CG CC
                                  _      CG  A
GAM1572  LOC256848 5'  TCCTGTGGGTGGTGGGG    39298    _   AGTA   C
                                TCC GTGG   GTGG GGGG
                                ||| ||||   |||| ||||
                                AGG CACC   CACC CCCC
                                  A   _____   A
GAM1572  LOC90233  5'  TCCGTGGACTAGGCGGGG   39299       G  GT
                                TCCGTGGA TA  GGCGGGG
                                |||||||| ||  |||||||
                                AGGCACCT AT  CCGCCCC
                                    G  __
GAM1572  LOC90874  3'  TCCGTGGAGAGGAGG      39300        T  T  C
                                TCCGTGGAG AG GG GG
                                ||||||||| || || ||
                                AGGCACCTC TC CT CC
                                          _  _  _
GAM1572  LOC92578  3'  TCCATGGAAATGAAGGCGGGG  39301        TAGT_
                                TCCGTGGAG    GGCGGGG
                                |||||||||    |||||||
                                AGGTACCTT    CCGCCCC
                                     TACTT
GAM1573  KAI1     5'  TGCCTGTGCCCACGTGTCGTCC 39304      AGATA  GGA
            A                    TGCCT    CA   TGTCGTCCA
                                 |||||    ||   |||||||||
                                 ACGGA    GT   ACAGCAGGT
                                    CACGG  GC_
GAM1573  MXI1     3'  TGCTTAAATACAGGTCCTC   39305     C       ATG  G
                                TGC TAGATACAGG   TC TC
                                ||| ||||||||||   || ||
                                ACG ATTTATGTCC   AG AG
                                  A        ___  G
GAM1573  MXI1     3'  TGCTTAAATACAGGTCCTC   39305     C       ATG  G
                                TGC TAGATACAGG   TC TC
                                ||| ||||||||||   || ||
                                ACG ATTTATGTCC   AG AG
                                  A        ___  G
GAM1573  FADS2    3'  TGCTTAGATGCAGGTCCCTCC  39306    C    A   ATG  G
                                TGC TAGAT CAGG   TC TCC
                                ||| ||||| ||||   || |||
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                                ACG ATCTA GTCC   GG AGG
                                  A    C   A__  G
GAM1573  FLJ21324  5'  TGCTTAATACAGGGAAGTCCA  39307    CTA      ATGTC
                                TGC   GATACAGG    GTCCA
                                |||   ||||||||    |||||
                                ACG   TTATGTCC    CAGGT
                                  AA_      CTT__
GAM1573  FLJ22389  5'  TGCTGGGATACAGGGTGATCG  39308    CTA      A  _
                                TGC   GATACAGG TG TCG
                                |||   |||||||| || |||
                                ACG   CTATGTCC AC AGC
                                  ACC      C  T
GAM1573  KIAA0152  3'  TGCCTGGATGCAAGAGGTGCCA 39309      A   A    T  C T
                                TGCCT GAT CAGGA GT G CCA
                                ||||| ||| ||||| || | |||
                                ACGGA CTA GTTCT CA C GGT
                                   C   C    C  _ _
GAM1573  LRP1B    5'  TGCCTGGAGCAGGATGT    39310      A  TA
                                TGCCT GA  CAGGATGT
                                ||||| ||  ||||||||
                                ACGGA CT  GTCCTACA
                                   C  C_
GAM1573  TIEG     3'  TGCCTAGATACAGTCAT    39311          GGAT
                                TGCCTAGATACA   GTCGT
                                ||||||||||||   |||||
                                ACGGATCTATGT   CAGTA
                                           ____
GAM1573  LOC147779 3'  TGCCTAGGCTGTGTCGTCCA  39312       ATACAGGA
                                TGCCTAG      TGTCGTCCA
                                |||||||      |||||||||
                                ACGGATC      ACAGCAGGT
                                    CGAC____
GAM1573  LOC158056 5'  TGCCAGATACAGGGTCC    39313     T       ATGTC
                                TGCC AGATACAGG    GTCC
                                |||| |||||||||    ||||
                                ACGG TCTATGTCC    CAGG
                                  _      _____
GAM1573  LOC223009 5'  TGCCAAGATGCAGGAGC    39314     T   A    T
                                TGCC AGAT CAGGA GT
                                |||| |||| ||||| ||
                                ACGG TCTA GTCCT CG
                                  T   C    _
GAM1573  LOC91097  3'  TGCTTAATACAGGGAAGTCCA  39307    CTA      ATGTC
                                TGC   GATACAGG    GTCCA
                                |||   ||||||||    |||||
                                ACG   TTATGTCC    CAGGT
                                  AA_      CTT__
GAM1574  PAH      3'  GCTTTTCAATAATGTATTT   39317    C      TAGA
                                GC TTTCAATA   GTGTTT
                                || ||||||||   ||||||
```

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                                CG AAAGTTAT    CATAAA
                                 A       TA__
GAM1574  FLJ23510  3'  GCTTTTCAAAATGAATGCTT   39318    C     T  A
                                GC TTTCAA AT GAGTGTTT
                                || |||||| || ||||||||
                                CG AAAGTT TA CTTACGAA
                                 A     T  _
GAM1574  FLJ33069  3'  CCTTTCAACTGCCGGTGTTT   39319         ATAGA
                                CCTTTCAAT    GTGTTT
                                |||||||||    ||||||
                                GGAAAGTTG    CACAAA
                                     ACGGC
GAM1574  HT021     3'  TCCACCTTTTAATATTCGTGTT 39320         C     AGA
              T                  TCCGCCTTT AATAT   GTGTTT
                                |||||||| |||||   ||||||
                                AGGTGGAAA TTATA   CACAAA
                                     A    AG_
GAM1574  LOC115574 3'  TCCCCTTTCAAGTGT       39321     G      ATATAG
                                TCC CCTTTCA     AGTGT
                                ||| |||||||     |||||
                                AGG GGAAAGT     TCACA
                                 _     _______
GAM1574  LOC200862 5'  CCTTTTCATTTTCAGAGTGTTT 39322       _  ATA_
                                CCTTT CA    TAGAGTGTTT
                                ||||| ||    ||||||||||
                                GGAAA GT    GTCTCACAAA
                                   A  AAAA
GAM1575  ATRN      3'  TGTGTTTGTGTGTGTATGTGTG 39325     _    A     ACC
                                TGT TTTGT TGTGTA   TGTGTG
                                ||| ||||| ||||||   ||||||
                                ACA AAACA ACACAT   ACACAC
                                  C    C     ___
GAM1575  EHD3      3'  TGTTTGTGTGTGTGTG      39326       T  A    AACCT
                                TGTTT GT TGTGT    GTG
                                ||||| || |||||    |||
                                ACAAA CA ACACA    CAC
                                   _ C    _____
GAM1575  ETF1      3'  TGTGTTTGTATGTGTAAGTG   39327     _          CCT
                                TGT TTTGTATGTGTAA   GTG
                                ||| ||||||||||||   |||
                                ACA AAACATACACATT   CAC
                                  C          ___
GAM1575  SNAP25    3'  TGTTTTGTGTGTGTGTGT    39328         A    AACCT
                                TGTTTTGT TGTGT    GTGT
                                |||||||| |||||    ||||
                                ACAAAACA ACACA    CACA
                                     C    _____
GAM1575  SNAP25    3'  TGTTTTGTGTGTGTGTGT    39328         A    AACCT
                                TGTTTTGT TGTGT    GTGT
                                |||||||| |||||    ||||
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                                ACAAAACA ACACA    CACA
                                    C    _____
GAM1575 SORCS3   3' TGTGTTGTATGTGTGTGT    39329    T       AACCT
                                TGT TTGTATGTGT    GTGT
                                ||| ||||||||||    ||||
                                ACA AACATACACA    CACA
                                  C       _____
GAM1575 TIMM44   3' TCTTGGCACTGTGTGACCTGTG 39330     TA__    A
           TG                    TTTTG   TGTGT ACCTGTGTG
                                |||||   ||||| |||||||||
                                AGAAC   ACACA TGGACACAC
                                   CGTG    C
GAM1575 CBX1     3' TGTTTTGTGTGTGTATGTGTG 39331       A     ACC
                                TGTTTTGT TGTGTA   TGTGTG
                                |||||||| ||||||   ||||||
                                ACAAAACA ACACAT   ACACAC
                                    C    ___
GAM1575 DKFZp762A227 3' TATTTTGTGTGTGTGTGT    39332       A    AACCT
                                TGTTTTGT TGTGT    GTGT
                                |||||||| |||||    ||||
                                ATAAAACA ACACA    CACA
                                    C    _____
GAM1575 FLJ10898 3' TGTATTGTGTGTGTGTGT    39333    T   A    AACCT
                                TGT TTGT TGTGT    GTGT
                                ||| |||| |||||    ||||
                                ACA AACA ACACA    CACA
                                  T   C    _____
GAM1575 FLJ25416 3' TGTTTTTTCCATTTAACCTGTG 39334      GTA   G
           TG                    TGTTTT   TGT TAACCTGTGTG
                                ||||||   ||| ||||||||||
                                ACAAAA   GTA ATTGGACACAC
                                   AAG   A
GAM1575 KIAA1623 3' TGTTCTGTGTGTGTGTGT    39335       A    AACCT
                                TGTTTTGT TGTGT    GTGT
                                |||||||| |||||    ||||
                                ACAAGACA ACACA    CACA
                                    C    _____
GAM1575 KIAA1828 5' TGTGTTTGTGTGTGTGTGT    39336    _    A    AACCT
                                TGT TTTGT TGTGT    GTGT
                                ||| ||||| |||||    ||||
                                ACA AAACA ACACA    CACA
                                  C    C    _____
GAM1575 KIAA1972 3' TTTTGTGTGTGTGTGT     39337      A    AACCT
                                TTTTGT TGTGT    GTGT
                                |||||| |||||    ||||
                                AAAACA ACACA    CACA
                                   C    _____
GAM1575 LHFP     3' TGTTGTGTGTGTGTGTGT    39338     T   A    AACCT
                                TGTT TGT TGTGT    GTGT
                                |||| ||| |||||    ||||
```

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                                ACAA ACA ACACA    CACA
                                  C  C    _____
GAM1575 SARM     3' TTCTGCTGTGGCCTGTGTG  39339      A   TAA
                                TTTTGT TGTG  CCTGTGTG
                                |||||| ||||  ||||||||
                                AAGACG ACAC  GGACACAC
                                   _   C__
GAM1575 LOC147054 5' TGTTTGTGTGTGTGTG     39326      T  A    AACCT
                                TGTTT GT TGTGT    GTG
                                ||||| || |||||    |||
                                ACAAA CA ACACA    CAC
                                   _ C    _____
GAM1575 LOC154860 3' TGTTTTGTGTGTGTGTCTG  39340       A    AAC
                                TGTTTTGT TGTGT  CTG
                                |||||||| |||||  |||
                                ACAAAACA ACACA  GAC
                                     C    CA_
GAM1575 LOC158116 3' TGTTTGTATTGTTCTGTGT  39341     T   G  AAC
                                TGTTT GTAT TGT  CTGTGT
                                ||||| |||| |||  ||||||
                                ACAAA CATA ACA  GACACA
                                   _   _  A__
GAM1575 LOC160382 3' TGTTTTATATGTGTGGAACAAT 39342          __  CT
          G                      TGTTTTGTATGTGT  AAC  GTG
                                ||||||||||||||  |||  |||
                                ACAAAATATACACA  TTG  TAC
                                       CC  T_
GAM1576 DMRT2    3' GCTTGGTGGTTCCACT     39345    _   ATTA
                                GCT GGTG   GTTCCACT
                                ||| ||||   ||||||||
                                CGA CCAC   CAAGGTGA
                                 A   _____
GAM1576 EGF      3' AGTAGGTGATTAGTCGTAGA  39346   CT       CCAC
                                AG  GGTGATTAGTT   TAGA
                                ||  ||||||||||   ||||
                                TC  CCACTAATCAG   ATCT
                                 AT        C___
GAM1576 HTR2A    3' ATGATCGTTGGTTCCACTAGAC 39347      A___
                                GTGATT   GTTCCACTAGAC
                                ||||||   ||||||||||||
                                TACTAG   CAAGGTGATCTG
                                   CAAC
GAM1576 ZNF278   3' AGCTGGTGGCTAGTTCCCAGGA 39348       AT     ACTA
                                AGCTGGTG  TAGTTCC   GA
                                ||||||||  |||||||   ||
                                TCGACCAC  ATCAAGG   CT
                                     CG     GTC_
GAM1576 FLJ14816 3' GCTGGTGATGGGGGCTTAGAC  39349       TA__  CCAC
                                GCTGGTGAT   GTT   TAGAC
                                |||||||||   |||   |||||
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                                CGACCACTA   CGA   ATCTG
                                     CCCC  ____
GAM1576 FLJ20811 3' AGGTGGTGATTGGCTAAGGCTG 39350   C      A  CCA_ A
            GA                    AG TGGTGATT GTT   CT GA
                                || |||||||| |||   || ||
                                TC ACCACTAA CGA   GA CT
                                 C       C  TTCC  C
GAM1576 KIAA0237 3' AGCTGGTGATGGTGGCAGA   39351         TA  TCCAC
                                AGCTGGTGAT  GT    TAGA
                                ||||||||||  ||    ||||
                                TCGACCACTA  CA    GTCT
                                     C_  CC___
GAM1576 RoXaN   3' AGCGGTGATTCTCCCTGCTAGA 39352    T     AG   A_
                                AGC GGTGATT  TTCC  CTAGA
                                ||| |||||||  ||||  |||||
                                TCG CCACTAA  AGGG  GATCT
                                  _      G_   AC
GAM1576 SZF1    3' GCTGATGATGCAGCATTGCTAG 39353        _   TCCA
            A                    GCTGGTGAT TAGT    CTAGA
                                |||||||||  ||||    |||||
                                CGACTACTA GTCG    GATCT
                                     C    TAAC
GAM1576 TOB2    3' GATGAAAGGAGTTTCACTAGAC 39354      TT__   C
                                GGTGA    AGTT CACTAGAC
                                |||||    |||| ||||||||
                                CTACT    TCAA GTGATCTG
                                   TTCC    A
GAM1576 LOC130612 3' AGCTGGTGACTGCAGAGTCTAG 39355         A  TCCA_
            AC                    AGCTGGTGATT GT     CTAGAC
                                ||||||||||| ||     ||||||
                                TCGACCACTGA CG     GATCTG
                                      _ TCTCA
GAM1576 LOC163682 5' AACTGGTGGGAGTGTCTGCTGG 39356       ATT  _  CA  A
            AC                    AGCTGGTG   AGT TC  CT GAC
                                ||||||||   ||| ||  || |||
                                TTGACCAC   TCA AG  GA CTG
                                     CC_   C  AC  C
GAM1576 LOC221312 5' GCGGTGACGGCTGCTAGA    39357    T     TA   CCA
                                GC GGTGAT  GTT   CTAGA
                                || ||||||  |||   |||||
                                CG CCACTG  CGA   GATCT
                                  _     C_   C__
GAM1576 LOC254170 3' AACTGGTGATATCAACTA    39358         TAGT  C
                                AGCTGGTGAT    TC ACTA
                                ||||||||||    || ||||
                                TTGACCACTA    AG TGAT
                                      T___  T
GAM1577 LRRC2    3' TGTTAAAAAGAAAAAAATGTA  39361            __
                                TGTTAAAAGGAAAA  ATGTA
                                ||||||||||||||  |||||
```

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                                ACAATTTTTCTTTT  TACAT
                                       TT
GAM1577  PPP1R2   3'  CTAACTGAAAGGGAAAAATGTA 39362     _  TT   A
                                CTA TTG  AAA GGAAAAATGTA
                                ||| |||  ||| ||||||||||
                                GAT GAC  TTT CCTTTTTACAT
                                  T  __  C
GAM1577  DKFZP434G1411 3'  TCTATTGCTAAAATTATGT   39363          GGAAAA
                                TCTATTGTTAAAA     ATGT
                                ||||||||||||     ||||
                                AGATAACGATTTT     TACA
                                       AA____
GAM1577  GPR105   3'  CTGTTTTCCAGAAAAATGT   39364      AAAA
                                TTGTT   GGAAAAATGT
                                |||||   ||||||||||
                                GACAA   TCTTTTTACA
                                   AAGG
GAM1577  KIAA1915  3'  TTGTTCCAGGAAAAATGT   39365      AAA
                                TTGTT   AGGAAAAATGT
                                |||||   ||||||||||
                                AACAA   TCCTTTTTACA
                                   GG_
GAM1577  SBBI31   3'  TCTAGTGTTAAAAGTTATGT   39366     T       GAAAA
                                TCTA TGTTAAAAG    ATGT
                                |||| |||||||||    ||||
                                AGAT ACAATTTTC    TACA
                                  C       AA___
GAM1577  ZFP106   3'  TCTGGTGTTAAAAGAATTTCAT 39367     AT        AAA_
            GT                   TCT  TGTTAAAAGGA   ATGT
                                |||  ||||||||||   ||||
                                AGA  ACAATTTTCTT   TACA
                                  CC         AAAG
GAM1577  LOC200292 5'  TCTGTTGGTAAAAGGAAA    39368     A   T
                                TCT TTG TAAAAGGAAA
                                ||| ||| ||||||||||
                                AGA AAC ATTTTCCTTT
                                  C   C
GAM1577  LOC57862  3'  TTGCTAAAGGGAGAATGT    39369        A   AA
                                TTGTTAAA GGA  AATGT
                                |||||||| |||  |||||
                                AACGATTT CCT  TTACA
                                     C   C_
GAM1577  LOC92140  3'  ATTGCTAGGGAAGGGAAAAATG 39370        ___  A
            TA                    ATTGTTA   AA GGAAAAATGTA
                                |||||||   || ||||||||||
                                TAACGAT   TT CCTTTTTACAT
                                    CCC  C
GAM1578  FGF2     3'  TCTAGGTAAGCTTCACTGGGT  39373          AGA   CA
                                TCTAGGTAAGTTT   GCT  GGT
                                ||||||||||||   |||  |||
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                                AGATCCATTCGAA  TGA  CCA
                                       G__  C_
GAM1578 FLT1    3' GGTTACTTAGAGCTCAGGT   39374    AAG
                                GGT  TTTAGAGCTCAGGT
                                |||  ||||||||||||||
                                CCA  GAATCTCGAGTCCA
                                  AT_
GAM1578 C12orf22 3' CTGGGTAGCTTCGAGAGCTCAG 39375   A   A   __
             GT                   CT GGTA GTTT  AGAGCTCAGGT
                                || |||| ||||  ||||||||||
                                GA CCAT CGAA  TCTCGAGTCCA
                                 C   _   GC
GAM1578 KIAA1915 3' TAGGGTAAGAGCTCAGG    39376    TAA  TT
                                TAGG  GT  AGAGCTCAGG
                                ||||  ||  ||||||||||
                                ATCC  CA  TCTCGAGTCC
                                  ___  T_
GAM1578 RNF13   3' TCTAGGTAACTTTATGGAGGT  39377       G   GAGCTC
                                TCTAGGTAA TTTA    AGGT
                                |||||||| ||||    ||||
                                AGATCCATT AAAT    TCCA
                                     G   ACC___
GAM1579 ARHGEF7  3' CAAGGGCAAGGAAGAACCGTAA 39380    AAA      __
                                CGA  CAAGGAAGA  TGTAG
                                |||  |||||||||  |||||
                                GTT  GTTCCTTCT  GCATT
                                  CCC       TG
GAM1579 ATP2B2   3' CGGAAACAAGGCAACATGCCGG 39381   A      _ G   A_
             CAA                  CG AAACAAGG AA ATGT  GCAA
                                || ||||||||| || ||||  ||||
                                GC TTTGTTCC TT TACG  CGTT
                                 C      G  G   GC
GAM1579 BAT1    5' GAAAACAAGGGGTGAAGAGTAG 39382         ____   T
                                GAAAACAAGG   AAGA GTAG
                                ||||||||||   |||| ||||
                                CTTTTGTTCC   TTCT CATC
                                     CCAC   _
GAM1579 CLASP2   3' GAAAAGAATGGGTGTAGCAA  39383      C  _  AAGA
                                GAAAA AA GG   TGTAGCAA
                                ||||| || ||   ||||||||
                                CTTTT TT CC   ACATCGTT
                                  C  A  C___
GAM1579 DSP     3' GAAGTCAAGGTATAGCA    39384    AA   AAGA
                                GAA  CAAGG   TGTAGCA
                                |||  |||||   |||||||
                                CTT  GTTCC   ATATCGT
                                  CA   ____
GAM1579 FGF5    3' AGAATTTAGATGTAGCAA   39385     ___
                                AGGA  AGATGTAGCAA
                                ||||  ||||||||||
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                                TCTT   TCTACATCGTT
                                  AAA
GAM1579  FGF5     3'  AGAATTTAGATGTAGCAA    39385      ___
                                AGGA   AGATGTAGCAA
                                ||||   ||||||||||
                                TCTT   TCTACATCGTT
                                  AAA
GAM1579  FOXE3    3'  ACGGAGAAGGATGTAGCA    39386    AA    _
                                AC  GGAAG ATGTAGCA
                                ||  ||||| ||||||||
                                TG  TCTTC TACATCGT
                                 CC    C
GAM1579  GEMIN5   5'  ACGCGGACAAGGAAGACG    39387     AAA
                                ACG   ACAAGGAAGATG
                                |||   ||||||||||||
                                TGC   TGTTCCTTCTGC
                                  GCC
GAM1579  GNA14    3'  AAAACAAGGAGTTTGCAA    39388          AGA
                                AAAACAAGGA   TGTAG
                                ||||||||||   |||||
                                TTTTGTTCCT   ACGTT
                                     CAA
GAM1579  GRLF1    3'  GAAAACGGGGGATCTAGC    39389       AA  AA   G
                                GAAAAC  GG  GAT TAGC
                                ||||||  ||  ||| ||||
                                CTTTTG  CC  CTA ATCG
                                   __ CC   G
GAM1579  H4FH     3'  GAAAATAAGAGTGCAGCAA   39390      C   GA  A
                                GAAAA AAG  AG TGTAGCAA
                                |||||| |||  || ||||||||
                                CTTTT TTC  TC ACGTCGTT
                                  A  __ _
GAM1579  HMG20A   3'  GAAGACAGGATGGTGTAGCAA  39391     A   A   AGA
                                GAA ACA GGA   TGTAGCAA
                                ||| ||| |||   ||||||||
                                CTT TGT CCT   ACATCGTT
                                  C   _   ACC
GAM1579  HPSE     3'  ACTGAAACAAGGAAGAAAGGTA 39392    GA          T__
            G                    AC  AAACAAGGAAGA   GTAG
                                ||  ||||||||||||   ||||
                                TG  TTTGTTCCTTCT   CATC
                                 AC          TTC
GAM1579  KCNA3    3'  AAAAACAAGGGCATAGGCA   39393          AAGA    _
                                GAAAACAAGG    TGTAG CA
                                ||||||||||    ||||| ||
                                TTTTTGTTCC    GTATC GT
                                     C___     C
GAM1579  MEF2C    3'  GAAAATAAGCAAAATGTAA   39394      C   G
                                GAAAA AAG AAGATGTAG
                                ||||| ||| |||||||||
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                                CTTTT TTC TTTTACATT
                                   A  G
GAM1579  MT1L     3'  GAAAAAAAGATGTAGCAA    39395      CAAG
                                GAAAA   GAAGATGTAGCAA
                                |||||   ||||||||||||
                                CTTTT   TTTCTACATCGTT
                                  ____
GAM1579  MUC3B    3'  GAGAGCAAGAGATGCAGCA   39396    AAA   GA
                                GA  CAAG  AGATGTAGCA
                                ||  ||||  ||||||||||
                                CT  GTTC  TCTACGTCGT
                                 CTC   __
GAM1579  NCOA6    5'  GAACACAAGGAAGTATAG    39397    A       A
                                GAA ACAAGGAAG TGTAG
                                ||| ||||||||| |||||
                                CTT TGTTCCTTC ATATC
                                  G       _
GAM1579  NXF2     3'  ACGAAGACAAAGAAGACAT   39398      A
                                ACGAA ACAAGGAAGATGT
                                ||||| ||||||||||||
                                TGCTT TGTTTCTTCTGTA
                                   C
GAM1579  NXF2     3'  ACGAAGACAAAGAAGACAT   39398      A
                                ACGAA ACAAGGAAGATGT
                                ||||| ||||||||||||
                                TGCTT TGTTTCTTCTGTA
                                   C
GAM1579  PHF1     3'  GAAACTGAGGAAGATGAGGCA 39399     ACA       TA
                                GAAA  AGGAAGATG  GCA
                                ||||  |||||||||  |||
                                CTTT  TCCTTCTAC  CGT
                                  GAC       TC
GAM1579  PITPNB   3'  GAAAACGAGGAGCAGGCA   39400      A   AGAT   _
                                GAAAAC AGGA   GTAG CA
                                |||||| ||||   |||| ||
                                CTTTTG TCCT   CGTC GT
                                   C   ____   C
GAM1579  PITX2    5'  ACGAAGACATGGGATGTGGGCA 39401     A  A  AA    A_
                                ACGAA ACA GG  GATGT  GCA
                                ||||| ||| ||  |||||  |||
                                TGCTT TGT CC  CTACA  CGT
                                   C  A __    CC
GAM1579  PNOC     3'  ACAAAAATACACTCTGATGTAG 39402      __  AGGAA
            CAA                   ACGAAA  ACA    GATGTAGCAA
                                ||||||  |||    ||||||||||
                                TGTTTT  TGT    CTACATCGTT
                                   TA  GAGA_
GAM1579  PTPRO    3'  ACAGAACAAGGAATGCAA    39403    AA      AG
                                ACG  AACAAGGA  ATGTAG
                                |||  ||||||||  ||||||
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                                TGT  TTGTTCCT  TACGTT
                                  C_      __
GAM1579  PTPRO    3'  ACAGAACAAGGAATGCAA    39403    AA      AG
                                ACG  AACAAGGA  ATGTAG
                                |||  ||||||||  ||||||
                                TGT  TTGTTCCT  TACGTT
                                  C_      __
GAM1579  PTPRO    3'  ACAGAACAAGGAATGCAA    39403    AA      AG
                                ACG  AACAAGGA  ATGTAG
                                |||  ||||||||  ||||||
                                TGT  TTGTTCCT  TACGTT
                                  C_      __
GAM1579  PTPRO    3'  ACAGAACAAGGAATGCAA    39403    AA      AG
                                ACG  AACAAGGA  ATGTAG
                                |||  ||||||||  ||||||
                                TGT  TTGTTCCT  TACGTT
                                  C_      __
GAM1579  PTPRO    3'  ACAGAACAAGGAATGCAA    39403    AA      AG
                                ACG  AACAAGGA  ATGTAG
                                |||  ||||||||  ||||||
                                TGT  TTGTTCCT  TACGTT
                                  C_      __
GAM1579  RAD52    3'  ACGAAAGTGGGAAAACGGCA  39404      ACAA      TA
                                ACGAAA   GGAAGATG  GCA
                                ||||||   ||||||||  |||
                                TGCTTT   CCTTTTGC  CGT
                                   CAC_      __
GAM1579  SCNN1G   3'  ACAAAAACAGGGATTTGGTGTG 39405        A   AGA__   A
           GC                    ACGAAAACA GGA    TGT GC
                                |||||||||  |||    ||| ||
                                TGTTTTTGT CCT    ACA CG
                                     C   AAACC   C
GAM1579  SLC16A1  3'  GAAAATGAAGACACAGCAA   39406     CAAG    TG
                                GAAAA   GAAGA  TAGCAA
                                |||||   |||||  ||||||
                                CTTTT   CTTCT  GTCGTT
                                   A___    GT
GAM1579  SMARCA1  3'  AACAAGAAAATAGCA      39407       GAT
                                AACAAGGAA   GTAGCA
                                |||||||||   ||||||
                                TTGTTCTTT   TATCGT
                                     ___
GAM1579  SMARCA1  3'  AACAAGAAAATAGCA      39407       GAT
                                AACAAGGAA   GTAGCA
                                |||||||||   ||||||
                                TTGTTCTTT   TATCGT
                                     ___
GAM1579  SNTB1    3'  CAAAAACAAGGGTCAGTAA   39408         AAGAT
                                CGAAAACAAGG    GTAG
                                ||||||||||    ||||
```

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                                GTTTTTGTTCC    CATT
                                      CAGT_
GAM1579  TNFRSF17  5'  GAAAACAAGGGAGCTACA    39409        AA  T  A
                                GAAAACAAGG  GA GT GCA
                                ||||||||||  || || |||
                                CTTTTGTTCC  CT CG TGT
                                     __  _  A
GAM1579  UBE2V1    3'  CAAAGCAAGGAAGTGT     39410     AA      A
                                CGAA  CAAGGAAG TGT
                                ||||  |||||||| |||
                                GTTT  GTTCCTTC ACA
                                  C_      _
GAM1579  UBE2V1    3'  CAAAGCAAGGAAGTGT     39410     AA      A
                                CGAA  CAAGGAAG TGT
                                ||||  |||||||| |||
                                GTTT  GTTCCTTC ACA
                                  C_      _
GAM1579  UBE2V1    3'  CAAAGCAAGGAAGTGT     39410     AA      A
                                CGAA  CAAGGAAG TGT
                                ||||  |||||||| |||
                                GTTT  GTTCCTTC ACA
                                  C_      _
GAM1579  VANGL2    3'  AAAATAAGGAAGAAGC     39411     C      TGT
                                AAAA AAGGAAGA   AGC
                                |||| ||||||||   |||
                                TTTT TTCCTTCT   TCG
                                  A      ____
GAM1579  COPS7A    3'  AAACAAGGGAGAGAGCA    39412       A   TGT
                                AAACAAGG AGA   AGCA
                                |||||||| |||   ||||
                                TTTGTTCC TCT   TCGT
                                    C   C__
GAM1579  CPSF2     3'  GAGAACAAGGAGTCTGTAA   39413    A      AGA
                                GA AACAAGGA   TGTAG
                                || ||||||||   |||||
                                CT TTGTTCCT   ACATT
                                 C       CAG
GAM1579  FLJ10110  3'  GAAAACAGGGGGAAGCAG    39414       A  AA  T
                                GAAAACA GG  GA GTAG
                                ||||||| ||  || ||||
                                CTTTTGT CC  CT CGTC
                                    _  CC  T
GAM1579  FLJ10970  3'  GAGACAAGGGAAGATGGCAA  39415    AA    _    TA
                                GA  ACAAGG AAGATG  GCAA
                                ||  |||||| ||||||  ||||
                                CT  TGTTCC TTCTAC  CGTT
                                 C_     C     __
GAM1579  FLJ20080  3'  GAAAAAAGGAAAAGCA     39416      C     ATGT
                                GAAAA AAGGAAG    AGCA
                                ||||| |||||||    ||||
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                                CTTTT TTCCTTT    TCGT
                                  _     _____
GAM1579  FLJ20519  3'  GAAATGAGGAAAATGAGCAA  39417     ACA       T
                                GAAA   AGGAAGATG AGCAA
                                ||||   ||||||||| |||||
                                CTTT   TCCTTTTAC TCGTT
                                  AC_       _
GAM1579  FLJ20666  3'  ACAGAAACAAGGAAGACA    39418     A
                                ACG AAACAAGGAAGATG
                                ||| ||||||||||||||
                                TGT TTTGTTCCTTCTGT
                                  C
GAM1579  FLJ20666  3'  ACAGAAACAAGGAAGACA    39418     A
                                ACG AAACAAGGAAGATG
                                ||| ||||||||||||||
                                TGT TTTGTTCCTTCTGT
                                  C
GAM1579  GHITM     3'  ACAAGATATTTGATGTAGCA  39419       AA___
                                ACAAGG    GATGTAGCA
                                ||||||    |||||||||
                                TGTTCT    CTACATCGT
                                   ATAAA
GAM1579  GIT2      3'  GAGGCCAAGGAAATGCGC    39420    AAA     A    A
                                GA   CAAGGA GATGT GC
                                ||   |||||| ||||| ||
                                CT   GTTCCT TTACG CG
                                 CCG     _    _
GAM1579  GIT2      3'  GAGGCCAAGGAAATGCGC    39420    AAA     A    A
                                GA   CAAGGA GATGT GC
                                ||   |||||| ||||| ||
                                CT   GTTCCT TTACG CG
                                 CCG     _    _
GAM1579  GIT2      3'  GAGGCCAAGGAAATGCGC    39420    AAA     A    A
                                GA   CAAGGA GATGT GC
                                ||   |||||| ||||| ||
                                CT   GTTCCT TTACG CG
                                 CCG     _    _
GAM1579  KIAA0159  3'  GAAAACAAGGAGATTGGCAA  39421          A  GTA
                                GAAAACAAGGA GAT   GCAA
                                |||||||||| |||   ||||
                                CTTTTGTTCCT CTA   CGTT
                                      _  AC_
GAM1579  KIAA0295  3'  ACAAAAACGAGGAGGCAG    39422        A   AGAT
                                ACGAAAAC AGGA    GTAG
                                |||||||| ||||    ||||
                                TGTTTTTG TCCT    CGTC
                                     C   C___
GAM1579  KIAA0493  5'  ACCAAAACAAGTGGTGGCA   39423    G      GAAGAT  A
                                AC AAAACAAG     GT GCA
                                || ||||||||     || |||
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                                TG TTTTGTTC     CA CGT
                                 G       AC____  C
GAM1579  KIAA0721  3'  GAAAACAAGAAATACGGTAG  39424          GAT_
                                GAAAACAAGGAA   GTAG
                                ||||||||||||  ||||
                                CTTTTGTTCTTT   CATC
                                      ATGC
GAM1579  KIAA0721  3'  GAAAACAAGAAATACGGTAG  39424          GAT_
                                GAAAACAAGGAA   GTAG
                                ||||||||||||  ||||
                                CTTTTGTTCTTT   CATC
                                      ATGC
GAM1579  KIAA0747  3'  ACGAAGGCAGGAAGACAGAGCA 39425      AACA      GT
                                ACGAA   AGGAAGAT  AGCA
                                |||||   ||||||||  ||||
                                TGCTT   TCCTTCTG  TCGT
                                   CCG_       TC
GAM1579  KIAA0876  3'  ACGAGGACAGGAATTCACAGCA 39426     AA   A   GA GT
            A                    ACGA  ACA GGAA  T  AGCAA
                                ||||  ||| ||||  |  |||||
                                TGCT  TGT CCTT  G  TCGTT
                                  CC   _   AA TG
GAM1579  KIAA0894  3'  GAAAACAGAGAATGTAA     39427       AG  AG
                                GAAAACA  GA  ATGTAG
                                |||||||  ||  ||||||
                                CTTTTGT  CT  TACATT
                                     CT  __
GAM1579  KIAA0971  3'  ACGAAAATGTGGAAGGTGTAA  39428       CAA    A
                                ACGAAAA   GGAAG TGTAG
                                |||||||   ||||| |||||
                                TGCTTTT   CCTTC ACATT
                                     ACA    C
GAM1579  KIAA1266  3'  GAAAACAGGGACAACAGTAA   39429       A   A   _
                                GAAAACA GGA GAT GTAG
                                ||||||| ||| ||| ||||
                                CTTTTGT CCT TTG CATT
                                     C   G   T
GAM1579  KIAA1514  3'  CAGGAACAAGGAAGGCGC    39430    AA        A
                                CG  AACAAGGAAG TGT
                                ||  |||||||||| |||
                                GT  TTGTTCCTTC GCG
                                 CC         C
GAM1579  KIAA1728  3'  CAAAGGCAAGGAAGAAAGT    39431     AA       T_
                                CGAA  CAAGGAAGA  GT
                                ||||  |||||||||  ||
                                GTTT  GTTCCTTCT  CA
                                  CC        TT
GAM1579  MGC10940  3'  CAGGAACAAGGAAACAGCA   39432    AA        ATG
                                CG  AACAAGGAAG   TAGCA
                                ||  ||||||||||   |||||
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                                GT  TTGTTCCTTT   GTCGT
                                 CC        ___
GAM1579  MGC11034  3'  GAAATGAAAAGATGTGGC    39433     ACAA       A
                                GAAA    GGAAGATGT GC
                                ||||    |||||||||| ||
                                CTTT    TTTTCTACA CG
                                  AC__        C
GAM1579  NKX2B     3'  GAAAGCAGGGGAAAACGCAA   39434     A  A_
                                GAAA CA  GGAAGATGTAG
                                |||| ||  ||||||||||
                                CTTT GT  CCTTTTGCGTT
                                  C  CC
GAM1579  PRO2730   3'  GAAAGCAAGGAAAAGCAG    39435     A       T
                                GAAA CAAGGAAGA GTAG
                                |||| ||||||||| ||||
                                CTTT GTTCCTTTT CGTC
                                  C       _
GAM1579  SLC16A4   5'  GAAAACAAGTGAGCATTGTAA  39436        GA  A__
                                GAAAACAAG  AG   TGTAG
                                |||||||||  ||   |||||
                                CTTTTGTTC  TC   ACATT
                                     AC  GTA
GAM1579  SSR1      3'  GAAAACATAGTTGGTGTAGCAA 39437       A  AAGA
                                GAAAACA GG    TGTAGCAA
                                |||||||  ||    ||||||||
                                CTTTTGT TC    ACATCGTT
                                    A  AACC
GAM1579  TLN2      3'  ACGGAGGCAAGAAAGCGTGCAA 39438     AAAA      A   A
                                ACG    CAAGGAAG TGT GCAA
                                |||    |||||||| ||| ||||
                                TGC    GTTCTTTC GCA CGTT
                                  CTCC       _  _
GAM1579  XYLT1     3'  GAAGACAAGGAACCTGTAG    39439     A       GA
                                GAA ACAAGGAA  TGTAG
                                ||| ||||||||  |||||
                                CTT TGTTCCTT  ACATC
                                  C       GG
GAM1579  LOC116028 3'  AAAACAGGGACGCAGCA     39440       A  AA
                                AAAACA GG  GATGTAGCA
                                ||||||  ||  |||||||||
                                TTTTGT CC  CTGCGTCGT
                                     _  __
GAM1579  LOC129880 3'  ACGAAAACCAGTCAGGTGTGGC 39441        A  GA  A   A
                                ACGAAAAC AG  AG TGT GC
                                ||||||||  ||  ||  ||| ||
                                TGCTTTTG TC  TC ACA CG
                                     G  AG  C   C
GAM1579  LOC130074 5'  CGAAACAAGGGGGGCGTGC   39442       A    AAGA   A
                                CGAAA CAAGG    TGT GC
                                |||||  |||||    |||  ||
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                                GCTTT GTTCC    GCA CG
                                   _     CCCC   _
GAM1579  LOC144266 5'  GAGAACAAGGAGATGTGGGCAA 39443     A       A     A_
                                GA AACAAGGA GATGT  GCAA
                                || |||||||| |||||  ||||
                                CT TTGTTCCT CTACA  CGTT
                                 C       _     CC
GAM1579  LOC145501 3'  GAAGGCAAGGAAGTGCAG     39444      AA       A
                                GAA  CAAGGAAG TGTAG
                                |||  |||||||| |||||
                                CTT  GTTCCTTC ACGTC
                                  CC       _
GAM1579  LOC148413 3'  GAAGACAGGGATGTGGCA     39445      A   A  AA     A
                                GAA ACA GG  GATGT GCA
                                ||| ||| ||  ||||| |||
                                CTT TGT CC  CTACA CGT
                                  C   _ __     C
GAM1579  LOC151438 5'  AAAGACAGGGGTGTAGCAA    39446      A   A  AAGA
                                GAA ACA GG    TGTAGCAA
                                ||| ||| ||    ||||||||
                                TTT TGT CC    ACATCGTT
                                  C   C  C___
GAM1579  LOC152765 3'  GAGAACAAGGAGGAGACGTAG  39447     A       __
                                GA AACAAGGA  AGATGTAG
                                || ||||||||  ||||||||
                                CT TTGTTCCT  TCTGCATC
                                 C       CC
GAM1579  LOC154214 3'  GAAAATGTGGAAAAATAGTGTA 39448       CAA      _____
              GC                  GAAAA   GGAAGA    TGTAGC
                                |||||   ||||||    ||||||
                                CTTTT   CCTTTT    ACATCG
                                   ACA      TATC
GAM1579  LOC155072 3'  GAAAACAAGTATGTGGCA     39449          GAAG    A
                                GAAAACAAG    ATGT GCA
                                |||||||||    |||| |||
                                CTTTTGTTC    TACA CGT
                                      A___    C
GAM1579  LOC157285 3'  GAAAACAGGGAGGACTTAG    39450        A   A   G
                                GAAAACA GGA GAT TAG
                                ||||||| ||| ||| |||
                                CTTTTGT CCT CTG ATC
                                    C   C   A
GAM1579  LOC158434 5'  GAAGAGGAAAATGTAA      39451      AACA
                                GAA    AGGAAGATGTAG
                                |||    ||||||||||||
                                CTT    TCCTTTTACATT
                                  C___
GAM1579  LOC159170 5'  CGGGAACAAGGAAAACGT     39452     AA
                                CG  AACAAGGAAGATGT
                                ||  ||||||||||||||
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                                GC  TTGTTCCTTTTGCA
                                 CC
GAM1579  LOC159178 5'  CGGGAACAAGGAAAACGT    39452    AA
                                CG  AACAAGGAAGATGT
                                ||  ||||||||||||||
                                GC  TTGTTCCTTTTGCA
                                 CC
GAM1579  LOC161190 5'  GAGAACTGGGAAGATGTGTGGC 39453    A   AA       A__
              A                  GA AAC  GGAAGATGT   GCA
                                || |||  |||||||||   |||
                                CT TTG  CCTTCTACA   CGT
                                 C   AC        CAC
GAM1579  LOC161489 5'  GAAGGCAAGGAAGGGCCACA   39454     AA       AT  A
                                GAA  CAAGGAAG  GT GCA
                                |||  ||||||||  || |||
                                CTT  GTTCCTTC  CG TGT
                                  CC       C_  G
GAM1579  LOC169611 3'  AAAACAAGGAAGAAAACA    39455            TGT
                                AAAACAAGGAAGA   AGCA
                                ||||||||||||   ||||
                                TTTTGTTCCTTCT   TTGT
                                        T__
GAM1579  LOC196214 5'  GAAGACGAGGATGATGCAG    39456     A  A    A
                                GAA AC AGGA GATGTAG
                                ||| || |||| |||||||
                                CTT TG TCCT CTACGTC
                                  C  C    A
GAM1579  LOC196812 3'  ACAGGAACAAGAATAGATGTAG 39457     AA       _
                                ACG  AACAAGGA AGATGTAG
                                |||  |||||||| ||||||||
                                TGT  TTGTTCTT TCTACATC
                                  CC       A
GAM1579  LOC200589 3'  AAAGACAAGGAAACTTGT    39458     A        A_
                                GAA ACAAGGAAG  TGT
                                ||| |||||||||  |||
                                TTT TGTTCCTTT  ACA
                                  C        GA
GAM1579  LOC202868 3'  GAAAACAAGTATGTGGCA    39449         GAAG    A
                                GAAAACAAG    ATGT GCA
                                |||||||||    |||| |||
                                CTTTTGTTC    TACA CGT
                                      A___    C
GAM1579  LOC255518 3'  GAAGCAACGTAATGTAGCA   39459     AA   GGAA
                                GAA  CAA    GATGTAGCA
                                |||  |||    |||||||||
                                CTT  GTT    TTACATCGT
                                  C_   GCA_
GAM1579  LOC51315  3'  GAAAATGAGGAAAAGCA     39460      CA     ATGT
                                GAAAA  AGGAAG    AGCA
                                |||||  ||||||    ||||
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                                CTTTT  TCCTTT    TCGT
                                  AC     ____
GAM1579  LOC90620  5'  AAACAAGGGACCGAGAGGTAG  39461        A____   T
                                AAACAAGG    AGA GTAG
                                ||||||||    ||| ||||
                                TTTGTTCC    TCT CATC
                                    CTGGC   C
GAM1579  LOC92080  3'  ACGAGGGAAGGAAGAAAGAGGG 39462     AAAC      TGTA__
           CA                     ACGA   AAGGAAGA     GCA
                                ||||   ||||||||     |||
                                TGCT   TTCCTTCT     CGT
                                  CCC_      TTCTCC
GAM1580  ATP1A2   3'  AAGAGGCTGGGAAAGAACTTGT 39465     TGA      CT  CC
                                AAGA   CTGGGAAG  AT  GT
                                ||||   ||||||||  ||  ||
                                TTCT   GACCCTTT  TG  CA
                                  CC_      CT  AA
GAM1580  CELSR2   3'  AGAGGCTGGGAAGCATCC    39466    TGA      T
                                AGA   CTGGGAAGC ATCC
                                |||   |||||||||| ||||
                                TCT   GACCCTTCG TAGG
                                  CC_       _
GAM1580  DLEC1    3'  GATGACTGAGATGAGCTTCTGT 39467          __    A  C
                                GATGACTGGGA  AGCT TC GT
                                ||||||||||  |||| || ||
                                CTACTGACTCT  TCGA AG CA
                                      AC    _  A
GAM1580  DLEC1    3'  GATGACTGAGATGAGCTTCTGT 39467          __    A  C
                                GATGACTGGGA  AGCT TC GT
                                ||||||||||  |||| || ||
                                CTACTGACTCT  TCGA AG CA
                                      AC    _  A
GAM1580  SURF4    3'  AGGTAACTGGGTTGAGTCCGT  39468    A       AAGCTA
                                AG TGACTGGG     TCCGT
                                || ||||||||     |||||
                                TC ATTGACCC     AGGCA
                                 C       AACTC_
GAM1580  C7orf10  3'  AAGATGGTAGGGAACAAAACGT 39469       ACT     G TATC
                                AAGATG   GGGAA C    CGT
                                ||||||   ||||| |    |||
                                TTCTAC   CCCTT G    GCA
                                   CAT    _ TTTT
GAM1580  CRF      3'  TGCTGGGAAGCTATCCA     39470    A
                                TG CTGGGAAGCTATCCG
                                || ||||||||||||||
                                AC GACCCTTCGATAGGT
                                 _
GAM1580  FEM-2    3'  GACTGGCTGGGCATATCTGTA  39471       GAA_  _    C
                                GACTGG    GC TATC GTA
                                ||||||    || |||| |||
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                                CTGACC   CG ATAG CAT
                                   GACC  T   A
GAM1580  MGC20255  3'  AAGATGACCTGATCCTGTCTGT 39472        GG  AG  A  C
                                AAGATGACT  GA  CT TC GT
                                |||||||||  ||  || || ||
                                TTCTACTGG  CT  GA AG CA
                                     A_  AG  C  A
GAM1580  LOC145989 3'  GAGACTGGGAAGTCCATA    39473    T       CTA
                                GA GACTGGGAAG   TCCGTA
                                || ||||||||||   ||||||
                                CT CTGACCCTTC   AGGTAT
                                 _       ____
GAM1581  MADH7    3'  CATGTCCCTCCCAGGGAC    39476        _   AA
                                CGTGTCCC CCTA  GAC
                                |||||||| ||||  |||
                                GTACAGGG GGGT  CTG
                                     A   CC
GAM1581  BM045    3'  CGGTCCCCTATCCAAGGAC   39477    T    ___   A
                                CG GTCCCC   CTAA GAC
                                || ||||||   |||| |||
                                GC CAGGGG   GGTT CTG
                                 _     ATA   C
GAM1581  BM045    3'  CGGTCCCCTATCCAAGGAC   39477    T    ___   A
                                CG GTCCCC   CTAA GAC
                                || ||||||   |||| |||
                                GC CAGGGG   GGTT CTG
                                 _     ATA   C
GAM1581  KIAA1493  3'  CGTATCCCCCACACCTTAAAGA 39478        ______
                                CGTGTCCCCC     TAAAGA
                                ||||||||||     ||||||
                                GCATAGGGGG     ATTTCT
                                      TGTGGA
GAM1581  RNPC1    3'  CATGTCCCCTCCTCCAGAC   39479        _ AA_
                                CGTGTCCCC CT   AGAC
                                ||||||||| ||   ||||
                                GTACAGGGG GG   TCTG
                                     A  AGG
GAM1581  LOC157695 3'  CATGTCCCCCTTTCAAGAC   39480         A__
                                CGTGTCCCCCT   AAGAC
                                ||||||||||   |||||
                                GTACAGGGGGA   TTCTG
                                      AAG
GAM1581  LOC221718 3'  CGTGTCCCTTTAGAAAAC    39481        CC  _
                                CGTGTCCC  TA AAGAC
                                ||||||||  || |||||
                                GCACAGGG  AT TTTTG
                                     AA  C
GAM1582  NDUFA10   3'  TAAAGCTATATGGCGTC     39484         AATC
                                TAAAGCTATAT    CGTT
                                ||||||||||    ||||
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                                ATTTCGATATA    GCAG
                                      CC__
GAM1582  TRAP240   3'  CTGAAGCCATATGTTGAAATTC 39485    A       AATCC_
             AT                   CT AAGCTATAT     GTTCAT
                                  || |||||||||     ||||||
                                  GA TTCGGTATA     TAAGTA
                                   C        CAACTT
GAM1582  C20orf177 3'  TAGAGCTACATAATCTTGTC   39486    A         CGT
                                  TA AGCTATATAATC   TC
                                  || ||||||||||||   ||
                                  AT TCGATGTATTAG   AG
                                   C          AAC
GAM1582  FLJ10839  3'  TAAAACTATAACAAAGTTCATC 39487          TAATCC
                                  TAAAGCTATA     GTTCATC
                                  ||||||||||     |||||||
                                  ATTTTGATAT     CAAGTAG
                                        TGTTT_
GAM1582  KIAA0820  3'  CTGAAGTATATAATCCGTT    39488    A   C
                                  CT AAG TATATAATCCGTT
                                  || ||| ||||||||||||||
                                  GA TTC ATATATTAGGCAA
                                   C   _
GAM1582  LOC134266 3'  CTAAACCTATATAATCTAGACA 39489       G         CGTT
             TC                   CTAAA CTATATAATC    CATC
                                  ||||| ||||||||||    ||||
                                  GATTT GATATATTAG    GTAG
                                     G         ATCT
GAM1582  LOC144512 5'  AAACTATATTTATTGTTCAT   39490         AATCC
                                  AAGCTATAT    GTTCAT
                                  |||||||||    ||||||
                                  TTTGATATA    CAAGTA
                                        AATAA
GAM1582  LOC201931 3'  TAAAAGCTATATGGTCCAT    39491    T        AA
                                  C AAAGCTATAT  TCCGT
                                  | ||||||||||  |||||
                                  A TTTCGATATA  AGGTA
                                   T         CC
GAM1582  LOC221718 3'  TAAAGCTAAATCATGTTCAT   39492         TAT    C_
                                  TAAAGCTA   AATC  GTTCAT
                                  ||||||||   ||||  ||||||
                                  ATTTCGAT   TTAG  CAAGTA
                                        ___    TA
GAM1582  LOC222159 5'  TAAGGCTATATAAGTCAGCCAG 39493    A       T____  __
             GTTCAT                    AA GCTATATAA    CC  GTTCAT
                                  || |||||||||    ||  ||||||
                                  TT CGATATATT    GG  CAAGTA
                                   C        CAGTC  TC
GAM1582  LOC254143 5'  AAACTATATTTATTGTTCAT   39490         AATCC
                                  AAGCTATAT    GTTCAT
                                  |||||||||    ||||||
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                                TTTGATATA    CAAGTA
                                     AATAA
GAM1582  LOC254827 5'  CTAAAGCTATATCAAGTGCAT  39494          AATCC  T
                                CTAAAGCTATAT    GT CAT
                                ||||||||||||    || |||
                                GATTTCGATATA    CA GTA
                                       GTT__  C
GAM1583  B3GALT5  5'  GAGGTGGGAGAGGAGACCCG  39497    A   C      G
                                GAG TGGG GAGGAGAT CTG
                                ||| |||| |||||||| |||
                                CTC ACCC CTCCTCTG GGC
                                  C   T      _
GAM1583  CADPS    5'  CGAGGTGGGCAAGGGG     39498     A       AGATGCT
                                CGAG TGGGCGAGG      GG
                                |||| |||||||||      ||
                                GCTC ACCCGTTCC      CC
                                  C       ________
GAM1583  CHRNE    3'  GATGGGCAGTGCTGG      39499       GAGG  A
                                GATGGGC    AG TGCTGG
                                |||||||    || ||||||
                                CTACCCG    TC ACGACC
                                     ____  _
GAM1583  CHST1    3'  GAGGTGGGAGAGGGAGG    39500    A   C   A  TGCT
                                GAG TGGG GAGG GA    GG
                                ||| |||| |||| ||    ||
                                CTC ACCC CTCC CT    CC
                                  C   T   _ _____
GAM1583  DNMT3L   5'  GAGGGGCGAGGAGCTGCGGG  39501    AT       A   T
                                GAG  GGGCGAGGAG TGC GGG
                                |||  |||||||||| ||| |||
                                CTC  CCCGCTCCTC ACG CCC
                                  __        G   _
GAM1583  DXF68S1E  5'  GAGGTGGGTGACGGGCTGCGGG 39502    A   C  _  AGA   T
                                GAG TGGG GA GG   TGC GGG
                                ||| |||| || ||   ||| |||
                                CTC ACCC CT CC   ACG CCC
                                  C   A  G  CG_  _
GAM1583  EFNA1    3'  GAGGTCTTGCTGGGAGATGCTG 39503    ATGG_  GA
            GG                    GAG    GC  GGAGATGCTGGG
                                |||    ||  ||||||||||||
                                CTC    CG  CCTCTACGACCC
                                  CAGAA  AC
GAM1583  ENG      5'  TGGGCGGGGAGGGGGTGCTGGG 39504       A   A___
                                TGGGCG GGAG    TGCTGGG
                                ||||||| ||||    |||||||
                                ACCCGC CCTC    ACGACCC
                                   C    CCCC
GAM1583  EPS8     5'  CGAGGTGGGAGGGGACCGG   39505     A   CG   A AT
                                CGAG TGGG  AGG G  GCTGG
                                |||| ||||  ||| |  |||||
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                                GCTC ACCC  TCC C  TGGCC
                                  C   __  C __
GAM1583  FOXI1   3'  AGATGGGCAGTGCTG      39506       GAGG  A
                                AGATGGGC   AG TGCTG
                                ||||||||   || |||||
                                TCTACCCG   TC ACGAC
                                     ____ _
GAM1583  FSTL1   3'  GAAGTGGAGAAGATGCTGGG  39507    A  GCG
                                GAG TGG  AGGAGATGCTGGG
                                ||| |||  ||||||||||||
                                CTT ACC  TCTTCTACGACCC
                                 C  ___
GAM1583  GSTM1   3'  CGAGGAGGCAGGTGCTGG   39508    AT  G  AGA
                                CGAG  GGGC AGG  TGCTGG
                                ||||  |||| |||  ||||||
                                GCTC  TCCG TCC  ACGACC
                                  C_  _  ___
GAM1583  GSTM2   3'  CGAGGAGGCAGGTGCTGG   39508    AT  G  AGA
                                CGAG  GGGC AGG  TGCTGG
                                ||||  |||| |||  ||||||
                                GCTC  TCCG TCC  ACGACC
                                  C_  _  ___
GAM1583  GSTM4   3'  CGAGGAGGCAGGTGCTGG   39508    AT  G  AGA
                                CGAG  GGGC AGG  TGCTGG
                                ||||  |||| |||  ||||||
                                GCTC  TCCG TCC  ACGACC
                                  C_  _  ___
GAM1583  HD      3'  GGGCAGAAGGGATGCTGGG   39509    _  A
                                GGGC GAGG GATGCTGGG
                                |||| |||| |||||||||
                                CCCG CTTC CTACGACCC
                                  T  C
GAM1583  KCNK3   3'  GAGATGGGGGTGCTG      39510       CGA  AGA
                                GAGATGGG  GG  TGCTG
                                ||||||||  ||  |||||
                                CTCTACCC  CC  ACGAC
                                     ___ ___
GAM1583  MEN1    3'  CGAGATGGGCTGGACCTCTGGG 39511        GA  GATG
                                CGAGATGGGC  GGA  CTGGG
                                ||||||||||  |||  |||||
                                GCTCTACCCG  CCT  GACCC
                                     A_  GGA_
GAM1583  MEN1    3'  CGAGATGGGCTGGACCTCTGGG 39511        GA  GATG
                                CGAGATGGGC  GGA  CTGGG
                                ||||||||||  |||  |||||
                                GCTCTACCCG  CCT  GACCC
                                     A_  GGA_
GAM1583  MEN1    3'  CGAGATGGGCTGGACCTCTGGG 39511        GA  GATG
                                CGAGATGGGC  GGA  CTGGG
                                ||||||||||  |||  |||||
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                                GCTCTACCCG  CCT   GACCC
                                     A_  GGA_
GAM1583  MEN1    3'  CGAGATGGGCTGGACCTCTGGG 39511        GA  GATG
                                CGAGATGGGC  GGA   CTGGG
                                ||||||||||  |||   |||||
                                GCTCTACCCG  CCT   GACCC
                                     A_  GGA_
GAM1583  MEN1    3'  CGAGATGGGCTGGACCTCTGGG 39511        GA  GATG
                                CGAGATGGGC  GGA   CTGGG
                                ||||||||||  |||   |||||
                                GCTCTACCCG  CCT   GACCC
                                     A_  GGA_
GAM1583  MEN1    3'  CGAGATGGGCTGGACCTCTGGG 39511        GA  GATG
                                CGAGATGGGC  GGA   CTGGG
                                ||||||||||  |||   |||||
                                GCTCTACCCG  CCT   GACCC
                                     A_  GGA_
GAM1583  MEN1    3'  CGAGATGGGCTGGACCTCTGGG 39511        GA  GATG
                                CGAGATGGGC  GGA   CTGGG
                                ||||||||||  |||   |||||
                                GCTCTACCCG  CCT   GACCC
                                     A_  GGA_
GAM1583  MIA     5'  TGAGCAAGGGGGTGCTGG    39512        AGA
                                TGGGCGAGG   TGCTGG
                                |||||||||   ||||||
                                ACTCGTTCC   ACGACC
                                     CCC
GAM1583  PAX5    3'  AGGCAAGTGGGGGATGCTGGG  39513       GA___
                                GGGCGAG    GATGCTGGG
                                |||||||    |||||||||
                                TCCGTTC    CTACGACCC
                                   ACCCC
GAM1583  PTGIR   3'  GAGATGGATGGGGAATCCAGG  39514        CGA  AG  G TG
                                GAGATGGG   GG  AT C  GG
                                ||||||||   ||  || |  ||
                                CTCTACCT   CC  TA G  CC
                                     AC_  CT  _ GT
GAM1583  SOX10   3'  GAGGTGGGCAAGGAACAGGG   39515    A        ATGCT
                                GAG TGGGCGAGGAG    GGG
                                ||| ||||||||||    |||
                                CTC ACCCGTTCCTT    CCC
                                  C         GT___
GAM1583  AMOTL1  3'  TGGGTGAGGAGACAGG      39516     C       GCT
                                TGGG GAGGAGAT   GGG
                                |||| ||||||||   |||
                                ACCC CTCCTCTG   TCC
                                  A       ____
GAM1583  ARP5    5'  GAGTGGAGCTGGGATGCTGGG  39517    A  _  GA  A
                                GAG TGG GC  GG GATGCTGGG
                                ||| ||| ||  || |||||||||
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                                CTC ACC CG  CC CTACGACCC
                                  _  T A_ _
GAM1583 ARTN     5' GAGGGGGGTAGATGCTGGG   39518    AT  CGA _
                                GAG  GGG  GG AGATGCTGGG
                                |||  |||  || ||||||||||
                                CTC  CCC  CC TCTACGACCC
                                 __  ____ A
GAM1583 C11orf11 3' CGAGGTGGGTAGGAGCCG   39519    A   CG   GAT  TG
                                CGAG TGGG  AGGA  GC  G
                                |||| ||||  ||||  ||  |
                                GCTC ACCC  TCCT  CG  C
                                  C   A_   ___ GT
GAM1583 C20orf102 3' CGGATGGGCGGGGGCAGG   39520    A      A  AGAT  T
                                CG GATGGGCG GG   GC GG
                                || |||||||| ||   || ||
                                GC CTACCCGC CC   CG CC
                                 _      _ C___  T
GAM1583 DKFZP564D0478 3' GAGATGGGTCCAATGCTGGG  39521        CGAGGA
                                GAGATGGG     GATGCTGGG
                                ||||||||     |||||||||
                                CTCTACCC     TTACGACCC
                                     AGG___
GAM1583 DKFZP586N0721 5' CGAGGTGGGGAGGGGAGAGAGG 39522     A   C   A  TGCT
                                CGAG TGGG GAGG GA   GG
                                |||| |||| |||| ||   ||
                                GCTC ACCC CTCC CT   CC
                                  C   _   C  CTCT
GAM1583 FADS2    3' CGAGATGGGGAGGGCTGG   39523        C   AGAT
                                CGAGATGGG GAGG   GCTGG
                                ||||||||| ||||   |||||
                                GCTCTACCC CTCC   CGACC
                                     _   _____
GAM1583 FLJ10052 3' GAGGTGGCTGAGCTATCTGGG 39524    ATG  GA  AG  G
                                GAG  GGC  GG  AT CTGGG
                                |||  |||  ||  || |||||
                                CTC  CCG  TC  TA GACCC
                                  CA_  AC  GA  _
GAM1583 FLJ14346 3' GAGGTGGGCAAGGGGGCTG   39525    A      AGAT
                                GAG TGGGCGAGG   GCTG
                                ||| |||||||||   ||||
                                CTC ACCCGTTCC   CGAC
                                  C       CC__
GAM1583 FLJ20489 3' GAGATGGGTGGGGGGCCACGG 39526       CGA  AGA  T
                                GAGATGGG  GG  TGC GG
                                ||||||||  ||  ||| ||
                                CTCTACCC  CC  GTG CC
                                     ACC  CCG  _
GAM1583 FLJ20542 3' CGAGATGCCTACGGGGATGCTG 39527      G__  A  A
           GG                   CGAGATG  GCG GG GATGCTGGG
                                |||||||  ||| || |||||||||
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                                GCTCTAC   TGC CC CTACGACCC
                                    GGA   _ _
GAM1583  FLJ20546  3'  AGGTGGGCGAGAGTTTGG    39528    A      G  ATGC
                                AG TGGGCGAG AG    TGG
                                || |||||||| ||    |||
                                TC ACCCGCTC TC    ACC
                                 C       _  AA__
GAM1583  KIAA0469  5'  CGGGATGGGCGGGGAGACG   39529    A      A
                                CG GATGGGCG GGAGATG
                                || |||||||| |||||||
                                GC CTACCCGC CCTCTGC
                                 C       C
GAM1583  KIAA0930  3'  GAGATGGGTGGGGGGCGATGGG 39530        CGA__  A   CT
                                GAGATGGG    GG GATG  GG
                                ||||||||    || ||||  ||
                                CTCTACCC    CC CTAC  CC
                                     ACCCC  G   __
GAM1583  KIAA1026  3'  GAAATGAGGAGGTGCTGG    39531        C   AGA
                                GAGATGGG GAGG   TGCTGG
                                |||||||| ||||   ||||||
                                CTTTACTC CTCC   ACGACC
                                     _   ____
GAM1583  MICAL    5'  CGAGATCGGGCGGGGATGCTGG 39532       _    A  A
              G                  CGAGAT GGGCG GG GATGCTGGG
                                |||||| ||||| || |||||||||
                                GCTCTA CCCGC CC CTACGACCC
                                   G    _ _
GAM1583  MSTP032   3'  GATGTGTAAGTGATGCTGGG   39533     GGCG   A
                                GATG    AGG GATGCTGGG
                                ||||    ||| |||||||||
                                CTAC    TTC CTACGACCC
                                  ACA_   A
GAM1583  NDRG4    3'  GAGATGGGATGAGGAGGACTG  39534        C_     AT
                                GAGATGGG  GAGGAG  GCTG
                                ||||||||  ||||||  ||||
                                CTCTACCC  CTCCTC  TGAC
                                     TA     C_
GAM1583  NDRG4    3'  GAGATGGGATGAGGAGGACTG  39534        C_     AT
                                GAGATGGG  GAGGAG  GCTG
                                ||||||||  ||||||  ||||
                                CTCTACCC  CTCCTC  TGAC
                                     TA     C_
GAM1583  PDGFC    5'  GAGGGGGTGGGGACGCGG    39535     AT   CGA  A    T
                                GAG  GGG   GG GATGC GG
                                |||  |||   || ||||| ||
                                CTC  CCC   CC CTGCG CC
                                  C_   AC_ _    _
GAM1583  PIP5K1C   3'  AGGTGGGCGAGGAACCTGGG   39536    A         ATG
                                AG TGGGCGAGGAG   CTGGG
                                || ||||||||||   |||||
```

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                                TC ACCCGCTCCTT   GACCC
                                 C         G__
GAM1583  PP3501   3'  GAGTGGGTGAGGAGTGAGG   39537     A   C     A  CT
                                GAG TGGG GAGGAG TG  GG
                                ||| |||| |||||| ||  ||
                                CTC ACCC CTCCTC AC  CC
                                  _   A     _ T_
GAM1583  RIN3     3'  GAGGTGCTCCTGAGATGCTGGG 39538    T  _  GAG_
                                GA GG GC    GAGATGCTGGG
                                || || ||    ||||||||||
                                CT CC CG    CTCTACGACCC
                                 _ A  AGGA
GAM1583  RNF40    3'  TGGGGAGGAGATGGGG      39539      C        CT
                                TGGG GAGGAGATG  GGG
                                |||| |||||||||  |||
                                ACCC CTCCTCTAC  CCC
                                  _       __
GAM1583  SCGF     3'  GATGGGCAAGGAGGCGGG    39540           AT  T
                                GATGGGCGAGGAG  GC GGG
                                ||||||||||||  || |||
                                CTACCCGTTCCTC  CG CCC
                                      __ _
GAM1583  SDC3     3'  AGGCACCTGGGGGATGCTGGG  39541       A___  A
                                GGGCG    GG GATGCTGGG
                                |||||    || |||||||||
                                TCCGT    CC CTACGACCC
                                   GGAC  C
GAM1583  STRAIT11499 3'  GAGATGGGTCGAAGAAGGTGCT 39542         _      A_
            GGG                    GAGATGGG CGAGGAG  TGCTGGG
                                |||||||| |||||||  |||||||
                                CTCTACCC GCTTCTT  ACGACCC
                                     A      CC
GAM1583  TBX21    5'  GATGGGCAGGGAGCAGGG    39543        G   A  T  T
                                GATGGGC AGG GA GC GGG
                                ||||||| ||| || || |||
                                CTACCCG TCC CT CG CCC
                                   _  _ _ T
GAM1583  TRAP95   3'  CGAGATGGGCAGCTG       39544          AGGAGAT  _
                                CGAGATGGGCG      GCT G
                                ||||||||||       ||| |
                                GCTCTACCCGT      CGA C
                                      _______  A
GAM1583  ZFP91    3'  GAGGGGGACTGAGATGCTGGG  39545     AT   C  G_
                                GAG  GGG GA  GAGATGCTGGG
                                |||  ||| ||  ||||||||||
                                CTC  CCC CT  CTCTACGACCC
                                  __  _ GA
GAM1583  LOC136345 3'  TGGGGGAGGTGGAGATGCTGGG 39546      C  ___
                                TGGG GA   GGAGATGCTGGG
                                |||| ||   ||||||||||||
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                                ACCC CT   CCTCTACGACCC
                                  C  CCA
GAM1583  LOC144231 5'  GAGATGGGTGATGGATGG    39547        C  _   GATGC
                                GAGATGGG GA GGA     TGG
                                |||||||| || |||     |||
                                CTCTACCC CT CCT     ACC
                                    A  A  ______
GAM1583  LOC144600 5'  GAGATGGGTGGGGGGCGATGGG 39530         CGA__  A    CT
                                GAGATGGG     GG GATG  GG
                                ||||||||     || ||||  ||
                                CTCTACCC     CC CTAC  CC
                                    ACCCC  G   __
GAM1583  LOC147057 3'  TGGGCCCTCGGGGGATGCTGGG 39548       GA__  A_
                                TGGGC    GG  GATGCTGGG
                                |||||    ||  |||||||||
                                ACCCG    CC  CTACGACCC
                                   GGAG  CC
GAM1583  LOC149461 3'  CGAGGCTGGCTGGATGCTGGG  39549      ATG   GA   GA
                                CGAG   GGC  GGA  TGCTGGG
                                ||||   |||  |||  |||||||
                                GCTC   CCG  CCT  ACGACCC
                                  CGA   A_   __
GAM1583  LOC152485 3'  TGGGTGAGGGGATGCTGGG    39550      C    A
                                TGGG GAGG GATGCTGGG
                                |||| |||| |||||||||
                                ACCC CTCC CTACGACCC
                                  A    C
GAM1583  LOC155032 5'  TGGGGGAGGTGGAGATGCTGGG 39546      C  ___
                                TGGG GA   GGAGATGCTGGG
                                |||| ||   ||||||||||||
                                ACCC CT   CCTCTACGACCC
                                  C  CCA
GAM1583  LOC163682 5'  CCAGGTGTGGGGGATGCTGGG  39551    G  A  _  CGA  A
                                C AG TG GG   GG GATGCTGGG
                                | || || ||   || |||||||||
                                G TC AC CC   CC CTACGACCC
                                 G  C  A  ___  _
GAM1583  LOC163882 3'  GAAGGTCCCCAGGAGATGTTGG 39552     T  GCG__       C
            G                    GA GG     AGGAGATG TGGG
                                || ||     |||||||| ||||
                                CT CC     TCCTCTAC ACCC
                                 T  AGGGG       A
GAM1583  LOC256221 5'  GAGATGGGCCAGGGACATGGG  39553         G   A   C
                                GAGATGGGC AGG GATG TGGG
                                ||||||||| ||| |||| ||||
                                CTCTACCCG TCC CTGT ACCC
                                     G   _   _
GAM1583  LOC56920  3'  TGGGTGGGAGATGCTGGG    39554      CGA
                                TGGG   GGAGATGCTGGG
                                ||||   ||||||||||||
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                                ACCC   CCTCTACGACCC
                                  AC_
GAM1584  PODXL     3'  TTGATGATAAACTGTCTTTGCT 39557          T         A
              A                   TTGATGATA AATTGTTTTT CTA
                                  ||||||||| |||||||||| |||
                                  AACTACTAT TTGACAGAAA GAT
                                        _         C
GAM1584  FKSG14    3'  TTGAATGATAAGAATTTTTACT 39558      _    TAATT
                                  TTGA TGATA     GTTTTTACT
                                  |||| |||||     |||||||||
                                  AACT ACTAT     TAAAAATGA
                                    T     TCT__
GAM1584  KIAA0557  3'  TTGATGATATAATTAGTT     39559             _
                                  TTGATGATATAATT GTT
                                  |||||||||||||| |||
                                  AACTACTATATTAA CAA
                                           T
GAM1584  PLCL1     3'  TGATGATATGATATTGTT     39560          A__
                                  TGATGATAT   ATTGTT
                                  |||||||||   ||||||
                                  ACTACTATA   TAACAA
                                        CTA
GAM1584  LOC133957 3'  TTGATAATATAATATTACT    39561             TGTTT
                                  TTGATGATATAAT     TTACT
                                  ||||||||||||     |||||
                                  AACTATTATATTA     AATGA
                                           T_____
GAM1584  LOC152851 3'  TTGATGACATGATTGTAAACC  39562           A     TTTT
                                  TTGATGATAT ATTGT    ACT
                                  |||||||||| |||||    |||
                                  AACTACTGTA TAACA    TGG
                                        C     TT__
GAM1585  RUNX1     5'  CAGCGCCGCCTTGGCTGTGGGT 39565       G       AACCGCA
                                  CAGCG TCGTTTT       GGT
                                  ||||| |||||||       |||
                                  GTCGC GGCGGAA       CCA
                                     _       CCGACAC
GAM1585  SLC2A8    3'  GGAGGGCTGACCGCAGGTC    39566    TC_   TTA
                                  GG   GTT   ACCGCAGGTC
                                  ||   |||   ||||||||||
                                  CC   CGA   TGGCGTCCAG
                                    TCC   C__
GAM1585  C11orf11  5'  AGCGGTGCCGCAGGT       39567       C TTTTAA
                                  AGCGGT G     CCGCAGGT
                                  |||||| |     ||||||||
                                  TCGCCA C     GGCGTCCA
                                     _ _______
GAM1585  LOC132880 5'  GGTGTTCCAACACGCTGCAGGT 39568     C       _ ____
              C                    GGT GTTTTAAC C   GCAGGTC
                                  ||| |||||||| |   |||||||
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                                CCA CAAGGTTG G   CGTCCAG
                                  _      T CGA
GAM1585 LOC152627 5' GGTTGTTTTAACCACAAGGT  39569    C        _
                                GGT GTTTTAACCGCA GGT
                                ||| |||||||||||| |||
                                CCA CAAAATTGGTGT CCA
                                  A         T
GAM1586 FLJ11800 3' TCTAGTTCTGCTGTTGCAA   39572     CGCC
                                TCTAG   GCTGTTGCAG
                                |||||   ||||||||||
                                AGATC   CGACAACGTT
                                   AAGA
GAM1586 VIT1    5' TCTAGTGTTGCAGTTG     39573     CGCCGC     AG
                                TCTAG    TGTTGCAG  TG
                                |||||    ||||||||  ||
                                AGATC    ACAACGTC  AC
                                  _______     A_
GAM1586 ZMPSTE24 5' TCTGCGCGCTGCTGGCAGTGT 39574    A   C    _  A
                                TCT GCGC GCTGTTG CAG GT
                                ||| |||| ||||||| ||| ||
                                AGA CGCG CGACGAC GTC CA
                                  _  _     C  A
GAM1586 LOC220575 3' TCTAGTTCTGCTGTTGCAA   39572     CGCC
                                TCTAG   GCTGTTGCAG
                                |||||   ||||||||||
                                AGATC   CGACAACGTT
                                   AAGA
GAM1586 LOC57099 5' CTGGCGCCGCTGGTGGTG   39575   A      T  CAGA
                                CT GCGCCGCTG TG   GTG
                                || |||||||| ||   |||
                                GA CGCGGCGAC AC   CAC
                                 C       C ____
GAM1586 LOC90591 3' TCTGTCGCCGCTGGAGTG   39576    AG      TTGCA
                                TCT  CGCCGCTG    GAGTG
                                |||  ||||||||    |||||
                                AGA  GCGGCGAC    CTCAC
                                  CA      _____
GAM1587 HEBP1   3' TGGCAGTAACTGACTTTGAAG 39579       C  A  GCATAC
                                TGGCAGTA CT AT    GAAG
                                |||||||| || ||    ||||
                                ACCGTCAT GA TG    CTTC
                                    T  C  AAA___
GAM1587 IL4R    3' TGGGGGTTCCATGCATACGA  39580    CA  A  TA
                                TGG  GT CC  ATGCATACGA
                                |||  || ||  ||||||||||
                                ACC  CA GG  TACGTATGCT
                                  CC  A __
GAM1587 RBM6    5' TAGCAGTACCTAGGCGGCGAAG 39581          AT  ATA
                                TGGCAGTACCTA  GC   CGAAG
                                ||||||||||||  ||   |||||
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                                ATCGTCATGGAT  CG   GCTTC
                                      C_  CC_
GAM1587  CYYR1    3'  TGGCAGTAGCTGGCATTGAAG  39582        C  AAT    AC
                                TGGCAGTA CT   GCAT  GAAG
                                |||||||| ||   ||||  ||||
                                ACCGTCAT GA   CGTA  CTTC
                                     C  C__    A_
GAM1587  EPN3     3'  TGGCAGCATCTGGAAGCGAAG  39583        C  AATGCATA
                                TGGCAGTA CT       CGAAG
                                |||||||| ||       |||||
                                ACCGTCGT GA       GCTTC
                                     A  CCTTC___
GAM1587  MGC20255 3'  TGGTAGTACCTAGGGCATA   39584     C       AT
                                TGG AGTACCTA  GCATA
                                ||| ||||||||  |||||
                                ACC TCATGGAT  CGTAT
                                  A       CC
GAM1587  PRO1635  3'  TGGCAATATGATTACATACGAA 39585        CCTAA
              G                  TGGCAGTA    TGCATACGAAG
                                |||||||||    ||||||||||
                                ACCGTTAT    ATGTATGCTTC
                                     ACTA_
GAM1588  C20orf1  3'  CAGTTGGTGAGGTTTTCT    39588    T         G
                                CA GTTGGTGAGGTT TCT
                                || ||||||||||| |||
                                GT CAACCACTCCAA AGA
                                 _          A
GAM1588  DYRK1A   3'  TACATGAAAGGTTGTTTC    39589       TTGGT       C
                                TACATG    GAGGTTGT TC
                                ||||||    |||||||| ||
                                ATGTAC    TTCCAACA AG
                                   T_____       A
GAM1588  CGRP-RCP 3'  CATGTTGGTGAGGCTGGTCT   39590              _
                                CATGTTGGTGAGGTTG TCT
                                |||||||||||||| |||
                                GTACAACCACTCCGAC AGA
                                          C
GAM1588  KIAA1244 3'  ATGTATTTATAGTTGTCTTCT  39591      TGG  A       C
                                ATGT   TG GGTTGTCT CT
                                ||||   || |||||||| ||
                                TACA   AT TCAACAGA GA
                                  TAA  A       A
GAM1588  KIAA1948 3'  ATGTTGGTGGAAGGCATTTCT  39592         __    TG_
                                ATGTTGGTG  AGGT   TCT
                                |||||||||  ||||   |||
                                TACAACCAC  TCCG   AGA
                                     CT    TAA
GAM1588  NR0B1    3'  TACCTGTTGGCAAATGTCTTCT 39593     A     TG  GT    C
                                TAC TGTTGG  AG  TGTCT CT
                                ||| ||||||  ||  ||||| ||
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                                ATG ACAACC  TT  ACAGA GA
                                  G     GT __    A
GAM1588  SGP28    3'  CATTTGGCTCACATGTCTCCT  39594     G    GAGGT
                                CAT TTGGT    TGTCTCCT
                                ||| |||||    ||||||||
                                GTA AACCG    ACAGAGGA
                                  _    AGTGT
GAM1588  SSH1     3'  CATGTTGGTTAGTTTCT     39595         GA   G
                                CATGTTGGT  GGTT TCT
                                |||||||||  |||| |||
                                GTACAACCA  TCAA AGA
                                     A_   _
GAM1588  LOC133308 3'  TACATCGTCTCCCTGAGGTTGT 39596      _  GG__         C
             CTTCT                  TACAT GTT    TGAGGTTGTCT CT
                                ||||| |||    |||||||||| ||
                                ATGTA CAG    ACTCCAACAGA GA
                                   G   AGGG         A
GAM1588  LOC145314 3'  TAATGTTGGTGTGGTTTTCT   39597   C       A   G
                                A ATGTTGGTG GGTT TCT
                                | |||||||| |||| |||
                                A TACAACCAC CCAA AGA
                                 T       A   A
GAM1588  LOC148764 3'  TGTTGATGATAGAATTCTC    39598         _ TTG
                                TGTTGGTGA GG   TCTC
                                |||||||| ||   ||||
                                ACAACTACT TC   AGAG
                                     A  TTA
GAM1588  LOC157503 5'  TACATGTTGTCTCTACTTGTCT 39599         GTGAGG_
                                TACATGTTG      TTGTCT
                                |||||||||      ||||||
                                ATGTACAAC      AACAGA
                                     AGAGATG
GAM1588  LOC91650  3'  ATGTTTTGATAAGGTTGT    39600      __
                                ATGT  TGGTGAGGTTGT
                                ||||  ||||||||||||
                                TACA  ACTATTCCAACA
                                  AA
GAM1588  LOC92578  5'  CGACTGGGGTTGTCTC      39601    _   TGA       C
                                TG TTGG   GGTTGTCT C
                                || ||||   |||||||| |
                                GC GACC   CCAACAGA G
                                 T    ___       A
GAM1589  ABLIM    3'  GTTGGGTAGTTCCCTTAA    39604          C
                                GTTGGGTAG TCCCTTAA
                                |||||||||  ||||||||
                                CAACCCATC AGGGAATT
                                     A
GAM1589  ABLIM    3'  GTTGGGTAGTTCCCTTAA    39604          C
                                GTTGGGTAG TCCCTTAA
                                |||||||||  ||||||||
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                                CAACCCATC AGGGAATT
                                     A
GAM1589  FLJ20374  3'  TGCTGGGTGGCTTTAACCCTT  39605        A  ____
                                TGTTGGGT GCT    CCCTT
                                |||||||| |||    |||||
                                ACGACCCA CGA    GGGAA
                                     C   AATT
GAM1589  LOC256781 5'  CTGAGGCTCCCTTGGGTTA   39606      TA      AA
                                TTGGG  GCTCCCTT  GTTA
                                |||||  ||||||||  ||||
                                GACTC  CGAGGGAA  CAAT
                                   __       CC
GAM1590  ITGAV     3'  TAAGGTCCAAATTTGGACTGCT 39609     A  GAT   GA
              T                  TAAG TC   GGT  GGACTGCTT
                                |||| ||   |||  |||||||||
                                ATTC AG   TTA  CCTGACGAA
                                   C  GT_   AA
GAM1590  LOC144144 5'  TAAGAACCCAATTGTGGGGGCT 39610      __    G   A  A
              GCTT                  TAAGA  TCGAT GTG GG CTGCTT
                                |||||  ||||| ||| || ||||||
                                ATTCT  GGTTA CAC CC GACGAA
                                   TG    A   C  C
GAM1590  LOC163081 3'  GATGTACAGTGAGGGTTGCTT  39611     CG       AC
                                GAT  ATGGTGAGG  TGCTT
                                |||  |||||||||  |||||
                                CTA  TGTCACTCC  ACGAA
                                  CA        CA
GAM1590  LOC220486 5'  TAAGAACCCAATTGTGGGGGCT 39610      __    G   A  A
              GCTT                  TAAGA  TCGAT GTG GG CTGCTT
                                |||||  ||||| ||| || ||||||
                                ATTCT  GGTTA CAC CC GACGAA
                                   TG    A   C  C
GAM1591  ACVR1B    3'  CGCACCGGGGCACTC      39614         CTGG
                                CGCACCGGG    GTACTC
                                |||||||||    ||||||
                                GCGTGGCCC    CGTGAG
                                             ____
GAM1591  CSPG3     3'  GCACTGGGCTAGAAAACT    39615     C      T_
                                GCAC GGGCTGGG  ACT
                                |||| ||||||||  |||
                                CGTG CCCGATCT  TGA
                                  A       TT
GAM1591  CYP4B1    3'  TCGAACCGAAATAGGTGCTC  39616     C     C    A
                                TCG ACCGGG TGGGT CTC
                                ||| |||||| ||||| |||
                                AGC TGGCTT ATCCA GAG
                                  T     T    C
GAM1591  DTNB      3'  CGCACAACAGATGGGTACT   39617      __   C
                                CGCAC  CGGG TGGGTACT
                                |||||  |||| ||||||||
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                                GCGTG  GTCT ACCCATGA
                                  TT   _
GAM1591  MYB     5'  CCGCACCGGGCTGCCGCCTC  39618          GGTA
                                TCGCACCGGGCTG   CTC
                                |||||||||||||   |||
                                GGCGTGGCCCGAC   GAG
                                      GGCG
GAM1591  NDUFA9  3'  CCGCCTGGCTGGGTGCTC   39619    ACCG      A
                                TCGC   GGCTGGGT CTC
                                ||||   |||||||| |||
                                GGCG   CCGACCCA GAG
                                  GA__      C
GAM1591  NRCAM   5'  TCCACTGGGCTAGACACC   39620   G  C     GT
                                TC CAC GGGCTGG  ACT
                                || ||| |||||||  |||
                                AG GTG CCCGATC  TGG
                                 _  A     TG
GAM1591  NRXN1   3'  GCACCAGGCGGCAAACTC   39621       T  GT_
                                GCACCGGGC GG   ACTC
                                |||||||||  ||   ||||
                                CGTGGTCCG CC   TGAG
                                     _ GTT
GAM1591  NRXN1   3'  GCACCAGGCGGCAAACTC   39621       T  GT_
                                GCACCGGGC GG   ACTC
                                |||||||||  ||   ||||
                                CGTGGTCCG CC   TGAG
                                     _ GTT
GAM1591  PREB    5'  TCGCCGCCGGGAGCACTC   39622    A_   CTG
                                TCGC  CCGGG   GGTACTC
                                ||||  |||||   |||||||
                                AGCG  GGCCC   TCGTGAG
                                  GC    ___
GAM1591  SLC29A2 3'  TCGCCCTGGGCTGGATCTC   39623    A  _      A
                                TCGC CC GGGCTGGGT CTC
                                |||| ||  ||||||||| |||
                                AGCG GG CCCGACCTA GAG
                                  _  A       _
GAM1591  SNRPN   5'  TCCACCACAGGTACT      39624   G   GGC
                                TC CACCG   TGGGTACT
                                || |||||   ||||||||
                                AG GTGGT   GTCCATGA
                                 _    ___
GAM1591  SNRPN   5'  TCCACCACAGGTACT      39624   G   GGC
                                TC CACCG   TGGGTACT
                                || |||||   ||||||||
                                AG GTGGT   GTCCATGA
                                 _    ___
GAM1591  SNRPN   5'  TCCACCACAGGTACT      39624   G   GGC
                                TC CACCG   TGGGTACT
                                || |||||   ||||||||
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                                AG GTGGT  GTCCATGA
                                 _   ___
GAM1591 SNRPN    5' TCCACCACAGGTACT     39624   G   GGC
                                TC CACCG  TGGGTACT
                                || |||||  ||||||||
                                AG GTGGT  GTCCATGA
                                 _   ___
GAM1591 SUFU     3' TCGCAGCATTCAGGTACT   39625     C  GGC
                                TCGCA CG  TGGGTACT
                                ||||| ||  ||||||||
                                AGCGT GT  GTCCATGA
                                  C  AA_
GAM1591 SVIL     3' GCACCGGAAGCAGTACTC   39626       CTG
                                GCACCGGG  GGTACTC
                                ||||||||  |||||||
                                CGTGGCCT  TCATGAG
                                     TCG
GAM1591 SVIL     3' GCACCGGAAGCAGTACTC   39626       CTG
                                GCACCGGG  GGTACTC
                                ||||||||  |||||||
                                CGTGGCCT  TCATGAG
                                     TCG
GAM1591 UBE2I    5' TCGCACTGGGCTGGACTC   39627      C     GT
                                TCGCAC GGGCTGG  ACTC
                                |||||| |||||||  ||||
                                AGCGTG CCCGACC  TGAG
                                   A     __
GAM1591 ADAR3    5' TCCCACTGGGCTGGGGGCCTC 39628   G  C     TA_
                                TC CAC GGGCTGGG  CTC
                                || ||| ||||||||  |||
                                AG GTG CCCGACCC  GAG
                                 G  A      CCG
GAM1591 CREG     3' GCACCAGGCTCAGGCAGCTC  39629        _   _
                                GCACCGGGCT GGGTA CTC
                                |||||||||| ||||| |||
                                CGTGGTCCGA TCCGT GAG
                                      G   C
GAM1591 DKFZP762D096 5' TCGCTGCTGGGCACCC     39630     ACCGG
                                TCGC    GCTGGGTACTC
                                ||||    ||||||||||
                                AGCG    CGACCCGTGGG
                                  A____
GAM1591 FLJ14621 5' CGCAGCCGCAGGTACT     39631     _  GGC
                                CGCA CCG  TGGGTACT
                                |||| |||  ||||||||
                                GCGT GGC  GTCCATGA
                                  C  ___
GAM1591 FLJ22794 5' TCAACTGGCTGGGTGCT    39632    C  CG      A
                                TCG AC  GGCTGGGT CT
                                ||| ||  |||||||| ||
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```
                                AGT TG  CCGACCCA GA
                                  _ A_       C
GAM1591  GEMIN6   5'  TCGCAACTCTGGGTACTC    39633      CCGGG
                                TCGCA    CTGGGTACTC
                                |||||    ||||||||||
                                AGCGT    GACCCATGAG
                                   TGA__
GAM1591  HPCAL4   3'  GCACCAAACAGGTGCTC     39634        T   A
                                GCACCGGGC GGGT CTC
                                ||||||||| |||| |||
                                CGTGGTTTG TCCA GAG
                                      _   C
GAM1591  HTMP10   3'  GCACCAGGCTGACCTC      39635          GTA
                                GCACCGGGCTGG   CTC
                                ||||||||||||   |||
                                CGTGGTCCGACT   GAG
                                       G__
GAM1591  KIAA1228 5'  CCGAGGCGGGCTGGGTGCTC  39636    CAC        A
                                TCG   CGGGCTGGGT CTC
                                |||   |||||||||| |||
                                GGC   GCCCGACCCA GAG
                                  TCC         C
GAM1591  KIAA1432 5'  TCGACTGGGCTTATGCTC    39637    C  C    GG  A
                                TCG AC GGGCT  GT CTC
                                ||| || |||||  || |||
                                AGC TG CCCGA  TA GAG
                                  _ A    A_  C
GAM1591  KIAA1453 3'  TCGCTGCTGGCCGAGTGCTC  39638     ACCG       A
                                TCGC    GGCTGGGT CTC
                                ||||    |||||||| |||
                                AGCG    CCGGCTCA GAG
                                  ACGA       C
GAM1591  MGC12760 3'  CCGCCGGGCCAGCAGCTC    39639     AC     TG G  _
                                TCGC  CGGGC  G TA CTC
                                ||||  |||||  | || |||
                                GGCG  GCCCG  C GT GAG
                                   __     GT _  C
GAM1591  MGC4796  3'  TCGTACTGGGAGCACTC     39640    C  C   CTG
                                TCG AC GGG   GGTACTC
                                ||| || |||   |||||||
                                AGC TG CCC   TCGTGAG
                                  A  A  ___
GAM1591  PAFAH2   3'  TCGCTGGGCTGAGTCT      39641      ACC        A
                                TCGC   GGGCTGGGT CT
                                ||||   ||||||||| ||
                                AGCG   CCCGACTCA GA
                                  A__        _
GAM1591  PF1      5'  CCTCCCGGGCTGGGTGCTC   39642    GCA         A
                                TC   CCGGGCTGGGT CTC
                                ||   |||||||||| |||
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                                GG   GGCCCGACCCA GAG
                                 AG_         C
GAM1591  SIPL     3'  TCACACCACCGGTGGGTA    39643        __  C
                                TCGCACCG  GG TGGGTA
                                ||||||||  || ||||||
                                AGTGTGGT  CC ACCCAT
                                     GG  _
GAM1591  TIEG     3'  TCGTGCCAGGCTGTGGGGCT   39644     CA      _  TA
                                TCG  CCGGGCTG GG  CT
                                |||  |||||||| ||  ||
                                AGC  GGTCCGAC CC  GA
                                  AC       A  CC
GAM1591  ZNF334    5'  TCGCACCAGGTCCAAGTCTC   39645         _ TG   A
                                TCGCACCGGG C  GGT CTC
                                |||||||||| |  ||| |||
                                AGCGTGGTCC G  TCA GAG
                                      A GT  _
GAM1591  LOC133688 5'  GCGCCGGGCTAAGGACTC    39646    A        T
                                GC CCGGGCTGGG ACTC
                                || ||||||||| ||||
                                CG GGCCCGATTC TGAG
                                 C         C
GAM1591  LOC143915 3'  CCGCTGGGCTAGCACTC     39647      ACC      G
                                TCGC   GGGCTGG TACTC
                                ||||   ||||||| |||||
                                GGCG   CCCGATC GTGAG
                                  A__      _
GAM1591  LOC145195 5'  TCGCACCGGCAGCAACT     39648         G TG   _
                                TCGCACCGG C  GGTA CT
                                ||||||||| |  |||| ||
                                AGCGTGGCC G  TCGT GA
                                      _ __    T
GAM1591  LOC150606 3'  TCCACTGGCAAATACT      39649    G   CG   T
                                TC CAC  GGC GGGTACT
                                || |||  ||| |||||||
                                AG GTG  CCG TTTATGA
                                 _   A_  _
GAM1591  LOC152845 5'  GCAGGGCCTGGGTACTC     39650     CC   _
                                GCA  GGGC TGGGTACTC
                                |||  |||| |||||||||
                                CGT  CCCG ACCCATGAG
                                  __    G
GAM1591  LOC160646 5'  CGTACAGGACTGGGTGCTC    39651    C  C       A
                                CG AC GGGCTGGGT CTC
                                || || ||||||||| |||
                                GC TG CCTGACCCA GAG
                                 A  T        C
GAM1591  LOC201799 5'  GCGCCGGGCTGCAGCCTC     39652    A       _   A
                                GC CCGGGCTG GGT CTC
                                || |||||||| ||| |||
```

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                                CG GGCCCGAC TCG GAG
                                 C       G  _
GAM1591  LOC203601 5'  CCGCCACCACTGGGTATTC   39653      _  GG       C
                                TCGC ACC  GCTGGGTA TC
                                |||| |||  |||||||| ||
                                GGCG TGG  TGACCCAT AG
                                  G  __       A
GAM1591  LOC221931 3'  TCTACCAAGTATGGGTGCT   39654    GC     C_    A
                                TC  ACCGGG  TGGGT CT
                                ||  ||||||  ||||| ||
                                AG  TGGTTC  ACCCA GA
                                 A_     AT    C
GAM1591  LOC257017 5'  CCAAATACGTGGGTACTC    39655      __ _
                                CCGG  GC TGGGTACTC
                                ||||  || |||||||||
                                GGTT  TG ACCCATGAG
                                  TA  C
GAM1591  LOC54499  3'  TCTCACTGGTAGAATACTC   39656    G   C  GCT
                                TC CAC GG   GGGTACTC
                                || ||| ||   ||||||||
                                AG GTG CC   CTTATGAG
                                 A   A  AT_
GAM1591  LOC91409  3'  TCCCACTGAGCAGGGTGCTC  39657    G   C    T    A
                                TC CAC GGGC GGGT CTC
                                || ||| |||| |||| |||
                                AG GTG CTCG CCCA GAG
                                 G   A    T    C
GAM1591  LOC92106  5'  TCGCCCTGGGCTCAAGGT    39658      A  _    __
                                TCGC CC GGGCT  GGGT
                                |||| || |||||  ||||
                                AGCG GG CCCGA  TCCA
                                  _ A     GT
GAM1591  LOC92379  3'  CCTGCCAGGGTGGGTACTC   39659    GCA    C
                                TC   CCGGG TGGGTACTC
                                ||   ||||| |||||||||
                                GG   GGTCC ACCCATGAG
                                 AC_    C
GAM1592  KIAA0555  5'  TGCTGAGACCCGGAGAAGCT  39662             TTAT
                                TGTTGAGACCCGGAG   GAGTT
                                ||||||||||||||   |||||
                                ACGACTCTGGGCCTC   TTCGA
                                                  ____
GAM1592  KIAA0555  5'  TGCTGAGACCCGGAGAAGCT  39662             TTAT
                                TGTTGAGACCCGGAG   GAGTT
                                ||||||||||||||   |||||
                                ACGACTCTGGGCCTC   TTCGA
                                                  ____
GAM1592  LOC51128  3'  GTTGAGACCTGGAACCAATGTG 39663         C   TT ___
            AGTT                  GTTGAGACC GGAG  A   TGAGTT
                                ||||||||| ||||  |   ||||||
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                                CAACTCTGG CCTT  T   ACTCAA
                                     A    GG TAC
GAM1593  AF1Q     3'  GAGGTAAGGCTAAAATAGG   39666           CTT
                                GAGGTAAGGCTAAA   GG
                                |||||||||||||   ||
                                CTCCATTCCGATTT   CC
                                      TAT
GAM1593  AP2B1    3'  AGGGATAAGGCTACTACAGGTA 39667    A        AACTT
              AG                  AG GGTAAGGCTA    GGTAAG
                                || ||||||||||    ||||||
                                TC CTATTCCGAT    CCATTC
                                 C        GATGT
GAM1593  COG7     3'  AGGGGTGAGACTAAAGGCGG   39668    A  A      CT
                                AG GGT AGGCTAAA  TGG
                                || ||| ||||||||  |||
                                TC CCA TCTGATTT  GCC
                                 C  C       CC
GAM1593  DCK      3'  AGAGGTGGGACTAAACTGTTAA 39669       AA       TGG
              G                   AGAGGT  GGCTAAACT   TAAG
                                ||||||  |||||||||   ||||
                                TCTCCA  CTGATTTGA   ATTC
                                   CC       CA_
GAM1593  GPR86    3'  GAGGTAAGGCCAGAAAGGTA   39670          AACTT
                                GAGGTAAGGCTA    GGTA
                                ||||||||||||    ||||
                                CTCCATTCCGGT    CCAT
                                      CTTT_
GAM1593  PDE4D    3'  AGGTAAGGTCATTTGGT     39671        C  AAC
                                AGGTAAGG TA   TTGGT
                                |||||||| ||   |||||
                                TCCATTCC GT   AACCA
                                     A  A__
GAM1593  SLC22A5  3'  AGAGGCTAGGGCTGGTAA    39672       A   CTAAAC
                                AGAGGT AGG     TTGGTAA
                                |||||| |||     |||||||
                                TCTCCG TCC     GACCATT
                                   A   C_____
GAM1593  SNX15    3'  GAGGTAGGGCCAGGCCCTGG   39673       A    AA_
                                GAGGTA GGCTA   CTTGG
                                |||||| |||||   |||||
                                CTCCAT CCGGT   GGACC
                                   C    CCG
GAM1593  TNS      3'  AGAGGTGGGAGCTAAGGCA   39674       AA_     ACTT
                                AGAGGT   GGCTAA   GGTA
                                ||||||   ||||||   ||||
                                TCTCCA   TCGATT   CCGT
                                   CCC     _____
GAM1593  AFAP     3'  AGGGGAAGGTTAAGCCTGG   39675    A  T   C   A
                                AG GG AAGG TAA CTTGG
                                || || |||| ||| |||||
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                                TC CC TTCC ATT GGACC
                                 _ C   A  C
GAM1593  FEM-2    3'  AGGGGTAAGGCTGGGCATGCAG 39676    A       AAACTT___
                GTA                  AG GGTAAGGCT       GGTA
                                || |||||||||       ||||
                                TC CCATTCCGA       CCAT
                                 C        CCCGTACGT
GAM1593  HTEX4    5'  AGATGTAAAGAGCTTGGTAAG  39677    G     CTAAA
                                AGA GTAAGG    CTTGGTAAG
                                ||| ||||||    |||||||||
                                TCT CATTTC    GAACCATTC
                                  A     TC___
GAM1593  HTEX4    5'  AGATGTAAAGAGCTTGGTAAG  39677    G     CTAAA
                                AGA GTAAGG    CTTGGTAAG
                                ||| ||||||    |||||||||
                                TCT CATTTC    GAACCATTC
                                  A     TC___
GAM1593  HTEX4    5'  AGATGTAAAGAGCTTGGTAAG  39677    G     CTAAA
                                AGA GTAAGG    CTTGGTAAG
                                ||| ||||||    |||||||||
                                TCT CATTTC    GAACCATTC
                                  A     TC___
GAM1593  KIAA1679  3'  GAGGCAAGGCTGCACCTG    39678          AA
                                GAGGTAAGGCT  ACTTG
                                ||||||||||  |||||
                                CTCCGTTCCGA  TGGAC
                                       CG
GAM1593  KIAA1966  3'  AGGGGAAGGCTAAACAATAG   39679    A  T        T_
                                AG GG AAGGCTAAAC  TGG
                                || || ||||||||||  |||
                                TC CC TTCCGATTTG  ATC
                                 _ C         TT
GAM1593  PRO0082   3'  AGAAGTAAGGCTAAATAAATA  39680             CTT
                                AGAGGTAAGGCTAAA   GGTA
                                ||||||||||||||   ||||
                                TCTTCATTCCGATTT   TTAT
                                          AT_
GAM1593  RRP46    3'  AGAGGCAAGGCTGGGCTGCTGG 39681           AAAC__
                                AGAGGTAAGGCT     TTGG
                                ||||||||||||     ||||
                                TCTCCGTTCCGA     GACC
                                       CCCGAC
GAM1593  TUB      3'  AGAGGTTGCTCAGCTTGGTAAG 39682       AAG   AAA
                                AGAGGT   GCT   CTTGGTAAG
                                ||||||   |||   |||||||||
                                TCTCCA   CGA   GAACCATTC
                                   A__   GTC
GAM1593  LOC123232 3'  GAGGTGAGGCTGCAACTGG   39683      A    A_   T
                                GAGGT AGGCT  AACT GG
                                ||||| |||||  |||| ||
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                                CTCCA TCCGA  TTGA CC
                                  C    CG   _
GAM1593  LOC158364 5'  AGAGGTGGGGCCAGGCA    39684       AA    AACTT
                                AGAGGT  GGCTA    GGTA
                                ||||||  |||||    ||||
                                TCTCCA  CCGGT    CCGT
                                  CC    _____
GAM1593  LOC204084 3'  GAGTCAGGCTGGGCTTGGTAAG 39685     GTA    AAA
                                GAG   AGGCT   CTTGGTAAG
                                |||   |||||  |||||||||
                                CTC   TCCGA   GAACCATTC
                                 AG_    CCC
GAM1593  LOC221583 3'  AGGGGTAAGGCCAGTGG     39686    A        AACT
                                AG GGTAAGGCTA    TGG
                                || ||||||||||    |||
                                TC CCATTCCGGT    ACC
                                 C        C___
GAM1594  BACH2     3'  TGTGAAGGTAACTATCACTCCT 39689      C  AA   CC
             G                   TGTG AA  TAAC  TCACTCCTG
                                ||||  ||  ||||  |||||||||
                                ACAC TT  ATTG  AGTGAGGAC
                                  _ CC    AT
GAM1594  CDH5      3'  TGTGGAGGTGGCCCTCACCCTG 39690      CAAAATAA      T
                                TGTG       CCCTCAC CCTG
                                ||||       ||||||| ||||
                                ACAC       GGGAGTG GGAC
                                  CTCCACC_      _
GAM1594  CREBL2    3'  TGTGAACATTCACTCCTG    39691     CAAAAT   CC
                                TGTG     AAC  TCACTCCTG
                                ||||     |||  |||||||||
                                ACAC     TTG  AGTGAGGAC
                                  _______  TA
GAM1594  EPS15     3'  TGTGCAAAATATTTTTCCTTAT 39692          AC___   CA_
             CTC                   TGTGCAAAATA    CCT   CTC
                                ||||||||||    |||   |||
                                ACACGTTTTAT    GGA   GAG
                                      AAAAA   ATA
GAM1594  IER5      3'  TGTGCGGAAACGCCACTCCTG  39693      AAAAT   C T
                                TGTGC    AAC C CACTCCTG
                                |||||    ||| | ||||||||
                                ACACG    TTG G GTGAGGAC
                                  CCT__   C _
GAM1594  RXRA      3'  TGTGGCATCTTCACTCCTG   39694     _  AAATAACCC
                                TGTG CA       TCACTCCTG
                                |||| ||       |||||||||
                                ACAC GT       AGTGAGGAC
                                  C  AGA_______
GAM1594  KIAA1309  3'  TGTGCTAAATAACCTTATGAAC 39695      A       CTCACTC
             TG                    TGTGC AAATAACC      CTG
                                ||||| ||||||||      |||
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                                ACACG TTTATTGG      GAC
                                  A       AATACTT
GAM1594 KIAA1510 5' TGGCAGACACAGCCTCACTCCT 39696    T   AA_   AC
            G                    TG GCA   ATA  CCTCACTCCTG
                                 || |||   |||  ||||||||||
                                 AC CGT   TGT  GGAGTGAGGAC
                                  _  CTG   C_
GAM1594 KIAA1853 3' TGCCCGGGGCCCTCACTCCTG 39697     AAAATAA
                                 TGC      CCCTCACTCCTG
                                 |||      ||||||||||||
                                 ACG      GGGAGTGAGGAC
                                   GGCCCC_
GAM1594 N6AMT1   3' TGTGCAAATAATTCTATAGGCC 39698        A   CC  CACT_
            TG                    TGTGCAAA TAA  CT    CCTG
                                 |||||||| |||  ||    ||||
                                 ACACGTTT ATT  GA    GGAC
                                      _  AA  TATCC
GAM1594 NMA      3' TGTGCAAATAATCCTTCA    39699        A  _  C
                                 TGTGCAAA TAA CC TCA
                                 |||||||| ||| || |||
                                 ACACGTTT ATT GG AGT
                                      _  A  A
GAM1594 ZNF238   3' TGTGCAAAATGCTTTTGCCT   39700         AACC  CACT
                                 TGTGCAAAAT    CT    CCT
                                 ||||||||||    ||    |||
                                 ACACGTTTTA    GA    GGA
                                       C___  AAAC
GAM1594 LOC256165 3' TGCAAAATCCAAGCGTTCCTG  39701        AA  CTCAC_
                                 TGCAAAAT  CC     TCCTG
                                 ||||||||  ||     |||||
                                 ACGTTTTA  GG     AGGAC
                                      __  TTCGCA
GAM1594 LOC91138  3' TATGCAAAAGGGTCTTCACTC  39702        TAACCC
                                 TGTGCAAAA     TCACTC
                                 |||||||||     ||||||
                                 ATACGTTTT     AGTGAG
                                       CCCAGA
GAM1595 BRCA1    3' AGTGCTAACTTCCAGTAAC   39705         GTG   C
                                 AGTGTTAGCT   CCAG AAC
                                 ||||||||||   |||| |||
                                 TCACGATTGA   GGTC TTG
                                       A__    A
GAM1595 FKBP10   3' AAGCTCAGCTGTGTCAG     39706      G       C
                                 AAGT TTAGCTGTG CAG
                                 |||| ||||||||| |||
                                 TTCG AGTCGACAC GTC
                                   _       A
GAM1595 INPP1    3' TGAATGTTAACCAGCA      39707   A      GCTGT
                                 A AGTGTTA    GCCAGCA
                                 | |||||||    |||||||
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                                A TTACAAT     TGGTCGT
                                 C      _____
GAM1595 KIAA0857 3' TAAAGTATGTGCTAGCAA    39708       TTAGC    C
                                TAAAGTG    TGTGC AGCAA
                                |||||||    ||||| |||||
                                ATTTCAT    ACACG TCGTT
                                     _____    A
GAM1595 PRDM2    3' TGAGGGTTAGCTGTAGGAGC  39709   A  T       CC
                                A AG GTTAGCTGTG  AGC
                                | || ||||||||||  |||
                                A TC CAATCGACAT  TCG
                                 C  C        CC
GAM1595 WISP2    3' TAAAGTGTTGCCTGCAGC    39710        A   G   C
                                TAAAGTGTT GCT TGC AGC
                                ||||||||| ||| ||| |||
                                ATTTCACAA CGG ACG TCG
                                      _  _  _
GAM1595 BNIP2    3' TAAAGTGTGGTTCTCTATTTAG 39711       TAG___   GCC
             CAA                  TAAAGTGT     CTGT   AGCAA
                                |||||||     ||||   |||||
                                ATTTCACA     GATA   TCGTT
                                     CCAAGA    AA_
GAM1595 FLJ10241 3' TAAAGTGTCAGTAGTAGC    39712         CT  GCC
                                TAAAGTGTTAG  GT   AGC
                                ||||||||||  ||   |||
                                ATTTCACAGTC  CA   TCG
                                      AT  ___
GAM1595 FLJ11181 3' TAAAATGTTAGCCAAGGCAA  39713           TGCCA
                                TAAAGTGTTAGCTG    GCAA
                                ||||||||||||||    ||||
                                ATTTTACAATCGGT    CGTT
                                       TC___
GAM1595 FLJ11259 3' ATATCAAGTTGTGCCAGCAAC 39714       _ C
                                GTGTTA G TGTGCCAGCAAC
                                |||||| | ||||||||||||
                                TATAGT C ACACGGTCGTTG
                                    T A
GAM1595 GALNT12  3' AGTGTTAACTGTGGTAGCAAC 39715           CC
                                AGTGTTAGCTGTG  AGCAAC
                                ||||||||||||  ||||||
                                TCACAATTGACAC  TCGTTG
                                       CA
GAM1595 GIT1     3' AAGGGCACTTGTGCCAG     39716     T  TA  _
                                AAG GT  GCT GTGCCAG
                                ||| ||  ||| |||||||
                                TTC CG  TGA CACGGTC
                                  C  __  A
GAM1595 H2AV     3' ATGTTAGCTGTACAGTGGC   39717           CA__
                                GTGTTAGCTGTGC   GC
                                ||||||||||||   ||
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                                TACAATCGACATG   CG
                                      TCAC
GAM1595 KIAA0599 5' TAAAGCGTTGGCCCGATAGTGC 39718        A _____
            CAGCA                  TAAAGTGTT GCT    GTGCCAGCA
                                |||||||||| |||    |||||||||
                                ATTTCGCAA CGG    CACGGTCGT
                                     C   GCTAT
GAM1595 KIAA1492 3' TAAAGTGTTAGATTGCAGC   39719         CTG   C
                                TAAAGTGTTAG   TGC AGC
                                ||||||||||   ||| |||
                                ATTTCACAATC   ACG TCG
                                      TA_   _
GAM1595 KIAA1681 3' AAGTGTCAGTCAAGCAA     39720        CT TGCC
                                AAGTGTTAG  G   AGCAA
                                |||||||||  |   |||||
                                TTCACAGTC  T   TCGTT
                                     AG ____
GAM1595 NUDT13   3' GTGCAAATGCCAGCAAC     39721     TAGCT
                                GTGT    GTGCCAGCAAC
                                ||||    ||||||||||
                                CACG    TACGGTCGTTG
                                  TT___
GAM1595 P1P373C6 3' TAAAGTGCTGGCTGAGGGCAA 39722        A   TGCCA
                                TAAAGTGTT GCTG    GCAA
                                |||||||||| ||||    ||||
                                ATTTCACGA CGAC    CGTT
                                     C   TCC__
GAM1595 PCSK7    3' GTATCCCAGCTGTGCCGGCA   39723      __      A
                                GTGTT  AGCTGTGCC GCA
                                |||||  ||||||||| |||
                                CATAG  TCGACACGG CGT
                                   GG       C
GAM1595 LOC145809 5' GTGTTGCCCAGCAAC      39724      A  TGTG
                                GTGTT GC   CCAGCAAC
                                ||||| ||   ||||||||
                                CACAA CG   GGTCGTTG
                                   _ ____
GAM1595 LOC145919 3' AAAGTGTTTAGTCAGCA    39725       AGCT  GC
                                AAAGTGTT   GT  CAGCA
                                ||||||||   ||  |||||
                                TTTCACAA   CA  GTCGT
                                     AT__  __
GAM1595 LOC164945 5' AAGCTGTTAGCCCCAGGGCAAC 39726    _      GTG  __
                                AAG TGTTAGCT   CCA  GCAAC
                                ||| ||||||||   |||  |||||
                                TTC ACAATCGG   GGT  CGTTG
                                  G       ___  CC
GAM1595 LOC203369 3' AGAGTTCGGATGCCAGCAA   39727    T   AGCT
                                AG GTT    GTGCCAGCAA
                                || |||    ||||||||||
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                                TC CAA    TACGGTCGTT
                                 T  GCC_
GAM1596 RPL10    3' TGTGTTGGTACAGGCTTCT   39730       C   AT
                                TGTGTTGG ACAG  TTCT
                                |||||||| ||||  ||||
                                ACACAACC TGTC  AAGA
                                     A   CG
GAM1596 SORCS3   3' GTGTTGGTGATTCTGCTG    39731       CACA   T  A
                                GTGTTGG   GATT CT CTG
                                |||||||   |||| || |||
                                CACAACC   CTAA GA GAC
                                    A___   _ C
GAM1596 TGFA     3' TGTGTTGGGCAGAATTCT    39732       CA   T
                                TGTGTTGG  CAGA TTCT
                                ||||||||  |||| ||||
                                ACACAACC  GTCT AAGA
                                     C_   T
GAM1596 AMOTL1   3' TGGTTGGCACAGGTGACACTGC 39733    T       ATTTC
                                TG GTTGGCACAG    TACTGC
                                || ||||||||||    ||||||
                                AC CAACCGTGTC    GTGACG
                                 _        CACT_
GAM1596 KIAA1238 3' TGTTGGGTTTTTCTACTG    39734      CACAGA
                                TGTTGG     TTTCTACTG
                                ||||||     |||||||||
                                ACAACC     AAAGATGAC
                                   CAA___
GAM1596 OPRL1    3' TGTGTTGGGCGTAGATGGGCTC 39735       _ AC   TT_  A
            TGC                   TGTGTTGG C  AGAT   CT CTGC
                                ||||||||  |  ||||   || ||||
                                ACACAACC G  TCTA   GA GACG
                                     C CA   CCC  _
GAM1596 PCDH17   3' GTGTAGCTTGGACTACTGC   39736     T   ACA  TTT
                                GTGT GGC   GA   CTACTGC
                                |||| |||   ||   |||||||
                                CACA TCG   CT   GATGACG
                                  _   AAC  ___
GAM1596 ZIM2     3' GTGTTGGCGCAGATGAAATGGC 39737       A    TTCTA__
            TGC                   GTGTTGGC CAGAT      CTGC
                                |||||||| |||||      ||||
                                CACAACCG GTCTA      GACG
                                     C    CTTTACC
GAM1596 LOC150862 5' TGTGTTGGATATTGACCTTTGC 39738       CACA_    CTA
            TG                    TGTGTTGG    GATTT   CTG
                                |||||||||    |||||  |||
                                ACACAACC    CTGGA   GAC
                                     TATAA    AAC
GAM1596 LOC163231 5' TGAACAGGTTTCTACTG     39739     C    A
                                TGG ACAG TTTCTACTG
                                ||| |||| |||||||||
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                                ACT TGTC AAAGATGAC
                                  _   C
GAM1596 LOC253815 5'  TGTGTTGGGCACAGGGCAGCTG 39740        _    ATTTCTA
                                TGTGTTGG CACAG      CTG
                                |||||||| |||||      |||
                                ACACAACC GTGTC      GAC
                                    C    CCGTC__
GAM1596 LOC255328 3'  TGTGTTGGATGGACCACTG   39741        CACA  TTT
                                TGTGTTGG   GA   CTACTG
                                ||||||||   ||   ||||||
                                ACACAACC   CT   GGTGAC
                                    TAC_  ___
GAM1596 LOC90670  3'  GTTAAACAGATTTTTATTGC   39742      C      C  C
                                GTTGG ACAGATTT TA TGC
                                ||||| |||||||| || |||
                                CAATT TGTCTAAA AT ACG
                                  _      A  A
GAM1596 LOC92370  3'  TGTATTGGCATGGATTCTATAC 39743         CA    C_
           TGC                    TGTGTTGGCA  GATTT  TACTGC
                                ||||||||||  |||||  ||||||
                                ACATAACCGT  CTAAG  ATGACG
                                     AC    AT
GAM1597 BC008967  5'  GATACAGCTAGAGAGAAGT   39746    C   A__
                                GAT CAGC   AGAGAAGT
                                ||| ||||   ||||||||
                                CTA GTCG   TCTCTTCA
                                  T   ATC
GAM1597 SELM      3'  CGGCTCTCAGCAAGAGAAGTA  39747    A_ _
                                CG  TC CAGCAAGAGAAGTA
                                ||  || ||||||||||||||
                                GC  AG GTCGTTCTCTTCAT
                                 CG  A
GAM1597 LOC152641 3'  TTAAACGACTTCACACCACGAG 39748        __ _  G  A
                                TTAAACGA  TC CA CA GAG
                                ||||||||  || || || |||
                                AATTTGCT  AG GT GT CTC
                                     GA  T  G  G
GAM1598 BCL7A     5'  TTTCACCTTAAGCCATTCC    39751       G      G__
                                TTTCAC TTAAGCT   CC
                                ||||||| |||||||   ||
                                AAAGTG AATTCGG   GG
                                   G      TAA
GAM1598 CKN1      3'  TTCATGTTTAAGCCAGATTCC  39752      C   AAGCT      _
                                TTCA GTT    GCCAGAT CC
                                |||| |||    ||||||| ||
                                AAGT CAA    CGGTCTA GG
                                  A  ATT__      A
GAM1598 EMR1      3'  TTCCATGTTAAGCTGAGAAGA  39753      C       CC_
                                TTTCA GTTAAGCTG   AGA
                                ||||| |||||||||   |||
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```
                                AAGGT CAATTCGAC   TCT
                                  A        TCT
GAM1598  KERA     5'  ACTTTAAGCTGTCAAGTC    39754    G       C   A
                                AC TTAAGCTG CAG TC
                                || |||||||| ||| ||
                                TG AATTCGAC GTT AG
                                 A       A   C
GAM1598  PODXL    3'  TTTCAGGTCGTCAGATCC    39755       C   AAGCT C
                                TTTCA GTT    G CAGATCC
                                ||||| |||    | |||||||
                                AAAGT CAG    C GTCTAGG
                                  C  _____ A
GAM1598  RAD52    3'  TTCCACGTTCAGACTTGGGTCC 39756         A  _  GCCAGA
              C                  TTTCACGTT AG CT     TCCC
                                ||||||||| || ||     ||||
                                AAGGTGCAA TC GA     AGGG
                                     G  T  ACCC__
GAM1598  RAD52    3'  TTCCACGTTCAGACTTGGGTCC 39756         A  _  GCCAGA
              C                  TTTCACGTT AG CT     TCCC
                                ||||||||| || ||     ||||
                                AAGGTGCAA TC GA     AGGG
                                     G  T  ACCC__
GAM1598  RAD52    3'  TTCCACGTTCAGACTTGGGTCC 39756         A  _  GCCAGA
              C                  TTTCACGTT AG CT     TCCC
                                ||||||||| || ||     ||||
                                AAGGTGCAA TC GA     AGGG
                                     G  T  ACCC__
GAM1598  RAD52    3'  TTCCACGTTCAGACTTGGGTCC 39756         A  _  GCCAGA
              C                  TTTCACGTT AG CT     TCCC
                                ||||||||| || ||     ||||
                                AAGGTGCAA TC GA     AGGG
                                     G  T  ACCC__
GAM1598  VBP1     3'  TTTCACGTTGGCCAAGATC    39757          AAGCT   _
                                TTTCACGTT    GCCA GATC
                                |||||||||    |||| ||||
                                AAAGTGCAA    CGGT CTAG
                                     C____    T
GAM1598  ARHGAP11A 5'  TTTCTCGTCTATTGCCAGAT   39758     A   AAGC
                                TTTC CGTT    TGCCAGAT
                                |||| ||||   ||||||||
                                AAAG GCAG    ACGGTCTA
                                  A   ATA_
GAM1598  DKFZP564D0462 5'  TTTCTTGTTTTTGTTCAGATCC 39759      AC   AAGCTGC
              C                  TTTC  GTT      CAGATCCC
                                ||||  |||      ||||||||
                                AAAG  CAA      GTCTAGGG
                                  AA   AAACAA_
GAM1598  FLJ21916  3'  TTTCAGTTGGGAAACAGGGATC 39760      C   ___    TGCCA
              CC                   TTTCA GTT   AAGC    GATCCC
                                ||||| |||   ||||    ||||||
```

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                                AAAGT CAA   TTTG    CTAGGG
                                  _  CCC    TCC__
GAM1598  GGA2     3'  TTCCCAAGGCTGCCAGGTCC   39761     A  TTAA      A
                                TTTC CG    GCTGCCAG TCC
                                |||| ||    |||||||| |||
                                AAGG GT    CGACGGTC AGG
                                  _ TC__       C
GAM1598  HCC-4    5'  TTTCGGTTTGCCAGAT     39762     AC   AAGC
                                TTTC  GTT    TGCCAGAT
                                ||||  |||    ||||||||
                                AAAG  CAA    ACGGTCTA
                                  C_  ____
GAM1598  RNF38    3'  TTTCACATTTTCCAGAT     39763         AAGCTG
                                TTTCACGTT     CCAGAT
                                |||||||||     ||||||
                                AAAGTGTAA     GGTCTA
                                     AA____
GAM1598  TSPAN-2  3'  TTTCAACTGCCAGATC      39764      CGTTAA
                                TTTCA     GCTGCCAGATC
                                |||||     ||||||||||
                                AAAGT     TGACGGTCTAG
                                  _______
GAM1598  LOC123855 5'  TTCACGTTGAGCTGGAACTCC  39765        A    CCAGA
                                TTCACGTT AGCTG    TCC
                                |||||||| |||||    |||
                                AAGTGCAA TCGAC    AGG
                                     C    CTTG_
GAM1598  LOC139221 3'  TTTCATGTTAAGCCTTTAGA   39766      C       GCC
                                TTTCA GTTAAGCT   AGA
                                ||||| ||||||||   |||
                                AAAGT CAATTCGG   TCT
                                   A       AAA
GAM1598  LOC151742 3'  GTTGCAACTGCCAGGTCC    39767     A_       A
                                GTT  AGCTGCCAG TCC
                                |||  ||||||||| |||
                                CAA  TTGACGGTC AGG
                                  CG        C
GAM1598  LOC203411 5'  TTTCACGTCAGCAGAT      39768          A  TGCC
                                TTTCACGTTA GC    AGAT
                                |||||||||| ||    ||||
                                AAAGTGCAGT CG    TCTA
                                     _  ____
GAM1599  MGAT5    5'  TTGATCATTTCACAATGTA    39771        CGATT
                                TTGATCAT    CAATGTA
                                ||||||||    |||||||
                                AACTAGTA    GTTACAT
                                     AAGT_
GAM1599  NBEA     3'  ACTTGATCAGTACAATGTA    39772        TCGATT
                                ACTTGATCA     CAATGTA
                                |||||||||     |||||||
```

```
                                TGAACTAGT     GTTACAT
                                     CAT___
GAM1599  DKFZP566D1346 3'  TACTGATGTGTCGATTCAATGT 39773      T   CA_
                                TACT GAT   TCGATTCAATGT
                                |||| |||   ||||||||||||
                                ATGA CTA   AGCTAAGTTACA
                                  _   CAC
GAM1599  KIAA0057  3'  TTGATCATTTGTTCCAAAATGT 39774        CGA   ___
           AC                     TTGATCAT   TTC   AATGTAC
                                |||||||||   |||   |||||||
                                AACTAGTA   AAG   TTACATG
                                     AAC   GTT
GAM1599  KIAA0193  3'  CTTGACCAAGGTCAATGTAC   39775        TCGAT
                                CTTGATCA    TCAATGTAC
                                ||||||||    |||||||||
                                GAACTGGT    AGTTACATG
                                     TCC__
GAM1599  KIAA0628  3'  CTTGATACAAGATCAATGTAC  39776       _  TC   T
                                CTTGAT CA  GAT CAATGTAC
                                |||||| ||  ||| ||||||||
                                GAACTA GT  CTA GTTACATG
                                   T  T_  _
GAM1599  MGC3232   3'  TTAATACAAATTCAATGTA    39777      C  C
                                TTGAT AT GATTCAATGTA
                                ||||| || ||||||||||
                                AATTA TG TTAAGTTACAT
                                  _  T
GAM1599  USP8      3'  ACTATGTACATCGATTTGATGT 39778     TGAT_      CA
                                ACT    CATCGATT  ATGT
                                |||    ||||||||  ||||
                                TGA    GTAGCTAA  TACA
                                  TACAT       AC
GAM1599  LOC149267 3'  TTGATCATGGAGGTAATGT    39779        C  TTC
                                TTGATCAT GA   AATGT
                                |||||||| ||   |||||
                                AACTAGTA CT   TTACA
                                     C  CCA
GAM1599  LOC158476 5'  TTGGACATATTCAATGTA     39780     AT   CG
                                TTG  CAT  ATTCAATGTA
                                |||  |||  ||||||||||
                                AAC  GTA  TAAGTTACAT
                                  CT   __
GAM1599  LOC221288 5'  CTTGATCAATTAATGT       39781        TCG   C
                                CTTGATCA   ATT AATGT
                                ||||||||   ||| |||||
                                GAACTAGT   TAA TTACA
                                     ___   _
GAM1600  TNFAIP1   3'  AGTGGGTACTATACGTGGCTAC 39784     C  AA     AC_   C
           GTT                    AG GG  ACTGTA   GGC ACGTT
                                || ||  ||||||   ||| |||||
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                                TC CC  TGATAT   CCG TGCAA
                                 A  CA     GCA   A
GAM1600  LOC115110 3'  AGGGAAACTGCTGGCTGTGTT  39785    C       AAC   CAC
                                AG GGAAACTGT   GGC   GTT
                                || |||||||||   |||   |||
                                TC CCTTTGACG   CCG   CAA
                                 _       A__   ACA
GAM1600  LOC129011 5'  AGCTGGGCAGGTGGCCACGTT  39786     _ AAACT   AC_
                                AGC GG    GTA   GGCCACGTT
                                ||| ||    |||   |||||||||
                                TCG CC    CGT   CCGGTGCAA
                                  A _____   CCA
GAM1601  BACH2    3'  ATGGCAGAAGTTAGGTTGGG   39789         T   ATAT
                                ATGGCAGAA TTG    TTGGG
                                ||||||||| |||    |||||
                                TACCGTCTT AAT    AACCC
                                      C   CC__
GAM1601  DSCR3    3'  TGGCAGGATTTGAAGGA     39790       A     TATTT
                                TGGCAG ATTTGA     GGGA
                                |||||| ||||||     ||||
                                ACCGTC TAAACT     TCCT
                                   C     _____
GAM1601  GPR84    3'  ATGGAGAGACTTGATTTGGGA  39791      C  _      AT
                                ATGG AGA ATTTGAT  TTGGGA
                                |||| ||| |||||||  ||||||
                                TACC TCT TGAACTA  AACCCT
                                  _  C      __
GAM1601  HMGN2    3'  ATGGCAGAATTTATCTGAA    39792          TGA
                                ATGGCAGAATT   TATTTGGG
                                ||||||||||   ||||||||
                                TACCGTCTTAA   ATAGACTT
                                          ___
GAM1601  LMO7     5'  TGGTAGAATCTTCTTTGGGAA  39793     C      GATA
                                TGG AGAATTT    TTTGGGAA
                                ||| |||||||    ||||||||
                                ACC TCTTAGA    AAACCCTT
                                  A      AG__
GAM1601  LMO7     5'  TGGTAGAATCTTCTTTGGGAA  39793     C      GATA
                                TGG AGAATTT    TTTGGGAA
                                ||| |||||||    ||||||||
                                ACC TCTTAGA    AAACCCTT
                                  A      AG__
GAM1601  SLC22A1LS 5'  TGGCAAAATTTGGGG       39794           ATATTT
                                TGGCAGAATTTG      GGG
                                ||||||||||||      |||
                                ACCGTTTTAAAC      CCC
                                          _______
GAM1601  UC28     3'  ATGGCAGAGTCTTACACTTGGG 39795         A   G
              AA                  ATGGCAGA TTT ATATTTGGGAA
                                ||||||||| ||| ||||||||||
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                                TACCGTCT AGA TGTGAACCCTT
                                    C   A
GAM1601  CLIPR-59  3'  ATGGGGTCTGTATTTGGG    39796     CAGAA    A
                                ATGG    TTTG TATTTGGG
                                ||||    |||| ||||||||
                                TACC    AGAC ATAAACCC
                                  CC___   _
GAM1601  FLJ12891  3'  ATGGCAGAGTATGACCTTCTGG 39797       ATT    A_
           G                     ATGGCAGA   TGAT  TTTGGG
                                ||||||||   ||||  ||||||
                                TACCGTCT   ACTG  AGACCC
                                    CAT    GA
GAM1601  GCHFR    3'  ATGGCGGTGATGATTTGGGAA  39798     AGAATT   _
                                ATGGC     TGAT ATTTGGGAA
                                |||||     |||| |||||||||
                                TACCG     ACTA TAAACCCTT
                                  CC____    C
GAM1601  KIAA0514  3'  ATGGCAGAGTTCTGAGGGTGGA 39799       A_    TATT
                                ATGGCAGA  TTTGA    TGGG
                                ||||||||  |||||    ||||
                                TACCGTCT  AGACT    ACCT
                                    CA    CCC_
GAM1601  KIAA1017  3'  ATGGCAGGATTTGGGG      39800       A    ATATTT
                                ATGGCAG ATTTG     GGG
                                ||||||| |||||     |||
                                TACCGTC TAAAC     CCC
                                    C    _______
GAM1601  KIAA1393  3'  ATGGCAGAATTTATCCGAA    39801         TGA
                                ATGGCAGAATT   TATTTGGG
                                ||||||||||   ||||||||
                                TACCGTCTTAA   ATAGGCTT
                                       ___
GAM1601  LHPP     3'  TGGTGAGTTCTGGGATTTGGGA 39802     CAGAA    AT
                                TGG    TTTG  ATTTGGGA
                                |||    ||||  ||||||||
                                ACC    AGAC  TAAACCCT
                                  ACTCA    CC
GAM1601  TCEA3    3'  ATAGCAGAGAGTTTGGGA    39803       ATTT  TA
                                ATGGCAGA   GA  TTTGGGA
                                ||||||||   ||  |||||||
                                TATCGTCT   CT  AAACCCT
                                     _____  C_
GAM1601  LOC116071 3'  GGCAGGGAGCTATTTGGGAA   39804      AATTTGA
                                GGCAG      TATTTGGGAA
                                |||||      ||||||||||
                                CCGTC      ATAAACCCTT
                                  CCTCG__
GAM1601  LOC127703 3'  ATGGAGAGATGGTTTGTTTGGG 39805     C   ATT  ATA__
           AA                    ATGG AGA   TG    TTTGGGAA
                                |||| |||   ||    ||||||||
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                                TACC TCT   AC    AAACCCTT
                                  _  CT_  CAAAC
GAM1601  LOC133688 3'  ATGGAAGAATTTGAAATGGAA  39806     C       TATT
                                ATGG AGAATTTGA   TGGGA
                                |||| |||||||||   |||||
                                TACC TCTTAAACT   ACCTT
                                  T       TT__
GAM1601  LOC143677 5'  GCAGAATGTAGGTTTGGG    39807       T  ATA
                                GCAGAAT TG   TTTGGG
                                ||||||| ||   ||||||
                                CGTCTTA AT   AAACCC
                                    C  CC_
GAM1601  LOC145540 3'  ATGGCAGAATTTATCTGAA   39792         TGA
                                ATGGCAGAATT   TATTTGGG
                                ||||||||||   ||||||||
                                TACCGTCTTAA   ATAGACTT
                                          ___
GAM1601  LOC148915 3'  ATGGCAGAATTTATCTGAA   39792         TGA
                                ATGGCAGAATT   TATTTGGG
                                ||||||||||   ||||||||
                                TACCGTCTTAA   ATAGACTT
                                          ___
GAM1601  LOC150580 3'  ATGGTAGAATTTATCTGAA   39808     C     TGA
                                ATGG AGAATT   TATTTGGG
                                |||| ||||||   ||||||||
                                TACC TCTTAA   ATAGACTT
                                  A     ___
GAM1601  LOC152212 3'  ATGGCAGAATTTATCTGAA   39792         TGA
                                ATGGCAGAATT   TATTTGGG
                                ||||||||||   ||||||||
                                TACCGTCTTAA   ATAGACTT
                                          ___
GAM1601  LOC152267 3'  ATGGCAGAATTTATCTGAA   39792         TGA
                                ATGGCAGAATT   TATTTGGG
                                ||||||||||   ||||||||
                                TACCGTCTTAA   ATAGACTT
                                          ___
GAM1601  LOC254000 3'  TGGCAGAATTTATCTGAA    39809         TGA
                                TGGCAGAATT   TATTTGGG
                                |||||||||   ||||||||
                                ACCGTCTTAA   ATAGACTT
                                          ___
GAM1601  LOC88584  3'  ATGGCAGAATTTATCTGAA   39792         TGA
                                ATGGCAGAATT   TATTTGGG
                                ||||||||||   ||||||||
                                TACCGTCTTAA   ATAGACTT
                                          ___
GAM1602  ANXA9     5'  AGTGGGGGTGTGTGCAGC    39812    C  A       C
                                AG GGG GTGTGTGCG GC
                                || ||| ||||||||| ||
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                                TC CCC CACACACGT CG
                                 A  C       _
GAM1602 CST1    3' GGGGGTGTGTACCATGTAC  39813    A      G  C
                                GGG GTGTGTGC CG GTAC
                                ||| |||||||| || ||||
                                CCC CACACATG GT CATG
                                  C       _ A
GAM1602 FGFRL1  3' GCATGTGTGCGTGCGT     39814    GGGA       C
                                GC   GTGTGTGCG GCGT
                                ||   ||||||||| ||||
                                CG   TACACACGC CGCA
                                 ____       A
GAM1602 NPR1    5' GGGAGTGTGCGTGCGTGT    39815          C  C
                                GGGAGTGTGTG GCG GT
                                |||||||||| ||| ||
                                CCCTCACACGC CGC CA
                                       A  A
GAM1602 RAB33A  5' GCGTGTGTGTGTGCGCGCGT  39816    GGA
                                GCG  GTGTGTGCGCGCGT
                                |||  ||||||||||||||
                                CGC  CACACACGCGCGCA
                                  ACA
GAM1602 SHH     5' GCGGGTGTGTGCGTGTGC    39817      AG      C__
                                GCGGG TGTGTGCG  GC
                                |||||  ||||||||  ||
                                CGCCC ACACACGC  CG
                                   __      ACA
GAM1602 WHSC1   3' CAGACACTGTGTGCGTGTGTA 39818     AG_      CGC
                                CGGG  TGTGTGCG  GTA
                                ||||  ||||||||  |||
                                GTCT  ACACACGC  CAT
                                  GTG       ACA
GAM1602 CAMTA1  3' ACGTGTGTGTGTGTGCGTGT  39819    GGA     C  C
                                GCG  GTGTGTG GCG GT
                                |||  ||||||| ||| ||
                                TGC  CACACAC CGC CA
                                  ACA      A  A
GAM1602 FLJ14084 3' GCGTGAGTGTGTGCGCGTGC  39820    G          C
                                GCG GAGTGTGTGCGCG GT
                                ||| ||||||||||||| ||
                                CGC CTCACACACGCGC CG
                                  A          A
GAM1602 FLJ25473 5' GCGGGAGTGTGTGCTGAGC   39821           GC_
                                GCGGGAGTGTGTGC  GC
                                ||||||||||||||  ||
                                CGCCCTCACACACG  CG
                                        ACT
GAM1602 KIAA0227 3' ACAACTGTGTGTGCGTGTGTAC 39822     GA       CGC
                                GCGG GTGTGTGCG  GTAC
                                ||||  |||||||||  ||||
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                                TGTT  CACACACGC   CATG
                                  GA        ACA
GAM1602  KIAA1904  3'  CAGGTGTGTGTGTGCGTGC   39823     A      C   C
                                CGGG GTGTGTG GCG GT
                                |||| ||||||| ||| ||
                                GTCC CACACAC CGC CG
                                  A      A   A
GAM1602  KIAA1904  3'  GGTGTGTGTGTGCGTGCGT   39824    GA_       C
                                GG   GTGTGTGCG GCGT
                                ||   ||||||||| ||||
                                CC   CACACACGC CGCA
                                 ACA        A
GAM1602  OSBPL2    3'  GCATGAGTGTGTGCGTGCGT   39825     G         C
                                GCG GAGTGTGTGCG GCGT
                                ||| |||||||||| ||||
                                CGT CTCACACACGC CGCA
                                  A          A
GAM1602  OSBPL2    3'  GCATGAGTGTGTGCGTGCGT   39825     G         C
                                GCG GAGTGTGTGCG GCGT
                                ||| |||||||||| ||||
                                CGT CTCACACACGC CGCA
                                  A          A
GAM1602  STK33     5'  GAGTGTGTGTGTGCGTGT    39826     A      C   C
                                GGG GTGTGTG GCG GT
                                ||| ||||||| ||| ||
                                CTC CACACAC CGC CA
                                  A      A   A
GAM1602  LOC147929 5'  GAGACGTGTGTGTGCGCGCGT  39827      ___
                                GGGA   GTGTGTGCGCGCGT
                                ||||   ||||||||||||||
                                CTCT   CACACACGCGCGCA
                                  GCA
GAM1602  LOC255146 5'  GCGGGAGCGTGTGTGATGC    39828            CGC_
                                GCGGGAGTGTGTG    GC
                                ||||||||||||    ||
                                CGCCCTCGCACAC    CG
                                        ACTA
GAM1602  LOC90632  5'  GCTTGTGTGTGCGTGCGT    39829    GGGA       C
                                GC    GTGTGTGCG GCGT
                                ||    ||||||||| ||||
                                CG    CACACACGC CGCA
                                 AA__        A
GAM1603  COL4A6    3'  TAACAATAATTCAGATTATATT 39832            _   T
                                TAACAATAATTCA ATT TATT
                                |||||||||||| ||| ||||
                                ATTGTTATTAAGT TAA ATAA
                                        C   T
GAM1603  COL4A6    3'  TAACAATAATTCAGATTATATT 39832            _   T
                                TAACAATAATTCA ATT TATT
                                |||||||||||| ||| ||||
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                                ATTGTTATTAAGT TAA ATAA
                                      C   T
GAM1603  TACC2    3'  ACAATCAAATCAATTTTATTTA 39833       AAT_
                                ACAAT    TCAATTTTATTTA
                                |||||    |||||||||||||
                                TGTTA    AGTTAAAATAAAT
                                   GTTT
GAM1603  PRKRIR   3'  TAACAAAATTCACATTTTATTT 39834       T     _
            A                    TAACAA AATTCA ATTTTATTTA
                                |||||| |||||| ||||||||||
                                ATTGTT TTAAGT TAAAATAAAT
                                   _     G
GAM1604  CDC42    3'  TTTGAAACAACAAAAAAAAATA 39837      T     __
            GTA                     TTTG AAATAA  AAAAAAAATAGTA
                                |||| ||||||  |||||||||||||
                                AAAC TTTGTT  TTTTTTTTATCAT
                                   _     GT
GAM1604  TACSTD2  3'  TTTGAAATAAAAAAAAAATA   39838     T
                                TTTG AAATAAAAAAAAAATA
                                |||| ||||||||||||||||
                                AAAC TTTATTTTTTTTTTAT
                                   _
GAM1604  KIAA1710 3'  TTTGTAAATAACAAAAAAACA  39839          A
                                TTTGTAAATAA AAAAAAATA
                                |||||||||| |||||||||
                                AAACATTTATT TTTTTTTGT
                                      G
GAM1604  LOC202934 3'  TTGCTAAAAAAAAAATAGTA   39840      AAA
                                TTGT   TAAAAAAAAAATAGTA
                                ||||   ||||||||||||||||
                                AACG   ATTTTTTTTTTATCAT
                                   ____
GAM1604  LOC255465 3'  TTGCTAAAAAAAAAAATAGTA  39841      AAAT
                                TTGT    AAAAAAAAAATAGTA
                                ||||    ||||||||||||||||
                                AACG    TTTTTTTTTTATCAT
                                   AT__
GAM1604  LOC54103  3'  TTTATAAATAAAAAAAAA    39842
                                TTTGTAAATAAAAAAAAA
                                ||||||||||||||||||
                                AAATATTTATTTTTTTTT

GAM1605  ALDH3A2   3'  ATGAAATATGTTCATTTTGAAG 39845      TTCG_
                                GTGA    GTTCATTTTGAAG
                                ||||    ||||||||||||
                                TACT    CAAGTAAAACTTC
                                   TTATA
GAM1605  ZNF24    3'  GACTTATGGTTCATTTTGA   39846      C__
                                GATT   GGTTCATTTTGA
                                ||||   ||||||||||||
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                                CTGA   CCAAGTAAAACT
                                  ATA
GAM1605  LOC151647 3'  TTAGTGGTGATCCATTTTGAAG 39847       ATTC
                                TTAGTG    GGTTCATTTTGAAG
                                ||||||    ||||||||||||||
                                AATCAC    CTAGGTAAAACTTC
                                   CA__
GAM1605  LOC51083  5'  GTGACTCGGTTTTGA       39848          CATT
                                GTGATTCGGTT    TTGA
                                ||||||||||    ||||
                                CACTGAGCCAA    AACT
                                       ____
GAM1606  ETS2      3'  TCGCTCCTTTGAGAATCTCA   39851      AAGGAG   A
                                TCGCT     TTT AGAATCTCA
                                |||||     ||| |||||||||
                                AGCGA     AAA TCTTAGAGT
                                   GG____   C
GAM1606  SLC31A1   3'  TCCTTAAGAGAAATGGGAATCT 39852    G  A    TTTAA_
            CA                    TC CT AGGAG     GAATCTCA
                                || || |||||     ||||||||
                                AG GA TTCTC     CTTAGAGT
                                 _ A    TTTACC
GAM1606  TLR5      5'  TCCTGAGACTATAGGAATCTCA 39853    G  A   AGTT  A
                                TC CT AGG    TA GAATCTCA
                                || || |||    || ||||||||
                                AG GA TCT    AT CTTAGAGT
                                 _ C   GAT_  C
GAM1606  CAMP-GEFII 3'  CGCTGGCAAATTTAAGAATCT  39854      AAG
                                CGCT   GAGTTTAAGAATCT
                                ||||   ||||||||||||||
                                GCGA   TTTAAATTCTTAGA
                                  CCG
GAM1606  FLJ20038  3'  TCTTAGGGAGTCTGATCTC    39855    GC  A      AA  A
                                TC  TA GGAGTTT  GA TCTC
                                ||  || |||||||  || ||||
                                AG  AT CCTCAGA  CT AGAG
                                 A_  C      __ _
GAM1606  FLJ20456  3'  AGATGTGTAAGAATCTCA    39856     _  T
                                GGA GT TAAGAATCTCA
                                ||| || ||||||||||
                                TCT CA ATTCTTAGAGT
                                  A  C
GAM1606  FLJ21069  5'  GCAACCTCTCTTAAGAATCTCA 39857    TAAGGAG
                                GC      TTTAAGAATCTCA
                                ||      ||||||||||||
                                CG      GAATTCTTAGAGT
                                 TTGGAGA
GAM1606  MGC20460  5'  TCCTAAGAAGAAAGGGTCTC   39858    G       TTT   AA
                                TC CTAAGGAG   AAG  TCTC
                                || ||||||||   |||  ||||
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                                AG GATTCTTC   TTC  AGAG
                                 _       T__   CC
GAM1606  LOC200918 3'  TCCTTAAGAGAAATGGGAATCT 39852    G  A    TTTAA_
              CA                  TC CT AGGAG     GAATCTCA
                                || || |||||     ||||||||
                                AG GA TTCTC     CTTAGAGT
                                 _ A    TTTACC
GAM1606  LOC51134  5'  GCTAAGGCAGAATCTC      39859        AGTTTA
                                GCTAAGG     AGAATCTC
                                |||||||     ||||||||
                                CGATTCC     TCTTAGAG
                                    G_____
GAM1607  EHM2     3'  TACCTTTTTTTGTAGTCA     39862        CTC
                                TACCTTTT   GTAGTCG
                                ||||||||   |||||||
                                ATGGAAAA   CATCAGT
                                     AAA
GAM1607  FLJ25449  3'  CCTTTTCTCATGTAAACTGTTT 39863          A  C  G_
                                CCTTTTCTCGT GT GA  GTTT
                                |||||||||||| || ||  ||||
                                GGAAAAGAGTA CA TT  CAAA
                                       _ T  GA
GAM1607  MGC2376  3'  TTTTCTCGTGCAAGTGGTTT   39864        A  CGA_
                                TTTTCTCGT GT    GGTTT
                                |||||||| ||    |||||
                                AAAAGAGCA CG    CCAAA
                                     _ TTCA
GAM1607  SYNCOILIN 3'  ACCTTTTCTCAGAGGTT     39865          TAGTC
                                ACCTTTTCTCG    GAGGTT
                                ||||||||||     ||||||
                                TGGAAAAGAGT    CTCCAA
                                       _____
GAM1608  ALDH8A1   3'  CATGGCTCACTGCAG       39868          CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACCGAGTG  AC GTC
                                     __  _
GAM1608  CUL3     3'  CATGGCTCACTCGAGG      39869          CG   C
                                CATGGCTCAC  TGA GG
                                ||||||||||  ||| ||
                                GTACCGAGTG  GCT CC
                                     A_  _
GAM1608  DCLRE1C  3'  CATGGCTCACTGCAG       39868          CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACCGAGTG  AC GTC
                                     __  _
GAM1608  GLRX2    5'  CACCATGGCTTTGGAAATGGG  39870          CACCGT  C
                                TACCATGGCT     GA GGG
                                ||||||||||     || |||
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                                GTGGTACCGA     TT CCC
                                      AACCT_  A
GAM1608  HS3ST3A1  3'  CACTATGAAAACTGTGACGGG  39871     C    CTC  C
                                TAC ATGG   AC GTGACGGG
                                ||| ||||   || ||||||||
                                GTG TACT   TG CACTGCCC
                                  A   TT_  A
GAM1608  MUC4      3'  CCATTGGACCGTGACGGG    39872      _  CTC
                                CCAT GG   ACCGTGACGGG
                                |||| ||   ||||||||||
                                GGTA CC   TGGCACTGCCC
                                  A  ___
GAM1608  SMAP      5'  ACCATGGCTCTGTGGG      39873         ACC   AC
                                ACCATGGCTC   GTG  GG
                                ||||||||||   |||  ||
                                TGGTACCGAG   CAC  CC
                                      A__   __
GAM1608  TACC1     3'  CATGGCTCACTGCAG       39868         CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACCGAGTG  AC GTC
                                      __  _
GAM1608  ZNF74     3'  CATGGCTCACTGCAG       39868         CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACCGAGTG  AC GTC
                                      __  _
GAM1608  AP4S1     3'  CATGGCTCACTGCAG       39868         CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACCGAGTG  AC GTC
                                      __  _
GAM1608  BACH      3'  CCATGGCTACTCGAGG      39874         C  CG   C
                                CCATGGCT AC  TGA GG
                                ||||||||  ||  ||| ||
                                GGTACCGA TG  GCT CC
                                     _  A_  _
GAM1608  CHERP     5'  CCATGGCTCCGGCCGCGGG   39875          ACC  GA
                                CCATGGCTC   GT  CGGG
                                |||||||||   ||  ||||
                                GGTACCGAG   CG  GCCC
                                     GC_  GC
GAM1608  DKFZP434O047 5'  TACCATGGGTCCCCATGGG   39876         C  A    AC
                                TACCATGG TC CCGTG  GG
                                ||||||||  || |||||  ||
                                ATGGTACC AG GGTAC  CC
                                     C  G    __
GAM1608  FLJ11259  3'  CATGGCTCACTGCAG       39868         CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
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                                GTACCGAGTG  AC GTC
                                   __  _
GAM1608  FLJ14466  3'  TACCATAGCTCACTGCAG    39877          CG  A
                                TACCATGGCTCAC  TG CGG
                                |||||||||||||  || |||
                                ATGGTATCGAGTG  AC GTC
                                   __  _
GAM1608  GMFB      3'  CATGGCTCAATACTGGG     39878        CC   AC
                                CATGGCTCA  GTG  GGG
                                |||||||||  |||  |||
                                GTACCGAGT  TAT  CCC
                                     __  GA
GAM1608  KIAA0090  3'  CCATGGCTTGCCAGAGAGG   39879        CA   T  C
                                CCATGGCT  CCG GA GGG
                                ||||||||  ||| || |||
                                GGTACCGA  GGT CT TCC
                                     AC  _  C
GAM1608  KIAA0429  5'  CATGGCTCATCCAACGG     39880         _  GT
                                CATGGCTCA CC  GACGG
                                |||||||||  ||  |||||
                                GTACCGAGT GG  TTGCC
                                     A  __
GAM1608  KIAA0451  3'  TGTGCTCACCAGACATGGG   39881    _       T  __
                                TG GCTCACCG GAC  GGG
                                || ||||||||  |||  |||
                                AC CGAGTGGT CTG  CCC
                                 A       _  TA
GAM1608  KIAA0853  3'  CATGGCTCACTGCAG       39868         CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACCGAGTG  AC GTC
                                   __  _
GAM1608  KIAA1023  3'  CCATGGCTCCATGGG       39882         CA    AC
                                CCATGGCT  CCGTG  GG
                                ||||||||  |||||  ||
                                GGTACCGA  GGTAC  CC
                                   __    __
GAM1608  KIAA1091  5'  CCGCGGCTGCCGTGACGGG   39883    A    CA
                                CC TGGCT  CCGTGACGGG
                                || |||||  ||||||||||
                                GG GCCGA  GGCACTGCCC
                                 C    C_
GAM1608  KIAA1423  3'  CATGGCTCACTGCAG       39868         CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACCGAGTG  AC GTC
                                   __  _
GAM1608  KIAA1771  3'  CATGGCTCACTGCAG       39868         CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
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                                GTACCGAGTG  AC GTC
                                      __  _
GAM1608  MGC10999  3'  ACTGTGGCTCACTGCAG     39884    CA      CG  A
                                AC  TGGCTCAC  TG CGG
                                ||  ||||||||  || |||
                                TG  ACCGAGTG  AC GTC
                                 AC       __  _
GAM1608  MGC16384  3'  ACCATGGCTCACTGCAG     39885          CG  A
                                ACCATGGCTCAC  TG CGG
                                ||||||||||||  || |||
                                TGGTACCGAGTG  AC GTC
                                      __  _
GAM1608  MGC29891  3'  ACCATGGCTCACTGCAG     39885          CG  A
                                ACCATGGCTCAC  TG CGG
                                ||||||||||||  || |||
                                TGGTACCGAGTG  AC GTC
                                      __  _
GAM1608  NAV3      3'  TACCATGGCCTAGCCCTTGGG  39886         CA__  GTGAC
                                TACCATGGCT    CC    GGG
                                ||||||||||    ||    |||
                                ATGGTACCGG    GG    CCC
                                      ATCG  AA___
GAM1608  RNO2      5'  CATGGCTCACTGTAGG       39887          C   AC
                                CATGGCTCAC GTG  GG
                                |||||||||| |||  ||
                                GTACCGAGTG CAT  CC
                                      A  __
GAM1608  SPTLC2    3'  CATGGCTCACTGCAG        39868          CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACCGAGTG  AC GTC
                                      __  _
GAM1608  THEA      3'  CATGGCTCACTGCAG        39868          CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACCGAGTG  AC GTC
                                      __  _
GAM1608  LOC120114 3'  TACCATGGCCACTGCACAGG   39888          T   C  G
                                TACCATGGC CAC GT ACGGG
                                ||||||||| ||| || |||||
                                ATGGTACCG GTG CG TGTCC
                                      _   A  _
GAM1608  LOC126906 3'  TACCATAGCTTATTGGCCCGTC 39889          CA_________   TGA
                  ACG                  ACCATGGCT         CCG   CG
                                |||||||||         |||   ||
                                TGGTATCGA         GGC   GC
                                      ATAACCIIIG   AGT
GAM1608  LOC143909 5'  ACCGTGGCTCACCTCGG      39890      A       GTGA
                                ACC TGGCTCACC    CGG
                                ||| |||||||||    |||
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                                TGG ACCGAGTGG    GCC
                                  C        A___
GAM1608  LOC145225 3'  CCATGGCTCCCCTAAGGG    39891          A  G   C
                                CCATGGCTC CC TGA GGG
                                ||||||||| || ||| |||
                                GGTACCGAG GG ATT CCC
                                     _ G   _
GAM1608  LOC147077 5'  CCTGGCTCACATCTGTGACGGG 39892    A       C___
                                CC TGGCTCAC    GTGACGGG
                                || ||||||||    ||||||||
                                GG ACCGAGTG    CACTGCCC
                                 _       TAGA
GAM1608  LOC152317 3'  CATGGCTCACTGCAG       39868          CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACCGAGTG  AC GTC

                                     __  _
GAM1608  LOC158337 3'  TACCATGGCTCTTGATGCCCGT 39893         A__________   TGA
                  CACGG                CATGGCTC         CCG   CGG
                                ||||||||         |||   |||
                                GTACCGAG         GGC   GCC
                                     AACTACIIIG   AGT
GAM1608  LOC196812 3'  TACTATGCTCACCACCTGGTGA 39894     CATG      _____   C
                  TGGG                 TAC    GCTCACC     GTGA GGG
                                |||    |||||||     |||| |||
                                ATG    CGAGTGG     CACT CCC
                                  ATA_      TGGAC    A
GAM1608  LOC197114 3'  CATGGCTCCCTGGTGATGGG   39895         A __    C
                                CATGGCTC CC  GTGA GGG
                                |||||||| ||  |||| |||
                                GTACCGAG GG  CACT CCC
                                     _ AC    A
GAM1608  LOC220070 3'  CATGGCTCACTGCAG       39868          CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACCGAGTG  AC GTC

                                     __  _
GAM1608  LOC220549 3'  CATGGCTCACTGCAG       39868          CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACCGAGTG  AC GTC

                                     __  _
GAM1608  LOC220739 3'  TACTGTGGCCCACACCGGCGGG 39896     CA       CG  A
                                TAC  TGGCTCAC  TG CGGG
                                |||  ||||||||  || ||||
                                ATG  ACCGGGTG  GC GCCC
                                  AC       TG  C
GAM1608  LOC221288 3'  ATGGCCCACTCTAAATATGGG  39897         CG   C___
                                ATGGCTCAC  TGA    GGG
                                |||||||||  |||    |||
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                                TACCGGGTG  ATT   CCC
                                     AG   TATA
GAM1608  LOC91250  5'  CATGGCTCACTGCAGG     39898         CG  A
                                CATGGCTCAC  TG CGGG
                                ||||||||||  || ||||
                                GTACCGAGTG  AC GTCC
                                     __  _
GAM1608  LOC91664  3'  TACCATGGATTGCCTGATGG   39899        CTCA  G   C
                                TACCATGG   CC TGA GG
                                ||||||||   || ||| ||
                                ATGGTACC   GG ACT CC
                                     TAAC  _   A
GAM1608  LOC92568  3'  CATGACTCACTGCAG       39900         CG  A
                                CATGGCTCAC  TG CGG
                                ||||||||||  || |||
                                GTACTGAGTG  AC GTC
                                     __  _
GAM1609  LOC90624  3'  TTTGATCAAGGGCCACTA    39903         TTCGTC
                                TTTGATCGAG     GCCACTA
                                ||||||||||     |||||||
                                AAACTAGTTC     CGGTGAT
                                     C_____
GAM1610  NEU3      3'  GACTTCAGTAGCTTCTGT    39906      ATGTA TG     C
                                GACT    T  GTAGCT CTGT
                                ||||    |  |||||| ||||
                                CTGA    A  CATCGA GACA
                                  _____ GT     A
GAM1610  PAPSS1    3'  GACTATGTGGTCCCCT      39907        ATT   AG
                                GACTATGT   GGT  CTCCT
                                ||||||||   |||  |||||
                                CTGATACA   CCA  GGGGA
                                     ___   __
GAM1610  G2        3'  GACTGTGGTTCTACCACTCCTG 39908      A  TA  GGTA
            T                    GACT TG  TT   GCTCCTGT
                                ||||  ||  ||   ||||||||
                                CTGA AC  AG   TGAGGACA
                                  C  CA  ATGG
GAM1610  KLK15     3'  CGCCCTGGGTAGCTCTTGTC   39909     ATT_      C
                                TGT   GGTAGCTC TGTC
                                |||   |||||||| ||||
                                GCG   CCATCGAG ACAG
                                  GGAC       A
GAM1610  MGC10612  3'  GACTGTGTGGCTCCTGT     39910      A   ATTGGTA
                                GACT TGT      GCTCCTGT
                                ||||  |||     ||||||||
                                CTGA ACA      CGAGGACA
                                  C   C_______
GAM1610  MGC5466   3'  GATAATGTATTGGGATAACTCT 39911     CT       __     C
            GT                    GA  ATGTATTGG  TAGCTC TGT
                                ||  |||||||||  |||||| |||
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                                CT  TACATAACC  ATTGAG ACA
                                 AT        CT     _
GAM1610  LOC158187 3'  GACAATGTTACAGGGCTTCTGT 39912     T    _  T  TA   C
                                GAC ATGT AT GG  GCT CTGT
                                ||| |||| || ||  ||| ||||
                                CTG TACA TG CC  CGA GACA
                                  T   A  T  __   A
GAM1610  LOC254749 5'  ACTATGCAGTGGTTTTTGTC  39913         T    AGCTCC
                                ACTATGTA TGGT     TGTC
                                |||||||| ||||     ||||
                                TGATACGT ACCA     ACAG
                                     C    AAA___
GAM1610  LOC255925 3'  GACTATGTTATTGGTGAAGGTG 39914         _     AGCTCC
              TC                  GACTATGT ATTGGT     TGTC
                                |||||||| ||||||     ||||
                                CTGATACA TAACCA     ACAG
                                     A     CTTCC_
GAM1611  APP      3'  TGAACAGGGATTCTTTTC    39917         AG  GCG
                                TGAGCAGG  TT   CTTTTC
                                ||||||||  ||   ||||||
                                ACTTGTCC  AA   GAAAAG
                                     CT  ___
GAM1611  CHRNB2    5'  TGAGCAGGCGGAGGCTTTTC   39918         AGTTGC
                                TGAGCAGG     GCTTTTC
                                ||||||||     |||||||
                                ACTCGTCC     CGAAAAG
                                     GCCTC_
GAM1611  DUSP1     5'  GCAGGGCGGCGCTTTTC     39919      A  T
                                GCAGG GT GCGCTTTTC
                                ||||| || |||||||||
                                CGTCC CG CGCGAAAAG
                                   _  C
GAM1611  FKRP     3'  TGGGCAGAACACTTTT      39920     A    AGTT
                                TG GCAGG    GCGCTTTT
                                || |||||    ||||||||
                                AC CGTCT    TGTGAAAA
                                 C    ____
GAM1611  HD       3'  TGAGCAGGGGCTCCCTTTC   39921         A   GCG
                                TGAGCAGG GTT   CTTTTC
                                |||||||| |||   ||||||
                                ACTCGTCC CGA   GGAAAG
                                     C   G__
GAM1611  IL20RA   3'  TGAGAGGACACTTTT      39922      C   AGTT
                                TGAG AGG    GCGCTTTT
                                |||| |||    ||||||||
                                ACTC TCC    TGTGAAAA
                                  _  ____
GAM1611  LSP1     3'  TGATCAGGAGTTTCTTTC    39923     G      GCG
                                TGA CAGGAGTT   CTTTT
                                ||| ||||||||   |||||
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                                ACT GTCCTCAA  GAAAG
                                  A      A__
GAM1611  MAN2B1   5'  GAGCAGAAGTGCTTTTC    39924        TGC
                                GAGCAGGAGT  GCTTTTC
                                ||||||||||  |||||||
                                CTCGTCTTCA  CGAAAAG
                                          ___
GAM1611  MLLT2    3'  GAGCGGGGGTTGCCTTC    39925    A A   G
                                GAGC GG GTTGC CTTT
                                |||| || ||||| ||||
                                CTCG CC CAACG GAAG
                                  C C   _
GAM1611  MTNR1B   3'  TGAGAAGGAGTTGGGCTC   39926    C     C
                                TGAG AGGAGTTG GCTT
                                |||| |||||||| ||||
                                ACTC TCCTCAAC CGAG
                                  T      C
GAM1611  MYO1C    3'  TGGCAGAGGCGCTTTT     39927   A   G  TT
                                TG GCAG AG  GCGCTTTT
                                || |||| ||  ||||||||
                                AC CGTC TC  CGCGAAAA
                                 _   _ __
GAM1611  OLFM1    5'  TGGGCGGGAGCTGCGCCCTC  39928   A  A
                                TG GC GGAGTTGCGCTTTT
                                || || ||||||||||||||
                                AC CG CCTCGACGCGGGAG
                                 C  C
GAM1611  OLFM1    5'  TGGGCGGGAGCTGCGCCCTC  39928   A  A
                                TG GC GGAGTTGCGCTTTT
                                || || ||||||||||||||
                                AC CG CCTCGACGCGGGAG
                                 C  C
GAM1611  OLFM1    5'  TGGGCGGGAGCTGCGCCCTC  39928   A  A
                                TG GC GGAGTTGCGCTTTT
                                || || ||||||||||||||
                                AC CG CCTCGACGCGGGAG
                                 C  C
GAM1611  PMX1     3'  TAAGTAGCCATGGCGCTTTTC 39929    C  GA  T
                                TGAG AG  GT GCGCTTTTC
                                |||| ||  || |||||||||
                                ATTC TC  TA CGCGAAAAG
                                  A  GG  C
GAM1611  RHCE     3'  TGAACAGGCCTTGTTTTTC   39930      AG   CGC
                                TGAGCAGG  TTG   TTTTC
                                ||||||||  |||   |||||
                                ACTTGTCC  AAC   AAAAG
                                    GG   A__
GAM1611  RHCE     3'  TGAACAGGCCTTGTTTTTC   39930      AG   CGC
                                TGAGCAGG  TTG   TTTTC
                                ||||||||  |||   |||||
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                                ACTTGTCC AAC  AAAAG
                                    GG  A__
GAM1611 RHCE    3' TGAACAGGCCTTGTTTTTC  39930      AG  CGC
                                TGAGCAGG TTG  TTTTC
                                |||||||| |||  |||||
                                ACTTGTCC AAC  AAAAG
                                    GG  A__
GAM1611 RHCE    3' TGAACAGGCCTTGTTTTTC  39930      AG  CGC
                                TGAGCAGG TTG  TTTTC
                                |||||||| |||  |||||
                                ACTTGTCC AAC  AAAAG
                                    GG  A__
GAM1611 RHD     3' TGAACAGGCCTTGTTTTTC  39930      AG  CGC
                                TGAGCAGG TTG  TTTTC
                                |||||||| |||  |||||
                                ACTTGTCC AAC  AAAAG
                                    GG  A__
GAM1611 RHD     3' TGAACAGGCCTTGTTTTTC  39930      AG  CGC
                                TGAGCAGG TTG  TTTTC
                                |||||||| |||  |||||
                                ACTTGTCC AAC  AAAAG
                                    GG  A__
GAM1611 THRB    5' GAGCAGGAGGTCTCTTTTC  39931       TTGCG
                                GAGCAGGAG   CTTTTC
                                |||||||||   ||||||
                                CTCGTCCTC   GAAAAG
                                     CAGA_
GAM1611 AP1G2   5' GAGCAGGGGTTGGTGCTC   39932      A  C_
                                GAGCAGG GTTG GCTT
                                ||||||| |||| ||||
                                CTCGTCC CAAC CGAG
                                    C  CA
GAM1611 AP1G2   5' GAGCAGGGGTTGGTGCTC   39932      A  C_
                                GAGCAGG GTTG GCTT
                                ||||||| |||| ||||
                                CTCGTCC CAAC CGAG
                                    C  CA
GAM1611 DKFZP727G051 3' TGGGCTAGGGGTTGGCTT   39933   A _ A  C
                                TG GC AGG GTTG GCTT
                                || || ||| |||| ||||
                                AC CG TCC CAAC CGAA
                                 C A  C  _
GAM1611 FLJ11193 5' CGGGCGGAAGCGCTTTT    39934   A A  TT
                                TG GC GGAG GCGCTTTT
                                || || ||||  ||||||||
                                GC CG CCTT CGCGAAAA
                                 C _  __
GAM1611 FLJ11413 3' TGAGCAGGAATGCCTC     39935       T G
                                TGAGCAGGAGT GC CTT
                                |||||||||| || |||
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                                ACTCGTCCTTA CG GAG
                                      _ _
GAM1611  FLJ13385  3'  AGCAGGAGTGTGAACTTTC   39936        _ C
                                AGCAGGAGT TG GCTTTT
                                ||||||||| || ||||||
                                TCGTCCTCA AC TGAAAG
                                    C  T
GAM1611  FLJ20856  3'  TGAGTGGAGTTTACACTTC   39937     CA    _
                                TGAG  GGAGTT GCGCTTT
                                ||||  |||||| |||||||
                                ACTC  CCTCAA TGTGAAG
                                  A_    A
GAM1611  FLJ20967  3'  TGAGCAGAGGTCATTTTC   39938       GA   CGC
                                TGAGCAG  GTTG   TTTTC
                                |||||||  ||||   |||||
                                ACTCGTC  CAGT   AAAAG
                                    TC   ____
GAM1611  HSPC009   3'  TGAGCAGGATTCAATTTC   39939        GTTG  CT
                                TGAGCAGGA   CG  TTTC
                                |||||||||   ||  ||||
                                ACTCGTCCT   GT  AAAG
                                     AA__  T_
GAM1611  IL14      5'  TGAGCAGGGCTTGCTT     39940        A  GC
                                TGAGCAGG GTT  GCTT
                                |||||||| |||  ||||
                                ACTCGTCC CGA  CGAA
                                    _  A_
GAM1611  KIAA0916  3'  TGAGCAGAGTTTAAACTTC   39941       G   GC_
                                TGAGCAG AGTT   GCTTT
                                ||||||| ||||   |||||
                                ACTCGTC TCAA   TGAAG
                                    _   ATT
GAM1611  KIAA1023  3'  GCAGGAGTCCCTTTC      39942        GCG
                                GCAGGAGTT   CTTTTC
                                |||||||||   ||||||
                                CGTCCTCAG   GGAAAG
                                     ____
GAM1611  MGC11082  3'  TGGCAGGAGTTAGCTTC    39943    A       C
                                TG GCAGGAGTTG GCTTT
                                || |||||||||| |||||
                                AC CGTCCTCAAT CGAAG
                                  _       _
GAM1611  PTPN21    3'  TGAGTTAGGCAAGCGCTTTT  39944     C_  AGTT
                                TGAG  AGG   GCGCTTTT
                                ||||  |||   ||||||||
                                ACTC  TCC   CGCGAAAA
                                  AA  GTT_
GAM1611  SSH2      3'  TGGGCAAGAGTCAAAGTTTTTC 39945    A       GCGC_
                                TG GCAGGAGTT    TTTTC
                                || |||||||||    |||||
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                                AC CGTTCTCAG     AAAAG
                                 C        TTTCA
GAM1611  LOC133688 3'  TGGCAGGGGTTCTCCTTC    39946    A     A   GCG
                                TG GCAGG GTT   CTTTT
                                || ||||| |||   |||||
                                AC CGTCC CAA   GGAAG
                                 _    C   GA_
GAM1611  LOC137991 5'  GCGGGAGCCAGGGCTTTTC    39947    A     GC_
                                GC GGAGTT   GCTTTTC
                                || ||||||   |||||||
                                CG CCTCGG   CGAAAAG
                                 C     TCC
GAM1611  LOC144848 3'  TGAGCAGGAGTCTGGTGCC    39948           GC__
                                TGAGCAGGAGTT    GCT
                                ||||||||||||    |||
                                ACTCGTCCTCAG    CGG
                                       ACCA
GAM1611  LOC148760 3'  TGAGCAGGATTTTATGACTTC  39949         GT___  C
                                TGAGCAGGA     TG GCTTT
                                |||||||||     || |||||
                                ACTCGTCCT     AC TGAAG
                                      AAAAT  _
GAM1611  LOC149501 3'  TGGGCAGGAGTCGGAGGACTC  39950    A         C___
                                TG GCAGGAGTTG    GCTT
                                || ||||||||||    ||||
                                AC CGTCCTCAGC    TGAG
                                 C         CTCC
GAM1611  LOC149653 3'  TGGGCAGGAGTGCCCTTT    39951    A       T  G
                                TG GCAGGAGT GC CTTT
                                || |||||||| || ||||
                                AC CGTCCTCA CG GAAA
                                 C       _  G
GAM1611  LOC151234 3'  TGAACAGGATTTGCGTTTTT   39952         G     C
                                TGAGCAGGA TTGCG TTTT
                                ||||||||| ||||| ||||
                                ACTTGTCCT AACGC AAAA
                                      A     A
GAM1611  LOC154007 3'  TGAGAATCAGAGCGCTTTT    39953      ___    AGTT
                                TGAG   CAGG    GCGCTTTT
                                ||||   ||||    ||||||||
                                ACTC   GTCT    CGCGAAAA
                                  TTA   _____
GAM1611  LOC157931 5'  GAGCAGGAAATGTTTTTC     39954         T  CGC
                                GAGCAGGAG TG   TTTTC
                                ||||||||| ||   |||||
                                CTCGTCCTT AC   AAAAG
                                      T  A__
GAM1611  LOC158527 5'  TGGGCAGAAGTTGGAACACTTT 39955    A         ___
                                TG GCAGGAGTTG   CGCTTT
                                || ||||||||||   ||||||
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                                AC CGTCTTCAAC   GTGAAA
                                 C        CTT
GAM1611  LOC219513 5'  TGAACAGGAATTTGCTTTT   39956          GC
                                TGAGCAGGAGTT  GCTTTT
                                ||||||||||||  ||||||
                                ACTTGTCCTTAA  CGAAAA
                                       A_
GAM1611  LOC255097 5'  GAGCAGGAGTCTTCTTTTC   39957          GCG
                                GAGCAGGAGTT   CTTTTC
                                ||||||||||   ||||||
                                CTCGTCCTCAG   GAAAAG
                                       AA_
GAM1612  EIF2AK3   3'  TGAGGGCTATAAAGCTTG    39960     A   CT  GATCT
                                TGA GGC  TA    GAGCTTG
                                ||| |||  ||    |||||||
                                ACT CCG  AT    TTCGAAC
                                  C   AT  _____
GAM1612  GFRA2     3'  AGCCTTGGTTAAGCTTGG    39961       AGATC
                                GGCCTT    TGAGCTTGG
                                ||||||    |||||||||
                                TCGGAA    ATTCGAACC
                                   CCA__
GAM1612  NTF5      3'  GGTCCTTAGATCAGCTGG    39962    _      TG   T
                                GG CCTTAGATC  AGCT GG
                                || |||||||||  |||| ||
                                CC GGAATCTAG  TCGA CC
                                 A        __   _
GAM1612  ODF2      3'  TGAGAGGTTTGCACTGAGCTTG 39963     _  CCTTAGAT
              G                  TGA AGG       CTGAGCTTGG
                                 ||| |||       ||||||||||
                                 ACT TCC       GACTCGAACC
                                   C   AAACGT__
GAM1612  DKFZP564I0422 3'  TGAGGCCTTACCTAGTTTGG   39964     A     AG   G  C
                                TGA GGCCTT  ATCT AG TTGG
                                ||| ||||||  |||| || ||||
                                ACT CCGGAA  TGGA TC AACC
                                  _     __    _ A
GAM1612  MGC15854  5'  TGAGGGCCTGGATCTGAG    39965     A    TA
                                TGA GGCCT  GATCTGAG
                                ||| |||||  ||||||||
                                ACT CCGGA  CTAGACTC
                                  C    C_
GAM1612  PMF1      3'  TAAAGGCCCCTGGGCTTG    39966         TAGAT   A
                                TGAAGGCCT    CTG GCTTG
                                |||||||||    ||| |||||
                                ATTTCCGGG    GAC CGAAC
                                       _____  C
GAM1612  RASD2     3'  TGGAGGCCGTGGATCTGAACTG 39967    A    TTA       T
              G                  TG AGGCC   GATCTGAGCT GG
                                 || |||||   |||||||||| ||
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                                AC TCCGG   CTAGACTTGA CC
                                 C    CAC       _
GAM1612  LOC144508 5'  GGCACATGGATCTGAGCTTGG  39968     CTTA_
                                GGC    GATCTGAGCTTGG
                                |||    ||||||||||||
                                CCG    CTAGACTCGAACC
                                  TGTAC
GAM1612  LOC147160 5'  TGAGGGCCCTAGAGCTTG    39969     A       TCTGA
                                TGA GGCCTTAGA    GCTTG
                                ||| |||||||||    |||||
                                ACT CCGGGATCT    CGAAC
                                  C       _____
GAM1612  LOC196410 3'  TGAGTGCCTTGGAGCTTG    39970     AG    AGATCT
                                TGA  GCCTT     GAGCTTG
                                |||  |||||     |||||||
                                ACT  CGGAA     CTCGAAC
                                  CA    C_____
GAM1612  LOC197003 3'  TGGGGGCCTTAATCTTTG    39971    AA     A    GAGC
                                TG  GGCCTT GATCT    TTG
                                ||  |||||| |||||    |||
                                AC  CCGGAA TTAGA    AAC
                                 CC     _    ____
GAM1612  LOC204084 3'  TGAAGATGAATTTCTGAGCTTG 39972       CCTTAGA
           G                     TGAAGG      TCTGAGCTTGG
                                ||||||      ||||||||||
                                ACTTCT      AGACTCGAACC
                                   ACTTAA_
GAM1612  LOC221398 3'  TGGAGGCCTTAGTCCTTG    39973    A       A  TGAG
                                TG AGGCCTTAG TC    CTTG
                                || |||||||| ||    ||||
                                AC TCCGGAATC AG    GAAC
                                 C       _ ____
GAM1613  B4GALT5   3'  GTGTACTTGATGGTAATTATG  39976     _ A_   A
                                GTG AC  GAT GTAATTATG
                                ||| ||  ||| |||||||||
                                CAC TG  CTA CATTAATAC
                                  A  AA   C
GAM1613  DLG5      3'  TGATAGTGACAATAACCATTAT 39977           A   TA
           G                     TGATAGTGACAG TAG  ATTATG
                                ||||||||||| |||  ||||||
                                ACTATCACTGTT ATT  TAATAC
                                      _  GG
GAM1614  CTNND2    5'  TTGCCCAACTGCAGCATC    39980        G    ACACC
                                TTGCCCAA TGCA    GTGTC
                                |||||||| ||||    |||||
                                AACGGGTT ACGT    CGTAG
                                   G    _____
GAM1614  MAOB      3'  TTACCCAAGTGTGTACTGTCC  39981          CAAC  CG
                                TTGCCCAAGTG   AC  TGTCC
                                ||||||||||   ||  |||||
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                                AATGGGTTCAC   TG  ACAGG
                                      ACA_  __
GAM1614  NAB2     5'  CCCCGCGCACGATGCCGTGTCC 39982     AA    ACA__
                                CCC  GTGCA    CCGTGTCC
                                |||  |||||    ||||||||
                                GGG  CGCGT    GGCACAGG
                                  G_    GCTAC
GAM1614  TFCP2    5'  TTGCCCCAGGAGACACCGTGTC 39983       A  TGCA
                                TTGCCC AG    ACACCGTGTC
                                ||||||  ||   ||||||||||
                                AACGGG TC    TGTGGCACAG
                                   G  CTC_
GAM1614  ARF6     3'  TTACCCAAGAACTGCTGTGT   39984        T  AACACC
                                TTGCCCAAG GC     GTGT
                                |||||||||  ||     ||||
                                AATGGGTTC TG     CACA
                                      T  ACGA__
GAM1614  HGRG8    3'  CCAAGTGCAAATGTC       39985         CACC
                                CCAAGTGCAA    GTGTC
                                ||||||||||    |||||
                                GGTTCACGTT    TACAG
                                      _____
GAM1614  KIAA1724 3'  CCAAGTGCAGCCTGTCC     39986        ACA  G
                                CCAAGTGCA   CC TGTCC
                                |||||||||   ||  |||||
                                GGTTCACGT   GG ACAGG
                                      C__  _
GAM1614  TREX1    5'  TGCAGCAGCAGCACCGTGTCC  39987     CCA  _   A
                                TGC   AGT GCA CACCGTGTCC
                                |||   ||| ||| ||||||||||
                                ACG   TCG CGT GTGGCACAGG
                                  ___   T   C
GAM1614  TREX1    5'  TGCAGCAGCAGCACCGTGTCC  39987     CCA  _   A
                                TGC   AGT GCA CACCGTGTCC
                                |||   ||| ||| ||||||||||
                                ACG   TCG CGT GTGGCACAGG
                                  ___   T   C
GAM1614  LOC131368 3'  CCCAAGTGACATGTGTC     39988        CA   CC
                                CCCAAGTG  ACA  GTGTC
                                ||||||||  |||  |||||
                                GGGTTCAC  TGT  CACAG
                                      __   A_
GAM1614  LOC201191 3'  GCCCAAGTGCAGCGC       39989          ACACC
                                GCCCAAGTGCA    GTGT
                                ||||||||||    ||||
                                CGGGTTCACGT    CGCG
                                      _____
GAM1614  LOC257464 5'  CAAGGTGACGCCGTGTCC    39990      _  CA  A
                                CAAG TG  AC CCGTGTCC
                                ||||  ||  ||  ||||||||
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                                GTTC AC  TG GGCACAGG
                                  C __  C
GAM1614 LOC90119 5' TTGCCTACCACCGTGT     39991      CAAG   AA
                                TTGCC    TGC  CACCGTGT
                                |||||    |||  ||||||||
                                AACGG    ATG  GTGGCACA
                                  _____  __
GAM1615 INHBB    3' AGCCCCCTCTTCTCTCCCT   39994    A      ___  C
                                AG CCCCCTC   TC CCCT
                                || |||||||   || ||||
                                TC GGGGGAG   AG GGGA
                                 _     AAG  A
GAM1615 JUNB     3' GATCGCCCCCTCTTCCCC    39995      GCAGA      C
                                GATCG    CCCCCTCT CCCC
                                |||||    |||||||| ||||
                                CTAGC    GGGGGAGA GGGG
                                  ______       A
GAM1615 LEP      3' GGCAGACCCCAAACCTCC    39996         C__
                                GGCAGACCCC   TCTCC
                                ||||||||||   |||||
                                CCGTCTGGGG   GGAGG
                                     TTT
GAM1615 MAL      3' TCAGCAGAGGATCTTTCTTTCC 39997        CCCC  C  CC_
           T                     TCGGCAGA   CT TC   CCT
                                 ||||||||   || ||   |||
                                 AGTCGTCT   GA AG   GGA
                                     CCTA  A  AAA
GAM1615 MAL      3' TCAGCAGAGGATCTTTCTTTCC 39997        CCCC  C  CC_
           T                     TCGGCAGA   CT TC   CCT
                                 ||||||||   || ||   |||
                                 AGTCGTCT   GA AG   GGA
                                     CCTA  A  AAA
GAM1615 MAL      3' TCAGCAGAGGATCTTTCTTTCC 39997        CCCC  C  CC_
           T                     TCGGCAGA   CT TC   CCT
                                 ||||||||   || ||   |||
                                 AGTCGTCT   GA AG   GGA
                                     CCTA  A  AAA
GAM1615 MAL      3' TCAGCAGAGGATCTTTCTTTCC 39997        CCCC  C  CC_
           T                     TCGGCAGA   CT TC   CCT
                                 ||||||||   || ||   |||
                                 AGTCGTCT   GA AG   GGA
                                     CCTA  A  AAA
GAM1615 NEUD4    3' GGCTTCCCCCTCTCCCCC    39998     AGA
                                GGC   CCCCCTCTCCCCC
                                |||   |||||||||||||
                                CCG   GGGGGAGAGGGGG
                                  AA_
GAM1615 WRN      5' GAGCGGAGACCCCCTCTTCCCC 39999    T  C        C
           T                     GA CGG AGACCCCCTCT CCCCT
                                 || ||| |||||||||| |||||
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                                CT GCC TCTGGGGGAGA GGGGA
                                 C  _         A
GAM1615 20D7-FC4 3' TCTGCCCCCCTCTTCCTCT   40000    G  AGA      C  C
                                TC GC   CCCCCTCT CC CT
                                || ||   |||||||| || ||
                                AG CG   GGGGGAGA GG GA
                                 A ___      A  A
GAM1615 BCAA     5' CCAGAGTCCCCTCTCTCC    40001     C  A   _
                                TCGG AG CCCC CTCTCC
                                |||| || |||| ||||||
                                GGTC TC GGGG GAGAGG
                                  _ A   A
GAM1615 BIRC1    3' GATTGGCAGACCTGTCCCCAAC 40002     C      C__   TC
             CCCT                   GAT GGCAGACC   CCTC  CCCCT
                                ||| ||||||||   ||||  |||||
                                CTA CCGTCTGG   GGGG  GGGGA
                                  A       ACA    TT
GAM1615 C5orf6   3' TCGGCAGACCCCTTCCTTCCCT 40003          C   CC
                                TCGGCAGACCCC TCT  CCCT
                                |||||||||||| |||  ||||
                                AGCCGTCTGGGG AGG  GGGA
                                       A   AA
GAM1615 CITED1   5' GAAGGACAGACCCTTTTTTTCC 40004    TC       CCTC__
             C                   GA  GGCAGACCC     TCCC
                                ||  |||||||||     ||||
                                CT  CTGTCTGGG     AGGG
                                 TC       AAAAAA
GAM1615 DKFZp434G171 5' GATCGGCAGGTGCCAAACTTCC 40005         AC_  CCT  C
                                GATCGGCAG   CC   CT CC
                                |||||||||   ||   || ||
                                CTAGCCGTC   GG   GA GG
                                     CAC  TTT  A
GAM1615 FLJ14594 3' ATCGGCAGACCTGTCCCC    40006          CCCTC
                                ATCGGCAGACC    TCCCC
                                ||||||||||    |||||
                                TAGCCGTCTGG    AGGGG
                                       AC___
GAM1615 FLJ20294 3' TCGGCAGATCACCAGGTCTCC  40007        ___  CCC
                                TCGGCAGA   CC   TCTCC
                                ||||||||   ||   |||||
                                AGCCGTCT   GG   AGAGG
                                    AGT  TCC
GAM1615 FLJ22938 3' TCTGCAATTTCCTCTCCCCCT  40008    G    ACCC
                                TC GCAG    CCTCTCCCCCT
                                || ||||    ||||||||||
                                AG CGTT    GGAGAGGGGGA
                                 A   AAA_
GAM1615 KIAA1086 3' GATTGGGGACCCCCTGCC    40009     C  CA      _
                                GAT GG  GACCCCCT CT
                                ||| ||  |||||||| ||
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                                CTA CC  CTGGGGGA GG
                                  A  C_       C
GAM1615  MGC16121  5'  GCTCACCCTTCCTCTCCCC   40010    AG   __
                                GC  ACCC  CCTCTCCCC
                                ||  ||||  |||||||||
                                CG  TGGG  GGAGAGGGG
                                 AG    AA
GAM1615  NFASC     3'  GATCTCCCCCTCTCCTC     40011     GGCAGA        CC
                                GATC     CCCCCTCTCC  C
                                ||||     ||||||||||  |
                                CTAG     GGGGGGAGAGG  G
                                  A_____         AA
GAM1615  LOC134853 5'  ATCGGCGGCTGCATCCTTCTCC 40012       AGACC___  C    C
              TCCT                    ATCGGC       CC TCTCC CCT
                                ||||||       || ||||| |||
                                TAGCCG       GG AGAGG GGA
                                    CCGACGTA  A     A
GAM1615  LOC147341 5'  CCAGCCCCCCTCTTTCTTCCT  40013      AGA       CCC__
                                TCGGC   CCCCCTCT    CCT
                                |||||   ||||||||    |||
                                GGTCG   GGGGGAGA    GGA
                                  ___       AAGAA
GAM1615  LOC151963 3'  GATCAGCAGGCCTCCTGACC   40014         A  C   CT
                                GATCGGCAG CC CCT  CC
                                |||||||||  || |||  ||
                                CTAGTCGTC GG GGA  GG
                                     C  A   CT
GAM1615  LOC201617 5'  ACAGCCTCCCCTCTCCTCCT   40015      AC_       C
                                GCAG   CCCCTCTCC CCT
                                ||||   ||||||||| |||
                                TGTC   GGGGAGAGG GGA
                                  GGA        A
GAM1615  LOC255330 3'  GATGCTTACTTCCTCTCCCC   40016     CG  AG  CC
                                GAT  GC  AC  CCTCTCCCC
                                |||  ||  ||  |||||||||
                                CTA  CG  TG  GGAGAGGGG
                                  __  AA  AA
GAM1615  LOC256867 5'  GATGGGCAGACCTGGCAGCTCT 40017     C       CC_____
              CC                    GAT GGCAGACC      CTCTCC
                                ||| ||||||||      ||||||
                                CTA CCGTCTGG      GAGAGG
                                  C        ACCGTC
GAM1615  LOC257153 5'  TCTGCTAGGTTTTCTCCCCCT  40018    G  _  ACCCCC
                                TC GC AG      TCTCCCCCT
                                || || ||      |||||||||
                                AG CG TC      AGAGGGGGA
                                 A  A  CAAA__
GAM1615  LOC54550  5'  AGCCCCCCTTCCCTCTCCCCCT 40019     AGA  __
                                GGC   CC  CCCTCTCCCCCT
                                |||   ||  ||||||||||||
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                              TCG  GG  GGGAGAGGGGGA
                                GGG  AA
GAM1615 LOC57106 3' TCGGCCTCCTCTCCCCCT   40020     AGACCC
                              TCGGC    CCTCTCCCCCT
                              |||||    ||||||||||
                              AGCCG    GGAGAGGGGGA
                                 GA____
GAM1615 LOC90297 5' GACCTGCACCTCCCTCTCCC  40021    G  AG  _
                              GATC GC  ACC CCCTCTCCC
                              |||| ||  ||| |||||||||
                              CTGG CG  TGG GGGAGAGGG
                                A  __  A
GAM1616 DMD    5' CTGACAGCTGTTTGCAGACCTC 40024         ___ _  TAA
          CT                   CTGACAGCTGT  CA ACC  TCCT
                              ||||||||||  || |||  ||||
                              GACTGTCGACA  GT TGG  AGGA
                                    AAC  C  ___
GAM1616 DMD    5' CTGACAGCTGTTTGCAGACCTC 40024         ___ _  TAA
          CT                   CTGACAGCTGT  CA ACC  TCCT
                              ||||||||||  || |||  ||||
                              GACTGTCGACA  GT TGG  AGGA
                                    AAC  C  ___
GAM1616 DMD    5' CTGACAGCTGTTTGCAGACCTC 40024         ___ _  TAA
          CT                   CTGACAGCTGT  CA ACC  TCCT
                              ||||||||||  || |||  ||||
                              GACTGTCGACA  GT TGG  AGGA
                                    AAC  C  ___
GAM1616 PCDH9   5' CTGGAGGCTGTCAAAACTCCT 40025    ACA     CCTAA
                              CTG  GCTGTCAA    TCCT
                              |||  ||||||||    ||||
                              GAC  CGACAGTT    AGGA
                                CTC      TTG__
GAM1616 PPARGC1  3' CCTGACAATTGTCATGCATCCT 40026       C    ACCTA
                              CCTGACAG TGTCA    ATCCT
                              |||||||| |||||    |||||
                              GGACTGTT ACAGT    TAGGA
                                   A    ACG__
GAM1616 PPEF1   3' CTGACATTTAACCTAATC   40027      GCTGTC
                              CTGACA     AACCTAATC
                              ||||||     |||||||||
                              GACTGT     TTGGATTAG
                                 AAA___
GAM1616 KIAA0057 3' CTGACAATGACCTAATCCT   40028       C  TCA
                              CTGACAG TG   ACCTAATCCT
                              ||||||| ||   ||||||||||
                              GACTGTT AC   TGGATTAGGA
                                    _ ___
GAM1616 KIAA0599 3' CTGGCAGCTGCCCTGAATC   40029    A     CAA  _
                              CTG CAGCTGT   CCT AATC
                              ||| |||||||   ||| ||||
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                                GAC GTCGACG   GGA TTAG
                                  C      ___   C
GAM1616  KIAA0638  3'  CCAGACAGCTGGAGGCCTGGTC 40030    T      TCAA   AA
                CT                  CC GACAGCTG    CCT  TCCT
                                || ||||||||    |||  ||||
                                GG CTGTCGAC    GGA  AGGA
                                 T       CTCC   CC
GAM1616  KIAA0935  3'  CCTGTTAGCTGTCATGCCT    40031      AC       A_
                                CCTG  AGCTGTCA  CCT
                                ||||  ||||||||  |||
                                GGAC  TCGACAGT  GGA
                                  AA       AC
GAM1616  KIAA1079  3'  TGGCAGCCACCTAGTCC     40032    A    GTCA    A
                                TG CAGCT    ACCTA TCC
                                || |||||    ||||| |||
                                AC GTCGG    TGGAT AGG
                                 C     _____     C
GAM1616  KIAA1676  5'  CCTGACAGCAGCAACACTTGGT 40033          T T    _  AA_
                CCT                   CCTGACAGC G CAAC CT   TCCT
                                ||||||||| | |||| ||   ||||
                                GGACTGTCG C GTTG GA   AGGA
                                      T _    T  ACC
GAM1616  KIAA1922  3'  CCTTACAGCTGTTGGCTCATGT 40034     G       CAAC  AA___
                TCCT                  CCT ACAGCTGT    CT     TCCT
                                ||| ||||||||    ||     ||||
                                GGA TGTCGACA    GA     AGGA
                                  A       ACC_  GTACA
GAM1616  NET-6    5'  CCTGACAGCTGCTTTGTCC    40035           CAACCTAA
                                CCTGACAGCTGT       TCC
                                ||||||||||||       |||
                                GGACTGTCGACG       AGG
                                      AAAC_____
GAM1616  ZW10     3'  CCTGACAGTTTGTTAGCTAAT  40036         C_   CAAC
                                CCTGACAG  TGT    CTAAT
                                ||||||||  |||    |||||
                                GGACTGTC  ACA    GATTA
                                     AA   ATC_
GAM1616  LOC144558 5'  CCTGTAGCTGTCAACTCT    40037      AC         _
                                CCTG  AGCTGTCAAC CT
                                ||||  |||||||||| ||
                                GGAC  TCGACAGTTG GA
                                  A_         A
GAM1616  LOC151234 3'  CCTGTTGGTGCCAACCTGATC  40038      ACAGC        A
                                CCTG     TGTCAACCT ATC
                                ||||     ||||||||| |||
                                GGAC     ACGGTTGGA TAG
                                  AACC_        C
GAM1616  LOC151623 5'  CCTGTAGCTGTCAACTCT    40037      AC         _
                                CCTG  AGCTGTCAAC CT
                                ||||  |||||||||| ||
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                                GGAC  TCGACAGTTG GA
                                  A_        A
GAM1616  LOC153914 5'  CCTGGTAGCTGGCCAGCCAATC 40039      AC    _  A  T
              CT                   CCTG  AGCTG TCA CC AATCCT
                                |||||  ||||| ||| || ||||||
                                GGAC  TCGAC GGT GG TTAGGA
                                  CA    C  C  _
GAM1616  LOC169026 3'  CCTGAGCAGCTCTAATCC    40040      _    GTCAAC
                                CCTGA CAGCT     CTAATCC
                                |||||  |||||     |||||||
                                GGACT GTCGA     GATTAGG
                                  C    _______
GAM1616  LOC221962 5'  CCTGTAGCTGTCAACTCT    40037      AC        _
                                CCTG  AGCTGTCAAC CT
                                ||||  |||||||||| ||
                                GGAC  TCGACAGTTG GA
                                  A_        A
GAM1616  LOC254122 3'  CTGACAGCTTCAGGTCCT    40041         G   A__
                                CTGACAGCT TCA   CCT
                                |||||||||  |||   |||
                                GACTGTCGA AGT   GGA
                                     _  CCA
GAM1616  LOC92391  3'  CCTGACAGCTTTTAATATCCT  40042          GTCAACCTA
                                CCTGACAGCT       ATCCT
                                ||||||||||       |||||
                                GGACTGTCGA       TAGGA
                                     AAATTA___
GAM1617  CTPS      3'  CAGAGACAGACATCTT      40045     C    GTCGT
                                CAG AGAT    AGACATCTT
                                ||| ||||    |||||||||
                                GTC TCTG    TCTGTAGAA
                                  _   _____
GAM1617  DYRK1A    3'  AACAGATGTTGTAATCTTGA   40046         C   GAC
                                AGCAGATGT GTA   ATCTTGA
                                |||||||||  |||   |||||||
                                TTGTCTACA CAT   TAGAACT
                                     A  ___
GAM1617  DYRK1A    3'  AACAGATGTTGTAATCTTGA   40046         C   GAC
                                AGCAGATGT GTA   ATCTTGA
                                |||||||||  |||   |||||||
                                TTGTCTACA CAT   TAGAACT
                                     A  ___
GAM1617  DYRK1A    3'  AACAGATGTTGTAATCTTGA   40046         C   GAC
                                AGCAGATGT GTA   ATCTTGA
                                |||||||||  |||   |||||||
                                TTGTCTACA CAT   TAGAACT
                                     A  ___
GAM1617  FCMD      3'  AGCTGACTCAGACATCTTGA   40047     A   GTCG
                                AGC GAT    TAGACATCTTGA
                                |||  |||    ||||||||||||
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                                TCG CTG   GTCTGTAGAACT
                                  A  A___
GAM1617 IRS1     3' CAGCAGATGAAATGTATCTTGA 40048        TCGTAGAC
                                CAGCAGATG      ATCTTGA
                                |||||||||      |||||||
                                GTCGTCTAC      TAGAACT
                                     TTTACA__
GAM1617 KCNA3    3' CAGATCAGGACATCTTG    40049    TG  TA
                                CAGA  TCG  GACATCTTG
                                ||||  |||  |||||||||
                                GTCT  AGT  CTGTAGAAC
                                  __  C_
GAM1617 MPP1     3' ACAGATGTGTCATTTTG    40050       C  AGA  C
                                GCAGATGT GT   CAT TTG
                                |||||||| ||   ||| |||
                                TGTCTACA CA   GTA AAC
                                    _ ____  A
GAM1617 ZHX1     3' CAGTAAATCAGACATCTTG   40051    A  TCG
                                CAG TG   TAGACATCTTG
                                ||| ||   ||||||||||
                                GTC AT   GTCTGTAGAAC
                                  _ TTA
GAM1617 C11orf21 5' CAGCAAATGCCCTGGTGTCTTG 40052         GTAGACA
                                CAGCAGATGTC      TCTTG
                                ||||||||||      |||||
                                GTCGTTTACGG      AGAAC
                                      GACCAC_
GAM1617 D2S448   3' GATTCCGCAGACATTTTG    40053    GT       C
                                GAT  CGTAGACAT TTG
                                |||  ||||||||| |||
                                CTA  GCGTCTGTA AAC
                                  AG        A
GAM1617 FAM3D    5' CAGCAGGTGCCGTAGGTCCCTG 40054       A       ACA
           A                     CAGCAG TGTCGTAG   TCTTGA
                                |||||| ||||||||   ||||||
                                GTCGTC ACGGCATC   GGGACT
                                   C       CA_
GAM1617 FUSIP1   3' CAGCCGGGCCTAGACATCTTGA 40055     AGAT   G
                                CAGC   GTC TAGACATCTTGA
                                ||||   ||| ||||||||||||
                                GTCG   CGG ATCTGTAGAACT
                                  GCC_  _
GAM1617 KIAA1808 5' CAGCGGGTGCCGTAGAGCCTCT 40056     AGA       CA_
                                CAGC   TGTCGTAGA   TCT
                                ||||   |||||||||   |||
                                GTCG   ACGGCATCT   AGA
                                  CCC        CGG
GAM1617 PDZ-GEF1 3' AGCAGATGAGGTGTCTTG    40057        TC  AGACA
                                AGCAGATG  GT    TCTTG
                                ||||||||  ||    |||||
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                                TCGTCTAC  CA    AGAAC
                                    TC  C____
GAM1617  RAB3GAP   3'  ACAGACACAAGACATCTTGA   40058       T  T
                                GCAGATG CG AGACATCTTGA
                                ||||||| || ||||||||||
                                TGTCTGT GT TCTGTAGAACT
                                   _ _
GAM1617  SYNJ2     3'  TGACAGATGCACAAACGTTTTG 40059    A      T      ATC
                                C GCAGATG CGTAGAC   TTG
                                | ||||||| |||||||   |||
                                A TGTCTAC GTGTTTG   AAC
                                 C       _      CAA
GAM1617  LOC112703 5'  ACGGATGTCGCAGGTCTTG    40060    A         ACA
                                GC GATGTCGTAG   TCTTG
                                || ||||||||||   |||||
                                TG CTACAGCGTC   AGAAC
                                 C         C__
GAM1617  LOC126031 5'  GCAGGACGTGGACATCTTG    40061     ATGT   A
                                GCAG    CGT GACATCTTG
                                ||||    ||| |||||||||
                                CGTC    GCA CTGTAGAAC
                                  CT__   C
GAM1617  LOC132332 3'  AGATGTCAAGTTAACATCTTGA 40062        TA__
                                AGATGTCG    GACATCTTGA
                                ||||||||    ||||||||||
                                TCTACAGT    TTGTAGAACT
                                    TCAA
GAM1617  LOC148534 3'  GCAGAAAAGACATCTTG     40063      TGTCGT
                                GCAGA     AGACATCTTG
                                |||||     ||||||||||
                                CGTCT     TCTGTAGAAC
                                  TT_____
GAM1617  LOC157556 5'  ACAGATGCAGCTGCATTTTGA  40064        C  AGA   C
                                GCAGATGT GT   CAT TTGA
                                |||||||| ||   ||| ||||
                                TGTCTACG CG   GTA AACT
                                    T  AC_   A
GAM1617  LOC256940 5'  CAGCAGATGTCTGGACCACTG  40065          GTA   ATC
                                CAGCAGATGTC   GAC   TTG
                                ||||||||||   |||   |||
                                GTCGTCTACAG   CTG   GAC
                                      AC_   GT_
GAM1617  LOC91565  3'  GCAGATGTCGTGGAAAACAGTT 40066          ___    TC
            TG                   GCAGATGTCGT   AGACA  TTG
                                ||||||||||   |||||  |||
                                CGTCTACAGCA   TTTGT  AAC
                                      CCT    CA
GAM1618  MMP15     3'  TTTGCCGGCTGTACAATTTAT  40069       AGC     _
                                TTTGCC   GGTTGTA GATTTAT
                                ||||||   ||||||| |||||||
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                                AAACGG   CCGACAT TTAAATA
                                   ___      G
GAM1618 RPS17    3'  TTTGCTGTTGTCCCAGATTTAT 40070      CAGCG   G
                                TTTGC    GTT TAGATTTAT
                                |||||    ||| |||||||||
                                AAACG    CAG GTCTAAATA
                                   ACAA_   G
GAM1618 FLJ14621 3'  TCTGCTGGTCAGATTTAT    40071      CAGC    GT
                                TTTGC    GGTT  AGATTTAT
                                |||||    ||||  ||||||||
                                AGACG    CCAG  TCTAAATA
                                   A___    __
GAM1618 NYD-SP26 3'  CTTGCCAAAAAGATTTAT    40072        CGGTTGT
                                TTTGCCAG      AGATTTAT
                                ||||||||      ||||||||
                                GAACGGTT      TCTAAATA
                                     TT_____
GAM1618 SEMA6B   3'  TTTGCCGGTGGTTGTAAAC   40073      AGC
                                TTTGCC   GGTTGTAGAT
                                ||||||   ||||||||||
                                AAACGG   CCAACATTTG
                                   CCA
GAM1618 SEMA6B   3'  TTTGCCGGTGGTTGTAAAC   40073      AGC
                                TTTGCC   GGTTGTAGAT
                                ||||||   ||||||||||
                                AAACGG   CCAACATTTG
                                   CCA
GAM1618 SEMA6B   3'  TTTGCCGGTGGTTGTAAAC   40073      AGC
                                TTTGCC   GGTTGTAGAT
                                ||||||   ||||||||||
                                AAACGG   CCAACATTTG
                                   CCA
GAM1618 LOC147991 3'  TCTGTCAGTGGTTTGAAATTTA 40074     C   C    GT
             T                   TTTG CAG GGTT  AGATTTAT
                                ||||  ||| ||||  ||||||||
                                AGAC GTC CCAA  TTTAAATA
                                   A  A    AC
GAM1619 DRPLA    3'  GGGTGCTCCAAGGTCCAATGTA 40077     A    CATCA
                                GGGT CTCT    CCAATGTA
                                ||||  ||||    ||||||||
                                CCCA GAGG    GGTTACAT
                                   C    TTCCA
GAM1619 DKFZP434B044 3'  AAGGGTACTTCATTTCACTGT  40078         C   __   CAA
                                AAGGGTACT TCA  TCAC   TGT
                                |||||||||  |||  ||||   |||
                                TTCCCATGA AGT  AGTG   ACA
                                     _   AA    ___
GAM1619 FLJ20378 3'  AAGGGCACTTCAAACTCAATGT 40079         C   TC   _
             A                    AAGGGTACT TCA  AC CAATGTA
                                |||||||||  |||  ||  |||||||
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                                TTCCCGTGA AGT  TG GTTACAT
                                     _  T_  A
GAM1619  FLJ21551  3'  AAGGTACTCTTATTACCCAATG 40080          C  CA_
            T                    AGGGTACTCT AT   CCAATGT
                                 |||||||||| ||   |||||||
                                 TTCCATGAGA TA   GGTTACA
                                      A  ATG
GAM1619  KIAA0326  3'  AGGGTTTCTCATCACTGATGTA 40081       AC        CA
                                 AGGGT  TCTCATCAC  ATGTA
                                 |||||  |||||||||  |||||
                                 TCCCA  AGAGTAGTG  TACAT
                                    A_        AC
GAM1619  LOC149685 5'  AAGGGTACTTCATGGCGCATGT 40082          C    CACCA
                                 AAGGGTACT TCAT     ATGT
                                 |||||||||| ||||     ||||
                                 TTCCCATGA AGTA     TACA
                                      _   CCGCG
GAM1619  LOC54516  3'  AAGGGTACTTTCACCCTATGT  40083         C     ACCA
                                 AAGGGTACT TCATC    ATGT
                                 |||||||||| |||||    ||||
                                 TTCCCATGA AGTGG    TACA
                                      A    GA__
GAM1620  COL19A1   3'  GCAGATAAGTTGTAAGCGTTT  40086         AC___    T
                                 GCAGATAA     AAGC GTTT
                                 ||||||||     |||| ||||
                                 CGTCTATT     TTCG CAAA
                                      CAACA   _
GAM1620  DNTT      3'  TAGAGATAGACAGTATTTCAG  40087     C     A   A C
                                 TAG AGATA ACA G TGTTTCAG
                                 ||| ||||| ||| | ||||||||
                                 ATC TCTAT TGT C ATAAAGTC
                                   _     C   _ _
GAM1620  TGIF      3'  TAACAGGAAGCTGTTT      40088        ATAAAC
                                 TAGCAG     AAGCTGTTT
                                 ||||||     |||||||||
                                 ATTGTC     TTCGACAAA
                                    C_____
GAM1620  TMOD3     3'  TAGCAGAAAGTAGAAATGTTTC 40089         TAAACAAGC
            AG                     TAGCAGA        TGTTTCAG
                                 |||||||        ||||||||
                                 ATCGTCT        ACAAAGTC
                                     TTCATCTTT
GAM1620  C5orf5    3'  CAGCGGATAAACAGTAACTCAG 40090      A       A C  T
                                 TAGC GATAAACA G TG TTCAG
                                 |||| |||||||| | || |||||
                                 GTCG CTATTTGT C AT GAGTC
                                   C       _ _  T
GAM1620  HUMAGCGB  5'  TAGCCCTCAAGGCTGTTTC   40091      AGATAAA   _
                                 TAGC       CAAG CTGTTTC
                                 ||||       |||| |||||||
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                                ATCG      GTTC GACAAAG
                                  GGA____   C
GAM1620  MAGEH1   5'  TAGCAATAAACAAGCCGTTCTC 40092       A         _
             AG                    TAGCAG TAAACAAGCTGT TTCAG
                                   |||||| |||||||||||| |||||
                                   ATCGTT ATTTGTTCGGCA GAGTC
                                     _         A
GAM1620  RGC32    3'  AGCAGGTAAACAAAGTCA    40093      A      CTGTT
                                   AGCAG TAAACAAG    TCA
                                   ||||| ||||||||    |||
                                   TCGTC ATTTGTTT    AGT
                                     C       C____
GAM1620  RP4-622L5 3'  TAGCAGATGATGAAGACACTCA 40094        AAAC   CTGT
             G                     TAGCAGAT    AAG    TTCAG
                                   ||||||||   |||   |||||
                                   ATCGTCTA   TTC   GAGTC
                                        CTAC   TGT_
GAM1620  TIGD5    3'  TAGCAGACAGGAGTTTC     40095        AAACA  CT
                                   TAGCAGAT    AG  GTTTC
                                   ||||||||    ||  |||||
                                   ATCGTCTG    TC  CAAAG
                                        _____  CT
GAM1620  TOSO     3'  CAGCAGATAGATGAGACTCCTT 40096         AACA  _  G
                                   TAGCAGATA    AG CT TTT
                                   |||||||||   || || |||
                                   GTCGTCTAT    TC GA GAA
                                        CTAC  T  G
GAM1620  UBP1     3'  TAGCAGACAAGCATTT      40097       TAAA    T
                                   TAGCAGA    CAAGC GTTT
                                   |||||||    ||||| ||||
                                   ATCGTCT    GTTCG TAAA
                                        ____    _
GAM1620  ZNF185   3'  GCAAATAGACAAGCTAAACA   40098       A      TTT
                                   GCAGATA ACAAGCTG   CA
                                   ||||||| ||||||||   ||
                                   CGTTTAT TGTTCGAT   GT
                                        C       TT_
GAM1620  LOC116411 3'  CAGCAGATAAACAAGTGAACAA 40099             C  TTT
                                   TAGCAGATAAACAAG TG   CAG
                                   |||||||||||||| ||   |||
                                   GTCGTCTATTTGTTC AC   GTT
                                             _  TT_
GAM1620  LOC133308 5'  GCAGATAAACGGTCTCA     40100         AAGCT
                                   GCAGATAAAC    GTTTCA
                                   ||||||||||    ||||||
                                   CGTCTATTTG    CAGAGT
                                         C____
GAM1620  LOC153077 3'  AGCAGATAAACAAATCTCAG   40101           GCT
                                   AGCAGATAAACAA   GTTTCAG
                                   ||||||||||||   |||||||
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                                TCGTCTATTTGTT   TAGAGTC
                                        ___
GAM1620 LOC165693 3' GCTGAATGAGCTGTTTCAG   40102    A  TAAACA
                                GC GA     AGCTGTTTCAG
                                || ||     ||||||||||
                                CG CT     TCGACAAAGTC
                                 A  TAC___
GAM1620 LOC199232 3' GATAAACAGAGTCTCAG     40103        AGCT
                                GATAAACA   GTTTCAG
                                ||||||||   |||||||
                                CTATTTGT   CAGAGTC
                                     CT__
GAM1620 LOC50999  3' AGCAGATAAACAGTATGTCT  40104          AGC
                                AGCAGATAAACA   TGTTT
                                ||||||||||||   |||||
                                TCGTCTATTTGT   ACAGA
                                       CAT
GAM1620 LOC63928  5' GCGAACAACGGGCTGTTTCAG 40105    AG   ACAA
                                GC  ATAA   GCTGTTTCAG
                                ||  ||||   ||||||||||
                                CG  TGTT   CGACAAAGTC
                                 CT   GCC_
GAM1620 LOC90110  3' TAGTGGAGAAACAAGCAAGC  40106    CA  T      T_
                                TAG  GA AAACAAGC  GT
                                |||  || ||||||||  ||
                                ATC  CT TTTGTTCG  CG
                                  AC  C      TT
GAM1620 LOC90381  3' TAGCAGATAAGGTGAGAGCCA 40107         ACA___
                                TAGCAGATAA     AGCTG
                                ||||||||||     |||||
                                ATCGTCTATT     TCGGT
                                      CCACTC
GAM1621 CELSR3    3' TTCTCGGTAAGGAGAGTTTGGG 40110      TC   CCC   C_______
           TCCTG                   TCGGT  AAG   GAG      CCTG
                                |||||  |||   |||      ||||
                                AGCCA  TTC   CTC      GGAC
                                   __   CT_   AAACCCA
GAM1621 CMAR      5' TCCTCAGCTTGAGCCC      40111         CAAGCCC
                                TTCTCGGTT      GAGCCC
                                |||||||||      ||||||
                                AGGAGTCGA      CTCGGG
                                     A_______
GAM1621 FGFR1     3' TTCTGGGTTCAAGCAGTTAGC  40112      C       CCG_
                                TTCT GGTTCAAGC    AGC
                                |||| |||||||||    |||
                                AAGA CCAAGTTCG    TCG
                                  C       TCAA
GAM1621 FGFR1     3' TTCTGGGTTCAAGCAGTTAGC  40112      C       CCG_
                                TTCT GGTTCAAGC    AGC
                                |||| |||||||||    |||
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                                AAGA CCAAGTTCG    TCG
                                  C       TCAA
GAM1621  FLJ10458  3'  TCTCGGCCTGGGGTCTGAGTCC 40113        CAAGCCC_  C
             TG                    TCTCGGTT       GAG CCTG
                                   ||||||||       ||| ||||
                                   AGAGCCGG       CTC GGAC
                                      ACCCCAGA   A
GAM1621  FLJ11850  3'  TCCTCGGTTTAAGGCCCT    40114         C   CCCGA
                                   TTCTCGGTT AAG    GCCCT
                                   |||||||||| |||    |||||
                                   AGGAGCCAA TTC    CGGGA
                                      A  _____
GAM1621  FLJ13241  3'  TTCTGGGTTCAAACGTGGCTCT 40115     C       CCGA  C
             G                     TTCT GGTTCAAGC    GC CTG
                                   |||| |||||||||    || |||
                                   AAGA CCAAGTTTG    CG GAC
                                     C       CAC_  A
GAM1621  FLJ13315  3'  TCCTTGGTTCAAGTGATCCTG  40116     C      CCC  GC
                                   TTCT GGTTCAAG   GA  CCTG
                                   |||| ||||||||   ||  ||||
                                   AGGA CCAAGTTC   CT  GGAC
                                     A       A__  A_
GAM1621  FLJ20308  3'  TCTGCAGGCCTGAGCTCT    40117    _  TTCAA   C    C
                                   TCT CGG    GCC GAGC CT
                                   ||| |||    ||| |||| ||
                                   AGA GTC    CGG CTCG GA
                                     C  _____   A   A
GAM1621  IL-23R    3'  TTCCTGGTTCAAGTGATTCTCC 40118    TC      CCC  GC__
             TG                    TTC  GGTTCAAG   GA    CCTG
                                   |||  ||||||||   ||    ||||
                                   AAG  CCAAGTTC   CT    GGAC
                                     GA       A__  AAGA
GAM1621  KIAA0057  3'  TTCTAGGTTCAAGCGATTCTCC 40119     C       CCGAGC
             TG                    TTCT GGTTCAAGC     CCTG
                                   |||| |||||||||     ||||
                                   AAGA CCAAGTTCG     GGAC
                                     T       CTAAGA
GAM1621  NIR3      3'  GGTCAGGCCTGAGCCCT     40120     T  A   C
                                   GGT CA GCC GAGCCCT
                                   ||| || ||| |||||||
                                   CCA GT CGG CTCGGGA
                                    _  C   A
GAM1621  RAI17     3'  TCTCTGTTCCCCAAGCCTGGGC 40121     G   ___    CGA
             CCTG                    TCTC GTTC   AAGCC   GCCCTG
                                   |||| ||||   |||||   ||||||
                                   AGAG CAAG   TTCGG   CGGGAC
                                     A   GGG    ACC
GAM1621  LOC148918 5'  TTCTGGGTTCAAGCAATTCTCC 40122      C       CCGAGC
             TG                    TTCT GGTTCAAGC     CCTG
                                   |||| |||||||||     ||||
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                                AAGA CCAAGTTCG     GGAC
                                  C       TTAAGA
GAM1621  LOC162655 5'  TTCTCGGCTTCAGGGGTGTCCT 40123        CA  CCCGAGC
           G                     TTCTCGGTT  AG      CCTG
                                 |||||||||  ||      ||||
                                 AAGAGCCGA  TC      GGAC
                                      AG  CCCACA_
GAM1621  LOC196529 3'  TTCTGGGTTCAAGAGATTCTCC 40124     C       CCC  GC__
           TG                    TTCT GGTTCAAG   GA    CCTG
                                 |||| ||||||||   ||    ||||
                                 AAGA CCAAGTTC   CT    GGAC
                                   C       T__  AAGA
GAM1621  LOC197196 3'  TTCTGGGTTCAAGTGATTCTCC 40125     C       CCC  GC__
           TG                    TTCT GGTTCAAG   GA    CCTG
                                 |||| ||||||||   ||    ||||
                                 AAGA CCAAGTTC   CT    GGAC
                                   C       A__  AAGA
GAM1621  LOC200251 5'  TTCTGGGTTCAAGCAATTCTCC 40122     C       CCGAGC
           TG                    TTCT GGTTCAAGC     CCTG
                                 |||| |||||||||      ||||
                                 AAGA CCAAGTTCG     GGAC
                                   C       TTAAGA
GAM1621  LOC205011 5'  TTCTGGGTTCAAGGCTTCT    40126     C       CCCGA  C_
                                 TTCT GGTTCAAG    GC  CT
                                 |||| ||||||||    ||  ||
                                 AAGA CCAAGTTC    CG  GA
                                   C       _____  AA
GAM1621  LOC221943 5'  CTCTCAGAGCCTGAGCCCT    40127       TTCA   C
                                 TTCTCGG    AGCC GAGCCCT
                                 |||||||    |||| |||||||
                                 GAGAGTC    TCGG CTCGGGA
                                      ____    A
GAM1621  LOC255621 3'  TTCTTGGTTCAAATTCAAA    40128     C       CC
                                 TTCT GGTTCAAG  CGAG
                                 |||| ||||||||  ||||
                                 AAGA CCAAGTTT  GTTT
                                   A       AA
GAM1621  LOC90092  3'  TTCTGGGTTCAAGCGATTCTTC 40129     C       CCGAGCC
           TG                    TTCT GGTTCAAGC      CTG
                                 |||| |||||||||      |||
                                 AAGA CCAAGTTCG      GAC
                                   C       CTAAGAA
GAM1621  LOC90233  3'  TTCTGGGTTCAAGCGATTCTCC 40130     C       CCGAGC
           TG                    TTCT GGTTCAAGC     CCTG
                                 |||| |||||||||      ||||
                                 AAGA CCAAGTTCG     GGAC
                                   C       CTAAGA
GAM1622  DKFZP434F1735 5'  TAAAACATAAATGTCATCA    40133        C     _
                                 TAAAACAT AATGTCG CA
                                 |||||||| ||||||| ||
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                                ATTTTGTA TTACAGT GT
                                     T      A
GAM1622 KIAA0155 3' ACATCAATACCAAGTTTGT   40134        GT  CAA
                                ACATCAAT  CG   TTTGT
                                ||||||||  ||   |||||
                                TGTAGTTA  GT   AAACA
                                     TG  TC_
GAM1622 KIAA0310 3' TAAAACACCAAACAGTTTG   40135          TGTC   A
                                TAAAACATCAA    GCA TTTG
                                ||||||||||    ||| ||||
                                ATTTTGTGGTT    TGT AAAC
                                      ____  C
GAM1622 KIAA0391 3' TAAAAAATCAATGTCAATGCTG 40136      C        CAAT
           T                     TAAAA ATCAATGTCG    TTGT
                                |||||  ||||||||||    ||||
                                ATTTT TAGTTACAGT    GACA
                                   T        TAC_
GAM1623 DPYSL2   3' GTGATGGAATGACCTACT    40139        CA
                                GTGATGGGG  GCCTACT
                                |||||||||  |||||||
                                CACTACCTT  TGGATGA
                                     AC
GAM1623 MME     3' TGTGATGGTGCCCTCTC     40140        GGCA   A
                                TGTGATGG   GCCT CTC
                                ||||||||   |||| |||
                                ACACTACC   CGGG GAG
                                     A___   A
GAM1623 MME     3' TGTGATGGTGCCCTCTC     40140        GGCA   A
                                TGTGATGG   GCCT CTC
                                ||||||||   |||| |||
                                ACACTACC   CGGG GAG
                                     A___   A
GAM1623 MME     3' TGTGATGGTGCCCTCTC     40140        GGCA   A
                                TGTGATGG   GCCT CTC
                                ||||||||   |||| |||
                                ACACTACC   CGGG GAG
                                     A___   A
GAM1623 MME     3' TGTGATGGTGCCCTCTC     40140        GGCA   A
                                TGTGATGG   GCCT CTC
                                ||||||||   |||| |||
                                ACACTACC   CGGG GAG
                                     A___   A
GAM1623 PIK3R1   3' ACTGGGGTGGGGAAGCTTATTC 40141      TGA    C   C  C
                                ACTG   TGGGG AGC TA TC
                                ||||   ||||| ||| || ||
                                TGAC   ACCCC TCG AT AG
                                  CCC    T   A  A
GAM1623 DPP9    3' CTGTGATGTGGCGGCTCC    40142         G   A  CTAC
                                CTGTGATG GGC GC    TCC
                                |||||||| ||| ||    |||
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                                GACACTAC CCG CG    AGG
                                    A   C ____
GAM1623  KIAA1423  3'  ACTGTGATGGGGTGGCACT   40143          CA  _
                                ACTGTGATGGGG  GC CT
                                ||||||||||||  || ||
                                TGACACTACCCC  CG GA
                                      AC  T
GAM1623  MGC13114  3'  ACTGTGATGGGGGAGGCT    40144          C  C
                                ACTGTGATGGGG AG CT
                                |||||||||||| || ||
                                TGACACTACCCC TC GA
                                      C  C
GAM1623  MGC13114  3'  ACTGTGATGGGGGAGGCT    40144          C  C
                                ACTGTGATGGGG AG CT
                                |||||||||||| || ||
                                TGACACTACCCC TC GA
                                      C  C
GAM1623  MGC13114  3'  ACTGTGATGGGGGAGGCT    40144          C  C
                                ACTGTGATGGGG AG CT
                                |||||||||||| || ||
                                TGACACTACCCC TC GA
                                      C  C
GAM1623  MGC13114  3'  ACTGTGATGGGGGAGGCT    40144          C  C
                                ACTGTGATGGGG AG CT
                                |||||||||||| || ||
                                TGACACTACCCC TC GA
                                      C  C
GAM1623  MGC3113   3'  CTGTGGTGGGGCAGTGAAC   40145      A      CCT
                                CTGTG TGGGGCAG   AC
                                |||||  ||||||||   ||
                                GACAC ACCCCGTC   TG
                                   C       ACT
GAM1623  LOC121506 5'  CCGACTCAGGGCAGCCTACTC  40146     TGA
                                CTG   TGGGGCAGCCTACTC
                                |||   ||||||||||||||||
                                GGC   GTCCCGTCGGATGAG
                                  TGA
GAM1623  LOC148223 3'  CTGGGATGGGGCAGCCAC    40147     T         T
                                CTG GATGGGGCAGCC AC
                                ||| ||||||||||| ||
                                GAC CTACCCCGTCGG TG
                                  C         _
GAM1623  LOC149506 5'  TGTGATGGGGCAGTTCCCA   40148           __
                                TGTGATGGGGCAG  CCTA
                                ||||||||||||  ||||
                                ACACTACCCCGTC  GGGT
                                      AA
GAM1623  LOC245744 3'  TGTGATGGGGCGGCAGCCCCG  40149          A  CTA
                                TGTGATGGGGC GC   CTCCG
                                ||||||||||| ||   |||||
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                                ACACTACCCCG CG   GGGGC
                                      C  TC_
GAM1623  LOC81569  5'  GTGGTGCCGCAGCCTACTC   40150     A  GG
                                GTG TG  GCAGCCTACTC
                                ||| ||  ||||||||||||
                                CAC AC  CGTCGGATGAG
                                  C  GG
GAM1624  ABCB10    3'  AAAATGAGGTGCCATGCTA   40153        A  T AA
                                AAGATGAG GT G  ATGCTA
                                |||||||| || |  ||||||
                                TTTTACTC CA C  TACGAT
                                     _  _ GG
GAM1624  AEGL1     3'  TGGGAGTTGAACCACA      40154     A      AAT
                                TG GAGTTGA   GCTACA
                                || |||||||   ||||||
                                AC CTCAACT   TGGTGT
                                 C      ___
GAM1624  CUGBP1    3'  AAAGGTGAGAGTTCAAGC    40155      A       G  AT
                                AAAG TGAGAGTT AA  GC
                                |||| |||||||| ||  ||
                                TTTC ACTCTCAA TT  CG
                                  C       G __
GAM1624  GBE1      3'  AGACATTTTCTGAAATGCTACA 40156      GAGAG
                                AGAT     TTGAAATGCTACA
                                ||||     ||||||||||||||
                                TCTG     GACTTTACGATGT
                                  TAAAA
GAM1624  MECP2     3'  AAAGTGACGCTTGAAATGCT   40157      A   GA   _
                                AAAG TGA  GTT GAAATGCT
                                |||| |||  ||| ||||||||
                                TTTC ACT  CGA CTTTACGA
                                  _   G_   A
GAM1624  PDGFRA    3'  AAAGATAGCAAAATGCTA    40158       GAG   T
                                AAAGAT   AGT GAAATGCTA
                                ||||||   ||| |||||||||
                                TTTCTA   TCG TTTTACGAT
                                     ___   _
GAM1624  PGK1      3'  AAGATGAGCTGAGATGCT    40159        GA    A
                                AAGATGA  GTTGA ATGCT
                                |||||||  ||||| |||||
                                TTCTACT  CGACT TACGA
                                     __     C
GAM1624  PIN4      3'  AAGATCAGAGTTGACTAAC   40160       G       AAT
                                AAGAT AGAGTTGA   GC
                                ||||| ||||||||   ||
                                TTCTA TCTCAACT   TG
                                   G       GAT
GAM1624  TCF12     3'  AAAAATGAGAGCAAGAGAAATG 40161           T___
            CTA                   AAAGATGAGAGT    GAAATGCTA
                                ||||||||||||    |||||||||
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                                TTTTTACTCTCG    CTTTACGAT
                                      TTCT
GAM1624  BMF      3'  GATGAACAAAATGCTACA    40162       AGT
                                GATGAG   TGAAATGCTACA
                                ||||||   ||||||||||||
                                CTACTT   GTTTTACGATGT
                                  ___
GAM1624  CAP350    3'  AAAGATGGGAGTTGAAGGTTTG 40163        A       A___
              C                   AAAGATG GAGTTGAA    TGC
                                ||||||| ||||||||    |||
                                TTTCTAC CTCAACTT    ACG
                                    C       CCAA
GAM1624  CAPNS2    3'  GGAAATGAGAGCTGTTGC    40164    A         AAA
                                A AGATGAGAGTTG   TGC
                                | ||||||||||||   |||
                                C TTTACTCTCGAC   ACG
                                 C          A__
GAM1624  CGI-57    3'  AAAGATCAGGGTTGAAGGTCC  40165       G  A     ATG
                                AAAGAT AG GTTGAA   CT
                                |||||| || ||||||   ||
                                TTTCTA TC CAACTT   GG
                                   G  C     CCA
GAM1624  DC8       3'  GGAGCTGAGAGTTGATGGC    40166    A  A        AAT
                                A AG TGAGAGTTGA   GC
                                | || ||||||||||   ||
                                C TC ACTCTCAACT   CG
                                 C  G         AC_
GAM1624  DKFZP564G0222 3'  AAAGATGATAGTTTATTTAC   40167         G    GAAA
                                AAAGATGA AGTT    TGC
                                |||||||| ||||    |||
                                TTTCTACT TCAA    ATG
                                     A    ATAA
GAM1624  DKFZp761D0614 3'  AGAGGGAAGTGAATGCTAC    40168     TGA    T   A
                                AGA   GAGT GAA TGCTAC
                                |||   |||| ||| ||||||
                                TCT   TTCA CTT ACGATG
                                  CCC   _  _
GAM1624  FLJ13215  3'  AAAGATGAGGGTAGTTTGATAT 40169          ___    _  A
              G                   AAAGATGAG   AGTT GA ATG
                                |||||||||   |||| || |||
                                TTTCTACTC   TCAA CT TAC
                                     CCA    A  A
GAM1624  FLJ14146  3'  AAGAAGACAGGATGCTAC    40170      T  G  TTGAA
                                AAGA GA AG     ATGCTAC
                                |||| || ||     |||||||
                                TTCT CT TC     TACGATG
                                  T  G  C____
GAM1624  FLJ20051  3'  AGATGAGAGTCTGAAATG    40171          _
                                AGATGAGAGT TGAAATG
                                |||||||||| |||||||
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                                TCTACTCTCA ACTTTAC
                                      G
GAM1624  FUBP3    3'  AGGGGAGAGTTGGCCAC     40172    AT      AAAT
                                AG  GAGAGTTG    GCTAC
                                ||  ||||||||    |||||
                                TC  CTCTCAAC    CGGTG
                                 CC       ____
GAM1624  HSPC155  5'  AAGATGAGACGTTGGGTTGCT  40173        _   AAA
                                AAGATGAGA GTTG   TGCT
                                ||||||||| ||||   ||||
                                TTCTACTCT CAAC   ACGA
                                      G    CCA
GAM1624  KIAA0534  3'  AAGATGAGATGTTGGGAAGTAC 40174        _   AAATGC
            A                    AAGATGAGA GTTG     TACA
                                ||||||||| ||||     ||||
                                TTCTACTCT CAAC     ATGT
                                      A    CCTTC_
GAM1624  KIAA1458  3'  AAAAATGAGAGGCCTGCTACA  40175          TTGAAA
                                AAAGATGAGAG     TGCTACA
                                ||||||||||     |||||||
                                TTTTTACTCTC     ACGATGT
                                       CGG___
GAM1624  KIAA1600  3'  AAAGATGAAGAAGAAAGTGCT  40176        G  TT   _
                                AAAGATGA AG  GAAA TGCT
                                |||||||| ||  |||| ||||
                                TTTCTACT TC  CTTT ACGA
                                     _ TT    C
GAM1624  NFAT5    3'  AAAGTGGCCAAAGATGCTACA  40177     A  AGA  TG  _
                                AAAG TG   GT  AA ATGCTACA
                                |||| ||   ||  || ||||||||
                                TTTC AC   CG  TT TACGATGT
                                  _ ___  GT  C
GAM1624  NFAT5    3'  AAAGTGGCCAAAGATGCTACA  40177     A  AGA  TG  _
                                AAAG TG   GT  AA ATGCTACA
                                |||| ||   ||  || ||||||||
                                TTTC AC   CG  TT TACGATGT
                                  _ ___  GT  C
GAM1624  LOC115557 3'  GATGGGAGCTGAAGGAAACT   40178     A       AT__
                                GATG GAGTTGAA    GCT
                                |||| ||||||||    |||
                                CTAC CTCGACTT    TGA
                                  C       CCTT
GAM1624  LOC145255 3'  AAAGATAAGGGTTGGGGCC    40179         A    AAAT
                                AAAGATGAG GTTG    GCT
                                ||||||||| ||||    |||
                                TTTCTATTC CAAC    CGG
                                      C    CC__
GAM1624  LOC147669 3'  AAAGATGAGGTCTTGCTA     40180         A   GAAA
                                AAAGATGAG GTT    TGCTA
                                ||||||||| |||    |||||
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                                TTTCTACTC CAG    ACGAT
                                      _  A___
GAM1624  LOC148760 3'  GATGAAAGTTGAAGACCA    40181           AT
                                GATGAGAGTTGAA  GCTA
                                ||||||||||||  ||||
                                CTACTTTCAACTT  TGGT
                                     C_
GAM1624  LOC149267 3'  AAAGATGCTAAGGGGATGCTAC 40182       A_   TTGAA
              A                  AAAGATG  GAG    ATGCTACA
                                ||||||| |||    ||||||||
                                TTTCTAC  TTC    TACGATGT
                                   GA   CCC__
GAM1624  LOC149300 5'  AAAGTGAGAGTTGTGCCTGCT  40183     A       AAA_
                                AAAG TGAGAGTTG    TGCT
                                |||| |||||||||    ||||
                                TTTC ACTCTCAAC    ACGA
                                  _       ACGG
GAM1624  LOC157507 5'  GATGAGAGATTGTTAATGC    40184       _   A_
                                GATGAGAG TTG  AATGC
                                |||||||| |||  |||||
                                CTACTCTC AAC  TTACG
                                     T   AA
GAM1624  LOC158709 3'  AGATGGGTAGATAGATGCTACA 40185      AG_  TTGAA
                                AGATG   AG    ATGCTACA
                                |||||   ||    ||||||||
                                TCTAC   TC    TACGATGT
                                   CCA  TATC_
GAM1624  LOC199678 3'  AAGAAGCTGAGGTGCTAC    40186     _    AA
                                GAGA GTTGA  TGCTAC
                                |||| |||||  ||||||
                                TTCT CGACT  ACGATG
                                  T    CC
GAM1624  LOC222160 5'  AAAATGAGAATTTGTGCTGCA  40187          GAAA   A
                                AAGATGAGAGTT    TGCT CA
                                ||||||||||||    |||| ||
                                TTTTACTCTTAA    ACGA GT
                                       AC__    C
GAM1624  LOC255650 3'  AAAGTTGGAAGGTGCTAC    40188       _  A_
                                AGAGTTG AA  TGCTAC
                                ||||||| ||  ||||||
                                TTTCAAC TT  ACGATG
                                     C  CC
GAM1624  LOC257443 3'  AAAAATGAGAGGCCTGCTACA  40175          TTGAAA
                                AAAGATGAGAG     TGCTACA
                                ||||||||||      |||||||
                                TTTTTACTCTC     ACGATGT
                                       CGG___
GAM1624  LOC91409  3'  GGAAGTGTCAGGAAATGCTA   40189   T   A   __
                                A GAG GTT  GAAATGCTA
                                | ||| |||  |||||||||
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                                C TTC CAG  CTTTACGAT
                                 C   A   TC
GAM1625  ELK1     3'  ACAGAGAAGTTGTGGAAGCTGT 40192         A    AC___
                                ATAGAGAA TTGT     CTGT
                                |||||||| ||||     ||||
                                TGTCTCTT AACA     GACA
                                     C    CCTTC
GAM1625  FLJ12568 3'  GAAAAATTGGAGTATATG    40193         TACCT
                                GAGAAATTG     GTATATG
                                |||||||||     |||||||
                                CTTTTTAAC     CATATAC
                                      CT___
GAM1625  KIAA1371 3'  ATAAAGGAATTGTACCCAGT   40194       A        _
                                ATAGAG AATTGTACCT GT
                                |||||| |||||||||| ||
                                TATTTC TTAACATGGG CA
                                    C         T
GAM1625  LANCL2   3'  ACAGAGAATCTGTATGT     40195        A     CC
                                ATAGAGAA TTGTA  TGT
                                |||||||| |||||  |||
                                TGTCTCTT GACAT  ACA
                                     A    __
GAM1625  MGC10067 3'  GAAGAGAAATTGTGTCTAT   40196   T        AC
                                A AGAGAAATTGT  CTGT
                                | ||||||||||  ||||
                                C TCTCTTTAACA  GATA
                                 T         CA
GAM1625  LOC144481 3'  GAAAAGTTGACCTGTAT     40197      A   T
                                GAGAA TTG ACCTGTAT
                                ||||| ||| ||||||||
                                CTTTT AAC TGGACATA
                                   C   _
GAM1625  LOC254045 3'  GAAAAGTTGACCTGTAT     40197      A   T
                                GAGAA TTG ACCTGTAT
                                ||||| ||| ||||||||
                                CTTTT AAC TGGACATA
                                   C   _
GAM1626  FLJ11838 3'  CAAGATATGTTTATTCAT    40200
                                TAAGATATGTTTATTCAT
                                ||||||||||||||||||
                                GTTCTATACAAATAAGTA

GAM1627  AGM1     3'  TGACTGAATTGTATACTT    40203   A   TTCT
                                A ACTG    AATTGTATACTT
                                | ||||    ||||||||||||
                                A TGAC    TTAACATATGAA
                                 C   _____
GAM1627  CTNND2   3'  TAAACTATTCTGTGTCTTGTGC 40204          AA___    ATA
                TTA                   TAAACTGTTCT    TTGT   CTTA
                                ||||||||||     ||||   ||||
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                                ATTTGATAAGA    AACA  GAAT
                                      CACAG   C__
GAM1627 PCDHA9   3' CTGTGATCTTGTATACTTA   40205     TCTAA
                                CTGT    TTGTATACTTA
                                ||||    ||||||||||
                                GACA    AACATATGAAT
                                  CTAG_
GAM1627 DIS3     3' AACTGTTCTAGTTACTACTT  40206         A  GTA
                                AACTGTTCTA TT   TACTT
                                |||||||||| ||  |||||
                                TTGACAAGAT AA   ATGAA
                                      C  TG_
GAM1627 DKFZP564I052 3'  TAAACTGTTTTAATATAAATAC 40207         C    TGT_
             TT                   TAAACTGTT TAAT    ATACTT
                                |||||||| ||||   ||||||
                                ATTTGACAA ATTA    TATGAA
                                      A    TATT
GAM1627 FLJ10898 3'  TAAACTGTTCTGCAT      40208          AATT
                                TAAACTGTTCT    GTAT
                                ||||||||||    ||||
                                ATTTGACAAGA    CGTA
                                      ____
GAM1627 FLJ20152  3'  TAAACTGTTTTGCATGCTT    40209         CTAA     A
                                TAAACTGTT    TTGTAT CTT
                                ||||||||    |||||| |||
                                ATTTGACAA    AACGTA GAA
                                     ____     C
GAM1627 KIAA1579  3'  CTGTTCTAGTACTCTTA     40210         ATT    A
                                CTGTTCTA   GTAT CTTA
                                ||||||||   |||| ||||
                                GACAAGAT   CATG GAAT
                                     ___    A
GAM1627 LIG-1    3'  AACTGTTCTGACCTTTTGCTT  40211         A   GTATA
                                AACTGTTCT ATT     CTT
                                ||||||||| |||     |||
                                TTGACAAGA TGG     GAA
                                      C   AAAAC
GAM1627 ZDHHC2   3'  TAAACTGTGCTACCCATATA   40212         T   A TG
                                TAAACTGT CTA T  TATA
                                |||||||| ||| |  ||||
                                ATTTGACA GAT G  ATAT
                                     C   G GT
GAM1627 LOC253936 3'  TAAACTGCTCTGAGACACGCTT 40213           AATTG  TA
                                TAAACTGTTCT    TA  CTT
                                ||||||||||    ||  |||
                                ATTTGACGAGA    GT  GAA
                                      CTCT_  GC
GAM1627 LOC254436 3'  TAAACTATTCTAAAGACTT   40214            TTGTAT
                                TAAACTGTTCTAA     ACTT
                                ||||||||||||     ||||
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                                ATTTGATAAGATT     TGAA
                                      TC____
GAM1628 PCDH9    5' TTTGATAGGGTTGGCTACTAT 40217      CGA   CGTC
                                TTTGAT   GTT    GCTACTAT
                                ||||||   |||    ||||||||
                                AAACTA   CAA    CGATGATA
                                   TCC   C___
GAM1628 ATP10D   3' TTTGATCAGGCTACT      40218       G  TTCGTC
                                TTTGATC AG     GCTACT
                                ||||||| ||     ||||||
                                AAACTAG TC     CGATGA
                                  _ _______
GAM1629 ANXA11   3' TTTGTTAGAAACAGACA     40221      CC       T
                                TTTG  AGAAACAGG CA
                                ||||  ||||||||| ||
                                AAAC  TCTTTGTCT GT
                                  AA       _
GAM1629 ANXA9    3' TTTGCCAAAAGAATTCGAGTAT 40222          ACAGG  A
              C                  TTTGCCAGAA    TC AGTATC
                                 ||||||||||    || ||||||
                                 AAACGGTTTT    AG TCATAG
                                      CTTA_  C
GAM1629 ETV3     3' TTTGTAGAAACAGGTTCCCAT  40223     CC       _ AA
                                TTTG  AGAAACAGGT C  GT
                                ||||  |||||||||| |  ||
                                AAAC  TCTTTGTCCA G  TA
                                  A_        A GG
GAM1629 TP53BP2  3' TTTGCCAAAAATAATCGTAT   40224         CA   AA
                                TTTGCCAGAAA  GGTC  GTAT
                                ||||||||||  ||||  ||||
                                AAACGGTTTTT  TTAG  CATA
                                      A_   __
GAM1629 FLJ10713 3' AGAAACAGGGGAAGTATC    40225        TC
                                AGAAACAGG  AAGTATC
                                |||||||||  |||||||
                                TCTTTGTCC  TTCATAG
                                     CC
GAM1629 KIAA0931 5' TTTGCAGATGCATTCAAGTATC 40226      C   AA  GG
                                TTTGC AGA  CA  TCAAGTATC
                                ||||| |||  ||  |||||||||
                                AAACG TCT  GT  AGTTCATAG
                                  _  AC  A_
GAM1629 PAK7     3' TTTGCCAGAAAAGTA      40227          CAGGTCA
                                TTTGCCAGAAA      AGTA
                                ||||||||||      ||||
                                AAACGGTCTTT      TCAT
                                      _______
GAM1629 SPRY4    3' TTTGCCAGGAAATAGGGTC   40228        _   CA_
                                TTTGCCAG AAA   GGTC
                                |||||||| |||   ||||
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                                AAACGGTC TTT   CCAG
                                    C   ATC
GAM1629  LOC134111 3'  TCTGCCAGGGGTGGTCGCAGTA 40229        AAACA   A_
             TC                   TTTGCCAG    GGTC  AGTATC
                                  ||||||||    ||||  ||||||
                                  AGACGGTC    CCAG  TCATAG
                                      CCCA_   CG
GAM1629  LOC149705 3'  CAGAGAGGTTTCAAGTAT    40230     AAC  __
                                  CAGA   AGG  TCAAGTAT
                                  ||||   |||  ||||||||
                                  GTCT   TCC  AGTTCATA
                                    C__   AA
GAM1629  LOC158310 5'  CTTGACACTGTAGGTCAAGT   40231     C  GAAAC
                                  TTTG CA     AGGTCAAGT
                                  |||| ||     |||||||||
                                  GAAC GT     TCCAGTTCA
                                    T  GACA_
GAM1629  LOC202025 3'  TTTGCTGTGGGTCAAGTAT    40232      CAGAAACA
                                  TTTGC       GGTCAAGTAT
                                  |||||       ||||||||||
                                  AAACG       CCAGTTCATA
                                     ACAC____
GAM1629  LOC203274 3'  TTTGCAGGAAACAGGAATC    40233      CA      __
                                  TTTGC  GAAACAGG  TC
                                  |||||  ||||||||  ||
                                  AAACG  CTTTGTCC  AG
                                     TC       TT
GAM1629  LOC221395 3'  TTTGTTCAACAAGGTCAAGT   40234     CCAGA   _
                                  TTTG    AACA GGTCAAGT
                                  ||||    |||| ||||||||
                                  AAAC    TTGT CCAGTTCA
                                    AAG__    T
GAM1629  LOC254659 5'  TTTGCCAGTGACAGTCTGTC   40235       AA   ___
                                  TTTGCCAG  ACAG   GTC
                                  ||||||||  ||||   |||
                                  AAACGGTC  TGTC   CAG
                                      AC    AGA
GAM1629  LOC51103  5'  TGCCAGAAACTGCTCTAAGT   40236        AGG  _
                                  TGCCAGAAAC   TC AAGT
                                  ||||||||||   || ||||
                                  ACGGTCTTTG   AG TTCA
                                       ACG  A
GAM1629  LOC92399  3'  TTTGCCAGCAGCAAGTAT    40237       AAA   GT
                                  TTTGCCAG   CAG  CAAGTAT
                                  ||||||||   |||  |||||||
                                  AAACGGTC   GTC  GTTCATA
                                             ___   __
GAM1630  ABCD4     3'  TCTTACAGATCTCACACTTCCA 40240        CCA_  CT  C
             G                    TCTTACGGA    GC  CT CCAG
                                  |||||||||    ||  || ||||
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                              AGAATGTCT   TG  GA GGTC
                                   AGAG  T_  A
GAM1630  ABCD4    3'  TCTTACAGATCTCACACTTCCA 40240        CCA_  CT  C
           G                   TCTTACGGA   GC  CT CCAG
                              |||||||||   ||  || ||||
                              AGAATGTCT   TG  GA GGTC
                                   AGAG  T_  A
GAM1630  ABCD4    3'  TCTTACAGATCTCACACTTCCA 40240        CCA_  CT  C
           G                   TCTTACGGA   GC  CT CCAG
                              |||||||||   ||  || ||||
                              AGAATGTCT   TG  GA GGTC
                                   AGAG  T_  A
GAM1630  ABCD4    3'  TCTTACAGATCTCACACTTCCA 40240        CCA_  CT  C
           G                   TCTTACGGA   GC  CT CCAG
                              |||||||||   ||  || ||||
                              AGAATGTCT   TG  GA GGTC
                                   AGAG  T_  A
GAM1630  AP1M1    3'  TCTTGAAGACCAGCCTCT    40241     AC
                              TCTT  GGACCAGCCTCT
                              ||||  ||||||||||||
                              AGAA  TCTGGTCGGAGA
                                CT
GAM1630  CKTSF1B1 3'  CACACCAGCCTCTCCCAG    40242    G
                              CG ACCAGCCTCTCCCAG
                              || ||||||||||||||||
                              GT TGGTCGGAGAGGGTC
                               G
GAM1630  IL1R1    3'  TCTTAGGGAAAGTCTCCCAG   40243      C   CC  CC
                              TCTTA GGA  AG  TCTCCCAG
                              ||||| |||  ||  ||||||||
                              AGAAT CCT  TC  AGAGGGTC
                                 C   T_  __
GAM1630  ITPKB    3'  TCTTACAGGGCCAGGGCTGCT  40244        A_   C_  _
                              TCTTACGG  CCAG  CT CT
                              ||||||||  ||||  || ||
                              AGAATGTC  GGTC  GA GA
                                   CC    CC  C
GAM1630  LGALS3BP 5'  GACCCAGAAGCCTCTCCCAG   40245     _____
                              GACC    AGCCTCTCCCAG
                              ||||    ||||||||||||
                              CTGG    TCGGAGAGGGTC
                                GTCT
GAM1630  NCKAP1   5'  CCTTCGCAGCAGCCTCTC    40246     A  GAC
                              TCTT CG   CAGCCTCTC
                              |||| ||   |||||||||
                              GGAA GC   GTCGGAGAG
                                _  GTC
GAM1630  PLA2G5   3'  CTTAGGAGCCTCTCTCA     40247     C   CCA      C
                              CTTA GGA   GCCTCTC CA
                              |||| |||   ||||||| ||
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                                GAAT CCT   CGGAGAG GT
                                  _  ___      A
GAM1630  ROBO1    5'  TCTTGCGGAGCCTCCC      40248      A    CCA
                                TCTT CGGA   GCCTCTC
                                |||| ||||   |||||||
                                AGAA GCCT   CGGAGGG
                                  C   ___
GAM1630  FLJ10081 5'  TCTTACGGCCGCGCGCTC    40249        A  A_  _
                                TCTTACGG CC  GC CTC
                                |||||||| ||  || |||
                                AGAATGCC GG  CG GAG
                                     _ CG  C
GAM1630  HEYL     3'  TCTCTGAGGGTCTCTCCCAG   40250      AC_  ACCAGC
                                TCTT   GG     CTCTCCCAG
                                ||||   ||     |||||||||
                                AGAG   CC     GAGAGGGTC
                                  ACT  CA____
GAM1630  KIAA0323 3'  TCTTAGATTCCTCTCCCA    40251      AC   CCAG
                                TCTT  GGA    CCTCTCCCA
                                ||||  |||    |||||||||
                                AGAA  TCT    GGAGAGGGT
                                  __   AA__
GAM1630  KIAA0939 3'  TCTTGGGGGCACTCTCCCAG   40252      AC  ACCA  _
                                TCTT  GG    GC CTCTCCCAG
                                ||||  ||    || |||||||||
                                AGAA  CC    CG GAGAGGGTC
                                  CC  _____  T
GAM1630  KIAA1391 3'  CCTTATGCTACCTCTCCCAG   40253      CGGACCA
                                TCTTA       GCCTCTCCCAG
                                |||||       ||||||||||
                                GGAAT       TGGAGAGGGTC
                                   ACGA___
GAM1630  KRTHB3   3'  TCTCACAGTGCTTCTTCCAG   40254        ACCA  C   C
                                TCTTACGG    GC TCT CCAG
                                ||||||||    || ||| ||||
                                AGAGTGTC    CG AGA GGTC
                                     A___  A   A
GAM1630  MYT1L    5'  TCTTACAGGAAGTCTTCTCTCC 40255       _  CCAGC_
                                TCTTAC GGA      CTCTCC
                                |||||| |||      ||||||
                                AGAATG CCT      GAGAGG
                                    T   TCAGAA
GAM1630  SEMA5A   3'  TTACAGACTGGCTCTTCAG    40256        CA  C   CC
                                TTACGGAC  GC TCT  CAG
                                ||||||||  || |||  |||
                                AATGTCTG  CG AGA  GTC
                                     AC  _   A_
GAM1630  LOC146443 5'  TCTGCAGGGCCTCTCCCA    40257     TAC  ACCA
                                TCT   GG    GCCTCTCCCA
                                |||   ||    ||||||||||
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                                AGA  CC   CGGAGAGGGT
                                  CGT ____
GAM1630 LOC149076 3' TCTGCGGACCAAGCTTTCT  40258    TA     _ C_
                                TCT  CGGACCA GC  TCT
                                |||  ||||||| ||  |||
                                AGA  GCCTGGT CG  AGA
                                  C_     T  AA
GAM1630 LOC152627 5' CTTCGTGAGCCAGCCTCTCC  40259    A  _  _
                                CTT CG GA CCAGCCTCTCC
                                ||| || || ||||||||||
                                GAA GC CT GGTCGGAGAGG
                                  _  A  C
GAM1630 LOC166341 3' TCTTGGGATGCCTCCCA    40260    AC  CCA  TC
                                TCTT  GGA  GCC  TCCCA
                                ||||  |||  |||  |||||
                                AGAA  CCT  CGG  AGGGT
                                  C_  A__  __
GAM1630 LOC221865 3' TCTTGTGGTCAGTGGCTGCCCC 40261    AC  AC  C__  C
          AG                      TCTT  GG  CAG  CT TCCCAG
                                ||||  ||  |||  || ||||||
                                AGAA  CC  GTC  GA GGGGTC
                                  CA  A_  ACC  C
GAM1630 LOC255152 5' TCTTACAGAGATTCCTTTTCTC 40262       CCAG  ___
                                TCTTACGGA   CC  TCTC
                                |||||||||   ||  ||||
                                AGAATGTCT   GG  AGAG
                                     CTAA  AAA
GAM1630 LOC55908  5' GGACCAGCCGCCGCCCAG   40263       _  T
                                GGACCAGCC TC CCCAG
                                ||||||||| || |||||
                                CCTGGTCGG GG GGGTC
                                     C  C
GAM1630 LOC91355  5' TCTTCTGCCAGCCCCTCTCC  40264    ACGGA       _
                                TCTT    CCAGCCTCTC CC
                                ||||    |||||||||| ||
                                AGAA    GGTCGGGGAG GG
                                  GAC__       A
GAM1630 LOC92017  5' TCTCACGGGTTAGTATCTCTCA 40265       ACC  CC   C
          G                      TCTTACGG  AG  TCTC CAG
                                |||||||  ||  |||| |||
                                AGAGTGCC  TC  AGAG GTC
                                    CAA  AT   A
GAM1631 CXCL13   3' TATTACTTATAACTGAATAAC  40268           T
                                TATTATTTATAACTGA GTAAC
                                |||||||||||||||| |||||
                                ATAATGAATATTGACT TATTG
                                                 _
GAM1631 RASGRP1  3' TATTATTTAAGCCACTGAT   40269       TA__
                                TATTATTTA   ACTGAT
                                |||||||||   ||||||
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                                ATAATAAAT   TGACTA
                                     TCGG
GAM1631 HTGN29   3' TATTATTTAAGTGATAATGACC 40270       TAAC    TA_
            C                   TATTATTTA   TGATG  ACCC
                                |||||||||   |||||  ||||
                                ATAATAAAT   ACTAT  TGGG
                                     TC__    TAC
GAM1631 JIK     5' TATTTATGATGCAACC     40271      TAAC
                                TATTTA   TGATGTAACC
                                ||||||   ||||||||||
                                ATAAAT   ACTACGTTGG
                                    ____
GAM1631 KIAA1430 3' TTTGCAACTGATGTGGTCC   40272    A       AA_
                                TTT TAACTGATGT  CC
                                ||| ||||||||||  ||
                                AAA GTTGACTACA  GG
                                  C        CCA
GAM1631 KIAA1764 5' TACTATTTATAACTGAAGC   40273           T
                                TATTATTTATAACTGA GT
                                |||||||||||||||| ||
                                ATGATAAATATTGACT CG
                                          T
GAM1631 RAN     3' TATTTACACCATGTAACCC   40274       A  G
                                TATTTATA CT ATGTAACCC
                                |||||||| || |||||||||
                                ATAAATGT GG TACATTGGG
                                    _ _
GAM1631 ZAK     3' TATTATTTGAAACTGATA    40275       AT
                                TATTATTT  AACTGATG
                                ||||||||  ||||||||
                                ATAATAAA  TTGACTAT
                                     CT
GAM1631 LOC151571 5' TCATTTATGATGTATATAACC  40276       AACTG
                                TTATTTAT    ATGTAACC
                                ||||||||    ||||||||
                                AGTAAATA    TATATTGG
                                     CTACA
GAM1631 LOC196989 3' TTATTTATAGCTCTATGTGCCC 40277       A  G_   AA
                                TTATTTATA CT  ATGT  CC
                                ||||||||| ||  ||||  ||
                                AATAAATAT GA  TACA  GG
                                     C  GA   CG
GAM1631 LOC221431 3' TATTATTTATGACCTGATATA  40278        AA_
                                TATTATTTAT   CTGATGTA
                                ||||||||||   ||||||||
                                ATAATAAATA   GACTATAT
                                      CTG
GAM1632 HDAC4    3' TGCTGGTGGGGCGTGGGCA   40281      T     CAAGA
                                TGCTG TGGGGCG    GCG
                                ||||| |||||||    |||
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                                ACGAC ACCCCGC    CGT
                                  C      ACC__
GAM1632 NID      3' TGTTGTTGGGGCTCAGGC    40282    C       GCA  A
                                TG TGTTGGGGC   AG GC
                                || |||||||||   || ||
                                AC ACAACCCCG   TC CG
                                 A        AG_  _
GAM1632 DDX17    5' GCTGTTGGGGCGGCGC      40283          CAAGA   A
                                GCTGTTGGGGCG    GCG C
                                ||||||||||||    ||| |
                                CGACAACCCCGC    CGC G
                                       _____  C
GAM1632 DKFZP761I2123 5' TGCTGCTTGGGGTCATGGGTGG 40284        _   _ CAAGA_
             CG                    TGCTGTT GGGG CG     GCG
                                |||||||| |||| ||     |||
                                ACGACGA CCCC GT     CGC
                                    A   A  ACCCAC
GAM1632 HSJ001348 5' TGCTGTTGGAGCGGCCGGCG   40285           _ AAGA
                                TGCTGTTGGGGCG C    GCG
                                |||||||||||| |    |||
                                ACGACAACCTCGC G    CGC
                                       C GC__
GAM1632 KIAA0410  3' CTGTTGTTAAGAGCGAC     40286       GGGCGC
                                CTGTTG     AAGAGCGAC
                                ||||||     |||||||||
                                GACAAC     TTCTCGCTG
                                   AA____
GAM1632 KIAA1218  5' TGCTGCTGGCAGAGTGA     40287        GGGC   A   C
                                TGCTGTTG    GCA GAG GA
                                ||||||||    ||| ||| ||
                                ACGACGAC    CGT CTC CT
                                     _____   _   A
GAM1632 MASA     5' TGCTGTTGGGGAGGGCGGAGGG 40288          C__  A_  A
             CG                    TGCTGTTGGGG   GC  AG GCG
                                |||||||||||   ||  || |||
                                ACGACAACCCC   CG  TC CGC
                                      TCC  CC  C
GAM1633 CD2      3' TGTGATGGAGCTCTCTGA    40291          AGCCTA   C
                                TGTGATGGGGC     CTC GA
                                ||||||||||      ||| ||
                                ACACTACCTCG     GAG CT
                                      A_____   A
GAM1633 CHRM1    3' TGTGTGGGGCAGGGCCG     40292      A       CCTACT
                                TGTG TGGGGCAG     CCG
                                ||||  ||||||||      |||
                                ACAC ACCCCGTC     GGC
                                  _       CC_____
GAM1633 PIK3R1   3' TGGGGAAGCTTATTCTGAA   40293      C   C  C  C
                                TGGGG AGC TA TC GAA
                                ||||| ||| || || |||
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                                ACCCC TCG AT AG CTT
                                   T  A  A  A
GAM1633  SDC2     3'  GTGATGGGGCAGGAATCTGA  40294          CCTAC  C
                                GTGATGGGGCAG    TC GA
                                ||||||||||||   || ||
                                CACTACCCCGTC    AG CT
                                      CTT__  A
GAM1633  B3GNT7   3'  TGCGGTGGGGCAGGGCTC   40295     A      CCTA
                                TGTG TGGGGCAG   CTC
                                |||| ||||||||   |||
                                ACGC ACCCCGTC   GAG
                                  C       CC__
GAM1633  EZF-2    5'  TGTGAGGGGGCAGCGCTCACTC 40296      T      _ _
                                TGTGA GGGGCAGC CT ACTC
                                ||||| |||||||| || ||||
                                ACACT CCCCGTCG GA TGAG
                                   C       C  G
GAM1633  RHOBTB2  5'  TGTGACGGGGTGGCTTCTA   40297         CA __
                                TGTGATGGGG  GC  CTA
                                ||||||||||  ||  |||
                                ACACTGCCCC  CG  GAT
                                      AC  AA
GAM1633  SEC61A1  3'  TGTGATAGGGTGGTAAGCCC  40298         C____
                                TGTGATGGGG    AGCCT
                                ||||||||||    |||||
                                ACACTATCCC    TCGGG
                                      ACCAT
GAM1633  TRIM29   3'  TGTGATGGGTTGGCCTCT    40299        GCA   A
                                TGTGATGGG   GCCT CT
                                |||||||||   |||| ||
                                ACACTACCC   CGGA GA
                                     AAC   _
GAM1633  LOC115399 3'  TGTGTTGGGGCAGCTGCTC   40300     A       CTA
                                TGTG TGGGGCAGC   CTC
                                |||| |||||||||   |||
                                ACAC ACCCCGTCG   GAG
                                  A       AC_
GAM1633  LOC128954 5'  TGGATGGGGCCCCTCT     40301    T      AG   A
                                TG GATGGGGC  CCT CT
                                || ||||||||  ||| ||
                                AC CTACCCCG  GGA GA
                                 _       G_  _
GAM1633  LOC149506 5'  TGTGATGGGGCAGTTCCCA   40148          __
                                TGTGATGGGGCAG  CCTA
                                ||||||||||||  ||||
                                ACACTACCCCGTC  GGGT
                                      AA
GAM1633  LOC150378 5'  TGTGTGGGGCAGGGGCACT   40302     A      CC_
                                TGTG TGGGGCAG   TACT
                                |||| ||||||||   ||||
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                                ACAC ACCCCGTC   GTGA
                                  _      CCC
GAM1633  LOC164397 5'  GTGATGGGGCAGTTTCCCA   40303          ___
                                GTGATGGGGCAG   CCTA
                                ||||||||||||  ||||
                                CACTACCCCGTC   GGGT
                                       AAA
GAM1633  LOC220394 5'  TGTGATGGACATATTCTGA   40304        G  GCCTAC  C
                                TGTGATGGG CA     TC GA
                                |||||||||  ||     || ||
                                ACACTACCT GT     AG CT
                                      _ ATA___  A
GAM1633  LOC245744 3'  TGTGATGGGGCGGCAGCCCCG  40149          A  CTA
                                TGTGATGGGGC GC   CTCCG
                                ||||||||||| ||   |||||
                                ACACTACCCCG CG   GGGGC
                                       C  TC_
GAM1634  GPC6     5'  CGCGCTCCTCGCCGCTGCCCAG 40307         AA   CA__  A
            CGT                   CGCGCTCCTC  CGC    CG CGT
                                ||||||||||  |||    || |||
                                GCGCGAGGAG  GCG    GT GCA
                                      CG   ACGG  C
GAM1634  HHIP     5'  CGCGCCCCTTGACGTCACCGC  40308         CA   C   GA
                                CGCGCTCCT  ACG CAC  CGT
                                |||||||||  ||| |||  |||
                                GCGCGGGGA  TGC GTG  GCG
                                      AC   A  __
GAM1634  HYAL3    5'  GCGTCCTGCGGCACGCCACGGC 40309     C   CA___      A
            GT                    GCG TCCT    ACGCCACG CGT
                                |||  ||||    |||||||| |||
                                CGC AGGA    TGCGGTGC GCA
                                  _   CGCCG       C
GAM1634  FLJ21159  5'  ACCGCTCTTCGGCCCAACG   40310    G    C  AAC   A
                                AC CGCTC TC   GCC CGACG
                                || ||||| ||   ||| |||||
                                TG GCGAG AG   CGG GTTGC
                                 _    A  C__  _
GAM1634  MGC1203   3'  GCTCCTCAGGCTCGGCGT    40311        AC  CA  A
                                GCTCCTCA  GC  CG CGT
                                ||||||||  ||  || |||
                                CGAGGAGT  CG  GC GCA
                                     C_  A_  C
GAM1634  LOC143384 5'  GCGCTCCTCACGACG       40312         AACGCC
                                GCGCTCCTC     ACGACG
                                |||||||||     ||||||
                                CGCGAGGAG     TGCTGC
                                              _____
GAM1635  FLJ11838  3'  CAAGATATGTTTATTCAT    40200
                                TAAGATATGTTTATTCAT
                                ||||||||||||||||||
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                                GTTCTATACAAATAAGTA

GAM1636  FLJ23416  3'  TAAGAATTTAGAAATCATC   40316          TA_
                                TAAGAATTTAGA  CATC
                                ||||||||||||  ||||
                                ATTCTTAAATCT  GTAG
                                      TTA
GAM1636  FLJ31153  3'  AGAATTCAGATATTTATATT  40317          CATC
                                AGAATTTAGATA   TATATT
                                ||||||||||||   ||||||
                                TCTTAAGTCTAT   ATATAA
                                      AA__
GAM1636  KIAA1545  3'  TAAGAATTTAGTAACGTCATAT 40318          AT  A  _
            ATT                   TAAGAATTTAG  AC TC TATATT
                                ||||||||||  || || ||||||
                                ATTCTTAAATC  TG AG ATATAA
                                      AT  C  T
GAM1636  MO25     3'  TAAAAATAAAATATATCTATAT 40319       TT    C
            T                    TAAGAAT  AGATA ATCTATATT
                                |||||||  ||||| |||||||||
                                ATTTTTA  TTTAT TAGATATAA
                                    T_    A
GAM1636  LOC222160 5'  TAAGGGTCTAGATACAACT   40320      AA        T
                                TAAG  TTTAGATACA CT
                                ||||  |||||||||| ||
                                ATTC  AGATCTATGT GA
                                  CC         T
GAM1637  EZH1     3'  TGGGACAGGTGGTCTACCT   40323     CGTC  C    C
                                TGG   GGC GGTGG CTACCT
                                |||   ||| ||||| ||||||
                                ACC   CTG CCACC GATGGA
                                  _____  T    A
GAM1637  TEM7     3'  TGGCGGCAGATGGCCT      40324      GTC  C
                                TGGC  GGC GGTGGCCT
                                ||||  ||| ||||||||
                                ACCG  CCG CTACCGGA
                                  ___  T
GAM1637  FLJ10081  3'  TGGTGTGGTATGATCCTACCTG 40325     C  C  CCG   _
                                TGG GT GG   GTGG CCTACCTG
                                ||| || ||   |||| ||||||||
                                ACC CA CC   TACT GGATGGAC
                                  A  _  A__    A
GAM1637  SFRS8    3'  TGGTGTGGCCGGCGTCT     40326     C  C       GC
                                TGG GT GGCCGGTG  CT
                                ||| || ||||||||  ||
                                ACC CA CCGGCCGC  GA
                                  A  _       A_
GAM1637  LOC200213 5'  TGGCGTCGGCCGCCCGGCCT  40327          G_
                                TGGCGTCGGCCG  TGGCCT
                                ||||||||||||  ||||||
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                                ACCGCAGCCGGC GCCGGA
                                      GG
GAM1637 LOC255218 3' GCAGGGTGGTGGCCTGTCTG  40328    TC CC      AC
                                GCG GG GGTGGCCT CTG
                                ||| || |||||||| |||
                                CGT CC CCACCGGA GAC
                                  C_ A_      CA
GAM1638 ABCD4    3' TCTTACAGATCTCACACTTCCA 40240         A_ CT C
          G                      TCTTACGGATC GC CT CCAG
                                ||||||||||| || || ||||
                                AGAATGTCTAG TG GA GGTC
                                      AG T_ A
GAM1638 ABCD4    3' TCTTACAGATCTCACACTTCCA 40240         A_ CT C
          G                      TCTTACGGATC GC CT CCAG
                                ||||||||||| || || ||||
                                AGAATGTCTAG TG GA GGTC
                                      AG T_ A
GAM1638 ABCD4    3' TCTTACAGATCTCACACTTCCA 40240         A_ CT C
          G                      TCTTACGGATC GC CT CCAG
                                ||||||||||| || || ||||
                                AGAATGTCTAG TG GA GGTC
                                      AG T_ A
GAM1638 ABCD4    3' TCTTACAGATCTCACACTTCCA 40240         A_ CT C
          G                      TCTTACGGATC GC CT CCAG
                                ||||||||||| || || ||||
                                AGAATGTCTAG TG GA GGTC
                                      AG T_ A
GAM1638 AP1M1    3' TCTTGAAGACCAGCCTCT    40241     AC
                                TCTT GGATCAGCCTCT
                                |||| ||||||||||||
                                AGAA TCTGGTCGGAGA
                                  CT
GAM1638 CLASP1   3' CAACATCAGTCTTTCCCAG   40331    _    C C
                                CGG ATCAG CT TCCCAG
                                ||| ||||| || ||||||
                                GTT TAGTC GA AGGGTC
                                  G    A A
GAM1638 IL1R1    3' TCTTAGGGAAAGTCTCCCAG  40243      C  TC CC
                                TCTTA GGA AG TCTCCCAG
                                ||||| ||| || ||||||||
                                AGAAT CCT TC AGAGGGTC
                                   C  T_ __
GAM1638 LGALS3BP 5' CAGAAGCCTCTCCCAG     40332     TC
                                CGGA AGCCTCTCCCAG
                                |||| ||||||||||||
                                GTCT TCGGAGAGGGTC
                                   __
GAM1638 NCKAP1   5' CCTTCGCAGCAGCCTCTC    40246     A GAT
                                TCTT CG  CAGCCTCTC
                                |||| ||  |||||||||
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                                GGAA GC   GTCGGAGAG
                                  _ GTC
GAM1638 PLA2G5   3' CTTAGGAGCCTCTCTCA     40247     C   TCA      C
                                CTTA GGA   GCCTCTC CA
                                |||| |||   ||||||| ||
                                GAAT CCT   CGGAGAG GT
                                  _  ___      A
GAM1638 RAD54L   3' TCTTGATGATTTTCTCCCAG  40333     ACG   CAGCC
                                TCTT   GAT    TCTCCCAG
                                ||||   |||    ||||||||
                                AGAA   CTA    AGAGGGTC
                                  CTA   AA___
GAM1638 FLJ11053 3' TCTCTGACAGTCTTTCCCAG  40334     ACG  T   C  C
                                TCTT   GA CAG CT TCCCAG
                                ||||   || ||| || ||||||
                                AGAG   CT GTC GA AGGGTC
                                  A__ _   A  A
GAM1638 FLJ22477 3' TCTCGTGAGTCTTTCTCCCAG 40335     AC GA  AGCC
                                TCTT  G  TC    TCTCCCAG
                                ||||  |  ||    ||||||||
                                AGAG  C  AG    AGAGGGTC
                                  CA TC  AA__
GAM1638 HEYL     3' TCTCTGAGGGTCTCTCCCAG  40250     AC_  ATCAGC
                                TCTT   GG     CTCTCCCAG
                                ||||   ||     |||||||||
                                AGAG   CC     GAGAGGGTC
                                  ACT  CA____
GAM1638 KCNS1    3' TCTTGTGGATCAACTCT     40336     AC       C
                                TCTT  GGATCAGC TCT
                                ||||  |||||||| |||
                                AGAA  CCTAGTTG AGA
                                  CA       _
GAM1638 KIAA0303 5' TCTTCCGGATCAAATTCCCAG 40337     A       CCTC
                                TCTT CGGATCAG    TCCCAG
                                |||| ||||||||    ||||||
                                AGAA GCCTAGTT    AGGGTC
                                  G       TA__
GAM1638 KIAA0323 3' TCTTAGATTCCTCTCCCA    40251     AC    CAG
                                TCTT  GGAT   CCTCTCCCA
                                ||||  ||||   |||||||||
                                AGAA  TCTA   GGAGAGGGT
                                  __    A__
GAM1638 KIAA0939 3' TCTTGGGGGCACTCTCCCAG  40252     AC  ATCA  _
                                TCTT  GG   GC CTCTCCCAG
                                ||||  ||   || |||||||||
                                AGAA  CC   CG GAGAGGGTC
                                  CC  _____ T
GAM1638 KIAA1391 3' CCTTATGCTACCTCTCCCAG  40253      CGGATCA
                                TCTTA      GCCTCTCCCAG
                                |||||      ||||||||||
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                                GGAAT      TGGAGAGGGTC
                                  ACGA___
GAM1638  KIAA1915  3'  TCTTGTCATGCCTCTCC     40338      ACGGA  _
                                TCTT    TCA GCCTCTCC
                                ||||    ||| ||||||||
                                AGAA    AGT CGGAGAGG
                                  C____   A
GAM1638  KRTHB3    3'  TCTCACAGTGCTTCTTCCAG   40254        ATCA  C   C
                                TCTTACGG   GC TCT CCAG
                                ||||||||   || ||| ||||
                                AGAGTGTC   CG AGA GGTC
                                    A___  A   A
GAM1638  MYT1L     5'  TCTTACAGGAAGTCTTCTCTCC 40255       _  TCAGC_
                                TCTTAC GGA     CTCTCC
                                |||||| |||     ||||||
                                AGAATG CCT     GAGAGG
                                   T   TCAGAA
GAM1638  LOC146443 5'  TCTGCAGGGCCTCTCCCA    40257     TAC  ATCA
                                TCT   GG   GCCTCTCCCA
                                |||   ||   ||||||||||
                                AGA   CC   CGGAGAGGGT
                                 CGT  ____
GAM1638  LOC155066 5'  TTACAGATCAGTGGCCTCC    40339         ___
                                TTACGGATCA   GCCTCT
                                ||||||||||   ||||||
                                AATGTCTAGT   CGGAGG
                                     CAC
GAM1638  LOC166341 3'  TCTTGGGATGCCTCCCA     40260     AC   CA   TC
                                TCTT  GGAT  GCC  TCCCA
                                ||||  ||||  |||  |||||
                                AGAA  CCTA  CGG  AGGGT
                                  C_   __   __
GAM1638  LOC221865 3'  TCTTGTGGTCAGTGGCTGCCCC 40261      AC  A   C__  C
            AG                    TCTT  GG TCAG   CT TCCCAG
                                ||||  || ||||   || ||||||
                                AGAA  CC AGTC   GA GGGGTC
                                  CA  _   ACC  C
GAM1638  LOC255152 5'  TCTTACAGAGATTCCTTTTCTC 40262         TCAG  ___
                                TCTTACGGA   CC   TCTC
                                |||||||||   ||   ||||
                                AGAATGTCT   GG   AGAG
                                     CTAA  AAA
GAM1638  LOC257289 5'  TCTCCATGGCCTCTCCC     40340     A  GATCA
                                TCTT CG    GCCTCTCCC
                                |||| ||    |||||||||
                                AGAG GT    CGGAGAGGG
                                  _ AC___
GAM1638  LOC91355  5'  TCTTCTGCCAGCCCCTCTCC   40264     ACGGA       _
                                TCTT    TCAGCCTCTC CC
                                ||||    |||||||||| ||
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                                AGAA    GGTCGGGGAG GG
                                  GAC__        A
GAM1638 LOC92017 5' TCTCACGGGTTAGTATCTCTCA 40265       ATC  CC    C
             G                    TCTTACGG   AG  TCTC CAG
                                  ||||||||   ||  |||| |||
                                  AGAGTGCC   TC  AGAG GTC
                                      CAA  AT    A
GAM1639 FLJ23132 3' TAGTATATGAGATGGTTA    40343       CT_
                                  TAGTATGT   ATGGTTA
                                  ||||||||   |||||||
                                  ATCATATA   TACCAAT
                                      CTC
GAM1639 MIG-6    3' CAGCTATGGTCTATGGTTA    40344     _  _
                                  TAGT ATG TCTATGGTTA
                                  |||| ||| ||||||||||
                                  GTCG TAC AGATACCAAT
                                    A   C
GAM1639 LOC151360 3' TAATATGTACTGTGGTTA    40345       _ A
                                  TAGTATGT CT TGGTTA
                                  |||||||| || ||||||
                                  ATTATACA GA ACCAAT
                                      T  C
GAM1639 LOC151361 3' TAATATGTACTGTGGTTA    40345       _ A
                                  TAGTATGT CT TGGTTA
                                  |||||||| || ||||||
                                  ATTATACA GA ACCAAT
                                      T  C
GAM1640 SYCP1    3' TCCAAAATATTTTAATAG    40348       TC_
                                  TCCAAAAT   TTAATAG
                                  ||||||||   |||||||
                                  AGGTTTTA   AATTATC
                                      TAA
GAM1640 KIAA0555 3' CCCGACTCTTGGTAGAAATTTA 40349    AAA     AA
                                  CC   ATTCTT  TAGAAATTTA
                                  ||   ||||||  ||||||||||
                                  GG   TGAGAA  ATCTTTAAAT
                                   GC_     CC
GAM1640 PTK9     3' TCCAGGATTCTTAATGCAATAA 40350     AA       A_ _
             TTT                    TCCA  ATTCTTAAT  GA AATTT
                                  ||||  |||||||||  || |||||
                                  AGGT  TAAGAATTA  TT TTAAA
                                    CC        CG  A
GAM1640 LOC91286 3' TCCAAAATTTTGAATAGA    40351        CTT
                                  TCCAAAATT   AATAGA
                                  |||||||||   ||||||
                                  AGGTTTTAA   TTATCT
                                       AAC
GAM1641 COX15    5' TCCACAACCCAGGGCTCTGTGG 40354       AA____    C
                                  TCCACAAC     CTCTG GG
                                  ||||||||     ||||| ||
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                                AGGTGTTG     GAGAC CC
                                     GGTCCC    A
GAM1641  COX15    5'  TCCACAACCCAGGGCTCTGTGG 40354        AA____    C
                                TCCACAAC     CTCTG GG
                                ||||||||     ||||| ||
                                AGGTGTTG     GAGAC CC
                                     GGTCCC    A
GAM1641  MEN1     5'  TCCACAACACACACCACGG   40355         _ T TG
                                TCCACAACA AC C  CGG
                                ||||||||| || |  |||
                                AGGTGTTGT TG G  GCC
                                      G  T GT
GAM1641  NDUFA1   5'  TCCCAGCAAGCCCCGCGG    40356     A  A  _
                                TCC CA CAA CTCTGCGG
                                ||| || ||| ||||||||
                                AGG GT GTT GGGGCGCC
                                  _ C   C
GAM1641  RTN2     3'  TCCCAGCAGGCCCCGCGG    40357     A  A  A_
                                TCC CA CA  CTCTGCGG
                                ||| || ||  ||||||||
                                AGG GT GT  GGGGCGCC
                                  _ C  CC
GAM1641  TOP3B    5'  CCCACAGCAAGCCCCGCGG   40358       A  _
                                TCCACA CAA CTCTGCGG
                                |||||| ||| ||||||||
                                GGGTGT GTT GGGGCGCC
                                    C   C
GAM1641  DKFZP434N178 3'  TCCACAAAAACTGCTTGG    40359        C    _ GC
                                TCCACAA AACT CT  GG
                                ||||||| |||| ||  ||
                                AGGTGTT TTGA GA  CC
                                     T    C  A_
GAM1641  EIF2S2   3'  TCCACAACAAGCTTTGCA    40360          _ C
                                TCCACAACAA CT TGCG
                                |||||||||| || ||||
                                AGGTGTTGTT GA ACGT
                                      C  A
GAM1641  FLJ20010 5'  CCCACAACTGAGCCTGCGG   40361         AAC_
                                TCCACAAC    TCTGCGG
                                ||||||||    |||||||
                                GGGTGTTG    GGACGCC
                                     ACTC
GAM1641  HSPC251  3'  TCCACAACAGTCTCTGTGG   40362         A_    C
                                TCCACAACA  CTCTG GG
                                |||||||||  ||||| ||
                                AGGTGTTGT  GAGAC CC
                                      CA    A
GAM1641  KIAA1094 5'  TCCACCGCAGGTCACTTCTGCG 40363       AA _____  _     III
            GC                    TCCAC  CA    ACT CTGCGG   C
                                ||||| ||    ||| ||||||   |
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                                AGGTG  GT    TGA GACGCC   G
                                  GC  CCAG   A     III
GAM1641  KIAA1317  3'  TCCACAACAACACAG       40364          TCT
                                TCCACAACAAC   GCGG
                                ||||||||||   ||||
                                AGGTGTTGTTG   TGTC
                                      ___
GAM1641  MGC16703  5'  CCCACAACCCCTGCGG      40365         AA
                                TCCACAAC  CTCTGCGG
                                ||||||||  ||||||||
                                GGGTGTTG  GGGACGCC
                                      __
GAM1641  MLZE      5'  TCCCAGCAACTCTAGCTGG   40366     A  A      _  _
                                TCC CA CAACTCT GC GG
                                ||| || ||||||| || ||
                                AGG GT GTTGAGA CG CC
                                  _  C      T  A
GAM1641  TP53TG3   3'  TCCACAGCAGCTCCCAG     40367       A  A    G
                                TCCACA CA CTCT CGG
                                ||||||  ||  ||||  |||
                                AGGTGT GT GAGG GTC
                                   C  C    _
GAM1641  LOC151040 3'  CCCACAACAGTCCCCGG     40368          AC   G
                                TCCACAACA  TCT CGG
                                |||||||||  |||  |||
                                GGGTGTTGT  AGG GCC
                                     C_   G
GAM1641  LOC157254 5'  TCCGCAACCCCCGCGG      40369     A    AA
                                TCC CAAC  CTCTGCGG
                                |||  ||||  ||||||||
                                AGG GTTG  GGGGCGCC
                                  C    __
GAM1641  LOC165757 5'  TCCGAACAGCCCTGCGG     40370     AC    A
                                TCC  AACA CTCTGCGG
                                |||  ||||  ||||||||
                                AGG  TTGT GGGACGCC
                                  C_    C
GAM1641  LOC199796 5'  TCCACAAACGACTTGTCTGTGG 40371         _ A  ___    C
                                TCCACAA C AC   TCTG GG
                                |||||||  |  ||   ||||  ||
                                AGGTGTT G TG   AGAC CC
                                    T C  AAC    A
GAM1641  LOC203696 5'  CCCACAACTGCCTGCGG     40372         AAC
                                TCCACAAC   TCTGCGG
                                ||||||||   |||||||
                                GGGTGTTG   GGACGCC
                                     AC_
GAM1641  LOC222252 3'  CCCACAACAGTCCCCGG     40368          AC   G
                                TCCACAACA  TCT CGG
                                |||||||||  |||  |||
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                                GGGTGTTGT  AGG GCC
                                     C_   G
GAM1641  LOC255849 5'  CCCACAGCATCCACTCTGTGG  40373       A ___     C
                                TCCACA CA   ACTCTG GG
                                |||||| ||   |||||| ||
                                GGGTGT GT   TGAGAC CC
                                   C  AGG     A
GAM1641  LOC257364 3'  CCCACAGCAAGCTGCTGG    40374       A   CT   _
                                TCCACA CAA  CTGC GG
                                |||||| |||  |||| ||
                                GGGTGT GTT  GACG CC
                                   C   C_    A
GAM1642  ADRA2B    3'  AGAAAGGGAAGCCCAGACATTG 40377     C   AACT TA
              G                  AGA AGG    G  CAGACATTGG
                                 ||| |||    |  ||||||||||
                                 TCT TCC    C  GTCTGTAACC
                                   T   CTT_ GG
GAM1642  CLCN5     5'  AGACAGGAGTTGATGTGCAATG 40378        AC  TACAGA  T
              G                  AGACAGGA  TG     CA TGG
                                 ||||||||  ||     || |||
                                 TCTGTCCT  AC     GT ACC
                                      CA  TACAC_  T
GAM1642  KRTHA4    3'  GAAGGAGTTGTCCAGACATTGG 40379    C    AC   A
                                 GA AGGA  TGT CAGACATTGG
                                 || ||||  ||| ||||||||||
                                 CT TCCT  ACA GTCTGTAACC
                                  _   CA   G
GAM1642  SHOX2     3'  GACAGGCGCGACATT      40380       AAC   ACA
                                 GACAGG   TGT   GACATT
                                 ||||||   |||   ||||||
                                 CTGTCC   GCG   CTGTAA
                                    ___   ___
GAM1642  SHOX2     3'  GACAGGCGCGACATT      40380       AAC   ACA
                                 GACAGG   TGT   GACATT
                                 ||||||   |||   ||||||
                                 CTGTCC   GCG   CTGTAA
                                    ___   ___
GAM1642  FLJ10545  3'  AGACAGAAACTGTAAGCCATTG 40381           C  A
              G                  AGACAGGAACTGTA AG CATTGG
                                 |||||||||||||| || ||||||
                                 TCTGTCTTTGACAT TC GTAACC
                                         _  G
GAM1642  FLJ12298  3'  AGACAGAATTTCACCATGTTGG 40382        ACTG   AGACA
                                 AGACAGGA    TAC     TTGG
                                 ||||||||    |||     ||||
                                 TCTGTCTT    GTG     AACC
                                      AAA_   GTAC_
GAM1642  FLJ13659  3'  AGACAGGATTTCACCATGTTGG 40383        ACTG   AGACA
                                 AGACAGGA    TAC     TTGG
                                 ||||||||    |||     ||||
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                                TCTGTCCT   GTG    AACC
                                    AAA_   GTAC_
GAM1642  FLJ20051  3'  AAACAGGAATTGTGTAACTGG  40384        C   ACAGAC
                                AGACAGGAA TGT     ATTGG
                                ||||||||| |||     |||||
                                TTTGTCCTT ACA     TGACC
                                    A   CAT___
GAM1642  FLJ20511  3'  AGACAGGAAGTGTACGATG   40385        C    A  CAT
                                AGACAGGAA TGTAC GA   TG
                                ||||||||| ||||| ||   ||
                                TCTGTCCTT ACATG CT   AC
                                    C    _ ___
GAM1642  KIAA0261  3'  AAACAGGAATTCCACATTG   40386        CTGTACAG
                                AGACAGGAA       ACATTG
                                |||||||||       ||||||
                                TTTGTCCTT       TGTAAC
                                    AAGG____
GAM1642  KIAA0317  3'  AGGCAGGAACTGTAGCAGCTCA 40387    A        _   ACATT
           GG                     AG CAGGAACTGTA CAG    GG
                                || ||||||||||| |||    ||
                                TC GTCCTTGACAT GTC    CC
                                 C         C   GAGT_
GAM1642  KIAA0889  3'  AGACAGGGTTTCACCATATTGG 40388       AACTG   AGAC
                                AGACAGG    TAC    ATTGG
                                |||||||    |||    |||||
                                TCTGTCC    GTG    TAACC
                                    CAAA_   GTA_
GAM1642  KIAA1001  3'  AGACAGGATTTCACCATGTTGG 40383       ACTG   AGACA
                                AGACAGGA    TAC    TTGG
                                ||||||||    |||    ||||
                                TCTGTCCT    GTG    AACC
                                    AAA_   GTAC_
GAM1642  KIAA1641  3'  AGACAGGATTTCACCATATTGG 40389       ACTG   AGAC
                                AGACAGGA    TAC    ATTGG
                                ||||||||    |||    |||||
                                TCTGTCCT    GTG    TAACC
                                    AAA_   GTA_
GAM1642  LIAS      3'  AGACAGGATTTCACCATGTTGG 40383       ACTG   AGACA
                                AGACAGGA    TAC    TTGG
                                ||||||||    |||    ||||
                                TCTGTCCT    GTG    AACC
                                    AAA_   GTAC_
GAM1642  PDCD6     3'  AGATAGGAACTGTGACATT    40390     C       ACA
                                AGA AGGAACTGT   GACATT
                                ||| |||||||||   ||||||
                                TCT TCCTTGACA   CTGTAA
                                  A        ____
GAM1642  LOC115574 3'  AGGCAGGGGTGGACATTG    40391    A    AAC  TACA
                                AG CAGG   TG    GACATTG
                                || ||||   ||    |||||||
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                                TC GTCC   AC    CTGTAAC
                                 C    CC_  ____
GAM1642  LOC127428 3'  AGACAGGGTTTCGCCATGTTGG 40392       AAC_   A  GACA
                                AGACAGG    TGT CA    TTGG
                                |||||||    ||| ||    ||||
                                TCTGTCC    GCG GT    AACC
                                    CAAA   _  AC__
GAM1642  LOC144563 5'  GACAGGAAGTTGACGTTG    40393       CT  ACA   A
                                GACAGGAA  GT   GAC TTG
                                ||||||||  ||   ||| |||
                                CTGTCCTT  CA   CTG AAC
                                    __  A__   C
GAM1642  LOC147229 3'  GGGCACAGGTCAGACATTGG   40394    A_  T_  A
                                GG  AC  GT CAGACATTGG
                                ||  ||  || ||||||||||
                                CC  TG  CA GTCTGTAACC
                                 CG  TC  _
GAM1642  LOC151632 5'  GACAGGAAGTTGACGTTG    40393       CT  ACA   A
                                GACAGGAA  GT   GAC TTG
                                ||||||||  ||   ||| |||
                                CTGTCCTT  CA   CTG AAC
                                    __  A__   C
GAM1642  LOC162137 3'  GACAGCAACAGGAGACATTGG  40395      G   TGTAC
                                GACAG AAC    AGACATTGG
                                ||||| |||    |||||||||
                                CTGTC TTG    TCTGTAACC
                                   G   TCC__
GAM1642  LOC200251 5'  AGGCAAGAACTGTGCCTAGCTT 40396    A        ACAGACA
            GG                   AG CAGGAACTGT      TTGG
                                || ||||||||||      ||||
                                TC GTTCTTGACA      AACC
                                 C        CGGATCG
GAM1642  LOC200904 5'  GACAGGAAGTTGACATTG    40397       CT  ACA
                                GACAGGAA  GT   GACATTG
                                ||||||||  ||   |||||||
                                CTGTCCTT  CA   CTGTAAC
                                    __  A__
GAM1642  LOC203083 5'  GACAGGAAGTTGATGTTG    40398       CT  ACA  CA
                                GACAGGAA  GT   GA  TTG
                                ||||||||  ||   ||  |||
                                CTGTCCTT  CA   CT  AAC
                                    __  A__  AC
GAM1642  LOC219919 5'  GACAGGAAGTTGACGTTG    40393       CT  ACA   A
                                GACAGGAA  GT   GAC TTG
                                ||||||||  ||   ||| |||
                                CTGTCCTT  CA   CTG AAC
                                    __  A__   C
GAM1642  LOC221540 3'  CAGGAGTCAGACATTG      40399      ACT  A
                                CAGGA   GT CAGACATTG
                                |||||   || |||||||||
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                                GTCCT   CA GTCTGTAAC
                                  ___  _
GAM1642  LOC221795 5'  GACAGGAAGTTGACGTTG    40393        CT  ACA   A
                                GACAGGAA  GT   GAC TTG
                                ||||||||  ||   ||| |||
                                CTGTCCTT  CA   CTG AAC
                                    __  A__   C
GAM1642  LOC254176 5'  GACAGGAAGTTGATGTTG    40398        CT  ACA  CA
                                GACAGGAA  GT   GA  TTG
                                ||||||||  ||   ||  |||
                                CTGTCCTT  CA   CT  AAC
                                    __  A__  AC
GAM1642  LOC256447 3'  AGGCAAGAGCTAAACATTG   40400    A    A   TACA
                                AG CAGGA CTG    GACATTG
                                || ||||| |||    |||||||
                                TC GTTCT GAT    TTGTAAC
                                 C    C  ____
GAM1642  LOC256515 5'  GACAGGAAGTTGACGTTG    40393        CT  ACA   A
                                GACAGGAA  GT   GAC TTG
                                ||||||||  ||   ||| |||
                                CTGTCCTT  CA   CTG AAC
                                    __  A__   C
GAM1642  LOC257466 5'  AGGAGGTGCTCGGACATTGG  40401     AC   ACA
                                AGGA  TGT   GACATTGG
                                ||||  |||   ||||||||
                                TCCT  ACG   CTGTAACC
                                  CC   AGC
GAM1642  LOC257545 3'  CAGGAGTCAGACATTG      40399      ACT  A
                                CAGGA   GT CAGACATTG
                                |||||   || |||||||||
                                GTCCT   CA GTCTGTAAC
                                  ___  _
GAM1642  LOC257598 3'  CAGGAGTCAGACATTG      40399      ACT  A
                                CAGGA   GT CAGACATTG
                                |||||   || |||||||||
                                GTCCT   CA GTCTGTAAC
                                  ___  _
GAM1643  AOC3     3'  CCTCAGGATTCGGGAGAAATTG 40404    _ A       TGCCA__
            CAGG                  CC CA GATTCGGGA      CAGG
                                || || |||||||||      ||||
                                GG GT CTAAGCCCT      GTCC
                                 A  C       CTTTAAC
GAM1643  DGUOK    3'  CCAAGACTTTGGGCAGTGCAGG 40405        C_  ATGCCA
                                CCAAGATT  GGG     CAGG
                                ||||||||  |||     ||||
                                GGTTCTGA  CCC     GTCC
                                    AA   GTCAC_
GAM1643  MPP2     3'  GACTCAGGGTGTCACAGG    40406        A  C
                                GATTCGGG TG CACAGG
                                |||||||| || ||||||
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                                CTGAGTCC AC GTGTCC
                                    C  A
GAM1643  NRXN2    3'  CCCAGCGGGTGCCACAG     40407      AGATT    A
                                CCCA    CGGG TGCCACAG
                                ||||    |||| ||||||||
                                GGGT    GCCC ACGGTGTC
                                  C____   _
GAM1643  NRXN2    3'  CCCAGCGGGTGCCACAG     40407      AGATT    A
                                CCCA    CGGG TGCCACAG
                                ||||    |||| ||||||||
                                GGGT    GCCC ACGGTGTC
                                  C____   _
GAM1643  NRXN2    3'  CCCAGCGGGTGCCACAG     40407      AGATT    A
                                CCCA    CGGG TGCCACAG
                                ||||    |||| ||||||||
                                GGGT    GCCC ACGGTGTC
                                  C____   _
GAM1643  POU4F1   3'  TCCCGGGATTGGAGAGCAGCCA 40408      AA   C   T__   C
            TAGG                  TCCC  GATT GGGA   GCCA AGG
                                ||||  |||| ||||   |||| |||
                                AGGG  CTAA CTCT   CGGT TCC
                                  CC   C   CGT    A
GAM1643  PPP4R1   3'  TCCCAAGAGTGGTCACAG    40409        TTCG  ATGC
                                TCCCAAGA   GG   CACAG
                                ||||||||   ||   |||||
                                AGGGTTCT   CC   GTGTC
                                     CA__  A___
GAM1643  RASD1    5'  TCCCAGGATCTGGGCACAG   40410      A   TC   ATGC
                                TCCCA GAT  GGG   CACAG
                                |||||| |||  |||   |||||
                                AGGGT CTA  CCC   GTGTC
                                  C   GA  ____
GAM1643  ARHF     3'  CCAAGAGTCTAGCCGCAGG   40411       T  GGGAT   A
                                CCAAGA TC    GCC CAGG
                                |||||| ||    ||| ||||
                                GGTTCT AG    CGG GTCC
                                   C  AT___   C
GAM1643  ARHGEF2  3'  CCAAGACGGATGTTGCAGG   40412        TCG    CCA
                                CCAAGAT   GGATG   CAGG
                                |||||||   |||||   ||||
                                GGTTCTG   CCTAC   GTCC
                                     ___    AAC
GAM1643  BCL2L1   3'  CCCAAGGCAAAGATGCCACAGG 40413       ATTC
                                CCCAAG   GGGATGCCACAGG
                                ||||||   ||||||||||||||
                                GGGTTC   TTCTACGGTGTCC
                                   CGT_
GAM1643  C20orf39 3'  TCCCAAGAGTGCGTATTGCTGC 40414        TT_  GGA   CACA
            GG                  TCCCAAGA   CG   TGC    GG
                                ||||||||   ||   |||    ||
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                                AGGGTTCT  GC  ACG   CC
                                    CAC  ATA  ACG_
GAM1643  DKFZP564D0462 3'  TCCCAGGATGGTGTTGCAGG  40415     A  TCG  A  CCA
                                TCCCA GAT  GG TG  CAGG
                                ||||| |||  || ||  ||||
                                AGGGT CTA  CC AC  GTCC
                                  C  ___  _  AAC
GAM1643  FLJ14100  3'  TCCCAGGATCCGGAGCAG   40416     A     ATGCCA
                                TCCCA GATTCGGG    CAG
                                ||||| ||||||||    |||
                                AGGGT CTAGGCCT    GTC
                                  C      C_____
GAM1643  KIAA0865  3'  CAAGATTTAGGTGCGTTAGG  40417      CG  A  CAC
                                CAAGATT  GG TGC  AGG
                                |||||||  || |||  |||
                                GTTCTAA  CC ACG  TCC
                                    AT  _  CAA
GAM1643  KIF13B   3'  CCAGGGACAGGTGCCACAGG  40418    AGATT   A
                                CCA    CGGG TGCCACAGG
                                |||    |||| |||||||||
                                GGT    GTCC ACGGTGTCC
                                  CCCT_   _
GAM1643  KIF13B   3'  TCCCAAGATGGTGCTACAGG  40419       TCG  A  C
                                TCCCAAGAT  GG TGC ACAGG
                                |||||||||  || ||| |||||
                                AGGGTTCTA  CC ACG TGTCC
                                     ___  _  A
GAM1643  KIF13B   3'  CCAGGGACAGGTGCCACAGG  40418    AGATT   A
                                CCA    CGGG TGCCACAGG
                                |||    |||| |||||||||
                                GGT    GTCC ACGGTGTCC
                                  CCCT_   _
GAM1643  MYH10    3'  CCAAGATTCCAAACCCACAGG  40420       G   G
                                CCAAGATTC GGAT CCACAGG
                                ||||||||| |||| |||||||
                                GGTTCTAAG TTTG GGTGTCC
                                     G  _
GAM1643  UBPH     3'  TCTGAAATCCAGGGATGCTGCA 40421    CCA    _     CA
            GG                   TC  AGATTC GGGATGC  CAGG
                                ||  |||||| |||||||  ||||
                                AG  TTTAGG CCCTACG  GTCC
                                 AC_     T      AC
GAM1643  LOC148638 5'  TCCCAGGATTCTTCCCTTACAG 40422      A    GGGATG  ___
            G                    TCCCA GATTC     CC   ACAGG
                                ||||| |||||     ||   |||||
                                AGGGT CTAAG     GG   TGTCC
                                  C    AA_____  GAA
GAM1643  LOC158332 3'  CAGGATTATGATGTCACAGG  40423    A   CGG   C
                                CA GATT   GATG CACAGG
                                || ||||   |||| ||||||
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                                GT CTAA   CTAC GTGTCC
                                 C   TA_   A
GAM1643  LOC159090 5'  TCCCAAGACTCTCACTGCAGG  40424          GGGA   CAC
                                TCCCAAGATTC   TGC   AGG
                                ||||||||||   |||  |||
                                AGGGTTCTGAG   ACG   TCC
                                      AGTG  ___
GAM1643  LOC196510 3'  TCCCAGGATTCCGAGCAG    40425      A   _  ATGCCA
                                TCCCA GATTC GGG    CAG
                                ||||| ||||| |||    |||
                                AGGGT CTAAG CTC    GTC
                                   C    G  ______
GAM1643  LOC257078 5'  TCCCAGGGTTGAAGTCGCCACA 40426      AGA  CG  A
            GG                    TCCCA   TT  GG TGCCACAGG
                                ||||||  ||  || |||||||||
                                AGGGT   AA  TC GCGGTGTCC
                                   CCC  CT  A
GAM1643  LOC90874  3'  TCCCAGGATATCTACCCCCCAC 40427      A  _  GGGATG
            AGG                   TCCCA GAT TC     CCACAGG
                                ||||| ||| ||     |||||||
                                AGGGT CTA AG     GGTGTCC
                                   C   T  ATGGGG
GAM1644  ADAM23    3'  CACCCCAACTTTAGCTCCGTAG 40430        A_____      C
            TCA                   CACCCCAA     CTCCGTAG CA
                                ||||||||     |||||||| ||
                                GTGGGGTT     GAGGCATC GT
                                     GAAATC       A
GAM1644  DIAPH2    3'  GGCTTCCTAAAAGACATAGCCA 40431     AC  C   CTC
            C                    GGC  CC AAA   CGTAGCCAC
                                |||  || |||   |||||||||
                                CCG  GG TTT   GTATCGGTG
                                  AA  A   TCT
GAM1644  FNTB     3'  CGGCACCCCACGCTGCCA     40432         AACTC   A
                                CGGCACCCCA     CGT GCCA
                                ||||||||||     ||| ||||
                                GCCGTGGGGT     GCG CGGT
                                      _____  A
GAM1644  GAMT     3'  CGACACCCTGGACTCCCGGC   40433        CAA    GTA
                                CGGCACCC   ACTCC   GC
                                ||||||||   |||||   ||
                                GCTGTGGG   TGAGG   CG
                                     ACC    GC_
GAM1644  IL12RB2   3'  GCACTCCAATACAGTAGCCAC  40434      C   _  TCC
                                GCAC CCAA AC   GTAGCCAC
                                |||| |||| ||   ||||||||
                                CGTG GGTT TG   CATCGGTG
                                  A   A  T__
GAM1644  LIMK1    3'  CGGGCCCCAGACTCCCCA     40435     CA     A     G
                                CGG  CCCCA ACTCC TA
                                |||  ||||| ||||| ||
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                                GCC  GGGGT TGAGG GT
                                  C_    C    G
GAM1644  LIMK1    3'  CGGGCCCCAGACTCCCCA    40435    CA    A    G
                                CGG  CCCCA ACTCC TA
                                |||  ||||| ||||| ||
                                GCC  GGGGT TGAGG GT
                                  C_    C    G
GAM1644  PSMD5    3'  GCATTCCAAACTCCTAGTTCCA 40436    CC       GTAG_
              C                  GCA  CCAAACTCC    CCAC
                                |||  |||||||||    ||||
                                CGT  GGTTTGAGG    GGTG
                                  AA        ATCAA
GAM1644  RPIP8    5'  CGGAGCCCCAAACCCGTCGC   40437    CA      T    A
                                CGG  CCCCAAAC CCGT GC
                                |||  |||||||| |||| ||
                                GCC  GGGGTTTG GGCA CG
                                  TC       _    G
GAM1644  SLC35A3  5'  CGGCTCCCGTCGCCGTAGCCAC 40438     A   CAAACT
                                CGGC CCC     CCGTAGCCAC
                                |||| |||     ||||||||||
                                GCCG GGG     GGCATCGGTG
                                  A   CAGC__
GAM1644  BPES     3'  GGTCCCCCAAACAACAAGCTAC 40439    CA       TC  T   C
                                GG  CCCCAAAC  CG AGC AC
                                ||  ||||||||  || ||| ||
                                CC  GGGGTTTG  GT TCG TG
                                 AG       TT  _   A
GAM1644  C1orf9   3'  GGCACTACAGCTCCGTAG    40440      CC  AA
                                GGCAC  CA  CTCCGTAG
                                |||||  ||  ||||||||
                                CCGTG  GT  GAGGCATC
                                   AT  C_
GAM1644  ESDN     3'  CACCTTCCACAGCTTTGTGGCC 40441      __   AA_  CC  A
              AC                  CACC  CCA   CT  GT GCCAC
                                ||||  |||   ||  || |||||
                                GTGG  GGT   GA  CA CGGTG
                                  AA   GTC  AA  C
GAM1644  FLJ10374 3'  CAGTGCCCCAAACACTGCCAC  40442     CA      TCCGTA
                                CGG  CCCCAAAC     GCCAC
                                |||  ||||||||     |||||
                                GTC  GGGGTTTG     CGGTG
                                  AC       TGA____
GAM1644  FLJ22283 5'  GGGACCCCAGCATAGCCA    40443    C     AACTC
                                GG ACCCCA     CGTAGCCA
                                || ||||||     ||||||||
                                CC TGGGGT     GTATCGGT
                                 C     C_____
GAM1644  GGA2     3'  GGCACTCCGCACTGAAACACCG 40444       _  _  _____   T
              T                  GGCAC CC CA    AAC CCGT
                                |||||  ||  ||    |||  ||||
```

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                                CCGTG GG GT    TTG GGCA
                                  A  C  GACT   T
GAM1644  GGA2     3'  GGCACTCCGCACTGAAACACCG 40444       _ _ ____   T
              T                    GGCAC CC CA    AAC CCGT
                                   ||||| || ||    ||| ||||
                                   CCGTG GG GT    TTG GGCA
                                     A  C  GACT   T
GAM1644  HSH2     3'  GGTGCCCCAAACCATCAGCGTC 40445    CA       CCG   __
              AC                    GG  CCCCAAACT   TAGC  CAC
                                    ||  |||||||||   ||||  |||
                                    CC  GGGGTTTGG   GTCG  GTG
                                     AC       TA_    CA
GAM1644  IL-17RC  3'  CGGACACCCCATCCTGTAGCCA 40446     _      AAC   _
              C                     CGG CACCCCA   TCC GTAGCCAC
                                    ||| |||||||   ||| ||||||||
                                    GCC GTGGGGT   AGG CATCGGTG
                                     T     ___   A
GAM1644  KIAA0326 3'  GCACCCCAAACTTCAGC     40447          CCG
                                    GCACCCCAAACT   TAGC
                                    ||||||||||||   ||||
                                    CGTGGGGTTTGA   GTCG
                                          A__
GAM1644  KIAA0339 3'  CGGCACCCCAGGTTTCCA    40448         AACTCC  AG
                                    CGGCACCCCA     GT  CCA
                                    ||||||||||     ||  |||
                                    GCCGTGGGGT     CA  GGT
                                          C_____   AA
GAM1644  KIAA0562 5'  GCACCCCAAGCTGCTGC     40449         A  CC  A
                                    GCACCCCAA CT  GT GC
                                    |||||||||  ||  ||  ||
                                    CGTGGGGTT GA  CG CG
                                          C  __  A
GAM1644  KIAA0682 3'  GGCACCCCAGGATCACCCCAT  40450         A____
                                    GGCACCCCA    ACTCCGT
                                    |||||||||    |||||||
                                    CCGTGGGGT    TGGGGTA
                                         CCTAG
GAM1644  KIAA0907 3'  GGTATCCCAAACTCCAGCC    40451    CAC       GT
                                    GG   CCCAAACTCC  AGCC
                                    ||   ||||||||||  ||||
                                    CC   GGGTTTGAGG  TCGG
                                     ATA         __
GAM1644  KIAA1462 3'  CAGTGTCCCAAACTCCTTCAC  40452     CAC       GTA
                                    CGG   CCCAAACTCC   GC
                                    |||   ||||||||||   ||
                                    GTC   GGGTTTGAGG   TG
                                      ACA         AAG
GAM1644  MGC4368  5'  GGCAACTCAGGGCAGCCA    40453     CCCCAA    C__
                                    GGCA     ACTC   GTAGCCA
                                    ||||     ||||   |||||||
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                                CCGT    TGAG  CGTCGGT
                                  _____   TCC
GAM1644 MGC5242  5' GGTGCCACATTCTTTGTAGCCA 40454   CA  C  AA  CC
            C                    GG  CC CA  CT  GTAGCCAC
                                 ||  || ||  ||  ||||||||
                                 CC  GG GT  GA  CATCGGTG
                                  AC  T  AA  AA
GAM1644 MGC7036  5' CGGCACCCAAAACTTTCCGC  40455       C   __
                                 CGGCACCC AAAC  TCCGT
                                 |||||||| ||||  |||||
                                 GCCGTGGG TTTG  AGGCG
                                      T   AA
GAM1644 MKRN1    3' GGACCCCAAAGCAGGGCCAC  40456   C      CTC  TA
                                 GG ACCCCAAA  CG  GCCAC
                                 || ||||||||  ||  |||||
                                 CC TGGGGTTT  GT  CGGTG
                                  _      C__  CC
GAM1644 MKRN4    3' GGACCCCAAAGCAGGGCCAC  40456   C      CTC  TA
                                 GG ACCCCAAA  CG  GCCAC
                                 || ||||||||  ||  |||||
                                 CC TGGGGTTT  GT  CGGTG
                                  _      C__  CC
GAM1644 MYT1     3' CGGGCCCCAAACGGGAAGTCAC 40457    CA      TCCGT  C
                                 CGG  CCCCAAAC    AG CAC
                                 |||  ||||||||    || |||
                                 GCC  GGGGTTTG    TC GTG
                                   C_      CCCT_  A
GAM1644 RASGRP4  3' GACACCCCAGAGGAAGCCAC  40458       AACTCCGT
                                 GGCACCCCA      AGCCAC
                                 |||||||||      ||||||
                                 CTGTGGGGT      TCGGTG
                                      CTCCT___
GAM1644 RRS1     5' GGCGGCCCAAACTCCGGC    40459    AC       TA
                                 GGC  CCCAAACTCCG  GC
                                 |||  ||||||||||  ||
                                 CCG  GGGTTTGAGGC  CG
                                   CC        __
GAM1644 TBX21    5' GGCACCTTCCCGTAGCC     40460      CCAAAC
                                 GGCACC     TCCGTAGCC
                                 ||||||     |||||||||
                                 CCGTGG     GGGCATCGG
                                    AA____
GAM1644 LOC143909 5' CAGCACCCCGAGTCTGTCGC  40461       AAAC  C  A
                                 CGGCACCCC    TC GT GC
                                 |||||||||    || || ||
                                 GTCGTGGGG    AG CA CG
                                      CTC_  A  G
GAM1644 LOC151568 5' GGCACCCCTAGGCACTGGCCGT 40462       AA___  __
                                 GGCACCCC     ACT  CCGT
                                 ||||||||     |||  ||||
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                                CCGTGGGG    TGA  GGCA
                                    ATCCG   CC
GAM1644  LOC159199 5'  CGGCACCCTGGGCCAGGCCA  40463       CAAACT   TA
                                CGGCACCC    CCG  GCCA
                                ||||||||    |||  ||||
                                GCCGTGGG    GGT  CGGT
                                    ACCC__  C_
GAM1644  LOC200186 5'  CGGCTCCTCCAGCCGTAGCCAC 40464     A  _   AACT
                                CGGC CC CCA   CCGTAGCCAC
                                |||| || |||   ||||||||||
                                GCCG GG GGT   GGCATCGGTG
                                  A  A   C___
GAM1644  LOC203636 3'  CGGCACCCCCGGCTCCCCCAC  40465       AAA   GTAG
                                CGGCACCCC   CTCC   CCAC
                                |||||||||   ||||   ||||
                                GCCGTGGGG   GAGG   GGTG
                                    GCC   G___
GAM1644  LOC204084 5'  CGACACCCGGATTGTGGCCAC  40466       CAAACTCC  A
                                CGGCACCC      GT GCCAC
                                ||||||||      || |||||
                                GCTGTGGG      CA CGGTG
                                    CCTAA___  C
GAM1644  LOC256855 3'  CGGGCCCGCTGTCGTAGCCAC  40467    CAC   AAACTC
                                CGG   CCC     CGTAGCCAC
                                |||   |||     |||||||||
                                GCC   GGG     GCATCGGTG
                                  C__   CGACA_
GAM1644  LOC90631  3'  CGGCACCCTGAACTCGGT    40468       CA    C
                                CGGCACCC  AACTC GT
                                ||||||||  ||||| ||
                                GCCGTGGG  TTGAG CA
                                    AC    C
GAM1644  LOC91464  3'  GGCATCCAAAGCAGCCA     40469     CC    CTCC
                                GGCA  CCAAA   GTAGCCA
                                ||||  |||||   |||||||
                                CCGT  GGTTT   CGTCGGT
                                  A_    _____
GAM1645  NFKBIL1   3'  TTTGAGATGTGGAACCAGGTCT 40472       C_   T   G
            T                    TTTGAG  GTGG GAT TAGGTCTT
                                 ||||||  |||| ||| ||||||||
                                 AAACTC  CACC TTG GTCCAGAA
                                    TA   _  _
GAM1645  NRF      3'  TTTGAGCTGATCTAGTAGGTCT 40473       G   GAT
            T                    TTTGAGC TGGT   GTAGGTCTT
                                 |||||||  ||||   |||||||||
                                 AAACTCG ACTA   CATCCAGAA
                                    _   GAT
GAM1646  ATP6V0E   3'  TGAGATGGCTCTTCCCTCT   40476      AAGC   GAA
                                TGAGA   GGT   TTCCCTCT
                                |||||   |||   ||||||||
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                                ACTCT   CCG   AAGGGAGA
                                  A___  AG_
GAM1646 BACH2   5' AGAAAGCATGCTTTCTTCT  40477       G  AA   CC
                                AGAAAGCG TG  TTC  TCT
                                |||||||| ||  |||  |||
                                TCTTTCGT AC  AAG  AGA
                                    _ GA  A_
GAM1646 CABC1   5' TGAGAAGTGGAACTCCCC   40478      AAGC   _
                                TGAGA   GGTG AATTCCCT
                                |||||   |||| ||||||||
                                ACTCT   TCAC TTGAGGGG
                                  _____  C
GAM1646 CPS1    3' TGAGAAAGTTGTGAATCAGTTC 40479       CG      C___
            CT                    TGAGAAAG  GTGAATT   CCT
                                |||||||  |||||||   |||
                                ACTCTTTC  CACTTAG   GGA
                                    AA      TCAA
GAM1646 EIF4E   3' TAAGAAGTACAAATTCCTTCTA 40480       AGCG TG     C
                                TGAGAA   G  AATTCC TCTA
                                ||||||   |  |||||| ||||
                                ATTCTT   T  TTAAGG AGAT
                                   CA__ GT     A
GAM1646 GPC3    3' TAAGAAAGTGGTTCCCT    40481        C   GAAT
                                TGAGAAAG GGT   TCCCT
                                |||||||| |||   |||||
                                ATTCTTTC CCA   AGGGA
                                    A  _____
GAM1646 IL12B   3' TGAGAAAGGGATTCC      40482        C  TGA
                                TGAGAAAG GG   ATTCC
                                |||||||| ||   |||||
                                ACTCTTTC CC   TAAGG
                                    _ ____
GAM1646 MAN2A2  3' GAGAAACAGTGATTCCTTCTA  40483      G     A   C
                                GAGAAA CGGTGA TTCC TCTA
                                |||||| |||||| |||| ||||
                                CTCTTT GTCACT AAGG AGAT
                                   _    _   A
GAM1646 PTGFR   3' TGAGAAAGAGCCTTTGTTTCTC 40484       C   GAATTCC_
            TA                    TGAGAAAG GGT       CTCTA
                                |||||||| |||       |||||
                                ACTCTTTC TCG       GAGAT
                                    _  GAAACAAA
GAM1646 TFAP4   3' TGGGAGAGTGGCGAATTC   40485    A  A  C
                                TG GA AG GGTGAATTC
                                || || || |||||||||
                                AC CT TC CCGCTTAAG
                                 C  C  A
GAM1646 TOP3A   3' TGAGAAAGTGGCGTTCTCT   40486        C   AATTCC
                                TGAGAAAG GGTG     CTCT
                                |||||||| ||||     ||||
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                                ACTCTTTC CCGC     GAGA
                                    A   AA____
GAM1646 UBE3A    5' TGAGGAGCTGGTGAATTC    40487     AA  _
                                TGAG  AGC GGTGAATTC
                                ||||  ||| |||||||||
                                ACTC  TCG CCACTTAAG
                                  C_  A
GAM1646 VAV2     3' GAGGTTGGTATTTCCCCTCT  40488    AAAGC   AA
                                GAG    GGTG  TTCCCTCT
                                |||    ||||  ||||||||
                                CTC    CCAT  AGGGGAGA
                                  CAA__   AA
GAM1646 ATP1B4   3' GAGGAACAGCAATTCTTTCT  40489    AA    G    CC
                                GAG  AGCGGT AATTC  TCT
                                |||  |||||| |||||  |||
                                CTC  TTGTCG TTAAG  AGA
                                  C_    _    AA
GAM1646 C13orf1  3' TAAGAAAGAATTCCCT     40490       GCGGT
                                TGAGAAA    GAATTCCCT
                                |||||||    |||||||||
                                ATTCTTT    CTTAAGGGA
                                     _____
GAM1646 CLDN8    3' AGAAAGCCATTCAATTTCCT  40491       G  G_   C
                                AGAAAGC GT  AATT CCT
                                ||||||| ||  |||| |||
                                TCTTTCG TA  TTAA GGA
                                    G  AG   A
GAM1646 ELF1     3' GAGAAAGTGGTGATCATCTA  40492       C    AT  CC
                                GAGAAAG GGTGA  TC  TCTA
                                ||||||| |||||  ||  ||||
                                CTCTTTC CCACT  AG  AGAT
                                    A    __  T_
GAM1646 FLJ10853 3' TGAGAAAGGACATCCCT    40493       C GT AAT
                                TGAGAAAG G  G   TCCCT
                                |||||||| |  |   |||||
                                ACTCTTTC C  T   AGGGA
                                    _ TG ___
GAM1646 FLJ20151 3' GAGGGCCTGAGTTCCCTCT  40494    AAA  GG   A
                                GAG   GC  TGA TTCCCTCT
                                |||   ||  ||| ||||||||
                                CTC   CG  ACT AAGGGAGA
                                  C__  G_   C
GAM1646 HES6     3' TGGGAGAGCGCTGGCAGCTCTA 40495    A  A    G  AATTCC
                                TG GA AGCG TG     CTCTA
                                || || |||| ||     |||||
                                AC CT TCGC AC     GAGAT
                                 C  C    G  CGTC__
GAM1646 KIAA0276 3' TGAAAAGTGGCCCCTC     40496       A C   GAATT
                                TGAGAA G GGT    CCCTC
                                |||||| | |||    |||||
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                                ACTTTT C CCG    GGGAG
                                   _ A  _____
GAM1646 KIAA0356 3' TGAGAAAGCGGTGGGCTC    40497          AA
                                TGAGAAAGCGGTG  TTC
                                ||||||||||||  |||
                                ACTCTTTCGCCAC  GAG
                                      CC
GAM1646 KIAA1000 3' TGGAAGCAATGATATTCCCT  40498    A  A     _
                                TG GAA GCGGTGA ATTCCCT
                                || ||| ||||||| |||||||
                                AC CTT CGTTACT TAAGGGA
                                 _  _     A
GAM1646 KIAA1889 3' TGAGAAAATGGTTTCTTTTCTA 40499       C  GAA  CC_
                                TGAGAAAG GGT   TTC   TCTA
                                |||||||| |||   |||   ||||
                                ACTCTTTT CCA   AAG   AGAT
                                     A  ___  AAA
GAM1646 LEC3    3' GAGGGAGTGAATTTCCTCTA  40500    AAAGC      C
                                GAG    GGTGAATT CCTCTA
                                |||    |||||||| ||||||
                                CTC    TCACTTAA GGAGAT
                                  CC___       A
GAM1646 PTD008  3' GAAAGGGCCAGGTTCCCTCTA  40501      C  GAA_
                                GAAAG GGT    TTCCCTCTA
                                ||||| |||    |||||||||
                                CTTTC CCG    AAGGGAGAT
                                   _  GTCC
GAM1646 RC3     5' GAGAGCCGTTTCCCTCT     40502      AA  G  GAA
                                GAGA  GC GT   TTCCCTCT
                                ||||  || ||   ||||||||
                                CTCT  CG CA   AAGGGAGA
                                  __ G  ___
GAM1646 RDGBB   3' TGACAAAGCAGTCTTTTTCTCT 40503     G       GAATTCC
            A                    TGA AAAGCGGT      CTCTA
                                ||| ||||||||      |||||
                                ACT TTTCGTCA      GAGAT
                                  G       GAAAAA_
GAM1646 UBP1    3' TGAGAAAACAGTGGATTCCCT  40504          A
                                TGAGAAAGCGGTG ATTCCCT
                                |||||||||||| |||||||
                                ACTCTTTTGTCAC TAAGGGA
                                      C
GAM1646 LOC152274 3' TAAGAAAGTTCCGATTTCC   40505       CGG  A
                                TGAGAAAG   TGA TTCC
                                ||||||||   ||| ||||
                                ATTCTTTC   GCT AAGG
                                     AAG   A
GAM1646 LOC152992 5' TGAGGCGGCTTCCCTC     40506     AAA    GAA
                                TGAG   GCGGT   TTCCCTC
                                ||||   |||||   |||||||
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                                ACTC   CGCCG   AAGGGAG
                                  ___    ___
GAM1646 LOC221922 5' AAGACCACTGGTTCCCTCT   40507     AA _  GAAT
                                GAGA  GC GGT    TCCCTCT
                                ||||  || |||    |||||||
                                TTCT  TG CCA    AGGGAGA
                                  GG  A  ____
GAM1647 ACCN2    3' CACCCAGAGCCCTGCCTGCT   40510       _  GAT
                                CACCCAGA CTT   CCTGCT
                                |||||||| |||   ||||||
                                GTGGGTCT GGG   GGACGA
                                    C   AC_
GAM1647 BCRP2    3' CAGTGCCATCTGTCCTGCT   40511    CAC   GACT  A
                                CAG   CCA    TG TCCTGCT
                                |||   |||    || |||||||
                                GTC   GGT    AC AGGACGA
                                  AC_   AG__  _
GAM1647 CA7      3' CAGCCCCAGGCTTGGACCCTG  40512     A    A   _
                                CAGC CCCAG CTTG ATCCTG
                                |||| ||||| |||| ||||||
                                GTCG GGGTC GAAC TGGGAC
                                  _    C   C
GAM1647 CD28     3' CAGCACCCAAGTACTGCT    40513         ACTTGATC
                                CAGCACCCAG       CTGCT
                                ||||||||||       |||||
                                GTCGTGGGTT       GACGA
                                     CAT_____
GAM1647 CELSR2   3' CAGAACCCAGACTTGAAACCTG 40514    C         T_
                                CAG ACCCAGACTTGA  CCTG
                                ||| ||||||||||||  ||||
                                GTC TGGGTCTGAACT  GGAC
                                  T         TT
GAM1647 CENTD2   3' CAGCACCCGCTTTCTGCT    40515       AGA   GATC
                                CAGCACCC   CTT   CTGCT
                                ||||||||   |||   |||||
                                GTCGTGGG   GAA   GACGA
                                    C__   A___
GAM1647 CENTD2   3' CAGCACCCGCTTTCTGCT    40515       AGA   GATC
                                CAGCACCC   CTT   CTGCT
                                ||||||||   |||   |||||
                                GTCGTGGG   GAA   GACGA
                                    C__   A___
GAM1647 COG4     3' CCAGACTTTGTTTCTCTGCT   40516       GA__ _
                                CCAGACTT    TC CTGCT
                                ||||||||    || |||||
                                GGTCTGAA    AG GACGA
                                    ACAA  A
GAM1647 ELAC2    3' AGACCCACTGATCCTG     40517    C    GAC
                                AG ACCCA   TTGATCCTG
                                || |||||   |||||||||
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                              TC TGGGT   GACTAGGAC
                                _   ___
GAM1647 GADD45B  3' CAGCAACTCAACAGATTCTGCT 40518      CCCA   TT   C
                              CAGCA    GAC  GAT CTGCT
                              |||||    |||  ||| |||||
                              GTCGT    TTG  CTA GACGA
                                 TGAG   T_   A
GAM1647 HSPCB    3' CAACATCCAATCCTGC      40519      C   GACTTG
                              CAGCA CCA     ATCCTGC
                              ||||| |||     |||||||
                              GTTGT GGT     TAGGACG
                                A  ______
GAM1647 HUNK     3' GCCTTCAGGTAATCCCTGCTA  40520    ACC   ACT     _
                              GC   CAG   TGATCC TGCTA
                              ||   |||   |||||| |||||
                              CG   GTC   ATTAGG ACGAT
                               GAA   C__     G
GAM1647 HYOU1    3' CAGCCCTAGCTCCTGC      40521      A  C  A TTGA
                              CAGC CC AG C    TCCTGC
                              |||| || || |    ||||||
                              GTCG GG TC G    AGGACG
                                _ A  _ ____
GAM1647 MIP      5' CAGTGCCTGGGTCCCTGCTA   40522     A_    A__
                              CAG  CTTG   TCCTGCTA
                              |||  ||||   ||||||||
                              GTC  GGAC   GGGACGAT
                                AC    CCA
GAM1647 MPP2     3' AGCTCAGACCTGTGCCTGCT   40523     ACC       AT
                              AGC   CAGACTTG  CCTGCT
                              |||   ||||||||  ||||||
                              TCG   GTCTGGAC  GGACGA
                                A__       AC
GAM1647 BRD2     5' CAGCACCCAGATTGGC      40524          C   ATCCT
                              CAGCACCCAGA TTG    GC
                              |||||||||||| |||    ||
                              GTCGTGGGTCT AAC    CG
                                          _  _____
GAM1647 C5orf6   3' CAGCACTTAAAACACCCTGCT  40525       CC_    TTG
                              CAGCAC   AGAC   ATCCTGCT
                              ||||||   ||||   ||||||||
                              GTCGTG   TTTG   TGGGACGA
                                 AAT   ___
GAM1647 C9orf14  3' GCATGCTTGATCCTGCT     40526     CCCAGA
                              GCA     CTTGATCCTGCT
                              |||     ||||||||||||
                              CGT     GAACTAGGACGA
                                AC____
GAM1647 CORTBP2  5' GCACTTAACCCGCTGCT     40527      CCA     ATC
                              GCAC   GACTTG   CTGCT
                              ||||   ||||||   |||||
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                                CGTG  TTGGGC  GACGA
                                  AA_    ___
GAM1647 DKFZP564O0423 3' CAGAACCCAGACTACATGCT  40528    C      TGATCC
                                CAG ACCCAGACT    TGCT
                                ||| |||||||||    ||||
                                GTC TGGGTCTGA    ACGA
                                  T       TGT___
GAM1647 FBXL9   3' CAGACCTAGGCTCAGCTGCT  40529    C  C A  ATC
                                CAG ACC AG CTTG  CTGCT
                                ||| ||| || ||||  |||||
                                GTC TGG TC GAGT  GACGA
                                  _  A C   C__
GAM1647 FLJ20294 3' CAGCCTCTGGATCCTGCT   40530    ACCCAGA  T
                                CAGC     CT GATCCTGCT
                                ||||     || |||||||||
                                GTCG     GA CTAGGACGA
                                  GA_____  C
GAM1647 IL-17RC  5' GCACCCAGGCCTGAGGCCCTG  40531       A   __
                                GCACCCAG CTTGA  TCCTG
                                |||||||| |||||  |||||
                                CGTGGGTC GGACT  GGGAC
                                    C    CC
GAM1647 KIAA0415 3' GCCCCACCCACATCCTGCT   40532   A   GA  TG
                                GC CCCA  CT  ATCCTGCT
                                || ||||  ||  ||||||||
                                CG GGGT  GG  TAGGACGA
                                 _   G_  TG
GAM1647 KIAA0494 3' AGCTCCAGGCCTGCCCTGCTA  40533    AC   A   A
                                AGC  CCAG CTTG TCCTGCTA
                                |||  |||| |||| ||||||||
                                TCG  GGTC GGAC GGGACGAT
                                  A_   C   _
GAM1647 KIAA0980  5' CAGACCCAGACTCTGC     40534    C      TGATC
                                CAG ACCCAGACT    CTGC
                                ||| |||||||||    ||||
                                GTC TGGGTCTGA    GACG
                                  _      _____
GAM1647 KIAA1586 3' AGAACTTAGCTGAGTCCTGCTA 40535   C  CC  A  T  _
                                AG AC  AG CT GA TCCTGCTA
                                || ||  || || || ||||||||
                                TC TG  TC GA CT AGGACGAT
                                 T  AA  _  _  C
GAM1647 KIAA1655 5' CAGACCCAGGCTCCTGCT   40536    C    ACTTGA
                                CAG ACCCAG     TCCTGCT
                                ||| ||||||     |||||||
                                GTC TGGGTC     AGGACGA
                                  _     CG____
GAM1647 L3MBTL2  5' CAGCACCCGATACCCTGCT   40537       A  CTTG
                                CAGCACCC GA    ATCCTGCT
                                |||||||| ||    ||||||||
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                                GTCGTGGG CT    TGGGACGA
                                    _  A___
GAM1647  LGI3     3'  CAGTACCCTGGTATCCTGCTA  40538     C    AGACTTG
                                CAG ACCC      ATCCTGCTA
                                ||| ||||      |||||||||
                                GTC TGGG      TAGGACGAT
                                  A   ACCA___
GAM1647  MGC13010  3'  CAGCACCCAGACTCTGCCCCTG 40539            GA_
                                CAGCACCCAGACTT   TCCTG
                                ||||||||||||||  |||||
                                GTCGTGGGTCTGAG   GGGAC
                                       ACG
GAM1647  SEC61A1   3'  AGCACCCAACTCTGC       40540         A  TGATC
                                AGCACCCAG CT    CTGC
                                ||||||||| ||    ||||
                                TCGTGGGTT GA    GACG
                                    _ _____
GAM1647  LOC118851 5'  CACCTCCTTGATCCTGCT    40541     CAGA
                                CACC    CTTGATCCTGCT
                                ||||    ||||||||||||
                                GTGG    GAACTAGGACGA
                                  AG__
GAM1647  LOC121506 3'  CAGGCCTAGTGATCCTG     40542     CA  C  ACT
                                CAG  CC AG   TGATCCTG
                                |||  || ||   ||||||||
                                GTC  GG TC   ACTAGGAC
                                  C_  A  ___
GAM1647  LOC127281 3'  CAGCTTCAGACTTGAGCT    40543     ACC       TCCT
                                CAGC   CAGACTTGA   GCT
                                ||||   |||||||||   |||
                                GTCG   GTCTGAACT   CGA
                                  AA_       _____
GAM1647  LOC142948 3'  GCCCCGCCCATATCCTGCT   40544    A   AGA  TG
                                GC CCC   CT  ATCCTGCT
                                || |||   ||  ||||||||
                                CG GGG   GG  TAGGACGA
                                 _   CG_  TA
GAM1647  LOC144308 3'  ACACCCAGGCTGCCTGCT    40545        A  TGAT
                                GCACCCAG CT    CCTGCT
                                |||||||| ||    ||||||
                                TGTGGGTC GA    GGACGA
                                    C  C___
GAM1647  LOC145725 5'  GCACCCAGACCTGAGCT     40546           TCCT
                                GCACCCAGACTTGA    GCT
                                ||||||||||||||    |||
                                CGTGGGTCTGGACT    CGA
                                       _____
GAM1647  LOC145732 5'  GCACCCAGACCTGAGCT     40546           TCCT
                                GCACCCAGACTTGA    GCT
                                ||||||||||||||    |||
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                                CGTGGGTCTGGACT   CGA
                                      ____
GAM1647  LOC147004 3'  GCCTCCAGCCAAAATCCTGCTA 40547    AC   A  T_
                                GC  CCAG CT  GATCCTGCTA
                                ||  |||| ||  ||||||||||
                                CG  GGTC GG  TTAGGACGAT
                                 GA   _  TT
GAM1647  LOC147057 5'  GCACCCAGAGCCTGCT     40548        CTTGAT
                                GCACCCAGA     CCTGCT
                                |||||||||     ||||||
                                CGTGGGTCT     GGACGA
                                     C_____
GAM1647  LOC149127 3'  CAGCACCCAGAGTGCTCG    40549          ___
                                CAGCACCCAGA   CTTG
                                ||||||||||   ||||
                                GTCGTGGGTCT   GAGC
                                      CAC
GAM1647  LOC169693 5'  CAGCACCCTGACCCTGCT    40550        AGACT
                                CAGCACCC    TGATCCTGCT
                                ||||||||    ||||||||||
                                GTCGTGGG    ACTGGGACGA
                                     _____
GAM1647  LOC196957 5'  GCACCCAGACCTGAGCT     40546           TCCT
                                GCACCCAGACTTGA    GCT
                                ||||||||||||||    |||
                                CGTGGGTCTGGACT    CGA
                                      ____
GAM1647  LOC196961 5'  GCACCCAGACCTGAGCT     40546           TCCT
                                GCACCCAGACTTGA    GCT
                                ||||||||||||||    |||
                                CGTGGGTCTGGACT    CGA
                                      ____
GAM1647  LOC197138 5'  GCACCCAGACCTGAGCT     40546           TCCT
                                GCACCCAGACTTGA    GCT
                                ||||||||||||||    |||
                                CGTGGGTCTGGACT    CGA
                                      ____
GAM1647  LOC200081 3'  GCACCCAGGCACCACTGCTA   40551        ACTTG  _
                                GCACCCAG    ATC CTGCTA
                                ||||||||    ||| ||||||
                                CGTGGGTC    TGG GACGAT
                                     CG___   T
GAM1647  LOC220763 3'  CAACATCCAATCCTGC      40519      C   GACTTG
                                CAGCA CCA     ATCCTGC
                                ||||| |||     |||||||
                                GTTGT GGT     TAGGACG
                                   A  _______
GAM1647  LOC92106  5'  CAGAATATTTTGGTCCTGCTA  40552      C____   A
                                CAGA    TTG TCCTGCTA
                                ||||    ||| ||||||||
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                                GTCT    AAC AGGACGAT
                                  TATAA  C
GAM1648 AK2     3' TGAGAGGTTACTCATGAA    40555    A       GT
                                TGA AGGTTACTCG  TGAA
                                ||| ||||||||||  ||||
                                ACT TCCAATGAGT  ACTT
                                  C       __
GAM1648 C7orf2  3' GAGGGGCCACGGTTGAATGGA  40556   AA    TC     CA
                                GA  GGTTAC  GGTTGAA  GA
                                ||  ||||||  |||||||  ||
                                CT  CCGGTG  CCAACTT  CT
                                 CC     __     AC
GAM1648 DYRK1A  3' TGAAAGGTTGTTTCTTGAACAG 40557        ACTCGG
                                TGAAAGGTT     TTGAACAG
                                |||||||||     ||||||||
                                ACTTTCCAA     AACTTGTC
                                     CAAAG_
GAM1648 EPHB2   3' TGAAGGTTATGAACA      40558     A    CTCGGT
                                TGAA GGTTA     TGAACA
                                |||| |||||     ||||||
                                ACTT CCAAT     ACTTGT
                                  _    _______
GAM1648 FKBP1A  3' TGAAAGGATACTCAATACAGA  40559       T      TGA
                                TGAAAGG TACTCGGT   ACAGA
                                ||||||| ||||||||   |||||
                                ACTTTCC ATGAGTTA   TGTCT
                                    T      ___
GAM1648 IGF1    3' TGAAAGGTTTTGATATTTTGAA 40560        ACTCGG__    C
           TAGA                 TGAAAGGTT       TTGAA AGA
                                |||||||||       ||||| |||
                                ACTTTCCAA       AACTT TCT
                                     AACTATAA    A
GAM1648 MJD     3' TGAAAGGTTAATTTGGTTAATA 40561        CTC_    AC
           AGA                  TGAAAGGTTA   GGTTGA  AGA
                                ||||||||||   ||||||  |||
                                ACTTTCCAAT   CCAATT  TCT
                                     TAAA    AT
GAM1648 MJD     3' TGAAAGGTTAATTTGGTTAATA 40561        CTC_    AC
           AGA                  TGAAAGGTTA   GGTTGA  AGA
                                ||||||||||   ||||||  |||
                                ACTTTCCAAT   CCAATT  TCT
                                     TAAA    AT
GAM1648 PDGFRB  3' TGAGGGGTAGCTGGCTGAACAG 40562    AA  TA  C
           A                    TGA  GGT  CT GGTTGAACAGA
                                |||  |||  || ||||||||||
                                ACT  CCA  GA CCGACTTGTCT
                                  CC   TC  _
GAM1648 PXN     3' TGAGGGCTTACTCAGACAG   40563    AA   _    TTGA
                                TGA  GGTT ACTCGG   ACAG
                                |||  |||| ||||||   ||||
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                                ACT  CCGA TGAGTC    TGTC
                                  C_    A     _____
GAM1648  CCT5     3'  AAAGGTTGTTTAAACAG     40564        ACTCGG
                                AAAGGTT      TTGAACAG
                                |||||||      ||||||||
                                TTTCCAA      AATTTGTC
                                    CA_____
GAM1648  CIB1     3'  GAAAGGTTCTTGGACAG     40565        A  C  TTGA
                                GAAAGGTT CT GG    ACAG
                                |||||||| || ||    ||||
                                CTTTCCAA GA CC    TGTC
                                    _ A _____
GAM1648  D2S448   3'  GAAAGGTTGCTCAGAACACAGA 40566         A     TTGA
                                GAAAGGTT CTCGG    ACAGA
                                |||||||| |||||    |||||
                                CTTTCCAA GAGTC    TGTCT
                                    C     TTG_
GAM1648  DKFZP564C196 3'  GAAAGGTTGCAGAGCAG     40567        ACTCG  T  A
                                GAAAGGTT     GT GA CAG
                                ||||||||     || || |||
                                CTTTCCAA     CG CT GTC
                                    ______ T  C
GAM1648  DKFZP564P1916 3'  TAAAAGGTTACTTCTATAGA   40568          _ GGTT
                                TGAAAGGTTACT C    GA
                                ||||||||||||| |    ||
                                ATTTTCCAATGA G    CT
                                    A ATAT
GAM1648  DZIP1    3'  TAAAAGGTTACTTGGAAACAGA 40569           C  TT
                                TGAAAGGTTACT GG  GAACAGA
                                ||||||||||||| ||  |||||||
                                ATTTTCCAATGA CC  TTTGTCT
                                    A  __
GAM1648  FLJ20793  3'  TGAGAGGTCACTTGACGAAA   40570     A      C  TT
                                TGA AGGTTACT GG  GAA
                                ||| |||||||| ||  |||
                                ACT TCCAGTGA CT  TTT
                                  C       A  GC
GAM1648  GEMIN7   3'  TGGAAGGTTACTAGTGA     40571    A       C   T
                                TG AAGGTTACT GGT GA
                                || |||||||| ||| ||
                                AC TTCCAATGA TCA CT
                                 C       _  _
GAM1648  GS3955   3'  TAAAAGGTTATTTCAGAGACAG 40572          C_    TT  A
            A                    TGAAAGGTTA  TCGG  GA CAGA
                                ||||||||||  ||||  || ||||
                                ATTTTCCAAT  AGTC  CT GTCT
                                    AA    T_  _
GAM1648  MGC23980  3'  TGAAAGGCTGACACTGAACAGA 40573          _  TCGG
                                TGAAAGGTT AC    TTGAACAGA
                                |||||||| ||    |||||||||
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                                ACTTTCCGA TG   GACTTGTCT
                                     C  T___
GAM1648  OR2C3    3'  TGATAGGTTACTCTATTGA   40574    A      G
                                TGA AGGTTACTC GTTGA
                                ||| ||||||||| |||||
                                ACT TCCAATGAG TAACT
                                  A       A
GAM1648  PRO0618  3'  TGAAAGATTACTATGATGGA  40575         C_  T
                                TGAAAGGTTACT  GGT GA
                                ||||||||||||  ||| ||
                                ACTTTCTAATGA  CTA CT
                                       TA   C
GAM1648  UST      3'  TGAAAGGTACTCCAGGCTG   40576       T   __
                                TGAAAGGT ACTC  GGTTG
                                |||||||| ||||  |||||
                                ACTTTCCA TGAG  CCGAC
                                     _   GT
GAM1648  LOC126282 3'  TGAAAGGTGGTCCCCAGA   40577       TACTC   GAA
                                TGAAAGGT    GGTT   CAGA
                                ||||||||    ||||   ||||
                                ACTTTCCA    CCAG   GTCT
                                     ______   GG_
GAM1648  LOC145919 5'  TGAAAAGTTGGTGGGCAG   40578       ACTC   T AA
                                TGAAAGGTT   GGT G  CAG
                                |||||||||   ||| |  |||
                                ACTTTTCAA   CCA C  GTC
                                     _____  _ CC
GAM1648  LOC255037 3'  AAAAGGTCTTTGGTTGGACAG  40579       ACTC    A
                                GAAAGGTT    GGTTG ACAG
                                ||||||||    ||||| ||||
                                TTTTCCAG    CCAAC TGTC
                                     AAA_    C
GAM1648  LOC90594  3'  TGAAAGGTTCTTGACA     40580       A  CGGT   A
                                TGAAAGGTT CT    TGA CA
                                ||||||||| ||    ||| ||
                                ACTTTCCAA GA    ACT GT
                                     _ _____  _
GAM1649  C4orf1   3'  TCCAAGGTCCCCACCCAGGT  40583       AT__
                                TCCGAGGTC    CCCAGGT
                                |||||||||    |||||||
                                AGGTTCCAG    GGGTCCA
                                     GGGT
GAM1649  FANCG    5'  CTCGCCTCTGGTTGGCCGGGT  40584       CGA   CATC  A
                                CTCGCCTC   GGT    CC GGT
                                ||||||||   |||    || |||
                                GAGCGGAG   CCA    GG CCA
                                     A__   ACC_  C
GAM1649  GATA4    3'  CCTCCAAGTCCCAGGT      40585       GTCA
                                CCTCCGAG    TCCCAGGT
                                ||||||||    ||||||||
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                                GGAGGTTC   AGGGTCCA
                                    ____
GAM1649 GLRX2    5' CCCGCCTCTGGATTCTTTTAGG 40586       C_ GG ATCCC
            T                    CTCGCCTC GA TC   AGGT
                                 |||||||| || ||   ||||
                                 GGGCGGAG CT AG   TCCA
                                     AC A_ AAAA_
GAM1649 GRB10    3' CTCGCTCTGGGTCCCCAGG   40587     C CGA   AT
                                 CTCGC TC  GGTC CCCAGG
                                 ||||| ||  |||| ||||||
                                 GAGCG AG  CCAG GGGTCC
                                   _ AC_   __
GAM1649 MEL      3' TCCCGATCACCCAGGT     40588    GA   T
                                 TCC GGTCA CCCAGGT
                                 |||  ||||| |||||||
                                 AGG CTAGT GGGTCCA
                                   G_    _
GAM1649 RXRG     3' GCCCAGGGGTCATCCTGGGT  40589     CCGA      CA
                                 GCCT   GGTCATCC GGT
                                 ||||   |||||||| |||
                                 CGGG   CCAGTAGG CCA
                                   TCC_      AC
GAM1649 TFCP2    5' CTCGTTCTTGGCTGCCCCAGGT 40590     CC CGA  CA
                                 CTCG TC  GGT TCCCAGGT
                                 |||| ||  ||| ||||||||
                                 GAGC AG  CCG GGGGTCCA
                                   A_ AA_  AC
GAM1649 TRPV4    3' CTCGCCTCTGGGGCCAAAGCAG 40591       CGA    TCC
            G                    CTCGCCTC  GGTCA  CAGG
                                 ||||||||  |||||  ||||
                                 GAGCGGAG  CCGGT  GTCC
                                     ACC    TTC
GAM1649 ARFGAP1  3' CCCGCCTCTGACCTCAGG    40592       C GGTCAT _
                                 CTCGCCTC GA    CC CAGG
                                 |||||||| ||    || ||||
                                 GGGCGGAG CT    GG GTCC
                                     A _______ A
GAM1649 C11orf11 3' CCCGCTTCTGGGGAAACTCCGG 40593     C CGA TC TC A
            GT                   CTCGC TC  GG A CC GGT
                                 ||||| ||  ||  |  || |||
                                 GGGCG AG  CC  T  GG CCA
                                   A ACC  TT GA  C
GAM1649 C21orf108 3' GCAGAGGTCATCCCAGG    40594    CTCC
                                 GC   GAGGTCATCCCAGG
                                 ||   ||||||||||||||
                                 CG   CTCCAGTAGGGTCC
                                  T___
GAM1649 CBX3     5' CGCCTCCGAGCTGCTCCGGGT 40595       GTCA  CA
                                 CGCCTCCGAG   TCC  GGT
                                 ||||||||||   |||  |||
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                                GCGGAGGCTC   AGG  CCA
                                     GACG   C_
GAM1649  FLJ00007  3'  CTCCCCTCCCAGGTTCCGGGT  40596    G    G   CA   CA
                                CTC CCTCC AGGT  TCC  GGT
                                ||| ||||| ||||  |||  |||
                                GAG GGAGG TCCA  AGG  CCA
                                  G    G   __   C_
GAM1649  FLJ13456  3'  CTCGCTCTGTTTCCCAGG    40597      C  CGAG  CA
                                CTCGC TC   GT  TCCCAGG
                                ||||| ||   ||  |||||||
                                GAGCG AG   CA  AGGGTCC
                                   _ A___  A_
GAM1649  FLJ20207  3'  CTCTCTTCCCAAACATCTCAGG 40598    GCC   G   T   C
            T                    CTC   TCC AGG CATC CAGGT
                                |||   ||| ||| |||| |||||
                                GAG   AGG TTT GTAG GTCCA
                                  AGA   G   _   A
GAM1649  HSPC232   5'  CTCGCCGCCGTTATCCCAGGT  40599      T   AGGTC
                                CTCGCC CCG    ATCCCAGGT
                                |||||| |||    |||||||||
                                GAGCGG GGC    TAGGGTCCA
                                   C   AA___
GAM1649  KIAA1484  3'  CTCGCCCCGGCCCCG      40600        CGA   CAT   A
                                CTCGCCTC   GGT   CCC G
                                ||||||||   |||   ||| |
                                GAGCGGGG   CCG   GGG C
                                     ___   ___   C
GAM1649  KIF13B    3'  CTCCCTCTGGTCAGGCCTGGGT 40601    G   CGA    TC  A_
                                CTC CCTC   GGTCA  CC  GGT
                                ||| ||||   |||||  ||  |||
                                GAG GGAG   CCAGT  GG  CCA
                                  _   A__    CC  AC
GAM1649  KIF13B    3'  CTCCCTCTGGTCAGGCCTGGGT 40601    G   CGA    TC  A_
                                CTC CCTC   GGTCA  CC  GGT
                                ||| ||||   |||||  ||  |||
                                GAG GGAG   CCAGT  GG  CCA
                                  _   A__    CC  AC
GAM1649  MGC15875  5'  CTCCTTCTGGCCATCCAGG    40602     GA__      C
                                CTCC    GGTCATCC AGG
                                ||||    |||||||| |||
                                GAGG    CCGGTAGG TCC
                                  AAGA       _
GAM1649  MGC3178   5'  CTCCCAGGTCATTCCAAGT    40603     G      C
                                CTCC AGGTCAT CCAGGT
                                |||| ||||||| ||||||
                                GAGG TCCAGTA GGTTCA
                                  G      A
GAM1649  PSCD1     5'  CTTTCCTCTGTGGATCCCAGGT 40604    CG   CGA  TC
                                CT  CCTC   GG  ATCCCAGGT
                                ||  ||||   ||  |||||||||
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                                GA  GGAG   CC  TAGGGTCCA
                                 AA    ACA  __
GAM1649  SRp25    5'  TCGTTCTGACGCCCCAGG    40605     CC  C  G  CAT
                                TCG  TC GA GT   CCCAGG
                                |||  || || ||   ||||||
                                AGC  AG CT CG   GGGTCC
                                  A_  A  G  ___
GAM1649  LOC145438 5'  CTCGCCTCGCTTCCTGGG    40606        CGAG  CA   CA
                                CTCGCCTC    GT  TCC  GG
                                ||||||||    ||  |||  ||
                                GAGCGGAG    CG  AGG  CC
                                     _____  A_   AC
GAM1649  LOC221596 5'  GCTTCCACTTCTCCCAGGT    40607    C    AGG  A
                                GC TCCG   TC TCCCAGGT
                                || ||||   || ||||||||
                                CG AGGT   AG AGGGTCCA
                                 A   GA_  _
GAM1649  LOC256715 3'  CTCGCCTCGGAGGCCAACTCCA 40608         C      TC_
              GGT                    CTCGCCTC GAGGTCA   CCAGGT
                                |||||||| |||||||   ||||||
                                GAGCGGAG CTCCGGT   GGTCCA
                                     C      TGA
GAM1650  IRS2     3'  GGATAGAGGGCGAGTTAAAT   40611        TCTT  A
                                GGATAGA    GC AGTTAAAT
                                |||||||    || ||||||||
                                CCTATCT    CG TCAATTTA
                                    CC__  C
GAM1650  TOMM22    3'  AGGGCACAGTTGCAAGTT    40612      _    ATC
                                AGGG ATAG   TTGCAAGTT
                                |||| ||||   |||||||||
                                TCCC TGTC   AACGTTCAA
                                  G   ___
GAM1650  ZNF255    5'  AGGGATAAAAAGCTACAAGTT  40613         TC_
                                AGGGATAGA   TTGCAAGTT
                                |||||||||   |||||||||
                                TCCCTATTT   GATGTTCAA
                                     TTC
GAM1650  LOC149153 5'  GGATAGATTGTGGCAGTTAAAT 40614         CT  CA
                                GGATAGAT  TG  AGTTAAAT
                                ||||||||  ||  ||||||||
                                CCTATCTA  AC  TCAATTTA
                                     AC  CG
GAM1650  LOC149773 5'  GGGATAGATCTTGAAAT     40615            C
                                GGGATAGATCTTG AAGT
                                |||||||||||| ||||
                                CCCTATCTAGAAC TTTA
                                          _
GAM1650  LOC256714 3'  GAGATATACAGTGCAAGTT    40616       G  CT
                                GGGATA AT  TGCAAGTT
                                |||||| ||  ||||||||
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                                CTCTAT TG  ACGTTCAA
                                   A  TC
GAM1651  COL19A1   3'  TTTGGTCTGAGCACTAGTTGCA 40619   CT     _________  TCAT
             AATGATC                  TGAGCAC       CGA    TT
                                  |||||||       |||    ||
                                  ACTCGTG       GTT    AG
                                AG      ATCAACIII   TACT
GAM1651  LOC158476 5'  TTTGGCTTGACATCCCCATTT  40620         G  _  GA
                                TTTGGCTTGA CA CC  TCATTT
                                |||||||||| || ||  ||||||
                                AAACCGAACT GT GG  GGTAAA
                                      _  A  __
GAM1652  CANX      3'  TAATCAATACATTTGGGA    40623      TATAG
                                TAGTT    ACATTTGGGA
                                |||||    ||||||||||
                                ATTAG    TGTAAACCCT
                                   TTA__
GAM1652  MAX       3'  TTTATAGTCTTATAGTAAAGGG 40624          _   ACATTT
                                TTTATAGTTT ATAG     GGG
                                |||||||||| ||||     |||
                                AAATATCAGA TATC     CCC
                                      A   ATTT__
GAM1652  MAX       3'  TTTATAGTCTTATAGTAAAGGG 40624          _   ACATTT
                                TTTATAGTTT ATAG     GGG
                                |||||||||| ||||     |||
                                AAATATCAGA TATC     CCC
                                      A   ATTT__
GAM1652  FLJ13646  3'  TTTATAGTTATACTAAATGGGA 40625        TATAG  ATT_
                                TTTATAGTT    AC   TGGGA
                                |||||||||    ||   |||||
                                AAATATCAA    TG   ACCCT
                                      TA___  ATTT
GAM1652  FLJ20725  3'  TTCATAGTTTATTTGG      40626          AGACAT
                                TTTATAGTTTAT     TTGG
                                ||||||||||||     ||||
                                AAGTATCAAATA     AACC
                                                 _______
GAM1652  LOC201824 3'  TTTATGGTATCATAGTATTTGG 40627      A  _     AC
             GA                   TTTAT GT TTATAG  ATTTGGGA
                                |||||  || ||||||  ||||||||
                                AAATA CA AGTATC  TAAACCCT
                                   C  T     A_
GAM1652  LOC257048 3'  TTTATGGTTTGTAACAATTTGG 40628      A   ATA   _
             GA                   TTTAT GTTT   GACA TTTGGGA
                                |||||  ||||   ||||  |||||||
                                AAATA CAAA   TTGT AAACCCT
                                   C    CA_    T
GAM1653  FLJ11838  3'  CAAGATATGTTTATTCAT    40200
                                TAAGATATGTTTATTCAT
                                ||||||||||||||||||
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                                GTTCTATACAAATAAGTA

GAM1654 HNRPA0   5' GCCGTTATCGTTGGTT     40632       AC   C
                                GTCGTTA  TCGT GGTT
                                |||||||  |||| ||||
                                CGGCAAT  AGCA CCAA
                                    __   A
GAM1654 LOC126231 5' CGCGTTGTTACTCGGG     40633      C   A   TC
                                CGCGT GTTA CTCG  GG
                                ||||| |||| ||||  ||
                                GCGCA CAAT GAGC  CC
                                  A   _   __
GAM1655 FLJ23416 3' TAAGAATTTAGAAATCATC   40316          TA_
                                TAAGAATTTAGA   CATC
                                ||||||||||||   ||||
                                ATTCTTAAATCT   GTAG
                                       TTA
GAM1655 FLJ31153 3' AGAATTCAGATATTTATATT  40317          CATC
                                AGAATTTAGATA    TATATT
                                ||||||||||||    ||||||
                                TCTTAAGTCTAT    ATATAA
                                       AA__
GAM1655 KIAA1545 3' TAAGAATTTAGTAACGTCATAT 40318          AT  A  _
            ATT                   TAAGAATTTAG  AC TC TATATT
                                ||||||||||  || || ||||||
                                ATTCTTAAATC  TG AG ATATAA
                                       AT  C  T
GAM1655 MO25     3' TAAAAATAAAATATATCTATAT 40319       TT    C
            T                    TAAGAAT  AGATA ATCTATATT
                                |||||||  ||||| |||||||||
                                ATTTTTA  TTTAT TAGATATAA
                                    T_    A
GAM1655 LOC222160 5' TAAGGGTCTAGATACAACT   40320      AA        T
                                TAAG  TTTAGATACA CT
                                ||||  |||||||||| ||
                                ATTC  AGATCTATGT GA
                                  CC         T
GAM1656 MYLK     3' TGATGGCATAATAAACCAA   40637   T   A        TG
                                A ATG CATAATAAAT  G
                                | ||| ||||||||||  |
                                A TAC GTATTATTTG  T
                                 C   C         GT
GAM1656 NARS     3' TACATGACATGCATTTGGT   40638          AATAAA
                                TATATGACAT     TTGGT
                                ||||||||||     |||||
                                ATGTACTGTA     AACCA
                                       CGTA__
GAM1656 PCDHA9   3' TGATGACATAGTAAATGCTTAG 40639   T      A    ___
            TAA                   A ATGACATA TAAAT   TGGTAA
                                | |||||||| |||||   ||||||
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                                A TACTGTAT ATTTA   ATCATT
                                 C       C     CGA
GAM1656  PHYH     3'  TATGACATAAAATTGGTA    40640          TA
                                TATGACATAA  AATTGGTA
                                ||||||||||  ||||||||
                                ATACTGTATT  TTAACCAT
                                          __
GAM1656  SMARCA2   3'  TATATGACAAATGAACTCACTG 40641          T___   AA
              G                  TATATGACA    AAT  ATTGG
                                |||||||||    |||  |||||
                                ATATACTGT    TTG  TGACC
                                     TTAC   AG
GAM1656  ARHGEF3   3'  TATGTACATAATAAAATGA   40642     _        T
                                TATG ACATAATAAA TGG
                                |||| ||||||||||| |||
                                ATAC TGTATTATTT ACT
                                  A         T
GAM1656  FLJ13910  3'  TATATATATAATAAACTGG   40643       AC
                                TATATG  ATAATAAATTGG
                                ||||||  ||||||||||||
                                ATATAT  TATTATTTGACC
                                   A_
GAM1657  SOX15    5'  AGTCGTTGCCGAGGAACTTG   40646    CA       TTT
                                AG  GTTGCCGA   ATTTG
                                ||  ||||||||   |||||
                                TC  CAACGGCT   TGAAC
                                 AG       CCT
GAM1657  FLJ13912  3'  CTAAAACATGGATTTATTT    40647        GTTGCC
                                CTAAAGCA     GATTTATTT
                                ||||||||     |||||||||
                                GATTTTGT     CTAAATAAA
                                     AC_____
GAM1657  KIAA0710  3'  CTGAAGCAGTTGGTGACTT    40648    A       CC
                                CT AAGCAGTTG  GATTT
                                || |||||||||  |||||
                                GA TTCGTCAAC  CTGAA
                                 C        CA
GAM1657  SIPL     3'  TAAGGCAGTTACTTTATTT    40649     A      CGA
                                TAA GCAGTTGC   TTTATTT
                                ||| ||||||||   |||||||
                                ATT CGTCAATG   AAATAAA
                                  C       ___
GAM1657  LOC131368 3'  AAGCAATTGCTTGATGATTTG  40650          C_   TT
                                AAGCAGTTGC  GAT  ATTTG
                                ||||||||||  |||  |||||
                                TTCGTTAACG  CTA  TAAAC
                                      AA   C_
GAM1657  LOC139770 3'  AAGCAGTTGTGTGACACTTG   40651         CCGATT
                                AAGCAGTTG     TATTTG
                                |||||||||     ||||||
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                                TTCGTCAAC     GTGAAC
                                     ACACT_
GAM1658 ADORA2B  5' CCGGTCCAGGCGCCGTGCC  40654        AT  G  C
                                CCGGTCCAG  CGC GT GCC
                                |||||||||  ||| || |||
                                GGCCAGGTC  GCG CA CGG
                                     C_  G  _
GAM1658 GCLC     5' CCGGGCTGACGGCGGTCGCCCG 40655     TCCA  C
                                CCGG   GAT GCGGTCGCCCG
                                ||||   ||| ||||||||||||
                                GGCC   CTG CGCCAGCGGGC
                                  CGA_  C
GAM1658 WT1      5' GGCCCAGATGCCGCCC     40656        CGCG
                                GGTCCAGAT   GTCGCCC
                                |||||||||   |||||||
                                CCGGGTCTA   CGGCGGG
                                     _____
GAM1658 WT1      5' GGCCCAGATGCCGCCC     40656        CGCG
                                GGTCCAGAT   GTCGCCC
                                |||||||||   |||||||
                                CCGGGTCTA   CGGCGGG
                                     _____
GAM1658 WT1      5' GGCCCAGATGCCGCCC     40656        CGCG
                                GGTCCAGAT   GTCGCCC
                                |||||||||   |||||||
                                CCGGGTCTA   CGGCGGG
                                     _____
GAM1658 WT1      5' GGCCCAGATGCCGCCC     40656        CGCG
                                GGTCCAGAT   GTCGCCC
                                |||||||||   |||||||
                                CCGGGTCTA   CGGCGGG
                                     _____
GAM1658 FLJ20359 3' GGCTGGATTGCAGCCACCCG  40657    CCA  C
                                GGT   GAT GCGGTCGCCCG
                                |||   ||| ||||||||||||
                                CCG   CTA CGTCGGTGGGC
                                  AC_   A
GAM1658 FLJ21736 3' GGTCCAGATGCCCTCCCC    40658       C  GG  G
                                GGTCCAGAT GC  TC CCC
                                ||||||||| ||  || |||
                                CCAGGTCTA CG  AG GGG
                                     _ GG  _
GAM1658 IDI1     5' CCGGTCCCGGATGGCGCCCG  40659      A_  CGC  T
                                CCGGTCC  GAT   GG CGCCCG
                                |||||||  |||   || ||||||
                                GGCCAGG  CTA   CC GCGGGC
                                    GC  ___  _
GAM1658 KIAA1171 3' GGTCCAGATCACTGGAAGGCCC 40660          _  TC_
             G                   GGTCCAGATCGC GG   GCCCG
                                 ||||||||||| ||   |||||
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                                CCAGGTCTAGTG CC   CGGGC
                                      A  TTC
GAM1658  KIAA1691  3'  CCGGTCCAGGTAGCTGCCG   40661        ATC  G
                                CCGGTCCAG   GC GTCG
                                |||||||||   || ||||
                                GGCCAGGTC   CG CGGC
                                     CAT  A
GAM1658  PTPRT     3'  GGTCCAGACTGCAAATGTC   40662        C  ___
                                GGTCCAGAT GCG   GTC
                                ||||||||| |||   |||
                                CCAGGTCTG CGT   CAG
                                     A   TTA
GAM1658  TPD52     5'  CCGGCTCGGATCGCC       40663      CCAGA   C
                                CCGGT     TCG GGTCGCC
                                |||||     ||| |||||||
                                GGCCG     AGC CTAGCGG
                                  _____   _
GAM1658  LOC112616 3'  GGTCCAGAGGCCTCGCC     40664        TC  GG
                                GGTCCAGA  GC  TCGCC
                                ||||||||  ||  |||||
                                CCAGGTCT  CG  AGCGG
                                    C_  G_
GAM1658  LOC154860 5'  CGGTTCGGGCCGCGGAGACTCC 40665      CCAGA     TC  _
           G                     CGGT     TCGCGG  GC CCG
                                ||||     ||||||  || |||
                                GCCA     GGCGCC  TG GGC
                                  AGCCC      TC  A
GAM1658  LOC165229 5'  CCTGTCCAGATCTTAGCTCG   40666    G       GC  _
                                CC GTCCAGATC  GG TCG
                                || |||||||||  || |||
                                GG CAGGTCTAG  TC AGC
                                 A        AA  G
GAM1658  LOC219513 3'  CCGGTCCAGGCTGCCCA     40667        GATCGC   C
                                CCGGTCCA      GGT GCCCG
                                ||||||||      ||| |||||
                                GGCCAGGT      CCG CGGGT
                                    _______   A
GAM1658  LOC222182 3'  GATCCAGATCCTTCCTGCC    40668         GCGG  _
                                GGTCCAGATC    TC GCC
                                ||||||||||    || |||
                                CTAGGTCTAG    GG CGG
                                     GAA_  A
GAM1659  BBOX1     3'  TGAGAGAAGTTACATGTTCAT  40671     A       _   G
                                TGA AGAAGTTAC TGTT GT
                                ||| ||||||||| |||| ||
                                ACT TCTTCAATG ACAA TA
                                  C        T   G
GAM1659  C1QB      5'  TGTGAGAGGTTACCACCGTGGT 40672    AA  A    TG __
           GATC                    TG  AGA GTTAC  T  TGGTGATC
                                ||  ||| |||||  |  ||||||||
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                                AC  TCT CAATG  G  ACCACTAG
                                 AC   C     GT GC
GAM1659  PPP2R2B   3'  TGGAAGAATTACTGTTAGC    40673    A     G
                                TG AAGAA TTACTGTTGGT
                                || ||||| ||||||||||
                                AC TTCTT AATGACAATCG
                                 C    _
GAM1659  APOF      3'  GAAAGAAGTTACTATTCAGTGA 40674              _
              TC                   GAAAGAAGTTACTGTT GGTGATC
                                |||||||||||||||| |||||||
                                CTTTCTTCAATGATAA TCACTAG
                                          G
GAM1659  DKFZP566J091 3'  TGGAAGAAGTTATTGCCA    40675    A       C
                                TG AAGAAGTTA TGTTG
                                || |||||||| |||||
                                AC TTCTTCAAT ACGGT
                                 C        A
GAM1659  FBXL3B    5'  TAAAGGAAGTTACTGAAAAAT  40676     A        TT_
                                TGAA GAAGTTACTG   GGT
                                |||| ||||||||||   |||
                                ATTT CTTCAATGAC   TTA
                                   C         TTT
GAM1659  KIAA0794  3'  TGAAGAAGTTACTTTGGT    40677     A       G
                                TGAA GAAGTTACT TTGGT
                                |||| ||||||||| |||||
                                ACTT CTTCAATGA AACCA
                                  _       _
GAM1659  KIAA1615  5'  TGAGAGAAGTTGATGACC    40678    A     TACTGT
                                TGA AGAAGT     TGGTGATC
                                ||| ||||||     ||||||||
                                ACT TCTTCA     ACTACTGG
                                 C     _______
GAM1659  KIAA1679  5'  TGAAAGAGGTCACTGTGCCAGT 40679        A     __  TG
                                TGAAAGA GTTACT  GT  GT
                                ||||||| ||||||  ||  ||
                                ACTTTCT CAGTGA  CG  CA
                                    C     CA  GT
GAM1659  N4BP3     3'  TGGGAGGAGCTACTGCCCAGGT 40680    AA  A        __
                                TG  AG AGTTACTGTT  GGT
                                ||  || ||||||||||  |||
                                AC  TC TCGATGACGG  CCA
                                 CC  C         GT
GAM1659  LOC129138 3'  TGGAAGAAGCTGGGAGCTGTGG 40681    A       A____    T
              T                   TG AAGAAGTT     CTGT GGT
                                || ||||||||     |||| |||
                                AC TTCTTCGA     GACA CCA
                                 C       CCCTC   _
GAM1659  LOC143425 3'  TGGAAAAAGTTACTTAAGAT   40682    A         GTT
                                TG AAGAAGTTACT   GGT
                                || ||||||||||   |||
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                                AC TTTTTCAATGA   CTA
                                 C          ATT
GAM1659  LOC166341 3'  GAAGCAGTTGCTGATAGAT   40683       TAC      _
                                GAAGT   TGTTGGT GAT
                                |||||   ||||||| |||
                                CTTCG   ACGACTA CTA
                                   TCA      T
GAM1660  EPHA2     3'  TCCCTGGTCATCTCCTCAGT   40686       A         A
                                TCCCTG TCATCTCCTCA GT
                                |||||| |||||||||| ||
                                AGGGAC AGTAGAGGAGT CA
                                   C         _
GAM1660  OSR1      3'  CTGATCATCTCACCTACT     40687          _ CAAG
                                CTGATCATCTC CT    TACT
                                |||||||||| ||    ||||
                                GACTAGTAGAG GG    ATGA
                                       T _____
GAM1660  PLOD2     3'  CCTGATATAAAATTCAAGTACT 40688       CATCTCC
                                CCTGAT      TCAAGTACT
                                ||||||      |||||||||
                                GGACTA      AGTTCATGA
                                   TATTTTA
GAM1660  RAD54B    3'  CTGACCATCTCTCCATACT    40689          CT  AG
                                CTGATCATCTC  CA  TACT
                                |||||||||| ||  ||||
                                GACTGGTAGAG  GT  ATGA
                                       AG  __
GAM1660  SEL1L     3'  CTGATCATTTCTTACATACT   40690        C  CTCAA
                                CTGATCAT TC     GTACT
                                |||||||| ||     |||||
                                GACTAGTA AG     TATGA
                                     A  AATG_
GAM1660  DIS3      3'  TCTCTGATCATCTTGAACTACT 40691     C        CCTC  G
                                TC CTGATCATCT    AA TACT
                                || ||||||||||    || ||||
                                AG GACTAGTAGA    TT ATGA
                                 A         AC__  G
GAM1660  FLJ22690  3'  CTGATCATCTCCCAGCACT    40692           CA
                                CTGATCATCTCCT  AGTACT
                                ||||||||||||  ||||||
                                GACTAGTAGAGGG  TCGTGA
                                              __
GAM1660  KIAA1858  3'  CTGCTGTCTCTTCAAGTACT   40693     ATCA   C
                                CTG    TCTC TCAAGTACT
                                |||    |||| |||||||||
                                GAC    AGAG AGTTCATGA
                                  GAC_    A
GAM1660  MGC23244  3'  CCCCTGACCTCAAGT       40694        TCATCT
                                TCCCTGA     CCTCAAGT
                                |||||||     ||||||||
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                                GGGGACT     GGAGTTCA
                                        ______
GAM1660 MGC4638   3' TCCCTGACATCTTCTCACAGGA 40695       T    C   _ T
             CT                   TCCCTGA CATCT CTCA AG ACT
                                  ||||||| ||||| |||| || |||
                                  AGGGACT GTAGA GAGT TC TGA
                                     _    A   G  C
GAM1660 SIAT4A    3' TCCCTGAGCGTCTCCCCAGC   40696       TCA      A
                                  TCCCTGA   TCTCCTCA GT
                                  |||||||   |||||||| ||
                                  AGGGACT   AGAGGGGT CG
                                     CGC      _
GAM1660 SLC5A7    3' TCCCTGATCACTTTTCAGC    40697         T  CC   A
                                  TCCCTGATCA CT  TCA GT
                                  |||||||||| ||  ||| ||
                                  AGGGACTAGT GA  AGT CG
                                        _ AA   _
GAM1660 LOC196283 3' TCCTTGGGCATCTCCTCCAGCA 40698     C  AT       A
                                  TCC TG  CATCTCCTC AGTA
                                  ||| ||  ||||||||| ||||
                                  AGG AC  GTAGAGGAG TCGT
                                    A  CC        G
GAM1660 LOC256520 3' CTTCCAGTTTCCTCAAGTGCT  40699    GA   TC_       A
                                  CT  TCA   TCCTCAAGT CT
                                  ||  |||   ||||||||| ||
                                  GA  GGT   AGGAGTTCA GA
                                   A_  CAA        C
GAM1660 LOC85479  5' TCTCTGTCATCTCCACTGTACT 40700    C   A       TCAA
                                  TC CTG TCATCTCC    GTACT
                                  || ||| ||||||||    |||||
                                  AG GAC AGTAGAGG    CATGA
                                   A   _       TGA_
GAM1660 LOC90378  5' TCCTCTTCTTTCTCAAGTACT  40701     CTGA  A   C_
                                  TCC    TC TCT  CTCAAGTACT
                                  |||    || |||  ||||||||||
                                  AGG    AG AGA  GAGTTCATGA
                                    _____  A   AA
GAM1660 LOC91351  3' TCCTCACTTTTTCAAGTACT   40702     CTGA    CTCC
                                  TCC    TCAT    TCAAGTACT
                                  |||    ||||    |||||||||
                                  AGG    AGTG    AGTTCATGA
                                    _____    AAAA
GAM1661 DUOX2     3' GGAAGTCAATTAGAGATGTGGG 40705          TCGA    A
                                  GGAGGTCAATT    AGAT TGGG
                                  ||||||||||    |||| ||||
                                  CCTTCAGTTAA    TCTA ACCC
                                         TC__    C
GAM1661 KLK4      3' GGGGTCAATTTCATG       40706     A        GAAGAT
                                  GG GGTCAATTTC      ATG
                                  || ||||||||||      |||
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                                CC CCAGTTAAAG     TAC
                                 _      ______
GAM1661  RPH3A    3'  GGAGATCAGCAGGGTATGG   40707       ATTTCGA  A_
                                GGAGGTCA     AG  TATGG
                                ||||||||     ||  |||||
                                CCTCTAGT     TC  ATACC
                                    CG_____  CC
GAM1661  LOC150372 3'  GGAGGCCAAGGCCAGGTGTGGG 40708        TT   AAGATA
                                GGAGGTCAA  TCG     TGGG
                                |||||||||  |||     ||||
                                CCTCCGGTT  GGT     ACCC
                                     CC   CCAC__
GAM1662  GSPT1    5'  CCCGGCCGGAGAGGAGTGGG   40711      G  TTC   A
                                TCCGG CG   AGA GAGTGGG
                                ||||| ||   ||| |||||||
                                GGGCC GC   TCT CTCACCC
                                   G  C__   C
GAM1662  M17S2    5'  CATTAGGGCGGAAAGAGTGGG  40712     CC    TTCA
                                CAT  GGGCG   GAAGAGTGGG
                                |||  |||||   ||||||||||
                                GTA  CCCGC   TTTCTCACCC
                                  AT    C___
GAM1662  M17S2    5'  CATTAGGGCGGAAAGAGTGGG  40712     CC    TTCA
                                CAT  GGGCG   GAAGAGTGGG
                                |||  |||||   ||||||||||
                                GTA  CCCGC   TTTCTCACCC
                                  AT    C___
GAM1662  MADD     5'  CCGGGCGCGCGCGGGGAGTGGG 40713        TCAGAA_
                                CCGGGCGT      GAGTGGG
                                ||||||||      |||||||
                                GGCCCGCG      CTCACCC
                                    CGCGCCC
GAM1662  C8orf6   5'  CATCAGAGCAGAAGGGTGG   40714     C   GTTC    A
                                CATC GGGC   AGAAG GTGG
                                |||| ||||   ||||| ||||
                                GTAG CTCG   TCTTC CACC
                                  T   _____    C
GAM1662  HABP2    3'  TCAGGGTGCCAAGGAGAGTGGG 40715    C   C  TC  A
                                TC GGG GT  AG AGAGTGGG
                                || ||| ||  || ||||||||
                                AG CCC CG  TC TCTCACCC
                                 T   A  GT  C
GAM1662  KIAA1041 3'  CACCTGGATCACAGGAGAGTGG 40716      C   CGTT   A
            G                    CATC GGG   CAG AGAGTGGG
                                 |||| |||   ||| ||||||||
                                 GTGG CCT   GTC TCTCACCC
                                   A  AGT_   C
GAM1662  KIAA1727 3'  ATCCGGGCTTTGGGGGAGGGTG 40717        GTTCAGA_  A
            GG                   ATCCGGGC       AG GTGGG
                                 ||||||||       || |||||
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                                TAGGCCCG       TC CACCC
                                    AAACCCCC  C
GAM1662 KLF16    3' CATCCTGGCGGTCAGGGTGGG 40718      G   T   AAGA
                                CATCC GGCG TCAG    GTGGG
                                ||||| |||| ||||    |||||
                                GTAGG CCGC AGTC    CACCC
                                   A   C   C___
GAM1662 NBR2     5' CATTAGGGCGGAAAGAGTGGG 40712     CC    TTCA
                                CAT  GGGCG    GAAGAGTGGG
                                |||  |||||    ||||||||||
                                GTA  CCCGC    TTTCTCACCC
                                  AT    C___
GAM1662 NFAT5    5' CATCCGGGTTATTCGGAGTGGG 40719        C_   AGAA
                                CATCCGGG  GTTC    GAGTGGG
                                ||||||||  ||||    |||||||
                                GTAGGCCC  TAAG    CTCACCC
                                    AA    C___
GAM1662 OBSCN    3' TCCGGGCAGAGCTGGAGAGTGG 40720        TTCAGA_
              G                  TCCGGGCG      AGAGTGGG
                                ||||||||      ||||||||
                                AGGCCCGT      TCTCACCC
                                    CTCGACC
GAM1662 PPM1A    5' CATCCGGGCGTTGGAGAGG   40721          CAGAA   T
                                CATCCGGGCGTT     GAG GG
                                ||||||||||||     ||| ||
                                GTAGGCCCGCAA     CTC CC
                                      C____   T
GAM1662 PRDM8    5' AGTGTTATTTTGGAAGAGTGGG 40722    C   CA____
                                GG GTT     GAAGAGTGGG
                                || |||     ||||||||||
                                TC CAA     CTTCTCACCC
                                 A   TAAAAC
GAM1662 RASAL2   3' TCTGGAGATAGGAGAGTGGG   40723    C   C  TC  A
                                TC GGG GT  AG AGAGTGGG
                                || ||| ||  || ||||||||
                                AG CCT TA  TC TCTCACCC
                                 A   C  __  C
GAM1662 LOC126961 3' ATCTGGCCGTGTGTAGAGTGGG 40724     C  G   TCAGA
                                ATC GG CGT     AGAGTGGG
                                ||| || |||     ||||||||
                                TAG CC GCA     TCTCACCC
                                  A  G   CACA_
GAM1662 LOC255040 3' CATTCGGACGAGAGTG      40725     C     TTCAGA
                                CAT CGGGCG     AGAGTG
                                ||| ||||||     ||||||
                                GTA GCCTGC     TCTCAC
                                  A     _______
GAM1662 LOC255041 3' CATTCGGACGAGAGTG      40725     C     TTCAGA
                                CAT CGGGCG     AGAGTG
                                ||| ||||||     ||||||
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                                GTA GCCTGC     TCTCAC
                                  A    _______
GAM1662 LOC257395 3' ATCTGGCCGTGTGTAGAGTGGG 40724     C  G   TCAGA
                                ATC GG CGT    AGAGTGGG
                                ||| || |||    ||||||||
                                TAG CC GCA    TCTCACCC
                                  A  G   CACA_
GAM1662 LOC56930 5' TCCTGGCCCTGGAAGAGTGGG 40726     G   G  CA
                                TCC GGC TT  GAAGAGTGGG
                                ||| ||| ||  ||||||||||
                                AGG CCG GA  CTTCTCACCC
                                  A  G  C_
GAM1662 LOC91397 5' GGCTGAGCTCAGGAGAGTGGG 40727     ___     A
                                GGC   GTTCAG AGAGTGGG
                                |||   |||||| ||||||||
                                CCG   CGAGTC TCTCACCC
                                  ACT     C
GAM1663 MAN1A1   3' ATCTGAACCAAATAGAATGCT 40730     G  CA  TT
                                ATC TG  GG  AAATAGAATGCT
                                ||| ||  ||  ||||||||||||
                                TAG AC  TT  TTTATCTTACGA
                                  _ __  GG
GAM1663 NET1     3' ATCGGCAGGTTAAATGAAT   40731      T         A
                                ATCG GCAGGTTAAAT GAAT
                                |||| |||||||||| ||||
                                TAGC CGTCCAATTTA CTTA
                                   _         _
GAM1663 RAB27A   3' CATGTTAAATAGAATGCT    40732    G
                                CA GTTAAATAGAATGCT
                                || ||||||||||||||
                                GT CAATTTATCTTACGA
                                 A
GAM1663 RUNX3    3' GTGCAGGCTGGTGGGATGCT  40733         AAATA  A
                                GTGCAGGTT    GA TGCT
                                |||||||||    || ||||
                                CACGTCCGA    CT ACGA
                                      CCACC  _
GAM1663 MRPL34   3' GCGCAGGTTCGAAATGCT    40734         AAATA
                                GTGCAGGTT    GAATGCT
                                |||||||||    |||||||
                                CGCGTCCAA    TTTACGA
                                      GC___
GAM1663 LOC118738 3' TCTGCAGGCAGAATG       40735    G      TAAAT
                                TC TGCAGGT    AGAATG
                                || |||||||    ||||||
                                AG ACGTCCG    TCTTAC
                                  _     ______
GAM1663 LOC157507 5' ATCGTGCAGCTTGGATAAA   40736         G  AA
                                ATCGTGCAG TT  ATAGA
                                ||||||||| ||  |||||
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                                TAGCACGTC AA  TATTT
                                     G  CC
GAM1664  ABCD1    5'  GGGCAGAGGGGGGCGTCTCTTC  40739        AAAATT   GG
                                GGGCAGAGG     TGT  CTTC
                                |||||||||     |||  ||||
                                CCCGTCTCC     GCA  GAAG
                                     CCC___   GA
GAM1664  CAPN1    3'  GGACAGAGGGGGGCGTTGGCTTC 40740        AAAATTTG
                                GGGCAGAGG       TGGCTTC
                                |||||||||       |||||||
                                CCTGTCTCC       ACCGAAG
                                     CCCGCA__
GAM1664  DAAM2    3'  GGACAGAGGCTGCTGTGGCTTC 40741        AAAAT
                                GGGCAGAGG    TTGTGGCTTC
                                |||||||||    ||||||||||
                                CCTGTCTCC    GACACCGAAG
                                     GAC__
GAM1664  DLEC1    3'  GGATGGAGTTTGTGGCTT    40742     CA   GAAAA
                                GGG  GAG    TTTGTGGCTT
                                |||  |||    ||||||||||
                                CCT  CTC    AAACACCGAA
                                  AC  _____
GAM1664  DLEC1    3'  GGATGGAGTTTGTGGCTT    40742     CA   GAAAA
                                GGG  GAG    TTTGTGGCTT
                                |||  |||    ||||||||||
                                CCT  CTC    AAACACCGAA
                                  AC  _____
GAM1664  EIF2C1   3'  GGGCAGGGGGGGATGCTTGCTTC 40743       A  AAAATT   G_
                                GGGCAG GG     TGT  GCTTC
                                |||||| ||     |||  |||||
                                CCCGTC CC     ACG  CGAAG
                                   _  CCCT__   AA
GAM1664  IGF2     5'  GGGCAGAGCGGGGGGGATGGCTT 40744        GAAAATTT
                                GGGCAGAG       GTGGCTT
                                ||||||||       |||||||
                                CCCGTCTC       TACCGAA
                                     GCCCCCC_
GAM1664  INPP5D   3'  GGGAGAGGGTCCAGTGGCTTC  40745     C    AAAATTT
                                GGG AGAGG      GTGGCTTC
                                ||| |||||      ||||||||
                                CCC TCTCC      CACCGAAG
                                  _    CAGGT__
GAM1664  KIF5C    3'  GGCCAGAGGAGGGTGACTTC   40746    G     AAATTT
                                GG CAGAGGA     GTGGCTTC
                                || |||||||     ||||||||
                                CC GTCTCCT     CACTGAAG
                                  G      CC____
GAM1664  ODF2     3'  GGGAGAGGAAAACCACCAGGCT 40747     C        TGT_
              TC                  GGG AGAGGAAAATT    GGCTTC
                                ||| ||||||||||    ||||||
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                                CCC TCTCCTTTTGG   CCGAAG
                                  _         TGGT
GAM1664  SHC1     5'  GGGAGAGGGACAAGTGGCTTC  40748     C     AAA  TT
                                GGG AGAGG   AT  GTGGCTTC
                                ||| |||||   ||  ||||||||
                                CCC TCTCC   TG  CACCGAAG
                                  _    C__  TT
GAM1664  STIM1    3'  GGGCAGAGGAAAAATACCTT   40749           TTT   G
                                GGGCAGAGGAAAA   GTG CTT
                                ||||||||||||   ||| |||
                                CCCGTCTCCTTTT   TAT GAA
                                       ___   G
GAM1664  BFAR     5'  GAGCAGAGGAAGAGGGAGAGGC 40750          AATTTGT_
            TTC                   GGGCAGAGGAA       GGCTTC
                                ||||||||||       ||||||
                                CTCGTCTCCTT       CCGAAG
                                      CTCCCTCT
GAM1664  C20orf139 3'  GGGAAGAGGGAAATACCT    40751     C     A    TTGTG
                                GGG AGAGG AAAT    GCTT
                                ||| ||||| ||||    ||||
                                CCC TCTCC TTTA     TGGA
                                  T    C   _____
GAM1664  C20orf178 3'  GGGCAAGGAAAAGCCTATGGCT 40752       G      _
            T                    GGGCA AGGAAAA TTTGTGGCTT
                                ||||| ||||||| ||||||||||
                                CCCGT TCCTTTT GGATACCGAA
                                   _      C
GAM1664  FLJ13725  5'  GAGTAGAGGGAGAAAGATGGTT 40753     C     AAAATTT    C
            TC                    GGG AGAGG      GTGG TTC
                                ||| |||||      |||| |||
                                CTC TCTCC      TACC AAG
                                  A    CTCTTTC    A
GAM1664  FLJ14564  3'  GGGCAGAGGCAGGTGTGAC   40754         AAAATT
                                GGGCAGAGG     TGTGGC
                                |||||||||     ||||||
                                CCCGTCTCC     ACACTG
                                      GTCC__
GAM1664  FLJ20694  3'  GGGCAGAGGAGGTGAAGAGCTT 40755          AAATTTGT
                                GGGCAGAGGA       GGCTT
                                ||||||||||       |||||
                                CCCGTCTCCT       TCGAA
                                      CCACTTC_
GAM1664  FLJ23186  3'  GGGGGGAGGAGGATGACTT   40756     CA    AAATTT
                                GGG  GAGGA     GTGGCTT
                                |||  |||||     |||||||
                                CCC  CTCCT     TACTGAA
                                  CC    CC____
GAM1664  GKAP42    5'  GGGCAGAGAAGCGGCT      40757          AAATTT
                                GGGCAGAGGA     GTGGCT
                                ||||||||||     ||||||
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                                CCCGTCTCTT     CGCCGA
                                       ______
GAM1664  HIF1AN   3'  GGCAGAGGAGCTGGCTT     40758         AAATTTG
                                GGCAGAGGA      TGGCTT
                                |||||||||      ||||||
                                CCGTCTCCT      ACCGAA
                                     CG_____
GAM1664  KIAA1202 3'  GGGTAGAAGCTTGTGGCTT   40759     C    AAAA
                                GGG AGAGG    TTTGTGGCTT
                                ||| |||||    ||||||||||
                                CCC TCTTC    GAACACCGAA
                                  A    ____
GAM1664  PAK6     3'  GGGCAGAGGGTGGGGCTGGGGC 40760         AAAAT_  T
            TTC                   GGGCAGAGG     TTG GGCTTC
                                |||||||||      ||| ||||||
                                CCCGTCTCC      GAC CCGAAG
                                     CACCCC   C
GAM1664  PFDN1    3'  GGGCAGAGGAGAAGCTGT    40761          A  T
                                GGGCAGAGGA AA TTGT
                                |||||||||| || ||||
                                CCCGTCTCCT TT GACA
                                     C  C
GAM1664  RAB40C   3'  GGGTGGAGGAGCGGCCAATGGC 40762     CA    AAATTT_
            TTC                   GGG  GAGGA      GTGGCTTC
                                |||  |||||      ||||||||
                                CCC  CTCCT      TACCGAAG
                                  AC    CGCCGGT
GAM1664  SRPUL    5'  GGGCAAAGGAAAGTGACTT   40763          ATTT
                                GGGCAGAGGAAA   GTGGCTT
                                ||||||||||||   |||||||
                                CCCGTTTCCTTT   CACTGAA
                                       _____
GAM1664  TSPEAR   3'  GGGCAAAGGGAAAGGCAGCTTC 40764         A   TTT TG
                                GGGCAGAGG AAA   G  GCTTC
                                ||||||||| |||   |  |||||
                                CCCGTTTCC TTT   C  CGAAG
                                     C   C__ GT
GAM1664  LOC145098 5'  GGGAGAGGGGGATGAACTT   40765     C    AAAATT  T
                                GGG AGAGG      TG GGCTT
                                ||| |||||      || |||||
                                CCC TCTCC      AC TTGAA
                                  _     CCCT__  _
GAM1664  LOC145693 5'  GAGCAGAGGAGGGTGATTT   40766         AAATTT   GC
                                GGGCAGAGGA     GTG  TT
                                ||||||||||     |||  ||
                                CTCGTCTCCT     CAC  AA
                                     CC_____   TA
GAM1664  LOC147958 5'  GGAGAGAGGCTGGCGGCTTC  40767     C    AAAATTT
                                GGG AGAGG      GTGGCTTC
                                ||| |||||      ||||||||
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                                CCT TCTCC      CGCCGAAG
                                  C    GAC____
GAM1664  LOC150378 5'  AGGTAGGGGAAATGGCTT    40768     C  A    AATTT
                                GGG AG GGAA    GTGGCTT
                                ||| || ||||    |||||||
                                TCC TC CCTT    TACCGAA
                                  A  C   _____
GAM1664  LOC152426 3'  GGGAAGAGGAAAGTGGGAGAGG 40769     C       ATTTGT__
           CTT                   GGG AGAGGAAA       GGCTT
                                ||| ||||||||       |||||
                                CCC TCTCCTTT       CCGAA
                                  T       CACCCTCT
GAM1664  LOC152793 3'  GGGCAGGAGAAAATCATCCCTT 40770       AG      TGTGG
           C                     GGGCAG  GAAAATT    CTTC
                                ||||||  |||||||    ||||
                                CCCGTC  CTTTTAG    GAAG
                                   CT      TAGG_
GAM1664  LOC170221 3'  GGGTGTAGGACCTGTGGCTTC  40771     CAG    AAA
                                GGG   AGGA   TTTGTGGCTTC
                                |||   ||||   ||||||||||
                                CCC   TCCT   GGACACCGAAG
                                  ACA   ___
GAM1664  LOC201382 5'  GGGCGAGGAGAATTTGCAA    40772      A    A     TG
                                GGGC GAGGA AATTTG  G
                                |||| ||||| ||||||  |
                                CCCG CTCCT TTAAAC  T
                                  _    C     GT
GAM1664  LOC220965 3'  GGCAGAGGAAAATAAACTT    40773           TTGT
                                GGCAGAGGAAAAT    GGCTT
                                ||||||||||||    |||||
                                CCGTCTCCTTTTA    TTGAA
                                        T___
GAM1664  LOC255308 3'  GGGAGAGGGAGATAACTT     40774     C    AAAATTT
                                GGG AGAGG      GTGGCTT
                                ||| |||||      |||||||
                                CCC TCTCC      TATTGAA
                                  _    CTC_____
GAM1664  LOC256094 3'  GGGCAGAGAGGAGAAAGAGGCT 40775         AAAATTTGT
           TC                    GGGCAGAGG        GGCTTC
                                |||||||||        ||||||
                                CCCGTCTCT        CCGAAG
                                     CCTCTTTCT
GAM1664  LOC91689  3'  GGGCAAAGGAAGATTATACTT  40776          A   TGTG
                                GGGCAGAGGAA ATT    GCTT
                                |||||||||| |||    ||||
                                CCCGTTTCCTT TAA    TGAA
                                       C   TA__
GAM1664  LOC92340  3'  GGGCAGAGGCGGGCTGACGTGG 40777         AAAATT__
           CTTC                    GGGCAGAGG       TGTGGCTTC
                                |||||||||       |||||||||
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                                CCCGTCTCC       GCACCGAAG
                                     GCCCGACT
GAM1665 ABCD1    3' GGGAGCCGGGGCCCCAC     40780       T      GTGG
                                GGGAGC CGGGGCC    CCAC
                                |||||| |||||||    ||||
                                CCCTCG GCCCCGG    GGTG
                                  _     _____
GAM1665 ABP1     3' GGAGTTCCCAGGTGTGGC    40781      __     GCC
                                GGAG  CTCGGG   GTGGC
                                ||||  ||||||   |||||
                                CCTC  GGGTCC   CACCG
                                  AA     A__
GAM1665 ADAM23   5' CGGGGCTCGGGGCTGGGC    25638      A       CGT
                                CGGG GCTCGGGGC   GGC
                                |||| |||||||||   |||
                                GCCC CGAGCCCCG   CCG
                                  _       AC_
GAM1665 ADRA2A   5' GAGCTCGGGGGTCCTATG    40782          __ _
                                GAGCTCGGGG  CC GTG
                                ||||||||||  || |||
                                CTCGAGCCCC  GG TAC
                                     CA  A
GAM1665 AF1Q     5' CGGGAGCTCCGGGGTCTGCG   40783         _   CC_
                                CGGGAGCTC GGGG   GTG
                                |||||||| ||||   |||
                                GCCCTCGAG CCCC   CGC
                                     G    AGA
GAM1665 BCL10    5' CGGGAGCTCGGGCTGCG     40784          G C
                                CGGGAGCTCGGG C GTG
                                |||||||||||| | |||
                                GCCCTCGAGCCC G CGC
                                      _ A
GAM1665 CACNA1C  3' CGGGAGCTCGGCGTGGCC    40785          GGC
                                CGGGAGCTCGG   CGTGGCC
                                ||||||||||   |||||||
                                GCCCTCGAGCC   GCACCGG
                                     ___
GAM1665 DDX11    3' CAGGAGCCTGTGGCCATG    40787        CGG
                                CGGGAGCT   GGCCGTG
                                ||||||||   |||||||
                                GTCCTCGG   CCGGTAC
                                    ACA
GAM1665 DDX11    3' CAGGAGCCCTGTGGCCATG   40786         GG_
                                CGGGAGCTC   GGCCGTG
                                |||||||||   |||||||
                                GTCCTCGGG   CCGGTAC
                                     ACA
GAM1665 EDN3     5' GGGGGTTCGAGGCCGGCC    40788     AGC       GT
                                GGG   TCGGGGCC  GGCC
                                |||   ||||||||  ||||
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                                CCC  AGCTCCGG  CCGG
                                  CCA      __
GAM1665 EPB49    3' GGAAGCTCGGGGTTTGCG    40789          CC_
                                GGGAGCTCGGGG  GTG
                                ||||||||||||  |||
                                CCTTCGAGCCCC  CGC
                                      AAA
GAM1665 HRB     5' CGGGAGCCGGGCAGCGCTGC  40790       T   GC_  G
                                CGGGAGC CGGG  CGT GC
                                ||||||| ||||  ||| ||
                                GCCCTCG GCCC  GCG CG
                                   _  GTC  A
GAM1665 IRS2    5' CGGGCGCTCGGGGTCCGCG   40791     A      _
                                CGGG GCTCGGGG CCGTG
                                |||| |||||||| |||||
                                GCCC CGAGCCCC GGCGC
                                  G       A
GAM1665 ITGA4   5' CGGGAGCTTCGGGTGCTCGCG 40792        _   _ _
                                CGGGAGCT CGGG GC CGTG
                                |||||||| |||| || ||||
                                GCCCTCGA GCCC CG GCGC
                                    A   A A
GAM1665 KCNJ10  5' CGGGGGCCGGGGCCGGGG   40793     A T      T
                                CGGG GC CGGGGCCG GG
                                |||| || |||||||| ||
                                GCCC CG GCCCCGGC CC
                                  C _      C
GAM1665 LHX5    5' GGGCGCACCGTGGCCA     40794     A TCGGG
                                GGG GC    GCCGTGGCCA
                                ||| ||    ||||||||||
                                CCC CG    TGGCACCGGT
                                  G _____
GAM1665 MBTPS1  5' CGGGAGCTCAGGGCCGGC   40795           GT
                                CGGGAGCTCGGGGCC  GGC
                                ||||||||||||||  |||
                                GCCCTCGAGTCCCGG  CCG
                                                __
GAM1665 MECP2   3' CGGGAGCTGGGGGTTGTG   40796       C   CC
                                CGGGAGCT GGGG  GTG
                                |||||||| ||||  |||
                                GCCCTCGA CCCC  CAC
                                    C   AA
GAM1665 MMP15   3' GGGAGCTGGGGGCTGCTGCGTG 40797     C   _________  GGCC
           GCCAC                AGCT GGGGC      CGT   AC
                                ||||  |||||      |||   ||
                                TCGA CCCCG       GCA   TG
                                  C    ACGACIII  CCGG
GAM1665 NR2C2   5' CGGGAGCCGGGGGCCGCG   40798       C
                                CGGGAGCT GGGGCCGTG
                                |||||||| |||||||||
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                                GCCCTCGG CCCCGGCGC
                                    C
GAM1665  PABPC4   5'  CGGGGCTCGGGGCCCGAGC   40799     A       GT
                                CGGG GCTCGGGGCC  GGC
                                |||| ||||||||||  |||
                                GCCC CGAGCCCCGG  TCG
                                  _       GC
GAM1665  PAX2     5'  CGGGGCTCGGGGCTGGGC    25638     A       CGT
                                CGGG GCTCGGGGC   GGC
                                |||| |||||||||   |||
                                GCCC CGAGCCCCG   CCG
                                  _       AC_
GAM1665  PAX2     5'  CGGGGCTCGGGGCTGGGC    25638     A       CGT
                                CGGG GCTCGGGGC   GGC
                                |||| |||||||||   |||
                                GCCC CGAGCCCCG   CCG
                                  _       AC_
GAM1665  PTPRO    5'  CGGGGACTCGGGGGCACGGCTG 40800     AG     C     CA
             CG                   CGGG  CTCGGGG CGTGGC  CG
                                |||| |||||||| ||||||  ||
                                GCCC  GAGCCCC GTGCCG  GC
                                  CT      C     AC
GAM1665  PTPRO    5'  CGGGGACTCGGGGGCACGGCTG 40800     AG     C     CA
             CG                   CGGG  CTCGGGG CGTGGC  CG
                                |||| |||||||| ||||||  ||
                                GCCC  GAGCCCC GTGCCG  GC
                                  CT      C     AC
GAM1665  RYR2     5'  CGGGGGCTGGAGGGGGCCGCG  40801     A  C___
                                CGGG GCT   GGGGCCGTG
                                |||| |||   |||||||||
                                GCCC CGA   CCCCGGCGC
                                  C  CCTC
GAM1665  SBF1     3'  GGGGGCTCGGGGCCTCAATAC  40802     A       GTG__
                                GGG GCTCGGGGCC    GC
                                ||| ||||||||||    ||
                                CCC CGAGCCCCGG    TG
                                  C        AGTTA
GAM1665  SCRT1    5'  CGGGGCTTGGGGGGGCTGCG   40803     A  C___    C
                                CGGG GCT   GGGGC GTG
                                |||| |||   ||||| |||
                                GCCC CGA   CCCCG CGC
                                  _  ACCC    A
GAM1665  SOX11    3'  CGGGAGCCCGGGGCGCGCG   40804          _
                                CGGGAGCTCGGGGC CGTG
                                |||||||||||||| ||||
                                GCCCTCGGGCCCCG GCGC
                                          C
GAM1665  TLE1     5'  CGGGCGCTCGGGGACTGTG   40805     A      _ C
                                CGGG GCTCGGGG C GTG
                                |||| |||||||| | |||
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                                GCCC CGAGCCCC G CAC
                                  G       T A
GAM1665 BAD     3' CGGGGGCTCGGGTCCCGG    40806     A      G  G
                                CGGG GCTCGGG CC TGG
                                |||| ||||||| || |||
                                GCCC CGAGCCC GG GCC
                                  C      A  _
GAM1665 BAD     3' CGGGGGCTCGGGTCCCGG    40806     A      G  G
                                CGGG GCTCGGG CC TGG
                                |||| ||||||| || |||
                                GCCC CGAGCCC GG GCC
                                  C      A  _
GAM1665 DDX12    3' CAGGAGCCCTGTGGCCAC    40807         GGGGCC
                                CGGGAGCTC     GTGGCCAC
                                |||||||||     ||||||||
                                GTCCTCGGG     CACCGGTG
                                     A_____
GAM1665 DKFZP434C131 3' CGGGGGCTCCGCTTGGCCATG  40808      A    GG___
                                CGGG GCTC     GGCCGTG
                                |||| ||||     |||||||
                                GCCC CGAG     CCGGTAC
                                  C    GCGAA
GAM1665 FLJ10490  5' CGGGAGCCGGGGTCGCG     40809        T     C
                                CGGGAGC CGGGG CGTG
                                ||||||| ||||| ||||
                                GCCCTCG GCCCC GCGC
                                     _     A
GAM1665 FLJ14106  5' CGGGAGCTGGGGCCCCAC     40810         C      GTGG
                                CGGGAGCT GGGGCC    CCAC
                                |||||||| ||||||    ||||
                                GCCCTCGA CCCCGG    GGTG
                                     _     _____
GAM1665 FLJ21438  5' CGGGAGTCCGGAGGCGGTTACG 40811        CT     CC    CC
                                CGGGAG  CGGGG  GTGG  ACG
                                ||||||  |||||  ||||  |||
                                GCCCTC  GCCTC  CGCC  TGC
                                   AG     __    AA
GAM1665 FLJ21988  3' GGGGTCTTGGGGCATGTGCGTG 40812   AG  C    _________  GGCC
             GCCAC                    CT GGGGC       CGT    AC
                                 || |||||       |||    ||
                                 GA CCCCG       GCA    TG
                                CA  A    TACACIII   CCGG
GAM1665 FLJ22635  3' CAGGAGCTCGGGGTGGGGTCGT 40813           C_____
             G                    CGGGAGCTCGGGG     CGTG
                                  ||||||||||||||     ||||
                                  GTCCTCGAGCCCC     GCAC
                                        ACCCCA
GAM1665 FLJ22693  5' GGAGCGCGGGCTGTGGC     40814       T    G C
                                GGAGC CGGG C GTGGC
                                ||||| |||| | |||||
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                                CCTCG GCCC G CACCG
                                  C   _ A
GAM1665 GLIS2    3' CGGGGGCTGGGAGGCCAGCCA 40815     A  C _   GT
                                CGGG GCT GG GGCC  GGCCA
                                |||| ||| || ||||  |||||
                                GCCC CGA CC CCGG  TCGGT
                                  C  C T   __
GAM1665 HCA112   3' GGAGCAGGGCTGTGGCCACG  40816     TC    C
                                GGAGC  GGGGC GTGGCCACG
                                |||||  ||||| |||||||||
                                CCTCG  TCCCG CACCGGTGC
                                  __    A
GAM1665 KIAA0705 3' CGGGCGGGTTGGCCGTGGCCGC 40817     AGCT  ___       A
            G                    CGGG   CGGG   GCCGTGGCC CG
                                ||||   ||||  ||||||||| ||
                                GCCC   GCCC   CGGCACCGG GC
                                  ____   AAC       C
GAM1665 KIAA1297 3' GGGGGCTCAGGGGCTGGTGCGT 40818     _   _________  GGCC
            GGCCAC                GCTC GGGGC       CGT   AC
                                |||| |||||       |||   ||
                                CGAG CCCCG       GCA   TG
                                  T    ACCACIII  CCGG
GAM1665 MGC15875 5' GGGAGCTCAGGTGGCCGTG   40819        _ _
                                GGGAGCTC GG GGCCGTG
                                |||||||| || |||||||
                                CCCTCGAG CC CCGGCAC
                                     T A
GAM1665 MGC26744 5' GGGGCTCGGAGGGTCGC    40820    A      CC  G
                                GGG GCTCGGGG  GT GC
                                ||| ||||||||  || ||
                                CCC CGAGCCTC  CA CG
                                  _      C_  G
GAM1665 N4BP3    3' CGGGACCTTGGGGCTGGTGCGT 40821   G  C   _________  GGCC
            GGCCAC                A CT GGGGC       CGT   AC
                                | || |||||       |||   ||
                                T GA CCCCG       GCA   TG
                                 G  A    ACCACIII  CCGG
GAM1665 OSR2     5' GGGTGCTTGGGGCCGGC    40822    A  C    GT
                                GGG GCT GGGGCC  GGC
                                ||| ||| ||||||  |||
                                CCC CGA CCCCGG  CCG
                                  A  A    __
GAM1665 PPP1R1A  5' CGGGACTCGGGGCTGGGGC   40823      G      CGT
                                CGGGA CTCGGGGC   GGC
                                ||||| ||||||||   |||
                                GCCCT GAGCCCCG   CCG
                                  _      ACC
GAM1665 PPP1R1B  5' CGGGACTCGGGGCTCGCCCCCC 40824      G      _  GG  A
            G                    CGGGA CTCGGGGC CGT  CC CG
                                ||||| |||||||| |||  || ||
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                                GCCCT GAGCCCCG GCG  GG GC
                                  _       A   GG  _
GAM1665  PTPRT    5'  CGGGGGCCGGGGCCGGGAC   40825      A  T       T
                                CGGG GC CGGGGCCG GGC
                                |||| || |||||||| |||
                                GCCC CG GCCCCGGC CTG
                                  C  _       C
GAM1665  RAB9A    5'  CGGGAGCTCTGGGCCGGCCCG  40826          G    GT    A
                                CGGGAGCTC GGGCC  GGCC CG
                                ||||||||| |||||  |||| ||
                                GCCCTCGAG CCCGG  CCGG GC
                                     A    __   _
GAM1665  TNRC9    5'  AGGAGCTCGGGAGCCGCG    40827           _
                                GGGAGCTCGGG GCCGTG
                                |||||||||| ||||||
                                TCCTCGAGCCC CGGCGC
                                      T
GAM1665  LOC124460 5'  CGGGAGGTCGGGGCCAGTG   40828       C       _
                                CGGGAG TCGGGGCC GTG
                                |||||| |||||||| |||
                                GCCCTC AGCCCCGG CAC
                                   C       T
GAM1665  LOC144373 3'  CAGGAGCCCTGTGGCCATG   40786         GG_
                                CGGGAGCTC   GGCCGTG
                                |||||||||   |||||||
                                GTCCTCGGG   CCGGTAC
                                     ACA
GAM1665  LOC148479 5'  GGGGGCTCGGGCGGCTGCG   40829     A      __ C
                                GGG GCTCGGG  GC GTG
                                ||| |||||||  || |||
                                CCC CGAGCCC  CG CGC
                                  C      GC  A
GAM1665  LOC152274 3'  GGGGGCTCAGGGCTGGTGCGTG 40830   A       _________  GGCC
            GCCAC                  GCTCGGGGC       CGT    AC
                                 |||||||||       |||    ||
                                 CGAGTCCCG       GCA    TG
                                C        ACCACIII   CCGG
GAM1665  LOC155066 3'  GGGAGCTCGGGTAAGCGTG   40831          GC__
                                GGGAGCTCGGG    CGTG
                                ||||||||||    ||||
                                CCCTCGAGCCC    GCAC
                                      ATTC
GAM1665  LOC207089 3'  CGGGAGCCTGGTGGCGGCCA  40832        TC  _  CGT
                                CGGGAGC  GG GGC   GGCCA
                                |||||||  || |||   |||||
                                GCCCTCG  CC CCG   CCGGT
                                   GA  A  ____
GAM1665  LOC221929 5'  CGGGGCTCGGGGCAGCAC    40833      A       CGT   C
                                CGGG GCTCGGGGC   GGC AC
                                |||| |||||||||   ||| ||
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                                GCCC CGAGCCCCG   TCG TG
                                  _      ___  _
GAM1665 LOC51112  5'  GGGACTCGGGGTGCCCGCG   40834     G     ___
                                GGGA CTCGGGG   CCGTG
                                |||| |||||||   |||||
                                CCCT GAGCCCC   GGCGC
                                  _      ACG
GAM1666 DKFZp434D177 3'  TGCTACATAGTCGTGTGA    40837         A  CAGCTA
                                TGCTACATA TC     GTGA
                                ||||||||| ||     ||||
                                ACGATGTAT AG     CACT
                                     C  CA____
GAM1666 FLJ20300  5'  TGCACATAGCTAGTGA     40838     T    AATCC
                                TGC ACAT    AGCTAGTGA
                                ||| ||||    |||||||||
                                ACG TGTA    TCGATCACT
                                  _   _____
GAM1666 FLJ22029  3'  TTGCTAGTGAGCTAGTGA    40839       CATAATCC
                                TTGCTA       AGCTAGTGA
                                ||||||       |||||||||
                                AACGAT       TCGATCACT
                                   CAC_____
GAM1666 KIAA0483  3'  GCTACATAATTTAGTAA     40840         CCAGC
                                GCTACATAAT    TAGTGA
                                ||||||||||    ||||||
                                CGATGTATTA    ATCATT
                                     A____
GAM1666 SDF1      3'  TTGCTACATAATCAAATGGTGA 40841           CAGCTA
              A                  TTGCTACATAATC     GTGAA
                                 ||||||||||||     |||||
                                 AACGATGTATTAG     CACTT
                                       TTTAC_
GAM1666 LOC144871 5'  TTGCTGACATAGCCAGTAGTGA 40842      _    AT    C
                                TTGCT ACATA  CCAG TAGTGA
                                ||||| |||||  |||| ||||||
                                AACGA TGTAT  GGTC ATCACT
                                   C    C_   _
GAM1666 LOC149332 3'  TACATAATTTCTCTAGTGA   40843        CCAG
                                TACATAAT   CTAGTGA
                                ||||||||   |||||||
                                ATGTATTA   GATCACT
                                     AAGA
GAM1666 LOC51064  3'  TTGCCACATGGCTAATG     40844         AATCCA
                                TTGCTACAT     GCTAGTG
                                |||||||||     |||||||
                                AACGGTGTA     CGATTAC
                                     C_____
GAM1667 BRCA1     3'  TGACATTGAATGTTCCTCAAA  40847          A    G
                                TGACATTGAGT TTTCT GAA
                                |||||||||| ||||| |||
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                                ACTGTAACTTA AAGGA TTT
                                      C     G
GAM1667  DDC      3'  TGAACATTGATTGCCCTGGAAA 40848    T       GTAT
                A                  A GACATTGA    TTCTGGAAAA
                                   | ||||||||    ||||||||||
                                   A TTGTAACT    GGGACCTTTT
                                    C       AAC_
GAM1667  ECM2     3'  ATGATACTGAGTATAACAGGA  40849      C        TTCT
                                   ATGA ATTGAGTAT    GGA
                                   |||| |||||||||    |||
                                   TACT TGACTCATA    CCT
                                     A        TTGT
GAM1667  ITGAM    3'  TGACTTGAATATCTGGAAA    40850      A      TT
                                   TGAC TTGAGTA  TCTGGAAA
                                   |||| |||||||  ||||||||
                                   ACTG AACTTAT  AGACCTTT

                                     _      __
GAM1667  MFAP3    3'  ATGACATTGGTGTGGAA     40851          A  ATTTC
                                   ATGACATTG GT     TGGAA
                                   |||||||||  ||     |||||
                                   TACTGTAAC CA     ACCTT
                                        _ C_____
GAM1667  NSF      3'  ATGATTGATTTTTCTGGA    40852      CA    GTA
                                   ATGA  TTGA   TTTCTGGA
                                   ||||  ||||   ||||||||
                                   TACT  AACT   AAAGACCT
                                     __    AA_
GAM1667  PCM1     3'  ATGCATTGAGTATGTAAGG    40853     A        TTCT
                                   ATG CATTGAGTAT    GG
                                   ||| ||||||||||    ||
                                   TAC GTAACTCATA    CC
                                     _         CATT
GAM1667  PTGS2    3'  TGACAATGAGATGTGGAAAA   40854      T    TATTTC
                                   TGACA TGAG      TGGAAAA
                                   ||||| ||||      |||||||
                                   ACTGT ACTC      ACCTTTT
                                      T    TAC___
GAM1667  SLC2A5   3'  GACAGGTATTTCTGGAAA    40855      TTGA
                                   GACA    GTATTTCTGGAAA
                                   ||||    ||||||||||||||
                                   CTGT    CATAAAGACCTTT
                                     C___
GAM1667  STAR     3'  GACTATATTTCTGGAA      40856     ATTGA
                                   GAC     GTATTTCTGGAA
                                   |||     |||||||||||||
                                   CTG     TATAAAGACCTT
                                     A_____
GAM1667  ABCA8    3'  ATGACATTTAGTATTTTTAG   40857         G      C
                                   ATGACATT AGTATTT TGG
                                   |||||||| ||||||| |||
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                                TACTGTAA TCATAAA ATC
                                    A      A
GAM1667 AFAP     3' TGAAGTTGAGATTTTCTGGAA 40858     CA    TA
                                TGA TTGAG TTTCTGGAA
                                ||| ||||| |||||||||
                                ACT AACTC AAAGACCTT
                                  TC    TA
GAM1667 AP3M1    3' ATGACAATAGTTTCTGGAA   40859       TTG   AT
                                ATGACA   AGT  TTCTGGAA
                                ||||||   |||  ||||||||
                                TACTGT   TCA  AAGACCTT
                                   TA_   __
GAM1667 ARHGEF3  3' ATGAAATTGGCCTCTGGA    40860      C    A  AT
                                ATGA ATTG GT  TTCTGGA
                                |||| |||| ||  |||||||
                                TACT TAAC CG  GAGACCT
                                  T   _ __
GAM1667 BRAG     3' ATGGCATTGAGTGGCACAGAA 40861     A       ATTTCT
                                ATG CATTGAGT     GGAA
                                ||| ||||||||     ||||
                                TAC GTAACTCA     TCTT
                                  C       CCGTG_
GAM1667 DKFZP564O043 3' ACAAATCAGTTTCTGGAAA   40862     TTG_   AT
                                ACA    AGT  TTCTGGAAA
                                |||    |||  |||||||||
                                TGT    TCA  AAGACCTTT
                                  TTAG   __
GAM1667 FBP17    3' ATGAAACCAATATTTCTGGAAA 40863      C  TG G
            A                    ATGA AT  A TATTTCTGGAAAA
                                |||| ||  | ||||||||||||
                                TACT TG  T ATAAAGACCTTTT
                                  T  GT _
GAM1667 FLJ10971 3' ATAACGGACTATTTCTGGA   40864       ATT  G
                                ATGAC   GA TATTTCTGGA
                                |||||   || ||||||||||
                                TATTG   CT ATAAAGACCT
                                   C__  G
GAM1667 FLJ23499 3' ATGGCATTGAATAGGAGTGAAA 40865     A       TTTC
            A                    ATG CATTGAGTA    TGGAAA
                                ||| |||||||||    ||||||
                                TAC GTAACTTAT    ACTTTT
                                  C        CCTC
GAM1667 HBOA     3' TGACACTGAAACTGGA      40866          TATTT
                                TGACATTGAG     CTGGA
                                ||||||||||     |||||
                                ACTGTGACTT     GACCT
                                      T_____
GAM1667 HPA2     3' ATGACATTTAGTCTCTTTGGA  40867        G   A   C
                                ATGACATT AGT TTT TGGA
                                |||||||| ||| ||| ||||
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                                TACTGTAA TCA AGA ACCT
                                    A   G   A
GAM1667 HRLP5    3' ATTGGATGTATTTCTGGAA   40868     A__
                                ATTG   GTATTTCTGGAA
                                ||||   ||||||||||||
                                TAAC   CATAAAGACCTT
                                  CTA
GAM1667 KIAA0033 3' ATGATGATGAATCTGGAAA   40869     CAT   GTATT
                                ATGA   TGA    TCTGGAAA
                                ||||   |||    ||||||||
                                TACT   ACT    AGACCTTT
                                  ___   ACTT_
GAM1667 KIAA0316 3' TGCATTGAGCTTTGGGAAA   40870    A      A  TCT
                                TG CATTGAGT TT   GGAAA
                                || ||||||| ||   |||||
                                AC GTAACTCG AA   CCTTT
                                 _      A  C__
GAM1667 KIAA1026 3' TGACATTAACTGAGTTTTGGAA 40871       ____    ATTTC
             AA                   TGACAT    TGAGT    TGGAAAA
                                ||||||   |||||    |||||||
                                ACTGTA    ACTCA    ACCTTTT
                                   ATTG    AA___
GAM1667 KIAA1102 3' TGACATTGACTCTTTGGAA   40872        GTA   C
                                TGACATTGA   TTT TGGAA
                                |||||||||   ||| |||||
                                ACTGTAACT   AGA ACCTT
                                     G__   A
GAM1667 KIAA1755 3' GACATTGAGTTCAGGGA     40873         ATT  T_
                                GACATTGAGT   TC  GGA
                                ||||||||||   ||  |||
                                CTGTAACTCA   AG  CCT
                                      ___  TC
GAM1667 KIAA1906 3' ATTGACTAGCTGGAAAA     40874      G  TTT
                                ATTGA TA   CTGGAAAA
                                ||||| ||   ||||||||
                                TAACT AT   GACCTTTT
                                   G  C__
GAM1667 MGC22014 3' TGGCATCGAGTGAGCAAAGAAA 40875    A      ATTTCT
                                TG CATTGAGT     GGAAA
                                || ||||||||     |||||
                                AC GTAGCTCA     TCTTT
                                 C       CTCGTT
GAM1667 NAPG     3' ATGACAGTGGAGTTCTGGAA   40876      TT_   ATT
                                ATGACA   GAGT   TCTGGAA
                                ||||||   ||||   |||||||
                                TACTGT   CTCA   AGACCTT
                                   CAC   ___
GAM1667 PARVA    3' ATGGCCTTGAGTATATCAGA   40877     ACA      T  T
                                ATG   TTGAGTAT TC GGA
                                |||   |||||||| || |||
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                                TAC   AACTCATA AG TCT
                                  CGG       T _
GAM1667  SLC2A10   3'  ATGTCATTGAGTGGGGAA    40878     A       ATTTCT
                                ATG CATTGAGT     GGAA
                                ||| ||||||||     ||||
                                TAC GTAACTCA     CCTT
                                  A       CC____
GAM1667  SLC5A7    3'  TGCAGAAGTATTTTTGGAAAA  40879    A  TT       C
                                TG CA  GAGTATTT TGGAAAA
                                || ||  |||||||| |||||||
                                AC GT  TTCATAAA ACCTTTT
                                 _ C_       A
GAM1667  LOC120105 5'  ATGAATCTGTAAATTTCTGG   40880      CA   AGT
                                ATGA  TTG   ATTTCTGG
                                ||||  |||   ||||||||
                                TACT  GAC   TAAAGACC
                                  TA   ATT
GAM1667  LOC143286 3'  TGATGTCTCCTGTTTCTGGAAA 40881     CA  GAGTA
              A                  TGA  TT    TTTCTGGAAAA
                                ||| ||    ||||||||||
                                ACT  AG    AAAGACCTTTT
                                  AC  AGGAC
GAM1667  LOC146506 3'  ATCACATGGAGTATTTCTGGAA 40882    G    T
                                AT ACAT GAGTATTTCTGGAA
                                || |||| ||||||||||||||
                                TA TGTA CTCATAAAGACCTT
                                 G    C
GAM1667  LOC150311 5'  TGACATGAGGAATTCTGGAAAA 40883       T   TAT
                                TGACAT GAG   TTCTGGAAAA
                                |||||| |||   ||||||||||
                                ACTGTA CTC   AAGACCTTTT
                                   _   CTT
GAM1667  LOC197358 3'  ATGACATTGATGTTTTTGATGA 40884          _  A   CTG
                                ATGACATTGA GT TTT   GA
                                |||||||||| || |||   ||
                                TACTGTAACT CA AAA   CT
                                      A  A   CTA
GAM1667  LOC201695 5'  ATGATAGGTAATTTCTGGAA   40885     CAT  A   _
                                ATGA   TG GTA TTTCTGGAA
                                ||||   || ||| |||||||||
                                TACT   AT CAT AAAGACCTT
                                  ___  C   T
GAM1667  LOC203113 3'  ATGGCATTAAGTAAAGGAAAA  40886     A       TTTCT
                                ATG CATTGAGTA    GGAAAA
                                ||| |||||||||    ||||||
                                TAC GTAATTCAT    CCTTTT
                                  C        TT___
GAM1667  LOC220477 5'  GACACCAAATTTCTGGAAAA   40887      TG   AT
                                GACAT  AGT  TTCTGGAAAA
                                |||||  |||  ||||||||||
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                                CTGTG  TTA  AAGACCTTTT
                                  GT  __
GAM1667  LOC220753 3'  GACATATTTCTGGAA      40888     TTGAG
                                GACA    TATTTCTGGAA
                                ||||    ||||||||||
                                CTGT    ATAAAGACCTT
                                 _____
GAM1667  LOC220883 3'  TGACACTGAAACTGGA     40866         TATTT
                                TGACATTGAG    CTGGA
                                ||||||||||    |||||
                                ACTGTGACTT    GACCT
                                      T____
GAM1667  LOC253430 5'  TGAGGTCCGCATTTCTGG    40889     CA  GA
                                TGA  TT  GTATTTCTGG
                                |||  ||  ||||||||||
                                ACT  AG  CGTAAAGACC
                                  CC  G_
GAM1667  LOC253926 5'  ATGACATTGTCCTTGGAA    40890        AGTA  TC
                                ATGACATTG   TT  TGGAA
                                |||||||||   ||  |||||
                                TACTGTAAC   AG  ACCTT
                                     ____ GA
GAM1667  LOC256130 3'  ACTAGAATGTTTCTGGAAA   40891    ATT   A
                                AC   GAGT TTTCTGGAAA
                                ||   |||| ||||||||||
                                TG   CTTA AAAGACCTTT
                                 AT_   C
GAM1667  LOC51136  3'  ATGACATTAGTATTTTGTGG  40892       G     C_
                                ATGACATT AGTATTT  TGG
                                ||||||||| |||||||  |||
                                TACTGTAA TCATAAA  ACC
                                     _     AC
GAM1668  ACVR1     5'  TACTCGGAGAGTAGAAGA    40895    CA      _
                                TAC  GGAGAGTA AAGA
                                |||  |||||||| ||||
                                ATG  CCTCTCAT TTCT
                                  AG      C
GAM1668  CAPZA1    3'  TACCAGAAGTGCTTGGAAG   40896        A  AAA
                                TACCAGGAG GT   GAAG
                                |||||||||  ||   ||||
                                ATGGTCTTC CG   CTTC
                                     A  AAC
GAM1668  CDH3      3'  CACCAGGAGGCCTAAGAAG   40897        A  A_
                                TACCAGGAG GT  AAGAAG
                                |||||||||  ||  ||||||
                                GTGGTCCTC CG  TTCTTC
                                     _ GA
GAM1668  CDH6      3'  CACCAGGACAGCGGAAG     40898        G   AAA
                                TACCAGGA AGT   GAAG
                                ||||||||  |||   ||||
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                                GTGGTCCT TCG   CTTC
                                     G   C__
GAM1668  CLN6     3'  TACCAGAAGATGTCCGGGAAG  40899          _  AAA_
                                TACCAGGAGA GT    GAAG
                                |||||||||| ||    ||||
                                ATGGTCTTCT CA    CTTC
                                      A  GGCC
GAM1668  FANCC    3'  CACCAGGAGTACCGAAG     40900        GA   AA
                                TACCAGGA  GTA  GAAG
                                ||||||||  |||  ||||
                                GTGGTCCT  CAT  CTTC
                                     __   GG
GAM1668  HAP1     3'  TACCAGGACAGCACTAGA    40901        G    A_
                                TACCAGGA AGTA  AGA
                                |||||||| ||||  |||
                                ATGGTCCT TCGT  TCT
                                     G    GA
GAM1668  HSD3B1   5'  CACCAGGAAACAGAAG      40902         GTAA
                                TACCAGGAGA    AGAAG
                                ||||||||||    |||||
                                GTGGTCCTTT    TCTTC
                                      G___
GAM1668  MLF2     3'  ACCAGGAGATTAAAGAAG    40903         G
                                ACCAGGAGA TAAAGAAG
                                ||||||||| ||||||||
                                TGGTCCTCT ATTTCTTC
                                      A
GAM1668  NHLH1    3'  CACCAGGAGTTGAAGAAG    40904         AGTA
                                TACCAGGAG    AAGAAG
                                |||||||||    ||||||
                                GTGGTCCTC    TTCTTC
                                      AAC_
GAM1668  PIK3R3   5'  CCAGGAGATATATAGAAG    40905         _   A
                                CCAGGAGA GTA AGAAG
                                |||||||| ||| |||||
                                GGTCCTCT TAT TCTTC
                                     A   A
GAM1668  PIK4CB   3'  ACCAGGAGGGGCAGGGAAG   40906         A_   AA
                                ACCAGGAG  GTA  GAAG
                                ||||||||  |||  ||||
                                TGGTCCTC  CGT  CTTC
                                     CC   CC
GAM1668  PKHD1    3'  CACCAGATGCCTAAAGAAG   40907         AGAG
                                TACCAGG    TAAAGAAG
                                |||||||    ||||||||
                                GTGGTCT    ATTTCTTC
                                    ACGG
GAM1668  PKNOX1   3'  TACCAGGAAACAGAAG      40908         GTAA
                                TACCAGGAGA    AGAAG
                                ||||||||||    |||||
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                                ATGGTCCTTT   TCTTC
                                     G___
GAM1668 SQLE     5' TACCAAGAGGAGCACGGA    40909        _   AA
                                TACCAGGAG AGTA  GA
                                ||||||||| ||||  ||
                                ATGGTTCTC TCGT  CT
                                     C   GC
GAM1668 TRIM14   3' ACCAGGAACTGCTAAGAAG   40910       A_ A
                                ACCAGGAG  GT AAGAAG
                                ||||||||  || ||||||
                                TGGTCCTT  CG TTCTTC
                                     GA  A
GAM1668 TYRP1    3' ACCAGATAAAAAAAGAAG    40911      A  T
                                ACCAGG GAG AAAGAAG
                                |||||| ||| |||||||
                                TGGTCT TTT TTTCTTC
                                   A  _
GAM1668 ATP6V0A1 3' CACCAGGAGGTGGGAAG    40912       A AAA
                                TACCAGGAG GT  GAAG
                                ||||||||| ||  ||||
                                GTGGTCCTC CA  CTTC
                                     _ CC_
GAM1668 CCRK     5' CACCAGGAGAACGGAAG    40913         TAAA
                                TACCAGGAGAG   GAAG
                                ||||||||||   ||||
                                GTGGTCCTCTT   CTTC
                                      GC__
GAM1668 CGI-57   3' TACCTGGGAGAAGAACCAGAAG 40914     A_    TAA__
                                TACC  GGAGAG    AGAAG
                                ||||  ||||||    |||||
                                ATGG  CCTCTT    TCTTC
                                  AC     CTTGG
GAM1668 DKFZP586M1120 3' ACCAGGAGGAGCGGAAG    40915       _  AAA
                                ACCAGGAG AGT  GAAG
                                |||||||| |||  ||||
                                TGGTCCTC TCG  CTTC
                                     C  C__
GAM1668 DMTF1    5' TACCAGGATGGAGGAAG    40916       __  TAAA
                                TACCAGGA  GAG   GAAG
                                ||||||||  |||   ||||
                                ATGGTCCT  CTC   CTTC
                                     AC  _____
GAM1668 EPS15R   3' TACCAAGAGGCTAAAGAAG   40917       AG
                                TACCAGGAG  TAAAGAAG
                                |||||||||  ||||||||
                                ATGGTTCTC  ATTTCTTC
                                      CG
GAM1668 FLJ10738 3' TACGGGAGAGCATGAAG    40918    CA      AA
                                TAC  GGAGAGTA  GAAG
                                |||  ||||||||  ||||
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                                ATG  CCTCTCGT  CTTC
                                  C_       A_
GAM1668 HCA4     3' ACCAGGAGGCAGGAAG      40919         A   AA
                                ACCAGGAG GTA  GAAG
                                |||||||| |||  ||||
                                TGGTCCTC CGT  CTTC
                                     _   C_
GAM1668 IL1RAPL1 5' ACTAGGAGAAAAATGAAG    40920    C      T  A
                                AC AGGAGAG AA GAAG
                                || ||||||| || ||||
                                TG TCCTCTT TT CTTC
                                 A      T  A
GAM1668 KIAA0125 5' ACCAGGAGGAGCGAGGGAAG  40921         _  AAA_
                                ACCAGGAG AGT    GAAG
                                |||||||| |||    ||||
                                TGGTCCTC TCG    CTTC
                                     C   CTCC
GAM1668 KIAA0352 3' TACCAAGAAAATGGGAGAAG  40922           AA_
                                TACCAGGAGAGT   AGAAG
                                ||||||||||||   |||||
                                ATGGTTCTTTTA   TCTTC
                                       CCC
GAM1668 KIAA0924 3' AGGAGAGCTACACAAAGAAGC 40923         _____     III
                                AGGAGAGT    AAAGAAG   C
                                ||||||||    |||||||   |
                                TCCTCTCG    TTTCTTC   G
                                     ATGTG      III
GAM1668 KIAA1607 3' CACCAGGAGGCTGAAG      40924         A  AAA
                                TACCAGGAG GT   GAAG
                                ||||||||| ||   ||||
                                GTGGTCCTC CG   CTTC
                                       _ A__
GAM1668 KIAA1881 3' CCTAGGAGAGCATGGAAA    40925    _       AA
                                CC AGGAGAGTA  GAAG
                                || |||||||||  ||||
                                GG TCCTCTCGT  CTTT
                                 A        AC
GAM1668 MGC14799 5' CACCAGGAAGCGGGAAG     40926         G   AAA
                                TACCAGGA AGT   GAAG
                                |||||||| |||   ||||
                                GTGGTCCT TCG   CTTC
                                     _   CC_
GAM1668 MGC16121 5' TACCAGGAACCGCAGAGA    40927         A_  A
                                TACCAGGAG  GTA AGA
                                |||||||||  ||| |||
                                ATGGTCCTT  CGT TCT
                                      GG   C
GAM1668 MGC3040  3' CAGGAAAAAATAGAGAAG    40928         __  A
                                CAGGAGA  GTA AGAAG
                                |||||||  ||| |||||
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                                GTCCTTT  TAT TCTTC
                                    TT   C
GAM1668  MGC4643   3'  TACCAGGAGCCGGCAAGGGAAG 40929         A__    A_
                                TACCAGGAG   GTAA  GAAG
                                |||||||||   ||||  ||||
                                ATGGTCCTC   CGTT  CTTC
                                     GGC    CC
GAM1668  NR1H4     5'  CCAGGAAACTAAGAGAAG    40930        G   _
                                CCAGGAGA TAA AGAAG
                                |||||||| ||| |||||
                                GGTCCTTT ATT TCTTC
                                    G   C
GAM1668  PRO0641   3'  CCAGGAAATGAAAAGAAG    40931        GT_
                                CCAGGAGA   AAAGAAG
                                ||||||||   |||||||
                                GGTCCTTT   TTTCTTC
                                    ACT
GAM1668  PSMD13    3'  CAGGAGAGACCCACAAAGAAG  40932        _____
                                CAGGAGAG    TAAAGAAG
                                ||||||||    ||||||||
                                GTCCTCTC    GTTTCTTC
                                    TGGGT
GAM1668  SMT3H2    5'  CACCAGGAGCGGCAGAAGAAG  40933         A_  _
                                TACCAGGAG  GTA AAGAAG
                                |||||||||  ||| ||||||
                                GTGGTCCTC  CGT TTCTTC
                                     GC   C
GAM1668  SSH2      3'  CACCAGGAAGATTAAGGAAG   40934        _ G   A
                                TACCAGGA GA TAA GAAG
                                |||||||| || ||| ||||
                                GTGGTCCT CT ATT CTTC
                                    T  A   C
GAM1668  STAT2     3'  CCAGGAGTAAAGGAAAGAAG   40935        ___  T
                                CCAGGAG   AG AAAGAAG
                                |||||||   || |||||||
                                GGTCCTC   TC TTTCTTC
                                    ATT  C
GAM1668  TIEG      3'  ACTAGGAATAATAAAGAAG    40936    C    _
                                AC AGGAG AGTAAAGAAG
                                || ||||| ||||||||||
                                TG TCCTT TTATTTCTTC
                                 A    A
GAM1668  LOC131744 3'  TACTCAGGTAAAGAAG      40937     _   AGAG
                                TAC CAGG    TAAAGAAG
                                ||| ||||    ||||||||
                                ATG GTCC    ATTTCTTC
                                  A   _____
GAM1668  LOC137964 5'  TACCAGAAGTACGAAGAAG    40938         A TA
                                TACCAGGAG G  AAGAAG
                                |||||||||  |  ||||||
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                                ATGGTCTTC T  TTCTTC
                                      A GC
GAM1668  LOC144571 3'  TACTAGGAAAGTGTAAAG    40939     C       __
                                TAC AGGAGAGT  AAAG
                                ||| ||||||||  ||||
                                ATG TCCTTTCA  TTTC
                                  A       CA
GAM1668  LOC145676 5'  TAAGGTAAGAGTAAAGAAG   40940   C  __
                                C AGG  AGAGTAAAGAAG
                                | |||  ||||||||||||
                                A TCC  TCTCATTTCTTC
                                 T   AT
GAM1668  LOC147160 5'  CACCAGGAGGCCCTGAAG    40941         A  AAA
                                TACCAGGAG GT   GAAG
                                ||||||||| ||   ||||
                                GTGGTCCTC CG   CTTC
                                      _ GGA
GAM1668  LOC149684 3'  ACTAGGAGAGCGGAGAAG    40942    C       AA
                                AC AGGAGAGT  AGAAG
                                || ||||||||  |||||
                                TG TCCTCTCG  TCTTC
                                 A       CC
GAM1668  LOC151647 5'  TACCAGGAGAAGCCCGAAG   40943         _  AAA
                                TACCAGGAGA GT   GAAG
                                |||||||||| ||   ||||
                                ATGGTCCTCT CG   CTTC
                                      T  GG_
GAM1668  LOC152941 3'  TACCAAGAGAAGCTGAAG    40944         _  AAA
                                TACCAGGAGA GT   GAAG
                                |||||||||| ||   ||||
                                ATGGTTCTCT CG   CTTC
                                      T  A__
GAM1668  LOC153894 3'  TACCAGAAGGTCCTGAAG    40945         A  AAA
                                TACCAGGAG GT   GAAG
                                ||||||||| ||   ||||
                                ATGGTCTTC CA   CTTC
                                      _ GGA
GAM1668  LOC154547 5'  CACCAGGAGCGGCAGAAGAAG  40933         A_  _
                                TACCAGGAG  GTA AAGAAG
                                |||||||||  ||| ||||||
                                GTGGTCCTC  CGT TTCTTC
                                      GC   C
GAM1668  LOC154743 3'  TACCAGAGTAAAGAAG      40946      GGA
                                TACCA   GAGTAAAGAAG
                                |||||   ||||||||||
                                ATGGT   CTCATTTCTTC
                                     ____
GAM1668  LOC158434 5'  ACTGGGAGAGACAAAGAAG   40947    CA    _
                                AC  GGAGAG TAAAGAAG
                                ||  |||||| ||||||||
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                                TG  CCTCTC GTTTCTTC
                                 AC      T
GAM1668  LOC158997 5'  CACCAGGAGCTGCAGAAGAAG  40948          A_   _
                                TACCAGGAG  GTA AAGAAG
                                |||||||||  ||| ||||||
                                GTGGTCCTC  CGT TTCTTC
                                     GA   C
GAM1668  LOC162333 5'  CACCAGGCTCCCAAAGAAG    40949        AGAG
                                TACCAGG    TAAAGAAG
                                |||||||    ||||||||
                                GTGGTCC    GTTTCTTC
                                   GAGG
GAM1668  LOC166341 3'  CACTGGGAGAACACAGAAG    40950     CA       A
                                TAC  GGAGAGTA AGAAG
                                |||  |||||||| |||||
                                GTG  CCTCTTGT TCTTC
                                  AC       G
GAM1668  LOC200058 3'  CCAGGAGAGCCTCTAGAGAAG  40951          AA____
                                CCAGGAGAGT      AGAAG
                                ||||||||||      |||||
                                GGTCCTCTCG      TCTTC
                                     GAGATC
GAM1668  LOC200845 5'  ACTAGGAAAATAGAGAAG     40952     C        A
                                AC AGGAGAGTA AGAAG
                                || |||||||| |||||
                                TG TCCTTTTAT TCTTC
                                 A        C
GAM1668  LOC220581 3'  ACTGGGAGAGCACCCCAAGAAG 40953     CA       ____
                                AC  GGAGAGTA    AAGAAG
                                ||  ||||||||    ||||||
                                TG  CCTCTCGT    TTCTTC
                                 AC       GGGG
GAM1668  LOC220930 3'  ACCACTAAAGTAAGGAAG     40954      GG       A
                                ACCA  AGAGTAA GAAG
                                ||||  ||||||| ||||
                                TGGT  TTTCATT CTTC
                                   GA       C
GAM1668  LOC221496 3'  TACCAGTAAGACTAGAGA     40955        _    G  A
                                TACCAG GAGA TA AGA
                                |||||| |||| || |||
                                ATGGTC TTCT AT TCT
                                    A   G  C
GAM1668  LOC221561 5'  CACCAGGAGCGGCAGAAGAAG  40933          A_   _
                                TACCAGGAG  GTA AAGAAG
                                |||||||||  ||| ||||||
                                GTGGTCCTC  CGT TTCTTC
                                     GC   C
GAM1668  LOC253263 3'  CACCAGAAAAAAAGAAG      40956          GT
                                TACCAGGAGA  AAAGAAG
                                ||||||||||  |||||||
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                                GTGGTCTTTT  TTTCTTC
                                        __
GAM1668  LOC254228 3'  CACCAGGAATAGGAAG      40957          _  TAAA
                                TACCAGGAG AG    GAAG
                                ||||||||| ||    ||||
                                GTGGTCCTT TC    CTTC
                                     A  ____
GAM1668  LOC255975 5'  CACCAGGAAGCAGAAG      40958         G   AA
                                TACCAGGA AGT  AGAAG
                                |||||||| |||  |||||
                                GTGGTCCT TCG  TCTTC
                                     _  __
GAM1668  LOC257591 5'  CACCAGGAGCGGCAGAAGAAG  40933          A_  _
                                TACCAGGAG  GTA AAGAAG
                                |||||||||  ||| ||||||
                                GTGGTCCTC  CGT TTCTTC
                                     GC   C
GAM1668  LOC51015  3'  ACTAGGAGGCGCAAAAAAG   40959    C     A_
                                AC AGGAG  GTAAAGAAG
                                || |||||  |||||||||
                                TG TCCTC  CGTTTTTTC
                                 A    CG
GAM1668  LOC90342  5'  TACCAGAACAAAGAAG      40960         GAG
                                TACCAGGA   TAAAGAAG
                                ||||||||   ||||||||
                                ATGGTCTT   GTTTCTTC
                                       ___
GAM1668  LOC90906  5'  CACCAGATTAAAGAAG      40961         AGAG
                                TACCAGG    TAAAGAAG
                                |||||||    ||||||||
                                GTGGTCT    ATTTCTTC
                                    A___
GAM1668  LOC91115  3'  TACCAGGAGGCAGAAG      40962          A  AA
                                TACCAGGAG GT  AGAAG
                                ||||||||| ||  |||||
                                ATGGTCCTC CG  TCTTC
                                     _  __
GAM1669  GPX4      3'  GCAGGTTTGCAGGCAGGCCGT  40965      C___
                                GCGG    GCAGGCAGGCCGT
                                ||||    ||||||||||||||
                                CGTC    CGTCCGTCCGGCA
                                  CAAA
GAM1669  HDAC7A    3'  ACTGTCAAAGCAGGCAGGCTGT 40966     A  _  C         C
                                GC TG CGG GCAGGCAGGC GT
                                || || ||| |||||||||| ||
                                TG AC GTT CGTCCGTCCG CA
                                 _ A  T         A
GAM1669  HDAC7A    3'  ACTGTCAAAGCAGGCAGGCTGT 40966     A  _  C         C
                                GC TG CGG GCAGGCAGGC GT
                                || || ||| |||||||||| ||
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                                TG AC GTT CGTCCGTCCG CA
                                 _ A  T       A
GAM1669 HR      5' GCGCGGGCGGTGGCGGTCG   40967   A C   CA  A C
                                GC TG GGCG  GGC GG CG
                                || || ||||  ||| || ||
                                CG GC CCGC  CCG CC GC
                                 C _   CA  _ A
GAM1669 LEF1    3' GCGTCGACTGGGCAGGCCGT  40968   ATG   GCA
                                GC  CGGC  GGCAGGCCGT
                                ||  ||||  ||||||||||
                                CG  GCTG  CCGTCCGGCA
                                 CA_   AC_
GAM1669 NUP50   5' CGCAGCGGCGCAGGGG     40969     T       CA
                                CGCA GCGGCGCAGG  GG
                                |||| ||||||||||  ||
                                GCGT CGCCGCGTCC  CC
                                  _       __
GAM1669 SFRP1   3' TGCGGGGGAACAGGCAGGCTGT 40970      C___       C
                                TGCGG   GCAGGCAGGC GT
                                |||||   ||||||||||  ||
                                ACGCC   TGTCCGTCCG CA
                                   CCCT       A
GAM1669 FLJ22056 3' CGCATGCGGGTGTGGGCCAGG 40971        CGCA_  _
                                CGCATGCGG    GGC AGG
                                |||||||||    ||| |||
                                GCGTACGCC    CCG TCC
                                     CACAC   G
GAM1669 H6PD    5' CGCGGCGGCGCAGGCCGC   40972    AT       AG
                                CGC  GCGGCGCAGGC  GC
                                |||  ||||||||||  ||
                                GCG  CGCCGCGTCCG  CG
                                  C_        G_
GAM1669 KIAA0284 3' GCGTGTGGTGCAGGCCAAGC  40973   A  C  C    _
                                GC TG GG GCAGGC AGGC
                                || || || |||||| ||||
                                CG AC CC CGTCCG TTCG
                                 C  A  A    G
GAM1669 MGC10870 5' CGTACGCGGCGTAGCGCGCGT 40974   C      CA  AG  _
                                CG ATGCGGCG  GGC  GC CGT
                                || ||||||||  |||  || |||
                                GC TGCGCCGC  TCG  CG GCA
                                 A       A_  __  C
GAM1669 THG-1   5' ACGCAGGCGGCGATCAGAGGCT 40975      T    CA_ C   C
            GT                    ACGCA GCGGCG   GG AGGC GT
                                |||||  ||||||   || |||| ||
                                TGCGT CGCCGC   TC TCCG CA
                                   C     TAG  _   A
GAM1669 LOC162022 5' CGCGGTGCAGTAGGCCG    40976      C   GC
                                TGCGG GCAG  AGGCCG
                                |||||  ||||  ||||||
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                                GCGCC CGTC  TCCGGC
                                  A   A_
GAM1669 LOC92267 5' GCGATGTGGCGCAGGGAG   40977   _  C     C
                                GC ATG GGCGCAGG AG
                                || ||| |||||||| ||
                                CG TAC CCGCGTCC TC
                                 C  A     C
GAM1670 BACE    3' TCACTTGCTCTGTGGGTA   40980     CAGGC      AA
                                TCGCT   TGTTCTGTG  TA
                                |||||   |||||||||  ||
                                AGTGA   ACGAGACAC  AT
                                  _____      CC
GAM1670 BACE    3' TCACTTGCTCTGTGGGTA   40980     CAGGC      AA
                                TCGCT   TGTTCTGTG  TA
                                |||||   |||||||||  ||
                                AGTGA   ACGAGACAC  AT
                                  _____      CC
GAM1670 BCLG    3' AGGCTGTTTACTAACGTGAATA 40981       C_____      III
           GC                   AGGCTGTT    TGTGAATAG  C
                                ||||||||    |||||||||  |
                                TCCGACAA    GCACTTATC  G
                                   ATGATT       III
GAM1670 BCLG    3' AGGCTGTTTACTAACGTGAATA 40981       C_____      III
           GC                   AGGCTGTT    TGTGAATAG  C
                                ||||||||    |||||||||  |
                                TCCGACAA    GCACTTATC  G
                                   ATGATT       III
GAM1670 BCLG    3' AGGCTGTTTACTAACGTGAATA 40981       C_____      III
           GC                   AGGCTGTT    TGTGAATAG  C
                                ||||||||    |||||||||  |
                                TCCGACAA    GCACTTATC  G
                                   ATGATT       III
GAM1670 COL4A3  3' GGTGATATTTTGTGAATAG  40982   C__   C
                                GG  TGTT TGTGAATAG
                                ||  |||| |||||||||
                                CC  ATAA ACACTTATC
                                 ACT   A
GAM1670 COL4A3  3' GGTGATATTTTGTGAATAG  40982   C__   C
                                GG  TGTT TGTGAATAG
                                ||  |||| |||||||||
                                CC  ATAA ACACTTATC
                                 ACT   A
GAM1670 COL4A3  3' GGTGATATTTTGTGAATAG  40982   C__   C
                                GG  TGTT TGTGAATAG
                                ||  |||| |||||||||
                                CC  ATAA ACACTTATC
                                 ACT   A
GAM1670 CYP4F3  3' TCGTTTGGGCTACTGTGAATAG 40983    CTCA   TT
                                TCG   GGCTG  CTGTGAATAG
                                |||   |||||  ||||||||||
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                              AGC   CCGAT  GACACTTATC
                                AAAC   __
GAM1670 PTGIS    3' GCCAGCTCCCTGTGA      40984     CA   G
                              GCT  GGCT TTCTGTGA
                              |||  |||| ||||||||
                              CGG  TCGA GGGACACT
                                __   _
GAM1670 WHSC1    3' TCGCATGGTACTGTGAATA   40985     TCA  CTGTT
                              TCGC   GG    CTGTGAATA
                              ||||  ||    |||||||||
                              AGCG   CC    GACACTTAT
                                TA_  AT___
GAM1670 CYP4F2   3' TCGTTTGGCTACTGTGAATAG  40986    CTCA    TT
                              TCG    GGCTG  CTGTGAATAG
                              |||    |||||  ||||||||||
                              AGC    CCGAT  GACACTTATC
                                AAA_    __
GAM1670 FLJ10120 3' GCCAGGCTGTTTCCTGTG    40987    T      __
                              GC CAGGCTGT  TCTGTG
                              || ||||||||  ||||||
                              CG GTCCGACA  GGACAC
                               _       AA
GAM1670 FLJ10460 3' TCGCCCAGGCTGTAGCGCA   40988           TC
                              TCGCTCAGGCTGT  TGTG
                              ||||||||||||  ||||
                              AGCGGGTCCGACA  GCGT
                                     TC
GAM1670 FLJ12078 5' GCCCAGGCTGTTCTTGA     40989           G
                              GCTCAGGCTGTTCT TGA
                              |||||||||||||| |||
                              CGGGTCCGACAAGA ACT
                                             _
GAM1670 FLJ22582 3' GCTCAGGCTGCCGGGGTG    40990           CT_
                              GCTCAGGCTGTT   GTG
                              ||||||||||||   |||
                              CGAGTCCGACGG   CAC
                                     CCC
GAM1670 GPS2     5' TCGCCAGGCTGTTGTCCATG   40991     T      __
                              TCGC CAGGCTGT  TCTGTG
                              |||| ||||||||  ||||||
                              AGCG GTCCGACA  AGGTAC
                                _       AC
GAM1670 MGC3329  3' TCGCCCAGGCTGTAGTGCA   40992           TC
                              TCGCTCAGGCTGT  TGTG
                              ||||||||||||  ||||
                              AGCGGGTCCGACA  ACGT
                                     TC
GAM1670 LOC219347 3' TCCTCAGGCTTCTGTG     40993    G      GT
                              TC CTCAGGCT  TCTGTG
                              || ||||||||  ||||||
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                                AG GAGTCCGA  AGACAC
                                 _     ___
GAM1670  LOC222160 3'  GCTCAGGCTGCTTTTGCA    40994          C_
                                GCTCAGGCTGTT  TGTG
                                ||||||||||||  ||||
                                CGAGTCCGACGA  ACGT
                                      AA
GAM1670  LOC254041 5'  TCGTCCAGGCTGTAGTGCA   40995    CT      TC
                                TCG  CAGGCTGT  TGTG
                                |||  ||||||||  ||||
                                AGC  GTCCGACA  ACGT
                                  AG       TC
GAM1670  LOC51145  3'  TCGCCCAGGCTGGAGGGGAGTG 40996          TTCT___
                                TCGCTCAGGCTG      GTG
                                ||||||||||||      |||
                                AGCGGGTCCGAC      CAC
                                      CTCCCCT
GAM1670  LOC92499  5'  TCGTCCAGGCTGTAGTGCA   40995    CT      TC
                                TCG  CAGGCTGT  TGTG
                                |||  ||||||||  ||||
                                AGC  GTCCGACA  ACGT
                                  AG       TC
GAM1671  APP     3'  TGTGTGCACATAAAACAGG   40999     _    AAC
                                TGTG GCACA   AAAACAGG
                                ||||  |||||   ||||||||
                                ACAC CGTGT   TTTTGTCC
                                  A    A__
GAM1671  CPO     3'  TTGTGGCACAAATGAAAAC   41000          C_
                                TTGTGGCACAAA  AAAAC
                                ||||||||||||  |||||
                                AACACCGTGTTT  TTTTG
                                      AC
GAM1671  DMD     5'  GCCAAGCACAGATAAAGCAGGC 41001    TGT     AAC   A
                                GT   GGCACA   AAA CAGGC
                                ||   ||||||   ||| |||||
                                CG   TCGTGT   TTT GTCCG
                                 GT_     CTA   C
GAM1671  DMD     5'  GCCAAGCACAGATAAAGCAGGC 41001    TGT     AAC   A
                                GT   GGCACA   AAA CAGGC
                                ||   ||||||   ||| |||||
                                CG   TCGTGT   TTT GTCCG
                                 GT_     CTA   C
GAM1671  INSRR    3'  TTGTTGGCAGCAAGGTAGGC   41002     _   CAAA   AAC
                                TTGT GGCA    CAA   AGGC
                                ||||  ||||    |||   ||||
                                AACA CCGT    GTT   TCCG
                                  A   C___   CCA
GAM1671  JUP     3'  CGTTGCTGGGGGAAAACAGA   41003      _  CACAAAC
                                CGTTG TGG      AAAACAGG
                                |||||  |||      ||||||||
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                                GCAAC ACC      TTTTGTCT
                                   G   CCC____
GAM1671  PKNOX1   3'  TATAGCAAATGAAACAGGC   41004       CAAACA
                                TGTGGCA     AAACAGGC
                                |||||||     ||||||||
                                ATATCGT     TTTGTCCG
                                    TTAC__
GAM1671  FLJ10852 3'  TGTGAAAGCAAAACAG     41005      CAC  A
                                TGTGG   AA CAAAACAG
                                |||||   || ||||||||
                                ACACT   TT GTTTTGTC
                                   ___  C
GAM1671  FLJ14640 5'  GTGTGGCACAGCGTACAGG   41006    T      AACAAA
                                GT GTGGCACA     ACAGG
                                || ||||||||     |||||
                                CA CACCGTGT     TGTCC
                                 _       CGCA__
GAM1671  FLJ20276 3'  TTGTGGGCCATACAAAACAGG  41007      CA  A
                                TTGTGG  CA ACAAAACAGG
                                ||||||  || ||||||||||
                                AACACC  GT TGTTTTGTCC
                                   CG  A
GAM1671  HSNOV1   3'  CTACAAAAACAAACAAAACAGG 41008    TG C_
            C                    TTG  G  ACAAACAAAACAGGC
                                |||  |  ||||||||||||||
                                GAT  T  TGTTTGTTTTGTCCG
                                  GT TT
GAM1671  KIAA1804 3'  GTTGTGTGCAAATGGACAAAGG 41009      _  CAA__   AAC
            C                    GTTGTG GCA    ACAA   AGGC
                                ||||||| |||    ||||   ||||
                                CAACAC CGT    TGTT   TCCG
                                   A   TTACC   ___
GAM1671  MAGEB1   5'  TGTGGTCAGGCAAAACAGG   41010      CA  AA
                                TGTGG  CA  CAAAACAGG
                                |||||  ||  |||||||||
                                ACACC  GT  GTTTTGTCC
                                   A_  CC
GAM1671  MAP3K3   3'  ATGGCCACAGGCAGGACAGGC  41011      _  AA  AA
                                GTGGC ACA  CA  ACAGGC
                                ||||| |||  ||  ||||||
                                TACCG TGT  GT  TGTCCG
                                   G   CC  CC
GAM1671  NAV3     3'  CGTGTGGCACAAAGGAGG    41012    T      CAAAAC
                                CGT GTGGCACAAA     AGG
                                ||| ||||||||||     |||
                                GCA CACCGTGTTT     TCC
                                  _        CC____
GAM1671  SRF      3'  CGTGTGGCACAAATGAAGTCAG 41013    T      CAAAA_
                                CGT GTGGCACAAA     CAG
                                ||| ||||||||||     |||
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                                GCA CACCGTGTTT     GTC
                                  _        ACTTCA
GAM1671  TRIM35   3'  TCATGACACAAGCAGAGCAGG  41014   TG       A  AAA
                                T  TGGCACAA CA   CAGG
                                |  |||||||| ||   ||||
                                A  ACTGTGTT GT   GTCC
                                 GT       C  CTC
GAM1671  UBN1     3'  CCTTGTGGCACAGACCTCACAA 41015       A_____   A     III
           GACAGGCG                 GGCACA     ACAA ACAGGC   G
                                ||||||     |||| ||||||   |
                                CCGTGT     TGTT TGTCCG   C
                                   CTGGAG    C     III
GAM1671  LOC115207 3'  GCTGAAAACAAAACAAAATAGG 41016     T_   C      C
           C                     GTTG  GGCA AAACAAAA AGGC
                                ||||  |||| |||||||| ||||
                                CGAC  TTGT TTTGTTTT TCCG
                                  TT   _       A
GAM1671  LOC149464 5'  GCTGTGTGGGGCAGAACAGGC  41017       GCACAAA  A
                                GTTGTG      CA AACAGGC
                                ||||||      || |||||||
                                CGACAC      GT TTGTCCG
                                   ACCCC__  C
GAM1671  LOC150951 5'  CGTTGTGGTTTTCAAAATGGGC 41018        CACAAA    CA
                                CGTTGTGG     CAAAA  GGC
                                ||||||||     |||||  |||
                                GCAACACC     GTTTT  CCG
                                     AAAA__     AC
GAM1672  PLAG1    3'  TCCGTGTTTGGTGACCTAAC   41021       C  _____
                                TCCGTG TTG    CCTAGC
                                |||||| |||    ||||||
                                AGGCAC AAC    GGATTG
                                   A   CACT
GAM1672  REST     5'  TCCGCTGCTGCGCCGCGAGCTC 41022      _   _   TA   A
                                TCCG TGCT TGCC  GCGA CTC
                                |||| |||| ||||  |||| |||
                                AGGC ACGA GCGG  CGCT GAG
                                  G   C   __   C
GAM1672  BM039    5'  CCGTGCCCCAGTGGACTCAC   41023       TTG    CGA
                                CCGTGC   CCTAG   ACTCAC
                                ||||||   |||||   ||||||
                                GGCACG   GGGTC   TGAGTG
                                   ___     ACC
GAM1672  FLJ13769 3'  TCCTTGCTTGCCTCAAACT    41024     G       AG
                                TCC TGCTTGCCT  CGAACT
                                ||| |||||||||  ||||||
                                AGG ACGAACGGA  GTTTGA
                                  A       __
GAM1672  FLJ14213 5'  TCCGTGCTTGCGTTTCTCTCAC 41025          CTAGCGAA
                                TCCGTGCTTGC       CTCAC
                                ||||||||||        |||||
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                                AGGCACGAACG       GAGTG
                                      CAAAGA__
GAM1672 KIAA0256 3' GTGCCTGCTTATGGAAGCT   41026        C  GC  _
                                GTGCTTGC TA  GAA CT
                                |||||||| ||  ||| ||
                                CACGGACG AT  CTT GA
                                     A  AC   C
GAM1672 KIAA1091 3' TCGGTGCTTGCTTAGAGGCAC 41027    C       C   CGA_
                                TC GTGCTTGC TAG    AC
                                || |||||||| |||    ||
                                AG CACGAACG ATC    TG
                                 C       A   TCCG
GAM1672 KIAA1161 5' TCCTGCTTGCCTGGCTCCAGCA 41028     G        A  GAACT
             C                   TCC TGCTTGCCT GC     CAC
                                ||| ||||||||| ||     |||
                                AGG ACGAACGGA CG     GTG
                                 _       C  AGGTC
GAM1672 KIAA1280 5' CCGTGCTTGGCCAGGACTCA   41029        C   C  A
                                CCGTGCTTG CTAG GA CTCA
                                ||||||||| |||| || ||||
                                GGCACGAAC GGTC CT GAGT
                                     C   _ _
GAM1672 KIAA1529 3' CATGCTTGCCTTCCTCA     41030          AGCGAA
                                CGTGCTTGCCT     CTCA
                                ||||||||||      ||||
                                GTACGAACGGA     GAGT
                                      AG____
GAM1672 OATPRP4  3' GTGCTTTGTAGCAGAACTCAC  41031       GCC   _
                                GTGCTT   TAGC GAACTCAC
                                ||||||   |||| ||||||||
                                CACGAA   ATCG CTTGAGTG
                                   AC_    T
GAM1672 TRIP-Br2 3' TCCGTGCTTATTTGAACT    41032         CCTAGC
                                TCCGTGCTTG     GAACT
                                ||||||||||     |||||
                                AGGCACGAAT     CTTGA
                                      AAA___
GAM1672 LOC144438 3' CCGTGCTTGTTTCAAACTCAC 41033        CCTAG
                                CCGTGCTTG    CGAACTCAC
                                |||||||||    |||||||||
                                GGCACGAAC    GTTTGAGTG
                                      AAA__
GAM1672 LOC149464 5' TCCGTGCTGGCCTGAGCTCA  41034        T   AGC  A
                                TCCGTGCT GCCT   GA CTCA
                                |||||||| ||||   || ||||
                                AGGCACGA CGGA   CT GAGT
                                     C    ___ C
GAM1672 LOC91355 5' GTGCCTTGCCAAACTCAC    41035     _    TAGC
                                GTGC TTGCC    GAACTCAC
                                |||| |||||    ||||||||
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                                CACG AACGG    TTTGAGTG
                                  G    ____
GAM1673 CD5      3'  AGCTGTTGTGCAGCAGAGTGTG 41038        C____      CTCA
              AG                   GCTGTTG    CAGGGTG    TGAG
                                   |||||||    |||||||    ||||
                                   CGACAAC    GTCTCAC    ACTC
                                      ACGTC     _____
GAM1673 CHRNA2   5'  AGCTGCTGCTGGATTCTGTGAG 41039         CA    G  CA
                                   AGCTGTTGC  GGGT CT  TGAG
                                   |||||||||  |||| ||  ||||
                                   TCGACGACG  CCTA GA  ACTC
                                        A_    A  C_
GAM1673 CYP1A2   3'  AGCAGTTGCCAGGGCTGGTGAG 41040     T         GCTCA
                                   AGC GTTGCCAGGGT     TGAG
                                   ||| ||||||||||     ||||
                                   TCG CAACGGTCCCG     ACTC
                                     T         ACC__
GAM1673 KIR2DL3  3'  ACTGTGGTGCTCATG       41041       TGCCAG
                                   GCTGT     GGTGCTCATG
                                   |||||     ||||||||||
                                   TGACA     CCACGAGTAC
                                             _______
GAM1673 NCYM     5'  TGTCTGCGTGCTCGTGAG    41042     _  CAGG     A
                                   TGT TGC    GTGCTC TGAG
                                   ||| |||    |||||| ||||
                                   ACA ACG    CACGAG ACTC
                                     G  _____      C
GAM1673 PPP1R12B 3'  GCTGCCTGGGGTGCTCATGAG  41043       A_
                                   GTTGCC  GGGTGCTCATGAG
                                   ||||||  ||||||||||||||
                                   CGACGG  CCCACGAGTACTC
                                      AC
GAM1673 C20orf110 3'  GCTGTTGCTGGTGTCTGA    41044         CAG    C  A
                                   GCTGTTGC   GGTG TC TGA
                                   ||||||||   |||| || |||
                                   CGACAACG   CCAC AG ACT
                                        A__    _ _
GAM1673 FOXP1    3'  TGTACCAAGCTTATGAG     41045     T    GGT   C
                                   TGT GCCAG   GCT ATGAG
                                   ||| |||||   ||| |||||
                                   ACA TGGTT   CGA TACTC
                                     _    ____   A
GAM1673 KIAA0590  3'  AGCTGTTGCTCAGGAGCC    41046         _    T
                                   AGCTGTTGC CAGGG GCT
                                   ||||||||| ||||| |||
                                   TCGACAACG GTCCT CGG
                                        A    _
GAM1673 KIAA0935  3'  GCTGTTGCCAGCATG       41047           GGTGCT
                                   GCTGTTGCCAG     CATG
                                   ||||||||||      ||||
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                                CGACAACGGTC     GTAC
                                        _______
GAM1673 KIAA1952 5' AACTGTTGCTCTCATG      41048         CAGGGTG
                                AGCTGTTGC      CTCATG
                                |||||||||      ||||||
                                TTGACAACG      GAGTAC
                                     A_______
GAM1673 KLHL6    3' GTTATTATAGTGCTCATGAG   41049      CCAG
                                GTTG    GGTGCTCATGAG
                                ||||    ||||||||||||
                                CAAT    TCACGAGTACTC
                                  AATA
GAM1673 N4BP3    3' AGTGGTTGCCAGGGGCT     41050    CT        T
                                AG  GTTGCCAGGG GCT
                                ||  |||||||||| |||
                                TC  CAACGGTCCC CGA
                                 AC         _
GAM1673 LOC199699 3' AGCTGTTGCACAGGACTAGTG  41051          _    GT   CA
                                AGCTGTTGC CAGG  GCT  TG
                                ||||||||| ||||  |||  ||
                                TCGACAACG GTCC  TGA  AC
                                     T    __   TC
GAM1673 LOC51336 5' GTTGCCAGGGGCTGA       41052          T   CAT
                                GTTGCCAGGG GCT   GA
                                |||||||||| |||   ||
                                CAACGGTCCC CGA   CT
                                          _  ____
GAM1673 LOC91056 3' AGCTGTTGCAAGGATGAAATGA 41053          C      CTC
             G                   AGCTGTTGC AGGGTG   ATGAG
                                |||||||||| ||||||   |||||
                                TCGACAACG TCCTAC   TACTC
                                     T     TT_
GAM1674 MET      3' GGACAAAGTGTGGACTGTTGCT 41056          C_  AC___
             T                   GGACAAAGTG  GA    GCTT
                                ||||||||||  ||    ||||
                                CCTGTTTCAC  CT    CGAA
                                      AC  GACAA
GAM1675 ADAM17   3' CAAACCACACAAGAACTGT    41059            _ G
                                TAAACCACACAAGG C GT
                                |||||||||||||| | ||
                                GTTTGGTGTGTTCT G CA
                                       T A
GAM1675 ADAM17   3' CAAACCACACAAGAACTGT    41059            _ G
                                TAAACCACACAAGG C GT
                                |||||||||||||| | ||
                                GTTTGGTGTGTTCT G CA
                                       T A
GAM1675 DLG4     3' CAGAAGGCGGCAGCATTT     41060    C       _
                                CA AAGGCGGTA CGTTT
                                || |||||||| |||||
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                                GT TTCCGCCGT GTAAA
                                 C        C
GAM1675 RPP30    3' TAAATCACACAAAGGT      41061      C       GC
                                TAAA CACACAAG  GGT
                                |||| ||||||||  |||
                                ATTT GTGTGTTT  CCA
                                  A      __
GAM1675 UGT1A1   3' TAAACACACAAGGTGGCAC   41062      C       C
                                TAAAC ACACAAGG GGTAC
                                ||||| |||||||| |||||
                                ATTTG TGTGTTCC CCGTG
                                   _       A
GAM1675 UGT1A4   3' TAAACACACAAGGTGGCAC   41062      C       C
                                TAAAC ACACAAGG GGTAC
                                ||||| |||||||| |||||
                                ATTTG TGTGTTCC CCGTG
                                   _       A
GAM1675 UGT1A9   3' TAAACACACAAGGTGGCAC   41062      C       C
                                TAAAC ACACAAGG GGTAC
                                ||||| |||||||| |||||
                                ATTTG TGTGTTCC CCGTG
                                   _       A
GAM1675 FLJ10408 5' TGACCACACACTCATGTGTTT  41063    A       AGG  GTAC
                                A ACCACACA   CG    GTTT
                                | ||||||||   ||    ||||
                                A TGGTGTGT   GT    CAAA
                                 C       GA_  ACA_
GAM1675 MGC3077  3' TAAACCACAAATACGT      41064         CAAGGC
                                TAAACCACA     GGTACGT
                                |||||||||     |||||||
                                ATTTGGTGT     TTATGCA
                                              _______
GAM1675 LOC147341 3' ACACGACCACAGTACGTTT   41065      AAG_
                                ACAC    GCGGTACGTTT
                                ||||    ||||||||||||
                                TGTG    TGTCATGCAAA
                                  CTGG
GAM1675 LOC221688 5' CCACACAAGGTTAGGTAATGTT 41066          C__    C_
          T                      CCACACAAGG   GGTA  GTTT
                                 ||||||||||   ||||  ||||
                                 GGTGTGTTCC   CCAT  CAAA
                                       AAT    TA
GAM1675 LOC51097 3' CCACTTAAGCAGCATGTTT   41067      ACA       C
                                CCAC   AGGCGGTA GTTT
                                ||||   |||||||| ||||
                                GGTG   TTCGTCGT CAAA
                                  AA_       A
GAM1676 ATRN     3' TGGGGATGCGTTTCTTGGG   41070    A  TCA  C C
                                TG GG   GC G TTCTTGGG
                                || ||   || | ||||||||
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                                AC CC   CG C AAGAACCC
                                 C  TA_  _ A
GAM1676  EGFL5    5'  TGGAGGTCAAAGTGGTTTTGGG 41071    T       CCGCTTC
                C                TG GAGGTCAG      TTGGGC
                                 || ||||||||      ||||||
                                 AC CTCCAGTT      AACCCG
                                  _       TCACCAA
GAM1676  ENTPD6   3'  GTGGGGTCAGCCCGAGGTGGGC 41072     A       GCTTCT
                                 GTG GGTCAGCC     TGGGC
                                 ||| ||||||||     |||||
                                 CAC CCAGTCGG     ACCCG
                                   C       GCTCC_
GAM1676  LAMA5    3'  TGTGAGGCAGCTGCAGGGG   41073       T   C  TTCTT
                                 TGTGAGG CAGC GC    GGG
                                 ||||||| |||| ||    |||
                                 ACACTCC GTCG CG    CCC
                                     _   A  TC___
GAM1676  USP1     3'  TGAGATTCTGCTTCTTGGG   41074       CAGCC
                                 TGAGGT    GCTTCTTGGG
                                 ||||||    ||||||||||
                                 ACTCTA    CGAAGAACCC
                                    AGA__
GAM1676  B3GNT7   3'  TGGAGGTCAGCAGCTTGGG   41075    T       C   TCT
                                 TG GAGGTCAGC GCT   TGGG
                                 || |||||||| |||   ||||
                                 AC CTCCAGTCG CGA   ACCC
                                  _       T   ___
GAM1676  C1orf24  3'  TGTGAGGTCAGCCTGG     41076           GCTTCT
                                 TGTGAGGTCAGCC     TGG
                                 ||||||||||||     |||
                                 ACACTCCAGTCGG     ACC
                                           _______
GAM1676  DCOHM    3'  TATGAGGTCACTCTTGGG    41077         GCCGC
                                 TGTGAGGTCA    TTCTTGGG
                                 ||||||||||    ||||||||
                                 ATACTCCAGT    GAGAACCC
                                           ______
GAM1676  DMWD     3'  TGTGAGGTCAGCAGGGAGGG  41078          CGCTTCTT
                                 TGTGAGGTCAGC      GGG
                                 ||||||||||||      |||
                                 ACACTCCAGTCG      CCC
                                        TCCCT___
GAM1676  IL18BP   3'  TGGAGGGCAGGGCTTCTTGGG 41079   T   T   CC
                                 TG GAGG CAG  GCTTCTTGGG
                                 || |||| |||  ||||||||||
                                 AC CTCC GTC  CGAAGAACCC
                                  _   C   C_
GAM1676  KIAA0280 3'  TGTGAGGTCCAGCTGTTAG   41080        AGCC   TC
                                 TGTGAGGTC   GCT  TTGG
                                 |||||||||   |||  ||||
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                                ACACTCCAG   CGA  AATC
                                     GT__   C_
GAM1676 KIAA1199 3' TGTGAGGTTGGCTCTTG    41081       CA  CGCT
                                TGTGAGGT  GC   TCTTG
                                ||||||||  ||   |||||
                                ACACTCCA  CG   AGAAC
                                     AC  ____
GAM1676 KIAA1323 5' TGAGGTCACCAGATTCTTGGG 41082       G   C_
                                TGAGGTCA CCG  TTCTTGGG
                                |||||||| |||  ||||||||
                                ACTCCAGT GGT  AAGAACCC
                                     _  CT
GAM1676 MGC9753  5' TGTGAGGTCAGTGTCCCTGG  41083         CCGC
                                TGTGAGGTCAG   TTCTTGG
                                ||||||||||   |||||||
                                ACACTCCAGTC   AGGGACC
                                      AC__
GAM1676 POFUT1   3' TGTAGGCTTTGTTTCTTGGG  41084    G   CAGCCGC
                                TGT AGGT      TTCTTGGG
                                ||| ||||      ||||||||
                                ACA TCCG      AAGAACCC
                                  _   AAACA__
GAM1676 LOC134266 3' TGGAGGTCAGCCTGG      41085    T       GCTTCT
                                TG GAGGTCAGCC     TGG
                                || ||||||||||     |||
                                AC CTCCAGTCGG     ACC
                                 _      _______
GAM1676 LOC145447 5' GTGAGATGTTTCTTGGG    41086       CAGCCGC
                                GTGAGGT     TTCTTGGG
                                |||||||     ||||||||
                                CACTCTA     AAGAACCC
                                    CA_____
GAM1676 LOC200081 3' TGTGAGGTTGGCAGCTCTTG  41087       CA  C   T
                                TGTGAGGT  GC GCT CTTG
                                ||||||||  || ||| ||||
                                ACACTCCA  CG CGA GAAC
                                     AC  T  _
GAM1677 CASP8    3' TGGTAGTGTGGAATTTAGC   41090      G     GGGC
                                TGGTAG TGTGGAA   GC
                                ||||||| |||||||   ||
                                ACCATC ACACCTT   CG
                                    _      AAAT
GAM1677 CASP8    3' TGGTAGTGTGGAATTTAGC   41090      G     GGGC
                                TGGTAG TGTGGAA   GC
                                ||||||| |||||||   ||
                                ACCATC ACACCTT   CG
                                    _      AAAT
GAM1677 CASP8    3' TGGTAGTGTGGAATTTAGC   41090      G     GGGC
                                TGGTAG TGTGGAA   GC
                                ||||||| |||||||   ||
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                                ACCATC ACACCTT   CG
                                   _     AAAT
GAM1677  CASP8    3'  TGGTAGTGTGGAATTTAGC   41090      G     GGGC
                                TGGTAG TGTGGAA   GC
                                |||||| |||||||   ||
                                ACCATC ACACCTT   CG
                                   _     AAAT
GAM1677  CDH5     3'  GGTGGGTGTGGAGGTGGCC   41091    A      A  GCGC
                                GGT GGTGTGGA GG   GCC
                                ||| |||||||| ||   |||
                                CCA CCACACCT CC   CGG
                                  C       _ AC__
GAM1677  CPNE7    3'  GGTGGGTGTGGGGGGCAC    41092    A     AA
                                GGT GGTGTGG  GGGCGC
                                ||| |||||||  ||||||
                                CCA CCACACC  CCCGTG
                                  C     __
GAM1677  FOSB     3'  GGTGGGTGTGGGAGACA     41093    A     AA
                                GGT GGTGTGG  GGGCG
                                ||| |||||||  |||||
                                CCA CCACACC  TCTGT
                                  C     C_
GAM1677  GRM1     3'  TGGAGGTGTGGGAGATCGG   41094    T      A _______
                                TGG AGGTGTGG AG    GG
                                ||| |||||||| ||    ||
                                ACC TCCACACC TC    CC
                                  _      C  TAGIII
GAM1677  MSN      3'  TGGGGGTGTGGAAGGGAC    41095    TA        C
                                TGG  GGTGTGGAAGGG GC
                                |||  |||||||||||| ||
                                ACC  CCACACCTTCCC TG
                                  C_         _
GAM1677  PIM1     5'  TGGCGGCGGGAGGGCGCGCC  41096    A   T   A
                                TGGT GGTG GGA GGGCGCGCC
                                |||| |||| ||| |||||||||
                                ACCG CCGC CCT CCCGCGCGG
                                   _   _  _
GAM1677  RASAL1   5'  TGGTGGGTGGGAGGCG     41097    A   T   AG
                                TGGT GGTG GGA  GGCG
                                |||| |||| |||  ||||
                                ACCA CCAC CCT  CCGC
                                  C   _  __
GAM1677  SELL     3'  TGCTAGGTGTGGAAGTCGG   41098    G        _____
                                TG TAGGTGTGGAAG    GG
                                || ||||||||||||    ||
                                AC ATCCACACCTTC    CC
                                 G          AGIII
GAM1677  TIMP3    5'  GGTGGGCTGGGGCGCGCC    41099    T  AA_
                                GGTG GG   GGGCGCGCC
                                |||| ||   |||||||||
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                                CCAC CC   CCCGCGCGG
                                  _ GAC
GAM1677  DKFZP434P211 3'  TGGAGGTGTGGGCAGTGG    41100     T       A_ _
                                TGG AGGTGTGG  AG GG
                                ||| ||||||||  || ||
                                ACC TCCACACC  TC CC
                                  _       CG  A
GAM1677  DKFZP761G1913 3'  TGGTGGTGTGGGAAGTTGG    41101      A      _  _____
                                TGGT GGTGTGG AAG     GG
                                |||| ||||||| |||     ||
                                ACCA CCACACC TTC     CC
                                  _      C   AAIII
GAM1677  FBXO24    3'  TGGCAGGTGGCGATAGGGGGCG 41102          _  AA__    C
              TGC                    TGGTAGGTG TGG    GGGCG GC
                                |||||||||| |||    ||||| ||
                                ACCGTCCAC GCT    CCCGC CG
                                     C   ATCC     A
GAM1677  FLJ21709  3'  TGGTAGGTGAGGGAGAAC     41103          T  A
                                TGGTAGGTG GG AGGGC
                                ||||||||| || |||||
                                ACCATCCAC CC TCTTG
                                     T  C
GAM1677  KIAA0182  3'  TGGTGGGTGTGAAGCTGG     41104      A     G  _____
                                TGGT GGTGTG AAG     GG
                                |||| |||||| |||     ||
                                ACCA CCACAC TTC     CC
                                  C     _  GAIII
GAM1677  KIAA0352  3'  TGGTGGGGTGGGGGGAAAC    41105      A  T    AA   C
                                TGGT GG GTGG  GGG GC
                                |||| || ||||  ||| ||
                                ACCA CC CACC  CCT TG
                                  C _    CC   T
GAM1677  KIAA0435  3'  TGGGAGGTGTGGGGGAGC     41106     T       AA   C
                                TGG AGGTGTGG  GGG GC
                                ||| ||||||||  ||| ||
                                ACC TCCACACC  CCC CG
                                  C        __   T
GAM1677  KIAA0894  3'  GGTAGGTGTGGGGGAAGGA    41107          ___
                                GGTAGGTGT   GGAAGGG
                                |||||||||   |||||||
                                CCATCCACA   CCTTCCT
                                     CCC
GAM1677  KIAA1904  3'  GGTGGGTGTGGGGCAGGGC    41108     A      A__
                                GGT GGTGTGG   AGGGC
                                ||| |||||||   |||||
                                CCA CCACACC   TCCCG
                                  C      CCG
GAM1677  NAC1      3'  TGGCAGGTGTGTGTGTGTTG 41109       GAAG__________  CGCG
              GCGCGCC                 GGTGTG          GG    CC
                                ||||||          ||    ||
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                                CCACAC          CC   GG
                                   ACACACACAAIII GCGC
GAM1677 PP5395   3' TGGGGGTGTGGAACAGGC   41110    TA      _
                                TGG GGTGTGGAA GGGC
                                ||| ||||||||| ||||
                                ACC CCACACCTT TCCG
                                  C_      G
GAM1677 PTRF     3' TGGAGGTGTGGGGAGGGGGGCG 41111    T     A_   C_
                                TGG AGGTGTGG AGGG GCG
                                ||| |||||||| |||| |||
                                ACC TCCACACC TCCC CGC
                                  _     CC   CC
GAM1677 RGS17    5' TGGAGGTGTGGGCAGCGCGCC 41112    T     AAG
                                TGG AGGTGTGG  GGCGCGCC
                                ||| ||||||||  ||||||||
                                ACC TCCACACC  TCGCGCGG
                                  _     CG_
GAM1677 RHOBTB1  3' TGGCAGGTGTGGAGCTGTGGC 41113          AG___
                                TGGTAGGTGTGGA   GGC
                                ||||||||||||    |||
                                ACCGTCCACACCT   CCG
                                       CGACA
GAM1677 SPIB     3' TGGTAGGTGAGCTTGCGC   41114       T AAGG
                                TGGTAGGTG GG  GCGC
                                ||||||||| ||  ||||
                                ACCATCCAC TC  CGCG
                                     _ GAA_
GAM1677 TEX27    3' TGGTAGATGTGGACTGGG   41115         A_
                                TGGTAGGTGTGGA GGG
                                |||||||||||| |||
                                ACCATCTACACCT CCC
                                       GA
GAM1677 LOC150174 3' TGGAGGTGTGGGCAGTGG   41100    T     A_ _
                                TGG AGGTGTGG AG GG
                                ||| ||||||| || ||
                                ACC TCCACACC TC CC
                                  _     CG A
GAM1677 LOC150213 3' TGGAGGTGTGGGCAGTGG   41100    T     A_ _
                                TGG AGGTGTGG AG GG
                                ||| ||||||| || ||
                                ACC TCCACACC TC CC
                                  _     CG A
GAM1677 LOC151429 3' TGGGGGTGTGGACACGC    41116    TA    AAGG
                                TGG GGTGTGG  GCGCGC
                                ||| ||||||| ||||||
                                ACC CCACACC  TGTGCG
                                  C_    _____
GAM1677 LOC157421 5' TGGTGGGGTGGAGGGCACA  41117    A T   A
                                TGGT GG GTGGA GGGCGCG
                                |||| || ||||| |||||||
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                                ACCA CC CACCT CCCGTGT
                                  C _    _
GAM1677  LOC253148 5'  TGGGAGGTGTGGGGGC      41118     T       AA
                                TGG AGGTGTGG  GGGC
                                ||| ||||||||  ||||
                                ACC TCCACACC  CCCG
                                  C       __
GAM1677  LOC253263 5'  TGGTAGGTTTGGAAGACCGGCG 41119        G     _______  CGCG
              CC                  GGTAGGT TGGAAG     GG    C
                                ||||||| ||||||     ||    |
                                CCATCCA ACCTTC     CC    G
                                    A     TGGIII  GCGC
GAM1677  LOC253502 3'  GGTGGGTGTGGGGGCAC     41092     A       AA
                                GGT GGTGTGG  GGGCGC
                                ||| |||||||  ||||||
                                CCA CCACACC  CCCGTG
                                  C      __
GAM1678  ANGPT2    3'  CAGTGCGCAGCCGTGACTTTCA 41122             TCTGCG
              G                   CAGTGCGTAGCCGT     TCAG
                                ||||||||||||||     ||||
                                GTCACGCGTCGGCA     AGTC
                                       CTGAA_
GAM1678  CDKN1C    5'  GTGGTGGACTCTTCTGCGTC   41123     C  A_  CG
                                GTG GT  GC  TTCTGCGTC
                                ||| ||  ||  |||||||||
                                CAC CA  TG  AAGACGCAG
                                  _  CC  AG
GAM1678  VNN1      3'  CAGTGCATGGCTGTTATCG    41124        A  C   CTG
                                CAGTGCGT GC GTT   CG
                                |||||||| || |||   ||
                                GTCACGTA CG CAA   GC
                                     C  A   TA_
GAM1678  FLJ13114  3'  AGTGCATAGCTGCTCAATGT   41125          C    TGC
                                AGTGCGTAGC GTTC   GT
                                |||||||||| ||||   ||
                                TCACGTATCG CGAG   CA
                                      A    TTA
GAM1678  LOC129433 3'  CAGTGCGTAGTGTTCTG     41126          CC
                                CAGTGCGTAG  GTTCTG
                                ||||||||||  ||||||
                                GTCACGCATC  CAAGAC
                                      A_
GAM1678  LOC196761 3'  GTGCTGCTGGCTGCGTCAG   41127     GTA  CGTT
                                GTGC   GC    CTGCGTCAG
                                ||||   ||    |||||||||
                                CACG   CG    GACGCAGTC
                                  A__  ACC_
GAM1678  LOC255299 5'  GTCGTAGCCAGTGGTGTCAG   41128    G       TTCTGC
                                GT CGTAGCCG     GTCAG
                                || ||||||||     |||||
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                                CA GCATCGGT     CAGTC
                                 _      CACCA_
GAM1678 LOC256784 5' GTGGTGGACTCTTCTGCGTC  41123    C A_ CG
                                GTG GT  GC  TTCTGCGTC
                                ||| ||  ||  |||||||||
                                CAC CA  TG  AAGACGCAG
                                  _ CC  AG
GAM1679 ABAT    5' GGATGCGCGCCCCGAGTTCCGG 41131    CAC    G_ TC   A
          C                      GG   GCGCGC  TG  TTCC GC
                                ||   ||||||  ||  |||| ||
                                CC   CGCGCG  GC  AAGG CG
                                 TA_     GG  TC   C
GAM1679 CDKN2A   3' AGGCATCGCGCACGTCCAG   41132      _      TGTCT
                                AGGCA CGCGCGCG    TCCAG
                                ||||| ||||||||     |||||
                                TCCGT GCGCGTGC    AGGTC
                                  A      _____
GAM1679 CDKN2B   3' AGGCATCGCGCACGTCCAG   41132      _      TGTCT
                                AGGCA CGCGCGCG    TCCAG
                                ||||| ||||||||     |||||
                                TCCGT GCGCGTGC    AGGTC
                                  A      _____
GAM1679 CSHL1    3' AGGTGGCTGCCGTCTTCCAGC  41133    CAC  GC  G
                                AGG   GC  GC TGTCTTCCAGC
                                |||   ||  || ||||||||||
                                TCC   CG  CG GCAGAAGGTCG
                                  AC_  A_  _
GAM1679 FLRT2    5' GGCGTATCACTGTGTCTTCTAG 41134    ACG_   GC      C
          C                      GGC    CGC  GTGTCTTC AGC
                                |||    |||  |||||||| |||
                                CCG    GTG  CACAGAAG TCG
                                  CATA   A_      A
GAM1679 G6PD     5' AGGTGCGCGCGCATCCCAGGCC 41135     CAC          ___
          AGC                     AGG   GCGCGCGTGTCTT   CCAGC
                                |||   ||||||||||||   |||||
                                TCC   CGCGCGCGTAGGG   GGTCG
                                  A__           TCC
GAM1679 ITPKB    3' GGGCGCGTGTGTGACCTTTAGC 41136    CAC    C    CTT ___
                                GG   GCGCG GTGT   CC   AGC
                                ||   ||||| ||||   ||   |||
                                CC   CGCGC CACA   GG   TCG
                                  ___     A    CT_  AAA
GAM1679 LDHB     5' AGCTGCGTGCGTCTCCTCCGGC 41137     AC   C    G     A
                                GGC  GCG GCGT TCTTCC GC
                                |||  ||| |||| |||||| ||
                                TCG  CGC CGCA AGGAGG CG
                                  A_   A    G     C
GAM1679 MUC4     3' GCACGCGCGCGTGCACAG    41138            CTTC
                                GCACGCGCGCGTGT    CAG
                                ||||||||||||||    |||
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                                CGTGCGCGCGCACG   GTC
                                       T___
GAM1679 MUC4    3' GCACGCGCGCGTGCACAG   41138          CTTC
                                GCACGCGCGCGTGT   CAG
                                ||||||||||||||  |||
                                CGTGCGCGCGCACG   GTC
                                       T___
GAM1679 PTPRN   3' GGCAGGCGTGCCCCTTCTGGC 41139    CGC  C G   CA
                                GGCA  GCG GT TCTTC  GC
                                ||||  ||| || |||||  ||
                                CCGT  CGC CG GGAAG  CG
                                  C__  A G   AC
GAM1679 SLC25A11 5' GGCGCGCGCACGCCCCTCCAGC 41140    A      G
                                GGC CGCGCGCGT TCTTCCAGC
                                ||| ||||||||| |||||||||
                                CCG GCGCGTGCG GGGAGGTCG
                                  C       _
GAM1679 SOST    5' GGCACGCCACCTTCCAG    41141       G  GTGT
                                GGCACGC CGC   CTTCCAG
                                ||||||| |||   |||||||
                                CCGTGCG GTG   GAAGGTC
                                   _  _____
GAM1679 SOX12   3' AGGCGCGTGCGTTGCCACCCGG 41142    AC  C  _  T  A
          C                      AGGC  GCG GCGT GTC TCC GC
                                ||||  ||| |||| ||| ||| ||
                                TCCG  CGC CGCA CGG GGG CG
                                  __  A   A  T  C
GAM1679 A2BP1   5' AGGCGCGCGCGTGGGTCCAGC  41143    AC      TCT
                                AGGC  GCGCGCGTG   TCCAGC
                                ||||  |||||||||   ||||||
                                TCCG  CGCGCGCAC   AGGTCG
                                  __       CC_
GAM1679 CLSTN1  5' GGAGCGCGCGCGGCGGACCCGG 41144   CA     T  CT_  A
          C                      GG  CGCGCGCG GT   TCC GC
                                ||  |||||||| ||   ||| ||
                                CC  GCGCGCGC CG   GGG CG
                                 TC       _ CCT   C
GAM1679 CNOT8   5' AGACGCGCGCGCGCGCCT   41145    A
                                AGGC CGCGCGCGTGTCT
                                |||| ||||||||||||
                                TCTG GCGCGCGCGCGGA
                                  C
GAM1679 DEPC-1  5' GGCGCGCCCGTGCAAACCC   41146    AC   G   CT_
                                GGC  GCGC CGTGT   TCC
                                |||  |||| |||||   |||
                                CCG  CGCG GCACG   GGG
                                  __   G    TTT
GAM1679 EIF3S9  3' AGGCATGCGGCGCCCTCC   41147     CGC  C
                                AGGCA   GCG GTGTCTTCC
                                |||||   ||| |||||||||
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                                TCCGT   CGC CGCGGGAGG
                                  A__  _
GAM1679 FEM-2    3' AGGCTGCGAGATCTTCCAG   41148     ACGC   CGT
                                AGGC   GCG   GTCTTCCAG
                                ||||   |||  |||||||||
                                TCCG   CGC   TAGAAGGTC
                                  A___  TC_
GAM1679 FEM1B    5' GGCACGTCCGCGACCCAG    41149      CG    TGTCT
                                GGCACG  CGCG    TCCAG
                                ||||||  ||||    |||||
                                CCGTGC  GCGC    GGGTC
                                   AG   T____
GAM1679 FLJ10008 3' GGCACGCTGCCCCTCCAG    41150       GC  GTG
                                GGCACGC  GC   TCTTCCAG
                                |||||||  ||   ||||||||
                                CCGTGCG  CG   GGGAGGTC
                                   A_  ___
GAM1679 FLJ12355 3' AGGCAAGCGCGCCTCTAG    41151     CGC     G   TCC
                                AGGCA   GCGCGT TCT   AG
                                |||||   |||||| |||   ||
                                TCCGT   CGCGCG AGA   TC
                                  T__     G   ___
GAM1679 FLJ13993 5' GGCACGTCCGCGCCTACTTCAG 41152       __    G  T    C
          C                      GGCACG  CGCGC TG CTTC AGC
                                ||||||  ||||| || |||| |||
                                CCGTGC  GCGCG AT GAAG TCG
                                   AG    G  _   _
GAM1679 FLJ20752 5' GCGCATGCGCGCTTCCAG    41153     __    T
                                GCGC  GCGTG CTTCCAG
                                ||||  ||||| |||||||
                                CGCG  CGCGC GAAGGTC
                                  TA    _
GAM1679 FLJ21087 5' GGCATGCACGTGCCCTCGGC   41154     CGC         CA
                                GGCA   GCGCGTGTCTTC  GC
                                ||||   ||||||||||||  ||
                                CCGT   CGTGCACGGGAG  CG
                                  A__          C_
GAM1679 FLJ21438 5' GCGCGCGTGGGGCGTCCAGC   41155         TCT__
                                GCGCGCGTG    TCCAGC
                                |||||||||    ||||||
                                CGCGCGCAC    AGGTCG
                                     CCCGC
GAM1679 KIAA0317 3' AGCATGCGGCATCTTCTGGC   41156     C   C  GT     CA
                                GGCA GCG GC  GTCTTC  GC
                                |||| ||| ||  ||||||  ||
                                TCGT CGC CG  TAGAAG  CG
                                  A  _  __     AC
GAM1679 KIAA0322 5' AGGGGCGCGCGCGGCTC     41157     CAC       T
                                AGG   GCGCGCGTG CTT
                                |||   ||||||||| |||
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                                TCC   CGCGCGCGC GAG
                                  C__       C
GAM1679 KIAA0769 5' AGCGCGCGCGTGTGTGAAAGGA 41158    A    C   CTTCC_
             GC                   GGC CGCGCG GTGT     AGC
                                ||| |||||| ||||     |||
                                TCG GCGCGC CACA     TCG
                                  C     A   CTTTCC
GAM1679 KIAA1054 3' GGCGCATGCGTGTGGTCCCAGC 41159    AC  C    C_
                                GGC  GCG GCGTGT  TTCCAGC
                                |||  ||| ||||||  |||||||
                                CCG  CGT CGCACA  AGGGTCG
                                  __  A     CC
GAM1679 KIAA1910 3' GGCACTGTCAGTTCTTCCAGC  41160     GCG  C  G
                                GGCAC   CG GT TCTTCCAGC
                                |||||   || || |||||||||
                                CCGTG   GT CA AGAAGGTCG
                                   ACA  _  _
GAM1679 MGC21945 5' GGCGCGCGCTCACGACTCCAGC 41161    A    G   T  T
                                GGC CGCGC CGTG CT CCAGC
                                ||| ||||| |||| || |||||
                                CCG GCGCG GTGC GA GGTCG
                                  C    A   T  _
GAM1679 MGC26778 3' AGGCACGTGTTACTATTTCCAG 41162       CGC_  G   C
                                AGGCACG   GC TGT TTCCAG
                                |||||||   || ||| ||||||
                                TCCGTGC   TG ATA AAGGTC
                                    ACAA  _   _
GAM1679 MGC2744  5' GGAAAAGCACTGTGTCTTCCAG 41163   CAC_   GC
             C                   GG   GCGC  GTGTCTTCCAGC
                                ||   ||||  ||||||||||||
                                CC   CGTG  CACAGAAGGTCG
                                 TTTT   A_
GAM1679 MMPL1    3' AGGCAGGTGTGCGTCCCCTGGC 41164     CGCGCGC      CA
                                AGGCA     GTGTCTTC  GC
                                |||||     ||||||||  ||
                                TCCGT     CGCAGGGG  CG
                                   CCACA__      AC
GAM1679 NIFU     5' GCACGCGTCCGCCTTCTGGC  41165        __     CA
                                GCGCGCGT  GTCTTC  GC
                                |||||||  ||||||  ||
                                CGTGCGCA  CGGAAG  CG
                                    GG     AC
GAM1679 NUDT3    5' GCGCGCGCGCCCCCGGC     41166          T  A
                                GCGCGCGTGTCT CC GC
                                |||||||||||| || ||
                                CGCGCGCGCGGG GG CG
                                       _  C
GAM1679 SPIB     3' AGGGCGCGCGCCAGC      41167     CAC      TGTCTT
                                AGG  GCGCGCG     CCAGC
                                |||  |||||||     |||||
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                                TCC   CGCGCGC     GGTCG
                                  ___     _______
GAM1679  LOC144266 5'  GGCACTGGTCAGTCTTCCAGC  41168      GCGCG  T
                                GGCAC     CG GTCTTCCAGC
                                |||||     || ||||||||||
                                CCGTG     GT CAGAAGGTCG
                                   ACCA_  _
GAM1679  LOC152282 5'  AGGTGGGCGGTCTCTTCCAGC  41169     CACGC   C  G
                                AGG     GCG GT TCTTCCAGC
                                |||     ||| || ||||||||||
                                TCC     CGC CA AGAAGGTCG
                                  ACC__   _  G
GAM1679  LOC153505 3'  AGGCGGCGCGCGCCCA      41170      AC       GTCTT
                                AGGC  GCGCGCGT    CCA
                                ||||  ||||||||     |||
                                TCCG  CGCGCGCG    GGT
                                  C_       ______
GAM1679  LOC158287 3'  AGGCATCTGCGCCCCTCCAGC  41171      CGC    GTG
                                AGGCA   GCGC   TCTTCCAGC
                                |||||   ||||   |||||||||
                                TCCGT   CGCG   GGGAGGTCG
                                   AGA    ___
GAM1679  LOC200269 3'  GGCCCGCGCGCCTCCAG     41172     A      GTGTC
                                GGC CGCGCGC     TTCCAG
                                ||| |||||||     ||||||
                                CCG GCGCGCG     GAGGTC
                                  G      ______
GAM1679  LOC201245 5'  GCGCGCGTGCAGGGAGCCCAG  41173          CT_____
                                GCGCGCGTGT      TCCAG
                                ||||||||||      |||||
                                CGCGCGCACG      GGGTC
                                     TCCCTC
GAM1679  LOC203668 5'  GGCGGGCGGGCTTCTTCCAGC  41174     AC   C  GTG
                                GGC  GCG GC   TCTTCCAGC
                                |||  ||| ||   |||||||||
                                CCG  CGC CG   AGAAGGTCG
                                  CC   C  A__
GAM1679  LOC219743 3'  AGGCACGGGCCTGCCTTCCAGC 41175        CGC  G
                                AGGCACG   GC TGTCTTCCAGC
                                |||||||   || ||||||||||
                                TCCGTGC   CG ACGGAAGGTCG
                                   C__  G
GAM1679  LOC255981 5'  GGCACGCGCGCCGTCCGCAGC  41176          G     TC
                                GGCACGCGCGC TGTCT  CAGC
                                |||||||||| |||||  ||||
                                CCGTGCGCGCG GCAGG  GTCG
                                      _    C_
GAM1679  LOC51093  5'  GGGTGTGCGCGCGCCGACCTCT 41177    CAC_       _ T    CA
            GGC                   GG    GCGCGCGT G CTTC  GC
                                ||    |||||||| | ||||  ||
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                                CC   CGCGCGCG C GGAG  CG
                                 CACA      G T   AC
GAM1679 LOC51219 5' AGGTGCGTGCCTGTAATCCCAG 41178    CAC  C  G  C_
            C                    AGG   GCG GC TGT  TTCCAGC
                                |||   ||| || |||  |||||||
                                TCC   CGC CG ACA  AGGGTCG
                                 A__   A  G   TT
GAM1679 LOC58509 5' AGCACGTGCGCGTCCA     41179       C    TGTCT
                                GGCACG GCGCG    TCCA
                                ||||||| |||||    ||||
                                TCGTGC CGCGC    AGGT
                                   A    _____
GAM1679 LOC90625 3' AGGGGGTACGTGTCTTCCAGC  41180    CACGCGC
                                AGG      GCGTGTCTTCCAGC
                                |||      ||||||||||||||
                                TCC      TGCACAGAAGGTCG
                                 CCCA___
GAM1680 CLECSF12 3' TAAAATTGCTCTGACTGT    41183         GT_
                                TAAAATTGTTT   CTGT
                                ||||||||||   ||||
                                ATTTTAACGAG   GACA
                                      ACT
GAM1680 MGC5149  3' AAATTGTTCTAAGTCTGT    41184        ___
                                AAATTGTTT   GTCTGT
                                |||||||||   ||||||
                                TTTAACAAG   CAGACA
                                     ATT
GAM1681 CACNB2   3' TTTTGGGGATGCTGTTAGT   41187       _  CCG  CC
                                TTTTGGGG TGC   GT  AGT
                                |||||||| |||   ||  |||
                                AAAACCCC ACG   CA  TCA
                                     T   A__  A_
GAM1681 GCK      5' TTTGGGGTTTGAGGTTCAGTC  41188       GCCC   C
                                TTTGGGGT   GGT CAGTC
                                ||||||||   ||| |||||
                                AAACCCCA   CCA GTCAG
                                     AACT   A
GAM1681 FLJ22794 5' TATTTTGGGGCATGGTCTGGTC 41189          CCC    CA
                                TATTTTGGGGTG   GGTC  GTC
                                ||||||||||||   ||||  |||
                                ATAAAACCCCGT   CCAG  CAG
                                      A__    AC
GAM1681 Spir-1   3' TATTTTGGGGGTGTAGT     41190         _ CCC
                                TATTTTGGGG TG   GGT
                                |||||||||| ||   |||
                                ATAAAACCCC AC   TCA
                                      C  A__
GAM1681 LOC150605 5' TATTTTGGGGAGACTGGT    41191         T_  CC
                                TATTTTGGGG  GC  GGT
                                |||||||||  ||  |||
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                                ATAAAACCCC  TG  CCA
                                     TC  A_
GAM1681  LOC158130 3'  TATTCTGGGGTGATCCAGT   41192          CCCG
                                TATTTTGGGGTG   GTCCAGT
                                ||||||||||||   |||||||
                                ATAAGACCCCAC   TAGGTCA
                                      ____
GAM1682  ACTN2    5'  GGCGGGCGGCGGGCGGCGGGC  41195       A  TCT  T   A
                                GGCGGGC GC   GC GGC GGC
                                ||||||| ||   || ||| |||
                                CCGCCCG CG   CG CCG CCG
                                    C  CC_ _   C
GAM1682  ALX3     3'  GGTGGGCAGCTCATTCTGCAGG 41196    C       TG_   G
                                GG GGGCAGCTC   CTG CAGG
                                || |||||||||   ||| ||||
                                CC CCCGTCGAG   GAC GTCC
                                 A       TAA  _
GAM1682  AP2A1    5'  GGCGGGCGGGCGGGCTGGCAGG 41197       A_  TCT
              C                  GGCGGGC  GC   GCTGGCAGGC
                                 |||||||  ||   ||||||||||
                                 CCGCCCG  CG   CGACCGTCCG
                                     CC  CC_
GAM1682  AP2A1    5'  GGCGGGCGGGCGGGCTGGCAGG 41197       A_  TCT
              C                  GGCGGGC  GC   GCTGGCAGGC
                                 |||||||  ||   ||||||||||
                                 CCGCCCG  CG   CGACCGTCCG
                                     CC  CC_
GAM1682  AP2A1    5'  TGGCGGGCGGGCGGGCGGG   41198       AGCTCT  T   A
                                 TGGCGGGC     GC GGC GG
                                 ||||||||     || ||| ||
                                 ACCGCCCG     CG CCG CC
                                      CC_____  C   C
GAM1682  AP2A1    5'  TGGCGGGCGGGCGGGCGGG   41198       AGCTCT  T   A
                                 TGGCGGGC     GC GGC GG
                                 ||||||||     || ||| ||
                                 ACCGCCCG     CG CCG CC
                                      CC_____  C   C
GAM1682  BGN      5'  GGCGGGCTGGGGTGGTGGGC  41199       AGCTC  C__   CA
                                 GGCGGGC    TG   TGG  GGC
                                 |||||||    ||   |||  |||
                                 CCGCCCG    AC   ACC  CCG
                                      ______  CCC   AC
GAM1682  CD7      3'  TGGGGGCCTGCTGGTGGG    41200     C   AGCT      CA
                                 TGG GGGC   CTGCTGG  GG
                                 ||| ||||   |||||||  ||
                                 ACC CCCG   GACGACC  CC
                                   _   _____      AC
GAM1682  CRHR1    5'  GGCGGGCGGCTGCGGGC     41201        A   CT  T
                                 GGCGGGC GCT  GC GGC
                                 ||||||| |||  || |||
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                                CCGCCCG CGA  CG CCG
                                    C  __  C
GAM1682 GFAP    3' GGTGGGTGCCGTCTGGCAGGC 41202    C  CA  CTG
                                GG GGG  GCT  CTGGCAGGC
                                || |||  |||  |||||||||
                                CC CCC  CGG  GACCGTCCG
                                 A  A_  CA_
GAM1682 NLGN2   5' TGGCGGGCAGCGCCCCGTGCAG 41203         T  G  _
            G                    TGGCGGGCAGC CT CTG GCAGG
                                ||||||||||| || ||| |||||
                                ACCGCCCGTCG GG GGC CGTCC
                                      C  _  A
GAM1682 VARS2   5' GGTGGGCGGCTCTCCAGG   41204   C   A   G TGG
                                GG GGGC GCTCT C  CAGG
                                || |||| ||||| |  ||||
                                CC CCCG CGAGA G  GTCC
                                 A  C   _ ___
GAM1682 VASP    5' GGCGGGCGGCTCGCCCACGGGC 41205      A  T  G  A
                                GGCGGGC GCTC GCT GC GGC
                                ||||||| |||| ||| || |||
                                CCGCCCG CGAG CGG TG CCG
                                    C  _  G  C
GAM1682 WBSCR5  5' TGGCGGGCGGGCAGGGCGGGC 41206      A_  TCT  T
                                TGGCGGGC  GC  GC GGC
                                ||||||||  ||  || |||
                                ACCGCCCG  CG  CG CCG
                                     CC  TCC  C
GAM1682 WBSCR5  5' TGGCGGGCGGGCAGGGCGGGC 41206      A_  TCT  T
                                TGGCGGGC  GC  GC GGC
                                ||||||||  ||  || |||
                                ACCGCCCG  CG  CG CCG
                                     CC  TCC  C
GAM1682 WBSCR5  5' TGGCGGGCGGGCAGGGCGGGC 41206      A_  TCT  T
                                TGGCGGGC  GC  GC GGC
                                ||||||||  ||  || |||
                                ACCGCCCG  CG  CG CCG
                                     CC  TCC  C
GAM1682 ZFP103  5' TGGCGGGCGGCGCCTCTCAGGC 41207      A  TCT  GG_
                                TGGCGGGC GC  GCT  CAGGC
                                |||||||| ||  |||  |||||
                                ACCGCCCG CG  CGG  GTCCG
                                     C  ___  AGA
GAM1682 ANP32B  5' TGGCGGGCGGCGTGCGGGCAGG 41208      A  TC  T
            C                    TGGCGGGC GC  TGC GGCAGGC
                                |||||||| ||  ||| |||||||
                                ACCGCCCG CG  ACG CCGTCCG
                                     C  C_  C
GAM1682 AP3D1   3' TGGTGGGGGCTCTGCCTGTGAG 41209    C  CA    _ GC
            G                    TGG GGG  GCTCTGC TG  AGG
                                ||| |||  ||||||| ||  |||
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                                ACC CCC  CGAGACG AC  TCC
                                  A  C_     G  AC
GAM1682 CABP4    3'  GGTGGGCAGCTGAGAGCAGG  41210    C      CTGCT
                                GG GGGCAGCT    GGCAGG
                                || ||||||||    ||||||
                                CC CCCGTCGA    TCGTCC
                                 A      CTC__
GAM1682 CARM1    3'  TGGCAGGCAGGGCTGGCAGGC 41211         CTCT
                                TGGCGGGCAG   GCTGGCAGGC
                                ||||||||||   ||||||||||
                                ACCGTCCGTC   CGACCGTCCG
                                      C___
GAM1682 cerk     5'  GGCGGGCGGCGGGCGGCGGGC 41195       A  TCT  T   A
                                GGCGGGC GC   GC GGC GGC
                                ||||||| ||   || ||| |||
                                CCGCCCG CG   CG CCG CCG
                                    C  CC_  _   C
GAM1682 CNOT8    5'  TGGCGGGCTGACGAGCTGGCGG 41212        A_  TCT     A
             GC                   TGGCGGGC  GC   GCTGGC GGC
                                ||||||||  ||   |||||| |||
                                ACCGCCCG  TG   CGACCG CCG
                                     AC  CT_     C
GAM1682 DKFZP434J154 3'  TGGTGGGCAGCCCCTGGGC   41213     C        GCT
                                TGG GGGCAGCTCT   GGC
                                ||| ||||||||||   |||
                                ACC CCCGTCGGGG   CCG
                                  A         AC_
GAM1682 ECE2     3'  TGGTGGGGGCTCTGCTGGAGGC 41214     C   CA        C
                                TGG GGG  GCTCTGCTGG AGGC
                                ||| |||  |||||||||| ||||
                                ACC CCC  CGAGACGACC TCCG
                                  A  C_        _
GAM1682 FAF1     5'  TGGCGGGCGAGCCGGCGGG   41215        AGCTCT     A
                                TGGCGGGC     GCTGGC GG
                                ||||||||     |||||| ||
                                ACCGCCCG     CGGCCG CC
                                     CT_____     C
GAM1682 FAM3B    5'  TGGCGGCAGCTCCCAG      41216       G      GCTGG
                                TGGCGG CAGCTCT     CAG
                                |||||| |||||||     |||
                                ACCGCC GTCGAGG     GTC
                                   _      ______
GAM1682 FLJ10482 5'  TGGCGGCAGCTCTGCCG     41217       G
                                TGGCGG CAGCTCTGCTG
                                |||||| ||||||||||
                                ACCGCC GTCGAGACGGC
                                   _
GAM1682 FLJ22693 5'  TGGCGGGCGGCTCTCGCAGG   41218        A    GCTG
                                TGGCGGGC GCTCT    GCAGG
                                |||||||| |||||    |||||
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                                ACCGCCCG CGAGA    CGTCC
                                    C     G___
GAM1682  FLJ23112  5'  TGGCGGGCAGCACTGG      41219          TCT
                                TGGCGGGCAGC   GCTGG
                                ||||||||||   |||||
                                ACCGCCCGTCG   TGACC
                                     ___
GAM1682  GDF10     3'  TGGCGGACAGCTCTCTCTGGGC 41220            G_   _
                                TGGCGGGCAGCTCT  CTGG C
                                ||||||||||||||  |||| |
                                ACCGCCTGTCGAGA  GACC G
                                      GA   C
GAM1682  HN1L      3'  TGGCAGGCGGCTCCTGCAGGC  41221         A    GCTG
                                TGGCGGGC GCTCT    GCAGGC
                                |||||||| |||||    ||||||
                                ACCGTCCG CGAGG    CGTCCG
                                    C     A___
GAM1682  HSPB7     3'  TAGCGAGGCTTTGCTGGCAGGC 41222        CA   C
                                TGGCGGG  GCT TGCTGGCAGGC
                                |||||||  ||| ||||||||||
                                ATCGCTC  CGA ACGACCGTCCG
                                    __   A
GAM1682  HUMZD58C02 3'  TGGCGGGCGGCGCTGCGAAGC  41223         A  T    T_
                                TGGCGGGC GC CTGC  GGC
                                |||||||| || ||||  |||
                                ACCGCCCG CG GACG  TCG
                                    C  C    CT
GAM1682  KIAA0350  3'  TGGTGGGCACATCTGCTGGCAG 41224     C     GC
            G                    TGG GGGCA  TCTGCTGGCAGG
                                ||| |||||  ||||||||||||
                                ACC CCCGT  AGACGACCGTCC
                                  A    GT
GAM1682  KIAA1100  3'  TGGCGGGCGGGCGGGCAGG    41225        AGCTCT  T
                                TGGCGGGC     GC GGCAGG
                                ||||||||     || ||||||
                                ACCGCCCG     CG CCGTCC
                                    CC_____  C
GAM1682  KIAA1909  5'  TGGTGGGAGGTGTGGCAGG    41226     C   C  CTC  C
                                TGG GGG AG   TG TGGCAGG
                                ||| ||| ||   || |||||||
                                ACC CCC TC   AC ACCGTCC
                                  A   _ C__  _
GAM1682  MAPKAPK5  5'  CGGCGGGCGGCTCTAGGC    41227         A     CT
                                TGGCGGGC GCTCTG  GGC
                                |||||||| ||||||  |||
                                GCCGCCCG CGAGAT  CCG
                                    C     __
GAM1682  MAPKAPK5  5'  CGGCGGGCGGCTCTAGGC    41227         A     CT
                                TGGCGGGC GCTCTG  GGC
                                |||||||| ||||||  |||
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                                GCCGCCCG CGAGAT  CCG
                                    C     __
GAM1682 MGC12921 3' TGGGGGCATTTTGGCAGG    41228     C    GCTCTGC
                                TGG GGGCA      TGGCAGG
                                ||| |||||      |||||||
                                ACC CCCGT      ACCGTCC
                                  _    AAA____
GAM1682 MGC2594  3' TGGCGGGCAGGCGGGTGGG   41229          CTCT  T  CA
                                TGGCGGGCAG   GC GG  GG
                                ||||||||||   || ||  ||
                                ACCGCCCGTC   CG CC  CC
                                      ____ C  AC
GAM1682 MGC3413  5' TGGCGGGCGACGGGCGGCGGGC 41230         A  TCT  T   A
                                TGGCGGGC GC   GC GGC GGC
                                |||||||| ||   || ||| |||
                                ACCGCCCG TG   CG CCG CCG
                                    C  CC_ _   C
GAM1682 PPIL2    3' TGGCTGGCAGCAGAGGGCAGGC 41231      G     TCTGCT
                                TGGC GGCAGC     GGCAGGC
                                |||| ||||||     |||||||
                                ACCG CCGTCG     CCGTCCG
                                  A     TCTC__
GAM1682 RPH3A    3' GGTGGGCAGCTAGAGCAGGC   41232    C       CTGCT
                                GG GGGCAGCT    GGCAGGC
                                || ||||||||    |||||||
                                CC CCCGTCGA    TCGTCCG
                                 A       TC___
GAM1682 SIMRP7   3' TGGGGGCAGCTTTGGGC     41233     C       C  CT
                                TGG GGGCAGCT TG  GGC
                                ||| |||||||| ||  |||
                                ACC CCCGTCGA AC  CCG
                                  _       A  __
GAM1682 SZF1     5' GGGCAGCTTCCGTGTGGGC    41234        _  C  GCA
                                GGGCAGCT CTG TG   GGC
                                |||||||| ||| ||   |||
                                CCCGTCGA GGC AC   CCG
                                    A   _  AC_
GAM1682 YAP      5' TGGCGGGCAGTCTTGCAGG    41235         C   GCTG
                                TGGCGGGCAG TCT    GCAGG
                                |||||||||| |||    |||||
                                ACCGCCCGTC AGA    CGTCC
                                      _   A___
GAM1682 LOC113146 3' TGGCGGATGCTGGCAG      41236        CAGCTC
                                TGGCGGG     TGCTGGCAG
                                |||||||     |||||||||
                                ACCGCCT     ACGACCGTC
                                      _______
GAM1682 LOC129198 3' TGGTGGGCAGCTCGCAGG    41237     C       TGCTG
                                TGG GGGCAGCTC    GCAGG
                                ||| |||||||||    |||||
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                                ACC CCCGTCGAG    CGTCC
                                  A      _____
GAM1682  LOC143392 3'  TGGCTGGCACTGGCAG     41238     G   AGCTCT
                                TGGC GGC     GCTGGCAG
                                |||| |||     ||||||||
                                ACCG CCG     TGACCGTC
                                  A  _______
GAM1682  LOC145801 5'  TGGCGGGCGGCGTGGGGGCAGG 41239        A  TC  CT
              C                  TGGCGGGC GC  TG  GGCAGGC
                                |||||||| ||  ||  |||||||
                                ACCGCCCG CG  AC  CCGTCCG
                                     C  C_  CC
GAM1682  LOC151174 5'  TGGTGGGCAGCCTGTGAGATGG 41240     C      T   C____
              C                  TGG GGGCAGC CTG     TGGC
                                ||| ||||||| |||     ||||
                                ACC CCCGTCG GAC     ACCG
                                  A      _   ACTCT
GAM1682  LOC196759 3'  GGTGGGCAGCTCCAGGTGCCTG 41241    C       T________   GGCA
              CA                   G GGGCAGCTC       GCT    G
                                | |||||||||       |||    |
                                C CCCGTCGAG       CGG    T
                                 A        GTCCAIII   ACGG
GAM1682  LOC202404 5'  TGGCCGGTGGTTCCTAGCAGG  41242      G  CAGC  TG
                                TGGC GG    TC  CTGGCAGG
                                |||| ||    ||  ||||||||
                                ACCG CC    AG  GATCGTCC
                                  G  ACCA  __
GAM1682  LOC222493 5'  TGGCGGGCGGCTCGGCAGG    41243        A    TGCT
                                TGGCGGGC GCTC    GGCAGG
                                |||||||| ||||    ||||||
                                ACCGCCCG CGAG    CCGTCC
                                     C    _____
GAM1682  LOC253687 3'  TGGCGGGCACCTCTGTGC     41244         G     CTG
                                TGGCGGGCA CTCTG   GC
                                ||||||||| |||||   ||
                                ACCGCCCGT GAGAC   CG
                                      G     A__
GAM1682  LOC254266 3'  TGGCAGGCAGTTCTGGG     41245          C    CT
                                TGGCGGGCAG TCTG  GG
                                |||||||||| ||||  ||
                                ACCGTCCGTC AGAC  CC
                                      A    __
GAM1682  LOC255535 5'  GGTGGGCATGGGCTTGGCAGGC 41246     C     GCTCT  _
                                GG GGGCA     GCT GGCAGGC
                                || |||||     ||| |||||||
                                CC CCCGT     CGA CCGTCCG
                                 A     ACC__   A
GAM1682  LOC58525  5'  TGGGGGCAGCCCAAGGTGGGC  41247     C       TGCT  CA
                                TGG GGGCAGCTC    GG  GGC
                                ||| |||||||||    ||  |||
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                                ACC CCCGTCGGG   CC  CCG
                                  _       TT__  AC
GAM1682 LOC91179 3' TGGCGGGCGGCGCTGCGAAGC 41223       A T   T_
                                TGGCGGGC GC CTGC  GGC
                                |||||||| || ||||  |||
                                ACCGCCCG CG GACG  TCG
                                     C  C    CT
GAM1683 ABCG2    3' TTCATGTTTAATTCAGTTT   41250      TA
                                TTCAT  TTTAATTTAGTTT
                                |||||  ||||||||||||
                                AAGTA  AAATTAAGTCAAA
                                   C_
GAM1683 TARDBP   3' ATTATTTAAATCAGTTTTATT 41251        T
                                ATTATTTAA TTAGTTTTATT
                                ||||||||| ||||||||||
                                TAATAAATT AGTCAAAATAA
                                      T
GAM1683 FJX1     3' TTCATTATTTGACTTAGT    41252         A
                                TTCATTATTT ATTTAGT
                                |||||||||| |||||||
                                AAGTAATAAA TGAATCA
                                      C
GAM1683 FLJ10287 3' TTCATTATCTAATTTCTATTTT 41253           A_
                   ATT                  TTCATTATTTAATTT  GTTTTATT
                                |||||||||||||||  ||||||||
                                AAGTAATAGATTAAA  TAAAATAA
                                        GA
GAM1683 LOC203365 3' TTCAGTACAACCTTAGTTTTAT 41254     T  TTAA
                   T                   TTCA TAT    TTTAGTTTTATT
                                |||| |||    ||||||||||||
                                AAGT ATG    GAATCAAAATAA
                                  C   TTG_
GAM1684 DSP      3' TAGAATGTCCTATCACT     41257        AA  C
                                TAGAATGTC  GTC ACT
                                |||||||||  ||| |||
                                ATCTTACAG  TAG TGA
                                     GA   _
GAM1684 FPRL1    3' TAAAATGCAAAGTCCACT    41258        C
                                TAGAATGT AAGTCCACT
                                |||||||| |||||||||
                                ATTTTACG TTCAGGTGA
                                      T
GAM1684 GNAS     3' CAGGATGTAGTCCACT      41259     A   CA
                                TAG ATGT  AGTCCACT
                                ||| ||||  ||||||||
                                GTC TACA  TCAGGTGA
                                  C   __
GAM1684 HIP2     3' TAGGTGTCAAATTCACT     41260     AA      C
                                TAG  TGTCAAGT CACT
                                |||  |||||||| ||||
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                                ATC  ACAGTTTA GTGA
                                  C_       A
GAM1684  HMMR     3'  TAAAATGTCAAAAGACACT   41261          TC_
                                TAGAATGTCAAG   CACT
                                ||||||||||||  ||||
                                ATTTTACAGTTT   GTGA
                                       TCT
GAM1684  HMMR     3'  TAAAATGTCAAAAGACACT   41261          TC_
                                TAGAATGTCAAG   CACT
                                ||||||||||||  ||||
                                ATTTTACAGTTT   GTGA
                                       TCT
GAM1684  KCNJ15   3'  TACAATTCAGTCCACT     41262    G   G   A
                                TA AAT TCA GTCCACT
                                || ||| ||| |||||||
                                AT TTA AGT CAGGTGA
                                 G   _   _
GAM1684  MADH5    3'  TAAAACAAGTCCACT      41263      TGT
                                TAGAA   CAAGTCCACT
                                |||||   ||||||||||
                                ATTTT   GTTCAGGTGA
                                  ____
GAM1684  PTGFRN   3'  TAGAACGTCCCTCTGTCACT  41264        AA___   C
                                TAGAATGTC    GTC ACT
                                |||||||||    ||| |||
                                ATCTTGCAG    CAG TGA
                                     GGAGA  _
GAM1684  PTPRG    3'  TAGAATGCAACCACT      41265       T   GT
                                TAGAATG CAA  CCACT
                                |||||||  |||  |||||
                                ATCTTAC GTT  GGTGA
                                   _  ___
GAM1684  SLC24A1  3'  TAGAATGTCTAATCCCT    41266        A    A
                                TAGAATGTC AGTCC CT
                                ||||||||| ||||| ||
                                ATCTTACAG TTAGG GA
                                     A    _
GAM1684  SNX2     3'  CAGAATGTCATGCCACAGTCCA 41267        _______      III
            CTA                   AGAATGTCA     AGTCCACT   A
                                |||||||||     ||||||||  |
                                TCTTACAGT     TCAGGTGA   T
                                     ACGGTG       III
GAM1684  SOCS5    3'  TAAAATGTAAGCCACT      41268        C   T
                                TAGAATGT AAG CCACT
                                ||||||||  ||| |||||
                                ATTTTACA TTC GGTGA
                                   _  _
GAM1684  ST7      3'  TAGAATATCTTCATCCACT   41269        AA_
                                TAGAATGTC   GTCCACT
                                |||||||||   |||||||
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                                ATCTTATAG   TAGGTGA
                                     AAG
GAM1684  TFG      3'  TAGAAAGTCAAGTCAATCACT  41270      T      ___
                                TAGAA GTCAAGTC   CACT
                                ||||| ||||||||   ||||
                                ATCTT CAGTTCAG   GTGA
                                   T       TTA
GAM1684  TIMM23   3'  TAAAATGTCAGAGGTACACT   41271         A__  C
                                TAGAATGTCA   GT CACT
                                ||||||||||   || ||||
                                ATTTTACAGT   CA GTGA
                                      CTC  T
GAM1684  C20orf164 3'  TAGTATGTCCTGCCCACT    41272     A    AA
                                TAG ATGTC  GTCCACT
                                ||| |||||  |||||||
                                ATC TACAG  CGGGTGA
                                  A    GA
GAM1684  DIAPH3   5'  GAATGTCAAGGACCCACT    41273         __
                                GAATGTCAAG  TCCACT
                                ||||||||||  ||||||
                                CTTACAGTTC  GGGTGA
                                      CT
GAM1684  DKFZp434D177 3'  TAGAATGTCTGGCAGATCACT  41274         A___  TC
                                TAGAATGTC   AG  CACT
                                |||||||||   ||  ||||
                                ATCTTACAG   TC  GTGA
                                      ACCG  TA
GAM1684  DKFZp761K1423 5'  CAGAGCCAGTCCACT      41275     AT   A
                                TAGA  GTCA GTCCACT
                                ||||  |||| |||||||
                                GTCT  CGGT CAGGTGA
                                   __   _
GAM1684  FLJ20727  5'  AGAATATCACTGTCCACT    41276         A_
                                AGAATGTCA  GTCCACT
                                |||||||||  |||||||
                                TCTTATAGT  CAGGTGA
                                      GA
GAM1684  FLJ22029  3'  CAAAATGAAGTCCACT      41277       TC
                                TAGAATG  AAGTCCACT
                                |||||||  |||||||||
                                GTTTTAC  TTCAGGTGA
                                   __
GAM1684  FLJ22969  3'  TAGAATGAGTCCACT       41278       TCA
                                TAGAATG   AGTCCACT
                                |||||||   ||||||||
                                ATCTTAC   TCAGGTGA
                                   ___
GAM1684  H2AV     3'  AAATGTCAAAGGTCTACT    41279         __  C
                                GAATGTCAA  GTC ACT
                                |||||||||  ||| |||
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                                TTTACAGTT  CAG TGA
                                     TC   A
GAM1684 HRI      3'  TAAAAGTTAAGTCCACT     41280      T  C
                                TAGAA GT AAGTCCACT
                                |||||| || |||||||||
                                ATTTT CA TTCAGGTGA
                                   _  A
GAM1684 KIAA0436 3'  CAGAAGTCTGAGTCCACT    41281      T   A_
                                TAGAA GTC  AGTCCACT
                                ||||| |||  ||||||||
                                GTCTT CAG  TCAGGTGA
                                   _   AC
GAM1684 LZIC     3'  TAAAAATCAAGTCCACT     41282      T
                                TAGAA GTCAAGTCCACT
                                ||||| ||||||||||||
                                ATTTT TAGTTCAGGTGA

                                   _
GAM1684 PLU-1    3'  CAGAATGTCTTCTCCACT    41283        AAG
                                TAGAATGTC   TCCACT
                                |||||||||   ||||||
                                GTCTTACAG   AGGTGA
                                     AAG
GAM1684 PLU-1    3'  CAGAATGTCTTCTCCACT    41283        AAG
                                TAGAATGTC   TCCACT
                                |||||||||   ||||||
                                GTCTTACAG   AGGTGA
                                     AAG
GAM1684 PSMD10   3'  TAAAATGTGGTCCACT     41284        CAA
                                TAGAATGT   GTCCACT
                                ||||||||   |||||||
                                ATTTTACA   CAGGTGA
                                     C__
GAM1684 STRIN    3'  GAATGTCAGCAAATCCACT   41285         ___
                                GAATGTCA   AGTCCACT
                                ||||||||   ||||||||
                                CTTACAGT   TTAGGTGA
                                     CGT
GAM1684 VEZATIN  3'  TAAAATGTGTCCACT      41286        CAA
                                TAGAATGT   GTCCACT
                                |||||||   |||||||
                                ATTTTACA   CAGGTGA
                                     ___
GAM1684 LOC145601 3'  AGAATGTCAAAAGCAGCACT   41287          TC___
                                AGAATGTCAAG    CACT
                                ||||||||||    ||||
                                TCTTACAGTTT    GTGA
                                      TCGTC
GAM1684 LOC145900 5'  CAGAATGCCACCACT      41288          AGT
                                TAGAATGTCA   CCACT
                                |||||||||   |||||
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                                GTCTTACGGT   GGTGA
                                      ___
GAM1684  LOC148918 5'  CAGGACATCAAGGTCCACT   41289     A      _
                                TAG ATGTCAAG TCCACT
                                ||| |||||||| ||||||
                                GTC TGTAGTTC AGGTGA
                                  C       C
GAM1684  LOC152059 5'  CAGATGGCAGAGTCCACT    41290     A  T  _
                                TAGA TG CA AGTCCACT
                                |||| || || ||||||||
                                GTCT AC GT TCAGGTGA
                                  _ C  C
GAM1684  LOC152215 3'  CAGCATACAAGTCCACT     41291     A   T
                                TAG ATG CAAGTCCACT
                                ||| ||| ||||||||||
                                GTC TAT GTTCAGGTGA
                                  G  _
GAM1684  LOC152756 3'  TAGAATATCAAAAGTACT    41292           TCC
                                TAGAATGTCAAG   ACT
                                ||||||||||||   |||
                                ATCTTATAGTTT   TGA
                                       TCA
GAM1684  LOC220020 5'  TAGAATGCCTTTCCACT     41293         AAG
                                TAGAATGTC   TCCACT
                                |||||||||   ||||||
                                ATCTTACGG   AGGTGA
                                     AA_
GAM1684  LOC221935 3'  TAGAATATTTCCCCCTCCACT  41294        __  AAG_
                                TAGAATG  TC    TCCACT
                                |||||||  ||    ||||||
                                ATCTTAT  AG    AGGTGA
                                    AA  GGGG
GAM1684  LOC254936 5'  CAGAATGCCACCACT       41288         AGT
                                TAGAATGTCA   CCACT
                                ||||||||||   |||||
                                GTCTTACGGT   GGTGA
                                      ___
GAM1685  AFG3L2    3'  GATGGTGTAGAGCAAGAAG    41297     T  _   CTGAA
                                GATG TG AGA     GCAAGAAG
                                |||| || |||     ||||||||
                                CTAC AC TCT     CGTTCTTC
                                  C  A  _____
GAM1685  ANKTM1    3'  TGTTGGGGACAGCAAGAAG    41298      A_   TGA
                                TGTTG  GAC   AGCAAGAAG
                                |||||  |||   |||||||||
                                ACAAC  CTG   TCGTTCTTC
                                  CC   ___
GAM1685  CDKN2C    3'  TGTTGAGATTGGCAAAA      41299        C  AA
                                TGTTGAGA TG  GCAAGA
                                ||||||| ||  ||||||
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                                ACAACTCT AC  CGTTTT
                                    A  __
GAM1685  CDKN2C   3'  TGTTGAGATTGGCAAAA     41299        C  AA
                                TGTTGAGA TG  GCAAGA
                                |||||||| ||  ||||||
                                ACAACTCT AC  CGTTTT
                                    A  __
GAM1685  CYP3A4   3'  TGTTGAGGATGGAATGCAAGA  41300       ACT_  _
                                TGTTGAG   GAA GCAAGA
                                |||||||   ||| ||||||
                                ACAACTC   CTT CGTTCT
                                   CTAC   A
GAM1685  FMR2     3'  GATGTGGGATTTCAAGAAG   41301      T A  CTGAAG
                                GATGT G GA     CAAGAAG
                                ||||| | ||     |||||||
                                CTACA C CT     GTTCTTC
                                  _ C  AAA___
GAM1685  FUT6     5'  ATGTTGAGGAACTGCAGGAGGA 41302        __  GAA   A  A
                                ATGTTGAG  ACT   GCA GA GA
                                ||||||||  |||   ||| || ||
                                TACAACTC  TGA   CGT CT CT
                                    CT   ___   C  C
GAM1685  HIP2     3'  GATGTTGGTGCTCCTCAAGAAG 41303       AGA  GAAG
            A                    GATGTTG   CT    CAAGAAGA
                                |||||||   ||   ||||||||
                                CTACAAC   GA    GTTCTTCT
                                    CAC  GGA_
GAM1685  PIK3CD   3'  GAGGCTGAGGCAAGAAGA    41304     A   A
                                GAG CTGA GCAAGAAGA
                                ||| |||| |||||||||
                                CTC GACT CGTTCTTCT
                                  C   C
GAM1685  PTPN7    3'  GATGTTGAGACTTGGAGATCAG 41305          GA_  CA_
                                GATGTTGAGACT   AG   AG
                                ||||||||||||   ||   ||
                                CTACAACTCTGA   TC   TC
                                       ACC  TAG
GAM1685  PTPN7    3'  GATGTTGAGACTTGGAGATCAG 41305          GA_  CA_
                                GATGTTGAGACT   AG   AG
                                ||||||||||||   ||   ||
                                CTACAACTCTGA   TC   TC
                                       ACC  TAG
GAM1685  PTPN7    3'  GATGTTGAGACTTGGAGATCAG 41305          GA_  CA_
                                GATGTTGAGACT   AG   AG
                                ||||||||||||   ||   ||
                                CTACAACTCTGA   TC   TC
                                       ACC  TAG
GAM1685  SAS      3'  GAGACTGAGGCAGGAGGA    41306        A   A  A
                                GAGACTGA GCA GA GA
                                |||||||| ||| || ||
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                                CTCTGACT CGT CT CT
                                     C   C  C
GAM1685 TNFRSF9  3' GAGACTGAGGCAGGAGGA    41306        A   A  A
                                GAGACTGA GCA GA GA
                                |||||||| ||| || ||
                                CTCTGACT CGT CT CT
                                     C   C  C
GAM1685 UMPS     3' TGAGAGACTGAGGCAGGAGGA  41307    TT       A   A  A
                                TG  GAGACTGA GCA GA GA
                                ||  |||||||| ||| || ||
                                AC  CTCTGACT CGT CT CT
                                 T_      C   C  C
GAM1685 CGI-96   3' TGTGGAGGCAAGAAGCAGGAAG 41308     T   ACT_     A
                                TGT GAG    GAAGCA GAAG
                                ||| |||    |||||| ||||
                                ACA CTC    CTTCGT CTTC
                                  C   CGTT     C
GAM1685 CYorf14  5' ATGCCTGGAGCAAGAAG     41309      TGAGA   A
                                ATGT     CTG AGCAAGAAG
                                ||||     ||| |||||||||
                                TACG     GAC TCGTTCTTC
                                  _____  C
GAM1685 FLJ10482 3' TGTTGGAAAGGGCAAGAAG    41310       A  CTGAA
                                TGTTG GA     GCAAGAAG
                                ||||| ||     ||||||||
                                ACAAC CT     CGTTCTTC
                                   _  TTCC_
GAM1685 FLJ10687 3' GTTGGGAGACTGAGGCAGGAGG 41311     __       A   A  A
             A                   GTT  GAGACTGA GCA GA GA
                                ||| |||||||| ||| || ||
                                CAA  CTCTGACT CGT CT CT
                                  CC       C   C  C
GAM1685 FLJ14594 3' GATGTGGAGACTGAGGCCCAGA 41312       T       A  A_
                                GATGT GAGACTGA GC  AGA
                                ||||| |||||||| ||  |||
                                CTACA CTCTGACT CG  TCT
                                   C       C  GG
GAM1685 FLJ20342 3' GAGGCTGAGGCAAGAAGA    41304     A   A
                                GAG CTGA GCAAGAAGA
                                ||| |||| |||||||||
                                CTC GACT CGTTCTTCT
                                  C   C
GAM1685 FLJ21156 3' TGTTGAGACTGGGTTGGTAGAA 41313          AAGCA__
             GA                   TGTTGAGACTG      AGAAGA
                                ||||||||||       ||||||
                                ACAACTCTGAC      TCTTCT
                                      CCAACCA
GAM1685 KCNT1    3' GATGCTGAGGCTGGGGAAG   41314         A  AAGCAA
                                GATGTTGAG CTG     GAAG
                                ||||||||| |||     ||||
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                                CTACGACTC GAC     CTTC
                                     C   CC____
GAM1685  KIAA1257  3'  CTGAGAGGCTGAAGCAGGAGGA 41315       __       A  A
                                TTGAGA  CTGAAGCA GA GA
                                ||||||  |||||||| || ||
                                GACTCT  GACTTCGT CT CT
                                   CC       C  C
GAM1685  KIAA1649  3'  TTGAGAGGCTGAAGCAGGAGGA 41316       __       A  A
                                TTGAGA  CTGAAGCA GA GA
                                ||||||  |||||||| || ||
                                AACTCT  GACTTCGT CT CT
                                   CC       C  C
GAM1685  KRT6IRS   3'  GATTTGAGACTGAGCTAGA   41317     G        A  A
                                GAT TTGAGACTGA GC AGA
                                ||| |||||||||| || |||
                                CTA AACTCTGACT CG TCT
                                  _        _  A
GAM1685  MGC4172   3'  GACGTTGAGGTGCAAGAAG   41318         ACTGAA
                                GATGTTGAG     GCAAGAAG
                                |||||||||     ||||||||
                                CTGCAACTC     CGTTCTTC
                                     CA____
GAM1685  PDZD2     3'  ATGTTGGGAGAGCTGGCAAGAA 41319       __   _  AA
              G                   ATGTT  GAGA CTG  GCAAGAAG
                                  |||||  |||| |||  ||||||||
                                  TACAA  CTCT GAC  CGTTCTTC
                                     CC    C  __
GAM1685  PRO0132   5'  GATGTTGAGGCAGGAGAA    41320         ACTGAA  __
                                GATGTTGAG     GCA  AGAA
                                |||||||||     |||  ||||
                                CTACAACTC     CGT  TCTT
                                     _______  CC
GAM1685  PRO0899   5'  TGCCAGACTGAAGCAGGAGGA  41321      G        A  A
                                TGTT AGACTGAAGCA GA GA
                                |||| ||||||||||| || ||
                                ACGG TCTGACTTCGT CT CT
                                  _        C  C
GAM1685  TSPEAR    3'  GATGTTGAAGGCTTCAGTCAAG 41322         A_  GA  _
                                GATGTTGAG  CT  AG CAAG
                                |||||||||  ||  || ||||
                                CTACAACTT  GA  TC GTTC
                                     CC  AG  A
GAM1685  LOC118611 3'  TGCTGAGATTGAAATTTAAAAG 41323         C    CA_
                                TGTTGAGA TGAAG   AGAAG
                                |||||||| |||||   |||||
                                ACGACTCT ACTTT   TTTTC
                                     A    AAA
GAM1685  LOC127396 3'  ATGTTGAGACTGGAA       41324           AAGCAA
                                ATGTTGAGACTG     GAA
                                ||||||||||||     |||
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                                TACAACTCTGAC     CTT
                                          ______
GAM1685  LOC146728 5'  GAAGTTGAAACCAGGGCA    41325    T        AA
                                GA GTTGAGACTG  GCA
                                || ||||||||||  |||
                                CT CAACTTTGGT  CGT
                                  T         CC
GAM1685  LOC147004 3'  ATGTTGAGCTGCAGGAG     41326        A  GAA   A  A
                                ATGTTGAG CT   GCA GA G
                                |||||||| ||   ||| || |
                                TACAACTC GA   CGT CT C
                                     _ ___   C  C
GAM1685  LOC149448 3'  GGTGTTACAGAGGCAAGAAGA  41327    A    AGACT  A
                                G TGTTG     GA GCAAGAAGA
                                | |||||     || |||||||||
                                C ACAAT     CT CGTTCTTCT
                                 C     GT___  C
GAM1685  LOC152286 3'  GATGTTGAACTGGGGCTGGA   41328         A   AA  AA
                                GATGTTGAG CTG  GC  GA
                                ||||||||| |||  ||  ||
                                CTACAACTT GAC  CG  CT
                                      _  CC  AC
GAM1685  LOC154877 5'  GAGGCTGAAGCAGGAGGA     41329     A       A  A
                                GAG CTGAAGCA GA GA
                                ||| |||||||| || ||
                                CTC GACTTCGT CT CT
                                  C       C  C
GAM1685  LOC203427 3'  GAGGCTGAAGCAGGAGGA     41329     A       A  A
                                GAG CTGAAGCA GA GA
                                ||| |||||||| || ||
                                CTC GACTTCGT CT CT
                                  C       C  C
GAM1685  LOC219920 5'  GATGAGGAAACTGAGGCAGGAA 41330      TT       A   A
            GA                    GATG  GAGACTGA GCA GAAGA
                                ||||  |||||||| ||| |||||
                                CTAC  CTTTGACT CGT CTTCT
                                  TC       C   C
GAM1685  LOC221632 3'  GATGTAGAATCAGAAGCAAGGA 41331      T   ACT       A
            GA                    GATGT GAG   GAAGCAAG AGA
                                ||||| |||   |||||||| |||
                                CTACA CTT   CTTCGTTC TCT
                                   T   AGT       C
GAM1685  LOC254945 5'  ATGTTGAGATGAGGAAG     41332         C   AGCAA
                                ATGTTGAGA TGA     GAAG
                                |||||||||  |||     ||||
                                TACAACTCT ACT     CTTC
                                      _  C____
GAM1685  LOC90190  3'  GATTTGAGGCTGAAGAGTCAG  41333     G    A     CAAGA
                                GAT TTGAG CTGAAG     AG
                                ||| ||||| ||||||     ||
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                                CTA AACTC GACTTC     TC
                                  _    C     TCAG_
GAM1685 LOC90979 5' GATGTTGAACAAGGGAAG    41334        GACTGAA   __
                                GATGTTGA      GCAA  GAAG
                                ||||||||      ||||  ||||
                                CTACAACT      TGTT  CTTC
                                    _______   CC
GAM1685 LOC91812 5' GACCCCGGCTGAGGCAGGA   41335    G   AGA   A   A
                                GAT TTG   CTGA GCA GA
                                ||| |||   |||| ||| ||
                                CTG GGC   GACT CGT CT
                                  G   C__   C   C
GAM1685 LOC91813 5' GACCCCGGCTGAGGCAGGA   41335    G   AGA   A   A
                                GAT TTG   CTGA GCA GA
                                ||| |||   |||| ||| ||
                                CTG GGC   GACT CGT CT
                                  G   C__   C   C
GAM1685 LOC92249 3' GATGTTGATGGTTGGAGCCTGA 41336        GAC_ A   AA
                                GATGTTGA    TG AGC  GA
                                ||||||||    || |||  ||
                                CTACAACT    AC TCG  CT
                                     ACCA  C   GA
GAM1686 STMN1    3' TCATTTGTGCGTTGGGT     41339        AACATT
                                TCGTTTG     CGTTGGGT
                                |||||||     ||||||||
                                AGTAAAC     GCAACCCA
                                    AC_____
GAM1686 FAM3C    3' GATTGTTTAAACATATAAGGT  41340     C        TCGTT
                                GAT GTTTGAACAT     GGGT
                                ||| ||||||||||     ||||
                                CTA CAAATTTGTA     TCCA
                                  A         TAT__
GAM1686 LOC91380 3' GATCGTTTGAGCTCAGGT    41341         ACATTC  _
                                GATCGTTTGA     GTT GGGT
                                ||||||||||     ||| ||||
                                CTAGCAAACT     CGA TCCA
                                    _______  G
GAM1687 DNAJC6   3' AAATTAGATGCTACATTT    41344        C  CA
                                AAATTAG AT  GCTACATTT
                                ||||||| ||  |||||||||
                                TTTAATC TA  CGATGTAAA
                                    _ __
GAM1687 KIAA0090 3' ATTAAATAGCATCATCTCATTT 41345        T      G  A
                                ATTAAAT AGCATCA CT CATTT
                                ||||||| ||||||| || |||||
                                TAATTTA TCGTAGT GA GTAAA
                                    _      A  _
GAM1687 KIAA0459 3' AATTAACAGTCAGCTGCATTT  41346         _     A
                                AATTAGCA TCAGCT CATTT
                                |||||||| |||||| |||||
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                                TTAATTGT AGTCGA GTAAA
                                    C     C
GAM1687  PPP1R15B  3'  ATTAAACTAGATCCAAGTTACA 41347         C   __  C
             TTT                  ATTAAATTAG ATC  AG TACATTT
                                  |||||||||| |||  || |||||||
                                  TAATTTGATC TAG  TC ATGTAAA
                                      _  GT  A
GAM1687  STATI2   3'  ATTAGATTAGCTTCAGCT    41348     A     A
                                  ATTA ATTAGC TCAGCT
                                  |||| |||||| ||||||
                                  TAAT TAATCG AGTCGA
                                    C     A
GAM1687  STATI2   3'  ATTAGATTAGCTTCAGCT    41348     A     A
                                  ATTA ATTAGC TCAGCT
                                  |||| |||||| ||||||
                                  TAAT TAATCG AGTCGA
                                    C     A
GAM1687  LOC144519 3'  ATTAAATTAACATTACAGCC   41349           __
                                  ATTAAATTAGCAT  CAGCT
                                  |||||||||||||  |||||
                                  TAATTTAATTGTA  GTCGG
                                        AT
GAM1687  LOC202347 3'  AAATTAGCACCATCATTACATT 41350          GC__
             T                    AAATTAGCATCA    TACATTT
                                  ||||||||||||    |||||||
                                  TTTAATCGTGGT    ATGTAAA
                                        AGTA
GAM1688  MXI1     3'  TGTTTTATCATTATCAAATGC  41353          ATTTC
                                  TGTTTTATTAT     TCAAATGC
                                  ||||||||||||    ||||||||
                                  ACAAAATAGTA     AGTTTACG
                                        AT___
GAM1688  MXI1     3'  TGTTTTATCATTATCAAATGC  41353          ATTTC
                                  TGTTTTATTAT     TCAAATGC
                                  ||||||||||||    ||||||||
                                  ACAAAATAGTA     AGTTTACG
                                        AT___
GAM1688  C20orf82  3'  TGTTTTGATATATTTCCATTGC 41354       AT       CAAA
                                  TGTTTT  TATATTTCT    TGC
                                  ||||||  |||||||||    |||
                                  ACAAAA  ATATAAAGG    ACG
                                     CT       TA__
GAM1688  EIF5     3'  GTTTTATTACATCAAATG    41355          TTTC
                                  GTTTTATTATA    TCAAATG
                                  ||||||||||||   |||||||
                                  CAAAATAATGT    AGTTTAC
                                         ____
GAM1688  FLJ10702  3'  GTTTTATTATATTGGGTGGAAT 41356          TCTCA_
             GC                   GTTTTATTATATT     AATGC
                                  ||||||||||||||    |||||
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                                CAAAATAATATAA     TTACG
                                      CCCACC
GAM1688  MGC26954  3'  GTTTTATTAGTGCTCAAATG  41357         TATTT
                                GTTTTATTA    CTCAAATG
                                |||||||||    ||||||||
                                CAAAATAAT    GAGTTTAC
                                   CAC__
GAM1688  PORIMIN   3'  GTTTTATTGTACTCCTATTAAA 41358        A      C__
           TG                     GTTTTATT TATTTCT   AAATG
                                |||||||| |||||||   |||||
                                CAAAATAA ATGAGGA   TTTAC
                                   C      TAA
GAM1688  LOC197358 3'  TGTTTTGTTTTATTTCCCA   41359       A  A
                                TGTTTT TT TATTTCTCA
                                |||||| || |||||||||
                                ACAAAA AA ATAAAGGGT
                                   C  A
GAM1688  LOC256158 5'  TGTCTTGGGGTTCTCAAATG  41360       ATTATAT
                                TGTTTT      TTCTCAAATG
                                ||||||      ||||||||||
                                ACAGAA      AAGAGTTTAC
                                   CCCC___
GAM1689  ACYP1     3'  CCATCATACAGGTAATATATAA 41363             C
                                TCGTTATACAGGTAATA ATAA
                                |||||||||||||||| ||||
                                GGTAGTATGTCCATTAT TATT
                                      A
GAM1689  B3GALT3   3'  TGTCATTATGCAGTACATA   41364         A   GTAA
                                TGTCGTTAT CAG    TACATA
                                ||||||||| |||    ||||||
                                ACAGTAATA GTC    ATGTAT
                                   C  _____
GAM1689  GNRHR     5'  TGTTATTACACATTAATGCATA 41365     CG      GG    A
           A                     TGT  TTATACA  TAAT CATAA
                                |||  |||||||  |||| |||||
                                ACA  AATGTGT  ATTA GTATT
                                  AT      A_   C
GAM1689  CASPR3    3'  TGTTTTTATACAGAACACATA  41366     CG       TA
                                TGT  TTATACAGG  ATACATA
                                |||  |||||||||  |||||||
                                ACA  AATATGTCT  TGTGTAT
                                  AA       __
GAM1689  FLJ22173  5'  TGTCCTTATACACATCAGGTAG 41367       ______   A      III
           TACATAAT                TATACA    GGTA TACATAA   T
                                ||||||    |||| |||||||   |
                                ATATGT    CCAT ATGTATT   A
                                   GTAGT   C      III
GAM1690  MDM1      3'  TATAAATAGTATCTTTTTTCA  41370              _
                                TATAAATAGTATTTTTTT CA
                                |||||||||||||||||| ||
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                                ATATTTATCATAGAAAAA GT
                                          A
GAM1690  FLJ23017  3'  TATAAATAATATTTTTTTCAC  41371
                                TATAAATAGTATTTTTTTCAT
                                ||||||||||||||||||||
                                ATATTTATTATAAAAAAAGTG

GAM1690  KIAA1673  3'  ATAGGTCATTCTTTTCATTAT  41372     __
                                ATAG  TATTTTTTTCATTAT
                                ||||  ||||||||||||||
                                TATC  GTAAGAAAAGTAATA
                                  CA
GAM1690  WDR7      3'  TATAATTCTATTTTTTTCATTA 41373      ATAG
           T                     TATAA   TATTTTTTTCATTAT
                                |||||   ||||||||||||||
                                ATATT   ATAAAAAAAGTAATA
                                   AAG_
GAM1691  APM1      3'  TATTAAATATAAATTGTCTAAA 41376        T    A
                                TATTAAATAT AAATT TCTAAA
                                |||||||||| ||||| ||||||
                                ATAATTTATA TTTAA AGATTT
                                      _    C
GAM1691  PPAT      3'  TAAATATTAAATTTCTAAAT  41377          A
                                TAAATATTAAATT TCTAAAT
                                |||||||||||| |||||||
                                ATTTATAATTTAA AGATTTA
                                                _
GAM1691  LOC146268 3'  TATTAAATATTAAATATC    41378           T
                                TATTAAATATTAAAT ATC
                                |||||||||||||| |||
                                ATAATTTATAATTTA TAG
                                                _
GAM1692  ITGB1     3'  GTAGATCAACTATTTCA     41381          CA
                                GTAGATCAACTA  TTCA
                                ||||||||||||  ||||
                                CATCTAGTTGAT  AAGT
                                      A_
GAM1692  KRAS2     3'  AATCAACTGCATGCACCAAAA  41382        A  T
                                GATCAACT CAT CATTAAAA
                                |||||||| ||| ||||||||
                                TTAGTTGA GTA GTGGTTTT
                                     C  C
GAM1692  KRAS2     3'  AATCAACTGCATGCACCAAAA  41382        A  T
                                GATCAACT CAT CATTAAAA
                                |||||||| ||| ||||||||
                                TTAGTTGA GTA GTGGTTTT
                                     C  C
GAM1692  PPAT      3'  GATCAAGCACTTCATTAAAA   41383       C  A
                                GATCAA TAC TTCATTAAAA
                                |||||| ||| ||||||||||
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                                CTAGTT GTG AAGTAATTTT
                                   C  _
GAM1692 ZNF174    3'  GTAGATCACTCATCTTTATTAA 41384        A A   C__
              A                    GTAGATCA CT CATT   ATTAAA
                                   |||||||| || ||||  ||||||
                                   CATCTAGT GA GTAG   TAATTT
                                      _ _   AAA
GAM1692 C6orf37   3'  GCAGAATGCATTCATTAAA   41385      TCAACTA
                                   GTAGA     CATTCATTAAA
                                   |||||     ||||||||||
                                   CGTCT     GTAAGTAATTT
                                     TAC____
GAM1692 FLJ13687  5'  GACACACATTCATTAA     41386     CA  T
                                   GAT  AC ACATTCATTAA
                                   |||  || ||||||||||
                                   CTG  TG TGTAAGTAATT
                                    __ _
GAM1692 KIAA0433  3'  GTACATTAACTACATTTTCAC  41387     G  C      __
                                   GTA AT AACTACAT  TCAT
                                   ||| || ||||||||  ||||
                                   CAT TA TTGATGTA  AGTG
                                     G  A       AA
GAM1692 KIAA1726  3'  AGATCAATTTCTTCATTAAA   41388       CTACA
                                   AGATCAA    TTCATTAAA
                                   |||||||    |||||||||
                                   TCTAGTT    AAGTAATTT
                                       AAAG_
GAM1692 LOC120103 3'  AGATCAACTACCATTA      41389          ATT
                                   AGATCAACTAC   CATTA
                                   ||||||||||   |||||
                                   TCTAGTTGATG   GTAAT
                                          ___
GAM1692 LOC143308 5'  GTAAATCAATGACCATTCATT  41390         CTA_
                                   GTAGATCAA    CATTCATT
                                   |||||||||    ||||||||
                                   CATTTAGTT    GTAAGTAA
                                         ACTG
GAM1693 CNR1      3'  TGGTTACAAAGGCATTAT    41393     GA
                                   TGGT  TGCGAGGGCATTAT
                                   ||||  ||||||||||||||
                                   ACCA  ATGTTTCCGTAATA
                                     __
GAM1693 NELL2     3'  CATGGTGATGTGAGACAC    41394         C   G
                                   TATGGTGATG GAGG CAT
                                   |||||||||| |||| |||
                                   GTACCACTAC CTCT GTG
                                         A   _
GAM1693 DKFZp586G0123 5'  ACTGGGCCATGGAGGGCATT   41395     AT  G  C
                                   ACT  GGT ATG GAGGGCATT
                                   |||  ||| ||| |||||||||
```

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                                TGA  CCG TAC CTCCCGTAA
                                  C_  G  _
GAM1693  KIAA1710  3'  ACTATGGTGTGTGAATAGG   41396        A  C  __
                                ACTATGGTG TG GA  GGG
                                ||||||||| || ||  |||
                                TGATACCAC AC CT  TCC
                                     _ A  TA
GAM1693  KIAA1972  3'  ACTTGGGAGGGCATT      41397     A   TGATGC
                                ACT TGG     GAGGGCATT
                                ||| |||     |||||||||
                                TGA ACC     CTCCCGTAA
                                  _  _______
GAM1693  MGC4677   5'  ATGGTGGTGCGGGACAT     41398       A    A
                                ATGGTG TGCG GGGCAT
                                |||||| |||| ||||||
                                TACCAC ACGC CCTGTA
                                   C   _
GAM1693  LOC257095 5'  TGGTAGATGAGGGCATTAT   41399      _   GC
                                TGGT GAT  GAGGGCATTAT
                                |||| |||  ||||||||||
                                ACCA CTA  CTCCCGTAATA
                                  T  __
GAM1694  KIAA0173  5'  GATCAAGCAGAGGAAAATAT  41402         ACTTTT
                                GATCAAGCA     AAATAT
                                |||||||||     ||||||
                                CTAGTTCGT     TTTATA
                                     CTCCT_
GAM1694  PRTD-NY3  3'  GTAAATCAGGCAGTTTTTA   41403        A   AC
                                GTAGATCA GCA  TTTTA
                                |||||||| |||  |||||
                                CATTTAGT CGT  AAAAT
                                     C   CA
GAM1694  LOC91170  3'  GTAGACAAGCAACTTTTA    41404      T
                                GTAGA CAAGCAACTTTTA
                                ||||| ||||||||||||
                                CATCT GTTCGTTGAAAAT
                                  _
GAM1695  CAV3      3'  GAACCCAGGCCCTTCCCTCAGT 41407          CTGA_ TG
            G                    GAATCCAGGCCC    T  GTG
                                ||||||||||||    |  |||
                                CTTGGGTCCGGG    A  CAC
                                      AAGGG GT
GAM1695  CDH12     5'  GAATCCAGGTTTGAGGT     41408        CCCC   TT
                                GAATCCAGG   TGA  GGT
                                |||||||||   |||  |||
                                CTTAGGTCC   ACT  CCA
                                     AA__   __
GAM1695  FGD1      3'  GAATCCAGGTCTCCTACCTCTG 41409        CC_   AT__
            GTG                   GAATCCAGG   CCTG   TGGTG
                                |||||||||   ||||   |||||
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                                CTTAGGTCC  GGAT   ACCAC
                                     AGA   GGAG
GAM1695 FSTL3    3' CCGAATCCGGGCTCTAAGGAGT 41410       A  CC   TT
            G                    TCGAATCC GGC  CTGA  GGTG
                                 |||||||| |||  ||||  ||||
                                 GGCTTAGG CCG  GATT  TCAC
                                     C  A_   CC
GAM1695 NPY2R    3' TCAATCCAGGTCCTAACGT   41411    G     CC    TG
                                 TC AATCCAGG  CCTGAT  GT
                                 || ||||||||  ||||||  ||
                                 AG TTAGGTCC  GGATTG  CA
                                  _      A_    __
GAM1695 PTPRF    3' TCTAGGCTCTCTGATTGGT   41412    C   CC_
                                 TC AGGC   CTGATTGGT
                                 || ||||   |||||||||
                                 AG TCCG   GACTAACCA
                                  A   AGA
GAM1695 PTPRF    3' TCTAGGCTCTCTGATTGGT   41412    C   CC_
                                 TC AGGC   CTGATTGGT
                                 || ||||   |||||||||
                                 AG TCCG   GACTAACCA
                                  A   AGA
GAM1695 RRP22    3' TCCAATCCAGGTCCCTGATTG  41413    G      C
                                 TC AATCCAGG CCCTGATTG
                                 || |||||||| |||||||||
                                 AG TTAGGTCC GGGACTAAC
                                  G      A
GAM1695 SCG3     3' GAATCCTGCTGATTGGTG    41414      AG  CCC
                                 GAATCC  GC   TGATTGGTG
                                 ||||||  ||   |||||||||
                                 CTTAGG  CG   ACTAACCAC
                                    A_ ___
GAM1695 SVIL     5' TCGAATCCAGCTTTTGAT    41415        GCCC  GA
                                 TCGAATCCAG   CT  TTGGT
                                 ||||||||||   ||  |||||
                                 AGCTTAGGTC   GA  AACTA
                                      ____  A_
GAM1695 KIAA1086 3' TCAAATCCAGGCCTCAGT    41416          CCTGA TG
                                 TCGAATCCAGGCC    T  GT
                                 ||||||||||||    |  ||
                                 AGTTTAGGTCCGG    A  CA
                                       _____ GT
GAM1695 LOC157681 5' GAATAGATTTTGATTGGTG   41417     CC   CCCC
                                 GAAT  AGG   TGATTGGTG
                                 ||||  |||   |||||||||
                                 CTTA  TCT   ACTAACCAC
                                   __  AAA_
GAM1696 EGLN3    3' TATTTTAGGTGCTGAGAGTATG 41420     G   A   GG
            T                    TAT TTAG TGC  GGGAGTATGT
                                 ||| |||| |||  ||||||||||
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                                ATA AATC ACG  CTCTCATACA
                                  A   C  A_
GAM1696  KIAA0286  3'  TATGTAGGGGCCTAGGGGGTGT 41421      T  AT  __    A  A
             GT                   TATGT AG  GC  GGGGG GT TGT
                                  ||||| ||  ||  ||||| || |||
                                  ATACA TC  CG  TCCCC CA ACA
                                    _  CC  GA    _  C
GAM1696  MGC32104  3'  TATTTTAGGTTCAAGGAGTATG 41422    G   ATG    G
             T                    TAT TTAG   CGGGG AGTATGT
                                  ||| ||||   ||||| |||||||
                                  ATA AATC   GTTCC TCATACA
                                    A   CAA    _
GAM1697  CSR1     3'  GCTGTCTGTAGGTGAGGCT   41425    C  _       A
                                  GCT GTC GTAGGTGAG CT
                                  ||| ||| ||||||||| ||
                                  CGA CAG CATCCACTC GA
                                    _  A       C
GAM1697  FLJ20374  3'  CAGGTGCTCTTCGTGAATG   41426        G   AG
                                  CAGGTGCTC TCGT  GTG
                                  ||||||||| ||||  |||
                                  GTCCACGAG AGCA  TAC
                                       A   CT
GAM1697  FLJ22215  5'  CAGGTGCTTCTCGGCAGG    41427        CG  _
                                  CAGGTGCT  TCG TAGG
                                  ||||||||  ||| ||||
                                  GTCCACGA  AGC GTCC
                                       AG  C
GAM1697  IMAGE:4907098 5'  CAGGTGCTTGAGCGTGAGGT   41428        CGT_  _
                                  CAGGTGCT   CGT AGGT
                                  ||||||||   ||| ||||
                                  GTCCACGA   GCA TCCA
                                       ACTC  C
GAM1697  IRF5     3'  CAGGTGCTCATCGGGGC     41429           TA
                                  CAGGTGCTCGTCG  GGT
                                  ||||||||||||  |||
                                  GTCCACGAGTAGC  CCG
                                         C_
GAM1697  LOC145719 5'  CAGGTTACATAGGTGAGC    41430      GCTCGT       A
                                  CAGGT     CGTAGGTGAG C
                                  |||||     |||||||||| |
                                  GTCCA     GTATCCACTC G
                                    AT____        C
GAM1697  LOC145720 5'  CAGGTTACATAGGTGAGC    41430      GCTCGT       A
                                  CAGGT     CGTAGGTGAG C
                                  |||||     |||||||||| |
                                  GTCCA     GTATCCACTC G
                                    AT____        C
GAM1697  LOC197114 5'  CAGGTTACATAGGTGAGC    41430      GCTCGT       A
                                  CAGGT     CGTAGGTGAG C
                                  |||||     |||||||||| |
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                                GTCCA     GTATCCACTC G
                                  AT____        C
GAM1697  LOC197117 5'  CAGGTTACATAGGTGAGC    41430      GCTCGT       A
                                CAGGT     CGTAGGTGAG C
                                |||||     |||||||||| |
                                GTCCA     GTATCCACTC G
                                  AT____        C
GAM1697  LOC199953 3'  CAGGTGCTCCTCAGGGGTGAGG 41431        G   TA     A
           CT                    CAGGTGCTC TCG  GGTGAG CT
                                |||||||||| |||  |||||| ||
                                GTCCACGAG AGT  CCACTC GA
                                     G   CC     C
GAM1697  LOC221773 3'  AGGTGCTTGTTGAATGAA    41432       C  CGTA
                                AGGTGCT GT    GGTGAG
                                ||||||| ||    ||||||
                                TCCACGA CA    TTACTT
                                    A  AC__
GAM1698  ETR101    3'  TCTGCGGAAGGCGCCCGCG    41435      A  TA  C
                                TCTGC GA  GG GCGCTTGCG
                                ||||| ||  || |||||||||
                                AGACG CT  TC CGCGGGCGC
                                  C  __  _
GAM1698  FLJ23590  5'  CCTGCAGGTAGGCGCGGGCA   41436       A       CTT
                                TCTGCAG TAGGCGCG   GCG
                                ||||||| ||||||||   |||
                                GGACGTC ATCCGCGC   CGT
                                    C       C__
GAM1698  KIAA1911  5'  CCGTCTTGGGTGCGCTTGCGCA 41437     CAGATA  C
                                CTG     GG GCGCTTGCGCA
                                |||     || ||||||||||
                                GGC     CC CGCGAACGCGT
                                  AGAAC_  A
GAM1698  LOC143110 3'  TCTGCGGATAAGCGGATTGCA  41438      A       CGC
                                TCTGC GATAGGCG   TTGCG
                                ||||| ||||||||   |||||
                                AGACG CTATTCGC   AACGT
                                  C       CT_
GAM1698  LOC147054 5'  TGCGCACGTGCGTGCTTGCGC  41439     AG  AG   C
                                TGC  AT  GCG GCTTGCGC
                                |||  ||  ||| ||||||||
                                ACG  TG  CGC CGAACGCG
                                  CG  CA   A
GAM1698  LOC221922 5'  TCTGCAGAGGGGCGTCAGAAGG 41440        TA   _  CTTGC
           CA                    TCTGCAGA  GGCG CG    GCA
                                |||||||  |||| ||    |||
                                AGACGTCT  CCGC GT    CGT
                                    CC    A  CTTC_
GAM1699  C8orf1    3'  TACAATTTTCGAAGTACTTACC 41443      CCTC       GGG
           A                     TATAA    CGAAGTAC   ACCA
                                |||||    ||||||||   ||||
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                                ATGTT   GCTTCATG   TGGT
                                  AAAA      AA_
GAM1699 RLBP1    5' ACTTCCTGTCAGGACCA    41444    C   GAA  A
                                AC TCC   GT CGGGACCA
                                || |||   || ||||||||
                                TG AGG   CA GTCCTGGT
                                 A  A__  _
GAM1699 FLJ20151 3' TATAACCTTTACTGGAC    41445        CCGAAG   G
                                TATAACCT     TAC GGAC
                                ||||||||     ||| ||||
                                ATATTGGA     ATG CCTG
                                     A_____   A
GAM1699 LAMB4    5' TATAACCTTGAAGACAA    41446        CC    T
                                TATAACCT  GAAG ACGG
                                ||||||||  |||| ||||
                                ATATTGGA  CTTC TGTT
                                     A_   _
GAM1699 LYPLA3   3' ACCTCTGGGTACAGGACCA   41447      CGAA
                                ACCTC    GTACGGGACCA
                                |||||    ||||||||||
                                TGGAG    CATGTCCTGGT
                                  ACC_
GAM1699 MRPS18B  3' CAACCTCCGCCTCCTGGGATCA 41448         AAGTAC    C
                                TAACCTCCG     GGGA CA
                                |||||||||     |||| ||
                                GTTGGAGGC     CCCT GT
                                      GGAGGA    A
GAM1699 LOC221583 3' TAACTTCCGAAGTATTCCA   41449     C       CGGGA
                                TAAC TCCGAAGTA     CCA
                                |||| |||||||||     |||
                                ATTG AGGCTTCAT     GGT
                                  A        AA___
GAM1699 LOC221832 5' TATAACCTCTGCAGAAGCTGGA 41450         C___     ACG
             C                   TATAACCTC    GAAGT   GGAC
                                |||||||||    |||||   ||||
                                ATATTGGAG    CTTCG   CCTG
                                      ACGT     A__
GAM1699 LOC253233 3' TATAACCTTCCAGGCC      41451         _  GAAGTAC   A
                                TATAACCT CC      GGG CC
                                |||||||| ||      ||| ||
                                ATATTGGA GG      TCC GG
                                     A  ________  _
GAM1699 LOC91516  5' CATGACCTCCGAGGCCAG    41452     A       A TA
                                TAT ACCTCCGA G  CGG
                                ||| ||||||||  |  |||
                                GTA TGGAGGCT C  GTC
                                  C       _ CG
GAM1700 ENAM     3' TGGTATAGAATGTCAGTGAT   41455     A  A  T
                                TGG TG GG AATGTCAGTGAT
                                ||| || || ||||||||||||
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                                ACC AT TC TTACAGTCACTA
                                  _ A _
GAM1700 LILRB4   3' CTGGCTGGGGTTCAGTGA    41456     A A  AATG
                                CTGG TG GGT    TCAGTGA
                                |||| || |||    |||||||
                                GACC AC CCA    AGTCACT
                                  G C  ____
GAM1700 PDE4B    5' CTGGATGAGGTGTCGGTGAT  41457          AAT  A
                                CTGGATGAGGT   GTC GTGAT
                                ||||||||||   ||| |||||
                                GACCTACTCCA   CAG CACTA
                                      ___  C
GAM1700 THBD     3' ACTGGATGGGGTGGAGCCTAGG 41458        A  AAT  _ T
             AT                   ACTGGATG GGT   GTC AG GAT
                                ||||||||| |||   ||| || |||
                                TGACCTAC CCA   CGG TC CTA
                                    C  CCT  A _
GAM1700 FLJ20489 5' CTGGAGAGGTAGTAGC     41459      T    AT  C
                                CTGGA GAGGTA  GT AGT
                                ||||| ||||||  || |||
                                GACCT CTCCAT  CA TCG
                                  _     __ _
GAM1700 FLJ22969 3' GGCAACAGTGATGTCGGTGAT  41460    ATGA  A    A
                                GG    GGT ATGTC GTGAT
                                ||    ||| ||||| |||||
                                CC    TCA TACAG CACTA
                                 GTTG  C    C
GAM1700 MAP3K2   3' ACTGATGTGTCAGTG      41461     G  AGGTAA
                                ACTG ATG     TGTCAGTG
                                |||| |||     ||||||||
                                TGAC TAC     ACAGTCAC
                                  _  _______
GAM1700 MGC2731  5' ACTGGATGGGGAATAGAGGAT  41462       A  T   TC  T
                                ACTGGATG GG AATG  AG GAT
                                ||||||| || ||||  || |||
                                TGACCTAC CC TTAT  TC CTA
                                    _ C   C_ _
GAM1700 PPP1R10  5' CTGGATGAGTGAATTTGGGTG  41463       GT  GTCA
                                CTGGATGAG  AAT   GTG
                                |||||||||  |||   |||
                                GACCTACTC  TTA   CAC
                                     AC  AACC
GAM1700 LOC148823 3' TGGATGGGGAGATGTTGGCA  41464      A  TA   CA
                                TGGATG GG  ATGT  GTG
                                ||||||  ||  ||||  |||
                                ACCTAC CC  TACA  CGT
                                   C  TC   AC
GAM1700 LOC94976 3' ACTGGATAGGTAGTTCCTTTG  41465      G   ATG  AG_
                                ACTGGAT AGGTA  TC  TG
                                ||||||| |||||  ||  ||
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                                TGACCTA TCCAT  AG  AC
                                   _    CA_ GAA
GAM1701  OPA1     3' TTAGAATCATTTCTGACTT  41468      ATCCTAAA
                                TTAGAAT      TCTGACTT
                                |||||||      ||||||||
                                AATCTTA      AGACTGAA
                                   GTAA____
GAM1701  OPA1     3' TTAGAATCATTTCTGACTT  41468      ATCCTAAA
                                TTAGAAT      TCTGACTT
                                |||||||      ||||||||
                                AATCTTA      AGACTGAA
                                   GTAA____
GAM1701  OPA1     3' TTAGAATCATTTCTGACTT  41468      ATCCTAAA
                                TTAGAAT      TCTGACTT
                                |||||||      ||||||||
                                AATCTTA      AGACTGAA
                                   GTAA____
GAM1701  OPA1     3' TTAGAATCATTTCTGACTT  41468      ATCCTAAA
                                TTAGAAT      TCTGACTT
                                |||||||      ||||||||
                                AATCTTA      AGACTGAA
                                   GTAA____
GAM1701  OPA1     3' TTAGAATCATTTCTGACTT  41468      ATCCTAAA
                                TTAGAAT      TCTGACTT
                                |||||||      ||||||||
                                AATCTTA      AGACTGAA
                                   GTAA____
GAM1701  PTPN12   3' GAATACTATAAATCTGGCTTT 41469      CC      A
                                GAATAT  TAAATCTG CTTT
                                ||||||  |||||||| ||||
                                CTTATG  ATTTAGAC GAAA
                                   AT       C
GAM1701  KIAA0133 3' TTAGAACATCTTAAGTCT   41470        C  A
                                TTAGAATATC TAA TCT
                                |||||||||| ||| |||
                                AATCTTGTAG ATT AGA
                                     A  C
GAM1701  KIAA1718 3' GAATATCCTAAATAAC     41471          CT
                                GAATATCCTAAAT  GAC
                                |||||||||||||  |||
                                CTTATAGGATTTA  TTG
                                                __
GAM1701  MGC15416 5' TTAGAGTGTCCCAAACCT   41472     ATA
                                TTAGA  TCCTAAATCT
                                |||||  ||||||||||
                                AATCT  AGGGTTTGGA
                                   CAC
GAM1701  LOC138046 3' AATATCACCTGACTT     41473      CTAA
                                AATATC   ATCTGACTT
                                ||||||   |||||||||
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                                TTATAG   TGGACTGAA
                                   ____
GAM1701 LOC158376 3'  TTAAAATATCTTATTTCTGGCT 41474         C  AA   A
             TT                  TTAGAATATC TA  TCTG CTTT
                                 |||||||||| ||  |||| ||||
                                 AATTTTATAG AT  AGAC GAAA
                                       A  AA   C
GAM1702 SHMT2    3'  TCGGTGAAGAGCTTCTGCTTCA 41477         C  AA  C___
             CCGTG                TCGGTGAAG GC  CT   CACCGTG
                                  ||||||||| ||  ||   |||||||
                                  AGCCACTTC CG  GA   GTGGCAC
                                       T  AA  CGAA
GAM1702 SORBS1   3'  TCGGTGAAATGCTGCCGT    41478         C  AACTCCA
                                 TCGGTGAAG GC     CCGT
                                 |||||||| ||      ||||
                                 AGCCACTTT CG     GGCA
                                       A  AC_____
GAM1702 LOC57109  3'  TCGGTAAAGCGTGGCCAGGCGT 41479          CAACT  C_
             G                    TCGGTGAAGCG    CCA  CGTG
                                  ||||||||||    |||  ||||
                                  AGCCATTTCGC    GGT  GCAC
                                        ACC__   CC
GAM1702 LOC92106  5'  TCGGTGAAGCGAAATTCTAC   41480         C  C  C
                                 TCGGTGAAGCG AA TC AC
                                 |||||||||| || || ||
                                 AGCCACTTCGC TT AG TG
                                        T  A  A
GAM1703 FLJ20730  5'  ACGTGGAGAAGCTACAGTA   41483    A   T__
                                 GCG TGGA   GCTACAGTA
                                 ||| ||||   |||||||||
                                 TGC ACCT   CGATGTCAT
                                   _    CTT
GAM1703 KIAA0061  3'  GCCAAATGCTACAGTAAA    41484    GAT
                                 GC   GGATGCTACAGTAAA
                                 ||   ||||||||||||||
                                 CG   TTTACGATGTCATTT
                                  G__
GAM1703 KIAA1376  3'  GCGTATCTACTACAGTA     41485     A  GA
                                 GCG TG  TGCTACAGTA
                                 ||| ||  ||||||||||
                                 CGC AT  ATGATGTCAT
                                   _ AG
GAM1703 ST7L     3'  TATCACAGTTGCTACAGT    41486       GAT  A
                                 TATCGC   GG TGCTACAGT
                                 ||||||   || |||||||||
                                 ATAGTG   TC ACGATGTCA
                                     ___  A
GAM1703 ST7L     3'  TATCACAGTTGCTACAGT    41486       GAT  A
                                 TATCGC   GG TGCTACAGT
                                 ||||||   || |||||||||
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                                ATAGTG   TC ACGATGTCA
                                   ___  A
GAM1703 ST7L    3' TATCACAGTTGCTACAGT    41486       GAT  A
                                TATCGC   GG TGCTACAGT
                                ||||||   || |||||||||
                                ATAGTG   TC ACGATGTCA
                                   ___  A
GAM1704 ACVR1B  3' AGCGCTACGATTACAGG     41489     A        ATGTG
                                AGC CTACGATTACA    GG
                                ||| ||||||||||     ||
                                TCG GATGCTAATGT    CC
                                 C        _____
GAM1704 GABRP   3' TAGCACCATTGGATGTGGG   41490        CGATTACA
                                TAGCACTA       ATGTGGG
                                ||||||||       |||||||
                                ATCGTGGT       TACACCC
                                     AACC____
GAM1704 FLJ10956 3' GCCACTGCACTCCAATGTGGGC 41491    _  A  ATTA
                                GC ACT CG    CAATGTGGGC
                                || ||| ||    ||||||||||
                                CG TGA GT    GTTACACCCG
                                 G   C  GAG_
GAM1704 KIAA1018 3' TAACACTGCTAATGTGGG    41492       ACGATTAC
                                TAGCACT       AATGTGGG
                                |||||||       ||||||||
                                ATTGTGA       TTACACCC
                                    CGA_____
GAM1704 MAWBP   3' AGTGCTACGATTACAGG     41493    CA        ATGTG
                                AG  CTACGATTACA    GG
                                ||  ||||||||||     ||
                                TC  GATGCTAATGT    CC
                                 AC        _____
GAM1704 LOC158709 5' GCAAGACAGGTTATGATGTGGG 41494     CT   A_   CA
            C                    GCA  ACG  TTA  ATGTGGGC
                                 |||  |||  |||  ||||||||
                                 CGT  TGT  AAT  TACACCCG
                                   TC   CC   AC
GAM1705 TMEPAI  3' GGTCAGATTGCGAATACCTGGG 41497    _  T  ATA        AA
            GC                     GG CG GT   CGAATACCTG  GC
                                   || || ||   ||||||||||  ||
                                   CC GT TA   GCTTATGGAC  CG
                                    A  C  AC_         CC
GAM1705 MAEA    3' GGTGTGTATACGAAACGACGC  41498    C         TACC   A
                                GG GTGTATACGAA    TGA GC
                                || ||||||||||     ||| ||
                                CC CACATATGCTT    GCT CG
                                 A         T___   G
GAM1705 MGC15429 3' GGCATGTATGTATCTGGG    41499         ACGAA  C   AA
                                GGCGTGTAT    TA CTG  G
                                |||||||||    || |||  |
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                                CCGTACATA    AT GAC  C
                                     C____  A   CC
GAM1705  P4HA2    5'  GGCTGTCCAGCAATACCTGAGG 41500     G   ATACG       A
              C                   GGC TGT    AATACCTGA GC
                                  ||| |||    ||||||||| ||
                                  CCG ACA    TTATGGACT CG
                                    _  GGTCG       C
GAM1705  ZIM3     5'  GGCGTGTATACTGAAAAG    41501          GAATACCT
                                  GGCGTGTATAC       GAAG
                                  ||||||||||        ||||
                                  CCGCACATATG       TTTC
                                        ACT_____
GAM1706  BST2     3'  CCGGAGGGAGGCTCTGGAG   41504     T      AG  GT
                                  CCG GAGGGAGG  TC  GAG
                                  ||| ||||||||  ||  |||
                                  GGC CTCCCTCC  AG  CTC
                                    _       G_  AC
GAM1706  RARB     5'  CACTCGAGGGGGAGGAAGTG   41505     C  TGA       TC
                                  CAC CG   GGGAGGAG  GTG
                                  ||| ||   ||||||||  |||
                                  GTG GC   CCCTCCTT  CAC
                                    A  TCC       __
GAM1706  C11orf25  5'  CCCGAGAGGGAGGCGGA     41506      T       AGT  T
                                  CCCG GAGGGAGG   CG GA
                                  |||| ||||||||   || ||
                                  GGGC CTCCCTCC   GC CT
                                    T       ___  _
GAM1706  C1orf26   3'  ACCCTGAGGGAGGTGAAGGAG  41507      G        AGTCGT
                                  ACCC TGAGGGAGG     GAG
                                  |||| |||||||||     |||
                                  TGGG ACTCCCTCC     CTC
                                    _        ACTTC_
GAM1706  CTAG2    3'  CCCTGAGGGAGCCTGA      41508     G      GGA   G
                                  CCC TGAGGGA   GTC TGA
                                  ||| |||||||   ||| |||
                                  GGG ACTCCCT   CGG ACT
                                    _     ____   _
GAM1706  DKFZP564I0422 5'  CGTGAGAGCTTAGTCGTGAG   41509         AGG
                                  CGTGAGGG   AGTCGTGAG
                                  ||||||||   |||||||||
                                  GCACTCTC   TCAGCACTC
                                       GAA
GAM1706  DKFZP564K0322 3'  CACTTGGAGGGAGGGCCCGTG  41510     CCGT       AG
                                  CAC    GAGGGAGG  TCGTG
                                  |||    ||||||||  |||||
                                  GTG    CTCCCTCC  GGCAC
                                    AAC_       CG
GAM1706  FLJ10374  3'  CCCGTGAGGGGGTCCTG     41511          A  AG  G
                                  CCCGTGAGGG GG  TC TG
                                  |||||||||| ||  || ||
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                                GGGCACTCCC CC  AG AC
                                      _ __  G
GAM1706 KIAA1138 3' CACCCGGGAGGGAGGGCCTG  41512       T      A  G
                                CACCCG GAGGGAGG GTC TG
                                |||||| |||||||| ||| ||
                                GTGGGC CTCCCTCC CGG AC
                                   C       _  _
GAM1706 KIAA1524 5' ACTTTGAGGGAGGAGAATG   41513    CCG         TC
                                AC  TGAGGGAGGAG  GTG
                                ||  ||||||||||  |||
                                TG  ACTCCCTCCTC  TAC
                                 AA_         T_
GAM1706 SCYD1    3' CACCAGTGGGGGCGTG     41514      C   A   AGGA T
                                CACC GTG GGG    G CGTG
                                |||| ||| |||    | ||||
                                GTGG CAC CCC    C GCAC
                                  T  _  _____ _
GAM1706 TOR2A    3' CCCGGGAGGGGGCTGCTGAG  41515     T    A  AGTCG
                                CCCG GAGGG GG     TGAG
                                |||| ||||| ||     ||||
                                GGGC CTCCC CC     ACTC
                                  C     _  GACG_
GAM1706 TP53TG3  3' CACTCGTGAGGGGGCTTCTTGA 41516     C       A  AG  G
          G                      CAC CGTGAGGG GG  TC TGAG
                                ||| |||||||| ||  || ||||
                                GTG GCACTCCC CC  AG ACTC
                                  A       _  GA  A
GAM1706 LOC123591 3' CACCCTGAGGGAGGCCAGGTG  41517       G        AGTC
                                CACCC TGAGGGAGG    GTG
                                ||||| |||||||||    |||
                                GTGGG ACTCCCTCC    CAC
                                   _        GGTC
GAM1706 LOC148181 5' CACTGTGAGGGAGGAGC     41518     CC
                                CAC  GTGAGGGAGGAGT
                                |||  ||||||||||||
                                GTG  CACTCCCTCCTCG
                                  A_
GAM1706 LOC154990 5' CACTGTGAGGGAGGAGC     41518     CC
                                CAC  GTGAGGGAGGAGT
                                |||  ||||||||||||
                                GTG  CACTCCCTCCTCG
                                  A_
GAM1706 LOC196500 3' CATGAGGGAGAGAGTGAG    41519          G  TC
                                CGTGAGGGAG AG  GTGAG
                                |||||||||| ||  |||||
                                GTACTCCCTC TC  CACTC
                                      _  T_
GAM1706 LOC255975 5' CACTGTGAGGGAGGAGC     41518     CC
                                CAC  GTGAGGGAGGAGT
                                |||  ||||||||||||
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                              GTG  CACTCCCTCCTCG
                                A_
GAM1707  ADAR    3'  TTCCCAGCTGCCGGAG     41522       CA   ACG
                              TTCCCAGT  TGT   CGGAG
                              ||||||||  |||   |||||
                              AAGGGTCG  ACG   GCCTC
                                 __   ____
GAM1707  ADAR    3'  TTCCCAGCTGCCGGAG     41522       CA   ACG
                              TTCCCAGT  TGT   CGGAG
                              ||||||||  |||   |||||
                              AAGGGTCG  ACG   GCCTC
                                 __   ____
GAM1707  ADAR    3'  TTCCCAGCTGCCGGAG     41522       CA   ACG
                              TTCCCAGT  TGT   CGGAG
                              ||||||||  |||   |||||
                              AAGGGTCG  ACG   GCCTC
                                 __   ____
GAM1707  ASTN    3'  TTCCCAGTCATGAGGGTGGGGA 41523          TACGC  A
                              TTCCCAGTCATG    GG GA
                              ||||||||||||    || ||
                              AAGGGTCAGTAC    CC CT
                                    TCCCA  C
GAM1707  ASTN    3'  TTCCCAATCATGCAGATGGAGA 41524           CGC
                              TTCCCAGTCATGTA   GGAGA
                              ||||||||||||||   |||||
                              AAGGGTTAGTACGT   CCTCT
                                    CTA
GAM1707  CA12    3'  TTCTCAGTCATGGCACTGA   41525    C      TA   G
                              TTC CAGTCATG  CGC GA
                              ||| ||||||||  ||| ||
                              AAG GTCAGTAC  GTG CT
                                A       C_   A
GAM1707  CAPN2   3'  TTCCCAGTTGGCTCATGGGA   41526       CAT  A  C  A
                              TTCCCAGT   GT CG GG GA
                              ||||||||   || || || ||
                              AAGGGTCA   CG GT CC CT
                                   AC_  A  A  _
GAM1707  COL4A5  3'  TTCCCAGTTCTGTACAAGCAGA 41527        CA    __
                              TTCCCAGT  TGTAC  GCGGA
                              ||||||||  |||||  |||||
                              AAGGGTCA  ACATG  CGTCT
                                   AG    TT
GAM1707  COL4A5  3'  TTCCCAGTTCTGTACAAGCAGA 41527        CA    __
                              TTCCCAGT  TGTAC  GCGGA
                              ||||||||  |||||  |||||
                              AAGGGTCA  ACATG  CGTCT
                                   AG    TT
GAM1707  COL4A5  3'  TTCCCAGTTCTGTACAAGCAGA 41527        CA    __
                              TTCCCAGT  TGTAC  GCGGA
                              ||||||||  |||||  |||||
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                                AAGGGTCA  ACATG  CGTCT
                                    AG    TT
GAM1707  CRHR1    3'  TTCCCAGTGGTGTCGGA    41528       CA   ACG
                                TTCCCAGT  TGT   CGGA
                                ||||||||  |||   ||||
                                AAGGGTCA  ACA   GCCT
                                    CC   ___
GAM1707  DXS1283E 3'  TCCTCAGTCATGTGGA     41529    _      ACGC
                                TCC CAGTCATGT    GGA
                                ||| |||||||||    |||
                                AGG GTCAGTACA    CCT
                                  A      _____
GAM1707  EPS15    5'  TTCCATCATGCAAGGGAG    41530     CA      CGC
                                TTCC  GTCATGTA   GGAG
                                ||||  ||||||||   ||||
                                AAGG  TAGTACGT   CCTC
                                  __       TC_
GAM1707  ICMT     3'  TTCCCAGCATGACAGAG     41531       T   TAC
                                TTCCCAG CATG   GCGGAG
                                |||||||  ||||   ||||||
                                AAGGGTC GTAC   TGTCTC
                                    _   ___
GAM1707  MAP1A    3'  TTCCCAGTCGTTTGGCAGAGA  41532        ATGTAC
                                TTCCCAGTC     GCGGAGA
                                |||||||||     |||||||
                                AAGGGTCAG     CGTCTCT
                                    CAAAC_
GAM1707  MUC4     3'  TCCCCAGTCAGGTTTGGAG   41533        T  ACGC
                                TTCCCAGTCA GT    GGAG
                                ||||||||||  ||    ||||
                                AGGGGTCAGT CA    CCTC
                                    C  AA__
GAM1707  NDUFB3   5'  TTCCCAGTATATGTGCA     41534       C    AC
                                TTCCCAGT ATGT  GCG
                                |||||||  ||||  |||
                                AAGGGTCA TATA  CGT
                                    _    CA
GAM1707  NDUFB9   5'  TCCCCGGCCGCGCGGAGA    41535      A   ATGTA
                                TTCCC GTC    CGCGGAGA
                                |||||  |||    ||||||||
                                AGGGG CGG    GCGCCTCT
                                   C   C_____
GAM1707  STARD4   3'  TTCCCAGCTATTCAGGAG    41536       CA   A  C
                                TTCCCAGT  TGT CG GGAG
                                ||||||||  ||| || ||||
                                AAGGGTCG  ATA GT CCTC
                                    __   A  _
GAM1707  SULT2B1  5'  CTCCCAGTTACTCCGGAG    41537       CATG   G_
                                TTCCCAGT    TAC  CGGAG
                                ||||||||    |||  |||||
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                                GAGGGTCA   ATG  GCCTC
                                    _____  AG
GAM1707  TFAP2C   3'  TTCCCAGTCTGTGCGGTGGAGA 41538        A   A  C_
                                TTCCCAGTC TGT CG  GGAGA
                                ||||||||| ||| ||  |||||
                                AAGGGTCAG ACA GC  CCTCT
                                     _  C  CA
GAM1707  TLR4     5'  TTCTGGTCTCACGCAGGAGA  41539    CCA  ATG   _
                                TTC  GTC  TACGC GGAGA
                                |||  |||  ||||| |||||
                                AAG  CAG  GTGCG CCTCT
                                  AC_  A__    T
GAM1707  TLR4     5'  TTCTGGTCTCACGCAGGAGA  41539    CCA  ATG   _
                                TTC  GTC  TACGC GGAGA
                                |||  |||  ||||| |||||
                                AAG  CAG  GTGCG CCTCT
                                  AC_  A__    T
GAM1707  TLR4     5'  TTCTGGTCTCACGCAGGAGA  41539    CCA  ATG   _
                                TTC  GTC  TACGC GGAGA
                                |||  |||  ||||| |||||
                                AAG  CAG  GTGCG CCTCT
                                  AC_  A__    T
GAM1707  TLX1     5'  CTCCTGGCTGCGCGGAG    41540    CA  CA  TA
                                TTCC  GT  TG  CGCGGAG
                                ||||  ||  ||  |||||||
                                GAGG  CG  AC  GCGCCTC
                                  AC  __  __
GAM1707  cerk     3'  TTCCCAGTTTGTGAGCAG    41541       CA  AC
                                TTCCCAGT  TGT  GCGG
                                ||||||||  |||  ||||
                                AAGGGTCA  ACA  CGTC
                                    A_  CT
GAM1707  CTPS2    3'  TTCCCAGTCATGTATTCA    41542          CG
                                TTCCCAGTCATGTA  CG
                                ||||||||||||||  ||
                                AAGGGTCAGTACAT  GT
                                       AA
GAM1707  DKFZP434K1772 5'  CCAGTACGCAGCTGGAGA    41543      C    C  _
                                CCAGT ATGTA GC GGAGA
                                ||||| ||||| || |||||
                                GGTCA TGCGT CG CCTCT
                                  _    _  A
GAM1707  FAM3D    5'  CTCCCAGTTGCTGGAG     41544       CA  ACGC
                                TTCCCAGT  TGT   GGAG
                                ||||||||  |||   ||||
                                GAGGGTCA  ACG   CCTC
                                    __  A___
GAM1707  FLJ14146 3'  TTCACAGTCATGCAGGGA    41545    C       CGC
                                TTC CAGTCATGTA   GGA
                                ||| ||||||||||   |||
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                                AAG GTCAGTACGT   CCT
                                  T        C__
GAM1707  FLJ20294  3'  TTCCCAGTCAGCTGTGAG    41546         T  ACGCG
                                TTCCCAGTCA GT    GAG
                                |||||||||| ||    |||
                                AAGGGTCAGT CG    CTC
                                      _  ACA__
GAM1707  FLJ20309  3'  TTCCAAGTCATGTGGA     41547     C       ACGC
                                TTCC AGTCATGT   GGA
                                |||| ||||||||   |||
                                AAGG TCAGTACA   CCT
                                  T      _____
GAM1707  FLJ21432  3'  TTCTCAGTCATGTACCACGCAG 41548    C         _  G
            A                    TTC CAGTCATGTAC GCG AGA
                                ||| |||||||||| ||| |||
                                AAG GTCAGTACATG TGC TCT
                                  A         G  G
GAM1707  FLJ23392  3'  TTCCCAGTGCCCTTGGAGA   41549       CAT  ACGC
                                TTCCCAGT   GT   GGAGA
                                ||||||||   ||   |||||
                                AAGGGTCA   CG   CCTCT
                                     ___  GGAA
GAM1707  KIAA0152  3'  TTCCCAGTCATGAGAACTCGG  41550          T__  G
                                TTCCCAGTCATG   AC CGG
                                ||||||||||||   || |||
                                AAGGGTCAGTAC   TG GCC
                                       TCT  A
GAM1707  KIAA0940  3'  TTCCCAGTCAAGTTGCAG    41551         T  AC
                                TTCCCAGTCA GT  GCGG
                                |||||||||| ||  ||||
                                AAGGGTCAGT CA  CGTC
                                      T  A_
GAM1707  KIAA1155  3'  TTCCCAATTATGTGGA     41552        C   ACGC
                                TTCCCAGT ATGT   GGA
                                |||||||| ||||   |||
                                AAGGGTTA TACA   CCT
                                     A   _____
GAM1707  KIAA1198  3'  TCTCCAGTCATGTGTGAGA   41553    _       ACGCG
                                TC CCAGTCATGT    GAGA
                                || ||||||||||    ||||
                                AG GGTCAGTACA    CTCT
                                  A        CA___
GAM1707  KIAA1553  3'  TTCCCAGTTGGTGCTCCTGGAG 41554       CA_   ACGC
            A                    TTCCCAGT   TGT   GGAGA
                                ||||||||   |||   |||||
                                AAGGGTCA   ACG   CCTCT
                                     ACC   AGGA
GAM1707  MKRN1    5'  TTCCGGTCCGGCTGCGGGGA  41555     CA  AT  AC   A
                                TTCC  GTC  GT  GCGG GA
                                ||||  |||  ||  |||| ||
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                                AAGG  CAG  CG  CGCC CT
                                  C_  GC  A_   C
GAM1707  NXN      5'  TTCCCAGTGGTGGCGTCGA   41556       CA  TAC   GA
                                TTCCCAGT  TG   GCG  GA
                                ||||||||  ||   |||  ||
                                AAGGGTCA  AC   CGC  CT
                                    CC  ___   AG
GAM1707  PIP3-E   3'  TTCCCAGTCAAGTGGA     41557         T  ACGC
                                TTCCCAGTCA GT    GGA
                                ||||||||||  ||    |||
                                AAGGGTCAGT CA    CCT
                                     T  ____
GAM1707  RPS6KB1  3'  TTCCCAGTTAATGTGTCTAAAG 41558        C_   ACGC
            A                    TTCCCAGT  ATGT    GGAGA
                                ||||||||  ||||    |||||
                                AAGGGTCA  TACA    TTTCT
                                    AT    CAGA
GAM1707  TSPEAR   3'  TCCCAGTCAGCTGGAG     41559        TGTAC  _
                                TCCCAGTCA    GC GGAG
                                |||||||||    || ||||
                                AGGGTCAGT    CG CCTC
                                     _____  A
GAM1707  TTTY12   5'  TTCTTAGTCCTGTACACATGA  41560     CC   A      _
                                TTC  AGTC TGTACGCG GA
                                |||  |||| |||||||| ||
                                AAG  TCAG ACATGTGT CT
                                  AA   G       A
GAM1707  LOC132338 5'  CTCCCAGTGTTGTGGAG     41561        CA   ACGC
                                TTCCCAGT  TGT    GGAG
                                ||||||||  |||    ||||
                                GAGGGTCA  ACA    CCTC
                                    CA  ____
GAM1707  LOC152426 3'  TCCCAGTCACCCTTGGAGA   41562         GTACGC
                                TCCCAGTCAT     GGAGA
                                ||||||||||     |||||
                                AGGGTCAGTG     CCTCT
                                     GGAA__
GAM1707  LOC157651 5'  CCAGCATTGCACGGAGA     41563     T   GTA
                                CCAG CAT   CGCGGAGA
                                |||| |||   ||||||||
                                GGTC GTA   GTGCCTCT
                                  _   AC_
GAM1707  LOC158318 5'  TTCCCAGTCCGTCAGGGAGA   41564         A   A  C
                                TTCCCAGTC TGT CG GGAGA
                                ||||||||| ||| || |||||
                                AAGGGTCAG GCA GT CCTCT
                                     _   _  C
GAM1707  LOC201475 3'  TTCCCAGTGTATGTACACTAGA 41565         C_       GG
                                TTCCCAGT  ATGTACGC  AGA
                                ||||||||  ||||||||  |||
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                                AAGGGTCA  TACATGTG  TCT
                                    CA       A_
GAM1707  LOC253142 3'  TTCTCAGCTATGACACAGAGA  41566    C   TC   T
                                TTC CAG  ATG ACGCGGAGA
                                ||| |||  ||| |||||||||
                                AAG GTC  TAC TGTGTCTCT
                                  A  GA  _
GAM1707  LOC91960  3'  TTCCCAGTTGGTGACAGA    41567       CA  TAC
                                TTCCCAGT  TG   GCGGA
                                ||||||||  ||   |||||
                                AAGGGTCA  AC   TGTCT
                                    __  CAC
GAM1708  ACPT    3'  CGGGCCGGGGCAGTCAGC    41570    A  TAC  A
                                CG GGC   CG GGGCAGTCAGC
                                || |||   || ||||||||||
                                GC CCG   GC CCCGTCAGTCG
                                 _  ___  _
GAM1708  ACPT    3'  CGGGCCGGGGCAGTCAGC    41570    A  TAC  A
                                CG GGC   CG GGGCAGTCAGC
                                || |||   || ||||||||||
                                GC CCG   GC CCCGTCAGTCG
                                 _  ___  _
GAM1708  ATF5    5'  CGAGGCTACAGAGCCATGGCC  41571       CG    AGTCA
                                CGAGGCTAC  AGGGC    GCC
                                |||||||||  |||||    |||
                                GCTCCGATG  TCTCG    CGG
                                    __    GTAC_
GAM1708  ATP6V1G2  3'  CGAGGCTACCAAGTTAAGTAGC 41572          GGC   C
                                CGAGGCTACCGAG   AGT AGC
                                ||||||||||||   ||| |||
                                GCTCCGATGGTTC   TCA TCG
                                      AAT  _
GAM1708  ATP6V1G2  3'  CGAGGCTACCAAGTTAAGTAGC 41572          GGC   C
                                CGAGGCTACCGAG   AGT AGC
                                ||||||||||||   ||| |||
                                GCTCCGATGGTTC   TCA TCG
                                      AAT  _
GAM1708  CD79A   3'  CGAGGCTGCTACAATCAGC   41573       ACCGAGG
                                CGAGGCT     GCAGTCAGC
                                |||||||     |||||||||
                                GCTCCGA     TGTTAGTCG
                                   CGA____
GAM1708  CD79A   3'  CGAGGCTGCTACAATCAGC   41573       ACCGAGG
                                CGAGGCT     GCAGTCAGC
                                |||||||     |||||||||
                                GCTCCGA     TGTTAGTCG
                                   CGA____
GAM1708  CH25H   3'  CAAGGCTATTGAGGTGAGC   41574       CC   GC
                                CGAGGCTA  GAGG  AGT
                                ||||||||  ||||  |||
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                                GTTCCGAT  CTCC  TCG
                                    AA    AC
GAM1708  CYFIP2    5'  GAGGCTACCGCAGGGCCCCGCG 41575          _    AGTCA
                CC                  GAGGCTACCG AGGGC    GCC
                                    |||||||||| |||||    |||
                                    CTCCGATGGC TCCCG    CGG
                                        G    GGGCG
GAM1708  GRIN2C    3'  GAGGCTACTGAGGTCACTGGCT 41576     C    __________  AGTCA
                GACTGC                  CTAC GAGG       GC    GC
                                    |||| ||||       ||    ||
                                    GATG CTCC       CG    CG
                                      A   AGTGAIIIC  ACTGA
GAM1708  ITGA2     3'  AGGTTACTGCCAGTCAGCC   41577    C   CGAGGG
                                    AGG TAC     CAGTCAGCC
                                    ||| |||     |||||||||
                                    TCC ATG     GTCAGTCGG
                                      A   ACG___
GAM1708  MNT       5'  CGAGAGCTGCCGGGGGGCGCGCC 41578     _   A   A   A_
                                    CGAG GCT CCG GGGC  GTC
                                    |||| ||| ||| ||||  |||
                                    GCTC CGA GGC CCCG  CGG
                                      T   C   C   CG
GAM1708  NDUFA10   3'  GGCTGCCGAGAGCTGGCC    41579     A       A_
                                    GGCT CCGAGGGC  GTC
                                    |||| ||||||||  |||
                                    CCGA GGCTCTCG  CGG
                                      C       AC
GAM1708  OSM       3'  CAAGGCAGGGGGGGCAGTCAGCC 41580       TACCGA
                                    CGAGGC     GGGCAGTCAGCC
                                    ||||||     ||||||||||||
                                    GTTCCG     CCCGTCAGTCGG
                                       TCCC__
GAM1708  PCDH11X   5'  GAGGCTATTCAGGCAGCC    41581       CCGA
                                    GAGGCTA    GGGCAGTC
                                    |||||||    ||||||||
                                    CTCCGAT    TCCGTCGG
                                        AAG_
GAM1708  PCDH11Y   5'  GAGGCTATTCAGGCAGCC    41581       CCGA
                                    GAGGCTA    GGGCAGTC
                                    |||||||    ||||||||
                                    CTCCGAT    TCCGTCGG
                                        AAG_
GAM1708  PHB       3'  CGGGGCTGTGGCCCAGTCAGCC 41582    A    ACCGAG   __
                                    CG GGCT     GGC  AGTCAGCC
                                    || ||||     |||  ||||||||
                                    GC CCGA     CCG  TCAGTCGG
                                     C    CA____   GG
GAM1708  SEZ6L     5'  CGGGGCTCCTGAGGGCAG    41583    A    A   _
                                    CG GGCT CC GAGGGCAG
                                    || |||| || ||||||||
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                                GC CCGA GG CTCCCGTC
                                 C   _ A
GAM1708 SLC2A5   3'  GGCCACCGAGTTAGTTGGCTGA 41584          _________  AGTCA
             CTGC                  CTACCGAG       GGC    GC
                                   ||||||||       |||    ||
                                   GGTGGCTC       CCG    CG
                                      AATCAAIII   ACTGA
GAM1708 TLL2     5'  CGAGGCAACCGGGAAGCAGCC  41585       T   A   C  T
                                   CGAGGC ACCG GGG AG CAGCC
                                   |||||| |||| ||| || |||||
                                   GCTCCG TGGC CCT TC GTCGG
                                      T   _  _ _
GAM1708 AFAP     3'  CGGGGCAGCCGGGGATCCAAGC 41586    A   TA   A   CAG  _
                                   CG GGC  CCG GGG   TCA GC
                                   || |||  ||| |||   ||| ||
                                   GC CCG  GGC CCC   GGT CG
                                    C  TC   _   TA_   T
GAM1708 ALK7     5'  CGAGGCAGCCGGGGCAGCACGG 41587       TA   A      CA_
             CC                     CGAGGC  CCG GGGCAGT   GCC
                                   ||||||  ||| |||||||   |||
                                   GCTCCG  GGC CCCGTCG   CGG
                                      TC   _      TGC
GAM1708 B3GNT7   3'  GCTGAGGGCAGGCAGC      41588     ACC       T
                                   GCT   GAGGGCAG CAGC
                                   |||   |||||||| ||||
                                   CGA   CTCCCGTC GTCG
                                     ___       C
GAM1708 C21orf6  3'  GAGGCCACTGAGAGTTGTTAG  41589         C     CA  C
                                   GAGGCTAC GAGGG  GT AG
                                   |||||||| |||||  || ||
                                   CTCCGGTG CTCTC  CA TC
                                       A     AA  A
GAM1708 FLJ20069 3'  GAGGCACCGTGCCCAGTCAGC  41590       T    AGGG
                                   GAGGC ACCG    CAGTCAGC
                                   ||||| ||||    ||||||||
                                   CTCCG TGGC    GTCAGTCG
                                      _    ACGG
GAM1708 FLJ22282 3'  GAGGCTACCCAGGGCACAATTT 41591          G     ________
             GGTC                     GAGGCTACC AGGGCA      GTC
                                   |||||||| ||||||       |||
                                   CTCCGATGG TCCCGT      CAG
                                        G     GTTAAAC
GAM1708 FLJ23022 3'  CGGGGCAGCCGGGACCTCAG   41592    A   TA   A   AG
                                   CG GGC  CCG GGGC  TCAG
                                   || |||  ||| ||||  ||||
                                   GC CCG  GGC CCTG  AGTC
                                    C  TC   _   G_
GAM1708 HIC2     3'  GAGGCAGCCGAGGCAGGGC   41593       TA     G   TCA
                                   GAGGC  CCGAGG CAG   GC
                                   |||||  |||||| |||   ||
```

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                                CTCCG  GGCTCC GTC   CG
                                   TC     _  C__
GAM1708  KIAA1297  5'  CGGGGCACTGAGGGCAGC    41594    A   T  C
                                CG GGC AC GAGGGCAGT
                                || ||| || |||||||||
                                GC CCG TG CTCCCGTCG
                                 C   _  A
GAM1708  MGC15937  5'  CGAGGCTCCGGGGGTGCC    41595       A   A   CA
                                CGAGGCT CCG GGG  GTC
                                ||||||| ||| |||  |||
                                GCTCCGA GGC CCC  CGG
                                    _  _  CA
GAM1708  RILP      3'  AGCTAGGCAGTCAGC      41596      ACCGA
                                GGCT    GGGCAGTCAGC
                                ||||    ||||||||||
                                TCGA    TCCGTCAGTCG

                                 _____
GAM1708  TIP120A   5'  CGAGGCTACAGAGCCAGC    41597         CGAG  C
                                CGAGGCTAC    GG AGTCAGC
                                |||||||||    || |||||||
                                GCTCCGATG    TC TCGGTCG
                                     ____ _
GAM1708  LOC115273 5'  CGGGGCACCGAGGGCGTC    41598    A   T       A
                                CG GGC ACCGAGGGC GTC
                                || ||| ||||||||| |||
                                GC CCG TGGCTCCCG CAG
                                 C   _        _
GAM1708  LOC158972 3'  CGGGTCTGGCAGTCAG      41599    A  _  ACCGAG
                                CG GG CT     GGCAGTCAG
                                || || ||     |||||||||
                                GC CC GA     CCGTCAGTC
                                 _  A  _______
GAM1708  LOC199923 3'  GAAGGACATGGGGCAGTCAG   41600      CT  CGA
                                GAGG  AC   GGGCAGTCAG
                                ||||  ||   ||||||||||
                                CTTC  TG   CCCGTCAGTC
                                  C_  TAC
GAM1708  LOC201514 5'  GAGGCGCCGGGACAGCC     41601      TA   A
                                GAGGC  CCG GGGCAGTC
                                |||||  ||| ||||||||
                                CTCCG  GGC CCTGTCGG
                                  C_   _
GAM1708  LOC203335 5'  CGGGGCGGCCGAGGGCCTGGGT 41602    A   TA      A___
            C                    CG GGC  CCGAGGGC    GTC
                                || |||  ||||||||    |||
                                GC CCG  GGCTCCCG    CAG
                                 C  CC       GACC
GAM1708  LOC221472 3'  CGGGGTTACCTGGGGCTTTCCC 41603    A  C   GA   AG__
            AG                    CG GG TACC  GGGC    TCAG
                                || || ||||  ||||    ||||
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                                GC CC ATGG  CCCG    GGTC
                                 C  A    AC    AAAG
GAM1708  LOC221710 5'  GGCAGAAGGGCAGTCGGC    41604     TACC        A
                                GGC    GAGGGCAGTC GC
                                |||    |||||||||| ||
                                CCG    TTCCCGTCAG CG
                                  TC__         C
GAM1708  LOC255452 3'  CGAGGGCTGCCGGGGGACGCCA 41605       _ A   A   CA
              GCC                    CGAGG CT CCG GGG  GTCAGCC
                                |||||| || ||| |||  |||||||
                                GCTCC GA GGC CCC  CGGTCGG
                                   C  C   C   TG
GAM1708  LOC256477 5'  GAGGGGAGGGGCAGTCAG    41606      CTACC    _
                                GAGG    GAGGG CAGTCAG
                                ||||    ||||| |||||||
                                CTCC    CTCCC GTCAGTC
                                  C_____    C
GAM1708  LOC257095 5'  CAAGGCTACCGGTCAGTC    41607           AGGG
                                CGAGGCTACCG    CAGTC
                                ||||||||||    |||||
                                GTTCCGATGGC    GTCAG
                                      CA__
GAM1709  ADCY8    5'  GGGGCGGAGCTGGGGGCGG    41610      A    G    A
                                GGGG GGAGC GGGGG GG
                                |||| ||||| ||||| ||
                                CCCC CCTCG CCCCC CC
                                  G    A    G
GAM1709  AQP5     5'  GGGGGGGCAGGGGGCGG     41611      A  A       A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGTCCCCC CC
                                  _ _       G
GAM1709  AR       5'  GGGGGGCGGGTGGGGAGAAGGG 41612     A  A    __       C
                                GGG GG GCGGG  GGGAGGAG GG
                                ||| || |||||  |||||||| ||
                                CCC CC CGCCC  CCCTCTTC CC
                                  _ _    AC       _
GAM1709  ARHG     5'  GGGGGAGCTGGGGGCGG     41613     A    G    A
                                GGG GGAGC GGGGG GG
                                ||| ||||| ||||| ||
                                CCC CCTCG CCCCC CC
                                  _    A    G
GAM1709  ARHGDIA  3'  GGGGAGGGGCTGGGGGGG    41614        A  G    A
                                GGGGAGG GC GGGGG GG
                                ||||||| || ||||| ||
                                CCCCTCC CG CCCCC CC
                                    C  A    _
GAM1709  B3GAT1    5'  GGAGAGGGGCGGCCACGGGCGG 41615        A   GGGGA  A
                                GGGGAGG GCGG    GG GCGG
                                ||||||| ||||    || ||||
```

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                                CCTCTCC CGCC    CC CGCC
                                   C   GGTG_ _
GAM1709 C1orf6   5' GAGGAGGAGGAGGGGCGG   41616        C    A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CTCCTCCTC CTCCCC CC
                                     _    G
GAM1709 C1QG    3' GGGGAGGGGGTGCAGTGGGGGT 41617       A___  __   A
          GG                  GGGGAGG   GCG  GGGGG GG
                              |||||||   |||  ||||| ||
                              CCCCTCC   CGT  CCCCC CC
                                 CCCA  CA    A
GAM1709 CACNG6   5' GGGCGGGAGCGAGGAGCG   41618   A     _
                              GG GCGGGGG GAGGAGCG
                              || ||||||| ||||||||
                              CC CGCCCTC CTCCTCGC
                               _     G
GAM1709 CALM3    3' GGGGTGGGGTGGGGAGG    41619     A AGC _
                              GGGG GG  GG GGGGAGG
                              |||| ||  || |||||||
                              CCCC CC  CC CCCCTCC
                                A ___ A
GAM1709 CALR    3' GGGGAGGGGGTGGGGGAGAGTG 41620       AGCG     G C
          G                   GGGGAGG   GGGGGAG AG GG
                              |||||||   ||||||| || ||
                              CCCCTCC   CCCCCTC TC CC
                                 CCCA     _ A
GAM1709 CAPON   5' GGGGAGGAGGTGGCGGCGGGAG 41622        CG  G  A_
          CGG                   GGGGAGGAG  GG GG  GGAGCGG
                              |||||||||  || ||  |||||||
                              CCCCTCCTC  CC CC  CCTCGCC
                                   CA  G  GC
GAM1709 CAPON   5' GGGGAGCGGTGGGGCTTGCGG  41621   A    _   AGGA
                              GG GGAGCGG GGGG   GCGG
                              || ||||||| ||||   ||||
                              CC CCTCGCC CCCC   CGCC
                               _     A   GAA_
GAM1709 CDC25B   5' GGGCGAGGGGTGGGGGGGG   41623    _   AGC    A
                              GGG GAGG   GGGGGG GG
                              ||| ||||   |||||| ||
                              CCC CTCC   CCCCCC CC
                                G   CCA    _
GAM1709 CDC25B   5' GGGCGAGGGGTGGGGGGGG   41623    _   AGC    A
                              GGG GAGG   GGGGGG GG
                              ||| ||||   |||||| ||
                              CCC CTCC   CCCCCC CC
                                G   CCA    _
GAM1709 COL11A2  3' GGGGAGGACAGGGGTGG    41624       G    GA
                              GGGGAGGA CGGGGG  GG
                              |||||||| ||||||  ||
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                                CCCCTCCT GTCCCC  CC
                                    _     A_
GAM1709 COL11A2  3' GGGGAGGACAGGGGTGG     41624        G     GA
                                GGGGAGGA CGGGGG  GG
                                |||||||| ||||||  ||
                                CCCCTCCT GTCCCC  CC
                                    _     A_
GAM1709 COL1A1   3' GGGCAGGAGCGGGCTGAGG   41625     G       GG
                                GGG AGGAGCGGG  GAGG
                                ||| |||||||||  ||||
                                CCC TCCTCGCCC  CTCC
                                  G       GA
GAM1709 CSNK1G2  3' GGGGCAGGAGTGGGGTAGGGCG 41626     _    C   GG   A
             G                   GGGG AGGAG GGGG  AGG GCGG
                                |||| ||||| ||||  ||| ||||
                                CCCC TCCTC CCCC  TCC CGCC
                                  G    A   A_  _
GAM1709 CTRL     3' GGAGGAGGGGTGGGGGCCCCGG 41627       C  _  A  AG_
                                GGAGGAG GGG GGG GG   CGG
                                ||||||| ||| ||| ||   |||
                                CCTCCTC CCC CCC CC   GCC
                                    _  A   _ GGG
GAM1709 DES      3' GGGGAGGGCGTGGGGAGG    41628       A  G
                                GGGGAGG GCG GGGGAGG
                                ||||||| ||| |||||||
                                CCCCTCC CGC CCCCTCC
                                    _  A
GAM1709 DLX2     3' GGGGAGGGCGGGCAGGCG    41629       A    G  AGGA
                                GGGGAGG GCGGG GG    GCG
                                ||||||| ||||| ||    |||
                                CCCCTCC CGCCC TC    CGC
                                    _    G ____
GAM1709 DNMT3L   5' GGGGGCGGGGAGGGGCG     41631     AGGA      A  A
                                GGGG   GCGGGGGG GG GCG
                                ||||   |||||||| || |||
                                CCCC   CGCCCCTC CC CGC
                                   ____      _ _
GAM1709 DNMT3L   5' GGGGAGGGGCGGGGGCGG    41630       A     GA
                                GGGGAGG GCGGGGG  GG
                                ||||||| |||||||  ||
                                CCCCTCC CGCCCCC  CC
                                    C     G_
GAM1709 ED1      5' AGGGAGGAGGAGGGGCGG    41632        C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| ||||||  ||
                                TCCCTCCTC CTCCCC CC
                                    _    G
GAM1709 EGFL5    3' GGGGGGGGCAGGGGGCGG    41633     A  A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
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                                CCCC CC CGTCCCCC CC
                                  _ C       G
GAM1709 EGLN1    5' GGGGAGGGCCGAGGGGCGG   41634       A G    AGGA
                                GGGGAGG GC GGGGG   GCGG
                                ||||||| || |||||   ||||
                                CCCCTCC CG CTCCC   CGCC
                                   _ G    _____
GAM1709 EIF4G1   3' GGGGAGGAGAGGGACACCTGGC 41635        C   GGAGGA
             GG                   GGGGAGGAG GGGG     GCGG
                                ||||||||| ||||     ||||
                                CCCCTCCTC CCCT     CGCC
                                     T   GTGGAC
GAM1709 EPS15    5' GGGGAGGAGGCGGAGGGAGCGG 41636         _      GGA
                                GGGGAGGAG CGGGGGGA  GCGG
                                ||||||||| ||||||||  ||||
                                CCCCTCCTC GCCTCCCT  CGCC
                                     C      ___
GAM1709 FBXL11   3' GGGGCGGGGTGGGGGGAAG   41637     A AGC
                                GGGG GG  GGGGGGAGG
                                ||||  ||  |||||||||
                                CCCC CC  CCCCCCTTC
                                  G  CCA
GAM1709 FCN2     3' GGGAGGAGTGTGGGGGTGG   41638       CG_   A
                                GGGAGGAG  GGGGG GG
                                ||||||||  ||||| ||
                                CCCTCCTC  CCCCC CC
                                     ACA    A
GAM1709 FHIT     3' GGGGAGAGGCGGGGGGGCG   41639      GA     AGGA
                                GGGGAG  GCGGGGGG   GCG
                                ||||||  ||||||||   |||
                                CCCCTC  CGCCCCCC   CGC
                                   TC      _____
GAM1709 FOS      5' GGGCGAGGGGCCGAGGGGCGG 41640    _   A G    AGGA
                                GGG GAGG GC GGGGG   GCGG
                                ||| |||| || |||||   ||||
                                CCC CTCC CG CTCCC   CGCC
                                  G   C G   _____
GAM1709 FOXG1B   5' GGGGGGGCGGCGGGCGG    41641     A A   G   A
                                GGGG GG GCGG GGG GG
                                |||| || |||| ||| ||
                                CCCC CC CGCC CCC CC
                                  _ _   G  G
GAM1709 FXR2     5' GGGGAGCCGCGGGGGGCGG   41642      GA     A
                                GGGGAG  GCGGGGGG GG
                                ||||||  |||||||| ||
                                CCCCTC  CGCCCCCC CC
                                   GG      G
GAM1709 FXYD1    3' GGGAAGGGGCGGCGGAGGGGGC 41643       A   G  GA  A
             GG                   GGGGAGG GCGG GG  GG GCGG
                                ||||||| |||| ||  || ||||
```

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                                CCCTTCC CGCC CC  CC CGCC
                                    C    G  TC  C
GAM1709  FXYD1    3'  GGGAAGGGGCGGCGGAGGGGGC 41643        A    G  GA  A
                GG                  GGGGAGG GCGG GG  GG GCGG
                                    ||||||| |||| ||  || ||||
                                    CCCTTCC CGCC CC  CC CGCC
                                        C    G  TC  C
GAM1709  GDF2     5'  GGGGAGGAGCTGGGAAGGAGCG 41644          GG
                G                    GGGGAGGAGC  GGGGAGGAGCGG
                                    ||||||||||  ||||||||||||
                                    CCCCTCCTCG  CCCTTCCTCGCC
                                          A_
GAM1709  GNA15    3'  GGGCAGGAGTACCCTGGGGGGC 41645     G    C_____     A
                GG                  GGG AGGAG     GGGGGG GG
                                    ||| |||||     |||||| ||
                                    CCC TCCTC     CCCCCC CC
                                      G    ATGGGA     G
GAM1709  GRB14    5'  GGGGAGGAGCGGCCGGTGG   41647          GG  A
                                    GGGGAGGAGCGG  GG GG
                                    ||||||||||||  || ||
                                    CCCCTCCTCGCC  CC CC
                                          GG  A
GAM1709  GRB14    5'  GGGGAGAGGGGAGGAGCGG   41646       GAGCG
                                    GGGGAG    GGGGGAGGAGCGG
                                    ||||||    ||||||||||||
                                    CCCCTC    TCCCCTCCTCGCC
                                              _____
GAM1709  GTF2IRD1  5'  GGAGAGGAGCGGAGAGCGG   41648             A
                                    GGGGAGGAGCGGGGGG GG
                                    |||||||||||||||| ||
                                    CCTCTCCTCGCCTCTC CC
                                               G
GAM1709  HNRPDL   5'  GAGGAGGGGCGGGGGCTGG   41649        A      GA
                                    GGGGAGG GCGGGGG  GG
                                    ||||||| |||||||  ||
                                    CTCCTCC CGCCCCC  CC
                                        C      GA
GAM1709  HOXC10   3'  GAGGAGGGGCGGGGAGAGGAAG 41650    A          ____   III
                GAGCGGC                 GG GCGGGGGGAGGA   GCGG   C
                                    ||  ||||||||||||    ||||  |
                                    CC CGCCCCTCTCCT    CGCC   G
                                     C          TCCT    III
GAM1709  IGFBP2   3'  GGAGAGGGGCGGGGGGCAGG   41651        A      _
                                    GGGGAGG GCGGGGGGG AGG
                                    ||||||| |||||||| |||
                                    CCTCTCC CGCCCCCC TCC
                                        C       G
GAM1709  INSR     3'  GGGGGCGGGTGGGGGGAACG   41652      AGGA    _   A
                                    GGGG    GCGGG GGG GGAGCG
                                    ||||    ||||| ||| ||||||
```

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                                CCCC   CGCCC CCC CCTTGC
                                  ____    A  C
GAM1709  ITGA6    5'  GGAGGGGAGCGGGGACCTGCAG 41653     A       GAGG_
            CGG                   GGGG GGAGCGGGGG    AGCGG
                                  |||| ||||||||||    |||||
                                  CCTC CCTCGCCCCT    TCGCC
                                    C        GGACG
GAM1709  JAM2     5'  GGGCGAGGAGCTGGGGGCGG  41654    _     G    A
                                  GGG GAGGAGC GGGGG GG
                                  ||| ||||||| ||||| ||
                                  CCC CTCCTCG CCCCC CC
                                    G      A    G
GAM1709  JUNB     3'  GGGGAGGGCAGGGGGCGG    41655       A       A
                                  GGGGAGG GCGGGGGG GG
                                  ||||||| |||||||| ||
                                  CCCCTCC CGTCCCCC CC
                                     _      G
GAM1709  KCNC3    5'  GGGGGGCGGGGCGGGAGGGGCG 41658    A  A    __    A
            G                     GGG GG GCGGGG  GGAGG GCGG
                                  ||| || ||||||  ||||| ||||
                                  CCC CC CGCCCC  CCTCC CGCC
                                    _ _     GC    C
GAM1709  KCNC3    5'  GGGAGGGGCGGGGACGCAGGGG 41656       A     G__  A
            CGG                   GGGAGG GCGGGGG   AGG GCGG
                                  |||||| |||||||   ||| ||||
                                  CCCTCC CGCCCCT   TCC CGCC
                                     C      GCG   C
GAM1709  KCNC3    3'  GGGAAGGGGCGGGGGGGACCG  41657       A       AG  G
                                  GGGGAGG GCGGGGGG  GA CG
                                  ||||||| ||||||||  || ||
                                  CCCTTCC CGCCCCCC  CT GC
                                     C       __  G
GAM1709  KCNF1    3'  GGGGAGGGTTGGGGGGACACAG 41659       AGC      GGA
                                  GGGGAGG   GGGGGGA   GCGG
                                  |||||||   |||||||   ||||
                                  CCCCTCC   CCCCCCT   TGTC
                                     CAA      G__
GAM1709  KCNK3    3'  GGGGATGAGGAAGGGGAG    41660      G   CG
                                  GGGGA GAG  GGGGGAG
                                  ||||| |||  |||||||
                                  CCCCT CTC  TCCCCTC
                                    A   CT
GAM1709  KCNQ2    5'  GGGGCGGAGCGCGGGGGGCGG  41661     A    _    AGGA
                                  GGGG GGAGCG GGGGG    GCGG
                                  |||| |||||| |||||    ||||
                                  CCCC CCTCGC CCCCC    CGCC
                                    G     G    _____
GAM1709  LASS1    3'  GGAGGGGGTGGAGGGGCG    41662      C   _    A
                                  GGAG GGGG GGAGG GCG
                                  |||| |||| ||||| |||
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                                CCTC CCCC CCTCC CGC
                                  _   A    C
GAM1709  LBX1    3'  GGGGAGGAGGCGGGAGTGG   41663        _     GA
                                GGGGAGGAG CGGGGG  GG
                                ||||||||| ||||||  ||
                                CCCCTCCTC GCCCTC  CC
                                     C     A_
GAM1709  LRP1    5'  GGCGGGGAGGGGGGGGTGG   41665   _ A   C     A
                                GG GG GGAG GGGGGG GG
                                || || |||| |||||| ||
                                CC CC CCTC CCCCCC CC
                                 G _   _     A
GAM1709  LRP1    5'  GGAGGGGGGGGTGGGGGGCG   41664     C     A__ A
                                GGAG GGGGGG   GG GCG
                                |||| ||||||   || |||
                                CCTC CCCCCC   CC CGC
                                  _     ACC  C
GAM1709  LSP1    3'  GGGGAGGGCGGGGGCGG    41666       A      GA
                                GGGGAGG GCGGGGG  GG
                                ||||||| |||||||  ||
                                CCCCTCC CGCCCCC  CC
                                   _      G_
GAM1709  MAP3K10  5'  GGGGAGGGGCCGGGGGCTGCGG 41667       A  G    AGGA
                                GGGGAGG GC GGGGG   GCGG
                                ||||||| || |||||   ||||
                                CCCCTCC CG CCCCC   CGCC
                                    C  G    GA__
GAM1709  MGMT    5'  GGGGCGGCGGGGGGGGGCG    41668     AGGA      A GA
                                GGGG   GCGGGGGG G  GCG
                                ||||   |||||||| |  |||
                                CCCC   CGCCCCCC C  CGC
                                  GC__      _ __
GAM1709  MGMT    5'  GGGGGGGGCGGGGGGGG    41669     A  A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCCC CC
                                  _ C      _
GAM1709  MIC2    5'  GGGGGCGGGTGAGGGGAGCGG  41670     AGGA    _  A
                                GGGG   GCGGG GGG GGAGCGG
                                ||||   ||||| ||| |||||||
                                CCCC   CGCCC CTC CCTCGCC
                                  ____    A  C
GAM1709  MKPX    5'  GAGGAGGAGCGGCGGGGCGG  41671          _   A
                                GGGGAGGAGCGG GGGG GG
                                |||||||||||| |||| ||
                                CTCCTCCTCGCC CCCC CC
                                       G   G
GAM1709  MNT     3'  GGGGAGGGGCAGCGGGTGG   41672       A   G  A
                                GGGGAGG GCGG GGG GG
                                ||||||| |||| ||| ||
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                                CCCCTCC CGTC CCC CC
                                    C   G  A
GAM1709 MSL3L1   5' GGCGGGGGGCGGGGAGGCG   41674   _ A A     AGGA
                                GG GG GG GCGGGGGGG   GCG
                                || || || ||||||||   |||
                                CC CC CC CGCCCCTC   CGC
                                 G _ _     ____
GAM1709 MSL3L1   5' GGGGAGGGCGGGCGGGGGCGG 41673      A   G A A
                                GGGGAGG GCGGG GG GG GCGG
                                ||||||| ||||| || || ||||
                                CCCCTCC CGCCC CC CC CGCC
                                    _   G _ _
GAM1709 MSL3L1   5' GGCGGGGGGCGGGGAGGCG   41674   _ A A     AGGA
                                GG GG GG GCGGGGGGG   GCG
                                || || || ||||||||   |||
                                CC CC CC CGCCCCTC   CGC
                                 G _ _     ____
GAM1709 MSL3L1   5' GGGGAGGGCGGGCGGGGGCGG 41673      A   G A A
                                GGGGAGG GCGGG GG GG GCGG
                                ||||||| ||||| || || ||||
                                CCCCTCC CGCCC CC CC CGCC
                                    _   G _ _
GAM1709 MSL3L1   5' GGCGGGGGGCGGGGAGGCG   41674   _ A A     AGGA
                                GG GG GG GCGGGGGGG   GCG
                                || || || ||||||||   |||
                                CC CC CC CGCCCCTC   CGC
                                 G _ _     ____
GAM1709 MSL3L1   5' GGGGAGGGCGGGCGGGGGCGG 41673      A   G A A
                                GGGGAGG GCGGG GG GG GCGG
                                ||||||| ||||| || || ||||
                                CCCCTCC CGCCC CC CC CGCC
                                    _   G _ _
GAM1709 NCALD    3' GGGGAAGAGAGGGGAGTGG  41675       C    A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CCCCTTCTC CCCCTC CC
                                     T    A
GAM1709 NCOA6IP  5' GGGAAGGGGCGGGACCACGGGC 41676      A    GGA_ A
           GG                    GGGGAGG GCGGGG   GG GCGG
                                ||||||| ||||||   || ||||
                                CCCTTCC CGCCCT   CC CGCC
                                   C    GGTG _
GAM1709 NEUROD2  5' GGGGAGGGGAGGGGGGGAGG  41677     __   C
                                GGGGA  GGAG GGGGGGAGG
                                |||||  |||| |||||||||
                                CCCCT  CCTC CCCCCCTCC
                                  CC   _
GAM1709 NPR1     5' GGGAAGGAGCAGGAGC     41678         GGGGGG
                                GGGGAGGAGC    AGGAGC
                                ||||||||||    ||||||
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                                CCCTTCCTCG     TCCTCG
                                       _______
GAM1709 NRXN1    5' GGGGAGCGGGCGGCGCGGAGTG 41679    A      G A__   C
             G                   GG GGAGCGGG GG   GGAG GG
                                 || |||||||| ||   |||| ||
                                 CC CCTCGCCC CC   CCTC CC
                                  _      G GCG    A
GAM1709 NTSR1    3' GGGGAGGGGTGGGGAGGAG   41680       AGC _
                                 GGGGAGG   GG GGGGAGGAG
                                 |||||||   || |||||||||
                                 CCCCTCC   CC CCCCTCCTC
                                     ___ A
GAM1709 PACSIN1  3' GGGGAGGGGCGGCAGTGG    41681       A   G  GA
                                 GGGGAGG GCGG GG  GG
                                 ||||||| |||| ||  ||
                                 CCCCTCC CGCC TC  CC
                                     C   G  A_
GAM1709 PAFAH1B1 5' GGGGGAGGGGAGGGGAGCG   41682    A   C     A
                                 GGG GGAG GGGGGG GGAGCG
                                 ||| |||| |||||| ||||||
                                 CCC CCTC CCCTCC CCTCGC
                                   _   _    _
GAM1709 PAX2     3' GGGGAGGGGCGGCAGGCGG   41684       A   G   A
                                 GGGGAGG GCGG GGG GG
                                 ||||||| |||| ||| ||
                                 CCCCTCC CGCC TCC CC
                                     C   G   G
GAM1709 PAX2     3' GGGAGGGGATGGGAGGAGTGG  41683      AGC  _      C
                                 GGGAGG   GGG GGGAGGAG GG
                                 ||||||   ||| |||||||| ||
                                 CCCTCC   CCT CCCTCCTC CC
                                    ___  A       A
GAM1709 PAX2     3' GGGGAGGGGCGGCAGGCGG   41684       A   G   A
                                 GGGGAGG GCGG GGG GG
                                 ||||||| |||| ||| ||
                                 CCCCTCC CGCC TCC CC
                                     C   G   G
GAM1709 PAX2     3' GGGAGGGGATGGGAGGAGTGG  41683      AGC  _      C
                                 GGGAGG   GGG GGGAGGAG GG
                                 ||||||   ||| |||||||| ||
                                 CCCTCC   CCT CCCTCCTC CC
                                    ___  A       A
GAM1709 PCTK3    3' GGGGAGGAGTGGAGGGTGG   41685        C     A
                                 GGGGAGGAG GGGGGG GG
                                 ||||||||| |||||| ||
                                 CCCCTCCTC CCTCCC CC
                                      A     A
GAM1709 PDE4A    3' GGGGGGCGGGGGGGGTGAGTGG  41686    A  A      AG   C
                                 GGG GG GCGGGGGGG  GAG GG
                                 ||| || ||||||||  ||| ||
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                                CCC CC CGCCCCCC  CTC CC
                                  _ _      CA   A
GAM1709  PDE4A    3'  GGGGAGGAGTGGAGGGGAACAG 41687         CG    A
                                GGGGAGGAG  GGGGG GGAGCGG
                                |||||||||  ||||| |||||||
                                CCCCTCCTC  CCTCC CCTTGTC
                                     A_    _
GAM1709  PDE4A    3'  AGGGGAGTGAGGGGAGGAGTGG 41688     A   C         C
                                GGG GGAG GGGGGGAGGAG GG
                                ||| |||| |||||||||| ||
                                TCC CCTC CTCCCCTCCTC CC
                                  _   A         A
GAM1709  PLOD3    5'  GGGGAGGGGCGGCGGCTCGG   41689        A   G  GA_
                                GGGGAGG GCGG GG   GG
                                |||||||| |||| ||   ||
                                CCCCTCC CGCC CC   CC
                                     C   G  GAG
GAM1709  PLOD3    5'  GGGAGGCGGGGGAGGGGCGG   41690       AGCG      A
                                GGGAGG   GGGGGAGG GCGG
                                ||||||   |||||||| ||||
                                CCCTCC   CCCCCTCC CGCC
                                    G___      C
GAM1709  PML      3'  GGCGAGGAGTGGGCTGGCGAGG 41691    G    C  __ _    C
            AGTGG                 GG GAGGAG GGG  GG GAGGAG GG
                                || |||||| |||  || |||||| ||
                                CC CTCCTC CCC  CC CTCCTC CC
                                 G    A  GA  G    A
GAM1709  PML      3'  GGCGAGGAGTGGGCTGGCGAGG 41691    G    C  __ _    C
            AGTGG                 GG GAGGAG GGG  GG GAGGAG GG
                                || |||||| |||  || |||||| ||
                                CC CTCCTC CCC  CC CTCCTC CC
                                 G    A  GA  G    A
GAM1709  PML      3'  GGCGAGGAGTGGGCTGGCGAGG 41691    G    C  __ _    C
            AGTGG                 GG GAGGAG GGG  GG GAGGAG GG
                                || |||||| |||  || |||||| ||
                                CC CTCCTC CCC  CC CTCCTC CC
                                 G    A  GA  G    A
GAM1709  PPP2R1A  3'  GGGGAGGACGGGAGGTGG    41692        G     A
                                GGGGAGGA CGGGGGG GG
                                |||||||| ||||||| ||
                                CCCCTCCT GCCCTCC CC
                                     _     A
GAM1709  PRDM16   3'  GGGGAGGATGCTGAGGAGTGG  41693        _ _    A
                                GGGGAGGA GC GGGGGG GG
                                |||||||| || |||||| ||
                                CCCCTCCT CG CTCCTC CC
                                     A A    A
GAM1709  PRDM2    3'  GGGGAGAGAGGGGTGG      41694        AGC    A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
```

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                                CCCCTCT  CTCCCC CC
                                   ___     A
GAM1709  PRKCA    3'  GGGGAGGGCTGGGGGCTGG   41695       A _    GA
                                GGGGAGG GC GGGGG  GG
                                ||||||| || |||||  ||
                                CCCCTCC CG CCCCC  CC
                                   _ A    GA
GAM1709  PROC     3'  GGGGGGGGGCGGGGGGGG    41696     A A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCCC CC
                                  C  C      _
GAM1709  PRODH    3'  GGCGGGGGCGGGGGGTGCTGG  41697    _ A A      AGGA _
                                GG GG GG GCGGGGGG   GC GG
                                || || || ||||||||   || ||
                                CC CC CC CGCCCCCC   CG CC
                                 G _ _      A___  A
GAM1709  PTPRF    3'  GGCGGAGGAGAGGGGAGCG   41698   A   C    A
                                GG GGAG GGGGGG GGAGCG
                                || |||| |||||| ||||||
                                CC CCTC CTCTCC CCTCGC
                                 G   _    _
GAM1709  PTPRF    3'  GGCGGAGGAGAGGGGAGCG   41698   A   C    A
                                GG GGAG GGGGGG GGAGCG
                                || |||| |||||| ||||||
                                CC CCTC CTCTCC CCTCGC
                                 G   _    _
GAM1709  PTPRG    5'  GGGGAGAGGCAGGGGGAGCGG  41699      GA      GGA
                                GGGGAG  GCGGGGGGA  GCGG
                                ||||||  |||||||||  ||||
                                CCCCTC  CGTCCCCCT  CGCC
                                   TC       ___
GAM1709  PXN      3'  GGGGAGGATGGAGAGTGG    41700       GC    A
                                GGGGAGGA  GGGGGG GG
                                ||||||||  |||||| ||
                                CCCCTCCT  CCTCTC CC
                                    A_     A
GAM1709  RAB13    5'  GGGGAGGGGTGGGGAGCGC   41702       AGC _    GA
                                GGGGAGG   GG GGGGAG  GC
                                |||||||   || ||||||  ||
                                CCCCTCC   CC CCCCTC  CG
                                   ___  A     G_
GAM1709  RAB13    5'  GGGGGAGCCGGGGGGAGG    41701    A    G
                                GGG GGAGC GGGGGGAGG
                                ||| ||||| ||||||||
                                CCC CCTCG CCCCCTCC
                                  _    G
GAM1709  RAB3A    3'  GGGGGGGGGGGGGGGTCCCAG  41703    A AGC    A AG_
                                GGGG GG   GGGGGG GG   CGG
                                |||| ||   |||||| ||   |||
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                                CCCC CC   CCCCCC CC   GTC
                                  _ ___     _ AGG
GAM1709  RANBP3   3'  GGGAGGGGGGTTTGGGGGGCGG 41704       AGC  ___  A  A
                                GGGAGG   GGG   GGG GG GCGG
                                ||||||   |||   ||| || ||||
                                CCCTCC   CCC   CCC CC CGCC
                                   C__   AAA   _ _
GAM1709  REST     5'  GGGGAGAGGTGGGGGAGG    41705       G  CG
                                GGGGAG AG  GGGGGAGG
                                |||||| ||  ||||||||
                                CCCCTC TC  CCCCCTCC
                                   _ CA
GAM1709  RHCG     3'  GGGGAGGGCAGGGGTGG     41706        A      GA
                                GGGGAGG GCGGGGG  GG
                                ||||||| |||||||  ||
                                CCCCTCC CGTCCCC  CC
                                   _      A_
GAM1709  RNH      5'  GGGGAGGGGTGGGTGGGGTGG  41707        AGC_ _   A
                                GGGGAGG    GG GGGG GG
                                |||||||    || |||| ||
                                CCCCTCC    CC CCCC CC
                                    CCAC  A    A
GAM1709  RNH      5'  GGGGAGGGGTGGGTGGGGTGG  41707        AGC_ _   A
                                GGGGAGG    GG GGGG GG
                                |||||||    || |||| ||
                                CCCCTCC    CC CCCC CC
                                    CCAC  A    A
GAM1709  RPA1     3'  GGGGATGGGGGGGGGGTGG    41708      _ AGC     A
                                GGGGA GG   GGGGGG GG
                                |||||  ||   |||||| ||
                                CCCCT CC   CCCCCC CC
                                   A  CC_     A
GAM1709  SALL1    3'  GGGGCGGGGTGGGGGGCAAGG  41709      A  AGC     __
                                GGGG GG   GGGGGG  AGG
                                ||||  ||   ||||||  |||
                                CCCC CC   CCCCCC  TCC
                                  G  CCA     GT
GAM1709  SCRT1    3'  GGGGAGGGGAGGGGGCTCGG   41710        AGC     A  AG
                                GGGGAGG   GGGGGG GG  CGG
                                |||||||   |||||| ||  |||
                                CCCCTCC   CCTCCC CC  GCC
                                   ___     _ GA
GAM1709  SF1      5'  GGGGCGGGCCGGGGGCGG    41711      A  A  G    A
                                GGGG GG GC GGGGG GG
                                |||| || || ||||| ||
                                CCCC CC CG CCCCC CC
                                  G  _  G    G
GAM1709  SIAT8E   5'  GGGGAGGGGGAGGGGCG     41712       GGAGCG       A
                                GGGGA     GGGGGAGG GCG
                                |||||     |||||||| |||
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                                CCCCT     CCCCCTCC CGC
                                  _______       C
GAM1709  SLC9A1   3'  GGGGAGGAGCTGTGCTGGGGTG 41713          GG____    A
              G                   GGGGAGGAGC     GGGG GG
                                  ||||||||||     |||| ||
                                  CCCCTCCTCG     CCCC CC
                                        ACACGA    A
GAM1709  SLC9A3R2 5'  GGGGGAGCTCGGGGGCGG    41714     A    G_    A
                                  GGG GGAGC  GGGGG GG
                                  ||| |||||  ||||| ||
                                  CCC CCTCG  CCCCC CC
                                    _    AG    G
GAM1709  SMG1     3'  GGGGAGGAGTAGGGAACGATGG 41715          CG     G  GC
                                  GGGGAGGAG  GGGGGA GA  GG
                                  |||||||||  ||||||  ||  ||
                                  CCCCTCCTC  TCCCTT CT  CC
                                        A_     G  A_
GAM1709  SOX11    3'  GGGGGGCCGGGGGAGG      41716     A  A  G
                                  GGG GG GC GGGGGAGG
                                  ||| || || ||||||||
                                  CCC CC CG CCCCCTCC
                                    _ _  G
GAM1709  SPI1     3'  GGGGAGGGGCGGGTGACGG    41717        A     G GA
                                  GGGGAGG GCGGG G  GG
                                  ||||||| ||||| |  ||
                                  CCCCTCC CGCCC C  CC
                                       C     A TG
GAM1709  SPI1     3'  GGAGTGGGGGGAGGGGCGG    41718      C        A
                                  GGAG GGGGGGAGG GCGG
                                  |||| ||||||||| ||||
                                  CCTC CCCCCCTCC CGCC
                                    A        C
GAM1709  SPTB     3'  GGGGAGGATGGAGGGCGG     41719         GC     A
                                  GGGGAGGA  GGGGGG GG
                                  ||||||||  |||||| ||
                                  CCCCTCCT  CCTCCC CC
                                       A_     G
GAM1709  SRD5A1   5'  GAGGAGGGGCGGCTACCGGAGG 41720         A    GG___     A
              GGCGG                    GGGGAGG GCGG     GGAGG GCGG
                                  ||||||| ||||     ||||| ||||
                                  CTCCTCC CGCC     CCTCC CGCC
                                       C    GATGG    C
GAM1709  TCF3     3'  GGGGGGGACGGGGGGGGCTCAGG 41721      A  AG      ____
                                  GGGG GG  CGGGGGG    AGG
                                  |||| ||  |||||||    |||
                                  CCCC CC  GCCCCCC    TCC
                                    _ CT      CGAG
GAM1709  TFAP2A   3'  GGTGAGGCGTGGGAGGGGCGG  41722    GA  A   GG     A
                                  GG  GG GCG  GGGAGG GCGG
                                  ||  || |||  |||||| ||||
```

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                                CC  TC CGC  CCCTCC CGCC
                                 AC  _  A_     C
GAM1709  TNFRSF11A 3'  GGGGGGAGTCGGGGGGAGG   41723      A   _
                                GGGG GGAG CGGGGGGAGG
                                |||| |||| ||||||||||
                                CCCC CCTC GCCCCCCTCC
                                  _   A
GAM1709  TNFSF5   3'  GGGGGGGGGGGGGGGGTTTCGG  41724      A  AGC     A  AG_
                                GGGG GG   GGGGGG GG   CGG
                                |||| ||   |||||| ||   |||
                                CCCC CC   CCCCCC CC   GCC
                                  _ C__     _ AAA
GAM1709  TSLP     5'  GGGGAGGAAGGTCAGGGAGGAG 41725          C  __
              CGG                    GGGGAGGAG GG  GGGGAGGAGCGG
                                |||||||||  ||  ||||||||||||
                                CCCCTCCTT CC  TCCCTCCTCGCC
                                    _ AG
GAM1709  TULP1    3'  GGGGAGGAGGGGGGCACAGCGG 41726         GC     AGG
                                GGGGAGGA  GGGGGG   AGCGG
                                ||||||||  ||||||   |||||
                                CCCCTCCT  CCCCCC   TCGCC
                                    __     GTG
GAM1709  UGCG     5'  GGGGGGTGGGGACGGAAGGGGC 41727      A  AGC  __     A
              GG                   GGGG GG   GGG  GGGAGG GCGG
                                |||| ||   |||  |||||| ||||
                                CCCC CC   CCC  CCTTCC CGCC
                                  _ AC_   TG     C
GAM1709  VAT1     3'  GGGGAGGGGCAGGGGAGAGCGG 41728         A      GA
                                GGGGAGG GCGGGGGG  GGAGCGG
                                |||||||  |||||||  |||||||
                                CCCCTCC CGTCCCC  TCTCGCC
                                    C      __
GAM1709  WSX1     5'  AGGGGGAGTGGGGAGGCG    41729      A   C     AGGA
                                GGGG GGAG GGGGGG    GCG
                                |||| |||| ||||||    |||
                                TCCC CCTC CCCCTC    CGC
                                  _    A     ____
GAM1709  YWHAE    3'  GGGGAGGAGTGAGGGGAAG    41730          C
                                GGGGAGGAG GGGGGGAGG
                                |||||||| |||||||||
                                CCCCTCCTC CTCCCCTTC
                                     A
GAM1709  20D7-FC4  3'  GGGGGGAGAGGGGAGG      41731      A   CG
                                GGGG GGAG  GGGGGAGG
                                |||| ||||  ||||||||
                                CCCC CCTC  TCCCCTCC
                                  _   __
GAM1709  ARHGEF9   5'  GGGGAGGGGAGGGGGATG    41732         AGC     A  GC
                                GGGGAGG   GGGGGG GGA  G
                                |||||||   |||||| |||  |
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                                CCCCTCC   CCTCCC CCT  C
                                   ___     _  A_
GAM1709  ATPW     5'  GGGGCGGGGGCGGGGCGAGGGC 41733      A  A_     G    A
                GG                  GGGG GG  GCGGGG GAGG GCGG
                                    |||| ||  |||||| |||| ||||
                                    CCCC CC  CGCCCC CTCC CGCC
                                      G  CC     G   _
GAM1709  BCL2L1    3'  GGGGAGAGTGGGGGGAAAA    41734        G  C
                                    GGGGAG AG GGGGGGAGGA
                                    |||||| || ||||||||||
                                    CCCCTC TC CCCCCCTTTT
                                       _ A
GAM1709  C20orf178 3'  GGGTGAGGAGTGGGCCAGAGTG 41735     _     C   GGGA    C
                G                    GGG GAGGAG GGG    GGAG GG
                                    ||| |||||| |||    |||| ||
                                    CCC CTCCTC CCC    TCTC CC
                                      A     A   GG__    A
GAM1709  C20orf46  3'  GGGCGGGAGCAGGGGGGTGG    41736     GA         A
                                    GGG  GGAGCGGGGGGG GG
                                    |||  |||||||||||| ||
                                    CCC  CCTCGTCCCCC CC
                                      GC          A
GAM1709  C2orf9    3'  GGGGAGGGGCGGGGGGGCAG   41737         A       AGGA
                                    GGGGAGG GCGGGGGGG    GCGG
                                    ||||||| ||||||||    ||||
                                    CCCCTCC CGCCCCCC    CGTC
                                        C       _____
GAM1709  CACNG4    3'  GGGTGGGGGCGAGGGGGCG    41738     GA  A       AGGA
                                    GGG  GG GCGGGGGG    GCG
                                    |||  || ||||||||    |||
                                    CCC  CC CGCTCCCC    CGC
                                      AC  C       _____
GAM1709  CAMKK1    3'  GGGGAGGGGCGGGAGTGG     41739         A      GA
                                    GGGGAGG GCGGGGG  GG
                                    ||||||| |||||||  ||
                                    CCCCTCC CGCCCTC  CC
                                        C      A_
GAM1709  CARM1     3'  GGGGGGGCGGGGGGGGG      41740      A  A       A
                                    GGGG GG GCGGGGGG GG
                                    |||| || |||||||| ||
                                    CCCC CC CGCCCCCC CC
                                       _ _       _
GAM1709  CITED2    3'  GGGGGGCGGCGGGGGGGACAG  41741     A  A   _    A  AG
                                    GGG GG GCGG GGGG GG  CGG
                                    ||| || |||| |||| ||  |||
                                    CCC CC CGCC CCCC CC  GTC
                                      _ _   G    _ CT
GAM1709  CLSTN1    5'  GGGAGGGGCGGGGGAGAGGAGC 41742        A      _
                GG                   GGGAGG GCGGGGG GAGGAGCGG
                                    |||||| ||||||| |||||||||
```

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                                CCCTCC CGCCCCC CTCCTCGCC
                                   C      T
GAM1709  CNIL     5'  GGGGAGGAGGAGCGGGGAGCGG 41743         C   G  A
                                GGGGAGGAG GGG GG GGAGCGG
                                ||||||||| ||| || |||||||
                                CCCCTCCTC CTC CC CCTCGCC
                                     _  G  _
GAM1709  CPLX1    3'  GGAGGATCTGTAGGGGGAGGGG 41744       GC___       A
           CGG                    GGAGGA    GGGGGGAGG GCGG
                                ||||||    ||||||||| ||||
                                CCTCCT    TCCCCCTCC CGCC
                                   AGACA       C
GAM1709  CPLX1    3'  GGGGAGGGGCGGGGGCTCCGCG 41745       A      GAGGA
           G                     GGGGAGG GCGGGGG    GCGG
                                ||||||| |||||||    ||||
                                CCCCTCC CGCCCCC    CGCC
                                   C      GAGG_
GAM1709  DDX39    3'  GGGAAGGGAGGTGGGAGGGGCG 41746       AGC  _     A
           G                     GGGGAGG   GGG GGGAGG GCGG
                                |||||||   ||| |||||| ||||
                                CCCTTCC   TCC CCCTCC CGCC
                                   C__  A     C
GAM1709  DGKZ     3'  GGGGCAGGAGCGGGGGCTGG   41747     _        GA
                                GGGG AGGAGCGGGGG  GG
                                |||| ||||||||||  ||
                                CCCC TCCTCGCCCCC  CC
                                  G         GA
GAM1709  DGKZ     3'  GGGGAGGGTCGCCGGAGCG   41748       AG  GGGGGA
                                GGGGAGG  CG     GGAGCG
                                |||||||  ||     ||||||
                                CCCCTCC  GC     CCTCGC
                                   CA  GG____
GAM1709  DKFZp547F072 5'  GGGGAGGGGTGGGGAGAAA   41749       AGC  _
                                GGGGAGG   GG GGGGAGGAG
                                |||||||   || |||||||||
                                CCCCTCC   CC CCCCTCTTT
                                   ___  A
GAM1709  DKFZp547O146 5'  GGGGTGGGGAGAGGGGCG    41750     AGGAGC       A
                                GGGG     GGGGGGAGG GCG
                                ||||     ||||||||| |||
                                CCCC     CCCCTCTCC CGC
                                  A_____        C
GAM1709  DKFZP564I1171 3'  AGGGAGGAGCGATCGGGAG   41751          G_
                                GGGGAGGAGCGG  GGGAG
                                ||||||||||||  |||||
                                TCCCTCCTCGCT  CCCTC
                                       AG
GAM1709  DKFZp762K222 5'  GGGGAGGGGGCGGGCGGGG   41752       A_    G  A
                                GGGGAGG  GCGGG GG GG
                                |||||||  ||||| || ||
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                                CCCCTCC  CGCCC CC CC
                                   CC    G _
GAM1709  FLJ10246  3'  GGAGAGGGACAATGGGGAGG  41753       AG  _
                                GGGGAGG  CGG GGGGAGG
                                |||||||  ||| |||||||
                                CCTCTCC  GTT CCCCTCC
                                   CT   A
GAM1709  FLJ13224  5'  GGGGAGGGTCGGGGGGCCAGG  41754       AG     __
                                GGGGAGG  CGGGGGG  AGG
                                |||||||  |||||||  |||
                                CCCCTCC  GCCCCCC  TCC
                                   CA      GG
GAM1709  FLJ13322  3'  GGGGAGAAGCAGGGGTGG    41755            GA
                                GGGGAGGAGCGGGGG  GG
                                ||||||||||||||  ||
                                CCCCTCTTCGTCCCC  CC
                                         A_
GAM1709  FLJ14280  3'  GGGGAGCGGTGGGAAAGGGGGG 41756      _______   C     A
          TGG                     GGGGA     GGAG GGGGGG GG
                                |||||     |||| |||||| ||
                                CCCCT     CCTT CCCCCC CC
                                   CGCCAC    T     A
GAM1709  FLJ14681  3'  GGGTGGGTTGGGGGGGAGCGG  41757     GA  AGCG    A
                                GGG  GG    GGGGG GGAGCGG
                                |||  ||    ||||| |||||||
                                CCC  CC    CCCCC CCTCGCC
                                  AC  AA__    _
GAM1709  FLJ20406  3'  GGGGCGGGGCGGGGGACGG    41758     A  A      GA
                                GGGG GG GCGGGGG  GG
                                ||||  || |||||||  ||
                                CCCC CC CGCCCCC  CC
                                  G  C      TG
GAM1709  FLJ23058  3'  GGGTGGGAGCGGGGGGCTGG   41759     GA         A_
                                GGG  GGAGCGGGGGG  GG
                                |||  ||||||||||  ||
                                CCC  CCTCGCCCCCC  CC
                                  AC          GA
GAM1709  FLJ23416  3'  GGGGAGGGCTGGGAGCGG    41760       A  G    A
                                GGGGAGG GC GGGGG GG
                                |||||||  ||  |||||  ||
                                CCCCTCC CG CCCTC CC
                                   _  A    G
GAM1709  FLJ23519  5'  GGGGAGGGGTGGGTGGGGTGG  41707       AGC_  _   A
                                GGGGAGG    GG GGGG GG
                                |||||||    ||  ||||  ||
                                CCCCTCC    CC CCCC CC
                                   CCAC  A    A
GAM1709  FLJ30213  5'  GGGGTGGGTGGGGGGAGG    41761      A  AGC
                                GGGG GG   GGGGGGGAGG
                                ||||  ||   |||||||||
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                                CCCC CC   CCCCCCTCC
                                  A  CA_
GAM1709  FLJ30567  3'  GGCGGAGGAGCTCCCCAGGGAG 41762    _      _____      A
              TGG                  GG GGAGGAGC     GGGGGG GG
                                || ||||||||     |||||| ||
                                CC CCTCCTCG     TCCCTC CC
                                 G       AGGGG      A
GAM1709  FOXH1     3'  GGGTGGGAGCGGGAGGGAGGAG 41763     GA       _
              CGG                  GGG  GGAGCGGG GGGAGGAGCGG
                                |||  |||||||| ||||||||||
                                CCC  CCTCGCCC CCCTCCTCGCC
                                  AC       T
GAM1709  FOXO3A    5'  GGGGAGGGGCGCCCGGGGGAGG 41764        A  ___       A
              GGCGG                   GGGGAGG GCG   GGGGGAGG GCGG
                                ||||||| |||   |||||||| ||||
                                CCCCTCC CGC   CCCCCTCC CGCC
                                    C   GGG       C
GAM1709  GBTS1     3'  GGGGAGGCAGCGGGGGGTCAG   41765        _       GA
                                GGGGAGG AGCGGGGGG  GG
                                ||||||| ||||||||  ||
                                CCCCTCC TCGCCCCC  TC
                                    G       AG
GAM1709  GDF11     5'  AGGGAGGTACTGGGGGGCGG   41766        A  _     A
                                GGGGAGG GC GGGGGG GG
                                ||||||| || |||||| ||
                                TCCCTCC TG CCCCCC CC
                                    A  A     G
GAM1709  HNRPA0    5'  GGGGGAGGGAAGGGGAGCG    41767     A    C     A
                                GGG GGAG GGGGGG GGAGCG
                                ||| |||| |||||| ||||||
                                CCC CCTC CCTTCC CCTCGC
                                  _   _     _
GAM1709  HRD1      3'  GGGGCCTGGGGGGGAGGGGCGG  41768      AGGAGC       A
                                GGGG     GGGGGGGAGG GCGG
                                ||||     ||||||||| ||||
                                CCCC     CCCCCCTCC CGCC
                                  GGA___        C
GAM1709  HSJ1      3'  GGGGAGAGAGCAGGGGCGG    41769        _       GA
                                GGGGAG GAGCGGGGG  GG
                                |||||| |||||||||  ||
                                CCCCTC CTCGTCCCC  CC
                                    T       G_
GAM1709  ILF3      5'  GGGGCGAGCGGGCGGGCGG    41770      AG      _  A
                                GGGG  GAGCGGG GGG GG
                                ||||  ||||||| ||| ||
                                CCCC  CTCGCCC CCC CC
                                  G_      G  G
GAM1709  KHDRBS3   5'  GAGGAGGAGCGGGCGCGGGCGG 41771              GGGA  A
                                GGGGAGGAGCGGG    GG GCGG
                                ||||||||||||    || ||||
```

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                                CTCCTCCTCGCCC   CC CGCC
                                      GCG_ _
GAM1709 KIAA0189 3' GGGGTGAAGGGGGAGTGG   41772     A   C     A
                                GGGG GGAG GGGGGG GG
                                |||| |||| |||||| ||
                                CCCC CTTC CCCCTC CC
                                  A   _     A
GAM1709 KIAA0211 5' GGGGCGGAGCGGGGGCGG   41773     A       GA
                                GGGG GGAGCGGGGG  GG
                                |||| ||||||||||  ||
                                CCCC CCTCGCCCCC  CC
                                  G        G_
GAM1709 KIAA0237 5' GGGGCGGGGAGGGGCG     41774    A      A  A
                                GG GCGGGGGG GG GCG
                                || |||||||| || |||
                                CC CGCCCCTC CC CGC
                                 C      _ _
GAM1709 KIAA0339 3' GGGTGGGGGGCGGAGGGCG   41775    A  AGC   G    A
                                GGG GG   GGG GGAGG GCG
                                ||| ||   ||| ||||| |||
                                CCC CC   CCC CCTCC CGC
                                 A ____  G    _
GAM1709 KIAA0444 5' GGGGAGGAGGGGAGGTGG   41776         C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CCCCTCCTC CCCTCC CC
                                      _     A
GAM1709 KIAA0537 5' GGGGAGGGGGAGCGAGGGGCGG 41777        AGC    _   A
                                GGGGAGG   GGGGG GAGG GCGG
                                |||||||   ||||| |||| ||||
                                CCCCTCC   CCCTC CTCC CGCC
                                    ___    G   C
GAM1709 KIAA0649 5' GGGGAGGCGGCGGGCCGGGGGC 41778        A_    G_  A  A
           GG                     GGGGAGG  GCGGG  GG GG GCGG
                                |||||||  |||||  || || ||||
                                CCCCTCC  CGCCC  CC CC CGCC
                                    GC    GG  _ _
GAM1709 KIAA0918 3' GGGGAGGAGAGAAGGAGAGGGG 41779         C    _   A
           CGG                     GGGGAGGAG GGGGG GAGG GCGG
                                |||||||| ||||| |||| ||||
                                CCCCTCCTC CTTCC CTCC CGCC
                                      T    T   C
GAM1709 KIAA1016 5' GGGGCGGGCGGGGAGGCG   41780     A  A      AGGA
                                GGGG GG GCGGGGGG   GCG
                                |||| || ||||||||   |||
                                CCCC CC CGCCCCTC   CGC
                                  G _      _____
GAM1709 KIAA1183 3' GGGGAGGGCGGGGGCCACAGGC 41781        A     GA__  A
           GG                     GGGGAGG GCGGGGG   GG GCGG
                                ||||||| |||||||   || ||||
```

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                                CCCCTCC CGCCCCC   TC CGCC
                                   _     GGTG  _
GAM1709  KIAA1321  3'  AGGGAGGAGTGGGGGGAAAA  41782        C
                                GGGGAGGAG GGGGGGAGGA
                                ||||||||| ||||||||||
                                TCCCTCCTC CCCCCCTTTT
                                   A
GAM1709  KIAA1337  3'  GGGGAGGGTTGCGGGGGGGCGG 41783       A__      AGGA
                                GGGGAGG  GCGGGGGG  GCGG
                                |||||||  ||||||||  ||||
                                CCCCTCC  CGCCCCCC  CGCC
                                   CAA     _____
GAM1709  KIAA1388  5'  GGGAGGGAGGAGAGGAGCG   41784      AGC
                                GGGAGG  GGGGGGAGGAGCG
                                ||||||  ||||||||||||
                                CCCTCC  CTCCTCTCCTCGC
                                  ___
GAM1709  KIAA1580  5'  GGGGCGGGGGCGGGGGCGGGGG 41785    A  A_     GA  A
          CGG                   GGGG GG  GCGGGGG  GG GCGG
                                |||| ||  |||||||  || ||||
                                CCCC CC  CGCCCCC  CC CGCC
                                  G  CC      GC  C
GAM1709  KIAA1910  5'  GGAGGGGGGCGGAGGGCG   41786     AGC   _    A
                                GGAGG  GGGG GGAGG GCG
                                |||||  |||| ||||| |||
                                CCTCC  CCCC CCTCC CGC
                                  ___   G    _
GAM1709  KIAA1949  5'  GGGGAGGCAAGGAGGGGCG   41787      GA      A  A
                                GGGGAG  GCGGGGGG GG GCG
                                ||||||  |||||||| || |||
                                CCCCTC  CGTTCCTC CC CGC
                                  __      _ _
GAM1709  KIAA1949  5'  GGGGAGGCAAGGAGGGGCG   41787      GA      A  A
                                GGGGAG  GCGGGGGG GG GCG
                                ||||||  |||||||| || |||
                                CCCCTC  CGTTCCTC CC CGC
                                  __      _ _
GAM1709  KIAA1949  5'  GGGGAGGCAAGGAGGGGCG   41787      GA      A  A
                                GGGGAG  GCGGGGGG GG GCG
                                ||||||  |||||||| || |||
                                CCCCTC  CGTTCCTC CC CGC
                                  __      _ _
GAM1709  MAGEF1   5'  GGGGAGGGGTTGGACAGCG   41788      AGC  GG   GG
                                GGGGAGG  GG  GGA  AGCG
                                |||||||  ||  |||  ||||
                                CCCCTCC  CC  CCT  TCGC
                                   ___  AA  G_
GAM1709  MASA     5'  GGGGAGGGCGGAGGGCGG   41789      A      A
                                GGGGAGG GCGGGGGG GG
                                ||||||| |||||||| ||
```

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                                CCCCTCC CGCCTCCC CC
                                   _      G
GAM1709  MGC:5244  5'  GGGGAGGGGTGGGGGTGC    41790       AGC  G   A  A
                                GGGGAGG   GG GGG GG GC
                                |||||||   || ||| || ||
                                CCCCTCC   CC CCC CC CG
                                   ___  A   _  A
GAM1709  MGC10882  3'  GGGGAGGGAAGGGGAGTGG   41791       AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   CCCCTC CC
                                   CTT     A
GAM1709  MGC21688  3'  GGGGAGGGTGGGGGGTTGCTGG 41792       AGC     AGGA  _
                                GGGGAGG   GGGGGG    GC GG
                                |||||||   ||||||    || ||
                                CCCCTCC   CCCCCC    CG CC
                                   CA_     AA__  A
GAM1709  MGC22014  3'  GGGGGTAAGGGAGGGGCGG   41793     AGGAGCG      A
                                GGGG      GGGGGAGG GCGG
                                ||||      |||||||| ||||
                                CCCC      TTCCCTCC CGCC
                                  CA_____       C
GAM1709  MGC25056  5'  GGGGAGGGCTGGGGGCTGG   41695       A  _    GA
                                GGGGAGG GC GGGGG  GG
                                ||||||| || |||||  ||
                                CCCCTCC CG CCCCC  CC
                                   _  A    GA
GAM1709  MGC2865   3'  GGGGGGCGAGGGGCGG     41794     A  A      A
                                GGG GG GCGGGGGG GG
                                ||| || |||||||| ||
                                CCC CC CGCTCCCC CC
                                  _  _      G
GAM1709  MGC3047   3'  GGGGAGGGGTGTGGAGGCG   41795       AGC  GG_   GA
                                GGGGAGG   GG   GGAG  GCG
                                |||||||   ||   ||||  |||
                                CCCCTCC   CC   CCTC  CGC
                                   ___  ACA   __
GAM1709  MGC35558  3'  GGGAAGGGGTGTAAGGAGTGG  41796       AGC  GGG     C
                                GGGGAGG   GG   GAGGAG GG
                                |||||||   ||   |||||| ||
                                CCCTTCC   CC   TTCCTC CC
                                   ___  ACA     A
GAM1709  MGC4415   3'  GGGGAGGGTGGAGATGAGGGGG 41797     ____   CG    A  A
            GCGG                   GGGA   GGAG  GGGGG GG GCGG
                                ||||   ||||  ||||| || ||||
                                CCCT   CCTC  CTCCC CC CGCC
                                  CCCA   TA    _  _
GAM1709  MMPL1     3'  GGGGAGGAGCTGGGTGTGG   41798         G   GGA
                                GGGGAGGAGC GGG   GG
                                |||||||||| |||   ||
```

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                                CCCCTCCTCG CCC   CC
                                      A   ACA
GAM1709  NECL1    3'  GGGGAGCAAGCGGGAGGGGCGG 41799    A      _     A
                                GG GGAGCGGG GGGAGG GCGG
                                || |||||||| |||||| ||||
                                CC CCTCGTTC CCCTCC CGCC
                                  _       G     C
GAM1709  NFAT5    5'  GGGGGGAGCGGCGGTGG     41800      A      G  GA
                                GGGG GGAGCGG GG  GG
                                |||| ||||||| ||  ||
                                CCCC CCTCGCC CC  CC
                                  _      G  A_
GAM1709  NFAT5    5'  GGGGGGAGCGGCGGTGG     41800      A      G  GA
                                GGGG GGAGCGG GG  GG
                                |||| ||||||| ||  ||
                                CCCC CCTCGCC CC  CC
                                  _      G  A_
GAM1709  NKX2B    5'  GGGGAGGGGGGAGTGG      41801        AGC      A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   CCCCTC CC
                                    ____      A
GAM1709  NKX2B    5'  GGGGGGAGTGGGGGGAGG    41802      A    C
                                GGGG GGAG GGGGGGAGG
                                |||| |||| |||||||||
                                CCCC CCTC CCCCCCTCC
                                  _   A
GAM1709  NLI-IF   5'  GGGGAGGGGTGGGAGGGAGG   41804        AGC_
                                GGGGAGG   GGGGGGAGG
                                |||||||   |||||||||
                                CCCCTCC   CCTCCCTCC
                                    CCAC
GAM1709  NLI-IF   5'  GGGGGGGAGGGGAGGGG     41803      A    C      A
                                GGGG GGAG GGGGGG GG
                                |||| |||| |||||| ||
                                CCCC CCTC CCCTCC CC
                                  C   _     _
GAM1709  NR5A1    3'  GGGAGGGGGCGGGGCGGGTGG  41805        A_     _  A_
                                GGGAGG  GCGGGG GG  GG
                                ||||||  |||||| ||  ||
                                CCCTCC  CGCCCC CC  CC
                                    CC     G  CA
GAM1709  P5CR2    3'  GGGGGGTGGCAGGGGCGG    41806      A  A_      GA
                                GGGG GG  GCGGGGG  GG
                                |||| ||  |||||||  ||
                                CCCC CC  CGTCCCC  CC
                                  _ AC      G_
GAM1709  PAK7     5'  GGGTAGGGGCAAGGGGGGCGG  41807     G   A       A GA
                                GGG AGG GCGGGGGG G  GCGG
                                ||| ||| ||||||||  |  ||||
```

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                                CCC TCC CGTTCCCC C  CGCC
                                  A  C      _ __
GAM1709  PALM     5'  GGGGAGGGGAGGGGGACGCGG  41808       AGC     A  _
                                GGGGAGG  GGGGGG GGA GCGG
                                |||||||  |||||| ||| ||||
                                CCCCTCC  CCTCCC CCT CGCC
                                   ___    _  G
GAM1709  PDGFC    5'  GGGGTGGGGACGCGGGGGAGCG 41809     A_  AG  G   AG
             G                   GGGG  GG  CG GGGG  GAGCGG
                                ||||  ||  || ||||  ||||||
                                CCCC  CC  GC CCCC  CTCGCC
                                  AC  CT  G   __
GAM1709  PF1      5'  GGGGAGGGTGATGGGGGGTGG  41810       AGC__     A
                                GGGGAGG    GGGGGG GG
                                |||||||    |||||| ||
                                CCCCTCC    CCCCCC CC
                                    CACTA     A
GAM1709  PGLYRP   3'  GGGGAGGAATGGGGTGCGG   41811        C   GGA
                                GGGGAGGAG GGGG  GG
                                |||||||||| ||||  ||
                                CCCCTCCTT CCCC  CC
                                     A   ACG
GAM1709  PPP1R12C  3'  GGGGAGGGGTGACGGGGTGG  41812       A___    _
                                GGGGAGG   GCGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   TGCCCC CC
                                    CCAC     A
GAM1709  PPP1R1B  5'  GGGGAGGGCGCGGGAGCG   41813       A  G  GAGG
                                GGGGAGG GCG GGG   AGCG
                                ||||||| ||| |||   ||||
                                CCCCTCC CGC CCC   TCGC
                                   _  G  ____
GAM1709  QKI      5'  GGAGAGGAGGGAGGGGCG   41814     C       A
                                GGAG GGGGGGAGG GCG
                                |||| ||||||||| |||
                                CCTC CCTCCCTCC CGC
                                  T       C
GAM1709  RAB5EP   5'  GGGGATGGGCGGGGAAGCG   41815      _ A    GGAG
                                GGGGA GG GCGGGG   GAGCG
                                ||||| || ||||||   |||||
                                CCCCT CC CGCCCC   TTCGC
                                  A _    ____
GAM1709  RBPMS    5'  GAGGAGGAGGAGGAGC     41816      GCG
                                GAGGA  GGGGGAGGAGC
                                |||||  ||||||||||
                                CTCCT  CCTCCTCCTCG
                                   ___
GAM1709  REPRIMO  3'  GGGGGGAGCAGGAGAAGAGTGG 41817     A       G   C
                                GGGG GGAGCGGGGG AGGAG GG
                                |||| |||||||||| ||||| ||
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                                CCCC CCTCGTCCTC TTCTC CC
                                  _       _    A
GAM1709 SCAMP-4  3' GGGGAGGAGGTGGTGGGCGG  41819        CG _  A
                                GGGGAGGAG  GG GGG GG
                                |||||||||  || ||| ||
                                CCCCTCCTC  CC CCC CC
                                     CA  A   G
GAM1709 SCAMP-4  3' GGGGAGGGGTGGGGTGGGG   41818       AGC   _ A
                                GGGGAGG   GGGG GG GG
                                |||||||   |||| || ||
                                CCCCTCC   CCCC CC CC
                                   CCA    A  _
GAM1709 SCYA22   3' GGGGGGGGTGGGGAGAGG    41820     A  AGC
                                GGGG GG   GGGGGGAGG
                                ||||  ||   |||||||||
                                CCCC CC   CCCCTCTCC
                                  _  CCA
GAM1709 SEMA6A   5' GGGGGCGGGGTGGGGGCG    41821     AGGA     _ A  A  _
                                GGGG    GCGGGG GG GG GC G
                                ||||    |||||| || || || |
                                CCCC    CGCCCC CC CC CG C
                                  _____     A  _  _  A
GAM1709 SFXN5    3' GGGGAGGGCGGGAAGGG     41822        A       A
                                GGGGAGG GCGGGGGG GG
                                ||||||| |||||||| ||
                                CCCCTCC CGCCCTTC CC
                                  _       _
GAM1709 SNTA1    5' GGGGAGGAGCTCTGGGGGCGG  41823         GG_   AGGA
                                GGGGAGGAGC   GGGG   GCGG
                                ||||||||||   ||||   ||||
                                CCCCTCCTCG   CCCC   CGCC
                                     AGA   _____
GAM1709 SPATA6   5' GGGGAGGGGCGGCGGGGAG   41824        A   _
                                GGGGAGG GCGG GGGGAG
                                ||||||| |||| ||||||
                                CCCCTCC CGCC CCCCTC
                                   C   G
GAM1709 SSH-3    3' GGGAGGGGGCGGGGGTGG    41825       A_     GA
                                GGGAGG  GCGGGGG  GG
                                ||||||  |||||||  ||
                                CCCTCC  CGCCCCC  CC
                                   CC      A_
GAM1709 STIM2    3' GGTGGGGAGTGGAGGGTGG   41826    _ A   C     A
                                GG GG GGAG GGGGGG GG
                                || || |||| |||||| ||
                                CC CC CCTC CCTCCC CC
                                 A  _   A     A
GAM1709 STX1B2   3' GGGGTGGAGGAGGGGTGG    41827     A   C     A
                                GGGG GGAG GGGGGG GG
                                |||| |||| |||||| ||
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                                CCCC CCTC CTCCCC CC
                                  A  _    A
GAM1709 STX1B2   3' GGGGATGGAGTGAAAGGGG  41828      _   C GG  A
                                GGGGA GGAG G  GGG GG
                                ||||| |||| |  ||| ||
                                CCCCT CCTC C  TCC CC
                                  A   A TT  _
GAM1709 T1A-2    5' GGGGGGGCCGGAGGGGTGG  41829     A  AG  _   A
                                GGGG GG  CGG GGGG GG
                                |||| ||  ||| |||| ||
                                CCCC CC  GCC CCCC CC
                                  C  G_  T   A
GAM1709 TETRAN   3' GGGGGGTGGGGGTCAGGCAG  41830     A  AGC    GA  A
                                GGGG GG   GGGGG  GG GCGG
                                |||| ||   |||||  || ||||
                                CCCC CC   CCCCC  TC CGTC
                                  _ A__     AG  _
GAM1709 TGIF2    5' GGCGGGGAGCGGGGGGCGCCGG 41831    _ A        AGGAG
                                GG GG GGAGCGGGGGG    CGG
                                || || ||||||||||    |||
                                CC CC CCTCGCCCCCC    GCC
                                 G  _        GCG__
GAM1709 WAC      5' GGGGAGGGGGGGAGAGC     41832      GGAGC      G
                                GGGGA    GGGGGGAG AGC
                                |||||    |||||||| |||
                                CCCCT    CCCCCCTC TCG
                                  _____      _
GAM1709 WAC      5' GGGGAGGGGGGGAGAGC     41832      GGAGC      G
                                GGGGA    GGGGGGAG AGC
                                |||||    |||||||| |||
                                CCCCT    CCCCCCTC TCG
                                  _____      _
GAM1709 WNT10A   5' GGGGGGGGCGGGGGGTGAAGAG 41833     A  A      __
           CGG                    GGGG GG GCGGGGGG  AGGAGCGG
                                |||| || ||||||||  ||||||||
                                CCCC CC CGCCCCCC  TTCTCGCC
                                  _ C       AC
GAM1709 LOC124044 3' GGGGAGGAGGGGGTGGGGCGG  41834        GC    GA  A
                                GGGGAGGA  GGGGG  GG GCGG
                                ||||||||  |||||  || ||||
                                CCCCTCCT  CCCCC  CC CGCC
                                    __    AC  _
GAM1709 LOC124783 5' GGCGGGGAGCGGGCTGGTGG  41835    _ A      G_  A
                                GG GG GGAGCGGG  GG GG
                                || || ||||||||  || ||
                                CC CC CCTCGCCC  CC CC
                                 G  _       GA  A
GAM1709 LOC131034 5' GGGGACGAGCGGGTGGCGG   41836      G      G  A
                                GGGGA GAGCGGG GG GG
                                ||||| ||||||| || ||
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                                CCCCT CTCGCCC CC CC
                                   G      A  G
GAM1709  LOC131583 3'  GGGCGGGAGCGGGGGCCGG   41837     GA        GA
                                GGG  GGAGCGGGGG  GG
                                |||  ||||||||||  ||
                                CCC  CCTCGCCCCC  CC
                                  GC         GG
GAM1709  LOC143677 3'  GGGAAGGGGTAGGGGGGTGG   41838        AGC_     A
                                GGGGAGG    GGGGGG GG
                                |||||||    |||||| ||
                                CCCTTCC    CCCCCC CC
                                    CCAT     A
GAM1709  LOC146515 3'  GGGGTGGGCGGGGGGAG     41839      A  A
                                GGGG GG GCGGGGGGAG
                                |||| || ||||||||||
                                CCCC CC CGCCCCCCTC
                                  A  _
GAM1709  LOC146988 5'  GGGGAGGGATAGGGAGTGG    41840        AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   TCCCTC CC
                                    CTA     A
GAM1709  LOC147160 5'  GGGGAAGGGGGGGGTGG     41841        AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTTC   CCCCCC CC
                                    C__     A
GAM1709  LOC148343 5'  GGGGAGTGGGCCCGGGGGGCGG 41842       ___ AG      A
                                GGGGA   GG  CGGGGGG GG
                                |||||   ||  ||||||| ||
                                CCCCT   CC  GCCCCCC CC
                                   CAC  GG      G
GAM1709  LOC151056 3'  AGGGTGGGGTGGGGGGAGGGGC 41843      A  AGC        A
            GG                    GGGG GG   GGGGGGAGG GCGG
                                |||| ||   |||||||| ||||
                                TCCC CC   CCCCCCTCC CGCC
                                  A  CCA        C
GAM1709  LOC151648 5'  GGGGGGAGGTGGGGCTGGCGG  41844      A    CG    GAGGA
                                GGGG GGAG  GGGG     GCGG
                                |||| ||||  ||||     ||||
                                CCCC CCTC  CCCC     CGCC
                                  _    CA    GAC__
GAM1709  LOC151878 5'  GGGGAGGGGTGGAGGGGCTGG  41845        AGC  GG    A  _
                                GGGGAGG   GG  GGAGG GC GG
                                |||||||   ||  ||||| || ||
                                CCCCTCC   CC  CCTCC CG CC
                                    ___  A_    C  A
GAM1709  LOC151878 5'  GGGGTAGGGGAGGGGTGG    41846      _  AGC      A
                                GGGG AGG   GGGGGG GG
                                |||| |||   |||||| ||
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                                CCCC TCC   CTCCCC CC
                                  A  C__     A
GAM1709  LOC153232 3'  GGGGGGGGGGGGGCGGGCAG   41847     A  AGC     A  A
                                GGGG GG   GGGGGG GG GCGG
                                |||| ||   |||||| || ||||
                                CCCC CC   CCCCCC CC CGTC
                                  _ ___     G  _
GAM1709  LOC153474 3'  AGGGAGGAGCGATCGGGAG   41751          G_
                                GGGGAGGAGCGG  GGGAG
                                ||||||||||||  |||||
                                TCCCTCCTCGCT  CCCTC
                                      AG
GAM1709  LOC153688 5'  GGGGGAAGTGGGGGCGG    41848     A   C    GA
                                GGGG GGAG GGGGG  GG
                                |||| |||| |||||  ||
                                CCCC CTTC CCCCC  CC
                                  _   A    G_
GAM1709  LOC154427 3'  GGGAGGGGCCGGGGGAGCGG  41849      A  G     GGA
                                GGGAGG GC GGGGGA   GCGG
                                |||||| || ||||||   ||||
                                CCCTCC CG CCCCCT   CGCC
                                   C  G     ___
GAM1709  LOC157226 5'  GGGGCGGTGGGGGGGAAAGGCGG 41851     A  AGC       GA
                                GGGG GG   GGGGGGGAG  GCGG
                                |||| ||   ||||||||  ||||
                                CCCC CC   CCCCCCTT  CGCC
                                  G  A__       TC
GAM1709  LOC157226 5'  GGGGACGGGAGGGGGGCG    41850     AGGA      A  A
                                GGGG   GCGGGGGG GG GCG
                                ||||   |||||||| || |||
                                CCCC   TGCCCTCC CC CGC
                                  _____       _  C
GAM1709  LOC158236 5'  AGGGGGAGGGGGAGGGGCGG  41852     A   C     A  A
                                GGGG GGAG GGGGGG GG GCGG
                                |||| |||| |||||| || ||||
                                TCCC CCTC CCCCTC CC CGCC
                                  _   _     _ _
GAM1709  LOC158819 5'  GGGGAGGAAAGAGGAGG     41853         CG
                                GGGGAGGAG  GGGGGAGG
                                |||||||||  ||||||||
                                CCCCTCCTT  TCTCCTCC
                                     __
GAM1709  LOC158972 3'  AGGGAGGAAGAGGAGGGGCGG  41854        GCG       A
                                GGGGAGGA   GGGGGAGG GCGG
                                ||||||||   |||||||| ||||
                                TCCCTCCT   TCTCCTCC CGCC
                                     ___       C
GAM1709  LOC162333 5'  GGGGAGGGTTGGTGATGGGGTG 41855        AGC  _____    A
            G                    GGGGAGG   GG    GGGG GG
                                |||||||   ||    |||| ||
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                                CCCCTCC   CC    CCCC CC
                                    CAA  ACTA    A
GAM1709  LOC197136 3'  GGGGAGGAGGGGGTGGGGCGG  41834        GC    GA  A
                                GGGGAGGA  GGGGG  GG GCGG
                                ||||||||  |||||  || ||||
                                CCCCTCCT  CCCCC  CC CGCC
                                    __     AC  _
GAM1709  LOC200862 5'  GGGAGGGAGCCCGGGAGCG   41856    GA    GG   GAGG
                                GGG  GGAGC  GGG    AGCG
                                |||  |||||  |||    ||||
                                CCC  CCTCG  CCC    TCGC
                                  TC    GG  _____
GAM1709  LOC203530 3'  GGGGGGTGGGGGGGGAAG     41857      A  AGC
                                GGGG GG   GGGGGGGAGG
                                ||||  ||   |||||||||
                                CCCC CC   CCCCCCTTC
                                  _  AC_
GAM1709  LOC221656 3'  GGGGGGGGGCGGGGGGCGGGCGG 41858      A  A       A  A
                                GGGG GG GCGGGGGG GG GCGG
                                |||| || |||||||| || ||||
                                CCCC CC CGCCCCCC CC CGCC
                                  _ C       G  _
GAM1709  LOC221656 3'  GGGCGGGGGGGCGGGCG      41859    A       A  A
                                GG GCGGGGGG GG GCG
                                || |||||||| || |||
                                CC CGCCCCCC CC CGC
                                  _       G  _
GAM1709  LOC221833 3'  GGAGAGGGGCGGGCGCAGGGTG 41860        A    _____   A
            G                    GGGGAGG GCGGG    GGG GG
                                |||||||  |||||    ||| ||
                                CCTCTCC CGCCC    CCC CC
                                    C    GCGT   A
GAM1709  LOC221876 3'  GGGGAGGGGTGTGGGGAAAG   41861        AGCG_
                                GGGGAGG    GGGGGAGG
                                |||||||    ||||||||
                                CCCCTCC    CCCCTTTC
                                    CCACA
GAM1709  LOC222166 5'  GGGCGGCGGGAGGAGCG     41862    A   G
                                GG GCGG GGGAGGAGCG
                                || |||| ||||||||||
                                CC CGCC CCCTCCTCGC
                                  _   G
GAM1709  LOC254532 5'  GGGGGGAGTGAGGGGCCGG   41864      A   C     A_
                                GGGG GGAG GGGGGG  GG
                                |||| |||| ||||||  ||
                                CCCC CCTC CTCCCC  CC
                                  _   A     GG
GAM1709  LOC254532 5'  GGGGAGGGGCGGGGTGGGG   41863        A     _ A
                                GGGGAGG GCGGGG GG GG
                                ||||||| |||||| || ||
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                                CCCCTCC CGCCCC CC CC
                                    C     A  _
GAM1709  LOC255031 5'  GGGCGAGGGGCGGGCGAAGAGC 41865     _   A    G G
                GG                  GGG GAGG GCGGG G AGGAGCGG
                                    ||| |||| ||||| | ||||||||
                                    CCC CTCC CGCCC C TTCTCGCC
                                      G   C    G _
GAM1709  LOC255259 5'  GGGGAGGAGGCGGGGGCCGG  41866         _    GA
                                    GGGGAGGAG CGGGGG  GG
                                    ||||||||| ||||||  ||
                                    CCCCTCCTC GCCCCC  CC
                                         C     GG
GAM1709  LOC257200 3'  GGGAAGGGGTGGGGGGTGG   41867       AGC     A
                                    GGGGAGG   GGGGGG GG
                                    |||||||   |||||| ||
                                    CCCTTCC   CCCCCC CC
                                        CCA     A
GAM1709  LOC257484 3'  GGGGGTAAGGGAGGGGCGG   41793     AGGAGCG      A
                                    GGGG      GGGGGAGG GCGG
                                    ||||      |||||||| ||||
                                    CCCC      TTCCCTCC CGCC
                                      CA_____       C
GAM1709  LOC64744  3'  GGGGAGAGGGTGGGAGGCG   41868       AGC  _    GA
                                    GGGGAGG   GGG GGGAG  GCG
                                    |||||||   ||| |||||  |||
                                    CCCCTCT   CCC CCCTC  CGC
                                        ___   A    __
GAM1709  LOC90233  5'  GGGGAGCGGCGGCCGACCGGGG 41869      GA   GG  A_  A
                CGG                   GGGGAG  GCGG  GG  GG GCGG
                                    ||||||  ||||  ||  || ||||
                                    CCCCTC  CGCC  CT  CC CGCC
                                       GC    GG  GG  C
GAM1709  LOC92080  5'  GGGGAGGGTGGTGGAGGAGCGG 41870       AGCG  G
                                    GGGGAGG    GG GGAGGAGCGG
                                    |||||||    || ||||||||||
                                    CCCCTCC    CC CCTCCTCGCC
                                        CA__  A
GAM1710  AK3      3'  CCTTTTGAAAGGCAGAGGAG   41873    CG      ATCT
                                    CC  TTGAAAGG    GGGAG
                                    ||  ||||||||    |||||
                                    GG  AACTTTCC    TCCTC
                                     AA       GTC_
GAM1710  ALDH3B2   3'  ACCCGTTGGAGGCGGGTGGGA  41874        AA   ATC_
                                    ACCCGTTG  AGG    TGGGA
                                    ||||||||  |||    |||||
                                    TGGGCAAC  TCC    ACCCT
                                         C_   GCCC
GAM1710  ASGR2    5'  GTGAAAGGTGTGGAGA      41875    T     ATC  _
                                    GT GAAAGG   TG GGAGA
                                    || ||||||   || |||||
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                                CA CTTTCC   AC CCTCT
                                 _    ___  A
GAM1710 C7      3' TCGATTCAGATTTGGGAGAA  41876     AA_   C
                                TTGA  GGAT TGGGAGAA
                                ||||  |||| ||||||||
                                AGCT  TCTA ACCCTCTT
                                  AAG   A
GAM1710 CELL    3' ACCCGTTGCAGGGACGGGGG  41877        AAA   CT
                                ACCCGTTG  GGAT  GGG
                                ||||||||  ||||  |||
                                TGGGCAAC  CCTG  CCC
                                    GTC   CC
GAM1710 EXTL1   3' ACCCATTGGGGGGCGGAGGGGGA 41878        AAA__  TCT
            G                    ACCCGTTG   GGA  GGGAG
                                ||||||||   |||  |||||
                                TGGGTAAC   CCT  CCCTC
                                    CCCCG  CC_
GAM1710 EZH1    3' CCGTTGGGGCCTGGGAG    41879       AAA  AT
                                CCGTTG  GG  CTGGGAG
                                ||||||  ||  |||||||
                                GGCAAC  CC  GACCCTC
                                   ___  CG
GAM1710 FUT1    3' TTGGAGGACCCAGGGGAGAA  41880     AA     __
                                TTG  AGGATCT  GGGAGAA
                                |||  |||||||  |||||||
                                AAC  TCCTGGG  CCCTCTT
                                  C_     TC
GAM1710 GAS7    3' TTGGGGGGTCCTAGGAGAA   41881     AAA  A
                                TTG  GG TCTGGGAGAA
                                |||  || ||||||||||
                                AAC  CC GGATCCTCTT
                                  CCC  A
GAM1710 IHPK1   3' CCCTTGAGCCCTGGGAG    41882     G   AAGGA
                                CCC TTGA    TCTGGGAG
                                ||| ||||    ||||||||
                                GGG AACT    GGACCCTC
                                  _   CG___
GAM1710 NUMB    3' CACCAAAAGGGGGTTTGGGGGA 41883    TT    ATC__   A
            A                    CG  GAAAGG    TGGG GAA
                                ||  ||||||    |||| |||
                                GT  TTTTCC    ACCC CTT
                                 GG     CCCAA   C
GAM1710 PGLS    3' TTGAAAGGAGAGCCCGGAGA  41884        T__  G
                                TTGAAAGGA  CT GGAGA
                                |||||||||  || |||||
                                AACTTTCCT  GG CCTCT
                                     CTC  G
GAM1710 POU4F1  3' GTTGAAAGGTTCTACCAGGA  41885        A  ___
                                GTTGAAAGG TCT  GGGA
                                ||||||||| |||  ||||
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                                CAACTTTCC AGA   TCCT
                                     A   TGG
GAM1710 PSG7     3' TTGAGGTTCCATGGGAGAA   41886      AA  A  __
                                TTGA  GG TCT  GGGAGAA
                                ||||  || |||  |||||||
                                AACT  CC AGG  CCCTCTT
                                  __  A   TA
GAM1710 RET      3' CCCAGGAGGGGTCTGGGGGAA 41887      TT  AA  A     A
                                CCCG  GA  GG TCTGGG GAA
                                ||||  ||  || |||||| |||
                                GGGT  CT  CC AGACCC CTT
                                  C_  CC  _     C
GAM1710 SNAPAP   3' GTGAAAGGAAGCAAGAG     41888    T      TC
                                GT GAAAGGA  TGGGAG
                                || |||||||  ||||||
                                CA CTTTCCT  GTTCTC
                                 _      TC
GAM1710 WNT8B    3' CCCTAGGTCTGGGAGA      41889     GTTGAA   A
                                CCC     AGG TCTGGGAGA
                                |||     ||| |||||||||
                                GGG     TCC AGACCCTCT
                                 A_____  _
GAM1710 CCR7     3' CCCTGTTGAGAGCCTGGGAG   41890     _    AA GA
                                CCC GTTGA  G  TCTGGGAG
                                ||| |||||  |  ||||||||
                                GGG CAACT  C  GGACCCTC
                                 A    __ TC
GAM1710 CD36L1   3' CCGCTGGGAGAGTCCGGGAGAA 41891       AA  GA
                                CCGTTG  AG  TCTGGGAGAA
                                ||||||  ||  ||||||||||
                                GGCGAC  TC  AGGCCCTCTT
                                   CC  TC
GAM1710 CLSTN1   3' ACCCTTGGGACTGGGAGA    41892     G   AAA   T
                                ACCC TTG   GGA CTGGGAGA
                                |||| |||   ||| ||||||||
                                TGGG AAC   CCT GACCCTCT
                                  _   ___   _
GAM1710 DKFZP434P0316 5' CCCGCTGGCCTGGGAGA     41893       GAAA  A
                                CCCGTT    GG TCTGGGAGA
                                ||||||    || |||||||||
                                GGGCGA    CC GGACCCTCT
                                  ____  _
GAM1710 FBP17    3' ACCCGTTGCAGGGACCGGAA   41894        AAA   T
                                ACCCGTTG   GGA CTGGGA
                                ||||||||   ||| ||||||
                                TGGGCAAC   CCT GGCCTT
                                     GTC   _
GAM1710 FLJ10352 3' CCTGTGAGAGAAGAGGAGAA   41895    GT   A   TCT
                                CC  TGA AGGA   GGGAGAA
                                ||  ||| ||||   |||||||
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                                GG  ACT TCTT   TCCTCTT
                                 AC   C    C__
GAM1710  FLJ12700  3'  GTTGGAATCTGGGAGAA     41896      AAA
                                GTTG   GGATCTGGGAGAA
                                ||||   ||||||||||||||
                                CAAC   CTTAGACCCTCTT
                                  ___
GAM1710  FLJ22167  5'  CCTGGCTCACAGGATCTGGG   41897    C_   GAA
                                CC  GTT   AGGATCTGGG
                                ||  |||   ||||||||||
                                GG  CGA   TCCTAGACCC
                                 AC   GTG
GAM1710  GMPPB     5'  GTAGAGGACTGGGAGAA     41898    TGAA    T
                                GT    AGGA CTGGGAGAA
                                ||    |||| |||||||||
                                CA    TCCT GACCCTCTT
                                 TC__    _
GAM1710  HAPIP     3'  CTGAGTGGGATCTGGGGGAA   41899      AA_        A
                                TTGA   GGATCTGGG GAA
                                ||||   ||||||||| |||
                                GACT   CCTAGACCC CTT
                                  CAC        C
GAM1710  KIAA0152  3'  CCTTTGAAAGGACGGAA     41900    G         CT
                                CC TTGAAAGGAT  GGGA
                                || ||||||||||  ||||
                                GG AACTTTCCTG  CCTT
                                 A         __
GAM1710  KIAA1391  3'  CCTTTGAAAGGGTACTGAA    41901    G       AT_
                                CC TTGAAAGG   CTGGG
                                || ||||||||   |||||
                                GG AACTTTCC   GACTT
                                 A       CAT
GAM1710  KIAA1405  3'  ACCTGGTTGGGGCTGCCCTGGG 41902     C_    AAAGGA_
            AG                    ACC  GTTG      TCTGGGAG
                                |||  ||||      ||||||||
                                TGG  CAAC      GGACCCTC
                                  AC    CCCGACG
GAM1710  MGC14844  3'  CATCAGATTTGGGAGA      41903      GAAA    C
                                CGTT    GGAT TGGGAGA
                                ||||    |||| |||||||
                                GTAG    TCTA ACCCTCT
                                  ____    A
GAM1710  MSRA      3'  GTTGAAAGCATTTTTACTGGAA 41904         G  _____
                                GTTGAAAG AT     CTGGGA
                                |||||||| ||     ||||||
                                CAACTTTC TA     GACCTT
                                     G  AAAAT
GAM1710  N4BP3     3'  GCTGAGAGCAGGGATCTGGGAG 41905       AA____
                                GTTGA     GGATCTGGGAG
                                |||||     ||||||||||
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                                CGACT     CCTAGACCCTC
                                   CTCGTC
GAM1710 SMOC1    3' CCCTTTGGGGGTCCGGAGAG  41906     G   AAA A    _
                                CCC TTG   GG TCTGG GAG
                                ||| |||   || ||||| |||
                                GGG AAC   CC AGGCC CTC
                                  A  C__  C    T
GAM1710 ZIN      3' CCTGCCCAGGTCTGGGAG    41907    C  TGAA   A
                                CC GT    AGG TCTGGGAG
                                || ||    ||| ||||||||
                                GG CG    TCC AGACCCTC
                                 A  GG__  _
GAM1710 LOC124446 5' CCTGCTGGAAGACAGGGAG   41908    C    A   ATCT
                                CC GTTG AAGG    GGGAG
                                || |||| ||||    |||||
                                GG CGAC TTCT    CCCTC
                                 A   C    GT__
GAM1710 LOC126248 3' CCTGCTGAGCCTGGGAG     41909    C     AAG A
                                CC GTTGA   G TCTGGGAG
                                || |||||   | ||||||||
                                GG CGACT   C GGACCCTC
                                 A    ____ _
GAM1710 LOC145547 3' CCCTTGAGGCCTGGGAG     41910     G    AA  A
                                CCC TTGA  GG TCTGGGAG
                                ||| ||||  || ||||||||
                                GGG AACT  CC GGACCCTC
                                  _    __  _
GAM1710 LOC146819 3' GTTAAAAGGGAAAAAAGAA   41911         ATCT
                                GTTGAAAGG    GGGAGAA
                                |||||||||    |||||||
                                CAATTTTCC    TTTTCTT
                                     CTT_
GAM1710 LOC146821 3' GTTAAAAGGGAAAAAAGAA   41911         ATCT
                                GTTGAAAGG    GGGAGAA
                                |||||||||    |||||||
                                CAATTTTCC    TTTTCTT
                                     CTT_
GAM1710 LOC150166 5' ACCCAGTGCTAGGATCTGGGAG 41912       T  AA
             A                   ACCCG TG  AGGATCTGGGAGA
                                 ||||| ||  ||||||||||||
                                 TGGGT AC  TCCTAGACCCTCT
                                    C  GA
GAM1710 LOC150605 5' ACCCGTTGGTGGGGGAG     41913        AAA  ATCT
                                ACCCGTTG   GG    GGGAG
                                ||||||||   ||    |||||
                                TGGGCAAC   CC    CCCTC
                                     CA_  _____
GAM1710 LOC151701 3' ACCTGTTTGAAGGCAGCCGGG 41914     C   GA    AT_
                                ACC GTT  AAGG   CTGGG
                                ||| |||  ||||   |||||
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                                TGG CAA  TTCC   GGCCC
                                  A   AC    GTC
GAM1710  LOC155036 5'  CGTTAGGTCTGGGAGAA     41915      GAA   A
                                CGTT   AGG TCTGGGAGAA
                                ||||   ||| ||||||||||
                                GCAA   TCC AGACCCTCTT
                                  ___   _
GAM1710  LOC157858 5'  CCGTTGTATCTGGGAGA     41916       AAAGG
                                CCGTTG    ATCTGGGAGA
                                ||||||    ||||||||||
                                GGCAAC    TAGACCCTCT
                                   A____
GAM1710  LOC196264 3'  ACCTGTTGAAAGAATAGAG   41917     C         CTG
                                ACC GTTGAAAGGAT   GGAG
                                ||| ||||||||||   ||||
                                TGG CAACTTTCTTA   TCTC
                                  A         ___
GAM1710  LOC220469 3'  ACCTGATGGGAGGGACAGGAGA 41918     CGT  AA   ATC
            A                    ACC   TG  AGG   TGGGAGAA
                                |||   ||  |||   ||||||||
                                TGG   AC  TCC   GTCCTCTT
                                  ACT  CC   CT_
GAM1710  LOC221760 3'  ACCTGTTGCAGGTGGGGAG   41919     C    AA   ATCT
                                ACC GTTG  AGG    GGGAG
                                ||| ||||  |||    |||||
                                TGG CAAC  TCC    CCCTC
                                  A   G_   AC__
GAM1710  LOC222237 3'  CCTGTTCAAAGGATCAAGAG   41920    C   G      T
                                CC GTT AAAGGATC GGGAG
                                || ||| |||||||| |||||
                                GG CAA TTTCCTAG TTCTC
                                 A  G       _
GAM1710  LOC257476 3'  CCCTTGAGCCCTGGGAG     41882     G    AAGGA
                                CCC TTGA    TCTGGGAG
                                ||| ||||    ||||||||
                                GGG AACT    GGACCCTC
                                  _    CG___
GAM1710  LOC64182  3'  CCTTGAAAGGGAACAGGA    41921    G       ATC
                                CC TTGAAAGG   TGGGA
                                || ||||||||   |||||
                                GG AACTTTCC   GTCCT
                                  _       CTT
GAM1711  B4GALT2   3'  GGCAAAGTGGCGGGGTG     41924      TTAC     A   C
                                GGCGG    GTGGCG GGT G
                                |||||    |||||| ||| |
                                CCGTT    CACCGC CCA C
                                   T____     C   A
GAM1711  RTN4      5'  GGGCGGTTGTGGGGGTG     41925        AC    CGA   C
                                GGGCGGTT  GTGG   GGT G
                                ||||||||  ||||   ||| |
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                                CCCGCCAA  CACC   CCA C
                                    __    C__   A
GAM1711  CARD6    3'  TGGGCGGATCACCTGAGGTCGG 41926        _   G GGC
                                TGGGCGG TTAC T   GAGGTCGG
                                ||||||| |||| |   ||||||||
                                ACCCGCC AGTG A   CTCCAGCC
                                   T   G ___
GAM1711  DKFZP434J037 3'  TGGGTGGATCACCTGAGGTCGG 41927      C  _   G GGC
                                TGGG GG TTAC T   GAGGTCGG
                                |||| || |||| |   ||||||||
                                ACCC CC AGTG A   CTCCAGCC
                                  A T   G ___
GAM1711  FLJ12387  3'  TGGGCGGTGCCCGGGGCGGGGT 41928        TA_  T   A
            CGG                   TGGGCGGT   CG GGCG GGTCGG
                                ||||||||   || |||| ||||||
                                ACCCGCCA   GC CCGC CCAGCC
                                    CGG  C   C
GAM1711  FLJ12747  3'  TGGGCGGATCACCTGAGGTCGG 41926        _   G GGC
                                TGGGCGG TTAC T   GAGGTCGG
                                ||||||| |||| |   ||||||||
                                ACCCGCC AGTG A   CTCCAGCC
                                   T   G ___
GAM1711  KIAA0889  3'  TGGGCGGATCACTTGAGGTCGG 41929        _   GTGGC
                                TGGGCGG TTAC    GAGGTCGG
                                ||||||| ||||    ||||||||
                                ACCCGCC AGTG    CTCCAGCC
                                   T   AA___
GAM1711  LOC143188 5'  TGGGCAGTTCTGGGGTG     41930        ACG   CGA   C
                                TGGGCGGTT   TGG   GGT G
                                |||||||||   |||   ||| |
                                ACCCGTCAA   ACC   CCA C
                                    G__   ___   A
GAM1711  LOC90072  3'  TGGGCGGATCACTTGAGGTCGG 41929        _   GTGGC
                                TGGGCGG TTAC    GAGGTCGG
                                ||||||| ||||    ||||||||
                                ACCCGCC AGTG    CTCCAGCC
                                   T   AA___
GAM1712  ABCD1    3'  GGGGCGGGGCAGGGGCCGG   41933     A_   T
                                GGGG  GGGC GGGGCCGG
                                ||||  |||| ||||||||
                                CCCC  CCCG CCCCGGCC
                                  GC   T
GAM1712  ACP1     5'  GGGCGGGGAGGGTCCGCGGG   41934     C      _  _
                                GGGC GGGGAGGG CTG GGG
                                |||| |||||||| ||| |||
                                CCCG CCCCTCCC GGC CCC
                                  _      A  G
GAM1712  ACP1     5'  GGGCGGGGAGGGTCCGCGGG   41934     C      _  _
                                GGGC GGGGAGGG CTG GGG
                                |||| |||||||| ||| |||
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                                CCCG CCCCTCCC GGC CCC
                                  _      A  G
GAM1712 ADCY7    5' GGGCTGGGGAGAGGGCCTCTGG 41935     C     GGCT    ___
             G                   GGGC GGGGAG   GGGGCC  GGG
                                 |||| ||||||   ||||||  |||
                                 CCCG CCCCTC   TCCCGG  CCC
                                   A    ____     AGA
GAM1712 ADORA2B  5' GGGCTGGGGCGCTGGTGGCCGG 41936     C   AGG   _
             G                   GGGC GGGG  GCTGG GGCCGGG
                                 |||| ||||  ||||| |||||||
                                 CCCG CCCC  CGACC CCGGCCC
                                   A  G__    A
GAM1712 AGRN     3' GGACTGGGCTGGGGCTGG    41937     GA       C
                                 GGG  GGGCTGGGGC GG
                                 |||  |||||||||| ||
                                 CCT  CCCGACCCCG CC
                                   GA       A
GAM1712 ANK1     3' GGGTTGGGGAGGGTGGGCAG  41938    CC      C   GC
                                 GGG  GGGGAGGG TGGG  CGG
                                 |||  |||||||| ||||  |||
                                 CCC  CCCCTCCC ACCC  GTC
                                   AA      _   __
GAM1712 ANK1     3' GGGTTGGGGAGGGTGGGCAG  41938    CC      C   GC
                                 GGG  GGGGAGGG TGGG  CGG
                                 |||  |||||||| ||||  |||
                                 CCC  CCCCTCCC ACCC  GTC
                                   AA      _   __
GAM1712 AOC3     3' GGGCTGGGGGAGTACCAGGGGC 41939     C_    GG _    C
             TGGG                  GGGC  GGGGAG  CT GGGGC GGG
                                 ||||  ||||||  || ||||| |||
                                 CCCG  CCCCTC  GG CCCCG CCC
                                   AC     AT  T    A
GAM1712 ARAF1    5' GGGCTGAGGTGGGGCTGGG   41940     C   A_
                                 GGGC GGGG  GGGCTGGG
                                 |||| ||||  ||||||||
                                 CCCG CTCC  CCCGACCC
                                   A   AC
GAM1712 ARHGDIA  3' GGGTGGGGGAGGGCTGAGG   41941    CC
                                 GGG  GGGGAGGGCTGGGG
                                 |||  ||||||||||||||
                                 CCC  CCCCTCCCGACTCC
                                   AC
GAM1712 ARIX     5' GGGCGGGGGCGGGGGCCGGG  41942     CGG  A   T
                                 GGGC   GG GGGC GGGGCCGGG
                                 ||||   || |||| |||||||||
                                 CCCG   CC CCCG CCCCGGCCC
                                   ___  _   C
GAM1712 ASGR2    5' GCTCTGAGGGCTGGGGCTGGG 41943    CGGG        C
                                 GC   GAGGGCTGGGGC GGG
                                 ||   ||||||||||| |||
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                                CG   CTCCCGACCCCG CCC
                                 AGA_         A
GAM1712 ASPH    3' GGGCTGGGAGGGCTGGAGAGG 41944     CG         CC
                                GGGC  GGGAGGGCTGGGG  GG
                                ||||  ||||||||||||  ||
                                CCCG  CCCTCCCGACCTC  CC
                                  A_          T_
GAM1712 ASPH    5' GGGCTGGTGAGGGCTGGTGG  41945     C  G      _
                                GGGC GG GAGGGCTGG GG
                                |||| || ||||||||| ||
                                CCCG CC CTCCCGACC CC
                                  A A        A
GAM1712 ASPH    3' GGGCTGGGAGGGCTGGAGAGG 41944     CG         CC
                                GGGC  GGGAGGGCTGGGG  GG
                                ||||  ||||||||||||  ||
                                CCCG  CCCTCCCGACCTC  CC
                                  A_          T_
GAM1712 ATP2B4   5' AGGCCGGGGAGTGGGCTGGG  41946         __
                                GGGCCGGGGA  GGGCTGGG
                                ||||||||||  ||||||||
                                TCCGGCCCCT  CCCGACCC
                                     CA
GAM1712 B4GALT2  3' GGGCTAGGGGGAGGGGGTCGGG 41947     CG  A  CT   C
                                GGGC  GGG GGG  GGGG CGGG
                                ||||  ||| |||  |||| ||||
                                CCCG  CCC CCT  CCCC GCCC
                                  AT  _  C_   A
GAM1712 B4GALT2  3' GGGCTAGGGGGAGGGGGTCGGG 41947     CG  A  CT   C
                                GGGC  GGG GGG  GGGG CGGG
                                ||||  ||| |||  |||| ||||
                                CCCG  CCC CCT  CCCC GCCC
                                  AT  _  C_   A
GAM1712 BACE2    5' GGGCTCGGGGGGCGCCGGG   41948     _   A _
                                GGGC CGGGG GG GCTGGG
                                |||| ||||| || ||||||
                                CCCG GCCCC CC CGGCCC
                                  A    _ G
GAM1712 BACE2    5' GGGCTCGGGGGGCGCCGGG   41948     _   A _
                                GGGC CGGGG GG GCTGGG
                                |||| ||||| || ||||||
                                CCCG GCCCC CC CGGCCC
                                  A    _ G
GAM1712 BACE2    5' GGGCTCGGGGGGCGCCGGG   41948     _   A _
                                GGGC CGGGG GG GCTGGG
                                |||| ||||| || ||||||
                                CCCG GCCCC CC CGGCCC
                                  A    _ G
GAM1712 BAIAP3   3' GGCCTGGGGAAGGGTTGGG   41950     _   _  C
                                GGCC GGGGA GGG TGGG
                                |||| ||||| ||| ||||
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                                CCGG CCCCT CCC ACCC
                                  A    T  A
GAM1712 BAIAP3   3' GGGGTGGGGGCCAGGGCCGGG 41949    CCGG A   TG
                                GGG   GG GGGC GGGCCGGG
                                |||   || ||||  ||||||||
                                CCC   CC CCCG  CCCGGCCC
                                  CA__ _   GT
GAM1712 BARHL1   3' GGGCTGAGGCTGGGGGCTGGGG 41951     C   A___      C
           TCGGG                  GGGC GGGG   GGGCTGGGG CGGG
                                |||| ||||   |||||||||| ||||
                                CCCG CTCC   CCCGACCCC GCCC
                                  A   GACC       A
GAM1712 BARHL1   3' GGGCCGGGCAGGGCCCCCTCCC 41952       G    GGGG_
           GGG                    GGGCCGGG AGGGCT    CCGGG
                                |||||||| ||||||    |||||
                                CCCGGCCC TCCCGG    GGCCC
                                    G     GGGAG
GAM1712 BCL2L2   3' GGGCAGGGGAAAGGAGGGGTTG 41953     C      CT   CC
           GG                     GGGC GGGGAGGG  GGGG  GGG
                                |||| ||||||||  ||||  |||
                                CCCG CCCCTTTC  CCCC  CCC
                                  T       CT   AA
GAM1712 BGN     3' GAGTCGGGGAGGGTTGAAAGG  41954    C       C  GG CC
                                GGG CGGGGAGGG TG  G  GG
                                ||| |||||||| ||  |  ||
                                CTC GCCCCTCCC AC  T  CC
                                  A       A  TT __
GAM1712 BRAF    5' GGGCGGGGAGGGGGCCGG    41955     C      CTGG
                                GGGC GGGGAGGG   GGCCGG
                                |||| ||||||||   ||||||
                                CCCG CCCCTCCC   CCGGCC
                                  _      _____
GAM1712 C21orf2  3' GGGCTGGGGAAGACGCTGGG  41956     C     __
                                GGGC GGGGAGG  GCTGGG
                                |||| |||||||  ||||||
                                CCCG CCCCTTC  CGACCC
                                  A      TG
GAM1712 CHAD    5' GGCTGGGACGCCTGGGGCCGGG 41957    C   AGGG
                                GGC GGGG   CTGGGGCCGGG
                                ||| ||||   ||||||||||
                                CCG CCCT   GACCCCGGCCC
                                  A   GCG_
GAM1712 COL6A2   3' GGGCCTGGGGAGACCTGGGGCT 41958      _     G     C
           GGG                    GGGCC GGGGAGG CTGGGGC GGG
                                ||||| ||||||| ||||||| |||
                                CCCGG CCCCTCT GACCCCG CCC
                                  A      G      A
GAM1712 COL6A2   3' GGGCTGGGCGGGGGCCGG    41959    GA   T
                                GGG  GGGC GGGGCCGG
                                |||  |||| ||||||||
```

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                                CCC  CCCG CCCCGGCC
                                  GA   C
GAM1712 COPE    3' GGGTGGGGAGGGCTGCAGGG  41960    CC       G  CC
                                GGG  GGGGAGGGCTG GG  GG
                                |||  |||||||||| ||  ||
                                CCC  CCCCTCCCGAC TC  CC
                                  A_        G  __
GAM1712 COX7A1   5' CGGCGGGGCTGGGGCTGG   41963    GGA       C
                                CGG   GGGCTGGGGC GG
                                |||   |||||||||| ||
                                GCC   CCCGACCCCG CC
                                  GC_       A
GAM1712 COX7A1   5' GGGCTGGGGCTGGGGCTGGGGC 41961     C   A__       C
            TGGG                  GGGC GGGG   GGGCTGGGGC GGG
                                |||| ||||   |||||||||| |||
                                CCCG CCCC   CCCGACCCCG CCC
                                  A   GAC        A
GAM1712 COX7A1   5' CGGGGCTGGGGCTGGGGCTGGG 41962      A__       C
                                CGGGG   GGGCTGGGGC GGG
                                |||||   |||||||||| |||
                                GCCCC   CCCGACCCCG CCC
                                   GAC        A
GAM1712 CSK     3' GGGCCGGAGGGGTGCAGGCTGG 41964        A  C  _   C
            G                   GGGCCGGGG GGG TG GGGC GGG
                                |||||||| ||| || |||| |||
                                CCCGGCCTC CCC AC TCCG CCC
                                     _  _ G   A
GAM1712 CYP11B1  3' GGGCCAGGTGGGGCTGGG    41965       GA
                                GGGCCGGG  GGGCTGGG
                                ||||||||  ||||||||
                                CCCGGTCC  CCCGACCC
                                    AC
GAM1712 DAG1    3' GGGCAGGGGAGAGGGGCTGGG  41966     C     GCT    C
                                GGGC GGGGAGG   GGGGC GGG
                                |||| |||||||   ||||| |||
                                CCCG CCCCTCT   CCCCG CCC
                                  T      ___     A
GAM1712 DES     3' GGGCTGGGGAGGTCTGCGGG   41967     C     G  _
                                GGGC GGGGAGG CTG GGG
                                |||| ||||||| ||| |||
                                CCCG CCCCTCC GAC CCC
                                  A      A  G
GAM1712 DGUOK   3' GGGCTGGGGATGGAAAGGTGGT 41968     C   _  CT  _  CC
            TGGG                  GGGC GGGGA GGG  GG GG  GGG
                                |||| ||||| |||  || ||  |||
                                CCCG CCCCT CCT  CC CC  CCC
                                  A    A  TT  A  AA
GAM1712 DGUOK   3' GGGCTGGGGATGGAAAGGTGGT 41968     C   _  CT  _  CC
            TGGG                  GGGC GGGGA GGG  GG GG  GGG
                                |||| ||||| |||  || ||  |||
```

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                                CCCG CCCCT CCT  CC CC  CCC
                                  A    A  TT  A  AA
GAM1712  DGUOK    3'  GGGCTGGGGATGGAAAGGTGGT 41968     C    _  CT  _  CC
             TGGG                  GGGC GGGGA GGG  GG GG  GGG
                                |||| ||||| |||  || ||  |||
                                CCCG CCCCT CCT  CC CC  CCC
                                  A    A  TT  A  AA
GAM1712  DGUOK    3'  GGGCTGGGGATGGAAAGGTGGT 41968     C    _  CT  _  CC
             TGGG                  GGGC GGGGA GGG  GG GG  GGG
                                |||| ||||| |||  || ||  |||
                                CCCG CCCCT CCT  CC CC  CCC
                                  A    A  TT  A  AA
GAM1712  DGUOK    3'  GGGCTGGGGATGGAAAGGTGGT 41968     C    _  CT  _  CC
             TGGG                  GGGC GGGGA GGG  GG GG  GGG
                                |||| ||||| |||  || ||  |||
                                CCCG CCCCT CCT  CC CC  CCC
                                  A    A  TT  A  AA
GAM1712  DLEC1    3'  GGGCCTGGGGCTGAGGGCTGGG 41969      _  ___
                                GGGCC GGGG  AGGGCTGGG
                                ||||| ||||  |||||||||
                                CCCGG CCCC  TCCCGACCC
                                  A   GAC
GAM1712  DLEC1    3'  GGGCCTGGGGCTGAGGGCTGGG 41969      _  ___
                                GGGCC GGGG  AGGGCTGGG
                                ||||| ||||  |||||||||
                                CCCGG CCCC  TCCCGACCC
                                  A   GAC
GAM1712  DMPK     5'  GGGCTAGGGGGTGAGGGCTGGG 41971     C___  _
                                GGGC   GGG GAGGGCTGGG
                                ||||   ||| ||||||||||
                                CCCG   CCC CTCCCGACCC
                                  ATCC  A
GAM1712  DMPK     5'  GGGTGAGGGCTGGGGGTTGGG  41970    _       CC_
                                GGG GAGGGCTGGGG  GGG
                                ||| ||||||||||  |||
                                CCC CTCCCGACCCC  CCC
                                  A        CAA
GAM1712  DNMT3A   5'  GGGCTGGGGGGCTGCTGGG   41972     C   A __
                                GGGC GGGG GG  GCTGGG
                                |||| |||| ||  ||||||
                                CCCG CCCC CC  CGACCC
                                  A   _ GA
GAM1712  DOC1     5'  GGGCCGGGCGGGGGCCGG    41973      GGGGA   T
                                GGGCC    GGGC GGGGCCGG
                                |||||    |||| ||||||||
                                CCCGG    CCCG CCCCGGCC
                                   _____  C
GAM1712  DOC1     5'  GGGCGGGGGCCGGGCCGG    41974     CGG  A      G
                                GGGC  GG GGGCTGGG CCGG
                                ||||  || |||||||| ||||
```

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                                CCCG   CC CCCGGCCC GGCC
                                  ___ _      _
GAM1712  DRIL1    5'  GGGCCGCGGGGGAGCCGG    41975       G  A   CTGG
                                GGGCCG GG GGG    GGCCGG
                                |||||| || |||    ||||||
                                CCCGGC CC CCC    TCGGCC
                                   G  _  ____
GAM1712  DUSP7    5'  GGCCCGGGGCCGGGGCCGG   41976      G   AGG
                                GGCC GGG   GCTGGGGCCGG
                                |||| |||   ||||||||||
                                CCGG CCC   CGGCCCCGGCC
                                  G  ___
GAM1712  EGFL4    3'  GGGCTGGGGGTGGCTGGA    41977      C    AG
                                GGGC GGGG  GGCTGGG
                                |||| ||||  |||||||
                                CCCG CCCC  CCGACCT
                                  A    CA
GAM1712  EGFL6    5'  GGCCTGGGGAGGGGCTGGG   41978      _      _
                                GGCC GGGGAGGG CTGGG
                                |||| |||||||| |||||
                                CCGG CCCCTCCC GACCC
                                  A       C
GAM1712  EGLN1    5'  GGGCCGGGAGGGCCGGG     41979        G
                                GGGCCGGG AGGGCTGGG
                                |||||||| |||||||||
                                CCCGGCCC TCCCGGCCC
                                   _
GAM1712  EIF4A1   3'  GAGCCCTGGCTGGGGCTGG   41980      GGGGAG       C
                                GGGCC     GGCTGGGGC GG
                                |||||     ||||||||| ||
                                CTCGG     CCGACCCCG CC
                                   GA____       A
GAM1712  EN1      3'  GGGCCGGCGATGCGGGTCGGG  41981       G  GG  T   GC
                                GGGCCGG GA  GC GGG  CGGG
                                ||||||| ||  || |||  ||||
                                CCCGGCC CT  CG CCC  GCCC
                                    G  A_  _   A_
GAM1712  ENG      5'  GGGCGGGGAGGGGGTGCTGGG  41982      C       CT  G  C
                                GGGC GGGGAGGG  GG GC GGG
                                |||| ||||||||  || || |||
                                CCCG CCCCTCCC  CC CG CCC
                                  _       __ A  A
GAM1712  ERBB3    3'  GGACTGGGGAAAAGGGGCTGGG 41983      C    ____
                                GGGC GGGGA    GGGCTGGG
                                |||| |||||    ||||||||
                                CCTG CCCCT    CCCGACCC
                                  A     TTTC
GAM1712  ESPN     3'  GGGCCTGGCTGGCTGGGGCTGG 41984       GG  AG       C
            G                    GGGCC  GG  GGCTGGGGC GGG
                                |||||  ||  ||||||||| |||
```

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                                CCCGG  CC  CCGACCCCG CCC
                                  A_  GA       A
GAM1712  FAAH     3'  GGGTCGGGAAGGGGCCAGGGCC 41985     C       _ TG
              GGG                  GGG CGGGGAGGG C  GGGCCGGG
                                ||| ||||||||| |  ||||||||
                                CCC GCCCTTCCC G  CCCGGCCC
                                  A       C GT
GAM1712  FDXR     3'  GGGCCGGGGCTGGGGCTGGG  41986        GAGG      C
                                GGGCCGGG   GCTGGGGC GGG
                                ||||||||   |||||||| |||
                                CCCGGCCC   CGACCCCG CCC
                                     ____      A
GAM1712  FDXR     3'  GGGCCGGGGCTGGGGCTGGG  41986        GAGG      C
                                GGGCCGGG   GCTGGGGC GGG
                                ||||||||   |||||||| |||
                                CCCGGCCC   CGACCCCG CCC
                                     ____      A
GAM1712  GA       5'  GGGTGGGGCTGGGGCTGGG  41987     GA        C
                                GGG  GGGCTGGGGC GGG
                                |||  |||||||||| |||
                                CCC  CCCGACCCCG CCC
                                  AC        A
GAM1712  GAS11    3'  GGGCTGGAGGGGGCTGAGG  41988      C   A
                                GGGC GGGG GGGCTGGGG
                                |||| |||| |||||||||
                                CCCG CCTC CCCGACTCC
                                  A   C
GAM1712  GDI1     3'  GGGCTGGGAGGGGCTGGG   41989      C   GA
                                GGGC GGG  GGGCTGGG
                                |||| |||  ||||||||
                                CCCG CCC  CCCGACCC
                                  A  TC
GAM1712  GNB2     3'  GGCCCGGGGAAGGGGGCTGGG  41990    G       CTG   C
                                GG CCGGGGAGGG   GGGC GGG
                                || ||||||||||   |||| |||
                                CC GGCCCCTTCC   CCCG CCC
                                 G        ___   A
GAM1712  GNB2     5'  GGGCCGCGGGACGGGGGCTGGG 41991       _   ___
                                GGGCCG GGGA   GGGCTGGG
                                |||||| ||||   ||||||||
                                CCCGGC CCCT   CCCGACCC
                                   G   GCC
GAM1712  GPI      3'  GGGCTGGGGGTTAGGCTGGG  41992     C   A__
                                GGGC GGGG   GGGCTGGG
                                |||| ||||   ||||||||
                                CCCG CCCC   TCCGACCC
                                  A   CAA
GAM1712  GUCY1A2  5'  GGGCGGGGAGGGCTGCGG   41993     C        G
                                GGGC GGGGAGGGCTG GG
                                |||| |||||||||| ||
```

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                                CCCG CCCCTCCCGAC CC
                                  _        G
GAM1712 HOXB5    3' GGGCTGGGGGTGGCACGGG   41994     C   AG  _
                                GGGC GGGG  GGC TGGG
                                |||| ||||  ||| ||||
                                CCCG CCCC  CCG GCCC
                                  A   CA  T
GAM1712 HSD11B2  5' GGGGCGGGGCGGGGCGGGGGCC 41995   C    A_   T       III
           GGGC                  G CGGGG  GGGC GGGGCCGGG  C
                                | |||||  |||| |||||||||  |
                                C GCCCC  CCCG CCCCGGCCC  G
                                 C    GC   C       III
GAM1712 HSD11B2  5' GGGCGGGGGCCGGGCCGG    41974     CGG  A      G
                                GGGC   GG GGGCTGGG CCGG
                                ||||   || |||||||| ||||
                                CCCG   CC CCCGGCCC GGCC
                                  ____ _      _
GAM1712 IKBKB    5' GGGCGGGGAAGGCGGGGCTGGG 41996     C       T    C
                                GGGC GGGGAGGGC GGGGC GGG
                                |||| ||||||||| ||||| |||
                                CCCG CCCCTTCCG CCCCG CCC
                                  _       _    A
GAM1712 IL12RB2  5' GGGCCGGGGCGGGGGTCGGG  41997         AGGGCT   C
                                GGGCCGGGG     GGGG CGGG
                                |||||||||     |||| ||||
                                CCCGGCCCC     CCCC GCCC
                                     GC____    A
GAM1712 IL12RB2  5' GGGCGGGGGTCGGGGCTGGG  41998     C   A__
                                GGGC GGGG   GGGCTGGG
                                |||| ||||   ||||||||
                                CCCG CCCC   CCCGACCC
                                  C   AGC
GAM1712 INPPL1   5' GGGCTGAGGCTGGGGCCGGG  41999     C GGGA
                                GGGC G   GGGCTGGGGCCGGG
                                |||| |   ||||||||||||||
                                CCCG C   TCCGACCCCGGCCC
                                  A ____
GAM1712 ITGA3    3' GGAAGGGGCTGGGGCTGG    42000       _     C
                                GGGAGGG CTGGGGC GG
                                ||||||| ||||||| ||
                                CCTTCCC GACCCCG CC
                                    C      A
GAM1712 ITGA3    3' GGAAGGGGCTGGGGCTGG    42000       _     C
                                GGGAGGG CTGGGGC GG
                                ||||||| ||||||| ||
                                CCTTCCC GACCCCG CC
                                    C      A
GAM1712 ITPKB    3' GGGCCAGGGAGGGCGTGGG   42001           _
                                GGGCCGGGGAGGGC TGGG
                                |||||||||||||| ||||
```

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                                CCCGGTCCCTCCCG ACCC
                                       C
GAM1712 JAK3    3' GGGCCAGGGCTTAAGGGGTTGG 42002        AGGGCT   CC
           G                    GGGCCGGGG    GGGG  GGG
                                |||||||||    ||||  |||
                                CCCGGTCCC    CCCC  CCC
                                     GAATT_   AA
GAM1712 JUNB    5' GGTCTGGGGAGGGTCCCTGCGG 42003    GCC      _ GGG  C
           G                    GG   GGGGAGGG CT   GC GGG
                                ||   |||||||| ||   || |||
                                CC   CCCCTCCC GG   CG CCC
                                 AGA      A  GA_ _
GAM1712 JUP     5' GGGTCGGGGTCGGGCCGGG   42005    C    A_
                                GGG CGGGG  GGGCTGGG
                                ||| |||||  ||||||||
                                CCC GCCCC  CCCGGCCC
                                  A    AG
GAM1712 JUP     5' GGGCCGGGTCGGGGTCGG    42004        GAGGGCT   C
                                GGGCCGGG     GGGG CGG
                                ||||||||     |||| |||
                                CCCGGCCC     CCCC GCC
                                     AG_____   A
GAM1712 KCNJ10  5' GGGCCGGGGCCGGGGTCGGG  42006        GAGG     C
                                GGGCCGGG   GCTGGGG CGGG
                                ||||||||   ||||||| ||||
                                CCCGGCCC   CGGCCCC GCCC
                                     _____      A
GAM1712 KCNK4   5' GGGCCGGGCGGGGGGCTCCTGG 42007        GA   CT   G_ _
           G                    GGGCCGGG  GGG  GGG  CC GGG
                                ||||||||  |||  |||  || |||
                                CCCGGCCC  CCC  CCC  GG CCC
                                     G_   __   GA  A
GAM1712 KCNK4   5' GGGCCGGGCGGGGGGCTCCTGG 42007        GA   CT   G_ _
           G                    GGGCCGGG  GGG  GGG  CC GGG
                                ||||||||  |||  |||  || |||
                                CCCGGCCC  CCC  CCC  GG CCC
                                     G_   __   GA  A
GAM1712 KIF5C   5' GGGTGGGGGGCCGGGGCCGGG  42008    CCG   A
                                GGG   GGG GGGCTGGGGCCGGG
                                |||   ||| ||||||||||||||
                                CCC   CCC CCCGGCCCCGGCCC
                                  A__   _
GAM1712 KIFC3   5' GGCCGGGCTGGCTGGGGCTGGG 42009        GAG       C
                                GGCCGGG   GGCTGGGGC GGG
                                |||||||   ||||||||| |||
                                CCGGCCC   CCGACCCCG CCC
                                     GA_       A
GAM1712 KLK4    3' GGTCTGGGGAAGGAGGGGTTGG 42010    GCC      CT   CC
           G                    GG   GGGGAGGG  GGGG  GGG
                                ||   ||||||||  ||||  |||
```

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                                CC  CCCCTTCC  CCCC  CCC
                                 AGA      T_   AA
GAM1712  KPNB1   5'  GGGATGGGGGTTGGGGGTCGGG 42011    CCG  A  GCT   C
                                GGG  GGG GG  GGGG CGGG
                                |||  ||| ||  |||| ||||
                                CCC  CCC CC  CCCC GCCC
                                  TA_  _ AAC   A
GAM1712  L1CAM   3'  GGCTGGGGAGTGGCTGGG   42012    C    _
                                GGC GGGGAG GGCTGGG
                                ||| |||||| |||||||
                                CCG CCCCTC CCGACCC
                                  A    A
GAM1712  L1CAM   3'  GGCTGGGGAGTGGCTGGG   42012    C    _
                                GGC GGGGAG GGCTGGG
                                ||| |||||| |||||||
                                CCG CCCCTC CCGACCC
                                  A    A
GAM1712  LFG     3'  GGGTGGGGAGGGATGGGGCTGG 42013    CC      C    C
            G                    GGG  GGGGAGGG TGGGGC GGG
                                |||  |||||||| |||||| |||
                                CCC  CCCCTCCC ACCCCG CCC
                                  A_      T    A
GAM1712  LIMK1   5'  GGGCCCGGCGGGGCTGGGGCTG 42014      G  GA       C
            GG                   GGGCC GG  GGGCTGGGGC GGG
                                |||||  ||  |||||||||| |||
                                CCCGG CC  CCCGACCCCG CCC
                                   G  GC        A
GAM1712  LIMK1   5'  GGGCCCGGCGGGGCTGGGGCTG 42014      G  GA       C
            GG                   GGGCC GG  GGGCTGGGGC GGG
                                |||||  ||  |||||||||| |||
                                CCCGG CC  CCCGACCCCG CCC
                                   G  GC        A
GAM1712  LIMK1   5'  GGGCTGGGGGCGGCCGGG   42015    C   AG
                                GGGC GGGG  GGCTGGG
                                ||||  ||||  |||||||
                                CCCG CCCC  CCGGCCC
                                  A   CG
GAM1712  LIMK1   5'  GGGCTGGGGGCGGCCGGG   42015    C   AG
                                GGGC GGGG  GGCTGGG
                                ||||  ||||  |||||||
                                CCCG CCCC  CCGGCCC
                                  A   CG
GAM1712  LOXL2   3'  GGGTGGGGGCCGGGCTGGG   42016    CC   A_
                                GGG  GGGG  GGGCTGGG
                                |||  ||||  ||||||||
                                CCC  CCCC  CCCGACCC
                                  AC   GG
GAM1712  MADH3   5'  GGCTGGGGAGGGCGTGCGGG  42017    C      _ _
                                GGC GGGGAGGGC TG GGG
                                ||| |||||||| || |||
```

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                                CCG CCCCTCCCG AC CCC
                                  A       C  G
GAM1712  MAML1    5'  GGGCCGGGCCCGGGGCCGG   42018        GAGGG
                                GGGCCGGG    CTGGGGCCGG
                                ||||||||    ||||||||||
                                CCCGGCCC    GGCCCCGGCC
                                    G____
GAM1712  MAP3K10  3'  GGGCTGGGGCAGGGCCTGGG   42019     C   _    _
                                GGGC GGGG AGGGC TGGG
                                |||| |||| ||||| ||||
                                CCCG CCCC TCCCG ACCC
                                  A   G    G
GAM1712  MAX      3'  GGGCTGGGAAGGGTCCGCACTG 42020     C      _  GG  C
            GG                    GGGC GGGGAGGG CTG  GC GGG
                                |||| |||||||| |||  || |||
                                CCCG CCCTTCCC GGC  TG CCC
                                  A       A  G_  A
GAM1712  MAX      3'  GGGCTGGGAAGGGTCCGCACTG 42020     C      _  GG  C
            GG                    GGGC GGGGAGGG CTG  GC GGG
                                |||| |||||||| |||  || |||
                                CCCG CCCTTCCC GGC  TG CCC
                                  A       A  G_  A
GAM1712  MECP2    3'  GGGCCGGGAGGGGTAGACCTGG 42021        G   CTG    _
            G                     GGGCCGGG AGGG   GGGCC GGG
                                |||||||| ||||   ||||| |||
                                CCCGGCCC TCCC   TCTGG CCC
                                    _   CA_    A
GAM1712  MFI2     5'  GGCTGGGGCCGGGCTGGGGCTG 42023     C   A_       C
            GG                    GGC GGGG  GGGCTGGGGC GGG
                                ||| ||||  |||||||||| |||
                                CCG CCCC  CCCGACCCCG CCC
                                  A   GG        A
GAM1712  MFI2     5'  GGGGCTGGCTGGGGCCGG    42022      AG
                                GGGG  GGCTGGGGCCGG
                                ||||  ||||||||||||
                                CCCC  CCGACCCCGGCC
                                  GA
GAM1712  MFI2     5'  GGGGCTGGCTGGGGCCGG    42022      AG
                                GGGG  GGCTGGGGCCGG
                                ||||  ||||||||||||
                                CCCC  CCGACCCCGGCC
                                  GA
GAM1712  MFI2     5'  GGCTGGGGCCGGGCTGGGGCTG 42023     C   A_       C
            GG                    GGC GGGG  GGGCTGGGGC GGG
                                ||| ||||  |||||||||| |||
                                CCG CCCC  CCCGACCCCG CCC
                                  A   GG        A
GAM1712  MIC2     5'  GGGCCGGGTGGGGCGAAGCCCG 42024        GA   TG  G
            GG                    GGGCCGGG  GGGC  GG CCGGG
                                ||||||||  ||||  || |||||
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                                CCCGGCCC  CCCG  TC GGCCC
                                    AC    CT  G
GAM1712  MYLK2    3'  GAGCTGGGGAGGGAACCGGG   42025      C       CTGG
                                GGGC GGGGAGGG    GGCCGGG
                                |||| ||||||||    |||||||
                                CTCG CCCCTCCC    TTGGCCC
                                  A      _____
GAM1712  NGFR     3'  GGGCTGAGGGAGGGTTGAGG   42027      C _      C
                                GGGC G GGGAGGG TGGGG
                                |||| | ||||||| |||||
                                CCCG C CCCTCCC ACTCC
                                  A T      A
GAM1712  NGFR     3'  GGGCTGGGGGGAACCCTGGGCTG 42026      C    A    G_   C
           GG                     GGGC GGGG GGGCT  GGGC GGG
                                |||| |||| |||||  |||| |||
                                CCCG CCCC CTTGG  CCCG CCC
                                  A   _    GA    A
GAM1712  NR1D1    3'  GGGCCAGGGGAGGGTTGTGGG  42028       _       C  _
                                GGGCC GGGGAGGG TG GGG
                                ||||| |||||||| || |||
                                CCCGG CCCCTCCC AC CCC
                                  T       A  A
GAM1712  NRIP1    5'  GGGCGGGCGTGGGGCCGG    42029     A   _
                                GGG GGGC TGGGGCCGG
                                ||| |||| |||||||||
                                CCC CCCG ACCCCGGCC
                                  G   C
GAM1712  NTSR1    3'  GGGTGGGGAGGAGTTGGG    42030     CC      _ C
                                GGG  GGGGAGG G TGGG
                                |||  ||||||| | ||||
                                CCC  CCCCTCC C ACCC
                                  A_      T A
GAM1712  OLFM1    5'  GGGCTGGGCAGGGCTGGGCTGG 42031      C   G        G C
           G                     GGGC GGG AGGGCTGGG C GGG
                                |||| ||| |||||||| | |||
                                CCCG CCC TCCCGACCC G CCC
                                  A   G        _ A
GAM1712  OLFM1    5'  GGGCTGGGCAGGGCTGGGCTGG 42031      C   G        G C
           G                     GGGC GGG AGGGCTGGG C GGG
                                |||| ||| |||||||| | |||
                                CCCG CCC TCCCGACCC G CCC
                                  A   G        _ A
GAM1712  OLFM1    5'  GGGCTGGGCAGGGCTGGGCTGG 42031      C   G        G C
           G                     GGGC GGG AGGGCTGGG C GGG
                                |||| ||| |||||||| | |||
                                CCCG CCC TCCCGACCC G CCC
                                  A   G        _ A
GAM1712  OTOF     3'  GGGCTGGGGAGCGGCTGGCGGG 42032      C     _     GGC
                                GGGC GGGGAG GGCTGG   CGGG
                                |||| |||||| ||||||   ||||
```

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                                CCCG CCCCTC CCGACC   GCCC
                                  A     G     ___
GAM1712  PACE     3'  GGCTGGGGCCGGGGCCGG    42033     C   GAGG
                                GGC GGG    GCTGGGGCCGG
                                ||| |||    ||||||||||
                                CCG CCC    CGGCCCCGGCC
                                  A  _____
GAM1712  PACSIN1  3'  GGGCTGGGAGGGCTGGCACAG  42034      CG         G  C
                                GGGC  GGGAGGGCTGG GC GG
                                ||||  |||||||||| || ||
                                CCCG  CCCTCCCGACC TG TC
                                  A_          G  _
GAM1712  PAH      5'  GGGCTGAGGGAGGGTGTGGG   42035      C _      C  _
                                GGGC G GGGAGGG TG GGG
                                |||| | ||||||| || |||
                                CCCG C CCCTCCC AC CCC
                                  A T       _  A
GAM1712  PEA15    3'  GGGTGGGGAGGGGCATCTTGGG 42036     CC       _ _____
                                GGG  GGGGAGGG C    TGGG
                                |||  |||||||| |    ||||
                                CCC  CCCCTCCC G    ACCC
                                  A_       C TAGA
GAM1712  PEX14    3'  GGGGCTGGGGCTGGGGCTGGG  42038      A__         C
                                GGGG   GGGCTGGGGC GGG
                                ||||   |||||||||| |||
                                CCCC   CCCGACCCCG CCC
                                  GAC          A
GAM1712  PEX14    3'  GGGCTGGGGAGGGGCTTGGG   42037      C       _  _
                                GGGC GGGGAGGG CT GGG
                                |||| |||||||| || |||
                                CCCG CCCCTCCC GA CCC
                                  A       C  A
GAM1712  PEX14    3'  GGGCCTGGGGCTGGGGCTGGG  42039       GGGGA         C
                                GGGCC     GGGCTGGGGC GGG
                                |||||     |||||||||| |||
                                CCCGG     CCCGACCCCG CCC
                                   AC___          A
GAM1712  PFKFB4   3'  GGGCTGGGGTGGGGGCTCTGGG 42040      C    A__     G_
                                GGGC GGGG   GGGCT  GGG
                                |||| ||||   |||||  |||
                                CCCG CCCC   CCCGA  CCC
                                  A    ACC     GA
GAM1712  PFKL     3'  GGGCTGGGGAGGGGCGTGGG   42041      C       _ _
                                GGGC GGGGAGGG C TGGG
                                |||| |||||||| | ||||
                                CCCG CCCCTCCC G ACCC
                                  A       C C
GAM1712  PIK3R2   5'  GGGCTGGGAGGGTCCGCTGGG  42042      CG     _____
                                GGGC  GGGAGG    GCTGGG
                                ||||  ||||||    ||||||
```

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                                CCCG  CCCTCC    CGACCC
                                  A_     CAGG
GAM1712  PKD1     3'  GAGCTGGGGAGGGGACCCTGGG 42043      C      ____
                                GGGC GGGGAGGG    CTGGG
                                |||| ||||||||    |||||
                                CTCG CCCCTCCC    GACCC
                                  A       CTGG
GAM1712  PKM2     3'  GGGCTGGAGGAGGGGCTCTGGG 42044      C  _     ___
                                GGGC GG GGAGGG   CTGGG
                                |||| || ||||||   |||||
                                CCCG CC CCTCCC   GACCC
                                  A  T     CGA
GAM1712  PLD2     3'  GGGCTGGGAGGGCCCTGGG   42045      CG       G_
                                GGGC  GGGAGGGCT  GGG
                                ||||  |||||||||  |||
                                CCCG  CCCTCCCGG  CCC
                                  A_       GA
GAM1712  POLR2E   3'  GAGCTGGGGTGGGGCTGGG   42046      C    A_
                                GGGC GGGG  GGGCTGGG
                                |||| ||||  ||||||||
                                CTCG CCCC  CCCGACCC
                                  A    AC
GAM1712  PPP1R8   5'  GAGGTAGGGTTGGGGCCGGG   42047      _    C
                                GGGG AGGG TGGGGCCGGG
                                |||| |||| ||||||||||
                                CTCC TCCC ACCCCGGCCC
                                  A    A
GAM1712  PPP2R4   3'  GGGATGGGGAGGGGCCACTGCT 42048      CC       _  GG  C
            GGG                   GGG  GGGGAGGG CTG  GC GGG
                                |||  |||||||| |||  || |||
                                CCC  CCCCTCCC GGT  CG CCC
                                  TA       C   GA  A
GAM1712  PPP3CB   5'  GGGCCGGGCGGGGTTGGG    42049        GA   C
                                GGGCCGGG  GGG TGGG
                                ||||||||  ||| ||||
                                CCCGGCCC  CCC ACCC
                                     GC   A
GAM1712  PPP4C    3'  GGGTTGGAGGGGGCAGGGGCCG 42050      CC    A    T
            GG                    GGG  GGGG GGGC GGGGCCGGG
                                |||  |||| |||| |||||||||
                                CCC  CCTC CCCG CCCCGGCCC
                                  AA   C    T
GAM1712  PRKACA   3'  GGGCTGGGAGGGCTGAGGGGCT 42051      CG       __    C
            GGG                   GGGC  GGGAGGGCT  GGGGC GGG
                                ||||  |||||||||  ||||| |||
                                CCCG  CCCTCCCGA  CCCCG CCC
                                  A_       CT    A
GAM1712  PSD      5'  GGGCTGGGGTGGGCCTGGG   42052      C    A   _
                                GGGC GGGG GGGC TGGG
                                |||| |||| |||| ||||
```

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                                CCCG CCCC CCCG ACCC
                                  A   A   G
GAM1712  PSD     5'  GGGCCAGGGAGTGGGCCGG   42053          GGCTG
                                GGGCCGGGGAG    GGGCCGG
                                ||||||||||    |||||||
                                CCCGGTCCCTC    CCCGGCC
                                      A____
GAM1712  PTMS    5'  GGTGCCGGGGCCGGGGCCGGG  42054   _    GAGG
                                GG GCCGGG   GCTGGGGCCGGG
                                || ||||||   ||||||||||||
                                CC CGGCCC   CGGCCCCGGCCC
                                 A    _____
GAM1712  PTPRJ   3'  GGGCAGGGGAAGCGGGGCCGGG 42055     C      G T
                                GGGC GGGGAGG C GGGGCCGGG
                                |||| ||||||| | |||||||||
                                CCCG CCCCTTC G CCCCGGCCC
                                  T     _ _
GAM1712  PVRL2   5'  GGGCCCGGGAGGGGACTGGG   42056      G     __
                                GGGCC GGGAGGG  CTGGG
                                ||||| |||||||  |||||
                                CCCGG CCCTCCC  GACCC
                                   G      CT
GAM1712  PYCR1   3'  GGGCCGGGAGGGGGCGTGGG   42057        _ A   _
                                GGGCCGGG G GGGC TGGG
                                |||||||| | |||| ||||
                                CCCGGCCC C CCCG ACCC
                                     T C   C
GAM1712  RAB3B   5'  GGGCCGGGGCGGGGCGCTGCGG 42058         A   C  GG  C
            G                    GGGCCGGGGG GGG TG  GC GGG
                                |||||||||| ||| ||  || |||
                                CCCGGCCCC CCC GC  CG CCC
                                     G   C  GA  _
GAM1712  RAB7    5'  GCGCTGGGGGCTCCGGGCCGGG 42059    CGG  A    G_
                                GC   GG GGGCT  GGGCCGGG
                                ||   || |||||  ||||||||
                                CG   CC CCCGA  CCCGGCCC
                                 CGA  _    GG
GAM1712  RAD21   5'  GGCCCGGGGAGGGGAAAAGGGT 42060    G        CT__   C
            CGGG                   GG CCGGGGAGGG   GGGG CGGG
                                || ||||||||||   |||| ||||
                                CC GGCCCCTCCC   TCCC GCCC
                                 G        CTTT   A
GAM1712  RFX1    3'  GGGCTGGGGAGAAGACGCTGGG 42061      C     _____
                                GGGC GGGGAGG   GCTGGG
                                |||| |||||||   ||||||
                                CCCG CCCCTCT   CGACCC
                                  A      TCTG
GAM1712  ROR2    5'  GGGCCGGGGCGCGGGGTCGGG  42062         AGG  T   C
                                GGGCCGGGGG  GC GGGG CGGG
                                |||||||||  || |||| ||||
```

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                                CCCGGCCCC  CG CCCC GCCC
                                     G__ _   A
GAM1712 RPIP8   5' AGGCCGGGGAGGGAGCTCTCCG 42063          CTGGGG
            GG                   GGGCCGGGGAGGG    CCGGG
                                ||||||||||||     |||||
                                TCCGGCCCCTCCC    GGCCC
                                      TCGAGA
GAM1712 RXRA    3' AGGCTGGGGAGGGGCCGG   42064    C   GGGCT
                                GGGC GGGGA   GGGGCCGG
                                |||| |||||   ||||||||
                                TCCG CCCCT   CCCCGGCC
                                  A   _____
GAM1712 RYR1    5' GGGCGGGAGGGCTGGG     42065    CG
                                GGGC  GGGAGGGCTGGG
                                ||||  ||||||||||||
                                CCCG  CCCTCCCGACCC
                                  __
GAM1712 RYR1    5' GGGCTGGGGGCGGGCTGGG  42066    C   A_
                                GGGC GGGG  GGGCTGGG
                                |||| ||||  ||||||||
                                CCCG CCCC  CCCGACCC
                                  A  CG
GAM1712 SCRT1   5' GGGCTTGGGGGGGCTGCGG  42067    C_  A    G
                                GGGC  GGGG GGGCTG GG
                                ||||  |||| |||||| ||
                                CCCG  CCCC CCCGAC CC
                                  AA  _    G
GAM1712 SF1     5' GGGCCGGGGGCGGCGGGGCCGG 42068        AG  T
            G                    GGGCCGGGG  GGC GGGGCCGGG
                                |||||||||  ||| |||||||||
                                CCCGGCCCC  CCG CCCCGGCCC
                                     CG  _
GAM1712 SLC6A8  5' GGGCCGGGGGGCGGCCGG   42069        AG  TGG
                                GGGCCGGGG  GGC  GGCCGG
                                |||||||||  |||  ||||||
                                CCCGGCCCC  CCG  CCGGCC
                                     __  ___
GAM1712 SLC8A2  3' GGGCTGGGGGGAAGGGCTGGG  42070    C___
                                GGGC   GGGGAGGGCTGGG
                                ||||   ||||||||||||
                                CCCG   CCCTTCCCGACCC
                                  ACCC
GAM1712 SMARCB1 5' GGGCTGGGGCGGGGCCGG   42071    C   AGGGC
                                GGGC GGGG   TGGGGCCGG
                                |||| ||||   |||||||||
                                CCCG CCCC   GCCCCGGCC
                                  A   _____
GAM1712 SNL     3' GGGCTGGGAGGAGGTGGCTGGG 42072    CG     CT  _  C
                                GGGC  GGGAGGG  GG GGC GGG
                                ||||  |||||||  || ||| |||
```

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                                CCCG  CCCTCCT  CC CCG CCC
                                  A_      __ A  A
GAM1712  SOX10    3'  AGGCTGGGGGGCAGGGGCTGGG  42073     CGG  A   T    C
                                GGGC   GG GGGC GGGGC GGG
                                ||||   || |||| ||||| |||
                                TCCG   CC CCCG CCCCG CCC
                                  A__ _   T    A
GAM1712  SPI1     3'  GGGCCGGCGGGGGGCTGCGGG   42074       _ A     _
                                GGGCCGG GG GGGCTG GGG
                                ||||||| || |||||| |||
                                CCCGGCC CC CCCGAC CCC
                                   G _     G
GAM1712  TAGLN    3'  GAGCTGGGGGAGGGCCGGG   42075     C_
                                GGGC  GGGGAGGGCTGGG
                                ||||  ||||||||||||
                                CTCG  CCCCTCCCGGCCC
                                  AC
GAM1712  TBR1     3'  GGGCCGCGGCGGGGCCGG    42076      G  AGGGC
                                GGGCCG GG    TGGGGCCGG
                                |||||| ||    |||||||||
                                CCCGGC CC    GCCCCGGCC
                                   G _____
GAM1712  TEM8     3'  GGGTTGGGGAGAGGCTGGG   42077     CC    _
                                GGG  GGGGAG GGCTGGG
                                |||  |||||| |||||||
                                CCC  CCCCTC CCGACCC
                                  AA     T
GAM1712  TFDP1    5'  GGGCTGGGGCCGGGCCGGG   42078     C   A_
                                GGGC GGGG  GGGCTGGG
                                |||| ||||  ||||||||
                                CCCG CCCC  CCCGGCCC
                                  A   GG
GAM1712  TFDP1    5'  AGGCGCGGGCTGGGGCCGGG   42079     CGGGGA
                                GGGC     GGGCTGGGGCCGGG
                                ||||     ||||||||||||||
                                TCCG     CCCGACCCCGGCCC
                                  CG____
GAM1712  TGFB1    3'  GGGGCGGGGTGGGGCCGG    42080     A  C
                                GGGG GGG TGGGGCCGG
                                |||| ||| |||||||||
                                CCCC CCC ACCCCGGCC
                                  G  C
GAM1712  THY1     3'  GGTGGGGGCTGGGGGTTGGG   42081    _ A       CC_
                                GG GG GGGCTGGGG   GGG
                                || || |||||||||   |||
                                CC CC CCCGACCCC   CCC
                                 A _       CAA
GAM1712  TMPRSS2  3'  GGGTTAGGGAGAGCAGGCTGGG 42082     CC       TG   C
                                GGG  GGGGAGGGC  GGGC GGG
                                |||  |||||||||  |||| |||
```

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                                CCC  TCCCTCTCG  TCCG CCC
                                  AA        __    A
GAM1712  TPSB1    3'  GGGCAGGGGAGGGCTGGAGGG  42083      C           CC
                                GGGC GGGGAGGGCTGGGG  GG
                                |||| ||||||||||||||  ||
                                CCCG CCCCTCCCGACCTC  CC
                                  T           __
GAM1712  TRAF5    5'  GGCCTGGGGCGGGGCCGG    42084      GGGGA    T
                                GGCC    GGGC GGGGCCGG
                                ||||    |||| ||||||||
                                CCGG    CCCG CCCCGGCC
                                  AC___   _
GAM1712  VASP     5'  GGGCCGGGGCGGGTCTCCGGG  42085          A  _  GGGG
                                GGGCCGGGG GGG CT   CCGGG
                                ||||||||| ||| ||   |||||
                                CCCGGCCCC CCC GA   GGCCC
                                     G  A  ____
GAM1712  WDR4     3'  GGGCTACGGCTGGGGCTGGG   42086      CGGGGAG        C
                                GGGC      GGCTGGGGC GGG
                                ||||      ||||||||| |||
                                CCCG      CCGACCCCG CCC
                                  ATG____       A
GAM1712  WDR4     3'  GGGCTACGGCTGGGGCTGGG   42086      CGGGGAG        C
                                GGGC      GGCTGGGGC GGG
                                ||||      ||||||||| |||
                                CCCG      CCGACCCCG CCC
                                  ATG____       A
GAM1712  ACY-3    3'  GGGTTGGGGAGGCCTGGCAAGG 42087     CC      G  GG   C
                                GGG  GGGGAGG CT  GGC GGG
                                |||  |||||| ||  ||| |||
                                CCC  CCCCTCC GA  CCG TCC
                                  AA      G __   T
GAM1712  ADAR3    5'  GGGCTGGGGGCCTCGGCTGGG  42088      C    AG___
                                GGGC GGGG    GGCTGGG
                                |||| ||||    |||||||
                                CCCG CCCC    CCGACCC
                                  A   CGGAG
GAM1712  AGS3     5'  GGGTCGGGGAGGCCGTGGG   42089     C       G  _
                                GGG CGGGGAGG CTG GGG
                                ||| |||||||| ||| |||
                                CCC GCCCCTCC GGC CCC
                                  A       _   A
GAM1712  ALOXE3   5'  GGGCTAGGGGCTGCGGGGCTGG 42090      C_   AGG  T    C
            G                    GGGC  GGGG   GC GGGGC GGG
                                ||||  ||||   || ||||| |||
                                CCCG  CCCC   CG CCCCG CCC
                                  AT   GA_ _    A
GAM1712  ALOXE3   5'  GGGCTGGGTAGGGCTGAGG   42091      C  G
                                GGGC GGG AGGGCTGGGG
                                |||| ||| ||||||||||
```

```
                                CCCG CCC TCCCGACTCC
                                  A  A
GAM1712 AP1M2    5' GAGTCGGGGAGGGAGCGCCGGG 42092     C       CT  G
                                GGG CGGGGAGGG  GG GCCGGG
                                ||| |||||||||  || ||||||
                                CTC GCCCCTCCC  TC CGGCCC
                                  A       __  G
GAM1712 APEG1    3' GGGTGGGGAGGGGAGGCTGGG  42093     CC      CT    C
                                GGG  GGGGAGGG  GGGGC GGG
                                |||  ||||||||  ||||| |||
                                CCC  CCCCTCCC  CTCCG CCC
                                  A_       __    A
GAM1712 BCAN     5' AGGCTACCCAGGGCTGGGGTTG 42094      CGGGG        CC
              GG                  GGGC    AGGGCTGGGG  GGG
                                ||||    ||||||||||  |||
                                TCCG    TCCCGACCCC  CCC
                                  ATGGG        AA
GAM1712 C1orf2   5' GGGTGGGGAGGGTAAAAGCGGG 42095     CC      CT    C
                                GGG  GGGGAGGG  GGGGC GGG
                                |||  ||||||||  ||||| |||
                                CCC  CCCCTCCC  TTTCG CCC
                                  A_       AT    _
GAM1712 C1orf2   5' GGGTGGGGAGGGTAAAAGCGGG 42095     CC      CT    C
                                GGG  GGGGAGGG  GGGGC GGG
                                |||  ||||||||  ||||| |||
                                CCC  CCCCTCCC  TTTCG CCC
                                  A_       AT    _
GAM1712 C1QTNF4  5' GGTGCTGGGGCCAGGGGCCGGG 42096    _ C    AGGGCT
                                GG GC GGGG     GGGGCCGGG
                                || || ||||     |||||||||
                                CC CG CCCC     CCCCGGCCC
                                 A  A    GGT___
GAM1712 C20orf100 3' GGGCTGGGGCTGGAGCTGGGGC 42097      C    A__
              CGGG                  GGGC GGGG   GGGCTGGGGCCGGG
                                |||| ||||   ||||||||||||||
                                CCCG CCCC   CTCGACCCCGGCCC
                                  A    GAC
GAM1712 C21orf69 3' GGGCGGGGAGGGCGCTCCTGGG 42098      C       TGGGG  _
                                GGGC GGGGAGGGC     CC GGG
                                |||| |||||||||     || |||
                                CCCG CCCCTCCCG     GG CCC
                                  _        CGA__  A
GAM1712 CARD11   5' GGGCCGGGAGGGGGCTGCGGG  42099         _ A     _
                                GGGCCGGG G GGGCTG GGG
                                |||||||| | |||||| |||
                                CCCGGCCC C CCCGAC CCC
                                     T C     G
GAM1712 CLSTN1   3' GGGCTGGGGCGGGGCTGGG   42100      C    A_
                                GGGC GGGG  GGGCTGGG
                                |||| ||||  ||||||||
```

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                                CCCG CCCC  CCCGACCC
                                  A   GC
GAM1712 CORO1B   3' GGGCTGGGCAGTGGTCGGG   42101     C  G  _  C
                                GGGC GGG AG GG TGGG
                                |||| ||| || || ||||
                                CCCG CCC TC CC GCCC
                                  A  G  A  A
GAM1712 CRF     3' GGGCCGGGGGCGTCATAGCCGG 42102        AGG  TGG__
           G                     GGGCCGGGG  GC   GGCCGGG
                                |||||||||  ||   |||||||
                                CCCGGCCCC  CG   TCGGCCC
                                     ___ CAGTA
GAM1712 CRYL1    5' GCCAGGGGCTGGGGCTGGG   42103       AGG      C
                                GCCGGGG  GCTGGGGC GGG
                                |||||||  |||||||| |||
                                CGGTCCC  CGACCCCG CCC
                                   ___      A
GAM1712 CSMD1    5' GGGCTGGCGGGGCCGGGGCCGG 42104     CG  GA
           G                     GGGC  GG  GGGCTGGGGCCGGG
                                ||||  ||  ||||||||||||||
                                CCCG  CC  CCCGGCCCCGGCCC
                                  A_  GC
GAM1712 CSMD1    5' GGGCTGGCGGGGCCGGGGCCGG 42104     CG  GA
           G                     GGGC  GG  GGGCTGGGGCCGGG
                                ||||  ||  ||||||||||||||
                                CCCG  CC  CCCGGCCCCGGCCC
                                  A_  GC
GAM1712 CYB5-M   3' GGGCTGGGCTCAGGGGCTGGG  42105     C  GA___
                                GGGC GGG    GGGCTGGG
                                |||| |||    ||||||||
                                CCCG CCC    CCCGACCC
                                  A  GAGTC
GAM1712 CYB5-M   3' GGGCTGGGCTCAGGGGCTGGG  42105     C  GA___
                                GGGC GGG    GGGCTGGG
                                |||| |||    ||||||||
                                CCCG CCC    CCCGACCC
                                  A  GAGTC
GAM1712 DCAMKL1  5' GGGCTGCGGGGCTGCAGGGCTG 42107     __   ____
           GG                    GGGC  CGGGG   AGGGCTGGG
                                ||||  |||||   |||||||||
                                CCCG  GCCCC   TCCCGACCC
                                  AC    GACG
GAM1712 DCAMKL1  5' GGGCTGGGGGGCGGCGGCGGGG 42106     C   AG_  __
           CCGGG                   GGGC GGGG  GGC  TGGGGCCGGG
                                |||| ||||  |||  ||||||||||
                                CCCG CCCC  CCG  GCCCCGGCCC
                                  A   CCG  CC
GAM1712 DCTN2    5' GGGTAGGGGAGAGGCTGGG   42108    CC    _
                                GGG  GGGGAG GGCTGGG
                                |||  |||||| |||||||
```

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                                CCC  CCCCTC CCGACCC
                                  AT     T
GAM1712  DKFZP434K028 3'  GGGTTGGCATGGGGCCGG    42109     AG  _
                                GGG  GGC TGGGGCCGG
                                |||  ||| |||||||||
                                CCC  CCG ACCCCGGCC
                                  AA   T
GAM1712  DKFZp434P2235 3'  GGGCTGGGGGTGCTGGGAGGGG 42110     C    A____  CT    C
           CTGGG                  GGC GGGG    GGG  GGGGC GGG
                                |||  ||||    |||  ||||| |||
                                CCG CCCC    CCC  CCCCG CCC
                                  A   CACGA  T_    A
GAM1712  DLGAP1   3'  GGGCTGAGGGGGGCCCGGG   42111     C    A    G
                                GGGC GGGG GGGCT GGG
                                |||| |||| ||||| |||
                                CCCG CTCC CCCGG CCC
                                  A   C    G
GAM1712  DLGAP1   3'  GGGCTGAGGGGGGCCCGGG   42111     C    A    G
                                GGGC GGGG GGGCT GGG
                                |||| |||| ||||| |||
                                CCCG CTCC CCCGG CCC
                                  A   C    G
GAM1712  DMWD     3'  AGGCTGGGGGCATGGGGTTGGG 42112     CGG  A   _    CC
                                GGGC   GG GGGC TGGGG  GGG
                                ||||   || |||| |||||  |||
                                TCCG   CC CCCG ACCCC  CCC
                                  A__  _   T    AA
GAM1712  DNAL4    3'  GGGCTGGGGGGGCTGCTGG   42113     C    A    G_
                                GGGC GGGG GGGCTG  GG
                                |||| |||| ||||||  ||
                                CCCG CCCC CCCGAC  CC
                                  A   _     GA
GAM1712  DRIL2    3'  GGACTGGGGAGGGCTGAAGAGG 42114     C        ____   C
           GCTGGG                 GGC GGGGAGGGCTG   GGGC GGG
                                |||  ||||||||||   |||| |||
                                CTG CCCCTCCCGAC   CCCG CCC
                                  A         TTCT   A
GAM1712  EEA1     5'  GGGCCGGGAGGGGACCGG    42115        G   CTGG
                                GGGCCGGG AGGG   GGCCGG
                                |||||||| ||||   ||||||
                                CCCGGCCC TCCC   CTGGCC
                                          _   ____
GAM1712  ERF      3'  GGGCTGAGGAGGGCTGGGAGTG 42116     C          CC
           GG                   GGGC GGGGAGGGCTGGGG  GGG
                                ||||  ||||||||||||||  |||
                                CCCG CTCCTCCCGACCCT  CCC
                                  A           CA
GAM1712  FLJ10211 5'  GGGCCTGGGGCCAGGGTCGGG  42117      GGGGA   TG   C
                                GGGCC    GGGC  GGG CGGG
                                |||||    ||||  ||| ||||
```

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                                CCCGG    CCCG  CCC GCCC
                                  AC___   GT   A
GAM1712  FLJ11743  5'  GGGCCGCGGGGCCCGGGTCGGG 42118      G  A  G    GC
                                GGGCCG GG GG CTGGG  CGGG
                                |||||| || || |||||  ||||
                                CCCGGC CC CC GGCCC  GCCC
                                   G  _  G    A_
GAM1712  FLJ12089  5'  GGGCCGGCGGCGGGGCTGGG   42119       _  A_
                                GGGCCGG GG  GGGCTGGG
                                |||||||  ||  ||||||||
                                CCCGGCC CC  CCCGACCC
                                    G  GC
GAM1712  FLJ12355  3'  GGGTTGGCGAACCCCGGGCCGG 42120    CC  G  G G  G
           G                     GGG  GG GA G CT GGGCCGGG
                                |||  || || | || ||||||||
                                CCC  CC CT T GG CCCGGCCC
                                  AA  G  _ G  G
GAM1712  FLJ12505  5'  GGGCCTGGGGCTGGGGCTGGG  42039      GGGGA       C
                                GGGCC    GGGCTGGGGC GGG
                                |||||    |||||||||| |||
                                CCCGG    CCCGACCCCG CCC
                                  AC___         A
GAM1712  FLJ12604  3'  GGCGTTGGCTGGGGCTGG    42121     C GGGAG       C
                                GGC G    GGCTGGGGC GG
                                ||| |    ||||||||| ||
                                CCG C    CCGACCCCG CC
                                  _ AA___        A
GAM1712  FLJ14810  3'  GGGTGGGGGATGGGTTGGG   42122     CC    _   C
                                GGG  GGGGA GGG TGGG
                                |||  ||||| ||| ||||
                                CCC  CCCCT CCC ACCC
                                  AC    A  A
GAM1712  FLJ20424  5'  GGCTGGGGAGGGCTGGCCAG   42123     C        GG
                                GGC GGGGAGGGCT  GGCCGG
                                ||| ||||||||||  ||||||
                                CCG CCCCTCCCGA  CCGGTC
                                  A         __
GAM1712  FLJ20424  5'  GGGCCGGGCGCAGGGGCTGGG  42124        GAGG  T    C
                                GGGCCGGG   GC GGGGC GGG
                                ||||||||   || ||||| |||
                                CCCGGCCC   CG CCCCG CCC
                                    G___  T    A
GAM1712  FLJ20519  5'  GGGGCTGGGCTCTTGGGGTTGG 42125     A_   ___   CC
           G                     GGGG  GGGCT   GGGG  GGG
                                ||||  |||||   ||||  |||
                                CCCC  CCCGA   CCCC  CCC
                                  GA    GAA   AA
GAM1712  FLJ22215  3'  GGGCGGGGATGGGGCCGG    42126     C    GGGC
                                GGGC GGGGA   TGGGGCCGG
                                |||| |||||   |||||||||
```

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                                CCCG CCCCT   ACCCCGGCC
                                  _   ____
GAM1712 FLJ22477 3' GGGCTGGGGCAGGTGCATGGGC 42127     C   _  _ TG   C
           TGGG                   GGGC GGGG AGG GC  GGGC GGG
                                |||| |||| ||| ||  |||| |||
                                CCCG CCCC TCC CG  CCCG CCC
                                  A   G  A TA   A
GAM1712 FLNC    5' GGGCTGGGGGTGCGGCCGG   42128     CGG A  C G
                                GGGC  GG GGG TG GGCCGG
                                ||||  || ||| || ||||||
                                CCCG  CC CCC AC CCGGCC
                                  A__ _  _ G
GAM1712 FOXH1   5' GGGCTGGGGCAGGCGGGCTGGG 42129     C   A   TG   C
                                GGGC GGGG GGGC  GGGC GGG
                                |||| |||| ||||  |||| |||
                                CCCG CCCC TCCG  CCCG CCC
                                  A   G   __   A
GAM1712 GIPC3   3' GGGCCGGGGCAGGGGGCTGGG 42130        A___
                                GGGCCGGGG   GGGCTGGG
                                |||||||||   ||||||||
                                CCCGGCCCC   CCCGACCC
                                    GTCC
GAM1712 HRMT1L3  5' GGGCTGGGGGGGCTGGG    42131     C   A
                                GGGC GGGG GGGCTGGG
                                |||| |||| ||||||||
                                CCCG CCCC CCCGACCC
                                  A   _
GAM1712 HSPC195  5' GGGCTGGGCAGGGCTGGG   42132     C  G
                                GGGC GGG AGGGCTGGG
                                |||| ||| |||||||||
                                CCCG CCC TCCCGACCC
                                  A  G
GAM1712 IRF7    3' GGGCTGGGGCCCGGGGCTGGG 42133     C   AGGG     C
                                GGGC GGGG   CTGGGGC GGG
                                |||| ||||   ||||||| |||
                                CCCG CCCC   GGCCCCG CCC
                                  A   G___     A
GAM1712 KBRAS2   3' GGGATGGGGAGTAGGCTGGG  42134    CC    __
                                GGG  GGGGAG  GGCTGGG
                                |||  ||||||  |||||||
                                CCC  CCCCTC  CCGACCC
                                  TA    AT
GAM1712 KIAA0295 3' GGGCTGGGGCAGGAGGGGCTGG 42135     C   A  CT   C
           G                    GGGC GGGG GGG  GGGGC GGG
                                |||| |||| |||  ||||| |||
                                CCCG CCCC TCC  CCCCG CCC
                                  A   G  T_   A
GAM1712 KIAA0339 3' AGGCTGGGGGGGTGCTGGG   42136     C   A _
                                GGGC GGGG GG GCTGGG
                                |||| |||| || ||||||
```

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                                TCCG CCCC CC CGACCC
                                  A   C A
GAM1712  KIAA0363  5'  GGCTCCCTCGGGCTGGGGCCGG 42137    CGGGGA
              G                   GGC     GGGCTGGGGCCGGG
                                  |||     |||||||||||||
                                  CCG     CCCGACCCCGGCCC
                                    AGGGAG
GAM1712  KIAA0561  5'  GGGCCGGGAGAGGGTCGGG   42138       _    C
                                  GGGCCGGG GAGGG TGGG
                                  |||||||| ||||| ||||
                                  CCCGGCCC CTCCC GCCC
                                       T    A
GAM1712  KIAA0616  3'  GGGCTGGGGATGGCGGATGGGC 42139     C    G  TG__   C
              TGGG                  GGGC GGGGA GGC   GGGC GGG
                                  |||| ||||| |||   |||| |||
                                  CCCG CCCCT CCG   CCCG CCC
                                    A    A  CCTA   A
GAM1712  KIAA0773  3'  GGGCTGGGGAGGGGCTACCTGG 42140     C      _ GGG  _
              G                   GGGC GGGGAGGG CT   GCC GGG
                                  |||| |||||||| ||   ||| |||
                                  CCCG CCCCTCCC GA   TGG CCC
                                    A       C ___   A
GAM1712  KIAA0792  3'  GGGCTGGGGAGGGACTGGCCAT 42141     C      _ GG   _
              GG                    GGGC GGGGAGGG CT  GGCCG GG
                                  |||| |||||||| ||  ||||| ||
                                  CCCG CCCCTCCC GA  CCGGT CC
                                    A       T __    A
GAM1712  KIAA0930  3'  GGGCAGGCCTGGGGCTGG    42142    G  G     C
                                  GGG AGG CTGGGGC GG
                                  ||| ||| ||||||| ||
                                  CCC TCC GACCCCG CC
                                    G  G      A
GAM1712  KIAA0963  3'  GGGTCAGGGAAGGGCTGGG   42143    C    _
                                  GGG CGGGGA GGGCTGGG
                                  ||| |||||| ||||||||
                                  CCC GTCCCT CCCGACCC
                                    A     T
GAM1712  KIAA1110  5'  GGGCCGGGGGCAGGCCGGG   42144        A_
                                  GGGCCGGGG  GGGCTGGG
                                  |||||||||  ||||||||
                                  CCCGGCCCC  TCCGGCCC
                                       CG
GAM1712  KIAA1110  3'  GGCCGGGTATTAGCTGGGGCTG 42145       GAG_      C
              GG                    GGCCGGG   GGCTGGGGC GGG
                                  |||||||   ||||||||| |||
                                  CCGGCCC   TCGACCCCG CCC
                                       ATAA       A
GAM1712  KIAA1171  3'  GGGCCAGGGGAGGGCACGGG  42146      _      _
                                  GGGCC GGGGAGGGC TGGG
                                  ||||| ||||||||| ||||
```

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                                CCCGG CCCCTCCCG GCCC
                                  T       T
GAM1712  KIAA1171  3'  GGCCTGGGGAGGGAACTGGG  42147     _      __
                                GGCC GGGGAGGG  CTGGG
                                |||| ||||||||  |||||
                                CCGG CCCCTCCC  GACCC
                                  A       TT
GAM1712  KIAA1280  5'  AGGCTGGGTGTCCTGGGGCCGG 42148     C   GAGGG
           G                     GGGC GGG    CTGGGGCCGGG
                                |||| |||    ||||||||||
                                TCCG CCC    GACCCCGGCCC
                                  A  ACAG_
GAM1712  KIAA1297  3'  GGGCCTGGGGGTTGTAGGGCTG 42149      _   _____
           GG                     GGGCC GGGG    AGGGCTGGG
                                ||||| ||||    |||||||||
                                CCCGG CCCC    TCCCGACCC
                                  A   CAACA
GAM1712  KIAA1602  3'  GGGCTGGGGGCTGGGGGCTGGG 42150     CGG  A       _ C
                                GGGC  GG GGGCTGGGG C GGG
                                ||||  || |||||||| | |||
                                CCCG  CC CCCGACCCC G CCC
                                  A__  _       C A
GAM1712  KIAA1706  3'  GGGCGGGGGAGGGCTGTGG   42151     C        _
                                GGGC GGGGAGGGCTG GG
                                |||| ||||||||||| ||
                                CCCG CCCCTCCCGAC CC
                                  C         A
GAM1712  KIAA1811  3'  GGGCCCGGGAAGAGGGGGTTGG 42152     G     CT   CC
           G                     GGGCC GGGAGGG  GGGG  GGG
                                ||||| |||||||  ||||  |||
                                CCCGG CCCTTCT  CCCC  CCC
                                  G      C_   AA
GAM1712  KIAA1855  3'  GAGGCTGCAGCTGGGGTTGGG  42153     AG__      CC
                                GGGG   GGCTGGGG  GGG
                                ||||   ||||||||  |||
                                CTCC   TCGACCCC  CCC
                                  GACG       AA
GAM1712  KIAA1862  3'  CGGGGCTGGGGCTGGGGCTGGG 41962      A__       C
                                CGGGG  GGGCTGGGGC GGG
                                |||||  ||||||||||| |||
                                GCCCC  CCCGACCCCG CCC
                                   GAC        A
GAM1712  KIAA1862  3'  GAGCTGGAGCCGGGGCTGGGGC 42154     C   A__       C
           TGGG                   GGGC GGGG  GGGCTGGGGC GGG
                                |||| ||||  |||||||||| |||
                                CTCG CCTC  CCCGACCCCG CCC
                                  A  GGC        A
GAM1712  KIAA1913  5'  GGGTTGGGGGCGGGGGCCGGG  42155    CCGG  A   T
                                GGG   GG GGGC GGGGCCGGG
                                |||   || |||| |||||||||
```

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                                CCC   CC CCCG CCCCGGCCC
                                  AA__ _   C
GAM1712 KIAA1938 3' GGGTGGGGGTGGTGGGGCTGGG 42156    CC   AG C    C
                                GGG  GGGG  GG TGGGGC GGG
                                |||  ||||  || |||||| |||
                                CCC  CCCC  CC ACCCCG CCC
                                  A_   CA _    A
GAM1712 KIAA1981 3' GGGTGGGGAGGGGCGCTGGG  42157    CC     ___
                                GGG  GGGGAGG   GCTGGG
                                |||  |||||||   ||||||
                                CCC  CCCCTCC   CGACCC
                                  A_     CCG
GAM1712 MGC15437 5' GGGCCAGGGGAGGGGGCTCGGG 42158        A  CT   _
                                GGGCCGGGG GGG  GGGGC CGGG
                                |||||||| |||  ||||| ||||
                                CCCGGTCCC CTC  CCCCG GCCC
                                     _  __    A
GAM1712 MGC15631 3' GGGCCGAGGAGGGGGCCCGGG 42159          CTG  G
                                GGGCCGGGGAGGG   GG CCGGG
                                ||||||||||||   || |||||
                                CCCGGCTCCTCCC   CC GGCCC
                                       ___  G
GAM1712 MGC2647  3' GGGCCGGGGCAGGGTCGGG   42160        _   C
                                GGGCCGGGG AGGG TGGG
                                |||||||| |||| ||||
                                CCCGGCCCC TCCC GCCC
                                     G   A
GAM1712 MGC4737  3' GGGCTGGGAGGGGTCTGGG   42161     C  GA  _
                                GGGC GGG  GGG CTGGG
                                ||||  |||  |||  |||||
                                CCCG CCC  CCC GACCC
                                  A  TC  A
GAM1712 MSE55    5' GGGCCGGGGGAGGGAGGTGGGC 42162        _   CTG_   C
           TGGG                  GGGCCGGGG AGGG   GGGC GGG
                                |||||||| ||||   |||| |||
                                CCCGGCCCC TCCC   CCCG CCC
                                     C   TCCA   A
GAM1712 MYL9     3' GGGCTGGGGTGTCAGGGGGCTG 42163     C   A_____
           GG                    GGGC GGGG     GGGCTGGG
                                ||||  ||||     ||||||||
                                CCCG CCCC     CCCGACCC
                                  A   ACAGTCC
GAM1712 NKG7     3' GGGCTGGGGAAGGGCTGGAAGG 42164     C   _      CC
           G                     GGGC GGGGA GGGCTGGGG  GGG
                                |||| ||||| |||||||||  |||
                                CCCG CCCCT CCCGACCTT  CCC
                                  A    T      __
GAM1712 OR2C3    3' GGGCTGGGAGGGCTCCGG    42165     CG      GGGG
                                GGGC  GGGAGGGCT   CCGG
                                ||||  |||||||||   ||||
```

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                                CCCG  CCCTCCCGA   GGCC
                                  A_      _____
GAM1712  OSBP2    5'  AGGCCGGGGGGCGGGGCCGG   42166        AGG  T
                                GGGCCGGGG   GC GGGGCCGG
                                |||||||||   || ||||||||
                                TCCGGCCCC   CG CCCCGGCC
                                     ___  _
GAM1712  OSBP2    5'  GGGCGGGGGGCAGGCCGG    42167     CG   A   TG
                                GGGC  GGG GGGC  GGGCCGG
                                ||||  ||| ||||  |||||||
                                CCCG  CCC CCCG  TCCGGCC
                                   __   _   __
GAM1712  PHYHIP   3'  GGGCCAGGGGAGGGCAGTGGG  42168      _       __
                                GGGCC GGGGAGGGC  TGGG
                                ||||| |||||||||  ||||
                                CCCGG CCCCTCCCG  ACCC
                                   T        TC
GAM1712  PITPNM   3'  GGGCTGGGGGGGGCCAGCGCTGG 42169     C    A    TG G  C
              G                  GGGC GGGG GGGC  G GC GGG
                                ||||  |||| ||||  | || |||
                                CCCG CCCC CCCG  C CG CCC
                                  A    _    GT G  A
GAM1712  PLA2G6   3'  GGGCCGGTGAGAGGCTGGG   42170       G   _
                                GGGCCGG GAG GGCTGGG
                                ||||||| ||| |||||||
                                CCCGGCC CTC CCGACCC
                                    A  T
GAM1712  PLXNC1   5'  GGGCTGGGGGGGCCGCCCCCGG 42171     C    A     GGG
              G                  GGGC GGGG GGGCTG   CCGGG
                                ||||  |||| ||||||   |||||
                                CCCG CCCC CCCGGC   GGCCC
                                  A    _     GGG
GAM1712  RAB35    3'  GGGCTGGGGAGGGGCGCGG   42172     C    GGGCT    _
                                GGGC GGGGA    GGGGC CGG
                                ||||  |||||    ||||| |||
                                CCCG CCCCT    CCCCG GCC
                                  A    _____    C
GAM1712  RABL4    5'  GGGCCGGGGGCGGATATCGGG  42173        AGG  T  GC_
                                GGGCCGGGG   GC GGG   CGGG
                                |||||||||   || |||   ||||
                                CCCGGCCCC   CG CCT   GCCC
                                     ___  _   ATA
GAM1712  RABL4    5'  GGGCAGGGGAGGGCTCCAGGTG 42174     C       G_   CC
              GG                   GGGC GGGGAGGGCT  GGG  GGG
                                ||||  ||||||||||  |||  |||
                                CCCG CCCCTCCCGA  TCC  CCC
                                  T        GG   A_
GAM1712  RASD2    5'  GGGCTGGGAATGGCGGGCCGGG 42175     C    G   TG
                                GGGC GGGGA GGC  GGGCCGGG
                                |||| ||||| |||  ||||||||
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                                CCCG CCCTT CCG  CCCGGCCC
                                  A    A  __
GAM1712 RBPMS    5' GGGCCGGGCAGGGCTGGG    42176        G
                                GGGCCGGG AGGGCTGGG
                                |||||||| |||||||||
                                CCCGGCCC TCCCGACCC
                                    G
GAM1712 RBPMS    5' GGGCTGGGGCGCGGGGCTGGG 42177     C   AGG  T    C
                                GGGC GGGG   GC GGGGC GGG
                                |||| ||||   || ||||| |||
                                CCCG CCCC   CG CCCCG CCC
                                  A   G__ _    A
GAM1712 RELB     5' GGGCTGCGGGGCGCGGGGCCGG 42178     __    AGG  T
            G                    GGGC  CGGGG   GC GGGGCCGGG
                                |||| |||||   || |||||||||
                                CCCG  GCCCC   CG CCCCGGCCC
                                  AC    G__ _
GAM1712 RNF10    5' GGGCTCGGGAGTCCGGGCCGGG 42179     CG    GG    G
                                GGGC  GGGAG  CTGGG CCGGG
                                |||| |||||  ||||| |||||
                                CCCG  CCCTC  GGCCC GGCCC
                                  AG    A_    _
GAM1712 SDC3     3' GGGCTGGTGGGGCCAGGCTGGG 42180     C___   A_
                                GGGC   GGGG  GGGCTGGG
                                ||||   ||||  ||||||||
                                CCCG   CCCC  TCCGACCC
                                  ACCA   GG
GAM1712 SEC61A1  5' GGGGCGGGGCCGGGGCCGG   42181     A_
                                GGGG  GGGCTGGGGCCGG
                                ||||  ||||||||||||
                                CCCC  CCCGGCCCCGGCC
                                  GC
GAM1712 SET07    3' GGGCGGGGAGGGCGCGGG    42182     C       _
                                GGGC GGGGAGGGC TGGG
                                |||| ||||||||| ||||
                                CCCG CCCCTCCCG GCCC
                                  _       C
GAM1712 SHANK3   5' GGGTCGGGGAGGGCTCGCGGG  42183     C        GGG  C
                                GGG CGGGGAGGGCT   GC GGG
                                ||| ||||||||||   || |||
                                CCC GCCCCTCCCGA   CG CCC
                                  A         G__ _
GAM1712 SLC26A10 5' AGGTTGGGGAGGAGGGGTTGGG 42184     CC       CT    CC
                                GGG  GGGGAGGG  GGGG  GGG
                                |||  ||||||||  ||||  |||
                                TCC  CCCCTCCT  CCCC  CCC
                                  AA       __    AA
GAM1712 SNTA1    5' GCTGGGGAGGGGGCCTCGGG   42185    C      CTGG   __
                                GC GGGGAGGG   GGCC  GGG
                                || ||||||||   ||||  |||
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                                CG CCCCTCCC   CCGG  CCC
                                 A      ____   AG
GAM1712  SPS      5'  GGGCCCGGGCGCCTGGGGCCGG 42186      G   AGGG
                 G                GGGCC GGG   CTGGGGCCGGG
                                  ||||| |||   ||||||||||
                                  CCCGG CCC   GACCCCGGCCC
                                    G  GCG_
GAM1712  STRAIT11499 5'  GGGCTGAGGGAGGGCGCCGGG  42187      C _      TGGG
                                  GGGC G GGGAGGGC   GCCGGG
                                  |||| | ||||||||   ||||||
                                  CCCG C CCCTCCCG   CGGCCC
                                    A T     ____
GAM1712  TBX21    5'  GGGCGGGGGACCCGAGGGCCGG 42188      C   A  G  _
                 G                GGGC GGGG GG CTG GGGCCGGG
                                  |||| |||| || ||| ||||||||
                                  CCCG CCCC CT GGC CCCGGCCC
                                    _   _ G  T
GAM1712  TIGD5    5'  GGGCCGGGGCGCGGTCGG    42191         AGGGC  G  C
                                  GGGCCGGGG    TG GG CGG
                                  |||||||||    || || |||
                                  CCCGGCCCC    GC CC GCC
                                       _____ G  A
GAM1712  TIGD5    5'  GGCCGGGGGCGGCGGGGCCGGG 42189         AG   T
                                  GGCCGGGG  GGC GGGGCCGGG
                                  ||||||||  ||| |||||||||
                                  CCGGCCCC  CCG CCCCGGCCC
                                      CG  _
GAM1712  TIGD5    5'  GGGCGCGGGGCTCGGGGCTGGG 42190      _    A___
                                  GGGC CGGGG   GGGCTGGG
                                  |||| |||||   ||||||||
                                  CCCG GCCCC   CCCGACCC
                                    C    GAGC
GAM1712  TNFRSF19L 3'  GGGCTGGGCAGGGCTAGGG   42192      C   G
                                  GGGC GGG AGGGCTGGGG
                                  |||| ||| ||||||||||
                                  CCCG CCC TCCCGATCCC
                                    A  G
GAM1712  TNRC6    3'  GGGCGGGGGGGGGGGGTTGGG   42193     C   A   CT   CC
                                  GGGC GGGG GGG  GGGG  GGG
                                  |||| |||| |||  ||||  |||
                                  CCCG CCCC CCC  CCCC  CCC
                                    _   _  __   AA
GAM1712  TNRC9    5'  GGGCCCGGGGCCGGGGGCCGGG 42194      G   AGG     _
                                  GGGCC GGG   GCTGGGG CCGGG
                                  ||||| |||   ||||||| |||||
                                  CCCGG CCC   CGGCCCC GGCCC
                                    G  ___      C
GAM1712  TOPBP1   5'  GGGCGGTGGCTGGGGTCGG   42195     CGG  AG      C
                                  GGGC   GG  GGCTGGGG CGG
                                  ||||   ||  |||||||| |||
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                                CCCG  CC  CCGACCCC GCC
                                  ___ A_      A
GAM1712  TRIM26   3'  AGCATCTGAGGGTTGGGGCTGG 42196    CGGG   C    C
             G                   GGC   GAGGG TGGGGC GGG
                                 |||   ||||| |||||| |||
                                 TCG   CTCCC ACCCCG CCC
                                   TAGA    A    A
GAM1712  WNT10A   5'  GGGCTGGGGACGGGAGGCTGGG 42197     C    G  CT   C
                                 GGGC GGGGA GG  GGGGC GGG
                                 |||| ||||| ||  ||||| |||
                                 CCCG CCCCT CC  CTCCG CCC
                                   A    G __    A
GAM1712  YWHAQ    5'  GGGCGCGGGGCCGGGGCCGGG  42198     _   GAGG
                                 GGGC CGGG   GCTGGGGCCGGG
                                 |||| ||||   ||||||||||||
                                 CCCG GCCC   CGGCCCCGGCCC
                                   C   _____
GAM1712  ZDHHC8   3'  GGGCTGGGGAGGGGGCTCTGGG 42199     C      _____
                                 GGGC GGGGAGGG   CTGGG
                                 |||| ||||||||   |||||
                                 CCCG CCCCTCCC   GACCC
                                   A       CCGA
GAM1712  LOC115330 3'  GGGCTGGGGAGGGTGTCAGGG  42200     C      C__
                                 GGGC GGGGAGGG   TGGGG
                                 |||| ||||||||   |||||
                                 CCCG CCCCTCCC   GTCCC
                                   A       ACA
GAM1712  LOC116113 3'  GGGCCGGGGTGGGAGACTGGG  42201         A   ___
                                 GGGCCGGGG GGG   CTGGG
                                 |||||||||| |||   |||||
                                 CCCGGCCCC CCC   GACCC
                                      A   TCT
GAM1712  LOC116173 3'  GGGCTGGGGTGGGGTTTGGCGG 42202     C   A   C__   __   C
           GCTGGG                  GGC GGGG GGG   TGG  GGC GGG
                                 ||| |||| |||   |||  ||| |||
                                 CCG CCCC CCC   ACC  CCG CCC
                                   A   A   CAA   GC   A
GAM1712  LOC121219 3'  GGCTGGGGAGGCAGGGCTGGG  42203     C      G T    C
                                 GGC GGGGAGG C GGGGC GGG
                                 ||| ||||||| | ||||| |||
                                 CCG CCCCTCC G TCCCG CCC
                                   A      _ _     A
GAM1712  LOC124930 3'  GGGTGGGGGAGGGGCTGGG   42204     CC       _
                                 GGG  GGGGAGGG CTGGG
                                 |||  |||||||| |||||
                                 CCC  CCCCTCCC GACCC
                                   AC       C
GAM1712  LOC128402 3'  GGGCTGTCCTGGCTGGGGCTGG 42205      CGGGGAG       C
             G                   GGGC      GGCTGGGGC GGG
                                 ||||      ||||||||| |||
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                                CCCG      CCGACCCCG CCC
                                  ACAGGA_        A
GAM1712  LOC143287 3'  GGGCTGCGGGCCGGGGGTCGGG 42206      CGGGGA       C_
                                GGGC     GGGCTGGGG  CGGG
                                ||||     |||||||||  ||||
                                CCCG     CCCGGCCCC  GCCC
                                  ACG___        CA
GAM1712  LOC144600 3'  GGGCAGGCCTGGGGCTGG    42142     G   G      C
                                GGG AGG CTGGGGC GG
                                ||| ||| ||||||| ||
                                CCC TCC GACCCCG CC
                                  G   G      A
GAM1712  LOC145694 5'  GGGCCGAGGCCTCGGGGCTGGG 42207          A____
                                GGGCCGGGG    GGGCTGGG
                                |||||||||    ||||||||
                                CCCGGCTCC    CCCGACCC
                                     GGAGC
GAM1712  LOC145719 5'  GGGGCTGGCTTTGGGGCTGGG  42208      AG   __    C
                                GGGG  GGCT  GGGGC GGG
                                ||||  ||||  ||||| |||
                                CCCC  CCGA  CCCCG CCC
                                  GA    AA     A
GAM1712  LOC145720 5'  GGGGCTGGCTTTGGGGCTGGG  42208      AG   __    C
                                GGGG  GGCT  GGGGC GGG
                                ||||  ||||  ||||| |||
                                CCCC  CCGA  CCCCG CCC
                                  GA    AA     A
GAM1712  LOC145988 5'  GGGTGGGGAGGGAGGCGGGGCT 42209     CC       C__     C
            GGG                   GGG  GGGGAGGG   TGGGGC GGG
                                |||  ||||||||   |||||| |||
                                CCC  CCCCTCCC   GCCCCG CCC
                                  A_       TCC      A
GAM1712  LOC145989 3'  GGGCTGGGAGGAGGTGGCTGGG 42072      CG      CT  _   C
                                GGGC  GGGAGGG  GG GGC GGG
                                ||||  |||||||  || ||| |||
                                CCCG  CCCTCCT  CC CCG CCC
                                  A_       __  A   A
GAM1712  LOC146782 3'  GGGCTGGGGGTGTTGGGAGGGG 42210     C    A____   CT     C
            CTGGG                   GGC GGGG     GGG  GGGGC GGG
                                ||| ||||     |||  ||||| |||
                                CCG CCCC     CCC  CCCCG CCC
                                  A    CACAA   T_     A
GAM1712  LOC146957 3'  GGGCTGGGAGGGATCTGGG    42211      CG      __
                                GGGC  GGGAGGG  CTGGG
                                ||||  |||||||  |||||
                                CCCG  CCCTCCC  GACCC
                                  A_       TA
GAM1712  LOC147229 3'  GGGTCGGAGAGGGTGCAGCCTG 42212     C        C  G    _
            GG                    GGG CGGGGAGGG TG GGCC GGG
                                ||| ||||||||| || |||| |||
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                                CCC GCCTCTCCC AC TCGG CCC
                                  A       _ G   A
GAM1712  LOC148046 3'  CGCTGACTGCTGGGGCTGGG  42213    GG  GG      C
                                CG  GA  GCTGGGGC GGG
                                ||  ||  |||||||| |||
                                GC  CT  CGACCCCG CCC
                                 GA  GA       A
GAM1712  LOC148696 5'  GAGCTGGGGAGGGTCTGACTGG 42214     C      _  GG  C
             G                   GGGC GGGGAGGG CTG  GC GGG
                                |||| |||||||| |||  || |||
                                CTCG CCCCTCCC GAC  TG CCC
                                  A       A  __ A
GAM1712  LOC149535 5'  GGAGCTGGGGCTGGGGCTGGG  42215     A__       C
                                GGGG   GGGCTGGGGC GGG
                                ||||   |||||||||| |||
                                CCTC   CCCGACCCCG CCC
                                  GAC         A
GAM1712  LOC149657 3'  GGGCGGGGAGTGCCAGGGCTGG 42216     C     G  TG   C
             G                   GGGC GGGGAG GC  GGGC GGG
                                |||| |||||| ||  |||| |||
                                CCCG CCCCTC CG  CCCG CCC
                                  _     A  GT   A
GAM1712  LOC150319 3'  AGGCCGGGGAGGGCTGGCTTGG 42217              GGCC
             G                   GGGCCGGGGAGGGCTGG    GGG
                                ||||||||||||||||    |||
                                TCCGGCCCCTCCCGACC    CCC
                                       GAA_
GAM1712  LOC150605 5'  GGGTTGGGAAGGAGTTGGG   42218    CC      _ C
                                GGG  GGGGAGG G TGGG
                                |||  ||||||| | ||||
                                CCC  CCCTTCC C ACCC
                                  AA      T A
GAM1712  LOC151632 5'  GGGCTGGAGACTTGGGCTGGG  42219     C    ____
                                GGGC GGGGA   GGGCTGGG
                                |||| |||||   ||||||||
                                CCCG CCTCT   CCCGACCC
                                  A    GAA
GAM1712  LOC152274 3'  GGGCTGGTGAGTGGTGGGGCTG 42220     C  G   _  C     C
             GG                  GGGC GG GAG GG TGGGGC GGG
                                |||| || ||| || |||||| |||
                                CCCG CC CTC CC ACCCCG CCC
                                  A  A   A  _     A
GAM1712  LOC152286 3'  GGTCTGGGGAGGGTTGATGG   42221    GCC      C  _
                                GG   GGGGAGGG TGG GG
                                ||   |||||||| ||| ||
                                CC   CCCCTCCC ACT CC
                                 AGA       A   A
GAM1712  LOC155066 3'  GGACTGACAGGCTGGGGTCGGG 42222     CG  GA       C
                                GGGC  GG  GGGCTGGGG CGGG
                                ||||  ||  |||||||| ||||
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                                CCTG  CT  TCCGACCCC GCCC
                                  A_  G_       A
GAM1712  LOC158055 3'  GGGCAGCGGGGCTGGGGCTGGG 42223      CG  GA        C
                                GGGC  GG  GGGCTGGGGC GGG
                                ||||  ||  |||||||||| |||
                                CCCG  TC  CCCGACCCCG CCC
                                  __  GC        A
GAM1712  LOC158104 5'  GGGCCGGGCTGGGGCTGG    42224      GGGGA       C
                                GGGCC    GGGCTGGGGC GG
                                |||||    |||||||||| ||
                                CCCGG    CCCGACCCCG CC
                                  _____        A
GAM1712  LOC158177 3'  AGGCTGGGGTAATCATGGGGCT 42225      C   AG GC_     C
            GGG                   GGGC GGGG  G   TGGGGC GGG
                                |||| ||||  |   |||||| |||
                                TCCG CCCC  T   ACCCCG CCC
                                  A   AT AGT     A
GAM1712  LOC164633 3'  GGGTGGGGACAGGGTGGGGCTG 42226     CC   __  C     C
            GG                    GGG  GGGGA  GGG TGGGGC GGG
                                |||  |||||  ||| |||||| |||
                                CCC  CCCCT  CCC ACCCCG CCC
                                  A_    GT  _     A
GAM1712  LOC196382 5'  GGGCGGGGAGGGCACGGG    42227      C       _
                                GGGC GGGGAGGGC TGGG
                                |||| |||||||| ||||
                                CCCG CCCCTCCCG GCCC
                                  _       T
GAM1712  LOC196477 5'  AGGCACGGGCTGGGGCCGGG   42229      CGGGGA
                                GGGC     GGGCTGGGGCCGGG
                                ||||     ||||||||||||||
                                TCCG     CCCGACCCCGGCCC
                                  TG____
GAM1712  LOC196477 5'  GGGTGGGACTGGGGCTGG    42228     GA        C
                                GGG  GGGCTGGGGC GG
                                |||  |||||||||| ||
                                CCC  CCTGACCCCG CC
                                  AC        A
GAM1712  LOC196500 3'  GGGCTGGGGAGTGTTCCGG    42230     C     GGC  GGG
                                GGGC GGGGAG   TG   CCGG
                                |||| ||||||   ||   ||||
                                CCCG CCCCTC   AC   GGCC
                                  A     ___  AA_
GAM1712  LOC196985 5'  GGGCAGGGGCGCGGGGCTGGG  42231      C   AGG  T    C
                                GGGC GGGG   GC GGGGC GGG
                                |||| ||||   || ||||| |||
                                CCCG CCCC   CG CCCCG CCC
                                  T   G__  _    A
GAM1712  LOC197114 5'  GGGGCTGGCTTTGGGGCTGGG  42208      AG   __    C
                                GGGG  GGCT  GGGGC GGG
                                ||||  ||||  ||||| |||
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                                CCCC  CCGA  CCCCG CCC
                                  GA    AA    A
GAM1712  LOC201522 3'  GGGCTGGGTGCGGGGCTGGG  42232     C   GA__
                                GGGC GGG    GGGCTGGG
                                |||| |||    ||||||||
                                CCCG CCC    CCCGACCC
                                  A   ACGC
GAM1712  LOC201705 5'  GGGTAGAGCTGGGGCTGG    42233     G         C
                                GGG AGGGCTGGGGC GG
                                ||| ||||||||||| ||
                                CCC TCTCGACCCCG CC
                                  A         A
GAM1712  LOC204994 5'  GGGCCGTGGGCAGGGGGCCGGG 42234       GGGA    T_
                                GGGCCG    GGGC  GGGGCCGGG
                                ||||||    ||||  |||||||||
                                CCCGGC    CCCG  CCCCGGCCC
                                   A___    TC
GAM1712  LOC219562 3'  GGGCTGGGGGTGCTGGGAGGGG 42110     C    A____   CT    C
            CTGGG                  GGC GGGG    GGG  GGGGC GGG
                                ||| ||||    |||  ||||| |||
                                CCG CCCC    CCC  CCCCG CCC
                                  A    CACGA   T_    A
GAM1712  LOC220018 5'  GGTCTGGGGAGGGGTCCCTTGG 42235    GCC       CTG GG  __
            G                   GG   GGGGAGGG   G  CC  GGG
                                ||   ||||||||   |  ||  |||
                                CC   CCCCTCCC   C  GG  CCC
                                 AGA       ___ AG  AA
GAM1712  LOC221424 5'  GGGCCGGGGATAGGGCCGGG   42236          GGGC
                                GGGCCGGGGA    TGGGGCCGGG
                                ||||||||||    ||||||||||
                                CCCGGCCCCT    ATCCCGGCCC
                                      _____
GAM1712  LOC221424 5'  GGGCCGCGGGCGGGGCCGG    42237       GGGA    T
                                GGGCCG    GGGC GGGGCCGG
                                ||||||    |||| ||||||||
                                CCCGGC    CCCG CCCCGGCC
                                   G___    _
GAM1712  LOC221935 3'  GGGCTGGGGAGGTCTGAGG    42238     C      G
                                GGGC GGGGAGG CTGGGG
                                |||| ||||||| ||||||
                                CCCG CCCCTCC GACTCC
                                  A      A
GAM1712  LOC253747 5'  GGGCTGGGGACCAGGGCTGGG  42239     C    ___
                                GGGC GGGGA   GGGCTGGG
                                |||| |||||   ||||||||
                                CCCG CCCCT   CCCGACCC
                                  A     GGT
GAM1712  LOC254263 5'  GGGCCGTGGGGGGCGCGGG    42240       _  A   _
                                GGGCCG GGG GGGC TGGG
                                |||||| ||| |||| ||||
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                                CCCGGC CCC CCCG GCCC
                                   A  _  C
GAM1712  LOC255276 5'  GGAGTTGGCTGGGGCTGG   42241     AG       C
                                GGGG  GGCTGGGGC GG
                                ||||  ||||||||| ||
                                CCTC  CCGACCCCG CC
                                  AA       A
GAM1712  LOC256115 5'  GGGCTGGGGTAGGCGGCGGTTG 42242     C   A   T  _  CC
            GG                    GGGC GGGG GGGC GG GG  GGG
                                |||| |||| |||| || ||  |||
                                CCCG CCCC TCCG CC CC  CCC
                                  A   A   _ G  AA
GAM1712  LOC256158 5'  GGGCTGGGGGGTGCCCTGGG  42243     C   A  _  G_
                                GGGC GGGG GG GCT  GGG
                                |||| |||| || |||  |||
                                CCCG CCCC CC CGG  CCC
                                  A   _ A  GA
GAM1712  LOC256923 3'  AGGCCGGGGAGGGGCACCGGG  42244           CTG G
                                GGGCCGGGGAGGG  G GCCGGG
                                ||||||||||||  | ||||||
                                TCCGGCCCCTCCC  C TGGCCC
                                       ___ G
GAM1712  LOC257152 5'  GGGCCGCGGAGTGAGGCCGGG  42245      G   GGC
                                GGGCCG GGAG  TGGGGCCGGG
                                |||||| ||||  ||||||||||
                                CCCGGC CCTC  ACTCCGGCCC
                                   G  ___
GAM1712  LOC257494 3'  AGCATCTGAGGGTTGGGGCTGG 42196    CGGG   C    C
            G                   GGC   GAGGG TGGGGC GGG
                                |||   ||||| |||||| |||
                                TCG   CTCCC ACCCCG CCC
                                  TAGA    A    A
GAM1712  LOC51107  3'  GGACCCCGGGCTGGGGCTGGG  42246     GGGGA       C
                                GGGCC    GGGCTGGGGC GGG
                                |||||    |||||||||| |||
                                CCTGG    CCCGACCCCG CCC
                                   GG___        A
GAM1712  LOC51112  5'  GCTGAGGCTGGGGCTGG    42248    C GGGA       C
                                GC G   GGGCTGGGGC GG
                                || |   |||||||||| ||
                                CG C   TCCGACCCCG CC
                                 A ____        A
GAM1712  LOC51112  5'  GGGTGCGGGGCCTCCGGGGCCG 42247    C_   AGGG
            GG                    GGG  CGGGG   CTGGGGCCGGG
                                |||  |||||   ||||||||||
                                CCC  GCCCC   GGCCCCGGCCC
                                  AC    GGA_
GAM1712  LOC56961  5'  GGGCAGGGGGAGGGTTGGG   42249     C_      C
                                GGGC  GGGGAGGG TGGG
                                ||||  |||||||| ||||
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                                CCCG  CCCCTCCC ACCC
                                  TC       A
GAM1712  LOC56961  5'  GGGCTGGGGGCGGGAGTCGCCG 42250     C   A_  CT  G_
             GG                   GGGC GGGG  GGG  GG  GCCGGG
                                  |||| ||||  |||  ||  ||||||
                                  CCCG CCCC  CCC  TC  CGGCCC
                                    A   CG  __  AG
GAM1712  LOC57118  5'  GCTGGGGAGGGGGCGCCGGG  42251    C      CT  G
                                  GC GGGGAGGG  GG GCCGGG
                                  || ||||||||  || ||||||
                                  CG CCCCTCCC  CC CGGCCC
                                   A       __  G
GAM1712  LOC64744  3'  GGACTGGGGAGGACGTTGGG  42252     C       __
                                  GGGC GGGGAGGGC  TGGG
                                  |||| |||||||||  ||||
                                  CCTG CCCCTCCTG  ACCC
                                    A        CA
GAM1712  LOC90249  5'  GAGCTGGAACTTGGGGCTGGG  42253     C   A___
                                  GGGC GGGG   GGGCTGGG
                                  |||| ||||   ||||||||
                                  CTCG CCTT   CCCGACCC
                                    A   GAAC
GAM1712  LOC90378  3'  GGGCTGGGGCAGGGGTGAGGCT 42254     C   _   C    C
             GGG                    GGGC GGGG AGGG TGGGGC GGG
                                  |||| |||| |||| |||||| |||
                                  CCCG CCCC TCCC ACTCCG CCC
                                    A   G   C    A
GAM1712  LOC91461  5'  GGGCCGGGGGAGCCTGGGCCGG 42255        A    G
             G                     GGGCCGGGG GGGCT GGGCCGGG
                                  |||||||||  ||||| ||||||||
                                  CCCGGCCCC CTCGG CCCGGCCC
                                       _    A
GAM1713  EFNB2    3'  TCCATGAGTGATGCAGATGTG  42258        A  _  _
                                  TCCATGAGT ATG AGA GTG
                                  |||||||||  |||  |||  |||
                                  AGGTACTCA TAC TCT CAC
                                       C   G   A
GAM1713  EHF      3'  CCATGAGTGGATACTGCTGA  42259       AAT  GAG   C
                                  CCATGAGT   GA   TGC GA
                                  ||||||||   ||   ||| ||
                                  GGTACTCA   CT   ACG CT
                                       C__  ATG   A
GAM1713  EYA2     3'  TCCGGAGTAATGAGACTA    42260     AT        G
                                  TCC  GAGTAATGAGA TG
                                  |||  ||||||||||| ||
                                  AGG  CTCATTACTCT AT
                                    C_         G
GAM1713  HIF1A    3'  TCCATGAGTAACTGC       42261           GAGAG
                                  TCCATGAGTAAT    TGC
                                  ||||||||||||    |||
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                              AGGTACTCATTG    ACG
                                    _____
GAM1713 HOXC11   3' TCCGGAATGGAGTGCCG    42262    AT  GTA   A
                              TCC  GA   ATG GAGTGCCG
                              |||  ||   ||| ||||||||
                              AGG  CT   TAC CTCACGGC
                                C_  ___   _
GAM1713 PKD1     3' TGGGGTGATGAGAGTGCC    42263    A_  A
                              TG  GT ATGAGAGTGCC
                              ||  || ||||||||||
                              AC  CA TACTCTCACGG
                               CC  C
GAM1713 STAU2    3' TCCATAAAGGAGTGCG     42264       TAATGA    C
                              TCCATGAG    GAGTGC G
                              ||||||||    |||||| |
                              AGGTATTT    CTCACG C
                                   C_____    A
GAM1713 AD158    5' TCCGGGCGCGAGAGTGTCGA  42265    ATGA  AAT    C
                              TCC   GT   GAGAGTG CGA
                              |||   ||   ||||||| |||
                              AGG   CG   CTCTCAC GCT
                                CCCG  ___     A
GAM1713 KIAA0152 3' CATGAGAACTCGGGGTGTCGA 42266      T   GAGA_   C
                              CATGAG AAT    GTG CGA
                              |||||| |||    ||| |||
                              GTACTC TTG    CAC GCT
                                 _  AGCCC   A
GAM1713 KIAA1337 3' TCCATGAGGAAAGCTGTGCTGA 42267       TAAT   A_   C
                              TCCATGAG   GAG  GTGC GA
                              ||||||||   |||  |||| ||
                              AGGTACTC   TTC  CACG CT
                                   CT__   GA   A
GAM1713 KLK7     3' TCCAGTGTTTGAGAGTGC    42268     TGA  AA
                              TCCA   GT  TGAGAGTGC
                              ||||   ||  |||||||||
                              AGGT   CA  ACTCTCACG
                                CA_  A_
GAM1713 KLK7     3' TCCAGTGTTTGAGAGTGC    42268     TGA  AA
                              TCCA   GT  TGAGAGTGC
                              ||||   ||  |||||||||
                              AGGT   CA  ACTCTCACG
                                CA_  A_
GAM1713 PPP2R3A  3' CAAGAGTGTAGAGTGCTGA   42269    T    AATG     C
                              CA GAGT    AGAGTGC GA
                              || ||||    ||||||| ||
                              GT CTCA    TCTCACG CT
                               T   CA__      A
GAM1713 PRO1598  3' TCCATGAGATGATGAGAA    42270        TA_
                              TCCATGAG   ATGAGAG
                              ||||||||   |||||||
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                                AGGTACTC   TACTCTT
                                     TAC
GAM1713  LOC115123 3'  TCCTTGAGTAATGGACGC    42271     A       A  G
                                TCC TGAGTAATG GA TGC
                                ||| ||||||||| || |||
                                AGG ACTCATTAC CT GCG
                                  A       _ _
GAM1713  LOC145566 5'  TCCAAGAGTGATTTTGCTGA   42272     T   AAT  GAG   C
                                TCCA GAGT   GA   TGC GA
                                |||| ||||   ||   ||| ||
                                AGGT CTCA   CT   ACG CT
                                  T   ___  AAA   A
GAM1713  LOC148887 3'  CCATGACTCCCGGAGAGTGCCG 42273       GTAAT_
                                CCATGA     GAGAGTGCCG
                                ||||||     ||||||||||
                                GGTACT     CTCTCACGGC
                                    GAGGGC
GAM1713  LOC150407 3'  TCCAGAGTGCCCAGGAGTGC   42274     T   AA_ GA
                                TCCA GAGT   T  GAGTGC
                                |||| ||||   |  ||||||
                                AGGT CTCA   G  CTCACG
                                  _    CGG TC
GAM1713  LOC163964 5'  TCCATGAGTGGTAGACTTACTG 42275         AATG   G_   C
           A                     TCCATGAGT    AGA  TGC GA
                                |||||||||    |||  ||| ||
                                AGGTACTCA    TCT  ATG CT
                                     CCA_   GA   A
GAM1714  NOTCH3   3'  GGCTATGGAACATGTCCAATCT 42278          C_   GCT  A
           GG                    GGCTATGGAAC  GTC   GT TGG
                                ||||||||||  |||   || |||
                                CCGATACCTTG  CAG   TA ACC
                                      TA   GT_  G
GAM1714  PRKCG    3'  GGCTGTAGAGGCTGTATG    42279     A   ACCGTC
                                GGCT TGGA     GCTGTATG
                                |||| ||||     ||||||||
                                CCGA ATCT     CGACATAC
                                  C   C_____
GAM1714  DDR1     3'  GGCTATGGGCCGTTGCT     42280        AA   C
                                GGCTATGG  CCGT GCT
                                ||||||||  |||| |||
                                CCGATACC  GGCA CGA
                                     C_    A
GAM1714  DDR1     3'  GGCTATGGGCCGTTGCT     42280        AA   C
                                GGCTATGG  CCGT GCT
                                ||||||||  |||| |||
                                CCGATACC  GGCA CGA
                                     C_    A
GAM1714  DDR1     3'  GGCTATGGGCCGTTGCT     42280        AA   C
                                GGCTATGG  CCGT GCT
                                ||||||||  |||| |||
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                                CCGATACC  GGCA CGA
                                    C_    A
GAM1714 KIAA1641 3' GGTCATGGAACTGTGTGTG   42281    C      C  CGCT  A
                                GG TATGGAAC GT    GT TG
                                || |||||||| ||    || ||
                                CC GTACCTTG CA    CA AC
                                 A       A _____  C
GAM1714 POMT1    3' GGCATGGAGCTGTAT       42282     T    ACCGTC
                                GGC ATGGA     GCTGTAT
                                ||| |||||     |||||||
                                CCG TACCT     CGACATA
                                  _    _______
GAM1714 LOC150244 5' GGCTATGGATGCTGTCGTCCCC 42283         AC_____   G  G  T
             CAGG                   GCTATGGA     CGTC CT TA GG
                                ||||||||     |||| || || ||
                                CGATACCT     GCAG GG GT CC
                                     ACGACA   _  G  _
GAM1714 LOC55908  3' GGCTGGGAGCGCCGCTGTGTGG 42284      AT   AC       A
                                GGCT  GGA  CGTCGCTGT TGG
                                ||||  |||  ||||||||| |||
                                CCGA  CCT  GCGGCGACA ACC
                                  C_  C_       C
GAM1715 CAV1     3' TTCAATTCATAAATTGTTGCTG 42287         TCAACATAC
                                TTCAATTC       GTTGCTG
                                ||||||||       |||||||
                                AAGTTAAG       CAACGAC
                                     TATTTAA__
GAM1715 SP1      5' TTCAATTTTCACCACAGCTG   42288       C   A   C
                                TTCAATT TCA CATA GTTG
                                ||||||| ||| |||| ||||
                                AAGTTAA AGT GTGT CGAC
                                    A   G   _
GAM1715 KIAA0438 3' TTCAGCTCTCAACATTGCT   42289      A        ACGT
                                TTCA TTCTCAACAT    TGCT
                                |||| ||||||||||    ||||
                                AAGT GAGAGTTGTA    ACGA
                                  C        _____
GAM1715 MGC21738 3' TTCAATTCTGACATTACC    42290         CAACAT
                                TTCAATTCT     ACGTTGCT
                                |||||||||     |||||||||
                                AAGTTAAGA     TGTAATGG
                                     C_____
GAM1715 PRO0132  5' TTCAATTCCTAAATTATTTGCT 42291         CAACATACG
             G                   TTCAATTCT       TTGCTG
                                |||||||||       ||||||
                                AAGTTAAGG       AACGAC
                                     ATTTAATA_
GAM1716 ACYP1    3' ATCATACAGGTAATATATAA   42294        A     C
                                GTTATACA GTAATA ATAA
                                |||||||| |||||| ||||
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                                TAGTATGT CATTAT TATT
                                    C     A
GAM1716 COG6     3' TTGTTATATACAACACATAA  42295       CAAG
                                TTGTTATA   TAATACATAA
                                ||||||||   ||||||||||
                                AACAATAT   GTTGTGTATT
                                    AT__
GAM1716 PTGFR    3' GTTGTTATAACAAACCATCAT 42296        _  TA  A
                                GTTGTTATA CAAG  AT CAT
                                ||||||||| ||||  || |||
                                CAACAATAT GTTT  TA GTA
                                     T   GG  _
GAM1716 C21orf7  3' AGTTGTCATGTGGGTAATACA 42297       ACAA
                                AGTTGTTAT   GTAATACA
                                |||||||||   ||||||||
                                TCAACAGTA   CATTATGT
                                    CACC
GAM1716 FLJ10901 3' AGGTGTTATACAAGACCAATA 42298   T       __
                                AG TGTTATACAAG  TAATA
                                || ||||||||||  |||||
                                TC ACAATATGTTC  GTTAT
                                 C         TG
GAM1716 POF1B    3' GTTGTTATACTGAATACAT   42299       AAGT
                                GTTGTTATAC   AATACAT
                                ||||||||||   |||||||
                                CAACAATATG   TTATGTA
                                    AC__
GAM1716 LOC245771 3' AGGTGTTATACAAGACCAATA 42298   T       __
                                AG TGTTATACAAG  TAATA
                                || ||||||||||  |||||
                                TC ACAATATGTTC  GTTAT
                                 C         TG
GAM1717 AKAP13   3' GACTGGGCCTTCTTCTGGC   42302    C   A  CC  _
                                GAC GGGCC TCT  CTG C
                                ||| ||||| |||  ||| |
                                CTG CCCGG AGA  GAC G
                                  A   A  A_  C
GAM1717 AKAP13   3' GACTGGGCCTTCTTCTGGC   42302    C   A  CC  _
                                GAC GGGCC TCT  CTG C
                                ||| ||||| |||  ||| |
                                CTG CCCGG AGA  GAC G
                                  A   A  A_  C
GAM1717 AKAP13   3' GACTGGGCCTTCTTCTGGC   42302    C   A  CC  _
                                GAC GGGCC TCT  CTG C
                                ||| ||||| |||  ||| |
                                CTG CCCGG AGA  GAC G
                                  A   A  A_  C
GAM1717 GDF2     5' GGGCCGGCATCTCCCTGCTGTT 42303     ___
             T                   GGGCC  ATCTCCCTGCTGTTT
                                 |||||  |||||||||||||||
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                                CCCGG   TAGAGGGACGACAAA
                                  CCG
GAM1717 ORC5L    3' GCTCAAACCCTGCTGTTT    42304    _ TCT
                                GC CA   CCCTGCTGTTT
                                || ||   ||||||||||
                                CG GT   GGGACGACAAA
                                 A  TT_
GAM1717 RASGRP2  5' GACCGGGGCGTCTTCCTGC    42305       CA   C
                                GACCGGGC  TCT CCTGC
                                ||||||||  ||| |||||
                                CTGGCCCG  AGA GGACG
                                     C_   A
GAM1717 ST5      3' GGGCCTTCTCCCCAGGCT    42306      A     __
                                GGGCC TCTCCCT  GCT
                                ||||| |||||||  |||
                                CCCGG AGAGGGG  CGA
                                   A      TC
GAM1717 ST5      3' GGGCCTTCTCCCCAGGCT    42306      A     __
                                GGGCC TCTCCCT  GCT
                                ||||| |||||||  |||
                                CCCGG AGAGGGG  CGA
                                   A      TC
GAM1717 TBL1X    3' GGGCCATCTTCCTCAGCCCTT  42307        C   __   G
                                GGGCCATCT CCT  GCT TT
                                ||||||||| |||  ||| ||
                                CCCGGTAGA GGA  CGG AA
                                     A   GT   G
GAM1717 FLJ11700 3' GGCTGAAGTCATTCCTGCTGTT 42308    CA___  TC_
            T                    GGC    TC   CCTGCTGTTT
                                |||    ||   ||||||||||
                                CCG    AG   GGACGACAAA
                                  ACTTC  TAA
GAM1717 FLJ12650 3' GGGCCTGATGTCCTGCTGTTT  42309      ATCTC_
                                GGGCC     CCTGCTGTTT
                                |||||     ||||||||||
                                CCCGG     GGACGACAAA
                                   ACTACA
GAM1717 FLJ14326 3' GGGCCCGAGGCCTGCTGTTT   42310      ATCTC
                                GGGCC    CCTGCTGTTT
                                |||||    ||||||||||
                                CCCGG    GGACGACAAA
                                   GCTCC
GAM1717 KIAA0240 3' GACTGGCCATCTCACAGGGTTT 42311    CG       CCTGCT
                                GAC  GGCCATCTC     GTTT
                                |||  |||||||||     ||||
                                CTG  CCGGTAGAG     CAAA
                                  A_        TGTCC_
GAM1717 NSE1     3' GACCGGGCCGGCTTCCCT    42312        AT  _
                                GACCGGGCC  CT CCCT
                                |||||||||  || ||||
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                                CTGGCCCGG  GA GGGA
                                     CC  A
GAM1717  TADA3L   3'  GACTGGCCACTGCTGT     42313    CG    TCTCC
                                GAC  GGCCA    CTGCTGT
                                |||  |||||    |||||||
                                CTG  CCGGT    GACGACA
                                  A_    _____
GAM1717  TADA3L   3'  GACTGGCCACTGCTGT     42313    CG    TCTCC
                                GAC  GGCCA    CTGCTGT
                                |||  |||||    |||||||
                                CTG  CCGGT    GACGACA
                                  A_    _____
GAM1717  LOC153222 3'  GAGCCATCTTTTTTTTGTTGTT 42314         CCC___  C
              T                   GGGCCATCT     TG TGTTT
                                |||||||||     || |||||
                                CTCGGTAGA     AC ACAAA
                                     AAAAAA  A
GAM1717  LOC200689 5'  GACCGGGCCGGCTTCCCT    42312         AT  _
                                GACCGGGCC  CT CCCT
                                |||||||||  || ||||
                                CTGGCCCGG  GA GGGA
                                     CC  A
GAM1717  LOC203292 5'  GGACCTCTTGCTGTTT     42315      A  CCC
                                GGGCC TCT   TGCTGTTT
                                |||||| |||   ||||||||
                                CCTGG AGA   ACGACAAA
                                  _  ____
GAM1717  LOC256880 5'  GGGTTCTTCCTTGCTGTTT   42316     CCA  _  C
                                GGG   TCT CC TGCTGTTT
                                |||   ||| || ||||||||
                                CCC   AGA GG ACGACAAA
                                  A__   A  A
GAM1717  LOC51285  3'  GACTGGGTCAGAGATGCTGTTT 42317     C   C  TCTCCC
                                GAC GGG CA     TGCTGTTT
                                ||| ||| ||     ||||||||
                                CTG CCC GT     ACGACAAA
                                  A   A  CTCT__
GAM1718  PCDHB9   3'  ATTGATCCTTATTTTAAGGTC  42320     TC  GCACATC
                                ATTG  CC      TTTAAGGTC
                                ||||  ||      |||||||||
                                TAAC  GG      AAATTCCAG
                                   TA  AATA___
GAM1718  RAB36    3'  TTGTTCTGCACATCCTGGC    42321     CCC       TAA
                                TTGT   GCACATCTT   GGT
                                ||||   |||||||||   |||
                                AACA   CGTGTAGGA   CCG
                                  AGA        ___
GAM1718  SNX9     3'  TCCCGTAATTATTAAGGTC   42322      CAC  CT
                                TCCCG   AT  TTAAGGTC
                                |||||   ||  ||||||||
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                                AGGGC  TA  AATTCCAG
                                  AT_  AT
GAM1718 HIC2     3'  CTGTTATGCAGCATTTTTGAGG 42323     CCC  _  C  A
             TC                   TTGT  GCA CAT TTT AGGTC
                                  ||||  ||| ||| ||| |||||
                                  GACA  CGT GTA AAA TCCAG
                                    ATA  C  A  C
GAM1718 KCNS1    3'  TTGTTCACACCTTTTTGAGGTC 42324     CCCG       A__
                                  TTGT   CACATCTTT  AGGTC
                                  ||||   |||||||||  |||||
                                  AACA   GTGTGGAAA  TCCAG
                                    A___       AAC
GAM1718 PIP5K2B  3'  ATCTTCACATCTTTGGGGT   42325     CCG       AA
                                  GTC  CACATCTTT  GGT
                                  |||  |||||||||  |||
                                  TAG  GTGTAGAAA  CCA
                                    AA_       CC
GAM1718 LOC147042 3'  TTGCCCCACTTTGGGGT     42326        ACATC  AA
                                  TTGTCCCGC    TTT  GGT
                                  |||||||||    |||  |||
                                  AACGGGGTG    AAA  CCA
                                       _____  CC
GAM1718 LOC169026 3'  TTGGCCTGCACATCTTCA    42327     T  C
                                  TTG CC GCACATCTTTA
                                  ||| || ||||||||||
                                  AAC GG CGTGTAGAAGT
                                    C  A
GAM1719 CYP1A2   3'  GCTTGAACCTGCGAGGTGGAG  42330    CC      T  TTTATA
                                  GC  TGAACCTG CG     GAG
                                  ||  |||||||| ||     |||
                                  CG  ACTTGGAC GC     CTC
                                   A_       _ TCCAC_
GAM1719 DISC1    3'  GCTTGAACCTGGGAGGTAGAG  42331    CC      TCGTTTA
                                  GC  TGAACCTG      TAGAG
                                  ||  ||||||||      |||||
                                  CG  ACTTGGAC      ATCTC
                                   A_       CCTCC__
GAM1719 FOXD2    3'  GCCCCGGGCCTGTCGCCCTGAG 42332       AA        ATA
                                  GCCCTG  CCTGTCGTTT   GAG
                                  ||||||  ||||||||||   |||
                                  CGGGGC  GGACAGCGGG   CTC
                                     CC         A__
GAM1719 FLJ14117 3'  GCCTAGAACTCTTATAGA    42333     CT   CTG  GT
                                  GCC  GAAC   TC  TTATAGA
                                  |||  ||||   ||  |||||||
                                  CGG  CTTG   AG  AATATCT
                                    AT    ___  __
GAM1719 ZNF333   3'  CCCTGGGTCTGCCACTGTAGAG 42334       AAC     TTTA
                                  CCCTG   CTGTCG    TAGAG
                                  |||||   ||||||    |||||
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                                GGGAC   GACGGT    ATCTC
                                   CCA     GAC_
GAM1719  LOC147054 5'  GCCCTGAACTTGTTTTCC    42335         C   CG
                                GCCCTGAAC TGT  TTT
                                ||||||||| |||  |||
                                CGGGACTTG ACA  AGG
                                     A   AA
GAM1719  LOC158014 5'  GCTCTGAGACTGTTACAGA   42336    C    AC    CGTT
                                GC CTGA  CTGT    TATAGA
                                || ||||  ||||    ||||||
                                CG GACT  GACA    ATGTCT
                                 A    CT    ____
GAM1719  LOC219920 5'  GCCTTGGGTCTGCCGTCCA   42337     C  AAC
                                GCC TG   CTGTCGTTTA
                                ||| ||   ||||||||||
                                CGG AC   GACGGCAGGT
                                  A  CCA
GAM1720  KIAA1915  3'  TAATTTAAAAGGATTAGA    42340          A
                                TAATTTAAAAG ATTAGA
                                |||||||||| ||||||
                                ATTAAATTTTC TAATCT
                                      C
GAM1720  LOC201287 5'  TTAATTTAAAAGAAGTTACTGT 42341            TTAG
           T                    TTAATTTAAAAGAA    ATTGTT
                                ||||||||||||||    ||||||
                                AATTAAATTTTCTT    TGACAA
                                      CAA_
GAM1720  LOC256207 5'  TTAATTTAAAAGAAGTTACTGT 42341            TTAG
           T                    TTAATTTAAAAGAA    ATTGTT
                                ||||||||||||||    ||||||
                                AATTAAATTTTCTT    TGACAA
                                      CAA_
GAM1721  CACNG3    5'  CTGCGGGCACCACTGGA     42344      AGAT   _
                                CTGC    GGGC TCACTGGA
                                ||||    |||| ||||||||
                                GACG    CCCG GGTGACCT
                                  ____    T
GAM1721  DLEC1     3'  CTGCAGATGGGGTGAGTCTGG  42345          CTCA__
                                CTGCAGATGGG     CTGG
                                ||||||||||      ||||
                                GACGTCTACCC     GACC
                                      CACTCA
GAM1721  DTR       3'  TTACTACAGATGGGTCACAGAA 42346            C    T
                                TTACTGCAGATGGG TCAC GGAA
                                |||||||||||||| |||| ||||
                                AATGATGTCTACCC AGTG TCTT
                                      _   _
GAM1721  HIP12     3'  CTGCAGATTCCAGCTGGAA    42347         GGGC  _
                                CTGCAGAT    TCA CTGGAA
                                ||||||||    ||| ||||||
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                                GACGTCTA   GGT GACCTT
                                    A___   C
GAM1721  KIF5C    3'  TACTGCAGATGGCTGGA     42348          GCTCA
                                TACTGCAGATGG    CTGGA
                                ||||||||||||   |||||
                                ATGACGTCTACC    GACCT
                                       _____
GAM1721  KLK13    3'  TGAGATGGGCTGATGGAA    42349    C       CAC
                                TG AGATGGGCT   TGGAA
                                || |||||||||   |||||
                                AC TCTACCCGA   ACCTT
                                 _       CT_
GAM1721  LMO2     3'  TTACTATGGATGGGCTGTGG  42350      CA      CAC
                                TTACTG  GATGGGCT   TGG
                                ||||||  ||||||||   |||
                                AATGAT  CTACCCGA   ACC
                                    AC       C__
GAM1721  SLC4A2   3'  TTACTGCAGGGGCAGTGG    42351        AT    TCAC
                                TTACTGCAG  GGGC   TGG
                                |||||||||  ||||   |||
                                AATGACGTC  CCCG   ACC
                                     __    TC__
GAM1721  TRPS1    3'  TTACTGCAATTAACTGG     42352         A  GGCTC
                                TTACTGCAG TG    ACTGG
                                |||||||||  ||    |||||
                                AATGACGTT AT    TGACC
                                     A  _____
GAM1721  C1orf34  3'  TCACTGCACTTACTGG      42353        AGATGG   C
                                TTACTGC     GCT ACTGG
                                |||||||     ||| |||||
                                AGTGACG     TGA TGACC
                                     _______  A
GAM1721  CLLD8    5'  TGCAGAATATCACTGGAA    42354       TGGGC
                                TGCAGA    TCACTGGAA
                                ||||||    |||||||||
                                ACGTCT    AGTGACCTT
                                   TAT__
GAM1721  FLJ12619 3'  CTGCACAATTCACTGGAA    42355     AG TG GC
                                CTGC  A  G  TCACTGGAA
                                ||||  |  |  |||||||||
                                GACG  T  T  AGTGACCTT
                                  __ GT A_
GAM1721  FLJ20446 3'  TTATTGCGACTTCCACTGGAA 42356     C   A   GGG T
                                TTA TGC GAT   C CACTGGAA
                                ||| ||| |||   | ||||||||
                                AAT ACG CTG   G GTGACCTT
                                  A   _   AA_ _
GAM1721  KIAA1877 5'  TTAATGCAGATGGGTGG     42357     C        CTCAC
                                TTA TGCAGATGGG    TGG
                                ||| ||||||||||    |||
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                                AAT ACGTCTACCC    ACC
                                  T       _____
GAM1721  MGC16309  3'  TTACTGGGGATGGGCTTCTG  42358      CA      CA
                                TTACTG  GATGGGCT  CTG
                                ||||||  ||||||||  |||
                                AATGAC  CTACCCGA  GAC
                                   CC       A_
GAM1721  MGC3040   3'  TTAATGCAGATGTGGGTGTTGG 42359    C      _  CTCAC
           A                     TTA TGCAGATG GG    TGGA
                                ||| |||||||| ||    ||||
                                AAT ACGTCTAC CC    ACCT
                                  T       A  CACA_
GAM1721  SHARP    3'  TTACTGCAGAGCCCTGG    42360         TGG  T A
                                TTACTGCAGA   GC C CTGG
                                ||||||||||   || | ||||
                                AATGACGTCT   CG G GACC
                                     ____  _ _
GAM1721  VMP      5'  CTGCAGATCTCTCGCTGG    42361        GGG   A
                                CTGCAGAT   CTC CTGG
                                ||||||||   ||| ||||
                                GACGTCTA   GAG GACC
                                     GA_   C
GAM1721  LOC126133 3'  TTACTGCATATGGATTCTGG  42362        G    CTCA
                                TTACTGCA ATGGG    CTGG
                                |||||||| |||||    ||||
                                AATGACGT TACCT    GACC
                                     A     AA__
GAM1721  LOC148753 3'  CTGCAGAGGCCACTGGA     42363        TG   T
                                CTGCAGA  GGC CACTGGA
                                |||||||  ||| |||||||
                                GACGTCT  CCG GTGACCT
                                     __   _
GAM1721  LOC152687 3'  TGCTGTGTAAAGACACTGGAA  42364     AGA_   CT
                                TGC    TGGG  CACTGGAA
                                |||    ||||  ||||||||
                                ACG    ATTT  GTGACCTT
                                  ACAC    CT
GAM1721  LOC196761 3'  TGCGGGATCTGGGCTCACTGGA 42365     A_  __
           A                     TGC  GA  TGGGCTCACTGGAA
                                |||  ||  ||||||||||||||
                                ACG  CT  ACCCGAGTGACCTT
                                  CC  AG
GAM1721  LOC219688 3'  TTACTGCAAATGGTGG      42366          GCTCAC
                                TTACTGCAGATGG     TGG
                                ||||||||||||      |||
                                AATGACGTTTACC     ACC
                                     _______
GAM1721  LOC255040 3'  TTACTGCGGATGGCACCGGAA  42367        A    GCT
                                TTACTGC GATGG   CACTGGAA
                                |||||||  |||||   ||||||||
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                                AATGACG CTACC   GTGGCCTT
                                   C    ___
GAM1721  LOC255041 3'  TTACTGCGGATGGCACCGGAA  42367       A    GCT
                                TTACTGC GATGG   CACTGGAA
                                ||||||| |||||   ||||||||
                                AATGACG CTACC   GTGGCCTT
                                   C    ___
GAM1721  LOC255783 3'  TTATTGCAGATGGACACGGA   42368     C        TC  T
                                TTA TGCAGATGGGC  AC GGA
                                ||| ||||||||||  || |||
                                AAT ACGTCTACCTG  TG CCT
                                  A        __ _
GAM1721  LOC84528  5'  CTGCAGATTCTGAGCTGGG    42369        ___     CACT
                                CTGCAGA   TGGGCT    GG
                                |||||||   ||||||    ||
                                GACGTCT   ACTCGA    CC
                                   AAG     C___
GAM1721  LOC92973  5'  CTGCGGGTCACTGGA      42370      AGAT   C
                                CTGC    GGG TCACTGGA
                                ||||    ||| ||||||||
                                GACG    CCC AGTGACCT
                                  ____  _
GAM1722  SKP2      5'  AGCCAGACCCGCTAAGCCTAG  42373      TTA  G
                                AGCCG   AC CCGCTAAGCCTAG
                                |||||   || ||||||||||||
                                TCGGT   TG GGCGATTCGGATC
                                  C__  _
GAM1722  SKP2      5'  AGCCAGACCCGCTAAGCCTAG  42373      TTA  G
                                AGCCG   AC CCGCTAAGCCTAG
                                |||||   || ||||||||||||
                                TCGGT   TG GGCGATTCGGATC
                                  C__  _
GAM1722  RAP140    3'  GTTTTTACATGACTAAGCCTAG 42374     A__  CC
                                GTT   ACG  GCTAAGCCTAG
                                |||   |||  ||||||||||
                                CAA   TGT  TGATTCGGATC
                                  AAA   AC
GAM1722  LOC149117 3'  AGCCTTGACAGCAAGCCTA    42375     GTTAAC  C  T
                                AGCC     GC GC AAGCCTA
                                ||||     || || |||||||
                                TCGG     TG CG TTCGGAT
                                  AAC____  T  _
GAM1722  LOC197387 5'  GCCGTTAACCCGCCTCTA    42376        G    AAGC
                                GCCGTTAAC CCGCT    CTA
                                ||||||||| |||||    |||
                                CGGCAATTG GGCGG    GAT
                                     _    A___
GAM1723  ZNF22     5'  ACTAGTGTTTCATTTCCTAGAG 42379        CC   AA__  AA_
            GTGTA                ACTGGTGT  CAT    TA   GTGTA
                                ||||||||  |||    ||   |||||
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                                TGATCACA GTA   AT  CACAT
                                    AA  AAGG CTC
GAM1723 AMOT     3' ACTGGTGTTCACATGGTAT  42380       CC   ATAAA
                                ACTGGTGT CATA   GTGT
                                |||||||| ||||   ||||
                                TGACCACA GTGT   CATA
                                    A_   AC___
GAM1723 C1orf17  3' GGTGTCTGGCTTAAAGTGTA 42381      CCATAA
                                GGTGTC    TAAAGTGTA
                                ||||||    |||||||||
                                CCACAG    ATTTCACAT
                                   ACCGA_
GAM1723 C3IP1    3' ACTGGTGCCTGTAATCACCCGG 42382       T CA   AAA___
           TG                    ACTGGTG CC  TAAT    GTG
                                |||||||  ||  ||||    |||
                                TGACCAC GG  ATTA    CAC
                                    _ AC   GTGGGC
GAM1723 DKFZP434G1411 3' ACTGATGACAGGTAAAGTGT  42383       TCC  TAA
                                ACTGGTG   CA   TAAAGTGT
                                |||||||   ||  ||||||||
                                TGACTAC   GT   ATTTCACA
                                    T__  CC_
GAM1723 FLJ13693 3' ACTGTGTCCCAAGTG      42384     G     TAATAA
                                ACTG TGTCCCA     AGTG
                                |||| |||||||     ||||
                                TGAC ACAGGGT     TCAC
                                  _      _______
GAM1723 KIAA0555 3' ACTAGTGTTTCCATGGGGTGT 42385       C_   AATAAA
                                ACTGGTGT  CCAT     GTGT
                                ||||||||  ||||     ||||
                                TGATCACA  GGTA     CACA
                                    AA   CCC___
GAM1723 KIAA1363 5' GGTGTCCTTGCAAAGTGT   42386       CATAA
                                GGTGTCC    TAAAGTGT
                                |||||||    ||||||||
                                CCACAGG    GTTTCACA
                                    AAC__
GAM1723 MGC13204 3' CTGGTGCCTGTAATCCCAGC  42387      T  CA   AA_
                                CTGGTG CC  TAAT   AGT
                                ||||||  ||  ||||   |||
                                GACCAC GG  ATTA   TCG
                                   _ AC    GGG
GAM1723 SEMA4G   5' ACAGGTGTCCCTGTAAGGTGT 42388    T      ATAA   A
                                AC GGTGTCCC    TAA GTGT
                                ||  ||||||||    ||| ||||
                                TG CCACAGGG    ATT CACA
                                 T       AC__   C
GAM1723 TRIM2    3' ACTGGTGTCCTACTACATGTG  42389         C  A   AA
                                ACTGGTGTCC AT ATA  GTG
                                ||||||||||  ||  |||  |||
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                                TGACCACAGG TG TGT  CAC
                                      A  A   A_
GAM1723  LOC127180 3'  TGGTTCTCACAAAGTGT     42390      G  C     TAA
                                TGGT TC CATAA   AGTGT
                                |||| || |||||   |||||
                                ACCA AG GTGTT   TCACA
                                  _  A    ___
GAM1723  LOC132617 3'  ACTGGTAATAAAGTG       42391        TCCCATA
                                ACTGGTG      ATAAAGTG
                                |||||||      ||||||||
                                TGACCAT      TATTTCAC
                                  ________
GAM1723  LOC150203 3'  ACTGGTGCCTGTAATCACCCTG 42392       T  CA    AAAG_
              T                  ACTGGTG CC  TAAT     TGT
                                |||||||  ||  ||||     |||
                                TGACCAC GG  ATTA     ACA
                                   _  AC    GTGGG
GAM1723  LOC154739 5'  TGGTGTCCTAATACATATGTA  42393        CA     AA_
                                TGGTGTCC  TAATA   GTGTA
                                ||||||||  |||||   |||||
                                ACCACAGG  ATTAT   TACAT
                                     __     GTA
GAM1723  LOC201689 5'  ACTTGTGTCCTAGAAAGTGTA  42394     G      CATAAT
                                ACT GTGTCC     AAAGTGTA
                                |||  ||||||     ||||||||
                                TGA CACAGG     TTTCACAT
                                  A     ATC___
GAM1723  LOC203276 3'  TGGTGTCCTAATACATATGTA  42393        CA     AA_
                                TGGTGTCC  TAATA   GTGTA
                                ||||||||  |||||   |||||
                                ACCACAGG  ATTAT   TACAT
                                     __     GTA
GAM1723  LOC203305 3'  TGGTGTCCTAATACATATGTA  42393        CA     AA_
                                TGGTGTCC  TAATA   GTGTA
                                ||||||||  |||||   |||||
                                ACCACAGG  ATTAT   TACAT
                                     __     GTA
GAM1723  LOC221504 3'  ACTGGTGTGCCATGGCAGTG   42395        C    AATAA
                                ACTGGTGT CCAT     AGTG
                                |||||||| ||||     ||||
                                TGACCACA GGTA     TCAC
                                     C    CCG__
GAM1723  LOC254243 3'  TGGTGTCCTAATACATATGTA  42393        CA     AA_
                                TGGTGTCC  TAATA   GTGTA
                                ||||||||  |||||   |||||
                                ACCACAGG  ATTAT   TACAT
                                     __     GTA
GAM1723  LOC257463 3'  ACTGGGGTTCTGCATAAAGTGT 42396      T  CCCATA
                                ACTGG GT     ATAAAGTGT
                                |||||  ||     |||||||||
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                                TGACC CA     TATTTCACA
                                  C  AGACG_
GAM1723 LOC90038 3' TGGTGTCCTAATACATATGTA 42393        CA    AA_
                                TGGTGTCC  TAATA   GTGTA
                                ||||||||  |||||   |||||
                                ACCACAGG  ATTAT   TACAT
                                     __    GTA
GAM1724 CARKL    3' CCTCCGGTCACATGGTTC    42399    C       TCA
                                CC CCGGTCACGT   GGTTC
                                || ||||||||||   |||||
                                GG GGCCAGTGTA   CCAAG
                                 A        ____
GAM1724 CDKN2B   3' CCTCAGTCTTCAGGTT     42400    C    ACG
                                CC CGGTC   TTCAGGTT
                                || |||||   ||||||||
                                GG GTCAG   AAGTCCAA
                                 A    ____
GAM1724 DXYS155E 3' CCTCGGCCACGCTCCCGTTC  42401    C        AG
                                CC CGGTCACGTTC  GTTC
                                || ||||||||||  ||||
                                GG GCCGGTGCGAG  CAAG
                                 A          GG
GAM1724 EXTL3    3' CCCGGCCAGCCGGGTGGGTTC 42402        C   CA___
                                CCCGGTCA GTT     GGTTC
                                |||||||| |||    |||||
                                GGGCCGGT CGG     CCAAG
                                     _  CCCAC
GAM1724 FCMD     3' CCCTCAGACATTCAGGTT    42403    C   TC
                                CCC CGG  ACGTTCAGGTT
                                ||| |||  ||||||||||
                                GGG GTC  TGTAAGTCCAA
                                 A  __
GAM1724 GALGT    3' CCCTACTGGGCATCAGGTTC  42404    CCC_  T  CGT
                                CCC    GG CA   TCAGGTTC
                                |||    || ||   ||||||||
                                GGG    CC GT   AGTCCAAG
                                  ATGA  C  ___
GAM1724 GGA1     3' CCCCCCAGTCACTGGGTTC   42405          GTTCA
                                CCCCCCGGTCAC    GGTTC
                                ||||||||||||    |||||
                                GGGGGGTCAGTG    CCAAG
                                      AC___
GAM1724 GP9      3' CCCCCTGGCTGGAGCCAGGTTC 42406      C   CACGT
                                CCCCC GGT    TCAGGTTC
                                ||||| |||    ||||||||
                                GGGGG CCG    GGTCCAAG
                                   A   ACCTC
GAM1724 HS3ST3A1 5' CCGCCCGAGTTCAGGTTC    42407    _    TCAC
                                CC CCCGG    GTTCAGGTTC
                                || |||||    ||||||||||
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                                GG GGGCT   CAAGTCCAAG
                                 C    ____
GAM1724 IHPK3   3' CCTCCGTCCTCCAGGTTC   42408   C  GT ACG
                                CC CCG  C   TTCAGGTTC
                                || |||  |   |||||||||
                                GG GGC  G   AGGTCCAAG
                                 A   AG ___
GAM1724 MSF     5' CCTCCCGGGCGGATCAGGTTC 42409   _   TCA  T_
                                CC CCCGG   CG  TCAGGTTC
                                || |||||   ||  |||||||||
                                GG GGGCC   GC  AGTCCAAG
                                 A    C__  CT
GAM1724 PCSK2   3' CCTTCAGGCCTCAGGTTC   42410   GG   C  _
                                CC  TCA GT TCAGGTTC
                                ||  ||| || ||||||||
                                GG  AGT CG AGTCCAAG
                                 A_   C  G
GAM1724 SLC30A4  5' CCCCAGGTCTGACAGGTTC  42411    C   ACGTT
                                CCCC GGTC    CAGGTTC
                                |||| ||||    |||||||
                                GGGG CCAG    GTCCAAG
                                  T   ACT__
GAM1724 SLC7A6   3' CCTGGCATTCAGGTTC     42412   C  CAC
                                CC GGT   GTTCAGGTTC
                                || |||   ||||||||||
                                GG CCG   TAAGTCCAAG
                                 A   ___
GAM1724 UPK1B   3' CCCGGTCAAGTGATTC     42413       C  TCA
                                CCCGGTCA GT   GGTTC
                                |||||||| ||   |||||
                                GGGCCAGT CA   CTAAG
                                     T  ___
GAM1724 WEE1    5' CCTCAGGTCCAGTCTCAGGTTC 42414   C _   ACG_
                                CC C GGTC   TTCAGGTTC
                                || | ||||   |||||||||
                                GG G CCAG   GAGTCCAAG
                                 A T   GTCA
GAM1724 AF9Q34   3' CCCGGGAACTCAGGTTC    42415     TC  GT
                                CCCGG  AC  TCAGGTTC
                                |||||  ||  ||||||||
                                GGGCC  TG  AGTCCAAG
                                   CT  __
GAM1724 AFAP    3' CCCTGTCGAATCCAGGTT   42416    G   AC
                                CCC GTC  GTTCAGGTT
                                ||| |||  |||||||||
                                GGG CAG  TAGGTCCAA
                                  A   CT
GAM1724 BATF    3' CCTTCCAGTCGTGACAGTTC  42417   CC    AC  TCA
                                CC  CCGGTC  GT   GGTTC
                                ||  ||||||  ||   |||||
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                                GG  GGTCAG  CA   TCAAG
                                 AA      __ CTG
GAM1724  C20orf110 3'  CCCCCAGGGATTCAGGTTC   42418       TCAC
                                CCCCCGG   GTTCAGGTTC
                                |||||||   ||||||||||
                                GGGGGTC   TAAGTCCAAG
                                    CC__
GAM1724  CLIPR-59  3'  CCCCCTGGGCCTTCAGGTTC  42419      C_   ACG
                                CCCCC  GGTC   TTCAGGTTC
                                |||||  ||||   |||||||||
                                GGGGG  CCGG   AAGTCCAAG
                                  AC   ____
GAM1724  CNOT8    3'  CCCTCACGTTTCAGGTT     42420     GG      _
                                CCC  TCACGTT CAGGTT
                                |||  ||||||| ||||||
                                GGG  AGTGCAA GTCCAA
                                 __      A
GAM1724  CXYorf1   3'  CCTCACTTGTTCAGGTTC    42421    GG   __
                                CC  TCAC  GTTCAGGTTC
                                ||  ||||  ||||||||||
                                GG  AGTG  CAAGTCCAAG
                                 __   AA
GAM1724  DKFZP566D193 3'  CCATTGTCTTGTTCAGGTTC  42422    CCG   AC
                                CC   GTC  GTTCAGGTTC
                                ||   |||  ||||||||||
                                GG   CAG  CAAGTCCAAG
                                 TAA   AA
GAM1724  FLJ12565  5'  CCCCCGGCCACTGGCGTTC   42423          _____
                                CCCCCGGTCAC    GTTC
                                ||||||||||    ||||
                                GGGGGCCGGTG    CAAG
                                      ACCG
GAM1724  GTPBP2    3'  CCTGGCCACACCAAGTT     42424    C       T
                                CC GGTCACGT CAGGTT
                                || |||||||| ||||||
                                GG CCGGTGTG GTTCAA
                                 A      _
GAM1724  HYPC     5'  CCCACCTGGCTCAGGTT     42425     _ C   CACGT
                                CCC CC GGT    TCAGGTT
                                ||| || |||    |||||||
                                GGG GG CCG    AGTCCAA
                                  T  A  _____
GAM1724  KIAA0152  3'  CCCCGGCCAACCAGGTTC    42426        CGT
                                CCCCGGTCA   TCAGGTTC
                                |||||||||   ||||||||
                                GGGGCCGGT   GGTCCAAG
                                     T__
GAM1724  KIAA0478  3'  CCCCTCTGGTTCCAGGTTC   42427     CC_   CACG
                                CCCC   GGT   TTCAGGTTC
                                ||||   |||   |||||||||
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                              GGGG  CCA   AGGTCCAAG
                                AGA  ____
GAM1724 KIAA1016 5' CCTGGCGCTCAGGTTC     42428    C  TCA
                              CC GG  CGTTCAGGTTC
                              || ||  ||||||||||
                              GG CC  GCGAGTCCAAG
                               A ___
GAM1724 KIAA1908 5' CCCCAGTCGTCGGTT      42429       AC  CA
                              CCCCGGTC GTT GGTT
                              |||||||| ||| ||||
                              GGGGTCAG CAG CCAA
                                   __ __
GAM1724 MAPK8IP3 5' CCCCAGCTGCCTCAGGTTC  42430       CACG
                              CCCCGGT   TTCAGGTTC
                              |||||||   |||||||||
                              GGGGTCG   GAGTCCAAG
                                  ACG_
GAM1724 MGC10960 3' CCCTCCAGCATCAGGTT    42431    _   T CGT
                              CCC CCGG CA  TCAGGTT
                              ||| |||| ||  |||||||
                              GGG GGTC GT  AGTCCAA
                                A  _ ___
GAM1724 MGC35521 3' CCCTGGTCACATGGTC     42432    C      TCA
                              CCC GGTCACGT  GGTT
                              ||| ||||||||  ||||
                              GGG CCAGTGTA  CCAG
                                A     ___
GAM1724 NCX     3' CCCTCTCGGCGCCTCAGGTTC 42433    GG A_  _
                              CCC  TC  CGT TCAGGTTC
                              |||  ||  ||| ||||||||
                              GGG  AG  GCG AGTCCAAG
                                AG  CC  G
GAM1724 PRO2405  3' CCCGAGGTATTCAGGTTC   42434    CC  CAC
                              CCC  GGT  GTTCAGGTTC
                              |||  |||  ||||||||||
                              GGG  CCA  TAAGTCCAAG
                                CT  ___
GAM1724 SULT1C2  5' CCTCCCGACTCAGGTT     42435   _   TCACG
                              CC CCCGG    TTCAGGTT
                              || |||||    ||||||||
                              GG GGGCT    GAGTCCAA
                               A   _____
GAM1724 SULT4A1  3' CCCTCCGCTCACGCCGCTC  42436   _  G     CAG
                              CCC CCG TCACGTT  GTTC
                              ||| ||| |||||||  ||||
                              GGG GGC AGTGCGG  CGAG
                                A  G    ___
GAM1724 UBP1    3' CCAGGTCAGCATAAGGTTC   42437   C   _  TC
                              CC GGTCA CGT  AGGTTC
                              || ||||| |||  ||||||
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                                GG CCAGT GTA  TCCAAG
                                 T    C   T_
GAM1724  LOC146957 3'  CCCACTGGCTGTCAGGTTC   42438    CCC   CAC  T
                                CCC   GGT   GT CAGGTTC
                                |||   |||   || |||||||
                                GGG   CCG   CA GTCCAAG
                                  TGA   A__  _
GAM1724  LOC149134 5'  CCTCCTGTGGCTTCAGGTT   42439    _  CC_   CACG
                                CC CC   GGT    TTCAGGTT
                                || ||   |||    ||||||||
                                GG GG   CCG    AAGTCCAA
                                 A  ACA   _____
GAM1724  LOC151445 3'  CCTGATCACGCTCCCGTTC   42440    C         AG
                                CC GGTCACGTTC  GTTC
                                || ||||||||||  ||||
                                GG CTAGTGCGAG  CAAG
                                 A         GG
GAM1724  LOC151959 5'  CCTCCCTGCGTCCTCAGGTTC  42441    _   CG_   ACG
                                CC CCC   GTC   TTCAGGTTC
                                || |||   |||   |||||||||
                                GG GGG   CAG   GAGTCCAAG
                                 A   ACG   ____
GAM1724  LOC157556 3'  CCCTCAGGTCCATGCGGGTTC  42442     C _    A   TCA
                                CCC C GGTC CGT   GGTTC
                                ||| | |||| |||   |||||
                                GGG G CCAG GTA   CCAAG
                                  A T    _   CGC
GAM1724  LOC91286  3'  CCTCCCAGGTTCCCAGGTTC   42443    _     TCACG
                                CC CCCGG     TTCAGGTTC
                                || |||||     |||||||||
                                GG GGGTC     GGGTCCAAG
                                 A    CAA__
GAM1724  LOC93082  3'  CCTCCTGCTTCAAGTCCAGGTT 42444    C  GG__   C
              C                  CC CC    TCA GTTCAGGTTC
                                || ||    ||| ||||||||||
                                GG GG    AGT CAGGTCCAAG
                                 A  ACGA   T
GAM1724  LOC96597  3'  CCCGTCTTGCCCAGGTTC    42445     G  AC
                                CCCG TC  GTTCAGGTTC
                                |||| ||  ||||||||||
                                GGGC AG  CGGGTCCAAG
                                  _  AA
GAM1725  IL1R1    3'  AAATGGCTCAATACCTTTTATT 42448      TAT    __
                                AAATG   GTTCA  ACCTTTTATT
                                |||||   |||||  ||||||||||
                                TTTAC   CGAGT  TGGAAAATAA
                                   ____    TA
GAM1725  PROS1    3'  GGATGTATGTTCATTCTT    42449    A        AC
                                A ATGTATGTTCA  CTT
                                | ||||||||||  |||
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                                C TACATACAAGT  GAA
                                 C          AA
GAM1725  ROCK2    3'  TGTATGTATCAGTCTCTCA   42450       _  AC
                                TGTATGT TCA  CTTTTA
                                ||||||| |||  ||||||
                                ACATACA AGT  GAGAGT
                                    T  CA
GAM1725  TRPM8    3'  GTATGTTCAATACATTATT   42451         CCTT
                                GTATGTTCAA   TTATT
                                ||||||||||   |||||
                                CATACAAGTT   AATAA
                                      ATGT
GAM1725  KIAA1389 3'  AAATGTATGTTCATCTC    42452          AC
                                AAATGTATGTTCA  CTT
                                ||||||||||||  |||
                                TTTACATACAAGT  GAG
                                       A_
GAM1725  KIAA1726 3'  TGTATGTTTCTTTACTTTTATT 42453       _ AAC_
              A                  TGTATGTT C   CTTTTATTA
                                ||||||||  |   |||||||||
                                ACATACAA G   GAAAATAAT
                                    A AAAT
GAM1725  MGC17347 3'  ATGTATGCTTCAACACACTTAT 42454        _   CT_
              T                  ATGTATGTT CAAC   TTTATT
                                ||||||||| ||||  ||||||
                                TACATACGA GTTG   GAATAA
                                    A   TGT
GAM1725  PADI1    3'  AAATGCATGTCGACATTTTTAT 42455         CAACC
              T                  AAATGTATGTT    TTTTATT
                                ||||||||||    |||||||
                                TTTACGTACAG    AAAATAA
                                      CTGTA
GAM1725  SMAP1    3'  AAATGTATGTTTTGTCTTCATT 42456         CAACC
                                AAATGTATGTT    TTTTATT
                                ||||||||||    |||||||
                                TTTACATACAA    GAAGTAA
                                      AACA_
GAM1725  LOC149620 3'  GTAATGCTCAACCTTTTATT   42457    _
                                GTA TGTTCAACCTTTTATT
                                ||| ||||||||||||||||
                                CAT ACGAGTTGGAAAATAA
                                  T
GAM1726  ARG2     3'  TGTTAGGGATGTGGATAGAATA 42460         GTCTACA
                                TGTTAGGGATG      AGAATA
                                ||||||||||      ||||||
                                ACAATCCCTAC      TCTTAT
                                      ACCTA__
GAM1726  BET3     3'  TTAGGGATTTCACTCAAGAAT  42461       GGT_  A
                                TTAGGGAT   CT CAAGAAT
                                ||||||||   || |||||||
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                                AATCCCTA    GA GTTCTTA
                                    AAGT  _
GAM1726  DNAJA4    5'  TGGTAGGGACACGATAAGAATA 42462     T      __   CTAC
                                TG TAGGGAT  GGT    AAGAATA
                                || |||||||  |||    |||||||
                                AC ATCCCTG  CTA    TTCTTAT
                                 C      TG  _____
GAM1726  FLJ20160  3'  TGTTAGGAACCAAATAAGAATA 42463          GGTCTAC
                                TGTTAGGGAT      AAGAATA
                                ||||||||||      |||||||
                                ACAATCCTTG      TTCTTAT
                                      GTTTA__
GAM1726  KIAA0097  5'  TGTAGGGGTGGAACGAAGA   42464     T    A   TCT  _
                                TGT AGGG TGG   AC AAGA
                                ||| |||| |||   || ||||
                                ACA TCCC ACC   TG TTCT
                                  _    C   T__  C
GAM1726  MGC4766   5'  TGTAGGGACGGTGGGAAT    42465     T       CTACAA
                                TGT AGGGATGGT     GAAT
                                ||| |||||||||      ||||
                                ACA TCCCTGCCA     CTTA
                                  _        CC_____
GAM1726  NET-7     3'  GTTGGGGGAAGGGCAAGAATA  42466     A_    T  TCTA
                                GTT  GGGA GG    CAAGAATA
                                |||  |||| ||    ||||||||
                                CAA  CCCT CC    GTTCTTAT
                                  CC    T  C___
GAM1726  PALM      3'  GAGACGGTGTCTGTGAGAAT   42467        __   ACA
                                GGGATGG  TCT   AGAAT
                                |||||||  |||   |||||
                                CTCTGCC  AGA   TCTTA
                                    AC   CAC
GAM1726  PTPRT     3'  TGTCAGGGAACATTTACAAGAA 42468          TG  C
                TA                    TGTTAGGGA  GT TACAAGAATA
                                |||||||||  || ||||||||||
                                ACAGTCCCT  TA ATGTTCTTAT
                                      TG  A
GAM1726  SYT13     3'  TGTTAGGGATGGTCTCCCCAAG 42469             A__
                                TGTTAGGGATGGTCT   CAAG
                                ||||||||||||||   ||||
                                ACAATCCCTACCAGA   GTTC
                                         GGG
GAM1726  WAP1      3'  TGTTTGGAAAACTCTGCAAGAA 42470      A    TGG   A
                TA                    TGTT GGGA   TCT CAAGAATA
                                ||||  ||||   |||  ||||||||
                                ACAA CCTT   AGA GTTCTTAT
                                  A    TTG   C
GAM1726  LOC146315 5'  GTTAGGGAGCAAGGCTGCAGGA 42471         T___  T  A  A
                                GTTAGGGA    GG CT CA GA
                                ||||||||    || || || ||
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                                CAATCCCT   CC GA GT CT
                                    CGTT  _  C  C
GAM1727  CACNA1C   5'  TGTAAAACAATTGTACACC   42474          CTTAA
                                TGTAAAACAAT    ACACC
                                ||||||||||    |||||
                                ACATTTTGTTA    TGTGG
                                      ACA__
GAM1727  CYP4F3    3'  TGTGAATACAGGCACACACCAC 42475    _  A   ATCTTAA
             C                   TGT AA ACA      ACACCACC
                                 ||| || |||      ||||||||
                                 ACA TT TGT      TGTGGTGG
                                   C  A   CCGTG__
GAM1727  DR1      3'  TAAAATTTCATAAACACCA   42476      CAA  T
                                TAAAA   TC TAAACACCA
                                |||||   || |||||||||
                                ATTTT   AG ATTTGTGGT
                                   AA_  T
GAM1727  ERBB2IP   3'  TATAAAACAGATTGCAAGTACC 42477         _  CT   AC
             ACC                   TGTAAAACA AT  TAA  ACCACC
                                 |||||||||  ||  |||  ||||||
                                 ATATTTTGT TA  GTT  TGGTGG
                                       C  AC   CA
GAM1727  SCN8A     3'  TGTAAACAATCTTTCAC     42478       A      AA
                                TGTAAA CAATCTT  AC
                                ||||||  |||||||  ||
                                ACATTT GTTAGAA  TG
                                    _      AG
GAM1727  SIRT1     3'  TGAAAAACAATCTATTTTACC  42479    T        TAAAC
                                TG AAAACAATCT    ACC
                                ||  ||||||||||    |||
                                AC TTTTGTTAGA    TGG
                                  T        TAAAA
GAM1727  TEC      3'  TGTACAACAATCCCACCA    42480     A       TAAA
                                TGTA AACAATCT    CACCA
                                ||||  ||||||||   |||||
                                ACAT TTGTTAGG    GTGGT
                                   G       ____
GAM1727  TRHDE     3'  TGTAGAACAAAAACACCA    42481     A    TCTT
                                TGTA AACAA    AAACACCA
                                ||||  |||||   ||||||||
                                ACAT TTGTT    TTTGTGGT
                                   C    ____
GAM1727  C(27)-3BETA-HSD 3'  TGAAAAACAATGGGAACATCAC 42482    T      CTTA   C
             C                   TG AAAACAAT    AACA CACC
                                 || ||||||||    |||| ||||
                                 AC TTTTGTTA    TTGT GTGG
                                  T       CCC_    A
GAM1727  CDC10     3'  TGTAAACAATCAAACCAC    42483       A    TTAAAC
                                TGTAAA CAATC     ACCAC
                                ||||||  |||||     |||||
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                                ACATTT GTTAG     TGGTG
                                   _    TT____
GAM1727  DKFZP564L0864 3'  TAAGACAATCTTAAAGTACAC  42484     A         CAC
                                TAA ACAATCTTAAA   CAC
                                ||| ||||||||||   |||
                                ATT TGTTAGAATTT   GTG
                                  C         CAT
GAM1727  Dlc2     3'  TGCAAAACAGTCCCAGCAACGC 42485         A    __  A  A
            CGCC                   TGTAAAACA TCTTA  AAC CC CC
                                |||||||| |||||  ||| || ||
                                ACGTTTTGT AGGGT  TTG GG GG
                                     C    CG  C  C
GAM1727  FLJ23878  3'  TGCAACAGTTTAAACACCA   42486     AA   ATC
                                TGTA  ACA   TTAAACACCA
                                ||||  |||   ||||||||||
                                ACGT  TGT   AATTTGTGGT
                                  __   CA_
GAM1727  FYCO1    3'  TAAAATTTCCAAAACACCA   42487      CAA   T
                                TAAAA   TCT AAACACCA
                                |||||   ||| ||||||||
                                ATTTT   AGG TTTGTGGT
                                   AA_   T
GAM1727  KIAA0630  3'  TGTAAAATATTAAAACACCACC 42488        CAATCTT
                                TGTAAAA      AAACACCACC
                                |||||||      ||||||||||
                                ACATTTT      TTTGTGGTGG
                                     ATAAT__
GAM1727  MGC4172   3'  GTAAAACAATTAGGGACACCAC 42489          CTTAA
            C                    GTAAAACAAT    ACACCACC
                                ||||||||||    ||||||||
                                CATTTTGTTA    TGTGGTGG
                                      ATCCC
GAM1727  SEMA3C    3'  TATAAAACTAAACACC      42490         AATCT
                                TGTAAAAC    TAAACACC
                                ||||||||    ||||||||
                                ATATTTTG    ATTTGTGG
                                      _____
GAM1727  LOC145225 3'  TGGAAAACAATCTACTCCCACC 42491    T        TAAACA
                                TG AAAACAATCT     CCACC
                                || ||||||||||     |||||
                                AC TTTTGTTAGA     GGTGG
                                 C         TGAG__
GAM1727  LOC152687 5'  TGTAAAACGATCTGCCAC    42492        A   TAAACA
                                TGTAAAAC ATCT     CCAC
                                |||||||| ||||     ||||
                                ACATTTTG TAGA     GGTG
                                     C   C_____
GAM1727  LOC253782 3'  TGTTAAACAATCTTTTAATACC 42493     A        AAAC_
                                TGT AAACAATCTT    ACC
                                ||| ||||||||||    |||
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                                ACA TTTGTTAGAA    TGG
                                  A        AATTA
GAM1728 CD5     3' CCTGCCACTCGGGGCAGCAG  42496         CACTC  A
                                CCTGTCACTT    CA CAG
                                ||||||||||    || |||
                                GGACGGTGAG    GT GTC
                                     CCCC_  C
GAM1728 CTRL    3' CTGCCATTCATTCCAACAG   42497       C   C
                                CTGTCA TTCA TCCAACAG
                                |||||| |||| ||||||||
                                GACGGT AAGT AGGTTGTC
                                   _   A
GAM1728 CUL4B   3' CCTAACGGCTCCAACAG    42498     TC  TTCA
                                CCTG  AC   CTCCAACAG
                                ||||  ||   |||||||||
                                GGAT  TG   GAGGTTGTC
                                  __ CC__
GAM1728 IHPK1   3' CAACCTGTCACGTGCCAACAG 42499          TTCACT
                                TAACCTGTCAC    CCAACAG
                                ||||||||||     |||||||
                                GTTGGACAGTG    GGTTGTC
                                     CAC___
GAM1728 ITGA1   3' ACCTGTCATTTTCCAA     42500        C  CAC
                                ACCTGTCA TT   TCCAA
                                |||||||| ||   |||||
                                TGGACAGT AA   AGGTT
                                   A ___
GAM1728 MASP1   3' ACCTGGAATTACTCCAACAG  42501      TCACTTC
                                ACCTG      ACTCCAACAG
                                |||||      ||||||||||
                                TGGAC      TGAGGTTGTC
                                  CTTAA__
GAM1728 SLC1A3  3' TAACCTGCACTTTGCTCACAG 42502       T    CA   CA
                                TAACCTG CACTT  CTC  ACAG
                                ||||||| |||||  |||  ||||
                                ATTGGAC GTGAA  GAG  TGTC
                                   _    AC   __
GAM1728 TRPM8   3' CCTTGTCACCTCCTCTGACAG 42503     _      A   CA
                                CCT GTCACTTC CTC  ACAG
                                ||| |||||||| |||  ||||
                                GGA CAGTGGAG GAG  TGTC
                                  A       _   AC
GAM1728 WASF1   5' TGCAACTTTACTCCAACA    42504     C   C
                                TGT ACTT ACTCCAACA
                                ||| |||| |||||||||
                                ACG TGAA TGAGGTTGT
                                  T   A
GAM1728 ZNF217  5' ACTTGTCACTCACCCCTCTAAC 42505    C      T     ___
            AG                    AC TGTCACT CACTCC   AACAG
                                || ||||||| ||||||   |||||
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                                TG ACAGTGA GTGGGG   TTGTC
                                 A      _     AGA
GAM1728  CCR7     3'  GCCCCTTCACTCCAGCAG    42506     A        A
                                GTC CTTCACTCCA CAG
                                ||| |||||||||| |||
                                CGG GAAGTGAGGT GTC
                                  G         C
GAM1728  DKFZP564G202 3'  TAACCTGTACTTCAAATGACAG 42507         C     CTCCA
                                TAACCTGT ACTTCA     ACAG
                                |||||||| ||||||     ||||
                                ATTGGACA TGAAGT     TGTC
                                      _     TTAC_
GAM1728  FLJ22104  3'  TGTCACCTCTTTATTCTAACAG 42508          AC___  C
                                TGTCACTTC     TC AACAG
                                |||||||||     || |||||
                                ACAGTGGAG     AG TTGTC
                                      AAATA  A
GAM1728  FLJ22690  3'  CTGTTGAGCATCTCCAACAG   42509      CACTT  _
                                CTGT     CA CTCCAACAG
                                ||||     || |||||||||
                                GACA     GT GAGGTTGTC
                                   ACTC_  A
GAM1728  KIAA0648  3'  CTCTCAAACTTCACTCTAACAG 42510    G  __        C
                                CT TC  ACTTCACTC AACAG
                                || ||  ||||||||| |||||
                                GA AG  TGAAGTGAG TTGTC
                                 G  TT        A
GAM1728  TRIP-Br2  3'  TAACCTGCACTCAAC       42511         T    TCACTC
                                TAACCTG CACT      CAAC
                                ||||||| ||||      ||||
                                ATTGGAC GTGA      GTTG
                                      _   _______
GAM1728  LOC152765 5'  CCTGTTTCACTCCAGCAG    42512       CAC        A
                                CCTGT   TTCACTCCA CAG
                                |||||   ||||||||| |||
                                GGACA   AAGTGAGGT GTC
                                   ___         C
GAM1728  LOC158263 3'  CTTTCATTCCTCCCAACAG    42513    G   C   AC
                                CT TCA TTC  TCCAACAG
                                || ||| |||  ||||||||
                                GA AGT AAG  GGGTTGTC
                                 A   _   GA
GAM1728  LOC257476 3'  CAACCTGTCACGTGCCAACAG  42499           TTCACT
                                TAACCTGTCAC      CCAACAG
                                ||||||||||      |||||||
                                GTTGGACAGTG      GGTTGTC
                                      CAC___
GAM1729  SEPN1     3'  GTGGAGGATGGGACAGTGCT   42516     ATA  AC       A
                                GTG   GA  GGACGGTG CT
                                |||   ||  |||||||| ||
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                                CAC   CT  CCTGTCAC GA
                                  CTC  AC      _
GAM1729  LOC144100 5'  TTCGTGACAGGACTCTGTGTG  42517         A  GGACG
                                TTCGTGATAG AC    GTG
                                |||||||||| ||    |||
                                AAGCACTGTC TG    CAC
                                     C  AGACA
GAM1729  LOC219401 5'  TTCTTGATAGAATGGGGT    42518    G      C  AC
                                TTC TGATAGAA GG  GGT
                                ||| |||||||| ||  |||
                                AAG ACTATCTT CC  CCA
                                  A      A  __
GAM1730  HGF      3'  GATGCCAGCACATATCT     42521     ACG   AA
                                GATG   CGG  CACATATCT
                                ||||   |||  |||||||||
                                CTAC   GTC  GTGTATAGA
                                  G__   __
GAM1730  GPR105   3'  GATGAGGGCACATATCT     42522     CGC  AA
                                GATGA   GG  CACATATCT
                                |||||   ||  |||||||||
                                CTACT   CC  GTGTATAGA
                                   ____  C_
GAM1730  UNC5D    3'  TAGATAACTAGATCAACACGTG 42523        GC  ___   ATA
           TCTC                   TAGATGAC  GGA   ACAC   TCTC
                                |||||||  |||   ||||   ||||
                                ATCTATTG  TCT   TGTG   AGAG
                                     A_   AGT    CAC
GAM1730  LOC150166 3'  TAGGGACGCGGAGTGATCT   42524     AT      ACACAT
                                TAG  GACGCGGA     ATCT
                                |||  ||||||||     ||||
                                ATC  CTGCGCCT     TAGA
                                  C_       CAC___
GAM1730  LOC163782 3'  GAGACGCGGAACCACTCT    42525    T        A   A
                                GA GACGCGGAAC CAT TCT
                                || |||||||||| ||| |||
                                CT CTGCGCCTTG GTG AGA
                                  _        _  _
GAM1730  LOC220963 3'  TAGTGGGCTTCACACATATCT  42526     A  AC  GGA
                                TAG TG  GC   ACACATATCT
                                ||| ||  ||   ||||||||||
                                ATC AC  CG   TGTGTATAGA
                                  _  C_  AAG
GAM1731  C20orf45  3'  TGTTCTTCTGTTTAAGTTAGA  42529       AAAT
                                TGTTTT    TTTAAGTTAGA
                                ||||||    ||||||||||
                                ACAAGA    AAATTCAATCT
                                   AGAC
GAM1731  R3HDM    3'  TTCCCCCAAATTTTAAGTT    42530    G
                                TT TTTTAAATTTTAAGTT
                                || ||||||||||||||||
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                                AA GGGGTTTAAAATTCAA
                                 G
GAM1731 LOC129450 3'  TACTGTTTTTAAGTCATTTTAA 42531        AA____       A
             GTTGGA                 ATTGTTTT     ATTTTAAGTT GA
                                ||||||||     |||||||||| ||
                                TGACAAAA     TAAAATTCAA CT
                                    ATTCAG        C
GAM1731 LOC90355  3'  GTTCCAGGTGAATTTTAAGTTA 42532      ____
             GA                   GTTTTA   AATTTTAAGTTAGA
                                ||||||   ||||||||||||||
                                CAAGGT   TTAAAATTCAATCT
                                   CCAC
GAM1732 ALPI    3'  CAGGTGCAGGGGTGTGGAA   42535       CGCT   C_
                                TAGGTGC   GGGTG  GAA
                                |||||||   |||||  |||
                                GTCCACG   CCCAC  CTT
                                    TC__    AC
GAM1732 KLF8    5'  GGTTCGCTGGGCCGAA     42536    GC      G
                                GGT  CGCTGGGT CGAA
                                |||  |||||||| ||||
                                CCA  GCGACCCG GCTT
                                 A_      _
GAM1732 LTB4R   5'  TAGGTGCTGTTTGCTAAAT   42537       CGC  GG   G
                                TAGGTGC   TG  TGC AAAT
                                |||||||   ||  ||| ||||
                                ATCCACG   AC  ACG TTTA
                                   ___  AA   A
GAM1732 ZNF266   3'  TAGGGTTGCTGTACAAAAT   42538     TGCC   GG
                                TAGG   GCT  GTGCGAAAT
                                ||||   |||  |||||||||
                                ATCC   CGA  CATGTTTTA
                                  CAA_  __
GAM1732 ARL8    5'  CAGGTGCCGCTGCGCCG     42539          G  G
                                TAGGTGCCGCTG GT CG
                                |||||||||||| || ||
                                GTCCACGGCGAC CG GC
                                       G  _
GAM1732 FLJ23191  5'  GGTGTGGTGTGCGAAA     42540     CCGC  _
                                GGTG   TGG GTGCGAAA
                                ||||   ||| ||||||||
                                CCAC   ACC CACGCTTT
                                  ____  A
GAM1732 HSPBP1   5'  GGCGCCGCCATCTGGCGGGA  42541         ___   C
                                GGTGCCGCTG  GGTG GA
                                ||||||||||  |||| ||
                                CCGCGGCGGT  CCGC CT
                                      AGA   C
GAM1732 IL1F10   3'  GGTGTCACTGAGCTGAAAT   42542     C      GC
                                GGTG CGCTGGGT  GAAAT
                                |||| ||||||||  |||||
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                                CCAC GTGACTCG  CTTTA
                                  A       A_
GAM1732  NAV1     5'  CAGGTGTCGCAGGCGGGA    42543       C   T    C
                                TAGGTG CGC GGGTG GA
                                |||||| ||| ||||| ||
                                GTCCAC GCG TCCGC CT
                                   A   _    C
GAM1732  PI4KII   3'  AGGTGCCAGAATTGTGAAAT   42544        CTGGG  C
                                AGGTGCCG    TG GAAAT
                                ||||||||    || |||||
                                TCCACGGT    AC CTTTA
                                     CTTA_  A
GAM1732  PLA2G3   3'  TAGGTGTCGCAGGGGGGAA   42545       C   T   TGC
                                TAGGTG CGC GGG   GAA
                                |||||| ||| |||   |||
                                ATCCAC GCG CCC   CTT
                                   A   T   CC_
GAM1732  RA-GEF-2 3'  TAGGTCCGCTAAAGAAA     42546      G       TGC
                                TAGGT CCGCTGGG   GAAA
                                ||||| ||||||||   ||||
                                ATCCA GGCGATTT   CTTT
                                  _      ____
GAM1732  RAB22A   3'  TACGCAAGACTGGGTGCGA   42547    G   CC
                                TA GTG  GCTGGGTGCGA
                                || |||  ||||||||||
                                AT CGT  TGACCCACGCT
                                 G   TC
GAM1732  LOC145540 5'  TAGGTGCTGGATGCG       42548       CGC
                                TAGGTGC   TGGGTGCG
                                |||||||   ||||||||
                                ATCCACG   ACCTACGC
                                   ____
GAM1732  LOC145622 3'  TAGAGTGCTGGCACAGTGGAA  42549     _   C_  TG   C
                                TAG GTGC  GC  GGTG GAA
                                ||| ||||  ||  |||| |||
                                ATC CACG  CG  TCAC CTT
                                  T   AC  TG   _
GAM1732  LOC152283 3'  AGGTGCCGCTGGATGGAA    42550            C
                                AGGTGCCGCTGGGTG GAA
                                |||||||||||||| |||
                                TCCACGGCGACCTAC CTT
                                      _
GAM1732  LOC220963 3'  TAGGTGCCTTGCAGTGGA    42551        GC  _   C
                                TAGGTGCC  TG GGTG GA
                                ||||||||  || |||| ||
                                ATCCACGG  AC TCAC CT
                                     A_  G   _
GAM1732  LOC253866 3'  TAGGTGCCAGGTGGA       42552        GCT    C
                                TAGGTGCC   GGGTG GA
                                ||||||||   ||||| ||
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                                ATCCACGG   TCCAC CT
                                   ___    _
GAM1732 LOC91266 5' TAGGTGCCGCTCGGGTGCA   42553          _
                                TAGGTGCCGCT GGGTGCG
                                |||||||||| |||||||
                                ATCCACGGCGA CCCACGT
                                      G
GAM1733 DDA3     3' CAGAGTCCAGTAGAGAATGCG 42556      A   TA
                                CAGAGT TCA  TAGAGAATGCG
                                |||||| |||  ||||||||||
                                GTCTCA GGT  ATCTCTTACGC
                                   _  C_
GAM1733 MGC35558 3' GCAAAGGCCATGGAGAATGCG 42557      TA   ATA
                                GCAGAG  TCAT   GAGAATGCG
                                ||||||  ||||   |||||||||
                                CGTTTC  GGTA   CTCTTACGC
                                   C_   C__
GAM1733 LOC150067 3' ACAGAGTATGAGAATG     42558        CATATA
                                GCAGAGTAT     GAGAATG
                                |||||||||     |||||||
                                TGTCTCATA     CTCTTAC
                                   _______
GAM1733 LOC154094 3' ACAGAGTATGAGAATG     42558        CATATA
                                GCAGAGTAT     GAGAATG
                                |||||||||     |||||||
                                TGTCTCATA     CTCTTAC
                                   _______
GAM1733 LOC51072  3' ACAGAGTATGAGAATG     42558        CATATA
                                GCAGAGTAT     GAGAATG
                                |||||||||     |||||||
                                TGTCTCATA     CTCTTAC
                                   _______
GAM1734 HPS4     3' TGACTATAACGTAATAGAACTG 42561          ______     III
             C                   TGATTATGAT    AGAACTG   C
                                ||||||||||    |||||||  |
                                ACTGATATTG    TCTTGAC   G
                                      CATTA      III
GAM1734 TIMP3    5' TGATATATGATAGAAGACTG   42562     _      __
                                TGAT TATGATAGA  ACTG
                                |||| |||||||||  ||||
                                ACTA ATACTATCT  TGAC
                                   T        TC
GAM1734 KIAA1674 3' TGATCATAGCTAGAACTG    42563        A_
                                TGATTATG  TAGAACTG
                                ||||||||  ||||||||
                                ACTAGTAT  ATCTTGAC
                                     CG
GAM1734 SLC26A7  3' TGATTTTAATGTCAGAACTG  42564      ___  A
                                TGATT   ATG TAGAACTG
                                |||||   ||| ||||||||
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                                ACTAA   TAC GTCTTGAC
                                  AAT   A
GAM1734  LOC162333 5'  TGATCATGTGGCAAAACTG   42565        A__
                                TGATTATG   TAGAACTG
                                ||||||||   ||||||||
                                ACTAGTAC   GTTTTGAC
                                    ACC
GAM1735  HNRPF     3'  TACTTAAACTACTTAAACTTA  42568     G          T
                                TAC TAAACTACTTAA CTTA
                                ||| |||||||||||| ||||
                                ATG ATTTGATGAATT GAAT
                                  A          T
GAM1735  TJP1      5'  CGTTAGACCTGCATCTTAGCA  42569     AAACT    A_
                                CGT    ACTT  ATCTTAGCA
                                |||    ||||  |||||||||
                                GCA    TGGA  TAGAATCGT
                                  ATC__    CG
GAM1735  DKFZp434A2417 3'  GTATACTACTTATAACCTAG   42570     A       AT_
                                GTA ACTACTTA   CTTAG
                                ||| ||||||||   |||||
                                CAT TGATGAAT   GGATC
                                  A       ATT
GAM1735  KIAA1718  3'  GTAAGCTACTTAAAGACTTA   42571      A       T__
                                GTAA CTACTTAA   CTTA
                                |||| ||||||||   ||||
                                CATT GATGAATT   GAAT
                                  C       TCT
GAM1735  PDE8A     3'  GTAACCATGATCTTAGC     42572      A   CTTA
                                GTAA CTA    ATCTTAGC
                                |||| |||    ||||||||
                                CATT GGT    TAGAATCG
                                  _   AC__
GAM1735  LOC162333 5'  GTTGAACTACTTGATCTGCA   42573    A_       A    TA
                                GT  AACTACTT ATCT  GCA
                                ||  |||||||| ||||  |||
                                CA  TTGATGAA TAGA  CGT
                                 AC       C   __
GAM1736  CAPS      3'  GGGGACCCGCAAGGGA      42577        T    TTGT
                                GGGGACC CGCGA    GGGA
                                ||||||| |||||    ||||
                                CCCCTGG GCGTT    CCCT
                                    _    _____
GAM1736  CAPS      3'  GGGGACCTCGGCGGG       42576          CGATT
                                GGGGACCTCG    GTGGG
                                ||||||||||    |||||
                                CCCCTGGAGC    CGCCC
                                     ______
GAM1736  CDK5R2    5'  GGGGACCCGGCGGTGGG     42578         C   ATT
                                GGGGACCT GCG   GTGGG
                                |||||||| |||   |||||
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                                CCCCTGGG CGC   CACCC
                                     C  ___
GAM1736 DNMT3L   5' GGGGACCTCAGTGGG      42579         CGATT
                                GGGGACCTCG    GTGGG
                                ||||||||||    |||||
                                CCCCTGGAGT    CACCC
                                      _____
GAM1736 DVL1     3' CAGGGGGCCTGTGCACCGCAGG 42580      A  C_ G   TG
                                CAGGGG CCT  GC ATTG  GG
                                |||||| |||  || ||||  ||
                                GTCCCC GGA  CG TGGC  CC
                                   C  CA _   GT
GAM1736 FOXE3    3' GGGGGGCAAACTTGTGGGAA  42581     ACCTC   __
                                GGGG    GCGA  TTGTGGGAA
                                ||||    ||||  |||||||||
                                CCCC    CGTT  AACACCCTT
                                  C____   TG
GAM1736 MMP25    3' AGGGGGGCCTTGTGGGA     42582      ACCTC  GA
                                AGGGG    GC  TTGTGGGA
                                |||||    ||  ||||||||
                                TCCCC    CG  AACACCCT
                                  C____  G_
GAM1736 PIK3R2   3' GGGGACCTGCGGTGGG      42583        C   ATT
                                GGGGACCT GCG   GTGGG
                                |||||||| |||   |||||
                                CCCCTGGA CGC   CACCC
                                     _  ___
GAM1736 PPP1R3D  3' CAGGGGACCTTGCAGCAGAA  42584         C   ATT TG
                                CAGGGGACCT GCG   G  GGA
                                |||||||||| |||   |  |||
                                GTCCCCTGGA CGT   C  CTT
                                      A  ___ GT
GAM1736 RUNX1    3' GGGGATTCCTTGTGGGA     42585      __  CGCGAT
                                GGGGA  CCT     TGTGGGA
                                |||||  |||     |||||||
                                CCCCT  GGA     ACACCCT
                                  AA  _______
GAM1736 BRPF3    3' TGAGGGACCTTGGGTGGGA   42586   A      CGCGATT
                                C GGGGACCT      GTGGGA
                                | ||||||||      ||||||
                                A TCCCTGGA      CACCCT
                                 C       ACC____
GAM1736 C22orf4  3' AGGGGACCTCGCGGCACAGAG  42587          ATTGT
                                AGGGGACCTCGCG    GGG
                                ||||||||||||    |||
                                TCCCCTGGAGCGC    CTC
                                      CGTGT
GAM1736 C5orf4   5' AGGGACCCATTGTGGG      42588        CGCG
                                GGGGACCT   ATTGTGGG
                                ||||||||   ||||||||
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                              TCCCTGGG   TAACACCC
                                  ____
GAM1736 C5orf4   3' AGGGACCCATTGTGGG     42588       CGCG
                              GGGGACCT   ATTGTGGG
                              ||||||||   ||||||||
                              TCCCTGGG   TAACACCC
                                  ____
GAM1736 CUL4A    5' GGGGAGACTTTGTGAGA    42589     CCTC  GA
                              GGGGA   GC  TTGTGGGA
                              |||||   ||  ||||||||
                              CCCCT   TG  AACACTCT
                                 C___  A_
GAM1736 FLJ12122 3' GGGTGGCCCCATTGTGGG   42590    GA_   GCG
                              GGG   CCTC   ATTGTGGG
                              |||   ||||   ||||||||
                              CCC   GGGG   TAACACCC
                                ACC   ___
GAM1736 FLJ13881 3' CAGGGGACCCAGGTGGG    42591        CGCGATT
                              CAGGGGACCT     GTGGG
                              ||||||||||     |||||
                              GTCCCCTGGG     CACCC
                                   TC_____
GAM1736 FLJ22246 5' CAGGGGACCTGGAGAATGGGGA 42592         CGC  T  T
                              CAGGGGACCT   GA TG GGGA
                              ||||||||||   || || ||||
                              GTCCCCTGGA   CT AC CCCT
                                   CCT  T  _
GAM1736 GOLGA3   3' CAGGGAACTAGAACTCGGTTGT 42593       _____   CGA
           GGGAA                GGGGAC    CTCG   TTGTGGGAA
                              ||||||    ||||  |||||||||
                              CCCTTG    GAGC   AACACCCTT
                                 ATCTT   C__
GAM1736 MGC20983 3' GGGGAGATTTACTGTGGGAA  42594     CCTCGCG
                              GGGGA     ATTGTGGGAA
                              |||||     ||||||||||
                              CCCCT     TGACACCCTT
                                 CTAAA__
GAM1736 MGC4734  5' GGGGAGGCCTCGCGGGA    42595     __    GATTGT
                              GGGGA  CCTCGC    GGGA
                              |||||  ||||||    ||||
                              CCCCT  GGAGCG    CCCT
                                 CC    _______
GAM1736 PIPPIN   5' GGGGACCTCAGCCAAGGGA   42596       _ GATTGT
                              GGGGACCTC GC    GGGA
                              |||||||||  ||    ||||
                              CCCCTGGAG CG    CCCT
                                   T  GTT___
GAM1736 PRKWNK2  3' CAGGTGACCTTGCGGTAG   42597     G   C  ATT
                              CAGG GACCT GCG  GTGG
                              ||||  ||||| |||  ||||
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                                GTCC CTGGA CGC   CATC
                                  A    A  ___
GAM1736  SDC3     5'  CAGGGAACTTTGCGAATAGA  42598        CTC   TT
                                CAGGGGAC  GCGA  GTGGG
                                ||||||||  ||||  |||||
                                GTCCCTTG  CGCT  TATCT
                                    AAA   __
GAM1736  LOC126122 3'  CAGGTGGCCTCGTGGGA    42599     _ A   GCGATT
                                CAGG GG CCTC    GTGGGA
                                |||| || ||||    ||||||
                                GTCC CC GGAG    CACCCT
                                  A _   _______
GAM1736  LOC126917 3'  CAGGGGACCCGTGGG      42600         CGCGATT
                                CAGGGGACCT     GTGGG
                                ||||||||||     |||||
                                GTCCCCTGGG     CACCC
                                               ________
GAM1736  LOC154790 3'  CAGGGGACCTCTGGGGCCCGGG 42601          GCGA__  T
              G                  CAGGGGACCTC     TTG GGG
                                 ||||||||||     ||| |||
                                 GTCCCCTGGAG    GGC CCC
                                      ACCCCG  _
GAM1736  LOC256211 5'  GGGGGTCTCTTGTGGAA    42602     AC   GCGA
                                GGGG  CTC   TTGTGGGA
                                ||||  |||   ||||||||
                                CCCC  GAG   AACACCTT
                                  CA  _____
GAM1736  LOC256405 5'  CAGTGGGCCTCTGTGGGA   42603    _  A   GCGAT
                                CAG GGG CCTC    TGTGGGA
                                ||| ||| ||||    |||||||
                                GTC CCC GGAG    ACACCCT
                                  A  _   ______
GAM1736  LOC257426 3'  GGGGACCTCAGCCAAGGGA   42596        _ GATTGT
                                GGGGACCTC GC    GGGA
                                |||||||| ||    ||||
                                CCCCTGGAG CG    CCCT
                                     T  GTT___
GAM1736  LOC85414  3'  CAGGGGACCTGATTGTTGGG  42604        CGC    _
                                CAGGGGACCT  GATTGT GGG
                                ||||||||||  |||||| |||
                                GTCCCCTGGA  CTAACA CCC
                                     ___    A
GAM1736  LOC91397  5'  AGGGAACCTTGCTTAGGGTGGG 42605        C  GATT_
                                AGGGGACCT GC    GTGGG
                                ||||||||| ||    |||||
                                TCCCTTGGA CG    CACCC
                                     A  AATCC
GAM1737  CBLB     3'  TGCCTTTAAATTCTGA     42608         GGATT
                                TGTCTTTAAG    TTCTGA
                                ||||||||||    ||||||
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                              ACGGAAATTT    AAGACT
                                    _____
GAM1737 CNGB3    3' CTGCTGGGGATTTTTTGA    42609    T TTAA      C
                              CTG CT   GGGATTTT TGA
                              ||| ||   |||||||| |||
                              GAC GA   CCCTAAAA ACT
                                _ C___      A
GAM1737 NR4A2    3' TGTCAGGATTTTCTGA     42610     TTTAA
                              TGTC    GGGATTTTCTGA
                              ||||    ||||||||||||
                              ACAG    TCCTAAAAGACT
                                   _____
GAM1737 PTPN18   3' TCTGTCTTTTGGGGGCTCTG  42611        AA  ATT
                              TCTGTCTTT  GGG  TTCTG
                              |||||||||  |||  |||||
                              AGACAGAAA  CCC  GAGAC
                                    AC  C__
GAM1737 PTPN7    5' TCTGTCTTTGAGGGCTGA    42612        A   ATTTT
                              TCTGTCTTT AGGG    CTGA
                              ||||||||| ||||    ||||
                              AGACAGAAA TCCC    GACT
                                    C  _____
GAM1737 PTPN7    5' TCTGTCTTTGAGGGCTGA    42612        A   ATTTT
                              TCTGTCTTT AGGG    CTGA
                              ||||||||| ||||    ||||
                              AGACAGAAA TCCC    GACT
                                    C  _____
GAM1737 STK38    3' TCTGTCTTAGGGATTTTCTG  42613       TA
                              TCTGTCTT  AGGGATTTTCTG
                              ||||||||  ||||||||||||
                              AGACAGAA  TCCCTAAAAGAC
                                    __
GAM1737 TMPRSS4  3' TCTGACTTTGGGGGATCCCC  42614     T   AA    TT
                              TCTG CTTT  GGGATT  C
                              |||| ||||  ||||||  |
                              AGAC GAAA  CCCTAG  G
                                T   CC     GG
GAM1737 YES1     3' TCTTTGAGCAATTCTGAC    42615      AA  ATT
                              TCTTT  GGG  TTCTGAC
                              |||||  |||  |||||||
                              AGAAA  CTC  AAGACTG
                                __  GTT
GAM1737 DKFZp434G179 3'  TCTGTCTTCAAGGTGGGACTGA 42616          GATTTT
          C                    TCTGTCTTTAAGG     CTGAC
                              ||||||||||||     |||||
                              AGACAGAAGTTCC     GACTG
                                     ACCCT_
GAM1737 FLJ12587 3' TCTGTCTTGGTCACCTTTCTG 42617       TAA  GA__
                              TCTGTCTT   GG   TTTTCTG
                              ||||||||   ||   |||||||
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                                AGACAGAA  CC   GAAAGAC
                                    ___ AGTG
GAM1737 FLJ13881 3' TCTGTGTTTAGGGGTCATCCT 42618     C   A  ATT
                                TCTGT TTTA GGG  TTCT
                                ||||| |||| |||  ||||
                                AGACA AAAT CCC  AGGA
                                   C   C  AGT
GAM1737 FLJ22969 3' TCTTCTTTAGGATTTCTG   42619    G   AA    T
                                TCT TCTTT  GGGATTT CTG
                                ||| |||||  ||||||| |||
                                AGA AGAAA  TCCTAAA GAC
                                  _   __    _
GAM1737 KIAA0555 3' TCTTCTTCCATATTTTCTGAC 42620    G   AAGGG
                                TCT TCTTT    ATTTTCTGAC
                                ||| |||||    ||||||||||
                                AGA AGAAG    TAAAAGACTG
                                  _    GTA__
GAM1737 KIAA1712 3' TCTTGAGGATTTTCTGA    42621     TAA
                                TCTT  GGGATTTTCTGA
                                ||||  ||||||||||||
                                AGAA  TCCTAAAAGACT
                                  C__
GAM1737 LGI4    5' TCTGTCTCTGTATTTTTGA   42622       AAGGG   C
                                TCTGTCTTT    ATTTT TGA
                                |||||||||    ||||| |||
                                AGACAGAGA    TAAAA ACT
                                     CA___   _
GAM1737 MGC2454  3' CCTGTCTTTGGGGGAATTT   42623       AA   T
                                TCTGTCTTT  GGGA TTT
                                |||||||||  |||| |||
                                GGACAGAAA  CCCT AAA
                                     CC   T
GAM1737 MP1     5' TCTGTCTATGAGGCTTCTGAC 42624      TTA  GAT
                                TCTGTCT  AGG  TTTCTGAC
                                |||||||  |||  ||||||||
                                AGACAGA  TCC  GAAGACTG
                                    TAC  ___
GAM1737 UPB1    3' TCTGTTCTTTAGGCCTTCTGAC 42625     _   AA  A
                                TCTGT CTTT  GGG TTTTCTGAC
                                ||||| ||||  ||| |||||||||
                                AGACA GAAA  TCC GGAAGACTG
                                   A   __  _
GAM1737 ZBRK1   5' TCTGTCTTTGTATCTTCTG   42626       AAGGG
                                TCTGTCTTT    ATTTTCTG
                                |||||||||    ||||||||
                                AGACAGAAA    TAGAAGAC
                                     CA___
GAM1737 ZNF31   5' CCTGTCTTTAAGGGCCTG    42627          ATTT
                                TCTGTCTTTAAGGG   TCTG
                                ||||||||||||||   ||||
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                                GGACAGAAATTCCC  GGAC
                                     ____
GAM1737  LOC116211 3'  TATCTTTAATGTTTTCTGA  42628       GGGA
                                TGTCTTTAA  TTTTCTGA
                                |||||||||  ||||||||
                                ATAGAAATT  AAAAGACT
                                    AC__
GAM1737  LOC129446 3'  TCTTTATGATTTTCTG    42629      AGG
                                TCTTTA  GATTTTCTG
                                ||||||  |||||||||
                                AGAAAT  CTAAAAGAC
                                   A__
GAM1737  LOC142954 3'  TCTGTCTACTTTATTTTCTG  42630      TTAAGGG
                                TCTGTCT     ATTTTCTG
                                |||||||     ||||||||
                                AGACAGA     TAAAAGAC
                                    TGAAA__
GAM1737  LOC143188 5'  TCTGTTTTCAATACTTTCTG  42631     C    GGG
                                TCTGT TTTAA  ATTTTCTG
                                ||||| |||||  ||||||||
                                AGACA AAGTT  TGAAAGAC
                                  A    A__
GAM1737  LOC149465 3'  TCTGTCTTTGTGATTCTGA  42632       AAGG  TT
                                TCTGTCTTT   GAT  TCTGA
                                |||||||||   |||  |||||
                                AGACAGAAA   CTA  AGACT
                                    CA__  __
GAM1737  LOC150113 5'  TGTCTTTTGGTTTTCTGAC  42633      AAG  A
                                TGTCTTT  GG TTTTCTGAC
                                |||||||  || |||||||||
                                ACAGAAA  CC AAAAGACTG
                                   A__  _
GAM1737  LOC161443 5'  CCTGTCTTTGGATTTTTGA  42634       AAG     C
                                TCTGTCTTT  GGATTTT TGA
                                |||||||||  ||||||| |||
                                GGACAGAAA  CCTAAAA ACT
                                    ___     _
GAM1737  LOC221035 3'  TCTGTCTTGGGATATTTGA  42635       TAA    TTTC
                                TCTGTCTT  GGGAT   TGA
                                ||||||||  |||||   |||
                                AGACAGAA  CCCTA   ACT
                                    ___    TAA_
GAM1737  LOC253613 3'  TCTGTTTTTAAGGGGAATGAC  42636     C      ATTTTC
                                TCTGT TTTAAGGG     TGAC
                                ||||| ||||||||     ||||
                                AGACA AAATTCCC     ACTG
                                  A       CTT___
GAM1737  LOC257017 5'  TCTGCTTTAAAAAATTCTGA  42637     T        TT
                                TCTG CTTTAAGGGAT  TCTGA
                                |||| ||||||||||  |||||
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                                AGAC GAAATTTTTTA  AGACT
                                  _       __
GAM1737 LOC51277 3' TCTGTCTTGGGGCCTG     42638       TAA  ATTT
                                TCTGTCTT  GGG   TCTG
                                ||||||||  |||   ||||
                                AGACAGAA  CCC   GGAC
                                    C__  _____
GAM1737 LOC55924 3' TGTCAGAGGGATTTTCTGA   42639     TTTA
                                TGTC   AGGGATTTTCTGA
                                ||||   ||||||||||||
                                ACAG   TCCCTAAAAGACT
                                  TC__
GAM1737 LOC91145 3' TGCTAGAAGATTTTCTGAC   42640    CTT  AG
                                TGT  TA  GGATTTTCTGAC
                                |||  ||  ||||||||||||
                                ACG  AT  TCTAAAAGACTG
                                 ___ CT
GAM1738 EDAR     3' TATGATCTCATTGTTCTGAATC 42643         _____  C
                                TATGATCTCA   TCT GATC
                                ||||||||||   ||| ||||
                                ATACTAGAGT   AGA TTAG
                                     AACA  C
GAM1738 RAB7L1   3' TGATCTCATTTTCCTCTCAAT  42644        CTCGA
                                TGATCTCAT    TCTCAAT
                                |||||||||    |||||||
                                ACTAGAGTA    AGAGTTA
                                     AAAGG
GAM1738 FPGT     3' TATGATTATTGATGAATCTCAA 42645      CTCATCTC
             T                   TATGAT       GATCTCAAT
                                 ||||||       |||||||||
                                 ATACTA       TTAGAGTTA
                                    ATAACTAC
GAM1738 LOC200014 5' GATCTCATCCTCATTGATC   42646       _ ___
                                GATCTCATC TC   GATC
                                ||||||||| ||   ||||
                                CTAGAGTAG AG   CTAG
                                     G  TAA
GAM1738 LOC254778 5' TATGAGCTCATCTCGTTCC   42647      T       A
                                TATGA CTCATCTCG TCT
                                ||||| ||||||||| |||
                                ATACT GAGTAGAGC AGG
                                   C       A
GAM1738 LOC255565 3' TATGATCTTATGCAAGTTACTC 42648       CATCTCGAT__
             AATC                  TATGATCT         CTCAATC
                                   ||||||||         |||||||
                                   ATACTAGA         GAGTTAG
                                      ATACGTTCAAT
GAM1738 LOC90010  3' TATGATCTTATGCAAGTTACTC 42648       CATCTCGAT__
             AATC                  TATGATCT         CTCAATC
                                   ||||||||         |||||||
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                                ATACTAGA        GAGTTAG
                                    ATACGTTCAAT
GAM1739 ABL1    3' CGCGAGGTGCCCAGTGGCAG  42651   GA      ___
                                CG AGGTGCCCA  GCAG
                                || |||||||||  ||||
                                GC TCCACGGGT  CGTC
                                 GC       CAC
GAM1739 ABL1    3' CGCGAGGTGCCCAGTGGCAG  42651   GA      ___
                                CG AGGTGCCCA  GCAG
                                || |||||||||  ||||
                                GC TCCACGGGT  CGTC
                                 GC       CAC
GAM1739 EPAC    5' CGGAAGGTGCCAGTGGG    42652         C  CA
                                CGGAAGGTGCC AG  GG
                                |||||||||| ||  ||
                                GCCTTCCACGG TC  CC
                                      _ AC
GAM1739 MDM2    5' CGAAAGCAGCAGGATCTCG   42653      GTGCC
                                CGGAAG   CAGCAGGATCTCG
                                ||||||   ||||||||||||
                                GCTTTC   GTCGTCCTAGAGC
                                  _____
GAM1739 MDM2    5' CGAAAGCAGCAGGATCTCG   42653      GTGCC
                                CGGAAG   CAGCAGGATCTCG
                                ||||||   ||||||||||||
                                GCTTTC   GTCGTCCTAGAGC
                                  _____
GAM1739 MDM2    5' CGAAAGCAGCAGGATCTCG   42653      GTGCC
                                CGGAAG   CAGCAGGATCTCG
                                ||||||   ||||||||||||
                                GCTTTC   GTCGTCCTAGAGC
                                  _____
GAM1739 MDM2    5' CGAAAGCAGCAGGATCTCG   42653      GTGCC
                                CGGAAG   CAGCAGGATCTCG
                                ||||||   ||||||||||||
                                GCTTTC   GTCGTCCTAGAGC
                                  _____
GAM1739 MDM2    5' CGAAAGCAGCAGGATCTCG   42653      GTGCC
                                CGGAAG   CAGCAGGATCTCG
                                ||||||   ||||||||||||
                                GCTTTC   GTCGTCCTAGAGC
                                  _____
GAM1739 PCDH12  5' GAGGGTGCCCATGGTCT    42654   A     GCA  A
                                GA GGTGCCCA  GG TCT
                                || ||||||||  || |||
                                CT CCACGGGT  CC AGA
                                 C      A__  _
GAM1739 SHMT2   3' GGTGCAGCAGGATTTCG    42655     CC      C
                                GGTGC  AGCAGGAT TCG
                                |||||  |||||||| |||
```

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                                CCACG  TCGTCCTA AGC
                                  __       A
GAM1739 CAMKK2   3' GGAAGGTGCCATGGTTTCC   42656         CAGCA  A_
                                GGAAGGTGCC    GG  TCT
                                ||||||||||    ||  |||
                                CCTTCCACGG    CC  AGG
                                    TA___  AA
GAM1739 DD96     3' GGGAGGTGCTCAGCTGAC    42657    A     C    AG
                                GG AGGTGC CAGC  GAT
                                || |||||| ||||  |||
                                CC TCCACG GTCG  CTG
                                 C     A   A_
GAM1739 DKFZp434E169 3'  GGCGTGCAGTGGCGGGATCTCG 42658    AAG    CCA_  A
                                GG   GTGC    GC GGATCTCG
                                ||   ||||    || ||||||||
                                CC   CACG    CG CCTAGAGC
                                 G__    TCAC  C
GAM1739 FLJ10803 3'  GGAGTGCAGTGGCAGGATCT   42659     AG    CCA_
                                GGA  GTGC    GCAGGATCT
                                |||  ||||    |||||||||
                                CCT  CACG    CGTCCTAGA
                                  __    TCAC
GAM1739 FLJ13265 3'  GAGGGTGCCCAGTTCCTCG    42660    A       CAGGA
                                GA GGTGCCCAG     TCTCG
                                || |||||||||     |||||
                                CT CCACGGGTC     GGAGC
                                 C        AA___
GAM1739 FLJ13621 3'  GGAGTGCAGTGGCGGGATCTCG 42661     AG    CCA_  A
                                GGA  GTGC    GC GGATCTCG
                                |||  ||||    || ||||||||
                                CCT  CACG    CG CCTAGAGC
                                  __    TCAC  C
GAM1739 FLJ20034 3'  GGAAGGTGCTCAACCTTCTCG  42662         C    AGGA
                                GGAAGGTGC CAGC    TCTCG
                                ||||||||| ||||    |||||
                                CCTTCCACG GTTG    AGAGC
                                     A    GA__
GAM1739 FLJ22969 3'  GGAAAGTGTTCAAGAGGTCT   42663        CC   C   A
                                GGAAGGTG  CAG AGG TCT
                                ||||||||  ||| ||| |||
                                CCTTTCAC  GTT TCC AGA
                                    AA   C   _
GAM1739 FLJ23469 5'  CGGAAGGTGCCGGGTTC     42664          CAGCA  A
                                CGGAAGGTGCC     GG TC
                                ||||||||||     || ||
                                GCCTTCCACGG     CC AG
                                     C____  A
GAM1739 HSU79303 3'  GGAAGGTGCCCAGGATCT    42665           GCA
                                GGAAGGTGCCCA   GGATCT
                                ||||||||||||   ||||||
```

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                                CCTTCCACGGGT  CCTAGA
                                    ____
GAM1739  KIAA0445  5'  CAGGGTGCCCAGTAGG     42666    AA       C
                                CGG  GGTGCCCAG AGG
                                |||  ||||||||| |||
                                GTC  CCACGGGTC TCC
                                  __       A
GAM1739  KIAA1940  5'  AGCTCCCCCAGCGGGATCTCG  42667    G__     A
                                GGT   CCCAGC GGATCTCG
                                |||   |||||| ||||||||
                                TCG   GGGTCG CCTAGAGC
                                  AGG     C
GAM1739  LOC145438 3'  GGAGTGCAGTGGCGGGATCTCG 42661    AG    CCA_  A
                                GGA  GTGC    GC GGATCTCG
                                |||  ||||    || ||||||||
                                CCT  CACG    CG CCTAGAGC
                                  __    TCAC  C
GAM1739  LOC146756 3'  GGAGTGCAGTGGCGGGATCTCG 42661    AG    CCA_  A
                                GGA  GTGC    GC GGATCTCG
                                |||  ||||    || ||||||||
                                CCT  CACG    CG CCTAGAGC
                                  __    TCAC  C
GAM1739  LOC147515 3'  GGAAGGTGCTAGTAAGAT    42668         CC  C
                                GGAAGGTGC  AG AGGAT
                                |||||||||  || |||||
                                CCTTCCACG  TC TTCTA
                                     A_  A
GAM1739  LOC149579 5'  CAGGGTGCCCAGTAGG     42666    AA       C
                                CGG  GGTGCCCAG AGG
                                |||  ||||||||| |||
                                GTC  CCACGGGTC TCC
                                  __       A
GAM1739  LOC149995 3'  GGAAGGTGCTAGTAAGAT    42668         CC  C
                                GGAAGGTGC  AG AGGAT
                                |||||||||  || |||||
                                CCTTCCACG  TC TTCTA
                                     A_  A
GAM1739  LOC152627 5'  GGAGTGAGTGGCGGGATCTCG  42669    AG   CCCA  A
                                GGA  GTG    GC GGATCTCG
                                |||  |||    || ||||||||
                                CCT  CAC    CG CCTAGAGC
                                  __   TCAC  C
GAM1739  LOC200213 5'  GGGCCAGCAGGATCTC     42670    T   C
                                GG GCC AGCAGGATCTC
                                || ||| ||||||||||
                                CC CGG TCGTCCTAGAG
                                  _  _
GAM1739  LOC221490 3'  AGTGCAGTGGCGGGATCTCG   42671      CCA_  A
                                GGTGC    GC GGATCTCG
                                |||||    || ||||||||
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                                TCACG   CG CCTAGAGC
                                   TCAC  C
GAM1739  LOC255452 3'  GGGGGTGCCCAGTGATC    42672    AA       CAG
                                GG  GGTGCCCAG   GATC
                                ||  |||||||||   ||||
                                CC  CCACGGGTC   CTAG
                                 C_       A__
GAM1739  LOC91862  3'  GGAGTGCAGTGGCGGGATCTCG 42661    AG   CCA_  A
                                GGA  GTGC   GC GGATCTCG
                                |||  ||||   || ||||||||
                                CCT  CACG   CG CCTAGAGC
                                  __   TCAC  C
GAM1739  LOC92689  5'  CGGGAGTGCCCAGCGGG    42673    AA       A
                                CGG  GGTGCCCAGC GG
                                |||  |||||||||| ||
                                GCC  TCACGGGTCG CC
                                  C_       C
GAM1740  APM1     3'  TGATGGAAAAAGATATACCA  42676     T__
                                TGATG   GGGGATATACCA
                                |||||   ||||||||||||
                                ACTAC   TTTCTATATGGT
                                   CTT
GAM1740  FABP2    3'  TGAATGGAAATATACCA    42677    T   GG
                                TGA GTGG  ATATACCA
                                |||  ||||  ||||||||
                                ACT TACC  TATATGGT
                                  _   TT
GAM1740  HLA-DMB  5'  TGATGTGGGGATACCCA    42678          A
                                TGATGTGGGGATAT CCA
                                |||||||||||||| |||
                                ACTACACCCCTATG GGT
                                          _
GAM1740  LAMP2    3'  TGATGTGTTAACTACCA    42679       GG   A
                                TGATGTG  GAT TACCA
                                |||||||  ||| |||||
                                ACTACAC  TTG ATGGT
                                    AA  _
GAM1740  NONO     3'  TGATTAAACAATATACCA   42680     GT  G
                                TGAT  GG GATATACCA
                                ||||  || |||||||||
                                ACTA  TT TTATATGGT
                                  AT  G
GAM1740  RUNX3    3'  TGATGTGAGAATCCA      42681          ATA
                                TGATGTGGGGAT   CCA
                                ||||||||||||   |||
                                ACTACACTCTTA   GGT
                                          ____
GAM1740  SVIL     5'  TGACGTGGGAATCCA      42682          ATA
                                TGATGTGGGGAT   CCA
                                ||||||||||||   |||
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                                ACTGCACCCTTA  GGT
                                      ___
GAM1740 SVIL    5' TGACGTGGGAATCCA      42682          ATA
                                TGATGTGGGGAT  CCA
                                ||||||||||||  |||
                                ACTGCACCCTTA  GGT
                                      ___
GAM1740 TP63    3' TAATATAAAATATACCA    42683        G
                                TGATGTGGG ATATACCA
                                ||||||||| ||||||||
                                ATTATATTT TATATGGT
                                      _
GAM1740 UBE1    3' TGATGAGGGAACACCA     42684      T   T
                                TGATG GGGGA ATACCA
                                ||||| ||||| ||||||
                                ACTAC TCCCT TGTGGT
                                    _   _
GAM1740 ALS2CR3 3' GATTATCAGGATATACCA   42685    _ G
                                GAT GT GGGATATACCA
                                ||| || ||||||||||||
                                CTA TA TCCTATATGGT
                                  A  G
GAM1740 BTN2A2  3' TGACCTATGATATACCA    42686    G  GG
                                TGAT TG  GATATACCA
                                |||| ||  |||||||||
                                ACTG AT  CTATATGGT
                                  G  A_
GAM1740 DKFZP762D096 3' TGATGTGGAGATTCCCCA  42687          ATA
                                TGATGTGGGGAT  CCA
                                ||||||||||||  |||
                                ACTACACCTCTA  GGT
                                      AGG
GAM1740 FLJ14124 5' TAATGTAGTTAAATATACCA  42688       __
                                TGATGTGG  GGATATACCA
                                ||||||||  ||||||||||
                                ATTACATC  TTTATATGGT
                                    AA
GAM1740 FLJ21820 3' TGATGTAGAAGCTATGCCA  42689        A_  A
                                TGATGTGGGG  TAT CCA
                                ||||||||||  ||| |||
                                ACTACATCTT  ATA GGT
                                     CG   C
GAM1740 HEMK    3' TGATGTAGGCTCACATCA    42690       GA   C
                                TGATGTGGG  TATA CA
                                |||||||||  |||| ||
                                ACTACATCC  GTGT GT
                                     GA   A
GAM1740 HTCD37  3' TATGAGAACAGTATACCA    42691       ___
                                TGTGGGGAT  ATACCA
                                |||||||||  ||||||
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                                ATACTCTTG  TATGGT
                                     TCA
GAM1740 KIAA1061 3' TGATGCGGGGATGGGGTACCA 42692         A___
                                TGATGTGGGGAT   TACCA
                                ||||||||||||  |||||
                                ACTACGCCCCTA  ATGGT
                                      CCCC
GAM1740 KIAA1116 3' TATGGATAAGATATACCA   42693     ___
                                TGTGG  GGATATACCA
                                |||||  ||||||||||
                                ATACC  TCTATATGGT
                                   TAT
GAM1740 MDS006   3' TGACGTGGTATACACCA    42694       GG
                                TGATGTGG ATATACCA
                                |||||||| ||||||||
                                ACTGCACC TATGTGGT
                                     A_
GAM1740 MGC10981 3' TGATGTGGTTACATGCCA   42695       GG   A
                                TGATGTGG ATAT CCA
                                |||||||| |||| |||
                                ACTACACC TGTA GGT
                                     AA   C
GAM1740 TAF9L    3' TGATCTGAATTATACCA    42696     G   GA
                                TGAT TGGG TATACCA
                                |||| |||| |||||||
                                ACTA ACTT ATATGGT
                                  G   A_
GAM1740 TTTY2    5' TGATGTGAAGCACCA      42697        ATA
                                TGATGTGGGG  TACCA
                                ||||||||||  |||||
                                ACTACACTTC  GTGGT
                                      ___
GAM1740 TTYH2    3' TGACGCGGATATACCA     42698      GG
                                TGATGT GGATATACCA
                                ||||||  ||||||||||
                                ACTGCG CCTATATGGT
                                     __
GAM1740 ZFP106   3' TGAGTAGAGACGTATGCCA  42699    T     TA __
                                TGA GTGGGGA TA CCA
                                ||| |||||||  ||  |||
                                ACT CATCTCT AT GGT
                                  _     GC AC
GAM1740 LOC143154 3' TGATAAAAATATACCA    42700      TG
                                TGATG GGGATATACCA
                                |||||  ||||||||||
                                ACTAT TTTTATATGGT
                                     __
GAM1740 LOC144363 3' TGTGCTGTTAATATACCA  42701    A _ GG
                                TG TG TG GATATACCA
                                || || ||  |||||||||
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                                AC AC AC  TTATATGGT
                                 _ G  AA
GAM1740  LOC149103 3'  TGATGGGAAGACATGCCA    42702      T      A
                                TGATG GGGGATAT CCA
                                ||||| |||||||| |||
                                ACTAC CTTCTGTA GGT
                                   C       C
GAM1740  LOC159148 5'  TGATGTGAAGCACCA      42697         ATA
                                TGATGTGGGG   TACCA
                                ||||||||||   |||||
                                ACTACACTTC   GTGGT
                                      ____
GAM1740  LOC165476 5'  TGAGTGGGAACAGCCA     42703     T       TA
                                TGA GTGGGGATA  CCA
                                ||| |||||||||  |||
                                ACT CACCCTTGT  GGT
                                  _       C_
GAM1740  LOC202934 5'  TGAGTGGGGACACAGCCA    42704     T       _
                                TGA GTGGGGATATA CCA
                                ||| |||||||||||| |||
                                ACT CACCCCTGTGT GGT
                                  _         C
GAM1740  LOC203107 3'  TGAGTAGAATATACCA      42705     T    G
                                TGA GTGGG ATATACCA
                                ||| ||||| ||||||||
                                ACT CATCT TATATGGT
                                  _    _
GAM1740  LOC219294 3'  TGATAAAAATATACCA      42700      TG
                                TGATG  GGGATATACCA
                                |||||  ||||||||||
                                ACTAT  TTTTATATGGT
                                    __
GAM1740  LOC222068 3'  TGTGTGGGGAAAGTACCA    42706    A      TA_
                                TG TGTGGGGA   TACCA
                                || ||||||||   |||||
                                AC ACACCCCT   ATGGT
                                  _       TTC
GAM1740  LOC254423 5'  TGATGTGGAGGATGCCA     42707        _   ATA
                                TGATGTGG GGAT   CCA
                                |||||||| ||||   |||
                                ACTACACC CCTA   GGT
                                     T   C__
GAM1740  LOC255465 5'  TGAGTGGGGACACAGCCA    42704     T       _
                                TGA GTGGGGATATA CCA
                                ||| |||||||||||| |||
                                ACT CACCCCTGTGT GGT
                                  _         C
GAM1741  ELMO1     3'  TACCAGTAATAATTACAAT    42710         T
                                TATCAGTGAT ATTACAAT
                                |||||||||| ||||||||
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                                ATGGTCATTA TAATGTTA
                                      T
GAM1741  FOS      3'  ATCAGTAACATTACAAT     42711         T
                                ATCAGTGAT ATTACAAT
                                ||||||||| ||||||||
                                TAGTCATTG TAATGTTA
                                      _
GAM1741  GPC5     3'  CATCAGTGGCTAAGTTACA   42712         AT __
                                TATCAGTG  TA  TTACA
                                ||||||||  ||  |||||
                                GTAGTCAC  AT  AATGT
                                     CG  TC
GAM1741  ITGB3    3'  TATCAGGACACATCACAAT   42713        T  _
                                TATCAG GAT TATTACAAT
                                |||||| ||| |||||||||
                                ATAGTC CTG GTAGTGTTA
                                   _  T
GAM1741  RDX      3'  TACCAGTGAGGAGCTTACAAT 42714         TTA__
                                TATCAGTGA    TTACAAT
                                |||||||||    |||||||
                                ATGGTCACT    AATGTTA
                                     CCTCG
GAM1741  RNGTT    3'  CATCAGTAGTTTTATTACAAT 42715         A__
                                TATCAGTG   TTATTACAAT
                                ||||||||   ||||||||||
                                GTAGTCAT   AATAATGTTA
                                     CAA
GAM1741  TIMELESS 5'  CATCAGTGGACCAACCAAT   42716         _   TTA
                                TATCAGTG ATTA   CAAT
                                |||||||| ||||   ||||
                                GTAGTCAC TGGT   GTTA
                                     C   TG_
GAM1741  DNCLI1   3'  ATCAGTGATTGAGACAAT    42717         ATT
                                ATCAGTGATT   ACAAT
                                ||||||||||   |||||
                                TAGTCACTAA   TGTTA
                                      CTC
GAM1741  FLJ10292 3'  CATCAGCAACTTACAAT     42718       TG  TA
                                TATCAG  AT  TTACAAT
                                ||||||  ||  |||||||
                                GTAGTC  TG  AATGTTA
                                   GT  __
GAM1741  FLJ10895 3'  TATCAGTTATTACAAT      42719        GAT
                                TATCAGT   TATTACAAT
                                |||||||   |||||||||
                                ATAGTCA   ATAATGTTA
                                     ____
GAM1741  FLJ23416 3'  TATCAAGTGATATGCACAAT  42720       _    TAT
                                TATCA GTGAT   TACAAT
                                ||||| |||||   ||||||
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                                ATAGT CACTA   GTGTTA
                                   T    TAC
GAM1741  MGC2628   3'  CATCAGCATCTTTACAAT    42721       G   A
                                TATCAGT ATT TTACAAT
                                ||||||| ||| |||||||
                                GTAGTCG TAG AATGTTA
                                    _  A
GAM1741  LOC115297 3'  TATCAGTGTATTAGACACA   42722        _   T_
                                TATCAGTG ATTA  TACA
                                |||||||| ||||  ||||
                                ATAGTCAC TAAT  GTGT
                                     A   CT
GAM1741  LOC257407 3'  ATCAGTGAATCACAAT      42723        TT
                                ATCAGTGA  ATTACAAT
                                ||||||||  ||||||||
                                TAGTCACT  TAGTGTTA
                                    __
GAM1742  NBEA      3'  AGTAAAATGGTTGCTGACT    42726        ACAG   ACC
                                AGTGAAGTG    GTT   GACT
                                |||||||||    |||   ||||
                                TCATTTTAC    CGA   CTGA
                                     CAA_  ____
GAM1742  PPP2R5A   3'  GTGAAGGACAGGTTGTGAGGAC 42727       T       ACC__
           T                    GTGAAG GACAGGTT     GACT
                                |||||| ||||||||     ||||
                                CACTTC CTGTCCAA     CTGA
                                   _       CACTC
GAM1742  AQP10     3'  AGTGAAGTGAGGGTTGTCC    42728         CA    A_
                                AGTGAAGTGA  GGTT  CC
                                ||||||||||  ||||  ||
                                TCACTTCACT  CCAA  GG
                                     C_    CA
GAM1742  DKFZp547D155 3'  GTGGGGTGACAGGAGTGGGACT 42729     AA       TTACC
                                GTG  GTGACAGG     GACT
                                |||  ||||||||     ||||
                                CAC  CACTGTCC     CTGA
                                  CC       TCACC
GAM1742  FLJ12592  3'  AGTGAAGTACAGTGAGGTTA   42730         AC___
                                AGTGAAGTG     AGGTTA
                                |||||||||     ||||||
                                TCACTTCAT     TCCAAT
                                     GTCAC
GAM1742  KIAA1191  5'  AGTGAAATGATGTGATGACTA  42731          CA_   TACC
                                AGTGAAGTGA   GGT    GACTA
                                ||||||||||   |||    |||||
                                TCACTTTACT   CTA    CTGAT
                                     ACA   ____
GAM1742  MESDC2    3'  GTGAAGTGGGGGGCACACT    42732        ACA   T  CG
                                GTGAAGTG   GGT AC  ACT
                                ||||||||   ||| ||  |||
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                                CACTTCAC   CCG TG  TGA
                                     CC_  _ __
GAM1742  LOC158288 5'  GTGGAATGACAGGCGTGAACTA 42733     A        TACC
                                GTG AGTGACAGGT    GACTA
                                ||| ||||||||||    |||||
                                CAC TTACTGTCCG    TTGAT
                                  C         CAC_
GAM1742  LOC196812 5'  AGTGAAGTAGCTTCTGACT    42734        GAC  G  ACC
                                AGTGAAGT   AG TT   GACT
                                ||||||||   || ||   ||||
                                TCACTTCA   TC AA   CTGA
                                     ___  G  GA_
GAM1742  LOC63923  3'  AGGAGGTGACAAACGTCCG    42735    T  A      TTA
                                AG GA GTGACAGG   CCG
                                || || ||||||||   |||
                                TC CT CACTGTTT   GGC
                                 _ C       GCA
GAM1743  ETV5      3'  ATACATAGAGAATCTAAGCTT  42738       TT___
                                ATATGT     ATCTAAGCTT
                                ||||||     ||||||||||
                                TATGTA     TAGATTCGAA
                                   TCTCT
GAM1743  LAMC1     3'  TACAAGCTGCCATCTAAG     42739      TA    T
                                TACAA  TGTT ATCTAAG
                                |||||  ||||  |||||||
                                ATGTT  ACGG TAGATTC
                                   CG   _
GAM1743  FLJ30681  3'  CAATATGTTGGTGGCAAGCTT  42740         TATC_
                                CAATATGTT    TAAGCTT
                                |||||||||    |||||||
                                GTTATACAA    GTTCGAA
                                     CCACC
GAM1743  KIAA1423  3'  TACAAAATGTATCTAAGCTT   42741      T    TT
                                TACAA ATGT  ATCTAAGCTT
                                ||||| ||||  ||||||||||
                                ATGTT TACA  TAGATTCGAA
                                   T    __
GAM1743  KIAA1843  3'  CAATACTTTCTAAGCTT     42742       GTTTA
                                CAATAT     TCTAAGCTT
                                ||||||     |||||||||
                                GTTATG     AGATTCGAA
                                   AA___
GAM1743  OR7C1     3'  ATATGGGCACTAAGCTT     42743       TT  T
                                ATATG  TA CTAAGCTT
                                |||||  ||  ||||||||
                                TATAC  GT GATTCGAA
                                   CC  _
GAM1743  USP25     3'  TACAAAATGTTCTACAGCTT   42744       T    TTA   _
                                TACAA ATGT   TCTA AGCTT
                                ||||| ||||   |||| |||||
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                                ATGTT TACA   AGAT TCGAA
                                  T   ___   G
GAM1743  LOC157663 3'  TACAATATGTTTAAAGC     42745           TCT
                                TACAATATGTTTA   AAGC
                                ||||||||||||   ||||
                                ATGTTATACAAAT   TTCG
                                       ___
GAM1743  LOC168667 3'  TACAACATGTTCAATGGCTT   42746           TCTAA
                                TACAATATGTTTA    GCTT
                                ||||||||||||    ||||
                                ATGTTGTACAAGT    CGAA
                                       TAC__
GAM1743  LOC254892 3'  CAATATGTTTATTGCT      42747           CTAA
                                CAATATGTTTAT    GCT
                                ||||||||||||   |||
                                GTTATACAAATA    CGA
                                       A___
GAM1744  C20orf45  3'  TGTTCTTCTGTTTAAGTTAGA  42529       AAAT
                                TGTTTT    TTTAAGTTAGA
                                ||||||   ||||||||||
                                ACAAGA    AAATTCAATCT
                                   AGAC
GAM1744  R3HDM     3'  TTCCCCCAAATTTTAAGTT    42530    G
                                TT TTTTAAATTTTAAGTT
                                || ||||||||||||||||
                                AA GGGGTTTAAAATTCAA
                                 G
GAM1744  LOC129450 3'  TACTGTTTTTAAGTCATTTTAA 42531         AA____        A
            GTTGGA                  ATTGTTTT     ATTTTAAGTT GA
                                ||||||||     |||||||||| ||
                                TGACAAAA     TAAAATTCAA CT
                                     ATTCAG         C
GAM1744  LOC90355  3'  GTTCCAGGTGAATTTTAAGTTA 42532       ____
            GA                    GTTTTA    AATTTTAAGTTAGA
                                ||||||   ||||||||||||||
                                CAAGGT    TTAAAATTCAATCT
                                   CCAC
GAM1745  AKAP13    3'  AAGCATCAACTCTGTGCCAG   42751     G         TTAT
                                AAG ATCAACTCTGT    CTAG
                                ||| ||||||||||    ||||
                                TTC TAGTTGAGACA    GGTC
                                  G         C___
GAM1745  CDC27     3'  GGTCAGTTACTCTGTTTATCTG 42752    A  ___          A
            GA                    GG TCA   ACTCTGTTTATCT GA
                                || |||   |||||||||||| ||
                                CC AGT   TGAGACAAATAGA CT
                                 _  CAA           C
GAM1745  EPB41     3'  AAGGATCAATGAGATCTAG    42753         CTC  TTT
                                AAGGATCAA   TG   ATCTAG
                                |||||||||   ||   ||||||
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                                TTCCTAGTT  AC  TAGATC
                                     ___ TC_
GAM1745 GPR4    3' GGAGATCGCTGTTTATCTAGA 42754   A    AACT
                                A GGATC   CTGTTTATCTAGA
                                | |||||   ||||||||||||
                                C TCTAG   GACAAATAGATCT
                                 C    C___
GAM1745 LARGE   3' AAGGATCAGATTTTCTATTT  42755       AC___
                                AAGGATCA    TCTGTTT
                                ||||||||    |||||||
                                TTCCTAGT    AGATAAA
                                     CTAAA
GAM1745 LARGE   3' AAGGATCAGATTTTCTATTT  42755       AC___
                                AAGGATCA    TCTGTTT
                                ||||||||    |||||||
                                TTCCTAGT    AGATAAA
                                     CTAAA
GAM1745 TEM7    3' AAGGACCAGCTTGTGAGTCTAG 42756       A  C   TTA
                                AAGGATCA CT TGT   TCTAG
                                |||||||| || |||   |||||
                                TTCCTGGT GA ACA   AGATC
                                     C  _   CTC
GAM1745 CENTB5  3' AAGAATCAATTCTGTTCTTCAG 42757       C      A  T
                                AAGGATCAA TCTGTTT TC AG
                                ||||||||| ||||||| || ||
                                TTCTTAGTT AGACAAG AG TC
                                      A      A  _
GAM1745 FADS1   3' AAGGATCAGCACCTATTT    42758       __  T
                                AAGGATCA  AC CTGTTT
                                ||||||||  || ||||||
                                TTCCTAGT  TG GATAAA
                                     CG  _
GAM1745 FLJ14936 3' GGAGATCGACTCCGCCTTCT  42759   A    A       A
                                A GGATC ACTCTGTTT TCT
                                | ||||| ||||||||| |||
                                C TCTAG TGAGGCGGA AGA
                                 C    C       _
GAM1745 FLJ21324 5' AAAGATCAATTCTAATCTGGA  42760       C   TTT   A
                                AAGGATCAA TCTG   ATCT GA
                                ||||||||| ||||   |||| ||
                                TTTCTAGTT AGAT   TAGA CT
                                      A   ___   C
GAM1745 FLJ31737 3' AGGATCAACTGTGTACCAG   42761        C   TTAT
                                AGGATCAACT TGT   CTAG
                                |||||||||| |||   ||||
                                TCCTAGTTGA ACA   GGTC
                                      C  T___
GAM1745 IDI1    3' GGGTTGACTCTGTCCCCTAG  42762    ATCA       A
                                GG   ACTCTGTTT TCTAG
                                ||   ||||||||| |||||
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                                CC    TGAGACAGG GGATC
                                 CAAC        _
GAM1745  KIAA1190  3'  AGGGGTTGGTTGTGCCCACCTA 42763     ATCAACTC_
            GA                    AGG        TGTTTATCTAGA
                                  |||        ||||||||||||
                                  TCC        ACGGGTGGATCT
                                    CCAACCAAC
GAM1745  KIAA1434  3'  AAAGATCAACTCTGCCTACCTA 42764
            GA                    AAGGATCAACTCTGTTTATCTAGA
                                  ||||||||||||||||||||||||
                                  TTTCTAGTTGAGACGGATGGATCT

GAM1745  KIAA1441  3'  AGGGTCCACTCTACTAG     42765     A  A     TTTAT
                                  AGG TC ACTCTG     CTAG
                                  ||| || ||||||     ||||
                                  TCC AG TGAGAT     GATC
                                    C  G     _____
GAM1745  PSR       3'  AGGAATCAACTTTAGCATCTGG 42766      _     CTGTT     A
            A                      AGGA TCAACT     TATCT GA
                                  |||| ||||||     |||||| ||
                                  TCCT AGTTGA     GTAGA CT
                                    T     AATC_     C
GAM1745  RNAHP     3'  AGCATCAACTCCCATTTAGA   42767    G       GTT   C
                                  AG ATCAACTCT   TAT TAGA
                                  || |||||||||   ||| ||||
                                  TC TAGTTGAGG   GTA ATCT
                                   G        ___   A
GAM1745  LOC151201 3'  GGGTCAACTGATTTATCT    42768    A     CT
                                  GG TCAACT  GTTTATCT
                                  || ||||||  ||||||||
                                  CC AGTTGA  TAAATAGA
                                   C     C_
GAM1745  LOC196485 5'  GGACTCAGAACTTATCTAGA   42769     TCAA   TG__
                                  GGA    CTC    TTTATCTAGA
                                  |||    |||    ||||||||||
                                  CCT    GAG    GAATAGATCT
                                    _____   TCTT
GAM1745  LOC202986 5'  GGACTCAGAACTTATCTAGA   42769     TCAA   TG__
                                  GGA    CTC    TTTATCTAGA
                                  |||    |||    ||||||||||
                                  CCT    GAG    GAATAGATCT
                                    _____   TCTT
GAM1745  LOC221981 3'  AGATCAACTTTAGGATTATCTG 42770         CTGT__     A
            GA                      GGATCAACT     TTATCT GA
                                  |||||||||     |||||| ||
                                  TCTAGTTGA     AATAGA CT
                                       AATCCT     C
GAM1745  LOC89894  3'  AAGGATCACTAGTGAATCT    42771         A  CT  TT
                                  AAGGATCA CT  GT  ATCT
                                  |||||||| ||  ||  ||||
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                                TTCCTAGT GA  CA  TAGA
                                    _ T_  CT
GAM1745 LOC91097 3' AAAGATCAATTCTAATCTGGA 42760        C   TTT   A
                                AAGGATCAA TCTG   ATCT GA
                                ||||||||| ||||   |||| ||
                                TTTCTAGTT AGAT   TAGA CT
                                    A   ___   C
GAM1745 LOC92579 3' AGGACCAACTTATCT      42772         CTGTT
                                AGGATCAACT    TATCT
                                ||||||||||    |||||
                                TCCTGGTTGA    ATAGA
                                      _____
GAM1746 MFAP4    3' TGCGGTAGCTGTGTTCTTGGC 42775          CCTGG
                                TGCGGTAGCTGT    TGGT
                                ||||||||||||    ||||
                                ACGCCATCGACA    ACCG
                                      CAAGA
GAM1746 PER2     3' TGTGGTGGCAGTCGCCTGTGGT 42776   C  A  T  _  G
                                TG GGT GC GTC CT GTGGT
                                || ||| || ||| || |||||
                                AC CCA CG CAG GG CACCA
                                 A  C  T  C  A
GAM1746 PRG3     3' TGCGGTAGTTCTCCCGCCTGGC 42777        _____  T
                                TGCGGTAG    CTG CCTGGT
                                ||||||||    ||| ||||||
                                ACGCCATC    GGC GGACCG
                                    AAGAG  _
GAM1746 RLN2     3' TGTTGTAGCTGTGGTAAT    42778    CG      CCT
                                TG  GTAGCTGT   GGTGGT
                                ||  ||||||||   ||||||
                                AC  CATCGACA   CCATTA
                                 AA       ___
GAM1746 SH3GL1   3' TGGGTGGCTGGTGGTGGC    42779    C   A   TCC
                                TG GGT GCTG   TGGTGGT
                                || ||| ||||   |||||||
                                AC CCA CGAC   ACCACCG
                                 _  C   C__
GAM1746 SNTB2    3' TGGGTAGCTGTGGCATGGTG   42780    C       CC__
                                TG GGTAGCTGT    TGGTG
                                || |||||||||    |||||
                                AC CCATCGACA    ACCAC
                                 _       CCGT
GAM1746 WWOX     3' TGCAGTGGTGGCCGTGGTGGTA 42781       AGCT   C
                                TGCGGT    GTC TGGTGGTA
                                ||||||    ||| ||||||||
                                ACGTCA    CGG ACCACCAT
                                    CCAC   C
GAM1746 WWOX     3' TGCAGTGGTGGCCGTGGTGGTA 42781       AGCT   C
                                TGCGGT    GTC TGGTGGTA
                                ||||||    ||| ||||||||
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                                ACGTCA   CGG ACCACCAT
                                   CCAC  C
GAM1746 AGPAT1   5' TGCGGCAGCGGTGGTGGC   42782       T  CCT
                                TGCGGTAGC GT  GGTGGT
                                ||||||||| ||  ||||||
                                ACGCCGTCG CA  CCACCG
                                     C ___
GAM1746 ATP9B    3' TGTGGTGCTTGCTTGGTAGC  42783   C  A  _ CC
                                TG GGT GCT GT  TGGTGGT
                                || ||| ||| ||  |||||||
                                AC CCA CGA CG  ACCATCG
                                 A  _  A A_
GAM1746 BY55     3' TGCTGTAGCTGTTTTAAAAGT 42784    G     CC  T
                                TGC GTAGCTGT  TGG GGT
                                ||| ||||||||  ||| |||
                                ACG CATCGACA  ATT TCA
                                  A       AA  T
GAM1746 FLJ11269 5' TGAGGTACTGGTGGTGGC   42785   C   G  TCC
                                TG GGTA CTG   TGGTGGT
                                || |||| |||   |||||||
                                AC CCAT GAC   ACCACCG
                                 T   _  C__
GAM1746 FLJ12838 3' TGTGGTATTGTGAAGGGTAAC 42786   C   GC  CCT  T
                                TG GGTA  TGT   GG GGTAAC
                                || ||||  |||   || ||||||
                                AC CCAT  ACA   TC CCATTG
                                 A   A_  CT_ _
GAM1746 FLJ20127 5' TGTGGAGTTGTTCCAGTAAT  42787   C  T  C   C TG
                                TG GG AG TGT C  GTGGT
                                || || || ||| |  |||||
                                AC CC TC ACA G  CATTA
                                 A  _ A  A GT
GAM1746 FLJ20127 5' TGTGGCGCTGGTGGTGGT   42788   C  A   TCC
                                TG GGT GCTG   TGGTGGT
                                || ||| ||||   |||||||
                                AC CCG CGAC   ACCACCA
                                 A  _   C__
GAM1746 KIAA0669 5' TGAGGTAGCGGTGGTGGC   42789   C    T  CCT
                                TG GGTAGC GT  GGTGGT
                                || |||||| ||  ||||||
                                AC CCATCG CA  CCACCG
                                 T    C ___
GAM1746 KIAA0987 3' TGGGTAGTGGTGGTGGT    42790   C    C  TCC
                                TG GGTAG TG   TGGTGGT
                                || ||||| ||   |||||||
                                AC CCATC AC   ACCACCA
                                 _   _ C__
GAM1746 KIAA1485 3' TGTGGTGTTGCTGGTGAT   42791   C  AGC  TC
                                TG GGT  TG  CTGGTGGT
                                || |||  ||  ||||||||
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                                AC CCA   AC  GACCACTA
                                 A   CA_ __
GAM1746  KIAA1643  3'  GGTAGCTGAGCTGGTGGC    42792        TC
                                GGTAGCTG  CTGGTGGT
                                ||||||||  ||||||||
                                CCATCGAC  GACCACCG
                                     TC
GAM1746  LATS1     3'  TGGGTAGGGTGGTGGTGGT   42793    C    CT  CC
                                TG GGTAG  GT  TGGTGGT
                                || |||||  ||  |||||||
                                AC CCATC  CA  ACCACCA
                                 _    C_  CC
GAM1746  PR48      3'  GCGGTGGCCCGGTGGT      42794       AGCT T
                                GCGGT    G CCTGGTGGT
                                |||||    | |||||||||
                                CGCCA    C GGGCCACCA
                                   C____ _
GAM1746  LOC120400 5'  TGTGGCACTGGTGGTGGT    42796    C    G   TCC
                                TG GGTA CTG   TGGTGGT
                                || |||| |||   |||||||
                                AC CCGT GAC   ACCACCA
                                 A    _   C__
GAM1746  LOC120400 5'  TGCGGAGTTGTTCCAGTAAT   42795      T  C   C TG
                                TGCGG AG TGT C  GTGGT
                                ||||| || ||| |  |||||
                                ACGCC TC ACA G  CATTA
                                   _ A   A GT
GAM1746  LOC148809 5'  TGCGTGGCTGTCCTGTTG    42797      GTA       G
                                TGCG   GCTGTCCTG TG
                                ||||   ||||||||| ||
                                ACGC   CGACAGGAC AC
                                  AC_        A
GAM1746  LOC158236 5'  TGCGGTTGCTGTGGTA      42798       A    CCTGGT
                                TGCGGT GCTGT     GGTA
                                |||||| |||||     ||||
                                ACGCCA CGACA     CCAT
                                   A    _______
GAM1746  LOC200597 3'  TGGGCAGCTCCTGGTGGTAA  42799    C     TG
                                TG GGTAGC  TCCTGGTGGTAA
                                || ||||||  ||||||||||||
                                AC CCGTCG  AGGACCACCATT
                                 _     __
GAM1746  LOC201324 5'  TGTGGTGCTTGCTTGGTAGC  42783    C   A   _  CC
                                TG GGT GCT GT  TGGTGGT
                                || ||| ||| ||  |||||||
                                AC CCA CGA CG  ACCATCG
                                 A   _   A  A_
GAM1746  LOC255271 5'  TGCGGTAGGTGTCTTGTTCAGT 42800        C    C  GT_
                                TGCGGTAG TGTC TG   GGT
                                |||||||| |||| ||   |||
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                                ACGCCATC ACAG AC   TCA
                                    C    A  AAG
GAM1746  LOC256784 5'  TGCTGGCTGTCCGGTGGT    42801     GGTA      T
                                TGC    GCTGTCC GGTGGT
                                |||    ||||||| ||||||
                                ACG    CGACAGG CCACCA
                                  AC__      _
GAM1747  8D6A     3'  AGCAGGAGTGTCTTAAGCACAG 42804      AAAAT    GGC_
                                AGTA    GGTG    AAGCACAG
                                ||||    ||||    ||||||||
                                TCGT    TCAC    TTCGTGTC
                                  CC___    AGAA
GAM1747  CBFA2T2   3'  AGTAAAATGACAAAGCACA   42805        A   TG GCA
                                AGTAAAA TGG  G   AGCACA
                                ||||||| |||  |   ||||||
                                TCATTTT ACT  T   TCGTGT
                                    _  GT ___
GAM1747  DLG4     3'  AGAAAAATGGTGGGGGCA    42806    T         CAA
                                AG AAAAATGGTGGG   GCA
                                || ||||||||||||   |||
                                TC TTTTTACCACCC   CGT
                                 _          C__
GAM1747  FOXI1    3'  AGTAAGTGTGGCCAGTACA    42807     AAAAT   _   A  C
                                AGTA    GGTG GGC AG ACA
                                ||||    |||| ||| || |||
                                TCAT    TCAC CCG TC TGT
                                  ______   A   G  A
GAM1747  GYPB     3'  AGCAAAGGAATAGCAGGTGCA  42808       __     TG  CAA
                                AGTAAA  AATGG  GG   GCA
                                ||||||  |||||  ||   |||
                                TCGTTT  TTATC  CC   CGT
                                   CC    GT  A__
GAM1747  GYPE     3'  AGCAAAGGAATAGCAGGTGCA  42808       __     TG  CAA
                                AGTAAA  AATGG  GG   GCA
                                ||||||  |||||  ||   |||
                                TCGTTT  TTATC  CC   CGT
                                   CC    GT  A__
GAM1747  ISL1     5'  AGTGAAATGGTGGTTGTACA   42809     AA        GCAA
                                AGT  AAATGGTGG    GCA
                                |||  |||||||||    |||
                                TCA  TTTACCACC    TGT
                                  C_        AACA
GAM1747  ITGA11    3'  AGTAAAGGTCGTACTATGCACA 42810       AAT   _ GG AA_
             G                   AGTAAA   GGT G  C   GCACAG
                                ||||||   ||| |  |   ||||||
                                TCATTT   CCA C  G   CGTGTC
                                   ___   G AT ATA
GAM1747  KCNJ6    5'  AGAAAAGTGGTGGACCACGCA  42811    T    A       AA_
                                AG AAAA TGGTGGGC   GCA
                                || |||| ||||||||   |||
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                                TC TTTT ACCACCTG   CGT
                                 _   C      GTG
GAM1747  MYH11    3'  AGTGAAAGTGTTTTTAAGCACA 42812    AAAAAT   GGC__
                G                AGT    GGTG    AAGCACAG
                                 |||    ||||    ||||||||
                                 TCA    TCAC    TTCGTGTC
                                  CTT___   AAAAA
GAM1747  MYH11    3'  AGTGAAAGTGTTTTTAAGCACA 42812    AAAAAT   GGC__
                G                AGT    GGTG    AAGCACAG
                                 |||    ||||    ||||||||
                                 TCA    TCAC    TTCGTGTC
                                  CTT___   AAAAA
GAM1747  MYH11    3'  AGTGAAAGTGTTTTTAAGCACA 42812    AAAAAT   GGC__
                G                AGT    GGTG    AAGCACAG
                                 |||    ||||    ||||||||
                                 TCA    TCAC    TTCGTGTC
                                  CTT___   AAAAA
GAM1747  PLAG1    3'  AATAAAAATGGTCATCTAGGGC 42813        _____  CAA
                ACAG               TAAAAATGGT    GGG  GCACAG
                                 ||||||||||    |||  ||||||
                                 ATTTTTACCA    TCC  CGTGTC
                                      GTAGA  ___
GAM1747  PPARGC1  3'  AATAAAAATGAGAGGAGCACAG 42814        GT  CA
                                 AGTAAAAATG  GGG  AGCACAG
                                 |||||||||  |||  |||||||
                                 TTATTTTTAC  TCC  TCGTGTC
                                      TC  __
GAM1747  PYGB     3'  AGTAACAATGAGGGGCACA   42815     A    T  CAA
                                 AGTAA AATGG GGG  GCACA
                                 ||||| ||||| |||  |||||
                                 TCATT TTACT CCC  CGTGT
                                   G   _  ___
GAM1747  SELP     3'  AGTAACAGGTGAGTCAAAGCAC 42816      AAAT    _  _
                AG                 AGTAA   GGTGGG CAA GCACAG
                                 |||||   |||||| ||| ||||||
                                 TCATT   CCACTC GTT CGTGTC
                                   GT__    A  T
GAM1747  SMCX     3'  AATAAAAAACTGTGAGCA    42817       TG_
                                 AGTAAAAA  GTGGGCA
                                 ||||||||  |||||||
                                 TTATTTTT  CACTCGT
                                     TGA
GAM1747  TRPV1    3'  GTAAGAGGAGCAAGCAC     42818     AAAT  T
                                 GTAA   GG GGGCAAGCAC
                                 ||||   || ||||||||||
                                 CATT   TC CTCGTTCGTG
                                   C___  _
GAM1747  TRPV1    3'  GTAAGAGGAGCAAGCAC     42818     AAAT  T
                                 GTAA   GG GGGCAAGCAC
                                 ||||   || ||||||||||
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                                CATT    TC CTCGTTCGTG
                                  C___  _
GAM1747  TRPV1    3'  GTAAGAGGAGCAAGCAC     42818      AAAT  T
                                GTAA    GG GGGCAAGCAC
                                ||||    || ||||||||||
                                CATT    TC CTCGTTCGTG
                                  C___  _
GAM1747  TRPV1    3'  GTAAGAGGAGCAAGCAC     42818      AAAT  T
                                GTAA    GG GGGCAAGCAC
                                ||||    || ||||||||||
                                CATT    TC CTCGTTCGTG
                                  C___  _
GAM1747  BCAA     3'  AGAAAAATGGCAAAGTACA   42819    T      TG GCA  C
                                AG AAAAATGG  G   AG ACA
                                || ||||||||  |   || |||
                                TC TTTTTACC  T   TC TGT
                                 _       GT ___  A
GAM1747  DKFZP586J1624 3'  GTAAGTGAAAGCACA       42820     AAAAT    GC
                                GTA    GGTGG  AAGCACA
                                |||    |||||  |||||||
                                CAT    TCACT  TTCGTGT
                                 ______    __
GAM1747  DNAJA2   3'  ATAAAAATCAAGCAC       42821        GGTGGG
                                GTAAAAAT     CAAGCAC
                                ||||||||     |||||||
                                TATTTTTA     GTTCGTG
                                   _______
GAM1747  FLJ10901 3'  AATAAAAAATTAGCAGGCA   42822         __   TG
                                AGTAAAAA  TGG  GGCA
                                ||||||||  |||  ||||
                                TTATTTTT  ATC  CCGT
                                     TA   GT
GAM1747  FLJ14327 3'  GTAAGAGGTAATTTAAGCACAG 42823      AAAT    GC_
                                GTAA    GGTGG   AAGCACAG
                                ||||    |||||   ||||||||
                                CATT    CCATT   TTCGTGTC
                                  CT__     AAA
GAM1747  FLJ21240 3'  TAAAAATTGTAAGCACA     42824        G   GGCA
                                TAAAAAT GTG    AGCACA
                                ||||||| |||    ||||||
                                ATTTTTA CAT    TCGTGT
                                   A  _____
GAM1747  KIAA1198 3'  ATAAAAATTAGCTGGGCA    42825         _ _
                                GTAAAAAT GG TGGGCA
                                |||||||| || ||||||
                                TATTTTTA TC ACCCGT
                                     A  G
GAM1747  KIAA1254 3'  AGTGAAAATAGGTGGGACA   42826     A    _     _
                                AGT AAAAT GGTGGG CA
                                ||| ||||| |||||| ||
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                                TCA TTTTA CCACCC GT
                                  C    T    T
GAM1747  KIAA1492  3'  AGTAACAGATGAATTGGGCAGG 42827      AA_   __    A
             CA                   AGTAA  ATGG  TGGGCA GCA
                                  |||||  ||||  |||||| |||
                                  TCATT  TACT  ACCCGT CGT
                                    GTC   TA    C
GAM1747  KIAA1712  3'  TAAAAATGTGGCCAAGCA    42828        G  G
                                  TAAAAATG TGG CAAGCA
                                  |||||||| ||| ||||||
                                  ATTTTTAC ACC GTTCGT
                                       _  G
GAM1747  MGC12466  3'  AGTAAAAAGTGGGCCAG     42829        AT      A
                                  AGTAAAA  GGTGGGC AG
                                  |||||||  ||||||| ||
                                  TCATTTT  TCACCCG TC
                                     __      G
GAM1747  MGC32043  3'  AGAGGAAATATTTTCAAGCACA 42830    TAA    GTGGG
             G                    AG  AAATG    CAAGCACAG
                                  ||  |||||    |||||||||
                                  TC  TTTAT    GTTCGTGTC
                                   TCC    AAAA_
GAM1747  NCBP2     3'  GTAAAAATGGGCTCGTGTGCA  42831       ATG     AA____
                                  GTAAAA  GTGGGC     GCA
                                  ||||||  ||||||     |||
                                  CATTTT  TACCCG     CGT
                                     ___     AGCACA
GAM1747  PP591     5'  AATAGGGGTCGCAAGCAC     42832       T  __
                                  AATGG GG  GCAAGCAC
                                  ||||| ||  ||||||||
                                  TTATC CC  CGTTCGTG
                                    C  AG
GAM1747  RCD-8     3'  AGTCAAGGTGGGCAGAGGGTAC 42833     AAAAAT       _  C__
             AG                   AGT     GGTGGGCA AG   ACAG
                                  |||     |||||||| ||   ||||
                                  TCA     CCACCCGT TC   TGTC
                                   GTT___       C  CCA
GAM1747  REPRIMO   3'  AGCAAAGTGGGCAGGC      42834       AAAT       A
                                  AGTAA    GGTGGGCA GC
                                  |||||    |||||||| ||
                                  TCGTT    TCACCCGT CG
                                     _____       C
GAM1747  TXNL2     3'  AATAAAAAATTAGGTGGGCA  42835        T___
                                  AGTAAAAA    GGTGGGCA
                                  ||||||||    ||||||||
                                  TTATTTTT    CCACCCGT
                                       TAAT
GAM1747  LOC145801 3'  AGTAAAAATGCTGTTACA    42836          G  G_
                                  AGTAAAAATG TG  GCA
                                  |||||||||| ||  |||
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                                TCATTTTTAC AC  TGT
                                      G  AA
GAM1747  LOC151050 5'  ATAAAAATTAGCCGGGCA    42837        _  _
                                GTAAAAAT GGT GGGCA
                                |||||||| ||| |||||
                                TATTTTTA TCG CCCGT
                                     A   G
GAM1747  LOC152804 3'  AGCAAAAAGAAAATGGCAGGCA 42838       _____   TG
                                AGTAAAA    ATGG  GGCA
                                |||||||    ||||  ||||
                                TCGTTTT    TACC  CCGT
                                    TCTTT   GT
GAM1747  LOC153218 3'  AGAAAAAGAATAAGCAAG    42839    T    TG
                                AG AAAAA  GTGGGCAAG
                                || |||||  |||||||||
                                TC TTTTT  TATTCGTTC
                                 _    CT
GAM1747  LOC153894 3'  GTAAGAATGGGGGCCACCAG   42840     A    T   AA  A
                                GTAA AATGG GGGC  GC CAG
                                |||| ||||| ||||  || |||
                                CATT TTACC CCCG  TG GTC
                                  C    _   G_ _
GAM1747  LOC162427 3'  AGAAAAATTAGCCGGGCA    42841    T   A   _
                                AG AAAA TGGT GGGCA
                                || |||| |||| |||||
                                TC TTTT ATCG CCCGT
                                 T   A   G
GAM1747  LOC196860 5'  AGTAAGGTTGGTCCAAGGCACA 42842      AAAT   _  G_   _
            G                    AGTAA   GGT GG  CAAG CACAG
                                |||||   ||| ||  |||| |||||
                                TCATT   CCA CC  GTTC GTGTC
                                  _____  A  AG   C
GAM1747  LOC221814 5'  ATAAAAATTAGCTGGGCA    42825        _  _
                                GTAAAAAT GG TGGGCA
                                |||||||| || ||||||
                                TATTTTTA TC ACCCGT
                                     A  G
GAM1747  LOC221815 5'  ATAAAAATTAGCTGGGCA    42825        _  _
                                GTAAAAAT GG TGGGCA
                                |||||||| || ||||||
                                TATTTTTA TC ACCCGT
                                     A  G
GAM1747  LOC222166 3'  AGCAGAGGTGGACAGGGTGCA  42843     AAAAT      A___
                                AGTA    GGTGGGCA   GCA
                                ||||    ||||||||   |||
                                TCGT    CCACCTGT   CGT
                                  CT___       CCCA
GAM1747  LOC245771 5'  AATAAAAAATTAGCAGGCA   42822        __  TG
                                AGTAAAAA  TGG  GGCA
                                ||||||||  |||  ||||
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                                TTATTTTT  ATC  CCGT
                                    TA   GT
GAM1747  LOC257295 3'  AGTAAAAATGCTGTTACA    42836          G  G_
                                AGTAAAAATG TG  GCA
                                |||||||||| ||  |||
                                TCATTTTTAC AC  TGT
                                     G  AA
GAM1747  LOC51193  5'  AGTAAAAAATGCCTCGCCGGGT 42844         _______ G   CAA
           GCA                    AGTAAAAA     TG TGGG   GCA
                                |||||||||     || ||||   |||
                                TCATTTTT     GC GCCC   CGT
                                    TACGGA  G    A__
GAM1747  LOC92148  5'  AGAAAAAATTAGCTGGGCA   42845    T     _ _
                                AG AAAAAT GG TGGGCA
                                || |||||| || ||||||
                                TC TTTTTA TC ACCCGT
                                 T     A  G
GAM1748  ABCD1    5'  ACTGTCGCTTTAGGCCCCCGGG 42848     C   GA  TA
                                GCTG CGC  TG  CCCCCGGG
                                |||| |||  ||  ||||||||
                                TGAC GCG  AT  GGGGGCCC
                                  A   AA  CC
GAM1748  ABCD4    3'  GCCGTTGCATCTCCCCCGGG   42849     CGA   ___
                                GCCG   TGTA   CCCCCGGG
                                ||||   ||||   ||||||||
                                CGGC   ACGT   GGGGGCCC
                                  A__    AGA
GAM1748  ATP11A   3'  AAGCTGCGACTTCACCCCCGGG 42850       C  GATG
                                AAGCTGC GC    TACCCCCGGG
                                ||||||| ||    ||||||||||
                                TTCGACG TG    GTGGGGGCCC
                                    C  AA__
GAM1748  BIRC7    5'  AGCTCCTGACCCCCG      42851      G  GCGA  T
                                AGCT CC    TG ACCCCCG
                                |||| ||    || |||||||
                                TCGA GG    AC TGGGGGC
                                  _  ____  _
GAM1748  BIRC7    5'  AGCTCCTGACCCCCG      42851      G  GCGA  T
                                AGCT CC    TG ACCCCCG
                                |||| ||    || |||||||
                                TCGA GG    AC TGGGGGC
                                  _  ____  _
GAM1748  DIAPH2   5'  AAGCTGCCGATTTCAGGCCCCC 42852         CGATGTA_
           GGG                    AAGCTGCCG       CCCCCGGG
                                |||||||||       ||||||||
                                TTCGACGGC       GGGGGCCC
                                     TAAAGTCC
GAM1748  DIAPH2   5'  AAGCTGCCGATTTCAGGCCCCC 42852         CGATGTA_
           GGG                    AAGCTGCCG       CCCCCGGG
                                |||||||||       ||||||||
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                                TTCGACGGC      GGGGGCCC
                                     TAAAGTCC
GAM1748 ECEL1    5' GCCGCCGCGGTGCAGACCTGGG 42853        A   CC  C
                                GCTGCCGCG TGTA  CC GGG
                                ||||||||| ||||  || |||
                                CGGCGGCGC ACGT  GG CCC
                                     C   CT  A
GAM1748 KIP2     3' GCTGCCACTGCTTTCCTGGG  42854       GA  ACC  C
                                GCTGCCGC  TGT  CC GGG
                                ||||||||  |||  || |||
                                CGACGGTG  ACG  GG CCC
                                     __  AAA  A
GAM1748 MFGE8    3' AAGCTGCCTGTGTCCTCTGGG 42855       GCGA  A  CCC
                                AAGCTGCC   TGT CC  GGG
                                ||||||||   ||| ||  |||
                                TTCGACGG   ACA GG  CCC
                                     AC__  _ AGA
GAM1748 MFI2     3' GCCGCCGCGGAAACTCCCCGGG 42856       ATGT  _
                                GCTGCCGCG   AC CCCCGGG
                                |||||||||   || |||||||
                                CGGCGGCGC   TG GGGGCCC
                                     CTT_  A
GAM1748 PIK3R3   5' AAGCTGCCGCAGCCTCGG    42857        ATGTAC  C
                                AAGCTGCCGCG    CC CGG
                                ||||||||||     || |||
                                TTCGACGGCGT    GG GCC
                                     C_____  A
GAM1748 SLC6A8   3' AAGCTGCCACTGCTGCTTCTGG 42858       GA_  ACCCCC
           G                     AAGCTGCCGC  TGT    GGG
                                ||||||||||  |||    |||
                                TTCGACGGTG  ACG    CCC
                                     ACG  AAGA__
GAM1748 TBL1X    5' AGCAGCCGCGCGCCGCCCCCGG 42859    T    A  A_
           G                     AGC GCCGCG TGT  CCCCCGGG
                                ||| |||||| |||  ||||||||
                                TCG CGGCGC GCG  GGGGGCCC
                                  T    _  GC
GAM1748 ARFRP1   3' GCTGCCGCTGCAGGGCCTGGG  42860       GA   CC_  C
                                GCTGCCGC  TGTA  CC GGG
                                ||||||||  ||||  || |||
                                CGACGGCG  ACGT  GG CCC
                                     __   CCC  A
GAM1748 CENTG2   5' GCGCCGCAGCCCCCGG     42861    T    ATGTA
                                GC GCCGCG    CCCCCGG
                                || ||||||    |||||||
                                CG CGGCGT    GGGGGCC
                                  _    C_____
GAM1748 DKFZP434B195 5' GCTGCCGCCAACCGGCCCTCGG 42862        _  GTA  C
           G                     GCTGCCGC GAT   CCC CGGG
                                ||||||||  |||   ||| ||||
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                                CGACGGCG TTG   GGG GCCC
                                    G  GCC  A
GAM1748 FLJ11618 3' AAGCTGCCTGTGTCGCCCACCC 42863       GCGA_  __    C
            CTGGG                   AAGCTGCC    TGT  ACCCC GGG
                                ||||||||    |||  ||||| |||
                                TTCGACGG    GCG  TGGGG CCC
                                    ACACA  GG    A
GAM1748 FLJ21742 3' GCTGCTGCTGACCCTTGGG   42864      C  GA  T   CC
                                GCTGC GC  TG ACCC  GGG
                                ||||| ||  || ||||  |||
                                CGACG CG  AC TGGG  CCC
                                  A  __ _   AA
GAM1748 JIK     5'  GCTGTCACCACCCCCGGG    42865     C   GATG
                                GCTG CGC    TACCCCCGGG
                                |||| |||    ||||||||||
                                CGAC GTG    GTGGGGGCCC
                                  A  _____
GAM1748 KIAA0963 5' AGCTGCCGCCGCTCACTTCCGG 42866        GATG   CC
            G                    AGCTGCCGC    TAC  CCGGG
                                |||||||||    |||  |||||
                                TCGACGGCG    GTG  GGCCC
                                     GCGA   AA
GAM1748 KIAA1199 5' GCGCCGCGAGCTCCCGG     42867    T      T  ACC
                                GC GCCGCGA GT   CCCGG
                                || ||||||| ||   |||||
                                CG CGGCGCT CG   GGGCC
                                 _      _ A__
GAM1748 KIAA1912 5' GCTGCCGCGGGAAATCCTCGGG 42868         ATGTAC  C
                                GCTGCCGCG     CC CGGG
                                |||||||||     || ||||
                                CGACGGCGC     GG GCCC
                                     CCTTTA  A
GAM1748 LHFPL2   5' AAGTGCTGCACCCCG      42869     C   CGCGA      C
                                AAG TGC    TGTACCCC G
                                ||| |||    |||||||| |
                                TTC ACG    ACGTGGGG C
                                  _  ______       A
GAM1748 MAGEF1   5' AGCCGCCGCGCAAGCCCCGGG  42870         ATGTAC
                                AGCTGCCGCG     CCCCGGG
                                ||||||||||     |||||||
                                TCGGCGGCGC     GGGGCCC
                                     GTTC__
GAM1748 MGC14128 5' GCTCCCGCACCCCCGG     42871     G   GATGT
                                GCT CCGC    ACCCCCGG
                                ||| ||||    ||||||||
                                CGA GGCG    TGGGGGCC
                                  G   ______
GAM1748 OPRL1    3' AAGCTGCCTGCTGCACTTCCCG 42872        GCGA    C_
            GG                    AAGCTGCC   TGTAC  CCCGGG
                                |||||||   |||||  ||||||
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                                TTCGACGG   ACGTG  GGGCCC
                                    ACG_    AA
GAM1748  PARVA    5'  GCTGCCGCGGGCCGGTCGGG  42873       AT  ACCCC
                                GCTGCCGCG  GT    CGGG
                                |||||||||  ||    ||||
                                CGACGGCGC  CG    GCCC
                                    C_  GCCA_
GAM1748  PCBP4    3'  GCTGCCGCAGCTCAGACCCCTG 42874       ATGT__    C
           GG                     GCTGCCGCG     ACCCC GGG
                                |||||||||     ||||| |||
                                CGACGGCGT     TGGGG CCC
                                    CGAGTC    A
GAM1748  PCBP4    3'  GCTGCCGCAGCTCAGACCCCTG 42874       ATGT__    C
           GG                     GCTGCCGCG     ACCCC GGG
                                |||||||||     ||||| |||
                                CGACGGCGT     TGGGG CCC
                                    CGAGTC    A
GAM1748  PCBP4    3'  GCTGCCGCAGCTCAGACCCCTG 42874       ATGT__    C
           GG                     GCTGCCGCG     ACCCC GGG
                                |||||||||     ||||| |||
                                CGACGGCGT     TGGGG CCC
                                    CGAGTC    A
GAM1748  PDZD2    5'  AGCCGCTGCTTTCTCCCCCGGG 42875      C  GATGTA
                                AGCTGC GC     CCCCCGGG
                                ||||||  ||    ||||||||
                                TCGGCG CG     GGGGGCCC
                                   A  AAAGA_
GAM1748  RNF13    5'  AAGTTGCATGAGTGCTTCCGGG 42876    C   CGC  _   ACCC
                                AAG TGC   GA TGT    CCGGG
                                |||  |||   ||  |||    |||||
                                TTC ACG   CT ACG    GGCCC
                                  A   TA_  C   AA__
GAM1748  SH3BGRL2 5'  AGCCGCCGGCAGCCTCTGGG   42877       CGAT   C  CC_
                                AGCTGCCG    GTA CC   GGG
                                ||||||||    |||  ||   |||
                                TCGGCGGC    CGT GG   CCC
                                    _____   C  AGA
GAM1748  Spir-2   3'  AAACTGCCGTTCGCATTCCTGG 42878        CGA    CC  C
           G                     AAGCTGCCG   TGTA  CC GGG
                                |||||||||   ||||  ||  |||
                                TTTGACGGC   GCGT  GG CCC
                                    AA_    AA  A
GAM1748  STK29    3'  AGCTGCCGCGGGGTGGACGGG  42879        AT  ACCCC
                                AGCTGCCGCG  GT    CGGG
                                ||||||||||  ||    ||||
                                TCGACGGCGC  CA    GCCC
                                    CC  CCT__
GAM1748  LOC138835 5'  AAGCTGCCGTGGAGATGGTTGG 42880         C___    TACCCCC
           G                     AAGCTGCCG   GATG      GGG
                                |||||||||   ||||      |||
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                                TTCGACGGC  CTAC     CCC
                                    ACCT   CAA____
GAM1748  LOC146488 3'  AAGCTGCCACTGCTGCTTCTGG 42858       GA_  ACCCCC
            G                    AAGCTGCCGC  TGT    GGG
                                 ||||||||||  |||    |||
                                TTCGACGGTG  ACG    CCC
                                    ACG  AAGA__
GAM1748  LOC148887 3'  AGCTGCCGGGGACGATGTCCCG 42881       ____    ACC
            GG                   AGCTGCCG  CGATGT  CCCGGG
                                 ||||||||  ||||||  ||||||
                                TCGACGGC  GCTACA  GGGCCC
                                    CCCT   ___
GAM1748  LOC149297 5'  AGCCGCCGGGCATCCTTGGG  42882       CGAT  C  CC
                                AGCTGCCG  GTA CC  GGG
                                ||||||||  ||| ||  |||
                                TCGGCGGC  CGT GG  CCC
                                    C___  A  AA
GAM1748  LOC149506 3'  AGCTGCCGTGGATCACTTCTTG 42883       C_  G  CCCC_
            GG                   AGCTGCCG  GAT TAC    GGG
                                 ||||||||  ||| |||    |||
                                TCGACGGC  CTA GTG    CCC
                                    AC  _  AAGAA
GAM1748  LOC150244 5'  GCTGCGTGCAGGCCCCCGGG  42884   C  A  __
                                GC GCG TGTA  CCCCCGGG
                                || ||| ||||  ||||||||
                                CG CGC ACGT  GGGGGCCC
                                 A  _   CC
GAM1748  LOC201911 3'  CTGCCGCGAGCCCCGG     42885       TGTAC
                                CTGCCGCGA    CCCCGG
                                |||||||||    ||||||
                                GACGGCGCT    GGGGCC
                                    C____
GAM1748  LOC219401 5'  AAACTGCCGCAGCGCTCCCTGG 42886        A  A  CC
            G                    AAGCTGCCGCG TGT CCC  GGG
                                 |||||||||| ||| |||  |||
                                TTTGACGGCGT GCG GGG  CCC
                                      C  A  A_
GAM1748  LOC220776 3'  AAGCTGTCCGTTTGCCCTGGG  42887     _  CGA  TAC  C
                                AAGCTG CCG   TG   CCC GGG
                                |||||| |||   ||   ||| |||
                                TTCGAC GGC   AC   GGG CCC
                                   A  AA_  ___   A
GAM1748  LOC221405 5'  AAGCTGCCAGTGGGGCCTTGGG 42888       CGA  TAC  CC
                                AAGCTGCCG   TG   CC  GGG
                                |||||||||   ||   ||  |||
                                TTCGACGGT   AC   GG  CCC
                                    C__  CCC  AA
GAM1748  LOC222832 5'  GCCGCCGCGTCCCCGG     42889       ATGTAC
                                GCTGCCGCG    CCCCGG
                                |||||||||    ||||||
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                                CGGCGGCGC     GGGGCC
                                     A_____
GAM1748 LOC91344 5' AGCTGCCAGGAGCAGTCCCTGG 42890        C T  CC  _
             G                    AGCTGCCG GA GTA  CCC GGG
                                  |||||||| || |||  ||| |||
                                  TCGACGGT CT CGT  GGG CCC
                                      C  _  CA  A
GAM1748 LOC91768 5' ACTGCCGCTCCCACTCCCGGG  42891        GATG  C
                                  GCTGCCGC   TAC CCCGGG
                                  ||||||||   ||| ||||||
                                  TGACGGCG   GTG GGGCCC
                                      AGG_  A
GAM1749 ITCH    3' CAGGCAACTGAAACAATC    42894      ATTCTT
                                  CGGG     CTGAAACAATC
                                  ||||     ||||||||||
                                  GTCC     GACTTTGTTAG
                                    GTT___
GAM1749 MTMR8   3' TACCGGCCCCTCTGGGGCAATC 42895       GA       AAA
                                  TACCGG  TTCTTCTG   CAATC
                                  ||||||  ||||||||   |||||
                                  ATGGCC  GGGGAGAC   GTTAG
                                     __       CCC
GAM1749 SLC7A5  3' CAAGTCTTCTGAGACA      42896      AT       A
                                  CGGG  TCTTCTGA ACA
                                  ||||  |||||||| |||
                                  GTTC  AGAAGACT TGT
                                    __       C
GAM1749 SPOCK   5' GGGATTCCAGTTTCTGAAATAA 42897         _____      C
             TC                    GGGATTCT   TCTGAAA AATC
                                   ||||||||   ||||||| ||||
                                   CCCTAAGG   AGACTTT TTAG
                                       TCAA      A
GAM1749 DKFZP434N093 3' CCTGGACTGAAACAAT      42898    G   TTCTT
                                  CC GGA     CTGAAACAAT
                                  || |||     ||||||||||
                                  GG CCT     GACTTTGTTA
                                   A  _____
GAM1749 DNAM-1  3' CAGGTTTTCTGAAACA      42899      A  C
                                  CGGG TT TTCTGAAACA
                                  |||| || ||||||||||
                                  GTCC AA AAGACTTTGT
                                     _ _
GAM1749 FLJ10300 5' TACCTCGCTTCTGAAACA    42900      GGGATT
                                  TACC     CTTCTGAAACA
                                  ||||     ||||||||||
                                  ATGG     GAAGACTTTGT
                                    AGC___
GAM1749 KIAA0669 3' CCAGGATTCTTTTGTTCAAT   42901          C  AAA
                                  CCGGGATTCTT TG   CAAT
                                  |||||||||| ||   ||||
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                                GGTCCTAAGAA AC   GTTA
                                      A  AA_
GAM1749  KIAA1157  3'  TACATGGTTCTGAAACAAT   42902    CG  ATTC
                                TAC  GG   TTCTGAAACAAT
                                |||  ||   ||||||||||||
                                ATG  CC   AAGACTTTGTTA
                                  TA  ____
GAM1749  USP25     3'  GGGATTCTCTTGAAATAATC   42903       TC    C
                                GGGATTCT  TGAAA AATC
                                ||||||||  ||||| ||||
                                CCCTAAGA  ACTTT TTAG
                                     GA    A
GAM1749  LOC145845 5'  CCAAGACTTTTGAAACA    42904      TT   C
                                CCGGGA  CTT TGAAACA
                                ||||||  ||| |||||||
                                GGTTCT  GAA ACTTTGT
                                   __  A
GAM1750  CLN5      5'  GGAAGCATTCTAGCCCTGAGAG 42907        _      A
                                GGAAGCAT CTGGTCCT AGAG
                                |||||||| |||||||| ||||
                                CCTTCGTA GATCGGGA TCTC
                                     A       C
GAM1750  CNN1      3'  TGGGGGAGCTTCTGGTCCT   42908    A  A   A
                                TG GG AGC TCTGGTCCT
                                || || ||| |||||||||
                                AC CC TCG AGACCAGGA
                                 C  C   A
GAM1750  COL4A5    3'  AGGGGGCATATGGTCTTAAGAG 42909     AA   C    C
                                AGG  GCAT TGGTC TAAGAG
                                |||  |||| ||||| ||||||
                                TCC  CGTA ACCAG ATTCTC
                                  CC   T    A
GAM1750  COL4A5    3'  AGGGGGCATATGGTCTTAAGAG 42909     AA   C    C
                                AGG  GCAT TGGTC TAAGAG
                                |||  |||| ||||| ||||||
                                TCC  CGTA ACCAG ATTCTC
                                  CC   T    A
GAM1750  COL4A5    3'  AGGGGGCATATGGTCTTAAGAG 42909     AA   C    C
                                AGG  GCAT TGGTC TAAGAG
                                |||  |||| ||||| ||||||
                                TCC  CGTA ACCAG ATTCTC
                                  CC   T    A
GAM1750  CYLN2     3'  TGAGGAAGCGTCCTGGTCTGGC 42910         A_      CTAA
            GAG                   TGAGGAAGC  TCTGGTC   GAG
                                |||||||||  |||||||   |||
                                ACTCCTTCG  GGACCAG    CTC
                                     CA      ACCG
GAM1750  DUOX1     3'  TGAGACACATCCTGGTCCT   42911      AA    _
                                TGAGG  GCATC TGGTCCT
                                |||||  ||||| |||||||
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                                ACTCT  TGTAG ACCAGGA
                                   G_    G
GAM1750 NEUROD2  3' TGGAGAAGCACTCCTTGGGAG 42912    AG     CTGG   AA_
                                TG  GAAGCAT   TCCT   GAG
                                ||  |||||||   ||||  |||
                                AC  CTTCGTG   AGGA   CTC
                                 CT      _____   ACC
GAM1750 SDHC     3' TGAGAAAGCATAAAATTAAGAG 42913          CT   CC
                                TGAGGAAGCAT  GGT  TAAGAG
                                ||||||||||  |||  ||||||
                                ACTCTTTCGTA  TTA  ATTCTC
                                       TT   __
GAM1750 C11orf11  5' TGAGTAGGCATCTGACTGGGAG 42914      GAA      TC  AA
                                TGAG   GCATCTGG  CT  GAG
                                ||||   ||||||||  ||  |||
                                ACTC   CGTAGACT  GA  CTC
                                  ATC       __  CC
GAM1750 C6orf33   3' TGGGGCAGCATCTATGTAGGAG 42915    A  A      GTCC  A
                                TG GG AGCATCTG    TA GAG
                                || || ||||||||    || |||
                                AC CC TCGTAGAT    AT CTC
                                 C  G       AC__  C
GAM1750 DKFZP434A0131 3' TGGGCAAGCACGGTCTTGGGAG 42916    A  _     CT   CTAA
                                TG GG AAGCAT  GGTC    GAG
                                || || ||||||  ||||    |||
                                AC CC TTCGTG  CCAG    CTC
                                 _  G     __    AACC
GAM1750 DKFZp434F142 3'  TGAGGAAGTTCTGGGCCTGGAG 42917        CA    T   AA
                                TGAGGAAG  TCTGG CCT  GAG
                                ||||||||  ||||| |||  |||
                                ACTCCTTC  AGACC GGA  CTC
                                     A_    C   C_
GAM1750 DKFZp547I094 5'  AGGAAGCACAGGTCTGGGAG   42918        CT   CTAA
                                AGGAAGCAT  GGTC    GAG
                                |||||||||  ||||    |||
                                TCCTTCGTG  CCAG    CTC
                                     T_    ACC_
GAM1750 FLJ12788  3' TGAGGGAACGTAGGCCTGAG   42919      A   ATCT  T   A
                                TGAGG AGC    GG CCT AG
                                ||||| |||    || ||| ||
                                ACTCC TTG    CC GGA TC
                                   C   CAT_ _   C
GAM1750 FLJ22301  3' TGGGGAACATGGTTCTGAGAG  42920    A  A    TC    C  A
                                TG GG AGCA  TGGT CT AGAG
                                || || ||||  |||| || ||||
                                AC CC TTGT  ACCA GA TCTC
                                 _  C    __    A  C
GAM1750 FLJ23590  5' TGAGGAAGCGGGTGCTTAAGAG 42921         ATCT   C  _
                                TGAGGAAGC    GGT CT AAGAG
                                |||||||||    ||| || |||||
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                                ACTCCTTCG   CCA GA TTCTC
                                    C___  C  A
GAM1750 KIAA0350 3' TGAGGAAGCGTCCTGAG    42922       ATCTG   AA
                                TGAGGAAGC   GTCCT  GAG
                                |||||||||   |||||  |||
                                ACTCCTTCG   CAGGA  CTC
                                    _____   __
GAM1750 KIAA1110 3' TGAGGAAGCAGAGGCCCTGGGA 42923        TCT    AA
          G                  TGAGGAAGCA  GGTCCT  GAG
                             |||||||||  ||||||  |||
                             ACTCCTTCGT  CCGGGA  CTC
                                   CT_    CC
GAM1750 MADHIP   5' TGAGGAAACACCACTTAAGAG  42924        TGGTCC
                             TGAGGAAGCATC    TAAGAG
                             ||||||||||||    ||||||
                             ACTCCTTTGTGG    ATTCTC
                                    TGA___
GAM1750 MADHIP   5' TGAGGAAACACCACTTAAGAG  42924        TGGTCC
                             TGAGGAAGCATC    TAAGAG
                             ||||||||||||    ||||||
                             ACTCCTTTGTGG    ATTCTC
                                    TGA___
GAM1750 MADHIP   5' TGAGGAAACACCACTTAAGAG  42924        TGGTCC
                             TGAGGAAGCATC    TAAGAG
                             ||||||||||||    ||||||
                             ACTCCTTTGTGG    ATTCTC
                                    TGA___
GAM1750 MGC14480 3' TGGGGAAGCATCTTCCAAG   42925   A      GG  T
                             TG GGAAGCATCT  TCC AAG
                             || ||||||||||  ||| |||
                             AC CCTTCGTAGA  AGG TTC
                              C       __  _
GAM1750 MGC15677 5' TGGGGAAGGCAATGGGGTCCTG 42926   A   _ TCT_    A
          AG                  TG GGAAG CA   GGTCCT AG
                              || ||||| ||   |||||| ||
                              AC CCTTC GT   CCAGGA TC
                               C    C  TACC    C
GAM1750 MGC2541  3' TGGGAAGCATGGTACCTCCTAG 42927   A    TC  ____   A
          GAG                   G GGAAGCA  TGG   TCCTA GAG
                                | |||||||  |||   ||||| |||
                                C CCTTCGT  ACC   AGGAT CTC
                                _     __  ATGG    C
GAM1750 STARD7   5' TGAGGAAGAGTCTCCTCTGAG  42928       CA  TGG   AA
                             TGAGGAAG  TC   TCCT  GAG
                             ||||||||  ||   ||||  |||
                             ACTCCTTC  AG   AGGA  CTC
                                  TC  ___   GA
GAM1750 ZNF220   3' TGGGGAAGGGTTTCAAGA   42929   A   CATCT   CC
                             TG GGAAG    GGT  TAAGA
                             || |||||    |||  |||||
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                                AC CCTTC    CCA  GTTCT
                                 C    _____  AA
GAM1750  LOC113763 3'  TGAGAAAGCAAGCCTCTTAAG  42930        TCT   _ _
                                TGAGGAAGCA   GGTC CT AAG
                                ||||||||||   |||| || |||
                                ACTCTTTCGT   TCGG GA TTC
                                      ___    A  A
GAM1750  LOC146243 3'  AGGAAGCATCAGGATAGGAG  42931        T  TCCTAA
                                AGGAAGCATC GG     GAG
                                |||||||||| ||     |||
                                TCCTTCGTAG CC     CTC
                                      T  TATC__
GAM1750  LOC219649 3'  TGAGGAAGGTCACAGTTAAGAG 42932        CA  _   CC
                                TGAGGAAG  TC TGGT  TAAGAG
                                ||||||||  || ||||  ||||||
                                ACTCCTTC  AG GTCA  ATTCTC
                                     C_  T   __
GAM1750  LOC221486 3'  TGGGGAGGCATCTGGCTCTCAG 42933    A   A      TC  A
                                TG GGA GCATCTGG  CT AG
                                || ||| ||||||||  || ||
                                AC CCT CGTAGACC  GA TC
                                 C   C       GA  G
GAM1750  LOC223009 5'  TGAGGAAGTTTTGGGCCTGGAG 42934        CATC   T   AA
                                TGAGGAAG    TGG CCT  GAG
                                ||||||||    ||| |||  |||
                                ACTCCTTC    ACC GGA  CTC
                                     AAA_   C   C_
GAM1750  LOC255975 5'  TGAGGCAGCACCTGCCTGGGAG 42935      A       GT   AA
                                TGAGG AGCATCTG  CCT  GAG
                                ||||| ||||||||  |||  |||
                                ACTCC TCGTGGAC  GGA  CTC
                                   G       __   CC
GAM1750  LOC51075  3'  TGAGGAAGCAAGAGTCCT    42936         TCT
                                TGAGGAAGCA   GGTCCT
                                ||||||||||   ||||||
                                ACTCCTTCGT   TCAGGA
                                      TC_
GAM1751  BACE     3'  AGAGCTAAAAAAGAGCTCTTT  42939        TTTGT  A
                                AGAGCTAAA    GA CTCTTT
                                |||||||||    || ||||||
                                TCTCGATTT    CT GAGAAA
                                     TTT__  C
GAM1751  BACE     3'  AGAGCTAAAAAAGAGCTCTTT  42939        TTTGT  A
                                AGAGCTAAA    GA CTCTTT
                                |||||||||    || ||||||
                                TCTCGATTT    CT GAGAAA
                                     TTT__  C
GAM1751  CDH19    3'  TAGAGCCAGGGCACAAAACTCT 42940        AATTTGT
              TT                  TAGAGCTA     GAACTCTTT
                                ||||||||     |||||||||
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                                ATCTCGGT      TTTGAGAAA
                                     CCCGTGT
GAM1751  COL19A1   3'  TAGAGTGGGTGTGAACTCTTT  42941      CTAAATT
                                TAGAG      TGTGAACTCTTT
                                |||||      ||||||||||||
                                ATCTC      ACACTTGAGAAA
                                   ACCC___
GAM1751  TSG       3'  GAGCTAAATCTCAACT      42942          GTG
                                GAGCTAAATTT   AACT
                                ||||||||||   ||||
                                CTCGATTTAGA   TTGA
                                      G__
GAM1751  FLJ11184  3'  GAGCTAAACTGAAACTCTTT   42943         T T
                                GAGCTAAATT G GAACTCTTT
                                |||||||||| | |||||||||
                                CTCGATTTGA C TTTGAGAAA
                                     _ _
GAM1751  FLJ14393  3'  TAGAGCCAAAGAAGCTCTT    42944         TTTGT  _
                                TAGAGCTAAA     GAA CTCTT
                                ||||||||||     ||| |||||
                                ATCTCGGTTT     CTT GAGAA
                                      _____  C
GAM1751  HSA243666 3'  CAGAGCTAGGTCTGTTCTTT   42945        AA    GAAC
                                TAGAGCTA  TTTGT    TCTTT
                                ||||||||  |||||    |||||
                                GTCTCGAT  AGACA    AGAAA
                                     CC    _____
GAM1751  PDZ-GEF1  3'  TAGAGCTAGATTTCTGTCTTT  42946        A    G  AAC
                                TAGAGCTA ATTT TG   TCTTT
                                |||||||| |||| ||   |||||
                                ATCTCGAT TAAA AC   AGAAA
                                     C    G  ___
GAM1751  PRO0902   3'  TAGGGCTATGAAACTCTT    42947     A    AATT  T
                                TAG GCTA    TG GAACTCTT
                                ||| ||||    || ||||||||
                                ATC CGAT    AC TTTGAGAA
                                  C   _____ _
GAM1752  DBY       3'  TGAATTGATGACTCCTGTTAAA 42950         A  AAAGA
              G                  TGGATTGAT AC     GTTAAAG
                                |||||||||  ||     |||||||
                                ACTTAACTA TG     CAATTTC
                                     C  AGGA_
GAM1752  GCLM      3'  TGGATTGATATGGAGGCAA    42951          ACAAA   T
                                TGGATTGATA     GAG TAA
                                ||||||||||     ||| |||
                                ACCTAACTAT     CTC GTT
                                      AC___   C
GAM1752  RAD52     3'  TGGATTGATACAAAGTAG     42952          A    _
                                TGGATTGATA CAAAG AG
                                |||||||||| ||||| ||
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                                ACCTAACTAT GTTTC TC
                                      _    A
GAM1752  RAD52    3'  TGGATTGATACAAAGTAG    42952         A    _
                                TGGATTGATA CAAAG AG
                                |||||||||| ||||| ||
                                ACCTAACTAT GTTTC TC
                                      _    A
GAM1752  RAD52    3'  TGGATTGATACAAAGTAG    42952         A    _
                                TGGATTGATA CAAAG AG
                                |||||||||| ||||| ||
                                ACCTAACTAT GTTTC TC
                                      _    A
GAM1752  RAD52    3'  TGGATTGATACAAAGTAG    42952         A    _
                                TGGATTGATA CAAAG AG
                                |||||||||| ||||| ||
                                ACCTAACTAT GTTTC TC
                                      _    A
GAM1752  RPL10    3'  TGGATTGGTAAGAATCA     42953       ATAACA
                                TGGATTG     AAGAGTTA
                                |||||||     ||||||||
                                ACCTAAC     TTCTTAGT
                                    CA____
GAM1752  SERPINH2 3'  TGGATTGATAGCAACAAAG   42954          ___
                                TGGATTGATA   ACAAAG
                                ||||||||||   ||||||
                                ACCTAACTAT   TGTTTC
                                      CGT
GAM1752  ADAMDEC1 3'  TGGACTGATAACAATATAGAA  42955             ___
                                TGGATTGATAACAA   AGAG
                                ||||||||||||||   ||||
                                ACCTGACTATTGTT   TCTT
                                       ATA
GAM1752  GIT2     3'  TGGATGGATTAGAGTTAA    42956      T   AACAA
                                TGGAT GAT    AGAGTTAA
                                ||||| |||    ||||||||
                                ACCTA CTA    TCTCAATT
                                   C   A____
GAM1752  KIAA1805 3'  TGGAGGAGCACAAAGAGTTAAA 42957     TT  TA
            G                    TGGA  GA  ACAAAGAGTTAAAG
                                ||||  ||  ||||||||||||||
                                ACCT  CT  TGTTTCTCAATTTC
                                  C_  CG
GAM1752  ZNF304   5'  TGGATTGTAACAAAAGC     42958       A     A
                                TGGATTG TAACAA GAGT
                                ||||||| |||||| ||||
                                ACCTAAC ATTGTT TTCG
                                      _    _
GAM1752  LOC151190 3'  TAGATTGATAATAAAAAG    42959          C
                                TGGATTGATAA AAAGAG
                                |||||||||| ||||||
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                                ATCTAACTATT TTTTTC
                                       A
GAM1752  LOC90844  3'  TGGATGATAACAATAAA     42960      T      A
                                TGGAT GATAACAA GAG
                                ||||| |||||||| |||
                                ACCTA CTATTGTT TTT
                                   _      A
GAM1753  LMNA      5'  GCAGGCGTGGGGATCTGG    42963      T  CGCGA
                                GCGGGT TG    GGATCTGG
                                |||||| ||    ||||||||
                                CGTCCG AC    CCTAGACC
                                   C  C____
GAM1753  C22orf20  5'  CGCGGGTTAGGATCT       42964        TGCGCG
                                CGCGGGTT     AGGATCT
                                ||||||||     |||||||
                                GCGCCCAA     TCCTAGA

                                   _______
GAM1753  LOC124446 5'  TCTGGGGCGAGGATTTG     42965    GC   TTTGC      C
                                TC  GGG    GCGAGGAT TG
                                ||  |||    |||||||| ||
                                AG  CCC    CGCTCCTA AC
                                 A_  _____      A
GAM1753  LOC222171 3'  TCTCGGGTTTGGAACTGG    42966    G      GCGCGA   T
                                TC CGGGTTT     GGA CTGG
                                || |||||||     ||| ||||
                                AG GCCCAAA     CCT GACC
                                 A      _______  T
GAM1753  LOC253805 3'  GCGGGTCTGTGCACACTCTGG  42967        C   AGGA
                                GCGGGTTTG GCG    TCTGG
                                ||||||||| |||    |||||
                                CGCCCAGAC CGT    AGACC
                                      A  GTG_
GAM1754  SPON1     3'  TGTTTCAGCTTAGTACAAGGTG 42970        GTACC    AC_
              GC                    TGTTTCAGC    GCAA   GGC
                                |||||||||    ||||   |||
                                ACAAAGTCG    TGTT   CCG
                                      AATCA    CCA
GAM1754  LOC149703 3'  TGTTTCATTTTCCAAACGGC   42971       GCGTACCG
                                TGTTTCA       CAAACGGC
                                |||||||       ||||||||
                                ACAAAGT       GTTTGCCG
                                    AAAAG___
GAM1754  LOC203365 3'  TTTCAGCGCGCATGTGGGTGGC 42972        TAC    AAC____
                                TTTCAGCG   CGCA      GGC
                                ||||||||   ||||      |||
                                AAAGTCGC   GCGT      CCG
                                    ___    ACACCCA
GAM1754  LOC203368 3'  TGTTTCAGCTGTATTGCAGGC  42973         _   CC   AAC
                                TGTTTCAGC GTA  GCA   GGC
                                ||||||||| |||  |||   |||
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                                ACAAAGTCG CAT  CGT   CCG
                                     A   AA  ___
GAM1754  LOC54518  3'  TGTTTCAGCATGTCTCTGGGCC 42974          ACCGCAAAC
                                TGTTTCAGCGT       GGCC
                                ||||||||||        ||||
                                ACAAAGTCGTA       CCGG
                                      CAGAGAC__
GAM1755  LASS1     3'  TGGCCGCAGGGACCTTGCTG   42977      TATTA
                                TGGTT    GACCTTGCTG
                                |||||    ||||||||||
                                ACCGG    CTGGAACGAC
                                   CGTCC
GAM1755  LDHB      5'  ATGGTGTATGGGGGCCTTGCTG 42978      T   TAGA_
                                ATGGT TAT    CCTTGCTG
                                ||||| |||    ||||||||
                                TACCA ATA    GGAACGAC
                                   C   CCCCC
GAM1755  SHANK2    3'  GGCTGGCAGGGCCTTGCTG    42979     TAT   A_
                                GGTT   TAG  CCTTGCTG
                                ||||   |||  ||||||||
                                CCGA   GTC  GGAACGAC
                                  CC_   CC
GAM1755  C1QR1     3'  TAAATGGCTTTGAGCAGTTTTT 42980          AT__   ACC
            GCTG                   TAAATGGTTT    TAG   TTGCTG
                                ||||||||||   |||  ||||||
                                ATTTACCGAA    GTC   AACGAC
                                      ACTC   AAA
GAM1755  C20orf12  3'  TAAGTGGTTTATTGAGAGCTG  42981     A       _   CCTT
                                TAA TGGTTTATT AGA    GCTG
                                ||| ||||||||| |||    ||||
                                ATT ACCAAATAA TCT    CGAC
                                  C        C  ____
GAM1755  KIAA0161  3'  ATGGTTTATATGCACCTTG    42982         TAG_
                                ATGGTTTAT    ACCTTG
                                |||||||||    ||||||
                                TACCAAATA    TGGAAC
                                      TACG
GAM1755  MGC17998  3'  TGATGGTTTCCCTTCCTTGCTG 42983    A      ATTAGA
                                A ATGGTTT     CCTTGCTG
                                | |||||||     ||||||||
                                A TACCAAA     GGAACGAC
                                 C      GGGAA_
GAM1755  LOC148709 5'  ATGGCTGTGTACCTTGCTG    42984       TATTAG
                                ATGGTT     ACCTTGCTG
                                ||||||     |||||||||
                                TACCGA     TGGAACGAC
                                   CACA__
GAM1755  LOC201692 5'  ATGGTTCATTAGCCCTG     42985           A
                                ATGGTTTATTAG CCTTG
                                |||||||||||| |||||
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                                TACCAAGTAATC GGGAC
                                           _
GAM1756 ADCY7    3' GCCATGAAATTCCTTTAT   42988    C   TCTA
                                GCC TGAA   TCCTTTAT
                                ||| ||||   ||||||||
                                CGG ACTT   AGGAAATA
                                  T   TA__
GAM1756 PLP1     3' CTAAAAGTTTATCCTTTAT  42989     TC__
                                CTGAA   TATCCTTTAT
                                |||||   ||||||||||
                                GATTT   ATAGGAAATA
                                   TCAA
GAM1757 COG4     3' TGGGCTGCTCGCTGCCTGCCG 42992      G_  CGAC
                                TGGGCTG CGC   CCTGCCG
                                |||||||  |||   |||||||
                                ACCCGAC  GCG   GGACGGC
                                    GA   AC__
GAM1757 MAP3K7IP1 3' TGGGCTGGCCCGACCCT    42993       G
                                TGGGCTGGC CCGACCCT
                                ||||||||| ||||||||
                                ACCCGACCG GGCTGGGA
                                          _
GAM1757 MUCDHL   3' TGGGCTGGTTGATGCCGC    42994      CGCC  CCC
                                TGGGCTGG   GA  TGCCGC
                                ||||||||   ||  ||||||
                                ACCCGACC   CT  ACGGCG
                                    AA__  ____
GAM1757 MUCDHL   3' TGGGCTGGTTGATGCCGC    42994      CGCC  CCC
                                TGGGCTGG   GA  TGCCGC
                                ||||||||   ||  ||||||
                                ACCCGACC   CT  ACGGCG
                                    AA__  ____
GAM1757 PPY      3' TGGGCTGGCGCTGCTCA     42995       CGACCC  _
                                TGGGCTGGCGC    TGC CG
                                ||||||||||     ||| ||
                                ACCCGACCGCG    ACG GT
                                       _______  A
GAM1757 RRP22    5' TGGGCCGGCGCCGCACCGTG  42996         _  C
                                TGGGCTGGCGCCG ACC TG
                                |||||||||||| ||| ||
                                ACCCGGCCGCGGC TGG AC
                                      G   C
GAM1757 C17orf26 3' TGGGCTGGCTCGGCCTTG    42997       GC  A  C
                                TGGGCTGGC  CG CC TG
                                |||||||||  || || ||
                                ACCCGACCG  GC GG AC
                                    A_  C  A
GAM1757 EDR1     5' TGGGCTGGGCGCCGGCTCG   42998       _   ACCCT  _
                                TGGGCTGG CGCCG   GC CG
                                |||||||| |||||    || ||
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                                ACCCGACC GCGGC    CG GC
                                    C    _____ A
GAM1757  FLJ10044  5'  TGGGTTGCCGGGGTTGCCGCG  42999     CTGGC   ACCC
                                TGGG    GCCG   TGCCGCG
                                ||||    ||||   |||||||
                                ACCC    CGGC   ACGGCGC
                                  AA___   CCCA
GAM1757  FLJ20651  3'  TGGGCTGGGCCATGCTTGC   43000       C   ACCC  C_
                                TGGGCTGG GCCG   TGC  GC
                                |||||||| ||||   |||  ||
                                ACCCGACC CGGT   ACG  CG
                                    _   ____  AA
GAM1757  KIAA0542  3'  TGGGCTGGCGCTGAGCCTG   43001         C  C
                                TGGGCTGGCGC GA CCTG
                                |||||||||| || ||||
                                ACCCGACCGCG CT GGAC
                                      A  C
GAM1757  KIAA0618  3'  TGGGCTGGCGTCTCCTGC    43002         CCGAC
                                TGGGCTGGCG    CCTGC
                                |||||||||    |||||
                                ACCCGACCGC    GGACG
                                     AGA__
GAM1757  PDE11A   5'  GGCTGGCGCCGACCCCACCCCG 43003            TG  G
                                GGCTGGCGCCGACCC  CC CG
                                |||||||||||||  || ||
                                CCGACCGCGGCTGGG  GG GC
                                      GT  G
GAM1757  PPY2     3'  TGGGCTGGCACTGCCC     43004          CGACCC   G
                                TGGGCTGGCGC     TGCC C
                                ||||||||||     |||| |
                                ACCCGACCGTG     ACGG G
                                    _______  _
GAM1757  QKI      5'  TGGGCTGGTCCCCGCCGC    43005        CGCCGA
                                TGGGCTGG     CCCTGCCGC
                                ||||||||     |||||||||
                                ACCCGACC     GGGGCGGCG
                                    A_____
GAM1757  SEMA5B   5'  TGGGCTGGCGGCCGGTCTG   43006         _  ACC
                                TGGGCTGGCG CCG   CTG
                                |||||||||| |||   |||
                                ACCCGACCGC GGC   GAC
                                     C   CA_
GAM1757  SYT12    3'  TGGGCTGACCTCCTGC     43007       GC   GAC
                                TGGGCTG  GCC   CCTGC
                                |||||||  |||   |||||
                                ACCCGAC  TGG   GGACG
                                    __  A__
GAM1757  LOC115708 3'  TGGGCTGGCCTGGTCTCCTAGC 43008         GCCGAC_   CC
             G                   TGGGCTGGC      CCTG  GCG
                                 |||||||||      ||||  |||
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                                ACCCGACCG      GGAT  CGC
                                     GACCAGA   __
GAM1757  LOC139248 5'  TGGGCTGGTGCGGAGCTGC   43009        C  C  CC
                                TGGGCTGG GC GA  CTGC
                                |||||||| || ||  ||||
                                ACCCGACC CG CT  GACG
                                     A  C  C_
GAM1757  LOC147639 3'  GGCTGCGGCCCTGCCG     43010      G  CCGA
                                GGCTG CG    CCCTGCCG
                                ||||| ||    ||||||||
                                CCGAC GC    GGGACGGC
                                   _  C___
GAM1757  LOC158696 3'  TGGGCTGGTGTTGAGTGCCA  43011        CGCC  CCC
                                TGGGCTGG    GA   TGCCG
                                ||||||||    ||   |||||
                                ACCCGACC    CT   ACGGT
                                     ACAA  C__
GAM1757  LOC196510 5'  TGGGCTGGCGGCGGGGAGCGCG 43012          C  ACCCT  C
                                TGGGCTGGCG CG     GC GCG
                                |||||||||| ||     || |||
                                ACCCGACCGC GC     CG CGC
                                      C  CCCT_  _
GAM1757  LOC253868 3'  GGGTACTGGCCCTGCCG     43013     __    GCCGAC
                                GGG  CTGGC     CCTGCCG
                                |||  |||||     |||||||
                                CCC  GACCG     GGACGGC
                                  AT    _______
GAM1757  LOC255397 5'  TGGGCTGGTGCGGTGCCCGC   43014        C  CGAC
                                TGGGCTGG GC    CCTGC
                                |||||||| ||    |||||
                                ACCCGACC CG    GGGCG
                                     A  CCAC
GAM1757  LOC91464  5'  TGGGCTGGCCCTGGC      43015         GCCGAC   CC
                                TGGGCTGGC     CCTG  GC
                                |||||||||     ||||  ||
                                ACCCGACCG     GGAC  CG
                                              _______   __
GAM1758  ABCB11    3'  GGTTCAAAAATGAAAGAC    43018     GGA    C
                                GGT   AAAAA GAAAGAC
                                |||   ||||| |||||||
                                CCA   TTTTT CTTTCTG
                                  AG_     A
GAM1758  ADAMTS5   3'  CAATGGAAAGGTGAAAGACA  43019         AAAC
                                CGGTGGAAA    GAAAGACA
                                |||||||||    ||||||||
                                GTTACCTTT    CTTTCTGT
                                     CCA_
GAM1758  AQP6      3'  CGGTGGAAGCGAAGAC      43020         AAAA    A
                                CGGTGGAA     CGAA GAC
                                ||||||||     |||| |||
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                                GCCACCTT   GCTT CTG
                                    C___   _
GAM1758 B4GALT5  3' GGGGAAAAACAAAGA      43021    T     A G
                                GG GGAAAAA C AAAGA
                                || ||||||| | |||||
                                CC CCTTTTT G TTTCT

                                _     _ _
GAM1758 CACNA1G  3' ACCCAGTGGAGAAAG      43022         AAAAAC
                                ACCCGGTGGA    GAAAG
                                ||||||||||    |||||
                                TGGGTCACCT    CTTTC

                                       _______
GAM1758 CAPN10   3' CCCGGTAGAGAAGAC      43023         AAAAAC   A
                                CCCGGTGGA    GAA GAC
                                |||||||||    ||| |||
                                GGGCCATCT    CTT CTG

                                       _______  _
GAM1758 CAPN10   3' CCCGGTAGAGAAGAC      43023         AAAAAC   A
                                CCCGGTGGA    GAA GAC
                                |||||||||    ||| |||
                                GGGCCATCT    CTT CTG

                                       _______  _
GAM1758 CSNK1E   5' CCCGTGGAAAAACGAA     43024     G      A
                                CCCG TGGAAAAA CGAA
                                |||| |||||||| ||||
                                GGGC ACCTTTTT GCTT

                                  _      _
GAM1758 DIBD1    5' CCTGGGGAAAAAAGAA     43025    C  T      C
                                CC GG GGAAAAAA GAA
                                || || |||||||| |||
                                GG CC CCTTTTTT CTT
                                 A  _      _
GAM1758 EHD3     3' CCAGGTGGAAAGAACATCTAAC 43026    C      A   AAA
           A                     CC GGTGGAAA AACG   GACA
                                || |||||||| ||||   ||||
                                GG CCACCTTT TTGT   TTGT
                                 T       C   AGA
GAM1758 IGF1     3' ACCCAGTGGGAGAAAAACTGAA 43027         A__     GA
           GA                     ACCCGGTGG   AAAAAC  AAGA
                                |||||||||   ||||||  ||||
                                TGGGTCACC   TTTTTG  TTCT
                                     CTC     AC
GAM1758 MMP2     3' CCAGTGGAGAAGAGAC      43028        AAAAAC  _
                                CCGGTGGA     GAA AGAC
                                ||||||||     ||| ||||
                                GGTCACCT     CTT TCTG
                                       _______  C
GAM1758 SLC25A14 5' CCAGAAGAGTGAAAGACA    43029     T   AAAAAC
                                CCGG GGA     GAAAGACA
                                |||| |||     ||||||||
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                                GGTC TCT     CTTTCTGT
                                  T  CA____
GAM1758  SLC25A14  5'  CCAGAAGAGTGAAAGACA    43029     T   AAAAAC
                                CCGG GGA     GAAAGACA
                                |||| |||     ||||||||
                                GGTC TCT     CTTTCTGT
                                  T  CA____
GAM1758  STX7      3'  CCAACAAAAAAATGAAAGACA  43030     TG     AC
                                CCGG  GAAAAA  GAAAGACA
                                ||||  ||||||  ||||||||
                                GGTT  TTTTTT  CTTTCTGT
                                  GT     A_
GAM1758  TSN       3'  CCTGGTGGAAAACAAAATGA   43031    C      AA     _
                                CC GGTGGAAA  ACGAAA GA
                                || ||||||||  |||||| ||
                                GG CCACCTTT  TGTTTT CT
                                 A       __      A
GAM1758  CDA11     3'  GATGGAAAGTGGAAGACA     43032       AAAC   A
                                GGTGGAAA    GAA GACA
                                ||||||||    ||| ||||
                                CTACCTTT    CTT CTGT
                                    CAC_  _
GAM1758  FLJ14431  3'  GGTGGAAATCAAAAGACA     43033       AAA
                                GGTGGAAA   CGAAAGACA
                                ||||||||   |||||||||
                                CCACCTTT   GTTTTCTGT
                                    A__
GAM1758  FLJ20699  3'  ACCCGGTGGAGCAGCTGACTGG 43034         AAAAAC  AA_
           AC                     ACCCGGTGGA     GA   GAC
                                ||||||||||     ||   |||
                                TGGGCCACCT     CT   CTG
                                     CGTCGA  GAC
GAM1758  GRIN3A    3'  ACCTGGTGAAAAGGTTAACG   43035     C      A___
                                ACC GGTGGAAA    AACG
                                ||| ||||||||    ||||
                                TGG CCACTTTT    TTGC
                                  A       CCAA
GAM1758  KIAA1492  3'  ACCCAGTGGAGCATGGAAGACA 43036         AAAAAC   A
                                ACCCGGTGGA     GAA GACA
                                ||||||||||     ||| ||||
                                TGGGTCACCT     CTT CTGT
                                     CGTAC_  _
GAM1758  PPP1R14C  3'  ACTCGGTGGAAAGCAGAC    43037    C       AAACGAA
                                AC CGGTGGAAA      AGAC
                                || |||||||||      ||||
                                TG GCCACCTTT      TCTG
                                 A       CG_____
GAM1758  RIP5      3'  ACCCGATGGAGAATCGAGGAAG 43038         AAAAA  __
           ACA                    ACCCGGTGGA    CGA  AAGACA
                                ||||||||||    |||  ||||||
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                                TGGGCTACCT    GCT  TTCTGT
                                      CTTA_   CC
GAM1758  STX12     3'  CCTGTGGAAAAGGGAAGTGGAC 43039    G       AAC   A__
              A                    CC GTGGAAAA   GAA   GACA
                                   || ||||||||   |||   ||||
                                   GG CACCTTTT   CTT   CTGT
                                    A       CC_   CAC
GAM1758  SYNCOILIN 3'  CCCAGGGAAAGTGAAAGACA   43040      T    AAAC
                                   CCCGG GGAAA    GAAAGACA
                                   ||||| |||||    ||||||||
                                   GGGTC CCTTT    CTTTCTGT
                                      _    CA__
GAM1758  LOC120425 5'  CCTCCTAGAAGTGAAAGACA   43041    GG_    AAAAC
                                   CC   TGGAA    GAAAGACA
                                   ||   |||||    ||||||||
                                   GG   ATCTT    CTTTCTGT
                                    AGG    CA___
GAM1758  LOC127703 3'  ACCCAGTGGAGAAGAAAG    43042         A  AAC
                                   ACCCGGTGGA AA   GAAAG
                                   |||||||||| ||   |||||
                                   TGGGTCACCT TT   CTTTC
                                         C  ___
GAM1758  LOC145624 5'  ACTCAGTGGAAAGAAACA    43043    C       _
                                   AC CGGTGGAAA AAACG
                                   || |||||||| |||||
                                   TG GTCACCTTT TTTGT
                                    A        C
GAM1758  LOC205418 5'  CAGTGGAAAATGAAAGA     43044         AAC
                                   CGGTGGAAAA   GAAAGA
                                   ||||||||||   ||||||
                                   GTCACCTTTT   CTTTCT
                                         A__
GAM1758  LOC221036 3'  GATGGAAAGTGGAAGACA    43032        AAAC   A
                                   GGTGGAAA    GAA GACA
                                   ||||||||    ||| ||||
                                   CTACCTTT    CTT CTGT
                                       CAC_   _
GAM1758  LOC256107 5'  ACCCAGTGGAAAGAAGAA    43045          A  C
                                   ACCCGGTGGAAA AA GAA
                                   |||||||||||| || |||
                                   TGGGTCACCTTT TT CTT
                                          C  _
GAM1758  LOC91170  3'  CCGGTGGAATGAAGGAC     43046        AAAAC   A
                                   CCGGTGGAA     GAA GAC
                                   |||||||||     ||| |||
                                   GGCCACCTT     CTT CTG
                                         A_____   C
GAM1758  LOC93380  5'  CCCAGCAAAAGAAGCGAAGGAC 43047      TG   A  A    A
                                   CCCGG  GAA AA CGAA GAC
                                   |||||  ||| || |||| |||
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                                GGGTC  TTT TT GCTT CTG
                                  GT   C C    C
GAM1759 ALPI     3'  CACCCAAGTCCTTGGGTC    43050      T    A  CGGC   A
                                CACC CAAG CC    TTG GTC
                                |||| |||| ||    ||| |||
                                GTGG GTTC GG    AAC CAG
                                  _    A _____   C
GAM1759 ANK1     3'  CCTCAGATTCTTAAGTC     43051       A  CCCGG
                                CCTCA GA    CTTGAGTC
                                ||||| ||    ||||||||
                                GGAGT CT    GAATTCAG
                                  _ AA___
GAM1759 ANK1     3'  CCTCAGATTCTTAAGTC     43051       A  CCCGG
                                CCTCA GA    CTTGAGTC
                                ||||| ||    ||||||||
                                GGAGT CT    GAATTCAG
                                  _ AA___
GAM1759 ASPH     3'  CAGCTCAAGGCGTTACTGAGT  43052    C     ACCCG   T
                                CA CTCAAG    GCT GAGT
                                || |||||     ||| ||||
                                GT GAGTTC    TGA CTCA
                                 C     CGCAA  _
GAM1759 ASPH     3'  CAGCTCAAGGCGTTACTGAGT  43052    C     ACCCG   T
                                CA CTCAAG    GCT GAGT
                                || |||||     ||| ||||
                                GT GAGTTC    TGA CTCA
                                 C     CGCAA  _
GAM1759 CD22     3'  CTCAAACCCGGAGTC       43053      A      CTTG
                                CTCA GACCCGG    AGTC
                                |||| |||||||    ||||
                                GAGT TTGGGCC    TCAG
                                  _      _____
GAM1759 CEACAM6  3'  CACCTCAGGCCTGAG       43054        AGACCC
                                CACCTCA     GGCTTGAG
                                |||||||     ||||||||
                                GTGGAGT     CCGGACTC
                                  _______
GAM1759 COL9A2   3'  CCTTAGGACTCCTGAGTCC   43055     CAA   CCGG
                                CCT   GAC   CTTGAGTCC
                                |||   |||   |||||||||
                                GGA   CTG   GGACTCAGG
                                  ATC   A___
GAM1759 CRMP1    3'  CCTCAGGGCTTGAGGTC     43056      A ACCC       _
                                CCTCA G   GGCTTGAG TC
                                ||||| |   |||||||| ||
                                GGAGT C   CCGAACTC AG
                                  _ _____       C
GAM1759 CTSL     5'  CACCTCAAGGCCAGCAGAGT  43057         AC    TT
                                CACCTCAAG  CCGGC  GAGT
                                |||||||||  |||||  ||||
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                                GTGGAGTTC  GGTCG  CTCA
                                    C_    T_
GAM1759  EDAR     3'  CACCTCAAAGGCCTGGC     43058        ACCC     A
                                CACCTCAAG    GGCTTG GT
                                |||||||||    |||||| ||
                                GTGGAGTTT    CCGGAC CG
                                    ____     _
GAM1759  FLRT1    5'  CCCAAGACCCTCTGGGT     43059        GG  T A
                                CTCAAGACCC  CT G GT
                                ||||||||||  || | ||
                                GGGTTCTGGG  GA C CA
                                    A_  _ C
GAM1759  FMO2     3'  CCTTCAGGGCCCGAGTC     43060     CA  ACCC
                                CCT  AG    GGCTTGAGTC
                                |||  ||    ||||||||||
                                GGA  TC    CCGGGCTCAG
                                  AG  ____
GAM1759  GNB1     3'  CACCTAAGGACTGAGT      43061      C   ACCC    T
                                CACCT AAG    GGCT GAGT
                                ||||| |||    |||| ||||
                                GTGGA TTC    CTGA CTCA
                                  _  ____   _
GAM1759  MPZ      3'  CCTCAAGACCTGGAGTC     43062         C  CTTG
                                CCTCAAGACC GG    AGTC
                                |||||||||| ||    ||||
                                GGAGTTCTGG CC    TCAG
                                    A  ____
GAM1759  PDGFB    5'  CACCTCAAGGCCCAAGTC    43063       GACCC    TG
                                CACCTCAA    GGCT  AGTC
                                ||||||||    ||||  ||||
                                GTGGAGTT    CCGG  TCAG
                                    _____   GT
GAM1759  PRV1     5'  CACCTCAAGGATCCTGGGTC  43064        ACCCGG    A
                                CACCTCAAG     CTTG GTC
                                |||||||||     |||| |||
                                GTGGAGTTC     GGAC CAG
                                    CTA___    C
GAM1759  TEM8     3'  CACCTCAAAGTTGGGT      43065       GACCC  C   A
                                CACCTCAA    GG TTG GT
                                ||||||||    || ||| ||
                                GTGGAGTT    TC AAC CA
                                    _____ _   C
GAM1759  TIMM23   5'  CCTCAAGCCTGGGTGGTCC   43066       A  C  CT  A
                                CCTCAAG CC GG  TG GTCC
                                ||||||| || ||  || ||||
                                GGAGTTC GG CC  AC CAGG
                                    _  A  C_  _
GAM1759  VPS26    3'  TCACAGGTCCTCCTGAGTCC  43067     _  AC  GG
                                TCA AG  CC  CTTGAGTCC
                                |||  ||  ||  |||||||||
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                                AGT TC  GG  GGACTCAGG
                                  G  CA  A_
GAM1759  WHSC1    3'  CACCACTGAGTTGGTTTGAGTC 43068     TCAA  CCC  C
             C                     CACC   GA   GG TTGAGTCC
                                   ||||   ||   || ||||||||
                                   GTGG   CT   CC AACTCAGG
                                     TGA_  CAA  A
GAM1759  ZNF256   5'  CTCAAGACTGGGCCACATATC  43069       CC   TGA_
                                   CTCAAGAC  GGCT   GTC
                                   ||||||||  ||||   |||
                                   GAGTTCTG  CCGG   TAG
                                        AC   TGTA
GAM1759  ARHF     3'  TCAAGCATAACTTGAGTC    43070      ACCC
                                   TCAAG   GGCTTGAGTC
                                   |||||   ||||||||||
                                   AGTTC   TTGAACTCAG
                                     GTA_
GAM1759  BCL2L1   3'  CACCTCAGGGCTGAGTC     43071       A ACCC   T
                                   CACCTCA G   GGCT GAGTC
                                   |||||||  |   |||| |||||
                                   GTGGAGT C   CCGA CTCAG
                                      _ ____   _
GAM1759  BMF      3'  CCTCAAGACTCAAAAGTCC   43072        C  CTT
                                   CCTCAAGAC CGG   GAGTCC
                                   |||||||| |||   ||||||
                                   GGAGTTCTG GTT   TTCAGG
                                        A  ___
GAM1759  CDT6     5'  CTCAAAGCTTGAGTC      43073      GACCC
                                   CTCAA    GGCTTGAGTC
                                   |||||    ||||||||||
                                   GAGTT    TCGAACTCAG
                                      _____
GAM1759  DKFZP434F2021 3'  ACCTCAAGACACAATGGT    43074         C  CT  A
                                   ACCTCAAGAC CGG  TG GT
                                   |||||||||| |||  || ||
                                   TGGAGTTCTG GTT  AC CA
                                        T  __  _
GAM1759  DKFZP434H0820 3'  CACCTCGGGGACCCAAAAGGAG 43075      AA_     CTT
             TCC                    CACCTC   GACCCGG   GAGTCC
                                    ||||||   |||||||   ||||||
                                    GTGGAG   CTGGGTT   CTCAGG
                                       CCC      TTC
GAM1759  FLJ12687  3'  ACCTCAAGAATCCAGAAGTC   43076        C_   CTT
                                   ACCTCAAGA  CCGG   GAGTC
                                   |||||||||  ||||   |||||
                                   TGGAGTTCT  GGTC   TTCAG
                                        TA   ___
GAM1759  FLJ20306  5'  CACCCAAGCCCTTGGGTC    43077     T   A   GGC   A
                                   CACC CAAG CCC   TTG GTC
                                   |||| |||| |||   ||| |||
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                                GTGG GTTC GGG   AAC CAG
                                  _   _  ___   C
GAM1759  FLJ21742  3'  CAACTCAAGATCCTCCAAGTC  43078    C      C  GGC TG
                                CA CTCAAGA CC   T  AGTC
                                || ||||||| ||   |  ||||
                                GT GAGTTCT GG   G  TCAG
                                 T      A  A__ GT
GAM1759  FLJ23186  3'  CCTGAAGACACTGAGTC     43079     C    CCG   T
                                CCT AAGAC   GCT GAGTC
                                ||| |||||   ||| |||||
                                GGA TTCTG   TGA CTCAG
                                  C    ___  _
GAM1759  GTPBG3    3'  CACTTCTAGATCACCTGAGT   43080     C  A   CCCG
                                CAC TC AGA    GCTTGAGT
                                ||| || |||    ||||||||
                                GTG AG TCT    TGGACTCA
                                  A  A   AG__
GAM1759  H2AFY2    3'  CACTCTTGGGACTCGGGTCGTC 43081     _  CAA   C   CTTGA
              C                  CAC CT   GAC CGG     GTCC
                                ||| ||   ||| |||     ||||
                                GTG GA   CTG GCC     CAGG
                                  A  ACC   A   CAG__
GAM1759  KCNK16    3'  CTCAAGACCACCTTGGGTC   43082         C G    A
                                CTCAAGACC G CTTG GTC
                                ||||||||| | |||| |||
                                GAGTTCTGG T GAAC CAG
                                      _ G    C
GAM1759  KIAA1005  3'  CACTTCAAACCCAGGT      43083     C   A      CTTGA
                                CAC TCA GACCCGG     GT
                                ||| ||| |||||||     ||
                                GTG AGT TTGGGTC     CA
                                  A  _      ______
GAM1759  KIAA1301  3'  TCAAGATTCTCCTGAGTCC   43084       CCCGG
                                TCAAGA     CTTGAGTCC
                                ||||||     |||||||||
                                AGTTCT     GGACTCAGG
                                   AAGA_
GAM1759  MGC13053  3'  CTCAGAGGCTTGAGTC      43085      A  CCC
                                CTCA GA   GGCTTGAGTC
                                |||| ||   ||||||||||
                                GAGT CT   CCGAACTCAG
                                  _ ___
GAM1759  MGC20258  5'  CACCTCAAGCCTGTGGGGTCC  43086         A  C__  CTTGA
                                CACCTCAAG CC   GG     GTCC
                                ||||||||| ||   ||     ||||
                                GTGGAGTTC GG   CC     CAGG
                                      _  ACA  C_____
GAM1759  MGC20533  5'  CACCTCAAGGCCCGACCC    43087          A
                                CACCTCAAG CCCGGCTT
                                ||||||||| ||||||||
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                                GTGGAGTTC GGGCTGGG
                                     C
GAM1759 MGC3265  3' ACTTCAAATCCATCAAGTCC  43088   C    A  CGGC TG
                                AC TCAAG CC    T  AGTCC
                                || ||||| ||    |  |||||
                                TG AGTTT GG    A  TCAGG
                                 A    A  T___ GT
GAM1759 MGC4827  3' CACCCAAGACTAAAGAGTC   43089     T     CCGGCTT
                                CACC CAAGAC      GAGTC
                                |||| ||||||      |||||
                                GTGG GTTCTG      CTCAG
                                  _     ATTT___
GAM1759 NOLC1    3' CACCTAGAGACCTGAG      43090      CA   CCC
                                CACCT  AGA   GGCTTGAG
                                |||||  |||   ||||||||
                                GTGGA  TCT   CTGGACTC
                                  __   ____
GAM1759 PHIP     5' CTCAAGACTAGGAAATC     43091        CC  CTT
                                CTCAAGAC  GG   GAGTC
                                ||||||||  ||   |||||
                                GAGTTCTG  CC   TTTAG
                                     AT  ___
GAM1759 RANBP6   5' CCTCTCAGAAGCTTGAGT    43092      A_   CCC
                                CCTC  AGA   GGCTTGAGT
                                ||||  |||   |||||||||
                                GGAG  TCT   TCGAACTCA
                                  AG  ___
GAM1759 RNAHP    3' CTCAAACCTGGAGCAATCC   43093     A    C  CTTG
                                CTCA GACC GG    AGTCC
                                |||| |||| ||    |||||
                                GAGT TTGG CC    TTAGG
                                  _    A  TCG_
GAM1759 THTPA    5' CACCTCAAAGCCCGAGAGTC  43094        GA    CTT
                                CACCTCAA  CCCGG   GAGTC
                                ||||||||  |||||   |||||
                                GTGGAGTT  GGGCT   CTCAG
                                     TC    ___
GAM1759 TRIP3    3' CACCTTAAGGACCCCAAGTC  43095      C   _   GGCT
                                CACCT AAG ACCC    TGAGTC
                                ||||| ||| ||||    ||||||
                                GTGGA TTC TGGG    GTTCAG
                                  A   C   ____
GAM1759 TUSP     5' CACCTCAAAGCTTGGCCCTGTG 43096         ACCC    GA_
            TCC                  CACCTCAAG   GGCTT   GTCC
                                |||||||||   |||||  ||||
                                GTGGAGTTT   CCGGG   CAGG
                                     CGAA    ACA
GAM1759 LOC126536 3' CAGCTCAAGGCTTGTTGTC   43097    C    GACCC     A_
                                CA CTCAA    GGCTTG  GTC
                                || |||||    ||||||  |||
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                                GT GAGTT    CCGAAC  CAG
                                 C    _____     AA
GAM1759  LOC132299 5'  CCTCCGAGGCCGAGTC     43098     AA  CCC    T
                                CCTC  GA   GGCT GAGTC
                                ||||  ||   |||| |||||
                                GGAG  CT   CCGG CTCAG
                                  G_  ___   _
GAM1759  LOC143720 3'  CACCCAAGACTAAAGAGTC   43089     T    CCGGCTT
                                CACC CAAGAC      GAGTC
                                |||| ||||||      |||||
                                GTGG GTTCTG      CTCAG
                                  _     ATTT___
GAM1759  LOC147669 5'  ACCTCAAGGCCAGGCTTGGGTC 43099        A  C     A
                                ACCTCAAG CC GGCTTG GTC
                                |||||||| || |||||| |||
                                TGGAGTTC GG CCGAAC CAG
                                     C  T     C
GAM1759  LOC202309 5'  CACCTCAAGATTGGTGTGTC   43100         CCC  CT  A
                                CACCTCAAGA   GG  TG GTC
                                ||||||||||   ||  || |||
                                GTGGAGTTCT   CC  AC CAG
                                     AA_  __  A
GAM1759  LOC221060 5'  CACCCCGGGGCCTAAACTCGAG 43101       AAGA  C_
           TC                    CACCTC    CC  GGCTTGAGTC
                                ||||||    ||  ||||||||||
                                GTGGGG    GG  TTGAGCTCAG
                                   CCCC  AT
GAM1759  LOC253866 5'  CACCTTGAGCCCCGGCCT    43102      CA  A
                                CACCT  AG CCCGGCTT
                                |||||  || ||||||||
                                GTGGA  TC GGGCCGGA
                                  AC  G
GAM1759  LOC255170 3'  CACCTTCAGACCTGAGTTGGGT 43103      CA    C GC   A
           CC                    CACCT  AGACC G  TTG GTCC
                                |||||  ||||| |  ||| ||||
                                GTGGA  TCTGG C  AAC CAGG
                                  AG    A TC   C
GAM1759  LOC256906 3'  CACCTCAAGGATCCTGGGTC   43064         ACCCGG   A
                                CACCTCAAG     CTTG GTC
                                |||||||||     |||| |||
                                GTGGAGTTC     GGAC CAG
                                     CTA___    C
GAM1759  LOC257364 3'  ACCTCAGCACCTTGAGTC    43104       AGACC  G
                                ACCTCA    CG CTTGAGTC
                                ||||||    || ||||||||
                                TGGAGT    GT GAACTCAG
                                   C_____  G
GAM1759  LOC51580  3'  CACTCAAGCCGTTTGAGTC   43105     C    AC   GC
                                CAC TCAAG  CCG  TTGAGTC
                                ||| |||||  |||  |||||||
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                                GTG AGTTC  GGC  AACTCAG
                                  _    __   A_
GAM1759 LOC90917 3' CTCAAGACCTCACAGGGTCC  43106        CG  TTGA
                                CTCAAGACC  GC   GTCC
                                |||||||||  ||   ||||
                                GAGTTCTGG  TG   CAGG
                                     AG  TCC_
GAM1759 LOC96652 3' CACCCAAGACTGTTGGGTC   43107     T    CCGGC  A
                                CACC CAAGAC    TTG GTC
                                |||| ||||||    ||| |||
                                GTGG GTTCTG    AAC CAG
                                  _     AC___   C
GAM1760 DLG5     5' GCGTCATAGTCCTTCTTGACC 43110     ACCC  AA
                                GCGT   GG  CTTCTTGACC
                                ||||   ||  ||||||||||
                                CGCA   TC  GAAGAACTGG
                                  GTA_  AG
GAM1760 FUT6     5' AAGTGTACCCGGAGCTGAAACC 43111     C       A  TCTT
                                AAG GTACCCGGA CT   GACC
                                ||| |||||||| ||   ||||
                                TTC CATGGGCCT GA   TTGG
                                  A       C  CT__
GAM1760 FLJ20225 3' AAGCGTGTAATTCTTGAC    43112       ACCCGG  C
                                AAGCGT     AA TTCTTGAC
                                ||||||     || ||||||||
                                TTCGCA     TT AAGAACTG
                                   CA____  _
GAM1760 FLJ20288 3' AGGGTCCTGGAACTTCTTG   43113    C  A  C
                                AG GT CC GGAACTTCTTG
                                || || || ||||||||||
                                TC CA GG CCTTGAAGAAC
                                 C  _  A
GAM1760 PPP1R3B  3' AAGTGTCCCCACTCTTGAC   43114    C  A   GAAC
                                AAG GT CCCG   TTCTTGAC
                                ||| || ||||   ||||||||
                                TTC CA GGGT   GAGAACTG
                                  A  G   _____
GAM1760 LOC145598 3' AAGCATACTTCATCTCTTTTTG 43115        C_  GAA  C
             A                   AAGCGTAC  CG   CTT TTGA
                                 ||||||||  ||   ||| ||||
                                 TTCGTATG  GT   GAA AACT
                                      AA  AGA   A
GAM1760 LOC167410 3' AGGGTACCCGGGGCTTGGCC  43116    C      AACTT   A
                                AG GTACCCGG    CTTG CC
                                || ||||||||    |||| ||
                                TC CATGGGCC    GAAC GG
                                 C       CC___   C
GAM1760 LOC92465 5' AAGTGTCCTAACCATCTTGAC  43117    C  AC  GG   _
                                AAG GT  CC  AACT TCTTGAC
                                ||| ||  ||  |||| |||||||
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                                TTC CA  GG  TTGG AGAACTG
                                  A  __  A_   T
GAM1761  GSTA4    3'  CTACCATTTTATTTATTACA  43120     AGTTT
                                CTAT    TTTTATTTATTACA
                                ||||    ||||||||||||||
                                GATG    AAAATAAATAATGT
                                  GT___
GAM1761  PDX1     3'  TCTAATAGTTTTTTTAATTTTA 43121     _        T  A
              CA                  TCTA TAGTTTTTTTA TT TTACA
                                ||||| |||||||||| || |||||
                                AGAT ATCAAAAAAAT AA AATGT
                                  T         T  _
GAM1761  FLJ12876 3'  TCTATATTTTTTTCATTTAC  43122       G
                                TCTATA TTTTTTTATTTAT
                                |||||| ||||||||||||
                                AGATAT AAAAAAGTAAATG
                                   A
GAM1761  HSD17B7  3'  CATAGTTCATAGTTTATTACA  43123        TTTTA
                                TATAGTTT    TTTATTACA
                                ||||||||    |||||||||
                                GTATCAAG    AAATAATGT
                                     TATC_
GAM1761  MGC14793 3'  TCTATGGTTTTCTCACTT    43124       A
                                TCTAT GTTTTTTTATTT
                                ||||| ||||||||||||
                                AGATA CAAAAGAGTGAA
                                   C
GAM1761  MGC3222  3'  TATAATTTAGAAATTTATTACA 43125        TTTT
                                TATAGTTT   ATTTATTACA
                                ||||||||   ||||||||||
                                ATATTAAA   TAAATAATGT
                                     TCTT
GAM1761  LOC122786 3'  TCTGTAGTTCTTTTACTT    43126     A
                                TCT TAGTTTTTTTATTT
                                ||| ||||||||||||||
                                AGA ATCAAGAAAATGAA
                                  C
GAM1762  C20orf50  5'  TCATCTGTAAAATTTTTC    43129
                                TCATTTGTAAAATTTTTT
                                ||||||||||||||||||
                                AGTAGACATTTTAAAAAG

GAM1762  ZNF347   3'  TCATTTGTAAGGTTTCTC    43130          AA
                                TCATTTGTAA  TTTTTT
                                ||||||||||  ||||||
                                AGTAAACATT  AAAGAG
                                      CC
GAM1763  ABCC3    3'  GGAGATGGCGTTGAAGAA    43133     AAC  C   G
                                GGA   AT GTG TGGAGAA
                                |||   || ||| |||||||
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                                CCT   TA CGC ACTTCTT
                                  C__  C   A
GAM1763  ABCD4    3'  GGAAAGGGAGATGTGGGGAGAA 43134      CATC___   T
                                GGAAA      GTGG GGAGAA
                                |||||      |||| ||||||
                                CCTTT      CACC CCTCTT
                                   CCCTCTA   _
GAM1763  ABCD4    3'  GGAAAGGGAGATGTGGGGAGAA 43134      CATC___   T
                                GGAAA      GTGG GGAGAA
                                |||||      |||| ||||||
                                CCTTT      CACC CCTCTT
                                   CCCTCTA   _
GAM1763  ABCD4    3'  GGAAAGGGAGATGTGGGGAGAA 43134      CATC___   T
                                GGAAA      GTGG GGAGAA
                                |||||      |||| ||||||
                                CCTTT      CACC CCTCTT
                                   CCCTCTA   _
GAM1763  ABCD4    3'  GGAAAGGGAGATGTGGGGAGAA 43134      CATC___   T
                                GGAAA      GTGG GGAGAA
                                |||||      |||| ||||||
                                CCTTT      CACC CCTCTT
                                   CCCTCTA   _
GAM1763  ARHGEF7  3'  GGAACACAGTGGGGGAAA    43135      A   C    T
                                GGAA CAT GTGG GGAGA
                                |||| ||| |||| |||||
                                CCTT GTG CACC CCTTT
                                  _   T    C
GAM1763  BMP1     3'  ACGGGCACAGTGGGGAGAA   43136      AA   TC    T
                                ACGG  ACA  GTGG GGAGAA
                                ||||  |||  |||| ||||||
                                TGCC  TGT  CACC CCTCTT
                                  CG   __   _
GAM1763  BMP1     3'  ACGGGCACAGTGGGGAGAA   43136      AA   TC    T
                                ACGG  ACA  GTGG GGAGAA
                                ||||  |||  |||| ||||||
                                TGCC  TGT  CACC CCTCTT
                                  CG   __   _
GAM1763  CBS      3'  GAAACATCCTAAGAGGAA    43137        G  _  T
                                GAAACATC TG G GGAG
                                |||||||| || | ||||
                                CTTTGTAG AT C CCTT
                                     G  T T
GAM1763  CD80     3'  GGAAACATGGCAAAAGAAGA  43138        C TG T_
                                GGAAACAT G  G  GGAGA
                                |||||||| |  |  |||||
                                CCTTTGTA C  T  CTTCT
                                     C GT TT
GAM1763  CHRNB1   3'  CGGAAGTTTGTGAATGAAGA  43139      ACATC   _
                                CGGAA    GTGG TGGAGA
                                |||||    |||| ||||||
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                                GCCTT    CACT ACTTCT
                                   CAAA_   T
GAM1763  DDAH2    5'  ACAGAGTTGGTGGAGAA    43140      AACATCG
                                ACGGA     TGGTGGAGAA
                                |||||     ||||||||||
                                TGTCT     ACCACCTCTT
                                   CA_____
GAM1763  DLC1     5'  CGGAAGCGCTGTGGGGAA    43141      ACAT  G   A
                                CGGAA   CGT GTGG GAA
                                |||||   ||| |||| |||
                                GCCTT   GCG CACC CTT
                                   C___  A   C
GAM1763  DYT1     3'  GGAAACAATGCCAGGGAGAA  43142       TC  _  T
                                GGAAACA  GT GG GGAGAA
                                |||||||  || || ||||||
                                CCTTTGT  CG TC CCTCTT
                                    TA  G  _
GAM1763  EBAG9    5'  GGAAAAATCGGCCTGGAGA   43143      C   TGG
                                GGAAA ATCG   TGGAGA
                                ||||| ||||   ||||||
                                CCTTT TAGC   ACCTCT
                                   T   CGG
GAM1763  ENAM     3'  ACGAAGACATAATGGAGGAG  43144      A   C   T
                                ACGGA ACAT GTGG GGAG
                                ||||| |||| |||| ||||
                                TGCTT TGTA TACC CCTC
                                   C   T   T
GAM1763  GDI1     3'  GGAACGTGGTGGGGGAA    43145      ACAT      A_
                                GGAA   CGTGGTGG  GAA
                                ||||   ||||||||  |||
                                CCTT   GCACCACC  CTT
                                  ____      CC
GAM1763  GNGT2    3'  CAGAGACCCAGCAGGTGGAG  43146      A  ATC  _
                                CGGA AC   GT GGTGGAG
                                |||| ||   || |||||||
                                GTCT TG   CG CCACCTC
                                  C  GGT  T
GAM1763  GRM6     3'  ACAGAAATGTTTCTCAGAGGAG 43147       CA__  GT  T
            A                    ACGGAAA   TC  GG GGAGA
                                |||||||   ||  || |||||
                                TGTCTTT   AG  TC CCTCT
                                    ACAA  AG  T
GAM1763  HMG20A   3'  ACAGAAATATGAGGAGGAA   43148       C  CGT  T
                                ACGGAAA AT   GG GGAG
                                ||||||| ||   || ||||
                                TGTCTTT TA   CC CCTT
                                    A  CT_  T
GAM1763  HNRPF    5'  GAAATGTCCACGGAGGAGA   43149      ACA     T
                                GGAA   TCGTGG GGAGA
                                ||||   |||||| |||||
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                                CTTT   GGTGCC CCTCT
                                  ACA     T
GAM1763  HOXC6    3'  GGAGGCGCGTGGAGAAA     43150     AACAT    G
                                GGA    CGTG TGGAGAAA
                                |||    |||| ||||||||
                                CCT    GCGC ACCTCTTT
                                  CC___   _
GAM1763  HPCAL1   3'  CGGCTGTGGTGGAGAAA     43151     AAACATC
                                CGG      GTGGTGGAGAAA
                                |||      ||||||||||||
                                GCC      CACCACCTCTTT
                                  GA_____
GAM1763  HPCAL1   3'  CGGCTGTGGTGGAGAAA     43151     AAACATC
                                CGG      GTGGTGGAGAAA
                                |||      ||||||||||||
                                GCC      CACCACCTCTTT
                                  GA_____
GAM1763  HR       3'  GGAAATCATGAAGGAG      43152      AC      T
                                GGAA  ATCGTGG GGAG
                                ||||  ||||||| ||||
                                CCTT  TAGTACT CCTC
                                  __      T
GAM1763  IGF2     3'  GGAAACGTCCGTGGTCAGGAG  43153       A_      __
                                GGAAAC  TCGTGGT  GGAG
                                ||||||  |||||||  ||||
                                CCTTTG  GGCACCA  CCTC
                                   CA      GT
GAM1763  IGFBP4   5'  ACGGGGACGTAGCGGGGGAA   43154      AAACAT       A_
                                ACGG     CGTGGTGG  GAA
                                ||||     ||||||||  |||
                                TGCC     GCATCGCC  CTT
                                  CCT___       CC
GAM1763  IL26     3'  GGAAACATTATTTGAAAA    43155         CG GG
                                GGAAACAT  T  TGGAGA
                                ||||||||  |  ||||||
                                CCTTTGTA  A  ACTTTT
                                     AT A_
GAM1763  JPH3     3'  GGAGCGACCCTGGTGGAGAA  43156     AAC   G
                                GGA   ATC TGGTGGAGAA
                                |||   ||| ||||||||||
                                CCT   TGG ACCACCTCTT
                                  CGC   G
GAM1763  KCND3    3'  CAGAAATAGTGGGGAAA     43157       CATC    T
                                CGGAAA    GTGG GGAGA
                                ||||||    |||| |||||
                                GTCTTT    CACC CCTTT
                                   AT__    _
GAM1763  KCNJ15   3'  GGAAATATTTTGAATGGAAA  43158       C  CG  _
                                GGAAA AT  TGG TGGAGA
                                ||||| ||  ||| ||||||
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                                CCTTT TA  ACT ACCTTT
                                   A  AA   T
GAM1763  LAMC1     3'  GGAAACATCAGAAGAAA     43159          TGGT
                                GGAAACATCG    GGAGAAA
                                ||||||||||    |||||||
                                CCTTTGTAGT    CTTCTTT
                                      _____
GAM1763  MAP3K7IP2 3'  GGAGACACGTTCAGGGAAGA   43160     A   T   ___  T
                                GGA ACA CGT   GG GGAGA
                                ||| ||| |||   || |||||
                                CCT TGT GCA   CC CTTCT
                                  C   _   AGT  _
GAM1763  MDM1      3'  GGAACAGAATGGAGAAA     43161      ACAT  TG
                                GGAA    CG  GTGGAGAAA
                                ||||    ||  |||||||||
                                CCTT    GT  TACCTCTTT
                                   _____  CT
GAM1763  NELL2     5'  CAGAGACAATGGAGAAA     43162      A   TCGTG
                                CGGA ACA     GTGGAGAAA
                                |||| |||     |||||||||
                                GTCT TGT     TACCTCTTT
                                   C   ______
GAM1763  PCDH9     5'  GGAAATATTGATGACAGGAGA  43163      C  C_   GT_
                                GGAAA AT  GTG   GGAGA
                                ||||| ||  |||   |||||
                                CCTTT TA  TAC   CCTCT
                                   A  AC   TGT
GAM1763  PCLO      3'  GGAAACACGAGTGGAAAA    43164       T  T
                                GGAAACA CG GGTGGAGAA
                                ||||||| || |||||||||
                                CCTTTGT GC TCACCTTTT
                                      _ _
GAM1763  PCM1      5'  AGATCTCATTGTGGTGGAGAA  43165     AA_   C
                                GGA   CAT GTGGTGGAGAA
                                |||   ||| ||||||||||
                                TCT   GTA CACCACCTCTT
                                  AGA   A
GAM1763  PITPN     3'  CGGAACACAATGGAGAGA    43166      A   C    T
                                CGGAA CAT GTGG GGAGA
                                ||||| ||| |||| |||||
                                GCCTT GTG TACC TCTCT
                                   _   T   _
GAM1763  PPP1R12B  3'  GGAAACATCAGGGAAAA     43167          T  T
                                GGAAACATCG GG GGAGA
                                |||||||||| || |||||
                                CCTTTGTAGT CC CTTTT
                                      _  _
GAM1763  PSME1     3'  ACAGAAGCAAGTTTGGGGAAAA 43168        A  TCG_   T
                                ACGGAA CA    TGG GGAGAA
                                |||||| ||    ||| ||||||
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                                TGTCTT GT    ACC CCTTTT
                                   C  TCAA  _
GAM1763  RAB38    3'  GGAGGTCATCTTGGGAGAAAA  43169     AA_   G   TG
                                GGA   CATC TGG  GAGAA
                                |||   |||| |||  |||||
                                CCT   GTAG ACC  CTTTT
                                  CCA    A   CT
GAM1763  RBBP2    5'  GGGAACCGGTGGAGAAAA    43170    A   ATCG
                                GG AAC    TGGTGGAGAAAA
                                || |||    ||||||||||||
                                CC TTG    GCCACCTCTTTT
                                 C  ____
GAM1763  RIMS1    5'  CGGAGGCGCGGCGGGAGA    43171      AACAT       _
                                CGGA     CGTGGTGG AGA
                                ||||     |||||||| |||
                                GCCT     GCGCCGCC TCT
                                   CC___       C
GAM1763  RNF14    3'  ACGGAAGATTAGGGAAAA    43172       ACATCG   T
                                ACGGAA     TGG GGAGAA
                                ||||||     ||| ||||||
                                TGCCTT     ATC CCTTTT
                                   CTA___  _
GAM1763  RTN1     3'  ACAGAAGCATTGCAGAGAAGA  43173       A   C TG T
                                ACGGAA CAT G  G GGAGA
                                |||||| ||| |  | |||||
                                TGTCTT GTA C  C CTTCT
                                   C   A GT T
GAM1763  SCN8A    3'  ACGTGAAGCCCATGTGGAGAA  43174     _  ACA    G
                                ACG GAA   TCGTG TGGAGAA
                                |||| |||   ||||| |||||||
                                TGC CTT   GGTAC ACCTCTT
                                  A   CG_    _
GAM1763  SLC10A1  3'  GGAAATGCTGGAGAAA      43175      ACATC   G
                                GGAA     GTG TGGAGAAA
                                ||||     ||| ||||||||
                                CCTT     TAC ACCTCTTT
                                   _____  G
GAM1763  SLC9A3R2 3'  GGAAACATGTGTGGAG      43176        C   G
                                GGAAACAT GTG TGGAG
                                |||||||| ||| |||||
                                CCTTTGTA CAC ACCTC
                                      _  _
GAM1763  SOD3     3'  GGAGACCTCTGGGTGGAGA   43177     A  A  GT
                                GGA AC TC  GGTGGAGA
                                ||| || ||  ||||||||
                                CCT TG AG  CCACCTCT
                                  C  G  AC
GAM1763  TNF      3'  GGAAACATCTGGAGAGA     43178         G   T
                                GGAAACATC TGG GGAGA
                                ||||||||| ||| |||||
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                                CCTTTGTAG ACC TCTCT
                                          _  _
GAM1763  UPK1B    3'  GGAAACATAGTGCAGATGAGAA 43179        C   GTG__
                                GGAAACAT GTG    GAGAA
                                |||||||| |||    |||||
                                CCTTTGTA CAC    CTCTT
                                     T  GTCTA
GAM1763  VNN1     3'  GAAAACAGTAGTGGTGGGGA  43180       TC_     A
                                GGAAACA  GTGGTGG GA
                                |||||||  ||||||| ||
                                CTTTTGT  CACCACC CT
                                    CAT     C
GAM1763  ZNF236   3'  GGAGACGTCGGTGTTGTTGAA 43181    A  A  _  G  GA
                                GGA AC TCG TG TG  GAA
                                ||| || ||| || ||  |||
                                CCT TG AGC AC AC  CTT
                                  C  C   C  A  AA
GAM1763  ABCA5    5'  GGAACTATCGTTGTAAGAG   43182     AC    G  _
                                GGAA  ATCGT GTG GAG
                                ||||  ||||| ||| |||
                                CCTT  TAGCA CAT CTC
                                  GA    A  T
GAM1763  ATP10D   5'  GGAAACATAGAGAGAA     43183       CGT  T
                                GGAAACAT   GG GGAGAA
                                ||||||||   || ||||||
                                CCTTTGTA   TC TCTCTT
                                           ___  _
GAM1763  ATP1B4   3'  GGAAACATTGTAGAGGAGA   43184       C    T
                                GGAAACAT GTGG GGAGA
                                |||||||| |||| |||||
                                CCTTTGTA CATC CCTCT
                                     A   T
GAM1763  C11orf9  3'  ACGGAACCAAATTGGGGAG   43185      A  TCG   T
                                ACGGAA CA   TGG GGAG
                                |||||| ||   ||| ||||
                                TGCCTT GT   ACC CCTC
                                   G  TTA  _
GAM1763  C12orf2  5'  GGAACACGGAGTGGAGAA    43186     A  T  TG
                                GGAA CA CG  GTGGAGAA
                                |||| || ||  ||||||||
                                CCTT GT GC  CACCTCTT
                                  _  _  CT
GAM1763  C1orf16  3'  GGGGACATGCACGATGGAGAA 43187    AA   _
                                GG  ACAT CGTGGTGGAGAA
                                ||  |||| ||||||||||||
                                CC  TGTA GTGCTACCTCTT
                                 CC    C
GAM1763  C20orf130 3'  GGAAACATCTTAGGGGAA    43188       GT_  T
                                GGAAACATC   GG GGAG
                                |||||||||   || ||||
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                                CCTTTGTAG   CC CCTT
                                     AAT  _
GAM1763  C20orf177 3'  GGATACATGACGGGGAAA    43189     A    CG   T
                                GGA ACAT  TGG GGAGA
                                ||| ||||  ||| |||||
                                CCT TGTA  GCC CCTTT
                                  A   CT   _
GAM1763  CAMKK2   3'  GGAAGGTTCCGTGGTGGGGA   43191      ACA_       A
                                GGAA   TCGTGGTGG GA
                                ||||   ||||||||| ||
                                CCTT   GGCACCACC CT
                                  CCAA       C
GAM1763  CAMKK2   3'  GGAAACAATGGGGAA       43190        TC    T
                                GGAAACA  GTGG GGAG
                                |||||||  |||| ||||
                                CCTTTGT  TACC CCTT

                                   __   _
GAM1763  CARM1    3'  CGGCAACATCGTGTAAAA    43192     A        G
                                CGG AACATCGTG TGGAG
                                ||| ||||||||| |||||
                                GCC TTGTAGCAC ATTTT
                                  G        _
GAM1763  CLECSF9  3'  GGGAACATCGGTAGAA      43193     A      GT
                                GG AACATC  GGTGGAG
                                || ||||||  |||||||
                                CC TTGTAG  CCATCTT
                                 C     __
GAM1763  DDX31    3'  GGAAATTCCCCAGGAGGAGA   43194       CA__   T  T
                                GGAAA    TCG GG GGAGA
                                |||||    ||| || |||||
                                CCTTT    GGT CC CCTCT
                                   AAGG   _  T
GAM1763  DIO2     3'  GGAGACAAAGATGGGGAGA    43195     A   TC_    T
                                GGA ACA   GTGG GGAGA
                                ||| |||   |||| |||||
                                CCT TGT   TACC CCTCT
                                  C   TTC   _
GAM1763  DIO2     3'  GGAGACAAAGATGGGGAGA    43195     A   TC_    T
                                GGA ACA   GTGG GGAGA
                                ||| |||   |||| |||||
                                CCT TGT   TACC CCTCT
                                  C   TTC   _
GAM1763  DKFZP434C171 3'  GGAAACACCTAGAGGAA     43196         G   T
                                GGAAACATC TGG GGAG
                                ||||||||| ||| ||||
                                CCTTTGTGG ATC CCTT
                                      _  T
GAM1763  DKFZP564D172 3'  GGAAACAAAAATGGGGAAGA   43197         TC_    T
                                GGAAACA   GTGG GGAGA
                                |||||||   |||| |||||
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                                CCTTTGT   TACC CTTCT
                                    TTT    C
GAM1763  DKFZp564K142 3'  GGAAATATGCAAGGAGGAG    43198      C  _  T  T
                                GGAAA AT CG GG GGAG
                                ||||| || || || ||||
                                CCTTT TA GT CC CCTC
                                   A  C  T  T
GAM1763  DKFZP564O1863 5'  ACGGAGGCAGCGGACGGAA    43199      AA  TC   _
                                ACGGA  CA  GTGG TGGAG
                                |||||  ||  |||| |||||
                                TGCCT  GT  CGCC GCCTT
                                   CC  __    T
GAM1763  DKFZP566E144 3'  GGAAACAGCATATTAGGAGAAA 43200        T    GT_
            A                    GGAAACA CGTG   GGAGAAAA
                                |||||||  ||||   ||||||||
                                CCTTTGT GTAT   CCTCTTTT
                                    C    AAT
GAM1763  DKFZP566J091 3'  GGATATATCAGGGAGAAAA    43201     AAC   GT  T
                                GGA   ATC  GG GGAGAAAA
                                |||   |||  || ||||||||
                                CCT   TAG  TC CCTCTTTT
                                  ATA   __  _
GAM1763  DKFZp761K1423 3'  ACTGAAATGATTGGTGGAGAAA 43202    G    CATCG
            A                    AC GAAA    TGGTGGAGAAAA
                                || ||||    ||||||||||||
                                TG CTTT    ACCACCTCTTTT
                                 A   ACTA_
GAM1763  FLJ10008  3'  CAGAGGACAAGGGTGGAGAA   43203     A_   TCGT
                                CGGA  ACA    GGTGGAGAA
                                ||||  |||   |||||||||
                                GTCT  TGT    CCACCTCTT
                                  CC   TC__
GAM1763  FLJ10842  3'  GGAAATACAGAAGGAGAAAA   43204      CAT  T  T
                                GGAAA   CG GG GGAGAAAA
                                |||||   || || ||||||||
                                CCTTT   GT CT CCTCTTTT
                                   AT_  _  T
GAM1763  FLJ10898  5'  GAAACGGCATGGGGGAGA    43205      AT    T
                                GAAAC  CGTGG GGAGA
                                |||||  ||||| |||||
                                CTTTG  GTACC CCTCT
                                   CC    C
GAM1763  FLJ14768  3'  GGAAACACTGGGGAGA      43206        CG   T
                                GGAAACAT  TGG GGAGA
                                ||||||||  ||| |||||
                                CCTTTGTG  ACC CCTCT
                                     __   _
GAM1763  FLJ20097  3'  GGGAACACGTTGATGGAAAA   43207    A   T   _
                                GG AACA CGT GGTGGAGAA
                                || |||| ||| |||||||||
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                                CC TTGT GCA CTACCTTTT
                                 C   _  A
GAM1763  FLJ20275  3'  GGAAACATTAGTGCTGGAGA  43208       C_  G
                                GGAAACAT  GTG TGGAGA
                                ||||||||  ||| ||||||
                                CCTTTGTA  CAC ACCTCT
                                    AT   G
GAM1763  FLJ21156  3'  GGAGGTCGTGGTAGTAGA   43209    AACA      _
                                GGA   TCGTGGTGG AGA
                                |||   ||||||||| |||
                                CCT   AGCACCATC TCT
                                  CC__       A
GAM1763  FLJ22679  3'  GGAGACATCGTAGGGGGAA  43210    A       T  A
                                GGA ACATCGTGG GG GAA
                                ||| ||||||||| || |||
                                CCT TGTAGCATC CC CTT
                                  C       _ C
GAM1763  FLJ22693  5'  GGAGACGCCGGCGGGAAA   43211    AACAT  _    A
                                GGA    CGT GGTGG GAAA
                                |||    ||| ||||| ||||
                                CCT    GCG CCGCC CTTT
                                  CT___   G   _
GAM1763  FLJ23392  5'  GGGAACTAGCGGAGAAA    43212    A  ATCG
                                GG AAC   TGGTGGAGAAA
                                || |||   ||||||||||
                                CC TTG   ATCGCCTCTTT
                                 C  _____
GAM1763  GTPBP1    3'  ACAGGGGTGGCGTGGTGGGGAA 43213     AAACAT      A
                                ACGG     CGTGGTGG GAA
                                ||||     |||||||| |||
                                TGTC     GCACCACC CTT
                                  CCCACC       C
GAM1763  HAPIP     3'  AGAAATGTTCAGCCTGGAGAAA 43214      CA_  TGG
            A                    GGAAA  TCG  TGGAGAAAA
                                |||||  |||  |||||||||
                                TCTTT  AGT  ACCTCTTTT
                                   ACA  CGG
GAM1763  HCA127    3'  GGAGACAGAAGTGGAGAAA   43215    A  TCGT
                                GGA ACA   GGTGGAGAAA
                                ||| |||   ||||||||||
                                CCT TGT   TCACCTCTTT
                                  C  CT__
GAM1763  HIC       3'  ACAGAAATATCGGTAAAAAGGA 43216       C   TGGT___
            GA                   ACGGAAA ATCG      GGAGA
                                |||||||  ||||      |||||
                                TGTCTTT TAGC      CCTCT
                                    A   CATTTTT
GAM1763  INSM2     3'  GGAACATTGACTACAGGGAGAA 43217     A  C____ TG T
                                GGAA CAT    G  G GGAGAA
                                |||| |||    |  | ||||||
```

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                                CCTT GTA    T  C CCTCTT
                                  _  ACTGA GT _
GAM1763  KIAA0179  3'  GGAACGTGGACGGAGA     43218     ACAT    _
                                GGAA   CGTGG TGGAGA
                                ||||   ||||| ||||||
                                CCTT   GCACC GCCTCT
                                  ____    T
GAM1763  KIAA0373  5'  GGAAACATTAGCGGGAGAG   43219       C_   TG
                                GGAAACAT  GTGG  GAG
                                ||||||||  ||||  |||
                                CCTTTGTA  CGCC  CTC
                                    AT    CT
GAM1763  KIAA0408  3'  GGATACACTGGTGGAGA     43220     A   CG
                                GGA ACAT  TGGTGGAGA
                                ||| ||||  |||||||||
                                CCT TGTG  ACCACCTCT
                                  A   __
GAM1763  KIAA0731  3'  GGAAAGGTCAGAGAAA      43221      CATCGT   _
                                GGAAA     GGT GGAGAAA
                                |||||     ||| |||||||
                                CCTTT     CCA TCTCTTT
                                  _______  G
GAM1763  KIAA0978  3'  GGAAACATGTTGGGAGAGA   43222       CG   TG
                                GGAAACAT  TGG  GAGA
                                ||||||||  |||  ||||
                                CCTTTGTA  ACC  CTCT
                                    CA   CT
GAM1763  KIAA1069  3'  GGAGACGTCTGACAAAGAAAA  43223     A  A  G   TG
                                GGA AC TC TGG  GAGAAAA
                                ||| || || |||  |||||||
                                CCT TG AG ACT  TTCTTTT
                                  C  C  _  GT
GAM1763  KIAA1522  3'  GAAAACACCCTGGAGAG     43224       G   T
                                GGAAACATC TGG GGAG
                                ||||||||| ||| ||||
                                CTTTTGTGG ACC TCTC
                                    G   _
GAM1763  KIAA1710  5'  GGAAGTCGAGCACTGGGGAAA  43225     ACA   _____   T
                                GGAA   TCG    TGG GGAGA
                                ||||   |||    ||| |||||
                                CCTT   AGC    ACC CCTTT
                                  C__   TCGTG   _
GAM1763  MGC10986  5'  GGAAGCCTCGGGTGGAGAA   43226     ACA   T
                                GGAA   TCG GGTGGAGAA
                                ||||   ||| |||||||||
                                CCTT   AGC CCACCTCTT
                                  CGG   _
GAM1763  MGC35558  3'  ACAGAAACAAACGTGGGGAAAA 43227         T_    T
                                ACGGAAACA  CGTGG GGAGAA
                                |||||||||  ||||| ||||||
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                                TGTCTTTGT  GCACC CCTTTT
                                     TT    _
GAM1763  MGC4549   3'  ACGGGCACTAGAAGGTGGAGAA 43228      AA  ATCGT
                                ACGG  AC    GGTGGAGAA
                                ||||  ||    |||||||||
                                TGCC  TG    CCACCTCTT
                                  CG  ATCTT
GAM1763  MGC5508   3'  ACAGGGTACCCTGGTGGAGA   43229      AAAC   G
                                ACGG    ATC TGGTGGAGA
                                ||||    ||| |||||||||
                                TGTC    TGG ACCACCTCT
                                  CCA_   G
GAM1763  NAG73     5'  GGACACATCGCTAAGGGGA    43230     A      ___  T
                                GGA ACATCGT   GG GGA
                                ||| |||||||   || |||
                                CCT TGTAGCG   CC CCT
                                  G      ATT  _
GAM1763  NFASC     3'  ACAGAGACATTGGGTCTGGAG  43231      A    CG   ___
                                ACGGA ACAT  TGG   TGGAG
                                ||||| ||||  |||   |||||
                                TGTCT TGTA  ACC   ACCTC
                                   C    __   CAG
GAM1763  OBTP      3'  GGAGGAGCAGGTGGAGAAA    43232     AACAT  T
                                GGA    CG GGTGGAGAAA
                                |||    || ||||||||||
                                CCT    GT CCACCTCTTT
                                  CCTC_  _
GAM1763  OR7E120   3'  TGAGACCCACAGGTGGAGAA   43233   C   AA  T  T
                                A GGA  CA CG GGTGGAGAA
                                | |||  || || |||||||||
                                A TCT  GT GT CCACCTCTT
                                 C   GG  _  _
GAM1763  PAK7      3'  GGAAACATTGTGGTGTGCAAAA 43234        C     GA_
                                GGAAACAT GTGGTG   GAAA
                                |||||||| ||||||   ||||
                                CCTTTGTA CACCAC   TTTT
                                     A     ACG
GAM1763  PRO0611   3'  TGAGAATTCTAGTGGAG     43235   C    ACA  G
                                A GGAA   TC TGGTGGAG
                                | ||||   || ||||||||
                                A TCTT   AG ATCACCTC
                                 C   A__  _
GAM1763  PRRG2     3'  CGGAAACGCGTGTGCCAGG    43236       AT   _  __
                                CGGAAAC  CGTG GT  GG
                                |||||||  |||| ||  ||
                                GCCTTTG  GCAC CG  CC
                                    C_   A  GT
GAM1763  RNF2      3'  GGAAACACACTTTGTGGGGAAA 43237        C____    T
              A                  GGAAACAT    GTGG GGAGAA
                                 ||||||||    |||| ||||||
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                                CCTTTGTG    CACC CCTTTT
                                    TGAAA   _
GAM1763 SDCCAG43 3' GGAAATCATGGAGAAG     43238     AC     T
                                GGAA ATCGTGG GGAG
                                |||| ||||||| ||||
                                CCTT TAGTACC CTTC
                                  __      T
GAM1763 SEZ6    3' GGGCATCGCAGGCGGGGAA   43240    AAA    _    A
                                GG  CATCGT GGTGG GAA
                                ||  |||||| ||||| |||
                                CC  GTAGCG CCGCC CTT
                                 C__     T    C
GAM1763 SEZ6    3' GGTGGTCATGTGGAGAAA    43239    AAACA    G
                                GG    TCGTG TGGAGAAA
                                ||    ||||| ||||||||
                                CC    AGTAC ACCTCTTT
                                 ACC__    _
GAM1763 SLC2A10  3' GGAAGCATCTAGAATGGAGAA 43241     A   GT_
                                GGAA CATC   GGTGGAGAA
                                |||| ||||  |||||||||
                                CCTT GTAG   TTACCTCTT
                                  C   ATC
GAM1763 SSBP4    5' ACGGCAGGCATCGTCCGCGCGG 43242     AAA_    _______ T
           GGGAG                 ACGG   CATCGT     GG GGAG
                                |||| ||||||     || ||||
                                TGCC   GTAGCA     CC CCTC
                                  GTCC     GGCGCG  C
GAM1763 STX11    5' GGGCGCACGGATGGAGAA    43243    AAA  T  T
                                GG  CA CG GGTGGAGAA
                                ||  || || |||||||||
                                CC  GT GC CTACCTCTT
                                 CGC  _  _
GAM1763 TP53TG3  3' GAAACATCAGCAGAGAAAA   43244        GT  TG
                                GAAACATC  GG  GAGAAAA
                                ||||||||  ||  |||||||
                                CTTTGTAG  TC  CTCTTTT
                                    __  GT
GAM1763 TTC2     3' ACGGAGACGTGATGAAG     43245      AACAT
                                ACGGA    CGTGGTGGAG
                                |||||    ||||||||||
                                TGCCT    GCACTACTTC
                                  CT___
GAM1763 ZFP91    3' GGAAATATGCAGTGGGAA    43246      C  C TG   A
                                GGAAA AT G  GTGG GAA
                                ||||| || |  |||| |||
                                CCTTT TA C  CACC CTT
                                  A  _ GT   _
GAM1763 ZNF304   3' GGAAAATCGTGTCAGGAAA   43247      C     GT_
                                GGAAA ATCGTG   GGAGA
                                ||||| ||||||   |||||
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                                CCTTT TAGCAC   CCTTT
                                   _     AGT
GAM1763  LOC115343 3'  GGCAGACATCAGGAAGGAGGAG 43248    AA_     T___  T
              A                    GG   ACATCG    GG GGAGA
                                   ||   ||||||    || |||||
                                   CC   TGTAGT    CC CCTCT
                                    GTC     CCTT  T
GAM1763  LOC123745 3'  GAAAACACCATGGGGAGA    43249            T
                                   GGAAACATCGTGG GGAGA
                                   |||||||||||| |||||
                                   CTTTTGTGGTACC CCTCT
                                              _
GAM1763  LOC124460 3'  CGAAGGCACAGTGGAGGAAA   43250      AA   C    T
                                   CGGA  CAT GTGG GGAGA
                                   ||||  ||| |||| |||||
                                   GCTT  GTG CACC CCTTT
                                     CC   T    T
GAM1763  LOC124538 3'  AGAAATGTTCGCACAGGGGAAA 43251      CA_   ___  T
                                   GGAAA   TCGT   GG GGAGA
                                   |||||   ||||   || |||||
                                   TCTTT   AGCG   CC CCTTT
                                      ACA    TGT  _
GAM1763  LOC139904 5'  GGAGGCACGCGATGAGGGAG   43252     AA  T    ___
                                   GGA  CA CGTGGT   GGAG
                                   |||  || ||||||   ||||
                                   CCT  GT GCGCTA   CCTC
                                     CC  _     CTC
GAM1763  LOC144321 3'  GGAAACATGTTTAGAAAA    43253         C  GG
                                   GGAAACAT GT  TGGAGAA
                                   |||||||| ||  |||||||
                                   CCTTTGTA CA  ATCTTTT
                                        _  A_
GAM1763  LOC144699 3'  GGAAACCCCGTGGGGAGA    43254        AT    T
                                   GGAAAC  CGTGG GGAGA
                                   ||||||  ||||| |||||
                                   CCTTTG  GCACC CCTCT
                                      GG    _
GAM1763  LOC145946 3'  GGAGACAATGAAGAGAA     43255     A   TC    T
                                   GGA ACA  GTGG GGAGAA
                                   ||| |||  |||| ||||||
                                   CCT TGT  TACT TCTCTT
                                     C   __   _
GAM1763  LOC146268 3'  GGAAACACTGGGGAG       43256         CG   T
                                   GGAAACAT  TGG GGAG
                                   ||||||||  ||| ||||
                                   CCTTTGTG  ACC CCTC
                                             __   _
GAM1763  LOC147118 3'  CAGAAACAGGTTTGGAGA    43257         TC  GG
                                   CGGAAACA  GT  TGGAGA
                                   ||||||||  ||  ||||||
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                                GTCTTTGT  CA  ACCTCT
                                    C_  A_
GAM1763  LOC147219 3'  GGAAGTTCAAATGTGAGAAAA  43258     ACA  T   _
                                GGAA   TCG GGTG GAGAAAA
                                ||||   ||| |||| |||||||
                                CCTT   AGT TTAC CTCTTTT
                                  CA_  _   A
GAM1763  LOC147858 5'  GGAAACAGAGAGTGGGGGAGA  43259       TC__   T
                                GGAAACA   GTGG GGAGA
                                |||||||   |||| |||||
                                CCTTTGT   CACC CCTCT
                                    CTCT   C
GAM1763  LOC147958 3'  ACGGGACATCGTGGCCGTGCGA 43260     AA       _____
            AG                    ACGG  ACATCGTGGT    GGAG
                                ||||  ||||||||||    ||||
                                TGCC  TGTAGCACCG    CTTC
                                  C_        GCACG
GAM1763  LOC148229 5'  ACGGGAAGGTCGTGGGGGA   43261     A  CA     T
                                ACGG AA  TCGTGG GGA
                                |||| ||  |||||| |||
                                TGCC TT  AGCACC CCT
                                  C  CC     C
GAM1763  LOC149878 3'  GAAAAGATGGTGGAGA     43262      CATC
                                GGAAA   GTGGTGGAGA
                                |||||   ||||||||||
                                CTTTT   TACCACCTCT
                                  C___
GAM1763  LOC151278 5'  GGAAATGCCGCGGTGGAGAA  43263      CA
                                GGAAA  TCGTGGTGGAGAA
                                |||||  ||||||||||||
                                CCTTT  GGCGCCACCTCTT
                                  AC
GAM1763  LOC152373 5'  GGAAAGGTGGAGAAA      43264      CATCGT
                                GGAAA     GGTGGAGAAA
                                |||||     ||||||||||
                                CCTTT     CCACCTCTTT
                                  _______
GAM1763  LOC153792 3'  ACGAAGACATCATGGAGAG   43265      A       T
                                ACGGA ACATCGTGG GGAG
                                ||||| ||||||||| ||||
                                TGCTT TGTAGTACC TCTC
                                  C       _
GAM1763  LOC153810 3'  GGAAGCATGGCGGGGGAG    43266     A  C   T
                                GGAA CAT GTGG GGAG
                                |||| ||| |||| ||||
                                CCTT GTA CGCC CCTC
                                  C  C   C
GAM1763  LOC154428 5'  CGGAGGAATCGTGGTCAGAA  43267     AAC      _
                                CGGA   ATCGTGGT GGAG
                                ||||   |||||||| ||||
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                                GCCT   TAGCACCA TCTT
                                  CCT       G
GAM1763  LOC154739 5'  GGAATGTCGTAGTAAAG     43268      ACA
                                GGAA   TCGTGGTGGAG
                                ||||   ||||||||||
                                CCTT   AGCATCATTTC
                                  AC_
GAM1763  LOC161635 5'  GGATGTATCATGGAGAAA     43269     AAC      T
                                GGA   ATCGTGG GGAGA
                                |||   ||||||| |||||
                                CCT   TAGTACC TCTTT
                                  ACA      _
GAM1763  LOC196477 3'  GGAAAAATCTATGAGGAAA    43270       C  _   T
                                GGAAA ATC GTGG GGAGA
                                ||||| ||| |||| |||||
                                CCTTT TAG TACT CCTTT
                                   T   A   _
GAM1763  LOC196513 3'  CAGAAACATTGAAGGAAA     43271         CG   T
                                CGGAAACAT  TGG GGAGA
                                |||||||||  ||| |||||
                                GTCTTTGTA  ACT CCTTT
                                     __   T
GAM1763  LOC196955 5'  GGAGCCAGGGTGGAGAAA     43272     AA  TCGT
                                GGA  CA    GGTGGAGAAA
                                |||  ||    ||||||||||
                                CCT  GT    CCACCTCTTT
                                  CG  C___
GAM1763  LOC199718 3'  GGAAAGATTCTGGAGAAA     43273      CATC  GG
                                GGAAA    GT  TGGAGAAA
                                |||||    ||  ||||||||
                                CCTTT    TA  ACCTCTTT
                                   C___  AG
GAM1763  LOC200298 3'  GGAGCCGGGTGGAGAAA     43274     AACA   T
                                GGA    TCG GGTGGAGAAA
                                |||    ||| ||||||||||
                                CCT    GGC CCACCTCTTT
                                  C___   _
GAM1763  LOC200779 5'  CGGAACGCAGGCGATGGGGAGA 43275       ACAT__  _   T
                                CGGAA     CG TGG GGAGA
                                |||||     || ||| |||||
                                GCCTT     GC ACC CCTCT
                                   GCGTCC  T   _
GAM1763  LOC201456 3'  GGAAGCATCAGTAGAGAA     43276      A    GT
                                GGAA CATC  GGTGGAGAA
                                |||| ||||  |||||||||
                                CCTT GTAG  TCATCTCTT
                                  C    __
GAM1763  LOC203317 3'  GGAAACATGTAAGAAAG     43277         C    TG
                                GGAAACAT GTGG  GAG
                                |||||||| ||||  |||
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                                CCTTTGTA CATT  TTC
                                     _   CT
GAM1763  LOC205143 5'  GGGGGCACCTTGGAGAGAA   43278    AAA   G   T
                                GG   CATC TGG GGAGAA
                                ||   |||| ||| ||||||
                                CC   GTGG ACC TCTCTT
                                 CCC    A  _
GAM1763  LOC219594 5'  GGAGGCATCAGCGGAGGAA   43279     AA   _   T
                                GGA  CATC GTGG GGAG
                                |||  |||| |||| ||||
                                CCT  GTAG CGCC CCTT
                                  CC    T   T
GAM1763  LOC222189 3'  GGCAGACATCAGGAAGGAGGAG 43248    AA_     T___  T
             A                   GG   ACATCG    GG GGAGA
                                ||   ||||||    || |||||
                                CC   TGTAGT    CC CCTCT
                                 GTC     CCTT  T
GAM1763  LOC245787 3'  GGCAGACATCAGGAAGGAGGAG 43248    AA_     T___  T
             A                   GG   ACATCG    GG GGAGA
                                ||   ||||||    || |||||
                                CC   TGTAGT    CC CCTCT
                                 GTC     CCTT  T
GAM1763  LOC253167 3'  GAAAACATTATGGGAGAA    43280        CG   TG
                                GGAAACAT  TGG  GAGAA
                                ||||||||  |||  |||||
                                CTTTTGTA  ACC  CTCTT
                                     AT   __
GAM1763  LOC253933 3'  TGAGACCCACAGGTGGAGA   43281   C   AA  T  T
                                A GGA  CA CG GGTGGAGA
                                | |||  || || ||||||||
                                A TCT  GT GT CCACCTCT
                                 C   GG  _ _
GAM1763  LOC254263 3'  GGAGACAGGGCTGGAGAAA   43282     A   TCGT  _
                                GGA ACA    GG TGGAGAAA
                                ||| |||    || ||||||||
                                CCT TGT    CC ACCTCTTT
                                  C   C___  G
GAM1763  LOC255040 5'  GGAGACATCGCGGAGGGAA   43283     A       T  A
                                GGA ACATCGTGG GG GAA
                                ||| ||||||||| || |||
                                CCT TGTAGCGCC CC CTT
                                  C        T  _
GAM1763  LOC255041 5'  GGAGACATCGCGGAGGGAA   43283     A       T  A
                                GGA ACATCGTGG GG GAA
                                ||| ||||||||| || |||
                                CCT TGTAGCGCC CC CTT
                                  C        T  _
GAM1763  LOC255105 3'  CGAGACCCACAGGTGGAGA   43284    _  AA  T  T
                                CG GA  CA CG GGTGGAGA
                                || ||  || || ||||||||
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                                GC CT  GT GT CCACCTCT
                                 T  GG  _  _
GAM1763  LOC255458 5'  GGAGTCTGGTGGAGAAA     43285     AACA  G
                                GGA    TC TGGTGGAGAAA
                                |||    || ||||||||||
                                CCT    AG ACCACCTCTTT
                                  C___  _
GAM1763  LOC255527 5'  CGGGGACACCACGGGGAG    43286     AA       T
                                CGG  ACATCGTGG GGAG
                                |||  ||||||||| ||||
                                GCC  TGTGGTGCC CCTC
                                  CC        _
GAM1763  LOC256222 3'  GAAGCATCTGGAGAAA      43287     A    GTGG
                                GAA CATC    TGGAGAAA
                                ||| ||||    ||||||||
                                CTT GTAG    ACCTCTTT
                                  C   _____
GAM1763  LOC256980 3'  AGAAGCATGGTGGGGAGA    43288     A   C    T
                                GGAA CAT GTGG GGAGA
                                |||| ||| |||| |||||
                                TCTT GTA CACC CCTCT
                                  C   C   _
GAM1763  LOC257249 3'  GGAGACGTTTGGTAACTGAGAA 43289     A  ATCG    ___
                                GGA AC    TGGTG   GAGAA
                                ||| ||    |||||   |||||
                                CCT TG    ACCAT   CTCTT
                                  C  CAA_    TGA
GAM1763  LOC257551 3'  GGAAACATCTGGAGAGA     43178         G   T
                                GGAAACATC TGG GGAGA
                                ||||||||| ||| |||||
                                CCTTTGTAG ACC TCTCT

                                     _   _
GAM1763  LOC257601 3'  GGAAACATCTGGAGAGA     43178         G   T
                                GGAAACATC TGG GGAGA
                                ||||||||| ||| |||||
                                CCTTTGTAG ACC TCTCT

                                     _   _
GAM1763  LOC89919  3'  GGAAGCACAGAGCTGGGGAGAA 43290      A   C__ _   T
                                GGAA CAT   G TGG GGAGAA
                                |||| |||   | ||| ||||||
                                CCTT GTG   C ACC CCTCTT
                                  C   TCT G   _
GAM1763  LOC91963  5'  GGAAAATTCAAAATGGAGAAAA 43291      CA   TG
                                GGAAA  TCG  GTGGAGAAAA
                                |||||  |||  ||||||||||
                                CCTTT  AGT  TACCTCTTTT
                                   TA   TT
GAM1764  C22orf20  3'  TCAGACTTTCACTCATGT    43294     A    CTGAA
                                TCA ACTT    ACTCATGT
                                ||| ||||    ||||||||
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                                AGT TGAA    TGAGTACA
                                  C   AG___
GAM1764  DRCTNNB1A 3'  TTCAACTTCTGCCATGTC   43295      A     AAAC
                                TTCAA CTTCTG   TCATGTC
                                ||||| ||||||   |||||||
                                AAGTT GAAGAC   GGTACAG
                                   _    ____
GAM1764  FLJ13448  3'  TTCTGGCTTCTGAAAACATGTC 43296    AAA       CT
           A                     TTC  CTTCTGAAA  CATGTCA
                                |||  |||||||||  |||||||
                                AAG  GAAGACTTT  GTACAGT
                                  ACC       T_
GAM1764  FLJ22060  3'  TTCAGCCTTCTGAAATAAATGG 43297     AA       CTCAT_
           TCA                    TTCA  CTTCTGAAA     GTCA
                                ||||  |||||||||     ||||
                                AAGT  GAAGACTTT     CAGT
                                  CG       ATTTAC
GAM1764  IPLA2(GAMMA) 3'  TTCAAAGTTAACTCATGTC   43298       C  CTGA
                                TTCAAA TT   AACTCATGTC
                                ||||||| ||   ||||||||||
                                AAGTTT AA   TTGAGTACAG
                                   C  ____
GAM1764  LOC123036 3'  CAAATTTCTGAAATCCTTCA   43299     C       C  ATG
                                CAAA TTCTGAAA TC   TCA
                                |||| ||||||| ||   |||
                                GTTT AAGACTTT AG   AGT
                                  A       _  GA_
GAM1764  LOC147409 3'  TTCAACTTCTGAGGGAGTC   43300      A      AACTCAT
                                TTCAA CTTCTGA      GTC
                                ||||| |||||||      |||
                                AAGTT GAAGACT      CAG
                                   _      CCCT___
GAM1764  LOC148438 3'  AAACTTCTGAAATGC       43301          ACTC
                                AAACTTCTGAA   ATGT
                                ||||||||||   ||||
                                TTTGAAGACTT   TACG
                                      ____
GAM1764  LOC151040 3'  TTCAATAAAGCTCATGTC    43302      ACTTC   A
                                TTCAA    TGAA CTCATGTC
                                |||||    |||| ||||||||
                                AAGTT    ATTT GAGTACAG
                                   _____   C
GAM1764  LOC199729 3'  TTCAAACTGCTGGAACAATG  43303        T  A  TC
                                TTCAAACT CTG AAC  ATG
                                |||||||| ||| |||  |||
                                AAGTTTGA GAC TTG  TAC
                                     C  C  T_
GAM1764  LOC220980 5'  TTCAAACTCCTGTTTATGT   43304          AAACTC
                                TTCAAACTTCTG    ATGT
                                ||||||||||||    ||||
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                                AAGTTTGAGGAC     TACA
                                      AAA___
GAM1764  LOC221174 5'  TTCAGCTTCTGAAAAATCA   43305     AA       C_
                                TTCA  CTTCTGAAA  TCA
                                ||||  |||||||||  |||
                                AAGT  GAAGACTTT  AGT
                                  C_       TT
GAM1764  LOC253314 3'  CTCAGGCCCCAACTCATGT   43306     AA   TGA
                                TTCA  CTTC   AACTCATGT
                                ||||  ||||   |||||||||
                                GAGT  GGGG   TTGAGTACA
                                  CC   ___
GAM1765  GLUD1     3'  GTGGTTACATGTAAACT     43309        C   AC
                                GTGGTTAC GTG  AAGCT
                                |||||||| |||  |||||
                                CACCAATG TAC  TTTGA
                                     _   A_
GAM1765  HDAC4     3'  CCCGTGGCTGTTGCACGCT   43310         ACCG  A  A
                                CCCGTGGTT    TG CA GCT
                                |||||||||    || || |||
                                GGGCACCGA    AC GT CGA
                                      CA__  _  G
GAM1765  APG-1     3'  CCCCGTGGTTACTTGCA     43311          CG  A
                                CCCCGTGGTTAC  TG CA
                                ||||||||||||  || ||
                                GGGGCACCAATG  AC GT
                                      A_  _
GAM1765  FLJ13315  5'  TCCCCGTAGGCCTGGCGAGCT  43312        _   ACC   CAA
                                TCCCCGT GGTT   GTGA   GCT
                                ||||||| ||||   ||||   |||
                                AGGGGCA CCGG   CGCT   CGA
                                    T   AC_   ___
GAM1765  ZNF197    3'  TCCCCGTGTTACCCAGGC    43313        G    GTGA  A
                                TCCCCGTG TTACC    CA GC
                                |||||||| |||||    || ||
                                AGGGGCAC AATGG    GT CG
                                     _    _____  C
GAM1765  LOC145501 3'  CCTGGCTACTGTGACAAGCT   43314    G     C
                                CC TGGTTAC GTGACAAGCT
                                || ||||||| ||||||||||
                                GG ACCGATG CACTGTTCGA
                                  _      A
GAM1765  LOC151996 3'  TCCTGTGGTTACAAAGC     43315     CC      CGTGAC
                                TCC  GTGGTTAC     AAGC
                                |||  ||||||||     ||||
                                AGG  CACCAATG     TTCG
                                  A_       T_____
GAM1765  LOC253574 5'  TCCCCGTGGGTTGTGAGAGCT  43316         TTACC   CA
                                TCCCCGTGG    GTGA  AGCT
                                |||||||||    ||||  ||||
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                                AGGGGCACC    CACT  TCGA
                                     CAA__   C_
GAM1766  ABCE1   3'  AAGGGCAGTTTCATTAC    43319     A  TCA
                                AAGG GC   TTTCATTAC
                                |||| ||   |||||||||
                                TTCC CG   AAAGTAATG
                                  _  TC_
GAM1766  ANKH    3'  AAGGCCTCTTTCATTAC    43320     AG   A
                                AAGG  CTC TTTCATTAC
                                ||||  ||| |||||||||
                                TTCC  GAG AAAGTAATG
                                  G_  _
GAM1766  ANKH    3'  AAGGCCTCTTTCATTAC    43320     AG   A
                                AAGG  CTC TTTCATTAC
                                ||||  ||| |||||||||
                                TTCC  GAG AAAGTAATG
                                  G_  _
GAM1766  CA12    3'  AAGGAACAGCCTCATTA    43321       TCA
                                AAGGAGC   TTTCATTA
                                |||||||   ||||||||
                                TTCCTTG   GGAGTAAT
                                    TC_
GAM1766  EGFL6   3'  AGAAGCTCATCAACTTAC   43322         TCA
                                AGGAGCTCATT   TTAC
                                ||||||||||   ||||
                                TCTTCGAGTAG   AATG
                                      TTG
GAM1766  GHR     3'  GAACTCTTTGTTTCATTAC   43323      A___
                                GAGCTC    TTTCATTAC
                                ||||||    |||||||||
                                CTTGAG    AAAGTAATG
                                   AAAC
GAM1766  LBR     3'  AAGGGCTCTTTTCATTAC    43324     A   A
                                AAGG GCTC TTTCATTAC
                                |||| |||| |||||||||
                                TTCC CGAG AAAGTAATG
                                  _   A
GAM1766  LFG     3'  AAGGAGCCCTGGCCTCATTAC 43325       A__
                                AAGGAGCTC   TTTCATTAC
                                |||||||||   |||||||||
                                TTCCTCGGG   GGAGTAATG
                                     ACC
GAM1766  MMP13   3'  AGATCCTCCATTTCATTAC   43326    G_  _
                                GGA  CTC ATTTCATTAC
                                |||  ||| ||||||||||
                                TCT  GAG TAAAGTAATG
                                  AG   G
GAM1766  MTAP    3'  AGAAGCTCACATTAC       43327       TTT
                                AGGAGCTCA   CATTAC
                                |||||||||   ||||||
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                                TCTTCGAGT   GTAATG
                                    ___
GAM1766 MTMR2    3' AAGAAGCTCCTTTGTTAC    43328        A  CA
                                AAGGAGCTC TTT  TTAC
                                ||||||||| |||  ||||
                                TTCTTCGAG GAA  AATG
                                     _  AC
GAM1766 SLC38A2  3' AGGCAAACCATTTCATTA    43329    __  T
                                AGG  AGC CATTTCATTA
                                |||  ||| ||||||||||
                                TCC  TTG GTAAAGTAAT
                                  GT  _
GAM1766 SMARCC2  3' AAGGAGCTTTCCTTAC      43330       CA   A
                                AAGGAGCT  TTTC TTAC
                                ||||||||  |||| ||||
                                TTCCTCGA  AAGG AATG
                                    __   _
GAM1766 SMARCC2  3' AAGGAGCTTTCCTTAC      43330       CA   A
                                AAGGAGCT  TTTC TTAC
                                ||||||||  |||| ||||
                                TTCCTCGA  AAGG AATG
                                    __   _
GAM1766 ABLIM    3' GGGGCCCACTCTGCATTA    43331    A      __
                                GG GCTCATTT  CATTA
                                || ||||||||  |||||
                                CC CGGGTGAG  GTAAT
                                 C       AC
GAM1766 ABLIM    3' GGGGCCCACTCTGCATTA    43331    A      __
                                GG GCTCATTT  CATTA
                                || ||||||||  |||||
                                CC CGGGTGAG  GTAAT
                                 C       AC
GAM1766 B9       3' AAGGCAGCCCTTCATTA     43332     _    AT
                                AAGG AGCTC  TTCATTA
                                |||| |||||  |||||||
                                TTCC TCGGG  AAGTAAT
                                  G    __
GAM1766 C20orf85 3' AGAAGCCTTATTCATTAC    43333       CAT
                                AGGAGCT   TTCATTAC
                                |||||||   ||||||||
                                TCTTCGG   AAGTAATG
                                    AAT
GAM1766 CLECSF9  3' AAGAAGCTTCTTACTCATTA  43334        _ AT_
                                AAGGAGCT C   TTCATTA
                                |||||||| |   |||||||
                                TTCTTCGA G   GAGTAAT
                                     A AAT
GAM1766 CYYR1    3' AAGGAACTCATTCAAAAC    43335          T  TT
                                AAGGAGCTCATT CA  AC
                                |||||||||||| ||  ||
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                                TTCCTTGAGTAA GT  TG
                                       _ TT
GAM1766  DKFZP434G1411 3'  AGGAGCTCATAAACTAC     43336          TTC
                                AGGAGCTCAT   ATTAC
                                ||||||||||  |||||
                                TCCTCGAGTA   TGATG
                                     TT_
GAM1766  DKFZp547E052 3'  AAGGAGCTCAGATATTAC    43337          TTTC
                                AAGGAGCTCA    ATTAC
                                ||||||||||   |||||
                                TTCCTCGAGT    TAATG
                                     CTA_
GAM1766  DKFZP564D172 3'  AAAGAGCTGCCCATCA      43338         CAT
                                AAGGAGCT   TTCATTA
                                ||||||||  |||||||
                                TTTCTCGA   GGGTAGT
                                    C__
GAM1766  DNM1L    3'  AAGGAACTGACCATCATTAC   43339         C  _
                                AAGGAGCT ATT TCATTAC
                                |||||||| ||| |||||||
                                TTCCTTGA TGG AGTAATG
                                    C   T
GAM1766  FLJ12476  3'  AAAGAGCATTTCATTA      43340        TC
                                AAGGAGC  ATTTCATTA
                                |||||||  |||||||||
                                TTTCTCG  TAAAGTAAT
                                      __
GAM1766  GNG3     3'  AAGGGGCTCACAACAATTAC   43341      A     TT  _
                                AAGG GCTCAT  CA TTAC
                                |||| ||||||  || ||||
                                TTCC CGAGTG  GT AATG
                                  C     TT  T
GAM1766  KIAA0125  3'  AGGGGTCCATTTCATCAC    43342     AGC
                                AGG   TCATTTCATTAC
                                |||   ||||||||||||
                                TCC   GGTAAAGTAGTG
                                  CCA
GAM1766  KIAA0179  3'  AGGGTCTCATTTCCTAC     43343     AG       A
                                AGG  CTCATTTC TTAC
                                |||  |||||||| ||||
                                TCC  GAGTAAAG GATG
                                  CA       _
GAM1766  KIAA1243  3'  AGGTGCTATCTCATTAC     43344     A   C
                                AGG GCT ATTTCATTAC
                                ||| ||| ||||||||||
                                TCC CGA TAGAGTAATG
                                  A  _
GAM1766  KIAA1494  3'  AAGGATCTTATTCATTAC    43345       G  CAT
                                AAGGA CT   TTCATTAC
                                ||||| ||   ||||||||
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                                TTCCT GA   AAGTAATG
                                   A  AT_
GAM1766 KIAA1573 3' AAGAACCACTTCATTAC     43346       T
                                AGGAGC CATTTCATTAC
                                |||||| ||||||||||
                                TTCTTG GTGAAGTAATG
                                   _
GAM1766 MGC1127  3' AGGCAGCTGTTCTCATTA    43347     _   CA
                                AGG AGCT  TTTCATTA
                                ||| ||||  ||||||||
                                TCC TCGA  AGAGTAAT
                                  G   CA
GAM1766 MGC12458 3' AAGAAGCCTTCATTAC      43348        CAT
                                AAGGAGCT   TTCATTAC
                                ||||||||   ||||||||
                                TTCTTCGG   AAGTAATG
                                   ____
GAM1766 MRP64    3' AAGAAGCCCCATTTTATTAC  43349         _   C
                                AAGGAGCTC ATTT ATTAC
                                ||||||||| |||| |||||
                                TTCTTCGGG TAAA TAATG
                                     G   A
GAM1766 NIP30    3' AAGGGCTCCATTTCATTAC   43350      A   _
                                AAGG GCTC ATTTCATTAC
                                |||| |||| ||||||||||
                                TTCC CGAG TAAAGTAATG
                                  _   G
GAM1766 NRF      5' AAGGAACCATGTCATTAC    43351       T   T
                                AAGGAGC CAT TCATTAC
                                ||||||| ||| |||||||
                                TTCCTTG GTA AGTAATG
                                   _  C
GAM1766 RRN3     3' AGGAAGTATTTCATTAC     43352      CTC
                                AGGAG   ATTTCATTAC
                                |||||   ||||||||||
                                TCCTT   TAAAGTAATG
                                   CA_
GAM1766 TSPEAR   3' AGGCTTCCATTTCATTAC    43353     AGC
                                AGG   TCATTTCATTAC
                                |||   ||||||||||||
                                TCC   GGTAAAGTAATG
                                  GAA
GAM1766 WNT2B    3' AAGGAGCCTCAACTAC      43354        CATT  _
                                AAGGAGCT    TCA TTAC
                                ||||||||    ||| ||||
                                TTCCTCGG    AGT GATG
                                     ____   T
GAM1766 WNT2B    3' AAGGAGCCTCAACTAC      43354        CATT  _
                                AAGGAGCT    TCA TTAC
                                ||||||||    ||| ||||
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                                TTCCTCGG   AGT GATG
                                    ____   T
GAM1766  LOC127396 5'  AAGGGTCTCTCTCCATTA    43355     AG   A
                                AAGG  CTC TTTCATTA
                                ||||  ||| ||||||||
                                TTCC  GAG GAGGTAAT
                                  CA   A
GAM1766  LOC148710 3'  AGGAGACGCAGTTCATTAC    43356     _ T  T
                                AGGAG C CA TTCATTAC
                                ||||| | || ||||||||
                                TCCTC G GT AAGTAATG
                                   T C  C
GAM1766  LOC149506 3'  AAGGGACTCCTCATTAC     43357     AG   AT
                                AAGG  CTC  TTCATTAC
                                ||||  |||  ||||||||
                                TTCC  GAG  GAGTAATG
                                  CT   __
GAM1766  LOC149992 3'  AGGAACTCAGAACTCATT    43358       T__
                                AGGAGCTCA   TTCATT
                                |||||||||   ||||||
                                TCCTTGAGT   GAGTAA
                                     CTT
GAM1766  LOC150481 3'  AGGAGCCCAACCCCTTAC    43359       _ TT A
                                AGGAGCTCA T  C TTAC
                                ||||||||| |  | ||||
                                TCCTCGGGT G  G AATG
                                     T GG _
GAM1766  LOC151005 3'  AGGAACTCAGAACTCATT    43358       T__
                                AGGAGCTCA   TTCATT
                                |||||||||   ||||||
                                TCCTTGAGT   GAGTAA
                                     CTT
GAM1766  LOC161823 3'  AAGTAGTTCACCTCATTA    43360     G  C
                                AAG AG TCATTTCATTA
                                ||| || ||||||||||
                                TTC TC AGTGGAGTAAT
                                  A  A
GAM1766  LOC219401 5'  AAGGAGCTTCTATTAC      43361       CATT  _
                                AAGGAGCT    TC ATTAC
                                ||||||||    || |||||
                                TTCCTCGA    AG TAATG
                                    ____  A
GAM1766  LOC221830 3'  AGCTTGTCATTTCATTAC    43362     ___
                                AGC   TCATTTCATTAC
                                |||   ||||||||||||
                                TCG   AGTAAAGTAATG
                                  AAC
GAM1766  LOC245811 3'  AAAGAGCTCAAGACTAC     43363       TTTC
                                AAGGAGCTCA    ATTAC
                                ||||||||||    |||||
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                                TTTCTCGAGT   TGATG
                                     TC__
GAM1767 ANXA4   3' TCTTCAGAATGTTTCTGGAGT 43366    _ ATTG ACC
                                TCT CA   GT  TCTGGAGT
                                ||| ||   ||  ||||||||
                                AGA GT   CA  AGACCTCA
                                  A CTTA A__
GAM1767 GATA4   3' TTCCCAGTTGTTGTTCTGGAGT 43367      A  GTACC
            C                    TTCTCA TTG    TCTGGAGTC
                                ||||||| |||    |||||||||
                                AAGGGT AAC    AGACCTCAG
                                   C  AACA_
GAM1767 GSTA4   5' TCAGGCTTTCTGGAGTC    43368    ATT  ACC
                                TCA  GGT  TCTGGAGTC
                                |||  |||  |||||||||
                                AGT  CCG  AGACCTCAG
                                 ___  AA_
GAM1767 MPHOSPH9 5' TTCTCAATTGGTGTCT     43369         ACC
                                TTCTCAATTGGT  TCT
                                ||||||||||||  |||
                                AAGAGTTAACCA  AGA
                                      C__
GAM1767 PDYN    3' TTCTAGCTGCTGCTTCTGGAGT 43370     CAA  GTACC
            C                    TTCT  TTG    TCTGGAGTC
                                ||||  |||    |||||||||
                                AAGA  GAC    AGACCTCAG
                                  TC_  GACGA
GAM1767 PIP5K1A  3' TCTTGTCAACACTTCTGGAGT  43371    CAA  GG  C
                                TCT  TT  TAC TCTGGAGT
                                |||  ||  ||| ||||||||
                                AGA  AG  GTG AGACCTCA
                                  AC_  TT  A
GAM1767 ATP6V1EL2 5' TCAGGAGTGTCTCTGGAGT   43372    ATT  AC
                                TCA  GGT  CTCTGGAGT
                                |||  |||  |||||||||
                                AGT  TCA  GAGACCTCA
                                  CC_  CA
GAM1767 DKFZP434P0721 3' TTCTCAATGCTGGAG      43373       T GTACCT
                                TTCTCAAT G    CTGGAG
                                |||||||| |    ||||||
                                AAGAGTTA C    GACCTC
                                     _ _______
GAM1767 FLJ11703 3' TTCTACCTCCATCTCTGGAGTC 43374    CAA  G  AC
                                TTCT  TT GT  CTCTGGAGTC
                                ||||  || ||  ||||||||||
                                AAGA  AG TA  GAGACCTCAG
                                  TGG  G  __
GAM1767 FLJ22160 3' TTCTCCGTGTCTCTGGAGTC  43375     AATTG  AC
                                TTCTC    GT  CTCTGGAGTC
                                |||||    ||  ||||||||||
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                                AAGAG    CA  GAGACCTCAG
                                  GCA__  __
GAM1767  SEMA4F   3'  TCATTGGTACAGACAGGTC   43376    A     CTC   A
                                TCA TTGGTAC   TGG GTC
                                ||| |||||||   ||| |||
                                AGT AACCATG   GTC CAG
                                  _      TCT   _
GAM1767  YR-29    3'  TCTTCAATTGGTGTGTAGT   43377    _     ACCTC  G
                                TCT CAATTGGT    TG AGT
                                ||| ||||||||    || |||
                                AGA GTTAACCA    AC TCA
                                  A       C____  A
GAM1767  LOC149422 3'  TTCCCACAGAGCCTCTGGAGTC 43378      AT   TA
                                TTCTCA  TGG  CCTCTGGAGTC
                                ||||||  |||  ||||||||||
                                AAGGGT  GTC  GGAGACCTCAG
                                   __   TC
GAM1767  LOC51028  3'  TTCTCAATTGATCGGGGT    43379         ACCTC   A
                                TTCTCAATTGGT    TGG GT
                                ||||||||||    ||| ||
                                AAGAGTTAACTA    GCC CA
                                       _____  C
GAM1767  LOC91344  3'  TTCCAATTGGTGTGTAGT    43380    T     ACCTC  G
                                TTC CAATTGGT    TG AGT
                                ||| ||||||||    || |||
                                AAG GTTAACCA    AC TCA
                                  _      C____  A
GAM1768  MS4A6A   3'  GTTGTGGCAGAAATTG     43383     A   TACA
                                GTTG GGCA   GAAATTG
                                |||| ||||   |||||||
                                CAAC CCGT   CTTTAAC
                                  A   _____
GAM1768  PTK7     3'  AGTTGAAGGCCAGAAATTG   43384      _  ATA
                                AGTTGA GGC   CAGAAATTG
                                |||||| |||   |||||||||
                                TCAACT CCG   GTCTTTAAC
                                   T   ___
GAM1768  AP1GBP1  3'  ACAGTTGATCCAGAAGTT    43385       GGCATA    A
                                ACAGTTGA     CAGAA TT
                                ||||||||     ||||| ||
                                TGTCAACT     GTCTT AA
                                     AG____     C
GAM1768  AP1GBP1  3'  ACAGTTGATCCAGAAGTT    43385       GGCATA    A
                                ACAGTTGA     CAGAA TT
                                ||||||||     ||||| ||
                                TGTCAACT     GTCTT AA
                                     AG____     C
GAM1768  ATP6V1H  3'  AACAATAAATACAGAAATT   43386      TGAGGC
                                AACAGT     ATACAGAAATT
                                ||||||     ||||||||||
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                                TTGTTA     TATGTCTTTAA
                                   TT____
GAM1768  FLJ13842  3'  AACAGTGGGTGTCCAGAAATTG 43387       T A  CATA
                                AACAGT G GG    CAGAAATTG
                                |||||| | ||    |||||||||
                                TTGTCA C CC    GTCTTTAAC
                                   _ _  ACAG
GAM1768  KIAA1076  3'  CAGCCTCTATATACAGAAGTTG 43388      GAGGC       A
                                CAGTT     ATACAGAA TTG
                                ||||||    |||||||| |||
                                GTCGG     TATGTCTT AAC
                                   AGATA       C
GAM1768  KIAA1718  3'  TTAAAATACAGAAATTG     43389      GC
                                TTGAG  ATACAGAAATTG
                                |||||  ||||||||||||
                                AATTT  TATGTCTTTAAC
                                   __
GAM1768  SCYA23    3'  AGTTGAGGCAAGAAA       43390          TAC
                                AGTTGAGGCA   AGAAA
                                ||||||||||   |||||
                                TCAACTCCGT   TCTTT
                                     ___
GAM1768  TRIM2     3'  AAGGTGAAATACAGAAATTG   43391      C___
                                GAGG    ATACAGAAATTG
                                ||||    ||||||||||||
                                TTCC    TATGTCTTTAAC
                                  ACTT
GAM1768  WFDC2     3'  GCTGGACCTCAGAAATTG     43392      A   ATA
                                GTTG GGC   CAGAAATTG
                                |||| |||   |||||||||
                                CGAC CTG   GTCTTTAAC
                                  _  GA_
GAM1768  LOC148418 3'  GTTGACACACAGAGATTG     43393      AG        A
                                GTTG  GCATACAGA ATTG
                                ||||  ||||||||| ||||
                                CAAC  TGTGTGTCT TAAC
                                   __        C
GAM1769  OA1       3'  GAGCAAGGTTTGGGGGCCGCTA 43396       ACTCGA  AA
                                GAGCAA     TG  GGCCGCTA
                                ||||||     ||  ||||||||
                                CTCGTT     AC  CCGGCGAT
                                    CCAA__  CC
GAM1769  PDGFB     3'  GGGCAAGACCGGAGGCCGCT   43397   A    AC   ATGA
                                G GCAA  TCG    AGGCCGCT
                                | ||||  |||    ||||||||
                                C CGTT  GGC    TCCGGCGA
                                 C    CT   C___
GAM1769  SNCB      5'  GGCAGACGCGGGGGCCGCTA   43398   A   A  T  ATGAA
                                G GCA AC CG     GGCCGCTA
                                | ||| || ||     ||||||||
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                                C CGT TG GC    CCGGCGAT
                                 _  C  C  CC___
GAM1769  TF       3'  GCAAACTCATGGATCATCT   43399        G   AA GC  _
                                GCAAACTC ATG  G  CG CT
                                |||||||| |||  |  || ||
                                CGTTTGAG TAC  C  GT GA
                                     _  __ TA  A
GAM1769  DKFZP434C131 3'  GAGCTCGATGACCCGGTTGCTA 43400      AAAC      A__  CC
                                GAGC   TCGATGA   GG  GCTA
                                ||||   |||||||   ||  ||||
                                CTCG   AGCTACT   CC  CGAT
                                  ____      GGG  AA
GAM1769  FLJ10099  5'  GGCGGGCCCGAGGCCGCTA   43401   A  AAA    TGAA
                                G GC   CTCGA   GGCCGCTA
                                | ||   |||||   ||||||||
                                C CG   GGGCT   CCGGCGAT
                                 _ CCC    ____
GAM1769  GOLGIN-67 3'  GCAAACTCGATATGCATGCTA  43402          AAG  C_
                                GCAAACTCGATG   GC  GCTA
                                ||||||||||||   ||  ||||
                                CGTTTGAGCTAT   CG  CGAT
                                      A__  TA
GAM1769  KIAA0855  3'  GCAAACTCGATATGCATGCTA  43402          AAG  C_
                                GCAAACTCGATG   GC  GCTA
                                ||||||||||||   ||  ||||
                                CGTTTGAGCTAT   CG  CGAT
                                      A__  TA
GAM1769  PRKCL2    3'  GAGCAAATGAAGGGTTGCTA   43403      AACTC      CC_
                                GAGCA    GATGAAGG   GCTA
                                |||||    ||||||||   ||||
                                CTCGT    TTACTTCC   CGAT
                                  _____      CAA
GAM1769  LOC134701 5'  GAGCTGGGCGGAAGGCCGCT   43404      AAACT  AT
                                GAGC    CG  GAAGGCCGCT
                                ||||    ||  ||||||||||
                                CTCG    GC  CTTCCGGCGA
                                  ACCC_ __
GAM1769  LOC144017 5'  GAGCGTGGCTCGGACCGCT   43405     AAA_   ATGAA
                                GAGC   CTCG    GGCCGCT
                                ||||   ||||    |||||||
                                CTCG   GAGC    CTGGCGA
                                  CACC   _____
GAM1769  LOC145988 3'  GCAAACTCGATATGCATGCTA  43402          AAG  C_
                                GCAAACTCGATG   GC  GCTA
                                ||||||||||||   ||  ||||
                                CGTTTGAGCTAT   CG  CGAT
                                      A__  TA
GAM1769  LOC204301 3'  GCAAACTCGATATGCACGCTA  43406          AAG  _
                                GCAAACTCGATG   GC CGCTA
                                ||||||||||||   || |||||
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                                CGTTTGAGCTAT   CG GCGAT
                                      A__  T
GAM1769  LOC220534 3'  GCAAACTCGATATGCGTGCTA  43407          AAG  C_
                                GCAAACTCGATG   GC  GCTA
                                ||||||||||||   ||  ||||
                                CGTTTGAGCTAT   CG  CGAT
                                      A__  CA
GAM1769  LOC254358 3'  GCAAACTCGATATGCATGCTA  43402          AAG  C_
                                GCAAACTCGATG   GC  GCTA
                                ||||||||||||   ||  ||||
                                CGTTTGAGCTAT   CG  CGAT
                                      A__  TA
GAM1769  LOC255718 5'  GAGACTTGAAAAGCCG      43408     CAA   C  TG
                                GAG   ACT GA  AAGGCCG
                                |||   ||| ||  |||||||
                                CTC   TGA CT  TTTCGGC
                                  ___   A  __
GAM1770  HNRPH3    3'  TTGATCCATTAGCCAATTTGGA 43411         _    TAATCC
              A                  TTGATCCAT GGTTA     GGAA
                                 |||||||||  |||||     ||||
                                 AACTAGGTA TCGGT     CCTT
                                      A    TAAA__
GAM1770  TTN       3'  GATCCACATAATTTGGA     43412        GGTT    CC
                                GATCCAT    ATAAT  GGA
                                |||||||    |||||  |||
                                CTAGGTG    TATTA  CCT
                                   _____    AA
GAM1770  KIAA0972  3'  TTGACCATGGTTAATGGA    43413      T       TAATCC
                                TTGA CCATGGTTA      GGA
                                ||||  |||||||||     |||
                                AACT GGTACCAAT      CCT
                                  _       TA_____
GAM1770  MIG-6     3'  TGGTCTATGGTTATACCACAA  43414    A  C       AT   G
                                TG TC ATGGTTATA  CCG AA
                                || ||  |||||||||  ||| ||
                                AC AG TACCAATAT  GGT TT
                                 C  A        __   G
GAM1770  TOR1B     3'  TTGATCCACGGTTGTGACCA   43415          ATAAT
                                TTGATCCATGGTT    CCG
                                ||||||||||||     |||
                                AACTAGGTGCCAA    GGT
                                      CACT_
GAM1770  YME1L1    3'  CATGGTCAATCTGGAA      43416        TA   C
                                CATGGTTA  ATC GGAA
                                ||||||||  ||| ||||
                                GTACCAGT  TAG CCTT
                                   __   A
GAM1770  YME1L1    3'  CATGGTCAATCTGGAA      43416        TA   C
                                CATGGTTA  ATC GGAA
                                ||||||||  ||| ||||
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                                GTACCAGT  TAG CCTT
                                    __   A
GAM1770  LOC161734 3'  TTGATCCAAGCCAGAAATCTGG 43417        T    T_   C
                                TTGATCCA GGTTA  AATC GG
                                |||||||| |||||  |||| ||
                                AACTAGGT TCGGT  TTAG CC
                                    _    CT   A
GAM1771  CITED2    3'  TAATTCACGCCGAAGAAGTTGG 43420        ACA   TC____
           G                     TAATTCAC   CGAA     GGG
                                |||||||   ||||     |||
                                ATTAAGTG   GCTT     CCC
                                    CG_   CTTCAA
GAM1771  FLJ11577  3'  TCCATGATTCACACATGA    43421       A       C
                                TCCGT ATTCACACA GA
                                ||||| |||||||| ||
                                AGGTA TAAGTGTGT CT
                                   C       A
GAM1771  KIAA0711  5'  TCCGTAATTCACTGCCAGG   43422          ACA  AATC
                                TCCGTAATTCAC   CG   GG
                                ||||||||||||  ||   ||
                                AGGCATTAAGTG   GT   CC
                                      ACG  ____
GAM1771  MGC15677  3'  GTAGCTCACACAAAATTATTGG 43423    A      C   C___
           G                     GTA TTCACACA GAAT   GGG
                                ||| |||||||| ||||   |||
                                CAT GAGTGTGT TTTA   CCC
                                  C       _   ATAA
GAM1772  ACO1      3'  CCTCAGTGCTCACTTGCT    43426   _        CA
                                CC CAGTGCTCACT  GCT
                                || ||||||||||  |||
                                GG GTCACGAGTGA  CGA
                                 A         A_
GAM1772  CHRNB2    3'  TCCTGGTAGCTCACTCGTCCAT 43427    CA  _      AG   A
           CCT                    TCC  GT GCTCACTC  CTG CCT
                                |||  || ||||||||  ||| |||
                                AGG  CA CGAGTGAG  GGT GGA
                                  AC  T       CA   A
GAM1772  CIT       5'  TCCTCGTGCTCTAGACTGACCT 43428    CA     ACTCA
                                TCC  GTGCTC    GCTGACCT
                                |||  ||||||    ||||||||
                                AGG  CACGAG    TGACTGGA
                                  AG     ATC__
GAM1772  CMAR      3'  TCCATGCTCACTCGGGAAGC   43429    CA       ____
                                TCC  GTGCTCACTC    AGC
                                |||  ||||||||||    |||
                                AGG  TACGAGTGAG    TCG
                                  __         CCCT
GAM1772  GJA5      5'  TCCCAGTGCTTGCTGC      43430          CACTCA    A
                                TCCCAGTGCT     GCTG C
                                ||||||||||     |||| |
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                                AGGGTCACGA     CGAC G
                                     A_____   _
GAM1772 KIF1B    3' ATGCTCACTACCACC      43431         CA   G
                                GTGCTCACT  GCT ACC
                                |||||||||  ||| |||
                                TACGAGTGA  TGG TGG
                                     __  _
GAM1772 SLC2A1   3' CCAGTGCTCCCAACTG     43432         A T
                                CCAGTGCTC C CAGCTG
                                |||||||||  | ||||||
                                GGTCACGAG G GTTGAC
                                     _ _
GAM1772 SPG7     3' TCCATGCTCACTCGGGAAGC  43429     CA        _____
                                TCC  GTGCTCACTC   AGC
                                |||  ||||||||||   |||
                                AGG  TACGAGTGAG   TCG
                                  __       CCCT
GAM1772 ALTE     3' TCCTGACCTCAGCTGAC    43433     CAG  CTCA       C
                                TCC   TG   CTCAGCTGA C
                                |||   ||   ||||||||| |
                                AGG   AC   GAGTCGACT G
                                  ___  TG__       A
GAM1772 ALTE     3' TCCTGACCTCAGCTGAC    43433     CAG  CTCA       C
                                TCC   TG   CTCAGCTGA C
                                |||   ||   ||||||||| |
                                AGG   AC   GAGTCGACT G
                                  ___  TG__       A
GAM1772 C21orf109 5' TCCCAGTGGTTACTCCAATGTA 43434        CTC   AGC  _
             C                   TCCCAGTG   ACTC   TG AC
                                |||||||   ||||   || ||
                                AGGGTCAC   TGAG   AC TG
                                     CAA   GTT  A
GAM1772 C4.4A    3' TCCCCGTGACAGCTGAC    43435     A   CTCACT
                                TCCC GTG     CAGCTGAC
                                |||| |||     ||||||||
                                AGGG CAC     GTCGACTG
                                  G  T_____
GAM1772 C5orf4   3' CCTGGTAAATGCTCAGCTGGCC 43437    CA   CTCA       A
             T                   CC  GTG   CTCAGCTG CCT
                                ||  |||   |||||||| |||
                                GG  CAT   GAGTCGAC GGA
                                 AC  TTAC       C
GAM1772 C5orf4   3' AGTGCTCAGCTGGCCT     43436        CTCA   A
                                AGTGCTCA   GCTG CCT
                                ||||||||   |||| |||
                                TCACGAGT   CGAC GGA
                                     _____   C
GAM1772 CDC14B   3' CCCCAGTGTTTAAAAGCTGGCC 43438        CTCACTC    A
             T                   TCCCAGTG      AGCTG CCT
                                ||||||||      ||||| |||
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                                GGGGTCAC      TCGAC GGA
                                     AAATTT_    C
GAM1772  DKFZP586N0721 5'  TCCCAGTGCTAGCTGCC     43439          CACTC    AC
                                TCCCAGTGCT    AGCTG  C
                                ||||||||||    |||||  |
                                AGGGTCACGA    TCGAC  G
                                      _____    GT
GAM1772  DKFZp761O0113 5'  AGTGCTCATTCCTACAACTGGC 43440         ___ _     A
           CT                    AGTGCTCA   CT CAGCTG CCT
                                ||||||||   || |||||| |||
                                TCACGAGT   GA GTTGAC GGA
                                     AAG  T     C
GAM1772  FEM-2    3'  TCCCAGTGCTGGCACCAGACCT 43441          __   T  GCT
                                TCCCAGTGCT  CAC CA   GACCT
                                ||||||||||  ||| ||   |||||
                                AGGGTCACGA  GTG GT   CTGGA
                                      CC   _  ___
GAM1772  FLJ12921  3'  TCCCAGTGGTCACTTCTGCT   43442        C    _ A
                                TCCCAGTG TCACT C GCT
                                |||||||| ||||| | |||
                                AGGGTCAC AGTGA G CGA
                                     C     A A
GAM1772  FLJ22595  3'  TCCCAGTGATCATTGCCA    43443        C   CTCA
                                TCCCAGTG TCA    GCTG
                                |||||||| |||    ||||
                                AGGGTCAC AGT    CGGT
                                     T   AA__
GAM1772  FZD9     3'  CCCCGGTGCTCACTTGCCTGAC 43444      A        CAG
           CT                    TCCC GTGCTCACT   CTGACCT
                                ||||  |||||||||   |||||||
                                GGGG CACGAGTGA   GACTGGA
                                  C        ACG
GAM1772  HRH4     3'  TCCCAGCTGCTCAGGTGGCT   43445       _     CTCA
                                TCCCAG TGCTCA    GCT
                                ||||||  ||||||    |||
                                AGGGTC ACGAGT    CGA
                                   G     CCAC
GAM1772  KIAA0675  5'  CCACTGCTTGCCAACTGAC    43446     G    CA T
                                CCA TGCT  C CAGCTGAC
                                |||  ||||  | ||||||||
                                GGT ACGA  G GTTGACTG
                                  G    AC _
GAM1772  KIAA0793  3'  CCAGTGCTTGCTCTAGGCCA   43447        CA   A__
                                CCAGTGCT  CTC   GCTG
                                ||||||||  |||   ||||
                                GGTCACGA  GAG   CGGT
                                     AC   ATC
GAM1772  KIAA0939  3'  TCCCAGGCTGCTGAC       43448        T   CACTCA
                                TCCCAG GCT     GCTGAC
                                ||||||  |||     ||||||
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                                AGGGTC CGA     CGACTG
                                  _  _______
GAM1772 KIAA1357 3' TCTCCGTGCTCACCAGACC   43449    _ A      T  GCT
                                TC CC GTGCTCAC CA   GACC
                                || || |||||||| ||   ||||
                                AG GG CACGAGTG GT   CTGG
                                 A  _      _ ___
GAM1772 KIAA1549 3' TCCAAACACCCACTCAGTTGA 43450    C  TG       C
                                TCC AG  CTCACTCAG TGA
                                ||| ||  ||||||||| |||
                                AGG TT  GGGTGAGTC ACT
                                  T  GT       A
GAM1772 MGC11082 3' TCCCAGCTGTTCATTCAGCCA 43451       GC_   C
                                TCCCAGT   TCA TCAGCTG
                                |||||||   ||| |||||||
                                AGGGTCG   AGT AGTCGGT
                                    ACA   A
GAM1772 RAB10    3' TCCCAGTGTTTAGCTCTCCAAC 43452       CTCA_   AG TG
             CT                   TCCCAGTG    CTC  C  ACCT
                                |||||||||    |||  |  ||||
                                AGGGTCAC    GAG  G  TGGA
                                    AAATC   A_ GT
GAM1772 RNF29    3' CCAGTGCTTTCTGCAACTA   43453       CA  _
                                CCAGTGCT  CT CAGCTG
                                ||||||||  || ||||||
                                GGTCACGA  GA GTTGAT
                                    AA  C
GAM1772 SAMHD1   3' CCTAGTGCCATGGCTGACCT   43454    C    T  CTCA
                                CC AGTGC CA    GCTGACCT
                                || ||||| ||    ||||||||
                                GG TCACG GT    CGACTGGA
                                 A    _  AC__
GAM1772 SEMA5B   3' TCCCAGTACTCACTGCC     43455           CA
                                TCCCAGTGCTCACT  GCT
                                ||||||||||||||  |||
                                AGGGTCATGAGTGA  CGG
                                                __
GAM1772 TBC1D2   5' TCCCAGTGATCATTTTTAACCT 43456       C   CTCAGC
                                TCCCAGTG TCA     TGACCT
                                |||||||| |||     ||||||
                                AGGGTCAC AGT     ATTGGA
                                    T   AAAA__
GAM1772 ZDHHC3   3' TCCCAGTGCCACAGGCT     43457        T   TCA
                                TCCCAGTGC CAC   GCT
                                ||||||||| |||   |||
                                AGGGTCACG GTG   CGA
                                    _  TC_
GAM1772 LOC118738 3' CCAGTGCTTATGCTATTGCCT  43458       CACTCA    A__
                                CCAGTGCT     GCTG   CCT
                                ||||||||     ||||   |||
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                                GGTCACGA     CGAT   GGA
                                    ATA___    AAC
GAM1772  LOC130507 5'  TCCCGCGTGTTTCCAGGCTGAC 43459      A_   CTCAC    _
                CT                   TCCC  GTG    TCAG CTGACCT
                                     ||||  |||    |||| |||||||
                                     AGGG  CAC    GGTC GACTGGA
                                       CG   AAA__    C
GAM1772  LOC137829 3'  TCCCAGTATTTGCTGCAAACT  43460        _____   _  CTC
                                     TCCCAGT    GCT CA   AGCT
                                     |||||||    ||| ||   ||||
                                     AGGGTCA    CGA GT   TTGA
                                         TAAA   C  ___
GAM1772  LOC152426 5'  CCTTGGACAATTCAGCTGACCT 43461     AG  CT  C_
                                     CC  TG  CA  TCAGCTGACCT
                                     ||  ||  ||  ||||||||||
                                     GG  AC  GT  AGTCGACTGGA
                                      A_  CT  TA
GAM1772  LOC157657 3'  TCCTGACCTCAGCTGAC     43433     CAG  CTCA       C
                                     TCC   TG    CTCAGCTGA C
                                     |||   ||    ||||||||| |
                                     AGG   AC    GAGTCGACT G
                                       ___  TG__        A
GAM1772  LOC164295 5'  TCCCAGTGCTGTGCTGAGGCCT 43462          CACTCA    __
                                     TCCCAGTGCT     GCTGA  CCT
                                     ||||||||||     |||||  |||
                                     AGGGTCACGA     CGACT  GGA
                                           CA_____     CC
GAM1772  LOC196472 5'  CAGTGCTCATTCGGGAGGGACC 43463         C  AGCT__
                T                    CAGTGCTCA TC      GACCT
                                     |||||||||  ||      |||||
                                     GTCACGAGT AG      CTGGA
                                           A  CCCTCC
GAM1772  LOC221935 3'  CCAGTGCTCACATCCTGGCT   43464          _  A__
                                     CCAGTGCTCAC TC   GCT
                                     ||||||||||| ||   |||
                                     GGTCACGAGTG AG   CGA
                                            T  GAC
GAM1772  LOC222787 5'  TCTCAGTGCTCTTTGCAGATCT 43465    C       ACTCA  T  C
                                     TC CAGTGCTC     GC GA CT
                                     || ||||||||     || || ||
                                     AG GTCACGAG     CG CT GA
                                      A       AAA__  T  A
GAM1772  LOC51212  3'  TCCCAATGTTGCCCAGGCTG   43466        CTCA    _
                                     TCCCAGTG    CTCAG CTG
                                     ||||||||    ||||| |||
                                     AGGGTTAC    GGGTC GAC
                                          AAC_     C
GAM1772  LOC90768  5'  TCCTCGGGTGACTCAGCTGACC 43467     CA__   CTC
                T                    TCC    GTG   ACTCAGCTGACCT
                                     |||    |||   ||||||||||||
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                                AGG   CAC  TGAGTCGACTGGA
                                  AGCC  ___
GAM1772 LOC90917 3' TCTCAGGGCTCACTCAGGGAC 43468   C  T       CT
                                TC CAG GCTCACTCAG  GAC
                                || ||| ||||||||||  |||
                                AG GTC CGAGTGAGTC  CTG
                                 A  C        C_
GAM1772 LOC93109 3' CCCCAGTGTTCACTCCCACCT 43469       C    AGC G
                                TCCCAGTG TCACTC   T ACCT
                                |||||||| ||||||   | ||||
                                GGGGTCAC AGTGAG   G TGGA
                                     A     ___ G
GAM1773 C20orf71 3' TATTGTAGGAGAGGATGGTATG 43472     GATGCT      A
                                TATTG     GGAGGATG TATG
                                |||||     |||||||| ||||
                                ATAAC     TCTCCTAC ATAC
                                   ATCC__       C
GAM1773 KIAA0884 3' TATTGGATTGCTGACGGTG   43473       _   GA  A
                                TATTGGAT GCTG  GG TG
                                |||||||| ||||  || ||
                                ATAACCTA CGAC  CC AC
                                     A   TG  _
GAM1773 LOC158476 3' CATTGGATGCTGGAGATAGAT  43474            AT
                                TATTGGATGCTGGAGG  GAT
                                ||||||||||||||||  |||
                                GTAACCTACGACCTCT  CTA
                                          AT
GAM1773 LOC219654 3' TATTAGATGCTGGAGGGCTG   43475            A_
                                TATTGGATGCTGGAGG  TG
                                ||||||||||||||||  ||
                                ATAATCTACGACCTCC  AC
                                          CG
GAM1774 RPL36A   3' TGAACATAAACTCAAGATTT   43478       TT    A
                                TGAACATA  TTCAA ATTT
                                ||||||||  ||||| ||||
                                ACTTGTAT  GAGTT TAAA
                                     TT    C
GAM1774 FLJ14803 3' TGAACATATTTAAAAAATTT   43479         TC
                                TGAACATATTT  AAAATTT
                                ||||||||||  |||||||
                                ACTTGTATAAA  TTTTAAA
                                      TT
GAM1774 HSPCAL3  3' TTCCTGATAACTTTCAAAATTT 43480    G   ACAT
                                TTC TGA    ATTTTCAAAATTT
                                ||| |||    ||||||||||||
                                AAG ACT    TGAAAGTTTTAAA
                                  G   AT__
GAM1774 LANCL2   3' CATGTACATATTTTTAAAATTT 43481     A       C
                                CGTG ACATATTTT AAAATTT
                                |||| ||||||||| |||||||
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                                GTAC TGTATAAAA TTTTAAA
                                  A       A
GAM1774  LOC91948  3'  TTCGTGAACAACAAAATT    43482         TATTTT
                                TTCGTGAACA     CAAAATT
                                ||||||||||     |||||||
                                AAGCACTTGT     GTTTTAA
                                     T_____
GAM1775  LSS       3'  CTGCACAGACTTGGGATGTT   43485        ATCGA   C
                                CTGCACAGA    GAT GTT
                                |||||||||    ||| |||
                                GACGTGTCT    CTA CAA
                                     GAACC   _
GAM1775  FLJ20605  3'  CAAAAATCGAGATTGTTTT    43486    C        C
                                CA AGAATCGAGAT GTTTT
                                || ||||||||||| |||||
                                GT TTTTAGCTCTA CAAAA
                                 _        A
GAM1775  FLJ23305  3'  CTGACACTTTTGAGATCGTTTT 43487    _   AGAATC
                                CTG CAC     GAGATCGTTTT
                                ||| |||     ||||||||||||
                                GAC GTG     CTCTAGCAAAA
                                  T   AAAA__
GAM1775  KIAA0662  3'  CTGCACAGACATCACTTGTTTT 43488        _    AGATC
                                CTGCACAGA ATCG    GTTTT
                                ||||||||| ||||    |||||
                                GACGTGTCT TAGT    CAAAA
                                     G    GAA__
GAM1775  RACGAP1   3'  ACAGAAGAAAATCGTTTT    43489      TC
                                ACAGAA  GAGATCGTTTT
                                ||||||  ||||||||||||
                                TGTCTT  TTTTAGCAAAA
                                   C_
GAM1775  TOM1L1    3'  CTGCACAGAGTCTACGTTTT   43490        A  GAGAT
                                CTGCACAGA TC    CGTTTT
                                ||||||||| ||    ||||||
                                GACGTGTCT AG    GCAAAA
                                     C  AT___
GAM1775  LOC120400 5'  GCACAGAATGCACTGTTTT    43491        _  AGATC
                                GCACAGAAT CG    GTTTT
                                ||||||||| ||    |||||
                                CGTGTCTTA GT    CAAAA
                                     C  GA___
GAM1775  LOC219688 5'  ACTGCACAGGATGGTT      43492        AATCGA   C
                                ACTGCACAG     GAT GTT
                                |||||||||     ||| |||
                                TGACGTGTC     CTA CAA
                                     _______  C
GAM1776  CENTD1    3'  CTTTACAAGGTTTGTTCA    43495        A  A
                                CTTTACAAG TT GTTCA
                                ||||||||| || |||||
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                                GAAATGTTC AA CAAGT
                                     C  A
GAM1776  CENTD1   3'  CTTTACAAGGTTTGTTCA    43495         A  A
                                CTTTACAAG TT GTTCA
                                ||||||||| || |||||
                                GAAATGTTC AA CAAGT
                                     C  A
GAM1776  GALNT7   3'  TTTACATGCACAGTTCATTGCC 43496       AGAT       CA
              A                  TTTACA   TAGTTCAT  CCA
                                ||||||   ||||||||  |||
                                AAATGT   GTCAAGTA  GGT
                                   ACGT       AC
GAM1776  HHLA1    5'  TTCACAAGGTAATGTCATCA   43497        AT   _
                                TTTACAAG  TAGT TCATCA
                                ||||||||  |||| ||||||
                                AAGTGTTC  ATTA AGTAGT
                                     C_   C
GAM1776  HMGCR    3'  CTCTACAAGAGACATCATCA   43498         TTAGT
                                CTTTACAAGA    TCATCA
                                ||||||||||    ||||||
                                GAGATGTTCT    AGTAGT
                                      CTGT_
GAM1776  HSPA4    3'  TTTACAAAGATTCAAAACATTA 43499       _   AGTT_  C
              CCA                  TTTACAA GATT    CAT ACCA
                                ||||||| ||||    ||| ||||
                                AAATGTT CTAA    GTA TGGT
                                     T   GTTTT   A
GAM1776  KAL1     3'  TTTACAAGATTACTTCTC    43500          G   A
                                TTTACAAGATTA TTC TC
                                |||||||||||| ||| ||
                                AAATGTTCTAAT AAG AG
                                      G   _
GAM1776  PIK3R2   5'  CCTTACAAGGGCCACTCGTCAC 43501        ATTA   A
                                CTTTACAAG   GTTC TCAC
                                |||||||||   |||| ||||
                                GGAATGTTC   TGAG AGTG
                                     CCGG   C
GAM1776  SYNGR1   3'  CTTTGAAGATCAAGAATCACCA 43502     AC       TTC
                                CTTT  AAGATTAG   ATCACCA
                                ||||  ||||||||  |||||||
                                GAAA  TTCTAGTT   TAGTGGT
                                  C_       CT_
GAM1776  ZFY      3'  CTTTACAAGCTTGTAGACACAC 43503        AT__   TT  T
                                CTTTACAAG   TAG  CA CAC
                                |||||||||   |||  || |||
                                GAAATGTTC   ATC  GT GTG
                                     GAAC   T_  _
GAM1776  ALDH9    5'  CTTTACAAGTGTTTTCGGGTTC 43504        ATTA_____
              ATCA                 CTTTACAAG       GTTCATCA
                                |||||||||       ||||||||
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                                GAAATGTTC       CAAGTAGT
                                    ACAAAAGCC
GAM1776 BTN1A1   3' CTTCACAGGATTAATTAATTGC 43505       A      C  CA
            CA                   CTTTACA GATTAGTT AT  CCA
                                ||||||| |||||||| ||  |||
                                GAAGTGT CTAATTAA TA  GGT
                                    C       T  AC
GAM1776 FLJ10110 3' TTTATAAGATCAGTACCTTCA  43506     C       _  A
                                TTTA AAGATTAGT TC TCA
                                |||| ||||||||| || |||
                                AAAT TTCTAGTCA GG AGT
                                  A       T  A
GAM1776 FLJ12529 3' CTTCACAAGGGTTCTTCA    43507         ATTA   A
                                CTTTACAAG   GTTC TCA
                                |||||||||   |||| |||
                                GAAGTGTTC   CAAG AGT
                                    C___   A
GAM1776 FLJ20220 3' CTTTAAAGATTAGTATTTATCA 43508      C       TC__
                                CTTTA AAGATTAGT   ATCA
                                ||||| |||||||||   ||||
                                GAAAT TTCTAATCA   TAGT
                                  _       TAAA
GAM1776 FLJ21657 3' CTTTACAAATTAGTTACC    43509       A      CATC
                                CTTTACA GATTAGTT   ACC
                                ||||||| ||||||||   |||
                                GAAATGT TTAATCAA   TGG
                                    _     _____
GAM1776 FLJ23056 3' CTTTACAAGGATTGGTTTAACA 43510        _  A  ___
            TCA                   CTTTACAAG ATT GTT   CATCA
                                ||||||||| ||| |||   |||||
                                GAAATGTTC TAA CAA   GTAGT
                                    C   C   ATT
GAM1776 ICB-1    3' CATAATCATGTTCATCATCA   43511    A   _      C
                                CA GATTA GTTCATCA CA
                                || ||||| |||||||| ||
                                GT TTAGT CAAGTAGT GT
                                 A    A       A
GAM1776 KIAA0626 3' CTTTGCCAAGAAGGCATCACCA 43512     A_    TT  TT
                                CTTT  CAAGA  AG  CATCACCA
                                ||||  |||||  ||  ||||||||
                                GAAA  GTTCT  TC  GTAGTGGT
                                  CG    __  C_
GAM1776 KIAA1198 3' TTTACAAAAACATCATCA    43513        TTAGT
                                TTTACAAGA    TCATCA
                                |||||||||    ||||||
                                AAATGTTTT    AGTAGT
                                    TGT__
GAM1776 RAI17    3' CTTTGCAAGACTAGAAATCA   43514     A       TTC
                                CTTT CAAGATTAG   ATCA
                                |||| |||||||||   ||||
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                                GAAA GTTCTGATC   TAGT
                                  C       TT_
GAM1776  LOC112840 5'  CTGTACACGTGTTCATCAC   43515    T   AGATTA
                                CT TACA     GTTCATCAC
                                || ||||     |||||||||
                                GA ATGT     CAAGTAGTG
                                 C   GCA___
GAM1776  LOC120105 5'  CTTTACAAGTTCAAGTTCATC  43516        A  _
                                CTTTACAAG TTA GTTCATC
                                ||||||||| ||| |||||||
                                GAAATGTTC AGT CAAGTAG
                                     A  T
GAM1776  LOC134266 3'  TTTACAAGCTTAACCACC    43517        A   GTTC
                                TTTACAAG TTA   ATCACC
                                |||||||| |||   ||||||
                                AAATGTTC AAT   TGGTGG
                                    G  _____
GAM1776  LOC152992 3'  TTTATGAAATACGGTTCATCAC 43518     CA   TA_
                                TTTA  AGAT   GTTCATCAC
                                ||||  ||||   |||||||||
                                AAAT  TTTA   CAAGTAGTG
                                  AC   TGC
GAM1776  LOC159065 5'  CTTTGCAGGATCAGCCATC   43519     A  A     T
                                CTTT CA GATTAGT CATC
                                |||| || ||||||| ||||
                                GAAA GT CTAGTCG GTAG
                                  C  C     _
GAM1777  BACH2    3'  AGAGGTGCACTTGCATCAGAC  43522     A  TT   GTA_
                                AGA GT  GTA    CATCAGAC
                                ||| ||  |||    ||||||||
                                TCT CA  CGT    GTAGTCTG
                                 C  __   GAAC
GAM1777  CASP7    3'  GAAGTGTGGGTCATCAGAC    43523      T  TA  A
                                GAAGT TG  GT CATCAGAC
                                ||||| ||  || ||||||||
                                CTTCA AC  CA GTAGTCTG
                                  C  C_  _
GAM1777  RAB38    3'  AGAAGTTTGTAACAGAC      43524          TACAT
                                AGAAGTTTGTAG    CAGAC
                                ||||||||||||    |||||
                                TCTTCAAACATT    GTCTG
                                          _____
GAM1777  TPMT     3'  AGAAGTTTGTACATGCAGGCCA 43525         AGT   _  A
                                AGAAGTTTGT   ACAT CAG CCA
                                ||||||||||   |||| ||| |||
                                TCTTCAAACA   TGTA GTC GGT
                                      ___   C   C
GAM1777  C5orf4   3'  GAGGTTTGTAGACTACAC    43526    A      __
                                GA GTTTGTAG  TACAT
                                || ||||||||  |||||
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                                CT CAAACATC  ATGTG
                                 C       TG
GAM1777 C5orf4   5' GAGGTTTGTAGACTACAC    43526    A      __
                                GA GTTTGTAG  TACAT
                                || ||||||||  |||||
                                CT CAAACATC  ATGTG
                                 C       TG
GAM1777 CG018    3' AGAATTCCCAGCATCAGACCA  43527     G   G   TA
                                AGAA TTT TAG  CATCAGACCA
                                |||| ||| |||  ||||||||||
                                TCTT AAG GTC  GTAGTCTGGT
                                  _  G  __
GAM1777 FLJ14840 5' AGTTGTAGTACGAATCCGTCAG 43528     T      A_______    A
             GCC                   AGTT GTAGTAC      TCAG CC
                                |||| |||||||      |||| ||
                                TCAA CATCATG      AGTC GG
                                  _      CTTAGGC    C
GAM1777 FLJ20132 5' AGGAGTTTGTAGATGCTCCCA  43529    A       TACA  AGA
                                AG AGTTTGTAG    TC   CCA
                                || |||||||||    ||   |||
                                TC TCAAACATC    AG   GGT
                                 C       TACG  ___
GAM1777 NR1H4    3' AAAGTTATACATCAGA      43530       TGTA
                                GAAGTT    GTACATCAGA
                                ||||||    ||||||||||
                                TTTCAA    TATGTAGTCT
                                           ____
GAM1777 LOC147057 3' AGAAGTTTGGGGACAGGAGAC  43531         TAGT   TC
                                AGAAGTTTG    ACA  AGAC
                                |||||||||    |||  ||||
                                TCTTCAAAC    TGT  TCTG
                                     CCC_   CC
GAM1777 LOC160897 3' AGAGTTTGTAGTATACAC    43532     A       __
                                AGA GTTTGTAGT  ACAT
                                ||| |||||||||  ||||
                                TCT CAAACATCA  TGTG
                                  _       TA
GAM1777 LOC161536 5' AGAAGTTTGAAGTTTTTGGACC 43533         T   ACATCA
             A                   AGAAGTTTG AGT      GACCA
                                |||||||||| |||      |||||
                                TCTTCAAAC TCA      CTGGT
                                     T   AAAAC_
GAM1777 LOC197358 3' GACTCCGTGGTGCATCAGAC   43534    AG    A  A
                                GA  TTTGT GT CATCAGAC
                                ||  ||||| || ||||||||
                                CT  AGGCA CA GTAGTCTG
                                 G_    C  C
GAM1778 ATP8A2   3' TGGCCAGCCATGCAGCAG    43537       A      G
                                TGGCCA CCATGCAG GG
                                |||||| |||||||| ||
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                                ACCGGT GGTACGTC TC
                                   C       G
GAM1778 CDK2     5'  TTGGCCAACTTGAAACAATGT  43538         CA  CA   G
                                TTGGCCAAC  TG  GGG AATGT
                                |||||||||  ||  ||| |||||
                                AACCGGTTG  AC  TTT TTACA
                                     A_  __   G
GAM1778 ENAM     3'  CTGGCCAGGGGGAGGGGAATGT 43539        ACCATGC
                                TTGGCCA      AGGGGAATGT
                                |||||||      ||||||||||
                                GACCGGT      TCCCCTTACA
                                    CCCCC__
GAM1778 WT1      3'  CTGGCTGACCTCGGGAATG   43540      CA   ATGCAG
                                TTGGC  ACC     GGGAATG
                                |||||  |||     |||||||
                                GACCG  TGG     CCCTTAC
                                   AC   AG____
GAM1778 WT1      3'  CTGGCTGACCTCGGGAATG   43540      CA   ATGCAG
                                TTGGC  ACC     GGGAATG
                                |||||  |||     |||||||
                                GACCG  TGG     CCCTTAC
                                   AC   AG____
GAM1778 WT1      3'  CTGGCTGACCTCGGGAATG   43540      CA   ATGCAG
                                TTGGC  ACC     GGGAATG
                                |||||  |||     |||||||
                                GACCG  TGG     CCCTTAC
                                   AC   AG____
GAM1778 WT1      3'  CTGGCTGACCTCGGGAATG   43540      CA   ATGCAG
                                TTGGC  ACC     GGGAATG
                                |||||  |||     |||||||
                                GACCG  TGG     CCCTTAC
                                   AC   AG____
GAM1778 FEM-2    3'  TGGCCAACCATTCTCTGAATGT 43541          GCAGGG
                                TGGCCAACCAT     GAATGT
                                ||||||||||     ||||||
                                ACCGGTTGGTA     CTTACA
                                      AGAGA_
GAM1778 SDC3     3'  TTGGCCAAATAGGTGAGGGG   43542        CCA__  C
                                TTGGCCAA     TG AGGGG
                                ||||||||     || |||||
                                AACCGGTT     AC TCCCC
                                     TATCC  _
GAM1778 LOC126767 5'  TGGCCAACCGCTGCAGGGATGT 43543          A_      GA
                                TGGCCAACC  TGCAGGG  ATGT
                                |||||||||  |||||||  ||||
                                ACCGGTTGG  ACGTCCC  TACA
                                     CG      __
GAM1778 LOC149108 3'  TTGGCCAATCATTGGATG    43544        CCATG  GG   A
                                TTGGCCAA     CA  GGA TG
                                ||||||||     ||  ||| ||
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                                AACCGGTT    GT  CCT AC
                                   A____  AA  _
GAM1778  LOC159199 5'  TTGGCCAACTGTGCGAGGA   43545        CA  A
                                TTGGCCAAC  TGC GGGGA
                                |||||||||  ||| |||||
                                AACCGGTTG  ACG CTCCT
                                   AC  _
GAM1778  LOC255426 3'  TTGGCTGGCATGCAGATCTCAG 43546      CAAC      GGAAT
           T                    TTGGC   CATGCAGG    GT
                                |||||   ||||||||    ||
                                AACCG   GTACGTCT    CA
                                  ACC_      AGAGT
GAM1779  C21orf2   3'  ACAGGACTGGTGTAGACAG   43549        CACA  CTC
                                ACAGGACTGG   TG  ACGG
                                ||||||||||   ||  ||||
                                TGTCCTGACC   AC  TGTC
                                     ____ ATC
GAM1779  CARD15    5'  ACAGGACTGGTGAGCCTGG   43550        CACAT  CAC
                                ACAGGACTGG    GCT  GG
                                ||||||||||    |||  ||
                                TGTCCTGACC    CGG  CC
                                     ACT__  A__
GAM1779  DMPK      3'  ACAGGACTGGAGCTGGGCGGA  43551        CACAT  CA_
                                ACAGGACTGG    GCT  CGGA
                                ||||||||||    |||  ||||
                                TGTCCTGACC    CGA  GCCT
                                     T____  CCC
GAM1779  GAB2      3'  GAACTATGCATGCTCATGG   43552      GCA      C
                                GGACTG  CATGCTCA GG
                                ||||||  |||||||| ||
                                CTTGAT  GTACGAGT CC
                                   AC_      A
GAM1779  GAB2      3'  GAACTATGCATGCTCATGG   43552      GCA      C
                                GGACTG  CATGCTCA GG
                                ||||||  |||||||| ||
                                CTTGAT  GTACGAGT CC
                                   AC_      A
GAM1779  GPR56     3'  ACGGGACTGGCATGGTC     43553    A      CA  C
                                AC GGACTGGCA  TG TC
                                || |||||||||  || ||
                                TG CCTGACCGT  AC AG
                                 C       __  C
GAM1779  IL5RA     3'  ACAAGACTGGTGTGTCTGG   43554        CACA  C  AC
                                ACAGGACTGG   TG TC  GG
                                ||||||||||   || ||  ||
                                TGTTCTGACC   AC AG  CC
                                     AC__  _  A_
GAM1779  KEL       5'  ACAGGACTGGCCTCTGGGTGGA 43555         ACA  CTCAC
                                ACAGGACTGGC   TG    GGA
                                ||||||||||   ||    |||
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                                TGTCCTGACCG  AC    CCT
                                      GAG  CCA__
GAM1779 MDH2    5' ACAGGAGCTGGTGACGCGG   43556      _   CAC   TCAC
                                ACAGGA CTGG  ATGC   GG
                                |||||| ||||  ||||   ||
                                TGTCCT GACC  TGCG   CC
                                   C   AC_  ____
GAM1779 PACSIN1  3' GGAGGGCTGGCACAGCCCGG  43557   C  A      T  T A
                                A AGG CTGGCACA GC C CGG
                                | ||| |||||||| || | |||
                                C TCC GACCGTGT CG G GCC
                                 C  C      _ _ _
GAM1779 PDGFRB   5' CAGGACTGGTGCAGGCTCCTGA 43558        CA  T   ACG
                                CAGGACTGG  CA GCTC   GA
                                |||||||||  || ||||   ||
                                GTCCTGACC  GT CGAG   CT
                                      AC  C    GA_
GAM1779 RASAL1   3' ACAGGACTAGGCACGTCTCTGG 43559        _    ATG   AC
                                ACAGGACT GGCAC   CTC  GG
                                |||||||| |||||   |||  ||
                                TGTCCTGA CCGTG   GAG  CC
                                     T    CA_  A_
GAM1779 REGL    3' CAGTATTGGCACAGCTTGG   43560    GAC     T   CAC
                                CAG   TGGCACA GCT   GG
                                |||   ||||||| |||   ||
                                GTC   ACCGTGT CGA   CC
                                  ATA      _   A__
GAM1779 SUFU    3' ACAGGACTGGTTACAGAGCTGG 43561         C_  T_  CAC
            A                    ACAGGACTGG  ACA  GCT   GGA
                                ||||||||||  |||  |||   |||
                                TGTCCTGACC  TGT  CGA   CCT
                                      AA   CT   ___
GAM1779 USP7    3' CAGGGCTGGTGCACGG     43562     A   CACA   TC
                                CAGG CTGG    TGC  ACGG
                                |||| ||||    |||  ||||
                                GTCC GACC    ACG  TGCC
                                  C   _____  __
GAM1779 ZK1     3' GGACTGGACATGGCTCACGGA  43563       C    _
                                GGACTGG ACATG CTCACGGA
                                ||||||| ||||| ||||||||
                                CCTGACC TGTAC GAGTGCCT
                                     _    C
GAM1779 DGKD    3' GGACTGGCAGAGCCACGG    43564        CAT  T
                                GGACTGGCA   GC CACGG
                                |||||||||   || |||||
                                CCTGACCGT   CG GTGCC
                                      CT_  _
GAM1779 FKBP3   5' GGCGGGGCCACTCACGGA    43565    ACT   A AT
                                GG   GGC C  GCTCACGGA
                                ||   ||| |  |||||||||
```

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                                CC  CCG G  TGAGTGCCT
                                 GCC  _ __
GAM1779  FLJ13052  3'  CAGGCTGGAGACTCACGG   43566    A   CACAT
                                CAGG CTGG   GCTCACGG
                                |||| ||||   ||||||||
                                GTCC GACC   TGAGTGCC
                                  _   TC___
GAM1779  FLJ20499  5'  ACGGGACTGCAGCCACCGCGGA 43567   A    G  CA   T A
                                AC GGACTG CA  TGC C CGGA
                                || |||||| ||  ||| | ||||
                                TG CCTGAC GT  GTG G GCCT
                                 C     _ CG  _ C
GAM1779  FLJ25442  5'  CAGGACTGGCCTCTAAACGG  43568        ACATG  C_
                                CAGGACTGGC   CT  ACGG
                                ||||||||||   ||  ||||
                                GTCCTGACCG   GA  TGCC
                                      GA___  TT
GAM1779  GIT2    3'  ACAGGGTTGGCCGGCTCCATTA 43569     AC   ACAT  _____
           CGG                   ACAGG  TGGC   GCTC   ACGG
                                ||||| ||||   ||||   ||||
                                TGTCC  ACCG   CGAG   TGCC
                                  CA   GC__   GTAA
GAM1779  GIT2    3'  ACAGGGTTGGCCGGCTCCATTA 43569     AC   ACAT  _____
           CGG                   ACAGG  TGGC   GCTC   ACGG
                                ||||| ||||   ||||   ||||
                                TGTCC  ACCG   CGAG   TGCC
                                  CA   GC__   GTAA
GAM1779  GIT2    3'  ACAGGGTTGGCCGGCTCCATTA 43569     AC   ACAT  _____
           CGG                   ACAGG  TGGC   GCTC   ACGG
                                ||||| ||||   ||||   ||||
                                TGTCC  ACCG   CGAG   TGCC
                                  CA   GC__   GTAA
GAM1779  HSPBP1   3'  GGGCTGGCACACCCTGG    43570   A      G  CAC
                                GG CTGGCACAT CT   GG
                                || |||||||| ||   ||
                                CC GACCGTGTG GA   CC
                                 C       G  ___
GAM1779  KIAA0275  3'  CAGGGCTGGATGACTCACGG  43571    A   CAC  _
                                CAGG CTGG   ATG CTCACGG
                                |||| ||||   ||| |||||||
                                GTCC GACC   TAC GAGTGCC
                                  C   ___   T
GAM1779  KIAA0298  3'  CAAGGCTGGCACATGGCAGGA  43572    A       CT  C
                                CAGG CTGGCACATG  CA GGA
                                |||| ||||||||||  || |||
                                GTTC GACCGTGTAC  GT CCT
                                  C       C_  _
GAM1779  KIAA0429  5'  GGGGCTCTGCTGCTCACGGA  43573   ACT  ACA__
                                GG  GGC   TGCTCACGGA
                                ||  |||   ||||||||||
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                                CC  CCG    ACGAGTGCCT
                                 ___  AGACG
GAM1779 KIAA0561 3' CAGGACTGGCATACTGG    43574        CA   CAC
                                CAGGACTGGCA TGCT  GG
                                |||||||||||  ||||  ||
                                GTCCTGACCGT ATGA  CC
                                    __   ___
GAM1779 KIAA1204 5' AGACTGGCAGCCGCGG     43575       CAT  T A
                                GGACTGGCA  GC C CGG
                                |||||||||  || | |||
                                TCTGACCGT  CG G GCC
                                    ___ _ C
GAM1779 LGI2     3' ACAGGACTGTTACACAAGC   43576        __    T
                                ACAGGACTG GCACA GC
                                |||||||||  ||||| ||
                                TGTCCTGAC TGTGT CG
                                     AA    T
GAM1779 RLUCL    3' CAGGTTGGTGCTCACAG    43577     AC  CACA
                                CAGG TGG   TGCTCACGG
                                ||||  |||   |||||||||
                                GTCC ACC   ACGAGTGTC
                                  A_  ____
GAM1779 SLC5A6   3' CAGAACTGGTACTGAAATGG  43578       C  A  CTCAC
                                CAGGACTGG AC TG    GG
                                |||||||||  || ||    ||
                                GTCTTGACC TG AC    CC
                                     A  _  TTTA_
GAM1779 ZD52F10  3' CAGGGCTGGCACAGGCTGG   43579     A      T  CAC
                                CAGG CTGGCACA GCT  GG
                                |||| ||||||||  |||  ||
                                GTCC GACCGTGT CGA  CC
                                  C      C  ___
GAM1779 LOC149722 5' CAAGCTTACATGCTCATGGA  43580     A  GGC       C
                                CAGG CT   ACATGCTCA GGA
                                ||||  ||  |||||||||  |||
                                GTTC GA   TGTACGAGT CCT
                                  _  A__       A
GAM1779 LOC151313 3' CAGGGCTGGCACCTGCCCA   43581     A     A
                                CAGG CTGGCAC TGCTCA
                                |||| |||||||  ||||||
                                GTCC GACCGTG ACGGGT
                                  C      G
GAM1779 LOC169026 3' CAGTGCTCACATCATGCTCGTG 43582     GA  G  _     AC
           GA                     CAG  CT GCA CATGCTC  GGA
                                |||  ||  |||  |||||||  |||
                                GTC  GA TGT GTACGAG  CCT
                                  AC  G   A      CA
GAM1779 LOC222066 5' ACAGGACTGTGCGTGCT     43583         _  ACA
                                ACAGGACTG GC   TGCT
                                |||||||||  ||   ||||
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                                TGTCCTGAC CG   ACGA
                                     A  C__
GAM1779  LOC51281  5'  ACGGGACTGCAGCCACCGCGGA 43567    A     G  CA   T A
                                AC GGACTG CA  TGC C CGGA
                                || |||||| ||  ||| | ||||
                                TG CCTGAC GT  GTG G GCCT
                                 C     _  CG   _ C
GAM1779  LOC89985  5'  ACTGGGTAATCCATGCTCATGG 43584      CA____       C
             A                   ACTGG     CATGCTCA GGA
                                |||||     |||||||| |||
                                TGACC     GTACGAGT CCT
                                   CATTAG       A
GAM1779  LOC90576  3'  GGACTGGACATGGCTCACGGA  43563       C    _
                                GGACTGG ACATG CTCACGGA
                                ||||||| ||||| ||||||||
                                CCTGACC TGTAC GAGTGCCT
                                    _    C
GAM1780  ADAM17    3'  CGTGAGATCCTCAAATGAC   43587    TCT_
                                CGT   TCCTCAAATGAC
                                |||   ||||||||||||
                                GCA   AGGAGTTTACTG
                                  CTCT
GAM1780  ARHGEF6   3'  TCCTGGGCTCAAATGATCC   43588     TC_       _
                                TTCT   CTCAAATGA CC
                                ||||   ||||||||| ||
                                AGGA   GAGTTTACT GG
                                   CCC        A
GAM1780  CDC2L2    5'  CTCTTCTTCCTCAGAACC    43589     G        AAT
                                CTC TTCTTCCTCA   GACC
                                ||| ||||||||||   ||||
                                GAG AAGAAGGAGT   TTGG
                                  _        C__
GAM1780  CKAP1     5'  CCGCTGCACCTCAAGTGATCC  43590      CTT     A  _
                                TCGTT   CCTCAA TGA CC
                                |||||   |||||| ||| ||
                                GGCGA   GGAGTT ACT GG
                                   CGT     C   A
GAM1780  CUL5      3'  CTCATTCTTAAATTAAATGACC 43591         CCTC_
             C                   CTCGTTCTT     AAATGACCC
                                |||||||||     |||||||||
                                GAGTAAGAA     TTTACTGGG
                                     TTTAA
GAM1780  CYP1A2    3'  TCCTGGGCTCAAATGATCC   43588     TC_       _
                                TTCT   CTCAAATGA CC
                                ||||   ||||||||| ||
                                AGGA   GAGTTTACT GG
                                   CCC        A
GAM1780  DDX10     3'  CTCATTCTTTCTCAGGGCTGGT 43592         C    AA__  AC
             CC                    CTCGTTCTT CTCA    TG  CC
                                ||||||||| ||||    ||  ||
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                                GAGTAAGAA GAGT    AC  GG
                                     A    CCCG  CA
GAM1780  GAB2     3'  TCCTTCTTCCTCCACTGGACCC 43593    G       AAAT_
                                TC TTCTTCCTC     GACCC
                                || |||||||||     |||||
                                AG AAGAAGGAG     CTGGG
                                 G        GTGAC
GAM1780  GAB2     3'  TCCTTCTTCCTCCACTGGACCC 43593    G       AAAT_
                                TC TTCTTCCTC     GACCC
                                || |||||||||     |||||
                                AG AAGAAGGAG     CTGGG
                                 G        GTGAC
GAM1780  GALNT3   3'  TCCTGAGCTCAAATGATCC    43594      TC_       _
                                TTCT   CTCAAATGA CC
                                ||||   ||||||||| ||
                                AGGA   GAGTTTACT GG
                                   CTC        A
GAM1780  GLP1R    3'  CTCATTCTTTCTCAACACC    43595         C     ATG
                                CTCGTTCTT CTCAA   ACC
                                ||||||||| |||||   |||
                                GAGTAAGAA GAGTT   TGG
                                     A    G__
GAM1780  GLRA3    5'  TCGTTCTTCCCTGACTGAGACC 43596           CAAAT__
              C                  TCGTTCTTCCT      GACCC
                                 ||||||||||       |||||
                                 AGCAAGAAGGG      CTGGG
                                       ACTGACT
GAM1780  HOXB3    3'  CTCGTCTTCCTCTACC      43597       T      AAATG
                                CTCGT CTTCCTC     ACC
                                ||||| |||||||     |||
                                GAGCA GAAGGAG     TGG
                                   _      A____
GAM1780  ID1      3'  GTTCTCCCTCAGATCC      43598           AAT  _
                                GTTCTTCCTCA   GA CC
                                ||||||||||   || ||
                                CAAGAGGGAGT   CT GG
                                      ___  A
GAM1780  ITGA6    3'  CTCGCTCTTCTTTCCGGATCC  43599          C_  AAAT  _
                                CTCGTTCTTC  TC    GA CC
                                |||||||||  ||    || ||
                                GAGCGAGAAG  AG    CT GG
                                     AA  GC__  A
GAM1780  KCNK6    3'  TCCTGGCCTCAAGTGATCC    43600      T_     A   _
                                TTCT  CCTCAA TGA CC
                                ||||  |||||| ||| ||
                                AGGA  GGAGTT ACT GG
                                   CC     C   A
GAM1780  MBD4     3'  CTCATGAGCTCAAATGATCC   43601       TCTTC        _
                                CTCGT     CTCAAATGA CC
                                |||||     ||||||||| ||
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                                GAGTA    GAGTTTACT GG
                                   CTC__        A
GAM1780  MEA     5'  GCTCCCCTCAAATGGCC     43602       T        A
                                GTTCT CCTCAAATG CC
                                ||||| ||||||||| ||
                                CGAGG GGAGTTTAC GG
                                   _        C
GAM1780  MLLT2   3'  CTAGCCCTTTCAAATGA     43603    C     CC
                                CT GTTCTT  TCAAATGA
                                || ||||||  ||||||||
                                GA CGGGAA  AGTTTACT
                                 T     __
GAM1780  NAPB    3'  CTCTTTCTTCCTAGACTGACC  43604     G        CAAA
                                CTC TTCTTCCT    TGACC
                                ||| ||||||||    |||||
                                GAG AAGAAGGA    ACTGG
                                  A        TCTG
GAM1780  NEF3    3'  CATCCCCCCTTAAGTGACCC   43605          C  A
                                CGTTCTTCCT AA TGACCC
                                |||||||||| || ||||||
                                GTAGGGGGGA TT ACTGGG
                                      A  C
GAM1780  PIK3R3  3'  TCAAACCTCTCAAATGACCC   43606     TT    C
                                TCG  CTTC TCAAATGACCC
                                |||  |||| ||||||||||
                                AGT  GGAG AGTTTACTGGG
                                  TT   _
GAM1780  PRKY    3'  TCCTCAGGCTCAAGTGATCC   43607       ___     A   _
                                TCTTC   CTCAA TGA CC
                                |||||   ||||| ||| ||
                                AGGAG   GAGTT ACT GG
                                   TCC     C   A
GAM1780  RTN4    3'  TCGTTCTTCCCTGACC       43608           CAAA
                                TCGTTCTTCCT    TGACC
                                ||||||||||    |||||
                                AGCAAGAAGGG    ACTGG
                                          ____
GAM1780  SIRT7   3'  TCGTTCTCCCTAGACC       43609           CAAAT
                                TCGTTCTTCCT     GACC
                                ||||||||||     ||||
                                AGCAAGAGGGA     CTGG
                                      T____
GAM1780  SLA2    3'  CTCTTTCTTCCTCTCCCTGATC 43610     G        AAA_  _
            C                    CTC TTCTTCCTC    TGA CC
                                ||| |||||||||    ||| ||
                                GAG AAGAAGGAG    ACT GG
                                  A        AGGG   A
GAM1780  SLC1A3  3'  ATTCTTCCTTAAAGAAGACC   43611          C  T__
                                GTTCTTCCT AAA   GACC
                                ||||||||| |||   ||||
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                                TAAGAAGGA TTT   CTGG
                                    A   CTT
GAM1780  STAR     5'  TCGTCCTTCCTGAGCC      43612          CAAAT  _
                                TCGTTCTTCCT    GA CC
                                ||||||||||    || ||
                                AGCAGGAAGGA    CT GG
                                     _____  C
GAM1780  TEM5     3'  GTTCTTCCCAAGACCC      43613        T   AT
                                GTTCTTCC CAA  GACCC
                                |||||||| |||  |||||
                                CAAGAAGG GTT  CTGGG
                                   _  __
GAM1780  XT3      3'  TCCTGACCTCAAGTGATCC   43614      T_     A  _
                                TTCT  CCTCAA TGA CC
                                ||||  |||||| ||| ||
                                AGGA  GGAGTT ACT GG
                                  CT     C   A
GAM1780  ZNF74    3'  TCCTAGGCTCAAATGATCC   43615      TC_       _
                                TTCT   CTCAAATGA CC
                                ||||   |||||||||| ||
                                AGGA   GAGTTTACT GG
                                  TCC        A
GAM1780  AKAP6    3'  CTTTTTCTTCCTCCTTGTACCC 43616    CG        AAATG
                                CT  TTCTTCCTC    ACCC
                                ||  |||||||||    ||||
                                GA  AAGAAGGAG    TGGG
                                 AA        GAACA
GAM1780  ATP10D   3'  CATTCCTGTCCTCAAATGA   43617       __
                                CGTTCT  TCCTCAAATGA
                                ||||||  ||||||||||||
                                GTAAGG  AGGAGTTTACT
                                   AC
GAM1780  C11orf25 3'  CTCTTTCTTCCTTTCCAACC  43618     G       CAAA
                                CTC TTCTTCCT    TGACC
                                ||| ||||||||    |||||
                                GAG AAGAAGGA    GTTGG
                                  A       AAG_
GAM1780  C1QTNF2  3'  TCCTGACCTCAAATGATCC   43619      T_        _
                                TTCT  CCTCAAATGA CC
                                ||||  |||||||||| ||
                                AGGA  GGAGTTTACT GG
                                  CT         A
GAM1780  C20orf45 3'  GTTCTTCCCCACCGCCC     43620          AA  A
                                GTTCTTCCTCA  TG CCC
                                ||||||||||||  || |||
                                CAAGAAGGGGT  GC GGG
                                      G_  _
GAM1780  CRK7     3'  CTCGCTCTGGCAAATGA     43621        TCCT
                                CTCGTTCT    CAAATGA
                                ||||||||    |||||||
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                                GAGCGAGA    GTTTACT
                                     CC__
GAM1780  DCLRE1A   3'  CCACACTTCTTCAAATGAC    43622     TT    C
                                TCG  CTTC TCAAATGAC
                                |||  |||| |||||||||
                                GGT  GAAG AGTTTACTG
                                  GT    A
GAM1780  dJ383J4.3 3'  TCCTGGCCTCAAATGATCC    43623     T_        _
                                TTCT  CCTCAAATGA CC
                                ||||  |||||||||| ||
                                AGGA  GGAGTTTACT GG
                                  CC         A
GAM1780  DKFZP564I0422 5'  CCCGTTCTTTCTCCCCGCCC   43624         C   AAA  A
                                CTCGTTCTT CTC   TG CCC
                                ||||||||| |||   || |||
                                GGGCAAGAA GAG   GC GGG
                                      A   GG_  _
GAM1780  DUSP14    5'  CTCCTTCTTCCTCAAGAGTCC  43625     G         ATGA
                                CTC TTCTTCCTCAA    CC
                                ||| ||||||||||    ||
                                GAG AAGAAGGAGTT    GG
                                  G          CTCA
GAM1780  FAM3D     3'  GTCCTTCCTCAGGACC      43626          AAT
                                GTTCTTCCTCA   GACC
                                ||||||||||   ||||
                                CAGGAAGGAGT   CTGG
                                      C__
GAM1780  FLJ10232  3'  TCCTGGGCTCAAATGATCC    43588     TC_       _
                                TTCT   CTCAAATGA CC
                                ||||   |||||||| ||
                                AGGA   GAGTTTACT GG
                                  CCC        A
GAM1780  FLJ20034  3'  TCCTGACCTCAAATGATCC    43619     T_        _
                                TTCT  CCTCAAATGA CC
                                ||||  |||||||||| ||
                                AGGA  GGAGTTTACT GG
                                  CT         A
GAM1780  FLJ22349  3'  CTCTTCTTCCTCCCGACC     43627     G       AAAT
                                CTC TTCTTCCTC    GACC
                                ||| |||||||||    ||||
                                GAG AAGAAGGAG    CTGG
                                  _        GG__
GAM1780  FLJ22405  3'  CTCATTCTCAGTGCAGGTGATC 43628         CCT_  AA  _
           C                     CTCGTTCTT    CA  TGA CC
                                ||||||||||    ||  ||| ||
                                GAGTAAGAG    GT  ACT GG
                                      TCAC  CC   A
GAM1780  FLJ22596  3'  TCCTGACCTCAAATGATCC    43619     T_        _
                                TTCT  CCTCAAATGA CC
                                ||||  |||||||||| ||
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                                AGGA  GGAGTTTACT GG
                                  CT        A
GAM1780  FLJ23604  3'  CGTTCTTTCTCAGAGCC    43629       C   AAT  _
                                CGTTCTT CTCA   GA CC
                                ||||||| ||||   || ||
                                GCAAGAA GAGT   CT GG
                                    A   ___  C
GAM1780  JAM1      3'  GTTCTCCAAATGACC      43630      CCT
                                GTTCTT   CAAATGACC
                                ||||||   |||||||||
                                CAAGAG   GTTTACTGG
                                   ___
GAM1780  JAM1      3'  GTTCTCCAAATGACC      43630      CCT
                                GTTCTT   CAAATGACC
                                ||||||   |||||||||
                                CAAGAG   GTTTACTGG
                                   ___
GAM1780  JAM1      3'  GTTCTCCAAATGACC      43630      CCT
                                GTTCTT   CAAATGACC
                                ||||||   |||||||||
                                CAAGAG   GTTTACTGG
                                   ___
GAM1780  JAM1      3'  GTTCTCCAAATGACC      43630      CCT
                                GTTCTT   CAAATGACC
                                ||||||   |||||||||
                                CAAGAG   GTTTACTGG
                                   ___
GAM1780  KIAA0227  3'  CTCATTCTCCAGGTGACC    43631       T  TCAAA
                                CTCGTTCT CC    TGACC
                                |||||||| ||    |||||
                                GAGTAAGA GG    ACTGG
                                    _  TCC__
GAM1780  KIAA1509  3'  CTCGCTCTGTGCGGATGACCC  43632       TCCTCAA
                                CTCGTTCT      ATGACCC
                                ||||||||      |||||||
                                GAGCGAGA      TACTGGG
                                    CACGCC_
GAM1780  KIAA1817  5'  TCGTTCTCCCTGTACCTGGCCC 43633         CAAA_  A
                                TCGTTCTTCCT    TG CCC
                                ||||||||||    || |||
                                AGCAAGAGGGA    AC GGG
                                     CATGG  C
GAM1780  KIAA1893  3'  CTCGTTCTACCTCACGTG    43634       T    AA
                                CTCGTTCT CCTCA  TG
                                |||||||| |||||  ||
                                GAGCAAGA GGAGT  AC
                                    T    GC
GAM1780  MGC21688  3'  CTCGTTCTTACCTTGGGCCC  43635       _  CAAA  A_
                                CTCGTTCTT CCT   TG  CCC
                                ||||||||| |||   ||  |||
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                                GAGCAAGAA GGA    AC  GGG
                                     T  _____  CC
GAM1780  MGC2780   5'  TTCTGGGCTCAAATGATCC    43636      TC_       _
                                TTCT   CTCAAATGA CC
                                ||||   |||||||||| ||
                                AAGA   GAGTTTACT GG
                                  CCC        A
GAM1780  PELI1     3'  CTCGTCCTTCTTCCTAAC     43637          C  AAA
                                CTCGTTCTTC TC   TGAC
                                |||||||||| ||   ||||
                                GAGCAGGAAG AG   ATTG
                                     A  G__
GAM1780  PRO2176   3'  TTCTTCCTCTAAATTAAGTGGC 43638         _  ______ A   III
            CCG                    TCTTCCTC AAA     TG CCC   G
                                ||||||||| |||     || |||   |
                                AGAAGGAG TTT     AC GGG   C
                                     A   AATTC  C   III
GAM1780  RoXaN     3'  TCCTGACTTCAAATGATCC    43639      TC  _      _
                                TTCT  CT CAAATGA CC
                                ||||  || ||||||| ||
                                AGGA  GA GTTTACT GG
                                  CT  A      A
GAM1780  Rpo1-2    3'  TCCTGCACTCAAATGATCC    43640      TC_       _
                                TTCT   CTCAAATGA CC
                                ||||   |||||||||| ||
                                AGGA   GAGTTTACT GG
                                  CGT        A
GAM1780  Rpo1-2    3'  TCCTGCACTCAAATGATCC    43640      TC_       _
                                TTCT   CTCAAATGA CC
                                ||||   |||||||||| ||
                                AGGA   GAGTTTACT GG
                                  CGT        A
GAM1780  VIT1      5'  TCCTGACCTCAAATGATCC    43619      T_        _
                                TTCT  CCTCAAATGA CC
                                ||||  |||||||||| ||
                                AGGA  GGAGTTTACT GG
                                  CT         A
GAM1780  WBSCR22   3'  TCCTGGCCTCAAATGATCC    43623      T_        _
                                TTCT  CCTCAAATGA CC
                                ||||  |||||||||| ||
                                AGGA  GGAGTTTACT GG
                                  CC         A
GAM1780  LOC124997 3'  CTCCTTCTTCCTTCCCGTCC   43641      G       CAAA  A
                                CTC TTCTTCCT    TG CC
                                ||| ||||||||    || ||
                                GAG AAGAAGGA    GC GG
                                  G       AGG_  A
GAM1780  LOC126755 3'  CTCGTTCTTGTGGTGAATGATC 43642          CCTCA_    _
            C                   CTCGTTCTT      AATGA CC
                                |||||||||      ||||| ||
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                                GAGCAAGAA     TTACT GG
                                     CACCAC    A
GAM1780  LOC131870 3'  CTCCTTCTTTCTCATGGAC   43643    G    C   AAT
                                CTC TTCTT CTCA   GAC
                                ||| ||||| ||||   |||
                                GAG AAGAA GAGT   CTG
                                  G    A   AC_
GAM1780  LOC134288 3'  CCTTTCCCCCCTTGAATGA   43644    CG      CA
                                CT  TTCTTCCT  AATGA
                                ||  ||||||||  |||||
                                GG  AGGGGGGA  TTACT
                                 AA       AC
GAM1780  LOC136345 5'  CTCTTTCTTCCTAACC     43645    G      CAAAT
                                CTC TTCTTCCT    GACC
                                ||| ||||||||    ||||
                                GAG AAGAAGGA    TTGG
                                  A      _____
GAM1780  LOC139483 5'  CTCTTCTTCCTCTGTCC    43646    G       AAA  A
                                CTC TTCTTCCTC   TG CC
                                ||| |||||||||   || ||
                                GAG AAGAAGGAG   AC GG
                                  _       ___  A
GAM1780  LOC143712 3'  CTCTTTCTTCCTCACC     43647    G       AAATG
                                CTC TTCTTCCTC    ACC
                                ||| |||||||||    |||
                                GAG AAGAAGGAG    TGG
                                  A      _____
GAM1780  LOC143888 3'  CTCTTCTTCCTTAAATATCC  43648    G      C    A
                                CTC TTCTTCCT AAATG CC
                                ||| |||||||| ||||| ||
                                GAG AAGAAGGA TTTAT GG
                                  _      A    A
GAM1780  LOC144603 3'  CTCATTCTCAGTGCAGGTGATC 43628         CCT_  AA  _
              C                  CTCGTTCTT    CA  TGA CC
                                |||||||||   ||  ||| ||
                                GAGTAAGAG    GT  ACT GG
                                     TCAC  CC   A
GAM1780  LOC145258 3'  CTCGTTCCTCTTTCTCGACCC  43649          ___   AAAT
                                CTCGTTCTTC   CTC    GACCC
                                ||||||||||   |||    |||||
                                GAGCAAGGAG   GAG    CTGGG
                                     AAA   ____
GAM1780  LOC145474 3'  CTTATTCTTCCAGTATGGCCC  43650    CG      TCAA   A
                                CT  TTCTTCC    ATG CCC
                                ||  |||||||    ||| |||
                                GA  AAGAAGG    TAC GGG
                                 AT      TCA_   C
GAM1780  LOC145801 3'  TCGTCTTCTTCTTCGCCC    43651      T    C  AAA  A
                                TCGT CTTC TC   TG CCC
                                |||| |||| ||   || |||
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                                AGCA GAAG AG   GC GGG
                                  _   A  AA_  _
GAM1780  LOC147341 5'  CTCTTTCTTCCTCACACACCC  43652     G        AATG
                                CTC TTCTTCCTCA    ACCC
                                ||| ||||||||||    ||||
                                GAG AAGAAGGAGT    TGGG
                                  A         GTG_
GAM1780  LOC147912 5'  CTCGATCTTCTTTCTGGCCGAC 43653      T    C_  AAA_
              CC                  CTCG TCTTC  TC    TGACCC
                                ||||| |||||  ||    ||||||
                                GAGC AGAAG  AG    GCTGGG
                                  T    AA  ACCG
GAM1780  LOC148343 5'  TCCTTCTTCCCCCGGACCC   43654    G       AAAT
                                TC TTCTTCCTC    GACCC
                                || |||||||||    |||||
                                AG AAGAAGGGG    CTGGG
                                 G        GC__
GAM1780  LOC149351 5'  CTCTTCTTCCTCATGGGCC   43655     G        AA  A_
                                CTC TTCTTCCTCA  TG  CC
                                ||| ||||||||||  ||  ||
                                GAG AAGAAGGAGT  AC  GG
                                  _         __ CC
GAM1780  LOC149705 3'  TCCTGACCTCAAATGATCC   43619      T_        _
                                TTCT  CCTCAAATGA CC
                                ||||  |||||||||| ||
                                AGGA  GGAGTTTACT GG
                                  CT         A
GAM1780  LOC151391 3'  CTCATTCTTCCTTGTCC     43656           CAAA  A
                                CTCGTTCTTCCT    TG CC
                                ||||||||||||    || ||
                                GAGTAAGAAGGA    AC GG
                                       _____  A
GAM1780  LOC151414 3'  CTGGCTGCCCCTCAAGTGGCC  43657    C   C       A  A
                                CT GTT TTCCTCAA TG CC
                                || ||| |||||||| || ||
                                GA CGA GGGGAGTT AC GG
                                 C   C       C  C
GAM1780  LOC151445 3'  CTCGTTCTCGCTCCTGA     43658          C   AAA
                                CTCGTTCTT CTC   TGA
                                ||||||||| |||   |||
                                GAGCAAGAG GAG   ACT
                                     C   G__
GAM1780  LOC162952 3'  CTCTTCTTCCTTGGTGGCC   43659     G       CAAA  A
                                CTC TTCTTCCT    TG CC
                                ||| ||||||||    || ||
                                GAG AAGAAGGA    AC GG
                                  _       ACC_  C
GAM1780  LOC163882 3'  CTTTTTCTTTCAAATGATCC   43660    CG    CC       _
                                CT  TTCTT  TCAAATGA CC
                                ||  |||||  |||||||| ||
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                                GA  AAGAA  AGTTTACT GG
                                 AA     __       A
GAM1780  LOC166983 5'  CTCGTTCCTCCAGACC      43661          TCAAAT
                                CTCGTTCTTCC     GACC
                                ||||||||||     ||||
                                GAGCAAGGAGG     CTGG
                                      T_____
GAM1780  LOC200597 3'  CTCCTTCTGGCTGATGACC    43662     G    TC  CAA
                                CTC TTCT  CT   ATGACC
                                ||| ||||  ||   ||||||
                                GAG AAGA  GA   TACTGG
                                  G    CC  C__
GAM1780  LOC200918 5'  CTCACGACTCCTCGAATGGCCC 43663      TTC     A    A
                                CTCG   TTCCTC AATG CCC
                                ||||   |||||| |||| |||
                                GAGT   GAGGAG TTAC GGG
                                   GCT     C    C
GAM1780  LOC203350 3'  TCCTGGGCTCAAATGATCC    43588      TC_       _
                                TTCT   CTCAAATGA CC
                                ||||   |||||||||| ||
                                AGGA   GAGTTTACT GG
                                   CCC        A
GAM1780  LOC221393 3'  CTCATTCTTCCTCCTGCCAACC 43664            AAA_
              C                  CTCGTTCTTCCTC    TGACCC
                                 ||||||||||||    ||||||
                                 GAGTAAGAAGGAG    GTTGGG
                                       GACG
GAM1780  LOC221632 3'  CTCTTCTTCCCATTGATCC    43665     G       CAAA  _
                                CTC TTCTTCCT    TGA CC
                                ||| ||||||||    ||| ||
                                GAG AAGAAGGG    ACT GG
                                  _       TA__   A
GAM1780  LOC245806 3'  CTCTTCTTCCTCATCACC     43666     G         AA G
                                CTC TTCTTCCTCA  T ACC
                                ||| ||||||||||  | |||
                                GAG AAGAAGGAGT  A TGG
                                  _         __ G
GAM1780  LOC253070 3'  CTCGTTCTCCCTCGCC       43667            AAAT A
                                CTCGTTCTTCCTC    G CC
                                ||||||||||||    | ||
                                GAGCAAGAGGGAG    C GG
                                       _____ _
GAM1780  LOC254413 5'  TCATTCTTCCTTGTCC       43668           CAAA  A
                                TCGTTCTTCCT    TG CC
                                ||||||||||    || ||
                                AGTAAGAAGGA    AC GG
                                       _____  A
GAM1780  LOC51036  3'  GCTAACCTTCAAATGACCC    43669     CTT   _
                                GTT   CCT CAAATGACCC
                                |||   ||| ||||||||||
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                                CGA   GGA GTTTACTGGG
                                  TT_   A
GAM1780 LOC63923 3' ATTCTTCCTCATAACACC    43670          AA   _
                                GTTCTTCCTCA  TGAC CC
                                ||||||||||  |||| ||
                                TAAGAAGGAGT  ATTG GG
                                      __    T
GAM1780 LOC90231 5' CTCCTTCTTCTCGGTGGCC   43671     G     C  AAA  A
                                CTC TTCTTC TC   TG CC
                                ||| |||||| ||   || ||
                                GAG AAGAAG AG   AC GG
                                  G     _ CC_  C
GAM1780 LOC92228 3' CTCATTCTTCCCTGGCC     43672          CAAA  A
                                CTCGTTCTTCCT    TG CC
                                ||||||||||||    || ||
                                GAGTAAGAAGGG    AC GG
                                      _____  C
GAM1781 ABCC3    3' TGAGTAGCTGCCGAAGGGGTCC 43675        CA  _   AGATG
             A                   TGAGTAGC  CC AAG    CCA
                                ||||||||  || |||    |||
                                ACTCATCG  GG TTC    GGT
                                     AC  C   CCCA_
GAM1781 ABCC3    3' TGAGTAGCTGCCGAAGGGGTCC 43675        CA  _   AGATG
             A                   TGAGTAGC  CC AAG    CCA
                                ||||||||  || |||    |||
                                ACTCATCG  GG TTC    GGT
                                     AC  C   CCCA_
GAM1781 ACPP     3' TGCGGCACCACTGAGAGATGC  43676    AGTA    CA
                                TG   GCCAC  AGAGATGC
                                ||   |||||  ||||||||
                                AC   TGGTG  TCTCTACG
                                  GCCG    AC
GAM1781 CALCB    3' TAAGTCAATGAGAGATGCCA   43677      AGCCACCA
                                TGAGT       AGAGATGCCA
                                |||||       ||||||||||
                                ATTCA       TCTCTACGGT
                                   GTTAC___
GAM1781 CBFA2T3  3' TGATAGCCACGCACACAGATGC 43678     G      _  AG_
             CA                   TGA TAGCCAC CA   AGATGCCA
                                ||| ||||||| ||   ||||||||
                                ACT ATCGGTG GT   TCTACGGT
                                  _      C  GTG
GAM1781 CLCA3    3' AAGAGCCTGCTGAGAGATGC   43679     T   ACCA_
                                GAG AGCC    AGAGATGC
                                ||| ||||    ||||||||
                                TTC TCGG    TCTCTACG
                                  _   ACGAC
GAM1781 DDX11    3' TGGGCAGGACGGAGATGCCA   43680    A   CC  CAA
                                TG GTAG  AC   GAGATGCCA
                                || ||||  ||   |||||||||
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                                AC CGTC  TG   CTCTACGGT
                                 C    C_  C__
GAM1781  DDX11    3'  TGGGCAGGACGGAGATGCCA  43680    A   CC  CAA
                                TG GTAG  AC   GAGATGCCA
                                || ||||  ||   |||||||||
                                AC CGTC  TG   CTCTACGGT
                                 C    C_  C__
GAM1781  EMS1     3'  TGAGTGGCCACAAATGCCA   43681      A    CAAG
                                TGAGT GCCAC    AGATGCCA
                                ||||| |||||    ||||||||
                                ACTCA CGGTG    TTTACGGT
                                   C    ____
GAM1781  EMS1     3'  TGAGTGGCCACAAATGCCA   43681      A    CAAG
                                TGAGT GCCAC    AGATGCCA
                                ||||| |||||    ||||||||
                                ACTCA CGGTG    TTTACGGT
                                   C    ____
GAM1781  FGFR1    3'  TGAGTAGCTGGGACTACAGGTG 43682       CACCAAG__  A
              CCA                  TGAGTAGC       AG TGCCA
                                |||||||||       || |||||
                                ACTCATCG       TC ACGGT
                                     ACCCTGATG  C
GAM1781  FGFR1    3'  TGAGTAGCTGGGACTACAGGTG 43682       CACCAAG__  A
              CCA                  TGAGTAGC       AG TGCCA
                                |||||||||       || |||||
                                ACTCATCG       TC ACGGT
                                     ACCCTGATG  C
GAM1781  HMGB2    3'  TGAGTAGCCCATCAAAAAGC  43683       ACCA    T
                                TGAGTAGCC    AGAGA GC
                                |||||||||    ||||| ||
                                ACTCATCGG    TTTTT CG
                                     GTAG    _
GAM1781  IRF2     3'  TGAGTAGCCCTGGGAGATCCA  43684       ACCAA    G
                                TGAGTAGCC    GAGAT CCA
                                |||||||||    ||||| |||
                                ACTCATCGG    CTCTA GGT
                                     GACC_    _
GAM1781  MEOX1    3'  TGGCAGCCAAGAGACGC    43685    A     CCA
                                TG GTAGCCA   AGAGATGC
                                || |||||||   ||||||||
                                AC CGTCGGT   TCTCTGCG
                                  _     ___
GAM1781  MEOX1    3'  TGGCAGCCAAGAGACGC    43685    A     CCA
                                TG GTAGCCA   AGAGATGC
                                || |||||||   ||||||||
                                AC CGTCGGT   TCTCTGCG
                                  _     ___
GAM1781  RNF12    5'  TGAGTAGCTGGTTGAGACCC  43686       CACCAA    G
                                TGAGTAGC     GAGAT CC
                                ||||||||     ||||| ||
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                                ACTCATCG     CTCTG GG
                                    ACCAA_    _
GAM1781  SLC7A5   3'  TGAGCTAGGGGAGATGCC    43687      _ CCACCAA
                                TGAGT AG      GAGATGCC
                                ||||| ||      ||||||||
                                ACTCG TC      CTCTACGG
                                   A  CC_____
GAM1781  TACC1    3'  TGAGTAACCACTGAGCTG    43688          CAA   A
                                TGAGTAGCCAC   GAG TG
                                ||||||||||   ||| ||
                                ACTCATTGGTG   CTC AC
                                      A__   G
GAM1781  TEGT     3'  GAGTTTGGCTTCAAGAGATG   43689      A__  CAC
                                GAGT   GC   CAAGAGATG
                                ||||   ||   |||||||||
                                CTCA   CG   GTTCTCTAC
                                   AAC  AA_
GAM1781  VDR      3'  TGAGTAGCCGCCAGCC      43690         A   AGAGAT
                                TGAGTAGCC CCA     GCC
                                ||||||||| |||     |||
                                ACTCATCGG GGT     CGG
                                     C  _______
GAM1781  C20orf29 3'  TGGGTAGGAGGGAGATGCCA   43691    A    CCACCAA
                                TG GTAG      GAGATGCCA
                                || ||||      |||||||||
                                AC CATC      CTCTACGGT
                                 C    CTCC___
GAM1781  DDX12    3'  TGGGCAGGACGGAGATGCCA   43680    A    CC  CAA
                                TG GTAG  AC   GAGATGCCA
                                || ||||  ||   |||||||||
                                AC CGTC  TG   CTCTACGGT
                                 C    C_  C__
GAM1781  DKFZP586F1318 3'  GAAAAGTTGAGAGATGCCA    43692     T  CCACCA
                                GAG AG     AGAGATGCCA
                                ||| ||     ||||||||||
                                CTT TC     TCTCTACGGT
                                  T  AAC___
GAM1781  DKFZp761N1114 3'  TGAATAGCCATTGAGAGAGC   43693          CCA    T
                                TGAGTAGCCA   AGAGA GC
                                ||||||||||   ||||| ||
                                ACTTATCGGT   TCTCT CG
                                      AAC    _
GAM1781  DOCK3    3'  AACCACCGAGAGATGCCA    43694        A
                                AGCCACC AGAGATGCCA
                                ||||||| ||||||||||
                                TTGGTGG TCTCTACGGT
                                    C
GAM1781  ESPL1    5'  TAAGTAGCCATCACAGGCCA   43695          C  AG  AT
                                TGAGTAGCCA CA  AG  GCCA
                                |||||||||| ||  ||  ||||
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                                ATTCATCGGT GT  TC  CGGT
                                     A  G_  __
GAM1781  EZFIT    5'  TGAGCAGCCATCCCTCTGC   43696        _  AAGAGA
                                TGAGTAGCCA CC     TGC
                                |||||||||| ||     |||
                                ACTCGTCGGT GG     ACG
                                     A  GAG___
GAM1781  FBXL9    5'  TGAGCAGCCACTGAGGTCCA  43697         CAA   ATG
                                TGAGTAGCCAC   GAG   CCA
                                ||||||||||   |||   |||
                                ACTCGTCGGTG   CTC   GGT
                                      A__   CA_
GAM1781  FLJ10932 3'  TGAGTAGCTAAGACTACAGGTG 43698       CACCAAG__  A
            CCA                    TGAGTAGC       AG TGCCA
                                |||||||        || |||||
                                ACTCATCG       TC ACGGT
                                     ATTCTGATG  C
GAM1781  FLJ13111 3'  TGAGCAGCTGCCGGTACTCCA  43699       CA  AAGAG  G
                                TGAGTAGC  CC    AT CCA
                                ||||||||  ||    || |||
                                ACTCGTCG  GG    TG GGT
                                     AC  CCA__  A
GAM1781  FLJ32332 5'  TGAGTGGCCACCAAGCCTTCCA 43700      A       AGATG
                                TGAGT GCCACCAAG    CCA
                                ||||| |||||||||    |||
                                ACTCA CGGTGGTTC    GGT
                                   C       GGAA_
GAM1781  GDAP2    3'  GCAGGCAACTCAAGAGATGC   43701     _ C  _
                                GTAG C AC CAAGAGATGC
                                |||| | || ||||||||||
                                CGTC G TG GTTCTCTACG
                                  C T  A
GAM1781  KIAA0125 3'  TGAGCAGCCACCAGGAGCC   43702          A A  T
                                TGAGTAGCCACCA G GA GCC
                                |||||||||||| | || |||
                                ACTCGTCGGTGGT C CT CGG
                                          _ _  _
GAM1781  KIAA0354 3'  CAGTCCATGGGAGATGCCA   43703    _  CCAA
                                TAG CCA   GAGATGCCA
                                ||| |||   |||||||||
                                GTC GGT   CTCTACGGT
                                  A  ACC_
GAM1781  KIAA1323 3'  TGAGTGTGCTAAGATGCC    43704     A_  CACCAA
                                TGAGT  GC     GAGATGCC
                                |||||  ||     ||||||||
                                ACTCA  CG     TTCTACGG
                                   CA  A_____
GAM1781  KIAA1582 5'  TGAGTAGCTGCACAACCCCA  43705       __  CAAGA  G
                                TGAGTAGC  CAC    GAT CCA
                                ||||||||  |||    ||| |||
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                                ACTCATCG  GTG    TTG GGT
                                    AC  _____  G
GAM1781  KIAA1668  3'  TGAGTAGCCATCAGGCC    43706        CCA  AGAT
                                TGAGTAGCCA  AG   GCC
                                ||||||||||  ||   |||
                                ACTCATCGGT  TC   CGG
                                    AG_  ____
GAM1781  MGC32043  3'  GTGGCTCAAATCAAGAGATG  43707   A  _  C__
                                GT GC CA  CAAGAGATG
                                || || ||  |||||||||
                                CA CG GT  GTTCTCTAC
                                 C  A  TTA
GAM1781  PRO0456   3'  TGAGCAGCTACTGTGTGCCA  43708       C  CAAGAGA
                                TGAGTAGC AC     TGCCA
                                |||||||| ||     |||||
                                ACTCGTCG TG     ACGGT
                                    A  ACAC___
GAM1781  PRO0902   3'  TGAGTAGCTTTTAGAATATG  43709       CACCA   _
                                TGAGTAGC    AGAG ATG
                                ||||||||    |||| |||
                                ACTCATCG    TCTT TAC
                                    AAAA_   A
GAM1781  SEMA4G    5'  TGAGTAGCCACAAGGCC    43710         C   AGAT
                                TGAGTAGCCAC AAG   GCC
                                |||||||||| |||   |||
                                ACTCATCGGTG TTC   CGG
                                      _  ____
GAM1781  STAF65(gamma) 3'  TGAGTAACCACAGTGATG   43711          CA  A
                                TGAGTAGCCAC  AG GATG
                                ||||||||||  || ||||
                                ACTCATTGGTG  TC CTAC
                                      __  A
GAM1781  STX4A     3'  TGAGCAGCTGCCAACCCC    43712       CA   AGAG  G
                                TGAGTAGC  CCA   AT CC
                                ||||||||  |||   || ||
                                ACTCGTCG  GGT   TG GG
                                    AC  ____  G
GAM1781  LOC112817 5'  AGCAGCTAGAGAGATGCCA   43713      CACCA
                                AGTAGC    AGAGATGCCA
                                ||||||    ||||||||||
                                TCGTCG    TCTCTACGGT
                                   ATC__
GAM1781  LOC115219 3'  TGAGTAATTGTTTTTAAATGCC 43714       CCACCAAG
           A                    TGAGTAG      AGATGCCA
                                |||||||      ||||||||
                                ACTCATT      TTTACGGT
                                    AACAAAAA
GAM1781  LOC132880 3'  GAGTCCAGTTAAGAGATG    43715     AG   CC_
                                GAGT  CCA   AAGAGATG
                                ||||  |||   ||||||||
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                                CTCA  GGT   TTCTCTAC
                                  __  CAA
GAM1781  LOC144231 5'  TGGTACACAAGAGATGCC    43716    A   GC   C
                                TG GTA  CAC AAGAGATGCC
                                || |||  ||| ||||||||||
                                AC CAT  GTG TTCTCTACGG
                                 _  __  _
GAM1781  LOC144373 3'  TGGGCAGGACGGAGATGCCA  43680    A    CC  CAA
                                TG GTAG  AC   GAGATGCCA
                                || ||||  ||   |||||||||
                                AC CGTC  TG   CTCTACGGT
                                 C   C_  C__
GAM1781  LOC148697 5'  AGTAACTGCTGGGAGATGCCA  43717       CACCAA
                                AGTAGC     GAGATGCCA
                                ||||||     |||||||||
                                TCATTG     CTCTACGGT
                                    ACGACC
GAM1781  LOC148894 3'  TGAGTAGCAGCAGATG      43718        CACCA  _
                                TGAGTAGC    AG AGATG
                                ||||||||    || |||||
                                ACTCATCG    TC TCTAC
                                     _____  G
GAM1781  LOC149840 3'  TGGGTGGCCACCAACACTGC   43719    A  A      GAGA
                                TG GT GCCACCAA   TGC
                                || || ||||||||   |||
                                AC CA CGGTGGTT   ACG
                                 C  C       GTG_
GAM1781  LOC151610 3'  TGGCTAGCCACCAGGATG    43720    AG       A A
                                TG  TAGCCACCA G GATG
                                ||  |||||||||| | ||||
                                AC  ATCGGTGGT C CTAC
                                 CG       _ _
GAM1781  LOC158427 3'  TGGGCAGCCACCATGGCAGTGC 43721    A        AG__  A
                                TG GTAGCCACCA   AG TGC
                                || ||||||||||   || |||
                                AC CGTCGGTGGT   TC ACG
                                 C         ACCG  _
GAM1781  LOC167040 5'  TGCGTAGCCACTGACCC     43722    A      CAAGA   G
                                TG GTAGCCAC    GAT CC
                                || ||||||||    ||| ||
                                AC CATCGGTG    CTG GG
                                 G       A____  _
GAM1781  LOC203769 5'  TGAGCAGCCGTCACTGCC    43723        AC  AGAGA
                                TGAGTAGCC  CA    TGCC
                                |||||||||  ||    ||||
                                ACTCGTCGG  GT    ACGG
                                     CA  G____
GAM1781  LOC256306 3'  TGAGTAGCCATGTAACCCC    43724         CCAAGA   G
                                TGAGTAGCCA     GAT CC
                                ||||||||||     ||| ||
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                                ACTCATCGGT     TTG GG
                                     ACA___   G
GAM1781 LOC64102 5' TGAGTCGGCTAACAGATGCCA 43725      A_ CACC G
                                TGAGT GC   AA AGATGCCA
                                ||||| ||   || ||||||||
                                ACTCA CG   TT TCTACGGT
                                   GC A___ G
GAM1782 ASB3     3' TAATGTACTGGTGATGAAGC  43728          TACA
                                TAATGTACTGGTG   AAGT
                                ||||||||||||   ||||
                                ATTACATGACCAC   TTCG
                                       TAC_
GAM1782 C1orf1   3' TAATGTGTGTAAAGTGCT    43729      ACTG   CA
                                TAATGT   GTGTA  AAGTGCT
                                ||||||   |||||  |||||||
                                ATTACA   CACAT  TTCACGA
                                   _____   __
GAM1782 CYBB     3' TAATGTTTGTAAAAGTGC    43730      ACTGG   C
                                TAATGT    TGTA AAAGTGC
                                ||||||    |||| |||||||
                                ATTACA    ACAT TTTCACG
                                   A_____   _
GAM1782 ASPN     3' AATGTGCTTGATAACAAAGTG  43731      A _   T
                                AATGT CT GGTG ACAAAGTG
                                ||||| || |||| ||||||||
                                TTACA GA CTAT TGTTTCAC
                                   C A   _
GAM1782 C22orf20 3' ATGTATTAGAGTTAAGTGCT  43732      C  T  ACA
                                ATGTA TGG GT   AAGTGCT
                                ||||| ||| ||   |||||||
                                TACAT ATC CA   TTCACGA
                                   A  T  A__
GAM1782 FLJ11193 3' TAATGTCTGGTACATGTAAGTG 43733      A      CA_
                                TAATGT CTGGTGTA   AAGTG
                                |||||| ||||||||   |||||
                                ATTACA GACCATGT   TTCAC
                                   _      ACA
GAM1782 FLJ32430 3' ATGTACTGGTGCTAGTG     43734          ACAA
                                ATGTACTGGTGT   AGTG
                                ||||||||||||   ||||
                                TACATGACCACG   TCAC
                                      A___
GAM1782 HIC      3' TAATATATTTGGAGCAAAGTGC 43735      C_  TGTA
             T                   TAATGTA  TGG   CAAAGTGCT
                                 |||||||  |||   |||||||||
                                 ATTATAT  ACC   GTTTCACGA
                                    AA   TC__
GAM1783 CBFA2T1  5' TGACAGGAGCACATGTGGCCTT 43738        AAGCTAC
                                TGACAGGAG     GGCCTT
                                |||||||||     ||||||
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                                ACTGTCCTC      CCGGAA
                                     GTGTACA
GAM1783 KHK     3' TGAGAGGAGAAGCTGGCTCT  43739    C       AC  _
                                TGA AGGAGAAGCT  GGC CT
                                ||| ||||||||||  ||| ||
                                ACT TCCTCTTCGA  CCG GA
                                  C         __  A
GAM1783 KHK     3' TGAGAGGAGAAGCTGGCTCT  43739    C       AC  _
                                TGA AGGAGAAGCT  GGC CT
                                ||| ||||||||||  ||| ||
                                ACT TCCTCTTCGA  CCG GA
                                  C         __  A
GAM1783 MYBL2   3' TGACGGAGCTCCCTGTGGCCTT 43740     A   AAG  AC__
                                TGAC GGAG   CT   GGCCTT
                                |||| ||||   ||   ||||||
                                ACTG CCTC   GG   CCGGAA
                                  _   GA_  GACA
GAM1783 NDUFA6  3' TGACAGGAAGAGCTGGC    43741       GA   AC
                                TGACAGGA  AGCT  GGC
                                ||||||||  ||||  |||
                                ACTGTCCT  TCGA  CCG
                                     TC   __
GAM1783 PPP1R3D  3' TGACAGGAGGCGCAGCTTA   43742        AA  TA   C
                                TGACAGGAG  GC  CGGC TTA
                                |||||||||  ||  |||| |||
                                ACTGTCCTC  CG  GTCG AAT
                                     __  C_   _
GAM1783 REQ     3' AGGAGAGAAACAGCCTTA    43743      A CT
                                AGGAGA G  ACGGCCTTA
                                ||||||  |  |||||||||
                                TCCTCT C  TGTCGGAAT
                                   _ TT
GAM1783 SCD     3' GGAGAGGCCCTGGCCTTAA   43744      A   AC
                                GGAGA GCT  GGCCTTAA
                                |||||  |||  ||||||||
                                CCTCT CGG  CCGGAATT
                                   C   GA
GAM1783 EDG2    5' TGCTAGGAGAAGCTGTGTACCT 43745    AC        ACG_
                                TG  AGGAGAAGCT    GCCT
                                ||  ||||||||||    ||||
                                AC  TCCTCTTCGA    TGGA
                                  GA         CACA
GAM1783 EDG2    5' TGCTAGGAGAAGCTGTGTACCT 43745    AC        ACG_
                                TG  AGGAGAAGCT    GCCT
                                ||  ||||||||||    ||||
                                AC  TCCTCTTCGA    TGGA
                                  GA         CACA
GAM1783 FLJ10357 3' TGAGAGGAGAAGCTGCACGC  43746     C        A  _
                                TGA AGGAGAAGCT CG GC
                                ||| |||||||||| || ||
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                                ACT TCCTCTTCGA GT CG
                                  C         C  G
GAM1783  FLJ10922  3'  CAGGGCCAACGGCCTT      43747      AGAA   _
                                CAGG    GCTA CGGCCTT
                                ||||    |||| |||||||
                                GTCC    CGGT GCCGGAA
                                  _____    T
GAM1783  FLJ23360  3'  TGACAGGAAAGGCTGTCAG    43748          A   A_
                                TGACAGGAGA GCT  CGG
                                |||||||||| |||  |||
                                ACTGTCCTTT CGA  GTC
                                      C   CA
GAM1783  KIAA0494  3'  GGAGCCAGCTACGGCTTTAA   43749      A_       C
                                GGAG  AGCTACGGC TTAA
                                ||||  |||||||||| ||||
                                CCTC  TCGATGCCG AATT
                                  GG        A
GAM1783  KIAA0515  5'  TGACTGGAGAAGCTCCTC     43750      A        ACGG
                                TGAC GGAGAAGCT    CCTT
                                |||| |||||||||    ||||
                                ACTG CCTCTTCGA    GGAG
                                  A        _____
GAM1783  KIAA1535  3'  TGATGGGACAAGCTACAG     43751      CA   G
                                TGA  GGA AAGCTACGG
                                |||  ||| |||||||||
                                ACT  CCT TTCGATGTC
                                  AC   G
GAM1783  KIAA1726  3'  TGGCAAGAGTCTGGCCTTA    43752    A     AAG  AC
                                TG CAGGAG   CT  GGCCTTA
                                || ||||||   ||  |||||||
                                AC GTTCTC   GA  CCGGAAT
                                 C     A__  __
GAM1783  MRPL48    5'  TGACGGAACGGCCTT       43753      A   GAAGCT
                                TGAC GGA     ACGGCCTT
                                |||| |||     ||||||||
                                ACTG CCT     TGCCGGAA
                                  _  _______
GAM1783  PCQAP     3'  TGACAGGAGGCGTGTGTCCTT  43754          AA  TACGG_
                                TGACAGGAG  GC     CCTT
                                |||||||||  ||     ||||
                                ACTGTCCTC  CG     GGAA
                                     __  CACACA
GAM1783  SAMHD1    3'  TGAAGGAGAAAGGCTTTA    43755     C       CTAC   C
                                TGA AGGAGAAG    GGC TTA
                                ||| ||||||||    ||| |||
                                ACT TCCTCTTT    CCG AAT
                                  _       ____  A
GAM1783  TRAF3     3'  CAGGAGAAGCTGCCT       43756           ACG
                                CAGGAGAAGCT   GCCT
                                ||||||||||   ||||
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                                GTCCTCTTCGA   CGGA
                                      ___
GAM1783  TSARG1    3'  TGACAAGAGAGGTCCCT     43757          AGCTAC  _
                                TGACAGGAGA     GG CCTT
                                ||||||||||     || ||||
                                ACTGTTCTCT     CC GGGA
                                      _______  A
GAM1783  LOC132321 5'  ACAGGAGAGGGCTCGGCTTTA  43758        A_  A   C
                                ACAGGAGA  GCT CGGC TTA
                                ||||||||  ||| |||| |||
                                TGTCCTCT  CGA GCCG AAT
                                     CC   _   A
GAM1783  LOC220538 3'  TGACAGGAGACAGCTGCACGA  43759          _   __
                                TGACAGGAGA AGCT  ACGG
                                |||||||||| ||||  ||||
                                ACTGTCCTCT TCGA  TGCT
                                      G   CG
GAM1784  CACNA2D2  3'  TCGGAGGTGAGATGTGATTTG  43762        A   A  __
                                TTGGAGGT AGAT TG  TTG
                                |||||||| |||| ||  |||
                                AGCCTCCA TCTA AC  AAC
                                     C   C  TA
GAM1784  CRABP2    3'  TTGGGGCTAGGACTGCTGACTT 43763      A  A  ATA
                                TTGG GGT AG   TGTTGACTT
                                |||| ||| ||   |||||||||
                                AACC CCG TC   ACGACTGAA
                                  _  A  CTG
GAM1784  ISGF3G    3'  TTGGTGGTAAGATGCCTCTT   43764      A      TA   GA
                                TTGG GGTAAGA  TGTT  CTT
                                |||| |||||||  ||||  |||
                                AACC CCATTCT  ACGG  GAA
                                  A      __   A_
GAM1784  MTCP1     5'  GGAGGTAAGAAGGTGACTT    43765          TAT  T
                                GGAGGTAAGA   GT GACTT
                                ||||||||||   || |||||
                                CCTCCATTCT   CA CTGAA
                                      TC_  _
GAM1784  NCOA4     3'  TTGGAGGTACAGGTATGCTGTG 43766          _ A      A_
           CTT                    TTGGAGGTA AG TATGTTG  CTT
                                ||||||||| || |||||||  |||
                                AACCTCCAT TC ATACGAC  GAA
                                     G  C      AC
GAM1784  PSMB9     3'  GGAGGTAAGGTCAGGTGGCTTA 43767         ATATGT  A
                                GGAGGTAAG     TG CTTA
                                |||||||||     || ||||
                                CCTCCATTC     AC GAAT
                                      CAGTCC  C
GAM1784  IRO039700 5'  TTGGAGGTGATGGTGAGCTT   43768         AAGAT   T  _
                                TTGGAGGT    ATG TGA CTT
                                ||||||||    ||| ||| |||
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                                AACCTCCA     TAC ACT GAA
                                     C____   C   C
GAM1784  KIAA0293  3'  TTGGAGGCTGGGATATGGTG   43769        AA_     T
                                TTGGAGGT   GATATG TG
                                ||||||||   |||||| ||
                                AACCTCCG   CTATAC AC
                                     ACC     C
GAM1784  LOC169943 5'  TTGAAGGTAAGATATGTCA    43770
                                TTGGAGGTAAGATATGTTG
                                ||||||||||||||||||
                                AACTTCCATTCTATACAGT

GAM1784  LOC221399 5'  TGGAGGTAAGATGTGAATTG   43771          AT__
                                TGGAGGTAAGAT    GTTG
                                ||||||||||||    ||||
                                ACCTCCATTCTA    TAAC
                                       CACT
GAM1784  LOC253776 3'  TTGGAGGTAGGGCATGGTG    43772        AGA    T
                                TTGGAGGTA   TATG TG
                                |||||||||   |||| ||
                                AACCTCCAT   GTAC AC
                                     CCC    C
GAM1785  ARF1      3'  CACATGGCTATGGAAT      43775          GAACC
                                TACATGGCTAT    GGAAT
                                ||||||||||     |||||
                                GTGTACCGATA    CCTTA
                                       _____
GAM1785  HTR4      3'  ACATGGCTGTGACGGA      43776        A   AC
                                ACATGGCT TGA  CGGA
                                |||||||| |||  ||||
                                TGTACCGA ACT  GCCT
                                     C   __
GAM1785  IL15      5'  CACATGGCCATATATTGGAATG 43777          AACC
                                TACATGGCTATG    GGAATG
                                ||||||||||||    ||||||
                                GTGTACCGGTAT    CCTTAC
                                       ATAA
GAM1785  MBL2      3'  TACATGGCAATGAAAAGGA    43778        T    CC
                                TACATGGC ATGAA  GGA
                                |||||||| |||||  |||
                                ATGTACCG TACTT  CCT
                                     T    TT
GAM1785  PIG8      3'  TAATGGCTATAAAGGGA     43779   C        CC
                                A ATGGCTATGAA  GGA
                                | ||||||||||  |||
                                A TACCGATATTT  CCT
                                 T         C_
GAM1785  TAGLN2    3'  TGATGGCTATGGGGAAGGGAAT 43780   C       AACC__
              G                  A ATGGCTATG     GGAATG
                                | |||||||||     ||||||
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                                A TACCGATAC     CCTTAC
                                 C        CCCTTC
GAM1785 ABLIM    3' TGTGCTGTGACCAGGATG    43781    _  A  A   A
                                TG GCT TGA CCGG ATG
                                || ||| ||| |||| |||
                                AC CGA ACT GGTC TAC
                                 A  C  _   C
GAM1785 ABLIM    3' TGTGCTGTGACCAGGATG    43781    _  A  A   A
                                TG GCT TGA CCGG ATG
                                || ||| ||| |||| |||
                                AC CGA ACT GGTC TAC
                                 A  C  _   C
GAM1785 BTN2A1   3' TACATGGCTGTGAGACCAA   43782        A  _
                                TACATGGCT TGA ACCGG
                                ||||||||| ||| |||||
                                ATGTACCGA ACT TGGTT
                                      C  C
GAM1785 FLJ12586 3' TACATGGCTGGAATA      43783        ATGAACC
                                TACATGGCT     GGAATG
                                |||||||||     ||||||
                                ATGTACCGA     CCTTAT
                                          _______
GAM1785 FLJ20950 3' TACATGGCCTGGGAAT     43784        A  AACC
                                TACATGGCT TG   GGAAT
                                ||||||||| ||   |||||
                                ATGTACCGG AC   CCTTA
                                          _ ____
GAM1785 KIAA0907 3' TAATGGCTATGAGACCAA   43785   C       _
                                A ATGGCTATGA ACCGG
                                | |||||||||| |||||
                                A TACCGATACT TGGTT
                                 T        C
GAM1785 MRPL48   3' TACTGGCTATGGGAAT     43786    A      AACC
                                TAC TGGCTATG   GGAAT
                                ||| ||||||||   |||||
                                ATG ACCGATAC   CCTTA
                                  _     ____
GAM1785 PME-1    3' CACATGGCTGGGCGGGATG   43787        ATGAAC  A
                                TACATGGCT     CGG ATG
                                |||||||||     ||| |||
                                GTGTACCGA     GCC TAC
                                      CCC___   C
GAM1785 STRAIT11499 5' TGGGATGACCGGAATG     43788    CT   A
                                TGG  ATGA CCGGAATG
                                |||  |||| ||||||||
                                ACC  TACT GGCCTTAC
                                  C_   _
GAM1786 ANPEP    3' TGTCCATCGAGAGCTTCTGCTC 43791          CCACCCC
                                TGTCTATCGGG     CTGCTC
                                ||||||||||      ||||||
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                                ACAGGTAGCTC      GACGAG
                                      TCGAA__
GAM1786 BCKDHA   3' TGTGCTGTCAGGTCCCCCTGCT 43792     _ A    CCA
             C                   TGT CT TCGGG   CCCCCTGCTC
                                ||| || |||||   ||||||||||
                                ACA GA AGTCC   GGGGGACGAG
                                  C  C    A__
GAM1786 CHD3    5' TCTATTCCCATCTCCCTGCTC  43793      CGGG   CC_
                                TCTAT    CCA   CCCTGCTC
                                |||||    |||   ||||||||
                                AGATA    GGT   GGGACGAG
                                   AG__   AGA
GAM1786 NUMB    3' GACCGCTACCCCCTGCTC    43794      ___
                                GGCC   ACCCCCTGCTC
                                ||||   ||||||||||
                                CTGG   TGGGGGACGAG
                                   CGA
GAM1786 RARG    3' TGTCCCTTTCACCCTCTGTTC  43795      ATCGGGC    C   C
                                TGTCT      CACCC CTG TC
                                |||||      ||||| ||| ||
                                ACAGG      GTGGG GAC AG
                                   GAAA___    A  A
GAM1786 RUNX3   3' TATCTATCTGGCCCTCCTGTTC 43796        G    ACCC    C
                                TGTCTATC GGCC    CCTG TC
                                |||||||| ||||    |||| ||
                                ATAGATAG CCGG    GGAC AG
                                     A    GA__    A
GAM1786 SOX11   3' TGCCCTCTGCCACCCCCTGCTC 43797      A  GG
                                TGTCT TC  GCCACCCCCTGCTC
                                ||||| ||  ||||||||||||||
                                ACGGG AG  CGGTGGGGGACGAG
                                   _ A_
GAM1786 USP5    3' GTCTATCGCTGCCCCTCTGCTC 43798        G_   A  CC
                                GTCTATCG  GCC CC  CTGCTC
                                ||||||||  ||| ||  ||||||
                                CAGATAGC  CGG GG  GACGAG
                                     GA   _ A_
GAM1786 ZNF256  5' TGCCTCCTCATCCCCTGCT   43799      ATCGGGC  C
                                TGTCT      CA CCCCTGCT
                                |||||      || ||||||||
                                ACGGA      GT GGGGACGA
                                   GGA_____  A
GAM1786 ctm-1   5' TGCCTTTGGCCGCCCCCTGCTC 43800      ATCG    A
                                TGTCT    GGCC CCCCCTGCTC
                                |||||    |||| ||||||||||
                                ACGGA    CCGG GGGGGACGAG
                                   AA__    C
GAM1786 DKFZp761K1824 3' GTCTACCACCTCCTGCT    43801      ATCGG     C
                                GTCT    GCCACC CCTGCT
                                ||||    |||||| ||||||
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                                CAGA    TGGTGG GGACGA
                                  _____     A
GAM1786  SMOC1    3'  TGTCCTGTCCCCTCCCCTGCT  43802      ATCGGG  AC
                                TGTCT     CC  CCCCTGCT
                                |||||     ||  ||||||||
                                ACAGG     GG  GGGGACGA
                                   ACAG__  GA
GAM1786  SYTL2    3'  TGTCTGTCTCCATTCCCTGCTC 43803      A  GGG   CC
                                TGTCT TC   CCA  CCCTGCTC
                                ||||| ||   |||  ||||||||
                                ACAGA AG   GGT  GGGACGAG
                                   C  A__   AA
GAM1786  SYTL2    3'  TGTCTGTCTCCATTCCCTGCTC 43803      A  GGG   CC
                                TGTCT TC   CCA  CCCTGCTC
                                ||||| ||   |||  ||||||||
                                ACAGA AG   GGT  GGGACGAG
                                   C  A__   AA
GAM1786  LOC145719 5'  GCCCAGGGCCACCTCTTGCT   43804      TC      CCC
                                GTCTA  GGGCCACC   TGCT
                                |||||  ||||||||   ||||
                                CGGGT  CCCGGTGG   ACGA
                                   __       AGA
GAM1786  LOC145720 5'  GCCCAGGGCCACCTCTTGCT   43804      TC      CCC
                                GTCTA  GGGCCACC   TGCT
                                |||||  ||||||||   ||||
                                CGGGT  CCCGGTGG   ACGA
                                   __       AGA
GAM1786  LOC197114 5'  GCCCAGGGCCACCTCTTGCT   43804      TC      CCC
                                GTCTA  GGGCCACC   TGCT
                                |||||  ||||||||   ||||
                                CGGGT  CCCGGTGG   ACGA
                                   __       AGA
GAM1786  LOC253039 3'  TCAAACCATCCCTTGCTC    43805        C   C
                                TCGGGCCA CCC TGCTC
                                |||||||| ||| |||||
                                AGTTTGGT GGG ACGAG
                                     A   A
GAM1787  LPHH1    3'  CCACAGGATTTTAAAGCCTACG 43808          C   CAG_
                                CTACAGGATTT AAA    GCG
                                |||||||||||| |||    |||
                                GGTGTCCTAAA TTT    TGC
                                       A   CGGA
GAM1787  C20orf121 3'  CACTGGCCAAACAGGTGGT    43809     A  ATT       C
                                TAC GG   TCAAACAGG GGT
                                ||| ||   ||||||||| |||
                                GTG CC   GGTTTGTCC CCA
                                  A ___        A
GAM1787  DKFZP586B2420 3'  CAGGACTCACAGGTGGT     43810         CAA     C
                                CAGGATTT   ACAGG GGT
                                ||||||||   ||||| |||
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                                GTCCTGAG   TGTCC CCA
                                   ___     A
GAM1787  FLJ10871  3'  CTGCAGGATTTCAGGGAAGT   43811    A        AACA  C
                                CT CAGGATTTCA    GG GGT
                                || ||||||||||    || |||
                                GA GTCCTAAAGT    CC TCA
                                 C         C___  T
GAM1787  FLJ14564  3'  TGACAGGATTTTAAGCA     43812    T       CAAAC
                                C ACAGGATTT     AGGCG
                                | |||||||||     |||||
                                A TGTCCTAAA     TTCGT
                                 C        A____
GAM1787  FLJ20086  3'  CTACAGGAGTTTCAACAATGGG 43813         _     A   GC
              T                  CTACAGGA TTTCAA CAG  GGT
                                 |||||||| |||||| |||  |||
                                 GATGTCCT AAAGTT GTT  CCA
                                      C      _   AC
GAM1787  JAM1     3'  GGAGGCCAAGGCAGGCGGT   43814     TT    A_
                                 GGA  TCAA  CAGGCGGT
                                 |||  ||||  ||||||||
                                 CCT  GGTT  GTCCGCCA
                                   CC    CC
GAM1787  KIAA0594  3'  CAGCATTTCAAAGCAGT     43815     G      ACA
                                 CAG ATTTCAA   GGCGGT
                                 ||| |||||||   ||||||
                                 GTC TAAAGTT   TCGTCA
                                   G      ___
GAM1787  KIAA0618  3'  CTACAGGATTGCAGGCA     43816          TCAAA
                                 CTACAGGATT    CAGGCG
                                 ||||||||||    ||||||
                                 GATGTCCTAA    GTCCGT
                                       C____
GAM1787  MGC2865   3'  TACAGGATTTGAGCCAAT    43817          CAAAC  G
                                 TACAGGATTT    AG CGGT
                                 ||||||||||    || ||||
                                 ATGTCCTAAA    TC GTTA
                                       C____  G
GAM1787  mPA-PLA1  3'  CTATGGGATTTCAAAAAAC   43818     CA        C
                                 CTA  GGATTTCAAA AGGC
                                 |||  |||||||||| ||||
                                 GAT  CCTAAAGTTT TTTG
                                   AC        _
GAM1787  MRPL33    3'  CTACAGGATTTCTGAATCAGT  43819           AAACAGG
                                 CTACAGGATTTC      CGGT
                                 ||||||||||||      ||||
                                 GATGTCCTAAAG      GTCA
                                        ACTTA__
GAM1787  LOC145719 3'  TACAGGATTTAAAAAAAG    43820          C   C
                                 TACAGGATTT AAA AGG
                                 |||||||||| ||| |||
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                                ATGTCCTAAA TTT TTC
                                     T   T
GAM1787  LOC145720 3'  TACAGGATTTAAAAAAAG    43820          C   C
                                TACAGGATTT AAA AGG
                                |||||||||| ||| |||
                                ATGTCCTAAA TTT TTC
                                     T   T
GAM1787  LOC146268 3'  CTACAGGGGTTCAAACAGAC   43821         AT
                                CTACAGG  TTCAAACAGGC
                                |||||||  ||||||||||
                                GATGTCC  AAGTTTGTCTG
                                   CC
GAM1787  LOC151475 3'  TACAGGATGTCAGGGAGT    43822         TTCAAA    C
                                TACAGGAT     CAGG GGT
                                ||||||||     |||| |||
                                ATGTCCTA     GTCC TCA
                                     CA_____   C
GAM1787  LOC197117 3'  TACAGGATTTAAAAAAAG    43820          C   C
                                TACAGGATTT AAA AGG
                                |||||||||| ||| |||
                                ATGTCCTAAA TTT TTC
                                     T   T
GAM1787  LOC221087 3'  CAGGAGCCTACAGGCGGTC    43823       TTTCAA
                                CAGGA     ACAGGCGGTC
                                |||||     ||||||||||
                                GTCCT     TGTCCGCCAG
                                   CGGA__
GAM1788  F-LAN-1   3'  TACACCATGGCCTCATCTA    43826         C  G__
                                TACGCCAT GG   TATCTA
                                |||||||| ||   ||||||
                                ATGTGGTA CC   GTAGAT
                                     _  GGA
GAM1788  TSPAN-3   3'  TACGCCATATGATCCTA     43827         CG   A
                                TACGCCAT  GGT TCTA
                                |||||||  ||| ||||
                                ATGCGGTA  CTA GGAT
                                     TA  _
GAM1788  LOC150935 5'  TACGCCATTGTTTTCCGGGTAT 43828         ________
                                TACGCCAT      CGGGTAT
                                |||||||      |||||||
                                ATGCGGTA      GCCCATA
                                     ACAAAAG
GAM1788  LOC254198 5'  CGCCATCATAAAGATCTA     43829         ___  T
                                CGCCATCG   GG ATCTA
                                ||||||||   || |||||
                                GCGGTAGT   TC TAGAT
                                     ATT  _
GAM1789  ADH4      3'  CCTGATGCTCTCTCTCTGC    43832          G  A   T
                                CCTGATGCTCTC TC TCT GC
                                |||||||||||| || ||| ||
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                                GGACTACGAGAG AG AGA CG
                                          _ _  _
GAM1789  EDN3     3'  TCTCTGATACCATCTT     43833    C      TCTCGT
                                TC CTGATGC     CATCTT
                                || |||||||     ||||||
                                AG GACTATG     GTAGAA
                                 A     _______
GAM1789  ITGB3    3'  CCTATGCTCTCCTTCTTTGC  43834     A      G_  ATC
                                CCTG TGCTCTC  TC   TTGC
                                |||| |||||||  ||   ||||
                                GGAT ACGAGAG  AG   AACG
                                  _      GA  A__
GAM1789  KNSL1    5'  TCCCTGGTACTCTCGGGCGCTG 43835       A       TCATC
              C                  TCCCTG TGCTCTCG     TTGC
                                ||||||| ||||||||     ||||
                                AGGGAC ATGAGAGC     GACG
                                   C       CCGC_
GAM1789  DEPP     3'  TCCCTGATGCCTCACCTTCTTG 43836         T   GT A
              C                  TCCCTGATGC CTC  C TCTTGC
                                |||||||||| |||  | ||||||
                                AGGGACTACG GAG  G AGAACG
                                      _   TG A
GAM1789  DKFZP566G1424 3'  TCTCTGATGCTACCCTTCTTG  43837    C       _   GTCA
                                TC CTGATGCT CTC    TCTTG
                                || |||||||| |||    |||||
                                AG GACTACGA GGG    AGAAC
                                 A       T   A___
GAM1789  DKFZp761A132 3'  CCCGGTGGGGTCATCTTG    43838      A  CTCTC
                                CCTG TG     GTCATCTTG
                                |||| ||     |||||||||
                                GGGC AC     CAGTAGAAC
                                  C  CC___
GAM1789  FLJ21736  3'  CCCTGATGGATTCTGTTGTCTT 43839         C__   C  CA
              G                  CCCTGATG   TCT GT  TCTTG
                                ||||||||   ||| ||  |||||
                                GGGACTAC   AGA CA  AGAAC
                                     CTA   _  AC
GAM1789  KIAA0352  3'  TCCCTGATGTCTTGTCCCTGC  43840         C   C   AT
                                TCCCTGATG TCT GTC  CTTGC
                                ||||||||| ||| |||  |||||
                                AGGGACTAC AGA CAG  GGACG
                                      _   A   __
GAM1789  KIAA0534  3'  TCATTGATGCTCTTGTCTC    43841    CC       C   A
                                TC  TGATGCTCT GTC TC
                                ||  ||||||||| ||| ||
                                AG  ACTACGAGA CAG AG
                                 TA        A   _
GAM1789  KIAA0795  5'  TCTTTGATGCTCTGCAGCTGC  43842    CC       C T  T  T
                                TC  TGATGCTCT G CA CT GC
                                ||  ||||||||| | || || ||
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                                AG  ACTACGAGA C GT GA CG
                                 AA        _ _  C  _
GAM1789  KIAA0964  3'  CCCTTGGACTGTCGTCATCTTG 43843     GAT   C
                                CCCT   GCT TCGTCATCTTG
                                ||||   ||| ||||||||||
                                GGGA   TGA AGCAGTAGAAC
                                  ACC   C
GAM1789  KIAA1775  3'  CCCTGATGCTCTTCTAGTTGC  43844          CG  ATC
                                CCCTGATGCTCT  TC   TTGC
                                ||||||||||||  ||   ||||
                                GGGACTACGAGA  AG   AACG
                                       __  ATC
GAM1789  KIAA1872  3'  CCCAGCCACTTTTGTCATCTTG 43845     TGA    CTC
                                CCC   TGCT   GTCATCTTG
                                |||   ||||   |||||||||
                                GGG   GTGA   CAGTAGAAC
                                  TCG    AAA
GAM1789  MGC27382  3'  TCCTTGATACTCTTTTTTTTTG 43846     C        CGTCATC
            C                    TCC TGATGCTCT       TTGC
                                ||| |||||||||       ||||
                                AGG ACTATGAGA       AACG
                                  A        AAAAAA_
GAM1789  ZNF220    3'  TGATTGCAAGTTCATCTTGC   43847      _  TCTCG
                                TGAT GC     TCATCTTGC
                                |||| ||     |||||||||
                                ACTA CG     AGTAGAACG
                                  A  TTCA_
GAM1789  LOC150372 5'  TCCCTGATCCTAGTCTTG    43848         G  CTCGTCA
                                TCCCTGAT CT       TCTTG
                                ||||||||  ||      |||||
                                AGGGACTA GA       AGAAC
                                     G  TC_____
GAM1789  LOC162540 3'  TCTTTGATGCCCTGATTTCTTG 43849    CC        C  CA
                                TC  TGATGCTCT GT  TCTTG
                                ||  |||||||||  ||  |||||
                                AG  ACTACGGGA TA  AGAAC
                                 AA        C  A_
GAM1789  LOC51313  3'  CTGATGCTCTTGCAGGCTG   43850          C T  TC
                                CTGATGCTCT G CA  TTG
                                ||||||||||  |  ||  |||
                                GACTACGAGA C GT  GAC
                                      A _  CC
GAM1789  LOC92552  3'  CCCACATCTCTCTCGTCATTTT 43851     TGATG_        C
            G                    CCC      CTCTCGTCAT TTG
                                |||      ||||||||||  |||
                                GGG      GAGAGCAGTA AAC
                                  TGTAGA         A
GAM1790  FLJ20344  3'  GCAGCATTCATAAGGTTTC   43854    C        TTCTCGA
                                GC GCATTCATA       TTTC
                                ||  |||||||||       ||||
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                                CG CGTAAGTAT      AAAG
                                 T        TCC____
GAM1790  LOC144455 3'  GCCGTCTTCATATTCCCTACTT 43855      CA         G
                                GCCG  TTCATATTCTC ATTT
                                |||| |||||||||| ||||
                                CGGC  AAGTATAAGGG TGAA
                                  AG         A
GAM1790  LOC163115 3'  GCTGCATTCATTCATAGGTTTC 43856    C       AT  TCGA_
            T                    GC GCATTCAT  TC     TTTCT
                                || ||||||||  ||     |||||
                                CG CGTAAGTA  AG     AAAGA
                                 A       __  TATCC
GAM1790  LOC92285  5'  ACTGCATTCATAAGGTTTC    43857    C        TTCTCGA
                                GC GCATTCATA      TTTC
                                || |||||||||      ||||
                                TG CGTAAGTAT      AAAG
                                 A        TCC____
GAM1791  KIFAP3    5'  TATCTTGAGAGGCAGGCG    43860        TA    TAT
                                TATCTTGA  AGGC   GCG
                                ||||||||  ||||   |||
                                ATAGAACT  TCCG   CGC
                                     C_    TC_
GAM1791  ZNF267    3'  TATCTTGAGTAAGGGTTGAGCA 43861         _     CTATGC
                                TATCTTGA TAAGG     GAGCA
                                |||||||| |||||     |||||
                                ATAGAACT ATTCC     CTCGT
                                     C     CAA___
GAM1791  ARHGEF9   3'  TATTTTCATAAGGCTTTG    43862     C  G       A
                                TAT TT ATAAGGCT TG
                                ||| || |||||||| ||
                                ATA AA TATTCCGA AC
                                  A  G       A
GAM1791  DKFZP564O0423 3'  TATTCTGAAGACTATGTGAG   43863     CT   TA       C
                                TAT  TGA  AGGCTATG GAG
                                |||  |||  |||||||| |||
                                ATA  ACT  TCTGATAC CTC
                                  AG   __       A
GAM1791  FLJ11753  3'  TATCTTGAAAAGGTTATA    43864         T    C
                                TATCTTGA AAGG TATG
                                |||||||| |||| ||||
                                ATAGAACT TTCC ATAT
                                     T    A
GAM1791  FLJ23311  5'  TCTTGATAGGGCTACTGGGCG  43865         A     ___
                                TCTTGATA GGCTAT   GCG
                                |||||||| ||||||   |||
                                AGAACTAT CCGATG   CGC
                                     C     ACC
GAM1791  HBXIP     3'  TATCTTGATAGCGGTCCATAGA 43866          A_  _    C
            GCA                     TATCTTGATA  GG CTATG GAGCA
                                |||||||||  || ||||| |||||
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                                ATAGAACTAT  CC GGTAT CTCGT
                                     CG  A    _
GAM1791  HUMAGCGB  5'  TATCTTAATGGGGTTGCG    43867        AA  CTA
                                TATCTTGAT  GG   TGCG
                                |||||||||  ||   ||||
                                ATAGAATTA  CC   ACGC
                                     CC  A__
GAM1791  PAFAH2    3'  TCTTGATAGGAGCTCATG    43868        A_   _
                                TCTTGATA  GGCT ATG
                                ||||||||  |||| |||
                                AGAACTAT  TCGA TAC
                                     CC    G
GAM1792  INHBB     5'  CGGGTCACTGCCGCACGGG   43871    A      GATC C
                                TG GTCACTGC    C CACGGG
                                || |||||||||    | ||||||
                                GC CAGTGACG    G GTGCCC
                                 C       _____ C
GAM1792  LIMK1     3'  TAAGTCATGGTCCCACGGG   43872       C  CGATC
                                TGAGTCA TG    CCCACGGG
                                |||||||  ||    ||||||||
                                ATTCAGT AC    GGGTGCCC
                                     _  CA___
GAM1792  LIMK1     3'  TAAGTCATGGTCCCACGGG   43872       C  CGATC
                                TGAGTCA TG    CCCACGGG
                                |||||||  ||    ||||||||
                                ATTCAGT AC    GGGTGCCC
                                     _  CA___
GAM1792  SLC22A1L  5'  TGAGTCACTGGGTCCCAGG   43873        CGA    CAC
                                TGAGTCACTG   TCCC   GGG
                                ||||||||||   ||||   |||
                                ACTCAGTGAC   AGGG   TCC
                                     CC_    ____
GAM1792  SRGAP1    5'  TGAGTCACTGTGTCTGGCGCCC 43874       CGA _________  CACG
              GTG                    GTCACTG   TC      CC    G
                                |||||||   ||      ||   |
                                CAGTGAC   AG      GG    C
                                     AC_  ACCGIIIC  GCAC
GAM1792  TBP       5'  TGGGTCACTGCAAAGATCACTA 43875    A       TCCC   ___
              TGGGC                   TG GTCACTGCGA    CAC   GGGC
                                || ||||||||||    |||   ||||
                                AC CAGTGACGTT    GTG   CCCG
                                 C        TCTA   ATA
GAM1792  C20orf154 3'  TGAGTCACTGTGATTACAG    43876         C   CCCC
                                TGAGTCACTG GAT    ACGG
                                |||||||||| |||    ||||
                                ACTCAGTGAC CTA    TGTC
                                     A   A___
GAM1792  DKFZP434J037 3'  TGAGTCACTGAGGTCCAAGG   43877          CGATCC   C
                                TGAGTCACTG     CCA GG
                                ||||||||||     ||| ||
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                                ACTCAGTGAC     GGT CC
                                     TCCA__   T
GAM1792  FLJ12242  3'  TAAGTCACAGCCCCACGGG   43878        TGCGAT
                                TGAGTCAC     CCCCACGGG
                                ||||||||     |||||||||
                                ATTCAGTG     GGGGTGCCC
                                    TC____
GAM1792  FLJ14816  3'  TGAGTCACTGGGTCCCCGG   43879         CGA    ACG
                                TGAGTCACTG   TCCCC   GG
                                ||||||||||   |||||   ||
                                ACTCAGTGAC   AGGGG   CC
                                     CC_    ___
GAM1792  PPP1R16B  3'  TGCAGTCACTCCCATGGG    43880    _     GCGATC    C
                                TG AGTCACT     CCCA GGG
                                || |||||||     |||| |||
                                AC TCAGTGA     GGGT CCC
                                 G      _______    A
GAM1792  SEC14L2   3'  GCAGCTGCGATCCCTGTGGG   43881    CA        CAC
                                GT  CTGCGATCCC   GGG
                                ||  ||||||||||   |||
                                CG  GACGCTAGGG   CCC
                                 TC         ACA
GAM1792  SPTLC2    3'  TGAGCCACTGCGCCCAGCCATG 43882           A   __   C
           GGC                    TGAGTCACTGCG TCC  CCA GGGC
                                ||||||||||||| |||  ||| ||||
                                ACTCGGTGACGC GGG  GGT CCCG
                                      _  TC   A
GAM1792  TOB2      3'  GCTCCTGGCCCCACGGGC    43883    CA   CGAT
                                GT  CTG    CCCCACGGGC
                                ||  |||    ||||||||||
                                CG  GAC    GGGGTGCCCG
                                 AG   C___
GAM1792  TOB2      3'  GCTCCTGGCCCCACGGGC    43883    CA   CGAT
                                GT  CTG    CCCCACGGGC
                                ||  |||    ||||||||||
                                CG  GAC    GGGGTGCCCG
                                 AG   C___
GAM1792  LOC222662 3'  TGGGTCACTGCAGTTCTGCGCC 43884         A_ ________  CACG
           CGTGGG                  TCACTGCG  TC      CC    GG
                                ||||||||  ||      ||    ||
                                AGTGACGT  AG      GG    CC
                                     CA  ACGIIIC  GCAC
GAM1792  LOC257096 5'  GAGTCACTGTGATTTTTGCCCG 43885         C   C________  CACG
           TG                    AGTCACTG GAT       CC    G
                                ||||||||  |||       ||    |
                                TCAGTGAC CTA       GG    C
                                     A   AAAAIIIC  GCAC
GAM1793  DKFZP586B0923 3'  TACATTACCCAGCATTTTTTC  43888         A   GC
                                TACGTTA CCC  AGCATTTTTTC
                                |||||||  |||  ||||||||||
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                                ATGTAAT GGG  TCGTAAAAAAG
                                      _  __
GAM1793  LOC150940 5'  GTTAGAAGCAGCATTTTTT   43889     ACCC
                                GTTA   GCAGCATTTTTT
                                ||||   ||||||||||||
                                CAAT   CGTCGTAAAAAA
                                  CTT_
GAM1793  LOC152897 3'  TACTTTGCAGACAGCATTTTTT 43890     GTTAACCC
                                TAC      GCAGCATTTTTT
                                |||      ||||||||||||
                                ATG      TGTCGTAAAAAA
                                 AAACGTC_
GAM1793  LOC253296 3'  CAACTGCAGCATTTTTT    43891     CC
                                TAAC  GCAGCATTTTTT
                                ||||  ||||||||||||
                                GTTG  CGTCGTAAAAAA
                                  A_
GAM1793  LOC253298 5'  CAACTGCAGCATTTTTT    43891     CC
                                TAAC  GCAGCATTTTTT
                                ||||  ||||||||||||
                                GTTG  CGTCGTAAAAAA
                                  A_
GAM1793  LOC257570 3'  CAACTGCAGCATTTTTT    43891     CC
                                TAAC  GCAGCATTTTTT
                                ||||  ||||||||||||
                                GTTG  CGTCGTAAAAAA
                                  A_
GAM1793  LOC257571 5'  CAACTGCAGCATTTTTT    43891     CC
                                TAAC  GCAGCATTTTTT
                                ||||  ||||||||||||
                                GTTG  CGTCGTAAAAAA
                                  A_
GAM1794  ADCY6    3'  ACCTTGGTCCCTTCAGCT    43894       ATAAC   CC
                                ACTTTGGT    CCC  CAGCT
                                ||||||||    |||  |||||
                                TGGAACCA    GGG  GTCGA
                                     _____  AA
GAM1794  ADCY6    3'  ACCTTGGTCCCTTCAGCT    43894       ATAAC   CC
                                ACTTTGGT    CCC  CAGCT
                                ||||||||    |||  |||||
                                TGGAACCA    GGG  GTCGA
                                     _____  AA
GAM1794  ASB1     3'  ACTTTAGTATAAGCCTCTCAGC 43895         C  CCC
           T                     ACTTTGGTATAA CC   CAGCT
                                 ||||||||||||  ||   |||||
                                 TGAAATCATATT GG   GTCGA
                                       C  AGA
GAM1794  ATP10C   3'  CTTTGGTATGTGCCATGCAGCT 43896        AAC  CCC
                                 CTTTGGTAT   CC   CAGCT
                                 |||||||||   ||   |||||
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                                GAAACCATA  GG  GTCGA
                                     CAC  TAC
GAM1794 BTG1     5' CTCGGACCTCCCCAGCT    43897     TATA  C
                                TTTGG   ACC CCCCAGCT
                                |||||   ||| ||||||||
                                GAGCC   TGG GGGGTCGA
                                  _____  A
GAM1794 LASS2    3' CTTTGCTCCTCCCCCAGCT   43898     GTATAA _
                                CTTTG    CC CCCCCAGCT
                                |||||    || |||||||||
                                GAAAC    GG GGGGGTCGA
                                  GA____  A
GAM1794 MMP19    5' CTTTAAAATTCCCCCAGCTA  43899     TATAACC
                                CTTTGG     CCCCCAGCTA
                                ||||||     ||||||||||
                                GAAATT     GGGGGTCGAT
                                   TTAA___
GAM1794 MMP19    5' CTTTAAAATTCCCCCAGCTA  43899     TATAACC
                                CTTTGG     CCCCCAGCTA
                                ||||||     ||||||||||
                                GAAATT     GGGGGTCGAT
                                   TTAA___
GAM1794 ADMP     5' CTTTGGCTCCTCCCCAGCT   43900     ATAA  C
                                CTTTGGT   CC CCCCAGCT
                                |||||||   || ||||||||
                                GAAACCG   GG GGGGTCGA
                                    A___  A
GAM1794 GOLGA2LY 3' CTTTGGCACTGCCCCCTGGCT 43901       AAC   CA
                                CTTTGGTAT  CCCCC  GCT
                                |||||||||  |||||  |||
                                GAAACCGTG  GGGGG  CGA
                                     AC_   AC
GAM1794 KIAA1163 3' GGTTTTCAACTTCCCCAGCT  43902    A__   CC
                                GGT  TAAC  CCCCAGCT
                                |||  ||||  ||||||||
                                CCA  GTTG  GGGGTCGA
                                  AAA   AA
GAM1794 KIAA1750 3' CTCAGCTACCTCCCCAGCT   43903   TG  ATA  C
                                TT  GT   ACC CCCCAGCT
                                ||  ||   ||| ||||||||
                                GA  CG   TGG GGGGTCGA
                                 GT  A__  A
GAM1794 KNSL6    3' ACTCTGACCCCCTCCCCAGCT 43904      TATAA  _
                                ACTTTGG    CCC CCCCAGCT
                                |||||||    ||| ||||||||
                                TGAGACT    GGG GGGGTCGA
                                    GG___  A
GAM1794 LANO     3' CTTTGACATAATTCCTCCAG  43905     GT   CC  C
                                CTTTG  ATAA  CC CCAG
                                |||||  ||||  || ||||
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                                GAAAC  TATT  GG GGTC
                                   TG    AA  A
GAM1794  MGC11287  3'  TCTGGGCCTCCCCAGCT     43906      TATAA  C
                                TTTGG     CC CCCCAGCT
                                |||||     || ||||||||
                                AGACC     GG GGGGTCGA
                                   C_____  A
GAM1794  URB       3'  TTTAGCACTAGAGCCCCTCCAG 43907        AAC__   _
                                TTTGGTAT     CCCC CCAG
                                ||||||||     |||| ||||
                                AAATCGTG     GGGG GGTC
                                     ATCTC    A
GAM1794  LOC147040 3'  CCTTGGGCCTTCCCCAGCTA   43908       TATAA  C_
                                CTTTGG     CC  CCCCAGCTA
                                ||||||     ||  |||||||||
                                GGAACC     GG  GGGGTCGAT
                                   C_____  AA
GAM1794  LOC147664 3'  ACCTTGGTAACCTCTGGCT    43909         TA   CCCCCA
                                ACTTTGGTA  ACC      GCT
                                |||||||||  |||     |||
                                TGGAACCAT  TGG      CGA
                                     __   AGAC__
GAM1794  LOC221794 5'  ACTCTACCCTCCCAGC      43910       GGTATA    C
                                ACTTT      ACCC CCCAGC
                                |||||      |||| ||||||
                                TGAGA      TGGG GGGTCG
                                   _______    A
GAM1794  LOC222414 3'  TTTGGTACAAAAACAGCT    43911          CCCCCC
                                TTTGGTATAA     CAGCT
                                ||||||||||     |||||
                                AAACCATGTT     GTCGA
                                     TTT___
GAM1794  LOC253681 3'  CCTTGGGCCTTCCCCAGCTA   43908       TATAA  C_
                                CTTTGG     CC  CCCCAGCTA
                                ||||||     ||  |||||||||
                                GGAACC     GG  GGGGTCGAT
                                   C_____  AA
GAM1794  LOC256158 5'  CTCTGGGCCCTCCCCAGCT    43912       TATAA   _
                                CTTTGG     CCC CCCCAGCT
                                ||||||     ||| ||||||||
                                GAGACC     GGG GGGGTCGA
                                   C_____   A
GAM1794  LOC256273 3'  TCTGGACTCCCCCAGCT      43913      TATA  C
                                TTTGG    AC CCCCCAGCT
                                |||||    || |||||||||
                                AGACC    TG GGGGGTCGA
                                   _____  A
GAM1794  LOC257431 3'  CTTTGGCACTGCCCCCTGGCT  43901          AAC     CA
                                CTTTGGTAT   CCCCC  GCT
                                |||||||||   |||||  |||
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                                GAAACCGTG  GGGGG  CGA
                                     AC_    AC
GAM1795 COL4A4   5' CCGCAAGTTGGAGGCGGGCTGG 43916        TTTACTACA
                                TCGCAAGTT       GGCTGG
                                |||||||||       ||||||
                                GGCGTTCAA       CCGACC
                                     CCTCCGC__
GAM1795 DAAM2    3' TCCAAGTGGCCACCTGCAGGCT 43917    G    TT    A_
           GG                    TC CAAGT  TTACT  CAGGCTGG
                                || |||||  |||||  ||||||||
                                AG GTTCA  GGTGG  GTCCGACC
                                 _    CC    AC
GAM1795 MN1      3' TCCAAAGACTGCAGGCTG    43918    G   TTTTT   A
                                TC CAAG    ACT CAGGCTG
                                || ||||    ||| |||||||
                                AG GTTT    TGA GTCCGAC
                                 _   C____   C
GAM1795 BICD2    3' GTACCTATGCTGCAGGCTGG   43919    T   __  A
                                GT TTTA  CT CAGGCTGG
                                || ||||  || ||||||||
                                CA GGAT  GA GTCCGACC
                                 T   AC  C
GAM1795 CNNM1    3' TCCAAGTTTTCCCTAAGGCTGG 43920    G       TA   C
                                TC CAAGTTTT  CTA AGGCTGG
                                || ||||||||  ||| |||||||
                                AG GTTCAAAA  GAT TCCGACC
                                 _       GG  _
GAM1795 FLJ00001 3' TCCAAGAACCTGCAGGCTG   43921    G   TTTTTA  A
                                TC CAAG     CT CAGGCTG
                                || ||||     || |||||||
                                AG GTTC     GA GTCCGAC
                                 _   TTG___  C
GAM1795 KIAA0152 3' GTTCTGTTGCTGCAGGCTGG   43922      TA__  A
                                GTTTT    CT CAGGCTGG
                                |||||    || ||||||||
                                CAAGA    GA GTCCGACC
                                   CAAC  C
GAM1795 KIAA0648 3' TCCAAGTTTTTGCAGAAGCTGG 43923    G       ACTAC
                                TC CAAGTTTTT     AGGCTGG
                                || |||||||||     |||||||
                                AG GTTCAAAAA     TTCGACC
                                 _       CGTC_
GAM1795 KIAA0830 5' CGCGAGCTCTGCAGGCTG    43924     A     TACTA
                                CGC AGTTTT     CAGGCTG
                                ||| ||||||     |||||||
                                GCG TCGAGA     GTCCGAC
                                  C     C____
GAM1795 LOC132617 3' TCGGTGCTGCTGCAGGCTG   43925     CAA   TTTA  A
                                TCG   GTT    CT CAGGCTG
                                |||   |||    || |||||||
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                                AGC   CGA    GA GTCCGAC
                                  CA_   C___  C
GAM1795  LOC136288 5'  AGTTTTTACACGGCTGG     43926         T  A
                                AGTTTTTAC AC GGCTGG
                                ||||||||| || ||||||
                                TCAAAAATG TG CCGACC
                                        _ _
GAM1796  AF5Q31    3'  TAGCTCACGGAAACCATCTTAT 43929      C   CAT
                                TAGC CAC   GGACCATCTTAT
                                |||| |||   ||||||||||||
                                ATCG GTG   TTTGGTAGAATA
                                  A   CC_
GAM1796  RRM2B     3'  TTAGCCCATCTGCAGCTT     43930        CCA  GAC  T
                                TTAGCCCA   TG   CA CTT
                                ||||||||   ||   || |||
                                AATCGGGT   AC   GT GAA
                                     AG_  ___  C
GAM1796  XK        3'  TCAGTTCACCATGGCTTA     43931      CC       ACCAT
                                TTAG  CACCATGG    CTTA
                                ||||  ||||||||    ||||
                                AGTC  GTGGTACC    GAAT
                                  AA       _____
GAM1796  FLJ10292  3'  TCAGTTTTTAATGGATCATCTT 43932      CCCACC    C
            AT                    TTAG     ATGGA CATCTTAT
                                ||||     ||||| ||||||||
                                AGTC     TACCT GTAGAATA
                                  AAAAAT    A
GAM1796  LOC115207 3'  ACCTATTATTGGACCATTTTAT 43933     CACCA_      C
                                GCC     TGGACCAT TTAT
                                |||     |||||||| ||||
                                TGG     ACCTGGTA AATA
                                  ATAATA       A
GAM1797  CETN1     3'  TCTAAGGTTTCACAAAATG    43936        GTCA   C
                                TCTAAGGTT    GCA GGATG
                                |||||||||    ||| |||||
                                AGATTCCAA    TGT TTTAC
                                     AG__   _
GAM1797  FGF2      5'  CCTGGGGTTCACGGATG      43937     AA   GTCAG
                                TCT  GGTT    CACGGATG
                                |||  ||||    ||||||||
                                GGA  CCAA    GTGCCTAC
                                  CC   _____
GAM1797  HRH2      5'  TCTAAGGTGTTGGGAATGA    43938        T  CAGCAC
                                TCTAAGGT GT     GGATGA
                                |||||||| ||     ||||||
                                AGATTCCA CA     CTTACT
                                     _ ACC___
GAM1797  MN1       3'  TCTGAGGTTGCCAGGACCATGA 43939     A        C  GG
                                TCT AGGTTGTCAG AC  ATGA
                                ||| |||||||||| ||  ||||
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                                AGA TCCAACGGTC TG  TACT
                                  C        C  G_
GAM1797  OCLN     5'  TCCTAGGGGGCAGCACGGATG  43940     A   TT T
                                TCT AGG  G CAGCACGGATG
                                ||| |||  | ||||||||||
                                AGG TCC  C GTCGTGCCTAC
                                  A   CC _
GAM1797  RFC4     5'  TAAGATTGTGATTCTGGATGAA 43941         CAGCAC
                                TAAGGTTGT     GGATGAA
                                |||||||||     |||||||
                                ATTCTAACA     CCTACTT
                                     CTAAGA
GAM1797  CDC42BPB 3'  TCTCGGGTTGTCAGGGGTG   43942     AA        CAC  A
                                TCT  GGTTGTCAG   GG TG
                                |||  |||||||||   || ||
                                AGA  CCAACAGTC   CC AC
                                  GC        ___  C
GAM1797  FLJ20558 3'  TAAAGTTGTCAAGGGGTG    43943           CAC  A
                                TAAGGTTGTCAG   GG TG
                                ||||||||||||   || ||
                                ATTTCAACAGTT   CC AC
                                      C__  C
GAM1797  HML2     5'  TCTGAGGTTGTCACAGCTGAA  43944     A       AGC    A
                                TCT AGGTTGTC   ACGG TGAA
                                ||| ||||||||   |||| ||||
                                AGA TCCAACAG   TGTC ACTT
                                  C        ____    G
GAM1797  KCNE4    3'  TCTAAGGTTGCTGGCTGATG   43945          CA  ACG
                                TCTAAGGTTGT  GC   GATG
                                ||||||||||  ||   ||||
                                AGATTCCAACG  CG   CTAC
                                      AC  A__
GAM1797  KIAA0335 3'  GGTTGTCAGTCACACTGA    43946          _   GA
                                GGTTGTCAG CACG  TGA
                                ||||||||| ||||  |||
                                CCAACAGTC GTGT  ACT
                                     A    G_
GAM1797  MAC30    5'  TAAGGTTGTCATGGTGTGAA   43947          GCAC  A_
                                TAAGGTTGTCA    GG  TGAA
                                ||||||||||    ||  ||||
                                ATTCCAACAGT    CC  ACTT
                                      A___  AC
GAM1797  LOC149837 3'  CTGAGGTTGGGCACCACGGATG 43948    A     T_  G
                                CT AGGTTG  CA CACGGATG
                                || ||||||  || ||||||||
                                GA TCCAAC  GT GTGCCTAC
                                  C     CC  G
GAM1797  LOC157421 5'  TCTAAGGTGTGGAGGGTGA   43949         T  CAGCAC  A
                                TCTAAGGT GT     GG TGA
                                |||||||| ||     || |||
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                                AGATTCCA CA     CC ACT
                                     _ CCT___  C
GAM1797 LOC205398 5' TAAGGCTGTCGGCTCCCTGA  43950         A  ACGGA
                                TAAGGTTGTC GC    TGA
                                |||||||||| ||    |||
                                ATTCCGACAG CG    ACT
                                      C  AGGG_
GAM1798 SCML1    3' CTCAGAATTAAGCAAATTAA  43953     A      AACT
                                CTCA GAATTAAG   TTAA
                                |||| ||||||||   ||||
                                GAGT CTTAATTC   AATT
                                  _      GTTT
GAM1798 ST7      3' TAACTCAGCTTAGAAGAACTTT 43954       AGAATT
             AA                   TAACTCA    AAGAACTTTAA
                                |||||||     ||||||||||||
                                ATTGAGT     TTCTTGAAATT
                                    CGAATC
GAM1798 ACTR1A   3' ACTCAAGAAAGCGAGTTTTAA  43955        TTAA  AC
                                ACTCAAGAA   GA  TTTAA
                                |||||||||   ||  |||||
                                TGAGTTCTT   CT  AAATT
                                     TCG_  CA
GAM1798 ERO1L    3' AACTCAAAAAGAACTTTA    43956        ATTA
                                AACTCAAGA   AGAACTTTA
                                |||||||||   |||||||||
                                TTGAGTTTT   TCTTGAAAT
                                            ____
GAM1798 PMAIP1   3' TAACTCAAAAATGTAACTTTAA 43957          TAAG
                                TAACTCAAGAAT   AACTTTAA
                                ||||||||||||   ||||||||
                                ATTGAGTTTTTA   TTGAAATT
                                       CA__
GAM1798 LOC153606 5' TCAAGAATTACACTTTAA    43958         AGA
                                TCAAGAATTA  ACTTTAA
                                ||||||||||  |||||||
                                AGTTCTTAAT  TGAAATT
                                      G__
GAM1798 LOC157503 3' TAACTGGAGAATTAAGAA    43959      CA
                                TAACT  AGAATTAAGAA
                                |||||  ||||||||||
                                ATTGA  TCTTAATTCTT
                                   CC
GAM1798 LOC220107 3' AAGAACCATGGAACTTTAA   43960       A_
                                AAGAATTA  GAACTTTAA
                                ||||||||  |||||||||
                                TTCTTGGT  CTTGAAATT
                                     AC
GAM1799 CD59     3' ATAAGCAAGTTTCTATTTTCCT 43963       TCC_     C
             AT                   GTGGGTAA   CTATTT CCTAT
                                |||||||    |||||| |||||
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                                TATTCGTT   GATAAA GGATA
                                    CAAA     A
GAM1799  FLJ11413  3'  TGGGTAATCCCAGAAATTCC  43964          TAT__
                                TGGGTAATCCC    TTCC
                                ||||||||||    ||||
                                ACCCATTAGGG    AAGG
                                    TCTTT
GAM1799  GIT2      3'  AGTAGGTGATTTCTTTTCCCTA 43965       A  CC  A
           T                     AGTGGGT AT  CT TTTCCCTAT
                                ||||||| ||  || |||||||||
                                TCATCCA TA  GA AAAGGGATA
                                    C  AA  _
GAM1799  GIT2      3'  AGTAGGTGATTTCTTTTCCCTA 43965       A  CC  A
           T                     AGTGGGT AT  CT TTTCCCTAT
                                ||||||| ||  || |||||||||
                                TCATCCA TA  GA AAAGGGATA
                                    C  AA  _
GAM1799  GIT2      3'  AGTAGGTGATTTCTTTTCCCTA 43965       A  CC  A
           T                     AGTGGGT AT  CT TTTCCCTAT
                                ||||||| ||  || |||||||||
                                TCATCCA TA  GA AAAGGGATA
                                    C  AA  _
GAM1799  KIAA0663  3'  GTGGGTCAGATTTCCCTA    43966      AATCCCT
                                GTGGGT      ATTTCCCTA
                                ||||||      |||||||||
                                CACCCA      TAAAGGGAT
                                   GTC_____
GAM1799  P24B      3'  AGTGGCTAATCCCTGGCCTA  43967      G      ATTTC
                                AGTGG TAATCCCT    CCTA
                                ||||| ||||||||    ||||
                                TCACC ATTAGGGA    GGAT
                                  G       CC___
GAM1799  PNAS-127  3'  GTTGGTATTTCTATTTCCTTAT 43968    G   ATCC      C
                                GT GGTA   CTATTTCC TAT
                                || ||||   |||||||| |||
                                CA CCAT   GATAAAGG ATA
                                 A   AAA_      A
GAM1799  RBM9      5'  GTGGGTAATTGATCTCTCT   43969        CCCT    C
                                GTGGGTAAT   ATTTC CT
                                |||||||||   ||||| ||
                                CACCCATTA   TAGAG GA
                                    AC__    A
GAM1799  LOC253019 3'  GTGGGTCAGATTTCCCTA    43966      AATCCCT
                                GTGGGT      ATTTCCCTA
                                ||||||      |||||||||
                                CACCCA      TAAAGGGAT
                                   GTC_____
GAM1799  LOC253975 3'  GTGGGGGTCAGATTTCCCTAT  43970      TAA  CCT
                                GTGGG   TC   ATTTCCCTAT
                                |||||   ||   ||||||||||
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                                CACCC  AG  TAAAGGGATA
                                  CC_ TC_
GAM1799 LOC90494 5' AGATGACCTTATTTCCCTA  43971    AAT C
                                GGGT  CC TATTTCCCTA
                                ||||  || ||||||||||
                                TCTA  GG ATAAAGGGAT
                                  CT_ A
GAM1800 ANXA4   3' TGCAAGTACAGCTTTAAAGC  43974       T AC__
                                TGCAAGTACA CT   AGC
                                |||||||||| ||   |||
                                ACGTTCATGT GA   TCG
                                      C AATT
GAM1800 BAZ2A   3' AGCACTTTTCTACAGCTGCAC 43975     A__     CA
                                AGTAC  TCTACAGC CAC
                                |||||  |||||||| |||
                                TCGTG  AGATGTCG GTG
                                  AAA      AC
GAM1800 BRDT    5' TACAAGTACATGTCCATGC   43976       CTA _
                                TGCAAGTACAT  CA GC
                                ||||||||||  || ||
                                ATGTTCATGTA  GT CG
                                      CAG A
GAM1800 C21orf33 3' TGTGAGAGCAGCCCAGCCACAC 43977   CA TA T A
          C                      TG AG CA CT CAGCCACACC
                                || || || || ||||||||||
                                AC TC GT GG GTCGGTGTGG
                                 AC TC C _
GAM1800 CD164   3' TGCAAGTAAAACAAACAGCTGT 43978      CATCT_   CAC
          ACC                     TGCAAGTA    ACAGC  ACC
                                ||||||||    |||||  |||
                                ACGTTCAT    TGTCG  TGG
                                    TTTGTT   ACA
GAM1800 CPD     3' TGCAAGTAGGTCTCTTCCACA 43979      CA  ACAG
                                TGCAAGTA TCT   CCACA
                                |||||||| |||   |||||
                                ACGTTCAT AGA   GGTGT
                                    CC  GAA_
GAM1800 GAN     3' TGCTGCTTCTTACAGCCA   43980    AA ACA  _
                                TGC GT  TCT ACAGCCA
                                ||| ||  ||| |||||||
                                ACG CG  AGA TGTCGGT
                                  A_ A__  A
GAM1800 GAN     3' GCCTCCAACATCTACAGCCACA 43981   AAGT_
                                GC   ACATCTACAGCCACA
                                ||   ||||||||||||||
                                CG   TGTAGATGTCGGTGT
                                 GAGGT
GAM1800 MMP8    3' TGAAAGTGGATACAGCCACA  43982   C  ACATC
                                TG AAGT   TACAGCCACA
                                || ||||   ||||||||||
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                                AC TTCA    ATGTCGGTGT
                                 T   CCT__
GAM1800 MPP2    3' AGTATACGCAGAGCCACACC  43983     C  C  C
                                AGTA AT TA AGCCACACC
                                |||| || || |||||||||
                                TCAT TG GT TCGGTGTGG
                                  A  C  C
GAM1800 RARG    3' TGCAGGTGCATCACACAGC   43984     A  A   _
                                TGCA GT CATC TACAGC
                                |||| || |||| ||||||
                                ACGT CA GTAG GTGTCG
                                  C  C   T
GAM1800 SHANK2  3' TGGAAGTACATCTGCTGAGCTC 43985   C       AC__   _  C
            ATAC                  TG AAGTACATCT   AGC CA AC
                                || ||||||||||   ||| || ||
                                AC TTCATGTAGA   TCG GT TG
                                 C        CGAC   A  A
GAM1800 SQSTM1  3' GCAGGTTACAGCCACA     43986     A  ACATC
                                GCA GT    TACAGCCACA
                                ||| ||    ||||||||||
                                CGT CA    ATGTCGGTGT
                                  C  _____
GAM1800 DKFZP566K1924 3' TGCAAGTTACATGTTACCA   43987       _   CTACA
                                TGCAAGT ACAT    GCCA
                                ||||||| ||||    ||||
                                ACGTTCA TGTA    TGGT
                                    A   CAA__
GAM1800 FBXO9   3' TACAGGTGCATGCCACCACACC 43988     A  A  _ ACA
                                TGCA GT CAT CT   GCCACACC
                                |||| || ||| ||   ||||||||
                                ATGT CA GTA GG   TGGTGTGG
                                  C  C   C  ___
GAM1800 FLJ11269 5' TGCAAGTATCTTTTGCTGCAC  43989       CA   ACA  CA
                                TGCAAGTA  TCT   GC  CAC
                                ||||||||  |||   ||  |||
                                ACGTTCAT  AGA   CG  GTG
                                     __   AAA  AC
GAM1800 FLJ20139 3' TACAGGTGCATGCCACCACACC 43988     A  A  _ ACA
                                TGCA GT CAT CT   GCCACACC
                                |||| || ||| ||   ||||||||
                                ATGT CA GTA GG   TGGTGTGG
                                  C  C   C  ___
GAM1800 FLJ22202 3' TGTGAGTACATCATACTCCA   43990    CA      _  AG
                                TG  AGTACATC TAC  CCA
                                ||  |||||||| |||  |||
                                AC  TCATGTAG ATG  GGT
                                 AC       T  A_
GAM1800 GIOT-2  3' TGAAGTTCACAGCCACA     43991    C   ACA  T
                                TG AAGT   TC ACAGCCACA
                                || ||||   || |||||||||
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                                AC TTCA   AG TGTCGGTGT
                                 _   ___  _
GAM1800 KIAA0752 3' TGCAGGCATGTGACACCACACC 43992     A   CATCT   G
                                TGCA GTA    ACA CCACACC
                                |||| |||    ||| ||||||||
                                ACGT CGT    TGT GGTGTGG
                                  C   ACAC_  _
GAM1800 KIAA1244 3' TACAGGTGCATCCTACCACACC 43993     A  A    ACA
                                TGCA GT CATCT   GCCACACC
                                |||| || |||||   ||||||||
                                ATGT CA GTAGG   TGGTGTGG
                                  C  C    A__
GAM1800 KIAA1559 3' TGCAAATACATACTATGCC   43994          _  CA
                                TGCAAGTACAT CTA  GCC
                                |||||||||||| |||  |||
                                ACGTTTATGTA GAT  CGG
                                       T   A_
GAM1800 KIAA1643 3' TGCAGCTGGTCAGCCACAC   43995     A  ACATCTA
                                TGCA GT      CAGCCACAC
                                |||| ||      |||||||||
                                ACGT CG      GTCGGTGTG
                                  _  ACCA___
GAM1800 KIAA1750 3' TGCATGTACAAAGCCACAC   43996     A    TCTAC
                                TGCA GTACA    AGCCACAC
                                |||| |||||    ||||||||
                                ACGT CATGT    TCGGTGTG
                                  A    T____
GAM1800 MBLR     3' TGCAAGGTATCAACAACCACAC 43997       TAC   T
                                TGCAAG   ATC ACAGCCACAC
                                ||||||   ||| ||||||||||
                                ACGTTC   TAG TGTTGGTGTG
                                   CA_   T
GAM1800 MGC20486 5' TGCGAGGGCACGGACGCCACAC 43998     A  TA   CT  A
            C                    TGC AG  CAT  AC GCCACACC
                                ||| ||  |||  || ||||||||
                                ACG TC  GTG  TG CGGTGTGG
                                  C  CC   CC  _
GAM1800 MSC      3' TGCAGTGACAGCCACAC     43999      A  ACATCT
                                TGCA GT     ACAGCCACAC
                                |||| ||     ||||||||||
                                ACGT CA     TGTCGGTGTG
                                  _  C_____
GAM1800 OSBPL5   3' TGCGGGGCCAGCTAAGCCACAC 44000     AAGTA  T   C
            C                    TGC    CA CTA AGCCACACC
                                |||    || ||| |||||||||
                                ACG    GT GAT TCGGTGTGG
                                  CCCCG  C  _
GAM1800 SRPK1    3' CAAGTACATCTCAATCA     44001          A  GC
                                CAAGTACATCT CA  CA
                                |||||||||| ||  ||
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                                GTTCATGTAGA GT  GT
                                      _ TA
GAM1800  TPD52    3'  TGCAAATATGTCTAGACAC   44002        CA  AC  C
                                TGCAAGTA  TCT  AG CAC
                                |||||||  |||  || |||
                                ACGTTTAT  AGA  TC GTG
                                     AC  __  T
GAM1800  LOC115708 3'  TACAAGTAACCCAGGCAGCCAC 44003        C   __
              AC                  TGCAAGTA ATCTA  CAGCCACAC
                                |||||||| |||||  |||||||||
                                ATGTTCAT TGGGT  GTCGGTGTG
                                     _   CC
GAM1800  LOC126066 5'  TGAAGTTCACAGCCACA    43991    C   ACA  T
                                TG AAGT   TC ACAGCCACA
                                || ||||   || |||||||||
                                AC TTCA   AG TGTCGGTGT
                                 _   ___  _
GAM1800  LOC130752 3'  TGAAGTACATCTGTTTGGCC   44004    C        ACA__
                                TG AAGTACATCT    GCC
                                || ||||||||||    |||
                                AC TTCATGTAGA    CGG
                                 _        CAAAC
GAM1800  LOC145608 5'  CAAGTACATGCTGCCCA    44005         _ ACA   A
                                CAAGTACAT CT   GCC CA
                                ||||||||| ||   ||| ||
                                GTTCATGTA GA   CGG GT
                                     C  ___  _
GAM1800  LOC147639 3'  TGCAAGTACATTTATTACA   44006          C___
                                TGCAAGTACAT   TACA
                                ||||||||||   ||||
                                ACGTTCATGTA   ATGT
                                      AATA
GAM1800  LOC148089 3'  AGTACATCCACTGGGTTGCACC 44007          AGCCA__
                                AGTACATCTAC      CACC
                                ||||||||||      ||||
                                TCATGTAGGTG      GTGG
                                      ACCCAAC
GAM1800  LOC158476 3'  TGCAAGTACACTGCATACAAC  44008          C___
                                TGCAAGTACAT   TACAGC
                                ||||||||||   ||||||
                                ACGTTCATGTG   ATGTTG
                                      ACGT
GAM1800  LOC197273 5'  TGAAGTACACAGCCAC     44009    C    ATCT
                                TG AAGTAC   ACAGCCAC
                                || ||||||   ||||||||
                                AC TTCATG   TGTCGGTG
                                 _   _____
GAM1800  LOC201810 3'  TACAGGTGTGTACCACCACACC 44010     A  ACATC   A
                                TGCA GT    TAC GCCACACC
                                |||| ||    ||| ||||||||
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                                ATGT CA    ATG TGGTGTGG
                                  C  CAC__  G
GAM1800  LOC256044 5'  TGAAAGTCACAGCCACA    44011   C   ACATC
                                TG AAGT    TACAGCCACA
                                || ||||    ||||||||||
                                AC TTCA    GTGTCGGTGT
                                 T  _____
GAM1800  LOC84549  3'  TGCAAGTACATTAACACAG   44012         C__
                                TGCAAGTACAT  TACAG
                                ||||||||||  |||||
                                ACGTTCATGTA  GTGTC
                                       ATT
GAM1800  LOC90594  5'  TGAAGTTCACAGCCACA    43991   C   ACA  T
                                TG AAGT  TC ACAGCCACA
                                || ||||  || |||||||||
                                AC TTCA  AG TGTCGGTGT
                                 _  ___ _
GAM1800  LOC93132  5'  TACAGGTGCATGCCACCACACC 43988     A  A  _  ACA
                                TGCA GT CAT CT  GCCACACC
                                |||| || ||| ||  ||||||||
                                ATGT CA GTA GG  TGGTGTGG
                                  C  C  C  ___
GAM1801  PFKFB4   3'  TCACACTTCACAAAGCCAACTG 44015   G        T  G
                                TC ACACTTCACAA GCT AACTG
                                || ||||||||||| ||| |||||
                                AG TGTGAAGTGTT CGG TTGAC
                                 _        T  _
GAM1801  dJ55C23.6 3'  GACACTTCCAAGACACTG    44016       A  __
                                GACACTTC CA  ATGCTG
                                |||||||| ||  ||||||
                                CTGTGAAG GT  TGTGAC
                                     _ TC
GAM1801  FLJ11101  3'  TCAACACTTCTTGCTGAACTG  44017         ACAA
                                TCGACACTTC   TGCTGAACTG
                                ||||||||||   ||||||||||
                                AGTTGTGAAG   ACGACTTGAC
                                      A___
GAM1801  HGC6.1.1  3'  GACGGTCACTGCTGAACTG   44018    ACT   AA
                                GAC  TCAC  TGCTGAACTG
                                |||  ||||  ||||||||||
                                CTG  AGTG  ACGACTTGAC
                                  CC_  __
GAM1801  HSPC043   5'  TCAGCACTTCACAATCACC   44019    A       _
                                TCG CACTTCACAAT GCT
                                ||| |||||||||| |||
                                AGT GTGAAGTGTTA TGG
                                  C         G
GAM1801  KPNB3    3'  GACACTTCACATTCAAGGGCTG 44020         AT_____
                                GACACTTCACA      GCTG
                                ||||||||||      ||||
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                                CTGTGAAGTGT      CGAC
                                      AAGTTCC
GAM1801  SYNPO2   3'  TCGTGCTTCACAATCAGCC   44021     ACA       __
                                TCG   CTTCACAAT  GCT
                                |||   |||||||||  |||
                                AGC   GAAGTGTTA  CGG
                                  AC_       GT
GAM1802  ADD1     3'  TACACAAGGACAGAGCACA   44024        CC    A
                                TACACAAGG  CAGGG CACA
                                |||||||||  ||||| ||||
                                ATGTGTTCC  GTCTC GTGT
                                      T_    _
GAM1802  ADD1     3'  TACACAAGGACAGAGCACA   44024        CC    A
                                TACACAAGG  CAGGG CACA
                                |||||||||  ||||| ||||
                                ATGTGTTCC  GTCTC GTGT
                                      T_    _
GAM1802  ANK1     3'  TACACAAGGCTGATTACTGTAC 44025        CCAGGG  ___
              A                  TACACAAGGC     AC   ACA
                                 ||||||||||     ||   |||
                                 ATGTGTTCCG     TG   TGT
                                       ACTAA_  ACA
GAM1802  ANK1     3'  TACACAAGGCTGATTACTGTAC 44025        CCAGGG  ___
              A                  TACACAAGGC     AC   ACA
                                 ||||||||||     ||   |||
                                 ATGTGTTCCG     TG   TGT
                                       ACTAA_  ACA
GAM1802  AOC3     3'  CATGAGGCAGGCAGACACAA  44026    CA   CC   __
                                CA  AGGC  AGG  GACACAA
                                ||  ||||  |||  |||||||
                                GT  TCCG  TCC  CTGTGTT
                                 AC    __   GT
GAM1802  CEBPA    3'  CACAAGGCACTGCTGGGCACA  44027        CCA___   A
                                CACAAGGC     GGG CACA
                                ||||||||     ||| ||||
                                GTGTTCCG     CCC GTGT
                                     TGACGA  _
GAM1802  CREBBP   3'  TACAAAAGGTCCAAGAACA   44028     C   C
                                TACA AAGG CCAGGGACA
                                |||| |||| |||||||||
                                ATGT TTCC GGTTCTTGT
                                  T   A
GAM1802  CSK      3'  ACACGGGACATGGGACACA   44029     AA  CC  _
                                ACAC  GG  CA GGGACACA
                                ||||  ||  || ||||||||
                                TGTG  CC  GT CCCTGTGT
                                  __  CT  A
GAM1802  EPHA2    3'  CAAAGGCCCAGGAAAGCAA   44030    C         CA
                                CA AAGGCCCAGGGA  CAA
                                || ||||||||||||  |||
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                                GT TTCCGGGTCCTT  GTT
                                 _         TC
GAM1802  GARP    3'  ACACAAGGCTTGGATTCAA   44031        CCAG   CA
                                ACACAAGGC   GGA  CAA
                                |||||||||   |||  |||
                                TGTGTTCCG   CCT  GTT
                                     AA__   AA
GAM1802  HUNK    3'  CACACACAGGGGCACA     44032      AGGCC    A
                                TACACA    CAGGG CACA
                                ||||||    ||||| ||||
                                GTGTGT    GTCCC GTGT
                                   _____    C
GAM1802  IMPA1   3'  TACACAAGACTTTAAAGCA   44033        CC_   A
                                TACACAAGGC   AGGG CA
                                ||||||||||   |||| ||
                                ATGTGTTCTG   TTTC GT
                                     AAA   _
GAM1802  ITGA6   3'  ACACATTAGGGACACAA     44034      AGGCCC
                                ACACA     AGGGACACAA
                                |||||     ||||||||||
                                TGTGT     TCCCTGTGTT
                                  AA____
GAM1802  LY95    5'  CAAGTACCCAGGGACACAA   44035     _
                                CAAG GCCCAGGGACACAA
                                |||| ||||||||||||||
                                GTTC TGGGTCCCTGTGTT
                                  A
GAM1802  NTSR1   3'  CACGTGAGGCCCAAAGCCAC  44036    A__       A
                                CAC   AGGCCCAGGG CAC
                                |||   |||||||||| |||
                                GTG   TCCGGGTTTC GTG
                                  CAC         G
GAM1802  SAA4    3'  TACCAGTTCCTGGGGACACAA  44037    A  AGG  CA
                                TAC CA   CC  GGGACACAA
                                ||| ||   ||  |||||||||
                                ATG GT   GG  CCCTGTGTT
                                  _  CAA  AC
GAM1802  SAFB    3'  CACGAGACAGGACACA      44038    A   CCA
                                CAC AGGC   GGGACACA
                                ||| ||||   ||||||||
                                GTG TCTG   TCCTGTGT
                                  C   ___
GAM1802  SHC1    3'  TACAAGAGGCCCAAATTCA   44039     CA       GA
                                TACA  AGGCCCAGG  CA
                                ||||  |||||||||  ||
                                ATGT  TCCGGGTTT  GT
                                   TC        AA
GAM1802  SIX2    3'  TACGGAGGGACCAGGACACA  44040    ACAA  C    G
                                TAC    GG CCAGG ACACA
                                |||    || ||||| |||||
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                                ATG   CC GGTCC TGTGT
                                  CCTC  T    _
GAM1802  TARBP2   3'  TACATGAGCCCAGAGGCA    44041     CAA       A
                                TACA  GGCCCAGGG CA
                                ||||  ||||||||| ||
                                ATGT  TCGGGTCTC GT
                                  AC_       C
GAM1802  TARBP2   3'  TACATGAGCCCAGAGGCA    44041     CAA       A
                                TACA  GGCCCAGGG CA
                                ||||  ||||||||| ||
                                ATGT  TCGGGTCTC GT
                                  AC_       C
GAM1802  TARBP2   3'  TACATGAGCCCAGAGGCA    44041     CAA       A
                                TACA  GGCCCAGGG CA
                                ||||  ||||||||| ||
                                ATGT  TCGGGTCTC GT
                                  AC_       C
GAM1802  TIMP3    3'  TACCCAGGGCCGAGTGACACA  44042     A  A   C  G
                                TAC CA GGCC AG GACACA
                                ||| || |||| || ||||||
                                ATG GT CCGG TC CTGTGT
                                  G  C   C  A
GAM1802  UBB      5'  CACCCACAGGGACACAA     44043     AAGG  _
                                CAC   CC CAGGGACACAA
                                |||   || ||||||||||
                                GTG   GG GTCCCTGTGTT
                                  _____  T
GAM1802  ATPW     5'  TACTCAAGAAAAGGACACA   44044     A    CCC
                                TAC CAAGG  AGGGACACA
                                ||| |||||  |||||||||
                                ATG GTTCT  TTCCTGTGT
                                  A    T__
GAM1802  BTBD3    3'  ACACTGCCAGGGACACA     44045     AG   C
                                ACA  GCC AGGGACACA
                                |||  ||| |||||||||
                                TGT  CGG TCCCTGTGT
                                  GA  _
GAM1802  CART     3'  TACACAAAGGTACACA      44046       GGCCC   G
                                TACACAA    AGG ACACA
                                |||||||    ||| |||||
                                ATGTGTT    TCC TGTGT
                                     _____  A
GAM1802  CASP9    3'  ACACAGGGATCATGGGACACAA 44047      A  CC  _
                                ACACA GG  CA GGGACACAA
                                ||||| ||  || |||||||||
                                TGTGT CC  GT CCCTGTGTT
                                   C  TA  A
GAM1802  CCNB3    3'  TACACAAAGTCATCCACAC   44048        CC  GGG
                                TACACAAGG  CA   ACAC
                                |||||||||  ||   ||||
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                                ATGTGTTTC  GT   TGTG
                                     A_  AGG
GAM1802  CDCA4    3'  TACAGTGGGGGACACAA     44049     CAA  CCCA
                                TACA   GG    GGGACACAA
                                ||||   ||    |||||||||
                                ATGT   CC    CCCTGTGTT
                                  CA_  ____
GAM1802  CHST4    3'  ACACAAGCATGGACACAA    44050       GCC  G
                                ACACAAG   CA GGACACAA
                                |||||||   || ||||||||
                                TGTGTTC   GT CCTGTGTT
                                    ___  A
GAM1802  CLIC4    3'  TACACAGTGAATGGACACAA  44051       A GCCCAG
                                TACACA G     GGACACAA
                                |||||| |     ||||||||
                                ATGTGT C     CCTGTGTT
                                   _ ACTTA_
GAM1802  D21S2056E 3'  CACAAGGCCAGCCACA      44052         CA  GA
                                CACAAGGCC  GG  CACA
                                |||||||||  ||  ||||
                                GTGTTCCGG  TC  GTGT
                                     __  G_
GAM1802  DIM1     3'  CACACAGGGAGGACACA     44053       A  CCCA
                                TACACA GG    GGGACACA
                                |||||| ||    ||||||||
                                GTGTGT CC    TCCTGTGT
                                   C  ____
GAM1802  DJ971N18.2 3'  TACACAAGAAAAGGATGCAA  44054         CCC    CA
                                TACACAAGG   AGGGA  CAA
                                |||||||||   |||||  |||
                                ATGTGTTCT   TTCCT  GTT
                                     T__    AC
GAM1802  DKFZp434F1719 3'  ACACAGGCCGGGCACA      44055      A   CA   A
                                ACACA GGCC  GGG CACA
                                ||||| ||||  ||| ||||
                                TGTGT CCGG  CCC GTGT
                                  _   __  _
GAM1802  ERO1L    3'  ACCAGGCCTTAGGGACACA   44056    A    C_
                                AC AGGCC  AGGGACACA
                                || |||||  |||||||||
                                TG TCCGG  TCCCTGTGT
                                 G    AA
GAM1802  FLJ11021  3'  TACACAAGACAGCGGACAC   44057         CC  _
                                TACACAAGGC  AG GGACAC
                                ||||||||||  || ||||||
                                ATGTGTTCTG  TC CCTGTG
                                     __  G
GAM1802  FLJ12783  3'  CATAAGAAAGGACACA     44058    C   CCC
                                CA AAGG   AGGGACACA
                                || ||||   |||||||||
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                                GT TTCT   TTCCTGTGT
                                 A  ___
GAM1802  FLJ12891  3'  TACACAAGGCTCTTCTGCACAA 44059          CCAGGGA
                                TACACAAGGC      CACAA
                                ||||||||||      |||||
                                ATGTGTTCCG      GTGTT
                                     AGAAGAC
GAM1802  FLJ20507  3'  CACAGGGTCTGAAGGACACA   44060      A  CCC_
                                CACA GG    AGGGACACA
                                |||| ||    |||||||||
                                GTGT CC    TTCCTGTGT
                                  C  AGAC
GAM1802  FLJ21742  3'  CACAAGGCCTGAATTCACACA  44061         CA  ___
                                CACAAGGCC  GGG   ACACA
                                |||||||||  |||   |||||
                                GTGTTCCGG  CTT   TGTGT
                                     A_   AAG
GAM1802  FLJ22283  5'  CACACAGTGCGGGACACA    44062       AG  CCA
                                TACACA  GC   GGGACACA
                                ||||||  ||   ||||||||
                                GTGTGT  CG   CCCTGTGT
                                   CA  ___
GAM1802  FLJ22746  3'  ACAAGGCCTAGTTACCAA    44063        C  GG  A
                                ACAAGGCC AG  AC CAA
                                |||||||| ||  || |||
                                TGTTCCGG TC  TG GTT
                                     A  AA  _
GAM1802  FLJ32926  3'  ACAGAGACAGGGACACA     44064     A  CC
                                ACA GG  CAGGGACACA
                                ||| ||  ||||||||||
                                TGT CT  GTCCCTGTGT
                                  _  CT
GAM1802  IL1F10    3'  CACAAGGCTAAAACGCA     44065        CCA    A
                                CACAAGGC   GGGAC CA
                                ||||||||   ||||| ||
                                GTGTTCCG   TTTTG GT
                                     A__     C
GAM1802  KCNS1     3'  ACACAAGGCCAAACA       44066         CAG
                                ACACAAGGCC   GGACA
                                ||||||||||   |||||
                                TGTGTTCCGG   TTTGT
                                             ___
GAM1802  KIAA0285  3'  CACGGGAACCAGGGACACA   44067     AA GC
                                CAC  G  CCAGGGACACA
                                |||  |  ||||||||||||
                                GTG  C  GGTCCCTGTGT
                                  CC TT
GAM1802  KIAA0746  5'  ACACAAGGCTGAGAGCA     44068         CC    A
                                ACACAAGGC  AGGG CA
                                |||||||||  |||| ||
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                                TGTGTTCCG  TCTC GT
                                     AC   _
GAM1802  KIAA0801  3'  ACATCAAGGTGGGGACACAA   44069    _    CCCA
                                ACA CAAGG   GGGACACAA
                                ||| |||||   |||||||||
                                TGT GTTCC   CCCTGTGTT
                                  A    AC__
GAM1802  KIAA1025  3'  TACAGAGGCTGAAAACACA   44070    CA   CCA
                                TACA  AGGC   GGGACACA
                                ||||  ||||   ||||||||
                                ATGT  TCCG   TTTTGTGT
                                  C_   AC_
GAM1802  KIAA1348  3'  TACACAAGCCCAAGCCA    44071       G    GA
                                TACACAAG CCCAGG  CA
                                |||||||| ||||||  ||
                                ATGTGTTC GGGTTC  GT
                                     _    G_
GAM1802  KIAA1372  5'  CACAAGCCCAGCACA      44072      G    GGA
                                CACAAG CCCAG   CACA
                                |||||| |||||   ||||
                                GTGTTC GGGTC   GTGT
                                     _    ___
GAM1802  KIAA1395  3'  CACACAGATGGGGACACA   44073      A  CCCA
                                TACACA GG   GGGACACA
                                |||||| ||   ||||||||
                                GTGTGT CT   CCCTGTGT
                                   _  AC__
GAM1802  KIAA1462  3'  CACACAAAGGGATACA     44074      GGCCC    C
                                TACACAA    AGGGA ACA
                                |||||||    ||||| |||
                                GTGTGTT    TCCCT TGT
                                   ______    A
GAM1802  KIAA1508  5'  ACACAAAGATGGGGCACAA   44075       CCCA  A
                                ACACAAGG   GGG CACAA
                                ||||||||   ||| |||||
                                TGTGTTTC   CCC GTGTT
                                     TAC_  _
GAM1802  KIAA1573  3'  CACAAAGCACAAACACAA    44076       C  GG
                                CACAAGGC CA  GACACAA
                                |||||||| ||  |||||||
                                GTGTTTCG GT  TTGTGTT
                                     T  __
GAM1802  KIAA1649  3'  CACAGGGCAGAACACAA     44077     A  CCA
                                CACA GGC   GGGACACAA
                                |||| |||   |||||||||
                                GTGT CCG   TCTTGTGTT
                                  C   ___
GAM1802  KIAA1649  5'  CACAGGGCAGAACACAA     44077     A  CCA
                                CACA GGC   GGGACACAA
                                |||| |||   |||||||||
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                                GTGT CCG   TCTTGTGTT
                                  C  ___
GAM1802 LAP1B    3' CATAAGAAAGGACACAA     44078    C    CCC
                                CA AAGG   AGGGACACAA
                                || ||||   ||||||||||
                                GT TTCT   TTCCTGTGTT
                                 A   ___
GAM1802 LEPROTL1 3' ACAAGGTCAAAGACACAA    44079       CC
                                ACAAGG  CAGGGACACAA
                                ||||||  ||||||||||||
                                TGTTCC  GTTTCTGTGTT
                                   A_
GAM1802 MGC12981 3' ACATGCAGAGCAGGGACACA  44080     CAA  CC
                                ACA   GG  CAGGGACACA
                                |||   ||  ||||||||||
                                TGT   TC  GTCCCTGTGT
                                  ACG  TC
GAM1802 MGC15438 5' ACACAGCAGTGAGGGGCACA  44081      A_  CCC    A
                                ACACA  GG   AGGG CACA
                                |||||  ||   |||| ||||
                                TGTGT  TC   TCCC GTGT
                                   CG  AC_   C
GAM1802 MGC4172  3' CAAGTGCCCAGGGGCACAA   44082      _       A
                                CAAG GCCCAGGG CACAA
                                |||| |||||||| |||||
                                GTTC CGGGTCCC GTGTT
                                  A       C
GAM1802 MGC4796  3' ACATGGGGCTAAGAACACA   44083     CAA   CC
                                ACA   GGC  AGGGACACA
                                |||   |||  |||||||||
                                TGT   CCG  TTCTTGTGT
                                  ACC   A_
GAM1802 MIC2L1   3' TACCAAAACAGGGACACA    44084     A     CC
                                TAC CAAGGC  AGGGACACA
                                ||| ||||||  |||||||||
                                ATG GTTTTG  TCCCTGTGT
                                  _     __
GAM1802 MKNK1    3' CACACAAGACCTGGGGACACA 44085          CA
                                TACACAAGGCC  GGGACACA
                                ||||||||||  ||||||||
                                GTGTGTTCTGG  CCCTGTGT
                                      AC
GAM1802 MKRN1    3' CACACAAGGCTTAAACCA    44086         CCAG    A
                                TACACAAGGC    GGAC CA
                                ||||||||||    |||| ||
                                GTGTGTTCCG    TTTG GT
                                      AA__    _
GAM1802 MRPS27   3' ACACAAGGTCTCAGGATGCACA 44087        CC_    A_
                                ACACAAGG   CAGGG  CACA
                                ||||||||   |||||  ||||
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                                TGTGTTCC  GTCCT  GTGT
                                    AGA    AC
GAM1802  PAPSS2   3'  TACAGAAGAGGACACAA    44088     C   GCCCA
                                TACA AAG    GGGACACAA
                                |||| |||    |||||||||
                                ATGT TTC    TCCTGTGTT
                                  C  _____
GAM1802  PPP1R16B 3'  TACACAAAGCTGCTGATACA  44089         CCAGG  C
                                TACACAAGGC    GA ACA
                                ||||||||||    || |||
                                ATGTGTTTCG    CT TGT
                                     ACGA_  A
GAM1802  PRRG2    3'  TACACAAGATGGCACA     44090         CCCAG  A
                                TACACAAGG    GG CACA
                                |||||||||    || ||||
                                ATGTGTTCT    CC GTGT
                                     A____  _
GAM1802  SRF      3'  CACAGGCCCAGCTACTCA    44091      A      GG  A
                                CACA GGCCCAG  AC CA
                                |||| |||||||  || ||
                                GTGT CCGGGTC  TG GT
                                  _      GA  A
GAM1802  TIX1     3'  ACACAAAGGGGGCACA      44092         CCCA   A
                                ACACAAGG   GGG CACA
                                ||||||||   ||| ||||
                                TGTGTTTC   CCC GTGT
                                    C___  _
GAM1802  YAP1     3'  TACATTAGGAACAAGGACA   44093      CA   CC
                                TACA  AGG  CAGGGACA
                                ||||  |||  ||||||||
                                ATGT  TCC  GTTCCTGT
                                  AA   TT
GAM1802  ZNF183   3'  TACAAAGGAAGGACAC      44094      C    CCC
                                TACA AAGG   AGGGACAC
                                |||| ||||   ||||||||
                                ATGT TTCC   TTCCTGTG
                                  _   ____
GAM1802  LOC143384 3'  CACAAAGCTCAAGGCACA   44095         C     A
                                CACAAGGC CAGGG CACA
                                |||||||| ||||| ||||
                                GTGTTTCG GTTCC GTGT
                                    A    _
GAM1802  LOC143879 3'  TACACAAAGTTCAGAGCCA   44096         CC     A
                                TACACAAGG  CAGGG CA
                                |||||||||  ||||| ||
                                ATGTGTTTC  GTCTC GT
                                     AA    G
GAM1802  LOC146443 5'  ACACAGGGAGACACA       44097       A  CCCA
                                ACACA GG   GGGACACA
                                ||||| ||   ||||||||
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                                TGTGT CC    CTCTGTGT
                                  _ ____
GAM1802  LOC147229 5'  TACATAGGAGCCAAAGACA    44098      CA   C_
                                TACA  AGG  CCAGGGACA
                                ||||  |||  |||||||||
                                ATGT  TCC  GGTTTCTGT
                                  A_   TC
GAM1802  LOC147669 5'  ACACAGGGACACAGGGACACA  44099       A  _ C
                                ACACA GG C CAGGGACACA
                                ||||| || | ||||||||||
                                TGTGT CC G GTCCCTGTGT
                                   C  T T
GAM1802  LOC148147 3'  TACACAAGTCCAAAACCA    44100         GC     GA
                                TACACAAG  CCAGG  CA
                                ||||||||  |||||  ||
                                ATGTGTTC  GGTTT  GT
                                     A_     TG
GAM1802  LOC149668 3'  CAACACCCAGGGACACAA    44101     G
                                CAA GCCCAGGGACACAA
                                ||| ||||||||||||||
                                GTT TGGGTCCCTGTGTT
                                  G
GAM1802  LOC159089 3'  TACACAAGGCCAGCATTTCACA 44102           C  GGA__
           A                     TACACAAGGCC AG     CACAA
                                ||||||||||| ||     |||||
                                ATGTGTTCCGG TC     GTGTT
                                       _  GTAAA
GAM1802  LOC160777 3'  ACACAGGCAGGATACA      44103       A   CCA    C
                                ACACA GGC   GGGA ACA
                                ||||| |||   |||| |||
                                TGTGT CCG   TCCT TGT
                                  _  ____   A
GAM1802  LOC196214 5'  CACGTGAGGGCAGGGACACA  44104     A__   CC
                                CAC   AGG  CAGGGACACA
                                |||   |||  ||||||||||
                                GTG   TCC  GTCCCTGTGT
                                  CAC   C_
GAM1802  LOC200093 3'  TACACTGGGAGACACA      44105       AA  CCCA
                                TACAC  GG   GGGACACA
                                |||||  ||   ||||||||
                                ATGTG  CC   CTCTGTGT
                                  A_  ____
GAM1802  LOC202934 3'  ACACTTGGATGGGGACACAA  44106      AA  CCCA
                                ACAC  GG   GGGACACAA
                                ||||  ||   |||||||||
                                TGTG  CC   CCCTGTGTT
                                  AA  TAC_
GAM1802  LOC253971 3'  TACACAAGCCTGGCACCAA   44107         G  CA  G  A
                                TACACAAG CC  GG AC CAA
                                |||||||| ||  || || |||
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                                ATGTGTTC GG  CC TG GTT
                                    _ A_  G  _
GAM1802 LOC89919 3' ACACAGGGACAGGGCACA    44108      A  CC    A
                                ACACA GG  CAGGG CACA
                                ||||| ||  ||||| ||||
                                TGTGT CC  GTCCC GTGT
                                  _ CT    _
GAM1803 FLRT2    5' TGAAATAATTAAAGCTAA    44111           A
                                TGAAATAATTAGA CTAG
                                |||||||||||| ||||
                                ACTTTATTAATTT GATT
                                       C
GAM1803 RERE     3' TGAAAGAAAAAAAACTAGAAAC 44112      T  TT
           AT                    TGAAA AA  AGAACTAGAAACAT
                                |||||| ||  ||||||||||||||
                                ACTTT TT  TTTTGATCTTTGTA
                                  C  TT
GAM1803 KIAA1016 3' AAATAATTAGAGAAAC      44113          ACTA
                                AAATAATTAGA   GAAAC
                                ||||||||||   |||||
                                TTTATTAATCT   CTTTG
                                     ____
GAM1803 MBLR     3' TGAAATAATGAGAAAAATAAAC 44114         T   CTAG
           AT                    TGAAATAAT AGAA   AAACAT
                                |||||||| ||||   ||||||
                                ACTTTATTA TCTT   TTTGTA
                                     C   TTTA
GAM1803 PXMP4    3' TAATGCAGCTACTAGAAACAT  44115     _  A_
                                TAAT TAG  ACTAGAAACAT
                                |||| |||  ||||||||||
                                ATTA GTC  TGATCTTTGTA
                                  C  GA
GAM1803 LOC157567 3' TGAAATAATTATGAACTA    44116          _
                                TGAAATAATTA GAACTA
                                |||||||||| ||||||
                                ACTTTATTAAT CTTGAT
                                       A
GAM1803 LOC158863 3' TGAAATAGTGAACCAGA     44117        ATTA
                                TGAAATA   GAACTAGA
                                |||||||   ||||||||
                                ACTTTAT   CTTGGTCT
                                    CA__
GAM1803 LOC51136 3' AAATAATTAGAATAGAA      44118          C
                                AAATAATTAGAA TAGAA
                                |||||||||||| |||||
                                TTTATTAATCTT ATCTT
                                       _
GAM1804 FLJ13912 3' TTACACTTGCAATGTTA      44121        ACG   TTC
                                TTACACTT   GCA   GTTA
                                |||||||   |||   ||||
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                                AATGTGAA  CGT  CAAT
                                   ___  TA_
GAM1804 PRO1600  3' TATTACATTGATGGCATTCA  44122       CTTAC
                                TATTACA    GGCATTCG
                                |||||||    ||||||||
                                ATAATGT    CCGTAAGT
                                    AACTA
GAM1805 BTK      3' AGGGAATCAAAGAAGAGGT   44125       A        A
                                AGGGAA TCAAAGAAGA GT
                                |||||| |||||||||| ||
                                TCCCTT AGTTTCTTCT CA
                                   _       C
GAM1805 CA12     3' AAGGAAATCAGAGGGAGA    44126         A  A_
                                AGGGAAATCA AG  AGA
                                |||||||||| ||  |||
                                TTCCTTTAGT TC  TCT
                                      C  CC
GAM1805 CARPX    3' GAAATCAAAGAATGCAGT    44127          GA_
                                GAAATCAAAGAA   AGT
                                ||||||||||||   |||
                                CTTTAGTTTCTT   TCA
                                       ACG
GAM1805 CDC27    3' AGGGAGATTAAAGAAAAA    44128      A  C
                                AGGGA AT AAAGAAGAA
                                ||||| || |||||||||
                                TCCCT TA TTTCTTTTT
                                  C  A
GAM1805 CYP8B1   3' AGGGAAATCAGGAGGAGGAGT  44129         A_  A  A
                                AGGGAAATCA  AG AG AGT
                                ||||||||||  || || |||
                                TCCCTTTAGT  TC TC TCA
                                      CC  C  C
GAM1805 DEDD     3' AGGGAAATAAAGGGGAAG    44130        C    AA
                                AGGGAAAT AAAG  GAAG
                                |||||||| ||||  ||||
                                TCCCTTTA TTTC  CTTC
                                   _   CC
GAM1805 ESRRG    3' AGGGAGGTGAAAGAAGAAA   44131      AATC
                                AGGGA    AAAGAAGAAG
                                |||||    ||||||||||
                                TCCCT    TTTCTTCTTT
                                  CCAC
GAM1805 GRAF     3' AGGGAAACAGAGAAGCCA    44132        CAA  A
                                AGGGAAAT   AGA GAAGTTA
                                ||||||||   ||| |||||||
                                TCCCTTTG   TCT CTTCGGT
                                   ___  _
GAM1805 IFNGR1   3' AGGAAAATCAGACTTCAAAGTT 44133         AAGAA_
                                AGGGAAATCA     GAAGTT
                                ||||||||||     ||||||
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                                TCCTTTTAGT     TTTCAA
                                     CTGAAG
GAM1805  MYCL2    3'  AGGGAGATCAAAAAGAAA    44134      A      A
                                AGGGA ATCAAAGA GAAG
                                ||||| |||||||| ||||
                                TCCCT TAGTTTTT CTTT
                                   C      _
GAM1805  MYO10    3'  GGGAAATCAGGTTGGGAGGTTA 44135         AAGAA_  A
                                GGGAAATCA     GA GTTA
                                |||||||||     || ||||
                                CCCTTTAGT     CT CAAT
                                     CCAACC  C
GAM1805  PBX3     3'  AGGGAAACAAAGAGTTAA    44136       T     AGAA
                                AGGGAAA CAAAGA   GTTAA
                                ||||||| ||||||   |||||
                                TCCCTTT GTTTCT   CAATT
                                   _    ____
GAM1805  PCDHA11  5'  AGGGAACTCAAAGAAAAAAT  44137      A
                                AGGGAA TCAAAGAAGAAGT
                                |||||| ||||||||||||
                                TCCCTT AGTTTCTTTTTTA
                                   G
GAM1805  PCDHA11  5'  AGGGAACTCAAAGAAAAAAT  44137      A
                                AGGGAA TCAAAGAAGAAGT
                                |||||| ||||||||||||
                                TCCCTT AGTTTCTTTTTTA
                                   G
GAM1805  POU3F1   3'  AGGGAAATATAAGGGGAAA   44138       CA   AA
                                AGGGAAAT  AAG  GAAG
                                ||||||||  |||  ||||
                                TCCCTTTA  TTC  CTTT
                                     TA   CC
GAM1805  RARRES3  3'  AGGGAAACAGAGGAAA     44139       CAA   A
                                AGGGAAAT   AGA GAAG
                                ||||||||   ||| ||||
                                TCCCTTTG   TCT CTTT
                                     ___   C
GAM1805  AFAP     3'  GGGAGACCAAGAAGTTAA    44140     A   AAGA
                                GGGA ATCA    AGAAGTTAA
                                |||| ||||    |||||||||
                                CCCT TGGT    TCTTCAATT
                                   C   ____
GAM1805  AKAP11   3'  GGGAAATCAAAAAGCTA     44141         AGAA
                                GGGAAATCAA    GAAGTTA
                                ||||||||||    |||||||
                                CCCTTTAGTT    TTTCGAT
                                     ____
GAM1805  CGI-57   3'  AGGGAAATCAAAAGTAAAAGT  44142          _ A
                                AGGGAAATCAAA G AGAAGT
                                |||||||||||| | ||||||
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                                TCCCTTTAGTTT C TTTTCA
                                       T A
GAM1805  DKFZP566D193 3'  GGGAAGTATGAGAAGTTAAT   44143      ATCAAA  A
                                GGGAA     GA GAAGTTAAT
                                |||||     || |||||||||
                                CCCTT     CT CTTCAATTA
                                   CATA__  _
GAM1805  DKFZP586M1120 3'  AGGGAAATCAGGGAAAGA    44144         AA_
                                AGGGAAATCA   GAAGA
                                ||||||||||   |||||
                                TCCCTTTAGT   TTTCT
                                      CCC
GAM1805  G2       3'  AGGGAAACAAAGAATCAG    44145       T      GA
                                AGGGAAA CAAAGAA  AG
                                ||||||| |||||||  ||
                                TCCCTTT GTTTCTT  TC
                                   _      AG
GAM1805  JIK      3'  AGGGAGATAAAGAAAAAG    44146      A  C
                                AGGGA AT AAAGAAGAAG
                                ||||| || ||||||||||
                                TCCCT TA TTTCTTTTTC
                                   C  _
GAM1805  KIAA0884  5'  AGGGAGGTCTGAAGAAGT    44147      AA  AAA
                                AGGGA  TC   GAAGAAGT
                                |||||  ||   ||||||||
                                TCCCT  AG   CTTCTTCA
                                   CC  A__
GAM1805  KIAA1198  3'  AGGGAAATCAGGCAAGAAAA  44148         ___
                                AGGGAAATCA   AAGAAGA
                                ||||||||||   |||||||
                                TCCCTTTAGT   TTCTTTT
                                      CCG
GAM1805  KIAA1266  3'  GGAAAATCAGAGACATAGT   44149         A   AGA
                                GGGAAATCA AGA   AGT
                                ||||||||| |||   |||
                                CCTTTTAGT TCT   TCA
                                      C   GTA
GAM1805  KIAA1509  3'  AGGGAAATCTAGGAAGGCAG  44150         AAA   A_
                                AGGGAAATC   GAAG  AG
                                |||||||||   ||||  ||
                                TCCCTTTAG   CTTC  TC
                                     ATC    CG
GAM1805  KIAA1535  3'  AGGGAAACAGAGACATC     44151        CAA   A  A
                                AGGGAAAT   AGA GA GTT
                                ||||||||   ||| || |||
                                TCCCTTTG   TCT CT TAG
                                     ___   _  G
GAM1805  KIAA1913  3'  AGGGCAATCAAAGAACTTAAAA 44152      A        ____
            GT                    AGGG AATCAAAGAA    GAAGT
                                ||||| ||||||||||    |||||
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                                TCCC TTAGTTTCTT    TTTCA
                                  G         GAAT
GAM1805  LRPPRC    3'  AGGGAAACCAAAGAGCCAA    44153            AGAA
                                AGGGAAATCAAAGA    GTTAA
                                ||||||||||||||    |||||
                                TCCCTTTGGTTTCT    CGGTT
                                                  _____
GAM1805  MGC20481  3'  AGGAAGTTGGAGGAGAAGCCA  44154       ATCAA  A
                                GGGAA     AG AGAAGTTA
                                |||||     || ||||||||
                                TCCTT     TC TCTTCGGT
                                   CAACC  C
GAM1805  SEC14L1   3'  GGGAGAATCAAAGAATCATTA  44155      _         GAA
                                GGGA AATCAAAGAA   GTTA
                                ||||| ||||||||||   ||||
                                CCCT TTAGTTTCTT   TAAT
                                  C         AG_
GAM1805  SENP8     3'  AGGGAGACCAAAGGAAATTAAT 44156       A       AA
                                AGGGA ATCAAAG  GAAGTTAAT
                                |||||| |||||||  |||||||||
                                TCCCT TGGTTTC  CTTTAATTA
                                  C      __
GAM1805  SIAT8C    5'  AGGGAAACCGGGGAAATC     44157          AAAGAA
                                AGGGAAATC      GAAGTT
                                |||||||||      ||||||
                                TCCCTTTGG      CTTTAG
                                     CCC___
GAM1805  TACTILE   3'  AGAGAGATCAAAGAAGAAGCCA 44158       A
                                AGGGA ATCAAAGAAGAAGTTA
                                ||||| ||||||||||||||||
                                TCTCT TAGTTTCTTCTTCGGT
                                  C
GAM1805  UBE2G1    3'  AGGGAAATTAAATGGAAACTTT 44159         C  __   AAG
            TAAT                   AGGGAAAT AAA  GAAG   TTAAT
                                |||||||| |||  ||||  |||||
                                TCCCTTTA TTT  CTTT   AATTA
                                     A   AC    GAA
GAM1805  LOC131368 3'  AGGCAAATTGGAGAAAAAGT   44160     G    CAA
                                AGG AAAT   AGAAGAAGT
                                |||  ||||   |||||||||
                                TCC TTTA   TCTTTTTCA
                                  G    ACC
GAM1805  LOC144453 3'  AAGGAAATTGAAGAGAA     44161         CA    A
                                AGGGAAAT  AAGA GAA
                                ||||||||  |||| |||
                                TTCCTTTA  TTCT CTT
                                     AC    _
GAM1805  LOC144577 3'  AGGGAAACAGAGAGGCT     44162         CAA   A  A
                                AGGGAAAT   AGA GA GTT
                                ||||||||   ||| || |||
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                                TCCCTTTG   TCT CT CGA
                                    ___   _  C
GAM1805  LOC148545 5'  AGGGAAGTTGAGAAAAAGTT   44163       ATCAA
                                AGGGAA    AGAAGAAGTT
                                ||||||    ||||||||||
                                TCCCTT    TCTTTTTCAA
                                   CAAC_
GAM1805  LOC149703 3'  AGGGAAATTCAAGAGAA     44164        CA   A
                                AGGGAAAT  AAGA GAA
                                ||||||||  |||| |||
                                TCCCTTTA  TTCT CTT
                                    AG   _
GAM1805  LOC158187 3'  GGGAAGGGAAGGAGAAGTTAAT 44165       ATCA  A
                                GGGAA   AAG AGAAGTTAAT
                                |||||   ||| ||||||||||
                                CCCTT   TTC TCTTCAATTA
                                   CCC_  C
GAM1805  LOC201562 3'  GGAAATTAACATAGGAAGTTAA 44166       C  AGAA_
           T                     GGAAAT AA    GAAGTTAAT
                                ||||||| ||    |||||||||
                                CCTTTA TT    CTTCAATTA
                                   A  GTATC
GAM1805  LOC206372 3'  AGGGAAGCAGGGAAGAAAT   44167       AT  AA
                                AGGGAA  CA  GAAGAAGT
                                ||||||  ||  ||||||||
                                TCCCTT  GT  CTTCTTTA
                                   C_  CC
GAM1805  LOC221399 5'  GGGGATCAGGGAAGAAGT    44168     AA   AA
                                GGG  ATCA  GAAGAAGT
                                |||  ||||  ||||||||
                                CCC  TAGT  CTTCTTCA
                                  C_   CC
GAM1805  LOC256756 5'  AGGTAAATCGAAGAAGAA    44169     G    A
                                AGG AAATC AAGAAGAA
                                ||| ||||| ||||||||
                                TCC TTTAG TTCTTCTT
                                  A    C
GAM1805  LOC51003  3'  AGGGAAATCAAAGAACAA    44170            G
                                AGGGAAATCAAAGAA AA
                                |||||||||||||| ||
                                TCCCTTTAGTTTCTT TT
                                         G
GAM1805  LOC56965  3'  GGTGAAGTCAAAGGGAAAGT   44171    _  A     AA
                                GG GAA TCAAAG  GAAGT
                                || ||| ||||||  |||||
                                CC CTT AGTTTC  TTTCA
                                 A  C     CC
GAM1805  LOC56965  3'  GGTGAAGTCAAAGGGAAAGT   44171    _  A     AA
                                GG GAA TCAAAG  GAAGT
                                || ||| ||||||  |||||
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                                CC CTT AGTTTC  TTTCA
                                 A  C     CC
GAM1806 KCNA5    3'  TCTCTTGGGATCTGGGCTATT  44174     CCA      _
                                TTTC   GGATCTGG TTATT
                                ||||   |||||||| |||||
                                AGAG   CCTAGACC GATAA
                                  AAC       C
GAM1806 RASD1    5'  TCTCCCAGGATCTGGGCAC   44175           T
                                TTTCCCAGGATCTGG TAT
                                |||||||||||||| |||
                                AGAGGGTCCTAGACC GTG
                                          C
GAM1806 SERPINE1 3'  TCTCCCAGGGTCTCAGGT   44176        A  __
                                TTTCCCAGG TCT  GGT
                                ||||||||| |||  |||
                                AGAGGGTCC AGA  CCA
                                      C  GT
GAM1806 SLC19A2  3'  TCCTAGGATAAATTATTAAAA  44177    C    CT
                                TCC AGGAT  GGTTATTAAAA
                                ||| |||||  ||||||||||
                                AGG TCCTA  TTAATAATTTT
                                 A    T_
GAM1806 CDW92    3'  TTTCCCAGATCTTGCTA     44178       G   G
                                TTTCCCAG ATCT GTTA
                                |||||||| |||| ||||
                                AAAGGGTC TAGA CGAT
                                     _   A
GAM1806 FLJ10916 3'  CTTCCTGGGATCTGAAGCCTAA 44179      CA      TTA
            A                    TTTCC  GGATCTGG   TTAAA
                                |||||  ||||||||   |||||
                                GAAGG  CCTAGACT   GATTT
                                  AC       TCG
GAM1806 FLJ11800 3'  CCAAAGGTTATTAAAA     44180      ATCT
                                CCAGG   GGTTATTAAAA
                                |||||   ||||||||||
                                GGTTT   CCAATAATTTT
                                  ____
GAM1806 KIAA0852 5'  TTTCCCAGGATTCTGTCCAGTA 44181         _  GT  T
            AA                   TTTCCCAGGAT CTG  TA TAAA
                                ||||||||||| |||  || ||||
                                AAAGGGTCCTA GAC  GT ATTT
                                      A  AG  C
GAM1806 KIAA1005 3'  TTTCGAGGATCTGGTTACC   44182     CC
                                TTTC  AGGATCTGGTTATT
                                ||||  ||||||||||||||
                                AAAG  TCCTAGACCAATGG
                                  C_
GAM1806 LATS1    3'  TTTCCTAATGGGTTATTAAAA  44183      C  GATCT
                                TTTCC AG    GGTTATTAAAA
                                ||||| ||    ||||||||||
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                                AAAGG TT    CCAATAATTTT
                                  A  AC___
GAM1806  MAD4     3'  TCTCCTGGGATCCAGGGTT   44184      CA     __
                                TTTCC  GGATCT  GGTT
                                |||||  ||||||  ||||
                                AGAGG  CCTAGG  CCAA
                                  AC     TC
GAM1806  SPINLW1   3'  TTTCCCAGGGTTAGTTTCTA   44185        ATC    A
                                TTTCCCAGG   TGGTT TTA
                                |||||||||   ||||| |||
                                AAAGGGTCC   ATCAA GAT
                                     CA_    A
GAM1806  LOC152926 3'  TTCCTTGGTACAGTTATTAAAA 44186     CA  ATC
                                TTCC  GG   TGGTTATTAAAA
                                ||||  ||   ||||||||||||
                                AAGG  CC   GTCAATAATTTT
                                  AA  AT_
GAM1806  LOC220549 5'  TTCCCGAATCCTGGTTATTAA  44187      A    _
                                TTCCC GGATC TGGTTATTAA
                                ||||| ||||| ||||||||||
                                AAGGG CTTAG ACCAATAATT
                                  _    G
GAM1806  LOC220575 3'  CCAAAGGTTATTAAAA      44180      ATCT
                                CCAGG    GGTTATTAAAA
                                |||||    ||||||||||||
                                GGTTT    CCAATAATTTT
                                  _____
GAM1806  LOC254249 5'  TTTCCCAGGACTGACTGG    44188          ___
                                TTTCCCAGGAT   CTGG
                                ||||||||||   ||||
                                AAAGGGTCCTG   GACC
                                     ACT
GAM1806  LOC254635 3'  TTTCCCAAGATTAAATGATTAT 44189          C___
           TAAAA                  TTTCCCAGGAT    TGGTTATTAAAA
                                |||||||||||    ||||||||||||
                                AAAGGGTTCTA    ACTAATAATTTT
                                     ATTT
GAM1806  LOC51605  3'  TTTCCCAGGTTGTCAACTATTA 44190        ATC_ GG
           AAA                    TTTCCCAGG    T  TTATTAAAA
                                |||||||||    |  |||||||||
                                AAAGGGTCC    G  GATAATTTT
                                     AACA TT
GAM1807  LOC90110  5'  TACTGGTATGATTTTATACAGC 44193        A   _____
                                TATTGGTAT ATTT    CAGT
                                ||||||||| ||||    ||||
                                ATGACCATA TAAA    GTCG
                                     C    ATAT
GAM1808  CACNA2D2  3'  TGGAGGACACTGGTGGCTAG   44196        _   ATCACG   A
                                TGGAGGAC CTG     GGC AG
                                |||||||| |||     ||| ||
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                                ACCTCCTG GAC     CCG TC
                                    T  CA____  A
GAM1808 CSF3    3' TGGGAGACCTGATACTCTCAAG 44197    AG      C GGG
                                TGG GACCTGAT AC  CAAG
                                ||| |||||||| ||  ||||
                                ACC CTGGACTA TG  GTTC
                                  CT      _ AGA
GAM1808 IL16    5' TGGAGGACTTGGTCTGTGGGC 44198       C A AC_
                                TGGAGGAC TG TC  GGGC
                                |||||||| || ||  ||||
                                ACCTCCTG AC AG  CCCG
                                    A C ACA
GAM1808 NR1H2   3' TGGAAGACTCGCTGGGCA   44199       C ATCAC
                                TGGAGGAC TG    GGGCA
                                |||||||| ||    |||||
                                ACCTTCTG GC    CCCGT
                                    A GA___
GAM1808 OAT     3' TGAAGGACTTGATTTAGAGG  44200       C   CAC_
                                TGGAGGAC TGAT   GGG
                                |||||||| ||||   |||
                                ACTTCCTG ACTA   TCC
                                    A   AATC
GAM1808 PDGFB   5' GGAGGACCTGGGCGCAG    44201        ATCAC _ A
                                GGAGGACCTG    GG GCA G
                                ||||||||||    || ||| |
                                CCTCCTGGAC    CC CGT C
                                    _____ G  C
GAM1808 PDGFB   3' GGAGGGGTGCGGGCAAG    44202     ACC ATCA
                                GGAGG  TG   CGGGCAAG
                                |||||  ||   ||||||||
                                CCTCC  AC   GCCCGTTC
                                  CC_ ____
GAM1808 SCNN1A  3' TGGAGCATACATAAACGGGCAA 44203     G__ C  TC
            GA                    TGGAG  AC TGA  ACGGGCAAGA
                                |||||  || |||  ||||||||||
                                ACCTC  TG ATT  TGCCCGTTCT
                                  GTA  T  __
GAM1808 TSNAX   5' TGAAGGACCTGGAGCAAG   44204        ATCAC
                                TGGAGGACCTG    GGGCAAG
                                ||||||||||    |||||||
                                ACTTCCTGGAC    CTCGTTC
                                    _____
GAM1808 TXNIP   3' TGGAGGTTCTGATCACAGG  44205      AC
                                TGGAGG  CTGATCACGGG
                                ||||||  ||||||||||
                                ACCTCC  GACTAGTGTCC
                                   AA
GAM1808 ABHD2   3' TGGGAGACCTGAAACAGG   44206    AG     TC
                                TGG  GACCTGA  ACGGG
                                |||  |||||||  |||||
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                                ACC  CTGGACT  TGTCC
                                  CT      T_
GAM1808 AKR1D1   5' TGGAGAACCTGACTGTAGG   44207          CAC
                                TGGAGGACCTGAT   GGG
                                ||||||||||||   |||
                                ACCTCTTGGACTG   TCC
                                     ACA
GAM1808 DDR2     3' GGAGGACCTGAGCCGTAGG   44208         _ AC
                                GGAGGACCTGA TC  GGG
                                |||||||||| ||  |||
                                CCTCCTGGACT GG  TCC
                                      C  CA
GAM1808 DKFZP586B2420 3' TGGAGGACCAGAGCAGGG    44209        T  T  C
                                TGGAGGACC GA CA GGG
                                ||||||||| || || |||
                                ACCTCCTGG CT GT CCC
                                     T  C  _
GAM1808 FLJ21742  3' TGGGGCACCTGATCATCAGG   44210     A  _       _
                                TGG GG ACCTGATCA CGGG
                                ||| || ||||||||| ||||
                                ACC CC TGGACTAGT GTCC
                                  _ G        A
GAM1808 FOXN4    3' TGGAGAGTCTGGAGCAAG    44211       AC   ATCAC
                                TGGAGG  CTG    GGGCAAG
                                ||||||  |||    |||||||
                                ACCTCT  GAC    CTCGTTC
                                   CA  ______
GAM1808 KIAA0182 3' TGGGGAGACAGTGGGCAAG   44212    A   CCT   CAC
                                TGG GGA   GAT   GGGCAAG
                                ||| |||   |||   |||||||
                                ACC CCT   CTG   CCCGTTC
                                  _  ___   TCA
GAM1808 MGC1842  3' TGGAGGACCTGGAGGGC     44213         ATCAC
                                TGGAGGACCTG    GGGC
                                ||||||||||    ||||
                                ACCTCCTGGAC    CCCG
                                      CT___
GAM1808 NAV1     5' TGGAGGACTTGATGGAGG    44214        C    CAC
                                TGGAGGAC TGAT   GGG
                                |||||||| ||||   |||
                                ACCTCCTG ACTA   TCC
                                     A   CC_
GAM1808 PDEF     5' TGGAGGACTGGGTCTGTGGG  44215        C  A_  AC_
                                TGGAGGAC TG  TC   GGG
                                |||||||| ||  ||   |||
                                ACCTCCTG AC  AG   CCC
                                     _ CC  ACA
GAM1808 SKIP     3' TGGCAGGACTACTTGGGCAAGA 44216     _    C  ATCAC
                                TGG AGGAC TG    GGGCAAGA
                                ||| ||||| ||    ||||||||
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                                ACC TCCTG AT    CCCGTTCT
                                  G    _ GAA__
GAM1808  SKIP     3'  TGGCAGGACTACTTGGGCAAGA 44216    _    C  ATCAC
                                TGG AGGAC TG    GGGCAAGA
                                ||| ||||| ||    ||||||||
                                ACC TCCTG AT    CCCGTTCT
                                  G    _ GAA__
GAM1808  LOC120425 3'  GGAGGGTCTGATCCAACGGG   44217      AC     __
                                GGAGG  CTGATC  ACGGG
                                |||||  ||||||  |||||
                                CCTCC  GACTAG  TGCCC
                                   CA     GT
GAM1808  LOC146315 5'  TGGAGACCTGATGCTGGG    44218      G      CAC
                                TGGAG ACCTGAT   GGG
                                ||||| |||||||   |||
                                ACCTC TGGACTA   CCC
                                   _      CGA
GAM1808  LOC152084 5'  TGGAGGACCGGGTCATCCCAGG 44219         TG___   A
                                TGGAGGACC     ATC CGGG
                                |||||||||     ||| ||||
                                ACCTCCTGG     TAG GTCC
                                      CCCAG   G
GAM1808  LOC152739 5'  TGGAGTACCTGATCCCACAAG  44220      G       ACGG
                                TGGAG ACCTGATC    GCAAG
                                ||||| ||||||||    |||||
                                ACCTC TGGACTAG    TGTTC
                                   A       GG__
GAM1808  LOC196549 3'  TGGAGGACTTGGCCACCAGC   44221        C  AT   G
                                TGGAGGAC TG  CAC GGC
                                |||||||| ||  ||| |||
                                ACCTCCTG AC  GTG TCG
                                     A  CG   G
GAM1808  LOC205398 5'  TGAAGGACCTGGCCAGCAAG   44222          AT  CGG
                                TGGAGGACCTG  CA   GCAAG
                                ||||||||||  ||   |||||
                                ACTTCCTGGAC  GT   CGTTC
                                      CG  ___
GAM1808  LOC51308  3'  TGGGGACCCTGGGCAA      44223     A     GATCAC
                                TGG GGACCT     GGGCAA
                                ||| ||||||     ||||||
                                ACC CCTGGG     CCCGTT
                                  _     A_____
GAM1808  LOC55924  3'  TGGGGAACCTGATGCTCCAGG  44224     A       CA__
                                TGG GGACCTGAT    CGGG
                                ||| |||||||||    ||||
                                ACC CTTGGACTA    GTCC
                                  C        CGAG
GAM1809  EPO      3'  ATTGCTGGCACTGGA       44227            CCC
                                ATTGCTGGTACT   GGA
                                ||||||||||||   |||
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                                TAACGACCGTGA  CCT
                                      ___
GAM1809 G6PD    3' TGTTGCTGGTGACAAGGAA  44228   A     _ TCCC
                                TG TTGCTGGT AC   GGAA
                                || |||||||| ||   ||||
                                AC AACGACCA TG   CCTT
                                 _      C  TT__
GAM1809 GEMIN5  5' TGATTGCTGGGCCAATGGA  44229       TACT C__
                                TGATTGCTGG   CC  GGA
                                ||||||||||   ||  |||
                                ACTAACGACC   GG  CCT
                                      C___ TTA
GAM1809 DDX17   5' GATTACTGATTCCTGGGACAT 44230       AC  C A
                                GATTGCTGGT  TCC GG ACAT
                                ||||||||||  ||| || ||||
                                CTAATGACTA  AGG CC TGTA
                                      __  A  C
GAM1809 FADS3   3' TGGTTGCTGGTGCCCTGA   44231   A     ACT  G
                                TG TTGCTGGT  CCC GA
                                || ||||||||  ||| ||
                                AC AACGACCA  GGG CT
                                 C      C__  A
GAM1809 FLJ21562 5' TGATTGCTGGTACTACTTGA  44232         CCCG
                                TGATTGCTGGTACT   GA
                                ||||||||||||||   ||
                                ACTAACGACCATGA   CT
                                      TGAA
GAM1809 KIAA0153 3' GATGCTGTGCTCCCGGA    44233    T   GTA
                                GAT GCTG  CTCCCGGA
                                ||| ||||  ||||||||
                                CTA CGAC  GAGGGCCT
                                  _   AC_
GAM1809 KIAA0222 5' TGGATGCTGGTACTCTCAG   44234   AT       C
                                TG  TGCTGGTACTC CGG
                                ||  |||||||||| |||
                                AC  ACGACCATGAG GTC
                                 CT         A
GAM1809 KLF12   3' TGGATGCTGGTATTCTTAACAC 44235   AT     C  CCGG
                                TG  TGCTGGTA TC   AACAT
                                ||  |||||||| ||   |||||
                                AC  ACGACCAT AG   TTGTG
                                 CT      A  AA__
GAM1809 KLK7    3' CTGGTACTTTTGGAACAT    44236       CCC
                                CTGGTACT  GGAACAT
                                ||||||||  |||||||
                                GACCATGA  CCTTGTA
                                     AAA
GAM1809 KLK7    3' CTGGTACTTTTGGAACAT    44236       CCC
                                CTGGTACT  GGAACAT
                                ||||||||  |||||||
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                                GACCATGA   CCTTGTA
                                    AAA
GAM1809  LOC144558 3'  TGATAGCTTCTGCCCGGAACAT 44237     T   GGTACT
                                TGAT GCT     CCCGGAACAT
                                |||| |||     ||||||||||
                                ACTA CGA     GGGCCTTGTA
                                  T   AGAC__
GAM1809  LOC151816 5'  TGGTTGTGGTACTCCTGGA    44238    A   C       C
                                TG TTG TGGTACTCC GGA
                                || ||| ||||||||| |||
                                AC AAC ACCATGAGG CCT
                                 C   _       A
GAM1809  LOC157278 3'  TGATAGCTTCTGCCCGGAACAT 44237     T   GGTACT
                                TGAT GCT     CCCGGAACAT
                                |||| |||     ||||||||||
                                ACTA CGA     GGGCCTTGTA
                                  T   AGAC__
GAM1809  LOC255461 5'  TGATAGCTTCTGCCCGGAACAT 44237     T   GGTACT
                                TGAT GCT     CCCGGAACAT
                                |||| |||     ||||||||||
                                ACTA CGA     GGGCCTTGTA
                                  T   AGAC__
GAM1809  LOC255516 5'  TGATAGCTTCTGCCCGGAACAT 44237     T   GGTACT
                                TGAT GCT     CCCGGAACAT
                                |||| |||     ||||||||||
                                ACTA CGA     GGGCCTTGTA
                                  T   AGAC__
GAM1809  LOC257068 3'  TGATTGCTGGACTCCTGG    44239        T    C
                                TGATTGCTGG ACTCC GG
                                |||||||||| ||||| ||
                                ACTAACGACC TGAGG CC
                                      _    A
GAM1810  BTAF1     3'  AAACCTATTGAGTACATATGTT 44242       A_   T
                                AAACCTAT  AGT ACATGTGTT
                                ||||||||  ||| |||||||||
                                TTTGGATA  TCA TGTATACAA
                                    AC   _
GAM1810  KIAA1240  3'  TAAAACCCAAACTACATGTGTT 44243        TAAG
                                TAAAACCTA    TTACATGTGTT
                                |||||||||    ||||||||||||
                                ATTTTGGGT    GATGTACACAA
                                     TT__
GAM1810  PPP1R15B  3'  TAAGCCCTATAAGTATTGT    44244     AA       TACA
                                TAA  CCTATAAGT    TGT
                                |||  |||||||||    |||
                                ATT  GGATATTCA    ACA
                                  CG        TA__
GAM1810  LOC151473 3'  TAAAACATACAACATGTGT    44245       C    AGTT
                                TAAAAC TATA    ACATGTGT
                                |||||| ||||    ||||||||
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                                ATTTTG ATGT    TGTACACA
                                   T  ____
GAM1810  LOC155438 3'  AAACCTATAATCGTGTGTT    44246          GTTACA
                                AAACCTATAA     TGTGTT
                                ||||||||||     ||||||
                                TTTGGATATT     ACACAA
                                    AGC___
GAM1810  LOC93538  3'  TAAAACTTAGAGTTACATGCAG 44247       CTATA       _
           TT                    TAAAAC     AGTTACATGT GTT
                                ||||||     |||||||||| |||
                                ATTTTG     TCAATGTACG CAA
                                   AATC_         T
GAM1811  CDH6      3'  TACAAAGGCAAACTTTCGCATG 44250       ATAC    C
           T                     TACAAA    AACT TTCGCATGT
                                ||||||    |||| |||||||||
                                ATGTTT    TTGA AAGCGTACA
                                   CCGT    _
GAM1811  PPP3CA    3'  TACAAATGCAACTCTTTTCTGT 44251       ATA       CGCA
                                TACAAA   CAACTCTT    TGT
                                ||||||   ||||||||    |||
                                ATGTTT   GTTGAGAA    ACA
                                   AC_       AAG_
GAM1811  PUM1      3'  CAAAATACAGTTCATCTTCTGT 44252         AC  T  GCA
                                CAAAATACA  TC TC   TGT
                                |||||||||  || ||   |||
                                GTTTTATGT  AG AG   ACA
                                     CA  T  AAG
GAM1811  RAD51C    3'  TACAAAATACTACTTTCATAAT 44253          A   C    C___
           ATGT                    TACAAAATAC ACT TTCG    ATGT
                                ||||||||||| ||| ||||    ||||
                                ATGTTTTATG TGA AAGT    TACA
                                     A   _    ATTA
GAM1811  SRGAP1    3'  TACAAAATACAAATGCCCG    44254          CTC
                                TACAAAATACAA   TTCG
                                ||||||||||||   ||||
                                ATGTTTTATGTT   GGGC
                                       TAC
GAM1811  TGFBR1    3'  TACAAAATACAATTGCATG    44255          CTC  C
                                TACAAAATACAA   TT GCATG
                                ||||||||||||   || |||||
                                ATGTTTTATGTT   AA CGTAC
                                      ___  _
GAM1811  WEE1      3'  CAAAATACAGCTTTCAACTGT  44256         A  C    CA
                                CAAAATACA CT TTCG  TGT
                                |||||||||  || ||||  |||
                                GTTTTATGT  GA AAGT  ACA
                                     C  _    TG
GAM1811  EDG1      3'  ACAAAATACAACCAT       44257           TCTTCG
                                ACAAAATACAAC      CAT
                                ||||||||||||      |||
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                                TGTTTTATGTTG     GTA
                                           ______
GAM1811 KIAA1817 3' AAAATACAGCTCTGCTGT    44258        A   TC  A
                                AAAATACA CTCT  GC TGT
                                |||||||| ||||  || |||
                                TTTTATGT GAGA  CG ACA
                                    C   __ _
GAM1811 LOC168537 3' CAAAATACAATTCATCCAT   44259         C  T  G
                                CAAAATACAA TC TC CAT
                                |||||||||| || || |||
                                GTTTTATGTT AG AG GTA
                                     A  T  _
GAM1811 LOC199678 3' AAATACAACTGATCTATGT   44260         CT  GC
                                AAATACAACT  TC  ATGT
                                ||||||||||  ||  ||||
                                TTTATGTTGA  AG  TACA
                                     CT  A_
GAM1811 LOC51320  3' TACGAAATGTAACTCTTCA   44261     A   AC
                                TAC AAAT  AACTCTTCG
                                ||| ||||  |||||||||
                                ATG TTTA  TTGAGAAGT
                                  C   CA
GAM1812 ATP7A    3' CTTTGCTTCTGGTAATGG    44264    A     ACGAA
                                CT TGCTTT    GGTAATGG
                                || ||||||    ||||||||
                                GA ACGAAG    CCATTACC
                                 A     A____
GAM1812 TBXA2R   5' CATGCTTTACAAAATGG     44265          GGTA
                                TATGCTTTACGAA    ATGG
                                ||||||||||||    ||||
                                GTACGAAATGTTT    TACC
                                           ____
GAM1812 CECR7    3' CATGTTTTACAACAATGG    44266     C      AGG
                                TATG TTTACGA   TAATGG
                                |||| |||||||   ||||||
                                GTAC AAATGTT   GTTACC
                                  A      ___
GAM1812 DKFZP434P0721 3' ACTGTGCTCTAAATAATGG   44267     A      CGAA
                                ACT TGCTTTA    GGTAATGG
                                ||| |||||||    ||||||||
                                TGA ACGAGAT    TTATTACC
                                  C      ____
GAM1812 FLJ14735 3' GCTTCTAAAAGGTAATGG    44268      AC
                                GCTTT  GAAGGTAATGG
                                |||||  ||||||||||
                                CGAAG  TTTCCATTACC
                                   AT
GAM1812 KIAA0630 3' ACTATGTTTTACACAATGGA  44269       C     AAGG
                                ACTATG TTTACG    TAATGGA
                                |||||| ||||||    |||||||
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                                TGATAC AAATGT   GTTACCT
                                  A    ____
GAM1812 RAB4B    3' ACAATGCTTTATGGGGGTAGGG 44270   T     CGAA   A__
            TGG                  AC ATGCTTTA   GGTA  TGG
                                || ||||||||   ||||  |||
                                TG TACGAAAT   CCAT  ACC
                                 T      ACCC   CCC
GAM1812 LOC153910 3' TATGCCTTTGTTAGGTGGA   44271       ACGA   AAT
                                TATGCTTT   AGGT  GGA
                                ||||||||   ||||  |||
                                ATACGGAA   TCCA  CCT
                                    ACAA   ___
GAM1812 LOC158364 5' ACTATGCTTTGGACATGG    44272        ACGAA  TA
                                ACTATGCTTT    GG  ATGG
                                ||||||||||    ||  ||||
                                TGATACGAAA    CC  TACC
                                      _____ TG
GAM1813 C14orf1  3' TTACAAAAGTTGTTACACAA  44275       GCCCAGGG
                                TTACAAAAG      ACACAA
                                |||||||||      ||||||
                                AATGTTTTC      TGTGTT
                                     AACAA___
GAM1813 CREBBP   3' TACAAAAGGTCCAAGAACA   44028       C
                                TACAAAAGG CCAGGGACA
                                ||||||||| |||||||||
                                ATGTTTTCC GGTTCTTGT
                                     A
GAM1813 EFNB1    3' TACAAAGGTGGGCACA     44276      A  CCCA   A
                                TACAAA GG   GGG CACA
                                |||||| ||   ||| ||||
                                ATGTTT CC   CCC GTGT
                                   _  A___   _
GAM1813 EPHA2    3' AAAGGCCCAGGAAAGCAA   44277         CA
                                AAAGGCCCAGGGA  CAA
                                ||||||||||||  |||
                                TTTCCGGGTCCTT  GTT
                                       TC
GAM1813 HGF      3' CTACAATTTAGGGACACA   44278      AAGGCCC
                                TTACAA      AGGGACACA
                                ||||||      |||||||||
                                GATGTT      TCCCTGTGT
                                   AAA____
GAM1813 MTMR8    3' CAAAAGGCTCAGGTCAACA   44279       C   GAC
                                CAAAAGGC CAGG   ACA
                                |||||||| ||||   |||
                                GTTTTCCG GTCC   TGT
                                     A   AGT
GAM1813 ODF2     3' AAAAGGCCAAATGGACACAA  44280       CAG_
                                AAAAGGCC   GGACACAA
                                ||||||||   ||||||||
```

```
                                TTTTCCGG   CCTGTGTT
                                    TTTA
GAM1813  RNF6     3'  TTACAAAAAGGCTGAACACAA  44281        _  CCAG
                                TTACAAAA GGC   GGACACAA
                                |||||||| |||   ||||||||
                                AATGTTTT CCG   CTTGTGTT
                                    T  A___
GAM1813  SHC1     3'  TACAAGAGGCCCAAATTCA   44039      A       GA
                                TACAA AGGCCCAGG  CA
                                ||||| |||||||||  ||
                                ATGTT TCCGGGTTT  GT
                                   C       AA
GAM1813  SIX2     3'  TACGGAGGGACCAGGACACA  44040    AAAA  C    G
                                TAC   GG CCAGG ACACA
                                |||   || ||||| |||||
                                ATG   CC GGTCC TGTGT
                                  CCTC  T    _
GAM1813  SLC2A6   3'  TTACAAAAGGGTGAACACA   44282        CCCAG
                                TTACAAAAGG    GGACACA
                                ||||||||||    |||||||
                                AATGTTTTCC    CTTGTGT
                                     CA___
GAM1813  STAU2    3'  AAAAGGCCTTAGCAATGCAA  44283       C_  G  CA
                                AAAAGGCC  AG GA  CAA
                                ||||||||  || ||  |||
                                TTTTCCGG  TC TT  GTT
                                    AA  G  AC
GAM1813  CHST3    3'  TTACGGGGTGCCGAAGGACAC  44284     AAAAG   C
                                TTAC    GCC AGGGACAC
                                ||||    ||| ||||||||
                                AATG    CGG TTCCTGTG
                                  CCCCA   C
GAM1813  COL21A1  3'  TTACAAAAGCATTAAGCACAA  44285       G CCA   A
                                TTACAAAAG C   GGG CACAA
                                ||||||||| |   ||| |||||
                                AATGTTTTC G   TTC GTGTT
                                     _ TAA   _
GAM1813  CXorf1   3'  TTACAAAAGTTCAATTTACAC  44286       GCC   GG_
                                TTACAAAAG   CAG   ACAC
                                |||||||||   |||   ||||
                                AATGTTTTC   GTT   TGTG
                                     AA_   AAA
GAM1813  DKFZP564G2022 3'  TTACAGAAAGTTCAGGAACA   44287      A   CC
                                TTACA AAGG  CAGGGACA
                                ||||| ||||  ||||||||
                                AATGT TTTC  GTCCTTGT
                                   C    AA
GAM1813  DKFZp761J139 5'  TTACAAAAGAGTGGGCCGGG   44288       _____   CA
                                TTACAAAA    GGCC  GGG
                                ||||||||    ||||  |||
```

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                              AATGTTTT    CCGG  CCC
                                  CTCAC   __
GAM1813 ESPL1    5' CAAAAGGCAAACACA      44289        CCAG
                              CAAAAGGC   GGACACA
                              ||||||||   |||||||
                              GTTTTCCG   TTTGTGT
                                     ____
GAM1813 FLJ20508 3' TTACAGATAGGCAAACACAA  44290     AA_   CCAG
                              TTACA  AGGC   GGACACAA
                              |||||  ||||   ||||||||
                              AATGT  TCCG   TTTGTGTT
                                 CTA  ____
GAM1813 FLJ20718 3' TCACAAAAGGCAAACA     44291         CCAG
                              TTACAAAAGGC   GGACA
                              ||||||||||   |||||
                              AGTGTTTTCCG   TTTGT
                                     ____
GAM1813 FLJ21820 3' TTACAGGAGACCCAGGTTCA  44292      AA       GA
                              TTACA  AGGCCCAGG  CA
                              |||||  |||||||||  ||
                              AATGT  TCTGGGTCC  GT
                                 CC       AA
GAM1813 FLJ25006 3' TTACAAAAAGGCTTACAAGATG 44293       _  CCA_   CA
          CA                   TTACAAAA GGC   GGGA  CA
                              ||||||||| |||   ||||  ||
                              AATGTTTT CCG   TTCT  GT
                                   T  AATG   AC
GAM1813 KIAA0825 3' ACAAAAGGCTCAGAATACA   44294        C   _
                              ACAAAAGGC CAGGG ACA
                              ||||||||| ||||| |||
                              TGTTTTCCG GTCTT TGT
                                   A   A
GAM1813 KIAA0914 3' TTACAAAATGCCTAAGTCA   44295       G  C  GA
                              TTACAAAA GCC AGG  CA
                              |||||||| ||| |||  ||
                              AATGTTTT CGG TTC  GT
                                   A  A  A_
GAM1813 KIAA0916 3' TTACAAAAAGGCAGTATACA  44296        CC  GG_
                              TTACAAAAGG  CAG   ACA
                              ||||||||||  |||   |||
                              AATGTTTTTC  GTC   TGT
                                   C_  ATA
GAM1813 MGC15438 5' CAGAAGGCAATAGGGACACA  44297   A   CC_
                              CA AAGGC   AGGGACACA
                              || |||||   |||||||||
                              GT TTCCG   TCCCTGTGT
                               C    TTA
GAM1813 MSTP031  3' TACAAAAGGAGATACA     44298        CCCAG  C
                              TACAAAAGG    GGA ACA
                              |||||||||    ||| |||
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                                ATGTTTTCC    TCT TGT
                                     _____  A
GAM1813  PAPSS2   3'  TACAGAAGAGGACACA     44299     A  GCCCA
                                TACA AAG    GGGACACA
                                |||| |||    ||||||||
                                ATGT TTC    TCCTGTGT
                                  C  _____
GAM1813  PRO0971  3'  TTACAAAAAGGCTAAGCACA  44300       _  CC  G
                                TTACAAAA GGC  AGG ACA
                                |||||||| |||  ||| |||
                                AATGTTTT CCG  TTC TGT
                                     T  A_  G
GAM1813  RGS7     3'  AAAAGGAAGAGACACA     44301      CCC
                                AAAAGG  AGGGACACA
                                ||||||  |||||||||
                                TTTTCC  TCTCTGTGT
                                   T__
GAM1813  SEMA5A   3'  TTACAAGAAGCCCAAAACA   44302      A      G
                                TTACAA AGGCCCAGG ACA
                                |||||| ||||||||| |||
                                AATGTT TTCGGGTTT TGT
                                   C       _
GAM1813  SMCR8    3'  TACAAAAAGCTGGGGACA    44303        CCA
                                TACAAAAGGC  GGGACA
                                ||||||||||  ||||||
                                ATGTTTTTCG  CCCTGT
                                      AC_
GAM1813  ZNF183   3'  CTACAAAGGAAGGACAC     44304      A  CCC
                                TTACAAA GG  AGGGACAC
                                ||||||| ||  ||||||||
                                GATGTTT CC  TTCCTGTG
                                     _ ___
GAM1813  ZNF387   3'  TTACAAAAGACCCAATTTACA  44305          GG_
                                TTACAAAAGGCCCAG  ACA
                                ||||||||||||||  |||
                                AATGTTTTCTGGGTT  TGT
                                        AAA
GAM1813  LOC122786 3'  TCACAAAAGAGGACA       44306       GCCCA
                                TTACAAAAG    GGGACA
                                |||||||||    ||||||
                                AGTGTTTTC    TCCTGT
                                     _____
GAM1813  LOC148918 5'  TTACAAAAGCAGATACA     44307       GCC  GG
                                TTACAAAAG  CAG  ACA
                                |||||||||  |||  |||
                                AATGTTTTC  GTC  TGT
                                     ___  TA
GAM1813  LOC149911 3'  CTACAAAAGGCTTGTTCCTAG  44308         _____  A
                                TTACAAAAGGC    CC GG
                                ||||||||||    || ||
```

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                                GATGTTTTCCG    GG TC
                                      AACAA  A
GAM1813  LOC151742 3'  TTACAAAGAGAGGACACA    44309       AG CCCA
                                TTACAAA  G   GGGACACA
                                |||||||  |   ||||||||
                                AATGTTT  C   TCCTGTGT
                                   CT ____
GAM1813  LOC157349 3'  TTAGAAAAGGCCTCCATGG   44310    C      __  G
                                TTA AAAAGGCC  CA GG
                                ||| ||||||||  || ||
                                AAT TTTTCCGG  GT CC
                                  C       AG  A
GAM1813  LOC199786 3'  TTACAAAAGCCTAAAGA     44311        G  C
                                TTACAAAAG CC AGGGA
                                ||||||||| || |||||
                                AATGTTTTC GG TTTCT
                                      _  A
GAM1813  LOC202986 5'  TCACAAAAGTTGAGGGACAC   44312       GCCC
                                TTACAAAAG   AGGGACAC
                                |||||||||   ||||||||
                                AGTGTTTTC   TCCCTGTG
                                     AAC_
GAM1813  LOC203414 3'  AAAAGGCCCAACGCACAA    44313         GGA
                                AAAAGGCCCAG   CACAA
                                ||||||||||   |||||
                                TTTTCCGGGTT   GTGTT
                                      GC_
GAM1813  LOC206338 5'  TTACAAAAAGTTTTTCCAGTGA 44314        C____   G
                                TTACAAAAGG    CCAG GA
                                ||||||||||    |||| ||
                                AATGTTTTTC    GGTC CT
                                      AAAAA   A
GAM1813  LOC219673 5'  TTACAAGAGACCCAGTTACA   44315      A      GG
                                TTACAA AGGCCCAG  ACA
                                ||||||  ||||||||  |||
                                AATGTT TCTGGGTC  TGT
                                   C       AA
GAM1813  LOC90231  3'  TTACAAAAGGTCCACTGG    44316        C  G_
                                TTACAAAAGG CCA  GG
                                |||||||||| |||  ||
                                AATGTTTTCC GGT  CC
                                      A   GA
GAM1813  LOC90591  3'  CTACAAAAGGATCTGATACAA  44317        CCCAGG  C
                                TTACAAAAGG     GA ACAA
                                ||||||||||     || ||||
                                GATGTTTTCC     CT TGTT
                                      TAGA__  A
GAM1814  ABCA1     3'  TCAAAGCAGGATGTTAGCC    44320       T__    AC
                                TCAAAGCG   TGTT  AGCC
                                ||||||||   ||||  ||||
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                                AGTTTCGT  ACAA  TCGG
                                    CCT   __
GAM1814 ACCN2   3' CCAAAGATCCTACAGCC    44321      C  G
                                TCAAAG GTT TTACAGCC
                                |||||| ||| ||||||||
                                GGTTTC TAG GATGTCGG
                                  _  _
GAM1814 ALDH3A2 3' TCACAGCCTGCTGCAGCC   44322    A  G   A
                                TCA AGC TTGTT CAGCC
                                ||| ||| ||||| |||||
                                AGT TCG GACGA GTCGG
                                  G  _    C
GAM1814 APXL    3' CAGAGCCCTCCACAGCC    44323    A  G  G
                                CA AGC TT TTACAGCC
                                || ||| || ||||||||
                                GT TCG GA GGTGTCGG
                                 C  G  _
GAM1814 BDP1    5' TCACGGCCGCTCACAGCC   44324    AAGC   _
                                TCA   GTTG TTACAGCC
                                |||   |||| ||||||||
                                AGT   CGGC AGTGTCGG
                                  GC__   G
GAM1814 COL9A1  5' CCAAAGCGTCCAGGCC     44325        GTTA  _
                                TCAAAGCGTT   CAG CC
                                ||||||||||   ||| ||
                                GGTTTCGCAG   GTC GG
                                     _____  C
GAM1814 DLST    3' TCAAACGTCAGCAGCC     44326     G    TTA
                                TCAAA CGTTG  CAGCC
                                ||||| |||||  |||||
                                AGTTT GCAGT  GTCGG
                                   _    C__
GAM1814 DMRT1   3' CAAATGTGTTACAGCC     44327     GC  T
                                CAAA  GT GTTACAGCC
                                ||||  || |||||||||
                                GTTT  CA CAATGTCGG
                                  A_  _
GAM1814 EDN1    5' TCAAAGCGATCCTTCAGCC  44328       _  G  A
                                TCAAAGCG TT TT CAGCC
                                |||||||| || || |||||
                                AGTTTCGC AG AA GTCGG
                                     T  G  _
GAM1814 HAS3    3' TCAAACGTTGTGAGCC     44329     G    TAC
                                TCAAA CGTTGT  AGCC
                                ||||| ||||||  ||||
                                AGTTT GCAACA  TCGG
                                   _    C__
GAM1814 HAS3    3' TCAAAACGCTGAGAACAGCC  44330         TT_
                                TCAAAGCGTTG  ACAGCC
                                ||||||||||  ||||||
```

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                                AGTTTTGCGAC   TGTCGG
                                      TCT
GAM1814  KIF3B    3'  TCAGAAGTGCCACAATACAGC  44331     _   C  TG __
                                TCA AAG GT  T  TACAGC
                                ||| ||| ||  |  ||||||
                                AGT TTC CG  G  ATGTCG
                                  C   A  GT TT
GAM1814  LHX4     3'  CCAAAGCACTGAGCAGCC    44332          TTA
                                TCAAAGCGTTG   CAGCC
                                ||||||||||   |||||
                                GGTTTCGTGAC   GTCGG
                                      TC_
GAM1814  MN1      5'  TCAGGACGCCGCCCGCAGCC  44333     AA       A_
                                TCA  GCGTTGTT  CAGCC
                                |||  ||||||||  |||||
                                AGT  TGCGGCGG  GTCGG
                                  CC       GC
GAM1814  PMX1     5'  CAGAGCGTTGTGCACCAGCC  44334    A       TA__
                                CA AGCGTTGT    CAGCC
                                || ||||||||    |||||
                                GT TCGCAACA    GTCGG
                                 C       CGTG
GAM1814  PMX1     5'  CAGAGCGTTGTGCACCAGCC  44334    A       TA__
                                CA AGCGTTGT    CAGCC
                                || ||||||||    |||||
                                GT TCGCAACA    GTCGG
                                 C       CGTG
GAM1814  PTP4A2   3'  TCAGAGTAACGCTACAGCC   44335     A  CGT
                                TCA AG   TGTTACAGCC
                                ||| ||   ||||||||||
                                AGT TC   GCGATGTCGG
                                  C  ATT
GAM1814  RAB7L1   3'  TCGAAGCATCACAGCC      44336    A   GTT
                                TC AAGC   GTTACAGCC
                                || ||||   |||||||||
                                AG TTCG   TAGTGTCGG
                                 C   ___
GAM1814  RNMT     3'  TCAAGTCTCCACAGCC      44337      AGC   G
                                TCAA   GTT TTACAGCC
                                ||||   ||| ||||||||
                                AGTT   CAG GGTGTCGG
                                   ___   A
GAM1814  SLC7A5   3'  TCAGGGCTGTGCCACAGGCC  44338     AA  GT      _
                                TCA  GC  TGTTACAG CC
                                |||  ||  |||||||| ||
                                AGT  CG  ACGGTGTC GG
                                  CC  AC       C
GAM1814  THBD     5'  TCATACATGTTACAGCC     44339     AA   T
                                TCA  GCGT GTTACAGCC
                                |||  |||| |||||||||
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                                AGT  TGTA CAATGTCGG
                                  A_   _
GAM1814  TNFRSF8   3'  CCAAAGCGTGCAGAGCC     44340         T  TAC
                                TCAAAGCGT GT   AGCC
                                |||||||||  ||   ||||
                                GGTTTCGCA CG   TCGG
                                      _  TC_
GAM1814  WNT5A     3'  TCACAGCGGGGCCACAGCC   44341     A    TT
                                TCA AGCG  GTTACAGCC
                                |||  ||||  |||||||||
                                AGT TCGC  CGGTGTCGG
                                  G    CC
GAM1814  ZNF239    5'  TCACAGCTCCGCACAGC     44342     A   G    T
                                TCA AGC TTGT ACAGC
                                |||  |||  ||||  |||||
                                AGT TCG GGCG TGTCG
                                  G   A    _
GAM1814  AD-020    3'  TCAAAGCATTAAACTGCC    44343          TT  A
                                TCAAAGCGTTG  AC GCC
                                ||||||||||  ||  |||
                                AGTTTCGTAAT  TG CGG
                                       T_  A
GAM1814  AD-020    3'  TCAAAGCATTAAACTGCC    44343          TT  A
                                TCAAAGCGTTG  AC GCC
                                ||||||||||  ||  |||
                                AGTTTCGTAAT  TG CGG
                                       T_  A
GAM1814  AKAP8     3'  TCAAGAGACATGTTACAGCC  44344      _  _   T
                                TCAA AG CGT GTTACAGCC
                                ||||  ||  |||  |||||||||
                                AGTT TC GTA CAATGTCGG
                                  C  T   _
GAM1814  BLP1      3'  TCCAAGCGTCAACAGC      44345     A       TT
                                TC AAGCGTTG  ACAGC
                                ||  ||||||||  |||||
                                AG TTCGCAGT  TGTCG
                                 G       __
GAM1814  DKFZp434N035 3'  CCAGAGCAGCGACAGCC     44346     A    TT  T
                                TCA AGCG  GT ACAGCC
                                |||  ||||  ||  ||||||
                                GGT TCGT  CG TGTCGG
                                  C    __  C
GAM1814  FLJ10619  3'  CAAAGGTGGAATTACAGCC   44347       C  T__
                                CAAAG GT   GTTACAGCC
                                |||||  ||   |||||||||
                                GTTTC CA   TAATGTCGG
                                   _  CCT
GAM1814  FLJ12132  3'  TCATAGCTCACTACAGCC    44349     A   G TG
                                TCA AGC T  TTACAGCC
                                |||  |||  |  ||||||||
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                                AGT TCG A  GATGTCGG
                                  A   _ GT
GAM1814  FLJ12132  3'  TCAAGCGACTCTTACAGCC   44348      A   _  G
                                TCAA GCG TT TTACAGCC
                                |||| ||| || ||||||||
                                AGTT CGC GA AATGTCGG
                                  _   T  G
GAM1814  FLJ12425  3'  CAAAGTGATCATTACAGCC   44350      C_  TG
                                CAAAG  GT  TTACAGCC
                                |||||  ||  ||||||||
                                GTTTC  TA  AATGTCGG
                                   AC  GT
GAM1814  FLJ12542  5'  CAAAGCGCCGCAGCC       44351          TTA
                                CAAAGCGTTG   CAGCC
                                ||||||||||   |||||
                                GTTTCGCGGC   GTCGG
                                             ____
GAM1814  FLJ14437  3'  TCAAAGCATTTCAAAGC     44352          G   C
                                TCAAAGCGTT TTA AGC
                                |||||||||| ||| |||
                                AGTTTCGTAA AGT TCG
                                      _   T
GAM1814  FLJ14442  3'  TCTAAGTATTCTACAGCC    44353    A   CG  G
                                TC AAG  TT TTACAGCC
                                || |||  || ||||||||
                                AG TTC  AA GATGTCGG
                                 A   AT  _
GAM1814  FLJ14957  3'  TCAAAACGCATAACAGCC    44354          TGTT
                                TCAAAGCGT    ACAGCC
                                |||||||||    ||||||
                                AGTTTTGCG    TGTCGG
                                     TAT_
GAM1814  FLJ22378  3'  TCAAAGCATCTCACAGGCC   44355          G     _
                                TCAAAGCGTT TTACAG CC
                                |||||||||| |||||| ||
                                AGTTTCGTAG AGTGTC GG
                                      _     C
GAM1814  FLJ22595  3'  TCAATACCTGTTACAGC     44356      A  G
                                TCAA GC TTGTTACAGC
                                |||| || ||||||||||
                                AGTT TG GACAATGTCG
                                  A  _
GAM1814  FLJ25012  3'  TCACAGCTCACTACAGCC    44357     A   G TG
                                TCA AGC T  TTACAGCC
                                ||| ||| |  ||||||||
                                AGT TCG A  GATGTCGG
                                  G   _ GT
GAM1814  GALNT12   3'  TCAAAGCAATGCAGCC      44358         T  TTA
                                TCAAAGCG TG   CAGCC
                                |||||||| ||   |||||
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                                AGTTTCGT AC   GTCGG
                                     T ___
GAM1814 HML2     5' TCTGAGGTTGTCACAGC     44359    AA  C
                                TC  AG GTTGTTACAGC
                                ||  || ||||||||||
                                AG  TC CAACAGTGTCG
                                 AC  _
GAM1814 HTATIP2  3' TCAAAGCAGGCCCCCCAGCC  44360        __  G  A
                                TCAAAGC  GTT TT CAGCC
                                |||||||  ||| || |||||
                                AGTTTCG  CGG GG GTCGG
                                    TC   G  _
GAM1814 JDD1     3' TCACAGCTTATTGCAGCC    44361     A   G    A
                                TCA AGC TTGTT CAGCC
                                ||| ||| ||||| |||||
                                AGT TCG AATAA GTCGG
                                  G  _    C
GAM1814 KIAA0748 3' CCAAAGCAAACTACAGC     44362        TTG
                                TCAAAGCG   TTACAGC
                                ||||||||   |||||||
                                GGTTTCGT   GATGTCG
                                     TT_
GAM1814 KIAA1006 3' TCAAAGCAGTCACAGC      44363        TT
                                TCAAAGCG  GTTACAGC
                                ||||||||  ||||||||
                                AGTTTCGT  CAGTGTCG
                                          __
GAM1814 KIAA1260 3' TCAAATGTCACAAGCC      44364      GCGT     _
                                TCAAA    TGTTACA GCC
                                |||||    ||||||| |||
                                AGTTT    ACAGTGT CGG
                                   _____      T
GAM1814 KIAA1340 3' TCAAAATGTCATCACAGC    44365       C  TG
                                TCAAAG GT  TTACAGC
                                |||||| ||  |||||||
                                AGTTTT CA  AGTGTCG
                                    A  GT
GAM1814 KIAA1348 3' CAAAGAGTCTACAGCC      44366      C   GT
                                CAAAG GTT  TACAGCC
                                ||||| |||  |||||||
                                GTTTC CAG  ATGTCGG
                                   T  __
GAM1814 KIAA1458 5' CCAAAGCGCCGCTGGCC     44367           ACA
                                TCAAAGCGTTGTT   GCC
                                ||||||||||||||  |||
                                GGTTTCGCGGCGA   CGG
                                        C__
GAM1814 KIAA1492 3' CAAAGCATCCATTATAGC    44368         _   C
                                CAAAGCGTT GTTA AGC
                                ||||||||| |||| |||
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                                GTTTCGTAG TAAT TCG
                                     G   A
GAM1814 KIAA1677 3' TCAAAACTGATTACAGC    44369      GTT
                                TCAAAGC  GTTACAGC
                                |||||||  ||||||||
                                AGTTTTG  TAATGTCG
                                   AC_
GAM1814 KIAA1701 5' CCAAAGCCACCACAGCC    44370      GT GT
                                TCAAAGC  T  TACAGCC
                                |||||||  |  |||||||
                                GGTTTCG  G  GTGTCGG
                                   __ TG
GAM1814 LIPG     3' TCAAAGCAGGCTGAGCAGC   44371      __   TTA
                                TCAAAGC  GTTG  CAGC
                                |||||||  ||||  ||||
                                AGTTTCG  CGAC  GTCG
                                   TC   TC_
GAM1814 MGC13090 3' CCAAAGCAGGCTGCAGCC   44372      TT   A
                                TCAAAGCG  GTT CAGCC
                                ||||||||  ||| |||||
                                GGTTTCGT  CGA GTCGG
                                    C_  C
GAM1814 MGC14859 3' TCAAAGCGGGGTCCAGCC   44373      TT   A
                                TCAAAGCG  GTT CAGCC
                                ||||||||  ||| |||||
                                AGTTTCGC  CAG GTCGG
                                    CC  _
GAM1814 MGC15631 3' TCACAGCTCCCTGCAGCC   44374    A  G  G  A
                                TCA AGC TT TT CAGCC
                                ||| ||| || || |||||
                                AGT TCG AG GA GTCGG
                                  G  _ G  C
GAM1814 MGC1842  5' CCAGAGCGGGCTACAGC    44375    A   TT
                                TCA AGCG  GTTACAGC
                                ||| ||||  ||||||||
                                GGT TCGC  CGATGTCG
                                  C   C_
GAM1814 MGC3178  3' TCAACAGCTGCCACAGCC   44376     AGC
                                TCAA  GTTGTTACAGCC
                                ||||  ||||||||||||
                                AGTT  CGACGGTGTCGG
                                  GT_
GAM1814 RPS6KB1  3' TCAAACGAGCCACAGC     44377     G  TT
                                TCAAA CG  GTTACAGC
                                ||||| ||  ||||||||
                                AGTTT GC  CGGTGTCG
                                   _ T_
GAM1814 SCDGF-B  3' TCAAAATTCTGTTACAGC   44378      CG
                                TCAAAG  TTGTTACAGC
                                ||||||  ||||||||||
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                                AGTTTT  GACAATGTCG
                                   AA
GAM1814  SCDGF-B   3'  TCAAAATTCTGTTACAGC    44378       CG
                                TCAAAG  TTGTTACAGC
                                ||||||  ||||||||||
                                AGTTTT  GACAATGTCG
                                   AA
GAM1814  STAM2     5'  TCAGGCGGCCGCTACGGCC   44379     AA  _      A
                                TCA  GCG TTGTTAC GCC
                                |||  ||| ||||||| |||
                                AGT  CGC GGCGATG CGG
                                  C_  C      C
GAM1814  TCEA3     3'  TCAAAGGCCCCCACAGCC    44380       C   G
                                TCAAAG GTT TTACAGCC
                                |||||| ||| ||||||||
                                AGTTTC CGG GGTGTCGG
                                   _  G
GAM1814  TRAF4     3'  CCAGGGCGGTGTTACAGC    44381     AA   T
                                TCA  GCG TGTTACAGC
                                |||  ||| |||||||||
                                GGT  CGC ACAATGTCG
                                  CC   C
GAM1814  TTTY13    3'  TCATAGCGGTCACAGC      44382     A    TT
                                TCA AGCG  GTTACAGC
                                ||| ||||  ||||||||
                                AGT TCGC  CAGTGTCG
                                  A   __
GAM1814  ZSIG11    5'  TCAAGGCAGCTCCACGGCC   44383     A  _  G   A
                                TCAA GC GTT TTAC GCC
                                |||| || ||| |||| |||
                                AGTT CG CGA GGTG CGG
                                  C  T   _    C
GAM1814  LOC118851 5'  TCAAACCAATCACAGC      44384       G  TT
                                TCAAA CG  GTTACAGC
                                ||||| ||  ||||||||
                                AGTTT GT  TAGTGTCG
                                   G  __
GAM1814  LOC129676 5'  TCAGGCACTGCTGCAGC     44385     AA       A
                                TCA  GCGTTGTT CAGC
                                |||  |||||||| ||||
                                AGT  CGTGACGA GTCG
                                  C_       C
GAM1814  LOC142827 3'  TCAAACTCCCACAGCC      44386       GCG  G
                                TCAAA   TT TTACAGCC
                                |||||   || ||||||||
                                AGTTT   GA GGTGTCGG
                                   ____  G
GAM1814  LOC144577 3'  TGAAGGTCTCCACAGCC     44387    A   C   G
                                C AAG GTT TTACAGCC
                                | ||| ||| ||||||||
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                                A TTC CAG GGTGTCGG
                                 C  _  A
GAM1814  LOC146819 3'  TCACGGTCAGCCACAGCC    44388     AAGC  _
                                TCA   GTT GTTACAGCC
                                |||   ||| |||||||||
                                AGT   CAG CGGTGTCGG
                                  GC__  T
GAM1814  LOC146821 3'  TCACGGTCAGCCACAGCC    44388     AAGC  _
                                TCA   GTT GTTACAGCC
                                |||   ||| |||||||||
                                AGT   CAG CGGTGTCGG
                                  GC__  T
GAM1814  LOC149073 5'  CCGAAGCGCCGCAGCC      44389    A       TTA
                                TC AAGCGTTG   CAGCC
                                || ||||||||   |||||
                                GG TTCGCGGC   GTCGG
                                 C       ____
GAM1814  LOC149654 5'  CCAAAGCGGCCACGGC      44390         TT    A
                                TCAAAGCG  GTTAC GC
                                ||||||||  ||||| ||
                                GGTTTCGC  CGGTG CG
                                     __    C
GAM1814  LOC151657 3'  TCAGAGGCAGACCACAGCC    44391     A  C  TG_
                                TCA AG GT   TTACAGCC
                                ||| || ||   ||||||||
                                AGT TC CG   GGTGTCGG
                                  C  _  TCT
GAM1814  LOC152687 5'  TCACACGTTTACAGCC      44392     AA    GT
                                TCA  GCGTT  TACAGCC
                                |||  |||||  |||||||
                                AGT  TGCAA  ATGTCGG
                                  G_    __
GAM1814  LOC153561 3'  TCACAGCTTACTGCAGCC    44393     A  G    A
                                TCA AGC TTGTT CAGCC
                                ||| ||| ||||| |||||
                                AGT TCG AATGA GTCGG
                                  G  _    C
GAM1814  LOC157918 3'  TGAAACAGTAGTTACAGC    44394    A   _  T
                                C AAGC GT GTTACAGC
                                | |||| || ||||||||
                                A TTTG CA CAATGTCG
                                 C   T  T
GAM1814  LOC157919 5'  TGAAACAGTAGTTACAGC    44394    A   _  T
                                C AAGC GT GTTACAGC
                                | |||| || ||||||||
                                A TTTG CA CAATGTCG
                                 C   T  T
GAM1814  LOC158293 3'  TCAAAGCAGTCCCTGTCAG   44395        _  G  A_
                                TCAAAGC GTT TT  CAG
                                ||||||| ||| ||  |||
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                                AGTTTCG CAG GA  GTC
                                    T   G  CA
GAM1814  LOC196528 3'  TCATAGCTCACTACAGCC    44349     A   G TG
                                TCA AGC T  TTACAGCC
                                ||| ||| |  ||||||||
                                AGT TCG A  GATGTCGG
                                  A  _ GT
GAM1814  LOC199848 5'  TCACAGCTCCTGCACAGCC    44397     A   G_    T
                                TCA AGC  TTGT ACAGCC
                                ||| |||  |||| ||||||
                                AGT TCG  GACG TGTCGG
                                  G   AG   _
GAM1814  LOC199848 5'  TCACAGCTCCCGCACAGCC    44396     A   G_    T
                                TCA AGC  TTGT ACAGCC
                                ||| |||  |||| ||||||
                                AGT TCG  GGCG TGTCGG
                                  G   AG   _
GAM1814  LOC199848 5'  TCACAGCTCCCGCACAGCC    44396     A   G_    T
                                TCA AGC  TTGT ACAGCC
                                ||| |||  |||| ||||||
                                AGT TCG  GGCG TGTCGG
                                  G   AG   _
GAM1814  LOC199858 3'  TCATGACAATTACAGCC      44398     AA   TT
                                TCA  GCG  GTTACAGCC
                                |||  |||  |||||||||
                                AGT  TGT  TAATGTCGG
                                  AC   __
GAM1814  LOC199883 3'  TCAAAGCAGTAGTTATGGC    44399        _ T    CA
                                TCAAAGC GT GTTA  GC
                                ||||||| || ||||  ||
                                AGTTTCG CA CAAT  CG
                                    T  T    AC
GAM1814  LOC199906 3'  TCAGAAGTCCCCACAGCC     44400     A  C   G
                                TCA AG GTT TTACAGCC
                                ||| || ||| ||||||||
                                AGT TT CAG GGTGTCGG
                                  C  _   G
GAM1814  LOC200020 3'  TCAAAGCAGTAGTTACGGC    44401        _ T    A
                                TCAAAGC GT GTTAC GC
                                ||||||| || ||||| ||
                                AGTTTCG CA CAATG CG
                                    T  T    C
GAM1814  LOC200301 5'  CAAAGATGTTACAGCC       44402       CGT
                                CAAAG   TGTTACAGCC
                                |||||   ||||||||||
                                GTTTC   ACAATGTCGG
                                   T__
GAM1814  LOC200470 5'  TCTGAGCGTCGCTCCAGC     44403     AA        A
                                TC  AGCGTTGTT CAGC
                                ||  ||||||||| ||||
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                                AG  TCGCAGCGA GTCG
                                 AC        G
GAM1814  LOC200473 3'  TCAGCAGCGGCTCACAGCC   44404     A_   TTG
                                TCA  AGCG   TTACAGCC
                                |||  ||||   ||||||||
                                AGT  TCGC   AGTGTCGG
                                  CG    CG_
GAM1814  LOC202134 3'  TCAAAGAGGTGCCACAGC    44405       CGT
                                TCAAAG   TGTTACAGC
                                ||||||   |||||||||
                                AGTTTC   ACGGTGTCG
                                    TCC
GAM1814  LOC204161 5'  CAGAGCAGCCACAGCC      44406    A    TT
                                CA AGCG  GTTACAGCC
                                || ||||  |||||||||
                                GT TCGT  CGGTGTCGG
                                 C   __
GAM1814  LOC221069 3'  TCAAACTGCTACGGCC      44407      GCG      A
                                TCAAA   TTGTTAC GCC
                                |||||   ||||||| |||
                                AGTTT   GACGATG CGG
                                   ___      C
GAM1814  LOC254122 3'  TCGAAGCGTTGGCAGCACAGC  44408    A       T___
                                TC AAGCGTTG    TACAGC
                                || ||||||||    ||||||
                                AG TTCGCAAC    GTGTCG
                                 C       CGTC
GAM1814  LOC257612 5'  TCAGGGCGCCCACAGCC     44409     AA     GT
                                TCA  GCGTT  TACAGCC
                                |||  |||||  |||||||
                                AGT  CGCGG  GTGTCGG
                                  CC    __
GAM1814  LOC51068  3'  TCAAAACGTAAGCCACAG    44410         T_
                                TCAAAGCGT  GTTACAG
                                |||||||||  |||||||
                                AGTTTTGCA  CGGTGTC
                                      TT
GAM1814  LOC91565  3'  TCAACAGCTCACCACAGC    44411      _   G TG
                                TCAA AGC T  TTACAGC
                                |||| ||| |  |||||||
                                AGTT TCG A  GGTGTCG
                                  G   _ GT
GAM1814  LOC96573  3'  CAAAGGCCTACAGCC       44412       C  TG
                                CAAAG GT  TTACAGCC
                                ||||| ||  ||||||||
                                GTTTC CG  GATGTCGG
                                   _  __
GAM1815  EYA1     3'  TTACATATAATACATTAGTG   44415            GGGG
                                TTACGTATAATATA    AGTG
                                ||||||||||||||    ||||
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                                AATGTATATTATGT   TCAC
                                      AA__
GAM1815 FUS1    3' TTACTGTAAGGGAGGGGGTG  44416     _  TAATAT    A
                                TTAC GTA     AGGGG GTG
                                |||| |||     ||||| |||
                                AATG CAT     TCCCC CAC
                                  A  TCCC__    _
GAM1815 WNT1    3' CGTATGAACCGCGGGGAGTG  44417      _  ATA
                                CGTAT AAT   GGGGAGTG
                                ||||| |||   ||||||||
                                GCATA TTG   CCCCTCAC
                                   C  GCG
GAM1815 DEFB118 3' AATTACATATTGGTGGGGGGTG 44418         AATATA   A
                                AATTACGTAT     GGGG GTG
                                ||||||||||     |||| |||
                                TTAATGTATA     CCCC CAC
                                      ACCAC_   _
GAM1816 ACATN   3' TGCCAACAATGTCAGACTA   44421        ___   A
                                TGTCAACA   TCA ACTA
                                ||||||||   ||| ||||
                                ACGGTTGT   AGT TGAT
                                     TAC   C
GAM1816 SH3BP4  3' GATTTGCCAGTATCAGTCCT  44422        AC    AA_
                                GATTTGTCA  ATCA   CT
                                |||||||||  ||||   ||
                                CTAAACGGT  TAGT   GA
                                      CA    CAG
GAM1816 LOC51026 3' CCATTTGTCAATATCATCCCA 44423   G       C    AA
                                C ATTTGTCAA ATCA  CTA
                                | |||||||||| ||||  |||
                                G TAAACAGTT TAGT  GGT
                                 G        A    AG
GAM1817 C18orf1 3' ATTATTTCTAGGGGCTTCCAA 44426         AATTA
                                ATTATTTCTA    TTCCAA
                                ||||||||||    ||||||
                                TAATAAAGAT    AAGGTT
                                      CCCCG
GAM1817 CYR61   3' ATCATTTACAAATTATTCCA  44427       C
                                ATTATTT TAAATTATTCCA
                                ||||||| ||||||||||||
                                TAGTAAA GTTTAATAAGGT
                                    T
GAM1817 TLL2    3' ATTATTTAAAAATTATTCCAA 44428       CT
                                ATTATTT  AAATTATTCCAA
                                |||||||  ||||||||||||
                                TAATAAA  TTTAATAAGGTT
                                    TT
GAM1817 ZNF215  3' AATTATTTACCCTGTTATTCCA 44429        _ AAA
                                GATTATTT CT   TTATTCCA
                                |||||||| ||   ||||||||
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                                TTAATAAA GG   AATAAGGT
                                    T  GAC
GAM1817  KIAA0794  3'  ACCATTATTTCTAACC     44430    G        ATTATT
                                AC ATTATTTCTAA     CC
                                || ||||||||||      ||
                                TG TAATAAAGATT     GG
                                 G         _______
GAM1817  RABEX5    3'  ACAATTATAAAATTATTCCAA  44431        TTCT
                                ACGATTAT    AAATTATTCCAA
                                ||||||||    ||||||||||||
                                TGTTAATA    TTTAATAAGGTT
                                    T___
GAM1817  LOC146820 3'  GATTGTTAGCAATTATTCCAA  44432     A  TCTA
                                GATT TT    AATTATTCCAA
                                |||| ||    ||||||||||
                                CTAA AA    TTAATAAGGTT
                                  C  TCG_
GAM1817  LOC200471 5'  GATTATTTCCTGATCTCCAA   44433         AA   AT
                                GATTATTTCT  ATT  TCCAA
                                ||||||||||  |||  |||||
                                CTAATAAAGG  TAG  AGGTT
                                     AC  __
GAM1818  INHBB     5'  GGTGCCCGGGAGAGCCG     44436      G    TC   G
                                GGTGCC CGGGG  GAG CCG
                                |||||| |||||  ||| |||
                                CCACGG GCCCT  CTC GGC
                                   _    __  _
GAM1818  IRTA2     3'  GGTGCTGTGGCCAAAGGCTGG  44437      CGCGG     _  C
                                GGTGC    GGTCGA GGC GG
                                |||||    |||||| ||| ||
                                CCACG    CCGGTT CCG CC
                                   ACA__     T   A
GAM1818  TNFSF9    3'  TCGGGAGGTCGAGGC      44438      TGCCGC
                                TCGG     GGGGTCGAGGC
                                ||||     ||||||||||
                                AGCC     CTCCAGCTCCG
                                  _______
GAM1818  KIAA0449  5'  GGTGCCGCGGGCATGGCTGG   44439          GT  A   C
                                GGTGCCGCGGG  CG GGC GG
                                ||||||||||  || ||| ||
                                CCACGGCGCCC  GT CCG CC
                                     __ A   A
GAM1818  OSBPL5    5'  TCGGTGCTCCGGGCCGGCCGG  44440       CG   G  GA
                                TCGGTGC  CGGG TC  GGCCGG
                                |||||||  |||| ||  ||||||
                                AGCCACG  GCCC GG  CCGGCC
                                    AG   _ __
GAM1818  PRDM12    3'  CCGGGCCGGGGGGTTGGGGCTGG 44441     T    C    CGA   C
                                TCGG GCCG GGGGT   GGC GG
                                |||| |||| |||||   ||| ||
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                                GGCC CGGC CCCCA   CCG CC
                                  _   _    ACC   A
GAM1818 LOC161931 3'  TCGGTCCCGCCGAGGCG    44442     G   GGGGT    C
                                TCGGT CCGC    CGAGGC G
                                ||||| ||||    |||||| |
                                AGCCA GGCG    GCTCCG C
                                  G   _____     A
GAM1819 AGTR1    3'  TCAATTCTGAAAAGTAGC    44445    T     TCATG  C
                                TC ATTCTGAA    GAG AGC
                                || ||||||||    ||| |||
                                AG TAAGACTT    TTC TCG
                                 T      _____  A
GAM1819 AGTR1    3'  TCAATTCTGAAAAGTAGC    44445    T     TCATG  C
                                TC ATTCTGAA    GAG AGC
                                || ||||||||    ||| |||
                                AG TAAGACTT    TTC TCG
                                 T      _____  A
GAM1819 AGTR1    3'  TCAATTCTGAAAAGTAGC    44445    T     TCATG  C
                                TC ATTCTGAA    GAG AGC
                                || ||||||||    ||| |||
                                AG TAAGACTT    TTC TCG
                                 T      _____  A
GAM1819 AGTR1    3'  TCAATTCTGAAAAGTAGC    44445    T     TCATG  C
                                TC ATTCTGAA    GAG AGC
                                || ||||||||    ||| |||
                                AG TAAGACTT    TTC TCG
                                 T      _____  A
GAM1819 AGTR1    3'  TCAATTCTGAAAAGTAGC    44445    T     TCATG  C
                                TC ATTCTGAA    GAG AGC
                                || ||||||||    ||| |||
                                AG TAAGACTT    TTC TCG
                                 T      _____  A
GAM1819 PRX      5'  TCAGTTCTGCATGGAGCAGCT  44446    TA    AAT
                                TC  TTCTG   CATGGAGCAGCT
                                ||  |||||   ||||||||||||
                                AG  AAGAC   GTACCTCGTCGA
                                 TC    ___
GAM1819 FLJ13449 3'  TCTGTCTGAAACAAGCAGC   44447    AT    T  TGG
                                TCT  TCTGAA CA   AGCAGC
                                |||  |||||| ||   ||||||
                                AGA  AGACTT GT   TCGTCG
                                  C_     T  ___
GAM1819 IMP-2    5'  TATTCTGAATCAACTTAGC   44448          TGG_
                                TATTCTGAATCA    AGC
                                ||||||||||||    |||
                                ATAAGACTTAGT    TCG
                                       TGAA
GAM1819 KIAA1026 3'  TCCATTCTGAAGGCAG     44449          ATCAT  A
                                TCTATTCTGA    GG GCAG
                                ||||||||||    || ||||
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                                AGGTAAGACT    TC CGTC
                                      _____ _
GAM1819 KIAA1321 3' TCTATGTTGAGTCCAACAGCT 44450      TC  A ATGGA
                                TCTAT  TGA TC    GCAGCT
                                ||||| ||| ||    ||||||
                                AGATA  ACT AG    TGTCGA
                                   CA  C GT___
GAM1819 KIAA1432 3' TATTCTGAACTAAGCAG    44451        CATG
                                TATTCTGAAT   GAGCAG
                                ||||||||||   ||||||
                                ATAAGACTTG   TTCGTC
                                      A___
GAM1819 PDCD6IP  3' TCTGATCTGAATCAGCTGAGC 44452    AT       TG_
                                TCT  TCTGAATCA   GAGC
                                |||  |||||||||   ||||
                                AGA  AGACTTAGT   CTCG
                                  CT       CGA
GAM1819 PRO2533  3' TATTCTGAAATAAGGAGTAGCT 44453        TCAT   C
                                TATTCTGAA    GGAG AGCT
                                |||||||||    |||| ||||
                                ATAAGACTT    CCTC TCGA
                                     TATT    A
GAM1819 TJP2     3' TCAGTTCTGAATTTGCACCAGC 44454    TA      CA  GAG
             T                   TC  TTCTGAAT  TG   CAGCT
                                 ||  ||||||||  ||   |||||
                                 AG  AAGACTTA  AC   GTCGA
                                  TC       A_  GTG
GAM1819 ZNF238   3' TCTATTCTGACTTGCTCTAAAG 44455         ATCA___
                                TCTATTCTGA      TGGAG
                                ||||||||||      |||||
                                AGATAAGACT      ATTTC
                                      GAACGAG
GAM1819 LOC147622 5' TCTACTCTGAAATCAGTGG   44456          _  _
                                TCTATTCTGAA TCA TGG
                                |||||||||||| ||| |||
                                AGATGAGACTT AGT ACC
                                      T  C
GAM1819 LOC150343 5' TCTATTCTGAACACCTCCCAGC 44457          T  GGAG
             T                   TCTATTCTGAA CAT    CAGCT
                                 |||||||||||| |||    |||||
                                 AGATAAGACTT GTG    GTCGA
                                      _  GAGG
GAM1819 LOC162137 3' TCTGTTCTGAATGATGGAA   44458    A      C
                                TCT TTCTGAAT ATGGAG
                                ||| |||||||| ||||||
                                AGA AAGACTTA TACCTT
                                  C       C
GAM1819 LOC221477 5' CCTATTCTGAGCTGGCAG    44459        ATCA  GA
                                TCTATTCTGA    TG  GCAG
                                ||||||||||    ||  ||||
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                                GGATAAGACT   AC  CGTC
                                     CG__  __
GAM1819  LOC51313  3'  TCTATTCTGAATTTGAAAC   44460          CA
                                TCTATTCTGAAT  TGGAGC
                                ||||||||||||  ||||||
                                AGATAAGACTTA  ACTTTG
                                      A_
GAM1820  COPG2     3'  TGATGCCACTAGCCTAAA    44463   T     A_
                                A ATGCCA  AGTTTAAA
                                | ||||||  ||||||||
                                A TACGGT  TCGGATTT
                                 C     GA
GAM1820  GCA       3'  CATATGCCATTTCTAAA     44464         AAG
                                TATATGCCA   TTTAAA
                                |||||||||   ||||||
                                GTATACGGT   AGATTT
                                     AA_
GAM1820  PDK4      3'  TATATGCCAGTTTAAA      44465         AA
                                TATATGCCA  GTTTAAA
                                |||||||||  |||||||
                                ATATACGGT  CAAATTT
                                      __
GAM1820  SMAC      5'  CATACACCAAGTTTAAA     44466          A
                                TATATGCCAA GTTTAAA
                                |||||||||| |||||||
                                GTATGTGGTT CAAATTT
                                      _
GAM1820  FLJ11113  3'  TATCTGCCATAGTCTAAA    44467     A    A
                                TAT TGCCA AGTTTAAA
                                ||| ||||| ||||||||
                                ATA ACGGT TCAGATTT
                                  G    A
GAM1820  KIAA0446  5'  CATATGCCAATCTATTTTAAA  44468          AG___
                                TATATGCCAA    TTTAAA
                                ||||||||||    ||||||
                                GTATACGGTT    AAATTT
                                      AGATA
GAM1820  LOC147343 5'  TATATTTCAAAGTTCAAA    44469       GC
                                TATAT  CAAAGTTTAAA
                                |||||  ||||||||||
                                ATATA  GTTTCAAGTTT
                                   AA
GAM1820  LOC222662 3'  TATATGCCAAATCCAAA     44470          G
                                TATATGCCAAA TTTAAA
                                |||||||||| ||||||
                                ATATACGGTTT AGGTTT
                                      _
GAM1821  BTK       3'  AGGGAATCAAAGAAGAGGT   44125        A        A
                                AGGGAA TCAAAGAAGA GT
                                |||||| |||||||||| ||
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                                TCCCTT AGTTTCTTCT CA
                                   _       C
GAM1821  CA12     3'  AAGGAAATCAGAGGGAGA    44126         A  A_
                                AGGGAAATCA AG  AGA
                                |||||||||| ||  |||
                                TTCCTTTAGT TC  TCT
                                     C  CC
GAM1821  CARPX    3'  GAAATCAAAGAATGCAGT    44127          GA_
                                GAAATCAAAGAA   AGT
                                ||||||||||||   |||
                                CTTTAGTTTCTT   TCA
                                      ACG
GAM1821  CDC27    3'  AGGGAGATTAAAGAAAAA    44128       A  C
                                AGGGA AT AAAGAAGAA
                                ||||| || |||||||||
                                TCCCT TA TTTCTTTTT
                                   C  A
GAM1821  CYP8B1   3'  AGGGAAATCAGGAGGAGGAGT  44129          A_  A  A
                                AGGGAAATCA  AG AG AGT
                                ||||||||||  || || |||
                                TCCCTTTAGT  TC TC TCA
                                     CC  C  C
GAM1821  DEDD     3'  AGGGAAATAAAGGGGAAG    44130        C    AA
                                AGGGAAAT AAAG  GAAG
                                |||||||| ||||  ||||
                                TCCCTTTA TTTC  CTTC
                                   _   CC
GAM1821  ESRRG    3'  AGGGAGGTGAAAGAAGAAA   44131       AATC
                                AGGGA    AAAGAAGAAG
                                |||||    ||||||||||
                                TCCCT    TTTCTTCTTT
                                   CCAC
GAM1821  GRAF     3'  AGGGAAACAGAGAAGCCA    44132        CAA   A
                                AGGGAAAT   AGA GAAGTTA
                                ||||||||   ||| |||||||
                                TCCCTTTG   TCT CTTCGGT
                                    ____   _
GAM1821  IFNGR1   3'  AGGAAAATCAGACTTCAAAGTT 44133          AAGAA_
                                AGGGAAATCA      GAAGTT
                                ||||||||||      ||||||
                                TCCTTTTAGT      TTTCAA
                                     CTGAAG
GAM1821  MYCL2    3'  AGGGAGATCAAAAAGAAA    44134       A       A
                                AGGGA ATCAAAGA GAAG
                                ||||| |||||||| ||||
                                TCCCT TAGTTTTT CTTT
                                   C       _
GAM1821  MYO10    3'  GGGAAATCAGGTTGGGAGGTTA 44135          AAGAA_  A
                                GGGAAATCA      GA GTTA
                                |||||||||      || ||||
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                                CCCTTTAGT     CT CAAT
                                     CCAACC  C
GAM1821  PBX3     3'  AGGGAAACAAAGAGTTAA    44136       T     AGAA
                                AGGGAAA CAAAGA    GTTAA
                                ||||||| ||||||    |||||
                                TCCCTTT GTTTCT    CAATT
                                   _     ____
GAM1821  PCDHA11  5'  AGGGAACTCAAAGAAAAAAT  44137       A
                                AGGGAA TCAAAGAAGAAGT
                                |||||| ||||||||||||
                                TCCCTT AGTTTCTTTTTTA
                                   G
GAM1821  PCDHA11  5'  AGGGAACTCAAAGAAAAAAT  44137       A
                                AGGGAA TCAAAGAAGAAGT
                                |||||| ||||||||||||
                                TCCCTT AGTTTCTTTTTTA
                                   G
GAM1821  POU3F1   3'  AGGGAAATATAAGGGGAAA   44138       CA   AA
                                AGGGAAAT  AAG  GAAG
                                ||||||||  |||  ||||
                                TCCCTTTA  TTC  CTTT
                                     TA   CC
GAM1821  RARRES3  3'  AGGGAAACAGAGGAAA     44139       CAA   A
                                AGGGAAAT   AGA GAAG
                                ||||||||   ||| ||||
                                TCCCTTTG   TCT CTTT
                                   ___   C
GAM1821  AFAP     3'  GGGAGACCAAGAAGTTAA    44140     A   AAGA
                                GGGA ATCA    AGAAGTTAA
                                |||| ||||    |||||||||
                                CCCT TGGT    TCTTCAATT
                                  C   ____
GAM1821  AKAP11   3'  GGGAAATCAAAAAGCTA     44141         AGAA
                                GGGAAATCAA    GAAGTTA
                                ||||||||||    |||||||
                                CCCTTTAGTT    TTTCGAT
                                     _____
GAM1821  CGI-57   3'  AGGGAAATCAAAAGTAAAAGT  44142          _ A
                                AGGGAAATCAAA G AGAAGT
                                |||||||||||| | ||||||
                                TCCCTTTAGTTT C TTTTCA
                                       T A
GAM1821  DKFZP566D193 3'  GGGAAGTATGAGAAGTTAAT   44143      ATCAAA  A
                                GGGAA     GA GAAGTTAAT
                                |||||     || |||||||||
                                CCCTT     CT CTTCAATTA
                                   CATA__  _
GAM1821  DKFZP586M1120 3'  AGGGAAATCAGGGAAAGA    44144         AA_
                                AGGGAAATCA   GAAGA
                                ||||||||||   |||||
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                                TCCCTTTAGT   TTTCT
                                     CCC
GAM1821 G2      3' AGGGAAACAAAGAATCAG    44145       T     GA
                                AGGGAAA CAAAGAA  AG
                                ||||||| |||||||  ||
                                TCCCTTT GTTTCTT  TC
                                   _     AG
GAM1821 JIK     3' AGGGAGATAAAGAAAAAG    44146      A  C
                                AGGGA AT AAAGAAGAAG
                                ||||| || ||||||||||
                                TCCCT TA TTTCTTTTTC
                                  C  _
GAM1821 KIAA0884 5' AGGGAGGTCTGAAGAAGT    44147      AA  AAA
                                AGGGA  TC   GAAGAAGT
                                |||||  ||   ||||||||
                                TCCCT  AG   CTTCTTCA
                                   CC  A__
GAM1821 KIAA1198 3' AGGGAAATCAGGCAAGAAAA  44148         ___
                                AGGGAAATCA   AAGAAGA
                                ||||||||||   |||||||
                                TCCCTTTAGT   TTCTTTT
                                     CCG
GAM1821 KIAA1266 3' GGAAAATCAGAGACATAGT   44149        A   AGA
                                GGGAAATCA AGA   AGT
                                ||||||||| |||   |||
                                CCTTTTAGT TCT   TCA
                                     C   GTA
GAM1821 KIAA1509 3' AGGGAAATCTAGGAAGGCAG  44150        AAA   A_
                                AGGGAAATC   GAAG  AG
                                |||||||||   ||||  ||
                                TCCCTTTAG   CTTC  TC
                                     ATC    CG
GAM1821 KIAA1535 3' AGGGAAACAGAGACATC     44151        CAA   A  A
                                AGGGAAAT   AGA GA GTT
                                ||||||||   ||| || |||
                                TCCCTTTG   TCT CT TAG
                                   ___   _  G
GAM1821 KIAA1913 3' AGGGCAATCAAAGAACTTAAAA 44152      A       ____
           GT                     AGGG AATCAAAGAA    GAAGT
                                ||||| ||||||||||    |||||
                                TCCC TTAGTTTCTT    TTTCA
                                  G         GAAT
GAM1821 LRPPRC   3' AGGGAAACCAAAGAGCCAA    44153           AGAA
                                AGGGAAATCAAAGA    GTTAA
                                ||||||||||||||    |||||
                                TCCCTTTGGTTTCT    CGGTT
                                     ____
GAM1821 MGC20481 3' AGGAAGTTGGAGGAGAAGCCA 44154      ATCAA  A
                                GGGAA    AG AGAAGTTA
                                |||||    || ||||||||
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                                TCCTT    TC TCTTCGGT
                                   CAACC  C
GAM1821  SEC14L1   3'  GGGAGAATCAAAGAATCATTA  44155     _       GAA
                                GGGA AATCAAAGAA   GTTA
                                |||| ||||||||||   ||||
                                CCCT TTAGTTTCTT   TAAT
                                   C        AG_
GAM1821  SENP8     3'  AGGGAGACCAAAGGAAATTAAT 44156      A      AA
                                AGGGA ATCAAAG  GAAGTTAAT
                                ||||| |||||||  |||||||||
                                TCCCT TGGTTTC  CTTTAATTA
                                   C      __
GAM1821  SIAT8C    5'  AGGGAAACCGGGGAAATC    44157        AAAGAA
                                AGGGAAATC     GAAGTT
                                |||||||||     ||||||
                                TCCCTTTGG     CTTTAG
                                     CCC___
GAM1821  TACTILE   3'  AGAGAGATCAAAGAAGAAGCCA 44158      A
                                AGGGA ATCAAAGAAGAAGTTA
                                ||||| ||||||||||||||||
                                TCTCT TAGTTTCTTCTTCGGT
                                   C
GAM1821  UBE2G1    3'  AGGGAAATTAAATGGAAACTTT 44159       C  __   AAG
            TAAT                   AGGGAAAT AAA  GAAG   TTAAT
                                |||||||| |||  ||||   |||||
                                TCCCTTTA TTT  CTTT   AATTA
                                     A   AC    GAA
GAM1821  LOC131368 3'  AGGCAAATTGGAGAAAAAGT   44160     G    CAA
                                AGG AAAT   AGAAGAAGT
                                ||| ||||   |||||||||
                                TCC TTTA   TCTTTTTCA
                                  G    ACC
GAM1821  LOC144453 3'  AAGGAAATTGAAGAGAA     44161        CA    A
                                AGGGAAAT  AAGA GAA
                                ||||||||  |||| |||
                                TTCCTTTA  TTCT CTT
                                     AC    _
GAM1821  LOC144577 3'  AGGGAAACAGAGAGGCT     44162        CAA   A  A
                                AGGGAAAT   AGA GA GTT
                                ||||||||   ||| || |||
                                TCCCTTTG   TCT CT CGA
                                     ___   _  C
GAM1821  LOC148545 5'  AGGGAAGTTGAGAAAAAGTT   44163       ATCAA
                                AGGGAA     AGAAGAAGTT
                                ||||||     ||||||||||
                                TCCCTT     TCTTTTTCAA
                                   CAAC_
GAM1821  LOC149703 3'  AGGGAAATTCAAGAGAA     44164        CA    A
                                AGGGAAAT  AAGA GAA
                                ||||||||  |||| |||
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                                TCCCTTTA  TTCT CTT
                                    AG    _
GAM1821  LOC158187 3'  GGGAAGGGAAGGAGAAGTTAAT 44165      ATCA   A
                                GGGAA    AAG AGAAGTTAAT
                                |||||    ||| ||||||||||
                                CCCTT    TTC TCTTCAATTA
                                   CCC_   C
GAM1821  LOC201562 3'  GGAAATTAACATAGGAAGTTAA 44166      C  AGAA_
           T                     GGAAAT AA     GAAGTTAAT
                                |||||| ||     |||||||||
                                CCTTTA TT     CTTCAATTA
                                   A  GTATC
GAM1821  LOC206372 3'  AGGGAAGCAGGGAAGAAAT    44167       AT  AA
                                AGGGAA  CA  GAAGAAGT
                                ||||||  ||  ||||||||
                                TCCCTT  GT  CTTCTTTA
                                   C_  CC
GAM1821  LOC221399 5'  GGGGATCAGGGAAGAAGT     44168     AA    AA
                                GGG  ATCA  GAAGAAGT
                                |||  ||||  ||||||||
                                CCC  TAGT  CTTCTTCA
                                  C_    CC
GAM1821  LOC256756 5'  AGGTAAATCGAAGAAGAA     44169     G     A
                                AGG AAATC AAGAAGAA
                                ||| ||||| ||||||||
                                TCC TTTAG TTCTTCTT
                                  A    C
GAM1821  LOC51003  3'  AGGGAAATCAAAGAACAA     44170             G
                                AGGGAAATCAAAGAA AA
                                |||||||||||||| ||
                                TCCCTTTAGTTTCTT TT
                                         G
GAM1821  LOC56965  3'  GGTGAAGTCAAAGGGAAAGT   44171    _  A     AA
                                GG GAA TCAAAG  GAAGT
                                || ||| ||||||  |||||
                                CC CTT AGTTTC  TTTCA
                                 A  C     CC
GAM1821  LOC56965  3'  GGTGAAGTCAAAGGGAAAGT   44171    _  A     AA
                                GG GAA TCAAAG  GAAGT
                                || ||| ||||||  |||||
                                CC CTT AGTTTC  TTTCA
                                 A  C     CC
GAM1822  ACE      3'  TCTCTGGTGGGAGGCCC     44474      C   CCTC
                                TCTCT GGT    GGGGCCC
                                ||||| |||    |||||||
                                AGAGA CCA    CTCCGGG
                                   _  CC__
GAM1822  ALAS1    5'  TCTCCTGGTCCCCACATCCC   44475     TC      GGG
                                TCTC  GGTCCTCG   CCC
                                ||||  ||||||||   |||
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                                AGAG  CCAGGGGT   GGG
                                  GA       GTA
GAM1822 ASC     5'  CCTCTGGATTGGGGCCCC    44476      C  TCCTC
                                TCTCT GG    GGGGCCCC
                                ||||| ||    ||||||||
                                GGAGA CC    CCCCGGGG
                                  _  TAA__
GAM1822 AXIN2    5'  TCTCTCTGTCTCTCTGGGGCC  44477       G  _  _____  GGC
                                TCTCTC GTC CTC    GG   C
                                |||||| ||| |||    ||   |
                                AGAGAG CAG GAG    CC   G
                                   A   A   AIIIC  CGG
GAM1822 CDKN2B   5'  TCTGCGGCTTGGGGCCCC    44478     _   CCTC
                                TCT CGGT    GGGGCCCC
                                ||| ||||    ||||||||
                                AGA GCCG    CCCCGGGG
                                  C    AA__
GAM1822 CFTR     5'  TCTCTCGGGCGCTGGGGTCCC  44479        TC_  C   _
                                TCTCTCGG   CT GGGG CCC
                                ||||||||   || |||| |||
                                AGAGAGCC   GA CCCC GGG
                                     CGC  _   A
GAM1822 CLDN5    3'  TCTTCCGGTGGGGGCCCC    44480     CT   CCTC
                                TCT  CGGT    GGGGCCCC
                                |||  ||||    ||||||||
                                AGA  GCCA    CCCCGGGG
                                  AG    C___
GAM1822 CNN2     3'  TCTCACGGAGCAGGGCCCC   44481      T   TCCT
                                TCTC CGG    CGGGGCCCC
                                |||| |||    |||||||||
                                AGAG GCC    GTCCCGGGG
                                  T   TC__
GAM1822 COL4A2   5'  CCTTTCGGTCCTCGGCC     44482     C       GG
                                TCT TCGGTCCTC  GGCC
                                ||| |||||||||  ||||
                                GGA AGCCAGGAG  CCGG
                                  A        __
GAM1822 CPNE6    5'  CTCTCGGTCGGGGGCTCC    44483         CTC    _
                                CTCTCGGTC   GGGGC CC
                                |||||||||   ||||| ||
                                GAGAGCCAG   CCCCG GG
                                     C__     A
GAM1822 CYP7B1   5'  TCTCTCGGCGGCGCCC      44484        TCCT   G
                                TCTCTCGG    CGG GCCC
                                ||||||||    ||| ||||
                                AGAGAGCC    GCC CGGG
                                     _____   G
GAM1822 DNASE1   5'  TCTCTTGTCTGGGGGCCCC   44485      CG   CTC
                                TCTCT  GTC   GGGGCCCC
                                |||||  |||   ||||||||
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                                AGAGA  CAG   CCCCGGGG
                                  A_   AC_
GAM1822  DVL1    3'  TCTCTCGTCTTCCGGTCCC   44486       G  C  G  G
                                TCTCTCG TC TC GG CCC
                                ||||||| || || || |||
                                AGAGAGC AG AG CC GGG
                                   _ A  G  A
GAM1822  EYA2    3'  TCGTCTCGGCTGTGGGGCCCC  44487   _     CCTC
                                TC TCTCGGT   GGGGCCCC
                                || |||||||   ||||||||
                                AG AGAGCCG   CCCCGGGG
                                 C     ACA_
GAM1822  FGFR2   5'  CTGCGGCCTCGGGGCCCC   44488   _  T
                                CT CGG CCTCGGGGCCCC
                                || ||| ||||||||||||
                                GA GCC GGAGCCCCGGGG
                                 C  _
GAM1822  FGFR2   5'  CTGCGGCCTCGGGGCCCC   44488   _  T
                                CT CGG CCTCGGGGCCCC
                                || ||| ||||||||||||
                                GA GCC GGAGCCCCGGGG
                                 C  _
GAM1822  FGFR2   5'  CTGCGGCCTCGGGGCCCC   44488   _  T
                                CT CGG CCTCGGGGCCCC
                                || ||| ||||||||||||
                                GA GCC GGAGCCCCGGGG
                                 C  _
GAM1822  FGFR2   5'  CTGCGGCCTCGGGGCCCC   44488   _  T
                                CT CGG CCTCGGGGCCCC
                                || ||| ||||||||||||
                                GA GCC GGAGCCCCGGGG
                                 C  _
GAM1822  FGFR2   5'  CTGCGGCCTCGGGGCCCC   44488   _  T
                                CT CGG CCTCGGGGCCCC
                                || ||| ||||||||||||
                                GA GCC GGAGCCCCGGGG
                                 C  _
GAM1822  FGFR2   5'  CTGCGGCCTCGGGGCCCC   44488   _  T
                                CT CGG CCTCGGGGCCCC
                                || ||| ||||||||||||
                                GA GCC GGAGCCCCGGGG
                                 C  _
GAM1822  FGFR2   5'  CTGCGGCCTCGGGGCCCC   44488   _  T
                                CT CGG CCTCGGGGCCCC
                                || ||| ||||||||||||
                                GA GCC GGAGCCCCGGGG
                                 C  _
GAM1822  FGFR2   5'  CTGCGGCCTCGGGGCCCC   44488   _  T
                                CT CGG CCTCGGGGCCCC
                                || ||| ||||||||||||
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                                GA GCC GGAGCCCCGGGG
                                 C  _
GAM1822  FGFR2    5'  CTGCGGCCTCGGGGCCCC    44488    _  T
                                CT CGG CCTCGGGGCCCC
                                || ||| ||||||||||||
                                GA GCC GGAGCCCCGGGG
                                 C  _
GAM1822  FGFR2    5'  CTGCGGCCTCGGGGCCCC    44488    _  T
                                CT CGG CCTCGGGGCCCC
                                || ||| ||||||||||||
                                GA GCC GGAGCCCCGGGG
                                 C  _
GAM1822  FGFR2    5'  CTGCGGCCTCGGGGCCCC    44488    _  T
                                CT CGG CCTCGGGGCCCC
                                || ||| ||||||||||||
                                GA GCC GGAGCCCCGGGG
                                 C  _
GAM1822  FSTL3    3'  CCTTGGTGAGGCAGGGCCCC  44489     C  CCT_
                                TCT GGT   CGGGGCCCC
                                ||| |||   |||||||||
                                GGA CCA   GTCCCGGGG
                                  A  CTCC
GAM1822  FUT3     3'  CTCCCGGGTGGGGCCCC     44490       TCCTC
                                CTCTCGG   GGGGCCCC
                                |||||||   ||||||||
                                GAGGGCC   CCCCGGGG
                                    CA___
GAM1822  GNPAT    5'  TCTTTCGCTCAGGACGGCCC  44491     C  GTC      __
                                TCT TCG  CTCGGGGC  CCC
                                ||| |||  ||||||||  |||
                                AGA AGC  GAGTCCTG  GGG
                                  A  ___      CC
GAM1822  GPC1     3'  CCTCAGCCCTCGGGGTCC    44493            _
                                TCTCGGTCCTCGGGG CC
                                |||||||||||||| ||
                                GGAGTCGGGAGCCCC GG
                                        A
GAM1822  GPC1     5'  TCTCTCGGATCCTGGCCGGGTC 44492        _  ___   G
              C                  TCTCTCGG TCCT  CGGG CC
                                 |||||||| ||||  |||| ||
                                 AGAGAGCC AGGA  GCCC GG
                                     T   CCG   A
GAM1822  GRIK1    5'  CTGAGCTCTCTCGGGGCTCC  44494    C  _ _     _
                                CT GG TC CTCGGGGC CC
                                || || || |||||||| ||
                                GA TC AG GAGCCCCG GG
                                 C  G  A      A
GAM1822  HSPG2    5'  TCTCTCGCTCGCTCGCTCC   44495       G  _   GGG
                                TCTCTCG TC CTCG  CC
                                ||||||| || ||||  ||
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                                AGAGAGC AG GAGC   GG
                                    G  C    GA_
GAM1822 ITPKB    3'  TCTCCGGTGGGGAGGCCCC   44496     T   CCTC
                                TCTC CGGT    GGGGCCCC
                                |||| ||||    ||||||||
                                AGAG GCCA    CTCCGGGG
                                  _    CCC_
GAM1822 LFG      5'  TCTCTCGGGGAAGGGGTCCC  44497       TCCTC   _
                                TCTCTCGG    GGGG CCC
                                ||||||||    |||| |||
                                AGAGAGCC    CCCC GGG
                                    CCTT_    A
GAM1822 MADH6    5'  TCTCTCGGCTCAGCTCC     44498       TC    GG
                                TCTCTCGG  CTCGG  CC
                                ||||||||  |||||  ||
                                AGAGAGCC  GAGTC  GG
                                    __     GA
GAM1822 MAP3K11  5'  TCCCTCGGTTCTGGAGCAGTCC 44499        C  C    ___
                                TCTCTCGGT CT GGGGC   CC
                                ||||||||| || |||||   ||
                                AGGGAGCCA GA CCTCG   GG
                                    A  _    TCA
GAM1822 MATK     3'  TCTCTCGGTCCTCTGGGGCC  44500          _____ GGC
                                TCTCTCGGTCCTC    GG   C
                                ||||||||||||    ||   |
                                AGAGAGCCAGGAG    CC   G
                                      AIIIC  CGG
GAM1822 MATK     3'  TCTCTCGGTCCTCTGGGGCC  44500          _____ GGC
                                TCTCTCGGTCCTC    GG   C
                                ||||||||||||    ||   |
                                AGAGAGCCAGGAG    CC   G
                                      AIIIC  CGG
GAM1822 MATK     3'  TCTCTCGGTCCTCTGGGGCC  44500          _____ GGC
                                TCTCTCGGTCCTC    GG   C
                                ||||||||||||    ||   |
                                AGAGAGCCAGGAG    CC   G
                                      AIIIC  CGG
GAM1822 OCLN     5'  CTCTCGGTTCCTGCCGCC    44501       _  CGGG  _
                                CTCTCGGT CCT    GCC CC
                                |||||||| |||    ||| ||
                                GAGAGCCA GGA    CGG GG
                                    A  _____   C
GAM1822 P53AIP1  3'  TCACCACAGCTCGGGGC     44502    _ T   TC
                                TC TC CGG  CTCGGGGC
                                || || |||  ||||||||
                                AG GG GTC  GAGCCCCG
                                 T  T  __
GAM1822 PAFAH1B2 5'  TCGCTCGGTCCCGTCGGTCCC 44503    T      __    GG
                                TC CTCGGTCC  TCGG  CCC
                                || ||||||||  ||||  |||
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                                AG GAGCCAGG  AGCC  GGG
                                 C       GC    A_
GAM1822  PCSK5    5'  TCGCTCCTCCCGGGGCCCC   44504     G    __
                                TCG TCCTC  GGGGCCCC
                                ||| |||||  ||||||||
                                AGC AGGAG  CCCCGGGG
                                  G    GG
GAM1822  PLXNA1   3'  TCTCTGCGACCCGGGGCCCC  44505      _  T  T
                                TCTCT CGG CC CGGGGCCCC
                                ||||| ||| || |||||||||
                                AGAGA GCT GG GCCCCGGGG
                                   C  _ _
GAM1822  POLG     5'  CCTCGGTCCTCACGGTGC    44506          _ _
                                TCTCGGTCCTCG GG GC
                                |||||||||||| || ||
                                GGAGCCAGGAGT CC CG
                                       G  A
GAM1822  RBM3     5'  TCTCCCGGTCCTTGAC      44507          CGG
                                TCTCTCGGTCCT   GGC
                                ||||||||||||   |||
                                AGAGGGCCAGGA   CTG
                                       A__
GAM1822  RRM2B    5'  TCCCCCGCCTCGGGGCTCC   44508       GT       _
                                TCTCTCG  CCTCGGGGC CC
                                |||||||  ||||||||| ||
                                AGGGGGC  GGAGCCCCG GG
                                   __        A
GAM1822  RRM2B    3'  TCTCAGTCCATAAGCCC     44509        TCG
                                TCTCGGTCC   GGGCCC
                                |||||||||   ||||||
                                AGAGTCAGG   TTCGGG
                                     TA_
GAM1822  SLC21A9  3'  CTCTTGGCCAGGTGGGGCCCC 44510     C   CTC_
                                CTCT GGTC    GGGGCCCC
                                |||| ||||    ||||||||
                                GAGA CCGG    CCCCGGGG
                                  A    TCCA
GAM1822  SOX4     3'  TCTCTCAGTCCCGGCGTTCC  44511         T  GG__
                                TCTCTCGGTCC CGG    CC
                                |||||||||| |||    ||
                                AGAGAGTCAGG GCC    GG
                                      _  GCAA
GAM1822  SYN3     3'  TCTTGGCCTCAGGACCCC    44512     C  T
                                TCT GG CCTCGGGGCCCC
                                ||| || ||||||||||||
                                AGA CC GGAGTCCTGGGG
                                  A  _
GAM1822  SYN3     3'  TCTTGGCCTCAGGACCCC    44512     C  T
                                TCT GG CCTCGGGGCCCC
                                ||| || ||||||||||||
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                                AGA CC GGAGTCCTGGGG
                                  A  _
GAM1822  SYN3     3'  TCTTGGCCTCAGGACCCC    44512     C  T
                                TCT GG CCTCGGGGCCCC
                                ||| || ||||||||||||
                                AGA CC GGAGTCCTGGGG
                                  A  _
GAM1822  TBX3     3'  TCTCTCGAGGGAGTCCGGGGCC 44513        _____   TC
              CC                  TCTCTCG    GTCC  GGGGCCCC
                                |||||||    ||||  ||||||||
                                AGAGAGC    CAGG  CCCCGGGG
                                   TCCCT   __
GAM1822  TEM5     3'  TCCCTCGGTTTCCATTTGGTCC 44514        __   TCGG  _
                                TCTCTCGG  TCC    GG CC
                                ||||||||  |||    || ||
                                AGGGAGCC  AGG    CC GG
                                    AA   TAAA  A
GAM1822  TEM6     3'  CCTCTCGGTCCTCACAGGC   44515          _
                                TCTCTCGGTCCTCG GGGC
                                |||||||||||||| ||||
                                GGAGAGCCAGGAGT TCCG
                                       G
GAM1822  TOP3B    5'  TCTCGGTCCTTCACACTCC   44516        _  GG  _
                                TCTCGGTCCT CG  GC CC
                                |||||||||| ||  || ||
                                AGAGCCAGGA GT  TG GG
                                     A  G_  A
GAM1822  TRPM2    5'  TCCCTTGGCTGGGGCCCC    44517      C   CCTC
                                TCTCT GGT    GGGGCCCC
                                ||||| |||    ||||||||
                                AGGGA CCG    CCCCGGGG
                                   A   A___
GAM1822  APOL4    3'  TCCCTCCGTTTGGGGTCCC   44518      G  CCTC   _
                                TCTCTC GT    GGGG CCC
                                |||||| ||    |||| |||
                                AGGGAG CA    CCCC GGG
                                   G  AA__    A
GAM1822  C1orf17  3'  TCTTGTTCTCAGAGCTCC    44519     CG  C      _
                                TCT  GT CTCGGGGC CC
                                |||  || |||||||| ||
                                AGA  CA GAGTCTCG GG
                                  A_  A       A
GAM1822  C1QTNF2  5'  CTCTCGGCGGGGCTCC      44520       TCCT     _
                                CTCTCGG    CGGGGC CC
                                |||||||    |||||| ||
                                GAGAGCC    GCCCCG GG
                                    _____      A
GAM1822  C20orf139 3'  CTCTTGGTTTTCAGAAGCCCC  44521      C   CC    _
                                CTCT GGT  TCGGG GCCCC
                                |||| |||  ||||| |||||
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                                GAGA CCA  AGTCT CGGGG
                                  A  AA    T
GAM1822  C20orf151 3'  CCTCTCGGTCCTCCAGCCCC  44522          G  G
                                TCTCTCGGTCCTC GG CCCC
                                |||||||||||| || ||||
                                GGAGAGCCAGGAG TC GGGG
                                       G  _
GAM1822  C20orf20  3'  TCTTTCAGGTCCATCGGGGTCC 44523    C  _   _    _
           C                    TCT TC GGTCC TCGGGG CCC
                                ||| || ||||| |||||| |||
                                AGA AG CCAGG AGCCCC GGG
                                  A T    T     A
GAM1822  C6orf33   5'  CTCCCGCCTCGGGGTCCC   44524      GT      _
                                CTCTCG  CCTCGGGG CCC
                                ||||||  |||||||| |||
                                GAGGGC  GGAGCCCC GGG
                                   __      A
GAM1822  CBLC      3'  CCTTCCAGCCCTTGGGGCTCC  44525    CT     C   _
                                TCT  CGGTCCT GGGGC CC
                                |||  ||||||| ||||| ||
                                GGA  GTCGGGA CCCCG GG
                                  AG      A    A
GAM1822  CGI-152   3'  TCCCTCCCGGGGCCC      44526     GG   T
                                TCTC  TCC CGGGGCCC
                                ||||  ||| ||||||||
                                AGGG  AGG GCCCCGGG
                                   __  _
GAM1822  CLIPR-59  3'  CCTTGGTGGTCGGGGCCCC   44527    C   CC
                                TCT GGT  TCGGGGCCCC
                                ||| |||  ||||||||||
                                GGA CCA  AGCCCCGGGG
                                  A   CC
GAM1822  CLIPR-59  3'  CCTCAGGGCCTTGGGGCC   44528     TC  T   C
                                TCTC  GG CCT GGGGCC
                                ||||  || ||| ||||||
                                GGAG  CC GGA CCCCGG
                                  TC  _   A
GAM1822  CLSTN1    5'  CTCTCGGAGCTCTCGGGGC   44529       TC__
                                CTCTCGG    CTCGGGGC
                                |||||||    ||||||||
                                GAGAGCC    GAGCCCCG
                                    TCGA
GAM1822  DKFZP434A043 3'  CTCTTGGTCCCCAGTTCC    44530     C       GG
                                CTCT GGTCCTCGG  CC
                                |||| |||||||||  ||
                                GAGA CCAGGGGTC  GG
                                  A        AA
GAM1822  DKFZP434C1715 3'  TCTCAGTCTTCAAAGGGTCCC  44531        C __   _
                                TCTCGGTC TC  GGGG CCC
                                |||||||| ||  |||| |||
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                                AGAGTCAG AG  TCCC GGG
                                     A  TT    A
GAM1822  DKFZP434H0820 3'  TCTCCCGGTCCTGGCCC     9439           CGG
                                TCTCTCGGTCCT   GGCCC
                                ||||||||||||   |||||
                                AGAGGGCCAGGA   CCGGG
                                          ___
GAM1822  DKFZp434N035 3'  TCTCTCGGTCCGCCC       44532          TCGGG
                                TCTCTCGGTCC    GCCC
                                ||||||||||     ||||
                                AGAGAGCCAGG    CGGG
                                          _____
GAM1822  DKFZp761G2113 3'  TCCCTCTCACCTTGGGGCCCC  44533       GGT   C
                                TCTCTC   CCT GGGGCCCC
                                ||||||   ||| ||||||||
                                AGGGAG   GGA CCCCGGGG
                                    AGT   A
GAM1822  FLJ10748  3'  CCTCTCGGTCAGAAC       44534          CTC
                                TCTCTCGGTC   GGGGC
                                ||||||||||   |||||
                                GGAGAGCCAG   TCTTG
                                          ___
GAM1822  FLJ11850  3'  TCTCCTCGGTTTAAGGCCC   44535     _    CCTC
                                TCTC TCGGT    GGGGCCC
                                |||| |||||    |||||||
                                AGAG AGCCA    TTCCGGG
                                  G     AA__
GAM1822  FLJ12377  5'  TCTCCGCCGCGGGGCCCC    44536     G T  T
                                TCTC G CC CGGGGCCCC
                                |||| | || |||||||||
                                AGAG C GG GCCCCGGGG
                                  G _  C
GAM1822  FLJ12697  3'  TCTCTCTGGCGGGCTCC     44537      _  CCTCG   _
                                TCTCTC GGT    GGGC CC
                                |||||| |||    |||| ||
                                AGAGAG CCG    CCCG GG
                                    A  _____   A
GAM1822  FLJ12875  3'  TCTGTTGCCCGGGGCCCC    44538    CG_ T  T
                                TCT   G CC CGGGGCCCC
                                |||   | || |||||||||
                                AGA   C GG GCCCCGGGG
                                  CAA _  _
GAM1822  FLJ13769  3'  TCTCTCGGTTCTGCCACC    44539        C  CGGG  _
                                TCTCTCGGT CT    GCC CC
                                |||||||| ||    ||| ||
                                AGAGAGCCA GA    CGG GG
                                     A  ____   T
GAM1822  FLJ20188  3'  TCTCTCAACCTGGGGC      44540        T   C
                                TCTCTCGG CCT GGGGC
                                |||||||| ||| |||||
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                                AGAGAGTT GGA CCCCG
                                    _  _
GAM1822  FLJ22386  5'  TCTTTCTGTCCTCGGTCC    44541    C  G      GG
                                TCT TC GTCCTCGG  CC
                                ||| || ||||||||  ||
                                AGA AG CAGGAGCC  GG
                                  A  A       A_
GAM1822  GPT2      3'  CCTCTCAGACGGGGTTCC    44542       TCCT    CC
                                TCTCTCGG   CGGGG  CC
                                ||||||||   |||||  ||
                                GGAGAGTC   GCCCC  GG
                                     T___    AA
GAM1822  GSK3A     3'  TCCCAGCCCCTCTTGGGGCTCC 44543         C___    _
                                TCTCGGTCCT   GGGGC CC
                                ||||||||||   |||||  ||
                                AGGGTCGGGG   CCCCG GG
                                      AGAA    A
GAM1822  HAND1     3'  CCTCTCCTCCCGGGGC     44544      GG   T
                                TCTCTC  TCC CGGGGC
                                ||||||  |||  ||||||
                                GGAGAG  AGG GCCCCG
                                   G_  _
GAM1822  KIAA0211  5'  TCTTTCGGCTTTGGAGCCCC   44545    C    CCTC
                                TCT TCGGT   GGGGCCCC
                                ||| |||||   ||||||||
                                AGA AGCCG   CCTCGGGG
                                  A    AAA_
GAM1822  KIAA0258  3'  CCTTGGTTCCCCAGGTCCC   44546    C  _     G
                                TCT GGT CCTCGGG CCC
                                ||| ||| ||||||| |||
                                GGA CCA GGGGTCC GGG
                                  A  A      A
GAM1822  KIAA0339  3'  TCGCTGGGCTTGGGGCCCC   44547   T  C   CCTC
                                TC CT GGT   GGGGCCCC
                                || || |||   ||||||||
                                AG GA CCG   CCCCGGGG
                                 C  C   AA__
GAM1822  KIAA0720  3'  TCTCTCGGCCTCCGCGTCCC  44548       CT  GGG
                                TCTCTCGGTC  CG   CCC
                                ||||||||||  ||   |||
                                AGAGAGCCGG  GC   GGG
                                      AG  GCA
GAM1822  KIAA1074  5'  TCTCTCGGCTCTTAACGGCC  44549       TC  CG _
                                TCTCTCGG  CT  G GGCC
                                ||||||||  ||  | ||||
                                AGAGAGCC  GA  T CCGG
                                     GA  AT G
GAM1822  KIAA1100  5'  TCTCTCGGCCCAGGCCC    44550         TCG
                                TCTCTCGGTCC   GGGCCC
                                ||||||||||   ||||||
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                                AGAGAGCCGGG  TCCGGG
                                     ___
GAM1822 KIAA1274 3' CTAGCACTCCTTGGGGCTCC  1924    CT  G   C   _
                                CT  CG TCCT GGGGC CC
                                ||  || |||| ||||| ||
                                GA  GT AGGA CCCCG GG
                                 TC  G   A    A
GAM1822 KIAA1668 5' CTCTGGCTTCGGGGCCCC   44551    C  CC
                                CTCT GGT  TCGGGGCCCC
                                |||| |||  ||||||||||
                                GAGA CCG  AGCCCCGGGG
                                  _  A_
GAM1822 KIAA1808 3' TCTCGCCAGGGGCCCC     44552     GT  TC
                                TCTCG  CC  GGGGCCCC
                                |||||  ||  ||||||||
                                AGAGC  GG  CCCCGGGG
                                  __  T_
GAM1822 KIAA1879 5' TCTCTCGGTGGGAAGCCC   44553       CCTC
                                TCTCTCGGT   GGGGCCC
                                |||||||||   |||||||
                                AGAGAGCCA   CTTCGGG
                                     CC__
GAM1822 KIAA1881 3' CCTCCCACTCGGGGC      44554      GTC
                                TCTCTCG  CTCGGGGC
                                |||||||  ||||||||
                                GGAGGGT  GAGCCCCG
                                     ___
GAM1822 KIAA1932 5' TCTCTCGGCCTGCCC      44555      T  CGGG
                                TCTCTCGG CCT   GCCC
                                |||||||| |||   ||||
                                AGAGAGCC GGA   CGGG
                                   _  _____
GAM1822 LALP1   5' CCTCTCGGTTCAGTCCC    44556       CC   GG
                                TCTCTCGGT  TCGG  CCC
                                |||||||||  ||||  |||
                                GGAGAGCCA  AGTC  GGG
                                     __   A_
GAM1822 LAP1B   5' CCTCTCGGATGGGGGCCC   44557      TCCTC
                                TCTCTCGG   GGGGCCC
                                ||||||||   |||||||
                                GGAGAGCC   CCCCGGG
                                    TAC__
GAM1822 LEC3    3' TCCCTCGGGAGGGGTCCC   44558      TCCTC  _
                                TCTCTCGG   GGGG CCC
                                ||||||||   |||| |||
                                AGGGAGCC   CCCC GGG
                                    CT___   A
GAM1822 MGC10731 5' TCTCCCGGGGGGCCC      44559      TCCTC
                                TCTCTCGG   GGGGCCC
                                ||||||||   |||||||
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                                AGAGGGCC    CCCCGGG
                                   _____
GAM1822 MGC15563 3' TCTCCGGCCCTTGGGGTCC   44560     T     C   _
                                TCTC CGGTCCT GGGG CC
                                |||| ||||||| |||| ||
                                AGAG GCCGGGA CCCC GG
                                  _     A   A
GAM1822 MGC15854 5' TCTCTCGGCCCCTGCCC     44561          CGGG
                                TCTCTCGGTCCT   GCCC
                                ||||||||||||   ||||
                                AGAGAGCCGGGG   CGGG
                                       A___
GAM1822 MGC17299 5' TCTCTCAGTCGCTGGTCCC   44562         _ C  GG
                                TCTCTCGGTC CT GG  CCC
                                |||||||||| || ||  |||
                                AGAGAGTCAG GA CC  GGG
                                      C  _  A_
GAM1822 MGC4238  3' CCTTGGTCCTGTTGGTGGGTCC 44563     C     CG____  _
             C                   TCT GGTCCT     GGG CCC
                                ||| ||||||     ||| |||
                                GGA CCAGGA     CCC GGG
                                  A     CAACCA   A
GAM1822 MOT8     5' CTCTCGGTCCGCCGCC      44564          TCGGG  _
                                CTCTCGGTCC    GCC CC
                                ||||||||||    ||| ||
                                GAGAGCCAGG    CGG GG
                                      _____  C
GAM1822 OSAP     3' TCTCTCAGTCCTAAAATCTGGG 44565         C__________  GGCC
             GCCCC                  CTCGGTCCT        GG   CC
                                |||||||||        ||   ||
                                GAGTCAGGA        CC   GG
                                     TTTTAGAIII  CCGG
GAM1822 PALM     3' TCACTCGGTCCCTGCCC     44566    T       CGGG
                                TC CTCGGTCCT   GCCC
                                || |||||||||   ||||
                                AG GAGCCAGGG   CGGG
                                 T       A___
GAM1822 PIP5K2B  5' CTCCGAACGCCTCGGGGCCCC  44567    T  T__
                                CTC CGG   CCTCGGGGCCCC
                                ||| |||   ||||||||||||
                                GAG GCT   GGAGCCCCGGGG
                                  _   TGC
GAM1822 PIP5K2B  5' CTCCGAACGCCTCGGGGCCCC  44567    T  T__
                                CTC CGG   CCTCGGGGCCCC
                                ||| |||   ||||||||||||
                                GAG GCT   GGAGCCCCGGGG
                                  _   TGC
GAM1822 POFUT1   3' CTCCAGTCTCGGGGCC      44568     T    C
                                CTC CGGTC TCGGGGCC
                                ||| ||||| ||||||||
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                                GAG GTCAG AGCCCCGG
                                  _   _
GAM1822 PV1      3' TCCCTTGGTCCTCAGGCC   44569      C       G
                                TCTCT GGTCCTCGGG CC
                                ||||| |||||||||| ||
                                AGGGA CCAGGAGTCC GG
                                   A       _
GAM1822 RALY     5' TCTCTGGGTTCCGCTGCCCC  44570      C  C T  GG
                                TCTCT GGT C CG  GCCCC
                                ||||| ||| | ||  |||||
                                AGAGA CCA G GC  CGGGG
                                   C  A _  GA
GAM1822 RP4-622L5 3' TCCCTCGGTTCCACCC     44571        _  TCGGG
                                TCTCTCGGT CC    GCCC
                                |||||||| ||    ||||
                                AGGGAGCCA GG    TGGG
                                     A _____
GAM1822 SERF2    5' TCTCTCGGGTCTCCGAAGC   44572       _  CT
                                TCTCTCGG TC  CGGGGC
                                |||||||| ||  ||||||
                                AGAGAGCC AG  GCTTCG
                                    C  AG
GAM1822 SMOC1    5' TCCTTCGCTCGGGGCCC    44573    TC  GTC
                                TC  TCG  CTCGGGGCCC
                                ||  |||  ||||||||||
                                AG  AGC  GAGCCCCGGG
                                 GA  ___
GAM1822 SP192    5' TCTCTCAGTCCCCTCGGGGCC 44574          _______ GGC
                                TCTCTCGGTCCTC    GG  C
                                ||||||||||||    ||  |
                                AGAGAGTCAGGGG    CC  G
                                       AGIIIC  CGG
GAM1822 SYT13    3' TCTGGGATCGGGGCCCC    44575    C  TCC
                                TCT GG  TCGGGGCCCC
                                ||| ||  ||||||||||
                                AGA CC  AGCCCCGGGG
                                  C  T__
GAM1822 TNFRSF19L 3' TCTCGGTCCTCACAGTCCC  44576         G  _
                                TCTCGGTCCTCG GG CCC
                                |||||||||||| || |||
                                AGAGCCAGGAGT TC GGG
                                       G  A
GAM1822 WBP11    5' TCTCTCGGTCAACCC      44577        CTCGG
                                TCTCTCGGTC    GGCCC
                                ||||||||||    |||||
                                AGAGAGCCAG    TTGGG
                                     _____
GAM1822 ZYG      3' TCCCTCGGAAGGGGCCCC   44578       TCCTC
                                TCTCTCGG    GGGGCCCC
                                ||||||||    ||||||||
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                                AGGGAGCC    CCCCGGGG
                                    TT___
GAM1822  LOC121504 3'  TCTATCCTCCATCGGGGCCC  44579    C  GG  _
                                TCT TC  TCC TCGGGGCCC
                                ||| ||  ||| |||||||||
                                AGA AG  AGG AGCCCCGGG
                                  T  G_  T
GAM1822  LOC124222 3'  CTCAGAGCCTCCTCGGGGCTCC 44580      ____       _
                                CTCGG   TCCTCGGGGC CC
                                |||||   |||||||||| ||
                                GAGTC   AGGAGCCCCG GG
                                   TCGG        A
GAM1822  LOC126133 5'  TCTCGCGGGCGCGGGGCCC   44581    T  TCCT
                                TCTC CGG   CGGGGCCC
                                |||| |||   ||||||||
                                AGAG GCC   GCCCCGGG
                                  C  CGC_
GAM1822  LOC127003 5'  TCTCTCGGTTCACACGCC    44582       CC  GG_
                                TCTCTCGGT  TCG  GCC
                                |||||||||  |||  |||
                                AGAGAGCCA  AGT  CGG
                                     __  GTG
GAM1822  LOC127943 5'  TCCCTCCCGGGGCCC      44526     GG  T
                                TCTC  TCC CGGGGCCC
                                ||||  ||| ||||||||
                                AGGG  AGG GCCCCGGG
                                   __  _
GAM1822  LOC148443 3'  TCTCAGTCTCAGTGCCCC    44583       C   G
                                TCTCGGTC TCGG GCCCC
                                |||||||| |||| |||||
                                AGAGTCAG AGTC CGGGG
                                     _   A
GAM1822  LOC149300 3'  CCTCTCGGTTTGCCAGCC    44584       ___  TCGG
                                TCTCTCGGT  CC   GGCC
                                |||||||||  ||   ||||
                                GGAGAGCCA  GG   TCGG
                                     AAC  ____
GAM1822  LOC149668 3'  CCTCTCGGTCCTGCTGGCCC  44585         CGG
                                TCTCTCGGTCCT  GGCCC
                                ||||||||||||  |||||
                                GGAGAGCCAGGA  CCGGG
                                      CGA
GAM1822  LOC149935 3'  TCACTCGGTCCACATACC    44586   T     T  GG
                                TC CTCGGTCC CG  GCC
                                || ||||||||  ||  |||
                                AG GAGCCAGG GT  TGG
                                 T      T  A_
GAM1822  LOC150094 3'  TCTCGGTCTTGAGGTCCC    44587       CTC   _
                                TCTCGGTC  GGGG CCC
                                ||||||||  |||| |||
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                                AGAGCCAG   CTCC GGG
                                    AA_    A
GAM1822  LOC150225 3'  CTCCCAGCCTTGGGGCCC    44588       T   C
                                CTCTCGG CCT GGGGCCC
                                ||||||| ||| |||||||
                                GAGGGTC GGA CCCCGGG
                                   _   A
GAM1822  LOC157562 5'  TCTGCCTGTCTTCGGGGCC   44589     C  G   C
                                TCT TC GTC TCGGGGCC
                                ||| || ||| ||||||||
                                AGA GG CAG AGCCCCGG
                                  C  A   A
GAM1822  LOC159091 5'  TCTCCCATGATCGGGGCC    44590       GTCC
                                TCTCTCG    TCGGGGCC
                                |||||||    ||||||||
                                AGAGGGT    AGCCCCGG
                                    ACT_
GAM1822  LOC162427 3'  TCTTTCAGTGAGGGCCCC    44591     C     CCTC
                                TCT TCGGT    GGGGCCCC
                                ||| |||||    ||||||||
                                AGA AGTCA    TCCCGGGG
                                  A    C___
GAM1822  LOC163250 5'  TCCCCCAGCCTTCGGGGTCCC  44592          C     _
                                TCTCTCGGTC TCGGGG CCC
                                |||||||||| |||||| |||
                                AGGGGGTCGG AGCCCC GGG
                                      A     A
GAM1822  LOC170394 5'  TCCAGCACCTCGGGGTCC    44593    T   _       _
                                TC CGGT CCTCGGGG CC
                                || |||| |||||||| ||
                                AG GTCG GGAGCCCC GG
                                  _   T       A
GAM1822  LOC220522 3'  TCCACAAACTTGGGGTCCC    44594     CT   TC  C   _
                                TCT  CGG  CT GGGG CCC
                                |||  |||  || |||| |||
                                AGG  GTT  GA CCCC GGG
                                  T_   T_  A    A
GAM1822  LOC221501 3'  CTCTCCGCCCTCGGGGTTCC   44595       G         CC
                                CTCTC GTCCTCGGGG  CC
                                ||||| ||||||||||  ||
                                GAGAG CGGGAGCCCC  GG
                                   G         AA
GAM1822  LOC221935 3'  CCTCTCCCTGGGGCCC      44596       GGT   C
                                TCTCTC   CCT GGGGCCC
                                ||||||   ||| |||||||
                                GGAGAG   GGA CCCCGGG
                                    ___   _
GAM1822  LOC222962 3'  CTCAGGCCTCGGGGCCCC    44597       T
                                CTCGG CCTCGGGGCCCC
                                ||||| ||||||||||||
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                                GAGTC GGAGCCCCGGGG
                                  C
GAM1822 LOC254587 5' CCTCTCGGTCCCCGGTTCC   44598            GG
                                TCTCTCGGTCCTCGG  CC
                                |||||||||||||||  ||
                                GGAGAGCCAGGGGCC  GG
                                       AA
GAM1822 LOC51112  5' TCCTGCCTCGGGGCCC     44599     CG T
                                TCT  G CCTCGGGGCCC
                                |||  | ||||||||||
                                AGG  C GGAGCCCCGGG
                                 A_ _
GAM1822 LOC80298  5' CCTCGGTCTCAAGAAGCTCC  44600        C __    _
                                TCTCGGTC TC  GGGGC CC
                                |||||||| ||  ||||| ||
                                GGAGCCAG AG  CTTCG GG
                                     _ TT    A
GAM1822 LOC90957  3' TCTCTCAGTCGAGCC       44601         CTCG
                                TCTCTCGGTC   GGGCC
                                ||||||||||   |||||
                                AGAGAGTCAG   CTCGG
                                      _____
GAM1822 LOC91585  5' TCCCGCTCACCTCGGGGCTCC  44602      G __       _
                                TCTCG T  CCTCGGGGC CC
                                ||||| |  ||||||||| ||
                                AGGGC A  GGAGCCCCG GG
                                   G GT       A
GAM1823 ABCD1     3' CTCGGCTGCGCTGCTGTGTGGC 44605     CCCA      CACTC
                                CTCG   CGCTGCTG    GGC
                                ||||   ||||||||    |||
                                GAGC   GCGACGAC    CCG
                                  CGAC      ACA__
GAM1823 ADRBK1    5' GCTCGCGCGGCGCTCGGC    44606    CCA  T  T  A
                                GC  CGC GC GC CTCGGC
                                ||  ||| || || ||||||
                                CG  GCG CG CG GAGCCG
                                 A__  _ C  C
GAM1823 ATP6V0A4  5' CTCGGTCTGCAGCAGGCACTCG 44607     CCCAC  T  T_
           GC                   CTCG    GC GC  GCACTCGGC
                                ||||    || ||  |||||||||
                                GAGC    CG CG  CGTGAGCCG
                                  CAGA_  T  TC
GAM1823 CDKN2B    5' CTTTCCCACGCTGCTCCGG   44608    CG        GCAC
                                CT  CCCACGCTGCT   TCGG
                                ||  ||||||||||   ||||
                                GA  GGGTGCGACGA   GGCC
                                 AA        _____
GAM1823 COL4A3    5' CTCGCCTCGCCACTCG      44609       CA   TGCTG
                                CTCGCC  CGC    CACTCG
                                ||||||  |||    ||||||
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                                GAGCGG  GCG    GTGAGC
                                   A_  _____
GAM1823  COL4A3   5'  CTCGCCTCGCCACTCG     44609      CA   TGCTG
                                CTCGCC  CGC    CACTCG
                                ||||||  |||    ||||||
                                GAGCGG  GCG    GTGAGC
                                   A_  _____
GAM1823  COL4A3   5'  CTCGCCTCGCCACTCG     44609      CA   TGCTG
                                CTCGCC  CGC    CACTCG
                                ||||||  |||    ||||||
                                GAGCGG  GCG    GTGAGC
                                   A_  _____
GAM1823  HOXA3    3'  TCTTCCGTGCACAGCACTCGGC 44610    GC  AC  T  T
                                TC  CC  GC GC GCACTCGGC
                                ||  ||  || || |||||||||
                                AG  GG  CG TG CGTGAGCCG
                                 AA  CA  _  T
GAM1823  MET      5'  CTCGCGCCCTCCACTCGGC   44611      CCAC   G  G
                                CTCGC   GCT CT CACTCGGC
                                |||||   ||| || ||||||||
                                GAGCG   CGG GA GTGAGCCG
                                   _____  _  G
GAM1823  PTEN     5'  CTCGCTCTGCCGCCGCTTGGC  44612      CCAC      ACTC
                                CTCGC   GCTGCTGC   GGC
                                |||||   ||||||||   |||
                                GAGCG   CGGCGGCG   CCG
                                   AGA_      AA__
GAM1823  ACTR3    5'  CTCGCCTGCTGCTGCTGCTGC  44613      CAC      ACTCG
                                CTCGCC  GCTGCTGC   GC
                                ||||||  ||||||||   ||
                                GAGCGG  CGACGACG   CG
                                   A__      ACGA_
GAM1823  CIDEB    5'  CACGCTTGTGCTGCACCTGGC  44614       ___      TC
                                CACGCT  GCTGCAC  GGC
                                ||||||  |||||||  |||
                                GTGCGA  CGACGTG  CCG
                                   ACA     GA
GAM1823  DKFZP434H0820 5'  GCCCGCGCTGCTCAGGC     44615      A      G  CTC
                                GCCC CGCTGCT CA   GGC
                                |||| ||||||| ||   |||
                                CGGG GCGACGA GT   CCG
                                  C     _ ___
GAM1823  FLJ10563 5'  CTCCTCCACGCTGCCCGG    44616     GC        GCACT
                                CTC  CCACGCTGCT    CGG
                                |||  ||||||||||    |||
                                GAG  GGTGCGACGG    GCC
                                  GA        _____
GAM1823  FLJ12443 5'  CTCGCCGCACGTTGCTGGC   44617       _   C    _
                                CTCGCC CACG TGCTG C
                                |||||| |||| ||||| |
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                                GAGCGG GTGC ACGAC G
                                   C   A   C
GAM1823 FLJ23251 5' TCGCCCCACGTTGCTCGG   44618      A  T C  AC
                                TCGCCC CGC G TGC  TCGG
                                |||||| ||| | |||  ||||
                                AGCGGG GTG C ACG  AGCC
                                   _  _ A  __
GAM1823 HAND2    3' TCGCCCACGCCGGGTCTGATTC 44619         ___  CAC
           GGC                  TCGCCCACGCTG  CTG  TCGGC
                                ||||||||||||  |||  |||||
                                AGCGGGTGCGGC  GAC  AGCCG
                                      CCA  TA_
GAM1823 KIAA0237 5' CCCGCCTGCGCTGCCGGC   44620      CA     _
                                CTCGCC  CGCTGCTG C
                                ||||||  |||||||| |
                                GGGCGG  GCGACGGC G
                                   AC      C
GAM1823 KIAA0476 5' CTCGCTCGGCCGGCTCGG   44621     CCA  CT   CA
                                CTCGC  CG  GCTG  CTCGG
                                |||||  ||  ||||  |||||
                                GAGCG  GC  CGGC  GAGCC
                                   A__  __   C_
GAM1823 KLF5     5' CTCGCCCACGCTGGCTTGGGTC 44622          _ GCAC
           GGC                  CTCGCCCACGCTG CT   TCGGC
                                ||||||||||||| ||   |||||
                                GAGCGGGTGCGAC GA   AGCCG
                                      C  ACCC
GAM1823 LCE      5' TCCCCACGCCGCTCGG     44623    G       TGCAC
                                TC CCCACGCTGC    TCGG
                                || ||||||||||    ||||
                                AG GGGTGCGGCG    AGCC
                                  _       ______
GAM1823 MGC2306  3' CCCGCCCATATTGCACTTGG  44624       CGC  C    C
                                CTCGCCCA  TG TGCACT GG
                                ||||||||  || |||||| ||
                                GGGCGGGT  AT ACGTGA CC
                                     ___  A    A
GAM1823 LOC127294 5' CACGTCAGCTGCACTTGGC   44625     CT_     C
                                CACG  GCTGCACT GGC
                                ||||  |||||||| |||
                                GTGC  CGACGTGA CCG
                                  AGT      A
GAM1823 LOC145601 3' CCACGGCCACTCGGC      44626      CT  TG
                                CCACG  GC  CACTCGGC
                                |||||  ||  ||||||||
                                GGTGC  CG  GTGAGCCG
                                     __  __
GAM1823 LOC197342 3' CTCCCCTGCGCTGCTGTTCCGG 44627    G  A_      CAC
           C                     CTC CCC  CGCTGCTG  TCGGC
                                ||| |||  ||||||||  |||||
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                                GAG GGG  GCGACGAC   GGCCG
                                  _  AC       AA_
GAM1823  LOC197358 5'  CTCCTCCACGCTGCGGGCCAGC 44628     GC       T_  A__
              TCGG                   CTC  CCACGCTGC  GC   CTCGG
                                |||  |||||||||  ||   |||||
                                GAG  GGTGCGACG  CG   GAGCC
                                  GA        CC  GTC
GAM1823  LOC220045 3'  GCCTGGCAGGCTGCGCTTGGC  44629     CAC  T_    A  C
                                GCC   GC  GCTGC CT GGC
                                |||   ||  ||||| || |||
                                CGG   CG  CGACG GA CCG
                                  AC_  TC    C  A
GAM1823  LOC221463 3'  GCCACGCCAGAACTCGG     44630     C     CTGC
                                GCC ACGCTG    ACTCGG
                                ||| ||||||    ||||||
                                CGG TGCGGT    TGAGCC
                                  _     CT__
GAM1823  LOC222488 3'  CTCGCCCATTCAGCCCACTCGG 44631         CGCT   G
              C                   CTCGCCCA    GCT CACTCGGC
                                ||||||||    ||| ||||||||
                                GAGCGGGT    CGG GTGAGCCG
                                     AAGT   _
GAM1823  LOC93166  5'  CGCCGTGGGCTGCTGCGCTTGG 44632      CAC_       A  C
              C                   CGCC    GCTGCTGC CT GGC
                                ||||    |||||||| || |||
                                GCGG    CGACGACG GA CCG
                                  CACC       C  A
GAM1824  PTPN2     3'  GCAATATATAGTAGAAA     44635          T   TA
                                GCAATATGT AGT  AAA
                                |||||||||  |||  |||
                                CGTTATATA TCA  TTT
                                     _  TC
GAM1824  KIAA1918  3'  GCAATAGAGTTAAAAAT     44636       TGTT
                                GCAATA    AGTTAAAAAT
                                ||||||    ||||||||||
                                CGTTAT    TCAATTTTTA
                                   C___
GAM1824  MGC2628   3'  AACGCAATGTGTTCACACAAA  44637         A    AGT_
                                AACGCAAT TGTT    TAAA
                                ||||||||  ||||    ||||
                                TTGCGTTA ACAA    GTTT
                                     C    GTGT
GAM1824  PRO2266   3'  GCAATATGCTTATTAAAA     44638          A
                                GCAATATGTT GTTAAAA
                                ||||||||||  |||||||
                                CGTTATACGA TAATTTT
                                      A
GAM1824  SAS10     3'  TAATACAATGACTTTAGTTAAA 44639     CG    _  G
              A                    TAA  CAAT AT TTAGTTAAAA
                                |||  ||||  ||  ||||||||||
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                                ATT  GTTA TG AATCAATTTT
                                  AT   C  A
GAM1825 NKX2H    3' GAGAGCGTTCCAGGCGT    44642     A      A
                                GAGA CGTTCCAG GTGT
                                |||| |||||||| ||||
                                CTCT GCAAGGTC CGCA
                                  C      _
GAM1825 SRD5A2   5' TGAGAGTTTGCAATGTCTAT  44643     AC   CCAG
                                TGAGA  GTT   AGTGTCTAT
                                |||||  |||   |||||||||
                                ACTCT  CAA   TTACAGATA
                                   __  ACG_
GAM1825 STAU     5' GAGGGCGTTCCAGGAACAATGT 44644    AA      ____
                                GAG  CGTTCCAG   AGTGT
                                |||  ||||||||   |||||
                                CTC  GCAAGGTC   TTACA
                                  CC      CTTG
GAM1825 STAU     5' GAGGGCGTTCCAGGAACAATGT 44644    AA      ____
                                GAG  CGTTCCAG   AGTGT
                                |||  ||||||||   |||||
                                CTC  GCAAGGTC   TTACA
                                  CC      CTTG
GAM1825 STAU     5' GAGGGCGTTCCAGGAACAATGT 44644    AA      ____
                                GAG  CGTTCCAG   AGTGT
                                |||  ||||||||   |||||
                                CTC  GCAAGGTC   TTACA
                                  CC      CTTG
GAM1825 DKFZp564I1922 3' TGAGGTGTTGTTCATGTCTAT  44645    AAC__   CAGA
                                TGAG   GTTC   GTGTCTAT
                                ||||   ||||   ||||||||
                                ACTC   CAAG   TACAGATA
                                  CACAA   ____
GAM1825 DPP3     3' TGAGAACGTTTTGAACCCTAGC 44646        _____ AG
                                TGAGAACGTT   CC  AGT
                                ||||||||||   ||  |||
                                ACTCTTGCAA   GG  TCG
                                     AACTT  GA
GAM1825 DPP3     3' TGAGAACGTTTTGAACCCTAGC 44646        _____ AG
                                TGAGAACGTT   CC  AGT
                                ||||||||||   ||  |||
                                ACTCTTGCAA   GG  TCG
                                     AACTT  GA
GAM1825 FLJ10290 5' TGAGAGCGTCCGGAGGT    44647     A  T  A  T
                                TGAGA CGT CC GAG GT
                                ||||| ||| || ||| ||
                                ACTCT GCA GG CTC CA
                                  C  _  C  _
GAM1825 FLJ14249 3' TGAGAATTTCCAAAGCAC   44648     CG     TG
                                TGAGAA  TTCCAGAG  T
                                ||||||  ||||||||  |
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                                ACTCTT  AAGGTTTC  G
                                   A_       GT
GAM1825  FLJ14249  3'  TGAGAATTTCCAAAGCAC    44648       CG       TG
                                TGAGAA  TTCCAGAG  T
                                ||||||  ||||||||  |
                                ACTCTT  AAGGTTTC  G
                                   A_       GT
GAM1825  FLJ20898  3'  GAGAATGTTCCAGATGAGC    44649      C       GT_
                                GAGAA GTTCCAGA   GT
                                |||||  ||||||||   ||
                                CTCTT CAAGGTCT   CG
                                   A       ACT
GAM1825  GMFB      3'  TGAGAACATTTTAGAGCAC    44650         CC    TG
                                TGAGAACGTT  AGAG  T
                                ||||||||||  ||||  |
                                ACTCTTGTAA  TCTC  G
                                      AA    GT
GAM1825  KIAA0089  3'  TGAGATCGTTCCAATCT     44651       A      GAGT
                                TGAGA CGTTCCA    GTCT
                                |||||  |||||||    ||||
                                ACTCT GCAAGGT    TAGA
                                   A     _____
GAM1825  KIAA0515  3'  GAGCCAGAGTGTCTA       44652     AACGTT
                                GAG     CCAGAGTGTCTA
                                |||     ||||||||||||
                                CTC     GGTCTCACAGAT
                                  _______
GAM1825  KIAA0557  3'  TGGAACGTTCCAGAACCCA    44653    A          TG
                                TG GAACGTTCCAGAG  TCTA
                                || ||||||||||||  ||||
                                AC CTTGCAAGGTCTT  GGGT
                                  _          __
GAM1825  KIAA1554  3'  TGAGAAAGTTTCAGAACAT    44654       C  C    TG
                                TGAGAA GTT CAGAG  T
                                |||||| ||| |||||  |
                                ACTCTT CAA GTCTT  A
                                   T  A    GT
GAM1825  MAPK8IP3  3'  GAGAGCGTTCCAGATGCC     44655      A       G
                                GAGA CGTTCCAGA TGTC
                                ||||  |||||||| ||||
                                CTCT GCAAGGTCT ACGG
                                  C       _
GAM1825  PGRMC1    3'  TGAGGGTGTCTGAGTGTCTAT  44656      AAC   CCA
                                TGAG   GTT   GAGTGTCTAT
                                ||||   |||   ||||||||||
                                ACTC   CAG   CTCACAGATA
                                  CCA   A__
GAM1825  LOC145508 3'  TGGGAACCTTCCAGAAAGGTTC 44657    A   G       TG__
            T                    TG GAAC TTCCAGAG    TCT
                                || |||| ||||||||    |||
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                                AC CTTG AAGGTCTT    AGA
                                 C   G       TCCA
GAM1825  LOC146452 3'  TGAGACACAGGAGTGTCTAT   44658      A  TTC  _
                                TGAGA CG   CAG AGTGTCTAT
                                ||||| ||   ||| |||||||||
                                ACTCT GT   GTC TCACAGATA
                                   _ ___   C
GAM1825  LOC253233 5'  TGGGAACGCTCCAGCCGTAT   44659    A        A_
                                TG GAACGTTCCAG  GTGT
                                || ||||||||||  ||||
                                AC CTTGCGAGGTC  CATA
                                 C         GG
GAM1826  ADAMTS5   3'  TAATTCTTTTATATTAAAAACA 44662            CAT
                                TAATTCTTTTGTATT   AGACA
                                ||||||||||||||   |||||
                                ATTAAGAAAATATAA   TTTGT
                                          TT_
GAM1826  CTSH      3'  TCTTTGCGTCATAGACAC    44663      T  AT
                                TCTTT GT  TCATAGACAC
                                ||||| ||  ||||||||||
                                AGAAA CG  AGTATCTGTG
                                   _  C_
GAM1826  DMD       3'  TAACTTTTTTGTACAATTGCAT 44664      C      T____
              AGAC                  TAATT TTTTGTAT    CATAGAC
                                ||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A       TTAAC
GAM1826  DMD       3'  TAACTTTTTTGTACAATTGCAT 44664      C      T____
              AGAC                  TAATT TTTTGTAT    CATAGAC
                                ||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A       TTAAC
GAM1826  DMD       3'  TAACTTTTTTGTACAATTGCAT 44664      C      T____
              AGAC                  TAATT TTTTGTAT    CATAGAC
                                ||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A       TTAAC
GAM1826  DMD       3'  TAACTTTTTTGTACAATTGCAT 44664      C      T____
              AGAC                  TAATT TTTTGTAT    CATAGAC
                                ||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A       TTAAC
GAM1826  DMD       3'  TAACTTTTTTGTACAATTGCAT 44664      C      T____
              AGAC                  TAATT TTTTGTAT    CATAGAC
                                ||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A       TTAAC
GAM1826  DMD       3'  TAACTTTTTTGTACAATTGCAT 44664      C      T____
              AGAC                  TAATT TTTTGTAT    CATAGAC
                                ||||| ||||||||    |||||||
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                                ATTGA AAAACATG    GTATCTG
                                   A      TTAAC
GAM1826 DMD     3' TAACTTTTTTGTACAATTGCAT 44664      C      T____
            AGAC                  TAATT TTTTGTAT    CATAGAC
                                |||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A      TTAAC
GAM1826 DMD     3' TAACTTTTTTGTACAATTGCAT 44664      C      T____
            AGAC                  TAATT TTTTGTAT    CATAGAC
                                |||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A      TTAAC
GAM1826 DMD     3' TAACTTTTTTGTACAATTGCAT 44664      C      T____
            AGAC                  TAATT TTTTGTAT    CATAGAC
                                |||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A      TTAAC
GAM1826 DMD     3' TAACTTTTTTGTACAATTGCAT 44664      C      T____
            AGAC                  TAATT TTTTGTAT    CATAGAC
                                |||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A      TTAAC
GAM1826 DMD     3' TAACTTTTTTGTACAATTGCAT 44664      C      T____
            AGAC                  TAATT TTTTGTAT    CATAGAC
                                |||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A      TTAAC
GAM1826 DMD     3' TAACTTTTTTGTACAATTGCAT 44664      C      T____
            AGAC                  TAATT TTTTGTAT    CATAGAC
                                |||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A      TTAAC
GAM1826 DMD     3' TAACTTTTTTGTACAATTGCAT 44664      C      T____
            AGAC                  TAATT TTTTGTAT    CATAGAC
                                |||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A      TTAAC
GAM1826 DMD     3' TAACTTTTTTGTACAATTGCAT 44664      C      T____
            AGAC                  TAATT TTTTGTAT    CATAGAC
                                |||||| ||||||||    |||||||
                                ATTGA AAAACATG    GTATCTG
                                   A      TTAAC
GAM1826 MTMR8    3' TAATTTTTTGTATTTTTAGTAG 44665      C       CA___
            ACA                   TAATT TTTTGTATT    TAGACA
                                |||||| |||||||||    ||||||
                                ATTAA AAAACATAA    ATCTGT
                                   _       AAATC
GAM1826 SHANK2   3' TTCTTTGCCAATAGACAC    44666       T  ATTC
                                TTCTTT GT    ATAGACAC
                                |||||| ||    ||||||||
                                AAGAAA CG    TATCTGTG
                                   _ GT__
GAM1826 EBNA1BP2 3' TTCTTTGTATTCAAAGA     44667       T      T
                                TTCTTT GTATTCA AGA
                                |||||| ||||||| |||
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                                AAGAAA CATAAGT TCT
                                  _      T
GAM1826  FLJ11004  5'  TTCTTTTTTTGGCATAGACA   44668        GTATT
                                TTCTTTT    CATAGACA
                                |||||||    ||||||||
                                AAGAAAA    GTATCTGT
                                   AAACC
GAM1826  FLJ32978  3'  TAATTCTTTTTGTACAACA   44669          _   TCATA
                                TAATTCTTTT GTAT    GACA
                                |||||||||| ||||    ||||
                                ATTAAGAAAA CATG    TTGT
                                     A   _____
GAM1826  KIAA0877  3'  ATTCTTTTGGTTCCCATAGGCA 44670         TA_     A
                                ATTCTTTTG   TTCATAG CA
                                |||||||||   ||||||| ||
                                TAAGAAAAC   GGGTATC GT
                                     CAA      C
GAM1826  KIAA1160  3'  TAATTTTTTTGTATTTTTAGTA 44671       C       CA___
            GACA                   TAATT TTTTGTATT    TAGACA
                                |||||| |||||||||    ||||||
                                ATTAA AAAACATAA    ATCTGT
                                   A        AAATC
GAM1826  NMNAT    3'  TAATTTTTTGTATTCTTAG   44672       C        A
                                TAATT TTTTGTATTC TAG
                                ||||| |||||||||| |||
                                ATTAA AAAACATAAG ATC
                                  _         A
GAM1826  LOC197053 3'  TTCCTTTGAGTAACATAGACA  44673        TATT_
                                TTCTTTTG    CATAGACA
                                ||||||||    ||||||||
                                AAGGAAAC    GTATCTGT
                                     TCATT
GAM1826  LOC221810 3'  TTCTTTTGAGTAATAGACA   44674        TATTC
                                TTCTTTTG    ATAGACA
                                ||||||||    |||||||
                                AAGAAAAC    TATCTGT
                                     TCAT_
GAM1826  LOC253039 3'  TTCTTTTGCATCTCTTCATAG  44675          _____
                                TTCTTTTGTAT   TCATAG
                                ||||||||||    ||||||
                                AAGAAAACGTA   AGTATC
                                      GAGA
GAM1826  LOC90233  3'  TAATTTTTTGTATTTTAGTAGA 44676       C       CA__
            CA                    TAATT TTTTGTATT    TAGACA
                                ||||| |||||||||    ||||||
                                ATTAA AAAACATAA    ATCTGT
                                  _        AATC
GAM1826  LOC90843  3'  TAATTCTTTTTGTGTGTGAGAC 44677          GTATTCAT
            AC                    TAATTCTTTT       AGACAC
                                ||||||||||       ||||||
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                                ATTAAGAAAA      TCTGTG
                                     ACACACAC
GAM1826 LOC91796 3' TAATTCTTAGTATATGGACAC 44678       TT   TCATA
                                TAATTCTT  GTAT    GACAC
                                ||||||||  ||||    |||||
                                ATTAAGAA  CATA    CTGTG
                                     T_   TAC__
GAM1827 GNAO1    3' TCGGTGCAGATGGGTA     44681      A  CCGT
                                TCGGTG CG   GTGGGTA
                                |||||| ||   |||||||
                                AGCCAC GT   TACCCAT
                                   _ C___
GAM1827 PRO2605  3' GGTGACGCTGTATGCCGG    44682       C    _____
                                GGTGACGC GTGTG    GG
                                |||||||| |||||    ||
                                CCACTGCG CATAC    CC
                                     A    GGIII
GAM1827 LOC150005 5' TCGGTGACATTGTGGCCTGGC 44683       GCCG    GTAC
                                TCGGTGAC   TGTGG   GC
                                ||||||||   |||||   ||
                                AGCCACTG   ACACC   CG
                                     TA__    GGAC
GAM1827 LOC257481 3' GGTGACGCTGTATGCCGG    44682       C    _____
                                GGTGACGC GTGTG    GG
                                |||||||| |||||    ||
                                CCACTGCG CATAC    CC
                                     A    GGIII
GAM1828 CAT      3' TAGAAAAATAAAAATTTCTGA  44686       AAC  TT
                                TAGAAAGA   GA  ATTTCTGA
                                ||||||||   ||  ||||||||
                                ATCTTTTT   TT  TAAAGACT
                                     A__  TT
GAM1828 FGA      3' TAGAAAGAAATTGGTTACTCCT 44687        CGA_
                                TAGAAAGAAA    TTATTTCT
                                ||||||||||    ||||||||
                                ATCTTTCTTT    AATGAGGA
                                      AACC
GAM1828 GAS1     3' TAAAAATAAATTATTTCTGAA  44688      GAAAC
                                TAGAAA    GATTATTTCTGAA
                                ||||||    |||||||||||||
                                ATTTTT    TTAATAAAGACTT
                                   AT___
GAM1828 ICMT     3' TAGAAATAAGTCATATTTCTGA 44689      GAAACGAT
                                TAGAAA       TATTTCTGA
                                ||||||       |||||||||
                                ATCTTT       ATAAAGACT
                                   ATTCAGT_
GAM1828 MEL      3' TAGAAAGAACGTCCGA      44690        A  ATTATT
                                TAGAAAGAA CG     TCTGA
                                ||||||||| ||     |||||
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                                ATCTTTCTT GC     AGGCT
                                   _ _______
GAM1828 NDUFA10  3' GAAACACTTTTATTTCTG    44691       A__
                                GAAACG   TTATTTCTG
                                ||||||   |||||||||
                                CTTTGT   AATAAAGAC
                                   GAA
GAM1828 TES      3' GAAAGAAACTTTATTTTGA   44692        GA     C
                                GAAAGAAAC  TTATTT TGA
                                |||||||||  |||||| |||
                                CTTTCTTTG  AATAAA ACT
                                     A_     _
GAM1828 DKFZp434E1822 3'  AGAGGGAAAGAACATTTCTGA  44693     AA    C  T
                                AGA  GAAA GA TATTTCTGA
                                |||  |||| || |||||||||
                                TCT  CTTT CT GTAAAGACT
                                  CC    _ T
GAM1828 FLJ11101  3'  GAAGAGGGACCTATTTCTGAA  44694     A  AACGA
                                GAA GA     TTATTTCTGAA
                                ||| ||     ||||||||||
                                CTT CT     GATAAAGACTT
                                  _  CCCTG
GAM1828 FLJ11715  3'  TAGAAAGAGACGGCTGTACTTT 44695        A   AT__    C
           GAA                    TAGAAAGA ACG    TATTT TGAA
                                ||||||| |||    ||||| ||||
                                ATCTTTCT TGC    ATGAA ACTT
                                     C   CGAC    _
GAM1828 KIAA1219  3'  TAGAAAGAGGAGGTTATCTTTA 44696        AACGA    ____
           CCTGA                  TAGAAAGA    TTATT    TCTGA
                                ||||||||     |||||    |||||
                                ATCTTTCT     AATAG    GGACT
                                     CCTCC     AAAT
GAM1828 KIAA1391  3'  TAGAAGAAGTTGCATTTCTGAA 44697      A   ACGAT
                                TAGAA GAA     TATTTCTGAA
                                ||||| |||     ||||||||||
                                ATCTT CTT     GTAAAGACTT
                                   _   CAAC_
GAM1828 MAWBP    5'  TAGAAACAGACGATCATT    44698       GAA
                                TAGAAA   ACGATTATT
                                ||||||   |||||||||
                                ATCTTT   TGCTAGTAA
                                   GTC
GAM1828 MGC11271  3'  GAAAGAAACAAATTCTGAA   44699          TTAT
                                GAAAGAAACGA    TTCTGAA
                                ||||||||||    |||||||
                                CTTTCTTTGTT    AAGACTT
                                       T___
GAM1828 SDC3     3'  CAGAAAGAAATGAAGTCTG   44700          C  TTATT
                                TAGAAAGAAA GA     TCTG
                                ||||||||| ||     ||||
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                                GTCTTTCTTT CT     AGAC
                                      A  TC___
GAM1828  LOC123036 3'  CAGAAAGAAATATATATTTTTG 44701          CGAT     C
              AA                    TAGAAAGAAA    TATTT TGAA
                                    ||||||||||    ||||| ||||
                                    GTCTTTCTTT    ATAAA ACTT
                                          ATAT     A
GAM1828  LOC145844 3'  GAAAGAATTTATTTCTG     44702        ACGA
                                    GAAAGAA    TTATTTCTG
                                    |||||||    |||||||||
                                    CTTTCTT    AATAAAGAC
                                       A___
GAM1828  LOC153218 3'  AAAAGAAATACTATTCTGAA   44703         CG      T
                                    GAAAGAAA  ATTATT CTGAA
                                    ||||||||  ||||||| |||||
                                    TTTTCTTT  TGATAA GACTT
                                       A_     _
GAM1828  LOC199232 3'  AGAAACGAGATATAATTCTGAA 44704         T_   __
                                    AGAAACGA  TAT  TTCTGAA
                                    ||||||||  |||  |||||||
                                    TCTTTGCT  ATA  AAGACTT
                                       CT   TT
GAM1828  LOC202934 5'  TAGGAAGAAACAGAAAACCTGA 44705     A      _  TTATT
              A                      TAG AAGAAAC GA     TCTGAA
                                    ||| ||||||| ||     ||||||
                                    ATC TTCTTTG CT     GGACTT
                                      C      T  TTT__
GAM1828  LOC203696 5'  TAGAGGGAGACGACTTCTGA   44706     AA  A    TAT
                                    TAGA  GA ACGAT   TTCTGA
                                    ||||  || |||||   ||||||
                                    ATCT  CT TGCTG   AAGACT
                                      CC  C    ___
GAM1828  LOC222252 5'  TAGACAAGTGGCATTATTTCTG 44707      AAGAAACG
              A                      TAGA       ATTATTTCTGA
                                    ||||       ||||||||||
                                    ATCT       TAATAAAGACT
                                      GTTCACCG
GAM1828  LOC91445  3'  CAGAAAGAGGCTGGATTTCTG  44708         AACGATT
                                    TAGAAAGA      ATTTCTG
                                    ||||||||      |||||||
                                    GTCTTTCT      TAAAGAC
                                       CCGACC_
GAM1828  LOC91948  3'  AGAAACGTTCTCTGAA      44709         ATTA
                                    AGAAACG    TTTCTGAA
                                    |||||||    ||||||||
                                    TCTTTGC    AGAGACTT
                                       A___
GAM1828  LOC93587  5'  CAGAAAGAAAGCCTTTCTG    44710          CGATTA
                                    TAGAAAGAAA     TTTCTG
                                    ||||||||||     ||||||
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                                GTCTTTCTTT     AAAGAC
                                     CGG___
GAM1829  DPYSL2   3'  GTGATGGAATGACCTACT    40139        CA
                                GTGATGGGG  GCCTACT
                                |||||||||  |||||||
                                CACTACCTT  TGGATGA
                                     AC
GAM1829  MME      3'  TGTGATGGTGCCCTCTC     40140        GGCA   A
                                TGTGATGG   GCCT CTC
                                ||||||||   |||| |||
                                ACACTACC   CGGG GAG
                                     A___   A
GAM1829  MME      3'  TGTGATGGTGCCCTCTC     40140        GGCA   A
                                TGTGATGG   GCCT CTC
                                ||||||||   |||| |||
                                ACACTACC   CGGG GAG
                                     A___   A
GAM1829  MME      3'  TGTGATGGTGCCCTCTC     40140        GGCA   A
                                TGTGATGG   GCCT CTC
                                ||||||||   |||| |||
                                ACACTACC   CGGG GAG
                                     A___   A
GAM1829  MME      3'  TGTGATGGTGCCCTCTC     40140        GGCA   A
                                TGTGATGG   GCCT CTC
                                ||||||||   |||| |||
                                ACACTACC   CGGG GAG
                                     A___   A
GAM1829  MSL3L1   3'  CTGTGATGGGGTGACACAATC  44713          CA  C  C
                                CTGTGATGGGG  GC TA TC
                                ||||||||||  || || ||
                                GACACTACCCC  TG GT AG
                                      AC  T  T
GAM1829  PIK3R1   3'  ACTGGGGTGGGGAAGCTTATTC 40141      TGA    C   C  C
                                ACTG   TGGGG AGC TA TC
                                ||||   ||||| ||| || ||
                                TGAC   ACCCC TCG AT AG
                                  CCC    T   A  A
GAM1829  USP6     5'  CTGTGATGGTCTATTCC     44714        GGCAGC   C
                                CTGTGATGG     CTA TCC
                                |||||||||     ||| |||
                                GACACTACC     GAT AGG
                                     A_____   A
GAM1829  C9orf5   3'  CTGTATGCAGTCTACTCCA   44715      ATGGG    C
                                CTGTG    GCAG CTACTCCA
                                |||||    |||| ||||||||
                                GACAT    CGTC GATGAGGT
                                   A____    A
GAM1829  DPP9     3'  CTGTGATGTGGCGGCTCC    40142        G   A  CTAC
                                CTGTGATG GGC GC    TCC
                                |||||||| ||| ||    |||
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                                GACACTAC CCG CG    AGG
                                    A   C _____
GAM1829  FAM3A    3'  ACTGTGATCGGGCTCCAGCTAC 44716        G   ___  C    C
              TTCA                    ACTGTGAT GGGC   AGC TACT CA
                                ||||||||| ||||   ||| |||| ||
                                TGACACTA CCCG   TCG ATGA GT
                                    G    AGG  _    A
GAM1829  FLJ11218 3'  TGTGATAGGCTTATTCC     44717         G AGCC  C
                                TGTGATGGG C    TA TCC
                                |||||||||| |    || |||
                                ACACTATCC G    AT AGG
                                     _ A___  A
GAM1829  FLJ14106 3'  CTTTGGTGGGGCAGATCCCA   44718    G  A      __
                                CT TG TGGGGCAG  CCTA
                                || || ||||||||  ||||
                                GA AC ACCCCGTC  GGGT
                                 A  C       TA
GAM1829  HSF2     3'  ACTGGATGGGGCTCACTCC    44719     T       AGCC
                                ACTG GATGGGGC    TACTCC
                                |||| ||||||||    ||||||
                                TGAC CTACCCCG    GTGAGG
                                  _       A___
GAM1829  KIAA0063 3'  TGTGGCTGCCCCTACTCCA    44720    A   G_  AG
                                TG TGG  GC  CCTACTCCA
                                || |||  ||  |||||||||
                                AC ACC  CG  GGATGAGGT
                                 _   GA  G_
GAM1829  KIAA1068 3'  TGTGGTGGGACAGTGTGCCT   44721      A      ____
                                TGTG TGGGGCA    GCCT
                                |||| |||||||    ||||
                                ACAC ACCCTGT    CGGA
                                  C       CACA
GAM1829  KIAA1323 5'  TGTGATGGTAACATCTGCTCCA 44722         _    GC  A
                                TGTGATGG GGCA  CT CTCCA
                                |||||||| ||||  || |||||
                                ACACTACC TTGT  GA GAGGT
                                     A    A_  C
GAM1829  KIAA1423 3'  ACTGTGATGGGGTGGCACT    40143           CA  _
                                ACTGTGATGGGG  GC CT
                                ||||||||||||  || ||
                                TGACACTACCCC  CG GA
                                      AC  T
GAM1829  MGC13114 3'  ACTGTGATGGGGGAGGCT    40144           C  C
                                ACTGTGATGGGG AG CT
                                |||||||||||| || ||
                                TGACACTACCCC TC GA
                                      C  C
GAM1829  MGC13114 3'  ACTGTGATGGGGGAGGCT    40144           C  C
                                ACTGTGATGGGG AG CT
                                |||||||||||| || ||
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                                TGACACTACCCC TC GA
                                      C  C
GAM1829  MGC13114  3'  ACTGTGATGGGGGAGGCT    40144          C  C
                                ACTGTGATGGGG AG CT
                                |||||||||||| || ||
                                TGACACTACCCC TC GA
                                      C  C
GAM1829  MGC13114  3'  ACTGTGATGGGGGAGGCT    40144          C  C
                                ACTGTGATGGGG AG CT
                                |||||||||||| || ||
                                TGACACTACCCC TC GA
                                      C  C
GAM1829  MGC3047   3'  TGTGATGGTGGCAGGTCCA   44723        _    CCTAC
                                TGTGATGG GGCAG    TCCA
                                |||||||| |||||    ||||
                                ACACTACC CCGTC    AGGT
                                     A    C____
GAM1829  MGC3113   3'  CTGTGGTGGGGCAGTGAAC   40145      A      CCT
                                CTGTG TGGGGCAG   AC
                                ||||| ||||||||   ||
                                GACAC ACCCCGTC   TG
                                   C       ACT
GAM1829  PTDSS2    3'  CTGTGCTGGGGCCTCCTCCA  44724      A     AGCCTA
                                CTGTG TGGGGC     CTCCA
                                ||||| ||||||     |||||
                                GACAC ACCCCG     GAGGT
                                   G     GAG___
GAM1829  LOC121506 5'  CCGACTCAGGGCAGCCTACTC  40146    TGA
                                CTG   TGGGGCAGCCTACTC
                                |||   ||||||||||||||
                                GGC   GTCCCGTCGGATGAG
                                  TGA
GAM1829  LOC149506 5'  TGTGATGGGGCAGTTCCCA   40148          __
                                TGTGATGGGGCAG  CCTA
                                ||||||||||||  ||||
                                ACACTACCCCGTC  GGGT
                                       AA
GAM1829  LOC245744 3'  TGTGATGGGGCGGCAGCCCC  44725         A  CTA
                                TGTGATGGGGC GC   CTCC
                                |||||||||| ||   ||||
                                ACACTACCCCG CG   GGGG
                                      C  TC_
GAM1829  LOC257487 5'  GTGACAGACTGGCCTGCTCCA 44726        GCA   A
                                GTGATGGG   GCCT CTCCA
                                ||||||||   |||| |||||
                                CACTGTCT   CGGA GAGGT
                                     GAC    C
GAM1829  LOC81569  5'  GTGGTGCCGCAGCCTACTC   40150    A  GG
                                GTG TG  GCAGCCTACTC
                                ||| ||  ||||||||||
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                                CAC AC  CGTCGGATGAG
                                  C  GG
GAM1829 LOC91531 5' TGTGTGTATAGCCTACTTCA  44727     A  GGGC       C
                                TGTG TG   AGCCTACT CA
                                |||| ||   |||||||| ||
                                ACAC AC   TCGGATGA GT
                                  _ ATA_      A
GAM1829 LOC92689 3' TGGAACAAAGGCAGTCTACTCC 44728    TG TG _    C
           A                     TG  A  G GGCAG CTACTCCA
                                 ||  |  | ||||| ||||||||
                                 AC  T  T CCGTC GATGAGGT
                                  CT GT T    A
GAM1830 ABCD4    3' TCTTACAGATCTCACACTTCCA 40240        CCA_  CT  C
           G                     TCTTACGGA   GC  CT CCAG
                                 |||||||||   ||  || ||||
                                 AGAATGTCT   TG  GA GGTC
                                      AGAG  T_  A
GAM1830 ABCD4    3' TCTTACAGATCTCACACTTCCA 40240        CCA_  CT  C
           G                     TCTTACGGA   GC  CT CCAG
                                 |||||||||   ||  || ||||
                                 AGAATGTCT   TG  GA GGTC
                                      AGAG  T_  A
GAM1830 ABCD4    3' TCTTACAGATCTCACACTTCCA 40240        CCA_  CT  C
           G                     TCTTACGGA   GC  CT CCAG
                                 |||||||||   ||  || ||||
                                 AGAATGTCT   TG  GA GGTC
                                      AGAG  T_  A
GAM1830 ABCD4    3' TCTTACAGATCTCACACTTCCA 40240        CCA_  CT  C
           G                     TCTTACGGA   GC  CT CCAG
                                 |||||||||   ||  || ||||
                                 AGAATGTCT   TG  GA GGTC
                                      AGAG  T_  A
GAM1830 AP1M1    3' TCTTGAAGACCAGCCTCT    40241     AC
                                TCTT  GGACCAGCCTCT
                                ||||  ||||||||||||
                                AGAA  TCTGGTCGGAGA
                                  CT
GAM1830 CKTSF1B1 3' CACACCAGCCTCTCCCAG    40242    G
                                CG ACCAGCCTCTCCCAG
                                || ||||||||||||||||
                                GT TGGTCGGAGAGGGTC
                                 G
GAM1830 IL1R1    3' TCTTAGGGAAAGTCTCCCAG   40243     C   CC  CC
                                TCTTA GGA  AG  TCTCCCAG
                                ||||| |||  ||  ||||||||
                                AGAAT CCT  TC  AGAGGGTC
                                  C  T_  __
GAM1830 ITPKB    3' TCTTACAGGGCCAGGGCTGCT  40244       A_   C_  _
                                TCTTACGG  CCAG  CT CT
                                ||||||||  ||||  || ||
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                                AGAATGTC  GGTC  GA GA
                                    CC    CC  C
GAM1830 LGALS3BP  5'  GACCCAGAAGCCTCTCCCAG  40245     ____
                                GACC    AGCCTCTCCCAG
                                ||||    ||||||||||||
                                CTGG    TCGGAGAGGGTC
                                  GTCT
GAM1830 NCKAP1    5'  CCTTCGCAGCAGCCTCTC    40246     A  GAC
                                TCTT CG   CAGCCTCTC
                                |||| ||   |||||||||
                                GGAA GC   GTCGGAGAG
                                  _ GTC
GAM1830 PLA2G5    3'  CTTAGGAGCCTCTCTCA     40247     C   CCA      C
                                CTTA GGA   GCCTCTC CA
                                |||| |||   ||||||| ||
                                GAAT CCT   CGGAGAG GT
                                  _  ___      A
GAM1830 ROBO1     5'  TCTTGCGGAGCCTCCC      40248     A    CCA
                                TCTT CGGA   GCCTCTC
                                |||| ||||   |||||||
                                AGAA GCCT   CGGAGGG
                                  C   ___
GAM1830 FLJ10081  5'  TCTTACGGCCGCGCGCTC    40249        A  A_  _
                                TCTTACGG CC  GC CTC
                                |||||||| ||  || |||
                                AGAATGCC GG  CG GAG
                                    _ CG  C
GAM1830 HEYL      3'  TCTCTGAGGGTCTCTCCCAG  40250     AC_  ACCAGC
                                TCTT   GG     CTCTCCCAG
                                ||||   ||     |||||||||
                                AGAG   CC     GAGAGGGTC
                                  ACT  CA____
GAM1830 KIAA0323  3'  TCTTAGATTCCTCTCCCA    40251     AC   CCAG
                                TCTT  GGA    CCTCTCCCA
                                ||||  |||    |||||||||
                                AGAA  TCT    GGAGAGGGT
                                  __   AA__
GAM1830 KIAA0939  3'  TCTTGGGGGCACTCTCCCAG  40252     AC  ACCA  _
                                TCTT  GG    GC CTCTCCCAG
                                ||||  ||    || |||||||||
                                AGAA  CC    CG GAGAGGGTC
                                  CC  ____  T
GAM1830 KIAA1391  3'  CCTTATGCTACCTCTCCCAG  40253      CGGACCA
                                TCTTA      GCCTCTCCCAG
                                |||||      ||||||||||
                                GGAAT      TGGAGAGGGTC
                                  ACGA___
GAM1830 KRTHB3    3'  TCTCACAGTGCTTCTTCCAG  40254        ACCA  C   C
                                TCTTACGG    GC TCT CCAG
                                ||||||||    || ||| ||||
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                                AGAGTGTC   CG AGA GGTC
                                    A___  A  A
GAM1830  MYT1L    5'  TCTTACAGGAAGTCTTCTCTCC 40255      _  CCAGC_
                                TCTTAC GGA     CTCTCC
                                |||||| |||     ||||||
                                AGAATG CCT     GAGAGG
                                   T  TCAGAA
GAM1830  SEMA5A   3'  TTACAGACTGGCTCTTCAG   40256       CA  C   CC
                                TTACGGAC  GC TCT  CAG
                                ||||||||  || |||  |||
                                AATGTCTG  CG AGA  GTC
                                    AC  _  A_
GAM1830  LOC146443 5'  TCTGCAGGGCCTCTCCCA    40257    TAC  ACCA
                                TCT   GG   GCCTCTCCCA
                                |||   ||   ||||||||||
                                AGA   CC   CGGAGAGGGT
                                  CGT  ____
GAM1830  LOC149076 3'  TCTGCGGACCAAGCTTTCT   40258    TA     _  C_
                                TCT  CGGACCA GC  TCT
                                |||  ||||||| ||  |||
                                AGA  GCCTGGT CG  AGA
                                  C_     T  AA
GAM1830  LOC152627 5'  CTTCGTGAGCCAGCCTCTCC   40259    A  _  _
                                CTT CG GA CCAGCCTCTCC
                                ||| || || ||||||||||
                                GAA GC CT GGTCGGAGAGG
                                  _  A  C
GAM1830  LOC166341 3'  TCTTGGGATGCCTCCCA    40260    AC   CCA   TC
                                TCTT  GGA   GCC  TCCCA
                                ||||  |||   |||  |||||
                                AGAA  CCT   CGG  AGGGT
                                  C_   A__   __
GAM1830  LOC221865 3'  TCTTGTGGTCAGTGGCTGCCCC 40261     AC  AC   C__  C
            AG                    TCTT  GG  CAG   CT TCCCAG
                                ||||  ||  |||   || ||||||
                                AGAA  CC  GTC   GA GGGGTC
                                   CA  A_   ACC  C
GAM1830  LOC255152 5'  TCTTACAGAGATTCCTTTTCTC 40262       CCAG  ___
                                TCTTACGGA   CC   TCTC
                                |||||||||   ||   ||||
                                AGAATGTCT   GG   AGAG
                                     CTAA  AAA
GAM1830  LOC55908  5'  GGACCAGCCGCCGCCCAG    40263       _  T
                                GGACCAGCC TC CCCAG
                                ||||||||| || |||||
                                CCTGGTCGG GG GGGTC
                                     C  C
GAM1830  LOC91355  5'  TCTTCTGCCAGCCCCTCTCC   40264     ACGGA       _
                                TCTT    CCAGCCTCTC CC
                                ||||    |||||||||| ||
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                                AGAA    GGTCGGGGAG GG
                                  GAC__        A
GAM1830 LOC92017 5' TCTCACGGGTTAGTATCTCTCA 40265       ACC  CC   C
            G                    TCTTACGG   AG  TCTC CAG
                                 ||||||||   ||  |||| |||
                                 AGAGTGCC   TC  AGAG GTC
                                     CAA  AT   A
GAM1831 COL4A4   3' TGAACAGGTTGAACTTTTAGGA 44732     _  CTATT  AG
            GG                   TGAA AGG    AT  TTAGGAGG
                                 |||| |||    ||  ||||||||
                                 ACTT TCC    TG  AATCCTCC
                                   G  AACT_ AA
GAM1831 SCN3A    3' TGAAAGCTATTGTAGGG    44733      G    ATA  T   A
                                 TGAAAG CTATT   GT AGG G
                                 |||||| |||||   || ||| |
                                 ACTTTC GATAA   CA TCC C
                                    _    ___ _  A
GAM1831 SLC22A2  5' TGAGGACTGTAGTTAGGAGG  44734    AA   ATTA
                                 TGA  GGCT   TAGTTAGGAGG
                                 |||  ||||   ||||||||||
                                 ACT  CTGA   ATCAATCCTCC
                                   C_   C___
GAM1831 TBL2     3' TGAAAGGCTTCCACCTGGGAGG 44735       A   AGTTA
                                 TGAAAGGCT TTAT    GGAGG
                                 |||||||| ||||    |||||
                                 ACTTTCCGA GGTG    CCTCC
                                     A   GAC__
GAM1831 TBL2     3' TGAAAGGCTTCCACCTGGGAGG 44735       A   AGTTA
                                 TGAAAGGCT TTAT    GGAGG
                                 |||||||| ||||    |||||
                                 ACTTTCCGA GGTG    CCTCC
                                     A   GAC__
GAM1831 DMWD     3' AGGGTTATGGCTAGGAGG    44736    CTA   A
                                 AGG   TTAT GTTAGGAGG
                                 |||   |||| |||||||||
                                 TCC   AATA CGATCCTCC
                                   C__   C
GAM1831 KIAA0953 3' CGAGGGCACAGTTAGGG    44737    AA   TATT      A
                                 TGA  GGC   ATAGTTAGG G
                                 |||  |||   ||||||||| |
                                 GCT  CCG   TGTCAATCC C
                                   C_  _____       _
GAM1831 SLC37A1  3' TGAAAGGCAGTTGTGAAG    44738       TATTAT   A_
                                 TGAAAGGC    AGTT  GGAG
                                 ||||||||    ||||  ||||
                                 ACTTTCCG    TCAA  CTTC
                                     _______   CA
GAM1831 LOC137593 3' AAAGGCTATTATGGTTGG    44739         A   A
                                 AAAGGCTATTAT GTT GG
                                 |||||||||||| ||| ||
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                                  TTTCCGATAATA CAA CC
                                        C  _
GAM1831  LOC146268 5'  GAAAGGCTGTTTAGGAG     44740        ATTATAG
                                  GAAAGGCT      TTAGGAG
                                  ||||||||      |||||||
                                  CTTTCCGA      AATCCTC
                                      CA_____
GAM1831  LOC219333 3'  TGGAAGGCTGTTTTAAAAGAGG 44741    A     A  A   TT
                                  TG AAGGCT TT TAG  AGGAGG
                                  || |||||| || |||  ||||||
                                  AC TTCCGA AA ATT  TTCTCC
                                   C     C  A  __
GAM1831  LOC221448 5'  TGAAAGGCTTTAAAAAGGAGG  44742        ATTA   TT
                                  TGAAAGGCT    TAG  AGGAGG
                                  |||||||||    |||  ||||||
                                  ACTTTCCGA    ATT  TCCTCC
                                        A___   TT
GAM1832  GABRQ    3'  AAGAAACTGAAAGGAGCACAG  44745         TA  A_
                                  AAGAAACTGAA  GA  ATAG
                                  ||||||||||  ||  ||||
                                  TTCTTTGACTT  CT  TGTC
                                         TC  CG
GAM1832  MDM1     3'  AAGAAACTGAAAAGGGGCTAG  44746         T  AAA_
                                  AAGAAACTGAA AG    TAG
                                  |||||||||| ||    |||
                                  TTCTTTGACTT TC    ATC
                                         T  CCCG
GAM1832  ZFY      3'  AAGAAACTGAATAGGATT     44747           AAATA
                                  AAGAAACTGAATAG     GATT
                                  ||||||||||||||     ||||
                                  TTCTTTGACTTATC     CTAA
                                                _____
GAM1832  DDX17    5'  AAGAAACTGAGTAGAGCCAAA  44748         A    AA
                                  AAGAAACTGA TAGA  TAGA
                                  |||||||||| ||||  ||||
                                  TTCTTTGACT ATCT  GTTT
                                         C    CG
GAM1832  FLJ20232  3'  AAGACACTGAATAGGAACAG   44749      A        A
                                  AAGA ACTGAATAG AATAG
                                  |||| ||||||||| |||||
                                  TTCT TGACTTATC TTGTC
                                    G        C
GAM1832  FLJ21551  3'  AGAACGAGACAGAAATAGGTTG 44750      ACT  A       A
                                  AGAA   GA TAGAAATAG TTG
                                  ||||   || ||||||||| |||
                                  TCTT   CT GTCTTTATC AAC
                                    GCT  _        C
GAM1832  KR18     3'  AAGAAACTGATGTGGAAATA   44751         ATA_
                                  AAGAAACTGA    GAAATA
                                  ||||||||||    ||||||
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                                TTCTTTGACT    CTTTAT
                                      ACAC
GAM1832  PEG10    3'  AGAAGCTGAACAGGAATA    44752      A       A
                                AGAA CTGAATAG AATA
                                |||| |||||||| ||||
                                TCTT GACTTGTC TTAT
                                  C       C
GAM1832  SCAND2   3'  AAGAGGTTTACAAAAATAGATT 44753      AACTGA
              G                  AAGA     ATAGAAATAGATTG
                                ||||     ||||||||||||||
                                TTCT     TGTTTTTATCTAAC
                                  CCAAA_
GAM1832  LOC157681 5'  GAAATAGAATAGATTTTGATTG 44754      CT      AATA
                                GAAA  GAATAGA    GATTG
                                ||||  |||||||    |||||
                                CTTT  CTTATCT    CTAAC
                                  AT      AAAA
GAM1832  LOC51125  3'  AGGAACTGAATAGTAGAAACAG 44755    A      ___
                                AG AACTGAA   TAGAAATAG
                                || |||||||   |||||||||
                                TC TTGACTT   ATCTTTGTC
                                 C      ATC
GAM1833  ASPH     3'  CAATTATTTCTGAGCCCA    44758           ATTAT
                                CGATTATTTCTGA     TCCA
                                ||||||||||||     ||||
                                GTTAATAAAGACT     GGGT
                                      C____
GAM1833  ASPH     3'  CAATTATTTCTGAGCCCA    44758           ATTAT
                                CGATTATTTCTGA     TCCA
                                ||||||||||||     ||||
                                GTTAATAAAGACT     GGGT
                                      C____
GAM1833  CDK10    5'  ACGCTTATTTCTGGGTGTCCAA 44759     A       AATTAT
                                ACG TTATTTCTG     TCCAA
                                ||| |||||||||     |||||
                                TGC AATAAAGAC     AGGTT
                                  G       CCAC__
GAM1833  KLHL3    3'  TTATTTCTGGACATTCC     44760         AAT
                                TTATTTCTG   TATTCC
                                |||||||||   ||||||
                                AATAAAGAC   GTAAGG
                                     CT_
GAM1833  NMB      3'  CGATATTTCTGGTGACCCA    44761      T      AATTAT
                                CGAT ATTTCTG     TCCA
                                |||| |||||||     ||||
                                GCTA TAAAGAC     GGGT
                                  _      CACT__
GAM1833  TLL2     3'  ATTATTTAAAAATTATTCCAA  44428       CT
                                ATTATTT  GAATTATTCCAA
                                |||||||  ||||||||||||
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                                TAATAAA  TTTAATAAGGTT
                                    TT
GAM1833  ZNF215   3'  AATTATTTACCCTGTTATTCCA 44429        _ GAA
                                GATTATTT CT   TTATTCCA
                                |||||||| ||   ||||||||
                                TTAATAAA GG   AATAAGGT
                                    T  GAC
GAM1833  MGC15875 3'  GACATCTGGGTTATTCCAA   44762    TATT   AA
                                GAT   TCTG  TTATTCCAA
                                |||   ||||  |||||||||
                                CTG   AGAC  AATAAGGTT
                                  T___   CC
GAM1833  PTPN3    3'  CGGGTGAATCTGAATTGTTCCA 44763    ATTATT      A
                                CG     TCTGAATT TTCCA
                                ||     |||||||| |||||
                                GC     AGACTTAA AAGGT
                                 CCACTT       C
GAM1833  RAB6C    3'  CGTTATTTCTGCTAATTC    44764    A      AATT
                                CG TTATTTCTG    ATTC
                                || |||||||||    ||||
                                GC AATAAAGAC    TAAG
                                 _       GAT_
GAM1833  RABEX5   3'  ACAATTATAAAATTATTCCAA  44431       TTCT
                                ACGATTAT    GAATTATTCCAA
                                ||||||||    ||||||||||||
                                TGTTAATA    TTTAATAAGGTT
                                    T___
GAM1833  LOC200471 5' GATTATTTCCTGATCTCCAA   44433        GA   AT
                                GATTATTTCT  ATT  TCCAA
                                ||||||||||  |||  |||||
                                CTAATAAAGG  TAG  AGGTT
                                     AC  __
GAM1833  LOC205251 5' GATTCACTGATTATTCCAA    44765     ATTT   A
                                GATT    CTGA TTATTCCAA
                                ||||    |||| |||||||||
                                CTAA    GACT AATAAGGTT
                                  GT__   _
GAM1834  ACK1     3'  TGCTGGGGCGGCCCTCAAGCC  44768    CGA      A  T
                                TGC   GGCGGCCC TCG GCT
                                |||   |||||||| ||| |||
                                ACG   CCGCCGGG AGT CGG
                                  ACC       _   T
GAM1834  CDK10    3'  GCTGGGGCGGCCCGCTTGTTGC 44769    CGA      ATCG  C
                                GC   GGCGGCCC    TG TGC
                                ||   ||||||||    || |||
                                CG   CCGCCGGG    AC ACG
                                 ACC       CGA_  A
GAM1834  KCNN2    5'  TGCCGAGGCTGCCCGTGGGGC  44770        G   ATC   CT
                                TGCCGAGGC GCCC   GTG  GC
                                |||||||| ||||   |||  ||
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                                ACGGCTCCG CGGG  CAC  CG
                                     A   ___  CC
GAM1834  CECR2    5'  TACTGAGGCGGCTGCGGCTGC  44771    C      CCAT  T
                                TGC GAGGCGGC   CG GCTGC
                                ||| ||||||||   || |||||
                                ATG CTCCGCCG   GC CGACG
                                  A      AC__  _
GAM1834  FLJ14816 3'  TGTCAAGGCGGCTCTGTG    44772    C      CCA  _
                                TG CGAGGCGGC   TC GTG
                                || |||||||||  || |||
                                AC GTTCCGCCG   AG CAC
                                 A       ___  A
GAM1834  FLJ20255 3'  TGCCGAGGCTGCTCCCTG    44773        G  _  ATCGTG
                                TGCCGAGGC GC CC     CTG
                                ||||||||| || ||     |||
                                ACGGCTCCG CG GG     GAC
                                     A  A  _______
GAM1834  HSPC065  5'  TGCCGAAGCGGCCCCT     44774           ATCGTG
                                TGCCGAGGCGGCCC     CT
                                ||||||||||||||     ||
                                ACGGCTTCGCCGGG     GA
                                                   _______
GAM1834  KIAA0800 5'  CCGAGGCGGCTCCGCCGCTGC  44775         _  AT GT
                                CCGAGGCGGC CC  C  GCTGC
                                |||||||||| ||  |  |||||
                                GGCTCCGCCG GG  G  CGACG
                                      A  CG __
GAM1834  KIAA0960 3'  TGGTTAAGCGCCTATCGTGCTG 44776    CCG    G  C
             C                   TG   AGGCG CC ATCGTGCTGC
                                ||   ||||| || ||||||||||
                                AC   TTCGC GG TAGCACGACG
                                 CAA    _  A
GAM1834  MCAM     3'  TGCCAGGCCCTTCGTGCTG   44777      AGGC    A
                                TGCCG   GGCCC TCGTGCTG
                                |||||   ||||| ||||||||
                                ACGGT   CCGGG AGCACGAC
                                   _____    A
GAM1834  MGC12966 3'  TGCCGAGGGGCCCTCTTCTG   44778        C    A  GTG
                                TGCCGAGG GGCCC TC   CTG
                                |||||||| ||||| ||   |||
                                ACGGCTCC CCGGG AG   GAC
                                      _    _  AA_
GAM1834  MICAL    5'  TGCGGGGCGGCCCGGGGCGTGC 44779     C A      AT__
                                TGC G GGCGGCCC    CGTGC
                                ||| | ||||||||    |||||
                                ACG C CCGCCGGG    GCACG
                                  _ C       CCCC
GAM1834  PER3     5'  TGCTGGGACGGCCCGCAGCCTG 44780     CGA      ATC  G
             C                   TGC   GGCGGCCC   GT CTGC
                                |||   ||||||||   || ||||
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                                ACG   CTGCCGGG   CG GACG
                                  ACC       CGT  _
GAM1834  PPAP2A   5'  TGCCGAGGCGCTCGTG     44781          G CCA
                                TGCCGAGGCG C   TCGTG
                                |||||||||| |   |||||
                                ACGGCTCCGC G   AGCAC
                                       _ ___
GAM1834  PYY2     3'  TGCCGAGGCGGTCCTCGC    44782          C  A
                                TGCCGAGGCGG CC TCGT
                                |||||||||| || ||||
                                ACGGCTCCGCC GG AGCG
                                      A  _
GAM1834  LOC165552 3'  TGCAGAGGCGGCTTGCC     44783     C       CCATCG
                                TGC GAGGCGGC     TGCT
                                ||| ||||||||     ||||
                                ACG CTCCGCCG     ACGG
                                  T       A_____
GAM1835  ABCD2    3'  TGCTATTATAGCCCAGTTTGA  44786     AC_       A
                                TGC   TGTGGCCCA TTTGA
                                |||   ||||||||| |||||
                                ACG   ATATCGGGT AAACT
                                  ATA        C
GAM1835  ADCY8    5'  CTGCACTGGGCTTTG       44787         T   CCAA
                                CTGCACTG GGC    TTTG
                                |||||||| |||    ||||
                                GACGTGAC CCG    AAAC
                                       _  ____
GAM1835  IMMP2L   5'  TGCCCTCGCCCAATTTG     44788     A  GTG
                                TGC CT   GCCCAATTTG
                                ||| ||   ||||||||||
                                ACG GG   CGGGTTAAAC
                                  _  AG_
GAM1835  ITGB3    3'  TGCACTGTGGCCTCTCAGA   44789           CAA  T
                                TGCACTGTGGCC   TT GA
                                ||||||||||||   || ||
                                ACGTGACACCGG   AG CT
                                       AG_  T
GAM1835  TERT     3'  CACAGCACCTCCCCCCAATTTG 44790     T    GTGG
              AC                  CAC GCACT    CCCAATTTGAC
                                ||| |||||    ||||||||||
                                GTG CGTGG    GGGTTAAACTG
                                  T    AGGG
GAM1835  UNC5C    3'  CTGCATCCCTGTCCAATTTGA  44791       _  G  GC
                                CTGCA CT TG  CCAATTTGA
                                ||||| || ||  |||||||||
                                GACGT GG AC  GGTTAAACT
                                   A  G  A_
GAM1835  C21orf93 3'  CTGGGCTGTGGCCCTGGGGAC  44792     CA        AATTT
                                CTG  CTGTGGCCC    GAC
                                |||  |||||||||    |||
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                                GAC  GACACCGGG    CTG
                                  CC        ACCC_
GAM1835  CLGN     3'  CACTGTAACTATAATTTGA   44793        CC_
                                CACTGTGGC   AATTTGA
                                |||||||||   |||||||
                                GTGACATTG   TTAAACT
                                     ATA
GAM1835  DKFZP434C1715 3'  CACTTGTGAAAAACCAATTTG  44794     _   C___
                                CACT GTGG    CCAATTTG
                                |||| ||||    ||||||||
                                GTGA CACT    GGTTAAAC
                                  A    TTTT
GAM1835  DKFZp547I224 3'  TGCACTGTGGTCTGA       44795         CCCAA
                                TGCACTGTGG     TTTGA
                                ||||||||||     |||||
                                ACGTGACACC     AGACT

                                      _____
GAM1835  DKFZp566H0824 5'  CTGCACTGTGGTCCAATGAC   44796          C    TT
                                CTGCACTGTGG CCAA  TGAC
                                |||||||||||| ||||  ||||
                                GACGTGACACC GGTT  ACTG
                                      A   __
GAM1835  FLJ00001  3'  CACTGCACAGTGGCCTGGTGAC 44797        T     CAATT
                                CACTGCAC GTGGCC     TGAC
                                |||||||| ||||||     ||||
                                GTGACGTG CACCGG     ACTG
                                     T     ACC__
GAM1835  FLJ12565  3'  CTCACTGTGGCCCTGA      44798    G        AATT
                                CT CACTGTGGCCC    TGA
                                || ||||||||||    |||
                                GA GTGACACCGGG    ACT

                                _        _____
GAM1835  FLJ22390  5'  CACTGCATTTGTGGTGGGCGTT 44799       C_    CCCAA_
            TGA                   CACTGCA  TGTGG     TTTGA
                                |||||||  |||||     |||||
                                GTGACGT  ACACC     AAACT
                                     AA    ACCCGC
GAM1835  GMEB2    3'  CACTGCAGTGTGGTTCCCA   44800        C    __
                                CACTGCA TGTGG  CCCA
                                ||||||| |||||  ||||
                                GTGACGT ACACC  GGGT
                                     C    AA
GAM1835  KIAA1301  3'  CACGGCACTGTGAAGGAAGTTT 44801     T       CCCAA_
            GA                    CAC GCACTGTGG     TTTGA
                                ||| |||||||||     |||||
                                GTG CGTGACACT     AAACT
                                  C        TCCTTC
GAM1835  KIAA1879  5'  GCACTGTGGCAATCTG      44802          CC
                                GCACTGTGGC  AATTTG
                                ||||||||||  ||||||
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                                CGTGACACCG  TTAGAC
                                          __
GAM1835  LYPLA2    3'  ACTGCACTGGGGCCAGCGAC   44803        T    CAATT
                                ACTGCACTG GGCC    TGAC
                                ||||||||| ||||    ||||
                                TGACGTGAC CCGG    GCTG
                                     C   TC___
GAM1835  SLC12A8   3'  CACTTATTGTGGCCCTCTG   44804     GCAC      AA
                                CACT   TGTGGCCC  TTTG
                                ||||   ||||||||  ||||
                                GTGA   ACACCGGG  AGAC
                                  ATA_      __
GAM1835  LOC115110 3'  CATTGTGCTGTGACCGCTTTGA 44805    C  CA      CAA
                                CA TG  CTGTGGCC   TTTGA
                                || ||  ||||||||   |||||
                                GT AC  GACACTGG   AAACT
                                 A  AC       CG_
GAM1835  LOC126282 3'  CACTGCACGTGGCCTCAAT   44806        T    _
                                CACTGCAC GTGGCC CAAT
                                |||||||| |||||| ||||
                                GTGACGTG CACCGG GTTA
                                     _     A
GAM1835  LOC149332 5'  CATTACACTGTAAATTTGA   44807    C       GCCC
                                CA TGCACTGTG    AATTTGA
                                || |||||||||    |||||||
                                GT ATGTGACAT    TTAAACT
                                 A       ____
GAM1835  LOC150157 3'  TGCACTGTGGTCTGA      44795         CCCAA
                                TGCACTGTGG    TTTGA
                                ||||||||||    |||||
                                ACGTGACACC    AGACT
                                          _____
GAM1835  LOC151098 5'  TGCACTGTGGTCTGA      44795         CCCAA
                                TGCACTGTGG    TTTGA
                                ||||||||||    |||||
                                ACGTGACACC    AGACT
                                          _____
GAM1835  LOC196890 3'  TGCACTGTGGTCTGA      44795         CCCAA
                                TGCACTGTGG    TTTGA
                                ||||||||||    |||||
                                ACGTGACACC    AGACT
                                          _____
GAM1835  LOC220469 3'  CACTGCAGCCTCCTGATTTGAC 44808      TG   CA___
                                CACTG  GCC    ATTTGAC
                                |||||  |||    |||||||
                                GTGAC  CGG    TAAACTG
                                   GT   AGGAC
GAM1835  LOC221454 5'  CTGCCCTGAACAATTTGAC   44809     A   TGGCC
                                CTGC CTG    CAATTTGAC
                                |||| |||    |||||||||
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                                GACG GAC    GTTAAACTG
                                  G  TT___
GAM1835  LOC221495 3'  CTGCAGAAGTCTAATTTGAC  44810     CTGT  CCC
                                CTGCA   GG  AATTTGAC
                                |||||   ||  ||||||||
                                GACGT   TC  TTAAACTG
                                   CT__  AGA
GAM1835  LOC253731 5'  CTGCACTGTGGCTCGA     44811         CCAAT
                                CTGCACTGTGGC    TTGA
                                ||||||||||||    ||||
                                GACGTGACACCG    AGCT
                                        _____
GAM1835  LOC253778 5'  TGCTCATATTCCAATTTGA   44812    ACT   GC
                                TGC   GTG  CCAATTTGA
                                |||   |||  |||||||||
                                ACG   TAT  GGTTAAACT
                                  AG_   AA
GAM1836  KIAA1046  3'  TTTCTATTTGGTGCAACGTT  44815         A   T
                                TTTCTATTTGGTG CAG CGTT
                                |||||||||||| ||| ||||
                                AAAGATAAACCAC GTT GCAA
                                        _  _
GAM1836  MGC14817  3'  TTTCATTTGGTGGCAGT    44816     T      A
                                TTTC ATTTGGTG CAGT
                                |||| |||||||| ||||
                                AAAG TAAACCAC GTCA
                                   _      C
GAM1836  MGC3048   3'  TATTTGGTTGCTGTTCT    44817       GACA  C
                                TATTTGGT    GT GTTCT
                                ||||||||    || |||||
                                ATAAACCA    CG CAAGA
                                     A___  A
GAM1836  NYD-SP12  3'  TTTCTTTTGGTGACAAGC    44818      A       _
                                TTTCT TTTGGTGACA GT
                                ||||| |||||||||| ||
                                AAAGA AAACCACTGT CG
                                   _        T
GAM1836  LOC149332 5'  TTTCTTTTTGATAAAGTTGTT  44819      A      C   C
                                TTTCT TTTGGTGA AGT GTT
                                ||||| |||||||| ||| |||
                                AAAGA AAACTATT TCA CAA
                                   A       _  A
GAM1836  LOC152503 3'  TTTCCATCTTAACAGTTGTTCT 44820        GG     C
                                TTTCTATTT  TGACAGT GTTCT
                                |||||||||  ||||||| |||||
                                AAAGGTAGA  ATTGTCA CAAGA
                                     __      A
GAM1836  LOC255238 3'  TTTCATTTGGTGGCAGT    44816     T      A
                                TTTC ATTTGGTG CAGT
                                |||| |||||||| ||||
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                                AAAG TAAACCAC GTCA
                                  _      C
GAM1837  BCL9     5'  TGCTGGGGGCAGTGGCAC    44823         _  CA  AG
                                TGCTGGGGG AGT  GG  AC
                                ||||||||| |||  ||  ||
                                ACGACCCCC TCA  CC  TG
                                     G  __  G_
GAM1837  CKN1     3'  TGGATAGTAGGAGACA     44824     GG   C
                                TGGG  AGT AGGAGACA
                                ||||  ||| ||||||||
                                ACCT  TCA TCCTCTGT
                                  A_  _
GAM1837  CYP2F1   5'  TGCTGAGCTGCAGGAGACAC  44825       GGA T
                                TGCTGGG   G CAGGAGACAC
                                |||||||   | ||||||||||
                                ACGACTC   C GTCCTCTGTG
                                    GA_ _
GAM1837  HCN2     3'  GCTGGGGGAACTGAGGCACCG  44826        TCAG   A
                                GCTGGGGGAG   GAG CACCG
                                ||||||||||   ||| |||||
                                CGACCCCCTT   CTC GTGGC
                                     GA__  C
GAM1837  KCNMB1   3'  CTGGGGGAGGATGGGTACCG  44827        TCA  AGAC
                                CTGGGGGAG   GG   ACCG
                                |||||||||   ||   ||||
                                GACCCCCTC   CC   TGGC
                                     CTA  CA__
GAM1837  MTMR6    5'  TGCTGGAGGAGGCCGGTAC   44828         TCA  AG
                                TGCTGGGGGAG   GG  AC
                                ||||||||||   ||  ||
                                ACGACCTCCTC   CC  TG
                                      CGG  A_
GAM1837  NCOR2    3'  TGGGGGAGTCGGCAGCCG    44829         A  AGACA
                                TGGGGGAGTC GG    CCG
                                |||||||||| ||    |||
                                ACCCCCTCAG CC    GGC
                                     _  GTC__
GAM1837  NR1I2    5'  TGCTAGGGCTAGGAGGCA    44830       GAGTC    A
                                TGCTGGGG    AGGAG CA
                                ||||||||    ||||| ||
                                ACGATCCC    TCCTC GT
                                    GA___    C
GAM1837  SLC7A5   3'  CTGGGGCAGGGGACAC     44831       GAGT   A
                                CTGGGG   CAGG GACAC
                                ||||||   |||| |||||
                                GACCCC   GTCC CTGTG
                                   ____   C
GAM1837  ACTR1A   3'  TGCAGTCAGGAGGCATCG   44832     TGGGGG       A  C
                                TGC     AGTCAGGAG CA CG
                                |||     ||||||||| || ||
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                                ACG     TCAGTCCTC GT GC
                                 _______       C  A
GAM1837 ADPRTL3  5' TGTGGGGGATTAGACATCG   44833   C     GTCAGG    C
                                TG TGGGGGA     AGACA CG
                                || |||||||     ||||| ||
                                AC ACCCCCT     TCTGT GC
                                 _     AA____    A
GAM1837 BTN3A1   5' TGCTGCATATCAGGAGATAC  44834     GGGGA       C
                                TGCTG    GTCAGGAGA AC
                                |||||    ||||||||| ||
                                ACGAC    TAGTCCTCT TG
                                   GTA__       A
GAM1837 C20orf44 3' TGCTGGAGGGGGTTGGGGAG  44835      _  A  CA_
                                TGCTGG GGG GT   GGAG
                                |||||| ||| ||   ||||
                                ACGACC CCC CA   CCTC
                                    T   C  ACC
GAM1837 Di-Ras2  3' TGGGGGAGTGAGGTGCCG    44836        C   AGACA
                                TGGGGGAGT AGG    CCG
                                ||||||||| |||    |||
                                ACCCCCTCA TCC    GGC
                                      C   AC___
GAM1837 DKFZP566G1424 5' TGTGGGGGAGTTGGGGTTACA  44837    C       CA  AG_
                                TG TGGGGGAGT  GG   ACA
                                || |||||||||  ||   |||
                                AC ACCCCCTCA  CC   TGT
                                 _       AC  CAA
GAM1837 DKFZp586I021 3' TGTTGGGGGAGATGGGAC    44838    C       TCA  A
                                TG TGGGGGAG   GG GAC
                                || ||||||||   || |||
                                AC ACCCCCTC   CC CTG
                                 A       TA_  _
GAM1837 FLJ12526 5' GCTGGGGGAATGTGGGGCGCCG 44839          CA  AGACA
                                GCTGGGGGAGT  GG    CCG
                                ||||||||||  ||    |||
                                CGACCCCCTTA  CC    GGC
                                      CA  CCGC_
GAM1837 FLJ13111 3' TGCTGGGGGGGTGGGGAG    44840        A  CA
                                TGCTGGGGG GT  GGAG
                                |||||||| ||  ||||
                                ACGACCCCC CA  CCTC
                                      C  CC
GAM1837 FLJ30213 5' TGCTGGGGGGGCAGAG      44841        A  CA
                                TGCTGGGGG GT  GGAG
                                |||||||| ||  ||||
                                ACGACCCCC CG  TCTC
                                      C  __
GAM1837 FLJ30567 3' TGTGGTTCACCAGGAGGCACCG 44842    C   GGGA      A
                                TG TGG    GTCAGGAG CACCG
                                || |||    |||||||| |||||
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                                AC ACC    TGGTCCTC GTGGC
                                 _  AAG_      C
GAM1837 HSU79275 5' TGCTGGTGGAGGACAC     44843       G   TCAGGA
                                TGCTGG GGAG     GACAC
                                |||||| ||||     |||||
                                ACGACC CCTC     CTGTG
                                   A  _______
GAM1837 KIAA0781 3' CTGGGGGAAAGGCAC      44844         TC  AGA
                                CTGGGGGAG  AGG  CAC
                                |||||||||  |||  |||
                                GACCCCCTT  TCC  GTG
                                      __  ____
GAM1837 KIAA1086 3' GCTGGGGGCGTGGGGATGCCG 44845        A  CA  GACA
                                GCTGGGGG GT  GGA   CCG
                                |||||||| ||  |||   |||
                                CGACCCCC CA  CCT   GGC
                                     G  CC   AC__
GAM1837 KIAA1887 5' TGCTGGGAGGGGGTAGTGGGGG 44846         _____  CA  A
             A                   TGCTGGGGG    AGT  GG GA
                                |||||||||    |||  || ||
                                ACGACCCTC    TCA  CC CT
                                     CCCCA   CC  _
GAM1837 KLF12    3' GCTGGGGGACAGGAGA     44847         GT
                                GCTGGGGGA  CAGGAGA
                                |||||||||  |||||||
                                CGACCCCCT  GTCCTCT
                                      __
GAM1837 MGC11271 5' TGCTGGGGTACAGGGGACACCG 44848        GAGT   A
                                TGCTGGGG    CAGG GACACCG
                                ||||||||    |||| |||||||
                                ACGACCCC    GTCC CTGTGGC
                                     AT__    C
GAM1837 MGC20255 3' GCTGGGGGCAGGGAC       44850        AGT   A
                                GCTGGGGG   CAGG GAC
                                ||||||||   |||| |||
                                CGACCCCC   GTCC CTG
                                     ___   _
GAM1837 MGC20255 3' TGCTGGGGGAGCAGGAGCC   44849          T    ACA
                                TGCTGGGGGAG CAGGAG   CC
                                |||||||||| ||||||   ||
                                ACGACCCCCTC GTCCTC   GG
                                      _    ___
GAM1837 PALMD    5' TGCTGGGGAGGCAGAC      44851        GAGTC  _
                                TGCTGGGG    AGG AGAC
                                ||||||||    ||| ||||
                                ACGACCCC    TCC TCTG
                                     _____  G
GAM1837 PLEK2    3' TGCTGGGGAAAAGTCAAGA   44852        __
                                TGCTGGGG  GAGTCAGGA
                                ||||||||  |||||||||
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                                ACGACCCC  TTCAGTTCT
                                    TT
GAM1837  SLC21A11  3'  TGCTGGAAACAGGAGGCAC   44853      GG AGT    A
                                TGCTGG  G   CAGGAG CAC
                                ||||||  |   |||||| |||
                                ACGACC  T   GTCCTC GTG
                                   TT ___     C
GAM1837  SR-BP1    3'  TGCTGAGGGGGTTGGGGACA  44854        A  CA  A
                                TGCTGGGGG GT  GG GACA
                                ||||||||| ||  || ||||
                                ACGACTCCC CA  CC CTGT
                                     C  AC  _
GAM1837  LOC136345 3'  TGCATGGGGGAGGTGGAGA   44855    _      TCA
                                TGC TGGGGGAG   GGAGA
                                ||| ||||||||   |||||
                                ACG ACCCCCTC   CCTCT
                                  T       CA_
GAM1837  LOC145676 5'  CCGTTAGTCAGGAGGCAC    44856    GGGG       A
                                CTG    AGTCAGGAG CAC
                                |||    ||||||||| |||
                                GGC    TCAGTCCTC GTG
                                  AA__        C
GAM1837  LOC146445 3'  TGGGGGAGAGGCAGACA     44857        TC  _
                                TGGGGGAG  AGG AGACA
                                ||||||||  ||| |||||
                                ACCCCCTC  TCC TCTGT
                                    __  G
GAM1837  LOC147040 5'  GGGAAGTACAGGAGACACCG   44858       _
                                GGGGAGT CAGGAGACACCG
                                ||||||| ||||||||||||
                                CCCTTCA GTCCTCTGTGGC
                                    T
GAM1837  LOC149506 5'  GCTGGGAAGGAGGGGAC     44859       __   TCA  A
                                GCTGGG  GGAG   GG GAC
                                ||||||  ||||   || |||
                                CGACCC  CCTC   CC CTG
                                   TT   ___  _
GAM1837  LOC150378 5'  TGCTGGGGGTGGTGGAGGCACC 44860         AGTCA   A
           G                     TGCTGGGGG     GGAG CACCG
                                |||||||||     |||| |||||
                                ACGACCCCC     CCTC GTGGC
                                     ACCA_    C
GAM1837  LOC155032 5'  TGCATGGGGGAGGTGGAGA   44855    _      TCA
                                TGC TGGGGGAG   GGAGA
                                ||| ||||||||   |||||
                                ACG ACCCCCTC   CCTCT
                                  T       CA_
GAM1837  LOC204820 3'  TGCTGGAGGGGAGCGGGCACCG 44861       __     CA  AGA
                                TGCTGG  GGGAGT  GG   CACCG
                                ||||||  ||||||  ||   |||||
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                                ACGACC  CCCTCG  CC   GTGGC
                                   TC     __  C__
GAM1837  LOC253681 5'  GGGAAGTACAGGAGACACCG   44858       _
                                GGGGAGT CAGGAGACACCG
                                ||||||| ||||||||||||
                                CCCTTCA GTCCTCTGTGGC
                                    T
GAM1837  LOC254345 5'  TGTTGGGGGAGGCGGGGGCCG  44862    C       TCA  AGACA
                                TG TGGGGGAG   GG    CCG
                                || ||||||||   ||    |||
                                AC ACCCCCTC   CC    GGC
                                 A       CG_  CCC__
GAM1837  LOC256087 5'  TGCCGGGAGCCCGGGAG     44863         AG  A
                                TGCTGGGGG  TC GGAG
                                |||||||||  || ||||
                                ACGGCCCTC  GG CCTC
                                      G_  C
GAM1837  LOC51112  5'  TGTTGGGGGAGTCAGAGA    44864    C         G
                                TG TGGGGGAGTCAG AGA
                                || ||||||||||||| |||
                                AC ACCCCCTCAGTC TCT
                                 A          _
GAM1837  LOC91801  3'  TGCGGGGGACAGAAGATGCCG  44865     T     GT      CA
                                TGC GGGGGA  CAGGAGA  CCG
                                ||| ||||||  |||||||  |||
                                ACG CCCCCT  GTCTTCT  GGC
                                  _     __       AC
GAM1837  LOC92840  3'  TGCTGGGGGGGCTGCGTGGGGA  44866         A  CA___  A
                                TGCTGGGGG GT     GG GA
                                ||||||||| ||     || ||
                                ACGACCCCC CG     CC CT
                                      _  ACGCA  C
GAM1838  ADAM29    3'  GAGGGTGTCACCCGAGG     44869      C    GCCGC
                                GAGG TGTC     GCCCGAGG
                                |||| ||||     ||||||||
                                CTCC ACAG     TGGGCTCC
                                  C   ______
GAM1838  DES       3'  AAAGGCTAGTGCCTGAGG    44870        _  CGCCGC   C
                                AGAGGCT GT     GCC GAGG
                                ||||||| ||     ||| ||||
                                TTTCCGA CA     CGG CTCC
                                    T _______   A
GAM1838  GPRK5     5'  GGCTGTCAGCGCCTGGGGT   44871         CC     CGA
                                GGCTGTCG  GCGCC   GGT
                                ||||||||  |||||   |||
                                CCGACAGT  CGCGG   CCA
                                     __     ACC
GAM1838  SOD3      3'  GAGGCTGTCAGCGTGAGCGGGG 44872          CC   CC__  A
              T                  GAGGCTGTCG  GCG    CG GGT
                                ||||||||||  |||    || |||
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                                CTCCGACAGT  CGC   GC CCA
                                    __  ACTC  C
GAM1838  BC022889  3'  GAGGCTGTCGCTGTAAACATAG 44873         CGCGCCCG_
           GT                    GAGGCTGTCGC       AGGT
                                 ||||||||||        ||||
                                 CTCCGACAGCG       TCCA
                                      ACATTTGTA
GAM1838  DATF1     5'  AGAGGCTGTTCCCGTGGAG   44874        CG  CGCCC
                                 AGAGGCTGT  CCG    GAG
                                 |||||||||  |||    |||
                                 TCTCCGACA  GGC    CTC
                                      AG   AC___
GAM1838  DATF1     5'  AGAGGCTGTTCCCGTGGAG   44874        CG  CGCCC
                                 AGAGGCTGT  CCG    GAG
                                 |||||||||  |||    |||
                                 TCTCCGACA  GGC    CTC
                                      AG   AC___
GAM1838  DATF1     5'  AGAGGCTGTTCCCGTGGAG   44874        CG  CGCCC
                                 AGAGGCTGT  CCG    GAG
                                 |||||||||  |||    |||
                                 TCTCCGACA  GGC    CTC
                                      AG   AC___
GAM1838  FADS1     5'  AGGGGCTGTCAGGCGCGTGCTC 44875    A     __ _  C  C  A
           GGGGT                    AG GGCTGTC  GC CG GC CG GGT
                                 || |||||||  || || || || |||
                                 TC CCGACAG  CG GC CG GC CCA
                                  C      TC  C  A  A  C
GAM1838  FBXL9     3'  GAGGCTGTGCTGCAGGGCTGGT 44876        C  C   CCCGA
                                 GAGGCTGT GC GCG     GGT
                                 |||||||| || |||     |||
                                 CTCCGACA CG CGT     CCA
                                      _  A   CCCGA
GAM1838  FLJ10724  3'  AGAGGCTGTCCTGGAGTGAGAG 44877         GCCGCGCCC
           GT                    AGAGGCTGTC        GAGGT
                                 ||||||||||        |||||
                                 TCTCCGACAG        CTCCA
                                      GACCTCACT
GAM1838  FLJ13909  5'  GAGGCTGTCGTGCCAGAAGAGG 44878         CCGC   C___
           T                     GAGGCTGTCG    GCC    GAGGT
                                 ||||||||||    |||    |||||
                                 CTCCGACAGC    CGG    CTCCA
                                      A___    TCTT
GAM1838  FLJ22393  5'  AGTATTGCCGCGCCCGGGGT  44879    C   C        A
                                 GG TGT GCCGCGCCCG GGT
                                 || ||| |||||||||| |||
                                 TC ATA CGGCGCGGGC CCA
                                  _  A         C
GAM1838  FOXD4     5'  GAGGCTGCGCTGCGGTACCTCG 44880        T   C C_______   CGA
                                 GAGGCTG CGC G      GCC   G
                                 ||||||| ||| |      |||   |
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                                CTCCGAC GCG C      TGG   C
                                    _  A GCCAIII   AGC
GAM1838 KIAA1776 3' AGAGGCCGGGCTTGCCTGAGGT 44881        TC  CGC   C
                                AGAGGCTG  GC   GCC GAGGT
                                |||||||| ||   ||| |||||
                                TCTCCGGC  CG   CGG CTCCA
                                    C_  AA_   A
GAM1838 KIAA1817 5' GAGGCTGTCCTTGTTGAGGT   44882        CG  GCGCCC
                                GAGGCTGT  CC     GAGGT
                                |||||||| ||     |||||
                                CTCCGACA  GG     CTCCA
                                    __  AACAA_
GAM1838 RAB40C   3' GAGGCTGCACGCAGGTGCCCGG 44883        _  CGC_    A
           GGT                    GAGGCTGT CGC    GCCCG GGT
                                |||||||| |||    ||||| |||
                                CTCCGACG GCG    CGGGC CCA
                                    T   TCCA    C
GAM1838 SEF     3' GAGGCTGTGTGTGCTGAGGT   44884        CGCCGC  CC
                                GAGGCTGT     GC  GAGGT
                                ||||||||     ||  |||||
                                CTCCGACA     CG  CTCCA
                                    CACA__  A_
GAM1838 LOC143392 3' AGAGGCTGTTGTCCTGATGCAG 44885        CG_  GC__  CCGA
           GGGT                   AGAGGCTGT   CC    GC    GGT
                                |||||||||   ||    ||    |||
                                TCTCCGACA   GG    CG    CCA
                                    ACA  ACTA  TCC_
GAM1838 LOC200301 5' AGAGGCTGCGGCGGTTGGGGT  44886        T  CC   CCCGA
                                AGAGGCTG CG  GCG     GGT
                                |||||||| ||  |||     |||
                                TCTCCGAC GC  CGC     CCA
                                    _  __   CAACC
GAM1838 LOC253868 3' GAGGCAGCCCTGCCCGGGGT   44887      TGTC   GC    A
                                GAGGC    GCC  GCCCG GGT
                                |||||    |||  ||||| |||
                                CTCCG    CGG  CGGGC CCA
                                   T___   GA    C
GAM1838 LOC91661  3' GAGGATTGTTGGAGCCCGGGGT 44888      C_   CGCCGC    A
                                GAGG  TGT     GCCCG GGT
                                ||||  |||     ||||| |||
                                CTCC  ACA     CGGGC CCA
                                  TA   ACCT__    C
GAM1839 FLJ13181  5' TCCCCGGATGCGCTTCCA    44891        CACCC   GA
                                TCCCCGGAT    CGT  TCG
                                |||||||||    |||  |||
                                AGGGGCCTA    GCG  GGT
                                    C____   AA
GAM1839 KIAA1754  3' TCCCTGGAGTGCCCCGCAACTG 44892      C   TCA    TG __
           CGTC                   TCCC GGA   CCCCG  AT  CGTC
                                |||| |||   |||||  ||  ||||
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                                AGGG CCT   GGGGC  TG  GCAG
                                  A   CAC    GT  AC
GAM1839  LOC201522 5'  TCTCCGGGTCCGCCCGCCGTC  44893    C    A  AC    GAT
                                TC CCGG TC  CCCGT   CGTC
                                || |||| ||  |||||   ||||
                                AG GGCC AG  GGGCG   GCAG
                                 A    C  GC    ____
GAM1839  LOC254243 3'  TCCCCGGATTCCCTCCTGTC   44894         CA  _  G  A
                                TCCCCGGAT  CC CC TG TC
                                |||||||||  || || || ||
                                AGGGGCCTA  GG GG AC AG
                                      AG  A  _  _
GAM1839  LOC90038  3'  TCCCCGGATTCCCTCCTGTC   44894         CA  _  G  A
                                TCCCCGGAT  CC CC TG TC
                                |||||||||  || || || ||
                                AGGGGCCTA  GG GG AC AG
                                      AG  A  _  _
GAM1840  CD69      3'  TGATTTAGGAAAGTCACAAACC 44897         _   TAGG_
              TA                  TGATTTAG AAA    AGACCTA
                                |||||||| |||    |||||||
                                ACTAAATC TTT    TTTGGAT
                                     C   CAGTG
GAM1840  CDH11     3'  TGATTTAAAAAAATACCT    44898          TAGGAG
                                TGATTTAGAAA     ACCT
                                ||||||||||     ||||
                                ACTAAATTTTT     TGGA
                                      TTA___
GAM1840  MME       3'  TGATTAGAAATCCTGGTCTACC 44899       T     AGGAGAC
                                TGATT AGAAAT      CTACC
                                ||||| ||||||      |||||
                                ACTAA TCTTTA      GATGG
                                  _     GGACCA_
GAM1840  MME       3'  TGATTAGAAATCCTGGTCTACC 44899       T     AGGAGAC
                                TGATT AGAAAT      CTACC
                                ||||| ||||||      |||||
                                ACTAA TCTTTA      GATGG
                                  _     GGACCA_
GAM1840  MME       3'  TGATTAGAAATCCTGGTCTACC 44899       T     AGGAGAC
                                TGATT AGAAAT      CTACC
                                ||||| ||||||      |||||
                                ACTAA TCTTTA      GATGG
                                  _     GGACCA_
GAM1840  MME       3'  TGATTAGAAATCCTGGTCTACC 44899       T     AGGAGAC
                                TGATT AGAAAT      CTACC
                                ||||| ||||||      |||||
                                ACTAA TCTTTA      GATGG
                                  _     GGACCA_
GAM1840  TNFSF4    3'  TGACTTAAAATAGGGGACCTGC 44900         A    A    A
              C                   TGATTTAGAA TAGG GACCT CC
                                |||||||||| |||| ||||| ||
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                                ACTGAATTTT ATCC CTGGA GG
                                      _   C    C
GAM1840  DKFZP434C0826 3'  TGATTTAAAATAGGAGA     44901          A
                                TGATTTAGAA TAGGAGA
                                |||||||||| |||||||
                                ACTAAATTTT ATCCTCT
                                      _
GAM1840  DKFZP586F1318 3'  ATTTAGAGACAAGTCTACC    44902        A    AGAC
                                ATTTAGA ATAGG   CTACC
                                ||||||| |||||   |||||
                                TAAATCT TGTTC   GATGG
                                    C    A___
GAM1840  FADS1     3'  TGATTTAGAAGTATGAAG     44903          A  _
                                TGATTTAGAA TA GGAG
                                |||||||||| || ||||
                                ACTAAATCTT AT CTTC
                                      C  A
GAM1840  KIAA1143  3'  TAATTTAGAGAGAGCCTA     44904         AATA   A
                                TGATTTAGA   GGAG CCTA
                                |||||||||   |||| ||||
                                ATTAAATCT   TCTC GGAT
                                     C___   _
GAM1840  KIAA1462  3'  TGATTAGAAATGGATCATACCT 44905       T     A   G___
           A                     TGATT AGAAAT GGA   ACCTA
                                |||||  ||||||  |||   |||||
                                ACTAA TCTTTA CCT   TGGAT
                                  _     _  AGTA
GAM1840  MGC12921  3'  TGACTTGGAAACGACCTA     44906       A    AGGA
                                TGATTT GAAAT   GACCTA
                                ||||||  |||||   ||||||
                                ACTGAA CTTTG   CTGGAT
                                   C    _____
GAM1840  NCOA2     3'  TAATTTAGAAATGAAAA      44907          A
                                TGATTTAGAAAT GGAGA
                                |||||||||||  |||||
                                ATTAAATCTTTA CTTTT
                                      _
GAM1840  SEC14L1   3'  TGATTTGGGAACAGGAAGCACC 44908        AGA     _ _
                                TGATTT   AATAGGA G ACC
                                ||||||   ||||||| | |||
                                ACTAAA   TTGTCCT C TGG
                                   CCC      T G
GAM1840  TCL6      3'  TGATTTAGAGAAGGGGAG     44909         _  TA
                                TGATTTAGA AA  GGAG
                                |||||||||  ||  ||||
                                ACTAAATCT TT  CCTC
                                      C  CC
GAM1840  TCL6      3'  TGATTTAGAGAAGGGGAG     44909         _  TA
                                TGATTTAGA AA  GGAG
                                |||||||||  ||  ||||
```

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                                ACTAAATCT TT  CCTC
                                     C  CC
GAM1840 UBXD2    3' TGATTTAGAAGAAGCTAC    44910        AAT    AC
                                TGATTTAGA   AGGAG  CTAC
                                |||||||||   |||||  ||||
                                ACTAAATCT   TCTTC  GATG
                                    ____    __
GAM1840 LOC253187 3' TGGTTCAGAAAGAAGCCT    44911    A     AT    A
                                TG TTTAGAA  AGGAG CCT
                                || |||||||  ||||| |||
                                AC AAGTCTT  TCTTC GGA
                                 C      __    _
GAM1840 LOC255326 3' TGGTTTAGAGGTAAGAAAC    44912    A     AA
                                TG TTTAGA  TAGGAGAC
                                || ||||||  ||||||||
                                AC AAATCT  ATTCTTTG
                                 C     CC
GAM1840 LOC91522  3' GACTCTGAGTGGGAGGCCTGCC 44913      A  AATA   A   A
                                GATTT GA    GGAG CCT CC
                                ||||| ||    |||| ||| ||
                                CTGAG CT    CCTC GGA GG
                                   A  CAC_   C   C
GAM1841 SERPINB4  5' GTGTGTCTGTGGAATGAAGG   44916       A____
                                GTGTGT    GAATGAAGG
                                ||||||    |||||||||
                                CACACA    CTTACTTCC
                                    GACAC
GAM1841 CDK5RAP3  5' TTCTGCCTTGTGTAGAATGGGG 44917     GTA  G        AA
             G                   TTC   CC TGTGTAGAATG  GG
                                |||   || ||||||||||  ||
                                AAG   GG ACACATCTTAC  CC
                                  AC_  A         CC
GAM1841 LOC145231 5' GTGCCGTGGAAAAATGAAGG   44918    A    TGT
                                GT CCGTG   AGAATGAAGG
                                || |||||   ||||||||||
                                CA GGCAC   TTTTACTTCC
                                 C    CT_
GAM1842 EHHADH   3' TGTATGATTCATAAGATTTC   44921      A    GGA
                                TGTGT ATTCA   AAGATTTC
                                ||||| |||||   ||||||||
                                ACATA TAAGT   TTCTAAAG
                                   C    A__
GAM1842 HGF      3' TGTACAGGAAGATTTC      44922      ATT     A
                                TGTA   CAGGAA GATTTC
                                ||||   |||||| ||||||
                                ACAT   GTCCTT CTAAAG
                                    ___     _
GAM1842 TCF19    5' TGTGTAATTCGGAGAAGA    44923          A  _
                                TGTGTAATTC GGA AAGA
                                |||||||||| ||| ||||
```

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                                ACACATTAAG CCT TTCT
                                      _  C
GAM1842  TCF19    5'  TGTGTAATTCGGAGAAGA    44923         A  _
                                TGTGTAATTC GGA AAGA
                                |||||||||| ||| ||||
                                ACACATTAAG CCT TTCT
                                      _  C
GAM1842  FLJ20151 3'  TGTGGAATTCAGGGAGAT    44924     T      AA
                                TGTG AATTCAGG  AGAT
                                |||| ||||||||  ||||
                                ACAC TTAAGTCC  TCTA
                                  C      C_
GAM1843  ACCN2    5'  CCCGCCCGCGCGCGC       44927     GCGCG
                                CCCGC    CCGCGTGCGC
                                |||||    ||||||||||
                                GGGCG    GGCGCGCGCG
                                     _____
GAM1843  ACP1     5'  CCCGCGCGCAGAGGCGCC    44928         CCGCGT
                                CCCGCGCGCG     GCGCC
                                ||||||||||     |||||
                                GGGCGCGCGT     CGCGG
                                     CTC___
GAM1843  ACP1     5'  CCCCCGCGCGCCTGCGCA    44929    G      GC
                                CCC CGCGCGCC  GTGCG
                                ||| ||||||||  |||||
                                GGG GCGCGCGG  CGCGT
                                  G       A_
GAM1843  ACP1     5'  CCCGCGCGCAGAGGCGCC    44928         CCGCGT
                                CCCGCGCGCG     GCGCC
                                ||||||||||     |||||
                                GGGCGCGCGT     CGCGG
                                     CTC___
GAM1843  ACP1     5'  CCCCCGCGCGCCTGCGCA    44929    G      GC
                                CCC CGCGCGCC  GTGCG
                                ||| ||||||||  |||||
                                GGG GCGCGCGG  CGCGT
                                  G       A_
GAM1843  ADA      5'  CCCTCGTGCGCCCCGGCGC   44930    G  C    G  T
                                CCC CG GCGCC CG GCGC
                                ||| || ||||| || ||||
                                GGG GC CGCGG GC CGCG
                                  A  A    G  _
GAM1843  ADAM12   5'  CGCGCACGGCCCGCGCC     44931         CC  G
                                CGCGCGCG  GC TGCGCC
                                ||||||||  || ||||||
                                GCGCGTGC  CG GCGCGG
                                     __  G
GAM1843  ADAMTS8  5'  CCCCGGCCCGCGTGCGCC    44932     G  C  G
                                CCC CG GC CCGCGTGCGCC
                                ||| || || ||||||||||
```

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                                GGG GC CG GGCGCACGCGG
                                  _ _ _
GAM1843 ADCY6    5' CCCGCGCGTCCTGGCC      44933        CG  GCG  C
                                CCCGCGCG  CC   TG GCC
                                ||||||||  ||   || |||
                                GGGCGCGC  GG   AC CGG
                                   A_ ____ _
GAM1843 ADPRT    5' CCTCGCGTGCGCTCACCCAGCC 44934    _   C   _  G  C
                                CC CGCG GCGC CGC TG GCC
                                || |||| |||| ||| || |||
                                GG GCGC CGCG GTG GT CGG
                                 A   A   A  G  _
GAM1843 ADPRT    5' CCTCGCCGCCTCGCGTGCGC   44935    _  G   GC
                                CC CGC CGC  CGCGTGCGC
                                || ||| |||  |||||||||
                                GG GCG GCG  GCGCACGCG
                                 A  _  GA
GAM1843 AGL      5' CCGTGCGCGCACTCGCC     44936     C     C  GTG
                                CCG GCGCGC GC   CGCC
                                ||| |||||| ||   ||||
                                GGC CGCGCG TG   GCGG
                                 A     _ A__
GAM1843 ALDH3B2  5' GCCGGCCGCGTGCGCC      44937    G  C
                                GC CG GCCGCGTGCGCC
                                || || ||||||||||||
                                CG GC CGGCGCACGCGG
                                  _ _
GAM1843 AP1M1    3' CCCGAGCGCGCCAGGTGC    44938     C       C
                                CCCG GCGCGCCG GTGC
                                |||| |||||||| ||||
                                GGGC CGCGCGGT CACG
                                  T       C
GAM1843 APP      5' CCCGCGCCGCCACCGC      44939       G     GTG
                                CCCGCGC CGCCGC   CGC
                                ||||||| ||||||   |||
                                GGGCGCG GCGGTG   GCG
                                   _     ____
GAM1843 ARHGAP6  5' CACGCGCCGCCGGTGCGC    44940        _   C
                                CGCGCGC GCCG GTGCGC
                                ||||||| |||| ||||||
                                GTGCGCG CGGC CACGCG
                                   G   _
GAM1843 ARHGAP6  5' CACGCGCCGCCGGTGCGC    44940        _   C
                                CGCGCGC GCCG GTGCGC
                                ||||||| |||| ||||||
                                GTGCGCG CGGC CACGCG
                                   G   _
GAM1843 B4GALT1  5' CCCGCGGCGCCGCAGGC     44941        C       T
                                CCCGCG GCGCCGCG GC
                                |||||| |||||||| ||
```

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                                GGGCGC CGCGGCGT CG
                                  _      C
GAM1843 BARX1    5' CCGCGGCCCACTCGTGCGCC  44942      C  G   __
                                CCGCG GC CCGC  GTGCGCC
                                ||||| || ||||  |||||||
                                GGCGC CG GGTG  CACGCGG
                                  _ _   AG
GAM1843 BMPR1B   5' CCACCCCGCGCGTGCGC    44943     GCG  C
                                CCGC  CGC GCGTGCGC
                                ||||  ||| ||||||||
                                GGTG  GCG CGCACGCG
                                  GG_  _
GAM1843 BYSL     5' CCCGCGGCGCCGCGGGC    44944       C       T
                                CCCGCG GCGCCGCG GC
                                |||||| |||||||| ||
                                GGGCGC CGCGGCGC CG
                                  _      C
GAM1843 CACNA1B  5' CCCGCGTGCATCCCCGGC   44945       C  _  G  T
                                CCCGCG GCG CC CG GC
                                |||||| ||| || || ||
                                GGGCGC CGT GG GC CG
                                   A  A  G  _
GAM1843 CCND3    5' CCCGCGCGCGCGCGC      44947          CGCGT
                                CCCGCGCGCGC   GCGC
                                ||||||||||    ||||
                                GGGCGCGCGCG   CGCG
                                   _____
GAM1843 CCND3    5' CGCGCGCGCGCGCCGC     44946         C   G
                                CGCGCGCGC GCGT CGC
                                ||||||||| |||| |||
                                GCGCGCGCG CGCG GCG
                                   _   _
GAM1843 CD72     3' CCGCTCAGCCCGTGCGCC   44948     G  C  G
                                CCGC CG GCC CGTGCGCC
                                |||| || ||| ||||||||
                                GGCG GT CGG GCACGCGG
                                  A  _  _
GAM1843 CDK2AP1  5' CCCGCGCGCGTCCGGGCGGC  44949          _  C  C
                                CCCGCGCGCG CCG GTG GC
                                |||||||||| ||| ||| ||
                                GGGCGCGCGC GGC CGC CG
                                     A  C  _
GAM1843 CDKN2D   5' CGCGGTGCACCCGCGTGCGC  44950     C_   _
                                CGCG  GCGCC GCGTGCGC
                                ||||  ||||| ||||||||
                                GCGC  CGTGG CGCACGCG
                                  CA    G
GAM1843 CYP51    5' CCCACGCGCGCCACCCCGTGCG 44951           ___
                                CCCGCGCGCGCCGC  GTGCG
                                ||||||||||||||  |||||
```

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                                GGGTGCGCGCGGTG  CACGC
                                      GGG
GAM1843  DIO3    3'  CCGCGCGCGACAGGTGGGTGCC 44952        C  C   C__
                                CCGCGCGCG CG GTG  GCC
                                ||||||||| || |||  |||
                                GGCGCGCGC GT CAC  CGG
                                     T  C   CCA
GAM1843  DKC1    5'  CACCGCGTGCGTGCCGCC   44953    G   CC    _
                                CGC CGCG  GCGTGC GCC
                                ||| ||||  |||||| |||
                                GTG GCGC  CGCACG CGG
                                  _   A_    G
GAM1843  DSCAM   5'  CGCCGCGCGCTGCGC      44954    G   C  G
                                CGC CGCGC GC TGCGC
                                ||| ||||| || |||||
                                GCG GCGCG CG ACGCG
                                  _    _ _
GAM1843  DTNBP1  5'  CCCGCGCTGTCACCGCGCGC  44955       G__
                                CCCGCGC  CGCCGCGTGC
                                |||||||  ||||||||||
                                GGGCGCG  GTGGCGCGCG
                                   ACA
GAM1843  DUSP5   5'  CCCGCGCCGCGCCCCGCGGGTG 44956       _   G   C__
           CC                    CCCGCGC GCGCC CGTG  GCC
                                ||||||| ||||| ||||  |||
                                GGGCGCG CGCGG GCGC  CGG
                                   G   G   CCA
GAM1843  DVL3    5'  CCCGCGCGCGGCCTGC     44957         CC  G
                                CCCGCGCGCG  GC TGC
                                ||||||||||  || |||
                                GGGCGCGCGC  CG ACG
                                     __ G
GAM1843  EFEMP2  5'  CCCGCGCGGCCCGCGGC    44958       C  G   C
                                CCCGCGCG GCC CGTG GC
                                |||||||| ||| |||| ||
                                GGGCGCGC CGG GCGC CG
                                  _  _   _
GAM1843  EMS1    5'  CCGCCGCGCCAGCCGC     44959    G     C  G
                                CCGC CGCGCCG GT CGC
                                |||| ||||||| || |||
                                GGCG GCGCGGT CG GCG
                                  _     _ _
GAM1843  EMS1    5'  CCGCCGCGCCAGCCGC     44959    G     C  G
                                CCGC CGCGCCG GT CGC
                                |||| ||||||| || |||
                                GGCG GCGCGGT CG GCG
                                  _     _ _
GAM1843  EN1     5'  CCCGCGCCGCACCCGCGT   44960       _   _
                                CCCGCGC GCGCC GCGT
                                ||||||| ||||| ||||
```

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                                GGGCGCG CGTGG CGCA
                                   G    G
GAM1843  EZH2    5'  CCCGCGCGCCGACTCGCGT   44962         __ _
                                CCCGCGCGC  GC CGCGT
                                |||||||||  || |||||
                                GGGCGCGCG  TG GCGCA
                                    GC  A
GAM1843  EZH2    5'  CCCGCGCGTCGCCCCCGCGCGC 44961        _  _ G
            C                    CCCGCGCG CGC C CGTGCGCC
                                |||||||| ||| | ||||||||
                                GGGCGCGC GCG G GCGCGCGG
                                    A  G G
GAM1843  EZH2    5'  CCCGCGCGTCGCCGGCGCACGC 44963        _  _______ CGTG
            G                    CCCGCGCG CGC     CG   CG
                                |||||||| |||     ||   ||
                                GGGCGCGC GCG     GC   GC
                                    A  GIIICC  GTGC
GAM1843  F2RL3   3'  CCCGCGCGCCCGCAC      44964         G   GTGC
                                CCCGCGCGC CCGC   GC
                                |||||||||  ||||   ||
                                GGGCGCGCG GGCG   TG
                                   _   _____
GAM1843  FANCC   5'  CCGCGCGCGCGCACACGTG   44965   _      _
                                CC CGCGCGCGC CGCGTG
                                || |||||||| ||||||
                                GG GCGCGCGCG GTGCAC
                                 C       T
GAM1843  FOS     5'  CGCTGCGCCGCGGCCGCC    44966    GC      TG
                                CGC  GCGCCGCG  CGCC
                                |||  ||||||||  ||||
                                GCG  CGCGGCGC  GCGG
                                  A_      CG
GAM1843  FPGS    3'  CCCGCGCCGCAGCACCTGCG  44967       G  __  G
                                CCCGCGC CGC  CGC TGCG
                                ||||||| |||  ||| ||||
                                GGGCGCG GCG  GTG ACGC
                                    _  TC  G
GAM1843  FUT4    5'  GCGCGCGCCCACCGCC      44968         G  G
                                GCGCGCGCC CGT CGCC
                                |||||||||  ||| ||||
                                CGCGCGCGG GTG GCGG
                                   _  _
GAM1843  GAD2    5'  CCCTGCGCGCGCGTGCGTGC  44969    _      C_
                                CCC GCGCGCGC  GCGTGC
                                ||| ||||||||  ||||||
                                GGG CGCGCGCG  CGCACG
                                  A       CA
GAM1843  GALR1   5'  CCCGCGCGCGCCCAGCGCC    44970         G  CGT
                                CCCGCGCGC CCG   GCGCC
                                |||||||||  |||   |||||
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                                GGGCGCGCG GGT   CGCGG
                                      _  ____
GAM1843  GAN      5'  CCTGCGCGCGCGCCCGCC    44971    GC     C   G
                                CC  GCGCGC GCGT CGCC
                                ||  |||||| |||| ||||
                                GG  CGCGCG CGCG GCGG
                                 A_     _   G
GAM1843  GCGR     5'  CCCGCGCGGCGCTGC       44972        C  C  G
                                CCCGCGCG GC GC TGC
                                |||||||| || || |||
                                GGGCGCGC CG CG ACG
                                      _ _ _
GAM1843  GRB14    5'  CCCGCGCGTGGCCCGGGGCGC  44973        C_  G  T_
                                CCCGCGCG  GCC CG  GCGC
                                ||||||||  ||| ||  ||||
                                GGGCGCGC  CGG GC  CGCG
                                     AC  _ CC
GAM1843  GUCY1A2  5'  CGGCGCATCGCCGTGCGCC   44974    C    C  _
                                CG GCGCG CGC GTGCGCC
                                || ||||| ||| |||||||
                                GC CGCGT GCG CACGCGG
                                 _    A  G
GAM1843  HCN4     5'  CCCGCGCGGGTCCCGGGCGTGC 44975        CG_ ___
           G                     CCCGCGCG   CC   GCGTGCG
                                ||||||||   ||   |||||||
                                GGGCGCGC   GG   CGCACGC
                                     CCA  GCC
GAM1843  HNRPD    5'  CCCGCGCTGCCGCGCGC     44976       GC
                                CCCGCGC  GCCGCGTGC
                                |||||||  |||||||||
                                GGGCGCG  CGGCGCGCG
                                   A_
GAM1843  HNRPD    5'  CCCGCGCTGCCGCGCGC     44976       GC
                                CCCGCGC  GCCGCGTGC
                                |||||||  |||||||||
                                GGGCGCG  CGGCGCGCG
                                   A_
GAM1843  HNRPDL   5'  CCCGCCGCGCGCACGCGTG   44977      _     _
                                CCCGC GCGCGC CGCGTG
                                ||||| |||||| ||||||
                                GGGCG CGCGCG GCGCAC
                                   G     T
GAM1843  HPS4     5'  CCTGCGCGCGCGGCAGAGAGGC 44978    C       C   TGC__
           C                     CC GCGCGCGC GCG    GCC
                                || |||||||| |||    |||
                                GG CGCGCGCG CGT    CGG
                                 A       C   CTCTC
GAM1843  HRB      5'  GCGCGCGCCGCCCGCGCC    44979          G
                                GCGCGCGCCGC TGCGCC
                                |||||||||| ||||||
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```
                                CGCGCGCGGCG GCGCGG
                                      G
GAM1843  ID4      5'  CGCGCGCGCCCTGCGC      44980          GCG
                                CGCGCGCGCC   TGCGC
                                ||||||||||   |||||
                                GCGCGCGCGG   ACGCG
                                      G__
GAM1843  IL10RA   5'  CCTGGGCGCGCCGCATCG    44981    GC_        G
                                CC   GCGCGCCGCGT CG
                                ||   |||||||||||| ||
                                GG   CGCGCGGCGTA GC
                                 ACC         _
GAM1843  IL6R     5'  CCCGCGCCGCGCTCGGC     44982        _    CG  T
                                CCCGCGC GCGC  CG GC
                                ||||||| ||||  || ||
                                GGGCGCG CGCG  GC CG
                                    G   A_ _
GAM1843  IRS1     5'  CGCGCGCGCGCGCGCGCC    44983         C
                                CGCGCGCGC GCGTGCGCC
                                ||||||||| |||||||||
                                GCGCGCGCG CGCGCGCGG
                                      _
GAM1843  JAK2     5'  CCCGACGCGCGCCGCAAGC   44984      _         T
                                CCCG CGCGCGCCGCG GC
                                |||| ||||||||||| ||
                                GGGC GCGCGCGGCGT CG
                                  T         T
GAM1843  JUND     5'  CCTGCGCCGCGCCACTTGTGCG 44985    C   _      ___
              CC                  CC GCGC GCGCCGC  GTGCGCC
                                || |||| |||||||  |||||||
                                GG CGCG CGCGGTG  CACGCGG
                                 A   G      AA
GAM1843  KCNF1    5'  CCCGCGCGCGCCCTCGCAGCC  44986          G_   C
                                CCCGCGCGCGCC  CGTG GCC
                                ||||||||||||  |||| |||
                                GGGCGCGCGCGG  GCGT CGG
                                      GA   _
GAM1843  KCNS2    5'  CCCGCGCCGCGCGGGGGCGC   44987       G   C   T___
                                CCCGCGC CGC GCG   GCGC
                                ||||||| ||| |||   ||||
                                GGGCGCG GCG CGC   CGCG
                                    _   _   CCC
GAM1843  LAD1     5'  CCCGCGCGCCCCGGCCGCGC   44988        G   C  _
                                CCCGCGCGC CCG GT GCGC
                                ||||||||| ||| || ||||
                                GGGCGCGCG GGC CG CGCG
                                      G   _  G
GAM1843  LAD1     5'  CCCCCGCGCGCCCCGGC     44989     G      G  T
                                CCC CGCGCGCC CG GC
                                ||| |||||||| || ||
```

```
                                GGG GCGCGCGG GC CG
                                  G       G  _
GAM1843  LASS1    3'  CCGCGCGCGACAAGCGCC    44990         CC   T
                                CCGCGCGCG  GCG GCGCC
                                |||||||||  ||| |||||
                                GGCGCGCGC  TGT CGCGG
                                     __   T
GAM1843  LYPLA1   5'  CGTGCGCGCCAACGCGGCC   44991    C       _   C
                                CG GCGCGCCG CGTG GCC
                                || |||||||| |||| |||
                                GC CGCGCGGT GCGC CGG
                                 A       T   _
GAM1843  LYPLA1   5'  CCGCGCGCGCCCGCGCG     44992          G
                                CCGCGCGCGCC CGTGCG
                                |||||||||||  ||||||
                                GGCGCGCGCGG GCGCGC
                                             _
GAM1843  MADH6    5'  CCGCGCGCGGCCAGCGGC    44993         _ _   T
                                CCGCGCGCG CC GCG GC
                                |||||||||  ||  |||  ||
                                GGCGCGCGC GG CGC CG
                                     C  T   _
GAM1843  MADH7    5'  CCCGCGCGGCCCGCGC      44994        C   G
                                CCCGCGCG GCC CGTGC
                                ||||||||  |||  |||||
                                GGGCGCGC CGG GCGCG
                                        _   _
GAM1843  MAP3K8   5'  CCCGCGTCGCCCGCACGC    44995       CG    G  TG
                                CCCGCG  CGCC CG  CGC
                                ||||||  ||||  ||  |||
                                GGGCGC  GCGG GC  GCG
                                   A_    _  GT
GAM1843  MAPK14   5'  CCCGCGCGCGCGGCTGC     44996          C  G
                                CCCGCGCGCGC GC TGC
                                ||||||||||  ||  |||
                                GGGCGCGCGCG CG ACG
                                     C  _
GAM1843  MAPK14   5'  CCCGCGCGCGCGGCTGC     44996          C  G
                                CCCGCGCGCGC GC TGC
                                ||||||||||  ||  |||
                                GGGCGCGCGCG CG ACG
                                     C  _
GAM1843  MAPK14   5'  CCCGCGCGCGCGGCTGC     44996          C  G
                                CCCGCGCGCGC GC TGC
                                ||||||||||  ||  |||
                                GGGCGCGCGCG CG ACG
                                     C  _
GAM1843  MAPK14   5'  CCCGCGCGCGCGGCTGC     44996          C  G
                                CCCGCGCGCGC GC TGC
                                ||||||||||  ||  |||
```

```
                                GGGCGCGCGCG CG ACG
                                      C  _
GAM1843  MBTPS2   5'  CCGCGCGCGCCTTACAGCC   44997          GCG  _
                                CCGCGCGCGCC   TGC GCC
                                ||||||||||   ||| |||
                                GGCGCGCGCGG   ATG CGG
                                      A__   T
GAM1843  MGAT2    5'  CCCCGCGCCGCCTGCGC     44998     GCG      G
                                CCC   CGCGCCGC TGCGC
                                |||   |||||||| |||||
                                GGG   GCGCGGCG ACGCG
                                  ___       G
GAM1843  MKPX     5'  CCCGTGCGCACCGGGCAGGCC  44999      C       C  C
                                CCCG GCGCGCCG GTG GCC
                                |||| |||||||| ||| |||
                                GGGC CGCGTGGC CGT CGG
                                  A       C  C
GAM1843  MMP25    3'  CCCAGCGCGCGTGCGCC     45000      C     CGC
                                CCCG GCGCGC   GTGCGCC
                                |||| ||||||   |||||||
                                GGGT CGCGCG   CACGCGG
                                  _     ____
GAM1843  MSF      5'  CCCCGCGCGCTGCGC       45001     G      CGCG
                                CCC CGCGCGC    TGCGC
                                ||| |||||||    |||||
                                GGG GCGCGCG    ACGCG
                                  _     _____
GAM1843  MSX1     5'  CCCGCGCGCGCCTCCCGCC   45002          GCGTG
                                CCCGCGCGCGCC    CGCC
                                ||||||||||||    ||||
                                GGGCGCGCGCGG    GCGG
                                      AGG__
GAM1843  MYO5A    5'  CCCCGCGCGCCTACGC      45003     G      GCG
                                CCC CGCGCGCC   TGCGC
                                ||| ||||||||   |||||
                                GGG GCGCGCGG   ATGCG
                                  _      ___
GAM1843  NAB2     5'  CCCGCGCACGATGCCGTGT   45004         ___   C
                                CCCGCGCGC   GCCG GT
                                |||||||||   |||| ||
                                GGGCGCGTG   CGGC CA
                                     CTA    A
GAM1843  NAP1     3'  CCCGCTGCGCATGCGC      45005      GC   CGC
                                CCCGC  GCGC   GTGCGC
                                |||||  ||||   ||||||
                                GGGCG  CGCG   TACGCG
                                  A_    ____
GAM1843  NDUFS6   3'  CCCGGCGTGCCACACGC     45006      C  C
                                CCCG GCG GCCGCGTGC
                                |||| ||| |||||||||
```

```
                                GGGC CGC CGGTGTGCG
                                  _  A
GAM1843  NTRK2    5'  CCCGGCGCGCCGGGCACC    45007     C      CGT
                                CCCG GCGCGCCG  GCGCC
                                |||| ||||||||  |||||
                                GGGC CGCGCGGC  CGTGG
                                  _      C__
GAM1843  NXT1     5'  CCCGCGCGCGGCCAGC     45008         _  CGTGC
                                CCCGCGCGCG CCG    GC
                                |||||||||| |||    ||
                                GGGCGCGCGC GGT    CG
                                     C  _____
GAM1843  PAIP2    5'  CCCCCGCTCGACGTGCGC    45009    G  G  CC
                                CCC CGC CG  GCGTGCGC
                                ||| ||| ||  ||||||||
                                GGG GCG GC  TGCACGCG
                                  G  A  __
GAM1843  PDGFB    5'  CCCGCTGCGCGCTCGGC     45010     _    CG  T
                                CCCGC GCGCGC  CG GC
                                ||||| ||||||  || ||
                                GGGCG CGCGCG  GC CG
                                   A     A_ _
GAM1843  PITX1    3'  CCCGCGTGCGTCCTCCGCGCC  45011      C  _  GCG
                                CCCGCG GCG CC  TGCGCC
                                |||||| ||| ||  ||||||
                                GGGCGC CGC GG  GCGCGG
                                   A  A  AG_
GAM1843  PLCG2    5'  CCCGCGCGCGCAGCCCGCG   45012         C  G
                                CCCGCGCGCGC GC TGCG
                                |||||||||| || ||||
                                GGGCGCGCGCG CG GCGC
                                     T  G
GAM1843  PPP3CC   5'  CCCGCCGGACGTGCGC     45013     G  CGCC
                                CCCGC CG   GCGTGCGC
                                ||||| ||   ||||||||
                                GGGCG GC   TGCACGCG
                                  _ C___
GAM1843  PTPRJ    5'  CCCGCCGTGCGCCCGAGC    45014     _ C    G  T
                                CCCGC G GCGCC CG GC
                                ||||| | ||||| || ||
                                GGGCG C CGCGG GC CG
                                   G A    _ T
GAM1843  PTPRJ    5'  CCCGCGCGCCCTGGAACGTGC  45015       G  ____
                                CCCGCGCGC CC   GCGTGC
                                |||||||| ||   ||||||
                                GGGCGCGCG GG   TGCACG
                                     _ ACCT
GAM1843  PTS      5'  CCCGCCGCGCGGCCGGTGC   45016     _   _  C
                                CCCGC GCGCG CCG GTGC
                                ||||| ||||| ||| ||||
```

```
                                GGGCG CGCGC GGC CACG
                                  G    C  _
GAM1843 ROBO1    5' CCCGCGCGGCGCCCAACATCGC 45017        _   __   G
              C                   CCCGCGCG CGCC  GCGT CGCC
                                  |||||||| ||||  |||| ||||
                                  GGGCGCGC GCGG  TGTA GCGG
                                     C   GT   _
GAM1843 RRP22    5' CCGGCGCCGCACCGTGCGCC  45018    C   _    GC
                                  CC GCGC GCGCC  GTGCGCC
                                  || |||| |||||  |||||||
                                  GG CGCG CGTGG  CACGCGG
                                   C   G    __
GAM1843 RTN2     5' CCGCCGCGCCCACGACGCC   45019     _   G    T
                                  CCGC GCGC CCGCG GCGCC
                                  |||| |||| ||||| |||||
                                  GGCG CGCG GGTGC TGCGG
                                    G   _    _
GAM1843 SHB      5' CCCGCGCGCCCGTGCCCG    45020        G   C  G
                                  CCCGCGCGC CCG GT CG
                                  ||||||||| ||| || ||
                                  GGGCGCGCG GGC CG GC
                                       _  A  G
GAM1843 SIX2     5' CCCGCCCGCGCGCGC      44927      GCGCG
                                  CCCGC    CCGCGTGCGC
                                  |||||    ||||||||||
                                  GGGCG    GGCGCGCGCG
                                           _____
GAM1843 SLC25A11 5' CCCGTGCGCGCGCGGC     45022     C    C   T
                                  CCCG GCGCGC GCG GC
                                  |||| |||||| ||| ||
                                  GGGC CGCGCG CGC CG
                                    A     _  _
GAM1843 SLC25A11 5' CCGTGCGCGCGCGGCCCC   45021     C    C   T  G
                                  CCG GCGCGC GCG GC CC
                                  ||| |||||| ||| || ||
                                  GGC CGCGCG CGC CG GG
                                    A     _  _  G
GAM1843 SLC25A15 5' CCCGCCGCGCCGGCGTGGCC  45023      G     _   C
                                  CCCGC CGCGCCG CGTG GCC
                                  ||||| ||||||| |||| |||
                                  GGGCG GCGCGGC GCAC CGG
                                     _      C   _
GAM1843 SLC30A4  5' CGCGCCCGCCGCGCCCGC    45024      G      G
                                  CGCGC CGCCGCGT CGC
                                  ||||| |||||||| |||
                                  GCGCG GCGGCGCG GCG
                                    G       G
GAM1843 SORCS2   5' CCGCGCGCCCCGCGGGAGGGC 45025        G    TGC__
                                  CCGCGCGC CCGCG    GC
                                  |||||||| |||||    ||
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                                GGCGCGCG GGCGC    CG
                                    G    CCTCC
GAM1843  SOX11    3'  CCCGCCGCGCCCCGCGC    45027      G    G
                                CCCGC CGCGCC CGTGC
                                ||||| |||||| |||||
                                GGGCG GCGCGG GCGCG
                                  _    G
GAM1843  SOX11    3'  CCCGCGGCGGGGCGCGC    45026      C  CC
                                CCCGCG GCG  GCGTGC
                                |||||| |||  ||||||
                                GGGCGC CGC  CGCGCG
                                  _  CC
GAM1843  SPTBN4   5'  CCGCATGCGCCGCCGCGCC   45028      C     G
                                CCGCG GCGCCGC TGCGCC
                                ||||| ||||||| ||||||
                                GGCGT CGCGGCG GCGCGG
                                  A     _
GAM1843  ST7      5'  CGCGCCGCCGCGCCGCC    45029      G      G
                                CGCGC CGCCGCGT CGCC
                                ||||| |||||||| ||||
                                GCGCG GCGGCGCG GCGG
                                  _      _
GAM1843  ST7      5'  CGCGCCGCCGCGCCGCC    45029      G      G
                                CGCGC CGCCGCGT CGCC
                                ||||| |||||||| ||||
                                GCGCG GCGGCGCG GCGG
                                  _      _
GAM1843  TACSTD1  5'  ACTCGCGGGAGGGCGTGCGCC  45030    G   CC___
                                GC CGCG    GCGTGCGCC
                                || ||||    |||||||||
                                TG GCGC    CGCACGCGG
                                 A   CCTCC
GAM1843  TLE1     5'  CCGCGTGCGCGGCGCC     45031      C   CGC T
                                CCGCG GCGC   G GCGCC
                                ||||| ||||   | |||||
                                GGCGC CGCG   C CGCGG
                                  A   ___ _
GAM1843  TLR5     5'  CCCCGCGCCGCCTGCGCC    45032    GCG      G
                                CCC   CGCGCCGC TGCGCC
                                |||   |||||||| ||||||
                                GGG   GCGCGGCG ACGCGG
                                  ___      G
GAM1843  TRRAP    3'  CCCGCGTGCCGTGGCGGCC   45033      CGC   C_  C
                                CCCGCG   GCCG  GTG GCC
                                ||||||   ||||  ||| |||
                                GGGCGC   CGGC  CGC CGG
                                  A__    AC   _
GAM1843  TXNRD2   5'  CCCGCCGCGCTGCCTGCGCC  45034     G    C  G
                                CCCGC CGCGC GC TGCGCC
                                ||||| ||||| || ||||||
```

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                                GGGCG GCGCG CG ACGCGG
                                  _    A  G
GAM1843  UGCG     5'  CCCGCCCGCGCGCTCTCGCC  45035      G    C  GTG
                                CCCGC CGCGC GC  CGCC
                                ||||| ||||| ||  ||||
                                GGGCG GCGCG CG  GCGG
                                  G    _  AGA
GAM1843  WASF3    5'  CCCGCCGCGCCGCGGC      45036      G       T
                                CCCGC CGCGCCGCG GC
                                ||||| ||||||||| ||
                                GGGCG GCGCGGCGC CG
                                  _       _
GAM1843  WISP2    5'  CGCGCGCGCGCGCGCGCGC   45037        _
                                CGCGCGCGC CGCGTGCGC
                                ||||||||| |||||||||
                                GCGCGCGCG GCGCGCGCG
                                     C
GAM1843  WNT2     5'  GCGCGCCTCCCGCGCGCC    45038      G_  G
                                GCGCGC  CC CGTGCGCC
                                ||||||  || ||||||||
                                CGCGCG  GG GCGCGCGG
                                  GA  _
GAM1843  WWOX     5'  CCCGCGCGCGTCGGGGCC    45039        C  CGTGC
                                CCCGCGCGCG CG   GCC
                                |||||||||| ||    |||
                                GGGCGCGCGC GC   CGG
                                     A  CC___
GAM1843  WWOX     3'  CGCCGCGCCGCGCAGTGC    45040    G       GC_
                                CGC CGCGCCGCGT  GC
                                ||| ||||||||||  ||
                                GCG GCGCGGCGCG  CG
                                  _       TCA
GAM1843  WWOX     5'  CCCGCGCGCGTCGGGGCC    45039        C  CGTGC
                                CCCGCGCGCG CG   GCC
                                |||||||||| ||    |||
                                GGGCGCGCGC GC   CGG
                                     A  CC___
GAM1843  WWOX     5'  CCCGCGCGCGTCGGGGCC    45039        C  CGTGC
                                CCCGCGCGCG CG   GCC
                                |||||||||| ||    |||
                                GGGCGCGCGC GC   CGG
                                     A  CC___
GAM1843  WWOX     5'  CCCGCGCGCGTCGGGGCC    45039        C  CGTGC
                                CCCGCGCGCG CG   GCC
                                |||||||||| ||    |||
                                GGGCGCGCGC GC   CGG
                                     A  CC___
GAM1843  WWOX     5'  CCCGCGCGCGTCGGGGCC    45039        C  CGTGC
                                CCCGCGCGCG CG   GCC
                                |||||||||| ||    |||
```

```
                                GGGCGCGCGC GC    CGG
                                     A  CC___
GAM1843  ZIC1     5'  CGCGCGCGCCGCGCGGCGC   45041          _
                                CGCGCGCGCCGCGTG CGC
                                |||||||||||||| |||
                                GCGCGCGCGGCGCGC GCG
                                        C
GAM1843  ZNF76    5'  CCCGCGCGCAGCCTCGTGC   45042       _  G
                                CCCGCGCGC GCC CGTGC
                                ||||||||| ||| |||||
                                GGGCGCGCG CGG GCACG
                                     T  A
GAM1843  AHCYL1   5'  CCCGCGCCGCCACCTCCGC   45043       G    GTG
                                CCCGCGC CGCCGC  CGC
                                ||||||| ||||||  |||
                                GGGCGCG GCGGTG  GCG
                                   _    GAG
GAM1843  APCL     3'  CCCTGCGCGCCGCAAAGGCC  45044    GC       TGC
                                CCC  GCGCGCCGCG  GCC
                                |||  ||||||||||  |||
                                GGG  CGCGCGGCGT  CGG
                                  A_        TTC
GAM1843  APXL2    5'  CCCGCGCGGGCCACAGGC    45045       C    T
                                CCCGCGCG GCCGCG GC
                                |||||||| |||||| ||
                                GGGCGCGC CGGTGT CG
                                     C    C
GAM1843  ARHU     5'  CCCGCCTGCGCGCCGCGCGC  45046     __
                                CCCGC  GCGCGCCGCGTGC
                                |||||  ||||||||||||
                                GGGCG  CGCGCGGCGCGCG
                                   GA
GAM1843  ARS2     5'  CCCGCGCTGCGCCTGCGT    45047       _   _
                                CCCGCGC GCGCC GCGT
                                ||||||| ||||| ||||
                                GGGCGCG CGCGG CGCA
                                     A    A
GAM1843  BRD2     5'  CGCGCGCGCGCGCTCGC     45048       C   G
                                CGCGCGCGC GCGT CGC
                                ||||||||| |||| |||
                                GCGCGCGCG CGCG GCG
                                     _   A
GAM1843  C20orf154 5'  CCCGCGCGGTGCTGAACC   45049       CGCC  G  C
                                CCCGCGCG   GC TG GCC
                                ||||||||   || || |||
                                GGGCGCGC   CG AC TGG
                                     CA__  _  T
GAM1843  C20orf28 3'  CCCGCGCGGCCCGGGC     45050       C  G  T
                                CCCGCGCG GCC CG GC
                                |||||||| ||| || ||
```

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                                GGGCGCGC CGG GC CG
                                   _  _  C
GAM1843  CAC-1    5'  CCCGCGCGCCCCGCACC     45051        G   GTGC
                                CCCGCGCGC CCGC   GCC
                                ||||||||| ||||   |||
                                GGGCGCGCG GGCG   TGG
                                   G  ____
GAM1843  CASKIN1  3'  CGCGCCGCGCCCAGACGCGCC  45052     _   G __
                                CGCGC GCGCC CG  TGCGCC
                                ||||| ||||| ||  ||||||
                                GCGCG CGCGG GT  GCGCGG
                                  G   _ CT
GAM1843  CBX4     5'  CCCGCGCCGCCCCGGC      45053       G   G  T
                                CCCGCGC CGCC CG GC
                                ||||||| |||| || ||
                                GGGCGCG GCGG GC CG
                                   _   G  _
GAM1843  CBX4     5'  CCCGCGCTGCCCGCGC      45054       GC  G
                                CCCGCGC  GCC CGTGC
                                |||||||  ||| |||||
                                GGGCGCG  CGG GCGCG
                                   A_  _
GAM1843  CDC14B   5'  CCCGCGCGGGCGCTGGCGCACG 45055       __  _______ CGTG
           CG                   CCCGCGC  GCGC    CG   CG
                                |||||||  ||||    ||   ||
                                GGGCGCG  CGCG    GC   GC
                                   CC   AIIICC  GTGC
GAM1843  CDC14B   5'  CCCGCGCGGGCGCTGGCGCACG 45055       __  _______ CGTG
           CG                   CCCGCGC  GCGC    CG   CG
                                |||||||  ||||    ||   ||
                                GGGCGCG  CGCG    GC   GC
                                   CC   AIIICC  GTGC
GAM1843  CDC14B   5'  CCCGCGCGCCCGCGCGC    45056       G
                                CCCGCGCGC CCGCGTGC
                                ||||||||| ||||||||
                                GGGCGCGCG GGCGCGCG
                                   _
GAM1843  CDC14B   5'  CCCGCGCGCCCGCGCGC    45056       G
                                CCCGCGCGC CCGCGTGC
                                ||||||||| ||||||||
                                GGGCGCGCG GGCGCGCG
                                   _
GAM1843  CDC14B   5'  CCCGCGCGGGCGCTGGCGCACG 45055       __  _______ CGTG
           CG                   CCCGCGC  GCGC    CG   CG
                                |||||||  ||||    ||   ||
                                GGGCGCG  CGCG    GC   GC
                                   CC   AIIICC  GTGC
GAM1843  CDC14B   5'  CCCGCGCGCCCGCGCGC    45056       G
                                CCCGCGCGC CCGCGTGC
                                ||||||||| ||||||||
```

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                                GGGCGCGCG GGCGCGCG
                                        _
GAM1843  CENTG2   5'  CCGCGCGCTGCGTACTGCGCC  45057        _  C_  G
                                CCGCGCGC GC  GC TGCGCC
                                ||||||||  ||  ||  ||||||
                                GGCGCGCG CG  TG ACGCGG
                                     A  CA  _
GAM1843  CENTG2   3'  CCGGCGCGTGCCGCGTGAC   45058    C    C      C
                                CC GCGCG GCCGCGTG GC
                                ||  |||||  ||||||||  ||
                                GG CGCGC CGGCGCAC TG
                                 C    A       _
GAM1843  CHST3    5'  CCCGCGCGGCCCGAGCTGTGCG 45059         C  ____  _
                                CCCGCGCG GCC   GC GTGCG
                                ||||||||  |||   ||  |||||
                                GGGCGCGC CGG   CG CACGC
                                     _  GCT  A
GAM1843  CHSY1    5'  CCCGCGCGCCCTCAGC      45060         G  G  T
                                CCCGCGCGC CC CG GC
                                |||||||||  ||  ||  ||
                                GGGCGCGCG GG GT CG
                                      _  A  _
GAM1843  DKFZP434A1315 5'  CCCGACGCGCATGCGC      45061      C     CGC
                                CCCG GCGCGC   GTGCGC
                                ||||  ||||||   ||||||
                                GGGC TGCGCG   TACGCG
                                  _     ____
GAM1843  DKFZP434B195 5'  CCCGCGTACGCGGAGCCGCGCC 45062       CG   C__  G
                                CCCGCG  CGC   GC TGCGCC
                                ||||||  |||   ||  ||||||
                                GGGCGC  GCG   CG GCGCGG
                                   AT   CCT  _
GAM1843  DKFZP434C128 3'  CCGCGCCGCCCTCCGTGC    45063       G    G__
                                CCGCGC CGCC   CGTGC
                                ||||||  ||||   |||||
                                GGCGCG GCGG   GCACG
                                   _   GAG
GAM1843  DKFZp762K222 5'  CCCGCGCGGCGGCAGCGC    45064        C  C   T
                                CCCGCGCG GC GCG GCGC
                                ||||||||  ||  |||  ||||
                                GGGCGCGC CG CGT CGCG
                                     _  C   _
GAM1843  EIF2B3   5'  CCCGCACGCGCAACCGC     45065          C  G
                                CCCGCGCGCGC GC TGC
                                ||||||||||  ||  |||
                                GGGCGTGCGCG TG GCG
                                       T  _
GAM1843  EMILIN-2  5'  CCCGCGCGCAGCGGGCGCGCC  45066          C  C
                                CCCGCGCGCG CG GTGCGCC
                                |||||||||  ||  |||||||
```

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                                GGGCGCGCGT GC CGCGCGG
                                      C  C
GAM1843 ESDN     5' CCCCGCGCGCCTCTGGCC    10999     G      GCG  C
                                CCC CGCGCGCC   TG GCC
                                ||| ||||||||   || |||
                                GGG GCGCGCGG   AC CGG
                                  _       AG_  _
GAM1843 FLJ10709 5' CGCGCGCGGCTGGGAGCAGCC  45067        CC  GT___  _
                                CGCGCGCG  GC    GC GCC
                                ||||||||  ||    || |||
                                GCGCGCGC  CG    CG CGG
                                     __ ACCCT  T
GAM1843 FLJ12132 5' CCGCGCGTGCGGCCACGCC    45068       C  C  G
                                CCGCGCG GC GC TGCGCC
                                ||||||| || || ||||||
                                GGCGCGC CG CG GTGCGG
                                    A  C  _
GAM1843 FLJ12587 5' CCCGCGCGAGCTCAACAGGC   45069        C  _  _  T
                                CCCGCGCG GC CG CG GC
                                |||||||| || || || ||
                                GGGCGCGC CG GT GT CG
                                     T  A  T  C
GAM1843 FLJ13955 5' CCCGCGCGGCCGTAGGTGC    45070        C    C__
                                CCCGCGCG GCCG   GTGC
                                |||||||| ||||   ||||
                                GGGCGCGC CGGC   CACG
                                     _    ATC
GAM1843 FLJ14566 5' CCCGTGCACACCATGTGTGTGC 45071     C       C__   C
             C                   CCCG GCGCGCCG   GTG GCC
                                ||||| |||||||||   ||| |||
                                GGGC CGTGTGGT   CAC CGG
                                  A       ACA   A
GAM1843 FLJ20330 5' CGCCAGTCCGCTGCGTGCGCC  45072     G  ___   C
                                CGC CG   CGC GCGTGCGCC
                                ||| ||   ||| |||||||||
                                GCG GT   GCG CGCACGCGG
                                  _  CAG   A
GAM1843 FLJ20421 5' CCCCGCGCGCCTGACTCGCC   45073     G       GCGTG
                                CCC CGCGCGCC     CGCC
                                ||| ||||||||     ||||
                                GGG GCGCGCGG     GCGG
                                  _       ACTGA
GAM1843 FLJ20647 5' CGGCAGCAGCCGCGTGCGCC   45074    C  _  _
                                CG GC GC GCCGCGTGCGCC
                                || || || ||||||||||||
                                GC CG CG CGGCGCACGCGG
                                 _ T  T
GAM1843 FLJ20958 5' CCCGGGCGCGCGCTCATGC    45075     __       CG
                                CCC  GCGCGCGC  CGTGC
                                |||  ||||||||  |||||
```

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                                GGG  CGCGCGCG  GTACG
                                  CC       A_
GAM1843  FLJ21613  5'  CCCGCGCCGCCACGCAC     45076        G      TG
                                CCCGCGC CGCCGCG  C
                                ||||||| |||||||  |
                                GGGCGCG GCGGTGC  G
                                   _      GT
GAM1843  FLJ23816  3'  CCCGCGCGTCCAGGTGC     45077        CG   C
                                CCCGCGCG  CCG GTGC
                                ||||||||  ||| ||||
                                GGGCGCGC  GGT CACG
                                    A_   C
GAM1843  FOXJ1     5'  CCCGCCGCGCTCTCTGGCC   45078      G    CGCG  C
                                CCCGC CGCGC    TG GCC
                                ||||| |||||    || |||
                                GGGCG GCGCG    AC CGG
                                  _    AGAG  _
GAM1843  GAL3ST2   5'  CCCTGCGCGCCGAGTGC     45079     GC       C
                                CCC  GCGCGCCG GTGC
                                |||  |||||||| ||||
                                GGG  CGCGCGGC CACG
                                  A_       T
GAM1843  GBTS1     5'  CCTGCGGCGCCGCGGC      45080    C  C       T
                                CC GCG GCGCCGCG GC
                                || ||| |||||||| ||
                                GG CGC CGCGGCGC CG
                                 A  _       _
GAM1843  GNB1L     5'  CCCAGCGTGCGCGCGGCCGCC  45081     _  C    C   TG
                                CCC GCG GCGC GCG  CGCC
                                ||| ||| |||| |||  ||||
                                GGG CGC CGCG CGC  GCGG
                                  T  A    _   CG
GAM1843  H2AFY     5'  CCCGCGCGGCCCGCGC      44994        C   G
                                CCCGCGCG GCC CGTGC
                                |||||||| ||| |||||
                                GGGCGCGC CGG GCGCG
                                   _  _
GAM1843  H2AFY     5'  CCCGCGCGGCCCGCGC      44994        C   G
                                CCCGCGCG GCC CGTGC
                                |||||||| ||| |||||
                                GGGCGCGC CGG GCGCG
                                   _  _
GAM1843  HAND2     5'  CCCGCCGCGCCCTCGGC     45082      G     G_  T
                                CCCGC CGCGCC  CG GC
                                ||||| ||||||  || ||
                                GGGCG GCGCGG  GC CG
                                   _     GA  _
GAM1843  HIC       5'  CCCTCGCGCCCTGCGC      45083     G    G  GCG
                                CCC CGCGC CC   TGCGC
                                ||| ||||| ||   |||||
```

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                                GGG GCGCG GG   ACGCG
                                  A    _ ____
GAM1843 HSRNAFEV 5' CCCGCGCGGCCCGGGGCC    45084        C   G  TGC
                                CCCGCGCG GCC CG   GCC
                                |||||||| ||| ||   |||
                                GGGCGCGC CGG GC   CGG
                                     _   _  CC_
GAM1843 HSSEXGENE 5' CCCACGCGCGCAGCCGCC    45085          C  GTG
                                CCCGCGCGCGC GC   CGCC
                                |||||||||||  ||   ||||
                                GGGTGCGCGCG CG   GCGG
                                      T  ____
GAM1843 HSU79274 5' CCCGACAGCACGCGTGCG    45086      _  C    C
                                CCCG CG GCGC GCGTGCG
                                |||| || |||| |||||||
                                GGGC GT CGTG CGCACGC
                                  T  _    _
GAM1843 HUMAGCGB 5' CCTCGCGTGCGTCCTGTGGGTG 45087    _    C   _  GC   C__
             CC                   CC CGCG GCG CC  GTG   GCC
                                || |||| ||| ||  |||   |||
                                GG GCGC CGC GG  CAC   CGG
                                 A    A   A  A_   CCA
GAM1843 IL-17RC  3' CGTGCGGGCCGTGCGCC     45088    C   C   GC
                                CG GCG GCC  GTGCGCC
                                || ||| |||  |||||||
                                GC CGC CGG  CACGCGG
                                 A   C   __
GAM1843 IL-17RE  3' CCCACGCGCGCCACGTGC     45090
                                CCCGCGCGCGCCGCGTGC
                                ||||||||||||||||||
                                GGGTGCGCGCGGTGCACG

GAM1843 IL-17RE  3' CCGCGCCGCCCAGAGCC      45089        G    G  TGC
                                CCGCGC CGCC CG   GCC
                                |||||| |||| ||   |||
                                GGCGCG GCGG GT   CGG
                                     _    _  CT_
GAM1843 IMAGE:4907098 5'  CCCACGTGCGCCGGATGAGC   45091        C     C   C
                                CCCGCG GCGCCG GTG GC
                                |||||| |||||| ||| ||
                                GGGTGC CGCGGC TAC CG
                                    A      C   T
GAM1843 ITPK1    5' CCGGCGCGCGCCGCGAGC     45092    C          T
                                CC GCGCGCGCCGCG GC
                                || ||||||||||| ||
                                GG CGCGCGCGGCGC CG
                                 C           T
GAM1843 KIAA0014 3' CCGCGCCGCCGGCTGCC      45093        G    C  GC
                                CCGCGC CGCCG GT  GCC
                                |||||| ||||| ||  |||
```

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                                GGCGCG GCGGC CG  CGG
                                  _    _ A_
GAM1843 KIAA0074 5' CGCGCGCGTCGAGACGCC    45094       C  CGT
                                CGCGCGCG CG   GCGCC
                                |||||||| ||   |||||
                                GCGCGCGC GC   TGCGG
                                    A  TC_
GAM1843 KIAA0211 5' CCGCGCGCGTCCCCAGCGCC   45095        _ G  T
                                CCGCGCGCG CC CG GCGCC
                                ||||||||| || || |||||
                                GGCGCGCGC GG GT CGCGG
                                     A  G  _
GAM1843 KIAA0319 5' CCCTCGCGCGCGCACCTGC    45096     G      _  G
                                CCC CGCGCGC CGC TGC
                                ||| ||||||| ||| |||
                                GGG GCGCGCG GTG ACG
                                  A      C   G
GAM1843 KIAA0397 5' CCCGCCGCGCTCCCGGC     45097      _   G  G  T
                                CCCGC GCGC CC CG GC
                                ||||| |||| || || ||
                                GGGCG CGCG GG GC CG
                                   G    A  _ _
GAM1843 KIAA0476 5' CCCGCCGCGCTGCGC       45098      G    CGCG
                                CCCGC CGCGC    TGCGC
                                ||||| |||||    |||||
                                GGGCG GCGCG    ACGCG
                                  _    _____
GAM1843 KIAA0534 5' CGCCCGCGGCCCGCGCC     45099     G   CC  G
                                CGC CGCG  GC TGCGCC
                                ||| ||||  || ||||||
                                GCG GCGC  CG GCGCGG
                                  G    __  G
GAM1843 KIAA0560 5' CCGCGCCGCACAAACGC     45100       G  C   T
                                CCGCGC CGC GCG GCGC
                                |||||| ||| ||| ||||
                                GGCGCG GCG TGT TGCG
                                   _  _  T
GAM1843 KIAA0561 5' CCCGCGGCGCCGCAGGAGGC  45101       C      TGC_
                                CCCGCG GCGCCGCG    GC
                                |||||| ||||||||    ||
                                GGGCGC CGCGGCGT    CG
                                   _       CCTC
GAM1843 KIAA0672 5' CACGCGCGCCGCGCAATGCC  45102            GC_
                                CGCGCGCGCCGCGT   GCC
                                ||||||||||||||   |||
                                GTGCGCGCGGCGCG   CGG
                                       TTA
GAM1843 KIAA0790 5' CCCGCGCGCAGCCTGC      45104         CC  G
                                CCCGCGCGCG  GC TGC
                                ||||||||||  || |||
```

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                                GGGCGCGCGT  CG ACG
                                     __  G
GAM1843  KIAA0790  5'  CCCGCGCGCGGGCCGTGCG   45103         CCG
                                CCCGCGCGCG   CGTGCG
                                ||||||||||   ||||||
                                GGGCGCGCGC   GCACGC
                                     CCG
GAM1843  KIAA0987  3'  CGCGTGCACCACACGCC     45106     C      GT
                                CGCG GCGCCGC  GCGCC
                                ||||  |||||||  |||||
                                GCGC CGTGGTG  TGCGG
                                  A      __
GAM1843  KIAA0987  5'  CCCGGGCGCGCCGCGGC     45105     C         T
                                CCCG GCGCGCCGCG GC
                                ||||  ||||||||||  ||
                                GGGC CGCGCGGCGC CG
                                  C         _
GAM1843  KIAA1028  5'  CGCGCGCGCGCGCCGC      44946         C    G
                                CGCGCGCGC GCGT CGC
                                |||||||||  ||||  |||
                                GCGCGCGCG CGCG GCG
                                     _    _
GAM1843  KIAA1028  5'  CGCGCGCGCGCGCGCGCC    44983         C
                                CGCGCGCGC GCGTGCGCC
                                |||||||||  |||||||||
                                GCGCGCGCG CGCGCGCGG
                                     _
GAM1843  KIAA1199  5'  CCCCGCGCCGCTTGCGC     45107     GCG       G
                                CCC   CGCGCCGC TGCGC
                                |||   ||||||||  |||||
                                GGG   GCGCGGCG ACGCG
                                  ____       A
GAM1843  KIAA1274  5'  CCCGGCGCGCGCTCTGGC     45108     C     C  G_  C
                                CCCG GCGCGC GC  TG GC
                                ||||  ||||||  ||  ||  ||
                                GGGC CGCGCG CG  AC CG
                                  _     _  AG  _
GAM1843  KIAA1280  5'  CCCGTGCACGCCGCAGC     45109     C         T
                                CCCG GCGCGCCGCG GC
                                ||||  ||||||||||  ||
                                GGGC CGTGCGGCGT CG
                                  A         _
GAM1843  KIAA1580  5'  CCGCGCCGCCCTTAGCGCC    45110       G    GCGT
                                CCGCGC CGCC    GCGCC
                                ||||||  ||||    |||||
                                GGCGCG GCGG    CGCGG
                                     _   GAAT
GAM1843  KIAA1668  3'  CCTGCATGTGCCGCGTGACC   45111    C   CGC       C
                                CC GCG   GCCGCGTG GCC
                                ||  |||   ||||||||  |||
```

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                                GG CGT   CGGCGCAC TGG
                                 A  ACA      _
GAM1843 KIAA1691 5' CCGCGCGCTCCTGGGCC    45112       G GCG C
                                CCGCGCGC CC   TG GCC
                                |||||||| ||   || |||
                                GGCGCGCG GG   AC CGG
                                    A ___  C
GAM1843 KIAA1855 3' GCGGGGCGCCGCGTGTGC   45114    C_       C
                                GCG  GCGCCGCGTG GC
                                |||  |||||||||| ||
                                CGC  CGCGGCGCAC CG
                                  CC        A
GAM1843 KIAA1855 3' CCGCGTGTGCTCGCGCGCG   45113     CGC _
                                CCGCG   GC CGCGTGCG
                                |||||   || ||||||||
                                GGCGC   CG GCGCGCGC
                                   ACA  A
GAM1843 KIAA1912 5' CCCGCGCGCGCGCCCGCGC   45115         C G
                                CCCGCGCGCGC GC TGCGC
                                |||||||||| || |||||
                                GGGCGCGCGCG CG GCGCG
                                      _ G
GAM1843 LANO    5' CCTTGCGCGCCGGGGGCGCC  45116   GC      CGT
                                CC  GCGCGCCG   GCGCC
                                ||  ||||||||   |||||
                                GG  CGCGCGGC   CGCGG
                                 AA       CCC
GAM1843 LGI3    5' CCCGCGCGGGCTGGCACC    45117       C CGCGT
                                CCCGCGCG GC    GCGCC
                                |||||||| ||    |||||
                                GGGCGCGC CG    CGTGG
                                    C  AC___
GAM1843 MAFB    3' CCCGCCCGCGCACCCGC     45118      G   C G
                                CCCGC CGCGC GC TGC
                                ||||| ||||| || |||
                                GGGCG GCGCG TG GCG
                                   G    _ G
GAM1843 MANBAL  5' CCCGCGCCGCCGCGCCGCC   45119       G     G
                                CCCGCGC CGCCGCGT CGCC
                                ||||||| |||||||| ||||
                                GGGCGCG GCGGCGCG GCGG
                                      _      _
GAM1843 MAP-1   5' CCCGCGCCGCCCGAGC      45120       G   G T
                                CCCGCGC CGCC CG GC
                                ||||||| |||| || ||
                                GGGCGCG GCGG GC CG
                                    _   _ T
GAM1843 MESDC2  5' CGCTGCGCCGCGCAGCGCC   45121    GC      _
                                CGC  GCGCCGCGT GCGCC
                                |||  ||||||||| |||||
```

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                                GCG  CGCGGCGCG CGCGG
                                  A_       T
GAM1843  MGC12760  5'  CCCGGCGAACCCGTGCGCC   45122     C   C   G
                                CCCG GCG GCC CGTGCGCC
                                |||| ||| ||| ||||||||
                                GGGC CGC TGG GCACGCGG
                                  _   T   _
GAM1843  MGC12945  5'  CCTGCGCGCCCGCGCGC    45123    C     G
                                CC GCGCGC CCGCGTGC
                                || |||||| ||||||||
                                GG CGCGCG GGCGCGCG
                                 A     _
GAM1843  MGC12992  5'  CCCTGCGCGCGCCGAGGGCC  45124     _        CGTGC
                                CCC GCGCGCGCCG     GCC
                                ||| ||||||||||     |||
                                GGG CGCGCGCGGC     CGG
                                  A         TCC__
GAM1843  MGC13251  3'  CCCTTGCGCGCGTGCGTGCGC 45125     __      CC
                                CCC  GCGCGCG  GCGTGCGC
                                |||  |||||||  ||||||||
                                GGG  CGCGCGC  CGCACGCG
                                  AA      A_
GAM1843  MGC15396  5'  CGCGCCGCTGCCCGCGCC    45126      G   C  G
                                CGCGC CGC GC TGCGCC
                                ||||| ||| || ||||||
                                GCGCG GCG CG GCGCGG
                                   _   A  G
GAM1843  MGC2655   5'  CCGCGCGCGACGCAACC     45127         C    TGC
                                CCGCGCGCG CGCG   GCC
                                ||||||||| ||||   |||
                                GGCGCGCGC GCGT   TGG
                                     T    ____
GAM1843  MGC2780   5'  CCCGTGCCTGCAGCGCGCGC   45128     C  GC  C
                                CCCG GC  GC GCGTGCGC
                                |||| ||  || ||||||||
                                GGGC CG  CG CGCGCGCG
                                  A  GA  T
GAM1843  MGC3062   5'  GCACGCGCACAGCGCC      45129         C   T
                                GCGCGCGC GCG GCGCC
                                |||||||| ||| |||||
                                CGTGCGCG TGT CGCGG
                                     _   _
GAM1843  MGC5442   5'  CCCGCCGCGCTACCGAGCGCC  45130       G     CG _ T
                                CCCGC CGCGC  C G GCGCC
                                ||||| |||||  | | |||||
                                GGGCG GCGCG  G C CGCGG
                                   _     AT G T
GAM1843  OSBP2     5'  CCCGCGCGCGGCCGAGCGGCC  45131          _   C   C
                                CCCGCGCGCG CCG GTG GCC
                                |||||||||| ||| ||| |||
```

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                                GGGCGCGCGC GGC CGC CGG
                                      C   T  _
GAM1843  OXCT2    5'  CCCTGCGTGCGCCTCGGGC   45132    _  C    G  T
                                CCC GCG GCGCC CG GC
                                ||| ||| ||||| || ||
                                GGG CGC CGCGG GC CG
                                  A   A    A  C
GAM1843  p47      5'  CCCGTGCGCCTTCCAAAGCGC  45133    C   G__  CGT
                                CCCG GCGC   CCG   GCGC
                                |||| ||||   |||   ||||
                                GGGC CGCG   GGT   CGCG
                                  A   GAA   TT_
GAM1843  P5       5'  CCTGCAGCGTGCCGCACGCC   45134   C  _  C    GT
                                CC GC GCG GCCGC  GCGCC
                                || || ||| |||||  |||||
                                GG CG CGC CGGCG  TGCGG
                                 A  T   A    __
GAM1843  PCCX2    5'  CGCGCGCGCTGACATGGC    45135        C_    C
                                CGCGCGCGC  GCGTG GC
                                |||||||||  ||||| ||
                                GCGCGCGCG  TGTAC CG
                                     AC    _
GAM1843  PDCD7    5'  CCCGGCATGCGTGCGC      45136     C   CGCC
                                CCCG GCG    GCGTGCGC
                                |||| |||    ||||||||
                                GGGC CGT    CGCACGCG
                                  _   A____
GAM1843  PDCD7    5'  CGCGCGCGCACTTCGCC     45137        C  GTG
                                CGCGCGCGC GC   CGCC
                                ||||||||| ||   ||||
                                GCGCGCGCG TG   GCGG
                                     _  AA_
GAM1843  PKMYT1   5'  CCGCGCGCGTTCACGGGC    45138        C_   T
                                CCGCGCGCG  CGCG GC
                                |||||||||  |||| ||
                                GGCGCGCGC  GTGC CG
                                     AA   C
GAM1843  PPP1R14C 5'  CCCCGCGCGCCCGAGC     45139    G      G  T
                                CCC CGCGCGCC CG GC
                                ||| |||||||| || ||
                                GGG GCGCGCGG GC CG
                                  _      _  T
GAM1843  PRKWNK2  5'  CCCGCGCCGCGCCCGGGC    45140        _    G  T
                                CCCGCGC GCGCC CG GC
                                ||||||| ||||| || ||
                                GGGCGCG CGCGG GC CG
                                    G    _  C
GAM1843  PTPN9    3'  CCTTGCGTGCACACGTGTGC   45141    GC   C  _     C
                                CC  GCG GC CGCGTG GC
                                ||  ||| || |||||| ||
```

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                                GG  CGC CG GTGCAC CG
                                 AA   A T     A
GAM1843  RAD51    5'  CCCGCGGGCGTGGCACGCGCC  45142       C   CC
                                CCCGCG GCG  GCGTGCGCC
                                |||||| |||  |||||||||
                                GGGCGC CGC  CGTGCGCGG
                                   C   AC
GAM1843  RAD51    5'  CCCGCGGGCGTGGCACGCGCC  45142       C   CC
                                CCCGCG GCG  GCGTGCGCC
                                |||||| |||  |||||||||
                                GGGCGC CGC  CGTGCGCGG
                                   C   AC
GAM1843  RAD52B   5'  CCTGCGCGGCTAACCCTCGCC  45143    C    C  C_  GTG
                                CC GCGCG GC  GC   CGCC
                                || ||||| ||  ||   ||||
                                GG CGCGC CG  TG   GCGG
                                 A    _  AT  GGA
GAM1843  RES4-25  5'  CCCGCTGCGCCCAAGGGCC   45144      GC    G  TGC
                                CCCGC  GCGCC CG   GCC
                                |||||  ||||| ||   |||
                                GGGCG  CGCGG GT   CGG
                                  A_    _  TCC
GAM1843  RI58     5'  CGCGTGCGCGTGCGCGCGCC   45145     C   C_
                                CGCG GCGC  GCGTGCGCC
                                |||| ||||  |||||||||
                                GCGC CGCG  CGCGCGCGG
                                  A   CA
GAM1843  RINZF    5'  CCCGCGCGCTCCCCGCGGC   45146        G  G   C
                                CCCGCGCGC CC CGTG GC
                                ||||||||| || |||| ||
                                GGGCGCGCG GG GCGC CG
                                     A  G   _
GAM1843  RNPC1    5'  CCGTGCGCGCCGAGCTGCGCC  45147     C       C _
                                CCG GCGCGCCG G TGCGCC
                                ||| |||||||| | ||||||
                                GGC CGCGCGGC C ACGCGG
                                  A       T G
GAM1843  SERP1    5'  CCCGCGCCGCCGGAGCGCC   45148       G    CGT
                                CCCGCGC CGCCG   GCGCC
                                ||||||| |||||   |||||
                                GGGCGCG GCGGC   CGCGG
                                   _    CT_
GAM1843  SLC21A11 5'  CCCGCGTGCCCCGAAGTAGC  45149       C  G   C_  C
                                CCCGCG GC CCG  GTG GC
                                |||||| || |||  ||| ||
                                GGGCGC CG GGC  CAT CG
                                   A  G   TT  _
GAM1843  SLC2A10  5'  CCCGCGCGCAGCGCCGCC    45150         CC   G
                                CCCGCGCGCG  GCGT CGCC
                                ||||||||||  |||| ||||
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                                GGGCGCGCGT  CGCG GCGG
                                    __   _
GAM1843  SLK      5'  CCCGCGCGAGCCCGGC      45151        C   G  T
                                CCCGCGCG GCC CG GC
                                |||||||| ||| || ||
                                GGGCGCGC CGG GC CG
                                     T  _ _
GAM1843  SMARCA4  5'  CCTCGCGCGCGCGCCCGCC   45152    G      C    G
                                CC CGCGCGC GCGT CGCC
                                || ||||||| |||| ||||
                                GG GCGCGCG CGCG GCGG
                                 A      _   G
GAM1843  SMARCA4  5'  CGCTGCGCGCGCGCTCGCC   45153     _     C    G
                                CGC GCGCGC GCGT CGCC
                                ||| |||||| |||| ||||
                                GCG CGCGCG CGCG GCGG
                                  A     _   A
GAM1843  SMARCA4  5'  CCCGCTGCGCGCGCGC      45154      GC   C
                                CCCGC  GCGC GCGTGC
                                |||||  |||| ||||||
                                GGGCG  CGCG CGCGCG
                                   A_   _
GAM1843  SNFT     5'  CCCGCCCGCGCGCCCTGC    45155      G    C  G_
                                CCCGC CGCGC GC  TGC
                                ||||| ||||| ||  |||
                                GGGCG GCGCG CG  ACG
                                   G    _ GG
GAM1843  Spir-2   5'  CCCGCGCGCCGGACCCGCGT   45156        G____
                                CCCGCGCGC    CCGCGT
                                |||||||||    ||||||
                                GGGCGCGCG    GGCGCA
                                     GCCTG
GAM1843  SULT4A1  5'  CCCGCGCCCGCGCCCGCGCC   45158       G  C  G
                                CCCGCGC CGC GC TGCGCC
                                ||||||| ||| || ||||||
                                GGGCGCG GCG CG GCGCGG
                                    G  _ G
GAM1843  SULT4A1  5'  CCCGCACGCGCCCGCGC     45157          G
                                CCCGCGCGCGCC CGTGC
                                |||||||||||| |||||
                                GGGCGTGCGCGG GCGCG
                                                _
GAM1843  SYNJ2    5'  CCCGCGCGCCCGCAACTTGCC  45159        G    TGC_
                                CCCGCGCGC CCGCG   GCC
                                ||||||||| |||||   |||
                                GGGCGCGCG GGCGT   CGG
                                     _    TGAA
GAM1843  T2BP     5'  CCCGCGCGCGCGGCCTGC     45160          C  G
                                CCCGCGCGCGC GC TGC
                                |||||||||| || |||
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                                GGGCGCGCGCG CG ACG
                                      C  G
GAM1843  TCF6L1   5'  CCCGCGTGCGACCCTCCGGCGT 45161       C  _ _____
              G                  CCCGCG GCG CC    GCGTG
                                 |||||| ||| ||    |||||
                                 GGGCGC CGC GG    CGCAC
                                    A   T  GAGGC
GAM1843  TNKS2    5'  CCCACGCGCGCCCCTCGC    45163          GCG
                                 CCCGCGCGCGCC   TGC
                                 ||||||||||||   |||
                                 GGGTGCGCGCGG   GCG
                                       GGA
GAM1843  TNKS2    5'  CCCGCGCGTGCGCAGTGGCC   45162       C  C  _  C
                                 CCCGCGCG GC GC GTG GCC
                                 |||||||| || || ||| |||
                                 GGGCGCGC CG CG CAC CGG
                                    A  _  T  _
GAM1843  TRAP-1   5'  CCCGCGCCGCCCCCGCGGCC   45164       G   G   C
                                 CCCGCGC CGCC CGTG GCC
                                 ||||||| |||| |||| |||
                                 GGGCGCG GCGG GCGC CGG
                                    _   G   _
GAM1843  TREX1    5'  CCCATGCGCGCCGAACG     45165     C       CGT
                                 CCCG GCGCGCCG   GCG
                                 |||| ||||||||   |||
                                 GGGT CGCGCGGC   TGC
                                   A       T__
GAM1843  TRIM28   5'  CCCGCCGCGCGCGGGACGC   45166      G    C  T_
                                 CCCGC CGCGC GCG  GCGC
                                 ||||| ||||| |||  ||||
                                 GGGCG GCGCG CGC  TGCG
                                    _    _  CC
GAM1843  TSCOT    5'  CCGTGCGCCGGGAGCGCGCC   45167     CGC     C__
                                 CCG   GCGCCG   GTGCGCC
                                 |||   ||||||   |||||||
                                 GGC   CGCGGC   CGCGCGG
                                   A__      CCT
GAM1843  TSPAN-5  5'  CCCTCGCGCGCCGAGGCC    45168     G       CGTGC
                                 CCC CGCGCGCCG    GCC
                                 ||| |||||||||    |||
                                 GGG GCGCGCGGC    CGG
                                   A        TC___
GAM1843  UBE3B    3'  CCCAGCGTGCGCACACACG   45169     _  C   C   TG
                                 CCC GCG GCGC GCG  CG
                                 ||| ||| |||| |||  ||
                                 GGG CGC CGCG TGT  GC
                                   T  A   _  GT
GAM1843  WIT-1    3'  CCCGCGCGCAGTGTGGC     45170          CCGC   C
                                 CCCGCGCGCG   GTG GC
                                 |||||||||    ||| ||
```

```
                                GGGCGCGCGT   CAC CG
                                     CA__  _
GAM1843 ZAK      5' CCCGCGCGGCTCCCACGT    45171        _ G_
                                CCCGCGCG C  CCGCGT
                                |||||||| |  ||||||
                                GGGCGCGC G  GGTGCA
                                     C AG
GAM1843 ZNF338   5' CCCGGCGTGCTGGGCGACC   45172     C  C  CGC  C
                                CCCG GCG GC  GTG GCC
                                |||| ||| ||  ||| |||
                                GGGC CGC CG  CGC TGG
                                  _  A  ACC  _
GAM1843 ZNF84    5' CCCGCGCGCCCGCGGC      45173        G    T
                                CCCGCGCGC CCGCG GC
                                ||||||||| ||||| ||
                                GGGCGCGCG GGCGC CG

                                     _    _
GAM1843 LOC115574 5' CCCGCGCCGCGCCCCCTCGCC 45174       _    GCGTG
                                CCCGCGC GCGCC    CGCC
                                ||||||| |||||    ||||
                                GGGCGCG CGCGG    GCGG
                                    G    GGGA_
GAM1843 LOC118672 5' CCTGCGCGCACGCGCAGCG   45175    C      _   T
                                CC GCGCGCGC CGCG GCG
                                || |||||||| |||| |||
                                GG CGCGCGTG GCGT CGC
                                 A       C   _
GAM1843 LOC124044 5' CCCCGCGCGCCGCGCGC     45176    G
                                CCC CGCGCGCCGCGTGC
                                ||| ||||||||||||||
                                GGG GCGCGCGGCGCGCG

                                  _
GAM1843 LOC125297 5' CCCGCGCGGCCAGGGGCGCC  45177       C   CGT
                                CCCGCGCG GCCG  GCGCC
                                |||||||| ||||  |||||
                                GGGCGCGC CGGT  CGCGG
                                     _   CCC
GAM1843 LOC126123 5' CCCGGCGCGCGCCTGCAGC   45178     _     _  T
                                CCCG CGCGCGCC GCG GC
                                |||| |||||||| ||| ||
                                GGGC GCGCGCGG CGT CG
                                  C       A  _
GAM1843 LOC126257 5' CCGCGCGCAGCCGGGCGGCC  45179       _   C  C
                                CCGCGCGC GCCG GTG GCC
                                |||||||| |||| ||| |||
                                GGCGCGCG CGGC CGC CGG
                                     T   C  _
GAM1843 LOC128844 5' CCTGCGTGCGCGCAGGCAGCC 45180   C  C   C  T _
                                CC GCG GCGC GCG GC GCC
                                || ||| |||| ||| || |||
```

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                                GG CGC CGCG CGT CG CGG
                                 A  A   _  C  T
GAM1843  LOC128989 3'  CCTGTGCACGTACATGTGCC  45181   GC_   CC   C
                                CC  GCGCG  GCGTG GCC
                                ||  |||||  ||||| |||
                                GG  CGTGC  TGTAC CGG
                                 ACA   A_   A
GAM1843  LOC133383 5'  CCGTGGGCGCACACAAGCGC  45182    CGC  _   T
                                CCG  GCGC CGCG GCGC
                                |||  |||| |||| ||||
                                GGC  CGCG GTGT CGCG
                                 ACC   T   T
GAM1843  LOC135892 5'  CCGCGCGTGCCCCATCATGC  45183      C  G___
                                CCGCGCG GCC   CGTGC
                                ||||||| |||   |||||
                                GGCGCGC CGG   GTACG
                                    A  GGTA
GAM1843  LOC148014 3'  CGCGCGTGCGTAGTCGCC   45184      CC   __
                                CGCGCG  GCGTG  CGCC
                                ||||||  |||||  ||||
                                GCGCGC  CGCAT  GCGG
                                   A_   CA
GAM1843  LOC148114 5'  CCCGCGCGCTGGCCACGC   45185       __
                                CCCGCGCGC  GCCGCGT
                                |||||||||  |||||||
                                GGGCGCGCG  CGGTGCG
                                     AC
GAM1843  LOC149478 5'  CCCACGCGCGCCCAGC     45186         G  T
                                CCCGCGCGCGCC CG GC
                                |||||||||||| || ||
                                GGGTGCGCGCGG GT CG
                                       _ _
GAM1843  LOC150135 3'  CCCTGCGCGCACCGGCTGTG  45187   _       _ _
                                CCC GCGCGCGCCG C GTG
                                ||| |||||||||| | |||
                                GGG CGCGCGTGGC G CAC
                                  A        C A
GAM1843  LOC151571 5'  CCCGCGCGCGCCCGGC     45188         G  T
                                CCCGCGCGCGCC CG GC
                                |||||||||||| || ||
                                GGGCGCGCGCGG GC CG
                                       _ _
GAM1843  LOC151647 5'  CCGCGCGCGCAGTCGGTGCGCC 45189         ___ C
                                CCGCGCGCGC   CG GTGCGCC
                                ||||||||||   || |||||||
                                GGCGCGCGCG   GC CACGCGG
                                     TCA  _
GAM1843  LOC153768 5'  CCCCGCGCGCCGCGGGC    45190    G        T
                                CCC CGCGCGCCGCG GC
                                ||| ||||||||||| ||
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                                GGG GCGCGCGGCGC CG
                                  _         C
GAM1843  LOC154043 5'  CCCCGCTCCGCGTGCGC     45191     GCG   G
                                CCC   CGC CCGCGTGCGC
                                |||   ||| ||||||||||
                                GGG   GCG GGCGCACGCG
                                  ____  A
GAM1843  LOC154789 5'  CCCCCGCGTGCTCTACGCC    45192     G    C  CGCG
                                CCC CGCG GC    TGCGCC
                                ||| |||| ||    ||||||
                                GGG GCGC CG    ATGCGG
                                  G    A  AG__
GAM1843  LOC154877 3'  CCACGCGTGCCAGATCCTGTGC 45193        C    C_____
                                CCGCGCG GCCG      GTGC
                                ||||||| ||||      ||||
                                GGTGCGC CGGT      CACG
                                    A    CTAGGA
GAM1843  LOC155382 5'  CCCGCGCCGCCCGGGC      45194        G    G  T
                                CCCGCGC CGCC CG GC
                                ||||||| |||| || ||
                                GGGCGCG GCGG GC CG
                                   _    _  C
GAM1843  LOC160954 5'  CCTGTGCGCGCCGGTGGC    45195    GC_      C   C
                                CC   GCGCGCCG GTG GC
                                ||   |||||||| ||| ||
                                GG   CGCGCGGC CAC CG
                                 ACA       _   _
GAM1843  LOC163115 3'  GCTGCGTGCGCGTGTGCC    45196    _   C  C    C
                                GC GCG GC GCGTG GCC
                                || ||| || ||||| |||
                                CG CGC CG CGCAC CGG
                                 A   A  _     A
GAM1843  LOC163126 5'  CCCAGTGCGCGTGCGTGGGCGC 45197      C_    CC    __
                                CCCG  GCGCG  GCGT  GCGC
                                ||||  |||||  ||||  ||||
                                GGGT  CGCGC  CGCA  CGCG
                                  CA    A_    CC
GAM1843  LOC199899 5'  CCCGCGCGCTGCTGGCGCACGC 45198          _  _______  CGTG
              G                  CCCGCGCGC GC      CG    CG
                                |||||||| ||      ||    ||
                                GGGCGCGCG CG      GC    GC
                                     A  AIIICC  GTGC
GAM1843  LOC201161 5'  CCTGCGCGCGCCCCCGCC    45199    C        GCGTG
                                CC GCGCGCGCC     CGCC
                                || |||||||||     ||||
                                GG CGCGCGCGG     GCGG
                                 A        GG___
GAM1843  LOC201780 5'  CCCGCCGCGTGCCTCTCGCC   45200       _   C   GCGTG
                                CCCGC GCG GCC     CGCC
                                ||||| ||| |||     ||||
```

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                                GGGCG CGC CGG    GCGG
                                  G   A   AGA__
GAM1843  LOC203197 5'  CCCGCGCCGCGCTGCGCC    45201       G   C  G
                                CCCGCGC CGC GC TGCGCC
                                ||||||| ||| || ||||||
                                GGGCGCG GCG CG ACGCGG
                                    _   _ _
GAM1843  LOC219513 5'  CGCACGCGCCCGCGGGC     45202         G    C
                                CGCGCGCGCC CGTG GC
                                |||||||||| |||| ||
                                GCGTGCGCGG GCGC CG
                                     _   C
GAM1843  LOC219654 5'  CCCGCGCGCTGCCCGCAGCC   45203         _  G    C
                                CCCGCGCGC GCC CGTG GCC
                                ||||||||| ||| |||| |||
                                GGGCGCGCG CGG GCGT CGG
                                     A  _   _
GAM1843  LOC219654 5'  CCCGCGCGCTGCCGGCGCACGC 45204         _ _______  CGTG
            G                    CCCGCGCGC GC     CG   CG
                                |||||||| ||     ||   ||
                                GGGCGCGCG CG     GC   GC
                                     A  GIIICC  GTGC
GAM1843  LOC220107 5'  CCCGCGCCGCGGTCCGCC    45205       G   C C  G
                                CCCGCGC CGC G GT CGCC
                                ||||||| ||| | || ||||
                                GGGCGCG GCG C CA GCGG
                                    _  _ _  G
GAM1843  LOC221184 5'  CCCGCGCGGCCACGGC      45206        C     T
                                CCCGCGCG GCCGCG GC
                                |||||||| |||||| ||
                                GGGCGCGC CGGTGC CG
                                    _     _
GAM1843  LOC221773 5'  CCCCGCGTGCCGTCCGCGCC   45207     G   C   CG
                                CCC CGCG GCCG  TGCGCC
                                ||| |||| ||||  ||||||
                                GGG GCGC CGGC  GCGCGG
                                  _   A   AG
GAM1843  LOC253070 3'  CCCACGCGCGCCCGCACCGCC  45208          G  TG _
                                CCCGCGCGCGCC CG  C GCC
                                |||||||||||| ||  | |||
                                GGGTGCGCGCGG GC  G CGG
                                      _  GT G
GAM1843  LOC253289 5'  CCTGCGCTGCCACGTGC     45209    C   GC
                                CC GCGC  GCCGCGTGC
                                || ||||  |||||||||
                                GG CGCG  CGGTGCACG
                                 A   A_
GAM1843  LOC253502 5'  CCCATGCGTGTCGTACACC    45210      C   CGCCG
                                CCCG GCG    CGTGCGCC
                                |||| |||    ||||||||
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                                GGGT CGC    GCATGTGG
                                  A  ACA__
GAM1843  LOC254038 5'  CCCGCGCGGCCAGGGGCGCC  45177       C   CGT
                                CCCGCGCG GCCG  GCGCC
                                |||||||| ||||  |||||
                                GGGCGCGC CGGT  CGCGG
                                    _   CCC
GAM1843  LOC254124 3'  CCCTGCGCGCCGCGGCTGC   45211    GC       T _
                                CCC  GCGCGCCGCG GC GC
                                |||  |||||||||| || ||
                                GGG  CGCGCGGCGC CG CG
                                 A_        _ A
GAM1843  LOC254351 3'  CGCGCCGCTGCGGCTGC    45212     G  C  T _
                                CGCGC CGC GCG GC GC
                                ||||| ||| ||| || ||
                                GCGCG GCG CGC CG CG
                                  _  A  _ A
GAM1843  LOC254552 5'  CCCGCGCGACGCGTCCCGCC  45213       CGC   G_
                                CCCGCGCG  CGCGT  CGCC
                                ||||||||  |||||  ||||
                                GGGCGCGC  GCGCA  GCGG
                                    T__    GG
GAM1843  LOC254573 5'  CCCGCCGCGCGCCCTCCCGC  45214     _     GCGTG
                                CCCGC GCGCGCC    CGC
                                ||||| |||||||    |||
                                GGGCG CGCGCGG    GCG
                                  G      GAGG_
GAM1843  LOC254670 5'  CCCGCGTGCGCTCCTGCGC   45215     C   CGCG
                                CCCGCG GCGC   TGCGC
                                |||||| ||||   |||||
                                GGGCGC CGCG   ACGCG
                                   A   AGG_
GAM1843  LOC255031 5'  CCGGCGCGTGCGCGAGCGC   45216    C   C_   T
                                CCG GCGCG  CGCG GCGC
                                ||| |||||  |||| ||||
                                GGC CGCGC  GCGC CGCG
                                  _    AC   T
GAM1843  LOC255040 3'  CCCGCGCGGCACTTGC     45217       C  C  G
                                CCCGCGCG GC GC TGC
                                |||||||| || || |||
                                GGGCGCGC CG TG ACG
                                    _ _  A
GAM1843  LOC255041 3'  CCCGCGCGGCACTTGC     45217       C  C  G
                                CCCGCGCG GC GC TGC
                                |||||||| || || |||
                                GGGCGCGC CG TG ACG
                                    _ _  A
GAM1843  LOC255718 5'  CCTGCGCGCCAGGCAGCGC   45218   GC     C  _
                                CC  GCGCGCCG GT GCGC
                                ||  |||||||| || ||||
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                                GG  CGCGCGGT CG CGCG
                                 A_       C  T
GAM1843  LOC256160 5'  CCCGCCGCGTGCCTCTCGCC   45200      _   C   GCGTG
                                CCCGC GCG GCC     CGCC
                                ||||| ||| |||     ||||
                                GGGCG CGC CGG     GCGG
                                   G   A   AGA__
GAM1843  LOC51285  5'  CCCGCGCAGTGCGCCCGCC   45219        CGCC   G
                                CCCGCGCG    GCGT CGCC
                                ||||||||    |||| ||||
                                GGGCGCGT    CGCG GCGG
                                     CA__    G
GAM1843  LOC57109  5'  CCCGCACGCGTTGCGC      45220          CCGCG
                                CCCGCGCGCG     TGCGC
                                ||||||||||     |||||
                                GGGCGTGCGC     ACGCG
                                      A____
GAM1843  LOC90183  3'  CCCGCCCGCGCACCCGC     45118      G    C  G
                                CCCGC CGCGC GC TGC
                                ||||| ||||| || |||
                                GGGCG GCGCG TG GCG
                                   G     _  G
GAM1843  LOC90459  5'  CCGGCGTGCGCGGAACGCC   45221     C   C  C   T_
                                CCG GCG GC GCG  GCGCC
                                ||| ||| || |||  |||||
                                GGC CGC CG CGC  TGCGG
                                  _   A  _   CT
GAM1843  LOC90835  5'  CGCACGCGTCCGCGCGGCC   45222         _      C
                                CGCGCGCG CCGCGTG GCC
                                |||||||| ||||||| |||
                                GCGTGCGC GGCGCGC CGG
                                     A      _
GAM1843  LOC90850  5'  CCGCGCGCCGCCCCTCGGCGCC 45223         _   G__  T
                                CCGCGCGC GCC   CG GCGCC
                                |||||||| |||   || |||||
                                GGCGCGCG CGG   GC CGCGG
                                     G   GGA  _
GAM1843  LOC90874  5'  CGCCGCGTGCGCGCGC      45224     G   CC
                                CGC CGCG  GCGTGCGC
                                ||| ||||  ||||||||
                                GCG GCGC  CGCGCGCG
                                  _    A_
GAM1843  LOC91547  5'  CCCGCGCCGCCTGCGCGCC   45225       G   GC
                                CCCGCGC CGCC  GTGCGCC
                                ||||||| ||||  |||||||
                                GGGCGCG GCGG  CGCGCGG
                                    _    A_
GAM1843  LOC93166  5'  CCCTGCGTGCGCTACATGC   45226     _  C   CG
                                CCC GCG GCGC  CGTGC
                                ||| ||| ||||  |||||
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                                GGG CGC CGCG  GTACG
                                  A  A   AT
GAM1844  ADAMTS3  3'  CAATATACAGTATTTACACAAC 45229        _______    TGT
             AGC                   AATATACA     ACATA   ACAGC
                                |||||||||     |||||   |||||
                                TTATATGT     TGTGT   TGTCG
                                   CATAAA    ___
GAM1844  BACH2    3'  ATATATAATATGTACAG     45230       CAAC
                                ATATA    ATATGTACAG
                                ||||||   ||||||||||
                                TATAT    TATACATGTC
                                  AT__
GAM1844  ELF3     3'  TACAGATATACAGTTTACAGC  45231      _      ACATATG
                                TACA ATATACA      TACAGC
                                |||| |||||||      ||||||
                                ATGT TATATGT      ATGTCG
                                  C      CAA____
GAM1844  GPR48    3'  ATATGCACAGTATGTACAG    45232      ACA  _
                                ATAT   ACA TATGTACAG
                                ||||   ||| |||||||||
                                TATA   TGT ATACATGTC
                                  CG_   C
GAM1844  IL18RAP  3'  TACAATACATGGTAGACATGAC 45233         CAAC__    T
             AG                   TACAATATA     ATATG ACAG
                                |||||||||     ||||| ||||
                                ATGTTATGT     TGTAC TGTC
                                   ACCATC    _
GAM1844  KCNJ6    3'  TACATAAGGCATATATATGTAC 45234      ATATA  AC_
             AG                   TACA    CA   ATATGTACAG
                                ||||    ||   ||||||||||
                                ATGT    GT   TATACATGTC
                                  ATTCC  ATA
GAM1844  PKD2     3'  TACATATACATAAATATGTACA 45235      A     AC_
             G                    TACA TATACA   ATATGTACAG
                                |||| ||||||   ||||||||||
                                ATGT ATATGT   TATACATGTC
                                  _     ATT
GAM1844  PLXNA1   3'  ATATATATACATGTACAGC   45236      CAAC
                                ATATA    ATATGTACAGC
                                |||||    |||||||||||
                                TATAT    TGTACATGTCG
                                  ATA_
GAM1844  PUM1     3'  TACAATATACAACACTATATGC 45237           ___
                                TACAATATACAACAT   ATGT
                                ||||||||||||||   ||||
                                ATGTTATATGTTGTG   TACG
                                         ATA
GAM1844  RAG1     3'  TACAATATACAACAAAATG   45238           T_
                                TACAATATACAACA  ATG
                                ||||||||||||||  |||
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                                ATGTTATATGTTGT  TAC
                                       TT
GAM1844  TP53BP2   3'  ACAATATACAAGGTGTGCAG  45239          CATA   A
                                ACAATATACAA    TGT CAG
                                ||||||||||    ||| |||
                                TGTTATATGTT    ACA GTC
                                     CC__   C
GAM1844  ZNF10     3'  TATACAACATTACAAGC     45240          ATG   _
                                TATACAACAT   TACA GC
                                |||||||||   |||| ||
                                ATATGTTGTA   ATGT CG
                                     ___   T
GAM1844  BAP29     3'  TACAATACAACCTATGT     45241      AT      A
                                TACA  ATACAAC TATGT
                                ||||  ||||||| |||||
                                ATGT  TATGTTG ATACA
                                  __      G
GAM1844  BM-002    3'  TACAATATAACAACATGTA   45242          _    TA
                                TACAATATA CAACA  TGTA
                                |||||||| |||||  ||||
                                ATGTTATAT GTTGT  ACAT
                                     T    __
GAM1844  BRD1      3'  ACAATATACAAACATGTACAGC 45243          C
                                ACAATATACAA ATATGTACAGC
                                |||||||||| ||||||||||
                                TGTTATATGTT TGTACATGTCG
                                          _
GAM1844  C11orf23  3'  TACAATATAAACATACGC    45244          C
                                TACAATATA AACATATGT
                                |||||||| |||||||||
                                ATGTTATAT TTGTATGCG
                                          _
GAM1844  C20orf80  5'  CAATATTTGTATGTACAG    45245       ACAACA
                                CAATAT     TATGTACAG
                                ||||||     |||||||||
                                GTTATA     ATACATGTC
                                   AAC___
GAM1844  CNOT7     3'  ATATACAAGCATGTGTGTAGC  45246          _  A   AC
                                ATATACAA CAT TGT  AGC
                                |||||||| ||| |||  |||
                                TATATGTT GTA ACA  TCG
                                     C   C   CA
GAM1844  COAS3     3'  ACAATATGCCCACATATGTACA 45247        ACA_
            G                    ACAATAT    ACATATGTACAG
                                |||||||    ||||||||||||
                                TGTTATA    TGTATACATGTC
                                   CGGG
GAM1844  CORTBP2   3'  TACATATATACAGATATACAG  45248      _      ACAT
                                TACA ATATACA    ATGTACAG
                                |||| |||||||    ||||||||
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                                ATGT TATATGT    TATATGTC
                                  A      C___
GAM1844  DKFZP434C1715 3'  AACATACAACTTCTACAG    45249          ATATG
                                AATATACAAC    TACAG
                                ||||||||||    |||||
                                TTGTATGTTG    ATGTC
                                     AAG__
GAM1844  DKFZp434M0331 5'  CAATGTACAACAGAGAGCATAG 45250      A      TAT_  C
           C                    CAAT TACAACA    GTA AGC
                                |||| |||||||    ||| |||
                                GTTA ATGTTGT    CGT TCG
                                  C      CTCT   A
GAM1844  DKFZP586N2124 3'  AATAACAACAATTATACAGC   45251      T     TA
                                AATA ACAACA  TGTACAGC
                                |||| ||||||  ||||||||
                                TTAT TGTTGT  ATATGTCG
                                  _     TA
GAM1844  DKFZp761B1514 3'  TACAGTATACAACATCTG    45252      A        A
                                TACA TATACAACAT TG
                                |||| ||||||||||  ||
                                ATGT ATATGTTGTA AC
                                  C        G
GAM1844  FLJ10094  3'  TACATATACAACTCTGTA    45253      A       ATA
                                TACA TATACAAC   TGTA
                                |||| ||||||||   ||||
                                ATGT ATATGTTG   ACAT
                                  _       AG_
GAM1844  H2AFJ    3'  TACAATATATACATATAT    22728         CA
                                TACAATATA  ACATATGT
                                |||||||||  ||||||||
                                ATGTTATAT  TGTATATA
                                     A_
GAM1844  KIAA1041  3'  TACAATATAGATATGTAC    45254         CAAC
                                TACAATATA    ATATGTAC
                                |||||||||    ||||||||
                                ATGTTATAT    TATACATG
                                     C___
GAM1844  KIAA1243  3'  ATATACAACAGTACCAC     45255          TAT    A
                                ATATACAACA   GTAC GC
                                ||||||||||   |||| ||
                                TATATGTTGT   CATG TG
                                     ___    G
GAM1844  KIAA1259  3'  CAATATAGACAGTGCATACAGC 45256        CA   TA_
                                CAATATA  ACA   TGTACAGC
                                |||||||  |||   ||||||||
                                GTTATAT  TGT   GTATGTCG
                                   C_   CAC
GAM1844  KIAA1350  3'  CACATATACACATACATATGTA 45257      _      _       C
           TAG                    TACA ATATACA ACATATGTA AG
                                |||| ||||||| ||||||||| ||
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                                GTGT TATGTGT TGTATACAT TC
                                  A      A        A
GAM1844  KIAA1681  3'  TACATATATACACACACTGTAC 45258      _      A    _
              AGC                   TACA ATATACA CATA TGTACAGC
                                    |||| ||||||| |||| ||||||||
                                    ATGT TATATGT GTGT ACATGTCG
                                      A      _   G
GAM1844  MAPKAPK5  3'  TACAAATATACAACTACACAG  45259       _       A   GT
                                    TACAA TATACAAC TAT  ACAG
                                    ||||| |||||||| |||  ||||
                                    ATGTT ATATGTTG ATG  TGTC
                                      T       _  __
GAM1844  MAPKAPK5  3'  TACAAATATACAACTACACAG  45259       _       A   GT
                                    TACAA TATACAAC TAT  ACAG
                                    ||||| |||||||| |||  ||||
                                    ATGTT ATATGTTG ATG  TGTC
                                      T       _  __
GAM1844  MGC2817   3'  TACAATATACACACATA     45260           A
                                    TACAATATACA CATATG
                                    |||||||||||| ||||||
                                    ATGTTATATGT GTGTAT
                                                 _
GAM1844  PHF3      3'  TACAAGATACAACATTTTAACA 45261       T       ATGT
              G                      TACAA ATACAACAT    ACAG
                                    ||||| |||||||||    ||||
                                    ATGTT TATGTTGTA    TGTC
                                      C        AAAT
GAM1844  RBM5      3'  AATATACAAATATACACAA    45262         C
                                    AATATACAA ATATGTACAG
                                    ||||||||| ||||||||||
                                    TTATATGTT TATATGTGTT
                                                 _
GAM1844  SP2       3'  TACAATATACACTGTACA     45263           A ATA
                                    TACAATATACA C   TGTACA
                                    |||||||||||| |   ||||||
                                    ATGTTATATGT G   ACATGT
                                                 _ ____
GAM1844  ZFP95     3'  CACAGTGTACAACACATAT    45264      ATA
                                    TACA   TACAACATATGT
                                    ||||   ||||||||||||
                                    GTGT   ATGTTGTGTATA
                                      CAC
GAM1844  ZFP95     3'  CACAGTGTACAACACATAT    45264      ATA
                                    TACA   TACAACATATGT
                                    ||||   ||||||||||||
                                    GTGT   ATGTTGTGTATA
                                      CAC
GAM1844  LOC126917 3'  TACATATATCTTTTATGTACAG 45265      A    CAACA
                                    TACA TATA     TATGTACAG
                                    |||| ||||     |||||||||
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                                ATGT ATAT     ATACATGTC
                                  _   AGAAA
GAM1844  LOC136015 3'  TACACATATACAATATGCATAT 45266     _      ____
              GT                  TACA ATATACAA    CATATGT
                                  |||| ||||||||    |||||||
                                  ATGT TATATGTT    GTATACA
                                    G       ATAC
GAM1844  LOC144231 3'  ATATACAACATCACAGC     45267          ATG
                                  ATATACAACAT   TACAGC
                                  ||||||||||   ||||||
                                  TATATGTTGTA   GTGTCG
                                        ___
GAM1844  LOC153222 3'  TACAATACACAGACTCTGT    45268          _ ATA
                                  TACAATATACA AC   TGT
                                  |||||||||| ||   |||
                                  ATGTTATGTGT TG   ACA
                                         C  AG_
GAM1844  LOC154788 3'  TACACATATACAATATGCATAT 45266     _      ____
              GT                  TACA ATATACAA    CATATGT
                                  |||| ||||||||    |||||||
                                  ATGT TATATGTT    GTATACA
                                    G       ATAC
GAM1844  LOC168667 5'  TACAATGAACAACACAGC    45269       AT       T
                                  TACAAT  ACAACATA GT
                                  ||||||  |||||||| ||
                                  ATGTTA  TGTTGTGT CG
                                     CT       _
GAM1844  LOC51101  3'  ATATACAGTATATGTACA    45270       AC
                                  ATATACA  ATATGTACA
                                  |||||||  |||||||||
                                  TATATGT  TATACATGT
                                      CA
GAM1844  LOC51186  3'  AATATACAAATGTAC       45271         CAT
                                  AATATACAA   ATGTAC
                                  |||||||||   ||||||
                                  TTATATGTT   TACATG
                                        ___
GAM1844  LOC91250  5'  TACAAAATAGCATGTACAG   45272      T  CAACA
                                  TACAA ATA    TATGTACAG
                                  ||||| |||    |||||||||
                                  ATGTT TAT    GTACATGTC
                                     T  C____
GAM1845  CD34      3'  AGGGGGCACATGGAGCTCAGT  45275          TG  A
                                  AGGGGGCACATG  GCT TAGT
                                  ||||||||||||  ||| ||||
                                  TCCCCCGTGTAC  CGA GTCA
                                         CT  _
GAM1845  NRXN2     5'  AGGGGGCATGGTGCCGAGT   45276       CA  TG  AT
                                  AGGGGGCA  TG  GCT  AGT
                                  ||||||||  ||  |||  |||
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                                TCCCCCGT  AC  CGG  TCA
                                    __  CA   C_
GAM1845  HIF3A     3'  AAGGGAGGCACATAGATGG   45277      _     __
                                AAGGG GGCACAT  GTGG
                                ||||| |||||||  ||||
                                TTCCC CCGTGTA  TACC
                                   T      TC
GAM1845  KIAA0552  5'  GGGGGCACTGTGGGCACAG   45278        A    C
                                GGGGGCAC TGTGG TATAG
                                |||||||| ||||| |||||
                                CCCCCGTG ACACC GTGTC
                                     _    C
GAM1845  KIAA0789  3'  GGGGGAACATGTGAGCAGAGT  45279      C     _  TAT
                                GGGGG ACATGTG GC   AGT
                                ||||| ||||||| ||   |||
                                CCCCC TGTACAC CG   TCA
                                   T      T  TC_
GAM1845  NEDD8     3'  AGGGGGCAGTGGCTATGGT   45280        CAT      A
                                AGGGGGCA   GTGGCTAT GT
                                ||||||||   |||||||| ||
                                TCCCCCGT   CACCGATA CA
                                    ___       C
GAM1845  LOC152441 3'  AAGGGGCCATGTGTGTATAA   45281        A     GC
                                AGGGGGC CATGTG  TATAG
                                ||||||| ||||||  |||||
                                TTCCCCG GTACAC  ATATT
                                    _     AC
GAM1845  LOC152992 5'  AAGGGGGCAATGTGGGCTA   45282         C     _
                                AAGGGGGCA ATGTGG CTA
                                ||||||||| |||||| |||
                                TTCCCCCGT TACACC GAT
                                     _     C
GAM1845  LOC257200 3'  AGGAGGGCACATGTGTATGAGT 45283     _         GCTAT
                                AGG GGGCACATGTG     AGT
                                ||| ||||||||||     |||
                                TCC CCCGTGTACAC     TCA
                                  T         ATAC_
GAM1846  CACNB1    3'  TGGGCACCATCCCACGGG    45286    A T     ATTC
                                TG G CACCGT    CCCACGGG
                                || | ||||||    ||||||||
                                AC C GTGGTA    GGGTGCCC
                                 C _     _____
GAM1846  LIMK1     3'  TAAGTCATGGTCCCACGGG   43872        CC  ATTC
                                TGAGTCA  GT    CCCACGGG
                                |||||||  ||    ||||||||
                                ATTCAGT  CA    GGGTGCCC
                                    AC  _____
GAM1846  LIMK1     3'  TAAGTCATGGTCCCACGGG   43872        CC  ATTC
                                TGAGTCA  GT    CCCACGGG
                                |||||||  ||    ||||||||
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                                ATTCAGT  CA   GGGTGCCC
                                   AC  _____
GAM1846  SRGAP1   5'  TGAGTCACTGTGTCTGGCGCCC 43874     C  AT  _________  CACG
            GTG                   GTCAC GT  TC      CC   G
                                  ||||| ||  ||      ||   |
                                  CAGTG CA  AG      GG   C
                                    A  C_  ACCGIIIC  GCAC
GAM1846  TPI1     5'  TGATTCACCGCAAGACTGTGGG 45287     G      TTCCCCAC
            C                    TGA TCACCGTA      GGGC
                                 ||| ||||||||      ||||
                                 ACT AGTGGCGT      CCCG
                                   A      TCTGACA_
GAM1846  ANGPTL4  3'  GAGTCACCGTCTTTCGTGGGC  45288        A_   CCCAC
                                 GAGTCACCGT  TTC    GGGC
                                 ||||||||||  |||    ||||
                                 CTCAGTGGCA  AAG    CCCG
                                      GA   CA___
GAM1846  FLJ12242  3'  TAAGTCACAGCCCCACGGG   43878       C TATT
                                 TGAGTCAC G   CCCCACGGG
                                 ||||||||  |   |||||||||
                                 ATTCAGTG C   GGGGTGCCC
                                      T _____
GAM1846  KIAA1391  3'  TGAGTCACTCTGTTTTTCGCCC 45289      C__  A_  ____  CACG
            GTG                   AGTCAC   GT  TTC   CC   G
                                  ||||||   ||  |||   ||   |
                                  TCAGTG   CA  AAG   GG   C
                                     AGA  AA   IIIC  GCAC
GAM1846  PPP1R16B  3'  TGCAGTCACTCCCATGGG    43880    _    CGTATTC   C
                                 TG AGTCAC      CCCA GGG
                                 || ||||||      |||| |||
                                 AC TCAGTG      GGGT CCC
                                  G     A_______    A
GAM1846  LOC145317 3'  TGAGTCACTGTCTTCTTTGTGC 45290    C  A  __________  CACG
            CCGTGGG                 CAC GT TTC       CC   GG
                                    ||| || |||       ||   ||
                                    GTG CA AAG       GG   CC
                                      A  G   AAACAIIIC  GCAC
GAM1846  LOC161536 5'  TGAGTCACTGGTTTCCTGCCCG 45291       C_  A  _____  CACG
            TG                    GAGTCAC  GT TTC    CC   G
                                  |||||||  || |||    ||   |
                                  CTCAGTG  CA AGG    GG   C
                                     AC  A   AIIIC  GCAC
GAM1846  LOC197319 3'  TGGGTCTGTCAGTCCCACGGG  45292   A   ACC  ATTC
                                 TG GTC   GT   CCCACGGG
                                 || |||   ||   ||||||||
                                 AC CAG   CA   GGGTGCCC
                                  C   A__  GTCA
GAM1846  LOC63928  5'  TGAGCCACCTCCTCCTTCGCGG 45293        GTA   CCA_
            GC                    TGAGTCACC   TTCC   CGGGC
                                  |||||||||   ||||   |||||
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                                ACTCGGTGG  GAGG   GCCCG
                                     AG_   AAGC
GAM1847 DNASE2   3' CATGACAACCTCTGCCTCC   45296    A      __ _
                                TAT ACAACCTC  CC CC
                                ||| ||||||||  || ||
                                GTA TGTTGGAG  GG GG
                                  C       AC  A
GAM1847 ENC1     3' TCTATAACAAACTTCTTAACAG 45297         _ C  CCCCA
           CC                    TCTATAACAA C TC    GGTC
                                ||||||||||| | ||    ||||
                                AGATATTGTT G AG    TCGG
                                     T A  AATTG
GAM1847 IL15RA   3' TCTCCCACCTTTCCCAGGTCC  45298    ATAACA   CC
                                TCT    ACCT  CCCAGGTCC
                                |||    ||||  |||||||||
                                AGA    TGGA  GGGTCCAGG
                                  GGG___   AA
GAM1847 PC       3' CCTAAACCTCCCCTGGGTCC   45299     TAAC      CA
                                TCTA   AACCTCCCC  GGTCC
                                ||||   |||||||||  |||||
                                GGAT   TTGGAGGGG  CCAGG
                                  ____       AC
GAM1847 PC       3' CCTAAACCTCCCCTGGGTCC   45299     TAAC      CA
                                TCTA   AACCTCCCC  GGTCC
                                ||||   |||||||||  |||||
                                GGAT   TTGGAGGGG  CCAGG
                                  ____       AC
GAM1847 FLJ10251 5' TCTATGACAACCCCACAT    45300      A   CCTC    G
                                TCTAT ACAA   CCCCA GT
                                ||||| ||||   ||||| ||
                                AGATA TGTT   GGGGT TA
                                   C   ____    G
GAM1847 FLJ20793 3' TCTATAACTATTTCCCCATGTC 45301        AACC    CAG
                                TCTATAAC   TCCCC  GTC
                                ||||||||   |||||  |||
                                AGATATTG   AGGGG  CAG
                                     ATAA   TA_
GAM1847 FLJ22474 3' TCTATACGGCCTGCGCCAGGTC 45302       ACAA  CCC
           C                     TCTATA   CCT  CCAGGTCC
                                ||||||   |||  ||||||||
                                AGATAT   GGA  GGTCCAGG
                                   GCC_  CGC
GAM1847 FLJ22965 3' TCTATAACGTCTCCCTCC    45303        AAC   _
                                TCTATAAC  CTCCC CC
                                ||||||||  ||||| ||
                                AGATATTG  GAGGG GG
                                     CA_   A
GAM1847 LOC125268 3' TCTGAGCAGCCAGGCCCAGGTC 45304    ATAA  A  TCC
                                TCT   CA CC   CCCAGGTC
                                |||   || ||   ||||||||
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                                AGA   GT GG  GGGTCCAG
                                  CTC_  C  TCC
GAM1847  LOC127254 5'  TCTATAACATTTCCTAGGCC  45305        ACC  CCC
                                TCTATAACA  TCC  AGGTC
                                |||||||||  |||  |||||
                                AGATATTGT  AGG  TCCGG
                                     AA_  A__
GAM1847  LOC149117 3'  TCTATGGAACCTCCCGGCC  45306     AAC      CCA
                                TCTAT  AACCTCCC  GGTC
                                |||||  ||||||||  ||||
                                AGATA  TTGGAGGG  CCGG
                                  CC_      ___
GAM1847  LOC257017 5'  TCTGTAAAAACCTCCCTATGT  45307    A  C      CCAG
                                TCT TAA AACCTCCC   GT
                                ||| ||| ||||||||   ||
                                AGA ATT TTGGAGGG   CA
                                  C  T      ATA_
GAM1847  LOC63929  3'  TCTAAACACTTTCCAGGTC   45308    T   ACCTCCC
                                TCTA AACA     CCAGGTC
                                |||| ||||     |||||||
                                AGAT TTGT     GGTCCAG
                                  _   GAAA___
GAM1848  ARNT2     3'  GAGAAGTAGACGTTGGG    45311       T  TGTT
                                GAGAAGT AGG   TGTTGGG
                                ||||||| |||   |||||||
                                CTCTTCA TCT   GCAACCC
                                   _  _____
GAM1848  ARVCF     3'  AGGGAGTTAGGTAGGATGGG  45312   A  A      TTTGT
                                AG GA GTTAGGTG    TGGG
                                || || ||||||||    ||||
                                TC CT CAATCCAT    ACCC
                                 C  _      CCT__
GAM1848  BLAME     3'  AGAGAAGTGGGTGTGG     45313       TA    TTGTT
                                AGAGAAGT  GGTGT    GG
                                ||||||||  |||||    ||
                                TCTCTTCA  CCACA    CC
                                     C_    _____
GAM1848  CYP21A2   3'  GAGGTTGGTTGAGTGCTGGGA  45314    AA  A  _ TT
                                GAG  GTT GGT G  TGTTGGGA
                                |||  ||| ||| |  ||||||||
                                CTC  CAA CCA C  ACGACCCT
                                  __  _  A TC
GAM1848  DLG4      5'  AGAGAAGTTGGGGTTTTACGGG 45315       A  T   GT
                                AGAGAAGTT GG GTTT  TGGG
                                ||||||||| || ||||  ||||
                                TCTCTTCAA CC CAAA  GCCC
                                     C  _   AT
GAM1848  FCER2     3'  GAGAGGGTGCTGTTGGG    45316    AGTTA    T
                                GAGA    GGTGTT GTTGGG
                                ||||    |||||| ||||||
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                                CTCT    CCACGA CAACCC
                                  C____     _
GAM1848  FCER2    3'  GAGAGGGTGCTGTTGGG     45316     AGTTA     T
                                GAGA    GGTGTT GTTGGG
                                ||||    |||||| ||||||
                                CTCT    CCACGA CAACCC
                                  C____     _
GAM1848  FCER2    3'  GAGAGGGTGCTGTTGGG     45316     AGTTA     T
                                GAGA    GGTGTT GTTGGG
                                ||||    |||||| ||||||
                                CTCT    CCACGA CAACCC
                                  C____     _
GAM1848  FCER2    3'  GAGAGGGTGCTGTTGGG     45316     AGTTA     T
                                GAGA    GGTGTT GTTGGG
                                ||||    |||||| ||||||
                                CTCT    CCACGA CAACCC
                                  C____     _
GAM1848  FCER2    3'  GAGAGGGTGCTGTTGGG     45316     AGTTA     T
                                GAGA    GGTGTT GTTGGG
                                ||||    |||||| ||||||
                                CTCT    CCACGA CAACCC
                                  C____     _
GAM1848  GYG2     3'  GAGAAGTTGGGGCGAGGGG   45317       A_   TTTGTT
                                GAGAAGTT  GGTG    GGG
                                ||||||||  ||||    |||
                                CTCTTCAA  CCGC    CCC
                                     CC   TC____
GAM1848  KCNK10   5'  AGAGGGCTTGGGTGTTTG    45318     AA  A_
                                AGAG  GTT  GGTGTTTG
                                ||||  |||  ||||||||
                                TCTC  CGA  CCACAAAC
                                  C_  AC
GAM1848  NID      3'  GAAAAGTTGTTGTTGGG     45319       TAGG   T
                                GAGAAGT   TGTT GTTGGG
                                |||||||   |||| ||||||
                                CTTTTCA   ACAA CAACCC
                                    ____   _
GAM1848  PCDHGA1  3'  GAGAAGCTGGGCTGGTTGGG  45320       A  T   T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                     _ _   C
GAM1848  PCDHGA10 3'  GAGAAGCTGGGCTGGTTGGG  45320       A  T   T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                     _ _   C
GAM1848  PCDHGA11 3'  GAGAAGCTGGGCTGGTTGGG  45320       A  T   T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
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                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848 PCDHGA11 3' GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848 PCDHGA12 3' GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848 PCDHGA2  3' GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848 PCDHGA3  3' GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848 PCDHGA4  3' GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848 PCDHGA5  3' GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848 PCDHGA6  3' GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848 PCDHGA7  3' GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848 PCDHGA8  3' GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848 PCDHGA9  3' GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
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                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848  PCDHGB1  3'  GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848  PCDHGB2  3'  GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848  PCDHGB3  3'  GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848  PCDHGB4  3'  GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848  PCDHGB5  3'  GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848  PCDHGB6  3'  GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848  PCDHGB7  3'  GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848  PCDHGC3  3'  GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848  PCDHGC3  3'  GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848  PCDHGC4  3'  GAGAAGCTGGGCTGGTTGGG  45320      A T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
```

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                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848 PCDHGC5  3' GAGAAGCTGGGCTGGTTGGG  45320       A  T  T
                                GAGAAGTT GG GTT GTTGGG
                                |||||||| || ||| ||||||
                                CTCTTCGA CC CGA CAACCC
                                    _ _  C
GAM1848 PKIG     3' AGAGGAGGTGTTGGTGTTGGGA 45321     AAGTT     __
                                AGAG    AGGTGTT  TGTTGGGA
                                ||||    |||||||  ||||||||
                                TCTC    TCCACAA  ACAACCCT
                                  C____     CC
GAM1848 RNASE1   5' GAGAAATTGGGTGTGTTCGGGA 45322       A    TTG
                                GAGAAGTT GGTGT   TTGGGA
                                |||||||| |||||   ||||||
                                CTCTTTAA CCACA   AGCCCT
                                    C    CA_
GAM1848 C4.4A    3' AGAGAAGTAGGTGAGAGGG   45323       T    TTTGTT
                                AGAGAAGT AGGTG     GGG
                                |||||||| |||||     |||
                                TCTCTTCA TCCAC     CCC
                                    _    TCT___
GAM1848 CHST8    5' GAGAAGCTGCTTGTTGGG    45324       TAGG
                                GAGAAGT   TGTTTGTTGGG
                                |||||||   ||||||||||
                                CTCTTCG   ACGAACAACCC
                                    _____
GAM1848 FLJ20359 3' AGCTAGGTGGGTGGGA     45325        TTT  T
                                AGTTAGGTG   GT GGGA
                                |||||||||   || ||||
                                TCGATCCAC   CA CCCT
                                    C__  _
GAM1848 FLJ23537 3' GAGGTGTTGGGAAGGATGTTGG 45326    AA   A  TGTT_
           G                     GAG  GTT GG    TGTTGGG
                                |||  ||| ||    |||||||
                                CTC  CAA CC    ACAACCC
                                  CA   C  TTCCT
GAM1848 KIAA1940 3' AGGAAGTTGGGTCCCTGGG   45327    A     A  T   G
                                AG GAAGTT GG GTTT TTGGG
                                || |||||| || |||| |||||
                                TC CTTCAA CC CAGG GACCC
                                  _    _ _   _
GAM1848 MGC2628  3' AGGGAGGTGGGTGCCTGCTGGG 45328    A  A  TA
                                AG GA GT  GGTGTTTGTTGGG
                                || || ||  ||||||||||||
                                TC CT CA  CCACGGACGACCC
                                 C  C  C_
GAM1848 MGC26954 3' AGGGAGGTGTCAAGGTGTTGGG 45329    TT     _____
           A                     AG  AGGTGTT    TGTTGGGA
                                ||  |||||||    ||||||||
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                                TC  TCCACAG    ACAACCCT
                                 CC      TTCC
GAM1848  ZDHHC8    3'  AGAGAAGTTGGTGGG       45330          A    TTTGTT
                                AGAGAAGTT GGTG     GG
                                ||||||||| ||||     ||
                                TCTCTTCAA CCAC     CC
                                    _   ______
GAM1848  LOC143677 5'  AGGTAAGTTAGGTGTTGTGTGG 45331    AG          _   T
                                AG  AAGTTAGGTGTT TGT GG
                                ||  |||||||||||| ||| ||
                                TC  TTCAATCCACAA ACA CC
                                 CA          C  _
GAM1848  LOC145813 5'  GAGGGGTGGCAGGTTGTTGGG  45332     AA  __     GTT
                                GAG  GT  TAGGT   TGTTGGG
                                |||  ||  |||||   |||||||
                                CTC  CA  GTCCA   ACAACCC
                                  CC  CC    ___
GAM1848  LOC147057 3'  AGAGAAGTGGGTGTTCCCTGGA 45333         TA      G
                                AGAGAAGT  GGTGTTT TTGGG
                                ||||||||  ||||||| |||||
                                TCTCTTCA  CCACAAG GACCT
                                     C_      G
GAM1848  LOC164395 5'  GAGAAGTTGGGTGCTTTCCCCC 45334         A      GT___
           GGG                    GAGAAGTT GGTGTTT     TGGG
                                ||||||||| |||||||     ||||
                                CTCTTCAA CCACGAA     GCCC
                                     C      AGGGG
GAM1848  LOC197049 3'  AGAGAGGGTGGGTGCTACTGGG 45335       AGTTA     TGT
                                AGAGA     GGTGTT   TGGG
                                |||||     ||||||   ||||
                                TCTCT     CCACGA   ACCC
                                   CCCAC     TG_
GAM1848  LOC256300 5'  AGAAGAGTTAGGTGCCGGG    45336     GA        TTGT
                                AGA  AGTTAGGTGT    TGGG
                                |||  ||||||||||    ||||
                                TCT  TCAATCCACG    GCCC
                                  TC         _____
GAM1849  PPT2      3'  TACAGTTATGTTTTGCCTCCTG 45339         T     CAA_  A
           T                     TACAGTT ATGTTT    TT TGT
                                ||||||| ||||||    || |||
                                ATGTCAA TACAAA    AG ACA
                                     _     ACGG  G
GAM1849  AD022     3'  AGCTTACCAATTATGT      45340        GTTT
                                AGTTTAT    CAATTATGT
                                |||||||    |||||||||
                                TCGAATG    GTTAATACA
                                     _____
GAM1849  EDG2      3'  TACAGTATGACTCCAATTATGT 45341        TT   _
           A                     TACAGT  ATG TTTCAATTATGTA
                                ||||||  ||| ||||||||||||
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                                ATGTCA  TAC GAGGTTAATACAT
                                   __   T
GAM1849  EDG2     3'  TACAGTATGACTCCAATTATGT 45341       TT  _
              A                  TACAGT  ATG TTTCAATTATGTA
                                 ||||||  ||| ||||||||||||
                                 ATGTCA  TAC GAGGTTAATACAT
                                    __   T
GAM1849  EML4     3'  TACAGTTTAGTTTTAAAGGCAT 45342         T   C  T__
              GT                   TACAGTTTA GTTT AA   TATGT
                                   |||||||||  |||| ||   |||||
                                   ATGTCAAAT CAAA TT   GTACA
                                      _   A  TCC
GAM1849  FLJ10525 3'  ATTTATGTAAATTATGTA    45343        TTC
                                   GTTTATGT   AATTATGTA
                                   ||||||||   |||||||||
                                   TAAATACA   TTAATACAT
                                      T__
GAM1849  KLHL8    3'  GTTCACCTTTTGATTATGTA   45344       G   CA
                                   GTTTAT TTT  ATTATGTA
                                   ||||||| |||  ||||||||
                                   CAAGTG AAA  TAATACAT
                                      G   AC
GAM1850  ATP6V1E1 3'  GGAAGGAGTGGTGTGCCAC   45347       A   A  AT
                                   GGAAG AGT GT  GTGTTAT
                                   ||||| ||| ||  |||||||
                                   CCTTC TCA CA  CACGGTG
                                     C   C  __
GAM1850  SCD      3'  TAGGAAGAAGTGAAAGTTGT   45348          ___  A
                                   TAGGAAGAAGT   AGT TGT
                                   ||||||||||   ||| |||
                                   ATCCTTCTTCA   TCA ACA
                                         CTT   _
GAM1850  TPS1     3'  TAGGAAGCAGTGGTGTT     45349      AGA     AT
                                   TAGGA   AGTAGT  GTGTT
                                   |||||   ||||||  |||||
                                   ATCCT   TCGTCA  CACAA
                                     ___     C_
GAM1850  TPSB1    3'  TAGGAAGCAGTGGTGTT     45349      AGA     AT
                                   TAGGA   AGTAGT  GTGTT
                                   |||||   ||||||  |||||
                                   ATCCT   TCGTCA  CACAA
                                     ___     C_
GAM1850  COVA1    3'  AGAAGACACTGATGTGTTATT  45350       AGTAGT
                                   GGAAGA     ATGTGTTATT
                                   ||||||     ||||||||||
                                   TCTTCT     TACACAATAA
                                      GTGAC_
GAM1850  DDX21    3'  TAGGAAGAAGTGGAGTACAT   45351          __
                                   TAGGAAGAAGT  AGTATGT
                                   ||||||||||  |||||||
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                                ATCCTTCTTCA  TCATGTA
                                      CC
GAM1850  LOC149386 3'  GGTAAGAAGTGGTGTGTCATT  45352    _     A  AT
                                GG AAGAAGT GT  GTGTTATT
                                || ||||||| ||  ||||||||
                                CC TTCTTCA CA  CACAGTAA
                                 A      C  __
GAM1851  DGKA     3'  TGTGCGCATGGGGAACA     45355    C      AAA
                                TG TGCGCATG   GAGCG
                                || ||||||||   |||||
                                AC ACGCGTAC   CTTGT
                                 _      CC_
GAM1851  MGAT1    3'  CTGGTCAAGAGAGCGAACG    45356    CG  TGAA
                                CTG  CA    AGAGCGAACG
                                |||  ||    ||||||||||
                                GAC  GT    TCTCGCTTGC
                                  CA  TC__
GAM1851  MYOD1    3'  TGCTGCGTGGAAAAAAC     45357       CAT
                                TGCTGCG   GAAAGAGC
                                |||||||   ||||||||
                                ACGACGC   CTTTTTTG
                                    AC_
GAM1851  DKFZp566H0824 5'  TGCGTGTGCATGAGAGAGCG   45358    _ C     A
                                TGC TG GCATGA AGAGCG
                                ||| || |||||| ||||||
                                ACG AC CGTACT TCTCGC
                                  C  A     C
GAM1851  KIAA1243  3'  ATACTGCAAGAAAGGGCGAA   45359       CAT    A
                                ATGCTGCG   GAAAG GCGAA
                                ||||||||   ||||| |||||
                                TATGACGT   CTTTC CGCTT
                                    T__    C
GAM1851  MGC2474   3'  TGCGGCGCATGAAGGC      45360     T       A A
                                TGC GCGCATGAA G GC
                                ||| ||||||||| | ||
                                ACG CGCGTACTT C CG
                                  C       _ _
GAM1851  SSI-1     3'  ATGCTGCGTGCACGGCGGGCG  45361       __    AAAGA
                                ATGCTGC  GCATG    GCG
                                |||||||  |||||    |||
                                TACGACG  CGTGC    CGC
                                    CA    CGCC_
GAM1851  LOC151512 5'  CGCTGCGCACCGAGCG      45362         GAAA
                                TGCTGCGCAT    GAGCG
                                ||||||||||    |||||
                                GCGACGCGTG    CTCGC
                                     G___
GAM1851  LOC152274 3'  ATGCTGCGCCTGGACAGCG   45363         A  AAAG
                                ATGCTGCGC TG    AGCG
                                |||||||| ||    ||||
```

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                                TACGACGCG AC    TCGC
                                     G  CTG_
GAM1851 LOC51619 3' ATGCTGCAGCTGGAGAGAG   45364       _ AT  A
                                ATGCTGC GC  GA AGAG
                                ||||||| ||  || ||||
                                TACGACG CG  CT TCTC
                                    T  AC  C
GAM1852 ATP8A2   3' GCCCAGTAGGTTGTAGATTTCT 45367     G___    AC
                                GCT    AGGTT  AGATTTCT
                                |||    |||||  ||||||||
                                CGG    TCCAA  TCTAAAGA
                                  GTCA    CA
GAM1852 FCGR2A   3' TGGCTGGGGTTGTCTTATTTCT 45368    A   A   ACAG_
             AA                   TG GCTG GGTT    ATTTCTAA
                                || |||| ||||    ||||||||
                                AC CGAC CCAA    TAAAGATT
                                 _   C    CAGAA
GAM1852 FUS2     3' TGGGCTGAGGCTTGTAGACT   45369    A       AC_
                                TG GCTGAGGTT   AGATT
                                || |||||||||   |||||
                                AC CGACTCCGA   TCTGA
                                 C        ACA
GAM1852 IRAK4    3' TAAGCTGACTCAGATTT     45370        GGTTA
                                TGAGCTGA    CAGATTT
                                ||||||||    |||||||
                                ATTCGACT    GTCTAAA
                                    GA___
GAM1852 PKHD1    3' TGACTGACTTCTAGATTTCT   45371     G   GG  AC
                                TGA CTGA  TT  AGATTTCT
                                ||| ||||  ||  ||||||||
                                ACT GACT  AG  TCTAAAGA
                                  _   GA  A_
GAM1852 POU2AF1  5' TGAGCTGAGGCTGTTTCC    45372          ACAGA
                                TGAGCTGAGGTT    TTTCT
                                ||||||||||||    |||||
                                ACTCGACTCCGA    AAAGG
                                       C____
GAM1852 BCMP1    3' GCTGAGGCACCAATTTCTAA   45373        T  A
                                GCTGAGGT AC GATTTCTAA
                                |||||||| || |||||||||
                                CGACTCCG TG TTAAAGATT
                                    _  G
GAM1852 FLJ23168 3' TGACCTGGCAAAGATTTCTAA 45374    G  GA   TAC
                                TGA CT  GGT   AGATTTCTAA
                                ||| ||  |||   ||||||||||
                                ACT GA  CCG   TCTAAAGATT
                                  G  __   TT_
GAM1852 KIAA1189 3' TGATTTGAGGTTATCAGACT   45375     GC       _
                                TGA  TGAGGTTA CAGATT
                                |||  |||||||| ||||||
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                                ACT  ACTCCAAT GTCTGA
                                  AA       A
GAM1852  MGC27382  3'  TGGCTGAAGATTTCT      45376    A    GGTTAC
                                TG GCTGA     AGATTTCT
                                || |||||     ||||||||
                                AC CGACT     TCTAAAGA
                                 _    _______
GAM1852  MRPL35    3'  TGAGGCTGGGAGGTGATTTCT  45377     _  A  TTACA
                                TGAG CTG GG    GATTTCT
                                |||| ||| ||    |||||||
                                ACTC GAC CC    CTAAAGA
                                  C  _  TCCA_
GAM1852  PARVB     3'  TGAGCTGATGTTGTACTTCT   45378       G   ACAG
                                TGAGCTGA GTT    ATTTCT
                                |||||||| |||    ||||||
                                ACTCGACT CAA    TGAAGA
                                     A   CA__
GAM1852  WIT-1     5'  GAGCTGAGGTTCCATTCT    45379         A  GAT
                                GAGCTGAGGTT CA   TTCT
                                |||||||||||  ||   ||||
                                CTCGACTCCAA GT   AAGA
                                      G  ___
GAM1852  LOC144455 3'  TGAGCTGAGGGTGCAGAT    45380         TTA
                                TGAGCTGAGG   CAGAT
                                ||||||||||   |||||
                                ACTCGACTCC   GTCTA
                                      CAC
GAM1852  LOC149535 3'  ACTGGAGAGAGATTTCTAA   45381     AG TTAC
                                GCTG  G    AGATTTCTAA
                                ||||  |    ||||||||||
                                TGAC  C    TCTAAAGATT
                                  CT TC__
GAM1852  LOC153856 3'  TGGCTTGAAAAAGATTTCTAA  45382    A  _    TTAC
                                TG GCT GAGG    AGATTTCTAA
                                || ||| ||||    ||||||||||
                                AC CGA CTTT    TCTAAAGATT
                                 _   A    T___
GAM1852  LOC202347 3'  CCGAGGTTGTGGATTTCTA    45383        ACA
                                CTGAGGTT   GATTTCTA
                                ||||||||   ||||||||
                                GGCTCCAA   CTAAAGAT
                                     CAC
GAM1853  ADAM28    3'  TGATGTTTTTATGTTTTGTTT  45386     A   G
                                TGA TGTT TTTATGTTTTGTTT
                                ||| |||| ||||||||||||||
                                ACT ACAA AAATACAAAACAAA
                                  _   _
GAM1853  AKAP13    3'  TTGAAGTTGTTACTTTTGTTT  45387      T     TATG
                                TTGAA GTTGTT    TTTTGTTT
                                ||||| ||||||    ||||||||
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                                AACTT CAACAA    AAAACAAA
                                  _     TG__
GAM1853  HDAC5    3'  TTGAATGTGTGACTTTTTGTTT 45388        T  TTATG
                                TTGAATGT GT     TTTTGTTT
                                |||||||| ||     ||||||||
                                AACTTACA CA     AAAACAAA
                                    _ CTGA_
GAM1853  MTMR6    3'  TTGGGGTTTTTATGTTTTGTTT 45389     AAT   G
                                TTG   GTT TTTATGTTTTGTTT
                                |||   ||| ||||||||||||||
                                AAC   CAA AAATACAAAACAAA
                                  CC_  _
GAM1853  SORCS1   3'  TTGATTGTTTATATTTTATGTT 45390     A   G____
            TTGTTT                TGA TGTT     TTTATGTTTTGTTT
                                ||| ||||     ||||||||||||||
                                ACT ACAA     AAATACAAAACAAA
                                  A   ATATA
GAM1853  STAT1    3'  AATGTTGTCTTCTTTGTTT    45391         TATG
                                AATGTTGTT    TTTTGTTT
                                |||||||||    ||||||||
                                TTACAACAG    GAAACAAA
                                     AA__
GAM1853  TXNRD1   3'  AATGTTTCACATTGTTTTGTTT 45392       GTT  _
                                AATGTT   TAT GTTTTGTTT
                                ||||||   ||| |||||||||
                                TTACAA   GTA CAAAACAAA
                                   AGT   A
GAM1853  FLJ11042 3'  TGAGAGTATTTGTGTTTTGTTT 45393     AT  T   A
                                TGA  GT GTTT TGTTTTGTTT
                                |||  || |||| ||||||||||
                                ACT  CA TAAA ACAAAACAAA
                                  CT  _   C
GAM1853  JDD1     3'  GAATGTTGTATTTTGTTT     45394         TTAT
                                GAATGTTGT    GTTTTGTTT
                                |||||||||    |||||||||
                                CTTACAACA    TAAAACAAA
                                     ____
GAM1853  MGC2817  3'  CTGAATGGTTCTGTGTTTTGTT 45395       TTG   A
            T                    TTGAATG   TTT TGTTTTGTTT
                                |||||||   ||| ||||||||||
                                GACTTAC   AGA ACAAAACAAA
                                    CA_   C
GAM1853  ZNF387   3'  TTGAATGTTGTCTTGTTT    45396           A
                                TTGAATGTTGTTT TGTTT
                                |||||||||||| |||||
                                AACTTACAACAGA ACAAA
                                      _
GAM1853  LOC221178 3'  TTGAATGTTTTTTGTTTTTGTT 45397         G   ATG
            T                    TTGAATGTT TTT   TTTTGTTT
                                |||||||| |||   ||||||||
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                                AACTTACAA AAA   AAAACAAA
                                     A   CA_
GAM1853  LOC91650  5'  TTGATGTCCTGAGATGTTTTGT 45398     A    GTTT_
              TT                   TTGA TGTT    ATGTTTTGTTT
                                   |||| ||||    ||||||||||
                                   AACT ACAG    TACAAAACAAA
                                     _   GACTC
GAM1854  CENTD2    3'  TGGAAGGAAGGCTGAAGTC   45401        C   AAGTG
                                   TGGAAGGA GGG    GAAGTC
                                   |||||||| |||    ||||||
                                   ACCTTCCT TCC    CTTCAG
                                        _  GA___
GAM1854  CENTD2    3'  TGGAAGGAAGGCTGAAGTC   45401        C   AAGTG
                                   TGGAAGGA GGG    GAAGTC
                                   |||||||| |||    ||||||
                                   ACCTTCCT TCC    CTTCAG
                                        _  GA___
GAM1854  CLCN4     5'  GGGGGGAAGACCCTGGAAGTCC 45402    AC    _____
                                   GG  GGGAAG   TGGAAGTCC
                                   ||  ||||||   |||||||||
                                   CC  CCCTTC   ACCTTCAGG
                                    C_     TGGG
GAM1854  ELK1      3'  GGGAGGTGGGGGGAGATGTCC   45403    A   AC   AAGT   A
                                   GG AGG  GGG   GGA GTCC
                                   || |||  |||   ||| ||||
                                   CC TCC  CCC   TCT CAGG
                                    C   A_   CC__   A
GAM1854  JPH2      5'  TGAAAGGGTGGGGTGGAGGGGT 45404        AC   AA    A__
              CC                     TGGAAGG  GGG  GTGGA   GTCC
                                   |||||||  |||  |||||   ||||
                                   ACTTTCC  CCC  CACCT   CAGG
                                       CA   __    CCC
GAM1854  NDRG2     3'  TGGGAGACGGGAGGGCACCC   45405     AA       A T  AAG
                                   TGG  GGACGGGA G GG   TCC
                                   |||  |||||||| | ||   |||
                                   ACC  TCTGCCCT C CC   GGG
                                     C_       _ _  GT_
GAM1854  PML       3'  TGGAAGGAGGGGCTAATAGGAG 45406        C   A_    A
              TC                     TGGAAGGA GGG  AGTGG AGTC
                                   |||||||| |||  ||||| ||||
                                   ACCTTCCT CCC  TTATC TCAG
                                       C   GA    C
GAM1854  PMM2      3'  GGCACTGGAGGTGGAAGTCC   45407    _  G   A
                                   GG AC GGA GTGGAAGTCC
                                   || || ||| ||||||||||
                                   CC TG CCT CACCTTCAGG
                                    G  A   C
GAM1854  PPP2R1A   3'  GGGAGGACGGGAGGTGGA    45408    A       A
                                   GG AGGACGGGA GTGGA
                                   || |||||||| |||||
```

```
                                CC TCCTGCCCT CACCT
                                 C        C
GAM1854  PPP3CA   3'  TGGAAGGATGAGAATTCTGTAA 45409         C     GTGG__
              GT                  TGGAAGGA GGGAA      AAGT
                                  |||||||| |||||      ||||
                                  ACCTTCCT CTCTT      TTCA
                                      A     AAGACA
GAM1854  RXRG     3'  GGAAAGTGCAGGGTGGGGGTCC 45410       A_    AA    AA
                                  GGAAGG  CGGG  GTGG  GTCC
                                  ||||||  ||||  ||||  ||||
                                  CCTTTC  GTCC  CACC  CAGG
                                     AC    __    CC
GAM1854  SGT      3'  TGGGAGGAGGGGAAACATGTC  45411     A    C     GT GAA
                                  TGG AGGA GGGAA  G   GTC
                                  ||| |||| |||||  |   |||
                                  ACC TCCT CCCTT  T   CAG
                                    C    C     TG A__
GAM1854  SLC6A8   3'  TGGAGGTGCGGGAAGTGCATCC 45412      A  A_        GAA
                                  TGGA GG  CGGGAAGTG   GTCC
                                  |||| ||  |||||||||   ||||
                                  ACCT CC  GCCCTTCAC   TAGG
                                    _ AC        G__
GAM1854  SOD3     3'  TGGAAGGATGGTGGGT      45413         C  GAAG   AA
                                  TGGAAGGA GG    TGG  GT
                                  |||||||| ||    |||  ||
                                  ACCTTCCT CC    ACC  CA
                                      A _____   __
GAM1854  STC1     3'  GGAGGGAGGGGAAGAGTC    45414     A   C     TGGA
                                  GGA GGA GGGAAG    AGTC
                                  ||| ||| ||||||    ||||
                                  CCT CCT CCCTTC    TCAG
                                    C   C     _____
GAM1854  TEGT     3'  TGGAAGGAGAGGAAGTCTGG   45415         C     T_____
                                  TGGAAGGA GGGAAG      GG
                                  |||||||| ||||||      ||
                                  ACCTTCCT TCCTTC      CC
                                      C      AGAIII
GAM1854  TRAF1    3'  TGGGAGGACAGGAAGCTCCGGA 45416    A         T_______  AAGT
              CTC                   G AGGACGGGAAG      GG    C
                                  | ||||||||||       ||    |
                                  C TCCTGTCCTTC      CC    G
                                   C          GAGGIII  TGAA
GAM1854  C1orf22  3'  AGGGGGGGGGGGTGGAAGTC   45417     AC_   AA
                                  AGG   GGG  GTGGAAGTC
                                  |||   |||  |||||||||
                                  TCC   CCC  CACCTTCAG
                                    CCC   CC
GAM1854  CALN1    3'  TGGAAGGGGGGAAGCATGTAGT 45418         AC       GA_
                                  TGGAAGG  GGGAAGTG   AGT
                                  |||||||  ||||||||   |||
```

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                                ACCTTCC  CCCTTCGT   TCA
                                   C_       ACA
GAM1854  dJ309H15.1 3'  TGGAAGGCGGGGGGCATTCGGA 45419      A    AA T________  AAGT
           CTC                    AAGG CGGG  G       GG    C
                                |||| ||||  |       ||    |
                                TTCC GCCC  C       CC    G
                                  _    CC GTAAGIII  TGAA
GAM1854  DKFZP434P211 3'  GGATGGGACCTGGAAGTC    45420     C    AG
                                GGA GGGA  TGGAAGTC
                                ||| ||||  ||||||||
                                CCT CCCT  ACCTTCAG
                                  A    GG
GAM1854  DKFZP547L112 5'  TGGAAGGACTGGGGTCCTGGAG 45421          _   AAG_    A
           TCC                    TGGAAGGAC GGG    TGGA GTCC
                                |||||||||  |||    |||| ||||
                                ACCTTCCTG CCC    ACCT CAGG
                                     A   CAGG   _
GAM1854  ERF      3'  TGGGGGGTGCGGGGCACACAGG 45422     AA  A_    AA__ TG AA
           TCC                    TGG  GG  CGGG    G  G  GTCC
                                |||  ||  ||||    |  |  ||||
                                ACC  CC  GCCC    T  C  CAGG
                                  CC  AC    CGTG GT __
GAM1854  FLJ10743  3'  GGAAGGGCAGCGAGAAGTCC   45423     C   A    _
                                GGA GGG AGTG GAAGTCC
                                ||| ||| |||| |||||||
                                CCT CCC TCGC CTTCAGG
                                  T   G    T
GAM1854  FLJ12387  3'  TGGGAGGACGGACTAAGGGGAG 45424     A       __   T   A
           GTCC                    TGG AGGACGGG  AAG GGA GTCC
                                ||| ||||||||  ||| ||| ||||
                                ACC TCCTGCCT  TTC CCT CAGG
                                  C       GA   C   C
GAM1854  FLJ12700  3'  TGGTGAGGGTGGAGGAAGTCC  45425     A_   ACG   AGT
                                TGG  AGG   GGA   GGAAGTCC
                                |||  |||   |||   ||||||||
                                ACC  TCC   CCT   CCTTCAGG
                                  AC   CA_   ___
GAM1854  KIAA0172  5'  TGAGAGGGATTCAGTGGAAGTC 45426   A   C    ___
           C                     A GGA GGGA   AGTGGAAGTCC
                                | ||| ||||   ||||||||||
                                A TCT CCCT   TCACCTTCAGG
                                 C   _    AAG
GAM1854  KIAA0446  3'  TGGCAGGGTGGGGGGTGGGGTC 45427     A   AC   AA    AA
                                TGG AGG  GGG  GTGG  GTC
                                ||| |||  |||  ||||  |||
                                ACC TCC  CCC  CACC  CAG
                                  G   CA   CC    C_
GAM1854  KIAA1219  3'  TGGAAGACGAGGAAGTCTGG   45428       G   _    T_____
                                TGGAAG ACG GGAAG     GG
                                |||||| ||| |||||     ||
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                                ACCTTC TGC CCTTC     CC
                                   _  T    AGAIII
GAM1854  PYY      5'  TGGAAGGCGAGGGAAGTC    45429        A    AAGT
                                TGGAAGG CGGG   GGAAGTC
                                ||||||| ||||   |||||||
                                ACCTTCC GCTC   CCTTCAG
                                   _   _____
GAM1854  SCAMP-4   3'  TGGGAGGACGGGAGGG      45430     A       A T
                                TGG AGGACGGGA G GG
                                ||| ||||||||| | ||
                                ACC TCCTGCCCT C CC
                                  C       _ _
GAM1854  SCYB10    3'  TGGGAGGATGGCAGTGGAAGTC 45431     A    C  GA
              C                  TGG AGGA GG  AGTGGAAGTCC
                                ||| |||| ||  ||||||||||
                                ACC TCCT CC  TCACCTTCAGG
                                  C    A  G_
GAM1854  TOLLIP    3'  GGACGGGGCGGCACAGAAGTCC 45432        AA___ TG
                                GGACGGG    G  GAAGTCC
                                |||||||    |  |||||||
                                CCTGCCC    T  CTTCAGG
                                    CGCCG GT
GAM1854  VEGFC     5'  TGGAAGGACCGGGGGGTGGGGGA 45433         G  AA    AAGT
              CC                  TGGAAGGAC GG  GTGG    CC
                                ||||||||| ||  ||||    ||
                                ACCTTCCTG CC  CACC    GG
                                     G  CC    CCCT
GAM1854  ZNF304    3'  TGGGGGGGGGGGGGAAGTC    45434     AA  AC   AAGT
                                TGG  GG  GGG    GGAAGTC
                                |||  ||  |||    |||||||
                                ACC  CC  CCC    CCTTCAG
                                  CC  C_  _____
GAM1854  LOC115330 3'  TGGAAGGATGTGGGGAGCGTCC 45435         C__   A   GGAA
                                TGGAAGGA   GGG AGT    GTCC
                                ||||||||   ||| |||    ||||
                                ACCTTCCT   CCC TCG    CAGG
                                     ACA   C   _____
GAM1854  LOC124961 3'  TGGGAGGACAGAGGAGGT    45436     A       AAGT   A
                                TGG AGGACGGG    GGA GT
                                ||| ||||||||    ||| ||
                                ACC TCCTGTCT    CCT CA
                                  C        _____   C
GAM1854  LOC132617 5'  TGGAAGAACGGGCCTGCGGGGT 45437            AA_   AA
              CC                  TGGAAGGACGGG   GTGG  GTCC
                                ||||||||||||   ||||  ||||
                                ACCTTCTTGCCC   CGCC  CAGG
                                       GGA    C_
GAM1854  LOC146956 3'  GAGGTTGGGGAAGTGGAAGT   45438    A  AC_
                                GA GG   GGGAAGTGGAAGT
                                || ||   ||||||||||||
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                                CT CC   CCCTTCACCTTCA
                                 _ AAC
GAM1854  LOC147700 3'  TGGGGGCGTCTGTGGAAGT   45439     AA  A  GGAA
                                TGG  GG CG    GTGGAAGT
                                |||  || ||    ||||||||
                                ACC  CC GC    CACCTTCA
                                  C_  _  AGA_
GAM1854  LOC148343 5'  TGGGAGAACGGGGAGTGGGCC  45440     A       A     AA
                                TGG AGGACGGG AGTGG  GTC
                                ||| |||||||| |||||  |||
                                ACC TCTTGCCC TCACC  CGG
                                  C       C    __
GAM1854  LOC150213 3'  GGATGGGACCTGGAAGTC    45420     C    AG
                                GGA GGGA  TGGAAGTC
                                ||| ||||  ||||||||
                                CCT CCCT  ACCTTCAG
                                  A   GG
GAM1854  LOC151057 3'  GAAATGAGGAAGTGGAGGT    45441      GAC         A
                                GAAG   GGGAAGTGGA GT
                                ||||   |||||||||| ||
                                CTTT   TCCTTCACCT CA
                                   AC_         C
GAM1854  LOC151521 3'  TGGAAGTGTGGGGGTGGGGTTC 45442       GAC   AA    AAG
                                TGGAAG   GGG  GTGG   TC
                                ||||||   |||  ||||   ||
                                ACCTTC   CCC  CACC   AG
                                    ACA   C_   CCA
GAM1854  LOC152402 3'  TGGAAGCGTGCGGAAGTC    45443       GA  GGAA
                                TGGAAG  CG    GTGGAAGTC
                                ||||||  ||    |||||||||
                                ACCTTC  GC    CGCCTTCAG
                                    __  A____
GAM1854  LOC158852 5'  TGGGAGGAAGGGAAGTAG    45444     A    C
                                TGG AGGA GGGAAGTGG
                                ||| |||| |||||||||
                                ACC TCCT CCCTTCATC
                                  C    T
GAM1854  LOC203427 5'  GAGGGACGGGAAGCCCCGTC   45445    A         GGAA
                                GA GGACGGGAAGT    GTC
                                || ||||||||||    |||
                                CT CCTGCCCTTCG    CAG
                                 C          GGG_
GAM1854  LOC203536 5'  TGGAAGGAAGGGAGGCGATGTC 45446         C    A    AA
                                TGGAAGGA GGGA GTGG  GTC
                                |||||||| |||| ||||  |||
                                ACCTTCCT CCCT CGCT  CAG
                                     T    C    A_
GAM1854  LOC219513 5'  TGGAAGGAGGGGCACAGGGTCC 45447         C   AAGT  AA
                                TGGAAGGA GGG    GG  GTCC
                                |||||||| |||    ||  ||||
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                                ACCTTCCT CCC   CC  CAGG
                                    C   GTGT  __
GAM1854  LOC221140 3'  TGGGAGAATGGGTAAGTTTGGA 45448   A   C   _   T_____  AAGT
              CTC                   G AGGA GGG AAG     GG   C
                                | |||| ||| |||     ||   |
                                C TCTT CCC TTC     CC   G
                                 C   A   A   AAAIII  TGAA
GAM1854  LOC89932  5'  TGGAGAGGTGGGAAGTGAGA   45449     _   AC      _
                                TGGA AGG  GGGAAGTG GA
                                |||| |||  |||||||| ||
                                ACCT TCC  CCCTTCAC CT
                                  C   A_       T
GAM1855  APLP2     3'  CAGGCTAATCTCTGTGGAAGC  45452       CA____
                                CAGGCTGG     TGGAAGC
                                ||||||||     |||||||
                                GTCCGATT     ACCTTCG
                                     AGAGAC
GAM1855  C1QA      3'  CAGGCGGAGCATGGAAGC    45453      T _
                                CAGGC G GCATGGAAGC
                                ||||| | ||||||||||
                                GTCCG C CGTACCTTCG
                                   C T
GAM1855  CDK10     5'  CCAGGCCAGGCTGGGGGC    45454       _   A   AA
                                CCAGGCT GGC TGG  GC
                                ||||||| ||| |||  ||
                                GGTCCGG CCG ACC  CG
                                     T   _   CC
GAM1855  CENPC1    5'  TACCAGGCCGCGGCCAAGC   45455        __   ATGG
                                TACCAGGCT  GGC    AAGC
                                |||||||||  |||   ||||
                                ATGGTCCGG  CCG    TTCG
                                     CG   G___
GAM1855  COMT      3'  TACCAGGCTGGGTGAGAGAGC  45456         CAT_ GA
                                TACCAGGCTGG    G  AGC
                                ||||||||||    |  |||
                                ATGGTCCGACC    C  TCG
                                       CACT TC
GAM1855  COMT      3'  TACCAGGCTGGGTGAGAGAGC  45456         CAT_ GA
                                TACCAGGCTGG    G  AGC
                                ||||||||||    |  |||
                                ATGGTCCGACC    C  TCG
                                       CACT TC
GAM1855  DGCR2     3'  CCAGGCTGGGACAGGGGC    45457        C    AA
                                CCAGGCTGG ATGG  GC
                                ||||||||| ||||  ||
                                GGTCCGACC TGTC  CG
                                     C    CC
GAM1855  DNASE1L1  3'  TACCAGGCATGCAGAAGC    45458        TG   TG
                                TACCAGGC  GCA  GAAGC
                                ||||||||  |||  |||||
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                                ATGGTCCG  CGT  CTTCG
                                    TA  __
GAM1855  DNMT3L   5'  CACCAGGCTATGGGGGC    45459        GGC   AA
                                TACCAGGCT   ATGG  GC
                                |||||||||   ||||  ||
                                GTGGTCCGA   TACC  CG
                                     ___    CC
GAM1855  DTR      3'  AGCTACAGGCATGGAAGC    45460     ___
                                GGCT   GGCATGGAAGC
                                ||||   ||||||||||
                                TCGA   CCGTACCTTCG
                                  TGT
GAM1855  EDN2     5'  CCAGGCTGGACTGGAGC     45461        CA   A
                                CCAGGCTGG  TGGA GC
                                |||||||||  ||||  ||
                                GGTCCGACC  ACCT CG
                                     TG   _
GAM1855  GLDC     3'  AACTGGCACATGTGGAAGC   45462        _____
                                GGCTGGCA    TGGAAGC
                                ||||||||    |||||||
                                TTGACCGT    ACCTTCG
                                    GTAC
GAM1855  GPC6     5'  ACACAGGCTGTGGGAGC     45463   _     GCA   A
                                AC CAGGCTG   TGG AGC
                                || |||||||   ||| |||
                                TG GTCCGAC   ACC TCG
                                 T      ___   C
GAM1855  GPRK6    3'  ACCAGGCTGTGGGAGC      45464        GCA   A
                                ACCAGGCTG   TGG AGC
                                |||||||||   ||| |||
                                TGGTCCGAC   ACC TCG
                                     ___   C
GAM1855  HDAC5    3'  CCAGAAGGTATGGAAGC     45465      CT  C
                                CCAGG  GG ATGGAAGC
                                |||||  ||  ||||||||
                                GGTCT  CC TACCTTCG
                                  T_  A
GAM1855  IL10     3'  CAGGCTTGGAATGGAAGC    45466       _  C
                                CAGGCT GG ATGGAAGC
                                ||||||  ||  ||||||||
                                GTCCGA CC TACCTTCG
                                   A  T
GAM1855  IL10RA   3'  TACCAGACTGGCACCTAAG   45467           GG
                                TACCAGGCTGGCAT  AAG
                                ||||||||||||||  |||
                                ATGGTCTGACCGTG  TTC
                                      GA
GAM1855  IL13     3'  CACCAGGCTGAGCCCTGG    45468         _  A_
                                TACCAGGCTG GC  TGG
                                |||||||||  ||  |||
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                                GTGGTCCGAC CG  ACC
                                      T  GG
GAM1855  IL1RAP   3'  AGCAGTGACCATGGAAGC    45469     __   _
                                GGC  TGGC ATGGAAGC
                                |||  |||| ||||||||
                                TCG  ACTG TACCTTCG
                                  TC    G
GAM1855  IL2RB    3'  TACCAGGCTGAGAAG       45470          GCAT
                                TACCAGGCTG    GGAAG
                                ||||||||||    |||||
                                ATGGTCCGAC    TCTTC
                                      _____
GAM1855  INHBB    3'  CCAGGCTGGGAAGAAGC     45471          CAT
                                CCAGGCTGG   GGAAGC
                                |||||||||   ||||||
                                GGTCCGACC   TCTTCG
                                      CT_
GAM1855  INPP5A   3'  TACACAGAAGAACGGCATGGGA 45472     _   C___       A
              G                   TAC CAGG    TGGCATGG AG
                                ||| ||||    |||||||| ||
                                ATG GTCT    GCCGTACC TC
                                  T    TCTT       C
GAM1855  ITGA3    3'  CCAGGCTGGCACAGAAAGC    45473             _
                                CCAGGCTGGCATGGAA GC
                                |||||||||||||||| ||
                                GGTCCGACCGTGTCTT CG
                                         T
GAM1855  ITGA3    3'  CCAGGCTGGCACAGAAAGC    45473             _
                                CCAGGCTGGCATGGAA GC
                                |||||||||||||||| ||
                                GGTCCGACCGTGTCTT CG
                                         T
GAM1855  KIT      3'  CACCACTATGGAAGC       45474      AG   GGC
                                TACC  GCT   ATGGAAGC
                                ||||  |||   ||||||||
                                GTGG  TGA   TACCTTCG
                                   __   ____
GAM1855  MADH7    3'  CCAGGCTGGGGACAGAGC    45475          C_    A
                                CCAGGCTGG  ATGGA GC
                                |||||||||  ||||| ||
                                GGTCCGACC  TGTCT CG
                                      CC    _
GAM1855  MTMR8    3'  CACCAGGCTAATGGGAG     45476          GC    A
                                TACCAGGCTG  ATGG AG
                                ||||||||||  |||| ||
                                GTGGTCCGAT  TACC TC
                                      __    C
GAM1855  MYBPH    3'  AGCCGTCGCTATGGAAGC    45477       __ _
                                GGCTG  GC ATGGAAGC
                                |||||  || ||||||||
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                                TCGGC  CG TACCTTCG
                                   AG  A
GAM1855  NEBL     5'  TACCAGGCTGGCCTCACAAG   45478          AT_ G
                                TACCAGGCTGGC   G AAG
                                ||||||||||||   | |||
                                ATGGTCCGACCG   T TTC
                                       GAG G
GAM1855  NONO     3'  TACCAGCTGGCACAGGAGC   45479       G        A
                                TACCAG CTGGCATGG AGC
                                ||||||| ||||||||| |||
                                ATGGTC GACCGTGTC TCG
                                   _        C
GAM1855  PACE     3'  CCGGGCTGGCCACGAGGGC   45480    A      _    AA
                                CC GGCTGGC ATGG  GC
                                || ||||||| ||||  ||
                                GG CCGACCG TGCT  CG
                                 C      G    CC
GAM1855  PBX1     3'  ACCAGGCTGACAGCTGGAGGC  45481           __    A
                                ACCAGGCTGGCA  TGGA GC
                                ||||||||||||  |||| ||
                                TGGTCCGACTGT  ACCT CG
                                       CG    C
GAM1855  PCTK3    3'  CCAGGCTGGCTGTCAGC     45482          A  GA
                                CCAGGCTGGC TG  AGC
                                |||||||||| ||  |||
                                GGTCCGACCG AC  TCG
                                      _  AG
GAM1855  PES1     3'  CAGGCTGGGCACAGAGGC    45483         _     A
                                CAGGCTGG CATGGA GC
                                |||||||| |||||| ||
                                GTCCGACC GTGTCT CG
                                     C     C
GAM1855  PIK3R3   3'  ACCACTGTATGGAAGC      45484     AG    GC
                                ACC  GCTG  ATGGAAGC
                                |||  ||||  ||||||||
                                TGG  TGAC  TACCTTCG
                                  __    A_
GAM1855  PLXNB2   3'  ACCTAGGGCATGGAGGC     45485     A  CT       A
                                ACC GG  GGCATGGA GC
                                ||| ||  |||||||| ||
                                TGG TC  CCGTACCT CG
                                  A __       C
GAM1855  PTK2B    3'  ACCAGGCTGGCTTAGGGAGC   45486          AT_  A
                                ACCAGGCTGGC   GG AGC
                                ||||||||||   || |||
                                TGGTCCGACCG   CC TCG
                                       AAT  C
GAM1855  RAB18    3'  AACTAGCCATTATGGAAGC    45487        ____
                                GGCTGGC    ATGGAAGC
                                |||||||    ||||||||
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                                TTGATCG   TACCTTCG
                                   GTAA
GAM1855 RASGRP1  3' TACCAGACTTTATAGGCATGGA 45488       _____        III
            AGCG                  CCAGGCT    GGCATGGAAGC   G
                                  |||||||    ||||||||||  |
                                  GGTCTGA    CCGTACCTTCG   C
                                     AATAT        III
GAM1855 RFP     3' CCAGGCTGAGCCAAGAAGC   45489       _ AT
                                  CCAGGCTG GC  GGAAGC
                                  |||||||| ||  ||||||
                                  GGTCCGAC CG  TCTTCG
                                       T  GT
GAM1855 RXRA    3' CACTGGGCTGAGCCAGGGAGGC 45490    CA    _ AT_  A
                                  TAC  GGCTG GC   GGA GC
                                  |||  ||||| ||   ||| ||
                                  GTG  CCGAC CG   CCT CG
                                    AC    T  GTC   C
GAM1855 SPAP1   3' CCAGGCTGGTGAGACACAGC   45491        CAT  ___
                                  CCAGGCTGG   GGA   AGC
                                  |||||||||   |||   |||
                                  GGTCCGACC   TCT   TCG
                                       AC_   GTG
GAM1855 SUFU    3' CCAGGCTGGCTGCAGC      45492         A  GA
                                  CCAGGCTGGC TG  AGC
                                  ||||||||||  ||  |||
                                  GGTCCGACCG AC  TCG
                                        _  G_
GAM1855 TCF1    3' CCAGGCTGGCCTCAGAGGC   45493         AT_  A
                                  CCAGGCTGGC   GGA GC
                                  ||||||||||   ||| ||
                                  GGTCCGACCG   TCT CG
                                       GAG   C
GAM1855 TNFRSF13C 3' CACCAAACTCCATGGGGGC   45494         GG    AA
                                  TACCAGGCT  CATGG  GC
                                  |||||||||  |||||  ||
                                  GTGGTTTGA  GTACC  CG
                                       G_    CC
GAM1855 WBP2    3' CCGGGCTGGCATGGGAAGC   45495    A        _
                                  CC GGCTGGCATGG AAGC
                                  || ||||||||||| ||||
                                  GG CCGACCGTACC TTCG
                                   C         C
GAM1855 WNT1    3' ACCAGGCTGGGACCCAGC    45496         C  GGA
                                  ACCAGGCTGG AT   AGC
                                  ||||||||||  ||   |||
                                  TGGTCCGACC TG   TCG
                                       C  GG_
GAM1855 WNT5B   5' ACTAGGCTACATTGGGGGC   45497    C     G  _  AA
                                  AC AGGCTG CAT GG  GC
                                  || |||||| ||| ||  ||
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                                TG TCCGAT GTA CC  CG
                                 A     _  A  CC
GAM1855  ZNF134   3'  CCAGGTGACTTGGAGGC     45498      C   A   A
                                CCAGG TGGC TGGA GC
                                ||||| |||| |||| ||
                                GGTCC ACTG ACCT CG
                                   _   A   C
GAM1855  ZNF22    3'  CACCATTCTCATGGAAG     45499      GG  GG
                                TACCA  CT  CATGGAAG
                                |||||  ||  ||||||||
                                GTGGT  GA  GTACCTTC
                                   AA  __
GAM1855  AMOT     3'  CACACAAACCATGGAAG     45500     _    TGG
                                TAC CAGGC   CATGGAAG
                                ||| |||||   ||||||||
                                GTG GTTTG   GTACCTTC
                                  T    ____
GAM1855  ASP      5'  ACCAGGCTGGTGAATCGC    45501         CA   A_
                                ACCAGGCTGG  TGGA  GC
                                ||||||||||  ||||  ||
                                TGGTCCGACC  ACTT  CG
                                      __    AG
GAM1855  ASP      5'  ACCAGGCTGGTGAATCGC    45501         CA   A_
                                ACCAGGCTGG  TGGA  GC
                                ||||||||||  ||||  ||
                                TGGTCCGACC  ACTT  CG
                                      __    AG
GAM1855  ATP6V1B2 3'  TACCAGCTGTGCAAAAAG    45502       G  _  T
                                TACCAG CTG GCA GGAAG
                                |||||| ||| ||| |||||
                                ATGGTC GAC CGT TTTTC
                                   _   A   _
GAM1855  C11orf21 3'  CACCAGGCAAGGGAGGC     45503         T  CAT   A
                                TACCAGGC GG   GGA GC
                                |||||||| ||   ||| ||
                                GTGGTCCG TC   CCT CG
                                     T  ____   C
GAM1855  C20orf97 3'  CACCAGCATCAGTGGAGGC    45504       G TGG  _   A
                                TACCAG C   CA TGGA GC
                                |||||| |   || |||| ||
                                GTGGTC G   GT ACCT CG
                                   _ TA_  C    C
GAM1855  CLSP     3'  ACCAGGCCCAAGGAGGC     45505         GG  T   A
                                ACCAGGCT  CA GGA GC
                                ||||||||  || ||| ||
                                TGGTCCGG  GT CCT CG
                                     __  T   C
GAM1855  DKFZP434A043 5'  CCAGGCTGAATGACAGGC    45506          C    AA_
                                CCAGGCTGG ATGG   GC
                                ||||||||| ||||   ||
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                                GGTCCGACT TACT   CG
                                     _    GTC
GAM1855  DKFZp434G171 3'  CAGGCTGGTCTCCATGGAGGC  45507         ____     A
                                CAGGCTGG    CATGGA GC
                                ||||||||    |||||| ||
                                GTCCGACC    GTACCT CG
                                     AGAG     C
GAM1855  DKFZP434P0111 3'  ACCAGGCCCACACTGGAGGC   45508        G  _   A
                                ACCAGGCT GCA TGGA GC
                                |||||||| ||| |||| ||
                                TGGTCCGG TGT ACCT CG
                                     G   G    C
GAM1855  DKFZP434P1750 5'  CCAGGCTGGACGTGGAGC    45509         _ A    A
                                CCAGGCTGG C TGGA GC
                                ||||||||| | |||| ||
                                GGTCCGACC G ACCT CG
                                     T C    _
GAM1855  FLJ00024  5'  CCAGGCTGGCAGACAGC     45510           T GA
                                CCAGGCTGGCA G  AGC
                                |||||||||||  |  |||
                                GGTCCGACCGT C  TCG
                                      _ TG
GAM1855  FLJ10043  3'  CACCAGGTTCTGAGAAGC    45511         __  GCAT
                                TACCAGG  CTG    GGAAGC
                                |||||||  |||    ||||||
                                GTGGTCC  GAC    TCTTCG
                                     AA  _____
GAM1855  FLJ10901  3'  CCAGGTAACATGGGGGC     45512       C       AA
                                CCAGG TGGCATGG  GC
                                |||||  ||||||||  ||
                                GGTCC ATTGTACC  CG
                                   _       CC
GAM1855  FLJ12788  3'  TACCAGGCACTTGGGAG     45513         TG  A   A
                                TACCAGGC  GC TGG AG
                                ||||||||  || ||| ||
                                ATGGTCCG  TG ACC TC
                                     __  A   C
GAM1855  FLJ13055  5'  CCAGGCTGGCAGACGC      45514           TG  A
                                CCAGGCTGGCA  GA GC
                                ||||||||||  || ||
                                GGTCCGACCGT  CT CG
                                      __  G
GAM1855  FLJ20254  3'  TACCAGCACAAGGATGGAGGC  45515       _  T_  C     A
                                TACCAG GC  GG ATGGA GC
                                ||||||  ||  ||  ||||| ||
                                ATGGTC TG  CC TACCT CG
                                    G  TT  _     C
GAM1855  FLJ20294  3'  TACCAGGCTGGTCCCAGGAAGC 45516           CAT__
                                TACCAGGCTGG     GGAAGC
                                ||||||||||     ||||||
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                                ATGGTCCGACC    CCTTCG
                                      AGGGT
GAM1855  FLJ20344  3'  ACCAGGCTGGCCAACATGG   45517          ____
                                ACCAGGCTGGC   ATGG
                                ||||||||||    ||||
                                TGGTCCGACCG   TACC
                                      GTTG
GAM1855  FLJ22471  3'  CCAGGCTGCCCTGGAGC    45518       G A_   A
                                CCAGGCTG C  TGGA GC
                                |||||||| |  |||| ||
                                GGTCCGAC G  ACCT CG
                                     _ GG   _
GAM1855  FLJ23042  3'  CCATGGCACATGGAAGC    45519    _  TG
                                CCA GGC  GCATGGAAGC
                                ||| |||  ||||||||||
                                GGT CCG  TGTACCTTCG
                                  A  __
GAM1855  FLJ32356  3'  CCAGGCTGCCGGACAGC    45520       G A   _
                                CCAGGCTG C TGGA AGC
                                |||||||| | |||| |||
                                GGTCCGAC G GCCT TCG
                                     _ _   G
GAM1855  HRIHFB2072 3'  TACACAAACTTATGGAAG   45521    _    GGC
                                TAC CAGGCT   ATGGAAG
                                ||| ||||||   |||||||
                                ATG GTTTGA   TACCTTC
                                  T    A__
GAM1855  HS6ST    3'  CCAGGCTGGACACTTGGGGGC  45522        _ __  AA
                                CCAGGCTGG CA  TGG  GC
                                ||||||||| ||  |||  ||
                                GGTCCGACC GT  ACC  CG
                                     T  GA   CC
GAM1855  HTMP10   3'  ACCAGGCTGCCTGGAAGC    45523       G A
                                ACCAGGCTG C TGGAAGC
                                ||||||||| | |||||||
                                TGGTCCGAC G ACCTTCG
                                     _ G
GAM1855  ITPK1    3'  CACCAGGCAGGGTGGGGGC   45524       T  CA   AA
                                TACCAGGC GG  TGG  GC
                                |||||||| ||  |||  ||
                                GTGGTCCG CC  ACC  CG
                                     T  C_   CC
GAM1855  KIAA0226 3'  CCAGGCTGCACAAGC      45525       G   GG
                                CCAGGCTG CAT  AAGC
                                |||||||| |||  ||||
                                GGTCCGAC GTG  TTCG
                                     _   __
GAM1855  KIAA0237 3'  CCAGGCTGCTGGAGC      45526       G A    A
                                CCAGGCTG C TGGA GC
                                |||||||| | |||| ||
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                                GGTCCGAC G ACCT CG
                                     _ _   _
GAM1855 KIAA0285 3' ACCAGGCTCAGCAGGAGGC   45527       _   T  A
                                ACCAGGCT GGCA GGA GC
                                |||||||| |||| ||| ||
                                TGGTCCGA TCGT CCT CG
                                    G   _  C
GAM1855 KIAA0478 3' CACCGGGACCCCATGGAAGC  45528     A _ GG
                                TACC GG CT  CATGGAAGC
                                |||| || ||  |||||||||
                                GTGG CC GG  GTACCTTCG
                                  C  T  G_
GAM1855 KIAA0478 3' CCAGGCTGGCCGGAGC      45529         A   A
                                CCAGGCTGGC TGGA GC
                                |||||||||| |||| ||
                                GGTCCGACCG GCCT CG
                                     _   _
GAM1855 KIAA0557 3' CCAGGCTGGGATGAAGGC    45530        C    A
                                CCAGGCTGG ATGGA GC
                                ||||||||| ||||| ||
                                GGTCCGACC TACTT CG
                                     C    C
GAM1855 KIAA0945 3' CCAGGCTGAAGGGGAAGC    45531        CAT
                                CCAGGCTGG   GGAAGC
                                |||||||||   ||||||
                                GGTCCGACT   CCTTCG
                                      TCC
GAM1855 KIAA0984 3' CCAGGCTCCGCATGGAGC    45532       G_     A
                                CCAGGCT  GCATGGA GC
                                |||||||  ||||||| ||
                                GGTCCGA  CGTACCT CG
                                   GG     _
GAM1855 KIAA1025 3' ACCAGGACATGGAAG       45533       CTG
                                ACCAGG   GCATGGAAG
                                ||||||   |||||||||
                                TGGTCC   TGTACCTTC
                                    ___
GAM1855 KIAA1655 3' CCAGGCTGTGCATGGAGGC   45534        _     A
                                CCAGGCTG GCATGGA GC
                                |||||||| ||||||| ||
                                GGTCCGAC CGTACCT CG
                                     A      C
GAM1855 KIAA1866 3' CCAGGCTGTCCACTTGGAAG  45535        ___ A
                                CCAGGCTG   GC TGGAAG
                                ||||||||   || ||||||
                                GGTCCGAC   TG ACCTTC
                                     AGG  A
GAM1855 KIAA1887 5' CACCAGGCTGGATCTGAGGGC 45536          CA_  AA
                                TACCAGGCTGG   TGG  GC
                                ||||||||||   |||  ||
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                                GTGGTCCGACC  ACT  CG
                                      TAG  CC
GAM1855 KIAA1904 3' CCACGGAAACATGGGAGC   45538    _ CT     A
                                CCA GG  GGCATGG AGC
                                ||| ||  ||||||| |||
                                GGT CC  TTGTACC TCG
                                  G  T_     C
GAM1855 KIAA1904 3' CACCAGGCCCGTCTGGGAGC  45537       GGCA  A
                                TACCAGGCT   TGG AGC
                                |||||||||   ||| |||
                                GTGGTCCGG   ACC TCG
                                     GCAG  C
GAM1855 KIAA1924 3' CACCGGGGCGGTGTGGGAGC  45539    A_  T CA  A
                                TACC  GGC GG  TGG AGC
                                ||||  ||| ||  ||| |||
                                GTGG  CCG CC  ACC TCG
                                  CC  _ AC  C
GAM1855 LAT1-3TM 3' CAGGCTGGTCATTACAAGC   45540       _  _ G
                                CAGGCTGG CAT G AAGC
                                |||||||| ||| | ||||
                                GTCCGACC GTA T TTCG
                                     A  A G
GAM1855 LAT1-3TM 5' CAGGCTGGTCATTACAAGC   45540       _  _ G
                                CAGGCTGG CAT G AAGC
                                |||||||| ||| | ||||
                                GTCCGACC GTA T TTCG
                                     A  A G
GAM1855 MGC15631 3' ACCAGGCTCGCGGGAGC    45541       G  AT  A
                                ACCAGGCT GC  GGA GC
                                |||||||| ||  ||| ||
                                TGGTCCGA CG  CCT CG
                                     G  C_  _
GAM1855 MGC26641 3' ACCAGGCTGGTCTGGAAG   45542        CA
                                ACCAGGCTGG  TGGAAG
                                ||||||||||  ||||||
                                TGGTCCGACC  ACCTTC
                                      AG
GAM1855 MGC4832  3' TACCAGGCAGCTCTGGAGGC  45543       T  A_  A
                                TACCAGGC GGC  TGGA GC
                                |||||||| |||  |||| ||
                                ATGGTCCG TCG  ACCT CG
                                     _  AG   C
GAM1855 OBTP     3' TACCGGCCGGCAGTGGGGGC  45544    A     _  AA
                                TACC GGCTGGCA TGG  GC
                                |||| |||||||| |||  ||
                                ATGG CCGGCCGT ACC  CG
                                  _      C  CC
GAM1855 OSBPL1A  3' TACCTAGGCCCCTGGGAGC   45545    _   GGCA  A
                                TACC AGGCT   TGG AGC
                                |||| |||||   ||| |||
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                                ATGG TCCGG   ACC TCG
                                  A    GG__  C
GAM1855 OSBPL1A  3' TACCTAGGCCCCTGGGAGC  45545    _   GGCA  A
                                TACC AGGCT   TGG AGC
                                |||| |||||   ||| |||
                                ATGG TCCGG   ACC TCG
                                  A    GG__  C
GAM1855 OSBPL1A  3' TACCTAGGCCCCTGGGAGC  45545    _   GGCA  A
                                TACC AGGCT   TGG AGC
                                |||| |||||   ||| |||
                                ATGG TCCGG   ACC TCG
                                  A    GG__  C
GAM1855 PARVA    3' CAGGCTGGCACACTAGAGC  45546        ___  A
                                CAGGCTGGCAT  GGA GC
                                ||||||||||  ||| ||
                                GTCCGACCGTG  TCT CG
                                      TGA  _
GAM1855 PEG10    3' ACCAGGCTAAAGGAAG     45547        CAT
                                ACCAGGCTGG  GGAAG
                                |||||||||  |||||
                                TGGTCCGATT  CCTTC
                                     T__
GAM1855 PEPP3    3' CAGGCTGGCTCCAGAGGC   45548       A_  A
                                CAGGCTGGC  TGGA GC
                                |||||||||  |||| ||
                                GTCCGACCG  GTCT CG
                                     AG   C
GAM1855 POFUT1   3' CCAGGCTGCTCAGAGC    45549       G A  A
                                CCAGGCTG C TGGA GC
                                |||||||| | |||| ||
                                GGTCCGAC G GTCT CG
                                    _ A  _
GAM1855 PP1628   3' CCAGACTGTGGCATGGGGGC 45550       __    AA
                                CCAGGCT  GGCATGG  GC
                                |||||||  |||||||  ||
                                GGTCTGA  CCGTACC  CG
                                    CA     CC
GAM1855 PRO0902  3' TACTAGGCTAGCTCATAG   45551    C     __
                                TAC AGGCTGGC  ATGG
                                |||  ||||||||  ||||
                                ATG TCCGATCG  TATC
                                  A       AG
GAM1855 RALGPS1A 5' CCAGGCCACAGGGAGC     45552       G  T  A
                                CCAGGCTG CA GGA GC
                                |||||||| || ||| ||
                                GGTCCGGT GT CCT CG
                                    _ C  _
GAM1855 SLC12A5  3' ACCAGGCTGGTGGAGC     45553       CA   A
                                ACCAGGCTGG  TGGA GC
                                |||||||||  |||| ||
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                                TGGTCCGACC  ACCT CG
                                   __   _
GAM1855  TNKS2    3'  TACTGGGCTAGTACAAAAGC   45554     CA     C TG
                                TAC  GGCTGG A  GAAGC
                                |||  |||||| |  |||||
                                ATG  CCGATC T  TTTCG
                                  AC     A GT
GAM1855  TRIM2    3'  AGTGCAAGACCATGGAAGC    45555    _  T_  _
                                AG GC  GGC ATGGAAGC
                                || ||  ||| ||||||||
                                TC CG  CTG TACCTTCG
                                 A  TT   G
GAM1855  LOC115051 3'  CCAGGCTGGACACTTGGGGGC  45522          _ __   AA
                                CCAGGCTGG CA  TGG  GC
                                |||||||||  ||  |||  ||
                                GGTCCGACC GT  ACC  CG
                                      T  GA   CC
GAM1855  LOC116113 3'  TACCAGGCCTCTTCCCATGGGG 45556         GG____     AA
              GC                   TACCAGGCT     CATGG  GC
                                |||||||||     |||||  ||
                                ATGGTCCGG     GTACC  CG
                                     AGAAGG     CC
GAM1855  LOC123096 3'  CACCAGGCTGTGCAAAGC    45557          _  TGG
                                TACCAGGCTG GCA   AAGC
                                |||||||||| |||   ||||
                                GTGGTCCGAC CGT   TTCG
                                      A  ___
GAM1855  LOC123643 5'  CACCAGGCAATGCAGGGAGC   45558        TG_   T   A
                                TACCAGGC   GCA GGA GC
                                ||||||||   ||| ||| ||
                                GTGGTCCG   CGT CCT CG
                                     TTA   C  _
GAM1855  LOC126302 3'  CAGGCTGAATGGTGGAGC    45559         C    A__
                                CAGGCTGG ATGG   AGC
                                |||||||| ||||   |||
                                GTCCGACT TACC   TCG
                                     _   ACC
GAM1855  LOC126302 3'  CAGGCTGAATGGTGGAGC    45559         C    A__
                                CAGGCTGG ATGG   AGC
                                |||||||| ||||   |||
                                GTCCGACT TACC   TCG
                                     _   ACC
GAM1855  LOC130589 3'  CCAACAGCAGCATGGGAG    45560     __  T      A
                                CCA  GGC GGCATGG AG
                                |||  ||| ||||||| ||
                                GGT  TCG TCGTACC TC
                                  TG  _      C
GAM1855  LOC133308 5'  CCAGGCTGAGCCGGGAGGC   45561          _ AT   A
                                CCAGGCTG GC  GGA GC
                                |||||||| ||  ||| ||
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                                GGTCCGAC CG  CCT CG
                                     T  GC   C
GAM1855  LOC142893 5'  TACCAGACGAAACAGGAAGC   45562        T_   T
                                TACCAGGC  GGCA GGAAGC
                                ||||||||  |||| ||||||
                                ATGGTCTG  TTGT CCTTCG
                                     CT   _
GAM1855  LOC143310 3'  ACCCACAGGGCATGGAAG    45563     AG  T_
                                ACC  GC  GGCATGGAAG
                                |||  ||  ||||||||||
                                TGG  TG  CCGTACCTTC
                                  G_  TC
GAM1855  LOC149175 3'  CAGGCTGGCAGAAGGGAGC   45564          T__  A
                                CAGGCTGGCA   GG AGC
                                ||||||||||   || |||
                                GTCCGACCGT   CC TCG
                                      CTT  C
GAM1855  LOC149684 5'  TACCAGGCGTGGCTCTAAGC   45565        _   ATGG
                                TACCAGGC TGGC    AAGC
                                |||||||| ||||    ||||
                                ATGGTCCG ACCG    TTCG
                                     C    AGA_
GAM1855  LOC150319 3'  CCAGGCTGGCTGGAGGC     45566         A   A
                                CCAGGCTGGC TGGA GC
                                |||||||||| |||| ||
                                GGTCCGACCG ACCT CG
                                      _   C
GAM1855  LOC152084 5'  CCAGGCTGAGGAAAGC      45567         CAT
                                CCAGGCTGG   GGAAGC
                                |||||||||   ||||||
                                GGTCCGACT   CTTTCG
                                     C__
GAM1855  LOC152719 5'  CCAGGCTGGGCGACAGAGC   45568         _ _   A
                                CCAGGCTGG C ATGGA GC
                                ||||||||| | ||||| ||
                                GGTCCGACC G TGTCT CG
                                     C C    _
GAM1855  LOC158471 3'  TACACAGAAAATATGGAAG   45569    _   CT  C
                                TAC CAGG  GG ATGGAAG
                                ||| ||||  || |||||||
                                ATG GTCT  TT TACCTTC
                                  T   T_  A
GAM1855  LOC159199 5'  TACCAGGCCGACGGAAG     45570          AT
                                TACCAGGCTGGC  GGAAG
                                ||||||||||||  |||||
                                ATGGTCCGGCTG  CCTTC
                                       __
GAM1855  LOC166341 3'  CATCCTGGGCATGGAAGC    45571    GG   _
                                CA  CTGG CATGGAAGC
                                ||  |||| |||||||||
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                                GT  GACC GTACCTTCG
                                 AG    C
GAM1855  LOC197423 5'  CAGGCTGGTCATTACAAGC    45540         _   _ G
                                CAGGCTGG CAT G AAGC
                                |||||||| ||| | ||||
                                GTCCGACC GTA T TTCG
                                     A   A G
GAM1855  LOC199745 3'  TACCAGGCTTGGCAAAAAGC   45572          _    T
                                TACCAGGCT GGCA GGAAGC
                                ||||||||| |||| ||||||
                                ATGGTCCGA CCGT TTTTCG
                                     A    _
GAM1855  LOC219513 5'  TACGGGCTTGGGGAAGC     45573     CA    _  CAT
                                TAC  GGCT GG   GGAAGC
                                |||  |||| ||   ||||||
                                ATG  CCGA CC   CCTTCG
                                  C_    A  ___
GAM1855  LOC219898 5'  CCAGGCTGACAAAAGC      45574           TG
                                CCAGGCTGGCA  GAAGC
                                ||||||||||  |||||
                                GGTCCGACTGT  TTTCG
                                       __
GAM1855  LOC220565 5'  CAGGCTGGTCATTACAAGC    45540         _   _ G
                                CAGGCTGG CAT G AAGC
                                |||||||| ||| | ||||
                                GTCCGACC GTA T TTCG
                                     A   A G
GAM1855  LOC245771 3'  CCAGGTAACATGGGGGC     45512       C       AA
                                CCAGG TGGCATGG  GC
                                ||||| ||||||||  ||
                                GGTCC ATTGTACC  CG
                                   _       CC
GAM1855  LOC254636 5'  CCAGGCTAGGAGGAAGC     45575          CAT
                                CCAGGCTGG   GGAAGC
                                |||||||||   ||||||
                                GGTCCGATC   CCTTCG
                                     CT_
GAM1855  LOC257101 5'  CCAGGCTGGGGGACAGGGAGC  45576          ____  T   A
                                CCAGGCTGG    CA GGA GC
                                |||||||||    || ||| ||
                                GGTCCGACC    GT CCT CG
                                     CCCT  C   _
GAM1855  LOC257364 3'  CCAGCAACATGGGAGC      45577      G T      A
                                CCAG C GGCATGG AGC
                                |||| | ||||||| |||
                                GGTC G TTGTACC TCG
                                   _ _      C
GAM1855  LOC51337  3'  CCAGGCTGGTCAGGAGGC    45578          _  T   A
                                CCAGGCTGG CA GGA GC
                                ||||||||| || ||| ||
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                                GGTCCGACC GT CCT CG
                                     A _  C
GAM1855 LOC89985 5' CCATGCTCATGGAAGC     45579    G  GG
                                CCA GCT  CATGGAAGC
                                ||| |||  |||||||||
                                GGT CGA  GTACCTTCG
                                  A  __
GAM1855 LOC90268 3' CCAGGCTGTCAGGAGC     45580       G  T  A
                                CCAGGCTG CA GGA GC
                                |||||||| || ||| ||
                                GGTCCGAC GT CCT CG
                                     A _  _
GAM1855 LOC91464 3' CCTGGGCTGGCATCCAAAGC  45581   A_      G_
                                CC  GGCTGGCAT  GAAGC
                                ||  |||||||||  |||||
                                GG  CCGACCGTA  TTTCG
                                  AC       GG
GAM1855 LOC91974 5' ACCAGGCTGGTCAACAGGAGGC 45582        _  T__  A
                                ACCAGGCTGG CA   GGA GC
                                |||||||||| ||   ||| ||
                                TGGTCCGACC GT   CCT CG
                                     A  TGT   C
GAM1855 LOC92360 3' CCAGGCTGGTCTGGAGC    45583       CA   A
                                CCAGGCTGG  TGGA GC
                                |||||||||  |||| ||
                                GGTCCGACC  ACCT CG
                                     AG   _
GAM1855 LOC92497 5' TACCAGGCAGGCTAAGAGC   45584       T  AT  A
                                TACCAGGC GGC  GGA GC
                                |||||||| |||  ||| ||
                                ATGGTCCG CCG  TCT CG
                                     T  AT  _
GAM1855 LOC92497 5' CAGGCTGAGTTCCTGGAAGC  45585       CA___
                                CAGGCTGG    TGGAAGC
                                ||||||||    |||||||
                                GTCCGACT    ACCTTCG
                                     CAAGG
GAM1856 CHES1    3' TGCCTGGTGCCACAAGCTTGGG 45588       CT  C  T
           TC                     TGCCTGG  CT TA GCTTGGGTC
                                ||||||| || || |||||||||
                                ACGGACC  GG GT CGAACCCAG
                                    AC  T  T
GAM1856 GUK1     5' TGCGCGGCTATGTTTGGGTC  45589    C   CTCT  C
                                TGC TGGCT    ATG TTGGGTC
                                ||| |||||    ||| |||||||
                                ACG GCCGA    TAC AACCCAG
                                  C    _____  A
GAM1856 LRAT     3' TGCTTGGGTTCTACTTGTTTGG 45590    C  CTC   GC__
           GT                     TGC TGG   TCTAT   TTGGGT
                                ||| |||   |||||   ||||||
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                                ACG ACC   AGATG    AACCCA
                                  A   CA_    AACA
GAM1856 VDR      3'  TGTCTGTTTTTCCTCCTTGGGT 45591    C   GCTC   ATG
              C                   TG CTG    TCT   CTTGGGTC
                                  || |||    |||   ||||||||
                                  AC GAC    AGG   GAACCCAG
                                   A   AAAA   AG_
GAM1856 XK       3'  TGCCTGTGCTCTGAGACCTTGG 45592       _    CTATG
              GTC                   TGCCTG GCTCT    CTTGGGTC
                                  |||||| |||||    ||||||||
                                  ACGGAC CGAGA    GAACCCAG
                                     A    CTCTG
GAM1856 DKFZP586P0123 5'  TGCTTGGCTTCTTGTGGT    45593    C    CTCTATG   _
                                  TGC TGGCT      CTTG GGT
                                  ||| |||||      |||| |||
                                  ACG ACCGA      GAAC CCA
                                    A    A_______    A
GAM1856 KIAA1870  3'  TGGCTGGCTCTTTGGTTGG   45594    C      CTA  C
                                  TG CTGGCTCT   TG TTGG
                                  || ||||||||   || ||||
                                  AC GACCGAGA   AC AACC
                                   C       A__  C
GAM1856 MGC14799  3'  TGCCTGGCTGTTTATGCCTAG  45595        CTC
                                  TGCCTGGCT   TATGCTTGG
                                  |||||||||   |||||||||
                                  ACGGACCGA   ATACGGATC
                                        CAA
GAM1856 PDZD2    5'  TGGCTCTTTGTTGAGT     45596       CTA  C
                                  TGGCTCT   TG TTGGGT
                                  |||||||   || ||||||
                                  ACCGAGA   AC AACTCA
                                     A__  _
GAM1856 RoXaN    3'  TGCCTGGCTCCTAGG      45597         CTATGCT
                                  TGCCTGGCTCT      TGGG
                                  ||||||||||      ||||
                                  ACGGACCGAGG      ATCC
                                                 _______
GAM1856 SYNE-2   5'  TGCCTGGCTCTCTGGA     45598           ATGCTT
                                  TGCCTGGCTCTCT     GGG
                                  ||||||||||||      |||
                                  ACGGACCGAGAGA     CCT
                                                 _______
GAM1856 SYNJ2BP  5'  CTGGCTTCCTACTTGGGTC   45599      C   A
                                  CTGGCT TCT TGCTTGGGTC
                                  |||||| ||| ||||||||||
                                  GACCGA AGG ATGAACCCAG
                                     _  _
GAM1856 LOC147137 3'  TGCTTGGCTCTCTGGACGGT   45600     C       AT  TTG
                                  TGC TGGCTCTCT  GC   GGT
                                  ||| |||||||||  ||   |||
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                                ACG ACCGAGAGA  TG   CCA
                                  A        CC  ___
GAM1856  LOC150197 3'  TGCCTGGCTCTTCCTGCATGGG 45601          CTA   T
              TC                  TGCCTGGCTCT   TGC TGGGTC
                                  ||||||||||   ||| ||||||
                                  ACGGACCGAGA   ACG ACCCAG
                                        AGG   T
GAM1856  LOC152315 5'  TGACTCTCTGTGATGGGGGTC  45602         A  CTT_
                                  TGGCTCTCT TG    GGGTC
                                  |||||||| ||    |||||
                                  ACTGAGAGA AC    CCCAG
                                        C  TACC
GAM1856  LOC221465 3'  TGCCTGGCCTCTGTCCTTG    45603         T    ATG
                                  TGCCTGGC CTCT   CTTG
                                  |||||||| ||||   ||||
                                  ACGGACCG GAGA   GAAC
                                        _    CAG
GAM1856  LOC253868 5'  TGCTTGTCCCCTGCTTGGGTC  45604     C  GC     A
                                  TGC TG  TCTCT TGCTTGGGTC
                                  ||| ||  ||||| ||||||||||
                                  ACG AC  AGGGG ACGAACCCAG
                                    A  __    _
GAM1856  LOC254122 3'  TGGCTCAGGTGTTTGGGTC    45605       TCTA  C
                                  TGGCTC    TG TTGGGTC
                                  ||||||    || |||||||
                                  ACCGAG    AC AACCCAG
                                      TCC_  A
GAM1857  AXIN1     3'  TGAGTACGAGGTCATCT     45608          A    AT
                                  TGAGTACGA GTCA  TCT
                                  |||||||| ||||  |||
                                  ACTCATGCT CAGT  AGA
                                        C   __
GAM1857  CYP3A4    3'  TGAGAAATGTTGATTCTCTTA  45609      TACGAA  CA
                                  TGAG     GT  ATTCTCTTA
                                  ||||     ||  |||||||||
                                  ACTC     CA  TAAGAGAAT
                                    TTTA__  AC
GAM1857  IL10      3'  TGGGTTCAAGCAATTCTCTT   45610    A  A G   T
                                  TG GT C AAG CAATTCTCTT
                                  || || | ||| ||||||||||
                                  AC CA G TTC GTTAAGAGAA
                                   C  A _  _
GAM1857  LAMC2     3'  TGAGTAGGAACATTCTCTTA   45611       C   GTCA
                                  TGAGTA GAA    ATTCTCTTA
                                  |||||| |||    |||||||||
                                  ACTCAT CTT    TAAGAGAAT
                                      C   G___
GAM1857  OTOR      3'  TGAGTTGAAAATCCTCTT    45612       AC   GTC
                                  TGAGT  GAA   AATTCTCTT
                                  |||||  |||   |||||||||
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                                ACTCA  CTT   TTAGGAGAA
                                  A_  ___
GAM1857 ASB13    3' TGGGTGCGGGCAGCCTCTCTTA 45613    A  A  A__   AAT
             C                   TG GT CG   AGTC   TCTCTTAC
                                 || || ||  ||||  ||||||||
                                 AC CA GC   TCGG   AGAGAATG
                                  C  C  CCG   ___
GAM1857 FLJ14054 3' TGAGTACGTGGCATTCT     45614        AA  CA
                                 TGAGTACG  GT  ATTCT
                                 ||||||||  ||  |||||
                                 ACTCATGC  CG  TAAGA
                                     AC  __
GAM1857 FLJ20040 3' GTACAAAGTTCTCTT       45615         CAAT
                                 GTACGAAGT    TCTCTT
                                 |||||||||    ||||||
                                 CATGTTTCA    AGAGAA
                                              ____
GAM1857 MGC10999 3' TGAGTTCAAGCGATTCTCTT   45616      A G    CA
                                 TGAGT C AAGT  ATTCTCTT
                                 ||||| | ||||  ||||||||
                                 ACTCA G TTCG  TAAGAGAA
                                   A _    C_
GAM1857 SLC5A7   3' TGGGTACAAAGTATACTCTT   45617    A       CAATT
                                 TG GTACGAAGT    CTCTT
                                 || |||||||||    |||||
                                 AC CATGTTTCA    GAGAA
                                  C        TAT__
GAM1857 LOC148137 3' TGAGTTCAAGCAATTCTCTT   45618      A G   T
                                 TGAGT C AAG CAATTCTCTT
                                 ||||| | ||| ||||||||||
                                 ACTCA G TTC GTTAAGAGAA
                                   A _   _
GAM1857 LOC155032 3' TGAGTATGTATTTCTCTTA    45619       CGAA  CAA
                                 TGAGTA    GT   TTCTCTTA
                                 ||||||    ||   ||||||||
                                 ACTCAT    CA   AAGAGAAT
                                     A___  TA_
GAM1857 LOC197358 3' TGGATATGAATTAAATTCTCTT 45620    AG  C   GTC
                                 TG  TA GAA   AATTCTCTT
                                 ||  || |||   |||||||||
                                 AC  AT CTT   TTAAGAGAA
                                  CT  A   AAT
GAM1857 LOC200317 3' TGAGTCCAAGCAATTCTCTT   45621      ACG   T
                                 TGAGT   AAG CAATTCTCTT
                                 |||||   ||| ||||||||||
                                 ACTCA   TTC GTTAAGAGAA
                                   GG_  _
GAM1858 ADAMTS1   3' ACACCTCACTGGTTAC      45624    _   CGT
                                 AC CCTC   GCTGGTTAC
                                 || ||||   |||||||||
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                                TG GGAG   TGACCAATG
                                 T  ___
GAM1858 GLUL     3' TCCACCCTTTGAGTTAC     45625       CCG  CT
                                TCCACCCT   TG  GGTTAC
                                ||||||||   ||  ||||||
                                AGGTGGGA   AC  TCAATG
                                    A__  __
GAM1858 MTMR2    5' TCGACTCTCCGTGCTGGCT    45626    C  C
                                TC AC CTCCGTGCTGGTT
                                || || ||||||||||||
                                AG TG GAGGCACGACCGA
                                 C  A
GAM1858 NKX3A    3' CCTGCCTTTTGTGCTGGCTA   45627    AC   CC_
                                CC  CCT   GTGCTGGTTA
                                ||  |||   ||||||||||
                                GG  GGA   CACGACCGAT
                                 AC   AAA
GAM1858 SEMG1    3' TCCATCCTTTCACATGGTTACC 45628     C   CCG  _
             GA                   TCCA CCT   TGC TGGTTACCGA
                                ||||| |||   ||| ||||||||||
                                AGGT GGA   GTG ACCAATGGCT
                                  A   AA_   T
GAM1858 TBL2     3' CCATCCTCCGTGAGTC      45629     C       CT
                                CCA CCTCCGTG  GGTT
                                ||| ||||||||  ||||
                                GGT GGAGGCAC  TCAG
                                  A       __
GAM1858 WDR4     3' CACCATCTGTGCCACCG     45630     C  C    GGTT
                                CACC TC GTGCT    ACCG
                                |||| || |||||    ||||
                                GTGG AG CACGG    TGGC
                                  T  A    _____
GAM1858 WDR4     3' CACCATCTGTGCCACCG     45630     C  C    GGTT
                                CACC TC GTGCT    ACCG
                                |||| || |||||    ||||
                                GTGG AG CACGG    TGGC
                                  T  A    _____
GAM1858 WHSC1L1  5' TCCGCCTCCGTGCTGGCC    45631     AC
                                TCC  CCTCCGTGCTGGTT
                                |||  ||||||||||||||
                                AGG  GGAGGCACGACCGG
                                  C_
GAM1858 WHSC1L1  5' TCCGCCTCCGTGCTGGCC    45631     AC
                                TCC  CCTCCGTGCTGGTT
                                |||  ||||||||||||||
                                AGG  GGAGGCACGACCGG
                                  C_
GAM1858 CLDN15   3' CACCTTCCCCCAGTTACCG   45632     C   GTG TG
                                CACC TCC   C  GTTACCG
                                |||| |||   |  |||||||
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                                GTGG AGG   G  CAATGGC
                                  A  G__ GT
GAM1858  FLJ12572  3'  TCCACCCTGTCGTGGCTCTACT 45633        C_   _ GG   C
              GA                  TCCACCCT  CGTG CT  TTAC GA
                                  ||||||||  |||| ||  |||| ||
                                  AGGTGGGA  GCAC GA  GATG CT
                                      CA   C  __   A
GAM1858  FLJ12581  3'  TCCACCCTCCATGAGATT    45634           CT
                                  TCCACCCTCCGTG  GGTT
                                  ||||||||||||  ||||
                                  AGGTGGGAGGTAC  CTAA
                                          T_
GAM1858  FLJ14466  3'  TCCACGCTCTGCCCCTTGCTGA 45635      C_____   G
                                  TCCAC     CTCC TGCTGG
                                  |||||     |||| ||||||
                                  AGGTG     GGGG ACGACT
                                     CGAGAC    A
GAM1858  FLJ23186  3'  TCCACCCCTCTGGTGTTGCTGG 45636       _ CG____
                                  TCCACCC TC     TGCTGG
                                  |||||||  ||     ||||||
                                  AGGTGGG AG     ACGACC
                                      G  ACCACA
GAM1858  KIAA1204  3'  TCCACCCTGCGTAGCTAC    45637        CC   C
                                  TCCACCCT  GTG TGGTTAC
                                  ||||||||  |||  |||||||
                                  AGGTGGGA  CGC ATCGATG
                                            __   _
GAM1858  KIAA1389  3'  CTCTCTGCCGTGGTTACCGA   45638     CG   __
                                  CTC  TGCT  GGTTACCGA
                                  |||  ||||  |||||||||
                                  GAG  ACGG  CCAATGGCT
                                    AG    CA
GAM1858  KIAA1798  5'  CCTCCGTGCTCTCTGCGA    45639         GG  AC
                                  CCTCCGTGCT  TT  CGA
                                  ||||||||||  ||  |||
                                  GGAGGCACGA  GA  GCT
                                        GA  C_
GAM1858  LY6G5B    5'  TCCACCCTTTAGTTATACTGA  45640        CC_____
                                  TCCACCCT     GTGCTGG
                                  ||||||||     |||||||
                                  AGGTGGGA     TATGACT
                                       AATCAA
GAM1858  MAC30     5'  TCCACGCAGCGCCTGGTTGCCG 45641      CCTC   G     A
                                  TCCAC    CGT CTGGTT CCG
                                  |||||    ||| |||||| |||
                                  AGGTG    GCG GACCAA GGC
                                     CGTC   _     C
GAM1858  RHOBTB2   3'  TCCACCCTCTGGGTCCTGG    45642         C__  G
                                  TCCACCCTC   GT CTGG
                                  |||||||||   || ||||
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                                AGGTGGGAG   CA GACC
                                      ACC  G
GAM1858  UBXD2     5'  TCCGCCCTCCGTCTTCGTCCG  45643      A       G  GGTTA
                                TCC CCCTCCGT CT     CCG
                                ||| |||||||| ||     |||
                                AGG GGGAGGCA GA     GGC
                                  C       _  AGCA_
GAM1858  LOC145783 3'  TCCGCCCTCCGTATCTGG     45644      A        _
                                TCC CCCTCCGTG CTGG
                                ||| ||||||||| ||||
                                AGG GGGAGGCAT GACC
                                  C        A
GAM1858  LOC146227 3'  CCACCCTCTGTGGGCTGG     45645          C  __
                                CCACCCTC GT  GCTGG
                                |||||||| ||  |||||
                                GGTGGGAG CA  CGACC
                                     A  CC
GAM1858  LOC146445 3'  TCCACGCCTCTCCAGTTGCTGA 45646        _    CG____
                                TCCAC CCTC      TGCTGG
                                ||||| ||||      ||||||
                                AGGTG GGAG      ACGACT
                                   C    AGGTCA
GAM1858  LOC201799 3'  TCCAAAGCTGGTTACTGA     45647       T_        C
                                TCCG  GCTGGTTAC GA
                                ||||  ||||||||| ||
                                AGGT  CGACCAATG CT
                                   TT         A
GAM1858  LOC203504 3'  TCCACCCTTCCTGGCTGG     45648          _  GT
                                TCCACCCT CC  GCTGG
                                |||||||| ||  |||||
                                AGGTGGGA GG  CGACC
                                     A  AC
GAM1858  LOC203536 5'  TCCACCCTCCTGTTGTT      45649           G  CTG
                                TCCACCCTCC TG   GTT
                                |||||||||| ||   |||
                                AGGTGGGAGG AC   CAA
                                      _  AA_
GAM1858  LOC219920 5'  TCCGTCCTCCATGGATACTGA  45650      AC        _____
                                TCC  CCTCCGTG    CTGG
                                |||  ||||||||    ||||
                                AGG  GGAGGTAC    GACT
                                  CA       CTAT
GAM1858  LOC92078  5'  CCACTAGTGCTGGTTGCCG    45651      CCTCC         A
                                CCAC     GTGCTGGTT CCG
                                ||||     ||||||||| |||
                                GGTG     CACGACCAA GGC
                                  AT___         C
GAM1859  ACTR1B    3'  CAACAGCCTGACATGGCGCTCA 45654      G    G   T  __
            A                    CAA AGCT TGG CA  GCGCTCAA
                                ||| |||| ||| ||  ||||||||
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                                GTT TCGG ACT GT  CGCGAGTT
                                  G   _  _ AC
GAM1859  CD28     3'  GGAGAGCTGTGGCACTATCTC  45655   A        CAGCG
                                C AGAGCTGTGGT    CTC
                                | ||||||||||    |||
                                C TCTCGACACCG    GAG
                                 C         TGATA
GAM1859  CELSR3   3'  CAAGAGCTGGGGTCCTTCTC  45656        T   AGCG
                                CAAGAGCTG GGTC   CTC
                                ||||||||| ||||   |||
                                GTTCTCGAC CCAG   GAG
                                      C   GAA_
GAM1859  FOLR1    5'  AAGAGCTGTGGTCAGTGGC   45657           C_
                                AAGAGCTGTGGTCAG  GC
                                |||||||||||||||  ||
                                TTCTCGACACCAGTC  CG
                                          AC
GAM1859  GAS7     3'  GACACGATTCAGCGCTCAA   45658   GC  TGG
                                GA  TG   TCAGCGCTCAA
                                ||  ||   ||||||||||
                                CT  GC   AGTCGCGAGTT
                                 GT  TA_
GAM1859  GAS7     3'  GACACGATTCAGCGCTCAA   45658   GC  TGG
                                GA  TG   TCAGCGCTCAA
                                ||  ||   ||||||||||
                                CT  GC   AGTCGCGAGTT
                                 GT  TA_
GAM1859  GPR85    3'  AAGGCTGTGGTCTCCCC     45659    A       AGCG
                                AAG GCTGTGGTC    CTC
                                ||| |||||||||    |||
                                TTC CGACACCAG    GGG
                                  _        AG__
GAM1859  INHBC    5'  CAACAGCTGTGGTCTCAA    45660    G       AGCGC
                                CAA AGCTGTGGTC    TCAA
                                ||| ||||||||||    ||||
                                GTT TCGACACCAG    AGTT
                                  G         _____
GAM1859  INSM1    3'  AAGAGCTGTCGGTTGTACA   45661         _  CA_
                                AAGAGCTGT GGT   GCG
                                ||||||||| |||   |||
                                TTCTCGACA CCA   TGT
                                      G   ACA
GAM1859  ITGB2    3'  CAAGAGCTGTGGCCAAGC    45662            C
                                CAAGAGCTGTGGTCAG GC
                                |||||||||||||||| ||
                                GTTCTCGACACCGGTT CG
                                                 _
GAM1859  MCF2     3'  CAAAAGCTGTGGTTTCAAC   45663          __
                                CAAGAGCTGTGG  TCAGC
                                ||||||||||||  |||||
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                                GTTTTCGACACC  AGTTG
                                      AA
GAM1859  OLIG2    3'  AAAGCCAGACAGCGCTC     45664       GT  T
                                AGAGCT  GG CAGCGCTC
                                ||||||  || ||||||||
                                TTTCGG  TC GTCGCGAG
                                   __  T
GAM1859  RANBP3   3'  AGAGCTGTGCCTGCTCAA    45665         G  AGC
                                AGAGCTGTG TC   GCTCAA
                                ||||||||| ||   ||||||
                                TCTCGACAC GG   CGAGTT
                                      _ A__
GAM1859  SPN      5'  CAAGAGCTGGGACCGGCTC    45666         T GT AGC
                                CAAGAGCTG G  C   GCTC
                                ||||||||| |  |   ||||
                                GTTCTCGAC C  G   CGAG
                                     C TG C__
GAM1859  VIPR2    5'  AGCTGGAGCGCGCTCAA     45667      TG  CA
                                AGCTG  GT  GCGCTCAA
                                |||||  ||  ||||||||
                                TCGAC  CG  CGCGAGTT
                                   CT  __
GAM1859  ADAMTS19 3'  CAAGAGCTGTGATCCAGC    45668            _
                                CAAGAGCTGTGGTC AGC
                                |||||||||||||| |||
                                GTTCTCGACACTAG TCG
                                       G
GAM1859  C20orf29 3'  AGGGGCTGTGGCCTGCCAGC   45669    A_       A  __
                                AG  GCTGTGGTC GC  GC
                                ||  ||||||||| ||  ||
                                TC  CGACACCGG CG  CG
                                 CC        A  GT
GAM1859  DNAJA3   3'  CAATGGGCTGTGGCTCAGC    45670     GA_      _
                                CAA   GCTGTGG TCAGC
                                |||   ||||||| |||||
                                GTT   CGACACC AGTCG
                                  ACC      G
GAM1859  FLJ10853 5'  GAGCAGCAGCGCTCAAC     45671      TGT  T
                                GAGC   GG CAGCGCTCAAC
                                ||||   || ||||||||||
                                CTCG   TC GTCGCGAGTTG
                                   ___  _
GAM1859  FLJ11383 5'  CAAGGCTGTGGTCTTGGC    45672      A        AGC
                                CAAG GCTGTGGTC   GC
                                |||| |||||||||   ||
                                GTTC CGACACCAG   CG
                                   _        AAC
GAM1859  FLJ22843 5'  AGGGCCATGGCGCTCA      45673     A     GTCA
                                AG GCTGTG    GCGCTCA
                                || ||||||    |||||||
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                                TC CGGTAC    CGCGAGT
                                 C     _____
GAM1859 KIAA0319 5' CAAGAACTGTGGTCACTGCT  45674             GC
                                CAAGAGCTGTGGTCA  GCT
                                |||||||||||||||  |||
                                GTTCTTGACACCAGT  CGA
                                          GA
GAM1859 KIAA0793 3' GAGCTGTGGCTTGAGCGGC   45675          C__   _
                                GAGCTGTGGT   AGCG C
                                ||||||||||   |||| |
                                CTCGACACCG   TCGC G
                                      AAC    C
GAM1859 KIAA1559 3' CAGGAGCTGCAGTCAGCGTTCA 45676    A     TG      C
                                CA GAGCTG  GTCAGCG TCA
                                || ||||||  ||||||| |||
                                GT CTCGAC  CAGTCGC AGT
                                 C     GT      A
GAM1859 KIAA1695 3' CAAGAGCTTGCCTTCTGCTCA  45677         _ GG  AGC
                                CAAGAGCT GT  TC   GCTCA
                                |||||||| ||  ||   |||||
                                GTTCTCGA CG  AG   CGAGT
                                     A  GA  A__
GAM1859 KIAA1822 5' AGAGCTGTGGTCCACGGC    45678           A   _
                                AGAGCTGTGGTC GCG C
                                |||||||||||| ||| |
                                TCTCGACACCAG TGC G
                                       G   C
GAM1859 MGC10960 3' CAAAGGCTGTGGTCAGTCATCA 45679      A         _ C
                                CAAG GCTGTGGTCAG CG TCA
                                |||| |||||||||| || |||
                                GTTT CGACACCAGTC GT AGT
                                  C          A  _
GAM1859 N4BP1    3' GAGCGCAAGCTCAGCGCTCA   45680      T TG __
                                GAGC G  G  TCAGCGCTCA
                                |||| |  |  ||||||||||
                                CTCG C  T  AGTCGCGAGT
                                  _ GT CG
GAM1859 OSBPL1A  5' AGAGCTGCTGTGCGCTC     45681         G  CA
                                AGAGCTGT GT  GCGCTC
                                |||||||| ||  ||||||
                                TCTCGACG CA  CGCGAG
                                     A  __
GAM1859 p25      3' AAGGGCTGTGGTGAGTCG    45682     A       C  _
                                AAG GCTGTGGT AG CG
                                ||| |||||||| || ||
                                TTC CGACACCA TC GC
                                  C       C  A
GAM1859 PDCD7    5' CAACGGCTGTAGCCGCTC    45683     GA       CAG
                                CAA  GCTGTGGT   CGCTC
                                |||  ||||||||   |||||
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                                GTT  CGACATCG   GCGAG
                                  GC       ___
GAM1859  PGGT1B    3'  AAAGTTGTGGTTCAAACTTCAA 45684      C     _  C  _
              C                    AGAG TGTGGT CAG GCT CAAC
                                   |||| |||||| ||| ||| ||||
                                   TTTC ACACCA GTT TGA GTTG
                                     A     A  _  A
GAM1859  PPP1R15B  5'  AGGGCCGCGGCGCTCA      45685    A     GTCA
                                   AG GCTGTG    GCGCTCA
                                   || ||||||    |||||||
                                   TC CGGCGC    CGCGAGT
                                    C     _____
GAM1859  RBAK      5'  AGGTGCTGGCCCGGGCGCTCAA 45686    C  _    A__
              C                    AG TG TGGTC   GCGCTCAAC
                                   || || |||||   |||||||||
                                   TC AC ACCGG   CGCGAGTTG
                                    C  G    GCC
GAM1859  SURB7     3'  CAAGAACTGTGGAAAAGC    45687          TC_
                                   CAAGAGCTGTGG   AGC
                                   ||||||||||||   |||
                                   GTTCTTGACACC   TCG
                                          TTT
GAM1859  ZNF297B   3'  AGGGGCTGTGGCAGCCC     45688    A_     T   G
                                   AG  GCTGTGG CAGC CT
                                   ||  ||||||| |||| ||
                                   TC  CGACACC GTCG GG
                                    CC      _   _
GAM1859  ZNF297B   3'  AGGGGCTGTGGCAGCCC     45688    A_     T   G
                                   AG  GCTGTGG CAGC CT
                                   ||  ||||||| |||| ||
                                   TC  CGACACC GTCG GG
                                    CC      _   _
GAM1859  ZNF31     5'  CAAAGGCTGTGGTGCCACCTC  45689      A       CA_  G
                                   CAAG GCTGTGGT   GC CTC
                                   |||| ||||||||   || |||
                                   GTTT CGACACCA   TG GAG
                                     C       CGG  _
GAM1859  LOC128439 5'  CAAGACGCTCTCTCTAGTGCTC 45690       _  ________  G
              AGC                    CAAGA GCT      GTG TCAGC
                                   ||||| |||      ||| |||||
                                   GTTCT CGA      CAC AGTCG
                                      G   GAGAGAT   G
GAM1859  LOC142941 5'  CAGGAGCTGTGATTGTGCTCA  45691    A        CAGC
                                   CA GAGCTGTGGT    GCTCA
                                   || ||||||||||    |||||
                                   GT CTCGACACTA    CGAGT
                                    C         ACA_
GAM1859  LOC144667 3'  CAAGGGCTGTGCTCAGCA    45692      A     G
                                   CAAG GCTGTG TCAGCG
                                   |||| |||||| ||||||
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                                GTTC CGACAC AGTCGT
                                  C     G
GAM1859  LOC145135 5'  CAAGAGCCACCTTGGTGTTCAG 45693        _______  G
                C                  CAAGAGCT     GTG TCAGC
                                   ||||||||     ||| |||||
                                   GTTCTCGG     CAC AGTCG
                                       TGGAAC   A
GAM1859  LOC146381 5'  AGGGGCTGCTGCGCTCAAC   45694    A_    GGTCA
                                   AG  GCTGT    GCGCTCAAC
                                   ||  |||||    |||||||||
                                   TC  CGACG    CGCGAGTTG
                                    CC     A____
GAM1859  LOC150596 3'  CAGGAACTGTGGTTATCAAC   45695    A       ___
                                   CA GAGCTGTGG   TCAGC
                                   || |||||||||   |||||
                                   GT CTTGACACC   AGTTG
                                    C        AAT
GAM1859  LOC158292 5'  CAAGGCTCTTGGTGTTCAGC   45696     A   G_  ___
                                   CAAG GCT  TGG   TCAGC
                                   |||| |||  |||   |||||
                                   GTTC CGA  ACC   AGTCG
                                     _   GA   ACA
GAM1859  LOC158376 5'  CAAGAGCTGTGGTCAGCTCCA  45697              GC
                                   CAAGAGCTGTGGTCAGC  TCA
                                   ||||||||||||||||  |||
                                   GTTCTCGACACCAGTCG  GGT
                                              A_
GAM1859  LOC162048 5'  CAAGAGCTTCCAGCTGC     45698        GTGG    _
                                   CAAGAGCT    TCAGC GC
                                   ||||||||    ||||| ||
                                   GTTCTCGA    GGTCG CG
                                        A___     A
GAM1859  LOC197439 5'  AGGGGCTGCTGCGCTCAAC   45694    A_    GGTCA
                                   AG  GCTGT    GCGCTCAAC
                                   ||  |||||    |||||||||
                                   TC  CGACG    CGCGAGTTG
                                    CC     A____
GAM1859  LOC219942 3'  AAGGGCTGTGGCGAAGGGC   45699    A      C_  C
                                   AAG GCTGTGGT  AG GC
                                   ||| ||||||||  || ||
                                   TTC CGACACCG  TC CG
                                     C       CT  C
GAM1859  LOC92017  5'  CAAGGGCTGTGATCAGAC    45700     A        C
                                   CAAG GCTGTGGTCAG GC
                                   |||| ||||||||||| ||
                                   GTTC CGACACTAGTC TG
                                     C         _
GAM1860  ACO1      3'  TCTCTTTCTGGCACTACT    45703        CA  CAG
                                   TCTCTTTC  GC   TTACT
                                   ||||||||  ||   |||||
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                                AGAGAAAG CG  GATGA
                                    AC  T__
GAM1860 AOC3    3' ATCCTTTCCAGCTCAGCTA  45704    T      _
                                ATC CTTTCCAGC CAGTTA
                                ||| ||||||||| ||||||
                                TAG GAAAGGTCG GTCGAT
                                  _       A
GAM1860 EPB42   5' ATCTCCTGGACCAGTTACT  45705      TCCA
                                ATCTCTT  GCCAGTTACT
                                |||||||  ||||||||||
                                TAGAGGA  TGGTCAATGA
                                   CC__
GAM1860 IL27    3' ATCTCTTCCCAGTTCATC   45706         CCA
                                ATCTCTTTCCAG  GTT
                                ||||||||||||  |||
                                TAGAGAAGGGTC  TAG
                                      AAG
GAM1860 NDRG2   3' ATCTCTTCCAGGAGCT     45707      T  CC
                                ATCTCTT CCAG  AGTT
                                ||||||| ||||  ||||
                                TAGAGAA GGTC  TCGA
                                   _  C_
GAM1860 PLAG1   5' CCTCTTTCCAGCAGCCA    45708         C
                                TCTCTTTCCAGC AGTTA
                                |||||||||||| |||||
                                GGAGAAAGGTCG TCGGT
                                          _
GAM1860 SVIL    5' TCTCTTTCCAATGAATACTA  45709        CCAGT
                                TCTCTTTCCAG   TACTA
                                ||||||||||    |||||
                                AGAGAAAGGTT   ATGAT
                                      ACTT_
GAM1860 TYR     5' TCTCTTTCCAGCTACT     45710         CAGT
                                TCTCTTTCCAGC  TACT
                                ||||||||||||  ||||
                                AGAGAAAGGTCG  ATGA
                                          ____
GAM1860 ZNF83   5' TCTTTCCAACATTACT     45711        CA
                                TCTTTCCAGC  GTTACT
                                |||||||||  ||||||
                                AGAAAGGTTG  TAATGA
                                          __
GAM1860 ARHGEF9 3' ATCTCTTTCCATTCCCATCCCT 45712        G_  A  TA
                                ATCTCTTTCCA  CC GT  CT
                                ||||||||||  || ||  ||
                                TAGAGAAAGGT  GG TA  GA
                                      AA  G  GG
GAM1860 BCAS4   3' TCACTTTCCAGCGTTCCT   45713   T      CA  A
                                TC CTTTCCAGC  GTT CT
                                || |||||||||  ||| ||
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                                AG GAAAGGTCG  CAA GA
                                 T       __  G
GAM1860  BCCIP    3'  TCTCTCTCCAGTACT      45714          CCAGT
                                TCTCTTTCCAG    TACT
                                ||||||||||    ||||
                                AGAGAGAGGTC    ATGA
                                      _____
GAM1860  BTN3A3   3'  TCTCTTTCCAAGTCAC     45715          GCC
                                TCTCTTTCCA   AGTTAC
                                ||||||||||   ||||||
                                AGAGAAAGGT   TCAGTG
                                     ___
GAM1860  C17orf1A 3'  CCTTTTTCCAGCCCGTTGCTA 45716     C       A   A
                                TCT TTTCCAGCC GTT CTA
                                ||| ||||||||| ||| |||
                                GGA AAAGGTCGG CAA GAT
                                  A       G   C
GAM1860  C20orf172 3'  TCTCTTTCCGAGCTGTACT   45717         _   CA  T
                                TCTCTTTCC AGC  GT ACT
                                ||||||||| |||  || |||
                                AGAGAAAGG TCG  CA TGA
                                     C   A_ _
GAM1860  CALN1    3'  ATCTCTCTCTAGCAGTC     45718         C   C
                                ATCTCTTTC AGC AGTT
                                ||||||||| ||| ||||
                                TAGAGAGAG TCG TCAG
                                     A  _
GAM1860  CDC26    5'  ATCTCTTTTCAAGCCGGCC    45719         _ C    A
                                ATCTCTTT C AGCC GTT
                                |||||||| | |||| |||
                                TAGAGAAA G TCGG CGG
                                     A T    C
GAM1860  CNNM1    3'  ATCTCTTTTCCAGTCCCAGACT 45720         _   __    TT
            A                    ATCTCTTT CCAG  CCAG  ACTA
                                ||||||||| ||||  ||||  ||||
                                TAGAGAAA GGTC  GGTC  TGAT
                                     A   AG   __
GAM1860  COVA1    3'  ATCTTTTTCCAACATTCTA   45721      C       CA   A
                                ATCT TTTCCAGC  GTT CTA
                                |||| ||||||||  ||| |||
                                TAGA AAAGGTTG  TAA GAT
                                  A       __  _
GAM1860  dJ383J4.3 3'  TCTCTTTCAGCATAGCAATTA  45722         C  _____
                                TCTCTTTC AGC    CAGTTA
                                |||||||| |||    ||||||
                                AGAGAAAG TCG    GTTAAT
                                     _  TATC
GAM1860  DKFZP434C1715 3'  TCTTTCCACCTTTACT      45723         G  AG
                                TCTTTCCA CC  TTACT
                                |||||||| ||  |||||
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                                AGAAAGGT GG  AATGA
                                    _  A_
GAM1860  DKFZP564M182 3'  TCCTTCCAGTTGAATCACT    45724         CC_
                                TCTTTCCAG   AGTTACT
                                |||||||||   |||||||
                                AGGAAGGTC   TTAGTGA
                                     AAC
GAM1860  DKFZP586M1120 3'  ATCTCTTTCAGTTAGTTGCT   45725         C  CC    A
                                ATCTCTTTC AG  AGTT CT
                                ||||||||| ||  |||| ||
                                TAGAGAAAG TC  TCAA GA
                                     _ AA    C
GAM1860  DNAH8    5'  TCTTCAACAGTTACTA      45726      TC    C
                                TCTT  CAGC AGTTACTA
                                ||||  |||| ||||||||
                                AGAA  GTTG TCAATGAT
                                  __   _
GAM1860  FBXO21   3'  ATCTCTTTCTAGTAACT     45727         CAGCC   T
                                ATCTCTTTC    AGT ACT
                                |||||||||    ||| |||
                                TAGAGAAAG    TCA TGA
                                     A____   T
GAM1860  FBXO25   5'  ATCTCTTCCAGCCATCTTCT   45728        T      GTTA
                                ATCTCTT CCAGCCA    CT
                                ||||||| |||||||    ||
                                TAGAGAA GGTCGGT    GA
                                   _      AGAA
GAM1860  FLJ12783 3'  TCTCTTCCCAGCCCTTCCCT   45729           AG TA
                                TCTCTTTCCAGCC  T  CT
                                |||||||||||||  |  ||
                                AGAGAAGGGTCGG  A  GA
                                       GA GG
GAM1860  FLJ13842 3'  CTCTTTCCAGAGTGACT     45730         CC   T
                                CTCTTTCCAG  AGT ACT
                                ||||||||||  ||| |||
                                GAGAAAGGTC  TCA TGA
                                     __   C
GAM1860  FLJ20337 3'  CCTCTTTCCAGAGTTA      45731          CC
                                TCTCTTTCCAG  AGTTA
                                ||||||||||  |||||
                                GGAGAAAGGTC  TCAAT
                                     __
GAM1860  FLJ20489 3'  CTCTTTCCAGCCTCTACTA   45732           AG
                                CTCTTTCCAGCC  TTACTA
                                ||||||||||||  ||||||
                                GAGAAAGGTCGG  GATGAT
                                       A_
GAM1860  FLJ20628 3'  TCTTCAAGTCAGTTACT     45733       CC  C
                                TCTTT  AG CAGTTACT
                                |||||  || ||||||||
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                                AGAAG  TC GTCAATGA
                                  T_  A
GAM1860  FLJ21588  3'  ATCTCTTTCCCGCTAGCGCAGC 45734          ____  _
             T                   ATCTCTTTCC   AGC CAGTT
                                 ||||||||||   ||| |||||
                                 TAGAGAAAGG   TCG GTCGA
                                      GCGA  C
GAM1860  GRO3     3'  TCCTTTCCAGCTGTCCCTA   45735   T      CA  TA
                                 TC CTTTCCAGC  GT  CTA
                                 || |||||||||  ||  |||
                                 AG GAAAGGTCG  CA  GAT
                                  _       A_  GG
GAM1860  GT650    3'  TCTCCAACACCAGTTGCTA   45736     TTCCA     A
                                 TCTCT    GCCAGTT CTA
                                 |||||    ||||||| |||
                                 AGAGG    TGGTCAA GAT
                                    TTG__      C
GAM1860  HMP19    3'  TCTCTTCCTGGCTGTCACT   45737       CA  CA
                                 TCTCTTTC  GC  GTTACT
                                 ||||||||  ||  ||||||
                                 AGAGAAGG  CG  CAGTGA
                                      AC  A_
GAM1860  HSA249128 3'  ACCTTTTTCCAGTCATCCATCT 45738     C     C  G  _
                                 ATCT TTTCCAG CA TTA CT
                                 |||| ||||||| || ||| ||
                                 TGGA AAAGGTC GT GGT GA
                                   A      A  A   A
GAM1860  IL18BP   3'  TCTCTTTCAGGCAAAGCACTA  45739       CA  C  T
                                 TCTCTTTC  GC AG TACTA
                                 ||||||||  || || |||||
                                 AGAGAAAG  CG TT GTGAT
                                      TC  T  C
GAM1860  KIAA0252  3'  TCTCTTCCCAGTTCAACAGCT  45740         C____
                                 TCTCTTTCCAG    CAGTT
                                 ||||||||||    |||||
                                 AGAGAAGGGTC    GTCGA
                                       AAGTT
GAM1860  KIAA0254  3'  ATCTTTTCCAGCTACC     45741     C      CAGT
                                 ATCT TTTCCAGC    TACT
                                 |||| ||||||||   ||||
                                 TAGA AAAGGTCG    ATGG
                                   _      ____
GAM1860  KIAA0286  3'  TCTCTTTCCTGCCAACT     45742        A   GTT
                                 TCTCTTTCC GCCA   ACT
                                 ||||||||| ||||   |||
                                 AGAGAAAGG CGGT   TGA
                                      A   ___
GAM1860  KIAA0323  3'  ATCTCTTCTCAGGGACCGCT   45743       TC  ___  A
                                 ATCTCTT  CAG   CC GTT
                                 |||||||  |||   || |||
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                                TAGAGAA  GTC   GG CGA
                                   GA   CCT  _
GAM1860  KIAA0459  3'  ATCCTTTTCCAGCCGCTTCT   45744     TC       A   A
                                ATC  TTTCCAGCC GTT CT
                                |||  ||||||||| ||| ||
                                TAG  AAAGGTCGG CGA GA
                                  GA        _   A
GAM1860  KIAA0564  3'  TCTCCTTCTGGCTGCTTCT    45745        CA  CA   A
                                TCTCTTTC  GC  GTT CT
                                ||||||||  ||  ||| ||
                                AGAGGAAG  CG  CGA GA
                                    AC  A_   A
GAM1860  KIAA0721  3'  TCTCTTTCCAGCTTCTCAAACT 45746           CAGTT__
             A                   TCTCTTTCCAGC      ACTA
                                ||||||||||||      ||||
                                AGAGAAAGGTCG      TGAT
                                      AAGAGTT
GAM1860  KIAA0721  3'  TCTCTTTCCAGCTTCTCAAACT 45746           CAGTT__
             A                   TCTCTTTCCAGC      ACTA
                                ||||||||||||      ||||
                                AGAGAAAGGTCG      TGAT
                                      AAGAGTT
GAM1860  KIAA1076  3'  TCACTTTCCAGAAATTA     45747    T       CC
                                TC CTTTCCAG  AGTTA
                                || ||||||||  |||||
                                AG GAAAGGTC  TTAAT
                                 T       T_
GAM1860  KIAA1389  3'  TCTTTCCAGCAGAGCAACTA   45748          C_   T
                                TCTTTCCAGC  AGT ACTA
                                ||||||||||  ||| ||||
                                AGAAAGGTCG  TCG TGAT
                                      TC   T
GAM1860  KIAA1766  3'  ACCTCTTTTTGGAGCCCACT   45749        CC__    AGT
                                ATCTCTTT    AGCC   TACT
                                ||||||||    ||||   ||||
                                TGGAGAAA    TCGG   GTGA
                                    AACC    ____
GAM1860  MGC32104  3'  TCTTTTCCAGCACTTA      45750     C       C G
                                TCT TTTCCAGC A TTA
                                ||| ||||||| | |||
                                AGA AAAGGTCG T AAT
                                  _       _ G
GAM1860  NXP-2     3'  CTCTTTCCAGAATTACTA     45751          CC
                                CTCTTTCCAG  AGTTACTA
                                ||||||||||  ||||||||
                                GAGAAAGGTC  TTAATGAT
                                           __
GAM1860  OS4       3'  CTCTTTCCAGTTACT       45752          GCCA
                                CTCTTTCCA    GTTACT
                                |||||||||    ||||||
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                                GAGAAAGGT   CAATGA
                                        ____
GAM1860  PFTK1    3'  ATCTCCTTTCAGAATACT    45753        C   CCAGT
                                ATCTCTTT CAG    TACT
                                |||||||| |||    ||||
                                TAGAGGAA GTC    ATGA
                                    A   TT___
GAM1860  RAB14    3'  TCTTTCCAAAGTGTACT    45754        CC  _
                                TCTTTCCAG  AGT TACT
                                |||||||||  ||| ||||
                                AGAAAGGTT  TCA ATGA
                                    __  C
GAM1860  LOC113444 3'  TCTTTCCAGTGCAGACT    45755        C_  TT
                                TCTTTCCAG  CAG  ACT
                                |||||||||  |||  |||
                                AGAAAGGTC  GTC  TGA
                                    AC  __
GAM1860  LOC120105 5'  TCTCTCCATCAGTTGCT    45756        GC    A
                                TCTTTCCA  CAGTT CT
                                ||||||||  ||||| ||
                                AGAGAGGT  GTCAA GA
                                    A_    C
GAM1860  LOC143720 3'  TCCCTTTCCAATACT      45757         CCAGT
                                TCTCTTTCCAG    TACT
                                ||||||||||    ||||
                                AGGGAAAGGTT    ATGA
                                        _____
GAM1860  LOC146909 3'  TCCTTTCCATTCCTCCGGTTGC 45758    T     G____  A   A
            TA                   TC CTTTCCA    CC GTT CTA
                                || |||||||    || ||| |||
                                AG GAAAGGT    GG CAA GAT
                                 _     AAGGA  C   C
GAM1860  LOC148530 5'  ATCTCTTCTGGCACAGTAGCT  45759        CCA  _   TA
                                ATCTCTTT   GC CAGT  CT
                                ||||||||   || ||||  ||
                                TAGAGAAG   CG GTCA  GA
                                    AC_  T   TC
GAM1860  LOC152316 3'  ATCTGTTTCCAGCCGAGCTCT  45760     C       _   A
                                ATCT TTTCCAGCC AGTT CT
                                |||| ||||||||| |||| ||
                                TAGA AAAGGTCGG TCGA GA
                                  C       C   _
GAM1860  LOC152742 3'  ATCTCTTCACATAGTTACTA   45761       TC  GCC
                                ATCTCTT  CA   AGTTACTA
                                |||||||  ||   ||||||||
                                TAGAGAA  GT   TCAATGAT
                                    GT  A__
GAM1860  LOC153592 3'  ATCTCTTTATCAGTCAC     45762        CCAGC
                                ATCTCTTT    CAGTTAC
                                ||||||||    |||||||
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                                TAGAGAAA    GTCAGTG
                                    TA___
GAM1860  LOC164127 3'  ATCTCCTTCTGGCTGCGCACT  45763        CA  CA_  T
                                ATCTCTTTC  GC   GT ACT
                                |||||||||  ||   || |||
                                TAGAGGAAG  CG   CG TGA
                                    AC  ACG  _
GAM1860  LOC170372 5'  TCCCTTTCTTTTCCAGCCAGTT 45764       _____        A
            GCT                   TCTCTT    TCCAGCCAGTT CT
                                ||||||    |||||||||||  ||
                                AGGGAA    AGGTCGGTCAA GA
                                   AGAAA         C
GAM1860  LOC200301 5'  ATCCTTTCCAGCCAGGACT   45765    T         TT
                                ATC CTTTCCAGCCAG  ACT
                                ||| ||||||||||||  |||
                                TAG GAAAGGTCGGTC  TGA
                                  _         C_
GAM1860  LOC203202 3'  ATCTCTTCCAGTTAACT     45766       TCCAG     _
                                ATCTCTT    CCAGTTA CT
                                |||||||    ||||||| ||
                                TAGAGAA    GGTCAAT GA
                                   _____      T
GAM1860  LOC203378 5'  CTCTTTCACAGAGTTACTA   45767       _  CC
                                CTCTTTC CAG  AGTTACTA
                                ||||||| |||  ||||||||
                                GAGAAAG GTC  TCAATGAT
                                    T  __
GAM1860  LOC219898 3'  ATCTTTTCTCAGCCACCCA   45768     C   _    G
                                ATCT TTTC CAGCCA TTA
                                |||| |||| |||||| |||
                                TAGA AAAG GTCGGT GGT
                                  _   A     G
GAM1860  LOC221463 3'  TCCTTTCCATTGGTTACT    45769    T     GCCA
                                TC CTTTCCA    GTTACT
                                || |||||||    ||||||
                                AG GAAAGGT    CAATGA
                                 _      AAC_
GAM1860  LOC222787 5'  TCCTTTCCAGTGTAGACT    45770    T     CCA  T_
                                TC CTTTCCAG   GT  ACT
                                || ||||||||   ||  |||
                                AG GAAAGGTC   CA  TGA
                                 _       A__  TC
GAM1860  LOC253782 3'  ATCCCTTTTTCCTCTTACTA  45771       CCAG  AG
                                ATCTCTTT    CC  TTACTA
                                ||||||||    ||  ||||||
                                TAGGGAAA    GG  AATGAT
                                    AA__  AG
GAM1860  LOC254158 3'  TCTTTTTCCAGCTGACACT   45772    C      CAGT
                                TCT TTTCCAGC    TACT
                                ||| ||||||||    ||||
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                                AGA AAAGGTCG    GTGA
                                  A       ACT_
GAM1860  LOC256980 5'  ATCTTTTTGGAACCAGTTGCTA 45773      C   CC       A
                                ATCT TTT  AGCCAGTT CTA
                                |||| |||  |||||||| |||
                                TAGA AAA  TTGGTCAA GAT
                                  A   CC       C
GAM1860  LOC56920  3'  ATCTCCTTCCAGCCAGTT    45774
                                ATCTCTTTCCAGCCAGTT
                                ||||||||||||||||||
                                TAGAGGAAGGTCGGTCAA

GAM1860  LOC63928  3'  ATCTCTTCCCACTGGGTTACT  45775          GCCA
                                ATCTCTTTCCA    GTTACT
                                ||||||||||    ||||||
                                TAGAGAAGGGT    CAATGA
                                      GACC
GAM1860  LOC91263  5'  ATCCTTTCCAGTGCTCT     45776     T      CCA   A
                                ATC CTTTCCAG   GTT CT
                                ||| ||||||||   ||| ||
                                TAG GAAAGGTC   CGA GA
                                  _       A__   _
GAM1861  CLN5      3'  TAACTGCCATATCAGAAAGAA  45779        CCTC  A  A
                                TAACTGCC    TG CA AAAGAA
                                ||||||||    || || ||||||
                                ATTGACGG    AT GT TTTCTT
                                     T___  A  C
GAM1861  CNN2      3'  AACTGCTCAGCTGACAAAA    45780       CCCT
                                AACTGC    CTGACAAAA
                                ||||||    |||||||||
                                TTGACG    GACTGTTTT
                                   AGTC
GAM1861  DIAPH2    3'  CTGCCTCCTGTAAAAAGAA    45781      C T   AC
                                CTGCC C CTG  AAAAAGAA
                                ||||| | |||  ||||||||
                                GACGG G GAC  TTTTTCTT
                                   A _   A_
GAM1861  EGR3      3'  AACTGCCCTGAGGCCTAAGA   45782        CTC   CAAA_
                                AACTGCCC   TGA    AAGA
                                ||||||||   |||    ||||
                                TTGACGGG   ACT    TTCT
                                     ___   CCGGA
GAM1861  HHEX      3'  CAACCATATCTCTGACAAAAAG 45783       CCC
              AA                  TAACTG   CTCTGACAAAAAGAA
                                ||||||   ||||||||||||||||
                                GTTGGT   GAGACTGTTTTTCTT
                                   ATA
GAM1861  HYAL2     3'  CTTCCCCTCTGGCAGGGAGA   45784    G       A  AAA
                                CT CCCCTCTG CA   AGA
                                || ||||||| ||   |||
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                                GA GGGGAGAC GT   TCT
                                 A       C  CCC
GAM1861  HYAL2    3'  CTTCCCCTCTGGCAGGGAGA   45784    G       A  AAA
                                CT CCCCTCTG CA   AGA
                                || |||||||| ||   |||
                                GA GGGGAGAC GT   TCT
                                 A       C  CCC
GAM1861  ITPR3    3'  TAACTACCCACAAGGAG     45785         CTCTG    AA
                                TAACTGCCC    ACAA  AG
                                |||||||||    ||||  ||
                                ATTGATGGG    TGTT  TC
                                      _____   CC
GAM1861  OSM      3'  TAACTCCCTAGCTTCACAAAGA 45786      G   CT_ G_    A
              GAA                   TAACT CCC   CT  ACAAA AGAA
                                |||||  |||   ||  |||||  ||||
                                ATTGA GGG   GA  TGTTT TCTT
                                   _   ATC  AG    C
GAM1861  PFKFB4   3'  TAACTCCCCTCTGTACACAGAG 45787      G       _   AAA
              A                   TAACT CCCCTCTG ACA   AGA
                                |||||  ||||||||  |||   |||
                                ATTGA GGGGAGAC TGT   TCT
                                   _       A   GTC
GAM1861  PLAG1    3'  TAACTGGCCCTACAAAAAG    45788       C    CTG
                                TAACTG CCCT   ACAAAAAG
                                ||||||  ||||   ||||||||
                                ATTGAC GGGA   TGTTTTTC
                                   C   ____
GAM1861  PTP4A2   3'  TAACTGCCTTCCACAAA     45789         CC   G
                                TAACTGCC  TCT ACAAA
                                ||||||||  ||| |||||
                                ATTGACGG  AGG TGTTT
                                     A_   _
GAM1861  SLC1A4   3'  CTGTCCCTTACATAAAAAAGAA 45790     C    CTGAC_
                                CTG CCCT      AAAAAGAA
                                ||| ||||      ||||||||
                                GAC GGGA      TTTTTCTT
                                  A    ATGTAT
GAM1861  TFE3     3'  AACTGCCCCTCAAGGAAGAA   45791           TGACAAA
                                AACTGCCCCTC       AAGAA
                                ||||||||||       |||||
                                TTGACGGGGAG       TTCTT
                                      TTCC____
GAM1861  YY1      3'  TAACTGCCCATTCTTTTAAAGA 45792         C_   GACAA
              A                   TAACTGCCC  TCT    AAAGAA
                                |||||||||  |||    ||||||
                                ATTGACGGG  AGA    TTTCTT
                                     TA   AAA__
GAM1861  BTN2A1   3'  CCGGTCCTCTGACAGGAAGA   45793     CC        AA
                                CTG  CCTCTGACA  AAGA
                                |||  |||||||||  ||||
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                                GGC  GGAGACTGT  TTCT
                                  CA        CC
GAM1861  CGI-142   3'  TAACTGCCTTGATAAAAG    45794         CCTC   CA
                                TAACTGCC    TGA  AAAAG
                                ||||||||    |||  |||||
                                ATTGACGG    ACT  TTTTC
                                    A___    A_
GAM1861  DKFZP434I216 3'  AACTGCCCCAGTAAAAAG    45795          TCTGAC
                                AACTGCCCC      AAAAAG
                                |||||||||      ||||||
                                TTGACGGGG      TTTTTC
                                     TCA___
GAM1861  FHX       3'  GCTTCTCTGACAGAGAAAGAA  45796    CC       A__
                                GC  CTCTGACA   AAAGAA
                                ||  ||||||||   ||||||
                                CG  GAGACTGT   TTTCTT
                                  AA       CTC
GAM1861  FLJ13117  3'  CTTCCCCTCCAAAAATGGTAAA 45797    G      TG C  _____
              GA                    CT CCCCTC  A AA    AAAGA
                                ||  ||||||  | ||    |||||
                                GA GGGGAG  T TT    TTTCT
                                 A     GT T  ACCA
GAM1861  FLJ22195  3'  CAACTGTCCTCACGGCAAAAAG 45798        CC    _  A
              AA                    TAACTG  CCTC TG CAAAAAGAA
                                ||||||  ||||  ||  |||||||||
                                GTTGAC  GGAG GC GTTTTTCTT
                                   A_    T  C
GAM1861  FLJ22833  5'  TAACTGCCCCGTTCTTTGGATA 45799          __   GACA__
              AAAG                    TAACTGCCCC  TCT     AAAAG
                                ||||||||||  |||     |||||
                                ATTGACGGGG  AGA     TTTTC
                                     CA   AACCTA
GAM1861  HSP105B   5'  GCCGTTCCTCTGACACTCAGAA 45800     ___        AAA
                                GCC   CCTCTGACA   AGAA
                                |||   |||||||||   ||||
                                CGG   GGAGACTGT   TCTT
                                  CAA        GAG
GAM1861  KIAA0016  3'  TAACTGCCCCTCTATACA    45801             _
                                TAACTGCCCCTCTG ACA
                                ||||||||||||| |||
                                ATTGACGGGGAGAT TGT
                                        A
GAM1861  KIAA1219  3'  TGCCCAGCTTAAAAAGAA    45802       CT  GAC
                                TGCCC  CT   AAAAAGAA
                                |||||  ||   ||||||||
                                ACGGG  GA   TTTTTCTT
                                   TC  A__
GAM1861  KIAA1271  3'  TAACTCCCCTCTGACCCAG    45803       G         AAAA
                                TAACT CCCCTCTGAC    AG
                                |||||  ||||||||||    ||
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                                ATTGA GGGGAGACTG    TC
                                  _        GG__
GAM1861  KIAA1388  5'  TAACTGCTCTGCCAAAGA    45804       CCC    ACAA
                                TAACTGC   TCTG    AAAGA
                                |||||||   ||||    |||||
                                ATTGACG   AGAC    TTTCT
                                   ___    GG__
GAM1861  SCYA22    3'  TAACTGCCTTTTGGCAGGGAGA 45805        CCTC  A  AAA
                                TAACTGCC    TG CA   AGA
                                ||||||||    || ||   |||
                                ATTGACGG    AC GT   TCT
                                     AAA_  C  CCC
GAM1861  SEC24B    3'  TAACTGTGACAAAAAGA     45806       CCCCTC
                                TAACTG     TGACAAAAAGA
                                ||||||     ||||||||||
                                ATTGAC     ACTGTTTTTCT
                                  _______
GAM1861  SEMA5B    3'  ACTGCCTCTGACCAGA      45807       CC     AAAA
                                ACTGCC  TCTGAC    AGA
                                ||||||  ||||||    |||
                                TGACGG  AGACTG    TCT
                                  __     G___
GAM1861  STK22D    3'  CAACTGCCCCGGGGACGATGAA 45808         TCT   AA__
            AG                    TAACTGCCCC   GAC    AAAG
                                ||||||||||   |||   ||||
                                GTTGACGGGG   CTG    TTTC
                                     CCC   CTAC
GAM1861  TBL1Y     5'  AACTGCCCTTCTGTTAAGA    45809        C    ACAAA
                                AACTGCCC TCTG     AAGA
                                |||||||| ||||     ||||
                                TTGACGGG AGAC     TTCT
                                     A    AA___
GAM1861  TBL1Y     5'  AACTGCCCTTCTGTTAAGA    45809        C    ACAAA
                                AACTGCCC TCTG     AAGA
                                |||||||| ||||     ||||
                                TTGACGGG AGAC     TTCT
                                     A    AA___
GAM1861  LOC149302 5'  CTGCCCGAGAAAAAGA      45810       CTCT  C
                                CTGCCC    GA AAAAAGA
                                ||||||    || |||||||
                                GACGGG    CT TTTTTCT
                                  _____  C
GAM1861  LOC152816 3'  ACTGCTGACAAAGAGA      45811       CCCTC      A
                                ACTGC     TGACAAA AGA
                                |||||     ||||||| |||
                                TGACG     ACTGTTT TCT
                                  ______      C
GAM1861  LOC161635 5'  CTGCCCCTCCCACTAGAAGA   45812          G  AAA
                                CTGCCCCTCT AC   AAGA
                                ||||||||||  ||   ||||
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                                GACGGGGAGG TG   TTCT
                                      G  ATC
GAM1861  LOC196047 3'  CTGCCCCTAGCTGCAGGAAGA  45813         __   A  AA
                                CTGCCCCT  CTG CA  AAGA
                                ||||||||  ||| ||  ||||
                                GACGGGGA  GAC GT  TTCT
                                     TC   _  CC
GAM1861  LOC254013 3'  ACTGTCTCTAAAAAAAGAA   45814      CCC     C
                                ACTG   CTCTGA AAAAAGAA
                                ||||   |||||| ||||||||
                                TGAC   GAGATT TTTTTCTT
                                  A__     _
GAM1861  LOC256642 3'  TAACTCCTGACAAAAAGA    45815      GCCCC
                                TAACT    TCTGACAAAAAGA
                                |||||    ||||||||||||
                                ATTGA    GGACTGTTTTTCT
                                  _____
GAM1861  LOC257407 5'  CTGGGGGACTCTGACAGGGAGA 45816     CCC__       AAA
              A                  CTG    CTCTGACA   AGAA
                                 |||    ||||||||   ||||
                                 GAC    GAGACTGT   TCTT
                                   CCCCT      CCC
GAM1861  LOC257472 3'  AACTGCCCCAGTAAAAAG    45795         TCTGAC
                                AACTGCCCC     AAAAAG
                                |||||||||     ||||||
                                TTGACGGGG     TTTTTC
                                     TCA___
GAM1861  LOC91812  5'  ACTGCTCTGACACTGAAAAG   45817      CCC      ___
                                ACTGC   TCTGACA   AAAAG
                                |||||   |||||||   |||||
                                TGACG   AGACTGT   TTTTC
                                   ___      GAC
GAM1861  LOC91813  5'  ACTGCTCTGACACTGAAAAG   45817      CCC      ___
                                ACTGC   TCTGACA   AAAAG
                                |||||   |||||||   |||||
                                TGACG   AGACTGT   TTTTC
                                   ___      GAC
GAM1861  LOC92997  3'  CTGGGGGACTCTGACAGGGAGA 45816     CCC__       AAA
              A                  CTG    CTCTGACA   AGAA
                                 |||    ||||||||   ||||
                                 GAC    GAGACTGT   TCTT
                                   CCCCT      CCC
GAM1862  FLJ23436  5'  CCGCGACCCGGCCTCGGTTGCC 45820         AAAT  G_  A
                                TCGCGACCC    GT  CG TTGCC
                                |||||||||    ||  || |||||
                                GGCGCTGGG    CG  GC AACGG
                                     C___  GA  C
GAM1862  HAND1     3'  GCGATCCAAGTGTGTGGTTGC  45821      C    A    CGA
                                GCGA CCAA TGTG   TTGC
                                |||| |||| ||||   ||||
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                                CGCT GGTT ACAC   AACG
                                  A   C   ACC
GAM1862  LOC220522 3'  CGCGATCTGGGTGTGATGGTGC 45822      CCCAAAT  C  __
             C                   CGCGA      GTG GAT  TGCC
                                 |||||      ||| |||  ||||
                                 GCGCT      CAC CTA  ACGG
                                   AGACC__   A   CC
GAM1862  LOC222223 3'  GACCCAAATCATTTGC      45823         GTG  A
                                 GACCCAAAT   CG TTGC
                                 |||||||||   || ||||
                                 CTGGGTTTA   GT AACG
                                       ___ A
GAM1862  LOC255328 3'  GACCCAAAGTGGAGCAGCC   45824         T   C  TT_
                                 GACCCAAA GTG GA   GCC
                                 |||||||| ||| ||   |||
                                 CTGGGTTT CAC CT   CGG
                                      _  _ CGT
GAM1863  ABCA4    3'  GCTGGCCAGTCCATTTGGA   45827     GC    TAAC
                                 GCT  GGCC   CCATTTGGA
                                 |||  ||||   |||||||||
                                 CGA  CCGG   GGTAAACCT
                                   __   TCA_
GAM1863  APOB     5'  GCTGCGGCCTGGCCTCGG    45828         AA  CAT
                                 GCTGCGGCCT  CC   TTGG
                                 ||||||||||  ||   ||||
                                 CGACGCCGGA  GG   AGCC
                                       CC  ___
GAM1863  EZH1     3'  GCTGGGGCCTGGCCCATTTGG  45829     C    AA
                                 GCTG GGCCT  CCCATTTGG
                                 |||| |||||  |||||||||
                                 CGAC CCGGA  GGGTAAACC
                                   C    CC
GAM1863  GLS      3'  GCAACCTTGACCCATTTGGA   45830       A_
                                 GCGGCCT  ACCCATTTGGA
                                 |||||||  ||||||||||
                                 CGTTGGA  TGGGTAAACCT
                                      AC
GAM1863  ID2      5'  TAGCTGCGCTTGGCACCGGGTC 45831    _____  _  AAC_____  ATTT
             CAAATGG                GC   GGC CT      CC    GG
                                 ||   ||| ||      ||   ||
                                 CG   CCG GG      GG   CC
                                  CGAA   T  CCCIIIA  TTTA
GAM1863  SNRPN    5'  GCTGCGGCCAGCCCTTGG    45832         TAA   AT
                                 GCTGCGGCC   CCC  TTGG
                                 |||||||||   |||  ||||
                                 CGACGCCGG   GGG  AACC
                                       TC_   __
GAM1863  SNRPN    5'  GCTGCGGCCAGCCCTTGG    45832         TAA   AT
                                 GCTGCGGCC   CCC  TTGG
                                 |||||||||   |||  ||||
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                                CGACGCCGG  GGG  AACC
                                     TC_  __
GAM1863  SNRPN    5'  GCTGCGGCCAGCCCTTGG    45832        TAA  AT
                                GCTGCGGCC  CCC  TTGG
                                |||||||||  |||  ||||
                                CGACGCCGG  GGG  AACC
                                     TC_  __
GAM1863  FLJ10241  3'  ACTGGAAATCCATTTGG     45833     C  CCT  C
                                GCTG GG  AA CCATTTGG
                                |||| ||  || ||||||||
                                TGAC CT  TT GGTAAACC
                                  _ ___ A
GAM1863  KIAA1872  3'  GCTGCGGCCAGCGCACTGGA  45834        TAACC  T
                                GCTGCGGCC    CATT GGA
                                |||||||||    |||| |||
                                CGACGCCGG    GTGA CCT
                                     TCGC_  _
GAM1863  PLAC6    3'  AGCTGCAAAAGTTTATTTGGA  45835        CCTAACCC
                                AGCTGCGG       ATTTGGA
                                ||||||||       |||||||
                                TCGACGTT       TAAACCT
                                     TTCAAA__
GAM1863  SSAT2    5'  TAGCCGCGGCCTGGTAAGTGGA 45836          AACCCATT
                                TAGCTGCGGCCT       TGGA
                                ||||||||||||       ||||
                                ATCGGCGCCGGA       ACCT
                                      CCATTC__
GAM1863  LOC126789 3'  TGTGGCCTAACTTTGG     45837    C      CCA
                                TG GGCCTAAC  TTTGG
                                || ||||||||  |||||
                                AC CCGGATTG  AAACC
                                 A      ___
GAM1863  LOC149271 3'  TAGCTGCAGTCTAGTCGTGTGG 45838        C  ACCCATT
                                TAGCTGCGG CTA      TGG
                                ||||||||| |||      |||
                                ATCGACGTC GAT      ACC
                                     A  CAGCAC_
GAM1863  LOC90719  3'  AGCTGCGGCCTGACTGATCCAA 45839         A ________ ATTT
            AG                    GCTGCGGCCT AC      CC   G
                                ||||||||||  ||      ||   |
                                CGACGCCGGA TG      GG   C
                                     C  ACTIIIA  TTTA
GAM1864  SHOX     3'  TTCAGCTCAGTGACAAGATAGG 45842       _   TTGTAT
            A                    TTCAGCT AGTG     GATAGGA
                                |||||||  ||||     |||||||
                                AAGTCGA TCAC     CTATCCT
                                    G   TGTT__
GAM1864  LOC221362 3'  AGCAGTGTTGTATATAAGA   45843     T        A
                                AGC AGTGTTGTATG TAGGA
                                |||  |||||||||| |||||
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                                TCG TCACAACATAT ATTCT
                                  _       _
GAM1864  LOC221576 3'  AGTTAGTGTTGTCAAATAGG   45844    C       AT
                                AG TAGTGTTGT  GATAGG
                                || |||||||||  ||||||
                                TC ATCACAACA  TTATCC
                                 A        GT
GAM1864  LOC257515 3'  AGTTAGTGTTGTCAAATAGG   45844    C       AT
                                AG TAGTGTTGT  GATAGG
                                || |||||||||  ||||||
                                TC ATCACAACA  TTATCC
                                 A        GT
GAM1864  LOC257572 3'  AGTTAGTGTTGTCAAATAGG   45844    C       AT
                                AG TAGTGTTGT  GATAGG
                                || |||||||||  ||||||
                                TC ATCACAACA  TTATCC
                                 A        GT
GAM1865  AKAP13    3'  CCGGTGTATCCCAACCACCC   45847     CGATTT
                                CCGG     TCCCAACCACCC
                                ||||     ||||||||||||
                                GGCC     AGGGTTGGTGGG
                                  ACAT__
GAM1865  CTLA1     3'  CCTGCAACCCCGACTGCCC    45848    G    TTT   A  CA
                                CC GCGAT   CCC AC  CCC
                                || |||||   ||| ||  |||
                                GG CGTTG   GGG TG  GGG
                                 A    ____  C  AC
GAM1865  CYP4F3    3'  CCTGCAATCCCAGCCACC     45849    G    TTT    A
                                CC GCGA   TCCCA CCACC
                                || ||||   ||||| |||||
                                GG CGTT   AGGGT GGTGG
                                 A    ____     C
GAM1865  GNE       3'  CCCGCAATCCCAGCCAC     45850     G   TTT    A
                                CCCG CGA   TCCCA CCAC
                                |||| |||   ||||| ||||
                                GGGC GTT   AGGGT GGTG
                                  _  ____     C
GAM1865  PAX5      3'  GGCTTCCTCTGACCACCC    45851     GA    CCA
                                GGC  TTTTC   ACCACCC
                                |||  |||||   |||||||
                                CCG  AGGAG   TGGTGGG
                                  A_     AC_
GAM1865  PK428     5'  CCCGGCTCCCAACCAC      45852       GATTT
                                CCCGGC     TCCCAACCAC
                                ||||||     ||||||||||
                                GGGCCG     AGGGTTGGTG
                                           ______
GAM1865  PRKAB1    5'  CCGACACTTTCCCAACC      45853       G
                                CCGGC ATTTTCCCAACC
                                ||||| ||||||||||||
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                                GGCTG TGAAAGGGTTGG
                                   _
GAM1865 PRX     3' CCGGGATTTTCCCCAACATCC 45854     C       AAC _
                                CCGG GATTTTCCC  CA CC
                                |||| |||||||||  || ||
                                GGCC CTAAAAGGG  GT GG
                                  _       GTT  A
GAM1865 RAP1    3' ACAATTTTTTTTAACCACC   45855       CCC_
                                GCGATTTT   AACCACC
                                ||||||||   |||||||
                                TGTTAAAA   TTGGTGG
                                    AAAA
GAM1865 RHEB2   5' GCGCGCTCCCAACCGCCC    45856    ATT       A
                                GCG  TTCCCAACC CCC
                                |||  ||||||||| |||
                                CGC  GAGGGTTGG GGG
                                  GC_       C
GAM1865 SIX3    5' CAGCGATTCCACCGCAATCGCC 45857         _ _  CCA
              C                  CGGCGATTTT CC CAA  CCC
                                ||||||||| || |||  |||
                                GTCGCTAAGG GG GTT  GGG
                                     T  C  AGC
GAM1865 SMARCA3  3' ACCAGGTAACTTCCCAAC   45858    C  CG   T
                                ACC GG  ATTT CCCAAC
                                ||| ||  |||| ||||||
                                TGG CC  TGAA GGGTTG
                                  T  AT  _
GAM1865 SMARCA3  3' ACCAGGTAACTTCCCAAC   45858    C  CG   T
                                ACC GG  ATTT CCCAAC
                                ||| ||  |||| ||||||
                                TGG CC  TGAA GGGTTG
                                  T  AT  _
GAM1865 THY1    3' CCCAGGCACAGCCCAACCAC  45859    _   ATTTT
                                CCC GGCG    CCCAACCAC
                                ||| ||||    |||||||||
                                GGG CCGT    GGGTTGGTG
                                  T   GTC__
GAM1865 TNS     3' CAGGTGTTTTCCCAACTGTCC 45860    CGA       CA_
                                CGG  TTTTCCCAAC  CC
                                |||  ||||||||||  ||
                                GTC  AAAAGGGTTG  GG
                                  CAC        ACA
GAM1865 TPMT    3' ACCTGCAATCCCAGCCAC    45861    CG   TTT   A
                                ACC  GCGA  TCCCA CCAC
                                |||  ||||  ||||| ||||
                                TGG  CGTT  AGGGT GGTG
                                  A_   ___    C
GAM1865 ZNF74   5' CCTGCAATCCCAACTAC     45862   G   TTT     C
                                CC GCGA  TCCCAAC AC
                                || ||||  ||||||| ||
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                                GG CGTT   AGGGTTG TG
                                 A  ___      A
GAM1865 ATIP1    3' CCGGTGGTGACGCTCCAGTTAC 45863     C___  T   CAACC
             CC                   CCGG   GAT TTCC    ACCC
                                  ||||   ||| ||||    ||||
                                  GGCC   CTG GAGG    TGGG
                                    ACCA  C   TCAA_
GAM1865 CECR6    3' GGCTTCTCTCCCAGCCACC   45864    GA      A
                                  GGC  TTTTCCCA CCACC
                                  |||  |||||||| |||||
                                  CCG  GAGAGGGT GGTGG
                                    AA      C
GAM1865 DSCR6    3' CCTGCAATCCCAGCCAC     45865    G   TTT    A
                                  CC GCGA   TCCCA CCAC
                                  || ||||   ||||| ||||
                                  GG CGTT   AGGGT GGTG
                                   A  ___    C
GAM1865 FLJ10895 3' GGTTCTCCAACCACCC      45866    CGATT  _
                                  GG    TTC CCAACCACCC
                                  ||    ||| ||||||||||
                                  CC    AAG GGTTGGTGGG
                                    _____  A
GAM1865 FLJ31762 5' GCGACTTTCTTGGCCACCC   45867        CCAA
                                  GCGATTTTC   CCACCC
                                  |||||||||   ||||||
                                  CGCTGAAAG   GGTGGG
                                       AACC
GAM1865 G4       3' ACCCTGGGTTTCCCAACCAC   45868     _ CGAT
                                  ACCC GG   TTTCCCAACCAC
                                  |||| ||   ||||||||||||
                                  TGGG CC   AAAGGGTTGGTG
                                    A  C___
GAM1865 KIAA0830 3' GGTTCCTCCTCCCAACTACC   45869    CGA_       C
                                  GG   TTTTCCCAAC ACC
                                  ||   |||||||||| |||
                                  CC   AGGAGGGTTG TGG
                                   AAGG        A
GAM1865 KIAA1115 5' ACCCTGCTAACACCCAACCATC 45870     G  GATTTT      _
             C                     ACCC GC     CCCAACCA CC
                                   |||| ||     |||||||| ||
                                   TGGG CG     GGGTTGGT GG
                                     A  ATTGT_      A
GAM1865 KIAA1441 5' ACCCGGCGGTCTCTACCC    45871        A   __
                                  ACCCGGCG TTTT  CCC
                                  ||||||||  ||||  |||
                                  TGGGCCGC AGAG  GGG
                                       C    AT
GAM1865 KIAA1691 5' ACCCGTCGACCCCCGCCTGGCC 45872      G    TT _  AA_  A
             GCCC                    ACCCG CGATT  C CC   CC CCC
                                     ||||| |||||  | ||   || |||
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                                TGGGC GCTGG  G GG   GG GGG
                                  A    GG C  ACC  C
GAM1865 KIAA1821 3' CCTGCAACTTTCCCAACCGCC 45873    G          A
                                CC GCGATTTTCCCAACC CC
                                || |||||||||||||| ||
                                GG CGTTGAAAGGGTTGG GG
                                 A           C
GAM1865 MADHIP   3' CGGTCCCCCCAACCACCC    45874    CGA  TT
                                CGG   TT  CCCAACCACCC
                                |||   ||  ||||||||||
                                GCC   AG  GGGTTGGTGGG
                                  ___  GG
GAM1865 MADHIP   3' CGGTCCCCCCAACCACCC    45874    CGA  TT
                                CGG   TT  CCCAACCACCC
                                |||   ||  ||||||||||
                                GCC   AG  GGGTTGGTGGG
                                  ___  GG
GAM1865 MAPK8IP3 5' CCCGGCCCTCCCCAGCTGCC  45875      GA      ACCA
                                CCCGGC  TTTTCCCA   CC
                                ||||||  ||||||||   ||
                                GGGCCG  GGAGGGGT   GG
                                   __      CGAC
GAM1865 MGC35558 3' CCGGCGACTCTAGCCACC    45876         CCCAA
                                CCGGCGATTTT    CCACC
                                ||||||||||    |||||
                                GGCCGCTGAGA    GGTGG
                                      TC___
GAM1865 MSTP028  3' ACCTAGTCTAGTCTCAACCACC 45877    CG CGATTT  C
             C                   ACC  G     TC CAACCACCC
                                |||  |     || |||||||||
                                TGG  C     AG GTTGGTGGG
                                  AT AGATC_  A
GAM1865 MYT1     3' GGCCGATTTCCAGCCATCC    45878    _     __  A
                                GGC GATTTTC  CCA CC
                                ||| |||||||  ||| ||
                                CCG CTAAAGG  GGT GG
                                  G      TC   A
GAM1865 NETO2    3' CCTGGCTCCATCCAACCACC   45879    C   GA   TC
                                CC GGC  TTT  CCAACCACC
                                || |||  |||  |||||||||
                                GG CCG  AGG  GGTTGGTGG
                                 A  __   TA
GAM1865 p25      3' ACCGGGCGATTCCGGTGACC   45880    C       CCCA
                                ACC GGCGATTTT    ACC
                                ||| |||||||||    |||
                                TGG CCGCTAAGG    TGG
                                  C        CCAC
GAM1865 SCYA28   3' ACCTGCAATCCCAGCCAC    45861    CG   TTT    A
                                ACC  GCGA   TCCCA CCAC
                                |||  ||||   ||||| ||||
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                                TGG  CGTT   AGGGT GGTG
                                  A_   ___    C
GAM1865  STIM2    5'  CCGGCGACTCCTCCGGCCGCCC 45881         TC  AA  A
                                CCGGCGATTT  CC  CC CCC
                                ||||||||||  ||  || |||
                                GGCCGCTGAG  GG  GG GGG
                                      GA  CC  C
GAM1865  TRF4-2   3'  GCATTTTCCCAACTGCC     45882    G         CA
                                GC ATTTTCCCAAC  CC
                                || ||||||||||  ||
                                CG TAAAAGGGTTG  GG
                                 _         AC
GAM1865  VEZATIN  3'  CAGAATTTTCCCAATCACC   45883     C         C
                                CGG GATTTTCCCAA CACC
                                ||| ||||||||||| ||||
                                GTC TTAAAAGGGTT GTGG
                                  _         A
GAM1865  LOC127428 3'  CCAGGCATGCATCTCAACCACC 45884    C    ATTT  C
             C                   CC GGCG    TC CAACCACCC
                                || ||||    || |||||||||
                                GG CCGT    AG GTTGGTGGG
                                 T    ACGT  A
GAM1865  LOC138389 3'  ACCGGGCACCTCCCAACC    45885     C    AT
                                ACC GGCG  TTTCCCAACC
                                ||| ||||  ||||||||||
                                TGG CCGT  GGAGGGTTGG
                                  C   __
GAM1865  LOC146667 3'  ACCTCGTGATCCAACCGCC   45886     _ GC   TTTC     A
                                ACC CG  GAT    CCAACC CC
                                ||| ||  |||    |||||| ||
                                TGG GC  CTA    GGTTGG GG
                                  A  A_  _____      C
GAM1865  LOC146990 5'  CCTCGCCCCTCCCAGCCACCC  45887    GG  A       A
                                CC  CG TTTTCCCA CCACCC
                                ||  || |||||||| ||||||
                                GG  GC GGGAGGGT GGTGGG
                                 A_  G       C
GAM1865  LOC147080 5'  GGCGATTTCCACTACCC     45888          CCA  C
                                GGCGATTTTC   AC ACCC
                                ||||||||||   || ||||
                                CCGCTAAAGG   TG TGGG
                                      ____  A
GAM1865  LOC152633 5'  CCCGGCGGGGCAACCACC    45889        ATTTTCC
                                CCCGGCG      CAACCACC
                                |||||||      ||||||||
                                GGGCCGC      GTTGGTGG
                                    CCC_____
GAM1865  LOC152641 5'  GGCGCTTTCCCACCACCC    45890      A       A
                                GGCG TTTTCCCA CCACCC
                                |||| |||||||| ||||||
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                                CCGC GAAAGGGT GGTGGG
                                  _      _
GAM1865  LOC153682 3'  ACCTCGTGATCCGACCACC    45891     _ GC   TTTC  A
                                ACC CG  GAT    CC ACCACC
                                ||| ||  |||    || ||||||
                                TGG GC  CTA    GG TGGTGG
                                  A  A_  ____  C
GAM1865  LOC155435 3'  GGCACCACTCCCAACCACCC   45892      ATT
                                GGCG   TTCCCAACCACCC
                                ||||   ||||||||||||
                                CCGT   GAGGGTTGGTGGG
                                  GGT
GAM1865  LOC158401 3'  ACCTAGTGATTTTCCCAATTAC 45893     CG C         CC
              C                  ACC  G GATTTTCCCAA  ACC
                                ||| | ||||||||||  |||
                                TGG  C CTAAAAGGGTT  TGG
                                  AT A          AA
GAM1865  LOC163115 5'  ACCCTGTTTTCCCAGCCATCC  45894     GGCGA       A  _
                                ACCC     TTTTCCCA CCA CC
                                ||||     |||||||| ||| ||
                                TGGG     AAAAGGGT GGT GG
                                  AC___       C   A
GAM1865  LOC164173 5'  ACCCGCGATTCCACACGATCAC 45895       G    TT   _  AC__
                                ACCCG CGAT  TCC CA    CAC
                                ||||| ||||  ||| ||    |||
                                TGGGC GCTA  AGG GT    GTG
                                  _    __   T  GCTA
GAM1865  LOC201516 3'  CCACTTTCCCAACCAC      45896    GGCG
                                CC    ATTTTCCCAACCAC
                                ||    ||||||||||||||
                                GG    TGAAAGGGTTGGTG
                                  ____
GAM1865  LOC219846 5'  CCGCGGGGCTCCCTCAGCCATC 45897    _   CGAT    _ A  _
              C                  CC CGG    TTTCC CA CCA CC
                                || |||    ||||| || ||| ||
                                GG GCC    GAGGG GT GGT GG
                                 C   CC__     A  C   A
GAM1865  LOC220729 3'  GCTGATTTTCCCACAACC    45898    _        ACC
                                GC GATTTTCCCA   ACC
                                || ||||||||||   |||
                                CG CTAAAAGGGT   TGG
                                  A         GT_
GAM1865  LOC257554 3'  ACCCTGGGTTTCCCAACCAC   45868     _ CGAT
                                ACCC GG    TTTCCCAACCAC
                                |||| ||    ||||||||||||
                                TGGG CC    AAAGGGTTGGTG
                                  A  C___
GAM1865  LOC91409  3'  CCCAGGTGCGTCTAACCACCC  45899      CGATTT  CC
                                CCCGG     TC  AACCACCC
                                |||||     ||  ||||||||
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                                GGGTC     AG  TTGGTGGG
                                   CACGC_  A_
GAM1866  AOC2     3'  AAACAGGGAAAAGTACA     45902        AA
                                AAACAGG  AGAAGTATA
                                |||||||  |||||||||
                                TTTGTCC  TTTTCATGT
                                    C_
GAM1866  CCRL1    3'  AAACAGGAAAAAAGATA     45903             T
                                AAACAGGAAAGAAG ATA
                                |||||||||||||| |||
                                TTTGTCCTTTTTTC TAT
                                                _
GAM1866  CHC1     3'  GGACAGGAAAGGGGCACA    45904    A        AA
                                A ACAGGAAAG  GTATA
                                | |||||||||  |||||
                                C TGTCCTTTC  CGTGT
                                 C        CC
GAM1866  DDX6     3'  AAAAAGGAAAGAAAGAGTTACT 45905     C       ___   A
                AT                   AAA AGGAAAGA   AGT TACTAT
                                ||| ||||||||   ||| ||||||
                                TTT TCCTTTCT   TCA ATGATA
                                  T       TTC  _
GAM1866  GAC1     3'  AAACAGGAGAAAAGAGTGAATC 45906         A    TATACT
                G                    AAACAGGA AGAAG     ATCG
                                |||||||| |||||     ||||
                                TTTGTCCT TTTTC     TAGC
                                    C     TCACT_
GAM1866  MMP19    5'  AACAGGAAGGAGGTCAGAGCCC 45907         A  A  ATACTA
                G                    AACAGGAA GA GT     TCG
                                |||||||| || ||     |||
                                TTGTCCTT CT CA     GGC
                                    C  C  GTCTCG
GAM1866  MMP19    5'  AACAGGAAGGAGGTCAGAGCCC 45907         A  A  ATACTA
                G                    AACAGGAA GA GT     TCG
                                |||||||| || ||     |||
                                TTGTCCTT CT CA     GGC
                                    C  C  GTCTCG
GAM1866  VAMP8    3'  ACAGGAAAGGAGACCCTC    45908         A  TAT   A
                                ACAGGAAAG AG   ACT TC
                                |||||||||  ||   ||| ||
                                TGTCCTTTC TC   TGG AG
                                    C  ___   G
GAM1866  C21orf109 5'  AAACAGGAAAGAAAGTTCACT  45909           _  A
                                AAACAGGAAAGAA GT TACT
                                |||||||||||||  || ||||
                                TTTGTCCTTTCTT CA GTGA
                                      T  A
GAM1866  FLJ10287 3'  AAACAGAAGAGAACATACT   45910         A   G
                                AAACAGGA AGAA TATACT
                                ||||||||  |||| ||||||
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                                TTTGTCTT TCTT GTATGA
                                    C   _
GAM1866 FLJ23462 3' CAGGAAAGACCCTAGCTAT   45911        AGTA _
                                CAGGAAAGA   TA CTAT
                                |||||||||   || ||||
                                GTCCTTTCT   AT GATA
                                    GGG_ C
GAM1866 GDAP1L1  5' CAGGAAAGAAGGAGGCTCCG  45912         TATA A
                                CAGGAAAGAAG   CT TCG
                                ||||||||||   || |||
                                GTCCTTTCTTC   GA GGC
                                     CTCC _
GAM1866 HIC2     3' GGAAAGAAAATAAGCTAT    45913        _ TA
                                GGAAAGAAG TA  CTAT
                                ||||||||| ||  ||||
                                CCTTTCTTT AT  GATA
                                    T  TC
GAM1866 KIAA1033 3' AAACAGAGAAAACAATACT   45914      GA   AGT
                                AAACAG  AAGA   ATACT
                                ||||||  ||||   |||||
                                TTTGTC  TTTT   TATGA
                                   TC   GT_
GAM1866 KNSL6    3' AACAGAAAAGGAGTGTCCCAT 45915        A   ATA
                                AACAGGAAAG AGT   CTAT
                                |||||||||| |||   ||||
                                TTGTCTTTTC TCA   GGTA
                                    C   CAG
GAM1866 MGC3184  3' AACAGGAAAGAATACAACT   45916         GTAT
                                AACAGGAAAGAA   ACT
                                ||||||||||||   |||
                                TTGTCCTTTCTT   TGA
                                     ATGT
GAM1866 LOC145623 3' GGAAAGAAGTGACAACC    45917        AT  T
                                GGAAAGAAGT  AC ATC
                                ||||||||||  || |||
                                CCTTTCTTCA  TG TGG
                                    C_  T
GAM1866 LOC151174 5' AAACAGGGGAGAATTCCCTTCG 45918      AA   GTATA  A
                                AAACAGG  AGAA    CT TCG
                                |||||||  ||||    || |||
                                TTTGTCC  TCTT    GG AGC
                                   CC    AAG__  A
GAM1866 LOC253664 3' AAACAGTAAAGAGAATACTAT  45919      G    A T
                                AAACAG AAAGA G ATACTAT
                                |||||| ||||| | |||||||
                                TTTGTC TTTCT C TATGATA
                                   A    _T
GAM1866 LOC91069  3' GGACAGGAAATGAGGTAAGCT  45920   A      _  A   TA
                                A ACAGGAAA GA GTA  CT
                                | ||||||| || |||  ||
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                                C TGTCCTTT CT CAT  GA
                                 C       A  C   TC
GAM1867  ADCY6    3'  TCCCAGGACACTATCTGGGGAA 45923       A TG  T   CA
                                TTCCAG G  TT ATC  GGGAA
                                |||||| |  || |||  |||||
                                AGGGTC T  GA TAG  CCCTT
                                   C GT  _   AC
GAM1867  ADCY6    3'  TCCCAGGACACTATCTGGGGAA 45923       A TG  T   CA
                                TTCCAG G  TT ATC  GGGAA
                                |||||| |  || |||  |||||
                                AGGGTC T  GA TAG  CCCTT
                                   C GT  _   AC
GAM1867  ALPP     3'  TCCAGATGTCTGGGGA      45924       G    ATCCA
                                TCCAGA TGTTT    GGGA
                                |||||| |||||    ||||
                                AGGTCT ACAGA    CCCT
                                   _    C_____
GAM1867  HOXA3    3'  TTCCGGCAGTCCAGGGAA    45925     AGAGT  TTA
                                TTCC    GT   TCCAGGGAA
                                ||||    ||   |||||||||
                                AAGG    CG   AGGTCCCTT
                                  C_____  TC_
GAM1867  LAMC1    3'  TTCCAAGGAAAAGAATTCAGGG 45926      __   TGTTT  C
            AAA                   TTCCA  GAG    AT CAGGGAAA
                                |||||  |||    || ||||||||
                                AAGGT  CTT    TA GTCCCTTT
                                   TC   TTCT_  A
GAM1867  MAP4     3'  CTCCAGGTAGATCCAGGGA   45927       A   TTT
                                TTCCAG GTG   ATCCAGGGA
                                |||||| |||   |||||||||
                                GAGGTC CAT   TAGGTCCCT
                                   _   C__
GAM1867  MAP4     3'  CTCCAGGTAGATCCAGGGA   45927       A   TTT
                                TTCCAG GTG   ATCCAGGGA
                                |||||| |||   |||||||||
                                GAGGTC CAT   TAGGTCCCT
                                   _   C__
GAM1867  MSH3     3'  TTCAAGAGTGTTTATACGTAGA 45928     C         CCAG
            AA                    TTC AGAGTGTTTAT    GGAAA
                                ||| ||||||||||    |||||
                                AAG TCTCACAAATA    TCTTT
                                  T          TGCA
GAM1867  RTKN     3'  TTCCAGGAAGGGTTTAGGGA   45929       __ T    ATCC
                                TTCCAG  AG GTTT    AGGGA
                                ||||||  || ||||    |||||
                                AAGGTC  TC CAAA    TCCCT
                                   CT  C   _____
GAM1867  UPK1B    3'  TCCAGAGTCACTCGGGGAA   45930        GTTTA  CA
                                TCCAGAGT    TC  GGGAA
                                ||||||||    ||  |||||
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                                AGGTCTCA    AG  CCCTT
                                    GTG__  C_
GAM1867 ZNF179   3' TCCAGGGTCATCGGGGAA   45931      A  GTT   CA
                                TCCAG GT   TATC  GGGAA
                                ||||| ||   ||||  |||||
                                AGGTC CA   GTAG  CCCTT
                                   C ___   C_
GAM1867 DKFZP566I1024 3' TTCCTGAATCATCCAGGGA   45932      A   GTT
                                TTCC GAGT   TATCCAGGGA
                                |||| ||||   ||||||||||
                                AAGG CTTA   GTAGGTCCCT
                                  A  ___
GAM1867 ECE2     3' TTCCTGCTTTGTCCAGGGA   45933     AGAG    A_
                                TTCC   TGTTT  TCCAGGGA
                                ||||   |||||  ||||||||
                                AAGG   ACGAA  AGGTCCCT
                                  ____    AC
GAM1867 FLJ13110 3' TCCAGAATCCAGGGA      45934       GTGTTT
                                TCCAGA     ATCCAGGGA
                                ||||||     |||||||||
                                AGGTCT     TAGGTCCCT
                                  ______
GAM1867 FLJ13646 3' AGAATGCTGCTAGGGAAA   45935        TATCC
                                AGAGTGTT    AGGGAAA
                                ||||||||    |||||||
                                TCTTACGA    TCCCTTT
                                    CGA__
GAM1867 FLJ20195 3' TTCCAGAGGCCGGTGGGGA   45936        T   TATCCA
                                TTCCAGAG GTT     GGGA
                                |||||||| |||     ||||
                                AAGGTCTC CGG     CCCT
                                    _  CCAC__
GAM1867 HMGN4    5' TTCTAGGTGTTTACTTAGAG   45937     C  A      CC
                                TTC AG GTGTTTAT  AGGG
                                ||| || ||||||||  ||||
                                AAG TC CACAAATG  TCTC
                                  A  _       AA
GAM1867 KIAA0914  3' TTCTCAGTTATCCAGGGAA   45938     _  AGTGT
                                TTC CAG    TTATCCAGGGAA
                                ||| |||    ||||||||||||
                                AAG GTC    AATAGGTCCCTT
                                  A  ______
GAM1867 KIAA1204  3' CTCCAGGGATTCCAGGGAAA  45939       AGTGTTTA
                                TTCCAG       TCCAGGGAAA
                                ||||||       ||||||||||
                                GAGGTC       AGGTCCCTTT
                                   CCTA_____
GAM1867 KIAA1430  3' TTCTAGATGTTTACACAGAGA  45940     C   G     TC
                                TTC AGA TGTTTA  CAGGGA
                                ||| ||| ||||||  ||||||
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                                AAG TCT ACAAAT  GTCTCT
                                  A  _     GT
GAM1867 KIAA1492 3' TTCCAAAGCATCCAGGGAA   45941        GTTT
                                TTCCAGAGT   ATCCAGGGAA
                                |||||||||   ||||||||||
                                AAGGTTTCG   TAGGTCCCTT
                                     ____
GAM1867 KIAA1643 3' TTCCAGAGGGTGCAGAGGGAA 45942        T  T  TCC
                                TTCCAGAG GT TA   AGGGAA
                                |||||||| || ||   ||||||
                                AAGGTCTC CA GT   TCCCTT
                                    C  C  C__
GAM1867 MGC19825 3' TCCTGGAGTGTTTTATGGGGAA 45943     A_       ATCCA
            A                    TCC  GAGTGTTT    GGGAAA
                                |||  ||||||||    ||||||
                                AGG  CTCACAAA    CCCTTT
                                  AC       ATAC_
GAM1867 MSE55    3' TCCAGAGTGGCAGTCGGGGGA  45944        TTTA  CA
                                TCCAGAGTG   TC  GGGA
                                |||||||||   ||  ||||
                                AGGTCTCAC   AG  CCCT
                                     CGTC  CC
GAM1867 NET-7    3' TTCCAGAGCTGCCTCGGGGAAA 45945        _    ATCCA
                                TTCCAGAG TGTTT    GGGAAA
                                |||||||| |||||    ||||||
                                AAGGTCTC ACGGA    CCCTTT
                                     G    GC___
GAM1867 OSBPL3   3' TCCTAGAGACATACATTTGGGG 45946    _   _  T   CCA_
            GAA                   TCC AGAG TGT TAT    GGGAA
                                ||| |||| ||| |||    |||||
                                AGG TCTC GTA GTA    CCCTT
                                  A   T   T   AACC
GAM1867 P311     3' TCTAGAGAACAACATTCAGGGA 45947    C   TGTT_  C
            AA                    TC AGAG    TAT CAGGGAAA
                                || ||||    ||| ||||||||
                                AG TCTC    GTA GTCCCTTT
                                 A   TTGTT   A
GAM1867 RTBDN    3' CTCTGGAGCTCCAGGGA     45948     CA   GTTTA
                                TTC  GAGT    TCCAGGGA
                                |||  ||||    ||||||||
                                GAG  CTCG    AGGTCCCT
                                  AC   ______
GAM1867 VPS39    3' TTCCTGCTATCCAGGGA     45949     AGAG   T
                                TTCC    TGTT ATCCAGGGA
                                ||||    |||| |||||||||
                                AAGG    ACGA TAGGTCCCT
                                     ____    _
GAM1867 LOC112476 3' TTCCAGAGTGCAGGGA      45950         TTTATC
                                TTCCAGAGTG     CAGGGA
                                ||||||||||     ||||||
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                                AAGGTCTCAC     GTCCCT
                                       ______
GAM1867  LOC132617 5'  CCAGCGTGTCCGGGGGAA    45951      A   TTTA   A_
                                CCAG GTG    TCC  GGGAA
                                |||| |||    |||  |||||
                                GGTC CAC    AGG  CCCTT
                                  G  ____   CC
GAM1867  LOC146475 5'  CTCCAGAGGCTCTAGGGAA    45952         T    ATCC
                                TTCCAGAG GTTT    AGGGAA
                                |||||||| ||||    ||||||
                                GAGGTCTC CGAG    TCCCTT
                                     _    A___
GAM1867  LOC148137 3'  TTCGAGGGTGGAGGCCAGGGAA 45953     C  A   TTTAT
                                TTC AG GTG     CCAGGGAA
                                ||| || |||     ||||||||
                                AAG TC CAC     GGTCCCTT
                                  C  C   CTCC_
GAM1867  LOC149705 3'  TTCCAAGTGTTTGTGCAATGGG 45954       G      ATC  __
                                TTCCA AGTGTTT   CA  GGG
                                ||||| |||||||   ||  |||
                                AAGGT TCACAAA   GT  CCC
                                   _      CAC  TA
GAM1867  LOC150577 3'  TTCCAGAGCTCCAGGGAA    45955         GTTTA
                                TTCCAGAGT    TCCAGGGAA
                                |||||||||    |||||||||
                                AAGGTCTCG    AGGTCCCTT
                                       ______
GAM1867  LOC159053 3'  TTCCAGAGGTTGCTTCTGGGGA 45956         T   TA_  CA
                                TTCCAGAG GTT   TC  GGGA
                                |||||||| |||   ||  ||||
                                AAGGTCTC CAA   AG  CCCT
                                     _  CGA  AC
GAM1867  LOC164714 5'  TCCAGCTTGTCCAGGGA     45957      AG  TTTA
                                TCCAG  TG    TCCAGGGA
                                |||||  ||    ||||||||
                                AGGTC  AC    AGGTCCCT
                                   GA  ____
GAM1867  LOC201952 3'  TTCCAGCGTGACCCAGGGAA   45958       A   TTT
                                TTCCAG GTG   ATCCAGGGAA
                                |||||| |||   ||||||||||
                                AAGGTC CAC   TGGGTCCCTT
                                   G   ___
GAM1867  LOC219722 3'  TTCCAGTGTCCCCAGGGA    45959      GA    TA
                                TTCCA  GTGTT  TCCAGGGA
                                |||||  |||||  ||||||||
                                AAGGT  CACAG  GGGTCCCT
                                       __    __
GAM1867  LOC255045 3'  AGAATGCTGCTAGGGAAA    45935         TATCC
                                AGAGTGTT     AGGGAAA
                                ||||||||     |||||||
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                                TCTTACGA    TCCCTTT
                                    CGA__
GAM1867  LOC256520 3'  GAGTGTTTACAAAGAAA    45960        TC
                                GAGTGTTTA  CAGGGAAA
                                |||||||||  ||||||||
                                CTCACAAAT  GTTTCTTT
                                    __
GAM1867  LOC89919  3'  TTCCAGAGATGTTTAGACTTGG 45961       _    TCCA_
           G                     TTCCAGAG TGTTTA    GGG
                                |||||||| ||||||    |||
                                AAGGTCTC ACAAAT    CCC
                                    T     CTGAA
GAM1867  LOC90019  3'  TTCCAAAGTCGAACTCCAGGGA 45962        GTTTA
                                TTCCAGAGT    TCCAGGGA
                                |||||||||    ||||||||
                                AAGGTTTCA    AGGTCCCT
                                     GCTTG
GAM1868  APXL     3'  GCTGTTTGTTTTCTTACTAT   45965     A   ATAAA
                                GCTG TTGT    TTTACTAT
                                |||| ||||    ||||||||
                                CGAC AACA    GAATGATA
                                  A   AAA__
GAM1868  BTN2A2   3'  AAGCTGATTGTGTAACTC    45966         ATA
                                AAGCTGATTGT   AATTT
                                ||||||||||   |||||
                                TTCGACTAACA   TTGAG
                                     CA_
GAM1868  FLJ10922 3'  GCTGATCCAAATTTACT     45967       GTA
                                GCTGATT   TAAATTTACT
                                |||||||   ||||||||||
                                CGACTAG   GTTTAAATGA
                                   ___
GAM1868  KIAA1724 3'  AACTGGCTACAAATTTACT   45968      ATTG
                                AGCTG   TATAAATTTACT
                                |||||   ||||||||||||
                                TTGAC   ATGTTTAAATGA
                                  CG__
GAM1868  MGC2835  3'  AAGCTGATTGATGTAAAT    45969        TA_
                                AAGCTGATTG   TAAAT
                                |||||||||   |||||
                                TTCGACTAAC   ATTTA
                                     TAC
GAM1868  PPP2R3A  5'  GCTCTCATAAATTTACTAT   45970    GATTG
                                GCT    TATAAATTTACTAT
                                |||    ||||||||||||||
                                CGA    GTATTTAAATGATA
                                  GA___
GAM1868  LOC222134 5'  AAGCTGATTGTGTCAATCT   45971         ATA
                                AAGCTGATTGT   AATTT
                                ||||||||||   |||||
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                                TTCGACTAACA  TTAGA
                                     CAG
GAM1868 LOC84549 3' TGATTATAATTTACTA     45972        TAA
                                TGATTGTA  ATTTACTA
                                ||||||||  ||||||||
                                ACTAATAT  TAAATGAT
                                    ___
GAM1869 DRF1    5' TATTACATTCGCGAGCTCCAT 45975       C  A  _  A
                                TATTACA TC CG GC TTCGT
                                ||||||| || || || |||||
                                ATAATGT AG GC CG AGGTA
                                   A  C  T  _
GAM1869 PRO1600  3' TATTACATTGATGGCATTCA  44122       CTCAC
                                TATTACA    GGCATTCG
                                |||||||    ||||||||
                                ATAATGT    CCGTAAGT
                                   AACTA
GAM1870 BAK1    5' TGGAGATGGAGGTCCCGAGG  45978       AT  GG  A
                                TGGAGATG  GGT  CCC GAGG
                                ||||||||  |||  ||| ||||
                                ACCTCTAC  CCA  GGG CTCC
                                    CT  __  _
GAM1870 CAPN5    3' ATGCAGATGGTGGTGGGAACGG 45979    G    A    CCCAGA
                                ATG AGATG TGGTGG     GG
                                ||| ||||| ||||||     ||
                                TAC TCTAC ACCACC     CC
                                  G    C     CTTG__
GAM1870 CYP46    3' TGAAGGGTGGCCCAGG      45980      ATGAT       A
                                TGGAG    GGTGGCCCAG G
                                |||||    |||||||||| |
                                ACTTC    CCACCGGGTC C
                                   _____       _
GAM1870 DYRK1A   3' ATGGTGGTGGTGGTGGTGATGG 45981     AGA  A    CCCA  _
                                ATGG   TG TGGTGG   GA GG
                                ||||   || ||||||   || ||
                                TACC   AC ACCACC   CT CC
                                  ACC  C     A___  A
GAM1870 GSTT1    3' TGGGGATGGTGGCTTCGGGAGG 45982    AGAT       CCA__
                                TGG   GATGGTGGC    GAGG
                                |||   |||||||||    ||||
                                ACC   CTACCACCG    CTCC
                                  C___        AAGCC
GAM1870 HYOU1    3' TGGAGATGAATGGGGAAAACAG 45983         _  T  CC__
            AGG                   TGGAGATGA TGG GG   CAGAGG
                                |||||||||| ||| ||   ||||||
                                ACCTCTACT ACC CC   GTCTCC
                                     T  _  TTTT
GAM1870 IL1RN    3' TGGAGATGGAGCTTGGAG    45984       TGA  T  CCA
                                TGGAGA  TGG GGC  GAG
                                ||||||  ||| |||  |||
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                                ACCTCT  ACC TCG  CTC
                                   ___  _  AAC
GAM1870 LENG4    5' GGAGGGTGGCCCAGAG     45985     ATGAT
                                GGAG   GGTGGCCCAGAG
                                ||||   ||||||||||||
                                CCTC   CCACCGGGTCTC
                                  _____
GAM1870 LIF      3' ATGGGGACGATGGGGA     45986     A      T  CCCAG
                                ATGG GATGATGG GG    A
                                |||| |||||||| ||    |
                                TACC CTGCTACC CC    T
                                  C      _ _____
GAM1870 MAP3K7IP1 3' GGAGGTGATGGTGGGAG    45987     A       CCCA
                                GGAG TGATGGTGG   GAG
                                |||| |||||||||   |||
                                CCTC ACTACCACC   CTC
                                  C      ____
GAM1870 MMP19    3' TGGGTGGTGGAGCCTCAGGG  45988    AGA  A  T  _  A
                                TGG  TG TGG GGCC CAG GG
                                |||  || ||| |||| ||| ||
                                ACC  AC ACC TCGG GTC CC
                                  C__  C  _   A  _
GAM1870 MMP19    3' TGGGTGGTGGAGCCTCAGGG  45988    AGA  A  T  _  A
                                TGG  TG TGG GGCC CAG GG
                                |||  || ||| |||| ||| ||
                                ACC  AC ACC TCGG GTC CC
                                  C__  C  _   A  _
GAM1870 MMP19    3' TGGGTGGTGGAGCCTCAGGG  45988    AGA  A  T  _  A
                                TGG  TG TGG GGCC CAG GG
                                |||  || ||| |||| ||| ||
                                ACC  AC ACC TCGG GTC CC
                                  C__  C  _   A  _
GAM1870 MMP19    3' TGGGTGGTGGAGCCTCAGGG  45988    AGA  A  T  _  A
                                TGG  TG TGG GGCC CAG GG
                                |||  || ||| |||| ||| ||
                                ACC  AC ACC TCGG GTC CC
                                  C__  C  _   A  _
GAM1870 MSN      3' TGGGGGGTGGTGGCCAGGG  45989    AGATGA     C  A
                                TGG    TGGTGGCC AG GG
                                |||    |||||||| || ||
                                ACC    ACCACCGG TC CC
                                  CCCC__      _ _
GAM1870 PMX1     3' TGGTGGTGGTATCCCAGAGG  45990    A    ___
                                TG TGGTGG  CCCAGAGG
                                ||  ||||||  ||||||||
                                AC ACCACC  GGGTCTCC
                                  C    ATA
GAM1870 PMX1     3' TGGTGGTGGTATCCCAGAGG  45990    A    ___
                                TG TGGTGG  CCCAGAGG
                                ||  ||||||  ||||||||
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                                AC ACCACC   GGGTCTCC
                                 C     ATA
GAM1870 RORA     5' TGGAGAATGATGGGGAG    45991       TG     CCCA
                                TGGAGA  ATGGTGG   GAG
                                ||||||  |||||||   |||
                                ACCTCT  TACTACC   CTC
                                   __      C___
GAM1870 RORA     5' TGGAGAATGATGGGGAG    45991       TG     CCCA
                                TGGAGA  ATGGTGG   GAG
                                ||||||  |||||||   |||
                                ACCTCT  TACTACC   CTC
                                   __      C___
GAM1870 SEPN1    3' ATGGAGGGTTCTGCCCAGAGG 45992       ATGAT  G__
                                ATGGAG    GGT   GCCCAGAGG
                                ||||||    |||   |||||||||
                                TACCTC    CCA   CGGGTCTCC
                                   _____  AGA
GAM1870 SLC25A5  3' ATGGAAATGGCTTTAGAG    45993      GAT    GGCCC
                                ATGGA   GATGGT    AGAG
                                |||||   ||||||    ||||
                                TACCT   TTACCG    TCTC
                                   ___     AAA__
GAM1870 UNC13    3' ATGGAGATGGGTAGA      45994        AT   GGCCC
                                ATGGAGATG  GGT    AGA
                                |||||||||  |||    |||
                                TACCTCTAC  CCA    TCT
                                   __  _____
GAM1870 WHSC1    3' TGCAGATGATGCTGTTGGAGG 45995    G      G  GCCCA
                                TG AGATGATG TG    GAGG
                                || ||||||||  ||    ||||
                                AC TCTACTAC AC    CTCC
                                 G      G  AAC__
GAM1870 WHSC1    3' TGCAGATGATGCTGTTGGAGG 45995    G      G  GCCCA
                                TG AGATGATG TG    GAGG
                                || ||||||||  ||    ||||
                                AC TCTACTAC AC    CTCC
                                 G      G  AAC__
GAM1870 WHSC1    3' TGCAGATGATGCTGTTGGAGG 45995    G      G  GCCCA
                                TG AGATGATG TG    GAGG
                                || ||||||||  ||    ||||
                                AC TCTACTAC AC    CTCC
                                 G      G  AAC__
GAM1870 BTBD3    3' GGGGAAGAAGTGGCCCAGAGG 45996    A  T  T
                                GG GA GA GGTGGCCCAGAGG
                                || || || ||||||||||||
                                CC CT CT TCACCGGGTCTCC
                                 C  T  _
GAM1870 C1orf16  3' ATGGAGATGGGGCAGGAG    45997        AT  TG CCCA
                                ATGGAGATG  GG  G   GAG
                                |||||||||  ||  |   |||
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                                TACCTCTAC  CC  C    CTC
                                     C_  GT _____
GAM1870  C5orf4    5'  GGAGATGGTGGTGATGATGAGG 45998        A     CCCA
                                GGAGATG TGGTGG    GAGG
                                ||||||| ||||||    ||||
                                CCTCTAC ACCACT    CTCC
                                    C     ACTA
GAM1870  C5orf4    3'  GGAGATGGTGGTGATGATGAGG 45998        A     CCCA
                                GGAGATG TGGTGG    GAGG
                                ||||||| ||||||    ||||
                                CCTCTAC ACCACT    CTCC
                                    C     ACTA
GAM1870  CRK7      3'  ATGTGAGATGGTGGAGAG    45999     GA  T      CCC
                                ATG  GA GATGGTGG   AGAG
                                |||  || ||||||||   ||||
                                TAC  CT CTACCACC   TCTC
                                  A_  _      ____
GAM1870  DKFZP434M131 3'  TGGTGATGGTGGCTGGAG    46000     AGA        CCA
                                TGG   TGATGGTGGC   GAG
                                |||   ||||||||||   |||
                                ACC   ACTACCACCG   CTC
                                  ____        AC_
GAM1870  EPS15R    3'  GGAGTGGGGTGGCCCGGAGG   46001     A  AT      A
                                GGAG TG  GGTGGCCC GAGG
                                |||| ||  |||||||| ||||
                                CCTC AC  CCACCGGG CTCC
                                   _  C_       C
GAM1870  FBH1      5'  TGGAGATGGCCCAGG       46002        TGATGG       A
                                TGGAGA     TGGCCCAG G
                                ||||||     |||||||| |
                                ACCTCT     ACCGGGTC C
                                     _______       _
GAM1870  FLJ00058  5'  TGGAGATGGATGCGTGGCCTGG 46003          _  _     CA
              AGG                    TGGAGATG ATG GTGGCC  GAGG
                                |||||||| ||| ||||||  ||||
                                ACCTCTAC TAC CACCGG  CTCC
                                     C  G     AC
GAM1870  FLJ10044  3'  TGGAGGTGGCTCCCAGAGG   46004      ATGA   GG
                                TGGAG   TGGT  CCCAGAGG
                                |||||   ||||  ||||||||
                                ACCTC   ACCG  GGGTCTCC
                                   C____   A_
GAM1870  FLJ11198  3'  TGGCCTACATGGTGGCCCAGGG 46005     AGATG         A
                                TGG    ATGGTGGCCCAG GG
                                |||    |||||||||||| ||
                                ACC    TACCACCGGGTC CC
                                  GGATG          _
GAM1870  FLJ13612  3'  ATGGAGATGCTGGCTCAGGGAG 46006          A   GGCCCA
              G                    ATGGAGATG TGGT     GAGG
                                |||||||| ||||     ||||
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                                TACCTCTAC ACCG     CTCC
                                     G   AGTCC_
GAM1870 FLJ21432 3' TGGGTGACTGCACCCAGAGG  46007    AGA   G  G
                                TGG  TGAT GTG CCCAGAGG
                                |||  |||| ||| ||||||||
                                ACC  ACTG CGT GGGTCTCC
                                  C__   A  _
GAM1870 FLJ25449 5' ATGGTGATGGTGGAGGTAGAGG 46008     AGA       CCC_
                                ATGG  TGATGGTGG   AGAGG
                                ||||  |||||||||   |||||
                                TACC  ACTACCACC   TCTCC
                                  ___       TCCA
GAM1870 KIAA0455 3' ATGGCGGTGGTGGTGAGAAG  46009     AGA A    CCC
                                ATGG  TG TGGTGG   AGAGG
                                ||||  || ||||||   |||||
                                TACC  GC ACCACC   TCTTC
                                  ___ C     AC_
GAM1870 KIAA0596 3' TGAAGGACCTGGCCCAGAGG  46010     AT   GG
                                TGGAG  GAT  TGGCCCAGAGG
                                |||||  |||  ||||||||||
                                ACTTC  CTG  ACCGGGTCTCC
                                   __  G_
GAM1870 KIAA0637 3' TGGAGATGCTGAAGCGGAGG  46011       A  T  CCA
                                TGGAGATG TGG GGC   GAGG
                                |||||||| ||| |||   ||||
                                ACCTCTAC ACT TCG   CTCC
                                     G  _  C__
GAM1870 KIAA0876 3' TGGGGAAGGCTCCCCAGAGG  46012    A  TGAT   GG
                                TGG GA   GGT  CCCAGAGG
                                ||| ||   |||  ||||||||
                                ACC CT   CCG  GGGTCTCC
                                  C  T___  AG
GAM1870 KIAA1045 3' TGGGGCATGTGGCCCAGAGG  46013    AGATGATG
                                TGG      GTGGCCCAGAGG
                                |||      ||||||||||||
                                ACC      CACCGGGTCTCC
                                  CCGTA___
GAM1870 KIAA1280 5' ATGGAGATGGTGTGTGCAG   46014       ATG   GCC
                                ATGGAGATG  GTG  CAG
                                |||||||||  |||  |||
                                TACCTCTAC  CAC  GTC
                                     CA_  AC_
GAM1870 MGC3036  3' TGGAGGGATGGTGGGGAG    46015     AT      CCCA
                                TGGAG  GATGGTGG   GAG
                                |||||  ||||||||   |||
                                ACCTC  CTACCACC   CTC
                                   C_      C___
GAM1870 MGC4093  3' TGTGGATGGTGGTGACGTTGGA 46016   GA   A     CCA_
            GG                    TG  GATG TGGTGGC   GAGG
                                ||  |||| |||||||   ||||
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                                AC  CTAC ACCACTG    CTCC
                                 AC    C      CAAC
GAM1870  PURB     3'  GGGGATGGTGGTTGGGTGGAGG 46017    A    A    _  CCCA
                                GG GATG TGGT GG    GAGG
                                || |||| |||| ||    ||||
                                CC CTAC ACCA CC    CTCC
                                 C    C    A  CAC_
GAM1870  RFX3     5'  ATGGAGATGGTGGTGGTGGGGA 46018         A     CCCA
              GG                   ATGGAGATG TGGTGG    GAGG
                                |||||||||| ||||||    ||||
                                TACCTCTAC ACCACC    CTCC
                                     C     ACCC
GAM1870  RFX3     5'  ATGGAGATGGTGGTGGTGGGGA 46018         A     CCCA
              GG                   ATGGAGATG TGGTGG    GAGG
                                |||||||||| ||||||    ||||
                                TACCTCTAC ACCACC    CTCC
                                     C     ACCC
GAM1870  SIMRP7   3'  TGGAGAGGTAGAGCCCCAGAGG 46019       TGAT    ___
                                TGGAGA    GGTGG   CCCAGAGG
                                ||||||    |||||   ||||||||
                                ACCTCT    CCATC   GGGTCTCC
                                    ____     TCG
GAM1870  SPBPBP   3'  ATGGGGATGGAGGTAGAG    46020      AGAT     T  CCC
                                ATGG    GATGG GG   AGAG
                                ||||    ||||| ||   ||||
                                TACC    CTACC CC   TCTC
                                  C___     T  A__
GAM1870  ZIC4     5'  TGGAGGTGGTGGTGGTTCTGCC 46021    A  A     C________  AGA
              TCTGG                  AG TG TGGTGG       CC   GG
                                || || ||||||       ||   ||
                                TC AC ACCACC       GG   CC
                                 C  C     AAGACIII  AGA
GAM1870  LOC116143 3'  TGGAGGCTGGCCCAGAG     46022      GATGAT  _
                                TGGA     GG TGGCCCAGAG
                                ||||     || ||||||||||
                                ACCT     CC ACCGGGTCTC
                                  _______  G
GAM1870  LOC127435 3'  GAGACTGTGGTGGTTTGGAGG  46023      GA     CCCA
                                GAGAT  TGGTGG    GAGG
                                |||||  ||||||    ||||
                                CTCTG  ACCACC    CTCC
                                   AC     AAAC
GAM1870  LOC127845 5'  TGGAGCGTGGCCCAGAG     46024      ATGATG
                                TGGAG     GTGGCCCAGAG
                                |||||     ||||||||||
                                ACCTC     CACCGGGTCTC
                                   G_____
GAM1870  LOC145826 5'  TGGAGATGACCAGACTCCAGGG 46025          GGT   _    A
                                TGGAGATGAT   GGC CCAG GG
                                ||||||||||   ||| |||| ||
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                                ACCTCTACTG   CTG GGTC CC
                                      GT_   A    _
GAM1870  LOC146227 5'  TGGTGATGATGGTGGTG     46026     A         CCCAGA
                                TGG GATGATGGTGG      G
                                ||| ||||||||||      |
                                ACC CTACTACCACC      C
                                  A         A_____
GAM1870  LOC146237 3'  GGAGATGGCCCCACCCAGAGG  46027       TGA    G__
                                GGAGA   TGGT   GCCCAGAGG
                                |||||   ||||   |||||||||
                                CCTCT   ACCG   TGGGTCTCC
                                   ___    GGG
GAM1870  LOC150333 5'  ATGGTGATGATGGAGA      46028      A       TGGCCC
                                ATGG GATGATGG      AGA
                                |||| ||||||||      |||
                                TACC CTACTACC      TCT
                                  A       _______
GAM1870  LOC151429 5'  TGGAAATGCAGGCCTAGGG    46029         ATGGT    C  A
                                TGGAGATG     GGCC AG GG
                                ||||||||     |||| || ||
                                ACCTTTAC     CCGG TC CC
                                     GT___    A  _
GAM1870  LOC151719 5'  TGGTGATGGTGGTGGTAGTAGA 46030     A    A     CCC_
            GG                    TGG GATG TGGTGG    AGAGG
                                ||| |||| ||||||    |||||
                                ACC CTAC ACCACC    TCTCC
                                  A   C      ATCA
GAM1870  LOC157349 3'  TGGAGATGAGGGGCTTAGAGG  46031         T  T   CC
                                TGGAGATGA GG GGC  AGAGG
                                ||||||||| || |||  |||||
                                ACCTCTACT CC CCG  TCTCC
                                     _  _   AA
GAM1870  LOC157931 3'  ATGGGGGATGGTGGCAAGTGG  46032      AGAT        CC  A
                                ATGG    GATGGTGGC  AG GG
                                ||||    |||||||||  || ||
                                TACC    CTACCACCG  TC CC
                                  CC__         T_  A
GAM1870  LOC158147 3'  TGGTGATGGTGGCTGGAG    46000     AGA         CCA
                                TGG   TGATGGTGGC   GAG
                                |||   ||||||||||   |||
                                ACC   ACTACCACCG   CTC
                                  ___          AC_
GAM1870  LOC165904 3'  ATGGAGATGGTGATGAAGGG   46033         A     CCC  A
                                ATGGAGATG TGGTGG   AG GG
                                ||||||||| ||||||   || ||
                                TACCTCTAC ACTACT   TC CC
                                     C     ___  _
GAM1870  LOC196955 5'  GGAGGTGATGGTGGTGCC    46034      A        C_____
                                GGAG TGATGGTGG     CC
                                |||| |||||||||     ||
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                                CCTC ACTACCACC    GG
                                  C       ACIII
GAM1870  LOC221463 3'  TGGTCCTGGTGGCCCAGGG   46035    AGATGA        A
                                TGG     TGGTGGCCCAG GG
                                |||     |||||||||||| ||
                                ACC     ACCACCGGGTC CC
                                  AGG___        _
GAM1870  LOC253148 5'  TGGTGATGGTGGTGGTGATGG  46036    A   A     CCCA  _
                                TGG GATG TGGTGG   GA GG
                                ||| |||| ||||||   || ||
                                ACC CTAC ACCACC   CT CC
                                  A   C     A___ A
GAM1870  LOC253148 5'  TGGTGGTGATGGTGGTGATGGG 46037    AGA       CCCA__
             AGG                  TGG   TGATGGTGG     GAGG
                                |||   |||||||||     ||||
                                ACC   ACTACCACC     CTCC
                                  ACC       ACTACC
GAM1870  LOC255473 5'  TGGGGATGGTGGTGGAG    46038    A   A     CCCAG
                                TGG GATG TGGTGG    AG
                                ||| |||| ||||||    ||
                                ACC CTAC ACCACC    TC
                                  C   C    _____
GAM1870  LOC255622 3'  GAGAGATGACCCAGAG     46039     TGAT
                                GAGA   GGTGGCCCAGAG
                                ||||   ||||||||||||
                                CTCT   CTACTGGGTCTC
                                  ____
GAM1870  LOC90249  5'  TGGTGGTGGTGGTGCTGAGG  46040    AGA  A    CCCA
                                TGG   TG TGGTGG   GAGG
                                |||   || ||||||   ||||
                                ACC   AC ACCACC   CTCC
                                  ___ C     ACGA
GAM1871  ASPH     3'  CAATTATTTCTGAGCCCA    44758          ATTAT
                                CGATTATTTCTGA    TCCA
                                ||||||||||||    ||||
                                GTTAATAAAGACT    GGGT
                                       C____
GAM1871  ASPH     3'  CAATTATTTCTGAGCCCA    44758          ATTAT
                                CGATTATTTCTGA    TCCA
                                ||||||||||||    ||||
                                GTTAATAAAGACT    GGGT
                                       C____
GAM1871  CDK10    5'  ACGCTTATTTCTGGGTGTCCAA 44759    A       AATTAT
                                ACG TTATTTCTG     TCCAA
                                ||| |||||||||     |||||
                                TGC AATAAAGAC     AGGTT
                                  G       CCAC__
GAM1871  KLHL3    3'  TTATTTCTGGACATTCC     44760         AAT
                                TTATTTCTG   TATTCC
                                |||||||||   ||||||
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                                AATAAAGAC   GTAAGG
                                     CT_
GAM1871  NMB      3'  CGATATTTCTGGTGACCCA   44761      T      AATTAT
                                CGAT ATTTCTG     TCCA
                                |||| |||||||     ||||
                                GCTA TAAAGAC     GGGT
                                  _      CACT__
GAM1871  TLL2     3'  ATTATTTAAAAATTATTCCAA  44428        CT
                                ATTATTT  GAATTATTCCAA
                                |||||||  ||||||||||||
                                TAATAAA  TTTAATAAGGTT
                                    TT
GAM1871  ZNF215   3'  AATTATTTACCCTGTTATTCCA 44429         _ GAA
                                GATTATTT CT   TTATTCCA
                                |||||||| ||   ||||||||
                                TTAATAAA GG   AATAAGGT
                                     T  GAC
GAM1871  MGC15875 3'  GACATCTGGGTTATTCCAA   44762     TATT   AA
                                GAT   TCTG  TTATTCCAA
                                |||   ||||  |||||||||
                                CTG   AGAC  AATAAGGTT
                                  T___   CC
GAM1871  PTPN3    3'  CGGGTGAATCTGAATTGTTCCA 44763    ATTATT       A
                                CG     TCTGAATT TTCCA
                                ||     |||||||| |||||
                                GC     AGACTTAA AAGGT
                                 CCACTT       C
GAM1871  RAB6C    3'  CGTTATTTCTGCTAATTC    44764    A       AATT
                                CG TTATTTCTG    ATTC
                                || |||||||||    ||||
                                GC AATAAAGAC    TAAG
                                 _       GAT_
GAM1871  RABEX5   3'  ACAATTATAAAATTATTCCAA  44431        TTCT
                                ACGATTAT    GAATTATTCCAA
                                ||||||||    ||||||||||||
                                TGTTAATA    TTTAATAAGGTT
                                     T___
GAM1871  LOC200471 5' GATTATTTCCTGATCTCCAA   44433         GA   AT
                                GATTATTTCT  ATT  TCCAA
                                ||||||||||  |||  |||||
                                CTAATAAAGG  TAG  AGGTT
                                      AC   __
GAM1871  LOC205251 5' GATTCACTGATTATTCCAA    44765     ATTT    A
                                GATT    CTGA TTATTCCAA
                                ||||    |||| |||||||||
                                CTAA    GACT AATAAGGTT
                                  GT__    _
GAM1872  DRF1     5'  TATTACATTCGCGAGCTCCAT  45975        C  A  _  A
                                TATTACA TC CG GC TTCGT
                                ||||||| || || || |||||
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                                ATAATGT AG GC CG AGGTA
                                    A  C  T  _
GAM1872  PRO1600  3'  TATTACATTGATGGCATTCA  44122       CTCAC
                                TATTACA    GGCATTCG
                                |||||||    ||||||||
                                ATAATGT    CCGTAAGT
                                    AACTA
GAM1873  AKR1B1   5'  GCCCAGTACGGTGCGGCCTTCG 46045    GA__  _ C_______  TTC
           GAGAACCC                TA   GCG C      GGG   TCC
                                ||   ||| |      |||   |||
                                AT   CGC G      CCT   GGG
                                 GCCA   C GAAGIII   CTT
GAM1873  MLLT2    5'  GCCCGGGGAGCGCCGCGTCC   46046      AGTA       G
                                GCCC    GAGCGCCG GTTC
                                ||||    |||||||| ||||
                                CGGG    CTCGCGGC CAGG
                                  CCC_      G
GAM1873  NOX4     5'  ACCCAGAGCCGGGTTTTC     46047       TAGAGC       C
                                GCCCAG     GCCGGGTT TC
                                ||||||     |||||||| ||
                                TGGGTC     CGGCCCAA AG
                                   T_____       A
GAM1873  PODXL    3'  GCCCAGAGCCTCTCCGGGTTCT 46048       T  AGCG_
           CC                    GCCCAG AG    CCGGGTTCTCC
                                |||||| ||    ||||||||||
                                CGGGTC TC    GGCCCAAGAGG
                                   _ GGAGA
GAM1873  PPP1R12B 3'  GCCCAGTAGGCTGCTATCT   46049         A  _  CGGGT
                                GCCCAGTAG GC GC    TCT
                                ||||||||| || ||    |||
                                CGGGTCATC CG CG    AGA
                                     _  A  AT___
GAM1873  TOP1     3'  GCCTGGTAGAACGCTGACAAAT 46050     CA       ___
           TCC                    GCC  GTAGAGCGC   CGGGTTCT
                                |||  |||||||||   ||||||||
                                CGG  CATCTTGCG   GTTTAAGG
                                  AC        ACT
GAM1873  UCP3     3'  GCCCAGCAGGGCTTCT      46051          AGCGCC  G
                                GCCCAGTAG     GG TTCT
                                |||||||||     || ||||
                                CGGGTCGTC     CC AAGA
                                     _______ G
GAM1873  ZNF266   5'  CCAGTAAAGTCCATTCT     46052         CG  GG
                                CCAGTAGAG  CC  GTTCT
                                |||||||||  ||  |||||
                                GGTCATTTC  GG  TAAGA
                                     A_  __
GAM1873  DKFZp434G179 3'  AGTAGAGCATATTTTTTGGAGA 46053        CC__________  TTC
           ACCC                    TAGAGCG         GGG   TCC
                                |||||||         |||   |||
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                                ATCTCGT         CCT   GGG
                                    ATAAAAAAIII   CTT
GAM1873  DKFZP547L112 3'  GTGGAGCAAGAGTTCTCC    46054    A    CC
                                GT GAGCG  GGGTTCTCC
                                || |||||  |||||||||
                                CA CTCGT  CTCAAGAGG
                                 C    T_
GAM1873  DKFZP586A011 3'  GCCCAGTAGAGGCTGCTGGAGA 46055         C  C_______  TTC
           C                     CCCAGTAGAG GC      GGG   T
                                ||||||||||  ||      |||   |
                                GGGTCATCTC CG      CCT   G
                                      _ ACGAIII   CTT
GAM1873  FLJ12056  3'  AGTAGAGATGGGGTTCTCC   46056       CGCC
                                AGTAGAG   GGGTTCTCC
                                |||||||   |||||||||
                                TCATCTC   CCCAAGAGG
                                    TAC_
GAM1873  FLJ14427  3'  GCCTAGATCCTCTGGGTTCTCC 46057    CAG   GCGCC_
                                GCC   TAGA     GGGTTCTCC
                                |||   ||||     |||||||||
                                CGG   ATCT     CCCAAGAGG
                                  ___    AGGAGA
GAM1873  FLJ14721  5'  CCCAGTGGGGTGCGCTCTGGAG 46058     AGA__   C_____  TTC
           AACC                  CAGT    GCGC     GGG   TC
                                ||||    ||||     |||   ||
                                GTCA    CGCG     CCT   GG
                                  CCCCA    AGAIII   CTT
GAM1873  FLJ20152  5'  ACCCAGTAGAGACGTTCT    46059         C  CGG
                                GCCCAGTAGAG GC   GTTCT
                                ||||||||||| ||   |||||
                                TGGGTCATCTC TG   CAAGA
                                      _ ___
GAM1873  FLJ20511  3'  CCTCAGGGGCCGGGTTTTC   46060   _   TAGAGC      C
                                CC CAG     GCCGGGTT TC
                                || |||     |||||||| ||
                                GG GTC     CGGCCCAA AG
                                 A   CC____       A
GAM1873  FLJ21709  3'  CCAGTAGAGTCTCCAGGCTCT  46061        CG_
                                CCAGTAGAG   CCGGGTTCT
                                |||||||||   |||||||||
                                GGTCATCTC   GGTCCGAGA
                                     AGA
GAM1873  GALNT12   3'  GCTTAGTAAAGCAAATTGTTCT 46062    CC       CCGG
           C                    GC  AGTAGAGCG   GTTCTC
                                ||  |||||||||   ||||||
                                CG  TCATTTCGT    CAAGAG
                                 AA       TTAA
GAM1873  HPCAL4    3'  GCCCAGTAGAGCTTGGGACC   46063          GCC   TT
                                GCCCAGTAGAGC   GGG  C
                                ||||||||||||   |||  |
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                              CGGGTCATCTCG  CCC  G
                                    AA_  TG
GAM1873 KIAA0557 3' GCACAGTAGGGCGCCGGGCC  46064   C    A
                              GC CAGTAG GCGCCGGGTT
                              || |||||| ||||||||||
                              CG GTCATC CGCGGCCCGG
                               T    C
GAM1873 KIAA0937 3' GCTCAGTGGGATGCAGGCTCT 46065   C   A_ GC  C
                              GC CAGT  GA  GC GGGTTCT
                              || ||||  ||  || |||||||
                              CG GTCA  CT  CG TCCGAGA
                               A   CC  A_  _
GAM1873 KIAA1196 3' GCCCAGTGGGGCCCCTTCTCC 46066       AGA  G  GGG
                              GCCCAGT  GC CC  TTCTCC
                              |||||||  || ||  ||||||
                              CGGGTCA  CG GG  AAGAGG
                                  CCC  G  ___
GAM1873 KIAA1280 5' CCAGCCCCGCCGGGTTCT   46067     AGAG
                              CCAGT   CGCCGGGTTCT
                              |||||   ||||||||||
                              GGTCG   GCGGCCCAAGA
                                GG__
GAM1873 KIAA1884 3' GCCCAGCAGAGTGCTGGGT  46068         C  C
                              GCCCAGTAGAG GC GGGT
                              |||||||||| || ||||
                              CGGGTCGTCTC CG CCCA
                                    A  A
GAM1873 MGC8407  5' GCTCAGCGGGGCGCCGAGGGCT 46069   C   AGA     TT
          CC                   GC CAGT  GCGCCGGG  CTCC
                              || ||||  ||||||||  ||||
                              CG GTCG  CGCGGCTC  GAGG
                               A   CCC      CC
GAM1873 NMES1   5' GCCTGGTGGGCGCCAAACCGTC 46070    CA  AGA    GG TC
          C                    GCC  GT  GCGCCG  T  TCC
                              ||| ||  ||||||  |  |||
                              CGG  CA  CGCGGT  G  AGG
                                AC  CC_    TT GC
GAM1873 PDE4DIP  5' GCCCAGTGGGGTCCCC     46071      AGAGCGCC
                              GCCCAGT      GGGTTCTC
                              |||||||      ||||||||
                              CGGGTCA      CCCAGGGG
                                  C_______
GAM1873 TRF4-2   5' CCAGAGGGGTAGGTTCTCC   46072    T  AGCGCC
                              CCAG AG     GGGTTCTCC
                              |||| ||     |||||||||
                              GGTC TC     TCCAAGAGG
                                _  CCCA__
GAM1873 LOC120856 3' GCCCAGTAAAGCTGACGTTTTT 46073          GC_  GG_
          C                    GCCCAGTAGAGC  CG  TTC
                              ||||||||||||  ||  |||
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                                CGGGTCATTTCG  GC  AAG
                                      ACT  AAA
GAM1873  LOC124512 5'  GCCCAGTAGGGCGTCGTTGG  46074       A  C _____
                                GCCCAGTAG GCG CG    GG
                                ||||||||| ||| ||    ||
                                CGGGTCATC CGC GC    CC
                                    C  A  AAIII
GAM1873  LOC136319 3'  CCCAGTAGAGTGCATTCT   46075        C  CGG
                                CCCAGTAGAG GC  GTTCT
                                |||||||||| ||  |||||
                                GGGTCATCTC CG  TAAGA
                                      A  ___
GAM1873  LOC136442 3'  GCACGGTGGAGCGCCAGCGTC  46076   CCA  A      _
                                GC  GT GAGCGCCGG GTT
                                ||  || ||||||||| |||
                                CG  CA CTCGCGGTC CAG
                                 TGC  C       G
GAM1873  LOC157740 5'  GCCTGTGGAGAGGGGTTCTC  46077    CA  A  CGCC
                                GCC  GT GAG   GGGTTCTC
                                |||  || |||   ||||||||
                                CGG  CA CTC   CCCAAGAG
                                 A_  C  TC__
GAM1873  LOC158292 5'  CCCAGTCCCGGGTTCTC    46078      AGAGCG
                                CCCAGT    CCGGGTTCTC
                                ||||||    ||||||||||
                                GGGTCA    GGCCCAAGAG
                                   G_____
GAM1873  LOC202934 3'  GCCCTAGTAGAGGTTCTC   46079    _    GCGCCG
                                GCCC AGTAGA    GGTTCTC
                                |||| ||||||    |||||||
                                CGGG TCATCT    CCAAGAG
                                  A    _______
GAM1873  LOC203078 5'  GCCCAGTAGAAGCGTCGCTGGA 46080       _  C _____  TTCT
           GAC                  CCAGTAGA GCG CG    GG   C
                                |||||||| ||| ||    ||   |
                                GGTCATCT CGC GC    CC   G
                                     T  A  GAIII  TCTT
GAM1873  LOC254100 5'  GCCCAGTACAGCGCTATTC   46081       G   CGG
                                GCCCAGTA AGCGC  GTTC
                                |||||||| |||||  ||||
                                CGGGTCAT TCGCG  TAAG
                                     G   A__
GAM1873  LOC254556 3'  CAGGTGGGCCAGGTTCTCC   46082    TAGAGC
                                CAG    GCCGGGTTCTCC
                                |||    ||||||||||||
                                GTC    CGGTCCAAGAGG
                                 CACC__
GAM1873  LOC91759  3'  CCAGTGGAGGCTGGATCC    46083     A  C  C
                                CCAGT GAG GC GGGTTC
                                ||||| ||| || ||||||
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                                GGTCA CTC CG CCTAGG
                                  C  _ A
GAM1873 LOC93134 3' CCAGTAGAGGCTTCCGGAGAC 46084        C C_____ TTC
                                CCAGTAGAG GC      GGG  T
                                ||||||||| ||      |||  |
                                GGTCATCTC CG      CCT  G
                                     _ AAGGIII  CTT
GAM1874 CUL3    3' GTGGTAGAATACAGCATGC  46087    A      A GG
                                GTG TAGAATACG TA GC
                                ||| ||||||||| ||  ||
                                CAC ATCTTATGT GT  CG
                                  C       C A_
GAM1874 HLF     3' TGTGTCAGTGATAGGGC    46088    A  AATAC
                                TGTG TAG    GATAGGGC
                                |||| |||    ||||||||
                                ACAC GTC    CTATCCCG
                                  A  A____
GAM1874 JRK     3' TGTGGGGAGAAACAGGGCC  46089    AT_  ATAC
                                TGTG  AGA   GATAGGGCC
                                ||||  |||   |||||||||
                                ACAC  TCT   TTGTCCCGG
                                  CCC  ____
GAM1874 PRPSAP1  3' TGGATAGTAATAGGGC    46090    T    AATAC
                                TG GATAG    GATAGGGC
                                || |||||    ||||||||
                                AC CTATC    TTATCCCG
                                 _    A____
GAM1874 SLC25A5  3' TGTTATAGAATACAACATGCC 46091    G         GG
                                TGT ATAGAATACGATA  GCC
                                ||| ||||||||||||  |||
                                ACA TATCTTATGTTGT  CGG
                                  A          A_
GAM1874 XKRY    5' TGTGATGGAATACAAGG    46092      A     AT
                                TGTGAT GAATACG  AGG
                                |||||| |||||||  |||
                                ACACTA CTTATGT  TCC
                                   C     __
GAM1874 XKRY    5' TGTGATGGAATACAAGG    46092      A     AT
                                TGTGAT GAATACG  AGG
                                |||||| |||||||  |||
                                ACACTA CTTATGT  TCC
                                   C     __
GAM1874 APOARGC  3' TGTGGTAAAACACCAAGGGCC 46093    A     GAT
                                TGTG TAGAATAC   AGGGCC
                                |||| ||||||||   ||||||
                                ACAC ATTTTGTG   TCCCGG
                                  C       GT_
GAM1874 ASB13   3' TGTGGGGAATACAAAGC    46094    ATA      TAG
                                TGTG  GAATACGA  GGC
                                ||||  ||||||||  |||
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                              ACAC  CTTATGTT  TCG
                                CC_     ___
GAM1874 BDG-29   3' TGTAGTGGAAGATAGGGC   46095    ATA  TAC
                              TGTG  GAA  GATAGGGC
                              ||||  |||  ||||||||
                              ACAT  CTT  CTATCCCG
                                CAC  ___
GAM1874 C20orf59 3' TGTGAGGAGGACAGGGC    46096     TA ATAC
                              TGTGA GA   GATAGGGC
                              |||||  ||  ||||||||
                              ACACT CT   CTGTCCCG
                                 C_ C___
GAM1874 CAMTA2   3' GTGATGGGGTAAGACAGGGCC 46097     AGAA C
                              GTGAT   TA GATAGGGCC
                              |||||   || |||||||||
                              CACTA   AT CTGTCCCGG
                                 CCCC T
GAM1874 DKFZp434K114 5' TGTTGTAGCAGCCGATAGGGC 46098    GA  AATA
                              TGT TAG   CGATAGGGC
                              |||  |||   |||||||||
                              ACA ATC   GCTATCCCG
                                AC  GTCG
GAM1874 ESDN     3' TGTGATAAATATAAGTGGG   46099       A CG TA
                              TGTGATAGA TA  A  GGG
                              |||||||||  ||  |  |||
                              ACACTATTT AT  T  CCC
                                    _ AT CA
GAM1874 KIAA0532 3' TGTGGTAAGAACATATAGGGCC 46100    AT_    CG
                              TGTG  AGAATA  ATAGGGCC
                              ||||  ||||||  ||||||||
                              ACAC  TCTTGT  TATCCCGG
                                CAT    A_
GAM1874 KIAA1536 3' TGTGATAGAAAATGGGC    46101       TAC  A
                              TGTGATAGAA  GAT GGGC
                              ||||||||||  ||| ||||
                              ACACTATCTT  TTA CCCG
                                    ___  _
GAM1874 MOST2    5' TGTGATAAGTGCCAAGGGGC  46102      AATA  TA
                              TGTGATAG   CGA  GGGC
                              ||||||||   |||  ||||
                              ACACTATT   GTT  CCCG
                                   CACG  C_
GAM1874 PCDH19   3' TGTTTTTAATATGATAGGGC  46103    GATAG  C
                              TGT    AATA GATAGGGC
                              |||    |||| ||||||||
                              ACA    TTAT CTATCCCG
                                AAAA_   A
GAM1874 LOC128346 3' TGTGTGAAGATAGGGC    46104    ATA  TAC
                              TGTG  GAA  GATAGGGC
                              ||||  |||  ||||||||
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                                ACAC   CTT   CTATCCCG
                                  A__   ___
GAM1874  LOC143274 3'  TGTGTAGAATACTCAAGG    46105      A       GA
                                TGTG TAGAATAC  TAGGG
                                |||| ||||||||  |||||
                                ACAC ATCTTATG  GTTCC
                                  _       A_
GAM1874  LOC158969 3'  GTGATAGATGCACTGGGGC    46106        A_   GATA
                                GTGATAGA  TAC    GGGC
                                ||||||||  |||    ||||
                                CACTATCT  GTG    CCCG
                                     AC   AC__
GAM1874  LOC159121 3'  TGTATAGAACATCAGGGCC    46107      A      CGA
                                TGTG TAGAATA   TAGGGCC
                                |||| |||||||   |||||||
                                ACAT ATCTTGT   GTCCCGG
                                  _      A__
GAM1874  LOC161978 5'  TGTGAGGAGAATAGGGC     46108      T_   ATACG
                                TGTGA  AGA     ATAGGGC
                                |||||  |||     |||||||
                                ACACT  TCT     TATCCCG
                                   CC   _____
GAM1874  LOC169966 3'  TGTGATAGAAAACGTGATGG   46109         T   ATAG
                                TGTGATAGAA ACG    GG
                                |||||||||| |||    ||
                                ACACTATCTT TGC    CC
                                      T   ACTA
GAM1874  LOC200853 3'  TGTGGTGGAAAAACACAGGGCC 46110      ATA   T_  G
                                TGTG   GAA  AC ATAGGGCC
                                ||||   |||  || ||||||||
                                ACAC   CTT  TG TGTCCCGG
                                  CAC   TT  _
GAM1874  LOC202754 3'  TGTGATAGAACGAGGG      46111         AT    TA
                                TGTGATAGA  ACGA  GGG
                                |||||||||  ||||  |||
                                ACACTATCT  TGCT  CCC
                                     __   __
GAM1874  LOC220776 3'  TGTGATAGGAGGGATCAGGCC  46112         AATAC   A
                                TGTGATAG     GAT GGGCC
                                ||||||||     ||| |||||
                                ACACTATC     CTA TCCGG
                                     CTCC_   G
GAM1875  SELPLG    3'  CTGCAGTTGGGATACT      46115          T   CG
                                CTGCAGTTGG GAT  ACT
                                |||||||||| |||  |||
                                GACGTCAACC CTA  TGA
                                     _   __
GAM1875  C20orf139 5'  CTGCAGTTGCTGGTAGGCCGC  46116         G  ATCGACTT
                                CTGCAGTTG TG       CCGC
                                ||||||||| ||       ||||
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                                GACGTCAAC AC      GGCG
                                     G  CATCC___
GAM1875  EPS8R1   3'  CAGAAGATCGACTTCCGC   46117    TTGGT
                                CAG    GATCGACTTCCGC
                                |||    ||||||||||||
                                GTC    CTAGCTGAAGGCG
                                  TT___
GAM1875  EPS8R1   3'  CAGAAGATCGACTTCCGC   46117    TTGGT
                                CAG    GATCGACTTCCGC
                                |||    ||||||||||||
                                GTC    CTAGCTGAAGGCG
                                  TT___
GAM1875  EPS8R1   3'  CAGAAGATCGACTTCCGC   46117    TTGGT
                                CAG    GATCGACTTCCGC
                                |||    ||||||||||||
                                GTC    CTAGCTGAAGGCG
                                  TT___
GAM1875  FLJ10748 3'  CTGCAGCTGGTGGAGTCATCT  46118          A__  A
                                CTGCAGTTGGTG   TCG CT
                                ||||||||||||   ||| ||
                                GACGTCGACCAC   AGT GA
                                       CTC   A
GAM1875  HUMGT198A 5'  TGTAGTTGGTGGTCCGGGCGC  46119    C      A  GACTTC
                                TG AGTTGGTG TC     CGC
                                || ||||||||  ||     |||
                                AC TCAACCAC AG     GCG
                                 A      C  GCCC__
GAM1875  ZNF387   3'  CTGCTGTTGGTAACTTC     46120     A     GATC
                                CTGC GTTGGT    GACTTC
                                |||| ||||||    ||||||
                                GACG CAACCA    TTGAAG
                                  A     _____
GAM1875  LOC139274 5'  CTGCAGTTGCTGGTGCTACT   46121        ___    ATCG
                                CTGCAGT   TGGTG   ACT
                                |||||||   |||||   |||
                                GACGTCA   ACCAC   TGA
                                    ACG    GA__
GAM1875  LOC204084 5'  CTGCAGTTGGAGGTCTGGCCG  46122         TGA  GACTT
                                CTGCAGTTGG   TC    CCG
                                ||||||||||   ||    |||
                                GACGTCAACC   AG    GGC
                                      TCC  ACC__
GAM1876  HMMR     3'  AGCCAAGGTGTTTTAGCC    46125       AC    ACA
                                AGCCAAG  GTTT   AGTC
                                |||||||  ||||   ||||
                                TCGGTTC  CAAA   TCGG
                                    CA   A__
GAM1876  HMMR     3'  AGCCAAGGTGTTTTAGCC    46125       AC    ACA
                                AGCCAAG  GTTT   AGTC
                                |||||||  ||||   ||||
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                                TCGGTTC  CAAA   TCGG
                                   CA    A__
GAM1876  TNS      3'  AGCCGAGCTGTTTATAATTCGA 46126      A  AC    C  G
                                AGCC AG  GTTTA AA TCGG
                                |||| ||  ||||| || ||||
                                TCGG TC  CAAAT TT AGCT
                                  C  GA    A  A
GAM1876  UFD1L    3'  AGCCAAGATGTTGCAAAT    46127        C   TA
                                AGCCAAGA GTT  CAAGT
                                |||||||| |||  |||||
                                TCGGTTCT CAA  GTTTA
                                    A   C_
GAM1876  C19orf7   5'  GCCAGGTGCCGAGAGTCGGAG  46128      A AC   TACA
                                GCCA G  GTT    AGTCGGAG
                                |||| |  |||    ||||||||
                                CGGT C  CGG    TCAGCCTC
                                  _ CA   CTC_
GAM1876  FLJ22624  5'  AGCCGAAGGTAAGGAGTCGGAG 46129      _   AC  TTACA
                                AGCC AAG  GT    AGTCGGAG
                                |||| |||  ||    ||||||||
                                TCGG TTC  CA    TCAGCCTC
                                  C   __  TTCC_
GAM1876  KIAA0763  3'  CCGAGAATTGATGAGTCGGAG  46130    A   C   TACA
                                CC AGA GTT    AGTCGGAG
                                || ||| |||    ||||||||
                                GG TCT TAA    TCAGCCTC
                                 C   _   CTAC
GAM1876  LOC145748 3'  AGCCAAGATGATTTTCAGTCGG 46131        C_   ACA
            AG                    AGCCAAGA  GTTT   AGTCGGAG
                                ||||||||  ||||   ||||||||
                                TCGGTTCT  TAAA   TCAGCCTC
                                    AC    AG_
GAM1876  LOC149086 3'  AGTCAAGATATTTACAAA    46132    C    CG
                                AG CAAGA  TTTACAAG
                                || |||||  ||||||||
                                TC GTTCT  AAATGTTT
                                 A    AT
GAM1876  LOC155061 3'  AGCTAGACGTTTGTGGTGCAG  46133     CA      ACAA  _
                                AGC  AGACGTTT    GT CGG
                                |||  ||||||||    || |||
                                TCG  TCTGCAAA    CA GTC
                                  A_       CAC_  C
GAM1876  LOC196872 3'  GCTAAGACATTTGTAATC    46134    C       ACA
                                GC AAGACGTTT   AGTC
                                || |||||||||   ||||
                                CG TTCTGTAAA   TTAG
                                 A        CA_
GAM1876  LOC91445  3'  AGCCAAACACCAGGAGTTGG   46135       ACGT   CA   C
                                AGCCAAG    TTA  AGT GG
                                |||||||    |||  ||| ||
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                                TCGGTTT   GGT  TCA CC
                                   GT__   CC   A
GAM1877  C21orf2   3'  AAGACGCTGGGGTCCCCGT   46138     G    TC  T
                                AAGA GCTG  GG GTCCCCGT
                                |||| ||||  || ||||||||
                                TTCT CGAC  CC CAGGGGCA
                                  G   __ _
GAM1877  CYP1A2    3'  AAGGGCTGAGTCCCCGT     46139     A    TCGGT
                                AAG GGCTG    GTCCCCGT
                                ||| |||||    ||||||||
                                TTC CCGAC    CAGGGGCA
                                  _    T____
GAM1877  DXYS155E  3'  GGCTGTCATCCTTGTAG     46140       GGT   CC
                                GGCTGTC   GTCC  GTAG
                                |||||||   ||||  ||||
                                CCGACAG   TAGG  CATC
                                   ___    AA
GAM1877  RAB3B     3'  AAGAGACTGTTCTCTAAGTCCC 46141          _ GGT__    C
            TGTAG                  AAGAGGCTGT C    GTCCC GTAG
                                |||||||||| |    ||||| ||||
                                TTCTCTGACA G    CAGGG CATC
                                    A AGATT    A
GAM1877  TEGT      3'  AAGAGGCTCTCCATTTTCTTTG 46142        G  G  G_  CCC
            TAG                   AAGAGGCT TC GT  TC   GTAG
                                |||||||| || ||  ||   ||||
                                TTCTCCGA AG TA  AG   CATC
                                   G  G  AA  AAA
GAM1877  WHSC1     3'  GAGGCTGTGACACCCCGT    46143       C GT T
                                GAGGCTGT G  G CCCCGT
                                |||||||| |  | ||||||
                                CTCCGACA C  T GGGGCA
                                   _ TG _
GAM1877  WHSC1     3'  GAGGCTGTGACACCCCGT    46143       C GT T
                                GAGGCTGT G  G CCCCGT
                                |||||||| |  | ||||||
                                CTCCGACA C  T GGGGCA
                                   _ TG _
GAM1877  WHSC1     3'  GAGGCTGTGACACCCCGT    46143       C GT T
                                GAGGCTGT G  G CCCCGT
                                |||||||| |  | ||||||
                                CTCCGACA C  T GGGGCA
                                   _ TG _
GAM1877  C20orf112 3'  AGGTGCCTGGTGGTGTCCCTGT 46144    AG  _  TC      C
                                AG  GC TG  GGTGTCCC GT
                                ||  || ||  |||||||| ||
                                TC  CG AC  CCACAGGG CA
                                 CA  G  CA       A
GAM1877  DKFZP566G1424 5'  AGGTGCCTGGTGGTGTCCCTGT 46144    AG  _  TC      C
                                AG  GC TG  GGTGTCCC GT
                                ||  || ||  |||||||| ||
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                                TC  CG AC  CCACAGGG CA
                                 CA  G  CA       A
GAM1877  KIAA1023  3'  AGGGGTTAAGCCTGTCCCCGT  46145    A  CT__   GG
                                AG GG    GTC  TGTCCCCGT
                                || ||    |||  |||||||||
                                TC CC    CGG  ACAGGGGCA
                                 C  AATT   __
GAM1877  LGALS12   5'  AGAGGCTGGCTCCCTGT     46146       GTC   G    C
                                AGAGGCT   GGT TCCC GT
                                |||||||   ||| |||| ||
                                TCTCCGA   CCG AGGG CA
                                    ___   _   A
GAM1877  RAI16     5'  GAAGCTGTCGGTGAAGTAG   46147           TCCCC
                                GAGGCTGTCGGTG    GTAG
                                ||||||||||||     ||||
                                CTTCGACAGCCAC    CATC
                                       TT___
GAM1877  LOC139522 5'  GAGGTCGCCGGTGTCTTCGT   46148     C        CC
                                GAGG TGTCGGTGTC  CGT
                                |||| ||||||||||  |||
                                CTCC GCGGCCACAG  GCA
                                  A        AA
GAM1877  LOC155179 3'  AGGGGTTAAGCCTGTCCCCGT  46145    A  CT__   GG
                                AG GG    GTC  TGTCCCCGT
                                || ||    |||  |||||||||
                                TC CC    CGG  ACAGGGGCA
                                 C  AATT   __
GAM1877  LOC221405 5'  AAAGGCTGTCTGTAGGTCCCCG 46149         G  __
            T                    AGAGGCTGTC GT  GTCCCCGT
                                ||||||||||  ||  ||||||||
                                TTTCCGACAG CA  CAGGGGCA
                                      A  TC
GAM1877  LOC221486 3'  GAGGCTGCAGCGCCCGTAG    46150       T    TC
                                GAGGCTG CGGTG  CCCGTAG
                                |||||||  |||||  |||||||
                                CTCCGAC GTCGC  GGGCATC
                                   _    __
GAM1877  LOC255002 5'  GAGGCTGTTGTCTTGTA     46151        CGG   CCC
                                GAGGCTGT   TGTC   GTA
                                ||||||||   ||||   |||
                                CTCCGACA   ACAG   CAT
                                    ___    AA_
GAM1878  ADAM23    5'  TCCCGGGCGCCGCTCCGTGTGG 46154    G  AA  AT       C
                                TC CG  GT  TCGCTCCGTG GG
                                || ||  ||  ||||||||||  ||
                                AG GC  CG  GGCGAGGCAC CC
                                 G  C_  C_        A
GAM1878  ADMP      5'  TCGCGAAATGATCCTGTGTGG  46155        AT  G  CC   C
                                TCGCGAAGT  TC CT  GTG GG
                                |||||||||  ||  ||  ||| ||
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                                AGCGCTTTA  AG GA  CAC CC
                                     CT  _  __   A
GAM1878 KIAA0556 3'  TCATGAAGTATTTGCCGGCC   46156    C      C  T_____
                                TCG GAAGTATT GC     CC
                                ||| |||||||| ||     ||
                                AGT CTTCATAA CG     GG
                                  A       A  GCCIII
GAM1879 DIAPH2   3'  GTAATGTTAGGATGGG     46159     AC    GCGC
                                GTAG  GTTG   GGATGGG
                                ||||  ||||   |||||||
                                CATT  CAAT   CCTACCC
                                  A_   _____
GAM1879 RASGRP4  3'  GAGCTGGTGTGGATGGGA    46160    C    CGC
                                GA GTTGG   GGATGGGA
                                || |||||   ||||||||
                                CT CGACC   CCTACCCT
                                 _    ACA
GAM1879 YF13H12  3'  TAGTGCATTAATAGTGGATGGG 46161     AGA     CGC_
             A                   TAGT   CGTTGG    GGATGGGA
                                ||||   ||||||   ||||||||
                                ATCA   GTAATT    CCTACCCT
                                  C__      ATCA
GAM1880 FLT4     3'  TTCCTCTTTGAAGTTTGT    46164     G        AC
                                TTC TCTTTGAAGT  TTGT
                                ||| ||||||||||  ||||
                                AAG AGAAACTTCA  AACA
                                  G         __
GAM1881 A1BG     3'  TGGAAGAGCACAGATGAAAGAG 46167         G   TC  T
             G                   TGGAAGAG ACG  GT AAAGAGG
                                |||||||| |||  || |||||||
                                ACCTTCTC TGT  TA TTTCTCC
                                     G   C_  C
GAM1881 AMD1     3'  TGGGGGAGACACCAGGGAGAGG 46168     AA   G  GT  TTAA
                                TGG  GAG AC  CG    AGAGG
                                |||  ||| ||  ||    |||||
                                ACC  CTC TG  GT    TCTCC
                                  CC   _  TG  CCC_
GAM1881 ARHGAP6  5'  TGGAGAAGGACGAGCAAAGAGG 46169      AG     TC  T
                                TGGA  AGGACG  GT AAAGAGG
                                ||||  ||||||  || |||||||
                                ACCT  TCCTGC  CG TTTCTCC
                                  CT     T_  _
GAM1881 CIT      3'  TGGGAGGGGAAGTCGTCAA   46170     A  A   C
                                TGG AG GGA GTCGTTAA
                                ||| || ||| ||||||||
                                ACC TC CCT CAGCAGTT
                                  C  C   T
GAM1881 DEDD     3'  TGGAAAAGGGAAATAAAGGG   46171         ACGTCGT    A
                                TGGAAGAGG      TAAAG GG
                                |||||||||      ||||| ||
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                                ACCTTTTCC      ATTTC CC
                                    CTTT___    _
GAM1881  ELAVL2   5'  GGGGGAGGACGTCTTAAAAGGG 46172    AA       G    ___
            AGG                   GG  GAGGACGTC TTAAA   GAGG
                                  ||  ||||||||| |||||   ||||
                                  CC  CTCCTGCAG AATTT   CTCC
                                   CC       _    TCC
GAM1881  HRH1     3'  GAGAAAGCTGTTAAAGAGG   46173      C  C
                                  GAGGA GT GTTAAAGAGG
                                  ||||| || ||||||||||
                                  CTCTT CG CAATTTCTCC
                                     T  A
GAM1881  LFG      3'  GGAGGAGGGCGAAGCCAAGGGA 46174     A   A  TC    A_
            GG                    GGA GAGG CG  GTTAA  GAGG
                                  ||| |||| ||  |||||  ||||
                                  CCT CTCC GC  CGGTT  CTCC
                                    C   C  TT    CC
GAM1881  MAPT     5'  GGGAGAGGACAGCGGAGGAGG  46175    A      T  TTAAA
                                  GG AGAGGACG CG    GAGG
                                  || |||||||| ||    ||||
                                  CC TCTCCTGT GC    CTCC
                                   C       C  CTC__
GAM1881  MAPT     5'  GGGAGAGGACAGCGGAGGAGG  46175    A      T  TTAAA
                                  GG AGAGGACG CG    GAGG
                                  || |||||||| ||    ||||
                                  CC TCTCCTGT GC    CTCC
                                   C       C  CTC__
GAM1881  MAPT     5'  GGGAGAGGACAGCGGAGGAGG  46175    A      T  TTAAA
                                  GG AGAGGACG CG    GAGG
                                  || |||||||| ||    ||||
                                  CC TCTCCTGT GC    CTCC
                                   C       C  CTC__
GAM1881  MAPT     5'  GGGAGAGGACAGCGGAGGAGG  46175    A      T  TTAAA
                                  GG AGAGGACG CG    GAGG
                                  || |||||||| ||    ||||
                                  CC TCTCCTGT GC    CTCC
                                   C       C  CTC__
GAM1881  MUC4     5'  GGAAGAGGACAAAAGAG     46176          TCGTT
                                  GGAAGAGGACG    AAAGAG
                                  ||||||||||     ||||||
                                  CCTTCTCCTGT    TTTCTC
                                       _____
GAM1881  MUC4     5'  GGAAGAGGACAAAAGAG     46176          TCGTT
                                  GGAAGAGGACG    AAAGAG
                                  ||||||||||     ||||||
                                  CCTTCTCCTGT    TTTCTC
                                       _____
GAM1881  MYL1     5'  TGGAAGAGGATGGTGGTT    46177          C_  C
                                  TGGAAGAGGA  GT GTT
                                  |||||||||  || |||
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                                ACCTTCTCCT  CA CAA
                                      AC  C
GAM1881  PAK4     3'  TGGGGGAGGGCCTGTCCCAGAG 46178     AA    AC  _  AA
              G                    TGG  GAGG  GTC GTT  AGAGG
                                   |||  ||||  ||| |||  |||||
                                   ACC  CTCC  CGG CAG  TCTCC
                                     CC   __   A   GG
GAM1881  PDYN     5'  TGGGAGGAGGTGCCAAAGAGG  46179     AA    C  C
                                   TGG  GAGGA GT GTTAAAGAGG
                                   |||  ||||| || ||||||||||
                                   ACC  CTCCT CA CGGTTTCTCC
                                     __    C  _
GAM1881  PKHD1    3'  TGGAAGAAGGGTAAAGAAG    46180         ACGTC  T
                                   TGGAAGAGG    GT AAAGAGG
                                   |||||||||    || |||||||
                                   ACCTTCTTC    CA TTTCTTC
                                        C_____  _
GAM1881  PPL      3'  GGGAGAGGACGACACCAAGGAG 46181    A       T  TT  A
              G                    GG AGAGGACG CG  AA GAGG
                                   || |||||||| ||  || ||||
                                   CC TCTCCTGC GT  TT CTCC
                                    C       T  GG  C
GAM1881  RAB5B    3'  CGGGGAGGAACACTAGGGAGG  46182     AA    CGT    AA
                                   TGG  GAGGA   CGTTA  GAGG
                                   |||  |||||   |||||  ||||
                                   GCC  CTCCT   GTGAT  CTCC
                                     C_    T__    CC
GAM1881  SLC25A11 3'  TGGAAGGGAAATAAATAGAGG  46183       A   C  CGTTAA
                                   TGGAAG GGA GT     AGAGG
                                   |||||| ||| ||     |||||
                                   ACCTTC CCT TA     TCTCC
                                      _   T  TTTA__
GAM1881  TCF2     3'  GGGAGAGGACACAGAG      46184     A       T GTTAA
                                   GG AGAGGACG C     AGAG
                                   || |||||||| |     ||||
                                   CC TCTCCTGT G     TCTC
                                    C       _ ______
GAM1881  DKFZP434C171 3'  TGGGTGAGGGCCAGGGAGAGG  46185     AA   AC    TTAA
                                   TGG  GAGG  GTCG    AGAGG
                                   |||  ||||  ||||    |||||
                                   ACC  CTCC  CGGT    TCTCC
                                     CA   __    CCC_
GAM1881  DKFZP564G092 5'  TGGAGGGGAGGGTAAAGAG    46186      A__    ACGTC  T
                                   TGGA   GAGG    GT AAAGAG
                                   ||||   ||||    || ||||||
                                   ACCT   CTCC    CA TTTCTC
                                     CCC    ______  _
GAM1881  FADS1    3'  GAGGAGTGGTTAAAGAG     46187       C  C
                                   GAGGA GT GTTAAAGAG
                                   ||||| || |||||||||
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                                CTCCT CA CAATTTCTC
                                   _ C
GAM1881  FLJ10246  3'  TGGGAGAGGGACAATGGGGAGG 46188     A    _   TCGTTAAA
                                TGG AGAGG ACG       GAGG
                                ||| ||||| |||       ||||
                                ACC TCTCC TGT       CTCC
                                  C    C   TACCC___
GAM1881  FLJ10468  3'  GAAGAGGATGTTGAGTTGCAGG 46189        C  C__   AA  _
           AGG                    GAAGAGGA GT   GTT  AG AGG
                                ||||||||  ||   |||  ||  |||
                                CTTCTCCT CA   CAA  TC TCC
                                     A  ACT   CG  C
GAM1881  FLJ12671  3'  TGGAAGAGGATGCTGTTAA    46190          C  C
                                TGGAAGAGGA GT GTTAA
                                ||||||||||  ||  |||||
                                ACCTTCTCCT CG CAATT
                                      A  A
GAM1881  KIAA0240  3'  TGGGAGAGGGTGCAAAGAGA   46191     A    AC  C  T
                                TGG AGAGG  GT GT AAAGAGG
                                |||  |||||  ||  ||  |||||||
                                ACC TCTCC  CA CG TTTCTCT
                                  C    __  _  _
GAM1881  KIAA0775  3'  TGGAAGAAGGGTTGAG      46192         ACGTC   AAA
                                TGGAAGAGG    GTT   GAG
                                |||||||||    |||   |||
                                ACCTTCTTC    CAA   CTC
                                     C_____   ____
GAM1881  MGC32043  3'  TGGAAGAGAGTGCATCAGAGAG 46193          AC  _    A
           G                     TGGAAGAGG  GT CGTTA AGAGG
                                |||||||||  ||  |||||  |||||
                                ACCTTCTCT  CA GTAGT TCTCC
                                     __  C    C
GAM1881  MGC4342   3'  TGGGGAAGGATGGCGGGAGAGG 46194     AA    CGT  TTAA
                                TGG  GAGGA   CG    AGAGG
                                |||  |||||   ||    |||||
                                ACC  TTCCT   GC    TCTCC
                                  CC    ACC  CC__
GAM1881  MRPL37    3'  TGGAAGAGAGGCAAGAG     46195         AC  CGTTA
                                TGGAAGAGG  GT    AAGAG
                                |||||||||  ||    |||||
                                ACCTTCTCT  CG    TTCTC
                                     C_  _____
GAM1881  PHRET1    3'  TGGAAGGGAACCAAAGG     46196       A   CGTC TT    A
                                TGGAAG GGA    G  AAAG G
                                ||||||  |||   |  ||||  |
                                ACCTTC CCT    T  TTTC C
                                   _  ____ GG   _
GAM1881  SEPT3     3'  GGAAGAGGGTGGGCAAAGGG   46197         AC  CGT    A
                                GGAAGAGG  GT   TAAAG GG
                                ||||||||  ||   |||||  ||
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                                CCTTCTCC  CA   GTTTC CC
                                    __  CCC    _
GAM1881  SPINT1   3'  TGGAAGAGGAGCTCGGGAG   46198         CG   TTAAA
                                TGGAAGAGGA  TCG    GAG
                                ||||||||||  |||    |||
                                ACCTTCTCCT  AGC    CTC
                                      CG   C____
GAM1881  SRPK1    3'  GGAAGAGGAAAATGCTTGAAGG 46199         CGTC   AAA
                                GGAAGAGGA   GTT   GAGG
                                |||||||||   |||   ||||
                                CCTTCTCCT   CGA   TTCC
                                     TTTA   AC_
GAM1881  STRN3    5'  TGGGGGAAGGGCCGGAGAG   46200     AA   AC   TTAA
                                TGG  GAGG  GTCG   AGAG
                                |||  ||||  ||||   ||||
                                ACC  CTTC  CGGC   TCTC
                                  CC   C_   C___
GAM1881  ZDHHC8   3'  TGAGAGAGGGTGCCCCAAAGAG 46201    GA    AC   G
            G                    TG  AGAGG  GTC TTAAAGAGG
                                ||  |||||  ||| |||||||||
                                AC  TCTCC  CGG GGTTTCTCC
                                 TC    CA   _
GAM1881  LOC112476 3'  GGAAGGGGGCGGGACGTGGAGA 46202      A  A  T__   TAA
            GG                   GGAAG GG CG   CGT   AGAGG
                                |||||  ||  ||   |||   |||||
                                CCTTC CC GC   GCA   TCTCC
                                   C  C  CCT   CC_
GAM1881  LOC127841 5'  TGGGAGGACGTTGCCATTCAGG 46203     AA      C    AA___
            AGG                    TGG  GAGGACGT GTTA    GAGG
                                |||  |||||||| ||||    ||||
                                ACC  CTCCTGCA CGGT    CTCC
                                  __       A    AAGTC
GAM1881  LOC143437 3'  TGGAAGGGGACAAAGAGAGG   46204       A    TCGTTAA
                                TGGAAG GGACG      AGAGG
                                ||||||  |||||      |||||
                                ACCTTC CCTGT      TCTCC
                                   C    TTC____
GAM1881  LOC145945 5'  TGGAGAGGGCTGAAAGGAG    46205     A   ACGTC  _   _
                                TGGA GAGG    GTT AAAG AG
                                ||||  ||||    ||| |||| ||
                                ACCT CTCC    CGA TTTC TC
                                  _   _____  C   C
GAM1881  LOC219654 3'  TGGAAGAGGCACAAAGG     46206        A  TCGT    A
                                TGGAAGAGG CG   TAAAG G
                                |||||||||  ||   |||||  |
                                ACCTTCTCC GT   GTTTC C
                                     _  ____   _
GAM1881  LOC221415 5'  TGGAAGAAGGGTTGGGAGG   46207        ACGTC   AAA
                                TGGAAGAGG    GTT   GAGG
                                |||||||||    |||   ||||
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                                ACCTTCTTC    CAA   CTCC
                                     C_____   CC_
GAM1881  LOC221833 3'  TGGGAGGAGGTCGGGGAGAGG  46208     AA    C    TTAA
                                TGG  GAGGA GTCG    AGAGG
                                |||  ||||| ||||    |||||
                                ACC  CTCCT CAGC    TCTCC
                                  __    C    CCC_
GAM1881  LOC245812 3'  TGGGGGTGGGATCAGTTAAAGA 46209     AAGA  AC  _
           GG                     TGG    GG  GTC GTTAAAGAGG
                                |||    ||  ||| ||||||||||
                                ACC    CC  TAG CAATTTCTCC
                                  CCCA  C_   T
GAM1881  LOC253531 3'  TGGAAGGGGACAAAGAGAGG   46204       A    TCGTTAA
                                TGGAAG GGACG      AGAGG
                                ||||||| |||||      |||||
                                ACCTTC CCTGT      TCTCC
                                   C    TTC_____
GAM1881  LOC55580  5'  TGGAGGAGGAGGAAGGGAAAGG 46210     A    CGTCGTT   A
           G                     TGGA GAGGA      AAAG GG
                                |||| |||||      |||| ||
                                ACCT CTCCT      TTTC CC
                                  C    CCTTCCC   _
GAM1881  LOC91397  5'  TGGAAGAGACGGACACCGGGAG 46211       ___   GT  TTAAA
           G                     TGGAAGA   GGAC  CG    GAGG
                                |||||||   ||||  ||    ||||
                                ACCTTCT   CCTG  GC    CTCC
                                    CTG    TG  C_____
GAM1882  ABCC3    3'  TCCAGGTCGATGGCAGC     46214     CAGT  G  _
                                TCCA    GG CG TGGCAGC
                                ||||    || || |||||||
                                AGGT    CC GC ACCGTCG
                                  _____  A  T
GAM1882  ABCC3    3'  TCCAGGTCGATGGCAGC     46214     CAGT  G  _
                                TCCA    GG CG TGGCAGC
                                ||||    || || |||||||
                                AGGT    CC GC ACCGTCG
                                  _____  A  T
GAM1882  ACVR1    5'  CAGTGGGCTATGGTCACA    46215         _   CAGC
                                CAGTGGGC GTGG    CACA
                                |||||||| ||||    ||||
                                GTCACCCG TACC    GTGT
                                     A    A___
GAM1882  BCL11B   3'  TCTACAGCGAATAGCAGCCA   46216    C      GC
                                TC ACAGTGG  GTGGCAGCCA
                                || |||||||  ||||||||||
                                AG TGTCGCT  TATCGTCGGT
                                 A      __
GAM1882  CASP7    3'  CAGTGGACACAGCCA       46217         GTG
                                CAGTGGGC   GCAGCCA
                                ||||||||   |||||||
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                              GTCACCTG  TGTCGGT
                                 ___
GAM1882 CASP7   3' CAGTGGACACAGCCA     46217      GTG
                              CAGTGGGC  GCAGCCA
                              ||||||||  |||||||
                              GTCACCTG  TGTCGGT
                                 ___
GAM1882 CASP7   3' CAGTGGACACAGCCA     46217      GTG
                              CAGTGGGC  GCAGCCA
                              ||||||||  |||||||
                              GTCACCTG  TGTCGGT
                                 ___
GAM1882 CASP7   3' CAGTGGACACAGCCA     46217      GTG
                              CAGTGGGC  GCAGCCA
                              ||||||||  |||||||
                              GTCACCTG  TGTCGGT
                                 ___
GAM1882 GRB10   5' TCTACAGTGGGTATCACGTGGC 46218   C     _____
                              TC ACAGTGGG   CGTGGC
                              || ||||||||   ||||||
                              AG TGTCACCC   GCACCG
                               A      ATAGT
GAM1882 IL13    3' TCCAAGTGCCAGCAGCCAC  46219    C  GG  G
                              TCCA AGT  GC TGGCAGCCAC
                              |||| |||  || ||||||||||
                              AGGT TCA  CG GTCGTCGGTG
                                _  __ _
GAM1882 ISL1    5' TCCACAGTGAAATGGTGG   46220        C__
                              TCCACAGTGGG  GTGG
                              ||||||||||  ||||
                              AGGTGTCACTT  CACC
                                    TAC
GAM1882 ITGA5   3' TCCACAGTGGGACGCCA    46221        CGTG  A
                              TCCACAGTGGG   GC GCCA
                              ||||||||||   || ||||
                              AGGTGTCACCC   TG CGGT
                                          _____  _
GAM1882 ITPKA   3' CACAGTGGGGACAAAGCTGC  46222        __  T   A
                              CACAGTGGG  CG GGC GC
                              |||||||||  || ||| ||
                              GTGTCACCC  GT TCG CG
                                    CT  T   A
GAM1882 LASS1   3' TCCACGTGGCACGGTTGC   46223     A   G   CA
                              TCCAC GTGG CGTGG  GC
                              ||||| |||| |||||  ||
                              AGGTG CACC GTGCC  CG
                                 _   _    AA
GAM1882 LZTR1   3' GTGGCTTCATGGCAGCCACA  46225    G__
                              GTGG  CGTGGCAGCCACA
                              ||||  ||||||||||||
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                                CACC   GTACCGTCGGTGT
                                  GAA
GAM1882  LZTR1    3'  CACAATGGGCAGGCGCCACA   46224          T   A
                                CACAGTGGGCG GGC GCCACA
                                |||||||||| ||| ||||||
                                GTGTTACCCGT CCG CGGTGT
                                          _  _
GAM1882  NUMA1    5'  TCCACAGGGTCAGCCA      46226        TGGGCGT  _
                                TCCACAG      GG CAGCCA
                                |||||||      || ||||||
                                AGGTGTC      CC GTCGGT
                                   ________ A
GAM1882  PCDHB4   3'  CACTAGACATGTGGTGGTCACA 46227    G    __    CAGC
                                CA TGGGC  GTGG    CACA
                                || |||||  ||||    ||||
                                GT ATCTG  CACC    GTGT
                                 G    TA    ACCA
GAM1882  PER2     3'  CAGTGGAAACAGCCA       46228        CGT
                                CAGTGGG   GGCAGCCA
                                |||||||   ||||||||
                                GTCACCT   TTGTCGGT
                                   ____
GAM1882  PITX3    5'  TCCCAGTAGCGGCGGCTGC    46229     A     G  _   A
                                TCC CAGTGG CG TGGC GC
                                ||| |||||| || |||| ||
                                AGG GTCATC GC GCCG CG
                                  _     _ C    A
GAM1882  PRSS8    3'  TCCATGGTGGGTGAGGGGCCA  46230      CA    CGT  CA
                                TCCA  GTGGG   GG  GCCA
                                ||||  |||||   ||  ||||
                                AGGT  CACCC   CC  CGGT
                                  AC    ACT  C_
GAM1882  RAP1B    3'  CACAGTGAGAATCTACAGCTGC 46231          C  G_    CA
            A                    CACAGTGGG GT  GCAGC  CA
                                |||||||||  ||  |||||  ||
                                GTGTCACTC TA  TGTCG  GT
                                     T  GA    AC
GAM1882  SCN4A    3'  TCTGCAGGGGAGGGGCCAC    46232    CA   T   CGT  CA
                                TC  CAG GGG   GG  GCCAC
                                ||  ||| |||   ||  |||||
                                AG  GTC CCC   CC  CGGTG
                                 AC   _   T__  C_
GAM1882  SNTB1    5'  GCGGGAGTTGGCAGCTGCA    46233      C  _     CA
                                GTGGG GT GGCAGC  CA
                                ||||| || ||||||  ||
                                CGCCC CA CCGTCG  GT
                                   T  A     AC
GAM1882  AFAP     3'  TCCTGGTGGGCGTGCAA     46234     ACA       G
                                TCC   GTGGGCGTG CAG
                                |||   ||||||||| |||
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                                AGG   CACCCGCAC GTT
                                  AC_       _
GAM1882 ATP5D    3' CCCATGGGTGGCAGCCAC    46235     CAG   CG
                                TCCA   TGGG  TGGCAGCCAC
                                ||||   ||||  ||||||||||
                                GGGT   ACCC  ACCGTCGGTG
                                  ___    __
GAM1882 C20orf81 5' CCCACAGTGGTGATGGCCGC   46236         GC    A
                                TCCACAGTGG  GTGGC GC
                                ||||||||||  ||||| ||
                                GGGTGTCACC  TACCG CG
                                     AC    G
GAM1882 DDM36    3' CACAGTGGTGTTAGCCACA   46237       GCG  GC
                                CACAGTGG   TG  AGCCACA
                                ||||||||   ||  |||||||
                                GTGTCACC   AC  TCGGTGT
                                   ___  AA
GAM1882 DKFZp434D177 5' CACAGGGCAGCCGGCAGCC   46238     GT    __
                                CACA  GGGCG  TGGCAGCC
                                ||||  |||||  ||||||||
                                GTGT  CCCGT  GCCGTCGG
                                  __    CG
GAM1882 DKFZP566C243 3' ACAGCTCAGTGGCAGCTGCA  46239      GGGC      CA
                                ACAGT   GTGGCAGC  CA
                                |||||   ||||||||  ||
                                TGTCG   CACCGTCG  GT
                                  AGT_      AC
GAM1882 FLJ10597 3' TCCAGCTGTGGCAGCCC    46240     CAGTGG _      A
                                TCCA     GC GTGGCAGCC C
                                ||||     || |||||||||  |
                                AGGT     CG CACCGTCGG G
                                  _______ A       C
GAM1882 FLJ10661 3' CAGGGATGTGGCAGCTGCA   46241    T  GC      CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
                                GTC CC  CACCGTCG  GT
                                  _ TA       AC
GAM1882 FLJ10661 3' CAGGGATGTGGCAGCTGCA   46241    T  GC      CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
                                GTC CC  CACCGTCG  GT
                                  _ TA       AC
GAM1882 FLJ10661 3' CAGGGATGTGGCAGCTGCA   46241    T  GC      CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
                                GTC CC  CACCGTCG  GT
                                  _ TA       AC
GAM1882 FLJ10661 3' CAGGGATGTGGCAGCTGCA   46241    T  GC      CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
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                                GTC CC  CACCGTCG  GT
                                  _ TA       AC
GAM1882  FLJ10661  3'  CAGGGATGTGGCAGCTGCA   46241    T  GC      CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
                                GTC CC  CACCGTCG  GT
                                  _ TA       AC
GAM1882  FLJ10936  5'  CATATGGGCGTGGTCAAC    46242   _        _
                                CA GTGGGCGTGG CAGC
                                || ||||||||||  ||||
                                GT TACCCGCACC GTTG
                                 A        A
GAM1882  FLJ11939  3'  TCCTGGTGTCGGGGGCAGCCAC 46243    ACA   GG  T_
           A                     TCC   GTG  CG  GGCAGCCACA
                                |||   |||  ||  ||||||||||
                                AGG   CAC  GC  CCGTCGGTGT
                                  AC_   A_  CC
GAM1882  FLJ14082  3'  CACAGTGGGTCCTCGGGCCA   46244        CG__   CA
                                CACAGTGGG   TGG  GCCA
                                |||||||||   |||  ||||
                                GTGTCACCC   GCC  CGGT
                                     AGGA   __
GAM1882  FLJ14154  3'  TCCCAGTGAATGCAGCCAC   46245    A     GCGTG
                                TCC CAGTGG    GCAGCCAC
                                ||| ||||||    ||||||||
                                AGG GTCACT    CGTCGGTG
                                  _     TA___
GAM1882  FLJ20208  3'  TCCCTGGTCACGGCAGC     46246    ACAG   G
                                TCC    TGG CGTGGCAGC
                                |||    ||| |||||||||
                                AGG    ACC GTGCCGTCG
                                  G___   A
GAM1882  FLJ21596  3'  TCCACAGCGGCTCTCTAGCTAC 46247         G GTGGC   C
           A                     TCCACAGTGG C    AGC ACA
                                |||||||||| |    ||| |||
                                AGGTGTCGCC G    TCG TGT
                                     _ AGAGA   A
GAM1882  GRIN3A   3'  CACAGTAGGGTGTAAGC     46248         C   GC
                                CACAGTGGG GTG  AGC
                                |||||||| |||  |||
                                GTGTCATCC CAC  TCG
                                     _  AT
GAM1882  HBOA     3'  TCCTGGTGGTGGCAGCCA    46249    ACAG   GC
                                TCC    TGG  GTGGCAGCCA
                                |||    |||  ||||||||||
                                AGG    ACC  CACCGTCGGT
                                  _____   AC
GAM1882  HIF3A    5'  TCCAGGTGGGCGCTGACGCC   46250     CA     _   A
                                TCCA  GTGGGCG TGGC GCC
                                ||||  ||||||| |||| |||
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                                AGGT  CACCCGC ACTG CGG
                                  C_      G   _
GAM1882 IGSF2    3' TCCCAGTGGCGCAGCCGC    46251     A     G  TG  A
                                TCC CAGTGG CG  GC GC
                                ||| |||||| ||  || ||
                                AGG GTCACC GC  CG CG
                                  _     _ GT  G
GAM1882 KIAA0546 3' GTGGCCATGGCAGTTACA    46252      G       CC
                                GTGG CGTGGCAG  ACA
                                |||| ||||||||  |||
                                CACC GTACCGTC  TGT
                                  G       AA
GAM1882 KIAA0869 3' TCCACGTTGGGCAGCCAC    46253       AG    GTGGC
                                TCCAC  TGGGC    AGCCAC
                                |||||  |||||    ||||||
                                AGGTG  ACCCG    TCGGTG
                                   CA    _____
GAM1882 KIAA1862 3' CCCACAGTGGCATGGCGGCTGC 46254          G     A  CA
             A                   TCCACAGTGG CGTGGC GC  CA
                                ||||||||||  ||||||  ||  ||
                                GGGTGTCACC GTACCG CG  GT
                                      _     C  AC
GAM1882 MGC16279 5' CAGGGATGTGGCAGCTGCA   46241     T  GC       CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
                                GTC CC  CACCGTCG  GT
                                  _ TA       AC
GAM1882 MGC16279 5' CAGGGATGTGGCAGCTGCA   46241     T  GC       CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
                                GTC CC  CACCGTCG  GT
                                  _ TA       AC
GAM1882 MGC16279 3' CAGGGATGTGGCAGCTGCA   46241     T  GC       CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
                                GTC CC  CACCGTCG  GT
                                  _ TA       AC
GAM1882 MGC16703 3' ATGGTGGCGACAGCCGCA    46255      GC       A
                                GTGG  GTGGCAGCC CA
                                ||||  |||||||||  ||
                                TACC  CGCTGTCGG GT
                                  AC        C
GAM1882 MYH7B    3' TCCACAGCTCGCTGGTGGTTGC 46256         GG  __    CA
                                TCCACAGT  GC  GTGG  GC
                                ||||||||  ||  ||||  ||
                                AGGTGTCG  CG  CACC  CG
                                     AG  AC   AA
GAM1882 PRO2730  3' ACAGTGGGTGGCATCC      46257         CG    G
                                ACAGTGGG  TGGCA CC
                                ||||||||  |||||  ||
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                                TGTCACCC  ACCGT GG
                                   __     A
GAM1882  RMP      5'  TCCACGGTGGGCGCCTCCA   46258      A       GGCAG
                                TCCAC GTGGGCGT     CCA
                                ||||| ||||||||     |||
                                AGGTG CACCCGCG     GGT
                                   C       GA___
GAM1882  SLC5A6   3'  TCCACAGTGGACCTGGTCA   46259          G  _
                                TCCACAGTGGGC TGG CA
                                |||||||||||| ||| ||
                                AGGTGTCACCTG ACC GT
                                      G   A
GAM1882  LOC146713 3'  GTGGAGGGGGTCAGCCACA   46260      CGT  _
                                GTGGG   GG CAGCCACA
                                |||||   || ||||||||
                                CACCT   CC GTCGGTGT
                                   CCC  A
GAM1882  LOC150967 5'  TCCACAGTTGGCGTGGGCCA   46261        G      CA
                                TCCACAGT GGCGTGG  GCCA
                                |||||||| |||||||  ||||
                                AGGTGTCA CCGCACC  CGGT
                                     A     __
GAM1882  LOC151778 5'  CACAGGGCGTGGCAGCCACA   46262      GT
                                CACA  GGGCGTGGCAGCCACA
                                ||||  ||||||||||||||||
                                GTGT  CCCGCACCGTCGGTGT
                                   __
GAM1882  LOC152274 3'  TCCTAGTGGGCATGTGCCA   46263     AC        GCA
                                TCC  AGTGGGCGTG   GCCA
                                |||  ||||||||||   ||||
                                AGG  TCACCCGTAC   CGGT
                                  A_        A__
GAM1882  LOC153416 3'  CACAGTGAGAATCTACAGCTGC 46231         C  G_    CA
            A                    CACAGTGGG GT  GCAGC  CA
                                |||||||| ||  |||||  ||
                                GTGTCACTC TA  TGTCG  GT
                                      T  GA    AC
GAM1882  LOC155340 5'  CACCGGGTGTGGCAGCCACA   46264    G   C
                                CA TGGG GTGGCAGCCACA
                                || |||| ||||||||||||
                                GT GCCC CACCGTCGGTGT
                                 G   A
GAM1882  LOC157450 3'  CAGGGATGTGGCAGCTGCA   46241     T  GC       CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
                                GTC CC  CACCGTCG  GT
                                  _  TA       AC
GAM1882  LOC157624 5'  TGGGATGATGGCAGCTACA   46265     C__       C
                                TGGG   GTGGCAGC ACA
                                ||||   |||||||| |||
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                                ACCC   TACCGTCG TGT
                                  TAC       A
GAM1882  LOC158490 3'  TCCACCGATGTGGCAGCTGCA  46266      AG   GC      CA
                                TCCAC  TGG  GTGGCAGC  CA
                                |||||  |||  ||||||||  ||
                                AGGTG  GCT  CACCGTCG  GT
                                  __   A_       AC
GAM1882  LOC158490 3'  TCCACAGATGTGGCAGCTGCA  46267       TGGGC      CA
                                TCCACAG    GTGGCAGC  CA
                                |||||||    ||||||||  ||
                                AGGTGTC    CACCGTCG  GT
                                    TA___       AC
GAM1882  LOC196872 3'  CCACAGGCATGGTGGCCACA   46268      GTG      CA
                                CCACA   GGCGTGG  GCCACA
                                |||||   |||||||  ||||||
                                GGTGT   CCGTACC  CGGTGT
                                  ____      AC
GAM1882  LOC219649 3'  TCCACACTGCCCCAGGCAGCCA 46269       G  GGCGT
             C                   TCCACA TG    GGCAGCCAC
                                ||||||| ||    |||||||||
                                AGGTGT AC    CCGTCGGTG
                                   G  GGGGT
GAM1882  LOC219686 3'  CACAGTGACATGGCTAC     46270        G     A
                                CACAGTGG CGTGGC GC
                                |||||||| |||||| ||
                                GTGTCACT GTACCG TG
                                    _     A
GAM1882  LOC220073 5'  CAGGGATGTGGCAGCTGCA   46241     T  GC      CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
                                GTC CC  CACCGTCG  GT
                                  _ TA       AC
GAM1882  LOC220073 5'  CAGGGATGTGGCAGCTGCA   46241     T  GC      CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
                                GTC CC  CACCGTCG  GT
                                  _ TA       AC
GAM1882  LOC220073 5'  CAGGGATGTGGCAGCTGCA   46241     T  GC      CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
                                GTC CC  CACCGTCG  GT
                                  _ TA       AC
GAM1882  LOC220883 3'  TCCTGGTGGTGGCAGCCA    46249     ACAG   GC
                                TCC    TGG  GTGGCAGCCA
                                |||    |||  ||||||||||
                                AGG    ACC  CACCGTCGGT
                                  _____   AC
GAM1882  LOC220980 5'  CACATATGAAATGGCAGCCACA 46271      GTG  C
                                CACA   GG GTGGCAGCCACA
                                ||||   || ||||||||||||
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                                GTGT  CT TACCGTCGGTGT
                                  ATA  T
GAM1882 LOC253841 3' TCCACAGTGGGCAGCCAC   46272          GTGGC
                                TCCACAGTGGGC    AGCCAC
                                ||||||||||||    ||||||
                                AGGTGTCACCCG    TCGGTG
                                      _____
GAM1882 LOC257441 5' CACAGGGCAGCCGGCAGCC   46238     GT   __
                                CACA  GGGCG  TGGCAGCC
                                ||||  |||||  ||||||||
                                GTGT  CCCGT  GCCGTCGG
                                  __    CG
GAM1882 LOC90133  3' TCCTGGAGTCTGTGGCAGCCAC 46273    ACAG   C___
                                TCC   TGGG   GTGGCAGCCAC
                                |||   ||||   ||||||||||
                                AGG   ACCT   CACCGTCGGTG
                                  _____   CAGA
GAM1882 LOC90288  3' CCACAGTGGGCAGGTAGAGCTG 46274          __   C   CA
            CA                    CCACAGTGGGC  GTGG AGC  CA
                                ||||||||||  |||| |||  ||
                                GGTGTCACCCG  CATC TCG  GT
                                      TC   _  AC
GAM1882 LOC91069  3' CAGGGATGTGGCAGCTGCA   46241    T  GC      CA
                                CAG GG  GTGGCAGC  CA
                                ||| ||  ||||||||  ||
                                GTC CC  CACCGTCG  GT
                                  _ TA       AC
GAM1882 LOC91960  3' GGACACAGTGGCAGCCACA   46275     ___
                                GGGC   GTGGCAGCCACA
                                ||||   ||||||||||||
                                CCTG   CACCGTCGGTGT
                                  TGT
GAM1882 LOC92661  3' TCCACCGTGAGGGCAGCCAC  46276      A    CGT
                                TCCAC GTGGG   GGCAGCCAC
                                ||||| |||||   |||||||||
                                AGGTG CACTC   CCGTCGGTG
                                   G    ___
GAM1882 LOC93070  5' CATATGGGCGTGGTCAAC    46242    _       _
                                CA GTGGGCGTGG CAGC
                                || ||||||||| ||||
                                GT TACCCGCACC GTTG
                                 A        A
GAM1883 GPR4      3' AGGCATGGTGGCTCACATTTGT 46279        CT   G  CCCTA
            GG                    AGGCATGG  GCT AC    TGG
                                ||||||||  ||| ||    |||
                                TCCGTACC  CGA TG    ACC
                                     AC   G  TAAAC
GAM1883 PAEP      5' AGCATGGCTGCGGCTGTG    46280          TGACCC  A
                                GGCATGGCTGC     CT TG
                                ||||||||||     || ||
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                                TCGTACCGACG     GA AC
                                      CC____  C
GAM1883 PET112L  3' GGGGTGGCTGCTGGTCGGCTGT 46281    CA       ACCC_  A
            GG                  GG  TGGCTGCTG    CT TGG
                                ||  |||||||||    || |||
                                CC  ACCGACGAC    GA ACC
                                 CC       CAGCC  C
GAM1883 SPR     3' AGGCAGGACTGCCCCTATG   46282      T  CT    A
                                AGGCA GG  GCTG CCCCTATG
                                ||||| ||  |||| ||||||||
                                TCCGT CC  TGAC GGGGATAC
                                  _ __   _
GAM1883 SUFU    3' GGCAGGTTGCTGACCAGGCCAT 46283     T  C      _______  TAT
            G                   GCA GG TGCTGACC     CC   G
                                ||| || ||||||||     ||   |
                                CGT CC ACGACTGG     GG   C
                                 _  A       TCCIII  TAT
GAM1883 APCL    3' AGGTGTGGCTGTGGCCCCCACG 46284     CA     C  A
            G                   AGG  TGGCTG TG CCCCTATGG
                                |||  |||||| || |||||||||
                                TCC  ACCGAC AC GGGGGTGCC
                                 AC     _  C
GAM1883 CENTA2   3' AGGAATGGCTGCTGACTGCGGC 46285          _________  CTAT
            CATAGGG                 TGGCTGCTGAC       CC    GG
                                ||||||||||       ||    ||
                                ACCGACGACTG       GG    CC
                                      ACGCCIII  TATC
GAM1883 DOCK3    3' AGGATGGCTGCTGGATACATGG 46286     C        ACCCC
                                AGG ATGGCTGCTG     TATGG
                                ||| ||||||||||     |||||
                                TCC TACCGACGAC     GTACC
                                 _        CTAT_
GAM1883 EFS2    3' AGGTATGGCTGCTGAGCACCAG 46287     C         CCC   T
            G                   AGG ATGGCTGCTGA   CTA GG
                                ||| ||||||||||   ||| ||
                                TCC TACCGACGACT   GGT CC
                                 A         CGT  _
GAM1883 FLJ12975 3' AGGCATGGTGGAGCATCTGTGG 46288        CT__  TGACCC  A
                                AGGCATGG   GC     CT TGG
                                ||||||||   ||     || |||
                                TCCGTACC   CG     GA ACC
                                    ACCT  TA____  C
GAM1883 FLJ22405 3' AGGCATGGCTTTGATTCTCTG  46289         GC   CCC  A
                                AGGCATGGCT  TGA   CT TG
                                ||||||||||  |||   || ||
                                TCCGTACCGA  ACT   GA AC
                                      A_   AA_  G
GAM1883 KIAA0210 3' AGGGTGGCTAGATCCCTGTGG  46290     CA     CT  C    A
                                AGG  TGGCTG  GA CCCT TGG
                                |||  ||||||  || |||| |||
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                                TCC  ACCGAT  CT GGGA ACC
                                  C_     __ A    C
GAM1883  KIAA0446  5'  AGGCATGGTGGCATGCACCTGT 46291        CT  _  ACC   A
              GG                  AGGCATGG  GC TG   CCT TGG
                                  ||||||||  || ||   ||| |||
                                  TCCGTACC  CG AC   GGA ACC
                                     AC  T  GT_   C
GAM1883  KIAA0447  3'  AGGCATGGTGGCACGTGCCTGT 46292        CT  TGACC   A
              GG                  AGGCATGG  GC    CCT TGG
                                  ||||||||  ||    ||| |||
                                  TCCGTACC  CG    GGA ACC
                                     AC  TGCAC   C
GAM1883  KIAA0802  5'  GGCATGGCTCGCTGGCCTCC   46293         _   A  _
                                  GGCATGGCT GCTG CC CC
                                  |||||||||  |||| || ||
                                  CCGTACCGA CGAC GG GG
                                       G   C  A
GAM1883  KLK15     3'  AGGCGGGGCTGCTGGCCAGCTG 46294      AT      A  C_  A
              TGG                   AGGC  GGCTGCTG CC  CT TGG
                                  ||||  ||||||||  ||  || |||
                                  TCCG  CCGACGAC GG  GA ACC
                                    CC       C  TC  C
GAM1883  KLK15     3'  AGGCGGGGCTGCTGGCCAGCTG 46294      AT      A  C_  A
              TGG                   AGGC  GGCTGCTG CC  CT TGG
                                  ||||  ||||||||  ||  || |||
                                  TCCG  CCGACGAC GG  GA ACC
                                    CC       C  TC  C
GAM1883  KLK15     3'  AGGCGGGGCTGCTGGCCAGCTG 46294      AT      A  C_  A
              TGG                   AGGC  GGCTGCTG CC  CT TGG
                                  ||||  ||||||||  ||  || |||
                                  TCCG  CCGACGAC GG  GA ACC
                                    CC       C  TC  C
GAM1883  KLK15     3'  AGGCGGGGCTGCTGGCCAGCTG 46294      AT      A  C_  A
              TGG                   AGGC  GGCTGCTG CC  CT TGG
                                  ||||  ||||||||  ||  || |||
                                  TCCG  CCGACGAC GG  GA ACC
                                    CC       C  TC  C
GAM1883  MAPK11    3'  AGATATGGCTGCTGGCCTTGG  46295    GC       ACC   A
                                  AG  ATGGCTGCTG   CCT TGG
                                  ||  ||||||||||   ||| |||
                                  TC  TACCGACGAC   GGA ACC
                                   TA        C__   _
GAM1883  N4BP3     3'  GGCATGGCCTGAGCCTGTGG   46296        TG   CC   A
                                  GGCATGGC  CTGA  CCT TGG
                                  ||||||||  ||||  ||| |||
                                  CCGTACCG  GACT  GGA ACC
                                       __   C_   C
GAM1883  NETO2     3'  GGTTGGCTGCTGGAAACAGTAT 46297    CA       ACCCC__
              GG                    GG  TGGCTGCTG      TATGG
                                  ||  |||||||||      |||||
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                                CC  ACCGACGAC      ATACC
                                 A_       CTTTGTC
GAM1883  RAB1B    3'  GGTGGGCTGCTGGGCCCCTGTG 46298    CAT       A_    A
              G                   GG   GGCTGCTG  CCCCT TGG
                                  ||   ||||||||  ||||| |||
                                  CC   CCGACGAC  GGGGA ACC
                                   AC_       CC    C
GAM1883  RASSF2   3'  GGCTGGTGCTGCTGTCCCTATG 46299     ATG_      AC
              G                   GGC    GCTGCTG  CCCTATGG
                                  |||    |||||||  ||||||||
                                  CCG    CGACGAC  GGGATACC
                                   ACCA      A_
GAM1883  RIN      5'  GGCTGGCTGCTGGTCCTCC    46300     A       A_ _
                                  GGC TGGCTGCTG  CC CC
                                  ||| |||||||||  || ||
                                  CCG ACCGACGAC  GG GG
                                   _       CA  A
GAM1883  TTTY11   3'  AAGTATGGCTGCTGCAATG    46301     C        ACCCCT
                                  AGG ATGGCTGCTG     ATG
                                  ||| ||||||||||     |||
                                  TTC TACCGACGAC     TAC
                                   A        GT____
GAM1883  TXN2     3'  AGGTGTGGCTGCCTGACTAGGC 46302        _   ________ CTAT
              CATAGGG                 TGGCTGC TGAC      CC    GG
                                  |||||||  ||||      ||    ||
                                  ACCGACG ACTG      GG    CC
                                      G    ATCCIII  TATC
GAM1883  LOC144603 3'  AGGCATGGCTTTGATTCTCTG  46289         GC   CCC  A
                                  AGGCATGGCT  TGA   CT TG
                                  ||||||||||  |||   || ||
                                  TCCGTACCGA  ACT   GA AC
                                        A_   AA_  G
GAM1883  LOC147229 3'  GGCTGTGGCTGCTGTCATG    46303     A_       ACCCC
                                  GGC  TGGCTGCTG    TATG
                                  |||  |||||||||    ||||
                                  CCG  ACCGACGAC    GTAC
                                   AC        A____
GAM1883  LOC149194 3'  GACAAACCACTGGTCTCTATGG 46304      T   TG   ACCC
                                  GGCA GGC  CTG    CTATGG
                                  |||| |||  |||    ||||||
                                  CTGT TTG  GAC    GATACC
                                    _   GT   CAGA
GAM1883  LOC150372 3'  AGGCATGGCTGCAGAGAGCCT  46305           T  CC_
                                  AGGCATGGCTGC GA   CCT
                                  ||||||||||||  ||   |||
                                  TCCGTACCGACG CT   GGA
                                         T  CTC
GAM1883  LOC196746 3'  GCATGGCTGCTGGAGGCGGTGG 46306            ACCCCTA
                                  GCATGGCTGCTG      TGG
                                  ||||||||||||      |||
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                                CGTACCGACGAC      ACC
                                      CTCCGCC
GAM1883  LOC219513 3'  GGCAGGCTGCTGAGCTG     46307     T       CCCCTA
                                GGCA GGCTGCTGA     TG
                                |||| |||||||||     ||
                                CCGT CCGACGACT     AC
                                  _       CG____
GAM1883  LOC219537 3'  GGCCGTGGCTGCTGAGCTG   46308     A_       CCCCTA
                                GGC  TGGCTGCTGA     TG
                                |||  ||||||||||     ||
                                CCG  ACCGACGACT     AC
                                  GC        CG____
GAM1883  LOC90133  5'  AGGGGTGGCTGCTGAAAGCCT  46309     CA       CC_
                                AGG  TGGCTGCTGA   CCT
                                |||  ||||||||||   |||
                                TCC  ACCGACGACT   GGA
                                  CC        TTC
GAM1884  CLOCK     3'  TGGCAGTGGTATGTCC     46312       CCA   ACA
                                TGGCAGTG   TAT   GTCC
                                ||||||||   |||   ||||
                                ACCGTCAC   ATA   CAGG
                                     C__   ___
GAM1884  DLG5      5'  TGGCCGTGTCATACAGT     46313     A  CCA
                                TGGC GTG   TATACAGT
                                |||| |||   ||||||||
                                ACCG CAC   GTATGTCA
                                  G   A__
GAM1884  GYPA      3'  TGTCAGTGCCATGCCC      46314    G       ATACA
                                TG CAGTGCCAT    GTCC
                                || |||||||||    ||||
                                AC GTCACGGTA    CGGG
                                 A       ______
GAM1884  NKX2E     5'  TGGCAGCGCCAGTCC       46315         TATACA   C
                                TGGCAGTGCCA     GTC C
                                ||||||||||      ||| |
                                ACCGTCGCGGT     CAG G
                                      _______   A
GAM1884  SLC4A7    3'  TGGCAGTGCTTTATATCAA    46316        CA   _
                                TGGCAGTGC  TATA CAG
                                |||||||||  |||| |||
                                ACCGTCACG  ATAT GTT
                                     AA    A
GAM1884  SUV39H1   3'  TAGCAGGGCATACAGTCTCA   46317       T  CAT      C
                                TGGCAG GC   ATACAGTC CA
                                ||||||  ||   |||||||| ||
                                ATCGTC CG   TATGTCAG GT
                                   C  ___       A
GAM1884  C13orf1   3'  TGGCGGGCACCTGTAGTCCCAC 46318     A_ TG  ATATAC
                                TGGC  G  CC     AGTCCCAC
                                ||||  |  ||     ||||||||
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                                ACCG  C  GG     TCAGGGTG
                                  CC GT  ACA___
GAM1884  CASPR4    3'  TGGCAGTGCTGCAAGCCCA   46319        CATATA   T
                                TGGCAGTGC     CAG CCCA
                                |||||||||     ||| ||||
                                ACCGTCACG     GTT GGGT
                                     AC____   C
GAM1884  DBR1      3'  TGGCGGGCACCTGTAGTCCCAC 46318     A_ TG  ATATAC
                                TGGC  G  CC     AGTCCCAC
                                ||||  |  ||     ||||||||
                                ACCG  C  GG     TCAGGGTG
                                  CC GT  ACA___
GAM1884  DKFZP761E2110 3'  TGGCAGTGTGCATCAGTAGTCC 46320        C_   ATAC
           CA                     TGGCAGTG  CAT    AGTCCCA
                                |||||||  |||    |||||||
                                ACCGTCAC  GTA    TCAGGGT
                                     AC   GTCA
GAM1884  DKFZp761G2113 3'  TGGCATGACAGTCCC      46321      G  CCATAT
                                TGGCA TG     ACAGTCCC
                                |||||  ||     ||||||||
                                ACCGT AC     TGTCAGGG
                                  _ _______
GAM1884  FHX       3'  TGGCAGTGTATACTCAGTTTCA 46322        CC    A    CC
           C                     TGGCAGTG  ATAT CAGT  CAC
                                |||||||  ||||  ||||  |||
                                ACCGTCAC  TATG GTCA  GTG
                                     A_    A    AA
GAM1884  FLJ10687  3'  TGGCACGTGCCTGTAGTCCCAC 46323      _    ATATAC
                                TGGCA GTGCC     AGTCCCAC
                                |||||  |||||     ||||||||
                                ACCGT CACGG     TCAGGGTG
                                   G    ACA___
GAM1884  FLJ20040  3'  TGGGAGTGTCTGCCTCAGTCCC 46324     C   CCATATA
           AC                     TGG AGTG      CAGTCCCAC
                                ||| ||||      |||||||||
                                ACC TCAC      GTCAGGGTG
                                  C    AGACGGA
GAM1884  FLJ21195  3'  TGGCAGTGAAAGTAGTATACGG 46325       CCA____    A  CC
           TTTCAC                   GGCAGTG      TATAC GT  CAC
                                |||||||      |||||  ||  |||
                                CCGTCAC      ATATG CA  GTG
                                     TTTCATC    C  AA
GAM1884  HRH4      3'  TGGCGAGTACCTGTAGTCCCAC 46326     _    ATATAC
                                TGGC AGTGCC     AGTCCCAC
                                ||||  ||||||     ||||||||
                                ACCG TCATGG     TCAGGGTG
                                  C     ACA___
GAM1884  KIAA0635  3'  TGGTATTGCAAACAGTCCCA   46327    CAG   CATAT
                                TGG   TGC    ACAGTCCCA
                                |||   |||    |||||||||
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                                ACC  ACG    TGTCAGGGT
                                  ATA  TT___
GAM1884  TBLR1    3'  TGGCAGTGTTATATGCC     46328        CC   ACA
                                TGGCAGTG  ATAT   GTC
                                ||||||||  ||||   |||
                                ACCGTCAC  TATA   CGG
                                    AA   ___
GAM1884  TNKS1BP1 3'  GGCAGGGATACAGTCCCA    46329      TGCCAT
                                GGCAG     ATACAGTCCCA
                                |||||     ||||||||||
                                CCGTC     TATGTCAGGGT
                                  CC____
GAM1884  ZNF304   3'  TGGCAGTGATATAATTCC    46330        CC    CAG
                                TGGCAGTG  ATATA   TCC
                                ||||||||  |||||   |||
                                ACCGTCAC  TATAT   AGG
                                    __    TA_
GAM1884  ZNF340   3'  TGGCAGTGTCCTGTGTCCCA   46331        _  ATATACA
                                TGGCAGTG CC      GTCCCA
                                |||||||| ||      ||||||
                                ACCGTCAC GG      CAGGGT
                                    A  ACA____
GAM1884  LOC126669 3'  GGTGGTGCGAACCTATAGTCCC 46332    CA    CATA_  C
           AC                     GG  GTGC    TA AGTCCCAC
                                ||  ||||    || ||||||||
                                CC  CACG    AT TCAGGGTG
                                 AC   CTTGG  A
GAM1884  LOC149734 3'  TGGCAGTGTGTGCTTTCAGTCC 46333        CCATATA_
           CA                     TGGCAGTG       CAGTCCCA
                                ||||||||       ||||||||
                                ACCGTCAC       GTCAGGGT
                                    ACACGAAA
GAM1884  LOC152300 3'  TGGCAGGTGCCTACAGTCCCA  46334       _   ATA
                                TGGCAG TGCC   TACAGTCCCA
                                |||||| ||||   ||||||||||
                                ACCGTC ACGG   ATGTCAGGGT
                                   C   ___
GAM1884  LOC153205 5'  TGGCAATGCCATGTGTCTCA   46335          ATACA   C
                                TGGCAGTGCCAT    GTC CA
                                ||||||||||||    ||| ||
                                ACCGTTACGGTA    CAG GT
                                      CA___   A
GAM1884  LOC254773 3'  TGCCAGTGTTGTATACAACAC  46336    G    CCA     TCC
                                TG CAGTG   TATACAG   CAC
                                || |||||   |||||||   |||
                                AC GTCAC   ATATGTT   GTG
                                 G    AAC     ___
GAM1885  DBY      3'  TGGTATCGTGAGCATTAC    46339       TTC  GA
                                TGGTAT   CG  AGCATTAC
                                ||||||   ||  ||||||||
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                                ACCATA  GC  TCGTAATG
                                   ___  AC
GAM1885  DDX3     3'  TGATATCTTGAGCATTAC    46340       TCCG  A
                                TGGTATT   GA GCATTAC
                                |||||||   || |||||||
                                ACTATAG   CT CGTAATG
                                   AA__  _
GAM1885  DMRT2    3'  TGGCATTTAGCAGGCATT    46341       C_  AA
                                TGGTATTT  CGG  GCATT
                                ||||||||  |||  |||||
                                ACCGTAAA  GTC  CGTAA
                                   TC  __
GAM1885  TEM8     3'  TGGTATTTTGGGAAGATCA   46342       CC    C
                                TGGTATTT  GGAAG ATTA
                                ||||||||  ||||| ||||
                                ACCATAAA  CCTTC TAGT
                                   AC   _
GAM1885  HTEX4    5'  TGATATTTCTGCATTATCA   46343       CGGAA    C
                                TGGTATTTC    GCATTA CA
                                |||||||||    |||||| ||
                                ACTATAAAG    CGTAAT GT
                                   A____     A
GAM1885  HTEX4    5'  TGATATTTCTGCATTATCA   46343       CGGAA    C
                                TGGTATTTC    GCATTA CA
                                |||||||||    |||||| ||
                                ACTATAAAG    CGTAAT GT
                                   A____     A
GAM1885  HTEX4    5'  TGATATTTCTGCATTATCA   46343       CGGAA    C
                                TGGTATTTC    GCATTA CA
                                |||||||||    |||||| ||
                                ACTATAAAG    CGTAAT GT
                                   A____     A
GAM1885  KLK7     3'  TGGTACTTTTGGAACAT     46344       CC   G
                                TGGTATTT  GGAA CAT
                                ||||||||  |||| |||
                                ACCATGAA  CCTT GTA
                                   AA   _
GAM1885  KLK7     3'  TGGTACTTTTGGAACAT     46344       CC   G
                                TGGTATTT  GGAA CAT
                                ||||||||  |||| |||
                                ACCATGAA  CCTT GTA
                                   AA   _
GAM1885  VIT1     5'  TGGTATTTCACATTA       46345       CGGAA
                                TGGTATTTC    GCATTA
                                |||||||||    ||||||
                                ACCATAAAG    TGTAAT
                                             _____
GAM1885  LOC147040 5'  TGGGTTTCCGGAATCCAACCA  46346    TA      GCATT
                                TGG  TTTCCGGAA    ACCA
                                |||  |||||||||    ||||
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                                ACC  AAAGGCCTT    TGGT
                                  C_       AGGT_
GAM1885  LOC222828 5'  TGGTTTCGGCGAGTGTTACCA  46347     AT   C  A_  CA
                                TGGT  TTC GG  AG  TTACCA
                                ||||  ||| ||  ||  ||||||
                                ACCA  AAG CC  TC  AATGGT
                                  __  _  GC  AC
GAM1885  LOC253681 5'  TGGGTTTCCGGAATCCAACCA  46346     TA       GCATT
                                TGG  TTTCCGGAA    ACCA
                                |||  |||||||||    ||||
                                ACC  AAAGGCCTT    TGGT
                                  C_       AGGT_
GAM1885  LOC257428 5'  TGGTATTTCCTGGTGTACCA   46348          _  AAGCAT
                                TGGTATTTCC GG     TACCA
                                ||||||||||  ||      |||||
                                ACCATAAAGG CC     ATGGT
                                      A  AC_____
GAM1886  BACE     3'  CACTGGGGTGAGGAGATGT    46351         A    CACT
                                CACTGGGGT AGGG    GTGT
                                |||||||||  ||||    ||||
                                GTGACCCCA TCCT    TACA
                                     C    C___
GAM1886  BACE     3'  CACTGGGGTGAGGAGATGT    46351         A    CACT
                                CACTGGGGT AGGG    GTGT
                                |||||||||  ||||    ||||
                                GTGACCCCA TCCT    TACA
                                     C    C___
GAM1886  CLASP1   3'  CTGGGGTAGGGACCTTGT    46352         A   C   G
                                CTGGGGTA GGG ACT TGT
                                ||||||||  ||| ||| |||
                                GACCCCAT CCC TGG ACA
                                     _   _   A
GAM1886  FUT6     5'  ACACTGGGGGGGCCAGTG    46353         TAA    ACT
                                ACACTGGGG   GGGC   GTG
                                |||||||||   ||||   |||
                                TGTGACCCC   CCCG   CAC
                                     ___    GT_
GAM1886  IL18RAP  3'  CACTGGGAAATCTTAGGGGTGT 46354     TA____    CAC_    III
            TGTGTA                 GGGG     AGGG    TGTGT   A
                                ||||     ||||    |||||   |
                                CCCT     TCCC    ACACA   T
                                  TTAGAA    CACA    III
GAM1886  KLK4     3'  CACAAGGGGGCACTGTGT    46355     T    TAAG
                                CAC GGGG    GGCACTGTGT
                                |||  ||||    ||||||||||
                                GTG TCCC    CCGTGACACA
                                  T    _____
GAM1886  MAML1    3'  CACTGGGGTAAGTGGAGCA    46356           ___
                                CACTGGGGTAAG   GGCA
                                ||||||||||||   ||||
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                                GTGACCCCATTC  TCGT
                                      ACC
GAM1886 TMPRSS2  3' CACTGAGGTAGCAATGTGT  46357       AAG  C
                                CACTGGGGT  GGCA TGTGT
                                |||||||||  |||| |||||
                                GTGACTCCA  TCGT ACACA
                                     ___   T
GAM1886 BACH    3' CTCGGGACAACACTGTGT   46358   G  TAAG
                                CT GGG   GGCACTGTGT
                                || |||   ||||||||||
                                GA CCC   TTGTGACACA
                                 G  TG__
GAM1886 CLDN15  3' CACTGTGGACGTGCACTGTGT 46359     G  TAAGG
                                CACTG GG    GCACTGTGT
                                ||||| ||    |||||||||
                                GTGAC CC    CGTGACACA
                                   A  TGCA_
GAM1886 CSR1    3' CTCAGGGGGCACTGTGT    46360   G  TAA
                                CT GGG  GGGCACTGTGT
                                || |||  ||||||||||
                                GA TCC  CCCGTGACACA
                                 G  ___
GAM1886 DKFZP564G202 3' CATTGAGGTAAGGGGCCCA   46361   C       CA
                                CA TGGGGTAAGGG  CTG
                                || ||||||||||  |||
                                GT ACTCCATTCCC  GGT
                                 A         CG
GAM1886 FLJ11722  3' ACATGGGGTTTCACTGTG   46362    C    AAGGG
                                ACA TGGGGT    CACTGTG
                                ||| ||||||    |||||||
                                TGT ACCCCA    GTGACAC
                                  _     AA___
GAM1886 HSA243666 3' CTGGGGTAAGGACACAGGTGT 46363           T_
                                CTGGGGTAAGGGCAC  GTGT
                                ||||||||||||||  ||||
                                GACCCCATTCCTGTG  CACA
                                         TC
GAM1886 KIAA0280  3' TGGGGTAAGGATATGT     46364         CAC
                                TGGGGTAAGGG   TGTGT
                                ||||||||||   |||||
                                ACCCCATTCCT   ATACA
                                     ___
GAM1886 LEP16   3' ACAGGGGTAAGGGAACATGT  46365   T       C  T
                                AC GGGGTAAGGG AC GTGT
                                || |||||||||| || ||||
                                TG CCCCATTCCC TG TACA
                                 T        T  _
GAM1886 UBXD2   3' ACTGGGGTAAGAGGTG     46366          CACT
                                ACTGGGGTAAGGG   GTG
                                ||||||||||||   |||
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                                TGACCCCATTCTC    CAC
                                      ____
GAM1886  LOC124997 3'  AACACTGTGGTAGGGGTG    46367       G    A   CACT
                                AACACTG GGTA GGG    GTG
                                ||||||| |||| |||    |||
                                TTGTGAC CCAT CCC    CAC
                                   A   _  ____
GAM1886  LOC125929 5'  CTGGGGTAAGAACCTGTGT   46368           A
                                CTGGGGTAAGGGC CTGTGT
                                |||||||||||| ||||||
                                GACCCCATTCTTG GACACA
                                      _
GAM1886  LOC143677 5'  CTGGGGTGGGGCAGTGT     46369       AA    CT
                                CTGGGGT  GGGCA  GTGT
                                |||||||  |||||  ||||
                                GACCCCA  CCCGT  CACA
                                   C_    __
GAM1886  LOC147711 5'  CTGGGGTAAGAACCTGTGT   46368           A
                                CTGGGGTAAGGGC CTGTGT
                                |||||||||||| ||||||
                                GACCCCATTCTTG GACACA
                                      _
GAM1886  LOC148809 5'  CTGGGGTTTCACTGTGT     46370       AAGGG
                                CTGGGGT    CACTGTGT
                                |||||||    ||||||||
                                GACCCCA    GTGACACA
                                   AA___
GAM1886  LOC161734 3'  CTGGTGAGGCACTGTGT     46371     GGTAA
                                CTGG    GGGCACTGTGT
                                ||||    ||||||||||
                                GACC    TCCGTGACACA
                                  AC___
GAM1886  LOC201911 3'  CACCGCGCGGGGCATTGTGT   46372      GG  AA    C
                                CACTG  GT  GGGCA TGTGT
                                |||||  ||  ||||| |||||
                                GTGGC  CG  CCCGT ACACA
                                   G_  C_    A
GAM1886  LOC256950 3'  CACTGGGGAGGGAGTCCTGTGT 46373        TA    CA__
                                CACTGGGG  AGGG    CTGTGT
                                ||||||||  ||||    ||||||
                                GTGACCCC  TCCC    GACACA
                                     __    TCAG
GAM1886  LOC81569  5'  AACAACTTGAAAGGGGTGCTGT 46374     _  GG  T    CA_
            GT                   AACA CT  GG AAGGG   CTGTGT
                                ||||  ||  ||  |||||   ||||||
                                TTGT GA  CT TTCCC   GACACA
                                  T  A_  _    CAC
GAM1886  LOC90917  3'  ACACTGGGGTGGGAAGATGT   46375         AA   CACT
                                ACACTGGGGT  GGG    GTGT
                                ||||||||||  |||    ||||
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                                TGTGACCCCA  CCC    TACA
                                      __   TTC_
GAM1887 HMG20B   3'  TCGGCTGGAGGAGAGCAGGAT  46378      CCCTAC   AAA
                                TTGGC     AGA   GCAGGAT
                                |||||     |||   |||||||
                                AGCCG     TCT   CGTCCTA
                                   ACCTCC  ___
GAM1887 NGFRAP1  5'  TTGGTGCTCTGACCAGCAGGAT 46379     CCC  ACA  AA
                                TTGG   CT   GA  AGCAGGAT
                                ||||   ||   ||  ||||||||
                                AACC   GA   CT  TCGTCCTA
                                  AC_  GA_  GG
GAM1887 SOX12    3'  CTGGTCCCTACAGGGAT     46380      C      AAAAGCA
                                TTGG CCCTACAG      GGAT
                                |||| ||||||||      ||||
                                GACC GGGATGTC      CCTA
                                  A      ________
GAM1887 SUFU     3'  CTGGCCCCTGCAGGAT      46381          ACAGAAAA
                                TTGGCCCCT      GCAGGAT
                                |||||||||      |||||||
                                GACCGGGGA      CGTCCTA
                                           _________
GAM1887 TNFRSF10B 3'  CTGGCCCCTGTAGAAGTTGC   46382          AC    AA_
                                TTGGCCCCT  AGAA   GC
                                |||||||||  ||||   ||
                                GACCGGGGA  TCTT   CG
                                     CA    CAA
GAM1887 UNC119   3'  TTGGCCCCTCATGGGGAGGGAT 46383          A  GAAAAGCA
                                TTGGCCCCT CA       GGAT
                                ||||||||| ||       ||||
                                AACCGGGGA GT       CCTA
                                     _  ACCCCTC_
GAM1887 UNC119   3'  TTGGCCCCTCATGGGGAGGGAT 46383          A  GAAAAGCA
                                TTGGCCCCT CA       GGAT
                                ||||||||| ||       ||||
                                AACCGGGGA GT       CCTA
                                     _  ACCCCTC_
GAM1887 ENDO180  3'  TTGGTCCCCACAGGGGA     46384      C      AAAAGCA
                                TTGG CCCTACAG      GGA
                                |||| ||||||||      |||
                                AACC GGGGTGTC      CCT
                                  A       C_______
GAM1887 FLJ11362 5'  TTGGCCCCGTGCTCCAGCAGGA 46385          TACAGAAA
           T                    TTGGCCCC       AGCAGGAT
                                ||||||||       ||||||||
                                AACCGGGG       TCGTCCTA
                                     CACGAGG_
GAM1887 FLJ13154 3'  TGGCCCCTGCTGGTACAGGAGC 46386          _______   AAA
           AGG                    TGGCCCCT     ACAG   AGCAGG
                                ||||||||     ||||   ||||||
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                              ACCGGGGA    TGTC  TCGTCC
                                  CGACCA  C__
GAM1887 FLJ13855 3' TTGGCCCCTGATACGGGA   46387       ACA AAA A
                              TTGGCCCCT  GA  GC GGA
                              |||||||||  ||  || |||
                              AACCGGGGA  CT  TG CCT
                                  ___ A__ C
GAM1887 FLJ23231 3' TTGACCCCTACAGGGGCAGCAG 46388         AAA_
          GAT                 TTGGCCCCTACAG   AGCAGGAT
                              ||||||||||||||  ||||||||
                              AACTGGGGATGTC   TCGTCCTA
                                    CCCG
GAM1887 KIAA0494 5' TTGGACCTCCGGAGCAGGA  46389    _ _ TACAGAAA
                              TTGG CC CC      AGCAGGA
                              |||| || ||      |||||||
                              AACC GG GG      TCGTCCT
                                T  A  CC_____
GAM1887 KIAA0781 3' TTGGTTTCTACAGAAAAG   46390    CCC
                              TTGG  CTACAGAAAAG
                              ||||  ||||||||||
                              AACC  GATGTCTTTTC
                                AAA
GAM1887 KIAA1643 3' TTGGCCCCTGCAGCCGGCCCGG 46391       A  AAAA A_
                              TTGGCCCCT CAG   GC  GG
                              ||||||||| |||   ||  ||
                              AACCGGGGA GTC   CG  CC
                                  C  GGC_  GG
GAM1887 KIAA1649 3' TCGGCCCCTGGAAAAAGCAGG  46392       ACA
                              TTGGCCCCT  GAAAAGCAGG
                              |||||||||  ||||||||||
                              AGCCGGGGA  TTTTTCGTCC
                                  CC_
GAM1887 KIAA1649 5' TCGGCCCCTGGAAAAAGCAGG  46392       ACA
                              TTGGCCCCT  GAAAAGCAGG
                              |||||||||  ||||||||||
                              AGCCGGGGA  TTTTTCGTCC
                                  CC_
GAM1887 MGC15705 5' CTGGCCCTAGCAGGAGCAGGAT 46393      C  _  AAA
                              TTGGCCC TA CAG  AGCAGGAT
                              ||||||| || |||  ||||||||
                              GACCGGG AT GTC  TCGTCCTA
                                 _ C  C__
GAM1887 MGC29891 3' TTGGCCCCTCAGAAAAA    46394       A
                              TTGGCCCCT CAGAAAAG
                              ||||||||| ||||||||
                              AACCGGGGA GTCTTTTT
                                  _
GAM1887 UNC5D   3' TTGGTTCCTGAGAAAAGCGAGA 46395    CC  AC     AG
          T                   TTGG  CCT  AGAAAAGC  GAT
                              ||||  |||  ||||||||  |||
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                                AACC  GGA  TCTTTTCG  CTA
                                  AA  C_      CT
GAM1887  YKT6     3'  TTGGCATCTACAGAAGCCAG   46396      CC     AA  A
                                TTGGC  CTACAGA  AGC GG
                                |||||  |||||||  ||| ||
                                AACCG  GATGTCT  TCG TC
                                   TA     __   G
GAM1887  LOC144558 3'  TTGTCCCTGGAGAGCAGGA   46397    GC   AC   AAA
                                TTG  CCCT  AGA   GCAGGA
                                |||  ||||  |||   ||||||
                                AAC  GGGA  TCT   CGTCCT
                                  A_   CC  ___
GAM1887  LOC149086 3'  TTGGCCCTACAGGGTCAGG   46398       C    AAAAG
                                TTGGCCC TACAG    CAGG
                                |||||||  |||||    ||||
                                AACCGGG ATGTC    GTCC
                                   _    CCA__
GAM1887  LOC151623 3'  TTGTCCCTGGAGAGCAGGA   46397    GC   AC   AAA
                                TTG  CCCT  AGA   GCAGGA
                                |||  ||||  |||   ||||||
                                AAC  GGGA  TCT   CGTCCT
                                  A_   CC  ___
GAM1887  LOC157278 3'  TTGTCCCTGGAGAGCAGGA   46397    GC   AC   AAA
                                TTG  CCCT  AGA   GCAGGA
                                |||  ||||  |||   ||||||
                                AAC  GGGA  TCT   CGTCCT
                                  A_   CC  ___
GAM1887  LOC219848 3'  TTGTGCTCTTTGAAGCAGGAT  46399    _  CC  ACA  AA
                                TTG GC  CT   GA  AGCAGGAT
                                ||| ||  ||   ||  ||||||||
                                AAC CG  GA   CT  TCGTCCTA
                                  A  A_  AA_  __
GAM1887  LOC221962 3'  TTGTCCCTGGAGAGCAGGA   46397    GC   AC   AAA
                                TTG  CCCT  AGA   GCAGGA
                                |||  ||||  |||   ||||||
                                AAC  GGGA  TCT   CGTCCT
                                  A_   CC  ___
GAM1887  LOC255461 3'  TTGTCCCTGGAGAGCAGGA   46397    GC   AC   AAA
                                TTG  CCCT  AGA   GCAGGA
                                |||  ||||  |||   ||||||
                                AAC  GGGA  TCT   CGTCCT
                                  A_   CC  ___
GAM1887  LOC255516 3'  TTGTCCCTGGAGAGCAGGA   46397    GC   AC   AAA
                                TTG  CCCT  AGA   GCAGGA
                                |||  ||||  |||   ||||||
                                AAC  GGGA  TCT   CGTCCT
                                  A_   CC  ___
GAM1887  LOC255995 3'  TTAGCCTCAGAGCAGG     46400      CCTA   AAA
                                TTGGCC   CAGA   GCAGG
                                ||||||   ||||   |||||
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                                AATCGG   GTCT  CGTCC
                                  A___   ___
GAM1888 FCER1A   3' TGTTACATGGTTTTATATT   46403    C   A
                                TGT ACAT GTTTTATATT
                                ||| |||| ||||||||||
                                ACA TGTA CAAAATATAA
                                  A   C
GAM1888 MLLT4    3' GTATTTCACATATGCTATAT  46404    G     GTT
                                GTAT TCACATA  TTATAT
                                |||| |||||||  ||||||
                                CATA AGTGTAT  GATATA
                                  A     AC_
GAM1888 OGT      3' AAGTATGTTATCTAGTTCC   46405       CACA
                                AAGTATGT   TAGTTTT
                                ||||||||   |||||||
                                TTCATACA   ATCAAGG
                                     ATAG
GAM1888 SH3GL3   3' AAGTATGTCCAGAGTTT    46406       A  T
                                AAGTATGTC CA AGTTT
                                ||||||||| || |||||
                                TTCATACAG GT TCAAA
                                     _ C
GAM1888 DOK4     3' AGTATGTCATAAGCCATATAT 46407       CAT  TT
                                AGTATGTCA  AGT  TATAT
                                |||||||||  |||  |||||
                                TCATACAGT  TCG  ATATA
                                     AT_  GT
GAM1888 KIAA1240 3' AAGTATTTCACAGCAGTTATAT 46408     G   _   T
                                AAGTAT TCACA TAGTT TAT
                                |||||| ||||| ||||| |||
                                TTCATA AGTGT GTCAA ATA
                                   A   C   T
GAM1889 ABAT     5' GCGCCCCGAGTTCCGGCAGC  46411   A  AG  CC
                                GC CCCC  GAG  CCGGCAGC
                                || ||||  |||  ||||||||
                                CG GGGG  CTC  GGCCGTCG
                                 C   __  AA
GAM1889 ACLY     5' AGCACCCCAGCAGCCGGTAGC 46412       G  CC  C
                                AGCACCCCAG AGCC  GG AGC
                                |||||||||| ||||  || |||
                                TCGTGGGGTC TCGG  CC TCG
                                     G   __ A
GAM1889 ADRA2A   5' CAGCTCTCCAGGAGCCGC    46413    ACC      CCG
                                CAGC  CCAGGAGCC  GC
                                ||||  |||||||||  ||
                                GTCG  GGTCCTCGG  CG
                                  AGA       ___
GAM1889 ALK      5' GCACTGGAGCGGCCCCGGCGGC 46414    CCCA  ___     A
                                GCAC   GGA  GCCCCGGC GC
                                ||||   |||  |||||||| ||
```

```
                                CGTG   CCT  CGGGGCCG CG
                                  A___  CGC      C
GAM1889 ARHGAP6  5' GCGCTCCAAGTGCCCCGGCGGC 46415   ACC   A     A
                                GC  CCAGG GCCCCGGC GC
                                ||  ||||| |||||||| ||
                                CG  GGTTC CGGGGCCG CG
                                 CGA   A      C
GAM1889 ARHGAP6  5' GCGCTCCAAGTGCCCCGGCGGC 46415   ACC   A     A
                                GC  CCAGG GCCCCGGC GC
                                ||  ||||| |||||||| ||
                                CG  GGTTC CGGGGCCG CG
                                 CGA   A      C
GAM1889 AVP     5' GCTCCCCAGGAGCCCACGGC  46416   A        _
                                GC CCCCAGGAGCCC CGGC
                                || |||||||||||| ||||
                                CG GGGGTCCTCGGG GCCG
                                 A         T
GAM1889 B3GAT1   3' CAGTGTCCCAGCAGCCCCTGC  46417    CAC   G    G
                                CAG  CCCAG AGCCCC GC
                                |||  ||||| |||||| ||
                                GTC  GGGTC TCGGGG CG
                                  ACA   G    A
GAM1889 B3GAT1   3' CAGTGTCCCAGCAGCCCCTGC  46417    CAC   G    G
                                CAG  CCCAG AGCCCC GC
                                |||  ||||| |||||| ||
                                GTC  GGGTC TCGGGG CG
                                  ACA   G    A
GAM1889 B4GALT1  3' AGCCCCCGCCCCTGGCAG   46418    A  AGGA   _
                                AGC CCCC   GCCCC GGCAG
                                ||| ||||   ||||| |||||
                                TCG GGGG   CGGGG CCGTC
                                  _  ____   A
GAM1889 BACH2    5' CAGCCCCCTCCCGGCA     46419     A  AGGAGC
                                CAGC CCCC     CCCGGCA
                                |||| ||||     |||||||
                                GTCG GGGG     GGGCCGT
                                  _   A_____
GAM1889 BDP1     5' CAGCCCCGAGCCCCGGCG   46420     A  CAG       A
                                CAGC CCC  GAGCCCCGGC G
                                |||| |||  |||||||||| |
                                GTCG GGG  CTCGGGGCCG C
                                  _  ___        C
GAM1889 CACNA1C  3' GCGGCCCCGGCCCGGCGGC   46421   A_   A AGC    A
                                GC  CCCC GG   CCCGGC GC
                                ||  |||| ||   |||||| ||
                                CG  GGGG CC   GGGCCG CG
                                 CC   _ ___     C
GAM1889 CD81     3' GCTCCCAGGAGAGGCCTGGC  46422    AC      C__  C
                                GC  CCCAGGAG   CC GGC
                                ||  ||||||||   || |||
```

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                                CG  GGGTCCTC   GG CCG
                                 A_       TCC  A
GAM1889  CDKN2C   5'  CAGGTCCCGGGACTCCCGGCAG 46423     CAC   A   GC
              C                   CAG   CCC GGA  CCCGGCAGC
                                  |||   ||| |||  |||||||||
                                  GTC   GGG CCT  GGGCCGTCG
                                    CA_   C   GA
GAM1889  CHRNA4   3'  AGTACCCCAGGGGCTGAAGC   46424    C       A  CCC
                                  AG ACCCCAGG GC   GGC
                                  || ||||||||  ||   |||
                                  TC TGGGGTCC CG   TCG
                                   A       C  ACT
GAM1889  CHST6    5'  CAGCACCCCAAAGCTTGGCGGC 46425          G   CC__
                                  CAGCACCCCAG AGC    CGGC
                                  ||||||||||| |||    ||||
                                  GTCGTGGGGTT TCG    GCCG
                                        _   AACC
GAM1889  COMT     5'  CAGTGCCTCAGAAGCAGC    46426     CA  C      CCC
                                  CAG  CC CAGGAGC   GGC
                                  |||  || |||||||   |||
                                  GTC  GG GTCTTCG   TCG
                                    AC  A      ___
GAM1889  CRYBA2   5'  CAGCGTCTCAAGAGCCCCG    46427      ACCC
                                  CAGC    CAGGAGCCCCG
                                  ||||    ||||||||||
                                  GTCG    GTTCTCGGGGC
                                    CAGA
GAM1889  DLEC1    3'  CAGCACCCCAGAGCAGGGC    46428          G   CCC
                                  CAGCACCCCAG AGC   GGC
                                  |||||||||| |||   |||
                                  GTCGTGGGGTC TCG   CCG
                                        _   TC_
GAM1889  DLEC1    3'  CAGCACCCCAGAGCAGGGC    46428          G   CCC
                                  CAGCACCCCAG AGC   GGC
                                  |||||||||| |||   |||
                                  GTCGTGGGGTC TCG   CCG
                                        _   TC_
GAM1889  DLEC1    5'  CAGCACCCCAGAGCAGGGC    46428          G   CCC
                                  CAGCACCCCAG AGC   GGC
                                  |||||||||| |||   |||
                                  GTCGTGGGGTC TCG   CCG
                                        _   TC_
GAM1889  ESPN     3'  GCAGTGAAAGGGTCCCGGCAGC 46429     CCCC_   AGC
                                  GCA    AGG   CCCGGCAGC
                                  |||    |||   |||||||||
                                  CGT    TCC   GGGCCGTCG
                                    CACTT   CA_
GAM1889  ESRRA    5'  CACCTGGGGCTCCGGCAGC    46430     CCA  A  C
                                  CACC   GG GC CCGGCAGC
                                  ||||   || || ||||||||
```

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                                GTGG  CC CG GGCCGTCG
                                  AC_ _ A
GAM1889  FANCA    5'  GCGCCTACAGCCCCGGCGGC  46431    A  CCAGG       A
                                GC CC    AGCCCCGGC GC
                                || ||    ||||||||| ||
                                CG GG    TCGGGGCCG CG
                                 C  ATG__       C
GAM1889  FASN     3'  CAGCACCCCACGGGTGGC    46432         _ AGCCCC
                                CAGCACCCCA GG     GGC
                                |||||||||| ||     |||
                                GTCGTGGGGT CC     CCG
                                      G  CA____
GAM1889  FNTA     3'  CAGCACCCAAGGAGCATCAG  46433        C     CC
                                CAGCACCC AGGAGC  CGG
                                |||||||| ||||||  |||
                                GTCGTGGG TCCTCG  GTC
                                     T     TA
GAM1889  FOXG1B   5'  GCACTGAGCGCTCCGGCAGC  46434     CCCA  A  C
                                GCAC   GG GC CCGGCAGC
                                ||||   || || ||||||||
                                CGTG   TC CG GGCCGTCG
                                  AC__  G  A
GAM1889  GAS7     3'  CAGCAGAGTCCTGGCAG     46435      CCCCAG   C  C
                                CAGCA     GAG CC GGCAG
                                |||||     ||| || |||||
                                GTCGT     CTC GG CCGTC
                                  _______  A  A
GAM1889  GNA11    3'  CAGCGCCACCCGCCCGGCAGC  46436     A  _  AGGAGC
                                CAGC CC CC     CCCGGCAGC
                                |||| || ||     |||||||||
                                GTCG GG GG     GGGCCGTCG
                                  C  T  GC____
GAM1889  GRB10    5'  GCCCCCAGGAGCGCGGC     46437    A        CC
                                GC CCCCAGGAGC  CGGC
                                || ||||||||||  ||||
                                CG GGGGTCCTCG  GCCG
                                 _         C_
GAM1889  ILF1     3'  CAGCTCGGTGAGTCCCGGCAG  46438     ACCCCAG   C
                                CAGC      GAG CCCGGCAG
                                ||||      ||| ||||||||
                                GTCG      CTC GGGCCGTC
                                  AGCCA__   A
GAM1889  ITGB1    5'  CCCCCGCAGCTCCGGCAGC   46439     AGG   C
                                CCCC   AGC CCGGCAGC
                                ||||   ||| ||||||||
                                GGGG   TCG GGCCGTCG
                                  GCG   A
GAM1889  ITPA     3'  CAGGACCCCAGGCCTGGCGGC  46440    C       AGC  C   A
                                CAG ACCCCAGG   CC GGC GC
                                ||| ||||||||   || ||| ||
```

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                                GTC TGGGGTCC   GG CCG CG
                                  C       ___  A   C
GAM1889 LENG4    3'  CAGCGGCCCAGCAGGCGGCAG  46441     AC    G  CCC
                                CAGC  CCCAG AG   CGGCAG
                                ||||  ||||| ||   ||||||
                                GTCG  GGGTC TC   GCCGTC
                                  CC    G  C__
GAM1889 LRP2     5'  AGCACACCGCACCGGCAG    46442      C  AGGA  C
                                AGCAC CC    GC CCGGCAG
                                ||||| ||    || |||||||
                                TCGTG GG    CG GGCCGTC
                                  T  _____  T
GAM1889 MAP3K7IP1 3'  GCAATCCTGGCCGACAGC    46443     CC  A  AGCC
                                GCA  CC GG    CCGGCAGC
                                |||  || ||   ||||||||
                                CGT  GG CC    GGCTGTCG
                                  TA  A  _____
GAM1889 MAPRE3   3'  CAGCACCCTGGGAAGTGTTGGG 46444        CA    CCCC__
              C                  CAGCACCC  GGAG     GGC
                                |||||||  ||||     |||
                                GTCGTGGG  CCTT     CCG
                                    AC    CACAAC
GAM1889 MFGE8    3'  ACCCCAGGGCCGACG       46445        A   CC   A
                                ACCCCAGG GCC  GGC G
                                |||||||| |||  ||| |
                                TGGGGTCC CGG  CTG C
                                    _   __   _
GAM1889 MLLT1    3'  CAGCCTCCCAGGACCCCGGC   46446     AC      G
                                CAGC  CCCAGGA CCCCGGC
                                ||||  ||||||| |||||||
                                GTCG  GGGTCCT GGGGCCG
                                  GA      _
GAM1889 MYOG     3'  GCACCCCAGAGCTGGC      46447         G   CCC
                                GCACCCCAG AGC   GGC
                                ||||||||| |||   |||
                                CGTGGGGTC TCG   CCG
                                    _   A__
GAM1889 NCKAP1   5'  CAGCAGCCCGCGCCCCGGCAGC 46448      C   AGGA
                                CAGCA CCC    GCCCCGGCAGC
                                ||||| |||    ||||||||||
                                GTCGT GGG    CGGGGCCGTCG
                                  C   CG__
GAM1889 NEUROD2  3'  GCTGCCCCAGGAGAGCGGC    46449    A_       CCC
                                GC  CCCCAGGAG   CGGC
                                ||  |||||||||   ||||
                                CG  GGGGTCCTC   GCCG
                                 AC        TC_
GAM1889 PKD2L1   5'  ACCCCAGGTGCCCACTCTCAGC 46450         A    CGG__
                                ACCCCAGG GCCC     CAGC
                                |||||||| ||||     ||||
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                                TGGGGTCC CGGG    GTCG
                                    A   TGAGA
GAM1889 PTPRH    3' CAGCACCCAGGAGTCTGGGAGC 46451        C    CCCC C
                                CAGCACCC AGGAG   GG AGC
                                |||||||| |||||   || |||
                                GTCGTGGG TCCTC   CC TCG
                                    _    AGAC  _
GAM1889 SLC22A2  5' CACTCCGGGGCTCCGGCAGC  46452    C A A C
                                CAC CC GG GC CCGGCAGC
                                ||| || || || ||||||||
                                GTG GG CC CG GGCCGTCG
                                  A C _ A
GAM1889 SMARCD2  3' GCATCCCAGGAGATGATGGCGG 46453    C      CCCC_  A
            C                    GCA CCCAGGAG    GGC GC
                                ||| ||||||||    ||| ||
                                CGT GGGTCCTC    CCG CG
                                  A       TACTA   C
GAM1889 SNL     3' CAGCAGGGGGGCCCCGGCGGC  46454     CCCCA A     A
                                CAGCA    GG GCCCCGGC GC
                                |||||    || |||||||| ||
                                GTCGT    CC CGGGGCCG CG
                                   CCC__ _      C
GAM1889 TMEFF2   5' GCGCCCCGCAGCCCGGCAGC  46455   A   AGG    C
                                GC CCCC   AGCCC GGCAGC
                                || ||||   ||||| ||||||
                                CG GGGG   TCGGG CCGTCG
                                 C   CG_   _
GAM1889 TMEPAI   5' GCAGCCCCGGGGGGCGTCGGCAG 46456    _   A A CC
                                GCA CCCC GG GC  CGGCAG
                                ||| |||| || ||  ||||||
                                CGT GGGG CC CG  GCCGTC
                                  C   C C CA
GAM1889 TNFRSF6B 5' CAGCACCCGGCACTGGCTGGCA 46457        CA  A  CCC__
            GC                    CAGCACCC  GG GC    GGCAGC
                                |||||||  || ||    ||||||
                                GTCGTGGG  CC TG    CCGTCG
                                    __  G  ACCGA
GAM1889 TRIM9    5' CAGCACCCTGGCCAGCGGCGGC 46458        CA  __   CC
                                CAGCACCC  GG  AGC  CGGC
                                ||||||||  ||  |||  ||||
                                GTCGTGGG  CC  TCG  GCCG
                                    A_  GG   CC
GAM1889 TRIM9    5' CAGCACCCTGGCCAGCGGCGGC 46458        CA  __   CC
                                CAGCACCC  GG  AGC  CGGC
                                ||||||||  ||  |||  ||||
                                GTCGTGGG  CC  TCG  GCCG
                                    A_  GG   CC
GAM1889 TRRAP    5' CAGCCCCGACCTCGGCG    46459     A  CAGGA  C   A
                                CAGC CCC    GCC CGGC G
                                |||| |||    ||| |||| |
```

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                                GTCG GGG    TGG GCCG C
                                  _  C____  A   C
GAM1889 TSSC4    3' ACACCCCAGGAGCTTCAGC   46460          CC
                                GCACCCCAGGAGC CGGC
                                |||||||||||| ||||
                                TGTGGGGTCCTCG GTCG
                                       AA
GAM1889 USP7     3' ACCCCAGGAAGGCAG      46461         CCCC
                                ACCCCAGGAG   GGCAG
                                |||||||||   |||||
                                TGGGGTCCTT   CCGTC
                                      _____
GAM1889 C11orf11 3' GCACCCCAGGGGGCCGGC   46462         AGCC
                                GCACCCCAGG   CCGGC
                                |||||||||   |||||
                                CGTGGGGTCC   GGCCG
                                      CCC_
GAM1889 C16orf5  3' AGCACCCCAGAGGCGCAA   46463         GA  CCCG
                                AGCACCCCAG  GC   GCAG
                                |||||||||  ||   ||||
                                TCGTGGGGTC  CG   CGTT
                                      TC  _____
GAM1889 C20orf102 5' GCTGCCCGGCTCCGGCAGC   46464    AC   A  AGCC
                                GC  CCC GG   CCGGCAGC
                                ||  ||| ||   ||||||||
                                CG  GGG CC   GGCCGTCG
                                 AC   _  GA__
GAM1889 C9orf7   3' GCACCTTAGGAGCCCTGTGGGC 46465      CC       C___
                                GCACC  AGGAGCCC   GGC
                                |||||  ||||||||   |||
                                CGTGG  TCCTCGGG   CCG
                                   AA       ACAC
GAM1889 CAMKK2   5' GCACTCCCATCCGGCAG    46466     _   GGAGCC
                                GCAC CCCA     CCGGCAG
                                |||| ||||     |||||||
                                CGTG GGGT     GGCCGTC
                                  A   A_____
GAM1889 CENTA1   3' CAGTCCCCAGCGGCCGGCAGC  46467    CA    GA   CC
                                CAG  CCCCAG  GCC  GGCAGC
                                |||  ||||||  |||  ||||||
                                GTC  GGGGTC  CGG  CCGTCG
                                 A_     GC   __
GAM1889 CHST3    3' CAGCGTTTCCAGGAGACGGC   46468     ACC_     CCC
                                CAGC   CCAGGAG   CGGC
                                ||||   |||||||   ||||
                                GTCG   GGTCCTC   GCCG
                                  CAAA      T__
GAM1889 COPS7A   5' GCTCCGTCACCTCCGGCAGC   46469    A  CCAGGA   _
                                GC CC     GCC CCGGCAGC
                                || ||     ||| ||||||||
```

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                                CG GG     TGG GGCCGTCG
                                 A  CAG___   A
GAM1889  D15Wsu75e 5'  CCCTCGGGCACCCGGCAGC   46470    CA  A  _
                                CCC  GG GC CCCGGCAGC
                                |||  || || |||||||||
                                GGG  CC CG GGGCCGTCG
                                  AG  _  T
GAM1889  DKFZP564O0423 3'  CAGCACTTCAGGAGGCCAAGG  46471       CC     _  CC
                                CAGCAC  CAGGAG CC  GG
                                ||||||  |||||| ||  ||
                                GTCGTG  GTCCTC GG  CC
                                    AA     C  TT
GAM1889  DKFZP761E2110 5'  GCGTCCCACCGCCGGCAGC   46472    AC   AGGA  _
                                GC  CCC    GCC CCGGCAGC
                                ||  |||    ||| ||||||||
                                CG  GGG    TGG GGCCGTCG
                                 CA  _____  C
GAM1889  DRIL2    5'  CAGGCCCCGGCGCGGCAG    46473    CA   A  A  CCC
                                CAG  CCCC GG GC   GGCAG
                                |||  |||| || ||   |||||
                                GTC  GGGG CC CG   CCGTC
                                  C_   _  G  ___
GAM1889  EIF2S2   5'  CAGCCCCAGGCCCCGGCG    46474     AC    GA      A
                                CAGC  CCCAG  GCCCCGGC G
                                ||||  |||||  |||||||| |
                                GTCG  GGGTC  CGGGGCCG C
                                  __    __       C
GAM1889  FLJ10829  3'  CAGACGTCCTGTGGCCCCGGC  46475    C  C_  AGGA
                                CAG AC  CC    GCCCCGGC
                                ||| ||  ||    ||||||||
                                GTC TG  GG    CGGGGCCG
                                  _  CA  ACAC
GAM1889  FLJ10925  5'  ACCCCGCACCGCCCCGGCAGC  46476      AGGA_
                                ACCCC    GCCCCGGCAGC
                                |||||    ||||||||||
                                TGGGG    CGGGGCCGTCG
                                   CGTGG
GAM1889  FLJ12666  5'  GCGCCTCCAGCACCCGGCAGC  46477    A  _   GA   C
                                GC CC CCAG  GCCC GGCAGC
                                || || ||||  |||| ||||||
                                CG GG GGTC  TGGG CCGTCG
                                 C  A   G_   _
GAM1889  FLJ14126  3'  CAGCTCCCAGGAGCACAGC   46478     AC       CC
                                CAGC  CCCAGGAGC  CGGC
                                ||||  |||||||||  ||||
                                GTCG  GGGTCCTCG  GTCG
                                  A_       T_
GAM1889  FLJ14154  3'  CAGCACCCTGAGAGCCCGTGGC 46479        CA     C_
                                CAGCACCC  GGAGCCC  GGC
                                ||||||||  |||||||  |||
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                                GTCGTGGG  TCTCGGG  CCG
                                    AC      CA
GAM1889  FLJ14827  5'  CCCCGGACCCCCGGCAGC    46480     A   G
                                CCCC GGA CCCCGGCAGC
                                |||| ||| ||||||||||
                                GGGG CCT GGGGCCGTCG
                                  _   G
GAM1889  FLJ20255  3'  GCTTTCCAGGAGCGGGGCAGC  46481    ACC       CCC
                                GC   CCAGGAGC   GGCAGC
                                ||   ||||||||   ||||||
                                CG   GGTCCTCG   CCGTCG
                                 AAA       CC_
GAM1889  FLJ21415  5'  CCCCTACGCGCCCGGCAGC   46482     AGGA  _
                                CCCC    GC CCCGGCAGC
                                ||||    || |||||||||
                                GGGG    CG GGGCCGTCG
                                  ATG_  C
GAM1889  FLJ22393  3'  GCACCCCTCTCTTCCGGCAGC  46483       AGGAGCC
                                GCACCCC      CCGGCAGC
                                |||||||      ||||||||
                                CGTGGGG      GGCCGTCG
                                    AGAGAA_
GAM1889  FLJ22692  3'  GCCACCCCAGTGCTGGCAG   46484    _     GA  CCC
                                GC ACCCCAG  GC   GGCAG
                                || |||||||  ||   |||||
                                CG TGGGGTC  CG   CCGTC
                                 G      A_  A__
GAM1889  FLJ22944  5'  CAGCACCCCAGGGCGGG     46485          A  CCC
                                CAGCACCCCAGG GC   GG
                                |||||||||||| ||   ||
                                GTCGTGGGGTCC CG   CC
                                       _  C__
GAM1889  FSD1      3'  CAGCAGCCTGGGCTTGGCGGC  46486      C  CA  A  CC__
                                CAGCA CC  GG GC    CGGC
                                ||||| ||  || ||    ||||
                                GTCGT GG  CC CG    GCCG
                                   C  A_  _  AACC
GAM1889  GLIS2     3'  CAGCACCCAGGAGCACAGC   46487        C     CC
                                CAGCACCC AGGAGC  CGGC
                                |||||||| ||||||  ||||
                                GTCGTGGG TCCTCG  GTCG
                                    _      T_
GAM1889  GPS2      5'  GCACCCCAGGGGACGCGGGC   46488          A_  CCC
                                GCACCCCAGG  GC   GGC
                                ||||||||||  ||   |||
                                CGTGGGGTCC  TG   CCG
                                      CC  CGC
GAM1889  GS3955    3'  CAGACTCCAGGAGCTTGC    46489     C  C       CCCG
                                CAG AC CCAGGAGC    GC
                                ||| || ||||||||    ||
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                                GTC TG GGTCCTCG    CG
                                  _ A       AA__
GAM1889 HSD-3.1   5' GCCGGGCCCAGCCCCGGCAG  46490    AC__    GGA
                                GC   CCCA  GCCCCGGCAG
                                ||   ||||  ||||||||||
                                CG   GGGT  CGGGGCCGTC
                                 GCCC   ___
GAM1889 HSPC189   3' ACCTGGGGCACCCGGCAGC   46491     CCA  A  _
                                ACC   GG GC CCCGGCAGC
                                |||   || || |||||||||
                                TGG   CC CG GGGCCGTCG
                                  AC_  _  T
GAM1889 IKKE      5' GCCACCCCAGGAGCTGGGAC  46492    _         CCC
                                GC ACCCCAGGAGC   GGC
                                || ||||||||||   |||
                                CG TGGGGTCCTCG   CTG
                                 G          ACC
GAM1889 KHDRBS3   5' CAGCCCCGATCCCCGGTG    46493     A   CAG  G     CA
                                CAGC CCC   GA CCCCGG  G
                                |||| |||   || ||||||  |
                                GTCG GGG   CT GGGGCC  C
                                  _   ___  A     AC
GAM1889 KIAA0014  3' CAGGACCCCAGACGGCAG    46494     C       AGCCC
                                CAG ACCCCAGG    CGGCAG
                                ||| ||||||||    ||||||
                                GTC TGGGGTCT    GCCGTC
                                  C       _____
GAM1889 KIAA0258  3' CAGCACCCAGGAGTCTACAGC  46495        C    CCCCG
                                CAGCACCC AGGAG    GCAGC
                                |||||||| |||||    |||||
                                GTCGTGGG TCCTC    TGTCG
                                     _    AGA__
GAM1889 KIAA0339  3' CAGTTTAGGGAGCCCCGGCAGC 46496     CACCCCA
                                CAG      GGAGCCCCGGCAGC
                                |||      ||||||||||||||
                                GTC      CCTCGGGGCCGTCG
                                  AAATC__
GAM1889 KIAA0469  3' CAGTACCCCAGAGGGGTGGC   46497     C      G  CCCC
                                CAG ACCCCAG AG    GGC
                                ||| ||||||| ||    |||
                                GTC TGGGGTC TC    CCG
                                  A      _  CCCA
GAM1889 KIAA0478  3' GCATCTGATGGGCCCCGGCAGC 46498     CCCCA_  A
                                GCA     GG GCCCCGGCAGC
                                |||     || ||||||||||
                                CGT     CC CGGGGCCGTCG
                                  AGACTA  _
GAM1889 KIAA0831  3' CAGCACCCTAGGAGGCCAAGGC 46499        C    _  CC
                                CAGCACCC AGGAG CC  GGC
                                |||||||| ||||| ||  |||
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                                GTCGTGGG TCCTC GG  CCG
                                    A    C  TT
GAM1889  KIAA1007  5'  GCACCTCAGGCGGCTCCGGCAG 46500      C   A_  C
             C                   GCACC CAGG  GC CCGGCAGC
                                 ||||| ||||  || ||||||||
                                 CGTGG GTCC  CG GGCCGTCG
                                   A   GC  A
GAM1889  KIAA1036  5'  ACACCCCAACTTGGCAG    46501        GGA  CCC
                                 GCACCCCA  GC  GGCAG
                                 ||||||||  ||  |||||
                                 TGTGGGGT  TG  CCGTC
                                     ___  AA_
GAM1889  KIAA1096  3'  CAGACCCCAGGAGGGTCGG   46502    C        CCC
                                 CAG ACCCCAGGAG  CGG
                                 ||| ||||||||||  |||
                                 GTC TGGGGTCCTC  GCC
                                   _       CCA
GAM1889  KIAA1157  5'  GCGCTCCAGGAGCGCCCAGGCG 46503    ACC      _  _  A
             GC                   GC  CCAGGAGC CCC GGC GC
                                 ||  |||||||| ||| ||| ||
                                 CG  GGTCCTCG GGG CCG CG
                                  CGA      C  T  C
GAM1889  KIAA1170  3'  CAGCACCCTGGGAGGTGGAGGC 46504        CA   CCCC_
                                 CAGCACCC  GGAG   GGC
                                 ||||||||  ||||   |||
                                 GTCGTGGG  CCTC   CCG
                                     AC   CACCT
GAM1889  KIAA1254  5'  GCGCCTCCTGCCCGGCAGC   46505   A  _  AGGA   C
                                 GC CC CC   GCCC GGCAGC
                                 || || ||   |||| ||||||
                                 CG GG GG   CGGG CCGTCG
                                  C  A  A___   _
GAM1889  KIAA1464  5'  GCTCCAGGAGCGCGGCAGC   46506   ACC      CC
                                 GC  CCAGGAGC  CGGCAGC
                                 ||  ||||||||  |||||||
                                 CG  GGTCCTCG  GCCGTCG
                                  A__      C_
GAM1889  KIF1C    3'  CAGCACTTCTGGGGAAGCAGC  46507      CCCA__  GCCCC
                                 CAGCAC    GGA   GGCAGC
                                 ||||||    |||   ||||||
                                 GTCGTG    CCT   TCGTCG
                                    AAGACC  _____
GAM1889  LGI2     3'  CAGACCCCAGGAGCTTGC    46508    C        CCCG
                                 CAG ACCCCAGGAGC   GC
                                 ||| ||||||||||   ||
                                 GTC TGGGGTCCTCG   CG
                                   _       AA__
GAM1889  MEF-2    3'  GCACTCCAGCAGCCTGGGC   46509     C   G   CC
                                 GCAC CCAG AGCC  GGC
                                 |||| |||| ||||  |||
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                                CGTG GGTC TCGG  CCG
                                  A   G   AC
GAM1889 MGC10870 5' GCTGTCCCAGGAGCCGGAGC  46510   AC_      CC
                                GC  CCCAGGAGCC  GGC
                                ||  ||||||||||  |||
                                CG  GGGTCCTCGG  TCG
                                 ACA       CC
GAM1889 MGC11303 5' GCGCCGAGTCCCGGCAG    46511   A  CCAG  C
                                GC CC   GAG CCCGGCAG
                                || ||   ||| ||||||||
                                CG GG   CTC GGGCCGTC
                                 C ____  A
GAM1889 MGC12921 3' CAGGCCCTTTAGCTCTCTGGCA 46512    CAC  AGG  CCC__
           GC                    CAG  CCC  AGC   GGCAGC
                                |||  |||  |||   ||||||
                                GTC  GGG  TCG   CCGTCG
                                 C__  AAA  AGAGA
GAM1889 MGC14161 5' GCGTCCCTCAGCCCGGCAGC  46513   A_  _  GAGC
                                GC  CCC CAG   CCCGGCAGC
                                ||  ||| |||   |||||||||
                                CG  GGG GTC   GGGCCGTCG
                                 CA  A  ____
GAM1889 MGC14859 3' ACCCTGGCCACCCGGCAGC   46514    CA  AGC
                                ACCC  GG  CCCGGCAGC
                                ||||  ||  |||||||||
                                TGGG  CC  GGGCCGTCG
                                  A_  GGT
GAM1889 MGC16279 5' AGACCTCAGGAGCCCGC    46515   C  C      CG
                                AG ACC CAGGAGCCC  GC
                                || ||| |||||||||  ||
                                TC TGG GTCCTCGGG  CG
                                 _  A       __
GAM1889 MGC5442  3' CAGCAGCCCCGGGAGGTGGC  46516     _   A   CCCC
                                CAGCA CCCC GGAG   GGC
                                ||||| |||| ||||   |||
                                GTCGT GGGG CCTC   CCG
                                   C   C   CA__
GAM1889 moblak   3' CCCAGGAGTCCAGGAAGC   46517       C  C  C
                                CCCAGGAG CC GG AGC
                                |||||||| || || |||
                                GGGTCCTC GG CC TCG
                                    A  T  T
GAM1889 NBL1     5' GCGCCCCAGGAGGCTCGGC   46518   A      CCC
                                GC CCCCAGGAG  CGGC
                                || |||||||||  ||||
                                CG GGGGTCCTC  GCCG
                                 C       CGA
GAM1889 NEIL2    3' GCACCCCAGGAAGGCGCAGC  46519         CCCCG
                                GCACCCCAGGAG   GCAGC
                                ||||||||||||   |||||
```

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                                CGTGGGGTCCTT    CGTCG
                                      CCG__
GAM1889 NXPH3    3' CAGCCCCCGGTTCTCCTGGCAG 46520     A   A AGC_ C
                                CAGC CCCC GG   CC GGCAG
                                |||| |||| ||   || |||||
                                GTCG GGGG CC   GG CCGTC
                                  _   _ AAGA A
GAM1889 P38IP    5' GCGCCGCCTGCTCGGCAGC   46521    A _ AGGA CC
                                GC CC CC   GC CGGCAGC
                                || || ||   ||  |||||||
                                CG GG GG   CG  GCCGTCG
                                 C  C  A___  A_
GAM1889 PGS1     5' GCGTCCCAGGAGCGCGGC    46522    AC       CC
                                GC  CCCAGGAGC  CGGC
                                ||  |||||||||  ||||
                                CG  GGGTCCTCG  GCCG
                                 CA       C_
GAM1889 PRO2389  3' ACACCCCAGATAATGGCAG   46523         AGCCCC
                                GCACCCCAGG     GGCAG
                                ||||||||||     |||||
                                TGTGGGGTCT     CCGTC
                                      ATTA__
GAM1889 RAB17    3' CAGCCCCCAGGAGTGGC     46524     A       CCCC
                                CAGC CCCCAGGAG   GGC
                                |||| |||||||||   |||
                                GTCG GGGGTCCTC   CCG
                                  _       A___
GAM1889 RGS7     5' GCACAGGCGGCTCCGGCAGC  46525     CCC  A_ C
                                GCAC  AGG  GC CCGGCAGC
                                ||||  |||  || ||||||||
                                CGTG  TCC  CG GGCCGTCG
                                  ___  GC  A
GAM1889 RLUCL    5' CAGCACTACCAGGCCCGGCAGC 46526       C_    AGC
                                CAGCAC  CCAGG   CCCGGCAGC
                                ||||||  |||||   |||||||||
                                GTCGTG  GGTCC   GGGCCGTCG
                                   AT    ___
GAM1889 RNPC1    3' GCCACCCCGGCAGGCGGCAGC  46527    _    A  AGCCC
                                GC ACCCC GG    CGGCAGC
                                || ||||| ||    |||||||
                                CG TGGGG CC    GCCGTCG
                                 G    _ GTCC_
GAM1889 RRS1     5' GCGGCCCAAACTCCGGCAGC   46528    AC    GA  C
                                GC  CCCAG  GC CCGGCAGC
                                ||  |||||  || ||||||||
                                CG  GGGTT  TG GGCCGTCG
                                 CC    __ A
GAM1889 SCYA28   3' CAGCACCCTGGGAGGCCAAGGC 46529        CA   _ CC
                                CAGCACCC  GGAG CC  GGC
                                ||||||||  |||| ||  |||
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                                GTCGTGGG  CCTC GG  CCG
                                    AC    C  TT
GAM1889  SDC3     3'  CAGCACCCCAGGGAGCAGGG   46530          _   CCC
                                CAGCACCCCAGG AGC   GG
                                |||||||||||| |||   ||
                                GTCGTGGGGTCC TCG   CC
                                      C   TC_
GAM1889  SES2     3'  CAGCTCCCAGGAGCAGGGC    46531      AC        CCC
                                CAGC  CCCAGGAGC   GGC
                                ||||  |||||||||   |||
                                GTCG  GGGTCCTCG   CCG
                                  A_        TC_
GAM1889  SNFT     5'  GCGCGCCAGTCCCGGCAGC    46532    ACC    GAGC
                                GC   CCAG    CCCGGCAGC
                                ||   ||||    |||||||||
                                CG   GGTC    GGGCCGTCG
                                 CGC    A___
GAM1889  STAG1    5'  CAGCACCCTGAGGGCCTGAAC  46533         C_   A   CC
                                CAGCACCC  AGG GCC  GGC
                                ||||||||  ||| |||  |||
                                GTCGTGGG  TCC CGG  TTG
                                     AC   _   AC
GAM1889  TLN1     3'  CAGCCCAGAAGGCTTTGGTAG  46534    C       _ CCC  C
                                CA CCCAGGAG C   GG AG
                                || |||||||| |   || ||
                                GT GGGTCTTC G   CC TC
                                 C       C AAA  A
GAM1889  TLN2     5'  ACCGCCCCAGCGAGGGTCCTGG 46535    A_      _   C__  C
            CAGC                    GC  CCCCAG GAG   CC GGCAGC
                                ||  |||||| |||   || ||||||
                                TG  GGGGTC CTC   GG CCGTCG
                                 GC     G   CCA  A
GAM1889  TU3A     3'  CAGTGGCCTGAGCCCGGCAGC  46536     CACC  AG     C
                                CAG    CC  GAGCCC GGCAGC
                                |||    ||  |||||| ||||||
                                GTC    GG  CTCGGG CCGTCG
                                  ACC_  A_     _
GAM1889  UBE3B    3'  GCAGCCCAGGAGCCCTGGAGGC 46537     C         C  CA
                                GCA CCCAGGAGCCC GG  GC
                                ||| ||||||||||| ||  ||
                                CGT GGGTCCTCGGG CC  CG
                                  C         A  TC
GAM1889  WBSCR17  3'  AGCATCTTCAAGGGTCCTGGCA 46538      CCC_   AGC  C
            GC                    AGCA    CAGG   CC GGCAGC
                                ||||    ||||   || ||||||
                                TCGT    GTTC   GG CCGTCG
                                  AGAA    CCA  A
GAM1889  LOC122792 5'  CAGTGACTCCAGCAGCGGCGGC 46539     C_  C    G   CC
                                CAG  AC CCAG AGC  CGGC
                                |||  || |||| |||  ||||
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                                GTC  TG GGTC TCG  GCCG
                                  AC  A    G   CC
GAM1889  LOC130327 3'  CAGACCCCAGGAGGTCAGC   46540     C        CCC
                                CAG ACCCCAGGAG   CGGC
                                ||| ||||||||||   ||||
                                GTC TGGGGTCCTC   GTCG
                                  _        CA_
GAM1889  LOC144519 5'  CAGCACTTTGGGAAGCCAAGGC 46541       CCCA_     CC
                                CAGCAC    GGAGCC  GGC
                                ||||||    ||||||  |||
                                GTCGTG    CTTCGG  CCG
                                   AAACC     TT
GAM1889  LOC146823 3'  CAGCCCTTCAGGAGCCAGC   46542      A  C_       CC
                                CAGC CC  CAGGAGCC  GGC
                                |||| ||  ||||||||  |||
                                GTCG GG  GTCCTCGG  TCG
                                  _  AA       __
GAM1889  LOC147229 3'  CAGCATCCCAGGAGGCCC    46543      C       C
                                CAGCA CCCAGGAG CCC
                                ||||| |||||||| |||
                                GTCGT GGGTCCTC GGG
                                   A       C
GAM1889  LOC147791 3'  CAGCATCCCGGCGGCGCAGGC  46544       _   CA_  A  CCC
                                CAGCA CCC   GG GC   GGC
                                ||||| |||   || ||   |||
                                GTCGT GGG   CC CG   CCG
                                   A   CCG  G  T__
GAM1889  LOC150135 3'  GCTCTCCCTCCCCGGCAGC   46545    AC_   AGGAG
                                GC   CCC    CCCCGGCAGC
                                ||   |||    ||||||||||
                                CG   GGG    GGGGCCGTCG
                                 AGA   A____
GAM1889  LOC150271 5'  CAGCACCCGGGAGTGGGGGC   46546        CA    CCCC
                                CAGCACCC  GGAG    GGC
                                ||||||||  ||||    |||
                                GTCGTGGG  CCTC    CCG
                                     C_    ACCC
GAM1889  LOC150622 5'  CAGTGCCCAGGAAGGGCAG    46547     CAC       CCCC
                                CAG   CCCAGGAG    GGCAG
                                |||   ||||||||    |||||
                                GTC   GGGTCCTT    CCGTC
                                  AC_       C___
GAM1889  LOC151429 3'  GCTCCCACTGACCCCGGCAGC  46548    A   CAG  G
                                GC CCC   GA CCCCGGCAGC
                                || |||   || ||||||||||
                                CG GGG   CT GGGGCCGTCG
                                 A   TGA  _
GAM1889  LOC153196 5'  ACCTGCAAGTCCCGGCAG    46549     C_    AGC
                                ACC  CAGG   CCCGGCAG
                                |||  ||||   ||||||||
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                                TGG  GTTC   GGGCCGTC
                                  AC    A__
GAM1889  LOC158263 3'  CAGGGCCCCAGGAGTCACTTAG 46550     CA        CCCC__
              C                    CAG  CCCCAGGAG      GGC
                                  |||  |||||||||      |||
                                  GTC  GGGGTCCTC      TCG
                                    CC        AGTGAA
GAM1889  LOC163609 5'  CAGGTCCCGGGGGCCCCGGC   46551     CAC   A  A
                                  CAG   CCC GG GCCCCGGC
                                  |||   ||| || ||||||||
                                  GTC   GGG CC CGGGGCCG
                                    CA_   C  C
GAM1889  LOC164537 5'  GCACCCCAGGATGCTGACGCCG 46552           _  C_____
              GC                   GCACCCCAGGA GC     CCGGC
                                  ||||||||||| ||     |||||
                                  CGTGGGGTCCT CG     GGCCG
                                         A  ACTGC
GAM1889  LOC166341 3'  GCACCCCAGGGGCTTCCAG    46553          A  C_
                                  GCACCCCAGG GC  CCGG
                                  |||||||||| ||  ||||
                                  CGTGGGGTCC CG  GGTC
                                        C  AA
GAM1889  LOC199678 3'  CAGCACCCGGGAGGGAATCAG  46554         CA    CCCCGG
                                  CAGCACCC  GGAG     CAG
                                  ||||||||  ||||     |||
                                  GTCGTGGG  CCTC     GTC
                                       C_    CCTTA_
GAM1889  LOC200057 5'  CAGCCGCTCCGCCCGGCAG    46555     ACC_  AGGA    C
                                  CAGC    CC    GCCC GGCAG
                                  ||||    ||    |||| |||||
                                  GTCG    GG    CGGG CCGTC
                                    GCGA  _____    _
GAM1889  LOC200220 5'  CAGCAGCCCAGGGGTCGGC    46556      C     AGCCC
                                  CAGCA CCCAGG     CGGC
                                  ||||| ||||||     ||||
                                  GTCGT GGGTCC     GCCG
                                     C     CCA__
GAM1889  LOC200314 5'  CAACACCCTGGGGAGGTAGC   46557         CA_    CCCC
                                  CAGCACCC   GGAG    GGC
                                  ||||||||   ||||    |||
                                  GTTGTGGG   CCTC    TCG
                                       ACC    CA__
GAM1889  LOC204804 3'  CAGCACTTTGGGACGCCACAG  46558       CCCA   _   C
                                  CAGCAC    GGA GCC CGG
                                  ||||||    ||| ||| |||
                                  GTCGTG    CCT CGG GTC
                                     AAAC   G   T
GAM1889  LOC206426 5'  CAGCCCCCTTCCCGGCAGC    46559      A    AGGAGC
                                  CAGC CCCC     CCCGGCAGC
                                  |||| ||||     |||||||||
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                                GTCG GGGG     GGGCCGTCG
                                  _   AA____
GAM1889  LOC219649 3'  CAGCACCTAAAAGCCCCTGGCA 46560       CC       _
                 G                 CAGCACC  AGGAGCCCC GGCAG
                                   ||||||| |||||||| |||||
                                   GTCGTGG  TTTTCGGGG CCGTC
                                      A_       A
GAM1889  LOC219994 5'  GCAGCCCCGGGAGCCCGG    46561    _   A     C
                                   GCA CCCC GGAGCCC GG
                                   ||| |||| ||||||| ||
                                   CGT GGGG CCTCGGG CC
                                     C   C     _
GAM1889  LOC220538 3'  AACATCCTGCTCACCGGCAGC  46562     C  CAGGA  C__
                                   AGCA CC    GC   CCGGCAGC
                                   |||| ||    ||   ||||||||
                                   TTGT GG    CG   GGCCGTCG
                                     A  A____  AGT
GAM1889  LOC221092 3'  CACCACCCCTCCCCGGCAG   46563    G     AGGAG
                                   CA CACCCC    CCCCGGCAG
                                   || ||||||    |||||||||
                                   GT GTGGGG    GGGGCCGTC
                                    G     A____
GAM1889  LOC221463 3'  CCCAGGAGCCCTCCCAGC    46564          CGG
                                   CCCAGGAGCCC   CAGC
                                   ||||||||||   ||||
                                   GGGTCCTCGGG   GTCG
                                         AGG
GAM1889  LOC253181 3'  AGCGCCTCGGGAGCCCCGAATA 46565     A  CCA        C_
                 GC                  AGC CC   GGAGCCCCGG  AGC
                                     ||| ||   ||||||||||  |||
                                     TCG GG   CCTCGGGGCT  TCG
                                       C  AGC         TA
GAM1889  LOC255838 5'  CAGCCTCACCTCGGCCCCGGCG 46566      ACC_  AGGA       A
                 GC                  CAGC    CC    GCCCCGGC GC
                                     ||||    ||    |||||||| ||
                                     GTCG    GG    CGGGGCCG CG
                                       GAGT  AGC_       C
GAM1889  LOC256107 5'  CAGCACCCAGGGGTCCGAGC   46567        C   AGCC   _
                                     CAGCACCC AGG    CCG GC
                                     |||||||| |||    ||| ||
                                     GTCGTGGG TCC    GGC CG
                                          _   CCA_   T
GAM1889  LOC256812 5'  GCCATCATAAGTCCTGGCAGC  46568    ACCC  G   C  C
                                     GC    CA GAG CC GGCAGC
                                     ||    || ||| || ||||||
                                     CG    GT TTC GG CCGTCG
                                      GTA_  A   A  A
GAM1889  LOC90120  5'  GCATTGGGCCCCGGCGGC    46569     CCCCA  A       A
                                     GCA     GG GCCCCGGC GC
                                     |||     || |||||||| ||
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                                CGT    CC CGGGGCCG CG
                                  AA___ _      C
GAM1889 LOC90148 3' CATCCCAGGAGCTCCCAGAG  46570   C      _    C
                                CA CCCAGGAGC CCCGG AG
                                || ||||||||| ||||| ||
                                GT GGGTCCTCG GGGTC TC
                                 A       A    _
GAM1889 LOC90529 5' AGCACCTGGTCCGGTCCCGGCA 46571       ____ A  AGC
           GC                    AGCACC   CC GG   CCCGGCAGC
                                ||||||   || ||  |||||||||
                                TCGTGG   GG CC   GGGCCGTCG
                                   ACCA  _  A__
GAM1889 LOC91069 3' AGACCTCAGGAGCCTGC    46572   C  C      CCG
                                AG ACC CAGGAGCC   GC
                                || ||| ||||||||   ||
                                TC TGG GTCCTCGG   CG
                                 _  A      A__
GAM1889 LOC91663 5' ACCCAGCAGGGCCCTGGC   46573     __   A   C
                                ACCC  CAGG GCCC GGC
                                ||||  |||| |||| |||
                                TGGG  GTCC CGGG CCG
                                  TC   _   A
GAM1890 MSN     3' TGTTATAGCTGGAGAGGA    46576        C  T  C
                                TGTTGTAGC GG GG GA
                                ||||||||| || || ||
                                ACAATATCG CC CT CT
                                     A  T  C
GAM1890 HUMGT198A 5' GTTGTAGTTGGTGGTCCG   46577       CC    CGAAC
                                GTTGTAG  GGTGG    TCG
                                |||||||  |||||    |||
                                CAACATC  CCACC    GGC
                                   AA    A____
GAM1890 LOC200325 5' TGTTGTAGTGGTGGCC     46578       CC     GAACT
                                TGTTGTAG  GGTGGC    C
                                ||||||||  ||||||    |
                                ACAACATC  CCACCG    G
                                   A_     _____
GAM1891 CDCA4    3' CAGGTGCATGGGCTGACCCT  46581       GTT  C
                                CGGGTGCG   GC TGACCCT
                                ||||||||   || |||||||
                                GTCCACGT   CG ACTGGGA
                                   ACC  _
GAM1891 FLJ20280 3' GAGCCACCATGCCTGACC    46582     _  G  T
                                GGGT GC GT GCCTGACC
                                |||| || || ||||||||
                                CTCG TG TA CGGACTGG
                                  G  G  _
GAM1891 LOC90625 5' GGGTGAGCTTGACCCT     46583      C   GCC
                                GGGTG GGTT   TGACCCT
                                ||||| ||||   |||||||
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                                CCCAC TCGA   ACTGGGA
                                  _   ___
GAM1892 8D6A     3'  ACAGGGCCGTTCTACCCCCTGG 46586       GATTGCCC
                                ACAGGGC      TCCCCTGG
                                |||||||      ||||||||
                                TGTCCCG      GGGGGACC
                                   GCAAGAT_
GAM1892 GALR1    5'  ACAGGGCGAGAGCTCTTTTGG  46587        TT  C  CCCC
                                ACAGGGCGA  GC CT   TGG
                                |||||||||  || ||   |||
                                TGTCCCGCT  CG GA   ACC
                                     CT  A  AA__
GAM1892 MSF      3'  GGGCTGCATTCTCCCCTGG   46588     GAT   C__
                                GGGC   TGC   CTCCCCTGG
                                ||||   |||   |||||||||
                                CCCG   ACG   GAGGGGACC
                                  ___   TAA
GAM1892 PDGFB    3'  AGGGCTGCACCCTCCCTTGGA  46589      GAT       C
                                AGGGC   TGCCCTCCC TGGA
                                |||||   ||||||||| ||||
                                TCCCG   GTGGGAGGG ACCT
                                   AC_       A
GAM1892 PIGN     3'  ACAGGCATATGCTCTCCTCTGG 46590      G  AT   C    C
                                ACAGG CG  TGC CTCC CTGG
                                ||||| ||  ||| |||| ||||
                                TGTCC GT  ACG GAGG GACC
                                   _ AT   A    A
GAM1892 SPOCK    5'  ACAGGGCGGTCTGGTAGTCCTG 46591        A  GCCCTCC
             G                   ACAGGGCG TT      CCTGG
                                ||||||||  ||      |||||
                                TGTCCCGC AG      GGACC
                                     C  ACCATCA
GAM1892 SURF4    3'  ACAGGGCGAGTGCAGCTGG    46592         T   CCTCCC
                                ACAGGGCGA TGC     CTGG
                                |||||||||  |||     ||||
                                TGTCCCGCT ACG     GACC
                                     C   TC_____
GAM1892 DOC2B    3'  GGGCGTGTCCCCTTCCCCTGG  46593      ATTG   _
                                GGGCG    CCCT CCCCTGG
                                |||||    |||| |||||||
                                CCCGC    GGGA GGGGACC
                                   ACAG    A
GAM1892 FLJ10565 5'  ACGGGGCGATCGTCCAGCTGCT 46594    A       C  TCCC_
             GGA                   AC GGGCGATTG CC     CTGGA
                                || |||||||||  ||     |||||
                                TG CCCGCTAGC GG     GACCT
                                 C        A  TCGAC
GAM1892 FLJ11608 3'  CAGAGTCTTACCCTCCTCTGG  46595      CGA       C
                                CAGGG   TTGCCCTCC CTGG
                                |||||   ||||||||| ||||
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                                GTCTC   AATGGGAGG GACC
                                  AG_       A
GAM1892  FLJ14442  3'  AGGGCAGGCCTCCTCTGG    46596       ATT   C   C
                                AGGGCG   GCC TCC CTGG
                                ||||||   ||| ||| ||||
                                TCCCGT   CGG AGG GACC
                                   C__   _   A
GAM1892  FLJ20699  3'  GGCAGTTCTCCCCTGG     46597     A  GCC
                                GGCG TT   CTCCCCTGG
                                |||| ||   |||||||||
                                CCGT AA   GAGGGGACC
                                  C ___
GAM1892  FLJ21044  5'  AGGGCAGCAGCTTCCCCTGG   46598       ATT  CC
                                AGGGCG   GC  TCCCCTGG
                                ||||||   ||  ||||||||
                                TCCCGT   CG  AGGGGACC
                                   CGT  A_
GAM1892  KIAA0363  5'  GGGCCGCCCTCCCCTGG     46599     GAT
                                GGGC   TGCCCTCCCCTGG
                                ||||   ||||||||||||
                                CCCG   GCGGGAGGGGACC
                                  ___
GAM1892  KIAA0757  3'  GGGCGCGAGGCCCTCCCTTGGA 46600       ATT_      C
                                GGGCG    GCCCTCCC TGGA
                                |||||    |||||||| ||||
                                CCCGC    CGGGAGGG ACCT
                                   GCTC       A
GAM1892  KIAA1879  5'  AACGGTGCCCTCCTCTGG    46601     AT      C
                                GGCG  TGCCCTCC CTGG
                                ||||  |||||||| ||||
                                TTGC  ACGGGAGG GACC
                                  C_       A
GAM1892  KIAA1981  3'  ACAGGCTGCCCCCTCTTCTCTG 46602       GCGA      CC____
            G                    ACAGG    TTGCCCTC     CTGG
                                |||||    ||||||||     ||||
                                TGTCC    GACGGGGG     GACC
                                  _____       AGAAGA
GAM1892  MGC20255  3'  GGGGTCTCCTCCCTCCCCTGG  46603     CGA  G_
                                GGG   TT  CCCTCCCCTGG
                                |||   ||  ||||||||||
                                CCC   AG  GGGAGGGGACC
                                  CAG  GA
GAM1892  p25      3'  CAGGGCGAGGTCCTCTGG    46604        TTGCCC   C
                                CAGGGCGA     TCC CTGG
                                ||||||||     ||| ||||
                                GTCCCGCT     AGG GACC
                                    CC_____   A
GAM1892  SEPT3    3'  GGGCTTTGCCCTCCCTTGG    46605     GA        C
                                GGGC  TTGCCCTCCC TGG
                                ||||  |||||||||| |||
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                                CCCG  AACGGGAGGG ACC
                                  A_        A
GAM1892  TUSP     3'  ACAGGTCAGCGCCCTCTCCTGG 46606      GCGAT      C
                                ACAGG     TGCCCTC CCTGG
                                |||||     ||||||| |||||
                                TGTCC     GCGGGAG GGACC
                                   AGTC_      A
GAM1892  LOC121273 3'  GGGCACCACCCTCTCTTCTGG  46607     G  TG    CC__
                                GGGC AT  CCCTC    CTGG
                                |||| ||  |||||    ||||
                                CCCG TG  GGGAG    GACC
                                  _ GT    AGAA
GAM1892  LOC126668 3'  ACAGGGCAGGTGGCCTCTGGA  46608        AT  C    CCC
                                ACAGGGCG  TG CCTC   TGGA
                                ||||||||  || ||||   ||||
                                TGTCCCGT  AC GGAG   ACCT
                                     CC  C   ___
GAM1892  LOC146774 3'  CAGGACAGACCCTTCCCCTGGA 46609        ATT    _
                                CAGGGCG   GCCCT CCCCTGGA
                                |||||||   ||||| ||||||||
                                GTCCTGT   TGGGA GGGGACCT
                                    C__     A
GAM1892  LOC148189 5'  AGGGCGGTGCGGATCCCTGGA  46610       AT   CCTC
                                AGGGCG  TGC    CCCTGGA
                                ||||||  |||    |||||||
                                TCCCGC  ACG    GGGACCT
                                   C_   CCTA
GAM1892  LOC150290 3'  GGGTGCTGCCCTCTTTCTTCTG 46611     CGA       CC_____
             G                  GGG   TTGCCCTC     CTGG
                                |||   ||||||||     ||||
                                CCC   GACGGGAG     GACC
                                  AC_       AAAGAA
GAM1892  LOC158301 3'  AGGGTTCCCTCCCCTGGA    46612      CGATTG
                                AGGG     CCCTCCCCTGGA
                                ||||     ||||||||||||
                                TCCC     GGGAGGGGACCT
                                  AA_____
GAM1892  LOC253868 3'  GGCAGGGCCCTCCCCTGGA    46613      ATT
                                GGCG   GCCCTCCCCTGGA
                                ||||   ||||||||||||
                                CCGT   CGGGAGGGGACCT
                                  CC_
GAM1893  CRIM1    3'  TTTTTGATTTCAACTCAAAATG 46616         G    GGA
             T                   TTTTTGATT TAGC   AAAATGT
                                 |||||||| ||||   |||||||
                                 AAAAACTAA GTTG   TTTTACA
                                      A   AG_
GAM1893  FGF2     3'  TTTTTAATTGGCTTAAAAATGT 46617          TA  GG
                                TTTTTGATTG  GC  AAAAATGT
                                |||||||||  ||  ||||||||
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                                AAAAATTAAC  CG  TTTTTACA
                                      __  AA
GAM1893  SLC10A2   3'  TTTCTGATTGATGGGAAA    46618         TAGC
                                TTTTTGATTG    GGAAA
                                ||||||||||    |||||
                                AAAGACTAAC    CCTTT
                                      TAC_
GAM1893  LOC147694 3'  TTCTTGGTAAGAGGAAAAATGT 46619       ATTGT  C
                                TTTTTG     AG GGAAAAATGT
                                ||||||     || ||||||||||
                                AAGAAC     TC CCTTTTTACA
                                   CAT__  T
GAM1893  LOC147990 3'  TTTTTGATTTCATTAAGAAAAA 46620        G  GC_
            TGT                    TTTTTGATT TA   GGAAAAATGT
                                ||||||||| ||   ||||||||||
                                AAAAACTAA GT   TCTTTTTACA
                                      A  AAT
GAM1893  LOC200339 3'  TTTTTGATTGTAGACATTGGGT 46621           _  GAAAAA
            GT                     TTTTTGATTGTAG CG     TGT
                                ||||||||||||| ||     |||
                                AAAAACTAACATC GT     ACA
                                        T  AACCC_
GAM1894  KIAA0628  3'  ACTCTTGGTTGCCCAGGCTAGA 46624        CA    C_  C
                                ACTTTTGGT  CCCA  CT GA
                                |||||||||  ||||  || ||
                                TGAGAACCA  GGGT  GA CT
                                      AC    CC  T
GAM1894  KREMEN2   3'  ACTTTTGGTCTCCCCAAGGCG  46625         A_    CCT
                                ACTTTTGGTC  CCCA   CG
                                ||||||||||  ||||   ||
                                TGAAAACCAG  GGGT   GC
                                      AG    TCC
GAM1894  ORF1-FL49 3'  ACATTTGGCCACTACCTTGAA  46626    T       CC    C
                                AC TTTGGTCAC  ACCT GAA
                                || |||||||||  |||| |||
                                TG AAACCGGTG  TGGA CTT
                                 T       A_    A
GAM1894  LOC148443 3'  ACTTCTGGTCATTTGCCATCT  46627          C___   C
                                ACTTTTGGTCA    CCA CT
                                ||||||||||    ||| ||
                                TGAAGACCAGT    GGT GA
                                      AAAC   A
GAM1894  LOC220980 5'  TTTTGGTCACTTGCTTCTCAA  46628         CCAC__
                                TTTTGGTCAC     CTCGA
                                ||||||||||     |||||
                                AAAACCAGTG     GAGTT
                                      AACGAA
GAM1895  DPP4      3'  TACAATGCTTTCCCATCACCC  46631       A  C       G
                                TACAAT CT TCCTATTAC CC
                                |||||| || ||||||||| ||
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                                ATGTTA GA AGGGTAGTG GG
                                   C  A       _
GAM1895  FOXE1    3'  TACAATCTTCTTTTTCACACCC 46632       AC   CCTA
              C                   TACAAT  TCT    TTACGCCCC
                                  ||||||  |||    |||||||||
                                  ATGTTA  AGA    AGTGTGGGG
                                     GA   AAA_
GAM1895  HOXC13   3'  TAAATACTCTTCTGCACCC   46633   C       C  ATTA
                                  A AATACTCT CT    CGCCC
                                  | ||||||| ||    |||||
                                  A TTATGAGA GA    GTGGG
                                   T       A  C___
GAM1895  MEN1     5'  TACCATGCTCTCCTACATGGCC 46634     A  A        TAC
                                  TAC AT CTCTCCTAT   GCC
                                  ||| || |||||||||   |||
                                  ATG TA GAGAGGATG   CGG
                                    G  C        TAC
GAM1895  PFKFB2   5'  TACGATCTCTCCTAAGATCCC  46635     A  A       TTACG
                                  TAC AT CTCTCCTA     CCC
                                  ||| || ||||||||     |||
                                  ATG TA GAGAGGAT     GGG
                                    C  _       TCTA_
GAM1895  RU2      3'  TACATGCTTTCCTATTAC    46636      ATA  C
                                  TACA   CT TCCTATTAC
                                  ||||   || |||||||||
                                  ATGT   GA AGGATAATG
                                    AC_  A
GAM1895  CHST3    3'  CAATACTCTTCCCAGGGCCC   46637          _   TTAC
                                  CAATACTCT CCTA    GCCC
                                  ||||||||| ||||    ||||
                                  GTTATGAGA GGGT    CGGG
                                       A    CC__
GAM1895  COVA1    3'  AATACTCTCCATTGGC      46638          T   AC
                                  AATACTCTCC ATT  GC
                                  |||||||||| |||  ||
                                  TTATGAGAGG TAA  CG
                                        _   C_
GAM1895  DKFZP564I052 3'  AATACTCTCTCCCACC      46639          _  ATTA
                                  AATACTCTC CT    CGCC
                                  ||||||||| ||    ||||
                                  TTATGAGAG GG    GTGG
                                       A  _____
GAM1895  MGC15705  3'  CACAGTACTCTTCAGCC     46640      A     CCTA   C
                                  TACA TACTCT    TTA GCC
                                  |||| ||||||    ||| |||
                                  GTGT ATGAGA    AGT CGG
                                    C     _____  _
GAM1895  WDR9     3'  TAAATACTCTTTTAGCCC    46641    C       CCTA   C
                                  A AATACTCT    TTA GCCC
                                  | ||||||||    ||| ||||
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                                A TTATGAGA    AAT CGGG
                                 T       A___   _
GAM1895  LOC121457 3'  TAAATACTCTTTATTAGCCCC  46642    C       CC     C
                                A AATACTCT  TATTA GCCCC
                                | ||||||||  ||||| |||||
                                A TTATGAGA  ATAAT CGGGG
                                 T       A_    _
GAM1895  LOC129011 5'  CAGTGCTCTCCTATCTGCTGCC 46643    ATA        AC__
              CC                    CA   CTCTCCTATT    GCCCC
                                ||   ||||||||||    |||||
                                GT   GAGAGGATAG    CGGGG
                                 CAC         ACGA
GAM1895  LOC145790 3'  TACATTGTTCTCCTACTGCA   46644      ATAC       A
                                TACA    TCTCCTATT CG
                                ||||    |||||||||  ||
                                ATGT    AGAGGATGA GT
                                   AACA        C
GAM1895  LOC159121 3'  ATACTCTCACAGCGCCCC    46645        CT  TA
                                ATACTCTC  AT  CGCCCC
                                ||||||||  ||  ||||||
                                TATGAGAG  TG  GCGGGG
                                     __  TC
GAM1896  DAZ      3'  TAGGGAAGAAGCCATTGA    46648     A  TATC
                                TAG GA    AGGCCATTGA
                                ||| ||    ||||||||||
                                ATC CT    TTCGGTAACT
                                  C  TC__
GAM1896  FLG      3'  TGTCTAGAGCTGTCAGCC    46649         ATA    G
                                TGTCTAGAG   TCAG CC
                                |||||||||   |||| ||
                                ACAGATCTC   AGTC GG
                                     GAC    _
GAM1896  FSTL1    3'  TATCTAGAGGCAGTTATTG   46650         ATAT   GCC
                                TGTCTAGAG    CAG   ATTG
                                |||||||||    |||   ||||
                                ATAGATCTC    GTC   TAAC
                                     C___   AA_
GAM1896  CYLC2    3'  TCTAGAGATCATTCATTGA   46651        TA   GGC
                                TCTAGAGA  TCA   CATTGA
                                ||||||||  |||   ||||||
                                AGATCTCT  AGT   GTAACT
                                     __   AA_
GAM1896  DKFZp761H079 3'  TATCTAGAAATATAGGCTATTG 46652            C    C
              A                   TGTCTAGAGATAT AGGC ATTGA
                                ||||||||||||| |||| |||||
                                ATAGATCTTTATA TCCG TAACT
                                       _   A
GAM1896  FLJ20417  3'  TGCCTAGAGGTCAATTATTG   46653         ATA    GCC
                                TGTCTAGAG   TCAG   ATTG
                                |||||||||   ||||   ||||
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                                ACGGATCTC  AGTT  TAAC
                                    C__   AA_
GAM1896 SIMRP7   3' TGTCTGAGGAGCCATT     46654      A  ATATCA
                                TGTCT GAG     GGCCATT
                                ||||| |||     |||||||
                                ACAGA CTC     TCGGTAA
                                  _  C_____
GAM1897 HTR1D    3' TATGCTAAGTAGTGAAATCT  46657      C__  CAC
                                TATGT  GTA  GTGAAATCT
                                |||||  |||  |||||||||
                                ATACG  CAT  CACTTTAGA
                                  ATT  ___
GAM1897 TAF4B    3' TATTCCACACACGTGGAAT   46658    GT       A
                                TAT  CGTACACGTG AAT
                                |||  |||||||||| |||
                                ATA  GTGTGTGCAC TTA
                                  AG        C
GAM1897 GT650    3' CATGTGCATGTGAAATCT    46659      C  CAC
                                TATGT GTA  GTGAAATCT
                                ||||| |||  |||||||||
                                GTACA CGT  CACTTTAGA
                                  _  A__
GAM1897 KIAA0298 3' TACTAAGTCTGTAAGTGAAATC 46660      T  _  CAC
           T                     TACTA GTC GTA  GTGAAATCT
                                |||||  ||| |||  |||||||||
                                ATGAT CAG CAT  CACTTTAGA
                                  T  A  T__
GAM1897 Rpo1-2   3' TACTATATCGTGCACTTAAA  46661         A  G
                                TACTATGTCGT CAC TGAA
                                |||||||||| ||| ||||
                                ATGATATAGCA GTG ATTT
                                      C  A
GAM1897 Rpo1-2   3' TACTATATCGTGCACTTAAA  46661         A  G
                                TACTATGTCGT CAC TGAA
                                |||||||||| ||| ||||
                                ATGATATAGCA GTG ATTT
                                      C  A
GAM1897 LOC204593 5' CTATTGTGGGCTCACGTGAA  46662     _ C_ A
                                CTAT GT  GT CACGTGAA
                                ||||  ||  || ||||||||
                                GATA CA  CG GTGCACTT
                                  A  CC  A
GAM1897 LOC51336 3' TACTATGTACGTGTAAAAC   46663       _  ACAC
                                TACTATGT CGT   GTGAAAT
                                |||||||| |||   |||||||
                                ATGATACA GCA   CATTTTG
                                     T  ____
GAM1898 APAF1    3' GGGAAAATGCTTTAGAAA    46666       CG  GAGGG
                                GGGAAAA  GC    TAGAAA
                                |||||||  ||    ||||||
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                              CCCTTTT  CG    ATCTTT
                                 A_  AA___
GAM1898  APAF1    3'  GGGAAAATGCTTTAGAAA    46666       CG  GAGGG
                              GGGAAAA  GC    TAGAAA
                              |||||||  ||    ||||||
                              CCCTTTT  CG    ATCTTT
                                 A_  AA___
GAM1898  AVPR1A   5'  GGGAGGGAGGCAGAAA     46667     AAAC  C    G
                              GGGA    GG GAGG TAGAAA
                              ||||    || |||| ||||||
                              CCCT    CC CTCC GTCTTT
                                ____  _   _
GAM1898  HEBP1    5'  GGCGAGGCGGCGAGGCGAGA   46668    _  AAA       GT
                              GG GA   CGGCGAGG  AGA
                              || ||   ||||||||  |||
                              CC CT   GCCGCTCC  TCT
                               G  CC_      GC
GAM1898  HR       3'  AGGATGCGGTGGTAGAAACG   46669     AAACG   AG
                              GGGA    GCG  GGTAGAAACG
                              ||||    |||  ||||||||||
                              TCCT    CGC  CCATCTTTGC
                                A____   CA
GAM1898  HTR6     5'  GGGTGGACGGCAAGGGAG    46670     AAA        T
                              GGG   ACGGCGAGGG AG
                              |||   |||||||||| ||
                              CCC   TGCCGTTCCC TC
                                ACC        _
GAM1898  INHBB    5'  GGGAAGGTGGCGAAAGAG    46671      AAC       T
                              GGGAA   GGCGAGGG AG
                              |||||   |||||||| ||
                              CCCTT   CCGCTTTC TC
                                 CCA      _
GAM1898  LHX1     5'  GAGAACGGCGGCGGGAACG   46672     AA     A_  TAGA
                              GGGA  ACGGCG  GGG    AACG
                              ||||  ||||||  |||    ||||
                              CTCT  TGCCGC  CCC    TTGC
                                __     CG   ____
GAM1898  MKI67    3'  GGGAAAACAGCAGGGAG     46673          G   T
                              GGGAAAACGGC AGGG AG
                              |||||||||| |||| ||
                              CCCTTTTGTCG TCCC TC
                                       _   _
GAM1898  NPY2R    5'  GGGAAAAGGCGAGGGCAAA   46674        C
                              GGGAAAA GGCGAGGGTAGA
                              ||||||| ||||||||||||
                              CCCTTTT CCGCTCCCGTTT
                                      _
GAM1898  NPY2R    3'  GGGAAAAGGCGAGGGCAAA   46674        C
                              GGGAAAA GGCGAGGGTAGA
                              ||||||| ||||||||||||
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                                CCCTTTT CCGCTCCCGTTT
                                     _
GAM1898 PCDH7    5' GGGAGGGCAGCGATAGA     46675     AAAC   G _
                                GGGA    GGC AG GGTAGA
                                ||||    ||| || ||||||
                                CCCT    CCG TC CTATCT
                                  C___   _ G
GAM1898 PCDH7    5' GGGAGGGCAGCGATAGA     46675     AAAC   G _
                                GGGA    GGC AG GGTAGA
                                ||||    ||| || ||||||
                                CCCT    CCG TC CTATCT
                                  C___   _ G
GAM1898 PCDH7    5' GGGAGGGCAGCGATAGA     46675     AAAC   G _
                                GGGA    GGC AG GGTAGA
                                ||||    ||| || ||||||
                                CCCT    CCG TC CTATCT
                                  C___   _ G
GAM1898 PKIA     5' GGGAAGGCAGCCTGGAAAC   46676      AA    GAG  TAG
                                GGGAA  CGGC   GG   AAAC
                                |||||  ||||   ||   ||||
                                CCCTT  GTCG   CC   TTTG
                                   CC    GA_ ____
GAM1898 PNUTL1   3' GGGAAGGGCAAGGGAG      46677      AAC       T
                                GGGAA   GGCGAGGG AG
                                |||||   |||||||| ||
                                CCCTT   CCGTTCCC TC
                                   C__       _
GAM1898 SIX2     3' GGGAGACGGCAAGTCGGC    46679     AA       __
                                GGGA  ACGGCGAG  GGT
                                ||||  ||||||||  |||
                                CCCT  TGCCGTTC  CCG
                                  C_       AG
GAM1898 SIX2     3' GGGAAAAGGCCTCAGGAGA   46678       C   GA_   T
                                GGGAAAA GGC   GGG AGA
                                ||||||| |||   ||| |||
                                CCCTTTT CCG   TCC TCT
                                    _   GAG   _
GAM1898 SLC28A1  3' GGGAGAACAGCCCTCAGAAGCG 46680      A     GAGGG    A
                                GGGA AACGGC     TAGAA CG
                                |||| ||||||     ||||| ||
                                CCCT TTGTCG     GTCTT GC
                                  C     GGA__     C
GAM1898 STX1A    3' GGGAGGATGGCAAGGGCAG   46681      AAAC
                                GGGA    GGCGAGGGTAG
                                ||||    ||||||||||
                                CCCT    CCGTTCCCGTC
                                  CCTA
GAM1898 ZNF277   5' GGGGTGGCACCAGTAGAAACG  46682     AAAAC    AG
                                GGG    GGCG  GGTAGAAACG
                                |||    ||||  ||||||||||
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                                CCC    CCGT  TCATCTTTGC
                                  CA___   GG
GAM1898 ARH2    3' GGGAAAGTGGCAGAAA     46683     AAACGGC  _
                                GGGA     GAG GGTAGAAA
                                ||||     ||| ||||||||
                                CCCT     TTC CCGTCTTT
                                  ________  A
GAM1898 CLDN15  3' GGGAAGACAGCGGGGCCCACG 46684     A    A   AGAA
                                GGGAA ACGGCG GGGT   ACG
                                ||||| |||||| ||||   |||
                                CCCTT TGTCGC CCCG   TGC
                                   C     _   GG__
GAM1898 CNOT3   5' GGGAAAACGACGGCGAGCAGA 46685          A_
                                GGGAAAACGGCG  GGGTAGA
                                ||||||||||||  |||||||
                                CCCTTTTGCTGC  CTCGTCT
                                       CG
GAM1898 FLJ13397 5' GGGACGGCGGCGGCAAA    46686     AAA    AG
                                GGGA  CGGCG  GGTAGA
                                ||||  |||||  ||||||
                                CCCT  GCCGC  CCGTTT
                                  ___    CG
GAM1898 KCND1   5' GGGCATCCAGAGGGTAGAAA  46687    AAAA  GC
                                GGG   CG  GAGGGTAGAAA
                                |||   ||  ||||||||||
                                CCC   GT  CTCCCATCTTT
                                  GTAG  __
GAM1898 KIAA0121 3' GGGAGGGGATAGAAAC     46688     AAAC  CGA
                                GGGA   GG   GGGTAGAAAC
                                ||||   ||   ||||||||||
                                CCCT   CC   CCTATCTTTG
                                  ____  ___
GAM1898 KIAA0212 3' GGGAAAACAGTGACAGGT   46689         C  _
                                GGGAAAACGG GA GGGT
                                |||||||||| || ||||
                                CCCTTTTGTC CT TCCA
                                      A  G
GAM1898 KIAA0257 3' GGGAAGACAGGTGGTGAAAACG 46690      A   CGAG   AG
                                GGGAA ACGG   GGT  AAACG
                                ||||| ||||   |||  |||||
                                CCCTT TGTC   CCA  TTTGC
                                   C   CA__   CT
GAM1898 KIAA1029 3' GGGAAATGCAGGTAGAAA   46691      ACG  GA
                                GGGAAA  GC  GGGTAGAAA
                                ||||||  ||  |||||||||
                                CCCTTT  CG  TCCATCTTT
                                   A__  __
GAM1898 KIAA1111 3' GGGCAAACAGAATGGGTGGA  46692    A    CGA   A
                                GGG AAACGG   GGGT GA
                                ||| ||||||   |||| ||
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                                CCC TTTGTC  CCCA CT
                                  G     TTA   C
GAM1898 KIAA1111 3' GGGAAATGGGGCAAACAGAA  46693      AC_    GG
                                GGGAAA  GGCGAG  TAGAA
                                ||||||  ||||||  |||||
                                CCCTTT  CCGTTT  GTCTT
                                   ACC    __
GAM1898 MGC10960 3' GGGAAAACGTGGGAAA     46694        GCGA  T
                                GGGAAAACG   GGG AGA
                                |||||||||   ||| |||
                                CCCTTTTGC   CCC TTT
                                     A___  _
GAM1898 MKRN1    5' GAGAGGACGGCGAGGCCAG   46695     AA       G
                                GGGA  ACGGCGAGG TAG
                                ||||  ||||||||| |||
                                CTCT  TGCCGCTCC GTC
                                  CC       G
GAM1898 RAI15    3' GGGAAAGCAGGCAATGGGAG  46696      A _    _  T
                                GGGAAA C GGCGA GGG AG
                                |||||| | ||||| ||| ||
                                CCCTTT G CCGTT CCC TC
                                   C T    A  _
GAM1898 REM      3' GGGAGGGCAGTAGGTGGAGACG 46697     AAAC   A_   A A
                                GGGA   GGCG  GGGT GA ACG
                                ||||   ||||  |||| || |||
                                CCCT   CCGT  TCCA CT TGC
                                  C___   CA   C  C
GAM1898 SEMA5A   5' GGGAAAGCAGCGCTCGGGAG  46698      A    A__   T
                                GGGAAA CGGCG   GGG AG
                                |||||| |||||   ||| ||
                                CCCTTT GTCGC   CCC TC
                                   C    GAG  _
GAM1898 LOC138389 5' GGGAAGGCAGGCAGA      46699      AAC   GA
                                GGGAA   GGC  GGGTAGA
                                |||||   |||  |||||||
                                CCCTT   CCG  TCCGTCT
                                   ____  __
GAM1898 LOC151009 5' GGCGAGGACGGCGAAGGT   46700    _  AA
                                GG GA  ACGGCGAGGGT
                                || ||  ||||||||||
                                CC CT  TGCCGCTTCCA
                                 G  CC
GAM1898 LOC152110 5' AGGAGAGCGAAGGTAGA    46701     AAAC
                                GGGA   GGCGAGGGTAGA
                                ||||   ||||||||||||
                                TCCT   TCGCTTCCATCT
                                  C___
GAM1898 LOC157653 5' AGGAAAGGACAGGGTGGAAA  46702      AC   G    A
                                GGGAAA  GGC AGGGT GAAA
                                ||||||  ||| ||||| ||||
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                                TCCTTT  CTG TCCCA CTTT
                                   C_  _    C
GAM1898  LOC205948 5'  GGGAGGAGGCGAGGGAAACG  46703     AAAC      TAG
                                GGGA   GGCGAGGG  AAACG
                                ||||   ||||||||  |||||
                                CCCT   CCGCTCCC  TTTGC
                                  CCT_      ____
GAM1898  LOC220739 3'  GGGGGGCGAGAAGTGGAA   46704    AAAAC     _ A
                                GGG    GGCGAGG GT GAA
                                |||    ||||||| || |||
                                CCC    CCGCTCT CA CTT
                                 C____      T  C
GAM1898  LOC253891 3'  GGAAGGTGGCGAGAGGAAA   46705     AAC      TA
                                GGAA   GGCGAGGG  GAAA
                                ||||   ||||||||  ||||
                                CCTT   CCGCTCTC  CTTT
                                  CCA      __
GAM1898  LOC254552 5'  GGGAAGAGGCGGGGCGA    46706     AAC   A   A
                                GGGAA   GGCG GGGT GA
                                |||||   |||| |||| ||
                                CCCTT   CCGC CCCG CT
                                   CT_   _   _
GAM1898  LOC255394 5'  AGGAGAACGGCGACGGAG   46707     A      G  T
                                GGGA AACGGCGA GG AG
                                |||| |||||||| || ||
                                TCCT TTGCCGCT CC TC
                                  C       G  _
GAM1898  LOC90309  5'  GGGAAAACGGAGTAAGGGAAA  46708        C__    T
                                GGGAAAACGG   GAGGG AGA
                                ||||||||||   ||||| |||
                                CCCTTTTGCC   TTCCC TTT
                                     TCA    _
GAM1898  LOC92697  3'  GGGAAAATGTGGCAGAAA   46709       CGGCGAG
                                GGGAAAA      GGTAGAAA
                                |||||||      ||||||||
                                CCCTTTT      CCGTCTTT
                                   ACA____
GAM1899  AIM1     3'  AGAGGTTCGAGATCAGCC    46712     TC_   CCC
                                AGAG   CGGG   ATCAGCC
                                ||||   ||||   |||||||
                                TCTC   GCTC   TAGTCGG
                                  CAA   ___
GAM1899  ANK1     3'  AGAGGTCATGCCGTCAGCCCAG 46713     TC  G   CA
                                AGAG  CG GCC  TCAGCCCAG
                                ||||  || |||  |||||||||
                                TCTC  GT CGG  AGTCGGGTC
                                  CA  A  C_
GAM1899  ANK1     3'  AGAGGTCATGCCGTCAGCCCAG 46713     TC  G   CA
                                AGAG  CG GCC  TCAGCCCAG
                                ||||  || |||  |||||||||
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                                TCTC  GT CGG  AGTCGGGTC
                                  CA  A   C_
GAM1899  ANK1     3'  AGAGGTCATGCCGTCAGCCCAG 46713     TC  G   CA
                                AGAG  CG GCC  TCAGCCCAG
                                ||||  || |||  |||||||||
                                TCTC  GT CGG  AGTCGGGTC
                                  CA  A   C_
GAM1899  ANK1     3'  AGAGGTCATGCCGTCAGCCCAG 46713     TC  G   CA
                                AGAG  CG GCC  TCAGCCCAG
                                ||||  || |||  |||||||||
                                TCTC  GT CGG  AGTCGGGTC
                                  CA  A   C_
GAM1899  ANK1     3'  AGAGGTCATGCCGTCAGCCCAG 46713     TC  G   CA
                                AGAG  CG GCC  TCAGCCCAG
                                ||||  || |||  |||||||||
                                TCTC  GT CGG  AGTCGGGTC
                                  CA  A   C_
GAM1899  AP1S1    3'  GTCCAGGCTCCCCTCCCAG   46714       _  ATCAG
                                GTCCGGGC CC    CCCAG
                                |||||||| ||    |||||
                                CAGGTCCG GG    GGGTC
                                    A  GGA__
GAM1899  AP2B1    5'  GAGCCGGAGAGCACAGCCCAG  46715    T    CC_  T
                                GAG CCGGG   CA CAGCCCAG
                                ||| |||||   || ||||||||
                                CTC GGCCT   GT GTCGGGTC
                                  _    CTC  _
GAM1899  B4GALT5  3'  GAGTTCGAGACCAGCC     46716     C   CCC
                                GAGT CGGG   ATCAGCC
                                ||||  ||||  |||||||
                                CTCA GCTC   TGGTCGG
                                  A   ____
GAM1899  CDH15    3'  GTCGGGCCCGGTGACCTCAG  46717     C     ATCA  _
                                GTC GGGCCC    GCC CAG
                                ||| ||||||    ||| |||
                                CAG CCCGGG    TGG GTC
                                  _     CCAC   A
GAM1899  CDKN2D   5'  GAGCCGGGCCCAACCC      46718     T       TCA
                                GAG CCGGGCCCA   GCCC
                                ||| |||||||||   ||||
                                CTC GGCCCGGGT   TGGG
                                  _       ____
GAM1899  GPR4     3'  GAGTTCAAGATCAGCC      46719     C   CCC
                                GAGT CGGG   ATCAGCC
                                ||||  ||||  |||||||
                                CTCA GTTC   TAGTCGG
                                  A   ____
GAM1899  GRAF     3'  GAGTTCGAGATCAGCCC     46720     C   CCC
                                GAGT CGGG   ATCAGCCC
                                ||||  ||||  ||||||||
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                                CTCA GCTC   TAGTCGGG
                                  A   ___
GAM1899  GRM1     3'  AAGATGAGGAGTCTGTCAGCCC 46721     GTCC   CCCA
                 AG                 AAGA   GGG   TCAGCCCAG
                                    ||||   |||   |||||||||
                                    TTCT   CTC   AGTCGGGTC
                                      ACTC   AGAC
GAM1899  GRM7     5'  AGGTCCGGGCCCTTCAG     46722    A       A
                                    AG GTCCGGGCCC TCAG
                                    || ||||||||| ||||
                                    TC CAGGCCCGGG AGTC
                                     _       A
GAM1899  IFRD2    3'  AAGTGTCCGGGCCCCCAG     46723    A       A
                                    AAG GTCCGGGCCC TCAG
                                    ||| ||||||||| ||||
                                    TTC CAGGCCCGGG GGTC
                                      A       _
GAM1899  KAL1     3'  AGAGTCCGGGCCTCTGAGC    46724          CATC
                                    AGAGTCCGGGCC   AGC
                                    ||||||||||||   |||
                                    TCTCAGGCCCGG   TCG
                                           AGAC
GAM1899  MHC2TA   3'  AAGAGTTCGAGACCAGCCC    46725      C   CCC
                                    AAGAGT CGGG  ATCAGCCC
                                    |||||| ||||  ||||||||
                                    TTCTCA GCTC  TGGTCGGG
                                      A   ___
GAM1899  PCDHB16  3'  GAGTTCAAGATCAGCC      46719     C   CCC
                                    GAGT CGGG  ATCAGCC
                                    |||| ||||  |||||||
                                    CTCA GTTC  TAGTCGG
                                      A   ___
GAM1899  PIK3CD   3'  GAGTTCGAGACCAGCCCAG    46726     C   CCC
                                    GAGT CGGG  ATCAGCCCAG
                                    |||| ||||  ||||||||||
                                    CTCA GCTC  TGGTCGGGTC
                                      A   ___
GAM1899  PIM2     3'  AAGAGTCCCGGGGCTCAG     46727       __   CCA
                                    AAGAGTCC  GGGC  TCAG
                                    ||||||||  ||||  ||||
                                    TTCTCAGG  CCCG  AGTC
                                       GC   ___
GAM1899  RBL2     5'  AGGGCCCGGGCCCGCAG     46728    A       AT
                                    AG GTCCGGGCCC  CAG
                                    || ||||||||||  |||
                                    TC CGGGCCCGGG  GTC
                                     C       C_
GAM1899  SEDL     3'  GAGTTTGAAACCAGCCC     46729     CC   CCC
                                    GAGT  GGG  ATCAGCCC
                                    ||||  |||  ||||||||
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                                CTCA  CTT   TGGTCGGG
                                  AA  ___
GAM1899  SFTPA2   3'  AAGAGTCAGGGCCCATCAG   46730       C
                                AAGAGTC GGGCCCATCAG
                                ||||||| ||||||||||
                                TTCTCAG CCCGGGTAGTC
                                   T
GAM1899  SLC7A6   3'  AGAGTTGGGCCCACAG     46731      CC     T
                                AGAGT  GGGCCCA CAG
                                |||||  ||||||| |||
                                TCTCA  CCCGGGT GTC
                                  A_     _
GAM1899  SMOH     5'  AGAATCCGGGCCCGGGCCC   46733          ATCA
                                AGAGTCCGGGCCC   GCCC
                                ||||||||||||   ||||
                                TCTTAGGCCCGGG   CGGG
                                      CC__
GAM1899  SMOH     3'  GGGCACCCATCAGCCCAG    46732     __
                                GGGC  CCATCAGCCCAG
                                ||||  ||||||||||||
                                CCCG  GGTAGTCGGGTC
                                  TG
GAM1899  SNX6     5'  GGAAGTCCGGGCCGTCGTCCAG 46734   A        CA  AGC
                                A GAGTCCGGGCC  TC   CCAG
                                | ||||||||||  ||   ||||
                                C TTCAGGCCCGG  AG   GGTC
                                 C         C_  CA_
GAM1899  TBX3     3'  GAGTCCGGGGCCCCTTCCCAG  46735        _   ATCAG
                                GAGTCCGGG CCC    CCCAG
                                ||||||||| |||    |||||
                                CTCAGGCCC GGG    GGGTC
                                     C   GAA__
GAM1899  XRCC3    3'  GTCTGAGGCCCCAGCCCAG   46736    C _    AT
                                GTC G GGCCC  CAGCCCAG
                                ||| | |||||  ||||||||
                                CAG C CCGGG  GTCGGGTC
                                  A T    __
GAM1899  ZFX      5'  GAGTTCGAGACCAGCC     46716     C   CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
                                CTCA GCTC   TGGTCGG
                                  A   ___
GAM1899  AP3S2    3'  GAGTTCGGGCCCAGCC     46737     C      TCA
                                GAGT CGGGCCCA   GCC
                                |||| ||||||||   |||
                                CTCA GCCCGGGT   CGG
                                  A       ___
GAM1899  ARPP-21  3'  AAAGTCACCATCAGCTCA    46738       CGGGC      C
                                AGAGTC    CCATCAGC CA
                                ||||||    |||||||| ||
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                                TTTCAG    GGTAGTCG GT
                                  T____       A
GAM1899  C22orf19  3'  GAGTTCGAGACCAGCC     46716     C   CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
                                CTCA GCTC   TGGTCGG
                                  A   ___
GAM1899  CAMKK1    3'  GTCCGAGCCCCCATACCAG   46739         A   GC
                                GTCCGGGCCC TCA  CCAG
                                |||||||||| |||  ||||
                                CAGGCTCGGG GGT  GGTC
                                      _  AT
GAM1899  DKFZP434A043 3'  AAGAGTCCGAGTAGCTCAG   46740          CCCA
                                AAGAGTCCGGG   TCAG
                                ||||||||||    ||||
                                TTCTCAGGCTC   AGTC
                                       ATCG
GAM1899  DKFZp564A176 3'  GAGGGCCGGGCCCACAGTCAG  46741     T_       T   CC
                                GAG  CCGGGCCCA CAG  CAG
                                |||  |||||||| |||  |||
                                CTC  GGCCCGGGT GTC  GTC
                                  CC        _  A_
GAM1899  EVI5      3'  GAGTTCGAGACCAGCCCAG   46726     C   CCC
                                GAGT CGGG   ATCAGCCCAG
                                |||| ||||   ||||||||||
                                CTCA GCTC   TGGTCGGGTC
                                  A   ___
GAM1899  FLJ00001  5'  GAGGGGCCGGGCCCGGGGCCCA 46742     T__      ATCA
           G                    GAG   CCGGGCCC    GCCCAG
                                |||   ||||||||    ||||||
                                CTC   GGCCCGGG    CGGGTC
                                  CCC       CCC_
GAM1899  FLJ10521  3'  AGAGTCCAGGCCCATCCAC   46743             A
                                AGAGTCCGGGCCCATC GC
                                |||||||||||||||| ||
                                TCTCAGGTCCGGGTAG TG
                                         G
GAM1899  FLJ10743  3'  GAGGTCCTGGAGTCAGCCCAG  46744     _  G  CCCA
                                GAG TCC GG    TCAGCCCAG
                                ||| ||| ||    |||||||||
                                CTC AGG CC    AGTCGGGTC
                                  C   A  TC__
GAM1899  FLJ12448  3'  AGTCTGGGTTTGCCAGCCCAG  46745      C   CCCA
                                AGTC GGG    TCAGCCCAG
                                |||| |||    |||||||||
                                TCAG CCC    GGTCGGGTC
                                  A   AAAC
GAM1899  FLJ20010  3'  GGGTGCTCCCATCAGCTCAG   46746     ____       C
                                GGG    CCCATCAGC CAG
                                |||    ||||||||| |||
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                                CCC   GGGTAGTCG GTC
                                  ACGA       A
GAM1899  FLJ20232  3'  AAGTGGTCCATCAGCTCA   46747     CC  GC      C
                                GAGT  GG  CCATCAGC CA
                                ||||  ||  |||||||| ||
                                TTCA  CC  GGTAGTCG GT
                                  __ A_      A
GAM1899  FLJ20507  3'  GTCTGGGGGGGCGTCAGCCCAG  46748    C___   CCA
                                GTC   GGGC   TCAGCCCAG
                                |||   ||||  |||||||||
                                CAG   CCCG   AGTCGGGTC
                                  ACCC   C__
GAM1899  FLJ20507  3'  GTCTGGGGGGGCGTCAGCCCAG  46748    C___   CCA
                                GTC   GGGC   TCAGCCCAG
                                |||   ||||  |||||||||
                                CAG   CCCG   AGTCGGGTC
                                  ACCC   C__
GAM1899  FLJ20695  5'  GAGTCCGGGTCCAAGGCCCAG  46749       C   TCA
                                GAGTCCGGG CCA   GCCCAG
                                ||||||||| |||   ||||||
                                CTCAGGCCC GGT   CGGGTC
                                     A   TC_
GAM1899  FLJ23233  5'  AAGGGCCCGGGCCACCC    46750    A       CATCA
                                AAG GTCCGGGCC    GCCC
                                ||| |||||||||    ||||
                                TTC CGGGCCCGG    TGGG
                                  C       _____
GAM1899  GABBR1    3'  GAGAGACCCAAATCAGCCCAG  46751    TCC     __
                                GAG   GGGCCCA  TCAGCCCAG
                                |||   |||||||  |||||||||
                                CTC   TCTGGGT  AGTCGGGTC
                                  ___      TT
GAM1899  GABBR1    3'  GAGAGACCCAAATCAGCCCAG  46751    TCC     __
                                GAG   GGGCCCA  TCAGCCCAG
                                |||   |||||||  |||||||||
                                CTC   TCTGGGT  AGTCGGGTC
                                  ___      TT
GAM1899  HA-1      3'  GAGTCCAGGGCCAGTATTCAG  46752      _    CA___
                                GAGTCC GGGCC    TCAG
                                |||||| |||||    ||||
                                CTCAGG CCCGG    AGTC
                                   T    TCATA
GAM1899  HARS2     3'  AGAGGCTGGACTCAGCCCAG   46753     TCC   CCA
                                AGAG   GGGC   TCAGCCCAG
                                ||||   ||||  |||||||||
                                TCTC   CCTG   AGTCGGGTC
                                  CGA   ___
GAM1899  IRF5      5'  GTCCGAGCTCGCTTTCCAG   46754       CCA  A  ___
                                GTCCGGGC   TC GC   CCAG
                                ||||||||   || ||   ||||
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                                CAGGCTCG  AG CG  GGTC
                                   ___ _ AAA
GAM1899 KIAA0022 3' GAGTTTGAGACCAGCCCAG  46755    CC  CCC
                                GAGT GGG  ATCAGCCCAG
                                |||| |||  ||||||||||
                                CTCA CTC  TGGTCGGGTC
                                  AA ___
GAM1899 KIAA0446 5' AAGAGCTCAAGGTCAGCC   46756    TC  CCCA
                                AAGAG CGGG  TCAGCC
                                ||||| ||||  ||||||
                                TTCTC GTTC  AGTCGG
                                  GA  C___
GAM1899 KIAA0544 3' GAGTTTGAGACCAGCCC    46757    CC  CCC
                                GAGT GGG  ATCAGCCC
                                |||| |||  ||||||||
                                CTCA CTC  TGGTCGGG
                                  AA ___
GAM1899 KIAA0889 3' GAGTTCGAGACCAGCCC    46758    C  CCC
                                GAGT CGGG  ATCAGCCC
                                |||| ||||  ||||||||
                                CTCA GCTC  TGGTCGGG
                                  A  ___
GAM1899 KIAA1041 3' AAGAGTTTGCAACCAGCCCAG 46759     CCGG CC
                                AAGAGT   GC ATCAGCCCAG
                                ||||||   || ||||||||||
                                TTCTCA   CG TGGTCGGGTC
                                   AA__ T_
GAM1899 KIF13B   3' GCCGGGCCCTCTGCCAGCCC  46760  T     A___
                                G CCGGGCCC   TCAGCCC
                                | ||||||||   |||||||
                                C GGCCCGGG   GGTCGGG
                                _      AGAC
GAM1899 LIECG3   3' GAGTTCGAGACCAGCC     46716    C  CCC
                                GAGT CGGG  ATCAGCC
                                |||| ||||  |||||||
                                CTCA GCTC  TGGTCGG
                                  A  ___
GAM1899 NR4A3    5' AAGGGTCCAGGCTCAGGGCCC 46761    A     C TCA
                                AAG GTCCGGGC CA  GCCC
                                ||| |||||||| ||  ||||
                                TTC CAGGTCCG GT  CGGG
                                  C      A CC_
GAM1899 SARM     3' GAATTCAAGATCAGCC     46762    C  CCC
                                GAGT CGGG  ATCAGCC
                                |||| ||||  |||||||
                                CTTA GTTC  TAGTCGG
                                  A  ___
GAM1899 SYNJ2    5' AGGGTCGGGCCCACTGC    46763   A  C     CA
                                AG GTC GGGCCCAT  GC
                                || ||| ||||||||  ||
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                                TC CAG CCCGGGTG  CG
                                 C  _       A_
GAM1899  TCL6     5'  GAGTTCGAAACCAGCC      46764      C    CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
                                CTCA GCTT   TGGTCGG
                                  A   ____
GAM1899  TCL6     5'  GAGTTCGAAACCAGCC      46764      C    CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
                                CTCA GCTT   TGGTCGG
                                  A   ____
GAM1899  WASL     5'  GAGTCCAGGGCCGTCTCTCC   46765       _     CA_  AG
                                GAGTCC GGGCC   TC  CC
                                ||||||| |||||   ||  ||
                                CTCAGG CCCGG   AG  GG
                                   T    CAG  A_
GAM1899  LOC115219 5'  GACTCCGGGCCCTCGCCC    46766    G       A  A
                                GA TCCGGGCCC TC GCCC
                                || |||||||| || ||||
                                CT AGGCCCGGG AG CGGG
                                 G       _ _
GAM1899  LOC116411 5'  GAGCTGGAGACCAGCCC     46767      CC   CCC
                                GAGT  GGG   ATCAGCCC
                                ||||  |||   ||||||||
                                CTCG  CCT   TGGTCGGG
                                  A_  C__
GAM1899  LOC126272 3'  AAGCGTTCGGGACCAGCC    46768     A  C    CCC
                                AAG GT CGGG   ATCAGCC
                                ||| || ||||   |||||||
                                TTC CA GCCC   TGGTCGG
                                 G  A   ____
GAM1899  LOC126661 3'  GAGTTCGAGACCAGCC      46716      C    CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
                                CTCA GCTC   TGGTCGG
                                  A   ____
GAM1899  LOC129880 3'  GAGCTGGAGACCAGCCC     46767      CC   CCC
                                GAGT  GGG   ATCAGCCC
                                ||||  |||   ||||||||
                                CTCG  CCT   TGGTCGGG
                                  A_  C__
GAM1899  LOC138128 5'  AGGTCCGGGCCACGCCC     46769    A       CATCA
                                AG GTCCGGGCC    GCCC
                                || |||||||||    ||||
                                TC CAGGCCCGG    CGGG
                                 _       TG___
GAM1899  LOC145725 3'  GAGTTCGAGACCAGCC      46716      C    CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
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                                CTCA GCTC   TGGTCGG
                                  A   ___
GAM1899  LOC145732 3'  GAGTTCGAGACCAGCC     46716     C   CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
                                CTCA GCTC   TGGTCGG
                                  A   ___
GAM1899  LOC151516 5'  CCAGACGCCCATCAGCTCAG   46770     __        C
                                CCGG  GCCCATCAGC CAG
                                ||||  |||||||||| |||
                                GGTC  CGGGTAGTCG GTC
                                  TG         A
GAM1899  LOC153688 3'  GAGTTCGAGACCAGCCC     46758     C   CCC
                                GAGT CGGG   ATCAGCCC
                                |||| ||||   ||||||||
                                CTCA GCTC   TGGTCGGG
                                  A   ___
GAM1899  LOC157858 5'  GAGTTTGAGACCAGCCCAG    46755     CC   CCC
                                GAGT  GGG   ATCAGCCCAG
                                ||||  |||   ||||||||||
                                CTCA  CTC   TGGTCGGGTC
                                  AA  ___
GAM1899  LOC196955 3'  AAGAGCTGGGCCCCGCCACCCA 46771       CC     ATCA
           G                     AAGAGT  GGGCCC    GCCCAG
                                ||||||  ||||||    ||||||
                                TTCTCG  CCCGGG    TGGGTC
                                   A_     GCGG
GAM1899  LOC196957 3'  GAGTTCGAGACCAGCC     46716     C   CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
                                CTCA GCTC   TGGTCGG
                                  A   ___
GAM1899  LOC196961 3'  GAGTTCGAGACCAGCC     46716     C   CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
                                CTCA GCTC   TGGTCGG
                                  A   ___
GAM1899  LOC197138 3'  GAGTTCGAGACCAGCC     46716     C   CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
                                CTCA GCTC   TGGTCGG
                                  A   ___
GAM1899  LOC201973 5'  GAGCCGGGCCGAGCCTCAG   46772     T      CATC   _
                                GAG CCGGGCC    AGCC CAG
                                ||| |||||||    |||| |||
                                CTC GGCCCGG    TCGG GTC
                                  _      C___    A
GAM1899  LOC219731 5'  AAGAGTTCAGTGTCAGCC    46773       C   GCCCA
                                AAGAGT CGG     TCAGCC
                                |||||| |||     ||||||
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                                TTCTCA GTC    AGTCGG
                                   A  AC___
GAM1899 LOC254504 5' GTCCGAACGCAGCTCAG    46774       CCAT   C
                                GTCCGGGC   CAGC CAG
                                ||||||||   |||| |||
                                CAGGCTTG   GTCG GTC
                                    C___   A
GAM1899 LOC85414  3' CAGTGCCTTCATCAGCCCAG  46775    _  __
                                CGG GCC  CATCAGCCCAG
                                ||| |||  ||||||||||
                                GTC CGG  GTAGTCGGGTC
                                  A  AA
GAM1899 LOC90507  3' GTCCTGGGTCCACCCCAG    22181    _  C   CAG
                                GTCC GGG CCAT   CCCAG
                                |||| ||| ||||   |||||
                                CAGG CCC GGTG   GGGTC
                                  A  A   ___
GAM1899 LOC91012  5' GAGTCCGAGACCAGCC     46776       CCC
                                GAGTCCGGG   ATCAGCC
                                |||||||||   |||||||
                                CTCAGGCTC   TGGTCGG
                                    ___
GAM1899 LOC91056  3' GAGTTCGAGACCAGCC     46716     C   CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
                                CTCA GCTC   TGGTCGG
                                  A   ___
GAM1899 LOC91759  5' GAGTCCTCATCGGCTCAG   46777      GGGCC   A  C
                                GAGTCC    CATC GC CAG
                                ||||||    |||| || |||
                                CTCAGG    GTAG CG GTC
                                   A____   C  A
GAM1900 BTEB1    3' AAGAGAATATCAAATGTGA   46780       ATGTT
                                AAGAGAATAT    ATGTGA
                                ||||||||||    ||||||
                                TTCTCTTATA    TACACT
                                     GTT__
GAM1900 DDT      3' GAAGAGGATTATGTGA      46781      AATATAT
                                GAAGAG      GTTATGTGA
                                ||||||      |||||||||
                                CTTCTC      TAATACACT
                                   C_______
GAM1900 CNNM1    3' AAGAGGGGACAAAGTTATGTG 46782      AAT  T_
                                AAGAG  ATA  GTTATGTG
                                |||||  |||  ||||||||
                                TTCTC  TGT  CAATACAC
                                  CCC  TT
GAM1900 COLEC12  3' GAGGAGAATCTATGTG     46783    A    ATATG
                                GA GAGAAT    TTATGTG
                                || ||||||    |||||||
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                                CT CTCTTA    GATACAC
                                 C    _____
GAM1900 COLEC12  3' GAGGAGAATCTATGTG     46783    A    ATATG
                                GA GAGAAT    TTATGTG
                                || ||||||    |||||||
                                CT CTCTTA    GATACAC
                                 C    _____
GAM1900 FLJ10477 3' GAAGAAATAATTTTTTATGTGA 46784       ATATATG
                                GAAGAGA      TTATGTGA
                                |||||||      ||||||||
                                CTTCTTT      AATACACT
                                    ATTAAAA
GAM1900 KIAA0247 3' GAGGCGACATTGTTATGTG   46785    A__   A
                                GAG   ATAT TGTTATGTG
                                |||   |||| |||||||||
                                CTC   TGTA ACAATACAC
                                  CGC   _
GAM1900 KIAA0436 3' AGAGAATAGTATAAGCAAGTGA 46786       _   TTAT_
                                AGAGAATA TATG    GTGA
                                |||||||| ||||    ||||
                                TCTCTTAT ATAT    CACT
                                    C    TCGTT
GAM1900 KIAA1715 3' AAGAGAATAATAGTGTG    46787       TAT  TA
                                AAGAGAATA   GT  TGTG
                                |||||||||   ||  ||||
                                TTCTCTTAT   TA  ACAC
                                    ___  TC
GAM1900 PTD011   3' GAAGAGTATATCATG      46788      AATA
                                GAAGAG   TATGTTATG
                                ||||||   |||||||||
                                CTTCTC   ATATAGTAC
                                   ____
GAM1900 LOC157306 3' GAGGAGAGAATATGAATATG  46789    A   AT    TT
                                GA GAGA  ATATG  ATGTG
                                || ||||  |||||  |||||
                                CT CTCT  TATAC  TATAC
                                 C   CT    T_
GAM1900 LOC253970 3' GAGAGAATATATATGTGA    46790    A      TGT
                                GA GAGAATATA   TATGTGA
                                || |||||||||   |||||||
                                CT CTCTTATAT   ATACACT
                                _      ___
GAM1901 CDH8     5' TTGTGGGGCCCTGCGCTGGC  46793        CGG  CGG
                                TTGTGGGGCCC   GC   GGC
                                ||||||||||||  ||   |||
                                AACACCCCGGG   CG   CCG
                                      A__  CGA
GAM1901 COL11A2  3' GTTGTGGGATTCCAGGTGGGC 46794       CC    CCG
                                GTTGTGGGG  CCGGG   GGGC
                                |||||||||  |||||   ||||
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                                CAACACCCT  GGTCC   CCCG
                                     AA    A__
GAM1901  COL11A2   3'  GTTGTGGGATTCCAGGTGGGC  46794        CC    CCG
                                GTTGTGGGG  CCGGG   GGGC
                                |||||||||  |||||   ||||
                                CAACACCCT  GGTCC   CCCG
                                     AA    A__
GAM1901  CYP17     3'  GTTGTGGGGCCACATAGGG   46795         C  GGCC
                                GTTGTGGGGCC CG    GGG
                                ||||||||||| ||    |||
                                CAACACCCCGG GT    CCC
                                      T  AT__
GAM1901  DAZ       5'  CGCTGTGGGGCTTCGAGTGG  46796         CC   CC
                                CGTTGTGGGGC  CGGG  GG
                                ||||||||||  ||||  ||
                                GCGACACCCCG  GCTC  CC
                                      AA   A_
GAM1901  KCNJ5     5'  GTTGTGGGGTCCTGTGGGC   46797         _  CC_
                                GTTGTGGGG CC   GGGC
                                |||||||| ||   ||||
                                CAACACCCC GG   CCCG
                                     A  ACA
GAM1901  LTA       3'  CGTGTGGGGCTCTGGTCGG   46798    T     CCCG  C
                                CGT GTGGGGC    GG CGG
                                ||| |||||||    || |||
                                GCA CACCCCG    CC GCC
                                  _      AGA_  A
GAM1901  MAD2L2    3'  CTGAGCGGCCCCGGGCTGGGGC 46799    T  _       C
                                TTG GG GGCCCCGGGC GGGGC
                                ||| || |||||||||| |||||
                                GAC TC CCGGGGCCCG CCCCG
                                  _ G        A
GAM1901  RECQL5    3'  GTTGTTGGGTCCTGGATAAGGG 46800      G   C  C   CC
                                GTTGT GGG CC GGG  GGGG
                                ||||| ||| || |||  ||||
                                CAACA CCC GG CCT  TCCC
                                   A   A  A   AT
GAM1901  ROR2      5'  AGAGCTTCGGGCCGGGGC    46801      CC
                                GGGGC  CGGGCCGGGGC
                                |||||  ||||||||||
                                TCTCG  GCCCGGCCCCG
                                   AA
GAM1901  SLC2A6    3'  TGTGGGCTGCCTGGGCTGGGGC 46802       __  CC   C
                                TGTGGG  GCC  GGGC GGGGC
                                ||||||  |||  |||| |||||
                                ACACCC  CGG  CCCG CCCCG
                                   GA  A_   A
GAM1901  SORCS2    3'  CGTGTGTGGGGTCTGGGGGGC  46803    _     CCCCG  CC
                                CGT TGTGGGG    GG  GGGGC
                                ||| |||||||    ||  |||||
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                                GCA ACACCCC    CC  CCCCG
                                  C      AGA__ __
GAM1901  TXNRD2   5'  CGTCGTGGGGCTTCTGGGG   46804         CCCGGGCC
                                CGTTGTGGGGC      GGGG
                                ||||||||||       ||||
                                GCAGCACCCCG      CCCC
                                      AAGA____
GAM1901  CDC42BPB 3'  GCTGTGCCGTGGGCCGGGGC  46805     GGG  CC
                                GTTGT  GCC  GGGCCGGGGC
                                |||||  |||  ||||||||||
                                CGACA  CGG  CCCGGCCCCG
                                   ___  CA
GAM1901  DAZ2     5'  CGCTGTGGGGCTTCGAGTGG  46796        CC   CC
                                CGTTGTGGGGC  CGGG  GG
                                ||||||||||  ||||  ||
                                GCGACACCCCG  GCTC  CC
                                      AA   A_
GAM1901  DAZ3     5'  CGCTGTGGGGCTTCGAGTGG  46796        CC   CC
                                CGTTGTGGGGC  CGGG  GG
                                ||||||||||  ||||  ||
                                GCGACACCCCG  GCTC  CC
                                      AA   A_
GAM1901  DAZ3     5'  CGCTGTGGGGCTTCGAGTGG  46796        CC   CC
                                CGTTGTGGGGC  CGGG  GG
                                ||||||||||  ||||  ||
                                GCGACACCCCG  GCTC  CC
                                      AA   A_
GAM1901  FLJ12697 3'  GTCGTGGGAGAAGCGGTCGGGG 46806       CCC_  GC
                                GTTGTGGGG   CGG  CGGGG
                                |||||||||   |||  |||||
                                CAGCACCCT   GCC  GCCCC
                                     CTTC   A_
GAM1901  FLJ20979 5'  CGTGTGGGGCCCGAAGGGG   46807    T      C   CC
                                CGT GTGGGGCCC GGG  GGGG
                                |||  |||||||||  |||  ||||
                                GCA CACCCCGGG CTT  CCCC
                                  _       _  __
GAM1901  FLJ22746 3'  TGTGGGGCTCCCACTGGGC   46808       _   GGCCG
                                TGTGGGGC CCCG    GGGC
                                |||||||| ||||    ||||
                                ACACCCCG GGGT    CCCG
                                    A   GA___
GAM1901  FLJ23059 3'  GCTGTGGGGACTGGCTGGGGC  46809       CCCCG   C
                                GTTGTGGGG    GGC GGGGC
                                |||||||||    ||| |||||
                                CGACACCCC    CCG CCCCG
                                     TGA__   A
GAM1901  HRIHFB2122 3'  GTGTGGGGCCTTGGCCCAGTGG 46810    T      CCG    G___
           GC                    GT GTGGGGCC   GGCC    GGGC
                                 || ||||||||   ||||    ||||
```

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                                CA CACCCCGG  CCGG   CCCG
                                 _      AA_   GTCA
GAM1901 KIAA1870 5' TTGTGGGGCTAGTCCTTTGGGG 46811        CCC  G ___
             C                   TTGTGGGGC  GG CC  GGGGC
                                 |||||||||  || ||  |||||
                                 AACACCCCG  TC GG  CCCCG
                                      A__  A  AAA
GAM1901 LRP15   5' GCGCCAGTCCCGGGCCGGGG  46812   T  G  GC
                                 GT GT GG  CCCGGGCCGGGG
                                 || || ||  ||||||||||||
                                 CG CG TC  GGGCCCGGCCCC
                                  _ G  A_
GAM1901 NIFU    5' GTGATAGAGTCGGGCCGGGGC 46813   T    CCC
                                 GT GTGGGG  CGGGCCGGGGC
                                 || ||||||  ||||||||||
                                 CA TATCTC  GCCCGGCCCCG
                                  C    A__
GAM1901 PALM    3' TGTGGGGTGGGGGCCGGGG   46814      CCCC
                                 TGTGGGG   GGGCCGGGG
                                 |||||||   |||||||||
                                 ACACCCC   CCCGGCCCC
                                     ACC_
GAM1901 RPF-1   3' GTTGTGGAGTCCCAAGGG    46815       C   GGCC
                                 GTTGTGGGG CCCG   GGGG
                                 ||||||||| ||||   ||||
                                 CAACACCTC GGGT   TCCC
                                      A  _____
GAM1901 STRN3   5' GTGTGTGGGGCCCCGGCCGGGG 46816   _         G
             C                    GT TGTGGGGCCCCGG CCGGGGC
                                  || |||||||||||| |||||||
                                  CA ACACCCCGGGGCC GGCCCCG
                                   C          _
GAM1901 LOC150150 5' CGTTCTGGGGCCCTGGGGACG  46817    G      C  C_
                                 CGTT TGGGGCCC GGG  CG
                                 |||| |||||||| |||  ||
                                 GCAA ACCCCGGG CCC  GC
                                   G       A  CT
GAM1901 LOC158062 3' GTTGTGGGGCCCTGGCCG   46818          CG
                                 GTTGTGGGGCCC  GGCCG
                                 ||||||||||||  |||||
                                 CAACACCCCGGG  CCGGC
                                       A_
GAM1902 AGTR1   5' GCCGCCTCGGCGTCCCGGCTG  46821    _     C C
                                 GCC CCTTGGC G CCCGGCTG
                                 ||| ||||||| | ||||||||
                                 CGG GGAGCCG C GGGCCGAC
                                   C      _ A
GAM1902 AGTR1   5' GCCGCCTCGGCGTCCCGGCTG  46821    _     C C
                                 GCC CCTTGGC G CCCGGCTG
                                 ||| ||||||| | ||||||||
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                                CGG GGAGCCG C GGGCCGAC
                                  C      _ A
GAM1902  AGTR1    5'  GCCGCCTCGGCGTCCCGGCTG  46821     _      C C
                                GCC CCTTGGC G CCCGGCTG
                                ||| ||||||| | ||||||||
                                CGG GGAGCCG C GGGCCGAC
                                  C      _ A
GAM1902  AGTR1    5'  GCCGCCTCGGCGTCCCGGCTG  46821     _      C C
                                GCC CCTTGGC G CCCGGCTG
                                ||| ||||||| | ||||||||
                                CGG GGAGCCG C GGGCCGAC
                                  C      _ A
GAM1902  BCLG     5'  CCCTGGCCACGGAATGGCTG   46822          CCC__
                                CCTTGGCCGC    GGCTG
                                ||||||||||    |||||
                                GGGACCGGTG    CCGAC
                                      CCTTA
GAM1902  BCLG     5'  CCCTGGCCACGGAATGGCTG   46822          CCC__
                                CCTTGGCCGC    GGCTG
                                ||||||||||    |||||
                                GGGACCGGTG    CCGAC
                                      CCTTA
GAM1902  CDH16    5'  GCTCCCTTGGTCCAGCTG    46823    _     CCGCC
                                GC CCCTTGG    CCGGCTG
                                || |||||||    |||||||
                                CG GGGAACC    GGTCGAC
                                 A      A____
GAM1902  CLECSF5  3'  GCTCCCTTGGCTGCCTGG    46824    _      C   CC
                                GC CCCTTGGC GCC  GG
                                || |||||||| |||  ||
                                CG GGGAACCG CGG  CC
                                 A       A  A_
GAM1902  CRHR1    3'  GCCCCCCAAAGCCCTGCCCTGG 46825        __   __   C
            CTG                   GCCCCTT  GGCC  GCCC GGCTG
                                |||||||  ||||  |||| |||||
                                CGGGGGGG  TCGG  CGGG CCGAC
                                    TT    GA    A
GAM1902  CRMP1    5'  ACGCGCGGCTGCCCCGGCTGC  46827     CCCT    C
                                ACGC    TGGC GCCCCGGCTGC
                                ||||    |||| ||||||||||
                                TGCG    GCCG CGGGGCCGACG
                                  C___    A
GAM1902  CRMP1    5'  CGCCCGCCGCCGCTCCGGCTGC 46826      _ TG    C
                                CGCCC CT  GCCGC CCGGCTGC
                                ||||| ||  ||||| ||||||||
                                GCGGG GG  CGGCG GGCCGACG
                                  C __     A
GAM1902  CTNS     3'  GCCCTTGGCTCACCCGGCTGC  46828     C    _    C
                                GCCC TTGGC CGCCC GGCTGC
                                |||| ||||| ||||| ||||||
```

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                                CGGG AACCG GTGGG CCGACG
                                  _    A    _
GAM1902  DBN1    5'  GCCCTTGGCCGCCCCGTGC   46829     C         _
                                GCCC TTGGCCGCCCCG GC
                                |||| |||||||||||| ||
                                CGGG AACCGGCGGGGC CG
                                  _         A
GAM1902  ICA1    5'  CGTCCCCGACCGTCCCGGCTGC 46830   _   TT    C
                                CG CCCC  GGCCG CCCGGCTGC
                                || ||||  ||||| |||||||||
                                GC GGGG  CTGGC GGGCCGACG
                                 A   __    A
GAM1902  IDH2    5'  CGCCGCTCCTCCCGGCTG    46831     C  TGG  GC
                                CGCC CT   CC  CCCGGCTG
                                |||| ||   ||  ||||||||
                                GCGG GA   GG  GGGCCGAC
                                  C  ___  A_
GAM1902  IRS2    5'  GCCCCCCTCCCCGGCT     46832      TTGG  G
                                GCCCC    CC CCCCGGCT
                                |||||    || ||||||||
                                CGGGG    GG GGGGCCGA
                                   _____ A
GAM1902  KNS2    3'  GCCTCCCTGCCGCCCTGGCTG  46833    _    G     C
                                GCC CCTTG CCGCCC GGCTG
                                ||| ||||| |||||| |||||
                                CGG GGGAC GGCGGG CCGAC
                                  A    _     A
GAM1902  KNS2    5'  CCCCTTGGCCGCCGAGC     46834           CC
                                CCCCTTGGCCGCC  GGC
                                ||||||||||||  |||
                                GGGGAACCGGCGG  TCG
                                       C_
GAM1902  PPP2R5A  5'  ACGCTTGGCAGCTCCGGCTGC  46835     CCC    C  C
                                ACGC   TTGGC GC CCGGCTGC
                                ||||   ||||| || ||||||||
                                TGCG   AACCG CG GGCCGACG
                                  ___    T  A
GAM1902  PPT2    3'  ACAGCTCAGCCACCTGTTCTGG 46836    CC  TG    CC____
            CTGC                 GC  CT  GCCGCC     GGCTGC
                                || ||  ||||||     ||||||
                                TG  GA  CGGTGG     CCGACG
                                 TC  GT     ACAAGA
GAM1902  RPL4    5'  ACGCTCCTCTCAGCCCGGCTGC 46837     _ _  TG   GCCC
                                ACGC CC CT  GCC    CGGCTGC
                                |||| || ||  |||    |||||||
                                TGCG GG GA  CGG    GCCGACG
                                  A  A  GT  _____
GAM1902  TLX1    5'  GCTTCCCCGCTCCGGCTGC   46838    C_  TTGG   C
                                GC  CC    CCGC CCGGCTGC
                                ||  ||    |||| ||||||||
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                                CG  GG    GGCG GGCCGACG
                                 AA _____   A
GAM1902  bA430M15.1 3'  CCTTTTGGCCACATGACTG   46839    CC      CCC
                                CC  TTGGCCGC   GGCTG
                                ||  ||||||||   |||||
                                GG  AACCGGTG   CTGAC
                                 AA       TA_
GAM1902  C1orf2   5'  CGCTCCCCGAGCTCCGGCTGC  46840    _   T   CGCC
                                CGC CCCT GGC    CCGGCTGC
                                ||| |||| |||    ||||||||
                                GCG GGGG TCG    GGCCGACG
                                  A   C   A___
GAM1902  C1orf2   5'  CGCTCCCCGAGCTCCGGCTGC  46840    _   T   CGCC
                                CGC CCCT GGC    CCGGCTGC
                                ||| |||| |||    ||||||||
                                GCG GGGG TCG    GGCCGACG
                                  A   C   A___
GAM1902  C20orf60  3'  GCCCCTTGCCGGGCTG     46841        G   CCCC
                                GCCCCTTG CCG    GGCTG
                                |||||||| |||    |||||
                                CGGGGAAC GGC    CCGAC
                                      _   _____
GAM1902  C5orf3    5'  GCCTCCCTAACGACTTCGGCTG 46842    _      C  CC
              C                  GCC CCTTGGC GC  CGGCTGC
                                ||| ||||||| ||  |||||||
                                CGG GGGATTG TG  GCCGACG
                                  A      C  AA
GAM1902  CIDEB     5'  CGCCCCTTCCTGGCGCCTCGGC 46843        ___    C   C
              TGC                   CGCCCCT   TGGC GCC CGGCTGC
                                |||||||   |||| ||| |||||||
                                GCGGGGA   ACCG CGG GCCGACG
                                    AGG    _   A
GAM1902  CLIC4     5'  GCTCCGGGACTGCTCCGGCTGC 46844    C  TT   C  C
                                GC CC  GGC GC CCGGCTGC
                                ||  ||  |||  ||  ||||||||
                                CG GG  CTG CG GGCCGACG
                                 A  CC   A  A
GAM1902  CPR2      3'  ACCCTTCTTGGCCGCCCACAGC 46845      __         _
                                GCCC  CTTGGCCGCCC CGGC
                                ||||  ||||||||||| ||||
                                TGGG  GAACCGGCGGG GTCG
                                  AA          T
GAM1902  FGD3      3'  CCCTTGGCCAGTGGTTGC    46846          CCCC  C
                                CCCTTGGCCG    GG TGC
                                ||||||||||    ||  |||
                                GGGAACCGGT    CC ACG
                                      CA__  A
GAM1902  FLJ00001  3'  CGCCTCTTGGCCAGCTG     46847      C      GCCCC
                                CGCC CTTGGCC    GGCTG
                                ||||  |||||||    |||||
```

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                                GCGG GAACCGG    TCGAC
                                  A     _____
GAM1902 FLJ10074 5' ACGCCTCCTGGCTGTTCCTGC 46848      C     CGCC  G
                                ACGCC CTTGGC    CC GC
                                ||||| ||||||    || ||
                                TGCGG GGACCG    GG CG
                                  A     ACAA  A
GAM1902 FLJ20967 3' CCCTTCCCTTCCGGCTGC    46849      GG  GCC
                                CCCTT  CC   CCGGCTGC
                                |||||  ||   ||||||||
                                GGGAA  GG   GGCCGACG
                                  G_  AA_
GAM1902 IMP13    5' GCCCCTTGGCTGCTGGC     46850          C  CCC
                                GCCCCTTGGC GC   GGC
                                |||||||||| ||   |||
                                CGGGGAACCG CG   CCG
                                     A  A__
GAM1902 KIAA0447 3' GCCTCTTGGTGCCCGGCTG   46851    C    CC    C
                                GCC CTTGG  GCCC GGCTG
                                ||| |||||  |||| |||||
                                CGG GAACC  CGGG CCGAC
                                  A    A_   _
GAM1902 KIAA0481 3' ACGTGCCTCCCATCCCGGCTG 46852    CC    GG   C
                                ACG  CCTT  CCG CCCGGCTG
                                |||  ||||  ||| ||||||||
                                TGC  GGAG  GGT GGGCCGAC
                                  AC   __   A
GAM1902 KIAA1634 5' ACGCCCCTTGGACGCCCCTCCC 46853          C     _____
           GGCTGC                  CGCCCCTTGG CGCCCC    GGCTGC
                                |||||||||| ||||||    ||||||
                                GCGGGGAACC GCGGGG    CCGACG
                                     T     AGGG
GAM1902 MGC29643 5' GCAGCGGAGGCTGCCCCGGCTG 46854    CCCTT_   C
           C                     GC     GGC GCCCCGGCTGC
                                ||     ||| ||||||||||
                                CG     CCG CGGGGCCGACG
                                 TCGCCT   A
GAM1902 MMPL1    3' CGTCCCCTGGCCTTGCTG    46855    C       GCCCCG
                                CG CCCTTGGCC     GCTG
                                || |||||||||     ||||
                                GC GGGGACCGG     CGAC
                                 A       AA_____
GAM1902 PF1      5' GCCGTCTGCGTCCCGGCTG   46856    CC   GC  C
                                GCC  TTG  CG CCCGGCTG
                                |||  |||  || ||||||||
                                CGG  GAC  GC GGGCCGAC
                                  CA   __  A
GAM1902 PHYHIP   5' GCGCTTGCTCCTCTCCCGGCTG 46857    CC   G_  GC_
           C                     GC  CTTG  CC   CCCGGCTGC
                                ||  ||||  ||   |||||||||
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                                CG  GAAC  GG   GGGCCGACG
                                 C_   GA  AGA
GAM1902  RAB6B    5'  GCGTCCCGGTCCCGGCTG    46858    CC    CCGC
                                GC  CTTGG   CCCGGCTG
                                ||  |||||   ||||||||
                                CG  GGGCC   GGGCCGAC
                                 CA    A___
GAM1902  SAE1     3'  CGCCCCTTGTCGAGCAGCTGC  46859        GC  CCC
                                CGCCCCTTG  CG   CGGCTGC
                                |||||||||  ||   |||||||
                                GCGGGGAAC  GC   GTCGACG
                                     A_  TC_
GAM1902  SAST     5'  CCTTCGGCCGCCTCCAGC    46860    C       _
                                CC TTGGCCGCC CCGGC
                                || |||||||| |||||
                                GG AGCCGGCGG GGTCG
                                 A        A
GAM1902  STMN4    3'  ACGCCCCTTGGCCACCCC    46861
                                ACGCCCCTTGGCCGCCCC
                                ||||||||||||||||||
                                TGCGGGGAACCGGTGGGG

GAM1902  TNKS2    5'  GCTCCCTGCCCCCCGGCTG   46862    _   TG   G
                                GC CCCT  GCC CCCCGGCTG
                                || ||||  ||| |||||||||
                                CG GGGA  CGG GGGGCCGAC
                                 A   ___  _
GAM1902  U5-100K  3'  CACCCCTTGGTGCGGGGCTG  46863         CC  CCC
                                CGCCCCTTGG  GC   GGCTG
                                ||||||||||  ||   |||||
                                GTGGGGAACC  CG   CCGAC
                                     A_  CC_
GAM1902  ZNF339   5'  GCCCCCTCCTCCCGGCTG    46864        GG  GC
                                GCCCCTT  CC  CCCGGCTG
                                |||||||  ||  ||||||||
                                CGGGGGA  GG  GGGCCGAC
                                   ___  A_
GAM1902  LOC115219 5'  ACTCCCCTTGGCCGCTGAAAGC 46865    G          CCC_
                                AC CCCCTTGGCCGC    GGC
                                || ||||||||||||    |||
                                TG GGGGAACCGGCG    TCG
                                 A           ACTT
GAM1902  LOC121536 5'  CGCCCCCGCCGCCGCCCTGGCT 46866        TG_      C
            GC                    CGCCCCT   GCCGCCC GGCTGC
                                |||||||   ||||||| ||||||
                                GCGGGGG   CGGCGGG CCGACG
                                    CGG      A
GAM1902  LOC124245 5'  ACGTCCCTTGGCCCTTCCG   46867    C        GCC
                                ACG CCCTTGGCC   CCG
                                ||| |||||||||   |||
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                                TGC GGGAACCGG   GGC
                                  A        GAA
GAM1902  LOC128665 5'  ACGCCCCTTGGCCCTCAGC    46868           GCCC
                                ACGCCCCTTGGCC    CGGC
                                ||||||||||||    ||||
                                TGCGGGGAACCGG    GTCG
                                      GA__
GAM1902  LOC147043 5'  CCACCTTGTCCCGGCTG     46869    _    GCCGC
                                CC CCTTG     CCCGGCTG
                                || |||||     ||||||||
                                GG GGAAC     GGGCCGAC
                                 T    A____
GAM1902  LOC147622 5'  ACACCCCTTGGCCATGCTG    46870           GCCCCG
                                ACGCCCCTTGGCC     GCTG
                                ||||||||||||      ||||
                                TGTGGGGAACCGG     CGAC
                                      TA____
GAM1902  LOC147958 5'  GCCCTGTGGCCGCCCTGC     46871      CT       CG
                                GCCC  TGGCCGCCC  GC
                                ||||  |||||||||  ||
                                CGGG  ACCGGCGGG  CG
                                  AC        A_
GAM1902  LOC150244 3'  GCTCTTCGGCCGCCCAAAAC   46872    CCC        C_
                                GC   TTGGCCGCCC  GGC
                                ||   ||||||||||  |||
                                CG   AGCCGGCGGG  TTG
                                 AGA         TT
GAM1902  LOC170261 5'  GCCTCCTTGGCCGCTAAGC    46873     _       CCC
                                GCC CCTTGGCCGC   GGC
                                ||| ||||||||||   |||
                                CGG GGAACCGGCG   TCG
                                  A         AT_
GAM1902  LOC196500 3'  GCCCCTTGGCCTCCTGCTTGGC 46874           G  CC___
            TGC                   GCCCCTTGGCC CC     GGCTGC
                                ||||||||||| ||     ||||||
                                CGGGGAACCGG GG     CCGACG
                                      A  ACGAA
GAM1902  LOC219537 5'  CACCAATGGCTGCCCCGGCTGC 46875      CCT    C
                                CGCC   TGGC GCCCCGGCTGC
                                ||||   |||| ||||||||||
                                GTGG   ACCG CGGGGCCGACG
                                  TT_    A
GAM1902  LOC219908 5'  CGCCCAGCGCCCCGGCTGC    46876       CTT   C
                                CGCCC   GGC GCCCCGGCTGC
                                |||||   ||| ||||||||||
                                GCGGG   TCG CGGGGCCGACG
                                   ___   _
GAM1902  LOC220581 5'  ACCCCCCGGGGTGGCTGCCTTG 46877    G    T___    C   CC
            GCTGC                 AC CCCC    TGGC GCC  GGCTGC
                                || ||||    |||| |||  ||||||
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                                TG GGGG   ACCG CGG  CCGACG
                                 G   CCCC   A  AA
GAM1902  LOC221687 5'  GCCCGGGAGCCGCTCCGGCTGC 46878     CTT    C
                                GCCC  GGCCGC CCGGCTGC
                                ||||  |||||| ||||||||
                                CGGG  TCGGCG GGCCGACG
                                  CCC     A
GAM1902  LOC253018 3'  ACCCTTCCACTCTGCTCTGGCT 46879     C  G  C__  CCC
           G                     GCCC TT GC   GC   GGCTG
                                ||||  || ||   ||   |||||
                                TGGG AG TG   CG   CCGAC
                                  A  G  AGA  AGA
GAM1902  LOC255718 5'  CGTCCTTTGGCCGCCTGGC   46880    C  C       CC
                                CG CC TTGGCCGCC  GGC
                                ||  || |||||||||  |||
                                GC GG AACCGGCGG  CCG
                                 A  A       A_
GAM1902  LOC256015 5'  ACCCCTTTTGGCTGCTGGC   46881       __    C  CCC
                                GCCCCT  TGGC GC   GGC
                                ||||||  |||| ||   |||
                                TGGGGA  ACCG CG   CCG
                                   AA    A  A__
GAM1902  LOC257051 5'  GCCTCCTTGGCCGCTAAGC   46873     _        CCC
                                GCC CCTTGGCCGC   GGC
                                ||| ||||||||||   |||
                                CGG GGAACCGGCG   TCG
                                  A         AT_
GAM1902  LOC257141 5'  GCCCCCGGCCCCGGCTG     46882       TGGCC
                                GCCCCT    GCCCCGGCTG
                                ||||||    ||||||||||
                                CGGGGG    CGGGGCCGAC
                                   C_____
GAM1902  LOC257548 3'  ACCCTTCCACTCTGCTCTGGCT 46879     C  G  C__  CCC
           G                     GCCC TT GC   GC   GGCTG
                                ||||  || ||   ||   |||||
                                TGGG AG TG   CG   CCGAC
                                  A  G  AGA  AGA
GAM1902  LOC257610 3'  ACCCTTCCACTCTGCTCTGGCT 46879     C  G  C__  CCC
           G                     GCCC TT GC   GC   GGCTG
                                ||||  || ||   ||   |||||
                                TGGG AG TG   CG   CCGAC
                                  A  G  AGA  AGA
GAM1902  LOC51605  5'  CGCCCCTCCTCCTCGGTTG   46883       TGG  G  C   C
                                CGCCCCT   CC CC CGG TG
                                |||||||   || || ||| ||
                                GCGGGGA   GG GG GCC AC
                                    ___  A  A   A
GAM1903  EN1       5'  TGGGCGCGCGCGGGACTTTGCG 46886    A       CC    C
           G                     TG GTGCGCGCG  GGCT TGCGG
                                || |||||||||  |||| |||||
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                                AC CGCGCGCGC  CTGA ACGCC
                                 C       C_   A
GAM1903  GPC6    5'  GCGCGCGCCGGCTCCCCCGG  46887           _ G
                                GCGCGCGCCGGCTC T CGG
                                ||||||||||||| | |||
                                CGCGCGCGGCCGAG G GCC
                                       G G
GAM1903  PIG3    5'  GAGTGGTTCTGGCTCTGCGG  46888     CGCGCGCC
                                GAGTG      GGCTCTGCGG
                                |||||      ||||||||||
                                CTCAC      CCGAGACGCC
                                   CAAGA___
GAM1903  RAB33A  5'  GTGCGTGCGCCGGCACCG   46889     C      T
                                GTGCG GCGCCGGC CTG
                                ||||| |||||||| |||
                                CACGC CGCGGCCG GGC
                                   A       T
GAM1903  FLJ10241 3'  TGAGTGTGGCTCTCTGCG   46890     CGC  GCCGG
                                TGAGTG  GC    CTCTGCG
                                ||||||  ||    |||||||
                                ACTCAC  CG    GAGACGC
                                   AC_  A____
GAM1903  FLJ13693 3'  TGAGAGCGTGGGCTCTGCG   46891    T  CGCGCC
                                TGAG GCG     GGCTCTGCG
                                |||| |||     |||||||||
                                ACTC CGC     CCGAGACGC
                                  T  AC____
GAM1903  LOC145719 5'  TGGGTGCGCTGCAGCAGCTGTG 46892    A    _  C    C
                                TG GTGCGC GCG CGGCT TG
                                || |||||| ||| ||||| ||
                                AC CACGCG CGT GTCGA AC
                                 C     A  C    C
GAM1903  LOC145720 5'  TGGGTGCGCTGCAGCAGCTGTG 46892    A    _  C    C
                                TG GTGCGC GCG CGGCT TG
                                || |||||| ||| ||||| ||
                                AC CACGCG CGT GTCGA AC
                                 C     A  C    C
GAM1903  LOC147958 3'  GAGTGCGTGGGGCCTCTGCGG  46893       CGCGCC  _
                                GAGTGCG     GGC TCTGCGG
                                |||||||     ||| |||||||
                                CTCACGC     CCG AGACGCC
                                    ACC___  G
GAM1903  LOC197114 5'  TGGGTGCGCTGCAGCAGCTGTG 46892    A    _  C    C
                                TG GTGCGC GCG CGGCT TG
                                || |||||| ||| ||||| ||
                                AC CACGCG CGT GTCGA AC
                                 C     A  C    C
GAM1904  ADH5    5'  GGCGGGGCGTGGGGGGG    46896        GTTC
                                GGCGGGGCG   GGGGGGG
                                |||||||||   |||||||
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                                CCGCCCCGC   CCCCCCC
                                    A___
GAM1904 ALDH3A2  5' GCGGCGGGGTGTAGGG     46897       CG  TC
                                GCGGCGGGG  GT  GGGG
                                |||||||||  ||  ||||
                                CGCCGCCCC  CA  TCCC
                                    A_  __
GAM1904 ANK1     3' AGCGGCGGGGCGGACGGGG   46898          TT
                                AGCGGCGGGGCGG  CGGGG
                                ||||||||||||  |||||
                                TCGCCGCCCCGCC  GCCCC
                                      T_
GAM1904 ANK1     3' AGCGGCGGGGCGGACGGGG   46898          TT
                                AGCGGCGGGGCGG  CGGGG
                                ||||||||||||  |||||
                                TCGCCGCCCCGCC  GCCCC
                                      T_
GAM1904 AQP5     5' GCGCGGGGCCGGCGCGGGGGGGG 46899    G    _  T
                                GCG CGGGGC GGT CGGGGGGG
                                ||| |||||| ||| ||||||||
                                CGC GCCCCG CCG GCCCCCCC
                                  _    G  C
GAM1904 AR       5' GGCGGGGGGGGCGGGTGGG    46900       C  TT   _
                                GGCGGGG GG  CGGG GGG
                                ||||||| ||  |||| |||
                                CCGCCCC CC  GCCC CCC
                                    _ C_   A
GAM1904 ATP6V0C  3' GGTGGGGCGCCGGGGG     46901    C     GT
                                GG GGGGCG  TCGGGGG
                                || ||||||  |||||||
                                CC CCCCGC  GGCCCCC
                                 A     __
GAM1904 AXIN1    3' AGGTGCCGGGGGATGGGGGGG 46902    CG  G   C  TTC
                                AG  GC GGG GG   GGGGGGG
                                ||  || ||| ||   |||||||
                                TC  CG CCC CC   CCCCCCC
                                 CA  G   _  TA_
GAM1904 BMP2     5' AGTGGAGGGGCGGTGGGG    46903    C  C      TC
                                AG GG GGGGCGGT  GGGG
                                || || ||||||||  ||||
                                TC CC CCCCGCCA  CCCC
                                 A  T      __
GAM1904 BMP8     5' GCGGCGGGCGGCGGGG      46904        G   TT
                                GCGGCGGG CGG  CGGGG
                                |||||||| |||  |||||
                                CGCCGCCC GCC  GCCCC
                                      _  __
GAM1904 CACNA2D2 5' CGGCGGCGGGGTTGGGGGG   46905       _ C   C
                                CGGCGG GG GGTT GGGGGG
                                |||||| || |||| ||||||
```

```
                                GCCGCC CC CCAA CCCCCC
                                   G _  _
GAM1904 CD5L    3' GCAGGCGGGGCCAGGGGGG  46906  _     GGTT
                                GC GGCGGGGC  CGGGGGGG
                                || ||||||||  ||||||||
                                CG CCGCCCCG  GTCCCCCC
                                 T     ____
GAM1904 CDK2AP1 5' AGCCGGCGGGGCGGCCGGGG 46907   _       T
                                AGC GGCGGGGCGGT CGGGG
                                ||| |||||||||| |||||
                                TCG CCGCCCCGCCG GCCCC
                                  G       _
GAM1904 CKB     5' GCGGCCGGGCGGGGGCGGGGG 46908     G    TT_
                                GCGGC GGGCGG  CGGGGG
                                ||||| ||||||  ||||||
                                CGCCG CCCGCC  GCCCCC
                                   G    CCC
GAM1904 DBH     3' AGCAGCGGGGCGGGGGCGGGGG 46909          TT_
                                AGCGGCGGGGCGG  CGGGGG
                                ||||||||||||  ||||||
                                TCGTCGCCCCGCC  GCCCCC
                                       CCC
GAM1904 DECR1   5' GCGGTTGGGCGCAGGGGG   46910    CG   GTT
                                GCGG  GGGCG  CGGGGGG
                                ||||  |||||  |||||||
                                CGCC  CCCGC  GTCCCCC
                                  AA   ___
GAM1904 DIA1    3' GGCGTGGGGTGCGCGGGGG  46911    _  CG  T
                                GGCG GGG  GT CGGGGG
                                |||| |||  || ||||||
                                CCGC CCC  CG GCCCCC
                                  A  CA  C
GAM1904 FAAH    5' GCGGCGGGGGGCGGAGCGGGGG 46912     __     TT
                                GCGGC  GGGGCGG  CGGGGG
                                |||||  |||||||  ||||||
                                CGCCG  CCCCGCC  GCCCCC
                                   CC      TC
GAM1904 FMNL    5' GGTGGTGGCGGTGGCGGGGG  46913   C _    T_
                                GG GG GGCGGT  CGGGGG
                                || || ||||||  ||||||
                                CC CC CCGCCA  GCCCCC
                                 A  A     CC
GAM1904 FOXD1   5' GCGGCGGGGCGGCGCATGGGGG 46914          T _
                                GCGGCGGGGCGGT CG GGGGG
                                |||||||||||| || |||||
                                CGCCGCCCCGCCG GT CCCCC
                                       C  A
GAM1904 GALR1   5' AGCGGCGGGGCGCGCGGGG   46915         GTT  G
                                AGCGGCGGGGCG  CG GGGG
                                ||||||||||||  || ||||
```

```
                                TCGCCGCCCCGC  GC CCCC
                                      ___ G
GAM1904 GNA15   5' AGGGCGGGGCGGTGGCGGG  46916   C       TC G
                                AG GGCGGGGCGGT GG GGG
                                || |||||||||| || |||
                                TC CCGCCCCGCCA CC CCC
                                 _       __ G
GAM1904 GNB1    3' GGGGGGCGGGGCGGGGG    46917   C     TT
                                GG GGGGCGG CGGGGG
                                || ||||||| ||||||
                                CC CCCCGCC GCCCCC
                                 _     CC
GAM1904 GNB3    5' CGGCGGGGGGTTGGGGGGG  46918       C  C
                                CGGCGGGG GGTT GGGGGGG
                                |||||||| |||| |||||||
                                GCCGCCCC CCAA CCCCCCC
                                      _  _
GAM1904 GTF2IRD1 5' AGGGCGGGGCGGCGCGGGG  46919   C       T
                                AG GGCGGGGCGGT CGGGG
                                || |||||||||| |||||
                                TC CCGCCCCGCCG GCCCC
                                 _       C
GAM1904 HCN2    3' GCGCGGGGCGATGAGGGGGG  46920    G      TC
                                GCG CGGGGCGGT GGGGGG
                                ||| ||||||||| ||||||
                                CGC GCCCCGCTA CCCCCC
                                 _       CT
GAM1904 HHIP    5' GGCGCGGGAGGATGGGGGGG  46921    _  C TTC
                                GGCG GGG GG  GGGGGGG
                                |||| ||| ||  |||||||
                                CCGC CCC CC  CCCCCCC
                                  G  T TA_
GAM1904 IL6R    5' GCGGCAGGGGTGGCAGGGG   46922     _  C  TC
                                GCGGC GGGG GGT GGGGG
                                ||||| |||| |||  |||||
                                CGCCG CCCC CCG  TCCCC
                                   T  A  __
GAM1904 IL6R    5' GGCAGGGGCGGGGCGGGG    46923    _     TT
                                GGC GGGGCGG CGGGG
                                ||| |||||||  |||||
                                CCG CCCCGCC GCCCC
                                  T     CC
GAM1904 KCNC3   5' GGGGGGCGGGGCGGGAGG    46924   C     TT
                                GG GGGGCGG CGGGGGG
                                || |||||||  |||||||
                                CC CCCCGCC GCCCTCC
                                 _     CC
GAM1904 LMO6    3' AGGGGCGGGGCGTGGGGG    46925   C      GTTC
                                AG GGCGGGGCG   GGGGG
                                || |||||||||   |||||
```

```
                                TC CCGCCCCGC   CCCCC
                                 C       A___
GAM1904  MGMT    5'  GCGGCGGGGGGGGCGGGGGGG  46926        C  TT
                                GCGGCGGGG GG  CGGGGGGG
                                |||||||| ||  ||||||||
                                CGCCGCCCC CC  GCCCCCCC
                                     _  CC
GAM1904  MKPX    5'  AGCGGCGGGGCGGGCGGGG   46927           TT
                                AGCGGCGGGGCGG  CGGGG
                                ||||||||||||  |||||
                                TCGCCGCCCCGCC  GCCCC
                                       C_
GAM1904  MSX2    3'  GCGGTGGGGGGCGGGGG    46928     C   C  TT
                                GCGG GGGG GG  CGGGGG
                                |||| |||| ||  ||||||
                                CGCC CCCC CC  GCCCCC
                                  A   _ __
GAM1904  MSX2    3'  GGTGGGGCGGTGGGGGG    46929    C      TC
                                GG GGGGCGGT  GGGGGG
                                || ||||||||  ||||||
                                CC CCCCGCCA  CCCCCC
                                 A       __
GAM1904  NPY2R   5'  AGCGGCTGGGCGGTTGG    46930      G      C
                                AGCGGC GGGCGGTT GG
                                |||||| |||||||| ||
                                TCGCCG CCCGCCAA CC
                                   A      _
GAM1904  NRG2    3'  GGCGGGCGGGGCGGAGGG    46931      G   TT
                                GGCGGG CGG  CGGGGGG
                                |||||| |||  |||||||
                                CCGCCC GCC  GCCTCCC
                                   _  CC
GAM1904  NRG2    3'  GGCGGGCGGGGCGGAGGG    46931      G   TT
                                GGCGGG CGG  CGGGGGG
                                |||||| |||  |||||||
                                CCGCCC GCC  GCCTCCC
                                   _  CC
GAM1904  NRG2    3'  GGCGGGCGGGGCGGAGGG    46931      G   TT
                                GGCGGG CGG  CGGGGGG
                                |||||| |||  |||||||
                                CCGCCC GCC  GCCTCCC
                                   _  CC
GAM1904  NRG2    3'  GGCGGGCGGGGCGGAGGG    46931      G   TT
                                GGCGGG CGG  CGGGGGG
                                |||||| |||  |||||||
                                CCGCCC GCC  GCCTCCC
                                   _  CC
GAM1904  OPTN    5'  GGCGGCGGCGGTGGCGGAGGGG 46932      _    T_
                                GGCGG GGCGGT  CGGGGGGG
                                ||||| ||||||  ||||||||
```

```
                                CCGCC CCGCCA  GCCTCCCC
                                   G     CC
GAM1904  OTP      3'  GCGGCGGGCGAGGGGGG     46933        G   TTC
                                GCGGCGGG CGG   GGGGGG
                                |||||||| |||   ||||||
                                CGCCGCCC GCT   CCCCCC
                                    _   ___
GAM1904  PCBP1    5'  AGCGGCGGGCGGCGTTCGGGGG 46934         G   __
                                AGCGGCGGG CGGT  TCGGGGG
                                ||||||||| ||||  |||||||
                                TCGCCGCCC GCCG  AGCCCCC
                                    _   CA
GAM1904  PDE4A    3'  GGCGGGGGGGCGGGGG       46935        C  TT
                                GGCGGGG GG  CGGGGG
                                ||||||| ||  ||||||
                                CCGCCCC CC  GCCCCC
                                    _ __
GAM1904  PLCD1    5'  GCGGCGCGGCGGGAGGGG    46936       G    TTC
                                GCGGCG GGCGG   GGGGGG
                                |||||| |||||   ||||||
                                CGCCGC CCGCC   CTCCCC
                                   G    ___
GAM1904  PTMS     5'  GCGCGCGGGGTGGGGCGGGGG  46937     _     C  TT
                                GCG GCGGGG GG  CGGGGG
                                ||| |||||| ||  ||||||
                                CGC CGCCCC CC  GCCCCC
                                  G     A  CC
GAM1904  PTPRS    3'  GCGGCCGGGGCCGGTGGGGGGG 46938      _    _  TC
                                GCGGC GGGGC GGT  GGGGGGG
                                ||||| ||||| |||  |||||||
                                CGCCG CCCCG CCA  CCCCCCC
                                   G    G  __
GAM1904  PTPRS    3'  GCGGCCGGGGCCGGTGGGGGGG 46938      _    _  TC
                                GCGGC GGGGC GGT  GGGGGGG
                                ||||| ||||| |||  |||||||
                                CGCCG CCCCG CCA  CCCCCCC
                                   G    G  __
GAM1904  PTPRS    3'  GCGGCCGGGGCCGGTGGGGGGG 46938      _    _  TC
                                GCGGC GGGGC GGT  GGGGGGG
                                ||||| ||||| |||  |||||||
                                CGCCG CCCCG CCA  CCCCCCC
                                   G    G  __
GAM1904  PTPRS    3'  GCGGCCGGGGCCGGTGGGGGGG 46938      _    _  TC
                                GCGGC GGGGC GGT  GGGGGGG
                                ||||| ||||| |||  |||||||
                                CGCCG CCCCG CCA  CCCCCCC
                                   G    G  __
GAM1904  PYGO2    3'  AGCAGCGGGGTGGGGGTGGGGG 46939          C  TTCG
              G                  AGCGGCGGGG GG   GGGGGG
                                ||||||||| ||   ||||||
```

```
                                TCGTCGCCCC CC    CCCCCC
                                     A  CCCA
GAM1904  RAD23B   5'  GGCGGTGGGGGTGGGGG     46940      _  C   TC
                                GGCGG GG GGT  GGGGG
                                ||||| || |||  |||||
                                CCGCC CC CCA  CCCCC
                                  A  C  __
GAM1904  RFX1     3'  GGCGGGTGGGGCGGGGGG    46941       GC  TT
                                GGCGGG  GG  CGGGGGG
                                ||||||  ||  |||||||
                                CCGCCC  CC  GCCCCCC
                                   A_  CC
GAM1904  SALL1    3'  AAGGGGCGGGGCGGGGTGGGGG 46942     C        TTC
            G                    AAG GGCGGGGCGG   GGGGGG
                                ||| ||||||||||   ||||||
                                TTC CCGCCCCGCC   CCCCCC
                                  C         CCA
GAM1904  SDC1     3'  AGTGGCAGGGCGGAGGGGG   46943    C        TTC
                                AG GGCGGGGCGG   GGGGGG
                                || ||||||||||   ||||||
                                TC CCGTCCCGCC   TCCCCC
                                 A        ___
GAM1904  SPTBN4   3'  GCGGCGGAGTGCAGGGGG    46944         CGGTT
                                GCGGCGGGG    CGGGGGG
                                |||||||||    |||||||
                                CGCCGCCTC    GTCCCCC
                                     AC___
GAM1904  SRD5A1   5'  GGCGGCGGCGCGGGGG     46945      _   GTT
                                GGCGG GGCG   CGGGGG
                                ||||| ||||   ||||||
                                CCGCC CCGC   GCCCCC
                                   G   ___
GAM1904  TGFB1    3'  GGCGGGGCGGGGTGGGG     46946         TTC  _
                                GGCGGGGCGG   GG GGGG
                                ||||||||||   || ||||
                                CCGCCCCGCC   CC CCCC
                                     ___  A
GAM1904  TPT1     5'  AGCGGCGCTCGGGGG       46947       GGGGCG
                                AGCGGC     GTTCGGGGG
                                ||||||     |||||||||
                                TCGCCG     CGAGCCCCC
                                     _______
GAM1904  VIPR1    3'  AGGGTGGGGTGGCAAGGGG   46948    C  C    C   TC
                                AG GG GGGG GGT  GGGGG
                                || || |||| |||  |||||
                                TC CC CCCC CCG  TCCCC
                                 _ A   A  T_
GAM1904  ZNF278   5'  GCGGCGGGGCGCGCACGGGGG  46949          _  T
                                GCGGCGGGGCG GT CGGGGG
                                |||||||||| || ||||||
```

```
                                CGCCGCCCCGC CG GCCCCC
                                      G  T
GAM1904  ZNF278   5'  GCGGCGGGGCGCGCACGGGGG  46949          _  T
                                GCGGCGGGGCG GT CGGGGG
                                |||||||||| || ||||||
                                CGCCGCCCCGC CG GCCCCC
                                      G  T
GAM1904  ZNF278   5'  GCGGCGGGGCGCGCACGGGGG  46949          _  T
                                GCGGCGGGGCG GT CGGGGG
                                |||||||||| || ||||||
                                CGCCGCCCCGC CG GCCCCC
                                      G  T
GAM1904  ZNF278   5'  GCGGCGGGGCGCGCACGGGGG  46949          _  T
                                GCGGCGGGGCG GT CGGGGG
                                |||||||||| || ||||||
                                CGCCGCCCCGC CG GCCCCC
                                      G  T
GAM1904  AF053356_CDS3 3'  AGGGTGGGGTGGGCTGGGG   46950    C  C   C_   C
                                AG GG GGGG  GGTT GGGG
                                || || ||||  |||| ||||
                                TC CC CCCC  CCGA CCCC
                                 _ A   AC   _
GAM1904  BCoR     5'  AGCGGGGGGCGGTTGGG     46951      C       C
                                AGCGG GGGGCGGTT GGG
                                ||||| ||||||||| |||
                                TCGCC CCCCGCCAA CCC
                                   _       _
GAM1904  BCoR     5'  AGCGGGGGGCGGTTGGG     46951      C       C
                                AGCGG GGGGCGGTT GGG
                                ||||| ||||||||| |||
                                TCGCC CCCCGCCAA CCC
                                   _       _
GAM1904  BMF      3'  GGGGGTGGAGGTCGGGGGGG  46952    C  _  C   T
                                GG GG GG GGT CGGGGGGG
                                || || || ||| ||||||||
                                CC CC CC CCA GCCCCCCC
                                 C  A  T  _
GAM1904  BRUNOL6  5'  GGAGGGGCGTAGAGGGGG    46953    C     GTTC
                                GG GGGGCG   GGGGGGG
                                || ||||||   |||||||
                                CC CCCCGC   CTCCCCC
                                 T     AT__
GAM1904  CACNA1I  3'  GCGGTGGGCGGCCGGGGG    46954     CG      T
                                GCGG  GGGCGGT CGGGGG
                                ||||  ||||||| ||||||
                                CGCC  CCCGCCG GCCCCC
                                  A_      _
GAM1904  CARM1    3'  AGTGGGGGGGCGGGGGGG    46955    C  C     TTC
                                AG GG GGGGCGG   GGGGG
                                || || |||||||   |||||
```

```
                                TC CC CCCCGCC   CCCCC
                                 A  C      ___
GAM1904  CASKIN1   3'  GCGGTGGGGCAGGGGGG     46956      C      GTTC
                                GCGG GGGGCG    GGGGGG
                                |||| ||||||    ||||||
                                CGCC CCCCGT    CCCCCC
                                  A     _____
GAM1904  CD36L1    3'  GGCTGTGGGGCTGGGGGG    46957     GG_  C    C
                                GGC   GG GGTT GGGGGG
                                |||   || |||| ||||||
                                CCG   CC CCGA CCCCCC
                                  ACA  _    _
GAM1904  CECR2     5'  GCGGGGGGCGGCGGCGCGGGGG 46958      C       T_  G
                                GCGG GGGGCGGT  CG GGGGG
                                |||| ||||||||  || |||||
                                CGCC CCCCGCCG  GC CCCCC
                                  _       CC  G
GAM1904  CEP3      5'  AGGGCGGGGCGGCGCGGGG    46919    C         T
                                AG GGCGGGGCGGT CGGGG
                                || ||||||||||| |||||
                                TC CCGCCCCGCCG GCCCC
                                 _         C
GAM1904  CITED2    3'  GGGGGGCGGCGGGGGGG     46959    C      TT
                                GG GGGGCGG  CGGGGGGG
                                || |||||||  ||||||||
                                CC CCCCGCC  GCCCCCCC
                                 _     __
GAM1904  DKFZP434M154 3'  AGCGGGGGGTGGGGG       46960        C   TC
                                GGCGGGG GGT  GGGGG
                                ||||||| |||  |||||
                                TCGCCCC CCA  CCCCC
                                    _  __
GAM1904  DKFZp547O146 3'  AGGGCGGGGCTGGGCTGGGGGG 46961    C       __    C
                  G              AG GGCGGGGC  GGTT GGGGGGG
                                || ||||||||  |||| |||||||
                                TC CCGCCCCG  CCGA CCCCCCC
                                 _       AC   _
GAM1904  EFNA5     5'  GGCGGTGGGATGGGGG      46962       _  C   TC
                                GGCGG GG GGT  GGGGG
                                ||||| || |||  |||||
                                CCGCC CC CTA  CCCCC
                                  A  _   __
GAM1904  FAM10A6   5'  GCGGTGGGCGAAGCTGGGGGG  46963      CG     TTCG
                                GCGG  GGGCGG   GGGGGG
                                ||||  ||||||   ||||||
                                CGCC  CCCGCT   CCCCCC
                                  A_     TCGA
GAM1904  FBP17     3'  GGCGTGGCGGGGGGGGGG    46964      G    TTC
                                GGCG GGCGG   GGGGGG
                                |||| |||||   ||||||
```

```
                                CCGC CCGCC   CCCCCC
                                  A     CC_
GAM1904  FLJ00060  3'  GCGGTGGGGGGGTAAGGGGG   46965      C    C   TC
                                GCGG GGGG GGT  GGGGGG
                                |||| |||| |||  ||||||
                                CGCC CCCC CCA  TCCCCC
                                  A    _   T_
GAM1904  FLJ12650  3'  GCGCCGGGGGTGGGCGCGGGG   46966     G     C  TT  G
                                GCG CGGGG GG  CG GGGG
                                ||| ||||| ||  || ||||
                                CGC GCCCC CC  GC CCCC
                                  G     A  C_  G
GAM1904  FLJ30473  5'  GCCGCGGGCGCGGGGGG     46967    G     G  GTT
                                GC GCGGG CG   CGGGGGG
                                || ||||| ||   |||||||
                                CG CGCCC GC   GCCCCCC
                                 G     _  ____
GAM1904  FLJ31978  3'  GGGGGGGCGGCGATGGGGGG   46968    C       TCG
                                GG GGGGCGGT   GGGGGG
                                || ||||||||   ||||||
                                CC CCCCGCCG   CCCCCC
                                 C       CTA
GAM1904  FOXO3A    5'  GCGGCGGGGCGGGGAGAAGGGG 46969            TTC__
              G                  GCGGCGGGGCGG    GGGGGG
                                 ||||||||||||    ||||||
                                 CGCCGCCCCGCC    TCCCCC
                                        CCTCT
GAM1904  HSRNAFEV  5'  GGCGGGGGTTGCGGGGGGG   46970       CG  _
                                GGCGGGG  GTT CGGGGGGG
                                |||||||  ||| ||||||||
                                CCGCCCC  CAA GCCCCCCC
                                    __   C
GAM1904  IMP13     5'  AGTGGTGGGGTGAGGGGGG   46971    C  C    C  TTC
                                AG GG GGGG GG   GGGGGG
                                || || |||| ||   ||||||
                                TC CC CCCC CT   CCCCCC
                                 A  A    A  ____
GAM1904  KHDRBS3   5'  GCGGCGGCGGCGGCACGGGGG  46972        _     T
                                GCGGCGG GGCGGT CGGGGG
                                ||||||| |||||| ||||||
                                CGCCGCC CCGCCG GCCCCC
                                    G     T
GAM1904  KIAA0339  3'  GCGCGGGGCGGTGGCGGCGGGG 46974     G       T_  _
              G                  GCG CGGGGCGGT  CGG GGGGG
                                 ||| |||||||||  ||| |||||
                                 CGC GCCCCGCCA  GCC CCCCC
                                   _       CC   G
GAM1904  KIAA0339  3'  GGCGGTGGCGGCGGGGGTGGGG 46973       _     TC  _
                                GGCGG GGCGGT  GGG GGGG
                                ||||| ||||||  ||| ||||
```

```
                                CCGCC CCGCCG  CCC CCCC
                                   A     CC   A
GAM1904  KIAA0537  5' GGTGGCGGCGGTGGCAGGGG  46975    C _     T_
                                GG GG GGCGGT  CGGGGG
                                || || ||||||  ||||||
                                CC CC CCGCCA  GTCCCC
                                 A  G     CC
GAM1904  KIAA0620  5' GCGGCGGGAGGCGGGGGGG   46976         C  TT
                                GCGGCGGGG GG  CGGGGGGG
                                |||||||||  ||  ||||||||
                                CGCCGCCCT CC  GCCCCCCC
                                      _  __
GAM1904  KIAA0767  3' GGCGGGGGCTGGGGG       46977        CG   C
                                GGCGGGG  GTT GGGGG
                                |||||||  ||| |||||
                                CCGCCCC  CGA CCCCC
                                   __   _
GAM1904  KIAA0930  3' GGGGGGCGATGGGCGGGGGG  46978    C       T__
                                GG GGGGCGGT   CGGGGGG
                                || ||||||||   |||||||
                                CC CCCCGCTA   GCCCCCC
                                 _       CCC
GAM1904  KIAA1086  3' GGCGGGGGGGTGGGTGGGG    46979        C   TC  _
                                GGCGGGG GGT  GG GGGG
                                ||||||| |||  || ||||
                                CCGCCCC CCA  CC CCCC
                                    _  C_  A
GAM1904  KIAA1100  5' AGGGGGCGGGGGAGGGGGG   46980    C      TTC_
                                GG GGGGCGG    GGGGGG
                                || |||||||    ||||||
                                TC CCCCGCC    CCCCCC
                                 _      CCCT
GAM1904  KIAA1981  5' GCGCGGGGCGCGGGGGG     46981     G      GTT
                                GCG CGGGGCG   CGGGGGG
                                ||| |||||||   |||||||
                                CGC GCCCCGC   GCCCCCC
                                  _     ____
GAM1904  Magmas    3' GCGGCGGGGTGGGCGGGGGG  46982         C  TT
                                GCGGCGGGG GG  CGGGGGG
                                |||||||||  ||  |||||||
                                CGCCGCCCC CC  GCCCCCC
                                     A  C_
GAM1904  MGC14386  5' GCGGCGGGGATGGGGGG     46983         CGGTTC
                                GCGGCGGGG     GGGGGG
                                |||||||||     ||||||
                                CGCCGCCCC     CCCCCC
                                     TA_____
GAM1904  MGC15730  5' GGCGGGGCGGCGGGGG      46984          TT
                                GGCGGGGCGG  CGGGGG
                                ||||||||||  ||||||
```

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                                CCGCCCCGCC  GCCCCC
                                     __
GAM1904  MGC20460  5'  GGCGGTGGTGGTGGAGGGGG  46985      _ C  TC
                                GGCGG GG GGT  GGGGGGG
                                ||||| || |||  |||||||
                                CCGCC CC CCA  CTCCCCC
                                   A  A   C_
GAM1904  MGC20460  5'  GCGGCGGAGGCGGTGGAGGGGG 46986       _    TC
                                GCGGCGG GGCGGT  GGGGGGG
                                ||||||| ||||||  |||||||
                                CGCCGCC CCGCCA  CTCCCCC
                                    T     C_
GAM1904  MGC2555   5'  GCGCGGGGCGGGCTCGGGG   46987    G      _
                                GCG CGGGGCGG TTCGGGG
                                ||| |||||||| |||||||
                                CGC GCCCCGCC GAGCCCC
                                  _       C
GAM1904  MIC2L1    3'  GCGGGGGGCGGTAAGGG     46988     C       TC
                                GCGG GGGGCGGT  GGGG
                                |||| ||||||||  ||||
                                CGCC CCCCGCCA  TCCC
                                  _       T_
GAM1904  P5CR2     3'  GGCAGGGGCGGCAGGGG     46989     _      TC
                                GGC GGGGCGGT  GGGGG
                                ||| ||||||||  |||||
                                CCG CCCCGCCG  TCCCC
                                  T       __
GAM1904  PPM1A     5'  GCGGCGGCGGCGGCAGCCGGGG 46990        _     __
                                GCGGCGG GGCGGT  TCGGGG
                                ||||||| ||||||  ||||||
                                CGCCGCC CCGCCG  GGCCCC
                                    G     TC
GAM1904  PRIC285   3'  AGGGTGGGGTGGGGTGGGG   46991    C  C    C  TTC  _
                                AG GG GGGG GG   GG GGGG
                                || || |||| ||   || ||||
                                TC CC CCCC CC   CC CCCC
                                 _  A    A  ___  A
GAM1904  RASD2     3'  GGTGGGGCAGCAGGGG      46992    C       TC
                                GG GGGGCGGT  GGGGG
                                || ||||||||  |||||
                                CC CCCCGTCG  TCCCC
                                 A       __
GAM1904  RNF10     5'  GCGGTGGCGGCGGCGTTGGGGG 46993      C  _     TCG
                                GCGG GG GGCGGT   GGGGG
                                |||| || ||||||   |||||
                                CGCC CC CCGCCG   CCCCC
                                  A  G     CAA
GAM1904  SEMA4G    5'  GGCGGTGGGGGTGGTGGGG   46994      _  C   TC  _
                                GGCGG GG GGT  GG GGGG
                                ||||| || |||  || ||||
```

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                                CCGCC CC CCA  CC CCCC
                                  A  C   __  A
GAM1904  SEMA6A   5'  GCGGGGGGCGGGGTGGGGG   46995     C      TTCG
                                GCGG GGGGCGG   GGGGG
                                |||| |||||||   |||||
                                CGCC CCCCGCC   CCCCC
                                  _      CCA_
GAM1904  SEMA6C   3'  AGGTGCGGGGCGAGGGG    46996    CG      GTTC
                                AG  GCGGGGCG   GGGGG
                                ||  ||||||||   |||||
                                TC  CGCCCCGC   TCCCC
                                 CA       _____
GAM1904  SMURF2   5'  GCGGCGGGCGGCACGGGGG   46997        G   T
                                GCGGCGGG CGGT CGGGGG
                                |||||||| |||| ||||||
                                CGCCGCCC GCCG GCCCCC
                                    _   T
GAM1904  SSAT2    5'  GGCGGGAGTCGGGGGGG    46998      GC   T
                                GGCGGG  GGT CGGGGGGG
                                ||||||  ||| ||||||||
                                CCGCCC  TCA GCCCCCCC
                                   __  _
GAM1904  SUI1     5'  GCGGCGGCGGCGGTGGCGGG  46999       _     TC  G
                                GCGGCGG GGCGGT  GG GGG
                                ||||||| ||||||  || |||
                                CGCCGCC CCGCCA  CC CCC
                                    G     __  G
GAM1904  TEB4     3'  GGTGGGGGGCGGGCGGGGGGG  47000    C_     TT
                                GG  GGGGCGG  CGGGGGGG
                                ||  |||||||  ||||||||
                                CC  CCCCGCC  GCCCCCCC
                                 AC      C_
GAM1904  TGIF2    5'  AGCGGGGGGGCGCCGGGGG    47001      C     GT
                                AGCGG GGGGCG  TCGGGGG
                                ||||| ||||||  |||||||
                                TCGCC CCCCGC  GGCCCCC
                                   _     __
GAM1904  TNFSF13  5'  GGCGGGGCGGGTAAGGG     47002          TTCG
                                GGCGGGGCGG   GGGGG
                                ||||||||||   |||||
                                CCGCCCCGCC   TTCCC
                                     CA__
GAM1904  UBXD1    5'  GCCGCGGGGGCGGGGGG     47003    G     CGGTT
                                GC GCGGGG    CGGGGGG
                                || ||||||    |||||||
                                CG CGCCCC    GCCCCCC
                                 G     C____
GAM1904  VEGFC    5'  GCGGCGGGAGCGGGTCCGGGG  47004        _   _
                                GCGGCGGG GCGG TTCGGGG
                                |||||||| |||| |||||||
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                                CGCCGCCC CGCC AGGCCCC
                                     T   C
GAM1904  LOC116113 3'  GGTGGGGCGGCGGGGGG    47005    C     TT
                                GG GGGGCGG  CGGGGGG
                                || |||||||  |||||||
                                CC CCCCGCC  GCCCCCC
                                 A     __
GAM1904  LOC122618 3'  GGAGGTGGGGCTCAGGGGGG   47006    C  _  C
                                GG GG GG GGTTCGGGGGGG
                                || || || ||||||||||||
                                CC CC CC CCGAGTCCCCCC
                                 T  A  _
GAM1904  LOC127696 5'  CGGCGGGGCGGGTGGGG    47007          TTCG
                                CGGCGGGGCGG   GGGG
                                ||||||||||   ||||
                                GCCGCCCCGCC   CCCC
                                      CA__
GAM1904  LOC131583 3'  GCTGGGGCGGGAGCGGGGG   47008    _     TT_
                                GC GGGGCGG   CGGGGG
                                || |||||||   ||||||
                                CG CCCCGCC   GCCCCC
                                 A      CTC
GAM1904  LOC144058 5'  GCGCCGGGGCGGAGGCCGGGG  47009     G      T__
                                GCG CGGGGCGG   TCGGGG
                                ||| ||||||||   ||||||
                                CGC GCCCCGCC   GGCCCC
                                  G       TCC
GAM1904  LOC144600 5'  GGGGGGCGATGGGCGGGGGG   46978    C      T__
                                GG GGGGCGGT   CGGGGGG
                                || ||||||||   |||||||
                                CC CCCCGCTA   GCCCCCC
                                 _      CCC
GAM1904  LOC148193 5'  GGCGGGGCGGGGAGGGG    47010         TTC
                                GGCGGGGCGG   GGGGGGG
                                ||||||||||   |||||||
                                CCGCCCCGCC   CCTCCCC
                                      ___
GAM1904  LOC151959 3'  GGCGGGGCGGGGTAGGGG    47011         TTCG
                                GGCGGGGCGG   GGGGG
                                ||||||||||   |||||
                                CCGCCCCGCC   TCCCC
                                      CCA_
GAM1904  LOC152273 3'  AGTGGTGGGGCGGTTATAG   47012    C  C      CG
                                AG GG GGGGCGGTT  GG
                                || || |||||||||  ||
                                TC CC CCCCGCCAA  TC
                                 A  A       TA
GAM1904  LOC155066 5'  AGCGGCGGGCGCGGACCGGGG  47013         _   TT
                                AGCGGCGGG GCGG  CGGGG
                                ||||||||| ||||  |||||
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                                TCGCCGCCC CGCC  GCCCC
                                     G    TG
GAM1904  LOC157226 5'  GCGGCGGGGGGGACGGGAGGG   47014         C  TT
                                GCGGCGGGG GG  CGGGGGGG
                                ||||||||| ||  ||||||||
                                CGCCGCCCC CC  GCCCTCCC
                                     _  T_
GAM1904  LOC158056 5'  GCGGCAGGGGCTGGGGGG    47015         CG   C
                                GCGGCGGGG  GTT GGGGGG
                                |||||||||  ||| ||||||
                                CGCCGTCCC  CGA CCCCCC
                                     __   _
GAM1904  LOC163250 5'  AGGGGCGGGGCGGCAGGGG    47016    C         TC
                                AG GGCGGGGCGGT  GGGGG
                                || ||||||||||  |||||
                                TC CCGCCCCGCCG  TCCCC
                                 C         __
GAM1904  LOC199992 3'  GGACGGTGGGGTGGGCTGGGG  47017   A   C   C_   C
                                A GCGG GGGG  GGTT GGGG
                                | |||| ||||  |||| ||||
                                C TGCC CCCC  CCGA CCCC
                                 C   A   AC   _
GAM1904  LOC203530 3'  AAGGGTGGGGGGGTGGGGGG   47018    C  C   C   TC
                                AAG GG GGGG GGT  GGGGGG
                                ||| || |||| |||  ||||||
                                TTC CC CCCC CCA  CCCCCC
                                  _  A   _  __
GAM1904  LOC204515 5'  GCGGTGGGCGGGCAGGGGG   47019     CG     TT
                                GCGG  GGGCGG  CGGGGGG
                                ||||  ||||||  |||||||
                                CGCC  CCCGCC  GTCCCCC
                                  A_     C_
GAM1904  LOC221463 3'  GCGGGGGGTGGTTCATAG    47020     C   C     G
                                GCGG GGGG GGTTCG GG
                                |||| |||| |||||| ||
                                CGCC CCCC CCAAGT TC
                                  _   A     A
GAM1904  LOC245811 5'  GCGGCGGGGTGGAGAGTGGGGG 47021         C  TTCG_
           G                     GCGGCGGGG GG     GGGGGG
                                |||||||||  ||    ||||||
                                CGCCGCCCC CC     CCCCCC
                                     A  TCTCA
GAM1904  LOC253181 3'  GCGCGGGGCGTCGTGGGGG   47022     G      GT   _
                                GCG CGGGGCG  TCG GGGGG
                                ||| |||||||  ||| |||||
                                CGC GCCCCGC  AGC CCCCC
                                  _      __   A
GAM1904  LOC257451 3'  AGCAGCGGGGTGGGGGTGGGGG 46939         C  TTCG
           G                     AGCGGCGGGG GG    GGGGGG
                                |||||||||| ||    ||||||
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                                TCGTCGCCCC CC    CCCCCC
                                      A  CCCA
GAM1904  LOC51030  5'  AGGGGCGGGGCGAGCGGGGG   47023    C        TT
                                AG GGCGGGGCGG  CGGGGG
                                || ||||||||||  ||||||
                                TC CCGCCCCGCT  GCCCCC
                                 C         C_
GAM1904  LOC92312  5'  GCGGTGGGGGGCTGGGG     47024      C    C    C
                                GCGG GGGG GGTT GGGG
                                |||| |||| |||| ||||
                                CGCC CCCC CCGA CCCC
                                  A    _    _
GAM1905  CLC       3'  TATTTTCTCTTCTGGTTTATAG 47027       G    G
               G                   TATTTT TCTTT GGTTTATAGG
                                |||||| ||||| ||||||||||
                                ATAAAA AGAAG CCAAATATCC
                                    G    A
GAM1905  EMP1      3'  TTTTGCTTTGGGTCAGAAGG   47028      T       TAT
                                TTTTG CTTTGGGTT   AGG
                                ||||| |||||||||   |||
                                AAAAC GAAACCCAG   TCC
                                   _        TCT
GAM1905  IL17      3'  TGCTTTGTTTTGCTTATAGGA  47029    T    G___
                                TG CTTTG    GTTTATAGGA
                                || |||||    ||||||||||
                                AC GAAAC    CGAATATCCT
                                 _     AAAA
GAM1905  PRKAR2B   3'  CATTTTGTCTTTATATAGG    47030           GGTT
                                TATTTTGTCTTTG    TATAGG
                                ||||||||||||    ||||||
                                GTAAAACAGAAAT    ATATCC
                                          ____
GAM1905  GPR64     3'  TTTTGTTTTCTTTATAGGA    47031       C   GGG
                                TTTTGT TTT   TTTATAGGA
                                |||||| |||   |||||||||
                                AAAACA AAG   AAATATCCT
                                    A  ___
GAM1905  ICAM4     3'  TATTTTATTTTTGGAGACAGG  47032        C     TTT
                                TATTTTGT TTTGGG   ATAGG
                                |||||||| ||||||   |||||
                                ATAAAATA AAACCT   TGTCC
                                     A     C__
GAM1905  ICAM4     3'  TATTTTATTTTTGGAGACAGG  47032        C     TTT
                                TATTTTGT TTTGGG   ATAGG
                                |||||||| ||||||   |||||
                                ATAAAATA AAACCT   TGTCC
                                     A     C__
GAM1905  KIAA0193  3'  CTTTGTATTTGGGTTTGTGGGA 47033       C        ATA
                                TTTTGT TTTGGGTTT   GGA
                                |||||| |||||||||   |||
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                                GAAACA AAACCCAAA   CCT
                                   T       CAC
GAM1905  KUB3     3'  TTTTATCTGGATTGTAGG    47034        TT    TA
                                TTTTGTCT  GGGTT  TAGG
                                ||||||||  |||||  ||||
                                AAAATAGA  CCTAA  ATCC
                                     __    C_
GAM1905  LOC150170 5'  TTTTGTCTTGGAGAGG     47035        T   TTTAT
                                TTTTGTCTT GGG    AGG
                                ||||||||| |||    |||
                                AAAACAGAA CTC    TCC
                                     C  _____
GAM1905  LOC150175 5'  TTTTGTCTTGGAGAGG     47035        T   TTTAT
                                TTTTGTCTT GGG    AGG
                                ||||||||| |||    |||
                                AAAACAGAA CTC    TCC
                                     C  _____
GAM1905  LOC158257 5'  CATTTTGTCTTTCCAAGTGGG  47036          _______
                                TATTTTGTCTT     TGGG
                                ||||||||||     ||||
                                GTAAAACAGAA     ACCC
                                      AGGTTC
GAM1905  LOC161978 5'  TATTTTGTCTATGGGTTC    47037          T
                                TATTTTGTCT TGGGTTT
                                |||||||||| |||||||
                                ATAAAACAGA ACCCAAG
                                     T
GAM1905  LOC221895 3'  TATTTTGTTTTGGGG      47038        C     TTTATA
                                TATTTTGT TTTGGG     G
                                |||||||| ||||||     |
                                ATAAAACA AAACCC     C
                                   _    _______
GAM1906  MGC34869  5'  GCCGTGGGCAAGTTA      47041          ATC
                                GCCGTGGGCA   GGTTG
                                ||||||||||   |||||
                                CGGCACCCGT   TCAAT
                                     ___
GAM1906  PNPASE    3'  CCGTTGTAGGCAAGTAAAGTTG 47042     CC       TC__
            TT                   CCG  GTGGGCAA    GGTTGTT
                                ||| ||||||||   |||||||
                                GGC  CATCCGTT    TCAACAA
                                  AA       CATT
GAM1906  LOC120196 3'  GTGGGCAATTTCAAATTTAG   47043         __   TTG
                                GTGGGCAA  TCGG   TTAG
                                ||||||||  ||||   ||||
                                CACCCGTT  AGTT   AATC
                                     AA    TA_
GAM1906  LOC149506 5'  CCGCTGTGGGCAGTGCCA    47044      C      ATCG  T
                                CCGC GTGGGCA    GT GTTA
                                |||| |||||||    || ||||
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                                GGCG CACCCGT    CA CGGT
                                  A     ____  _
GAM1906  LOC159199 5'  CCTCGTGGGCAGTCAGGTG   47045    GC      A   T
                                CC  CGTGGGCA TCGG TG
                                ||  |||||||| |||| ||
                                GG  GCACCCGT AGTC AC
                                 A_      C   C
GAM1906  LOC222166 5'  CCGCCGTGGGGGTTG      47046         CAATC
                                CCGCCGTGGG    GGTTG
                                ||||||||||    |||||
                                GGCGGCACCC    CCAAC
                                              _____
GAM1907  ATP5J    5'  CTGGGAGGCGGGAGGGGG    47049     TCTA      A
                                TTGGG   AGGCGGGA GGGG
                                |||||   |||||||| ||||
                                GACCC   TCCGCCCT CCCC
                                  ____      C
GAM1907  BSN      3'  TTGGGCTTTGGAGAAGGGG   47050     T  AA  CG
                                TTGGG CT  GG  GGAAGGGG
                                ||||| ||  ||  ||||||||
                                AACCC GA  CC  TCTTCCCC
                                  _ AA  __
GAM1907  RAB3A    3'  TTAAAAAAAGGCGGGGGGGGG  47051     TCT      AA
                                TTGGG   AAGGCGGG  GGGG
                                |||||   ||||||||  ||||
                                AATTT   TTCCGCCC  CCCC
                                  TT_       CC
GAM1907  SF3A1    3'  CTGGGTCTGGGGCAGGGGG   47052       AA     AA
                                TTGGGTCT  GGCGGG  GGG
                                ||||||||  ||||||  |||
                                GACCCAGA  CCGTCC  CCC
                                    CC     __
GAM1907  SPTBN4   3'  AGGTAAAGGCGGGGAGGGG   47053     CT      A
                                GGGT  AAGGCGGG AGGGG
                                ||||  |||||||| |||||
                                TCCA  TTCCGCCC TCCCC
                                  T_       C
GAM1907  DKFZP434P211 3'  TTGGGCTCCCTGGGGAGGGGG  47054      _  AAGGC   A
                                TTGGG TCT    GGGA GGGG
                                ||||| |||    |||| ||||
                                AACCC AGG    CCCT CCCC
                                  G   GAC__   C
GAM1907  DKFZp547J036 3'  TAGGCCTCGGTGGGGGGGGG   47055       AA  C   AA
                                TGGGTCT  GG GGG  GGGG
                                |||||||  || |||  ||||
                                ATCCGGA  CC CCC  CCCC
                                   G_  A   CC
GAM1907  LOC150174 3'  TTGGGCTCCCTGGGGAGGGGG  47054      _  AAGGC   A
                                TTGGG TCT    GGGA GGGG
                                ||||| |||    |||| ||||
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                                AACCC AGG    CCCT CCCC
                                   G  GAC__   C
GAM1907  LOC150213 3'  TTGGGCTCCCTGGGGAGGGGG  47054      _  AAGGC   A
                                TTGGG TCT    GGGA GGGG
                                ||||| |||    |||| ||||
                                AACCC AGG    CCCT CCCC
                                   G  GAC__   C
GAM1907  LOC150236 5'  TTGGGCTCCCTGGGGAGGGGG  47054      _  AAGGC   A
                                TTGGG TCT    GGGA GGGG
                                ||||| |||    |||| ||||
                                AACCC AGG    CCCT CCCC
                                   G  GAC__   C
GAM1907  LOC255170 3'  TTGGGTCCTGGCCCGAGAAGGG 47056        AA  __
            G                    TTGGGTCT  GGC  GGGAAGGGG
                                ||||||||  |||  |||||||||
                                AACCCAGG  CCG  CTCTTCCCC
                                    A_  GG
GAM1908  FLJ20320  5'  TCTTGTAGGCTTTGAT     47059    G       G
                                TC TTGTAGGCTT TGAT
                                || |||||||||| ||||
                                AG AACATCCGAA ACTA
                                 _       _
GAM1908  KIAA1535  5'  TCGCTGTAGGGGTGGATG    47060         CTT   ATA
                                TCGTTGTAGG   GTG   GATG
                                ||||||||||   |||   ||||
                                AGCGACATCC   CAC   CTAC
                                     C__   ____
GAM1908  KRTAP3-3  3'  GTTGTAGGTACTGAGATAGGTG 47061        C_  T    A
            A                    GTTGTAGG  TTG GATAG TGA
                                ||||||||  ||| ||||| |||
                                CAACATCC  GAC CTATC ACT
                                    AT  T    C
GAM1908  PRO0899   5'  GTTGAAGGGCTATAGATGA   47062     TA_   TGTG
                                GTTG   GGCT    ATAGATGA
                                ||||   ||||    ||||||||
                                CAAC   CCGA    TATCTACT
                                  TTC   _____
GAM1909  FLJ20707  3'  TAATCTTTCTTTTAAAAC    47065     A
                                TGAT TTTCTTTTAAAAC
                                |||| ||||||||||||
                                ATTA AAAGAAAATTTTG
                                  G
GAM1909  FLJ31153  3'  TCTGGTATTTCTCCCAAA    47066     A
                                TTTG TATTTCTTTTAAA
                                |||| ||||||||||||
                                AGAC ATAAAGAGGGTTT
                                  C
GAM1909  KIAA0053  3'  TTTGATGTTTCCCTCAAA    47067       A
                                TTTGAT TTTCTTTTAAA
                                |||||| ||||||||||
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                                AAACTA AAAGGGAGTTT
                                   C
GAM1909 KIAA1573 3' TAACATTTCTTTTAAAAC    47068
                                TGATATTTCTTTTAAAAC
                                ||||||||||||||||||
                                ATTGTAAAGAAAATTTTG

GAM1909 LIPI    3' TTCCATCCTTTCTTTTAAAAC 47069    G  A_
                                TTT AT  TTTCTTTTAAAAC
                                ||| ||  ||||||||||||
                                AAG TA  AAAGAAAATTTTG
                                  G  GG
GAM1909 LOC129831 3' TTTAATATTTCTTTACAAAA  47070          _
                                TTTGATATTTCTTT TAAAA
                                |||||||||||||| |||||
                                AAATTATAAAGAAA GTTTT
                                         T
GAM1909 LOC145870 3' TTTAATGTCTCCTTTAAAAC  47071       A
                                TTTGAT TTTCTTTTAAAAC
                                |||||| ||||||||||||
                                AAATTA AGAGGAAATTTTG
                                   C
GAM1909 LOC146159 5' TGATTCTTCTTTTAAAAC    47072     A
                                TGAT TTTCTTTTAAAAC
                                |||| ||||||||||||
                                ACTA GAAGAAAATTTTG
                                  A
GAM1909 LOC153642 3' TTTGATACTTCCACTAAA    47073          T
                                TTTGATATTTCT TTAAA
                                |||||||||||| |||||
                                AAACTATGAAGG GATTT
                                         T
GAM1910 GPR18    5' TAACGCTTGGCGTCGGAGT    47076      GAGAAA
                                TAACGC     GGCGTCGGAGT
                                ||||||     ||||||||||
                                ATTGCG     CCGCAGCCTCA
                                   AA____
GAM1910 GRM6     5' CGCGGGGAGGGACACCGGGGTC 47077     A_  AA   GT   A
                                CGCG  GA  GGC  CGG GTC
                                ||||  ||  |||  ||| |||
                                GCGC  CT  CTG  GCC CAG
                                  CC  CC   TG   C
GAM1910 ZAP128   5' GCGGGGAAGGCCAGAGTC    47078    AGA    GT
                                GCG   AAGGC  CGGAGTC
                                |||   |||||  |||||||
                                CGC   TTCCG  GTCTCAG
                                  CCC    __
GAM1910 LOC153546 5' ACGCCGAGCGGTGTCGGAGT  47079     GA  AA  C
                                ACGC  GA  GG GTCGGAGT
                                ||||  ||  || ||||||||
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                                TGCG  CT  CC CAGCCTCA
                                  G_  CG  A
GAM1910  LOC253386 5'  GCGGGGAAGGCCAGAGTC    47078     AGA    GT
                                GCG   AAGGC  CGGAGTC
                                |||   |||||  |||||||
                                CGC   TTCCG  GTCTCAG
                                  CCC    __
GAM1911  DMRT2     3'  TGAGGACAAGGGATACTGTCT  47082     AAT   __      A
                                TGA   GGGC  GGGATACT TCT
                                |||   ||||  |||||||| |||
                                ACT   CCTG  CCCTATGA AGA
                                  ___   TT      C
GAM1911  ETV3      3'  TATGAATGGAGTTTGGTACTAT 47083       A   CG__  A
              CT                  TATGAA TGGG    GG TACTATCT
                                |||||| ||||    || ||||||||
                                ATACTT ACCT    CC ATGATAGA
                                   _    CAAA  _
GAM1911  SCA1      3'  TGAAACGAAGAAAGTACTAT   47084         C GG _
                                TGAAATGGG G  A TACTAT
                                |||||||| |  | ||||||
                                ACTTTGCTT C  T ATGATA
                                     _ TT C
GAM1911  CFP1      3'  TGAAATGACCAGTACTAT    47085        G   GA
                                TGAAATGG CGG  TACTAT
                                |||||||| |||  ||||||
                                ACTTTACT GTC  ATGATA
                                     G  __
GAM1911  INA       3'  TATGAAATGGGCAGGGATA   47086          _
                                TATGAAATGGGC GGGATA
                                |||||||||||| ||||||
                                ATACTTTACCCG CCCTAT
                                       T
GAM1911  KIAA0984  3'  TATGAGGTGGAAACACTAT   47087      AAT  GC GG
                                TATGA   GG  G  ATACTAT
                                |||||   ||  |  |||||||
                                ATACT   CC  C  TGTGATA
                                   ___  AC TT
GAM1911  PSMD12    3'  ATGAAATGGAATCAAGTGTTAT 47088          __   ATAC
              CT                  ATGAAATGGG  CGGG   TATCT
                                |||||||||  ||||   |||||
                                TACTTTACCT  GTTC   ATAGA
                                     TA   ACA_
GAM1911  LOC143425 3'  TGAAAAGAAAAATACTATCT   47089      TG  CG
                                TGAAA  GG  GGATACTATCT
                                |||||  ||  ||||||||||||
                                ACTTT  TC  TTTATGATAGA
                                   __  TT
GAM1911  LOC149464 5'  TGAAGTGGGTGGGATACT    47090      A   C
                                TGAA TGGG GGGATACT
                                |||| |||| ||||||||
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                                ACTT ACCC CCCTATGA
                                  C    A
GAM1911  LOC151963 3'  TATGAAATAGTAATATACT   47091          GCGGG
                                TATGAAATGG    ATACT
                                ||||||||||    |||||
                                ATACTTTATC    TATGA
                                      ATTA_
GAM1911  LOC203350 3'  GAGATGGGGTCTCACTATCT  47092    A    CGGGA
                                GA ATGGG    TACTATCT
                                || |||||    ||||||||
                                CT TACCC    GTGATAGA
                                 C    CAGA_
GAM1911  LOC257489 3'  TATGAGAATACGAGATATTAT  47093      AATGG      C
                                TATGA    GCGGGATA TAT
                                |||||    |||||||| |||
                                ATACT    TGCTCTAT ATA
                                   CTTA_       A
GAM1912  BCL11B   3'  CATTCCCTCCCCCCTTTT    47096       A  G
                                TATTCC CT TCCCCTTTT
                                |||||| || |||||||||
                                GTAAGG GA GGGGGAAAA
                                   _ G
GAM1912  CEACAM5  5'  TCTGCTGTCCTTCCTCCCTCT  47097    CA     C_   TT
                                TC  CTGTCC  CTT  CTCT
                                ||  ||||||  |||  ||||
                                AG  GACAGG  GGA  GAGA
                                 AC     AA   GG
GAM1912  GATA2    3'  CCGTCCCCTCCTTTTCTCTA   47098          ___
                                CTGTCCCCTT   TTCTCTA
                                ||||||||||   |||||||
                                GGCAGGGGAG   AAGAGAT
                                      GAA
GAM1912  KMO      3'  TATTCCACTTTATTTTTTCTCT 47099          GTCCCC
                                TATTCCACT     TTTTCTCT
                                |||||||||     ||||||||
                                ATAAGGTGA     AAAAGAGA
                                      AATAA_
GAM1912  Nrap     3'  TTCCACTGTCTCCACCCT    47100          C  TTTT
                                TTCCACTGTC CC    CTCT
                                |||||||||| ||    ||||
                                AAGGTGACAG GG    GGGA
                                      A  T___
GAM1912  OAS3     3'  TTCCTGTTCCTTCCTCT     47101      AC   CCC
                                TTCC  TGT   CTTTTCTCT
                                ||||  |||   |||||||||
                                AAGG  ACA   GGAAGGAGA
                                   __   A__
GAM1912  OCA2     3'  TATTCCACTGTGTCTC      47102          CCCCTTT
                                TATTCCACTGT      TCTC
                                ||||||||||       ||||
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                                ATAAGGTGACA      AGAG
                                      C_______
GAM1912 PITX2    3' ATTCAGTGGTTTCCTTTTCTCT 47103     CACT  CC
             A                   ATTC    GT  CCTTTTCTCTA
                                 ||||    ||  ||||||||||
                                 TAAG    CA  GGAAAAGAGAT
                                   TCAC  AA
GAM1912 SCTR     3' TTCCCTGTCCCTTTCT      47104      A      CT
                                 TTCC CTGTCCC  TTTCT
                                 |||| |||||||  |||||
                                 AAGG GACAGGG  AAAGA
                                   _      __
GAM1912 SLC1A4   3' CATTCCCTCTCCTTTTTTCT   47105       A  G   CC
                                 TATTCC CT TCC  TTTTCT
                                 |||||| || |||  ||||||
                                 GTAAGG GA AGG  AAAAGA
                                    _ G   AA
GAM1912 SNCA     3' TTCCATTTTCTCTACCTCTTCT 47106      CTG  C___
                                 TTCCA   TC    CCTTTTCT
                                 |||||   ||    ||||||||
                                 AAGGT   AG    GGAGAAGA
                                    AAA  AGAT
GAM1912 SNCA     3' TTCCATTTTCTCTACCTCTTCT 47106      CTG  C___
                                 TTCCA   TC    CCTTTTCT
                                 |||||   ||    ||||||||
                                 AAGGT   AG    GGAGAAGA
                                    AAA  AGAT
GAM1912 UBE2G2   3' TATTCCATCGTCCCCTGGAAGT 47107        C       TTTC_
             CT                    TATTCCA TGTCCCCT     TCT
                                   |||||||  ||||||||     |||
                                   ATAAGGT GCAGGGGA     AGA
                                      A       CCTTC
GAM1912 XYLB     3' TATGCCACTGTCTTATCTTTT  47108     T       CC__
                                 TAT CCACTGTC    CTTTT
                                 ||| ||||||||    |||||
                                 ATA GGTGACAG    GAAAA
                                   C       AATA
GAM1912 ABCC13   3' TATGCCACTGTCTTTCCT    47109     T       CCC
                                 TAT CCACTGTC   TTTTCT
                                 ||| ||||||||   ||||||
                                 ATA GGTGACAG   AAAGGA
                                   C       ___
GAM1912 AP1GBP1  3' TTCTACTGTTCTCTCT      47110     C     CCCCT
                                 TTC ACTGT     TTTCTCT
                                 ||| |||||     |||||||
                                 AAG TGACA     AGAGAGA
                                   A    ______
GAM1912 BC022889 3' ATTCCACCTTTTTTCTCT    47111         GTCCCC
                                 ATTCCACT      TTTTCTCT
                                 ||||||||      ||||||||
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                                TAAGGTGG     AAAAGAGA
                                   AA____
GAM1912  C20orf177 3'  ATTCCACTGTCTCTC       47112          CCCTTT
                                ATTCCACTGTC     TCTC
                                ||||||||||     ||||
                                TAAGGTGACAG     AGAG
                                      _______
GAM1912  DDX33     3'  ACTTTCCATTCCTTTTCTCTA  47113     G  ___
                                ACT TCC   CCTTTTCTCTA
                                ||| |||   ||||||||||
                                TGA AGG   GGAAAAGAGAT
                                  A   TAA
GAM1912  DKFZp434O0515 5'  CATTCCACTGTGATTTTCT    47114          CCCC
                                TATTCCACTGT    TTTTCT
                                ||||||||||    ||||||
                                GTAAGGTGACA    AAAAGA
                                      CT__
GAM1912  DKFZP761G1913 3'  CCACTGTCTTTCTCT       47115        CCCT
                                CCACTGTC    TTTCTCT
                                ||||||||    |||||||
                                GGTGACAG    AAAGAGA
                                     _____
GAM1912  ERp44     3'  TTCCACTGTCACCTCCCT     47117          C  TTT
                                TTCCACTGTC CC   TCTCT
                                |||||||||| ||   |||||
                                AAGGTGACAG GG   AGGGA
                                      T  ___
GAM1912  ERp44     3'  TATTTCACTCTCCTCTCT     47116      C    G   CCTTT
                                TATT CACT TCC     TCTCT
                                |||| |||| |||     |||||
                                ATAA GTGA AGG     AGAGA
                                  A    G  _____
GAM1912  FKSG28    3'  CTCCGCTGTTCTCTCTCT     47118      A    CCCC
                                TTCC CTGT    TTTTCTCT
                                |||| ||||    ||||||||
                                GAGG GACA    GAGAGAGA
                                  C    A___
GAM1912  FLJ11286  3'  TTCCTCTGTCCCCTAGGCCCTA 47119      A       TTT
                                TTCC CTGTCCCCT   CTCTA
                                |||| |||||||||   |||||
                                AAGG GACAGGGGA   GGGAT
                                  A        TCC
GAM1912  FLJ13111  3'  TTCTTCCATCTTTTTCTCT    47120     CA    CCC
                                TTC  CTGTC   TTTTCTCT
                                |||  |||||   ||||||||
                                AAG  GGTAG   AAAAGAGA
                                  AA    A__
GAM1912  FLJ14011  5'  TTCCACTGTGAATTCTCT     47121          CCCCTT
                                TTCCACTGT     TTCTCT
                                |||||||||     ||||||
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                                AAGGTGACA     AAGAGA
                                     CTT___
GAM1912 FLJ22415 3' CATTCCTAGATCCCTTTTTCTC 47122       ACT    C
             TA                   TATTCC   GTCCC TTTTCTCTA
                                  ||||||   ||||| |||||||||
                                  GTAAGG   TAGGG AAAAGAGAT
                                     ATC    A
GAM1912 GOLGA1   3' TATTCCACTCTTCCTCTT    47123        G_   C
                                  TATTCCACT  TCC CTT
                                  |||||||||  ||| |||
                                  ATAAGGTGA  AGG GAA
                                     GA   A
GAM1912 KIAA1028 3' CATTTCACTGCCTTTCTCT   47124     C      CCCT
                                  TATT CACTGTC    TTTCTCT
                                  |||| |||||||    |||||||
                                  GTAA GTGACGG    AAAGAGA
                                    A     _____
GAM1912 KIAA1999 3' TTCCACTGTCATTATGCTTTT 47125        CC_____
                                  TTCCACTGTC     CTTTT
                                  ||||||||||     |||||
                                  AAGGTGACAG     GAAAA
                                     TAATAC
GAM1912 MGC2306  3' CCGTCCCCTCCTTTTCTCTA  47098         ___
                                  CTGTCCCCTT   TTCTCTA
                                  |||||||||   |||||||
                                  GGCAGGGGAG   AAGAGAT
                                     GAA
GAM1912 PLP1     3' TACTTCACTGTCCTTTATCT  47126     C      CCTTT
                                  TATT CACTGTCC    TCT
                                  |||| ||||||||    |||
                                  ATGA GTGACAGG    AGA
                                    A       AAAT_
GAM1912 PTPRT    3' TATTCACTGTCCTGCTTT    47127      C      C_
                                  TATTC ACTGTCC  CTTT
                                  ||||| |||||||  ||||
                                  ATAAG TGACAGG  GAAA
                                     _      AC
GAM1912 SDC3     3' TTCCACTGTCTTTTTCT     47128         CCC
                                  TTCCACTGTC   TTTTCT
                                  |||||||||   ||||||
                                  AAGGTGACAG   AAAAGA
                                     A__
GAM1912 SDCCAG1  5' TATTCCACTGTTTCTCC     47129          CCCCTT
                                  TATTCCACTGT     TTCTCT
                                  ||||||||||     ||||||
                                  ATAAGGTGACA     AAGAGG
                                                 ______
GAM1912 SURB7    3' TTCTTACTGTCTTCTCC     47130     C_     CCCTT
                                  TTC  ACTGTC    TTCTCT
                                  |||  ||||||    ||||||
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                                AAG  TGACAG    AAGAGG
                                  AA    _____
GAM1912  TBX21    3'  TTCCAGCCCCTTTTCTCT    47131      CT T
                                TTCCA  G CCCCTTTTCTCT
                                |||||  | ||||||||||||
                                AAGGT  C GGGGAAAAGAGA
                                  __ _
GAM1912  TRIM5    5'  TATTCCACTGCTCCTGCCT   47132         _  __
                                TATTCCACTG TCC  CCT
                                |||||||||| |||  |||
                                ATAAGGTGAC AGG  GGA
                                      G   AC
GAM1912  TRIM5    5'  TATTCCACTGCTCCTGCCT   47132         _  __
                                TATTCCACTG TCC  CCT
                                |||||||||| |||  |||
                                ATAAGGTGAC AGG  GGA
                                      G   AC
GAM1912  TRIM5    5'  TATTCCACTGCTCCTGCCT   47132         _  __
                                TATTCCACTG TCC  CCT
                                |||||||||| |||  |||
                                ATAAGGTGAC AGG  GGA
                                      G   AC
GAM1912  UK114    3'  TTCCACTATCTTCTCC      47133          CCCTT
                                TTCCACTGTC    TTCTCT
                                |||||||||    ||||||
                                AAGGTGATAG    AAGAGG
                                  _____
GAM1912  LOC121838 5'  TCCACACATGGCCTTTTCTCT  47134      TGTCC_
                                TCCAC     CCTTTTCTCT
                                |||||     ||||||||||
                                AGGTG     GGAAAAGAGA
                                   TGTACC
GAM1912  LOC122786 3'  TTCCACTGTACCCTACATCT   47135         C    TT_
                                TTCCACTGT CCCT   TCT
                                |||||||| ||||   |||
                                AAGGTGACA GGGA   AGA
                                      T    TGT
GAM1912  LOC124402 3'  TCCCACAATCCTTTTCTCT    47136       TGTCC
                                TTCCAC    CCTTTTCTCT
                                ||||||    ||||||||||
                                AGGGTG    GGAAAAGAGA
                                   TTA__
GAM1912  LOC125228 3'  TATTCCACTTTTTTCT      47137         GTCCCC
                                TATTCCACT     TTTTCT
                                |||||||||     ||||||
                                ATAAGGTGA     AAAAGA
                                      A_____
GAM1912  LOC147689 5'  CACTGTCTGTCTTCTCTA    47138        CCC
                                CACTGTC   TTTTCTCTA
                                |||||||   |||||||||
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                                GTGACAG   AGAAGAGAT
                                   AC_
GAM1912  LOC148530 5'  TTCCCTGTCCCTTCTCT     47139      A      CTT
                                TTCC CTGTCCC   TTCTCT
                                |||| |||||||   ||||||
                                AAGG GACAGGG   AAGAGA
                                  _      ___
GAM1912  LOC150378 5'  CCCCACTTCCCTTTTCTCTA   47140        GTC
                                TTCCACT   CCCTTTTCTCTA
                                |||||||   ||||||||||||
                                GGGGTGA   GGGAAAAGAGAT
                                   A__
GAM1912  LOC150935 3'  TTCTTTGTCCTTCCCCTCTA   47141     CAC     CC  TT
                                TTC   TGTCC  TT  CTCTA
                                |||   |||||  ||  |||||
                                AAG   ACAGG  AG  GAGAT
                                  AA_    A_ GG
GAM1912  LOC153339 3'  ATTCCACCTCCCCCTTTTTTTC 47142        GT       C_
            T                    ATTCCACT  CCCCTTTT  TCT
                                |||||||| ||||||||  |||
                                TAAGGTGG  GGGGAAAA  AGA
                                    AG       AA
GAM1912  LOC153442 5'  TCCGAATGTCTTTTTCTCTA   47143     AC_   CCC
                                TCC   TGTC   TTTTCTCTA
                                |||   ||||   |||||||||
                                AGG   ACAG   AAAAGAGAT
                                  CTT    A__
GAM1912  LOC157681 3'  TTCAACAGCCTTTTCTCTA    47144     C  TGTCC
                                TTC AC     CCTTTTCTCTA
                                ||| ||     ||||||||||
                                AAG TG     GGAAAAGAGAT
                                  T  TC___
GAM1912  LOC158088 3'  TTCCATCTCTTTTCTCT     47145      CTG  CC
                                TTCCA   TC  CTTTTCTCT
                                |||||   ||  |||||||||
                                AAGGT   AG  GAAAAGAGA
                                   ___  A_
GAM1912  LOC202404 5'  TATTCTCGCTGTCCTCCTCTCT 47146       CA_     C
                                TATTC   CTGTCC CTTTTCT
                                |||||   |||||| |||||||
                                ATAAG   GACAGG GGAGAGA
                                   AGC     A
GAM1912  LOC221140 3'  CATTGTTCCCTTTCCATTTCT  47147    C   C      ___
                                CA TGT CCCTTTTC   TCT
                                || ||| ||||||||   |||
                                GT ACA GGGAAAGG   AGA
                                 A  A       TAA
GAM1912  LOC222136 3'  TATCCTGCTGCTTTCTCT    47148      CA    CCCCT
                                TATTC  CTGT    TTTCTCT
                                |||||  ||||    |||||||
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                                ATAGG  GACG    AAAGAGA
                                  AC   _____
GAM1912  LOC253012 5'  TTCCACTGTTTTTCC      47149         CCCC
                                TTCCACTGT   TTTTCT
                                |||||||||   ||||||
                                AAGGTGACA   AAAAGG
                                     ____
GAM1912  LOC51336  5'  TTCAACAGAATTCTTTTCTCTA 47150    C  TGTCCC
                                TTC AC     CTTTTCTCTA
                                ||| ||     ||||||||||
                                AAG TG     GAAAAGAGAT
                                  T  TCTTAA
GAM1912  LOC90155  5'  TATTCCACAGTTTTCTCC    47151        T  CCCCT
                                TATTCCAC GT    TTTCTCT
                                |||||||| ||    |||||||
                                ATAAGGTG CA    AAAGAGG
                                     T _____
GAM1912  LOC92710  3'  TATTCCACTGGCCCAGATCT   47152         T   CTTT
                                TATTCCACTG CCC    TCT
                                |||||||||| |||    |||
                                ATAAGGTGAC GGG    AGA
                                      C   TCT_
GAM1913  FBXL11    3'  TGGCGTCTCTCTTCTCAGTGGC 47155    A      C_  ACCC
                                TG CGTCTCTC  CT    TGGC
                                || ||||||||  ||    ||||
                                AC GCAGAGAG  GA    ACCG
                                 C       AA  GTC_
GAM1913  LFG       3'  TCTGGTGCCTCTCCCGCCCTAT 47157     AC       ____  C
            CCTGGC                  CTG  GTCTCTCCC    TA CCTGGC
                                |||  |||||||||   || ||||||
                                GAC  CGGAGAGGG    AT GGACCG
                                  CA        CGGG  A
GAM1913  LFG       3'  TCTGACGCCTCTCCTG      47156           CTACCC
                                TCTGACGTCTCTCC     TG
                                ||||||||||||||     ||
                                AGACTGCGGAGAGG     AC
                                     _______
GAM1913  NEBL      5'  CTGACGTCTCTGGTGCTCTGGC 47158          CCCTACC
                                CTGACGTCTCT      CTGGC
                                ||||||||||       |||||
                                GACTGCAGAGA      GACCG
                                      CCACGA_
GAM1913  STK24     5'  TCTGCTGGCTCTCTGCCTTGGC 47159     ACGT    CCTA  C
                                TCTG    CTCTC    CC TGGC
                                ||||    |||||    || ||||
                                AGAC    GAGAG    GG ACCG
                                  GACC     AC__  A
GAM1913  FBXO24    3'  CCTGAACATTCTTACCCTGG   47160      _   C   CCC
                                TCTGA CGT TCT   TACCCTGG
                                ||||| ||| |||   ||||||||
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                                GGACT GTA AGA   ATGGGACC
                                  T  _  ___
GAM1913  FBXO24    3'  CCTGAACATTCTTACCCTGG   47160      _  C   CCC
                                TCTGA CGT TCT   TACCCTGG
                                ||||| ||| |||   ||||||||
                                GGACT GTA AGA   ATGGGACC
                                  T  _  ___
GAM1913  FLJ20005  3'  TCTGACGTCCCTCACTGG    47161           CCTACC
                                TCTGACGTCTCTC     CTGG
                                ||||||||||||      ||||
                                AGACTGCAGGGAG     GACC
                                       T_____
GAM1913  KIAA0298  3'  TCTGAGTCCTCCTGCCTTGGC  47162      C   T    CTA  C
                                TCTGA GTC CTCC   CC TGGC
                                ||||| ||| ||||   || ||||
                                AGACT CAG GAGG   GG ACCG
                                  _  _    AC_  A
GAM1913  KIAA0493  5'  TCTGGGGTCTCTCCCTCTGGC  47163     AC        ACC
                                TCTG  GTCTCTCCCT   CTGGC
                                ||||  ||||||||||   |||||
                                AGAC  CAGAGAGGGA   GACCG
                                  CC        ___
GAM1913  KIAA1950  3'  CGTCTCCCCTCTTTATTCTGGC 47164         _  ACC__
                                CGTCTCTCC CT     CTGGC
                                |||||||| ||     |||||
                                GCAGAGGGG GA     GACCG
                                     A  AATAA
GAM1913  PSTPIP2   3'  TCTGACATTTAAACCCTGG   47165        CTCTCCCT
                                TCTGACGT       ACCCTGG
                                ||||||||       |||||||
                                AGACTGTA       TGGGACC
                                    AATT____
GAM1913  LOC147160 5'  TCTGGCTCTCCACCCTGG    47166      AC T     CT
                                TCTG  G CTCTCC  ACCCTGG
                                ||||  | ||||||  |||||||
                                AGAC  C GAGAGG  TGGGACC
                                  __ _    __
GAM1913  LOC161877 5'  TCTGAAGTCTCCCCCTCTGGC  47167      C         ACC
                                TCTGA GTCTCTCCCT   CTGGC
                                ||||| ||||||||||   |||||
                                AGACT CAGAGGGGGA   GACCG
                                  T        ___
GAM1913  LOC202301 5'  TCTGGCGTTCTCTCCCTA    47168      A  _
                                TCTG CGT CTCTCCCTA
                                |||| ||| |||||||||
                                AGAC GCA GAGAGGGAT
                                  C   A
GAM1913  LOC255565 3'  TCTGACATTTCATCCTGG    47169        C  TCCCTAC
                                TCTGACGT TC      CCTGG
                                |||||||| ||      |||||
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                                AGACTGTA AG      GGACC
                                    A  TA_____
GAM1914  COL19A1   3'  TTTATAAGCCAAATATCAAAT  47172       TTAA
                                TTTATA   GAATATCAAAT
                                ||||||   ||||||||||
                                AAATAT   TTTATAGTTTA
                                   TCGG
GAM1914  GRAF      3'  TAACTTAAAGAATATCAAA   47173       TATT
                                TAATTTA   AAGAATATCAAA
                                |||||||   ||||||||||
                                ATTGAAT   TTCTTATAGTTT
                                    ____
GAM1914  KIAA1718  3'  AATTTATGTTAAGGATATCAAA 47174       A    A
              T                  AATTTAT TTAAG ATATCAAAT
                                 ||||||| ||||| |||||||||
                                 TTAAATA AATTC TATAGTTTA
                                    C    C
GAM1914  ZNF33A    3'  TTACACTGAATATCAAAT    47175       AA
                                TTATATT  GAATATCAAAT
                                |||||||  ||||||||||
                                AATGTGA  CTTATAGTTTA
                                    __
GAM1915  TMSB4Y    5'  GTGGAATGTTCCGGAATAAA  47178     AC  _
                                GTG  GT TTCCGGAATAAA
                                |||  || ||||||||||||
                                CAC  TA AAGGCCTTATTT
                                  CT  C
GAM1915  CSNK1G1   3'  TATGTGACTTTTGTCCAGAA  47179       GTT__
                                TATGTGAC    TCCGGAA
                                ||||||||    |||||||
                                ATACACTG    AGGTCTT
                                     AAAAC
GAM1915  DKFZp547A023 3'  CATGTTCATCTGGAATAAAAA  47180      GA    CC
                                TATGT  CGTTT  GGAATAAAAA
                                |||||  |||||  ||||||||||
                                GTACA  GTAGA  CCTTATTTTT
                                   A_    __
GAM1915  FLJ20635  3'  TATGTGACGGTTTCGCAATCAG 47181        _   _____
              A                  TATGTGACG TTTC    CGGA
                                 ||||||||| ||||    ||||
                                 ATACACTGC AAAG    GTCT
                                     C   CGTTA
GAM1915  KLHL6     3'  TATGTGTGTTTCCCGAA     47182       AC     G
                                TATGTG  GTTTCC GAA
                                ||||||  |||||| |||
                                ATACAC  CAAAGG CTT
                                   A_     G
GAM1915  SLC2A13   3'  TATGTGACATTTCCCTTAGGAA 47183           ____
                                TATGTGACGTTTCC   GGAA
                                ||||||||||||||   ||||
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                                ATACACTGTAAAGG   CCTT
                                      GAAT
GAM1915 UGT2B10  3' TATGTGAAGATTGGAATAAAAA 47184       CGTTTCC
                                TATGTGA     GGAATAAAAA
                                |||||||     ||||||||||
                                ATACACT     CCTTATTTTT
                                    TCTAA__
GAM1915 LOC150271 3' TATGTGACTGTTTTTGGA    47185        _   CC
                                TATGTGAC GTTT  GGA
                                |||||||| ||||  |||
                                ATACACTG CAAA  CCT
                                     A   AA
GAM1916 BCAT2    3' TATCCTTGACCGCACGAC    47188      C_  ACG
                                TATCT  GAC   CGCACGAC
                                |||||  |||   ||||||||
                                ATAGG  CTG   GCGTGCTG
                                   AA  ___
GAM1916 LOC150299 3' ATCTCGACTCACTGCGAC    47189        A   GCA
                                ATCTCGAC CGC   CGAC
                                |||||||| |||   ||||
                                TAGAGCTG GTG   GCTG
                                     A   AC_
GAM1917 CRHR1    3' GCTAGTGGTCCTGCCCCA    47192      A  C  AAA
                                GCTA TG GT   CCTGCCCCA
                                |||| || ||   |||||||||
                                CGAT AC CA   GGACGGGGT
                                  C  _  ___
GAM1917 DDEF2    3' TGCTAATGTGTAAATTTCC    47193        C    CCTG
                                TGCTAATG GTAAA    CC
                                |||||||| |||||    ||
                                ACGATTAC CATTT    GG
                                     A    AAA_
GAM1917 HK1      5' TCGCTGGCAGATCTGCCCC    47194      AAT   TAAAC
                                TTGCT   GCG    CTGCCCC
                                |||||   |||    |||||||
                                AGCGA   CGT    GACGGGG
                                   C__   CTA__
GAM1917 RFP      3' TTGCTTGAAGTGATCTGCCCCA 47195      AA  CGTAAAC
                                TTGCT  TG      CTGCCCCA
                                |||||  ||      ||||||||
                                AACGA  AC      GACGGGGT
                                   __  TTCACTA
GAM1917 C20orf26 3' TTGTAAAGCGAGCCTGCCCCA  47196    C   T   TAAA
                                TTG TAA GCG    CCTGCCCCA
                                ||| ||| |||    |||||||||
                                AAC ATT CGC    GGACGGGGT
                                  _   T   TC__
GAM1917 C20orf39  3' TTGCTAATGCGGTGGCACTCTG 47197          TAA__  _
                                TTGCTAATGCG     AC CTG
                                ||||||||||     || |||
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                                AACGATTACGC    TG GAC
                                      CACCG  A
GAM1917  DKFZP434J193 3'  CTAGTGGCACCCTGCCCCA   47198    A  C   AA
                                CTA TG GTA  CCTGCCCCA
                                ||| || |||  |||||||||
                                GAT AC CGT  GGACGGGGT
                                  C  _   G_
GAM1917  FLJ22644  3'  TTGCAGCACACAACCTGCCC   47199     TAAT   TA_
                                TTGC   GCG   AACCTGCCC
                                ||||   |||   |||||||||
                                AACG   CGT   TTGGACGGG
                                  T___   GTG
GAM1917  NCOA2    3'  TTGCTAATGTTAACAGCCC   47200        CGTA   CT
                                TTGCTAATG   AAC  GCCC
                                |||||||||   |||  ||||
                                AACGATTAC   TTG  CGGG
                                      AA__   T_
GAM1917  PFTK1    3'  CTGCAGCGAGGCCTGCCCCA  47201     TAAT   TAAA
                                TTGC   GCG   CCTGCCCCA
                                ||||   |||   |||||||||
                                GACG   CGC   GGACGGGGT
                                  T___   TCC_
GAM1917  PRO0386  5'  TTGTAAAGCTAACCTGCCTCA 47202    C   T  GTA      C
                                TTG TAA GC   AACCTGCC CA
                                ||| ||| ||   |||||||| ||
                                AAC ATT CG   TTGGACGG GT
                                  _   T  A__       A
GAM1917  LOC200853 3'  TTACTAACAACCTGCC     47203        GCGTA
                                TTGCTAAT    AACCTGCC
                                ||||||||    ||||||||
                                AATGATTG    TTGGACGG
                                      _____
GAM1917  LOC221399 5'  TTGCTAATGCATCTG       47204          AAAC
                                TTGCTAATGCGT    CTG
                                ||||||||||||   |||
                                AACGATTACGTA    GAC
                                      ____
GAM1917  LOC92606  3'  TTGTTAATGCATATACCTCC   47205    C       A   G
                                TTG TAATGCGTA ACCT CC
                                ||| ||||||||| |||| ||
                                AAC ATTACGTAT TGGA GG
                                  A       A   _
GAM1918  ITGA6    3'  GATGGACGTCTGCGCAGC    47208        CG   _
                                GATGGACG  TTGT CAGC
                                ||||||||  |||| ||||
                                CTACCTGC  GACG GTCG
                                     A_   C
GAM1918  MSX2     3'  TCGTGTGGCCCTGTCAGC    47209     A  GAC  G
                                TCG TG   GC TTGTCAGC
                                ||| ||   || ||||||||
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                                AGC AC   CG GACAGTCG
                                  _ AC_  G
GAM1918 FLJ10925 5' CATCTGTGGACACAATC     47210     GA      TT
                                CATC  TGGACGCG  GTC
                                ||||  ||||||||  |||
                                GTAG  ACCTGTGT  TAG
                                  AC       __
GAM1918 FLJ20542 3' CATCGGTCCTGGGTTGTCAGC 47211      A___   ACGC
                                CATCG   TGG   GTTGTCAGC
                                |||||   |||   |||||||||
                                GTAGC   ACC   CAACAGTCG
                                  CAGG  ____
GAM1918 FLJ23056 3' ATGGGCAGTGTGTTGTCAGC  47212     A  C___
                                ATGG CG   GTTGTCAGC
                                |||| ||   |||||||||
                                TACC GT   CAACAGTCG
                                  C  CACA
GAM1918 HTCD37   3' CATCGATGAATGTTCAG     47213        CGCGT  _
                                CATCGATGGA    TGT CAG
                                ||||||||||    ||| |||
                                GTAGCTACTT    ACA GTC
                                      _____  A
GAM1918 KIAA0265 3' ATGGTCACTGGTTGTCAGC   47214     A  __
                                ATGG CGC  GTTGTCAGC
                                |||| |||  |||||||||
                                TACC GTG  CAACAGTCG
                                  A  AC
GAM1918 KIAA1719 5' CATCGATGGACAGGATGT    47215         CGT
                                CATCGATGGACG  TGT
                                ||||||||||||  |||
                                GTAGCTACCTGT  ACA
                                      CCT
GAM1918 LRRFIP2  3' TCAATGGACAAAAGTCAG    47216        CGTT
                                TCGATGGACG   GTCAG
                                ||||||||||   |||||
                                AGTTACCTGT   CAGTC
                                     TTT_
GAM1918 LRRFIP2  3' TCAATGGACAAAAGTCAG    47216        CGTT
                                TCGATGGACG   GTCAG
                                ||||||||||   |||||
                                AGTTACCTGT   CAGTC
                                     TTT_
GAM1918 MDS006   3' CATCATGGGTGTGACCAGC   47217     G   ACGC  TG
                                CATC ATGG   GT  TCAGC
                                |||| ||||   ||  |||||
                                GTAG TACC   CA  GGTCG
                                  _   CA__  CT
GAM1918 PHYHIP   3' GATGCACGTCGCAAGC      47218     GA      C
                                GATG  CGCGTTGT AGC
                                ||||  |||||||| |||
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                                CTAC  GTGCAGCG TCG
                                  __      T
GAM1918  LOC152485 3'  TCGATGAGCTTGTTGGC     47219       AC  G   CA
                                TCGATGG  GC TTGT  GC
                                |||||||  || ||||  ||
                                AGCTACT  CG AACA  CG
                                   __ _   AC
GAM1918  LOC157278 3'  CATCGATGGGAGTTTTGCTTAG 47220        ACGCG   C_
           C                     CATCGATGG    TTGT  AGC
                                |||||||||    ||||  |||
                                GTAGCTACC    AACG  TCG
                                     CTCAA   AA
GAM1918  LOC170174 5'  ATCGCTTCCAGTTGTCAGC   47221     ATGGA  C
                                ATCG    CG GTTGTCAGC
                                ||||    || |||||||||
                                TAGC    GT CAACAGTCG
                                  GAAG_ _
GAM1918  LOC197285 3'  GATGGACATGTTCAGC      47222       C  TG
                                GATGGACG GT  TCAGC
                                |||||||| ||  |||||
                                CTACCTGT CA  AGTCG
                                    A __
GAM1918  LOC203232 3'  TCGGGGAACCAGTCAGC     47223     AT   G  TT
                                TCG  GGAC CG  GTCAGC
                                |||  |||| ||  ||||||
                                AGC  CTTG GT  CAGTCG
                                  CC   _ __
GAM1918  LOC254173 3'  TCATGGATGCGCTGCCAGC   47224    G    C
                                TC ATGGA GCGTTGTCAGC
                                || ||||| ||||||||||
                                AG TACCT CGCGACGGTCG
                                 _    A
GAM1918  LOC255104 3'  GATGGTGCCTGTCAGC      47225      AC  G
                                GATGG  GC TTGTCAGC
                                |||||  || ||||||||
                                CTACC  CG GACAGTCG
                                  A_  _
GAM1919  ADD2     5'  CAGCGGCTCCGCGGCG      47228       T   TT
                                CAGCGGCT CTGT  GCG
                                |||||||| ||||  |||
                                GTCGCCGA GGCG  CGC
                                    _   C_
GAM1919  ADD2     5'  CAGCGGCTCCGCGGCG      47228       T   TT
                                CAGCGGCT CTGT  GCG
                                |||||||| ||||  |||
                                GTCGCCGA GGCG  CGC
                                    _   C_
GAM1919  ADD2     5'  CAGCGGCTCCGCGGCG      47228       T   TT
                                CAGCGGCT CTGT  GCG
                                |||||||| ||||  |||
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                                GTCGCCGA GGCG  CGC
                                     _    C_
GAM1919  ADD2     5'  CAGCGGCTCCGCGGCG      47228        T    TT
                                CAGCGGCT CTGT  GCG
                                |||||||| ||||  |||
                                GTCGCCGA GGCG  CGC
                                     _    C_
GAM1919  ADD2     5'  CAGCGGCTCCGCGGCG      47228        T    TT
                                CAGCGGCT CTGT  GCG
                                |||||||| ||||  |||
                                GTCGCCGA GGCG  CGC
                                     _    C_
GAM1919  ADD2     5'  CAGCGGCTCCGCGGCG      47228        T    TT
                                CAGCGGCT CTGT  GCG
                                |||||||| ||||  |||
                                GTCGCCGA GGCG  CGC
                                     _    C_
GAM1919  ADD2     5'  CAGCGGCTCCGCGGCG      47228        T    TT
                                CAGCGGCT CTGT  GCG
                                |||||||| ||||  |||
                                GTCGCCGA GGCG  CGC
                                     _    C_
GAM1919  APLP2    3'  CAGCGGCTGCTGCTTGGCA   47229         T      C
                                CAGCGGCT CTGTTTG GCA
                                |||||||| ||||||| |||
                                GTCGCCGA GACGAAC CGT
                                     C      _
GAM1919  CAPN10   3'  CAGCGGCTCCTGCAGCA     47230           TT
                                CAGCGGCTTCTGT  GCG
                                ||||||||||||  |||
                                GTCGCCGAGGACG  CGT
                                       T_
GAM1919  CAPN10   3'  CAGCGGCTCCTGCAGCA     47230           TT
                                CAGCGGCTTCTGT  GCG
                                ||||||||||||  |||
                                GTCGCCGAGGACG  CGT
                                       T_
GAM1919  FACL3    5'  CAGCAGCTTCTGAGGGTGGCAA 47231           TT__  C
                                CAGCGGCTTCTG    TG GCAA
                                ||||||||||||    || ||||
                                GTCGTCGAAGAC    AC CGTT
                                       TCCC  _
GAM1919  GGA3     3'  CAGTGGCTTCAGTGAATGCCA  47232     C     __ TT   G
                                CAG GGCTTC  TG  TGC CA
                                ||| ||||||  ||  ||| ||
                                GTC CCGAAG  AC  ACG GT
                                  A     TC  TT  _
GAM1919  GGA3     3'  CAGTGGCTTCAGTGAATGCCA  47232     C     __ TT   G
                                CAG GGCTTC  TG  TGC CA
                                ||| ||||||  ||  ||| ||
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                                GTC CCGAAG  AC  ACG GT
                                  A     TC  TT  _
GAM1919  GLI2     3'  AGCGGCCATTGCGCAACA    47233        TCTGT
                                AGCGGCT    TTGCGCAACA
                                |||||||    ||||||||||
                                TCGCCGG    AACGCGTTGT
                                   T____
GAM1919  GMPR     5'  CAGCGGCTCCTGGCTGCGGC   47234           T   _
                                CAGCGGCTTCTG TTGCG C
                                |||||||||||| ||||| |
                                GTCGCCGAGGAC GACGC G
                                       C    C
GAM1919  NEUROD2  5'  CAGCGGCTCCTCAAGGCGGC   47235          GTTT  _
                                CAGCGGCTTCT   GCG C
                                ||||||||||    ||| |
                                GTCGCCGAGGA   CGC G
                                      GTTC   C
GAM1919  PRKY     3'  CAGTGATTTCCATTGCGCAACA 47236     C GC      T
            A                    CAG G  TTCTGTT GCGCAACAA
                                ||| |  ||||||| |||||||||
                                GTC C  AAGGTAA CGCGTTGTT
                                  A TA      _
GAM1919  RFX2     5'  CAGCGGCTCCCGCGGCG     47237           TT
                                CAGCGGCTTCTGT  GCG
                                ||||||||||||  |||
                                GTCGCCGAGGGCG  CGC
                                       C_
GAM1919  SERPINB5 3'  GCGGCTTCCTGATCCAGCAA   47238         __  TT C
                                GCGGCTTCT  GT  G GCAA
                                |||||||||  ||  | ||||
                                CGCCGAAGG  TA  T CGTT
                                     AC  GG _
GAM1919  SLC25A11 3'  CAGTGGCTATAGGCGCAGCA   47239     C    TCT  TT    A
                                CAG GGCT   GT  GCGCA CA
                                ||| ||||   ||  ||||| ||
                                GTC CCGA   TA  CGCGT GT
                                  A   ___  TC    C
GAM1919  TCF7     3'  CAGAGGCTTCTGGCTGGCAA   47240     C       T   C
                                CAG GGCTTCTG TTG GCAA
                                ||| |||||||| ||| ||||
                                GTC CCGAAGAC GAC CGTT
                                  T       C   _
GAM1919  TNS      3'  GGCTCTGTTTGGTTTGACAA   47241      T      CGCA_
                                GGCT CTGTTTG    ACAA
                                |||| |||||||    ||||
                                CCGA GACAAAC    TGTT
                                  _      CAAAC
GAM1919  VTN      5'  CAGCGGCTGCTGCAGCA     47242         T   TT
                                CAGCGGCT CTGT  GCG
                                |||||||| ||||  |||
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                                GTCGCCGA GACG  CGT
                                    C    T_
GAM1919 APPD     3'  CAGGGTTTCTGTTCTTGCAA  47243     C  C       GC
                                CAG GG TTCTGTTT  GCAA
                                ||| || ||||||||  ||||
                                GTC CC AAGACAAG  CGTT
                                  _ A       AA
GAM1919 C6orf26  3'  GCGGCTTGTCCCCAGCGGCA  47244       TC    ___  _
                                GCGGCT  TGTTT   GCG CA
                                ||||||  |||||   ||| ||
                                CGCCGA  ACAGG   CGC GT
                                   __    GGT   C
GAM1919 DKFZp586I021 3'  CAGCAGCTTGGGTGTGACG   47245         CT  T  _
                                CAGCGGCTT  GT TG CG
                                |||||||||  || || ||
                                GTCGTCGAA  CA AC GC
                                     CC  C  T
GAM1919 DKFZP586M1120 5'  GCGGTTCCACGCAGCA     47246     C   GTTT    A
                                GCGG TTCT   GCGCA CA
                                |||| ||||   ||||| ||
                                CGCC AAGG   TGCGT GT
                                  _   ____    C
GAM1919 FLJ10891  3'  CAGTGGATTTGCACAA     47247     C  CTTCT
                                CAG GG    GTTTGCGCAA
                                ||| ||    ||||||||||
                                GTC CC    TAAACGTGTT
                                  A _____
GAM1919 HSPC213   3'  AGCGGCCTTCCAGTGTAGCA   47248       _   _  T  C
                                AGCGGC TTCT GT TG GCA
                                |||||| |||| || || |||
                                TCGCCG AAGG CA AT CGT
                                   G   T  C  _
GAM1919 jdp2     3'  GGCTATCTGTTCATAACAA   47249     _     GC_
                                GGCT TCTGTTT   GCAA
                                |||| |||||||   ||||
                                CCGA AGACAAG   TGTT
                                  T      TAT
GAM1919 KIAA1045  3'  CAGGGCTTCTCCTTGTGGCAA  47250     C     G   C_
                                CAG GGCTTCT TTTG  GCAA
                                ||| |||||||  ||||  ||||
                                GTC CCGAAGA GAAC  CGTT
                                  _     G   AC
GAM1919 KIAA1266  3'  CAGCGGCTCTGAGCTTGCAGCA 47251         CT_    _
                                CAGCGGCTT   GTTTGC GCA
                                |||||||||   |||||| |||
                                GTCGCCGAG   CGAACG CGT
                                     ACT     T
GAM1919 KIAA1580  5'  ACGGCTCCCTGCGCGGCA    47252         GTT    AA
                                GCGGCTTCT   TGCGC  CA
                                |||||||||   |||||  ||
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                                TGCCGAGGG  ACGCG  GT
                                    ___    CC
GAM1919 KIAA1643 3' CAGCGGCCTCATGAGACGCA  47253        _ TTT
                                CAGCGGCTTC TG  GCGCA
                                |||||||||| ||  |||||
                                GTCGCCGGAG AC  TGCGT
                                     T  TC_
GAM1919 KIAA1872 3' CAGCGGCTCTTCTTGTGCAA  47254       T G  C
                                CAGCGGCT CT TTTG GCAA
                                |||||||| || |||| ||||
                                GTCGCCGA GA GAAC CGTT
                                    _ A  A
GAM1919 MYO3B    3' CAGTGCTTTCTTACGCAA    47255    CG  CTG
                                CAG  GCTT  TTTGCGCAA
                                |||  ||||  |||||||||
                                GTC  CGAA  GAATGCGTT
                                  A_  A__
GAM1919 PPIE     3' CAGTGGCTTTTTTGCACA    47256    C   CTG
                                CAG GGCTT  TTTGCGCA
                                ||| |||||  ||||||||
                                GTC CCGAA  AAACGTGT
                                  A   A__
GAM1919 RNASE7   3' CAGTGACTTCTTTCTTGCGCAA 47257    C     G_
           CA                   CAG GGCTTCT  TTTGCGCAACA
                                ||| |||||||  ||||||||||
                                GTC CTGAAGA  GAACGCGTTGT
                                  A      AA
GAM1919 RYD5     3' ACGGCTGCTTGTGTGGCA    47258      T _ T C
                                GCGGCT CT GT TG GCA
                                |||||| || || || |||
                                TGCCGA GA CA AC CGT
                                   C A C _
GAM1919 SMARCF1  3' CAGCGTTTTCTGTTTCCA    47259     GC     G
                                CAGCG  TTCTGTTT CG
                                |||||  |||||||| ||
                                GTCGC  AAGACAAA GT
                                   AA      G
GAM1919 SMARCF1  3' CAGCGTTTTCTGTTTCCA    47259     GC     G
                                CAGCG  TTCTGTTT CG
                                |||||  |||||||| ||
                                GTCGC  AAGACAAA GT
                                   AA      G
GAM1919 SMARCF1  3' CAGCGTTTTCTGTTTCCA    47259     GC     G
                                CAGCG  TTCTGTTT CG
                                |||||  |||||||| ||
                                GTCGC  AAGACAAA GT
                                   AA      G
GAM1919 TCF6L1   3' GGCTTCTACAATTTGTAACAA  47260       ___   CGC
                                GGCTTCT  GTTTG  AACAA
                                |||||||  |||||  |||||
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                                CCGAAGA  TAAAC  TTGTT
                                   TGT    A__
GAM1919  LOC135932 5'  CAGCGCTCTGTGTAGCAA   47261     G  T   T  C
                                CAGCG CT CTGT TG GCAA
                                ||||| || |||| || ||||
                                GTCGC GA GACA AT CGTT
                                  _ _   C  _
GAM1919  LOC145820 3'  AGCAGCTTTATTTGTAACA   47262       C    CGC
                                AGCGGCTT TGTTTG  AACA
                                |||||||| ||||||  ||||
                                TCGTCGAA ATAAAC  TTGT
                                   _    A__
GAM1919  LOC146050 3'  CAGTGGCTTCTGCTTATTGCA 47263    C        C_
                                CAG GGCTTCTGTTTG GCA
                                ||| |||||||||||| |||
                                GTC CCGAAGACGAAT CGT
                                  A          AA
GAM1919  LOC150935 3'  CAGCAGGTTTCTGCAGCA   47264    _ C    TT
                                CAGC GG TTCTGT GCG
                                |||| || |||||| |||
                                GTCG CC AAGACG CGT
                                  T A    T_
GAM1919  LOC152048 3'  GCGGTCTCCGCACGCAAC   47265     CT   TT
                                GCGG TCTGT GCGCAAC
                                ||||  |||||  |||||||
                                CGCC AGGCG TGCGTTG
                                  AG   __
GAM1919  LOC154760 5'  CAGCGCTCTGTGTAGCAA   47261     G  T   T  C
                                CAGCG CT CTGT TG GCAA
                                ||||| || |||| || ||||
                                GTCGC GA GACA AT CGTT
                                  _ _   C  _
GAM1919  LOC163700 5'  AGCGGCTTTTGTTGGACG   47266       C   T_
                                AGCGGCTT TGTT GCG
                                |||||||| ||||  |||
                                TCGCCGAA ACAA TGC
                                   A   CC
GAM1919  LOC200058 3'  CAGCGGCCTTGGTGCA     47267        C  TT
                                CAGCGGCTT TG TGCG
                                ||||||||| ||  ||||
                                GTCGCCGGA AC ACGT
                                   _ C_
GAM1919  LOC201627 3'  AGTGGCTTCTGGCCAGGTGCG 47268   C      _ ___
                                AG GGCTTCTG TT  TGCG
                                || |||||||| ||  ||||
                                TC CCGAAGAC GG  ACGC
                                 A      C  TCC
GAM1919  LOC203069 5'  CAGCTGCTTCTGCAGCA    47269     G      TT
                                CAGC GCTTCTGT GCG
                                |||| ||||||||  |||
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                                GTCG CGAAGACG  CGT
                                  A       T_
GAM1919  LOC203954 5'  CAGCGGCTTCCGTCCTGCAGCA 47270            _  _
              A                   CAGCGGCTTCTGTT TGC GCAA
                                  |||||||||||||| ||| ||||
                                  GTCGCCGAAGGCAG ACG CGTT
                                        G   T
GAM1919  LOC221688 3'  CAGGGTTTCTGTTTTTCAA   47271     C  C      GCG
                                  CAG GG TTCTGTTT   CAA
                                  ||| || ||||||||   |||
                                  GTC CC AAGACAAA   GTT
                                    _ A       AA_
GAM1919  LOC253219 5'  CAGCGGCTGTTCGGCA      47272        TCT    C
                                  CAGCGGCT   GTTTG GCA
                                  ||||||||   ||||| |||
                                  GTCGCCGA   CAAGC CGT
                                     ____    _
GAM1919  LOC253219 3'  CAGCGGCTGTTCGGCA      47272        TCT    C
                                  CAGCGGCT   GTTTG GCA
                                  ||||||||   ||||| |||
                                  GTCGCCGA   CAAGC CGT
                                     ____    _
GAM1919  LOC253827 3'  CAGGGCTTCTGTTTAAGCAA   47273     C         C
                                  CAG GGCTTCTGTTTG GCAA
                                  ||| |||||||||||| ||||
                                  GTC CCGAAGACAAAT CGTT
                                    _         T
GAM1919  LOC92078  5'  CAGGGCTTCTGTGGTGCGCAAC 47274     C       T_
              A                   CAG GGCTTCTGT  TGCGCAACA
                                  ||| |||||||||  |||||||||
                                  GTC CCGAAGACA  ACGCGTTGT
                                    _       CC
GAM1920  ABCD1    3'  GGGGTGGTGCCCGGCCCGAGG  47277    A   G   GA
                                  GG GTGG GTC  CGGCCCGAGG
                                  || |||| |||  ||||||||||
                                  CC CACC CGG  GCCGGGCTCC
                                   C   A  __
GAM1920  ACP1     5'  GGGTGGGGTCACCTGGAGG   47278    A      GACG   C_
                                  GG GTGGGGTC    GCC  GAGG
                                  || ||||||||    |||  ||||
                                  CC CACCCCAG    TGG  CTCC
                                    _       _____  AC
GAM1920  ACP1     5'  GGGTGGGGTCACCTGGAGG   47278    A      GACG   C_
                                  GG GTGGGGTC    GCC  GAGG
                                  || ||||||||    |||  ||||
                                  CC CACCCCAG    TGG  CTCC
                                    _       _____  AC
GAM1920  ATRN     3'  GGAGTGGGGTTAGTGTTGGGGA 47279          CGAC___  CCCGA
                                  GGAGTGGGGT      GG    GGA
                                  ||||||||||      ||    |||
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                                CCTCACCCCA      CC    CCT
                                     ATCACAA  _____
GAM1920  CELL    3'  GGAGTGGGGTGGCAAAGG   47280         CGAC  CC
                                GGAGTGGGGT   GGC  GAGG
                                ||||||||||   |||  ||||
                                CCTCACCCCA   CCG  TTCC
                                     _____  T_
GAM1920  CHST1   5'  GGAGTAGGGTCGCCGGGG   47281          ACGGC  A
                                GGAGTGGGGTCG    CCG GG
                                ||||||||||||    ||| ||
                                CCTCATCCCAGC    GGC CC
                                      _____  C
GAM1920  CHST1   3'  GGAGTGGGGTGAGCTGGGG   47282         C  CG  CCGA
                                GGAGTGGGGT GA  GC   GG
                                |||||||||| ||  ||   ||
                                CCTCACCCCA CT  CG   CC
                                     _ __  ACC_
GAM1920  CXCL16  5'  GAGGACGACGGCCCGAGGA   47283     T
                                GGGG CGACGGCCCGAGGA
                                |||| ||||||||||||||
                                CTCC GCTGCCGGGCTCCT
                                  T
GAM1920  ENIGMA  3'  GGAGTGGGGTGGGAG      47284         CGAC  CCC
                                GGAGTGGGGT   GG   GAG
                                ||||||||||   ||   |||
                                CCTCACCCCA   CC   CTC
                                     ____  ___
GAM1920  GRN     3'  GAGTGGGGTCCCGAG      47285         CGACGG
                                GAGTGGGGT    CCCGAG
                                |||||||||    ||||||
                                CTCACCCCA    GGGCTC
                                     _______
GAM1920  HYOU1   3'  GGAGTGGGGCTGGGGAGG   47286         CGAC  CCC
                                GGAGTGGGGT   GG   GAGG
                                ||||||||||   ||   ||||
                                CCTCACCCCG   CC   CTCC
                                     A___  C__
GAM1920  KCNC3   3'  GGGTGGGGTCTGCAAGG    47287    A      GACGGCC
                                GG GTGGGGTC      CGAGG
                                || ||||||||      |||||
                                CC CACCCCAG      GTTCC
                                  _       AC_____
GAM1920  LASS1   3'  GGGTGGGGCCGGGTCCACGGGG 47288    A       AC  _  _  A
                                GG GTGGGGTCG  GG CC CG GG
                                || |||||||||  || || || ||
                                CC CACCCCGGC  CC GG GC CC
                                  _       __  A  T  C
GAM1920  MADH7   5'  GCGGCGGCGGCCCGAG      47289      _  TCGA
                                GTGG GG   CGGCCCGAG
                                ||||  ||   |||||||||
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                                CGCC CC   GCCGGGCTC
                                  G ____
GAM1920 MEIS2   3' GGTGTGGGGTCATCTGGGGA 47290   A      AC_ CCCGA
                                GG GTGGGGTCG  GG   GGA
                                || |||||||||  ||   |||
                                CC CACCCCAGT  CC   CCT
                                 A       AGA _____
GAM1920 MFI2    5' GGGCTGGGTCCGGGTCCGAGGA 47291   A G   GA  C_
                                GG GT GGGTC  CGG  CCGAGGA
                                || || |||||  |||  |||||||
                                CC CG CCCAG  GCC  GGCTCCT
                                 _ A    __  CA
GAM1920 MFI2    5' GGGCTGGGTCCGGGTCCGAGGA 47291   A G   GA  C_
                                GG GT GGGTC  CGG  CCGAGGA
                                || || |||||  |||  |||||||
                                CC CG CCCAG  GCC  GGCTCCT
                                 _ A    __  CA
GAM1920 MSF     3' GGGTGGTGGGAGGGCCTGGGG 47292   A  _ TC  C   CGA
                                GG GTGG GG  GA GGCC  GG
                                || |||| ||  || ||||  ||
                                CC CACC CC  CT CCGG  CC
                                 _   A __  C   ACC
GAM1920 NESH    5' GGGATGGGGTCGGAGACTGGGG 47293   AG      AC  CCGA
          A                      GG  TGGGGTCG  GGC   GGA
                                ||  ||||||||  |||   |||
                                CC  ACCCCAGC  CTG   CCT
                                 CT      CT  ACC_
GAM1920 NORE1   3' GTGGGGCACAGCCTGGGG   47294      CG    CGA
                                GTGGGGT  ACGGCC  GG
                                |||||||  ||||||  ||
                                CACCCCG  TGTCGG  CC
                                    __    ACC
GAM1920 NUCB1   3' GGAGTGGGGTCAGCTCTGGGA 47295        GAC  CCGA
                                GGAGTGGGGTC  GGC   GGA
                                ||||||||||  |||   |||
                                CCTCACCCCAG  TCG   CCT
                                     ___  AGAC
GAM1920 OPHN1   3' GTGGGGTCGGGGGAGG     47296       AC  CCC
                                GTGGGGTCG  GG  GAGG
                                |||||||||  ||  ||||
                                CACCCCAGC  CC  CTCC
                                    C_ ___
GAM1920 PAX2    3' GGGTGGGGTCAGACGGGG   47297   A     _   CCCGA
                                GG GTGGGGTC GACGG   GG
                                || |||||||| |||||   ||
                                CC CACCCCAG CTGCC   CC
                                 _      T   _____
GAM1920 PCDHGA1 3' GGAGTGGGGTGGGGAG     47298        CGAC  CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
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                              CCTCACCCCA  CC  CTC
                                   _____ C__
GAM1920 PCDHGA10 3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                              GGAGTGGGGT  GG  GAG
                              ||||||||||  ||  |||
                              CCTCACCCCA  CC  CTC
                                   _____ C__
GAM1920 PCDHGA11 3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                              GGAGTGGGGT  GG  GAG
                              ||||||||||  ||  |||
                              CCTCACCCCA  CC  CTC
                                   _____ C__
GAM1920 PCDHGA11 3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                              GGAGTGGGGT  GG  GAG
                              ||||||||||  ||  |||
                              CCTCACCCCA  CC  CTC
                                   _____ C__
GAM1920 PCDHGA12 3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                              GGAGTGGGGT  GG  GAG
                              ||||||||||  ||  |||
                              CCTCACCCCA  CC  CTC
                                   _____ C__
GAM1920 PCDHGA2  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                              GGAGTGGGGT  GG  GAG
                              ||||||||||  ||  |||
                              CCTCACCCCA  CC  CTC
                                   _____ C__
GAM1920 PCDHGA3  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                              GGAGTGGGGT  GG  GAG
                              ||||||||||  ||  |||
                              CCTCACCCCA  CC  CTC
                                   _____ C__
GAM1920 PCDHGA4  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                              GGAGTGGGGT  GG  GAG
                              ||||||||||  ||  |||
                              CCTCACCCCA  CC  CTC
                                   _____ C__
GAM1920 PCDHGA5  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                              GGAGTGGGGT  GG  GAG
                              ||||||||||  ||  |||
                              CCTCACCCCA  CC  CTC
                                   _____ C__
GAM1920 PCDHGA6  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                              GGAGTGGGGT  GG  GAG
                              ||||||||||  ||  |||
                              CCTCACCCCA  CC  CTC
                                   _____ C__
GAM1920 PCDHGA7  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                              GGAGTGGGGT  GG  GAG
                              ||||||||||  ||  |||
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                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGA8  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGA9  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGB1  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGB2  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGB3  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGB4  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGB5  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGB6  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGB7  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGC3  3' GGAGTGGGGTGGGGAG    47298       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
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                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGC3  3' GGAGTGGGGTGGGGAG    47298       CGAC  CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGC4  3' GGAGTGGGGTGGGGAG    47298       CGAC  CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PCDHGC5  3' GGAGTGGGGTGGGGAG    47298       CGAC  CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1920 PEX14    3' GAGTGGGGTTGGGGCTGGGGA 47299      CGAC  CCGA
                                GAGTGGGGT   GGC   GGA
                                |||||||||   |||   |||
                                CTCACCCCA   CCG   CCT
                                     ACC_  ACC_
GAM1920 PLAT     5' GGGTGGGGTCGGTGGCCCCGG 47300   A      AC    GA
                                GG GTGGGGTCG  GGCCC  GG
                                || |||||||||  |||||  ||
                                CC CACCCCAGC  CCGGG  CC
                                 _       CA    G_
GAM1920 PLAT     5' GGGTGGGGTCGGTGGCCCCGG 47300   A      AC    GA
                                GG GTGGGGTCG  GGCCC  GG
                                || |||||||||  |||||  ||
                                CC CACCCCAGC  CCGGG  CC
                                 _       CA    G_
GAM1920 RAD54L   5' GGAGTGGGGATGATGGTCCCA 47301      TC  C  _
                                GGAGTGGGG  GA GG CCCG
                                |||||||||  || || ||||
                                CCTCACCCC  CT CC GGGT
                                     TA  A  A
GAM1920 SHANK2   3' GGAGTGGGGTTGATGCTCA   47302      C  CG  C
                                GGAGTGGGGT GA  GC CG
                                |||||||||| ||  || ||
                                CCTCACCCCA CT  CG GT
                                     A  A_  A
GAM1920 SMT3H1   3' GGAGTGGGGTGGGAG      47284       CGAC  CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ ___
GAM1920 SOX10    3' GGAGTGGGGCTGACTGAGCAGG 47303       C  __  CCG
                                GGAGTGGGGT GAC  GGC  AGG
                                |||||||||| |||  |||  |||
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                                CCTCACCCCG CTG  TCG   TCC
                                     A   AC  ___
GAM1920  TGFB1    5'  GGAATGGGGGCGCCTGAGG   47304        T GACG   C
                                GGAGTGGGG C   GCC GAGG
                                ||||||||| |   ||| ||||
                                CCTTACCCC G   CGG CTCC
                                     C ____   A
GAM1920  ZAP70    3'  GGGTGGGGCTGAGGGTGGGGA  47305    A     C  C  CCCGA
                                GG GTGGGGT GA GG    GGA
                                || ||||||| || ||    |||
                                CC CACCCCG CT CC    CCT
                                 _     A  C  ACC__
GAM1920  AIF1     5'  GAAGTGGGGTTGGGGAGTTGAG 47306         CGAC  CCC_
            G                    GGAGTGGGGT   GG   GAGG
                                ||||||||||   ||   ||||
                                CTTCACCCCA   CC   CTCC
                                     ACC_  TCAA
GAM1920  APPD     3'  GCAGTGGAGCTGGCTTGGGGA  47307   G     CGAC   CCGA
                                G AGTGGGGT   GGC   GGA
                                | ||||||||   |||   |||
                                C TCACCTCG   CCG   CCT
                                 G      A___   AACC
GAM1920  BTBD2    3'  GGAGTGGACAGACGGCCTGGGG 47308       GTC     CGA
                                GGAGTGGG  GACGGCC  GG
                                ||||||||  |||||||  ||
                                CCTCACCT  CTGCCGG  CC
                                     GT_     ACC
GAM1920  C20orf108 3'  GGAGTGGGGTTGGGGCTTAGGA 47309        CGAC   CCG
                                GGAGTGGGGT   GGC   AGGA
                                ||||||||||   |||   ||||
                                CCTCACCCCA   CCG   TCCT
                                     ACC_  AA_
GAM1920  C20orf54  3'  GGGCGGGGTCGGCGGCC    47310    A      A
                                GG GTGGGGTCG CGGCC
                                || |||||||| |||||
                                CC CGCCCCAGC GCCGG
                                 _       C
GAM1920  DDR2     3'  GGAGTGGGGGTGACCAGG    47311        TCGAC   CG
                                GGAGTGGGG    GGCC  AGG
                                |||||||||    ||||  |||
                                CCTCACCCC    CTGG  TCC
                                     CA___   __
GAM1920  DKFZp434G171 3'  GGAGTGGAAGGCCTGGGG    47312        TCGAC   CGA
                                GGAGTGGGG    GGCC   GG
                                |||||||||    ||||  ||
                                CCTCACCTT    CCGG   CC
                                     _____   ACC
GAM1920  DKFZP586N0721 3'  GGAGTGGGGCTTGGTTCAGAGG 47313         CGAC  CC _
            A                    GGAGTGGGGT   GG  C GAGGA
                                ||||||||||   ||  | |||||
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                                CCTCACCCCG   CC  G CTCCT
                                     AA__  AA T
GAM1920  FLJ10260  5' GGGTGGGAGCAGGCCCGAGGA  47314    A    GT  AC
                                GG GTGGG  CG  GGCCCGAGGA
                                || |||||  ||  ||||||||||
                                CC CACCC  GT  CCGGGCTCCT
                                 _    TC  __
GAM1920  FLJ13769  3' GGTGTGGGGTTGGCAGGAGG  47315    A     CGAC   CC
                                GG GTGGGGT   GGC  GAGG
                                || |||||||   |||  ||||
                                CC CACCCCA   CCG  CTCC
                                 A     A___  TC
GAM1920  FLJ14326  3' GGAGTGGGGTATGTGTCGAGG  47316         CGACGGCC
                                GGAGTGGGGT      CGAGG
                                ||||||||||      |||||
                                CCTCACCCCA      GCTCC
                                     TACACA__
GAM1920  FLJ14810  3' GGGTGGGGGTTGGCATTGGGAG 47317    A     TCGAC   CC___
            G                    GG GTGGGG    GGC    GAGG
                                || ||||||    |||    ||||
                                CC CACCCC    CCG    CTCC
                                 _    CAA__   TAACC
GAM1920  FLJ20128  3' GGAGTGGGGCTGACCAAGG   47318         C  CGGC
                                GGAGTGGGGT GA   CCGAGG
                                |||||||||| ||   ||||||
                                CCTCACCCCG CT   GGTTCC
                                     A  _____
GAM1920  FLJ20359  3' GGAGTGGGGTCTGCAG     47319          GACG  CCG
                                GGAGTGGGGTC   GC   AG
                                ||||||||||   ||  ||
                                CCTCACCCCAG   CG   TC
                                      A___  ____
GAM1920  FLJ21459  3' GGATTGGGGTCGGGGAGG    47320     G      AC  CCC
                                GGA TGGGGTCG  GG   GAGG
                                ||| ||||||||  ||   ||||
                                CCT ACCCCAGC  CC   CTCC
                                  A       __  ____
GAM1920  FLJ22671  3' GGAGGTGGGGATGCCTGGGGA  47321     _    TCGACG   CGA
                                GGAG TGGGG     GCC   GGA
                                |||| |||||     |||   |||
                                CCTC ACCCC     CGG   CCT
                                   C    TA_____   ACC
GAM1920  HXCP2    3' GTGGGGTCGGGGGATGG     47322         AC  CCC  _
                                GTGGGGTCG  GG   GA GG
                                |||||||||  ||   || ||
                                CACCCCAGC  CC   CT CC
                                     C_  ____  A
GAM1920  KIAA0057  3' GGAGTGAGGACAGGAGGTGGCC 47323         T  AC_____   C
            TGAGG                  GGAGTGGGG CG     GGCC GAGG
                                |||||||| ||     |||| ||||
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                                CCTCACTCC GT     CCGG CTCC
                                     T  CCTCCA    A
GAM1920  KIAA0296  3'  GGAGTGGGGTCGTGGG      47324           AC  CCCGA
                                GGAGTGGGGTCG  GG    G
                                ||||||||||||  ||    |
                                CCTCACCCCAGC  CC    C
                                      A_  _____
GAM1920  KIAA0397  3'  GAGGTGGGGTCGGTTGGTGGCT 47325   GA       AC____   CCGA
           GGGGA                  GTGGGGTCG     GGC   GGA
                                  |||||||||     |||   |||
                                  CACCCCAGC     CCG   CCT
                                TC       CAACCA   ACC_
GAM1920  KIAA1171  3'  GGGTGGGGTCCGCCAGG     47326    A      GACG   CG
                                GG GTGGGGTC    GCC  AGG
                                || ||||||||    |||  |||
                                CC CACCCCAG    CGG  TCC
                                 _       G___   __
GAM1920  KIAA1388  3'  GGGTGGGGCTGGAAGAGG    47327    A      CGAC  CCC
                                GG GTGGGGT    GG   GAGG
                                || |||||||    ||   ||||
                                CC CACCCCG    CC   CTCC
                                 _      A___  TT_
GAM1920  KIAA1910  3'  GGGTGGGGTAGAGGGTGGGG   47328    A      C  C  CCCGA
                                GG GTGGGGT GA GG    GG
                                || ||||||| || ||    ||
                                CC CACCCCA CT CC    CC
                                 _      T  C  ACC__
GAM1920  KIAA1938  3'  GGAGTGGGGTGGGGAG      47298          CGAC  CCC
                                GGAGTGGGGT   GG   GAG
                                ||||||||||   ||   |||
                                CCTCACCCCA   CC   CTC
                                      _____  C__
GAM1920  LAP1B     5'  GGGTGGGGGCGATAGAAGGA  47329    A     T   CG CCC
                                GG GTGGGG CGA  G   GAGGA
                                || |||||| |||  |   |||||
                                CC CACCCC GCT  C   TTCCT
                                 _      C   AT ____
GAM1920  MACMARCKS 5'  GGGTGGGGCTGGCGCCCGAGG  47330    A      CGACG
                                GG GTGGGGT    GCCCGAGG
                                || |||||||    ||||||||
                                CC CACCCCG    CGGGCTCC
                                 _      ACCG_
GAM1920  MGC11115  3'  GGGTGGGGTCCTGAGGCCTGGG 47331    A       __ C    CGA
           G                    GG GTGGGGTC  GA GGCC   GG
                                || ||||||||  || ||||   ||
                                CC CACCCCAG  CT CCGG   CC
                                 _      GA  _    ACC
GAM1920  MGC2705   3'  GGAGTGGGGGTGGCTCAGG   47332         TCGAC   C G
                                GGAGTGGGG    GGC C AGG
                                |||||||||    ||| | |||
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                                CCTCACCCC    CCG G TCC
                                     CA___   A _
GAM1920 MGC5149  3' GGGCTGGATGGCCCGAGG    47333     C_ C
                                GGGT  GA GGCCCGAGG
                                |||| || |||||||||
                                CCCG  CT CCGGGCTCC
                                  AC  A
GAM1920 MSTP028  3' GGAGTGGGGGCGGTGAGAGGA 47334        TCGA  CCC
                                GGAGTGGGG   CGG  GAGGA
                                |||||||||   |||  |||||
                                CCTCACCCC   GCC  CTCCT
                                     C___   ACT
GAM1920 OSBPL5   3' GGGTGGGGTGGTTCCAGG    47335    A     CGAC  C_ G
                                GG GTGGGGT   GG  CC AGG
                                || |||||||   ||  || |||
                                CC CACCCCA   CC  GG TCC
                                 _     _____ AA  _
GAM1920 PMX2B    3' GGAGTGGGGTTGAAATGAGG  47336        C  CGGCCC
                                GGAGTGGGGT GA     GAGG
                                |||||||||| ||     ||||
                                CCTCACCCCA CT     CTCC
                                     A  TTA___
GAM1920 RPS6KA4  3' GGAGTGGGGTGGGGTAGGAGAG 47337         CGAC__  CCC
           GA                    GGAGTGGGGT    GG  GAGGA
                                |||||||||     ||  |||||
                                CCTCACCCCA    CC  CTCCT
                                     CCCCAT  T__
GAM1920 SCAM-1   3' GGAGTGGGGTGGGGAG     47298         CGAC  CCC
                                GGAGTGGGGT   GG  GAG
                                |||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____  C__
GAM1920 SHANK3   3' GGAGTGGGGCCGGTGGGCCAGG 47338          AC_   CG
                                GGAGTGGGGTCG  GGCC  AGG
                                ||||||||||||  ||||  |||
                                CCTCACCCCGGC  CCGG  TCC
                                      CAC   __
GAM1920 THG-1    3' GGGTGGGGTGTCTGCCGGGGA  47339    A     CGACG  C A
                                GG GTGGGGT    GCC G GGA
                                || |||||||    ||| | |||
                                CC CACCCCA    CGG C CCT
                                 _     CAGA_  _ C
GAM1920 TMG4     5' GGGTGAGGTCCTGCCTCGGTCC 47340   A      GA____  C  A
           GGGGA                 G GTGGGGTC     CGG CCG GGA
                                | ||||||||     ||| ||| |||
                                C CACTCCAG     GCC GGC CCT
                                 _      GACGGA  A  C
GAM1920 LOC124976 3' GGAGTGGGGTCCTGGCTTGGGG 47341          GAC  CCGA
                                GGAGTGGGGTC  GGC   GG
                                ||||||||||  |||   ||
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                                CCTCACCCCAG  CCG   CC
                                     GA_  AACC
GAM1920  LOC125268 3'  AGAGTGGGACGTGGGCGGCCTG 47342        T  A___    CGA
           GGG                   GGAGTGGGG CG   CGGCC  GG
                                 ||||||||| ||   |||||  ||
                                 TCTCACCCT GC   GCCGG  CC
                                     _ ACCC    ACC
GAM1920  LOC127702 3'  GGAGTGGGGCTGGCCTGGCGAG 47343         CGAC   ___
           G                    GGAGTGGGGT   GGCC  CGAGG
                                ||||||||||   ||||  |||||
                                CCTCACCCCG   CCGG  GCTCC
                                     A___   ACC
GAM1920  LOC146562 3'  GGAGTGGGGTCGGGTGGGG   47344          AC  CCCGA
                                GGAGTGGGGTCG  GG    GG
                                ||||||||||||  ||    ||
                                CCTCACCCCAGC  CC    CC
                                     __ ACC__
GAM1920  LOC147791 5'  GGAGTAGGGGGTGCGGCCTGGG 47345        TCGA    CGA
           G                    GGAGTGGGG   CGGCC  GG
                                |||||||||   |||||  ||
                                CCTCATCCC   GCCGG  CC
                                     CCAC    ACC
GAM1920  LOC148046 3'  GGAGTGGGGCGGCTGTAG    47346        TCGA   CCG
                                GGAGTGGGG   CGGC   AG
                                |||||||||   ||||  ||
                                CCTCACCCC   GCCG   TC
                                     _____   ACA
GAM1920  LOC150951 5'  GGAGTGGGTGTTGGTGGAGCCA 47347        _ CGAC__   CG
           GG                   GGAGTGGG GT     GGCC  AGG
                                |||||||| ||     ||||  |||
                                CCTCACCC CA     TCGG  TCC
                                    A  ACCACC   __
GAM1920  LOC151610 3'  AGAGTAGAGATGGTCTGAGGA  47348        TCGAC  CCC
                                GGAGTGGGG    GG   GAGGA
                                |||||||||    ||   |||||
                                TCTCATCTC    CC   CTCCT
                                     TA___  AGA
GAM1920  LOC152283 5'  GGAGTGGAGGGCAAGG      47349        TCGAC   CC
                                GGAGTGGGG    GGC  GAGG
                                |||||||||    |||  ||||
                                CCTCACCTC    CCG  TTCC
                                     _____   __
GAM1920  LOC164537 5'  GGGGTGGGGGCCCGAGG     47350    A     TCGACG
                                GG GTGGGG     GCCCGAGG
                                || ||||||     ||||||||
                                CC CACCCC     CGGGCTCC
                                 C     _______
GAM1920  LOC197379 5'  GAAGTGGGGTCGACGGGCGGTA 47351             _ CCG
           GG                   GGAGTGGGGTCGACGG C   AGG
                                |||||||||||||||| |   |||
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                                CTTCACCCCAGCTGCC G   TCC
                                        C CCA
GAM1920  LOC207043 3'  GGAGTGGGGACGGCAAAGG   47352        TCG    CC
                                GGAGTGGGG   ACGGC  GAGG
                                |||||||||   |||||  ||||
                                CCTCACCCC   TGCCG  TTCC
                                     ____    T_
GAM1920  LOC221218 3'  GAGTGGGGTTGGTGGAGG    47353        CGAC  CCC
                                GAGTGGGGT    GG   GAGG
                                |||||||||    ||   ||||
                                CTCACCCCA    CC   CTCC
                                     A___  AC_
GAM1920  LOC222031 3'  GGAGGGGGCCAGCCTGAGG   47356     T     GAC    C
                                GGAG GGGGTC   GGCC GAGG
                                |||| ||||||   |||| ||||
                                CCTC CCCCGG   TCGG CTCC
                                  _     ____    A
GAM1920  LOC222031 3'  GGGTGGGGGTCGGGGGCAGCGA   47354    A       AC   C_
                                GG GTGGGGTCG  GGC  CGA
                                || |||||||||  |||  |||
                                CC CACCCCAGC  CCG  GCT
                                 _       C_   TC
GAM1920  LOC222031 3'  GGGTGGGGGGTGACCCAAAG    47355    A     TCGAC
                                GG GTGGGG    GGCCCGAGG
                                || ||||||    |||||||||
                                CC CACCCC    CTGGGTTTC
                                 _     CA____
GAM1920  LOC253841 3'  GGAGTGGGGTCAGGTGGTCCAG 47357          AC_  C  G
            G                    GGAGTGGGGTCG   GG CC AGG
                                ||||||||||||   || || |||
                                CCTCACCCCAGT   CC GG TCC
                                       CCA  A  _
GAM1920  LOC90784  5'  GGGTGGAGGTTGATGGTGTAGG 47358    A   _   C  C  CCCG
            A                    GG GTGG GGT GA GG    AGGA
                                || |||| ||| || ||    ||||
                                CC CACC CCA CT CC    TCCT
                                 _   T   A  A  ACA_
GAM1920  LOC91319  3'  GGAGTGGGGCCGGGGCCTGGGG 47359          AC    CGA
                                GGAGTGGGGTCG  GGCC   GG
                                ||||||||||||  ||||   ||
                                CCTCACCCCGGC  CCGG   CC
                                       C_    ACC
GAM1920  LOC93259  5'  GGAGTGGGTGTGACCTGAGG   47360        _ CGAC    C
                                GGAGTGGG GT    GGCC GAGG
                                ||||||||  ||    |||| ||||
                                CCTCACCC CA    CTGG CTCC
                                     A  _____    A
GAM1921  AFP       5'  AGTTATTTTGTTATTGGC    47363         AC    A
                                AGTTATTTT  TATTG GC
                                |||||||||  |||||  ||
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                                TCAATAAAA  ATAAC CG
                                     CA    _
GAM1921  COX6A1   3'  TAAGTTATTTATTTAAGCCA  47364         TACTA
                                TAAGTTATTT    TTGAGCCA
                                ||||||||||    ||||||||
                                ATTCAATAAA    AATTCGGT
                                     TA___
GAM1921  GPR34    3'  AATTATTTTGCTGTTAGAGCCA 47365        A  A  _
                                AGTTATTTT CT TT GAGCCA
                                ||||||||| || || ||||||
                                TTAATAAAA GA AA CTCGGT
                                     C  C  T
GAM1921  IL18R1   3'  TAAGTTATTTTACTCTTTTTAG 47366          ATTG__  C
            TCA                   TAAGTTATTTTACT     AG CA
                                ||||||||||||||     || ||
                                ATTCAATAAAATGA     TC GT
                                       GAAAAA  A
GAM1921  SLC10A2  3'  AGTTATTTTCCCCTGGCAGCC  47367        A  A  __
                                AGTTATTTT CT TTG  AGCC
                                ||||||||| || |||  ||||
                                TCAATAAAA GG GAC  TCGG
                                     _ G   CG
GAM1921  FLJ13798 3'  GTTATCCTTGAGCCA      47368       TACTA
                                GTTATTT    TTGAGCCA
                                |||||||    ||||||||
                                CAATAGG    AACTCGGT
                                     _____
GAM1921  KIAA0433 3'  TAAGTTATTTAACTACCAATGC 47369         T    TG _
                                TAAGTTATTT ACTAT  A GC
                                |||||||||| |||||  | ||
                                ATTCAATAAA TGATG  T CG
                                     T    GT A
GAM1921  KIAA1500 3'  TAAATTATTTTAGAGCCA    47370          CTATT
                                TAAGTTATTTTA    GAGCCA
                                ||||||||||||    ||||||
                                ATTTAATAAAAT    CTCGGT
                                     _____
GAM1921  SARM     3'  AAGTTATTTTCCAGAGCCA    47371         A   TT
                                AAGTTATTTT CTA  GAGCCA
                                |||||||||| |||  ||||||
                                TTCAATAAAA GGT  CTCGGT
                                     _  __
GAM1921  LOC144453 3'  GTTATTTTATTTCTAAAGCCA  47372        CTATT_
                                GTTATTTTA     GAGCCA
                                |||||||||     ||||||
                                CAATAAAAT     TTCGGT
                                     AAAGAT
GAM1921  LOC200058 3'  TAAGTTATCTTGCCCAAAGTCA 47373          A  ATT   C
            C                    TAAGTTATTTT CT   GAG CAC
                                ||||||||||| ||   ||| |||
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                                ATTCAATAGAA GG   TTC GTG
                                      C  GT_   A
GAM1921  LOC203080 5'  TAAGTTAATCTTTGAGCCA    47374        T   ACTA
                                TAAGTTA TTT    TTGAGCCA
                                ||||||| |||    ||||||||
                                ATTCAAT AGA    AACTCGGT
                                    T  ____
GAM1921  LOC219673 5'  AGCTATGATTGAGCCA      47375       TTTACT
                                AGTTAT     ATTGAGCCA
                                ||||||     |||||||||
                                TCGATA     TAACTCGGT
                                   C_____
GAM1921  LOC220980 5'  AAGTTGTTTCTCAGTTGAGCCA 47376      A    ACTA
              C                  AAGTT TTTT    TTGAGCCAC
                                |||||  ||||    |||||||||
                                TTCAA AAAG    AACTCGGTG
                                   C    AGTC
GAM1922  PTGFRN    3'  TGTCAATGCAGAATCTAATGTT 47379        A  AC   _
                                TGTCAAT CA  AGTC AATGTT
                                ||||||| ||  |||| ||||||
                                ACAGTTA GT  TTAG TTACAA
                                    C  C_    A
GAM1922  TNFAIP1   3'  CATGTCAGTGAGTTCAATGTT  47380        ATACAACAG
                                TATGTCA        TCAATGTT
                                |||||||        ||||||||
                                GTACAGT        AGTTACAA
                                    CACTCA___
GAM1922  VDAC2     3'  TCAATGGTAACAGTCAATGTT  47381       AC_
                                TCAAT   AACAGTCAATGTT
                                |||||   ||||||||||||
                                AGTTA   TTGTCAGTTACAA
                                   CCA
GAM1922  FLJ22729  3'  ATGTTCACAACAGTTGGTGTT  47382      CAA        CAA
                                ATGT   TACAACAGT   TGTT
                                ||||   |||||||||   ||||
                                TACA   GTGTTGTCA   ACAA
                                   A__        ACC
GAM1922  FLJ23604  5'  TGCTGTGAAAACAGTCAGTGTT 47383     CAATAC       A
                                TGT      AACAGTCA TGTT
                                |||      |||||||| ||||
                                ACG      TTGTCAGT ACAA
                                  ACACTT       C
GAM1922  KIAA1229  3'  TATGTCAAACAGCAGATG    47384        TACA    CA
                                TATGTCAA    ACAGT  ATG
                                ||||||||    |||||  |||
                                ATACAGTT    TGTCG  TAC
                                     _____     TC
GAM1922  LOC145474 3'  TATATCAATACAATGGTC    47385           CA
                                TATGTCAATACAA  GTC
                                ||||||||||||  |||
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                                ATATAGTTATGTT  CAG
                                       AC
GAM1922  LOC219902 5'  CATGTTAGCAACTGGTCAATGT 47386      CAATA   A_
              T                 TATGT    CAAC  GTCAATGTT
                                |||||    ||||  |||||||||
                                GTACA    GTTG  CAGTTACAA
                                  ATC__   AC
GAM1923  ASB2     3'  GTGAGTTTTCCAGAACAAG   47389     C   ATATAA
                                GTG GTT     CCAGAACAAG
                                |||  |||     ||||||||||
                                CAC CAA     GGTCTTGTTC
                                  T  AA____
GAM1923  DGCR6    3'  GCGGCTGAGACCAGAACAAGC  47390     C   ATATA
                                GTG GTT    ACCAGAACAAGC
                                |||  |||    ||||||||||||
                                CGC CGA    TGGTCTTGTTCG
                                  _  CTC__
GAM1923  MYLK     5'  GTGCGTTAATGTGACTAAACAA 47391        TATAACCA
              G                  GTGCGTTA       GAACAAG
                                 ||||||||       |||||||
                                 CACGCAAT       TTTGTTC
                                     TACACTGA
GAM1923  MYLK     5'  GTGCGTTAATGTGACTAAACAA 47391        TATAACCA
              G                  GTGCGTTA       GAACAAG
                                 ||||||||       |||||||
                                 CACGCAAT       TTTGTTC
                                     TACACTGA
GAM1923  AKAP12   3'  GTGGGTTATATAACTGA     47392     C       CA
                                GTG GTTATATAAC  GA
                                |||  ||||||||||  ||
                                CAC CAATATATTG  CT
                                  C        A_
GAM1923  AKAP12   3'  GTGGGTTATATAACTGA     47392     C       CA
                                GTG GTTATATAAC  GA
                                |||  ||||||||||  ||
                                CAC CAATATATTG  CT
                                  C        A_
GAM1923  DGCR6L   3'  GCGGCTGAGACCAGAACAAGC  47390     C   ATATA
                                GTG GTT    ACCAGAACAAGC
                                |||  |||    ||||||||||||
                                CGC CGA    TGGTCTTGTTCG
                                  _  CTC__
GAM1923  FLJ13154 3'  GTGTAACAACCAGAGTAAGC   47393     CGTTAT       AC
                                GTG     ATAACCAGA  AAGC
                                |||     |||||||||  ||||
                                CAC     TGTTGGTCT  TTCG
                                  AT_____        CA
GAM1923  KIAA0057 3'  GTGGCCAAAATTAGAACAAGC  47394     C    TATAACC
                                GTG GTTA      AGAACAAGC
                                |||  ||||      |||||||||
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                                CAC CGGT      TCTTGTTCG
                                  _   TTTAA__
GAM1923 KIAA0140 3' GTACGTCTGGTCAGAACAAGC 47395       ATATAAC
                                GTGCGTT      CAGAACAAGC
                                |||||||      ||||||||||
                                CATGCAG      GTCTTGTTCG
                                    ACCA___
GAM1923 KIAA0215 3' ATGTGTTATATAACCGGAAAGC 47396    C        A  CA
                                GTG GTTATATAACC GAA  AGC
                                ||| |||||||||| |||  |||
                                TAC CAATATATTGG CTT  TCG
                                  A        C  __
GAM1923 KIAA1673 3' TGTGTTATATAACTTAAGA   47397    C       C__
                                TG GTTATATAAC   AGA
                                || ||||||||||   |||
                                AC CAATATATTG   TCT
                                 A         AAT
GAM1924 CCR2     3' GAAAGTTCTGCTCTGTCCCCAC 47400        CACCACA_
             TT                  GAAAGTTCT       CCCACTT
                                 |||||||||       |||||||
                                 CTTTCAAGA       GGGTGAA
                                      CGAGACAG
GAM1924 PDE4A    3' GAAGGAGGCCCCACACCTGCTT 47401     AGTTC  A      CA
                                GAA     TC CCACACC  CTT
                                |||     || |||||||  |||
                                CTT     GG GGTGTGG  GAA
                                  CCTCC  _      AC
GAM1924 TRPC5    3' CGAAAGTTCCTCATTTCTCTTA 47402        _  CCACACCC
             CTT                  CGAAAGTTC TCA       ACTT
                                  ||||||||| |||       ||||
                                  GCTTTCAAG AGT       TGAA
                                       G   AAAGAGAA
GAM1924 USP6     3' GAAAGTTCTCTATCAGACAGCT 47403        ACCA  CC  _
             T                    GAAAGTTCTC    CA  CA CTT
                                  ||||||||||    ||  || |||
                                  CTTTCAAGAG    GT  GT GAA
                                        ATA_  CT  C
GAM1924 ZNF200   5' GCAACCACACACCACACTC   47404    TC    C    _
                                GT  TCAC ACACC CACTT
                                ||  |||| ||||| |||||
                                CG  GGTG TGTGG GTGAG
                                 TT   _    T
GAM1924 C6orf35  3' CGAGAGCCACACCCACT     47405     A  TTCTCA
                                CGA AG     CCACACCCACT
                                ||| ||     ||||||||||
                                GCT TC     GGTGTGGGTGA
                                  C _______
GAM1924 FLJ14743 5' CGAGAGCTCTGCAGCCCACTT  47406     A     _  CCACA
                                CGA AGTTCT CA    CCCACTT
                                ||| |||||| ||    |||||||
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                                GCT TCGAGA GT    GGGTGAA
                                  C     C  C____
GAM1924  FLJ20160  3'  GAAAGTCCTCATTGAACTCCA  47407          CCAC  _
                                GAAAGTTCTCA   AC CCA
                                ||||||||||   || |||
                                CTTTCAGGAGT   TG GGT
                                      AACT  A
GAM1924  KIAA1553  3'  GAGAGTTCCCACGTGTGTCCAC 47408    A       CACAC_
              TT                 GA AGTTCTCAC     CCACTT
                                || |||||||||     ||||||
                                CT TCAAGGGTG     GGTGAA
                                  C       CACACA
GAM1924  KIAA1649  3'  CGAGAAGTCTGCACCCACT   47409    _   T  CACCA
                                CGA AAGT CT    CACCCACT
                                ||| |||| ||    ||||||||
                                GCT TTCA GA    GTGGGTGA
                                  C   _ C____
GAM1924  KIAA1649  3'  CGAGAAGTCTGCACCCACT   47409    _   T  CACCA
                                CGA AAGT CT    CACCCACT
                                ||| |||| ||    ||||||||
                                GCT TTCA GA    GTGGGTGA
                                  C   _ C____
GAM1924  MSTP028   3'  CAAAAGTTCTCACATACAC   47410          C_
                                CGAAAGTTCTCAC  ACAC
                                ||||||||||||  ||||
                                GTTTTCAAGAGTG  TGTG
                                      TA
GAM1924  NFAT5    3'  GAGATTCTACTAACCCACTT   47411    AA    C  CAC
                                GA  GTTCT AC   ACCCACTT
                                ||  ||||| ||   ||||||||
                                CT  TAAGA TG   TGGGTGAA
                                  C_    _  AT_
GAM1924  LOC112817 3'  GAAAATTCCCTTACTGTGCCTA 47412          __  CACA  C
              CTT                  GAAAGTTCTC  AC    CC ACTT
                                ||||||||||  ||    || ||||
                                CTTTTAAGGG  TG    GG TGAA
                                      AA  ACAC  A
GAM1924  LOC113763 3'  AAGGACCTTCATACCCACTT   47413     TT  CAC  C
                                AAG  CT   CA ACCCACTT
                                |||  ||   || ||||||||
                                TTC  GG   GT TGGGTGAA
                                  CT  AA_  A
GAM1924  LOC145333 5'  AAAATCAGAGCCACACCCACTT 47414       CTCA
                                AAAGTT    CCACACCCACTT
                                ||||||    ||||||||||||
                                TTTTAG    GGTGTGGGTGAA
                                    TCTC
GAM1924  LOC146506 3'  AAGTTCTCATCACTGGCTACAC 47415         C   ACC___
              TT                   AAGTTCTCA CAC     CACTT
                                |||||||| |||     |||||
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                                TTCAAGAGT GTG     GTGAA
                                     A   ACCGAT
GAM1924  LOC150279 3'  ATCCTCACTGCACCTGCTT   47416        CA    CA
                                GTTCTCAC  CACC  CTT
                                ||||||||  ||||  |||
                                TAGGAGTG  GTGG  GAA
                                     AC    AC
GAM1924  LOC220573 3'  GAAAGTTCTCTATCAGACAACT 47417         AC_  C  CC
              T                  GAAAGTTCTC   CA AC  ACTT
                                 ||||||||||   || ||  ||||
                                 CTTTCAAGAG   GT TG  TGAA
                                       ATA  C  T_
GAM1924  LOC90639  5'  GAAGGTTCTCACTTCCTACTT  47418     A      CACA  C
                                GAA GTTCTCAC    CC ACTT
                                ||| ||||||||    || ||||
                                CTT CAAGAGTG    GG TGAA
                                  C       AA__  A
GAM1925  FLRT2     3'  TGATTTGTGTGAAATGAC    47421     CCG       C
                                TGA   TGTGTGAAA GAC
                                |||   |||||||||| |||
                                ACT   ACACACTTT CTG
                                  AA_       A
GAM1925  ZNF236    3'  GCAATGGAACGGCCGCT     47422     T   A    A
                                GTG GTG AACG CCGCT
                                ||| ||| |||| |||||
                                CGT TAC TTGC GGCGA
                                  _  C    C
GAM1925  MGC14136  3'  GTGTGTGAAGCAAGCTC     47423         A   CC
                                GTGTGTGAA CGA  GCTC
                                |||||||||| |||  ||||
                                CACACACTT GTT  CGAG
                                     C  __
GAM1925  PTDSS2    3'  TGTGTGAAAGGAAGGCTC    47424         C  CC
                                TGTGTGAAA GA  GCTC
                                ||||||||| ||  ||||
                                ACACACTTT CT  CGAG
                                     C  TC
GAM1925  SLC5A7    3'  TGACTGGTGTGAAAACACT   47425     CGT       CGAC
                                TGAC   GTGTGAAA    CGCT
                                ||||   ||||||||    ||||
                                ACTG   CACACTTT    GTGA
                                  AC_       T___
GAM1925  LOC126961 3'  TGGCCGTGTGTAGAGTGGGCTC 47426     A       AAACGACC
                                TG CCGTGTGTG       GCTC
                                || |||||||||       ||||
                                AC GGCACACAT       CGAG
                                 C        CTCACC__
GAM1925  LOC257395 3'  TGGCCGTGTGTAGAGTGGGCTC 47426     A       AAACGACC
                                TG CCGTGTGTG       GCTC
                                || |||||||||       ||||
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                                AC GGCACACAT       CGAG
                                 C        CTCACC__
GAM1926 CDC23    3'  TCTGTATAATCACCAATGTTA  47429        ACTG   __
                                TCTGTATAA    CACC  TGTTA
                                |||||||||    ||||  |||||
                                AGACATATT    GTGG  ACAAT
                                     A___    TT
GAM1926 CUL3     3'  TCTGTATCATTACCTGTTA    47430       AAACTGC
                                TCTGTAT      ACCTGTTA
                                |||||||      ||||||||
                                AGACATA      TGGACAAT
                                   GTAA___
GAM1926 SLC7A6   3'  TATCTGTAAGAGCTGCATCTA  47431        TAAA    C
                                TATCTGTA    CTGCA CTG
                                ||||||||    ||||| |||
                                ATAGACAT    GACGT GAT
                                     TCTC    A
GAM1926 ACAA2    5'  CGTATAAAGGCCACTGTTA    47432        CT  AC
                                TGTATAAA  GC  CTGTTA
                                ||||||||  ||  ||||||
                                GCATATTT  CG  GACAAT
                                     C_  GT
GAM1926 CDW92    3'  TATTTGTAAAACAGGACCTGTT 47433     C    T    TGC
             A                   TAT TGTA AAAC   ACCTGTTA
                                ||| |||| ||||   ||||||||
                                ATA ACAT TTTG   TGGACAAT
                                  A   _    TCC
GAM1926 DKFZP434P0721 3'  TATCTGTATAGAACTGTCAGCT 47434          _    _ C
                                TATCTGTATA AACTG CA CT
                                |||||||||| ||||| || ||
                                ATAGACATAT TTGAC GT GA
                                     C    A  C
GAM1926 FLJ13841  3'  TATTTGTATAAATAGCCTCT   47435     C       CT  AC
                                TAT TGTATAAA  GC  CT
                                ||| ||||||||  ||  ||
                                ATA ACATATTT  CG  GA
                                  A       AT  GA
GAM1926 H2AFZ    3'  TCTGTACAAAACCAAATGTT   47436         CTGC  ___
                                TCTGTATAAA    ACC   TGTT
                                ||||||||||    |||   ||||
                                AGACATGTTT    TGG   ACAA
                                     ____   TTT
GAM1926 LEPROTL1  3'  TATCTGTAAGACTAACAAGTTA 47437        TAA    C  CT
                                TATCTGTA   ACTG AC  GTTA
                                ||||||||   |||| ||  ||||
                                ATAGACAT   TGAT TG  CAAT
                                     TC_    _  TT
GAM1926 LOC146332 3'  TACCTGTGTGAACTGGCACTTG 47438        ATA    _   C
                                TATCTGT   AACTG CAC TG
                                |||||||   ||||| ||| ||
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                                ATGGACA   TTGAC GTG AC
                                    CAC    C  A
GAM1926 LOC148604 5' TATCTGTAAGACTGGAGTT   47439       TAA   CACCT
                                TATCTGTA  ACTG   GTT
                                ||||||||  ||||   |||
                                ATAGACAT  TGAC   CAA
                                    TC_   CT___
GAM1926 LOC91286 5' TATCTGAATAAACTGTCC   47440      T      CA
                                TATCTG ATAAACTG  CC
                                ||||||| ||||||||  ||
                                ATAGAC TATTTGAC  GG
                                   T      A_
GAM1927 BLAME   3' TGTGGAGGGAGAGCTGCAGG  47443       TA    CC
                                TGTGGAGG  AGAGCT  CGGG
                                ||||||||  ||||||  ||||
                                ACACCTCC  TCTCGA  GTCC
                                    C_    C_
GAM1927 CBFA2T2  3' TGTGGAGGGGGAGGAGGGG  47444       TAA  CTCCC
                                TGTGGAGG  GAG   GGGG
                                ||||||||  |||   ||||
                                ACACCTCC  CTC   CCCC
                                    CC_   CT___
GAM1927 CENTD2   5' TGGAGGTATCTCCGGGG    47445       AGAGC  _
                                TGGAGGTA   TC CCGGGG
                                ||||||||   || ||||||
                                ACCTCCAT   AG GGCCCC
                                    _____  A
GAM1927 FGD1    3' TGTGGGGTGGGGGCTCCCAG  47446     A  AAGA
                                TGTGG GGT   GCTCCCGG
                                ||||| |||   ||||||||
                                ACACC CCA   CGAGGGTC
                                  _  CCCC
GAM1927 FKBP10   3' TGTGGAGGGGAGGTATGGTGGG 47447       TA  AGCTCCC
           GG                    TGTGGAGG  AG     GGGGG
                                ||||||||  ||     |||||
                                ACACCTCC  TC     CCCCC
                                    CC  CATACCA
GAM1927 GAS11   3' TGTGGAGGTGAGAGCCCCAG  47448       A   T
                                TGTGGAGGT AGAGC CCCGG
                                ||||||||| ||||| |||||
                                ACACCTCCA TCTCG GGGTC
                                    C    _
GAM1927 GDI1    3' GTGGGGGTAAGAGCGGTGGGGG 47449     A      TCCC
                                GTGG GGTAAGAGC   GGGGG
                                |||| |||||||||   |||||
                                CACC CCATTCTCG   CCCCC
                                  C       CCA_
GAM1927 IHPK1   3' TGTGGAGGAAGGGCATGGGG  47450       T  A  TCCC
                                TGTGGAGG AAG GC   GGGG
                                |||||||| ||| ||   ||||
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                                ACACCTCC TTC CG   CCCC
                                    _  C  TA__
GAM1927  OBP2A    3'  TGGAGGTGCAGACCCGGGGG  47451      A_  GCT
                                TGGAGGT  AGA  CCCGGGGG
                                |||||||  |||  ||||||||
                                ACCTCCA  TCT  GGGCCCCC
                                   CG  ___
GAM1927  OBP2B    3'  TGGAGGTGCAGACCCGGGGG  47451      A_  GCT
                                TGGAGGT  AGA  CCCGGGGG
                                |||||||  |||  ||||||||
                                ACCTCCA  TCT  GGGCCCCC
                                   CG  ___
GAM1927  SLC38A3  3'  TGGGGTCTTTGGCTCCCGGGGG 47452    A  AAGA_
                                TGG GGT    GCTCCCGGGGG
                                ||| |||    ||||||||||
                                ACC CCA    CGAGGGCCCCC
                                  _  GAAAC
GAM1927  B3GAT3   3'  TGGAGGTAGGAAGGGG     47453       A  CTCCC
                                TGGAGGTA GAG    GGGG
                                |||||||| |||    ||||
                                ACCTCCAT CTT    CCCC
                                   C  _____
GAM1927  C22orf5  3'  TGTGGAGGGGGAGAGGAGGGG  47454       TA_  CTCCC
                                TGTGGAGG  AGAG   GGGG
                                ||||||||  ||||   ||||
                                ACACCTCC  TCTC   CCCC
                                   CCC   CT___
GAM1927  CENTA1   3'  GTGGAGGTGGGGGGAGGGCGGG 47455       AA___  CTCC
           G                  GTGGAGGT   GAG   CGGGG
                              ||||||||   |||   |||||
                              CACCTCCA   CTC   GCCCC
                                 CCCCC  CC__
GAM1927  DKFZP434B103 3'  TGTGGAGGAAGGGGCTTCTGCC 47456     T  A_  T_______  CGGG
           CCCG                GAGG AAG  GC      CC   G
                               |||| |||  ||      ||   |
                               CTCC TTC  CG      GG   C
                                 _  CC  AAGACIII  GGGC
GAM1927  EPB41L1  3'  TGTGGGGTGGGGGAAGGGG   47457     A  AA__  CTCCC
                              TGTGG GGT   GAG   GGGG
                              ||||| |||   |||   ||||
                              ACACC CCA   CTT   CCCC
                                 _  CCCC  _____
GAM1927  FLJ12529 3'  GTGGAGGTGGGGATGGGGTTGG 47458       AA_  GCTCCC_
           GGG                 GTGGAGGT  GA     GGGGG
                               ||||||||  ||     |||||
                               CACCTCCA  CT     CCCCC
                                  CCC  ACCCCAA
GAM1927  FLJ20313 5'  TGGGGTCCTCCAGTTCCCGGGG 47459    A  AAG__  C
           G                   TGG GGT    AG TCCCGGGGG
                               ||| |||    || |||||||||
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                                ACC CCA    TC AGGGCCCCC
                                  _  GGAGG  A
GAM1927  GBTS1    3'  TGTGGATGTGGCTGGTCCCGGG 47460      G  AAGAGC
              GG                  TGTGGA GT     TCCCGGGGG
                                  |||||| ||     |||||||||
                                  ACACCT CA     AGGGCCCCC
                                     A  CCGACC
GAM1927  GPS1     3'  GTGGAGGTGGGGAGGGGG    47461       AA_  CTCCC
                                  GTGGAGGT  GAG    GGGG
                                  ||||||||  |||    ||||
                                  CACCTCCA  CTC    CCCC
                                       CCC  _____
GAM1927  KIAA0596 3'  TGTGGAGGCAGGAGTTCCAAGG 47462         A  C  C
                                  TGTGGAGGTA GAG TCC GGG
                                  |||||||||| ||| ||| |||
                                  ACACCTCCGT CTC AGG TCC
                                        C  A  T
GAM1927  KIAA1691 3'  TGTGGAGGGAAGGGCCGGG   47463       T  A  TCC
                                  TGTGGAGG AAG GC  CGGG
                                  |||||||| ||| ||  ||||
                                  ACACCTCC TTC CG  GCCC
                                       C  C  ___
GAM1927  p25      3'  TGTGGAGGGAGAGTGGGG    47464       TA   CTCCC
                                  TGTGGAGG  AGAG    GGGG
                                  ||||||||  ||||    ||||
                                  ACACCTCC  TCTC    CCCC
                                       C_   A____
GAM1927  PILR(ALPHA) 5'  TGTGGAGGGGCCGCCTGGGGG  47465       TAAGA  C  _
                                  TGTGGAGG    GCT CC GGGGG
                                  ||||||||    ||| || |||||
                                  ACACCTCC    CGG GG CCCCC
                                       C____  C  A
GAM1927  PPY2     3'  TGTGGAGGGGAGAGCTGGG   47466       TA    CCC
                                  TGTGGAGG  AGAGCT  GGG
                                  ||||||||  ||||||  |||
                                  ACACCTCC  TCTCGA  CCC
                                       CC    ___
GAM1927  PSKH1    3'  TGTGGAGGAAGGGGCTTGGG  47467       T  A_  CCC
                                  TGTGGAGG AAG  GCT  GGG
                                  |||||||| |||  |||  |||
                                  ACACCTCC TTC  CGA  CCC
                                       _  CC  A__
GAM1927  RAI17    3'  TGTGGAGGTGGGACGTGGG   47468       AA  GCTCC  _
                                  TGTGGAGGT  GA    CG GGG
                                  |||||||||  ||    || |||
                                  ACACCTCCA  CT    GC CCC
                                       CC  _____  A
GAM1927  SH3BGRL2 3'  TGTGGAGGTAAGAGTTTCC   47469          C_
                                  TGTGGAGGTAAGAG  TCC
                                  ||||||||||||||  |||
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                                ACACCTCCATTCTC  AGG
                                      AA
GAM1927  LOC148398 5'  TGTGGAAGTAGGGGCTGACGG  47470        AGA   CC
                                TGTGGAGGTA   GCT  CGG
                                ||||||||||   |||  |||
                                ACACCTTCAT   CGA  GCC
                                     CCC   CT
GAM1927  LOC149271 3'  TGTGGTGGGTGGGAGGTGGGG  47471      A_   AA   CTCCC
                                TGTGG  GGT  GAG    GGGG
                                |||||  |||  |||    ||||
                                ACACC  CCA  CTC    CCCC
                                   AC   CC   CA___
GAM1927  LOC149422 3'  TGCGGAGGATCGCTTCCGGGGG 47472        TAAGA   C
                                TGTGGAGG    GCT CCGGGGG
                                ||||||||    ||| |||||||
                                ACGCCTCC    CGA GGCCCCC
                                     TAG__   A
GAM1927  LOC150197 5'  GTGGAGGTGTTTGCCCTGGGGG 34959        AAGA  T  C
                                GTGGAGGT    GC CC GGGGG
                                ||||||||    || || |||||
                                CACCTCCA    CG GG CCCCC
                                     CAAA  _  A
GAM1927  LOC157918 5'  TGTGGAGGTTGGGGGAGTGGGG 47473        AA___   CTCCC
                                TGTGGAGGT    GAG    GGGG
                                |||||||||    |||    ||||
                                ACACCTCCA    CTC    CCCC
                                     ACCCC   A____
GAM1927  LOC199991 3'  TGTGGAGGGCTCTCCTGGGGG  47474        TAAGA   _  _
                                TGTGGAGG    GCTC CC GGGGG
                                ||||||||    |||| || |||||
                                ACACCTCC    CGAG GG CCCCC
                                     _____   A  A
GAM1927  LOC201522 3'  TGTGGAGGGGCTGCCTGGGGG  47475        TAAGA  _  C
                                TGTGGAGG    GCT CC GGGGG
                                ||||||||    ||| || |||||
                                ACACCTCC    CGA GG CCCCC
                                     C____   C  A
GAM1927  LOC221218 3'  GTGGAGGTGAGAGACAGGGG   47476        A   CTCC
                                GTGGAGGT AGAG   CGGGGG
                                |||||||| ||||   ||||||
                                CACCTCCA TCTC   GTCCCC
                                     C   T___
GAM1927  LOC253776 3'  TGGAGGTAGGGCATGGTGGGGG 47477        A A  TCCC_
                                TGGAGGTA G GC    GGGGG
                                |||||||| | ||    |||||
                                ACCTCCAT C CG    CCCCC
                                     _ C  TACCA
GAM1927  LOC254532 5'  TGTGGAGGGGAGGGGCGGGG   47478        TAA   CTCC
                                TGTGGAGG   GAG   CGGGG
                                ||||||||   |||   |||||
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                                ACACCTCC  CTC   GCCCC
                                    C__   CCC_
GAM1927  LOC255102 3'  TGTGGAGGTGGGAGTCAGGG  47479        AA  CTCC
                                TGTGGAGGT  GAG   CGGGG
                                |||||||||  |||   |||||
                                ACACCTCCA  CTC   GTCCC
                                    CC  A___
GAM1927  LOC255452 3'  TGTGGAGGCAAGTGGG     47480         AGCTCCC
                                TGTGGAGGTAAG     GGG
                                ||||||||||||     |||
                                ACACCTCCGTTC     CCC
                                      A_______
GAM1927  LOC256980 3'  TGTGGAGGTGGGATTTAGCTGG 47481    AAG_____  T______  CGGG
           CCCCCGGG               GGT     AGC    CC   GG
                                |||     |||    ||   ||
                                CCA     TCG    GG   CC
                                  CCCTAAA  ACCIII  GGGC
GAM1927  LOC257476 3'  TGTGGAGGAAGGGCATGGGG  47450       T  A  TCCC
                                TGTGGAGG AAG GC   GGGG
                                |||||||| ||| ||   ||||
                                ACACCTCC TTC CG   CCCC
                                    _  C  TA__
GAM1927  LOC90643  3'  TGTGGAGGAAGAGCTGAATCAG 47482       T     CC__
           G                    TGTGGAGG AAGAGCT   CGGG
                                |||||||| |||||||   ||||
                                ACACCTCC TTCTCGA   GTCC
                                    _     CTTA
GAM1927  LOC91818  3'  TGTGGAGGAAGAGCTGAATCAG 47482       T     CC__
           G                    TGTGGAGG AAGAGCT   CGGG
                                |||||||| |||||||   ||||
                                ACACCTCC TTCTCGA   GTCC
                                    _     CTTA
GAM1928  KIAA1128  3'  TCTTGGATTGAGCATTCACTGC 47485        AAACT  _  C
           G                    TCTTGGGTT    CAT CAC GCG
                                |||||||||    ||| ||| |||
                                AGAACCTAA    GTA GTG CGC
                                    CTC__   A  A
GAM1928  LANO    5'  TCTTGGGTTAGCTCGCTTCTCG 47486        AA  ATCAC_
           CG                   TCTTGGGTTA  CTC    CGCG
                                |||||||||  |||    ||||
                                AGAACCCAAT  GAG    GCGC
                                    C_  CGAAGA
GAM1928  MYNN    3'  TCTTGGGCTGATACTATC    47487        AA_  C
                                TCTTGGGTT   ACT ATC
                                |||||||||   ||| |||
                                AGAACCCGA   TGA TAG
                                    CTA  _
GAM1928  RNF10   5'  TCTTGGGTTTAGACTCGCCG  47488        AA_   ATCA
                                TCTTGGGTT   ACTC   CCG
                                |||||||||   ||||   |||
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                                AGAACCCAA  TGAG   GGC
                                     ATC   C___
GAM1928 SCYA21   3' TCTTGGGTTCAGGCTTCAAGCG 47489        AAACTCA  CC
                                TCTTGGGTT     TCA  GCG
                                |||||||||     |||  |||
                                AGAACCCAA     AGT  CGC
                                     GTCCGA_  T_
GAM1928 YAP     5' CCCTGGGTTCGTCGCCGC   47490        TAAAC  A  A
                                TCTTGGGT    TC TC CCGC
                                ||||||||    || || ||||
                                GGGACCCA    AG AG GGCG
                                     _____  C  C
GAM1929 IRS2    5' CTCGGCGGCGCCGCGCCC   47493     ACA  A       G
                                TTCG   GC GCGCCGCGC CC
                                ||||   || |||||||| ||
                                GAGC   CG CGCGGCGCG GG
                                  ___  C       _
GAM1929 SLC30A4  5' CTCGAGGGCAGTGCCGCGCGTC 47494      CA   C      _
            CC                    TTCGA  GCAG GCCGCGCG CCC
                                |||||  |||| |||||||| |||
                                GAGCT  CGTC CGGCGCGC GGG
                                   CC   A       A
GAM1929 TERF2   5' TCCGATCGCCGCGCGCCC   47495      CAGCAG
                                TTCGA     CGCCGCGCGCCC
                                |||||     ||||||||||||
                                AGGCT     GCGGCGCGCGGG
                                   A_____
GAM1929 DCOHM   3' TTCAGCAGCAGCTCATGC   47496     A      GC  C
                                TTCG CAGCAGC  CG GC
                                |||| |||||||  || ||
                                AAGT GTCGTCG  GT CG
                                  C      A_  A
GAM1929 ESDN    5' CTCGGCAGCCCCGCGCGCC   47497     ACA    G
                                TTCG   GCAGC CCGCGCGCC
                                ||||   ||||| |||||||||
                                GAGC   CGTCG GGCGCGCGG
                                  ___    G
GAM1929 FLJ12089 5' TTCACAGCAGCTGCTCC    47498     G      GCCGC  G
                                TTC ACAGCAGC    GC CC
                                ||| ||||||||    || ||
                                AAG TGTCGTCG    CG GG
                                  _      A____  A
GAM1929 FLJ30791 5' TCTGGCAGCAGCGGTGCAGCTC 47499    GA_      CC   C  _
            C                     TC   CAGCAGCG  GCG GC CC
                                ||   ||||||||  ||| || ||
                                AG   GTCGTCGC  CGT CG GG
                                 ACC       CA   _  A
GAM1929 KIAA0493 5' TTCGACAAGTCCTAGTCGTGCG 47500        CAGCGC__  C
            CCC                     TTCGACAG       CG GCGCCC
                                ||||||||       || ||||||
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                                AAGCTGTT      GC CGCGGG
                                    CAGGATCA  A
GAM1929  RAB24    5'  TTCGGCAGCGCCCCGTGTGCCC 47501     ACA      G  C__
             C                   TTCG   GCAGCGCC CG   GCCCC
                                 ||||   |||||||| ||   |||||
                                 AAGC   CGTCGCGG GC   CGGGG
                                   ___      G  ACA
GAM1929  TRIM15   3'  TTCGCCGCCCTTCGCGCGCCCC 47502     ACA  AGCGC
                                 TTCG   GC    CGCGCGCCCC
                                 ||||   ||    ||||||||||
                                 AAGC   CG    GCGCGCGGGG
                                   GG_  GGAA_
GAM1929  ZAK      3'  TTCGGTGACAGCACCGCCCC  47503     ACA       GCG
                                 TTCG   GCAGCGCCGC   CCC
                                 ||||   ||||||||||   |||
                                 AAGC   TGTCGTGGCG   GGG
                                   CAC        ___
GAM1929  LOC121536 5'  TTCAGCAGCAGCGCCGCCACCG 47504     A         G   _
             CC                    TTCG CAGCAGCGCCGC CGCC CC
                                   |||| |||||||||||| |||| ||
                                   AAGT GTCGTCGCGGCG GTGG GG
                                     C          _    C
GAM1929  LOC147463 5'  TCCGACGCCGCGCGCC      47505       AGCAGC       _
                                 TTCGAC     GCCGCGCGC C
                                 ||||||     ||||||||| |
                                 AGGCTG     CGGCGCGCG G
                                    _______        A
GAM1929  LOC196985 5'  TCCGACAGCAGGGGGCGCCCC  47506          CGCCGC
                                 TTCGACAGCAG     GCGCCCC
                                 ||||||||||     |||||||
                                 AGGCTGTCGTC     CGCGGGG
                                       CCC___
GAM1929  LOC196986 5'  TCCGACAGCAGGGGGCGCCCC  47506          CGCCGC
                                 TTCGACAGCAG     GCGCCCC
                                 ||||||||||     |||||||
                                 AGGCTGTCGTC     CGCGGGG
                                       CCC___
GAM1929  LOC254100 5'  CTCGGTAGCAGCCGACACGCCC 47507     AC   GC   _
             C                    TTCG  AGCA  GCCG CGCGCCCC
                                  ||||  ||||  |||| ||||||||
                                  GAGC  TCGT  CGGC GTGCGGGG
                                    CA   __   T
GAM1930  ARCN1    3'  ATCATGCCATTGCATTCCAGC  47510         CA  A_
                                 ATCATGCCAT  CG  TCAGC
                                 ||||||||||  ||  |||||
                                 TAGTACGGTA  GT  GGTCG
                                       AC  AA
GAM1930  DMXL1    5'  TCATGCCACGGGTCAGCGGC  47511         CACGA    A
                                 TCATGCCAT    TCAGC GC
                                 |||||||||    ||||| ||
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                                AGTACGGTG    AGTCG CG
                                     CCC__    C
GAM1930  ESR1    3'  CATCATGCATCACCACAG    47512        C    G T
                                CATCATGC ATCAC A CAG
                                |||||||| ||||| | |||
                                GTAGTACG TAGTG T GTC
                                     _    G _
GAM1930  GNAI3   3'  ATCATACTACATCAGCAG    47513        CATC  G
                                ATCATGC   AC ATCAGCAG
                                |||||||   || ||||||||
                                TAGTATG   TG TAGTCGTC
                                    A___  _
GAM1930  LGR6    5'  GCCAGCGAACACGGTCAGCAGC 47514      T____   A
                                GCCA    CACG TCAGCAGC
                                ||||    |||| ||||||||
                                CGGT    GTGC AGTCGTCG
                                  CGCTT   C
GAM1930  RUNX1   3'  CATGTGTCAAAATCAGCAG   47515     CCA   C
                                CATG   TCA GATCAGCAG
                                ||||   ||| |||||||||
                                GTAC   AGT TTAGTCGTC
                                  AC_   T
GAM1930  SAS     3'  ATCATGCCATTGCACTCCAGC  47516         __   GA
                                ATCATGCCAT  CAC  TCAGC
                                ||||||||||  |||  |||||
                                TAGTACGGTA  GTG  GGTCG
                                     AC   A_
GAM1930  ZFP161  3'  CATCATCCTGGGTGTCAGCAGC 47517       G  ATCACGA
                                CATCAT CC      TCAGCAGC
                                |||||| ||      ||||||||
                                GTAGTA GG      AGTCGTCG
                                   _ ACCCAC_
GAM1930  ZNF157  3'  TCATGCCATTGCACTCCAGC   47518        __   GA
                                TCATGCCAT  CAC  TCAGC
                                |||||||||  |||  |||||
                                AGTACGGTA  GTG  GGTCG
                                     AC   A_
GAM1930  ZNF36   3'  CATCATACTGTTCAGCAG    47519        CATCACGA
                                CATCATGC       TCAGCAG
                                ||||||||       |||||||
                                GTAGTATG       AGTCGTC
                                     ACA_____
GAM1930  C11orf25 3'  CATCATGCAGTCACTCAGCAGC 47520        CA    GA
                                CATCATGC  TCAC  TCAGCAGC
                                ||||||||  ||||  ||||||||
                                GTAGTACG  AGTG  AGTCGTCG
                                     TC   __
GAM1930  FLJ11196 3'  CATCAGCCATCATCAAAATAGT 47521      T      _   TC_  CA
            GGC                    CATCA GCCATCA CGA   AG  GC
                                |||||  ||||||| |||   ||  ||
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                                GTAGT CGGTAGT GTT   TC  CG
                                  _     A   TTA  AC
GAM1930  FLJ13441  3'  CATCATGCCATGTCAGGGCAGC 47522         CACGA  __
                                CATCATGCCAT    TCA  GCAGC
                                ||||||||||    |||  |||||
                                GTAGTACGGTA    AGT  CGTCG
                                     C____   CC
GAM1930  FLJ20034  3'  ATCATGCCATTGTACTCCAGC  47523         C__  GA
                                ATCATGCCAT   AC  TCAGC
                                ||||||||||   ||  |||||
                                TAGTACGGTA   TG  GGTCG
                                     ACA  A_
GAM1930  FLJ22353  3'  CATGCCACAGGAATCAGCAGC  47524        CAC
                                CATGCCAT   GATCAGCAGC
                                ||||||||   ||||||||||
                                GTACGGTG   TTAGTCGTCG
                                    TCC
GAM1930  H2AFJ    3'  CATCGTGCCATCAGAGC    47525     A      C  TCA
                                CATC TGCCATCA GA   GC
                                |||| ||||||| ||   ||
                                GTAG ACGGTAGT CT   CG
                                  C      _ ___
GAM1930  KIAA1922  5'  ATCATGCCATTGCACTCCAGC  47516         __  GA
                                ATCATGCCAT  CAC  TCAGC
                                ||||||||||  |||  |||||
                                TAGTACGGTA  GTG  GGTCG
                                     AC   A_
GAM1930  NKD2     3'  CATCATGCCAGCACCTGCAG   47526         T   GATCA
                                CATCATGCCA CAC    GCAG
                                |||||||||| |||    ||||
                                GTAGTACGGT GTG    CGTC
                                     C   GA___
GAM1930  NTF2     3'  CATCATGCACAACACCTCAGTG 47527        _ T   GA   CA
            GC                    CATCATGC CA CAC  TCAG  GC
                                |||||||| || |||  ||||  ||
                                GTAGTACG GT GTG  AGTC  CG
                                     T  T   G_   AC
GAM1930  OSBPL2   3'  ATCATGCCATTGCACTCCAGC  47516         __  GA
                                ATCATGCCAT  CAC  TCAGC
                                ||||||||||  |||  |||||
                                TAGTACGGTA  GTG  GGTCG
                                     AC   A_
GAM1930  OSBPL2   3'  ATCATGCCATTGCACTCCAGC  47516         __  GA
                                ATCATGCCAT  CAC  TCAGC
                                ||||||||||  |||  |||||
                                TAGTACGGTA  GTG  GGTCG
                                     AC   A_
GAM1930  PRO1866  5'  TGCTACTGATTCAGCAGC    47528     C  CAC  _
                                TGC AT   GAT CAGCAGC
                                ||| ||   ||| |||||||
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                                ACG TG   CTA GTCGTCG
                                  A  A__   A
GAM1930  PRRG1    3'  CATTATATCCAATATCAGCAG  47529     C  _  TCACG
                                CAT ATG CCA    ATCAGCAG
                                ||| ||| |||    ||||||||
                                GTA TAT GGT    TAGTCGTC
                                  A   A   TA___
GAM1930  LOC112817 3'  ATCATGCCATTGCACTCCAGC  47516          __  GA
                                ATCATGCCAT  CAC  TCAGC
                                ||||||||||  |||  |||||
                                TAGTACGGTA  GTG  GGTCG
                                      AC   A_
GAM1930  LOC120114 3'  ATCATGCCATTGCACTCTAGC  47530          CA  A  _
                                ATCATGCCAT  CG TC AGC
                                ||||||||||  || || |||
                                TAGTACGGTA  GT AG TCG
                                      AC  G  A
GAM1930  LOC130951 5'  CACCGTGCCTGGCGGATCAGCA 47531     A   ATCAC
              GC                  CATC TGCC    GATCAGCAGC
                                ||||| ||||    ||||||||||
                                GTGG ACGG    CTAGTCGTCG
                                  C   ACCGC
GAM1930  LOC143425 3'  TCTGCCATCACACATCAGC   47532    A       _
                                TC TGCCATCACG ATCAGC
                                || ||||||||| ||||||
                                AG ACGGTAGTGT TAGTCG
                                 _       G
GAM1930  LOC148137 3'  ATCATGCCATTGTACTACAGC  47533          C__  GAT
                                ATCATGCCAT   AC   CAGC
                                ||||||||||   ||   ||||
                                TAGTACGGTA   TG   GTCG
                                      ACA  AT_
GAM1930  LOC157507 5'  CATCATGCCACTGCACTCCAGC 47534           __  GA
              AG                  CATCATGCCAT  CAC  TCAGCAG
                                ||||||||||  |||  |||||||
                                GTAGTACGGTG  GTG  GGTCGTC
                                      AC   A_
GAM1930  LOC201227 3'  ATCATCCAGGCTCAGCAG    47535      G   TCACGA
                                ATCAT CCA     TCAGCAG
                                ||||| |||     |||||||
                                TAGTA GGT     AGTCGTC
                                  _  CCG___
GAM1930  LOC203378 3'  CATGCCATCACACGCAGC    47536          AT
                                CATGCCATCACG  CAGC
                                ||||||||||||  ||||
                                GTACGGTAGTGT  GTCG
                                       GC
GAM1930  LOC219731 5'  TCTGTCATATTTCCAGCAGC   47537    A  C   CACGA
                                TC TG CAT    TCAGCAGC
                                || || |||    ||||||||
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                                AG AC GTA    GGTCGTCG
                                 _ A  TAAA_
GAM1930  LOC220766 5'  ATCATGCCTTGTATGATTGGCA 47538        ATCAC_  CA
           GC                    ATCATGCC    GAT  GCAGC
                                 ||||||||    |||  |||||
                                 TAGTACGG    CTA  CGTCG
                                     AACATA  AC
GAM1930  LOC221710 5'  CATCAGCAGCAGGACGATCAGC 47539      T  __  TC
           AGC                    CATCA GC  CA  ACGATCAGCAGC
                                 ||||| ||  ||  ||||||||||||
                                 GTAGT CG  GT  TGCTAGTCGTCG
                                    _ TC  CC
GAM1930  LOC222985 5'  CATCGTGTTGCCATGGCAATTC 47540     A___    CA   _
           AGC                    CATC   TGCCAT  CGAT CAGC
                                 ||||   ||||||  |||| ||||
                                 GTAG   ACGGTA  GTTA GTCG
                                   CACA    CC   A
GAM1930  LOC254423 3'  CACTGTGCCATCAGGAGTGGC  47541    CA      C  TCA
                                 CAT  TGCCATCA GA  GC
                                 |||  |||||||| ||  ||
                                 GTG  ACGGTAGT CT  CG
                                  AC      C  CAC
GAM1930  LOC257463 3'  ATCATGCCATTGCACTCCAGC  47516         __  GA
                                 ATCATGCCAT  CAC  TCAGC
                                 ||||||||||  |||  |||||
                                 TAGTACGGTA  GTG  GGTCG
                                      AC  A_
GAM1930  LOC91661  3'  TGCCCTCGTGATCAGCAGC   47542     A  AC
                                 TGCC TC  GATCAGCAGC
                                 |||| ||  ||||||||||
                                 ACGG AG  CTAGTCGTCG
                                   G  CA
GAM1930  LOC93408  5'  ATCATGCCATTGCGCTCCAGC  47543        CA  A_
                                 ATCATGCCAT  CG  TCAGC
                                 ||||||||||  ||  |||||
                                 TAGTACGGTA  GC  GGTCG
                                      AC  GA
GAM1931  CGI-96    3'  ACTCTGATGGGGCTGTTGGACG 47546    AC  ATACTAG
                                 ACT  GAT     TGTTGGACG
                                 |||  |||     |||||||||
                                 TGA  CTA     ACAACCTGC
                                  GA  CCCCG__
GAM1931  MIG-6     3'  ACTACGATGAGCTACTTCAGTG 47547       A___   __   TT
           GG                    ACTACGAT   TACT  AGTG  GG
                                 ||||||||   ||||  ||||  ||
                                 TGATGCTA   ATGA  TCAC  CC
                                     CTCG   AG   __
GAM1931  LOC91695  3'  ACTCTGATGGGGCTGTTGGACG 47546    AC  ATACTAG
                                 ACT  GAT     TGTTGGACG
                                 |||  |||     |||||||||
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                                TGA  CTA      ACAACCTGC
                                  GA   CCCCG__
GAM1932  TFAP2C    3'  ATTGTTGATCTGTTGATC    47550      GG   C     C
                                GTTG  TGA TCTGT GATC
                                ||||  ||| ||||| ||||
                                TAAC  ACT AGACA CTAG
                                  A_  _    A
GAM1932  ALOX15B   3'  GTTGGGTGACCATAAGGTCCA  47551           C  TCGA
                                GTTGGGTGACT TG    TCCA
                                |||||||||| ||    ||||
                                CAACCCACTGG AT    AGGT
                                       T  TCC_
GAM1932  FLJ20374  3'  GCTGGGTGGCTTTAACCC    47552         ACT  GTC
                                GTTGGGTG   CT   GATCC
                                ||||||||   ||   |||||
                                CGACCCAC   GA   TTGGG
                                     C__  AA_
GAM1932  GRIN3A    3'  CGATGGGTGACTGCTGATC    47553    T       _  _
                                CG TGGGTGACT CTG TC
                                || |||||||| ||| ||
                                GC ACCCACTGA GAC AG
                                 T       C   T
GAM1932  HUMZD58C02 5'  CGTTGGGTCGCGGGTCC     47554         GACTC  T  A_
                                CGTTGGGT     TG CG  TCC
                                ||||||||     || ||  |||
                                GCAACCCA     GC GC  AGG
                                     ______  _  CC
GAM1932  KIAA1458  3'  GTTTGATGATCTCTGTCG     47555     G    _
                                GTT GGTGA CTCTGTCG
                                ||| ||||| ||||||||
                                CAA CTACT GAGACAGC
                                  A    A
GAM1932  TCBAP0758 3'  GTTGGGGATTCAGATGAGATCC 47556        T  C  TGTC__
           A                     GTTGGG GA TC      GATCCA
                                ||||||  || ||      ||||||
                                CAACCC CT AG      CTAGGT
                                   _  A  TCTACT
GAM1932  LOC157653 5'  GTGGGTGACACCTGGTCC     47557    T      _    TCGA
                                GT GGGTGAC TCTG    TCC
                                || |||||| ||||    |||
                                CA CCCACTG GGAC    AGG
                                 _      T    C___
GAM1932  LOC196410 3'  ACGTTGGGAGACTAGTC      47558         T    CT
                                ACGTTGGG GACT  GTC
                                |||||||| ||||  |||
                                TGCAACCC CTGA  CAG
                                     T    T_
GAM1932  LOC219942 3'  GTTGGGTGACTCCCTTCC     47559            GT GA
                                GTTGGGTGACTCT  C  TCC
                                ||||||||||||  |  |||
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                                CAACCCACTGAGG  G  AGG
                                       __ A_
GAM1932  LOC257443 3'  GTTTGATGATCTCTGTCG    47555     G    _
                                GTT GGTGA CTCTGTCG
                                ||| ||||| ||||||||
                                CAA CTACT GAGACAGC
                                  A    A
GAM1933  BAK1     3'  TCTACACCCCTGGATTACACTG 47562         A  AAT
                                TCTGCACC CC   GATTACACTG
                                |||||||| ||   ||||||||||
                                AGATGTGG GG   CTAATGTGAC
                                     _ AC_
GAM1933  MTR      3'  TCTGCACCATGACAC       47563          CCAA   TTA
                                TCTGCACCA    TGA   CAC
                                |||||||||    |||   |||
                                AGACGTGGT    ACT   GTG
                                       _____   ___
GAM1933  NBS1     3'  TCTGCACCACTGAAGCCA    47564          CAA   TTA
                                TCTGCACCAC   TGA   CA
                                ||||||||||   |||   ||
                                AGACGTGGTG   ACT   GT
                                       ___   TCG
GAM1933  TNFSF8   3'  TCTGCCCACCACACTACA    47565      A     ATG
                                TCTGC CCACCA   ATTACA
                                ||||| ||||||   ||||||
                                AGACG GGTGGT   TGATGT
                                   _     G__
GAM1933  DKFZP586C1619 5'  TCTGCACCACCGAGTACCGCGA 47566          AAT  T  _____
           CTG                    CTGCACCACC   GA TAC    ACTG
                                ||||||||||   || |||    ||||
                                GACGTGGTGG   CT ATG    TGAC
                                      ___  C   GCGC
GAM1933  FLJ10849  3'  TGCTACCAATGATACA      47567     ACC        T
                                TGC   ACCAATGAT ACA
                                |||   ||||||||| |||
                                ACG   TGGTTACTA TGT
                                  A__        _
GAM1933  FLJ12505  3'  TCTGCAGCCAGAGGTTACACTG 47568        _   CCAATGA
                                TCTGCA CCA      TTACACTG
                                |||||| |||      ||||||||
                                AGACGT GGT      AATGTGAC
                                   C   CTCC___
GAM1933  FLJ23189  3'  TCTTCACCACCAATGGAGCCAC 47569     G         ATTA
           TG                     TCT CACCACCAATG    CACTG
                                ||| ||||||||||    |||||
                                AGA GTGGTGGTTAC    GTGAC
                                  A         CTCG
GAM1933  KIAA0367  3'  TGCACCACTACACTGAACACTG 47570         __  A   TT
                                TGCACCAC  CA TGA  ACACTG
                                ||||||||  || |||  ||||||
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                                ACGTGGTG  GT ACT  TGTGAC
                                    AT  G  __
GAM1933  N4BP1    3'  TCTGTACAACTGCGTTTACACT 47571     C  C  CAA  A
             G                   TCTG AC AC   TG TTACACTG
                                 |||| || ||   || ||||||||
                                 AGAC TG TG   GC AATGTGAC
                                   A  T  AC_  A
GAM1933  NLP_1    5'  TCTGCACCGTTCGATGCCTGTT 47572        ACCA_   ATTAC_
             ACTG                 TCTGCACC    ATG     ACTG
                                  ||||||||    |||     ||||
                                  AGACGTGG    TAC     TGAC
                                     CAAGC   GGACAA
GAM1933  PELI2    3'  TCTGTCCACCAGTCACACT    47573     CA     ATGA
                                 TCTG  CCACCA    TTACACT
                                 ||||  ||||||    |||||||
                                 AGAC  GGTGGT    AGTGTGA
                                   A_     C___
GAM1933  TREX1    5'  TCTGACCACCTCCACATTACAC 47574     C     AA  _
             TG                   TCTG ACCACC  TG ATTACACTG
                                  |||| ||||||  || |||||||||
                                  AGAC TGGTGG  GT TAATGTGAC
                                    _     AG  G
GAM1933  TREX1    5'  TCTGACCACCTCCACATTACAC 47574     C     AA  _
             TG                   TCTG ACCACC  TG ATTACACTG
                                  |||| ||||||  || |||||||||
                                  AGAC TGGTGG  GT TAATGTGAC
                                    _     AG  G
GAM1933  LOC134265 3'  CTGCACCACCAATGCTTCAGCA 47575            A_  _
             CTG                    CTGCACCACCAATG  TTA CACTG
                                    ||||||||||||||  ||| |||||
                                    GACGTGGTGGTTAC  AGT GTGAC
                                           GA   C
GAM1933  LOC151304 3'  TCTGCACCTCAATGGTCA    47576        AC    A
                                 TCTGCACC  CAATG TTA
                                 ||||||||  ||||| |||
                                 AGACGTGG  GTTAC AGT
                                     A_    C
GAM1933  LOC152317 3'  TCTGGTTGCCAATGACCAGTAA 47577     CACCA       C__
             CTG                   TCTG    CCAATGATTA   ACTG
                                   ||||    ||||||||||   ||||
                                   AGAC    GGTTACTGGT   TGAC
                                     CAAC_        CAT
GAM1933  LOC202404 5'  TCTGTACCAATAACAC     47578     CACC     ATT
                                 TCTG   ACCAATG   ACAC
                                 ||||   |||||||   ||||
                                 AGAC   TGGTTAT   TGTG
                                   A___      ____
GAM1933  LOC50999  3'  TCTGCTAATATGTTACACTG   47579      ACCACCA   A
                                 TCTGC      ATG TTACACTG
                                 |||||      ||| ||||||||
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                                AGACG      TAC AATGTGAC
                                  ATTA___  _
GAM1934  DACH     3'  GTTGTTGTCAACATCCA     47582    CA       C
                                GT  TTGTCGGCA TCCA
                                ||  ||||||||| ||||
                                CA  AACAGTTGT AGGT
                                 AC       _
GAM1934  ROCK2    3'  AATCATTGTTGGTTCAACC    47583        C  CAC  C
                                AGTCATTGT GG   TC ACC
                                ||||||||| ||   || |||
                                TTAGTAACA CC   AG TGG
                                     A  A__  T
GAM1934  TLR1     3'  AGTCATTGTTGGAACTTCC    47584        C  C  _
                                AGTCATTGT GG ACT CC
                                ||||||||| || ||| ||
                                TCAGTAACA CC TGA GG
                                     A  T   A
GAM1934  ARHGEF9  3'  AGTCACTGTTGCCCATCCA    47585        CG  ACT   C
                                AGTCATTGT  GC   CCA CCA
                                |||||||||  ||   ||| |||
                                TCAGTGACA  CG   GGT GGT
                                     A_  ___   A
GAM1934  KIAA1826 5'  AATCATTGTCTTCCATTCA    47586        GGCAC    CC
                                AGTCATTGTC    TCCA  CA
                                ||||||||||    ||||  ||
                                TTAGTAACAG    AGGT  GT
                                     A____    AA
GAM1934  LOC145934 5'  AGTCATTGTCTCCATCCA    47587        GGCAC    C
                                AGTCATTGTC    TCCA CCA
                                ||||||||||    |||| |||
                                TCAGTAACAG    AGGT GGT
                                     _____    A
GAM1934  LOC150407 3'  AGTCCGGCACTCTGCCCA    47588     ATTGT      CA
                                AGTC    CGGCACTC  CCCA
                                ||||    ||||||||  ||||
                                TCAG    GCCGTGAG  GGGT
                                  _____       AC
GAM1934  LOC153711 5'  GTCGTCGTCCACCACCCA    47589     A    G CACT
                                GTC TTGTC G    CCACCCA
                                ||| ||||| |    |||||||
                                CAG AGCAG T    GGTGGGT
                                  C    G ____
GAM1934  LOC158549 5'  AGCCATTGTTCCTGTCCA    47590        CGGCAC   AC_
                                AGTCATTGT     TCC   CCA
                                |||||||||     |||   |||
                                TCGGTAACA     AGG   GGT
                                     _______  ACA
GAM1934  LOC158969 3'  AGGTATTGTGGTCCACCCA    47591    TC    C  CAC
                                AG  ATTGT GG   TCCACCCA
                                ||  ||||| ||   ||||||||
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                                TC  TAACA CC   AGGTGGGT
                                 CA    _ ___
GAM1934  LOC221688 5'  GTCATTGTCTCTCTTGCCCAT  47592        GGCA   CA_
                                GTCATTGTC   CTC   CCCAT
                                |||||||||   |||   |||||
                                CAGTAACAG   GAG   GGGTA
                                     A___   AAC
GAM1934  LOC256444 5'  AGTCATTGTCTCCATCCA    47587        GGCAC   C
                                AGTCATTGTC    TCCA CCA
                                ||||||||||    |||| |||
                                TCAGTAACAG    AGGT GGT
                                     _____   A
GAM1934  LOC51015  3'  AATCATTGTTGGTACGTCA   47593        C  C  TC
                                AGTCATTGT GG AC  CA
                                ||||||||| || ||  ||
                                TTAGTAACA CC TG  GT
                                     A  A  CA
GAM1935  JJAZ1     3'  ATATATGAAATAATTTCTAGA  47596       AA
                                GTATAT  GGATAGTTTCTAGA
                                ||||||  ||||||||||||||
                                TATATA  TTTATTAAAGATCT
                                   C_
GAM1935  PCM1      3'  AGTATGTAAGGACAGAGTTAGA 47597      A       TTTC
                                AGTAT TAAGGATAG   TAGA
                                ||||| |||||||||   ||||
                                TCATA ATTCCTGTC   ATCT
                                   C       TCA_
GAM1935  TGFBR2    5'  TAGTATACAAGTATAATTT   47598         G
                                TAGTATATAAG ATAGTTT
                                |||||||||| |||||||
                                ATCATATGTTC TATTAAA
                                     A
GAM1935  UBL3      3'  ATATATAAGTATTTCTAG    47599        GATA
                                GTATATAAG   GTTTCTAG
                                |||||||||   ||||||||
                                TATATATTC   TAAAGATC
                                     A___
GAM1935  BDG-29    3'  CAGTATATGGTTTTCTAG    47600       AA  ATAG
                                TAGTATAT  GG   TTTCTAG
                                ||||||||  ||   |||||||
                                GTCATATA  CC   AAAGATC
                                    __  A___
GAM1936  FLRT2     3'  AGGGAGATTAAAACATATAAGT 47603      CATCT  TG
                                AGGGAGA    AG  ATATAAGT
                                |||||||    ||  ||||||||
                                TCCCTCT    TT  TATATTCA
                                    AAT__  TG
GAM1936  KIAA1821  3'  AGAGAGACATTTACAGTG    47604        C__
                                AGGGAGACAT   TAGTG
                                ||||||||||   |||||
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                                TCTCTCTGTA   GTCAC
                                     AAT
GAM1936  LOC123872 3'  AGGGAGACATTTATGAT     47605         CTA
                                AGGGAGACAT   GTGAT
                                ||||||||||   |||||
                                TCCCTCTGTA   TACTA
                                     AA_
GAM1937  MCP     3'  TATGGCTGTCAGAGTCC     47608       GC    AT
                                TATGGC  GTCG  GGTCC
                                ||||||  ||||  |||||
                                ATACCG  CAGT  TCAGG
                                   A_   C_
GAM1937  SOX12    3'  CACTGGCCAAGTCGATGGTCTC 47609      AT   GC_        C
            T                    CACT  GGC   GTCGATGGTC CT
                                ||||  |||   |||||||||| ||
                                GTGA  CCG   CAGCTACCAG GA
                                  __  GTT         A
GAM1937  XYLB     3'  CACTTGGGAGATGGTCCC    47610      A   CGCGTC
                                CACT TGG     GATGGTCCC
                                |||| |||     |||||||||
                                GTGA ACC     CTACCAGGG
                                  _  CT_____
GAM1937  DKFZp762L0311 3'  CACTGTCTTGGTGTCGATGGTC 47611      A___   CGC
                                CACT    TGG   GTCGATGGTC
                                ||||    |||   ||||||||||
                                GTGA    ACC   CAGCTACCAG
                                  CAGA   A__
GAM1937  LOC153577 5'  TATGGCCGTGGTCCC       47612       G   CGAT
                                TATGGC CGT    GGTCCC
                                |||||| |||    ||||||
                                ATACCG GCA    CCAGGG
                                   _   ____
GAM1937  LOC157860 3'  CATGGTGTCTCGATGGTTCCT  47613       CGCG       C
                                TATGG    TCGATGGT CCT
                                |||||    |||||||| |||
                                GTACC    AGCTACCA GGA
                                   ACAG       A
GAM1938  DRG2     3'  GAAGGGCCCCCAACCCAA    47616      AA    G
                                GAAG  CCTC TGACCCAA
                                ||||  |||| ||||||||
                                CTTC  GGGG GTTGGGTT
                                  CC    _
GAM1938  MAPK14   3'  GAAACACCTTGGCCCAAATAC  47617      A    CG  A
                                GAAG ACCT  TG CCCAAATAC
                                |||| ||||  || |||||||||
                                CTTT TGGA  AC GGGTTTATG
                                  G   __ C
GAM1938  MAPK14   3'  GAAACACCTTGGCCCAAATAC  47617      A    CG  A
                                GAAG ACCT  TG CCCAAATAC
                                |||| ||||  || |||||||||
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                                CTTT TGGA  AC GGGTTTATG
                                  G   __ C
GAM1938 MAPK14   3' GAAACACCTTGGCCCAAATAC 47617     A   CG  A
                                GAAG ACCT  TG CCCAAATAC
                                |||| ||||  || |||||||||
                                CTTT TGGA  AC GGGTTTATG
                                  G   __ C
GAM1938 NSF      3' AGACCTTTAACCAAATAC    47618    A  CG   C
                                AGA CCT  TGACC AAATAC
                                ||| |||  ||||| ||||||
                                TCT GGA  ATTGG TTTATG
                                  _  A_   _
GAM1938 RET      3' TGAAGAACCAAAACTTCAA   47619        TCGT  C_
                                TGAAGAACC   GAC  CAA
                                |||||||||   |||  |||
                                ACTTCTTGG   TTG  GTT
                                      TT__   AA
GAM1938 SLC10A2  3' TGAAGAGCTCTTTGCCAAATAC 47620      AC   GTGAC
                                TGAAGA  CTC    CCAAATAC
                                ||||||  |||    ||||||||
                                ACTTCT  GAG    GGTTTATG
                                   C_   AAAC_
GAM1938 ZNF266   3' TGAAAACCCTATGTCCAAATAC 47621      A   CG  AC
                                TGAAGA CCT  TG  CCAAATAC
                                |||||| |||  ||  ||||||||
                                ACTTTT GGG  AC  GGTTTATG
                                   _  AT  A_
GAM1938 BICD2    3' TGAAAAACCCCAGAATCTGAAT 47622          T  CCCA_
            AC                    TGAAGAACCTCG GA    AATAC
                                ||||||||||||| ||    |||||
                                ACTTTTTGGGGT CT    TTATG
                                      _ TAGAC
GAM1938 GRP3     3' TGAAGACTGCCCCAAATA    47623      AC  C  GA
                                TGAAGA  CT GT  CCCAAATA
                                ||||||  || ||  ||||||||
                                ACTTCT  GA CG  GGGTTTAT
                                   __  _  __
GAM1938 KIAA0630 3' TGAAGAAACTCCAAAT     47624      ACCTCGT  _
                                TGAAGA     GAC CCAAAT
                                ||||||     ||| ||||||
                                ACTTCT     TTG GGTTTA
                                   _______  A
GAM1938 KIAA0769 3' TGAAAAATACCCAAAT     47625      CCTCGTG
                                TGAAGAA     ACCCAAAT
                                |||||||     ||||||||
                                ACTTTTT     TGGGTTTA
                                   A______
GAM1938 KIAA0895 3' TGAAGAACCATTTGAATCCA  47626        TCG  C_
                                TGAAGAACC   TGA  CCA
                                |||||||||   |||  |||
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                                ACTTCTTGG  ACT  GGT
                                     TAA  TA
GAM1938 SS-56    3' GAAGTTTCAGACCCAAATA   47627     AACC  T
                                GAAG   TCG GACCCAAATA
                                ||||   ||| ||||||||||
                                CTTC   AGT CTGGGTTTAT
                                  AA__  _
GAM1938 SUCLA2   3' TGAAGAACTTTGTATCCAA   47628       CTC  AC
                                TGAAGAAC  GTG  CCAA
                                ||||||||  |||  ||||
                                ACTTCTTG  CAT  GGTT
                                     AAA  A_
GAM1938 UNC5D    3' TGAGGAGTTAACCCAAAT    47629    A  ACCTCG
                                TGA GA     TGACCCAAAT
                                ||| ||     ||||||||||
                                ACT CT     ATTGGGTTTA
                                  C  CA____
GAM1938 ZMPSTE24 3' TGAAGACATCACCCAAAT    47630      ACCT  G
                                TGAAGA   CGT ACCCAAAT
                                ||||||   ||| ||||||||
                                ACTTCT   GTA TGGGTTTA
                                    ____  G
GAM1938 LOC121838 5' AGGGACCCTATCCCCAAATAC 47631    A_   CG GA
                                AG  ACCT  T  CCCAAATAC
                                ||  ||||  |  |||||||||
                                TC  TGGG  A  GGGTTTATG
                                 CC   AT G_
GAM1938 LOC149010 3' TGAAAACCACCCTCCCAAATAC 47632      A  TCGTGA
                                TGAAGA CC     CCCAAATAC
                                |||||| ||     |||||||||
                                ACTTTT GG     GGGTTTATG
                                   _  TGGGA_
GAM1938 LOC200933 3' TGAAGGCCCTCATGACCCA   47633      AA
                                TGAAG  CCTCGTGACCCA
                                |||||  ||||||||||||
                                ACTTC  GGAGTACTGGGT
                                   CG
GAM1939 DAP      3' TGGCATTGCTGTTCCCTGCC   47636     CGA      ATA
                                TGGCA   CTGTTCCT   TGCT
                                |||||   ||||||||   ||||
                                ACCGT   GACAAGGG   ACGG
                                   AAC      ___
GAM1939 KIAA0442 3' TGTTACGGCTGTTCCCAGACT 47637    GC   A      TAT
                                TG  ACG CTGTTCCTA   GCT
                                ||  ||| |||||||||   |||
                                AC  TGC GACAAGGGT   TGA
                                 AA   C       C__
GAM1939 SIX1     5' GGCGCGGCTGTTCCTAACCTC  47638    A  A       TATG
                                GGC CG CTGTTCCTA    CTC
                                ||| || |||||||||    |||
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                                CCG GC GACAAGGAT    GAG
                                  C  C        TG__
GAM1939  DAMS     5'  GATTGTTCCTATACAGCT    47639    C         _
                                GA TGTTCCTATAT GCT
                                || |||||||||| |||
                                CT ACAAGGATATG CGA
                                 A          T
GAM1939  FLJ13612  3'  TGGCATGCTGTTCCTCCTG   47640      CGA       ATA
                                TGGCA   CTGTTCCT   TG
                                |||||   ||||||||   ||
                                ACCGT   GACAAGGA   AC
                                   AC_       GG_
GAM1939  KIAA0194  3'  TGGCTGACTGTTCCTCCCT   47641      AC        ATATG
                                TGGC  GACTGTTCCT    CT
                                ||||  ||||||||||    ||
                                ACCG  CTGACAAGGA    GA
                                  A_        GG___
GAM1939  KIAA0939  3'  TGGCACAACTGTAGATGGTGCT 47642           TCCTATA
              C                   TGGCACGACTGT      TGCTC
                                ||||||||||||      |||||
                                ACCGTGTTGACA      ACGAG
                                       TCTACC_
GAM1940  AQP6     3'  AAGCAGAGTGGCTGTCTG    47645      A       AAT
                                AAGCA GAGTGGCT   GTCTG
                                ||||| ||||||||   |||||
                                TTCGT CTCACCGA   CAGAC
                                  _      ____
GAM1940  AQP6     3'  AAGCAGAGTGGCTGTCTG    47645      A       AAT
                                AAGCA GAGTGGCT   GTCTG
                                ||||| ||||||||   |||||
                                TTCGT CTCACCGA   CAGAC
                                  _      ____
GAM1940  ARF4L    3'  TGAGTGAGAGTGGCGGCTG   47646   A  CA       TAAT T
                                C AG  AGAGTGGC    G CTG
                                | ||  ||||||||    | |||
                                A TC  TCTCACCG    C GAC
                                 C  AC       C____ _
GAM1940  CALM1    5'  GGAGCGAGGGTGGCTGCACCAG 47647   A   A  A     AA GT T
              C                   C AGC AG GTGGCT  T  C GC
                                | ||| || ||||||  |  | ||
                                C TCG TC CACCGA  G  G CG
                                 C   C  C     C_ TG T
GAM1940  CALU     3'  TGAGAAAGAGTAAAGAGCTAAT 47648   A  C     _____       C
              GTTTG                  C AG AAGAGT    GGCTAATGT TG
                                | || ||||||    ||||||||| ||
                                A TC TTCTCA    TCGATTACA AC
                                 C  T     TTTC        A
GAM1940  CDC23    3'  GCAAGATAATGTCTG       47649        GTGGC
                                GCAAGA     TAATGTCTG
                                ||||||     |||||||||
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                                CGTTCT    ATTACAGAC
                                      _____
GAM1940  DNMT3B   3'  AGCTAAGAGTGGCCCCTG    47650    _       AATG
                                AGC AAGAGTGGCT   TCTG
                                ||| ||||||||||   ||||
                                TCG TTCTCACCGG   GGAC
                                  A       ____
GAM1940  EXTL1    3'  CAGGCACGCAGTTAATGTCTGC 47651    A   AGA TG C
                                CA GCA   G  G TAATGTCTGC
                                || |||   |  | ||||||||||
                                GT CGT   C  C ATTACAGACG
                                 C   G__ GT A
GAM1940  GPLD1    3'  GAGTAAGCAGAATGTCTG    47652      _  T_
                                GAGTG GC  AATGTCTG
                                ||||| ||  ||||||||
                                CTCAT CG  TTACAGAC
                                   T  TC
GAM1940  RFXAP    3'  CAAACAAGAAATGTCT      47653         GTGGCT
                                CAAGCAAGA     AATGTCT
                                |||||||||     |||||||
                                GTTTGTTCT     TTACAGA
                                      _______
GAM1940  RPL10    3'  CAAGGAGGGTGGTTAATCTGC  47654     CA  A    CTAAT
                                CAAG  AG GTGG    GTCTGC
                                ||||  || ||||    ||||||
                                GTTC  TC CACC    TAGACG
                                  C_  C    AAT__
GAM1940  SECTM1   3'  CAAGCAAGCCGGTGTCTG    47655        AG   CTAA
                                CAAGCAAG  TGG    TGTCTG
                                ||||||||  |||    ||||||
                                GTTCGTTC  GCC    ACAGAC
                                    G_  _____
GAM1940  SPAG8    3'  GCAATGGCCACCATGTCTGC   47656     AGA      __
                                GCA   GTGGCTA  ATGTCTGC
                                |||   |||||||  ||||||||
                                CGT   TACCGGT  TACAGACG
                                  ___       GG
GAM1940  SPG4     3'  AACAATTGTTTAATGTCTG    47657       GAG  GC
                                AGCAA   TG  TAATGTCTG
                                |||||   ||  |||||||||
                                TTGTT   AC  ATTACAGAC
                                   A__  AA
GAM1940  TMEM2    3'  AAGTAAGAGTGACTCATTCCTG 47658     C        AATG
              C                  AAG AAGAGTGGCT    TCTGC
                                 ||| ||||||||||    |||||
                                 TTC TTCTCACTGA    GGACG
                                   A         GTAA
GAM1940  ABLIM    3'  CAAGCAAGAGCTGGTCTCATCT 47659          _  _  AA
              GC                   CAAGCAAGAG TGG CT  TGTCTGC
                                   |||||||||| ||| ||  |||||||
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                                GTTCGTTCTC ACC GA  GTAGACG
                                     G   A __
GAM1940  ABLIM     3'  CAAGCAAGAGCTGGTCTCATCT 47659          _  _ AA
              GC                   CAAGCAAGAG TGG CT  TGTCTGC
                                |||||||||| ||| ||  |||||||
                                GTTCGTTCTC ACC GA  GTAGACG
                                     G   A __
GAM1940  C20orf188 3'  CAGGCAGGAGCGGCTGCCT   47660    A   A      AAT
                                CA GCA GAGTGGCT   GTCT
                                || ||| ||||||||   ||||
                                GT CGT CTCGCCGA   CGGA
                                 C   C      ___
GAM1940  C6orf33   3'  CAGGCGTGATGGCTAATGTCTG 47661    A  AA  G
                                CA GC  GA TGGCTAATGTCTG
                                || ||  || ||||||||||||
                                GT CG  CT ACCGATTACAGAC
                                 C  CA  _
GAM1940  CL25084   3'  AAGCGAGACAAATGTCTG    47662     AA   TG  T
                                AAGC  GAG  GC AATGTCTG
                                ||||  |||  || ||||||||
                                TTCG  CTC  TG TTACAGAC
                                  __   __ T
GAM1940  DKFZp761B1514 3'  CAAGAACGATGTCTGC     47663        GCTA
                                CAAGAGTG    ATGTCTGC
                                ||||||||    ||||||||
                                GTTCTTGC    TACAGACG
                                     _____
GAM1940  DKFZp761N1114 3'  AGATAAGCTATTGATGTCTGC  47664     GT    ___
                                AGA  GGCTA   ATGTCTGC
                                |||  |||||   ||||||||
                                TCT  TCGAT   TACAGACG
                                  AT    AAC
GAM1940  E2F5      3'  AAGTGGCAGTGAACGTCTG   47665        T___
                                GAGTGGC    AATGTCTG
                                |||||||    ||||||||
                                TTCACCG    TTGCAGAC
                                    TCAC
GAM1940  ESDN      3'  AGTAAGCTATAATGTCTG    47666     _   __
                                AGTG GCTA  ATGTCTG
                                |||| ||||  |||||||
                                TCAT CGAT  TACAGAC
                                  T    AT
GAM1940  FLJ10579  3'  AAGAAAGCAATGTCTG      47667      T   T
                                AAGAG GGC AATGTCTG
                                ||||| ||| ||||||||
                                TTCTT TCG TTACAGAC
                                   _  _
GAM1940  FLJ10702  3'  AAGCAAGTAGTGTCT       47668      AG    CTAA
                                AAGCA  AGTGG   TGTCT
                                |||||  |||||   |||||
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                                TTCGT  TCATC    ACAGA
                                  __   _____
GAM1940  FLJ12688  3'  AGCCAAGGGTGGCCAGTTCTGC 47669     _  A      ATG
                                AGC AAG GTGGCTA   TCTGC
                                ||| ||| |||||||   |||||
                                TCG TTC CACCGGT   AGACG
                                  G   C      CA_
GAM1940  FLJ20013  3'  AGACGCCCAGCTAATGTTTG   47670     _ __       C
                                AGA GT  GGCTAATGT TG
                                ||| ||  |||||||||| ||
                                TCT CG  TCGATTACA AC
                                  G  GG        A
GAM1940  FLJ21742  3'  AAAAGCGCAGATGTCTGC    47671        G TA
                                AAGAGTG C  ATGTCTGC
                                |||||||  |  ||||||||
                                TTTTCGC G  TACAGACG
                                    _ TC
GAM1940  KIAA0513  3'  AGCAGGAGTGGCTCTGGGTGC  47672      A       AA  TC
                                AGCA GAGTGGCT  TG  TGC
                                |||| ||||||||  ||  |||
                                TCGT CTCACCGA  AC  ACG
                                  C       G_  CC
GAM1940  KIAA1198  3'  CAGGCAGAGTGGCTCACGCCTG 47673    A   A       A
                                CA GCA GAGTGGCT ATGTCTG
                                || ||| |||||||| |||||||
                                GT CGT CTCACCGA TGCGGAC
                                 C   _       G
GAM1940  KIAA1853  3'  CAAGCAAGATGGCTGATGC    47674         G     A
                                CAAGCAAGA TGGCT ATGT
                                ||||||||| ||||| ||||
                                GTTCGTTCT ACCGA TACG
                                      _    C
GAM1940  KIAA1854  3'  CAAGGGGTAAATAATGTCTGC  47675      A_    C
                                CAAG  GTGG TAATGTCTGC
                                ||||  |||| ||||||||||
                                GTTC  CATT ATTACAGACG
                                  CC    T
GAM1940  KIAA1944  3'  GAGTGAGAACCAATGTCTG    47676      ___
                                GAGTG   GCTAATGTCTG
                                |||||   ||||||||||
                                CTCAC   TGGTTACAGAC
                                   TCT
GAM1940  MFN1      3'  AGCAAAAGTGGTAGCTATTTG  47677          CTAA   C
                                AGCAAGAGTGG    TGT TG
                                ||||||||||    ||| ||
                                TCGTTTTCACC    ATA AC
                                       ATCG   A
GAM1940  MGC13016  3'  GCAGGGAATGATGTCTGC    47678     A_    GCTA
                                GCA  GAGTG    ATGTCTGC
                                |||  |||||    ||||||||
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                                CGT  CTTAC    TACAGACG
                                  CC    ____
GAM1940  MGC14288  3'  AGCAAATTATTTAATGTCTG   47679       AG  GC
                                AGCAAG  TG  TAATGTCTG
                                ||||||  ||  |||||||||
                                TCGTTT  AT  ATTACAGAC
                                   A_  AA
GAM1940  MGC16491  3'  CAGGCAGGAGGGCTCCTTGC   47680    A   A   T    AA_
                                CA GCA GAG GGCT   TGT
                                || ||| ||| ||||   |||
                                GT CGT CTC CCGA   ACG
                                 C   C   _    GGA
GAM1940  MGC16703  3'  AGCTGGGACCACAGGTGTCTGC 47681     AA_  G G  TAA
                                AGC   GA T GC   TGTCTGC
                                |||   || | ||   |||||||
                                TCG   CT G TG   ACAGACG
                                  ACC  _ G  TCC
GAM1940  MGC20496  3'  TGACTAAGAAGGTAATGTTTGC 47682   A  _    T  C     C
                                A GC AAGAG GG TAATGT TGC
                                | || ||||| || ||||||| |||
                                A TG TTCTT CC ATTACA ACG
                                 C  A    _  _     A
GAM1940  PCYT2     3'  AAGGAGAGTGGCGAAGCTGC   47683     CA       T  T T
                                AAG  AGAGTGGC AA G CTGC
                                |||  |||||||| || | ||||
                                TTC  TCTCACCG TT C GACG
                                  C_       C  _ _
GAM1940  PTD012    3'  AGCCAACTAGTTGCTAATGTTT 47684     AAG__   G       C
            G                    AGC     AGT GCTAATGT TG
                                |||     ||| |||||||| ||
                                TCG     TCA CGATTACA AC
                                  GTTGA   A       A
GAM1940  PTPRR     3'  TGAGCAGAACAGCTAGTGTTTG 47685   A   A   TG   A   C
            C                    C AGCA GAG  GCTA TGT TGC
                                | |||| |||  |||| ||| |||
                                A TCGT CTT  CGAT ACA ACG
                                 C   _   GT    C   A
GAM1940  PTPRR     3'  TGAGCAGAACAGCTAGTGTTTG 47685   A   A   TG   A   C
            C                    C AGCA GAG  GCTA TGT TGC
                                | |||| |||  |||| ||| |||
                                A TCGT CTT  CGAT ACA ACG
                                 C   _   GT    C   A
GAM1940  SIAT4B    5'  GCAGGAGTGGCTGTCC      47686     A       AAT
                                GCA GAGTGGCT   GTCT
                                ||| ||||||||   ||||
                                CGT CTCACCGA   CAGG
                                  C       ___
GAM1940  SLC25A18  3'  CAGGCCAGAGTGGCCCCACCTG 47687    A  A        AA GT
            C                    CA GC AGAGTGGCT  T  CTGC
                                || || |||||||||  |  ||||
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                                GT CG TCTCACCGG  G  GACG
                                 C  G        G_ TG
GAM1940  ST7L     3'  TGAGTGAGAATGGCTATCATTG 47688    A  CA        A   C
              C                   C AG  AGAGTGGCTA TGT TGC
                                | ||  |||||||||| ||| |||
                                A TC  TCTTACCGAT GTA ACG
                                 C  AC         A   _
GAM1940  ST7L     3'  TGAGTGAGAATGGCTATCATTG 47688    A  CA        A   C
              C                   C AG  AGAGTGGCTA TGT TGC
                                | ||  |||||||||| ||| |||
                                A TC  TCTTACCGAT GTA ACG
                                 C  AC         A   _
GAM1940  LOC144266 5'  AGCTGTGCTAATGTTTG     47689     AAGA   G      C
                                AGC    GTG CTAATGT TG
                                |||    ||| ||||||| ||
                                TCG    CAC GATTACA AC
                                  A___   _      A
GAM1940  LOC144667 3'  GCGAAGTGGCTCACATCTG    47690    AA       A
                                GC  GAGTGGCT ATGTCTG
                                ||  |||||||| |||||||
                                CG  TTCACCGA TGTAGAC
                                 C_       G
GAM1940  LOC145501 3'  TGAGAAGAGTGGCCCTTCCTCT 47691    A  C        AATG_
              GC                  C AG AAGAGTGGCT     TCTGC
                                | || ||||||||||     |||||
                                A TC TTCTCACCGG     AGACG
                                 C  _         GAAGG
GAM1940  LOC147639 5'  CAAGCAAGGGGATGTTTG    47692        AGT  CTA    C
                                CAAGCAAG   GG   ATGT TG
                                ||||||||   ||   |||| ||
                                GTTCGTTC   CC   TACA AC
                                     C__  ____    A
GAM1940  LOC147694 3'  TGACAAGAAAAAATGTCTG    47693    A      TGGCT
                                A GCAAGAG     AATGTCTG
                                | |||||||     ||||||||
                                A TGTTCTT     TTACAGAC
                                 C      TT___
GAM1940  LOC152215 3'  AGCAAGGGGTCTAGATGTCTGC 47694        AGT  _   _
                                AGCAAG   GG CTA ATGTCTGC
                                ||||||   || ||| ||||||||
                                TCGTTC   CC GAT TACAGACG
                                   C__  A   C
GAM1940  LOC158709 3'  CAATGGGAGAATAAATGTCTG  47695     GCA_     GCT
                                CAA    AGAGTG   AATGTCTG
                                |||    ||||||   ||||||||
                                GTT    TCTTAT   TTACAGAC
                                  ACCC      ___
GAM1940  LOC219287 5'  CAGGCAGGAAGCATGTCTG    47696    A   A  GT   TA
                                CA GCA GA  GGC  ATGTCTG
                                || ||| ||  |||  |||||||
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                                GT CGT CT  TCG  TACAGAC
                                 C   C __  __
GAM1940  LOC221466 3'  AGGAAAGAGTGGTCCTTCTGC  47697    C_      _ AATG
                                AG  AAGAGTGG CT    TCTGC
                                ||  |||||||| ||    |||||
                                TC  TTCTCACC GG    AGACG
                                 CT       A  A___
GAM1940  LOC254532 5'  GCAGAGTGGCTCACGCCTG   47698    A       A
                                GCA GAGTGGCT ATGTCTG
                                ||| |||||||| |||||||
                                CGT CTCACCGA TGCGGAC
                                  _      G
GAM1940  LOC56270  3'  AGAGTGGCCTGGTGTCTG    47699         AA_
                                AGAGTGGCT   TGTCTG
                                |||||||||   ||||||
                                TCTCACCGG   ACAGAC
                                      ACC
GAM1941  HMGCS2    3'  AAGAGGTCTTCTCTCCATTGC  47702          A  GCA   C
                                AAGAGGTCTTC TC   CAT GC
                                |||||||||||  ||   ||| ||
                                TTCTCCAGAAG AG   GTA CG
                                      _ AG_   A
GAM1941  KCNE2     3'  AAAGAGGTCTTCAGCACA    47703           TC
                                AAAGAGGTCTTCA  GCACA
                                ||||||||||||  |||||
                                TTTCTCCAGAAGT  CGTGT
                                       __
GAM1941  MYH11     3'  AAAGAGGTCTCGTTTCCTCGC  47704          CA_____
                                AAAGAGGTCTT     TCGC
                                ||||||||||      ||||
                                TTTCTCCAGAG     AGCG
                                      CAAAGG
GAM1941  TACSTD1   3'  AAAGATGTCTTCGTCCCAC   47705      G     A  G
                                AAAGA GTCTTC TC CAC
                                ||||| |||||| || |||
                                TTTCT CAGAAG AG GTG
                                   A     C  G
GAM1941  UBE4A     3'  AAAGAGTCTTCATTTTGC    47706       G      C__
                                AAAGAG TCTTCAT   GC
                                ||||||| |||||||  ||
                                TTTCTC AGAAGTA   CG
                                   _      AAA
GAM1941  C20orf28  3'  GGAGAGGTCTTCGATCCGC   47707   A        A__
                                A AGAGGTCTTC   TCGC
                                | ||||||||||  ||||
                                C TCTCCAGAAG   GGCG
                                 C         CTA
GAM1941  FLJ14213  3'  GGAGGGGTCCTCATCCTGGTTG 47708   A  A       _______
             C                   A AG GGTCTTCATC     GC
                                | || ||||||||||      ||
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                                C TC CCAGGAGTAG     CG
                                 C  C        GACCAA
GAM1941  KIAA0007  3'  GGAAAGGTCTTTATCTGCAC  47709   A       C  _
                                A AGAGGTCTT ATC GCAC
                                | ||||||||| ||| ||||
                                C TTTCCAGAA TAG CGTG
                                 C       A  A
GAM1941  KIAA1228  3'  AAAGAGGCTTTACAGTCGC   47710       TC  _ _
                                AAAGAGG  TT CA TCGC
                                |||||||  || || ||||
                                TTTCTCC  AA GT AGCG
                                    GA  T  C
GAM1941  LOC148915 3'  AAAGAAGTCTTCATCTCA    47711            G
                                AAAGAGGTCTTCATC CA
                                |||||||||||||| ||
                                TTTCTTCAGAAGTAG GT
                                          A
GAM1941  LOC203292 5'  AAAGAGGTTTCATTCTGC    47712       C    _ _
                                AAAGAGGT TTCAT C GC
                                |||||||| ||||| | ||
                                TTTCTCCA AAGTA G CG
                                    _    A A
GAM1942  NFIA    3'  GGCGTAATCCATTATAGTG   47715    AA   AT_
                                GGC  TGAT   TTATAGTG
                                |||  ||||   ||||||||
                                CCG  ATTA   AATATCAC
                                  C_   GGT
GAM1942  NOL4    3'  GCCCCTGATATTTATGGTG   47716   AA_       A
                                GC   TGATATTTAT GTG
                                ||   |||||||||| |||
                                CG   ACTATAAATA CAC
                                 GGG        C
GAM1942  PRO1575  5'  GGCGCTGACCCTGTTATAGTG  47717    AA   AT__
                                GGC  TGAT    TTATAGTG
                                |||  ||||    ||||||||
                                CCG  ACTG    AATATCAC
                                  CG   GGAC
GAM1942  LOC129127 5'  CAGCAATGGTCAGTAGTG    47718       ATA  TA
                                CGGCAATG   TT  TAGTG
                                ||||||||   ||  |||||
                                GTCGTTAC   AG  ATCAC
                                    C__  TC
GAM1942  LOC157798 5'  ACAGCGATGATATTTTAGTG  47719      A       A
                                ACGGC ATGATATTT TAGTG
                                ||||| ||||||||| |||||
                                TGTCG TACTATAAA ATCAC
                                  C       _
GAM1943  TRHDE    3'  TGAGAATATCATTTCTGTTTT  22422     A       AAA
                                TGA AATATCATT   TTGTTTT
                                ||| |||||||||   |||||||
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                                ACT TTATAGTAA   GACAAAA
                                  C       A__
GAM1943  B3GNT5    3'  TGAAAACGTCATTAAAATCAGC 22423       TA       TT__
                TT                  TGAAAA  TCATTAAA    GTTT
                                    ||||||  ||||||||    ||||
                                    ACTTTT  AGTAATTT    CGAA
                                       GC       TAGT
GAM1943  FLJ10607  3'  AAAACATTTAAATTGTTTTA   22424       CA
                                    AAAATAT  TTAAATTGTTTTA
                                    |||||||  ||||||||||||
                                    TTTTGTA  AATTTAACAAAAT
                                             __
GAM1943  FLJ20060  3'  TGAAGAATCATTAAGCCTGTTT 22425      AAT       A_
                                    TGAA   ATCATTAA  TTGTTT
                                    ||||   ||||||||  ||||||
                                    ACTT   TAGTAATT  GACAAA
                                      CT_       CG
GAM1943  FLJ23563  3'  TGAAAATTATCATTAATGATTT 22426        _       ATT
                TA                  TGAAAAT ATCATTAA   GTTTTA
                                    |||||||  ||||||||   ||||||
                                    ACTTTTA TAGTAATT   TAAAAT
                                       A       AC_
GAM1943  LOC148418 3'  GAAAATATCGTTACCCCATTT  22427         A   AA TG
                                    GAAAATATC TTA  T  TTT
                                    |||||||||  |||  |  |||
                                    CTTTTATAG AAT  G  AAA
                                          C   GG GT
GAM1943  LOC222001 3'  TGAAGAATCATTAAGCCTGTTT 22425      AAT       A_
                                    TGAA   ATCATTAA  TTGTTT
                                    ||||   ||||||||  ||||||
                                    ACTT   TAGTAATT  GACAAA
                                      CT_       CG
GAM1943  LOC56899  3'  AAAATTCACAAAATTGTTTT   22428      A    T
                                    AAAAT TCAT AAATTGTTTT
                                    |||||  ||||  ||||||||||
                                    TTTTA AGTG TTTAACAAAA
                                       _    T
GAM1944  ACCN1     3'  TGGGCAGCTTGGGGAAA     47723     AG    TATAT
                                    TGG  AGCT     TGGGGGAA
                                    |||  ||||     ||||||||
                                    ACC  TCGA     ACCCCTTT
                                      CG   _____
GAM1944  ACHE      3'  GGAGGGGGAGGTTGGGGGAAAA 47724      AGCTTATA
                                    GGAG       TTGGGGGAAAA
                                    ||||       ||||||||||
                                    CCTC       AACCCCCTTTT
                                      CCCCTCC_
GAM1944  ARG1      3'  TGTAGAGTTTATACTAATTGGA 47725    G   C       GG_
                AAA                 TG AGAG TTATATTG   GGAAAA
                                    || |||| ||||||||   ||||||
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                                AC TCTC AATATGAT   CCTTTT
                                 A   A       TAA
GAM1944 CACNG2   5' TGGAGAGTTATAAAAAAAGGGA 47726       C    TT__
                                TGGAGAG TTATA   GGGGGA
                                ||||||| |||||   ||||||
                                ACCTCTC AATAT   TTCCCT
                                    _   TTTT
GAM1944 CENTD2   5' GGAGGCCCCTGGGGGA     47727     A   ATA
                                GGAG GCTT   TTGGGGGA
                                |||| ||||  ||||||||
                                CCTC CGGG   GACCCCCT
                                  _   ____
GAM1944 CHRNB4   3' TGGGAAGCCCTGGGGGAA    47728    AG   TATA
                                TGG  AGCT   TTGGGGGAA
                                |||  ||||   |||||||||
                                ACC  TCGG   GACCCCCTT
                                  CT   _____
GAM1944 CNN1     3' TGGGGGCTTTGCTGGGGGA   47729    AGA   ATA
                                TGG   GCTT   TTGGGGGA
                                |||   ||||  ||||||||
                                ACC   CGAA   GACCCCCT
                                  CC_   AC_
GAM1944 DPYSL3   3' TGGGAAGCTTGTGGCAAGGAA 47730    AG    ATAT  __
                                TGG  AGCTT   TGG  GGGAA
                                |||  |||||   |||  |||||
                                ACC  TCGAA   ACC  TCCTT
                                  CT    C___  GT
GAM1944 EGR1     5' TGGAGAGCTGGTGTCGGGG   47731        TATA
                                TGGAGAGCT   TTGGGG
                                |||||||||   ||||||
                                ACCTCTCGA   AGCCCC
                                     CCAC
GAM1944 GRM1     5' TGGAGGCGTTTGTAAGGGAA  47732      A  TTATAT
                                TGGAG GC     TGGGGGAA
                                ||||| ||     ||||||||
                                ACCTC CG     ATTCCCTT
                                   _ CAAAC_
GAM1944 GSS      3' TGGAAAGCTGGGGGAA      47733         TATATT
                                TGGAGAGCT     GGGGGAA
                                |||||||||     |||||||
                                ACCTTTCGA     CCCCCTT
                                     _______
GAM1944 HAL      3' TGGAGAGCTTGTTGAAG     47734          ATA
                                TGGAGAGCTT   TTGGGG
                                ||||||||||   ||||||
                                ACCTCTCGAA   AACTTC
                                     C__
GAM1944 KCNJ4    3' TGAAGAGTCAGTGGGGGAA   47735       C   TAT
                                TGGAGAG TTA   TGGGGGAA
                                ||||||| |||   ||||||||
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                                ACTTCTC AGT   ACCCCCTT
                                   _  C__
GAM1944  LOXL2    3'  TGGAGGGTTTCATTGGAAGA  47736      AGC  A
                                TGGAG  TT TATTGGGGGA
                                |||||  || ||||||||||
                                ACCTC  AA GTAACCTTCT
                                   CC_  A
GAM1944  MAPK4    3'  TGGGAGTGTTGGGGGAA    47737    A  CTTATA
                                TGG GAG    TTGGGGGAA
                                ||| |||    |||||||||
                                ACC CTC    AACCCCCTT
                                  _  AC____
GAM1944  MASP1    3'  TGGAGGGCTTATATCTTGGA  47738      A       GGG
                                TGGAG GCTTATATT  GGA
                                ||||| |||||||||  |||
                                ACCTC CGAATATAG  CCT
                                   C       AA_
GAM1944  MGST2    5'  TGGGGACCGGGTGGGGGGAAA 47739    A  G  TATATT
                                TGG GA CT    GGGGGAAA
                                ||| || ||    ||||||||
                                ACC CT GG    CCCCCTTT
                                  C  _  CCCAC_
GAM1944  NFE2L1   3'  GAGAGCTTGTGTGTTTGGGGA  47740       ATA___
                                GAGAGCTT    TTGGGGG
                                ||||||||    |||||||
                                CTCTCGAA    AACCCCT
                                     CACACA
GAM1944  NID      3'  TGGGGGGCTAGTATTGGGAAAA 47741    AGA  TA    GG
                                TGG  GCT  TATTGGG  AA
                                |||  |||  |||||||  ||
                                ACC  CGA  ATAACCC  TT
                                  CCC  TC     TT
GAM1944  NRXN2    3'  TGGAGGGCTTGGGAAGA    47742      A   ATATT
                                TGGAG GCTT   GGGGGA
                                ||||| ||||   ||||||
                                ACCTC CGAA   CCTTCT
                                   C   C____
GAM1944  NRXN2    3'  TGGAGGGCTTGGGAAGA    47742      A   ATATT
                                TGGAG GCTT   GGGGGA
                                ||||| ||||   ||||||
                                ACCTC CGAA   CCTTCT
                                   C   C____
GAM1944  NRXN2    3'  TGGAGGGCTTGGGAAGA    47742      A   ATATT
                                TGGAG GCTT   GGGGGA
                                ||||| ||||   ||||||
                                ACCTC CGAA   CCTTCT
                                   C   C____
GAM1944  NSD1     3'  TGGAAAAGTTGGGGGAAA   47743       CTTATA
                                TGGAGAG    TTGGGGGAAA
                                |||||||    ||||||||||
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                              ACCTTTT     AACCCCCTTT
                                  C_____
GAM1944  PACE4    3'  GGAGAGTTTTGGGGAAA     47744       C  ATA
                              GGAGAG TT   TTGGGGGAA
                              |||||| ||   |||||||||
                              CCTCTC AA   AACCCCTTT
                                _  ____
GAM1944  PAWR     5'  TGGAGGAGCTTGTAGGGGA   47745      _    ATAT
                              TGGAG AGCTT    TGGGGGA
                              ||||| |||||    |||||||
                              ACCTC TCGAA    ATCCCCT
                                 C    C___
GAM1944  PCDHA9   3'  GAGAGCTTGTACTCTGAGA   47746        A    GG
                              GAGAGCTT TATT  GGGA
                              |||||||| ||||  ||||
                              CTCTCGAA ATGA  CTCT
                                   C    GA
GAM1944  PPP6C    3'  TGGGGATGGGATGGGGGAAAA  47747     A  GCTTATAT
                              TGG GA       TGGGGGAAAA
                              ||| ||       ||||||||||
                              ACC CT       ACCCCCTTTT
                                C  ACCCT___
GAM1944  SLC22A12 3'  TGGAGGGGCAGCCCTGGGGGA  47748      A_  TTATA
                              TGGAG  GC    TTGGGGGA
                              |||||  ||    ||||||||
                              ACCTC  CG    GACCCCCT
                                 CC  TCGG_
GAM1944  SLC4A4   3'  TGGAGAGCTCTATAAGTGAGAA 47749         A   T  _
                              TGGAGAGCTT TAT GG GGGAA
                              |||||||||| ||| || |||||
                              ACCTCTCGAG ATA TC CTCTT
                                    _  T  A
GAM1944  TFRC     3'  TGGAGGCTTATGGGGGAA    47750      A    TAT
                              TGGAG GCTTA   TGGGGGAA
                              ||||| |||||   ||||||||
                              ACCTC CGAAT   ACCCCCTT
                                _    ____
GAM1944  TMC1     5'  TGGAGGGCTTGTGAAAGAAA  47751      A   ATAT  GG
                              TGGAG GCTT    TG  GGAAA
                              ||||| ||||    ||  |||||
                              ACCTC CGAA    AC  TCTTT
                                 C    C___  TT
GAM1944  TNFRSF4  3'  TGGAAGAGTAGTGGGGGGAAA 47752     _  CTTATATT
                              TGGA GAG       GGGGGAAA
                              |||| |||       ||||||||
                              ACCT CTC       CCCCCTTT
                                T   ATCAC___
GAM1944  ZNF195   3'  TGGAGACTTATATTTCATGAAA 47753       G       GGGG
                              TGGAGA CTTATATT    GAAA
                              |||||| ||||||||    ||||
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                                ACCTCT GAATATAA   CTTT
                                   _      AGTA
GAM1944  AKAP7    3'  TGTAGAGCTTATGTCAAAG   47754   G       A TG
                                TG AGAGCTTAT T  GGG
                                || ||||||||| |  |||
                                AC TCTCGAATA A  TTC
                                 A        C GT
GAM1944  AKAP7    3'  TGTAGAGCTTATGTCAAAG   47754   G       A TG
                                TG AGAGCTTAT T  GGG
                                || ||||||||| |  |||
                                AC TCTCGAATA A  TTC
                                 A        C GT
GAM1944  AKAP7    3'  TGTAGAGCTTATGTCAAAG   47754   G       A TG
                                TG AGAGCTTAT T  GGG
                                || ||||||||| |  |||
                                AC TCTCGAATA A  TTC
                                 A        C GT
GAM1944  ARHGAP5  3'  TGGAGATAAGTTTGGGGGAA  47755      GCTTATA
                                TGGAGA     TTGGGGGAA
                                ||||||     |||||||||
                                ACCTCT     AACCCCCTT
                                   ATTCA__
GAM1944  C1orf27  5'  TGGAGATTTATGTTTGAAAG  47756      GC   A_  GG
                                TGGAGA  TTAT  TTG  GG
                                ||||||  ||||  |||  ||
                                ACCTCT  AATA  AAC  TC
                                   A_   CA   TT
GAM1944  CECR7    3'  GAGAGCTTATGGAATAGGAGA 47757        AT__
                                GAGAGCTTAT   TGGGGGA
                                ||||||||||   |||||||
                                CTCTCGAATA   ATCCTCT
                                      CCTT
GAM1944  CNTN6    3'  TGGAGAGCATATATACAGAA  47758       T    T G
                                TGGAGAGC TATAT G GGGA
                                |||||||| ||||| | ||||
                                ACCTCTCG ATATA T TCTT
                                     T    _ G
GAM1944  CTBS     3'  TGGAGGGTTGGGGGAAA    47759     AGCTTATA
                                TGGAG      TTGGGGGAAA
                                |||||      ||||||||||
                                ACCTC      AACCCCCTTT
                                  CC_______
GAM1944  DKFZp434F142 3'  TGGAGAGCTTGATTTGAGAA  47760        ATA
                                TGGAGAGCTT   TTGGGGG
                                ||||||||||   |||||||
                                ACCTCTCGAA   AACTCTT
                                      CTA
GAM1944  DNAL4    3'  TGGGGTCAAGTTGGGGGAA  47761    AGAGC   TA
                                TGG    TTA  TTGGGGGAA
                                |||    |||  |||||||||
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                              ACC    AGT  AACCCCCTT
                                CC___   TC
GAM1944  FLJ00060  3'  TGGAGAGCATTAGGGAA     47762        TTAT
                              TGGAGAGC    ATTGGGGGA
                              ||||||||    |||||||||
                              ACCTCTCG    TAATCCCTT
                                   ____
GAM1944  FLJ10209  3'  GGAGAGCTTGGGGGA       47763        TATAT
                              GGAGAGCT    TGGGGGA
                              ||||||||    |||||||
                              CCTCTCGA    ACCCCCT
                                   _____
GAM1944  FLJ13114  3'  TGGGGATTTATCACCAGGGAAA 47764     A  GC   _  TG
            A                  TGG GA  TTAT AT  GGGGAAA
                              ||| ||  |||| ||  |||||||
                              ACC CT  AATA TG  CCCTTTT
                                C  A_   G  GT
GAM1944  KIAA0247  3'  GAGGGCTCCTGGGGGA     47765     A   ATA
                              GAG GCTT   TTGGGGGA
                              ||| ||||   ||||||||
                              CTC CGAG   GACCCCCT
                                C   ___
GAM1944  KIAA0367  3'  TGGAGGCTTATGGAGGA     47766      A    TAT
                              TGGAG GCTTA   TGGGGGA
                              ||||| |||||   |||||||
                              ACCTC CGAAT   ACCTCCT
                                  _    ___
GAM1944  KIAA1372  3'  TGGGGAGCCTGCTAGGGAA   47767     A     ATA
                              TGG GAGCTT   TTGGGGGA
                              ||| ||||||   ||||||||
                              ACC CTCGGA   GATCCCTT
                                C     C__
GAM1944  KIAA1484  3'  TGGGGATTTATTTGGGAGA   47768     A  GC   A
                              TGG GA  TTAT TTGGGGGA
                              ||| ||  |||| ||||||||
                              ACC CT  AATA AACCCTCT
                                C  A_   _
GAM1944  KLK14    3'  TGGGGGCTTGGTGGGGAGAA  47769     AGA   ATAT   _
                              TGG   GCTT   TGGGG GAA
                              |||   ||||   ||||| |||
                              ACC   CGAA   ACCCC CTT
                                CC_   CC__    T
GAM1944  LSM3     3'  TGGAGAGCTTGAGAAAA     47770        TATAT   GG
                              TGGAGAGCT    TGGG  AA
                              |||||||||    ||||  ||
                              ACCTCTCGA    ACTC  TT
                                   _____   TT
GAM1944  MAAT1    5'  TGGAGAGCTTGTCGTTGTTGG 47771         ATA_  GG
                              TGGAGAGCTT   TTG  GG
                              ||||||||||   |||  ||
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                                ACCTCTCGAA   AAC  CC
                                     CAGC   AA
GAM1944  PROL3    3'  TGGAGAATTTACAGGGAAAA  47772       C   ATT
                                TGGAGAG TTAT   GGGGGAAA
                                ||||||| ||||  ||||||||
                                ACCTCTT AATG   TCCCTTTT
                                   A   ___
GAM1944  PSKH1    3'  TGGGGAACTGGGGGGAA    47773    A    TATATT
                                TGG GAGCT    GGGGGAA
                                ||| |||||    |||||||
                                ACC CTTGA    CCCCCTT
                                  C    C_____
GAM1944  PSMD1    3'  TGGAGATCTTATATTTATTTGA 47774      G      GGGG_
           AAA                    TGGAGA CTTATATT    GAAAA
                                ||||||| ||||||||    |||||
                                ACCTCT GAATATAA    CTTTT
                                   A       ATAAA
GAM1944  RALY     3'  TGGGATGCGTTGGGGGA    47775    A  _  TTATA
                                TGG GA GC    TTGGGGGA
                                ||| || ||    ||||||||
                                ACC CT CG    AACCCCCT
                                  _  A  C____
GAM1944  TRIM2    3'  TGGGGGGTCTGTACTGGGAGGA 47776    AGAG_  TA     _
                                TGG    CT  TATTGGG GGA
                                |||    ||  ||||||| |||
                                ACC    GA  ATGACCC CCT
                                  CCCCA  C_     T
GAM1944  XPO5     3'  GGAGGGCTTGTGGGAGAA    47777     A   ATAT
                                GGAG GCTT   TGGGGGAA
                                |||| ||||   ||||||||
                                CCTC CGAA   ACCCTCTT
                                  C   C___
GAM1944  LOC116113 3'  GGAGAGCTGGTGGGGGA    47778       TATAT
                                GGAGAGCT    TGGGGGA
                                ||||||||    |||||||
                                CCTCTCGA    ACCCCCT
                                     CC___
GAM1944  LOC126661 5'  TGGGGAACTGGGGGAA    47779    A    TATATT
                                TGG GAGCT    GGGGGAA
                                ||| |||||    |||||||
                                ACC CTTGA    CCCCCTT
                                  C    _______
GAM1944  LOC133688 3'  GGAGAGCTTATAGGAAG    47780         TT
                                GGAGAGCTTATA  GGGGG
                                ||||||||||||  |||||
                                CCTCTCGAATAT  CCTTC
                                              __
GAM1944  LOC145127 3'  TGGAGTGTTTATTGGAGAA   47781      AGCTTA
                                TGGAG     TATTGGGGGA
                                |||||     ||||||||||
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                                ACCTC     ATAACCTCTT
                                  ACAA__
GAM1944  LOC148171 5'  TGGGGAGCTTGGCTTGAGGA  47782     A     ATA
                                TGG GAGCTT  TTGGGGG
                                ||| ||||||  |||||||
                                ACC CTCGAA  AACTCCT
                                  C     CCG
GAM1944  LOC148760 3'  GGGGAGCTTGTTGGAGAA    47783    A     ATA
                                GG GAGCTT  TTGGGGGA
                                || ||||||  ||||||||
                                CC CTCGAA  AACCTCTT
                                 C     C__
GAM1944  LOC149124 5'  TGGGGAGCTTGGCTTGAGGA  47782     A     ATA
                                TGG GAGCTT  TTGGGGG
                                ||| ||||||  |||||||
                                ACC CTCGAA  AACTCCT
                                  C     CCG
GAM1944  LOC149606 3'  TGGAGAGTTGAGGGGAA     47784       CTTATA  _
                                TGGAGAG     TTG GGGGAA
                                |||||||     ||| ||||||
                                ACCTCTC     AAC CCCCTT
                                    _______  T
GAM1944  LOC150967 3'  GAGGGCTTACATACAGGGGA  47785     A      _
                                GAG GCTTATAT TGGGGGA
                                ||| |||||||| |||||||
                                CTC CGAATGTA GTCCCCT
                                  C       T
GAM1944  LOC151429 3'  GAGAGGGCAGTGGGGGAAA   47786      CTTA  T
                                GAGAG   TA TGGGGGAAA
                                |||||   || |||||||||
                                CTCTC   GT ACCCCCTTT
                                   CC__  C
GAM1944  LOC152426 3'  GGAGAGCTTGTCAAGGAA    47787        ATA TG
                                GGAGAGCTT  T  GGGGA
                                |||||||||  |  |||||
                                CCTCTCGAA  A  TCCTT
                                      C__ GT
GAM1944  LOC153592 3'  GGGGAGTTTATTAGGAGAA   47788    A  C  A
                                GG GAG TT TATTGGGGGAA
                                || ||| || ||||||||||
                                CC CTC AA ATAATCCTCTT
                                 C  _  _
GAM1944  LOC158263 3'  TGGAGAGCTGTGGAAG      47789        TATAT
                                TGGAGAGCT    TGGGGG
                                |||||||||    ||||||
                                ACCTCTCGA    ACCTTC
                                      C____
GAM1944  LOC158654 5'  TGGGGAGTGTATTCAGGAGA  47790    A  CT  A TG
                                TGG GAG  TAT T  GGGGA
                                ||| |||  ||| |  |||||
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                                ACC CTC  ATA A  CCTCT
                                  C   AC   _ GT
GAM1944  LOC159110 3'  TAGAGAAAGTTGGGGGAAA   47791       CTTATA
                                TGGAGAG     TTGGGGGAAA
                                |||||||     ||||||||||
                                ATCTCTT     AACCCCCTTT
                                    TC_____
GAM1944  LOC159116 3'  TAGAGAAAGTTGGGGGAAA   47791       CTTATA
                                TGGAGAG     TTGGGGGAAA
                                |||||||     ||||||||||
                                ATCTCTT     AACCCCCTTT
                                    TC____
GAM1944  LOC164714 5'  TGGAGAGCTGGTGATGGGGG  47792        TATAT
                                TGGAGAGCT    TGGGGG
                                |||||||||    ||||||
                                ACCTCTCGA    ACCCCC
                                     CCACT
GAM1944  LOC203078 3'  TGGTTCTGTGTATTGGGGGAA 47793    AGAG  TA_
                                TGG    CT   TATTGGGGGAA
                                |||    ||   ||||||||||
                                ACC    GA   ATAACCCCCTT
                                  AA__  CAC
GAM1944  LOC221272 3'  GAGGGCTTGTGCAGGAAA    47794     A    ATAT  G
                                GAG GCTT    TG GGGAAA
                                ||| ||||    || ||||||
                                CTC CGAA    AC TCCTTT
                                  C    C___  G
GAM1944  LOC222183 3'  TGGAGGAGCTTGGGGGA     47795      _    TATAT
                                TGGAG AGCT    TGGGGGA
                                ||||| ||||    |||||||
                                ACCTC TCGA    ACCCCCT
                                   C   _____
GAM1944  LOC256855 5'  GGGAGTTACTGGGGGA      47796    A   CTTA
                                GG GAG    TATTGGGGGA
                                || |||    ||||||||||
                                CC CTC    ATGACCCCCT
                                 _   A___
GAM1944  LOC257428 5'  TGGAGAACTTTCTGGGGAA   47797         ATA
                                TGGAGAGCTT   TTGGGGGA
                                ||||||||||   ||||||||
                                ACCTCTTGAA   GACCCCTT
                                     A__
GAM1944  LOC56920  3'  TGGAGAGCCTGACAATGGGGA 47798          _   T
                                TGGAGAGCTT ATA TGGGGG
                                |||||||||| ||| ||||||
                                ACCTCTCGGA TGT ACCCCT
                                     C   T
GAM1944  LOC90643  3'  TGGAGGAGGTTGGGGGAAA   47799      _  CTTATA
                                TGGAG AG     TTGGGGGAAA
                                ||||| ||     ||||||||||
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                                ACCTC TC     AACCCCCTTT
                                  C  C_____
GAM1944 LOC91818 3' TGGAGGAGGTTGGGGGAAAA  47800      _ CTTATA
                                TGGAG AG     TTGGGGGAAAA
                                ||||| ||     ||||||||||
                                ACCTC TC     AACCCCCTTTT
                                  C  C_____
GAM1944 LOC92095 5' TGGGAGCTTGGGGGA      47801     A    TATAT
                                TGG GAGCT    TGGGGGA
                                ||| |||||    |||||||
                                ACC CTCGA    ACCCCCT
                                  _    _____
GAM1944 LOC92096 5' TGGGAGCTTGGGGGA      47801     A    TATAT
                                TGG GAGCT    TGGGGGA
                                ||| |||||    |||||||
                                ACC CTCGA    ACCCCCT
                                  _    _____
GAM1945 ABCB11   3' AGGAAAATGACTGTAAAAG   47804          GAAGAT
                                AGGAAAATGAC     GAAG
                                ||||||||||     ||||
                                TCCTTTTACTG     TTTC
                                      ACAT__
GAM1945 ABCD3    3' CACAGGAAAATGAAACTGAAG 47805           CGAAGA
                                TACAGGAAAATGA     TGAAG
                                ||||||||||||     |||||
                                GTGTCCTTTTACT     ACTTC
                                      TTG___
GAM1945 BPAG1    3' ACAGGAAAATGTCATGA     47806          A GAAG
                                ACAGGAAAATG C    ATGA
                                |||||||||| |    ||||
                                TGTCCTTTTAC G    TACT
                                      A ____
GAM1945 CD28     3' ACAGGAAAATGATGGAAG    47807          C_
                                ACAGGAAAATGA  GAAG
                                ||||||||||  ||||
                                TGTCCTTTTACT  CTTC
                                      AC
GAM1945 CHST1    3' CAGGAAGGACACGAAGATGA  47808       AATG
                                CAGGAA    ACGAAGATGA
                                ||||||    ||||||||||
                                GTCCTT    TGCTTCTACT
                                   CCTG
GAM1945 EGFL5    5' CAGGAATGGAGATGAA      47809      AA  ACGA
                                CAGGA  ATG    AGATGAA
                                |||||  |||    |||||||
                                GTCCT  TAC    TCTACTT
                                   __   C___
GAM1945 ENAM     3' TACAGAGAGAAAAAGATGA   47810       AAAAT  C
                                TACAGG    GA GAAGATGA
                                ||||||    || ||||||||
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                                ATGTCT    CT TTTCTACT
                                   CT___  T
GAM1945  FHIT     3'  TACAGGATGGTGAGATGAA   47811       AAA  AC  A
                                TACAGGA   TG  GA GATGAA
                                |||||||   ||  || ||||||
                                ATGTCCT   AC  CT CTACTT
                                   ___  CA  _
GAM1945  GCN1L1   3'  CACAGGAAAAGGTGAGAGATG  47812         __   C  A
                                TACAGGAAAA  TGA GA GATG
                                ||||||||||  ||| || ||||
                                GTGTCCTTTT  ACT CT CTAC
                                      CC  _ _
GAM1945  GJA5     3'  CAGGAAGATTCCGTAGATGAAG 47813       A  GA  A
                                CAGGAA AT  CG AGATGAAG
                                ||||||  ||  || ||||||||
                                GTCCTT TA  GC TCTACTTC
                                   C  AG  A
GAM1945  HNRPDL   3'  TACAGGGAGAAGATGAA     47814       AAAAT  C
                                TACAGG    GA GAAGATGAA
                                ||||||    || |||||||||
                                ATGTCC    CT CTTCTACTT
                                   _____  _
GAM1945  PIK3CD   3'  TACAGTAGAGAAAGATGA    47815       GAAAAT  C
                                TACAG     GA GAAGATGA
                                |||||     || ||||||||
                                ATGTC     CT TTTCTACT
                                   AT____  C
GAM1945  PPP2R5C  3'  GGAGAACATGAAGATGAAG   47816     A   GAC
                                GGA AAT   GAAGATGAAG
                                |||  |||   ||||||||||
                                CCT TTG   CTTCTACTTC
                                  C   TA_
GAM1945  PRG2     5'  CAGACAGAGATGAAGATGAAG  47817     AAAAT  C
                                CAGG    GA GAAGATGAAG
                                ||||    || ||||||||||
                                GTCT    CT CTTCTACTTC
                                   GTCT_  A
GAM1945  PRKY     3'  CAGAAGGAGACAGATGAAG   47818      AAAT   GA
                                CAGGA   GAC  AGATGAAG
                                |||||   |||  ||||||||
                                GTCTT   CTG  TCTACTTC
                                   CCT_   __
GAM1945  RRAS2    3'  TGAGGAGAGAAAGAGAAGATGA 47819   C    AAAT__  C
                                A AGGA     GA GAAGATGA
                                | ||||     || ||||||||
                                A TCCT     CT CTTCTACT
                                 C   CTCTTT  _
GAM1945  TIMM17A  3'  CAGGAAAATGACCTGTTCTGAA 47820          GAAGA_
            G                    CAGGAAAATGAC     TGAAG
                                ||||||||||||     |||||
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                                GTCCTTTTACTG     ACTTC
                                      GACAAG
GAM1945  TMOD4    3'  TACAGGAAAGGAGGACAGATGA 47821         AT  C  _
                                TACAGGAAA  GA GA AGATGA
                                |||||||||  || || ||||||
                                ATGTCCTTT  CT CT TCTACT
                                     C_  C  G
GAM1945  YY1      3'  TACAGGAAAATACTTTTGAAG  47822          A GAAGA
                                TACAGGAAAATG C    TGAAG
                                ||||||||||||| |    |||||
                                ATGTCCTTTTAT G    ACTTC
                                      _ AAA__
GAM1945  C20orf188 3'  TACAGGAAAATGAGGCAGA   47823           CGA
                                TACAGGAAAATGA   AGA
                                ||||||||||||   |||
                                ATGTCCTTTTACT   TCT
                                       CCG
GAM1945  CALN1    3'  GGAATTCCGAGATGAAGATGAA 47824     AA_  C__
             G                   GGAA   TGA   GAAGATGAAG
                                ||||   |||   ||||||||||
                                CCTT   GCT   CTTCTACTTC
                                  AAG   CTA
GAM1945  DKFZp434I099 3'  TACAGGAAAATCATGAGAAG   47825        ___   C
                                TACAGGAAA   ATGA GAAG
                                |||||||||   |||| ||||
                                ATGTCCTTT   TACT CTTC
                                      TAG   _
GAM1945  DKFZP564D166 3'  GGAAAACAATGAAAGATGAAG  47826       TG C_
                                GGAAAA  A  GAAGATGAAG
                                ||||||  |  ||||||||||
                                CCTTTT  T  TTTCTACTTC
                                    GT AC
GAM1945  FLJ21709  3'  GGAAAGAAGGAAGATGA     47827      AT  C
                                GGAAA  GA GAAGATGA
                                |||||  ||  ||||||||
                                CCTTT  TT CTTCTACT
                                   C_  C
GAM1945  KIAA1036  3'  CACAGGAAGTGAGATGA     47828        AA   CGAA
                                TACAGGAA  TGA    GATGA
                                ||||||||  |||    |||||
                                GTGTCCTT  ACT    CTACT
                                     C_  _____
GAM1945  KIAA1559  3'  GGTAAGTGAAGAAGATGAAG   47829    A  A   C
                                GG AA TGA GAAGATGAAG
                                || ||  ||| ||||||||||
                                CC TT ACT CTTCTACTTC
                                 A  C   T
GAM1945  KIAA1674  3'  AGGAAATGAAAAGATG      47830       A   C
                                AGGAAA TGA GAAGATG
                                ||||||  ||| |||||||
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                                TCCTTT ACT TTTCTAC
                                     _  _
GAM1945 KLHL4    3' TACAGGAAGGTGACAGACA   47831       AA   GA
                                TACAGGAA TGAC AGATG
                                |||||||| |||| |||||
                                ATGTCCTT ACTG TCTGT
                                    CC   __
GAM1945 SEMA3E   3' GGAAAATTTGGTGAGATGAAG 47832      GACGA_
                                GGAAAAT    AGATGAAG
                                |||||||    ||||||||
                                CCTTTTA    TCTACTTC
                                   AACCAC
GAM1945 SLC21A14 5' GGAAAAGAAAAGATGAAG   47833      T  C
                                GGAAAA GA GAAGATGAAG
                                |||||| || ||||||||||
                                CCTTTT CT TTTCTACTTC
                                     _  _
GAM1945 TIAM2    3' TACAGAAAAATGTGTGATGAAG 47834        ACGAA
                                TACAGGAAAATG   GATGAAG
                                ||||||||||||   |||||||
                                ATGTCTTTTTAC   CTACTTC
                                      ACA__
GAM1945 LOC146229 3' AGGAAAATGGAAAATGAAG  47836       AC
                                AGGAAAATG GAAGATGAAG
                                ||||||||| ||||||||||
                                TCCTTTTAC CTTTTACTTC
                                     __
GAM1945 LOC146229 3' TACAGGAAGTGAGTGAAG   47835       AA  C_
                                TACAGGAA TGA GAAG
                                |||||||| ||| ||||
                                ATGTCCTT ACT CTTC
                                    C_  CA
GAM1945 LOC150279 3' AGGAAAGTTCTGAGATGAAG 47837      ATGAC A
                                AGGAAA   GA GATGAAG
                                ||||||   || |||||||
                                TCCTTT   CT CTACTTC
                                   CAAGA _
GAM1945 LOC151473 3' GGAAAATGAAAGTAATGAAG 47838       CGAA
                                GGAAAATGA  GATGAAG
                                |||||||||  |||||||
                                CCTTTTACT  TTACTTC
                                     TTCA
GAM1945 LOC151778 5' GGTAGATGGTGAAGATGAAG 47839   AAA  AC
                                GG  ATG GAAGATGAAG
                                ||  ||| ||||||||||
                                CC  TAC CTTCTACTTC
                                 ATC  CA
GAM1945 LOC155340 5' GGTAGATGGTGAAGATGAAG 47839   AAA  AC
                                GG  ATG GAAGATGAAG
                                ||  ||| ||||||||||
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                                CC   TAC  CTTCTACTTC
                                 ATC   CA
GAM1945  LOC170395 3'  AGGAAATGAAAAGATG      47830       A   C
                                AGGAAA TGA GAAGATG
                                ||||||| ||| |||||||
                                TCCTTT ACT TTTCTAC
                                   _   _
GAM1945  LOC255620 5'  GGTAGATGGTGAAGATGAAG  47839    AAA   AC
                                GG   ATG  GAAGATGAAG
                                ||   |||  ||||||||||
                                CC   TAC  CTTCTACTTC
                                 ATC   CA
GAM1945  LOC51184  3'  AGGAAAATGGGAAGATA     47840         AC
                                AGGAAAATG  GAAGATG
                                |||||||||  |||||||
                                TCCTTTTAC  CTTCTAT
                                     C_
GAM1945  LOC91137  3'  AGAAAATGTGTAGGGATGAAG 47841        ACGAA_
                                GGAAAATG     GATGAAG
                                ||||||||     |||||||
                                TCTTTTAC     CTACTTC
                                   ACATCC
GAM1946  KIAA1061  3'  TTCTGGGTTCTGCAGTGT    47844          G TAC
                                TTTTGGGTTCTG C   TGT
                                |||||||||||| |   |||
                                AAGACCCAAGAC G   ACA
                                     _ TC_
GAM1946  LGALS8    3'  TATTTTGGTTTTTGTAGCAGCT 47845        GTTC__    TA
           GT                    TATTTTGG     TGGC  CTGT
                                ||||||||     ||||  ||||
                                ATAAAACC     ATCG  GACA
                                   AAAAAC    TC
GAM1946  TUBGCP3   3'  TTTGGGTTGCACTGTA      47846        CTG  T
                                TTTGGGTT   GC ACTGTA
                                ||||||||   || ||||||
                                AAACCCAA   CG TGACAT
                                    ___  _
GAM1946  LOC154421 3'  CATTTTGGGTTTGGAGCTGT   47847          C   CTA
                                TATTTTGGGTT TGG   CTGT
                                |||||||||| |||   ||||
                                GTAAAACCCAA ACC   GACA
                                     _   TC_
GAM1947  BDKRB2    3'  CACCTGTTTTCTTCCTCCA    47850       C___
                                CACCTG    CTTCTTTCA
                                ||||||    |||||||||
                                GTGGAC    GAAGGAGGT
                                   AAAA
GAM1947  HSPB3     5'  TCCACTGCCTTCAGTCA      47851       C      TT
                                TCCAC TGCCTTC  TCA
                                ||||| |||||||  |||
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                                AGGTG ACGGAAG  AGT
                                  _      TC
GAM1947 KLHL1    3' CTGCCTTCTTTCTAGCAA    47852          AAT
                                CTGCCTTCTTTC   CAA
                                ||||||||||||  |||
                                GACGGAAGAAAG   GTT
                                      ATC
GAM1947 SURF6    3' CACCTGTTTTCTTTCAACC   47853       CC
                                CACCTG  TTCTTTCAATC
                                ||||||  ||||||||||||
                                GTGGAC  AAGAAAGTTGG
                                   AA
GAM1947 ZNF146   3' CTGCTCTGCTCAATCAAT    47854      CT  _
                                CTGC  TCT TTCAATCAAT
                                ||||  ||| ||||||||||
                                GACG  AGA GAGTTAGTTA
                                  __  C
GAM1947 C1orf10  3' TCCAGCTGTCTTCTTCCA    47855      C  C
                                TCCA CTG CTTCTTTCA
                                |||| ||| |||||||||
                                AGGT GAC GAAGAAGGT
                                  C  A
GAM1947 DKFZP566J2046 3' CCGCCTCCCGGGTTCAAT    47856          ___
                                CTGCCTTCT   TTCAAT
                                |||||||||   ||||||
                                GGCGGAGGG   AAGTTA
                                     CCC
GAM1947 FLJ10726 3' TCTGCCAGCCTTCTTTCA    47857    CA  T
                                TC  CC GCCTTCTTTCA
                                ||  || ||||||||||||
                                AG  GG CGGAAGAAAGT
                                 AC  T
GAM1947 FLJ10898 5' TCCACCTGCTCTTTTTTC    47858         _  C
                                TCCACCTGC CTT TTTC
                                ||||||||| ||| ||||
                                AGGTGGACG GAA AAAG
                                      A  A
GAM1947 FLJ20038 3' TCCACTCTGTCTCAATCA    47859       _  CCTTC
                                TCCAC CTG    TTTCAATCA
                                ||||| |||    |||||||||
                                AGGTG GAC    AGAGTTAGT
                                  A  _____
GAM1947 KIAA0872 3' TGCCTGTCATTCAAGTCAAT  47860       _ T    _
                                TGCCT TC TTCAA TCAAT
                                ||||| || ||||| |||||
                                ACGGA AG AAGTT AGTTA
                                  C  T    C
GAM1947 KIAA1131 5' CTGCCAGTCCTGTCAATCAAT 47861       T_   _
                                CTGCC  TCTT TCAATCAAT
                                |||||  |||| |||||||||
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                                GACGG  AGGA AGTTAGTTA
                                   TC    C
GAM1947  NMT1     3'  CCTGCCTGCCAGCCAGTCA    47862       T  T_   A
                                CCTGCCT CT  TCA TCA
                                ||||||| ||  ||| |||
                                GGACGGA GG  GGT AGT
                                    C  TC   C
GAM1947  SCIN     5'  CACTTCCTTCTTCCACGACAAT 47863     CTG        AT_
                                CAC   CCTTCTTTCA   CAAT
                                |||   ||||||||||   ||||
                                GTG   GGAAGAAGGT   GTTA
                                  AA_        GCT
GAM1947  SLC5A7   3'  CCCCTTTCTCTTTTTTCAATCA 47864   A   GC__   C        III
             ATA                   CCT    CTT TTTCAATCAAT   A
                                 |||    ||| ||||||||||   |
                                 GGA    GAA AAAGTTAGTTA   T
                                _   AAGA   A         III
GAM1947  SSH2     3'  CTGCTTCCTTCCCTCAA     47865      C      AA
                                CTGC TTCTTTC  TCAA
                                |||| |||||||  ||||
                                GACG AAGGAAG  AGTT
                                   _      GG
GAM1947  LOC143437 5'  TCCTCCTGTTTTCTGGCAAT   47866     A    CC    TT
                                TCC CCTG  TTCT  CAAT
                                ||| ||||  ||||  ||||
                                AGG GGAC  AAGA  GTTA
                                  A    AA    CC
GAM1947  LOC150147 3'  TCCATCTATCAATCAATCA    47867      C   CCT  TT
                                TCCA CTG   TC  TCAATCA
                                |||| |||   ||  |||||||
                                AGGT GAT   AG  AGTTAGT
                                  A   ___  TT
GAM1947  LOC151278 3'  TCCACCTGCTTCTCCAAT     47868         C     T
                                TCCACCTGC TTCTT CAAT
                                ||||||||| ||||| ||||
                                AGGTGGACG AAGAG GTTA
                                                _    _
GAM1947  LOC151457 5'  CTGTTTCCTTCCACCACATCAA 47869      ___      T   _
             T                   CTG   CCTTCT TCA ATCAAT
                                 |||   |||||| ||| ||||||
                                 GAC   GGAAGG GGT TAGTTA
                                   AAA      T   G
GAM1947  LOC151458 5'  CTGTTTCCTTCCACCACATCAA 47869      ___      T   _
             T                   CTG   CCTTCT TCA ATCAAT
                                 |||   |||||| ||| ||||||
                                 GAC   GGAAGG GGT TAGTTA
                                   AAA      T   G
GAM1947  LOC153146 5'  TCCCCTGCCTTCTTGGCAA    47870     A         T_
                                TCC CCTGCCTTCTT  CAA
                                ||| ||||||||||  |||
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                                AGG GGACGGAAGAA  GTT
                                  _        CC
GAM1947  LOC154789 5'  CACCTTCCTTTCCAAT     47871      G    CT
                                CACCT CCTT  TTCAAT
                                ||||| ||||  ||||||
                                GTGGA GGAA  AGGTTA
                                   A   __
GAM1947  LOC155060 3'  CCTGCCTGCTCCAACAAT    47872       T   T   T
                                CCTGCCT CTT CAA CAAT
                                ||||||| ||| ||| ||||
                                GGACGGA GAG GTT GTTA
                                    C  _  _
GAM1947  LOC158237 3'  TCCACTCTGTCTCAATCA    47859      _  CCTTC
                                TCCAC CTG    TTTCAATCA
                                ||||| |||    |||||||||
                                AGGTG GAC    AGAGTTAGT
                                   A  _____
GAM1947  LOC199863 5'  CCTGCCTTTTTCTTATGGTCAA 47873       ___   TCAA
           T                     CCTGCCT   TCTT   TCAAT
                                |||||||   ||||   |||||
                                GGACGGA   AGAA   AGTTA
                                    AAA   TACC
GAM1947  LOC200734 3'  CACTTTTCTTCTTTCTTCAAT  47874    CTGC      AA
                                CAC   CTTCTTTC  TCAAT
                                |||   ||||||||  |||||
                                GTG   GAAGAAAG  AGTTA
                                  AAAA      A_
GAM1947  LOC221069 3'  CTGCCTCCCGGGTTCAATCAAT 47875        ___
                                CTGCCTTCT   TTCAATCAAT
                                |||||||||   ||||||||||
                                GACGGAGGG   AAGTTAGTTA
                                     CCC
GAM1947  LOC221773 3'  TCCACCTGCATCGAGATCA   47876       CT  TTTCA
                                TCCACCTGC  TC    ATCA
                                |||||||||  ||    ||||
                                AGGTGGACG  AG    TAGT
                                     T_  CTC__
GAM1947  LOC222001 5'  CTGTTTTCTTCCATTTCAAT   47877    CC      A_
                                CTG  TTCTTTCA  TCAAT
                                |||  ||||||||  |||||
                                GAC  AAGAAGGT  AGTTA
                                  AA       AA
GAM1947  LOC253531 5'  TCCTCCTGTTTTCTGGCAAT   47866    A   CC   TT
                                TCC CCTG  TTCT  CAAT
                                ||| ||||  ||||  ||||
                                AGG GGAC  AAGA  GTTA
                                  A   AA   CC
GAM1947  LOC255104 3'  TCCATTTCCTTTCCCTTTCA   47878     ___  GCC
                                TCCA   CCT   TTCTTTCA
                                ||||   |||   ||||||||
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                                AGGT   GGA   GGGAAAGT
                                  AAA   AA_
GAM1947  LOC55974  3'  CATCTCCTAGGCCCCAATCAAT 47879    C  G   TC_ TT
                                CA CT CCT   T  CAATCAAT
                                || || |||   |  ||||||||
                                GT GA GGA   G  GTTAGTTA
                                 A  _   TCC GG
GAM1947  LOC92017  5'  TCCACCTGCTTTTCTCCTCA   47880        C_    _
                                TCCACCTGC  TTCTT TCA
                                |||||||||  ||||| |||
                                AGGTGGACG  AAGAG AGT
                                      AA    G
GAM1948  CUGBP1    3'  TCAAAGGTGAGAGTTCAAGCAT 8405         A     ATGAC
                                TTAAAGGT AGAGTT    GCAT
                                |||||||| ||||||    ||||
                                AGTTTCCA TCTCAA    CGTA
                                     C     GTT__
GAM1948  PCK1      3'  TAAAGGTAAGGAACAATG    8406          _ TT
                                TAAAGGTAAG AG  ATG
                                |||||||||| ||  |||
                                ATTTCCATTC TT  TAC
                                      C  GT
GAM1948  KIAA1872  3'  GGGGAGGGTTTATGACGCAT   8407     TA  A  _
                                GG  AG GTT ATGACGCAT
                                ||  || ||| |||||||||
                                CC  TC CAA TACTGCGTA
                                 CC  C   A
GAM1948  LOC124602 3'  AGGTGGGGAATGTGACGCAT   8408      AA_   TA
                                AGGT   GAGT  TGACGCAT
                                ||||   ||||  ||||||||
                                TCCA   CTTA  ACTGCGTA
                                  CCC    C_
GAM1948  LOC149628 3'  TTAAAGGTGAAAGAAATATG   8409         __    T
                                TTAAAGGT  AAGAG TATG
                                ||||||||  ||||| ||||
                                AATTTCCA  TTCTT ATAC
                                     CT    T
GAM1948  LOC203397 3'  AGGTGGGGAATGTGACGCAT   8408      AA_   TA
                                AGGT   GAGT  TGACGCAT
                                ||||   ||||  ||||||||
                                TCCA   CTTA  ACTGCGTA
                                  CCC    C_
GAM1949  CASP8     3'  AAAGATTTCAAACAAATTTT   47884          GAT
                                AAAGATTTCAAA   GTTTT
                                ||||||||||||   |||||
                                TTTCTAAAGTTT   TAAAA
                                       GTT
GAM1949  CASP8     3'  AAAGATTTCAAACAAATTTT   47884          GAT
                                AAAGATTTCAAA   GTTTT
                                ||||||||||||   |||||
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                                TTTCTAAAGTTT  TAAAA
                                      GTT
GAM1949  GRM1     3'  TAAAGATTCTAAGATGATTTT  47885       CA    _
                                TAAAGATTT  AAGATG TTTT
                                |||||||||  |||||| ||||
                                ATTTCTAAG  TTCTAC AAAA
                                     A_     T
GAM1949  NDN      3'  ACTCCACGAGGGTGTTTTCTG  47886     A_  A_
                                ATTTCA  AG  TGTTTTCTG
                                ||||||  ||  |||||||||
                                TGAGGT  TC  ACAAAAGAC
                                   GC  CC
GAM1949  PCDHA1   3'  AGAATTTCAAAGCATTCT    47887    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA1   3'  AGAATTTCAAAGCATTCT    47887    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA10  3'  AGAATTTCAAAGCATTCT    47887    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA10  3'  AGAATTTCAAAGCATTCT    47887    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA11  3'  AGAATTTCAAAGCATTCT    47887    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA12  3'  AGAATTTCAAAGCATTCT    47887    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA13  3'  AGAATTTCAAAGCATTCT    47887    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA2   3'  AGAATTTCAAAGCATTCT    47887    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
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                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA3   3' AGAATTTCAAAGCATTCT    47887    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA4   3' AGAATTTCAAAGCATTCT    47887    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA5   3' AGAATTTCAAAGCATTCT    47887    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA6   3' AGAATTTCAAAGCATTCT    47887    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA6   3' AGAATTTCAAAGCATTCT    47887    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA7   3' AGAATTTCAAAGCATTCT    47887    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA8   3' AGAATTTCAAAGCATTCT    47887    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHA9   3' AGAATTTCAAAGCATTCT    47887    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHAC1  3' AGAATTTCAAAGCATTCT    47887    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1949  PCDHAC2  3' AGAATTTCAAAGCATTCT    47887    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
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                                TCT AAAGTTTC    AAGA
                                  T      GT___
GAM1949 ASPN     3' AAAATTTCCCTGTTTTCTG  47888       AAAGA
                                AAGATTTC    TGTTTTCTG
                                ||||||||    |||||||||
                                TTTTAAAG    ACAAAAGAC
                                    GG___
GAM1949 C1QR1    3' AGACAGATGTTTTCT      47889     TTCAA
                                AGAT    AGATGTTTTCT
                                ||||    ||||||||||
                                TCTG    TCTACAAAAGA
                                 _____
GAM1949 KIAA1764 3' AGATTTCAAATGCTTT     47890       AA
                                AGATTTCA  GATGTTTT
                                ||||||||  ||||||||
                                TCTAAAGT  TTACGAAA
                                  __
GAM1949 KIAA1877 3' AAGATGGATGTTTTCT     47891      TTCAAA
                                AAGAT     GATGTTTTCT
                                |||||     ||||||||||
                                TTCTA     CTACAAAAGA
                                  C_____
GAM1949 MGC10981 3' GATTTCAACCCAGCTTTTCTG 47892       AGAT   _
                                GATTTCAA    GTTTT CTG
                                ||||||||    ||||| |||
                                CTAAAGTT    CGAAA GAC
                                    GGGT    A
GAM1949 LOC143173 5' AGATTTCAAAGATGGTCTG  47893          TTT
                                AGATTTCAAAGATG   TCTG
                                ||||||||||||||   ||||
                                TCTAAAGTTTCTAC   AGAC
                                       C__
GAM1949 LOC144608 3' AAGATTTTAAGTAGTTTTCTG 47894      CA   AT
                                AAGATTT  AAG  GTTTTCTG
                                |||||||  |||  ||||||||
                                TTCTAAA  TTC  CAAAAGAC
                                   A_   AT
GAM1949 LOC54466 3' AAGATTTCATTTTTTCT    47895       AAGATG
                                AAGATTTCA     TTTTCT
                                |||||||||     ||||||
                                TTCTAAAGT     AAAAGA
                                    AA_____
GAM1949 LOC55924 3' AGATGTCAGAGGGATTTTCTG 47896     T   A  AT
                                AGAT TCA AG  GTTTTCTG
                                |||| ||| ||  ||||||||
                                TCTA AGT TC  TAAAAGAC
                                  C   C  CC
GAM1950 FCMD     5' TTTGGATTTGGAAAGGAA    47899           A
                                TTTGGATTTGGAAA GAA
                                |||||||||||||| |||
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                                AAACCTAAACCTTT CTT
                                       C
GAM1950 GORASP1  3' AGTGTTTGGGACTTGAAA   47900    A   _
                                AGT TTTGG ATTTGGAA
                                ||| ||||| ||||||||
                                TCA AAACC TGAACTTT
                                  C   C
GAM1950 HUNK     3' TGAGTACTTGGGAGGAA    47901         ATTT
                                TGAGTATTTGG   GGAA
                                ||||||||||   ||||
                                ACTCATGAACC   CCTT
                                      CT__
GAM1950 KCNA6    3' GAGTATTTGGCTCTGAGAA  47902        A   _
                                GAGTATTTGG TTTG GAA
                                |||||||||| |||| |||
                                CTCATAAACC AGAC CTT
                                      G   T
GAM1950 LENG4    3' GTATTTAGCTGGGGAAGA   47903       AT   AA
                                GTATTTGG  TTGG  AAGA
                                ||||||||  ||||  ||||
                                CATAAATC  GACC  TTCT
                                     __   CC
GAM1950 SLC13A3  3' TGAGTGCTCACTTGGAAAGGA 47904     A  GG      A
                                TGAGT TTT  ATTTGGAAA GA
                                ||||| |||  |||||||||| ||
                                ACTCA GAG  TGAACCTTT CT
                                   C  __       C
GAM1950 SNX9     3' GAAATAGGATTTGGGGAAGAA 47905    TATTT      AA
                                GAG    GGATTTGG  AAGAA
                                |||    ||||||||  |||||
                                CTT    CCTAAACC  TTCTT
                                  TAT__      CC
GAM1950 TRPS1    3' TGAGTATTTGAACATCTAAAGG 47906          TT_____
            A                    TGAGTATTTGGAT     GGA
                                ||||||||||||      |||
                                ACTCATAAACTTG     CCT
                                       TAGATTT
GAM1950 XK       3' TGAGGTAGGTTGGAAAAG   47907    TATTT  AT
                                TGAG    GG  TTGGAAAAG
                                ||||    ||  |||||||||
                                ACTC    CC  AACCTTTTC
                                  CAT__  __
GAM1950 DKFZp434N2435 5' GTATTGCTGAAGTTGGAAAAG 47908      __   T
                                GTATT  TGGA TTGGAAAAG
                                |||||  |||| |||||||||
                                CATAA  ACTT AACCTTTTC
                                  CG   C
GAM1950 FLJ10035 3' TGAGTTTTGGACAAAGA    47909      A     TT
                                TGAGT TTTGGAT  GGA
                                ||||| |||||||  |||
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                                ACTCA AAACCTG  TCT
                                  _      TT
GAM1950  FLJ10813  3'  AGTACTTAGATTTGGAAGAGAA 47910              A
                                AGTATTTGGATTTGGAA AGAA
                                |||||||||||||||| ||||
                                TCATGAATCTAAACCTT TCTT
                                          C
GAM1950  FLJ20618  3'  TGATGTGTAGTTTGGAAAAGAA 47911     GTATT   A
                                TGA    TGG TTTGGAAAAGAA
                                |||    ||| ||||||||||||
                                ACT    ATC AAACCTTTTCTT
                                  ACAC_  _
GAM1950  FLJ30058  3'  TGAATAATTTGGAGGGGGA   47912       _     TTT
                                TGAGTA TTTGGA   GGA
                                |||||| ||||||   |||
                                ACTTAT AAACCT   CCT
                                    T     CCC
GAM1950  IRAK3     3'  TGAGGGTTTGGGAAAAAAGAA  47913     TA    ATTT
                                TGAG  TTTGG    GGAAAAGAA
                                ||||  |||||    |||||||||
                                ACTC  AAACC    TTTTTTCTT
                                  CC    C___
GAM1950  KIAA0391  3'  GAGTATTTGGGAATTAGAAGAG 47914          AT_     A
                                GAGTATTTGG   TTGGAA AG
                                ||||||||||   |||||| ||
                                CTCATAAACC   AATCTT TC
                                       CTT     C
GAM1950  KIAA1161  3'  TGATATTTGGATGGGGA     47915     G       TT
                                TGA TATTTGGAT  GGA
                                ||| |||||||||  |||
                                ACT ATAAACCTA  CCT
                                  _       CC
GAM1950  LEAP-2    5'  TGGGTATTTGGATAAGAA    47916    A        TT
                                TG GTATTTGGAT  GGAA
                                || ||||||||||  ||||
                                AC CATAAACCTA  TCTT
                                 C         T_
GAM1950  MGC3123   3'  TGAGTATTTGGCTGAGAA    47917          ATTT
                                TGAGTATTTGG    GGAA
                                ||||||||||    ||||
                                ACTCATAAACC    TCTT
                                       GAC_
GAM1950  nexilin   3'  TGATGCTTATTTGGAAAAGAA  47918     GTATTTGG
                                TGA       ATTTGGAAAAGAA
                                |||       ||||||||||||||
                                ACT       TAAACCTTTTCTT
                                  ACGAA___
GAM1950  NICN1     3'  TGAGCATATCTCTTGGAAA    47919        TTGGA
                                TGAGTAT    TTTGGAAA
                                |||||||    ||||||||
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                                ACTCGTA    GAACCTTT
                                    TAGA_
GAM1950 Nup43    5' TGGTTATTTGGATGGTGAAG  47920    AG      TT  AA
                                TG  TATTTGGA  TGG  AAG
                                ||  ||||||||  |||  |||
                                AC  ATAAACCT  ACC  TTC
                                 CA       __   AC
GAM1950 PRO0650  5' TGAGAGTTTGGATTGTGG    47921     TA      _
                                TGAG  TTTGGATT TGG
                                ||||  |||||||| |||
                                ACTC  AAACCTAA ACC
                                  TC       C
GAM1950 TSC22    3' TGAGTGTTTAATACTGGAAAAG 47922      A    AT
             A                   TGAGT TTTGG  TTGGAAAAGA
                                |||||| |||||  ||||||||||
                                ACTCA AAATT  GACCTTTTCT
                                   C    AT
GAM1950 LOC132112 3' TGGGTGTTTAGATCAGGA    47923    A  A      T
                                TG GT TTTGGATT GGA
                                || || |||||||| |||
                                AC CA AAATCTAG CCT
                                 C  C       T
GAM1950 LOC146745 5' TGGGTACTTGGGATACGGGAA  47924    A      _  TT_
                                TG GTATTTGG AT   GGAA
                                || |||||||| ||   ||||
                                AC CATGAACC TA   CCTT
                                 C       C  TGC
GAM1950 LOC153951 3' TGACAGTTGGATTTGGAGGAG  47925     G  T        AA
                                TGA TA TTGGATTTGGA  AG
                                ||| || ||||||||||  ||
                                ACT GT AACCTAAACCT  TC
                                  _  C         CC
GAM1950 LOC158696 3' AGTATTTGGGAAACTGAAA    47926         AT__
                                AGTATTTGG    TTGGAA
                                |||||||||    ||||||
                                TCATAAACC    GACTTT
                                     CTTT
GAM1950 LOC201243 5' TGGGTACTTGGGATACGGGAA  47924    A      _  TT_
                                TG GTATTTGG AT   GGAA
                                || |||||||| ||   ||||
                                AC CATGAACC TA   CCTT
                                 C       C  TGC
GAM1950 LOC254946 3' TGGCCTGATTTGGAGAAG    47927    A  ATTTG      A
                                TG GT     GATTTGGA AAG
                                || ||     |||||||| |||
                                AC CG     CTAAACCT TTC
                                 _  GA___       C
GAM1951 RB1CC1   3' TTGTTATTTAAATGACCTCTA  47930          ATAA
                                TTGTTATTTAAA    TTCTA
                                ||||||||||||    |||||
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                                AACAATAAATTT   GAGAT
                                       ACTG
GAM1951  TRHDE    3'  CTACTAATTTAAAATAATTCTA 47931       TT
                                TTATTG  ATTTAAAATAATTCTA
                                ||||||  ||||||||||||||||
                                GATGAT  TAAATTTTATTAAGAT
                                  __
GAM1951  FLJ21919 3'  TTATTGTCATTTAAAAACAACT 47932          _
                                TTATTGTTATTTAAAA TAATT
                                |||||||||||||||| |||||
                                AATAACAGTAAATTTT GTTGA
                                          T
GAM1951  MEGF10   3'  TATTTCTAAAATAATTCT    47933     A
                                TGTT TTTAAAATAATTCT
                                |||| ||||||||||||||
                                ATAA AGATTTTATTAAGA
                                  _
GAM1951  LOC153883 3'  CTATTGCCAAAAAAATGATTCT 47934        TTT    A
           A                     TTATTGTTA   AAAAT ATTCTA
                                |||||||||   ||||| ||||||
                                GATAACGGT   TTTTA TAAGAT
                                      TT_    C
GAM1951  LOC91960 3'  TTAATATTTAAAATAATTCTA  47935     T
                                TTG TATTTAAAATAATTCTA
                                ||| ||||||||||||||||
                                AAT ATAAATTTTATTAAGAT
                                  T
GAM1952  S100A8   3'  TTGAGGTATTGATGACTTTATT 47938     AT    AT
           A                     TTGA  GTATT  TGATTTTATTA
                                ||||  |||||  ||||||||||
                                AACT  CATAA  ACTGAAATAAT
                                  C_    CT
GAM1952  XRCC4    3'  TTCAATGTATCAAAAATTTTAT 47939    G       TT
           TA                     TT AATGTATTA  GATTTTATTA
                                || |||||||||  ||||||||||
                                AA TTACATAGT  TTAAAATAAT
                                  G        TT
GAM1952  XRCC4    3'  TTCAATGTATCAAAAATTTTAT 47939    G       TT
           TA                     TT AATGTATTA  GATTTTATTA
                                || |||||||||  ||||||||||
                                AA TTACATAGT  TTAAAATAAT
                                  G        TT
GAM1952  XRCC4    3'  TTCAATGTATCAAAAATTTTAT 47939    G       TT
           TA                     TT AATGTATTA  GATTTTATTA
                                || |||||||||  ||||||||||
                                AA TTACATAGT  TTAAAATAAT
                                  G        TT
GAM1952  My015    3'  TGAATGTATTATATCAATTTT  47940        __  TG
                                TGAATGTAT  TAT  ATTTT
                                |||||||||  |||  |||||
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                                ACTTACATA  ATA  TAAAA
                                     AT   GT
GAM1952  LOC51290  3'  TTGAATATATTGCACAATATTT 47941          __   TG_
             TATTA                  TTGAATGTAT  TAT   ATTTTATTA
                                ||||||||||  |||   |||||||||
                                AACTTATATA  GTG   TAAAATAAT
                                     AC   TTA
GAM1953  FLJ13105  3'  TCAATAATAATATTTTCAA   47944     T
                                TCA TAATAATATTTTTAA
                                ||| ||||||||||||||
                                AGT ATTATTATAAAAGTT
                                  T
GAM1954  TREM1     3'  TACAGATTTAATTCATGTT   47947          ATT
                                TATAGATTTAAT   TGTT
                                ||||||||||||   ||||
                                ATGTCTAAATTA   ACAA
                                       AGT
GAM1954  BCAA      3'  TAAGATTTAATACAGTTTAT   47948   T        TT
                                A AGATTTAATAT  GTTTAT
                                | ||||||||||  ||||||
                                A TCTAAATTATG  CAAATA
                                 T         T_
GAM1954  BRPF3     3'  CATAGATTTTTCTCTGTTTAT  47949         AATA
                                TATAGATTT    TTTGTTTAT
                                |||||||||    |||||||||
                                GTATCTAAA    AGACAAATA
                                     AAG_
GAM1954  C20orf38  3'  TATAGTTTAATATCTATATCA  47950       A          TT
                                TATAG TTTAATATTTGT  ATCA
                                |||||  ||||||||||||  ||||
                                ATATC AAATTATAGATA  TAGT

                                  _          __
GAM1954  KIAA1434  3'  TATAGATTTATATATTTAGTTT 47951          _     _
             A                   TATAGATTTA ATATTT GTTTA
                                ||||||||||  ||||||  |||||
                                ATATCTAAAT TATAAA CAAAT
                                     A     T
GAM1955  DKFZP564G092 5'  TATACAATTTTTAATATA    47954
                                TATATAATTTTTAATATA
                                |||||||||||||||||
                                ATATGTTAAAAATTATAT

GAM1955  KIAA1503  3'  TATATATTTTTAATAAATTAGT 47955        A        T
                                TATATA TTTTTAATA AATTAGT
                                ||||||  |||||||||  |||||||
                                ATATAT AAAAATTAT TTAATCA
                                  _       _
GAM1955  LOC146802 3'  TAATCTTTAATATAACAGT    47956              T
                                TAATTTTTAATATAAT AGT
                                |||||||||||||||  |||
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                                ATTAGAAATTATATTG TCA
                                                _
GAM1956  FLJ10036  3'  TATATTCCATTAAACTAAAAT  47959          TC   T
                                TATATTCTATT  GCT AAAAT
                                ||||||||||  ||| |||||
                                ATATAAGGTAA  TGA TTTTA
                                      TT  _
GAM1956  FLJ20152  3'  TATATATTCTATCTTCCCAA  47960            CG
                                TATATATTCTATTT  CTTAA
                                ||||||||||||||  |||||
                                ATATATAAGATAGA  GGGTT
                                        A_
GAM1956  KIAA0895  3'  TACATATTCTGTTTCATAAAA  47961          A     CT
                                TATATATTCT TTTCG  TAAAA
                                ||||||||||| |||||  |||||
                                ATGTATAAGA AAAGT  ATTTT
                                      C    __
GAM1956  LOC151194 3'  TATACATTTTATTTCCCC    47962         C      G
                                TATATATT TATTTC CT
                                |||||||| |||||| ||
                                ATATGTAA ATAAAG GG
                                     A     G
GAM1957  IGF1      3'  TATTAGATATTATTTTAAT   47965             A
                                TATTAGATATTAT TTAAT
                                |||||||||||| |||||
                                ATAATCTATAATA AATTA
                                       A
GAM1957  ARF4      3'  TTAGATATCCAATTTCAT    47966          ATAT
                                TTAGATATT    TAATTTCAT
                                |||||||||    |||||||||
                                AATCTATAG    GTTAAAGTA
                                       ____
GAM1958  ABH       3'  AGAGATAGTTGTGATTAATTT  47969     T    A    T
                                AGA GATAG TGTG ATTAATTT
                                ||| ||||| |||| ||||||||
                                TCT CTATC ACAC TAATTAAA
                                  _    A   _
GAM1958  PTHR2     3'  AAGATATAGATGCAGCAT    47970        A      _
                                AAGATG TAGATGT GTAT
                                |||||| ||||||| ||||
                                TTCTAT ATCTACG CGTA
                                     _      T
GAM1958  ASAH      3'  AAGATAATGATATATTAATTT  47971         A      AT
                                AAGATGAT GATGTGT  TAATTT
                                |||||||| |||||||  ||||||
                                TTCTATTA CTATATA  ATTAAA
                                       _     __
GAM1959  ITPR2     3'  TCATGTATTAATCTCAATATAT 47974         A      T_
                TT                   TCATGTAT TAATTTT  TATATTT
                                |||||||| |||||||  |||||||
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                                AGTACATA ATTAGAG  ATATAAA
                                   _     TT
GAM1959  MEF2C    3'  ATGTACATATTTTTATATTT  47975        AT
                                ATGTATATA  TTTTTATATTT
                                |||||||||  ||||||||||
                                TACATGTAT  AAAAATATAAA
                                   __
GAM1959  PSMB9    3'  TCATGTATAGGGCTCTTTATAT 47976        TAA
           TT                    TCATGTATA  TTTTTTATATTT
                                 |||||||||  ||||||||||||
                                 AGTACATAT  GAGAAATATAAA
                                      CCC
GAM1959  TNS      3'  TCATGTATATATTATATAATAT 47977         ATTTTTT
           TT                    TCATGTATATA     ATATTT
                                 ||||||||||      ||||||
                                 AGTACATATAT     TATAAA
                                       AATATAT
GAM1959  C1orf19  3'  TGCATATAATTTTTTATACTT  47978
                                 TGTATATAATTTTTTATATTT
                                 |||||||||||||||||||||
                                 ACGTATATTAAAAAATATGAA

GAM1960  ARTN     3'  CAATATGTGTCCTTCAAAT   47981     __
                                 TAATA  TGTTCTTCAAAT
                                 |||||  ||||||||||||
                                 GTTAT  ACAGGAAGTTTA
                                    AC
GAM1960  ARTN     3'  CAATATGTGTCCTTCAAAT   47981     __
                                 TAATA  TGTTCTTCAAAT
                                 |||||  ||||||||||||
                                 GTTAT  ACAGGAAGTTTA
                                    AC
GAM1960  ARTN     3'  CAATATGTGTCCTTCAAAT   47981     __
                                 TAATA  TGTTCTTCAAAT
                                 |||||  ||||||||||||
                                 GTTAT  ACAGGAAGTTTA
                                    AC
GAM1960  ARTN     3'  CAATATGTGTCCTTCAAAT   47981     __
                                 TAATA  TGTTCTTCAAAT
                                 |||||  ||||||||||||
                                 GTTAT  ACAGGAAGTTTA
                                    AC
GAM1960  GG2-1    3'  CAATATGCTTTTCTTCAAATA 47982       ___
                                 TAATATGT   TCTTCAAATA
                                 ||||||||   ||||||||||
                                 GTTATACG   AGAAGTTTAT
                                      AAA
GAM1960  KCNV1    3'  CAATATGTTCTTAAATA     47983         C
                                 TAATATGTTCTT AAATA
                                 |||||||||||| |||||
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                                GTTATACAAGAA TTTAT
                                      _
GAM1960  LOC115123 3'  CAAAACATTCTTCAAATA    47984     T
                                TAA ATGTTCTTCAAATA
                                ||| ||||||||||||||
                                GTT TGTAAGAAGTTTAT
                                  T
GAM1960  LOC89919  3'  CAACACGTTCTTCAAATA    47985
                                TAATATGTTCTTCAAATA
                                ||||||||||||||||||
                                GTTGTGCAAGAAGTTTAT

GAM1961  ERBB4    3'  AACATTGTGGTTCCTC      47988        C  C  AAAAA
                                AACATTGT GG TC    CTC
                                |||||||| || ||    |||
                                TTGTAACA CC AG    GAG
                                     _  A  _____
GAM1961  MFAP3    5'  TTGGAGAACTCAAAAACT    47989     TC  _
                                TTG  GG CTCAAAAACT
                                |||  || ||||||||||
                                AAC  CT GAGTTTTTGA
                                  CT  T
GAM1961  POU2AF1  5'  TGATGAGCCCAAAAGCTCC   47990    TC_       A
                                TG   GGCTCAAAA CTCC
                                ||   ||||||||| ||||
                                AC   TCGGGTTTT GAGG
                                 TAC        C
GAM1961  PTX3     3'  AACATTATCCTCAAAAGCT    47991         GG      A
                                AACATTGTC  CTCAAAA CT
                                |||||||||  ||||||| ||
                                TTGTAATAG  GAGTTTT GA
                                     __      C
GAM1961  RP42     3'  ACATTTTCTAAATAAAAGCTCC 47992       G  GGCTC    A
              C                  ACATT TC     AAAA CTCCC
                                |||||  ||     |||| |||||
                                TGTAA AG     TTTT GAGGG
                                   A  ATTTA    C
GAM1961  VASP     3'  CTATAGCATTTAAAAACTCCC  47993      C   TC__
                                TTGT GGC    AAAAACTCCC
                                ||||  |||    ||||||||||
                                GATA TCG    TTTTTGAGGG
                                  _   TAAA
GAM1961  C21orf108 3'  CATGTGCAGGGAAACTCCC    47994     _   C  CTCAA
                                CAT TGT GG     AAACTCCC
                                |||  ||| ||    ||||||||
                                GTA ACG CC     TTTGAGGG
                                  C   T  C_____
GAM1961  CSMD1    3'  TTGCCACTGAAAACTCCC     47995       G  CA
                                TTGTCG CT  AAAACTCCC
                                ||||||  ||  |||||||||
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                                AACGGT GA  TTTTGAGGG
                                   _ C_
GAM1961  DAMS     3'  GCCTAAGCTTTGAAAACTCCC  47996     __    CA_
                                GTC  GGCT   AAAACTCCC
                                |||  ||||   |||||||||
                                CGG  TCGA   TTTTGAGGG
                                  AT    AAC
GAM1961  DKFZP434P0111 3'  ACATTGTCTGCCAGGACT    47997        G  T  AAA
                                ACATTGTC GC CA   ACT
                                ||||||||  || ||   |||
                                TGTAACAG CG GT   TGA
                                     A  _  CC_
GAM1961  DKFZp761B1514 3'  GTCATCACTCAAAAGTTCC   47998      __       AC
                                GTCG  GCTCAAAA  TCC
                                ||||  ||||||||  |||
                                CAGT  TGAGTTTT  AGG
                                  AG       CA
GAM1961  FLJ10483  3'  AACATTGTCAGACTTGGAAGAG 47999          _  CAAAAAC__
            TTCCC                   AACATTGTCGG CT        TCCC
                                ||||||||||| ||        ||||
                                TTGTAACAGTC GA        AGGG
                                      T  ACCTTCTCA
GAM1961  FLJ11106  3'  TTGTCGACAAACTTCC      48000         TCAA    _
                                TTGTCGGC    AAACT CC
                                ||||||||    ||||| ||
                                AACAGCTG    TTTGA GG
                                     _____     A
GAM1961  FLJ11149  3'  AACATTGTACGGTTTAAACT   48001         _  CTCAA
                                AACATTGT CGG     AAACT
                                ||||||||  |||     |||||
                                TTGTAACA GCC     TTTGA
                                     T   AAA__
GAM1961  FLJ14260  3'  ATTTCCAGTCAAAAACT     48002     GT   C
                                ATT  CGG TCAAAAACT
                                |||  ||| |||||||||
                                TAA  GTC AGTTTTTGA
                                  AG  _
GAM1961  FLJ22938  5'  TTGTCTGGAAAAACTCC     48003       _  CTC
                                TTGTC GG   AAAAACTCC
                                |||||  ||   |||||||||
                                AACAG CC   TTTTTGAGG
                                   A  ___
GAM1961  KIAA0007  3'  CATTGGTATTAAAAACTCCC   48004       TCGGCTC
                                CATTG      AAAAACTCCC
                                |||||      ||||||||||
                                GTAAC      TTTTTGAGGG
                                   CATAA__
GAM1961  KIAA1371  3'  AACACTGTCTTAAAACT     48005         GGCTCA
                                AACATTGTC     AAAACT
                                |||||||||     ||||||
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                                TTGTGACAG     TTTTGA
                                     AA____
GAM1961  MRPL18   3'  AACATTATTGCTGTAAAACTTC 48006       CG   CA    _
             C                    AACATTGT  GCT  AAAACT CC
                                  ||||||||  |||  |||||| ||
                                  TTGTAATA  CGA  TTTTGA GG
                                      A_   CA     A
GAM1961  LOC148266 3'  CACTGTCATACACAGAATTCC  48007       GCT  AA_  C
                                  CATTGTCG   CA   AA TCC
                                  ||||||||   ||   || |||
                                  GTGACAGT   GT   TT AGG
                                      AT_  GTC  A
GAM1961  LOC219513 5'  ACATTGTCGCTCCCCTTCC   48008       G   AAAAAC
                                  ACATTGTCG CTC     TCC
                                  |||||||||| |||     |||
                                  TGTAACAGC GAG     AGG
                                      _   GGGA__
GAM1961  LOC221272 3'  TTGTGCAGGAAAACTCCC    48009     _   CTCA
                                  TTGT CGG    AAAACTCCC
                                  |||| |||    |||||||||
                                  AACA GTC    TTTTGAGGG
                                    C   C___
GAM1961  LOC253970 5'  ACACTGTCACTAGAGCTCCC   48010       G  CAAAAA
                                  ACATTGTCG CT     CTCCC
                                  |||||||||  ||     |||||
                                  TGTGACAGT GA     GAGGG
                                       _  TCTC__
GAM1961  LOC51036  3'  CACAGAGCTTAAAAACTCC    48011     TGTC    C
                                  CAT    GGCT AAAAACTCC
                                  |||    |||| |||||||||
                                  GTG    TCGA TTTTTGAGG
                                    TC__    A
GAM1961  LOC91661  3'  CAGTGTCAGCTTCGGGGACTCC 48012     T       _ AAAA
                                  CA TGTCGGCT C    ACTCC
                                  || ||||||||  |    |||||
                                  GT ACAGTCGA G    TGAGG
                                   C       A CCCC
GAM1961  LOC93349  3'  AACACTGTTGGCTTCCCGGAGA 48013       C    _ AAAA__
             CTCC                     AACATTGT GGCT C     ACTCC
                                  |||||||| |||| |     |||||
                                  TTGTGACA CCGA G     TGAGG
                                       A    A GGCCTC
GAM1962  AQP3     3'  GGACAGTCAGTGGATG      48016       C  ATATG
                                  GGGCAG CA     GTGGATG
                                  ||||||  ||     |||||||
                                  CCTGTC GT     CACCTAC
                                     A  _____
GAM1962  ATP2B2   3'  GGGTGCCTGGATGGATGGGTGC 48017     CA   AAT    _   A
                                  GGG  GCC   ATGG TGG TGC
                                  |||  |||   |||| ||| |||
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                                CCC  CGG   TACC ACC ACG
                                  A_   ACC    T   C
GAM1962  FOS      3'  TCGGGCAGTGGCACTTGTGGGT 48018         CCAATATG    A
                GC                  TCGGGCAG       GTGG TGC
                                    ||||||||       |||| |||
                                    AGCCCGTC       CACC ACG
                                       ACCGTGAA    C
GAM1962  IGF1     3'  CCGGGCATAGTGGTGGGTG    48019        GCCAATA     A
                                    TCGGGCA      TGGTGG TG
                                    |||||||      |||||| ||
                                    GGCCCGT      ACCACC AC
                                       ATC____     C
GAM1962  RSN      3'  TCGGGGGGCCAATAAATG     48020       CA      T
                                    TCGGG  GCCAATA GGTG
                                    |||||  ||||||| ||||
                                    AGCCC  CGGTTAT TTAC
                                       CC      _
GAM1962  USP6     5'  CGTCCAGGTCGATGTGGTGGAT 48021     GG   CCA_  A
                G                    CG  CAG    AT TGGTGGATG
                                    ||  |||    || |||||||||
                                    GC  GTC    TA ACCACCTAC
                                     AG   CAGC  C
GAM1962  CGRP-RCP  5'  TCGGGCAGCTCGTAGCCTCGTG 48022          CAATA    GGA_
                C                    TCGGGCAGC     TGGT    TGC
                                    |||||||||     ||||    |||
                                    AGCCCGTCG     ATCG    ACG
                                          AGC__    GAGC
GAM1962  FLJ20856  5'  GGGCAGGCACATGGTGGGTGC  48023       CCA       A
                                    GGGCAG   ATATGGTGG TGC
                                    ||||||   ||||||||| |||
                                    CCCGTC   TGTACCACC ACG
                                       CG_       C
GAM1962  MYT1     3'  TCGGGGGCCTGGGTGGATG    48024       CA   AATAT
                                    TCGGG  GCC    GGTGGATG
                                    |||||  |||    ||||||||
                                    AGCCC  CGG    CCACCTAC
                                       C_   AC____
GAM1962  LOC127534 3'  GGGCAGCTGGGTGAATA     48025        CAATAT
                                    GGGCAGC     GGTGGATG
                                    |||||||     ||||||||
                                    CCCGTCG     CCACTTAT
                                       AC_____
GAM1962  LOC153232 3'  CGGGCAGGGGTGGTGGTGGATG 48026         CCAATA
                                    CGGGCAG     TGGTGGATG
                                    |||||||     |||||||||
                                    GCCCGTC     ACCACCTAC
                                       CCCACC
GAM1962  LOC162333 5'  GAGCAGCCAGTGGGTTGGTGC  48027          ATAT  _  A
                                    GGGCAGCCA    GGT GG TGC
                                    |||||||||    ||| || |||
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                                CTCGTCGGT   CCA CC ACG
                                     CAC_   A  _
GAM1962  LOC254100 3'  TCGGGCAGCCAGATGG      48028          ATAT
                                TCGGGCAGCCA   GGTGG
                                ||||||||||    |||||
                                AGCCCGTCGGT   CTACC
                                      ____
GAM1963  FRAT2     3'  TGAGAAAGCTCCTGGCAT     48031     A        TTTAT
                                TGA AAAGCTTCTG    GCAT
                                ||| ||||||||||    ||||
                                ACT TTTCGAGGAC    CGTA
                                  C       _____
GAM1963  GAN       3'  TGAAAAAGTTTCTGATCCCTAT 48032        C    ___
               G                 TGAAAAAG TTCTG   TTTATG
                                ||||||||| |||||   ||||||
                                ACTTTTTC AAGAC   GGATAC
                                     A    TAG
GAM1963  NFRKB     5'  CGGAAAAGCTTCTGGGCA     48033     A        TTTAT
                                TG AAAAGCTTCTG    GCA
                                || ||||||||||     |||
                                GC TTTTCGAAGAC    CGT
                                 C         C____
GAM1963  SIM2      3'  TGAAAGGATTTCTGTTTAC    48034       AAGC
                                TGAAA    TTCTGTTTAT
                                |||||    ||||||||||
                                ACTTT    AAGACAAATG
                                   CCTA
GAM1963  PITPNM    3'  TGGAAAAGCCTCTGCGCCCATG 48035     A          __
                                TG AAAAGCTTCTGT  TTATG
                                || ||||||||||||  |||||
                                AC TTTTCGGAGACG  GGTAC
                                 C          CG
GAM1963  SLC37A1   3'  TGGAAAAGCCTCTGGGGCGATG 48036     A         TTTAT  _
                                TG AAAAGCTTCTG    GC ATG
                                || ||||||||||     || |||
                                AC TTTTCGGAGAC    CG TAC
                                 C         CC___  C
GAM1963  LOC149910 3'  AGGGTCATTTATGCATG     48037     CT  T
                                AG  TC GTTTATGCATG
                                ||  || ||||||||||
                                TC  AG TAAATACGTAC
                                 CC  _
GAM1963  LOC221954 5'  GCTTCTGTCCACATCATG     48038           _
                                GCTTCTGTTTATG CATG
                                |||||||||||| ||||
                                CGAAGACAGGTGT GTAC
                                        A
GAM1964  ZIC4      3'  TTAATATTTTATGGCCTTGGC  48041         AAGTG   A
                                TTAGTATT    ATG CCTTGGC
                                ||||||||    ||| |||||||
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                                AATTATAA    TAC GGAACCG
                                    AA___   C
GAM1965 B4GALT7  3' TGGCAACAACCAGCTAGAGC  48044   AG      CAATA
                                TG  AACAACCA    AGAGC
                                ||  ||||||||    |||||
                                AC  TTGTTGGT    TCTCG
                                 CG      CGA__
GAM1965 ETS2     3' TGAGAACAATTATAAGA     48045        CCACA
                                TGAGAACAA    ATAAGA
                                |||||||||    ||||||
                                ACTCTTGTT    TATTCT
                                    AA___
GAM1965 GPR48    3' TGAGAACATTACATGAAGC   48046       ACC   ATAA
                                TGAGAACA   ACA   GAGC
                                ||||||||   |||   ||||
                                ACTCTTGT   TGT   TTCG
                                    AA_   AC__
GAM1965 LGI1     5' TAAGAACAGGTCACATAGGAG 48047       AC_   A  A
                                TGAGAACA   CACA TA GAG
                                ||||||||   |||| || |||
                                ATTCTTGT   GTGT AT CTC
                                    CCA   _  C
GAM1965 NPC2     3' TGAGAACCAGCCACCCGGAGC 48048       AA_   AATAA
                                TGAGAAC   CCAC    GAGC
                                |||||||   ||||    ||||
                                ACTCTTG   GGTG    CTCG
                                    GTC   GGC__
GAM1965 SLC24A1  3' AGAAACACAACAATAAGAG   48049     CA  C
                                AGAA  AC ACAATAAGAG
                                ||||  || ||||||||||
                                TCTT  TG TGTTATTCTC
                                  TG  T
GAM1965 CMG1     5' TGGGACAACCACGAGAAC    48050    A  A     AATA
                                TG GA CAACCAC    AGAGC
                                || || |||||||    |||||
                                AC CT GTTGGTG    TCTTG
                                 C  _      C___
GAM1965 DKFZP586M1120 3' TGAGAACAATCATGCTGGGAGC 48051         C  CAATAA
                                TGAGAACAA CA     GAGC
                                ||||||||| ||     ||||
                                ACTCTTGTT GT     CTCG
                                    A  ACGACC
GAM1965 ENDOGLYX1 3' TGAGAACTATCACAAGAACAGC 48052       AAC    T  G
                                TGAGAAC   CACAA AA AGC
                                |||||||   ||||| || |||
                                ACTCTTG   GTGTT TT TCG
                                    ATA    C  G
GAM1965 FENS-1   3' TGACAACAGCCACAAGAAC   48053    G   A    ATA
                                TGA AACA CCACA   AGAGC
                                ||| |||| |||||   |||||
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                                ACT TTGT GGTGT   TCTTG
                                  G   C    ___
GAM1965  FLJ21324  5'  TGAGAACAAACTGCAGAG    48054        CC  AATA
                                TGAGAACAA  AC   AGAG
                                |||||||||  ||   ||||
                                ACTCTTGTT  TG   TCTC
                                     __ ACG_
GAM1965  FLJ31168  3'  TGAGAACAGACCACCATGAGC  48055       _    AATAA
                                TGAGAACA ACCAC    GAGC
                                |||||||| |||||    ||||
                                ACTCTTGT TGGTG    CTCG
                                     C    GTA__
GAM1965  HSPC111   3'  TGAGAACAGTTCCTTCCCCAGA 48056       A__  ACAATA
            GC                    TGAGAACA   CC     AGAGC
                                |||||||   ||     |||||
                                ACTCTTGT   GG     TCTCG
                                     CAA  AAGGGG
GAM1965  HTCD37    3'  TGAAACAGTCACAATAAG    48057      A  AC
                                TGAGA CA  CACAATAAG
                                |||||  ||  |||||||||
                                ACTTT GT  GTGTTATTC
                                   _ CA
GAM1965  JM11      3'  TGAGAGCAACCACACCCCAGGG 48058      A       ATA_  A
            C                    TGAGA CAACCACA    AG GC
                                |||||  ||||||||    || ||
                                ACTCT GTTGGTGT    TC CG
                                   C       GGGG  C
GAM1965  KIAA0265  3'  TAAGAGCAACAACAAAGAGC   48059      A    C    TA
                                TGAGA CAAC ACAA  AGAGC
                                |||||  ||||  ||||  |||||
                                ATTCT GTTG TGTT  TCTCG
                                   C    T    __
GAM1965  KIAA0472  3'  AGGACAGACCACAATAAG    48060    A  _
                                AG ACA ACCACAATAAG
                                || ||| ||||||||||
                                TC TGT TGGTGTTATTC
                                 C   C
GAM1965  KIAA0669  3'  AGTACATATTACAATAAGAG   48061    A  ACC_
                                AG ACA    ACAATAAGAG
                                || |||    ||||||||||
                                TC TGT    TGTTATTCTC
                                 A   ATAA
GAM1965  KIAA1036  3'  TGAGAACAGCCTGAACAAA    48062        A  AC
                                TGAGAACA CC  AATAAG
                                |||||||| ||  ||||||
                                ACTCTTGT GG  TTGTTT
                                     C  AC
GAM1965  KIAA1155  3'  TGAGCACAACAATTCAAGAG   48063     A    CACAA
                                TGAG ACAAC    TAAGAG
                                ||||  |||||    ||||||
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                                ACTC TGTTG    GTTCTC
                                  G    TTAA_
GAM1965 KLF12    3' GAGAACAATTGTAAGATGC   48064       CCACAA    _
                                GAGAACAA     TAAGA GC
                                ||||||||     ||||| ||
                                CTCTTGTT     ATTCT CG
                                     AAC___    A
GAM1965 MGC2477  3' TGAAACAACCACTGAG     48065      A     AATAA
                                TGAGA CAACCAC    GAG
                                ||||| |||||||    |||
                                ACTTT GTTGGTG    CTC
                                  _     A____
GAM1965 MGC3130  3' TGGGAGCAACCACAGAAGC   48066    A A      ATAA
                                TG GA CAACCACA    GAGC
                                || || ||||||||    ||||
                                AC CT GTTGGTGT    TTCG
                                 C  C       C___
GAM1965 MGC4618  3' TGAGGACTGAAATAAGAGC   48067     A  AACCAC
                                TGAG AC     AATAAGAGC
                                |||| ||     |||||||||
                                ACTC TG     TTATTCTCG
                                  C  ACT___
GAM1965 NAPG     5' TGAGAACAGCCTGTGCAACATG 48068        A  A___    A_
           GAGC                   TGAGAACA CC    CAATA  GAGC
                                |||||||| ||    |||||  ||||
                                ACTCTTGT GG    GTTGT  CTCG
                                     C  ACAC    AC
GAM1965 NDP52    3' TGAGAACAAATACACTCAAGGG 48069        CC   A_   A
           C                    TGAGAACAA  ACA  TAAG GC
                                |||||||||  |||  |||| ||
                                ACTCTTGTT  TGT  GTTC CG
                                     TA   GA    C
GAM1965 PPP1R3B  3' TAAGAACAGCCAGTTTTAGGAG 48070        A   CAA_  A
                                TGAGAACA CCA    TA GAG
                                |||||||| |||    || |||
                                ATTCTTGT GGT    AT CTC
                                     C   CAAA  C
GAM1965 SERPINA7 5' TGAGACAACCACTGAGGGAGC  48071      A      AATAA
                                TGAGA CAACCAC    GAGC
                                ||||| |||||||    ||||
                                ACTCT GTTGGTG    CTCG
                                  _      ACTCC
GAM1965 TLN2     3' TGAGAACAAGCACGCAGGGC   48072        C   AATA  A
                                TGAGAACAA CAC    AG GC
                                ||||||||| |||    || ||
                                ACTCTTGTT GTG    TC CG
                                     C   CG__  C
GAM1965 TUSP     3' TGAGAACACCCCTGTAAAGAGC 48073        A  ACAAT
                                TGAGAACA CC    AAGAGC
                                |||||||| ||    ||||||
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                                ACTCTTGT GG    TTCTCG
                                     G  GACAT
GAM1965  LOC124152 3'  GAAAACTGGTAATAAGAGC   48074       AACCAC
                                GAGAAC     AATAAGAGC
                                ||||||     |||||||||
                                CTTTTG     TTATTCTCG
                                   ACCA__
GAM1965  LOC137886 3'  TAAGAACAACTGCATTAAG   48075         CA  A
                                TGAGAACAAC  CA TAAG
                                ||||||||||  || ||||
                                ATTCTTGTTG  GT ATTC
                                      AC  A
GAM1965  LOC146268 5'  GAAGGTCCAGACAATAAGAG  48076     CAA  __
                                GAA   CC  ACAATAAGAG
                                |||   ||  ||||||||||
                                CTT   GG  TGTTATTCTC
                                  CCA  TC
GAM1965  LOC147639 5'  TGAGAACAGCCAGGTCTCTCAG 48077         A   CAATA___
            AG                    TGAGAACA CCA       AGAG
                                ||||||||| |||       ||||
                                ACTCTTGT GGT       TCTC
                                     C   CCAGAGAG
GAM1965  LOC149305 5'  TGAGAACACCAATCAGAGC   48078         A   CAATA
                                TGAGAACA CCA     AGAGC
                                ||||||||| |||    |||||
                                ACTCTTGT GGT     TCTCG
                                     _   TAG__
GAM1965  LOC158301 3'  TGAGAACAATTCCAATGAAG   48079         CCA   _
                                TGAGAACAA   CAAT AAG
                                |||||||||   |||| |||
                                ACTCTTGTT   GTTA TTC
                                      AAG    C
GAM1965  LOC221272 3'  AAAACCTATTACAATAAGAG   48080       AACC_
                                AGAAC     ACAATAAGAG
                                |||||     ||||||||||
                                TTTTG     TGTTATTCTC
                                   GATAA
GAM1965  LOC221931 3'  TGAGAACCACACAATAAGGGC  48081        AAC        A
                                TGAGAAC   CACAATAAG GC
                                |||||||   ||||||||| ||
                                ACTCTTG   GTGTTATTC CG
                                     GT_        C
GAM1965  LOC51291  3'  GAGTGACCACAACCAAAG    48082     AACA       A
                                GAG    ACCACAAT AGAG
                                |||    |||||||| ||||
                                CTC    TGGTGTTG TTTC
                                  AC__       G
GAM1965  LOC51605  3'  AGAACAAAGAATAAGAG     48083        CCAC
                                AGAACAA    AATAAGAG
                                |||||||    ||||||||
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                                TCTTGTT   TTATTCTC
                                   TC__
GAM1966 CPNE3   3' CAAAATGATGTGTCATCTA   48086   C   CA
                                CA AATGA  TGTCATCTA
                                || |||||  |||||||||
                                GT TTACT  ACAGTAGAT
                                 T    AC
GAM1966 CYP1B1  3' TATTACACAAGGCATAT    48087        TGA
                                TATTACACAA   CATGT
                                ||||||||||   |||||
                                ATAATGTGTT   GTATA
                                      CC_
GAM1966 EGR3    3' TATCATGCAGTGACATGCAT  48088     CA  A     T
                                TATTA  CA TGACATG CAT
                                |||||  || ||||||| |||
                                ATAGT  GT ACTGTAC GTA
                                   AC  C     _
GAM1966 IL15    3' TATTACTCAATGACATTTTTCT 48089      A       GTCA
                                TATTAC CAATGACAT    TCT
                                |||||| |||||||||    |||
                                ATAATG GTTACTGTA    AGA
                                    A       AAA_
GAM1966 LARS2   3' TATTACACTAAAAAAGTCATCT 48090       AATGACAT
                                TATTACAC       GTCATCT
                                ||||||||       |||||||
                                ATAATGTG       CAGTAGA
                                     ATTTTTT_
GAM1966 OXTR    3' TACAAAACTGTGTCATCT    48091     C   GACA
                                TACA AAT    TGTCATCT
                                |||| |||    ||||||||
                                ATGT TTG    ACAGTAGA
                                  T   AC__
GAM1966 PCDHB11  3' TATTCACAATGATATGC    48092     A      C
                                TATT CACAATGA ATGT
                                |||| |||||||| ||||
                                ATAA GTGTTACT TACG
                                  _       A
GAM1966 PPIL1   3' CATTACATGTCATTCTATGTCA 48093       CA__  GAC
            TCTA                   TATTACA    AT   ATGTCATCTA
                                |||||||    ||   ||||||||||
                                GTAATGT    TA   TACAGTAGAT
                                    ACAG  AGA
GAM1966 PRKY    3' CACAATGACACCCGACTA    48094         G  AT
                                CACAATGACAT TC  CTA
                                |||||||||| ||  |||
                                GTGTTACTGTG GG  GAT
                                       _ CT
GAM1966 ENDOFIN  3' TATTACACATGAGAATGT    48095        A   C_
                                TATTACACA TGA  ATGT
                                ||||||||| |||  ||||
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                                ATAATGTGT ACT  TACA
                                      _  CT
GAM1966  FLJ22531  5'  TTACACAATGAAGAGCAT    48096          CAT T
                                TTACACAATGA   G CAT
                                ||||||||||   | |||
                                AATGTGTTACT   C GTA
                                     TCT _
GAM1966  KIAA0630  5'  TATTCACCTGAGCCATGTCATC 48097     A   AATGA_
            TA                    TATT CAC     CATGTCATCTA
                                ||||| |||     ||||||||||
                                ATAA GTG     GTACAGTAGAT
                                  _  GACTCG
GAM1966  KIAA1046  3'  TATTACACATGGCATGC     48098         A  A
                                TATTACACA TG CATGT
                                ||||||||| || |||||
                                ATAATGTGT AC GTACG
                                      _ C
GAM1966  KIAA1500  3'  TATTACACAATGTGAAGGCTCT 48099           ACATGTCA
                                TATTACACAATG       TCT
                                ||||||||||||       |||
                                ATAATGTGTTAC       AGA
                                      ACTTCCG_
GAM1966  PRO0767   5'  ATTACATAGCACTCATGTCAT  48100       CA__  GA
                                ATTACA   AT  CATGTCAT
                                ||||||   ||  ||||||||
                                TAATGT   TG  GTACAGTA
                                   ATCG  A_
GAM1966  STHM      3'  TATTACCTGGTGACATCATCC  48101       ACAA    TG
                                TATTAC   TGACA  TCATCT
                                ||||||   |||||  ||||||
                                ATAATG   ACTGT  AGTAGG
                                   GACC    __
GAM1966  LOC129831 3'  TATTTCACAATGAGTTTATC   48102      A       CA_
                                TATT CACAATGA   TGTC
                                |||| ||||||||   ||||
                                ATAA GTGTTACT   ATAG
                                  A       CAA
GAM1966  LOC145662 3'  CACAATGAAAATTCTATGTCAT 48103         C_______
                                CACAATGA      ATGTCAT
                                ||||||||      |||||||
                                GTGTTACT      TACAGTA
                                     TTTAAGA
GAM1966  LOC145846 3'  TATTACACAAGGGTATCAC    48104          TGACA
                                TATTACACAA     TGTCAT
                                ||||||||||     ||||||
                                ATAATGTGTT     ATAGTG
                                      CCC__
GAM1966  LOC146839 3'  TATTACATATGAACACATC    48105        CA   _
                                TATTACA  ATGA CATGTC
                                |||||||  |||| ||||||
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                                ATAATGT  TACT GTGTAG
                                   A_   T
GAM1966  LOC256471 3'  TATTCACAATGACATGT     48106      A
                                TATT CACAATGACATGT
                                |||| ||||||||||||
                                ATAA GTGTTACTGTACA
                                  _
GAM1966  LOC90786  5'  TACACAATGAATGGGTCTA    48107          C   TCA
                                TACACAATGA ATG   TCTA
                                |||||||||| |||   ||||
                                ATGTGTTACT TAC   AGAT
                                      _  CC_
GAM1967  CARKL     3'  TGAAGTACACATTGA       48110           AGGC
                                TGAAGTACACA    TTGA
                                ||||||||||    ||||
                                ACTTCATGTGT    AACT
                                       ____
GAM1967  EDN3      3'  TGAAATACACACAGAGGATT   48111           ___   C
                                TGAAGTACACA   AGG TT
                                ||||||||||   ||| ||
                                ACTTTATGTGT   TCC AA
                                      GTC   T
GAM1967  EIF4EBP2  3'  TGAAGTACAAGAGGACTC    48112          CA   _
                                TGAAGTACA  AGG CTT
                                |||||||||  ||| |||
                                ACTTCATGT  TCC GAG
                                      TC   T
GAM1967  GCH1      3'  TGAAGTCTGTTGAACTTGAATT 48113       ACACAA       C
            CA                    TGAAGT     GGCTTGAAT CA
                                ||||||     ||||||||| ||
                                ACTTCA     TTGAACTTA GT
                                   GACAAC        A
GAM1967  SYNGR2    3'  TGAGGACACAAGAGCCTGGTCC 48114     A T      _     AA
                                TGA G ACACAAG GCTTG  TCC
                                ||| | ||||||| |||||  |||
                                ACT C TGTGTTC CGGAC  AGG
                                  _ C      T     C_
GAM1967  TNFSF6    3'  TGAGGTAGCAAGGCCCA     48115     A   CA
                                TGA GTA  CAAGGCTTG
                                ||| |||  |||||||||
                                ACT CAT  GTTCCGGGT
                                  C   C_
GAM1967  TYRP1     5'  TGAAGCACGTAGAGGAAAATCC 48116        ACA_   CTT
            A                    TGAAGTAC    AGG   GAATCCA
                                ||||||||    |||   |||||||
                                ACTTCGTG    TCC   TTTAGGT
                                     CATC   T__
GAM1967  VLDLR     3'  AAGTACACAAGCTTGATCCA   48117          G     A
                                AAGTACACAAG CTTGA TCCA
                                |||||||||| ||||| ||||
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                                TTCATGTGTTC GAACT AGGT
                                      _   _
GAM1967 AUH     3' TGAAGTACACGGATGGGTCCA 48118        AA  CT  AA
                                TGAAGTACAC  GG  TG  TCCA
                                ||||||||||  ||  ||  ||||
                                ACTTCATGTG  CC  AC  AGGT
                                      __  T_  CC
GAM1967 BDG-29  3' CGAGTACACAAGGTGTCC    48119    A       CT  AA
                                TGA GTACACAAGG  TG  TCC
                                ||| ||||||||||  ||  |||
                                GCT CATGTGTTCC  AC  AGG
                                  _       __ __
GAM1967 C1QTNF7  3' TGAAATACACAGGGTCTC    48120         A  _
                                TGAAGTACACA GG CTT
                                |||||||||||| || |||
                                ACTTTATGTGT CC GAG
                                       C  A
GAM1967 C2F     5' GTTCACGAGGCTTGAATCCA  48121    A   A
                                GT CAC AGGCTTGAATCCA
                                || ||| ||||||||||||||
                                CA GTG TCCGAACTTAGGT
                                 A   C
GAM1967 FLJ10330 3' GAAGCTTGAGGCTTGAATC   48122      ACACA
                                GAAGT    AGGCTTGAATC
                                |||||    ||||||||||||
                                CTTCG    TCCGAACTTAG
                                   AAC__
GAM1967 FLJ11767 3' GTACACAAGGGGAACTCCA   48123        CTT  _
                                GTACACAAGG   GAA TCCA
                                ||||||||||   ||| ||||
                                CATGTGTTCC   CTT AGGT
                                      C__   G
GAM1967 FLJ12716 3' TGAGTACACACTGAAT     48124     A     AGGC
                                TGA GTACACA    TTGAAT
                                ||| |||||||    ||||||
                                ACT CATGTGT    GACTTA
                                  _     _____
GAM1967 FLJ23017 3' TGGAGAGCACAAGGCTCTTCCC 48125    A  TA       GAA
           A                     TG AG  CACAAGGCTT   TCCA
                                || ||  ||||||||||   ||||
                                AC TC  GTGTTCCGAG   GGGT
                                 C  TC        AA_
GAM1967 KIAA0895 3' TGAAGAACCATTTGAATCC   48126      T  A  AGGC
                                TGAAG AC CA    TTGAATCC
                                ||||| || ||    ||||||||
                                ACTTC TG GT    AACTTAGG
                                   T  _  A___
GAM1967 KIAA1254 3' TGAAGTACACACATTAGAAT  48127          AGGCTT
                                TGAAGTACACA     GAAT
                                ||||||||||      ||||
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                                ACTTCATGTGT     CTTA
                                      GTAAT_
GAM1967 OSBPL1A  3' TGAAATGCACAAGGCCTCC   48128      A      TGAA
                                TGAAGT CACAAGGCT   TCC
                                |||||| |||||||||   |||
                                ACTTTA GTGTTCCGG   AGG
                                   C       _____
GAM1967 OSBPL1A  3' TGAAATGCACAAGGCCTCC   48128      A      TGAA
                                TGAAGT CACAAGGCT   TCC
                                |||||| |||||||||   |||
                                ACTTTA GTGTTCCGG   AGG
                                   C       _____
GAM1967 OSBPL1A  3' TGAAATGCACAAGGCCTCC   48128      A      TGAA
                                TGAAGT CACAAGGCT   TCC
                                |||||| |||||||||   |||
                                ACTTTA GTGTTCCGG   AGG
                                   C       _____
GAM1967 SEC61A1  3' GTGCACAGACAAATCC     48129    A   A   TT
                                GT CACA GGC  GAATCC
                                || |||| |||  ||||||
                                CA GTGT CTG  TTTAGG
                                 C   _  __
GAM1967 SPBPBP   3' TGAAGTACAAAGGTTGA    48130        C   C
                                TGAAGTACA AAGG TTGA
                                ||||||||| |||| ||||
                                ACTTCATGT TTCC AACT
                                      _   _
GAM1967 STAT2    3' GAGTCACACAGGCCTGA    48131    AG    A
                                GA  TACACA GGCTTGA
                                ||  |||||| |||||||
                                CT  GTGTGT CCGGACT
                                 CA     _
GAM1967 VAV3     3' TGAGGTAAAGGTCTTGAATC  48132    A  CAC   _
                                TGA GTA   AAGG CTTGAATC
                                ||| |||   |||| ||||||||
                                ACT CAT   TTCC GAACTTAG
                                  C  ___   A
GAM1967 LOC133088 5' TGGAGTAATGAGCTCAAATCC  48133   A   CACAA   TG
                                TG AGTA    GGCT  AATCC
                                || ||||    ||||  |||||
                                AC TCAT    TCGA  TTAGG
                                 C   TAC__   GT
GAM1967 LOC150862 5' TGGGGTGCACAAAGCTTG   48134    AA  A
                                TG  GT CACAAGGCTTG
                                ||  || ||||||||||
                                AC  CA GTGTTTCGAAC
                                 CC  C
GAM1967 LOC158357 3' TGAACTACACAATAGGATT   48135     G    __   C
                                TGAA TACACA  AGG TT
                                |||| ||||||  ||| ||
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                                ACTT ATGTGT  TCC AA
                                  G     TA   T
GAM1967  LOC165257 5'  TGGGGCACACAAGACGAATCC  48136    AA         TT
                                TG  GTACACAAGGC  GAATCC
                                ||  ||||||||||  ||||||
                                AC  CGTGTGTTCTG  CTTAGG
                                 CC         __
GAM1967  LOC222166 3'  TGAAGTACACTGGAAATC    48137          AA  CTT
                                TGAAGTACAC  GG   GAATC
                                ||||||||||  ||   |||||
                                ACTTCATGTG  CC   TTTAG
                                      A_  ___
GAM1968  ANKRD3    3'  TTACATCCAAGAACCGCCCT   48140          AAA__
                                TTACATCCAA    GTTCT
                                ||||||||||    |||||
                                AATGTAGGTT    CGGGA
                                      CTTGG
GAM1968  COPA      3'  ATTACATCCTGCTCCTTTCTAG 48141         AAAAA   ___
                                ATTACATCC    GTTC   TCTAG
                                |||||||||    ||||   |||||
                                TAATGTAGG    CGAG   AGATC
                                     A____   GAA
GAM1968  ETF1      3'  TTACATCCAATTTCTCT     48142          AAAG
                                TTACATCCAA    TTCTCT
                                ||||||||||    ||||||
                                AATGTAGGTT    AAGAGA
                                      A___
GAM1968  KL        3'  ATTTCATCCTTATTCTCTAG   48143     A    AAAAA
                                ATT CATCC     GTTCTCTAG
                                ||| |||||     |||||||||
                                TAA GTAGG     TAAGAGATC
                                  A     AA___
GAM1968  SFRS2IP   5'  TTACGTCCACTCTCTA      48144      A    AAAAG
                                TTAC TCCA     TTCTCTA
                                |||| ||||    |||||||
                                AATG AGGT     GAGAGAT
                                  C   _____
GAM1968  DKFZP572C163 5'  CATTACATTCATAAAGTT    48145        C  A
                                CATTACAT CA AAAGTT
                                |||||||| || ||||||
                                GTAATGTA GT TTTCAA
                                     A  A
GAM1968  FLJ22756  3'  CATTACACTCAAGGGTCCT   48146       TC   AAA
                                CATTACA  CAA   GTTCT
                                |||||||  |||   |||||
                                GTAATGT  GTT   CAGGA
                                    GA   CC_
GAM1968  PAIP1     3'  CATGACATTTAAAAAGCCCT   48147     T    CC
                                CAT ACAT  AAAAAGTTCT
                                ||| ||||  ||||||||||
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                                GTA TGTA  TTTTTCGGGA
                                  C    AA
GAM1968  PRMT3    3'  ATTACATCCTGATTTTCTAG  48148        AAAAA  C
                                ATTACATCC    GTT TCTAG
                                |||||||||    ||| |||||
                                TAATGTAGG    TAA AGATC
                                     AC___   A
GAM1968  SCYB11   3'  CATCAAATCTAGAAGGTTCTCT 48149      C  CAAAAA
              AG                  CATTA ATC     GTTCTCTAG
                                |||||  |||     |||||||||
                                GTAGT TAG     CAAGAGATC
                                   T   ATCTTC
GAM1968  LOC129138 3'  CATTACATCTGCAAAGCCCC  48150        CAA
                                CATTACATC   AAAGTTCT
                                |||||||||   ||||||||
                                GTAATGTAG   TTTCGGGG
                                     ACG
GAM1968  LOC221662 3'  TCACATCTAAAGTTCC      48151       CAA
                                TTACATC   AAAGTTCT
                                |||||||   ||||||||
                                AGTGTAG   TTTCAAGG
                                   A__
GAM1968  LOC256112 3'  CATTACATCCAAAAGGTT    48152           A
                                CATTACATCCAAAA GTT
                                |||||||||||||| |||
                                GTAATGTAGGTTTT CAA
                                        C
GAM1968  LOC57406  3'  TTACATCCAAGGGTTCT     48153         AAA
                                TTACATCCAA   GTTCT
                                ||||||||||   |||||
                                AATGTAGGTT   CAAGA
                                     CC_
GAM1969  ARNT2    3'  TAAACTGTCCACTGACACCTGC 48156    C       CC  T T
              T                  TAA CTGTCCAC  GC C CTGCT
                                ||| ||||||||  || | |||||
                                ATT GACAGGTG  TG G GACGA
                                  T       AC  T _
GAM1969  CPD      3'  CTGTCCCATCTCTGC      48157     CCA   C
                                CTGT   CCCG TCTCTGC
                                ||||   |||| |||||||
                                GACA   GGGT AGAGACG
                                     ___   _
GAM1969  CSNK1G2  5'  CCTCTCCACGGTGACTCTGCT  48158    G    CCGCT
                                CCT TCCAC    CTCTGCT
                                ||| |||||    |||||||
                                GGA AGGTG    GAGACGA
                                  G    CCACT
GAM1969  GDF2     3'  ACCTGCCCGCCTGTGC      48159      TCCA    T  C
                                ACCTG   CCCGC CT TGC
                                |||||   ||||| || |||
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                                TGGAC   GGGCG GA ACG
                                  _____   _ C
GAM1969 PRX     3' CCTGCTGTGCCCTCTGCT   48160      CCACCC
                                CCTGT    GCTCTCTGCT
                                |||||    ||||||||||
                                GGACG    CGGGAGACGA
                                  ACA___
GAM1969 RIMS1   5' CCTGCCCGCCCCCTCTGCT  48161       A  G T
                                CCTGTCC CCC C CTCTGCT
                                ||||||| ||| | |||||||
                                GGACGGG GGG G GAGACGA
                                   C  _ _
GAM1969 SLC2A4  3' CCTGTCCTGCTCTCTGCT   48162       ACCC
                                CCTGTCC   GCTCTCTGCT
                                |||||||   ||||||||||
                                GGACAGG   CGAGAGACGA
                                   A___
GAM1969 SORBS1  3' TAACCTATCTGCTTGGCCATCT 48163        CACCC_  C
           GCT                    TAACCTGTC    GCT TCTGCT
                                |||||||||    ||| ||||||
                                ATTGGATAG    CGG AGACGA
                                     ACGAAC  T
GAM1969 XPC     3' ACCTGTACTTCTCTGC     48164      CCACCC  _
                                ACCTGT    GCT CTCTGC
                                ||||||    ||| ||||||
                                TGGACA    TGA GAGACG
                                  _______  A
GAM1969 AFAP    3' ACCTGTCCTCCGGCCAGCT  48165       A  C  CTCT
                                ACCTGTCC CC GCT   GCT
                                |||||||| || |||   |||
                                TGGACAGG GG CGG   CGA
                                   A  C  T___
GAM1969 AKR1B10 5' GTCTCACGTCCTGCTCTCTG  48166    _  __ _
                                GTC CAC  CC GCTCTCTG
                                ||| |||  || ||||||||
                                CAG GTG  GG CGAGAGAC
                                  A  CA  A
GAM1969 ChGn    5' AACTTGTCCACCCTTTTTGCT 48167    C       GCTCTC
                                AAC TGTCCACCC    TGCT
                                ||| |||||||||    ||||
                                TTG ACAGGTGGG    ACGA
                                  A       AAAA__
GAM1969 FLJ14437 3' ACCTGTCCGCCTTTCTCC   48168       A  CGC
                                ACCTGTCC CC  TCTCT
                                |||||||| ||  |||||
                                TGGACAGG GG  AGAGG
                                   C  AA_
GAM1969 FLJ20967 3' AACCTGTCCCATGCCTCTCTGC 48169        ACCCG
           T                    AACCTGTCC   CTCTCTGCT
                                |||||||||   |||||||||
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                              TTGGACAGG    GAGAGACGA
                                   GTACG
GAM1969 KIAA0821  3' AACCTGTCCATCTGC      48170        CCCGCTC   _
                              AACCTGTCCA     TCTG C
                              ||||||||||     |||| |
                              TTGGACAGGT     AGAC G
                                   _______   A
GAM1969 MGC10960  3' GCCATCCGCTCTCTGCT    48171   T   C
                              G CCA CCGCTCTCTGCT
                              | ||| ||||||||||||
                              C GGT GGCGAGAGACGA
                               _  A
GAM1969 MGC3123   3' CCTGGCCGCTCCCAATGCT   48172    TCCAC      __
                              CCTG    CCGCTCTC  TGCT
                              ||||    ||||||||  ||||
                              GGAC    GGCGAGGG  ACGA
                                C____      TT
GAM1969 LOC148293 3' CCACCATTCTGCTCTCTGCT  48173     C____
                              CCACC    GCTCTCTGCT
                              |||||    ||||||||||
                              GGTGG    CGAGAGACGA
                                 TAAGA
GAM1969 LOC150538 3' CCGTCTGTTCCCTTCTCTGCT 48174     CA__  GC
                              CTGTC   CCC  TCTCTGCT
                              |||||   |||  ||||||||
                              GGCAG   GGG  AGAGACGA
                                 ACAA  A_
GAM1969 LOC158117 3' TAACCTCTTAACCTCTCTGCT 48175     GTCC  CGC
                              TAACCT   ACC  TCTCTGCT
                              ||||||   |||  ||||||||
                              ATTGGA   TGG  AGAGACGA
                                 GAAT  ___
GAM1969 LOC197342 3' ACCTGGTGCTGCTCTCTGCT  48176     TCCACCC
                              ACCTG     GCTCTCTGCT
                              |||||     ||||||||||
                              TGGAC     CGAGAGACGA
                                 CACGA__
GAM1969 LOC203275 3' TAACCTCTTAACCTCTCTGCT 48175     GTCC  CGC
                              TAACCT   ACC  TCTCTGCT
                              ||||||   |||  ||||||||
                              ATTGGA   TGG  AGAGACGA
                                 GAAT  ___
GAM1969 LOC254018 3' CTGTCCATGGCTGTCTCTGCT 48177      CCC  __
                              CTGTCCA  GC  TCTCTGCT
                              |||||||  ||  ||||||||
                              GACAGGT  CG  AGAGACGA
                                 AC_  AC
GAM1969 LOC254873 3' CCTGTCCTGCTCTCTGCT   48162      ACCC
                              CCTGTCC   GCTCTCTGCT
                              |||||||   ||||||||||
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                                GGACAGG   CGAGAGACGA
                                   A___
GAM1969 LOC256529 5' CCTGTCCATCTACTTGCT   48178       CCC  CTC
                                CCTGTCCA  GCT  TGCT
                                ||||||||  |||  ||||
                                GGACAGGT  TGA  ACGA
                                   AGA  ___
GAM1969 LOC90785  3' CCTGTCCATCCTCACACTTGCT 48179      _ _  T  C
                                CCTGTCCA CC CGC CT TGCT
                                |||||||| || ||| || ||||
                                GGACAGGT GG GTG GA ACGA
                                   A A  T  _
GAM1969 LOC91522  3' CCTGTCCACTTTCCGGCAGCT  48180       ___  CTCTCT
                                CCTGTCCAC  CCG    GCT
                                |||||||||  |||    |||
                                GGACAGGTG  GGC    CGA
                                   AAA  CGT___
GAM1970 GALNT2    3' AAACTAACGCAACCGCAGTAAG 48183      TGA       A
                                AAATTG  GCAACCGCA TAAG
                                ||||||  ||||||||| ||||
                                TTTGAT  CGTTGGCGT ATTC
                                  TG_       C
GAM1970 PRKAR2B   3' TAAACTGTGGGCATGCTGATAA 48184       A  ACC  A_
          G                    TAAATTGTG GCA  GC  ATAAG
                               ||||||||| |||  ||  |||||
                               ATTTGACAC CGT  CG  TATTC
                                  C  A__  AC
GAM1970 UBE4A     3' TAAGTTATGAGCAATACCA   48185    A       __
                               TAA TTGTGAGCA  ACCG
                               ||| |||||||||  ||||
                               ATT AATACTCGT  TGGT
                                 C        TA
GAM1970 FLJ30681  3' ACTGTGAGTAACCTATAAG   48186       C   GCA
                               ATTGTGAG AACC   ATAAG
                               |||||||| ||||   |||||
                               TGACACTC TTGG   TATTC
                                  A   A__
GAM1970 KIAA0515  3' AATTGTGAGAGCAGTAA     48187       CAACC  A
                               AATTGTGAG    GCA TAA
                               |||||||||    ||| |||
                               TTAACACTC    CGT ATT
                                  T_____  C
GAM1970 TTTY13    5' TGTGAGCAACAATAAG      48188       ACC
                               TGTGAGCA   GCAATAAG
                               ||||||||   ||||||||
                               ACACTCGT   TGTTATTC
                                  ___
GAM1970 LOC90321  3' TGTGTGCTAACTGCAATAA   48189     A  _  C
                               TGTG GC AAC GCAATAA
                               |||| || ||| |||||||
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                                ACAC CG TTG CGTTATT
                                  A A   A
GAM1970 LOC92283 5' TAAGTTGTGAGCAATGAACAA 48190     A        CC_
                                TAA TTGTGAGCAA   GCAA
                                ||| ||||||||||   ||||
                                ATT AACACTCGTT   TGTT
                                  C         ACT
GAM1971 PCDHB9   3' TAGTACCTTCTTTGTGG     48193         GTAAC
                                TAGTACCTT    TTTTGTGG
                                |||||||||    ||||||||
                                ATCATGGAA    GAAACACC
                                             _____
GAM1971 FLJ23511 5' TTAGGATCTTGTAACCTAGGT 48194      TAC        TTGT
                                TTAG   CTTGTAACTT    GGT
                                ||||   ||||||||||    |||
                                AATC   GAACATTGGA    CCA
                                  CTA         T___
GAM1971 IL1RAPL1 3' TTAGTACTCTGTAGTG      48195        C    ACTTTT
                                TTAGTAC TTGTA     GTG
                                ||||||| |||||     |||
                                AATCATG GACAT     CAC
                                   A    _______
GAM1971 NET-2    3' TTAGTATTTTCTAACTTCCTAT 48196       CC  G     _
          G                      TTAGTA  TT TAACTTT TGTG
                                ||||||  || ||||||| ||||
                                AATCAT  AA ATTGAAG ATAC
                                   AA  G      G
GAM1971 LOC149386 3' TTAGATTAATGTGCTTTTGTGG 48197     TACCT   AA
          T                     TTAG    TGT  CTTTTGTGGT
                                ||||    |||  ||||||||||
                                AATC    ACA  GAAAACACCA
                                  TAATT   C_
GAM1971 LOC219920 5' GTGCCTTGCATTTTTGTGGT   48198    A      AC
                                GT CCTTGTA  TTTTGTGGT
                                || |||||||  |||||||||
                                CA GGAACGT  AAAACACCA
                                 C      A_
GAM1971 LOC51136  3' TTAGTATTTTGTGGCCTTGATA 48199       CC    AA    T
          GT                    TTAGTA  TTGT  CTTT GTGGT
                                ||||||  ||||  |||| |||||
                                AATCAT  AACA  GGAA TATCA
                                   AA   CC    C
GAM1972 ADAMTS9  3' AGGCAGAGAACTGGAGTTGT   48202         ATA   AG
                                AGGCAGAGAA   GAG  TGT
                                ||||||||||   |||  |||
                                TCCGTCTCTT   CTC  ACA
                                     GAC   A_
GAM1972 BDKRB2   3' AGGCAGAGGAGAGTG       48203         AAATA
                                AGGCAGAG    GAGAGTG
                                ||||||||    |||||||
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                                TCCGTCTC    CTCTCAC
                                        _____
GAM1972 CACNA2D2 3' GGCAGAGAAAAGGAAATG   48204        T  AG
                                GGCAGAGAAA AG  AGTG
                                |||||||||| ||  ||||
                                CCGTCTCTTT TC  TTAC
                                      _  CT
GAM1972 CASP10   3' GGCCAGAGGAGCAAAGTGTA  48205   _   AAAT  _
                                GGC AGAG   AG AGAGTGTA
                                ||| ||||   || ||||||||
                                CCG TCTC   TC TTTCACAT
                                  G   C___  G
GAM1972 CASP10   3' GGCCAGAGGAGCAAAGTGTA  48205   _   AAAT  _
                                GGC AGAG   AG AGAGTGTA
                                ||| ||||   || ||||||||
                                CCG TCTC   TC TTTCACAT
                                  G   C___  G
GAM1972 CBFB     3' AGGTTGAGAAATAGACCGTA  48206    CA       GA
                                AGG  GAGAAATAGA  GTG
                                |||  ||||||||||  |||
                                TCC  CTCTTTATCT  CAT
                                  AA        GG
GAM1972 CBFB     3' AGGTTGAGAAATAGACCGTA  48206    CA       GA
                                AGG  GAGAAATAGA  GTG
                                |||  ||||||||||  |||
                                TCC  CTCTTTATCT  CAT
                                  AA        GG
GAM1972 CD59     3' AGGCAAGGAAATAGCTTTAAC 48207      A     AGAGTG
                                AGGCAG GAAATAG     TAAC
                                |||||| |||||||     ||||
                                TCCGTT CTTTATC     ATTG
                                   C      GAA___
GAM1972 CDH1     3' AGGCAGAGGGACACACCAGTGT 48208       AA   GAG_
            A                    AGGCAGAG  ATA   AGTGTA
                                |||||||| |||   ||||||
                                TCCGTCTC  TGT   TCACAT
                                     CC   GTGG
GAM1972 COCH     3' AGGAGAGAAATAGAAAA    48209    C
                                AGG AGAGAAATAGAGAG
                                ||| ||||||||||||||
                                TCC TCTCTTTATCTTTT
                                  _
GAM1972 CREBL2   3' AGGGAGAAAGTAAGTGTA   48210    CA   AT  A
                                AGG  GAGAA  AG GAGTGTA
                                |||  |||||  || |||||||
                                TCC  CTCTT  TC TTCACAT
                                  __    __ A
GAM1972 DAAM2    3' AGGCAGAAGATAGGCAGC   48211       AA   AG
                                AGGCAGAG  ATAG  AGT
                                ||||||||  ||||  |||
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                                TCCGTCTT  TATC  TCG
                                    C_    CG
GAM1972  FBXL11   3'  AGCAGAGAGGGAGTGT      48212        AATA A
                                GGCAGAGA    G GAGTGT
                                ||||||||    | ||||||
                                TCGTCTCT    C CTCACA
                                    _____ C
GAM1972  G6PT1    3'  AGGCGCAGAAATGGAAAGT    48213      AG     A
                                AGGC  AGAAAT GAGAGT
                                ||||  |||||| ||||||
                                TCCG  TCTTTA CTTTCA
                                  CG     C
GAM1972  GARP     3'  AGGCAGAGAAGGAGGAGAGC   48214          ATA_
                                AGGCAGAGAA    GAGAGT
                                ||||||||||    ||||||
                                TCCGTCTCTT    CTCTCG
                                     CCTC
GAM1972  GFRA2    3'  GGCAGAGAGGGAGGGCAA     48215        AATA A   T
                                GGCAGAGA    G GAG GTAA
                                ||||||||    | ||| ||||
                                CCGTCTCT    C CTC CGTT
                                    _____ C   C
GAM1972  GNA15    3'  AGGCAGAGAAGAGAGCG      48216        AAT
                                AGGCAGAGA   AGAGAGTG
                                |||||||||   ||||||||
                                TCCGTCTCT   TCTCTCGC
                                    ___
GAM1972  GRLF1    3'  AGGAGAGGGGTAGAGAGC     48217     C    AAA
                                AGG AGAG   TAGAGAGT
                                ||| ||||   ||||||||
                                TCC TCTC   ATCTCTCG
                                  _    CCC
GAM1972  IFNGR1   3'  AGGCAGAGAAAAGAAAA      48218          T
                                AGGCAGAGAAA AGAGAG
                                |||||||||||| ||||||
                                TCCGTCTCTTT TCTTTT
                                    _
GAM1972  IHPK1    3'  GGCAGGGAGAAAGCAGTG     48219      A  AAT   _
                                GGCAG GA   AGAG AGTG
                                ||||| ||   |||| ||||
                                CCGTC CT   TTTC TCAC
                                   C  C__    G
GAM1972  IL10RA   3'  AGGCAGAGGAGCAGGCA      48220        AAATA  _  T
                                AGGCAGAG     GAG AG GTA
                                ||||||||     ||| || |||
                                TCCGTCTC     CTC TC CGT
                                    _____   G  _
GAM1972  LRP4     3'  AGGCAGGGAAGAGAATGT     48221       A  AAT
                                AGGCAG GA   AGAGAGTGT
                                ||||||  ||   |||||||||
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                                TCCGTC CT   TCTCTTACA
                                   C ___
GAM1972 MECP2    3' GGCAGAGAAGCAGGTG      48222         A  AGA
                                GGCAGAGAA TAG   GTG
                                ||||||||| |||   |||
                                CCGTCTCTT GTC   CAC
                                    C  ___
GAM1972 NELL2    5' AGGCAGAGACAATGGAGAAAGC 48223         _  A    T
                                AGGCAGAGA AAT GAGAG GT
                                ||||||||| ||| ||||| ||
                                TCCGTCTCT TTA CTCTT CG
                                    G  C    T
GAM1972 PCDH11X  3' AGTAGAGAAATAGGTTGTA   48224    C       AGAG
                                GG AGAGAAATAG    TGTA
                                || ||||||||||    ||||
                                TC TCTCTTTATC    ACAT
                                 A        CA__
GAM1972 PCDH11X  3' AGTCAGAGAAATAACTTGTAA 48225    G       AGAG
                                AG CAGAGAAATAG    TGTAA
                                || ||||||||||    |||||
                                TC GTCTCTTTATT    ACATT
                                 A         GA__
GAM1972 PCDH11X  3' AGTCAGAGAAATAACTTGTAA 48225    G       AGAG
                                AG CAGAGAAATAG    TGTAA
                                || ||||||||||    |||||
                                TC GTCTCTTTATT    ACATT
                                 A         GA__
GAM1972 PCDH11X  3' AGTAGAGAAATAGGTTGTA   48224    C       AGAG
                                GG AGAGAAATAG    TGTA
                                || ||||||||||    ||||
                                TC TCTCTTTATC    ACAT
                                 A        CA__
GAM1972 PCDH11Y  3' AGTAGAGAAATAGGTTGTA   48224    C       AGAG
                                GG AGAGAAATAG    TGTA
                                || ||||||||||    ||||
                                TC TCTCTTTATC    ACAT
                                 A        CA__
GAM1972 PIK3C2B  3' GGCAAGGGGTAGAAAATG    48226     G  AAA
                                GGCA AG   TAGAGAGTG
                                |||| ||   |||||||||
                                CCGT TC   ATCTTTTAC
                                  _  CCC
GAM1972 PLAG1    3' AGACAGAGAAGTTTGTA     48227        AATAG  AG
                                AGGCAGAGA    AG  TGTA
                                |||||||||    ||  ||||
                                TCTGTCTCT    TC  ACAT
                                     _____  AA
GAM1972 SELL     3' GGCAGGGGAAAGGAGAGC    48228      A_   TA
                                GGCAG  GAAA  GAGAGT
                                |||||  ||||  ||||||
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                                CCGTC  CTTT  CTCTCG
                                  CC    C_
GAM1972  SPOCK    3'  GGCAGGGGGAAAAAGTACAGTG 48229      A__    T  AG_
              T                   GGCAG   GAAA AG   AGTGT
                                  |||||   |||| ||   |||||
                                  CCGTC   CTTT TC   TCACA
                                     CCC    T  ATG
GAM1972  SPTBN4   3'  GGCAGAGAGGGGGGGCAGGAAT  48230        AA____  A
                                  GGCAGAGA     TAG GAGT
                                  ||||||||     ||| ||||
                                  CCGTCTCT     GTC CTTA
                                       CCCCCC  _
GAM1972  SRM      3'  AGGCAGAGAGATGGCGC     48231         AATA  GA
                                  AGGCAGAGA    GA  GTGT
                                  |||||||||    ||  ||||
                                  TCCGTCTCT    CT  CGCG
                                       ____ AC
GAM1972  TACC1    3'  AGGCAGAGGAGAGTA       48233         AAATA
                                  AGGCAGAG     GAGAGTG
                                  ||||||||     |||||||
                                  TCCGTCTC     CTCTCAT
                                       _____
GAM1972  TACC1    3'  AGGCAGAGGGGGGAGAAAGTG   48232         AAAT
                                  AGGCAGAG    AGAGAGTG
                                  ||||||||    ||||||||
                                  TCCGTCTC    TCTTTCAC
                                       CCCC
GAM1972  TAF4     3'  GGCAGAGAGGAGAGCG       48234         AATA
                                  GGCAGAGA    GAGAGTG
                                  ||||||||    |||||||
                                  CCGTCTCT    CTCTCGC
                                       C___
GAM1972  TGFB1    3'  AGGCAGAGAGGGAGAGAG     48235         AAT
                                  AGGCAGAGA   AGAGAG
                                  |||||||||   ||||||
                                  TCCGTCTCT   TCTCTC
                                        CCC
GAM1972  THRA     3'  AGGCAGAGAAAGGGGGAAGGGC 48236          TAGA_  T
                                  AGGCAGAGAAA     GAG GT
                                  ||||||||||     ||| ||
                                  TCCGTCTCTTT     TTC CG
                                         CCCCC   C
GAM1972  TUFT1    3'  AGGCAGAGGAAAGGGAGAG    48237         _  TA
                                  AGGCAGAG AAA  GAGAG
                                  |||||||| |||  |||||
                                  TCCGTCTC TTT  CTCTC
                                       C   CC
GAM1972  XRCC5    3'  AGGCAGAGTAATGTGGTAA    48238         A  AGAGA  _
                                  AGGCAGAG AAT    GTG TAA
                                  |||||||| |||    ||| |||
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                                TCCGTCTC TTA    CAC ATT
                                    A  _____  C
GAM1972  ASB10    5'  AGGCAGAGAGAGAGAGAG    48239        AAT
                                AGGCAGAGA  AGAGAG
                                |||||||||  ||||||
                                TCCGTCTCT  TCTCTC
                                     CTC
GAM1972  BRAG     3'  AGGCAGAGAAATGGAGCCTGTA 48240          A  AG
                                AGGCAGAGAAAT GAG  TGTA
                                |||||||||||| |||  ||||
                                TCCGTCTCTTTA CTC  ACAT
                                      C  GG
GAM1972  BTBD2    3'  AGCAGAGAAATGGGAAT     48241          AGA
                                GGCAGAGAAAT  GAGT
                                ||||||||||  ||||
                                TCGTCTCTTTA  CTTA
                                      CC_
GAM1972  C20orf150 3'  AGGCAGAGGGTAGAGCATG   48242        AAA    A
                                AGGCAGAG  TAGAG GTG
                                ||||||||  ||||| |||
                                TCCGTCTC  ATCTC TAC
                                     CC_   G
GAM1972  DJ159A19.3 3'  AGGCAGAGGGGCAGGAGC    48243        AAA  A
                                AGGCAGAG  TAG GAGT
                                ||||||||  ||| ||||
                                TCCGTCTC  GTC CTCG
                                     CCC  _
GAM1972  DKFZP434H132 3'  AGGCAAGAAATAGGGAGTA   48244      G      A
                                AGGCA AGAAATAG GAGTG
                                ||||| |||||||| |||||
                                TCCGT TCTTTATC CTCAT
                                   _      C
GAM1972  DKFZP434H132 3'  AGGCAAGAAATAGGGAGTA   48244      G      A
                                AGGCA AGAAATAG GAGTG
                                ||||| |||||||| |||||
                                TCCGT TCTTTATC CTCAT
                                   _      C
GAM1972  DKFZP564I0422 3'  GGCAGAAAATAATGTAA    48245        ATAGAG
                                GGCAGAGAA     AGTGTAA
                                |||||||||     |||||||
                                CCGTCTTTT     TTACATT
                                     A_____
GAM1972  FLJ10922  3'  AGGTAGAGGAAAGAATG    48246    C   AAAT
                                AGG AGAG   AGAGAGTG
                                ||| ||||   ||||||||
                                TCC TCTC   TTTCTTAC
                                  A   C___
GAM1972  FLJ11099  3'  GGCAGGGAGGAGAGTGC    48247      A  AATA
                                GGCAG GA   GAGAGTGT
                                ||||| ||   ||||||||
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                                CCGTC CT    CTCTCACG
                                   C  C___
GAM1972  FLJ11722  3'  AGGCAGAGGGCTGGAGCCCAA  48248        AAATAGA    G
                                AGGCAGAG      GAGT TAA
                                ||||||||      |||| |||
                                TCCGTCTC      CTCG GTT
                                     CCGAC__    G
GAM1972  FLJ12921  3'  GGCAGGGAGGTAGAGAGT    48249      A  AA
                                GGCAG GA  TAGAGAGT
                                ||||| ||  ||||||||
                                CCGTC CT  ATCTCTCA
                                   C  CC
GAM1972  FLJ13769  3'  AGGCAGAGAGGTGCA       48250          AATAGA A
                                AGGCAGAGA     G GTGTA
                                |||||||||     | |||||
                                TCCGTCTCT     C CACGT
                                      _______ _
GAM1972  FLJ14249  3'  AGGCAGAGGAGGGATAGAGGC  48251        AA___     A
                                AGGCAGAG     ATAGAG GT
                                ||||||||     |||||| ||
                                TCCGTCTC     TATCTC CG
                                     CTCCC     _
GAM1972  FLJ14249  3'  AGGCAGAGGAGGGATAGAGGC  48251        AA___     A
                                AGGCAGAG     ATAGAG GT
                                ||||||||     |||||| ||
                                TCCGTCTC     TATCTC CG
                                     CTCCC     _
GAM1972  FLJ14564  3'  AGGCAGAGATAATAGATGAA   48252          _     _
                                AGGCAGAGA AATAGA GAG
                                ||||||||| |||||| |||
                                TCCGTCTCT TTATCT CTT
                                     A     A
GAM1972  FLJ20154  3'  GGCAGAGAGGCAGAGAGC    48253         AA
                                GGCAGAGA  TAGAGAGT
                                ||||||||  ||||||||
                                CCGTCTCT  GTCTCTCG
                                     CC
GAM1972  FLJ20802  3'  AGCAGAGAAATGGAGGAGAAGG 48254           A___    T
            C                    GGCAGAGAAAT    GAGAG GT
                                ||||||||||    ||||| ||
                                TCGTCTCTTTA    CTCTT CG
                                      CCTC     C
GAM1972  FLJ21870  3'  GGCAGAGAAGAGGTACA     48255        AAT    A
                                GGCAGAGA   AGAG GTGTA
                                ||||||||   |||| |||||
                                CCGTCTCT   TCTC CATGT
                                     ___    _
GAM1972  FLJ30567  3'  AGGCAGAGGGAAAGAGCA    48256        AAAT
                                AGGCAGAG    AGAGAGTG
                                ||||||||    ||||||||
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                                TCCGTCTC   TTTCTCGT
                                    CC__
GAM1972 HABP2    3' GGCTGAGGAATAAAGATGTG  48257    A  A     _
                                GGC GAG AATAGAGA GTG
                                ||| ||| |||||||| |||
                                CCG CTC TTATTTCT CAC
                                  A  C      A
GAM1972 HIP-55   3' AGGCAGAGGGACAGAGAA    48258       AA
                                AGGCAGAG  ATAGAGAG
                                ||||||||  ||||||||
                                TCCGTCTC  TGTCTCTT
                                    CC
GAM1972 HSPC065  3' AGGCAGAGAAGGGAAAAT    48259        ATA
                                AGGCAGAGAA   GAGAGT
                                ||||||||||   ||||||
                                TCCGTCTCTT   CTTTTA
                                     CC_
GAM1972 IGF2AS   3' AGGCAGAGAGGTGAGTGT    48260       AATAGA
                                AGGCAGAGA     GAGTGT
                                |||||||||     ||||||
                                TCCGTCTCT     CTCACA
                                    CCA___
GAM1972 KIAA0795 3' AAGCAGAGAAGTGGAGAGAGC 48261        AT__
                                AGGCAGAGAA    AGAGAGT
                                ||||||||||    |||||||
                                TTCGTCTCTT    TCTCTCG
                                     CACC
GAM1972 KIAA0995 5' AGGCAGAGAAAGAGGC      48262        AT   A
                                AGGCAGAGAA  AGAG GT
                                ||||||||||  |||| ||
                                TCCGTCTCTT  TCTC CG
                                      __   _
GAM1972 KIAA1001 3' AGGCGGAAGAATGGAGTGCAA 48263     A_    ATAGA
                                AGGC  GAGAA    GAGTGTAA
                                ||||  |||||    ||||||||
                                TCCG  TTCTT    CTCACGTT
                                  CC    AC___
GAM1972 KIAA1467 3' AGGAGAGAAATAAGTG      48264     C      GAG
                                AGG AGAGAAATA   AGTG
                                ||| |||||||||   ||||
                                TCC TCTCTTTAT   TCAC
                                  _       ____
GAM1972 KIAA1908 5' AGGCAGAGGGTAGGAGC     48265       AAA  A
                                AGGCAGAG   TAG GAGT
                                ||||||||   ||| ||||
                                TCCGTCTC   ATC CTCG
                                    CC_  _
GAM1972 KLHL8    5' AGGCAGAAGGTAGATGTA    48266       AAA   GAG
                                AGGCAGAG   TAGA   TGTA
                                ||||||||   ||||   ||||
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                                TCCGTCTT  ATCT  ACAT
                                    CC_   ___
GAM1972 LIPG     5' AGGCAGAGAAGGTGGAAAAT  48267        ATA_
                                AGGCAGAGAA   GAGAGT
                                ||||||||||   ||||||
                                TCCGTCTCTT   CTTTTA
                                     CCAC
GAM1972 MGC11386 3' AGGCAGGAAATAAATAGTAAC 48268      A      GAGT
                                AGGCAG GAAATAGA   GTAAC
                                |||||| ||||||||   |||||
                                TCCGTC CTTTATTT   CATTG
                                   _      AT__
GAM1972 NKX2C    3' AGGCAGAGGGAGAGAAGC    48269       AAAT     T
                                AGGCAGAG   AGAGAG GT
                                ||||||||   |||||| ||
                                TCCGTCTC   TCTCTT CG
                                    CC__     _
GAM1972 OLFM2    3' AGGCGGGGAGAAAGGGCGT   48270     A__   AATA  A
                                AGGC  GAGA   GAG GTGT
                                ||||  ||||   ||| ||||
                                TCCG  CTCT   TTC CGCA
                                  CCC   _____  C
GAM1972 PHACS    5' AGGCAGAGGAAGTGT       48271       AAATA  G
                                AGGCAGAG    GA AGTGT
                                ||||||||    || |||||
                                TCCGTCTC    CT TCACA
                                      ______ _
GAM1972 POLD4    5' AGGCAGAGAAGGAGGCAA    48272       AAT  A   T
                                AGGCAGAGA   AG GAG GTAA
                                |||||||||   || ||| ||||
                                TCCGTCTCT   TC CTC CGTT
                                     ___  _   _
GAM1972 RNF8     3' AGGTGGAGAAAAGAGAG     48273     CA     T
                                AGG  GAGAAA AGAGAG
                                |||  |||||| ||||||
                                TCC  CTCTTT TCTCTC
                                  AC     _
GAM1972 SCYA18   5' AGGCAGAGAAGTGGTCAGAGT 48274        ATAG__
                                AGGCAGAGAA     AGAGT
                                ||||||||||     |||||
                                TCCGTCTCTT     TCTCA
                                     CACCAG
GAM1972 SLC26A10 5' AGGCAGAGAAAATGGGGGGTGG 48275         TA_________
             AGA                   AGGCAGAGAAA        GAGA
                                ||||||||||         ||||
                                TCCGTCTCTTT        CTCT
                                      TACCCCCCAC
GAM1972 SNAP29   3' GGCAGAGAAATAAGTG      48276          GAG
                                GGCAGAGAAATA   AGTG
                                ||||||||||||   ||||
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                                CCGTCTCTTTAT   TCAC
                                      ___
GAM1972 TLOC1    5' AAGCAGAGAAGTGGATCAGAGA 48277          A_____
                                AGGCAGAGAA     TAGAGA
                                ||||||||||     ||||||
                                TTCGTCTCTT     GTCTCT
                                     CACCTA
GAM1972 TNKS1BP1 5' AGGCAGAGAGGTATGAGC    48278         AA  GA
                                AGGCAGAGA  TA  GAGT
                                |||||||||  ||  ||||
                                TCCGTCTCT  AT  CTCG
                                     CC  A_
GAM1972 TP53TG3  3' AGGTGAGAGATAGAAAA     48279     CA    A
                                AGG  GAGA ATAGAGAG
                                |||  |||| ||||||||
                                TCC  CTCT TATCTTTT
                                  A_   C
GAM1972 TSPAN-2  3' AGGCAGAGAGATAAACTAAAGC 48280         A    ___
                                AGGCAGAGA ATAGA   GAGT
                                ||||||||| |||||   ||||
                                TCCGTCTCT TATTT   TTCG
                                     C    GAT
GAM1972 TUSP     3' GGCAGAGAGAGTAGAGGC    48281         AA_    A
                                GGCAGAGA   TAGAG GT
                                ||||||||   ||||| ||
                                CCGTCTCT   ATCTC CG
                                     CTC    _
GAM1972 UBE2G1   3' AGGCAGAGAAATATGAAG    48282           GA
                                AGGCAGAGAAATA  GAG
                                ||||||||||||  |||
                                TCCGTCTCTTTAT  TTC
                                       AC
GAM1972 ZAK      3' AGGCAGAAAATATGTGTA     48283          ATAGAGA
                                AGGCAGAGAA      GTGTA
                                ||||||||||      |||||
                                TCCGTCTTTT      CACAT
                                     ATA____
GAM1972 ZNF337   3' AGGAGGTTGGGGAGAGTGTAAC 48284     C  AGAAATA
                                AGG AG      GAGAGTGTAAC
                                ||| ||      ||||||||||
                                TCC TC      CTCTCACATTG
                                  _  CAACCC_
GAM1972 ZNF384   3' AGGCAGAGAAGGAGAGAGGC   48285         AT     T
                                AGGCAGAGAA  AGAGAG GT
                                ||||||||||  ||||||  ||
                                TCCGTCTCTT  TCTCTC CG
                                     CC     _
GAM1972 LOC121344 3' AGGCCAGAGAACAGGTGT    48286      _     A   AGA
                                AGGC AGAGAA TAG   GTGT
                                |||| |||||| |||   ||||
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                                TCCG TCTCTT GTC   CACA
                                  G     _  ____
GAM1972  LOC128077 3'  AGGCAGAGAAGGAATAAGGTA  48287          AT  A   T
                                AGGCAGAGAA  AG GAG GTA
                                ||||||||||  || ||| |||
                                TCCGTCTCTT  TT TTC CAT
                                     CC  A   _
GAM1972  LOC132241 5'  AAGCAGAGAAGTAGGCTCAGAG 48288          A  _____
              C                  AGGCAGAGAA TAG    AGAGT
                                ||||||||||| |||    |||||
                                TTCGTCTCTT ATC    TCTCG
                                     C   CGAG
GAM1972  LOC133688 3'  AGGCAGAGAATAGAAAGAAGC  48289          A      T_
                                AGGCAGAGAA TAGAGAG  GT
                                ||||||||||| |||||||  ||
                                TCCGTCTCTT ATCTTTC  CG
                                     _      TT
GAM1972  LOC145216 3'  AGGCAGAGAGCTGGGGAAAAGC 48290          AATA___
                                AGGCAGAGA       GAGAGT
                                |||||||||       ||||||
                                TCCGTCTCT       TTTTCG
                                     CGACCCC
GAM1972  LOC145371 3'  AGGTAGAGAATGGAGGTG    48291     C      ATA   A
                                AGG AGAGAA   GAG GTG
                                ||| ||||||   ||| |||
                                TCC TCTCTT   CTC CAC
                                  A     AC_  _
GAM1972  LOC148014 3'  GGCGAGGGATAGAGAGGT    48292     A   AA       T
                                GGC GAG  ATAGAGAG GT
                                ||| |||  |||||||| ||
                                CCG CTC  TATCTCTC CA
                                  _  CC       _
GAM1972  LOC148508 3'  AGGCAGAGGGAGATGTG     48293         AAATA   _
                                AGGCAGAG     GAGA GTG
                                ||||||||     |||| |||
                                TCCGTCTC     CTCT CAC
                                     C____    A
GAM1972  LOC148645 3'  GGCAGAGGAGAGAGCAT     48294         AAAT
                                GGCAGAG    AGAGAGTGT
                                |||||||    |||||||||
                                CCGTCTC    TCTCTCGTA
                                    C___
GAM1972  LOC148932 3'  AGGCAGAGGGATGAGTA     48295         AAATA  _
                                AGGCAGAG     GA GAGTG
                                ||||||||     || |||||
                                TCCGTCTC     CT CTCAT
                                     C____  A
GAM1972  LOC149422 3'  AGGCAGAGAAGGAAATGT    48296          AAT  AG
                                AGGCAGAGA   AG  AGTGT
                                |||||||||   ||  |||||
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                                TCCGTCTCT   TC  TTACA
                                    ___  CT
GAM1972  LOC149464 5'  AGGCAGAGGCAATGGAGGT   48297        A_   A   A
                                AGGCAGAG  AAT GAG GT
                                ||||||||  ||| ||| ||
                                TCCGTCTC  TTA CTC CA
                                    CG   C   _
GAM1972  LOC150319 3'  AGGCAGAGGGGCAGGTGCGAC  48298        AAATAG  A   TA
                                AGGCAGAG     AG GTG  AC
                                ||||||||     || |||  ||
                                TCCGTCTC     TC CAC  TG
                                    CCCG__ _   GC
GAM1972  LOC152766 3'  AGGCGAGAAATAGGTCTAA   48299      A        AGA  G
                                AGGC GAGAAATAG   GT TAA
                                |||| |||||||||   || |||
                                TCCG CTCTTTATC   CA ATT
                                  _        ___  G
GAM1972  LOC158563 5'  AGGCAGAGAGAAGAGAGGC   48300         AAT     T
                                AGGCAGAGA   AGAGAG GT
                                |||||||||   |||||| ||
                                TCCGTCTCT   TCTCTC CG
                                    CT_     _
GAM1972  LOC163341 3'  AGGCAGAGGAATGGAGAGT   48301        A   A
                                AGGCAGAG AAT GAGAGT
                                |||||||| ||| ||||||
                                TCCGTCTC TTA CTCTCA
                                    C   C
GAM1972  LOC197049 3'  AGGCAGAAGGGGTGAAAAGTA  48302        AAATA_
                                AGGCAGAG     GAGAGTG
                                ||||||||     |||||||
                                TCCGTCTT     TTTTCAT
                                    CCCCAC
GAM1972  LOC199231 3'  AGGCAGAGAGGAGCATAA    48303         AATA A
                                AGGCAGAGA    G GAGTGTAA
                                |||||||||    | ||||||||
                                TCCGTCTCT    C CTCGTATT
                                    _____ _
GAM1972  LOC201617 5'  AGGCAGAGAAAGAGAGAG    48304          T
                                AGGCAGAGAAA AGAGAG
                                |||||||||| ||||||
                                TCCGTCTCTTT TCTCTC
                                    C
GAM1972  LOC201799 3'  AGGCAGAAAAATAGACAAGT   48305            _
                                AGGCAGAGAAATAGA GAGT
                                |||||||||||||| ||||
                                TCCGTCTTTTTATCT TTCA
                                      G
GAM1972  LOC219920 5'  AGGCAGAGAAGGTGAGTG    48306          ATAGA
                                AGGCAGAGAA     GAGTG
                                ||||||||||     |||||
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                                TCCGTCTCTT    CTCAC
                                     CCA__
GAM1972  LOC220032 3'  AGGCAGAGAGAGGAAGAAGC  48307        AATA    T
                                AGGCAGAGA   GAGAG GT
                                |||||||||   ||||| ||
                                TCCGTCTCT   TTCTT CG
                                     CTCC    _
GAM1972  LOC221322 3'  AGGCAGAGAAGAGAA      48308        AAT
                                AGGCAGAGA   AGAGAG
                                |||||||||   ||||||
                                TCCGTCTCT   TCTCTT
                                     ___
GAM1972  LOC221398 3'  GGCAGAGAGATGACAAGGGT  48309       A  AGA   T
                                GGCAGAGA AT   GAG GT
                                |||||||| ||   ||| ||
                                CCGTCTCT TA   TTC CA
                                     C  CTG   C
GAM1972  LOC254552 3'  AGGCAGAGAGGGTAGACAG   48310       AA_   G
                                AGGCAGAGA   TAGA AG
                                |||||||||   |||| ||
                                TCCGTCTCT   ATCT TC
                                     CCC    G
GAM1972  LOC255223 3'  AGGCAGAAGGGGTGAAAAGTA  48302       AAATA_
                                AGGCAGAG     GAGAGTG
                                ||||||||     |||||||
                                TCCGTCTT     TTTTCAT
                                     CCCCAC
GAM1972  LOC256021 3'  AGGCATGGAAATAGACATG   48311     GA      GA
                                AGGCA  GAAATAGA  GTG
                                |||||  ||||||||  |||
                                TCCGT  CTTTATCT  TAC
                                   AC       G_
GAM1972  LOC256094 3'  GGCAGAGAGGAGAAAGAGGC  48312       AAT_    T
                                GGCAGAGA    AGAGAG GT
                                ||||||||    |||||| ||
                                CCGTCTCT    TTTCTC CG
                                     CCTC     _
GAM1972  LOC257476 3'  GGCAGGGAGAAAGCAGTG    48219     A  AAT   _
                                GGCAG GA   AGAG AGTG
                                |||||  ||   |||| ||||
                                CCGTC CT   TTTC TCAC
                                   C  C__   G
GAM1972  LOC51644  3'  AGGCAGAGAGAGGGTA      48313       AATA   A
                                AGGCAGAGA    GAG GTG
                                |||||||||    ||| |||
                                TCCGTCTCT    CTC CAT
                                     _____  C
GAM1972  LOC81558  3'  GGCGGAGAGTATAGAGTCGC  48314    A   A_    AG
                                GGC GAGA  ATAGAG  TGT
                                |||  ||||  ||||||  |||
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                                CCG CTCT  TATCTC  GCG
                                  C   CA    A_
GAM1972 LOC91010 3' GGCAGAGAAATAAGGGCA   48315          A  A
                                GGCAGAGAAAT GAG GTG
                                |||||||||||| ||| |||
                                CCGTCTCTTTA TTC CGT
                                       _  C
GAM1972 LOC91266 5' AGGCAGAGAGGGAGAGGGT   48316        AATA   T
                                AGGCAGAGA   GAGAG GT
                                |||||||||   ||||| ||
                                TCCGTCTCT   CTCTC CA
                                     CC__    C
GAM1972 LOC91585 3' AGGCAGAGGGATTGGACTGT  48317        AA  AGA  G
                                AGGCAGAG  AT   GA TGT
                                ||||||||  ||   || |||
                                TCCGTCTC  TA   CT ACA
                                     CC  AC_  G
GAM1973 BACH2    3' TTCACGGGACAGGAGTTTTT  48320       TC_  T
                                TTCACG   CA GAGTTTTT
                                ||||||   || ||||||||
                                AAGTGC   GT CTCAAAAA
                                   CCT  C
GAM1973 CHST6    3' TTTCACTTCCGAGTTTT     48321       G   AT
                                TTTCAC TCC  GAGTTTT
                                |||||| |||  |||||||
                                AAAGTG AGG  CTCAAAA
                                   A  __
GAM1973 COX7C    3' TTTCACGTCATAAGTTT     48322         C
                                TTTCACGTC ATGAGTTT
                                ||||||||| ||||||||
                                AAAGTGCAG TATTCAAA
                                       _
GAM1973 FEZ1     3' TTTCACATCCACATAATTTTT  48323           _
                                TTTCACGTCCATG AGTTTTT
                                |||||||||||| |||||||
                                AAAGTGTAGGTGT TTAAAAA
                                       A
GAM1973 POU2AF1  3' TTTCTCCAGAGTTTTT      48324      ACG    T
                                TTTC   TCCA GAGTTTTT
                                ||||   |||| ||||||||
                                AAAG   AGGT CTCAAAAA
                                    ___   _
GAM1973 TMSB4Y   5' TTTCGCGCTCATGAGCTT    48325      A  TC
                                TTTC CG  CATGAGTTT
                                |||| ||  |||||||||
                                AAAG GC  GTACTCGAA
                                  C  GA
GAM1973 WASF1    3' TTTCACATGGAAAAGTTTTT  48326         CCAT
                                TTTCACGT   GAGTTTTT
                                ||||||||   ||||||||
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                                AAAGTGTA   TTCAAAAA
                                    CCTT
GAM1973 WNT5A    5' TCTCCTCCGTGAGTTTTT   48327     ACG  A
                                TTTC  TCC TGAGTTTTT
                                ||||  ||| |||||||||
                                AGAG  AGG ACTCAAAAA
                                  G__  C
GAM1973 CHL1     3' TTTCATATCCATAAGTTTT   48328     CG
                                TTTCA  TCCATGAGTTTT
                                |||||  ||||||||||||
                                AAAGT  AGGTATTCAAAA
                                   AT
GAM1973 FLJ20413 3' CTTCATGTCTGAGTTTT    48329     C  CA
                                TTTCA GTC  TGAGTTTT
                                ||||| |||  ||||||||
                                GAAGT CAG  ACTCAAAA
                                   A  __
GAM1973 KIAA1679 3' TTTCACATCAGCTTTT     48330       CATG
                                TTTCACGTC   AGTTTTT
                                |||||||||   |||||||
                                AAAGTGTAG   TCGAAAA
                                     ____
GAM1973 RHOBTB2  3' TTCCACGTCTGGCCTTT    48331       CA  A
                                TTTCACGTC  TG GTTTTT
                                |||||||||  || ||||||
                                AAGGTGCAG  AC CGGAAA
                                     __ _
GAM1973 TCF17    3' TTTCACATCCATTACATTT   48332         GA_
                                TTTCACGTCCAT  GTTT
                                ||||||||||||  ||||
                                AAAGTGTAGGTA  TAAA
                                      ATG
GAM1973 LOC116143 3' TTTCAAGTCCAAAGTCTTT   48333     C    T
                                TTTCA GTCCA GAGTTTTT
                                ||||| ||||| ||||||||
                                AAAGT CAGGT TTCAGAAA
                                   T   _
GAM1973 LOC146177 3' TTTCTCCCTGAGTTTTT    48334     ACG  A
                                TTTC  TCC TGAGTTTTT
                                ||||  ||| |||||||||
                                AAAG  AGG ACTCAAAAA
                                   ___  G
GAM1973 LOC146699 3' TTTGCACATCTGAGTTTTT   48335    _    CA
                                TTT CACGTC  TGAGTTTTT
                                ||| ||||||  |||||||||
                                AAA GTGTAG  ACTCAAAAA
                                  C    __
GAM1973 LOC220930 3' TTTCATATCCATGACTTT    48336     CG     G
                                TTTCA  TCCATGA TTT
                                |||||  ||||||| |||
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                                AAAGT  AGGTACT AAA
                                  AT      G
GAM1973 LOC51131 3' TCTCATCCATGAGTTTTT    48337    A
                                TC CGTCCATGAGTTTTT
                                || ||||||||||||||
                                AG GTAGGTACTCAAAAA
                                 A
GAM1974 GRIK3    3' GCTGCATCTTTGGGCATCCTTT 48340     A         TTA
           GT                    GCT CATTTTTGGGC   TTTTGT
                                 ||| ||||||||||   ||||||
                                 CGA GTAGAAACCCG   GAAACA
                                   C         TAG
GAM1974 HIP2     3' TACATTTTTGTTATTTTGT    48341          GGC
                                 TACATTTTTG   TTATTTTGT
                                 ||||||||||   |||||||||
                                 ATGTAAAAAC   AATAAAACA
                                      ____
GAM1974 EFA6R    3' CTACGTTTTCCTTCCTTATTTT 48342      A    GGG_
           GT                    CTAC TTTTT    CTTATTTTGT
                                 |||| |||||    ||||||||||
                                 GATG AAAAG    GAATAAAACA
                                   C    GAAG
GAM1974 GBTS1    3' GCTACATTTGTGGTCATTTGT  48343         T  GCTTAT
                                 GCTACATTT TGG     TTTGT
                                 ||||||||| |||     |||||
                                 CGATGTAAA ACC     AAACA
                                       C   AGT___
GAM1974 GTSE1    3' GCTAATTTTTGTACTTTTTGT  48344      C      GG   AT
                                 GCTA ATTTTTG  CTT  TTTGT
                                 |||| |||||||  |||  |||||
                                 CGAT TAAAAAC  GAA  AAACA
                                   _      AT  __
GAM1974 KIAA0710 3' GCTGCATTCTTGGGACTT    48345     A        _
                                 GCT CATTTTTGGG CTT
                                 ||| |||||||||| |||
                                 CGA GTAAGAACCC GAA
                                   C         T
GAM1974 KIAA0738 3' GCTAATTTTTAAAAATTATTTT 48346      C        C_
           GT                    GCTA ATTTTTGGG  TTATTTTGT
                                 |||| |||||||||  |||||||||
                                 CGAT TAAAAATTT  AATAAAACA
                                   _        TT
GAM1974 KIAA1276 3' GCTAATTTTTGTATATTTTGT  48347      C      GGCT
                                 GCTA ATTTTTG    TATTTTGT
                                 |||| |||||||    ||||||||
                                 CGAT TAAAAAC    ATAAAACA
                                   _      AT__
GAM1974 NEUGRIN  3' GCTACATTTTACTTTATTTTGT 48348          TGG   _
                                 GCTACATTTT   GCTT ATTTTGT
                                 ||||||||||   |||| |||||||
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                                CGATGTAAAA   TGAA TAAAACA
                                     ___   A
GAM1974  LOC122553 3'  TACATTTTTATAGTTTTTATTT 48349          GGC___
             TGT                   TACATTTTTG     TTATTTTGT
                                   ||||||||||     |||||||||
                                   ATGTAAAAAT     AATAAAACA
                                        ATCAAA
GAM1974  LOC152002 3'  GCTAATTTTTAAAATATTTTGT 48350      C        CT
                                   GCTA ATTTTTGGG  TATTTTGT
                                   |||| |||||||||  ||||||||
                                   CGAT TAAAAATTT  ATAAAACA
                                     _        T_
GAM1974  LOC220753 3'  TCTCTGGGTTTGTTTTGT    48351         C  A
                                   TTTTTGGG TT TTTTGT
                                   |||||||| || ||||||
                                   AGAGACCC AA AAAACA
                                        A  C
GAM1975  AMD1      3'  TAGTATATAAACCCACAGTGT  48354        CAAGTT       C
                                   TGGTATA     ATTCACAG GT
                                   |||||||     |||||||| ||
                                   ATCATAT     TGGGTGTC CA
                                        ATT___       A
GAM1975  SLC6A14   3'  TAGTATGCAAGTTATCAC    48355       A       T
                                   TGGTAT CAAGTTAT CAC
                                   |||||| |||||||| |||
                                   ATCATA GTTCAATA GTG
                                      C       _
GAM1976  ANXA5     3'  TGACGTGTATGTGTTG      48358          CTAT
                                   TGACGTGTAT    TGTTG
                                   ||||||||||    |||||
                                   ACTGCACATA    ACAAC
                                         C___
GAM1976  PPP3CA    3'  TGAATGGACTTTTGTTGTTGT  48359     C   TAT  A
                                   TGA GTG   CT TTGTTGTTGT
                                   ||| |||   || ||||||||||
                                   ACT TAC   GA AACAACAACA
                                     _   CT_  A
GAM1976  CAMTA1    3'  TGCGTGTGTGTTGTTG      48360     A    ATCTAT
                                   TG CGTGT      TGTTGTTG
                                   || |||||      ||||||||
                                   AC GCACA      ACAACAAC
                                     _     C_____
GAM1976  EREG      3'  TAATGTATTTTTTGTTGTTGT  48361    C     CTA
                                   A GTGTAT   TTGTTGTTGT
                                   | ||||||   ||||||||||
                                   A TACATA   AACAACAACA
                                    T     AAA
GAM1976  MGC12466  3'  TGACAGAGGTGTTTTGTTGTTG 48362      ____    ATCTA
             TTGT                    TGAC    GTGT     TTGTTGTTGT
                                     ||||    ||||     ||||||||||
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                                ACTG   CACA    AACAACAACA
                                  TCTC   AAAC_
GAM1976 MRPL3    3' TGACATGTGTGATTTTGTTGT 48363       ATCTATTG
                                TGACGTGT      TTGTTGT
                                ||||||||      |||||||
                                ACTGTACA      AACAACA
                                    CACTAA__
GAM1976 OSBPL8   3' ACATGCCCTATTTATTGTTGTT 48364      ATC___
             GT                   ACGTGT     TATTGTTGTTGT
                                ||||||     ||||||||||||
                                TGTACG     ATAACAACAACA
                                   GGATAA
GAM1976 LOC132321 3' TGATTGTATCTATCATATTTGT 48365    CG       TG TG
                                TGA  TGTATCTAT  T  TTGT
                                |||  |||||||||  |  ||||
                                ACT  ACATAGATA  A  AACA
                                  A_       GT TA
GAM1976 LOC145676 5' TGAATCTTTTTGTTGTTGT   48366   T   A_
                                TG ATCT  TTGTTGTTGT
                                || ||||  ||||||||||
                                AC TAGA  AACAACAACA
                                 T   AA
GAM1976 LOC147514 3' TGTTTTGTATTTGTTGTTGTTG 48367    ACG    CTA
             T                   TG   TGTAT   TTGTTGTTGT
                                ||   |||||   ||||||||||
                                AC   ACATA   AACAACAACA
                                 AAA    AAC
GAM1976 LOC151201 5' TGATCATGTTGTTGTTGTTGT  48368    _    ATCTA
                                TGA CGTGT    TTGTTGTTGT
                                ||| |||||    ||||||||||
                                ACT GTACA    AACAACAACA
                                  A    AC___
GAM1976 LOC200273 3' TGTTTTGTATTTGTTGTTGTTG 48367    ACG    CTA
             T                   TG   TGTAT   TTGTTGTTGT
                                ||   |||||   ||||||||||
                                AC   ACATA   AACAACAACA
                                 AAA    AAC
GAM1976 LOC220534 3' TGTAACTTTTTGTTGTTGT   48369     T  A_
                                TGTA CT  TTGTTGTTGT
                                |||| ||  ||||||||||
                                ACAT GA  AACAACAACA
                                  T  AA
GAM1976 LOC93190  3' GTGTAAGTTTGTTGTTGT    48370      TCTA
                                GTGTA    TTGTTGTTGT
                                |||||    ||||||||||
                                CACAT    AACAACAACA
                                   TCA_
GAM1977 LOC147976 3' TGGTACCCTGGGGGCTGTGGT  48373        C   TCTAGACA
                                TGGTATCC GGG       TGGT
                                |||||||| |||       ||||
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                                ACCATGGG CCC       ACCA
                                    A   CCGAC___
GAM1977  LOC153243 5'  TGGGTCCCCTAATGGACATGGT 48374     TA    GG  CTA
                                TGG  TCCC  GT   GACATGGT
                                |||  ||||  ||   ||||||||
                                ACC  GGGG  TA   CTGTACCA
                                  CA    AT  C__
GAM1978  B3GALT2   3'  CATGCTTGTTATTGCATG    48377      G      __
                                CATG TTGTTAT  TATG
                                |||| |||||||  ||||
                                GTAC AACAATA  GTAC
                                  G      AC
GAM1978  CASP8AP2  3'  TACATGGTTTTATTATA     48378         G
                                TACATGGTT TTATTATG
                                ||||||||| ||||||||
                                ATGTACCAA AATAATAT
                                          _
GAM1978  DMRT2     3'  TGGTTGTTATGGATTT      48379          TAT
                                TGGTTGTTAT   GGTTT
                                ||||||||||   |||||
                                ACCAACAATA   CTAAA
                                      C__
GAM1978  EDN2      3'  CACGGTTGCTCCTGGTTT    48380          ATTA
                                CATGGTTGTT    TGGTTT
                                ||||||||||    ||||||
                                GTGCCAACGA    ACCAAA
                                      GG__
GAM1978  LASS2     3'  TACGATGGTTGTTATTGAGG   48381     _          AT
                                TAC ATGGTTGTTATT  GG
                                ||| ||||||||||||  ||
                                ATG TACCAACAATAA  CC
                                  C          CT
GAM1978  SLC4A4    3'  TACATGGTTTTTAAACAATTTA 48382         G   TT TG
              T                  TACATGGTT TTA  A  GTTTAT
                                 |||||||| |||  |  ||||||
                                 ATGTACCAA AAT  T  TAAATA
                                      A   T_ GT
GAM1978  FLJ23093  3'  TACATGGTGTTGCTTTTAT   48383         __   A
                                TACATGGT  TGTT TTAT
                                ||||||||  |||| ||||
                                ATGTACCA  ACGA AATA
                                    CA    A
GAM1978  HSN44A4A  3'  TGGGCGCTTTATGGTTTAT   48384     T    A
                                TGG TGTT TTATGGTTTAT
                                ||| |||| ||||||||||
                                ACC GCGA AATACCAAATA
                                  C    _
GAM1978  PRO0800   3'  ATGGATGACTTAGTGGTTTAT  48385     T  TTA   _
                                ATGG TG   TTA TGGTTTAT
                                |||| ||   ||| ||||||||
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                                TACC AC   AAT ACCAAATA
                                  T TG_   C
GAM1978 LOC253776 3'  TACATAGTGATATGGTTT    48386        TGTTAT
                                TACATGGT     TATGGTTT
                                ||||||||     ||||||||
                                ATGTATCA     ATACCAAA
                                     CT____
GAM1978 LOC256937 5'  TGATGGTTGTTAGCTGTGTTTA 48387    C        TTA  _
          T                      A ATGGTTGTTA   TG GTTTAT
                                | ||||||||||   || ||||||
                                A TACCAACAAT   AC CAAATA
                                 C         CG_  A
GAM1979 DACH     3'  TAAAATGGGCACATTTTACTT  48390        GA   C_
                                TAGAATGGG  ACAT  TACTT
                                |||||||||  ||||  |||||
                                ATTTTACCC  TGTA  ATGAA
                                     G_    AA
GAM1979 GAS7     3'  AGGGTGGGGGGGCATCCACT   48391    AA    AA
                                AG  TGGGG  CATCTACT
                                ||  |||||  ||||||||
                                TC  ACCCC  GTAGGTGA
                                 CC    CC
GAM1979 GAS7     3'  AGGGTGGGGGGGCATCCACT   48391    AA    AA
                                AG  TGGGG  CATCTACT
                                ||  |||||  ||||||||
                                TC  ACCCC  GTAGGTGA
                                 CC    CC
GAM1979 SLC17A4   5'  TAGGGACTGGCATTTACTTACT 48392       A___   C
                                TGGGGA    CAT TACTTACT
                                ||||||    ||| ||||||||
                                ATCCCT    GTA ATGAATGA
                                    GACC   A
GAM1979 C1orf19   3'  GAATGGGGAAGTCAACCC    48393         CA  T
                                GAATGGGGAA  TC ACTT
                                ||||||||||  || ||||
                                CTTACCCCTT  AG TGGG
                                      C_  T
GAM1979 CNOT8    3'  GAATGGGGAAGACTTA      48394         CATCT
                                GAATGGGGAA     ACTTA
                                ||||||||||     |||||
                                CTTACCCCTT     TGAAT
                                      C_____
GAM1979 KIAA0978  3'  GGGGCATCTACTTGCT      48395      AA       A
                                GGGG  CATCTACTT CT
                                ||||  ||||||||| ||
                                CCCC  GTAGATGAA GA
                                  __        C
GAM1979 KIAA1229  3'  GAATGGGATCTATTTA      48396        GAAC    C
                                GAATGGG    ATCTA TTA
                                |||||||    ||||| |||
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                                CTTACCC   TAGAT AAT
                                    ____    A
GAM1979 KIAA1297 3' TAGAACGGGGAGCGTCCACT  48397          ACA
                                TAGAATGGGGA  TCTACT
                                ||||||||||  ||||||
                                ATCTTGCCCCT  AGGTGA
                                     CGC
GAM1979 KIAA1889 3' CAGAAAGCGGGGAACGTTTACT 48398     __      ATC    A
          TGCT                   TAGAA  TGGGGAAC  TACTT CT
                                ||||| ||||||||  ||||| ||
                                GTCTT  GCCCCTTG  ATGAA GA
                                   TC      CAA    C
GAM1979 MTHFD2   3' TAAAATGGGGAGAACTTAC   48399          ACATCT
                                TAGAATGGGGA    ACTTAC
                                ||||||||||     ||||||
                                ATTTTACCCCT    TGAATG
                                     CT____
GAM1980 FLJ14009 5' TAGAATGCCCTGATAAT    48402      C    TTC
                                TAGAA GCTCT  GATGAT
                                ||||| |||||  ||||||
                                ATCTT CGGGA  CTATTA
                                   A   ___
GAM1980 KIAA0332 3' GAATGCTCTTTCATTTGAT   48403    C       A_
                                GAA GCTCTTTCG  TGAT
                                ||| |||||||||  ||||
                                CTT CGAGAAAGT  ACTA
                                  A       AA
GAM1980 PRO1768  3' CAGGGCGCTTTTCAATGAT   48404    AA   C
                                TAG  CGCT TTTCGATGAT
                                |||  |||| ||||||||||
                                GTC  GCGA AAAGTTACTA
                                  CC   _
GAM1981 ADAMTS5  3' TATTGGTTTTGTAAAACAATTA 48407      T      TCT TG
                                TATTG GTTTTGTA  A  ATTA
                                ||||| ||||||||  |  ||||
                                ATAAC CAAAACAT  T  TAAT
                                   _      TT_ GT
GAM1981 FLJ10099 3' TATTGTTGTTACTATGATT   48408      GTTT   AT
                                TATTGT   TGT  CTATGATT
                                ||||||   |||  ||||||||
                                ATAACA   ACA  GATACTAA
                                    ____   AT
GAM1981 KPNB3    5' TATTGTGTTTTCTGTTGCTTCT 48409        _____   A
          A                     TATTGTGTTT    TGT TCTA
                                ||||||||||    ||| ||||
                                ATAACACAAA    ACG AGAT
                                     AGACA   A
GAM1981 SLC38A4  3' TGTTGTTGCTCTATGATT    48410     _   A
                                TGTT TTGT TCTATGATT
                                |||| |||| |||||||||
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                                ACAA AACG AGATACTAA
                                  C   _
GAM1981  LOC221814 5'  CATTGTGTTTTGTAAGGCTG  48411           TCTA
                                TATTGTGTTTTGTA   TG
                                ||||||||||||||  ||
                                GTAACACAAAACAT   AC
                                      TCCG
GAM1982  ASPH    3'  TAATAGCTTTTAAATCATGTTT 48414       ATCTTTAG
           AA                   TAATAGC      TATGTTTAA
                                |||||||      |||||||||
                                ATTATCG      GTACAAATT
                                   AAAATTTA
GAM1982  ASPH    3'  TAATAGCTTTTAAATCATGTTT 48414       ATCTTTAG
           AA                   TAATAGC      TATGTTTAA
                                |||||||      |||||||||
                                ATTATCG      GTACAAATT
                                   AAAATTTA
GAM1982  GALNT1   3'  AGCATCCCCATGTGTTT    48415        GTA
                                AGCATCTTTA   TGTTT
                                ||||||||||  |||||
                                TCGTAGGGGT   ACAAA
                                     AC_
GAM1982  SCN3A    3'  ATAGCCTTTAAACTATGTTTAA 48416     AT    __
                                ATAGC  CTTTAG  TATGTTTAA
                                |||||  ||||||  |||||||||
                                TATCG  GAAATT  ATACAAATT
                                  __     TG
GAM1982  MGC14353  3'  TAATAGCACTCTATTGTTTA  48417       T    GTA
                                TAATAGCA CTTTA   TGTTTA
                                |||||||| |||||  ||||||
                                ATTATCGT GAGAT   ACAAAT
                                    _    A__
GAM1982  LOC196394 3'  TAATAGCACTTTAAAGATGTTT 48418       T    T_
           AA                   TAATAGCA CTTTAG  ATGTTTAA
                                ||||||||| ||||||  ||||||||
                                ATTATCGT GAAATT  TACAAATT
                                    _     TC
GAM1982  LOC219540 3'  AGCATCTTTAACATTTTTAA  48419          G
                                AGCATCTTTAGTAT TTTAA
                                |||||||||||||| |||||
                                TCGTAGAAATTGTA AAATT
                                      A
GAM1982  LOC253675 3'  TAATACATCTTTGGTACAT   48420     G     A
                                TAATA CATCTTT GTATGT
                                ||||| ||||||| ||||||
                                ATTAT GTAGAAA CATGTA
                                  _     C
GAM1983  YES1     3'  CTGATCTGGTCATATTTT    48423      C  GGTA
                                TTGATC GG    TTATATTTT
                                ||||||  ||   |||||||||
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                                GACTAG CC    AGTATAAAA
                                   A _____
GAM1983  KIAA1000  3'  TTGGCCTGGAGTCATATTTTC  48424     AT C     AT
                                TTG  C GGGGT  TATATTTTC
                                |||  | |||||  |||||||||
                                AAC  G CCTCA  GTATAAAAG
                                  CG A    __
GAM1983  LOC145788 5'  TTAATCCGGGGAGCTGTTTTC  48425          TATTATA
                                TTGATCCGGGG      TTTTC
                                ||||||||||       |||||
                                AATTAGGCCCC      AAAAG
                                      TCGAC__
GAM1984  COL17A1   5'  GAGTGATCTTTCAAAAAT    48428    AC        T
                                GA  GATCTTTCGA GAT
                                ||  |||||||||| |||
                                CT  CTAGAAAGTT TTA
                                 CA         T
GAM1984  COL17A1   5'  GAGTGATCTTTCAAAAAT    48428    AC        T
                                GA  GATCTTTCGA GAT
                                ||  |||||||||| |||
                                CT  CTAGAAAGTT TTA
                                 CA         T
GAM1984  FLJ12750  3'  TAGGACTGTCTTTCGAAAAT   48429     A  GA       T
                                TAG AC  TCTTTCGA GAT
                                |||  ||  |||||||| |||
                                ATC TG  AGAAAGCT TTA
                                  C  AC       T
GAM1985  PPARG     3'  TAAAACGCTTTTTCACAGTAAA 48432         C    G  GA
           T                     TAGAACGCT TTTC AT  TAAAT
                                |||||||||  ||||  ||  |||||
                                ATTTTGCGA AAAG TG  ATTTA
                                      A    _  TC
GAM1985  WHSC1     5'  TAGAACACTCTGATG       48433          TTC
                                TAGAACGCTCT   GATG
                                ||||||||||    ||||
                                ATCTTGTGAGA   CTAC
                                      ___
GAM1985  WHSC1     5'  TAGAACACTCTGATG       48433          TTC
                                TAGAACGCTCT   GATG
                                ||||||||||    ||||
                                ATCTTGTGAGA   CTAC
                                      ___
GAM1985  WHSC1     5'  TAGAACACTCTGATG       48433          TTC
                                TAGAACGCTCT   GATG
                                ||||||||||    ||||
                                ATCTTGTGAGA   CTAC
                                      ___
GAM1985  WHSC1     5'  TAGAACACTCTGATG       48433          TTC
                                TAGAACGCTCT   GATG
                                ||||||||||    ||||
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                                ATCTTGTGAGA  CTAC
                                        ____
GAM1985  PPP1R14C  3'  AGAACGCTCTTGAATAA    48434          TC
                                AGAACGCTCTT  GATGA
                                ||||||||||  |||||
                                TCTTGCGAGAA  TTATT
                                      C_
GAM1986  AK2       3'  TTTGTCCTAGGTCCCCTG    48437        T  A    G
                                TTTGTCCT AG GTTTT TG
                                |||||||| || ||||| ||
                                AAACAGGA TC CAGGG AC
                                    _ _    G
GAM1986  APOA2     5'  TCTGTCCTTGGTGTCTGTG   48438         AGA  _
                                TTTGTCCTT   GT TTTGTG
                                |||||||||   || ||||||
                                AGACAGGAA   CA AGACAC
                                     C__  C
GAM1986  BGN       3'  TGTCCCTGGGGTTTTGTG    48439        AGA
                                TGTCCTT   GTTTTGTG
                                |||||||   ||||||||
                                ACAGGGA   CAAAACAC
                                    CCC
GAM1986  CDH11     3'  TTGTCCTTTCTAATTTTGTG  48440        AG_
                                TTGTCCTT   AGTTTTGTG
                                ||||||||   |||||||||
                                AACAGGAA   TTAAAACAC
                                     AGA
GAM1986  CHN2      3'  TTTATCCTTAGCTGT       48441         AGTT
                                TTTGTCCTTAG   TTGT
                                ||||||||||   ||||
                                AAATAGGAATC   GACA
                                       ____
GAM1986  LMO2      3'  TCTGTCCTTCCCTTGTG     48442         AGAGT
                                TTTGTCCTT    TTTGTG
                                |||||||||    ||||||
                                AGACAGGAA    GAACAC
                                     GG___
GAM1986  MYOD1     3'  TGTCCTTGCCCTGTG       48443        AGA
                                TGTCCTT   GTTTTGTG
                                |||||||   ||||||||
                                ACAGGAA   CGGGACAC
                                      ___
GAM1986  PBX2      3'  TTTGTCCTCTGGAAGCCT    48444         A__
                                TTTGTCCTT   GAGTTT
                                |||||||||   ||||||
                                AAACAGGAG   TTCGGA
                                     ACC
GAM1986  PLCB4     3'  TTGTGTTCAGAAGTTTTGTG  48445      CC   _
                                TTGT  TTAGA GTTTTGTG
                                ||||  ||||| ||||||||
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                                AACA  AGTCT CAAAACAC
                                  CA    T
GAM1986  SUFU     3'  CTTGTCCTTTTATTTGTG    48446         AGAGT
                                TTTGTCCTT    TTTGTG
                                |||||||||    ||||||
                                GAACAGGAA    AAACAC
                                     AAT__
GAM1986  TMOD2    3'  TTTGTCCTTGAGATAACATG   48447         A   TTT_
                                TTTGTCCTT GAG    TGTG
                                ||||||||| |||    ||||
                                AAACAGGAA CTC    GTAC
                                     _  TATT
GAM1986  TTN      3'  TTTGTCATGATAATTTTGTG   48448       CTTAG
                                TTTGTC    AGTTTTGTG
                                ||||||    |||||||||
                                AAACAG    TTAAAACAC
                                   TACTA
GAM1986  TTN      3'  TTTGTCATGATAATTTTGTG   48448       CTTAG
                                TTTGTC    AGTTTTGTG
                                ||||||    |||||||||
                                AAACAG    TTAAAACAC
                                   TACTA
GAM1986  TTN      3'  TTTGTCATGATAATTTTGTG   48448       CTTAG
                                TTTGTC    AGTTTTGTG
                                ||||||    |||||||||
                                AAACAG    TTAAAACAC
                                   TACTA
GAM1986  C3IP1    3'  CTTGTCCCCAAAGTTTTGTG   48449
                                TTTGTCCTTAGAGTTTTGTG
                                ||||||||||||||||||||
                                GAACAGGGGTTTCAAAACAC

GAM1986  CLIC5    3'  TTTGTCCTTGGCCTTG      48450         AGA
                                TTTGTCCTT   GTTTTG
                                |||||||||   ||||||
                                AAACAGGAA   CGGAAC
                                     C__
GAM1986  COQ7     3'  TTTGTCCTTGAAGTTTTA    48451         AG
                                TTTGTCCTT  AGTTTTG
                                |||||||||  |||||||
                                AAACAGGAA  TCAAAAT
                                     CT
GAM1986  CORTBP2  3'  TTGTCCTTGGTTTCTGTG    48452         AGAG
                                TTGTCCTT    TTTTGTG
                                ||||||||    |||||||
                                AACAGGAA    AAGACAC
                                     CCA_
GAM1986  DKFZP434B195 3'  TTTGTCCTTAGCGGCTCTG   48453          A_
                                TTTGTCCTTAG  GTTTTG
                                ||||||||||  ||||||
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                                AAACAGGAATC  CGAGAC
                                      GC
GAM1986  DKFZP434F0318 3'  TCTGTCCTTGGTCATCTGTG   48454         AGAGT
                                TTTGTCCTT    TTTGTG
                                |||||||||    ||||||
                                AGACAGGAA    AGACAC
                                     CCAGT
GAM1986  DOCK3    3'  CTTGTCCTTGGGGCCTTTGTG  48455         AGA  _
                                TTTGTCCTT   GT TTGTG
                                |||||||||   || ||||||
                                GAACAGGAA   CG AAACAC
                                     CCC  G
GAM1986  FLJ12691  3'  TTTGTCTTTGAGCCCCAT    48456       C  A     TG
                                TTTGTC TT GAGTTT  T
                                |||||| || ||||||  |
                                AAACAG AA CTCGGG  A
                                   _ A     GT
GAM1986  FLJ21817  3'  TTTGTCCTTAAAAAACTG    48457           TT
                                TTTGTCCTTAGAG  TTG
                                ||||||||||||  |||
                                AAACAGGAATTTT  GAC
                                       TT
GAM1986  FLJ32783  3'  TTTGTTCAGCAAGTTTTGTG   48458      CCTTA
                                TTTGT    GAGTTTTGTG
                                |||||    ||||||||||
                                AAACA    TTCAAAACAC
                                   AGTCG
GAM1986  GT650    5'  TTGTCCTTAGGCTGTG      48459         A  TT
                                TTGTCCTTAG GT  TGTG
                                |||||||||| ||  ||||
                                AACAGGAATC CG  ACAC
                                      _ __
GAM1986  KIAA0280  3'  TTTGTCCCTTTCTAGCTTTGTG 48460         AG__
                                TTTGTCCTT    AGTTTTGTG
                                |||||||||    |||||||||
                                AAACAGGGA    TCGAAACAC
                                     AAGA
GAM1986  KIAA0643  3'  TTTGTCCCTGTGTTGTG     48461         AGA  T
                                TTTGTCCTT   GT TTGTG
                                |||||||||   || |||||
                                AAACAGGGA   CA AACAC
                                     ___  C
GAM1986  KIAA1348  3'  TTGTCCTTAAGCCTTTGTG   48462          AG
                                TTGTCCTTAG  TTTTGTG
                                ||||||||||  |||||||
                                AACAGGAATT  GAAACAC
                                      CG
GAM1986  KIAA1710  3'  TTTGTCCTTAAAAAGGAGTG  48463           TTTT
                                TTTGTCCTTAGAG   GTG
                                ||||||||||||   |||
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                                AAACAGGAATTTT  CAC
                                     TCCT
GAM1986 KIAA1762 3' TTTGGTTAGAGTTTTGTG  48464    TCC
                                TTTG  TTAGAGTTTTGTG
                                ||||  ||||||||||||
                                AAAC  AATCTCAAAACAC
                                  C__
GAM1986 MGC3036  3' TCTGTCCTTGCAGCATGTG  48465      AG  TT
                                TTTGTCCTT  AGT  TGTG
                                |||||||||  |||  ||||
                                AGACAGGAA  TCG  ACAC
                                     CG  T_
GAM1986 MYH7B    3' TTTGTCCCTAGGACTGTG    48466      AGTT
                                TTTGTCCTTAG   TTGTG
                                ||||||||||   |||||
                                AAACAGGGATC   GACAC
                                      CT__
GAM1986 MYOZ3    3' TTTGCAATCAGGTTTTGTG   48467    CC   A
                                TTTGT  TTAG GTTTTGTG
                                |||||  |||| ||||||||
                                AAACG  AGTC CAAAACAC
                                   TT   _
GAM1986 OR2C3    3' TTTGTCCTTTAGATACACTG  48468      _  GTT_
                                TTTGTCCTT AGA   TTG
                                |||||||| |||   |||
                                AAACAGGAA TCT   GAC
                                     A  ATGT
GAM1986 PDE10A   3' TTTGTCCTGAGGCTGTG    48469      TA  TT
                                TTTGTCCT  GAG  TTGTG
                                ||||||||  |||  |||||
                                AAACAGGA  CTC  GACAC
                                     __  C_
GAM1986 PIK3C2G  3' TGTCCTTAATACCCTGTG   48470      AG
                                TGTCCTTAG  TTTTGTG
                                |||||||||  |||||||
                                ACAGGAATT  GGGACAC
                                     AT
GAM1986 STRN3    3' TTTATCCAAACATTTTGTG   48471      TTAGA
                                TTTGTCC    GTTTTGTG
                                |||||||    ||||||||
                                AAATAGG    TAAAACAC
                                    TTTG_
GAM1986 TIX1     3' CTTGTCCTTGGAGCCACATG  48472      A   TT
                                TTTGTCCTT GAGT  TGTG
                                ||||||||| ||||  ||||
                                GAACAGGAA CTCG  GTAC
                                     C   GT
GAM1986 LOC143785 3' TTTGCCTATAGTTTTGTG   48473    T  TAG
                                TTTG CCT   AGTTTTGTG
                                |||| |||   |||||||||
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                                AAAC GGA   TCAAAACAC
                                  _   TA_
GAM1986  LOC146880 3'  CTTGTTCTTAGATCTGTG    48474      C     GT
                                TTTGT CTTAGA  TTTGTG
                                ||||| ||||||  ||||||
                                GAACA GAATCT  AGACAC
                                   A     __
GAM1986  LOC148529 5'  TTTGTACCTTAGGCAAATG    48475      _     A  TTT
                                TTTGT CCTTAG GT   GTG
                                ||||| |||||| ||   |||
                                AAACA GGAATC CG   TAC
                                   T     _  TT_
GAM1986  LOC150480 5'  TTTGTCCTTCAGATTTG     48476         AG  T
                                TTTGTCCTT  AG TTTG
                                |||||||||  || ||||
                                AAACAGGAA  TC AAAC
                                      G_  T
GAM1986  LOC151571 5'  CTTGTCATAACAGTTTTGTG   48477       CT  _
                                TTTGTC  TAG AGTTTTGTG
                                ||||||  ||| |||||||||
                                GAACAG  ATT TCAAAACAC
                                   T_  G
GAM1986  LOC153937 5'  TTGTCTTTCTAAGTTTTGTG   48478      C  A_
                                TTGTC TT  GAGTTTTGTG
                                ||||| ||  ||||||||||
                                AACAG AA  TTCAAAACAC
                                   A  GA
GAM1986  LOC158279 5'  TTTGTCCTTCAGATTTG     48476         AG  T
                                TTTGTCCTT  AG TTTG
                                |||||||||  || ||||
                                AAACAGGAA  TC AAAC
                                      G_  T
GAM1986  LOC164390 5'  TTTGTCCTTGGCTGGGTTGTG  48479         AGA  ___
                                TTTGTCCTT   GTT   TTGTG
                                |||||||||   |||   |||||
                                AAACAGGAA   CGA   AACAC
                                      C__   CCC
GAM1986  LOC164397 5'  CTTGTCCTTGGAGACACTG    48480         A   TT_
                                TTTGTCCTT GAG   TTG
                                ||||||||| |||   |||
                                GAACAGGAA CTC   GAC
                                      C   TGT
GAM1986  LOC197317 5'  TTTATCAAGTTTTGT       48481       CTTA
                                TTTGTC    GAGTTTTGT
                                ||||||    |||||||||
                                AAATAG    TTCAAAACA
                                   ____
GAM1986  LOC203202 3'  TTTGTCTTAGGTCCTG      48482       C    A
                                TTTGTC TTAG GTTTTG
                                |||||| |||| ||||||
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                                AAACAG AATC CAGGAC
                                     _   _
GAM1986  LOC203286 5'  TTTGTCTTCAGTCCTGTG    48483       C  AG
                                TTTGTC TT  AGTTTTGTG
                                ||||||  ||  |||||||||
                                AAACAG AA  TCAGGACAC
                                   _  G_
GAM1986  LOC219855 3'  TGTCCTTAGGCAGCCCTG    48484         __
                                TGTCCTTAG  AGTTTTG
                                |||||||||  |||||||
                                ACAGGAATC  TCGGGAC
                                     CG
GAM1986  LOC220864 5'  TTTGTCCTTCAGATTTG     48476         AG  T
                                TTTGTCCTT  AG TTTG
                                |||||||||  ||  ||||
                                AAACAGGAA  TC AAAC
                                     G_  T
GAM1986  LOC221543 5'  TTTGCCTTCGCTTTGTG     48485     T    AGA
                                TTTG CCTT   GTTTTGTG
                                ||||  ||||   ||||||||
                                AAAC GGAA   CGAAACAC
                                  _    G__
GAM1986  LOC253626 3'  TTATTTTTAGAGTTTTGTG    48486      CC
                                TTGT  TTAGAGTTTTGTG
                                ||||  ||||||||||||
                                AATA  AATCTCAAAACAC
                                  AA
GAM1986  LOC254428 3'  TTTCTCCCAATTTTGTG     48487     G    TAG
                                TTT TCCT   AGTTTTGTG
                                |||  ||||   |||||||||
                                AAA AGGG   TTAAAACAC
                                  G   ___
GAM1986  LOC254778 3'  TTTGTCCTTGAAAATTG     48488         A   TT
                                TTTGTCCTT GAG  TTG
                                |||||||||  |||  |||
                                AAACAGGAA CTT  AAC
                                     _   TT
GAM1986  LOC256113 5'  TTTGCCTTCACATTTTGTG    48489     T    AGA
                                TTTG CCTT   GTTTTGTG
                                ||||  ||||   ||||||||
                                AAAC GGAA   TAAAACAC
                                  _    GTG
GAM1986  LOC257596 5'  TTTGCCTTCGCTTTGTG     48485     T    AGA
                                TTTG CCTT   GTTTTGTG
                                ||||  ||||   ||||||||
                                AAAC GGAA   CGAAACAC
                                  _    G__
GAM1986  LOC91408  3'  TTTGTCCTTAAATATTG     48490          GTT
                                TTTGTCCTTAGA   TTG
                                ||||||||||||   |||
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                                AAACAGGAATTT   AAC
                                      AT_
GAM1986 LOC92710 3' TTCTCCCAGAGTTTTGTG    48491    G   T
                                TT TCCT AGAGTTTTGTG
                                || |||| ||||||||||
                                AA AGGG TCTCAAAACAC
                                 G   _
GAM1987 CENTD1   3' TAATATACAAGGTTTCTCAAAG 48494          A   G_  _ C
            TGCA                  TGATATACAA GTTT  CAA G GCA
                                |||||||||| ||||  ||| | |||
                                ATTATATGTT CAAA  GTT C CGT
                                      C   GA   T A
GAM1987 CENTD1   3' TAATATACAAGGTTTCTCAAAG 48494          A   G_  _ C
            TGCA                  TGATATACAA GTTT  CAA G GCA
                                |||||||||| ||||  ||| | |||
                                ATTATATGTT CAAA  GTT C CGT
                                      C   GA   T A
GAM1987 EGR4     3' TGCTGTACAAAGTCCCGCGC   48495    ATA       TGCAA
                                TG   TACAAAGTT    GCGC
                                ||   |||||||||    ||||
                                AC   ATGTTTCAG    CGCG
                                 GAC        GG___
GAM1987 GAK      3' TGATTACAAAGTGCGGTGCA   48496     A      T___
                                TGAT TACAAAGT    TGCA
                                |||| ||||||||    ||||
                                ACTA ATGTTTCA    ACGT
                                  _       CGCC
GAM1987 HAP1     3' TGATATGCAAAGTCCATGCA   48497       A      __
                                TGATAT CAAAGTT  TGCA
                                |||||| |||||||  ||||
                                ACTATA GTTTCAG  ACGT
                                   C      GT
GAM1987 LIFR     5' TGATAATGGTCTTGCAAGTGCA 48498       TACAAAG       C
                                TGATA      TTTGCAAG GCA
                                |||||      |||||||| |||
                                ACTAT      GAACGTTC CGT
                                   TACCA__       A
GAM1987 NBEA     3' TGATGTACAAAGTATCAAACG  48499     A       TTG
                                TGAT TACAAAGT   CAAGCG
                                |||| ||||||||   ||||||
                                ACTA ATGTTTCA   GTTTGC
                                  C       TA_
GAM1987 KIAA1789 5' TGATATACAAAAGTTGTGTATG 48500       _ T_________   AAGC
            CGCTTGC                TACAAA GT        TGC    GC
                                |||||| ||        |||    ||
                                ATGTTT CA        ACG    CG
                                   T  ACACATIII   CGAA
GAM1987 NLN      3' TGATATACAAAGATAAATGCA  48501          TT___
                                TGATATACAAAG    TGCA
                                ||||||||||||    ||||
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                                ACTATATGTTTC    ACGT
                                      TATTT
GAM1987 PRO2958  3' TATACAAATCTGAAGTGCA   48502       G   C  C
                                TATACAAA TTTG AAG GCA
                                |||||||| |||| ||| |||
                                ATATGTTT AGAC TTC CGT
                                    _   _  A
GAM1987 LOC92399 3' GATATACAGGCTAATTAAGTGC 48503       AA  TGC_  C
           A                     GATATACA  GTT   AAG GCA
                                |||||||| |||   ||| |||
                                CTATATGT  CGA   TTC CGT
                                    C_  TTAA  A
GAM1988 CALM1    3' ATACATGCAGATTTTGTGTGTG 48506       _______  C
                                ATGCGTGC    TGTG GTG
                                ||||||||    |||| |||
                                TATGTACG    ACAC CAC
                                    TCTAAA   A
GAM1988 CDH1     3' TCATGCGTAGTGGTGC     48507        CT  C
                                TCATGCGTG  GTG GTGC
                                |||||||||  ||| ||||
                                AGTACGCAT  CAC CACG
                                    __  _
GAM1988 CLTC     3' AATCATGGTGCTCTTTGC    48508       C   G__
                                AATCATG GTGCT  TGC
                                ||||||| |||||  |||
                                TTAGTAC CACGA  ACG
                                    _   GAA
GAM1988 EGFL4    3' TCATGTGTGTATGCGTG     48509      C  C
                                TCATG GTG TGTGCGTG
                                ||||| ||| ||||||||
                                AGTAC CAC ATACGCAC
                                   A  _
GAM1988 MNT      3' ATGTGTGCGTGTGCGTGC    48510     C  _
                                ATG GTGC TGTGCGTGC
                                ||| |||| |||||||||
                                TAC CACG ACACGCACG
                                  A   C
GAM1988 PLXNA1   3' AATCATGCATGCCCCGTGGTGC 48511          __  C
                                AATCATGCGTGCT  GTG GTGC
                                ||||||||||||  ||| ||||
                                TTAGTACGTACGG  CAC CACG
                                      GG  _
GAM1988 PTPRZ1   5' ATCGTGCGTGCGTATGTG    48512    A     T  C
                                ATC TGCGTGC GTG GTG
                                ||| ||||||| ||| |||
                                TAG ACGCACG CAT CAC
                                  C      _  A
GAM1988 ARHGEF10 3' TCATTCGGAGCGTGCGTGC   48513     G  T_  T
                                TCAT CG  GC GTGCGTGC
                                |||| ||  || ||||||||
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                                AGTA GC  CG CACGCACG
                                  A  CT  _
GAM1988  FLJ12649  3'  AATCATATACTGTGTGTGC   48514      GC      C
                                AATCAT  GTGCTGTG GTGC
                                ||||||  |||||||| ||||
                                TTAGTA  TATGACAC CACG
                                   __       A
GAM1988  FLJ21916  3'  CCATGGCTGTGCGTGC     48515      CGT
                                TCATG   GCTGTGCGTGC
                                |||||   ||||||||||
                                GGTAC   CGACACGCACG
                                   ____
GAM1988  FLJ22055  3'  CATCGTGTGTGTGCATGC   48516    G   C_
                                CAT CGTG  TGTGCGTGC
                                ||| ||||  |||||||||
                                GTA GCAC  ACACGTACG
                                  _   AC
GAM1988  FLJ25348  5'  TCATGCTGCCCCGTGGTG   48517      _ G    C
                                TCATGC GT CTGTG GTG
                                |||||| || ||||| |||
                                AGTACG CG GGCAC CAC
                                   A  G    _
GAM1988  GPS2      5'  ATCATGCCAATGCGTGC    48518      GTGCT
                                ATCATGC    GTGCGTGC
                                |||||||    ||||||||
                                TAGTACG    TACGCACG
                                    GT____
GAM1988  KIAA0828  3'  ATCATGCGTGGTCTGGTG   48519        CTG  C
                                ATCATGCGTG   TG GTG
                                ||||||||||   || |||
                                TAGTACGCAC   AC CAC
                                     CAG  _
GAM1988  KIAA1170  3'  CATGGTGGTGCGTGC      48520     C   CT
                                CATG GTG  GTGCGTGC
                                |||| |||  ||||||||
                                GTAC CAC  CACGCACG
                                  _  ___
GAM1988  KIAA1550  3'  CATGCGTCTATGTGTGC    48521       G    C
                                CATGCGT CTGTG GTGC
                                ||||||| ||||| ||||
                                GTACGCA GATAC CACG
                                   _    A
GAM1988  KIAA1958  3'  AACCACATATTGTGCGTG   48522     AT    C
                                AATC  GCGTG TGTGCGTG
                                ||||  ||||| ||||||||
                                TTGG  TGTAT ACACGCAC
                                  __    A
GAM1988  MGC23884  3'  AATCATGTGTACGCATGTGTG  48523       C   _   C
                                AATCATG GTGC TGTG GTG
                                ||||||| |||| |||| |||
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                                TTAGTAC CATG GTAC CAC
                                   A   C   A
GAM1988 p25      3' GCTGTGGCTGTGTGCGTGC   48524   _  _   __
                                GC GTG CTGT  GCGTGC
                                || ||| ||||  ||||||
                                CG CAC GACA  CGCACG
                                 A  C   CA
GAM1988 PRC1     3' CATGTGTGTTCATACATGC   48525     C  CT_
                                CATG GTG  GTGCGTGC
                                |||| |||  ||||||||
                                GTAC CAC  TATGTACG
                                  A  AAG
GAM1988 TReP-132 5' AATCATGCTGCTTTCATGC   48526       G   GTG
                                AATCATGC TGCT  CGTGC
                                |||||||| ||||  |||||
                                TTAGTACG ACGA  GTACG
                                    _   AA_
GAM1988 TReP-132 5' AATCATGCTGCTTTCATGC   48526       G   GTG
                                AATCATGC TGCT  CGTGC
                                |||||||| ||||  |||||
                                TTAGTACG ACGA  GTACG
                                    _   AA_
GAM1988 TReP-132 5' AATCATGCTGCTTTCATGC   48526       G   GTG
                                AATCATGC TGCT  CGTGC
                                |||||||| ||||  |||||
                                TTAGTACG ACGA  GTACG
                                    _   AA_
GAM1988 LOC116068 3' CATGCGTGCACACATGC    48527        T TG
                                CATGCGTGC G  CGTGC
                                ||||||||| |  |||||
                                GTACGCACG T  GTACG
                                     _ GT
GAM1988 LOC135932 3' CATGCGTGCCCATGC      48528        GTG
                                CATGCGTGCT  CGTGC
                                ||||||||||  |||||
                                GTACGCACGG  GTACG
                                    ____
GAM1988 LOC144871 3' CATGGTGGTGCGTGC      48520     C  CT
                                CATG GTG  GTGCGTGC
                                |||| |||  ||||||||
                                GTAC CAC  CACGCACG
                                  _  __
GAM1988 LOC149912 5' TCAGGTACCATGTGTGC    48529    TGC      C
                                TCA  GTGCTGTG GTGC
                                |||  |||||||| ||||
                                AGT  CATGGTAC CACG
                                  C__      A
GAM1988 LOC152794 5' CATGGTGGTGCGTGC      48520     C  CT
                                CATG GTG  GTGCGTGC
                                |||| |||  ||||||||
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                                GTAC CAC  CACGCACG
                                  _  __
GAM1988  LOC153546 3'  TCGAGCGTGCTAACGTG     48530    AT      T
                                TC  GCGTGCTG GCGTG
                                ||  |||||||| |||||
                                AG  CGCACGAT TGCAC
                                 CT      _
GAM1988  LOC153711 5'  TCTGCGTGTACGTGTGTG    48531    A    C_   C
                                TC TGCGTG  TGTG GTG
                                || ||||||  |||| |||
                                AG ACGCAC  GCAC CAC
                                 _    AT   A
GAM1988  LOC253181 3'  TCTGCGCGGTGCGTGC      48532    A    CT
                                TC TGCGTG  GTGCGTGC
                                || ||||||  ||||||||
                                AG ACGCGC  CACGCACG
                                 _    __
GAM1988  LOC257115 5'  TCTGCGCGGTGCGTGC      48532    A    CT
                                TC TGCGTG  GTGCGTGC
                                || ||||||  ||||||||
                                AG ACGCGC  CACGCACG
                                 _    __
GAM1988  LOC92305  3'  ACGCTGTGTCTGTGTGTGC    48533     _  _   C
                                ATGC GTG CTGTG GTGC
                                |||| ||| ||||| ||||
                                TGCG CAC GACAC CACG
                                  A  A    A
GAM1989  CHRNE     3'  CCGCATGTCCTTGCTTTC     48536     A__
                                TCGCG   TCTTGCTTTC
                                |||||   ||||||||||
                                GGCGT   GGAACGAAAG
                                   ACA
GAM1989  MAPRE1    3'  ACGATGCCTCTTGCTTT      48537     C  GA
                                ACGAT GC  TCTTGCTTT
                                ||||| ||  |||||||||
                                TGCTA CG  AGAACGAAA
                                  _ G_
GAM1989  SSPN      3'  CAATTTGGATCTTGCTTTCT   48538     CGC
                                CGAT   GATCTTGCTTTCT
                                ||||   |||||||||||||
                                GTTA   CTAGAACGAAAGA
                                  AAC
GAM1989  USP6      3'  CACCTTCATGATCTTGCTTTCT 48539     GA   C
                                CAC  TCG GATCTTGCTTTCT
                                |||  ||| |||||||||||||
                                GTG  AGT CTAGAACGAAAGA
                                 GA   A
GAM1989  WASF1     5'  GATCGGATGTGCTTTCT      48540     C   CT
                                GATCG GAT  TGCTTTCT
                                ||||| |||  ||||||||
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                                CTAGC CTA  ACGAAAGA
                                  _  C_
GAM1989  AD-003   3'  CGGGTCCCACCTTGCTTT    48541    A_  G G
                                CG  TC C ATCTTGCTTT
                                ||  || | ||||||||||
                                GC  AG G TGGAACGAAA
                                 CC  G _
GAM1989  KIAA0976  3'  ACCATGCGTAATCTTGCTTTCT 48542     CGAT  CG
                                ACCA   CG  ATCTTGCTTTCT
                                ||||   ||  ||||||||||||
                                TGGT   GC  TAGAACGAAAGA
                                  AC__  AT
GAM1989  S164     5'  ACGATCTGAGCTCCTTTCT   48543       GC  T   G
                                ACGATC  GA CTT CTTTCT
                                ||||||  || ||| ||||||
                                TGCTAG  CT GAG GAAAGA
                                   A_  C   _
GAM1989  SIMRP7   3'  CCACGGCGCCCTCCTTCTTGCT 48544      AT   GA____
            TTCT                  CCACG  CGC     TCTTGCTTTCT
                                |||||  |||     ||||||||||
                                GGTGC  GCG     AGAACGAAAGA
                                  C_   GGAGGA
GAM1989  LOC144524 5'  CCACCGTTCCTTGCTTT     48545      GAT  CGA
                                CCAC   CG   TCTTGCTTT
                                ||||   ||   |||||||||
                                GGTG   GC   GGAACGAAA
                                  ___  AA_
GAM1989  LOC153469 3'  ACCATGATAGCGATACTTTCT  48546      C   C    CTT
                                ACCA GAT GCGAT   GCTTTCT
                                |||| ||| |||||   |||||||
                                TGGT CTA CGCTA   TGAAAGA
                                  A   T    ___
GAM1989  LOC154791 3'  CCATGGCGCGATCTCAGCT   48547     CGAT       _
                                CCA    CGCGATCTT GCT
                                |||    ||||||||| |||
                                GGT    GCGCTAGAG CGA
                                  ACC_        T
GAM1989  LOC157860 3'  CCATCTGCCCTTGCTTTCT   48548     CGA  GCGA
                                CCA   TC    TCTTGCTTTCT
                                |||   ||    ||||||||||
                                GGT   AG    GGAACGAAAGA
                                  ___  ACG_
GAM1989  LOC197196 3'  ACCATGCTTGGCTGTGCTTTCT 48549      CGATC  GAT_  _
                                ACCA     GC    CT TGCTTTCT
                                ||||     ||    || ||||||||
                                TGGT     CG    GA ACGAAAGA
                                  A_____  AACC  C
GAM1989  LOC199837 5'  CATGATGACTGTGCTTTCT   48550    C   CGC   CT
                                CA GAT   GAT  TGCTTTCT
                                || |||   |||  ||||||||
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                                GT CTA   CTG  ACGAAAGA
                                 A  ___   AC
GAM1989  LOC220573 3'  CACCTTCATGATCTTGCTTTCT 48539     GA   C
                                CAC  TCG GATCTTGCTTTCT
                                |||  ||| ||||||||||||
                                GTG  AGT CTAGAACGAAAGA
                                  GA   A
GAM1990  ANKH     5'  GCGGCTCCTCCTCGCGGCTGC  48553     A       AAAAT
                                GCG CTCCTCCTC    CTGC
                                ||| |||||||||    ||||
                                CGC GAGGAGGAG    GACG
                                  C       CGCC_
GAM1990  ANKH     5'  GCGGCTCCTCCTCGCGGCTGC  48553     A       AAAAT
                                GCG CTCCTCCTC    CTGC
                                ||| |||||||||    ||||
                                CGC GAGGAGGAG    GACG
                                  C       CGCC_
GAM1990  JJAZ1    3'  CAGGATTTCTTCAAAATCTG   48554     C  CTCC  C
                                CAG GA   TC TCAAAATCTG
                                ||| ||   || ||||||||||
                                GTC CT   AG AGTTTTAGAC
                                  _ AA__  A
GAM1990  MAX      3'  CAGCGACTCTGTGCTGCGAATC 48555         CTC_  CAA
           TG                   CAGCGACTC   CT   AATCTG
                                |||||||||   ||   ||||||
                                GTCGCTGAG   GA   TTAGAC
                                     ACAC  CGC
GAM1990  MAX      3'  CAGCGACTCTGTGCTGCGAATC 48555         CTC_  CAA
           TG                   CAGCGACTC   CT   AATCTG
                                |||||||||   ||   ||||||
                                GTCGCTGAG   GA   TTAGAC
                                     ACAC  CGC
GAM1990  RERE     3'  CAGCAACTCTTCCTGCTCCCTC 48556         C   CAAAA_
           TGC                    CAGCGACTC TCCT     TCTGC
                                |||||||||| ||||     |||||
                                GTCGTTGAG AGGA     AGACG
                                     A   CGAGGG
GAM1990  RPS6KA2  3'  GCGCCTCCTCCCATCTAGTCTG 48557     A       CAAAA_
           C                     GCG CTCCTCCT     TCTGC
                                ||| ||||||||     |||||
                                CGC GAGGAGGG     AGACG
                                  G       TAGATC
GAM1990  SIAH2    3'  GCAGGCTCCCTAAATCTGC   48558     ACTC    CA
                                GCG   CTCCT  AAATCTGC
                                |||   |||||  ||||||||
                                CGT   GAGGG  TTTAGACG
                                  CC__    A_
GAM1990  SIRT2    5'  CAGCGGCTCCTCCCTCAGAGTC 48559       A     _   AAA
           T                     CAGCG CTCCTCC TCA   TCT
                                ||||| ||||||| |||   |||
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                                GTCGC GAGGAGG AGT   AGA
                                   C      G   CTC
GAM1990 ALS2CR2  5' CAGCGACTCTCTTCAGGCTGC 48560        C  C   AAAT
                                CAGCGACTC TC TCA    CTGC
                                ||||||||| || |||    ||||
                                GTCGCTGAG AG AGT    GACG
                                     _ A   CC__
GAM1990 DKFZP434P211 3' AGCGGCTCCTCCTGCTG     48561      A       CAAAAT
                                AGCG CTCCTCCT      CTG
                                |||| ||||||||      |||
                                TCGC GAGGAGGA      GAC
                                   C       C_____
GAM1990 FLJ20511 3' CAGCAGCTTCTGGGAAAAATCT 48562       A  C  CCTC
             GC                   CAGCG CT CT    AAAATCTGC
                                |||||| || ||    |||||||||
                                GTCGT GA GA    TTTTAGACG
                                   C  A  CCCT
GAM1990 FLJ22477 5' GCGCTCCTCCTCGGGGTCTG   48563     A       AAAA
                                GCG CTCCTCCTC    TCTG
                                ||| |||||||||    ||||
                                CGC GAGGAGGAG    AGAC
                                  _       CCCC
GAM1990 FLJ23185 3' CAGCAGCTCTTCCCTCTG    48564       A   C    CAAAA
                                CAGCG CTC TCCT     TCTG
                                ||||| ||| ||||     ||||
                                GTCGT GAG AGGG     AGAC
                                   C   A   _____
GAM1990 KIAA0321  5' ACAACAGCTCCTCAAGGTCTGC 48565       TC       AA
                                GCGAC  CTCCTCAA  TCTGC
                                |||||  ||||||||  |||||
                                TGTTG  GAGGAGTT  AGACG
                                   TC       CC
GAM1990 KIAA0630  3' GATTCCTCCTCCCTCATGC   48566    C       AAAA  _
                                GA TCCTCCTC    TC TGC
                                || |||||||    || |||
                                CT AGGAGGAG    AG ACG
                                 A       GG__  T
GAM1990 PTR4     3' AGCGACATACTCGAAATCTGC  48567       TCCTC   A
                                AGCGAC     CTC AAATCTGC
                                ||||||     ||| ||||||||
                                TCGCTG     GAG TTTAGACG
                                    TAT__   C
GAM1990 RAB2     5' ACGGCTCCTCCTCCCGCTGC   48568     A       AAAAT
                                GCG CTCCTCCTC     CTGC
                                ||| |||||||||     ||||
                                TGC GAGGAGGAG     GACG
                                  C        GGC__
GAM1990 RAB40C   3' TCCAGGTCCTCAAAGTCTG   48569     ___       A
                                TCC   TCCTCAAA TCTG
                                |||   |||||||| ||||
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                                AGG   AGGAGTTT AGAC
                                  TCC       C
GAM1990  TU12B1-TY 3'  CAGCGACAAGTTAAAATCTG   48570        TCCTCCTC
                                CAGCGAC       AAAATCTG
                                |||||||       ||||||||
                                GTCGCTG       TTTTAGAC
                                    TTCAA___
GAM1990  LOC147111 3'  GCCGGCTCCTCCTCCAGACAGT 48571    _ A        AAAA___
           CTGC                   GC G CTCCTCCTC      TCTGC
                                || | |||||||||       |||||
                                CG C GAGGAGGAG      AGACG
                                 G C        GTCTGTC
GAM1990  LOC150174 3'  AGCGGCTCCTCCTGCTG     48561      A       CAAAAT
                                AGCG CTCCTCCT     CTG
                                |||| ||||||||      |||
                                TCGC GAGGAGGA     GAC
                                  C       C_____
GAM1990  LOC150213 3'  AGCGGCTCCTCCTGCTG     48561      A       CAAAAT
                                AGCG CTCCTCCT     CTG
                                |||| ||||||||      |||
                                TCGC GAGGAGGA     GAC
                                  C       C_____
GAM1990  LOC150236 5'  AGCGGCTCCTCCTGCTG     48561      A       CAAAAT
                                AGCG CTCCTCCT     CTG
                                |||| ||||||||      |||
                                TCGC GAGGAGGA     GAC
                                  C       C_____
GAM1991  BID      3'  TGTGTAGATTTACAGA      48574      C   ATA
                                TGTG AGA   TTTACAGA
                                |||| |||   ||||||||
                                ACAC TCT   AAATGTCT
                                  A  ___
GAM1991  MOCS2    5'  GTGTAGAAATCCACAGA     48575     C    T
                                GTG AGAA ATTTACAGA
                                ||| |||| |||||||||
                                CAC TCTT TAGGTGTCT
                                  A   _
GAM1991  SLC26A4  3'  TGTGCAAATATTTTCAAA    48576         A    A
                                TGTGCAGA TATTT CAGA
                                |||||||| ||||| ||||
                                ACACGTTT ATAAA GTTT
                                     _    A
GAM1991  TARDBP   3'  TGGCAGAATATTTACAG     48577     T
                                TG GCAGAATATTTACAG
                                || ||||||||||||||
                                AC CGTCTTATAAATGTC
                                 _
GAM1991  FLJ10726 3'  TGTCAGAACATACAGA      48578     G      TT
                                TGT CAGAATA  TACAGA
                                ||| |||||||  ||||||
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                                ACA GTCTTGT  ATGTCT
                                  _     __
GAM1991  KIAA1240  3'  TGTACAGAATACAAAAGA    48579          TTAC
                                TGTGCAGAATAT    AGA
                                ||||||||||||    |||
                                ACATGTCTTATG    TCT
                                       TTT_
GAM1991  OATPRP4   3'  TGTAGCAGAACTCACAG     48580    _     AT
                                TGT GCAGAAT  TTACAG
                                ||| |||||||  ||||||
                                ACA CGTCTTG  AGTGTC
                                  T      __
GAM1991  LOC118487 3'  ACTAAGTATTTACAGACG    48581    A  A
                                GC GA TATTTACAGACG
                                || || ||||||||||||
                                TG TT ATAAATGTCTGC
                                 A  C
GAM1991  LOC123745 3'  TGTATAGAATGACTGTACAGA  48582     C    _  _
                                TGTG AGAAT ATT TACAGA
                                |||| ||||| ||| ||||||
                                ACAT TCTTA TGA ATGTCT
                                   A    C  C
GAM1991  LOC149577 3'  TGTGCAAATGCCCACAG     48583        ATA
                                TGTGCAGA   TTTACAG
                                ||||||||   |||||||
                                ACACGTTT   GGGTGTC
                                     AC_
GAM1991  LOC201283 3'  GTGCAGAGTATTCACAAA    48584        A
                                GTGCAGA TATTTACAGA
                                ||||||| ||||||||||
                                CACGTCT ATAAGTGTTT
                                    C
GAM1991  LOC201626 3'  TGAGCAGAATATGAAAGTACAG 48585    T       T_____
            A                    TG GCAGAATAT     TACAGA
                                || |||||||||     ||||||
                                AC CGTCTTATA     ATGTCT
                                 T        CTTTC
GAM1991  LOC254975 5'  TGTGCAGAGCACTTAACTGGAC 48586        A     _ A_
            G                    TGTGCAGA TATTTA C  GACG
                                ||||||| |||||| |  ||||
                                ACACGTCT GTGAAT G  CTGC
                                     C     T AC
GAM1991  LOC256714 3'  TGTCTAGAATATTTTACAG   48587     GC       _
                                TGT  AGAATATTT ACAG
                                |||  ||||||||| ||||
                                ACA  TCTTATAAA TGTC
                                  GA        A
GAM1991  LOC51691  3'  TGTACAAAGATTTACAGA    48588        AT
                                TGTGCAGA  ATTTACAGA
                                ||||||||  |||||||||
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                                ACATGTTT  TAAATGTCT
                                    C_
GAM1991  LOC57826  3'  TGTGCAGAAGTCTACTAGA   48589        TA   _
                                TGTGCAGAA  TTTAC AGA
                                |||||||||  ||||| |||
                                ACACGTCTT  AGATG TCT
                                    C_    A
GAM1991  LOC92973  5'  TGTGCAGATATGACAAA    48590       A  TT
                                TGTGCAGA TAT  ACAGA
                                ||||||||  |||  |||||
                                ACACGTCT ATA  TGTTT
                                    _  C_
GAM1992  ATP10B    3'  TATGTTATAGGGGAATAGT   23802        ATTCTA
                                TATGTTGTG    GAATAGT
                                |||||||||    |||||||
                                ATACAATAT    CTTATCA
                                    CCC___
GAM1993  G1P3      5'  CCGGAGCCTGCTGATAG    48594    AGAT
                                CCG   GGGCCTGCTGATAG
                                |||   ||||||||||||||
                                GGC   CTCGGACGACTATC
                                 ____
GAM1993  G1P3      5'  CCGGAGCCTGCTGATAG    48594    AGAT
                                CCG   GGGCCTGCTGATAG
                                |||   ||||||||||||||
                                GGC   CTCGGACGACTATC
                                 ____
GAM1993  G1P3      5'  CCGGAGCCTGCTGATAG    48594    AGAT
                                CCG   GGGCCTGCTGATAG
                                |||   ||||||||||||||
                                GGC   CTCGGACGACTATC
                                 ____
GAM1993  LARGE     3'  CCTGGGCCACTGCTGATAGA  48595   GAGA   __
                                CC   TGGGCC  TGCTGATAGA
                                ||   ||||||  ||||||||||
                                GG   ACCCGG  ACGACTATCT
                                 ____    TG
GAM1993  LARGE     3'  CCTGGGCCACTGCTGATAGA  48595   GAGA   __
                                CC   TGGGCC  TGCTGATAGA
                                ||   ||||||  ||||||||||
                                GG   ACCCGG  ACGACTATCT
                                 ____    TG
GAM1993  PPT2      3'  CCTGAGATGGGCCTCATAG   48596   _      GCTG
                                CC GAGATGGGCCT   ATAG
                                || ||||||||||   ||||
                                GG CTCTACCCGGA   TATC
                                 A        G___
GAM1993  PPT2      3'  CCTGAGATGGGCCTCATAG   48596   _      GCTG
                                CC GAGATGGGCCT   ATAG
                                || ||||||||||   ||||
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                                GG CTCTACCCGGA    TATC
                                 A         G___
GAM1993  FLJ22055  3'  GAGATGGGTGGAGATGGA    48597        CC  CT   A
                                GAGATGGG  TG  GAT GA
                                ||||||||  ||  ||| ||
                                CTCTACCC  AC  CTA CT
                                     __  CT   C
GAM1993  HSPC195   3'  CGAGATGGGGCTCCCCAGA   48598         C  G  GA
                                CGAGATGGG CT CT  TAGA
                                ||||||||| || ||  ||||
                                GCTCTACCC GA GG  GTCT
                                     C  G  __
GAM1993  KIAA0354  3'  CACTGACATGGATGCCTTGATA 48599     C  G   __   GC
            GA                    CAC GA ATGG  GCCT  TGATAGA
                                ||| || ||||  ||||  |||||||
                                GTG CT TACC  CGGA  ACTATCT
                                  A  G    TA   __
GAM1993  MGC3113   3'  GAGGGGCCTGCTGCAGA     48600     AT        A
                                GAG  GGGCCTGCTG TAGA
                                |||  ||||||||||| ||||
                                CTC  CCCGGACGAC GTCT
                                  __        _
GAM1993  MGC5139   5'  CACCAGGTGGGCCTGCTA    48601      G  A
                                CACC AG TGGGCCTGCTG
                                |||| || ||||||||||
                                GTGG TC ACCCGGACGAT
                                  _  C
GAM1993  OCLM      5'  CACTGAGATGGGGCTGCTA   48602     C       C
                                CAC GAGATGGG CTGCTG
                                ||| |||||||| ||||||
                                GTG CTCTACCC GACGAT
                                  A       C
GAM1993  LOC146802 3'  CACTGATAGTCTGCTGGTAG   48603     CGA    GC     A
                                CAC   GATGG  CTGCTG TAG
                                |||   |||||  |||||| |||
                                GTG   CTATC  GACGAC ATC
                                  A__     A_     C
GAM1993  LOC199714 3'  CCTGACTGCATGTCTGCTGAT  48604    GA   GG  _____
                                CC  GAT  GC    CTGCTGAT
                                ||  |||  ||    ||||||||
                                GG  CTG  CG    GACGACTA
                                 A_   A_  TACA
GAM1993  LOC255057 3'  CACCGACGTGGGCCCTG     48605       GA     TG
                                CACCGA  TGGGCC  CTG
                                ||||||  ||||||  |||
                                GTGGCT  ACCCGG  GAC
                                   GC     __
GAM1993  LOC257397 5'  CACTGAAATGGGCTGAATAG   48606     C        C  CT
                                CAC GAGATGGGC TG  GATAG
                                ||| ||||||||| ||  |||||
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                                GTG CTTTACCCG AC  TTATC
                                  A       _ __
GAM1993  LOC91689  3'  CCGAGCCTTTCTGCTGATAG  48607      ATGGGC
                                CCGAG     CTGCTGATAG
                                |||||     ||||||||||
                                GGCTC     GACGACTATC
                                   GGAAA_
GAM1994  COL4A3    3'  ATAACACTAGTTTAATG     48610        ACTTC    A
                                ATAACACT     GGTT GATG
                                ||||||||     |||| ||||
                                TATTGTGA     TCAA TTAC
                                     _____   A
GAM1994  COL4A3    3'  ATAACACTAGTTTAATG     48610        ACTTC    A
                                ATAACACT     GGTT GATG
                                ||||||||     |||| ||||
                                TATTGTGA     TCAA TTAC
                                     _____   A
GAM1994  COL4A3    3'  ATAACACTAGTTTAATG     48610        ACTTC    A
                                ATAACACT     GGTT GATG
                                ||||||||     |||| ||||
                                TATTGTGA     TCAA TTAC
                                     _____   A
GAM1994  STAT1     3'  CATAACATTTGCTAGATG    48611        CTACTTCG
                                CATAACA       GTTAGATG
                                |||||||       ||||||||
                                GTATTGT       CGATCTAC
                                   AAA_____
GAM1994  AKAP6     3'  TGAACACTGCAACTAGATG    48612    T     ACTT GG
                                A AACACT    C  TTAGATG
                                | ||||||    |  |||||||
                                A TTGTGA    G  GATCTAC
                                 C     C___ TT
GAM1994  BM046     3'  CACTATCTTAGTTAGATGT    48613      _   C
                                CACTA CTT GGTTAGATGT
                                ||||| ||| ||||||||||
                                GTGAT GAA TCAATCTACA
                                   A  _
GAM1994  DKFZP761L0424 3'  AACACTACTTTCAAATGT     48614          CGG
                                AACACTACTT   TTAGATGT
                                ||||||||||   ||||||||
                                TTGTGATGAA   AGTTTACA
                                     ____
GAM1994  ENPP4     3'  ACAACACTATTCTTTGGATGT  48615         C   GG  A
                                ATAACACTA TTC  TT GATGT
                                ||||||||| |||  || |||||
                                TGTTGTGAT AAG  AA CTACA
                                     _  A_  C
GAM1994  ICK       3'  CACAGTGTTACTTTATTAGATG 48616      ACAC     CG
              T                  CATA    TACTT  GTTAGATGT
                                ||||    |||||  |||||||||
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                                GTGT   ATGAA  TAATCTACA
                                  CACA    A_
GAM1994  KIAA0830  3'  ACACTAAACAATTGGATGT   48617      CTT    A
                                ACACTA  CGGTT GATGT
                                ||||||  ||||| |||||
                                TGTGAT  GTTAA CTACA
                                   TT_    C
GAM1994  KIAA1040  3'  CATGACCTTACTGGTCAGATGT 48618    A  AC   TC
                                CAT AC  TACT  GGTTAGATGT
                                ||| ||  ||||  ||||||||||
                                GTA TG  ATGA  CCAGTCTACA
                                  C  GA   __
GAM1994  PRO0902   3'  CTACTATCAATTAGATGT    48619      _
                                CTACT TCGGTTAGATGT
                                ||||| ||||||||||||
                                GATGA AGTTAATCTACA
                                   T
GAM1994  LOC146050 3'  CATAACACTATACCAGGT    48620          CT  _
                                CATAACACTA  TC GGT
                                ||||||||||  || |||
                                GTATTGTGAT  GG CCA
                                      AT  T
GAM1994  LOC221929 3'  ACAATACCAGGTTAGATG    48621     C    TC
                                ACA TACT  GGTTAGATG
                                ||| ||||  |||||||||
                                TGT ATGG  CCAATCTAC
                                  T   T_
GAM1995  PPFIA3    3'  GCGAGGCGGGCGCGCGCACTCC 48624         A_      _
                                GCGAGGCG  CGCGTGT CTCC
                                ||||||||  ||||||| ||||
                                CGCTCCGC  GCGCGCG GAGG
                                     CC      T
GAM1995  TIMM44    3'  CCTGCGGGGGAGTGTCTC    48625    GC   A  C  CGC
                                CC  GCG GG GA   GTGTCTC
                                ||  ||| || ||   |||||||
                                GG  CGC CC CT   CACAGAG
                                 A_   C  _ ____
GAM1995  C12orf3   3'  ACGTGCATGTGCGTGTCTC    48626     AG   AC_
                                GCG  GCG   GCGTGTCTC
                                |||  |||   |||||||||
                                TGC  CGT   CGCACAGAG
                                  A_   ACA
GAM1995  C20orf39  5'  CCGCGCGAAGGTGGCCACCA   48627         _____   G  G
                                CCGCGCGA    GGC AC CG
                                ||||||||    ||| || ||
                                GGCGCGCT    CCG TG GT
                                     TCCA   G  _
GAM1995  C20orf4   3'  CCGTGTAGGCAGATGTCTC    48628     CGCG    ACGC
                                CCG    AGGCG    GTGTCTC
                                |||    |||||    |||||||
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                                GGC   TCCGT   TACAGAG
                                  ACA_    C___
GAM1995 LGI3    5' CCGCGCGGGCTGGCACCTC   48629       A  GACGC TG
                                CCGCGCG GGC    G  TCTC
                                ||||||| |||    |  ||||
                                GGCGCGC CCG    C  GGAG
                                   _  AC___ GT
GAM1995 MGC4415  3' CCGCGCGGGGCGGCGGC    48630       A   AC  T
                                CCGCGCG GGCG  GCG GT
                                ||||||| ||||  ||| ||
                                GGCGCGC CCGC  CGC CG
                                   C   __  _
GAM1995 MOT8    5' CCGCTCACGGTGCGTGTCTCC 48631     GCGAG  AC
                                CCGC    GCG  GCGTGTCTCC
                                ||||    |||  ||||||||||
                                GGCG    TGC  CGCACAGAGG
                                  AG___   CA
GAM1995 NET-5   3' CCGCTGGGGCGGTATCTC    48632     GCGA   ACGC
                                CCGC   GGCG   GTGTCTC
                                ||||   ||||   |||||||
                                GGCG   CCGC   CATAGAG
                                  ACC_   _____
GAM1995 PRKWNK2  5' CCGCGATGAGGCGGCGCGTCT 48633      C_    AC
                                CCGCG  GAGGCG  GCGTGTCT
                                |||||  ||||||  ||||||||
                                GGCGC  CTCCGC  CGCGCAGA
                                   TA    __
GAM1995 SEC61A1  5' CCGCGTGAGGCGACGCTGCC  48634      C       G
                                CCGCG GAGGCGACGC TGTC
                                ||||| |||||||||| ||||
                                GGCGC CTCCGCTGCG ACGG
                                   A       _
GAM1995 TNFAIP3  3' CCACGCGACTTGTGTGTCT   48635       AG  GACGC
                                CCGCGCG  GC    GTGTCT
                                |||||||  ||    ||||||
                                GGTGCGC  TG    CACAGA
                                   __  AACA_
GAM1995 LOC124930 3' CCCGCGAGGCGGTGGCTC    48636    G       ACGC   T
                                CC CGCGAGGCG    GTG CTC
                                || |||||||||    ||| |||
                                GG GCGCTCCGC    CAC GAG
                                 _       _____   C
GAM1995 LOC128823 5' GCGTGTGAGGGTCTGTGTCTCC 48637     C__    CGACGC
                                GCG   GAGG     GTGTCTCC
                                |||   ||||     ||||||||
                                CGC   CTCC     CACAGAGG
                                  ACA   CAGA__
GAM1995 LOC144165 5' GCGCGAGGCTGGCATGTTCC   28244         GAC     C
                                GCGCGAGGC   GCGTGT TCC
                                |||||||||   |||||| |||
```

```
                                CGCGCTCCG  CGTACA AGG
                                    AC_    _
GAM1995  LOC145375 5'  GCGCGAGGCGGCGCAGGGGTCT 48638        A   T__
                                GCGCGAGGCG CGCG  GTCT
                                |||||||||| ||||  ||||
                                CGCGCTCCGC GCGT  CAGA
                                     C   CCC
GAM1995  LOC221766 3'  CCCCACGGCGTGTGTCTCC   48639   G  GA   ACGC
                                CC CGC  GGCG   GTGTCTCC
                                || |||  ||||   ||||||||
                                GG GTG  CCGC   CACAGAGG
                                 G  __   A___
GAM1996  ABCC1     5'  CGGCGGCGGGCACCGGGCGGCG 48642   A  A   G  AC_
           G                     CG CG CGGG CG   GGCGGCGG
                                || || |||| ||   ||||||||
                                GC GC GCCC GT   CCGCCGCC
                                 C  C   _  GGC
GAM1996  ABCC1     5'  CGGCGGCGGGCACCGGGCGGCG 48642   A  A   G  AC_
           G                     CG CG CGGG CG   GGCGGCGG
                                || || |||| ||   ||||||||
                                GC GC GCCC GT   CCGCCGCC
                                 C  C   _  GGC
GAM1996  ABCC1     5'  CGGCGGCGGGCACCGGGCGGCG 48642   A  A   G  AC_
           G                     CG CG CGGG CG   GGCGGCGG
                                || || |||| ||   ||||||||
                                GC GC GCCC GT   CCGCCGCC
                                 C  C   _  GGC
GAM1996  ABCC1     5'  CGGTGGCGCGGGCGGCGG    48643    _   AC
                                CGG GGCG  GGCGGCGG
                                ||| ||||  ||||||||
                                GCC CCGC  CCGCCGCC
                                  A   GC
GAM1996  ABCC1     5'  CGGTGGCGCGGGCGGCGG    48643    _   AC
                                CGG GGCG  GGCGGCGG
                                ||| ||||  ||||||||
                                GCC CCGC  CCGCCGCC
                                  A   GC
GAM1996  ABCC1     5'  CGGCGGCGGGCACCGGGCGGCG 48642   A  A   G  AC_
           G                     CG CG CGGG CG   GGCGGCGG
                                || || |||| ||   ||||||||
                                GC GC GCCC GT   CCGCCGCC
                                 C  C   _  GGC
GAM1996  ABCC1     5'  CGGTGGCGCGGGCGGCGG    48643    _   AC
                                CGG GGCG  GGCGGCGG
                                ||| ||||  ||||||||
                                GCC CCGC  CCGCCGCC
                                  A   GC
GAM1996  ABCC1     5'  CGGCGGCGGGCACCGGGCGGCG 48642   A  A   G  AC_
           G                     CG CG CGGG CG   GGCGGCGG
                                || || |||| ||   ||||||||
```

```
                                GC GC GCCC GT   CCGCCGCC
                                 C  C    _ GGC
GAM1996  ABCC1    5'  CGGCGGCGGGCACCGGGCGGCG 48642    A  A    G  AC_
              G                  CG CG CGGG CG   GGCGGCGG
                                 || || |||| ||   ||||||||
                                GC GC GCCC GT   CCGCCGCC
                                 C  C    _ GGC
GAM1996  ADRA2A   5'  CGGGGACGGCGGCGGCGG    48644      _ A
                                CGGGG CG CGGCGGCGG
                                ||||| || |||||||||
                                GCCCC GC GCCGCCGCC
                                   T  C
GAM1996  ADRBK2   5'  CGAGCTTTGGCGGCGGCGGCGG 48645     CGG__    A
                                CGA    GGCG CGGCGGCGG
                                |||    |||| |||||||||
                                GCT    CCGC GCCGCCGCC
                                  CGAAA   C
GAM1996  AP1M1    5'  CGGCCGAGGGCGGTGGCGGCGG 48646    A_ _    AC
                                CG  CG GGGCG  GGCGGCGG
                                ||  || |||||  ||||||||
                                GC  GC CCCGC  CCGCCGCC
                                 CG  T    CA
GAM1996  ARIH1    5'  GACGGCTGGTGGCGGCGG    48647      __ CGAC
                                GACGG  GG   GGCGGCGG
                                |||||  ||   ||||||||
                                CTGCC  CC   CCGCCGCC
                                   GA  A___
GAM1996  AXUD1    5'  CGGCAGCGGCGGCGGCGGCGG  48648    A  _   A
                                CG CGG GGCG CGGCGGCGG
                                || ||| |||| |||||||||
                                GC GTC CCGC GCCGCCGCC
                                 C  G   C
GAM1996  BARX1    5'  CGGCGGCGGCGGCGACGG    48649    _   A
                                CGG GGCG CGGCGGCGG
                                ||| |||| |||||||||
                                GCC CCGC GCCGCTGCC
                                  G   C
GAM1996  BARX1    5'  CGGTTTGGCGGCGGCGGCGG   48650    ___   A
                                CGG   GGCG CGGCGGCGG
                                |||   |||| |||||||||
                                GCC   CCGC GCCGCCGCC
                                  AAA   C
GAM1996  BCL11A   5'  CGGGGCGGGCGGCGGCGG    48651       A_
                                CGGGGCG  CGGCGGCGG
                                |||||||  |||||||||
                                GCCCCGC  GCCGCCGCC
                                    CC
GAM1996  BCL11A   5'  CGGGGCGGGCGGCGGCGG    48651       A_
                                CGGGGCG  CGGCGGCGG
                                |||||||  |||||||||
```

```
                                GCCCCGC  GCCGCCGCC
                                    CC
GAM1996 BCL11A   5' CGGGGCGGGCGGCGGCGG    48651       A_
                                CGGGGCG  CGGCGGCGG
                                |||||||  |||||||||
                                GCCCCGC  GCCGCCGCC
                                    CC
GAM1996 BMP8     5' TCGGCGGGCGGCGGGCGGCGG 48652     A  AC  _   AC
                                TCG CG  GG GGCG  GGCGGCGG
                                |||  ||  ||  ||||  ||||||||
                                AGC GC  CC CCGC  CCGCCGCC
                                  C  __  G   __
GAM1996 BTG1     5' TCGGCGGCGCGGCCCCGACGGC 48653     A  A  G   GA
             GG                   TCG CG CG GGC  CGGCGGCGG
                                |||  ||  ||  |||  |||||||||
                                AGC GC GC CCG  GCTGCCGCC
                                  C  C  G   GG
GAM1996 CALCA    5' CGGTGGCAGCGGCGGCGG    48654     _    A
                                CGG GGCG CGGCGGCGG
                                |||  ||||  |||||||||
                                GCC CCGT GCCGCCGCC
                                  A   C
GAM1996 CDK2AP1  5' CGCGAGGGCGGCGGCGGCGG   48655    A  _    A
                                CG CG GGGCG CGGCGGCGG
                                ||  ||  |||||  |||||||||
                                GC GC CCCGC GCCGCCGCC
                                  _  T    C
GAM1996 CDK5R2   3' CGGCGGTAACAGCGGCGG    48656     _  CG
                                CGG GG  ACGGCGGCGG
                                |||  ||  ||||||||||
                                GCC CC  TGTCGCCGCC
                                  G  AT
GAM1996 CLTCL1   5' CGGCGGCGGCGGCGGCAGCGG  48657    A  _   A
                                CG CGG GGCG CGGCGGCGG
                                ||  |||  ||||  |||||||||
                                GC GCC CCGC GCCGTCGCC
                                  C   G   C
GAM1996 COL6A2   3' TCGACTGCGGGGCCCGGGCGGC 48658       GA     GAC
             GG                   TCGAC  CGGGGC   GGCGGCGG
                                |||||  ||||||   ||||||||
                                AGCTG  GCCCCG   CCGCCGCC
                                    AC     GGC
GAM1996 CPT1A    5' CGGCAGCGGCGGCGGCGGCGG  48648    A  _   A
                                CG CGG GGCG CGGCGGCGG
                                ||  |||  ||||  |||||||||
                                GC GTC CCGC GCCGCCGCC
                                  C   G   C
GAM1996 CRKL     5' TCTGCGGCGGTAGGGGCGGCGG 48659    GA  A   GGCGAC
                                TC  CG CGG     GGCGGCGG
                                ||  ||  |||     ||||||||
```

```
                                AG  GC GCC     CCGCCGCC
                                 AC  C   ATCC__
GAM1996 CSDA     5'  CGCGGCGCAGGCGGCGGCGG   48660    A   G   A_
                                CG CGG GCG  CGGCGGCGG
                                || ||| |||  |||||||||
                                GC GCC CGT  GCCGCCGCC
                                 _   G   CC
GAM1996 CSNK2A2  5'  CGCAGAGGGTGGCGGCGGCGG  48661    AC  C   GCGA
                                CG  GA GGG    CGGCGGCGG
                                ||  || |||    |||||||||
                                GC  CT CCC    GCCGCCGCC
                                 GT  _   ACC_
GAM1996 CUL3     5'  CGGCGGCGGGGGCGGCGGCGGC 48662    A  A     _  A
              GG                    CG CG CGGGG CG CGGCGGCGG
                                || || ||||| || |||||||||
                                GC GC GCCCC GC GCCGCCGCC
                                 C  C    C  C
GAM1996 CUL3     5'  CGCGATGGCGGCGGCGGCGG   48663    A   _    A
                                CG CGG GGCG CGGCGGCGG
                                || ||| |||| |||||||||
                                GC GCT CCGC GCCGCCGCC
                                 _   A    C
GAM1996 E2F1     5'  GACAGGCGGCGGCGGCG     48664       G  A
                                GACGGG CG CGGCGGCG
                                |||||| || ||||||||
                                CTGTCC GC GCCGCCGC
                                    _  C
GAM1996 ETF1     5'  CGGCGGCGGCTCGCGGCGGCGG 48665    A   _   GA_
                                CG CGG GGC   CGGCGGCGG
                                || ||| |||   |||||||||
                                GC GCC CCG   GCCGCCGCC
                                 C   G   AGC
GAM1996 EXT1     5'  CGGCTGGAGGCGGCGGCGGCGG 48667    AC__     A
                                CG    GGGGCG CGGCGGCGG
                                ||    |||||| |||||||||
                                GC    CTCCGC GCCGCCGCC
                                 CGAC     C
GAM1996 EXT1     5'  CGGCGGCGGCGCTGGGTGGCGG 48666    A   _   AC____
              CGG                   CG CGG GGCG     GGCGGCGG
                                || ||| ||||     ||||||||
                                GC GCC CCGC     CCGCCGCC
                                 C   G    GACCCA
GAM1996 FBXO7    5'  CGGCGACGGGGACGGCGGCGG  48668    A       CG
                                CG CGACGGGG  ACGGCGGCGG
                                || ||||||||  ||||||||||
                                GC GCTGCCCC  TGCCGCCGCC
                                 C       __
GAM1996 FHL1     5'  CGGCGGTGGCGGCGGCG     48669    A   _   GAC
                                CG CGG GGC   GGCGGCG
                                || ||| |||   |||||||
```

```
                                GC GCC CCG   CCGCCGC
                                 C  A  ___
GAM1996  FMNL     5'  CGGGAGGCGGCGGCGGCGG   48670    AC     A
                                CG  GGGGCG CGGCGGCGG
                                ||  |||||| |||||||||
                                GC  CTCCGC GCCGCCGCC
                                 C_     C
GAM1996  FMR2     5'  CGGCGGCGGCAGCGGCGGCGG  48671    A  _   A
                                CG CGG GGCG CGGCGGCGG
                                || ||| |||| |||||||||
                                GC GCC CCGT GCCGCCGCC
                                 C  G   C
GAM1996  FMR2     5'  CGGCAGCGGCGGCGGCGGCGG  48648    A  _   A
                                CG CGG GGCG CGGCGGCGG
                                || ||| |||| |||||||||
                                GC GTC CCGC GCCGCCGCC
                                 C  G   C
GAM1996  FMR2     5'  CGGCCAGGCGGCGGCGGCGG   48672     ___   A
                                CGG   GGCG CGGCGGCGG
                                |||   |||| |||||||||
                                GCC   CCGC GCCGCCGCC
                                  GGT   C
GAM1996  FOXE1    5'  CGAGGCGGGCAGCGGCGG    48673       A_
                                CGGGGCG  CGGCGGCGG
                                |||||||  |||||||||
                                GCTCCGC  GTCGCCGCC
                                    CC
GAM1996  FOXG1B   5'  CGGGGGGAAACGGCGGCGG   48674    AC   C
                                CG  GGGG GACGGCGGCGG
                                ||  |||| ||||||||||
                                GC  CCCC TTGCCGCCGCC
                                 C_   T
GAM1996  GCLM     5'  ACGGCGGCTGGGCGGCGGCGG  48675     _  GA__
                                ACGG GGC   CGGCGGCGG
                                |||| |||   |||||||||
                                TGCC CCG   GCCGCCGCC
                                  G  ACCC
GAM1996  GMDS     5'  TCGGCGGCAGGGCGGAGCGCGG 48676     A  A     AC   G
                                TCG CG CGGGGCG  GGCG CGG
                                ||| || |||||||  |||| |||
                                AGC GC GTCCCGC  TCGC GCC
                                  C  C      C_   _
GAM1996  GNB2     5'  CCGCGGCGGAGGCGGCGGCGGC 48677     A  A  _   A
            GG                    TCG CG CGG GGCG CGGCGGCGG
                                ||| || ||| |||| |||||||||
                                GGC GC GCC CCGC GCCGCCGCC
                                  _  C   T   C
GAM1996  GPC1     5'  TCGCGGTCCAGAGGCGGCGGCG 48678     A  A__    CGA
            G                     TCG CG   CGGGG   CGGCGGCGG
                                ||| ||   |||||   |||||||||
```

```
                                AGC GC   GTCTC   GCCGCCGCC
                                  _ CAG    C__
GAM1996 GSPT1    5' CGACGACAGAGGCGGCGGCGG 48679         CGA
                                CGACGACGGGG   CGGCGGCGG
                                ||||||||||   |||||||||
                                GCTGCTGTCTC   GCCGCCGCC
                                      C__
GAM1996 GTF2E2   5' TCACCACTGGCGGTGGCGGCGG 48680    G  G  GG   AC
                                TC AC AC  GGCG  GGCGGCGG
                                || || ||  ||||  ||||||||
                                AG TG TG  CCGC  CCGCCGCC
                                 _ G  A_   CA
GAM1996 GUCY1A2  5' CGGCGGCGGAGGCGGCGGTGGC 48681    A  A  _   A  C
            GG                    CG CG CGG GGCG CGG GGCGG
                                || || ||| |||| ||| |||||
                                GC GC GCC CCGC GCC CCGCC
                                 C  C   T   C  A
GAM1996 HDAC5    5' CGGCGGCGGCAGCAGCGGCGGC 48682    A  A  _   A
            GG                    CG CG CGG GGCG CGGCGGCGG
                                || || ||| |||| |||||||||
                                GC GC GCC TCGT GCCGCCGCC
                                 C  C   G   C
GAM1996 HDAC5    5' CGGCGGCGGCAGCAGCGGCGGC 48682    A  A  _   A
            GG                    CG CG CGG GGCG CGGCGGCGG
                                || || ||| |||| |||||||||
                                GC GC GCC TCGT GCCGCCGCC
                                 C  C   G   C
GAM1996 HHIP     5' CGGCGGCGGGGCAGGCGG    48683    A  A     AC
                                CG CG CGGGGCG  GGCGG
                                || || |||||||  |||||
                                GC GC GCCCCGT  CCGCC
                                 C  C     __
GAM1996 HIVEP1   5' TCGCGACCCCCGCGGCGGCGGC 48684     A   GGG_  A
            GG                    TCG CGAC   GCG CGGCGGCGG
                                ||| ||||   ||| |||||||||
                                AGC GCTG   CGC GCCGCCGCC
                                  _   GGGG  C
GAM1996 JAG2     5' CGGCAGAGGCGGCGGCGGCGG  48685    A  _   A
                                CG CGG GGCG CGGCGGCGG
                                || ||| |||| |||||||||
                                GC GTC CCGC GCCGCCGCC
                                 C  T   C
GAM1996 KCNMB4   5' CGACGCCCCCGGCGGCGGCGG  48686      GGG_ A
                                CGACG   CG CGGCGGCGG
                                |||||   || |||||||||
                                GCTGC   GC GCCGCCGCC
                                   GGGG  C
GAM1996 KCNQ3    5' AACGAGGCGGCGGCGGCGG   48687         A
                                GACGGGGCG CGGCGGCGG
                                ||||||||| |||||||||
```

```
                                TTGCTCCGC GCCGCCGCC
                                     C
GAM1996  KIF3B    5'  CGAAAGCGGGCGGCGGCGGCGG 48688     CG__     A
                                CGA    GGGCG CGGCGGCGG
                                |||    ||||| |||||||||
                                GCT    CCCGC GCCGCCGCC
                                  TTCG     C
GAM1996  KIF5B    5'  CGGCGGCAGCGGCGGCGG    48689     _    A
                                CGG GGCG CGGCGGCGG
                                ||| |||| |||||||||
                                GCC CCGT GCCGCCGCC
                                  G    C
GAM1996  KPNA3    5'  CGGCTGCGGCGGCGGCGGCGG  48690     ____     A
                                CGG    GGCG CGGCGGCGG
                                |||    |||| |||||||||
                                GCC    CCGC GCCGCCGCC
                                  GACG    C
GAM1996  LAMC1    5'  CGGCGCGGGCGGTGGCGGCGG  48691    A  _    AC
                                CG CG GGGCG  GGCGGCGG
                                || || |||||  ||||||||
                                GC GC CCCGC  CCGCCGCC
                                 C  G    CA
GAM1996  LAMP2    5'  CGGCGACGGCGGCGACGGCGGC 48692    A     _
              GG                  CG CGACGG GGCGACGGCGGCGG
                                  || |||||| ||||||||||||||
                                  GC GCTGCC CCGCTGCCGCCGCC
                                   C     G
GAM1996  LAMP2    5'  CGGCGACGGCGGCGACGGCGGC 48692    A     _
              GG                  CG CGACGG GGCGACGGCGGCGG
                                  || |||||| ||||||||||||||
                                  GC GCTGCC CCGCTGCCGCCGCC
                                   C     G
GAM1996  LIMK1    5'  TCGACGGGGGGCGGGGCCCGGC 48693       AC     AC  __
              GG                  TCGACG  GGGGCG  GGC  GGCGG
                                  ||||||  ||||||  |||  |||||
                                  AGCTGC  CCCCGC  CCG  CCGCC
                                     C_     C_   GG
GAM1996  LIMK1    5'  TCGACGGGGGGCGGGGCCCGGC 48693       AC     AC  __
              GG                  TCGACG  GGGGCG  GGC  GGCGG
                                  ||||||  ||||||  |||  |||||
                                  AGCTGC  CCCCGC  CCG  CCGCC
                                     C_     C_   GG
GAM1996  LMO4     5'  CGGAGGCGGCGGCGGCGG    48694     _    A
                                CGG GGCG CGGCGGCGG
                                ||| |||| |||||||||
                                GCC CCGC GCCGCCGCC
                                  T    C
GAM1996  LMO4     5'  CGAGAGGCGGCGGCG       48695     C     GAC
                                CGA GGGGC   GGCGGCG
                                ||| |||||   |||||||
```

```
                                GCT CTCCG   CCGCCGC
                                  _   ____
GAM1996 LRP8    5' TCGGCGGCGGGGCGGGCTCAG 48697    A A     AC  GG
                                TCG CG CGGGGCG  GGC  CGG
                                ||| || |||||||  |||  |||
                                AGC GC GCCCCGC  CCG  GTC
                                  C C      __   A_
GAM1996 LRP8    5' CGGTGACGCTCGGCGGCGG   48696    _   A_
                                CGG GGCG  CGGCGGCGG
                                ||| ||||  |||||||||
                                GCC CTGC  GCCGCCGCC
                                  A   GA
GAM1996 LRP8    5' TCGGCGGCGGGGCGGGCTCAG 48697    A A     AC  GG
                                TCG CG CGGGGCG  GGC  CGG
                                ||| || |||||||  |||  |||
                                AGC GC GCCCCGC  CCG  GTC
                                  C C      __   A_
GAM1996 LRP8    5' CGGTGACGCTCGGCGGCGG   48696    _   A_
                                CGG GGCG  CGGCGGCGG
                                ||| ||||  |||||||||
                                GCC CTGC  GCCGCCGCC
                                  A   GA
GAM1996 LRP8    5' TCGGCGGCGGGGCGGGCTCAG 48697    A A     AC  GG
                                TCG CG CGGGGCG  GGC  CGG
                                ||| || |||||||  |||  |||
                                AGC GC GCCCCGC  CCG  GTC
                                  C C      __   A_
GAM1996 LRP8    5' CGGTGACGCTCGGCGGCGG   48696    _   A_
                                CGG GGCG  CGGCGGCGG
                                ||| ||||  |||||||||
                                GCC CTGC  GCCGCCGCC
                                  A   GA
GAM1996 MAF     5' CGAGCTGCGGTGGCGGCGG   48699     __  AC
                                CGGG  GCG  GGCGGCGG
                                ||||  |||  ||||||||
                                GCTC  CGC  CCGCCGCC
                                  GA   CA
GAM1996 MAF     5' CGCGAGCTGCGGTGGCGGCGG 48698    A   __  AC
                                CG CGGG  GCG  GGCGGCGG
                                || ||||  |||  ||||||||
                                GC GCTC  CGC  CCGCCGCC
                                  _   GA   CA
GAM1996 MAP2K2  5' CGCGGGCCGGCGGCGGCGG   48700    A   G  A
                                CG CGGG CG CGGCGGCGG
                                || |||| || |||||||||
                                GC GCCC GC GCCGCCGCC
                                  _   G  C
GAM1996 ME1     5' TCGGCGGCGGGGTCAGGCCGGG 48701     A  A    _ GA__   C
            GCGG                    TCG CG CGGGG C    CGG GGCGG
                                ||| || ||||| |    ||| |||||
```

```
                                AGC GC GCCCC G    GCC CCGCC
                                  C  C     A TCCG  _
GAM1996  MECP2    5'  CGGCGCGGCGGCGGCGGCGG   48702    A  G    A
                                CG CG GGCG CGGCGGCGG
                                || || |||| |||||||||
                                GC GC CCGC GCCGCCGCC
                                 C  G    C
GAM1996  MGAT3    5'  ACGGCGGCAGCAGCGGCGGCGG 48703     A  _    A
                                ACG CGG GGCG CGGCGGCGG
                                ||| ||| |||| |||||||||
                                TGC GCC TCGT GCCGCCGCC
                                  C   G    C
GAM1996  NDUFS7   3'  CGGCGACAGGCTCCGGCGGCGG 48704    A      G GA
                                CG CGACGGG C  CGGCGGCGG
                                || ||||||| |  |||||||||
                                GC GCTGTCC G  GCCGCCGCC
                                 C      _ AG
GAM1996  NR2F2    5'  CGGCGGCGGGGCGGCGGCGG   48705    A  A     GAC
                                CG CG CGGGGC   GGCGGCGG
                                || || ||||||   ||||||||
                                GC GC GCCCCG   CCGCCGCC
                                 C  C     ____
GAM1996  NRG1     5'  CGGCGGTGGCGGCGGCG     48669    A  _   GAC
                                CG CGG GGC   GGCGGCG
                                || ||| |||   |||||||
                                GC GCC CCG   CCGCCGC
                                 C   A   ____
GAM1996  PDAP1    5'  CGGCGGCTGCGGCGGCGG    48706     _   GA
                                CGG GGC  CGGCGGCGG
                                ||| |||  |||||||||
                                GCC CCG  GCCGCCGCC
                                  G   AC
GAM1996  POU4F1   5'  CGCGGCGGCTGGCGGCG     48707    A  _   GAC
                                CG CGG GGC   GGCGGCG
                                || ||| |||   |||||||
                                GC GCC CCG   CCGCCGC
                                 _   G   A__
GAM1996  PPP2R5E  5'  TCAGCGTTCCGGTGGCGGCGGC 48708     A  A__   _   GAC
            GG                    TCG CG   CGG GGC   GGCGGCGG
                                ||| ||   ||| |||   ||||||||
                                AGT GC   GCC CCG   CCGCCGCC
                                  C  AAG   A   ____
GAM1996  PPP6C    5'  CGGCAACAGCGGCGGCGGCGG  48709    A   GG   A
                                CG CGAC  GGCG CGGCGGCGG
                                || ||||  |||| |||||||||
                                GC GTTG  TCGC GCCGCCGCC
                                 C    __    C
GAM1996  PRSS11   5'  CGACTCTGGCGGCGGCGGCGG  48710      GG_   A
                                CGAC   GGCG CGGCGGCGG
                                ||||   |||| |||||||||
```

```
                                GCTG   CCGC GCCGCCGCC
                                  AGA    C
GAM1996  PTP4A2   5'  CGGCGGCGGTAGCGGTGGCGGC 48714    A  A  _   AC
                GG                  CG CG CGG GGCG  GGCGGCGG
                                    || || ||| ||||  ||||||||
                                    GC GC GCC TCGC  CCGCCGCC
                                     C  C   A    CA
GAM1996  PTP4A2   5'  CGGCCCGGCGGCGGCGGCGG  48713    ___   A
                                    CGG   GGCG CGGCGGCGG
                                    |||   |||| |||||||||
                                    GCC   CCGC GCCGCCGCC
                                      GGG    C
GAM1996  PTP4A2   5'  CGGCCCGGCGGCGGCGGCGG  48713    ___   A
                                    CGG   GGCG CGGCGGCGG
                                    |||   |||| |||||||||
                                    GCC   CCGC GCCGCCGCC
                                      GGG    C
GAM1996  PTP4A2   5'  CGGCGGCGGCGGCGGCGGCGG 48711    A  _   A
                                    CG CGG GGCG CGGCGGCGG
                                    || ||| |||| |||||||||
                                    GC GCC CCGC GCCGCCGCC
                                     C   G    C
GAM1996  PTP4A2   5'  CGGTAGCGGTGGCGGCGG    48712    _   AC
                                    CGG GGCG  GGCGGCGG
                                    ||| ||||  ||||||||
                                    GCC TCGC  CCGCCGCC
                                      A    CA
GAM1996  PTP4A2   5'  CGGCGGCGGCGGCGGCGGCGG 48711    A  _   A
                                    CG CGG GGCG CGGCGGCGG
                                    || ||| |||| |||||||||
                                    GC GCC CCGC GCCGCCGCC
                                     C   G    C
GAM1996  PTP4A2   5'  CGGCGGCGGTAGCGGTGGCGGC 48714    A  A  _   AC
                GG                  CG CG CGG GGCG  GGCGGCGG
                                    || || ||| ||||  ||||||||
                                    GC GC GCC TCGC  CCGCCGCC
                                     C  C   A    CA
GAM1996  PTP4A2   5'  CGGTAGCGGTGGCGGCGG    48712    _   AC
                                    CGG GGCG  GGCGGCGG
                                    ||| ||||  ||||||||
                                    GCC TCGC  CCGCCGCC
                                      A    CA
GAM1996  RFX2     5'  CGGCGGTGGCGGCGGCG     48669    A  _  GAC
                                    CG CGG GGC   GGCGGCG
                                    || ||| |||   |||||||
                                    GC GCC CCG   CCGCCGC
                                     C  A  ___
GAM1996  RNTRE    5'  CGGCGCGGCGGCGGCGGCGG  48702    A  G   A
                                    CG CG GGCG CGGCGGCGG
                                    || || |||| |||||||||
```

```
                                GC GC CCGC GCCGCCGCC
                                 C G   C
GAM1996 RNTRE   5' CGGCGCGGCGCGGCGGCGGCGG 48715   A A  G  A
                                CG CG CGG GCG CGGCGGCGG
                                || || ||| ||| |||||||||
                                GC GC GCC CGC GCCGCCGCC
                                 C _  G  C
GAM1996 ROR1    5' CGCTGAGGCGGCGGCGGCGG  48716   AC    A
                                CG  GGGGCG CGGCGGCGG
                                ||  |||||| |||||||||
                                GC  CTCCGC GCCGCCGCC
                                 GA    C
GAM1996 RREB1   5' CGGCCGGCGGCGGCGGCG   48717    __   A
                                CGG  GGCG CGGCGGCG
                                |||  |||| ||||||||
                                GCC  CCGC GCCGCCGC
                                  GG   C
GAM1996 SCNN1B  5' CGGCGGTGGCGGAGGCGGCGG 48718   A  _   AC
                                CG CGG GGCG  GGCGGCGG
                                || ||| ||||  ||||||||
                                GC GCC CCGC  CCGCCGCC
                                 C  A   CT
GAM1996 SH3BP4  5' CGCGGGACTCACGGCGGCGG  48719   A    G_
                                CG CGGGGC  ACGGCGGCGG
                                || ||||||  ||||||||||
                                GC GCCCTG  TGCCGCCGCC
                                 _    AG
GAM1996 SH3BP4  5' ACGGCGGCGGCGGCGGCG   48720    _   A
                                ACGG GGCG CGGCGGCG
                                |||| |||| ||||||||
                                TGCC CCGC GCCGCCGC
                                  G   C
GAM1996 SLC25A1 5' TCGGTCCGCGGTGGCGGCGGCG 48721    A__  A  _  GAC
           G                     TCG   CG CGG GGC   GGCGGCGG
                                |||   || ||| |||   ||||||||
                                AGC   GC GCC CCG   CCGCCGCC
                                  CAG  _  A  ___
GAM1996 SLC6A8  5' CGGCGGTGGCGGCGGCG    48669   A  _  GAC
                                CG CGG GGC   GGCGGCG
                                || ||| |||   |||||||
                                GC GCC CCG   CCGCCGC
                                 C  A  ___
GAM1996 SLIT3   5' CGCTCCGGGCGGCGGCGGCGG 48722   ACG_   A
                                CG   GGGCG CGGCGGCGG
                                ||   ||||| |||||||||
                                GC   CCCGC GCCGCCGCC
                                 GAGG   C
GAM1996 SOX18   5' CGGTGGGGACGGCGGTGG   48723    _ C      C
                                CGG GG GACGGCGG GG
                                ||| || |||||||| ||
```

```
                                GCC CC CTGCCGCC CC
                                  A C       A
GAM1996 TBL1X    5' CGGGCGCGGCGGCGGCGG    48724      _  A
                                CGGG GCG CGGCGGCGG
                                |||| ||| |||||||||
                                GCCC CGC GCCGCCGCC
                                  G  C
GAM1996 TM4SF2   5' CGGCGGCGGCAGGCGGCG    48725     _   A _
                                CGG GGCG C GGCGGCG
                                ||| |||| | |||||||
                                GCC CCGC G CCGCCGC
                                  G   C T
GAM1996 TMEFF2   5' ACGGCGGCAGCAGAGGCGGCGG 48726     A  _  _ __
             CGG                  ACG CGG GGC GA  CGGCGGCGG
                                ||| ||| ||| ||  |||||||||
                                TGC GCC TCG CT  GCCGCCGCC
                                  C  G  T  CC
GAM1996 TRC8     5' TCGAGGTGGAGCAGGCGGCGG  48727     CGAC     AC
                                TCGA   GGGGCG  GGCGGCGG
                                ||||   ||||||  |||||||||
                                AGCT   CCTCGT  CCGCCGCC
                                  CCA_     __
GAM1996 USP7     5' CCGCGGCGGGCGGCGGCGGCGG 48728     A  A    G  A
                                TCG CG CGGG CG CGGCGGCGG
                                ||| || |||| || |||||||||
                                GGC GC GCCC GC GCCGCCGCC
                                  _ C   _ C
GAM1996 USP7     5' CGGCGAGCCGGGGCGGCGGCGG 48729   A  __      A       III
             CGGC                   CGA  CGGGGCG CGGCGGCGG   C
                                 |||  ||||||| |||||||||   |
                                 GCT  GCCCCGC GCCGCCGCC   G
                                C   CG      C        III
GAM1996 YWHAB    5' CGGAATCGGCGGCGGCGG    48730      _ A
                                CGGGG CG CGGCGGCGG
                                ||||| || |||||||||
                                GCCTT GC GCCGCCGCC
                                   A  C
GAM1996 YWHAB    5' CGGAATCGGCGGCGGCGG    48730      _ A
                                CGGGG CG CGGCGGCGG
                                ||||| || |||||||||
                                GCCTT GC GCCGCCGCC
                                   A  C
GAM1996 ZNF219   5' CGGCGGCGGCGGGCGGCG    48732    A  _   AC
                                CG CGG GGCG  GGCGGCG
                                || ||| ||||  |||||||
                                GC GCC CCGC  CCGCCGC
                                 C  G   __
GAM1996 ZNF219   5' CGGCGGCGGAGCGGGCGGCGGC 48731    A  A      A_
             GG                   CG CG CGGGGCG  CGGCGGCGG
                                || || |||||||  |||||||||
```

```
                                GC GC GCCTCGC  GCCGCCGCC
                                 C  C      CC
GAM1996  ZNF278   5'  CGAAGGCGGCGGCGGCG     48733     CG    A
                                CGA  GGGCG CGGCGGCG
                                |||  ||||| ||||||||
                                GCT  TCCGC GCCGCCGC
                                  __     C
GAM1996  ZNF278   5'  CGAAGGCGGCGGCGGCG     48733     CG    A
                                CGA  GGGCG CGGCGGCG
                                |||  ||||| ||||||||
                                GCT  TCCGC GCCGCCGC
                                  __     C
GAM1996  ZNF278   5'  CGAAGGCGGCGGCGGCG     48733     CG    A
                                CGA  GGGCG CGGCGGCG
                                |||  ||||| ||||||||
                                GCT  TCCGC GCCGCCGC
                                  __     C
GAM1996  ZNF278   5'  CGAAGGCGGCGGCGGCG     48733     CG    A
                                CGA  GGGCG CGGCGGCG
                                |||  ||||| ||||||||
                                GCT  TCCGC GCCGCCGC
                                  __     C
GAM1996  ADNP     5'  CGGGGGCCGGACAGCGGCGG   48734     AC    __
                                CG  GGGGC  GACGGCGGCGG
                                ||  |||||  ||||||||||
                                GC  CCCCG  CTGTCGCCGCC
                                  __     GC
GAM1996  ADNP     5'  CGGCGGCACGGCGGTGGCGG   48736     A  G  A  C
                                CG CGG GCG CGG GGCGG
                                || ||| ||| ||| |||||
                                GC GCC TGC GCC CCGCC
                                 C  G  C  A
GAM1996  ADNP     5'  CGGCGGCGGCGGGCGGATGGCG 48735     A  A  __   AC_
            GCGG                    CG CG CGG  GGCG   GGCGGCGG
                                || || |||  ||||   ||||||||
                                GC GC GCC  CCGC   CCGCCGCC
                                 C  C   GC    CTA
GAM1996  AP1S2    5'  GGCCGGCGGCGGCGGCGG     48737     __    A
                                GG  GGCG CGGCGGCGG
                                ||  |||| |||||||||
                                CC  CCGC GCCGCCGCC
                                 GG    C
GAM1996  ARHGEF3  5'  TCCACGATGCCGGGCGGCGGCG 48738     G     ___    GCGA
            G                    TC ACGA   CGGG    CGGCGGCGG
                                || ||||   ||||   |||||||||
                                AG TGCT   GCCC    GCCGCCGCC
                                 G   ACG   ____
GAM1996  BART1    3'  AACAGAGGGTGGTGGCGGCGG  48739      AC   GCGAC
                                GACG  GGG    GGCGGCGG
                                ||||  |||    ||||||||
```

```
                                TTGT  CCC    CCGCCGCC
                                  CT   ACCA_
GAM1996  C14orf4   5'  TCCACCGCAGCGGCGGCGGCGG 48740    G  GA  G    A
                                TC AC  CG GGCG CGGCGGCGG
                                || ||  || |||| |||||||||
                                AG TG  GC TCGC GCCGCCGCC
                                 G __  G   C
GAM1996  C20orf81  5'  GATGGCCGCGGCGGCGG     48741    CG  G  A
                                GA  GG CG CGGCGGCGG
                                ||  || || |||||||||
                                CT  CC GC GCCGCCGCC
                                 A_  G  _
GAM1996  C22orf20  5'  CGGCGGCGGGGCGGGGGCGCGG 48742    A  A      AC    G
                                CG CG CGGGGCG  GGCG CGG
                                || || |||||||  |||| |||
                                GC GC GCCCCGC  CCGC GCC
                                 C  C      CC   _
GAM1996  CACNA1H   5'  CGGCGGAGGCGACGGCGGCGG  48743    A  _
                                CG CGG GGCGACGGCGGCGG
                                || ||| ||||||||||||||
                                GC GCC CCGCTGCCGCCGCC
                                 C   T
GAM1996  CHSY1     5'  ACGACGGCGACGACGGCGGCGG 48744         _
                                ACGACGG GGCGACGGCGGCGG
                                ||||||| ||||||||||||||
                                TGCTGCC CTGCTGCCGCCGCC
                                    G
GAM1996  CNOT7     5'  TCGGCGGCGGTGGCGGTGGCGG 48745     A  A  _   AC
                                TCG CG CGG GGCG  GGCGG
                                ||| || ||| ||||  |||||
                                AGC GC GCC CCGC  CCGCC
                                  C  C   A   CA
GAM1996  CNOT7     5'  CGGTGGCGGTAGCGGCGGCGG  48746     _   A___
                                CGG GGCG   CGGCGGCGG
                                ||| ||||   |||||||||
                                GCC CCGC   GCCGCCGCC
                                  A   CATC
GAM1996  CNOT7     5'  CGGTGGCGGTAGCGGCGGCGG  48746     _   A___
                                CGG GGCG   CGGCGGCGG
                                ||| ||||   |||||||||
                                GCC CCGC   GCCGCCGCC
                                  A   CATC
GAM1996  CNOT7     5'  TCGGCGGCGGTGGCGGTGGCGG 48745     A  A  _   AC
                                TCG CG CGG GGCG  GGCGG
                                ||| || ||| ||||  |||||
                                AGC GC GCC CCGC  CCGCC
                                  C  C   A   CA
GAM1996  CUL2      5'  CGGAGGCGGCGGCGGCGG    48694     _   A
                                CGG GGCG CGGCGGCGG
                                ||| |||| |||||||||
```

```
                                GCC CCGC GCCGCCGCC
                                  T   C
GAM1996 DDX17    5' GACGACCGATGGCGGCGG    48747      GGGG  C
                                GACGAC   CGA GGCGGCGG
                                ||||||   ||| ||||||||
                                CTGCTG   GCT CCGCCGCC
                                   ____  A
GAM1996 DGKD     3' TCGACGGCGGGGGCGCTGCGG 48748      A   _ ACG
                                TCGACG CGGGG CG  GCGG
                                |||||| ||||| ||  ||||
                                AGCTGC GCCCC GC  CGCC
                                   C    C  GA_
GAM1996 DKFZP434D1335 5' CGGCGCGGCGGCGGCGGCGG  48702   A G   A
                                CG CG GGCG CGGCGGCGG
                                || || |||| |||||||||
                                GC GC CCGC GCCGCCGCC
                                 C  G   C
GAM1996 DKFZp761A052 5'  TCGGCGGCGGAGGCGGCGGCGG 48749    A A  _   A
            CGG                   TCG CG CGG GGCG CGGCGGCGG
                                ||| || ||| |||| |||||||||
                                AGC GC GCC CCGC GCCGCCGCC
                                  C  C   T   C
GAM1996 DXS9928E  5' CGGCGGCGGCGGCGGGCGGCGG 48750    A  A  _   A_
            CGG                   CG CG CGG GGCG  CGGCGGCGG
                                || || ||| ||||  |||||||||
                                GC GC GCC CCGC  GCCGCCGCC
                                 C  C   G   CC
GAM1996 DZIP1    5' TCGCTTCCGCGGCGGCGGCGG  48751    ACGA  G   GAC
                                TCG   CG GGC   GGCGGCGG
                                |||   || |||   ||||||||
                                AGC   GC CCG   CCGCCGCC
                                  GAAG  G  ___
GAM1996 FLJ13187  5' CCGACGGCCGCGGGCGGCGGCG 48752       A_ _   A
            GCGG                   TCGACG  CG GGGCG CGGCGGCGG
                                ||||||  || ||||| |||||||||
                                GGCTGC  GC CCCGC GCCGCCGCC
                                   CG  G   C
GAM1996 FLJ13262  3' CGCGCGGCAGCGGCGGCG   48753   A  G   A
                                CG CG GGCG CGGCGGCG
                                || || |||| ||||||||
                                GC GC CCGT GCCGCCGC
                                 _  G   C
GAM1996 FLJ14466  5' GACGGCGGACGGCGGCGG   48754     GGC
                                GACGG   GACGGCGGCGG
                                |||||   ||||||||||
                                CTGCC   CTGCCGCCGCC
                                  GC_
GAM1996 FLJ14466  5' GACGGCGGACGGCGGCGG   48754     GGC
                                GACGG   GACGGCGGCGG
                                |||||   ||||||||||
```

```
                                CTGCC  CTGCCGCCGCC
                                  GC_
GAM1996 FLJ20506 5' GAGGGGGCGGCGGCGGCGG  48755   C    A
                                GA GGGGCG CGGCGGCGG
                                || |||||| |||||||||
                                CT CCCCGC GCCGCCGCC
                                 C    C
GAM1996 FLJ32356 5' CGGTGGCGGCGACGGCGGCGG 48756   AC _
                                CG  GG GGCGACGGCGGCGG
                                ||  || ||||||||||||||
                                GC  CC CCGCTGCCGCCGCC
                                 CA  G
GAM1996 H3F3A    5' CGACGGCGGCGCGGCGGCGG  48757      _   A
                                CGACGG GGCG CGGCGGCGG
                                |||||| |||| |||||||||
                                GCTGCC CCGC GCCGCCGCC
                                   G   _
GAM1996 HSU79303 5' CGGGGACCGACGGCGGCG   48758     __
                                CGGGG  CGACGGCGGCG
                                |||||  ||||||||||
                                GCCCC  GCTGCCGCCGC
                                   TG
GAM1996 KHDRBS3  5' CGGCCGGAAGGCGGCGGCGGCG 48759   A_  __   A
           G                     CG  CGG  GGCG CGGCGGCGG
                                ||  |||  |||| |||||||||
                                GC  GCC  CCGC GCCGCCGCC
                                 CG   TT   C
GAM1996 KHSRP    5' GAGGAGGCGGCGGCGGCGG   48760   C    A
                                GA GGGGCG CGGCGGCGG
                                || |||||| |||||||||
                                CT CTCCGC GCCGCCGCC
                                 C    C
GAM1996 KIAA0133 5' ACGGCGGCAGCGGCGGCG   48761     _   A
                                ACGG GGCG CGGCGGCG
                                |||| |||| ||||||||
                                TGCC CCGT GCCGCCGC
                                  G   C
GAM1996 KIAA0205 5' CCGGCGGCGGGGCCGGCGG   48762    A A    GA
                                TCG CG CGGGGC  CGGCGG
                                ||| || ||||||  ||||||
                                GGC GC GCCCCG  GCCGCC
                                  C  C    __
GAM1996 KIAA0215 5' CGGTTGGGCGGCGGCGGCGG  48763   ACG   A
                                CG   GGGCG CGGCGGCGG
                                ||   ||||| |||||||||
                                GC   CCCGC GCCGCCGCC
                                 CAA   C
GAM1996 KIAA0280 5' CGAAAACGGCGGCGGCGGCGG 48764    C   _  GAC
                                CGA GACGG GGC   GGCGGCGG
                                ||| ||||| |||   ||||||||
```

```
                                GCT TTGCC CCG   CCGCCGCC
                                  T    G  ___
GAM1996 KIAA0339 3' CGCGGGGCGGTGGCGGCGG   48765    A     AC
                                CG CGGGGCG  GGCGGCGG
                                || |||||||  ||||||||
                                GC GCCCCGC  CCGCCGCC
                                 _     CA
GAM1996 KIAA0537 5' ACGGCGGCGGCGGCGGCG    48720     _   A
                                ACGG GGCG CGGCGGCG
                                |||| |||| ||||||||
                                TGCC CCGC GCCGCCGC
                                  G   C
GAM1996 KIAA1026 5' CGGCGGTGGCGAGGCGGCGG  48766    A  _    C
                                CG CGG GGCGA GGCGGCGG
                                || ||| ||||| ||||||||
                                GC GCC CCGCT CCGCCGCC
                                 C  A    _
GAM1996 KIAA1393 3' GGGCATGGCGGCGGCGGCGG  48767     _____  A
                                GGG   GCG CGGCGGCGG
                                |||   ||| |||||||||
                                CCC   CGC GCCGCCGCC
                                  GTAC  C
GAM1996 KIAA1545 5' GACTCGCGGCGGCGGCG     48768     GA  G   GAC
                                GAC  CG GGC   GGCGGCG
                                |||  || |||   |||||||
                                CTG  GC CCG   CCGCCGC
                                  A_  G  ___
GAM1996 KIAA1735 5' CGGGAACGGCGGCGGCGG    48769      _ A
                                CGGGG CG CGGCGGCGG
                                ||||| || |||||||||
                                GCCCT GC GCCGCCGCC
                                   T  C
GAM1996 KIAA1813 5' TCGGCTCGACGCGGCGGCGGCG 48770     A__    G   GAC
           G                     TCG   CGACG GGC   GGCGGCGG
                                |||   ||||| |||   ||||||||
                                AGC   GCTGC CCG   CCGCCGCC
                                  CGA    G  ___
GAM1996 KIAA1813 5' CGACGCGGCGGCGGCGGTGG  48771      G   A    C
                                CGACG GGCG CGGCGG GG
                                ||||| |||| |||||| ||
                                GCTGC CCGC GCCGCC CC
                                   G   C     A
GAM1996 KIAA1957 5' TCGATGCGGGCGGCGGCGGCGG 48772      CGACG    A
                                TCGA    GGGCG CGGCGGCGG
                                ||||    ||||| |||||||||
                                AGCT    CCCGC GCCGCCGCC
                                  ACG__    C
GAM1996 KIAA1972 5' TCGGAGGGAGGGGGCGGCGGCG 48773     AC__  C     A
           GCGG                   TCG   GA GGGGCG CGGCGGCGG
                                |||   || |||||| |||||||||
```

```
                                AGC    CT CCCCGC GCCGCCGCC
                                  CTCC  C     C
GAM1996  KPNA6    5'  CGGCGGAGGCAACGGCGG    48774    A  _
                                CG CGG GGCGACGGCGG
                                || ||| ||||||||||
                                GC GCC CCGTTGCCGCC
                                 C   T
GAM1996  LEPROTL1  5'  TCCACGACCCGAGGCGGCGGCG 48775    G    __    GAC
              G                   TC ACGAC  GGGGC   GGCGGCGG
                                || |||||  |||||   ||||||||
                                AG TGCTG  CTCCG   CCGCCGCC
                                 G    GG    ___
GAM1996  LRP1B    5'  CGGCCCGGCGGCGGCGGCGG   48713     ___    A
                                CGG   GGCG CGGCGGCGG
                                |||   |||| |||||||||
                                GCC   CCGC GCCGCCGCC
                                  GGG    C
GAM1996  MAP2K5   5'  CGGCGGCGGCTGCGGCGGCGG  48776    A  _  GA
                                CG CGG GGC  CGGCGGCGG
                                || ||| |||  |||||||||
                                GC GCC CCG  GCCGCCGCC
                                 C   G   AC
GAM1996  MGC10818  5'  GAGTAGGGCGGCGGCGGCGG   48777    C_     A
                                GA  GGGGCG CGGCGGCGG
                                ||  |||||| |||||||||
                                CT  TCCCGC GCCGCCGCC
                                 CA     C
GAM1996  MGC15730  5'  CGGCGGTGGCGGGGCGGCGG   48778    A  _   AC
                                CG CGG GGCG  GGCGGCGG
                                || ||| ||||  ||||||||
                                GC GCC CCGC  CCGCCGCC
                                 C   A    C_
GAM1996  MO25     5'  CCGGCGACGGGCTCCCGCGGCG 48779       _____  A       III
              GCGGCGGC                 ACGGG    GCG CGGCGGCGG   C
                                |||||    ||| |||||||||  |
                                TGCCC    CGC GCCGCCGCC   G
                                   GAGGG   C       III
GAM1996  NLN      5'  TCGGCGTGGGGCGGCGAGGCGG 48780     A  AC     A   C
                                TCG CG  GGGGCG CGG GGCGG
                                ||| ||  |||||| ||| |||||
                                AGC GC  CCCCGC GCT CCGCC
                                  C  A_     C  _
GAM1996  PAPSS2   5'  ACGGCGGCGGCGGCGGCG    48720      _   A
                                ACGG GGCG CGGCGGCG
                                |||| |||| ||||||||
                                TGCC CCGC GCCGCCGC
                                  G    C
GAM1996  PLXNC1   5'  CGGAGACGCGGGCGGCGGCGGC 48781    AC    _    A
              GG                   CG  GACG GGGCG CGGCGGCGG
                                ||  |||| ||||| |||||||||
```

```
                                GC  CTGC CCCGC GCCGCCGCC
                                 CT   G    C
GAM1996  PPM1A    5'  CGGCCGAGGCGGCGGCGGCGG  48782    A_     A
                                CG  CGGGGCG CGGCGGCGG
                                ||  ||||||| |||||||||
                                GC  GCTCCGC GCCGCCGCC
                                 CG      C
GAM1996  PRP4     5'  GACTCCTCGGCGGCGGTGGCGG 48783     GACGG   A  C
                                GAC    GGCG CGG GGCGG
                                |||    |||| ||| |||||
                                CTG    CCGC GCC CCGCC
                                  AGGAG   C  A
GAM1996  PTP4A1   5'  CGGCGACACAGGCGGTGGCGGT 48785    A   _   AC   C
            GG                    CG CGACG GGGCG  GGCGG GG
                                || ||||| |||||  ||||| ||
                                GC GCTGT TCCGC  CCGCC CC
                                 C    G    CA    A
GAM1996  PTP4A1   5'  TCGTGGCGGAGCGGCGGTGGCG 48784     ACGA     A  C
            G                     TCG    CGGGGCG CGG GGCGG
                                |||    ||||||| ||| |||||
                                AGC    GCCTCGC GCC CCGCC
                                  ACC_     C  A
GAM1996  R3HDM    5'  CGACGGCGGGGCTGGGTGG   48786      A     GAC  C
                                CGACG CGGGGC   GG GG
                                |||||  ||||||   || ||
                                GCTGC GCCCCG   CC CC
                                   C     AC_  A
GAM1996  Rab11-FIP3 5'  TCGGCGGCGCGGGCGGGCGCGC 48787     A  A  _    AC   _
            G                     TCG CG CG GGGCG  GGCG GCG
                                |||  ||  ||  |||||  ||||  |||
                                AGC GC GC CCCGC  CCGC CGC
                                  C  C  G    __    G
GAM1996  RBPMS    5'  CGGCGAGTCTGCGACGGCGGCG 48788    A   ____
            G                     CG CGGG   GCGACGGCGGCGG
                                ||  ||||   ||||||||||||
                                GC GCTC   CGCTGCCGCCGCC
                                 C    AGA
GAM1996  RICH1    5'  CGGCGGTGGCGGCGGCG     48669    A   _   GAC
                                CG CGG GGC   GGCGGCG
                                ||  |||  |||   |||||||
                                GC GCC CCG   CCGCCGC
                                 C   A   ____
GAM1996  RNAC     5'  CGGCGACACCGACGGCGGCGG  48789    A    GGG
                                CG CGACG   CGACGGCGGCGG
                                ||  |||||   ||||||||||||
                                GC GCTGT   GCTGCCGCCGCC
                                 C    G__
GAM1996  SAST     5'  CGGCGGAGGCGGCGGCGGCGG  48790    A   _   A
                                CG CGG GGCG CGGCGGCGG
                                ||  |||  ||||  |||||||||
```

```
                                GC GCC CCGC GCCGCCGCC
                                 C  T   C
GAM1996 SFRS4   5' ACGGCGGCAGCGGCGGCGGCGG 48791    A  _   A
                                ACG CGG GGCG CGGCGGCGG
                                ||| ||| |||| |||||||||
                                TGC GCC TCGC GCCGCCGCC
                                  C  G   C
GAM1996 SHARP   5' CGGCGGCGGCGGCTGCGGCGGT 48792   A A  _  GA    C
            GG                   CG CG CGG GGC  CGGCGG GG
                                || || ||| |||  |||||| ||
                                GC GC GCC CCG  GCCGCC CC
                                 C  C   G   AC    A
GAM1996 SLI     5' TCCACTCGGCGGCGGCGGCGG  48793   G  GACGG   A
                                TC AC    GGCG CGGCGGCGG
                                || ||    |||| |||||||||
                                AG TG    CCGC GCCGCCGCC
                                 G  AG___   C
GAM1996 SMOC1   5' CGGGGCCCTCGCGGCGGCGG   48794      GA___
                                CGGGGC    CGGCGGCGG
                                ||||||    |||||||||
                                GCCCCG    GCCGCCGCC
                                   GGAGC
GAM1996 SPTLC2  5' CGGTGGCAGCGGCGGCGG    48654    _   A
                                CGG GGCG CGGCGGCGG
                                ||| |||| |||||||||
                                GCC CCGT GCCGCCGCC
                                  A   C
GAM1996 SSBP4   5' ACGGCCGCGGCGGCGGCG    48795     G_  A
                                ACGG  GCG CGGCGGCG
                                ||||  ||| ||||||||
                                TGCC  CGC GCCGCCGC
                                  GG   C
GAM1996 SUCLG2  5' TCGGCACGGGGCAGTAGGGCGG 48796    A G      AC  C
                                TCG C ACGGGGCG  GG GGCGG
                                ||| | ||||||||  || |||||
                                AGC G TGCCCCGT  TC CCGCC
                                  C _       CA  _
GAM1996 SUI1    5' CGGAAGGCGGCGGCGGCGG   48797    __   A
                                CGG  GGCG CGGCGGCGG
                                |||  |||| |||||||||
                                GCC  CCGC GCCGCCGCC
                                  TT   C
GAM1996 TAF6L   5' CGACGGCGGCGGGGGCGGTGGC 48798      A ____     AC
            GGCGG                  CGACG C   GGGGCG  GGCGGCGG
                                ||||| |   ||||||  ||||||||
                                GCTGC G   CCCCGC  CCGCCGCC
                                   C CCGC     CA
GAM1996 TEX27   5' GAGGAGGCGGTGGCGGCGG   48801   C     AC
                                GA GGGGCG  GGCGGCGG
                                || ||||||  ||||||||
```

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                                CT CTCCGC  CCGCCGCC
                                 C     CA
GAM1996  TEX27    5'  CGGCGGCGGAGCTCGGCGGCGG 48800    A  A     GA
                                CG CG CGGGGC  CGGCGGCGG
                                || || ||||||  |||||||||
                                GC GC GCCTCG  GCCGCCGCC
                                 C  C     A_
GAM1996  TEX27    5'  TCGGCGGCGGCAGCGGTGGCGG 48799     A  A  _   AC
              CGG                   TCG CG CGG GGCG  GGCGGCGG
                                ||| || ||| ||||  ||||||||
                                AGC GC GCC TCGC  CCGCCGCC
                                  C  C   G   CA
GAM1996  UAP1     5'  CGGCGGCGGGGCGGGCCG    48802    A  A     AC   GG
                                CG CG CGGGGCG  GGC  CG
                                || || |||||||  |||  ||
                                GC GC GCCCCGC  CCG  GC
                                 C  C      __  __
GAM1996  ZDHHC2   5'  CGGCGGCGGGGTGCGCTGCGG  48803    A  A   __  ACG
                                CG CG CGGG  GCG   GCGG
                                || || ||||  |||   ||||
                                GC GC GCCC  CGC   CGCC
                                 C  C   CA   GA_
GAM1996  LOC115708 5'  CCGCGACGCGCGGCGGCGGCGG 48804     A    GG   A
                                TCG CGACG  GCG CGGCGGCGG
                                ||| |||||  ||| |||||||||
                                GGC GCTGC  CGC GCCGCCGCC
                                  _    G_   C
GAM1996  LOC124801 5'  CGGCCGGCGGCGGCGGCG    48717     __   A
                                CGG  GGCG CGGCGGCG
                                |||  |||| ||||||||
                                GCC  CCGC GCCGCCGC
                                  GG   C
GAM1996  LOC124987 5'  CCGCGACGGGGCGGGGCGAGGG 48805     A        AC  ___
              CGG                   TCG CGACGGGGCG  GGC   GGCGG
                                ||| ||||||||||  |||   |||||
                                GGC GCTGCCCCGC  CCG   CCGCC
                                  _        C_  CTC
GAM1996  LOC131583 5'  CCGGCGCAGCTGGGCGGCGGCG 48806     A  ACG__    A
              GCGG                   TCG CG    GGGCG CGGCGGCGG
                                ||| ||    ||||| |||||||||
                                GGC GC    CCCGC GCCGCCGCC
                                  C  GTCGA    C
GAM1996  LOC133728 5'  CCGGCACAGGTGGTGGCGGCGG 48807     A G    GCGAC
                                TCG C ACGGG    GGCGGCGG
                                ||| | |||||    ||||||||
                                GGC G TGTCC    CCGCCGCC
                                  C _    ACCA_
GAM1996  LOC134121 3'  GATGACGGGGCACTGGGTGG   48808    C       AC_  C
                                GA GACGGGGCG   GG GG
                                || |||||||||   || ||
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                                CT CTGCCCCGT   CC CC
                                 A        GAC  A
GAM1996  LOC143384 5'  GAAGACGCGGCTGACGGCGGTG 48809    C   G  _      C
                 G                GA GACG GGC GACGGCGG GG
                                 || |||| ||| |||||||| ||
                                CT CTGC CCG CTGCCGCC CC
                                 T   G  A      A
GAM1996  LOC146057 5'  CCGCGTTTACTGGCGGCGGCGG 48810    A ___ GG   A
                 CGG                TCG CG  AC  GGCG CGGCGGCGG
                                 ||| ||  ||  |||| |||||||||
                                GGC GC  TG  CCGC GCCGCCGCC
                                  _ AAA  A_   C
GAM1996  LOC146745 5'  ACGGCGGTGGCGGCGGCG    48813    A  _  GAC
                                ACG CGG GGC   GGCGGCG
                                ||| ||| |||   |||||||
                                TGC GCC CCG   CCGCCGC
                                  C   A  ___
GAM1996  LOC146745 5'  CGACGGCGACAACGGCGGTGG  48811       _       C
                                CGACGG GGCGACGGCGG GG
                                |||||| |||||||||| ||
                                GCTGCC CTGTTGCCGCC CC
                                   G         A
GAM1996  LOC146745 5'  CGGCGACAACGGCGGTGGCGGC 48812    A    _   AC
                 GG                 CG CGACGG GGCG  GGCGGCGG
                                 || |||||| ||||  ||||||||
                                GC GCTGTT CCGC  CCGCCGCC
                                 C     G   CA
GAM1996  LOC147341 5'  CGCGCGGCGGCGGCGGCG    48814    A  G   A
                                CG CG GGCG CGGCGGCG
                                || || |||| ||||||||
                                GC GC CCGC GCCGCCGC
                                 _ G   C
GAM1996  LOC150067 5'  GAGGAGGCGGCGGCGGCGG    48760    C     A
                                GA GGGGCG CGGCGGCGG
                                || |||||| |||||||||
                                CT CTCCGC GCCGCCGCC
                                 C     C
GAM1996  LOC151127 5'  CGGTAGCAGCGGCGGCGG     48815    _   A
                                CGG GGCG CGGCGGCGG
                                ||| |||| |||||||||
                                GCC TCGT GCCGCCGCC
                                  A   C
GAM1996  LOC152267 5'  CGGCGATGGCGACGGCGGCGG  48816    A  _
                                CG CGG GGCGACGGCGGCGG
                                || ||| ||||||||||||||
                                GC GCT CCGCTGCCGCCGCC
                                 C   A
GAM1996  LOC152719 5'  GACGGGCGTGGCGGCG      48817       G  AC
                                GACGGG CG  GGCGGCG
                                |||||| ||  |||||||
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                                CTGCCC GC  CCGCCGC
                                   _ A_
GAM1996  LOC162417 5'  TCGGCGACGGGCGACTGG    48818     A      G   _
                                TCG CGACGGG CGAC GG
                                ||| ||||||| |||| ||
                                AGC GCTGCCC GCTG CC
                                  C      _   A
GAM1996  LOC196500 5'  CGCGGGGCGGCGGCGGTGG   48819    A      A     C
                                CG CGGGGCG CGGCGG GG
                                || ||||||| |||||| ||
                                GC GCCCCGC GCCGCC CC
                                 _      C     A
GAM1996  LOC201203 5'  ACGACGGCGGCGGCGGCG    48820        _  GAC
                                ACGACGG GGC   GGCGGCG
                                ||||||| |||   |||||||
                                TGCTGCC CCG   CCGCCGC
                                    G  ___
GAM1996  LOC201243 5'  CGACGGCGACAACGGCGGTGG  48811        _         C
                                CGACGG GGCGACGGCGG GG
                                |||||| |||||||||| ||
                                GCTGCC CTGTTGCCGCC CC
                                   G          A
GAM1996  LOC201243 5'  CGGCGACAACGGCGGTGGCGGC 48812    A     _   AC
          GG                      CG CGACGG GGCG  GGCGGCGG
                                || |||||| ||||  ||||||||
                                GC GCTGTT CCGC  CCGCCGCC
                                 C     G    CA
GAM1996  LOC201243 5'  ACGGCGGTGGCGGCGGCG    48813     A  _  GAC
                                ACG CGG GGC   GGCGGCG
                                ||| ||| |||   |||||||
                                TGC GCC CCG   CCGCCGC
                                  C   A  ___
GAM1996  LOC201915 5'  TCGGGCGGCGGGGCGCGCGG   48821     A_ A      A  G
                                TCG  CG CGGGGCG CG CGG
                                |||  || ||||||| || |||
                                AGC  GC GCCCCGC GC GCC
                                  CC  C      _ _
GAM1996  LOC220549 5'  CGGCTGAGCGGCGGCGGCGG   48822    ACG     A
                                CG   GGGCG CGGCGGCGG
                                ||   ||||| |||||||||
                                GC   CTCGC GCCGCCGCC
                                 CGA    C
GAM1996  LOC220558 5'  CGCGGCGCAGGCGGCGGCGG   48660    A   G   A_
                                CG CGG GCG  CGGCGGCGG
                                || ||| |||  |||||||||
                                GC GCC CGT  GCCGCCGCC
                                 _  G   CC
GAM1996  LOC221424 5'  CGCGGTCGCGGCGGCGGCGG   48823    A   G_   A
                                CG CGG  GCG CGGCGGCGG
                                || |||  ||| |||||||||
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                                GC GCC  CGC GCCGCCGCC
                                 _  AG   C
GAM1996  LOC256000 5'  CGCTGGGCCGCGGCGGCGG   48824    AC   G  A
                                CG  GGG CG CGGCGGCGG
                                ||  ||| || |||||||||
                                GC  CCC GC GCCGCCGCC
                                 GA   G  _
GAM1996  LOC51072  5'  GAGGAGGCGGCGGCGGCGG   48760    C     A
                                GA GGGGCG CGGCGGCGG
                                || |||||| |||||||||
                                CT CTCCGC GCCGCCGCC
                                 C     C
GAM1996  LOC56926  5'  ACGGGACGGCGGCGGCGG    48825         A
                                ACGGGGCG CGGCGGCGG
                                |||||||| |||||||||
                                TGCCCTGC GCCGCCGCC
                                     C
GAM1996  LOC64150  5'  GACGCTGGCGGCGGCGGCGG  48826     ACGG   A
                                GACG   GGCG CGGCGGCGG
                                ||||   |||| |||||||||
                                CTGC   CCGC GCCGCCGCC
                                  GA__   C
GAM1996  LOC90120  5'  CGCAGTGGCGGCGGCGG     48827    A  _  GAC
                                CG CGG GGC   GGCGGCGG
                                || ||| |||   ||||||||
                                GC GTC CCG   CCGCCGCC
                                 _  A  ____
GAM1996  LOC91272  5'  CGATGGCGGCAGGGGCGGTGG  48828    C  _   AC    C
                                CGA GG GGCG  GGCGG GG
                                ||| || ||||  ||||| ||
                                GCT CC CCGT  CCGCC CC
                                  A  G   CC    A
GAM1996  LOC91408  5'  ACGGCGGCGGCGGCGGCG    48720     _   A
                                ACGG GGCG CGGCGGCG
                                |||| |||| ||||||||
                                TGCC CCGC GCCGCCGC
                                  G   C
GAM1996  LOC91408  5'  ACGACGGCGGCGGCGGCG    48820       _  GAC
                                ACGACGG GGC   GGCGGCG
                                ||||||| |||   |||||||
                                TGCTGCC CCG   CCGCCGC
                                    G  ____
GAM1996  LOC92299  5'  CGGCGGCTGCTTTGGCGGCGG  48829    A  G_  GAC
                                CG CGG  GC   GGCGGCGG
                                || |||  ||   ||||||||
                                GC GCC  CG   CCGCCGCC
                                 C  GA  AAA
GAM1997  EIF3S1    3'  GGGTTTTGGTCATTTTAATTT  48832          G   _
                                GGGTTTTGGT ATTT AATTT
                                |||||||||| |||| |||||
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                                CCCAAAACCA TAAA TTAAA
                                     G   A
GAM1997  FLJ12476  3'  GGTTTTGGTGTTGTAATTT   48833        ATT
                                GGTTTTGGTG   TAATTT
                                ||||||||||  ||||||
                                CCAAAACCAC   ATTAAA
                                     AAC
GAM1997  PRO2958   3'  CAGGAATCTGATTTAATTT   48834     TT  GG
                                CGGG  TT  TGATTTAATTT
                                ||||  ||  ||||||||||
                                GTCC  AG  ACTAAATTAAA
                                  TT  __
GAM1997  RNAHP     3'  GGGTTTCTTGTTTAATTT    48835       GG  A
                                GGGTTTT  TG TTTAATTT
                                |||||||  ||  ||||||||
                                CCCAAAG  AC AAATTAAA
                                    A_  _
GAM1997  ZDHHC5    5'  GGCAATGGTGGTTTAATTT   48836     TT    A
                                GGT  TGGTG TTTAATTT
                                |||  |||||  ||||||||
                                CCG  ACCAC AAATTAAA
                                  TT    C
GAM1997  LOC257485 3'  GGGTTTTGGCCATTTTAATTT  48837         G   _
                                GGGTTTTGGT ATTT AATTT
                                ||||||||||  ||||  |||||
                                CCCAAAACCG TAAA TTAAA
                                     G   A
GAM1998  LOC90470  3'  TAATGCTATCTACTTTGTATT  48840        G  G   CC
                                TAATGCTG TC ACT  GTATT
                                ||||||||  ||  |||  |||||
                                ATTACGAT AG TGA  CATAA
                                    _  A   AA
GAM1998  LOC90841  3'  ATGCTGGCATCTTTGTATT   48841        T  A  CC
                                ATGCTGG CG CT  GTATT
                                |||||||  ||  ||  |||||
                                TACGACC GT GA  CATAA
                                    _  A  AA
GAM1999  HT002     3'  TGGCCAACACGGTGAAACCCTG 48844      G       ACGA_
           TG                     TGGCC AACACGGT    TTTGTG
                                |||||  ||||||||    ||||||
                                ACCGG TTGTGCCA    GGACAC
                                  _       CTTTG
GAM1999  LOC219731 5'  GGCTGGGCATGGTGACTTGTG  48845     CGAA  C   AC
                                GGC    CA GGT  GATTTGTG
                                |||    ||  |||  ||||||||
                                CCG    GT CCA  CTGAACAC
                                  ACCC  A   __
GAM2000  ADRBK1    3'  GCGGTGGAGGAGACCTGGTA   48848     GA       GGAG
                                GCGG  GAGGAGATC    GGTA
                                ||||  |||||||||    ||||
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                                CGCC  CTCCTCTGG   CCAT
                                  AC       A___
GAM2000 ANP32A   3' GGGAGAGGGGATATGGGTA   48849       A  CGGA
                                GGGAGAGG GAT   GGGTA
                                |||||||| |||   |||||
                                CCCTCTCC CTA   CCCAT
                                    C   TA__
GAM2000 AQP2     3' GCGGGAGAGGAGGGACGGGGT 48850         ATC  __
                                GCGGGAGAGGAG  GGA  GGGT
                                ||||||||||||  |||  ||||
                                CGCCCTCTCCTC  CCT  CCCA
                                       ___  GC
GAM2000 AR       5' GGGAGGGGGGGGAAGGCAGGGT  48851     A  A_  TC  _
                                GGGAG GG  GA  GG AGGGT
                                ||||| ||  ||  || |||||
                                CCCTC CC  CT  CC TCCCA
                                   C  CC  T_  G
GAM2000 ASPH     3' GCTGGAGAGGAGGGAAGGT   48852    G      ATC
                                GC GGAGAGGAG  GGAGGGT
                                || |||||||||  |||||||
                                CG CCTCTCCTC  CCTTCCA
                                 A       ___
GAM2000 ASPH     3' GCTGGAGAGGAGGGAAGGT   48852    G      ATC
                                GC GGAGAGGAG  GGAGGGT
                                || |||||||||  |||||||
                                CG CCTCTCCTC  CCTTCCA
                                 A       ___
GAM2000 BCL11B   3' GCGGGAGAGGTGGTGGT     48853        AGATC  AG
                                GCGGGAGAGG    GG  GGT
                                ||||||||||    ||  |||
                                CGCCCTCTCC    CC  CCA
                                      A____  A_
GAM2000 BCL2L2   3' AGTGGGAGAGGAGGGTGG    48854    C       ATC  A
                                AG GGGAGAGGAG  GG GG
                                || ||||||||||  || ||
                                TC CCCTCTCCTC  CC CC
                                 A       ___ A
GAM2000 CARPX    5' CGGGGCATGGTCGGAGGGT   48855     AGA_  AGA
                                CGGG   GG  TCGGAGGGT
                                ||||   ||  |||||||||
                                GCCC   CC  AGCCTCCCA
                                  CGTA  ___
GAM2000 CBFA2T3  3' GCGCGGAGAGGAGAGAGG    48856    _       TCG
                                GCG GGAGAGGAGA  GAGG
                                ||| ||||||||||  ||||
                                CGC CCTCTCCTCT  CTCC
                                  G       ___
GAM2000 CXCL16   3' GGGGGAGGAACAACTGGT    48857    A    AT  AG
                                GGG GAGGAG  CGG  GGT
                                ||| ||||||  |||  |||
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                                CCC CTCCTT  GTT  CCA
                                  C     __   GA
GAM2000  CYP8B1   3'  AGTAGGAGAGGGGAGGAGGGTA 48858    CG      A  TC
                                AG  GGAGAGG GA  GGAGGGTA
                                ||  |||||||  ||  ||||||||
                                TC  CCTCTCC CT  CCTCCCAT
                                 AT      C  __
GAM2000  DUSP6    5'  GCGGGAGAGGGCGGGG      48859          AGAT   A
                                GCGGGAGAGG    CGG GG
                                ||||||||||    |||  ||
                                CGCCCTCTCC    GCC CC
                                      C___   _
GAM2000  EGR3     5'  GCGGGAGAGGGCCCCAGGGGGT 48860          AGA    A
              A                  GCGGGAGAGG   TCGG GGGTA
                                ||||||||||   ||||  |||||
                                CGCCCTCTCC   GGTC CCCAT
                                      CGG    C
GAM2000  FANCA    3'  GGGAGGGTCGGAGGGT      48861       A  AGA
                                GGGAG GG   TCGGAGGGT
                                |||||  ||   |||||||||
                                CCCTC CC   AGCCTCCCA
                                  _  ___
GAM2000  GALR1    5'  AGCGGGAGCGGGGATCCGG    48862         A  A   _
                                AGCGGGAG GG GATC GG
                                ||||||||  ||  ||||  ||
                                TCGCCCTC CC CTAG CC
                                     G  C    G
GAM2000  KRT14    3'  GCAGGAGAGGGGATCTTCCAGT 48863          A    GGAG
                                GCGGGAGAGG GATC    GGT
                                ||||||||||  ||||    |||
                                CGTCCTCTCC CTAG    TCA
                                      C    AAGG
GAM2000  LTB4R    5'  AGTGAGAGAGGAAAGAGGG    48864    C        ATC
                                AG GGGAGAGGAG   GGAGGG
                                ||  ||||||||||   ||||||
                                TC CTCTCTCCTT   TCTCCC
                                 A         ____
GAM2000  MAPT     5'  AGCGGAGGAGGAGAAGGT     48865      GA      TCGGA
                                AGCGG  GAGGAGA    GGGT
                                |||||  |||||||    ||||
                                TCGCC  CTCCTCT    TCCA
                                  TC      ______
GAM2000  MAPT     5'  AGCGGAGGAGGAGAAGGT     48865      GA      TCGGA
                                AGCGG  GAGGAGA    GGGT
                                |||||  |||||||    ||||
                                TCGCC  CTCCTCT    TCCA
                                  TC      ______
GAM2000  MAPT     5'  AGCGGAGGAGGAGAAGGT     48865      GA      TCGGA
                                AGCGG  GAGGAGA    GGGT
                                |||||  |||||||    ||||
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                                TCGCC  CTCCTCT    TCCA
                                  TC     _____
GAM2000  MAPT    5'  AGCGGAGGAGGAGAAGGT    48865      GA      TCGGA
                                AGCGG  GAGGAGA    GGGT
                                |||||  |||||||    ||||
                                TCGCC  CTCCTCT    TCCA
                                  TC     _____
GAM2000  MECP2   3'  GCGGGAGGGGAGGTGC      48866       A  AGATCG   _
                                GCGGGAG GG     GAGG GT
                                |||||||  ||     ||||  ||
                                CGCCCTC CC     CTCC CG
                                   _ _______   A
GAM2000  MEN1    5'  GGCTGGAGGTCCTGGAGGGT   48867    AGA    A  __
                                GG   GGAG TC  GGAGGGT
                                ||   ||||  ||  |||||||
                                CC   CCTC AG  CCTCCCA
                                 GA_    C  GA
GAM2000  MSI1    3'  CGGGAGAGGGGCGGGT      48868         AGATC  A
                                CGGGAGAGG     GG GGGT
                                |||||||||     ||  ||||
                                GCCCTCTCC     CC CCCA
                                     _____  G
GAM2000  PAK4    3'  AGGGGGAGAGGGGGCTGGGT   48869    C       AGATC  A_
                                AG GGGAGAGG     GG  GGGT
                                ||  ||||||||    ||  ||||
                                TC CCCTCTCC     CC  CCCA
                                 C       C_____  GA
GAM2000  PRKACA  3'  AGTGGGAGAGGGGGGCAGGAGGG 48870    C       AGATC
           T                     AG GGGAGAGG     GGAGGGT
                                ||  ||||||||    |||||||
                                TC CCCTCTCC     CCTCCCA
                                 A       CCCGT
GAM2000  RAB3A   3'  GCGGGGGGGGGGGTTCAGGAGGG 48871       AGA  AGA  _
           T                     GCGGG   GG   TC GGAGGGT
                                |||||   ||   ||  |||||||
                                CGCCC   CC   AG CCTCCCA
                                   CCC  CCA  T
GAM2000  REST    5'  GGGAGAGGTGGGGGAGGGT   48872         AGATC
                                GGGAGAGG     GGAGGGT
                                ||||||||     |||||||
                                CCCTCTCC     CCTCCCA
                                     ACCC_
GAM2000  RFP     5'  AGTGGGGCAGGAAAGGGT    48873    C   AG    GATCG
                                AG GGG  AGGA     GAGGGT
                                ||  |||  ||||     ||||||
                                TC CCC  TCCT     TTCCCA
                                 A   CG   _____
GAM2000  SHANK2  3'  AGCGGGAGAGCTTGAGGGT   48874          GAGATCG
                                AGCGGGAGAG      GAGGGT
                                ||||||||||      ||||||
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                                TCGCCCTCTC      CTCCCA
                                      GAA____
GAM2000  SOX11    3'  AGCGGGAGGGGAGGCGG     48875        A    AT
                                AGCGGGAG GGAG  CGG
                                |||||||| ||||  |||
                                TCGCCCTC CCTC  GCC
                                     C    C_
GAM2000  TAL1     3'  AGAGGGAGAGGGCTAGGGT    48876    C      AGATCGG
                                AG GGGAGAGG      AGGGT
                                || ||||||||      |||||
                                TC CCCTCTCC      TCCCA
                                 T       CGA____
GAM2000  XYLB     3'  AGGGGGAGAGGAGAGATGGT   48877    C        TCG  G
                                AG GGGAGAGGAGA   GA GGT
                                || ||||||||||   || |||
                                TC CCCTCTCCTCT   CT CCA
                                 C          ___  A
GAM2000  AEBP1    5'  GCGGGAGAGAGGATGGGG    48879        GA   C  A
                                GCGGGAGAG  GAT GG GG
                                |||||||||  ||| || ||
                                CGCCCTCTC  CTA CC CC
                                      TC   _ _
GAM2000  AEBP1    5'  GCGGAGAGGGGATCGAGACGGG 48878      G     A     _ _
               T                 GCGG AGAGG GATCG GA GGGT
                                 |||| ||||| ||||| || ||||
                                 CGCC TCTCC CTAGC CT CCCA
                                   _    C    T  G
GAM2000  AIF1     3'  GGGGGAGGAGAAAACAGGTA   48880     A      TCGGA
                                GGG GAGGAGA     GGGTA
                                ||| |||||||     |||||
                                CCC CTCCTCT     TCCAT
                                  C      TTTG_
GAM2000  ASB10    5'  AGTGGGGAGGAGGAGAGG    48881    C   A     ATC
                                AG GGG GAGGAG   GGAGG
                                || ||| ||||||   |||||
                                TC CCC CTCCTC   TCTCC
                                 A   _      C__
GAM2000  C20orf110 3'  AGGGGAGGGGGATCATAGGGTA 48882    C     A  A    G
                                AG GGGAG GG GATCG AGGGTA
                                || ||||| || ||||| ||||||
                                TC CCCTC CC CTAGT TCCCAT
                                 _     _ C     A
GAM2000  C20orf27  3'  AGTGGGAGAGGAGGACGA    48883    C        AT
                                AG GGGAGAGGAG  CGG
                                || ||||||||||  |||
                                TC CCCTCTCCTC  GCT
                                 A         CT
GAM2000  C22orf5   3'  AGGGGGAGAGGAGGGGCTTGGT 48884    C        ATC  AG_
                                AG GGGAGAGGAG   GG   GGT
                                || ||||||||||   ||   |||
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                                TC CCCTCTCCTC   CC   CCA
                                 C        C__  GAA
GAM2000 CENTG1   3' GCTGGGAGAGGTCACGGGGGT 48885    _      AGAT   A
                                GC GGGAGAGG    CGG GGGT
                                || ||||||||    ||| ||||
                                CG CCCTCTCC    GCC CCCA
                                 A       AGT_  _
GAM2000 CORO1B   3' GCGGCGGAGGAGATGAAGG   48886     GA       C
                                GCGG  GAGGAGAT GGAGG
                                ||||  |||||||| |||||
                                CGCC  CTCCTCTA CTTCC
                                  GC       _
GAM2000 DKFZP761D0211 3' GCGGGAGAGAGGCCCAGGGT   48887         G  AT GG
                                GCGGGAGAG AG  C  AGGGT
                                ||||||||| ||  |  |||||
                                CGCCCTCTC TC  G  TCCCA
                                      _ CG G_
GAM2000 DKFZp762E1511 5'  AACGGGGGGGGGAGATTTTGGGG 48888       AGA     CGGA
              T                  AGCGGG   GGAGAT    GGGT
                                ||||||   ||||||    ||||
                                TTGCCC   CCTCTA    CCCA
                                   CCC     AAAC
GAM2000 DKFZp762M136 3'  AGCAGGAGAGGGGAGAGGTGAG 48889          __    TCG
              GGT                  AGCGGGAGA  GGAGA   GAGGGT
                                |||||||||  |||||   ||||||
                                TCGTCCTCT  CCTCT   CTCCCA
                                     CC     CCA
GAM2000 EFNA5    5' GCGGTGGGATGGGGGGT     48890      GAGA  A   C  A
                                GCGG    GG GAT GG GGGT
                                ||||    || ||| || ||||
                                CGCC    CC CTA CC CCCA
                                  A___  _   C  _
GAM2000 EMILIN   3' GGAGGGAGCGGAGGGT      48891      A    AT
                                GGAG GGAG  CGGAGGGT
                                |||| ||||  ||||||||
                                CCTC CCTC  GCCTCCCA
                                  _   __
GAM2000 EPB41L1   3' GCGGGAGAGAGGAAGGT     48892          AGATC
                                GCGGGAGAGG    GGAGGGT
                                ||||||||||    |||||||
                                CGCCCTCTCT    CCTTCCA
                                      ______
GAM2000 FLJ13544  3' AGCGGGAAGGAGAGG       48893        G     TCGGAG
                                AGCGGGA AGGAGA     GG
                                |||||||| ||||||     ||
                                TCGCCCT TCCTCT     CC
                                  _     _______
GAM2000 FLJ13855  3' AGGGGAGGGGAGAAAGGT    48894    C    A    TCGG
                                AG GGGAG GGAGA    AGGGT
                                || ||||| |||||    |||||
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                                TC CCCTC CCTCT    TTCCA
                                 _    C    ____
GAM2000  FLJ14299  3' GGGAGAGGGAGGAGGGT    48895        A  TC
                                GGGAGAGG GA  GGAGGGT
                                |||||||| ||  |||||||
                                CCCTCTCC CT  CCTCCCA
                                    _ __
GAM2000  KIAA0451  3' GGGAGAGTGAGGAGGGT    48896       GA  TC
                                GGGAGAG  GA  GGAGGGT
                                |||||||  ||  |||||||
                                CCCTCTC  CT  CCTCCCA
                                   A_ __
GAM2000  KIAA0557  3' GGGGGAGCAGGTGGGGGGTA  48897     A   G  ATC  A
                                GGG GAG AG   GG GGGTA
                                ||| ||| ||   || |||||
                                CCC CTC TC   CC CCCAT
                                  C   G  CAC  _
GAM2000  KIAA1100  3' AGAGGGAGAGGAGATTGG    48898    C          C
                                AG GGGAGAGGAGAT GG
                                || ||||||||||| ||
                                TC CCCTCTCCTCTA CC
                                 T          A
GAM2000  KIAA1855  3' GCGGGAGGACAGGGAGGGT   48899        A  AGATC
                                GCGGGAG GG    GGAGGGT
                                ||||||| ||    |||||||
                                CGCCCTC CT    CCTCCCA
                                    _ GTC__
GAM2000  KIAA1893  3' AGTGGGAGAGGGGATGG     48900    C       A   C
                                AG GGGAGAGG GAT GG
                                || |||||||| ||| ||
                                TC CCCTCTCC CTA CC
                                 A       C  _
GAM2000  KIAA1938  3' GGGGAGGGTCCAGGGGTA    48901     A   AGA   A
                                GGG GAGG   TCGG GGGTA
                                ||| ||||   |||| |||||
                                CCC CTCC   GGTC CCCAT
                                  _    CA_   _
GAM2000  LHPP      3' GGAGGGGAGGCAGGGGT     48902      A   AT   A
                                GGAG GGAG  CGG GGGT
                                |||| ||||  ||| ||||
                                CCTC CCTC  GTC CCCA
                                  C    C_   _
GAM2000  MGC26914  3' GGGAGAGGGGGGGGCACGGGGGT 48903         AGAT___  A
            A                    GGGAGAGG      CGG GGGTA
                                ||||||||      ||| |||||
                                CCCTCTCC      GCC CCCAT
                                    CCCCCGT  _
GAM2000  MGC2941   3' AGTGGGGAGGAAGGATAGGGT  48904    C  A    ATCGG
                                AG GGG GAGGAG    AGGGT
                                || ||| ||||||    |||||
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                                TC CCC CTCCTT    TCCCA
                                 A  _     CCTA_
GAM2000  PALMD    5'  GGGAGAGGAGCGGGGGT    48905        AT  A
                                GGGAGAGGAG  CGG GGGT
                                ||||||||||  ||| ||||
                                CCCTCTCCTC  GCC CCCA
                                      __  _
GAM2000  RAB1B    3'  GGGAGAGGAAAGGGT      48906        GATCG
                                GGGAGAGGA    GAGGGT
                                |||||||||    ||||||
                                CCCTCTCCT    TTCCCA
                                     _____
GAM2000  RAB3D    3'  GCAGGAGAGGGGTGGGT    48907         AGATC  A
                                GCGGGAGAGG    GG GGGT
                                ||||||||||    || ||||
                                CGTCCTCTCC    CC CCCA
                                     _____ A
GAM2000  RAB6C    5'  GCGGGAGAGAGACGGAGGGT  48908        G  T
                                GCGGGAGAG AGA CGGAGGGT
                                ||||||||| ||| ||||||||
                                CGCCCTCTC TCT GCCTCCCA
                                     _  _
GAM2000  SCAMP5   3'  GGGAGAAGGGAAGGT      48909        AGATC
                                GGGAGAGG    GGAGGGT
                                ||||||||    |||||||
                                CCCTCTTC    CCTTCCA
                                     _____
GAM2000  SIMRP7   3'  AGAGGGAGGTCCTGGAGGGTA  48910     A   A __
                                GGAG GGAG TC  GGAGGGTA
                                |||| |||| ||  ||||||||
                                TCTC CCTC AG  CCTCCCAT
                                  _   C  GA
GAM2000  TNKS1BP1 3'  GGGGGGAGTTCGGAGGGT   48911     AGA   A
                                GGG   GGAG TCGGAGGGT
                                |||   |||| |||||||||
                                CCC   CCTC AGCCTCCCA
                                  C__   A
GAM2000  TOB2     5'  GCGGGGATGGCGGATCGGAGGG 48912      A  _  A_
            T                    GCGGG GA GG  GATCGGAGGGT
                                 ||||| || ||  ||||||||||
                                 CGCCC CT CC  CTAGCCTCCCA
                                   _ A  GC
GAM2000  TUBB5    3'  AGCGGGGAGGGAGGG      48913       A   AGATCG
                                AGCGGG GAGG     GAGGG
                                ||||||| ||||     |||||
                                TCGCCC CTCC     CTCCC
                                   _   _______
GAM2000  LOC144501 5'  AGCAGGAGGGCCCAGGGGGGT  48914        A  AGATC  A
                                AGCGGGAG GG     GG GGGT
                                |||||||| ||     || ||||
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                                TCGTCCTC CC    CC CCCA
                                    _ GGGTC _
GAM2000  LOC146268 3'  AGCAGGGGACCATACGGAGGGT 48915      AGA  GAT__
                                AGCGGG  GGA   CGGAGGGT
                                ||||||  |||   ||||||||
                                TCGTCC  CCT   GCCTCCCA
                                   ___  GGTAT
GAM2000  LOC146452 3'  GGAAGAGGAGAGGGT     48916         TCGGA
                                GGGAGAGGAGA   GGGT
                                ||||||||||    ||||
                                CCTTCTCCTCT   CCCA
                                      _____
GAM2000  LOC170261 5'  GGGAGAGGAGAGGAGG     48917         TC
                                GGGAGAGGAGA GGAGG
                                |||||||||| |||||
                                CCCTCTCCTCT CCTCC
                                      __
GAM2000  LOC197350 3'  CGGGGGGATGGGGGGT     48918     AGA A  C A
                                CGGG  GG GAT GG GGGT
                                ||||  || ||| || ||||
                                GCCC  CC CTA CC CCCA
                                  ___ _  C _
GAM2000  LOC203076 3'  AGCGGGAGGGGATGGGG    48919       A A  C A
                                AGCGGGAG GG GAT GG GG
                                |||||||| || ||| || ||
                                TCGCCCTC CC CTA CC CC
                                     _ _  _ _
GAM2000  LOC206389 5'  AGCGGGAGAGGGGCTGGT   48920         AGATC AG
                                AGCGGGAGAGG   GG GGT
                                ||||||||||    || |||
                                TCGCCCTCTCC   CC CCA
                                      _____ GA
GAM2000  LOC220020 5'  GCTGGGAGAGGAGAGGGT   48921   _       TCGGA
                                GC GGGAGAGGAGA   GGGT
                                || ||||||||||    ||||
                                CG CCCTCTCCTCT   CCCA
                                 A       _____
GAM2000  LOC221272 3'  AGTGGTGGGAGTAGGAGGGTA 48922   C GAGA  ATC
                                AG GG   GGAG  GGAGGGTA
                                || ||   ||||  ||||||||
                                TC CC   CCTC  CCTCCCAT
                                 A AC__   AT_
GAM2000  LOC221336 5'  AGGTGGGAGGTGGAGGGT   48923   CG A  AGATC
                                AG GG GAGG    GGAGGGT
                                || || ||||    |||||||
                                TC CC CTCC    CCTCCCA
                                 CA _   A____
GAM2000  LOC221495 3'  GCCGGGGGGTCGGGGGGT   48924   _ AGA AGA  A
                                GC GGG  GG  TCGG GGGT
                                || |||  ||  |||| ||||
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                                CG CCC   CC   AGCC CCCA
                                 G   C__ ___    C
GAM2000  LOC221655 3'  AGTGGGGGCGGGGGGAAGGTA  48925    C   AGA  AGATC
                                AG GGG   GG    GGAGGGTA
                                || |||   ||    ||||||||
                                TC CCC   CC    CCTTCCAT
                                 A   ___  GCCCC
GAM2000  LOC256364 5'  AGTGGGAGGGGAGAGCAGACAG 48926    C    A    T   G
            TA                   AG GGGAG GGAGA CGGA GGTA
                                || ||||| ||||| |||| ||||
                                TC CCCTC CCTCT GTCT TCAT
                                 A    C    C   G
GAM2000  LOC257051 5'  GGGAGAGGAGAGGAGG      48917          TC
                                GGGAGAGGAGA  GGAGG
                                ||||||||||  |||||
                                CCCTCTCCTCT  CCTCC

                                      __
GAM2000  LOC51133  5'  GCCGGAGGGCGGGGGGT     48927    G   A  AGAT   A
                                GC GGAG GG    CGG GGGT
                                || |||| ||    ||| ||||
                                CG CCTC CC    GCC CCCA
                                 G   _ ____   C
GAM2000  LOC90630  5'  GCGGAGAGGAGATGGGG     48928     G       C  A
                                GCGG AGAGGAGAT GG GG
                                |||| |||||||| || ||
                                CGCC TCTCCTCTA CC CC

                                  _       _ _
GAM2000  LOC91208  5'  GCGGAGAGGAGATGGGG     48928     G       C  A
                                GCGG AGAGGAGAT GG GG
                                |||| |||||||| || ||
                                CGCC TCTCCTCTA CC CC

                                  _       _ _
GAM2001  NR1I2    5'  GAGGGAGAGGGAGACCACGAT  48931     AAT    T  TT
                                GAG   GAGAG GA  GCCACGAT
                                |||   ||||| ||  ||||||||
                                CTC   CTCTC CT  TGGTGCTA
                                  C__    C  C_
GAM2001  KIAA0057  3'  GAGAATGAGGGTTGCTTGA   48932        A  GAT   CAC
                                GAGAATGAG GT   TGC   GA
                                |||||||| ||   |||   ||
                                CTCTTACTC CA   ACG   CT
                                     C  ___   AA_
GAM2001  PCYT1B   3'  GAGAGTGAGAGAGAACTG    48933     A     T_
                                GAGA TGAGAG  GATTG
                                |||| ||||||  |||||
                                CTCT ACTCTC  TTGAC
                                  C     TC
GAM2001  RAI17    3'  AAGATGGGGGTGATTGCC    48934     A  AGA
                                GAGA TG   GTGATTGCC
                                |||| ||   |||||||||
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                                TTCT AC   CACTAACGG
                                  _ CCC
GAM2001  LOC145902 5'  GGAAGAACGTGGTTGCCACG   48935   A   T   A   A
                                G GAA GAG GTG TTGCCACG
                                | ||| ||| ||| ||||||||
                                C CTT CTT CAC AACGGTGC
                                _  _   G   C
GAM2001  LOC160711 5'  GAGGGTGAAAGTGAACACTGAT 48936     AA       TTGC  _
                                GAG  TGAGAGTGA    CAC GAT
                                |||  |||||||||    ||| |||
                                CTC  ACTTTCACT    GTG CTA
                                  CC        T___   A
GAM2001  LOC201382 5'  AGAATGAGCAAAATATTGCCA  48937        AGTG__
                                AGAATGAG     ATTGCCA
                                ||||||||     |||||||
                                TCTTACTC     TAACGGT
                                     GTTTTA
GAM2002  ADAM10   5'  TCGCTCCACTTCAGGGGCC   48940         CC   ACC
                                TCGCTCCGC  CAG   GCC
                                |||||||||  |||   |||
                                AGCGAGGTG  GTC   CGG
                                     AA   CC_
GAM2002  BCL7A    3'  TCGCTCCACCCTGCCTGCTCCG 48941          CAGA  _  _
           A                     TCGCTCCGCCC    CC GC CCGA
                                ||||||||||    || || ||||
                                AGCGAGGTGGG    GG CG GGCT
                                      AC__  A  A
GAM2002  CEBPD    3'  CGCTCCGCTCCGGGCCGTCG   48942        C  AGA   CC
                                CGCTCCGC CC   CCG  CG
                                |||||||| ||   |||  ||
                                GCGAGGCG GG   GGC  GC
                                     A  CCC   A_
GAM2002  DSCAM    5'  CGCTCCGCCCGGCCCG      48943          CAGACC
                                CGCTCCGCCC     GCCCG
                                ||||||||||     |||||
                                GCGAGGCGGG     CGGGC
                                      C_____
GAM2002  EMS1     3'  CACACCGCCCCAGGCTGCCCG  48944     T       ACC
                                CGC CCGCCCCAG   GCCCG
                                ||| |||||||||   |||||
                                GTG GGCGGGGTC   CGGGC
                                  T       CGA
GAM2002  EMS1     3'  CACACCGCCCCAGGCTGCCCG  48944     T       ACC
                                CGC CCGCCCCAG   GCCCG
                                ||| |||||||||   |||||
                                GTG GGCGGGGTC   CGGGC
                                  T       CGA
GAM2002  FOXD2    5'  TCCTCCGCCCCCTGCCCGA   48945    G       AGACC
                                TC CTCCGCCCC    GCCCGA
                                || |||||||||    ||||||
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                                AG GAGGCGGGG    CGGGCT
                                 _       GA___
GAM2002  GPR48    5'  TCGCTCCGCTGCCCTCCGA   48946        CCCAGA  GC
                                TCGCTCCGC     CC  CCGA
                                |||||||||     ||  ||||
                                AGCGAGGCG     GG  GGCT
                                     ACG___  A_
GAM2002  HIF1A    5'  TCGCTCCGGCCTAAGCGC    48947        _ CC  AC
                                TCGCTCCG CC  AG  CGC
                                ||||||||  ||  ||  |||
                                AGCGAGGC GG  TC  GCG
                                     C  AT  __
GAM2002  MAN1A1   5'  TCCTGCGTAGCCAGGCCGCCCG 48948     _ C___    A
              AC                   TCC GC    CCAG CCGCCCGAC
                                ||| ||    |||| |||||||||
                                AGG CG    GGTC GGCGGGCTG
                                  A  CATC    C
GAM2002  MAOB     5'  TCGCCCCGTTCCAGGCCTCCC  48949        CC    A  G
                                TCGCTCCG  CCAG CC CCC
                                ||||||||  |||| || |||
                                AGCGGGGC  GGTC GG GGG
                                     AA    C  A
GAM2002  MAP7     5'  CCGCTCCGCCCTTTCCTCG    48950          CAGACCG  _
                                TCGCTCCGCCC      CC CG
                                ||||||||||       || ||
                                GGCGAGGCGGG      GG GC
                                      AAA_____  A
GAM2002  MTNR1A   5'  TCGTCCGCCCGCCCG      48951     C      CAGACC
                                TCG TCCGCCC     GCCCG
                                ||| |||||||     |||||
                                AGC AGGCGGG     CGGGC
                                  _     _______
GAM2002  S100A10  5'  TCGCCCGCCCCAGACAGAGC   48952      T         C__
                                TCGC CCGCCCCAGAC   GC
                                |||| ||||||||||   ||
                                AGCG GGCGGGGTCTG   CG
                                  _         TCT
GAM2002  TIA1     5'  ACTCCGCCTCCTCCTCCG    48953         _ AGA  GC
                                GCTCCGCC CC   CC  CCG
                                ||||||||  ||   ||  |||
                                TGAGGCGG GG   GG  GGC
                                     A  A__  A_
GAM2002  TIA1     5'  ACTCCGCCTCCTCCTCCG    48953         _ AGA  GC
                                GCTCCGCC CC   CC  CCG
                                ||||||||  ||   ||  |||
                                TGAGGCGG GG   GG  GGC
                                     A  A__  A_
GAM2002  TR2      5'  TCGCTCTCGCTCCTGGCCCG  48954        _  C  AGACC
                                TCGCTC CGC CC    GCCCG
                                ||||||  ||| ||    |||||
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                                AGCGAG GCG GG    CGGGC
                                   A  A AC___
GAM2002 CBCIP2   5' TCGCCCCGCCCGGCTCG    48955         CAGACC  C
                                TCGCTCCGCCC    GC CG
                                ||||||||||     || ||
                                AGCGGGGCGGG    CG GC
                                      C_____  A
GAM2002 CTNNBIP1 5' TCGGTCCCTGGGCCGCCCGAC 48956    CTCCG  CAGA
                                TCG    CCC   CCGCCCGAC
                                |||    |||   |||||||||
                                AGC    GGG   GGCGGGCTG
                                  CA___   ACCC
GAM2002 DKFZP434N178 3' TCGCTCCGTCCCACGTCCCG  48957       C   GAC _
                                TCGCTCCG CCCA   CG CCCG
                                |||||||| ||||   || ||||
                                AGCGAGGC GGGT   GC GGGC
                                     A   ___  A
GAM2002 DKFZP564O1863 5' CCGCTTTGCCCCAGAAGGC   48958      CC      CC
                                TCGCT  GCCCCAGA  GC
                                |||||  ||||||||  ||
                                GGCGA  CGGGGTCT  CG
                                   AA       TC
GAM2002 FLJ10900 3' TCACTCCGCTCCAGCCCCG   48959        C   A  GC
                                TCGCTCCGC CCAG CC  CCG
                                |||||||||  |||| ||  |||
                                AGTGAGGCG GGTC GG  GGC
                                     A   _  __
GAM2002 FLJ10900 3' TCACTCCGCTCCAGCCCCG   48959        C   A  GC
                                TCGCTCCGC CCAG CC  CCG
                                |||||||||  |||| ||  |||
                                AGTGAGGCG GGTC GG  GGC
                                     A   _  __
GAM2002 NLI-IF   5' CGCTCCGCTCCGGCCGGAC   48960       C  AGACC  C
                                CGCTCCGC CC    GCC GAC
                                ||||||||  ||    ||| |||
                                GCGAGGCG GG    CGG CTG
                                     A  C_____  C
GAM2002 NTN1     3' TCGCCCCGCCCTCGGGCCCGCC 48961         CAGA__
           CG                    TCGCTCCGCCC    CCGCCCG
                                ||||||||||     |||||||
                                AGCGGGGCGGG    GGCGGGC
                                      AGCCCG
GAM2002 PIP5K2A  5' TCGCTCCGCCCGCTCG     48962         CAGACC  C
                                TCGCTCCGCCC    GC CG
                                ||||||||||     || ||
                                AGCGAGGCGGG    CG GC
                                      _______ A
GAM2002 PPP1R1A  5' CCGCTCCGCTCCGGCCC    48963        C  AGACC
                                TCGCTCCGC CC    GCCC
                                |||||||| ||    ||||
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                                GGCGAGGCG GG    CGGG
                                     A  C____
GAM2002  SAP30    5'  TCTCTCCGCTCCGGCAGCGGC  48964    G    _ __  ACC
                                TC CTCCGC CC  CAG   GC
                                || |||||| ||  |||   ||
                                AG GAGGCG GG  GTC   CG
                                 A     A  CC   GC_
GAM2002  SLC21A11  5'  CCGCTCCGGCCGCCGCCCGAC  48965       C  CAGA
                                TCGCTCCG CC    CCGCCCGAC
                                |||||||| ||    |||||||||
                                GGCGAGGC GG    GGCGGGCTG
                                     C  C___
GAM2002  LOC124930 3'  GCTCCGCCCTAGGACAGGAC   48966       C  AC  CCC
                                GCTCCGCCC AG  CG   GAC
                                ||||||||| ||  ||   |||
                                CGAGGCGGG TC  GT   CTG
                                     A  CT  C__
GAM2002  LOC124944 5'  CGCAGTCGCTTAGACCGCTCG  48967     TC_   CCC      C
                                CGC   CGC   AGACCGC CG
                                |||   |||   ||||||| ||
                                GCG   GCG   TCTGGCG GC
                                  TCA   AA_      A
GAM2002  LOC144058 5'  CGCTCCGCCATGCGCTCGAC   48968       CCAGAC   C
                                CGCTCCGCC     CGC CGAC
                                |||||||||     ||| ||||
                                GCGAGGCGG     GCG GCTG
                                     TAC___   A
GAM2002  LOC146517 3'  TCCTTCCGCCCCAGGCAC    48969    GC       AC
                                TC  TCCGCCCCAG  CGC
                                ||  ||||||||||  |||
                                AG  AGGCGGGGTC  GTG
                                 GA        C_
GAM2002  LOC147817 5'  GCTTTGTCCCAAACCCCCG    48970     CCGC      G
                                GCT    CCCAGACC CCCG
                                |||    |||||||| ||||
                                CGA    GGGTTTGG GGGC
                                  AACA       _
GAM2002  LOC155382 5'  CCGCTCCGCTCCGCTCCG    48971        CCCAGA   _
                                TCGCTCCGC     CCGC CCG
                                |||||||||     |||| |||
                                GGCGAGGCG     GGCG GGC
                                     A_____    A
GAM2002  LOC221424 5'  TCGCCCCGCCCCCTGCCCG    48972          AGACC
                                TCGCTCCGCCCC    GCCCG
                                ||||||||||||    |||||
                                AGCGGGGCGGGG    CGGGC
                                       GA___
GAM2002  LOC221710 5'  CTCCGCCCCAGGCCC       48973          ACC
                                CTCCGCCCCAG   GCCC
                                ||||||||||   ||||
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                                GAGGCGGGGTC  CGGG
                                      ___
GAM2002 LOC256664 5' TCGGTCCGCCCCGGACCGACCT 48974    C      A   _ _
          CG                    TCG TCCGCCCC GACCG CC CG
                                ||| |||||||| ||||| || ||
                                AGC AGGCGGGG CTGGC GG GC
                                  C      C    T  A
GAM2002 LOC51246 5' TCGCCCCGCCCCGCCC     48975          AGACC
                                TCGCTCCGCCCC   GCCC
                                ||||||||||||   ||||
                                AGCGGGGCGGGG   CGGG
                                      ______
GAM2002 LOC93622 3' CGCTCCGCTCCAGACCCGCGCG 48976       C     _ C
                                CGCTCCGC CCAGACC GC CG
                                |||||||| ||||||| || ||
                                GCGAGGCG GGTCTGG CG GC
                                     A     G  C
GAM2003 ADRA2A   5' AGCGGCCCATGGCCCGGGTCCC 48979       CA_   ACG
                                AGCGGCCC  GCCCG  CCC
                                ||||||||  |||||  |||
                                TCGCCGGG  CGGGC  GGG
                                     TAC   CCA
GAM2003 ATF4     5' CAGCGGCCGCGCCCCGCCCAC  48980       CCA   GA
                                CAGCGGCC  GCCC  CGCCCAC
                                ||||||||  ||||  |||||||
                                GTCGCCGG  CGGG  GCGGGTG
                                     CG_   __
GAM2003 BACE2    5' CAGCGGCCCAGCCCCTCCC   48981       C    GACG
                                CAGCGGCCC AGCCC   CCC
                                ||||||||| |||||   |||
                                GTCGCCGGG TCGGG   GGG
                                     _    GA__
GAM2003 BACE2    5' CAGCGGCCCAGCCCCTCCC   48981       C    GACG
                                CAGCGGCCC AGCCC   CCC
                                ||||||||| |||||   |||
                                GTCGCCGGG TCGGG   GGG
                                     _    GA__
GAM2003 BACE2    5' CAGCGGCCCAGCCCCTCCC   48981       C    GACG
                                CAGCGGCCC AGCCC   CCC
                                ||||||||| |||||   |||
                                GTCGCCGGG TCGGG   GGG
                                     _    GA__
GAM2003 BDKRB2   3' CAGCAGCCCTGCTGGCGTTTGC 48982       CA  C__  AC_
                                CAGCGGCCC  GC   CG   GC
                                |||||||||  ||   ||   ||
                                GTCGTCGGG  CG   GC   CG
                                     A_  ACC  AAA
GAM2003 CACNA1C  3' ACCACTGCCGGCCCGACGCCCA 48983    G  C_  A
                                GC GC  CC GCCCGACGCCCA
                                || ||  || ||||||||||||
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                                TG TG  GG CGGGCTGCGGGT
                                 G  AC  C
GAM2003  CACNA1C   3'  GCGGCCCCGGCCCGGCGGCGC  48984        A    A___
                                GCGGCCCC GCCCG   CGC
                                |||||||| |||||   |||
                                CGCCGGGG CGGGC   GCG
                                     C    CGCC
GAM2003  CAPN7     5'  GCGGCCCCAGCGGCCC      48985          CCGAC
                                GCGGCCCCAGC    GCCC
                                ||||||||||    ||||
                                CGCCGGGGTCG    CGGG
                                      C____
GAM2003  CDC25A    5'  CACCGGCCTCGGCCGCGCGCC  48986    G    CCA  _  A
                                CA CGGCC   GCC CG CGCC
                                || |||||   ||| || ||||
                                GT GCCGG   CGG GC GCGG
                                 G    AGC   C  _
GAM2003  CDR2      5'  CAGCGGCCCCCGCCGCCGTCCC 48987         A  CGA  _
                                CAGCGGCCCC GCC   CG CCC
                                |||||||||| |||   || |||
                                GTCGCCGGGG CGG   GC GGG
                                      G   CG_  A
GAM2003  CSK       5'  CAGCGGCCTGCGGGACGGTCCA 48988        CCA  CC   C_
                                CAGCGGCC   GC  GACG  CCA
                                ||||||||   ||  ||||  |||
                                GTCGCCGG   CG  CTGC  GGT
                                     A__  CC   CA
GAM2003  DHFR      5'  CAGCGCCCCCAGCGCCC     48989      G      CCGAC
                                CAGCG CCCCAGC    GCCC
                                ||||| |||||||    ||||
                                GTCGC GGGGTCG    CGGG
                                   G     ______
GAM2003  DNM2      5'  GCGGCCCCCGGCCCGAGCGC   48990        A_     _
                                GCGGCCCC  GCCCGA CGC
                                ||||||||  |||||| |||
                                CGCCGGGG  CGGGCT GCG
                                     GC     C
GAM2003  EGLN2     5'  CAGCGGCCGCAGCTCACCAC   48991        C   C  A
                                CAGCGGCC CAGC CG CGC
                                |||||||| |||| || |||
                                GTCGCCGG GTCG GT GTG
                                     C   A  G
GAM2003  FBXL2     5'  CGGCGCCGGCGACGCCC     48992      C  A  CC
                                CGGC CC GC  GACGCCC
                                |||| || ||  |||||||
                                GCCG GG CG  CTGCGGG
                                  C  C  __
GAM2003  FBXW1B    5'  GCGGCCCCGGCGGCCCCGC   48993        A___   GA
                                GCGGCCCC   GCCC  CGC
                                ||||||||   ||||  |||
```

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                              CGCCGGGG   CGGG  GCG
                                  CCGC   __
GAM2003  FBXW1B   5'  GCGGCCCCGGCGGCCCCGC   48993       A___   GA
                              GCGGCCCC   GCCC  CGC
                              ||||||||   ||||  |||
                              CGCCGGGG   CGGG  GCG
                                  CCGC   __
GAM2003  FBXW1B   5'  GCGGCCCCGGCGGCCCCGC   48993       A___   GA
                              GCGGCCCC   GCCC  CGC
                              ||||||||   ||||  |||
                              CGCCGGGG   CGGG  GCG
                                  CCGC   __
GAM2003  FGFR1    5'  GCGCCTCCAGCCCGGGC    48994    G _     AC
                              GCG CC CCAGCCCG  GC
                              ||| || ||||||||  ||
                              CGC GG GGTCGGGC  CG
                                _ A      C_
GAM2003  FGFR1    5'  GCGCCTCCAGCCCGGGC    48994    G _     AC
                              GCG CC CCAGCCCG  GC
                              ||| || ||||||||  ||
                              CGC GG GGTCGGGC  CG
                                _ A      C_
GAM2003  FGFR1    5'  GCGCCTCCAGCCCGGGC    48994    G _     AC
                              GCG CC CCAGCCCG  GC
                              ||| || ||||||||  ||
                              CGC GG GGTCGGGC  CG
                                _ A      C_
GAM2003  FGFR1    5'  GCGCCTCCAGCCCGGGC    48994    G _     AC
                              GCG CC CCAGCCCG  GC
                              ||| || ||||||||  ||
                              CGC GG GGTCGGGC  CG
                                _ A      C_
GAM2003  FGFR1    5'  GCGCCTCCAGCCCGGGC    48994    G _     AC
                              GCG CC CCAGCCCG  GC
                              ||| || ||||||||  ||
                              CGC GG GGTCGGGC  CG
                                _ A      C_
GAM2003  FGFR1    5'  GCGCCTCCAGCCCGGGC    48994    G _     AC
                              GCG CC CCAGCCCG  GC
                              ||| || ||||||||  ||
                              CGC GG GGTCGGGC  CG
                                _ A      C_
GAM2003  FOXD2    5'  GCGGCCCGCCGGCGCCCA    48995      CA  C A
                              GCGGCCC  GCC G CGCCCA
                              |||||||  ||| | ||||||
                              CGCCGGG  CGG C GCGGGT
                                  __  _ C
GAM2003  GAS7     3'  CAGCAGTCCCAGCCCTGC    48996      C      GAC
                              CAGCGG CCCAGCCC   GC
                              |||||| ||||||||  ||
```

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                                GTCGTC GGGTCGGG   CG
                                   A       A__
GAM2003  GAS7     3'  CAGCAGTCCCAGCCCTGC    48996       C       GAC
                                CAGCGG CCCAGCCC   GC
                                |||||| ||||||||   ||
                                GTCGTC GGGTCGGG   CG
                                   A       A__
GAM2003  GNB2     5'  CAGTGGCCCCAGCCCCGC    48997     C         GA
                                CAG GGCCCCAGCCC  CGC
                                ||| ||||||||||  |||
                                GTC CCGGGGTCGGG  GCG
                                  A         __
GAM2003  HIP12    5'  GCAGCCCCAGCCTAGGCAC   48998           CGA_
                                GCGGCCCCAGCC    CGC
                                ||||||||||||    |||
                                CGTCGGGGTCGG    GTG
                                      ATCC
GAM2003  HNRPA2B1  5'  CAGTCGCTTCAGCCCGATTTCC 48999     CG  CC      CG_
              C                  CAG  GC  CAGCCCGA   CCC
                                |||  ||  ||||||||   |||
                                GTC  CG  GTCGGGCT   GGG
                                  AG  AA       AAA
GAM2003  HNRPA2B1  5'  CAGTCGCTTCAGCCCGATTTCC 48999     CG  CC      CG_
              C                  CAG  GC  CAGCCCGA   CCC
                                |||  ||  ||||||||   |||
                                GTC  CG  GTCGGGCT   GGG
                                  AG  AA       AAA
GAM2003  HS3ST3A1  5'  CAGCGGCCCCCGCCACTCTGC  49000         A  CGAC_
                                CAGCGGCCCC GCC    GC
                                |||||||||| |||    ||
                                GTCGCCGGGG CGG    CG
                                      G  TGAGA
GAM2003  HTRA3    3'  CAGCAGCCCTGGCCCTAC    49001         CA   G
                                CAGCGGCCC  GCCC AC
                                |||||||||  |||| ||
                                GTCGTCGGG  CGGG TG
                                      AC   A
GAM2003  HYOU1    3'  CAGCAGCCCTAGCTCCTGC   8228          C  _  GAC
                                CAGCGGCCC AGC CC   GC
                                |||||||| ||| ||   ||
                                GTCGTCGGG TCG GG   CG
                                      A  A  A__
GAM2003  LASS1    3'  CAGCGGTGCCAGCCCACCTCGC 49002       CC       A__
                                CAGCGG  CCAGCCCG   CGC
                                ||||||  ||||||||   |||
                                GTCGCC  GGTCGGGT   GCG
                                   AC       GGA
GAM2003  LMO4     5'  GCGGCCCCCGCCCCCGCCC   49003         A   GA
                                GCGGCCCC GCCC  CGCCC
                                |||||||| ||||  |||||
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                                CGCCGGGG CGGG  GCGGG
                                     G   G_
GAM2003  M11S1    5'  GCGGCCCCGGCTCCCGC     49004        A  _  GA
                                GCGGCCCC GC CC  CGC
                                |||||||| || ||  |||
                                CGCCGGGG CG GG  GCG
                                     C  A  __
GAM2003  MAP3K7IP1 3'  CAGCGGCCCCTGCCTCAGCCCA 49005          A  _  AC
              C                  CAGCGGCCCC GCC CG  GCCCAC
                                 |||||||||| ||| ||  ||||||
                                 GTCGCCGGGG CGG GT  CGGGTG
                                      A  A  __
GAM2003  MAPK3    5'  GCGGCCCCGCCCGAGGCCC   32484        A     C
                                GCGGCCCC GCCCGA GCCC
                                |||||||| |||||| ||||
                                CGCCGGGG CGGGCT CGGG
                                     _     C
GAM2003  MEN1     5'  GCGGCCCCTGCCCCGC     49006        A    GA
                                GCGGCCCC GCCC  CGC
                                |||||||| ||||  |||
                                CGCCGGGG CGGG  GCG
                                     A   __
GAM2003  MEN1     5'  GCGGCCCCTGCCCCGC     49006        A    GA
                                GCGGCCCC GCCC  CGC
                                |||||||| ||||  |||
                                CGCCGGGG CGGG  GCG
                                     A   __
GAM2003  MGAT2    5'  CAGCGGCCCTGCGTCCTCTGC  49007         CA  __  GAC
                                CAGCGGCCC  GC  CC   GC
                                |||||||||  ||  ||   ||
                                GTCGCCGGG  CG  GG   CG
                                      A_  CA  AGA
GAM2003  MSF      3'  AGCAGCCAGCCCGGTGCC    49008        CC     AC
                                AGCGGCC  AGCCCG  GCC
                                |||||||  ||||||  |||
                                TCGTCGG  TCGGGC  CGG
                                     __     CA
GAM2003  MYL5     5'  CAGGGCCCCAGGTCTTGCCCA  49009     C       CCCGAC
                                CAG GGCCCCAG     GCCCA
                                ||| ||||||||     |||||
                                GTC CCGGGGTC     CGGGT
                                  _       CAGAA_
GAM2003  NRXN2    5'  GCGGCCCCGGCCCCGC      49010        A    GA
                                GCGGCCCC GCCC  CGC
                                |||||||| ||||  |||
                                CGCCGGGG CGGG  GCG
                                     C   __
GAM2003  NRXN2    5'  GCGGCCCCGGCCCCGC      49010        A    GA
                                GCGGCCCC GCCC  CGC
                                |||||||| ||||  |||
```

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                                CGCCGGGG CGGG  GCG
                                    C   __
GAM2003  PDE4A    5'  CAGCAGCCCTGGTTACATGGCC 49011        _______ __
                CG                  CAGCGGCCC    CA  GCCCG
                                    |||||||||    ||  |||||
                                    GTCGTCGGG    GT  CGGGC
                                       ACCAAT  AC
GAM2003  PGF      3'  GCGGCCCCAGCAGGATCCGC  49012          CC  __
                                    GCGGCCCCAGC  GA  CGC
                                    ||||||||||  ||  |||
                                    CGCCGGGGTCG  CT  GCG
                                          TC  AG
GAM2003  POLS     3'  AGCGGTCCCGGCCCCAACGC  49013      C   A   _
                                    AGCGG CCC GCCC GACGC
                                    ||||| ||| |||| |||||
                                    TCGCC GGG CGGG TTGCG
                                       A  C   G
GAM2003  POU2AF1  5'  CAGCGGCCCCGGCCCAGAGCGC 49014          A   _ _
                                    CAGCGGCCCC GCCC GA CGC
                                    |||||||||| |||| || |||
                                    GTCGCCGGGG CGGG CT GCG
                                          C   T  C
GAM2003  POU3F2   5'  CAGCGGGCAGCTCCGACGCCC  49015       CCC   _
                                    CAGCGG   CAGC CCGACGCCC
                                    ||||||   |||| |||||||||
                                    GTCGCC   GTCG GGCTGCGGG
                                       C__   A
GAM2003  PPP5C    5'  CAGCGGCACCCGGCCGAACC   49016       _  A   C  C
                                    CAGCGGC CCC GCC GA GCC
                                    ||||||| ||| ||| || |||
                                    GTCGCCG GGG CGG CT TGG
                                       T   C   _ _
GAM2003  PRKAR2A  5'  ACGGCCCCGGCTCACGTCGC   49017        A  C__  A
                                    GCGGCCCC GC   CG CGC
                                    |||||||| ||   || |||
                                    TGCCGGGG CG   GC GCG
                                       C  AGT  A
GAM2003  PRKCABP  3'  GCGGCCCCGCCCCGC       49018        A   GA
                                    GCGGCCCC GCCC  CGC
                                    |||||||| ||||  |||
                                    CGCCGGGG CGGG  GCG
                                       _   __
GAM2003  PRSS8    3'  GGCCCCAGCCCAGAACAC    49019          __
                                    GGCCCCAGCCC  GACGC
                                    ||||||||||  |||||
                                    CCGGGGTCGGG  TTGTG
                                          TC
GAM2003  RAB3A    3'  CAGCGGCCTCGGCCCACCGC  49020        CCA    A
                                    CAGCGGCC   GCCCG CGC
                                    ||||||||   ||||| |||
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                                GTCGCCGG  CGGGT GCG
                                    AGC    G
GAM2003  RAB4A    3'  AGCGGCCCCAGCTTACA    49021          CCG
                                AGCGGCCCCAGC  ACG
                                ||||||||||||  |||
                                TCGCCGGGGTCG  TGT
                                      AA_
GAM2003  RHBDL    3'  CAGCAGCCCTGAGACGTCC   49022        CAGCCC   C
                                CAGCGGCCC    GACG CC
                                |||||||||    |||| ||
                                GTCGTCGGG    CTGC GG
                                    ACT___   A
GAM2003  SLC7A5   3'  CAGCGGCCCCAGCCATTTCAC  49023           CGA_
                                CAGCGGCCCCAGCC   CGC
                                ||||||||||||||   |||
                                GTCGCCGGGGTCGG   GTG
                                      TAAA
GAM2003  SLC9A5   5'  CAGCGGCCGCCGGCCCGCGTCC 49024        _ A    A C
                                CAGCGGCC CC GCCCG CG CC
                                |||||||| || ||||| || ||
                                GTCGCCGG GG CGGGC GC GG
                                    C C    _ A
GAM2003  SOLH     5'  GCGGCCCCGGCCCCCGGGCCC  49025        A   GAC_
                                GCGGCCCC GCCC   GCCC
                                |||||||| ||||   ||||
                                CGCCGGGG CGGG   CGGG
                                    C   GGCC
GAM2003  TCL1B    3'  CAGGGCCCCAGTGAAGCCCA  49026    C      CCC  C
                                CAG GGCCCCAG   GA GCCCA
                                ||| ||||||||   || |||||
                                GTC CCGGGGTC   CT CGGGT
                                  _      A__  T
GAM2003  TFEB     3'  GCAGCCCCCGCGCTCA     49027        AGCC  A   C
                                GCGGCCCC   CG CGC CA
                                ||||||||   || ||| ||
                                CGTCGGGG   GC GCG GT
                                    _____  _   A
GAM2003  TJP1     5'  GCTGCCCCAGCAACTCCCAC  49028    G      CC   G
                                GC GCCCCAGC  GAC CCCAC
                                || ||||||||  ||| |||||
                                CG CGGGGTCG  TTG GGGTG
                                 A       __  A
GAM2003  TSSC4    3'  CAGTGCTTCCAGCCCACACCC  49029    CG  C_     G
                                CAG  GC  CCAGCCC ACGCCC
                                |||  ||  ||||||| ||||||
                                GTC  CG  GGTCGGG TGTGGG
                                  A_  AA      _
GAM2003  VENTX2   3'  CAGGGCCCCAGCATCCTCGC  49030     C       __  GA
                                CAG GGCCCCAGC  CC  CGC
                                ||| |||||||||  ||  |||
```

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                                GTC CCGGGGTCG  GG  GCG
                                  _       TA  A_
GAM2003  ZNF26    5'  GGCCATCCCCACGCCCAC    49031     CCAG   G
                                GGCC    CCC ACGCCCAC
                                ||||    ||| ||||||||
                                CCGG    GGG TGCGGGTG
                                  TA__   G
GAM2003  ZNF76    5'  GCCGGCCCCACAACCCGCCTGC 49032    _     __    AC_
                                GC GGCCCCA  GCCCG   GC
                                || |||||||  |||||   ||
                                CG CCGGGGT  TGGGC   CG
                                 G      GT    GGA
GAM2003  BM036    5'  CAGCGGCCTACACCGTCCA   49033        CCA  _   ACGC
                                CAGCGGCC   GC CCG    CCA
                                ||||||||   || |||    |||
                                GTCGCCGG   TG GGC    GGT
                                     A__  T   A___
GAM2003  BNIP-S   5'  GGTTGTCCCAGCCCCCAACAC  49034    C___      __
                                GG    CCCAGCCC  GACGC
                                ||    ||||||||  |||||
                                CC    GGGTCGGG  TTGTG
                                 AACA       GG
GAM2003  CHST3    5'  GCGGCCCCGACCCTCCGC    49035        A    GA
                                GCGGCCCC GCCC  CGC
                                |||||||| ||||  |||
                                CGCCGGGG TGGG  GCG
                                     C    AG
GAM2003  CRR9     5'  GCGCCCCCGGCCCGCCCGC    49036     G    A    A_
                                GCG CCCC GCCCG  CGC
                                ||| |||| |||||  |||
                                CGC GGGG CGGGC  GCG
                                  G    C     GG
GAM2003  DDX34    3'  CAGTGCTCCCAGCCCCCC    49037     CG  _      GACG
                                CAG  GC CCCAGCCC    CCC
                                |||  || ||||||||    |||
                                GTC  CG GGGTCGGG    GGG
                                  A_  A       _____
GAM2003  DKFZP434M154 5'  AGCGGTCCTGGCCCGACAC    49038       C  CA
                                AGCGG CC  GCCCGACGC
                                ||||| ||  |||||||||
                                TCGCC GG  CGGGCTGTG
                                   A  AC
GAM2003  DKFZp762K222 5'  CAGCTGCCCCAGCCTGGAGC   49039      G        C_  C
                                CAGC GCCCCAGCC  GA GC
                                |||| |||||||||  || ||
                                GTCG CGGGGTCGG  CT CG
                                  A        AC  _
GAM2003  DPP8     5'  CAGCGGCCTTGGCCTCGGAGGC 49040         CCA   _  AC_
                                CAGCGGCC   GCC CG   GC
                                ||||||||   ||| ||   ||
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                                GTCGCCGG  CGG GC  CG
                                    AAC  A  CTC
GAM2003  DXS1357E  5'  CAGCAGCCCCGGCCCCGC   49041        A   GA
                                CAGCGGCCCC GCCC  CGC
                                |||||||||| ||||  |||
                                GTCGTCGGGG CGGG  GCG
                                    C   __
GAM2003  FLJ10206  5'  AGCGGCCCGAGCCTGCGC   49042       C   CGA
                                AGCGGCCC AGCC  CGC
                                |||||||| ||||  |||
                                TCGCCGGG TCGG  GCG
                                    C   AC_
GAM2003  FLJ10811  5'  AGCGTCCCCAGCCGAGCTCA  49043     G      C  C  C
                                AGCG CCCCAGCC GA GC CA
                                |||| |||||||| || || ||
                                TCGC GGGGTCGG CT CG GT
                                  A      _ _ A
GAM2003  FLJ11370  3'  CAGCGGCCTCATGACCTGC   49044       C __  CGAC
                                CAGCGGCC CA  GCC   GC
                                |||||||| ||  |||   ||
                                GTCGCCGG GT  TGG   CG
                                    A  AC  A___
GAM2003  FLJ12355  5'  CACCGGCCCCAGCCCCGC   49045   G        GA
                                CA CGGCCCCAGCCC  CGC
                                || ||||||||||||  |||
                                GT GCCGGGGTCGGG  GCG
                                 G         __
GAM2003  FLJ12517  3'  CAGCGGCCCCAGTTGATGCC  49046         CCC  C
                                CAGCGGCCCCAG  GA GCC
                                ||||||||||||  || |||
                                GTCGCCGGGGTC  CT CGG
                                      AA_  A
GAM2003  FLJ12610  5'  CAGCGGCCGCGAGAGCGCCCAC 49047       CCA  CC  _
                                CAGCGGCC  GC  GA CGCCCAC
                                ||||||||  ||  || |||||||
                                GTCGCCGG  CG  CT GCGGGTG
                                    ___  CT  C
GAM2003  FLJ12768  3'  CAGCGTCCCAGCCCAGC    49048      GC       AC
                                CAGCG  CCCAGCCCG  GC
                                |||||  |||||||||  ||
                                GTCGC  GGGTCGGGT  CG
                                  A_       __
GAM2003  FLJ13881  5'  GCGGCCCCGCTCCAGCCGATCC 49049       A  _  A_  C_
           AC                   GCGGCCCC GC CCG  CG  CCAC
                                |||||||| || |||  ||  ||||
                                CGCCGGGG CG GGT  GC  GGTG
                                    _ A  CG  TA
GAM2003  FLJ14251  3'  CAGTGACCCCAGCTTTTCAC  49050    C       CCGA
                                CAG GGCCCCAGC   CGC
                                ||| |||||||||   |||
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                                GTC CTGGGGTCG    GTG
                                  A        AAAA
GAM2003  FLJ14775  5'  GCGGCCGCCACGCCCA      49051       CCA   CG
                                GCGGCC   GCC  ACGCCCA
                                ||||||   |||  |||||||
                                CGCCGG   CGG  TGCGGGT
                                   ____   __
GAM2003  FLJ20542  3'  CAGCAGCCCCAGCGAGATGCCT 49052            CC  C   C
              AC                    CAGCGGCCCCAGC  GA GCC AC
                                    ||||||||||||  || ||| ||
                                    GTCGTCGGGGTCG  CT CGG TG
                                           CT  A   A
GAM2003  FLJ22378  3'  CAGCGTCCCAGCCCCAC     49053       GC       G
                                    CAGCG  CCCAGCCC AC
                                    |||||  ||||||||  ||
                                    GTCGC  GGGTCGGG TG
                                       A_       G
GAM2003  FLJ22551  5'  ACGGCCCCAGCCCGGCGAACA  49054             A  CC
                                    GCGGCCCCAGCCCG CG  CA
                                    ||||||||||||||  ||  ||
                                    TGCCGGGGTCGGGC GC  GT
                                           C  TT
GAM2003  FLJ23436  5'  GCGGCCCAGCCCGGGC      49055        C     AC
                                    GCGGCCC AGCCCG  GC
                                    |||||||  ||||||  ||
                                    CGCCGGG TCGGGC  CG
                                       _     C_
GAM2003  GMPPB     5'  CAGCGGCCGTAGCCGCGTCCCA 49056         CC    C A  _
                                    CAGCGGCC  AGCC G CG CCCA
                                    ||||||||  |||| | || ||||
                                    GTCGCCGG  TCGG C GC GGGT
                                         CA   _ _  A
GAM2003  GTSE1     3'  GCTGGCCCCAGTCCCTCAGCCC 49057    _       _   GAC
              AC                    GC GGCCCCAG CCC   GCCCAC
                                    || ||||||||  |||   ||||||
                                    CG CCGGGGTC GGG   CGGGTG
                                     A       A   AGT
GAM2003  HIC2      5'  CAGCGGCCCTTGTCCTCAGCGC 49058          CAG_  _  A
                                    CAGCGGCCC    CC CG CGC
                                    |||||||||    || || |||
                                    GTCGCCGGG    GG GT GCG
                                         AACA  A  C
GAM2003  HIC2      3'  CAGCGGCCCAGCCCGGATCGC  49059         C     A__
                                    CAGCGGCCC AGCCCG   CGC
                                    |||||||||  ||||||   |||
                                    GTCGCCGGG TCGGGC   GCG
                                         _     CTA
GAM2003  KCNJ9     3'  GGCCCCAGCCTTCTGATCAC   49060         C___  _
                                    GGCCCCAGCC    GA CGC
                                    ||||||||||    || |||
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                                CCGGGGTCGG   CT GTG
                                     AAGA  A
GAM2003  KIAA0063  3'  CAGTGGCCCCAAGGTCCTGC  49061    C      C__  GAC
                                CAG GGCCCCAG  CC  GC
                                ||| ||||||||  ||  ||
                                GTC CCGGGGTT  GG  CG
                                  A       CCA  A__
GAM2003  KIAA0089  5'  GCGGCCCCGCCCCTTTCGC   49062       A   GA__
                                GCGGCCCC GCCC   CGC
                                |||||||| ||||   |||
                                CGCCGGGG CGGG   GCG
                                     _   GAAA
GAM2003  KIAA0140  3'  GGCCCCAGCCCCTGGGCCC   49063         GAC_
                                GGCCCCAGCCC   GCCC
                                ||||||||||   ||||
                                CCGGGGTCGGG   CGGG
                                      GACC
GAM2003  KIAA0427  3'  CAGGGCCCCAGCTGCCC    49064    C       CCGAC
                                CAG GGCCCCAGC    GCCC
                                ||| |||||||||    ||||
                                GTC CCGGGGTCG    CGGG
                                  _       A____
GAM2003  KIAA0475  5'  GCGGCCCCGGCCGCCC     49065       A  CGAC
                                GCGGCCCC GCC   GCCC
                                |||||||| |||   ||||
                                CGCCGGGG CGG   CGGG
                                     C  ____
GAM2003  KIAA0534  5'  GCGGCCCCGCCTCGCCC    49066       A  CGA
                                GCGGCCCC GCC  CGCCC
                                |||||||| |||  |||||
                                CGCCGGGG CGG  GCGGG
                                     _  A__
GAM2003  KIAA0537  5'  GCTTTGGCCCCGGCCCCCGC  49067   ___    A   GA
                                GC  GGCCCC GCCC  CGC
                                ||  |||||| ||||  |||
                                CG  CCGGGG CGGG  GCG
                                 AAA    C   G_
GAM2003  KIAA0557  3'  CAGCGGCCTCACTTGTTGATCA 49068       C  GCCC__  _
            C                    CAGCGGCC CA     GA CGC
                                ||||||||  ||     || |||
                                GTCGCCGG GT     CT GTG
                                     A  GAACAA  A
GAM2003  KIAA0711  3'  CAGCGGCCCCGACTCCCCA   49069        AGCCC  G_
                                CAGCGGCCCC    GAC  CCCA
                                ||||||||||    |||  ||||
                                GTCGCCGGGG    CTG  GGGT
                                      _____  AG
GAM2003  KIAA0790  5'  GCGGCCCCGGCCACCCC    49070       A  CG  G
                                GCGGCCCC GCC  AC CCC
                                |||||||| |||  || |||
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                                CGCCGGGG CGG  TG GGG
                                     C  __ _
GAM2003  KIAA1183  3'  CAGCGGCCTACAGCACCTGC  49071       C_   _ GAC
                                CAGCGGCC  CAGC CC   GC
                                ||||||||  |||| ||   ||
                                GTCGCCGG  GTCG GG   CG
                                     AT    T  A__
GAM2003  KIAA1196  3'  CAGTAGCCCCCACGCCA    49072    CG    AGCC G    C
                                CAG  GCCCC    C ACGCC A
                                |||  |||||    | |||||  |
                                GTC  CGGGG    G TGCGG T
                                  AT    _____ _    A
GAM2003  KIAA1303  3'  CAGCGGCCCCCTGCTGACAGC  49073        A  CC  _
                                CAGCGGCCCC GC  GAC GC
                                ||||||||||  ||  |||  ||
                                GTCGCCGGGG CG  CTG CG
                                      A  A_   T
GAM2003  KIAA1458  5'  GCTGGCCCCAGCCGAACTGC  49074   _       C  _
                                GC GGCCCCAGCC GAC GC
                                ||  ||||||||||  |||  ||
                                CG CCGGGGTCGG TTG CG
                                 A         C   A
GAM2003  KIAA1494  5'  GCGGCCCCACCGCGC      49075        GC   A
                                GCGGCCCCA  CCG CGC
                                |||||||||  |||  |||
                                CGCCGGGGT  GGC GCG
                                           __  _
GAM2003  KIAA1691  3'  AGCGGCCCCAGCCGTGCC    49076           CGAC
                                AGCGGCCCCAGCC    GCC
                                ||||||||||||||    |||
                                TCGCCGGGGTCGG    CGG
                                       CA__
GAM2003  MAPKAPK3  5'  GCGGCCCCAGCCTGGCGC    49077           CGA
                                GCGGCCCCAGCC   CGC
                                ||||||||||||   |||
                                CGCCGGGGTCGG   GCG
                                       ACC
GAM2003  MGC11257  3'  CAGCGGCCCCGCCCCGC     49078         A   GA
                                CAGCGGCCCC GCCC  CGC
                                |||||||||| ||||  |||
                                GTCGCCGGGG CGGG  GCG
                                          _   __
GAM2003  MGC13114  3'  CAGTGCTCCCAGCCCCAC    49079     CG  _      G
                                CAG  GC CCCAGCCC AC
                                |||  ||  |||||||| ||
                                GTC  CG GGGTCGGG TG
                                  A_  A       G
GAM2003  MGC14421  5'  CAGGGCCCCAGCGCCC      49080     C       CCGAC
                                CAG GGCCCCAGC    GCCC
                                ||| |||||||||    ||||
```

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                                GTC CCGGGGTCG    CGGG
                                  _      _____
GAM2003 MGC14839 3' AGCGGCCCCGCACCTGC     49081         A _ GAC
                                AGCGGCCCC GC CC   GC
                                ||||||||| || ||   ||
                                TCGCCGGGG CG GG   CG
                                     _ T  A__
GAM2003 MGC16703 5' GCGGCGCCAGCCCACCTCCCAC 49082       C       ACG
                                GCGGC CCAGCCCG   CCCAC
                                ||||| ||||||||   |||||
                                CGCCG GGTCGGGT   GGGTG
                                   C       GGA
GAM2003 MGC1842  5' GCGGCCCCGCTGCCTCCGC   49083         A __ GA
                                GCGGCCCC GC  CC  CGC
                                |||||||| ||  ||  |||
                                CGCCGGGG CG  GG  GCG
                                     _ AC  AG
GAM2003 MGC23280 5' GCGGCCCCGCAGGTTGCCCA  49084         A  CCGAC
                                GCGGCCCC GC    GCCCA
                                |||||||| ||    |||||
                                CGCCGGGG CG    CGGGT
                                     _ TCCAA
GAM2003 MGC2817  5' CAGCGGCCGCCGGCTCCCCCCG 49085         _ AG__   GA
           C                     CAGCGGCC CC    CCC  CGC
                                |||||||| ||    |||  |||
                                GTCGCCGG GG    GGG  GCG
                                     C  CCGA   GG
GAM2003 MGC29898 5' CAGCGGCCCTAGCCCCAC    49086         C    G
                                CAGCGGCCC AGCCC AC
                                ||||||||| ||||| ||
                                GTCGCCGGG TCGGG TG
                                     A    G
GAM2003 MGC5306  5' CAGTGGCCCCAACCGCGCAC  49087     C        _ A
                                CAG GGCCCCAGCC CG CGC
                                ||| |||||||||| || |||
                                GTC CCGGGGTTGG GC GTG
                                  A        C _
GAM2003 MRPL41   5' AGCGGCCCCGGCTCCGGCGC  49088         A _  A
                                AGCGGCCCC GC CCG CGC
                                ||||||||| || ||| |||
                                TCGCCGGGG CG GGC GCG
                                     C  A   C
GAM2003 NECL1    3' TGACGGCCCCAGCAGTCCCCAC 49089    A         CCGACG
                                C GCGGCCCCAGC     CCCAC
                                | ||||||||||     |||||
                                A TGCCGGGGTCG     GGGTG
                                 C          TCAG__
GAM2003 PIGQ     3' CAGCAGCCTGGCGATGCTCAC  49090         CCAGCC   C  C
                                CAGCGGCC     CGA GC CAC
                                ||||||||     ||| || |||
```

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                                GTCGTCGG     GCT CG GTG
                                     ACC___   A  A
GAM2003  PIP5K2A   5'  GCGGCCCCGGCGCGCCGC    49091        A  C  A
                                GCGGCCCC GC CG CGC
                                |||||||| || || |||
                                CGCCGGGG CG GC GCG
                                     C  C  G
GAM2003  PPAP2C    5'  GCCGGTCCCAGCGCGTCCC   49092    _ C     C  ACG
                                GC GG CCCAGC CG   CCC
                                || || |||||| ||   |||
                                CG CC GGGTCG GC   GGG
                                 G  A     C  A__
GAM2003  PRDM15    3'  GCGGCCCCGGCCCAGGAC    49093        A   __
                                GCGGCCCC GCCC  GAC
                                |||||||| ||||  |||
                                CGCCGGGG CGGG  CTG
                                     C    TC
GAM2003  PRO0082   3'  CAGTGGCCCAGCACATTCCA   49094     C    C   C  ACGC
                                CAG GGCCC AGC CG    CCA
                                ||| ||||| ||| ||    |||
                                GTC CCGGG TCG GT    GGT
                                  A    _   T  AA__
GAM2003  Rab11-FIP3 3'  GCGGCCCCAGCTCAGCTGC    49095          C  AC_
                                GCGGCCCCAGC CG   GC
                                |||||||||| ||   ||
                                CGCCGGGGTCG GT   CG
                                       A  CGA
GAM2003  RISC      3'  CAGCGGCCTCAGCTCAGC     49096        C    C  AC
                                CAGCGGCC CAGC CG  GC
                                |||||||| |||| ||  ||
                                GTCGCCGG GTCG GT  CG
                                     A   A  __
GAM2003  RNASE6PL  5'  CAGCGACCCCAGCTCCTCCAC  49097           _  GA
                                CAGCGGCCCCAGC CC  CGC
                                |||||||||||| ||  |||
                                GTCGCTGGGGTCG GG  GTG
                                       A  AG
GAM2003  SEC15B    5'  CAGCCGCCCCAGCCTCTGGC   49098     G       CGAC
                                CAGC GCCCCAGCC    GC
                                |||| |||||||||    ||
                                GTCG CGGGGTCGG    CG
                                  G        AGAC
GAM2003  SLC21A11  5'  GCGCCCCAGCGGATCTCGCCC  49099     G      CCGA__
                                GCG CCCCAGC     CGCCC
                                ||| |||||||     |||||
                                CGC GGGGTCG     GCGGG
                                  _      CCTAGA
GAM2003  TCEA2     5'  CAGCGACCCCCGCGCCC     49100          AGCC  A
                                CAGCGGCCCC    CG CGCCC
                                ||||||||||    || |||||
```

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                                GTCGCTGGGG   GC GCGGG
                                     ____ _
GAM2003 WIT-1    3' CAGCGGCTCCAGGCACTGC   49101      C   CC  AC
                                CAGCGGC CCAG  CG  GC
                                ||||||| ||||  ||  ||
                                GTCGCCG GGTC  GT  CG
                                    A   C_ GA
GAM2003 YME1L1   5' CAGCGACCTCACCCGCCTGC  49102       CCA    AC_
                                CAGCGGCC  GCCCG  GC
                                ||||||||  |||||  ||
                                GTCGCTGG  TGGGC  CG
                                    AG_   GGA
GAM2003 YME1L1   5' CAGCGACCTCACCCGCCTGC  49102       CCA    AC_
                                CAGCGGCC  GCCCG  GC
                                ||||||||  |||||  ||
                                GTCGCTGG  TGGGC  CG
                                    AG_   GGA
GAM2003 YME1L1   5' CAGCGACCTCACCCGCCTGC  49102       CCA    AC_
                                CAGCGGCC  GCCCG  GC
                                ||||||||  |||||  ||
                                GTCGCTGG  TGGGC  CG
                                    AG_   GGA
GAM2003 ZNF258   3' CAGCAGTTCCAGAAAGCCCAC 49103     CC   CCC  C
                                CAGCGG  CCAG  GA GCCCAC
                                ||||||  ||||  || ||||||
                                GTCGTC  GGTC  TT CGGGTG
                                   AA   ___  T
GAM2003 LOC112616 5' GCGGCCCCAGCTCGCCC    49104        CCGA
                                GCGGCCCCAGC   CGCCC
                                ||||||||||   |||||
                                CGCCGGGGTCG   GCGGG
                                     A___
GAM2003 LOC124460 3' CAGCGGCCTCAGGCTCAGGGCC 49105       C  _ C  AC
                                CAGCGGCC CAG C CG  GCC
                                |||||||| ||| | ||  |||
                                GTCGCCGG GTC G GT  CGG
                                    A  C A  CC
GAM2003 LOC125943 5' GACCCCAGCTCTCGAAGTCAC  49106       C__  ___
                                GGCCCCAGC  CGA  CGC
                                |||||||||  |||  |||
                                CTGGGGTCG  GCT  GTG
                                    AGA  TCA
GAM2003 LOC126123 5' ACGGCCCCGGCGCGCGCC   49107       A  C  A
                                GCGGCCCC GC CG CGCC
                                |||||||| || || ||||
                                TGCCGGGG CG GC GCGG
                                    C  C  _
GAM2003 LOC126299 5' GCGGCCCCCGCTCCGGC    49108       A  _  AC
                                GCGGCCCC GC CCG  GC
                                |||||||| || |||  ||
```

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                                CGCCGGGG CG GGC  CG
                                    G  A  __
GAM2003  LOC126364 5'  CAGCGGCCACGGCCAGCACCGT 49109        ____   _  A_
                CCGC                CAGCGGCC   CCAGC CCG  CGC
                                    ||||||||   ||||| |||  |||
                                    GTCGCCGG   GGTCG GGC  GCG
                                       TGCC    T   AG
GAM2003  LOC138307 5'  CGGCCCTGGTGACACCCAC   49110       CAGCCC
                                    CGGCCC     GACGCCCAC
                                    ||||||     |||||||||
                                    GCCGGG     CTGTGGGTG
                                      ACCA__
GAM2003  LOC145853 5'  CAGCGGCCCCGTGGCCTCCCGC 49111          A__  CGA
                                    CAGCGGCCCC   GCC   CGC
                                    ||||||||||   |||   |||
                                    GTCGCCGGGG   CGG   GCG
                                         CAC   AGG
GAM2003  LOC146174 5'  CAGCGGCCTCACGCCTCCCGC  49112        C  _  CGA
                                    CAGCGGCC CA GCC   CGC
                                    |||||||| || |||   |||
                                    GTCGCCGG GT CGG   GCG
                                       A  G   AGG
GAM2003  LOC150481 3'  CAGTGGATCCTGGCCCCCCAC  49113     C  CC  A_   GACG
                                    CAG GG  CC  GCCC    CCCAC
                                    ||| ||  ||  ||||    |||||
                                    GTC CC  GG  CGGG    GGGTG
                                      A  TA  AC   _____
GAM2003  LOC154881 5'  GCGGCCCCGGGCACTCCC    49114        A_  CCG  G
                                    GCGGCCCC  GC   AC CCC
                                    ||||||||  ||   || |||
                                    CGCCGGGG  CG   TG GGG
                                       CC  ___  A
GAM2003  LOC157355 3'  AGTGGTCCCAGCCCTTCAC   49115    C  C       GA
                                    AG GG CCCAGCCC  CGC
                                    || || ||||||||  |||
                                    TC CC GGGTCGGG  GTG
                                     A  A       AA
GAM2003  LOC158125 5'  GGCCCCAGCCCCTCAACG    49116          ___
                                    GGCCCCAGCCC   GACG
                                    ||||||||||   ||||
                                    CCGGGGTCGGG   TTGC
                                          GAG
GAM2003  LOC162022 5'  CAGTGGCTCGGGCCCCACGCCC 49117     C   CCCA   G
                CAC                   CAG GGC    GCCC ACGCCCAC
                                    |||  |||    |||| ||||||||
                                    GTC CCG    CGGG TGCGGGTG
                                      A   AGCC    G
GAM2003  LOC163126 5'  GCTGCCCTGGCCAACGCC    49118    G    CA   C
                                    GC GCCC  GCC GACGCC
                                    || ||||  ||| ||||||
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                                CG CGGG  CGG TTGCGG
                                 A   AC  _
GAM2003  LOC164121 5'  GCTCTCCAGCCCGACGCCCAC  49119   GGCC
                                GC   CCAGCCCGACGCCCAC
                                ||   ||||||||||||||||
                                CG   GGTCGGGCTGCGGGTG
                                 AGA_
GAM2003  LOC165246 5'  CAGCAGCCCCAGCCACTCCA  49120          CG  GC
                                CAGCGGCCCCAGCC  AC  CCA
                                ||||||||||||||  ||  |||
                                GTCGTCGGGGTCGG  TG  GGT
                                       __  A_
GAM2003  LOC166219 5'  CAGCAGCCCCAGCGCGCCC   49121          CC A
                                CAGCGGCCCCAGC  G CGCCC
                                ||||||||||||||  | |||||
                                GTCGTCGGGGTCG  C GCGGG
                                       __ _
GAM2003  LOC170095 5'  GCGGCCCCAGCCCGGGC    49122          AC
                                GCGGCCCCAGCCCG  GC
                                ||||||||||||||  ||
                                CGCCGGGGTCGGGC  CG
                                       C_
GAM2003  LOC200226 5'  CAGCAGCCCCGCGCC      49123        A  CCGAC  C
                                CAGCGGCCCC GC    GC C
                                |||||||||| ||    || |
                                GTCGTCGGGG CG    CG G
                                     _ _____  A
GAM2003  LOC200779 5'  CAGCGGCCGCAGAAAGCCCAC  49124       C   CCC  C
                                CAGCGGCC CAG   GA GCCCAC
                                |||||||| |||   || ||||||
                                GTCGCCGG GTC   TT CGGGTG
                                    C   ___  T
GAM2003  LOC205418 5'  CAGCGGCCCCGGGCTCTCTCTC 49125        A_  CCGACGC
           CAC                   CAGCGGCCCC  GC     CCAC
                                |||||||||  ||     ||||
                                GTCGCCGGGG  CG     GGTG
                                     CC  AGAGAGA
GAM2003  LOC205418 5'  CAGCGGCCCCGGGCTCTCTCTC 49125        A_  CCGACGC
           CAC                   CAGCGGCCCC  GC     CCAC
                                |||||||||  ||     ||||
                                GTCGCCGGGG  CG     GGTG
                                     CC  AGAGAGA
GAM2003  LOC220686 5'  CAGCGGCCCTTGTCCTCAGCGC 49058        CAG_  _  A
                                CAGCGGCCC   CC CG CGC
                                |||||||||   || || |||
                                GTCGCCGGG   GG GT GCG
                                     AACA  A  C
GAM2003  LOC221421 5'  CAGCGGCTCCGCTCAACGC   49126       C  A  C
                                CAGCGGC CC GC CGACGC
                                ||||||| || || ||||||
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                                GTCGCCG GG CG GTTGCG
                                    A  _  A
GAM2003  LOC256158 5'  AGCGGCCCCGGCTCCAAGCAC  49127        A  _   _
                                AGCGGCCCC GC CCGA CGC
                                ||||||||| || |||| |||
                                TCGCCGGGG CG GGTT GTG
                                    C  A   C
GAM2003  LOC90362  5'  CAGCGGCCGCAGCAGCGCCTCA 49128       C   CCGA   _
                                CAGCGGCC CAGC   CGCC CA
                                |||||||| ||||   |||| ||
                                GTCGCCGG GTCG   GCGG GT
                                    C   TC__   A
GAM2003  LOC91179  5'  CAGCGGCCCTCGGCCACC   49129       CA_  CGAC
                                CAGCGGCCC  GCC   GCC
                                |||||||||  |||   |||
                                GTCGCCGGG  CGG   TGG
                                    AGC  ____
GAM2003  LOC91355  5'  CAGCGTCCCCAGCACACCCAC  49130     G     CCG
                                CAGCG CCCCAGC  ACGCCCAC
                                ||||| |||||||  ||||||||
                                GTCGC GGGGTCG  TGTGGGTG
                                  A     ___
GAM2003  LOC92405  5'  GCGGCCCCGCAGACCCTCA   49131       A  CC  G  _
                                GCGGCCCC GC  GAC CC CA
                                |||||||| ||  ||| || ||
                                CGCCGGGG CG  CTG GG GT
                                    _  T_  _  A
GAM2003  LOC93624  5'  CAGCGGCCTCAGCTTCAGGCGC 49132       C   C_  A_
                                CAGCGGCC CAGC  CG  CGC
                                |||||||| ||||  ||  |||
                                GTCGCCGG GTCG  GT  GCG
                                    A   AA  CC
GAM2004  ARNT2    3'  GGTGCTGCTTGGTCACTCTGGG 49135   C_   CA___  C  C
            CA                   GG  CTGCT    AC CTG GGCA
                                ||  |||||    || ||| ||||
                                CC  GACGA    TG GAC CCGT
                                 AC    ACCAG  A  _
GAM2004  ATF5     3'  GGCCTGCTCATCTTCCCGCACT 49136        A___  TGCG
                                GGCCTGCTCA   CCC   GCACT
                                ||||||||||   |||   |||||
                                CCGGACGAGT   GGG   CGTGA
                                    AGAA  ____
GAM2004  CRAT     3'  CGTCCTGCTCAGCCTCTGCA  49137   G     A  _
                                CG CCTGCTCA CC CTGCG
                                || |||||||| || |||||
                                GC GGACGAGT GG GACGT
                                 A      C  A
GAM2004  CRAT     3'  CGTCCTGCTCAGCCTCTGCA  49137   G     A  _
                                CG CCTGCTCA CC CTGCG
                                || |||||||| || |||||
```

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                                GC GGACGAGT GG GACGT
                                 A       C  A
GAM2004  DHCR7    5'  GGCCTGCTTGCGCGCC      49138        CAACCC   _  A
                                GGCCTGCT     TGCG GC C
                                ||||||||     |||| || |
                                CCGGACGA     ACGC CG G
                                    _______   G  C
GAM2004  DUSP1    5'  CAGCGTGATCGGCCCTGCGG   49139      C  C  AA
                                CGGC TG TC  CCCTGCGG
                                |||| || ||  ||||||||
                                GTCG AC AG  GGGACGCC
                                  C  T  CC
GAM2004  GPR48    5'  CGGCCTCTCCCGCGGCC     49140       G  CAAC       A
                                CGGCCT CT    CCTGCGGC C
                                ||||||  ||    |||||||| |
                                GCCGGA GA    GGGCGCCG G
                                   _ _____       C
GAM2004  KLHL2    5'  GGCCCGCTCGGCCGGGCGCGC  49141         AA  CT  _
                                GGCCTGCTC  CC  GCG GC
                                |||||||||  ||  ||| ||
                                CCGGGCGAG  GG  CGC CG
                                     CC  CC   G
GAM2004  PTGER4   5'  CCTGCTCAGTCTGGAAACT   49142         ACC   C  C
                                CCTGCTCA   CTG GG ACT
                                ||||||||   ||| || |||
                                GGACGAGT   GAC CT TGA
                                     CA_  _  T
GAM2004  CIDEB    5'  CGGCCTGCTCAGCCTGCAGCGC 49143          AC       A
              T                  CGGCCTGCTCA  CCTGCGGC CT
                                ||||||||||  |||||||| ||
                                GCCGGACGAGT  GGACGTCG GA
                                      C_       C
GAM2004  FLJ10898 5'  GGTTTTTCAACCCCAGGACT   49144    CCTGC       C  C
                                GG    TCAACCCTG GG ACT
                                ||    ||||||||| || |||
                                CC    AGTTGGGGT CC TGA
                                 AAAA_       _ _
GAM2004  FLJ20059 3'  GGCCTGCCTCAGCCTCCCAAAG 49145        _  A___   TGCG_
              TGC                  GGCCTGC TCA    CCC    GC
                                ||||||| |||    |||    ||
                                CCGGACG AGT    GGG    CG
                                   G   CGGA   TTTCA
GAM2004  KIAA0556 3'  GGTTTGATCAACCCCTGAC   49146    CC  C      GC
                                GG  TG TCAACCCT  GGC
                                ||  || ||||||||  |||
                                CC  AC AGTTGGGG  CTG
                                 AA  T       A_
GAM2004  KIAA1161 5'  GGCCTGCATGGCCCTGCAA   49147        TCAA
                                GGCCTGC    CCCTGCGG
                                |||||||    ||||||||
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                                CCGGACG   GGGACGTT
                                    TACC
GAM2004 KIAA1465 3' GGCGCGCGGTCCTGCGGCGCT 49148    C  TCAAC      A
                                GGC TGC    CCTGCGGC CT
                                ||| |||    |||||||| ||
                                CCG GCG    GGACGCCG GA
                                  C  CCA__      C
GAM2004 MAPKAP1  5' CGGCCCGCTCAGCTGCCGC   49149         ACC   G
                                CGGCCTGCTCA  CTGC GC
                                ||||||||||  |||| ||
                                GCCGGGCGAGT  GACG CG
                                      C__   G
GAM2004 MGC20470 3' GGCCTGCTCAATCTGCAA    49150         CC
                                GGCCTGCTCAA  CTGCGG
                                ||||||||||  ||||||
                                CCGGACGAGTT  GACGTT
                                      A_
GAM2004 N4BP3    3' GGCCTGCCTGACCTGGCCAC   49151       CA  CT  G
                                GGCCTGCT  ACC  GC GC
                                ||||||||  |||  || ||
                                CCGGACGG  TGG  CG TG
                                    AC   AC  G
GAM2004 PAK7     3' GGTCTGTTGAACCCTGCCGG   49152    C  CTC      _
                                GG CTG   AACCCTGC GG
                                || |||   |||||||| ||
                                CC GAC   TTGGGACG CC
                                 A  AAC       G
GAM2004 PEPP3    3' CAGCCTGGCTCCCTGCGGCA   49153       _ CAA
                                CGGCCTG CT   CCCTGCGGCA
                                |||||||  ||   ||||||||||
                                GTCGGAC GA   GGGACGCCGT
                                    C  ___
GAM2004 PTPRT    3' GGCCTGCTCAGTGGGGGCACT  49154         ACCCTGC
                                GGCCTGCTCA      GGCACT
                                ||||||||||      ||||||
                                CCGGACGAGT      CCGTGA
                                      CACCC__
GAM2004 TAS1R1   3' CGGCCTGCTCGACCTTCGACCC 49155         A  CTG   A
           T                     CGGCCTGCTC ACC   CGGC CT
                                ||||||||||  |||   |||| ||
                                GCCGGACGAG TGG   GCTG GA
                                      C   AA_   G
GAM2004 LOC138389 3' CGGCCTGCTGGGCGCGTGC   49156       CAACCC   _
                                CGGCCTGCT     TGCG GC
                                |||||||||     |||| ||
                                GCCGGACGA     GCGC CG
                                      CCC___    A
GAM2004 LOC146506 3' GGCCTGCTGGGCCAGGCACT  49157       CAA  CTGC
                                GGCCTGCT   CC    GGCACT
                                ||||||||   ||    ||||||
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                                CCGGACGA  GG   CCGTGA
                                    CCC  T___
GAM2004  LOC147057 3'  CGGCCCCCAGCCCTGCGGCACT 49158      TG   A
                                CGGCC  CTCA CCCTGCGGCACT
                                |||||  |||| ||||||||||||
                                GCCGG  GGGT GGGACGCCGTGA
                                  __   C
GAM2004  LOC147136 5'  GGCCTTCTTCTGCGGCACT   49159      G  CAACC
                                GGCCT CT    CTGCGGCACT
                                ||||| ||    ||||||||||
                                CCGGA GA    GACGCCGTGA
                                  A  A____
GAM2004  LOC150271 5'  GGTCCGCGGTCCTGCGGCGCT  49160    C   TCAAC      A
                                GG CTGC    CCTGCGGC CT
                                || ||||    |||||||| ||
                                CC GGCG    GGACGCCG GA
                                 A   CCA__       C
GAM2004  LOC154789 5'  GGCCTGCTCAAGTTTGAAGC   49161          CCC  C
                                GGCCTGCTCAA   TG GGC
                                ||||||||||   || |||
                                CCGGACGAGTT   AC TCG
                                     CAA  T
GAM2004  LOC154860 5'  CGACCTGCTCAACTGCGCACT  49162           CC   G
                                CGGCCTGCTCAAC  TGCG CACT
                                ||||||||||||  |||| ||||
                                GCTGGACGAGTTG  ACGC GTGA
                                       __   _
GAM2004  LOC155382 5'  CGGCCCGCTCGGCCCGC     49163          AAC
                                CGGCCTGCTC   CCTGC
                                ||||||||||   |||||
                                GCCGGGCGAG   GGGCG
                                     CC_
GAM2004  LOC201705 5'  GCCTGCTCAGTCCTGGGACT   49164         AC   C  C
                                GCCTGCTCA  CCTG GG ACT
                                |||||||||  |||| || |||
                                CGGACGAGT  GGAC CC TGA
                                     CA   _ _
GAM2004  LOC203378 3'  CAGCCTGCTCAACCTGTAA   49165           C  CG
                                CGGCCTGCTCAACC TG  G
                                |||||||||||||| ||  |
                                GTCGGACGAGTTGG AC  T
                                       _ AT
GAM2004  LOC255926 3'  GCCTGCTCAGTCCCGACAGCA  49166         A_  T
                                GCCTGCTCA  CCC GCGGCA
                                |||||||||  ||| ||||||
                                CGGACGAGT  GGG TGTCGT
                                     CA  C
GAM2005  HOXA7    3'  TATGATCTGATGTCATGG    49169     _     ATTATTT
                                TATG TCTGAT      TCATGG
                                |||| ||||||      ||||||
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                                ATAC AGACTA      AGTACC
                                  T     C_______
GAM2005  IL10RA   3'  TGTCTGATACTGTCTTGGC   49170          ATTT  A
                                TGTCTGATATT    TC TGGC
                                ||||||||||    || ||||
                                ACAGACTATGA    AG ACCG
                                      C___  A
GAM2005  IL8      3'  TATGTTCTGGATATTTCATGG  49171      _  _    ATTT
                                TATGT CTG ATATT    TCATGG
                                ||||| ||| |||||    ||||||
                                ATACA GAC TATAA    AGTACC
                                  A  C    _____
GAM2005  GMFB     3'  TATGTCTGATTCCAGTATGG   49172         A   TTTTC
                                TATGTCTGAT TTA    ATGG
                                |||||||||| |||    ||||
                                ATACAGACTA GGT    TACC
                                      A  CA___
GAM2005  KIAA0215 3'  TGTCTGATAATCATGG      49173         TTATTT
                                TGTCTGATA     TCATGG
                                |||||||||     ||||||
                                ACAGACTAT     AGTACC
                                      T_____
GAM2005  KIAA1718 3'  TATGTCTGGGTTATTTTATG   49174        ATA      C
                                TATGTCTG   TTATTTT ATG
                                ||||||||   ||||||| |||
                                ATACAGAC   AATAAAA TAC
                                     CC_     _
GAM2005  MGC15873 3'  TGTCCCATATTTTCATGGC    49175      G    ATT
                                TGTCT ATATT   TTCATGGC
                                ||||| |||||   ||||||||
                                ACAGG TATAA   AAGTACCG
                                  G    ___
GAM2005  LOC221830 3'  TATGTCTGGTACTAAATAAATG 49176        A    TTTTC
           GC                     TATGTCTG TATTA    ATGGC
                                ||||||||| |||||    |||||
                                ATACAGAC ATGAT    TACCG
                                     C    TTATT
GAM2006  AGRN     3'  CAGCGGGCGCGGGGCTCTGGTG 49179     AT  AT      CGAC
           C                     CAGC  GT  CGGGGCTC   GC
                                ||||  ||  ||||||||   ||
                                GTCG  CG  GCCCCGAG   CG
                                  CC  C_      ACCA
GAM2006  ANK1     3'  GCGGCCAGGGGGCTCTGACG   49180    AT  ATC     C
                                GC  GT   GGGGCTC GACG
                                ||  ||   ||||||| ||||
                                CG  CG   CCCCGAG CTGC
                                 C_  GTC      A
GAM2006  ANK1     3'  GCGGCCAGGGGGCTCTGACG   49180    AT  ATC     C
                                GC  GT   GGGGCTC GACG
                                ||  ||   ||||||| ||||
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                                CG  CG   CCCCGAG CTGC
                                 C_  GTC      A
GAM2006  EDNRA    5'  TGTCCCGGGCTCCGGCGC    49181     A  G       A
                                TGT TC GGGCTCCG CGC
                                ||| || |||||||| |||
                                ACA GG CCCGAGGC GCG
                                  _ G       C
GAM2006  SORCS2   3'  CACCATCCAGGGCTCTGGCG   49182    G   GTA       CGA
                                CA CAT   TCGGGGCTC   CG
                                || |||   |||||||||   ||
                                GT GTA   GGTCCCGAG   GC
                                 G  ___        ACC
GAM2006  HERPUD1  5'  GCGGTGTCGGGGCTCCG     49183    AT  A
                                GC  GT TCGGGGCTCCG
                                ||  || ||||||||||
                                CG  CA AGCCCCGAGGC
                                 C_  C
GAM2006  PME-1    3'  CAGATGTATCGCCTGAG     49184     C       GGGCT  _  C
                                CAG ATGTATCG    CC GA G
                                ||| ||||||||    || || |
                                GTC TACATAGC    GG CT C
                                  _      _____  A  A
GAM2006  TRAF3    3'  CAGCGTATGTCGGGGCTC    49185      A   A
                                CAGC TGT TCGGGGCTC
                                |||| ||| |||||||||
                                GTCG ATA AGCCCCGAG
                                  C   C
GAM2006  LOC134265 5'  CAGGGCGCAGGGGCTCCGGCGC 49186     CA    TC       A
                                CAG  TGTA  GGGGCTCCG CGC
                                |||  ||||  ||||||||| |||
                                GTC  GCGT  CCCCGAGGC GCG
                                  CC   __        C
GAM2006  LOC205251 3'  GCGGACCGGGGCTCCGGCGC   49187    ATGT         A
                                GC   ATCGGGGCTCCG CGC
                                ||   |||||||||||| |||
                                CG   TGGCCCCGAGGC GCG
                                 CC__          C
GAM2007  BCL11A   3'  CACTTTTTTGTTTCTCTC    49190          C  G
                                CACTTTTTTGT TC CTT
                                |||||||||| || |||
                                GTGAAAAAACA AG GAG
                                       A  A
GAM2007  COL4A3   3'  CTTTTTTAGCTTCAGTG     49191        TCTC     A
                                CTTTTTTG   GCTTCA TG
                                ||||||||   |||||| ||
                                GAAAAAAT   CGAAGT AC
                                     _____     C
GAM2007  COL4A3   3'  CTTTTTTAGCTTCAGTG     49191        TCTC     A
                                CTTTTTTG   GCTTCA TG
                                ||||||||   |||||| ||
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                                GAAAAAAT   CGAAGT AC
                                    ____     C
GAM2007 Nrap     3' TTTTTTGCTCCTTCAATGT   49192       T  G
                                TTTTTTG CTC CTTCAATGT
                                ||||||| ||| |||||||||
                                AAAAAAC GAG GAAGTTACA
                                  _  _
GAM2007 FLJ11996 5' CACTTTTTTCCTTCAGTG    49193       TGTC  G    A
                                CACTTTTT   TC CTTCA TG
                                ||||||||   || ||||| ||
                                GTGAAAAA   AG GAAGT AC
                                    ____ _    C
GAM2007 FLJ21126 3' CTTTTTTTCTGGCTTCAGTGT  49194       G  C     A
                                CTTTTTT TCT GCTTCA TGT
                                ||||||| ||| |||||| |||
                                GAAAAAA AGA CGAAGT ACA
                                   _  C     C
GAM2007 GL004    5' CCTTTAACTTGCTTCAATGT   49195      TTGT  C
                                CTTTT   CT GCTTCAATGT
                                |||||   || ||||||||||
                                GGAAA   GA CGAAGTTACA
                                  TT__  A
GAM2007 MRPS30   3' TTTTTTGTCTCAAAAATCAATG 49196          CT__
           T                    TTTTTTGTCTCG   TCAATGT
                                |||||||||||   |||||||
                                AAAAAACAGAGT   AGTTACA
                                     TTTT
GAM2007 UXS1     3' TTTTTTGTCCCGCTTAATGT   49197           C
                                TTTTTTGTCTCGCTT AATGT
                                |||||||||||||| |||||
                                AAAAAACAGGGCGAA TTACA
                                      _
GAM2007 LOC143902 3' TTCTTTGTCTACTATAATGT   49198         C  TC
                                TTTTTTGTCT GCT  AATGT
                                |||||||||| |||  |||||
                                AAGAAACAGA TGA  TTACA
                                    _  TA
GAM2007 LOC146520 5' TTTTTTGTCTCTCCCTTTTGT  49199         G  CAA
                                TTTTTTGTCTC CTT   TGT
                                |||||||||| |||   |||
                                AAAAAACAGAG GGG   ACA
                                     A  AAA
GAM2007 LOC151094 3' CTTGCATTTTCGCTTTAATGT  49200      C___    C
                                TTTGT   TCGCTT AATGT
                                |||||   |||||| |||||
                                GAACG   AGCGAA TTACA
                                  TAAA    A
GAM2007 LOC91138  5' CACTTTTTTGTTTCCTT     49201          C  G
                                CACTTTTTTGT TC CTT
                                |||||||||| || |||
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                                GTGAAAAAACA AG GAA
                                      A  _
GAM2008  FCMD     3'  TCTGTGATTATTTATTTAGTTA 49204        CTC   GAGT
              T                  TCTGTGATT   TAT   GTTAT
                                 |||||||||   |||   |||||
                                 AGACACTAA   ATA   CAATA
                                       TAA   AAT_
GAM2008  KIAA0705  3'  TCTGTGATGTTCTTCACGTTAT 49205        TC   ATGA
                                 TCTGTGAT  TCT   GTGTTAT
                                 ||||||||  |||   |||||||
                                 AGACACTA  AGA   TGCAATA
                                      CA   AG__
GAM2008  KIAA0848  3'  TCTGTATTCTCTAGTT      49206       A      TGAGT
                                 TCTGTG TTCTCTA    GTT
                                 ||||||| |||||||    |||
                                 AGACAT AAGAGAT    CAA
                                      _     _____
GAM2008  KIAA0914  3'  TCTGTAGATGAGTGTT      49207       ATTCTCT
                                 TCTGTG      ATGAGTGTT
                                 ||||||      |||||||||
                                 AGACAT      TACTCACAA
                                    C_______
GAM2008  KIAA1724  3'  CTGTGGTTTTCTGAGTGTTAT  49208      A  C   AT
                                 CTGTG TT TCT  GAGTGTTAT
                                 ||||| || |||  |||||||||
                                 GACAC AA AGA  CTCACAATA
                                    C  A  __
GAM2008  TU3A     3'  TCTGTGATTCTCTTGGCCTT   49209          A  A  G
                                 TCTGTGATTCTCT TG GT TT
                                 |||||||||||| || || ||
                                 AGACACTAAGAGA AC CG AA
                                        _ _  G
GAM2008  LOC151720 5'  TCTGGGTTCTCTATTCTGT   49210     TGA      GAG
                                 TCTG   TTCTCTAT   TGT
                                 ||||   ||||||||   |||
                                 AGAC   AAGAGATA   ACA
                                   CC_      AG_
GAM2008  LOC219333 3'  TGTGATTCTCTGTGGCATGT   49211         A  A_
                                 TGTGATTCTCT TG  GTGT
                                 |||||||||| ||  ||||
                                 ACACTAAGAGA AC  TACA
                                       C  CG
GAM2008  LOC221738 3'  TGTGATTCTCTGTTCATGT   49212         ATGA
                                 TGTGATTCTCT   GTGT
                                 ||||||||||   ||||
                                 ACACTAAGAGA   TACA
                                       CAAG
GAM2009  ADORA1   3'  GGGTATCTCTTCAGAGCC    49215       G__   CT  A
                                 GGGTATCT   CAG  GG CC
                                 ||||||||   |||  || ||
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                                CCCATAGA  GTC  TC GG
                                    GAA  __ _
GAM2009  ATP2A3   3'  CGGGTGGCAAGTTGGACC    49216      ATCT  _ C
                                CGGGT   GCA G TGGACC
                                |||||   ||| | ||||||
                                GCCCA   CGT C ACCTGG
                                  C___  T A
GAM2009  BRCA1    3'  GAGCAGCAGCTGGAC      49217      TCT
                                GGGTA  GCAGCTGGAC
                                |||||  ||||||||||
                                CTCGT  CGTCGACCTG
                                  ___
GAM2009  GATA6    5'  GGCGCCGCGGCTGGACC    49218    AT   A
                                GGT  CTGC GCTGGACC
                                |||  |||| ||||||||
                                CCG  GGCG CGACCTGG
                                 C_   C
GAM2009  GNB3     5'  GGGCTCTGGCTGGAC      49219    A   CA
                                GGGT TCTG  GCTGGAC
                                |||| ||||  |||||||
                                CCCG AGAC  CGACCTG
                                  _   __
GAM2009  KCNJ8    5'  CGGGCGCGGCGGCTGGACC   49220      ATCT  A
                                CGGGT   GC GCTGGACC
                                |||||   || ||||||||
                                GCCCG   CG CGACCTGG
                                  CGC_  C
GAM2009  KERA     3'  TACGGTATCTGCATAAG    49221      G      GCT
                                TACGG TATCTGCA  GG
                                ||||| ||||||||  ||
                                ATGCC ATAGACGT  TC
                                  _      AT_
GAM2009  KRT6B    3'  ACTCCTCATCTGCAGCTGGACC 49222   GGG_
                                AC   TATCTGCAGCTGGACC
                                ||   ||||||||||||||||
                                TG   GTAGACGTCGACCTGG
                                 AGGA
GAM2009  NGB      3'  CACTCCTTCTGCAGCTGGAC  49223    GGGTA
                                TAC    TCTGCAGCTGGAC
                                |||    ||||||||||||
                                GTG    AGACGTCGACCTG
                                 AGGA_
GAM2009  SLC10A2  3'  GGGTATCACTGGACC      49224       TGCA
                                GGGTATC   GCTGGACC
                                |||||||   ||||||||
                                CCCATAG   TGACCTGG
                                  ____
GAM2009  VCY      3'  TGAGGTCTGGCAGCTGGGCC  49225   C   ATCT      A
                                A GGGT   GCAGCTGG CC
                                | ||||   |||||||| ||
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                                A TCCA    CGTCGACC GG
                                 C    GAC_       C
GAM2009  VCY      3'  TGAGGTCTGGCAGCTGGGCC   49225    C    ATCT       A
                                A GGGT    GCAGCTGG CC
                                | ||||    |||||||| ||
                                A TCCA    CGTCGACC GG
                                 C    GAC_       C
GAM2009  WISP1    3'  GGCATGGTCTGCAGCTGG    49226      ___
                                GGTA   TCTGCAGCTGG
                                ||||   ||||||||||
                                CCGT   AGACGTCGACC
                                  ACC
GAM2009  ZNF189   5'  TACGAGGATCCCTGGCTGG   49227       T    GCA
                                TACGGG ATCT   GCTGG
                                |||||| ||||   |||||
                                ATGCTC TAGG   CGACC
                                    C    GAC
GAM2009  CXorf9   3'  TACAGCCTTTGCAGCTGG    49228      G ATC
                                TACGG T   TGCAGCTGG
                                ||||| |   |||||||||
                                ATGTC G   ACGTCGACC
                                   _ GAA
GAM2009  DKFZP434N014 5'  CACGGGTACAGTGGCTGGA    49229         CTGCA
                                TACGGGTAT    GCTGGA
                                |||||||||    ||||||
                                GTGCCCATG    CGACCT
                                     TCAC_
GAM2009  DKFZP586I2223 3'  CACGGTCTTGCAGCTGGA    49230      GTATC
                                TACGG    TGCAGCTGGA
                                |||||    ||||||||||
                                GTGCC    ACGTCGACCT
                                   AGA__
GAM2009  FLJ21156  3'  GGGTCTGCGGGGCTGGGCC   49231     TA    A__    A
                                GGG  TCTGC   GCTGG CC
                                |||  |||||   ||||| ||
                                CCC  AGACG   CGACC GG
                                  __    CCC    C
GAM2009  HSPF2    5'  TACGGGTACCTCTTTGGAC   49232          GCAGC
                                TACGGGTATCT    TGGAC
                                ||||||||||    |||||
                                ATGCCCATGGA    ACCTG
                                     GAA__
GAM2009  KCND1    5'  GGGTATCTAGACGGGCC     49233        CA  T  A
                                GGGTATCTG  GC GG CC
                                |||||||||  || || ||
                                CCCATAGAT  TG CC GG
                                     C_  C  _
GAM2009  KIAA1393  5'  CACGTCGCTCTGCAGCTGGA  49234     GGTA
                                TACG    TCTGCAGCTGGA
                                ||||    ||||||||||||
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                                GTGC   AGACGTCGACCT
                                  AGCG
GAM2009 KIAA1582 5' TACAGGCCAGGCAGCTGG   49235      ATCT
                                TACGGGT   GCAGCTGG
                                |||||||   ||||||||
                                ATGTCCG   CGTCGACC
                                   GTC_
GAM2009 KIAA1649 3' CACGTGGCTGCAGCTGGAC   49236    _ TAT
                                TACG GG   CTGCAGCTGGAC
                                |||| ||   ||||||||||||
                                GTGC CC   GACGTCGACCTG
                                  A ___
GAM2009 KIAA1649 3' CACGTGGCTGCAGCTGGAC   49236    _ TAT
                                TACG GG   CTGCAGCTGGAC
                                |||| ||   ||||||||||||
                                GTGC CC   GACGTCGACCTG
                                  A ___
GAM2009 MGC12760 3' CAGCTGACTCTGCAGCTGGGCC 49237    GTA__       A
                                CGG    TCTGCAGCTGG CC
                                |||    |||||||||||| ||
                                GTC    AGACGTCGACC GG
                                 GACTG         C
GAM2009 MIDORI   3' CAGGCTGCAGCTGGGCC    49238    TAT       A
                                CGGG   CTGCAGCTGG CC
                                ||||   |||||||||| ||
                                GTCC   GACGTCGACC GG
                                  ___         C
GAM2009 NRM      3' GGGTATGGAGCTGGACC    49239     TC  C
                                GGGTA  TG AGCTGGACC
                                |||||  || |||||||||
                                CCCAT  AC TCGACCTGG
                                   __  C
GAM2009 NRM      3' GGGTATGGAGCTGGACC    49239     TC  C
                                GGGTA  TG AGCTGGACC
                                |||||  || |||||||||
                                CCCAT  AC TCGACCTGG
                                   __  C
GAM2009 NRM      3' GGGTATGGAGCTGGACC    49239     TC  C
                                GGGTA  TG AGCTGGACC
                                |||||  || |||||||||
                                CCCAT  AC TCGACCTGG
                                   __  C
GAM2009 PADI3    3' GGAAACGCAGCTGGACC    49240    TATC
                                GGG    TGCAGCTGGACC
                                |||    ||||||||||||
                                CCT    GCGTCGACCTGG
                                  TT__
GAM2009 PARVA    3' GGGTTGCAGCTGGAC      49241     ATC
                                GGGT   TGCAGCTGGAC
                                ||||   ||||||||||
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                              CCCA  ACGTCGACCTG
                                ___
GAM2009 PPAP2C   3' GGGCATCAGCTGGAC      49242       TGC
                              GGGTATC  AGCTGGAC
                              |||||||  ||||||||
                              CCCGTAG  TCGACCTG
                                ____
GAM2009 PPP1R16A 5' GGGCAGCTAGCTGGAC     49243      TCT _
                              GGGTA  GC AGCTGGAC
                              |||||  || ||||||||
                              CCCGT  CG TCGACCTG
                                 ___ A
GAM2009 LOC143524 5' CGGGTGGAACGGCTGGACC  49244      ATCT  A
                              CGGGT   GC GCTGGACC
                              |||||   || ||||||||
                              GCCCA   TG CGACCTGG
                                 CCT_ C
GAM2009 LOC144501 3' GGGCCCCACAGCTGGACC   49245     A  TG
                              GGGT TC  CAGCTGGACC
                              |||| ||  ||||||||||
                              CCCG GG  GTCGACCTGG
                                _ GT
GAM2009 LOC144559 5' CGGGTGGAACGGCTGGACC  49244      ATCT  A
                              CGGGT   GC GCTGGACC
                              |||||   || ||||||||
                              GCCCA   TG CGACCTGG
                                 CCT_ C
GAM2009 LOC147958 3' GGGTTCCACAGCTGGGCC   49246     A  TG     A
                              GGGT TC  CAGCTGG CC
                              |||| ||  ||||||| ||
                              CCCA AG  GTCGACC GG
                                _ GT     C
GAM2009 LOC149579 3' CAGCTGACTCTGCAGCTGGGCC 49237     GTA__        A
                              CGG    TCTGCAGCTGG CC
                              |||    |||||||||| ||
                              GTC    AGACGTCGACC GG
                                GACTG         C
GAM2009 LOC150819 5' GGATGCTGCAGCTGGAC    49247     AT
                              GGGT  CTGCAGCTGGAC
                              ||||  ||||||||||||
                              CCTA  GACGTCGACCTG
                                C_
GAM2009 LOC158061 3' AGGTCCTTCTGCAGCTGGGCC  49248     A__        A
                              GGGT   TCTGCAGCTGG CC
                              ||||   |||||||||| ||
                              TCCA   AGACGTCGACC GG
                                GGA         C
GAM2009 LOC196759 3' GAGGCTGCAGCTGGACC    49249     TAT
                              GGG   CTGCAGCTGGACC
                              |||   ||||||||||||
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                                CTC   GACGTCGACCTGG
                                  C__
GAM2009  LOC199864 3'  GAGGCTGCAGCTGGACC     49249     TAT
                                GGG   CTGCAGCTGGACC
                                |||   ||||||||||||||
                                CTC   GACGTCGACCTGG
                                  C__
GAM2009  LOC220045 3'  CAAGGCTGTGGCTGGACC     49250      TAT   CA
                                CGGG   CTG  GCTGGACC
                                ||||   |||  ||||||||
                                GTTC   GAC  CGACCTGG
                                  C__   AC
GAM2009  LOC220071 5'  CGGGCGGAACGGCTGGACC    49251       ATCT  A
                                CGGGT    GC GCTGGACC
                                |||||    || ||||||||
                                GCCCG    TG CGACCTGG
                                   CCT_  C
GAM2009  LOC220954 3'  CAGGTATCTGGCAAAGGCC    49252          _   CT  A
                                CGGGTATCTG CAG  GG CC
                                |||||||||| |||  || ||
                                GTCCATAGAC GTT  CC GG
                                      C   T_ _
GAM2009  LOC255515 5'  CGGGTGGAACGGCTGGACC    49244       ATCT  A
                                CGGGT    GC GCTGGACC
                                |||||    || ||||||||
                                GCCCA    TG CGACCTGG
                                   CCT_  C
GAM2009  LOC92305  3'  GGGTAGCCTGGGCTGGACC    49253       _    CA
                                GGGTA TCTG  GCTGGACC
                                ||||| ||||  ||||||||
                                CCCAT GGAC  CGACCTGG
                                   C    C_
GAM2010  BAZ2A     3'  CACTGCGCGCTGTGTGTGTGA  49256     C  _      CAACGC
                                CAC GT CGCTGTG     GTGA
                                ||| || |||||||     ||||
                                GTG CG GCGACAC     CACT
                                  A  C      ACA___
GAM2010  NCOR2     3'  CACCGCTGCGGCAACGATGTGT 49257       C  T T     C___
            GAA                   CACCGT GC G GCAACG    GTGAA
                                |||||| || | ||||||    |||||
                                GTGGCG CG C CGTTGC    CACTT
                                   A  _ _     TACA
GAM2010  RECK      5'  ACCGCCGCCGCCGGACGCGTG  49258          GCA
                                ACCGTCGCTGT   ACGCGTG
                                ||||||||||   |||||||
                                TGGCGGCGGCG   TGCGCAC
                                      GCC
GAM2010  FLJ10057  3'  CACTGTTGCTGTGCTGCA     49259     C  C      AAC
                                CAC GT GCTGTGC   GCG
                                ||| || |||||||   |||
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                                GTG CA CGACACG   CGT
                                  A A      A__
GAM2010  RAB17    3'  CACCGTCGCTGTGCTGCG    49260           AAC
                                CACCGTCGCTGTGC   GCG
                                |||||||||||||  |||
                                GTGGCAGCGACACG   CGC
                                       A__
GAM2010  RoXaN    3'  CCTCGCTGTGTGACACTG    49261    G      CA   G
                                CC TCGCTGTG  ACGC TG
                                || ||||||||  |||| ||
                                GG AGCGACAC  TGTG AC
                                 _      AC   _
GAM2010  LOC115110 3'  CGCTGCGCTGTGTTCTGCGTG  49262     __      CAAC
                                CGT  CGCTGTG   GCGTG
                                |||  |||||||   |||||
                                GCG  GCGACAC   CGCAC
                                  AC      AAGA
GAM2011  CDKN1A   3'  AAAGTCACTAAGAATCATTTAT 49265     C  _  TT
                                AGAG CAC AGG  TCATTTAT
                                |||| ||| |||  ||||||||
                                TTTC GTG TTC  AGTAAATA
                                  A  A  TT
GAM2011  RPL15    3'  AAAGCTGCAGGTTTCATC    49266      CA
                                AGAGC  CAGGTTTCATT
                                |||||  ||||||||||
                                TTTCG  GTCCAAAGTAG
                                   AC
GAM2011  BG1      3'  AGAGCTGATCTCATTT      49267      CACA
                                AGAGC   GGTTTCATTT
                                |||||   ||||||||||
                                TCTCG   CTAGAGTAAA
                                  A___
GAM2011  CASPR3   3'  AGAGGGCTGTTCCATTTATC  49268     CCACAG
                                AGAG     GTTTCATTTATC
                                ||||     ||||||||||||
                                TCTC     CAAGGTAAATAG
                                  CCGA__
GAM2011  CCNE2    3'  GAGCCACAGCATTTAT      49269        GTTT
                                GAGCCACAG   CATTTAT
                                |||||||||   |||||||
                                CTCGGTGTC   GTAAATA
                                     ____
GAM2011  CCNE2    3'  GAGCCACAGCATTTAT      49269        GTTT
                                GAGCCACAG   CATTTAT
                                |||||||||   |||||||
                                CTCGGTGTC   GTAAATA
                                     ____
GAM2011  DGKD     3'  TGAAGCCACAGTCAGCTGTTTA 49270   A       GTTTCA_
            TC                    A GAGCCACAG      TTTATC
                                | |||||||||      ||||||
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                                A TTCGGTGTC      AAATAG
                                 C       AGTCGAC
GAM2011  DKFZP434K2235 3'  TAAGAACCAAGCTTTATTTAT  49271         CA    C
                                TAAGAGCCA  GGTTT ATTTAT
                                |||||||||  ||||| ||||||
                                ATTCTTGGT  TCGAA TAAATA
                                     __    A
GAM2011  KIAA0205  3'  GAGATTGGTTTCATTTAT    49272     CCACA
                                GAG    GGTTTCATTTAT
                                |||    ||||||||||||
                                CTC    CCAAAGTAAATA
                                  TAA__
GAM2011  KIAA0217  3'  AGAGTTTGGGTTTCACAGATC  49273     CCACA      TT
                                AGAG    GGTTTCAT  ATC
                                ||||    ||||||||  |||
                                TCTC    CCAAAGTG  TAG
                                  AAAC_       TC
GAM2011  MGC5306   3'  TAAGAGCTCTGGGTTTCAC   49274       CACA
                                TAAGAGC    GGTTTCAT
                                |||||||    ||||||||
                                ATTCTCG    CCAAAGTG
                                     AGAC
GAM2011  LOC125929 3'  TAAGAGCATGGGTTTCATTT   49275       CACA
                                TAAGAGC    GGTTTCATTT
                                |||||||    ||||||||||
                                ATTCTCG    CCAAAGTAAA
                                     TAC_
GAM2011  LOC219557 3'  TAAGAGACATGGGCACATTATC 49276      C  CA   TT    T
                                TAAGAG CA  GGT  CATT ATC
                                |||||| ||  |||  |||| |||
                                ATTCTC GT  CCG  GTAA TAG
                                    T  AC   T_   _
GAM2012  TMLHE     3'  TAGAGTTTGACACAATATTATT 49279       ATAC  A
                                TAGAGT    GA ACAATATTATT
                                ||||||    || ||||||||||
                                ATCTCA    CT TGTTATAATAA
                                     AA__  G
GAM2013  CR1       3'  TTCCAAGCTCTTCTTACTG    49282     G    _ _
                                TTC CAAGC CT CTTACTG
                                ||| ||||| || |||||||
                                AAG GTTCG GA GAATGAC
                                  _     A  A
GAM2013  GFI1      3'  TTTCACAGCCCTACTG      49283        A    CT
                                TTTCGCA GCCT  TACTG
                                ||||||| ||||  |||||
                                AAAGTGT CGGG  ATGAC
                                     _   __
GAM2013  IGHMBP2   3'  TTTCCCAAGCCCCACCTG    49284      G       TTA
                                TTTC CAAGCCTC   CTG
                                |||| ||||||||   |||
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                                AAAG GTTCGGGG  GAC
                                  G      TG_
GAM2013 SH3BP2   3' TTTCCCAAGCCCCAGAACTG  49285     G      TT_
                                TTTC CAAGCCTC  ACTG
                                |||| ||||||||  ||||
                                AAAG GTTCGGGG  TGAC
                                  G      TCT
GAM2013 SPAG8    3' TTCCGCAAATGTTTACTG    49286       CCTC
                                TTTCGCAAG   TTACTG
                                |||||||||   ||||||
                                AAGGCGTTT   AATGAC
                                     ACA_
GAM2013 DDX31    3' TTTCACAAGCCTCCTCTG    49287           A
                                TTTCGCAAGCCTCTT CTG
                                |||||||||||||| |||
                                AAAGTGTTCGGAGGA GAC
                                                _
GAM2013 FLJ11342 3' TTTCACACTTTCTTACTG    49288       AGCC
                                TTTCGCA   TCTTACTG
                                |||||||   ||||||||
                                AAAGTGT   AGAATGAC
                                    GAA_
GAM2013 FLJ11577 5' TTTCACAAGCCTTTCACTG   49289         C
                                TTTCGCAAGCCT TTACTG
                                |||||||||||| ||||||
                                AAAGTGTTCGGA AGTGAC
                                       A
GAM2013 FLJ13195 3' TTTCACAAGCTCAGCACT    49290        C  T_
                                TTTCGCAAGC TC  TACT
                                |||||||||| ||  ||||
                                AAAGTGTTCG AG  GTGA
                                      _  TC
GAM2013 KIAA1867 3' TCTCGTGGAGCCTTACTG    49291      CA_    CT
                                TTTCG   AGCCT  TACTG
                                |||||   |||||  |||||
                                AGAGC   TCGGA  ATGAC
                                   ACC    __
GAM2013 MGC13007 3' TTTCACAAACCTACTG      49292         CTT
                                TTTCGCAAGCCT   ACTG
                                ||||||||||||   ||||
                                AAAGTGTTTGGA   TGAC
                                                ___
GAM2013 MGC14839 3' TTTCCAGGCCTCACTG      49293     G  A    TT
                                TTTC CA GCCTC  ACTG
                                |||| || |||||  ||||
                                AAAG GT CGGAG  TGAC
                                  _  C     __
GAM2013 MGC19556 5' TTTCCAAGCCTCAGCTG     49294      G       TTA
                                TTTC CAAGCCTC   CTG
                                |||| ||||||||   |||
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                                AAAG GTTCGGAG   GAC
                                  _      TC_
GAM2013  NS1-BP    3'  TTTCTTAAGCTCATTACTG   49295     GC   C  _
                                TTTC  AAGC TC TTACTG
                                ||||  |||| || ||||||
                                AAAG  TTCG AG AATGAC
                                  AA   _ T
GAM2013  PRO1257   3'  TTTCGCAAGCATTTTAGCTG  49296        CTC  _
                                TTTCGCAAGC   TTA CTG
                                ||||||||||   ||| |||
                                AAAGCGTTCG   AAT GAC
                                     TAA   C
GAM2013  LOC149952 3'  TCTCGCAAGCAGCACTACTG  49297        CTC_
                                TTTCGCAAGC    TTACTG
                                ||||||||||    ||||||
                                AGAGCGTTCG    GATGAC
                                     TCGT
GAM2013  LOC150519 3'  TCCCACAAATCTTACTG     49298   TT    CC
                                T  CGCAAG  TCTTACTG
                                |  ||||||  ||||||||
                                A  GTGTTT  AGAATGAC
                                 GG     __
GAM2013  LOC152220 3'  TTCACATCTCTTACTG      49299      AGC
                                TTCGCA   CTCTTACTG
                                ||||||   |||||||||
                                AAGTGT   GAGAATGAC
                                   A__
GAM2013  LOC253430 5'  TTCCGAGCCCCTTCTG      49300      CA      A
                                TTTCG  AGCCTCTT CTG
                                |||||  |||||||| |||
                                AAGGC  TCGGGGAA GAC
                                  __      _
GAM2013  LOC253675 3'  TTTCACAAGCTCATCCTG    49301        C  TTA
                                TTTCGCAAGC TC   CTG
                                |||||||||| ||   |||
                                AAAGTGTTCG AG   GAC
                                     _  TAG
GAM2013  LOC255621 3'  TTTCTAAAGCCTCTTGCTG   49302     GC      A
                                TTTC  AAGCCTCTT CTG
                                ||||  ||||||||| |||
                                AAAG  TTCGGAGAA GAC
                                  AT       C
GAM2013  LOC255855 5'  TTTCGCAACCTACTCATCTG  49303       G  _   _
                                TTTCGCAA CCT CTTA CTG
                                |||||||| ||| |||| |||
                                AAAGCGTT GGA GAGT GAC
                                     _  T   A
GAM2013  LOC92876  5'  TTTCGCAACCTACTCATCTG  49303       G  _   _
                                TTTCGCAA CCT CTTA CTG
                                |||||||| ||| |||| |||
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                                AAAGCGTT GGA GAGT GAC
                                    _  T   A
GAM2014  HOXB3    5'  CAAAGGTCTCCTAAAAGC    49306    T        CATTC
                                CAA AGGTCTCCTAG    AGC
                                ||| ||||||||||    |||
                                GTT TCCAGAGGATT    TCG
                                  _        T_____
GAM2014  ITGB1    3'  CAAAAGGTCCCCATTCAGC   49307    T      TAGC
                                CAA AGGTCTCC   ATTCAGC
                                ||| ||||||||   |||||||
                                GTT TCCAGGGG   TAAGTCG
                                  T      _____
GAM2014  YWHAG    3'  CAGTAGGCTTCTAGCACC    49308    A   T  C
                                CA TAGG CT CTAGCATT
                                || |||| || ||||||||
                                GT ATCC GA GATCGTGG
                                 C   _ A
GAM2014  C9orf5   3'  AATAGATCTGCCATTCAG    49309        _ TAGC
                                AATAGGTCT CC   ATTCAG
                                ||||||||| ||   ||||||
                                TTATCTAGA GG   TAAGTC
                                     C _____
GAM2014  CST8     5'  GGTTCTCCTAGGTCTTCAGCA  49310    _     CA_
                                GGT CTCCTAG   TTCAGCA
                                ||| |||||||   |||||||
                                CCA GAGGATC   AAGTCGT
                                  A      CAG
GAM2014  FHOD2    5'  TAGGTTCATAGCATTCAGCA   49311      C  C
                                TAGGT TC TAGCATTCAGCA
                                ||||| || ||||||||||||
                                ATCCA AG ATCGTAAGTCGT
                                   _ T
GAM2014  FLJ11274 5'  GGGTCCTAGGGGTTCAGCA   49312    TC     CA_
                                GG  TCCTAG   TTCAGCA
                                ||  ||||||   |||||||
                                CC  AGGATC   AAGTCGT
                                 C_     CCC
GAM2014  FLJ12425 3'  AAAAGGCTGGCATTCAG     49313    T   T  CCTA
                                AA AGG CT    GCATTCAG
                                || ||| ||    ||||||||
                                TT TCC GA    CGTAAGTC
                                 T   _ C____
GAM2014  FLJ12595 5'  AATGGGTCTCTGGCATCCA   49314     A     CTA
                                AAT GGTCTC   GCATTCA
                                ||| ||||||   |||||||
                                TTA CCAGAG   CGTAGGT
                                  C     AC_
GAM2014  FLJ13441 3'  GGTCTCCTCCTCATCAGC    49315        AG_   T
                                GGTCTCCT   CAT CAGC
                                ||||||||   ||| ||||
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                                CCAGAGGA   GTA GTCG
                                    GGA  _
GAM2014  FLJ23499  3'  CAACAGGTTTCCTTAGTGTGCT 49316      C   A_________  ATTCA
            GAAG                   TAGGT TCCT       GC    G
                                |||||  ||||       ||    |
                                GTCCA AGGA       CG    C
                                   A   ATCACIIIA  ACTTA
GAM2014  FLJ23516  3'  CAATGGTTTCATCCATTCAGCA 49317     A   C  CTAG
                                CAAT GGT TC    CATTCAGCA
                                ||||  ||| ||   |||||||||
                                GTTA CCA AG    GTAAGTCGT
                                   _   A  TAG_
GAM2014  KIAA1764  3'  CAATAGGTCTGCTGGTCTATGC 49318      C  A__________  ATTCA
            TGAATGC                  GGTCT CT        GC    GC
                                |||||  ||        ||    ||
                                CCAGA GA        CG    CG
                                   C  CCAGATIIIA  ACTTA
GAM2014  MGC10814  5'  CAGTGCCTGGCATTCAGC    49319    GTCT   A
                                TAG    CCT GCATTCAGC
                                |||    ||| |||||||||
                                GTC    GGA CGTAAGTCG
                                  AC__   C
GAM2014  MGC16703  5'  AGGTCTCCTGCCTCCTCGGC   49320        A  AT__  A
                                AGGTCTCCT GC    TC GC
                                |||||||||  ||    ||  ||
                                TCCAGAGGA CG    AG CG
                                     _  GAGG  C
GAM2014  UBCE7IP5  3'  CAATGGGTCTCCTCCAG     49321      A       AGCAT
                                CAAT GGTCTCCT     TCAG
                                ||||  ||||||||     ||||
                                GTTA CCAGAGGA     GGTC
                                  C       _____
GAM2014  LOC144681 3'  CAGGTCTCAGTTCAG       49322        CT  CA
                                TAGGTCTC  AG  TTCAG
                                ||||||||  ||  |||||
                                GTCCAGAG  TC  AAGTC
                                     __  __
GAM2014  LOC144682 3'  CAGGTCTCAGTTCAG       49322        CT  CA
                                TAGGTCTC  AG  TTCAG
                                ||||||||  ||  |||||
                                GTCCAGAG  TC  AAGTC
                                     __  __
GAM2014  LOC145053 5'  CAGGTCTCCTGCGCTAGC    49323         A  A  C
                                TAGGTCTCCT GC TT AGC
                                |||||||||| || || |||
                                GTCCAGAGGA CG GA TCG
                                     _  C  _
GAM2014  LOC151414 3'  CGAGGGGAAGGTAGCATTCAGC 49324   T   TCTCC_
            A                    A AGG     TAGCATTCAGCA
                                | |||     ||||||||||||
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                                G TCC     ATCGTAAGTCGT
                                 C   CCTTCC
GAM2014  LOC154214 3'  AATAGGTGCATTCAG       49325        CTCCTA
                                AATAGGT     GCATTCAG
                                |||||||     ||||||||
                                TTATCCA     CGTAAGTC
                                        _______
GAM2014  LOC196955 3'  CAACAGGTCTCCATTGGTGTGC 49326        TA__________  ATTCA
              TGAATGC                 GGTCTCC         GC    GC
                                |||||||         ||    ||
                                CCAGAGG         CG    CG
                                    TAACCACIIIA  ACTTA
GAM2014  LOC222112 3'  CAATAGTCTCCTGACTCCCTGT 49327       G     AG A_____
              TCAG                    CAATAG TCTCCT  C     TTCAG
                                |||||| ||||||  |     |||||
                                GTTATC AGAGGA  G     AAGTC
                                    _     CT AGGGAC
GAM2014  LOC51667  3'  TGATAGGTCTCTTAGCTAGCA  49328    A       C    ATTC
                                C ATAGGTCTC TAGC    AGCA
                                | |||||||||| ||||    ||||
                                A TATCCAGAG ATCG    TCGT
                                 C        A    A___
GAM2014  LOC90643  3'  ATAGGTCTCCAGCTCTTCAG   49329         T   A_
                                ATAGGTCTCC AGC  TTCAG
                                |||||||||| |||  |||||
                                TATCCAGAGG TCG  AAGTC
                                     _  AG
GAM2014  LOC90957  3'  CAATAGGTCTTTAGTTC     49330         CC   CA
                                CAATAGGTCT  TAG  TTC
                                ||||||||||  |||  |||
                                GTTATCCAGA  ATC  AAG
                                     A_  __
GAM2015  AKAP1     3'  GAGATAGAAGGAAGAAGAGG   49333        TCTGCAA
                                GAGATAGAA      AAGAGG
                                |||||||||      ||||||
                                CTCTATCTT      TTCTCC
                                     CCTTC__
GAM2015  AKAP1     3'  GAGATAGAAGGAAGAAGAGG   49333        TCTGCAA
                                GAGATAGAA      AAGAGG
                                |||||||||      ||||||
                                CTCTATCTT      TTCTCC
                                     CCTTC__
GAM2015  COL19A1   3'  GAGATGGTACAAAAGGGG    49334      AGAATC       A
                                GAGAT     TGCAAAAG GG
                                |||||     |||||||| ||
                                CTCTA     ATGTTTTC CC
                                   CC____       C
GAM2015  CYP1B1    3'  TGAGAAGCAGCACAAAAGAGGA 49335      T  AATCT
                                TGAGA AG    GCAAAAGAGGA
                                ||||| ||    ||||||||||
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                                ACTCT TC    TGTTTTCTCCT
                                  _ GTCG_
GAM2015 DCK     3' TGAGGAAGACAAAAGAGG    49336     AT  AATCT
                                TGAG  AG    GCAAAAGAGG
                                ||||  ||    ||||||||||
                                ACTC  TC    TGTTTTCTCC
                                  CT  _____
GAM2015 EGLN2   5' TGAGGTAGCACACAAAAAGGG 49337     A   AATC      A
                                TGAG TAG    TGCAAAAG GG
                                |||| |||    |||||||| ||
                                ACTC ATC    GTGTTTTT CC
                                  C  GT__       C
GAM2015 FGFR1   3' TGAGACAGCTAAGCTAGGGGAG 49338       AATCT  AAAA_
            GA                    TGAGATAG    GC    GAGGA
                                |||||||     ||    |||||
                                ACTCTGTC    CG    CTCCT
                                    GATT_ ATCCC
GAM2015 FGFR1   3' TGAGACAGCTAAGCTAGGGGAG 49338       AATCT  AAAA_
            GA                    TGAGATAG    GC    GAGGA
                                |||||||     ||    |||||
                                ACTCTGTC    CG    CTCCT
                                    GATT_ ATCCC
GAM2015 JTB     3' TGAGATAGGGTCTCTAAGA   49339       AA  GCAA
                                TGAGATAG  TCT   AAGA
                                ||||||||  |||   ||||
                                ACTCTATC  AGA   TTCT
                                    CC  GA__
GAM2015 MUC4    5' TGGGAAGAGGACAAAAGAGG  49340   A  T  ATCT
                                TG GA AGA   GCAAAAGAGG
                                || || |||   ||||||||||
                                AC CT TCT   TGTTTTCTCC
                                 C  _  CC__
GAM2015 MUC4    5' TGGGAAGAGGACAAAAGAGG  49340   A  T  ATCT
                                TG GA AGA   GCAAAAGAGG
                                || || |||   ||||||||||
                                AC CT TCT   TGTTTTCTCC
                                 C  _  CC__
GAM2015 PSEN1   5' TGAGAAGAATCTGAGAGG    49341     T     CAAA
                                TGAGA AGAATCTG   AGAGG
                                ||||| ||||||||   |||||
                                ACTCT TCTTAGAC   TCTCC
                                  _     _____
GAM2015 PTPRC   3' TGAGTAGAACAAGGAG     49342     A   ATCT   AA
                                TGAG TAGA   GCAA  GAG
                                |||| ||||   ||||  |||
                                ACTC ATCT   TGTT  CTC
                                  _   _____   C_
GAM2015 PTPRC   3' TGAGTAGAACAAGGAG     49342     A   ATCT   AA
                                TGAG TAGA   GCAA  GAG
                                |||| ||||   ||||  |||
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                                ACTC ATCT    TGTT  CTC
                                  _   _____    C_
GAM2015  ASB13    3'  TGAGGATGGTCCGTAAAAGAGG 49343      ATAGAA    C
             A                   TGAG      TCTG AAAAGAGGA
                                 ||||      |||| |||||||||
                                 ACTC      AGGC TTTTCTCCT
                                   CTACC_    A
GAM2015  C20orf139 3'  TGAGACAGAGAGAAAGGGG    49344         ATCTGCA    A
                                 TGAGATAGA       AAAG GG
                                 |||||||||       |||| ||
                                 ACTCTGTCT       TTTC CC
                                      CTC_____    C
GAM2015  CSTF1    3'  TGAGACAGGACGTGGGGGAGGA 49345         A  C  CAAAA
                                 TGAGATAG AT TG     GAGGA
                                 |||||||| || ||     |||||
                                 ACTCTGTC TG AC     CTCCT
                                      C  C  CCC__
GAM2015  DKFZp434E2220 5'  TGAATAGAATCTGTAATATAGG 49346      A        CAAAAG
                                 TGAG TAGAATCTG      AGG
                                 |||| |||||||||      |||
                                 ACTT ATCTTAGAC      TCC
                                   _        ATTATA
GAM2015  FARSL    3'  TGGGACAGGTGGGAAAGAGGA  49347    A    AATC  CA
                                 TG GATAG    TG  AAAGAGGA
                                 || |||||    ||  ||||||||
                                 AC CTGTC    AC  TTTCTCCT
                                  C     C___  CC
GAM2015  FLJ22548 3'  GAGCAATTTGCAAAAGGGGA   49348     ATAG   C       A
                                 GAG    AAT TGCAAAAG GGA
                                 |||    ||| |||||||| |||
                                 CTC    TTA ACGTTTTC CCT
                                   G___   A       C
GAM2015  FLJ32499  5'  TGAGACAGAAAAACAAGGGAGG 49349          TCT    AA
             A                   TGAGATAGAA   GCAA  GAGGA
                                 ||||||||||   ||||  |||||
                                 ACTCTGTCTT   TGTT  CTCCT
                                      TT_    CC
GAM2015  GNG4     3'  TGAGTAGGAGCCAAAAGAGGA  49350      A   AATCT  _
                                 TGAG TAG     GC AAAAGAGGA
                                 |||| |||     || |||||||||
                                 ACTC ATC     CG TTTTCTCCT
                                   _   CT___  G
GAM2015  HCDI     3'  TGGGAAAGAGGACTGGGAGAGG 49351    A  T   AT_   CAAA
             A                   TG GA AGA   CTG    AGAGGA
                                 || || |||   |||    ||||||
                                 AC CT TCT   GAC    TCTCCT
                                  C  T   CCT   CC__
GAM2015  MAB21L2   3'  TGAGGGTAGAGGTTCAGGAGAG 49352      A_    ATCTG  AA
             G                   TGAG  TAGA    CA  AGAGG
                                 ||||  ||||    ||  |||||
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                                ACTC  ATCT    GT  TCTCC
                                  CC    CCAA_  CC
GAM2015  MARCKS    3'  TGAGATGGGATCTGTGGGGAGG 49353       AGA    CAAAA
                                TGAGAT   ATCTG    GAGG
                                ||||||   |||||    ||||
                                ACTCTA   TAGAC    CTCC
                                   CCC    ACCC_
GAM2015  OR1F2     5'  TGAGGAAGAACACAAAGAGGA  49354     AT    CT    A
                                TGAG  AGAAT  GCAAA GAGGA
                                ||||  |||||  ||||| |||||
                                ACTC  TCTTG  TGTTT CTCCT
                                  CT    __    _
GAM2015  PDE4DIP   3'  AGGTAGCTGCACAAAAGG    49355    A   AAT    A
                                AG TAG   CTGCA AAGAGG
                                || |||   ||||| ||||||
                                TC ATC   GACGT TTTTCC
                                 C  ___    G
GAM2015  RAP140    5'  GAGATGGAATCAAAGAGG    49356      A    TGCA
                                GAGAT GAATC    AAAGAGG
                                ||||| |||||    |||||||
                                CTCTA CTTAG    TTTCTCC
                                  C    ____
GAM2015  SLC12A8   3'  TGGGACAGCTCCAAAAGAGGA  49357    A    AAT  G
                                TG GATAG   CT CAAAAGAGGA
                                || |||||   || ||||||||||
                                AC CTGTC   GA GTTTTCTCCT
                                 C    ___  G
GAM2015  THEA      3'  TGAGGAGGATTAGTAAAAGAGG 49358     ATA  ATCTGC
            A                    TGAG   GA     AAAAGAGGA
                                ||||   ||     |||||||||
                                ACTC   CT     TTTTCTCCT
                                  CTC  AATCA_
GAM2015  TINF2     3'  TGAGGTGAGAGCAAGCAAAGAG 49359     AT_   ATCT    A
            GA                   TGAG   AGA    GCAAA GAGGA
                                ||||   |||    ||||| |||||
                                ACTC   TCT    CGTTT CTCCT
                                  CAC   CGTT    _
GAM2015  TTTY9     3'  TGAGATCAATTGTAAAGGAGGA 49360       AG   C  C   A
                                TGAGAT  AAT TG AAA GAGGA
                                ||||||  ||| || ||| |||||
                                ACTCTA  TTA AC TTT CTCCT
                                   G_   _ A   C
GAM2015  LOC149175 3'  TGGGAAGGAGGCCTGAGGAGAG 49361    A  TA  A_   CAAA
            GA                   TG GA  GA  TCTG    AGAGGA
                                || ||  ||  ||||    ||||||
                                AC CT  CT  GGAC    TCTCCT
                                 C  TC  CC    TCC_
GAM2015  LOC153688 3'  TGAGATAAGGGATGGGGGAGAG 49362         AATC  CAAA
            GA                   TGAGATAG    TG    AGAGGA
                                ||||||||    ||    ||||||
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                                ACTCTATT   AC   TCTCCT
                                     CCCT  CCCC
GAM2015  LOC162333 5'  TGAGCTAGAGTCAAGAGG    49363     A   A  TGCAA
                                TGAG TAGA TC    AAGAGG
                                |||| |||| ||    ||||||
                                ACTC ATCT AG    TTCTCC
                                  G   C _____
GAM2015  LOC202152 3'  TGAGATAGGCTGAGAG     49364       AAT   CAAA
                                TGAGATAG   CTG   AGAG
                                ||||||||   |||   ||||
                                ACTCTATC   GAC   TCTC
                                     C__   _____
GAM2015  LOC253092 5'  TGAAATAGATGATGAGAGG   49365        ATC  CAAA
                                TGAGATAGA   TG   AGAGG
                                |||||||||   ||   |||||
                                ACTTTATCT   AC   TCTCC
                                      ACT  _____
GAM2015  LOC254428 3'  TAGAAGCCAAGAAAGAGGA   49366      T   CA
                                TAGAA CTG  AAAGAGGA
                                ||||| |||  ||||||||
                                ATCTT GGT  TTTCTCCT
                                   C   TC
GAM2015  LOC64116  5'  TGAGATAAAGAGGACAAAGGGG 49367        ATCT    AGA
           GA                    TGAGATAGA   GCAAA   GGA
                                |||||||||   |||||   |||
                                ACTCTATTT   TGTTT   CCT
                                      CTCC    CCC
GAM2015  LOC90408  5'  TGAGACAGAAAGTATAAGGAGG 49368         TCTGCAAAA
           A                     TGAGATAGAA       GAGGA
                                ||||||||||       |||||
                                ACTCTGTCTT       CTCCT
                                      TCATATTC_
GAM2015  LOC91035  5'  CGAGATGGAGAAAAGAGG    49369       A  ATCTGC
                                TGAGAT GA     AAAAGAGG
                                |||||| ||     ||||||||
                                GCTCTA CT     TTTTCTCC
                                   C  C_____
GAM2016  DAZ      3'  CTTCACTTCTTTCACTGA    49372          GCTCA
                                CTTCATTTCT    CACTGA
                                ||||||||||    ||||||
                                GAAGTGAAGA    GTGACT
                                      AA___
GAM2016  DAZ      3'  CTTCACTTCTTTCACTGA    49372          GCTCA
                                CTTCATTTCT    CACTGA
                                ||||||||||    ||||||
                                GAAGTGAAGA    GTGACT
                                      AA___
GAM2016  FUS2     3'  CCTTTATTCAGCCACACTGA   49373     CAT   T  T
                                CCTT   TTC GC CACACTGA
                                ||||   ||| || ||||||||
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                                GGAA   AAG CG GTGTGACT
                                  AT_   T  _
GAM2016  FUT4     3'  TTCATTTCTGCACTG       49374          TCAC
                                TTCATTTCTGC    ACTG
                                ||||||||||    ||||
                                AAGTAAAGACG    TGAC
                                       ____
GAM2016  MMP19    5'  ACCTCCATTGCTCATGCTGA   49375        TTC     CA
                                ACCTTCAT   TGCTCA  CTGA
                                ||||||||   ||||||  ||||
                                TGGAGGTA   ACGAGT  GACT
                                     ___      AC
GAM2016  MMP25    3'  CCTTCTGTCCTCATGCTGA    49376      ATT  TG    CA
                                CCTTC   TC  CTCA  CTGA
                                |||||   ||  ||||  ||||
                                GGAAG   AG  GAGT  GACT
                                   AC_  __    AC
GAM2016  MSH2     3'  TACCTTCATTCCATTACTG    49377           TGCTCAC
                                TACCTTCATTTC      ACTG
                                ||||||||||||      ||||
                                ATGGAAGTAAGG      TGAC
                                      TAA____
GAM2016  THBD     3'  TACATTTATTTCCATACACTGA 49378     C  C      CTC
                                TAC TT ATTTCTG   ACACTGA
                                ||| || |||||||   |||||||
                                ATG AA TAAAGGT   TGTGACT
                                  T  A      A__
GAM2016  UPF3A    3'  CTTCAGGACTCACACTG     49379      TTTCT
                                CTTCA    GCTCACACTG
                                |||||    ||||||||||
                                GAAGT    TGAGTGTGAC
                                   CC___
GAM2016  UPF3A    3'  CTTCAGGACTCACACTG     49379      TTTCT
                                CTTCA    GCTCACACTG
                                |||||    ||||||||||
                                GAAGT    TGAGTGTGAC
                                   CC___
GAM2016  AAK1     3'  CTTTATTTCTGCTGCTCTGA   49380     C       CACA
                                CTT ATTTCTGCT    CTGA
                                ||| |||||||||    ||||
                                GAA TAAAGACGA    GACT
                                  A        CGA_
GAM2016  BDG-29   3'  TTCATTCCCCTATACTGA    49381         G  CAC
                                TTCATTTCT CT   ACTGA
                                |||||||||  ||   |||||
                                AAGTAAGGG GA   TGACT
                                      _  TA_
GAM2016  DKFZp434I1610 3'  CCCACACTGCTTACATTGA   49382     T  TTT    C   C
                                CCT CA   CTGCT ACA TGA
                                |||  ||   ||||| ||| |||
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                                GGG GT   GACGA TGT ACT
                                  T ___    A  A
GAM2016  DKFZP586L151 3'  TTCATTTCTGCTCCTG      49383           ACA
                                TTCATTTCTGCTC  CTG
                                |||||||||||||  |||
                                AAGTAAAGACGAG  GAC
                                       ___
GAM2016  FLJ12057  3'  TACCTCCATTTAGCACTG     49384          CT  TCAC
                                TACCTTCATTT  GC   ACTG
                                ||||||||||  ||   ||||
                                ATGGAGGTAAA  CG   TGAC
                                      T_ ____
GAM2016  FLJ14957  3'  TCTTCCTTCTCACACTG      49385    A    G
                                TC TTTCT CTCACACTG
                                || ||||| |||||||||
                                AG AAGGA GAGTGTGAC
                                 _    A
GAM2016  HIC       3'  CCTCGTTTAAATACACACTGA  49386     A  CTGCT
                                CTTC TTT    CACACTGA
                                |||| |||    ||||||||
                                GGAG AAA    GTGTGACT
                                  C  TTTAT
GAM2016  HSA249128 3'  TTCATTTCCACAGCACTGA    49387        TG TCA
                                TTCATTTC  C   CACTGA
                                ||||||||  |   ||||||
                                AAGTAAAG  G   GTGACT
                                     GT TC_
GAM2016  IL18BP    5'  CCTTCACCTTCACACTG      49388        CTGC
                                CCTTCATTT   TCACACTG
                                |||||||||   ||||||||
                                GGAAGTGGA   AGTGTGAC
                                       ____
GAM2016  KIAA0229  3'  CTTCATTTGGCCACTG       49389        CT  TCA
                                CTTCATTT  GC   CACTG
                                ||||||||  ||   |||||
                                GAAGTAAA  CG   GTGAC
                                     C_  ___
GAM2016  MGC20255  3'  TTCATTTCTGCCTCTG       49390          CACA
                                TTCATTTCTGCT   CTG
                                ||||||||||||   |||
                                AAGTAAAGACGG   GAC
                                       A___
GAM2016  VEZATIN   3'  CTTCACTCTCACATTG       49391        TCTG     C
                                CTTCATT   CTCACA TG
                                |||||||   |||||| ||
                                GAAGTGA   GAGTGT AC
                                     ____     A
GAM2016  ZNF294    3'  ACTTTCATTTCTGAAGGCTGA  49392    C        CTCACA
                                AC TTCATTTCTG     CTGA
                                || ||||||||||     ||||
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                                TG AAGTAAAGAC     GACT
                                 A        TTCC__
GAM2016  LOC138354 5'  TACTTTTCTTTCTGCTGCTGCT 49393    C  CA      CACA
                GA                TAC TT  TTTCTGCT   CTGA
                                  ||| ||  ||||||||   ||||
                                  ATG AA  AAAGACGA   GACT
                                    A  AG       CGAC
GAM2016  LOC143872 5'  CTTCATTCAAATACACTGA   49394       CTGCTC
                                  CTTCATTT     ACACTGA
                                  ||||||||     |||||||
                                  GAAGTAAG     TGTGACT
                                       TTTA__
GAM2016  LOC145813 3'  ATTTCGTTTACCACACTG    49395      ___   T
                                  ATTTC   TGC CACACTG
                                  |||||   ||| |||||||
                                  TAAAG   ATG GTGTGAC
                                     CAA   _
GAM2016  LOC147072 5'  CTTCATTTTCCTCACGCTG   49396       CTG    A
                                  CTTCATTT   CTCAC CTG
                                  ||||||||   ||||| |||
                                  GAAGTAAA   GAGTG GAC
                                       AG_    C
GAM2016  LOC149600 5'  CTCATCATGTCACACTGA    49397      TC  C
                                  TTCATT  TG TCACACTGA
                                  ||||||  || |||||||||
                                  GAGTAG  AC AGTGTGACT
                                     T_  _
GAM2016  LOC149911 3'  CTTTATTTCTGCCCATCTTGA  49398    C         CAC
                                  CTT ATTTCTGCTCA   TGA
                                  ||| ||||||||||   |||
                                  GAA TAAAGACGGGT   ACT
                                    A          AGA
GAM2016  LOC152215 3'  CCGGATTCTGTTCACACTG   49399    TTCAT    C
                                  CC     TTCTG TCACACTG
                                  ||     ||||| ||||||||
                                  GG     AAGAC AGTGTGAC
                                   CCT__     A
GAM2016  LOC152404 5'  CTTCTGTGTCGCTCACACTG   49400     ATTTC
                                  CTTC     TGCTCACACTG
                                  ||||     ||||||||||
                                  GAAG     GCGAGTGTGAC
                                    ACACA
GAM2016  LOC161321 5'  TACTTTCATTTCTGCTATCCCT 49401    C          CACA
                GA                TAC TTCATTTCTGCT    CTGA
                                  ||| ||||||||||||    ||||
                                  ATG AAGTAAAGACGA    GACT
                                    A           TAGG
GAM2016  LOC253003 3'  CCTTTGTTACAGTCACACTGA  49402     CA  TCTGC
                                  CCTT  TT     TCACACTGA
                                  ||||  ||     |||||||||
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                                GGAA  AA    AGTGTGACT
                                  AC  TGTC_
GAM2016  LOC253336 5'  TTCATTTCTTCTGACTGA    49403        G  CAC
                                TTCATTTCT CT   ACTGA
                                ||||||||| ||   |||||
                                AAGTAAAGA GA   TGACT
                                     A  C__
GAM2017  ADD1    3'  TGCCCGCGTAGCAGGCCCTGC  49406     G   CTCTTT
                                TGCC GCGT     GGCCCTGC
                                |||| ||||     ||||||||
                                ACGG CGCA     CCGGGACG
                                  G   TCGT__
GAM2017  ADD1    3'  TGCCCGCGTAGCAGGCCCTGC  49406     G   CTCTTT
                                TGCC GCGT     GGCCCTGC
                                |||| ||||     ||||||||
                                ACGG CGCA     CCGGGACG
                                  G   TCGT__
GAM2017  ATP11A   3'  CTGCCGGCGTGGCCT      49407        CTCTTT   C
                                CTGCCGGCGT     GGCC T
                                ||||||||||     |||| |
                                GACGGCCGCA     CCGG A
                                     _______   A
GAM2017  DGKG     5'  GGCGTCTTCCCGCCTGC     49408       C  G  C
                                GGCGTCT TTT GCC TGC
                                ||||||| ||| ||| |||
                                CCGCAGA AGG CGG ACG
                                   _  G  _
GAM2017  GPR48    3'  GTCCCTTTTTTGGCCCTGC   49409       ___
                                GTCTCTT   TGGCCCTGC
                                |||||||   |||||||||
                                CAGGGAA   ACCGGGACG
                                   AAA
GAM2017  C1orf34  3'  CTGAGCCTTTGGTCCTGC    49410    CC  GTCT    C
                                CTG  GGC   CTTTGG CCTGC
                                |||  |||   |||||| |||||
                                GAC  TCG   GAAACC GGACG
                                  __  _____     A
GAM2017  C8orf13  3'  CTGCTGGGGTCTTAACTTG   49411    C  C   CTT   CC
                                CTGC GG GTCT   TGGC  TG
                                |||| || ||||   ||||  ||
                                GACG CC CAGA   ATTG  AC
                                  A  C   ___   A_
GAM2017  C8orf17  5'  CTGCACGGCGAAGTGGCTCTG  49412     _   TCTCTT   C
                                CTGC CGGCG     TGGC CTG
                                |||| |||||     |||| |||
                                GACG GCCGC     ACCG GAC
                                  T    TTC___   A
GAM2017  CST8     5'  CTGTTAGCGTCAGCCCAGCCCT 49413    CC     TC  TG
            G                    CTG  GGCGTC  TT  GCCCTG
                                |||  ||||||  ||  ||||||
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                                GAC  TCGCAG  GG  CGGGAC
                                  AA     TC  GT
GAM2017  DJ473B4   5'  TGTCAGCGTCTCTAGGCTGC   49414    C       TT   CC
                                TG CGGCGTCTCT  GGC  TGC
                                || ||||||||||  |||  |||
                                AC GTCGCAGAGA  CCG  ACG
                                 A        T_  __
GAM2017  DKFZP566J091 3'  CTGCCGGCCTCTCCCACTTCTG 49415        G     TGGCC
           C                     CTGCCGGC TCTCTT     CTGC
                                |||||||| ||||||     ||||
                                GACGGCCG AGAGGG     GACG
                                    G     TGAA_
GAM2017  FLJ10851  3'  TGCTGGCTCTTGGCCCTG    49416     C   G   CTT
                                TGC GGC TCT   TGGCCCTG
                                ||| ||| |||   ||||||||
                                ACG CCG AGA   ACCGGGAC
                                  A  _  ___
GAM2017  FLJ12057  5'  CTGCCGGCGTCTTCTTCTCCTC 49417          _   GGC_
           CTGC                   CTGCCGGCGTCT CTTT    CCTGC
                                ||||||||||| ||||    |||||
                                GACGGCCGCAGA GAAG    GGACG
                                      A    AGGA
GAM2017  FLJ20689  3'  TGCTGGTGTCTCTTTTGAGGC  49418     C  C      ___
                                TGC GG GTCTCTTT   GGC
                                ||| || ||||||||   |||
                                ACG CC CAGAGAAA   CCG
                                  A  A       ACT
GAM2017  FLJ20689  3'  TGCTGGTGTCTCTTTTGAGGC  49418     C  C      ___
                                TGC GG GTCTCTTT   GGC
                                ||| || ||||||||   |||
                                ACG CC CAGAGAAA   CCG
                                  A  A       ACT
GAM2017  FLJ20694  3'  CTGCTGGCTTCTCCCCGATGTC 49419      C   G       C__
           CTG                    CTGC GGC TCTCTTTGG   CCTG
                                |||| ||| |||||||||   ||||
                                GACG CCG AGAGGGGCT   GGAC
                                  A   A       ACA
GAM2017  KIAA1856  3'  TGCCGCGCACGATGGCCTTG   49420      G   CTCTT    C
                                TGCCG CGT     TGGCC TG
                                ||||| |||     ||||| ||
                                ACGGC GCG     ACCGG AC
                                   _   TGCT_    A
GAM2017  KIAA1879  3'  CTGCTGCTGTTTCTTCGTGC   49421      CG  _  C     _
                                CTGC  GC GT TCTTTG GC
                                ||||  || || |||||| ||
                                GACG  CG CA AGAAGC CG
                                  A_  A  A     A
GAM2017  PSKH1     5'  CGGCGTCTCGGCGGCTCTGC   49422         TT    C
                                CGGCGTCTC  TGGC CTGC
                                |||||||||  |||| ||||
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                                GCCGCAGAG  GCCG GACG
                                     CC    A
GAM2017  YAP      5'  CTGCTGGAGTCTCTTCCT    49423      C  C      TGGC
                                CTGC GG GTCTCTT    CCT
                                |||| || |||||||    |||
                                GACG CC CAGAGAA    GGA
                                  A  T     _____
GAM2017  LOC204970 3'  CTGCTGGTTCCAGCCCTG    49424      C  CG   CTTT
                                CTGC GG  TCT    GGCCCTG
                                |||| ||  |||    |||||||
                                GACG CC  AGG    TCGGGAC
                                  A  A_  _____
GAM2017  LOC219842 5'  GGCTCTCTCTACCTG       49425      G       GC
                                GGC TCTCTTTG  CCTG
                                ||| ||||||||  ||||
                                CCG AGAGAGAT  GGAC
                                  _       __
GAM2017  LOC221486 3'  CAGCTGTGCTTTGGCCCTG    49426      GTCT
                                CGGC    CTTTGGCCCTG
                                ||||    ||||||||||
                                GTCG    GAAACCGGGAC
                                  ACAC
GAM2017  LOC222136 3'  CGGCGTCTCTATCCTGC      49427          TTGGC
                                CGGCGTCTCT     CCTGC
                                ||||||||||     |||||
                                GCCGCAGAGA     GGACG
                                     TA___
GAM2017  LOC253971 3'  CTGCCGGCTTCTGCTTTTGC   49428         G  _   G
                                CTGCCGGC TCT CTTT GC
                                |||||||| ||| |||| ||
                                GACGGCCG AGA GAAA CG
                                     A  C   A
GAM2017  LOC255043 5'  CTGCTGGGGTTCCAGGGCCCTG 49429      C  C  C   TT
                                CTGC GG GT TCT  GGCCCTG
                                |||| || || |||  |||||||
                                GACG CC CA AGG  CCGGGAC
                                  A  C  _   TC
GAM2017  LOC51207  5'  CTGCCGGCTTTCAGCCGCCTG  49430        GTCTC  TG   __
                                CTGCCGGC    TT  GCC  CTG
                                ||||||||    ||  |||  |||
                                GACGGCCG    AA  CGG  GAC
                                     A____  GT   CG
GAM2017  LOC54505  5'  CTGAGCCTCTTTTTGGCCTTGC 49431     CC   G   C      C
                                CTG  GGC TCT TTTGGCC TGC
                                |||  ||| ||| ||||||| |||
                                GAC  TCG AGA AAACCGG ACG
                                  __   G   A      A
GAM2018  CSHL1     3'  TGGAGCAGCCCGTAGTT     49434          AA
                                TGGAGCAGCCT  TAGTT
                                ||||||||||  |||||
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                                ACCTCGTCGGG  ATCAA
                                      C_
GAM2018  CSHL1    3'  TGGAGCAGCCCGTAGTT     49434          AA
                                TGGAGCAGCCT  TAGTT
                                |||||||||||  |||||
                                ACCTCGTCGGG  ATCAA
                                      C_
GAM2018  CSHL1    3'  TGGAGCAGCTCTAAGTT     49435         _  AT
                                TGGAGCAGC CTA  AGTT
                                |||||||||| |||  ||||
                                ACCTCGTCG GAT  TCAA
                                     A  __
GAM2018  ITGA1    3'  ATGGAGCAACCTAGGAGCT   49436           AT
                                ATGGAGCAGCCTA  AGTT
                                ||||||||||||  ||||
                                TACCTCGTTGGAT  TCGA
                                       CC
GAM2018  C1orf19  3'  ATGAAGCAGTCTGATGGGTCT  49437         C  A  A_
                                ATGGAGCAG CT AT  GTTT
                                |||||||||  || ||  ||||
                                TACTTCGTC GA TA  CAGA
                                     A  C  CC
GAM2018  GNG10    3'  ATGGGGCAGCCTAATGC     49438      A         A
                                ATGG GCAGCCTAAT GT
                                |||| ||||||||||  ||
                                TACC CGTCGGATTA CG
                                  C         _
GAM2018  HMP19    3'  ATGGAGCCAGTTTAA       49439        AGCCTAA
                                ATGGAGC      TAGTTTAA
                                |||||||      ||||||||
                                TACCTCG      GTCAAATT
                                          ________
GAM2018  KIAA0376 3'  TGGGGCAGCCCAGAGTT     49440     A       AT
                                TGG GCAGCCTA  AGTT
                                |||  ||||||||  ||||
                                ACC CGTCGGGT  TCAA
                                  C       C_
GAM2018  KIAA1522 3'  ATGGAGCACCTGGCAGAAC   49441         G   AA   TTT
                                ATGGAGCA CCT  TAG   AAC
                                |||||||| |||  |||   |||
                                TACCTCGT GGA  GTC   TTG
                                     _   CC   ____
GAM2018  RAB9A    3'  ATGAAGCAGCAACATTAGTTTA 49442          CTAA_
              A                  ATGGAGCAGC     TAGTTTAA
                                 ||||||||||     ||||||||
                                 TACTTCGTCG     ATCAAATT
                                       TTGTA
GAM2019  BCRP2    3'  CTCTGGAAAGCTGTCTTT     49445      AACAA
                                CTCT     AAAGCTGTCTTT
                                ||||     ||||||||||||
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                                GAGA    TTTCGACAGAAA
                                  CC___
GAM2019  CALCR    3'  TCTCTATTAGAAAGCCGCTTT  49446       ACAA      T
                                TCTCTA   AAAGCTG CTTT
                                ||||||   ||||||| ||||
                                AGAGAT   TTTCGGC GAAA
                                   AATC     _
GAM2019  CD8A     3'  TCTCCAACAATTGTCTTTA   49447         AAAGC
                                TCTCTAACAA    TGTCTTTA
                                ||||||||||    ||||||||
                                AGAGGTTGTT    ACAGAAAT
                                      A____
GAM2019  ITPKB    3'  TCTCTACAAAAAGCAGT     49448       A       T
                                TCTCTA CAAAAAGC GT
                                |||||| |||||||| ||
                                AGAGAT GTTTTTCG CA
                                   _       T
GAM2019  LRRC2    3'  AACAAAAAACTGATTTTA    49449          TC
                                AACAAAAAGCTG  TTTA
                                ||||||||||||  ||||
                                TTGTTTTTTGAC  AAAT
                                      TA
GAM2019  NACA     3'  TCCAACAAGAAGCCATAACTTT 49450        A      __
              A                  TCTAACAA AAGCTGT  CTTTA
                                 |||||||| |||||||  |||||
                                 AGGTTGTT TTCGGTA  GAAAT
                                    C      TT
GAM2019  PRIM2A   3'  TCCCCAAAGCTGTTTTTA    49451       CAAAA     C
                                TCTCTAA    AGCTGT TTTA
                                |||||||    |||||| ||||
                                AGGGGTT    TCGACA AAAT
                                   ______     A
GAM2019  PRKCN    3'  TCTCTGACAGTGCCTTTA    49452      A   AAAA C
                                TCTCT ACA    G TGTCTTTA
                                ||||| |||    | ||||||||
                                AGAGA TGT    C ACGGAAAT
                                   C  _____ _
GAM2019  REV3L    3'  TAACAAAAATGTCTTT      49453         GC
                                TAACAAAAA  TGTCTTT
                                |||||||||  |||||||
                                ATTGTTTTT  ACAGAAA
                                      __
GAM2019  ZNF80    3'  TCTAACATGCTATCTTTA    49454       AAAA
                                TCTAACA    GCTGTCTTTA
                                |||||||    ||||||||||
                                AGATTGT    CGATAGAAAT
                                   A___
GAM2019  DEPP     3'  TCTCTACAGAAGCCTTTA    49455       A  AAAA CT
                                TCTCTA CA    G  GTCTTTA
                                |||||| ||    |  |||||||
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                                AGAGAT GT    C  CGGAAAT
                                   _  ____ TT
GAM2019  FKSG79    5'  TCTCTAGAGAAACTATCTTT   49456       ACAAA
                                TCTCTA     AAGCTGTCTTT
                                ||||||     ||||||||||
                                AGAGAT     TTTGATAGAAA
                                   CTC__
GAM2019  FLJ10697  3'  TAACAAAAATGTCTTT      49453         GC
                                TAACAAAAA  TGTCTTT
                                |||||||||  |||||||
                                ATTGTTTTT  ACAGAAA
                                   __
GAM2019  FLJ22479  3'  TCTCTAACAAAAATGCCACACA 49457            _  TG CTT
            TAC                    TCTCTAACAAAAA GC  T   TAC
                                |||||||||||||| ||  |   |||
                                AGAGATTGTTTTT CG  G   ATG
                                      A  GT TGT
GAM2019  GPR107    3'  TAACAAAAAACCTGTTTTA    49458         G    C
                                TAACAAAAA CTGT TTTA
                                |||||||||  ||||  ||||
                                ATTGTTTTT GACA AAAT
                                     G   _
GAM2019  KIAA0987  3'  TCTCTGCCAGTGTCTTTA    49459       AA  AAAA C
                                TCTCT  CA    G TGTCTTTA
                                |||||  ||    | ||||||||
                                AGAGA  GT    C ACAGAAAT
                                   CG  _____ _
GAM2019  KIAA1884  3'  TCCTAACTCTGTCTTTA     49460     T    AAAAAG
                                TC CTAAC     CTGTCTTTA
                                || |||||     |||||||||
                                AG GATTG     GACAGAAAT
                                  _    A_____
GAM2019  MGC4268   3'  TCTCTAACATGAGTTGTTTTA  49461         AAA  C   C
                                TCTCTAACA   AG TGT TTTA
                                |||||||||   || ||| ||||
                                AGAGATTGT   TC ACA AAAT
                                     AC_  A  _
GAM2019  S164      3'  TCTAACAGGCCAATCTTTAC   49462        AAAA   _
                                TCTAACA    GCTG TCTTTAC
                                |||||||    |||| |||||||
                                AGATTGT    CGGT AGAAATG
                                   C___    T
GAM2019  WNT16     3'  TCTTTACAAAACACTGTCTTTA 49463     CTA     A
            C                    TCT   ACAAAA GCTGTCTTTAC
                                |||   |||||| ||||||||||
                                AGA   TGTTTT TGACAGAAATG
                                  AA_     G
GAM2019  WNT16     3'  TCTTTACAAAACACTGTCTTTA 49463     CTA     A
            C                    TCT   ACAAAA GCTGTCTTTAC
                                |||   |||||| ||||||||||
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                                AGA   TGTTTT TGACAGAAATG
                                  AA_     G
GAM2019  LOC148696 5'  TCTCTAACCTGTCTTT      49464         AAAAAG
                                TCTCTAAC     CTGTCTTT
                                ||||||||     ||||||||
                                AGAGATTG     GACAGAAA
                                          _______
GAM2019  LOC221543 3'  TCTTACACCTGTCTTTA     49465     A   AAAAG
                                TCT ACA     CTGTCTTTA
                                ||| |||     |||||||||
                                AGA TGT     GACAGAAAT
                                  A   G____
GAM2019  LOC221543 5'  TCTAACAAAGAGCAGCCT    49466         A   T
                                TCTAACAAA AGC GTCT
                                ||||||||| ||| ||||
                                AGATTGTTT TCG CGGA
                                      C   T
GAM2019  LOC255065 3'  TCTCTACAGAAAGCTAT     49467       A  A
                                TCTCTA CA AAAGCTGT
                                |||||| || ||||||||
                                AGAGAT GT TTTCGATA
                                   _  C
GAM2019  LOC257596 3'  TCTTACACCTGTCTTTA     49465     A   AAAAG
                                TCT ACA     CTGTCTTTA
                                ||| |||     |||||||||
                                AGA TGT     GACAGAAAT
                                  A   G____
GAM2019  LOC257596 5'  TCTAACAAAGAGCAGCCT    49466         A   T
                                TCTAACAAA AGC GTCT
                                ||||||||| ||| ||||
                                AGATTGTTT TCG CGGA
                                      C   T
GAM2019  LOC90494  5'  TCTCTAATAAATGTGCCTTTA  49468       C   AAGC
                                TCTCTAA AAA    TGTCTTTA
                                ||||||| |||    ||||||||
                                AGAGATT TTT    ACGGAAAT
                                   A   AC__
GAM2020  CHRNB4    3'  TTAAAAGAAAAAAAAAAAGAT  49471         C_
                                TTAAAAGA  AAAAAGGAGAT
                                ||||||||  ||||||||||
                                AATTTTCT  TTTTTTTTCTA
                                     TT
GAM2020  CTSS      3'  TTAAAAGACAAAGAG       49472           AAA
                                TTAAAAGACAA   GGAG
                                ||||||||||   ||||
                                AATTTTCTGTT   TCTC
                                          ___
GAM2020  INPP1     3'  TCAAAAGACAGAGAT       49473           AAAAG
                                TTAAAAGACA    GAGAT
                                ||||||||||    |||||
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                                AGTTTTCTGT    CTCTA
                                      _____
GAM2020 OVOL1    3' TTAAAAAATAAAAGGAAATA  49474       CA
                                TTAAAAGA  AAAAGGAGATA
                                ||||||||  ||||||||||
                                AATTTTTT  TTTTCCTTTAT
                                     A_
GAM2020 RNTRE    3' CTAAAAGACAAGGAA      49475        AAA
                                TTAAAAGACA   AGGAG
                                ||||||||||   |||||
                                GATTTTCTGT   TCCTT
                                      ___
GAM2020 SLC7A7   3' TTAAAAGAAAAGAGGAG    49476       C   A
                                TTAAAAGA AAA AGGAG
                                |||||||| ||| |||||
                                AATTTTCT TTT TCCTC
                                     _  C
GAM2020 SP3      3' TTAAAAAATAAAAAGAAAATA 49477       C
                                TTAAAAGA AAAAAGGAGATA
                                |||||||| ||||||||||||
                                AATTTTTT TTTTTCTTTTAT
                                     A
GAM2020 XYLB     3' TAAAAGACAGGAAAAGAGAGAT 49478        __   _
                                TAAAAGACA  AAAAG GAGAT
                                |||||||||  ||||| |||||
                                ATTTTCTGT  TTTTC CTCTA
                                      CC    T
GAM2020 caspr5   3' TCAAAAGACAGGAGA      49479        AAAA
                                TTAAAAGACA   GGAGA
                                ||||||||||   |||||
                                AGTTTTCTGT   CCTCT
                                      _____
GAM2020 DKFZp564K142 3' TTAAAAGAAAACTAAGGAGAT 49480       C  A_
                                TTAAAAGA AA  AAGGAGAT
                                |||||||| ||  ||||||||
                                AATTTTCT TT  TTCCTCTA
                                     T  GA
GAM2020 FLJ20514 3' AAAGACAAGAAAAGATA    49481       AA
                                AAAGACAA  AGGAGATA
                                ||||||||  ||||||||
                                TTTCTGTT  TTTTCTAT
                                     C_
GAM2020 FLJ22670 3' TCAAAAGACAGGAAA      49482        AAAA
                                TTAAAAGACA   GGAGA
                                ||||||||||   |||||
                                AGTTTTCTGT   CCTTT
                                      _____
GAM2020 FLJ32743 3' TTAAAAGACCAAGAAAAGATA 49483       A  A
                                TTAAAAGAC AA AGGAGATA
                                ||||||||| || ||||||||
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                                AATTTTCTG TT TTTTCTAT
                                     G  C
GAM2020  HRH4     3'  CTAAAAGACAAGGAAGAG    49484          AA
                                TTAAAAGACAA  AGGAG
                                ||||||||||  |||||
                                GATTTTCTGTT  TTCTC
                                      CC
GAM2020  KIAA0016 3'  TTAAAATACAAGGAGATA    49485       G   AAA
                                TTAAAA ACA   AGGAGATA
                                |||||| |||   ||||||||
                                AATTTT TGT   TCCTCTAT
                                   A  ___
GAM2020  KIAA0438 3'  TTAACAGACAAAGAAGAAATA 49486      A      A
                                TTAA AGACAAA AGGAGATA
                                |||| ||||||| ||||||||
                                AATT TCTGTTT TTCTTTAT
                                  G      C
GAM2020  KIAA1430 3'  TTAAAAAACAAAAGAAAATA   49487           A
                                TTAAAAGACAAAA GGAGATA
                                |||||||||||| |||||||
                                AATTTTTTGTTTT CTTTTAT
                                                _
GAM2020  KIAA1456 3'  TTAAAAGACAGAGGAA      49488          AAA
                                TTAAAAGACA   AGGAG
                                |||||||||   |||||
                                AATTTTCTGT   TCCTT
                                      C__
GAM2020  KIAA1576 3'  TCAAGAGACAGGAAAGAAG    49489     A    A_
                                TTAA AGACA  AAAGGAG
                                |||| |||||  |||||||
                                AGTT TCTGT  TTTCTTC
                                  C    CC
GAM2020  KRTAP3-1 3'  CTAAAAGACAGAAGGGAG    49490          A  A
                                TTAAAAGACA AA GGAG
                                |||||||||| || ||||
                                GATTTTCTGT TT CCTC
                                      C  C
GAM2020  MGC22014 3'  AAAAACAAAGAGAAAATA    49491          A
                                AAAGACAAA AGGAGATA
                                |||||||| ||||||||
                                TTTTTGTTT TCTTTTAT
                                     C
GAM2020  MGC3251  3'  TTAAAAAACAAGGGAAAT    49492          AAA
                                TTAAAAGACAA  GGAGAT
                                ||||||||||  ||||||
                                AATTTTTTGTT  CCTTTA
                                      C__
GAM2020  MSTP031  3'  TCAAAAAAATACAAAAGGAGAT 49493         CA__
            A                    TTAAAAGA   AAAAGGAGATA
                                ||||||||   ||||||||||
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                                AGTTTTTT   TTTTCCTCTAT
                                    TATG
GAM2020  PRO0971   3'  GACATAAAAAAGGAGATA   49494    ___
                                GACA  AAAAGGAGATA
                                ||||  ||||||||||
                                CTGT  TTTTCCTCTAT
                                  ATT
GAM2020  LOC115297 3'  TTAAAAGACAAAGGAAGAGA  49495         A_
                                TTAAAAGACAAA  AGGAGA
                                ||||||||||||  ||||||
                                AATTTTCTGTTT  TTCTCT
                                      CC
GAM2020  LOC124245 3'  TAAAAGACAGGAAAT      49496       AAAA
                                TAAAAGACA   GGAGAT
                                |||||||||   ||||||
                                ATTTTCTGT   CCTTTA
                                     ____
GAM2020  LOC145314 3'  TTAGGAGACAGCAGAAGAT   49497    AA   AAA
                                TTA  AGACA  AGGAGAT
                                |||  |||||  |||||||
                                AAT  TCTGT  TCTTCTA
                                  CC    CG_
GAM2020  LOC151632 5'  TCAAGGGACAGGAAGGAGAT  49498    AA   AA
                                TTAA  GACA  AAGGAGAT
                                ||||  ||||  ||||||||
                                AGTT  CTGT  TTCCTCTA
                                  CC    CC
GAM2020  LOC154215 3'  TAAAAGACAATTGTAGATA   49499       AAAGG
                                TAAAAGACAA    AGATA
                                ||||||||||    |||||
                                ATTTTCTGTT    TCTAT
                                     AACA_
GAM2020  LOC158730 3'  TTAAAAGACAAGGAAATA    49500       AAA
                                TTAAAAGACA  AGGAGATA
                                ||||||||||  ||||||||
                                AATTTTCTGT  TCCTTTAT
                                     ___
GAM2020  LOC200904 5'  TCAAGGGACAGGAAGGAGAT  49498    AA   AA
                                TTAA  GACA  AAGGAGAT
                                ||||  ||||  ||||||||
                                AGTT  CTGT  TTCCTCTA
                                  CC    CC
GAM2020  LOC202934 3'  TCAAAAGACAAAGAGAAAAT  49501         A
                                TTAAAAGACAAA AGGAGAT
                                ||||||||||||| |||||||
                                AGTTTTCTGTTT TCTTTTA
                                      C
GAM2020  LOC203083 5'  TCAAGGGACAGGAAGGAGAT  49498    AA   AA
                                TTAA  GACA  AAGGAGAT
                                ||||  ||||  ||||||||
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                                AGTT  CTGT  TTCCTCTA
                                  CC    CC
GAM2020  LOC219919 5'  TCAAGGGACAGGAAGGAGAT   49498      AA    AA
                                TTAA  GACA  AAGGAGAT
                                ||||  ||||  ||||||||
                                AGTT  CTGT  TTCCTCTA
                                  CC    CC
GAM2020  LOC221178 3'  AGACAAAGAAAAGGAGAT    49502        ___
                                AGACAAA   AAGGAGAT
                                |||||||   ||||||||
                                TCTGTTT   TTCCTCTA
                                    CTT
GAM2020  LOC221472 3'  TTAAAAGCTCCCCAGGAGATA  49503        ACAAAA
                                TTAAAAG     AGGAGATA
                                |||||||     ||||||||
                                AATTTTC     TCCTCTAT
                                    GAGGGG
GAM2020  LOC221641 5'  AAAAACAGAAGAAGATA     49504        AA
                                AAAGACA  AAGGAGATA
                                |||||||  |||||||||
                                TTTTTGT  TTCTTCTAT
                                    C_
GAM2020  LOC221795 5'  TCAAGGGACAGGAAGGAGAT   49498      AA    AA
                                TTAA  GACA  AAGGAGAT
                                ||||  ||||  ||||||||
                                AGTT  CTGT  TTCCTCTA
                                  CC    CC
GAM2020  LOC254176 5'  TCAAGGGACAGGAAGGAGAT   49498      AA    AA
                                TTAA  GACA  AAGGAGAT
                                ||||  ||||  ||||||||
                                AGTT  CTGT  TTCCTCTA
                                  CC    CC
GAM2020  LOC255465 3'  TCAAAAGACAAAGAGAAAAT   49501           A
                                TTAAAAGACAAA AGGAGAT
                                ||||||||||| |||||||
                                AGTTTTCTGTTT TCTTTTA
                                       C
GAM2020  LOC256515 5'  TCAAAGGACAGGAAGGAGAT   49505       A    AA
                                TTAAA GACA  AAGGAGAT
                                ||||| ||||  ||||||||
                                AGTTT CTGT  TTCCTCTA
                                   C    CC
GAM2020  LOC256594 5'  TCAAGGGACAGGAAGGAGAT   49498      AA    AA
                                TTAA  GACA  AAGGAGAT
                                ||||  ||||  ||||||||
                                AGTT  CTGT  TTCCTCTA
                                  CC    CC
GAM2020  LOC257471 3'  TTAAAAAATAAAAAGAAAATA  49477         C
                                TTAAAAGA AAAAAGGAGATA
                                |||||||| ||||||||||||
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                                AATTTTTT TTTTTCTTTTAT
                                     A
GAM2020  LOC257484 3'  AAAAACAAAGAGAAAATA    49491         A
                                AAAGACAAA AGGAGATA
                                ||||||||| ||||||||
                                TTTTTGTTT TCTTTTAT
                                     C
GAM2020  LOC51186  3'  TTAAAAGACAGAGAC       49506         AAAAG
                                TTAAAAGACA    GAGAT
                                ||||||||||    |||||
                                AATTTTCTGT    CTCTG
                                      _____
GAM2020  LOC91137  3'  TTAAAAAACAAAGTCAAGATA 49507          AAG
                                TTAAAAGACAAA   GAGATA
                                ||||||||||||   ||||||
                                AATTTTTTGTTT   TTCTAT
                                      CAG
GAM2020  LOC92935  3'  TTAAAAGAGCAAAAGAAATA   49508        CAA
                                TTAAAAGA   AAAGGAGATA
                                ||||||||   ||||||||||
                                AATTTTCT   TTTTCTTTAT
                                     CG_
GAM2021  ARF4L     3'  TAGAGTCACAGTTTACATTTAC 49511     A_  G  AAA
                                TAGA  CA GG   TTTACATTTAC
                                ||||  || ||   ||||||||||
                                ATCT  GT TC   AAATGTAAATG
                                   CA  G  ___
GAM2021  ARNTL     3'  TAGAACAAGGGAAACATTTA   49512       _    ATTT
                                TAGAACA GGGAA    ACATTTA
                                ||||||| |||||    |||||||
                                ATCTTGT CCCTT    TGTAAAT
                                     T    _____
GAM2021  PCDHB2    3'  ACAAAGAAAATTTACATTTA   49513        _
                                ACAGGGAAA TTTACATTTA
                                ||||||||| ||||||||||
                                TGTTTCTTT AAATGTAAAT
                                      T
GAM2021  CNOT7     3'  AAACAGGGAAATAAATTAC    49514          ___
                                GAACAGGGAAAT   TTAC
                                ||||||||||||   ||||
                                TTTGTCCCTTTA   AATG
                                      TTT
GAM2021  FLJ12700  3'  AGGAGAAATTTACATTTA    49515    _
                                AGG GAAATTTACATTTA
                                ||| ||||||||||||||
                                TCC CTTTAAATGTAAAT
                                  T
GAM2021  FLJ13657  3'  AACTAGGAAATTTGCATTTAC  49516     A       A
                                AAC GGGAAATTT CATTTAC
                                ||| ||||||||| |||||||
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                                TTG TCCTTTAAA GTAAATG
                                  A       C
GAM2021  KIAA0515  3'  TAGAGCAGTGAAACATTTA   49517     A  G  ATTT
                                TAGA CAG GAA   ACATTTA
                                |||| ||| |||   |||||||
                                ATCT GTC CTT   TGTAAAT
                                  C  A  ____
GAM2021  MGC13090  3'  AGAACAGGGAGGTCTCACAGTT 49518         AA_    _
           TA                    AGAACAGGGA   TTTACA TTTA
                                ||||||||||   |||||| ||||
                                TCTTGTCCCT   GAGTGT AAAT
                                     CCA     C
GAM2021  PRO1866   5'  TAGGAGGGTTTACATTTA    49519    AAC   AAA
                                TAG   AGGG   TTTACATTTA
                                |||   ||||   ||||||||||
                                ATC   TCCC   AAATGTAAAT
                                  C__   ___
GAM2021  LOC149182 3'  GAATAGGGAAATTCATCAT    49520    C       _
                                GAA AGGGAAATTTA CAT
                                ||| ||||||||||| |||
                                CTT TCCCTTTAAGT GTA
                                  A         A
GAM2021  LOC151196 5'  ACAGGGAAGCACATTTA     49521       ATT
                                ACAGGGAA   TACATTTA
                                ||||||||   ||||||||
                                TGTCCCTT   GTGTAAAT
                                    C__
GAM2021  LOC51194  3'  CAGGATTTACATTTA      49522     GAA
                                CAGG   ATTTACATTTA
                                ||||   ||||||||||
                                GTCC   TAAATGTAAAT
                                  ___
GAM2022  CNTNAP2   3'  TTTCCATTTTATTCAGCCGGG  49525       GC___  C
                                TTTCCATT    CA CCGGG
                                ||||||||    || |||||
                                AAAGGTAA    GT GGCCC
                                    AATAA  C
GAM2022  ELK3      5'  TTTCTAGGAGGACCCGGGCGAA 49526     CATTGCC
           A                     TTTC      ACCCGGGCGAAA
                                ||||      ||||||||||||
                                AAAG      TGGGCCCGCTTT
                                  ATCCTCC
GAM2022  FLRT2     3'  TTTCCATTTGTTACACAAGGAA 49527       GCC_  C   C
           A                     TTTCCATT    AC CGGG GAAA
                                ||||||||    || |||| ||||
                                AAAGGTAA    TG GTTC CTTT
                                    ACAA  T   _
GAM2022  HLCS      3'  TTCCCATTGTCATTTCCATGTA 49528       C  C__   GGC
           AAA                     TTTCCATTG CA   CCG   GAAA
                                ||||||||| ||   |||   ||||
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                                AAGGGTAAC GT   GGT   TTTT
                                     A  AAA   ACA
GAM2022  HMGCR    3'  CACTGCCACTTCCATGAAAA  49529        __  GGC
                                CATTGCCAC  CCG   GAAAA
                                |||||||||  |||   |||||
                                GTGACGGTG  GGT   CTTTT
                                     AA   A__
GAM2022  INSR     3'  TTTCCATCTGCTGGGGGCG   49530       _  CACCC
                                TTTCCAT TGC    GGGCG
                                |||||||  |||    |||||
                                AAAGGTA ACG    CCCGC
                                   G   ACC__
GAM2022  KLF7     3'  TTTCCATTGGCAACAGCGGG  49531        _ C  C_
                                TTTCCATTG C AC  CGGG
                                |||||||||  | ||  ||||
                                AAAGGTAAC G TG  GCCC
                                     C T  TC
GAM2022  LCT      3'  TTTCCATTTTACTCAGCAA   49532        GCC  C   G
                                TTTCCATT   AC CGG CGA
                                ||||||||   || ||| |||
                                AAAGGTAA   TG GTC GTT
                                     AA_  A   _
GAM2022  MLPH     3'  TTTCCATTCCATTCATGAAA  49533        G   CC  GGC
                                TTTCCATT CCA  CG   GAAA
                                ||||||||  |||  ||   ||||
                                AAAGGTAA GGT  GT   CTTT
                                     _   AA  A__
GAM2022  NAPB     3'  CATTGCCACCCCCAGTAGTGGG 49534          _________  C
            GA                    CATTGCCACCC       GGG GA
                                  ||||||||||        ||| ||
                                  GTAACGGTGGG       CCC CT
                                       GGTCATCA  _
GAM2022  SCD      3'  TTTCCATTCCATCTAGCAAAA  49535        G   CCCG
                                TTTCCATT CCA    GGCGAAA
                                ||||||||  |||    |||||||
                                AAAGGTAA GGT    TCGTTTT
                                     _   AGA_
GAM2022  ZNF146   3'  TTTCTGTTCCCACTTTTAGTGA 49536     CA  G    CCG_  C
            AAA                     TTTC  TT CCAC    GG GAAAA
                                    ||||  || ||||    || |||||
                                    AAAG  AA GGTG    TC CTTTT
                                      AC  G    AAAA  A
GAM2022  FLJ11017 5'  TTTCTGTTACCACCTGAGGG  49537     CA       C__
                                TTTC  TTGCCACC   GGG
                                ||||  ||||||||   |||
                                AAAG  AATGGTGG   CCC
                                  AC       ACT
GAM2022  FLJ13110 3'  TCTCCATTGTAAAATGGCGAAA 49538         CCACCCG
            A                    TTTCCATTG      GGCGAAAA
                                 |||||||||      ||||||||
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                                AGAGGTAAC      CCGCTTTT
                                     ATTTTA_
GAM2022  FLJ20281  5'  TTTCCATTCTCATTTCCTAGTG 49539        GC  C__  G  C
              AA                   TTTCCATT  CA   CC GG GAA
                                   ||||||||  ||   || || |||
                                   AAAGGTAA  GT   GG TC CTT
                                       GA  AAA  A  A
GAM2022  FLJ20345  5'  TTTCTTGCCACCCGAA      49540      CA
                                   TTTC  TTGCCACCCGGG
                                   ||||  ||||||||||||
                                   AAAG  AACGGTGGGCTT
                                     __
GAM2022  FLJ20371  5'  TCTCTGTTGCCACCCGCGG    49541      CA        _
                                   TTTC  TTGCCACCCG GG
                                   ||||  |||||||||| ||
                                   AGAG  AACGGTGGGC CC
                                     AC         G
GAM2022  KIAA0342  5'  TTCCCATTGCTGTCCTGGA    49542          CA_  C
                                   TTTCCATTGC   CC GGG
                                   ||||||||||   || |||
                                   AAGGGTAACG   GG CCT
                                        ACA  A
GAM2022  KIAA0586  5'  CTTCCATTCCTCTCCGGGTGGA 49543         G  AC_    C_
              AA                   TTTCCATT CC   CCGGG  GAAA
                                   |||||||| ||   |||||  ||||
                                   GAAGGTAA GG   GGCCC  CTTT
                                       _ AGA     AC
GAM2022  KIAA1613  3'  TTTCCATTCCCATCCTATAGAA 49544         G   C  GGGC
                                   TTTCCATT CCA CC    GAA
                                   |||||||| ||| ||    |||
                                   AAAGGTAA GGT GG    CTT
                                       G   A  ATAT
GAM2022  KIAA1866  3'  TTTCCATTACTACCAGGA     49545          C   C
                                   TTTCCATTGC ACC GGG
                                   |||||||||| ||| |||
                                   AAAGGTAATG TGG CCT
                                        A   T
GAM2022  RHO6      3'  TCTCCGTTGCTGCCTCCTTAGA 49546       A___     A  C____
              GGG                      TTTCC    TTGCC CC     GGG
                                       |||||    ||||| ||     |||
                                       AGAGG    GACGG GG     CCC
                                          CAAC     A  AATCT
GAM2022  RHOBTB1   5'  TTCCCAGTCCCGGGCGA     49547       TTGCCA
                                       TTTCCA     CCCGGGCGA
                                       ||||||     |||||||||
                                       AAGGGT     GGGCCCGCT
                                          CA____
GAM2022  LOC148894 3'  TTCTCATTGCCACCCAAA     49548     _
                                       TTC CATTGCCACCCGGG
                                       ||| ||||||||||||||
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                                AAG GTAACGGTGGGTTT
                                  A
GAM2022  LOC157918 3'  TTTCCACTTGCTGCCAAG    49549        _  CAC
                                TTTCCATT GC   CCGGG
                                |||||||| ||   |||||
                                AAAGGTGA CG   GGTTC
                                    A  AC_
GAM2022  LOC157919 5'  TTTCCACTTGCTGCCAAG    49549        _  CAC
                                TTTCCATT GC   CCGGG
                                |||||||| ||   |||||
                                AAAGGTGA CG   GGTTC
                                    A  AC_
GAM2022  LOC158226 3'  TTTCCATTTCAAACAAGTGAAA 49550        GC  CC    C
                                TTTCCATT  CA  CGGG GAAA
                                |||||||  ||  |||| ||||
                                AAAGGTAA  GT  GTTC CTTT
                                    A_  TT    A
GAM2022  LOC163231 3'  TTTCCATTGTGATGAACGA    49551        CCACCC
                                TTTCCATTG     GGGCGA
                                |||||||||     ||||||
                                AAAGGTAAC     CTTGCT
                                    ACTA__
GAM2022  LOC200382 5'  TTTCCATTCCCACCGCGGCCG  49552        G    _  G
                                TTTCCATT CCACC CGG CG
                                |||||||| ||||| ||| ||
                                AAAGGTAA GGTGG GCC GC
                                    G    C   G
GAM2022  LOC219855 3'  TTTCCATTGTCTTGCCCATGGG 49553        CCA__  __  C
           GA                    TTTCCATTG    CCC  GGG GA
                                |||||||||    |||  ||| ||
                                AAAGGTAAC    GGG  CCC CT
                                    AGAAC   TA  _
GAM2022  LOC254559 3'  TCTCCATTGTCATAAAAGCTGA 49554        C  CCC   _
           AAA                    TTTCCATTG CA   GGGC GAAAA
                                |||||||||  ||   |||| |||||
                                AGAGGTAAC GT   TTCG CTTTT
                                    A  ATT    A
GAM2022  LOC255645 3'  TTCCACCAGGCCTTGGGTGAA  49555        __  ACCC   C
                                TTCCATT  GCC    GGG GAA
                                |||||||  |||    ||| |||
                                AAGGTGG  CGG    CCC CTT
                                   TC   AA__   A
GAM2022  LOC51008  3'  TTTCCATTTTACAAGCTGA   49556        GCCACC    _
                                TTTCCATT     CGGGC GA
                                ||||||||     ||||| ||
                                AAAGGTAA     GTTCG CT
                                    AAT___     A
GAM2022  LOC90246  3'  TTTCCATTGCTGCTGTAACAAA 49557         CACCCG
                                TTTCCATTGC     GGCGAA
                                ||||||||||     ||||||
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                                AAAGGTAACG     TTGTTT
                                     ACGACA
GAM2022 LOC90408 5' TCTCCATTGCCATCAGGGA   49558          CC   C
                                TTTCCATTGCCA  CGGG GA
                                ||||||||||||  |||| ||
                                AGAGGTAACGGT  GTCC CT
                                      A_   _
GAM2022 LOC91115 3' TTTCCATTCCTCAGGTGGGGA 49559        G  ACCC__   C
                                TTTCCATT CC     GGG GA
                                ||||||||  ||     ||| ||
                                AAAGGTAA GG     CCC CT
                                    _ AGTCCA  _
GAM2023 COG3     3' TAAGTGAACACTTAAAACTGTA 49562         G CA  TT
             C                   TAAGTGAACA C  AG  TTGTAC
                                 ||||||||||  |  ||  ||||||
                                 ATTCACTTGT G  TT  GACATG
                                      _ AA  TT
GAM2023 GAC1     3' AGGGGACAGCCAAGCCAGGC   49563    TGA        TT
                                AG   ACAGCCAAGTT  GT
                                ||   ||||||||||||  ||
                                TC   TGTCGGTTCGG  CG
                                 CCC          TC
GAM2023 INSRR    3' GTGAGGAGTCAGGCTCTGC    49564      AC  C  A
                                GTGA  AG CA GTTTTGT
                                ||||  || || |||||||
                                CACT  TC GT CGAGACG
                                  CC  A  C
GAM2023 SLC25A15 3' TAAGGAACCTGGAGGTTTTGTA 49565      T    AGCCAA
             C                   TAAG GAAC     GTTTTGTAC
                                 |||| ||||     |||||||||
                                 ATTC CTTG     CAAAACATG
                                   _   GACCTC
GAM2023 UQCRFS1  3' TAAGTGAATGCCTGAAAGT   49566        CA  ___
                                TAAGTGAA  GCC   AAGT
                                ||||||||  |||   ||||
                                ATTCACTT  CGG   TTCA
                                     A_   ACT
GAM2023 FLJ10305 3' GTGGGCAGCCAGCTCTGT    49567     AA     A
                                GTG  CAGCCA GTTTTGT
                                |||  |||||| |||||||
                                CAC  GTCGGT CGAGACA
                                  CC     _
GAM2023 FLJ20294 3' AGTGAGTAGCCAAGCCAGGC  49568      AC       TT
                                AGTGA  AGCCAAGTT  GT
                                |||||  |||||||||  ||
                                TCACT  TCGGTTCGG  CG
                                   CA       TC
GAM2023 IMPACT   3' AAGTGAACAGTTAATCACTTAT 49569         CC  GT_
                                AAGTGAACAG  AA   TTTGT
                                ||||||||||  ||   |||||
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                                TTCACTTGTC TT  GAATA
                                     AA AGT
GAM2023 KIAA1904 3' GTGGCAGCCAAGCGACATGT  49570    AA      TT__
                                GTG CAGCCAAGT  TGT
                                ||| ||||||||  |||
                                CAC GTCGGTTCG  ACA
                                  C_      CTGT
GAM2023 PCDH17   3' GTAAACAGTTAAGTCAGC   49571       CC    TT
                                GTGAACAG AAGTT GT
                                |||||||| ||||| ||
                                CATTTGTC TTCAG CG
                                     AA   T_
GAM2023 LOC149461 3' AGTAAACAGCCGGGCTGGTGC 49572         AA  T_
                                AGTGAACAGCC GTT TGT
                                |||||||||| ||| |||
                                TCATTTGTCGG CGA ACG
                                      CC  CC
GAM2023 LOC149830 3' GTGAAAGCCAAGCCCCA    49573     C       TT
                                GTGAA AGCCAAGTT G
                                ||||| |||||||| |
                                CACTT TCGGTTCGG T
                                   _       GG
GAM2023 LOC150351 3' TAAGTGAATGCCTGAAAGT   49566       CA  ___
                                TAAGTGAA GCC  AAGT
                                |||||||| |||  ||||
                                ATTCACTT CGG  TTCA
                                     A_  ACT
GAM2023 LOC163115 5' AGGAGAAACCAGTTTTGT   49574   T AC    A
                                AG GA AGCCA GTTTTGT
                                || ||  ||||| |||||||
                                TC CT  TTGGT CAAAACA
                                 _ CT    _
GAM2023 LOC256366 5' TAAGTGATGGCCAGTCCTGC  49575       ACA   A
                                TAAGTGA  GCCA GTTTTGT
                                |||||||  |||| |||||||
                                ATTCACT  CGGT CAGGACG
                                     AC_   _
GAM2024 BCL11B   3' TGTTTTGCTTTTCATTCAA   49578      T   GA
                                TGTTTT GCTT  CGTTCAA
                                |||||| ||||  |||||||
                                ACAAAA CGAA  GTAAGTT
                                   _   AA
GAM2024 CDH18    5' TCTGTTCTTGCTCCTCTTCA  49579          GACG
                                TCTGTTTTTGCTT   TTCA
                                ||||||||||||   ||||
                                AGACAAGAACGAG   AAGT
                                       GAG_
GAM2024 CPSF6    3' CCTCTGTTTTTTTTGAC    49580          GC
                                CCTCTGTTTTT  TTGAC
                                ||||||||||  |||||
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                                GGAGACAAAAA  AACTG
                                      A_
GAM2024  D12S2489E 3'  CCTGTTTTTGTTTGTTTCC    49581          C   ACG
                                TCTGTTTTTG TTG   TTC
                                |||||||||| |||   |||
                                GGACAAAAAC AAC   AGG
                                      A   AA_
GAM2024  DSCR3     3'  CCTCTGTTTTCTGCTACTCAGT 49582         _    TGAC_
           T                     CCTCTGTTT TTGCT    GTT
                                |||||||| |||||    |||
                                GGAGACAAA GACGA    CAA
                                      A    TGAGT
GAM2024  EDAR      3'  TCTGTTTTTATTCCCATT    49583          C  GA
                                TCTGTTTTTG TT  CGTT
                                |||||||||| ||  ||||
                                AGACAAAAAT AA  GTAA
                                      _  GG
GAM2024  FANCD2    3'  TCTATTTTTGTATGTTTCAA   49584         CT  ACG
                                TCTGTTTTTG  TG   TTCAA
                                |||||||||  ||   |||||
                                AGATAAAAAC  AC   AAGTT
                                      AT  A__
GAM2024  HLF       5'  CCTCGTTTTGCAAAATGTTCAA 49585      T    T  TT  C
                                CCTC GTTTT GC  GA GTTCAA
                                |||| ||||| ||  || ||||||
                                GGAG CAAAA CG  TT CAAGTT
                                  _    _ TT  A
GAM2024  IL2RA     3'  CCTCTGTTTTTTTAGAAATTCAA 49586          GCTT  C
                                CCTCTGTTTTT    GA GTTCAA
                                ||||||||||    || ||||||
                                GGAGACAAAAA    CT TAAGTT
                                      AT__  T
GAM2024  MYO9A     3'  TGTTTTTGCTTTCCCCA     49587          GACG
                                TGTTTTTGCTT    TTCA
                                ||||||||||    ||||
                                ACAAAAACGAA    GGGT
                                      AG__
GAM2024  PSAP      3'  CCTTTGTTTTGCTGCTTTGTTC 49588     C     __    GAC
           AA                     CCT TGTTTT  TGCTT   GTTCAA
                                ||| ||||||  |||||   ||||||
                                GGA ACAAAA  ACGAA   CAAGTT
                                  A     CG    A__
GAM2024  SLC9A5    3'  CTCTGTTTGGGGAATGTTCA   49589        TTGCTT  C
                                CTCTGTTT     GA GTTCA
                                ||||||||     || |||||
                                GAGACAAA     TT CAAGT
                                     CCCC__  A
GAM2024  ZNF24     3'  TTTTTAGCCTGACGTTCAA    49590      _
                                TTTTT GCTTGACGTTCAA
                                ||||| ||||||||||||
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                                AAAAA CGGACTGCAAGTT
                                   T
GAM2024  DKFZp434M0331 5'  TCTGTTTTTTTTGCATTCA   49591         GC   A
                                TCTGTTTTT  TTG CGTTCA
                                |||||||||  ||| ||||||
                                AGACAAAAA  AAC GTAAGT
                                     A_  _
GAM2024  FLJ12783  3'  CCTCTAGTTTTTGGTTTGA   49592      _      C_
                                CCTCT GTTTTTG  TTGA
                                ||||| |||||||  ||||
                                GGAGA CAAAAAC  AACT
                                   T      CA
GAM2024  HERPUD1   3'  TCTGCTTTTGCTTGCTCA    49593           GAC
                                TCTGTTTTTGCTT   GTTCA
                                ||||||||||||   |||||
                                AGACGAAAACGAA   CGAGT
                                      ___
GAM2024  KIAA0022  3'  TCGGTTTTTGCTTGCACA    49594    T        _
                                TC GTTTTTGCTTG ACG
                                || ||||||||||| |||
                                AG CAAAAACGAAC TGT
                                 C          G
GAM2024  KIAA0769  3'  CCTTGTTTTTTGCTCTGTTCAA 49595     CTG        GAC
                                CCT   TTTTTGCTT   GTTCAA
                                |||   |||||||||   ||||||
                                GGA   AAAAACGAG   CAAGTT
                                  ACA        A__
GAM2024  KIAA0882  3'  CCTCTGTCTTTGCTGCTACTTT 49596            TG_  G
            CA                    CCTCTGTTTTTGCT   AC TTCA
                                |||||||||||||   || ||||
                                GGAGACAGAAACGA   TG AAGT
                                         CGA  A
GAM2024  KIAA1209  3'  CTTTGATTTTGCTTTTTATTCA 49597    C  T       GAC
            A                     CT TG TTTTGCTT   GTTCAA
                                || || ||||||||   ||||||
                                GA AC AAAACGAA   TAAGTT
                                 A  T       AAA
GAM2024  KIAA1463  3'  TCTGTCTTTGTGATTCTTCA   49598          CT   CG_
                                TCTGTTTTTG  TGA   TTCA
                                |||||||||  |||   ||||
                                AGACAGAAAC  ACT   AAGT
                                      __  AAG
GAM2024  KIAA1854  3'  CCTCTAATTCTTGCTTGGCGTT 49599       _        A
                                CCTCTG TTTTTGCTTG CGTT
                                |||||| |||||||||| ||||
                                GGAGAT AAGAACGAAC GCAA
                                   T         C
GAM2024  KIAA1912  3'  CTCTGTTTGAGATGTTCA    49600         TTGCTT  C
                                CTCTGTTT     GA GTTCA
                                ||||||||     || |||||
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                                GAGACAAA     CT CAAGT
                                     CT_____ A
GAM2024  MGC7036   3'  TCTGTTTTTCTTGATTTCA   49601        G    CG
                                TCTGTTTTT CTTGA  TTCA
                                ||||||||| |||||  ||||
                                AGACAAAAA GAACT  AAGT
                                     _    A_
GAM2024  MYOZ2     3'  CCTTTGTTTTTGTTTGTGTCC  49602     C       C   AC
                                CCT TGTTTTTG TTG  GTTC
                                ||| |||||||| |||  ||||
                                GGA ACAAAAAC AAC  CAGG
                                  A       A  A_
GAM2024  SRPK1     3'  TCTGTTTTTGCTTACATT    49603           A
                                TCTGTTTTTGCTTG CGTT
                                |||||||||||||| ||||
                                AGACAAAAACGAAT GTAA

                                     _
GAM2024  TCL6      5'  TCGGTTTTCTCCTGTGTTCA   49604    T    TG   AC
                                TC GTTTT  CTTG  GTTCA
                                || |||||  ||||  |||||
                                AG CAAAA  GGAC  CAAGT
                                 C    GA   A_
GAM2024  TCL6      5'  TCGGTTTTCTCCTGTGTTCA   49604    T    TG   AC
                                TC GTTTT  CTTG  GTTCA
                                || |||||  ||||  |||||
                                AG CAAAA  GGAC  CAAGT
                                 C    GA   A_
GAM2024  TCL6      5'  TCGGTTTTCTCCTGTGTTCA   49604    T    TG   AC
                                TC GTTTT  CTTG  GTTCA
                                || |||||  ||||  |||||
                                AG CAAAA  GGAC  CAAGT
                                 C    GA   A_
GAM2024  TCL6      5'  TCGGTTTTCTCCTGTGTTCA   49604    T    TG   AC
                                TC GTTTT  CTTG  GTTCA
                                || |||||  ||||  |||||
                                AG CAAAA  GGAC  CAAGT
                                 C    GA   A_
GAM2024  TCL6      5'  TCGGTTTTCTCCTGTGTTCA   49604    T    TG   AC
                                TC GTTTT  CTTG  GTTCA
                                || |||||  ||||  |||||
                                AG CAAAA  GGAC  CAAGT
                                 C    GA   A_
GAM2024  LOC150468 5'  TCTGATCTTGCTTGATGTT    49605     T       C
                                TCTG TTTTGCTTGA GTT
                                |||| |||||||||| |||
                                AGAC AGAACGAACT CAA
                                  T        A
GAM2024  LOC157983 3'  TCTGTTTTTATCTTGAGTT    49606         _    C
                                TCTGTTTTTG CTTGA GTT
                                |||||||||| ||||| |||
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                                AGACAAAAAT GAACT CAA
                                      A    _
GAM2024  LOC167601 5'  CTCTTTTTTGCTCTTTCA    49607     G       GACG
                                CTCT TTTTTGCTT    TTCA
                                |||| |||||||||    ||||
                                GAGA AAAAACGAG    AAGT
                                  _       A___
GAM2024  LOC200488 5'  CCTGCCACCCTTGACGTT    49608       TTTG
                                TCTGTT    CTTGACGTT
                                ||||||    |||||||||
                                GGACGG    GAACTGCAA
                                   TGG_
GAM2024  LOC203289 3'  TCTGTTTTTATCTTGAGTT    49606          _    C
                                TCTGTTTTTG CTTGA GTT
                                |||||||||| ||||| |||
                                AGACAAAAAT GAACT CAA
                                      A    _
GAM2024  LOC221399 5'  TGTTTTTGCTGGCTCAA     49609          TGAC
                                TGTTTTTGCT    GTTCAA
                                ||||||||||    ||||||
                                ACAAAAACGA    CGAGTT
                                      C___
GAM2024  LOC221495 3'  TCTGTTTTTGCCTGACCCCC   49610              G
                                TCTGTTTTTGCTTGAC TTC
                                |||||||||||||||| |||
                                AGACAAAAACGGACTG GGG
                                         G
GAM2024  LOC222602 5'  CTTTGATTTTGCTCTTCTCAA  49611    C  T      GACG
                                CT TG TTTTGCTT    TTCAA
                                || || ||||||||    |||||
                                GA AC AAAACGAG    GAGTT
                                 A  T       AA__
GAM2024  LOC256544 3'  TCTGTTTTTATCTTGAGTT    49606          _    C
                                TCTGTTTTTG CTTGA GTT
                                |||||||||| ||||| |||
                                AGACAAAAAT GAACT CAA
                                      A    _
GAM2024  LOC257000 5'  CCCTTGCCTTGGCGTTCA    49612    TC   TTTTG    A
                                CC  TGT    CTTG CGTTCA
                                ||  |||    |||| ||||||
                                GG  ACG    GAAC GCAAGT
                                 GA  _____    C
GAM2024  LOC51123  3'  CCTTTATTTTTGCTGATCA   49613     C        T  CGT
                                CCT TGTTTTTGCT GA   TCA
                                ||| |||||||||| ||   |||
                                GGA ATAAAAACGA CT   AGT
                                  A        _ ____
GAM2024  LOC56959  5'  CCTCTGTTTCTAACACTG    49614           _ _
                                CCTCTGTTTTTG C TTG
                                |||||||||||| | |||
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                                GGAGACAAAGAT G GAC
                                       T T
GAM2024  LOC57117  5'  ATTCTCAGCTTGGCGTTCA   49615       _    A
                                GTTTTT GCTTG CGTTCA
                                |||||| ||||| ||||||
                                TAAGAG CGAAC GCAAGT
                                   T    C
GAM2025  AXL       3'  GAATTGCAGATTCTAGAGCTTT 49618     G        CC_
                                GAA TGCAGATTTT   GCTTT
                                ||| ||||||||||   |||||
                                CTT ACGTCTAAGA   CGAAA
                                  A         TCT
GAM2025  AXL       3'  GAATTGCAGATTCTAGAGCTTT 49618     G        CC_
                                GAA TGCAGATTTT   GCTTT
                                ||| ||||||||||   |||||
                                CTT ACGTCTAAGA   CGAAA
                                  A         TCT
GAM2025  RYR2      3'  AAGTGCAAACTGCTT       49619          TTCC
                                AAGTGCAGATT    GCTT
                                ||||||||||    ||||
                                TTCACGTTTGA    CGAA
                                      ____
GAM2025  TTN       3'  GAGGTGCAGATAGCTTGCTTT  49620    A      TTTCC
                                GA GTGCAGAT    GCTTT
                                || ||||||||    |||||
                                CT CACGTCTA    CGAAA
                                 C       TCGAA
GAM2025  TTN       3'  GAGGTGCAGATAGCTTGCTTT  49620    A      TTTCC
                                GA GTGCAGAT    GCTTT
                                || ||||||||    |||||
                                CT CACGTCTA    CGAAA
                                 C       TCGAA
GAM2025  TTN       3'  GAGGTGCAGATAGCTTGCTTT  49620    A      TTTCC
                                GA GTGCAGAT    GCTTT
                                || ||||||||    |||||
                                CT CACGTCTA    CGAAA
                                 C       TCGAA
GAM2025  ALOX15B   3'  TTCTTGGTAGATTTTCTGCTTT 49621     GAA  GC      C
                                TTC   GT  AGATTTTC GCTTT
                                |||   ||  |||||||| |||||
                                AAG   CA  TCTAAAAG CGAAA
                                  AAC  __       A
GAM2025  LOC120534 5'  TTCTAGCAAATTTTCCG     49622     GAAGT
                                TTC    GCAGATTTTCCG
                                |||    ||||||||||||
                                AAG    CGTTTAAAAGGC
                                  AT___
GAM2025  LOC144600 3'  GAAATGCAATAGCTCGCTTT   49623         ATTTTC
                                GAAGTGCAG     CGCTTT
                                |||||||||     ||||||
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                                CTTTACGTT     GCGAAA
                                     ATCGA_
GAM2026  AMPD1    5'  TCTAGGATAGCACAGTAG    49626      AA      AA
                                TCTA  ATAGCAT  GGTGG
                                ||||  |||||||  |||||
                                AGAT  TATCGTG  TCATC
                                  CC      __
GAM2026  BSN      3'  ACAGCATGGGGGTGGGTAA   49627       AA_
                                ATAGCAT   GGTGGGTAA
                                |||||||   |||||||||
                                TGTCGTA   CCACCCATT
                                    CCC
GAM2026  CTSZ     3'  TCTAAAGTGACATAAGAATGG  49628       ATA       _
                                TCTAAA   GCATAAGG TGG
                                ||||||   |||||||| |||
                                AGATTT   TGTATTCT ACC
                                   CAC       T
GAM2026  EXO1     3'  TAAAATGGCACAGAATGA    49629       A     AG
                                TAAAAT GCATA  GTGG
                                |||||| |||||  ||||
                                ATTTTA CGTGT  TACT
                                   C     CT
GAM2026  EXO1     3'  TAAAATGGCACAGAATGA    49629       A     AG
                                TAAAAT GCATA  GTGG
                                |||||| |||||  ||||
                                ATTTTA CGTGT  TACT
                                   C     CT
GAM2026  EXO1     3'  TAAAATGGCACAGAATGA    49629       A     AG
                                TAAAAT GCATA  GTGG
                                |||||| |||||  ||||
                                ATTTTA CGTGT  TACT
                                   C     CT
GAM2026  FGF2     3'  TAAAATAGCATATTTTAGTGA  49630          A___
                                TAAAATAGCATA    GGTGG
                                ||||||||||||    |||||
                                ATTTTATCGTAT    TCACT
                                      AAAA
GAM2026  GABPA    3'  TCTAAAATATATGCTCAAAGTA 49631          ___  A
            A                    TCTAAAATA   GC TAAGGTGG
                                ||||||||||   || ||||||||
                                AGATTTTAT   CG GTTTCATT
                                     ATA  A
GAM2026  INMT     3'  TCTAAGATAGCTGTAAGGC   49632       A     A_
                                TCTAA ATAGC  TAAGGT
                                |||||  |||||  ||||||
                                AGATT TATCG  ATTCCG
                                   C     AC
GAM2026  JAM2     3'  TAAAATAGCAAGTTCAGGTGA  49633          TA___
                                TAAAATAGCA     AGGTGG
                                ||||||||||     ||||||
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                                ATTTTATCGT    TCCACT
                                      TCAAG
GAM2026 KRAS2    3' TAAAATAAGCATTTAAGGTAA 49634       _  __
                                TAAAATA GCA  TAAGGTGG
                                ||||||| |||  ||||||||
                                ATTTTAT CGT  ATTCCATT
                                    T   AA
GAM2026 KRAS2    3' TAAAATAAGCATTTAAGGTAA 49634       _  __
                                TAAAATA GCA  TAAGGTGG
                                ||||||| |||  ||||||||
                                ATTTTAT CGT  ATTCCATT
                                    T   AA
GAM2026 MDFI     3' TCTGAGAGGACATGGGTGGGTA 49635     AAAATA    AA
                                TCT     GCAT  GGTGGGTA
                                |||     ||||  ||||||||
                                AGA     TGTA  CCACCCAT
                                  CTCTCC    C_
GAM2026 RFXAP    3' TCTAAAGAAGCATAAGCTAA   49636      AT      G
                                TCTAAA  AGCATAAG TGG
                                ||||||  |||||||| |||
                                AGATTT  TCGTATTC ATT
                                   CT       G
GAM2026 SCA1     3' TCTGAAATAGCACGGTA     49637     A       AA
                                TCT AAATAGCAT  GGTG
                                ||| |||||||||  ||||
                                AGA TTTATCGTG  CCAT
                                  C        __
GAM2026 THPO     5' TCTGGGGAGCAGATGGGTA   49638     AAAAT    TAA
                                TCT    AGCA   GGTGGGTA
                                |||    ||||   ||||||||
                                AGA    TCGT   CTACCCAT
                                  CCCC_   ____
GAM2026 TTR      3' TCTAACATAGCATATGAGGTGA 49639      A      __
                                TCTAA ATAGCATA  AGGTGG
                                ||||| ||||||||  ||||||
                                AGATT TATCGTAT  TCCACT
                                   G       AC
GAM2026 ABT1     3' AAACAGTAAGGTGGGT      49640       CA
                                AAATAG  TAAGGTGGGT
                                ||||||  ||||||||||
                                TTTGTC  ATTCCACCCA
                                        __
GAM2026 BDG-29   3' CAAAATAGTTACGTGGGTAA  49641        CA  AG
                                TAAAATAG  TA  GTGGGTAA
                                ||||||||  ||  ||||||||
                                GTTTTATC  AT  CACCCATT
                                    A_  G_
GAM2026 C1QTNF3  3' TAAAATAGCATTGTATGTGA  49642         AAG__
                                TAAAATAGCAT    GTGG
                                ||||||||||     ||||
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                                ATTTTATCGTA    CACT
                                      ACATA
GAM2026 CAS1     3' TAAAATAGGAGGTGGGTAA   49643       CATA
                                TAAAATAG   AGGTGGGTAA
                                ||||||||   ||||||||||
                                ATTTTATC   TCCACCCATT
                                    C___
GAM2026 DKFZP564J102 5' TCTGACGATAGGGAAGGTGGGT 49644    AAA_   CAT
             A                   TCT   ATAG   AAGGTGGGTA
                                 |||   ||||  ||||||||||
                                 AGA   TATC   TTCCACCCAT
                                   CTGC   CC_
GAM2026 DMTF1    3' TAAAATAGCCTGAGATGA    49645       ATA
                                TAAAATAGC   AGGTGG
                                |||||||||   ||||||
                                ATTTTATCG   TCTACT
                                      GAC
GAM2026 DNAM-1   3' TCTAAGGTAGACCTTGGGTA  49646     AA  C  AAGG
                                TCTAA  TAG AT   TGGGTA
                                |||||  ||| ||   ||||||
                                AGATT  ATC TG   ACCCAT
                                   CC   _  GA__
GAM2026 FER1L4   3' TCTGGGGTAGCTCACATGGGTA 49647    AAAA   A  AG
             A                   TCT   TAGC TA  GTGGGTAA
                                 |||   |||| ||  ||||||||
                                 AGA   ATCG GT  TACCCATT
                                   CCCC   A  G_
GAM2026 FLJ13031 5' TCTGAAATAGCAGGGC     49648     A      TAAGGT
                                TCT AAATAGCA     GGGT
                                ||| ||||||||     ||||
                                AGA TTTATCGT     CCCG
                                  C      _______
GAM2026 KIAA0534 3' TAAAAAGACCATAGGTGGGTA 49649      TA  ATA
                                TAAAA  GC   AGGTGGGTA
                                |||||  ||   |||||||||
                                ATTTT  TG   TCCACCCAT
                                   TC  GTA
GAM2026 KIAA1463 3' TCTAAAATGGCATTAGATAA   49650       A   A
                                TCTAAAAT GCAT AGGTGG
                                |||||||| |||| ||||||
                                AGATTTTA CGTA TCTATT
                                     C    A
GAM2026 KIAA1545 3' TCTAAAGAGCATAAAAT     49651      AT
                                TCTAAA  AGCATAAGGT
                                ||||||  ||||||||||
                                AGATTT  TCGTATTTTA
                                   C_
GAM2026 KIAA1786 3' TCTAAAATAGCTGAAT      49652          ATAAGG
                                TCTAAAATAGC     TGGGT
                                ||||||||||      |||||
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                                AGATTTTATCG     ACTTA
                                        _______
GAM2026  MGC15435  5'  TAAATTAGACAGTGGGTAA   49653     A   CATAA
                                TAAA TAG    GGTGGGTAA
                                |||| |||    |||||||||
                                ATTT ATC    TCACCCATT
                                  A  TG___
GAM2026  PTPRR     3'  TCTAGAAGCCTTGGGTGGGTAA 49654     AAAT   ATAA
                                TCTA   AGC   GGTGGGTAA
                                ||||   |||   |||||||||
                                AGAT   TCG   CCACCCATT
                                  CT__   GAAC
GAM2026  PTPRR     3'  TCTAGAAGCCTTGGGTGGGTAA 49654     AAAT   ATAA
                                TCTA   AGC   GGTGGGTAA
                                ||||   |||   |||||||||
                                AGAT   TCG   CCACCCATT
                                  CT__   GAAC
GAM2026  SH3BGRL2  3'  TAAAATGGCATAAGTTGA    49655      A     G
                                TAAAAT GCATAAG TGG
                                |||||| ||||||| |||
                                ATTTTA CGTATTC ACT
                                   C      A
GAM2026  LOC143943 3'  CCTAAAATGTAGATTAAGGTGG 49656       __  CA
           GT                    TCTAAAA  TAG  TAAGGTGGGT
                                |||||||  |||  ||||||||||
                                GGATTTT  ATC  ATTCCACCCA
                                    AC   TA
GAM2026  LOC149302 5'  TAAAATAGCAAAACAGAT    49657        TA   TG
                                TAAAATAGCA  AGG  GGT
                                ||||||||||  |||  |||
                                ATTTTATCGT  TTT  CTA
                                      __  GT
GAM2026  LOC157507 3'  TCTAAAATGCGTGAGC      49658       A  ATAAG
                                TCTAAAAT GC    GTGGGT
                                |||||||| ||    ||||||
                                AGATTTTA CG    CACTCG
                                      _ ______
GAM2026  LOC220469 3'  TCTAAAGTAGCAATGGAAGTA  49659      A    TAA  T
                                TCTAAA TAGCA   GG GGGTA
                                |||||| |||||   || |||||
                                AGATTT ATCGT   CC TTCAT
                                   C    TA_  _
GAM2026  LOC221823 3'  TAAAATAGCATAACCTAG    49660          GG
                                TAAAATAGCATAA  TGG
                                ||||||||||||  |||
                                ATTTTATCGTATT  ATC
                                       GG
GAM2026  LOC51336  5'  TAAAATGGCTAAAATGG     49661       A  A
                                TAAAAT GC TAAGGTGG
                                |||||| || ||||||||
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                                ATTTTA CG ATTTTACC
                                   C  _
GAM2027  PCDH11Y   3'  TAGTACGCTCTGTCATGA    49664        GC   C  G
                                TAGTACGC  CTG CG GA
                                ||||||||  ||| || ||
                                ATCATGCG  GAC GT CT
                                     A_   A  A
GAM2027  SLC1A2    5'  GTGCGCGCCTGGGGAG     49665    A      CC
                                GT CGCGCCTG  GGGAG
                                || ||||||||  |||||
                                CA GCGCGGAC  CCCTC
                                 C       __
GAM2027  DKFZP564O0523 3'  GTGCACGCCTGTAATCCCAGA  49666    A      ____  G
                                GT CGCGCCTG    CC GGA
                                || ||||||||    || |||
                                CA GTGCGGAC    GG TCT
                                 C       ATTA  G
GAM2027  FLJ12438  3'  GCGCCTGCCAGAGGGGAGA   49667         ____
                                GCGCCTGCC    GGGAGA
                                |||||||||    ||||||
                                CGCGGACGG    CCCTCT
                                     TCTC
GAM2027  LOC51042  5'  GTGCGCGCCTGTCCGGCGGGAG 49668    A      _ ___
                                GT CGCGCCTG CC   GGGAG
                                || |||||||| ||   |||||
                                CA GCGCGGAC GG   CCCTC
                                 C       A  CCG
GAM2028  NOVA1     3'  AACATTATCAGCTATCAAT   49671         ATA
                                AACATTATCA   TTATCAAT
                                ||||||||||   ||||||||
                                TTGTAATAGT   GATAGTTA
                                     C__
GAM2028  NOVA1     3'  AACATTATCAGCTATCAAT   49671         ATA
                                AACATTATCA   TTATCAAT
                                ||||||||||   ||||||||
                                TTGTAATAGT   GATAGTTA
                                     C__
GAM2028  TRRAP     3'  AACATTATCAATGCTCA     49672          ATTA
                                AACATTATCAAT    TCA
                                ||||||||||||    |||
                                TTGTAATAGTTA    AGT
                                      CG__
GAM2029  CD79B     3'  ACACCGTTTATTCCACGGGG   49675       GAA_
                                ACACCGT    TCCACGGGG
                                |||||||    |||||||||
                                TGTGGCA    AGGTGCCCC
                                   AATA
GAM2029  CD79B     3'  ACACCGTTTATTCCACGGGG   49675       GAA_
                                ACACCGT    TCCACGGGG
                                |||||||    |||||||||
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                                TGTGGCA   AGGTGCCCC
                                    AATA
GAM2029  EDARADD  5' ACCGTGGGACCACGGGGA   49676      AAT
                                ACCGTG  CCACGGGGA
                                ||||||  |||||||||
                                TGGCAC  GGTGCCCCT
                                   CCT
GAM2029  MAP1A    3' AACACAGCAGCACGGGGA   49677     C  AATC
                                AACAC GTG   CACGGGGA
                                ||||| |||   ||||||||
                                TTGTG CGT   GTGCCCCT
                                  T  C___
GAM2029  MEF2D    3' CACCGTGAATTGCAGGG    49678       CCA
                                CACCGTGAAT  CGGGG
                                ||||||||||  |||||
                                GTGGCACTTA  GTCCC
                                     AC_
GAM2029  MEN1     5' AACACACACCACGGGG     49679     _ TGAAT
                                AACAC CG    CCACGGGG
                                ||||| ||    ||||||||
                                TTGTG GT    GGTGCCCC
                                  T _____
GAM2029  PTPRA    5' AACACCGTGAACACCAGG    49680       TC  G
                                AACACCGTGAA  CAC GGG
                                ||||||||||  ||| |||
                                TTGTGGCACTT  GTG TCC
                                      __  G
GAM2029  SMARCA1  3' ACCATGAATACACTGGA    49681       C  GG
                                ACCGTGAAT CAC  GGA
                                ||||||||| |||  |||
                                TGGTACTTA GTG  CCT
                                     T  A_
GAM2029  SMARCA1  3' ACCATGAATACACTGGA    49681       C  GG
                                ACCGTGAAT CAC  GGA
                                ||||||||| |||  |||
                                TGGTACTTA GTG  CCT
                                     T  A_
GAM2029  TBL1X    5' ACAGTGACCTCCACGGGGA   49682    C   A_
                                AC GTGA  TCCACGGGGA
                                || ||||  ||||||||||
                                TG CACT  AGGTGCCCCT
                                 T   GG
GAM2029  TNFRSF6B 3' ACACGTGCCCACGGGG     49683     C  AA
                                ACAC GTG  TCCACGGGG
                                |||| |||  |||||||||
                                TGTG CAC  GGGTGCCCC
                                  _  __
GAM2029  TNFRSF6B 3' ACACGTGCCCACGGGG     49683     C  AA
                                ACAC GTG  TCCACGGGG
                                |||| |||  |||||||||
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                                TGTG CAC  GGGTGCCCC
                                  _  __
GAM2029 C17orf31 3' CATGACTGTCCACGGGGA   49684     A__
                                CGTGA  TCCACGGGGA
                                |||||  ||||||||||
                                GTACT  AGGTGCCCCT
                                   GAC
GAM2029 CXYorf1  5' AACACCTGTGGACACAGGGA 49685      _  AATC
                                AACACC GTG   CACGGGGA
                                |||||| |||   ||||||||
                                TTGTGG CAC   GTGTCCCT
                                   A  CT__
GAM2029 DKFZP434G1411 3' CACCATGAATAAAAGGA    49686        CCAC
                                CACCGTGAAT   GGGGA
                                ||||||||||   |||||
                                GTGGTACTTA   TTCCT
                                     TT__
GAM2029 DKFZp762P2111 3' AACACTGAGCCCTTGGGGA  49687    CG  AT  AC
                                AACAC  TGA  CC  GGGGA
                                |||||  |||  ||  |||||
                                TTGTG  ACT  GG  CCCCT
                                   __  CG  AA
GAM2029 FLJ10057 3' AACAGCGCCACGGGG     49688    CC  AAT
                                AACA  GTG  CCACGGGG
                                ||||  |||  ||||||||
                                TTGT  CGC  GGTGCCCC
                                  __  ___
GAM2029 FLJ10936 5' ACGCCGGAGCCCACGGGGA  49689   A  T  AT
                                AC CCG GA  CCACGGGGA
                                || ||| ||  |||||||||
                                TG GGC CT  GGTGCCCCT
                                 C  _  CG
GAM2029 FLJ14075 5' CACCGTAATCCCGGGA     49690       A  A
                                CACCGTGA TCC CGGGG
                                |||||||| ||| |||||
                                GTGGCATT AGG GCCCT
                                  _  _
GAM2029 FLJ20643 5' CATCGTCAAATCCGTGGGGA  49691   C  _    AC
                                CA CGT GAATCC  GGGGA
                                || ||| ||||||  |||||
                                GT GCA TTTAGG  CCCCT
                                 A  G    CA
GAM2029 FLJ22635 3' CACCTGCCCACGGGG      49692    G  AA
                                CACC TG  TCCACGGGG
                                ||||  ||  |||||||||
                                GTGG AC  GGGTGCCCC
                                  _  __
GAM2029 FLJ22969 3' AACACTCTGAATCCAGGG   49693     CG     C
                                AACAC  TGAATCCA GGG
                                |||||  |||||||| |||
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                                TTGTG  ACTTAGGT CCC
                                  AG      _
GAM2029  HSNOV1   3'  AACACTTGAATCCAGGA     49694       CG       C
                                AACAC  TGAATCCA GGG
                                |||||  |||||||| |||
                                TTGTG  ACTTAGGT CCT
                                  A_       _
GAM2029  HTEX4    5'  CACTGTGAATCTCGTATTGGGG 49695     C      CAC____    III
              AT                  CAC GTGAATC      GGGGA   T
                                |||  |||||||      |||||   |
                                GTG CACTTAG      CCCCT   A
                                  A      AGCATAA    III
GAM2029  HTEX4    5'  CACTGTGAATCTCGTATTGGGG 49695     C      CAC____    III
              AT                  CAC GTGAATC      GGGGA   T
                                |||  |||||||      |||||   |
                                GTG CACTTAG      CCCCT   A
                                  A      AGCATAA    III
GAM2029  HTEX4    5'  CACTGTGAATCTCGTATTGGGG 49695     C      CAC____    III
              AT                  CAC GTGAATC      GGGGA   T
                                |||  |||||||      |||||   |
                                GTG CACTTAG      CCCCT   A
                                  A      AGCATAA    III
GAM2029  ICK      5'  CCGCGAACGCAGGCGGGG    49696        C  __
                                CCGTGAAT CA  CGGGG
                                |||||||| ||  |||||
                                GGCGCTTG GT  GCCCC
                                     C  CC
GAM2029  KIAA0447 5'  CACCGTGACCGCCCGGGG    49697        AT_  A
                                CACCGTGA   CC CGGGG
                                ||||||||   || |||||
                                GTGGCACT   GG GCCCC
                                     GGC  _
GAM2029  KIAA0552 5'  ACCTGAATCCAACAGGGA    49698     G       _
                                ACC TGAATCCA CGGGGA
                                |||  |||||||| ||||||
                                TGG ACTTAGGT GTCCCT
                                  _       T
GAM2029  KIAA1813 3'  AACAGTGAACACGGGG      49699     CC    TC
                                AACA  GTGAA  CACGGGG
                                ||||  |||||  |||||||
                                TTGT  CACTT  GTGCCCC
                                   __    __
GAM2029  MAPK11   3'  ACATATGAACACGGGGA     49700     CC    TC
                                ACA  GTGAA  CACGGGGA
                                |||  |||||  ||||||||
                                TGT  TACTT  GTGCCCCT
                                  A_    __
GAM2029  MGC10485 5'  ACAGCCGGCTCCACGGGG    49701     _  TGAA
                                ACA CCG    TCCACGGGG
                                ||| |||    |||||||||
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                                TGT GGC    AGGTGCCCC
                                  C   CG__
GAM2029  RAB14    3'  ACACTGTGAACACAGGGA    49702      C     TC
                                ACAC GTGAA  CACGGGGA
                                |||| |||||  ||||||||
                                TGTG CACTT  GTGTCCCT
                                  A    __
GAM2029  RNB6     3'  AACACCATGAGCGCTGGGGA   49703          ATCCAC
                                AACACCGTGA     GGGGA
                                ||||||||||     |||||
                                TTGTGGTACT     CCCCT
                                     CGCGA_
GAM2029  SLC39A3  3'  ACACCATGACCATGGGG     49704         AT   C
                                ACACCGTGA  CCA GGGG
                                |||||||||  ||| ||||
                                TGTGGTACT  GGT CCCC
                                     __   A
GAM2029  LOC149579 5'  CACCTAACCCCACGGGG     49705      G   AT
                                CACC TGA  CCACGGGG
                                |||| |||  ||||||||
                                GTGG ATT  GGTGCCCC
                                  _   GG
GAM2029  LOC165229 5'  CACAGTTCCACGGGGA      49706     C  GAA
                                CAC GT   TCCACGGGGA
                                ||| ||   ||||||||||
                                GTG CA   AGGTGCCCCT
                                  T  ____
GAM2029  LOC199993 5'  CACCGTGACCGCCCGGGG    49697         AT_  A
                                CACCGTGA   CC CGGGG
                                ||||||||   || |||||
                                GTGGCACT   GG GCCCC
                                     GGC  _
GAM2029  LOC200093 5'  AACACCTGTGGACACAGGGA   49685        _   AATC
                                AACACC GTG    CACGGGGA
                                |||||| |||    ||||||||
                                TTGTGG CAC    GTGTCCCT
                                   A   CT__
GAM2029  LOC200317 3'  CACTGTCCCACGGGGA      49707     C  GAA
                                CAC GT   TCCACGGGGA
                                ||| ||   ||||||||||
                                GTG CA   GGGTGCCCCT
                                  A  ____
GAM2029  LOC204200 5'  GCGAAGGGTCCACGGGGA    49708       ____
                                GTGAA   TCCACGGGGA
                                |||||   ||||||||||
                                CGCTT   AGGTGCCCCT
                                   CCC
GAM2029  LOC204823 3'  ACCACTCTTCCCACGGGGA   49709       GAA_
                                ACCGT    TCCACGGGGA
                                |||||    ||||||||||
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                                TGGTG   GGGTGCCCCT
                                  AGAA
GAM2029  LOC222223 5'  ACACCGTGCAGTCATCACGA  49710       AA_ __
                                ACACCGTG  TC  CACGG
                                ||||||||  ||  |||||
                                TGTGGCAC  AG  GTGCT
                                    GTC  TA
GAM2029  LOC256447 3'  AACATTGGGAACACAGGGA  49711    CCGT  TC
                                AACA   GAA  CACGGGGA
                                ||||   |||  ||||||||
                                TTGT   CTT  GTGTCCCT
                                  AACC  __
GAM2029  LOC257068 3'  AACCCTGTGAATTGGGA    49712    A _    CCAC
                                AAC CC GTGAAT   GGGG
                                ||| || ||||||   ||||
                                TTG GG CACTTA   CCCT
                                  _ A    A___
GAM2029  LOC51035  5'  ACACCGCGGCTTCCGCGGGGA 49713       AA_  A
                                ACACCGTG  TCC CGGGGA
                                ||||||||  ||| ||||||
                                TGTGGCGC  AGG GCCCCT
                                    CGA  C
GAM2029  LOC51246  3'  AACACCGTGGACTGGGG    49714       A  CCAC
                                AACACCGTG AT   GGGG
                                |||||||| ||   ||||
                                TTGTGGCAC TG   CCCC
                                    C  A___
GAM2029  LOC51706  3'  GGACCTGTTGCCACGGGGA  49715  C  G  AAT
                                A ACC TG  CCACGGGGA
                                | ||| ||  |||||||||
                                C TGG AC  GGTGCCCCT
                                 C  _ AAC
GAM2029  LOC91040  5'  AACACCTGTGGACACAGGGA  49685      _  AATC
                                AACACC GTG   CACGGGGA
                                |||||| |||   ||||||||
                                TTGTGG CAC   GTGTCCCT
                                   A  CT__
GAM2029  LOC93070  5'  ACGCCGGAGCCCACGGGGA  49689   A  T  AT
                                AC CCG GA  CCACGGGGA
                                || ||| ||  |||||||||
                                TG GGC CT  GGTGCCCCT
                                 C  _  CG
GAM2030  TNS       3'  CGAGCTCAACAGCTGCCTGTTC 49718    _ C    CGCC
                                CGAG TC GCGGT   GCCTGTTC
                                |||| || |||||   ||||||||
                                GCTC AG TGTCG   CGGACAAG
                                  G  T    A___
GAM2030  DKFZp566H0824 5'  CGAGTTTCCGATGCGCCTGTT  49719      CCG   C  C
                                CGAGT   CGGT GC GCCTGTT
                                |||||   |||| || |||||||
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                                GCTCA   GCTA CG CGGACAA
                                  AAG   _ _
GAM2030  EPB41L1   5'  CGGGCTCTGCGGAGCAGCCTGT 49720    A _  C    TC  C
            TC                    CG G TC GCGG  GC GCCTGTTC
                                  || | || ||||  || ||||||||
                                  GC C AG CGCC  CG CGGACAAG
                                   C G  A    T_  T
GAM2030  FLJ21709  3'  GAGTCCGCTGTCGCCCAGCAGG 49721         G     __  CT
            TT                    GAGTCCGC GTCGCC  GC  GTT
                                  |||||||| ||||||  ||  |||
                                  CTCAGGCG CAGCGG  CG  CAA
                                       A     GT  TC
GAM2030  TESK2    5'  GCCGCTCCCCCCGCCTGTT   49722   T   GG  G
                                  G CCGC  TC CCGCCTGTT
                                  | ||||  || |||||||||
                                  C GGCG  GG GGCGGACAA
                                  _    AG  G
GAM2030  LOC150271 5'  CGGGTCCGCGGTCCTGC     49723    A       CGCCG
                                  CG GTCCGCGGT    CCTGT
                                  || |||||||||    |||||
                                  GC CAGGCGCCA    GGACG
                                   C       _____
GAM2030  LOC205095 3'  AGCCGCGTTGCTGCCTGTTC   49724    T    GTC  C
                                  AG CCGCG   GC GCCTGTTC
                                  || |||||   || ||||||||
                                  TC GGCGC   CG CGGACAAG
                                   _    AA_  A
GAM2030  LOC255452 3'  GAGTCTGGGGGATGCCCTGTTC 49725      CGC_  TC   GC
                                  GAGTC   GG  GCC  CTGTTC
                                  |||||   ||  |||  ||||||
                                  CTCAG   CC  CGG  GACAAG
                                     ACCC  TA  __
GAM2031  AP3S2    5'  ACGGTTCTCTCCTCGTGC    49728          G    CAT
                                  ACGGTTCTCTC CTCGT   GC
                                  |||||||||| |||||   ||
                                  TGCCAAGAGAG GAGCA   CG
                                           _    ___
GAM2031  C20orf139 5'  GGTCTCTCGCTGCAGTTGC    49729     T      C  CA_
                                  GGT CTCTCGCT GT   TGC
                                  ||| |||||||| ||   |||
                                  CCA GAGAGCGA CG   ACG
                                    _       _  TCA
GAM2031  CIDEB    5'  GGTTCTCTCCTGTGC      49730         G  C  CAT
                                  GGTTCTCTC CT GT   GC
                                  ||||||||| || ||   ||
                                  CCAAGAGAG GA CA   CG
                                           _ _  ___
GAM2031  LOC200301 3'  GACGGTTCCCTCCGCCCATGTC 49731           _    __
                                  GACGGTTCTCTC GCTC  GTC
                                  |||||||||||| ||||  |||
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                                CTGCCAAGGGAG CGGG  CAG
                                      G    TA
GAM2031  LOC255374 5'  CGGTTCTCCGCTCCGCAACC   49732        T    GT  T
                                CGGTTCTC CGCTC  CA GCC
                                |||||||| |||||  || |||
                                GCCAAGAG GCGAG  GT TGG
                                     _    GC  _
GAM2032  FBXL2     3'  TTTACATGCATCCATTCATTAC 49735       G  G
           T                     TTTATA TG ATCCATTCATTACT
                                 |||||| || ||||||||||||||
                                 AAATGT AC TAGGTAAGTAATGA
                                    _ G
GAM2032  C22orf19  3'  TTTATGGTGATCCACTTCTACT 49736      A   G      CA
                                 TTTAT GTG ATCCATT  TTACT
                                 ||||| ||| |||||||  |||||
                                 AAATA CAC TAGGTGA  GATGA
                                    C  _      A_
GAM2032  DKFZP547N043 3'  TTATAGTGGCTATTTGTTACT  49737         ATCC   CA
                                 TTATAGTGG    ATT  TTACT
                                 |||||||||    |||  |||||
                                 AATATCACC    TAA  AATGA
                                      GA__   AC
GAM2032  KIAA0608  3'  TTTACAACCAAATCTGTTCATT 49738        TG_   CA
           ACT                    TTTATAG   GATC  TTCATTACT
                                  |||||||   ||||  |||||||||
                                  AAATGTT   TTAG  AAGTAATGA
                                      GGT    AC
GAM2032  RI58      3'  TTTACAGTGAGAATTCATTA   49739         _ TCC
                                 TTTATAGTG GA   ATTCATTA
                                 ||||||||| ||   ||||||||
                                 AAATGTCAC CT   TAAGTAAT
                                      T ____
GAM2032  SIAT8C    5'  TAATGGACCATTCATTACT    49740        T
                                 TAGTGGA CCATTCATTACT
                                 ||||||| ||||||||||||
                                 ATTACCT GGTAAGTAATGA
                                     _
GAM2032  LOC144108 3'  TTTATAGTGGGACCTGAGCTAC 49741          AT  ATTCA
           T                     TTTATAGTGG  CC     TTACT
                                 ||||||||||  ||     |||||
                                 AAATATCACC  GG     GATGA
                                      CT  ACTC_
GAM2032  LOC145978 3'  TAATGATTATTCATTAC     49742        ATCC
                                 TAGTGG    ATTCATTAC
                                 ||||||    |||||||||
                                 ATTACT    TAAGTAATG
                                    AA__
GAM2032  LOC51170  3'  AGTGTGATCCATTTATTA    49743      _      C
                                 AGTG GATCCATT ATTA
                                 |||| |||||||| ||||
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                                TCAC CTAGGTAA TAAT
                                  A       A
GAM2033  OAS2     3'  TGGATATATCAGGTATATCTTG 49746          TATGC  C
                GT                  TGGATGTATC     TA CTTGGT
                                    ||||||||||     || ||||||
                                    ACCTATATAG     AT GAACCA
                                          TCCAT  A
GAM2033  UTY      5'  TGGAGTGTCTGTGCTGGGTACC 49747    T  A   A   T________  CTTG
                AAG                   A GT TCT TGC       AC    G
                                    | || ||| |||       ||    |
                                    T CA AGA ACG       TG    C
                                     _ C   C   ACCCAIII  GTTC
GAM2033  DKFZp586H0623 3'  TGGGTGGCCTAGGCTACCTTGG 49748     A  TA    T
                T                   TGG TG  TCTA GCTACCTTGGT
                                    ||| ||  |||| ||||||||||
                                    ACC AC  GGAT CGATGGAACCA
                                      C  C_    C
GAM2033  LOC147991 5'  TGGCTGTATTTATACCACTTGG 49749     A     C       C
                T                   TGG TGTAT TATGCTAC TTGGT
                                    ||| ||||| |||||||| |||||
                                    ACC ACATA ATATGGTG AACCA
                                      G     A       _
GAM2034  LFG      3'  TAGCAGGAGCCCGCTGGCAGTG 49752         A     AATTGT
                A                   TAGTAGGA CCCGC      GTGA
                                    |||||||| |||||      ||||
                                    ATCGTCCT GGGCG      CACT
                                          C     ACCGT_
GAM2034  PMX1     5'  TAATAGGAGCCTGTAATTACGT 49753         A  CGC
                G                   TAGTAGGA CC   AATTGTGTG
                                    |||||||| ||   |||||||||
                                    ATTATCCT GG   TTAATGCAC
                                          C  ACA
GAM2034  PMX1     5'  TAATAGGAGCCTGTAATTACGT 49753         A  CGC
                G                   TAGTAGGA CC   AATTGTGTG
                                    |||||||| ||   |||||||||
                                    ATTATCCT GG   TTAATGCAC
                                          C  ACA
GAM2034  RERE     3'  GTAGGAATTCACAATTAGTGA  49754        CC       T
                                    GTAGGAA  CGCAATTG GTGA
                                    |||||||  |||||||| ||||
                                    CATCCTT  GTGTTAAT CACT
                                         AA       _
GAM2034  SCAP2    3'  TAATAGGAATTAAATGTGTGA  49755         CCCGCAAT
                                    TAGTAGGAA       TGTGTGA
                                    |||||||||       |||||||
                                    ATTATCCTT       ACACACT
                                          AATTT___
GAM2034  DMWD     3'  GTGGGTCACCAGTTGTGTGA   49756    A  A_   CGCAA
                                    GT GG  ACC     TTGTGTGA
                                    || ||  |||     ||||||||
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                                CA CC  TGG    AACACACT
                                 C  AG   TC___
GAM2034  LOC143188 5'  TAGTAGGAGCTCACAGACATG  49757        ACC    AT
                                TAGTAGGA   CGCA  TGTG
                                ||||||||   ||||  ||||
                                ATCATCCT   GTGT  GTAC
                                     CGA    CT
GAM2034  LOC148936 5'  CAGTAGGGACTGTGTG      49758       A  CCGCAAT
                                TAGTAGG AC      TGTGTG
                                |||||||  ||      ||||||
                                GTCATCC TG      ACACAC
                                    C  ________
GAM2034  LOC148938 5'  CAGTAGGGACTGTGTG      49758       A  CCGCAAT
                                TAGTAGG AC      TGTGTG
                                |||||||  ||      ||||||
                                GTCATCC TG      ACACAC
                                    C  ________
GAM2035  DFNA5     3'  TATTATTGTGCAGAAAAAACG  49761        _  C    T
                                TATTATTG GCG AAGG GCG
                                ||||||||  |||  ||||  |||
                                ATAATAAC CGT TTTT TGC
                                     A   C    T
GAM2035  MASP2     3'  TATTATTGGGTCCATGGTG    49762        CG_  A
                                TATTATTGG   CA GGTG
                                |||||||||   ||  ||||
                                ATAATAACC   GT CCAC
                                      CAG  A
GAM2035  KIAA0528  3'  TATTATTGTGCAAAGGAGGAA  49763        _  C    TGC
                                TATTATTG GCG AAGG   GAA
                                |||||||  |||  ||||   |||
                                ATAATAAC CGT TTCC   CTT
                                     A   _    TC_
GAM2035  LOC144703 5'  TATTATTGCTGCAAGGAAC    49764        GC     T
                                TATTATTG  GCAAGG GC
                                ||||||||  ||||||  ||
                                ATAATAAC  CGTTCC TG
                                     GA     T
GAM2035  LOC92755  5'  CTGGAGCAGCGAGGTGCGAACG 49765      C  ____
                                TTGG GCA   AGGTGCGAACG
                                ||||  |||   ||||||||||
                                GACC CGT   TCCACGCTTGC
                                  T   CGC
GAM2036  LOC165254 3'  CGCGCTCGCCGCGGCTTC     49768            G
                                CGCGTTCGCCGCGGC TC
                                ||||||||||||||  ||
                                GCGCGAGCGGCGCCG AG
                                          A
GAM2037  ADAMTS13  5'  GCCAGCCCGAGGAGTGGAGC   49771      T  __    AAACAA
                                GCCA GTT  GGGAG     AGC
                                ||||  |||  |||||     |||
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                              CGGT CGG  TCCTC     TCG
                                _  GC    ACC___
GAM2037 ADAMTS13 5' GCCAGCCCGAGGAGTGGAGC  49771     T  __    AAACAA
                              GCCA GTT  GGGAG     AGC
                              |||| |||  |||||     |||
                              CGGT CGG  TCCTC     TCG
                                _  GC    ACC___
GAM2037 ADAMTS13 5' GCCAGCCCGAGGAGTGGAGC  49771     T  __    AAACAA
                              GCCA GTT  GGGAG     AGC
                              |||| |||  |||||     |||
                              CGGT CGG  TCCTC     TCG
                                _  GC    ACC___
GAM2037 BCL11B   3' TGCCTGTTTCTTAAACAGAGCA 49772     A   GGGAG    A
                              TGCC TGTT    AAACA AGCA
                              |||| ||||    ||||| ||||
                              ACGG ACAA    TTTGT TCGT
                                _   AGAA_    C
GAM2037 CKTSF1B1 3' ACCTGAGGGACAAAGCA    49773    A  TT   GAAA
                              GCC TG  GGGA   CAAAGCA
                              ||| ||  ||||   |||||||
                              TGG AC  CCCT   GTTTCGT
                                _ T_   _____
GAM2037 CYP2B6   3' CCAGCCTGGGAGACAGAGCA  49774    TG      AA  A
                              CCA  TTGGGAGA  CA AGCA
                              |||  ||||||||  || ||||
                              GGT  GACCCTCT  GT TCGT
                                CG       __ C
GAM2037 DDB2     5' GCCTCTGGGGAGAAACAAGGC 49775    A_  TT        A
                              GCC  TG  GGGAGAAACAA GC
                              |||  ||  ||||||||||| ||
                              CGG  AC  CCCTCTTTGTT CG
                                AG  __         C
GAM2037 DLC1     5' TGTCCTGGCTGGGAGCGAAGC 49776    _ AT      AAACA
                              TG CC  GTTGGGAG    AAGC
                              || ||  ||||||||    ||||
                              AC GG  CGACCCTC    TTCG
                               A  AC       GC___
GAM2037 ESR1     3' TGCAGTTGGAAACAGAGC    49777    CAT     GAA   A
                              TGC   GTTGGGA   ACA AGC
                              |||   |||||||   ||| |||
                              ACG   CAACCTT   TGT TCG
                                T__      ___   C
GAM2037 FGF2     3' TGCCACGTGAGAGCAGAGC   49778        T    AAA  A
                              TGCCATGT GGGAG   CA AGC
                              |||||||| |||||   || |||
                              ACGGTGCA CTCTC   GT TCG
                                   _    ___ C
GAM2037 GPC4     3' TGCTTGTAAGAAACAAGGC   49779    CATG   GG      A
                              TGC    TTG  AGAAACAA GC
                              |||    |||  |||||||| ||
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                                ACG   AAC  TCTTTGTT CG
                                 ____  AT      C
GAM2037  GUCY1A2  3'  TGCTTGTTCTCAACAAAGC   49780    CA   GGGAGA
                                TGC  TGTT    AACAAAGC
                                |||  ||||    ||||||||
                                ACG  ACAA    TTGTTTCG
                                 A_   GAG___
GAM2037  HDAC5    3'  CCATATCCAGGGAGACAAAGCA 49781       __    AA
                                CCATGTT  GGGAGA  CAAAGCA
                                |||||||  ||||||  |||||||
                                GGTATAG  CCCTCT  GTTTCGT
                                   GT    __
GAM2037  MEOX1    3'  GCTGGTGTTGGGAGACAGAGC  49782    CA_       AA  A
                                GC   TGTTGGGAGA  CA AGC
                                ||   ||||||||||  || |||
                                CG   ACAACCCTCT  GT TCG
                                 ACC        __  C
GAM2037  MEOX1    3'  GCTGGTGTTGGGAGACAGAGC  49782    CA_       AA  A
                                GC   TGTTGGGAGA  CA AGC
                                ||   ||||||||||  || |||
                                CG   ACAACCCTCT  GT TCG
                                 ACC        __  C
GAM2037  NPAS2    5'  GCCGCCGCTGGGAGACGAGGC  49783    A_       AACAAA
                                GCC  TGTTGGGAGA    GC
                                |||  ||||||||||    ||
                                CGG  GCGACCCTCT    CG
                                 CG        GCTC__
GAM2037  RBBP9    3'  CCAGCCTGGGAGACAGAGCA   49774    TG      AA  A
                                CCA  TTGGGAGA  CA AGCA
                                |||  ||||||||  || ||||
                                GGT  GACCCTCT  GT TCGT
                                 CG       __  C
GAM2037  SLC16A2  3'  TGCCATGTGTATACAAGAA   49784        ___  G
                                TGCCATGT   TG GAGAA
                                ||||||||   || |||||
                                ACGGTACA   AT TTCTT
                                     CAT  G
GAM2037  TCF12    3'  TATTATTAGAAATAAAGCA   49785      GG    C
                                TGTTG  AGAAA AAAGCA
                                |||||  ||||| ||||||
                                ATAAT  TCTTT TTTCGT
                                   AA    A
GAM2037  XRCC2    3'  CCAGCCTGGGAGACAGAGCA   49774    TG      AA  A
                                CCA  TTGGGAGA  CA AGCA
                                |||  ||||||||  || ||||
                                GGT  GACCCTCT  GT TCGT
                                 CG       __  C
GAM2037  XRCC5    3'  TGCTTGTTGGGAGGAAGC    49786    CA       AAACA
                                TGC  TGTTGGGAG    AAGC
                                |||  |||||||||    ||||
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                                ACG  ACAACCCTC    TTCG
                                  A_       C____
GAM2037  C20orf97  3'  TGCATGTGTGTGGAACAAAGCA 49787    C   _ _  GAA
                                TGC ATGT TG GGA   ACAAAGCA
                                ||| |||| || |||   ||||||||
                                ACG TACA AC CCT   TGTTTCGT
                                  _   C  A  ___
GAM2037  CGI-203   5'  TGCCAAGGACCAAGAAACAAAG 49788      TGTTGG
                                TGCCA     GAGAAACAAAG
                                |||||     ||||||||||
                                ACGGT     TTCTTTGTTTC
                                   TCCTGG
GAM2037  DKFZp761F2014 3'  TGCCAGGACGAAGCAAAGC   49789    TG  _  A
                                TGT  GGA GAA CAAAGC
                                |||  ||| ||| ||||||
                                ACG  CCT CTT GTTTCG
                                  GT   G   C
GAM2037  FBXO30    5'  TGCCATTAGGCAAAG      49790      GT   AGAAA
                                TGCCAT  TGGG    CAAAG
                                ||||||  ||||    |||||
                                ACGGTA  ATCC    GTTTC
                                   __   _____
GAM2037  FER1L4    3'  CCAACCTGGGAGACAGAGC   49791    TG      AA  A
                                CCA  TTGGGAGA  CA AGC
                                |||  ||||||||  || |||
                                GGT  GACCCTCT  GT TCG
                                  TG       __  C
GAM2037  FER1L4    3'  CCAACCTGGGAGACAGAGC   49791    TG      AA  A
                                CCA  TTGGGAGA  CA AGC
                                |||  ||||||||  || |||
                                GGT  GACCCTCT  GT TCG
                                  TG       __  C
GAM2037  FLJ10346  5'  GCCTGGGAGACAGAGC     49792    ATGT     AA  A
                                GCC   TGGGAGA  CA AGC
                                |||   |||||||  || |||
                                CGG   ACCCTCT  GT TCG
                                  _____     __  C
GAM2037  FLJ11710  3'  CCAGCCTGGGAGACAGAGCA  49774    TG      AA  A
                                CCA  TTGGGAGA  CA AGCA
                                |||  ||||||||  || ||||
                                GGT  GACCCTCT  GT TCGT
                                  CG       __  C
GAM2037  FLJ12221  3'  TGCCGGGAAAAATGGAAACA  49793          CA_
                                TGTTGGGAGAAA   AAGCA
                                ||||||||||||   |||||
                                ACGGCCCTTTTT   TTTGT
                                       ACC
GAM2037  FLJ12788  3'  TGCTGGGGTGGAGAAACAGAG  49794        _____     A
                                TGTTGGG   AGAAACA AG
                                |||||||   ||||||| ||
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                                ACGACCC   TCTTTGT TC
                                   CACC      C
GAM2037  FLJ20045  3'  CCAGCCTGGGAAACAAAGC   49795    T  TG  A
                                CCA GT  GG GAAACAAAGC
                                ||| ||  || ||||||||||
                                GGT CG  CC CTTTGTTTCG
                                  _  GA  _
GAM2037  FLJ20150  3'  TGCTAGATGCCAGAGACAAAG  49796    C__   TG G   AA
                                TGC   ATGT  G AGA  CAAAG
                                |||   ||||  | |||  |||||
                                ACG   TACG  C TCT  GTTTC
                                  ATC    GT _  __
GAM2037  FLJ21106  5'  GCCATGGGGGAAACAAAG    49797      TT   A
                                GCCATG  GGG GAAACAAAG
                                ||||||  ||| |||||||||
                                CGGTAC  CCC CTTTGTTTC
                                   __   _
GAM2037  FLJ22282  3'  TGGCATATCGGGAGGCAAAGCA 49798    C        AAA
                                TG CATGTTGGGAG   CAAAGCA
                                || ||||||||||   |||||||
                                AC GTATAGCCCTC   GTTTCGT
                                 C         C__
GAM2037  FLJ23024  3'  GCCTGGGAGACAGAGCA     49799     ATGT      AA  A
                                GCC    TGGGAGA  CA AGCA
                                |||    |||||||  || ||||
                                CGG    ACCCTCT  GT TCGT
                                  _____      __ C
GAM2037  FLJ23047  3'  TGTGGGCTAAAGAAACAAGGCA 49800     T  _____      A
                                TGT GGG    AGAAACAA GCA
                                ||| |||    |||||||| |||
                                ACA CCC    TCTTTGTT CGT
                                  _  GATT       C
GAM2037  FREQ     3'  TGCTGCGGGAAGGGACAA    49801     CA   T    AA
                                TGC  TGT GGGAG  ACAA
                                |||  ||| |||||  ||||
                                ACG  ACG CCTTC  TGTT
                                  __  C    CC
GAM2037  HRH4     3'  CCAGCCTGGGAGACAGAGCA   49774     TG       AA  A
                                CCA  TTGGGAGA  CA AGCA
                                |||  ||||||||  || ||||
                                GGT  GACCCTCT  GT TCGT
                                  CG       __ C
GAM2037  HSPC129  3'  TGCAGTTGAGAGGCAAAGC    49802     CAT      AAA
                                TGC   GTTGGGAG   CAAAGC
                                |||   ||||||||   ||||||
                                ACG   CAACTCTC   GTTTCG
                                  T__       C__
GAM2037  KIAA0459 3'  GCTCCCTGGGGGAAGCAGGGCA 49803    CATG    A   A  AA
                                GC    TTGGG GAA CA  GCA
                                ||    ||||| ||| ||  |||
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                                CG   GACCC CTT GT  CGT
                                 AGG_    C   C  CC
GAM2037  KIAA0515  3'  TGCTGCTGGGAGTGAAGC    49804     CA       AAACA
                                TGC  TGTTGGGAG    AAGC
                                |||  |||||||||    ||||
                                ACG  ACGACCCTC    TTCG
                                  __       AC___
GAM2037  KIAA0603  3'  TGCTAGTTGGCACAAAGC    49805     CAT    GAGAA
                                TGC   GTTGG    ACAAAGC
                                |||   |||||    |||||||
                                ACG   CAACC    TGTTTCG
                                  AT_    G____
GAM2037  KIAA0644  3'  GCCATGTTGGGGGCACAAGCA  49806          AGAA    A
                                GCCATGTTGGG    ACAA GCA
                                ||||||||||    |||| |||
                                CGGTACAACCC    TGTT CGT
                                       CCG_   _
GAM2037  KIAA1244  3'  GCTATAAAAAGAAACAAAGCA  49807    CA   TG
                                GC  TGT  GGAGAAACAAAGCA
                                ||  |||  ||||||||||||||
                                CG  ATA  TTTCTTTGTTTCGT
                                 __   TT
GAM2037  KIAA1610  3'  CCAGCAGAAGAGAAACAGAG   49808     T  T_       A
                                CCA GT  GGGAGAAACA AG
                                ||| ||  |||||||||| ||
                                GGT CG  TTCTCTTTGT TC
                                  _ TC        C
GAM2037  KIAA1884  3'  TGCTGTTGGAAGCAAAG     49809     CA       AAA
                                TGC  TGTTGGGAG   CAAAG
                                |||  |||||||||   |||||
                                ACG  ACAACCTTC   GTTTC
                                  __       ____
GAM2037  KIAA1975  5'  CCAGGCCGGGAGACAAAG    49810     T       AA
                                CCA GTTGGGAGA  CAAAG
                                ||| |||||||||  |||||
                                GGT CGGCCCTCT  GTTTC
                                  C       __
GAM2037  MGC13114  3'  GCCATGTTGATGCAGAGC    49811          GAGAAA  A
                                GCCATGTTGG     CA AGC
                                ||||||||||     || |||
                                CGGTACAACT     GT TCG
                                       AC_____  C
GAM2037  MGC22014  3'  TGCTGTGTGGTACAAAGC    49812     CA   T  GAGAA
                                TGC  TGT GG    ACAAAGC
                                |||  ||| ||    |||||||
                                ACG  ACA CC    TGTTTCG
                                  AC   _  A_____
GAM2037  NEIL2     3'  GCCAGGGAGACAGAGC      49813      TGTT     AA  A
                                GCCA    GGGAGA  CA AGC
                                ||||    ||||||  || |||
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                                CGGT   CCCTCT  GT TCG
                                  ____    __ C
GAM2037  NFAT5   3'  GCCTGAGAGACAGAGCA    49814    ATGT     AA  A
                                GCC   TGGGAGA  CA AGCA
                                |||   |||||||  || ||||
                                CGG   ACTCTCT  GT TCGT
                                  ____     __ C
GAM2037  P2RXL1  3'  TGCTAGGAACACTGGGGACAGA 49815   C____ TG    A  AA  A
           GCA                    GC    A  TTGGG GA  CA AGCA
                                ||    |  ||||| ||  || ||||
                                CG    T  GACCC CT  GT TCGT
                                 ATCCT GT    _ __  C
GAM2037  PGRMC2  3'  ATGTTAAGTGAAATAAGGCA  49816       A   C  A
                                ATGTTGGG GAAA AA GCA
                                |||||||| |||| || |||
                                TACAATTC CTTT TT CGT
                                     A   A  C
GAM2037  PLSCR4  3'  TGTCAATAAAAAGAAGCAAAGC 49817    TG ____    A
           A                    TGT  G   GAGAA CAAAGCA
                                |||  |   ||||| |||||||
                                ACA  T   TTCTT GTTTCGT
                                  GT ATTT    C
GAM2037  POFUT1  3'  CCAGCCTGGGAGACAGAGCA  49774    TG      AA  A
                                CCA  TTGGGAGA  CA AGCA
                                |||  ||||||||  || ||||
                                GGT  GACCCTCT  GT TCGT
                                  CG       __ C
GAM2037  RNF38   3'  TGCTATTGCAAACAAAGC    49818    CA    G  GAA
                                TGC  TGTTG GA   ACAAAGC
                                |||  ||||| ||   |||||||
                                ACG  ATAAC TT   TGTTTCG
                                  __    G  ___
GAM2037  SLAC2-B  3'  ATGTTAGGAGGGAAGTAAAGCA 49819         AAAC__
                                ATGTTGGGAG     AAAGCA
                                ||||||||||     ||||||
                                TACAATCCTC     TTTCGT
                                     CCTTCA
GAM2037  UBE3B   3'  TGCCATGTTTCCATCAAAGTAG 49820        GGGA__  ACAA
           AGCA                   TGCCATGTT     GAA   AGCA
                                |||||||||     |||   ||||
                                ACGGTACAA     TTT   TCGT
                                     AGGTAG   CATC
GAM2037  UBF-fl  3'  GCCTGGGAGACAGAGC     49792    ATGT     AA  A
                                GCC   TGGGAGA  CA AGC
                                |||   |||||||  || |||
                                CGG   ACCCTCT  GT TCG
                                  ____     __ C
GAM2037  ZNF338  3'  CCAGCCTGGGAAACAGAGC   49821    T  TG  A    A
                                CCA GT  GG GAAACA AGC
                                ||| ||  || |||||| |||
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                                GGT CG  CC CTTTGT TCG
                                  _ GA  _     C
GAM2037  LOC128272 3'  TGCCAAGGCCACAGAAGC    49822      TGTT   AGAA  _
                                TGCCA    GGG    ACA AAGC
                                |||||    |||    ||| ||||
                                ACGGT    TCC    TGT TTCG
                                   _____   GG__   C
GAM2037  LOC137964 3'  TGTAAAAGAAACAAGGCA    49823     T         A
                                TGT GGGAGAAACAA GCA
                                ||| ||||||||||| |||
                                ACA TTTTCTTTGTT CGT
                                  _         C
GAM2037  LOC138199 3'  GCCTGGGAGACAGAGC      49792     ATGT      AA  A
                                GCC    TGGGAGA  CA AGC
                                |||    |||||||  || |||
                                CGG    ACCCTCT  GT TCG
                                  _____      __ C
GAM2037  LOC149684 3'  TACCTGGGGAAACAAAG     49824     ATGT    A
                                TGCC    TGGG GAAACAAAG
                                ||||    |||| |||||||||
                                ATGG    ACCC CTTTGTTTC
                                   _____   _
GAM2037  LOC150568 5'  TGTCGGCTGAGACAAAGC    49825       GA  A
                                TGTTGG  GA ACAAAGC
                                ||||||  || |||||||
                                ACAGCC  CT TGTTTCG
                                    GA  C
GAM2037  LOC150759 3'  TGCATCCTGGGGATGAAGC    49826     C  G    A  AACA
                                TGC AT TTGGG GA    AAGC
                                ||| || ||||| ||    ||||
                                ACG TA GACCC CT    TTCG
                                  _ G    _  AC__
GAM2037  LOC151171 5'  GCCGTACTGGGAGCGAGGCA   49827     A       AAACAAA
                                GCC TGTTGGGAG      GCA
                                ||| |||||||||      |||
                                CGG ATGACCCTC      CGT
                                  C        GCTC___
GAM2037  LOC151283 3'  TGTGATATTGGGAGACAAAG   49828    CC        AA
                                TG  ATGTTGGGAGA  CAAAG
                                ||  ||||||||||  |||||
                                AC  TATAACCCTCT  GTTTC
                                  AC         __
GAM2037  LOC153959 5'  CCATGCTGACCAGAAACAAAGC 49829         G_
              A                  CCATGTTGG  AGAAACAAAGCA
                                |||||||||  ||||||||||||
                                GGTACGACT  TCTTTGTTTCGT
                                     GG
GAM2037  LOC154282 3'  TGCTATGTTGGGAGATCCA    49830     C         AA
                                TGC ATGTTGGGAGA  CA
                                ||| ||||||||||  ||
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                                ACG TACAACCCTCT  GT
                                  A          AG
GAM2037  LOC158235 3'  TGCTATGAAGAGAAATAAAGCA 49831     C   TT       C
                                TGC ATG  GGGAGAAA AAAGCA
                                ||| |||  |||||||| ||||||
                                ACG TAC  TTCTCTTT TTTCGT
                                  A  __       A
GAM2037  LOC200399 5'  TGCATCCTGGGGATGAAGC    49826     C  G     A  AACA
                                TGC AT TTGGG GA    AAGC
                                ||| || ||||| ||    ||||
                                ACG TA GACCC CT    TTCG
                                  _  G     _  AC__
GAM2037  LOC221074 3'  TGCAATGAAAGAAACAAAG    49832     CATGT  GG
                                TGC     TG  AGAAACAAAG
                                |||     ||  ||||||||||
                                ACG     AC  TCTTTGTTTC
                                  TT___  TT
GAM2037  LOC221773 3'  CCAGCCTGGGAGACAGAGCA   49774     TG       AA  A
                                CCA  TTGGGAGA  CA AGCA
                                |||  ||||||||  || ||||
                                GGT  GACCCTCT  GT TCGT
                                  CG       __  C
GAM2037  LOC222070 5'  CCAGCCTGGGAGACAGAGCA   49774     TG       AA  A
                                CCA  TTGGGAGA  CA AGCA
                                |||  ||||||||  || ||||
                                GGT  GACCCTCT  GT TCGT
                                  CG       __  C
GAM2037  LOC253148 5'  TGCCAGTGCAGGCAAGGC     49833       _   T  GAGAAA   A
                                TGCCA TGT GG      CAA GC
                                ||||| ||| ||      ||| ||
                                ACGGT ACG CC      GTT CG
                                   C   T _______   C
GAM2037  LOC253612 5'  CCAGCCTGGGAGACAGAGC    49834     TG       AA  A
                                CCA  TTGGGAGA  CA AGC
                                |||  ||||||||  || |||
                                GGT  GACCCTCT  GT TCG
                                  CG       __  C
GAM2037  LOC253897 3'  TGTAAAAGAAACAAGGCA     49823     T         A
                                TGT GGGAGAAACAA GCA
                                ||| ||||||||||| |||
                                ACA TTTTCTTTGTT CGT
                                  _          C
GAM2037  LOC91960  5'  CGCCAGGAATGGGGAAGCAAGG 49835       TGT_   A   A   A
             C                   TGCCA    TGGG GAA CAA GC
                                |||||    |||| ||| ||| ||
                                GCGGT    ACCC CTT GTT CG
                                   CCTT    _   C   C
GAM2038  SOX12    3'  GTGGCTTTGTCAGCGA      49838      A   ACGATT
                                GTGG TTTG      TCAGCGA
                                |||| ||||      |||||||
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                                CACC AAAC     AGTCGCT
                                  G  _______
GAM2039  ATP7B    3'  GCCGTGCAGGGAGGCTCCTGC  49841   G          CGAA
                                G CGTGCAGGGAGGC   GC
                                | ||||||||||||    ||
                                C GCACGTCCCTCCG   CG
                                 G          AGGA
GAM2039  DDX11    3'  GGCTGCAGGGATGGCAAGGCGG 49842    G      _  C  A
              C                  GGC TGCAGGGA GGC GA GCGGC
                                 ||| |||||||| ||| || |||||
                                 CCG ACGTCCCT CCG TT CGCCG
                                   _      A  _  C
GAM2039  DFFA     5'  GTCGCGGGAGGCCGGAGCGGC  49843   _ A       A
                                 GT GC GGGAGGCCG AGCGGC
                                 || || ||||||||| ||||||
                                 CA CG CCCTCCGGC TCGCCG
                                  G _       C
GAM2039  EGLN2    5'  GGTGTGCAAGGAGGTGGCGCCG 49844          _________   AAG
              CTTCG                 GTGCAGGGAG      GCCG  CG
                                 ||||||||||      ||||  ||
                                 CACGTTCCTC      CGGC  GC
                                       CACCGIII   GAA
GAM2039  GNA15    5'  GGTGCGCAGGGAGGCTGC    49845   C        CGAA
                                 GG GTGCAGGGAGGC   GC
                                 || ||||||||||||   ||
                                 CC CGCGTCCCTCCG   CG
                                  A         A___
GAM2039  HCFC1    3'  GGCCTGCAGGGAGGTCTGCGCC 49846        _________   AAG
              GCTTCGG                GCAGGGAG       GCCG  CGG
                                 ||||||||       ||||  |||
                                 CGTCCCTC       CGGC  GCC
                                      CAGACGIII   GAA
GAM2039  HSF4     5'  GGCGTTCAGCTCGGCCGAAGCG 49847      G  GGA
              GC                   GGCGT CAG   GGCCGAAGCGGC
                                 ||||| |||   ||||||||||||
                                 CCGCA GTC   CCGGCTTCGCCG
                                   A  GAG
GAM2039  IFNAR2   5'  GGCGGGCGGGGGGACAAAAGCGG 49848     T  A   A   C
              C                   GGCG GC GGG GGC GAAGCGGC
                                 |||| || ||| ||| ||||||||
                                 CCGC CG CCC CTG TTTCGCCG
                                   C  C   _   T
GAM2039  ITGA9    3'  CGTGTGACCTGGCCGAAGTGGC 49849      CAGGGA      C
                                 CGTG     GGCCGAAG GGC
                                 ||||     |||||||| |||
                                 GCAC     CCGGCTTC CCG
                                   ACTGGA       A
GAM2039  JAG2     5'  GGCGTGCAGGGGCGGCGG    49850          AG  CGAA
                                 GGCGTGCAGGG  GC   GCGG
                                 ||||||||||  ||   ||||
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                                CCGCACGTCCC CG   CGCC
                                     __ C___
GAM2039 KLF8    5' GGTTCGCTGGGCCGAAGTGGC 49851   CG  AGGGA      C
                                GG TGC    GGCCGAAG GGC
                                || |||    |||||||| |||
                                CC GCG    CCGGCTTC CCG
                                 AA  AC___      A
GAM2039 PDGFB   5' GGTGCGCAGGGAGGCAGGC   49852   C         CGAA
                                GG GTGCAGGGAGGC   GC
                                || ||||||||||||   ||
                                CC CGCGTCCCTCCG   CG
                                 A         TC__
GAM2039 PIGR    3' GGGTGCAGGGAGCAGGCGG   49853   C       G CGAA
                                GG GTGCAGGGAG C   GCGG
                                || ||||||||||  |   ||||
                                CC CACGTCCCTC G   CGCC
                                 _        _ TC__
GAM2039 SOX12   3' GGGTGTGGGGAGGCCGGAGGGG 49854   C  CA       A  C
            C                    GG GTG  GGGAGGCCG AG GGC
                                || |||  |||||||| || |||
                                CC CAC  CCCTCCGGC TC CCG
                                 _  AC       C  C
GAM2039 C20orf150 3' GTGGCAGGGAGCCAGCGG    49855    _     G  GA
                                GTG CAGGGAG CC  AGCGG
                                ||| ||||||| ||  |||||
                                CAC GTCCCTC GG  TCGCC
                                 C     _ __
GAM2039 dJ309H15.1 3' GGCTGTGGGGAGAGAAAGCGGC 49856    _  CA     CC
                                GGC GTG  GGGAGG  GAAGCGGC
                                ||| |||  ||||||  ||||||||
                                CCG CAC  CCCTCT  TTTCGCCG
                                 A  __     C_
GAM2039 DKFZp762K222 5' GGCGTGCGGGAGGCCGGAGGGG 49857        A       AA___
            CGGC                    GGCGTGC GGGAGGCCG    GCGGC
                                ||||||| |||||||||    |||||
                                CCGCACG CCCTCCGGC    CGCCG
                                   _       CTCCC
GAM2039 FKBP4   5' GGCGTGCGGGAGGCCGGGCGCG 49858        A       AA_
            GC                    GGCGTGC GGGAGGCCG   GCGGC
                                ||||||| |||||||||   |||||
                                CCGCACG CCCTCCGGC   CGCCG
                                   _       CCG
GAM2039 FKBP8   3' GGTGTGCAGAGGGGGTGGCGCC 49859       A __________   AAG
            GCTTCGG                 GCAGGG G       GCCG   CGG
                                |||||| |       ||||   |||
                                CGTCTC C       CGGC   GCC
                                   C CCACCGIII   GAA
GAM2039 FLJ20019 5' GTGTCAGGGAGGCCTGC    49860    _       GAA
                                GTG CAGGGAGGCC   GC
                                ||| ||||||||||   ||
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                                CAC GTCCCTCCGG   CG
                                  A        A__
GAM2039  FLJ21459  3'  AGCACCTTGGGAGGCCGAGGCG 49861      TGCA        A
             G                    GGCG    GGGAGGCCGA GCGG
                                  ||||    |||||||||| ||||
                                  TCGT    CCCTCCGGCT CGCC
                                    GGAA         C
GAM2039  FLJ23191  5'  AGCGTGCGGGGGCTGGGCGGC  49862        A   A   CGAA
                                  GGCGTGC GGG GGC    GCGGC
                                  ||||||| ||| |||    |||||
                                  TCGCACG CCC CCG    CGCCG
                                      _  _  ACC_
GAM2039  FLJ25132  5'  GGCGTGCAGCGGAGGGAGCGGC 49863          _     CCGA
                                  GGCGTGCAG GGAGG    AGCGGC
                                  |||||||| |||||    ||||||
                                  CCGCACGTC CCTCC    TCGCCG
                                       G    C___
GAM2039  GBTS1     3'  GGCGTGCAGGCGGGCGTTCCGG 49864          GA   CGAAGC
             GC                     GGCGTGCAGG  GGC     GGC
                                    ||||||||||  |||     |||
                                    CCGCACGTCC  CCG     CCG
                                         GC   CAAGGC
GAM2039  HGC6.1.1  5'  GGCGTCAGGGGAGACCTGGGGC 49865       G    _    GAA_
             GGC                      GGCGT CAGGG AGGCC    GCGGC
                                      ||||| ||||| |||||    |||||
                                      CCGCA GTCCC TCTGG    CGCCG
                                        _     C     ACCC
GAM2039  HSPC065   3'  GGATGGTAAGGGGCTGAAGCGG 49866    C   C_   A   C
             C                      GG GTG  AGGG GGC GAAGCGGC
                                    || |||  |||| ||| ||||||||
                                    CC TAC  TTCC CCG CTTCGCCG
                                     _  CA    _   A
GAM2039  KIAA0150  3'  GGTTGCACCTGCCGAAGCGG   49867    CG    GGGAG
                                    GG  TGCA    GCCGAAGCGG
                                    ||  ||||    ||||||||||
                                    CC  ACGT    CGGCTTCGCC
                                     A_   GGA__
GAM2039  KIAA0237  5'  GGCCTCCACAGGCCGAGGCGGC 49868     GTG  GGG      A
                                    GGC   CA   AGGCCGA GCGGC
                                    |||   ||   ||||||| |||||
                                    CCG   GT   TCCGGCT CGCCG
                                      GAG  G__      C
GAM2039  KIAA0544  3'  GGTGTGCAGGGAGCTGGGTGCC 49869          __________    AAG
             GCTTCGG                  GCAGGGAG       GCCG   CGG
                                      ||||||||       ||||   |||
                                      CGTCCCTC       CGGC   GCC
                                           GACCCAIII    GAA
GAM2039  KIAA0544  3'  GGGTGCAGGGGTGGGGAGCGGC 49870    C       A_  CCGA
                                    GG GTGCAGGG  GG    AGCGGC
                                    || ||||||||  ||    ||||||
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                                CC CACGTCCC  CC    TCGCCG
                                 _       CA  CC__
GAM2039  KIAA0553  3'  GGCAAAAGAGGCTGAGGTGG   49871      TGC       C  AGC
                                GGCG   AGGGAGGC GA   GG
                                ||||   |||||||| ||   ||
                                CCGT   TTTCTCCG CT   CC
                                  ___       A  CCA
GAM2039  KIAA0668  3'  AGCGTGTGGGGGAAGCGG    49872       CA   AGGCC
                                GGCGTG  GGG    GAAGCGG
                                ||||||  |||    |||||||
                                TCGCAC  CCC    CTTCGCC
                                   AC  ______
GAM2039  KIAA1138  3'  GGAGTGCAGGGGTGGGGCGGC  49873    C       A_  CCGAA
                                GG GTGCAGGG  GG    GCGGC
                                || ||||||||  ||    |||||
                                CC CACGTCCC  CC    CGCCG
                                 T       CA  C_____
GAM2039  KIAA1172  5'  GGCTGCGCCCGAAGCG      49874     _   AGGGAGG
                                GGC GTGC      CCGAAGCG
                                ||| ||||      ||||||||
                                CCG CGCG      GGCTTCGC
                                  A   _________
GAM2039  KIAA1184  3'  GGCTGTAGGGAGGCCACTGAGG 49875     G  C        AAGC
            C                    GGC TG AGGGAGGCCG    GGC
                                ||| || ||||||||||    |||
                                CCG AC TCCCTCCGGT    CCG
                                  _ A         GACT
GAM2039  MARK2     5'  GGGTGCGGGGAGGCCGGG    49876    C    A       AAGC
                                GG GTGC GGGAGGCCG    GG
                                || |||| |||||||||    ||
                                CC CACG CCCTCCGGC    CC
                                 _    C       _____
GAM2039  MGC12966  3'  GGCTGTGCTCGGAGTGGCGCCG 49877  _    AG    ________    AAG
            CTTCG                    GTGC  GGAG      GCCG   CG
                                 ||||  ||||      ||||   ||
                                 CACG  CCTC      CGGC   GC
                                A    AG    ACCGIII    GAA
GAM2039  MGC15476  5'  GGCGTGCAGGGGGCTGGGC    49878          A   CGAA
                                GGCGTGCAGGG GGC    GC
                                |||||||||| |||    ||
                                CCGCACGTCCC CCG    CG
                                       _   ACC_
GAM2039  R32184_3  3'  GGCGTGGGGGAGGCCCCCAGC  49879       CA       GA_
                                GGCGTG  GGGAGGCC   AGC
                                ||||||  ||||||||   |||
                                CCGCAC  CCCTCCGG   TCG
                                   C_       GGG
GAM2039  RASGRP4   3'  GGTGTGCAGGAAGGCCAGG    49880    C           AAGC
                                GG GTGCAGGGAGGCCG    GG
                                || ||||||||||||||    ||
```

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                                CC CACGTCCTTCCGGT   CC
                                 A          ____
GAM2039  SDC3     3'  GGCTGCAGGGAGGCACTGTGGC 49881     G         CGAAGC
                                GGC TGCAGGGAGGC     GGC
                                ||| ||||||||||      |||
                                CCG ACGTCCCTCCG     CCG
                                  _         TGACA_
GAM2039  TBC1D2   3'  GGCTGTGGGGAGGGGAGGTGGC 49882     _  CA     CC  AGC
                                GGC GTG  GGGAGG  GA   GGC
                                ||| |||  ||||||  ||   |||
                                CCG CAC  CCCTCC  CT   CCG
                                  A  __     C_  CCA
GAM2039  LOC120772 5'  GCGTGCAGGGGGGCTGAGC   49883          A   C  A
                                GCGTGCAGGG GGC GA GC
                                |||||||||| ||| || ||
                                CGCACGTCCC CCG CT CG
                                       C   A  _
GAM2039  LOC143916 3'  AGCAGTTTGGGAGGCCGAGGTG 49884     _ GCA        AGC
              G                  GGC GT   GGGAGGCCGA   GG
                                ||| ||   ||||||||||   ||
                                TCG CA   CCCTCCGGCT   CC
                                  T  AA_        CCA
GAM2039  LOC150244 5'  GGCGTGCAGGGCGAGGGCGGC  49885          AGGC   A_
                                GGCGTGCAGGG   CGA  GCGGC
                                ||||||||||    |||  |||||
                                CCGCACGTCCC   GCT  CGCCG
                                      ____  CC
GAM2039  LOC201245 5'  GCGTGCAGGGAGCCCAGTGGC  49886          G  GA  C
                                GCGTGCAGGGAG CC  AG GGC
                                ||||||||||| ||  || |||
                                CGCACGTCCCTC GG  TC CCG
                                       G  __  A
GAM2039  LOC203260 5'  GGCGGGCGGTGCCGAAGCGG   49887     T  AG  AG
                                GGCG GC  GG  GCCGAAGCGG
                                |||| ||  ||  ||||||||||
                                CCGC CG  CC  CGGCTTCGCC
                                  C  __  A_
GAM2039  LOC204820 3'  GGGCAGGGAGGCCTTGAGC   49888    CGT        GA_
                                GG   GCAGGGAGGCC   AGC
                                ||   ||||||||||   |||
                                CC   CGTCCCTCCGG   TCG
                                 ___         AAC
GAM2039  LOC219818 3'  GGCTTGTGGGGAAAGCGG    49889     G  CA   GGCCG
                                GGC TG  GGGA    AAGCGG
                                ||| ||  ||||    ||||||
                                CCG AC  CCCT    TTCGCC
                                  A  AC   _____
GAM2039  LOC220753 5'  GGTGTGCAGGTGAGGCTGGA   49890    C     _    C_
                                GG GTGCAGG GAGGC  GA
                                || ||||||| |||||  ||
```

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                                CC CACGTCC CTCCG  CT
                                 A      A    AC
GAM2039  LOC222865 5'  GGCGGTGCGGGGAGGTGCGG  49891     _  A    CCGAA
                                GGCG TGC GGGAGG    GCGG
                                |||| ||| ||||||    ||||
                                CCGC ACG CCCTCC    CGCC
                                  C  C     A____
GAM2039  LOC254076 5'  GGCTTGCAGGGCGTCGAGGCGG 49892    G     AGGC  A
           C                     GGC TGCAGGG   CGA GCGGC
                                ||| |||||||   ||| |||||
                                CCG ACGTCCC   GCT CGCCG
                                  A     GCA_  C
GAM2039  LOC254173 3'  GTGCAGGAGCACGAAGCGGC  49893      GA  _
                                GTGCAGG  GGC CGAAGCGGC
                                |||||||  ||| |||||||||
                                CACGTCC  TCG GCTTCGCCG
                                   __  T
GAM2039  LOC256867 5'  GCGTGCAGGGGGGCTGAGC   49883       A  C  A
                                GCGTGCAGGG GGC GA GC
                                |||||||||| ||| || ||
                                CGCACGTCCC CCG CT CG
                                     C  A  _
GAM2040  ABCC1    5'  GGCGGCGGGCACCGGGCGGCGG 49896       _  T  A_  A
                                GGCGGCGGG GC CG  CG CGG
                                ||||||||| || ||  || |||
                                CCGCCGCCC TG GC  GC GCC
                                     G  _  CC  C
GAM2040  ABCC1    5'  GGCGGCGGGCACCGGGCGGCGG 49896       _  T  A_  A
                                GGCGGCGGG GC CG  CG CGG
                                ||||||||| || ||  || |||
                                CCGCCGCCC TG GC  GC GCC
                                     G  _  CC  C
GAM2040  ABCC1    5'  GGCGGCGGGCACCGGGCGGCGG 49896       _  T  A_  A
                                GGCGGCGGG GC CG  CG CGG
                                ||||||||| || ||  || |||
                                CCGCCGCCC TG GC  GC GCC
                                     G  _  CC  C
GAM2040  ABCC1    5'  GGCGGCGGGCACCGGGCGGCGG 49896       _  T  A_  A
                                GGCGGCGGG GC CG  CG CGG
                                ||||||||| || ||  || |||
                                CCGCCGCCC TG GC  GC GCC
                                     G  _  CC  C
GAM2040  ABCC1    5'  GGCGGCGGGCACCGGGCGGCGG 49896       _  T  A_  A
                                GGCGGCGGG GC CG  CG CGG
                                ||||||||| || ||  || |||
                                CCGCCGCCC TG GC  GC GCC
                                     G  _  CC  C
GAM2040  ABCC1    5'  GGCGGCGGGCACCGGGCGGCGG 49896       _  T  A_  A
                                GGCGGCGGG GC CG  CG CGG
                                ||||||||| || ||  || |||
```

```
                                CCGCCGCCC TG GC  GC GCC
                                     G  _  CC  C
GAM2040  ABCC4    5'  AGGCGGCGGTGGCCGCGGG   49897        _  T  A  AC
                                AGGCGGCGG GGC CG CG  GG
                                ||||||||| ||| || ||  ||
                                TCCGCCGCC CCG GC GC  CC
                                     A  _  _  __
GAM2040  ACTN2    5'  AGGCGGCGGGCGGCGG     49898         GCTCGA  A
                                AGGCGGCGGG     CG CGG
                                ||||||||||     || |||
                                TCCGCCGCCC     GC GCC
                                      _______  C
GAM2040  ALDH3B1  3'  AGGCGGCGCGGCGATTGCGGCG 49899        G  TCGA_  A
            G                    AGGCGGCG GGC     CG CGG
                                ||||||||| |||     || |||
                                TCCGCCGC CCG     GC GCC
                                     G  CTAAC  C
GAM2040  ANKH     5'  GGCGACGGGGGGCGACGG     49900         CTCGA
                                GGCGGCGGGG     CGACGG
                                ||||||||||     ||||||
                                CCGCTGCCCC     GCTGCC
                                     C____
GAM2040  ANKH     5'  GGCGACGGGGGGCGACGG     49900         CTCGA
                                GGCGGCGGGG     CGACGG
                                ||||||||||     ||||||
                                CCGCTGCCCC     GCTGCC
                                     C____
GAM2040  AQP3     5'  AGGCGGCGGCGCTGTCGGGCGG 49901        G  CGA  A_
                                AGGCGGCGG GCT   CG  CGG
                                ||||||||| |||   ||  |||
                                TCCGCCGCC CGA   GC  GCC
                                     G  CA_  CC
GAM2040  AQP5     5'  AGGCGGCGGAGGAGGTGGA   49902         CTC  CGAC
                                AGGCGGCGGGG   GA   GGA
                                ||||||||||   ||   |||
                                TCCGCCGCCTC   CT   CCT
                                     ___  CCA_
GAM2040  AQP6     5'  GGCAGCGGGGCTCATGGGA   49903          ACGAC
                                GGCGGCGGGGCTCG    GGA
                                ||||||||||||||    |||
                                CCGTCGCCCCGAGT    CCT
                                      AC___
GAM2040  ARD1     5'  GGCGGCGGGGCTCGCGGG    49904          A  AC
                                GGCGGCGGGGCTCG CG  GG
                                |||||||||||||| ||  ||
                                CCGCCGCCCCGAGC GC  CC
                                     _  __
GAM2040  BAPX1    3'  AGGCAGCGGCACTGCGGTGG  49905        G  CGA  AC
                                AGGCGGCGG GCT   CG  GG
                                ||||||||| |||   ||  ||
```

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                                TCCGTCGCC TGA   GC  CC
                                    G   C__  CA
GAM2040  BCL11A   5'  GGCGGCGGCGGCGGCGGCGGCG 49906        _  T_  A  A
             G                   GGCGGCGG GGC  CG CG CGG
                                 |||||||| |||  || || |||
                                 CCGCCGCC CCG  GC GC GCC
                                    G   CC  C  C
GAM2040  BCL11A   5'  GGCGGCGGCGGCGGCGGCGGCG 49906        _  T_  A  A
             G                   GGCGGCGG GGC  CG CG CGG
                                 |||||||| |||  || || |||
                                 CCGCCGCC CCG  GC GC GCC
                                    G   CC  C  C
GAM2040  BCL11A   5'  GGCGGCGGCGGCGGCGGCGGCG 49906        _  T_  A  A
             G                   GGCGGCGG GGC  CG CG CGG
                                 |||||||| |||  || || |||
                                 CCGCCGCC CCG  GC GC GCC
                                    G   CC  C  C
GAM2040  BMP2     5'  GGCGGTGGGGCTCGGAGA    49907      C      AC
                                 GGCGG GGGGCTCG  GA
                                 ||||| ||||||||  ||
                                 CCGCC CCCCGAGC  CT
                                   A       CT
GAM2040  BTG1     5'  GGCGCTGGGGCTCGGCGGCG   49908     GC      A  A
                                 GGCG  GGGGCTCG CG CG
                                 ||||  |||||||| || ||
                                 CCGC  CCCCGAGC GC GC
                                   GA       C  C
GAM2040  CACNA1A  5'  GGCGGCGGCGGCTCGGCGCCTC 49909        _    A  A__
             GG                    GGCGGCGG GGCTCG CG   CGG
                                   |||||||| |||||| ||   |||
                                   CCGCCGCC CCGAGC GC   GCC
                                      G     C  GGA
GAM2040  CACNA1A  5'  GGCGGCGGCGGCTCGGCGCCTC 49909        _    A  A__
             GG                    GGCGGCGG GGCTCG CG   CGG
                                   |||||||| |||||| ||   |||
                                   CCGCCGCC CCGAGC GC   GCC
                                      G     C  GGA
GAM2040  DNCI1    5'  AGGTGGCGGGGCCGGCGCGG   49910     C      T  A  A
                                 AGG GGCGGGGC CG CG CGG
                                 ||| |||||||| || || |||
                                 TCC CCGCCCCG GC GC GCC
                                   A       _  C  _
GAM2040  DNMT3B   5'  GGCGGCGGAGCCGCGG      49911          TCGA  A
                                 GGCGGCGGGGC    CG CGG
                                 ||||||||||||    || |||
                                 CCGCCGCCTCG    GC GCC
                                                ____  _
GAM2040  E2F1     5'  AGGCGGCGGCGGCGGCGCGG   49912         _  TCGA  A
                                 AGGCGGCGG GGC    CG CGG
                                 |||||||| |||    || |||
```

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                                TCCGCCGCC CCG    GC GCC
                                     G   CC__  _
GAM2040  FKBP1A   5'  GGCGGGCGGCGCGACGG     49913      _  G  TCGAC
                                GGCGG CGG GC     GACGG
                                ||||| ||| ||     |||||
                                CCGCC GCC CG     CTGCC
                                  C   G  _____
GAM2040  FKBP1A   5'  GGCGGGCGGCGCGACGG     49913      _  G  TCGAC
                                GGCGG CGG GC     GACGG
                                ||||| ||| ||     |||||
                                CCGCC GCC CG     CTGCC
                                  C   G  _____
GAM2040  FMR2     5'  AGGCGGCGGCGGCGGGCGG   49914         _  TCGACGA
                                AGGCGGCGG GGC      CGG
                                |||||||||  |||      |||
                                TCCGCCGCC CCG      GCC
                                     G   CCC_____
GAM2040  FOXD1    5'  GGTGGCGGGGCCCGGGCGG   49915    C         ACGA
                                GG GGCGGGGCTCG    CGG
                                ||  ||||||||||    |||
                                CC CCGCCCCGGGC    GCC
                                 A          CC__
GAM2040  FOXG1B   5'  GGCGGCGCGGCGACCGG     49916       G   TC   GA
                                GGCGGCG GGC  GAC  CGG
                                |||||||  |||  |||  |||
                                CCGCCGC CCG  CTG  GCC
                                   G   __   __
GAM2040  G6PT1    5'  GGCGGCGAAGAGGCGGCGG   49917         CTCGA  A
                                GGCGGCGGGGG     CG CGG
                                ||||||||||     ||  |||
                                CCGCCGCTTC     GC GCC
                                     TCC__  C
GAM2040  GAS1     5'  AGGCGCGGGGAGCGGCGGA   49918      G    CTCGA  A
                                AGGCG CGGGG     CG CGGA
                                |||||  |||||     ||  ||||
                                TCCGC GCCCC     GC GCCT
                                  _     TC___  C
GAM2040  GATA2    5'  GGCTGGCGGGGCTTACAGG   49919     _       CG   AC
                                GGC GGCGGGGCT  ACG  GG
                                |||  |||||||||  |||  ||
                                CCG CCGCCCCGA  TGT  CC
                                  A        A_   __
GAM2040  HCN2     3'  GGCAGCGGGAAGCCGGCGG   49920         CTCGA  A
                                GGCGGCGGGGG     CG CGG
                                ||||||||||     ||  |||
                                CCGTCGCCCT     GC GCC
                                     TCG__  C
GAM2040  HIC1     5'  AGGCGGCGGGGCCGGCG     49921           T  A
                                AGGCGGCGGGGC CG CG
                                ||||||||||||  ||  ||
```

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                                TCCGCCGCCCCG GC GC
                                      _ C
GAM2040 IL6R    5' AGGGGCGGGGCGGGGCGGTGG 49922    C      TCGA AC
                                AGG GGCGGGGC   CG GG
                                ||| ||||||||   || ||
                                TCC CCGCCCCG   GC CC
                                  _      CCCC CA
GAM2040 LAMA5   5' GCGGCGGGAGCCCGGCGG    49923       _    ACGA
                                GCGGCGGG GCTCG   CGG
                                |||||||| |||||   |||
                                CGCCGCCC CGGGC   GCC
                                     T    C___
GAM2040 MEN1    3' AGGCGGCAGGGGAGGCGG    49924         CTC CGA
                                AGGCGGCGGGG  GA  CGG
                                ||||||||||  ||  |||
                                TCCGCCGTCCC  CT  GCC
                                      ___ CC_
GAM2040 MYO6    5' GGCGGCGGGGCTACCTGTACGG 49925          CGACG_
                                GGCGGCGGGGCT    ACGG
                                ||||||||||||    ||||
                                CCGCCGCCCCGA    TGCC
                                      TGGACA
GAM2040 NFATC1  5' GGCGGCGGGGAGTGGAGCGGCG 49926         CTC_ _ A
          G                     GGCGGCGGGG   GA CG CGG
                                |||||||||   || || |||
                                CCGCCGCCCC   CT GC GCC
                                     TCAC  C  C
GAM2040 NR2F2   5' GGCGGCGGCGGCTCCCCGGG  49927       _    GA AC
                                GGCGGCGG GGCTC  CG  GG
                                |||||||| |||||  ||  ||
                                CCGCCGCC CCGAG  GC  CC
                                     G    GG ___
GAM2040 PDGFB   5' GGCGGCGGGCCCGGGCGGCGG 49928        G   A_ A
                                GGCGGCGGG CTCG  CG CGG
                                ||||||||| ||||  || |||
                                CCGCCGCCC GGGC  GC GCC
                                     _   CC  C
GAM2040 PRSS11  5' GGCGGCGGCGGCGGTGGCGGCG 49929       _  TCGA_ A
          GAC                   GGCGGCGG GGC    CG CGGAC
                                |||||||| |||    || |||||
                                CCGCCGCC CCG    GC GCCTG
                                     G  CCACC  C
GAM2040 PYGL    5' GGCGGCGGGCTGCGCGGCGG  49930       G _ A A
                                GGCGGCGGG CT CG CG CGG
                                ||||||||| || || || |||
                                CCGCCGCCC GA GC GC GCC
                                     _ C _ C
GAM2040 RAD52   3' GGCGGCGGCGAGGACGG    49931       GGCT  C
                                GGCGGCGG   CGA GACGG
                                ||||||||   ||| |||||
```

```
                                CCGCCGCC   GCT CTGCC
                                    ____  C
GAM2040  RET     5'  GCGGCGGACGCGACGGAC    49932       GCT  A
                                GCGGCGGG  CG CGACGGAC
                                ||||||||  || ||||||||
                                CGCCGCCT  GC GCTGCCTG
                                    ___ _
GAM2040  RET     5'  GCGGCGGACGCGACGGAC    49932       GCT  A
                                GCGGCGGG  CG CGACGGAC
                                ||||||||  || ||||||||
                                CGCCGCCT  GC GCTGCCTG
                                    ___ _
GAM2040  RET     5'  GCGGCGGACGCGACGGAC    49932       GCT  A
                                GCGGCGGG  CG CGACGGAC
                                ||||||||  || ||||||||
                                CGCCGCCT  GC GCTGCCTG
                                    ___ _
GAM2040  RET     5'  GCGGCGGACGCGACGGAC    49932       GCT  A
                                GCGGCGGG  CG CGACGGAC
                                ||||||||  || ||||||||
                                CGCCGCCT  GC GCTGCCTG
                                    ___ _
GAM2040  RXRA    5'  AGGCAGCGGGCGGCGG      49933        GCTCGA  A
                                AGGCGGCGGG    CG CGG
                                ||||||||||    || |||
                                TCCGTCGCCC    GC GCC
                                    _______ C
GAM2040  SFRP1   5'  AGGCGCGGGGCGGCGG      49934      G    TCGAC A
                                AGGCG CGGGGC    G CGG
                                |||||  ||||||    | |||
                                TCCGC GCCCCG    C GCC
                                  _    ______ C
GAM2040  SMARCA5  5'  GGTGGGCGGGGCCAGACGG   49935   C_      CGAC
                                GG  GGCGGGGCT   GACGG
                                ||  |||||||||   |||||
                                CC  CCGCCCCGG   CTGCC
                                 AC       T___
GAM2040  ST14    5'  AGGCGGCGGGATTCCGG     49936        GC  GACGA
                                AGGCGGCGGG  TC    CGG
                                ||||||||||  ||    |||
                                TCCGCCGCCC  AG    GCC
                                     TA  _____
GAM2040  TM4SF2   5'  GGCGGCGGCGGCAGGCGGCGG  49937       _  TCGA  A
                                GGCGGCGG GGC    CG CGG
                                ||||||||  |||   || |||
                                CCGCCGCC CCG    GC GCC
                                    G   TCC_  C
GAM2040  USF2    3'  GGCGGCGGCGGCTGCGTGGTGG 49938       _   _  ACGA_____
            TGGCGG                  GCGGCGG GGCT CG       CGG
                                ||||||| |||| ||       |||
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                                CGCCGCC CCGA GC        GCC
                                    G    C  ACCACCACC
GAM2040  VIM      5'  GGCGGCGGTGGCGCGGAC    49939         _   T  AC
                                GGCGGCGG GGC CG  GAC
                                |||||||| ||| ||  |||
                                CCGCCGCC CCG GC  CTG
                                    A   C  __
GAM2040  ZNF219   5'  GGCGGCGGCGGCGGCGGCGGCG 49906         _   T_  A  A
              G                  GGCGGCGG GGC  CG CG CGG
                                |||||||| |||  || || |||
                                CCGCCGCC CCG  GC GC GCC
                                    G   CC  C  C
GAM2040  ZNF219   5'  GGCGGCGGCGGCGGGCGGCGG  49940         _   TCGA  A
                                GGCGGCGG GGC    CG CGG
                                |||||||| |||    || |||
                                CCGCCGCC CCG    GC GCC
                                    G   CCC_  C
GAM2040  ZNF7     5'  GGTGGCTGGGCTCGACCAC    49941    C   G       G
                                GG GGC GGGCTCGAC AC
                                || ||| |||||||||  ||
                                CC CCG CCCGAGCTG TG
                                 A  A       G
GAM2040  C9orf10  5'  GGCGGCGGGGGGCGCGG      49942          CTCGA  A
                                GGCGGCGGGG     CG CGG
                                ||||||||||     || |||
                                CCGCCGCCCC     GC GCC
                                    C_____  _
GAM2040  CACNG4   3'  GGCAGCGGGAGGGGAGGTGGCG 49943          CTC  CGA__
              GA                  GGCGGCGGGG   GA    CGGA
                                ||||||||||   ||    ||||
                                CCGTCGCCCT   CT    GCCT
                                    CCC  CCACC
GAM2040  CAM-KIIN 5'  GGCGGCGGGCTTGCTGCCGGAC 49944         G  CGACGA
                                GGCGGCGGG CT     CGGAC
                                ||||||||| ||     |||||
                                CCGCCGCCC GA     GCCTG
                                    _  ACGACG
GAM2040  CENTG2   5'  AGGCGCGGGGCTGGCCCGCGG  49945      G     CGA_  A
                                AGGCG CGGGGCT    CG CGG
                                ||||| |||||||    || |||
                                TCCGC GCCCCGA    GC GCC
                                   _      CCGG  _
GAM2040  CPLX1    3'  AGGCGGCGGGCGCGG       49946          GCTCGA  A
                                AGGCGGCGGG     CG CGG
                                ||||||||||     || |||
                                TCCGCCGCCC     GC GCC
                                               _______  _
GAM2040  DKFZp434N035 3'  AGGGGCGGGGCTCGTAAGGAC  49947     C         ACGAC
                                AGG GGCGGGGCTCG    GGAC
                                ||| ||||||||||     ||||
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                                TCC CCGCCCCGAGC    CCTG
                                  _        ATT__
GAM2040  DNAL4    3'  GGCAGTGGGGCTCCCAGGA   49948      C     GA  AC
                                GGCGG GGGGCTC  CG  GGA
                                ||||| |||||||  ||  |||
                                CCGTC CCCCGAG  GT  CCT
                                   A      G_  __
GAM2040  DSCR6    5'  GGGGCGGGGCGGCGCGG    49949    C      TCGA  A
                                GG GGCGGGGC   CG CGG
                                || ||||||||   || |||
                                CC CCGCCCCG   GC GCC
                                 _      CC__  _
GAM2040  DXS9928E 5'  GGCGGCGGCGGCGGCGGCGGCG 49906        _  T_  A  A
              G                  GGCGGCGG GGC  CG CG CGG
                                 |||||||| |||  || || |||
                                 CCGCCGCC CCG  GC GC GCC
                                     G   CC  C  C
GAM2040  E        5'  GGGTGCCGGGGCTCATCGCCGG 49950    CG  _      A  A
                                 GG  GC GGGGCTCG CG CGG
                                 ||  || |||||||| || |||
                                 CC  CG CCCCGAGT GC GCC
                                  CA  G       A  G
GAM2040  EPB41L1  5'  GGCGGCGCGGGGTCGCGGCGG  49951        _  C   A  A
                                 GGCGGCG GGG TCG CG CGG
                                 ||||||| ||| ||| || |||
                                 CCGCCGC CCC AGC GC GCC
                                     G   C   _  C
GAM2040  FLJ13110 5'  GGCGGCGCGGCTCGGCTAGG   49952        G     ACGAC
                                 GGCGGCG GGCTCG    GG
                                 ||||||| ||||||    ||
                                 CCGCCGC CCGAGC    CC
                                     G     CGAT_
GAM2040  GDAP2    5'  GGCGGCGGGCGGCACGGA    49953         GCT  A G
                                 GGCGGCGGG   CG C ACGGA
                                 |||||||||   || | |||||
                                 CCGCCGCCC   GC G TGCCT
                                       ___  C _
GAM2040  KIAA0193 5'  GGCGGCGGGCTCCGG       49954         G   GACGA
                                 GGCGGCGGG CTC    CGG
                                 ||||||||| |||    |||
                                 CCGCCGCCC GAG    GCC
                                       _  _____
GAM2040  KIAA0633 5'  AGCGGCGGAGCGCGGCGGA   49955          T  ACGA
                                 GGCGGCGGGGC CG   CGGA
                                 |||||||||||| ||   ||||
                                 TCGCCGCCTCG GC   GCCT
                                       C  C___
GAM2040  KIAA0649 5'  AGGCGGCGGGCCGGGGGCGG  49956          G T  ACGA
                                 AGGCGGCGGG C CG   CGG
                                 |||||||||| | ||   |||
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                                TCCGCCGCCC G GC   GCC
                                     _ _  CCCC
GAM2040 KIAA0963 5' AGGCGGCGGGACTCCAGGAC  49957          GAC
                                AGGCGGCGGGGCTC  GAC
                                |||||||||||||  |||
                                TCCGCCGCCCTGAG  CTG
                                    GTC
GAM2040 KIAA1511 5' AGGCGGCGGCGGCTGCTCGG  49958       _  CGACGA
                                AGGCGGCGG GGCT    CGG
                                ||||||||| ||||    |||
                                TCCGCCGCC CCGA    GCC
                                    G   CGA___
GAM2040 KIAA1912 5' GGCGGCGGGGGTCGCGCTGG  49959       C  A  AC
                                GGCGGCGGGG TCG CG  GG
                                |||||||||| ||| ||  ||
                                CCGCCGCCCC AGC GC  CC
                                     C  _ GA
GAM2040 KIAA1924 3' GGCGCTGGGGCTCGCGGGGG  49960    GC     A  AC
                                GGCG  GGGGCTCG CG  GG
                                ||||  |||||||| ||  ||
                                CCGC  CCCCGAGC GC  CC
                                  GA      _ CC
GAM2040 KIAA1940 5' GGCGGCGGGCTCGGGA     49961       G   ACGAC
                                GGCGGCGGG CTCG    GGA
                                ||||||||| ||||    |||
                                CCGCCGCCC GAGC    CCT
                                     _   _____
GAM2040 MAPKAPK2 5' GGTCGCGGGGCTCCGTGG    49962   CG      GA  AC
                                GG  GCGGGGCTC  CG  GG
                                ||  |||||||||  ||  ||
                                CC  CGCCCCGAG  GC  CC
                                 AG       __  A_
GAM2040 MAPKAPK2 5' GGTCGCGGGGCTCCGTGG    49962   CG      GA  AC
                                GG  GCGGGGCTC  CG  GG
                                ||  |||||||||  ||  ||
                                CC  CGCCCCGAG  GC  CC
                                 AG       __  A_
GAM2040 MGC10485 5' GGCAGTGGGCGCCGACGGAC  49963    CG   TCGA
                                GGCGG  GGGC   CGACGGAC
                                |||||  ||||   ||||||||
                                CCGTC  CCCG   GCTGCCTG
                                  A_   CG__
GAM2040 MGC10772 5' GGCGGCGGCACGGGCGGCGG  49964       G  TCGA  A
                                GGCGGCGG GC   CG CGG
                                |||||||| ||   || |||
                                CCGCCGCC TG   GC GCC
                                    G  CCC_  C
GAM2040 MGC9564  5' GGCGGCGGGGCGCGCGAGCGA 49965        T  A  _
                                GGCGGCGGGGC CG CGA CGG
                                |||||||||| || ||| |||
```

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                                CCGCCGCCCCG GC GCT GCT
                                      C _  C
GAM2040 MSRA    5' GGCGGCAGGGGCGCGGGCGG  49966      _    T  ACGA
                                GGCGGC GGGGC CG    CGG
                                |||||| ||||| ||    |||
                                CCGCCG CCCCG GC    GCC
                                   T    C  CC__
GAM2040 PCDH17  5' AGGCAGCGGCGGCGGCGGA   49967        _  TCGAC A
                                AGGCGGCGG GGC    G CGGA
                                ||||||||| |||    | ||||
                                TCCGTCGCC CCG    C GCCT
                                     G  _____ C
GAM2040 PEG10   3' AGGCGGCGGCTGTGGCGGCGG 49968      GG   CGA_  A
                                AGGCGGC  GGCT   CG CGG
                                |||||||  ||||   || |||
                                TCCGCCG  CCGA   GC GCC
                                   __   CACC  C
GAM2040 PIGQ    5' GGCGGCGGGGTCCGG      49969         C  GACGA
                                GGCGGCGGGG TC    CGG
                                |||||||||| ||    |||
                                CCGCCGCCCC AG    GCC
                                      _ _____
GAM2040 PODLX2  3' AGGCGCGGGGCTGGTGCGG   49970     G     CGACGA
                                AGGCG CGGGGCT     CGG
                                ||||| |||||||     |||
                                TCCGC GCCCCGA     GCC
                                  _      CCAC__
GAM2040 PRKWNK2 5' GGCGGCGGGGCGTCCGCGG   49971         TCGA  A
                                GGCGGCGGGGC   CG CGG
                                ||||||||||   || |||
                                CCGCCGCCCCG   GC GCC
                                      CAG_  _
GAM2040 Rab11-FIP3 5' GGCGGCGAGGATCCGGGCGGCG 49972        C_  A_  A
          GA                    GGCGGCGGGG  TCG  CG CGGA
                                |||||||||  |||  || ||||
                                CCGCCGCTCC  GGC  GC GCCT
                                      TA   CC  C
GAM2040 RBPMS   5' GGCGCCGGGGCTCCCTCGG   49973     G      GACGA
                                GGCG CGGGGCTC    CGG
                                |||| ||||||||    |||
                                CCGC GCCCCGAG    GCC
                                  G       GGA__
GAM2040 SBBI26  5' AGGCGGCGGTGGCTCGGCCA  49974        _    A_
                                AGGCGGCGG GGCTCG  CG
                                ||||||||| ||||||  ||
                                TCCGCCGCC CCGAGC  GT
                                     A     CG
GAM2040 SLC16A10 5' GGCGGCGGAGCCCCTGGCGG  49975          GACGA
                                GGCGGCGGGGCTC    CGG
                                ||||||||||||    |||
```

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                                CCGCCGCCTCGGG    GCC
                                      GACC_
GAM2040  SMURF2    5'  GGCGGCGGGGGCGGCGG    49976         CTCGA  A
                                GGCGGCGGGG    CG CGG
                                ||||||||||    || |||
                                CCGCCGCCCC    GC GCC
                                      C____  C
GAM2040  TGFB1I1   3'  AGGGGCGGGGCTCTCCAGTGG  49977    C       GA  AC
                                AGG GGCGGGGCTC  CG  GG
                                ||| ||||||||||  ||  ||
                                TCC CCGCCCCGAG  GT  CC
                                  _       AG  CA
GAM2040  LOC116113 3'  GGCGGCGGGGGGGAGAGGCGG   49978         CTC  CGA
                                GGCGGCGGGG   GA   CGG
                                ||||||||||   ||   |||
                                CCGCCGCCCC   CT   GCC
                                      CCT  CC_
GAM2040  LOC124987 5'  GGCGGTGGGGCCAATGGGG    49979      C    T   CGAC
                                GGCGG GGGGC CGA    GG
                                ||||| ||||| |||    ||
                                CCGCC CCCCG GTT    CC
                                   A    _  ACC_
GAM2040  LOC127703 5'  GGGTGCGGGGCTCCCGGG    49980    CG       GA  AC
                                GG  GCGGGGCTC  CG  GG
                                ||  |||||||||  ||  ||
                                CC  CGCCCCGAG  GC  CC
                                 CA       G_  __
GAM2040  LOC138835 5'  AGGCGGCGGGCTCTCCGGG    49981          G   GA  AC
                                AGGCGGCGGG CTC  CG  GG
                                |||||||||| |||  ||  ||
                                TCCGCCGCCC GAG  GC  CC
                                      _   AG  __
GAM2040  LOC144596 3'  GGCGGCGGCGGCTGCGTGGTGG 49938        _   _  ACGA_____
            TGGCGG                  GCGGCGG GGCT CG       CGG
                                |||||||  |||| ||       |||
                                CGCCGCC CCGA GC       GCC
                                    G   C  ACCACCACC
GAM2040  LOC148530 5'  AGGCGGCGGGTCAGCGGCGG   49982         GC   A  A
                                AGGCGGCGGG  TCG CG CGG
                                |||||||||  ||| || |||
                                TCCGCCGCCC  AGT GC GCC
                                      __   C  C
GAM2040  LOC149414 5'  AGGCGCGGGGCTGCCGG     49983      G      CGACGA
                                AGGCG CGGGGCT     CGG
                                ||||| |||||||     |||
                                TCCGC GCCCCGA     GCC
                                   _      CG_____
GAM2040  LOC197342 5'  GGCGCTGGGGCTCGATGCGG   49984      GC       CGA
                                GGCG  GGGGCTCGA   CGG
                                ||||  |||||||||   |||
```

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                                CCGC  CCCCGAGCT   GCC
                                  GA        AC_
GAM2040  LOC200325 5'  GGCAGCGGATGCAGCGGTGG   49985         _  TCGA  AC
                                GGCGGCGGG GC    CG  GG
                                ||||||||| ||    ||  ||
                                CCGTCGCCT CG    GC  CC
                                     A  TC__  CA
GAM2040  LOC201549 5'  GGCGGCTGGGCTCGCGGA    49986       G      ACGA
                                GGCGGC GGGCTCG    CGGA
                                |||||| |||||||    ||||
                                CCGCCG CCCGAGC    GCCT
                                   A      _____
GAM2040  LOC201915 5'  GGCGGCGGGGCGCGCGGG    49987          T  A  AC
                                GGCGGCGGGGC CG CG  GG
                                |||||||||| || ||  ||
                                CCGCCGCCCCG GC GC  CC
                                      C  _  __
GAM2040  LOC221424 5'  AGGTTGGTGGGGCCGCGGG    49989     C_  C     T  A  AC
                                AGG  GG GGGGC CG CG  GG
                                |||  || ||||| || ||  ||
                                TCC  CC CCCCG GC GC  CC
                                  AA  A    _  _  __
GAM2040  LOC221424 5'  AGGCGGCAGGGCTGAGTGG    49988           C  CGAC
                                AGGCGGCGGGGCT GA    GG
                                |||||||||||| ||    ||
                                TCCGCCGTCCCGA CT    CC
                                       _  CA__
GAM2040  LOC253219 5'  AGCTGGCGGGGCGCACGG    49990     _       T GACG
                                GGC GGCGGGGC C    ACGG
                                ||| |||||||| |    ||||
                                TCG CCGCCCCG G    TGCC
                                  A       C _____
GAM2040  LOC254901 5'  AGCGGCGGAGGCGGCGG     49991         _  TCGAC A
                                GGCGGCGG GGC     G CGG
                                |||||||| |||     | |||
                                TCGCCGCC CCG     C GCC
                                     T   ______ C
GAM2040  LOC255057 5'  GGCGGCGGGCTGGCGGCGG    49992         G  CGA  A
                                GGCGGCGGG CT   CG CGG
                                ||||||||| ||   || |||
                                CCGCCGCCC GA   GC GCC
                                      _  CC_  C
GAM2040  LOC256639 5'  GGCCGGCGGGGCTGTGCCGG   49993     _       CGACGA
                                GGC GGCGGGGCT      CGG
                                ||| |||||||||      |||
                                CCG CCGCCCCGA      GCC
                                  G        CACG__
GAM2040  LOC257478 3'  GGTGGCCGGGGGGCGGCGGAC  49994     C  _   CTCGA  A
                                GG GGC GGGG     CG CGGAC
                                || ||| ||||     || |||||
```

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                                CC CCG CCCC    GC GCCTG
                                 A  G   CC___  C
GAM2040 LOC51205 5' GGCGCCGGGGCTCAGCGG   49995     G       ACGA
                                GGCG CGGGGCTCG   CGG
                                |||| |||||||||   |||
                                CCGC GCCCCGAGT   GCC
                                  G       C___
GAM2041 CRHR1    3' TAGTGCTGTGGCCGCAAG   49998    _   CA
                                TGG GTTG  GCCGCAAG
                                ||| ||||  ||||||||
                                ATC CGAC  CGGCGTTC
                                 A   AC
GAM2041 TBL1X    3' GCTTGCGGCCGCAGGC     49999    G  _      CC
                                GC TTG GGTTGCAG  GC
                                || ||| ||||||||  ||
                                CG AAC CCGGCGTC  CG
                                 _  G      __
GAM2041 FLJ22028 3' GTTGGGCTGCATTCAAAGC   50000          GC  C
                                GTTGGGTTGCA  CG AAGC
                                ||||||||||  || ||||
                                CAACCCGACGT  GT TTCG
                                      AA  _
GAM2041 FLJ25132 5' TTGGTGCGAGCAGCCGCGGGC 50001     _ T_      AA
                                TTGG GT  GCAGCCGC  GC
                                |||| ||  ||||||||  ||
                                AACC CG  CGTCGGCG  CG
                                  A  CT       CC
GAM2041 GS3955   5' GCGAGTGCGGCTGCAGGC    50002    T_ _      CC
                                GCG  TG GGTTGCAG  GC
                                |||  || ||||||||  ||
                                CGC  AC CCGACGTC  CG
                                 TC  G      __
GAM2041 MGC1842  3' TTGGGTGGGCAGCTGCAG    50003       T_    C   A
                                TTGGGT  GCAGC GCA G
                                ||||||  ||||| ||| |
                                AACCCA  CGTCG CGT C
                                   CC    A   C
GAM2041 LOC149579 5' TCGCGCTGGGCGTGCTCGTGGG 50004          _  AGCC__
            C                    TCGCGTTGGGT TGC     GC
                                ||||||||||| |||     ||
                                AGCGCGACCCG ACG     CG
                                      C   AGCACC
GAM2041 LOC158572 3' GCAGTTCCTCTGGTTGCAGGC  50005   _  G____      CC
                                GC GTT    GGTTGCAG  GC
                                || |||    ||||||||  ||
                                CG CAA    CCAACGTC  CG
                                 T  GGAGA      __
GAM2041 LOC159199 3' GTTGGCTGTGGCTGCAAGC   50006      G   CA  C
                                GTTGG TTG  GC GCAAGC
                                ||||| |||  || ||||||
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                                CAACC GAC  CG CGTTCG
                                  _  AC  A
GAM2041  LOC219730 5'  TCGCGCTGCCTGGCCGGCCGCA 50007        ___     CA
                                TCGCGTTG  GGTTG  GCCGCA
                                ||||||||  |||||  ||||||
                                AGCGCGAC  CCGGC  CGGCGT
                                    GGA   __
GAM2041  LOC221312 5'  GCGAAGTTGCAGCTGC     50008     TT        C
                                GCG  GGGTTGCAGC GC
                                |||  ||||||||| ||
                                CGC  TTCAACGTCG CG
                                  __        A
GAM2042  ABCD1    5'  TCTCGGGCAGAGGGGGCG    50011    GC         AA
                                TC  CGGGCGGGGGGG  GCG
                                ||  |||||||||||  |||
                                AG  GCCCGTCTCCCC  CGC
                                 A_         __
GAM2042  AQP5     5'  GCCGGCGGGGGGCGCC      50012      G     GGAA
                                GCCGG CGGGGG   GCGCC
                                ||||| ||||||   |||||
                                CGGCC GCCCCC   CGCGG
                                  _    _____
GAM2042  CACNG1   5'  TCGCCGAGGCGTGGGTGCC   50013       _   GG   GAAGC
                                TCGCCG GGCG  GGG    GCC
                                |||||| ||||  |||    |||
                                AGCGGC CCGC  CCC    CGG
                                   T   A_   A_____
GAM2042  DLX4     3'  TCGCTGGGTGGGTGGGAGC   50014     C   C   G   A
                                TCGC GGG GGG GGGA GC
                                |||| ||| ||| |||| ||
                                AGCG CCC CCC CCCT CG
                                  A   A   A   _
GAM2042  DLX4     3'  TCGCTGGGTGGGTGGGAGC   50014     C   C   G   A
                                TCGC GGG GGG GGGA GC
                                |||| ||| ||| |||| ||
                                AGCG CCC CCC CCCT CG
                                  A   A   A   _
GAM2042  FUS1     3'  GCCGGGGCAGGGGGTGC     50015       _     GAA
                                GCCGGG CGGGGGG   GC
                                ||||||| |||||||   ||
                                CGGCCC GTCCCCC   CG
                                   C      A__
GAM2042  G6PT1    5'  TCGTGGGCGGGAAGGTGCC   50016     CC         AAGC
                                TCG  GGGCGGGGGGG   GCC
                                |||  ||||||||||   |||
                                AGC  CCCGCCCTTCC   CGG
                                  A_         A___
GAM2042  HOXB9    5'  GCAGGGGGAAGGGAAGCGC   50017    C   C
                                GC GGG GGGGGGGAAGCGC
                                || ||| ||||||||||||
```

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                                CG CCC CCTTCCCTTCGCG
                                 T  _
GAM2042 LMO2     5' GCCGGGCGGCGGGGGCGC    50018        G   AA
                                GCCGGGCGG GGGG  GCGC
                                ||||||||| ||||  ||||
                                CGGCCCGCC CCCC  CGCG
                                   G   __
GAM2042 MTCP1    5' CGCCGGTACTCGGGAGGCGCC 50019      _ GG    AA
                                CGCCGG GC  GGGGG  GCGCC
                                |||||| ||  |||||  |||||
                                GCGGCC TG  CCCTC  CGCGG
                                  A  AG    __
GAM2042 NGB      3' GCCGGGCGGGGTCGCCTGGGCG 50020        __________  AAGCG
             CTTCC                GGGCGGGG       GGG    CC
                                |||||||        |||    ||
                                CCCGCCCC       CCC    GG
                                   AGCGGAIII   GCGAA
GAM2042 SERPIND1 3' TCACCGGAGCGGGAGGTGC   50021       _      GAA
                                TCGCCGG GCGGGGGGG   GC
                                ||||||| ||||||||   ||
                                AGTGGCC CGCCCTCC   CG
                                   T       A__
GAM2042 SORBS1   5' TCGCCGGGCGGGCGGGCTGCGC 50022          G   AA
                                TCGCCGGGCGGG GGG  GCGC
                                |||||||||||| |||  ||||
                                AGCGGCCCGCCC CCC  CGCG
                                    G   GA
GAM2042 ZRF1     5' TCCCGGGCGGAGGGCGC     50023    G       GGAA
                                TC CCGGGCGGGGG    GCGC
                                || ||||||||||    ||||
                                AG GGCCCGCCTCC    CGCG
                                 _        _____
GAM2042 ARHGEF4  3' GCTGGGCAGGGCTGGGTGC   50024    C      __   AA
                                GC GGGCGGGG  GGG  GC
                                || ||||||||  |||  ||
                                CG CCCGTCCC  CCC  CG
                                 A       GA   A_
GAM2042 BPES     3' CCGCCGGGGCCGGAGGTGCCC  50025       _ G    GAAGC
                                TCGCCGGG C GGGGG    GCCC
                                |||||||| | |||||    ||||
                                GGCGGCCC G CCTCC    CGGG
                                   C G    A_____
GAM2042 CARD11   3' TCACCGGGTGGGGCGGAGCG   50026       C   G   A
                                TCGCCGGG GGGG GGA GCG
                                |||||||| |||| ||| |||
                                AGTGGCCC CCCC CCT CGC
                                   A   G   _
GAM2042 CDK5R1   5' CGCCGGGCGGGGGCTCGCCC   50027          GGAAG
                                CGCCGGGCGGGGG    CGCCC
                                ||||||||||||    |||||
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                                GCGGCCCGCCCCC    GCGGG
                                       GA___
GAM2042  DKFZP586M1120 5'  GCTGGGGAACCAAGCGCCC   50028    G    __
                                GC GGGGGG  AAGCGCCC
                                || ||||||  ||||||||
                                CG CCCCTT  TTCGCGGG
                                 A     GG
GAM2042  DPP9     3'  CGCTGGGCGGGACAAAGTGCC  50029    C      G G  C
                                CGC GGGCGGGG G AAG GCC
                                ||| |||||||| | ||| |||
                                GCG CCCGCCCT T TTC CGG
                                  A       G _  A
GAM2042  EDR2     3'  CAGTCGGGAGGAGGCGCC    50030    G      AA
                                CGG CGGGGGGG  GCGCC
                                ||| ||||||||  |||||
                                GTC GCCCTCCT  CGCGG
                                  A       C_
GAM2042  FLJ11193  5'  TCTCCGGGCGGAAGCGC    50031    G    GGGGG
                                TC CCGGGC    GGAAGCGC
                                || ||||||    ||||||||
                                AG GGCCCG    CCTTCGCG
                                 A    ______
GAM2042  FLJ13262  5'  TCGCGGGCGGGGGGACCCCGGCG 50032     C       GAA__
            CCC                    TCGC GGGCGGGGGG    GCGCCC
                                |||| ||||||||||    ||||||
                                AGCG CCCGCCCCCT    CGCGGG
                                  _        GGGGC
GAM2042  IGF2AS   5'  CCGCCGGGCGGTAAAGTGCC   50033          GGGG   C
                                TCGCCGGGCGGG   GAAG GCC
                                ||||||||||    |||| |||
                                GGCGGCCCGCC    TTTC CGG
                                       A___    A
GAM2042  KIAA0211  5'  TCTCCGTACGGGGGAGCG    50034    G  GG    GGA
                                TC CCG  CGGGGG   AGCG
                                || |||  ||||||   ||||
                                AG GGC  GCCCCC   TCGC
                                 A  AT     ___
GAM2042  KIAA1095  5'  CCGCCGGGCGGCCGGGCGCCC  50035          GG  GAA
                                TCGCCGGGCGG  GG   GCGCCC
                                ||||||||||  ||   ||||||
                                GGCGGCCCGCC  CC   CGCGGG
                                       GG  ___
GAM2042  KIAA1509  3'  CCTGGGGTAAAGGGAAGTGC   50036   _  CG       C
                                CC GGG  GGGGGGAAG GC
                                || |||  |||||||| ||
                                GG CCC  TTTCCCTTC CG
                                 A  CA       A
GAM2042  PRSS21   5'  CGCCGGGCCCGGGGCGCC    50037        GG   GGAA
                                CGCCGGGC  GGG   GCGCC
                                ||||||||  |||   |||||
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                                GCGGCCCG  CCC   CGCGG
                                    GG  ____
GAM2042  PRSS21   5'  CGCCGGGCCCGGGGCGCC   50037       GG  GGAA
                                CGCCGGGC  GGG   GCGCC
                                ||||||||  |||   |||||
                                GCGGCCCG  CCC   CGCGG
                                    GG  ____
GAM2042  SAST     5'  TCGTAGGAGGAGGGGGAGCGCC 50038    CC  C     A
           C                     TCG  GGG GGGGGGG AGCGCCC
                                |||  ||| ||||||| |||||||
                                AGC  TCC CCTCCCC TCGCGGG
                                 A_  T     C
GAM2042  SEMA5A   5'  CCTGGGTGGGAGAAGGGAGCGT 50039   _  C  ___   A  _
           CC                    CC GGG GGG   GGGGA GCG CC
                                || ||| |||   ||||| ||| ||
                                GG CCC CCC   TCCCT CGC GG
                                 A  A  TCT    _  A
GAM2042  SLC21A11  5'  GCCGGGCGGGGGGTGCGCGCC  50040         GGAA
                                GCCGGGCGGGGGG   GCGCC
                                ||||||||||||   |||||
                                CGGCCCGCCCCC   CGCGG
                                      ACG_
GAM2042  SNFT     3'  GCTGGGCAGAGGAGTGTCC   50041   C       AAGCG
                                GC GGGCGGGGGGG    CC
                                || ||||||||||    ||
                                CG CCCGTCTCCTC    GG
                                 A        ACA__
GAM2042  VI       5'  TCTCCGGCGGGGAGCGCC    50042   G   G   GGGA
                                TC CCGG CGGGG   AGCGCC
                                || |||| |||||   ||||||
                                AG GGCC GCCCC   TCGCGG
                                 A  _   ____
GAM2042  VIAAT    3'  TCTCCGGAATGGGAAGCGC   50043   G   CGGGG
                                TC CCGGG    GGGAAGCGC
                                || |||||    |||||||||
                                AG GGCCT    CCCTTCGCG
                                 A   TA___
GAM2042  LOC116411 5'  GCCGGGCGGGGGGGCTGACCC  50044         GAAGC
                                GCCGGGCGGGGGG    GCCC
                                ||||||||||||    ||||
                                CGGCCCGCCCCCC    TGGG
                                      GAC__
GAM2042  LOC153572 3'  GCTGGCGGGGGGGCGGCGCCC 50045   CG      GAA_
                                GC  GGCGGGGGG   GCGCCC
                                ||  |||||||||   ||||||
                                CG  CCGCCCCCC   CGCGGG
                                 A_       GCCG
GAM2042  LOC157753 5'  CCGCCGGGTGGGCAGCGCC   50046       C  GGGGA
                                TCGCCGGG GGG    AGCGCC
                                |||||||| |||    ||||||
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                                GGCGGCCC CCC    TCGCGG
                                    A  G____
GAM2042  LOC222128 5'  TCCCGGGCGGGGGAGGCC    50047    G          AAGC
                                TC CCGGGCGGGGGGG   GCC
                                || ||||||||||||   |||
                                AG GGCCCGCCCCCTC   CGG
                                 _         _____
GAM2042  LOC257408 5'  GCTGGGCGCCGGGGAAGCGC  50048    C    GG
                                GC GGGCG  GGGGAAGCGC
                                || |||||  ||||||||||
                                CG CCCGC  CCCCTTCGCG
                                 A    GG
GAM2042  LOC59346  5'  CGCCGCGGGGAGGTGCC     50049     GG       AAGC
                                CGCC  GCGGGGGGG   GCC
                                ||||  |||||||||   |||
                                GCGG  CGCCCCTCC   CGG
                                  __       A___
GAM2043  AKT1     3'  AGAACTGTGACACAG       50052       AACTT
                                AGAACT    GTGACACAG
                                ||||||    |||||||||
                                TCTTGA    CACTGTGTC
                                   ______
GAM2043  ARHGDIA  3'  ATAGAACCTGGGGGGCACAGAA 50053        AACTTGTGA
                                ATAGAACT       CACAGAA
                                ||||||||       |||||||
                                TATCTTGG       GTGTCTT
                                    ACCCCCC__
GAM2043  MUC4     3'  CAGGACTGGTTCTGACACAG  50054    A  AAC  G
                                TAG ACT   TT TGACACAG
                                ||| |||   || ||||||||
                                GTC TGA   AA ACTGTGTC
                                  C  CC_  G
GAM2043  PAK4     3'  TAAAACTAACTCGAGGCAG   50055          TGACA
                                TAGAACTAACTTG    CAG
                                ||||||||||||    |||
                                ATTTTGATTGAGC    GTC
                                       TCC__
GAM2043  PLA2G4C  3'  ACAGAGCTAACTTGTGCAGA  50056     A       ACA
                                ATAGA CTAACTTGTG  CAGA
                                ||||| ||||||||||  ||||
                                TGTCT GATTGAACAC  GTCT
                                   C       ___
GAM2043  VAPB     3'  ACAGAACTGAAGACACGGA   50057       AACTTGT    A
                                ATAGAACT      GACAC GA
                                ||||||||      ||||| ||
                                TGTCTTGA      CTGTG CT
                                    CTT____    C
GAM2043  EIF4B    3'  TAAAACTAGGACACAGA     50058        ACTTGT
                                TAGAACTA     GACACAGA
                                ||||||||     ||||||||
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                                ATTTTGAT     CTGTGTCT
                                     C_____
GAM2043  FAM8A1   3'  AGAATTATACTTTGACACAGAA 50059     C _   G
                                AGAA TA ACTT TGACACAGAA
                                |||| || |||| ||||||||||
                                TCTT AT TGAA ACTGTGTCTT
                                  A  A   _
GAM2043  FLJ23560 3'  ACAGAGCTGAGACACAGA    50060      ACTAAC   T
                                ATAGA     TTG GACACAGA
                                ||||||     ||| ||||||||
                                TGTCT     GAC CTGTGTCT
                                   C_____   T
GAM2043  HSPC129  5'  TAAAACTAACTGTGACGACAGA 50061          T    _
                                TAGAACTAACT GTGAC ACAGA
                                |||||||||||| ||||| |||||
                                ATTTTGATTGA CACTG TGTCT
                                       _    C
GAM2043  KIAA0514  3'  AGAATCTGCATGTGACACAGAA 50062     _ AACT
                                AGAA CT    TGTGACACAGAA
                                |||| ||    ||||||||||||
                                TCTT GA    ACACTGTGTCTT
                                  A  CGT_
GAM2043  PDK2     3'  ATAAAACTAACTATATACACAG 50063          TGTG
              AA                  ATAGAACTAACT    ACACAGAA
                                |||||||||||    ||||||||
                                TATTTTGATTGA    TGTGTCTT
                                       TATA
GAM2043  SEMA3C   3'  ATAGATTGGCCATAAACACAGA 50064      ACTAA  TGT
              A                   ATAGA    CT   GACACAGAA
                                |||||    ||   |||||||||
                                TATCT    GG   TTGTGTCTT
                                   AACC_  TAT
GAM2043  WFDC3    3'  CAGGACTGGTGGGACACAGAA  50065     A   AACT  T
                                TAG ACT    TG GACACAGAA
                                ||| |||    || |||||||||
                                GTC TGA    AC CTGTGTCTT
                                  C   CC__  C
GAM2043  LOC139673 3'  TAAAACTAGGACACAGA     50058        ACTTGT
                                TAGAACTA     GACACAGA
                                ||||||||     ||||||||
                                ATTTTGAT     CTGTGTCT
                                     C_____
GAM2043  LOC145463 3'  ATAGAGCTAACTCAGTAACA   50066      A     _
                                ATAGA CTAACTT GTGACA
                                ||||| ||||||| ||||||
                                TATCT GATTGAG CATTGT
                                   C      T
GAM2043  LOC148343 5'  CCAATTTGTGACATAGAA    50067      C       C
                                CTAA TTGTGACA AGAA
                                |||| |||||||| ||||
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                                GGTT AACACTGT TCTT
                                  A       A
GAM2043  LOC204804 3'  TAGAACCAGCACACGGA     50068        ACTT  G    A
                                TAGAACTA    GT ACAC GA
                                ||||||||    || |||| ||
                                ATCTTGGT    CG TGTG CT
                                    ____ _    C
GAM2043  LOC256594 5'  TAGAATGTGACACAG       50069       CTAACT
                                TAGAA     TGTGACACAG
                                |||||     ||||||||||
                                ATCTT     ACACTGTGTC
                                  _______
GAM2043  LOC51014  3'  ATAAAACTGAACAGTGCAGAA  50070        _   TT   ACA
                                ATAGAACT AAC  GTG   CAGAA
                                |||||||| |||  |||   |||||
                                TATTTTGA TTG  CAC   GTCTT
                                    C   T_   ___
GAM2043  LOC51691  3'  AAACTAACTTTAACATTAGAA  50071          G    C_
                                GAACTAACTT TGACA  AGAA
                                |||||||||| |||||  ||||
                                TTTGATTGAA ATTGT  TCTT
                                     _    AA
GAM2043  LOC90750  3'  TAGACTAACTCACAG       50072      A     TGTGA
                                TAGA CTAACT    CACAG
                                |||| ||||||    |||||
                                ATCT GATTGA    GTGTC
                                  _    ______
GAM2044  HTR6      5'  GGTGGACGGCAAGGGAGTG   50075    CA       TTCCT
                                GG  GACGGCAAG    GGTG
                                ||  |||||||||    ||||
                                CC  CTGCCGTTC    TCAC
                                 AC       CC___
GAM2044  NRD1      5'  CGGTGGCGGCCGGCCCTGGTG  50076     CAGA   AA  T
                                CGG   CGGC  GT CCTGGTG
                                |||   ||||  || |||||||
                                GCC   GCCG  CG GGACCAC
                                  ACC_   GC  _
GAM2044  PACSIN1   3'  CGGCAGACGGCGGGCGGT    50077          AA  TCCT
                                CGGCAGACGGC  GT   GGT
                                ||||||||||  ||   |||
                                GCCGTCTGCCG  CG   CCA
                                     CC  ____
GAM2044  PML       3'  ACGGCAGGGCGCTCCTGGT   50078       AC   AA
                                ACGGCAG  GGC  GTTCCTGGT
                                |||||||  |||  |||||||||
                                TGCCGTC  CCG  CGAGGACCA
                                  __   __
GAM2044  PML       3'  ACGGCAGGGCGCTCCTGGT   50078       AC   AA
                                ACGGCAG  GGC  GTTCCTGGT
                                |||||||  |||  |||||||||
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                                TGCCGTC  CCG  CGAGGACCA
                                   __  __
GAM2044  SIRPB2   3'  CGATGGATGGGAGTCCTGGTG  50079    CA  C  CA   T
                                CGG  GA GG  AGT CCTGGTG
                                |||  || ||  ||| |||||||
                                GCT  CT CC  TCA GGACCAC
                                  AC  A  C_  _
GAM2044  SIRPB2   3'  CGATGGATGGGAGTCCTGGTG  50079    CA  C  CA   T
                                CGG  GA GG  AGT CCTGGTG
                                |||  || ||  ||| |||||||
                                GCT  CT CC  TCA GGACCAC
                                  AC  A  C_  _
GAM2044  SPAG8    5'  CGGTGGAGGCAAGTCCTCTG   50080    CA  C       _
                                CGG  GA GGCAAGTTC CTG
                                |||  || |||||||||| |||
                                GCC  CT CCGTTCAGG GAC
                                  AC  _       A
GAM2044  ANKRD5   3'  GGTAACAAGTTCTTGGT    50081    CAGAC       C
                                GG    GGCAAGTTC TGGT
                                ||    |||||||||| ||||
                                CC    TTGTTCAAG ACCA
                                 A____       A
GAM2044  FLJ10520 5'  GGTAGCTGGCAAGTCAGGC   50082    C  AC      CCT
                                GG AG  GGCAAGTT   GGT
                                || ||  ||||||||   |||
                                CC TC  CCGTTCAG   CCG
                                 A  GA      T__
GAM2044  FLJ12122 5'  GGCTTCAGGTTCCTGGT    50083    AGA   CAA
                                GGC   CGG   GTTCCTGGT
                                |||   |||   |||||||||
                                CCG   GTC   CAAGGACCA
                                  AA_  ___
GAM2044  FLJ20034 5'  CGCCAGAGCCTTGTTCCTGGTG 50084    G   CG  AA_
                                CG CAGA  GC   GTTCCTGGTG
                                || ||||  ||   ||||||||||
                                GC GTCT  CG   CAAGGACCAC
                                 G   __  GAA
GAM2044  KCNV1    5'  GGCACGGCCCCTGGTG     50085    AG    AAGT
                                GGC  ACGGC   TCCTGGTG
                                |||  |||||   ||||||||
                                CCG  TGCCG   GGGACCAC
                                   __   _____
GAM2044  KIAA0478 3'  GGCAGACAGCCCTGCCTGGTG  50086         AAGTT
                                GGCAGACGGC    CCTGGTG
                                ||||||||||    |||||||
                                CCGTCTGTCG    GGACCAC
                                     GGAC_
GAM2044  KIAA1878 3'  CGGCAACGCTTCCTGGT     50087       A  G AAG
                                CGGCAG CG C   TTCCTGGT
                                |||||| || |   ||||||||
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                                GCCGTT GC G   AAGGACCA
                                  _  _ ___
GAM2044  PKMYT1    5'  CGGTAGACGGTAAGTTCC    50088     C     C
                                CGG AGACGG AAGTTCC
                                ||| |||||| |||||||
                                GCC TCTGCC TTCAAGG
                                  A     A
GAM2044  LOC147157 3'  GGTGTGACGGCACTTCCTGGTG 50089    CA_      AG
                                GG   GACGGCA  TTCCTGGTG
                                ||   |||||||  |||||||||
                                CC   CTGCCGT  AAGGACCAC
                                 ACA      G_
GAM2044  LOC151429 3'  GGCAGAGGCAGGTCCCTG    50090       C    A
                                GGCAGA GGCA GTTCCTG
                                |||||| |||| |||||||
                                CCGTCT CCGT CAGGGAC
                                   _   C
GAM2044  LOC153579 5'  GGCAGATGAGTCCTGGTG    50091       C GCA   T
                                GGCAGA G   AGT CCTGGTG
                                |||||| |   ||| |||||||
                                CCGTCT C   TCA GGACCAC
                                   A ___   _
GAM2045  CALB1     5'  TGGGCGCGGGCGCTGCCG    50094    A     AGCTG
                                TG GCGCGG    GCGTTGCCG
                                || ||||||    |||||||||
                                AC CGCGCC    CGCGACGGC
                                 C    ______
GAM2045  CISH      5'  TGGGCGCGGAGCGCGTGC    50095    A       TG    T
                                TG GCGCGGAGC  GCGT GC
                                || |||||||||  |||| ||
                                AC CGCGCCTCG  CGCA CG
                                 C       __   _
GAM2045  CISH      5'  TGGGCGCGGAGCGCGTGC    50095    A       TG    T
                                TG GCGCGGAGC  GCGT GC
                                || |||||||||  |||| ||
                                AC CGCGCCTCG  CGCA CG
                                 C       __   _
GAM2045  CNGB1     3'  TGAGTCGGGGCTGGCGTGC    50096     _ C  A      T
                                TGAG CG GG GCTGGCGT GC
                                |||| || || |||||||| ||
                                ACTC GC CC CGACCGCA CG
                                  A  _  _       _
GAM2045  CTSB      5'  CGGAGCGGTTGGCGTTGCCG   50097       ___
                                CGGAGC   TGGCGTTGCCG
                                ||||||   ||||||||||
                                GCCTCG   ACCGCAACGGC
                                   CCA
GAM2045  F12       3'  TGGCGCGGAGCTGGCCGC    50098    A         GT
                                TG GCGCGGAGCTGGC  TGC
                                || ||||||||||||  |||
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                                AC CGCGCCTCGACCG  GCG
                                  _       __
GAM2045 KCNN2    5' GCGCGGAGCCCAGACTGCCGA 50099        __  GT
                                GCGCGGAGCT  GGC  TGCCGA
                                ||||||||||  |||  ||||||
                                CGCGCCTCGG  CTG  ACGGCT
                                     GT  __
GAM2045 KLF4     5' TGGCGCGGAGCTGCGAAC    50100    A       G  TT
                                TG GCGCGGAGCTG CG  GC
                                || ||||||||||| ||  ||
                                AC CGCGCCTCGAC GC  TG
                                  _        _ T_
GAM2045 MAGEA8   5' TGGGCCGGAGCTGGGC     50101    A G      C
                                TG GC CGGAGCTGG GT
                                || || ||||||||| ||
                                AC CG GCCTCGACC CG
                                 C _       _
GAM2045 TNFSF7   5' GCGCGGAGCGCTGCCG     50102        TGGC
                                GCGCGGAGC   GTTGCCG
                                |||||||||   |||||||
                                CGCGCCTCG   CGACGGC
                                     ____
GAM2045 TPI1     5' TGGGCGTGGAGCCGGCAGCCGA 50103    A  C       TT
                                TG GCG GGAGCTGGCG  GCCGA
                                || ||| ||||||||||  |||||
                                AC CGC CCTCGGCCGT  CGGCT
                                 C  A        __
GAM2045 USP13    5' GAGCGCGGGGGTCTGCCG    50104       AGCT  CG
                                GAGCGCGG   GG  TTGCCG
                                ||||||||   ||  ||||||
                                CTCGCGCC   CC  GACGGC
                                     ____ A_
GAM2045 DKFZp547O146 3'  TGAGTGCGGAGCTAGGAACGA  50105     C       CGTTGC
                                TGAG GCGGAGCTGG     CGA
                                |||| ||||||||||     |||
                                ACTC CGCCTCGATC     GCT
                                  A        CTT___
GAM2045 FLJ12541 3' TGAGGTGGAGCTGGGCTG   50106     CGC      C
                                TGAG   GGAGCTGG GTTG
                                ||||   |||||||| ||||
                                ACTC   CCTCGACC CGAC
                                  CA_      _
GAM2045 FLJ12783 5' GAGCGCGGGGCTCCCGCCG   50107       AGCT  G_
                                GAGCGCGG   GGC  TTGCCG
                                ||||||||   |||  ||||||
                                CTCGCGCC   CCG  GGCGGC
                                     ____  AG
GAM2045 FLJ20707 5' CGGGCGCGGAGTTGCC     50108    A     GCTGGC
                                TG GCGCGGA     GTTGCC
                                || |||||||     ||||||
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                                GC CGCGCCT     CAACGG
                                 C     _______
GAM2045 KIAA0415 3' GCGTGGAGCTGGTGGCTG    50109     C       C_
                                GCG GGAGCTGG  GTTG
                                ||| ||||||||  ||||
                                CGC CCTCGACC  CGAC
                                  A       AC
GAM2045 KIAA0522 3' TGAGTGAGGAGCTGGATATGC  50110      CGC       CGT
                                TGAG   GGAGCTGG   TGC
                                ||||   ||||||||   |||
                                ACTC   CCTCGACC   ACG
                                  ACT       TAT
GAM2045 MFN1     3' TGATGCATTATCTGGCGTTGC  50111     GC   GAG_
                                TGA  GCG    CTGGCGTTGC
                                |||  |||    ||||||||||
                                ACT  CGT    GACCGCAACG
                                  A_   AATA
GAM2045 MGC14436 5' TGGGCGGGGGGCTTTCGGCTGA 50112    A   C  A   GG  TT  C
                                TG GCG GG GCT  CG  GC GA
                                || ||| || |||  ||  || ||
                                AC CGC CC CGA  GC  CG CT
                                 C   C  C   AA  __  A
GAM2045 SLC26A10 5' TGAGCGCGGAGATGGTCAGTT  50113          C   _ _
                                TGAGCGCGGAG TGG C GTT
                                |||||||||||| ||| | |||
                                ACTCGCGCCTC ACC G CAA
                                       T   A T
GAM2045 LOC126661 3' TGGGCATGGAGCTGAAAGATGC 50114    A   C       CGT_
                                TG GCG GGAGCTGG    TGC
                                || ||| ||||||||    |||
                                AC CGT CCTCGACT    ACG
                                 C   A       TTCT
GAM2045 LOC205085 5' TGGGCGCGGAGCTGGGGCCA   50115    A         CGTT
                                TG GCGCGGAGCTGG    GCCG
                                || ||||||||||||    ||||
                                AC CGCGCCTCGACC    CGGT
                                 C          C___
GAM2045 LOC255452 5' TGGCTGCGGAGCTGGCGCCA   50116    A _         GTT
                                TG GC GCGGAGCTGGC   GCCG
                                || || ||||||||||||  ||||
                                AC CG CGCCTCGACCG   CGGT
                                 _ A          ____
GAM2045 LOC93320  5' TGGGCGGGGCCGCAGCGTTGCC 50117    A   C  A   __
           G                     TG GCG GG GCTG  GCGTTGCCG
                                || ||| || ||||  |||||||||
                                AC CGC CC CGGC  CGCAACGGC
                                 C   _  _    GT
GAM2046 C20orf177 5' TAGTGCTCAAAATATTCTTGCT 50120     C         _ CA
           CAA                    TAG GCTCAGAATAT CT  TTCAA
                                ||| ||||||||||| ||  |||||
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                                ATC CGAGTTTTATA GA  GAGTT
                                  A         A  AC
GAM2046  CTAGE-1   3'  TAACGTTTTCAATCTCATTCA  50121      C__   GAAT
                                TAGCG   TCA    ATCTCATTCA
                                |||||   |||    ||||||||||
                                ATTGC   AGT    TAGAGTAAGT
                                   AAA  ____
GAM2046  DKFZp761O0113 5'  TAGCGGTCACCTCATT      50122       C   GAATA
                                TAGCG TCA     TCTCATT
                                ||||| |||     |||||||
                                ATCGC AGT     GGAGTAA
                                   C  _____
GAM2046  FLJ10377  3'  GCCACACAATATCTCATT    50123     _ G
                                GCT CA AATATCTCATT
                                ||| || ||||||||||
                                CGG GT TTATAGAGTAA
                                  T  G
GAM2046  KIAA0310  3'  AGCGCAAAATATTTTATTCAA  50124       TC      CTC
                                AGCGC  AGAATAT   ATTCAA
                                |||||  |||||||   ||||||
                                TCGCG  TTTTATA   TAAGTT
                                   __      AAA
GAM2046  SCYB10    5'  TAGGCTCAGAATATGTC     50125     C         C
                                TAG GCTCAGAATAT TC
                                ||| ||||||||||| ||
                                ATC CGAGTCTTATA AG
                                  _         C
GAM2046  LOC157507 5'  CACAAGAATATCTTGTTCAA   50126     TC        CA
                                CGC  AGAATATCT  TTCAA
                                |||  |||||||||  |||||
                                GTG  TCTTATAGA  AAGTT
                                  T_        AC
GAM2046  LOC203025 5'  TAGGCTAAGAATATCTTGTTC  50127     C   C       CA
                                TAG GCT AGAATATCT  TTC
                                ||| ||| |||||||||  |||
                                ATC CGA TCTTATAGA  AAG
                                  _  T        AC
GAM2047  BARX1     3'  TGGGACCTGGGTCTGGCT    19343         AGC    G
                                TGGGATCTG   CTGG CT
                                |||||||||   |||| ||
                                ACCCTGGAC   GACC GA
                                     CCA   _
GAM2047  FBN2      3'  TAGGATTTGAGCCTGGGCC    50130       C
                                TGGGAT TGAGCCTGGGCT
                                |||||| ||||||||||||
                                ATCCTA ACTCGGACCCGG
                                   A
GAM2047  RNF12     5'  TGGAATCTGAGTTTTCCATATT 50131          CCTGGG  _
              G                  TGGGATCTGAG     CTA ATTG
                                ||||||||||      ||| ||||
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                                ACCTTAGACTC     GGT TAAC
                                      AAAA__   A
GAM2047 PLAA     3' TGGGATCTAAGCCTGGAGTTAA 50132             CT__
             ATTG                   TGGGATCTGAGCCTGGG    AATTG
                                ||||||||||||||||   |||||
                                ACCCTAGATTCGGACCT    TTAAC
                                       CAAT
GAM2047 SIMRP7   3' TGGGATCTGAGCTGGGCCA   50133          C
                                TGGGATCTGAGC TGGGCTA
                                |||||||||||| |||||||
                                ACCCTAGACTCG ACCCGGT
                                      _
GAM2047 TJP4     3' TGGGCTGGGTTGGGCTGATTG 50134     AT   AGCC     A
                                TGGG  CTG   TGGGCT ATTG
                                ||||  |||   |||||| ||||
                                ACCC  GAC   ACCCGA TAAC
                                  __  CCA_     C
GAM2047 LOC200953 5' TGGGATCTGGTCCTGTCT    50135        AG   GG
                                TGGGATCTG  CCTG  CT
                                |||||||||  ||||  ||
                                ACCCTAGAC  GGAC  GA
                                     CA   A_
GAM2048 GLRX     3' GCCCGGTCAACCTTCT     50138     CA  GTGCG
                                GCCC  GT    TAACCTTCT
                                ||||  ||    |||||||||
                                CGGG  CA    GTTGGAAGA
                                  C_ _____
GAM2048 OSR1     3' TGGCCCAGTGTGTGTCTCCTT  50139    C       C  AA
                                TG CCCAGTGTG GT  CCTT
                                || |||||||| ||  ||||
                                AC GGGTCACAC CA  GGAA
                                 C       A  GA
GAM2048 PRKY     3' TGCACAGTGTAACCTT     50140     CC      CGTA
                                TGC  CAGTGTG    ACCTT
                                |||  |||||||   |||||
                                ACG  GTCACAT    TGGAA
                                  T_     _____
GAM2048 ZNF138   3' CCCCAGTATGAATTTTCT    50141          C  AACC
                                CCCCAGTGTG GT    TTCT
                                |||||||||| ||    ||||
                                GGGGTCATAC TA    AAGA
                                     T  A___
GAM2048 C6orf5   3' TGCCCGGCTAACTTTC      50142      CAGT T  G    C
                                TGCCC    G GC TAAC TTC
                                |||||    | || |||| |||
                                ACGGG    C CG ATTG AAG
                                   _____ _  _    A
GAM2048 FLJ11800 3' GCCCCAGTGTTCACCAAACCTT 50143          GCGT__
                                GCCCCAGTGT     AACCTT
                                ||||||||||     ||||||
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                                CGGGGTCACA     TTGGAA
                                     AGTGGT
GAM2048  FLJ13391  5'  CCTCCTCTGTGACCTTCTT   50144    _ AG   CGTA
                                CC CC  TGTG   ACCTTCTT
                                || ||  ||||   ||||||||
                                GG GG  ACAC   TGGAAGAA
                                 A  AG   ____
GAM2048  FLJ14260  5'  CCAGTATGAGTTTTCTT     50145        C  AACC
                                CCAGTGTG GT   TTCTT
                                |||||||| ||   |||||
                                GGTCATAC CA   AAGAA
                                     T  A___
GAM2048  MASA      3'  TACCTCAGTGCACCTT      50146      C     GCGTA
                                TGCC CAGTGT    ACCTT
                                |||| ||||||    |||||
                                ATGG GTCACG    TGGAA
                                  A    _____
GAM2048  LOC148760 3'  TACCTCAGAATGTGGCCTTCTT 50147      C   __   C TAA
                                TGCC CAG  TGTG G   CCTTCTT
                                |||| |||  |||| |   |||||||
                                ATGG GTC  ACAC C   GGAAGAA
                                  A  TT   _ ___
GAM2048  LOC151446 3'  CAGTGTACGCCTTTCTT     50148          AACC
                                CAGTGTGCGT    TTCTT
                                ||||||||||    |||||
                                GTCACATGCG    AAGAA
                                     GA__
GAM2048  LOC154930 5'  CCCCAGTATGAATTTTCT     50141          C  AACC
                                CCCCAGTGTG GT    TTCT
                                |||||||||| ||    ||||
                                GGGGTCATAC TA    AAGA
                                     T  A___
GAM2048  LOC222193 5'  CCTCAGTCCGGACCTTCT     50149    C    G  CGTA
                                CC CAGT TG    ACCTTCT
                                || |||| ||    |||||||
                                GG GTCA GC    TGGAAGA
                                 A    G  C___
GAM2049  BCAT1     3'  TAGAATGTTGCTCGGGGTACAC 50152      _   CAATGAAGA
           AG                     TAGA TGT        GTACACAG
                                |||| |||         ||||||||
                                ATCT ACA        CATGTGTC
                                  T   ACGAGCCC_
GAM2049  DSCR3     3'  GATGTCAACTGGCCACA     50153          GAAGA  A
                                GATGTCAAT     GT CACA
                                |||||||||     || ||||
                                CTACAGTTG     CG GTGT
                                     AC___  _
GAM2049  NPR2L     3'  AGATGTCAGTGAGAGCA     50154          A   A
                                AGATGTCA TGA GAGTA
                                |||||||| ||| |||||
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                                TCTACAGT ACT CTCGT
                                     C   _
GAM2049  TRAP240   3'  TAGAGTCAATGAAAAATA    50155      T
                                TAGA GTCAATGAAGAGTA
                                |||| ||||||||||||||
                                ATCT CAGTTACTTTTTAT
                                  _
GAM2049  DKFZp761O17121 3'  GTCAATGGGAGAGTACACAG   50156        A_
                                GTCAATG  AGAGTACACAG
                                |||||||  ||||||||||
                                CAGTTAC  TCTCATGTGTC
                                     CC
GAM2049  FLJ20967  3'  AGGTGTCAATGAGGACTCCA   50157    A        A  GTA
                                AG TGTCAATGA GA   CA
                                || |||||||| ||   ||
                                TC ACAGTTACT CT   GT
                                 C        C  GAG
GAM2049  FYCO1     3'  TAGATGTAGTGTACACA     50158        CAATGA  A
                                TAGATGT     AG GTACACA
                                |||||||     || |||||||
                                ATCTACA     TC CATGTGT
                                    _______ A
GAM2049  GABBR1    3'  GTACATGGAGGGTACACAG    50159    CA   A  A
                                GT  ATG AG GTACACAG
                                ||  ||| || ||||||||
                                CA  TAC TC CATGTGTC
                                 TG   C  C
GAM2049  GABBR1    3'  GTACATGGAGGGTACACAG    50159    CA   A  A
                                GT  ATG AG GTACACAG
                                ||  ||| || ||||||||
                                CA  TAC TC CATGTGTC
                                 TG   C  C
GAM2049  KIAA0662  3'  TAAATGTTAATGAAGAAC     50160        C
                                TAGATGT AATGAAGAGT
                                ||||||| ||||||||||
                                ATTTACA TTACTTCTTG
                                     A
GAM2049  KIAA1297  5'  CAGATGTCAGTGACTCCAGACA 50161          A   AG__  T
            C                    TAGATGTCA TGA    AG ACAC
                                |||||||| |||    || ||||
                                GTCTACAGT ACT    TC TGTG
                                      C   GAGG  _
GAM2049  MCM10     3'  TAAATGTCAATGTTAAAT    50162           AA
                                TAGATGTCAATG  GAGT
                                ||||||||||||  ||||
                                ATTTACAGTTAC  TTTA
                                       AA
GAM2049  LOC115073 3'  AGATGTCAGTGAAGGTA     50163         A    A
                                AGATGTCA TGAAG GTA
                                |||||||| ||||| |||
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                                TCTACAGT ACTTC CAT
                                     C    _
GAM2049  LOC131583 3'  AGATGTCAGTGACAGCGCA   50164        A  AG  TA
                                AGATGTCA TGA  AG  CA
                                |||||||| |||  ||  ||
                                TCTACAGT ACT  TC  GT
                                     C   G_  GC
GAM2049  LOC146330 5'  TAGTTGTCAATGAACTCACAG  50165    A       GAGTA
                                TAG TGTCAATGAA    CACAG
                                ||| ||||||||||    |||||
                                ATC ACAGTTACTT    GTGTC
                                  A        GA___
GAM2049  LOC151248 5'  TAGATGCCAAAGTTTTAGTGTA 50166         TGA___  A
              CA                  TAGATGTCAA     AG GTACA
                                ||||||||||     || |||||
                                ATCTACGGTT     TC CATGT
                                     TCAAAA  A
GAM2049  LOC151473 3'  TAGATGTCATGGATCACA    50167        A  AA  GTA
                                TAGATGTCA TG  GA   CACA
                                |||||||| ||  ||   ||||
                                ATCTACAGT AC  CT   GTGT
                                     _  __  A__
GAM2050  HEM1     5'  CTAAGTCAGGGTTCTCATGC  50170       AA   CC_
                                CTAGGTCA  GTTC   TGC
                                ||||||||  ||||   |||
                                GATTCAGT  CAAG   ACG
                                     CC    AGT
GAM2050  IL2RB    3'  CCAGGTCAGAGTTAGCTG    50171       A   CC
                                CTAGGTCA AGTT  CTG
                                |||||||| ||||  |||
                                GGTCCAGT TCAA  GAC
                                     C    TC
GAM2050  IRTA1    5'  CCAGGTCAGCCCAGATTGCCAA 50172       AAGTT  _____
              A                   CTAGGTCA    CCC    TGCCAAA
                                |||||||     |||   |||||||
                                GGTCCAGT    GGG    ACGGTTT
                                     C_____   TCTA
GAM2050  LZTR1    3'  CTAGATCAGGGTTCAGTGACAA 50173       AA   CC  C
                                CTAGGTCA  GTTC  TG CAA
                                ||||||||  ||||  || |||
                                GATCTAGT  CAAG  AC GTT
                                     CC    TC  T
GAM2050  NGB      3'  GGTCAGAGGGAGTGCCAAAA  50174      A  TTCCC
                                GGTCA AG    TGCCAAAA
                                ||||| ||    ||||||||
                                CCAGT TC    ACGGTTTT
                                   C  CCTC_
GAM2050  PRPF31   3'  CAGGTTCTCCCTGCCA     50175      CAAAG
                                TAGGT    TTCCCTGCCA
                                |||||    ||||||||||
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                                GTCCA    GAGGGACGGT
                                  A____
GAM2050 SCNN1A   3' TAGGAAAGTTCCTTGTCAAA  50176     TC      C C
                                TAGG  AAAGTTCC TG CAAA
                                ||||  |||||||| || ||||
                                ATCC  TTTCAAGG AC GTTT
                                  __       A  A
GAM2050 SYNGR1   3' CTGGGCAGGTCCCTGCCA    50177    A   CAA  T
                                CT GGT   AG TCCCTGCCA
                                || |||   || |||||||||
                                GA CCG   TC AGGGACGGT
                                 C   ___  C
GAM2050 ZIC1     3' GGTACCAAGCCTTTGCCAAAA 50178    CA_    CCC
                                GGT   AAGTT   TGCCAAAA
                                |||   |||||   ||||||||
                                CCA   TTCGG   ACGGTTTT
                                  TGG    AA_
GAM2050 ATPAF1   3' TAAGGTCAAAGTGGCCA     50179   T       TCCCT
                                C AGGTCAAAGT    GCCA
                                | ||||||||||    ||||
                                A TCCAGTTTCA    CGGT
                                 T        C____
GAM2050 C20orf55 3' CTAGGCCAGCTGCCAA      50180        AAGTTCC
                                CTAGGTCA      CTGCCAA
                                ||||||||      |||||||
                                GATCCGGT      GACGGTT
                                    C_______
GAM2050 DCLRE1A  3' TAGGTCGAAATGCCAAA     50181       A   TTCCC
                                TAGGTC AAG    TGCCAAA
                                |||||| |||    |||||||
                                ATCCAG TTT    ACGGTTT
                                   C  ______
GAM2050 DKFZP586M0622 5' CTAAGTTTCCCTGCCA      50182       CAAAG
                                CTAGGT    TTCCCTGCCA
                                ||||||    ||||||||||
                                GATTCA    AAGGGACGGT
                                          ______
GAM2050 DKFZp762A227 3' AGTCAAGGGTCTGCCAA     50183       A_  TCC
                                GGTCAA  GT   CTGCCAA
                                ||||||  ||   |||||||
                                TCAGTT  CA   GACGGTT
                                   CC  ___
GAM2050 FLJ00024 3' GGTTTTATTTCTGCCAAAA   50184    CAAA   CC
                                GGT   GTT  CTGCCAAAA
                                |||   |||  |||||||||
                                CCA   TAA  GACGGTTTT
                                  AAA_   A_
GAM2050 FLJ11726 3' TAGATCAAAGTTTCCCTG    50185          _
                                TAGGTCAAAGTT CCCTG
                                |||||||||||| |||||
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                                ATCTAGTTTCAA GGGAC
                                      A
GAM2050  FLJ12443  5' CTGGATCAGAGTTCCCCA    50186    A    A
                                CT GGTCA AGTTCCCTG
                                || ||||| |||||||||
                                GA CTAGT TCAAGGGGT
                                 C    C
GAM2050  FLJ14708  3' CCAGGTCAGAGGGCCAA     50187        A  TTCCCT
                                CTAGGTCA AG     GCCAA
                                |||||||| ||     |||||
                                GGTCCAGT TC     CGGTT
                                     C  C_____
GAM2050  FLJ20399  3' CTAGGCTGATGGCCCCTGCCA  50188       CAAAGT
                                CTAGGT     TCCCTGCCA
                                ||||||     |||||||||
                                GATCCG     GGGGACGGT
                                   ACTACC
GAM2050  FUSIP1    3' CTAGGTTAACAGTTCTACCAAA 50189       CAA_    CC
                                CTAGGT   AGTTC  TGCCAAA
                                ||||||   |||||  |||||||
                                GATCCA   TCAAG  ATGGTTT
                                   ATTG    __
GAM2050  KIAA0582  5' CTAGGTCAGGGTTCTGC     50190        AA   CC
                                CTAGGTCA  GTTC  TGC
                                ||||||||  ||||  |||
                                GATCCAGT  CAAG  ACG
                                     CC   __
GAM2050  KIAA0582  5' CTAGGTCAGGGTTCTGC     50190        AA   CC
                                CTAGGTCA  GTTC  TGC
                                ||||||||  ||||  |||
                                GATCCAGT  CAAG  ACG
                                     CC   __
GAM2050  KIAA0821  3' CCAGGTTAGAGTCCCCTG    50191       CAA
                                CTAGGT   AGTTCCCTG
                                ||||||   |||||||||
                                GGTCCA   TCAGGGGAC
                                   ATC
GAM2050  KIAA1036  3' CTAGGTTCTTCCCTGCCA    50192       CAAAG
                                CTAGGT    TTCCCTGCCA
                                ||||||    ||||||||||
                                GATCCA    AAGGGACGGT
                                   AG___
GAM2050  KIAA1199  3' CTGGGTCAGGGCTCCTGCCAAA 50193    A    AA    C
                                CT GGTCA  GTTCC TGCCAAA
                                || |||||  ||||| |||||||
                                GA CCAGT  CGAGG ACGGTTT
                                 C    CC    _
GAM2050  KIAA1786  3' TAGGCCAAGGTTCCAGCTTTTC 50194        A    CT  _____
            AAAA                   TAGGTCAA GTTCC  GC    CAAAA
                                |||||||| |||||  ||   |||||
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                                ATCCGGTT CAAGG  CG    GTTTT
                                     C     T_  AAAA
GAM2050  MGC29891  5'  CTAGTTAAGACTCCCTGTCAA  50195      GTCA  _      C
                                CTAG    AAG TTCCCTG CAA
                                ||||    ||| ||||||| |||
                                GATC    TTC GAGGGAC GTT
                                  AA__   T      A
GAM2050  MGC3248   3'  CTAGGTCAAAATGCTAAA    50196          TTCCC   C
                                CTAGGTCAAAG     TGC AAA
                                ||||||||||     ||| |||
                                GATCCAGTTTT     ACG TTT
                                      _____  A
GAM2050  NFAT5     3'  CTAGATTAAAGTGGCCAAA    50197       C     TCCCT
                                CTAGGT AAAGT     GCCAAA
                                |||||| |||||     ||||||
                                GATCTA TTTCA     CGGTTT
                                   A    C____
GAM2050  NFAT5     3'  CTAGATTAAAGTGGCCAAA    50197       C     TCCCT
                                CTAGGT AAAGT     GCCAAA
                                |||||| |||||     ||||||
                                GATCTA TTTCA     CGGTTT
                                   A    C____
GAM2050  PPP1R16B  3'  CAGGTCCCCTCCCCTGCTAAAA 50198        AAAG       C
                                TAGGTC    TTCCCTGC AAAA
                                ||||||    |||||||| ||||
                                GTCCAG    AGGGGACG TTTT
                                   GGG_       A
GAM2050  SEMA5A    3'  AGTCCCCCCTGCCAA       50199      AAAG
                                GGTC    TTCCCTGCCAA
                                ||||    ||||||||||
                                TCAG    GGGGGACGGTT
                                  ____
GAM2050  LOC120856 3'  CAGGTCAAGAATGCCAAA     50200         A TTCCC
                                TAGGTCAA G     TGCCAAA
                                |||||||| |     |||||||
                                GTCCAGTT C     ACGGTTT
                                     _ TT___
GAM2050  LOC126302 5'  TGAGGTCAAAGGGGCCAAA    50201    T       TTCCCT
                                C AGGTCAAAG      GCCAAA
                                | |||||||||      ||||||
                                A TCCAGTTTC      CGGTTT
                                 C        CC____
GAM2050  LOC143286 5'  CTAGGCCAGAGTTCTCTTGC   50202         A     C  _
                                CTAGGTCA AGTTC CT GC
                                |||||||| ||||| || ||
                                GATCCGGT TCAAG GA CG
                                     C     A  A
GAM2050  LOC144563 5'  CTGGGACAGGGGTCCCTGCCA  50203     A  T  AAGT
                                CT GG CA    TCCCTGCCA
                                || || ||    |||||||||
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                                GA CC GT   AGGGACGGT
                                 C  T  CCCC
GAM2050  LOC149072 5'  CTAGGCCAGGACCCGTTGC   50204       AA TT  __
                                CTAGGTCA  G  CCC  TGC
                                ||||||||  |  |||  |||
                                GATCCGGT  C  GGG  ACG
                                    __ CT   CA
GAM2050  LOC151475 5'  CAGGTCAAGGTCAGGCCTG   50205       A  C__
                                TAGGTCAA GTT   CCTG
                                ||||||||  |||   ||||
                                GTCCAGTT CAG   GGAC
                                    C   TCC
GAM2050  LOC151632 5'  CTGGGACAGGGGTCCCTGCCA  50203   A  T  AAGT
                                CT GG CA   TCCCTGCCA
                                || || ||   |||||||||
                                GA CC GT   AGGGACGGT
                                 C  T  CCCC
GAM2050  LOC200904 5'  CTGGGACAGGGGTCCCTGCCA  50203   A  T  AAGT
                                CT GG CA   TCCCTGCCA
                                || || ||   |||||||||
                                GA CC GT   AGGGACGGT
                                 C  T  CCCC
GAM2050  LOC203083 5'  CTGGGACAGGGGTCCCTGCCA  50203   A  T  AAGT
                                CT GG CA   TCCCTGCCA
                                || || ||   |||||||||
                                GA CC GT   AGGGACGGT
                                 C  T  CCCC
GAM2050  LOC219919 5'  CTGGGACAGGGGTCCCTGCCA  50203   A  T  AAGT
                                CT GG CA   TCCCTGCCA
                                || || ||   |||||||||
                                GA CC GT   AGGGACGGT
                                 C  T  CCCC
GAM2050  LOC221795 5'  CTGGGACAGGGGTCCCTGCCA  50203   A  T  AAGT
                                CT GG CA   TCCCTGCCA
                                || || ||   |||||||||
                                GA CC GT   AGGGACGGT
                                 C  T  CCCC
GAM2050  LOC254176 5'  CTGGGACAGGGGTCCCTGCCA  50203   A  T  AAGT
                                CT GG CA   TCCCTGCCA
                                || || ||   |||||||||
                                GA CC GT   AGGGACGGT
                                 C  T  CCCC
GAM2050  LOC256515 5'  CTGGGACAGGGGTCCCTGCCA  50203   A  T  AAGT
                                CT GG CA   TCCCTGCCA
                                || || ||   |||||||||
                                GA CC GT   AGGGACGGT
                                 C  T  CCCC
GAM2050  LOC56996  3'  GGGGTCCCTCTGCCAAA    50206   TCAAA   _
                                GG    GTTCC CTGCCAAA
                                ||    ||||| ||||||||
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                                CC    CAGGG GACGGTTT
                                 C____    A
GAM2050 LOC93512 3' CCAGGTTCTCCTGCCA     50207      CAAAGT _
                                CTAGGT    TC CCTGCCA
                                ||||||    || |||||||
                                GGTCCA    AG GGACGGT
                                   ______ A
GAM2051 ELAVL2   3' ACTTGCCTTTGTTGTATAGTTT 50210         AGGCAC
           T                    ACTTGCTTTT    ATAGTTTT
                                ||||||||||    ||||||||
                                TGAACGGAAA    TATCAAAA
                                     CAACA_
GAM2051 ABHD3    3' TTGTTTTACACAATAGTTTT  50211    C   G  C
                                TTG TTTTA GCA ATAGTTTT
                                ||| ||||| ||| ||||||||
                                AAC AAAAT TGT TATCAAAA
                                  _   G  _
GAM2051 MGC10067 3' CTGCTTTTATGACAATGGTTTT 50212        _  C  A
                                TTGCTTTTA GGCA AT GTTTT
                                ||||||||| |||| || |||||
                                GACGAAAAT CTGT TA CAAAA
                                     A   _ C
GAM2051 MGC3184  3' TTGTTTTAATAACATAGTTTT  50213    C    GC
                                TTG TTTTAG  ACATAGTTTT
                                ||| ||||||  ||||||||||
                                AAC AAAATT  TGTATCAAAA
                                  _    AT
GAM2051 PCDH17   3' GCTTTTAGTTGAAGTAGTTTT  50214       GCACA_
                                GCTTTTAG    TAGTTTT
                                ||||||||    |||||||
                                CGAAAATC    ATCAAAA
                                     AACTTC
GAM2051 POF1B    3' ACTTTCTAACTACATAGTTTT  50215      AG _
                                GCTTTT  GC ACATAGTTTT
                                ||||||  || ||||||||||
                                TGAAAG  TG TGTATCAAAA
                                   AT  A
GAM2052 MGC4734  3' TGCTATTTGGGCTAGTCA    50218     G     C _
                                TGCTA TTTGGGC AG CG
                                ||||| ||||||| || ||
                                ACGAT AAACCCG TC GT
                                  _     A  A
GAM2052 MGC9564  3' TGCAGTTTGGGCTGGAA    50219    T      CAGC
                                TGC AGTTTGGGC   GAA
                                ||| |||||||||   |||
                                ACG TCAAACCCG   CTT
                                  _      AC__
GAM2052 PDEF     5' TGCTGTTTGGGCTGGCG    50220     A      CA
                                TGCT GTTTGGGC  GCG
                                |||| ||||||||  |||
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                                ACGA CAAACCCG  CGC
                                  _      AC
GAM2052  LOC135154 3'  GCTTGAACCTGGCGGGGCGG   50221        A_   AAA
                                GTTTGGGCC  GCG   CGG
                                |||||||||  |||   |||
                                CGAACTTGG  CGC   GCC
                                     AC   CCC
GAM2052  LOC220686 5'  GCAGCAGCCAGCGGGGCGG    50222    T   TTG      AAA
                                GC AGT   GGCCAGCG   CGG
                                || |||   ||||||||   |||
                                CG TCG   TCGGTCGC   GCC
                                 _  ___       CCC
GAM2052  LOC51133  5'  GCTGCAGGGCCAGCGGGGCGG  50223     A  TT       AAA
                                GCT GT  GGGCCAGCG   CGG
                                ||| ||  |||||||||   |||
                                CGA CG  CCCGGTCGC   GCC
                                  _ T_       CCC
GAM2053  KCNH8    3'  TATTGTTCAGGAATAACAATC  50226         AT   AT
                                TATTGTTTA  GAA  TAACAATC
                                |||||||||  |||  ||||||||
                                ATAACAAGT  CTT  ATTGTTAG
                                     C_   __
GAM2053  LOC145231 3'  TTGTCATATGAATTAACAATC  50227       TA    A
                                TTGTT  ATGAA TTAACAATC
                                |||||  ||||| |||||||||
                                AACAG  TACTT AATTGTTAG
                                   TA    _
GAM2054  CAPZA1    3'  ATAACAGGTTACAATAGA     50230         C   GTCA
                                ATAACAGG TTA    AATAGA
                                ||||||||| |||    ||||||
                                TATTGTCC AAT    TTATCT
                                     _   G___
GAM2054  COL7A1    3'  CATCACAGGCTTGGGTCAA    50231     A       A_
                                CAT ACAGGCTT  GTCAA
                                ||| ||||||||  |||||
                                GTA TGTCCGAA  CAGTT
                                  G       CC
GAM2054  MEN1      5'  CAAACAGGCCCAGGTGAGTAGA 50232    T         TCAAA
              A                  A AACAGGCTTAG     TAGAA
                                | ||||||||||     |||||
                                G TTGTCCGGGTC     ATCTT
                                 T          CACTC
GAM2054  RXRA      3'  ACAGGTCTGGTTAAATAGAA   50233       CT A  C
                                ACAGG  T GT AAATAGAA
                                |||||  | || ||||||||
                                TGTCC  A CA TTTATCTT
                                   AG C  A
GAM2054  TEM7      3'  CGAACAGGCCATCAGAATAG   50234    T      TA   _
                                A AACAGGCT  GTCA AATAG
                                | ||||||||  |||| |||||
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                                G TTGTCCGG  TAGT TTATC
                                 C       __   C
GAM2054  TNFSF4   3'  CATAACAGATTAAAATAGA   50235        C  GTC
                                CATAACAGG TTA   AAATAGA
                                ||||||||| |||   |||||||
                                GTATTGTCT AAT   TTTATCT
                                      _  ____
GAM2054  ARHU     3'  TAACAGGAATAAATAGAA    50236       CTT  C
                                TAACAGG   AGT AAATAGAA
                                |||||||   ||| ||||||||
                                ATTGTCC   TTA TTTATCTT
                                     ___  _
GAM2054  FBXO21   3'  ATAACAGGGCTTTTTAAAATGG 50237        _  AGTC   A
              A                  ATAACAGG CTT    AAAT GA
                                ||||||||| |||    |||| ||
                                TATTGTCC GAA    TTTA CT
                                     C   AAAT    C
GAM2054  FLJ32468 5'  ACAGAAAAAGTCAAATGGAA   50238      CTT       A
                                ACAGG   AGTCAAAT GAA
                                |||||   |||||||| |||
                                TGTCT   TCAGTTTA CTT
                                   TTT       C
GAM2054  GT650    3'  AGGCCACTGGTCAAATAGAA   50239      TA__
                                AGGCT    GTCAAATAGAA
                                |||||    ||||||||||
                                TCCGG    CAGTTTATCTT
                                   TGAC
GAM2054  HAPIP    3'  AGGCTGAAGCAAATAGAA    50240      T_  T
                                AGGCT  AG CAAATAGAA
                                |||||  || |||||||||
                                TCCGA  TC GTTTATCTT
                                   CT  _
GAM2054  HRIHFB2436 3'  CAGGCCCATCCAAATGGAA   50241        GT    A
                                CAGGCTTA  CAAAT GAA
                                ||||||||  ||||| |||
                                GTCCGGGT  GTTTA CTT
                                     AG    C
GAM2054  KIAA0057  3'  TGAACAGGCTAGAGTAGA    50242   T      T  TCAAA
                                A AACAGGCT AG    TAGA
                                | ||||||||  ||    ||||
                                A TTGTCCGA TC    ATCT
                                 C       _  TC___
GAM2054  KIAA1061  3'  ACAGCAAGTCAAATGGA     50243     G TT       A
                                ACAG C  AGTCAAAT GA
                                ||||  |  |||||||| ||
                                TGTC G  TCAGTTTA CT
                                   _ T_       C
GAM2054  KIAA1374  3'  ACAATTTAGAGGTCAAATAGAA 50244     GCTTA__
                                ACAG      GTCAAATAGAA
                                ||||      ||||||||||
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                                TGTT      CAGTTTATCTT
                                  AAATCTC
GAM2054  KIAA1948  3'  ATAACAGGATTAGTTTTTAGAA 50245        C    CAAA
                                ATAACAGG TTAGT    TAGAA
                                |||||||| |||||    |||||
                                TATTGTCC AATCA    ATCTT
                                     T    AAA_
GAM2054  MGC5242   3'  CATACAGAGGGAGTCAAAT   50246     A   CTT
                                CATA CAGG   AGTCAAAT
                                |||| ||||   ||||||||
                                GTAT GTCT   TCAGTTTA
                                  _   CCC
GAM2054  OATL1     5'  TGAGGTCCCAGTCAGATAGAA  50247   C  _      A
                                A AGG CTTAGTCA ATAGAA
                                | ||| |||||||| ||||||
                                A TCC GGGTCAGT TATCTT
                                 C  A       C
GAM2054  PRO0386   5'  GGCATTAAGTCAAATAGAA    50248    TT__
                                GGC    AGTCAAATAGAA
                                |||    ||||||||||||
                                CCG    TCAGTTTATCTT
                                  TAAT
GAM2054  PRO2831   5'  GGTGGTAATCAAATAGAA    50249    CT_
                                GG   TAGTCAAATAGAA
                                ||   ||||||||||||
                                CC   ATTAGTTTATCTT
                                 ACC
GAM2054  RAE1      3'  CAACAGGCAGTGGAATGGA   50250        TT   CA   A
                                TAACAGGC  AGT  AAT GA
                                ||||||||  |||  ||| ||
                                GTTGTCCG  TCA  TTA CT
                                     __  CC   C
GAM2054  TLR10     5'  CAAAACAGGAAACAAATAGAA  50251    T     CTTAGT
                                CA AACAGG     CAAATAGAA
                                || ||||||     |||||||||
                                GT TTGTCC     GTTTATCTT
                                 T     TTT___
GAM2054  YKT6      3'  ACAGGCGCCTCTCAAATAGAA  50252       _  AG
                                ACAGGC TT  TCAAATAGAA
                                |||||| ||  ||||||||||
                                TGTCCG GG  AGTTTATCTT
                                   C  AG
GAM2054  LOC157567 3'  TAACAGGGCCTCCAAATAG   50253        _   AG
                                TAACAGG CTT  TCAAATAG
                                ||||||| |||  ||||||||
                                ATTGTCC GGA  GGTTTATC
                                     C  __
GAM2054  LOC221893 3'  GACGGAGTCCAAATAGAA    50254     TT   _
                                GGC  AGTC AAATAGAA
                                |||  |||| ||||||||
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                                CTG  TCAG TTTATCTT
                                  CC    G
GAM2055  EHD3     3'  TTCAGTGGCCATGAAGCAAGCC 50257      ATA  AGG  TA
              AG                    TTCA   GC   GG  CAAGCCAG
                                |||||   ||   ||  ||||||||
                                AAGT   CG   CT  GTTCGGTC
                                  CAC  GTA  TC
GAM2055  PIP5K1A   3'  TTCAATAGTGGAGGCAAAG   50258        CA     C
                                TTCAATAG  GGGGTA AAG
                                ||||||||  ||||||  |||
                                AAGTTATC  CTCCGT TTC
                                     AC     _
GAM2055  FLJ20452  3'  TTCAGAAGCAGAAGTCA     50259      AT       A
                                TTCA  AGCAGGGGT CA
                                ||||  |||||||||  ||
                                AAGT  TCGTCTTCA GT
                                  CT       _
GAM2055  LOC148758 3'  TTCAGTGCGGGGCGCAAGCCAG 50260      ATA  A    TA
                                TTCA   GC GGGG  CAAGCCAG
                                ||||   || ||||  ||||||||
                                AAGT   CG CCCC  GTTCGGTC
                                  CA_  _    GC
GAM2055  LOC153163 3'  TTCTGTAGCCAAAAGCAAGCCA 50261     AA   _    TA
              G                    TTC  TAGC AGGGG  CAAGCCAG
                                |||  |||| |||||  ||||||||
                                AAG  ATCG TTTTC  GTTCGGTC
                                  AC    G    __
GAM2055  LOC201100 5'  TTCAGAGCAGGAGAGC      50262      AT       TACA
                                TTCA  AGCAGGGG    AGC
                                ||||  ||||||||    |||
                                AAGT  TCGTCCTC    TCG
                                  C_       ____
GAM2055  LOC90342  3'  TAGCAGGAGGAAAGCCAG    50263         TAC
                                TAGCAGGGG   AAGCCAG
                                |||||||||   |||||||
                                ATCGTCCTC   TTCGGTC
                                     CT_
GAM2055  LOC91960  5'  TTCAATAGAGAAGCC       50264         C   GGTACA
                                TTCAATAG AGG     AGCC
                                ||||||||  |||     ||||
                                AAGTTATC TCT     TCGG
                                          _  _______
GAM2056  RFX2     3'  CAACTGCAGCGGCTACG     50267    T   A  A
                                CA CTG CA CGGCTACG
                                ||  |||  ||  ||||||||
                                GT GAC GT GCCGATGC
                                 T   _  C
GAM2056  SCNN1G   3'  TGGCATCTGGCAGTAGCT    50268         A  AC
                                TGGCATCTG CA  GGCT
                                |||||||||  ||  ||||
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                                ACCGTAGAC GT  TCGA
                                     C  CA
GAM2056  SUV39H1   3'  TGGCATCTGATAGCAGGGC   50269        CAAC   TAC
                                TGGCATCTGA   GGC   GC
                                ||||||||||   |||  ||
                                ACCGTAGACT   TCG   CG
                                     A___   TCC
GAM2056  WHSC1     3'  TGGCATCTGAAGTGGGACAATG 50270        CAAC_  TAC
           C                     TGGCATCTGA   GGC   GC
                                ||||||||||   |||  ||
                                ACCGTAGACT   CTG   CG
                                     TCACC   TTA
GAM2056  KIAA1644  3'  TGGCATCTGGCACATAGTAAGT 50271        A  AC_  CTAC_
           GCGC                    TGGCATCTG CA   GG    GCGC
                                ||||||||| ||   ||    ||||
                                ACCGTAGAC GT   TC    CGCG
                                     C  GTA  ATTCA
GAM2056  NIR1      5'  GGCTCCGGCGGCTACGCGC   50272    A   ACAA
                                GGC TCTG   CGGCTACGCGC
                                ||| ||||   ||||||||||
                                CCG AGGC   GCCGATGCGCG
                                  _   C___
GAM2056  NKX2C     3'  TGGTGCAACGGCTGTGCG    50273    CATC  A      AC
                                TGG   TG CAACGGCT  GCG
                                |||   || ||||||||  |||
                                ACC   AC GTTGCCGA  CGC
                                  _____ _      CA
GAM2056  PI4KII    3'  GGCATCTGGACTACGG      50274        ACAAC     C
                                GGCATCTG    GGCTACG G
                                ||||||||    ||||||| |
                                CCGTAGAC    CTGATGC C
                                     ______      A
GAM2056  LOC195977 3'  TGGCACCTGGTGGCAGCTTGCG 50275        ACAA    AC
                                TGGCATCTG   CGGCT  GCG
                                |||||||||   |||||  |||
                                ACCGTGGAC   GTCGA  CGC
                                     CACC    A_
GAM2056  LOC196694 5'  TGGCGCCGCCGCGGCTACGCGC 50276     AT   ACAA
                                TGGC  CTG   CGGCTACGCGC
                                ||||  |||   ||||||||||
                                ACCG  GGC   GCCGATGCGCG
                                  C_  GGC_
GAM2056  LOC200300 5'  TGGCATCTGGGCTTGGCTGTGC 50277        ACAAC   AC
           G                     TGGCATCTG    GGCT  GCG
                                |||||||||    ||||  |||
                                ACCGTAGAC    CCGA  CGC
                                     CCGAA   CA
GAM2056  LOC200304 5'  TGGCATCTGGGCTTGGCTGTGC 50277        ACAAC   AC
           G                     TGGCATCTG    GGCT  GCG
                                |||||||||    ||||  |||
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                                ACCGTAGAC    CCGA  CGC
                                     CCGAA   CA
GAM2056  LOC257457 5'  TGCCATCTGACGATGGCGC   50278   G      AAC   TAC
                                TG CATCTGAC   GGC   GC
                                || ||||||||   |||   ||
                                AC GTAGACTG   CCG   CG
                                 G      CTA  ___
GAM2057  CREB1    3'  ATATAACTCAAGGGATTGG   50281       ATT_
                                ATATAGCT   GGATTGG
                                ||||||||   |||||||
                                TATATTGA   CCTAACC
                                     GTTC
GAM2057  FLJ13193  3'  CACCATGTAGACCAGGTTGG  50282      A  _  TT  A
                                TACCAT TAG CTA  GG TTGG
                                |||||| ||| |||  || ||||
                                GTGGTA ATC GGT  CC AACC
                                   C   T  __  _
GAM2057  KIAA1026  3'  TACCTGTAGCTATTTTTGGGC  50283     ATA      GGATT
                                TACC   TAGCTATT    GGC
                                ||||   ||||||||    |||
                                ATGG   ATCGATAA    CCG
                                  AC_      AAAC_
GAM2057  LEPROTL1  3'  ATATAGCTGGACTTGGC    50284       ATT    _
                                ATATAGCT   GGATT GGC
                                ||||||||   ||||| |||
                                TATATCGA   CCTGA CCG
                                     ___    A
GAM2057  NUDT11   3'  ATATAGCCTGTTGGC      50285       AT  GA
                                ATATAGCT  TG  TTGGC
                                ||||||||  ||  |||||
                                TATATCGG  AC  AACCG
                                     __  __
GAM2057  LOC221337 3'  TACCATATACTATTCTGCTTGG 50286       G    GGA_
            C                    TACCATATA CTATT    TTGGC
                                ||||||||| |||||    |||||
                                ATGGTATAT GATAA    AACCG
                                     _    GACG
GAM2058  STARD5   3'  GGGTAACAGGCAGATGGAGT   50289       C   CGAC
                                GGGTAATAG CGGA    GGAGT
                                ||||||||| ||||    |||||
                                CCCATTGTC GTCT    CCTCA
                                     C   A___
GAM2058  CPR2     3'  GGGTGGTGAAGACAACGATGGA 50290     AATAGCC     ___
            GT                   GGGT      GGACGAC   GGAGT
                                ||||      |||||||   |||||
                                CCCA      TCTGTTG   CCTCA
                                  CCACT__      CTA
GAM2058  PIP5K1C   3'  GGGTGATGAGTCGGAAACAAAG 50291     A  _  C   C
            TC                   GGGT AT AG CGGA GACGGAGTC
                                |||| || || |||| |||||||||
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                                CCCA TA TC GCCT TTGTTTCAG
                                  C  C  A   _
GAM2058  PPP1R10   3'  GGGTAATACTGGAAAGGGGT   50292        G C   C  C  A
                                GGGTAATA C GGA GA GG GT
                                |||||||| | ||| || || ||
                                CCCATTAT G CCT TT CC CA
                                    _ A   _  C  _
GAM2059  ANKRD3    3'  CATGTGGGCACGTGTGTGTGGT 50295      AAAC_       AT
           T                    CATGT    CGTGTGTGT  GTT
                                |||||    |||||||||  |||
                                GTACA    GCACACACA  CAA
                                   CCCGT       C_
GAM2059  BAT5      3'  CATGTAATGCAGGATGTATGTT 50296       AACC   ___
                                CATGTA   GTGT   GTGTATGTT
                                ||||||   ||||   |||||||||
                                GTACAT   TACG   TACATACAA
                                   _____   TCC
GAM2059  CYLC2     3'  TAAACTGTGTGTGTGTGT    50297      C       A
                                TAAAC GTGTGTGT TGT
                                ||||| |||||||| |||
                                ATTTG CACACACA ACA
                                   A       C
GAM2059  DJ971N18.2 3'  CATGTAAACCTGGCTGT     50298          G  TG
                                CATGTAAACC TG  TGT
                                |||||||||| ||  |||
                                GTACATTTGG AC  ACA
                                      _  CG
GAM2059  FLJ12707  3'  GTCTAGGCCGTGTGTGGCATA  50299    AAA__       _
                                GT    CCGTGTGTG TATG
                                ||    ||||||||| ||||
                                CA    GGCACACAC GTAT
                                 GATCC        C
GAM2059  FLJ14260  5'  TGTAAGTGCTTGTATGTT    50300      ACC    G
                                TGTAA   GTGT TGTATGTT
                                |||||   |||| ||||||||
                                ACATT   CACG ACATACAA
                                   ___    A
GAM2059  SEMA4G    3'  CATGTGTGATACAGGTGTGTGT 50301      AA___  C_
                                CATGT    AC  GTGTGTGT
                                |||||    ||  ||||||||
                                GTACA    TG  CACACACA
                                   CACTA  TC
GAM2059  SEMA4G    3'  CATGTGTGATACAGGTGTGTGT 50301      AA___  C_
                                CATGT    AC  GTGTGTGT
                                |||||    ||  ||||||||
                                GTACA    TG  CACACACA
                                   CACTA  TC
GAM2059  Spir-2    3'  ATATAGACTGTGTGTATA    50302      A  C
                                ATGTA AC GTGTGTGTA
                                ||||| || |||||||||
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                                TATAT TG CACACATAT
                                   C  A
GAM2059  LOC132235 5'  TGCGTGCGTGTGTGTGTGT   50303    AAAC       A
                                TGT   CGTGTGTGT TGT
                                |||   ||||||||| |||
                                ACG   GCACACACA ACA
                                  CAC_       C
GAM2059  LOC148603 3'  ATGTGTGTGTGTGTGTGTGTT  50304     AAACC      A
                                ATGT    GTGTGTGT TGTT
                                ||||    |||||||| ||||
                                TACA    CACACACA ACAA
                                  CACA_      C
GAM2059  LOC149111 3'  TATAAATAGCCTGTGTATGTTA 50305      CC  G
                                TGTAAA  GT TGTGTATGTTA
                                ||||||  || ||||||||||
                                ATATTT  CG ACACATACAAT
                                    AT  G
GAM2059  LOC149301 3'  ATGTAGACAGTGTGTGCACAT  50306      A  C
                                ATGTA AC GTGTGTGTATGT
                                ||||| || ||||||||||||
                                TACAT TG CACACACGTGTA
                                   C  T
GAM2059  LOC221766 3'  TGCAAGTGCGTGAGTGTGTGTT 50307      AC_   T   A
                                TGTAA   CGTG GTGT TGTT
                                |||||   |||| |||| ||||
                                ACGTT   GCAC CACA ACAA
                                   CAC    T    C
GAM2060  ABCC1    3'  TGTTTTGGTTGTCTGGGTTTGG 50310       CA_   AG__
                                TGTTTTGG   TCTG    TGG
                                ||||||||   ||||    |||
                                ACAAAACC   AGAC    ACC
                                     AAC    CCAA
GAM2060  ABCC1    3'  TGTTTTGGTTGTCTGGGTTTGG 50310       CA_   AG__
                                TGTTTTGG   TCTG    TGG
                                ||||||||   ||||    |||
                                ACAAAACC   AGAC    ACC
                                     AAC    CCAA
GAM2060  ABCC1    3'  TGTTTTGGTTGTCTGGGTTTGG 50310       CA_   AG__
                                TGTTTTGG   TCTG    TGG
                                ||||||||   ||||    |||
                                ACAAAACC   AGAC    ACC
                                     AAC    CCAA
GAM2060  RNTRE    3'  TGTTTTGGTATCTGTAGTG    50311       C    _
                                TGTTTTGG ATCTG AGTG
                                |||||||| ||||| ||||
                                ACAAAACC TAGAC TCAC
                                     A    A
GAM2060  LOC143677 5'  TGTTTTGGAATTTGAGTGCA   50312       C  C     G
                                TGTTTTGG AT TGAGTG CG
                                |||||||| || |||||| ||
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                                ACAAAACC TA ACTCAC GT
                                     T A     _
GAM2060  LOC167040 5'  TGTCTTGGCATTTGGGGTCGT  50313          C  AGT  CG
                                TGTTTTGGCAT TG   GG  CGT
                                |||||||||| ||   ||  |||
                                ACAGAACCGTA AC   CC  GCA
                                      A ___  CA
GAM2061  FER      5'  GGGACAAAGAAGATACTT    50316          AC
                                GGGACAAAGAA  TATTT
                                |||||||||||  |||||
                                CCCTGTTTCTT  ATGAA
                                      CT
GAM2061  GGCX     3'  CGGGCAAATTATTTTACC    50317      A    GAAAC
                                TGGG CAAA    TATTTTACC
                                |||| ||||    |||||||||
                                GCCC GTTT    ATAAAATGG
                                  _   A____
GAM2061  HOXC13   3'  TGGGGCAAAGGCAGCTCCCACC 50318      A    AAACTA
            T                    TGGG CAAAG     TTTTACCT
                                |||| |||||     ||||||||
                                ACCC GTTTC     AGGGTGGA
                                  C    CGTCG_
GAM2061  ARHGEF3  3'  GGACAAAGAGGTTACTAATCT  50319         A___   T
                                GGACAAAGA   ACTA TTT
                                |||||||||   |||| |||
                                CCTGTTTCT   TGAT AGA
                                     CCAA   T
GAM2061  FLJ10898 5'  GGAGAAATGACTTTACCT    50320     CAAA   CT
                                GGA   GAAA  ATTTTACCT
                                |||   ||||  |||||||||
                                CCT   CTTT  TGAAATGGA
                                  ____   AC
GAM2061  KIAA0869 3'  TGGAACAAAGGAAATACTT   50321          A  C
                                TGGGACAAAG AA TATTT
                                |||||||||| || |||||
                                ACCTTGTTTC TT ATGAA
                                     C  T
GAM2061  KIAA1724 3'  TGGGACAAAGAAAATTCT    50322           CT
                                TGGGACAAAGAAA  ATTTT
                                |||||||||||||  |||||
                                ACCCTGTTTCTTT  TAAGA
                                      __
GAM2061  MGC12981 3'  GGACAAAGGACCAATTACCT  50323         AA   TT
                                GGACAAAG  ACTA  TTACCT
                                ||||||||  ||||  ||||||
                                CCTGTTTC  TGGT  AATGGA
                                     C_   T_
GAM2061  MGC23937 3'  TGGGACAAAGAACTGACTCT  50324           A  _
                                TGGGACAAAGAA CT ATTTT
                                |||||||||||| || |||||
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                                ACCCTGTTTCTT GA TGAGA
                                      _ C
GAM2061  PRO0650   5'  TGAGACAACTATTTTAC     50325        AAGAA
                                TGGGACA    ACTATTTTAC
                                |||||||    ||||||||||
                                ACTCTGT    TGATAAAATG
                                     _____
GAM2061  LOC144932 3'  GGGACAAAGTTTGATTTTTACC 50326          AAACTA
           T                     GGGACAAAG     TTTTACCT
                                 |||||||||     ||||||||
                                 CCCTGTTTC     AAAATGGA
                                       AAACTA
GAM2061  LOC147639 5'  TGGAGCAAAGAAATAGCCGCCT 50327     GA       CTATT TA
                                TGG  CAAAGAAA    T  CCT
                                |||  ||||||||    |  |||
                                ACC  GTTTCTTT    G  GGA
                                  TC       ATC__ GC
GAM2061  LOC199958 3'  GGACAAAGACTAATTT      50328         AA   T
                                GGACAAAGA  CTA TTT
                                |||||||||  ||| |||
                                CCTGTTTCT  GAT AAA
                                     __   T
GAM2061  LOC202052 3'  TGGGATGAAGAAACTTTAC    50329       CA       ATT
                                TGGGA  AAGAAACT   TTAC
                                |||||  ||||||||   ||||
                                ACCCT  TTCTTTGA   AATG
                                   AC       ___
GAM2061  LOC221042 3'  TGGGAAAGAGGACATCTTAC   50330       CA    AAC
                                TGGGA  AAGA   TATTTTAC
                                |||||  ||||   ||||||||
                                ACCCT  TTCT   GTAGAATG
                                   __    CCT
GAM2061  LOC221576 3'  GGACAGAGAAATCCACTT     50331       A    _
                                GGACA AGAAA CTATTT
                                ||||| ||||| ||||||
                                CCTGT TCTTT GGTGAA
                                   C    A
GAM2061  LOC257515 3'  GGACAGAGAAATCCACTT     50331       A    _
                                GGACA AGAAA CTATTT
                                ||||| ||||| ||||||
                                CCTGT TCTTT GGTGAA
                                   C    A
GAM2061  LOC257572 3'  GGACAGAGAAATCCACTT     50331       A    _
                                GGACA AGAAA CTATTT
                                ||||| ||||| ||||||
                                CCTGT TCTTT GGTGAA
                                   C    A
GAM2061  LOC90787  5'  TGGGACTAGGGAGCCTCCTACC 50332        AAA_  AA  AT
           T                     TGGGAC    GA  CT  TTTACCT
                                 ||||||    ||  ||  |||||||
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                                ACCCTG   CT  GA  GGATGGA
                                   ATCC  CG  __
GAM2062  AGXT     5'  AACCTGGGGCTGCACTGG    50335        ACTAGA     C
                                GACCTGGG     TTGCAC GG
                                ||||||||     |||||| ||
                                TTGGACCC     GACGTG CC
                                     C_____     A
GAM2062  CASP7    5'  CTGGGACTGGCACAGTCGGC   50336        AGATT   ___
                                CTGGGACT    GCAC   CGGC
                                ||||||||    ||||  ||||
                                GACCCTGA    CGTG   GCCG
                                     C____    TCA
GAM2062  CXorf6   3'  GACCTGGGAACTGGCTGG    50337        CTAG   CACC
                                GACCTGGGA   ATTG   GG
                                |||||||||   ||||   ||
                                CTGGACCCT   TGAC   CC
                                     ____   CGA_
GAM2062  EPHA1    5'  GACCTGGGACCTGGGACAGTGG 50338         AGATT   CC
              C                  GACCTGGGACT    GCA  GGC
                                 ||||||||||    |||  |||
                                 CTGGACCCTGG    TGT  CCG
                                      ACCC_   CA
GAM2062  HIRA     3'  CCTGGGACTGCCTTGCTGGC   50339        AGA   ACC
                                CCTGGGACT   TTGC   GGC
                                |||||||||   ||||   |||
                                GGACCCTGA   AACG   CCG
                                     CGG    A__
GAM2062  HOXD4    5'  GAGCTGGGACTGGGCAAGCTGG 50340    C      AGATT_  ACC
              C                  GA CTGGGACT     GC   GGC
                                 || ||||||||     ||   |||
                                 CT GACCCTGA     CG   CCG
                                  C       CCCGTT  A__
GAM2062  MMP11    3'  CCTGGGACAGGATTGAGG    50341        TA    CACC
                                CCTGGGAC  GATTG    GG
                                ||||||||  |||||    ||
                                GGACCCTG  CTAAC    CC
                                     TC    T___
GAM2062  SIAT8E   3'  CCTTGGGTTAGATCTCTCGG   50342     _  AC     GCAC
                                CCT GGG  TAGATT    CGG
                                ||| |||  ||||||    |||
                                GGA CCC  ATCTAG    GCC
                                  A  A_     AGA_
GAM2062  TNFRSF10B 3'  GACCTGGGACCGGACTGGC    50343         TA    _
                                GACCTGGGAC  GATTG C
                                ||||||||||  ||||| |
                                CTGGACCCTG  CTGAC G
                                      GC    C
GAM2062  DKFZP586G1122 3'  GACCTGGGGCTAGGGCATGG   50344        A   ATT   CC
                                GACCTGGG CTAG   GCA  GG
                                |||||||| ||||   |||  ||
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                                CTGGACCC GATC   CGT  CC
                                     C    C__   A_
GAM2062  DOC-1R    5'  GACCCGGGGCTGGGCTGCCGG  50345        A  AGATT  A_
                                GACCTGGG CT     GC  CCGG
                                |||||||| ||     ||  ||||
                                CTGGGCCC GA     CG  GGCC
                                     C  CC___  AC
GAM2062  FLJ20234  3'  CCTGGGACTAGCCCGCTGG    50346          A    ACC
                                CCTGGGACTAG TTGC   GG
                                |||||||||| ||||   ||
                                GGACCCTGATC GGCG   CC
                                      G    A__
GAM2062  FLJ20378  5'  CCTGGGACGAGGCGGGGC     50347        T  ATT  ACC
                                CCTGGGAC AG   GC   GGC
                                |||||||| ||   ||   |||
                                GGACCCTG TC   CG   CCG
                                     C  ___  CC_
GAM2062  FLJ23058  3'  GACCTGGGATTGGGGTGCAGGG 50348         CTAGAT    CC
              C                  GACCTGGGA     TGCA  GGC
                                 |||||||||     ||||  |||
                                 CTGGACCCT     ACGT  CCG
                                      AACCCC    C_
GAM2062  HSA404617 5'  CCTGGGACCAGGCCGG      50349          ATTGCA
                                 CCTGGGACTAG     CCGG
                                 ||||||||||      ||||
                                 GGACCCTGGTC     GGCC
                                       C_____
GAM2062  KIAA1181  3'  TGGGACCAGATTGAGGGC     50350           CACC
                                 TGGGACTAGATTG    GGC
                                 ||||||||||||    |||
                                 ACCCTGGTCTAAC    CCG
                                       TC__
GAM2062  KIAA1511  3'  GACTTGGGTTGATCCTAACTGG 50351     C    ACTA    GC_  C
              C                  GAC TGGG    GATT   AC GGC
                                 ||| ||||    ||||   || |||
                                 CTG ACCC    CTAG   TG CCG
                                   A    AA__    GAT  A
GAM2062  KIAA1937  5'  CCTGGGACCAGCTCCTTTGCAT 50352          A____     C
              CGG                  CCTGGGACTAG     TTGCA CGG
                                   ||||||||||     ||||| |||
                                   GGACCCTGGTC     AACGT GCC
                                        GAGGA     A
GAM2062  LIN-28    3'  GACCTGGAGCTGCTGCTGG    50353        GA  AGA    ACC
                                 GACCTGG  CT   TTGC   GG
                                 |||||||  ||   ||||   ||
                                 CTGGACC  GA   GACG   CC
                                     TC  C__    A__
GAM2062  MGC20460  5'  GACCTGGAGGCTGCAAGGC   50354        GACT  AT    CC
                                 GACCTGG    AG  TGCA  GGC
                                 |||||||    ||  ||||  |||
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                                CTGGACC   TC  ACGT  CCG
                                    ____  CG   T_
GAM2062  MGC4737   3'  GACCTGGGCTGGATGGGC    50355       A  A   T_
                                GACCTGGG CT GAT  GC
                                |||||||| || |||  ||
                                CTGGACCC GA CTA  CG
                                    _  C   CC
GAM2062  LOC112868 5'  CCTGGGACAGTGCGGCTGGC   50356       T  AT   ACC_
                                CCTGGGAC AG  TGC   GGC
                                |||||||| ||  |||   |||
                                GGACCCTG TC  ACG   CCG
                                    _ __  CCGA
GAM2062  LOC148171 5'  GACCTGGGCCTGGGGAGCTTGG 50357       A  AGATT  ACC
           C                     GACCTGGG CT    GC   GGC
                                |||||||| ||    ||   |||
                                CTGGACCC GA    CG   CCG
                                    G  CCCCT  AA_
GAM2062  LOC149124 5'  GACCTGGGCCTGGGGAGCTTGG 50357       A  AGATT  ACC
           C                     GACCTGGG CT    GC   GGC
                                |||||||| ||    ||   |||
                                CTGGACCC GA    CG   CCG
                                    G  CCCCT  AA_
GAM2062  LOC201242 5'  GACTTGGATTGCCAGCACCGGC 50358    C   ACTAGATT
                                GAC TGGG       GCACCGGC
                                ||| ||||       ||||||||
                                CTG ACCT       CGTGGCCG
                                  A   AACGGT__
GAM2062  LOC220070 3'  GACCTGGGCTGACATTGG    50359       A  A   TGCACC
                                GACCTGGG CT GAT     GG
                                |||||||| || |||     ||
                                CTGGACCC GA CTG     CC
                                    _ _   TAA___
GAM2062  LOC221712 5'  GACCTGGGACTGGAGCTGG   50360        A  TT  ACC
                                GACCTGGGACT GA  GC   GG
                                |||||||||| ||  ||   ||
                                CTGGACCCTGA CT  CG   CC
                                      C  __  A__
GAM2062  LOC253181 5'  GACCTGGGCTGGGGGCCCGGC  50361       A  AGATT  A
                                GACCTGGG CT    GC CCGGC
                                |||||||| ||    || |||||
                                CTGGACCC GA    CG GGCCG
                                    _  CCCC_  _
GAM2062  LOC51112  5'  GACCTGGGGCGGTGTCCTGGC  50362       ACTAGAT  CA  _
                                GACCTGGG      TG  CC GGC
                                ||||||||      ||  || |||
                                CTGGACCC      AC  GG CCG
                                    CGCC___  A_  A
GAM2062  LOC90342  5'  GACCTGGGGCAGGCCCGAC   50363       AC   ATT  A
                                GACCTGGG  TAG   GC CCGGC
                                ||||||||  |||   || |||||
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                                CTGGACCC  GTC   CG GGCTG
                                    C_  ___  _
GAM2063  ATP5B    5'  GCACCAGAATCCAGTACT    50366          _
                                GCACCAGGATCCAG ACT
                                |||||||||||||| |||
                                CGTGGTCTTAGGTC TGA
                                      A
GAM2063  BACH2    3'  GCACTTGCATCAGACTGGT   50367     CAGG   C
                                GCAC    ATC AGACTGGT
                                ||||    ||| ||||||||
                                CGTG    TAG TCTGACCA
                                  AACG  _
GAM2063  DPYSL3   3'  CCAGGATCGAGAGAATC     50368       C   CT
                                CCAGGATC AGA  GGTC
                                |||||||| |||  ||||
                                GGTCCTAG TCT  TTAG
                                    C   C_
GAM2063  FBLN1    3'  ACCATCGTAACCAGACTGGTCC 50369     GGAT__
                                ACCA     CCAGACTGGTCC
                                ||||     ||||||||||||
                                TGGT     GGTCTGACCAGG
                                  AGCATT
GAM2063  FLRT2    3'  GCTACAACATCAGACTGGTCC  50370    AC   G   C
                                GC  CAG ATC AGACTGGTCC
                                ||  ||| ||| ||||||||||
                                CG  GTT TAG TCTGACCAGG
                                 AT   G   _
GAM2063  FOXO1A   3'  CACACCAGGATCTGAAAATC   50371          CA  CT
                                CGCACCAGGATC  GA  GGTC
                                ||||||||||||  ||  ||||
                                GTGTGGTCCTAG  CT  TTAG
                                      A_  T_
GAM2063  GRB10    3'  ACACTGATGGGACTGGTC    50372     CAG   CCA
                                GCAC   GAT   GACTGGTC
                                ||||   |||   ||||||||
                                TGTG   CTA   CTGACCAG
                                  A__   CC_
GAM2063  MAP1A    5'  ACCAGGATGATGGTC       50373        CCA  C
                                ACCAGGAT   GA TGGTC
                                ||||||||   || |||||
                                TGGTCCTA   CT ACCAG
                                    ___  _
GAM2063  MGA      3'  GCACCAGGAGGCTGGT      50374         TCCA A
                                GCACCAGGA    G CTGGT
                                |||||||||    | |||||
                                CGTGGTCCT    C GACCA
                                     _____ C
GAM2063  SLC17A4  3'  GCACCAGGATCTAGCACATC  50375          C  ACTG
                                GCACCAGGATC AG    GTC
                                |||||||||| ||    |||
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                                CGTGGTCCTAG TC   TAG
                                      A  GTG_
GAM2063  SLC2A3   3'  ACGATGTTGGCCAGACTGGTC  50376    CACCA  AT
                                ACG    GG  CCAGACTGGTC
                                |||    ||  ||||||||||
                                TGC    CC  GGTCTGACCAG
                                  TACAA  __
GAM2063  SLC38A3  5'  ACCACCAGGAGCACTGGTC   50377    G      TCCAG
                                AC CACCAGGA    ACTGGTC
                                || ||||||||    |||||||
                                TG GTGGTCCT    TGACCAG
                                 _      CG___
GAM2063  STAT1    5'  CGCGCAGGATCCGGAAGGGC   50378    AC      A  CT
                                CGC  CAGGATCC GA  GGT
                                |||  |||||||| ||  |||
                                GCG  GTCCTAGG CT  CCG
                                  C_      C  TC
GAM2063  STAT1    5'  CGCGCAGGATCCGGAAGGGC   50378    AC      A  CT
                                CGC  CAGGATCC GA  GGT
                                |||  |||||||| ||  |||
                                GCG  GTCCTAGG CT  CCG
                                  C_      C  TC
GAM2063  TBL2     3'  CGCACCAGGGTGGCGTGGTCC  50379        ATCCAGAC
                                CGCACCAGG      TGGTCC
                                |||||||||      ||||||
                                GCGTGGTCC      ACCAGG
                                     CACCGC__
GAM2063  UBE2V1   3'  GCACCGGATTCAAGGT     50380      A   C   ACT
                                GCACC GGAT CAG   GGT
                                ||||| |||| |||   |||
                                CGTGG CCTA GTT   CCA
                                   _   A  ___
GAM2063  UBE2V1   3'  GCACCGGATTCAAGGT     50380      A   C   ACT
                                GCACC GGAT CAG   GGT
                                ||||| |||| |||   |||
                                CGTGG CCTA GTT   CCA
                                   _   A  ___
GAM2063  C11orf21 3'  ACCAGGATTCACTGTCC     50381       C AG   G
                                ACCAGGAT C  ACTG TCC
                                |||||||| |  |||| |||
                                TGGTCCTA G  TGAC AGG
                                    A __   _
GAM2063  CECR7    5'  CGCCTCAGGATCCAGGGT    50382     AC       ACT
                                CGC  CAGGATCCAG   GGT
                                |||  ||||||||||   |||
                                GCG  GTCCTAGGTC   CCA
                                  GA        ____
GAM2063  DKFZP566B183 5'  GCGACCAGTCCAATCAGGCTGG 50383    _    GATC__   A
            TC                    GC ACCAG     CAG CTGGTC
                                  || |||||     ||| ||||||
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                                CG TGGTC     GTC GACCAG
                                 C    AGGTTA   C
GAM2063  FLJ10040  3' ACGTCCAGGATCTGGCC     50384     CA       CAGAC
                                ACG  CCAGGATC    TGGTC
                                |||  ||||||||    |||||
                                TGC  GGTCCTAG    ACCGG
                                 A_      _____
GAM2063  FLJ14326  3' ACCATTTTGACCAGACTGGTC  50385      GGAT__
                                ACCA     CCAGACTGGTC
                                ||||     ||||||||||
                                TGGT     GGTCTGACCAG
                                  AAAACT
GAM2063  FLJ21687  3' ACGCGCCGGATCCAGGTTGG   50386      A  A       AC
                                ACGC CC GGATCCAG  TGG
                                |||| || ||||||||  |||
                                TGCG GG CCTAGGTC  ACC
                                  C _       CA
GAM2063  FLJ23263  5' GCACCAGAAGGCTGGTC     50387         ATCC  A
                                GCACCAGG    AG CTGGTC
                                ||||||||    || ||||||
                                CGTGGTCT    TC GACCAG
                                     _____  C
GAM2063  GKAP42    5' CGCACTGGGCGTTGGGACTGGT 50388       CA  ATCCA_
           C                     CGCAC  GG     GACTGGTC
                                |||||  ||     ||||||||
                                GCGTG  CC     CTGACCAG
                                   AC  GCAACC
GAM2063  GMPPB     5' ACGGCCAGGATCACGTGGTCC  50389     CA       CAG  _
                                ACG  CCAGGATC   AC TGGTCC
                                |||  ||||||||   || ||||||
                                TGC  GGTCCTAG   TG ACCAGG
                                 C_       ___  C
GAM2063  KIAA0229  3' ACCCAATTCAGACTGGT     50390     A    GATC
                                GC CCAG    CAGACTGGT
                                || ||||    |||||||||
                                TG GGTT    GTCTGACCA
                                 _    AA__
GAM2063  KIAA1718  3' GCACCCCTAGACTGGTC     50391       AGGAT  _
                                GCACC    CC AGACTGGTC
                                |||||    || |||||||||
                                CGTGG    GG TCTGACCAG
                                   _____  A
GAM2063  KIAA1798  5' GCTCAGGATCCACGCCTTC    50392     AC       GA  GG
                                GC  CAGGATCCA  CT  TC
                                ||  |||||||||  ||  ||
                                CG  GTCCTAGGT  GG  AG
                                 A_       GC  A_
GAM2063  MAPK6     5' ACATTCAGTGTTGGACTGGTCC 50393     C_  GATCCA
                                GCA  CAG     GACTGGTCC
                                |||  |||     |||||||||
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                                TGT  GTC     CTGACCAGG
                                  AA   ACAAC_
GAM2063  MGC13251  3'  GCACCAGGGACTGGT      50394        ATCCA
                                GCACCAGG    GACTGGT
                                ||||||||    |||||||
                                CGTGGTCC    CTGACCA
                                          _____
GAM2063  NKIR      3'  GCACCAGTCCCCGGGTTGGTCC 50395       GA   AGAC
                                GCACCAG  TCC    TGGTCC
                                |||||||  |||    ||||||
                                CGTGGTC  GGG    ACCAGG
                                    AG   CCCA
GAM2063  PRAM-1    3'  CGCGCCGGGATCCAGGGCTCC  50396     A  A      ACT  _
                                CGC CC GGATCCAG   GG TCC
                                ||| || ||||||||   || |||
                                GCG GG CCTAGGTC   CC AGG
                                  C  C       ___  G
GAM2063  RES4-22   5'  GCACCAGAGACTGGTC      50397       GATCC
                                GCACCAG    AGACTGGTC
                                |||||||    |||||||||
                                CGTGGTC    TCTGACCAG
                                          _____
GAM2063  SES2      5'  CGCGCCAGGACCCGGT      50398     A       AGACT
                                CGC CCAGGATCC    GGT
                                ||| |||||||||    |||
                                GCG GGTCCTGGG    CCA
                                  C       _____
GAM2063  SH3BGRL2  3'  GCACCACTCGAGACTGGTC   50399       GGA  C
                                GCACCA   TC AGACTGGTC
                                ||||||   || |||||||||
                                CGTGGT   AG TCTGACCAG
                                   G__  C
GAM2063  Spir-2    3'  CCAGGATCTAGAACCTTC    50400        C   _  GG
                                CCAGGATC AGA CT  TC
                                |||||||| ||| ||  ||
                                GGTCCTAG TCT GG  AG
                                     A   T  A_
GAM2063  ZNF271    3'  ACGTATCCGGATCCAGTGTGGT 50401     CA_  A      AC
                                ACG   CC GGATCCAG  TGGT
                                |||   || ||||||||  ||||
                                TGC   GG CCTAGGTC  ACCA
                                  ATA  _       AC
GAM2063  LOC122609 3'  ACACACCAGGGCTGGT      50402          ATCCAGA
                                ACGCACCAGG      CTGGT
                                ||||||||||      |||||
                                TGTGTGGTCC      GACCA
                                      C_______
GAM2063  LOC126328 5'  ACGCGCCGGGGACCGGC     50403      A  A  ATCCA
                                ACGC CC GG    GACTGGT
                                |||| || ||    |||||||
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                                TGCG GG CC    CTGGCCG
                                  C  C _____
GAM2063  LOC143909 5'  GCCCGGGAGACTGGTC     50404    A  A   TCCA
                                GC CC GGA   GACTGGTC
                                || || |||   ||||||||
                                CG GG CCT   CTGACCAG
                                 _  C  ____
GAM2063  LOC147136 5'  CACCAGGATCTGGGCC     50405         CAGAC   T
                                CACCAGGATC    TGG CC
                                ||||||||||    ||| ||
                                GTGGTCCTAG    ACC GG
                                      _____  C
GAM2063  LOC148932 3'  GCGGTCAGGATCCCTGGT    50406    AC_      AGA
                                GC   CAGGATCC   CTGGT
                                ||   ||||||||  |||||
                                CG   GTCCTAGG   GACCA
                                 CCA      ___
GAM2063  LOC149301 5'  GCCCAGGATCTACCCTTC    50407    A      CAG   GG
                                GC CCAGGATC   ACT  TC
                                || ||||||||  |||  ||
                                CG GGTCCTAG   TGG  AG
                                 _      A__   GA
GAM2063  LOC149657 3'  ACGCGGCAGGATCCGGGAGGC  50408     AC       AGACT
                                ACGC  CAGGATCC    GGT
                                ||||  ||||||||    |||
                                TGCG  GTCCTAGG    CCG
                                  CC       CCCT_
GAM2063  LOC152402 5'  GCTGCCAGGATCTAGACT    50409    A_      C
                                GC  CCAGGATC AGACT
                                ||  |||||||| |||||
                                CG  GGTCCTAG TCTGA
                                 AC       A
GAM2063  LOC153577 5'  CGCTGGGATCCAGGCTTCC    50410     ACCA      A  GG
                                CGC   GGATCCAG CT  TCC
                                |||   |||||||| ||  |||
                                GCG   CCTAGGTC GA  AGG
                                  AC__       C  __
GAM2063  LOC157226 5'  ACCACCAGGATCTGTAAC    50411    G        CA_
                                AC CACCAGGATC   GAC
                                || ||||||||||   |||
                                TG GTGGTCCTAG   TTG
                                 _        ACA
GAM2063  LOC165552 3'  GCACGTTCCCGCCAGACTGGTC 50412      CAGGAT_
            C                    GCAC      CCAGACTGGTCC
                                ||||      ||||||||||||
                                CGTG      GGTCTGACCAGG
                                  CAAGGGC
GAM2063  LOC220021 3'  CCTCTGGATTCAGACTGGTCC  50413    A__    C
                                CC   GGAT CAGACTGGTCC
                                ||   |||| ||||||||||
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                                GG   CCTA GTCTGACCAGG
                                 AGA    A
GAM2063  LOC221410 3'  ACAGTGTGAGTTCAGACTGGTC 50414     CCAG  TC_
                                GCA    GA   CAGACTGGTC
                                |||    ||   ||||||||||
                                TGT    CT   GTCTGACCAG
                                  CACA  CAA
GAM2063  LOC221466 5'  GCTGGATCCAGCCAGCCTGGTC 50415    ACCA       A____
                                GC    GGATCCAG     CTGGTC
                                ||    ||||||||     ||||||
                                CG    CCTAGGTC     GACCAG
                                 A___       GGTCG
GAM2063  LOC91661  3'  GCACCAGGGACTGGT       50394         ATCCA
                                GCACCAGG     GACTGGT
                                ||||||||     |||||||
                                CGTGGTCC     CTGACCA
                                      _____
GAM2064  NEU1      3'  TGGTAAAGGGAAGGTGATTTT  50418    TC     A
                                TG  AAAGG GAAGGTGATTTT
                                ||  ||||| ||||||||||||
                                AC  TTTCC CTTCCACTAAAA
                                 CA    _
GAM2064  PTP4A2    3'  TATGTCAAAGGAAAAAGGT    50419             _
                                TATGTCAAAGGAGAA GGT
                                |||||||||||||| |||
                                ATACAGTTTCCTTTT CCA
                                        T
GAM2064  SLC2A2    3'  ATGTCAAAGGAGACGATTATTT 50420            A   G
              T                  ATGTCAAAGGAGA GGT ATTTT
                                |||||||||||| ||| |||||
                                TACAGTTTCCTCT CTA TAAAA
                                      G   A
GAM2064  FLJ12571  3'  TATGTCAAAGTAGAAGCTG    50421          G     G
                                TATGTCAAAG AGAAG TG
                                |||||||||| ||||| ||
                                ATACAGTTTC TCTTC AC
                                     A    G
GAM2064  MBLL39    3'  TGTCTTGGATATTGGTGATTTT 50422      AAA   GAA_
                                TGTC   GGA    GGTGATTTT
                                ||||   |||    |||||||||
                                ACAG   CCT    CCACTAAAA
                                  AA_   ATAA
GAM2064  METAP1    3'  TATGTAAAGGAGAGGTG     50423       C       A
                                TATGT AAAGGAGA GGTG
                                ||||| |||||||| ||||
                                ATACA TTTCCTCT CCAC
                                   _       _
GAM2064  SHARP     3'  TATGTCGGGGGATTTGATTTT  50424       AAA   GAAGG
                                TATGTC   GGA     TGATTTT
                                ||||||   |||     |||||||
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                                ATACAG   CCT    ACTAAAA
                                   CCC   AA___
GAM2064  LOC150054 5'  ATGTTAAAGGGGAGAACAATTT 50425     C    A  AG TG
              T                    ATGT AAAGG GA  G  ATTTT
                                   |||| ||||| ||  |  |||||
                                   TACA TTTCC CT  T  TAAAA
                                     A    C  CT GT
GAM2064  LOC166034 5'  TGTAAAGGAGAAGGGATTTT   50426    C        T
                                   TGT AAAGGAGAAGG GATTTT
                                   ||| |||||||||| ||||||
                                   ACA TTTCCTCTTCC CTAAAA
                                     _        _
GAM2065  ALS2     3'  CATGTAGCTGACATACCC    50429    _   __
                                   CA GTAG  GACATACCC
                                   || ||||  |||||||||
                                   GT CATC  CTGTATGGG
                                    A   GA
GAM2065  AXUD1    3'  CTCAGGTACAAGGTGTTCC   50430         GT   ACATA
                                   CTCAGGTACA  AGG    CC
                                   ||||||||||  |||    ||
                                   GAGTCCATGT  TCC    GG
                                         __  ACAA_
GAM2065  CLOCK    3'  CTCAGGTACATACATA      50431          GTAGG
                                   CTCAGGTACA    ACATA
                                   ||||||||||    |||||
                                   GAGTCCATGT    TGTAT
                                         A____
GAM2065  CUL3     3'  CTCAAGTATGGTAAAAGTGTCC 50432        CA     CATA
                                   CTCAGGTA  GTAGGA   CC
                                   ||||||||  ||||||   ||
                                   GAGTTCAT  CATTTT   GG
                                        AC     CACA
GAM2065  FUT8     3'  CTCAGATATAGGCAC       50433        ACA    A
                                   CTCAGGT   GTAGG CAT
                                   |||||||   ||||| |||
                                   GAGTCTA   TATCC GTG
                                        ___    _
GAM2065  GPM6B    3'  TCATGTACAGTAAGTCAT    50434     G        A
                                   TCA GTACAGTAGG CAT
                                   ||| ||||||||| |||
                                   AGT CATGTCATTC GTA
                                     A         A
GAM2065  MAGEA8   3'  TCAGGTACATAGGGTACAC   50435         G   AC
                                   TCAGGTACA TAGG  ATAC
                                   |||||||| ||||  ||||
                                   AGTCCATGT ATCC  TGTG
                                         _   CA
GAM2065  MYB      3'  GGTACAATAAATGTACC     50436          ACA
                                   GGTACAGTAGG   TACC
                                   ||||||||||   ||||
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                                CCATGTTATTT  ATGG
                                      AC_
GAM2065 NOS1    3' TCAGGTACATGGGCGTGGACCC 50437       GTA ACAT_
                                TCAGGTACA  GG   ACCC
                                |||||||||  ||   ||||
                                AGTCCATGT  CC   TGGG
                                     AC_ GCACC
GAM2065 SLC6A3  3' CCAGGGATAGGACATGCTCC  50438     TACA      AC_
                                TCAGG  GTAGGACAT  CC
                                |||||  |||||||||  ||
                                GGTCC  TATCCTGTA  GG
                                   C___      CGA
GAM2065 SPTBN1  5' CCAGGTACAGTCTGTCATGCC 50439        AGGA  A
                                TCAGGTACAGT   CAT CC
                                ||||||||||   ||| ||
                                GGTCCATGTCA   GTA GG
                                      GACA  C
GAM2065 TJP1    3' TCATGTACAGTAAGTCAT   50434    G      A
                                TCA GTACAGTAGG CAT
                                ||| |||||||||| |||
                                AGT CATGTCATTC GTA
                                  A        A
GAM2065 VMD2    3' TCAGGCTGTTGTAGGACAT   50440      ACA_
                                TCAGGT   GTAGGACAT
                                ||||||   |||||||||
                                AGTCCG   CATCCTGTA
                                    ACAA
GAM2065 WSX1    3' CTCAGGTAAGTGACTCAGCC  50441       C  AG  A  C
                                CTCAGGTA AGT  GAC TA CC
                                |||||||| |||  ||| || ||
                                GAGTCCAT TCA  CTG GT GG
                                     _  __  A  C
GAM2065 CL25084 3' TCAGGTACTAGAATTTACATA 50442       _ TAGG_
                                TCAGGTAC AG    ACATA
                                |||||||| ||    |||||
                                AGTCCATG TC    TGTAT
                                     A  TTAAA
GAM2065 COLEC12 3' CAGGTGTGGTGGCATACCCC  50443     ACA  A  A
                                CAGGT  GT GG CATACCCC
                                |||||  || || ||||||||
                                GTCCA  CA CC GTATGGGG
                                   CAC  _  _
GAM2065 CXorf9  3' CTCAGGCAGGTGGGATGTGCCC 50444       CA  A  CATA
                                CTCAGGTA  GT GGA   CCC
                                ||||||||  || |||   |||
                                GAGTCCGT  CA CCT   GGG
                                     C_  C  ACAC
GAM2065 FBXO27  3' CTCAGTACAGTAGGGCCC    50445     G      ACATA
                                CTCAG TACAGTAGG    CCC
                                ||||| |||||||||    |||
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                                GAGTC ATGTCATCC    GGG
                                  _       C____
GAM2065  FLJ20195  3'  CCCAGGTACGGTAGTCC    50446        A   GACATA
                                CTCAGGTAC GTAG     CC
                                |||||||||  ||||     ||
                                GGGTCCATG CATC     GG
                                     C    A_____
GAM2065  FLJ20511  3'  TCAGGTACTGTGTCAAGATGTG 50447       AG___    CATA
              CC                  TCAGGTAC    TAGGA   CC
                                |||||||||    |||||   ||
                                AGTCCATG    GTTCT   GG
                                    ACACA    ACAC
GAM2065  FLJ30663  3'  CTCAGGTACAGTGTAAGG    50448          ___
                                CTCAGGTACAGT   AGG
                                ||||||||||||   |||
                                GAGTCCATGTCA   TCC
                                       CAT
GAM2065  FRAG1     3'  AGGTATAGAACACCACC     50449     ACA       _
                                AGGT   GTAGGACAT ACC
                                ||||   |||||||||| |||
                                TCCA   TATCTTGTG TGG
                                  ___        G
GAM2065  KIAA1211  3'  GGCACAGTGATATCCC      50450        AG  C  A
                                GGTACAGT  GA AT CCC
                                ||||||||  || || |||
                                CCGTGTCA  CT TA GGG
                                    __  A  _
GAM2065  NUDE1     3'  CTCAAGTACTAGCCCAT     50451        AG   GA
                                CTCAGGTAC  TAG  CAT
                                |||||||||  |||  |||
                                GAGTTCATG  ATC  GTA
                                    __  GG
GAM2065  P24B      3'  CTCAGGTACAGAGAACCCC   50452         T    ATA
                                CTCAGGTACAG AGGAC   CCC
                                ||||||||||| |||||   |||
                                GAGTCCATGTC TCTTG   GGG
                                  _    ___
GAM2065  Spir-1    3'  TCAGATACGCACACAT      50453        A   GG
                                TCAGGTAC GTA  ACAT
                                |||||||| |||  ||||
                                AGTCTATG CGT  TGTA
                                    _  G_
GAM2065  LOC116150 3'  CTCAGGTATTAACCATGCCCC  50454       CAG   GA   A
                                CTCAGGTA   TAG  CAT CCCC
                                ||||||||   |||  ||| ||||
                                GAGTCCAT   ATT  GTA GGGG
                                    A__   G_   C
GAM2065  LOC125704 3'  CTCAGGCATACTCATACTCC   50455       CAGTAGGA    _
                                CTCAGGTA       CATAC CC
                                ||||||||       ||||| ||
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                                GAGTCCGT       GTATG GG
                                    ATGA____    A
GAM2065  LOC144453 3'  CTCAGGTACCAGTGGCAT    50456         _  A  A
                                CTCAGGTAC AGT GG CAT
                                ||||||||| ||| || |||
                                GAGTCCATG TCA CC GTA
                                   G  _ _
GAM2065  LOC145868 3'  CAGGTACAGCCGACCATGCCC  50457          A GA  A
                                CAGGTACAGT G  CAT CCC
                                |||||||||| |  ||| |||
                                GTCCATGTCG C  GTA GGG
                                    G TG  C
GAM2065  LOC152048 3'  CTCAGGTACGATGGCCGCC   50458         A  A  ACATA  _
                                CTCAGGTAC GT GG    CC CC
                                ||||||||| || ||    || ||
                                GAGTCCATG TA CC    GG GG
                                    C  _ _____  C
GAM2065  LOC152404 5'  CTCAGGACATGGCGTACTCC   50459       T  GTA  ACA  _
                                CTCAGG ACA  GG  TAC CC
                                |||||| |||  ||  ||| ||
                                GAGTCC TGT  CC  ATG GG
                                   _  A__  GC_  A
GAM2065  LOC58486  5'  CTCAGGTATGGTACACC    50460        CAGTA  AC
                                CTCAGGTA    GG  ATACC
                                ||||||||    ||  |||||
                                GAGTCCAT    CC  TGTGG
                                    A____  A_
GAM2065  LOC91689  3'  CTCAGGTATGGGGCAGAATCCC 50461        CA__     CATA
                                CTCAGGTA   GTAGGA   CCC
                                ||||||||   ||||||   |||
                                GAGTCCAT   CGTCTT   GGG
                                    ACCC    A___
GAM2066  FLG      3'  GACCTTTTTGCCTTTCAGTGC  50464       CTCCG  __   C
                                GACCTT    GCC  TCAG GC
                                ||||||    |||  |||| ||
                                CTGGAA    CGG  AGTC CG
                                   AAA__  AA   A
GAM2066  SCN3A    3'  TTGGGTTTCTCCTCAGCA    50465     ACC     GGCC
                                TTGG   TTCTCC   TCAGCG
                                ||||   ||||||   ||||||
                                AACC   AAGAGG   AGTCGT
                                  CA_    ____
GAM2066  FLJ11850  3'  TTGGACCTTCTCTGCTGGAGC  50466          CG  CTC
                                TTGGACCTTCTC  GC   AGC
                                ||||||||||||  ||   |||
                                AACCTGGAAGAG  CG   TCG
                                      A_  ACC
GAM2066  GNG11    5'  TTGGCTTTCTCCGGGACG    50467     ACC       CCTCA
                                TTGG   TTCTCCGG    GCG
                                ||||   ||||||||    |||
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                                AACC  AAGAGGCC    TGC
                                  GA_      C____
GAM2066 MGC13053 5' TGGACCTTCTCTGGAGGCG   50468         C  CCTCA
                                TGGACCTTCTC GG    GCG
                                |||||||||||  ||    |||
                                ACCTGGAAGAG CC    CGC
                                      A  TC___
GAM2066 NIFU    5' GACCTTCTCAAGATGGCGC   50469        C  CCTCA
                                GACCTTCTC GG    GCGC
                                |||||||||  ||    ||||
                                CTGGAAGAG TC    CGCG
                                     T  TAC__
GAM2066 PTPRT   3' TTGGACCTTCACTGGTTCTGGC 50470        TCC  CC  A_
                                TTGGACCTTC  GG  TC  GC
                                ||||||||||  ||  ||  ||
                                AACCTGGAAG  CC  AG  CG
                                      TGA  A_  AC
GAM2066 LOC256158 5' TTGGTCTTCTCCCCAACAGCG  50471     AC     GG  T_
                                TTGG  CTTCTCC  CC  CAGCG
                                ||||  |||||||  ||  |||||
                                AACC  GAAGAGG  GG  GTCGC
                                  A_      __  TT
GAM2067 GABRA1   5' TTGTCTATGTTATCATGGA   50474    C       _  AT
                                TTG TCTATGTTA CA  TGGG
                                |||  |||||||||  ||  ||||
                                AAC AGATACAAT GT  ACCT
                                  _       A  __
GAM2067 HHEX    3' TCTCTGCTTGAATTGGGA    50475    A   AC
                                TCT TGTT  AATTGGGA
                                |||  ||||  ||||||||
                                AGA ACGA  TTAACCCT
                                  G   AC
GAM2067 TMPRSS4  3' CTTGCTCTGTGTCTGACTTTGG 50476        A   ACAA_
             G                   CTTGCTCT TGTT    TTGGG
                                |||||||| ||||    |||||
                                GAACGAGA ACAG    AACCC
                                     C   ACTGA
GAM2067 FLJ13166 3' CTGCTCTCCTAATTGGGA    50477       ATGTTAC
                                TTGCTCT      AATTGGGA
                                |||||||      ||||||||
                                GACGAGA      TTAACCCT
                                    GGA____
GAM2067 IMAGE145052 3' ACTTGCTCTCATGTTGCTTTGG 50478         _    ACAA
                                ACTTGCTCT ATGTT   TTGG
                                |||||||||  |||||   ||||
                                TGAACGAGA TACAA   AACC
                                     G    CGA_
GAM2067 KIAA0820  3' ACTTGCTCTGCTGTCTGGG   50479         A_   ACAAT
                                ACTTGCTCT  TGTT    TGGG
                                |||||||||  ||||    ||||
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                                TGAACGAGA  ACAG    ACCC
                                     CG   _____
GAM2067  KIAA1023  3'  CTGCTTTTGTAATTGGG    50480      CTA   TAC
                                TTGCT   TGT   AATTGGG
                                |||||   |||   |||||||
                                GACGA   ACA   TTAACCC
                                   AA_   ___
GAM2067  KIAA1870  5'  ACTTGCCTATGTTGCTACTGGG 50481       T      ACA
              A                  ACTTGC CTATGTT   ATTGGGA
                                |||||| |||||||   |||||||
                                TGAACG GATACAA   TGACCCT
                                   _      CGA
GAM2067  MGC5338   5'  CTTGCTCTAAGCTTGGG    50482         T  TACAA
                                CTTGCTCTA GT     TTGGG
                                ||||||||| ||     |||||
                                GAACGAGAT CG     AACCC
                                     T  _____
GAM2067  LOC145463 3'  ACTTGCTCTCATGTTGCTTTGG 50478          _    ACAA
                                ACTTGCTCT ATGTT    TTGG
                                ||||||||| |||||    ||||
                                TGAACGAGA TACAA    AACC
                                     G    CGA_
GAM2067  LOC146880 3'  TTGCCCTATGTGATGCCCGGTT 50483           TACAA____
              GGGA                 TTGCTCTATGT        TTGGGA
                                ||||||||||         ||||||
                                AACGGGATACA        AACCCT
                                     CTACGGGCC
GAM2067  LOC154222 3'  CTTGCTCTAGACTAAATAGTTG 50484          TG   CAA__
              GG                   CTTGCTCTA  TTA     TTGGG
                                |||||||||  |||     |||||
                                GAACGAGAT  GAT     AACCC
                                     CT   TTATC
GAM2067  LOC155179 3'  CTGCTTTTGTAATTGGG    50480      CTA   TAC
                                TTGCT   TGT   AATTGGG
                                |||||   |||   |||||||
                                GACGA   ACA   TTAACCC
                                   AA_   ___
GAM2067  LOC197053 3'  TTACTGCATTGTAATTGGGA   50485      C   GTTAC
                                TTGCT TAT     AATTGGGA
                                ||||| |||     ||||||||
                                AATGA GTA     TTAACCCT
                                   C   ACA__
GAM2067  LOC85569  3'  GCTCGTGTTATAATTGGG    50486      TA    C
                                GCTC  TGTTA AATTGGG
                                ||||  ||||| |||||||
                                CGAG  ACAAT TTAACCC
                                   C_     A
GAM2068  CORO1C    3'  ATAATATCTTATCTTCATTTA  50489          CTAAA
                                ATAATATCTT     TCATTTA
                                ||||||||||     |||||||
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                                TATTATAGAA     AGTAAAT
                                     TAGA_
GAM2068  ZNF140    3'  TATAACATTTTCTGAATTCACT 50490         C    _  A
              TAA                    TATAATAT TTCT AA TCATTTAA
                                     |||||||| |||| || ||||||||
                                     ATATTGTA AAGA TT AGTGAATT
                                          A    C  A
GAM2068  CHUK      3'  ATAATATCTTCTAAATTACTTA 50491               C
                                     ATAATATCTTCTAAAT ATTTA
                                     |||||||||||||||| |||||
                                     TATTATAGAAGATTTA TGAAT
                                               A
GAM2068  DKFZp761B1514 3'  TATAATTCTTCTAAATATCATT 50492        A       __
              T                      TATAAT TCTTCTAA  ATCATTT
                                     |||||| ||||||||  |||||||
                                     ATATTA AGAAGATT  TAGTAAA
                                        _       TA
GAM2068  LEC3      3'  TACAATATCTTCTAAATC     50493
                                     TATAATATCTTCTAAATC
                                     ||||||||||||||||||
                                     ATGTTATAGAAGATTTAG

GAM2068  SCOP      3'  TACAATATTATTAAATCATTTA 50494         CTTC
                                     TATAATAT    TAAATCATTTA
                                     ||||||||    ||||||||||
                                     ATGTTATA    ATTTAGTAAAT
                                          ATA_
GAM2069  HIP2      3'  TTCATATTTAAGAATTCT     50497           _
                                     TTCATATTTAA AATTCT
                                     |||||||||| ||||||
                                     AAGTATAAATT TTAAGA
                                           C
GAM2069  HARC      3'  TTCATACTTGATTCCAAAATTG 50498          AAA       _
              A                       TTCATATTT   ATTCTAAA TTGA
                                     |||||||||   |||||||| ||||
                                     AAGTATGAA   TAAGGTTT AACT
                                          C__        T
GAM2069  KIAA1678  3'  TTCACATTTAAAATTACT     50499             _
                                     TTCATATTTAAAATT CT
                                     |||||||||||||| ||
                                     AAGTGTAAATTTTAA GA
                                               T
GAM2069  PAIP1     3'  TTCATATTTGAAATTCAATTCA 50500          A      TAA__
              TTG                      TTCATATTT AAATTC     ATTG
                                     ||||||||| ||||||     ||||
                                     AAGTATAAA TTTAAG     TAAC
                                          C      TTAAG
GAM2069  SV2       3'  TTCATATTTGCAGCCCAAATTG 50501          AAAAT
              A                       TTCATATTT     TCTAAATTGA
                                     |||||||||     ||||||||||
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                                AAGTATAAA    GGGTTTAACT
                                     CGTC_
GAM2069  LOC54499  3'  TACATAAAATTCTAAGTTGA  50502    T        A
                                TAT TAAAATTCTAA TTGA
                                ||| |||||||||| ||||
                                ATG ATTTTAAGATT AACT
                                  T         C
GAM2069  LOC56267  3'  TTCATCTTAAGTTCTAAATTGA 50503     A    AA
                                TTCAT TTTAA  TTCTAAATTGA
                                ||||| |||||  ||||||||||
                                AAGTA GAATT  AAGATTTAACT
                                   _    C_
GAM2069  LOC91813  5'  TTCATCTTTAAAATTCCA    50504     A
                                TTCAT TTTAAAATTCTA
                                ||||| ||||||||||
                                AAGTA AAATTTTAAGGT
                                   G
GAM2070  GNE       3'  TTAATACATTAGTAAGCAGAGT 50507       T       ATC
                T                TTAATAC ATTAGTAAG   AGTT
                                ||||||| |||||||||   ||||
                                AATTATG TAATCATTC   TCAA
                                    _       GTC
GAM2070  MS4A1     3'  TTAATGTATTAGTCAACCAGTT 50508     AC      AA
                                TTAAT  TATTAGT  GATCAGTT
                                |||||  |||||||  ||||||||
                                AATTA  ATAATCA  TTGGTCAA
                                   C_     G_
GAM2070  POLS      3'  TTAGTACAGGCCTACAGATCAG 50509    A   TATTAGTA
                TT                TTA TAC       AGATCAGTT
                                ||| |||       |||||||||
                                AAT ATG       TCTAGTCAA
                                  C   TCCGGATG
GAM2070  SUN1      3'  TTAATACTATTCCTGTCAGTT  50510         AGTAAGA
                                TTAATACTATT      TCAGTT
                                ||||||||||      ||||||
                                AATTATGATAA      AGTCAA
                                      GGAC___
GAM2070  LOC90155  3'  TTAGTACTATTAGTTAGAT   50511    A        A
                                TTA TACTATTAGT AGAT
                                ||| |||||||||| ||||
                                AAT ATGATAATCA TCTA
                                  C         A
GAM2071  EIF2C1    3'  GTCACATGAGACACCTGT    50514        CCA    C
                                GTCACGTGA   ACACC GT
                                |||||||||   ||||| ||
                                CAGTGTACT   TGTGG CA
                                      C__     A
GAM2071  NXF2      3'  TATGTCACGTGGCCTGCA    50515         A  AA
                                TATGTCACGTG CC  CA
                                |||||||||| ||  ||
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                                ATACAGTGCAC GG  GT
                                      C  AC
GAM2071 NXF2     3'  TATGTCACGTGGCCTGCA    50515          A  AA
                                TATGTCACGTG CC  CA
                                |||||||||||  ||  ||
                                ATACAGTGCAC GG  GT
                                      C  AC
GAM2071 ZNF267   3'  TATGCCACATTCTTAACATTTG 50516         GACC   CCC
             TA                   TATGTCACGT   AACA  GTA
                                |||||||||    ||||  |||
                                ATACGGTGTA   TTGT  CAT
                                     AGAA   AAA
GAM2071 KIAA0632 3'  TGTCCTCACCAACACCTGT   50517     ACGTG       C
                                TGTC    ACCAACACC GT
                                ||||    ||||||||| ||
                                ACAG    TGGTTGTGG CA
                                  GAG__       A
GAM2071 LOC125704 3'  TATATACACATGCTGACACCCG 50518      _     ACCA
             T                   TATGT CACGTG   ACACCCGT
                                ||||| ||||||   ||||||||
                                ATATA GTGTAC   TGTGGGCA
                                   T    GAC_
GAM2072 DVL3     3'  TACGGAACTGTCCATAGAGAT  50521    TA      ___ _
                                TA  GAACTGTC   AG GAT
                                ||  ||||||||   || |||
                                AT  CTTGACAG   TC CTA
                                 GC       GTA  T
GAM2072 GARP     3'  TATAAAACGGGGATAAAATAT  50522        TGTCA
                                TATAGAAC    GGATAAAATAT
                                ||||||||    ||||||||||
                                ATATTTTG    CCTATTTTATA
                                     CC___
GAM2072 MYO10    3'  AAACTTGGGATAAAATAT    50523      GTCA
                                GAACT   GGATAAAATAT
                                |||||   ||||||||||
                                TTTGA   CCTATTTTATA
                                   AC__
GAM2072 CCNG2    3'  TATAAGAAAATGCGGATAAAAT 50524     _  C_  CA
             AT                   TATA GAA  TGT  GGATAAAATAT
                                |||| |||  |||  ||||||||||
                                ATAT CTT  ACG  CCTATTTTATA
                                  T  TT  __
GAM2072 FAM8A1   3'  CATAGAACTATATAAAATAT  50525         CAGG
                                TATAGAACTGT   ATAAAATAT
                                ||||||||||   |||||||||
                                GTATCTTGATA   TATTTTATA
                                      ____
GAM2072 FLJ22643 3'  TATAAGGCTGTCAAACTAAAA  50526      AA      A
                                TATAG  CTGTCAGG TAAAA
                                |||||  |||||||| |||||
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                                ATATT  GACAGTTT ATTTT
                                   CC       G
GAM2072  FLJ23790  5'  TATACAACTGTCATCAGATA   50527      G       __
                                TATA AACTGTCA  GGATA
                                |||| ||||||||  |||||
                                ATAT TTGACAGT  TCTAT
                                   G       AG
GAM2072  FLJ25082  3'  TGAGAACCCAGGATAAA     50528    T     GT
                                A AGAACT  CAGGATAAA
                                | ||||||  |||||||||
                                A TCTTGG  GTCCTATTT
                                 C     __
GAM2072  KIAA0373  5'  TATAGAACTATTCAAAGATA   50529           _  _
                                TATAGAACTGT CAG GATA
                                |||||||||||| ||| ||||
                                ATATCTTGATA GTT CTAT
                                        A   T
GAM2072  KIAA1598  3'  TAAGAACTCTGATAAAATA    50530    T     GTCAG
                                A AGAACT    GATAAAATA
                                | ||||||     |||||||||
                                A TCTTGA    CTATTTTAT
                                 T     GA___
GAM2072  LOC149705 3'  GAAACCAGGATGAAATAT     50531      CTG       A
                                GAA   TCAGGAT AAATAT
                                |||   ||||||| ||||||
                                CTT   GGTCCTA TTTATA
                                  T__       C
GAM2072  LOC202316 3'  TATAGAACATCCAAAATAAGAT 50532          TG        A
              AT                  TATAGAAC  TCAGGATAA ATAT
                                |||||||||  ||||||||| ||||
                                ATATCTTG  GGTTTTATT TATA
                                     TA        C
GAM2072  LOC257319 3'  TAGAAATGTGGATAAAAT     50533       C   CA
                                TAGAA TGT  GGATAAAAT
                                ||||| |||  |||||||||
                                ATCTT ACA  CCTATTTTA
                                   T  __
GAM2073  EIF2S3    3'  TATTTGTCCATGGGAACAA    50536      G       TGTAT
                                TATT TGTCCATG    CAA
                                |||| ||||||||    |||
                                ATAA ACAGGTAC     GTT
                                  _       CCTT_
GAM2073  GALNT3    3'  TATTGTGTTTTCCACATA     50537        ___
                                TATTGTG   TCCATGTG
                                |||||||   ||||||||
                                ATAACAC   AGGTGTAT
                                    AAA
GAM2073  HTR2C     3'  TACTGTGTTTATATGTGTA    50538         CC__
                                TATTGTGT    ATGTGTA
                                ||||||||    |||||||
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                                ATGACACA    TACACAT
                                    AATA
GAM2073  IGF1R    3'  TATTGTGTCCAGTTCCCCCAAA 50539          T  GTA_
             TA                   TATTGTGTCCA GT    TCAAATA
                                  ||||||||||| ||    |||||||
                                  ATAACACAGGT CA    GGTTTAT
                                        _  AGGG
GAM2073  MADH4    3'  TATTGTGTCTGTGGTACAGTCA 50540         CA  T  ___
             A                    TATTGTGTC  TG GTA   TCAA
                                  |||||||||  || |||   ||||
                                  ATAACACAG  AC CAT   AGTT
                                       AC  _   GTC
GAM2073  DKFZp761D0614 3'  TATTGTATTCACTTTTGTCAAA 50541         C   GTGTA
             TA                   TATTGTGT CAT    TCAAATA
                                  ||||||||| |||    |||||||
                                  ATAACATA GTG    AGTTTAT
                                       A   AAAAC
GAM2073  FLJ13114  3'  TATTGTGCTGATGAGTCAAAT  50542         CCAT   TA
                                  TATTGTGT    GTG  TCAAAT
                                  ||||||||    |||  ||||||
                                  ATAACACG    TAC  AGTTTA
                                       AC__   TC
GAM2073  HEMK     3'  TTGGTCCCATGCATCA      50543     T    A
                                  TTG GTCC TGTGTATCA
                                  ||| |||| |||||||||
                                  AAC CAGG GTACGTAGT
                                    _   _
GAM2073  LANO     3'  TATTGTGGTTGTATATC     50544        TCCA
                                  TATTGTG    TGTGTATC
                                  |||||||    ||||||||
                                  ATAACAC    ACATATAG
                                      CA__
GAM2073  PRO2831   5'  TGTGTCTGGTGGTAATCAAATA 50545       CAT   T__
                                  TGTGTC   GTG   ATCAAATA
                                  ||||||   |||   ||||||||
                                  ACACAG   CAC   TAGTTTAT
                                     AC_   CAT
GAM2073  LOC149332 3'  TTGTGTCCGTGTGTACCCAAT  50546        A       A
                                  TTGTGTCC TGTGTATC AAT
                                  |||||||| |||||||| |||
                                  AACACAGG ACACATGG TTA
                                       C       G
GAM2073  LOC255104 3'  CATTGTGTCTGTGTGACTCA   50547         CA    TA
                                  TATTGTGTC  TGTG  TCA
                                  |||||||||  ||||  |||
                                  GTAACACAG  ACAC  AGT
                                       AC    TG
GAM2073  LOC90494  5'  TATTGTGCTATCAAA       50548         CCATGTG
                                  TATTGTGT      TATCAAA
                                  ||||||||      |||||||
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                                ATAACACG      ATAGTTT
                                        ________
GAM2074 BAT4     5' GGTTAGGAAAGGCCCTCAG   50551        TC_
                                GGTTAGGAG   CCCTCAG
                                |||||||||   |||||||
                                CCAATCCTT   GGGAGTC
                                     TCC
GAM2074 PPP2R5A  5' GCCATCGCGGGTCCCCTC    50552    G   A_ A
                                GC GTT  GG GTCCCCTC
                                || |||  || ||||||||
                                CG TAG  CC CAGGGGAG
                                 G   CG _
GAM2074 TAL1     5' TACGCGGTTGCCTCCTCA    50553        AGGA   C
                                TACGCGGTT    GTC CCTCA
                                |||||||||    ||| |||||
                                ATGCGCCAA    CGG GGAGT
                                     _____   A
GAM2074 ESPL1    5' GCTGGTTGCAAGCCCTCAG   50554    _   AG   TC
                                GC GGTT  GAG  CCCTCAG
                                || ||||  |||  |||||||
                                CG CCAA  TTC  GGGAGTC
                                 A   CG   __
GAM2074 FLJ10094 5' TGAGTGCAGGGTCCCCTC    50555    C   _    A
                                G GGT TAGG GTCCCCTC
                                | ||| |||| ||||||||
                                A TCA GTCC CAGGGGAG
                                 C   C   _
GAM2074 KHDRBS3  5' CGCGGTTAGGCGGGCCCTC   50556         AGTC
                                CGCGGTTAGG    CCCTC
                                ||||||||||    |||||
                                GCGCCAATCC    GGGAG
                                      GCCC
GAM2074 PALM     3' GCGGGGTGTCCCCTCA      50557      TTA  A
                                GCGG   GG GTCCCCTCA
                                ||||   || |||||||||
                                CGCC   CC CAGGGGAGT
                                  ___  A
GAM2074 PRO2289  3' ACGCGGTCTCCATCCTCTC   50558        AGGA   C
                                ACGCGGTT    GTCC CTC
                                ||||||||    |||| |||
                                TGCGCCAG    TAGG GAG
                                     AGG_    A
GAM2074 ZIN      3' CGAGGCTGGGAGTCCCCTCAG 50559    C    A
                                CG GGTT GGAGTCCCCTCAG
                                || |||| ||||||||||||
                                GC CCGA CCTCAGGGGAGTC
                                 T   C
GAM2074 LOC90529 3' GCGCTTCAGGAGTCCCTTCAG 50560     G_         C
                                GCG  TTAGGAGTCCC TCAG
                                |||  |||||||||| ||||
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                                CGC  AGTCCTCAGGG AGTC
                                  GA         A
GAM2075  AR       3'  GGCTGGCACAGAGTA       50563          C  AAT
                                GGCTGGCACA GG   GTA
                                |||||||||| ||   |||
                                CCGACCGTGT CT   CAT
                                        _ ____
GAM2075  CTSD     3'  GGACGGCCTGGTGTGGGGTAG  50564        _  CACAC  AAT
                                GGACGGC TGG    GG   GTAG
                                ||||||| |||    ||   ||||
                                CCTGCCG ACC    CC   CATC
                                    G   ACA__  C__
GAM2075  FLJ14525 3'  GGAGGCTGGCACATGATGT   50565     C        CG  A
                                GGA GGCTGGCACA  GA TGT
                                ||| ||||||||||  || |||
                                CCT CCGACCGTGT  CT ACA
                                  _        A_  _
GAM2075  FLJ22056 3'  GGAGGCTGGCACGTGCA     50566     C        ACGGAA
                                GGA GGCTGGCAC     TGTA
                                ||| |||||||||      ||||
                                CCT CCGACCGTG     ACGT
                                  _       C_____
GAM2075  KIAA0705 5'  GGACGGCTGGGCAGAGGTA   50567          CACA    AT
                                GGACGGCTGG   CGGA  GTA
                                ||||||||||   ||||  |||
                                CCTGCCGACC   GTCT  CAT
                                       C___   C_
GAM2075  KIAA1858 3'  GGAGGCTGGCATGACCCTGT   50568     C       CAC  AA_
                                GGA GGCTGGCA   GG   TGT
                                ||| ||||||||   ||   |||
                                CCT CCGACCGT   CT   ACA
                                  _      A__  GGG
GAM2075  RAB1B    3'  GGACGGCTCGAGCTGGGAGTGT 50569         __  ACAC   A
              AG                  GGACGGCT  GGC    GGA TGTAG
                                ||||||||  |||    ||| |||||
                                CCTGCCGA  TCG    CCT ACATC
                                     GC   AC__   C
GAM2075  LOC145540 5'  GACGGTGGCGGGATGTA     50570       C   ACAC  A
                                GACGG TGGC    GG ATGTA
                                ||||| ||||    || |||||
                                CTGCC ACCG    CC TACAT
                                  _   _____  C
GAM2075  LOC151150 3'  AGATGGCTGGCATGTAAATG   50571     C       CACG
                                GGA GGCTGGCA    GAATG
                                ||| ||||||||    |||||
                                TCT CCGACCGT    TTTAC
                                  A       ACA_
GAM2075  LOC200860 3'  GGAGGCTGGGGAATGT      50572     C     CACAC
                                GGA GGCTGG    GGAATGT
                                ||| ||||||    |||||||
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                                CCT CCGACC    CCTTACA
                                  _    _____
GAM2076 GLI2     5' CACGGGGTTGATGGGGTGGGG 50575    T     TAT  AC
                                CAC GGGTTGA  TGG  TGGGG
                                ||| |||||||  |||  |||||
                                GTG CCCAACT  ACC  ACCCC
                                  C     ___  CC
GAM2076 KCNE1L   3' CACTGGGATGAAAACTGGG   50576      T  TATT
                                CACTGGG TGA   GGACTGGG
                                ||||||| |||   ||||||||
                                GTGACCC ACT   TTTGACCC
                                    T  ____
GAM2076 MEF2B    5' CTGGGTTGGCGGAGGCTGGGG 50577       ATATT A
                                CTGGGTTG    GG CTGGGG
                                ||||||||    || ||||||
                                GACCCAAC    CC GACCCC
                                     CGCCT _
GAM2076 SLC39A4  3' ACTGGAGTTGGGACTGGG    50578     _  ATATT
                                ACTGG GTTG    GGACTGGG
                                ||||| ||||    ||||||||
                                TGACC CAAC    CCTGACCC
                                  T  _____
GAM2076 SLC39A4  3' ACTGGAGTTGGGACTGGG    50578     _  ATATT
                                ACTGG GTTG    GGACTGGG
                                ||||| ||||    ||||||||
                                TGACC CAAC    CCTGACCC
                                  T  _____
GAM2076 TIMP3    5' CTGGGTTGGACATGACTGGGG 50579       _  TG
                                CTGGGTTG ATAT  GACTGGGG
                                |||||||| ||||  ||||||||
                                GACCCAAC TGTA  CTGACCCC
                                     C  __
GAM2076 TNFRSF10B 3' CACTGGGTGATGTTGGATGGG 50580       T  A   C
                                CACTGGGT GAT TTGGA TGGG
                                |||||||| ||| ||||| ||||
                                GTGACCCA CTA AACCT ACCC
                                     _  C   _
GAM2076 AGPAT1   3' CACTGGGTGGGTAGGTGTGGGG 50581       TGATATT  AC
                                CACTGGGT     GG  TGGGG
                                ||||||||     ||  |||||
                                GTGACCCA     CC  ACCCC
                                     CCCAT__  AC
GAM2076 AGPAT1   3' CACTGGGTGGGTAGGTGTGGGG 50581       TGATATT  AC
                                CACTGGGT     GG  TGGGG
                                ||||||||     ||  |||||
                                GTGACCCA     CC  ACCCC
                                     CCCAT__  AC
GAM2076 FLJ32670 3' CACTGGGTTTATTGAAACTGGG 50582       GA     _
             G                   CACTGGGTT  TATTGGA CTGGGG
                                 |||||||||  ||||||| ||||||
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                                GTGACCCAA  ATAACTT GACCCC
                                    __      T
GAM2076  KIAA0630  3'  GCTTATTGGACTGGGG     50583     GA
                                GTT  TATTGGACTGGGG
                                |||  ||||||||||||
                                CGA  ATAACCTGACCCC
                                  __
GAM2076  KIAA1388  3'  ACTGGGTTGAGCTGACTGGGG  50584         TATTG
                                ACTGGGTTGA    GACTGGGG
                                ||||||||||    ||||||||
                                TGACCCAACT    CTGACCCC
                                     CGA__
GAM2076  KIAA1904  3'  CACTGGGCTGGGAAGTTGGGG  50585         ATATT   C__
                                CACTGGGTTG    GGA   TGGGG
                                ||||||||||    |||   |||||
                                GTGACCCGAC    CCT   ACCCC
                                     ______   TCA
GAM2076  TJP4      5'  CTGGGGTTGGACTGGG      50586      TTGATA
                                CTGGG     TTGGACTGGG
                                |||||     ||||||||||
                                GACCC     AACCTGACCC
                                  C_____
GAM2076  LOC115861 5'  CTGGGTTGGGTGCTGGG     50587        ATATT  A_
                                CTGGGTTG    GG  CTGGG
                                ||||||||    ||  |||||
                                GACCCAAC    CC  GACCC
                                     ______  AC
GAM2076  LOC144347 3'  CTGGGCTGCCCCAGGCTGGGG  50588         ATA TG A
                                CTGGGTTG   T  G CTGGGG
                                ||||||||   |  | ||||||
                                GACCCGAC   G  C GACCCC
                                    GG_ GT C
GAM2076  LOC144817 3'  CATAGGGTTTCTAAGGACTGGG 50589    CT    GA  TT
            G                    CA  GGGTT  TA  GGACTGGGG
                                 ||  |||||  ||  |||||||||
                                 GT  CCCAA  AT  CCTGACCCC
                                  AT    AG  T_
GAM2076  LOC148085 3'  CACAGGGTTGATTGATCAGTTG 50590     T      __  TG AC
            GGG                    CAC GGGTTGAT  AT  G  TGGGG
                                   ||| ||||||||  ||  |  |||||
                                   GTG CCCAACTA  TA  C  ACCCC
                                     T       AC  GT A_
GAM2076  LOC148764 5'  TGGGTATTCTGTGGACTGGGG  50591      TGATAT
                                TGGGT     TGGACTGGGG
                                |||||     ||||||||||
                                ACCCA     ACCTGACCCC
                                  TAAGAC
GAM2076  LOC149345 3'  GGGTTGTAGACTGGG       50592       ATAT
                                GGGTTG    TGGACTGGG
                                ||||||    |||||||||
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                              CCCAAC   ATCTGACCC
                                   ____
GAM2077 ABCE1   3' TAAGTGCACAGAAAAAAGCA  50595       AAA  TT
                              TAAGTGCA  AAA AGCA
                              ||||||||  ||| ||||
                              ATTCACGT  TTT TCGT
                                   GTC  TT
GAM2077 ATP6V0E 3' AAGTGCAAAAAAGGCAAA   50596         ATTA
                              AAGTGCAAAAAA   GCAAA
                              ||||||||||||   |||||
                              TTCACGTTTTTT   CGTTT
                                    C___
GAM2077 COX11   3' TAAGTGAAAAAAATTAG    50597      C
                              TAAGTG AAAAAAATTAG
                              |||||| ||||||||||
                              ATTCAC TTTTTTTAATC
                                   _
GAM2077 EMX2    3' AAGTGCAAAAAACAAAAA   50598        AATTA
                              AAGTGCAAAAA   GCAAAAG
                              ||||||||||    |||||||
                              TTCACGTTTTT   TGTTTTT
                                   _____
GAM2077 BCDO    3' TAAGTGCAAAAGGTAACAAA 50599        AAAT
                              TAAGTGCAAAA   TAGCAAA
                              ||||||||||   |||||||
                              ATTCACGTTTT   ATTGTTT
                                    CC__
GAM2077 CAMTA1  3' TAAGGCAAAAAAATTAA    50600     T
                              TAAG GCAAAAAAATTAG
                              |||| ||||||||||||
                              ATTC CGTTTTTTTAATT
                                  _
GAM2077 CHERP   3' CAAGTGCAAAACTCAAGCA  50601        AAATT
                              TAAGTGCAAAA   AGCA
                              ||||||||||    ||||
                              GTTCACGTTTT   TCGT
                                    GAGT_
GAM2077 CLECSF9 3' AGGCAAATGTAGCAAAA    50602   T   AAAAT
                              AG GCAAA   TAGCAAAA
                              || |||||   ||||||||
                              TC CGTTT   ATCGTTTT
                                _   AC___
GAM2077 CLUL1   3' TAAGTGCAAAAGCAAA     50603        AAAATT
                              TAAGTGCAAA    AGCAAA
                              ||||||||||    ||||||
                              ATTCACGTTT    TCGTTT
                                   _____
GAM2077 KIAA0783 3' TAAGTGCAAAAAAAGCAAAAA 50604         ATT
                              TAAGTGCAAAAAA  AGCAAAAG
                              ||||||||||||  ||||||||
```

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                                ATTCACGTTTTTTT  TCGTTTTT
                                        ___
GAM2077  KIAA0894  3'  AATGCAAAGAAAACTACTCAAA 50605       _     G_
                AG                   AGTGCAAA AAAATTA  CAAAAG
                                     |||||||| |||||||  ||||||
                                     TTACGTTT TTTTGAT  GTTTTC
                                         C      GA
GAM2077  KIAA1486  5'  TAAGTGCAATAACCAG     50606         AAA
                                     TAAGTGCAA   AATTAG
                                     |||||||||   ||||||
                                     ATTCACGTT   TTGGTC
                                         A__
GAM2077  KIAA1918  3'  TAAGTGCAATAGAGTTAAAAAT 50607        _______
                TAA                  TAAGTGCAA      AAAAATTAG
                                     |||||||||      |||||||||
                                     ATTCACGTT      TTTTTAATT
                                         ATCTCAA
GAM2077  KRTAP4-7  3'  TAAGTGCAGAAAAGTTTATTAG 50608        A   ____    C
                AAA                  TAAGTGCA AAAA    ATTAG AAA
                                     |||||||| ||||    ||||| |||
                                     ATTCACGT TTTT    TAATC TTT
                                         C    CAAA    _
GAM2077  LOC124801 3'  TAAGAGCAAAAGGACAGCA    50609     T     AAAT
                                     TAAG GCAAAA    TAGCA
                                     |||| ||||||    |||||
                                     ATTC CGTTTT    GTCGT
                                       T     CCT_
GAM2077  LOC137492 3'  AGTGCAGAAAAATTTCTCAAA  50610       A      AG_
                                     AGTGCA AAAAATT   CAAA
                                     |||||| |||||||   ||||
                                     TCACGT TTTTTAA   GTTT
                                        C      AGA
GAM2077  LOC145873 3'  TAAGTACAAAAAAATCAA    50611
                                     TAAGTGCAAAAAAATTAG
                                     ||||||||||||||||||
                                     ATTCATGTTTTTTTAGTT

GAM2077  LOC221288 3'  AGTGCAAAAATAGCAGAAG   50612         AAT    A
                                     AGTGCAAAAA   TAGCA AAG
                                     ||||||||||   ||||| |||
                                     TCACGTTTTT   ATCGT TTC
                                            ___     C
GAM2078  KCNJ1    5'  TGGCATTTACTGAAGGTGTTTT 50615       GC   AG  A
                TT                    TGGCAT  GCT  AG TGTTTTTT
                                      ||||||  |||  || ||||||||
                                      ACCGTA  TGA  TC ACAAAAAA
                                         AA   CT  C
GAM2078  PEA15    3'  GCATGTGAATTTAATGTTTTTT 50616       CGCTAGA
                                      GCATG      GATGTTTTTT
                                      |||||      ||||||||||
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                                CGTAC      TTACAAAAAA
                                   ACTTAAA
GAM2078  DKFZp566D234 3'  TGGTGCAAGAGATGTTTTTT  50617    CA   CT
                                TGG  TGCG  AGAGATGTTTTTT
                                |||  ||||  ||||||||||||
                                ACC  ACGT  TCTCTACAAAAAA
                                  __   __
GAM2078  GPR105   3'  TGGCAGTGCTAGAGATG    50618      TGC
                                TGGCA  GCTAGAGATG
                                |||||  ||||||||||
                                ACCGT  CGATCTCTAC
                                   CA_
GAM2078  TUSP     5'  TGGCTTGCGTTGCTTTT    50619     A   CTAGAGA
                                TGGC TGCG      TGTTTTT
                                |||| ||||      |||||||
                                ACCG ACGC      ACGAAAA
                                  A   A_______
GAM2078  LOC204823 3'  TGGGTGCATTTGGATGTTTTTT 50620    CA   CTAGA
                                TGG  TGCG    GATGTTTTTT
                                |||  ||||    ||||||||||
                                ACC  ACGT    CTACAAAAAA
                                 C_   AAAC_
GAM2079  CDKN2A   3'  AGAATATATAAAAAATGA    50623        TG
                                AGAATGTGT  AAAAAATGA
                                |||||||||  |||||||||
                                TCTTATATA  TTTTTTACT
                                     __
GAM2079  CDKN2A   3'  AGAATATATAAAAAATGA    50623        TG
                                AGAATGTGT  AAAAAATGA
                                |||||||||  |||||||||
                                TCTTATATA  TTTTTTACT
                                     __
GAM2079  CDKN2A   3'  AGAATATATAAAAAATGA    50623        TG
                                AGAATGTGT  AAAAAATGA
                                |||||||||  |||||||||
                                TCTTATATA  TTTTTTACT
                                     __
GAM2079  CDKN2A   3'  AGAATATATAAAAAATGA    50623        TG
                                AGAATGTGT  AAAAAATGA
                                |||||||||  |||||||||
                                TCTTATATA  TTTTTTACT
                                     __
GAM2079  COL10A1  3'  GAAAAGCCTTGAAAGAATG   50624     T_  G     A
                                GAA  GT TTGAAA AATG
                                |||  ||  ||||||  ||||
                                CTT  CG AACTTT TTAC
                                  TT  G     C
GAM2079  ESRRBL1  3'  GAATGCTATGAAAAATGA    50625       GT      A
                                GAATGT  TGAAAAA TGA
                                ||||||  |||||||  |||
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                                CTTACG  ACTTTTT ACT
                                   AT     _
GAM2079  IDH1     3'  TAGAACATGAGAAAAAGTGA   50626        TT     A
                                TAGAATGTG  GAAAAA TGA
                                |||||||||  |||||| |||
                                ATCTTGTAC  CTTTTT ACT
                                     T_     C
GAM2079  KCNAB1   3'  TAAAATGTAGTAAAAAATGA   50627         TTG
                                TAGAATGTG   AAAAAATGA
                                |||||||||   |||||||||
                                ATTTTACAT   TTTTTTACT
                                     CA_
GAM2079  MAGP2    5'  TAGAATGTGTGTTACAATGA   50628         TGAAAA
                                TAGAATGTGT     AATGA
                                ||||||||||     |||||
                                ATCTTACACA     TTACT
                                      CAATG_
GAM2079  MEN1     3'  GAATGTATACTTAAAAATGA   50629        TGA_
                                GAATGTGT    AAAAATGA
                                ||||||||    ||||||||
                                CTTACATA    TTTTTACT
                                     TGAA
GAM2079  PIK3R3   3'  AGAATGAAAAAAAAAATGA    50630       TGTT
                                AGAATG    GAAAAAATGA
                                ||||||    ||||||||||
                                TCTTAC    TTTTTTTACT
                                   TTT_
GAM2079  POLH     3'  AGAATGTGAAGAAAATGA     50631        TT    AA
                                AGAATGTG  GAAA  ATGA
                                ||||||||  ||||  ||||
                                TCTTACAC  CTTT  TACT
                                     TT    __
GAM2079  RARA     3'  AAATGTGCTTAAAATGA      50632        GAA
                                GAATGTGTT   AAAATGA
                                |||||||||   |||||||
                                TTTACACGA   TTTTACT
                                     A__
GAM2079  RNF17    3'  CAGAAACATTGAAAAAATGA   50633      T TG
                                TAGAA G  TTGAAAAAATGA
                                |||||| |  ||||||||||||
                                GTCTT T  AACTTTTTTACT
                                   _ GT
GAM2079  RRM2B    3'  CAGACATTTGAAAAAATGA    50634      ATGTG
                                TAGA    TTGAAAAAATGA
                                ||||    ||||||||||||
                                GTCT    AACTTTTTTACT
                                  GTA__
GAM2079  SPOCK    3'  TAGAATGTCTCTGAAAATG    50635        G  GAA
                                TAGAATGT TT   AAAATG
                                ||||||||  ||   ||||||
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                                ATCTTACA AG   TTTTAC
                                    G  AC_
GAM2079  SYT1     3'  GAATGCATGGCTGGAAAAATGA 50636       ___    A
                                GAATGT   GTTG AAAAATGA
                                ||||||   |||| ||||||||
                                CTTACG   CGAC TTTTTACT
                                   TAC    C
GAM2079  TLL1     3'  TGTGTTTTGAAAAAATGA    50637      __
                                TGTGT  TGAAAAAATGA
                                |||||  ||||||||||
                                ACACA  ACTTTTTTACT
                                  AA
GAM2079  UBL1     3'  AATGTCCTGAAAAAGGTGA   50638      G      A_
                                AATGT TTGAAAAA  TGA
                                ||||| ||||||||  |||
                                TTACA GACTTTTT  ACT
                                  G       CC
GAM2079  VANGL2   3'  GAATGGGAAGAAAAAATGA   50639      TGTT
                                GAATG   GAAAAAATGA
                                |||||   ||||||||||
                                CTTAC   CTTTTTTACT
                                  CCTT
GAM2079  VNN2     3'  CAGAGTAGCCAAAAAAATG   50640     A  T  TG
                                TAGA TG GT  AAAAAATG
                                |||| || ||  ||||||||
                                GTCT AT CG  TTTTTTAC
                                  C  _  GT
GAM2079  VNN2     3'  CAGAGTAGCCAAAAAAATG   50640     A  T  TG
                                TAGA TG GT  AAAAAATG
                                |||| || ||  ||||||||
                                GTCT AT CG  TTTTTTAC
                                  C  _  GT
GAM2079  B1       3'  AGAATTCTGTGAAAAAATG   50641      G_   T
                                AGAAT  TGT GAAAAAATG
                                |||||  ||| |||||||||
                                TCTTA  ACA CTTTTTTAC
                                  AG   _
GAM2079  C1QR1    3'  TAGATGTGTTGCATCATGA   50642     A      AAAAA
                                TAGA TGTGTTG    ATGA
                                |||| |||||||    ||||
                                ATCT ACACAAC    TACT
                                  _      GTAG_
GAM2079  CAPN6    3'  TAGAAGTACTGAAAAATGA   50643      T        A
                                TAGAA GTGTTGAAAAA TGA
                                ||||| |||||||||| |||
                                ATCTT CATGACTTTTT ACT
                                  _        _
GAM2079  CLIC5    3'  AGAATGTGTCTCAAGTGA    50644          GAAA  A
                                AGAATGTGTT    AA TGA
                                ||||||||||    || |||
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                                TCTTACACAG    TT ACT
                                      AG__  C
GAM2079  CXorf1    3'  GAATATGTAGAATCAAAATGA  50645        T  __
                                GAATGTGT GAA  AAAATGA
                                |||||||| |||  |||||||
                                CTTATACA CTT  TTTTACT
                                     T   AG
GAM2079  D4ST-1    3'  AAATGCATCAGAAAAATG    50646        GA
                                GAATGTGTT  AAAAATG
                                |||||||||  |||||||
                                TTTACGTAG  TTTTTAC
                                      TC
GAM2079  DKFZp566D133 3'  GATTGTGGGAAAAAAATGA   50647    A   TT
                                GA TGTG  GAAAAAATGA
                                || ||||  ||||||||||
                                CT ACAC  TTTTTTTACT
                                 A   CC
GAM2079  DREV1     3'  GAATGTGTTGATCTGATGA   50648          AAAA
                                GAATGTGTTGA    ATGA
                                ||||||||||    ||||
                                CTTACACAACT    TACT
                                      AGAC
GAM2079  FLJ23342  3'  TAGAGATGTGTAAAAATGA    50649     _     TGA
                                TAGA ATGTGT   AAAAATGA
                                |||| ||||||   ||||||||
                                ATCT TACACA   TTTTTACT
                                  C     ___
GAM2079  HZFW1     3'  GAATGTGTTCCCAGAAATGA   50650        GAAA_
                                GAATGTGTT     AAATGA
                                |||||||||     ||||||
                                CTTACACAA     TTTACT
                                      GGGTC
GAM2079  KIAA0062  3'  CAGACTTTGAAAAAATG     50651      ATGTG
                                TAGA     TTGAAAAAATG
                                ||||     ||||||||||
                                GTCT     AACTTTTTTAC
                                  GA___
GAM2079  KIAA0884  5'  TAAAATGTGAAAACAAAAATGA 50652         TTGA_
                                TAGAATGTG     AAAAATGA
                                |||||||||     ||||||||
                                ATTTTACAC     TTTTTACT
                                      TTTTG
GAM2079  KIAA1915  3'  CAGAATATATGGAAAGAATG   50653         T   A
                                TAGAATGTGT GAAA AATG
                                |||||||||| |||| ||||
                                GTCTTATATA CTTT TTAC
                                      C   C
GAM2079  MEGF10    3'  TAGAATATGCAATTTAAAAATG 50654          TGA__
                                TAGAATGTGT     AAAAATG
                                ||||||||||     |||||||
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                                ATCTTATACG    TTTTTAC
                                      TTAAA
GAM2079  MRPS33   3'  TAGAATGTGTTCAAGAAAC   50655         G  A
                                TAGAATGTGTT AA AAAT
                                |||||||||||  || ||||
                                ATCTTACACAA TT TTTG
                                      G  C
GAM2079  MRPS33   3'  TAGAATGTGTTCAAGAAAC   50655         G  A
                                TAGAATGTGTT AA AAAT
                                |||||||||||  || ||||
                                ATCTTACACAA TT TTTG
                                      G  C
GAM2079  PI15     5'  GAGAGTGAAGAAAAAATGA   50656    AT   TT
                                GA  GTG  GAAAAAATGA
                                ||  |||  ||||||||||
                                CT  CAC  CTTTTTTACT
                                 CT   TT
GAM2079  RFX4     3'  CAGAATGTGTACCAATGA    50657         TGAAAA
                                TAGAATGTGT     AATGA
                                ||||||||||     |||||
                                GTCTTACACA     TTACT
                                      TGG___
GAM2079  SEMA4F   3'  TAGAATGTTGTTGATTTTTAAT 50658        _    AAA__
           G                     TAGAATGT GTTGA     AATG
                                ||||||||  |||||     ||||
                                ATCTTACA CAACT     TTAC
                                     A     AAAAA
GAM2079  TUCAN    3'  CAGAATAATGGAAAAAATGA   50659       TGTT
                                TAGAATG    GAAAAAATGA
                                |||||||    ||||||||||
                                GTCTTAT    CTTTTTTACT
                                    TAC_
GAM2079  LOC126767 5'  TGTGCACAGTGAAAAAATG    50660      _____
                                TGTGT    TGAAAAAATG
                                |||||    ||||||||||
                                ACACG    ACTTTTTTAC
                                   TGTC
GAM2079  LOC150848 5'  TAAAATGTGTTGATTCTATG   50661           AAAA
                                TAGAATGTGTTGA    ATG
                                ||||||||||||    |||
                                ATTTTACACAACT    TAC
                                       AAGA
GAM2079  LOC199777 3'  GACTGTGCAGAAAAATGA     50662    A    T     A
                                GA TGTGT GAAAAA TGA
                                || ||||| |||||| |||
                                CT ACACG CTTTTT ACT
                                 G    T     _
GAM2079  LOC203339 3'  TAGAATGCTAAATGGAAAATGA 50663        GT__  AA
                                TAGAATGT    TG  AAAATGA
                                ||||||||    ||  |||||||
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                                ATCTTACG   AC  TTTTACT
                                    ATTT  C_
GAM2079  LOC221002 3'  TAAAATGTAGTTGAAGAATGA  50664        _     AA
                                TAGAATGT GTTGAA  AATGA
                                |||||||| ||||||  |||||
                                ATTTTACA CAACTT  TTACT
                                    T     C_
GAM2079  LOC253959 3'  GATTGTGGGAAAAAAAATGA   50665    A    TT_
                                GA TGTG   GAAAAAATGA
                                || ||||   ||||||||||
                                CT ACAC   TTTTTTTACT
                                 A    CCT
GAM2079  LOC90693  3'  AAATGTGTTATAGAAATGA    50666          AAA
                                GAATGTGTTG   AAATGA
                                ||||||||||   ||||||
                                TTTACACAAT   TTTACT
                                     ATC
GAM2080  ENAM      3'  AAGACACTGTGCTAGGT     50669     T   T     A
                                AAG TACT GTGCTA GT
                                ||| |||| |||||| ||
                                TTC GTGA CACGAT CA
                                  T   _     C
GAM2080  PRKY      3'  TCTTAAAAGTTATTTGTG    50670     C       C
                                TCT AAAAGTTA TTGTG
                                ||| |||||||| |||||
                                AGA TTTTCAAT AACAC
                                  A       A
GAM2080  TIMM17A   3'  TCTCAGAAGTCACTTCAAG   50671      A       GTGC
                                TCTCA AAGTTACTT   TAAG
                                ||||| |||||||||   ||||
                                AGAGT TTCAGTGAA   GTTC
                                   C       ____
GAM2080  TNC       3'  TCAAAAGTACTTGTGCT     50672         T
                                TCAAAAGT ACTTGTGCT
                                |||||||| |||||||||
                                AGTTTTCA TGAACACGA
                                      _
GAM2080  EPLIN     3'  TCCAAAGTTACTTCCAAGT   50673    A       GTG
                                TC AAAGTTACTT   CTAAGT
                                || ||||||||||   ||||||
                                AG TTTCAATGAA   GGTTCA
                                 G       ___
GAM2080  HIC       3'  TCAAAAGTTTGCTAAG      50674          ACTTG
                                TCAAAAGTT    TGCTAAG
                                |||||||||    |||||||
                                AGTTTTCAA    ACGATTC
                                      _____
GAM2080  HT012     3'  TCAAAAATTACAATTGTTTGAG 50675          __   GCTA
             T                   TCAAAAGTTAC  TTGT    AGT
                                ||||||||||  ||||   |||
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                                AGTTTTTAATG  AACA    TCA
                                      TT    AAC_
GAM2080  KIAA1900  3'  TCTGAGAGTTACTTGAGGCAAG 50676     CAAA       T_  T
              T                    TCT    AGTTACTTG  GC AAGT
                                   |||    |||||||||  || ||||
                                   AGA    TCAATGAAC  CG TTCA
                                     CTC_       TC  _
GAM2080  MASA     3'  TCTCAAACTGTGCTAA      50677        AGTTAC
                                   TCTCAAA     TTGTGCTAA
                                   |||||||     |||||||||
                                   AGAGTTT     GACACGATT

                                   _______
GAM2080  ZF       3'  TCAAAAGTTCTTATCAAGT    50678          A    GC
                                   TCAAAAGTT CTTGT  TAAGT
                                   |||||||||| |||||  |||||
                                   AGTTTTCAA GAATA  GTTCA

                                      _    ___
GAM2080  LOC151826 3'  TCAAAGGATCTCTGTGCTAGGT 50679       A_   A  T     A
                                   TCAAA  GTT CT GTGCTA GT
                                   |||||  ||| || |||||| ||
                                   AGTTT  TAG GA CACGAT CA
                                      CC   A  _     C
GAM2081  EP300    5'  GCTCCGACGGCACCCGA     50682    C       CAC
                                   GC CCGACGGC   CCCGA
                                   || ||||||||   |||||
                                   CG GGCTGCCG   GGGCT
                                    A       T___
GAM2081  F2RL1    5'  GCCCCGACGCCGGGCGCG    50683          G  ACCC  A
                                   GCCCCGACG CC    CG CG
                                   |||||||||| ||    || ||
                                   CGGGGCTGC GG    GC GC
                                         _  CCC_  _
GAM2081  FTH1     5'  ACCCCGACGACTCTCGGCGAAG 50684           CACCC  A
                                   GCCCCGACGGC     CG CGAAG
                                   ||||||||||||    || |||||
                                   TGGGGCTGCTG     GC GCTTC
                                         AGA___  C
GAM2081  HAGH     5'  GCCCCGACTGCCACGGGCCG   50685         G    C___
                                   GCCCCGAC GCCAC   CCG
                                   |||||||| |||||   |||
                                   CGGGGCTG CGGTG   GGC
                                        A     CCC
GAM2081  LEF1     5'  GCCCCGGCGGCCACCCCG     50686        A
                                   GCCCCG CGGCCACCCCG
                                   |||||| ||||||||||
                                   CGGGGC GCCGGTGGGGC
                                      C
GAM2081  POLG     3'  GCCTGCACCACCCCGATGAAG  50687     CCGACG        C
                                   GCC     GCCACCCCGA GAAG
                                   |||     |||||||||| ||||
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                                CGG     TGGTGGGGCT CTTC
                                  ACG___        A
GAM2081 TBL3     5' CCCGGCAGCCACCGCCGCG   50688     A      _  A
                                CCCG CGGCCACC CCG CG
                                |||| |||||||| ||| ||
                                GGGC GTCGGTGG GGC GC
                                  C       C  _
GAM2081 C11orf21 3' GCCTCGTGGCCACCCCCAC   50689    C  AC       G
                                GCC CG  GGCCACCCC AC
                                ||| ||  ||||||||| ||
                                CGG GC  CCGGTGGGG TG
                                  A  A_       G
GAM2081 C20orf81 5' GCCCCGACGGCGCCTCA     50690          CA  C
                                GCCCCGACGGC  CC CG
                                ||||||||||  || ||
                                CGGGGCTGCCG  GG GT
                                       C_  A
GAM2081 IRX1     5' GCCCCCGGTCGGCCCGACGA   50691      GA   CCAC
                                GCCCC  CGG   CCCGACGA
                                |||||  |||   ||||||||
                                CGGGG  GCC   GGGCTGCT
                                   __  AGCC
GAM2081 KIAA0410 5' GCCCCAACGGCGGCGA      50692          CACCCC A
                                GCCCCGACGGC     G CGA
                                ||||||||||     | |||
                                CGGGGTTGCCG     C GCT
                                       _______ C
GAM2081 KIAA0495 5' GCCCCGACTGCCACCCACCA  50693        G      CGA
                                GCCCCGAC GCCACCC   CG
                                |||||||| |||||||   ||
                                CGGGGCTG CGGTGGG   GT
                                     A      TG_
GAM2081 MAP-1    5' GCCTGGCCGGGCCCCGACGA  50694    CCGAC   A__
                                GCC    GGCC   CCCCGACGA
                                |||    ||||   |||||||||
                                CGG    CCGG   GGGGCTGCT
                                  A____    CCC
GAM2081 MGC10724 5' CCCGAAGTGGTCCCGACGAAG 50695      C  CCAC
                                CCCGA GG    CCCGACGAAG
                                ||||| ||    ||||||||||
                                GGGCT TC    GGGCTGCTTC
                                   _ ACCA
GAM2081 SPACA1   5' GCCCCGACGGCCGTCCGA    50696          ACC
                                GCCCCGACGGCC   CCGA
                                ||||||||||||   ||||
                                CGGGGCTGCCGG   GGCT
                                       CA_
GAM2081 TCFL5    5' CCCTCGACGGCCGCCTCG    50697     _      A  C
                                CCC CGACGGCC CC CG
                                ||| |||||||| || ||
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                                GGG GCTGCCGG GG GC
                                  A       C  A
GAM2081  TLN2     3'  GCCCCGACGGCCTTCCG     50698           ACC
                                GCCCCGACGGCC   CCG
                                ||||||||||||  |||
                                CGGGGCTGCCGG   GGC
                                       AA_
GAM2081  TRAF3    5'  GCCCCGTGGCCACCCTTCCCG  50699       AC       CGA_
                                GCCCCG  GGCCACCC    CG
                                ||||||  ||||||||    ||
                                CGGGGC  CCGGTGGG    GC
                                   A_       AAGG
GAM2081  LOC112868 3'  GCCCTGGGGCCACCCCACA    50700      CGAC        G
                                GCCC    GGCCACCCC ACG
                                ||||    ||||||||| |||
                                CGGG    CCGGTGGGG TGT
                                  ACC_       _
GAM2081  LOC254057 3'  GCCCCGACGACTGCCCTTCCCC 50701          ____   A__
            G                    GCCCCGACG   GCC   CCCCG
                                |||||||||   |||   |||||
                                CGGGGCTGC   CGG   GGGGC
                                     TGA   GAA
GAM2081  LOC256117 5'  GCCCCGACGGCTGCGGGCCCCG 50702           CA____
                                GCCCCGACGGC     CCCCG
                                ||||||||||      |||||
                                CGGGGCTGCCG     GGGGC
                                       ACGCCC
GAM2081  LOC58525  5'  GCCCCGGCGACCACCTCCTTCA 50703       A       _  GA
                                GCCCCG CGGCCACC CC  CG
                                |||||| |||||||| ||  ||
                                CGGGGC GCTGGTGG GG  GT
                                   C       A  AA
GAM2082  BCL7A    5'  CGCCGGAGTGCGGCTCCG    50706          _   GA
                                CGCCGGAGTG GGC  CG
                                |||||||||| |||  ||
                                GCGGCCTCAC CCG  GC
                                       G   AG
GAM2082  CDH15    5'  GCCGGAGTGCACCCGCGACCCG 50707         G  GA_
                                GCCGGAGTG GC   CGACCCG
                                ||||||||| ||   |||||||
                                CGGCCTCAC TG   GCTGGGC
                                     G  GGC
GAM2082  DUSP7    5'  CGATGTGCGACGACTCG     50708    GA   G       C
                                CG  GTG GCGACGAC CG
                                ||  ||| |||||||| ||
                                GC  TAC CGCTGCTG GC
                                  __   A       A
GAM2082  EGLN3    5'  GCGGAGCTCCACGACCCG    50709    C    GGG G
                                GC GGAGT   C ACGACCCG
                                || |||||   | ||||||||
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                                CG CCTCG   G TGCTGGGC
                                 _    AG_ _
GAM2082  EGLN3    5'  GCGGAGCTCCACGACCCG    50709    C    GGG G
                                GC GGAGT   C ACGACCCG
                                || |||||   | ||||||||
                                CG CCTCG   G TGCTGGGC
                                 _    AG_ _
GAM2082  ELF3     5'  ACCGGAGTGGCGGAGTCCG    50710         G  ACGAC
                                GCCGGAGTGG CG    CCG
                                |||||||||| ||    |||
                                TGGCCTCACC GC    GGC
                                      _ CTCA_
GAM2082  GLUL     5'  CAGCTGGAGCGCGACCC     50711     AG  _  A
                                CGG  TGG GCG CGACCC
                                |||  ||| ||| ||||||
                                GTC  ACC CGC GCTGGG
                                  G_  T  _
GAM2082  GPC6     5'  CGCCGGAGTGTGCGGCAA    50712         G  A
                                CGCCGGAGTG GCG CGA
                                |||||||||| ||| |||
                                GCGGCCTCAC CGC GTT
                                      A  C
GAM2082  IGFBP4   5'  GCCGGAGGGGAGCAAGCC    50713       T  CGA  C
                                GCCGGAG GGG  CGA CC
                                ||||||| |||  ||| ||
                                CGGCCTC CCC  GTT GG
                                    _  TC_  C
GAM2082  NDUFA10  3'  GCTGGAGCAGAAGGCGGCCCG  50714    C    ___    ACGA
                                GC GGAGT  GGGCG   CCCG
                                || |||||  |||||   ||||
                                CG CCTCG  TCCGC   GGGC
                                 A   TCT   C___
GAM2082  P3       5'  CGCCCGAGTGGGCGATCG    50715     G       _
                                CGCC GAGTGGGCGA CG
                                |||| |||||||||| ||
                                GCGG CTCACCCGCT GC
                                  G        A
GAM2082  PDLIM1   5'  GCTGTGGCGGGCGACGACCCG  50716    CGGA
                                GC   GTGGGCGACGACCCG
                                ||   ||||||||||||||
                                CG   CGCCCGCTGCTGGGC
                                 ACAC
GAM2082  PPP2R2C  5'  CGCTGGAAGATGACGACCCG   50717    C   T  GC
                                CGC GGAG GG  GACGACCCG
                                ||| |||| ||  |||||||||
                                GCG CCTT CT  CTGCTGGGC
                                  A   _ A_
GAM2082  SPAG6    5'  GATCGTGGCGACGACTCG    50718    G _       C
                                GA TG GGCGACGAC CG
                                || || ||||||||| ||
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                                CT GC CCGCTGCTG GC
                                 A  A        A
GAM2082 ALK7     5' GCCGGGGCAGCACGGCCCG   50719      A TG G G   A
                                GCCGG G  G C ACG CCCG
                                ||||| |  | | ||| ||||
                                CGGCC C  C G TGC GGGC
                                   C GT _ _  C
GAM2082 C2orf9   5' CCGGGGGGAACGACCCG    50720     AGT   C
                                CCGG   GGG GACGACCCG
                                ||||   ||| |||||||||
                                GGCC   CCC TTGCTGGGC
                                  ___  C
GAM2082 C6orf31  5' GCCGGAGTGGGGGGTCCTCG   50721          CGACGA _
                                GCCGGAGTGGG     CC CG
                                ||||||||||      || ||
                                CGGCCTCACCC     GG GC
                                       CCA___  A
GAM2082 FLJ11743 3' CACCGGAGCGAACGGCCCG   50722            ACGA
                                CGCCGGAGTGGGCG   CCCG
                                ||||||||||||||   ||||
                                GTGGCCTCGCTTGC   GGGC
                                        C___
GAM2082 FLJ22246 5' CGCTGGAGCGGGTCGCCG    50723     C       _ A
                                CGC GGAGTGGG CG CG
                                ||| |||||||| || ||
                                GCG CCTCGCCC GC GC
                                  A       A  G
GAM2082 FLJ22341 3' CCTGGGGTGGCTCCGCCCG   50724    _ A   G GA  A
                                CC GG GTGG C  CG CCCG
                                || || |||| |  || ||||
                                GG CC CACC G  GC GGGC
                                 A  C   _ AG  _
GAM2082 FLJ32421 5' GCCGGAGTCACGTGACCCG   50725        GG   AC
                                GCCGGAGT  GCG  GACCCG
                                ||||||||  |||  ||||||
                                CGGCCTCA  TGC  CTGGGC
                                     G_   A_
GAM2082 GNB1L    5' GCCGGAGTCGGGAACGCC    50726        G  C    A
                                GCCGGAGT GG GACG CC
                                |||||||| || |||| ||
                                CGGCCTCA CC TTGC GG
                                     G  C   _
GAM2082 KIAA1940 5' CGCCGCGGGCGACGGCCCG   50727     GGA        A
                                CGCC   GTGGGCGACG CCCG
                                ||||   |||||||||| ||||
                                GCGG   CGCCCGCTGC GGGC
                                  ___         C
GAM2082 MD-2     5' GCCGAAGTGGGAGCGGCCCG   50728          CGA  A
                                GCCGGAGTGGG   CG CCCG
                                ||||||||||   || ||||
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                                CGGCTTCACCC  GC GGGC
                                      TC_  C
GAM2082  MGC13159  5'  CGCCGGAGCTGCTGCCGGGCCC 50729        GG  GA_  A_
            G                    CGCCGGAGT  GC   CG  CCCG
                                 |||||||||  ||   ||  ||||
                                 GCGGCCTCG  CG   GC  GGGC
                                      A_  ACG  CC
GAM2082  MGC15482  5'  CGCCGGAGGGGTGACGCC    50730        T   C    A
                                 CGCCGGAG GGG GACG CC
                                 ||||||||| ||| |||| ||
                                 GCGGCCTC CCC CTGC GG
                                      _   A    _
GAM2082  MGC20806  3'  CGCGTGGAACAGACGACCCG   50731     CGGA    _ _
                                 CGC    GTGGG C GACGACCCG
                                 |||    ||||| | |||||||||
                                 GCG    CACCT G CTGCTGGGC
                                  _____    T T
GAM2082  NPEPL1    5'  GCCAGAGCTCCTCGGTGACCCG 50732        GGG_  AC
                                 GCCGGAGT    CG  GACCCG
                                 ||||||||    ||  ||||||
                                 CGGTCTCG    GC  CTGGGC
                                      AGGA  CA
GAM2082  p25       3'  CGTGTGGGCGAGGTGACCCG   50733    GA       C__
                                 CG  GTGGGCGA   GACCCG
                                 ||  ||||||||   ||||||
                                 GC  CACCCGCT   CTGGGC
                                  A_       CCA
GAM2082  SCYB14    5'  CGTCGGAGCGGCGGCCC     50734    C       G  ACGA
                                 CG CGGAGTGG CG    CCC
                                 || |||||||| ||    |||
                                 GC GCCTCGCC GC    GGG
                                  A       _ C___
GAM2082  SLC16A3   3'  CACTGATCGGGCGACGATCCG  50735     CG  G         C
                                 CGC  GA TGGGCGACGA CCG
                                 |||  || ||||||||||| |||
                                 GTG  CT GCCCGCTGCT GGC
                                   A_  A         A
GAM2082  TRIM11    3'  CCGGAGTGGAGCCAAGGCCCG  50736         _  GACGA
                                 CCGGAGTGG GC     CCCG
                                 |||||||| ||     ||||
                                 GGCCTCACC CG     GGGC
                                      T  GTTCC
GAM2082  LOC112885 3'  CGACGGAGTGCCCCAGGCCCG  50737    C      GG  GA  A_
                                 CG CGGAGT  GC  CG  CCCG
                                 || ||||||  ||  ||  ||||
                                 GC GCCTCA  CG  GT  GGGC
                                  T     __  GG  CC
GAM2082  LOC148479 5'  GCTGGAGCGGGGCCGCCCG   50738    C       CGA  A
                                 GC GGAGTGGG   CG CCCG
                                 || ||||||||   || ||||
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                                CG CCTCGCCC   GC GGGC
                                 A       CG_ _
GAM2082  LOC151571 5'  GCCCGTGTTCGACGACCCG   50739     GGA   GG
                                GCC   GTG  CGACGACCCG
                                |||   |||  ||||||||||
                                CGG   CAC  GCTGCTGGGC
                                  G__   AA
GAM2082  LOC158581 3'  CACCGGAGAAAACTGACGACCC 50740         TG  _
              G                  CGCCGGAG  GGC GACGACCCG
                                |||||||||  ||| |||||||||
                                GTGGCCTC  TTG CTGCTGGGC
                                     TT   A
GAM2082  LOC205313 5'  GCCAGCACAGGCGACGGCC   50741       A TG      A
                                GCCGG G  GGCGACG CC
                                ||||| |  ||||||| ||
                                CGGTC T  CCGCTGC GG
                                   G GT      C
GAM2082  LOC221424 5'  CGCTGGGGCGGGGGCGGCCCG  50742     C  A    CGA  A
                                CGC GG GTGGG   CG CCCG
                                ||| || |||||   || ||||
                                GCG CC CGCCC   GC GGGC
                                  A  C    CC_  C
GAM2082  LOC93550  5'  CCTGGGCAAAGGCGGCCCG   50743    GGAG      ___  A
                                CC    TGGGCGA   CG CCCG
                                ||    |||||||   || ||||
                                GG    ACCCGTT   GC GGGC
                                  _____      TCC  C
GAM2083  APBA2     3'  TGGGGAGCCAGCGTCCGTGG   50746    A       AGCC  _  _
                                TG GGAGCCAG    CG CCG GG
                                || ||||||||    || ||| ||
                                AC CCTCGGTC    GC GGC CC
                                 C       _____  A   A
GAM2083  B4GALT3   3'  TGAGGAGCTGAGGGTGGGG   50747        CA   CCCGCC
                                TGAGGAGC  GAG     GGGG
                                ||||||||  |||     ||||
                                ACTCCTCG  CTC     CCCC
                                     A_   CCA___
GAM2083  B4GALT6   5'  TGGGAGGCCAGAGAGTCGGGG  50748    A   _     CCCGC
                                TG GGAG CCAGAG    CGGGG
                                || |||| ||||||    |||||
                                AC CCTC GGTCTC    GCCCC
                                  _   C     TCA__
GAM2083  BAK1      3'  TGAGGAGCATGGAGGGTGGGG  50749        CA_   CCCGCC
                                TGAGGAGC   GAG     GGGG
                                ||||||||   |||     ||||
                                ACTCCTCG   CTC     CCCC
                                     TAC   CCA___
GAM2083  CARD10    3'  TGAGAGGCCAGAGCCAAGGG   50750     GA       CGCC
                                TGAG  GCCAGAGCC    GGGG
                                ||||  |||||||||    ||||
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                                ACTC  CGGTCTCGG   TCCC
                                  TC       T___
GAM2083  CDO1    5'  TGAGCGAGCCAAGGAGCTGGGG 50751     _    __   CCGCC
                                TGAG GAGCCA  GAGC    GGGG
                                |||| ||||||  ||||    ||||
                                ACTC CTCGGT  CTCG    CCCC
                                  G     TC    A____
GAM2083  COL6A2  3'  TGAGAGCCAGCCTGTCGGGG  50752     G    GA   CGC
                                TGAG AGCCA  GCC   CGGGG
                                |||| |||||  |||   |||||
                                ACTC TCGGT  CGG   GCCCC
                                  _    __  ACA
GAM2083  EPHB6   5'  TGGGGCGCCGGGAGAATCCTGG 50753    A  A   A_   CCCG  _
            GG                    TG GG GCC  GAG    CC GGGG
                                || || |||  |||    || ||||
                                AC CC CGG  CTC    GG CCCC
                                 C  G   CC   TTA_  A
GAM2083  GAA     3'  TGGGGGCCAGAGCCCCGG    50754    A  A        GC
                                TG GG GCCAGAGCCC  CGG
                                || || ||||||||||  |||
                                AC CC CGGTCTCGGG  GCC
                                 _ C         __
GAM2083  IPF1    5'  CGGGAGCTGGAGCCGGGG    50755    A    CA    CGCC
                                TG GGAGC  GAGCC   GGGG
                                || |||||  |||||   ||||
                                GC CCTCG  CTCGG   CCCC
                                 _    AC    _____
GAM2083  LTB4R   5'  TGAGGAGCAGGAGTGAGGG   50756        CA   CCCGCC
                                TGAGGAGC  GAG     GGGG
                                ||||||||  |||     ||||
                                ACTCCTCG  CTC     TCCC
                                     TC   AC_____
GAM2083  MADH7   5'  GGGGCGCCCGCCGGGG      50757    A  CAGA
                                GG GC   GCCCGCCGGGG
                                || ||   ||||||||||
                                CC CG   CGGGCGGCCCC
                                 C  _____
GAM2083  MSF     3'  CGGGGAGCCAGGCCTGGGG   50758    A      A   CGCC
                                TG GGAGCCAG GCC   GGGG
                                || ||||||| |||   ||||
                                GC CCTCGGTC CGG   CCCC
                                 C       _   A___
GAM2083  MSI1    3'  GGAGCCAGACGCTGTTGGGG   50759         _ CCGCC
                                GGAGCCAGA GC    GGGG
                                |||||||| ||    ||||
                                CCTCGGTCT CG    CCCC
                                     G  ACAA_
GAM2083  NFE2    3'  TGAGGAGCCGAGTCAGGG    50760         A   CCCGC
                                TGAGGAGCC GAG    CGGGG
                                |||||||| |||    |||||
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                                ACTCCTCGG CTC    GTCCC
                                     _  A____
GAM2083  PES1    3'  TGAGGGGTCAGGGCTGGCTGGA 50761      AGC  A  CC  C
                                TGAGG  CAG GC  GC GGG
                                |||||  ||| ||  || |||
                                ACTCC  GTC CG  CG CCT
                                   CCA  C  AC  A
GAM2083  PIM2    5'  TGGGGAGCCAGGGCTGGGG   50762    A      A  CCGCC
                                TG GGAGCCAG GC    GGGG
                                || ||||||||| ||    ||||
                                AC CCTCGGTC CG    CCCC
                                 C       C  A____
GAM2083  PSCD4   3'  TGAGGACCAGAGAGGG      50763       G     CCCGCC
                                TGAGGA CCAGAG     GGG
                                |||||| ||||||     |||
                                ACTCCT GGTCTC     CCC
                                   _     T_____
GAM2083  RAD50   5'  GGGGCTGCCCGCCGGGG     50764    A  CAGA
                                GG GC   GCCCGCCGGGG
                                || ||   ||||||||||
                                CC CG   CGGGCGGCCCC
                                 C  A___
GAM2083  RAD50   5'  GGGGCTGCCCGCCGGGG     50764    A  CAGA
                                GG GC   GCCCGCCGGGG
                                || ||   ||||||||||
                                CC CG   CGGGCGGCCCC
                                 C  A___
GAM2083  RPL10   3'  TGGGAGCCACAGGCTGGGG   50765    A     G  CCC  C
                                TG GGAGCCA AG   GC GGGG
                                || ||||||| ||   || ||||
                                AC CCTCGGT TC   CG CCCC
                                 _     G  ___  A
GAM2083  TNP1    3'  AGGGCAGAGCCCGCTGGGG   50766     A  C       C
                                AGG GC AGAGCCCGC GGGG
                                ||| || ||||||||| ||||
                                TCC CG TCTCGGGCG CCCC
                                  _ _       A
GAM2083  VEGF    3'  TGGGGAGCCAGGGGATCGGGGA 50767    A      AGCCCGC
                                TG GGAGCCAG      CGGGGA
                                || ||||||||      ||||||
                                AC CCTCGGTC      GCCCCT
                                 C       CCCTA__
GAM2083  ARF6    5'  GAGGAGCCGGGGCCGGGG    50768        AGAGCCC
                                GAGGAGCC      GCCGGGG
                                ||||||||      |||||||
                                CTCCTCGG      CGGCCCC
                                     CCC_____
GAM2083  C20orf108 3'  TGAGGAGCCGAAGCCAAGG   50769        A   CCC
                                TGAGGAGCC GAG   GCCGGGG
                                ||||||||| |||   |||||||
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                                ACTCCTCGG CTT   CGGTTCC
                                      _  ___
GAM2083  C20orf55  5'  TGAGGAGCCAGAGATCCGGG  50770          CCCG
                                TGAGGAGCCAGAG   CCGGG
                                ||||||||||||   |||||
                                ACTCCTCGGTCTC   GGCCC
                                    TA__
GAM2083  CAM-KIIN  5'  TGAGGAGCCAAGCGGG     50771        G  CCGCC
                                TGAGGAGCCA AGC    GGG
                                |||||||||| |||    |||
                                ACTCCTCGGT TCG    CCC
                                      _  _____
GAM2083  CXYorf1   3'  GAGGAGCCCCGCGCTGGGGA  50772       AGAG  _  C
                                GAGGAGCC   CC CGC GGGGA
                                ||||||||   || ||| |||||
                                CTCCTCGG   GG GCG CCCCT
                                     ____  C  A
GAM2083  DKFZP434N014 3'  TAAGGAGCCAGGAGGAATGGGG 50773          _  CCCGCC
                                TGAGGAGCCAG AG     GGGG
                                |||||||||| ||     ||||
                                ATTCCTCGGTC TC     CCCC
                                      C  CTTA__
GAM2083  DKFZp547I094 5'  GAGGAGCCAGGATCGGGG    50774         AGCCCGC
                                GAGGAGCCAG      CGGGG
                                |||||||||      |||||
                                CTCCTCGGTC      GCCCC
                                      CTA____
GAM2083  DKFZP547L112 5'  CGGGAGCCAGAGTCCAGGG   50775    A       CCCG
                                TG GGAGCCAGAG   CCGGGG
                                || ||||||||||   ||||||
                                GC CCTCGGTCTC   GGTCCC
                                 _       A___
GAM2083  DKFZp547O146 5'  TGGGAGCCAGAGGTTGGGG   50776    A       CCCGCC
                                TG GGAGCCAGAG    GGGG
                                || ||||||||||    ||||
                                AC CCTCGGTCTC    CCCC
                                 _       CAA___
GAM2083  DKFZP566G1424 5'  TGAGGGCCAGAGCTGGATCCCC 50777    A     _________  GCCGG
            GGG                  GG GCCAGAGC      CC    G
                                || ||||||||      ||    |
                                CC CGGTCTCG      GG    C
                                 _      ACCTIIIA  GGCCG
GAM2083  DOC2A    3'  TGAGGAGCGCGGGGCCTGGG  50778       CAGA  CC_  G
                                TGAGGAGC   GC   GCC GGG
                                ||||||||   ||   ||| |||
                                ACTCCTCG   CG   CGG CCC
                                     ____  CCC   A
GAM2083  FLJ10743  3'  AGGAGCCAGGGCTGGGG    50779         A  CCGCC
                                AGGAGCCAG GC    GGGG
                                |||||||| ||    ||||
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                                TCCTCGGTC CG    CCCC
                                     C  A____
GAM2083  FLJ11526  5'  GAGGAGCCTTCTGCCGGGG   50780       AGAGCCC
                                GAGGAGCC     GCCGGGG
                                ||||||||     |||||||
                                CTCCTCGG     CGGCCCC
                                     AAGA___
GAM2083  FLJ12666  5'  TGAGGGGCCAGGGACCGGGA  50781     A    AGCCC
                                TGAGG GCCAG    GCCGGGG
                                ||||| |||||    |||||||
                                ACTCC CGGTC    TGGCCCT
                                   C    CC___
GAM2083  FLJ12788  3'  TGAGGAGCTGTGAGTAATCTGG 50782       CA_   CCCGCC
            GG                   TGAGGAGC   GAG     GGGG
                                ||||||||   |||     ||||
                                ACTCCTCG   CTC     CCCC
                                     ACA   ATTAGA
GAM2083  FLJ13798  5'  TGAGGAGCCAGAGGCTAGCATA 50783          _ CC  CG
            GGA                   TGAGGAGCCAGAG C  GC  GGGA
                                ||||||||||||| |  ||  ||||
                                ACTCCTCGGTCTC G  CG  TCCT
                                       C AT  TA
GAM2083  FLJ14009  3'  GAGGAGCCGGAGTGGGATCCCC 50784     A  __________  GCCG
            GGCGG                 GAGCC GAG       CCC    GG
                                ||||| |||       |||    ||
                                CTCGG CTC       GGG    CC
                                   C   ACCCTIIIA   GCCG
GAM2083  FLJ14800  3'  TGGGGAGCCAGAGACCTAG   50785    A       CCC   GG
                                TG GGAGCCAGAG   GCC  GG
                                || ||||||||||   |||  ||
                                AC CCTCGGTCTC   TGG  TC
                                 C        ___   A_
GAM2083  GR6       5'  AGGGGCCGGGGCCCACCAGG   50786    A   AGA
                                AGG GCC   GCCCGCCGGG
                                ||| |||   ||||||||||
                                TCC CGG   CGGGTGGTCC
                                  C   CCC
GAM2083  HUMZD58C02 3'  TGAGGGGCCTGGGCCCGGGG   50787      A   AGA   GCC
                                TGAGG GCC   GCCC   GGGG
                                ||||| |||   ||||   ||||
                                ACTCC CGG   CGGG   CCCC
                                   C   ACC   ___
GAM2083  KIAA0169  5'  TGAGGAGCCGGCAGCGGGGG   50788        AGA  CC  C
                                TGAGGAGCC   GC  GC GGGG
                                |||||||||   ||  || ||||
                                ACTCCTCGG   CG  CG CCCC
                                     C__  T_  C
GAM2083  KIAA0227  3'  TGAGGAGCCAGAAGAAGTGGGG 50789           CCCGCC
            A                   TGAGGAGCCAGAG     GGGGA
                                ||||||||||||     |||||
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                                ACTCCTCGGTCTT     CCCCT
                                      CTTCA_
GAM2083  KIAA0522  3'  TGAGGAGCTGGATATGCGGGG  50790        CA  GCCC  C
                                TGAGGAGC  GA    GC GGGG
                                ||||||||  ||    || ||||
                                ACTCCTCG  CT    CG CCCC
                                     AC  ATA_  _
GAM2083  KIAA0757  3'  TGGGGAGTCCAGCTGGGG    50791    A   _  GAGCCC  C
                                TG GGAG CCA     GC GGGG
                                || |||| |||     || ||||
                                AC CCTC GGT     CG CCCC
                                 C   A  _______ A
GAM2083  KIAA0870  3'  TGAGAAGCTGGAGCTCCGTGG  50792        CA   _  CC
                                TGAGGAGC  GAGC CCG  GG
                                ||||||||  |||| |||  ||
                                ACTCTTCG  CTCG GGC  CC
                                     AC   A  A_
GAM2083  KIAA1036  3'  TGAGGAGCCAGGCTTTGGGGA  50793          A  CCGCC
                                TGAGGAGCCAG GC    GGGGA
                                ||||||||||| ||    |||||
                                ACTCCTCGGTC CG    CCCCT
                                      _ AAA__
GAM2083  KIAA1076  3'  GAGGGGCCGGAGCCAGGGG   50794     A  A    CGCC
                                GAGG GCC GAGCC   GGGG
                                |||| ||| |||||   ||||
                                CTCC CGG CTCGG   CCCC
                                  C  C    T___
GAM2083  KIAA1509  3'  AGGAGCCAGCTGGAGGCTGGGG 50795         AGCCC_  C
                                AGGAGCCAG     GC GGGG
                                |||||||||     || ||||
                                TCCTCGGTC     CG CCCC
                                     GACCTC  A
GAM2083  KIAA1855  3'  TGAGGAGCTGGGAAATGGGGA  50796        CA_  CCCGCC
                                TGAGGAGC   GAG     GGGGA
                                ||||||||   |||     |||||
                                ACTCCTCG   CTT     CCCCT
                                     ACC   TA____
GAM2083  LR8       3'  TGAGGAGCCAGGAGTGGGG   50797          _  CCCGCC
                                TGAGGAGCCAG AG     GGGG
                                |||||||||| ||     ||||
                                ACTCCTCGGTC TC     CCCC
                                      C  A_____
GAM2083  MAFB      3'  TGAGGAGCCAGTGTTTCTCCGA 50798          AGCCCG_
                                TGAGGAGCCAG      CCGG
                                ||||||||||      ||||
                                ACTCCTCGGTC      GGCT
                                      ACAAAGA
GAM2083  MGC4549   3'  GGAGCCAGAGCCCCAAGGCTGG 50799           ____  C
              GG                  GGAGCCAGAGCCC   GC GGGG
                                ||||||||||||   || ||||
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                                CCTCGGTCTCGGG   CG CCCC
                                      GTTC  A
GAM2083  PBX4     3'  TGAGGAGCAGGGGCTCATGGG  50800        C  A_  C  CC
                                TGAGGAGC AG  GC CG  GGG
                                |||||||| ||  || ||  |||
                                ACTCCTCG TC  CG GT  CCC
                                     _  CC  A  A_
GAM2083  PEMT     3'  GGGGCAGCCCACGCCGGGG   50801    A  CAG    __
                                GG GC   AGCCC  GCCGGGG
                                || ||   |||||  |||||||
                                CC CG   TCGGG  CGGCCCC
                                 C  ___    TG
GAM2083  PEPP3    3'  TGGGGAGCCAGGACCTCAGG   50802    A      AG  CGC
                                TG GGAGCCAG  CC   CGGG
                                || ||||||||  ||   ||||
                                AC CCTCGGTC  GG   GTCC
                                 C       CT  A__
GAM2083  PRDM12   3'  TGCGGGGCCGGGGTGCCGGGGA 50803    A  A   AGAGCCC
                                TG GG GCC      GCCGGGGA
                                || || |||      ||||||||
                                AC CC CGG      CGGCCCCT
                                 G  C   CCCCA__
GAM2083  QSCN6    3'  TGAGGAGCTGGAGGCTGG    50804        CA   CCC  C
                                TGAGGAGC  GAG   GC GG
                                ||||||||  |||   || ||
                                ACTCCTCG  CTC   CG CC
                                     AC   ___  A
GAM2083  RAB40C   3'  TGGGAGCCAGGGCCCCGG    50805    A      A   GC
                                TG GGAGCCAG GCCC  CGG
                                || |||||||| ||||  |||
                                AC CCTCGGTC CGGG  GCC
                                 _       C   __
GAM2083  RASGRP4  3'  TGGGGGGCCAGGGCCACCAGGG 50806    A  A    A   C
                                TG GG GCCAG GCC GCCGGGG
                                || || ||||| ||| |||||||
                                AC CC CGGTC CGG TGGTCCC
                                 C  C    C  _
GAM2083  SDC3     3'  TGAGGAGCCAGGCCTGCCGGGG 50807          A   C
                                TGAGGAGCCAG GCC GCCGGGG
                                |||||||||| ||| |||||||
                                ACTCCTCGGTC CGG CGGCCCC
                                     _  A
GAM2083  SHANK3   5'  TGGGAGGCCAGAGCTCGCTCTC 50808    A   _     C  ___
            GGG                    TG GGAG CCAGAGC CGC   CGGG
                                || |||| ||||||| |||   ||||
                                AC CCTC GGTCTCG GCG   GCCC
                                 _   C      A  AGA
GAM2083  SHANK3   3'  GAGGGGCCGGAGATGGATCCCC 50809   A  A  __________  GCCG
            GGCGG                  G GCC GAG       CCC   GG
                                | ||| |||       |||   ||
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                                C CGG CTC        GGG    CC
                                 C   C   TACCTIIIA   GCCG
GAM2083  TBC1D2    3'  TGAGGGCCAGAGAGGG      50810       A      CCCGCC
                                TGAGG GCCAGAG      GGG
                                ||||| |||||||      |||
                                ACTCC CGGTCTC      CCC
                                   _      T_____
GAM2083  TOB2      3'  TGAGAAGCCAGGACATTGCCTG 50811          A_____   C
              CCGGGG                  GAGGAGCCAG      GCC GCCGGGG
                                ||||||||||      ||| |||||||
                                CTCTTCGGTC      CGG CGGCCCC
                                      CTGTAA   A
GAM2083  TRIM11    3'  TGGGGAGCCAGGGTTCCCCGGA 50812     A       AGC_  G
                                TG GGAGCCAG    CC CCGGG
                                || ||||||||    || |||||
                                AC CCTCGGTC    GG GGCCT
                                 C       CCAA  _
GAM2083  Ubc6p     3'  TGAGGAGCCGGGAGCTCCG    50813         A_    _
                                TGAGGAGCC  GAGC CCG
                                |||||||||  |||| |||
                                ACTCCTCGG  CTCG GGC
                                      CC    A
GAM2083  LOC116236 3'  TGAGGAGCACAGAGCTGGATCC 50814      _     _________  GCCGG
              CCGGCGG                  AGC CAGAGC       CC     GG
                                ||| ||||||       ||     ||
                                TCG GTCTCG       GG     CC
                                  T     ACCTIIIA  GGCCG
GAM2083  LOC126528 3'  TGAGGAGCAGGGCCTGG     50815         C  A   CGCC
                                TGAGGAGC AG GCC    GG
                                |||||||| || |||    ||
                                ACTCCTCG TC CGG    CC
                                     _ C   A___
GAM2083  LOC144165 5'  TGAGGAGCTGCGGTCCGCGG   50816         CAGA  CCG   G
                                TGAGGAGC    GC   CCG GG
                                ||||||||    ||   ||| ||
                                ACTCCTCG    CG   GGC CC
                                     A___  CCA   G
GAM2083  LOC150372 5'  GAGGAGCCAGGGGGCTGCGGGG 50817          A__  CC  C
              A                   GAGGAGCCAG   GC  GC GGGGA
                                ||||||||||   ||  || |||||
                                CTCCTCGGTC   CG  CG CCCCT
                                      CCC  A_  _
GAM2083  LOC152189 5'  GAGGGGGGCGCCCGCCGGGG   50818      AGCCAGA
                                GAGG      GCCCGCCGGGG
                                ||||      ||||||||||
                                CTCC      CGGGCGGCCCC
                                  CCCCG__
GAM2083  LOC155006 3'  TGGGGAGTGATGAGCCGGGGA  50819     A   CCA  GCCC
                                TG GGAG   GA    GCCGGGGA
                                || ||||   ||    ||||||||
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                                AC CCTC   CT    CGGCCCCT
                                 C    A__  ACT_
GAM2083  LOC158287 3'  TGAGGAGCAGAGCAAGGGG    50820        C     CCGCC
                                TGAGGAGC AGAGC     GGGG
                                |||||||| |||||     ||||
                                ACTCCTCG TCTCG     CCCC
                                     _     TT___
GAM2083  LOC163682 3'  GAGGGCCAGGGCCAGGG     50821      A     AGCCC
                                GAGG GCCAG     GCCGGGG
                                |||| |||||     |||||||
                                CTCC CGGTC     CGGTCCC
                                  _     C____
GAM2083  LOC164582 5'  TGGGGAACCAGAGCCTGGGA   50822     A          CGCC
                                TG GGAGCCAGAGCC    GGGG
                                || ||||||||||||    ||||
                                AC CCTTGGTCTCGG    CCCT
                                 C          A___
GAM2083  LOC196463 3'  GAGGGGCCAGAGCTGGGA     50823      A       CCGCC
                                GAGG GCCAGAGC     GGGG
                                |||| ||||||||     ||||
                                CTCC CGGTCTCG     CCCT
                                  C       A____
GAM2083  LOC200093 3'  GAGGAGCCCTGCGCTGGGGA   50824         AGAGCC   C
                                GAGGAGCC     CGC GGGGA
                                ||||||||     ||| |||||
                                CTCCTCGG     GCG CCCCT
                                     GAC___   A
GAM2083  LOC204804 3'  TGAGGGACCAGAGCTGGGA    50825      AG      CCGCC
                                TGAGG  CCAGAGC     GGGG
                                |||||  |||||||     ||||
                                ACTCC  GGTCTCG     CCCT
                                   CT      A____
GAM2083  LOC221832 3'  TGAGGGGCCAGAGCTGTCGAAG 50826       A       C__  CC
            GG                    TGAGG GCCAGAGC   CG  GGGG
                                |||||  ||||||||   ||  ||||
                                ACTCC CGGTCTCG   GC  TCCC
                                   C       ACA  T_
GAM2083  LOC253866 5'  TGAGAGGCCAGAGCGGGCGTGG 50827      GA       CC  C_
            GG                    TGAG  GCCAGAGC  GC  GGGG
                                ||||  ||||||||  ||  ||||
                                ACTC  CGGTCTCG  CG  CCCC
                                   TC       CC  CA
GAM2083  LOC255031 5'  TGGGGAACCAGGGAGCGCTGGG 50828    A       AGCC   C
            GA                    TG GGAGCCAG    CGC GGGGA
                                || ||||||||    ||| |||||
                                AC CCTTGGTC    GCG CCCCT
                                 C       CCTC   A
GAM2083  LOC59346  5'  GAGGAGCCCGGCGCCGGGGA   50829         AGAGCC
                                GAGGAGCC     CGCCGGGGA
                                ||||||||     |||||||||
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                                CTCCTCGG     GCGGCCCCT
                                     GCC___
GAM2083  LOC85479  5'  TGAGGAGCCAGGTGCCTTTAGG 50830          A_   CGCCG
                                TGAGGAGCCAG  GCC    GGG
                                ||||||||||  |||    |||
                                ACTCCTCGGTC  CGG    TCC
                                      CA   AAA__
GAM2083  LOC91040  3'  GAGGAGCCCCACGCTGGGGA  50831        AGAG  _   C
                                GAGGAGCC   CC CGC GGGGA
                                ||||||||   || ||| |||||
                                CTCCTCGG   GG GCG CCCCT
                                     ____  T   A
GAM2083  LOC91179  3'  TGAGGGGCCTGGGCCCGGGG  50787      A   AGA   GCC
                                TGAGG GCC   GCCC   GGGG
                                ||||| |||   ||||   ||||
                                ACTCC CGG   CGGG   CCCC
                                   C   ACC   ___
GAM2084  ADAR     3'  TGAAGATAACAGTGGGCAGAA  50834         _   T  CAA
                                TGAAGATAA AGTG GC   AGAA
                                |||||||| |||| ||   ||||
                                ACTTCTATT TCAC CG   TCTT
                                     G   C  ___
GAM2084  ADAR     3'  TGAAGATAACAGTGGGCAGAA  50834         _   T  CAA
                                TGAAGATAA AGTG GC   AGAA
                                |||||||| |||| ||   ||||
                                ACTTCTATT TCAC CG   TCTT
                                     G   C  ___
GAM2084  ADAR     3'  TGAAGATAACAGTGGGCAGAA  50834         _   T  CAA
                                TGAAGATAA AGTG GC   AGAA
                                |||||||| |||| ||   ||||
                                ACTTCTATT TCAC CG   TCTT
                                     G   C  ___
GAM2084  C18orf1  3'  TGAAGATAAATGCAGA      50835         AGT   CAA
                                TGAAGATAA   GTGC   AGA
                                |||||||||   ||||   |||
                                ACTTCTATT   TACG   TCT
                                     ___    ___
GAM2084  CYP51    5'  GAAGATAACTTACCTGAAGA   50836         AGTG   A_
                                GAAGATAA    TGCC  AAGA
                                ||||||||    ||||  ||||
                                CTTCTATT    ATGG  TTCT
                                     GA__    AC
GAM2084  LASS2    3'  TGAAGAAGTAATAGCCAAAGAA 50837       TAA   T
                                TGAAGA   AGTG GCCAAAGAA
                                ||||||   |||| |||||||||
                                ACTTCT   TTAT CGGTTTCTT
                                   TCA   _
GAM2084  OPHN1    3'  TGAAGACAGAATACAAAG     50838         A   TGC
                                TGAAGATA AGTG   CAAAG
                                |||||||| ||||   |||||
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                                ACTTCTGT TTAT   GTTTC
                                     C   ___
GAM2084  PBX1     3'  GAAATAGCATCCCAAAGAA   50839    TAA    G
                                GA   AGTGT CCAAAGAA
                                ||   ||||| ||||||||
                                CT   TCGTA GGTTTCTT
                                 TTA    G
GAM2084  SFTPA2   3'  TGAAGATATAGGCTCAGGGAAA 50840        A  T  GC  AA
                                TGAAGATA AG GT  CA  GAAA
                                |||||||| || ||  ||  ||||
                                ACTTCTAT TC CG  GT  CTTT
                                     A  _  A_  CC
GAM2084  SLC22A2  3'  TGAGAATAAAGTGAGCTGGAA  50841     AG       T  CAAA
                                TGA  ATAAAGTG GC    GAA
                                |||  |||||||| ||    |||
                                ACT  TATTTCAC CG    CTT
                                  CT       T  AC__
GAM2084  SMPX     3'  TGAAGATAAAGTAAGAA     50842           TGCCAA
                                TGAAGATAAAGTG     AGAA
                                ||||||||||||      ||||
                                ACTTCTATTTCAT     TCTT
                                                  _______
GAM2084  TCFL4    3'  TGAAGATAAAATGGGGCTGGGA 50843           T_  CAAA
                AA                  TGAAGATAAAGTG  GC    GAAA
                                ||||||||||||  ||    ||||
                                ACTTCTATTTTAC  CG    CTTT
                                       CC  ACC_
GAM2084  UC28     3'  TGAAGAAAACAAAACCAAAGAA 50844       T  AGTGT
                A                    TGAAGA AA     GCCAAAGAAA
                                ||||||  ||     ||||||||||
                                ACTTCT TT     TGGTTTCTTT
                                   T  GTTT_
GAM2084  WARS     3'  GAACACTGGTGTGCCAAGGGAA 50845     G  AAA       A_
                                GAA AT   GTGTGCCAA  GAA
                                |||  ||   |||||||||  |||
                                CTT TG   CACACGGTT  CTT
                                  G  AC_        CC
GAM2084  XK       3'  TAAGGTGGTTTCCAAAGAAA   50846     A   TG__
                                TAA GTG    CCAAAGAAA
                                |||  |||    |||||||||
                                ATT CAC    GGTTTCTTT
                                  C   CAAA
GAM2084  ABCA10   3'  TGAATATAAGTTGGCTAAAGAA 50847     G    AG  T  C
                A                    TGAA ATAA  TG GC AAAGAAA
                                |||| ||||  || || |||||||
                                ACTT TATT  AC CG TTTCTTT
                                  A   CA  _  A
GAM2084  C20orf72 3'  TGAAAATGGCTACCCAAAGAA  50848        AAA  GTG
                                TGAAGAT   GT   CCAAAGAA
                                |||||||   ||   ||||||||
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                                ACTTTTA  CG  GGTTTCTT
                                   C__  ATG
GAM2084  C8orf14   5'  AAAGAGTGTGCCAGAGAAA   50849      TAAA      A
                                GAAGA   GTGTGCCA AGAAA
                                |||||   |||||||| |||||
                                TTTCT   CACACGGT TCTTT
                                  _____       C
GAM2084  CLIC4     3'  TAAAGATAAAATGCTTGAGGAA 50850            GCCAAA
                                TGAAGATAAAGTGT     GAA
                                ||||||||||||||     |||
                                ATTTCTATTTTACG     CTT
                                        AACTC_
GAM2084  DKFZP434P211 3'  TGAAGACAGAGCTTGCAGA   50851        A  G  CAA
                                TGAAGATA AGT TGC   AGA
                                |||||||| ||| |||   |||
                                ACTTCTGT TCG ACG   TCT
                                     C  A  ___
GAM2084  DKFZp566H0824 5'  TGAGGATGGAAGTGCCAAAAA  50852     A  AAAGT
                                TGA GAT    GTGCCAAAGA
                                ||| |||    ||||||||||
                                ACT CTA    CACGGTTTTT
                                  C  CCTT_
GAM2084  FLJ00012  3'  AGATAAAAATACAAAGAAA   50853        T   C
                                AGATAAAG GTGC AAAGAAA
                                |||||||| |||| |||||||
                                TCTATTTT TATG TTTCTTT
                                       _   _
GAM2084  FLJ13063  5'  TGAAGAATGGTCACCAAAG   50854       TAAA  G
                                TGAAGA   GT TGCCAAAG
                                ||||||   || ||||||||
                                ACTTCT   CA GTGGTTTC
                                   TAC_  _
GAM2084  GABARAPL1 3'  TGAGATAAGGGGCACCAAAGA  50855     A    AGT TG
                                TGA GATAA   G  CCAAAGA
                                ||| |||||   |  |||||||
                                ACT CTATT   C  GGTTTCT
                                  _    CCC GT
GAM2084  KIAA0057  3'  TGAAATAAACGTGCCAGGGA   50856     A     G      AA
                                TGA GATAAA TGTGCCA  GA
                                ||| |||||| |||||||  ||
                                ACT TTATTT GCACGGT  CT
                                  _     _      CC
GAM2084  KIAA0087  3'  GAAGTAAAATGCCAAGGA    50857      A   GT      A
                                GAAG TAAA  GTGCCAA GA
                                |||| ||||  ||||||| ||
                                CTTC ATTT  TACGGTT CT
                                  _   __      C
GAM2084  KIAA0185  3'  TGAAAATAAAGCAAGCGAAGA  50858           T  CA
                                TGAAGATAAAGTG GC  AAGA
                                |||||||||||| ||  ||||
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                                ACTTTTATTTCGT CG  TTCT
                                       T  C_
GAM2084  KIAA0513  3'  TGAAGTTAAAGTGCTTGGAAA  50859      A      GCCAAA
                                TGAAG TAAAGTGT     GAAA
                                ||||| ||||||||     ||||
                                ACTTC ATTTCACG     CTTT
                                   A       AAC___
GAM2084  KIAA1724  3'  TGAAGACAAAGAAATAGAAGAA 50860          TGTGCCA
            A                    TGAAGATAAAG      AAGAAA
                                ||||||||||      ||||||
                                ACTTCTGTTTC      TTCTTT
                                      TTTATC_
GAM2084  KIAA1918  3'  TAAAGATGAGGACCAAAGAA   50861       AA  TGT
                                TGAAGAT  AG   GCCAAAGAA
                                |||||||  ||   |||||||||
                                ATTTCTA  TC   TGGTTTCTT
                                    C_  C__
GAM2084  MAPK8IP3  3'  TGAACATGAGCAAGCGCAAAGA 50862     G  AA   T  _
            AA                    TGAA AT  AGTG GC CAAAGAAA
                                |||| ||  |||| || ||||||||
                                ACTT TA  TCGT CG GTTTCTTT
                                  G  C_   T  C
GAM2084  PRO1617   5'  TGGGGACAATGCCCCAAAGAAA 50863    AA   AA   G
                                TG  GATA  GTGT CCAAAGAAA
                                ||  ||||  |||| |||||||||
                                AC  CTGT  TACG GGTTTCTTT
                                 CC   __   G
GAM2084  PROZ     3'  TGAGATAAAGAGTTCCAGGGAA 50864     A     T  G   AA
            A                    TGA GATAAAG GT CCA  GAAA
                                ||| ||||||| || |||  ||||
                                ACT CTATTTC CA GGT  CTTT
                                  _     T  A   CC
GAM2084  SEPT1    3'  TGAAGACAGAGTCTGGGAGAA  50865       A  G  CCAA
                                TGAAGATA AGT TG    AGAA
                                |||||||| ||| ||    ||||
                                ACTTCTGT TCA AC    TCTT
                                    C   G  CC__
GAM2084  TCL6     3'  TGAAAATAAACTATGAAGAAA  50866         G   CCA
                                TGAAGATAAA TGTG   AAGAAA
                                |||||||||| ||||   ||||||
                                ACTTTTATTT ATAC   TTCTTT
                                      G   ___
GAM2084  TCL6     3'  TGAAAATAAACTATGAAGAAA  50866         G   CCA
                                TGAAGATAAA TGTG   AAGAAA
                                |||||||||| ||||   ||||||
                                ACTTTTATTT ATAC   TTCTTT
                                      G   ___
GAM2084  TRIM5    5'  TGAAGACAGGCCAGGGAA    50867        AAGTGT   AA
                                TGAAGATA     GCCA  GAA
                                ||||||||     ||||  |||
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                                ACTTCTGT     CGGT  CTT
                                    C_____    CC
GAM2084  TRIM5    5'  TGAAGACAGGCCAGGGAA    50867        AAGTGT    AA
                                TGAAGATA     GCCA  GAA
                                ||||||||     ||||  |||
                                ACTTCTGT     CGGT  CTT
                                    C_____    CC
GAM2084  TRIM5    5'  TGAAGACAGGCCAGGGAA    50867        AAGTGT    AA
                                TGAAGATA     GCCA  GAA
                                ||||||||     ||||  |||
                                ACTTCTGT     CGGT  CTT
                                    C_____    CC
GAM2084  UGT2B10  3'  GAGAGATTTGTGCCAAGGA    50868    _   AAAG      A
                                GA AGAT    TGTGCCAA GA
                                || ||||    |||||||| ||
                                CT TCTA    ACACGGTT CT
                                 C    A___       C
GAM2084  ZFP91    3'  TGAAGATAAGTGTGCCGCAG   50869         A      AA
                                TGAAGATAA GTGTGCC  AG
                                ||||||||| |||||||  ||
                                ACTTCTATT CACACGG  TC
                                      _      CG
GAM2084  LOC145813 5'  TGAGGGACAGTGCCAAAGA    50870     A_   AAGT
                                TGA  GATA    GTGCCAAAGA
                                |||  ||||    ||||||||||
                                ACT  CTGT    CACGGTTTCT
                                  CC    _____
GAM2084  LOC148545 3'  GATAAAATGTTCTGAAGAA    50871          GCCA
                                GATAAAGTGT    AAGAA
                                ||||||||||    |||||
                                CTATTTTACA    TTCTT
                                      AGAC
GAM2084  LOC149072 5'  TGAGATAATGGATGCCAAAGAA 50872     A    AGT
                                TGA GATAA   GTGCCAAAGAA
                                ||| |||||   ||||||||||||
                                ACT CTATT   TACGGTTTCTT
                                  _    ACC
GAM2084  LOC150311 5'  TGGAGATAAAGGTGTTCACTAG 50873    A      T   C_  A_
              A                  TG AGATAAAG GTG  CA  AGA
                                || |||||||| |||  ||  |||
                                AC TCTATTTC CAC  GT  TCT
                                 C       _   AA  GA
GAM2084  LOC152275 5'  TGAGGATAAAGTTGCCA     50874     A      G
                                TGA GATAAAGT TGCCA
                                ||| |||||||| |||||
                                ACT CTATTTCA ACGGT
                                  C       _
GAM2084  LOC157273 5'  TGGAGATAAAGGCCCTAGAAA  50875    A      TGT   AA
                                TG AGATAAAG   GCC  AGAAA
                                || ||||||||   |||  |||||
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                                AC TCTATTTC   CGG  TCTTT
                                 C       ___   GA
GAM2084  LOC157349 5'  TGAAGACAGGGCCTGAAGAA   50876       AA  G  CCA
                                TGAAGATA  GT TG   AAGAA
                                ||||||||  || ||   |||||
                                ACTTCTGT  CG AC   TTCTT
                                    CC  G  ___
GAM2084  LOC196500 3'  TGAGAGGTAAAGTGTGCAGGAA 50877     _  A        CAAA
           A                     TGA AG TAAAGTGTGC    GAAA
                                ||| || ||||||||||    ||||
                                ACT TC ATTTCACACG    CTTT
                                  C  C        TC__
GAM2084  LOC196955 5'  TGAAGACAGGGCCTAGAA    50878       AAGTGT   AA
                                TGAAGATA     GCC  AGAA
                                ||||||||     |||  ||||
                                ACTTCTGT     CGG  TCTT
                                    CC_____   A_
GAM2084  LOC199787 3'  TGGAGGGAAAGTGTAGAAAAGA 50879    A  AT       CC
           AA                    TG AG  AAAGTGTG  AAAGAAA
                                || ||  ||||||||  |||||||
                                AC TC  TTTCACAT  TTTCTTT
                                 C  CC       CT
GAM2084  LOC220370 3'  TGAAGACAGATCCCAGAG    50880       AAGT  G   A
                                TGAAGATA    GT CCA AG
                                ||||||||    || ||| ||
                                ACTTCTGT    TA GGT TC
                                    C___  G   C
GAM2084  LOC221810 3'  TGAAGATAAAAGCTGAGAGAA  50881         T  GCCAA
                                TGAAGATAAAG GT     AGAA
                                ||||||||||| ||     ||||
                                ACTTCTATTTT CG     TCTT
                                      _  ACTC_
GAM2084  LOC91408  3'  TGAAGATGAAGTTGTTCCTCAA 50882       A   _  G  A_
           G                     TGAAGAT AAGT GT CC  AAG
                                ||||||| |||| || ||  |||
                                ACTTCTA TTCA CA GG  TTC
                                    C   A  A  AG
GAM2084  LOC91431  5'  TGATAGATGATGGTCCAAAGAA 50883     _   AAA   TG
           A                     TGA AGAT   GTG  CCAAAGAAA
                                ||| ||||   |||  |||||||||
                                ACT TCTA   TAC  GGTTTCTTT
                                  A   C__   CA
GAM2084  LOC92539  5'  TGAAGAGAGGAGCATCAAAGAA 50884       TAAAGT  GC
           A                     TGAAGA     GT  CAAAGAAA
                                ||||||     ||  ||||||||
                                ACTTCT     CG  GTTTCTTT
                                   CTCCT_  TA
GAM2085  ACADL    3'  ACATGTTTAGTGTTTCCTCGC  50887     G     CGCT
                                ACA GTTTAG    TTTTCTCGC
                                ||| ||||||    |||||||||
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                                TGT CAAATC    AAAGGAGCG
                                  A     AC__
GAM2085  BDKRB2   3'  ACATGTTTACATGATTTTCTCG 50888     G    G  CT_
                                ACA GTTTA CG   TTTTCTCG
                                ||| ||||| ||   ||||||||
                                TGT CAAAT GT   AAAAGAGC
                                  A    _  ACT
GAM2085  RAD17    5'  AGATTTCCTCTTTTTCTCGC   50889       AGCG
                                AGGTTT    CTTTTTCTCGC
                                ||||||    ||||||||||
                                TCTAAA    GAAAAAGAGCG
                                   GGA_
GAM2085  TBX6     5'  AGTTTGGCGCTTCCGGC     50890      A    TTT   C
                                GGTTT GCGCT   TCT GC
                                ||||| |||||   ||| ||
                                TCAAA CGCGA   AGG CG
                                   C     ___   C
GAM2085  TBX6     5'  AGTTTGGCGCTTCCGGC     50890      A    TTT   C
                                GGTTT GCGCT   TCT GC
                                ||||| |||||   ||| ||
                                TCAAA CGCGA   AGG CG
                                   C     ___   C
GAM2085  LOC118742 3'  CAGCATCCGCTTTTTCT     50891     _   TAG
                                CAG GTT   CGCTTTTTCT
                                ||| |||   ||||||||||
                                GTC TAG   GCGAAAAAGA
                                  G   ___
GAM2085  LOC158978 5'  CAGGTCTTTCCTTTTCT     50892       AGCG
                                CAGGTTT    CTTTTTCT
                                |||||||    ||||||||
                                GTCCAGA    GGAAAAGA
                                   AA__
GAM2085  LOC160414 5'  AAGCAAAGCGCTTTTTCTTGCC 50893      TT          C
                                AGGT  AGCGCTTTTTCT GCC
                                ||||  |||||||||||| |||
                                TTCG  TCGCGAAAAAGA CGG
                                  TT          A
GAM2086  ABCB10   3'  AAAATCACACTTTATAAA     50896          CTCG
                                AAAATCACAC    GTGGA
                                ||||||||||    |||||
                                TTTTAGTGTG    TATTT
                                     AAA_
GAM2086  CELSR1   3'  AAAATTACACCTCAGGG     50897      C        T
                                AAAAT ACACCTCGG GG
                                ||||| |||||||| ||
                                TTTTA TGTGGAGTC CC
                                  A        _
GAM2086  CPLX2    5'  ATCACACCTTCCTGTTGGA    50898         _ G_  _
                                ATCACACCT C  GT GGA
                                ||||||||| |  || |||
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                                TAGTGTGGA G  CA CCT
                                    A GA  A
GAM2086  CTPS     3'  TAAAATCACGCTTCAGAGA   50899        ACC   T
                                TAAAATCAC   TCGG GGA
                                |||||||||   |||| |||
                                ATTTTAGTG   AGTC TCT
                                    CGA   _
GAM2086  DAPK1    3'  TAAAATCACCCTGGAGGA    50900        A   C  T
                                TAAAATCAC CCT GG GGA
                                ||||||||| ||| || |||
                                ATTTTAGTG GGA CC CCT
                                    _   _  T
GAM2086  GCA      3'  TAAAAACACACAGAAAGGGAA  50901      T    CTC_  T
                                TAAAA CACAC    GG GGAA
                                ||||| |||||    || ||||
                                ATTTT GTGTG    TC CCTT
                                   T    TCTT  _
GAM2086  GNB5     3'  TAAAATCAGCACTTCCAGAGG  50902        _  C_   T
                                TAAAATCA CAC  TCGG GG
                                |||||||| |||  |||| ||
                                ATTTTAGT GTG  GGTC CC
                                    C   AA    T
GAM2086  GNB5     3'  TAAAATCAGCACTTCCAGAGG  50902        _  C_   T
                                TAAAATCA CAC  TCGG GG
                                |||||||| |||  |||| ||
                                ATTTTAGT GTG  GGTC CC
                                    C   AA    T
GAM2086  KCNJ1    5'  TAAGATCACACCAGGAAGA   50903     A      TC  T
                                TAA ATCACACC  GG GGA
                                ||| ||||||||  || |||
                                ATT TAGTGTGG  CC TCT
                                  C       T_  T
GAM2086  KL       3'  AAAATCATACCTCTAAAGA   50904        C    GGT
                                AAAATCA ACCTC   GGA
                                ||||||| |||||   |||
                                TTTTAGT TGGAG   TCT
                                    A    ATT
GAM2086  MAPK10   3'  TAAAATTACACTTTATGGAAAA 50905       C   CTCG
                                TAAAAT ACAC   GTGGAAAG
                                |||||| ||||   ||||||||
                                ATTTTA TGTG   TACCTTTT
                                   A   AAA_
GAM2086  MAPK10   3'  TAAAATTACACTTTATGGAAAA 50905       C   CTCG
                                TAAAAT ACAC   GTGGAAAG
                                |||||| ||||   ||||||||
                                ATTTTA TGTG   TACCTTTT
                                   A   AAA_
GAM2086  PKHD1    3'  TAAAACATGCCTCCCAGAAAGA 50906       T  CA   GGT
                                TAAAA CA  CCTC   GGAAAGA
                                ||||| ||  ||||   |||||||
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                                ATTTT GT  GGAG   TCTTTCT
                                  _ AC    GG_
GAM2086  SMS      3'  AAAATCACATTCTAATGG    50907         CC  _
                                AAAATCACA  TC GGTGG
                                |||||||||  || |||||
                                TTTTAGTGT  AG TTACC
                                     A_  A
GAM2086  TBR1     3'  TAAAATCACGCTCGGAGA    50908         AC    T
                                TAAAATCAC  CTCGG GGA
                                |||||||||  ||||| |||
                                ATTTTAGTG  GAGCC TCT
                                     C_    _
GAM2086  CNOT3    5'  AAATCACACTTCCTACTCAGAG 50909          _______    T
              G                  AAATCACAC     CTCGG GG
                                |||||||||      ||||| ||
                                TTTAGTGTG     GAGTC CC
                                     AAGGAT    T
GAM2086  COPB     5'  AAAATCACGCCTCTGGGA    50910         A   GGT
                                AAAATCAC CCTC   GGA
                                |||||||| ||||   |||
                                TTTTAGTG GGAG   CCT
                                     C   AC_
GAM2086  DKFZP564O0423 3'  AAATCACATTTTCTTGGGGA   50911         C___  C  T
                                AAATCACA   CT GG GGA
                                ||||||||   || || |||
                                TTTAGTGT   GA CC CCT
                                     AAAA  A  _
GAM2086  DYRK4    3'  AAATCACTGGTGGAAAG     50912         ACCTC
                                AAATCAC    GGTGGAAAG
                                |||||||    |||||||||
                                TTTAGTG    CCACCTTTC
                                    A____
GAM2086  ERG-1    5'  TAAAGTCACACCCTCCCTTGAA 50913      A      _  GG_
                                TAAA TCACACC TC   TGGA
                                |||| ||||||| ||   ||||
                                ATTT AGTGTGG AG   ACTT
                                  C      G  GGA
GAM2086  FLJ13902 3'  AAATCACAGCTGTTGGTGAGA  50914         C  C__   _
                                AAATCACA CT   GGTG GA
                                |||||||| ||   |||| ||
                                TTTAGTGT GA   CCAC CT
                                     C  CAA    T
GAM2086  HSPC142  3'  AAAATCACACAGGGAA      50915          CTC  T
                                AAAATCACAC   GG GGAA
                                ||||||||||   || ||||
                                TTTTAGTGTG   TC CCTT
                                      ___  _
GAM2086  IKKE     3'  AAATCACAAGGGAGTGGAGAGA 50916         CCTC     A
                                AAATCACA    GGTGGA AGA
                                ||||||||    |||||| |||
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                                TTTAGTGT   TCACCT TCT
                                    TCCC    C
GAM2086 KIAA0295 3' TAAAATCATGTACTTGTAGACA 50917       CACCTCG    A
            GA                   TAAAATCA     GTGGA AGA
                                 |||||||      ||||| |||
                                 ATTTTAGT     CATCT TCT
                                    ACATGAA    G
GAM2086 KIAA0564 3' TAAAAGTCACGTGGAAAG    50918     _   ACCTCG
                                 TAAAA TCAC    GTGGAAAG
                                 ||||| ||||    ||||||||
                                 ATTTT AGTG    CACCTTTC
                                   C   _______
GAM2086 KIAA0783 3' TAAAATCACACTTATAAAAGA  50919        CTCGGTG
                                 TAAAATCACAC     GAAAGA
                                 ||||||||||      ||||||
                                 ATTTTAGTGTG     TTTTCT
                                       AATA___
GAM2086 KIAA1042 3' TCACACCTCAAAAAAGA     50920         TG
                                 TCACACCTCGG  GAAAGA
                                 ||||||||||  ||||||
                                 AGTGTGGAGTT  TTTTCT
                                          __
GAM2086 KIAA1387 3' TAAAACTTGCAGCTCTGGAAAG 50921      CA_  C   GG
            A                    TAAAAT   CA CTC  TGGAAAGA
                                 ||||||   || |||  ||||||||
                                 ATTTTG   GT GAG  ACCTTTCT
                                    AAC  C   __
GAM2086 KIAA1718 3' TAAAATACAGAAATTGGAAAGA 50922      C   CCTCGG
                                 TAAAAT ACA     TGGAAAGA
                                 |||||| |||     ||||||||
                                 ATTTTA TGT     ACCTTTCT
                                    _   CTTTA_
GAM2086 KIAA1727 3' TCACAGAGGTGGAAAGA     50923      CCTC
                                 TCACA    GGTGGAAAGA
                                 |||||    ||||||||||
                                 AGTGT    CCACCTTTCT
                                    CT__
GAM2086 KIAA1789 5' TAAAATCATTCTGACCCTAGGG 50924        C____    CG T
            A                    TAAAATCA    ACCT  G GGA
                                 ||||||||    ||||  | |||
                                 ATTTTAGT    TGGG  C CCT
                                      AAGAC    AT _
GAM2086 LANO     3' AAAATCACACCGGGAGA     50925         TC  TG
                                 AAAATCACACC  GG  GA
                                 ||||||||||  ||  ||
                                 TTTTAGTGTGG  CC  CT
                                        __ CT
GAM2086 MGC19556 3' TAAAATCAATCACCAGGAAAG  50926        __    TCGGT
                                 TAAAATCA  CACC    GGAAAG
                                 ||||||||  ||||    ||||||
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                                ATTTTAGT  GTGG    CCTTTC
                                    TA   T____
GAM2086  PAXIP1L   3'  TAAAATTGCACATCTTAAAAAG 50927      CA   C  GG
             A                   TAAAAT  CAC TC  TGGAAAGA
                                 ||||||  ||| ||  ||||||||
                                 ATTTTA  GTG AG  ATTTTTCT
                                    AC   T  A_
GAM2086  RAB14    3'  TAAAATCACACTTAAAAG    50928          CTCGGTG
                                 TAAAATCACAC      GAAAG
                                 ||||||||||       |||||
                                 ATTTTAGTGTG      TTTTC
                                       AA_____
GAM2086  SV2B     3'  AAATCGACGGTGGAAAG     50929       ACACCT
                                 AAATC     CGGTGGAAAG
                                 |||||     ||||||||||
                                 TTTAG     GCCACCTTTC
                                    CT____
GAM2086  LOC129293 3'  CAAAGTCACATTCCTTGGAAAG 50930      A    CC  GG
             A                   TAAA TCACA  TC  TGGAAAGA
                                 |||| |||||  ||  ||||||||
                                 GTTT AGTGT  AG  ACCTTTCT
                                   C    A_  GA
GAM2086  LOC148734 5'  TAAAACCACAAAGGTGGGGAGA 50931          CCTC    AA
                                 TAAAATCACA    GGTGG  AGA
                                 ||||||||||    |||||  |||
                                 ATTTTGGTGT    CCACC  TCT
                                       TT__     CC
GAM2086  LOC151005 3'  CAAGATCACACCGGACAAGGGA 50932     A       T__   T
                                 TAA ATCACACC   CGG GGA
                                 ||| ||||||||   ||| |||
                                 GTT TAGTGTGG   GTT CCT
                                   C       CCT   C
GAM2086  LOC151877 3'  TAAAATCACACATCTGATAAA  50933          C  _
                                 TAAAATCACAC TC GGTGGA
                                 |||||||||| || ||||||
                                 ATTTTAGTGTG AG CTATTT
                                       T  A
GAM2086  LOC154789 3'  AAAATCACATCTCAGGAA    50934         C    T
                                 AAAATCACA CTCGG GGA
                                 ||||||||| ||||| |||
                                 TTTTAGTGT GAGTC CTT
                                      A    _
GAM2086  LOC162962 3'  TAAAATCATGGTGGAAG     50935        CACCTC      A
                                 TAAAATCA      GGTGGAA G
                                 ||||||||      ||||||| |
                                 ATTTTAGT      CCACCTT C
                                      A_____       C
GAM2086  LOC169026 3'  AAAATCACAGCGTGGAGAG    50936         CCTCG    A
                                 AAAATCACA     GTGGA AG
                                 |||||||||     ||||| ||
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                                TTTTAGTGT    CACCT TC
                                     CG___    C
GAM2086  LOC245744 3'  TCACACCTCGGGCACCTGGA  50937          _____
                                TCACACCTCGG    TGGA
                                ||||||||||    ||||
                                AGTGTGGAGCC    ACCT
                                    CGTGG
GAM2086  LOC54103  5'  ACAGCGCTCGGTGGAAGGA   50938    C__       A
                                ACA  CTCGGTGGAA GA
                                |||  |||||||||| ||
                                TGT  GAGCCACCTT CT
                                  CGC        C
GAM2086  LOC90317  3'  TAAAATCATGGTGGAA      50939        CACCTC
                                TAAAATCA     GGTGGAA
                                ||||||||     |||||||
                                ATTTTAGT     CCACCTT
                                     A_____
GAM2087  EHD4      3'  CTGTATAAAGGCTTTTATCC   50942    C   TCC T
                                CTG ATA   G CTTTTATCC
                                ||| |||   | |||||||||
                                GAC TAT   C GAAAATAGG
                                  A   TTC _
GAM2087  PTPRO     3'  CTACTGCTGTCTTTTGTC    50943       ATATCC      A
                                TTACTGC     GTCTTTT TC
                                |||||||     ||||||| ||
                                GATGACG     CAGAAAA AG
                                     A_____      C
GAM2087  LOC134145 3'  CCTTAATTCGTCTTTTATC   50944    GCAT  C
                                CT    AT CGTCTTTTATC
                                ||    || ||||||||||
                                GG    TA GCAGAAAATAG
                                 AAT_  A
GAM2087  LOC202754 3'  TTACTGCATCTTTGAT      50945        TATCCG    T
                                TTACTGCA     TCTTT AT
                                ||||||||     ||||| ||
                                AATGACGT     AGAAA TA
                                     _______    C
GAM2087  LOC254531 5'  TTATTACATATCCTTCCATTTA 50946    C       G  _
            T                    TTA TGCATATCC TCT TTTAT
                                ||| ||||||||| ||| |||||
                                AAT ATGTATAGG AGG AAATA
                                  A        A   T
GAM2087  LOC255338 5'  TTACTACATTCACTTTTGTCC  50947        A  CGT    A
                                TTACTGCAT TC   CTTTT TCC
                                |||||||||  ||   ||||| |||
                                AATGATGTA AG   GAAAA AGG
                                      _ T__     C
GAM2088  COX6C     3'  TTTCAAAGTATTTGTTAATTGT 50950          C_    TTC
                                TTTCAAAGTA  TGTTG   GT
                                ||||||||||  |||||   ||
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                                AAAGTTTCAT  ACAAT   CA
                                      AA    TAA
GAM2088  MS4A4A   3'  TTTCAAGTGCTGTTGCCTCAT  50951      A  A     _
                                TTTCAA GT CTGTTGT TCGT
                                ||||||| || ||||||| ||||
                                AAAGTT CA GACAACG AGTA
                                   _ C      G
GAM2088  SURF6    3'  TTTCAGATACTGTTGTGTC   50952      AA       _
                                TTTCA  GTACTGTTGT TC
                                |||||  |||||||||| ||
                                AAAGT  TATGACAACA AG
                                  C_        C
GAM2088  TLL2     3'  TTTCAAGGTGCTATTGTT    50953      A  A
                                TTTCAA GT CTGTTGTT
                                |||||| || ||||||||
                                AAAGTT CA GATAACAA
                                   C  C
GAM2088  FLJ10514 3'  TTTCAAAGTACTTTTATT    50954          G
                                TTTCAAAGTACT TTGTT
                                |||||||||||| |||||
                                AAAGTTTCATGA AATAA
                                      A
GAM2088  FLJ13187 3'  TTTCAAAGACTGTAGTTGT   50955       T    T  C
                                TTTCAAAG ACTGT GTT GT
                                |||||||| ||||| ||| ||
                                AAAGTTTC TGACA CAA CA
                                   _    T  _
GAM2088  HSRTSBETA 3'  TTTCAAAGTACAGTTTAATGT  50956         T  GTTC
                                TTTCAAAGTAC GTT   GT
                                |||||||||||| |||   ||
                                AAAGTTTCATG CAA   CA
                                      T  ATTA
GAM2088  KIAA1493  3'  TTTCAAAAGTATCTGTGTTGT  50957      _  _  T  C
                                TTTCAAA GTA CTGT GTT GT
                                ||||||| ||| |||| ||| ||
                                AAAGTTT CAT GACA CAA CA
                                   T  A   _  _
GAM2088  MRPL35   3'  TTTCAAAGTACTTTGCTGT   50958         G   C
                                TTTCAAAGTACT TTGTT GT
                                |||||||||||| ||||| ||
                                AAAGTTTCATGA AACGA CA
                                      _    _
GAM2088  VEZATIN  5'  TTTCAAAGTCTGTGTGTC    50959       A  _
                                TTTCAAAGT CTGT TGTT
                                ||||||||| |||| ||||
                                AAAGTTTCA GACA ACAG
                                      _  C
GAM2088  LOC152627 5'  TTTCAAAGTACTATTAATGT  50960           TTC
                                TTTCAAAGTACTGTTG  GT
                                ||||||||||||||||  ||
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                                AAAGTTTCATGATAAT   CA
                                         TA_
GAM2088  LOC197039 3'  TTTCAAGTACTGTAACTGTGTC 50961       A     ___  _
                                TTTCAA GTACTGT   TGT TC
                                |||||| |||||||   ||| ||
                                AAAGTT CATGACA   ACA AG
                                   _     TTG   C
GAM2089  CHI3L1   3'  TGTCTTGTAGGATGTTTGGCT  50964     A   TCGTT
                                TGTC TGTA    GTGTTTGGCT
                                |||| ||||    ||||||||||
                                ACAG ACAT    TACAAACCGA
                                  A   CC___
GAM2089  FLJ11783  3'  TGTCATGTATGTGGCCTTTGG  50965         C  T  G
                                TGTCATGTAT GT GT TTTGG
                                |||||||||| || || |||||
                                ACAGTACATA CA CG AAACC
                                      _ C  G
GAM2089  OLFM3    3'  TGTCAGGTGTCTGGTTTGG   50966      T  A  GT  T
                                TGTCA GT TC  TG GTTTGG
                                ||||| || ||  || ||||||
                                ACAGT CA AG  AC CAAACC
                                   C  C  __ _
GAM2089  PLCE1    3'  TGTATGTGTTGTCTATGGC   50967     C   ATC    GTT
                                TGT ATGT   GTTGT   TGGC
                                ||| ||||   |||||   ||||
                                ACA TACA   CAACA   ACCG
                                  _   ___    GAT
GAM2089  LOC144486 3'  TGTCATGTATAGTTTACTGGCT 50968         C   GTGT
                                TGTCATGTAT GTT    TTGGCT
                                |||||||||| |||    ||||||
                                ACAGTACATA CAA    GACCGA
                                      T   AT__
GAM2089  LOC153397 3'  TGTTGTATGTTGTACCTTATTG 50969    CA    C     T____
            GCT                   GT  TGTAT GTTGTG    TTGGCT
                                ||  ||||| ||||||    ||||||
                                CA  ACATA CAACAT    AACCGA
                                 __    _     GGAAT
GAM2090  FLJ20127  5'  TGTGTGGCGCTGGTGGTGG   50972      AGACT T   T_
                                TGTGT    G CGTT  TGGTGG
                                |||||    | ||||  ||||||
                                ACACA    C GCGA  ACCACC
                                   _____ C    CC
GAM2090  KIAA1719  3'  TGTGTGGGTTGTGTTCTGGT   50973      AGAC   C
                                TGTGT    TGT GTTTTGGT
                                |||||    ||| ||||||||
                                ACACA    ACA CAAGACCA
                                   CCCA  _
GAM2090  WBSCR21   5'  TGTGGGGGCTGTCACCGTGGT  50974      TAGA      TT
                                TGTG   CTGTCGT  TGGT
                                ||||   |||||||  ||||
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                                ACAC    GACAGTG  ACCA
                                  CCCC      GC
GAM2090  LOC120400 5'  TGTGTGGCACTGGTGGTGG    50975      AG_    TCGTTT
                                TGTGT   ACTG     TGGTGG
                                |||||   ||||     ||||||
                                ACACA   TGAC     ACCACC
                                   CCG    C_____
GAM2091  PKIA      3'  TCATTTTGTTTTCATAAGCAAT 50978     C_    C     AA
           C                     TCA  TTGTT TCATA  AGCGGTC
                                 |||  ||||| |||||  |||||||
                                 AGT  AACAA AGTAT  TCGTTAG
                                  AA    A    __
GAM2091  PVT1      3'  TCACCTGCAGTGGTTTTGTGAA 50979    TCTCATA_____       III
           AGCGGTCG                 GT          AAAGCGGTC   G
                                 ||          |||||||||   |
                                 CG          TTTCGCCAG   C
                                  TCACCAAAACAC        III
GAM2091  UTY       3'  TTGTTCTCTAAAAGAGGT     50980         A     C
                                 TTGTTCTC TAAAAG GGT
                                 |||||||| |||||| |||
                                 AACAAGAG ATTTTC CCA
                                      _     T
GAM2091  KIAA0630  3'  TCACTTGTTTTTAAAAGCA    50981         CTCA
                                 TCACTTGTT    TAAAAGCG
                                 |||||||||    ||||||||
                                 AGTGAACAA    ATTTTCGT
                                       AA__
GAM2091  KIAA1941  3'  TCACTTGTTCTCAATCAGAGTC 50982            TAAA  C
                                 TCACTTGTTCTCA    AG GGTC
                                 ||||||||||||    || ||||
                                 AGTGAACAAGAGT    TC TCAG
                                         TAG_  _
GAM2091  SR-BP1    3'  TCATTTGTTCCCATGGGT     50983     C        AAAAGC
                                 TCA TTGTTCTCAT      GGT
                                 ||| ||||||||||      |||
                                 AGT AACAAGGGTA      CCA
                                   A         C_____
GAM2091  TAF9L     3'  CACTTGTTCTTCAGTGGT     50984          CATAAA  C
                                 CACTTGTTCT      AG GGT
                                 ||||||||||      || |||
                                 GTGAACAAGA      TC CCA
                                       AG____  A
GAM2091  LOC200830 3'  TCATTTATTCTCATACTTATGG 50985     C          AAAGC_
           GT                      TCA TTGTTCTCATA      GGT
                                 ||| ||||||||||      |||
                                 AGT AATAAGAGTAT      CCA
                                   A          GAATAC
GAM2091  LOC202024 3'  TCCTTGTCCCAGAAGTGGT    50986    A      T  TAA   C
                                 TC CTTGTTC CA   AAG GGT
                                 || ||||||| ||   ||| |||
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                                AG GAACAGG GT   TTC CCA
                                 _     _ C__   A
GAM2092 ETS1    5' GCGGCGAAGTGAGCGCGCTCG 50989    A  CCCG
                                GCG TGG   GAGCGCGCTCG
                                ||| |||   ||||||||||
                                CGC GCT   CTCGCGCGAGC
                                  C  TCA_
GAM2092 GRIN2C  5' TCGCGATGGCTCGAGTGCGAGC 50990       C _________  CGCG
            GCGCT                 CGATGGC CG      GAG   CT
                                ||||||| ||      |||   ||
                                GCTACCG GC      CTC   GA
                                    A  TCACIIIG   GCGC
GAM2092 HDGF    5' GCGCGGTGGGTGCGCGCTC   50991    A  CCC  A
                                GCG TGG   GG GCGCGCTC
                                ||| |||   || ||||||||
                                CGC GCC   CC CGCGCGAG
                                  _   AC_  A
GAM2092 CPLX1   5' CAGCGGCGGGGCGCGCTC    50992    A   CC  A
                                CG TGGC  GG GCGCGCTC
                                || ||||  || ||||||||
                                GT GCCG  CC CGCGCGAG
                                 C    C_ _
GAM2092 LOC115265 5' TCGCGGGGGCCTGCGCGCTCG  50993      AT   CGGA
                                TCGCG  GGCC   GCGCGCTCG
                                |||||  ||||   |||||||||
                                AGCGC  CCGG   CGCGCGAGC
                                   CC    A___
GAM2092 LOC124801 5' GCGCGCACGGAGCGTGCT    50994    ATG  C     C
                                GCG   GC CGGAGCG GCT
                                |||   || ||||||| |||
                                CGC   CG GCCTCGC CGA
                                  G__  T      A
GAM2092 LOC220595 5' TCGCAATGGTCTGGACTC    50995        CCC  AGCGC
                                TCGCGATGG   GG    GCTC
                                |||||||||   ||    ||||
                                AGCGTTACC   CC    TGAG
                                      AGA  _____
GAM2092 LOC222133 5' TCGGCCCTCCCGGAGCGCGCTC 50996    CGATGG
             G                   TCG     CCCGGAGCGCGCTCG
                                |||     ||||||||||||||||
                                AGC     GGGCCTCGCGCGAGC
                                  CGGGA_
GAM2093 ABCD4   3' CGCCACAGTGTGGCTCTCC   50999    G TCT   C
                                CGT G   GTG GGCTCTCC
                                ||| |   ||| ||||||||
                                GCG T   CAC CCGAGAGG
                                  G GT_   A
GAM2093 ARF1    3' CGTGGCCGGCTCTCC      51000       CTGTG
                                CGTGGT    CGGCTCTCC
                                ||||||    |||||||||
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                                GCACCG    GCCGAGAGG
                                      _____
GAM2093  ATP8A2   3'  TGGTCTGTTAACACCTTTC   51001       __  G  C
                                TGGTCTGT  GCG CT TC
                                ||||||||  ||| || ||
                                ACCAGACA  TGT GA AG
                                     AT   G  A
GAM2093  B4GALT4  5'  CGTGGCCTGCCTCTTCC    51002        GCGG  _
                                CGTGGTCTGT   CTCT CC
                                ||||||||||   |||| ||
                                GCACCGGACG   GAGA GG
                                     ____   A
GAM2093  CDH17    3'  GTGGGTCTGTGTCATTTCC   51003    _    _ GCTC
                                GTGG TCTGTG CG   TCC
                                |||| ||||||  ||   |||
                                CACC AGACAC GT   AGG
                                  C     A  AA__
GAM2093  FSTL1    3'  CACTGGTCTGTGCCTCC    51004    G       GGCT
                                CAC TGGTCTGTGC   CTCC
                                |||  ||||||||||   ||||
                                GTG ACCAGACACG   GAGG
                                _       ____
GAM2093  GARP     3'  CACGTGGCTCTGCAGCACTC  51005      T  G    T
                                CACGTGG CT TGCGGC CTC
                                |||||||  ||  ||||||  |||
                                GTGCACC GA ACGTCG GAG
                                    _ G     T
GAM2093  GDF5     3'  GTGGCACCTGTGGCTCTCC   51006     __   GC
                                GTGGT  CTGT  GGCTCTCC
                                |||||  ||||  ||||||||
                                CACCG  GACA  CCGAGAGG
                                   TG   __
GAM2093  ITGAM    3'  GTGGTCTGGGCAGAGTCC    51007       T   CTC
                                GTGGTCTG GCGG   TCC
                                |||||||| ||||   |||
                                CACCAGAC CGTC   AGG
                                     C    TC_
GAM2093  MAPT     3'  CACGTGGCTTCCTCTCC     51008      T  GTGCGG
                                CACGTGG CT     CTCTCC
                                |||||||  ||     ||||||
                                GTGCACC GA     GAGAGG
                                    _  AG____
GAM2093  MAPT     3'  CACGTGGCTTCCTCTCC     51008      T  GTGCGG
                                CACGTGG CT     CTCTCC
                                |||||||  ||     ||||||
                                GTGCACC GA     GAGAGG
                                    _  AG____
GAM2093  MAPT     3'  CACGTGGCTTCCTCTCC     51008      T  GTGCGG
                                CACGTGG CT     CTCTCC
                                |||||||  ||     ||||||
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                                GTGCACC GA     GAGAGG
                                   _ AG____
GAM2093  MAPT     3'  CACGTGGCTTCCTCTCC     51008        T  GTGCGG
                                CACGTGG CT     CTCTCC
                                ||||||| ||     ||||||
                                GTGCACC GA     GAGAGG
                                   _ AG____
GAM2093  MEIS2    3'  CATGATCTCCAGTGTGGTTCT  51009         ___  C  C
                                CGTGGTCT   GTG GG TCT
                                ||||||||   ||| || |||
                                GTACTAGA   CAC CC AGA
                                     GGT   A  A
GAM2093  MLN      5'  CACGTGGTCTGAGTGGGTCT   51010          TGC  C
                                CACGTGGTCTG   GG TCT
                                ||||||||||   || |||
                                GTGCACCAGAC   CC AGA
                                      TCA  C
GAM2093  MOCS1    3'  GTGGTCTGGCAGGAGTCC    51011        T    CTC
                                GTGGTCTG GCGG   TCC
                                |||||||| ||||   |||
                                CACCAGAC CGTC   AGG
                                   _   CTC
GAM2093  MXI1     5'  CGTGGTTTGTTTACCTCTCCC  51012       C   GCGG
                                CGTGGT TGT    CTCTCCC
                                |||||| |||    |||||||
                                GCACCA ACA    GAGAGGG
                                   A   AATG
GAM2093  MYO1E    3'  CACCTGGTCTGTGCCTGGAGCT 51013     G        ____
            CC                    CAC TGGTCTGTGC    GGCTCT
                                ||| ||||||||||    ||||||
                                GTG ACCAGACACG    TCGAGG
                                  G         GACC
GAM2093  NFKB1    5'  CGCGGGTGGGCTCTC       51014       TCT   C
                                CGTGG   GTG GGCTCTC
                                |||||   ||| |||||||
                                GCGCC   CAC CCGAGAG
                                   ___   _
GAM2093  PCDH12   5'  TGACCGTGTGGCTCTCC     51015     T    C
                                TGG CTGTG GGCTCTCC
                                ||| ||||| ||||||||
                                ACT GGCAC CCGAGAGG
                                  _    A
GAM2093  PDGFRB   3'  GTGATCTGGAATCTCCC     51016        TGC GC
                                GTGGTCTG   G  TCTCCC
                                ||||||||   |  ||||||
                                CACTAGAC   C  AGAGGG
                                     ___ TT
GAM2093  PODXL    5'  CGCGCTGCGGCGGCTCTTCC   51017      GT   _      _
                                CGTG  CTGTG CGGCTCT CC
                                ||||  ||||| ||||||| ||
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                                GCGC  GACGC GCCGAGA GG
                                  __    C     A
GAM2093  RXRA     3'  CGCTGGTGTGCGGCTCTC    51018    _   CT
                                CG TGGT  GTGCGGCTCTC
                                || ||||  ||||||||||||
                                GC ACCA  CACGCCGAGAG
                                 G   __
GAM2093  S100A11  5'  CGGGTCTGGAGCCTCTCC    51019    T    T_  GG
                                CG GGTCTG  GC  CTCTCC
                                || ||||||  ||  ||||||
                                GC CCAGAC  CG  GAGAGG
                                  _    CT  __
GAM2093  SLC4A1AP  3'  CACATGGTCCACAAGGTTTTCT 51020        TG  C  C__
                                CACGTGGTC  TG GG   TCT
                                |||||||||  || ||   |||
                                GTGTACCAG  GT CC   AGA
                                     GT  T  AAA
GAM2093  SOX15    3'  GTATGTTGTGCGGCTCTCCC   51021    GTC
                                GTG   TGTGCGGCTCTCCC
                                |||   ||||||||||||||
                                CAT   ACACGCCGAGAGGG
                                  ACA
GAM2093  20D7-FC4  3'  CGTGGTGGGCTCTCC      51022      CTGT C
                                CGTGGT    G GGCTCTCC
                                ||||||    | ||||||||
                                GCACCA    C CCGAGAGG
                                   _____ _
GAM2093  C6orf33   3'  CACTGGTCTGTGCACCC    51023    G        G
                                CAC TGGTCTGTGCG CTC
                                ||| ||||||||||| |||
                                GTG ACCAGACACGT GGG
                                  _        _
GAM2093  CAT56     3'  CATGGGTCTGTGTCAGACTC  51024     _    _  _
                                CGTGG TCTGTG CGG CTC
                                ||||| |||||| ||| |||
                                GTACC AGACAC GTC GAG
                                   C     A  T
GAM2093  CLLD8     5'  CGCGGGTGGGGCTCTCC    51025     TCT   C
                                CGTGG   GTG GGCTCTCC
                                |||||   ||| ||||||||
                                GCGCC   CAC CCGAGAGG
                                   ___   C
GAM2093  DKFZP434E2135 3'  GTGATCCATGAGGTTTTCTC  51026        C  C__
                                GTGGTCTGTG GG   TCTC
                                |||||||||| ||   ||||
                                CACTAGGTAC CC   AGAG
                                     T  AAA
GAM2093  FLJ10898  5'  CACGTGGCCTCTTCTCC    51027         GTGCGGC
                                CACGTGGTCT      TCTCC
                                ||||||||||      |||||
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                                GTGCACCGGA      AGAGG
                                    GA_____
GAM2093  FLJ14166  3'  GTGGTCTGTGTCCAGTTCCC   51028          __   C
                                GTGGTCTGTG  CGG TCTC
                                ||||||||||  ||| ||||
                                CACCAGACAC  GTC AGGG
                                    AG   A
GAM2093  FLJ20079  3'  CATTTGGTCTGCGGTATTCTCT 51029    CG       CGG__
                                CA  TGGTCTGTG    CTCT
                                ||  |||||||||    ||||
                                GT  ACCAGACGC    GAGA
                                 AA        CATAA
GAM2093  FLJ20432  3'  CACGTGTTCTGTGCACATTC   51030       G       G TC
                                CACGTG TCTGTGCG C  TC
                                ||||||| |||||||| |  ||
                                GTGCAC AGACACGT G  AG
                                   A       _ TA
GAM2093  FLJ32356  3'  CACTCGGTGTGCGGCT      51031     G    CT
                                CAC TGGT  GTGCGGCT
                                ||| ||||  ||||||||
                                GTG GCCA  CACGCCGA
                                 A   __
GAM2093  GMPPA     5'  CGTGTGTCTGTGGATTCTC    51032      _      C GC
                                CGTG GTCTGTG G  TCTC
                                |||| ||||||| |  ||||
                                GCAC CAGACAC C  AGAG
                                  A      _ TA
GAM2093  GS3955    3'  ACGTGGTCAGTCAGCTCC     51033        T  G
                                ACGTGGTC GT CGGCTCT
                                |||||||| || |||||||
                                TGCACCAG CA GTCGAGG
                                    T  _
GAM2093  HS6ST     3'  CACGTGGCTTGTGCAAGACC   51034        TC    __
                                CACGTGG  TGTGC  GGCT
                                |||||||  |||||  ||||
                                GTGCACC  ACACG  CTGG
                                    GA    TT
GAM2093  KIAA0711  5'  TGGTCTCAGGAGCTCTCCC    51035       GTGC
                                TGGTCT    GGCTCTCCC
                                ||||||    |||||||||
                                ACCAGA    TCGAGAGGG
                                   GTCC
GAM2093  KIAA0767  3'  CACGTGGTCAGTTTTCATCTCC 51036          T  GCGGC
            C                    CACGTGGTC GT     TCTCCC
                                |||||||||  ||     ||||||
                                GTGCACCAG CA     AGAGGG
                                    T  AAAGT
GAM2093  KIAA0774  5'  CGTGGTCTGGCAATGTCT     51037          T    C_
                                CGTGGTCTG GCGG  TCT
                                |||||||||  ||||  |||
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                                GCACCAGAC CGTT  AGA
                                     _    AC
GAM2093  KIAA1086  3'  CACCTGGCCCTGTGGCTCTCCC 51038     G     G  C
                                CAC TGGTCT TG GGCTCTCCC
                                ||| |||||| || |||||||||
                                GTG ACCGGG AC CCGAGAGGG
                                  G     _  A
GAM2093  MGC16179  3'  GTGGTCTTGGACTCTCC     51039        G  C
                                GTGGTCT TG GGCTCTCC
                                ||||||| || ||||||||
                                CACCAGA AC CTGAGAGG
                                     _ _
GAM2093  MGC3165  3'  CAGGATCAGTGCGGCTCT    51040    T   T
                                CG GGTC GTGCGGCTCT
                                || |||| ||||||||||
                                GT CTAG CACGCCGAGA
                                 C   T
GAM2093  MGC4054  5'  CGCTGCAAGCGCGGCTCT    51041     G  CT
                                CGT GT  GTGCGGCTCT
                                ||| ||  ||||||||||
                                GCG CG  CGCGCCGAGA
                                  A  TT
GAM2093  MGC4643  3'  CACGTGTCTGTACCTCC     51042       G      GGCT
                                CACGTG TCTGTGC    CTCC
                                |||||| |||||||    ||||
                                GTGCAC AGACATG    GAGG
                                     _     _____
GAM2093  PDZD2    5'  CACTGGTCTGTGCCTGGAGCCC 51043     G        _____
                                CAC TGGTCTGTGC    GGCTC
                                ||| ||||||||||    |||||
                                GTG ACCAGACACG    TCGGG
                                  _         GACC
GAM2093  POMT2    3'  GTGGACGGAATGCGGCTCTC   51044      TCT__
                                GTGG     GTGCGGCTCTC
                                ||||     ||||||||||||
                                CACC     TACGCCGAGAG
                                   TGCCT
GAM2093  PYY2     3'  CGTGGTCTGCAGGTCTCCC    51045          C  C
                                CGTGGTCTGTG GG TCTCCC
                                |||||||||||| || ||||||
                                GCACCAGACGT CC AGAGGG
                                     _ _
GAM2093  RSP3     5'  CACGTGCTCCTGCTCTTCC    51046       G   GTGCG    _
                                CACGTG TCT     GCTCT CC
                                |||||| |||     ||||| ||
                                GTGCAC AGG     CGAGA GG
                                    G   A_____     A
GAM2093  UNC5D    3'  GTGGTCTGTCTTACCTCTC    51047         GCG  _
                                GTGGTCTGT   GC TCTC
                                |||||||||   || ||||
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                                CACCAGACA   TG AGAG
                                     GAA  G
GAM2093  WHIP     3'  TGGTCTGTTCTAACTTCC    51048        GC_   C
                                TGGTCTGT   GGCT TCC
                                ||||||||   |||| |||
                                ACCAGACA   TTGA AGG
                                     AGA   _
GAM2093  LOC115051 3'  CACGTGGCTTGTGCAAGACC   51034        TC    __
                                CACGTGG  TGTGC  GGCT
                                |||||||  |||||  ||||
                                GTGCACC  ACACG  CTGG
                                     GA    TT
GAM2093  LOC124402 3'  CGTGGTCTCTGAAGTTCT    51049        G  C  C
                                CGTGGTCT TG GG TCT
                                |||||||| || || |||
                                GCACCAGA AC TC AGA
                                     G  T  A
GAM2093  LOC143451 3'  CATGTGTCTGTGCTGGAGTCTC 51050     _      _  C_
                                CGTG GTCTGTGC GG  TCTC
                                |||| |||||||| ||  ||||
                                GTAC CAGACACG CC  AGAG
                                  A       A  TC
GAM2093  LOC145125 3'  CATGTGTCTGTGCTGGAGTCTC 51050     _      _  C_
                                CGTG GTCTGTGC GG  TCTC
                                |||| |||||||| ||  ||||
                                GTAC CAGACACG CC  AGAG
                                  A       A  TC
GAM2093  LOC146818 5'  CACGTGTCTGTGCCTC      51051       G      GG
                                CACGTG TCTGTGC  CTC
                                |||||| |||||||  |||
                                GTGCAC AGACACG  GAG
                                  _     __
GAM2093  LOC149276 5'  GCTGGGGCCTGGCTCTCCC    51052    ___     GTGC
                                GT   GGTCT    GGCTCTCCC
                                ||   |||||   |||||||||
                                CG   CCGGA    CCGAGAGGG
                                 ACC    ____
GAM2093  LOC149296 5'  GTGGTCTGTGCATATCC     51053           GCTC
                                GTGGTCTGTGCG    TCC
                                ||||||||||||   |||
                                CACCAGACACGT    AGG
                                      AT__
GAM2093  LOC153811 3'  GTGGGGTCTGTGAATGCTTCC  51054    __      CG_   C
                                GT  GGTCTGTG   GCT TCC
                                ||  ||||||||   ||| |||
                                CA  CCAGACAC   CGA AGG
                                 CC       TTA  _
GAM2093  LOC158056 5'  GTGGTCTGAGTGAGGCCC    51055        __   C
                                GTGGTCT  GTG GGCTC
                                |||||||  ||| |||||
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                                CACCAGA  CAC CCGGG
                                    CT   T
GAM2093  LOC158056 5'  CACTGGACCCCTGGCTCTCC   51056     G   _   G GC
                                CAC TGG TCT T  GGCTCTCC
                                ||| ||| ||| |  ||||||||
                                GTG ACC GGG A  CCGAGAGG
                                  _   T   G __
GAM2093  LOC158263 3'  ACTCAGGCATGTGGCTCTCC   51057    GT_   CT   C
                                AC   GGT  GTG GGCTCTCC
                                ||   |||  ||| ||||||||
                                TG   CCG  TAC CCGAGAGG
                                 AGT   __   A
GAM2093  LOC159201 5'  ACTTGGTCTGCTCGAAGGTTTT 51058    G       G   C_____
             CTC                    AC TGGTCTGT CGG     TCTC
                                || ||||||| |||      ||||
                                TG ACCAGACG GCT     AGAG
                                 A       A   TCCAAA
GAM2093  LOC219940 5'  GTGGGCCAGTGGCTCTCCC    51059      _  T  GC
                                GTGG TC GT  GGCTCTCCC
                                |||| || ||  |||||||||
                                CACC GG CA  CCGAGAGGG
                                  C  T  __
GAM2093  LOC220135 5'  CGGGGTCTGTGAACCTCTC    51060    T       CGG
                                CG GGTCTGTG   CTCTC
                                || ||||||||   |||||
                                GC CCAGACAC   GAGAG
                                 C       TTG
GAM2093  LOC221399 5'  CATATGGTCTAGGCTTCT    51061    CG      TGC   _
                                CA  TGGTCTG   GGCT CT
                                ||  |||||||   |||| ||
                                GT  ACCAGAT   CCGA GA
                                 AT      ____    A
GAM2093  LOC221692 3'  GTGGGGCCGGCTCTCC      51062      TCT  G
                                GTGG   GT CGGCTCTCC
                                ||||   || |||||||||
                                CACC   CG GCCGAGAGG
                                  C__  _
GAM2093  LOC254440 3'  CATGTGTCTGTGCTGGAGTCTC 51050      _      _  C_
                                CGTG GTCTGTGC GG  TCTC
                                |||| |||||||| ||  ||||
                                GTAC CAGACACG CC  AGAG
                                  A       A  TC
GAM2093  LOC254559 5'  GTGGGCCGCGCGGCTCTCC    51063      T
                                GTGG CTGTGCGGCTCTCC
                                |||| ||||||||||||||
                                CACC GGCGCGCCGAGAGG
                                  C
GAM2093  LOC255027 5'  CGTGGTCGGCGTCTTCC     51064        T T   G  C
                                CGTGGTC G GCG CT TCC
                                ||||||| | ||| || |||
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                                GCACCAG C CGC GA AGG
                                  _ _   A  _
GAM2093  LOC255446 3'  ACGTGGGGATGTGGCTCT    51065       TCT   C
                                ACGTGG   GTG GGCTCT
                                ||||||   ||| ||||||
                                TGCACC   TAC CCGAGA
                                   CC_   A
GAM2093  LOC86651  3'  ACCTGGTCTGTATGGTTTCC  51066    G       C  CTC
                                AC TGGTCTGTG GG   TCC
                                || |||||||| ||   |||
                                TG ACCAGACAT CC   AGG
                                 G       A  AA_
GAM2093  LOC95076  3'  CACTGGTCTGTGTACCC     51067     G       CG
                                CAC TGGTCTGTG  GCTC
                                ||| |||||||||  ||||
                                GTG ACCAGACAC  TGGG
                                  _       A_
GAM2094  GPR23     5'  GGCACCAATTTTATCTA     51070         ATTAAC
                                GGCACTAAT     TTATCTA
                                |||||||||     |||||||
                                CCGTGGTTA     AATAGAT
                                    A_____
GAM2094  AOP2      3'  GGCACTAATATTGCTCA     51071           AA
                                GGCACTAATATT  CTTA
                                ||||||||||||  ||||
                                CCGTGATTATAA  GAGT
                                     C_
GAM2094  FLJ14775  3'  CGGCACTATCATTGTACTT   51072        A   A_
                                CGGCACTA TATT  ACTT
                                |||||||| ||||  ||||
                                GCCGTGAT GTAA  TGAA
                                    A   CA
GAM2094  KIAA0716  3'  GGCATTAGCATCCCTATCTA  51073     C  A   AA
                                GGCA TA TATT  CTTATCTA
                                |||| || ||||  ||||||||
                                CCGT AT GTAG  GGATAGAT
                                  A  C   __
GAM2094  MGC24009  3'  GGCACTAATGATTGGCTT    51074         _  AA
                                GGCACTAAT ATT  CTT
                                ||||||||| |||  |||
                                CCGTGATTA TAA  GAA
                                    C   CC
GAM2094  LOC221495 5'  GGCACAATATTAACGCCTCTA  51075      T       TTA
                                GGCAC AATATTAAC   TCTA
                                ||||| |||||||||   ||||
                                CCGTG TTATAATTG   AGAT
                                  _       CGG
GAM2095  MTL5      3'  TAGAGATTTCTAGACTAAGACA 51078        A  _  T  CC
                                TAGAGATT TC AG AT  AAGACA
                                |||||||| || || ||  ||||||
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                                ATCTCTAA AG TC TG  TTCTGT
                                     _  A  _  A_
GAM2095  PTGS2    3'  TACAGATTTAAATCCAAGACA  51079    G    ATCAGT
                                TA AGATT     ATCCAAGACA
                                || |||||     ||||||||||
                                AT TCTAA     TAGGTTCTGT
                                 G    ATT___
GAM2095  TEC      3'  TAGGTATTTATTTATCCAAGA  51080    AG   ATCAG
                                TAG  ATT    TATCCAAGA
                                |||  |||    |||||||||
                                ATC  TAA    ATAGGTTCT
                                  CA   ATAA_
GAM2095  APOL4    3'  TAGAGATTGCGGTAAAGAC   51081       ATCA   TCC
                                TAGAGATT   GTA   AAGAC
                                ||||||||   |||   |||||
                                ATCTCTAA   CAT   TTCTG
                                     CGC_   ___
GAM2095  AQP9     3'  GAGAATATCAGTATTTATACA  51082     T       CCAAG
                                GAGA TATCAGTAT    ACA
                                |||| |||||||||    |||
                                CTCT ATAGTCATA    TGT
                                   T       AATA_
GAM2095  BAIAP1   3'  TAGAGATTTCAGAACAAG    51083       A    TATC
                                TAGAGATT TCAG    CAAG
                                |||||||| ||||   ||||
                                ATCTCTAA AGTC    GTTC
                                     _   TT__
GAM2095  FBXO30   3'  AGAGATTGTCAACCAAGACA   51084       A    TAT
                                AGAGATT TCAG   CCAAGACA
                                ||||||| ||||   ||||||||
                                TCTCTAA AGTT   GGTTCTGT
                                    C   ___
GAM2095  FLJ23153 3'  AGATACGTATGTATCCAAGACA 51085     TATCA_
                                AGAT     GTATCCAAGACA
                                ||||     ||||||||||||
                                TCTA     CATAGGTTCTGT
                                  TGCATA
GAM2095  KIAA0057 3'  GAGATTATGATCCGAGA     51086       CAGT   A
                                GAGATTAT    ATCC AGA
                                ||||||||    |||| |||
                                CTCTAATA    TAGG TCT
                                     C___    C
GAM2095  KIAA0674 5'  AGAGGTTGTCAGCACCA     51087     A  A     T
                                AGAG TT TCAGTA CCA
                                |||| || |||||| |||
                                TCTC AA AGTCGT GGT
                                  C  C     _
GAM2095  KIAA1514 3'  TAGAGGTTGCCAAGACA     51088      ATTATCA  AT
                                TAGAG      GT  CCAAGACA
                                |||||      ||  ||||||||
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                                ATCTC      CA  GGTTCTGT
                                  ________  AC
GAM2095  MGC2941   3'  CAGAGATTATGTGTCGGGACA  51089         CA  A  CAA
                                TAGAGATTAT  GT TC   GACA
                                ||||||||||  || ||   ||||
                                GTCTCTAATA  CA AG   CTGT
                                     __  C  CC_
GAM2095  SERHL     3'  GAGATTATTAGCCAGGAGACA  51090        C   ATCCA
                                GAGATTAT AGT    AGACA
                                |||||||| |||    |||||
                                CTCTAATA TCG    TCTGT
                                    A   GTCC_
GAM2095  LOC115265 3'  TAGTGACAGGTATCCAAG    51091     A   TATCA
                                TAG GAT    GTATCCAAG
                                ||| |||    |||||||||
                                ATC CTG    CATAGGTTC
                                  A   TC___
GAM2095  LOC148137 3'  GAGGATTATCAGAATAGAGAC  51092     _       TATCCA
                                GAG ATTATCAG     AGAC
                                ||| ||||||||     ||||
                                CTC TAATAGTC     TCTG
                                  C       TTATC_
GAM2095  LOC149086 5'  GATATCAAAGCCAAGACA    51093     T    TAT
                                GAT ATCAG   CCAAGACA
                                ||| |||||   ||||||||
                                CTA TAGTT   GGTTCTGT
                                  _     TC_
GAM2095  LOC157867 5'  CAGAGATTTGCAGATTCAAGA  51094         AT   T  C
                                TAGAGATT  CAG AT CAAGA
                                ||||||||  ||| || |||||
                                GTCTCTAA  GTC TA GTTCT
                                    AC   _  A
GAM2095  LOC257048 3'  TAGAGGATTCAACATCTGGGAC 51095       ATTA       CAA
              A                  TAGAG    TCAGTATC   GACA
                                 |||||    ||||||||   ||||
                                 ATCTC    AGTTGTAG   CTGT
                                    CTA_       ACC
GAM2096  NPHS2     3'  TTTTGCATTCACTCTGAAACAT 51098      T    _   A
              TT                  TTTT CATTC TTCT GAAACATTT
                                  |||| ||||| |||| |||||||||
                                  AAAA GTAAG GAGA CTTTGTAAA
                                    C    T   _
GAM2096  SLC39A1   3'  TTTTTTTTTTTTCTAGAAACAT 51099       CA  C
                                TTTTT  TT TTCTAGAAACAT
                                |||||  || ||||||||||||
                                AAAAA  AA AAGATCTTTGTA
                                   AA  A
GAM2096  TKT       3'  TTTTTCATTTTTCTCAAAACAT 51100         C   A
                                TTTTTCATT TTCT GAAACAT
                                ||||||||| |||| |||||||
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                                AAAAAGTAA AAGA TTTTGTA
                                     A    G
GAM2096  ATIP1    3'  TTTTGCATTCTACATGAAACAT 51101      T     TCTA
                TT                  TTTT CATTCT    GAAACATTT
                                    |||| ||||||    |||||||||
                                    AAAA GTAAGA    CTTTGTAAA
                                      C     TGTA
GAM2096  DKFZp434P2235 3'  TTTTTCATTTCAACAGGAAACA 51102          _ TTCTA
                TTT                 TTTTTCATT C    GAAACATTT
                                    ||||||||| |    |||||||||
                                    AAAAAGTAA G    CTTTGTAAA
                                        A TTGTC
GAM2096  NET-2    3'  TTTTTTACTCTCTAGAAA    51103      C    T
                                    TTTTT ATTCT CTAGAAA
                                    ||||| ||||| |||||||
                                    AAAAA TGAGA GATCTTT
                                      A    _
GAM2096  PGCP     3'  TTTTTTGTTCTTCCAAAAA    51104      CA
                                    TTTTT  TTCTTCTAGAAA
                                    |||||  ||||||||||||
                                    AAAAA  AAGAAGGTTTTT
                                      AC
GAM2096  UHRF1    3'  TTTTTCAATCTGTGAAAAACAT 51105       T   TCT
                TT                  TTTTTCA TCT   AGAAACATTT
                                    ||||||| |||   ||||||||||
                                    AAAAAGT AGA   TTTTTGTAAA
                                        T   CAC
GAM2096  VIT      3'  TTTTTCATCCTTCTAAACATTT 51106            GA
                                    TTTTTCATTCTTCTA  AACATTT
                                    ||||||||||||||  |||||||
                                    AAAAAGTAGGAAGAT  TTGTAAA
                                                __
GAM2096  LOC253782 3'  TTTTTCATTTTTCCAGAAA    51107         C
                                    TTTTTCATT TTCTAGAAA
                                    ||||||||| |||||||||
                                    AAAAAGTAA AAGGTCTTT
                                        A
GAM2097  WRB      3'  TTTAGTAGCGGTATTAA     51110      A      C
                                    TTTAG TAGCGGTA TGA
                                    ||||| |||||||| |||
                                    AAATC ATCGCCAT ATT
                                      _       A
GAM2097  B3GNT5   3'  TTTAGATATTATAACTTTGATG 51111        GCGGT  __
                T                   TTTAGATA    ACT  GATGT
                                    ||||||||    |||  |||||
                                    AAATCTAT    TGA  CTACA
                                        AATAT   AA
GAM2097  FLJ12572 3'  TTTAGCACACTGCTGATGTCC  51112      ATA  GGTA
                                    TTTAG   GC    CTGATGTCC
                                    |||||   ||    |||||||||
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                                AAATC  TG   GACTACAGG
                                  GTG  AC__
GAM2097 KIAA1432 3' TTTAGATAGTGGTACGAAT   51113        C    T
                                TTTAGATAG GGTAC GAT
                                ||||||||| ||||| |||
                                AAATCTATC CCATG TTA
                                    A    C
GAM2097 LOC130074 3' TTTAAATAGCCATCATGATGTC 51114         G  AC
          CA                    TTTAGATAGC GT  TGATGTCCA
                                |||||||||| ||  |||||||||
                                AAATTTATCG TA  ACTACAGGT
                                    G  GT
GAM2097 LOC153243 3' TAGGTGGCGATCTCGATGTCCA 51115    ATA    AC
                                TAG  GCGGT  TGATGTCCA
                                |||  |||||  |||||||||
                                ATC  CGCTA  GCTACAGGT
                                  CAC    GA
GAM2098 ADRA1A   5' CCGAAGCTGGGTGCG      51118        AGCC
                                TCGAAGCTGG   GTGTG
                                ||||||||||   |||||
                                GGCTTCGACC   CACGC
                                     ____
GAM2098 ADRA1A   5' CCGAAGCTGGGTGCG      51118        AGCC
                                TCGAAGCTGG   GTGTG
                                ||||||||||   |||||
                                GGCTTCGACC   CACGC
                                     ____
GAM2098 ADRA1A   5' CCGAAGCTGGGTGCG      51118        AGCC
                                TCGAAGCTGG   GTGTG
                                ||||||||||   |||||
                                GGCTTCGACC   CACGC
                                     ____
GAM2098 ARHGEF7  5' GAAGTCCGAGTGTGCAAA   51119    _   AGCC
                                GAAG CTGG   GTGTGCAAA
                                |||| ||||   |||||||||
                                CTTC GGCT   CACACGTTT
                                  A  ____
GAM2098 BMP1     3' TCGAGGCTGGAGCAGGGGTG  51120    A      CGT_
                                TCGA GCTGGAGC   GTG
                                |||| ||||||||   |||
                                AGCT CGACCTCG   CAC
                                  C      TCCC
GAM2098 CRTL1    5' GAAGCTGGAGATCAAGTG    51121        C_  T
                                GAAGCTGGAG  CG GTG
                                ||||||||||  || |||
                                CTTCGACCTC  GT CAC
                                     TA  T
GAM2098 DIO1     3' TCAAAGACCGTGTGCA      51122      CTGGA
                                TCGAAG    GCCGTGTGCA
                                ||||||    ||||||||||
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                                AGTTTC    TGGCACACGT
                                      _____
GAM2098  EGR1     5'  CCGGGGCTGGAGCTGCA     51123     AA      CGTG
                                TCG  GCTGGAGC   TGCA
                                |||  ||||||||   ||||
                                GGC  CGACCTCG   ACGT
                                  CC      ____
GAM2098  FAAH     5'  CGAAGCTGGAGAGGTCGTA   51124          C___
                                CGAAGCTGGAG   CGTG
                                ||||||||||   ||||
                                GCTTCGACCTC   GCAT
                                      TCCA
GAM2098  FASN     5'  CGAGGCTGGAGCGCGGC     51125     A      C   T
                                CGA GCTGGAGC GTG GC
                                ||| |||||||| ||| ||
                                GCT CGACCTCG CGC CG
                                  C      _  _
GAM2098  FY       5'  GCTGGAGGAGCAGTGCAA    51126       CC  _
                                GCTGGAG  GT GTGCAA
                                |||||||  || ||||||
                                CGACCTC  CG CACGTT
                                    CT  T
GAM2098  HDAC7A   3'  GAGCCTGGGGCTGTGTGCAAA 51127    AG    A  C
                                GA  CTGG GC GTGTGCAAA
                                ||  |||| || |||||||||
                                CT  GACC CG CACACGTTT
                                 CG    C  A
GAM2098  HDAC7A   3'  GAGCCTGGGGCTGTGTGCAAA 51127    AG    A  C
                                GA  CTGG GC GTGTGCAAA
                                ||  |||| || |||||||||
                                CT  GACC CG CACACGTTT
                                 CG    C  A
GAM2098  MBD1     3'  TCGAAGCTGGAGGTGGTG    51128          CC_
                                TCGAAGCTGGAG   GTG
                                ||||||||||||   |||
                                AGCTTCGACCTC   CAC
                                      CAC
GAM2098  MBD1     3'  TCGAAGCTGGAGGTGGTG    51128          CC_
                                TCGAAGCTGGAG   GTG
                                ||||||||||||   |||
                                AGCTTCGACCTC   CAC
                                      CAC
GAM2098  MBD1     3'  TCGAAGCTGGAGGTGGTG    51128          CC_
                                TCGAAGCTGGAG   GTG
                                ||||||||||||   |||
                                AGCTTCGACCTC   CAC
                                      CAC
GAM2098  MBD1     3'  TCGAAGCTGGAGGTGGTG    51128          CC_
                                TCGAAGCTGGAG   GTG
                                ||||||||||||   |||
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                                AGCTTCGACCTC  CAC
                                      CAC
GAM2098 RTKN     3'  TCAAAGCTGGTTAGTGCA    51129         AGCCGT
                                TCGAAGCTGG     GTGCA
                                ||||||||||     |||||
                                AGTTTCGACC     CACGT
                                     AAT___
GAM2098 TNFRSF6B 3'  TCTGAGCTGGAGCTGCTGGC  51130    GA       C  GT
                                TC  AGCTGGAGC GT  GC
                                ||  |||||||| ||  ||
                                AG  TCGACCTCG CG  CG
                                 AC        A  AC
GAM2098 CST8     5'  TCAGGGCTGGAGCTGTGGGCA 51131     AA       C   T
                                TCG  GCTGGAGC GTG GCA
                                |||  |||||||| ||| |||
                                AGT  CGACCTCG CAC CGT
                                  CC       A   C
GAM2098 DKFZP434C0826 5'  AGCTGGAACTAGGTAGCA    51132         C__   T
                                AGCTGGAGC   GTG GCA
                                |||||||||   ||| |||
                                TCGACCTTG   CAT CGT
                                     ATC  _
GAM2098 DKFZp547H236 3'  GAAGCTGGAGGACCAGGCG    51133          __   T
                                GAAGCTGGAG  CCG GTG
                                ||||||||||  ||| |||
                                CTTCGACCTC  GGT CGC
                                     CT   C
GAM2098 FLJ10058 5'  TCGAAGCTGGAGTGCA      51134          GCCGT
                                TCGAAGCTGGA    GTGCA
                                ||||||||||     |||||
                                AGCTTCGACCT    CACGT
                                        _____
GAM2098 FLJ20097 3'  TCAAGCTGGAACTGCA      51135    G        CGTG
                                TC AAGCTGGAGC    TGCA
                                || ||||||||||    ||||
                                AG TTCGACCTTG    ACGT
                                 _       _____
GAM2098 FLJ20485 3'  TCGAGGCTGCAGTGCAA     51136     A    G GCCGT
                                TCGA GCTG A    GTGCAA
                                |||| |||| |    ||||||
                                AGCT CGAC T    CACGTT
                                  C   G _____
GAM2098 KIAA0255 3'  CCGAGCTGGAGCTGTGC     51137      A       CG
                                TCGA GCTGGAGC  TGTGC
                                |||| ||||||||  |||||
                                GGCT CGACCTCG  ACACG
                                   _      __
GAM2098 KIAA0461 3'  GAAGCTGGCAGTGAAAAA    51138         AGCCGT   C
                                GAAGCTGG     GTG AAAA
                                ||||||||     ||| ||||
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                                CTTCGACC     CAC TTTT
                                     GT____   T
GAM2098  KIAA1950  3'  GAAGCTGGGTGGCAGTGTG   51139        A__  C
                                GAAGCTGG   GC GTGTG
                                ||||||||   || |||||
                                CTTCGACC   CG CACAC
                                     CAC  T
GAM2098  LGI3      5'  CGGAGCTGGAGCCGCAGC    51140    A          T
                                CG AGCTGGAGCCGTG GC
                                || ||||||||||||| ||
                                GC TCGACCTCGGCGT CG
                                 C          _
GAM2098  SCAMP-4   3'  CGAGGCTGGAGCCGCACA    51141    A         GT
                                CGA GCTGGAGCCGT  GCA
                                ||| ||||||||||  |||
                                GCT CGACCTCGGCG  TGT
                                  C         __
GAM2098  LOC132946 5'  GAAGCTAGAGAGTGCA      51142         CCGT
                                GAAGCTGGAG    GTGCA
                                ||||||||||    |||||
                                CTTCGATCTC    CACGT
                                      T____
GAM2098  LOC137797 3'  TCGGGGCTGGGCCGCATA    51143     AA     A
                                TCG  GCTGG GCCGTGTG
                                |||  ||||| ||||||||
                                AGC  CGACC CGGCGTAT
                                  CC     _
GAM2098  LOC158125 5'  GAGGGCTGCTGTGTGCAA    51144    A_   GGA  C
                                GA  GCT   GC GTGTGCAA
                                ||  |||   || ||||||||
                                CT  CGA   CG CACACGTT
                                 CC   ___  A
GAM2098  LOC170127 5'  CCGGGGCTGGCCGTGCG     51145     AA    GA
                                TCG  GCTG  GCCGTGTG
                                |||  ||||  ||||||||
                                GGC  CGAC  CGGCACGC
                                  CC    __
GAM2098  LOC202781 5'  CCGGGGCTGGAGCTGCACCGC  51146     AA       C TG _
                                TCG  GCTGGAGC G  T GC
                                |||  |||||||| |  | ||
                                GGC  CGACCTCG C  G CG
                                  CC       A GT G
GAM2098  LOC256230 5'  TCGGAGCTGGAGCAGCTGT    51147     A        C _
                                TCG AGCTGGAGC G TGT
                                ||| ||||||||| | |||
                                AGC TCGACCTCG C ACA
                                  C        T G
GAM2098  LOC256231 5'  TCGGAGCTGGAGCAGCTGT    51147     A        C _
                                TCG AGCTGGAGC G TGT
                                ||| ||||||||| | |||
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                                AGC TCGACCTCG C ACA
                                  C       T G
GAM2098 LOC54557 5' TCGGGGCTGGAGCCCGGC   51148    AA      G T
                                TCG  GCTGGAGCC TG GC
                                |||  ||||||||| || ||
                                AGC  CGACCTCGG GC CG
                                  CC       _ _
GAM2098 LOC93550 5' GAAGCTGGCGTCACGCCCAAA 51149       AGC    G
                                GAAGCTGG   CGTGT CAAA
                                ||||||||   ||||| ||||
                                CTTCGACC   GTGCG GTTT
                                     GCA    G
GAM2099 ARVCF    3' CCGAAGGTCAGTCCCGGAGG  51152     ATCT   AC
                                TCGAA   TCA  CCCGGAGG
                                |||||   |||  ||||||||
                                GGCTT   AGT  GGGCCTCC
                                   CC__   CA
GAM2099 LHX5     3' TCGAAATCTCTTGACCCTCCG 51153        CAA__ _
                                TCGAAATCTT    CC CCG
                                ||||||||||    || |||
                                AGCTTTAGAG    GG GGC
                                      AACTG  A
GAM2099 OLIG2    3' GAATCTTTTCCCGGAGG    51154    A   CAAC
                                GAA TCTT    CCCGGAGG
                                ||| ||||    ||||||||
                                CTT AGAA    GGGCCTCC
                                  _    AA__
GAM2099 A2BP1    5' TCTTCAGCCCCGGAGGCG   51155      A
                                TCTTCA CCCCGGAGGCG
                                |||||| ||||||||||
                                AGAAGT GGGGCCTCCGC
                                   C
GAM2099 FLJ20013 3' TCAAATCTTCAACCCTGCG  51156   G        _____
                                TC AAATCTTCAACCC    CG
                                || ||||||||||||    ||
                                AG TTTAGAAGTTGGG    GC
                                 _          ACIII
GAM2099 GMFB     3' TCAAGTCTTTGACCCCAAA   51157    AA   CA
                                TCGA  TCTT  ACCCCGGA
                                ||||  ||||  ||||||||
                                AGTT  AGAA  TGGGGTTT
                                  C_   AC
GAM2099 KIAA0237 3' TCAGATCTTCAACTCTCCCA  51158    AA      ___
                                TCG  ATCTTCAAC   CCCG
                                |||  |||||||||  ||||
                                AGT  TAGAAGTTG   GGGT
                                  C_       AGA
GAM2099 PTR4     3' TCGAAATCTGCAGCTCTCCTCC 51159        _______ AAC
             CG                   TCGAAATCT      TC   CCCG
                                |||||||||      ||   ||||
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                                AGCTTTAGA      AG   GGGC
                                     CGTCGAG  GA_
GAM2099  LOC253128 5'  TCGTGATCTGCTCCCGGAGGCG 51160     AA    TCAAC
                                TCG  ATCT    CCCGGAGGCG
                                |||  ||||    ||||||||||
                                AGC  TAGA    GGGCCTCCGC
                                  AC    CGA__
GAM2099  LOC254228 3'  GAAATCTTAACCCCCAAG    51161        C     G
                                GAAATCTT AACCCC GAG
                                |||||||| |||||| |||
                                CTTTAGAA TTGGGG TTC
                                     _     G
GAM2100  HTR2C    5'  CGGCAGTCGGTGCGCTGGCGAA 51164        A_ ________   GCTT
              GCCG                   GCAGTCG  GC      GCG    CG
                                |||||||  ||      |||    ||
                                CGTCAGC  CG      CGC    GC
                                     CA  CGAIIIC   TTCG
GAM2100  JAG2     5'  CGGGGTCGAGCGCAGCGC    51165     CA         TTC
                                CGG  GTCGAGCGCGGC   GC
                                |||  ||||||||||||   ||
                                GCC  CAGCTCGCGTCG   CG
                                  C_          ____
GAM2100  LASS1    3'  CGTGGTTGAGCGCCGGCGGCC  51166    GCA  C     _   TTC
                                CG   GT GAGCGC GGC   GCC
                                ||   || ||||||  |||   |||
                                GC   CA CTCGCG CCG   CGG
                                 AC_  A     G   C__
GAM2100  NDUFB10  5'  CGGCGGCGGGCGCGGACT    51167      A T  A     _
                                CGGC G CG GCGCGG CT
                                |||| | || |||||| ||
                                GCCG C GC CGCGCC GA
                                  C _  C     T
GAM2100  NLGN2    5'  ACGGTAGTTGAGCGTGGCT    51168      C   C    C
                                ACGG AGT GAGCG GGCT
                                |||| ||| ||||| ||||
                                TGCC TCA CTCGC CCGA
                                  A   A    A
GAM2100  PABPC4   5'  CGGCGGCGGGCGCGGGGCAGGC 51169      A T  A     CTTC_
              C                   CGGC G CG GCGCGG     GCC
                                |||| | || ||||||     |||
                                GCCG C GC CGCGCC     CGG
                                  C _  C     CCGTC
GAM2100  PDGFB    5'  ACGGCAGTCGATGGTTCG    51170          GCGC  C
                                ACGGCAGTCGA    GG TTCG
                                ||||||||||    || ||||
                                TGCCGTCAGCT    CC AAGC
                                      A___  _
GAM2100  RAC3     5'  CGGCGGCGGGCGCGGCC     51171      A T  A
                                CGGC G CG GCGCGGCT
                                |||| | || ||||||||
```

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                                GCCG C GC CGCGCCGG
                                  C _  C
GAM2100 RHEB2    5' CGGCGGCGGGCGCGGCTGCC  51172     A T  A      TC
                                CGGC G CG GCGCGGCT  GCC
                                |||| | || ||||||||  |||
                                GCCG C GC CGCGCCGA  CGG
                                  C _  C       __
GAM2100 SNX13    5' CGGCGGTTTTACTCGGCTTCGC 51173     A  CGA  G
                                CGGC GT   GC CGGCTTCGC
                                |||| ||   || |||||||||
                                GCCG CA   TG GCCGAAGCG
                                  C  AAA  A
GAM2100 DKFZP434G1411 5' CGGGGTCGAGCGCCCCTGCC  51174    CA       GG  TC
                                CGG  GTCGAGCGC  CT  GCC
                                |||  |||||||||  ||  |||
                                GCC  CAGCTCGCG  GG  CGG
                                  C_        __  GA
GAM2100 FLJ31564 5' GGCAGTCGCGCGCGCGGCT   51175        A__
                                GGCAGTCG   GCGCGGCT
                                ||||||||   ||||||||
                                CCGTCAGC   CGCGCCGA
                                     GCG
GAM2100 MGC10526 5' GGCAGTCGGGCGGCCCTCGTGC 51176        AGC      C___
             C                   GGCAGTCG   GCGGCTT   GCC
                                ||||||||   |||||||   |||
                                CCGTCAGC   CGCCGGG   CGG
                                     C__      AGCA
GAM2100 MGC2654   3' GGCTGTTGAGGGCAATGTTTCG 51177     A  C   C   C__
             C                   GGC GT GAG GCGG   TTCGC
                                ||| || ||| ||||   |||||
                                CCG CA CTC CGTT   AAGCG
                                  A  A   C   ACA
GAM2100 MP1      3' GCAGTCGAGCGCCACGGC    51178          G  TTC
                                GCAGTCGAGCGC GC   GC
                                |||||||||||| ||   ||
                                CGTCAGCTCGCG TG   CG
                                       G  C__
GAM2100 PDE8A    5' CGGCGGCGAGCGCGGATC    51179      A T       CT
                                CGGC G CGAGCGCGG  TC
                                |||| | |||||||||  ||
                                GCCG C GCTCGCGCC  AG
                                  C _       T_
GAM2100 LOC146774 5' CGGCAGTCGCAGTGTTCACAGC 51180        AG_____
             C                   CGGCAGTCG      CGCGGCT
                                |||||||||      |||||||
                                GCCGTCAGC      GTGTCGG
                                     GTCACAA
GAM2100 LOC158436 5' GGCAGAGGCGGCTTCGC     51181      GTC   C
                                GGCA   GAG GCGGCTTCGC
                                ||||   ||| ||||||||||
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                                CCGT   CTC CGCCGAAGCG
                                  ___  _
GAM2100 LOC221710 5'  ACGGCGGTGAGCGCGGGC    51182      A  C      _
                                ACGGC GT GAGCGCGG C
                                ||||| || |||||||| |
                                TGCCG CA CTCGCGCC G
                                   C  _      C
GAM2101 FLJ10508 3'  TCTGTTATCATGGTATCTGTG  51185    CGG  A      A
                                TCT   TGT ATGGTATCT TG
                                |||   ||| |||||||| ||
                                AGA   ATA TACCATAGA AC
                                  CA_  G       C
GAM2101 FLJ12697 3'  CCTCGGTGTAGTGGTGTCT   51186         A   A
                                TCTCGGTGTA TGGT TCT
                                |||||||||| |||| |||
                                GGAGCCACAT ACCA AGA
                                      C   C
GAM2101 KIAA0089 3'  TCTTGGTGTGGATGCCATG   51187    C    AAT  TAT
                                TCT GGTGT   GG   CTATG
                                ||| |||||   ||   |||||
                                AGA CCACA   CC   GGTAC
                                  A    ___  TAC
GAM2101 RNF8     3'  TCTTGGTTGTAATCTATGA   51188    C  _  ATGGT
                                TCT GGT GTA    ATCTATGA
                                ||| ||| |||    ||||||||
                                AGA CCA CAT    TAGATACT
                                  A  A  _____
GAM2101 ZNF304   3'  TCTGGTGTGAGTCCTATGA   51189    C    AAT   A
                                TCT GGTGT   GGT TCTATGA
                                ||| |||||   ||| |||||||
                                AGA CCACA   TCA GGATACT
                                  _    C__  _
GAM2101 LOC163231 5'  TCTCGTTGTAATGAATGA    51191      G      TATCT
                                TCTCG TGTAATGG    ATGA
                                ||||| ||||||||    ||||
                                AGAGC ACATTACT    TACT
                                   A      _____
GAM2101 LOC163231 5'  TCTCAGTGTGATGAAAGAGTGA 51190         A   TATCTA
             G                   TCTCGGTGT ATGG     TGAG
                                 |||||||| ||||     ||||
                                 AGAGTCACA TACT     ACTC
                                      C   TTCTC_
GAM2102 ALDH8A1  3'  TGATGAAAGAAACACTATGAAA 51194    G        GC
             A                   TGA TGAAAGAGATA  ATGAAAA
                                 ||| ||||||||||  |||||||
                                 ACT ACTTTCTTTGT  TACTTTT
                                   _        GA
GAM2102 ALOX15   3'  TGGGTGCAGAGACCATGAAAA  51195   A  AA    AG
                                 TG GTG  AGAGAT  CATGAAAA
                                 || |||  ||||||  ||||||||
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                                AC CAC  TCTCTG  GTACTTTT
                                 C  G_     __
GAM2102  CCR2    3'  TGAGTGAAGAAATTATGAA   51196        A    AGC
                                TGAGTGAA GAGAT   ATGAA
                                |||||||| |||||   |||||
                                ACTCACTT CTTTA   TACT
                                     _    A__
GAM2102  COLQ    3'  TGGTGGAAGCAGCATGAAA   51197    A  AAA  A
                                TG GTG   GAG TAGCATGAAA
                                || |||   ||| ||||||||||
                                AC CAC   TTC GTCGTACTTT
                                 _  C__   _
GAM2102  COLQ    3'  TGGTGGAAGCAGCATGAAA   51197    A  AAA  A
                                TG GTG   GAG TAGCATGAAA
                                || |||   ||| ||||||||||
                                AC CAC   TTC GTCGTACTTT
                                 _  C__   _
GAM2102  COLQ    3'  TGGTGGAAGCAGCATGAAA   51197    A  AAA  A
                                TG GTG   GAG TAGCATGAAA
                                || |||   ||| ||||||||||
                                AC CAC   TTC GTCGTACTTT
                                 _  C__   _
GAM2102  COLQ    3'  TGGTGGAAGCAGCATGAAA   51197    A  AAA  A
                                TG GTG   GAG TAGCATGAAA
                                || |||   ||| ||||||||||
                                AC CAC   TTC GTCGTACTTT
                                 _  C__   _
GAM2102  COLQ    3'  TGGTGGAAGCAGCATGAAA   51197    A  AAA  A
                                TG GTG   GAG TAGCATGAAA
                                || |||   ||| ||||||||||
                                AC CAC   TTC GTCGTACTTT
                                 _  C__   _
GAM2102  COLQ    3'  TGGTGGAAGCAGCATGAAA   51197    A  AAA  A
                                TG GTG   GAG TAGCATGAAA
                                || |||   ||| ||||||||||
                                AC CAC   TTC GTCGTACTTT
                                 _  C__   _
GAM2102  DISC1   3'  TGAGTGAAACAGGTTCCACG  51198        G  ATAG
                                TGAGTGAAA AG    CATG
                                ||||||||| ||    ||||
                                ACTCACTTT TC    GTGC
                                     G  CAAG
GAM2102  FBXL5   3'  TGAGTAAAGTGCATGAAA    51199        AGAGATA
                                TGAGTGAA      GCATGAAA
                                ||||||||      ||||||||
                                ACTCATTT      CGTACTTT
                                     CA_____
GAM2102  FBXL5   3'  TGAGTAAAGTGCATGAAA    51199        AGAGATA
                                TGAGTGAA      GCATGAAA
                                ||||||||      ||||||||
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                                ACTCATTT      CGTACTTT
                                    CA_____
GAM2102  FXYD6    3'  GAGTGAAAGGAGTCCATGAA   51200         A  TAG
                                GAGTGAAAG GA   CATGAA
                                ||||||||| ||   ||||||
                                CTCACTTTC CT   GTACTT
                                    _ CAG
GAM2102  IGFBP4   3'  TGAGTGAAGGAATGAGTGA    51201         A   AT  CA
                                TGAGTGAA GAG  AG  TGA
                                |||||||| |||  ||  |||
                                ACTCACTT CTT  TC  ACT
                                    C   AC __
GAM2102  IL1F5    3'  TGAGGGAAGAGATAGGAAA    51202      T   A      CAT
                                TGAG GAA GAGATAG   GAAA
                                |||| ||| |||||||   ||||
                                ACTC CTT CTCTATC   CTTT
                                  C  _      ___
GAM2102  MFGE8    3'  GTGAAAAGCCAGCATGA      51203      A   A
                                GTGAA GAG TAGCATGA
                                ||||| ||| ||||||||
                                CACTT TTC GTCGTACT
                                  _  G
GAM2102  PARK2    3'  AGTGAAAGGGATCCAGGA     51204         A   AG  T
                                AGTGAAAG GAT  CA GA
                                |||||||| |||  || ||
                                TCACTTTC CTA  GT CT
                                    C   G_  C
GAM2102  PARK2    3'  AGTGAAAGGGATCCAGGA     51204         A   AG  T
                                AGTGAAAG GAT  CA GA
                                |||||||| |||  || ||
                                TCACTTTC CTA  GT CT
                                    C   G_  C
GAM2102  PARK2    3'  AGTGAAAGGGATCCAGGA     51204         A   AG  T
                                AGTGAAAG GAT  CA GA
                                |||||||| |||  || ||
                                TCACTTTC CTA  GT CT
                                    C   G_  C
GAM2102  PHLDA3   3'  TGAGGTGGTGGGTAGCATGAA  51205      _  AAAGAGA
                                TGAG TG      TAGCATGAA
                                |||| ||      |||||||||
                                ACTC AC      ATCGTACTT
                                  C  CACCC__
GAM2102  POU3F4   3'  GAGTGAGAGAGAAAGGAAA    51206       A    T  CAT
                                GAGTGA AGAGA AG   GAAA
                                |||||| ||||| ||   ||||
                                CTCACT TCTCT TC   CTTT
                                    C    T ___
GAM2102  PPT2     5'  TGAGGAAAGAGAACGCA      51207      T      TA
                                TGAG GAAAGAGA  GCA
                                |||| ||||||||  |||
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                                ACTC CTTTCTCT  CGT
                                  _      TG
GAM2102  PPT2    5'  TGAGGAAAGAGAACGCA    51207     T     TA
                                TGAG GAAAGAGA  GCA
                                |||| ||||||||  |||
                                ACTC CTTTCTCT  CGT
                                  _      TG
GAM2102  PSD     5'  AGTGGAAGAGATAGATG    51208     A      C
                                AGTG AAGAGATAG ATG
                                |||| ||||||||| |||
                                TCAC TTCTCTATC TAC
                                  C      _
GAM2102  RAB11A  3'  AGTGAAGCCATAGCATGAAAA  51209      A AG
                                AGTGAA G  ATAGCATGAAAA
                                |||||| |  ||||||||||||
                                TCACTT C  TATCGTACTTTT
                                   _ GG
GAM2102  SCD     3'  TGAGTGAAGGGGCACAACAC  51210       AGAG_
                                TGAGTGAA    ATAGCAT
                                ||||||||    |||||||
                                ACTCACTT    TGTTGTG
                                     CCCCG
GAM2102  SLC16A1  3'  TAAGTGAAAGGGGTCACAAAA  51211        AGATAG  TG
                                TGAGTGAAAG     CA  AAA
                                ||||||||||     ||  |||
                                ATTCACTTTC     GT  TTT
                                      CCCA__  GT
GAM2102  SORD    3'  TGAGTGGCAGATTTTCATGAAA 51212      AA   GATAG
            A                    TGAGTG  AGA    CATGAAAA
                                ||||||  |||    ||||||||
                                ACTCAC  TCT    GTACTTTT
                                   CG   AAAA_
GAM2102  WAS     3'  TGAGTGAAGAGAACTGA     51213       A   TA  A
                                TGAGTGAA GAGA  GC TGA
                                |||||||| ||||  || |||
                                ACTCACTT CTCT  TG ACT
                                      _   __  _
GAM2102  ALS2CR3  3'  TGAGTGAAGGGGAACGAAA   51214       AGA  TAGC
                                TGAGTGAA   GA   ATGAAA
                                ||||||||   ||   ||||||
                                ACTCACTT   CT   TGCTTT
                                     CCC  _____
GAM2102  CTPS2   3'  AGTGGGAATGCATGAAA    51215     AAA  ATA
                                AGTG   GAG   GCATGAAA
                                ||||   |||   ||||||||
                                TCAC   CTT   CGTACTTT
                                  C__   A__
GAM2102  DDM36   3'  TGAGTGAAGAGGAGGCAGGA  51216       A  ATA  T
                                TGAGTGAA GAG   GCA GA
                                |||||||| |||   ||| ||
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                                ACTCACTT CTC   CGT CT
                                     _  CTC   C
GAM2102 dJ309H15.1 3'  GTGAAAGAGACAATAGA     51217           CAT
                                GTGAAAGAGATAG   GA
                                ||||||||||||   ||
                                CACTTTCTCTGTT   CT
                                       AT_
GAM2102 DKFZp547E052 3'  TGAGTGGAAAGATAACTAA   51218       AA       A
                                TGAGTG  AGAGATAGC TGA
                                ||||||  ||||||||| |||
                                ACTCAC  TTTCTATTG ATT
                                   C_       _
GAM2102 DPCR1    3'  TGGTGGAAGAGACAGGAAA   51219    A  A       CAT
                                TG GTG AAGAGATAG   GAAA
                                || ||| |||||||||   ||||
                                AC CAC TTCTCTGTC   CTTT
                                 _  C        ___
GAM2102 FLJ10241  3'  TGAGTGAAGACAAATG      51220        AAG     C
                                TGAGTGA   AGATAG ATG
                                |||||||   |||||| |||
                                ACTCACT   TCTGTT TAC
                                     ___     _
GAM2102 FLJ10890  3'  TGAGTAAAGAGAAAGAGA    51221         A   T  CAT
                                TGAGTGAA GAGA AG   GA
                                |||||||| |||| ||   ||
                                ACTCATTT CTCT TC   CT
                                     _   T  T__
GAM2102 FLJ12650  3'  GAGTGAAAGGGAGAGGCTG   51222         A  T  CA
                                GAGTGAAAG GA AG  TG
                                ||||||||| || ||  ||
                                CTCACTTTC CT TC  AC
                                      C  C  CG
GAM2102 H-L(3)MBT 3'  TGAGTGGGTAGAGAGCAGA   51223       AA_    TA   T
                                TGAGTG   AGAGA  GCA GA
                                ||||||   |||||  ||| ||
                                ACTCAC   TCTCT  CGT CT
                                   CCA    __   _
GAM2102 KIAA0240  5'  TGAGTAAAGGATGCTGATGAA  51224         A A   A  __
                                TGAGTGAA G GAT GC  ATGAA
                                |||||||| | ||| ||  |||||
                                ACTCATTT C CTA CG  TACTT
                                     _ _   _ AC
GAM2102 KLF12    3'  TGAGGAGGGAGATAACTGA   51225     T  AA      A
                                TGAG GA  GAGATAGC TGA
                                ||||  ||  |||||||| |||
                                ACTC CT  CTCTATTG ACT
                                  _  CC       _
GAM2102 MGC10854  3'  TGGGTAAGAAAGGCATGAAA  51226    A   A   ATA
                                TG GTGA AGAG   GCATGAAA
                                || |||| ||||   ||||||||
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                                AC CATT TTTC   CGTACTTT
                                 C   C   ___
GAM2102  MGC29667  3'  TGAGGGAAAGCAATAGCATGA  51227     T    AG
                                TGAG GAAAG  ATAGCATGA
                                |||| |||||  |||||||||
                                ACTC CTTTC  TATCGTACT
                                  C    GT
GAM2102  PLCL1     5'  TGGTGAAAGAGGCACTGAA   51228    A       ATA  _
                                TG GTGAAAGAG   GCA TGAA
                                || |||||||||   ||| ||||
                                AC CACTTTCTC   CGT ACTT
                                 _       ___  G
GAM2102  PRO0097   5'  AGTGGAAGAGATATACATAAA  51229     A       _
                                AGTG AAGAGATA GCATGAA
                                |||| |||||||| |||||||
                                TCAC TTCTCTAT TGTATTT
                                  C       A
GAM2102  RAI17     3'  TGAGCGAGAGAGACAGACG   51230       A       C
                                TGAGTGA AGAGATAG ATG
                                ||||||| |||||||| |||
                                ACTCGCT TCTCTGTC TGC
                                   C       _
GAM2102  SARCOSIN  3'  TGAGTGAAACAGATTCACAAAA 51231         G    AG  TG
                                TGAGTGAAA AGAT  CA  AAA
                                ||||||||| ||||  ||  |||
                                ACTCACTTT TCTA  GT  TTT
                                     G    A_  GT
GAM2102  SEMA5B    3'  TGGGTTGGAAGATAACCATGA  51232    A  GAAA      _
                                TG GT    GAGATAGC ATGA
                                || ||    |||||||| ||||
                                AC CA    TTCTATTG TACT
                                 C  ACC_       G
GAM2102  TCL6      5'  GTGAACTGAGATAGCATGAAAA 51233      A_
                                GTGAA  GAGATAGCATGAAAA
                                |||||  ||||||||||||||
                                CACTT  CTCTATCGTACTTTT
                                   GA
GAM2102  TCL6      5'  GTGAACTGAGATAGCATGAAAA 51233      A_
                                GTGAA  GAGATAGCATGAAAA
                                |||||  ||||||||||||||
                                CACTT  CTCTATCGTACTTTT
                                   GA
GAM2102  TCL6      5'  GTGAACTGAGATAGCATGAAAA 51233      A_
                                GTGAA  GAGATAGCATGAAAA
                                |||||  ||||||||||||||
                                CACTT  CTCTATCGTACTTTT
                                   GA
GAM2102  TCL6      5'  GTGAACTGAGATAGCATGAAAA 51233      A_
                                GTGAA  GAGATAGCATGAAAA
                                |||||  ||||||||||||||
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                                CACTT  CTCTATCGTACTTTT
                                   GA
GAM2102  LOC116166 3'  TGAGTGGCAGATTTTCATGAAA 51212       AA   GATAG
            A                   TGAGTG  AGA    CATGAAAA
                                ||||||  |||    ||||||||
                                ACTCAC  TCT    GTACTTTT
                                   CG   AAAA_
GAM2102  LOC130612 5'  TGAGTGAAAGAGGCTGTGCAGA 51234          ATA__   T
                                TGAGTGAAAGAG    GCA GA
                                ||||||||||||    ||| ||
                                ACTCACTTTCTC    CGT CT
                                      CGACA  _
GAM2102  LOC145622 5'  GTGAAAGAGCTCACTGAAA   51235        ATA  A
                                GTGAAAGAG   GC TGAAA
                                |||||||||   || |||||
                                CACTTTCTC   TG ACTTT
                                     GAG  _
GAM2102  LOC221477 3'  TGTAGTGGGAGGCCACATGAAA 51236    _   AAA   ATA
                                TG AGTG   GAG   GCATGAAA
                                || ||||   |||   ||||||||
                                AC TCAC   CTC   TGTACTTT
                                 A   C__   CGG
GAM2102  LOC255645 3'  TGAATGAAAGAGCTCTGAAA   51237          ATAGCA
                                TGAGTGAAAGAG     TGAAA
                                ||||||||||||     |||||
                                ACTTACTTTCTC     ACTTT
                                      GAG___
GAM2102  LOC90198  5'  TGAGTGAAGAGATGTCTGAA   51238        A    AGCA
                                TGAGTGAA GAGAT    TGAA
                                |||||||| |||||    ||||
                                ACTCACTT CTCTA    ACTT
                                    _    CAG_
GAM2103  CGGBP1    3'  TAAGCATATTGTGAAATTCTG  51241        AC   ATC_
                                TAAGCATAT  TGT    TTCTG
                                |||||||||  |||    |||||
                                ATTCGTATA  ACA    AAGAC
                                     __   CTTT
GAM2103  DKFZP566A1524 3'  TAAACATATACATCTTCTG    51242          TGT
                                TAAGCATATAC   ATCTTCTG
                                ||||||||||||  ||||||||
                                ATTTGTATATG   TAGAAGAC
                                      ___
GAM2103  GFPT1     3'  TATGAGCATACACTGCCACTG  51243     A         ATCTT
                                TAT AGCATATACTGT     CTG
                                ||| ||||||||||||    |||
                                ATA TCGTATGTGACG     GAC
                                  C          GT___
GAM2103  KIAA0410  3'  TATTAGCATATATTACACTCTG 51244     A       CTG   C
                                TAT AGCATATA   TAT TTCTG
                                ||| ||||||||   ||| |||||
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                                ATA TCGTATAT   ATG GAGAC
                                  A       A__   T
GAM2103  KIAA0895  3'  TACAAGTATATACTGAAGCT   51245       C       TAT
                                TATAAG ATATACTG   CT
                                |||||| ||||||||   ||
                                ATGTTC TATATGAC   GA
                                   A       TTC
GAM2103  LOC200624 5'  AAGCATATGTAACTTCTG    51246        TAC    T
                                AAGCATA   TGTA CTTCTG
                                |||||||   |||| ||||||
                                TTCGTAT   ACAT GAAGAC
                                    ___    T
GAM2103  LOC200942 3'  TAAGCATATGTGTGTCCT    51247         AC   A
                                TAAGCATAT  TGT TCTT
                                |||||||||  ||| ||||
                                ATTCGTATA  ACA AGGA
                                     C_   C
GAM2103  LOC203411 3'  AACAAATACTGTATTTTCTG   51248      T       C
                                AGCA ATACTGTAT TTCTG
                                |||| ||||||||| |||||
                                TTGT TATGACATA AAGAC
                                  T        A
GAM2103  LOC219731 5'  TATATGCATATCATCTTCT    51249      A     ACTG
                                TATA GCATAT    TATCTTCT
                                |||| ||||||    ||||||||
                                ATAT CGTATA    GTAGAAGA
                                  A     _____
GAM2104  TOX      3'  TAATAGTTTTTTGTTTGC    51252           TACCA
                                TAATAGTTTTTT     TTTGC
                                ||||||||||||     |||||
                                ATTATCAAAAAA     AAACG
                                       C_____
GAM2104  KIAA0171  3'  TTAATGGATTTTTACCTTTGCA 51253       AGTT       A
                                TTAAT    TTTTTACC TTTGCA
                                |||||    |||||||| ||||||
                                AATTA    AAAAATGG AAACGT
                                   CCT_       _
GAM2104  KIAA0472  3'  CAGTTACTTTATCATTTGCA   51254      T    C
                                TAGTT TTTTA CATTTGCA
                                ||||| ||||| ||||||||
                                GTCAA GAAAT GTAAACGT
                                   T    A
GAM2105  AFM      5'  TTATGGAATTTAGACTCTT    51257      AT    C
                                TTGT  GATT AGACTCTT
                                ||||  |||| ||||||||
                                AATA  TTAA TCTGAGAA
                                  CC    A
GAM2105  GPR18    5'  TTGTATTTTGTTTTAGACTCTT 51258       GATTC___
            T                    TTGTAT       AGACTCTTT
                                ||||||       |||||||||
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                                AACATA       TCTGAGAAA
                                   AAACAAAA
GAM2105 MGC4126  3' TTTGTAGAGACTGGACTCTTT 51259       T_   CA
                                TTTGTA  GATT  GACTCTTT
                                ||||||  ||||  ||||||||
                                AAACAT  CTGA  CTGAGAAA
                                   CT    C_
GAM2105 PDGFC    3' TTATTTGATGATTCAATAC   51260       T       _
                                TTATTTG ATGATTCAG AC
                                ||||||| ||||||||| ||
                                AATAAAC TACTAAGTT TG
                                   _       A
GAM2105 LOC253795 5' TTTGTATGAAAATCTCTTT   51261         TTCAGA
                                TTTGTATGA     CTCTTT
                                |||||||||     ||||||
                                AAACATACT     GAGAAA
                                      TTTA__
GAM2106 C7orf2   3' AAAAATCCAAGTTACAAG    51264          AA
                                AAAAATCCAAG  ACAAG
                                ||||||||||  |||||
                                TTTTTAGGTTC  TGTTC
                                      AA
GAM2106 CLECSF11  5' AAAAATCCAAAAAATTAG    51265           CA
                                AAAAATCCAAGAAA  AG
                                ||||||||||||  ||
                                TTTTTAGGTTTTTT  TC
                                      AA
GAM2106 CYP4F3   3' AAAATCCAACAATAAGAAG   51266        G  AC
                                AAAATCCAA AA  AAGAAG
                                ||||||||| ||  ||||||
                                TTTTAGGTT TT  TTCTTC
                                      G  A_
GAM2106 GJA1     3' AAAACCCAAGAATACCAG    51267          _  A
                                AAAATCCAAGAA AC AG
                                |||||||||||| || ||
                                TTTTGGGTTCTT TG TC
                                      A  G
GAM2106 GOCAP1   3' AAAACCCTCCTACAAGAAG   51268       AAGAA
                                AAAATCC    ACAAGAAG
                                |||||||    ||||||||
                                TTTTGGG    TGTTCTTC
                                   AGGA_
GAM2106 IDH3G    3' AATCCAAGGAGCAAACCAAGAA 51269        ____   _     III
            GC                    AATCCAAG   AAAC AAGAAG  C
                                ||||||||   |||| ||||||  |
                                TTAGGTTC   TTTG TTCTTC  G
                                   CTCG   G     III
GAM2106 IGF1     3' AAAAATCCAAAAAATTAG    51265           CA
                                AAAAATCCAAGAAA  AG
                                ||||||||||||  ||
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                                TTTTTAGGTTTTTT  TC
                                      AA
GAM2106  JAM3     3'  AAAAACCCAAGACACTGGAAG  51270          A  AA
                                AAAAATCCAAGA AC  GAAG
                                |||||||||||| ||  ||||
                                TTTTTGGGTTCT TG  CTTC
                                      G  AC
GAM2106  LAMC2    3'  AAAATCCAAGGAAATACAGAAG 51271          _  CA_
                                AAAATCCAAG AAA   AGAAG
                                |||||||||| |||   |||||
                                TTTTAGGTTC TTT   TCTTC
                                      C   ATG
GAM2106  MX2      3'  AATCAGGGAAACAAGAAG    51272      CAA
                                AATC   GAAACAAGAAG
                                ||||   ||||||||||
                                TTAG   CTTTGTTCTTC
                                  TCC
GAM2106  NHP2L1   3'  AAAAATCCAGAAACCAG     51273         A    A
                                AAAAATCCA GAAAC AG
                                ||||||||| ||||| ||
                                TTTTTAGGT CTTTG TC
                                      _    G
GAM2106  NSF      3'  AAAACCCAAAACAAAGAAG   51274          AAC
                                AAAATCCAAGA   AAGAAG
                                ||||||||||   ||||||
                                TTTTGGGTTTT   TTCTTC
                                      GT_
GAM2106  PIWIL1   3'  ATCTATGAGAAACAAGAAG   51275     CA__
                                ATC    AGAAACAAGAAG
                                |||    ||||||||||||
                                TAG    TCTTTGTTCTTC
                                  ATAC
GAM2106  RECQL5   3'  ACACAGAGAAACAAGAAG    51276   TC  _
                                A  CA AGAAACAAGAAG
                                |  || ||||||||||||
                                T  GT TCTTTGTTCTTC
                                 GT  C
GAM2106  SDHC     3'  GGAAATCCAAGAAAAAG     51277   A         C
                                A AAATCCAAGAAA AAG
                                | ||||||||||| |||
                                C TTTAGGTTCTTT TTC
                                 C          _
GAM2106  SLC21A9  3'  AAAACCTGGGAAACAAGA    51278       CAA
                                AAAATC   GAAACAAGA
                                ||||||   |||||||||
                                TTTTGG   CTTTGTTCT
                                    ACC
GAM2106  TIF1     3'  AAAAATCCAAGAAGTGGGAAG 51279           ACAA
                                AAAAATCCAAGAA    GAAG
                                ||||||||||||    ||||
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                                TTTTTAGGTTCTT   CTTC
                                      CACC
GAM2106 TNFRSF1B 3' AAAAACCCAAGGGCTCCAGAAG 51280          AAACA_
                                AAAAATCCAAG     AGAAG
                                ||||||||||     |||||
                                TTTTTGGGTTC     TCTTC
                                      CCGAGG
GAM2106 USH3A    3' AAAACTCCAAGAAGACAGAGA  51281      A      _  _
                                AAAA TCCAAGAA ACA AGA
                                |||| |||||||| ||| |||
                                TTTT AGGTTCTT TGT TCT
                                  G       C  C
GAM2106 CDC14B   3' AAAAATCCAATGTTACAGGGAA 51282         GAA_  A_
             G                   AAAAATCCAA   ACA  GAAG
                                ||||||||||   |||  ||||
                                TTTTTAGGTT   TGT  CTTC
                                      ACAA   CC
GAM2106 CDC14B   3' AAAAATCCAATGTTACAGGGAA 51282         GAA_  A_
             G                   AAAAATCCAA   ACA  GAAG
                                ||||||||||   |||  ||||
                                TTTTTAGGTT   TGT  CTTC
                                      ACAA   CC
GAM2106 CTBS     3' AAAAATGCAAGAAACTAG    51283       C       A
                                AAAAAT CAAGAAAC AG
                                |||||| |||||||| ||
                                TTTTTA GTTCTTTG TC
                                   C       A
GAM2106 DATF1    3' AAAACTGAGAAACAAGAA    51284      CCA
                                AAAAT   AGAAACAAGAA
                                |||||   ||||||||||||
                                TTTTG   TCTTTGTTCTT
                                   AC_
GAM2106 DATF1    3' AAAACTGAGAAACAAGAA    51284      CCA
                                AAAAT   AGAAACAAGAA
                                |||||   ||||||||||||
                                TTTTG   TCTTTGTTCTT
                                   AC_
GAM2106 DATF1    3' AAAACTGAGAAACAAGAA    51284      CCA
                                AAAAT   AGAAACAAGAA
                                |||||   ||||||||||||
                                TTTTG   TCTTTGTTCTT
                                   AC_
GAM2106 DDX18    3' AAAAATCCTCACAAAACAAGAA 51285        AA__
             G                   AAAAATCC    GAAACAAGAAG
                                ||||||||    ||||||||||||
                                TTTTTAGG    TTTTGTTCTTC
                                     AGTG
GAM2106 FLJ12619 3' AAAAATCCAGGATGAACAAG   51286        A  __
                                AAAAATCCA GA  AACAAG
                                |||||||| ||  ||||||
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                                TTTTTAGGT CT  TTGTTC
                                     C  AC
GAM2106  FLJ13081  3'  AAAAATCCAATAGAATCAAA   51287          __   A
                                AAAAATCCA  AGAA CAAG
                                |||||||||  |||| ||||
                                TTTTTAGGT  TCTT GTTT
                                     TA    A
GAM2106  FLJ20986  5'  AAAAATCCAACAAATGGCAAG  51288          G  ___
                                AAAAATCCAA AAA   CAAG
                                |||||||||| |||   ||||
                                TTTTTAGGTT TTT   GTTC
                                      G   ACC
GAM2106  KIAA0390  5'  AAAAATCCAAGCAAG       51289          AAA
                                AAAAATCCAAG   CAAG
                                ||||||||||   ||||
                                TTTTTAGGTTC   GTTC
                                      ___
GAM2106  KIAA0820  3'  AATCCTAAAAACAAGAAG    51290       A
                                AATCC AGAAACAAGAAG
                                ||||| ||||||||||||
                                TTAGG TTTTTGTTCTTC
                                   A
GAM2106  KIAA1237  3'  AAACCCATGAACAAGAAG    51291        A   A
                                AAATCCA GAA CAAGAAG
                                ||||||| ||| |||||||
                                TTTGGGT CTT GTTCTTC
                                     A  _
GAM2106  KIAA1674  3'  AAAATCCACAGAAGGCAAGAAG 51292          _   A_
                                AAAATCCA AGAA  CAAGAAG
                                |||||||| ||||  |||||||
                                TTTTAGGT TCTT  GTTCTTC
                                     G    CC
GAM2106  KIAA1755  3'  AATCCAAGACAAGGAAG     51293          AA   _
                                AATCCAAGA  CAAG AAG
                                |||||||||  |||| |||
                                TTAGGTTCT  GTTC TTC
                                     __    C
GAM2106  KIAA1906  3'  AAAAATCCAAAAGTCAAGAAG  51294            AA
                                AAAAATCCAAGA  CAAGAAG
                                ||||||||||||  |||||||
                                TTTTTAGGTTTT  GTTCTTC
                                      CA
GAM2106  KIAA1946  3'  AAACACCTGGAAACAAGAAG   51295     _ AA
                                AAAT CC  GAAACAAGAAG
                                |||| ||  ||||||||||||
                                TTTG GG  CTTTGTTCTTC
                                  T  AC
GAM2106  LANCL2    3'  AAAATCCAAACAGGAAG     51296          GAA   A
                                AAAATCCAA   ACA GAAG
                                |||||||||   ||| ||||
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                                TTTTAGGTT   TGT CTTC
                                    ___   C
GAM2106  MAN1C1   3'  AAAAACCAAGAAACCAAAAG   51297      T       A
                                AAAAA CCAAGAAAC AGAAG
                                ||||| ||||||||| |||||
                                TTTTT GGTTCTTTG TTTTC
                                  _       G
GAM2106  OSBPL2   5'  AAAAATCCAATAGACACTGAAG 51298         GAA   A_
                                AAAAATCCAA   ACA  GAAG
                                ||||||||||   |||  ||||
                                TTTTTAGGTT   TGT  CTTC
                                     ATC   GA
GAM2106  OSBPL2   5'  AAAAATCCAATAGACACTGAAG 51298         GAA   A_
                                AAAAATCCAA   ACA  GAAG
                                ||||||||||   |||  ||||
                                TTTTTAGGTT   TGT  CTTC
                                     ATC   GA
GAM2106  PER3     3'  AAAATTCCAAGAACTGTCAAAG 51299      A       ACAA_
                                AAAA TCCAAGAA    GAAG
                                |||| ||||||||    ||||
                                TTTT AGGTTCTT    TTTC
                                  A       GACAG
GAM2106  PRO2037  3'  AAAAATCCAACTCACAGAAG   51300         GAA   A
                                AAAAATCCAA   ACA GAAG
                                ||||||||||   ||| ||||
                                TTTTTAGGTT   TGT CTTC
                                     GAG  _
GAM2106  SE57-1   3'  AAAAATCTGAAAACAAGA    51301       CAA
                                AAAAATC   GAAACAAGA
                                |||||||   |||||||||
                                TTTTTAG   TTTTGTTCT
                                    AC_
GAM2106  TNFRSF21 3'  AAAAATCAGAAACAGAAG    51302       CA      A
                                AAAAATC  AGAAACA GAAG
                                |||||||  ||||||| ||||
                                TTTTTAG  TCTTTGT CTTC
                                    __     _
GAM2106  TNRC6    3'  AAAAATCTGTAAACAAGAAG   51303       CAAG
                                AAAAATC    AAACAAGAAG
                                |||||||    ||||||||||
                                TTTTTAG    TTTGTTCTTC
                                    ACA_
GAM2106  LOC145241 3'  AAAATCACAACAGACAAGAAG  51304       _   GAA
                                AAAATC CAA   ACAAGAAG
                                |||||| |||   ||||||||
                                TTTTAG GTT   TGTTCTTC
                                   T   GTC
GAM2106  LOC148195 3'  AAAATCCAAGATCAGGAAG   51305          AA  A
                                AAAATCCAAGA  CA GAAG
                                ||||||||||  ||  ||||
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                                TTTTAGGTTCT  GT CTTC
                                      A_  C
GAM2106  LOC150297 5'  AAAAAGTCCAAGAGGCACAAG  51306      _      A__
                                AAAAA TCCAAGA   ACAAG
                                ||||| |||||||   |||||
                                TTTTT AGGTTCT   TGTTC
                                   C       CCG
GAM2106  LOC153768 3'  AAAAATCCAGCAAGAA      51307          AGAAA
                                AAAAATCCA     CAAGAA
                                |||||||||     ||||||
                                TTTTTAGGT     GTTCTT
                                      C____
GAM2106  LOC158187 3'  AAAAATCCTAAGAACACTAAAA 51308         _    _  A
              G                  AAAAATCC AAGAA AC AGAAG
                                ||||||||| ||||| || |||||
                                TTTTTAGG TTCTT TG TTTTC
                                     A     G  A
GAM2106  LOC161829 3'  AATCCAAAAGTCAAGAAG     51309          AA
                                AATCCAAGA  CAAGAAG
                                |||||||||  |||||||
                                TTAGGTTTT  GTTCTTC
                                      CA
GAM2106  LOC197131 3'  AAAAGCCAGGAACCAAGAAG   51310      T   A   A
                                AAAA CCA GAA CAAGAAG
                                |||| ||| ||| |||||||
                                TTTT GGT CTT GTTCTTC
                                   C   C   G
GAM2106  LOC201725 3'  AAAAACCAAGAAAACCAAG    51311       T       __
                                AAAAA CCAAGAAA  CAAG
                                ||||| ||||||||  ||||
                                TTTTT GGTTCTTT  GTTC
                                   _       TG
GAM2106  LOC219842 5'  AAAACTCCAAGAACAAG      51312      A       A
                                AAAA TCCAAGAA CAAG
                                |||| |||||||| ||||
                                TTTT AGGTTCTT GTTC
                                   G       _
GAM2106  LOC256280 3'  AAAATTGGAGAAACAAGAA    51313       CCA
                                AAAAT   AGAAACAAGAA
                                |||||   ||||||||||
                                TTTTA   TCTTTGTTCTT
                                   ACC
GAM2106  LOC91496  5'  AATCCAAAACAGAGACAAGAAG 51314        _____  A
                                AATCCA    AGA ACAAGAAG
                                ||||||    ||| ||||||||
                                TTAGGT    TCT TGTTCTTC
                                    TTTG   C
GAM2107  COL10A1   3'  TCTGCAATCATAGAAAAGTT   51317           TAGT
                                TTTGCAATCATA    GAGTT
                                ||||||||||||    |||||
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                                AGACGTTAGTAT   TTCAA
                                     CTT_
GAM2107 PLXNA2   3' TTTGCAATTTGTGCAAAGTTCT 51318       CATATAGT
                                TTTGCAAT      GAGTTCT
                                ||||||||      |||||||
                                AAACGTTA      TTCAAGA
                                    AACACGT_
GAM2107 MGC15619 5' TTTGCAATCGATGTGATTGTCT 51319       ATATA   GT_
           A                     TTTGCAATC    GTGA  TCTA
                                 |||||||||    ||||  ||||
                                 AAACGTTAG    CACT  AGAT
                                     CTA__    AAC
GAM2107 PRO1257  5' TTTGCAATCCTATGTGTTCTA  51320       ATATA  A
                                TTTGCAATC    GTG GTTCTA
                                |||||||||    ||| ||||||
                                AAACGTTAG    TAC CAAGAT
                                     GA___   A
GAM2107 TU3A     3' GCAATCATGTACATCTCT    51321       ATA  AG_
                                GCAATCAT   GTG   TTCT
                                ||||||||   |||   ||||
                                CGTTAGTA   CAT   GAGA
                                    ___   GTA
GAM2108 ELAC1    3' GCTATCATCAATCCTGCCTGTC 51324    _     ATAC   A
           C                     GC ATCATCGG   GCCT TCC
                                 || ||||||||   |||| |||
                                 CG TAGTAGTT   CGGA AGG
                                  A      AGGA   C
GAM2108 HT002    3' GCACCATCTCAGGTGCCTGTCC 51325       GGATAC   A
                                GCATCATC     GCCT TCC
                                ||||||||     |||| |||
                                CGTGGTAG     CGGA AGG
                                     AGTCCA   C
GAM2109 RAD23A   3' TAAATAAACATGAATATATAT  51328   T   TT
                                A GATG  TGTGAATATATAT
                                | ||||  ||||||||||||
                                A TTAT  GTACTTATATATA
                                 T   TT
GAM2109 RECK     3' ATGAATACCGATGAATATATAT 51329     TGT  _
                                ATGA   TTG TGAATATATAT
                                ||||   ||| ||||||||||
                                TACT   GGC ACTTATATATA
                                  TAT   T
GAM2109 SVIL     3' ATGGTGTTTATATAAATATATA 51330     A   __
           T                     ATG TGTT  TGTGAATATATAT
                                 ||| ||||  ||||||||||||
                                 TAC ACAA  ATATTTATATATA
                                   C   AT
GAM2109 SVIL     3' ATGGTGTTTATATAAATATATA 51330     A   __
           T                     ATG TGTT  TGTGAATATATAT
                                 ||| ||||  ||||||||||||
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                                TAC ACAA  ATATTTATATATA
                                  C    AT
GAM2109  BCMP1    3'  ATGTGTGTGAGTATATAT    51331      T    A
                                ATGT TGTGA TATATAT
                                |||| ||||| |||||||
                                TACA ACACT ATATATA
                                  C    C
GAM2109  KIAA0052 3'  AATGATGTTTGATTTAAATAT  51332          ___
                                AATGATGTTTG   TGAATAT
                                ||||||||||   |||||||
                                TTACTACAAAC   ATTTATA
                                      TAA
GAM2109  KIAA0993 3'  TGAATGCATGTGCATATAT   51333   T    T   A
                                A GATGT TGTG ATATAT
                                | ||||| |||| ||||||
                                A TTACG ACAC TATATA
                                 C    T   G
GAM2109  PRO2176  3'  TAAATGGTATGAATATATAT   51334       ATGTT
                                TAAATG    TGTGAATATATAT
                                ||||||    ||||||||||||
                                ATTTAC    ATACTTATATATA
                                   C____
GAM2109  LOC145622 3'  TAAATGTTGTCTGTATATAT   51335       A       A
                                TAAATG TGTTTGTG ATAT
                                |||||| |||||||| ||||
                                ATTTAC ACAGACAT TATA
                                   A       A
GAM2110  DLEU2    3'  CTACCATATAGTTATAATTATA 51338     TT    A
                                CTG  GTATA TTATAATTATA
                                |||  ||||| ||||||||||
                                GAT  TATAT AATATTAATAT
                                  GG    C
GAM2110  PTPRG    3'  CTGTTGTATAAGATTATA    51339          __
                                CTGTTGTATA  ATTATA
                                ||||||||||  ||||||
                                GACAACATAT  TAATAT
                                      TC
GAM2110  LOC169545 5'  TCTGTTGTAATGCTTATTATA  51340         TAATTATA
                                TCTGTTGTA       ATTATA
                                |||||||||       ||||||
                                AGACAACAT       TAATAT
                                    TACGAA__
GAM2111  PBX2     3'  TATTTAACATATTTGGCAATAA 51343      A       TTT_
            CTC                   TATT AACATATTT    ATAACTC
                                |||| |||||||||   |||||||
                                ATAA TTGTATAAA    TATTGAG
                                  A       CCGT
GAM2111  FLJ11016 3'  TATTAAACTTATTTCCTAT   51344        A
                                TATTAAAC TATTTTTTAT
                                |||||||| ||||||||||
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                                ATAATTTG ATAAAGGATA
                                    A
GAM2111  MGC2603   3'  TTAAACATAGAGTATATAACT  51345        TTTTT
                                TTAAACATA    TATAACT
                                |||||||||    |||||||
                                AATTTGTAT    ATATTGA
                                     CTCAT
GAM2111  PRO0097   5'  TAAACATATTTCTTAGCTC   51346           TAA
                                TAAACATATTTTTTA   CTC
                                ||||||||||||||   |||
                                ATTTGTATAAAGAAT   GAG
                                        C__
GAM2112  P23       3'  ATCATGGGACTGGGAAG     51349       AC
                                ATCATG  GATTGGGAAG
                                ||||||  ||||||||||
                                TAGTAC  CTGACCCTTC
                                   C_
GAM2112  SLC9A6    3'  TAGAATATTTACACATTTGGGA 51350        CATG   A
           AG                     TAGAATAT    ACG TTGGGAAG
                                ||||||||    ||| ||||||||
                                ATCTTATA    TGT AACCCTTC
                                     AATG   A
GAM2112  C21orf108 3'  CACCATGTTGGGAAG       51351        ACGA
                                TATCATG    TTGGGAAG
                                |||||||    ||||||||
                                GTGGTAC    AACCCTTC
                                     ____
GAM2112  FLJ13215  3'  TAGAATATTTTGGTCTTTGGGA 51352        CA  ACGA
           AG                     TAGAATAT  TG    TTGGGAAG
                                ||||||||  ||    ||||||||
                                ATCTTATA  AC    AACCCTTC
                                     AA  CAGA
GAM2112  FLJ13215  3'  TAGAATATTCTGGTCTTTGGG  51354        CA  ACGA
                                TAGAATAT  TG    TTGGG
                                |||||||  ||    |||||
                                ATCTTATA  AC    AACCC
                                     AG  CAGA
GAM2112  FLJ13215  3'  TAGAATATTCTGGTCGTTGGA  51353        CA  A_  A
                                TAGAATAT  TG  CG TTGGG
                                |||||||  ||  ||  |||||
                                ATCTTATA  AC  GC AACCT
                                     AG  CA  _
GAM2112  KIAA0265  3'  TAGAATATTGTATGACATGG   51355        C__     AT
                                TAGAATAT   ATGACG  TGG
                                ||||||||   ||||||  |||
                                ATCTTATA   TACTGT  ACC
                                     ACA     __
GAM2112  LOC158435 3'  TAGAATAGTCATGGTGCTGAG  51356        _    ACGA
                                TAGAATA TCATG    TTGGG
                                |||||||  |||||    |||||
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                                ATCTTAT AGTAC   GACTC
                                    C    CAC_
GAM2112  LOC199858 5'  GAATACCATGATGGTGGG    51357          CGAT
                                GAATATCATGA   TGGG
                                ||||||||||   ||||
                                CTTATGGTACT   ACCC
                                      ACC_
GAM2112  LOC203292 3'  ATCATGGGACTGGGAAG     51349       AC
                                ATCATG  GATTGGGAAG
                                ||||||  ||||||||||
                                TAGTAC  CTGACCCTTC
                                   C_
GAM2112  LOC92465  5'  CAGGATGTCATGACATGGGA   51358     A  A       AT
                                TAG AT TCATGACG  TGGGA
                                ||| || ||||||||  |||||
                                GTC TA AGTACTGT  ACCCT
                                  C  C       __
GAM2113  ALDH2     3'  TAGGAAAAATTTCTCTTTTCA  51361         CTGA_
                                TAGGAAAAA    TTTTTCA
                                |||||||||    |||||||
                                ATCCTTTTT    GAAAAGT
                                     AAAGA
GAM2113  C7        3'  TAGGGAAAACTATCTCAAAT   51362      A      ATT
                                TAGG AAAACTG   TTTCAAAT
                                |||| |||||||   ||||||||
                                ATCC TTTTGAT   AGAGTTTA
                                  C      ____
GAM2113  IL13RA1   3'  GGCAAGAACTGAGGAGTCTCAA 51363    _  A     TT__
             ATA                   GG AA AACTGA    TTTCAAATA
                                || || ||||||    |||||||||
                                CC TT TTGACT    AGAGTTTAT
                                 G  C     CCTC
GAM2113  PCDH1     5'  GGAAGGGTGATTTTTCAA     51364      AAAC
                                GGAA    TGATTTTTCAA
                                ||||    ||||||||||
                                CCTT    ACTAAAAAGTT
                                  CCC_
GAM2113  TDO2      3'  CAGGGGAAACTGATTTTT     51365      AA
                                TAGG  AAACTGATTTTT
                                ||||  ||||||||||||
                                GTCC  TTTGACTAAAAA
                                  CC
GAM2113  B7-H1     3'  TAGGAAAAACTCATACATAAAT 51366          G  TTTTC
             A                   TAGGAAAAACT AT     AAATA
                                ||||||||||| ||     |||||
                                ATCCTTTTTGA TA     TTTAT
                                      G  TGTA_
GAM2113  CYP2E     3'  GGAAAATATTTATTTTCAAATA 51367       ACTGAT
                                GGAAAA     TTTTCAAATA
                                ||||||     ||||||||||
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                                CCTTTT     AAAAGTTTAT
                                   ATAAAT
GAM2113  HNRPA3    3'  AGAAAAACTGAACTACACAAAT 51368          TTTTT_
              A                    GGAAAAACTGA     CAAATA
                                   ||||||||||     ||||||
                                   TCTTTTTGACT     GTTTAT
                                      TGATGT
GAM2113  KIAA1253  3'  GGAATACTGTTTTCAAATA   51369     AA   AT
                                   GGAA  ACTG  TTTTCAAATA
                                   ||||  ||||  ||||||||||
                                   CCTT  TGAC  AAAAGTTTAT
                                     A_   __
GAM2113  KIAA1939  3'  GGAAAGGCTGATCTTACA    51370      AA      T
                                   GGAAA  CTGATTTT CA
                                   |||||  |||||||| ||
                                   CCTTT  GACTAGAA GT
                                      CC       T
GAM2113  KLF12     3'  GGAAAGGCCTGATTTCAAATA  51371      AA_     TT
                                   GGAAA   CTGATT  TCAAATA
                                   |||||   ||||||  |||||||
                                   CCTTT   GACTAA  AGTTTAT
                                      CCG     __
GAM2113  MGC15606  3'  TAGGAGAAGCTAATTCAAATA  51372      A  A    TTT
                                   TAGGA AA CTGAT   TCAAATA
                                   ||||| || |||||   |||||||
                                   ATCCT TT GATTA   AGTTTAT
                                      C  C    ___
GAM2113  MRPL45    3'  GGAAAAACTGATATCCAA    51373          TT
                                   GGAAAAACTGAT  TTCAA
                                   ||||||||||||  |||||
                                   CCTTTTTGACTA  AGGTT
                                          T_
GAM2113  LOC116150 3'  TAGGAGTTATTTTTCAAATA   51374      AAAACTG
                                   TAGGA      ATTTTTCAAATA
                                   |||||      ||||||||||||
                                   ATCCT      TAAAAAGTTTAT
                                      CAA____
GAM2113  LOC133686 3'  TAAGAAAAATTGATTCTC    51375         C
                                   TAGGAAAAA TGATTTTT
                                   |||||||| ||||||||
                                   ATTCTTTTT ACTAAGAG
                                        A
GAM2113  LOC135293 3'  AGGAAAGACACTGGCTTCAAAT 51376       A__    ATT
              A                     AGGAAA   ACTG   TTTCAAATA
                                   ||||||   ||||   |||||||||
                                   TCCTTT   TGAC   GAAGTTTAT
                                      CTG    C__
GAM2113  LOC158332 3'  TAGGAGAAACTGATTCCT    51377      A
                                   TAGGA AAACTGATTTTT
                                   ||||| ||||||||||||
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                                ATCCT TTTGACTAAGGA
                                   C
GAM2113  LOC204084 5'  TAGGAGAAGCTGATCTCT    51378       A  A
                                TAGGA AA CTGATTTTT
                                ||||| || |||||||||
                                ATCCT TT GACTAGAGA
                                   C  C
GAM2113  LOC220988 3'  AGAAAAACTGAACTACACAAAT 51368           TTTTT_
            A                   GGAAAAACTGA     CAAATA
                                ||||||||||     ||||||
                                TCTTTTTGACT     GTTTAT
                                      TGATGT
GAM2113  LOC255515 3'  GGAAACCATTTTTCAAAT    51379      AA   G
                                GGAA  ACT ATTTTTCAAAT
                                ||||  ||| ||||||||||
                                CCTT  TGG TAAAAAGTTTA
                                  __  _
GAM2114  CCNF     3'  TTCTTTCTTACATTTGCAG    51382        CTTG
                                TTCTTTCT    GTTTGCAG
                                ||||||||    ||||||||
                                AAGAAAGA    TAAACGTC
                                    ATG_
GAM2114  DMD      5'  TGGATCCTTTTTCTTTTGGCAG 51383    A      C    GGTTT
                                TG ATTCTTT TCTT     GCAG
                                || ||||||| ||||     ||||
                                AC TAGGAAA AGAA     CGTC
                                 C      A    AAC__
GAM2114  DMD      5'  TGGATCCTTTTTCTTTTGGCAG 51383    A      C    GGTTT
                                TG ATTCTTT TCTT     GCAG
                                || ||||||| ||||     ||||
                                AC TAGGAAA AGAA     CGTC
                                 C      A    AAC__
GAM2114  EPHB1    3'  TTCTTTTTCCTTTTTGCAG    51384       C    GG
                                TTCTTT TCTT  TTTGCAG
                                |||||| ||||  |||||||
                                AAGAAA AGGA  AAACGTC
                                   A    A_
GAM2114  FSHR     5'  TGATTTCTTTCTGCATTTGCAG 51385     A       CTTG
                                TGA TTCTTTCT    GTTTGCAG
                                ||| ||||||||    ||||||||
                                ACT AAGAAAGA    TAAACGTC
                                  A       CG__
GAM2114  HEPH     3'  TGAGTTTTTCTCTTGGTC     51386     A  C
                                TGA TT TTTCTCTTGGTT
                                ||| || ||||||||||||
                                ACT AA AAAGAGAACCAG
                                  C  _
GAM2114  HEPH     3'  TGAGTTTTTCTCTTGGTC     51386     A  C
                                TGA TT TTTCTCTTGGTT
                                ||| || ||||||||||||
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                                ACT AA AAAGAGAACCAG
                                  C  _
GAM2114  IGF1     3'  TAAATTCTTTCTTTATCAGT   51387          C__ TG
                                TGAATTCTTTCT   T  GT
                                ||||||||||||  |  ||
                                ATTTAAGAAAGA   A  CA
                                      AAT GT
GAM2114  ARPP-21  3'  TGAATTCCTTTCCATTTGCAG  51388         C   TG
                                TGAATTCTTT TCT  GTTTGCAG
                                |||||||||| |||  ||||||||
                                ACTTAAGGAA AGG  TAAACGTC
                                      _  __
GAM2114  C17      3'  TGGGTTCTTTCTCTGGTCTCAG 51389    AA       T    G
                                TG  TTCTTTCTCT GGTTT CAG
                                ||  |||||||||| ||||| |||
                                AC  AAGAAAGAGA CCAGA GTC
                                 CC        _    _
GAM2114  KIAA0828 3'  TGAATTCTTTCTTGTATAGT   51390          CT__
                                TGAATTCTTTCT    TGGT
                                ||||||||||||    ||||
                                ACTTAAGAAAGA    ATCA
                                      ACAT
GAM2114  KIAA1157 3'  TGAGTTCTTTCCTGAGCA    51391     A      CT   TTT
                                TGA TTCTTTCT  TGG   GCA
                                ||| ||||||||  |||   |||
                                ACT AAGAAAGG  ACT   CGT
                                  C       __  ___
GAM2114  KIAA1867 3'  TGGGTTCTTCCTGTGGCTT   51392    AA      CT
                                TG  TTCTTTCT  TGGTTT
                                ||  ||||||||  ||||||
                                AC  AAGAAGGA  ACCGAA
                                 CC       C_
GAM2114  LPAAT-gamma1 3'  TGAATTCTTTACTCTTGGCTCA 51393          _
                                TGAATTCTTT CTCTTGGTTTG
                                |||||||||| ||||||||||
                                ACTTAAGAAA GAGAACCGAGT
                                      T
GAM2114  MGC17919 3'  TTCTTTCTTTCCAGTGCAG   51394        C_ TG  TT
                                TTCTTTCT  T  GT  GCAG
                                ||||||||  |  ||  ||||
                                AAGAAAGA  G  CA  CGTC
                                    AA GT  __
GAM2114  PPP1R14C 3'  TGAATTCTTTCACTTTGG    51395          T  _
                                TGAATTCTTTC CTT GG
                                |||||||||| ||| ||
                                ACTTAAGAAAG GAA CC
                                      T  A
GAM2114  SEPT3    3'  TGAGTTCTTTCACCCTGCA   51396     A     T  TGGT
                                TGA TTCTTTC CT    TTGCA
                                ||| ||||||| ||    |||||
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                                ACT AAGAAAG GG    GACGT
                                  C      T _____
GAM2114  LOC113444 3'  TGAATTCTTTCCAGTGCA    51397          CTT   TT
                                TGAATTCTTTCT   GGT  GCA
                                ||||||||||||   |||  |||
                                ACTTAAGAAAGG   TCA  CGT
                                       ____   __
GAM2114  LOC145988 5'  TGAACTTTTTCTTGGCTGCAG  51398     TT   C      T
                                TGAA  CTTT TCTTGGTT GCAG
                                ||||  |||| |||||||| ||||
                                ACTT  GAAA AGAACCGA CGTC
                                  __   A      _
GAM2114  LOC149460 3'  TGGGTTCTTTTCTCCCTCTGCA 51399    AA     _    GG
              G                  TG  TTCTTT CTCTT  TTTGCAG
                                 ||  |||||| |||||  |||||||
                                 AC  AAGAAA GAGGG  AGACGTC
                                  CC     A    __
GAM2114  LOC151146 5'  TGGGCTCTTTCCCTTTGT    51400    AA        G
                                TG  TTCTTTCTCTT GT
                                ||  ||||||||||| ||
                                AC  GAGAAAGGGAA CA
                                 CC         A
GAM2114  LOC91963  3'  TAAATTCTTTCTCTTTTCTTG  51401           GG
                                TGAATTCTTTCTCTT  TTTG
                                ||||||||||||||  ||||
                                ATTTAAGAAAGAGAA  GAAC
                                       AA
GAM2115  HSD11B2   3'  TAAAATGTGGCAATTGGGAAG  51404       ATCA  A
                                TAAAAT    TG CGATTGGGAAG
                                ||||||    || ||||||||||
                                ATTTTA    AC GTTAACCCTTC
                                   C___  C
GAM2115  P23       3'  ATCATGGGACTGGGAAG     51349       AC
                                ATCATG  GATTGGGAAG
                                ||||||  ||||||||||
                                TAGTAC  CTGACCCTTC
                                   C_
GAM2115  SLC9A6    3'  AATATTTACACATTTGGGAAG  51405      CATG   A
                                AATAT    ACG TTGGGAAG
                                |||||    ||| ||||||||
                                TTATA    TGT AACCCTTC
                                   AATG   A
GAM2115  BTN2A1    3'  CAAGATATCATGAAACCAGGAA 51406     A       C   TG
              G                  TAA ATATCATGA GAT  GGAAG
                                 ||| ||||||||| |||  |||||
                                 GTT TATAGTACT TTG  CCTTC
                                  C        _  GT
GAM2115  C21orf108 3'  CACCATGTTGGGAAG       51351        ACGA
                                TATCATG    TTGGGAAG
                                |||||||    ||||||||
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                                GTGGTAC    AACCCTTC
                                      ____
GAM2115 KIAA0894 3' TAAAATATCATGGCAGACTCAG 51407          A _    G
                                TAAAATATCATG C GATT GG
                                |||||||||||| | |||| ||
                                ATTTTATAGTAC G CTGA TC
                                      C T    G
GAM2115 NESHBP   3' TAAAATACCATGAATAGGGA  51408          CGATT
                                TAAAATATCATGA    GGGA
                                ||||||||||||     ||||
                                ATTTTATGGTACT    CCCT
                                       TAT__
GAM2115 LOC203292 3' ATCATGGGACTGGGAAG    51349       AC
                                ATCATG  GATTGGGAAG
                                ||||||  ||||||||||
                                TAGTAC  CTGACCCTTC
                                   C_
GAM2116 CARPX    3' AGGCTTGGGGGAAAGAA     51411      CGA   TT
                                AGGCT   GGG  GGAAAGAA
                                |||||   |||  ||||||||
                                TCCGA   CCC  CCTTTCTT
                                   A__   __
GAM2116 ENO2     3' AGGGAACCTAGGGTTGGGGAGA 51412     C__  G       AA
                                AGG   TC AGGGTTGG  AGA
                                |||   || ||||||||  |||
                                TCC   GG TCCCAACC  TCT
                                  CTT  A       CC
GAM2116 EPHA2    3' GGCCCGAGGGTCTAAAGAA   51413          GG
                                GGCTCGAGGGTT  AAAGAA
                                ||||||||||||  ||||||
                                CCGGGCTCCCAG  TTTCTT
                                       A_
GAM2116 FACL4    3' AAGGCAAGTTGGGAAGA     51414      TCGA      A
                                AAGGC    GGGTTGG AAGA
                                |||||    ||||||| ||||
                                TTCCG    TTCAACC TTCT
                                   _____      C
GAM2116 FACL4    3' AAGGCAAGTTGGGAAGA     51414      TCGA      A
                                AAGGC    GGGTTGG AAGA
                                |||||    ||||||| ||||
                                TTCCG    TTCAACC TTCT
                                   _____      C
GAM2116 INPP1    5' AGGACGAGGGTTGGGGAG    51415     CT        AA
                                AGG  CGAGGGTTGG  AG
                                |||  ||||||||||  ||
                                TCC  GCTCCCAACC  TC
                                  T_         CC
GAM2116 LALBA    3' AAGCTTTGGGGGAACAGAA   51416      CGA   TT   _
                                AGGCT   GGG  GGAA AGAA
                                |||||   |||  |||| ||||
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                                TTCGA  CCC  CCTT TCTT
                                  AA_  __   G
GAM2116  MME     3'  TAAGGCTGAGAGAAAGAA   51417      C    TT
                                TAAGGCT GAGGG  GGAA
                                ||||||| |||||  ||||
                                ATTCCGA CTCTC  TCTT
                                    _    TT
GAM2116  MME     3'  TAAGGCTGAGAGAAAGAA   51417      C    TT
                                TAAGGCT GAGGG  GGAA
                                ||||||| |||||  ||||
                                ATTCCGA CTCTC  TCTT
                                    _    TT
GAM2116  MME     3'  TAAGGCTGAGAGAAAGAA   51417      C    TT
                                TAAGGCT GAGGG  GGAA
                                ||||||| |||||  ||||
                                ATTCCGA CTCTC  TCTT
                                    _    TT
GAM2116  MME     3'  TAAGGCTGAGAGAAAGAA   51417      C    TT
                                TAAGGCT GAGGG  GGAA
                                ||||||| |||||  ||||
                                ATTCCGA CTCTC  TCTT
                                    _    TT
GAM2116  MN1     3'  TAAGGTTGAGGGGGAAGGAA  51418     CTC    TT   A
                                TAAGG  GAGGG  GGAA GAA
                                |||||  |||||  |||| |||
                                ATTCC  CTCCC  CCTT CTT
                                  AA_    __   C
GAM2116  NOS2A   3'  ATAAGACTTGAGGCTGG    51419      C   G
                                ATAAGGCT GAGG TTGG
                                |||||||| |||| ||||
                                TATTCTGA CTCC GACC
                                    A   _
GAM2116  NRXN2   3'  GGATTGGAGGGCTTGGGAAGA  51420   CTC_     _ A
                                GG   GAGGGTT GG AAGA
                                ||   ||||||| || ||||
                                CC   CTCCCGA CC TTCT
                                 TAAC      A  C
GAM2116  NRXN2   3'  GGATTGGAGGGCTTGGGAAGA  51420   CTC_     _ A
                                GG   GAGGGTT GG AAGA
                                ||   ||||||| || ||||
                                CC   CTCCCGA CC TTCT
                                 TAAC      A  C
GAM2116  NRXN2   3'  GGATTGGAGGGCTTGGGAAGA  51420   CTC_     _ A
                                GG   GAGGGTT GG AAGA
                                ||   ||||||| || ||||
                                CC   CTCCCGA CC TTCT
                                 TAAC      A  C
GAM2116  POU2AF1  3'  AAGGAAGGAAGGGGTTGGAAAG 51421     CTC __
                                AAGG  GA  GGGTTGGAAAG
                                ||||  ||  ||||||||||
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                                TTCC  CT  CCCAACCTTTC
                                  TTC  TC
GAM2116  POU2AF1   3'  AAGGAAGGAAGGGGTTGGAAAG 51421     CTC  __
                                AAGG  GA  GGGTTGGAAAG
                                ||||  ||  ||||||||||
                                TTCC  CT  CCCAACCTTTC
                                  TTC  TC
GAM2116  RPH3AL   3'  ATAAGGTCGGGGGCTGA    51422      C  A
                                ATAAGG TCG GGGTTGG
                                |||||| ||| |||||||
                                TATTCC AGC CCCGACT
                                   _  C
GAM2116  RTN2     3'  AAGGCTCGGGCCGAGGAG    51423      GA     AA
                                AAGGCTC  GGGTTGG  AG
                                |||||||  |||||||  ||
                                TTCCGAG  CCCGGCT  TC
                                   __     CC
GAM2116  TPTE     3'  GGCAGGGTTGGAAAGAA     51424     TCG
                                GGC  AGGGTTGGAAAGAA
                                |||  ||||||||||||||
                                CCG  TCCCAACCTTTCTT
                                  ___
GAM2116  ZNF10    5'  AAGGTTCGATGGGAGAA     51425     C  _  TT
                                AAGG TCGA GGG  GGAA
                                |||| |||| |||  ||||
                                TTCC AGCT CCC  TCTT
                                  A  A  __
GAM2116  ZNF144   3'  AGGCTTGGCTGGAAGA     51426     CGAG     A
                                AGGCT   GGTTGGAA GA
                                |||||   |||||||| ||
                                TCCGA   CCGACCTT CT
                                  A___      _
GAM2116  C20orf110 3'  AGGCAAGAAGGGTTGGAGGGA  51427     TC_      AA
                                AGGC  GAGGGTTGGA  GA
                                ||||  |||||||||  ||
                                TCCG  TTCCCAACCT  CT
                                  TTC       CC
GAM2116  DKFZp547E052 3'  AGCCTTTGGGGTTGGAAAG   51428     CGA_
                                GGCT   GGGTTGGAAAG
                                ||||   ||||||||||
                                TCGG   CCCAACCTTTC
                                  AAAC
GAM2116  DKFZp547M072 3'  AGGGTCGGGGGGGGAAAG    51429    C  A  TT
                                AGG TCG GGG  GGAAAG
                                ||| ||| |||  ||||||
                                TCC AGC CCC  CCTTTC
                                  C  _  C_
GAM2116  DKFZP564F0522 3'  ATAAGGTTGAAGGAGGAA   51430      CTC    TT
                                ATAAGG  GAGGG  GGAA
                                ||||||  |||||  ||||
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                                TATTCC   CTTCC  CCTT
                                   AA_    T_
GAM2116 DKFZP727G051 3' GGCTGAAAAGGGGGAAGAA   51431     C__    TT   A
                                GGCT   GAGGG  GGAA GAA
                                ||||   |||||  |||| |||
                                CCGA   TTCCC  CCTT CTT
                                  CTT    __   _
GAM2116 FLJ20337 3' AAGGAAGAGGGTTGGGAAGAA  51432     CTC       A
                                AAGG   GAGGGTTGG AAGAA
                                ||||   ||||||||| |||||
                                TTCC   CTCCCAACC TTCTT
                                  TT_       C
GAM2116 GRIN3A   3' AGGCTGGAGGATCATTAGA   51433      C       GAA
                                AGGCT GAGGGTTG   AGA
                                ||||| ||||||||   |||
                                TCCGA CTCCTAGT   TCT
                                   C       AA_
GAM2116 HRD1     3' ACAGGGCTGAAGAGTTGGAGAG 51434     A   C        A
                                ATA GGCT GAGGGTTGGA AG
                                ||| |||| |||||||||| ||
                                TGT CCGA TTCTCAACCT TC
                                  C   C         C
GAM2116 IMP13    5' GGCTGGAGGGTCACGGGAGAG  51435     C      ___   A
                                GGCT GAGGGTT   GGA AG
                                |||| |||||||   ||| ||
                                CCGA CTCCCAG   CCT TC
                                  C      TGC   C
GAM2116 KIAA0335 3' ATAAGGCTGGTGGAAG      51436        CGAG   T    A
                                ATAAGGCT    GGT GGAA G
                                ||||||||    ||| |||| |
                                TATTCCGA    CCA CCTT C
                                     ____   _    _
GAM2116 KIAA0515 3' TAAAGGCTTGGGATAAAGA   51437   T     CGA   TTGG
                                A AAGGCT   GGG    AAAGA
                                | ||||||   |||    |||||
                                A TTCCGA   CCC    TTTCT
                                 T     A__   TA__
GAM2116 KIAA0552 5' ATAAGGCTGGGATAAAAGA   51438        CGA   TTG
                                ATAAGGCT   GGG   GAAAGA
                                ||||||||   |||   ||||||
                                TATTCCGA   CCC   TTTTCT
                                     ___   TA_
GAM2116 KIAA1100 3' GGAAGGGAGGGGTTGGAGAG  51439   T   CTC    _    A
                                A AAGG   GAGGG TTGGA AG
                                | ||||   ||||| ||||| ||
                                C TTCC   CTCCC AACCT TC
                                 C    ___     C    C
GAM2116 KIAA1169 3' TAAGGCTGGGGCTGTGGGA   51440        CGA     GAAA
                                TAAGGCT   GGGTTG    GA
                                |||||||   ||||||    ||
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                                ATTCCGA  CCCGAC   CT
                                   C__     ACC_
GAM2116 KIAA1554 3' GGCTGAAAGCAGAAAGAA   51441     C     T
                                GGCT GAGGGT GGAAAGAA
                                |||| |||||| ||||||||
                                CCGA CTTTCG TCTTTCTT
                                  _     _
GAM2116 KIAA1656 5' ATAAGGCCTCGGGAGAAGGAA 51442       _  A  TT
                                ATAAGGC TCG GGG  GGAA
                                ||||||| ||| |||  ||||
                                TATTCCG AGC CTC  CCTT
                                   G   C   TT
GAM2116 KIAA1678 3' AGGTCATTTAGTTGGAAGGAA 51443    C  AG_     A
                                AGG TCG   GGTTGGAA GAA
                                ||| |||   |||||||| |||
                                TCC AGT   TCAACCTT CTT
                                  _  AAA      C
GAM2116 KIAA1941 3' TAAGGCTGAATTGAA      51444       CGA
                                TAAGGCT   GGGTTGGA
                                |||||||   ||||||||
                                ATTCCGA   CTTAACTT
                                   ___
GAM2116 KR19    3' ATAAGGCCTGAGGGTGGA    51445       TC     T
                                ATAAGGC  GAGGGT GGA
                                |||||||  |||||| |||
                                TATTCCG  CTCCCA CCT
                                   GA    _
GAM2116 MSH5    5' AGGCTCCTTTGGAAAGA     51446      GAGGG
                                AGGCTC    TTGGAAAGA
                                ||||||    |||||||||
                                TCCGAG    AACCTTTCT
                                  GA___
GAM2116 PTPN3   3' ATAAGGTTTCAAGTGGAGGA  51447      C_   _ TT
                                ATAAGG  TCGAG GG  GGA
                                ||||||  ||||| ||  |||
                                TATTCC  AGTTC CC  CCT
                                   AA    A  T_
GAM2116 Rpo1-2  3' AGGGAACCTGGGGTTGGAAAG 51448    C__  GA
                                AGG   TC  GGGTTGGAAAG
                                |||   ||  ||||||||||
                                TCC   GG  CCCAACCTTTC
                                  CTT  AC
GAM2116 Rpo1-2  3' AGGGAACCTGGGGTTGGAAAG 51448    C__  GA
                                AGG   TC  GGGTTGGAAAG
                                |||   ||  ||||||||||
                                TCC   GG  CCCAACCTTTC
                                  CTT  AC
GAM2116 SP329   5' GGCTAGGCTCGGAAGA     51449     CG  G    A
                                GGCT  AGG TTGGAA GA
                                ||||  ||| |||||| ||
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                                CCGA  TCC AGCCTT CT
                                  __  G     _
GAM2116  SPR1     3'  AGGCTAAATTGGGAAGA     51450       CGA      A
                                AGGCT   GGGTTGG AAGA
                                |||||   ||||||| ||||
                                TCCGA   TTTAACC TTCT
                                   ___      C
GAM2116  ZNF317   3'  AGGCTTAAGGGTTATTTAGA   51451       CG       GAA
                                AGGCT  AGGGTTG   AGA
                                |||||  |||||||   |||
                                TCCGA  TCCCAAT   TCT
                                   AT       AAA
GAM2116  LOC127602 5'  GAAAGGCTTGTGGAAAGA    51452    T     CGAGG  T
                                A AAGGCT     GT GGAAAGA
                                | ||||||     || |||||||
                                C TTCCGA     CA CCTTTCT
                                 T     A____  _
GAM2116  LOC138639 3'  ATAAGGCTTGGTGTGTTGAGAA 51453         CGAGG_   _
                                ATAAGGCT     GTTG GAA
                                ||||||||     |||| |||
                                TATTCCGA     CAAC CTT
                                     ACCACA    T
GAM2116  LOC144667 3'  GGCCCCAGGGTTGGGGAGA    51454       G        AA
                                GGCTC AGGGTTGG  AGA
                                ||||| ||||||||  |||
                                CCGGG TCCCAACC  TCT
                                   G       CC
GAM2116  LOC145989 3'  AGCAGGGAGGGTTGGAAGGA   51455     TC_         A
                                GGC   GAGGGTTGGAA GA
                                |||   |||||||||||| ||
                                TCG   CTCCCAACCTT CT
                                  TCC          C
GAM2116  LOC149722 5'  AAGGCTTGAGGATCCAGG     51456        C       __
                                AAGGCT GAGGGTT  GG
                                |||||| |||||||  ||
                                TTCCGA CTCCTAG  CC
                                   A      GT
GAM2116  LOC150605 5'  AGGGGAGGGTTGGGAAG     51457     CTC        A
                                AGG   GAGGGTTGG AAG
                                |||   |||||||||| |||
                                TCC   CTCCCAACC TTC
                                  C__        C
GAM2116  LOC199786 3'  GGAAGGTGGGGTTGGAGGGAA  51458    T    CTCGA       AA
                                A AAGG     GGGTTGGA  GAA
                                | ||||     ||||||||  |||
                                C TTCC     CCCAACCT  CTT
                                 C    AC____       CC
GAM2116  LOC200812 5'  CAAGGACAGGTTGGAGAG     51459       CTCGA       A
                                TAAGG     GGGTTGGA AG
                                |||||     |||||||| ||
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                                GTTCC    TCCAACCT TC
                                  TG___      C
GAM2116  LOC202759 3'  ATAAGGCCTGAGGGTGGA    51445       TC     T
                                ATAAGGC  GAGGGT GGA
                                |||||||  |||||| |||
                                TATTCCG  CTCCCA CCT
                                   GA     _
GAM2116  LOC221931 5'  AGGGTTGGAGGAGTGGGAAGAA 51460     CTC_   GT   A
                                AGG   GAGG  TGG AAGAA
                                |||   ||||  ||| |||||
                                TCC   CTCC  ACC TTCTT
                                 CAAC   TC   C
GAM2116  LOC254085 5'  AGGAGAAGGTTGGAGGGA    51461     CTC        AA
                                AGG   GAGGGTTGGA  GA
                                |||   ||||||||||  ||
                                TCC   CTTCCAACCT  CT
                                 T__        CC
GAM2116  LOC255102 3'  CAAGGACAGGTTGGAGAG    51459      CTCGA      A
                                TAAGG    GGGTTGGA AG
                                |||||    |||||||| ||
                                GTTCC    TCCAACCT TC
                                  TG___      C
GAM2116  LOC255925 3'  CAAGGACAGGTTGGAGAG    51459      CTCGA      A
                                TAAGG    GGGTTGGA AG
                                |||||    |||||||| ||
                                GTTCC    TCCAACCT TC
                                  TG___      C
GAM2116  LOC256248 5'  AAGGGTTTTAAAGTTGGAAAG  51462     CTCG_
                                AAGG    AGGGTTGGAAAG
                                ||||    ||||||||||||
                                TTCC    TTTCAACCTTTC
                                  CAAAA
GAM2116  LOC51026  3'  AAGGCTGATTTTGGAAAGAA   51463      C  GGG
                                AAGGCT GA   TTGGAAAGAA
                                |||||| ||   ||||||||||
                                TTCCGA CT   AACCTTTCTT
                                   _  AA_
GAM2116  LOC51075  3'  GGCTTGAGGAAGCAAGA     51464     C    TT  A
                                GGCT GAGGG  GG AAGA
                                |||| |||||  || ||||
                                CCGA CTCCT  TC TTCT
                                  A    __ G
GAM2116  LOC51644  3'  TAAGGCTGAGGCAGAGAGA   51465       C   GTT   A
                                TAAGGCT GAGG   GGA AGA
                                ||||||| ||||   ||| |||
                                ATTCCGA CTCC   TCT TCT
                                    _   G__   C
GAM2116  LOC81558  3'  ATAGGGCTGAGAGGATGGG   51466     A   C_     T
                                ATA GGCT  GAGGGT GG
                                ||| ||||  |||||| ||
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                                TAT CCGA  CTCCTA CC
                                  C    CT     C
GAM2116 LOC92379 3' ATAAGGCTTGAGTGTGAG    51467        C   G  T
                                ATAAGGCT GAG GT GG
                                |||||||| ||| || ||
                                TATTCCGA CTC CA TC
                                     A   A  C
GAM2117 FBLN2    3' TAATGTACATGTACTACT    51470        T  _
                                TAATGTAC TGT TTACT
                                |||||||| ||| |||||
                                ATTACATG ACA GATGA
                                     T   T
GAM2117 PLN      3' ATGTGTTAATTTACTGTTTAT  51471     ACTT
                                ATGT    GTTTACTGTTTAT
                                ||||    ||||||||||||
                                TACA    TAAATGACAAATA
                                  CAAT
GAM2117 KIAA1586 5' ATGTACTTGTGCATTTATA    51472         TTAC
                                ATGTACTTGT    TGTTTATA
                                ||||||||||    ||||||||
                                TACATGAACA    GTAAATAT
                                     C___
GAM2117 KUB3     3' TAATGTATTTATTTACTA     51473       C
                                TAATGTA TTGTTTACTG
                                ||||||| ||||||||||
                                ATTACAT AATAAATGAT
                                     A
GAM2117 LOC168448 3' TAATGACTTGTTTGCTG     51474      T      A
                                TAATG ACTTGTTT CTG
                                ||||| |||||||| |||
                                ATTAC TGAACAAA GAC
                                   _       C
GAM2118 ADRB3    3' TGGCTAAAGTGAGAGAGGCC   51477    A      _ A__
                                TG CTAAAGTG GA   GCC
                                || |||||||| ||   |||
                                AC GATTTCAC CT   CGG
                                  C       T  CTC
GAM2118 MCCC2    5' TGGCTGGGGCGGAAGCTGAGC  51478    A  AAA      C  C
                                TG CT   GTGGAAGC TGA GC
                                || ||   |||||||| ||| ||
                                AC GA   CGCCTTCG ACT CG
                                  C  CCC       _  _
GAM2118 MOCS1    3' TGATTAAAGGAACCTGACG   51479     C    T  AA
                                TGA TAAAG GG  GCCTGACG
                                ||| ||||| ||  ||||||||
                                ACT ATTTC CT  TGGACTGC
                                  A    _ __
GAM2118 RFNG     3' TGCTGGGGTGGAAGCCTG    51480    A  AAA
                                TG CT   GTGGAAGCCTG
                                || ||   ||||||||||
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                                AC GA   CACCTTCGGAC
                                 _ CCC
GAM2118  FLJ14957  3'  TGACTAAAGGGAGGAATCGGCC 51481         T__   ___
                                TGACTAAAG   GGAA   GCC
                                |||||||||   ||||   |||
                                ACTGATTTC   CCTT   CGG
                                     CCT    AGC
GAM2118  FLJ21919  5'  TGATAGGGTGGAAGCGAAAC   51482     C  AA      CT
                                TGA TA  GTGGAAGC  GAC
                                ||| ||  ||||||||  |||
                                ACT AT  CACCTTCG  TTG
                                  _ CC       CT
GAM2118  GGA2      3'  TGACACCCAGAGCCTGACG    51483     TAAAGT   A
                                TGAC     GGA GCCTGACG
                                ||||     ||| ||||||||
                                ACTG     TCT CGGACTGC
                                  TGGG__   _
GAM2118  GGA2      3'  TGACACCCAGAGCCTGACG    51483     TAAAGT   A
                                TGAC     GGA GCCTGACG
                                ||||     ||| ||||||||
                                ACTG     TCT CGGACTGC
                                  TGGG__   _
GAM2118  GPT2      3'  TGTACTGGGAGAAGCCTGATGC 51484    _   AAAGT        C
            C                    TG ACT     GGAAGCCTGA GCC
                                || |||    |||||||||| |||
                                AC TGA    TCTTCGGACT CGG
                                 A   CCC__         A
GAM2118  MGC23445  5'  GACTGCAACAGGCCTGACG    51485      AA  TG AA
                                GACT  AG  G  GCCTGACG
                                ||||  ||  |  ||||||||
                                CTGA  TT  C  CGGACTGC
                                  CG  GT __
GAM2118  PELI1     5'  CTAAAGTGGGAGTAATCGC    51486         A  CC   _
                                CTAAAGTGG AG  TGA CGC
                                ||||||||| ||  ||| |||
                                GATTTCACC TC  ATT GCG
                                     C  __   A
GAM2118  LOC220846 3'  TGGCTAAAGTGAGAGAGGCC   51477    A       _  A__
                                TG CTAAAGTG GA   GCC
                                || ||||||| ||   |||
                                AC GATTTCAC CT   CGG
                                 C       T  CTC
GAM2118  LOC253782 3'  TGACAAAGTAAGCTGATGC    51487      T     GA   C   C
                                TGAC AAAGTG  AGC TGA GC
                                |||| ||||||  ||| ||| ||
                                ACTG TTTCAT  TCG ACT CG
                                  _     __   _  A
GAM2118  LOC51093  5'  TGCTGGAGTGGAAGATTTGAGG 51488    A  AA       CC_  __
            CGCC                    TG CT  AGTGGAAG   TGA  CGCC
                                || ||  ||||||||   |||  ||||
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                                AC GA  TCACCTTC   ACT  GCGG
                                 _ CC       TAA   CC
GAM2119  AHR      3'  TTTTTGGAGACGGAGCTCGG   51491        _ AAGTT
                                TTTTTGG GA     GGGCTCGG
                                ||||||| ||     ||||||||
                                AAAAACC CT     CTCGAGCC
                                    T  GC___
GAM2119  BAZ1B    3'  TTTTTGGGGGGGGTGGGAGGAGC 51492         AAA  T   CTC
                                TTTTTGGG   GT GGG   GGC
                                ||||||||   || |||   |||
                                AAAAACCC   CA CCC   TCG
                                     CCC  _   TCC
GAM2119  EHD2     3'  TTTTTGGGAAGAAGCCTTGGC  51493          A TT  G  C
                                TTTTTGGGAA G  GG CT GGC
                                |||||||||| |  || || |||
                                AAAAACCCTT C  TC GA CCG
                                      _ T_  G  A
GAM2119  GPC1     3'  TTTTTGGCAAAGTCAGTCCTTG 51494        G     TG G_  C
             GCC                   TTTTTGG AAAGT  G  CT GGCC
                                |||||||  |||||  |  || ||||
                                AAAAACC TTTCA  C  GA CCGG
                                    G    GT AG  A
GAM2119  NFKB2    5'  TCCGGAGTTGGGCTTGGC    51495       GAA        C
                                TTTGG   AGTTGGGCT GGC
                                |||||   ||||||||| |||
                                AGGCC   TCAACCCGA CCG
                                   ___         A
GAM2119  SHMT1    3'  TCTTTGGGAAGGTGACATTTGG 51496          A  TG   TC__
             C                    TTTTTGGGAA GT  GGC    GGC
                                |||||||||| ||  |||    |||
                                AGAAACCCTT CA  CTG    CCG
                                     C  __   TAAA
GAM2119  WNT3A    3'  TCTTTGGGAGGGCCTCGG    51497         AAGTT   _
                                TTTTTGGGA    GGGC TCGG
                                |||||||||    |||| ||||
                                AGAAACCCT    CCCG AGCC
                                   _____   G
GAM2119  FKBP5    3'  TTTTTGGGAAGCTACTGG    51498         A   GG   C
                                TTTTTGGGAA GTT  GCT GG
                                |||||||||| |||  ||| ||
                                AAAAACCCTT CGA  TGA CC
                                   _  __  _
GAM2119  FLJ12221 5'  TCTTTGGGGGGCTCGG      51499        AAAGTT
                                TTTTTGGG     GGGCTCGG
                                ||||||||     ||||||||
                                AGAAACCC     CCCGAGCC
                                   _______
GAM2119  FLJ13215 3'  TCTTTGGGAAGAACACC     51500         AGTT   TCG
                                TTTTTGGGAA   GGGC  GCC
                                ||||||||||   ||||  |||
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                                AGAAACCCTT   CTTG  TGG
                                     ____   ___
GAM2119 KIAA1373 3' TTTTTGGAAAAGGCTTTGG   51501        AGTT   C_
                                TTTTTGGGAA   GGGCT  GG
                                ||||||||||   |||||  ||
                                AAAAACCTTT   TCCGA  CC
                                     ____    AA
GAM2119 MDS033   3' TTTTTTGGAAAGTTAGGGTC  51502     G       C
                                TTTTT GGAAAGTTGGG TC
                                ||||| |||||||||| ||
                                AAAAA CCTTTCAATCC AG
                                   A         C
GAM2119 MFN2     3' TTTTTGGGAGAGGTGTTGCTGG 51503     A  T _________  TCG
           CCGAGC                 TGGGA AG TG      GGC   GC
                                ||||| || ||       |||   ||
                                ACCCT TC AC       CCG   CG
                                   C  C  AACGAIII   GCT
GAM2119 LOC125058 3' TTTTGGGAAGTGTGTTTGGCT  51504        A___   G
                                TTTTGGGAA    GTT GGCT
                                |||||||||    ||| ||||
                                AAAACCCTT    CAA CCGA
                                     CACA   A
GAM2119 LOC170127 3' TTCTTGGGGCTGCCGGGCTTGG 51505       AAA      C
           CC                     TTTTTGGG   GTTGGGCT GGCC
                                ||||||||   |||||||| ||||
                                AAGAACCC   CGGCCCGA CCGG
                                     CGA       A
GAM2119 LOC203369 3' TTTTTGGGAAAGATGAATGGGC 51506          T    CTC
           C                     TTTTTGGGAAAG TGGG   GGCC
                                ||||||||||| ||||   ||||
                                AAAAACCCTTTC ACTT   CCGG
                                       T    AC_
GAM2120 HSPG2    3' TGTGGGGCACCAGCCCACAA   51509    C  CAA      A
                                TG GG   CACCAGCC GCAA
                                || ||   |||||||| ||||
                                AC CC   GTGGTCGG TGTT
                                 A  CC_       G
GAM2120 MBD3     3' TGTGGCACCACCAGCCGCA    51510    C    A      A
                                TG GGCA CACCAGCC GCA
                                || |||| |||||||| |||
                                AC CCGT GTGGTCGG CGT
                                 A    G       _
GAM2120 RFNG     3' CGGCAACAGCAAAGCA      51511        C   CC
                                CGGCAACA CAG  AGCA
                                |||||||| |||  ||||
                                GCCGTTGT GTT  TCGT
                                     C   __
GAM2120 SLC2A3   3' TGCGGCAATATCAGAACCCAA  51512        CAC   ___
                                TGCGGCAA   CAG   CCAG
                                ||||||||   |||   ||||
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                                ACGCCGTT  GTC  GGTT
                                    ATA  TTG
GAM2120 THY1    3' GCTCAGGCACCAGCCAGCA  51513   GG A_
                                GC  CA  CACCAGCCAGCA
                                ||  ||  ||||||||||||
                                CG  GT  GTGGTCGGTCGT
                                 A_  CC
GAM2120 UNG     5' TGTGGAACAGGTCCCAGCAAAA 51514   C C   CCAG
          G                      TG GG AACA   CCAGCAAAAG
                                || || ||||   ||||||||||
                                AC CC TTGT   GGTCGTTTTC
                                 A _   CCAG
GAM2120 CYP2A7  5' GGGACACAGCCAGCAA     51515   CA  C
                                GG  ACAC AGCCAGCAA
                                ||  |||| |||||||||
                                CC  TGTG TCGGTCGTT
                                 C_  _
GAM2120 CYP2A7  5' GGGACACAGCCAGCAA     51515   CA  C
                                GG  ACAC AGCCAGCAA
                                ||  |||| |||||||||
                                CC  TGTG TCGGTCGTT
                                 C_  _
GAM2120 EDG2    5' TGCGGCAACTTCCCTCCAG  51516       A_ AG
                                TGCGGCAAC  CC  CCAG
                                |||||||||  ||  ||||
                                ACGCCGTTG  GG  GGTC
                                     AA  GA
GAM2120 FLJ10687 3' GACAGTCACCAGCCAGCA  51517    A_
                                GGCA  CACCAGCCAGCA
                                ||||  ||||||||||||
                                CTGT  GTGGTCGGTCGT
                                  CA
GAM2120 FLJ21324 5' GCGGCAACCCCTGCTGGCA  51518       A A CA
                                GCGGCAAC CC GC  GCA
                                |||||||| || ||  |||
                                CGCCGTTG GG CG  CGT
                                     G  A  AC
GAM2120 FREQ    3' TGCGGCAAACACCAAAGCAA  51519       _    CC
                                TGCGGCAA CACCAG  AGCAA
                                |||||||| ||||||  |||||
                                ACGCCGTT GTGGTT  TCGTT
                                     T    __
GAM2120 GS3955  5' TGCGGTCAGCGCTGCAACAAAA 51520    CAACAC  ____
          G                     GCGG    CAGC   CAGCAAAAG
                                ||||    ||||   |||||||||
                                CGCC    GTCG   GTTGTTTTC
                                  A_____   CGAC
GAM2120 KIAA0469 3' TGTGGTCATACCAGCCAG  51521   C _ AC
                                TG GG CA  ACCAGCCAG
                                || || ||  |||||||||
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                                AC CC GT  TGGTCGGTC
                                 A  A  A_
GAM2120  KIAA1838  5'  TGCGCCAACACCAGCCGCA   51522     G        A
                                TGCG CAACACCAGCC GCA
                                |||| |||||||||| |||
                                ACGC GTTGTGGTCGG CGT
                                  G         _
GAM2120  MGC2628   3'  TGCTGGGGCAGCCAGCAA    51523    _  CAACAC
                                TGC GG     CAGCCAGCAA
                                ||| ||     ||||||||||
                                ACG CC     GTCGGTCGTT
                                  A  CC____
GAM2120  LOC144195 3'  TGCGGCAATATCAGAACCCAA  51512        CAC  ___
                                TGCGGCAA   CAG   CCAG
                                ||||||||   |||   ||||
                                ACGCCGTT   GTC   GGTT
                                     ATA   TTG
GAM2120  LOC148759 5'  TACGGCAACACTGCGAG     51524          CA  C
                                TGCGGCAACAC  GC AG
                                ||||||||||  || ||
                                ATGCCGTTGTG  CG TC
                                      A_  C
GAM2120  LOC151194 5'  TGCGGCAACCCTCCAG      51525         A  AG
                                TGCGGCAAC CC  CCAG
                                |||||||| ||  ||||
                                ACGCCGTTG GG  GGTC
                                     _  A_
GAM2120  LOC152317 3'  TGTGGAAAAACCAGCAAA    51526    C  C  CACC
                                TG GG AA    AGCCAGCAAA
                                || || ||    ||||||||||
                                AC CC TT    TTGGTCGTTT
                                 A  T  _____
GAM2120  LOC199796 5'  GCGCAGAACCAGCCAGC     51527     G  AC
                                GCG CA  ACCAGCCAGC
                                ||| ||  ||||||||||
                                CGC GT  TGGTCGGTCG
                                  _  CT
GAM2120  LOC221935 3'  TGCTGCGAGCAGCCAGCAGAAG 51528     G  AACAC       A
                                TGC GC     CAGCCAGCA AAG
                                ||| ||     ||||||||| |||
                                ACG CG     GTCGGTCGT TTC
                                  A  CTC__        C
GAM2121  AGPAT2    3'  TGCCGTGGGCGCGAGTCCC    51531           C  CG
                                TGCCGTGGGCGCG GG  CCC
                                |||||||||||| ||  |||
                                ACGGCACCCGCGC TC  GGG
                                       _  A_
GAM2121  AGPAT2    3'  TGCCGTGGGCGCGAGTCCC    51531           C  CG
                                TGCCGTGGGCGCG GG  CCC
                                |||||||||||| ||  |||
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                                ACGGCACCCGCGC TC  GGG
                                       _ A_
GAM2121  CRLF1    5'  TGCCGGGGGCGCGCGGCG    51532      T
                                TGCCG GGGCGCGCGGCG
                                ||||| ||||||||||||
                                ACGGC CCCGCGCGCCGC
                                   C
GAM2121  DLC1     5'  CCGTGAGCCGGCGCTCC     51533        GCG     C
                                CCGTGGGC   CGGCGC CC
                                ||||||||   |||||| ||
                                GGCACTCG   GCCGCG GG
                                     ___     A
GAM2121  GPRC5B   3'  TGCCGTGGTGCCTGCCTTCCA  51534        GC  GCGGC   C_
                                TGCCGTGG  GC    GCC  CCA
                                ||||||||  ||    |||  |||
                                ACGGCACC  CG    CGG  GGT
                                     A_  GA___   AA
GAM2121  LETM1    3'  TGCTGTGGGCGCACTGGAC    51535     C        _  C
                                TGC GTGGGCGCGC GG GC
                                ||| ||||||||| || ||
                                ACG CACCCGCGTG CC TG
                                  A         A  _
GAM2121  LMO2     3'  TGCCATGGAGACGGCG      51536         CGC
                                TGCCGTGGG   GCGGCG
                                |||||||||   ||||||
                                ACGGTACCT   TGCCGC
                                     C__
GAM2121  RANBP3   5'  TGCTGCGGGCACTGCCCCC   51537     C       GCGGC
                                TGC GTGGGCGC    GCCCCC
                                ||| ||||||||    ||||||
                                ACG CGCCCGTG    CGGGGG
                                  A       A_____
GAM2121  RPA3     5'  TGCTGTGGGTGCTGCGTACC   51538     C    C  _   GC
                                TGC GTGGG GC GCG  GCC
                                ||| ||||| || |||  |||
                                ACG CACCC CG CGC  TGG
                                  A    A A   A_
GAM2121  TGFBI    3'  TGCCGTGGTGCATTCCTCC    51539        GC   CGGCG  C
                                TGCCGTGG  GCG    CC CC
                                ||||||||  |||    || ||
                                ACGGCACC  CGT    GG GG
                                     A_   AA___  A
GAM2121  THBD     5'  TGCCGTGCGCGCAGCCCC     51540       GG       G
                                TGCCGT  GCGCGCGGC CCC
                                ||||||  ||||||||| |||
                                ACGGCA  CGCGCGTCG GGG
                                     __       _
GAM2121  TIA1     5'  TGCTGTCGCGGCGGCGCCTCCA 51541     C  GG   C       C
                                TGC GT  GCG GCGGCGCC CCA
                                ||| ||  ||| |||||||| |||
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                                ACG CA  CGC CGCCGCGG GGT
                                  A  G_  _      A
GAM2121  TIA1     5'  TGCTGTCGCGGCGGCGCCTCCA 51541     C  GG   C       C
                                TGC GT  GCG GCGGCGCC CCA
                                ||| ||  ||| |||||||| |||
                                ACG CA  CGC CGCCGCGG GGT
                                  A  G_  _      A
GAM2121  VCP      3'  GCTGTGGGCGCACCCC      51542     C       GCGGC
                                GC GTGGGCGC    GCCCC
                                || ||||||||    |||||
                                CG CACCCGCG    TGGGG
                                 A      _____
GAM2121  ACP33    5'  TGCCGTGGCCGCCCC       51543         G GCGCGG
                                TGCCGTGG C     CGCCCC
                                |||||||| |     ||||||
                                ACGGCACC G     GCGGGG

                                   _ _______
GAM2121  ALK7     5'  GCTGGCGGTGCGCGGCGCTCC  51544    C_   GC       C
                                GC  GTGG  GCGCGGCGC CC
                                ||  ||||  ||||||||| ||
                                CG  CGCC  CGCGCCGCG GG
                                 AC   A_       A
GAM2121  ATP6V1B1 3'  ATGGAGCGTGCGGCGCCCCCA  51545      _   C
                                GTGG GCG GCGGCGCCCCCA
                                |||| ||| ||||||||||||
                                TACC CGC CGCCGCGGGGGT
                                  T   A
GAM2121  CDC14B   5'  TGCCGCGGCCGGCGCCCCC   51546        G GCG
                                TGCCGTGG C   CGGCGCCCCC
                                |||||||| |   ||||||||||
                                ACGGCGCC G   GCCGCGGGGG

                                   _ ____
GAM2121  CDC14B   5'  TGCCGCGGCCGGCGCCCCC   51546        G GCG
                                TGCCGTGG C   CGGCGCCCCC
                                |||||||| |   ||||||||||
                                ACGGCGCC G   GCCGCGGGGG

                                   _ ____
GAM2121  CDC14B   5'  TGCCGCGGCCGGCGCCCCC   51546        G GCG
                                TGCCGTGG C   CGGCGCCCCC
                                |||||||| |   ||||||||||
                                ACGGCGCC G   GCCGCGGGGG

                                   _ ____
GAM2121  FLJ11700 3'  TGCCGTGGATGCTGACCCTGTT 51547        GC  GC   G _____
            CCCA                  GCCGTGG  GC  GGC CC    CCCA
                                |||||||  ||  ||| ||    ||||
                                CGGCACC  CG  CTG GG    GGGT
                                    TA  A_   _  ACAA
GAM2121  FLJ20257 5'  TGCTGTGAGGCGCCCTCCCC  51548     C    C    GGCG
                                TGC GTGGG GCGC    CCCC
                                ||| ||||| ||||    ||||
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                                ACG CACTC CGCG   GGGG
                                  A    _   GGA_
GAM2121 GPS2     5' TGCCGTGGGCGCTCGGGCC  51549         G  C
                                TGCCGTGGGCGC CGG GCC
                                |||||||||||| ||| |||
                                ACGGCACCCGCG GCC CGG
                                       A  _
GAM2121 ICAM4    3' GCTGTGGGCGCGGGGCTCC  51550   C      C  G
                                GC GTGGGCGCG GGC CC
                                || ||||||||| ||| ||
                                CG CACCCGCGC CCG GG
                                 A       C  A
GAM2121 KIAA0449 5' GCTGTGGGGTGAGCGCCCCC  51551   C   CGCGC
                                GC GTGGG   GGCGCCCCC
                                || |||||   |||||||||
                                CG CACCC   TCGCGGGGG
                                 A   CAC__
GAM2121 KIAA0672 3' GCCGTGGGCCAGCGTCTCC  51552       GCG   CCC
                                GCCGTGGGC  CGGCG  CC
                                |||||||||  |||||  ||
                                CGGCACCCG  GTCGC  GG
                                     ___   AGA
GAM2121 KIAA1257 5' TGCTGGCCGCCGGCGCTCC  51553   CG  G  G   C
                                TGC  TGG CGC CGGCGC CC
                                |||  ||| ||| |||||| ||
                                ACG  ACC GCG GCCGCG GG
                                  __  G  _    A
GAM2121 KIAA1813 5' CCGCCTCCGCGGCGCCCCC  51554    GGGCG
                                CCGT   CGCGGCGCCCCC
                                ||||   ||||||||||||
                                GGCG   GCGCCGCGGGGG
                                  GAG__
GAM2121 MGC10966 5' GTGGGCGCCGACCCCTCCA  51555       G  G  _
                                GTGGGCGC CGGC CCC CCA
                                |||||||| |||| ||| |||
                                CACCCGCG GCTG GGG GGT
                                     _  _  A
GAM2121 MGC2705  3' TGCCGTGGGGTGGCCCC    51556       CGCGC  G
                                TGCCGTGGG    GGC CCC
                                |||||||||    ||| |||
                                ACGGCACCC    CCG GGG
                                     CA___  _
GAM2121 SLIT1    5' GCTTGCGCGCGGCGCCCC   51557   GG
                                GT  GCGCGCGGCGCCCC
                                ||  ||||||||||||||
                                CG  CGCGCGCCGCGGGG
                                 AA
GAM2121 LOC123316 5' TGCCGAGAGCCTGGCGCCCC  51558     T   GCGC
                                TGCCG GGGC   GGCGCCCC
                                ||||| ||||   ||||||||
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                                ACGGC CTCG    CCGCGGGG
                                  T    GA__
GAM2121  LOC133957 5'  TGCGCAGGCGCGGCGCCCCCA  51559     C TG     GC
                                TGC G  GGCGC  GGCGCCCCCA
                                ||| |  |||||  ||||||||||
                                ACG C  CCGCG  CCGCGGGGGT
                                  _ GT    __
GAM2121  LOC146136 5'  TGTCATGGCACACAGGTGTTCC 51560    C     G      CGCCC
                                TG CGTGG CGCGCGG    CC
                                || ||||| |||||||    ||
                                AC GTACC GTGTGTC    GG
                                 A    _      CACAA
GAM2121  LOC164584 5'  TGCCATGGGCGGCGTCCC    51566         GCGC    C  C
                                TGCCGTGGGC    GGCG CC C
                                ||||||||||    |||| || |
                                ACGGTACCCG    CCGC GG G
                                      _____   A  A
GAM2121  LOC164584 5'  TGCCGTGGGCGGCGTCC     51561         GCGC    _
                                TGCCGTGGGC    GGCG CC
                                ||||||||||    |||| ||
                                ACGGCACCCG    CCGC GG
                                      _____   A
GAM2121  LOC164584 5'  GCCGTGGGCGGCGTCC      51564         GCGC    _
                                GCCGTGGGC    GGCG CC
                                |||||||||    |||| ||
                                CGGCACCCG    CCGC GG
                                      _____   A
GAM2121  LOC164584 5'  GCCGTGGACGGCGTCC      51565        GCGC     _
                                GCCGTGG    GCGGCG CC
                                |||||||    |||||| ||
                                CGGCACC    TGCCGC GG
                                     _____     A
GAM2121  LOC164584 5'  TGCCGTGGGCGGCGTCC     51561         GCGC    _
                                TGCCGTGGGC    GGCG CC
                                ||||||||||    |||| ||
                                ACGGCACCCG    CCGC GG
                                      _____   A
GAM2121  LOC164584 5'  TGCCGTGGGCGGCGTCC     51561         GCGC    _
                                TGCCGTGGGC    GGCG CC
                                ||||||||||    |||| ||
                                ACGGCACCCG    CCGC GG
                                      _____   A
GAM2121  LOC164584 5'  GCCGTGGGCGGCGTCCC     51562         GCGC    C  C
                                GCCGTGGGC    GGCG CC C
                                |||||||||    |||| || |
                                CGGCACCCG    CCGC GG G
                                      _____   A  A
GAM2121  LOC164584 5'  TGCCGTGGGCGGCATCC     51563          C  GGCG
                                TGCCGTGGGCG GC    CC
                                |||||||||| ||    ||
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                                ACGGCACCCGC CG    GG
                                      _ TA__
GAM2121  LOC164584 5'  GCCGTGGGCGGCGTCC      51564         GCGC   _
                                GCCGTGGGC    GGCG CC
                                |||||||||    |||| ||
                                CGGCACCCG    CCGC GG
                                     _____    A
GAM2121  LOC164584 5'  TGCCGTGGGCGGCATCC      51563          C  GGCG
                                TGCCGTGGGCG GC    CC
                                |||||||||||  ||    ||
                                ACGGCACCCGC CG    GG
                                      _ TA__
GAM2121  LOC201382 5'  TGCCATGGTGAGTAGGTGCTTC 51567        GCGCGC  C  CC
            CA                    TGCCGTGG     GG GC  CCA
                                |||||||      || ||  |||
                                ACGGTACC     CC CG  GGT
                                     ACTCAT  A  AA
GAM2121  LOC254848 5'  TGCCGCGGGAGTAACGGCG    51568         CGC_
                                TGCCGTGGG    GCGGCG
                                |||||||||    ||||||
                                ACGGCGCCC    TGCCGC
                                     TCAT
GAM2122  A1BG     3'  AGACCAGCCTGGGCAACATAG  51571      AAACA    A___
                                AGAC    CAGTT    CAACATAG
                                ||||    |||||    ||||||||
                                TCTG    GTCGG    GTTGTATC
                                  _____    ACCC
GAM2122  APAF1    3'  AGACCAGCCTAGACAACATAG  51572      AAACA    ___
                                AGAC    CAGTT   ACAACATAG
                                ||||    |||||   |||||||||
                                TCTG    GTCGG   TGTTGTATC
                                  _____    ATC
GAM2122  APAF1    3'  AGACCAGCCTAGACAACATAG  51572      AAACA    ___
                                AGAC    CAGTT   ACAACATAG
                                ||||    |||||   |||||||||
                                TCTG    GTCGG   TGTTGTATC
                                  _____    ATC
GAM2122  CASP10   3'  AGACCAGCTTAGGCAACATAG  51573      AAACA    A___
                                AGAC    CAGTT    CAACATAG
                                ||||    |||||    ||||||||
                                TCTG    GTCGA    GTTGTATC
                                  _____    ATCC
GAM2122  CASP10   3'  AGACCAGCTTAGGCAACATAG  51573      AAACA    A___
                                AGAC    CAGTT    CAACATAG
                                ||||    |||||    ||||||||
                                TCTG    GTCGA    GTTGTATC
                                  _____    ATCC
GAM2122  CASP8    3'  AAACACAGTTATTCACAG    51574          CAA
                                AAACACAGTTA   CATAG
                                ||||||||||   |||||
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                                TTTGTGTCAAT   GTGTC
                                      AA_
GAM2122  CDH1     3'  AGACCAGCTTGGGCAACATAGC 51575      AAACA     A___
                                AGAC    CAGTT    CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTCGA    GTTGTATCG
                                  _____    ACCC
GAM2122  DDEF2    3'  AACAAATGCAGTTAACAG    51576       CA     CAAC
                                GACAAA  CAGTTA    ATAG
                                ||||||  ||||||    ||||
                                TTGTTT  GTCAAT    TGTC
                                   AC    ____
GAM2122  EIF4G2   3'  CAAATGCAGTTACATCATAGC  51577      CA       A
                                CAAA  CAGTTACA CATAGC
                                ||||  |||||||| ||||||
                                GTTT  GTCAATGT GTATCG
                                  AC       A
GAM2122  FGFR2    3'  AGGCAGACACAGTCATTCAT   51578    A  A       CAA
                                AG CA ACACAGTTA   CAT
                                || || |||||||||   |||
                                TC GT TGTGTCAGT   GTA
                                 C  C       AA_
GAM2122  GRM6     3'  AGACCAGCCTGGGCAACATAG  51571      AAACA     A___
                                AGAC    CAGTT    CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCGG    GTTGTATC
                                  _____    ACCC
GAM2122  IQGAP1   3'  AAACAAACACCAAAGCTTACAA 51579          ___   _   C
            TATAG                   AGACAAACAC   AGTT ACAA ATAG
                                ||||||||||   |||| |||| ||||
                                TTTGTTTGTG   TCGA TGTT TATC
                                      GTT    A    A
GAM2122  KLRD1    3'  AGACCAGCCTGGGCAACATAGC 51580      AAACA     A___
                                AGAC    CAGTT    CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTCGG    GTTGTATCG
                                  _____    ACCC
GAM2122  KLRD1    3'  AGACCAGCCTGGGCAACATAGC 51580      AAACA     A___
                                AGAC    CAGTT    CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTCGG    GTTGTATCG
                                  _____    ACCC
GAM2122  PCOLN3   3'  AGACAAACAGCACAGCACA   51581       AC    T   A
                                AGACAA  ACAGT ACA CATA
                                ||||||  ||||| ||| ||||
                                TCTGTT  TGTCG TGT GTGT
                                   __    _   C
GAM2122  RPP30    3'  AGACCAGCCTCAGCAACATAG  51582      AAACA     A___
                                AGAC    CAGTT    CAACATAG
                                ||||    |||||   ||||||||
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                                TCTG    GTCGG    GTTGTATC
                                  _____    AGTC
GAM2122  SLC4A4   3'  AGACAAACAGGTTACAATGTAG 51583        CA      CA
                                AGACAAACA  GTTACAA  TAG
                                |||||||||  |||||||  |||
                                TCTGTTTGT  CAATGTT  ATC
                                    C_      AC
GAM2122  SULT1C1  3'  AGACCAGCCTGGGCAACATAGC 51580     AAACA    A___
                                AGAC    CAGTT    CAACATAGC
                                ||||    |||||    |||||||||
                                TCTG    GTCGG    GTTGTATCG
                                  _____    ACCC
GAM2122  TAF1A    3'  AAACAGACATAGTTACAAAGAG 51584      A  C      CAT
           C                     AGACA ACA AGTTACAA   AGC
                                |||||  |||  ||||||||   |||
                                TTTGT TGT TCAATGTT   TCG
                                  C   A       TC_
GAM2122  TAF1A    3'  AAACAGACATAGTTACAAAGAG 51584      A  C      CAT
           C                     AGACA ACA AGTTACAA   AGC
                                |||||  |||  ||||||||   |||
                                TTTGT TGT TCAATGTT   TCG
                                  C   A       TC_
GAM2122  TNFRSF9  3'  AGACCAGCCTGTACAACAT    51585     AAACA   ___
                                AGAC    CAGT   TACAACAT
                                ||||    ||||   ||||||||
                                TCTG    GTCG   ATGTTGTA
                                  _____    GAC
GAM2122  AD7C-NTP 3'  AGACCAGCCTGGGCAACATAGC 51580     AAACA    A___
                                AGAC    CAGTT    CAACATAGC
                                ||||    |||||    |||||||||
                                TCTG    GTCGG    GTTGTATCG
                                  _____    ACCC
GAM2122  BCAR3    3'  AGAAAGCAACCAGCCAACATAG 51586     CA__  A   TA
           C                     AGA    AAC CAGT  CAACATAGC
                                |||    ||| ||||  |||||||||
                                TCT    TTG GTCG  GTTGTATCG
                                  TTCG  _   __
GAM2122  COLEC12  3'  AGACCAGCCTGGGCAACATAGC 51580     AAACA    A___
                                AGAC    CAGTT    CAACATAGC
                                ||||    |||||    |||||||||
                                TCTG    GTCGG    GTTGTATCG
                                  _____    ACCC
GAM2122  DAPK2    3'  GAGCAAAATTACAACATGGC   51587   _   CACA       A
                                GA CAAA    GTTACAACAT GC
                                || ||||    |||||||||| ||
                                CT GTTT    TAATGTTGTA CG
                                 C   _____        C
GAM2122  FLJ10232 5'  AGACCAGCCTGGGCAACATAGC 51580     AAACA    A___
                                AGAC    CAGTT    CAACATAGC
                                ||||    |||||    |||||||||
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                                TCTG    GTCGG   GTTGTATCG
                                  _____   ACCC
GAM2122  FLJ12888  3'  AGACCAATCTGGGCAACATAGC 51588     AAACA    A___
                                AGAC    CAGTT   CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTTAG   GTTGTATCG
                                  _____   ACCC
GAM2122  FLJ13769  5'  AGACCAGCCTAGGCAACATAG  51589     AAACA    A___
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCGG   GTTGTATC
                                  _____   ATCC
GAM2122  FLJ20147  3'  AGACCAGTCTGGGCAACATAGC 51590     AAACA    A___
                                AGAC    CAGTT   CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTCAG   GTTGTATCG
                                  _____   ACCC
GAM2122  FLJ22316  5'  AGACCAGCCTGGGCAACATAGC 51580     AAACA    A___
                                AGAC    CAGTT   CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTCGG   GTTGTATCG
                                  _____   ACCC
GAM2122  FLJ32334  3'  AGACCAGCCTGGGCAACATAGC 51580     AAACA    A___
                                AGAC    CAGTT   CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTCGG   GTTGTATCG
                                  _____   ACCC
GAM2122  KIAA0173  3'  AGACAAACCACACAT      51591       ACAGT    A
                                AGACAAAC    TACA CAT
                                ||||||||    |||| |||
                                TCTGTTTG    GTGT GTA
                                  _____   _
GAM2122  KIAA0186  3'  AGACCAGCTTGGGCAACATAG  51592     AAACA    A___
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCGA   GTTGTATC
                                  _____   ACCC
GAM2122  KIAA0493  3'  AGACAAACATAACATACACA   51593       CAGTT   _
                                AGACAAACA    ACA ACATA
                                |||||||||    ||| |||||
                                TCTGTTTGT    TGT TGTGT
                                     AT___   A
GAM2122  KIAA0532  3'  AGACCAGCTGGGCAACATAG   51594     AAACA    A__
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCGA   GTTGTATC
                                  _____   CCC
GAM2122  KIAA0828  3'  AGACCAGCCTGGGCAACATAG  51571     AAACA    A___
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
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                                TCTG    GTCGG   GTTGTATC
                                  _____   ACCC
GAM2122 KIAA1010 3' AGACCAGCCTGGGCAACATAGC 51580    AAACA   A___
                                AGAC    CAGTT   CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTCGG   GTTGTATCG
                                  _____   ACCC
GAM2122 KIAA1257 3' AGACCAGCCTGGGCAACATAGC 51580    AAACA   A___
                                AGAC    CAGTT   CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTCGG   GTTGTATCG
                                  _____   ACCC
GAM2122 KIAA1559 3' AGACCAGCCTGGGCAACATAG  51571    AAACA   A___
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCGG   GTTGTATC
                                  _____   ACCC
GAM2122 KIAA1915 3' ACAGACATATACAACATGGC   51595    A   CAGT      A
                                ACA ACA   TACAACAT GC
                                ||| |||   |||||||| ||
                                TGT TGT   ATGTTGTA CG
                                  C  AT__      C
GAM2122 KIAA1937 3' ACAAACACACACACATAG    51596       GT   A
                                ACAAACACA  TACA CATAG
                                |||||||||  |||| |||||
                                TGTTTGTGT  GTGT GTATC
                                     __   _
GAM2122 KIAA1962 3' AGACCAGTCTGGGCAACATAG  51597    AAACA   A___
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCAG   GTTGTATC
                                  _____   ACCC
GAM2122 KLHL6    3' AGACAAACATGTAAGCCATGGC 51598       CA  TACAA   A
                                AGACAAACA  GT    CAT GC
                                |||||||||  ||    ||| ||
                                TCTGTTTGT  CA    GTA CG
                                     A_  TTCG_   C
GAM2122 NCBP2    3' CAAAGCAATACAACATAGC   51599     CA   T
                                CAAA  CAGT ACAACATAGC
                                ||||  |||| ||||||||||
                                GTTT  GTTA TGTTGTATCG
                                  C_   _
GAM2122 PGS1     3' GACGGGGTAGTTACAACATGC  51600    AAACAC       A
                                GAC     AGTTACAACAT GC
                                |||     |||||||||||| ||
                                CTG     TCAATGTTGTA CG
                                  CCCCA_         _
GAM2122 PRO0899  5' AGACCAGCCTGGGCAACATAG  51571    AAACA   A___
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
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                              TCTG    GTCGG   GTTGTATC
                                _____   ACCC
GAM2122 RAB33B   3' CAGCCTGGACAACATAGC   51601     ___
                              CAGTT   ACAACATAGC
                              |||||   ||||||||||
                              GTCGG   TGTTGTATCG
                                 ACC
GAM2122 RNF8     3' AGACCAGCCTAGGCAACATAG 51589    AAACA   A___
                              AGAC    CAGTT   CAACATAG
                              ||||    |||||   ||||||||
                              TCTG    GTCGG   GTTGTATC
                                _____   ATCC
GAM2122 SAE1     3' AAACAAAGGACCAACATAGC  51602     C  TTA
                              AAACA AG   CAACATAGC
                              ||||| ||   ||||||||
                              TTTGT TC   GTTGTATCG
                                 T  CTG
GAM2122 SNAPC1   3' AGACCAGCCTGAGCAACATAGC 51603    AAACA   A___
                              AGAC    CAGTT   CAACATAGC
                              ||||    |||||   |||||||||
                              TCTG    GTCGG   GTTGTATCG
                                _____   ACTC
GAM2122 STARD7   3' GACAAGGCACTTAACATAGC  51604     ACA  G   CA
                              GACAA   CA TTA  ACATAGC
                              |||||   || |||  |||||||
                              CTGTT   GT AAT  TGTATCG
                                 CC_  G  __
GAM2122 STARD7   3' GACAAGGCACTTAACATAGC  51604     ACA  G   CA
                              GACAA   CA TTA  ACATAGC
                              |||||   || |||  |||||||
                              CTGTT   GT AAT  TGTATCG
                                 CC_  G  __
GAM2122 TANK     5' AGATGAAGACAGTTACACA   51605    CA  C       A
                              AGA  AA ACAGTTACA CA
                              |||  || |||||||| ||
                              TCT  TT TGTCAATGT GT
                                AC  C       _
GAM2122 TANK     5' AGATGAAGACAGTTACACA   51605    CA  C       A
                              AGA  AA ACAGTTACA CA
                              |||  || |||||||| ||
                              TCT  TT TGTCAATGT GT
                                AC  C       _
GAM2122 TRIM35   3' AGACCAGCTTGGGCAACATAG  51592    AAACA   A___
                              AGAC    CAGTT   CAACATAG
                              ||||    |||||   ||||||||
                              TCTG    GTCGA   GTTGTATC
                                _____   ACCC
GAM2122 UBCE7IP5 3' AGACCAGTCTGGACAACATAGC 51606    AAACA    ___
                              AGAC    CAGTT   ACAACATAGC
                              ||||    |||||   ||||||||||
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                                TCTG    GTCAG   TGTTGTATCG
                                  _____    ACC
GAM2122  LOC114932 3'  AGACAATGTGCCACAAAACATA 51607      ACACA    __
             GC                   AGACAA    GTTACA  ACATAGC
                                  ||||||    ||||||  |||||||
                                  TCTGTT    CGGTGT  TGTATCG
                                    ACA__     TT
GAM2122  LOC115098 5'  AGACCAGCCTGGGCAACATAGC 51580     AAACA    A___
                                  AGAC    CAGTT    CAACATAGC
                                  ||||    |||||    |||||||||
                                  TCTG    GTCGG    GTTGTATCG
                                    _____    ACCC
GAM2122  LOC115219 3'  AGACCAACCTGGACAACATAGC 51608     A   ACAGTT
                                  AGAC AAC     ACAACATAGC
                                  |||| |||     ||||||||||
                                  TCTG TTG     TGTTGTATCG
                                    G   GACC__
GAM2122  LOC124871 3'  AGACCAGCCTGGGCAACATAG  51571     AAACA    A___
                                  AGAC    CAGTT    CAACATAG
                                  ||||    |||||    ||||||||
                                  TCTG    GTCGG    GTTGTATC
                                    _____    ACCC
GAM2122  LOC134121 3'  AGATGCAACACAGGCATAG   51609     CA_      TTACAA
                                  AGA   AACACAG     CATAG
                                  |||   |||||||     |||||
                                  TCT   TTGTGTC     GTATC
                                    ACG      C_____
GAM2122  LOC150587 3'  AGACCAGCCTGGGCAACATAG  51571     AAACA    A___
                                  AGAC    CAGTT    CAACATAG
                                  ||||    |||||    ||||||||
                                  TCTG    GTCGG    GTTGTATC
                                    _____    ACCC
GAM2122  LOC154877 3'  AGACCAGCCTGGGCAACATAG  51571     AAACA    A___
                                  AGAC    CAGTT    CAACATAG
                                  ||||    |||||    ||||||||
                                  TCTG    GTCGG    GTTGTATC
                                    _____    ACCC
GAM2122  LOC157653 5'  GACGCAGTGGGTTACAACGTAG 51610     AAACACA      A
             C                    GAC      GTTACAAC TAGC
                                  |||      |||||||| ||||
                                  CTG      CAATGTTG ATCG
                                    CGTCACC       C
GAM2122  LOC157867 5'  AGACCAGCCTAGGCAACATAGC 51611     AAACA    A___
                                  AGAC    CAGTT    CAACATAGC
                                  ||||    |||||    |||||||||
                                  TCTG    GTCGG    GTTGTATCG
                                    _____    ATCC
GAM2122  LOC203427 3'  AGACCAGCCTGGGCAACATAGC 51580     AAACA    A___
                                  AGAC    CAGTT    CAACATAGC
                                  ||||    |||||    |||||||||
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                                TCTG    GTCGG   GTTGTATCG
                                  _____   ACCC
GAM2122  LOC219333 3'  AAACAAACACAACATA     51612         GTTACA
                                AGACAAACACA     ACATA
                                ||||||||||     |||||
                                TTTGTTTGTGT     TGTAT
                                        _______
GAM2122  LOC221960 3'  AGACCAGCCTGGGCAACATAG  51571     AAACA    A___
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCGG   GTTGTATC
                                  _____   ACCC
GAM2122  LOC257463 3'  AGACCAGCCTGGGCAACATAGC 51580     AAACA    A___
                                AGAC    CAGTT   CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTCGG   GTTGTATCG
                                  _____   ACCC
GAM2122  LOC51622  3'  AGACCAGCCTGGGCAACATAG  51571     AAACA    A___
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCGG   GTTGTATC
                                  _____   ACCC
GAM2122  LOC89231  3'  AGACCAGCCTGGGCAACATAG  51571     AAACA    A___
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCGG   GTTGTATC
                                  _____   ACCC
GAM2122  LOC91380  3'  AGACCAGTCTAAGCAACATAG  51613     AAACA    A___
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCAG   GTTGTATC
                                  _____   ATTC
GAM2123  ACP1      3'  AAATGCTGATGAAGA      51616       TACTG
                                AAATGT    TGATGAAGA
                                ||||||    |||||||||
                                TTTACG    ACTACTTCT
                                      _____
GAM2123  ACP1      3'  AAATGCTGATGAAGA      51616       TACTG
                                AAATGT    TGATGAAGA
                                ||||||    |||||||||
                                TTTACG    ACTACTTCT
                                      _____
GAM2123  BRCA1     3'  TAAAATGTCACTCTGAGA    51617          G  T
                                TAAAATGTTACT TGA GA
                                |||||||||||| ||| ||
                                ATTTTACAGTGA ACT CT
                                       G  _
GAM2123  C18orf1   3'  ATGTTACTGTGTGCAAAG    51618         AT_
                                ATGTTACTGTG  GAAG
                                ||||||||||  ||||
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                                TACAATGACAC   TTTC
                                      ACG
GAM2123  CLASP2    3'  TAAAATGCTACTGAGAAGA   51619          TGAT
                                TAAAATGTTACTG   GAAGA
                                ||||||||||||   |||||
                                ATTTTACGATGAC   CTTCT
                                      T___
GAM2123  MFAP3     3'  AAAATGTTACTTCTTCTAAGAA 51620         GTGATG
                                AAAATGTTACT     AAGAA
                                ||||||||||     |||||
                                TTTTACAATGA     TTCTT
                                      AGAAGA
GAM2123  PCDHGA7   3'  TAAAGTGTCACCACTGAAG   51621     A     TG GA
                                TAAA TGTTAC  T  TGAAG
                                |||| ||||||  |  |||||
                                ATTT ACAGTG  G  ACTTC
                                  C     GT __
GAM2123  PPP1CB    3'  AAATGCTACTGCACAATAGA   51622          ATGA
                                AAATGTTACTGTG   AGA
                                ||||||||||||   |||
                                TTTACGATGACGT   TCT
                                      GTTA
GAM2123  SIP       3'  TAAAACTGTTCTAATGAAGAA  51623    TT    ___
                                TG  ACTGT   GATGAAGAA
                                ||  |||||   |||||||||
                                AT  TGACA   TTACTTCTT
                                 TT    AGA
GAM2123  STAU2     3'  ATGTATACAGATGAAGAA    51624     _   TGT
                                ATGT TAC   GATGAAGAA
                                |||| |||   |||||||||
                                TACA ATG   CTACTTCTT
                                  T   T__
GAM2123  TCF20     5'  TAAAACGCTGTGGTGAAG    51625       TTA    A
                                TAAAATG   CTGTG TGAAG
                                |||||||   ||||| |||||
                                ATTTTGC   GACAC ACTTC
                                    ___    C
GAM2123  TTC3      5'  TGTTTGCTGAATGAAGAA    51626     A_   T
                                TGTT  CTG GATGAAGAA
                                ||||  ||| |||||||||
                                ACAA  GAC TTACTTCTT
                                  AC   _
GAM2123  AP3D1     3'  TAAAATGTCATTATCTCTGAAG 51627         C   GA_
           AA                    TAAAATGTTA TGT   TGAAGAA
                                ||||||||||  |||   |||||||
                                ATTTTACAGT ATA   ACTTCTT
                                      A   GAG
GAM2123  DKFZp434C0328 3'  AAATGTTACTGAAAGA      51628          TGAT
                                AAATGTTACTG    GAAGA
                                ||||||||||    |||||
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                                TTTACAATGAC    TTTCT
                                       ____
GAM2123  DKFZP564L0864 3'  TAAAGTGTTACTGTGACA    51629      A
                                TAAA TGTTACTGTGATG
                                |||| ||||||||||||
                                ATTT ACAATGACACTGT
                                  C
GAM2123  DKFZP761C169 3'  AAATGTTGCAGTGATGAAGAA  51630        ACT
                                AAATGTT   GTGATGAAGAA
                                |||||||   ||||||||||
                                TTTACAA   CACTACTTCTT
                                    CGT
GAM2123  ESM1     3'  TAAAATGTTGGCTGTGTGTTGA 51631         A_    A  AA
             A                   TAAAATGTT  CTGTG TG  GAA
                                |||||||||  ||||| ||  |||
                                ATTTTACAA  GACAC AC  CTT
                                     CC    _  AA
GAM2123  FLJ10898  5'  TGCTTCTGTGATGGAGAA    51632      A       A
                                TGTT CTGTGATG AGAA
                                |||| |||||||| ||||
                                ACGA GACACTAC TCTT
                                  A       C
GAM2123  FLJ13195  3'  AAATGTTACTTTGGAGAA    51633          G  AT
                                AAATGTTACT TG  GAA
                                |||||||||| ||  |||
                                TTTACAATGA AC  CTT
                                     A  CT
GAM2123  FLJ20619  3'  AAATCTTACTGTGTGCTTGA   51634      G       A  AA_
                                AAAT TTACTGTG TG   GA
                                |||| |||||||| ||   ||
                                TTTA AATGACAC AC   CT
                                  G       _  GAA
GAM2123  HSC3     3'  AAATGTTATATATTTGAAGA   51635        C    A_
                                AAATGTTA TGTG  TGAAGA
                                |||||||| ||||  ||||||
                                TTTACAAT ATAT  ACTTCT
                                     _    AA
GAM2123  KIAA0022  3'  AAAATGTTACTGGAATAAGGA  51636           TG    A
                                AAAATGTTACTG  ATGA GA
                                ||||||||||||  |||| ||
                                TTTTACAATGAC  TATT CT
                                      CT    C
GAM2123  KIAA0227  3'  AAAATGTTATTCGCGAAGAA   51637         CTG  A
                                AAAATGTTA   TG TGAAGAA
                                |||||||||   || |||||||
                                TTTTACAAT   GC GCTTCTT
                                     AA_  _
GAM2123  KIAA0284  3'  AAAATAACAGTGATGAAGA    51638       TT  T
                                AAAATG  AC GTGATGAAGA
                                ||||||  || ||||||||||
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                                TTTTAT  TG CACTACTTCT
                                   __ T
GAM2123  KIAA0391  3'  TAAAATGTTTAGTGTGAGGAA  51639        AC_    T
                                TAAAATGTT   TGTGA GAA
                                |||||||||   ||||| |||
                                ATTTTACAA   ACACT CTT
                                      ATC    C
GAM2123  KIAA0594  3'  TAAAATGTTTATAAAGAAGAA  51640        AC    T
                                TAAAATGTT  TGTGA GAAGAA
                                |||||||||  ||||| ||||||
                                ATTTTACAA  ATATT CTTCTT
                                      __    T
GAM2123  KIAA1010  3'  TGCTTGGATGAAGAA      51641     AC  T
                                TGTT  TG GATGAAGAA
                                ||||  || |||||||||
                                ACGA  AC CTACTTCTT

                                   __ _
GAM2123  KIAA1203  3'  TAAAATGTCTCTAAAGATGAAG 51642        A   T_
                                TAAAATGTT CTG  GATGAAG
                                ||||||||| |||  |||||||
                                ATTTTACAG GAT  CTACTTC
                                      A   TT
GAM2123  PCSK7    3'  AAAATGTTGCTGTGAAAAGA   51643        A     T
                                AAAATGTT CTGTGA GAAGA
                                |||||||| |||||| |||||
                                TTTTACAA GACACT TTTCT
                                      C     _
GAM2123  PPP4R2   5'  GTTACTATTAATGGAGAA    51644        _   A
                                GTTACTGT GATG AGAA
                                |||||||| ||||| ||||
                                CAATGATA TTAC TCTT
                                      A   C
GAM2123  PRO1575  5'  AAATGTTAAGCTGAATGAAGA  51645        __   T
                                AAATGTTA  CTG GATGAAGA
                                ||||||||  ||| ||||||||
                                TTTACAAT  GAC TTACTTCT
                                      TC  _
GAM2123  SAMP14   3'  TAAAGTGCTACCAATGGAGA   51646     A      GT    A
                                TAAA TGTTACT  GATG AGA
                                |||| |||||||  |||| |||
                                ATTT ACGATGG  TTAC TCT
                                   C      __    C
GAM2123  TA-KRP   3'  AAATGTCACAAGGATGAAG   51647         TGT
                                AAATGTTAC   GATGAAG
                                |||||||||   |||||||
                                TTTACAGTG   CTACTTC
                                      TTC
GAM2123  TIAF1    3'  ATGCAGCTGTGATGGAGA    51648      TA       A
                                ATGT  CTGTGATG AGA
                                ||||  |||||||| |||
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                                TACG  GACACTAC TCT
                                  TC       C
GAM2123  UMP-CMPK  3'  TAAAATGTTGTGATTACTAGA  51649        TAC     GA__
                                TAAAATGT   TGTGAT    AGA
                                ||||||||   ||||||    |||
                                ATTTTACA   ACACTA    TCT
                                     ___      ATGA
GAM2123  ZNF220    3'  TAAAATGTTCAAGATTGTGAAG 51650         ACTG__  A
           AA                     TAAAATGTT     TG TGAAGAA
                                ||||||||||     || |||||||
                                ATTTTACAA     AC ACTTCTT
                                     GTTCTA  _
GAM2123  LOC120826 5'  TAAGATGTTACTGGATA     51651     A        T
                                TAA ATGTTACTG GATG
                                ||| |||||||||| ||||
                                ATT TACAATGAC CTAT
                                  C       _
GAM2123  LOC148641 5'  AATGCAGGTGATGAAGA     51652       TACT
                                AATGT    GTGATGAAGA
                                |||||    ||||||||||
                                TTACG    CACTACTTCT
                                   TC__
GAM2123  LOC148645 3'  CAAAATGGGGCTGATGAAGA   51653        TTACTG
                                TAAAATG     TGATGAAGA
                                |||||||     |||||||||
                                GTTTTAC     ACTACTTCT
                                     CCCG__
GAM2123  LOC197287 3'  AAATGTTACTGTGTGGAG     51654           A  A
                                AAATGTTACTGTG TG AG
                                |||||||||||||| || ||
                                TTTACAATGACAC AC TC
                                        _  C
GAM2123  LOC200854 5'  GTTACTATTAATGGAGAA     51644         _    A
                                GTTACTGT GATG AGAA
                                |||||||| |||| ||||
                                CAATGATA TTAC TCTT
                                     A    C
GAM2124  MAP3K14   3'  TGTGTTGCAACAACCTGAAAA  51657            G  A
                                TGTGTTGCAACAGC CT AAAA
                                |||||||||||||| || ||||
                                ACACAACGTTGTTG GA TTTT
                                        _  C
GAM2124  AKAP12    3'  TGTGTTGCAACATTGTTCTTAA 51658           GCG__  A
           AA                     TGTGTTGCAACA     CT AAAA
                                ||||||||||||     || ||||
                                ACACAACGTTGT     GA TTTT
                                       AACAA  A
GAM2124  AKAP12    3'  TGTGTTGCAACATTGTTCTTAA 51658           GCG__  A
           AA                     TGTGTTGCAACA     CT AAAA
                                ||||||||||||     || ||||
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                                ACACAACGTTGT    GA TTTT
                                      AACAA  A
GAM2124  FLJ11783  3'  TGTGTTGTTAGCTTAAAAAAT  51659       CAAC   GC
                                TGTGTTG   AGC  TAAAAAAT
                                |||||||   |||  ||||||||
                                ACACAAC   TCG  ATTTTTTA
                                    AA__   A_
GAM2124  KIAA1910  5'  TGCCCAGCCAATGGCGCTGGAA 51660    GTT  AACA_    AA
           AAT                    TGT   GC    GCGCT  AAAAT
                                |||   ||    |||||  |||||
                                ACG   CG    CGCGA  TTTTA
                                  GGT  GTTAC    CC
GAM2124  MCM10    3'  TGTAGAAATCCAGTGCTAAAAA 51661     TTGCAA   C
           AT                    TGTG     CAG GCTAAAAAAT
                                ||||     ||| ||||||||||
                                ACAT     GTC CGATTTTTTA
                                  CTTTAG   A
GAM2124  RAB14    3'  TGTGATGCAACAGTGTAAGCAA 51662     T      C____  T
           AA                    TGTG TGCAACAG    GC AAAA
                                |||| ||||||||    || ||||
                                ACAC ACGTTGTC    CG TTTT
                                  T       ACATT  _
GAM2124  SDCBP    3'  TGTGTTGACTAAAAA      51663       CAACAGC
                                TGTGTTG      GCTAAAAA
                                |||||||      ||||||||
                                ACACAAC      TGATTTTT
                                      _______
GAM2124  LOC120892 3'  TGTTTGCAACAGCAACAAA   51664    G        C
                                TGT TTGCAACAGCG TAAA
                                ||| ||||||||||| ||||
                                ACA AACGTTGTCGT GTTT
                                  _        T
GAM2124  LOC130813 3'  GTGTTGCAGCAGCCAGCT    51665       A   __
                                GTGTTGCA CAGC  GCT
                                |||||||| ||||  |||
                                CACAACGT GTCG  CGA
                                    C    GT
GAM2124  LOC151742 3'  TGTGTTGCAACTGCCA      51666         AGC
                                TGTGTTGCAAC   GCTA
                                ||||||||||   ||||
                                ACACAACGTTG   CGGT
                                      A__
GAM2125  LILRB4   3'  TTGTCTGACTTCTGTTT     51669    _    GGTCTATA
                                TTG CTGAC      TTCTGTTT
                                ||| |||||      ||||||||
                                AAC GACTG      AAGACAAA
                                  A   _________
GAM2125  KIAA0635  5'  TTACTTACTATATTCTGTTT  51670      GACGGT
                                TTGCT     CTATATTCTGTTT
                                |||||     ||||||||||||
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                                AATGA     GATATAAGACAAA
                                  AT____
GAM2126 HTRA3    3'  TGTTCACAGGGGCAGAGGC   51673        AA_    A
                                TGTTTACG   GCAGA GC
                                ||||||||   ||||| ||
                                ACAAGTGT   CGTCT CG
                                     CCC    C
GAM2126 MAB21L1  3'  AGATTGTTTGCACTGCGGA   51674         A  AA  A
                                AGATTGTTT CG  GC GA
                                ||||||||| ||  || ||
                                TCTAACAAA GT  CG CT
                                     C  GA  C
GAM2126 C22orf4  3'  GATTTTTAAAACAGAAGCA   51675      GTTTAC
                                GATT     GAAGCAGAAGCA
                                ||||     ||||||||||||
                                CTAA     TTTTGTCTTCGT
                                  AAA___
GAM2126 FLJ23121 3'  TAGATTTTTTCTCTCCAGAAGC 51676       G   ACGAAG
             A                   TAGATT TTT     CAGAAGCA
                                ||||||| |||     ||||||||
                                ATCTAA AAA     GTCTTCGT
                                   A   GAGAG_
GAM2126 FLJ31121 3'  GATACACTGAGGCAGAAGCA   51677     TGTT   _  A
                                GAT    TAC GA GCAGAAGCA
                                |||    ||| || |||||||||
                                CTA    GTG CT CGTCTTCGT
                                  T___   A  C
GAM2126 HEMK     3'  GATTGTTTGCACCGCCTGGGCA 51678         A  AA  AGAA
                                GATTGTTT CG  GC    GCA
                                |||||||| ||  ||    |||
                                CTAACAAA GT  CG    CGT
                                     C  GG  GACC
GAM2126 KIAA0152 3'  TTGGAAACAGAGGCAGAAGCA  51679     TTT  _  A
                                TTG   AC GA GCAGAAGCA
                                |||   || || |||||||||
                                AAC   TG CT CGTCTTCGT
                                  CTT  T  C
GAM2126 OSMR     3'  GATGTCTATGGAGCAGAAG    51680     T    CGA
                                GAT GTTTA   AGCAGAAG
                                ||| |||||   ||||||||
                                CTA CAGAT   TCGTCTTC
                                  _    ACC
GAM2126 TSPEAR   3'  TGTTGCAGAAGCAGGAGCA    51681      TAC      A
                                TGTT   GAAGCAG AGCA
                                ||||   ||||||| ||||
                                ACAA   CTTCGTC TCGT
                                  CGT      C
GAM2126 LOC122553 3'  GATTGGTTAATTCAGAAGCA   51682       T   CGAAG
                                GATTG TTA    CAGAAGCA
                                ||||| |||    ||||||||
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                                CTAAC AAT    GTCTTCGT
                                  C  TAA__
GAM2126 LOC203530 3'  AGATTTGCCCGTGGGGCAGAAG 51683      _   ACGAA
            CA                    AGATT GTTT    GCAGAAGCA
                                  ||||| ||||    |||||||||
                                  TCTAA CGGG    CGTCTTCGT
                                    A   CACCC
GAM2127 POLI    3'  TGACCATGATATTCTTTTTATT 51686    TAA  T         C
            GA                    TG  GT GTATTCTTTTTAT GA
                                  ||  || |||||||||||| ||
                                  AC  TA TATAAGAAAAATA CT
                                   TGG  C          A
GAM2127 LAMP3   3'  TATAAGCTGATTTGTTCTTTTT 51687         TA___
                                  TGTAAGTTG    TTCTTTTT
                                  |||||||||    ||||||||
                                  ATATTCGAC    AAGAAAAA
                                       TAAAC
GAM2127 SMCR5   3'  TGGAAGTTGCTACCTTTTATTG 51688    T     ATT      C
            A                     TG AAGTTGT   CTTTTTAT GA
                                  || |||||||  |||||||| ||
                                  AC TTCAACG   GGAAAATA CT
                                   C      AT_      A
GAM2128 KRT1    3'  GGTCACTGCTGAACTGTTTCTC 51691    _  CTC      CTC
                                  GG CAC   CTGAACTG   CTC
                                  || |||   ||||||||  |||
                                  CC GTG   GACTTGAC   GAG
                                   A  AC_      AAA
GAM2128 PRX     3'  TCGGCCCCTGGGGGCTGCTCCT 51692      ACC    AA__
            C                     TCGGC   TCCTG   CTGCTCCTC
                                  |||||   |||||   |||||||||
                                  AGCCG   GGGAC   GACGAGGAG
                                     ____    CCCC
GAM2128 SNTB1   5'  TCGGTCCTCCTGAGCCGACT   51693     CA      A  _
                                  TCGG  CCTCCTGA CTG CT
                                  ||||  |||||||| ||| ||
                                  AGCC  GGAGGACT GGC GA
                                    A_      C   T
GAM2128 SOX10   3'  TCGTCACCTCCTGGGATGCGTC 51694    G       AAC   TC
            TC                    TCG CACCTCCTG   TGC  CTC
                                  ||| |||||||||   |||  |||
                                  AGC GTGGAGGAC   ACG  GAG
                                    A       CCT   CA
GAM2128 APXL2   3'  GCACCTTAAGTGCTCCTC    51695       CC   AC
                                  GCACCT  TGA  TGCTCCTC
                                  ||||||  |||  ||||||||
                                  CGTGGA  ATT  ACGAGGAG
                                     __   C_
GAM2128 BCCIP   3'  TCAGCACCACTGTTCC      51696        TCCTGA   C
                                  TCGGCACC     ACTG TCC
                                  ||||||||     |||| |||
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                                AGTCGTGG     TGAC AGG
                                   _______   A
GAM2128 BICD2    3'  TCGGCCCTCCTGATACCCT   51697      A      AC   T
                                TCGGC CCTCCTGA  TGC CCT
                                ||||| ||||||||  ||| |||
                                AGCCG GGAGGACT  ATG GGA
                                  _       __  _
GAM2128 DKFZP564J0863 5'  TCAGTGCCTGTAACTGCTC   51698     CACCT   _
                                TCGG    CCTG AACTGCTC
                                ||||    |||| ||||||||
                                AGTC    GGAC TTGACGAG
                                  AC___   A
GAM2128 FLJ20034  3'  TCAGCACCTCTGGCT      51699         C  AACT
                                TCGGCACCTC TG   GCT
                                |||||||||| ||   |||
                                AGTCGTGGAG AC   CGA
                                   _ _____
GAM2128 FLJ30681  3'  ACCTTTTTCTGAACTGCTTCTC 51700     C___       C
                                ACCT   CTGAACTGCT CTC
                                ||||   |||||||||| |||
                                TGGA   GACTTGACGA GAG
                                  AAAA        A
GAM2128 KIAA0418  3'  GGCACCTGGGAACTGCT    51701       CCT
                                GGCACCT   GAACTGCT
                                |||||||   ||||||||
                                CCGTGGA   CTTGACGA
                                    CC_
GAM2128 KIAA0864  5'  TCGTGCCTCCAGCTGCTCCTC  51702    GCA    TGAA
                                TCG   CCTCC   CTGCTCCTC
                                |||   |||||   |||||||||
                                AGC   GGAGG   GACGAGGAG
                                  AC_    TC__
GAM2128 MAST205   3'  GGCCCCTCCTGAGGCTGGGCTC 51703     A      A_ __
                                GGC CCTCCTGA  CT  GCTC
                                ||| ||||||||  ||  ||||
                                CCG GGAGGACT  GA  CGAG
                                  G       CC  CC
GAM2128 MGC4607   3'  TCGGCAGCTCCCTGCTCCT   51704      C   TGAA
                                TCGGCA CTCC   CTGCTCCT
                                |||||| ||||   ||||||||
                                AGCCGT GAGG   GACGAGGA
                                   C   _____
GAM2128 STI2     5'  TCAAGCTCCTGAATTGCTTCTC 51705     CAC      C   C
                                TCGG   CTCCTGAA TGCT CTC
                                ||||   |||||||| |||| |||
                                AGTT   GAGGACTT ACGA GAG
                                  C__      A   A
GAM2128 TBDN100   3'  GGACCTCCTATCTCCT     51706   C      AACTG
                                GG ACCTCCTG    CTCCT
                                || ||||||||    |||||
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                                CC TGGAGGAT    GAGGA
                                 _      A____
GAM2128 VPS39    3' GGCGCCACACACTGCTCCTC  51707    A  TCCTGA
                                GGC CC     ACTGCTCCTC
                                ||| ||     ||||||||||
                                CCG GG     TGACGAGGAG
                                  C  TGTG__
GAM2128 WSB1     3' TCGGCAGCTCCTGAACTTCT  51708      C        G
                                TCGGCA CTCCTGAACT CT
                                |||||| |||||||||| ||
                                AGCCGT GAGGACTTGA GA
                                   C         A
GAM2128 LOC122886 5' TCGTACTCACACTGCTCCT   51709    GCAC   CTGA
                                TCG    CTC    ACTGCTCCT
                                |||    |||    |||||||||
                                AGC    GAG    TGACGAGGA
                                  AT__   TG__
GAM2128 LOC166929 3' GGCACCTCTTTAACAAGCTC  51710       CTG   T_
                                GGCACCTC   AAC  GCTC
                                ||||||||   |||  ||||
                                CCGTGGAG   TTG  CGAG
                                    AAA   TT
GAM2128 LOC170394 5' TCGCGCCTCTCCCTCTTGCTCC 51711    _ AC    GAAC
          TC                    TCG GC  CTCCT    TGCTCCTC
                                ||| ||  |||||    ||||||||
                                AGC CG  GAGGG    ACGAGGAG
                                  G  GA    AGA_
GAM2128 LOC254531 5' GGCTCCTGAAGCTGCTCCTC  51712    ACC     _
                                GGC   TCCTGAA CTGCTCCTC
                                |||   ||||||| |||||||||
                                CCG   AGGACTT GACGAGGAG
                                  ____      C
GAM2128 LOC255242 5' TCGAACTTGAACTGCTCTTC  51713     C  CTCC       C
                                TCGG AC    TGAACTGCTC TC
                                |||| ||    |||||||||| ||
                                AGCT TG    ACTTGACGAG AG
                                  _ A___        A
GAM2128 LOC90639  3' TCGGCACCTGCTGGGGTCTC  51714       C   AACTG
                                TCGGCACCT CTG    CTC
                                ||||||||| |||    |||
                                AGCCGTGGA GAC    GAG
                                    C   CCCA_
GAM2128 LOC91450  3' TCGGCTTTTCACCTGCTCCTC 51715     ACC  CTGAA
                                TCGGC   TC    CTGCTCCTC
                                |||||   ||    |||||||||
                                AGCCG   AG    GACGAGGAG
                                  AAA  TG___
GAM2129 ABCA1    3' CCCGTGCCTGGAGACAC    51718     AGG    TTA
                                CCCG   GTCT   GAGACAC
                                ||||   ||||   |||||||
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                              GGGC  CGGA  CTCTGTG
                                A__   C__
GAM2129 GRIN2B   3' TCCCCAAGGCACCGGGGGACAC 51719        GT  TTAGA
                              TCCCCGAGG  CT    GACAC
                              |||||||||  ||    |||||
                              AGGGGTTCC  GG    CTGTG
                                   GT  CCCC_
GAM2129 MAN2A2   3' GAGGCTAGAGACACC      51720     GTCT
                              GAGG   TTAGAGACACC
                              ||||   ||||||||||
                              CTCC   GATCTCTGTGG
                                  ____
GAM2129 NTF5     3' CCCTGAGGTCTCTCAGCA    51721     GA      AG  A
                              CCC  GGGTCTTT  AG CA
                              |||  ||||||||  || ||
                              GGG  TCCAGAGA  TC GT
                                AC       G_  _
GAM2129 OTC      5' TCCCCTGGTTAGAGATAC    51722      GA  GTCT     C
                              TCCCC  GG   TTAGAGA AC
                              |||||  ||   ||||||| ||
                              AGGGG  CC   AATCTCT TG
                                 A_  ____      A
GAM2129 SCTR     5' TCCCCGAGGGCGCCCCGAC   51723          _   AGA
                              TCCCCGAGGGT CTTT   GAC
                              |||||||||| ||||   |||
                              AGGGGCTCCCG GGGG   CTG
                                     C   ___
GAM2129 SPR      3' CCTGGGGATAGAGACACC    51724    GA   TCTT
                              CC  GGG   TAGAGACACC
                              ||  |||   ||||||||||
                              GG  CCC   ATCTCTGTGG
                               A_  CT__
GAM2129 TAF11    3' TCCTTGGAGGCCTGAGATAC  51725    CCGA    TTA   C
                              TCC   GGGTCT   GAGA AC
                              |||   ||||||   |||| ||
                              AGG   TCCGGA   CTCT TG
                                AACC     ___   A
GAM2129 C1orf25  5' TCCCCGAGGCGTTACGACGCC 51726        _ CTTTAGA   A
                              TCCCCGAGG GT      GAC CC
                              |||||||| ||      ||| ||
                              AGGGGCTCC CA      CTG GG
                                   G  ATG____   C
GAM2129 CENTA1   3' TCCCCAAGGGTTCAGACAC   51727         CTTTAG
                              TCCCCGAGGGT    AGACAC
                              ||||||||||     ||||||
                              AGGGGTTCCCA    TCTGTG
                                     AG____
GAM2129 CITED1   3' TCCTCCATCTTTAGGGACAC  51728    _ GAGG      A
                              TCC CC   GTCTTTAG GACAC
                              ||| ||   |||||||| |||||
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                                AGG GG    TAGAAATC CTGTG
                                  A _____       C
GAM2129 CXorf1    3' CCCTTGATGACTTGGAGACA  51729     GAG   C_   A
                                CCC   GGT  TTT GAGACA
                                |||   |||  ||| ||||||
                                GGG   CTA  GAA CTCTGT
                                  AA_   CT   C
GAM2129 DKFZP434P1750 5' CCCTCGAGGCCCAGAGATGCC  51730     _    G  TTT    CA
                                CCC CGAGG TC   AGAGA  CC
                                ||| ||||| ||   |||||  ||
                                GGG GCTCC GG   TCTCT  GG
                                  A    G ___     AC
GAM2129 DKFZp761H079 5' TCCCCGGGGGCCTCCGGCAC  51731       A      AGAGA
                                TCCCCG GGGTCTTT    CAC
                                |||||| ||||||||    |||
                                AGGGGC CCCGGAGG    GTG
                                   C       CC___
GAM2129 FBXO21    3' CCCGAGGGCTCCGTGGAGAC  51732        _  TTA
                                CCCGAGGG TCT   GAGAC
                                |||||||| |||   |||||
                                GGGCTCCC AGG   CTCTG
                                    G   CAC
GAM2129 FLJ00001  3' CCAAGGCCTTTGGAGATAC   51733      G    A   C
                                CCGAGG TCTTT GAGA AC
                                |||||| ||||| |||| ||
                                GGTTCC GGAAA CTCT TG
                                   _    C   A
GAM2129 FLJ11142  3' CCCGAGGGCCCTGGAAGGCA  51734          TA  A
                                CCCGAGGGTCTT  GAG CA
                                ||||||||||||  ||| ||
                                GGGCTCCCGGGA  TTC GT
                                      CC   C
GAM2129 FLJ12448  3' TCCCCAGGGTGGGGGGGACACC 51735      G    CTTTAGA
                                TCCCC AGGGT      GACACC
                                ||||| |||||      ||||||
                                AGGGG TCCCA      CTGTGG
                                   _    CCCCCC_
GAM2129 FLJ14124  3' TCCCCGAGGGAGGGAC      51736         TCTTT  A
                                TCCCCGAGGG    AG GAC
                                ||||||||||    || |||
                                AGGGGCTCCC    TC CTG
                                      _____  C
GAM2129 FLJ14596  5' CCTGAGGGTCCGGCAAGGCAC  51737    C      TTA   A
                                CC GAGGGTCT   GAG CAC
                                || ||||||||   ||| |||
                                GG CTCCCAGG   TTC GTG
                                  A       CCG   C
GAM2129 FYCO1     3' TCTCCGGGGGGTCCCCTGGCAC 51738    C   A_      AGAGA
              C                  TC CCG  GGGTCTTT    CACC
                                || |||  ||||||||    ||||
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                                AG GGC  CCCAGGGG    GTGG
                                 A  CC       ACC__
GAM2129  KIAA0239  3'  CCTCGAGGGTCTGGGACAC   51739    C       TTAGA
                                CC CGAGGGTCT    GACAC
                                || |||||||||    |||||
                                GG GCTCCCAGA    CTGTG
                                 A       CC___
GAM2129  KIAA1862  5'  TCCTTGAAGGTGATGGACACC  51740    CC    CTTTAGA
                                TCC  GAGGGT     GACACC
                                |||  ||||||     ||||||
                                AGG  CTTCCA     CTGTGG
                                  AA    CTAC___
GAM2129  MGC15416  5'  TCCCCGAGGGTCTTGCAG    51741            _
                                TCCCCGAGGGTCTT TAG
                                |||||||||||||| |||
                                AGGGGCTCCCAGAA GTC
                                         C
GAM2129  OSBPL7    5'  TCCCCAGGGTCCATGGACGCC  51742      G     TTAGA  A
                                TCCCC AGGGTCT    GAC CC
                                ||||| |||||||    ||| ||
                                AGGGG TCCCAGG    CTG GG
                                   _      TAC__  C
GAM2129  PGLYRP    3'  CCTGGATCTCTTAGAGACAC   51743    GA      _
                                CC  GGGTCTTT AGAGACAC
                                ||  |||||||| ||||||||
                                GG  CCTAGAGA TCTCTGTG
                                 A_      A
GAM2129  RASSF2    3'  TCCACCTTCCTTTGGAGGCACC 51744    _ GAGGG    A  A
                                TCC CC    TCTTT GAG CACC
                                ||| ||    ||||| ||| ||||
                                AGG GG    GGAAA CTC GTGG
                                  T  AA___    C  C
GAM2129  SHANK3    3'  CCCTCGGGGGTCTTTGAC    51745    _ A      AGA
                                CCC CG GGGTCTTT   GAC
                                ||| || ||||||||   |||
                                GGG GC CCCAGAAA   CTG
                                  A  C      ___
GAM2129  SLC2A10   3'  CCTTGGGGGCTCTGCCAGCACC 51746   GA_  T   AG_  A
                                CC   GGG CTTT   AG CACC
                                ||   ||| ||||   || ||||
                                GG   CCC GAGA   TC GTGG
                                 AAC   C   CGG  _
GAM2129  SLC5A6    3'  TCCCAGAGGACCAGGGACACC  51747     C   GT TTT  A
                                TCCC GAGG  C   AG GACACC
                                |||| ||||  |   || ||||||
                                AGGG CTCC  G   TC CTGTGG
                                  T   TG ___  C
GAM2129  SLC6A13   3'  CCCAAGGGTCTCAGAGGGACAC 51748          T_  A
                                CCCGAGGGTCTT  AG GACAC
                                ||||||||||||  || |||||
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                                GGGTTCCCAGAG  TC CTGTG
                                      TC  C
GAM2129  SMOC1    3'  CCGAGGGTCACTAAGATAC    51749        TTTA    C
                                CCGAGGGTC    GAGA AC
                                |||||||||    |||| ||
                                GGCTCCCAG    TTCT TG
                                     TGA_    A
GAM2129  TIMM22   3'  TCCTGAGTGCCTGCAGAGACAC 51750     CC   G    T
                                TCC  GAG GTCT TAGAGACAC
                                |||  ||| |||| |||||||||
                                AGG  CTC CGGA GTCTCTGTG
                                  A_   A    C
GAM2129  TIP-1    3'  CCCCCGAGGGGCAGAGGCAC   51751         TCTT     A
                                TCCCCGAGGG    TAGAG CAC
                                ||||||||||    ||||| |||
                                GGGGGCTCCC    GTCTC GTG
                                      C___     C
GAM2129  ZNF31    5'  TCCTGGGGGGTCTTTACAGA   51752     CCGA       G
                                TCC    GGGTCTTTA AGA
                                |||    ||||||||| |||
                                AGG    CCCAGAAAT TCT
                                  ACCC        G
GAM2129  LOC146177 5'  TCCTTGAGGGTACTTCTTGTAC 51753     CC     _    AGAG
           AC                     TCC  GAGGGT CTTT    ACAC
                                |||  |||||| ||||    ||||
                                AGG  CTCCCA GAAG    TGTG
                                  AA      T    AACA
GAM2129  LOC148918 5'  TCTTCGGGGGTTCCCTGAGACG 51754    CC  A    _    A    A
           CC                     TC  CG GGGT CTTT GAGAC CC
                                ||  || |||| |||| ||||| ||
                                AG  GC CCCA GGGA CTCTG GG
                                 AA  C    A    _     C
GAM2129  LOC150067 5'  TCCGCGAGGGGACGAGACACC  51755     C      TCTTTA
                                TCC CGAGGG      GAGACACC
                                ||| ||||||      ||||||||
                                AGG GCTCCC      CTCTGTGG
                                  C      CTG___
GAM2129  LOC153146 5'  TCTCCCGAGGGTGAGAG     51756    _        CTTT
                                TC CCCGAGGGT    AGAG
                                || |||||||||    ||||
                                AG GGGCTCCCA    TCTC
                                 A        C___
GAM2129  LOC200230 3'  TCTCCAGGTCAGAGAC      51757    C  GA     TTT
                                TC CC  GGGTC   AGAGAC
                                || ||  |||||   ||||||
                                AG GG  TCCAG   TCTCTG
                                 A  __    ____
GAM2129  LOC200597 3'  TCCCTCAGGATCTTGGGGACAC 51758      CG       TAGA
                                TCCC  AGGGTCTT    GACAC
                                ||||  ||||||||    |||||
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                                AGGG  TCCTAGAA   CTGTG
                                  AG       CCC_
GAM2129  LOC200939 3'  TCCTCCAGGGTCTACA     51759     _ G      TTAGAG
                                TCC CC AGGGTCT     ACA
                                ||| || |||||||     |||
                                AGG GG TCCCAGA     TGT
                                 A  _     _______
GAM2129  LOC203411 5'  GAGGGGGCAGAGACACC     51760      TCTT
                                GAGGG   TAGAGACACC
                                |||||   ||||||||||
                                CTCCC   GTCTCTGTGG
                                  CC__
GAM2129  LOC253594 5'  TCTCCACGGTTAGAGACAC   51761    C   AG   CTT
                                TC CCG  GGT   TAGAGACAC
                                || |||  |||   |||||||||
                                AG GGT  CCA   ATCTCTGTG
                                 A  G_  ___
GAM2129  LOC51072  5'  TCCGCGAGGGGACGAGACACC  51755     C      TCTTTA
                                TCC CGAGGG     GAGACACC
                                ||| ||||||     ||||||||
                                AGG GCTCCC     CTCTGTGG
                                  C     CTG___
GAM2130  CLCN4    3'  TCAAAATAAGGATGTGTCC   51764         AA   CCGA
                                TCAAAATAA  GATG   GTCT
                                |||||||||  ||||   ||||
                                AGTTTTATT  CTAC   CAGG
                                     C_   A___
GAM2130  EVI2A    3'  TCAAAACAAAAGTACACAGT   51765          A  CG
                                TCAAAATAAAAG TGC  AGT
                                |||||||||||| |||  |||
                                AGTTTTGTTTTC ATG  TCA
                                       _  TG
GAM2130  RARB     3'  AAATAAAAGATGCAGT      51766           CG
                                AAATAAAAGATGC  AGT
                                ||||||||||||  |||
                                TTTATTTTCTACG  TCA
                                       __
GAM2130  RARB     3'  AAATAAAAGATGCAGT      51766           CG
                                AAATAAAAGATGC  AGT
                                ||||||||||||  |||
                                TTTATTTTCTACG  TCA
                                       __
GAM2130  RBM3     3'  AAAAAAAAAGATGGAACTGTCT 51767      T       CCGA_
            A                    AAAA AAAAGATG     GTCTA
                                ||||| ||||||||     |||||
                                TTTT TTTTCTAC     CAGAT
                                  T       CTTGA
GAM2130  RP1      3'  CCAAAATAAGAGAACCTGAGTC 51768         A  T  _
            T                    TCAAAATAA AGA GCC GAGTCT
                                |||||||||  ||| ||| ||||||
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                                GGTTTTATT TCT TGG CTCAGA
                                     C  _  A
GAM2130 ATE1     3'  TCAAAATAAAAAATGTCT    51769          GCCGA
                                TCAAAATAAAAGAT    GTCT
                                |||||||||||||    ||||
                                AGTTTTATTTTTTA    CAGA
                                      _____
GAM2130 BIRC8    5'  TCAAAATAAAAGCTGCGGA   51770          A  C
                                TCAAAATAAAAG TGC GA
                                |||||||||||| ||| ||
                                AGTTTTATTTTC ACG CT
                                      G  C
GAM2130 C1orf19  3'  ATAAAAGATGAAGCAGTCT   51771         CCG_
                                ATAAAAGATG   AGTCT
                                |||||||||    |||||
                                TATTTTCTAC   TCAGA
                                      TTCG
GAM2130 FLJ10726 3'  CCAAAATAGAAGACAAGACGTC 51772       A    GCCGA
          T                     TCAAAATA AAGAT    GTCT
                                |||||||| |||||    ||||
                                GGTTTTAT TTCTG    CAGA
                                     C    TTCTG
GAM2130 FLJ21791 3'  TCAAAATAAGAGATGAGT    51773        A   GCC
                                TCAAAATAA AGAT   GAGT
                                ||||||||| ||||   ||||
                                AGTTTTATT TCTA   CTCA
                                     C   ___
GAM2130 HSMPP8   3'  TCAAAACAAGGGCACAAGGTCT 51774       AAGAT  _   _
                                TCAAAATAA    GC CGAG TCT
                                |||||||||    || |||| |||
                                AGTTTTGTT    CG GTTC AGA
                                     CC___  T   C
GAM2130 KIAA0630 3'  AAAATAAAATAGGCAAGTCT  51775       GAT  C
                                AAAATAAAA   GC GAGTCT
                                |||||||||   || ||||||
                                TTTTATTTT   CG TTCAGA
                                     ATC  _
GAM2130 KIAA0841 3'  TCAAAATAAAAATGCCAGT   51776        A    G
                                TCAAAATAAA GATGCC AGT
                                |||||||||| |||||| |||
                                AGTTTTATTT TTACGG TCA
                                      _    _
GAM2130 MGC16309 5'  AAAATAAAAGGCTGCTGGTCT 51777        A_  CGA
                                AAAATAAAAG  TGC   GTCT
                                ||||||||||  |||   ||||
                                TTTTATTTTC  ACG   CAGA
                                      CG   AC_
GAM2130 P115     3'  AAATAAAAGATGTGTGTTCTA 51778         CCGAG
                                AAATAAAAGATG    TCTA
                                ||||||||||||    ||||
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                                TTTATTTTCTAC    AGAT
                                      ACACA
GAM2130 YKT6     3' TCAAAATAAAAATGGCCAGTCT 51779          AT   G
                                TCAAAATAAAAG  GCC AGTCT
                                |||||||||||  ||| |||||
                                AGTTTTATTTTT  CGG TCAGA
                                      AC  _
GAM2130 LOC131870 3' TCAAGACAAGAGCAAGTCT   51780     AATAA   T  C
                                TCAA    AAGA GC GAGTCT
                                ||||    |||| || ||||||
                                AGTT    TTCT CG TTCAGA
                                  CTG__   _ _
GAM2130 LOC150371 3' AAAATAAAATGATGTCCAAA  51781         _   _
                                AAAATAAAA GATG CCGAG
                                ||||||||| |||| |||||
                                TTTTATTTT CTAC GGTTT
                                      A   A
GAM2130 LOC92095  3' TCAAAAAAAAGATGCCA     51782       T
                                TCAAAA AAAAGATGCCG
                                |||||| ||||||||||
                                AGTTTT TTTTCTACGGT
                                   _
GAM2130 LOC92096  3' TCAAAAAGAAGATGCCA     51783       TAA
                                TCAAAA   AAGATGCCG
                                ||||||   |||||||||
                                AGTTTT   TTCTACGGT
                                   TC_
GAM2131 INPP5B   3' TGGAATATGGGGAGAGT     51786    TT     TATAG
                                TG  ATATGG    GGAGAGT
                                ||  ||||||    |||||||
                                AC  TATACC    CCTCTCA
                                 CT    ______
GAM2131 FLJ10508  3' TCTGTTATCATGGTATCTGTGG 51787        _     A___
          G                      TCTGTTAT ATGGTAT    GGG
                                ||||||||| |||||||   |||
                                AGACAATA TACCATA    CCC
                                     G      GACA
GAM2131 MAD4     3' TCTGCTATGTGGTTTGCGGG   51788        A   ATA_
                                TCTGTTAT TGGT    GGG
                                |||||||| ||||   |||
                                AGACGATA ACCA    CCC
                                     C    AACG
GAM2131 MGC15476  3' CTGTTAGGAGTGGGGAGAGT   51789       TAT  TATA
                                CTGTTA   GG    GGGAGAGT
                                ||||||   ||    ||||||||
                                GACAAT   CC    CCCTCTCA
                                   ___  TCAC
GAM2131 LOC153338 3' TCTGTGCTCTTGGTGGGGAGAG 51790      TATA_   ATA
          T                     TCTGT    TGGT   GGGAGAGT
                                |||||    ||||   ||||||||
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                                AGACA    ACCA   CCCTCTCA
                                  CGAGA   C__
GAM2131  LOC153339 5'  TGTTTAAAAAAAGGGAGAGT   51791     A  TG TAT
                                TGTT TA  G   AGGGAGAGT
                                |||| ||  |   |||||||||
                                ACAA AT  T   TCCCTCTCA
                                  _  TT TT_
GAM2131  LOC196761 3'  TCTGTTGAAATAGAGGGAGAGT 51792       ATAT    T
                                TCTGTT    GGTA AGGGAGAGT
                                ||||||    |||| |||||||||
                                AGACAA    TTAT TCCCTCTCA
                                   CT__    C
GAM2131  LOC90378  3'  TCTGTTATGAGGGCTGAGGG   51793       AT_   AT
                                TCTGTTAT   GGT  AGGG
                                ||||||||   |||  ||||
                                AGACAATA   CCG  TCCC
                                     CTC   AC
GAM2132  ARR3      3'  TGATTTATTAGAGTGTTACAGT 51796         A  AA_
                                TGATTTATTA AG   TATAGT
                                |||||||||| ||   ||||||
                                ACTAAATAAT TC   ATGTCA
                                      C  ACA
GAM2132  PPM1D     3'  TGATTTATTAGATGAATATA   51797         AA_
                                TGATTTATTA   GAATATA
                                |||||||||   |||||||
                                ACTAAATAAT   CTTATAT
                                      CTA
GAM2132  DKFZp434B0417 3'  TGATTTATTACGAACAGGTTTG 51798          AA    TA
                                TGATTTATTA  GAATA  GTTTG
                                |||||||||  |||||  |||||
                                ACTAAATAAT  CTTGT  CAAAC
                                      G_    C_
GAM2132  SCGB1D2   3'  TGATTTATTAAAGCAAGACGTT 51799           AATATA
                                TGATTTATTAAAG     GTT
                                ||||||||||||     |||
                                ACTAAATAATTTC     CAA
                                       GTTCTG
GAM2132  LOC257465 3'  TGATTTATAGAGAATATAG    51800        TAA
                                TGATTTAT   AGAATATAG
                                ||||||||   |||||||||
                                ACTAAATA   TCTTATATC
                                     TC_
GAM2133  HAL       3'  AGTCAACTGGTGGAGAGC    51803          __
                                AGTCAATTGGT  AGAGT
                                ||||||||||  |||||
                                TCAGTTGACCA  TCTCG
                                       CC
GAM2133  JAM2      3'  CAAAGCAGAGTTTTATAA    51804     TT
                                CAA  GGTAGAGTTTTATAA
                                |||  ||||||||||||||
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                                GTT  TCGTCTCAAAATATT
                                  __
GAM2133 BRAG     3'  AGTTAATTGGCAGAGAAATTA  51805     C         TT_
                                AGT AATTGGTAGAG   TTA
                                ||| ||||||||||   |||
                                TCA TTAACCGTCTC   AAT
                                  A         TTT
GAM2133 DKFZp547E052 3'  AGTAATTGGTTTACATTTATAA 51806     C      AGAGT
              C                  AGT AATTGGT     TTTATAAC
                                ||| |||||||     ||||||||
                                TCA TTAACCA     AAATATTG
                                  _      AATGT
GAM2133 KIAA1157  3'  AGACAGAAGTGAGTTTTATAA  51807    T  ATT   A
                                AG CA   GGT GAGTTTTATAA
                                || ||   ||| ||||||||||
                                TC GT   TCA CTCAAAATATT
                                 T  CT_  _
GAM2133 LOC92935  3'  GCCTCAAGAGTTTTATAA    51808     AATTGGT
                                GTC      AGAGTTTTATAA
                                |||      ||||||||||||
                                CGG      TCTCAAAATATT
                                  AGT____
GAM2134 ATRX     3'  AATTATTTCAGCACATATAACT 51811      C   T   G
                                AGTTA TTC GCA CATATAACT
                                ||||| ||| ||| |||||||||
                                TTAAT AAG CGT GTATATTGA
                                   A   T   _
GAM2134 ATRX     3'  AATTATTTCAGCACATATAACT 51811      C   T   G
                                AGTTA TTC GCA CATATAACT
                                ||||| ||| ||| |||||||||
                                TTAAT AAG CGT GTATATTGA
                                   A   T   _
GAM2134 IL22RA2   3'  AGTACTTGCATATAAC      51812     T    CTGCA
                                AGT ACTT    GCATATAAC
                                ||| ||||    |||||||||
                                TCA TGAA    CGTATATTG
                                  _   _____
GAM2134 RECK     3'  GTTGCTTACAACATATAA    51813     A  TC
                                GTT CT  TGCAGCATATAA
                                ||| ||  ||||||||||||
                                CAA GA  ATGTTGTATATT
                                  C  __
GAM2134 SELL     5'  AGTTCTTCTGCAGCCCAT    51814      A        A
                                AGTT CTTCTGCAGC TAT
                                |||| |||||||||| |||
                                TCAA GAAGACGTCG GTA
                                  _        G
GAM2134 SWAP70   3'  GTTGCTTCTCAATTATAACTA  51815     A    G   CA
                                GTT CTTCT CAG  TATAACTA
                                ||| ||||| |||  ||||||||
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                                CAA GAAGA GTT  ATATTGAT
                                  C    _  A_
GAM2134  My015    3'  AGTTGTTTTCTGACCACATAAC 51816     AC_    CAG
                T                  AGTT   TTCTG   CATATAACT
                                   ||||   |||||  |||||||||
                                   TCAA   AAGAC   GTGTATTGA
                                     CAA    TG_
GAM2134  NY-REN-60 3'  GTTATTTCTAAGTGCATATAAC 51817     C    CA_
                T                  GTTA TTCTG   GCATATAACT
                                   |||| |||||   ||||||||||
                                   CAAT AAGAT   CGTATATTGA
                                     A    TCA
GAM2134  TOB2     3'  AGTTCCTTCTGCAGTGTTTTCC 51818     A       CATATAA
                T                  AGTT CTTCTGCAG      CT
                                   |||| |||||||||      ||
                                   TCAA GAAGACGTC      GA
                                     G       ACAAAAG
GAM2134  LOC153339 5'  GTTGTTTCTGCAGAAATAACTA 51819     AC       CAT
                                   GTT  TTCTGCAG   ATAACTA
                                   |||  ||||||||   |||||||
                                   CAA  AAGACGTC   TATTGAT
                                     CA       TT_
GAM2135  MAT1A    3'  TCGAGTGTGAGCCAAGTTAGA  51822      ATATAC
                                   TCGA     GGGCCAAGTTAGA
                                   ||||     ||||||||||||
                                   AGCT     CTCGGTTCAATCT
                                     CACA__
GAM2135  MEF2C    3'  GAATATGGGCAAGTTAG     51823       AC    C
                                   GAATAT  GGGC AAGTTAG
                                   ||||||  |||| |||||||
                                   CTTATA  CCCG TTCAATC

                                      __   _
GAM2135  KIAA0355  5'  TCAATATACCCAAAAAAGTTAG 51824    G      GGG   ____
                AA                   C AATATAC   CCA    AGTTAGAA
                                   | |||||||   |||    ||||||||
                                   G TTATATG   GGT    TCAATCTT
                                    _      ___   TTTT
GAM2135  LOC200169 3'  GAATACACTCCAAGTT      51825        GGG
                                   GAATATAC   CCAAGTT
                                   ||||||||   |||||||
                                   CTTATGTG   GGTTCAA
                                        A__
GAM2136  AGRN     3'  TGGGATGGGGGTGGGGAAGGG  51829           T    T
                                   TGGGATGGGGGTG GGGA GGGG
                                   |||||||||||| |||| ||||
                                   ACCCTACCCCCAC CCCT TCCC

                                      _   _
GAM2136  AGRN     3'  TGGGGCTGGGGGTGGGGATGGG 51828        _____          III
                ATGGGGGC                TGGGGGTG    TGGGATGGGGG   C
                                   ||||||||    ||||||||||   |
```

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                                ACCCCCAC   ACCCTACCCCC  G
                                    CCCT        III
GAM2136 AK1     3' TGAGGTGGGGGTGAGGGGG   51830     A      T  AT
                                TGGG TGGGGGTG GGG  GG
                                |||| |||||||| |||  ||
                                ACTC ACCCCCAC CCC  CC
                                  C       T  __
GAM2136 ARVCF   3' TAGGATGGGGGGAGTGGGGTGG 51831          T_   A
           GGG                    TGGGATGGGGG  GTGGG TGGGGG
                                |||||||||||  ||||| ||||||
                                ATCCTACCCCC  CACCC ACCCCC
                                      CT    C
GAM2136 BAT1    3' TGGGGTGGGGGGCTGTCAGGGG  51832     A     G  GGAT
                                TGGG TGGGGGT TG   GGGG
                                |||| ||||||| ||   ||||
                                ACCC ACCCCCG AC   CCCC
                                  C      _ AGT_
GAM2136 BAT1    3' TGGGGTGGGGGGCTGTCAGGGG  51832     A     G  GGAT
                                TGGG TGGGGGT TG   GGGG
                                |||| ||||||| ||   ||||
                                ACCC ACCCCCG AC   CCCC
                                  C      _ AGT_
GAM2136 BSN     3' TGGGGTGGGGAGGGGTGGGGG  51833     A    TGT  A
                                TGGG TGGGGG   GGG TGGGGG
                                |||| ||||||   ||| ||||||
                                ACCC ACCCCT   CCC ACCCCC
                                  C     ____  C
GAM2136 C1QG    3' TGGGGAGGGGGTGCAGTGGGGG 51834     AT     TG GA
                                TGGG  GGGGGTG  G  TGGGGG
                                ||||  |||||||  |  ||||||
                                ACCC  CCCCCAC  C  ACCCCC
                                  CT      GT __
GAM2136 C5R1    3' TGGGGGGGGGTGGGGGG    51835     AT    T   AT
                                TGGG  GGGGG GTGGG  GGG
                                ||||  ||||| |||||  |||
                                ACCC  CCCCC CACCC  CCC
                                   __    _   __
GAM2136 DCTN1   5' GGGGTGGGGGCAGTGATGGGGG 51836     A      TGG
                                GGG TGGGGGTG   GATGGGGG
                                ||| ||||||||   ||||||||
                                CCC ACCCCCGT   CTACCCCC
                                  C       CA_
GAM2136 EMX2    5' TGGGGTGGGGGTGGGGGTGGGG 51837     A      T  A
           G                    TGGG TGGGGGTG GGG TGGGGG
                                |||| |||||||| ||| ||||||
                                ACCC ACCCCCAC CCC ACCCCC
                                  C       _  C
GAM2136 EMX2    5' TGGGGGTGGGGGTGGGG    51838        T  A
                                TGGGGGTG GGG TGGGG
                                |||||||| ||| |||||
```

```
                                ACCCCCAC CCC ACCCC
                                     _  C
GAM2136  FGD1    3'  TGGGCAACTAGAGTGTGGGGTG 51839     ATG__       A
              GGGG                   TGGG    GGGGTGTGGG TGGGGG
                                |||||    |||||||||| ||||||
                                ACCC    TCTCACACCC ACCCCC
                                  GTTGA        C
GAM2136  FMNL    5'  GGCGGTGGCGGGGGGTGGGGG  51840    A  G   T  A
                                GG TGG GGTG GGG TGGGGG
                                || ||| |||| ||| ||||||
                                CC GCC CCGC CCC ACCCCC
                                 _  A   _  C
GAM2136  GCGR    3'  GGGGTGGGGGGGTAGGTGGGGG  51841    A    T   A
                                GGG TGGGGG GTGGG TGGGGG
                                ||| |||||| ||||| ||||||
                                CCC ACCCCC CATCC ACCCCC
                                 C    _    _
GAM2136  HLCS    3'  TGGGGTGGGGGGTGGGGACAGG  51842     A      T
                                TGGG TGGGGGTG GGGATGGG
                                |||| |||||||| ||||||||
                                ACCC ACCCCCAC CCCTGTCC
                                  C      _
GAM2136  HNF3B   3'  TGGGGGTGTTGGGGTGGGG   51843        _  A
                                TGGGGGTGT GGG TGGGG
                                ||||||||| ||| |||||
                                ACCCCCACA CCC ACCCC
                                     A  C
GAM2136  HOXB5   5'  TGGGGGGGGGGGTTGGGGGGGTG 51844     AT    GT__  A
              GGGG                   TGGG  GGGGGT   GGG TGGGGG
                                ||||  ||||||   ||| ||||||
                                ACCC  CCCCCA   CCC ACCCCC
                                  CC    ACCC  C
GAM2136  HOXC4   3'  TGGGGGCATGGGGTGGGG   51845          A
                                TGGGGGTGTGGG TGGGG
                                |||||||||||| |||||
                                ACCCCCGTACCC ACCCC
                                      C
GAM2136  KPNB1   5'  GGGATGGGGGTTGGGG     51846         GTGGGA
                                GGGATGGGGGT    TGGGG
                                ||||||||||     |||||
                                CCCTACCCCCA    ACCCC
                                     _____
GAM2136  LIF     3'  TGGGTGGGAGTGGGATGGGGG  51847    A     GT
                                TGGG TGGGGGT  GGGATGGGGG
                                |||| |||||||  ||||||||||
                                ACCC ACCCTCA  CCCTACCCCC
                                  _     __
GAM2136  MECP2   3'  TGGGAGTGGGGGAGGTGGGGG  51848     _    TGT  A
                                TGGGA TGGGGG   GGG TGGGGG
                                ||||| ||||||   ||| ||||||
```

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                                ACCCT ACCCCC   TCC ACCCCC
                                  C     ___  _
GAM2136 MNT     3' TGGGGGTGGGACCCGGGATGGG 51849     ATG   TG
             GG                   TGGG  GGGG  TGGGATGGGGG
                                  ||||  ||||  ||||||||||
                                  ACCC  CCCT  GCCCTACCCCC
                                    CCA   GG
GAM2136 MOCS2   3' TGAGGTGGGGTTGGTGGGG   51850     A    GTGTG  A
                                  TGGG TGGGG    GG TGGGG
                                  |||| |||||    || |||||
                                  ACTC ACCCC    CC ACCCC
                                    C    AA___  _
GAM2136 MSN     3' GGGGTGGGGGTGTGGAAGGG   51851     A          T
                                  GGG TGGGGGTGTGGGA GGG
                                  ||| ||||||||||||| |||
                                  CCC ACCCCCACACCTT CCC
                                    C          _
GAM2136 MSX2    3' TGGTGGGGCGGTGGGG      51852     _  T   GA
                                  TGG GGG GTGG  TGGGG
                                  ||| ||| ||||  |||||
                                  ACC CCC CGCC  ACCCC
                                    A  _   __
GAM2136 PAK4    3' TGGGGCGGGGGTGACCCGGGGG 51853      A       TGGGA
                                  TGGG TGGGGGTG    TGGGGG
                                  |||| ||||||||    ||||||
                                  ACCC GCCCCCAC    GCCCCC
                                    C       TGG__
GAM2136 PGM1    5' TGGGGTGAGGGCACGGCGGGTG 51854      A      ___    A
             GGGG                    TGGG TGGGGGT   GTGGG TGGGGG
                                  |||| |||||||   ||||| ||||||
                                  ACCC ACTCCCG   CGCCC ACCCCC
                                    C      TGC   _
GAM2136 PIK3R3  3' TGGGTGTGGGGCATGATGGGGG 51855      A _      GG
                                  TGGG TG GGGGTGT  GATGGGGG
                                  |||| || |||||||  ||||||||
                                  ACCC AC CCCCGTA  CTACCCCC
                                    _ A      __
GAM2136 PRKACA  3' TGGGATGGGGGGTGTGGGTGGGG 51856              A
             G                     TGGGATGGGGGGTGTGGG TGGGGG
                                  ||||||||||||||||| ||||||
                                  ACCCTACCCCCACACCC ACCCCC
                                                    _
GAM2136 RING1   3' TGGGCTGGGGGGTACTGGGG   51857      A       TGGGA
                                  TGGG TGGGGGTG    TGGGG
                                  |||| ||||||||    |||||
                                  ACCC ACCCCCAT    ACCCC
                                    G       G____
GAM2136 SLC2A4  3' TGGGGAGGAAAGGGGATGGGGG 51858      AT    TGT
                                  TGGG  GGGGG   GGGATGGGGG
                                  ||||  |||||   ||||||||||
```

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                                ACCC  CTCCT   CCCTACCCCC
                                  __    TTC
GAM2136  SOD3     3'  TGGGTGGGGAGGGGTGGGG   51859     A     TGT   A
                                TGGG TGGGGG   GGG TGGGG
                                |||| ||||||   ||| |||||
                                ACCC ACCCCT   CCC ACCCC
                                  _     ____  C
GAM2136  SPTBN4   3'  TGGGGTGGGGGGTGGTGAGTGGG 51860      A      _   A
                                TGGG TGGGGGTG TGGG TGGG
                                |||| |||||||| |||| ||||
                                ACCC ACCCCCAC ACTC ACCC
                                  C       C   _
GAM2136  ZFP36L1  3'  GGGGTGGGGGGGGGTGGGG    51861     A     TGT   A
                                GGG TGGGGG   GGG TGGGG
                                ||| ||||||   ||| |||||
                                CCC ACCCCC   CCC ACCCC
                                  C     ____  _
GAM2136  20D7-FC4 3'  TGGGGTGAGGGAGAGGATGGGG 51862      A     TGT
           G                     TGGG TGGGGG   GGGATGGGGG
                                |||| ||||||   ||||||||||
                                ACCC ACTCCC   TCCTACCCCC
                                  C     TC_
GAM2136  ACAS2L   3'  TGGGTCATGTGTGGGGTGGGGG 51863      ATGGGG      A
                                TGGG     GTGTGGG TGGGGG
                                ||||     ||||||| ||||||
                                ACCC     CACACCC ACCCCC
                                  AGTA__      C
GAM2136  BCL2L1   3'  TGGAACAAGTGTGGGGTGGGGG 51864       GG       A
                                TGGGAT  GGGTGTGGG TGGGGG
                                ||||||  ||||||||| ||||||
                                ACCTTG  TTCACACCC ACCCCC
                                  __        C
GAM2136  CDH22    3'  TGGGGGAAACCTGGGGTGGGGG 51865      AT   GG G    A
                                TGGG  GGG  T TGGG TGGGGG
                                ||||  |||  | |||| ||||||
                                ACCC  CCT  G ACCC ACCCCC
                                  __   TT G    C
GAM2136  CXYorf1  3'  TGGTGGTGGGGGCGGTGGGGG  51866     GA_     GTG  A
                                TGG   TGGGGGT   GG TGGGGG
                                |||   |||||||   || ||||||
                                ACC   ACCCCCG   CC ACCCCC
                                  ACC      ____ _
GAM2136  DKFZp547J036 3'  TGGGGGGGGGGGTGTGTGGGG   51867      AT       GGA
                                TGGG  GGGGGTGTG   TGGGG
                                ||||  |||||||||   |||||
                                ACCC  CCCCCACAC   ACCCC
                                  CC        ____
GAM2136  EPB41L1  3'  GGGTGAAGGGTGTGGGGTGGGG 51868     A  _       A
           G                     GGG TGG GGGTGTGGG TGGGGG
                                ||| ||| ||||||||| ||||||
```

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                                CCC ACT CCCACACCC ACCCCC
                                  _  T       C
GAM2136  FLJ10305  3'  TGGGGTGGGGGGTGGGGTG    51869     A      T   A
                                TGGG TGGGGGTG GGG TG
                                |||| |||||||| ||| ||
                                ACCC ACCCCCAC CCC AC
                                  C       _  _
GAM2136  FLJ10748  3'  TGGAGATGGGGGGTGGGGG    51870    _       TGGGAT
                                TGG GATGGGGGGTG     GGGG
                                ||| ||||||||||      ||||
                                ACC CTACCCCCAC      CCCC
                                  T        _______
GAM2136  FLJ12816  3'  TGGGATGGGGGTGAAGTGGGGG  51871         G  T   A
                                TGGGATGGGG TG GGG TGGGGG
                                |||||||||| || ||| ||||||
                                ACCCTACCCC AC TTC ACCCCC
                                          _  _  _
GAM2136  FLJ14708  3'  TGGGACGGGGGCCCATGGGGG  51872           G GGG
                                TGGGATGGGGGGT T   ATGGGGG
                                |||||||||||| |   |||||||
                                ACCCTGCCCCCG G   TACCCCC
                                       G ___
GAM2136  FLJ14950  3'  TGGGTGGGGGTGGGGTGGGGG  51874      A      T   A
                                TGGG TGGGGGTG GGG TGGGGG
                                |||| |||||||| ||| ||||||
                                ACCC ACCCCCAC CCC ACCCCC
                                  _       _  _
GAM2136  FLJ14950  3'  TGGGGTGGGGGGTGGGTGTGGG  51873      A      T  GA
                                TGGG TGGGGGTG GG  TGGG
                                |||| |||||||| ||  ||||
                                ACCC ACCCCCAC CC  ACCC
                                  C       _  AC
GAM2136  FLJ30213  5'  GGGATGGGGGGTGGGTGGGGG   51875          GT   A
                                GGGATGGGGGGT  GGG TGGGGG
                                ||||||||||  ||| ||||||
                                CCCTACCCCCCA  CCC ACCCCC
                                          __  _
GAM2136  HCNP      3'  GGGGTGGGGAGGGGGGATGGGG 51876     A     TGT
            G                    GGG TGGGGG   GGGATGGGGG
                                ||| ||||||   ||||||||||
                                CCC ACCCCT   CCCTACCCCC
                                  C     CCC
GAM2136  HXCP2     3'  GGTGGGGGTCGGGGGGATGGGGG  51877    A    G  T
                                GG TGGGG TG GGGATGGGGG
                                || ||||| || ||||||||||
                                CC ACCCC GC CCCTACCCCC
                                  _    A  C
GAM2136  IMP13     3'  AGGGGTGGATGGGATGGGG   51878        __
                                GGGGGGTG  TGGGATGGGG
                                |||||||  ||||||||||
```

```
                                TCCCCAC  ACCCTACCCC
                                   CT
GAM2136  KIAA0227  3'  TGGGAATGGGGGGTGGGGGTGGG 51879      _      T  A
             GG                    TGGGA TGGGGGTG GGG TGGGGG
                                   ||||| |||||||| ||| ||||||
                                   ACCCT ACCCCCAC CCC ACCCCC
                                     T       _  C
GAM2136  KIAA0418  3'  TGGGGTAGGGTAGGGGTGGGGG 51880     ATG     T  A
                                   TGGG   GGGGTG GGG TGGGGG
                                   ||||   |||||| ||| ||||||
                                   ACCC   TCCCAT CCC ACCCCC
                                     CA_     C  _
GAM2136  KIAA0418  3'  TGGGATGGGGTGTGGTGGGG   51881          G    GA
                                   TGGGATGGGG TGTGG  TGGGG
                                   |||||||||| |||||  |||||
                                   ACCCTACCCC ACACC  ACCCC

                                        _    __
GAM2136  KIAA0563  5'  TGGGGTAGGGTGGGATGGGGG  51882      A    GTG
                                   TGGG TGGGG   TGGGATGGGGG
                                   |||| |||||   ||||||||||
                                   ACCC ATCCC   ACCCTACCCCC
                                     C    ___
GAM2136  KIAA1205  3'  GGGATGGGCAGTGGGTGGGGG  51883        GGT    A
                                   GGGATGGG   GTGGG TGGGGG
                                   ||||||||   ||||| ||||||
                                   CCCTACCC   CACCC ACCCCC
                                        GT_    _
GAM2136  KIAA1266  3'  TGGGCTGGAGGGGTGGGG    51884      A     TGTG  A
                                   TGGG TGGGGG    GG TGGGG
                                   |||| ||||||    || |||||
                                   ACCC ACCTCC    CC ACCCC
                                     G     _____  _
GAM2136  KIAA1328  3'  GATGGGGGGTGGGGG       51885         T    AT
                                   GATGGGGG GTGGG  GG
                                   |||||||| |||||  ||
                                   CTACCCCC CACCC  CC

                                        _    __
GAM2136  KIAA1453  3'  TGGGGTGGGGGCTGAAGGGGG  51886      A      GTG   T
                                   TGGG TGGGGGT   GGA GGGGG
                                   |||| |||||||   ||| |||||
                                   ACCC ACCCCCG   CTT CCCCC
                                     C      A__   _
GAM2136  KIAA1465  3'  TGGGGTGGGGGGTGGGAGG    51887      A      GT    T
                                   TGGG TGGGGGT  GGGA GG
                                   |||| |||||||  |||| ||
                                   ACCC ACCCCCA  CCCT CC
                                     C      __    _
GAM2136  KIAA1817  3'  GGGGTGGGGGGGCGTGGGG    51888     A     T   GGA
                                   GGG TGGGGG GTG   TGGGG
                                   ||| |||||| |||   |||||
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                                CCC ACCCCC CGC   ACCCC
                                  C     _  ___
GAM2136 KIAA1910 3' TGGGGGTGGGGTAGAGGGTGGG 51889     ATG     T   A
             GG                    TGGG   GGGGTG GGG TGGGGG
                                   ||||   |||||| ||| ||||||
                                   ACCC   CCCCAT TCC ACCCCC
                                     CCA     C   C
GAM2136 MGC10924 3' GGGGTGGGGGGTGGGGGTGGGGG 51890     A       T   A
                                   GGG TGGGGGTG GGG TGGGGG
                                   ||| |||||||| ||| ||||||
                                   CCC ACCCCCAC CCC ACCCCC
                                     C       _   C
GAM2136 MGC15631 3' TGGGGTGGGAGACGGGATGGGG 51891     A     TGT
             G                      TGGG TGGGGG   GGGATGGGGG
                                   |||| ||||||   ||||||||||
                                   ACCC ACCCTC   CCCTACCCCC
                                     C     TG_
GAM2136 MGC8407  3' TGGGATGTGGGGGGCATGGGGG  51892       G   TGT  G
                                   TGGGATG GGG   GG ATGGGGG
                                   ||||||| |||   || |||||||
                                   ACCCTAC CCC   CC TACCCCC
                                       A   ___  G
GAM2136 MISS     3' TGGGGTGGGGGGTGGCTACAGGG 51893      A       TGGG
                                   TGGG TGGGGGTG    ATGGGG
                                   |||| ||||||||    ||||||
                                   ACCC ACCCCCAC    TGTCCC
                                     C       CGA_
GAM2136 MSI2     3' TGGGATGGGGAGTGAGGCTGGT 51894          _   T  GA__
             GGGGG                    TGGGATGGGG GTG GG    TGGGGG
                                   |||||||||| ||| ||    ||||||
                                   ACCCTACCCC CAC CC    ACCCCC
                                         T   T  GACC
GAM2136 PP1628   5' TGGGTGGGGGGTGTAGGGGG   51895      A         AT
                                   TGGG TGGGGGGTGTGGG  GGG
                                   |||| ||||||||||||  |||
                                   ACCC ACCCCCCACATCC  CCC
                                     _          __
GAM2136 PP5395   3' TGGTGTGGGGGGTGTGGAACAGG 51896     GA
                                   TGG  TGGGGGGTGTGGGATGGG
                                   |||  ||||||||||||||||||
                                   ACC  ACCCCCCACACCTTGTCC
                                     AC
GAM2136 RNF40    3' TGGGGTGGGGAGGAGATGGGGG 51897      A     TGT
                                   TGGG TGGGGG   GGGATGGGGG
                                   |||| ||||||   ||||||||||
                                   ACCC ACCCCT   CTCTACCCCC
                                     C     C__
GAM2136 SARM     3' GGAGGTGGGCCATGAGGGTGGG 51898     T _   ___ T   A
             GG                     GGA GG GGGT   G GGG TGGGGG
                                   ||| || ||||   | ||| ||||||
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                                  CCT CC CCCG   C CCC ACCCCC
                                    _ A    GTA T  _
GAM2136 SDC3     3'  TGGGATGTGGGTGAGGGGTGGG 51899        G    T  A
                GG                   TGGGATG GGGTG GGG TGGGGG
                                     ||||||| ||||| ||| ||||||
                                     ACCCTAC CCCAC CCC ACCCCC
                                        A    T  C
GAM2136 SHAPY    3'  TGGGGTAGGAGTGAGGGTGGGG 51900      A       T  A
                G                    TGGG TGGGGGTG GGG TGGGGG
                                     |||| |||||||| ||| ||||||
                                     ACCC ATCCTCAC CCC ACCCCC
                                       C       T  _
GAM2136 STRAIT11499 3'  TGGGGTGGGGGGTGGGGACGGG  51901      A       T
                                     TGGG TGGGGGTG GGGATGGG
                                     |||| |||||||| ||||||||
                                     ACCC ACCCCCAC CCCTGCCC
                                       C       _
GAM2136 TEB4     3'  AGGATGTGGGTGTGGGGTGGGG 51902        G       A
                G                    GGGATG GGGTGTGGG TGGGGG
                                     |||||| ||||||||| ||||||
                                     TCCTAC CCCACACCC ACCCCC
                                        A        C
GAM2136 TED      3'  TGGGGTGGGGGGTAGGTTGGGGG 51903      A       T  GA
                                     TGGG TGGGGGTG GG  TGGGGG
                                     |||| |||||||| ||  ||||||
                                     ACCC ACCCCCAT CC  ACCCCC
                                       C       _ A_
GAM2136 TRIP10   3'  TGGGTTGGGGGGTGGAGGGGG   51904      A       T  AT
                                     TGGG TGGGGGTG GGG  GGGG
                                     |||| |||||||| |||  ||||
                                     ACCC ACCCCCAC CTC  CCCC
                                       A       _  __
GAM2136 UBP1     3'  TAGGATGGTGGGGGGTGGGG    51906        G  TGT   A
                                     TGGGATGG GG   GGG TGGGG
                                     ||||||||  ||   ||| |||||
                                     ATCCTACC CC   CCC ACCCC
                                        A ____  _
GAM2136 UBP1     3'  GGGGTGGGGGGGTTAGGGTGGGG 51905     A     TG    A
                G                    GGG TGGGGG  TGGG TGGGGG
                                     ||| ||||||  |||| ||||||
                                     CCC ACCCCC  ATCC ACCCCC
                                       C     CA   C
GAM2136 ZIN      3'  TGGGAGGATGGGGGGATGGGGG  51907      TGG    T
                                     TGGGA   GGGTG GGGATGGGGG
                                     |||||   ||||| ||||||||||
                                     ACCCT   CCTAC CCCTACCCCC
                                        ____    C
GAM2136 LOC146512 3'  TGGGTGGGGGGTGTGGGATG    51908      A
                                     TGGG TGGGGGGTGTGGGATG
                                     |||| ||||||||||||||
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                                ACCC ACCCCCACACCCTAC
                                   _
GAM2136  LOC146562 3'  TGGGAGTGGGGTCGGGTGGGGG 51909      TG    G   A
                                TGGGA  GGGGT TGGG TGGGGG
                                |||||  ||||| |||| ||||||
                                ACCCT  CCCCA GCCC ACCCCC
                                   CA    _   _
GAM2136  LOC153525 5'  GGGGTGGGGGTGGGGGTGGGGG 51890    A      T  A
                                GGG TGGGGGTG GGG TGGGGG
                                ||| |||||||| ||| ||||||
                                CCC ACCCCCAC CCC ACCCCC
                                  C       _  C
GAM2136  LOC155032 3'  TGGGATGGGGCTGGAAGGGGG  51910         GTG    T
                                TGGGATGGGG   TGGGA GGGGG
                                ||||||||||   ||||| |||||
                                ACCCTACCCC   ACCTT CCCCC
                                      G__    _
GAM2136  LOC162333 5'  TGGGATGTGCTATTGGGGATGG 51911       GGGG__  T
            GGG                   TGGGATG     TG GGGATGGGGG
                                |||||||     || ||||||||||
                                ACCCTAC     AC CCCTACCCCC
                                    ACGATA  _
GAM2136  LOC200093 3'  TGGTGGTGGGGGGCGGTGGGGG  51866    GA_     GTG  A
                                TGG   TGGGGGT   GG TGGGGG
                                |||   |||||||   || ||||||
                                ACC   ACCCCCG   CC ACCCCC
                                  ACC      ___  _
GAM2136  LOC201220 5'  TGGGGTAGGGTGGGATGGGGG  51882     A    GTG
                                TGGG TGGGG   TGGGATGGGGG
                                |||| |||||   ||||||||||
                                ACCC ATCCC   ACCCTACCCCC
                                  C    ___
GAM2136  LOC220058 5'  TGGGGTGGGGGGTGGCTTGGG  51912     A     T   GA
                                TGGG TGGGGG GTGG  TGGG
                                |||| |||||| ||||  ||||
                                ACCC ACCCCC CACC  ACCC
                                  C     _   GA
GAM2136  LOC221337 3'  GGGATGGGTGGGGGGTGGGGG   51913       _ TGT   A
                                GGGATGGG GG   GGG TGGGGG
                                |||||||| ||   ||| ||||||
                                CCCTACCC CC   CCC ACCCCC
                                    A ___   _
GAM2136  LOC221337 3'  TGGGTGGGGGGTGGGG       51914      A       TGGGAT
                                TGGG TGGGGGTG     GGG
                                |||| ||||||||     |||
                                ACCC ACCCCCAC     CCC
                                  _      _______
GAM2136  LOC254057 5'  TGGGAGGGGGGTGACGGGG    51915       T     GTGG
                                TGGGA GGGGGGT    GATGGGG
                                ||||| ||||||    |||||||
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                                ACCCT CCCCCA   CTGCCCC
                                  _    ____
GAM2136 LOC254873 3' TGGGGAGGAAAGGGGATGGGGG 51858     AT    TGT
                                TGGG GGGGG  GGGATGGGGG
                                |||| |||||  ||||||||||
                                ACCC CTCCT  CCCTACCCCC
                                  __    TTC
GAM2136 LOC57333 3' GGGTTGGGGGGTGTGACAGGG  51916    A      GG
                                GGG TGGGGGTGT GATGGGG
                                ||| ||||||||| |||||||
                                CCC ACCCCCACA CTGTCCC
                                  A      __
GAM2136 LOC91040 3' TGGTGGTGGGGGGCGGTGGGGG 51866    GA_     GTG A
                                TGG  TGGGGGT  GG TGGGGG
                                |||  ||||||| || ||||||
                                ACC  ACCCCCG  CC ACCCCC
                                  ACC     ___ _
GAM2136 LOC92340 3' TGGGATGAGGGGTGGGGG   51917         T    AT
                                TGGGATGGGGG GTGGG GG
                                |||||||||| ||||| ||
                                ACCCTACTCCC CACCC CC
                                      _   __
GAM2137 COG5    3' TGAATGGGTTAGCACAAAGTG 51920      ACATA  G
                                TGAATG    GGC ACAAAGTG
                                ||||||    ||| ||||||||
                                ACTTAC    TCG TGTTTCAC
                                   CCAA_  _
GAM2137 FBXL5   3' TGATGACATAGGGACAGTG   51921    A      C   AA
                                TGA TGACATAGG GACA GTG
                                ||| ||||||||| |||| |||
                                ACT ACTGTATCC CTGT CAC
                                  _      _  __
GAM2137 FBXL5   3' TGATGACATAGGGACAGTG   51921    A      C   AA
                                TGA TGACATAGG GACA GTG
                                ||| ||||||||| |||| |||
                                ACT ACTGTATCC CTGT CAC
                                  _      _  __
GAM2137 HGF     3' AATGACACAAAATAAAGTG   51922         CGAC
                                AATGACATAGG   AAAGTG
                                ||||||||||   ||||||
                                TTACTGTGTTT   TTTCAC
                                      TA__
GAM2137 NARS    3' TGAATAACTTGGATAAAGTGA 51923       ATA CGAC
                                TGAATGAC  GG   AAAGTGA
                                ||||||||  ||   |||||||
                                ACTTATTG  CC   TTTCACT
                                    AA_ TA__
GAM2137 NFE2L1  3' TGAATGACATGCGTGATGTTG 51924        AG  ACAAAG
                                TGAATGACAT GCG    TG
                                |||||||||| |||    ||
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                                ACTTACTGTA  CGC     AC
                                      __  ACTACA
GAM2137  TIE      3'  TGAATGACAGGCCGGGAGTG   51925         TA   GACAA
                                TGAATGACA  GGC    AGTG
                                |||||||||  |||    ||||
                                ACTTACTGT  CCG    TCAC
                                      __  GCCC_
GAM2137  TLR4     3'  GAATGACATCGAGTGACAAAGT 51926         A_  C
              GA                  GAATGACAT  GG GACAAAGTGA
                                |||||||||  || ||||||||||
                                CTTACTGTA  TC CTGTTTCACT
                                      GC  A
GAM2137  TLR4     3'  GAATGACATCGAGTGACAAAGT 51926         A_  C
              GA                  GAATGACAT  GG GACAAAGTGA
                                |||||||||  || ||||||||||
                                CTTACTGTA  TC CTGTTTCACT
                                      GC  A
GAM2137  TLR4     3'  GAATGACATCGAGTGACAAAGT 51926         A_  C
              GA                  GAATGACAT  GG GACAAAGTGA
                                |||||||||  || ||||||||||
                                CTTACTGTA  TC CTGTTTCACT
                                      GC  A
GAM2137  ATP6V0A1  3'  TAAATGACTCACAGACAGGGTG 51927         ATAG  _   AA
              A                   TGAATGAC   GC GACA  GTGA
                                ||||||||   || ||||  ||||
                                ATTTACTG   TG CTGT  CACT
                                     AG__  T   CC
GAM2137  DDR2     3'  GAGTGGCATAGGCATGGGTGA  51928    A  A      ACAAA
                                GA TG CATAGGCG    GTGA
                                || || ||||||||    ||||
                                CT AC GTATCCGT    CACT
                                 C  C      ACC__
GAM2137  DKFZP564F013 3'  GAATGGTAAGAGCAAAGTGA   51929      ACA   CGA
                                GAATG   TAGG   CAAAGTGA
                                |||||   ||||   ||||||||
                                CTTAC   ATTC   GTTTCACT
                                   C__   TC_
GAM2137  DKFZP727C091 3'  TGAAGGAAACATGGCAAAGTGA 51930      T__    A    CAA
                                TGAA   GACAT GGCGA   AGTGA
                                ||||   ||||| |||||   |||||
                                ACTT   TTGTA CCGTT   TCACT
                                   CCT    _   ___
GAM2137  KIAA0836  3'  TGATGGGCAAGGCAAAGTGA   51931     CATA    __
                                TGA    GGCGA  CAAAGTGA
                                |||    |||||  ||||||||
                                ACT    CCGTT  GTTTCACT
                                  AC__     CC
GAM2137  KIAA1240  3'  GATGTAAACGGTGGCAAAGTGA 51932     CA     A___
                                GA  TAGGCG    CAAAGTGA
                                ||  ||||||    ||||||||
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                                CT  ATTTGC    GTTTCACT
                                 AC     CACC
GAM2137  TONDU     5'  TGAATGACACAGGTGACA    51933           C
                                TGAATGACATAGG GACA
                                |||||||||||| ||||
                                ACTTACTGTGTCC CTGT
                                       A
GAM2137  LOC149657 3'  TGACACAGGCAAGGTGA     51934           CAAA
                                TGACATAGGCGA    GTGA
                                ||||||||||||    ||||
                                ACTGTGTCCGTT    CACT
                                       C___
GAM2137  LOC153811 3'  TGGGTGACATAGATATTGTGA  51935    AA       CGACAAA
                                TG  TGACATAGG      GTGA
                                ||  |||||||||      ||||
                                AC  ACTGTATCT      CACT
                                 CC        ATAA___
GAM2137  LOC157653 5'  GACGTAGGCGACAAAAAGA    51936    A         T
                                GAC TAGGCGACAAAG GA
                                ||| |||||||||||| ||
                                CTG ATCCGCTGTTTT CT
                                  C          T
GAM2137  LOC221143 3'  TGAATATGAGGACAAAGTG    51937       ACATA  C
                                TGAATG     GG GACAAAGTG
                                ||||||     || |||||||||
                                ACTTAT     TC CTGTTTCAC
                                    AC___  _
GAM2138  CKTSF1B1  3'  TAGTGTTGAGGAAATTCT    51940           T
                                TAGTGTTGAGG AATTCT
                                |||||||||| ||||||
                                ATCACAACTCC TTAAGA
                                       T
GAM2138  MME       3'  GTGACTTATAATTCTAGAA    51941     TTGAG
                                GTG    GTAATTCTAGAA
                                |||    ||||||||||||
                                CAC    TATTAAGATCTT
                                  TGAA_
GAM2138  MME       3'  GTGACTTATAATTCTAGAA    51941     TTGAG
                                GTG    GTAATTCTAGAA
                                |||    ||||||||||||
                                CAC    TATTAAGATCTT
                                  TGAA_
GAM2138  MME       3'  GTGACTTATAATTCTAGAA    51941     TTGAG
                                GTG    GTAATTCTAGAA
                                |||    ||||||||||||
                                CAC    TATTAAGATCTT
                                  TGAA_
GAM2138  MME       3'  GTGACTTATAATTCTAGAA    51941     TTGAG
                                GTG    GTAATTCTAGAA
                                |||    ||||||||||||
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                                CAC    TATTAAGATCTT
                                  TGAA_
GAM2138 DRIM    3' TAGTGTTGTGTGCCTAG    51942       AG  AAT
                                TAGTGTTG GT   TCTAG
                                |||||||| ||   |||||
                                ATCACAAC CA   GGATC
                                    A_ C__
GAM2138 GPS2    5' GTGTTGGGGAATTCCAG    51943      A  T
                                GTGTTG GG AATTCTAG
                                |||||| || ||||||||
                                CACAAC CC TTAAGGTC
                                   _ C
GAM2138 KIAA1441 3' TAGTGTTGGGCTCAGAAA   51944       A   AAT  T
                                TAGTGTTG GGT   TC AGAAA
                                |||||||| |||   || |||||
                                ATCACAAC CCG   AG TCTTT
                                    _  ___  _
GAM2138 KIAA1889 3' GTGTTTGGCACTAGAAA    51945     GA    ATT
                                GTGTT  GGTA   CTAGAAA
                                |||||  ||||   |||||||
                                CACAA  CCGT   GATCTTT
                                  A_   ___
GAM2138 POT1    3' TAGGTTGAGGTGAAATAGA   51946    T      AATTC
                                TAG GTTGAGGT    TAGA
                                ||| ||||||||    ||||
                                ATC CAACTCCA    ATCT
                                  _       CTTT_
GAM2138 LOC112840 3' TAGTGGTGAGGTAAAGGCAAAA 51947      T      TTCTA
            G                    TAGTG TGAGGTAA    GAAAG
                                |||||  ||||||||    |||||
                                ATCAC ACTCCATT    TTTTC
                                  C       TCCG_
GAM2138 LOC253128 3' GTGATGAGATCCCCTAGAA   51948    T     AAT
                                GTG TGAGGT   TCTAGAA
                                ||| ||||||   |||||||
                                CAC ACTCTA   GGATCTT
                                  T     GG_
GAM2139 ADAMTS5  3' TGACAAGGGGGAGACA     51951      T    TAAAT
                                TGACAA GGGGG    GACA
                                |||||| |||||    ||||
                                ACTGTT CCCCC    CTGT
                                   _    T____
GAM2139 ARF3    3' CAATGGGGCAAGACAA     51952       G   AT
                                CAATGGGG TAA  GACAA
                                |||||||| |||  |||||
                                GTTACCCC GTT  CTGTT
                                   _  __
GAM2139 ISL1    3' AATGACATGAAAAGTGGCAA  51953       AT__  _
                                AATGACA   GGG GGTAA
                                |||||||   ||| |||||
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                                TTACTGT   TTC CCGTT
                                   ACTT   A
GAM2139 MOG     3' AATGAAGAGAAAAGGTAGATGA 51954      CAAT_     A
           CA                    AATGA    GGGGGTA ATGACA
                                 |||||    ||||||| ||||||
                                 TTACT    TTTCCAT TACTGT
                                   TCTCT      C
GAM2139 NCOR2   3' AACGACGTGTGTAAATGACA  51955      AAT GGG
                                 AATGAC   G   GTAAATGACA
                                 ||||||   |   ||||||||||
                                 TTGCTG   C   CATTTACTGT
                                    ___ ACA
GAM2139 NFRKB   5' TGGAACTCATAAATGACA    51956      ___
                                 TGGGG   GTAAATGACA
                                 |||||   ||||||||||
                                 ACCTT   TATTTACTGT
                                   GAG
GAM2139 PCDHB9  3' AATGAACAAGGATGGCAA    51957      _  T  _
                                 AATGA CAA GGG GGTAA
                                 ||||| ||| ||| |||||
                                 TTACT GTT CCT CCGTT
                                   T  _  A
GAM2139 PCSK2   3' ATGCAATGGGAATTGATGA   51958     A        AA
                                 ATG CAATGGGGGT  ATGA
                                 ||| ||||||||||  ||||
                                 TAC GTTACCCTTA  TACT
                                   _         AC
GAM2139 PKHD1   3' AATGCATGAATTTTAAATGACA 51959     A  A   GG_
                                 AATG CA TGGG   TAAATGACA
                                 |||| || ||||   |||||||||
                                 TTAC GT ACTT   ATTTACTGT
                                   _ _    AAA
GAM2139 SLC25A17 3' ATGACAATTAAGGTGACA    51960        GG    AAAT
                                 ATGACAAT  GGGT    GACA
                                 ||||||||  ||||    ||||
                                 TACTGTTA  TCCA    CTGT
                                    AT    ____
GAM2139 SSX2    3' ATGGCAATGGGAAAAGCAGATG 51961     A      ___    A  A
           GCA                    ATG CAATGGG   GGTA ATG CA
                                  ||| |||||||   |||| ||| ||
                                  TAC GTTACCC   TCGT TAC GT
                                    C      TTT    C   C
GAM2139 TRPS1   3' AATGAATACAGAGGTGAGTGA  51962      CA      AAA
                                 AATGA  ATGGGGGT   TGA
                                 |||||  ||||||||   |||
                                 TTACT  TGTCTCCA   ACT
                                   TA       CTC
GAM2139 WHN     3' ATGAAGATGGGGGAATAA    51963     CA      TA
                                 ATGA  ATGGGGG  AATGA
                                 ||||  |||||||  |||||
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                                TACT  TACCCCC  TTATT
                                  TC     __
GAM2139  FLJ10986  3'  GACAATACAGAAATGA     51964       G   TA
                                GACAATG GGG  AATGA
                                ||||||| |||  |||||
                                CTGTTAT TCT  TTACT
                                   G  __
GAM2139  FLJ11280  5'  AATGAGATGGGGGAGATA    51965      CA      TAA
                                AATGA  ATGGGGG   ATG
                                |||||  |||||||  |||
                                TTACT  TACCCCC   TAT
                                  C_     TC_
GAM2139  FLJ13231  3'  AATGACAAAACAATTAAATGAC 51966        TGGGGG
            AA                   AATGACAA     TAAATGACAA
                                ||||||||     ||||||||||
                                TTACTGTT     ATTTACTGTT
                                    TTGTTA
GAM2139  FLJ20509  5'  ATGACAATGGAATGACA     51967          GGTAA
                                ATGACAATGGG    ATGACA
                                ||||||||||    ||||||
                                TACTGTTACCT    TACTGT
                                          _____
GAM2139  FLJ20761  5'  ATGACAATCTCTAAGGTGAATG 51968        G___    A
            ACA                   ATGACAAT    GGGGT AATGACA
                                ||||||||    ||||| |||||||
                                TACTGTTA    TTCCA TTACTGT
                                    GAGA    C
GAM2139  FLJ21458  5'  ATGACAGGAGAGGTGAC     51969       AT     AAAT
                                ATGACA  GGGGGT    GAC
                                ||||||  ||||||    |||
                                TACTGT  TCTCCA    CTG
                                   CC     ____
GAM2139  FLJ22035  3'  TGAAGAAATAAATGACA     51970     CAAT  GG
                                TGA    GG  GTAAATGACA
                                |||    ||  ||||||||||
                                ACT    TC  TATTTACTGT
                                  ____  TT
GAM2139  FLJ23563  3'  ACAGTCAATAAATGACAA     51971     G_
                                ATGG  GGTAAATGACAA
                                ||||  ||||||||||||
                                TGTC  TTATTTACTGTT
                                  AG
GAM2139  KIAA0141  3'  ATGAACAGAGGTGAATG     51972     CA      A
                                ATGA  ATGGGGGT AATG
                                ||||  |||||||| ||||
                                TACT  TGTCTCCA TTAC
                                  __       C
GAM2139  KIAA0240  3'  ATGACAATGGGGGGTCATCCCCA 51973             AAATGA
                                ATGACAATGGGGGGT     CA
                                ||||||||||||||     ||
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                                TACTGTTACCCCCA     GT
                                       GTAGGG
GAM2139 KIAA0317 3' GACAAGGCTTGTAGGTGACAA 51974      T GG_  AA
                                GACAA GG   GTA  TGACAA
                                ||||| ||   |||  ||||||
                                CTGTT CC   CAT  ACTGTT
                                   _ GAA   CC
GAM2139 KIAA0416 3' AATGGCAATGGTCATCCTGA  51975     A     GG  AAA
                                AATG CAATGG  GT   TGA
                                |||| ||||||  ||   |||
                                TTAC GTTACC  TA   ACT
                                  C     AG  GG_
GAM2139 KIAA0451 5' TGGCAATGGGAGATTTTGGACA 51976    A       TAAAT_
                                TG CAATGGGGG      GACA
                                || |||||||||      ||||
                                AC GTTACCCTC      CTGT
                                 C        TAAAAC
GAM2139 KIAA1054 3' GACAGTGTGGGTAAGTGGCA  51977     A G     A A
                                GACA TG GGGTAA TG CA
                                |||| || |||||| || ||
                                CTGT AC CCCATT AC GT
                                  C A     C  C
GAM2139 KIAA1724 3' AATGACATTAAAATGACA    51978        A  GGGGT
                                AATGACA TG     AAATGACA
                                ||||||| ||     ||||||||
                                TTACTGT AT     TTTACTGT
                                    A _____
GAM2139 KIAA1866 3' AATGACAAATGAGTGGCAA   51979         _   _
                                AATGACAA TGGG GGTAA
                                |||||||| |||| |||||
                                TTACTGTT ACTC CCGTT
                                     T   A
GAM2139 KIAA1922 3' AATGACAATCCACAAGTGGCAA 51980          ____  _
                                AATGACAAT    GGG GGTAA
                                |||||||||    ||| |||||
                                TTACTGTTA    TTC CCGTT
                                     GGTG   A
GAM2139 LSM5     3' AATGACAGAAAAGTAAGTGGCA 51981        AT       A  A
            A                    AATGACA  GGGGGTAA TG CAA
                                ||||||| ||||||| || |||
                                TTACTGT  TTTTCATT AC GTT
                                    C_       C  C
GAM2139 LSM5     3' AATGGTCACGTAAATGACA   51982       GG__
                                AATGG    GTAAATGACA
                                |||||    ||||||||||
                                TTACC    CATTTACTGT
                                   AGTG
GAM2139 OS4      3' TGGCAATGGAAGGGATGA    51983    A       TAA
                                TG CAATGGGGG   ATGA
                                || |||||||||   ||||
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                                AC GTTACCTTC   TACT
                                 C        CC_
GAM2139  RFX4     3'  AATGACAAGACAGATGGCAA   51984        __    _
                                AATGACA  ATGGG GGTAA
                                |||||||  ||||| |||||
                                TTACTGT  TGTCT CCGTT
                                    TC     A
GAM2139  USP24    3'  TGGCAGTAAAAATGACAA    51985     G    __
                                TGG GGTAA  ATGACAA
                                |||  |||||  |||||||
                                ACC TCATT  TACTGTT
                                  G     TT
GAM2139  ZF5128   3'  GATAATGGGGGTGAGACA    51986    C       AAAT
                                GA AATGGGGGT    GACA
                                || |||||||||    ||||
                                CT TTACCCCCA    CTGT
                                 A        CT__
GAM2139  LOC120105 3'  ACAATCAACAGAAGTGACAA   51987    TG _        AAAT
                                A  A CAATGGGGGT    GACAA
                                |  | ||||||||||    |||||
                                T  T GTTGTCTTCA    CTGTT
                                 GT A        _____
GAM2139  LOC130026 3'  AATGCAATGGACTGGATGACAA 51988      A      __  TAA
                                AATG CAATGGG  GG   ATGACAA
                                |||| |||||||  ||   |||||||
                                TTAC GTTACCT  CC   TACTGTT
                                   _      GA  ____
GAM2139  LOC143196 3'  ATGACAATGTGGAAGACA    51989         GG  TAAAT
                                ATGACAATG  GG    GACA
                                |||||||||  ||    ||||
                                TACTGTTAC  CC    CTGT
                                     A_  TT____
GAM2139  LOC149351 3'  ATGACAACTAATTTGAGTGGTA 51990        _______   _
            A                    ATGACAA     TGGG GGTAA
                                |||||||     |||| |||||
                                TACTGTT     ACTC CCATT
                                    GATTAA    A
GAM2139  LOC149464 3'  ATGAGGATGAGGATGATGA   51991      CA       AA
                                ATGA  ATGGGGGT  ATGA
                                ||||  ||||||||  ||||
                                TACT  TACTCCTA  TACT
                                  CC       C_
GAM2139  LOC157931 5'  ATGAAATGGCAAAATGACA   51992      C     G GT
                                ATGA AATGG G  AAATGACA
                                |||| ||||| |  ||||||||
                                TACT TTACC T  TTTACTGT
                                  _     G __
GAM2139  LOC161725 5'  ATGGAAATGGAGCTGCAAGTGA 51993     AC      __    A
            CAA                    ATG  AATGGGG  GTAA TGACAA
                                |||  |||||||  |||| ||||||
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                                TAC  TTACCTC  CGTT ACTGTT
                                  CT      GA    C
GAM2139  LOC199704 3'  TGCAAGTCTTGGTAGATGACA  51994    A   TGGG_   A
                                TG CAA     GGTA ATGACA
                                || |||     |||| ||||||
                                AC GTT     CCAT TACTGT
                                  _   CAGAA    C
GAM2139  LOC199907 3'  AATAGCACTACAGGTAAATGA  51995     A  A  G
                                AATG CA TG GGGTAAATGA
                                |||| || || ||||||||||
                                TTAT GT AT TCCATTTACT
                                  C  G  G
GAM2139  LOC220758 5'  TGGCAATGGGGGTCAACAA   51996    A        AAA
                                TG CAATGGGGGT   TGACAA
                                || ||||||||||   ||||||
                                AC GTTACCCCCA   GTTGTT
                                 C         ___
GAM2139  LOC221895 3'  AATGAAAATGGGTATGATGA   51997      C     GGTAA
                                AATGA AATGGG     ATGA
                                ||||| ||||||     ||||
                                TTACT TTACCC     TACT
                                   T     ATAC_
GAM2139  LOC254057 3'  TGATAAAGAGAAATGACAA    51998     CAAT    T
                                TGA    GGGGG AAATGACAA
                                |||    ||||| |||||||||
                                ACT    TTCTC TTTACTGTT
                                  AT__    _
GAM2139  LOC254778 3'  TGACAATGGAATTGATGA     51999          GTAA
                                TGACAATGGGG    ATGA
                                ||||||||||    ||||
                                ACTGTTACCTT    TACT
                                      AAC_
GAM2139  LOC257453 3'  ATGGCAATGGGAAAAGCAGATG 51961     A     ___    A  A
            GCA                    ATG CAATGGG   GGTA ATG CA
                                ||| |||||||   |||| ||| ||
                                TAC GTTACCC   TCGT TAC GT
                                  C      TTT    C   C
GAM2139  LOC81034  3'  AATAGCAATGGAATGACA     52000      A      GGTAA
                                AATG CAATGGG     ATGACA
                                |||| |||||||     ||||||
                                TTAT GTTACCT     TACTGT
                                  C      ______
GAM2139  LOC91974  3'  AATAACACAGTGAATGACA    52001        ATGGG   A
                                AATGACA     GGT AATGACA
                                |||||||     ||| |||||||
                                TTATTGT     TCA TTACTGT
                                    G_____   C
GAM2139  LOC93297  3'  AATCACATCTTGTAAATGACA  52002     G   ATGGGG
                                AAT ACA     GTAAATGACA
                                ||| |||     ||||||||||
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                                TTA TGT     CATTTACTGT
                                  G   AGAA__
GAM2140  MAT1A    3'  TCGAGTGTGAGCCAAGTTAGA  51822      ATATAC
                                TCGA     GGGCCAAGTTAGA
                                ||||     ||||||||||||
                                AGCT     CTCGGTTCAATCT
                                  CACA__
GAM2140  MEF2C    3'  GAATATGGGCAAGTTAG     51823       AC    C
                                GAATAT  GGGC AAGTTAG
                                ||||||  |||| |||||||
                                CTTATA  CCCG TTCAATC
                                   __   _
GAM2140  KIAA0355  5'  TCAATATACCCAAAAAAGTTAG 51824    G      GGG   ____
              AA                  C AAATATAC   CCA    AGTTAGAA
                                | |||||||   |||    ||||||||
                                G TTATATG   GGT    TCAATCTT
                                _     ___   TTTT
GAM2140  LOC200169 3'  GAATACACTCCAAGTT      51825        GGG
                                GAATATAC   CCAAGTT
                                ||||||||   |||||||
                                CTTATGTG   GGTTCAA
                                     A__
GAM2141  AICDA    3'  TATAAATTTATGAAGCTTTGA  52006          AT   A
                                TATAAATTTA  AAG CTTTGA
                                ||||||||||  ||| ||||||
                                ATATTTAAAT  TTC GAAACT
                                      AC  _
GAM2141  DKFZp434A2417 3'  TATAAAATAAGACTTTG     52007       TTTA
                                TATAAA    ATAAGACTTTG
                                ||||||    ||||||||||
                                ATATTT    TATTCTGAAAC
                                   ____
GAM2141  FLJ10781  3'  AAACTCAAAGACTTTGA     52008         TA
                                AAATTTAA  AGACTTTGA
                                ||||||||  |||||||||
                                TTTGAGTT  TCTGAAACT
                                   __
GAM2141  UBE3B    3'  TACAAATTTAATAAAGCCTTTG 52009              A_
              A                   TATAAATTTAATAAG  CTTTGA
                                ||||||||||||||  ||||||
                                ATGTTTAAATTATTT  GAAACT
                                      CG
GAM2141  LOC126823 3'  TGAAATTTAATAAGCATTTGA  52010    T         AC
                                A AAATTTAATAAG  TTTGA
                                | ||||||||||||  |||||
                                A TTTAAATTATTC  AAACT
                                 C          GT
GAM2141  LOC148446 5'  TACAAATTACTGTGAGACTTTG 52011         TAATA_
                                TATAAATT     AGACTTTG
                                ||||||||     ||||||||
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                                ATGTTTAA     TCTGAAAC
                                     TGACAC
GAM2141  LOC256239 3'  TATAAATTTCAGACTTTGA   52012        AATA
                                TATAAATTT    AGACTTTGA
                                |||||||||    |||||||||
                                ATATTTAAA    TCTGAAACT
                                     G___
GAM2142  B3GALT2   5'  AGCTGCAATGTAAAGCA     52015       AATAG    A
                                AGCTGCAA     GTGAA CA
                                ||||||||     ||||| ||
                                TCGACGTT     CATTT GT
                                     A____     C
GAM2142  CFTR      3'  GCTTGCAAAACACAAGTG     52016     _      __
                                GCT GCAAAATA  GGTG
                                ||| ||||||||  ||||
                                CGA CGTTTTGT  TCAC
                                  A       GT
GAM2142  EPO       3'  AGGTGCGAAAACAGGTAA     52017    C  _
                                AG TGC AAAATAGGTGA
                                || ||| ||||||||||
                                TC ACG TTTTGTCCATT
                                 C   C
GAM2142  GAGED2    3'  AAGCTGCAAAACTTTATTGA   52018          AGG__
                                AAGCTGCAAAAT     TGA
                                ||||||||||     |||
                                TTCGACGTTTTG     ACT
                                      AAATA
GAM2142  GAGED2    3'  AAGCTGCAAAACTTTATTGA   52018          AGG__
                                AAGCTGCAAAAT     TGA
                                ||||||||||     |||
                                TTCGACGTTTTG     ACT
                                      AAATA
GAM2142  GAGED2    3'  AAGCTGCAAAACTTTATTGA   52018          AGG__
                                AAGCTGCAAAAT     TGA
                                ||||||||||     |||
                                TTCGACGTTTTG     ACT
                                      AAATA
GAM2142  HDAC4     3'  TAAGCTACAAGATGA       52019         AAAT
                                TAAGCTGCA    AGGTGA
                                |||||||||    ||||||
                                ATTCGATGT    TCTACT
                                     ____
GAM2142  IRS2      3'  TAAGCTGCAGTATGAACA     52020         AAATAG    A
                                TAAGCTGCA     GTGAA CA
                                |||||||||     ||||| ||
                                ATTCGACGT     TACTT GT
                                     CA____    _
GAM2142  LANCL1    3'  AGCTGTGAAATAGGCACA     52021       CA       GAA
                                AGCTG  AAATAGGT   ACA
                                |||||  ||||||||   |||
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                                TCGAC  TTTATCCG   TGT
                                  AC       ___
GAM2142  MAP3K5   3'  TAAGTTACAAAATAGAGTCAA  52022      C        _  G
                                TAAG TGCAAAATAG GT AA
                                |||| |||||||||| || ||
                                ATTC ATGTTTTATC CA TT
                                  A         T  G
GAM2142  MYO1C    3'  GCTGCAAAAGATGCAGATG    52023          ____
                                GCTGCAAAA    TAGGTG
                                |||||||||    ||||||
                                CGACGTTTT    GTCTAC
                                     CTAC
GAM2142  NOV      3'  AGTGCAATGTGAAACA      52024    C    AATAG
                                AG TGCAA     GTGAAACA
                                || |||||     ||||||||
                                TC ACGTT     CACTTTGT
                                 _     A____
GAM2142  PCDH7    3'  TAATTTGCAAAATACAGTG    52025     GC       _
                                TAA  TGCAAAATA GGTG
                                |||  ||||||||| ||||
                                ATT  ACGTTTTAT TCAC
                                  AA        G
GAM2142  PFKFB3   3'  TAAGCTGCAGAAATGGAAA    52026          _   A  T
                                TAAGCTGCA AAAT GG GA
                                ||||||||| |||| || ||
                                ATTCGACGT TTTA CC TT
                                     C    _  T
GAM2142  PPP2CB   3'  TAAGCGCAAAAGGAGATGA    52027      T     T_
                                TAAGC GCAAAA  AGGTGA
                                ||||| ||||||  ||||||
                                ATTCG CGTTTT  TCTACT
                                   _     CC
GAM2142  PPP3R1   3'  AGCTGCAAGTCTTTTGAAACAA 52028         AATAGG
                                AGCTGCAA     TGAAACAA
                                ||||||||     ||||||||
                                TCGACGTT     ACTTTGTT
                                     CAGAAA
GAM2142  RAB7L1   3'  TAAGCTCAGAAGTAGGTGA    52029       G  A  _
                                TAAGCT CA AA TAGGTGA
                                |||||| || || |||||||
                                ATTCGA GT TT ATCCACT
                                   _  C  C
GAM2142  SEL1L    3'  CAAGCAAATTACAGAGTAGGTG 52030       ____    AAA
                                TAAGC   TGCA   TAGGTG
                                |||||   ||||   ||||||
                                GTTCG   ATGT   ATCCAC
                                   TTTA   CTC
GAM2142  SHANK2   3'  CTGCAAAAGGTTTTGGAACA   52031        AT    GA___
                                CTGCAAA  AGGT    AACA
                                |||||||  ||||    ||||
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                                GACGTTT  TCCA    TTGT
                                   __    AAACC
GAM2142  SLC30A4   3'  TGACTGCAGGATAAATAA    52032   A    AA
                                A GCTGCA  ATAGGTGA
                                | ||||||  ||||||||
                                A TGACGT  TATTTATT
                                 C     CC
GAM2142  STE       5'  TAAGCTGCAAAAAAAGATGA   52033          T_
                                TAAGCTGCAAAA  AGGTGA
                                ||||||||||||  ||||||
                                ATTCGACGTTTT  TCTACT
                                       TT
GAM2142  TEM7      3'  AGGTGCAGGAATAGGTAA    52034    C   A_
                                AG TGCA  AATAGGTGA
                                || ||||  |||||||||
                                TC ACGT  TTATCCATT
                                 C   CC
GAM2142  TRPM6     3'  AGCTGCAAAGTGCCCTGGACA  52035       AATA   AA____
                                AGCTGCAA   GGTG    ACA
                                ||||||||   ||||    |||
                                TCGACGTT   TCAC    TGT
                                     _____  GGGACC
GAM2142  UBE4A     3'  TAAGCTGCACAATTGAGTA   52036        A  A_
                                TAAGCTGCA AAT  GGTG
                                |||||||||  |||  ||||
                                ATTCGACGT TTA  TCAT
                                      G   AC
GAM2142  ARHGEF11  5'  AACTGCAAAGTACAGATAA   52037         __
                                AGCTGCAAA  ATAGGTGA
                                |||||||||  ||||||||
                                TTGACGTTT  TGTCTATT
                                      CA
GAM2142  BIKE      3'  AGCTGCAAAATCATTAGTAA  52038         A___
                                AGCTGCAAAAT   GGTGA
                                ||||||||||    |||||
                                TCGACGTTTTA   TCATT
                                       GTAA
GAM2142  DEFCAP    5'  AGCTGCAAGGCTGAGAAGAGGT 52039        ________  T
            G                    AGCTGCAA      AA AGGTG
                                 ||||||||      || |||||
                                 TCGACGTT      TT TCCAC
                                     CCGACTC  C
GAM2142  DEFCAP    5'  AGCTGCAAGGCTGAGAAGAGGT 52039        ________  T
            G                    AGCTGCAA      AA AGGTG
                                 ||||||||      || |||||
                                 TCGACGTT      TT TCCAC
                                     CCGACTC  C
GAM2142  DKFZP564D0462 3'  TAAGCTGCATAATAGTATG   52040         A    _
                                TAAGCTGCA AATAG GTG
                                ||||||||| ||||| |||
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                                ATTCGACGT TTATC TAC
                                     A    A
GAM2142 ELKS    3' AAGCTGCAGGCGGGGACA   52041      AAATA   AA_
                                AAGCTGCA   GGTG  ACA
                                ||||||||   ||||  |||
                                TTCGACGT   CCGC  TGT
                                     _____  CCC
GAM2142 FENS-1  3' TAAACTGCAGAAAATAGA   52042       __
                                TAAGCTGCA  AAATAGG
                                |||||||||  |||||||
                                ATTTGACGT  TTTATCT
                                     CT
GAM2142 FLJ11149 3' TGACTGCAAAGAAAATGA   52043   A     AT
                                A GCTGCAAA  AGGTGA
                                | ||||||||  ||||||
                                A TGACGTTT  TTTACT
                                 C       CT
GAM2142 FLJ12484 3' TAAGCTGCAAGCAAAGATG   52044       AAT_
                                TAAGCTGCAA   AGGTG
                                ||||||||||   |||||
                                ATTCGACGTT   TCTAC
                                     CGTT
GAM2142 FLJ12747 3' TAAGCTACAAAAATTAAATG   52045         __
                                TAAGCTGCAAAA  TAGGTG
                                ||||||||||||  ||||||
                                ATTCGATGTTTT  ATTTAC
                                      TA
GAM2142 FLJ12985 3' TAAACTGCAAGGTATGAAC   52046       AAAT   A_
                                TAAGCTGCA   AGGTG  AAC
                                |||||||||   |||||  |||
                                ATTTGACGT   TCCAT  TTG
                                     ____   AC
GAM2142 FLJ13910 3' AAGTTGCAAAATATTTGGTGA  52047    C      ___
                                AAG TGCAAAATA   GGTGA
                                ||| |||||||||   |||||
                                TTC ACGTTTTAT   CCACT
                                  A       AAA
GAM2142 FLJ20200 3' CAAGTTGCAGAACAAGTGA   52048    C   A
                                TAAG TGCA AATAGGTGA
                                |||| |||| |||||||||
                                GTTC ACGT TTGTTCACT
                                  A   C
GAM2142 FLJ20548 3' GCTTGCAACACCATGAAACAA  52049    _   A  AG
                                GCT GCAA AT  GTGAAACAA
                                ||| |||| ||  |||||||||
                                CGA CGTT TG  TACTTTGTT
                                  A   G  G_
GAM2142 FLJ20666 5' TAAGCTGCAGTGTAATACA   52050       AAATAG   A
                                TAAGCTGCA    GTGA ACA
                                |||||||||    |||| |||
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                                ATTCGACGT     CATT TGT
                                    CA____    A
GAM2142  FLJ21551  3'  TAAGCTTGCAAAAACAAAAGCA 52051       _     T___   TG
             A                   TAAGCT GCAAAA    AGG  A
                                 |||||| ||||||    |||  |
                                 ATTCGA CGTTTT    TTC  T
                                    A     TGTT   GT
GAM2142  FLJ22693  3'  TAAGCAGCAAAGTCAACA    52052      T   AATA   GA
                                 TAAGC GCAA    GGT  AACA
                                 ||||| ||||    |||  ||||
                                 ATTCG CGTT    TCA  TTGT
                                   T    _____   G_
GAM2142  FLJ30574  5'  TAAGCTGCAAAAAGAAAGTTAC 52053          T   TGAA_
             A                   TAAGCTGCAAAA AGG     ACA
                                 |||||||||||| |||     |||
                                 ATTCGACGTTTT TCT     TGT
                                       _  TTCAA
GAM2142  GC20     3'  TAAGCTGCAACGTACATG    52054         AA  G
                                 TAAGCTGCAA  TA GTG
                                 ||||||||||  || |||
                                 ATTCGACGTT  AT TAC
                                       GC  G
GAM2142  KIAA0010  3'  TAAGCTCAGAATAGCTGA    52055       G  A    G
                                 TAAGCT CA AATAG TGA
                                 |||||| || ||||| |||
                                 ATTCGA GT TTATC ACT
                                    _ C    G
GAM2142  KIAA0298  3'  TAAGCTGCAAGATGGGGA    52056         A  A  T
                                 TAAGCTGCAA AT GG GA
                                 |||||||||| || || ||
                                 ATTCGACGTT TA CC CT
                                       C  C  _
GAM2142  KIAA0423  5'  CAAGCTGCAGAAGAGGCAA    52057         A  T   TG
                                 TAAGCTGCA AA AGG  A
                                 ||||||||| || |||  |
                                 GTTCGACGT TT TCC  T
                                       C  C   GT
GAM2142  KIAA0469  3'  TAAGTGCAAAATAAGGGTAA   52058      C       __
                                 TAAG TGCAAAATA  GGTGA
                                 |||| |||||||||  |||||
                                 ATTC ACGTTTTAT  CCATT
                                   _       TC
GAM2142  KIAA0478  3'  TAAGCTGCAAATCTGGTGA    52059          ATA
                                 TAAGCTGCAAA   GGTGA
                                 ||||||||||||  |||||
                                 ATTCGACGTTT   CCACT
                                       AGA
GAM2142  KIAA0759  3'  GCTGCAGAGTCCAGTGAAACAA 52060       AAATA_
                                 GCTGCA     GGTGAAACAA
                                 ||||||     ||||||||||
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                                CGACGT     TCACTTTGTT
                                   CTCAGG
GAM2142  KIAA0783  3'  TAAGTGCAAAAAAAGCAA    52061     C      T   TG
                                TAAG TGCAAAA AGG  A
                                |||| ||||||| |||  |
                                ATTC ACGTTTT TTC  T
                                  _      T   GT
GAM2142  KIAA0836  3'  TAAGCTCAGAATAAGTAA    52062       G  A
                                TAAGCT CA AATAGGTGA
                                |||||| || |||||||||
                                ATTCGA GT TTATTCATT
                                   _ C
GAM2142  KIAA0853  3'  TAAGTTGCAAAATAAACTAAGG 52063     C      _______
            TA                    TAAG TGCAAAAT     AGGTG
                                |||| ||||||||     |||||
                                ATTC ACGTTTTA     TCCAT
                                  A       TTTGAT
GAM2142  KIAA0864  3'  TAAGCTGCATCAGTGGAACAA  52064        AAATA    A
                                TAAGCTGCA    GGTG AACAA
                                |||||||||    |||| |||||
                                ATTCGACGT    TCAC TTGTT
                                     AG___    C
GAM2142  KIAA0895  3'  TAAGCTGATAAGGTGAAACAA  52065       CAAAAT
                                TAAGCTG     AGGTGAAACAA
                                |||||||     ||||||||||
                                ATTCGAC     TCCACTTTGTT
                                    TAT___
GAM2142  KIAA0992  3'  AAGCTGTACATGTGAAACA   52066      CAAA   G
                                AAGCTG    ATA GTGAAACA
                                ||||||    ||| ||||||||
                                TTCGAC    TGT CACTTTGT
                                   A___   A
GAM2142  KIAA1028  3'  AACTGCAAAGATCTAGGCA   52067        A___
                                AGCTGCAAA    TAGGTG
                                |||||||||    ||||||
                                TTGACGTTT    ATCCGT
                                     CTAG
GAM2142  KIAA1034  3'  TAAGCTGCCAGATAGGAAGCCA 52068        AAA    T  AA
                                TAAGCTGC   ATAGG GA  CA
                                ||||||||   ||||| ||  ||
                                ATTCGACG   TATCC TT  GT
                                     GTC    _  CG
GAM2142  KIAA1109  5'  AACTGCAAGTTTAGGGAA    52069        AA_   T
                                AGCTGCAA   TAGG GAA
                                ||||||||   |||| |||
                                TTGACGTT   ATCC CTT
                                     CAA   _
GAM2142  KIAA1889  5'  AGCTGCAAGATGTGGATGA   52070        A  A__
                                AGCTGCAA AT   GGTGA
                                ||||||||  ||   |||||
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                                TCGACGTT TA   CTACT
                                    C  CAC
GAM2142  KIAA1958  3'  TAAGTGCAGAACCAACAAAACA 52071      C    A   AG TG
             A                   TAAG TGCA AAT  G  AAACAA
                                 |||| |||| |||  |  ||||||
                                 ATTC ACGT TTG  T  TTTGTT
                                   _   C   GT GT
GAM2142  KIAA1979  3'  AACTGCAAGGTATGAAC     52072        AAAT    A_
                                 AGCTGCA    AGGTG  AAC
                                 |||||||    |||||  |||
                                 TTGACGT    TCCAT  TTG
                                     ____    AC
GAM2142  MGC4832   3'  CAAGCTGCAGAGTGGAGCGTGA 52073         AAAT__  _
                                 TAAGCTGCA     AG GTGA
                                 |||||||||     || ||||
                                 GTTCGACGT     TC CACT
                                      CTCACC  G
GAM2142  NAP1L1    3'  AGCTGCAAAAACAAAAACAA   52074          TAGGT
                                 AGCTGCAAAA    GAAACAA
                                 ||||||||||    |||||||
                                 TCGACGTTTT    TTTTGTT
                                      TGT__
GAM2142  PELI2     3'  TAAGCTGCAAGGGAAGGTGA   52075          AAT_
                                 TAAGCTGCAA    AGGTGA
                                 ||||||||||    ||||||
                                 ATTCGACGTT    TCCACT
                                      CCCT
GAM2142  PRDM12    3'  TGACTGCAAAGTGTGAGAGGCG 52076    A      AT_____
             A                    A GCTGCAAA      AGGTGA
                                  | ||||||||      ||||||
                                  A TGACGTTT      TCCGCT
                                   C       CACACTC
GAM2142  PRO1596   3'  AGCTGCAAATTGAAACA     52077         ATAGG
                                 AGCTGCAAA     TGAAACA
                                 |||||||||     |||||||
                                 TCGACGTTT     ACTTTGT
                                      A____
GAM2142  PXR2b     3'  AGCTGCAAGGGGAGACA     52078        AAAT   T  A
                                 AGCTGCA    AGG GA ACA
                                 |||||||    ||| || |||
                                 TCGACGT    TCC CT TGT
                                     ____   C  C
GAM2142  SURB7     3'  TAAACTGAGGTGAAA       52079        CAAAAT
                                 TAAGCTG     AGGTGAAA
                                 |||||||     ||||||||
                                 ATTTGAC     TCCACTTT
                                     _______
GAM2142  TU3A      3'  TAAGCTGCAAAGGAGACTGGAA 52080          AT   _  A
             CA                    TAAGCTGCAAA  AGG TG AACA
                                   ||||||||||  ||| || ||||
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                                ATTCGACGTTT  TCT AC TTGT
                                      CC   G  C
GAM2142  LOC124245 3'  AACTGCAAAATCCAAAATG    52081          ___
                                AGCTGCAAAAT   AGGTG
                                ||||||||||   |||||
                                TTGACGTTTTA   TTTAC
                                      GGT
GAM2142  LOC129563 3'  AGCTGCAAAAATTAAATAA    52082          __
                                AGCTGCAAAA  TAGGTGA
                                |||||||||  |||||||
                                TCGACGTTTT  ATTTATT
                                      TA
GAM2142  LOC143154 3'  TAAGCTGCAAATCTATAGCAA  52083          A_  _  TG
                                TAAGCTGCAAA  TA GG  A
                                ||||||||||  || ||  |
                                ATTCGACGTTT  AT TC  T
                                      AG  A  GT
GAM2142  LOC144584 5'  TAAGCTGCAAATACCAAAGGTG 52084          AT____
                                TAAGCTGCAAA     AGGTG
                                ||||||||||     |||||
                                ATTCGACGTTT     TCCAC
                                      ATGGTT
GAM2142  LOC146819 3'  AGCTGCAAAATAATGTGA    52085          _
                                AGCTGCAAAATAG GTGA
                                |||||||||||| ||||
                                TCGACGTTTTATT CACT
                                       A
GAM2142  LOC146821 3'  AGCTGCAAAATAATGTGA    52085          _
                                AGCTGCAAAATAG GTGA
                                |||||||||||| ||||
                                TCGACGTTTTATT CACT
                                       A
GAM2142  LOC147057 3'  TAATTTGCAAAACAAAAAGCGA 52086     GC       ___
                                TAA  TGCAAAATA   GGTGA
                                |||  |||||||||   |||||
                                ATT  ACGTTTTGT   TCGCT
                                  AA        TTT
GAM2142  LOC147660 3'  AACTGCAAGGTATGAAC     52072        AAAT    A_
                                AGCTGCA    AGGTG  AAC
                                |||||||    |||||  |||
                                TTGACGT    TCCAT  TTG
                                     ____     AC
GAM2142  LOC149910 3'  AGCTGCAGAGAGGCGTGGAACA 52087        AAAT    A__
                                AGCTGCA    AGGTG   AACA
                                |||||||    |||||   ||||
                                TCGACGT    TCCGC   TTGT
                                    CTC_    ACC
GAM2142  LOC152905 3'  GCTGCAAAAAAAAAAACAA    52088         TAGGT
                                GCTGCAAAA     GAAACAA
                                |||||||||     |||||||
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                                CGACGTTTT    TTTTGTT
                                     TTT__
GAM2142  LOC153914 5'  GCTGCAAAATAATTTAAACAA  52089          GTG
                                GCTGCAAAATAG   AAACAA
                                ||||||||||||  ||||||
                                CGACGTTTTATT   TTTGTT
                                   AAA
GAM2142  LOC158435 5'  TAAGCTGCATGCACACAGAGAT 52090        AA_ ____
           GA                    TAAGCTGCA   AT   AGGTGA
                                |||||||||  ||   ||||||
                                ATTCGACGT   TG   TCTACT
                                     ACG  TGTC
GAM2142  LOC201229 3'  AACTGCAAGGATACAAACAA   52091        AATA   _
                                AGCTGCAA    GGTG AAACAA
                                ||||||||    |||| ||||||
                                TTGACGTT    CTAT TTTGTT
                                     C___    G
GAM2142  LOC201283 3'  TAAGCTGCTAAAAACTAAAACA 52092        A   T  G
                                TAAGCTGC AAA AG TGAAACA
                                |||||||| ||| || |||||||
                                ATTCGACG TTT TT ATTTTGT
                                     A   _  G
GAM2142  LOC203221 5'  TGACTGCAAAGTGTCCACA    52093    A      AATA    AA_
                                A GCTGCAA    GGTG   ACA
                                | |||||||    ||||   |||
                                A TGACGTT    TCAC   TGT
                                 C      _____    AGG
GAM2142  LOC219294 3'  TAAGCTGCAAATCTATAGCAA  52083          A_  _  TG
                                TAAGCTGCAAA  TA GG  A
                                ||||||||||  || ||  |
                                ATTCGACGTTT  AT TC  T
                                      AG  A  GT
GAM2142  LOC255196 3'  AGCTGCAAGGATGTAAGTGA   52094        AA___
                                AGCTGCAA    TAGGTGA
                                ||||||||    |||||||
                                TCGACGTT    ATTCACT
                                     CCTAC
GAM2142  LOC255624 3'  TAAACTGCAAGGTATGAAC    52046        AAAT    A_
                                TAAGCTGCA    AGGTG  AAC
                                |||||||||    |||||  |||
                                ATTTGACGT    TCCAT  TTG
                                     ____     AC
GAM2142  LOC91351  3'  AGCTGCAAGGAAAACA      52095       AAAT   T
                                AGCTGCA    AGG GAAACA
                                |||||||    ||| ||||||
                                TCGACGT    TCC TTTTGT
                                     ____   _
GAM2142  LOC91664  3'  AACTGCAAGGTATGAACAA    52096       AAAT    A_
                                AGCTGCA    AGGTG  AACAA
                                |||||||    |||||  |||||
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                                TTGACGT   TCCAT  TTGTT
                                   ____    AC
GAM2142 LOC92876 5' TAAGCTTCAAAATAGATAA   52097      G
                                TAAGCT CAAAATAGGTGA
                                |||||| ||||||||||||
                                ATTCGA GTTTTATCTATT
                                   A
GAM2142 LOC93129 3' AGCTTGCAAAACCCAAGGGA  52098    _    ___  T
                                AGCT GCAAAAT  AGG GA
                                |||| |||||||  ||| ||
                                TCGA CGTTTTG  TCC CT
                                  A     GGT  _
GAM2143 AK2      3' TGGCATAACCAACTTCCTTTT 52101    TACA  __
                                TGGC   AACT  TTTCCTTTT
                                ||||   ||||  |||||||||
                                ACCG   TTGG  GAAGGAAAA
                                  TA__   TT
GAM2143 ATP8A2   3' TGGCTCAATGCCCTTTT    52102     A  ACTTT
                                TGGCT CAA    TCCTTTT
                                ||||| |||    |||||||
                                ACCGA GTT    GGGAAAA
                                  _  AC___
GAM2143 C1orf1   3' TGTCTACTTTCCTTTT     52103   G   AAACT
                                TG CTAC    TTTCCTTTT
                                || ||||    |||||||||
                                AC GATG    AAAGGAAAA
                                 A  _____
GAM2143 CARP     3' TGGCTTCACTGTCCTTTTC   52104     ACAA  TT
                                TGGCT   ACT  TCCTTTTC
                                |||||   |||  ||||||||
                                ACCGA   TGA  AGGAAAAG
                                  AG__   C_
GAM2143 CRTAP    3' TGGCTTTCTTCCTTTT     52105     ACAAAC
                                TGGCT    TTTTCCTTTT
                                |||||    ||||||||||
                                ACCGA    AGAAGGAAAA
                                  A_____
GAM2143 ENC1     3' GCAACTTCTTTTCCTTTT   52106   T  AAA
                                GC AC  CTTTTCCTTTT
                                || ||  ||||||||||||
                                CG TG  GAAAAGGAAAA
                                 T  AA_
GAM2143 FLRT2    3' TGACTATGCCTCTTCCTTTTC 52107     CAAA
                                TGGCTA   CTTTTCCTTTTC
                                ||||||   ||||||||||||
                                ACTGAT   GAGAAGGAAAAG
                                   ACG_
GAM2143 FOXD1    3' TAACCATTTTTCCTTTTC   52108     CAAAC
                                TGGCTA   TTTTCCTTTTC
                                ||||||   ||||||||||
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                                ATTGGT    AAAAGGAAAAG
                                  A____
GAM2143  FZD3    3'  TGGCTACAAATTAAAATTTTTC 52109         CTTTTCC
                                TGGCTACAAA      TTTTC
                                ||||||||||      |||||
                                ACCGATGTTT      AAAAG
                                     AATTTTA
GAM2143  GNAS    3'  TGGCCTTTTTTCCTTTT    52110      ACAAAC
                                TGGCT    TTTTCCTTTT
                                |||||    ||||||||||
                                ACCGG    AAAAGGAAAA
                                  AA____
GAM2143  GNAS    3'  TGGCCTTTTTTCCTTTT    52110      ACAAAC
                                TGGCT    TTTTCCTTTT
                                |||||    ||||||||||
                                ACCGG    AAAAGGAAAA
                                  AA____
GAM2143  GNAS    3'  TGGCCTTTTTTCCTTTT    52110      ACAAAC
                                TGGCT    TTTTCCTTTT
                                |||||    ||||||||||
                                ACCGG    AAAAGGAAAA
                                  AA____
GAM2143  GNAS    3'  TGGCCTTTTTTCCTTTT    52110      ACAAAC
                                TGGCT    TTTTCCTTTT
                                |||||    ||||||||||
                                ACCGG    AAAAGGAAAA
                                  AA____
GAM2143  HAS3    3'  TGGCAAACTTTCCTTTT    52111     TAC      T
                                TGGC   AAACTTT CCTTTT
                                ||||   ||||||| ||||||
                                ACCG   TTTGAAA GGAAAA
                                  ___      _
GAM2143  HMGA2   3'  TGGCCACAAGCTTTTTTTTTC  52112         A    CC
                                TGGCTACAA CTTTT  TTTTC
                                ||||||||| |||||  |||||
                                ACCGGTGTT GAAAA  AAAAG
                                     C    A_
GAM2143  IFNAR2  3'  GCTACTATTTTCCTTTTC    52113      AAAC
                                GCTAC    TTTTCCTTTTC
                                |||||    ||||||||||||
                                CGATG    AAAAGGAAAAG
                                  AT__
GAM2143  IGF2R   3'  TGGCTGTTTTTTTTTCCTTTT  52114      ACAAAC
                                TGGCT    TTTTCCTTTT
                                |||||    ||||||||||
                                ACCGA    AAAAGGAAAA
                                  CAAAAA
GAM2143  LEP     3'  CGGCCAAACTTTTTTTTTT   52115     TA       CC
                                TGGC  CAAACTTTT  TTTT
                                ||||  |||||||||  ||||
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                                GCCG  GTTTGAAAA  AAAA
                                  __       AA
GAM2143  MTMR2    3'  TGGGTACAAACTGAACATTTTC 52116     C       TTTCC
                                TGG TACAAACT     TTTTC
                                ||| ||||||||     |||||
                                ACC ATGTTTGA     AAAAG
                                  C       CTTGT
GAM2143  NR1D1    3'  TGGTTTGCTTTTCCTTTTC   52117     CTACAAA
                                TGG      CTTTTCCTTTTC
                                |||      ||||||||||||
                                ACC      GAAAAGGAAAAG
                                  AAAC___
GAM2143  PBX3     3'  GGCTACAAAAACGCTTTCCTTT 52118         __ _
              TC                  GGCTACAA  AC TTTTCCTTTTC
                                ||||||||  || ||||||||||
                                CCGATGTT  TG GAAAGGAAAAG
                                     TT  C
GAM2143  POU5F1   3'  TGGCACAAACTCCAGGTTTTC  52119      T       TCC
                                TGGC ACAAACTTT   TTTTC
                                |||| |||||||||   |||||
                                ACCG TGTTTGAGG   AAAAG
                                  _       TCC
GAM2143  POU5F1   3'  TGGCACAAACTCCAGGTTTTC  52119      T       TCC
                                TGGC ACAAACTTT   TTTTC
                                |||| |||||||||   |||||
                                ACCG TGTTTGAGG   AAAAG
                                  _       TCC
GAM2143  PPP2R2C  3'  TGGCGGTGAACGCTTCCTTTCC 52120      TACA   T
                                TGGC    AAC TTTCCTTTTC
                                ||||    ||| ||||||||||
                                ACCG    TTG GAAGGAAAGG
                                  CCAC   C
GAM2143  RAD54B   3'  AGCTACATTCCTTTT       52121        AACTT
                                GGCTACA    TTCCTTTT
                                |||||||    ||||||||
                                TCGATGT    AAGGAAAA
                                     _____
GAM2143  TLR3     5'  GCTAGCCTTTCCTTTT      52122      CAAA
                                GCTA    CTTTTCCTTTT
                                ||||    ||||||||||
                                CGAT    GGAAAGGAAAA
                                  C___
GAM2143  TRPM6    3'  TGGTTTTCCACCTTCCTTTTC  52123     CTACAA    T
                                TGG     ACTTT CCTTTTC
                                |||     ||||| |||||||
                                ACC     TGGAA GGAAAAG
                                  AAAAGG    _
GAM2143  AIF1     3'  GGCCTGTTGGCTTTTCCTTTTC 52124      ACAAA_
                                GGCT     CTTTTCCTTTTC
                                ||||     ||||||||||||
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                                CCGG     GAAAAGGAAAAG
                                  ACAACC
GAM2143 BCCIP    3' TGACTATTCCTTTTC      52125       CAAACTT
                                TGGCTA     TTCCTTTTC
                                ||||||     |||||||||
                                ACTGAT     AAGGAAAAG
                                  _______
GAM2143 C1orf22  3' TGGTTAAATTTTTTCCTTTTC 52126     C  CAAAC
                                TGG TA    TTTTCCTTTTC
                                ||| ||    ||||||||||
                                ACC AT    AAAAGGAAAAG
                                  A  TTAA_
GAM2143 DKFZP761C169 3' GCTACATTTTCCTTTT     52127       AAC
                                GCTACA   TTTTCCTTTT
                                ||||||   ||||||||||
                                CGATGT   AAAAGGAAAA
                                  ___
GAM2143 DNAJA4   5' TGGTCATAAACATCCCTTTTC 52128     C  C    TT
                                TGG TA AAAC  TTCCTTTTC
                                ||| || ||||  |||||||||
                                ACC GT TTTG  AGGGAAAAG
                                  A  A    T_
GAM2143 FBXO27   3' TGATCCAAACTTTTTCTTTT  52129     CTA       C
                                TGG   CAAACTTTT CTTTT
                                |||   ||||||||| |||||
                                ACT   GTTTGAAAA GAAAA
                                  AG_       A
GAM2143 FBXO27   3' TGGCCCAAACTTTTTTTTTT  52130      A       CC
                                TGGCT CAAACTTTT  TTTT
                                ||||| |||||||||  ||||
                                ACCGG GTTTGAAAA  AAAA
                                  _       AA
GAM2143 FLJ10508 3' TGGTGCAAATTCTTCCCTTT  52131     CTA    C
                                TGG   CAAA TTTTCCTTTT
                                |||   |||| ||||||||||
                                ACC   GTTT AGAAGGGAAA
                                  AC_    A
GAM2143 FLJ20825 3' TGGCCTTTTCCTTTT      52132      TACAAA
                                TGGC     CTTTTCCTTTT
                                ||||     ||||||||||
                                ACCG     GAAAAGGAAAA
                                  _______
GAM2143 FLJ21432 3' GGCTATGTCTCCTTTTC     52133      CAAACT
                                GGCTA     TTTCCTTTTC
                                |||||     ||||||||||
                                CCGAT     AGAGGAAAAG
                                  AC_____
GAM2143 FYCO1    3' TGGCTGTGTACCTCCTTTTC  52134      ACAA   TT
                                TGGCT    ACT  TCCTTTTC
                                |||||    |||  ||||||||
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                                ACCGA   TGG  AGGAAAAG
                                  CACA  __
GAM2143 HIC     3' GCCTACTTTTCCTTTT     52135     ACAA
                                GCT   ACTTTTCCTTTT
                                |||   ||||||||||||
                                CGG   TGAAAAGGAAAA
                                 A___
GAM2143 HSPC019  3' GGCTGCCTTTTCCTTTT    52136     ACAAA
                                GGCT    CTTTTCCTTTT
                                ||||    ||||||||||||
                                CCGA    GAAAAGGAAAA
                                  CG___
GAM2143 JDD1    3' TGGGTACAAACTTGCCTTTC  52137    C       TT
                                TGG TACAAACTT  CCTTTT
                                ||| |||||||||  ||||||
                                ACC ATGTTTGAA  GGAAAG
                                  C       C_
GAM2143 KHSRP   3' TGACTTTTTTTTTTCCTTTT  52138     ACAAAC
                                TGGCT    TTTTCCTTTT
                                |||||    ||||||||||
                                ACTGA    AAAAGGAAAA
                                  AAAAA_
GAM2143 KIAA0265 3' TGATTATTCCTTTTCCTTTTC 52139   GC  CAAA
                                TG  TA   CTTTTCCTTTTC
                                ||  ||   ||||||||||||
                                AC  AT   GAAAAGGAAAAG
                                 TA  AAG_
GAM2143 KIAA0350 3' TGGCTACATTCCTCCTTTTC  52140       AAC
                                TGGCTACA  TTTTCCTTTTC
                                ||||||||  ||||||||||||
                                ACCGATGT  AGGAGGAAAAG
                                    A__
GAM2143 KIAA0663 3' TGGCTTTCTTCCTTTT     52105     ACAAAC
                                TGGCT    TTTTCCTTTT
                                |||||    ||||||||||
                                ACCGA    AGAAGGAAAA
                                  A_____
GAM2143 KIAA1010 3' TGACTGCAAGTTTCTCCTTTC 52141     A  AC
                                TGGCT CAA  TTTTCCTTTT
                                ||||| |||  ||||||||||
                                ACTGA GTT  AAGAGGAAAG
                                  C  CA
GAM2143 KIAA1634 3' TGGTTACTTTCTTTCCTTTT  52142    C  AAAC
                                TGG TAC   TTTTCCTTTT
                                ||| |||   ||||||||||
                                ACC ATG   GAAAGGAAAA
                                 A  AAA_
GAM2143 KIAA1798 3' GCTACAAACTTACTTTC    52143         TTC
                                GCTACAAACTT  CTTTT
                                ||||||||||  |||||
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                                CGATGTTTGAA   GAAAG
                                      T__
GAM2143  MAB21L2   5'  GGCTTGTTTTTTCCTTTTC   52144     ACAAAC
                                GGCT     TTTTCCTTTTC
                                ||||     ||||||||||
                                CCGA     AAAAGGAAAAG
                                  ACAA__
GAM2143  MGC10871  3'  TGGTCACAAACTCCTTTT    52145    C      TTT
                                TGG TACAAAC   TCCTTTT
                                ||| |||||||   |||||||
                                ACC GTGTTTG   AGGAAAA
                                  A      ___
GAM2143  MGC2488   3'  GCTACATGCTTCCTTTTC    52146      AACT
                                GCTACA    TTTCCTTTTC
                                ||||||    ||||||||||
                                CGATGT    GAAGGAAAAG
                                   AC__
GAM2143  MGC3265   3'  TGGCTTGGATTTCCTTCTC    52147     ACAAACT
                                TGGCT      TTTCCTTTTC
                                |||||      ||||||||||
                                ACCGA      AAAGGAAGAG
                                   ACCT___
GAM2143  nexilin   3'  TGGCACTCCTGGTTTCCTTTT  52148     T  AAA  __
                                TGGC AC   CT  TTTCCTTTT
                                |||| ||   ||  |||||||||
                                ACCG TG   GA  AAAGGAAAA
                                  _ AG_  CC
GAM2143  PTPNS1    3'  TGGTTCGACCTCTTCCTTTTC  52149     CTACAAA
                                TGG      CTTTTCCTTTTC
                                |||      ||||||||||||
                                ACC      GAGAAGGAAAAG
                                  AAGCTG_
GAM2143  UST       3'  TGGCTCCATCCTCCTTTTC    52150      A  AAC
                                TGGCT CA   TTTTCCTTTTC
                                ||||| ||   ||||||||||
                                ACCGA GT   AGGAGGAAAAG
                                   G  ___
GAM2143  ZER6      3'  TGGCTACACAGTTCCTTTC    52151        AACTT
                                TGGCTACA     TTCCTTTT
                                ||||||||     ||||||||
                                ACCGATGT     AAGGAAAG
                                     GTC__
GAM2143  LOC115207 3'  TGGTACAAACTTCCAACTTTC  52152     C         CC
                                TGG TACAAACTTTT  TTTTC
                                ||| ||||||||||  |||||
                                ACC ATGTTTGAAGG  GAAAG
                                  _         TT
GAM2143  LOC133482 5'  TGGCTTTTTTCCTTTT      52153       ACAAAC
                                TGGCT     TTTTCCTTTT
                                |||||     ||||||||||
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                                ACCGA     AAAAGGAAAA
                                  A_____
GAM2143  LOC145652 3'  TGGACTACTTCTTCCTTTT   52154    _   AAAC
                                TGG CTAC   TTTTCCTTTT
                                ||| ||||   ||||||||||
                                ACC GATG   AGAAGGAAAA
                                  T   A___
GAM2143  LOC145945 5'  TGTCTACTTTCTTTTCCTTTT  52155    G   AAA
                                TG CTAC   CTTTTCCTTTT
                                || ||||   ||||||||||
                                AC GATG   GAAAAGGAAAA
                                 A   AAA
GAM2143  LOC146310 5'  TGGACAACCTTTTTCCTTTTC  52156    CT   AC_
                                TGG  ACAA   TTTTCCTTTTC
                                |||  ||||   ||||||||||
                                ACC  TGTT   AAAAGGAAAAG
                                  __   GGA
GAM2143  LOC147514 3'  GGCTACAAACTTTCCTC     52157          T
                                GGCTACAAACTTT CCTT
                                |||||||||||| ||||
                                CCGATGTTTGAAA GGAG
                                          _
GAM2143  LOC147990 3'  TGGCTTTTTTATTTCCTTTTC  52158      ACAAACT
                                TGGCT      TTTCCTTTTC
                                |||||      ||||||||||
                                ACCGA      AAAGGAAAAG
                                   AAAAAT_
GAM2143  LOC149529 3'  GCTGCAAACTTTTGCCTTTT   52159    A       _
                                GCT CAAACTTTT CCTTTT
                                ||| ||||||||| ||||||
                                CGA GTTTGAAAA GGAAAA
                                  C       C
GAM2143  LOC158130 3'  TGGCTAGAATTTTCCTTT    52160      C  AC
                                TGGCTA AA  TTTTCCTTT
                                |||||| ||  |||||||||
                                ACCGAT TT  AAAAGGAAA
                                   C  __
GAM2143  LOC196478 5'  GCTACAAATCCATTTTC     52161       CTTT  _
                                GCTACAAA    TCC TTTTC
                                ||||||||    ||| |||||
                                CGATGTTT    AGG AAAAG
                                     _____   T
GAM2143  LOC200273 3'  GGCTACAAACTTTCCTC     52157          T
                                GGCTACAAACTTT CCTT
                                |||||||||||| ||||
                                CCGATGTTTGAAA GGAG
                                          _
GAM2143  LOC221272 3'  TAGCTACTTTCCTTTT      52162       AAACT
                                TGGCTAC     TTTCCTTTT
                                |||||||     |||||||||
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                              ATCGATG    AAAGGAAAA
                                     _____
GAM2143  LOC221272 3'  GCAGGTAAACTTTTCCTTTTC  52163    TAC_
                              GC   AAACTTTTCCTTTTC
                              ||   ||||||||||||||
                              CG   TTTGAAAAGGAAAAG
                               TCCA
GAM2143  LOC222255 3'  TGGCCGCAGCCCTCCTTTT   52164     TA  AA  TT
                              TGGC  CA  CT  TCCTTTT
                              ||||  ||  ||  |||||||
                              ACCG  GT  GG  AGGAAAA
                                GC  CG  __
GAM2143  LOC245771 5'  TGGCTGATGATCTCTCCTTTT 52165      ACAAAC
                              TGGCT     TTTTCCTTTT
                              |||||     ||||||||||
                              ACCGA     GAGAGGAAAA
                                 CTACTA
GAM2143  LOC253019 3'  TGGCTTTCTTCCTTTT     52105      ACAAAC
                              TGGCT     TTTTCCTTTT
                              |||||     ||||||||||
                              ACCGA     AGAAGGAAAA
                                 A_____
GAM2143  LOC253975 3'  TGGCTTTCTTCCTTTT     52105      ACAAAC
                              TGGCT     TTTTCCTTTT
                              |||||     ||||||||||
                              ACCGA     AGAAGGAAAA
                                 A_____
GAM2143  LOC51064  5'  TGGCAGCAGGAGCTCCTTTTC 52166     TA  AACTT
                              TGGC  CA    TTCCTTTTC
                              ||||  ||    |||||||||
                              ACCG  GT    GAGGAAAAG
                                TC  CCTC_
GAM2143  LOC51634  3'  TGGCTACAGGGTTTCATTTT  52167       AACT   C
                              TGGCTACA   TTTC TTTT
                              ||||||||   |||| ||||
                              ACCGATGT   AAAG AAAA
                                   CCC_   T
GAM2143  LOC56964  3'  TGGCTGAAACCTCCTTTTC   52168     AC    TT
                              TGGCT  AAACT  TCCTTTTC
                              |||||  |||||  ||||||||
                              ACCGA  TTTGG  AGGAAAAG
                                 C_    __
GAM2143  LOC92935  3'  GGCTACAAACCTCTTTTC    52169         TTC
                              GGCTACAAACTT   CTTTTC
                              ||||||||||||   ||||||
                              CCGATGTTTGGA   GAAAAG
                                             ___
GAM2144  PCDHA1    3'  TTGTATTCATATTTCTCTTT  52172        TCAATG
                              TTGTATTCAT     TCTCTTT
                              ||||||||||     |||||||
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                                AACATAAGTA    AGAGAAA
                                     TAA___
GAM2144 PCDHA1   3' TTGTATTCATATTTCTCTTT  52172       TCAATG
                                TTGTATTCAT    TCTCTTT
                                ||||||||||    |||||||
                                AACATAAGTA    AGAGAAA
                                     TAA___
GAM2144 PCDHA10  3' TTGTATTCATATTTCTCTTT  52172       TCAATG
                                TTGTATTCAT    TCTCTTT
                                ||||||||||    |||||||
                                AACATAAGTA    AGAGAAA
                                     TAA___
GAM2144 PCDHA10  3' TTGTATTCATATTTCTCTTT  52172       TCAATG
                                TTGTATTCAT    TCTCTTT
                                ||||||||||    |||||||
                                AACATAAGTA    AGAGAAA
                                     TAA___
GAM2144 PCDHA11  3' TTGTATTCATATTTCTCTTT  52172       TCAATG
                                TTGTATTCAT    TCTCTTT
                                ||||||||||    |||||||
                                AACATAAGTA    AGAGAAA
                                     TAA___
GAM2144 PCDHA12  3' TTGTATTCATATTTCTCTTT  52172       TCAATG
                                TTGTATTCAT    TCTCTTT
                                ||||||||||    |||||||
                                AACATAAGTA    AGAGAAA
                                     TAA___
GAM2144 PCDHA13  3' TTGTATTCATATTTCTCTTT  52172       TCAATG
                                TTGTATTCAT    TCTCTTT
                                ||||||||||    |||||||
                                AACATAAGTA    AGAGAAA
                                     TAA___
GAM2144 PCDHA2   3' TTGTATTCATATTTCTCTTT  52172       TCAATG
                                TTGTATTCAT    TCTCTTT
                                ||||||||||    |||||||
                                AACATAAGTA    AGAGAAA
                                     TAA___
GAM2144 PCDHA3   3' TTGTATTCATATTTCTCTTT  52172       TCAATG
                                TTGTATTCAT    TCTCTTT
                                ||||||||||    |||||||
                                AACATAAGTA    AGAGAAA
                                     TAA___
GAM2144 PCDHA4   3' TTGTATTCATATTTCTCTTT  52172       TCAATG
                                TTGTATTCAT    TCTCTTT
                                ||||||||||    |||||||
                                AACATAAGTA    AGAGAAA
                                     TAA___
GAM2144 PCDHA5   3' TTGTATTCATATTTCTCTTT  52172       TCAATG
                                TTGTATTCAT    TCTCTTT
                                ||||||||||    |||||||
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                                AACATAAGTA     AGAGAAA
                                     TAA___
GAM2144  PCDHA6   3' TTGTATTCATATTTCTCTTT  52172        TCAATG
                                TTGTATTCAT     TCTCTTT
                                ||||||||||     |||||||
                                AACATAAGTA     AGAGAAA
                                     TAA___
GAM2144  PCDHA6   3' TTGTATTCATATTTCTCTTT  52172        TCAATG
                                TTGTATTCAT     TCTCTTT
                                ||||||||||     |||||||
                                AACATAAGTA     AGAGAAA
                                     TAA___
GAM2144  PCDHA7   3' TTGTATTCATATTTCTCTTT  52172        TCAATG
                                TTGTATTCAT     TCTCTTT
                                ||||||||||     |||||||
                                AACATAAGTA     AGAGAAA
                                     TAA___
GAM2144  PCDHA8   3' TTGTATTCATATTTCTCTTT  52172        TCAATG
                                TTGTATTCAT     TCTCTTT
                                ||||||||||     |||||||
                                AACATAAGTA     AGAGAAA
                                     TAA___
GAM2144  PCDHA9   3' TTGTATTCATATTTCTCTTT  52172        TCAATG
                                TTGTATTCAT     TCTCTTT
                                ||||||||||     |||||||
                                AACATAAGTA     AGAGAAA
                                     TAA___
GAM2144  PCDHAC1  3' TTGTATTCATATTTCTCTTT  52172         TCAATG
                                TTGTATTCAT     TCTCTTT
                                ||||||||||     |||||||
                                AACATAAGTA     AGAGAAA
                                     TAA___
GAM2144  PCDHAC2  3' TTGTATTCATATTTCTCTTT  52172         TCAATG
                                TTGTATTCAT     TCTCTTT
                                ||||||||||     |||||||
                                AACATAAGTA     AGAGAAA
                                     TAA___
GAM2144  FLJ11726 3' TTTGTATTCTTCTGCC      52173         A   AA
                                TTTGTATTC TTC  TGTC
                                ||||||||| |||  ||||
                                AAACATAAG AAG  ACGG
                                      _  __
GAM2144  FLJ20666 3' TTTGTGTTCTCTTTGTCTCTTT 52174      A   AT  AA
                                TTTGT TTC  TC  TGTCTCTTT
                                ||||| |||  ||  |||||||||
                                AAACA AAG  AG  ACAGAGAAA
                                   C   __  AA
GAM2144  PEGASUS  3' TTTATATTCATTTCCACACCT  52175          _ A  GT
                                TTTGTATTCATT C AT  CT
                                |||||||||||| | ||  ||
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                                AAATATAAGTAA G TG  GA
                                      A G  TG
GAM2144  SH3BGRL   3'  TTTGTATTCATTTTGAATGT   52176          C__
                                TTTGTATTCATT   AATGT
                                ||||||||||||  |||||
                                AAACATAAGTAA   TTACA
                                      AAC
GAM2144  LOC153546 5'  TTTGTATTTCTTCGTCGCCT   52177        CA   AA
                                TTTGTATT  TTC  TGTCT
                                ||||||||  |||  |||||
                                AAACATAA  AAG  GCGGA
                                     AG   CA
GAM2144  LOC219818 3'  TTTGTGTTCTTCAATGT     52178       A   A
                                TTTGT TTC TTCAATGT
                                ||||| ||| ||||||||
                                AAACA AAG AAGTTACA
                                   C  _
GAM2144  LOC253805 5'  TTTGTATTGTTCAATGT     52179        CA
                                TTTGTATT  TTCAATGT
                                ||||||||  ||||||||
                                AAACATAA  AAGTTACA
                                     C_
GAM2145  AK2       3'  TGGCATAACCAACTTCCTTTTT 52182      TACA   __       C
              CA                  TGGC    AACT  TTTCCTTTT CA
                                ||||    ||||  |||||||||  ||
                                ACCG    TTGG  GAAGGAAAA GT
                                  TA__    TT        A
GAM2145  CRTAP     3'  TGGCTTTCTTCCTTTTCC    52183       ACAAAC
                                TGGCT     TTTTCCTTTTCC
                                |||||     ||||||||||||
                                ACCGA     AGAAGGAAAAGG
                                   A_____
GAM2145  CXorf6    5'  TGATTACAAGCCGACTTTTCCA 52184    GC     A  TTTC
                                TG  TACAA CT    CTTTTCCA
                                ||  ||||| ||    ||||||||
                                AC  ATGTT GG    GAAAAGGT
                                 TA     C  CT__
GAM2145  EPHB2     3'  TGGCACCAGTTTTTCTTTTCCA 52185      T  AAAC     C
                                TGGC AC    TTTTC TTTTCCA
                                |||| ||    ||||| |||||||
                                ACCG TG    AAAAG AAAAGGT
                                  _  GTCA    _
GAM2145  FZD3      3'  TGGCTACAAATTAAAATTTTTC 52186          CTTTTCC
              CA                  TGGCTACAAA      TTTTCCA
                                ||||||||||      |||||||
                                ACCGATGTTT      AAAAGGT
                                      AATTTTA
GAM2145  HMGA2     3'  TGGCCACAAGCTTTTTTTTTC  52112         A     CC
                                TGGCTACAA CTTTT  TTTTC
                                |||||||| |||||  |||||
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                                ACCGGTGTT GAAAA  AAAAG
                                     C    A_
GAM2145 SLC2A4   3' GGCTGCAGGGATTCTTTTCCA 52187     A  AACTT   C
                                GGCT CA    TTC TTTTCCA
                                |||| ||    ||| |||||||
                                CCGA GT    AAG AAAAGGT
                                  C  CCCT_  _
GAM2145 ATP10B   3' TGGTTATAACTTTTCCCT    52188    C  CA
                                TGG TA  AACTTTTCCTT
                                ||| ||  ||||||||||
                                ACC AT  TTGAAAAGGGA
                                  A  A_
GAM2145 BCCIP    3' TGACTATTCCTTTTC       52125       CAAACTT
                                TGGCTA      TTCCTTTTC
                                ||||||      |||||||||
                                ACTGAT      AAGGAAAAG
                                  ________
GAM2145 C20orf30 3' TGGCAGGCAACACTTTTCC   52189     TA_  _
                                TGGC   CAA ACTTTTCC
                                ||||   ||| ||||||||
                                ACCG   GTT TGAAAAGG
                                  TCC   G
GAM2145 DKFZP564O043 3' TAGCTATAAATTTTTCCCTTCC 52190       C   C
                                TGGCTA AAA TTTTCCTTTTC
                                |||||| ||| ||||||||||
                                ATCGAT TTT AAAAGGGAAGG
                                   A   A
GAM2145 FLJ11710 3' TGGCATAGATTCCCCTTTCCA  52191     TACAAACT
                                TGGC       TTTCCTTTTCCA
                                ||||       ||||||||||||
                                ACCG       AAGGGGAAAGGT
                                  TATCT___
GAM2145 FLJ23233 3' TGGCTGAAACCTTTTTCC    52192      AC       CCTT
                                TGGCT  AAACTTTT    TTCC
                                |||||  ||||||||    ||||
                                ACCGA  TTTGGAAA    AAGG
                                  C_       _____
GAM2145 JDD1     3' TGGGTACAAACTTGCCTTTCCA 52193     C       TTC
                                TGG TACAAACTT   CTTTTCCA
                                ||| |||||||||   ||||||||
                                ACC ATGTTTGAA   GGAAAGGT
                                  C        C__
GAM2145 KIAA0265 3' TGATTATTCCTTTTCCTTTTC  52139    GC  CAAA
                                TG  TA    CTTTTCCTTTTC
                                ||  ||    ||||||||||||
                                AC  AT    GAAAAGGAAAAG
                                 TA  AAG_
GAM2145 KIAA0663 3' TGGCTTTCTTCCTTTTCC    52183      ACAAAC
                                TGGCT     TTTTCCTTTTCC
                                |||||     ||||||||||||
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                                ACCGA     AGAAGGAAAAGG
                                  A_____
GAM2145 KIAA1010 3' TGACTGCAAGTTTCTCCTTTCC 52194      A  AC       T
             A                   TGGCT CAA  TTTTCCTTT CCA
                                 ||||| |||  ||||||||| |||
                                 ACTGA GTT  AAGAGGAAA GGT
                                   C   CA       _
GAM2145 KIAA1576 3' TGGCTCAAACTTTTGACC    52195      A       __
                                 TGGCT CAAACTTTT  CC
                                 ||||| |||||||||  ||
                                 ACCGA GTTTGAAAA  GG
                                   _       CT
GAM2145 KIAA1634 3' TGGTTACTTTCTTTCCTTTTTC 52196    C   AAAC       C
             A                   TGG TAC    TTTTCCTTTT CA
                                 ||| |||    |||||||||| ||
                                 ACC ATG    GAAAGGAAAA GT
                                  A  AAA_       A
GAM2145 KIAA1798 3' GCTACAAACTTACTTTC     52143          TTC
                                 GCTACAAACTT   CTTTT
                                 ||||||||||   |||||
                                 CGATGTTTGAA   GAAAG
                                       T__
GAM2145 KNSL7    3' TAGCTACAGGCTTTTATTTTT  52197        AA    CC
                                 TGGCTACA  CTTTT  TTTT
                                 ||||||||  |||||  ||||
                                 ATCGATGT  GAAAA  AAAA
                                     CC    TA
GAM2145 LALP1    3' GCTACAAATTTCATTTC     52198        CT    CT
                                 GCTACAAA  TTTC  TTTC
                                 ||||||||  ||||  ||||
                                 CGATGTTT  AAAG  AAAG
                                     __    T_
GAM2145 MGC2488  3' GCTACATGCTTCCTTTTC    52146       AACT
                                 GCTACA    TTTCCTTTTC
                                 ||||||    ||||||||||
                                 CGATGT    GAAGGAAAAG
                                    AC__
GAM2145 nexilin  3' TGGCACTCCTGGTTTCCTTTT  52148     T  AAA  __
                                 TGGC AC   CT  TTTCCTTTT
                                 |||| ||   ||  |||||||||
                                 ACCG TG   GA  AAAGGAAAA
                                   _ AG_  CC
GAM2145 NKX2B    3' TGCCTACAGGGTTTTCTTTTCC 52199    G     AAC     C
             A                   TG CTACA   TTTTC TTTTCCA
                                 || |||||   ||||| |||||||
                                 AC GATGT   AAAAG AAAAGGT
                                  G    CCC    _
GAM2145 STX18    3' TGGTGTGCACTGTTTCCTTTTT 52200     CTACAA  _       C
             CA                    TGG     ACT TTTCCTTTT CA
                                   |||     ||| ||||||||| ||
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                                ACC      TGA AAAGGAAAA GT
                                  ACACG_  C        A
GAM2145  ZNF271    5'  TGGCTAAAACTTTTACT     52201        C       C
                                TGGCTA AAACTTTT CT
                                |||||| |||||||| ||
                                ACCGAT TTTGAAAA GA
                                   _       T
GAM2145  ZNF317    3'  TGGCCACAAATTTTCTCC     52202          C     CTTT
                                TGGCTACAAA TTTTC    TCC
                                |||||||||| |||||    |||
                                ACCGGTGTTT AAAAG    AGG
                                     _    _____
GAM2145  LOC115207 3'  TGGTACAAACTTCCAACTTTC  52152      C          CC
                                TGG TACAAACTTTT  TTTTC
                                ||| ||||||||||  |||||
                                ACC ATGTTTGAAGG  GAAAG
                                  _         TT
GAM2145  LOC133482 5'  TGGCTTTTTTCCTTTT      52153       ACAAAC
                                TGGCT     TTTTCCTTTT
                                |||||     ||||||||||
                                ACCGA     AAAAGGAAAA
                                   A_____
GAM2145  LOC147080 5'  TGGCTACAAATTTGGCGATTTC 52203          CTTTTCCT
            CA                    TGGCTACAAA       TTTCCA
                                |||||||||       ||||||
                                ACCGATGTTT       AAAGGT
                                      AAACCGCT
GAM2145  LOC147990 3'  TGGCTTTTTTATTTCCTTTTC  52158       ACAAACT
                                TGGCT      TTTCCTTTTC
                                |||||      ||||||||||
                                ACCGA      AAAGGAAAAG
                                   AAAAAT_
GAM2145  LOC149529 3'  GCTGCAAACTTTTGCCTTTT   52159     A        _
                                GCT CAAACTTTT CCTTTT
                                ||| ||||||||| ||||||
                                CGA GTTTGAAAA GGAAAA
                                  C        C
GAM2145  LOC158130 3'  TGGCTAGAATTTTCCTTT     52160       C  AC
                                TGGCTA AA  TTTTCCTTT
                                |||||| ||  |||||||||
                                ACCGAT TT  AAAAGGAAA
                                   C  __
GAM2145  LOC196478 5'  GCTACAAATCCATTTTC      52161         CTTT  _
                                GCTACAAA    TCC TTTTC
                                ||||||||    ||| |||||
                                CGATGTTT    AGG AAAAG
                                     _____   T
GAM2145  LOC219894 3'  TGGTTTCAAACTTTTCTTCT   52204     CTA         C
                                TGG   CAAACTTTTC TTTT
                                |||   |||||||||| ||||
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                                ACC   GTTTGAAAAG AAGA
                                  AAA        _
GAM2145  LOC219988 5'  GCTACAAATTTTGTGCTTTC   52205        C   TC_
                                GCTACAAA TTT   CTTTT
                                |||||||| |||   |||||
                                CGATGTTT AAA   GAAAG
                                     A   CAC
GAM2145  LOC221272 3'  TAGCTACTTTCCTTTTC     52206        AAACT
                                TGGCTAC    TTTCCTTTTC
                                |||||||    ||||||||||
                                ATCGATG    AAAGGAAAAG
                                           _____
GAM2145  LOC221272 3'  GCAGGTAAACTTTTCCTTTTC  52163    TAC_
                                GC    AAACTTTTCCTTTTC
                                ||    ||||||||||||||
                                CG    TTTGAAAAGGAAAAG
                                 TCCA
GAM2145  LOC245771 5'  TGGCTGATGATCTCTCCTTTTT 52207       ACAAAC        C
            CA                    TGGCT     TTTTCCTTTT CA
                                |||||     |||||||||| ||
                                ACCGA     GAGAGGAAAA GT
                                   CTACTA         A
GAM2145  LOC253019 3'  TGGCTTTCTTCCTTTTCC    52183       ACAAAC
                                TGGCT     TTTTCCTTTTCC
                                |||||     ||||||||||||
                                ACCGA     AGAAGGAAAAGG
                                   A_____
GAM2145  LOC253975 3'  TGGCTTTCTTCCTTTTCC    52183       ACAAAC
                                TGGCT     TTTTCCTTTTCC
                                |||||     ||||||||||||
                                ACCGA     AGAAGGAAAAGG
                                   A_____
GAM2145  LOC254873 3'  GGCTGCAGGGATTCTTTTCCA  52187      A  AACTT   C
                                GGCT CA    TTC TTTTCCA
                                |||| ||    ||| |||||||
                                CCGA GT    AAG AAAAGGT
                                  C  CCCT_  _
GAM2145  LOC51634  3'  TGGCTACAGGGTTTCATTTT   52167        AACT    C
                                TGGCTACA    TTTC TTTT
                                ||||||||    |||| ||||
                                ACCGATGT    AAAG AAAA
                                     CCC_    T
GAM2146  HAL      3'  TTTATATTCATTCCTTATCTCC 52210           AA
            TT                    TTTGTATTCATTC  TGTCTCCTT
                                ||||||||||||  |||||||||
                                AAATATAAGTAAG  ATAGAGGAA
                                        GA
GAM2146  KCNJ16   3'  TATTTATTCCAGCCTCCTT   52211      C    AAT
                                TATT ATTC   GTCTCCTT
                                ||||  ||||   ||||||||
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                                ATAA TAAG   CGGAGGAA
                                  A   GT_
GAM2146 NEBL     3'  TTGTAAAACATTCAATGT    52212      TT_
                                TTGTA   CATTCAATGT
                                |||||   ||||||||||
                                AACAT   GTAAGTTACA
                                   TTT
GAM2146 PKHD1    5'  TCTGTTTCTGTCTCCT      52213      A   ATTCAA
                                TTTGT TTC     TGTCTCCT
                                ||||| |||     ||||||||
                                AGACA AAG     ACAGAGGA
                                  _  _______
GAM2146 FLJ11726 3'  TTTGTATTCTTCTGCC      52173         A   AA
                                TTTGTATTC TTC  TGTC
                                ||||||||| |||  ||||
                                AAACATAAG AAG  ACGG
                                    _  __
GAM2146 KIAA1553 3'  TTTGCATTCGACTGTTTCCTT  52214         ATTCAA   C
                                TTTGTATTC     TGT TCCTT
                                |||||||||     ||| |||||
                                AAACGTAAG     ACA AGGAA
                                     CTG___   A
GAM2146 PEGASUS  3'  TTTATATTCATTTCCACACCT  52175           _ A  GT
                                TTTGTATTCATT C AT  CT
                                |||||||||||| | ||  ||
                                AAATATAAGTAA G TG  GA
                                       A G  TG
GAM2146 PRP4     3'  TTTGTATTTACTCAAACCCTT  52215        C     TGTC
                                TTTGTATT ATTCAA    TCCTT
                                |||||||| ||||||    |||||
                                AAACATAA TGAGTT    GGGAA
                                     A     T___
GAM2146 SH3BGRL  3'  TTTGTATTCATTTTGAATGT   52176           C__
                                TTTGTATTCATT   AATGT
                                ||||||||||||   |||||
                                AAACATAAGTAA   TTACA
                                       AAC
GAM2146 LOC151512 5'  TCTGTTCATCCTCCTCTCCTT  52216      AT     AATG
                                TTTGT  TCATTC    TCTCCTT
                                |||||  ||||||    |||||||
                                AGACA  AGTAGG    AGAGGAA
                                   __     AGG_
GAM2146 LOC153546 5'  TTTGTATTTCTTCGTCGCCTT  52217        CA   AAT   T
                                TTTGTATT  TTC   GTC CCTT
                                ||||||||  |||   ||| ||||
                                AAACATAA  AAG   CAG GGAA
                                     AG   ___   C
GAM2146 LOC158402 5'  TTTGAATCTGGTCAATGTCTCC 52218      T   CAT
             TT                   TTTG ATT   TCAATGTCTCCTT
                                ||||| |||   ||||||||||||
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                                AAAC TAG   AGTTACAGAGGAA
                                  T   ACC
GAM2146  LOC219818 3'  TTTGTGTTCTTCAATGT     52178       A   A
                                TTTGT TTC TTCAATGT
                                ||||| ||| ||||||||
                                AAACA AAG AAGTTACA
                                   C   _
GAM2146  LOC253805 5'  TTTGTATTGTTCAATGT     52179         CA
                                TTTGTATT  TTCAATGT
                                ||||||||  ||||||||
                                AAACATAA  AAGTTACA
                                     C_
GAM2146  LOC54103  5'  TTTGTATTCCATTCTTTTCT   52219          _   AATG
                                TTTGTATTC ATTC    TCT
                                ||||||||| ||||    |||
                                AAACATAAG TAAG    AGA
                                      G    AAA_
GAM2146  LOC90529  3'  TTCGTATTACTGATGTTTCCTT 52220         C   CA    C
                                TTTGTATT ATT  ATGT TCCTT
                                |||||||| |||  |||| |||||
                                AAGCATAA TGA  TACA AGGAA
                                     _  C_    A
GAM2147  AK2       3'  TGGCATAACCAACTTCCTTTTT 52182      TACA   __       C
            CA                    TGGC    AACT  TTTCCTTTT CA
                                ||||    ||||  ||||||||| ||
                                ACCG    TTGG  GAAGGAAAA GT
                                  TA__    TT        A
GAM2147  CRTAP     3'  TGGCTTTCTTCCTTTTCC     52183       ACAAAC
                                TGGCT     TTTTCCTTTTCC
                                |||||     ||||||||||||
                                ACCGA     AGAAGGAAAAGG
                                  A_____
GAM2147  CXorf6    5'  TGATTACAAGCCGACTTTTCCA 52184     GC     A  TTTC
                                TG  TACAA CT    CTTTTCCA
                                ||  ||||| ||    ||||||||
                                AC  ATGTT GG    GAAAAGGT
                                 TA    C  CT__
GAM2147  EPHB2     3'  TGGCACCAGTTTTTCTTTTCCA 52185      T  AAAC    C
                                TGGC AC    TTTTC TTTTCCA
                                |||| ||    ||||| |||||||
                                ACCG TG    AAAAG AAAAGGT
                                  _  GTCA    _
GAM2147  FZD3      3'  TGGCTACAAATTAAAATTTTTC 52186          CTTTTCC
            CA                    TGGCTACAAA      TTTTCCA
                                ||||||||||      |||||||
                                ACCGATGTTT      AAAAGGT
                                      AATTTTA
GAM2147  HMGA2     3'  TGGCCACAAGCTTTTTTTTTC  52112         A    CC
                                TGGCTACAA CTTTT  TTTTC
                                ||||||||| |||||  |||||
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                                ACCGGTGTT GAAAA  AAAAG
                                     C    A_
GAM2147  SLC2A4   3'  GGCTGCAGGGATTCTTTTCCA  52187     A  AACTT   C
                                GGCT CA    TTC TTTTCCA
                                |||| ||    ||| |||||||
                                CCGA GT    AAG AAAAGGT
                                  C  CCCT_  _
GAM2147  ATP10B   3'  TGGTTATAACTTTTCCCT    52188     C  CA
                                TGG TA  AACTTTTCCTT
                                ||| ||  ||||||||||
                                ACC AT  TTGAAAAGGGA
                                  A  A_
GAM2147  BCCIP    3'  TGACTATTCCTTTTC       52125       CAAACTT
                                TGGCTA      TTCCTTTTC
                                ||||||      |||||||||
                                ACTGAT      AAGGAAAAG

                                _______
GAM2147  C20orf30 3'  TGGCAGGCAACACTTTTCC   52189     TA_  _
                                TGGC   CAA ACTTTTCC
                                ||||   ||| ||||||||
                                ACCG   GTT TGAAAAGG
                                  TCC   G
GAM2147  DKFZP564O043 3'  TAGCTATAAATTTTTCCCTTCC 52190       C   C
                                TGGCTA AAA TTTTCCTTTTC
                                |||||| ||| ||||||||||
                                ATCGAT TTT AAAAGGGAAGG
                                   A   A
GAM2147  FLJ11710 3'  TGGCATAGATTCCCCTTTCCA  52191     TACAAACT
                                TGGC       TTTCCTTTTCCA
                                ||||       ||||||||||||
                                ACCG       AAGGGGAAAGGT
                                  TATCT___
GAM2147  FLJ23233 3'  TGGCTGAAACCTTTTTCC    52192      AC       CCTT
                                TGGCT  AAACTTTT    TTCC
                                |||||  ||||||||    ||||
                                ACCGA  TTTGGAAA    AAGG
                                  C_       _____
GAM2147  JDD1     3'  TGGGTACAAACTTGCCTTTCCA 52193     C       TTC
                                TGG TACAAACTT   CTTTTCCA
                                ||| |||||||||   ||||||||
                                ACC ATGTTTGAA   GGAAAGGT
                                  C        C__
GAM2147  KIAA0265 3'  TGATTATTCCTTTTCCTTTTC  52139    GC  CAAA
                                TG  TA    CTTTTCCTTTTC
                                ||  ||    ||||||||||||
                                AC  AT    GAAAAGGAAAAG
                                 TA  AAG_
GAM2147  KIAA0663 3'  TGGCTTTCTTCCTTTTCC    52183      ACAAAC
                                TGGCT     TTTTCCTTTTCC
                                |||||     ||||||||||||
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                                ACCGA     AGAAGGAAAAGG
                                  A_____
GAM2147  KIAA1010  3'  TGACTGCAAGTTTCTCCTTTCC 52194      A   AC       T
              A                   TGGCT CAA  TTTTCCTTT CCA
                                  ||||| |||  ||||||||| |||
                                  ACTGA GTT  AAGAGGAAA GGT
                                    C   CA       _
GAM2147  KIAA1576  3'  TGGCTCAAACTTTTGACC    52195      A       __
                                  TGGCT CAAACTTTT  CC
                                  ||||| |||||||||  ||
                                  ACCGA GTTTGAAAA  GG
                                    _       CT
GAM2147  KIAA1634  3'  TGGTTACTTTCTTTCCTTTTTC 52196    C   AAAC       C
              A                   TGG TAC    TTTTCCTTTT CA
                                  ||| |||    |||||||||| ||
                                  ACC ATG    GAAAGGAAAA GT
                                    A  AAA_       A
GAM2147  KIAL1798  3'  GCTACAAACTTACTTTC     52143          TTC
                                  GCTACAAACTT   CTTTT
                                  ||||||||||   |||||
                                  CGATGTTTGAA   GAAAG
                                        T__
GAM2147  KNSL7    3'  TAGCTACAGGCTTTTATTTTT  52197        AA    CC
                                  TGGCTACA  CTTTT  TTTT
                                  ||||||||  |||||  ||||
                                  ATCGATGT  GAAAA  AAAA
                                       CC    TA
GAM2147  LALP1    3'  GCTACAAATTTCATTTC     52198        CT    CT
                                  GCTACAAA  TTTC  TTTC
                                  ||||||||  ||||  ||||
                                  CGATGTTT  AAAG  AAAG
                                       __    T_
GAM2147  MGC2488  3'  GCTACATGCTTCCTTTTC    52146       AACT
                                  GCTACA    TTTCCTTTTC
                                  ||||||    ||||||||||
                                  CGATGT    GAAGGAAAAG
                                     AC__
GAM2147  nexilin  3'  TGGCACTCCTGGTTTCCTTTT  52148     T  AAA  __
                                  TGGC AC   CT  TTTCCTTTT
                                  |||| ||   ||  |||||||||
                                  ACCG TG   GA  AAAGGAAAA
                                    _  AG_  CC
GAM2147  NKX2B    3'  TGCCTACAGGGTTTTCTTTTCC 52199    G     AAC     C
              A                   TG CTACA   TTTTC TTTTCCA
                                  || |||||   ||||| |||||||
                                  AC GATGT   AAAAG AAAAGGT
                                   G    CCC    _
GAM2147  STX18    3'  TGGTGTGCACTGTTTCCTTTTT 52200     CTACAA  _       C
              CA                    TGG     ACT TTTCCTTTT CA
                                  |||     ||| ||||||||| ||
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                                ACC      TGA AAAGGAAAA GT
                                  ACACG_  C        A
GAM2147  ZNF271    5'  TGGCTAAAACTTTTACT     52201        C       C
                                TGGCTA AAACTTTT CT
                                |||||| |||||||| ||
                                ACCGAT TTTGAAAA GA
                                   _       T
GAM2147  ZNF317    3'  TGGCCACAAATTTTCTCC     52202          C     CTTT
                                TGGCTACAAA TTTTC    TCC
                                |||||||||| |||||    |||
                                ACCGGTGTTT AAAAG    AGG
                                     _    _____
GAM2147  LOC115207 3'  TGGTACAAACTTCCAACTTTC  52152      C          CC
                                TGG TACAAACTTTT  TTTTC
                                ||| ||||||||||  |||||
                                ACC ATGTTTGAAGG  GAAAG
                                  _         TT
GAM2147  LOC133482 5'  TGGCTTTTTTCCTTTT      52153       ACAAAC
                                TGGCT     TTTTCCTTTT
                                |||||     ||||||||||
                                ACCGA     AAAAGGAAAA
                                   A_____
GAM2147  LOC147080 5'  TGGCTACAAATTTGGCGATTTC 52203          CTTTTCCT
           CA                     TGGCTACAAA       TTTCCA
                                |||||||||       ||||||
                                ACCGATGTTT       AAAGGT
                                     AAACCGCT
GAM2147  LOC147990 3'  TGGCTTTTTTATTTCCTTTTC  52158       ACAAACT
                                TGGCT      TTTCCTTTTC
                                |||||      ||||||||||
                                ACCGA      AAAGGAAAAG
                                   AAAAAT_
GAM2147  LOC149529 3'  GCTGCAAACTTTTGCCTTTT   52159     A        _
                                GCT CAAACTTTT CCTTTT
                                ||| ||||||||| ||||||
                                CGA GTTTGAAAA GGAAAA
                                  C        C
GAM2147  LOC158130 3'  TGGCTAGAATTTTCCTTT     52160       C  AC
                                TGGCTA AA  TTTTCCTTT
                                |||||| ||  |||||||||
                                ACCGAT TT  AAAAGGAAA
                                   C  __
GAM2147  LOC196478 5'  GCTACAAATCCATTTTC      52161         CTTT  _
                                GCTACAAA    TCC TTTTC
                                ||||||||    ||| |||||
                                CGATGTTT    AGG AAAAG
                                     _____   T
GAM2147  LOC219894 3'  TGGTTTCAAACTTTTCTTCT   52204     CTA         C
                                TGG   CAAACTTTTC TTTT
                                |||   |||||||||| ||||
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                                ACC   GTTTGAAAAG AAGA
                                  AAA        _
GAM2147  LOC219988 5'  GCTACAAATTTTGTGCTTTC   52205        C   TC_
                                GCTACAAA TTT   CTTTT
                                |||||||| |||   |||||
                                CGATGTTT AAA   GAAAG
                                     A   CAC
GAM2147  LOC221272 3'  TAGCTACTTTCCTTTTC     52206        AAACT
                                TGGCTAC    TTTCCTTTTC
                                |||||||    ||||||||||
                                ATCGATG    AAAGGAAAAG
                                           _____
GAM2147  LOC221272 3'  GCAGGTAAACTTTTCCTTTTC  52163    TAC_
                                GC    AAACTTTTCCTTTTC
                                ||    ||||||||||||||
                                CG    TTTGAAAAGGAAAAG
                                 TCCA
GAM2147  LOC245771 5'  TGGCTGATGATCTCTCCTTTTT 52207       ACAAAC         C
            CA                    TGGCT     TTTTCCTTTT CA
                                |||||     |||||||||| ||
                                ACCGA     GAGAGGAAAA GT
                                   CTACTA         A
GAM2147  LOC253019 3'  TGGCTTTCTTCCTTTTCC    52183       ACAAAC
                                TGGCT     TTTTCCTTTTCC
                                |||||     ||||||||||||
                                ACCGA     AGAAGGAAAAGG
                                   A_____
GAM2147  LOC253975 3'  TGGCTTTCTTCCTTTTCC    52183       ACAAAC
                                TGGCT     TTTTCCTTTTCC
                                |||||     ||||||||||||
                                ACCGA     AGAAGGAAAAGG
                                   A_____
GAM2147  LOC254873 3'  GGCTGCAGGGATTCTTTTCCA  52187      A  AACTT   C
                                GGCT CA    TTC TTTTCCA
                                |||| ||    ||| |||||||
                                CCGA GT    AAG AAAAGGT
                                  C  CCCT_   _
GAM2147  LOC51634  3'  TGGCTACAGGGTTTCATTTT   52167        AACT    C
                                TGGCTACA    TTTC TTTT
                                ||||||||    |||| ||||
                                ACCGATGT    AAAG AAAA
                                     CCC_    T
GAM2148  COL4A3    3'  TAACAATATCATTTTAAAAC   52224             TG
                                TAACAATATCATTTT  GAT
                                ||||||||||||||  |||
                                ATTGTTATAGTAAAA  TTG
                                          TT
GAM2148  COL4A3    3'  TAACAATATCATTTTAAAAC   52224             TG
                                TAACAATATCATTTT  GAT
                                ||||||||||||||  |||
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                                ATTGTTATAGTAAAA  TTG
                                      TT
GAM2148  COL4A3   3'  TAACAATATCATTTTAAAAC  52224           TG
                                TAACAATATCATTTT  GAT
                                |||||||||||||||  |||
                                ATTGTTATAGTAAAA  TTG
                                      TT
GAM2148  MLLT2    3'  CAATATCACTTGCAGTGTT   52225         T  A
                                CAATATCATTT TGG TGTT
                                |||||||||||| ||| ||||
                                GTTATAGTGAA GTC ACAA
                                      C  _
GAM2148  GNB4     3'  ACAGTATCATTTCTGTCTGTT  52226    A       GA
                                ACA TATCATTTTTG  TGTT
                                ||| ||||||||||  ||||
                                TGT ATAGTAAAGAC  ACAA
                                  C         AG
GAM2148  KIAA1219 3'  TAACAGGAATCCTTGGATGTT  52227     ATATC
                                TAACA    ATTTTTGGATGTT
                                |||||    |||||||||||||
                                ATTGT    TAGGAACCTACAA
                                   CCT__
GAM2148  KIAA1718 3'  TAACAGTATGCACCTTGGATGT 52228     A  _    T
           T                     TAACA TAT CATTTT GGATGTT
                                |||||| ||| |||||| |||||||
                                ATTGT ATA GTGGAA CCTACAA
                                   C  C    _
GAM2148  VCY2     5'  AACAATATCACCTGGGTGTT   52229         TT   A
                                AACAATATCAT  TTGG TGTT
                                ||||||||||  |||| ||||
                                TTGTTATAGTG  GACC ACAA
                                      __   C
GAM2148  VCY2     5'  AACAATATCACCTGGGTGTT   52229         TT   A
                                AACAATATCAT  TTGG TGTT
                                ||||||||||  |||| ||||
                                TTGTTATAGTG  GACC ACAA
                                      __   C
GAM2148  LOC146669 5'  ACAATATCATCGGCAGGTGTT  52230         TTT_  A
                                ACAATATCATT    GG TGTT
                                ||||||||||    || ||||
                                TGTTATAGTAG    CC ACAA
                                      CCGT  _
GAM2148  LOC197273 3'  AACAAAGCTATTTTTGGATGTT 52231      TATC
                                AACAA    ATTTTTGGATGTT
                                |||||    |||||||||||||
                                TTGTT    TAAAAACCTACAA
                                   TCGA
GAM2149  REV1L    3'  TATGCTACAGTAAAATAATTA  52234      _  A
                                TGTGT ACA GTAAAATAATTA
                                ||||| ||| ||||||||||||
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                                ATACG TGT CATTTTATTAAT
                                  A  _
GAM2149  LOC130752 3'  TATTGTGCTATCAAGTAA    52235        A__
                                TATTGTGT   CAAGTAA
                                ||||||||   |||||||
                                ATAACACG   GTTCATT
                                     ATA
GAM2150  SVIL     3'  GTTGTGTTTATTCTG      52238     A   CG
                                GTTG TGT  TTATTCTG
                                |||| |||  ||||||||
                                CAAC ACA  AATAAGAC
                                  _  __
GAM2150  SVIL     3'  GTTGTGTTTATTCTG      52238     A   CG
                                GTTG TGT  TTATTCTG
                                |||| |||  ||||||||
                                CAAC ACA  AATAAGAC
                                  _  __
GAM2150  ARL5     3'  TGTGCTGATTTGTATTCTGA  52239    C     GTC  T
                                TG GTTGAT   GT ATTCTGA
                                || ||||||   || |||||||
                                AC CGACTA   CA TAAGACT
                                 A     AA_ _
GAM2150  DQX1     3'  TGCTTTGGTGTCACCCTGA   52240    G   AT  C
                                TGC TTG  GT GTTATTCTGA
                                ||| |||  || ||||||||||
                                ACG AAC  CA CAGTGGGACT
                                  A  __ _
GAM2150  FLJ13962 3'  GTTGGCATTGTTATTCTG    52241     AT  C
                                GTTG  GT GTTATTCTG
                                ||||  || |||||||||
                                CAAC  TA CAATAAGAC
                                   CG  A
GAM2150  FTSJ1    3'  CGTTGATGAGATGATATTTTGA 52242        TCGT__   C
                                CGTTGATG     TATT TGA
                                ||||||||     |||| |||
                                GCAACTAC     ATAA ACT
                                     TCTACT    A
GAM2150  KIAA0992 3'  TGCTTTGATGTCTAGTCCCTG  52243    G      GTTA
                                TGC TTGATGTC    TTCTG
                                ||| ||||||||    |||||
                                ACG AACTACAG    GGGAC
                                  A       ATCA
GAM2150  KIAA1396 3'  TGCGTTGATCTCACTG      52244        G   TTATT
                                TGCGTTGAT TCG     CTG
                                ||||||||| |||     |||
                                ACGCAACTA AGT     GAC
                                     G  _____
GAM2150  LANO     3'  GTGTGAGTCTATTCTG      52245    _   T   GT
                                GT TGA GTC  TATTCTG
                                || ||| |||  |||||||
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                                CA ACT CAG  ATAAGAC
                                 C  _  __
GAM2150 LANO     3' GTGTGAGTCTATTCTG     52245   _  T  GT
                                GT TGA GTC  TATTCTG
                                || ||| |||  |||||||
                                CA ACT CAG  ATAAGAC
                                 C  _  __
GAM2150 LOC122618 5' TGCCTTGGTGTCTATCCTGA  52246    G  A   GT
                                TGC TTG TGTC  TATTCTGA
                                ||| ||| ||||  ||||||||
                                ACG AAC ACAG  ATAGGACT
                                 G  C   __
GAM2150 LOC133584 3' TGCATTGATGTGTGATCTCTG  52247          C  TA_
                                TGCGTTGATGT GT   TTCTG
                                |||||||||| ||   |||||
                                ACGTAACTACA CA   GAGAC
                                      _ CTA
GAM2150 LOC139248 5' TGTGTTGTTGTCACTCTGA   52248    C   A   GTT
                                TG GTTG TGTC   ATTCTGA
                                || |||| ||||   |||||||
                                AC CAAC ACAG   TGAGACT
                                 A   A   ___
GAM2150 LOC151056 3' GTTGATGTTTTAGTCTG     52249        CG   T
                                GTTGATGT  TTA TCTG
                                ||||||||  ||| ||||
                                CAACTACA  AAT AGAC
                                     A_  C
GAM2150 LOC158696 5' TGCATTGATGTCTGTAACTTAT 52250        _ ____   C   III
            TTTGAT                TTGATGTC GT   TATT TGA   T
                                ||||||||  ||   |||| |||   |
                                AACTACAG CA   ATAA ACT   A
                                     A  TTGA   A   III
GAM2150 LOC222224 3' TGTGTTGATGTTAGCATCTGA  52251    C      CGTTAT
                                TG GTTGATGT     TCTGA
                                || ||||||||     |||||
                                AC CAACTACA     AGACT
                                 A       ATCGT_
GAM2151 AR       5' TGCGGGAAGCTCCAGAG     52254    A      CT  C
                                TG CGGGAAGC  TA GAG
                                || ||||||||  || |||
                                AC GCCCTTCG  GT CTC
                                 _       AG  _
GAM2151 CKAP1    5' GACGGGACTTACGAG       52255       AGC
                                GACGGGA   CTTACGAG
                                |||||||   ||||||||
                                CTGCCCT   GAATGCTC
                                     ___
GAM2151 GRP      5' GACGGGAAGCCCTTGGAG    52256           AC
                                GACGGGAAGCCTT  GAG
                                ||||||||||||  |||
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                                CTGCCCTTCGGGA CTC
                                      AC
GAM2151 HDAC4    3' CGGCGGGAAGCCGCGAG    52257    A       TTA
                                TG CGGGAAGCC  CGAG
                                || |||||||||  ||||
                                GC GCCCTTCGG  GCTC
                                 C       C__
GAM2151 ROBO1    3' TGACAGGAGGCATCTTGAG   52258       A  C  AC
                                TGACGGGA GC TT  GAG
                                |||||||| || ||  |||
                                ACTGTCCT CG AG  CTC
                                     C  T  AA
GAM2151 ROBO1    3' TGACAGGAGGCATCTTGAG   52258       A  C  AC
                                TGACGGGA GC TT  GAG
                                |||||||| || ||  |||
                                ACTGTCCT CG AG  CTC
                                     C  T  AA
GAM2151 SPAP1    3' TGACAGGAGGTGCCTCCTGAG 52259       A__    AC
                                TGACGGGA  GCCTT  GAG
                                ||||||||  |||||  |||
                                ACTGTCCT  CGGAG  CTC
                                     CCA    GA
GAM2151 SPAP1    3' TGACAGGAGGTGCCTCCTGAG 52259       A__    AC
                                TGACGGGA  GCCTT  GAG
                                ||||||||  |||||  |||
                                ACTGTCCT  CGGAG  CTC
                                     CCA    GA
GAM2151 BOLL     5' TGGCGGGAAGCCTCAACG    52260    A       _
                                TG CGGGAAGCCTTA CG
                                || ||||||||||| ||
                                AC GCCCTTCGGAGT GC
                                 C         T
GAM2151 C20orf160 3' TAACGGGAGGCACACAGAG   52261       A  CT  _
                                TGACGGGA GC  TAC GAG
                                |||||||| ||  ||| |||
                                ATTGCCCT CG  GTG CTC
                                     C  T_  T
GAM2151 CARD9    3' TGACGGGACAGCACAAG     52262       _  CTT
                                TGACGGGA AGC  ACGAG
                                |||||||| |||  |||||
                                ACTGCCCT TCG  TGTTC
                                     G  ___
GAM2151 Di-Ras2  3' TGACAGGAAGACTGCTGAG   52263       C  TAC
                                TGACGGGAAG CT  GAG
                                |||||||||| ||  |||
                                ACTGTCCTTC GA  CTC
                                      T  CGA
GAM2151 DKFZP564C196 5' TGGCAGGAAGCCGCCAAG   52264    A       TTA
                                TG CGGGAAGCC  CGAG
                                || |||||||||  ||||
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                                AC GTCCTTCGG   GTTC
                                 C        CG_
GAM2151  DKFZP586I2223 3'  TGAGGGAGAAAGCCTGAG    52265     C   ___    TAC
                                TGA GGGA   AGCCT   GAG
                                ||| ||||   |||||   |||
                                ACT CCCT   TCGGA   CTC
                                  _    CTT    ___
GAM2151  DKFZP586I2223 3'  TGAGGGAGAAAGCCTGAG    52265     C   ___    TAC
                                TGA GGGA   AGCCT   GAG
                                ||| ||||   |||||   |||
                                ACT CCCT   TCGGA   CTC
                                  _    CTT    ___
GAM2151  DKFZP586I2223 3'  TGAGGGAGAAAGCCTGAG    52265     C   ___    TAC
                                TGA GGGA   AGCCT   GAG
                                ||| ||||   |||||   |||
                                ACT CCCT   TCGGA   CTC
                                  _    CTT    ___
GAM2151  FLJ13052  3'  TGCGGGAAGCTCCTCACG    52266    A      __
                                TG CGGGAAGC  CTTACG
                                || ||||||||  ||||||
                                AC GCCCTTCG  GAGTGC
                                  _       AG
GAM2151  GSG2      3'  TGACTGGAAACCTGTGAG    52267      G       TAC
                                TGAC GGAAGCCT   GAG
                                |||| ||||||||   |||
                                ACTG CCTTTGGA   CTC
                                   A       CA_
GAM2151  KBRAS2    3'  TGATGGGAAGCCCAGAG     52268     C       TAC
                                TGA GGGAAGCCT   GAG
                                ||| |||||||||   |||
                                ACT CCCTTCGGG   CTC
                                  A        T__
GAM2151  NUDEL     3'  GACGGGAAGGCTGGCGAG    52269          C  TA
                                GACGGGAAG CT  CGAG
                                ||||||||| ||  ||||
                                CTGCCCTTC GA  GCTC
                                      C  CC
GAM2151  SCYA5     3'  TGAGGGGAAGCCTCCCAAG   52270     C       TA
                                TGA GGGAAGCCT  CGAG
                                ||| |||||||||  ||||
                                ACT CCCTTCGGA  GTTC
                                  C        GG
GAM2151  ZNF183    5'  TGACGGAAGAGGACTGCGAG  52271          _  CC  A
                                TGACGGGA AG  TT CGAG
                                |||||||| ||  || ||||
                                ACTGCCTT TC  GA GCTC
                                     C  CT  C
GAM2151  LOC133308 5'  TGACGAGACACCGCGAG     52272          A   TTA
                                TGACGGGA GCC   CGAG
                                |||||||| |||   ||||
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                                ACTGCTCT TGG   GCTC
                                     G   C__
GAM2151  LOC133728 5'  TGGCGGCAGTCCCACGAG    52273    A   GA  C
                                TG CGG  AG CTTACGAG
                                || |||  || ||||||||
                                AC GCC  TC GGGTGCTC
                                 C   G_  A
GAM2151  LOC153196 5'  TGCGGGAAGCCTTGAG      52274    A         AC
                                TG CGGGAAGCCTT  GAG
                                || ||||||||||  |||
                                AC GCCCTTCGGAA  CTC
                                 _         __
GAM2151  LOC91266  3'  TGACGGTGCCCACGAG      52275       GAA    T
                                TGACGG   GCCT ACGAG
                                ||||||   |||| |||||
                                ACTGCC   CGGG TGCTC
                                   A__   _
GAM2151  LOC91445  3'  TGATGGGAAACCTGTGAG    52276     C       TAC
                                TGA GGGAAGCCT   GAG
                                ||| |||||||||   |||
                                ACT CCCTTTGGA   CTC
                                  A        CA_
GAM2152  BAZ1B     3'  TATGATGCTGGTGAATACACAA 52279         AATA_
                                TATGATGC     AATACACGA
                                ||||||||     |||||||||
                                ATACTACG     TTATGTGTT
                                     ACCAC
GAM2152  LAMC2     3'  TATGGTGCAATAAGAC      52280      A       ATACAC
                                TATG TGCAATAA      GAC
                                |||| ||||||||      |||
                                ATAC ACGTTATT      CTG
                                  C       _______
GAM2152  PCDHB7    3'  TATGATGCATTAAAAGCA     52281          A    TA
                                TATGATGCA TAAA  CA
                                ||||||||| ||||  ||
                                ATACTACGT ATTT  GT
                                     A    TC
GAM2152  SHOC2     3'  TATGATATAATAAATACA     52282        C
                                TATGATG AATAAATACA
                                ||||||| ||||||||||
                                ATACTAT TTATTTATGT
                                   A
GAM2152  TP63      3'  ATGCTCAAATACATGAC      52283      AA       C
                                ATGC  TAAATACA GAC
                                ||||  |||||||| |||
                                TACG  GTTTATGT CTG
                                  A_       A
GAM2152  STIP-1    3'  TATGATGCTAATAAATGACACA 52284          _      _
            A                    TATGATGC AATAAAT ACACGA
                                ||||||||| ||||||| ||||||
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                                ATACTACG TTATTTA TGTGTT
                                    A      C
GAM2153  CALU     3'  GGTGGCATTATTAAATTA    52287      AGA
                                GGTGG   ATTATTAAATTA
                                |||||   ||||||||||||
                                CCACC   TAATAATTTAAT
                                   G__
GAM2153  DKFZP564B1162 3'  TACGGTGAGAAAGATTA     52288       G    TT
                                TACGGTG AGAA  ATTA
                                ||||||| ||||  ||||
                                ATGCCAC TCTT  TAAT
                                    _   TC
GAM2153  KIAA1598  3'  GGTGAGGAGAGTTCAAATTAC  52289     __    ATTA
                                GGT  GGAGA    TTAAATTAC
                                |||  |||||    |||||||||
                                CCA  CCTCT    AGTTTAATG
                                  CT    CA__
GAM2154  AMD1     3'  TTTTTGCGTTTTTTCTTCATTT 52292      _    ___
             TTC                  TTTTT CGTTT  TTTTCGTTTTTT
                                |||||| |||||  ||||||||||||
                                AAAAA GCAAA  AGAAGTAAAAAG
                                   C    AA
GAM2154  BCL6     3'  TTTTTTGTTCTTTTTGTTTTTT 52293      C      C
             T                   TTTTT GTTTTTTT GTTTTTTT
                                |||||| |||||||| ||||||||
                                AAAAA CAAGAAAA CAAAAAAA
                                   A       A
GAM2154  BCL6     3'  TTTTTTGTTCTTTTTGTTTTTT 52293      C      C
             T                   TTTTT GTTTTTTT GTTTTTTT
                                |||||| |||||||| ||||||||
                                AAAAA CAAGAAAA CAAAAAAA
                                   A       A
GAM2154  CASP1    3'  TTTTTTTTTTTTTTCATTTTTC 52294      CG
                                TTTTT  TTTTTTTCGTTTTTT
                                |||||  ||||||||||||||
                                AAAAA  AAAAAAAGTAAAAAG
                                   AA
GAM2154  CASP1    3'  TTTTTTTTTTTTTTCATTTTTC 52294      CG
                                TTTTT  TTTTTTTCGTTTTTT
                                |||||  ||||||||||||||
                                AAAAA  AAAAAAAGTAAAAAG
                                   AA
GAM2154  CASP1    3'  TTTTTTTTTTTTTTCATTTTTC 52294      CG
                                TTTTT  TTTTTTTCGTTTTTT
                                |||||  ||||||||||||||
                                AAAAA  AAAAAAAGTAAAAAG
                                   AA
GAM2154  CASP1    3'  TTTTTTTTTTTTTTCATTTTTC 52294      CG
                                TTTTT  TTTTTTTCGTTTTTT
                                |||||  ||||||||||||||
```

AAAAA AAAAAAAGTAAAAAG
AA
GAM2154 CASP1 3' TTTTTTTTTTTTTTCATTTTTC 52294 CG
TTTTT TTTTTTTCGTTTTTT
AAAAA AAAAAAAGTAAAAAG
AA
GAM2154 DDX3 5' TTTTTCGTTTTTTTTGTTTTT 52296 C
TTTTTCGTTTTTTT GTTTTT
AAAAAGCAAAAAAA CAAAAA
A
GAM2154 DDX3 5' TTTCGTTTTTCGTTTTTTT 52295 TT
TTTCGTTTT TCGTTTTTTT
AAAGCAAAA AGCAAAAAAA
GAM2154 DDX3 5' TTTTTCGTTTTTTTTGTTTTT 52296 C
TTTTTCGTTTTTTT GTTTTT
AAAAAGCAAAAAAA CAAAAA
A
GAM2154 DDX3 5' TTTCGTTTTTCGTTTTTTT 52295 TT
TTTCGTTTT TCGTTTTTTT
AAAGCAAAA AGCAAAAAAA
GAM2154 DDX6 3' TTTTTTGCTTTTTTCCCCCCCT 52297 C G
T TTTTT GTTTTTTTC TTTTTTT
AAAAA CGAAAAAAG GGGGGAA
A G
GAM2154 EBF 3' TTTTTCCTTTTTTTCTTTTTTT 52298 G G
TTTTTC TTTTTTTC TTTTTTT
AAAAAG AAAAAAAG AAAAAAA
G
GAM2154 ETV5 3' TTTTTCGTTTTTTTGCTTT 52299 C
TTTTTCGTTTTTTT GTTTT
AAAAAGCAAAAAAA CGAAA
GAM2154 LMO4 3' TTTTTCTTTTTTTCATTCTTTT 52300 G
TTTTTC TTTTTTTCGTTTTTTT
AAAAAG AAAAAAAGTAAGAAAA
GAM2154 MECP2 3' TCGTTTTTTTTTCTTTTTT 52301 CG
TCGTTTTTTT TTTTTTT

```
                                AGCAAAAAAA  GAAAAAA
                                     AA
GAM2154  NFIB     3'  TTTTTCTTTTTTTCCTTTTTTT 52302       G       G
                                TTTTTC TTTTTTTC TTTTTTT
                                ||||||| |||||||| |||||||
                                AAAAAG AAAAAAAG AAAAAAA
                                   _       G
GAM2154  NFIB     3'  TTTTCCTTTTTTTTTCATTTTT 52303       G_
              TC                  TTTTTC  TTTTTTTCGTTTTTTT
                                ||||||  ||||||||||||||||
                                AAAAGG  AAAAAAAGTAAAAAAG
                                   AA
GAM2154  NFIB     3'  TTTTTCCTTTTTTCTTTTTTTC 52304       G       G
                                TTTTTC TTTTTTTC TTTTTTTC
                                ||||||| |||||||| ||||||||
                                AAAAAG GAAAAAAG AAAAAAAG
                                   _       _
GAM2154  PPP4C    3'  TTTTTTTTTTTTTTCATTTTTC 52294       CG
                                TTTTT  TTTTTTTCGTTTTTT
                                |||||  ||||||||||||||
                                AAAAA  AAAAAAAGTAAAAAG
                                   AA
GAM2154  PRDM2    3'  TTTTTCATTTCCCAATTTGTTT 52305            TC___
              TTTTC                TTTTTCGTTTTTT    GTTTTTTTC
                                ||||||||||||    |||||||||
                                AAAAAGTAAAGGG    CAAAAAAAG
                                      TTAAA
GAM2154  RPP30    3'  TTTTTCGCTTTTAATGTTTTTT 52307           TTC
              T                   TTTTTCGTTTTT   GTTTTTTT
                                ||||||||||||  ||||||||
                                AAAAAGCGAAAA   CAAAAAAA
                                      TTA
GAM2154  RPP30    3'  TTTTTTTTTTTTTTCGCTTTT  52306       CG
                                TTTTT  TTTTTTTCGTTTTT
                                |||||  |||||||||||||
                                AAAAA  AAAAAAAGCGAAAA
                                   AA
GAM2154  TKT      3'  TTTTTTTTTTTTTTCATTTTTC 52294       CG
                                TTTTT  TTTTTTTCGTTTTTT
                                |||||  |||||||||||||||
                                AAAAA  AAAAAAAGTAAAAAG
                                   AA
GAM2154  UBQLN2   3'  TTTTTTTTTTTTTTCATTTTTT 52308       CG
                                TTTTT  TTTTTTTCGTTTTTT
                                |||||  |||||||||||||||
                                AAAAA  AAAAAAAGTAAAAAA
                                   AA
GAM2154  CPEB1    3'  TTTTTTTTTTTCCCCGCTTTTC 52309       CG    TT
                                TTTTT  TTTTT  CGTTTTTT
                                |||||  |||||  ||||||||
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                                AAAAA  AAAAG  GCGAAAAG
                                  AA     GG
GAM2154  DKFZp547J036 3'  TTTTTTTTTTTTTTCCTTTTTT 52310       CG       G
           T                     TTTTT  TTTTTTTC TTTTTTT
                                 |||||  |||||||| |||||||
                                 AAAAA  AAAAAAAG AAAAAAA
                                   AA       G
GAM2154  DKFZP564C103 3'  TTTTTTTTTTTTTTCGTTTT   52311       CG
                                 TTTTT  TTTTTTTCGTTTT
                                 |||||  ||||||||||||
                                 AAAAA  AAAAAAAGCAAAA
                                   AA
GAM2154  DKFZp761D112 3'  TTTTTTTTTTTTTTCATTTTTC 52294       CG
                                 TTTTT  TTTTTTTCGTTTTTT
                                 |||||  |||||||||||||||
                                 AAAAA  AAAAAAAGTAAAAAG
                                   AA
GAM2154  DPCR1    3'  TCCGTTTTTTTTGTTTTTTT   52312           C
                                 TTCGTTTTTTT GTTTTTTT
                                 ||||||||||| ||||||||
                                 AGGCAAAAAAA CAAAAAAA
                                       A
GAM2154  FLJ00024  5'  TTTTCCGTTTTTTTGGTTTTTC 52313            C
                                 TTTTTCGTTTTTTT GTTTTTT
                                 |||||||||||||| |||||||
                                 AAAAGGCAAAAAAA CAAAAAG
                                       C
GAM2154  FLJ10276  3'  TTTTTCTTTTTTTCCTTTTTTC 52314       G       G
                                 TTTTTC TTTTTTTC TTTTTTT
                                 ||||||| |||||||| |||||||
                                 AAAAAG AAAAAAAG AAAAAAG
                                    _       G
GAM2154  FLJ10346  3'  TTTTTTTTTTTTTTCCCCTTTT 52315       CG       G
           TC                      TTTTT  TTTTTTTC TTTTTTTC
                                 |||||  |||||||| ||||||||
                                 AAAAA  AAAAAAAG GGAAAAAG
                                   AA       G
GAM2154  FLJ20015  3'  TTTTTCTTTTTTTTCATTTTTT 52316       G
           T                     TTTTTC TTTTTTTCGTTTTTTT
                                 |||||| ||||||||||||||||
                                 AAAAAG AAAAAAAGTAAAAAAA
                                    A
GAM2154  FLJ20406  3'  TTTTTTTTTTTTTTCGCTTTC  52317       CG
                                 TTTTT  TTTTTTTCGTTTTT
                                 |||||  ||||||||||||||
                                 AAAAA  AAAAAAAGCGAAAG
                                   AA
GAM2154  FLJ21901  3'  TTTTTTTTTTTTTTCCTTTTTT 52310       CG       G
           T                     TTTTT  TTTTTTTC TTTTTTT
                                 |||||  |||||||| |||||||
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                                AAAAA  AAAAAAAG AAAAAAA
                                  AA       G
GAM2154  FLJ21945  3'  TTTTTTTTTTTTTTCCGTTTC   52318      CG
                                TTTTT  TTTTTTTCGTTTT
                                |||||  ||||||||||||
                                AAAAA  AAAAAAGGCAAAG
                                  AA
GAM2154  GALNT6    3'  TTCTTCTTCTTTTTTGTTTTTT 52319       G      C
           T                     TTTTTC TTTTTTT GTTTTTTT
                                 ||||||| ||||||| ||||||||
                                 AAGAAG AGAAAAA CAAAAAAA
                                   A      A
GAM2154  KIAA0266  3'  TTTTTCCTTTTTTTCTTTTTT  52320       G       G
                                TTTTTC TTTTTTTC TTTTTT
                                |||||| |||||||| ||||||
                                AAAAAG AAAAAAAG AAAAAA
                                   G       _
GAM2154  MGC4734   3'  CTTTTCGTTTTTTTGTTTTTTT 52321             C
                                TTTTTCGTTTTTTT GTTTTTTT
                                |||||||||||||| ||||||||
                                GAAAAGCAAAAAAA CAAAAAAA
                                                _
GAM2154  MKRN4     3'  TTTCCGTTTTTGTTTTTTT    52322          TTC
                                TTTTCGTTTTT   GTTTTTTT
                                ||||||||||   ||||||||
                                AAAGGCAAAAA   CAAAAAAA
                                                ___
GAM2154  TCL6      3'  TTTTTTTTTTTTTTCCTTTTTT 52310       CG       G
           T                     TTTTT  TTTTTTTC TTTTTTT
                                 |||||  |||||||| |||||||
                                 AAAAA  AAAAAAAG AAAAAAA
                                   AA       G
GAM2154  TCL6      3'  TTTTTTTTTTTTTTCCTTTTTT 52310       CG       G
           T                     TTTTT  TTTTTTTC TTTTTTT
                                 |||||  |||||||| |||||||
                                 AAAAA  AAAAAAAG AAAAAAA
                                   AA       G
GAM2154  WIT-1     3'  TTTTTCTTTTCCCCATTTTTTT 52323       G     TT
           C                     TTTTTC TTTTT  CGTTTTTTTC
                                 |||||| |||||  ||||||||||
                                 AAAAAG AAAAG  GTAAAAAAAG
                                   _    GG
GAM2154  LOC130617 3'  TTTTTTTTTTTTTTCCTTTTTT 52310       CG       G
           T                     TTTTT  TTTTTTTC TTTTTTT
                                 |||||  |||||||| |||||||
                                 AAAAA  AAAAAAAG AAAAAAA
                                   AA       G
GAM2154  LOC146714 5'  TTTCTTTTCTTTTTTGTTTTTT 52324       CG       C
           TC                     TTTTT  TTTTTTT GTTTTTTTC
                                  |||||  ||||||| |||||||||
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                                AAAGA  AGAAAAA CAAAAAAAG
                                  AA       A
GAM2154  LOC151360 3'  TTTTTTTTTTTTTTTCGGCTTTT 52325      CG        _
                TT                 TTTTT  TTTTTTTCG TTTTTTT
                                   |||||  ||||||||| |||||||
                                   AAAAA  AAAAAAAGC GAAAAAA
                                     AA        C
GAM2154  LOC153222 3'  TTTCTTTTTTTTCTCCTTTTTT 52326      CG       G
                T                  TTTTT  TTTTTTTC TTTTTTT
                                   |||||  |||||||| |||||||
                                   AAAGA  AAAAAGAG AAAAAAA
                                     AA       G
GAM2154  LOC161357 3'  TTTTTCTTTTTTTCATTTTTTT 52328       G
                                   TTTTTC TTTTTTTCGTTTTTTT
                                   ||||||| ||||||||||||||||
                                   AAAAAG AAAAAAAGTAAAAAAA

                                    _
GAM2154  LOC161357 3'  TTTTTCATTTTTTTTTTTTTTT 52327            CG
                                   TTTTTCGTTTTTTT  TTTTTT
                                   |||||||||||||  ||||||
                                   AAAAAGTAAAAAAA  AAAAAA
                                         AA
GAM2154  LOC199863 5'  TTTTTCATTTTTTTTTCCTTTT 52329            CG
                C                  TTTTTCGTTTTTTT  TTTTTTTC
                                   |||||||||||||  ||||||||
                                   AAAAAGTAAAAAAA  AGGAAAAG
                                         A_
GAM2154  LOC220555 3'  TTTTTGATTTTTTTCTTTTTTT 52330      C       G
                C                  TTTTT GTTTTTTTC TTTTTTTC
                                   ||||| ||||||||| ||||||||
                                   AAAAA TAAAAAAAG AAAAAAAG
                                     C       _
GAM2154  LOC51594  3'  TTTTTTTTTTTTTTCGTTTC  52331      CG
                                   TTTTT  TTTTTTTCGTTTT
                                   |||||  ||||||||||||
                                   AAAAA  AAAAAAAGCAAAG
                                     AA
GAM2154  LOC91035  5'  TTTTTGTTTTTTTCTCCCTTTT 52332      C       G
                C                  TTTTT GTTTTTTTC TTTTTTTC
                                   ||||| ||||||||| ||||||||
                                   AAAAA CAAAAAAAG GGGAAAAG
                                     _       A
GAM2155  GPRC5B    3'  TACACGAAATCCCCT      52335        TAGGA
                                   TACGCGGA    ATCCCCT
                                   ||||||||    |||||||
                                   ATGTGCTT    TAGGGGA

                                        _____
GAM2155  SYNGR3    3'  CACGCGGGTCCACCCCCTC   52336       ATAGGA
                                   TACGCGG     ATCCCCTC
                                   |||||||     ||||||||
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                                GTGCGCC     TGGGGGAG
                                    CAGG__
GAM2155  FLJ10420  3'  CACAGTGAGGAATCCCTTCAG  52337      AT       C
                                CGCGG  AGGAATCCC TCAG
                                |||||  ||||||||| ||||
                                GTGTC  TCCTTAGGG AGTC
                                   AC        A
GAM2155  FLJ22173  5'  GCCTGGGCATCATCCCCTCAG  52338    __ A  GGA
                                GC  GG TA   ATCCCCTCAG
                                ||  || ||   ||||||||||
                                CG  CC GT   TAGGGGAGTC
                                 GA  C  AG_
GAM2155  KIAA0595  3'  ACACTGGGGATCCCCTCAG   52339     _ ATA   A
                                ACGC GG   GGA TCCCCTCAG
                                |||| ||   ||| |||||||||
                                TGTG CC   CCT AGGGGAGTC
                                  A ____  _
GAM2155  KIAA1056  3'  GGCTGGGAATCCCCTCAG    52340    ATA
                                GG   GGAATCCCCTCAG
                                ||   ||||||||||||||
                                CC   CCTTAGGGGAGTC
                                 GAC
GAM2155  TTTY13    3'  TACGATGGTGGTAATCCCCT   52341     C_  ATA  _
                                TACG  GG   GG AATCCCCT
                                ||||  ||   || ||||||||
                                ATGC  CC   CC TTAGGGGA
                                  TA  A__  A
GAM2155  ZIN       3'  CGAGGCTGGGAGTCCCCTCAG  50559    C  ATA   A
                                CG GG   GGA TCCCCTCAG
                                || ||   ||| |||||||||
                                GC CC   CCT AGGGGAGTC
                                 T  GAC   C
GAM2155  LOC255146 3'  TACGCGGAGGGGCCTCA     52342        TA  AATCC
                                TACGCGGA  GG    CCTCA
                                ||||||||  ||    |||||
                                ATGCGCCT  CC    GGAGT
                                    CC  _____
GAM2156  GPC1      3'  AAGGCAGGCGAGGCCAGGCC   52345        A  A_  _
                                AAGGCAGGC AG  CAG CT
                                |||||||||  ||  |||  ||
                                TTCCGTCCG TC  GTC GG
                                    C  CG   C
GAM2156  TEK       3'  TGAGTAGGCAAGACATTTATT  52346    A  C       GC
                                A GG AGGCAAGACA  TATT
                                | || ||||||||||  ||||
                                A TC TCCGTTCTGT  ATAA
                                 C  A        AA
GAM2156  CABP2     3'  TAAGGCAGGCAAGGGCACT    52347           ACA
                                TAAGGCAGGCAAG   GCT
                                ||||||||||||   |||
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                                ATTCCGTCCGTTC  TGA
                                      CCG
GAM2156 CABP2    3' TAAGGCAGGCAAGGGCACT   52347          ACA
                                TAAGGCAGGCAAG  GCT
                                ||||||||||||  |||
                                ATTCCGTCCGTTC  TGA
                                      CCG
GAM2156 DNM1L    3' TGAAGCAAAAGTAGCTATT   52348  C      C_
                                G AGGCAAGA  AGCTATT
                                | ||||||||  |||||||
                                A TTCGTTTT  TCGATAA
                                 C       CA
GAM2156 E2F6     3' AGGAGGCAAGATGTCTATT   52349    C      CAG
                                AGG AGGCAAGA  CTATT
                                ||| ||||||||  |||||
                                TCC TCCGTTCT  GATAA
                                  _       ACA
GAM2156 FLJ12363 3' GCAGGCAAGTTACGGCTATT  52350        __ A
                                GCAGGCAAG  AC GCTATT
                                |||||||||  || ||||||
                                CGTCCGTTC  TG CGATAA
                                      AA  C
GAM2156 FLJ13868 3' GGCAGGCAGTGACGAGCT    52351        A_  _
                                GGCAGGCA  GAC AGCT
                                ||||||||  ||| ||||
                                CCGTCCGT  CTG TCGA
                                     CA   C
GAM2156 FLJ21140 3' AGAGCTCCACTGACAGCTATT 52352   _ AGG  A_
                                AG GC   CA  GACAGCTATT
                                || ||   ||  ||||||||||
                                TC CG   GT  CTGTCGATAA
                                 T  AG_  GA
GAM2156 FLJ21478 3' TAAGGCAGGAGGGGAAGCT   52353        CAA_  C
                                TAAGGCAGG    GA AGCT
                                |||||||||    || ||||
                                ATTCCGTCC    CT TCGA
                                      TCCC  _
GAM2156 KATNB1   3' GGCAAAGCTGGGCAGCTATT  52354      _ AAGA
                                GGCAG GC    CAGCTATT
                                ||||| ||    ||||||||
                                CCGTT CG    GTCGATAA
                                   T  ACCC
GAM2156 KIAA0215 3' TAAAGCAGGTAAGAATACT   52355        C   CA
                                TAAGGCAGG AAGA  GCT
                                ||||||||| ||||  |||
                                ATTTCGTCC TTCT  TGA
                                      A   TA
GAM2156 KIAA0349 3' TAAGGTAGGAAAGACAACT   52356      C  C
                                TAAGG AGG AAGACAGCT
                                ||||| ||| |||||||||
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                                ATTCC TCC TTCTGTTGA
                                   A   T
GAM2156 KIAA1068 3' AGGCAGGCAAAGCACATT    52357         GAC  _
                                AGGCAGGCAA   AGC TATT
                                ||||||||||   ||| ||||
                                TCCGTCCGTT   TCG GTAA
                                     ___   T
GAM2156 KIAA1111 3' AAGGCAGGCAGGATGCT     52358         A  CA
                                AAGGCAGGCA GA  GCT
                                |||||||||| ||  |||
                                TTCCGTCCGT CT  CGA
                                      C  A_
GAM2156 KIAA1145 5' CAAGGCAGGCAGGCTA      52359          AGACA
                                TAAGGCAGGCA    GCTA
                                ||||||||||     ||||
                                GTTCCGTCCGT    CGAT
                                      C____
GAM2156 MAIL     3' TAAGGCAGGCAGATGGC     52360          A  CA
                                TAAGGCAGGCA GA  GC
                                |||||||||| ||  ||
                                ATTCCGTCCGT CT  CG
                                      _ AC
GAM2156 MEGF11   3' AGGGGAAGGCAGCTATT     52361     CA  C   A
                                AGG  GG AAG CAGCTATT
                                |||  || ||| ||||||||
                                TCC  CC TTC GTCGATAA
                                  __ _  C
GAM2156 MGC16153 3' TAAGGCAGGAGCTAGCT     52362         CA  AC
                                TAAGGCAGG  AG  AGCT
                                |||||||||  ||  ||||
                                ATTCCGTCC  TC  TCGA
                                     __ GA
GAM2156 PADI1    3' AGGTCGGAGTCAGCTATT    52363     CA  CA  A
                                AGG  GG  AG CAGCTATT
                                |||  ||  || ||||||||
                                TCC  CC  TC GTCGATAA
                                  AG  __  A
GAM2156 PRO1992  3' TAAGGCAGGCGGATCACC    52364          AA  CA
                                TAAGGCAGGC  GA  GCT
                                |||||||||  ||  |||
                                ATTCCGTCCG  CT  TGG
                                      C_  AG
GAM2156 TP53TG3  3' CAAGAATTTGAAGGCAGCTATT 52365       CAGGC   A
                                TAAGG    AAG CAGCTATT
                                |||||    ||| ||||||||
                                GTTCT    TTC GTCGATAA
                                   TAAAC   C
GAM2156 ZFD25    5' TAAGGCAGGCAGGAGAGACT   52366          A  C  _
                                TAAGGCAGGCA GA AG CT
                                |||||||||| || || ||
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                                ATTCCGTCCGT CT TC GA
                                      C  C  T
GAM2156  LOC131744 3'  AAGGCAGGTGCCAATTATT   52367       CAAGA  C
                                AAGGCAGG    CAG TATT
                                ||||||||    ||| ||||
                                TTCCGTCC    GTT ATAA
                                    ACG__   A
GAM2156  LOC134957 3'  GGAAAGTCCAAGACAGCT    52368    C  __
                                GG AGG  CAAGACAGCT
                                || |||  ||||||||||
                                CC TTC  GTTCTGTCGA
                                 T   AG
GAM2156  LOC138199 3'  TAAGGCAGGAAGATCGCT    52369       C   CA
                                TAAGGCAGG AAGA  GCT
                                ||||||||| ||||  |||
                                ATTCCGTCC TTCT  CGA
                                     _   AG
GAM2156  LOC142948 5'  AAGGCAGGCAAGGCAGCC    52370         A
                                AAGGCAGGCAAG CAGCT
                                |||||||||||| |||||
                                TTCCGTCCGTTC GTCGG
                                      C
GAM2156  LOC145842 5'  TAAGGCAAAGCATGGCTATT   52371       _  AGACA
                                TAAGGCAG GCA    GCTATT
                                |||||||| |||    ||||||
                                ATTCCGTT CGT    CGATAA
                                     T  AC___
GAM2156  LOC148085 3'  TAAGGCAGGAACTGGCT     52372       CAA  A_
                                TAAGGCAGG   GAC  GCT
                                |||||||||   |||  |||
                                ATTCCGTCC   TTG  CGA
                                     ___   AC
GAM2156  LOC151361 5'  AGGCAGGCAAAAATGCTATT   52373         CA
                                AGGCAGGCAAGA  GCTATT
                                ||||||||||||  ||||||
                                TCCGTCCGTTTT  CGATAA
                                      TA
GAM2156  LOC152343 3'  AAGAAACAAAGACAGTTATT   52374    C    _   C
                                AGG AGGCAA GACAG TATT
                                ||| |||||| ||||| ||||
                                TTC TTTGTT CTGTC ATAA
                                  _     T    A
GAM2156  LOC203378 3'  CAAGGCAGGCAAACCCACT    52375         ACA
                                TAAGGCAGGCAAG   GCT
                                ||||||||||||   |||
                                GTTCCGTCCGTTT   TGA
                                      GGG
GAM2156  LOC205327 3'  AAGGCAGGGTGCAGTTATT    52376       CAAGA  C
                                AAGGCAGG    CAG TATT
                                ||||||||    ||| ||||
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                                TTCCGTCC    GTC ATAA
                                     CAC__   A
GAM2156 LOC56181 3' GGTGAGGAAGGCAGCTATT   52377    C_  C  A
                                GG  AGG AAG CAGCTATT
                                ||  ||| ||| ||||||||
                                CC  TCC TTC GTCGATAA
                                 AC  _  C
GAM2156 LOC90155 3' AGGCAGGAAAACAGCTATT   52378       C
                                AGGCAGG AAGACAGCTATT
                                ||||||| ||||||||||||
                                TCCGTCC TTTTGTCGATAA
                                      _
GAM2157 KLHL1    3' TTAATTGTAATTAAAATTTACA 52381       GAATT
                                TTAATTG    TTGGAATTTACA
                                |||||||    ||||||||||||
                                AATTAAC    AATTTTAAATGT
                                     ATT__
GAM2157 FLJ22595 3' TTAATAGGGAATACGAATTTAC 52382     T_    TTTG
             A                   TTAAT  GGAAT   GAATTTACA
                                 |||||  |||||   |||||||||
                                 AATTA  CCTTA   CTTAAATGT
                                    TC    TG__
GAM2157 OSBPL3   3' TTAATTGGAATTCTTTTCTCT  52383           GGAA
                                TTAATTGGAATTTT   TTT
                                ||||||||||||||   |||
                                AATTAACCTTAAGA   AGA
                                       AAAG
GAM2157 RPS27L   3' TTAATTAGAATTATGGAATTTA 52384          T
                                TTAATTGGAATT TGGAATTTA
                                |||||||||||| |||||||||
                                AATTAATCTTAA ACCTTAAAT
                                       T
GAM2157 LOC125129 3' TTAAATGAAGTTGGAATTTACA 52385     T   ATT
                                TTAA TGGA   TTGGAATTTACA
                                |||| ||||   ||||||||||||
                                AATT ACTT   AACCTTAAATGT
                                  T   C__
GAM2157 LOC196442 3' TTAATCTCTTGGAATTTAC   52386      GGAA
                                TTAATT   TTTTGGAATTTAC
                                ||||||   ||||||||||||||
                                AATTAG   AGAACCTTAAATG
                                     ____
GAM2157 LOC253693 3' TTAATCTCTTGGAATTTAC   52386      GGAA
                                TTAATT   TTTTGGAATTTAC
                                ||||||   ||||||||||||||
                                AATTAG   AGAACCTTAAATG
                                     ____
GAM2158 PRKG2    3' TAATGGTCTTCCAAAGATAT   52389     AA      _
                                TAAT  TTTTCCAA GATGT
                                ||||  |||||||| |||||
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                                ATTA  AGAAGGTT CTATA
                                  CC       T
GAM2158  UBQLN2    3'  TAATATTTTTAGATGTACA    52390      A    CCA
                                TAATA TTTT   AGATGTACA
                                ||||| ||||   |||||||||
                                ATTAT AAAA   TCTACATGT
                                  A   ___
GAM2158  CDC2L5    3'  AATTTGTGAAGATGTACAAT   52391      TCC
                                AATTT   AAGATGTACAAT
                                |||||   ||||||||||||
                                TTAAA   TTCTACATGTTA
                                  CAC
GAM2158  CDC2L5    3'  AATTTGTGAAGATGTACAAT   52391      TCC
                                AATTT   AAGATGTACAAT
                                |||||   ||||||||||||
                                TTAAA   TTCTACATGTTA
                                  CAC
GAM2158  KIAA0836  3'  TAATAAGTTTCCAAAATA    52392       T
                                TAATAA TTTCCAAGATG
                                ||||||| ||||||||||
                                ATTATT AAAGGTTTTAT
                                   C
GAM2158  ZNF345    3'  TAAGAATTTTCCAAAAGTA    52393     T          T
                                TAA AATTTTCCAAGA GTA
                                ||| |||||||||||| |||
                                ATT TTAAAAGGTTTT CAT
                                  C          _
GAM2158  LOC115294 3'  AATAATTTTCCAAGTCTTCCAA 52394             ATGTA
           T                     AATAATTTTCCAAG     CAAT
                                ||||||||||||||     ||||
                                TTATTAAAAGGTTC     GTTA
                                       AGAAG
GAM2158  LOC147947 5'  ATAATTCTCCAGCATCACA    52395          A ATG
                                ATAATTTTCCA G   TACA
                                |||||||||||  |   ||||
                                TATTAAGAGGT C   GTGT
                                      _ GTA
GAM2158  LOC153688 3'  TAATGATTTTTCAAGATGCA   52396      A    C
                                TAAT ATTTT CAAGATGTA
                                |||| ||||| |||||||||
                                ATTA TAAAA GTTCTACGT
                                  C    A
GAM2158  LOC200132 3'  TTCTCCATATGTGTACAAT    52397       AGA_
                                TTTTCCA    TGTACAAT
                                |||||||    ||||||||
                                AAGAGGT    ACATGTTA
                                    ATAC
GAM2158  LOC222342 5'  TAATAATTTCCCAATAGT     52398           GAT
                                TAATAATTTTCCAA   GT
                                ||||||||||||||   ||
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                                ATTATTAAAGGGTT  CA
                                       AT_
GAM2159 DLD     3' AGCTGTGAGAATATCCTG   52401     TTAA  TTA
                                AGCT   AG  AATATCCTG
                                ||||   ||  |||||||||
                                TCGA   TC  TTATAGGAC
                                  CAC_ ___
GAM2159 DNMT3B  3' AGCTTTGCAGTTTTCCCTG  52402      AA   AAATA
                                AGCTTT AGTT   TCCTG
                                |||||| ||||   |||||
                                TCGAAA TCAA   GGGAC
                                   CG   AA___
GAM2159 GALNT3  3' AGCTTTAAATGAGTCAAGTATT 52403       ___     A  C
             CTGC                  AGCTTTAA  AGTTAA TAT CTGC
                                |||||||| ||||||| ||| ||||
                                TCGAAATT  TCAGTT ATA GACG
                                     TAC     C  A
GAM2159 MME     3' AGTTTTCAGTTTATCCTG   52404   C  AA   AAA
                                AG TTT  AGTT   TATCCTG
                                || |||  ||||   |||||||
                                TC AAA  TCAA   ATAGGAC
                                 _  AG   ___
GAM2159 MME     3' AGTTTTCAGTTTATCCTG   52404   C  AA   AAA
                                AG TTT  AGTT   TATCCTG
                                || |||  ||||   |||||||
                                TC AAA  TCAA   ATAGGAC
                                 _  AG   ___
GAM2159 MME     3' AGTTTTCAGTTTATCCTG   52404   C  AA   AAA
                                AG TTT  AGTT   TATCCTG
                                || |||  ||||   |||||||
                                TC AAA  TCAA   ATAGGAC
                                 _  AG   ___
GAM2159 MME     3' AGTTTTCAGTTTATCCTG   52404   C  AA   AAA
                                AG TTT  AGTT   TATCCTG
                                || |||  ||||   |||||||
                                TC AAA  TCAA   ATAGGAC
                                 _  AG   ___
GAM2159 B3GALT6 3' AGTTTTAAAGTGCTCCTG   52405   C     TAAATA
                                AG TTTAAAGT    TCCTG
                                || ||||||||    |||||
                                TC AAATTTCA    AGGAC
                                 A      CG____
GAM2159 FBXO9   3' GGACTCTTATTAAATATCCTG 52406  A   AAA
                                A GCTTT  GTTAAATATCCTG
                                | |||||  ||||||||||||||
                                C TGAGA  TAATTTATAGGAC
                                 C    A__
GAM2159 GHITM   3' AGTTTTAAAGTTATTTCCT  52407   C      AATA
                                AG TTTAAAGTTA   TCCT
                                || ||||||||||   ||||
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                                TC AAATTTCAAT    AGGA
                                 A         AA__
GAM2159  KIAA1826  3'  AAGCTTTAAAATTGCGTCTTGC 52408           AAATA  C
                                AAGCTTTAAAGTT     TC TGC
                                |||||||||||||     || |||
                                TTCGAAATTTTAA     AG ACG
                                      CGC__  A
GAM2159  LAMB4     3'  AAGCTTTAAAGTATCTTG    52409          TAAAT   C
                                AAGCTTTAAAGT     ATC TG
                                ||||||||||||     ||| ||
                                TTCGAAATTTCA     TAG AC
                                      _____  A
GAM2159  MEP50     3'  AAGCTTTACTGAGAAATATTTT 52410        AAGTT     CC
               GC                   AAGCTTTA     AAATAT  TGC
                                ||||||||     ||||||  |||
                                TTCGAAAT     TTTATA  ACG
                                    GACTC     AA
GAM2159  MIG2      3'  AGCTTTTAAAGTTAAATAT   52411       _
                                AGCTTT AAAGTTAAATAT
                                ||||||| ||||||||||||
                                TCGAAA TTTCAATTTATA
                                   A
GAM2159  ZNF17     5'  GCTTTAAAGTTGTGACCTG   52412          AAATAT
                                GCTTTAAAGTT      CCTG
                                ||||||||||       ||||
                                CGAAATTTCAA      GGAC
                                      CACT__
GAM2159  LOC152078 3'  GCTTTAAAATTAGCTG      52413          AATATC
                                GCTTTAAAGTTA      CTG
                                ||||||||||||      |||
                                CGAAATTTTAAT      GAC
                                      C_____
GAM2159  LOC203522 3'  GCTTCAACAATATCCTG     52414        AGTTA
                                GCTTTAA     AATATCCTG
                                |||||||     |||||||||
                                CGAAGTT     TTATAGGAC
                                    G____
GAM2159  LOC257277 5'  AGCTTCTTAAATATCTTG    52415        AAAG       C
                                AGCTTT    TTAAATATC TG
                                ||||||    ||||||||| ||
                                TCGAAG    AATTTATAG AC
                                     ____        A
GAM2160  FLJ22965  3'  TAATACAGTTGAATGGATA   52418     CGA   TGC
                                TAA   GGT   TGAATGGATA
                                |||   |||   ||||||||||
                                ATT   TCA   ACTTACCTAT
                                  ATG   ___
GAM2160  KIAA0779  5'  TACAGCGCCTGCTGCTGAATGG 52419      A  AG_
                                TATA CG   GTTGCTGAATGG
                                ||||  ||   ||||||||||||
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                                ATGT GC   CGACGACTTACC
                                  C  GGA
GAM2160  PLP1     3'  ACGATGACTGAATGGAT     52420      GGTT
                                ACGA    GCTGAATGGAT
                                ||||    ||||||||||
                                TGCT    TGACTTACCTA
                                  AC__
GAM2161  ARHGAP6  3'  GTTGAATGCCAAGTTCC     52423       C  T
                                GTTGG AT TCAAGTTCC
                                ||||| || |||||||||
                                CAACT TA GGTTCAAGG
                                   _ C
GAM2161  CREM     3'  TCTTTCAAGGTTTCAAGTTCC  52424     A   TT  CA
                                TCT TCG  GG  TTTCAAGTTCC
                                ||| |||  ||  ||||||||||
                                AGA AGT  CC  AAAGTTCAAGG
                                  A  T_  __
GAM2161  CYBB     3'  TCTATCTTGGCATTGTGTGGTT 52425       G       TCAA_
              C                  TCTATC TTGGCATT     GTTC
                                ||||||| ||||||||     ||||
                                AGATAG AACCGTAA     CAAG
                                   _       CACAC
GAM2161  EXTL2    3'  CTAAAGAGGCATTTCAGGTT   52426     TCGTT       A
                                CTA     GGCATTTCA GTT
                                |||     ||||||||| |||
                                GAT     CCGTAAAGT CAA
                                  TTCT_       C
GAM2161  MYCL1    3'  TATTATTGGCATTTTAAAGT   52427     CG       C_
                                TAT  TTGGCATTT  AAGT
                                |||  |||||||||  ||||
                                ATA  AACCGTAAA  TTCA
                                  AT        AT
GAM2161  SOCS5    3'  TCTTGGAGTTTCAAGTT     52428     G    CA
                                TC TTGG  TTTCAAGTT
                                || ||||  |||||||||
                                AG AACC  AAAGTTCAA
                                 _   TC
GAM2161  SPOCK    3'  TATCATTGTTTTTCGAGTT    52429        GCA    A
                                TATCGTTG   TTTC AGTT
                                ||||||||   |||| ||||
                                ATAGTAAC   AAAG TCAA
                                     AA_    C
GAM2161  BTN3A1   3'  TCAGAGCATTTTAAGTTC    52430     TT      C
                                TCG  GGCATTT AAGTTC
                                |||  ||||||| ||||||
                                AGT  TCGTAAA TTCAAG
                                  C_      A
GAM2161  ELKS     3'  TCTATTTTGGTCAAGTTC    52431      CG    CATT
                                TCTAT  TTGG    TCAAGTTC
                                |||||  ||||    ||||||||
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                                AGATA  AACC    AGTTCAAG
                                  A_   _____
GAM2161  FLJ13441  5'  TCTCACAGCATTTTAAGTTCC  52432     ATCGT       C
                                TCT    TGGCATTT AAGTTCC
                                |||    |||||||| |||||||
                                AGA    GTCGTAAA TTCAAGG
                                  GT___       A
GAM2161  IMPACT    3'  TCTATCATTAGTTCAAGTT    52433          CAT
                                TCTATCGTTGG   TTCAAGTT
                                ||||||||||   ||||||||
                                AGATAGTAATC   AAGTTCAA
                                     ___
GAM2161  KIAA0648  3'  TCTATCATTGGTATCCATTGTT 52434          CAT    A_
              CC                  TCTATCGTTGG   TTCA  GTTCC
                                ||||||||||   ||||  |||||
                                AGATAGTAACC   AGGT  CAAGG
                                      AT_    AA
GAM2161  LOC152804 3'  TCTATTTTTAAAAATCAAGTTC 52435      CG    CATT
                                TCTAT  TTGG    TCAAGTTC
                                |||||  ||||    ||||||||
                                AGATA  AATT    AGTTCAAG
                                  AA    TTT_
GAM2162  SS18      3'  TTGAGACCAAAACAATCAA    52438      AT       _
                                TTGA  CCAAAACA TCAG
                                ||||  |||||||| ||||
                                AACT  GGTTTTGT AGTT
                                  CT       T
GAM2162  TLX1      5'  TTGACTCTGGGACATCAATCA  52439      A  CAAA
                                TTGA TC    ACATCAGTTA
                                |||| ||    ||||||||||
                                AACT AG    TGTAGTTAGT
                                  G  ACCC
GAM2162  DCLRE1A   3'  TTGAACCTAAAACATCAGC    52440        C
                                TTGAATC AAAACATCAGT
                                ||||||| ||||||||||
                                AACTTGG TTTTGTAGTCG
                                    A
GAM2162  DCTD      3'  TTGAGCCAAAACAACAG      52441      AT       T
                                TTGA  CCAAAACA CAG
                                ||||  |||||||| |||
                                AACT  GGTTTTGT GTC
                                  C_       T
GAM2162  KIAA0205  3'  TGAATCCAAGACAGCAAC     52442         AACAT    T
                                TGAATCCAA     CAGT AAC
                                |||||||||     |||| |||
                                ACTTAGGTT     GTCG TTG
                                     CT___    _
GAM2162  KIAA0342  5'  TTGGACCAAAACAGATCCAACA 52443      AAT       TCAG
                                TTG   CCAAAACA    TTAACA
                                |||   ||||||||    ||||||
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                                AAC  GGTTTTGT   GGTTGT
                                  CT_      CTA_
GAM2162 KIAA0978 3' TGAATCCAGAAGCACTTAACA 52444       A  CAT  G
                                TGAATCCA AA  CA TTAACA
                                |||||||| ||  || ||||||
                                ACTTAGGT TT  GT AATTGT
                                     C  C__  G
GAM2162 MGC27382 3' TTAAATCCAAAGTCAATC   52445         ACA
                                TTGAATCCAAA  TCAGTT
                                ||||||||||  ||||||
                                AATTTAGGTTT  AGTTAG
                                      C__
GAM2162 SDC3    5' TTGAATCCAGGCAGCAGC   52446        AAA  T
                                TTGAATCCA  CA CAGT
                                |||||||||  || ||||
                                AACTTAGGT  GT GTCG
                                     CC_  C
GAM2162 ZDHHC2  3' TTGGATCCAAAACATGTTA  52447    A        CA
                                TTG ATCCAAAACAT  GTTA
                                ||| ||||||||||  ||||
                                AAC TAGGTTTTGTA  CAAT
                                  C        __
GAM2162 LOC116150 3' TTGAACCCAGAATACCAG   52448        A  C
                                TTGAATCCA AA ATCAG
                                |||||||| || |||||
                                AACTTGGGT TT TGGTC
                                     C  A
GAM2162 LOC221584 3' TGAGTCTAAAACATCAGGTCAA 52449    A  C       _
                                TGA TC AAAACATCAG TTAA
                                ||| || |||||||||| ||||
                                ACT AG TTTTGTAGTC AGTT
                                  C  A        C
GAM2162 LOC222193 3' TTGATCTTCAACATCAGTTA  52450     A  CAA
                                TTGA TC  AACATCAGTTA
                                |||| ||  ||||||||||
                                AACT AG  TTGTAGTCAAT
                                  _  AAG
GAM2162 LOC255652 3' TGAATCCAAAATGAATCAG   52451         C__
                                TGAATCCAAAA  ATCAG
                                ||||||||||  |||||
                                ACTTAGGTTTT  TAGTC
                                      ACT
GAM2163 ADCY7   3' AACTTTACGGGGTTCATGGGGA 52454        A  AAC_  T
                                AACTTTATG GG   TGG GA
                                |||||||| ||   ||| ||
                                TTGAAATGC CC   ACC CT
                                     C  AAGT  C
GAM2163 ATRN    3' CTTTATGAGAGGTGAG     52455         AACT
                                CTTTATGAGG   GGTGAG
                                ||||||||||  ||||||
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                              GAAATACTCT   CCACTC
                                    ____
GAM2163 BLAME   3' ACTTTATGAATAGTGGTG   52456        GAAC
                              ACTTTATGAG   TGGTG
                              ||||||||||   |||||
                              TGAAATACTT   ACCAC
                                   ATC_
GAM2163 CLCN1   3' CTTTATGAGGAGGTCGTGGGAG 52457         AC___  T
                              CTTTATGAGGA    TGG GAG
                              ||||||||||    ||| |||
                              GAAATACTCCT    ACC CTC
                                    CCAGC  _
GAM2163 DTR     3' AACTTATGAGGGGAAGTG   52458      T    AACT
                              AACTT ATGAGG   GGTG
                              ||||| ||||||   ||||
                              TTGAA TACTCC   TCAC
                                 _    CCT_
GAM2163 EZH2    3' ACTTTGCAGCTGGTGAGAA   52459     ATGA  AA
                              ACTTT   GG  CTGGTGAGAA
                              |||||   ||  ||||||||||
                              TGAAA   TC  GACCACTCTT
                                 CG__  __
GAM2163 HLA-A   3' TTTAAGAGGGAAGTAAGAA   52460    T   AACT
                              TTTA GAGG   GGTGAGAA
                              |||| ||||   ||||||||
                              AAAT CTCC   TCATTCTT
                                T   CT__
GAM2163 HLALS   3' ACTCTATGGGGGACAGAGGA   52461       A  A  T  T
                              ACTTTATG GG AC GG GA
                              |||||||| || || || ||
                              TGAGATAC CC TG CT CT
                                   C  C  T  C
GAM2163 KCNJ10  3' AACTTCATGGTGGTGGTGGGA  52462        A_  AAC    A
                              AACTTTATG  GG   TGGTG GA
                              |||||||||  ||   ||||| ||
                              TTGAAGTAC  CC   ACCAC CT
                                   CA  ___    C
GAM2163 LPXN    3' TTTATAAGGAATCTGAAGAG   52463         _   T
                              TTTATGAGGAA CTGG GAG
                              |||||||||||| |||| |||
                              AAATATTCCTT GACT CTC
                                    A   T
GAM2163 LRP4    3' CTCTACGCTGGTGAG      52464       AGGAA
                              CTTTATG    CTGGTGAG
                              |||||||    ||||||||
                              GAGATGC    GACCACTC
                                   _____
GAM2163 NDUFA2  3' CTTTATGAGGAATAGGAGAA   52465          C   T
                              CTTTATGAGGAA TGG GAGAA
                              |||||||||||| ||| |||||
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                                GAAATACTCCTT ATC CTCTT
                                          _  _
GAM2163 UVRAG    3' TTTATAAACCATGGTGAG    52466       GAAC
                                TTTATGAG   TGGTGAG
                                ||||||||   |||||||
                                AAATATTT   ACCACTC
                                    GGT_
GAM2163 ZNF146   3' TTTATGAGGAAACTTTTAA   52467         _ GG
                                TTTATGAGGAA CT  TGA
                                |||||||||| ||  |||
                                AAATACTCCTT GA  ATT
                                      T  AA
GAM2163 C1orf8   3' CTCTATGAGGAGTGGA      52468         ACTG  A
                                CTTTATGAGGA   GTG GA
                                ||||||||||    ||| ||
                                GAGATACTCCT   CAC CT
                                          ____  _
GAM2163 DMRTB1   3' AACTTTATGGAGGGGGAA    52469        _  AACT  T
                                AACTTTATG AGG   GG GAG
                                ||||||||| |||   || |||
                                TTGAAATAC TCC   CC CTT
                                    C  ____ _
GAM2163 FLJ13189 3' TTTGTGAGGAACAAGTGAG   52470    A      T
                                TTT TGAGGAAC GGTGAG
                                ||| |||||||| ||||||
                                AAA ACTCCTTG TCACTC
                                  C       T
GAM2163 FLJ14442 3' TTTATGAAGAAACTAAGAG   52471         _   T
                                TTTATGAGGAA CTGG GAG
                                |||||||||| |||| |||
                                AAATACTTCTT GATT CTC
                                      T   _
GAM2163 FLJ20509 3' CTTTGTGAGAATGAGA      52472     A    AACTG
                                CTTT TGAGG    GTGAGA
                                |||| |||||    ||||||
                                GAAA ACTCT    TACTCT
                                  C    _____
GAM2163 GT650    3' AACTGTGTGAGGAAGGGA    52473     TTA     CT  T
                                AACT   TGAGGAA  GG GA
                                ||||   |||||||  || ||
                                TTGA   ACTCCTT  CC CT
                                  CAC     __ _
GAM2163 HSPC228  3' AACTCTATGAGGGAGGGA    52474         AACT  T
                                AACTTTATGAGG   GG GA
                                ||||||||||||   || ||
                                TTGAGATACTCC   CC CT
                                      CT__  _
GAM2163 KIAA0711 3' TTCATGAGGAGTGTGGA     52475         ACTG  A
                                TTTATGAGGA   GTG GA
                                |||||||||    ||| ||
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                                AAGTACTCCT    CAC CT
                                     CA__  _
GAM2163  KIAA0825  3'  CTTTATGAGGCTGAGGA     52476          AA    T
                                CTTTATGAGG  CTGG GA
                                ||||||||||  |||| ||
                                GAAATACTCC  GACT CT
                                     __    C
GAM2163  KIAA1463  3'  AACTTCATGAGGAAAGG     52477             CT
                                AACTTTATGAGGAA  GG
                                ||||||||||||||  ||
                                TTGAAGTACTCCTT  CC
                                       T_
GAM2163  KIAA1673  3'  AACTTTTTGAGGGATAATGAA  52478       A     AAC
                                AACTTT TGAGG   TGGTGAG
                                ||||||| |||||   |||||||
                                TTGAAA ACTCC   ATTACTT
                                   A    CT_
GAM2163  PRO1914   5'  AACTTTATAGGAATGA      52479        G     C
                                AACTTTAT AGGAA TGG
                                |||||||| ||||| |||
                                TTGAAATA TCCTT ACT
                                     _    _
GAM2163  Rabip4R   3'  CTTATGAGGAGAAATTAGA    52480          ACT   G
                                TTTATGAGGA   GGT AGA
                                ||||||||||   ||| |||
                                GAATACTCCT   TTA TCT
                                     CT_   A
GAM2163  RFX4      3'  TTTATGAAGGAACCGTGAA    52481        _      G
                                TTTATGA GGAACTG TGAG
                                ||||||| ||||||| ||||
                                AAATACT CCTTGGC ACTT
                                   T      _
GAM2163  SPAG4L    5'  AACTCTGGGAGCTGGTGAG    52482       TA  A   A
                                AACTT  TG GGA CTGGTGAG
                                |||||  || ||| ||||||||
                                TTGAG  AC CCT GACCACTC
                                   __  _   C
GAM2163  LOC124739 3'  CTTTACGAGGGAGGCGGAGA   52483          AACT    _
                                CTTTATGAGG    GGTG AGA
                                ||||||||||    |||| |||
                                GAAATGCTCC    CCGC TCT
                                     CT__     C
GAM2163  LOC133022 3'  TTATGAAACACTGGTGGGA    52484        A      A
                                TTATGAGG ACTGGTG GA
                                |||||||| ||||||| ||
                                AATACTTT TGACCAC CT
                                     G      C
GAM2163  LOC143279 3'  AACTTTATGAGAATTCCAG    52485           A_ TG
                                AACTTTATGAGGA  C  G
                                ||||||||||||  |  |
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                                TTGAAATACTCTT  G  C
                                      AA GT
GAM2163  LOC146167 3'  CTTTATGAGGAAAAGA      52486          CTGGT
                                CTTTATGAGGAA    GAGA
                                ||||||||||||    ||||
                                GAAATACTCCTT    TTCT
                                      _____
GAM2163  LOC158709 3'  ACTGTATGAGGACAAAGGGAG  52487     T      ACT_  T
                                ACT TATGAGGA    GG GAG
                                ||| ||||||||    || |||
                                TGA ATACTCCT    CC CTC
                                  C       GTTT  _
GAM2163  LOC167555 3'  AACTTTTGTGAGGAATAGG    52488       A_     CT
                                AACTTT  TGAGGAA  GG
                                ||||||  |||||||  ||
                                TTGAAA  ACTCCTT  CC
                                    AC      AT
GAM2163  LOC203411 5'  CTTTATGAGGGGGCAGAG     52489         AACT  _
                                CTTTATGAGG    GGT GAG
                                ||||||||||    ||| |||
                                GAAATACTCC    CCG CTC
                                      C___    T
GAM2163  LOC92973  5'  TTTATGAAGCCATCTGAGAG   52490        AA__   T
                                TTTATGAGG    CTGG GAG
                                |||||||||    |||| |||
                                AAATACTTC    GACT CTC
                                     GGTA   _
GAM2164  INMT      3'  CATACTTAACCTTATAGA     52493          TATA
                                TATACTTAAC    CTTATAGA
                                ||||||||||    ||||||||
                                GTATGAATTG    GAATATCT
                                      _____
GAM2164  PRKCN     3'  TACTGAACAGTCATTATAGACT 52494      T   TATAC
                                TACT AAC     TTATAGACT
                                |||| |||     |||||||||
                                ATGA TTG     AATATCTGA
                                  C   TCAGT
GAM2164  LOC158549 5'  TGACTTAATTATACTCAT     52495    T     C
                                A ACTTAA TATACTTAT
                                | ||||||| |||||||||
                                A TGAATT ATATGAGTA
                                 C      A
GAM2164  LOC199986 5'  TTAACTCATACCATAGACT    52496       _    T
                                TTAACT ATACT ATAGACT
                                |||||| ||||| |||||||
                                AATTGA TATGG TATCTGA
                                    G    _
GAM2165  CD74      3'  CCTTGCTGCATTGTTATCTGCT 52499         AATAGGC    A
                                TCTTGCTG      TATCT CT
                                ||||||||      ||||| ||
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                                GGAACGAC      ATAGA GA
                                    GTAACA_    C
GAM2165 LEF1     3' CTGCTGAACGCATCT      52500        AG  T
                                TTGCTGAAT  GC ATCT
                                |||||||||  || ||||
                                GACGACTTG  CG TAGA
                                    __ _
GAM2165 MUCDHL   3' TCTTGCTGAGGGGCATCGGCT 52501        ATA  T  TA
                                TCTTGCTGA   GGC ATC  CT
                                |||||||||   ||| |||  ||
                                AGAACGACT   CCG TAG  GA
                                    CC_  _  CC
GAM2165 MUCDHL   3' TCTTGCTGAGGGGCATCGGCT 52501        ATA  T  TA
                                TCTTGCTGA   GGC ATC  CT
                                |||||||||   ||| |||  ||
                                AGAACGACT   CCG TAG  GA
                                    CC_  _  CC
GAM2165 TPM4     3' TCCTGCTGAGTGGGTCATTACT 52502        ATA  C  C
                                TCTTGCTGA   GG TAT TACT
                                |||||||||   || ||| ||||
                                AGGACGACT   CC GTA ATGA
                                    CAC  A  _
GAM2165 VIM      3' TCTTGCTGGTAATATATTGCT  52503        __   G___
                                TCTTGCTG  AATA   GCT
                                ||||||||  ||||   |||
                                AGAACGAC  TTAT   CGA
                                    CA   ATAA
GAM2165 DREV1    3' TCTTGCTAATGGGTTCCTCTA  52504        ATA  CTA_
                                TCTTGCTGA   GG   TCTA
                                |||||||||   ||   ||||
                                AGAACGATT   CC   AGAT
                                    AC_  AAGG
GAM2165 FLJ10178 3' TCTTGCTGAAAACAGTTACT   52505        TA   TATC
                                TCTTGCTGAA  GGC   TACT
                                ||||||||||  |||   ||||
                                AGAACGACTT  TTG   ATGA
                                    __   TCA_
GAM2165 FLJ10619 3' TCTTCTGGGTAGACTAT     52506     G   AA
                                TCTT CTG  TAGGCTAT
                                |||| |||  ||||||||
                                AGAA GAC  ATCTGATA
                                  _  CC
GAM2165 FLJ20811 3' TTGATGAATAGGTTCACTA   52507     C      CTA  T
                                TTG TGAATAGG   TC ACTA
                                ||| ||||||||   || ||||
                                AAC ACTTATCC   AG TGAT
                                  T      A__  _
GAM2165 MGC3169  3' TCTTGCTGGAGACAGGTCT   52508        A__    _
                                TCTTGCTG   ATAGG CT
                                ||||||||   ||||| ||
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                                AGAACGAC   TGTCC GA
                                     CTC     A
GAM2165  SIAT4A    3'  CCTTGCTGAGTAGATGCT    52509         A   __
                                TCTTGCTGA TAG  GCT
                                |||||||||  |||  |||
                                GGAACGACT ATC  CGA
                                     C   TA
GAM2165  LOC146237 3'  TTGCTGAATTACACCTCT    52510         _ G   A
                                TTGCTGAAT A GCT TCT
                                |||||||||  | |||  |||
                                AACGACTTA T TGG AGA
                                     A G   _
GAM2165  LOC56267  3'  TCTTACTGCCAGCGTTATCTAC 52511         AATA   __
               T                 TCTTGCTG    GGC  TATCTACT
                                |||||||||    |||  ||||||||
                                AGAATGAC    TCG  ATAGATGA
                                     GG__    CA
GAM2166  GNG5      3'  TATTATGGCACATGTGTTACA  52514         _    A
                                TATTATGGCA ATGT TTACA
                                ||||||||||  ||||  |||||
                                ATAATACCGT TACA AATGT
                                      G    C
GAM2166  SLC22A3   3'  TTATACAGTATTACAACA    52515       G  AT
                                TTATG CA  GTATTACAACA
                                |||||  ||  ||||||||||||
                                AATAT GT  CATAATGTTGT
                                     _  __
GAM2166  FLJ13110  3'  TTATGGCATATCTGAAACAGCA 52516         A   ATT__   A
               G                  TTATGGCA TGT     ACA CAG
                                |||||||| |||     ||| |||
                                AATACCGT ATA     TGT GTC
                                     _   GACTT   C
GAM2166  SB52      3'  CTATGGCAATGTAGTTTACA   52517           __
                                TTATGGCAATGTA  TTACA
                                ||||||||||||  |||||
                                GATACCGTTACAT  AATGT
                                       CA
GAM2167  DMD       5'  TGCCGTGAATAGTGAGGT    52520      AT   TAT
                                TGCT  GTG   ATAGTGAGGT
                                ||||  |||   ||||||||||
                                ACGG  CAC   TATCACTCCA
                                   __   T__
GAM2167  DMD       5'  TGCCGTGAATAGTGAGGT    52520      AT   TAT
                                TGCT  GTG   ATAGTGAGGT
                                ||||  |||   ||||||||||
                                ACGG  CAC   TATCACTCCA
                                   __   T__
GAM2167  EHD3      3'  TGCATATGTGTGTGTGCAT   52521     _     ATATA   AG
                                TGC TATGTGT    GTG  GTAT
                                |||  |||||||    |||  ||||
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                                ACG ATACACA    CAC  CGTA
                                  T      _____   A_
GAM2167  IL20RA   3'  TGCTATGTGCATATGGGAAGT  52522           AGT
                                TGCTATGTGTATAT   GAGGT
                                ||||||||||||||  |||||
                                ACGATACACGTATA   CTTCA
                                       CC_
GAM2167  KAL1     3'  TGTCTGTGTGTATATACATGTA 52523    _ A        GTGAG
              T                  TG CT TGTGTATATA    GTAT
                                || || ||||||||||    ||||
                                AC GA ACACATATAT    CATA
                                 A  C        GTA__
GAM2167  KCNJ3    3'  TGTATGTGTATGTATGTG    52524    C       A  _
                                TG TATGTGTAT TA GTG
                                || |||||||| || |||
                                AC ATACACATA AT CAC
                                 _       C  A
GAM2167  PCP4     3'  TGCTATGCGTGTGTGG      52525         ATATA   A
                                TGCTATGTGT    GTG GG
                                ||||||||||    ||| ||
                                ACGATACGCA    CAC CC
                                      _____  A
GAM2167  PPAT     3'  TGTATGTGTACATGTA      52526    C        A
                                TG TATGTGTATAT GTG
                                || ||||||||||| |||
                                AC ATACACATGTA CAT
                                 _       _
GAM2167  TAT      3'  TGTGTAAAGTGAGGTA      52527       TAT
                                TGTGTA   AGTGAGGTA
                                ||||||   |||||||||
                                ACACAT   TCACTCCAT
                                   T__
GAM2167  VIPR1    3'  TGTATGTGTAGCAGGGTGAGGT 52528    C      _ TA
              AT                  TG TATGTGTA TA  GTGAGGTAT
                                || ||||||| ||  |||||||||
                                AC ATACACAT GT  CACTCCATA
                                 _      C  CC
GAM2167  BCMP1    3'  TGCTATATGTGTGTGAG     52529         ATATA
                                TGCTATGTGT    GTGAG
                                ||||||||||    |||||
                                ACGATATACA    CACTC
                                      CA___
GAM2167  BY55     5'  CACGGATGTAGTGAGGTAT   52530     TG ATA
                                TATG  T   TAGTGAGGTAT
                                ||||  |   ||||||||||
                                GTGC  A   ATCACTCCATA
                                  CT C__
GAM2167  CACNA1I  3'  TGTCTATGTGTGTGTGTA    52531    _      ATATA   AG
                                TG CTATGTGT    GTG  GTA
                                || ||||||||    |||  |||
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                                AC GATACACA    CAC  CAT
                                 A      _____  A_
GAM2167 CSR1     3' TGCATGTGTATGTGTGCAT   52533    T      ATA   AG
                                TGC ATGTGTAT   GTG  GTAT
                                ||| ||||||||   |||  ||||
                                ACG TACACATA   CAC  CGTA
                                  _      ___   A_
GAM2167 CSR1     3' TGCATGTGTATATATGTG    52532    T        _
                                TGC ATGTGTATATA GTG
                                ||| |||||||||| |||
                                ACG TACACATATAT CAC
                                  _        A
GAM2167 DKFZP572C163 3' TGTTATGTGGTAAGGT     52534    C     TATATA
                                TG TATGTG     GTGAGGT
                                || ||||||     |||||||
                                AC ATACAC     CATTCCA
                                 A    _______
GAM2167 KIAA0970 3' TGTTATGTGTATATGTG     52535    C        A
                                TG TATGTGTATAT GTG
                                || |||||||||| |||
                                AC ATACACATATA CAC
                                 A        _
GAM2167 KIAA1247 3' TGTGCAGCTGGTGAGGTAT   52536       TATA
                                TGTGTA   GTGAGGTAT
                                ||||||   |||||||||
                                ACACGT   CACTCCATA
                                    CGAC
GAM2167 KIAA1309 3' TGCATGTGTGTATGTG     52537    T    A  A
                                TGC ATGTGT TAT GTG
                                ||| |||||| ||| |||
                                ACG TACACA ATA CAC
                                  _     C  _
GAM2167 KIAA1918 3' TGCATGTGTATGTATGTG    52538    T      A _
                                TGC ATGTGTAT TA GTG
                                ||| |||||||| || |||
                                ACG TACACATA AT CAC
                                  _       C  A
GAM2167 KLHL6    3' TGTATGTGTATATGTG      52539    C        A
                                TG TATGTGTATAT GTG
                                || |||||||||| |||
                                AC ATACACATATA CAC
                                  _        _
GAM2167 MGC15482 3' TGTATGTGTATGTATGTG    52524    C       A _
                                TG TATGTGTAT TA GTG
                                || |||||||| || |||
                                AC ATACACATA AT CAC
                                  _       C  A
GAM2167 OSBPL8   3' TGTGTATATGGCACAAGGT   52540         A __
                                TGTGTATAT GT  GAGGT
                                |||||||| ||  |||||
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                                ACACATATA CG  TTCCA
                                     C  TG
GAM2167  P101-PI3K 3'  TGCCATGTGTGTGTGGT     52541          ATATA   A
                                TGCTATGTGT     GTG GGT
                                ||||||||||     ||| |||
                                ACGGTACACA     CAC CCA
                                      _____   A
GAM2167  SSBP2     3'  TGTATGTGTATATGTCTGTAT  52542    C         A  GAG
                                TG TATGTGTATAT GT   GTAT
                                || ||||||||||| ||   ||||
                                AC ATACACATATA CA   CATA
                                 _         _ GA_
GAM2167  TSPAN-2   3'  TGTTCTGTGTATATATAAGTAT 52543    CTA         GTGA
                                TG   TGTGTATATA    GGTAT
                                ||   ||||||||||    |||||
                                AC   ACACATATAT    TCATA
                                 AAG         AT__
GAM2167  USP25     3'  TGTATGTGTATATATGTG     52544    C          _
                                TG TATGTGTATATA GTG
                                || ||||||||||| |||
                                AC ATACACATATAT CAC
                                 _          A
GAM2167  LOC121536 3'  TGTTATGTGTATATATGTA    52545    C          _
                                TG TATGTGTATATA GTG
                                || ||||||||||| |||
                                AC ATACACATATAT CAT
                                 A          A
GAM2167  LOC145622 3'  TGTCTGTATATATAGTG      52546    CTA
                                TG   TGTGTATATAGTG
                                ||   ||||||||||||
                                AC   ACATATATATCAC
                                 AG_
GAM2167  LOC151127 3'  TGCATATGTGTGTATGTG     52547     _      A   A
                                TGC TATGTGT TAT GTG
                                ||| ||||||| ||| |||
                                ACG ATACACA ATA CAC
                                  T      C  _
GAM2168  COL6A2    3'  CGGCCTAGAGCTCCTCCTCGGG 52550       CA___        AA
           C                     CGGTC     CTCCTCCTC  GC
                                |||||     |||||||||  ||
                                GCCGG     GAGGAGGAG  CG
                                   ATCTC         CC
GAM2168  EPAC      5'  CCCACCTTCATGTTTCTTTTCA 52551       GG  CACTC_  CC
           AGC                    TCCAC  TC     CT  TCAAGC
                                |||||  ||     ||  ||||||
                                GGGTG  AG     GA  AGTTCG
                                   GA  TACAAA  AA
GAM2168  KCNJ5     3'  GGTTCCTCCCCACAGC      52552     CCAC        _
                                GGT    TCCTCCTCA AGC
                                |||    ||||||||| |||
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                                CCA    AGGAGGGGT TCG
                                 _____       G
GAM2168 KCNK7    3' TCCTGGCTGCTTCCTCCTCA  52553    AC  CCAC
                                TCC  GGT   TCCTCCTCA
                                |||  |||   |||||||||
                                AGG  CCG   AGGAGGAGT
                                  A_  ACGA
GAM2168 KCNK7    3' TCCTGGCTGCTTCCTCCTCA  52553    AC  CCAC
                                TCC  GGT   TCCTCCTCA
                                |||  |||   |||||||||
                                AGG  CCG   AGGAGGAGT
                                  A_  ACGA
GAM2168 KCNK7    3' TCCTGGCTGCTTCCTCCTCA  52553    AC  CCAC
                                TCC  GGT   TCCTCCTCA
                                |||  |||   |||||||||
                                AGG  CCG   AGGAGGAGT
                                  A_  ACGA
GAM2168 KCNK7    3' TCCTGGCTGCTTCCTCCTCA  52553    AC  CCAC
                                TCC  GGT   TCCTCCTCA
                                |||  |||   |||||||||
                                AGG  CCG   AGGAGGAGT
                                  A_  ACGA
GAM2168 NFATC3   5' GCTGCAGCTCCTCCTCAGGC  52554    C_ _       A
                                GT  CA CTCCTCCTCA GC
                                ||  || |||||||||| ||
                                CG  GT GAGGAGGAGT CG
                                 AC  C         C
GAM2168 RBM6     5' TCCACGGCCCGCTCCTCC    52555         A
                                TCCACGGTCC CTCCTCC
                                |||||||||| |||||||
                                AGGTGCCGGG GAGGAGG
                                      C
GAM2168 20D7-FC4 5' AGCCTAGCTTTCTCCTCAAGC 52556     CA_ C_
                                GGTC   CT  CTCCTCAAGC
                                ||||   ||  ||||||||||
                                TCGG   GA  GAGGAGTTCG
                                  ATC  AA
GAM2168 DKFZP434H132 5'  TCCAGGGCTACCTCCTCCTTAA 52557      C   CCA      C
             G                   TCCA GGT   CTCCTCCT AAG
                                ||||  |||   |||||||| |||
                                AGGT CCG   GAGGAGGA TTC
                                  C   ATG       A
GAM2168 FLJ10535 3' ACAGCCCACTCCTTCTCAGGC  52558           C    A
                                ACGGTCCACTCCT CTCA GC
                                |||||||||||| |||| ||
                                TGTCGGGTGAGGA GAGT CG
                                       A   C
GAM2168 FLJ12688 3' CAACCGCTTCTCCTCAAG    52559     T  A  C
                                CGG CC CT CTCCTCAAG
                                ||| || || |||||||||
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                                GTT GG GA GAGGAGTTC
                                  _ C A
GAM2168 FLJ14154 3' TCCCTCTCCCTCCTCCTCAGGC 52560    ACGG  A       A
                                TCC   TCC CTCCTCCTCA GC
                                |||   ||| |||||||||| ||
                                AGG   AGG GAGGAGGAGT CG
                                  GAG_  _       C
GAM2168 MYH7B   3' CCCTGCCTGCTCCTCCTTGAGC 52561   ACG  CA      CA
                                CC  GTC  CTCCTCCT  AGC
                                ||  |||  ||||||||  |||
                                GG  CGG  GAGGAGGA  TCG
                                 GA_  AC      AC
GAM2168 PHF5A   3' CACAGTCAGTTCCTCAAGC   52562       CACTCC
                                CACGGTC    TCCTCAAGC
                                |||||||    |||||||||
                                GTGTCAG    AGGAGTTCG
                                    TCA___
GAM2168 PIP3-E  3' TCCACAGTCCATTTCATACAGG 52563         CTCCTCCT  A
             C                   TCCACGGTCCA       CA GC
                                ||||||||||       || ||
                                AGGTGTCAGGT       GT CG
                                      AAAGTAT_  C
GAM2168 RoXaN   3' CACAGTCCAGCTCAAG      52564         CTCCTC
                                CACGGTCCA    CTCAAG
                                |||||||||    ||||||
                                GTGTCAGGT    GAGTTC
                                    C_____
GAM2168 LOC126382 5' TCCCGGCGCCTCCTCAAG    52565    A   CCACT
                                TCC CGGT    CCTCCTCAAG
                                ||| ||||    ||||||||||
                                AGG GCCG    GGAGGAGTTC
                                  _   C____
GAM2168 LOC157506 3' ACAGAGCTCTTCCTCAAG    52566     TCCA  C
                                ACGG   CTC TCCTCAAG
                                ||||   ||| ||||||||
                                TGTC   GAG AGGAGTTC
                                  TC__  A
GAM2168 LOC158376 5' TCCATGGCCCACTGAGCAACCT 52567     C      CCT___
                                TCCA GGTCCACT     CCT
                                |||| ||||||||     |||
                                AGGT CCGGGTGA     GGA
                                  A       CTCGTT
GAM2168 LOC160418 5' CATGGTCTACCTCGTTCAGGC  52568   C   CACT   C_  A
                                CA GGTC   CCTC  TCA GC
                                || ||||   ||||  ||| ||
                                GT CCAG   GGAG  AGT CG
                                 A   AT__   CA  C
GAM2168 LOC202309 3' TCCACTGTCCTCCCTCAAG   52569     G   ACTCC
                                TCCAC GTCC    TCCTCAAG
                                ||||| ||||    ||||||||
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                                AGGTG CAGG    GGGAGTTC
                                  A   A____
GAM2168 LOC219653 3' CACGGACACCTCCTCAAG   52570      TCC  T
                                CACGG  AC CCTCCTCAAG
                                |||||  || ||||||||||
                                GTGCC  TG GGAGGAGTTC
                                  ___  T
GAM2168 LOC219920 3' CCCACTCCTCCTCCTCAG   52571      GGTCCA       A
                                TCCAC    CTCCTCCTCA G
                                |||||    |||||||||| |
                                GGGTG    GAGGAGGAGT C
                                  AG____       C
GAM2168 LOC93349  3' CACACCCTTCTTCCTCAAG   52572     GT  AC  C
                                CACG  CC  TC TCCTCAAG
                                ||||  ||  || ||||||||
                                GTGT  GG  AG AGGAGTTC
                                  __  GA  A
GAM2169 BMP4      3' TAATGACTCATTTTATTACCAC 52575       C__________  TAAG
           TTATG                  TGACTCAT       CCA   TG
                                |||||||        |||   ||
                                ACTGAGTA       GGT   AC
                                    AAATAAIIIT  GAAT
GAM2169 BMP4      3' TAATGACTCATTTTATTACCAC 52575       C__________  TAAG
           TTATG                  TGACTCAT       CCA   TG
                                |||||||        |||   ||
                                ACTGAGTA       GGT   AC
                                    AAATAAIIIT  GAAT
GAM2169 BMP4      3' TAATGACTCATTTTATTACCAC 52575       C__________  TAAG
           TTATG                  TGACTCAT       CCA   TG
                                |||||||        |||   ||
                                ACTGAGTA       GGT   AC
                                    AAATAAIIIT  GAAT
GAM2169 LOC221755 5' TGACTCATCCCACACTG    52576          AG
                                TGACTCATCCCATA  TG
                                ||||||||||||||  ||
                                ACTGAGTAGGGTGT  AC
                                      G_
GAM2170 ECM2      3' TCTGTGTGTTAGTGAATCAG  52579      _  GCCTTA
                                TCTGTG GT     TGAATCAG
                                |||||| ||     ||||||||
                                AGACAC CA     ACTTAGTC
                                  A  ATC____
GAM2170 IAPP      3' TCTGTGGTCTTTTAATTGAAGA 52580       GC   A   ATC_
           C                    TCTGTGGT  CTT TGA    AGAC
                                ||||||||  ||| |||    ||||
                                AGACACCA  GAA ATT    TCTG
                                    __   A   AACT
GAM2170 IL17      3' TGTGGTGCCTTGATCAGAC   52581         TA   A
                                TGTGGTGCCT  TGA TCAGAC
                                ||||||||||  ||| ||||||
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                                ACACCACGGA  ACT AGTCTG
                                          __  _
GAM2170 MBP      3'  TCTGTGCTGCCCCACGTTGGAC 52582       G       AATCA
                                TCTGTG TGCCTTATG    GAC
                                |||||| |||||||||    |||
                                AGACAC ACGGGGTGC    CTG
                                   G        AAC__
GAM2170 SELP     3'  TGGTCTTCTTGTGAGTCAGA   52583     GC_   A   A
                                TGGT   CTT TGA TCAGA
                                ||||   ||| ||| |||||
                                ACCA   GAA ACT AGTCT
                                  GAA   C   C
GAM2170 FLJ11222 3'  TCTGTAGTGTTGTAGAAATCGG 52584        CCT  T    A
             A                   TCTGTGGTG   TA GAATC GA
                                |||||||||   || ||||| ||
                                AGACATCAC   AT TTTAG CT
                                     AAC  C    C
GAM2170 FLJ14800 3'  TCTGTGGTGCCTGAGCAG    52585          TAT  AT
                                TCTGTGGTGCCT   GA  CAG
                                ||||||||||||   ||  |||
                                AGACACCACGGA   CT  GTC
                                       ____  C_
GAM2170 KIAA0430 3'  TGTGTGCAGAATCAGA      52586     G   CTTAT
                                TGTG TGC    GAATCAGA
                                |||| |||    ||||||||
                                ACAC ACG    CTTAGTCT
                                  _   T_____
GAM2170 N4BP2    3'  TGGGGGGCATGAATCAG     52587    T  T  CTT
                                TG GG GC   ATGAATCAG
                                || || ||   |||||||||
                                AC CC CG   TACTTAGTC
                                 C  C  ___
GAM2170 SSB-4    3'  TCTGTGCTGCCCATCAG     52588       G    TATGA
                                TCTGTG TGCCT    ATCAG
                                |||||| |||||    |||||
                                AGACAC ACGGG    TAGTC
                                   G    ______
GAM2170 LOC149013 3'  TCTGTAGTGCTGGAATGAGTCA 52589          CTT_   A
             G                   TCTGTGGTGC    ATGA TCAG
                                ||||||||||    |||| ||||
                                AGACATCACG    TACT AGTC
                                      ACCT    C
GAM2170 LOC150498 3'  TCTGTGGTTCCAGTCAGA    52590        G  TTATGAA
                                TCTGTGGT CC      TCAGA
                                |||||||| ||      |||||
                                AGACACCA GG      AGTCT
                                     A  TC_____
GAM2170 LOC150759 3'  TATGGGATGAATCAGA      52591       TGCCTT
                                TGTGG     ATGAATCAGA
                                |||||     ||||||||||
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                                ATACC     TACTTAGTCT
                                  C_____
GAM2170 LOC254543 5'  TCTGTGGTGTCATTAACA    52592        CC   GAAT
                                TCTGTGGTG  TTAT   CA
                                |||||||||  ||||   ||
                                AGACACCAC  AGTA   GT
                                     __   ATT_
GAM2171 CD8A     3'  AAGTGCATGTTTGGGACAGCAG 52595        ATCA_  TT
             T                   AAGTGCATGT    AT  TAGT
                                 ||||||||||    ||  ||||
                                 TTCACGTACA    TG  GTCA
                                       AACCC  TC
GAM2171 CDK2AP1   3'  AAAGATGCAAACAGTTTTAGTC 52596     _   TGTAT  A
                                AAAG TGCA    CA TTTTAGTC
                                |||| ||||    || ||||||||
                                TTTC ACGT    GT AAAATCAG
                                  T   TT___  C
GAM2171 DGUOK    3'  AGTGCAGGCCCAATTTTGGTC  52597      T  A      A
                                AGTGCA GT TCAATTTT GTC
                                |||||| || |||||||| |||
                                TCACGT CG GGTTAAAA CAG
                                   C  _       C
GAM2171 C1orf17   3'  AAAGTGCAGGTGTTCAGT    52598        T  ATCAAT
                                AAAGTGCA GT     TTTAGT
                                |||||||| ||     ||||||
                                TTTCACGT CA     AAGTCA
                                     C  C_____
GAM2171 DKFZp434F2322 3'  AAAGTGCAGATTTTTAGT    52599        T  ATCAA
                                AAAGTGCA GT    TTTTAGT
                                |||||||| ||    |||||||
                                TTTCACGT TA    AAAATCA
                                     C  _____
GAM2171 FLJ10504  3'  AAAGTGCATATGTTGGTGTAGC 52600          ATCAATT___
             TAGTC                  AAAGTGCATGT        TTAGTC
                                    ||||||||||         ||||||
                                    TTTCACGTATA        GATCAG
                                         CAACCACATC
GAM2171 KIAA0522  3'  AAAGTGCATTGTCTTCAGT   52601         _  ATCAA
                                AAAGTGCAT GT    TTTTAGT
                                |||||||| ||    |||||||
                                TTTCACGTA CA    GAAGTCA
                                     A  _____
GAM2171 MGC14793  3'  AGAGCTGTAACAAATTTTAGT  52602    T  A   T  _
                                AG GC TGTA CAA TTTTAGT
                                || || |||| ||| |||||||
                                TC CG ACAT GTT AAAATCA
                                 T  _   T  T
GAM2171 TIEG     3'  AAAGTGCAGTGTATCTTAGAGT 52603        _     AA  TT
             C                   AAAGTGCA TGTATC  TT  AGTC
                                 |||||||| ||||||  ||  ||||
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                                TTTCACGT ACATAG  AA  TCAG
                                    C     __ TC
GAM2171  USP20    3'  AAGTGCATATATTTTCTAGT   52604          CAA
                                AAGTGCATGTAT   TTTTAGT
                                ||||||||||||  |||||||
                                TTCACGTATATA   AAGATCA
                                      A__
GAM2171  LOC149386 3'  AAAATGCAAACAGTTTTAGT   52605        TGTAT  A
                                AAAGTGCA    CA TTTTAGT
                                ||||||||    || |||||||
                                TTTTACGT    GT AAAATCA
                                    TT___  C
GAM2172  CACNA1D  5'  TGAGCGACTACTGTGTGCA   52608     ACC_   G
                                TGA   TTGC TGTGTGCA
                                |||   |||| ||||||||
                                ACT   GATG ACACACGT
                                  CGCT   _
GAM2172  CD34     3'  CCTCTGAGGTGTGTGC      52609        ACCTTGC
                                TCTCTGA      GTGTGTGC
                                |||||||      ||||||||
                                GGAGACT      CACACACG
                                    C_______
GAM2172  CYLN2    3'  CCTCTGTGTGTGTGTG      52610       AACCT  C
                                TCTCTG    TG GTGTGTG
                                ||||||    || |||||||
                                GGAGAC    AC CACACAC
                                   ______ A
GAM2172  MLLT2    3'  TGAGGCTTCCAATGTGCAA   52611     AC   G  T
                                TGA  CTT CG GTGTGCAA
                                |||  ||| || ||||||||
                                ACT  GAA GT TACACGTT
                                  CC   G  _
GAM2172  RAB36    3'  TCCTGTCCGTGTGTGTGCA   52612    T   AA  TT C
                                TC CTG  CC  G GTGTGTGCA
                                || |||  ||  | |||||||||
                                AG GAC  GG  C CACACACGT
                                 _   A_  __ A
GAM2172  RAG2     5'  TCTCTGAATCTTTGCCGC    52613        C   _  G
                                TCTCTGAA CTT GC TGT
                                |||||||| ||| || |||
                                AGAGACTT GAA CG GCG
                                    A   A  _
GAM2172  SLC6A3   3'  CCTCTGAACAGACTGTGTGTGC 52614         CTT  _
            AA                    TCTCTGAAC   GC GTGTGTGCAA
                                |||||||||   || ||||||||||
                                GGAGACTTG   TG CACACACGTT
                                     TC_  A
GAM2172  C8orf13  3'  TCTCTGTCGTGTGTGTGTGTG  52615       AACCT  C
                                TCTCTG    TG GTGTGTG
                                ||||||    || |||||||
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                                AGAGAC    AC CACACAC
                                   AGCAC  A
GAM2172  FLJ10578  3'  TGAATGTTGTGTGCAA     52616     CCT  CG
                                TGAA   TG  TGTGTGCAA
                                ||||   ||  |||||||||
                                ACTT   AC  ACACACGTT
                                  ___  A_
GAM2172  FLJ11637  3'  TCTGAACCATGTATGTG     52617        TTGC
                                TCTGAACC   GTGTGTG
                                ||||||||   |||||||
                                AGACTTGG   CATACAC
                                    TA__
GAM2172  FLJ12154  5'  TCTTTGTATTCGTGTGTGTGCA 52618     C  AACC   C
           A                     TCT TG    TTG GTGTGTGCAA
                                ||| ||    ||| ||||||||||
                                AGA AC    AGC CACACACGTT
                                  A  ATA_   A
GAM2172  KIAA1622  3'  CCTGGGTTTTGTACGTATGCAA 52619     AACC   CG
                                TCTG    TTG  TGTGTGCAA
                                ||||    |||  |||||||||
                                GGAC    AAC  GCATACGTT
                                  CCAA   AT
GAM2172  KIAA1764  5'  TCTAACTCCTGTGTGCA     52620      AC  TGCG
                                TCTGA  CT    TGTGTGCA
                                |||||  ||    ||||||||
                                AGATT  GG    ACACACGT
                                  GA  _____
GAM2172  LIPI     3'  TCTCTGGATCTTGTATGTGCA  52621       AAC   GC
                                TCTCTG   CTT  GTGTGTGCA
                                ||||||   |||  |||||||||
                                AGAGAC   GAA  CATACACGT
                                   CTA   __
GAM2172  MIC2L1   3'  CCTGGGTGCTGCGTGTGTG   52622     AACC
                                TCTG    TTGCGTGTGTG
                                ||||    ||||||||||
                                GGAC    GACGCACACAC
                                  CCAC
GAM2172  NICE-1   3'  CTGAGCACCTGCTGTGTGCAA  52623      __   T  G
                                CTGA  ACCT GC TGTGTGCAA
                                ||||  |||| || |||||||||
                                GACT  TGGA CG ACACACGTT
                                  CG    _  _
GAM2172  PFTK1    3'  TCAGAATACTGTGTGTGCA   52624    T   CCT   _
                                TC GAA   TGC GTGTGTGCA
                                || |||   ||| |||||||||
                                AG CTT   ATG CACACACGT
                                 T  ___   A
GAM2172  VAV3     3'  TCTCTGAAATTTTTGGTGCA  52625        CCTTGCG  T
                                TCTCTGAA      TG GTGCA
                                ||||||||      || |||||
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                                AGAGACTT      AC CACGT
                                     TAAAA__  _
GAM2172  LOC130813 3'  CCTCTGAATCTTACGTGTA   52626        C
                                TCTCTGAA CTTGCGTGTG
                                |||||||| ||||||||||
                                GGAGACTT GAATGCACAT
                                     A
GAM2172  LOC144564 5'  CCTCTGGATTTCCATGTGCA   52627       AACC  G
                                TCTCTG    TT CGTGTGTG
                                ||||||    || ||||||||
                                GGAGAC    AA GTACACGT
                                    CTA_  G
GAM2172  LOC144571 5'  TCTTTTAACCTTGCTGTGCA   52628     CTG       GTG
                                TCT   AACCTTGC   TGTGCA
                                |||   ||||||||   ||||||
                                AGA   TTGGAACG   ACACGT
                                  AAA       ____
GAM2172  LOC200488 5'  TCACTGGGAAGCTGTGTGTGCA 52629    T   AACCTT  _
                                TC CTG      GC GTGTGTGCA
                                || |||      || ||||||||||
                                AG GAC      CG CACACACGT
                                 T   CCTT__  A
GAM2172  LOC255000 3'  TCTGAACTTTTCGCGTGCAA   52630        C  GCG
                                TCTGAAC TT   TGTGTGCAA
                                ||||||| ||   |||||||||
                                AGACTTG AA   GCGCACGTT
                                     _  AA_
GAM2172  LOC256113 3'  TCTCTGAACTTATTTAAAATGT 52631         CTTGC____
              GTG                   TCTCTGAAC        GTGTGTG
                                |||||||||        |||||||
                                AGAGACTTG        TACACAC
                                     AATAAATTT
GAM2172  LOC92285  5'  CTTTGAATCTTCTCATGTGTA  52632    C    C   G_
                                CT TGAA CTT  CGTGTGTG
                                || |||| |||  ||||||||
                                GA ACTT GAA  GTACACAT
                                 A    A   GA
GAM2172  LOC92340  3'  TCTGAACCTTGTCCTTGTA    52633          CGTG
                                TCTGAACCTTG    TGTG
                                ||||||||||    ||||
                                AGACTTGGAAC    ACAT
                                      AGGA
GAM2173  DKFZP434L1717 3'  TATTAGGTAGTTGTTTTA    52636        AT
                                TATTAGG  TAGTTGTTTTA
                                |||||||  ||||||||||
                                ATAATCC  ATCAACAAAAT
                                     __
GAM2173  LOC132720 3'  TTAGGATTATCTGATTTTA    52637         G  _
                                TTAGGATTA TTG TTTTA
                                ||||||||| ||| |||||
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                                AATCCTAAT GAC AAAAT
                                     A   T
GAM2173  LOC157567 3'  CCTATATTAGGATAAGGTTTT  52638          T  TT
                                TCTATATTAGGAT AG  GTTTT
                                |||||||||||| ||  |||||
                                GGATATAATCCTA TC  CAAAA
                                      T  __
GAM2174  PAH      3'  TATACAGATTTGCTTTTC    52641          A  A
                                TATACAGATTTG TTT TC
                                |||||||||||| ||| ||
                                ATATGTCTAAAC GAA AG
                                      _  A
GAM2174  RNTRE    3'  ACAGATGCCTATATCTATTA  52642       TTGATT
                                ACAGAT     TATCTATTA
                                ||||||     |||||||||
                                TGTCTA     ATAGATAAT
                                   CGGAT_
GAM2174  RISC     3'  TATACAGATGTTGATTTACTCT 52643        _      _
                                TATACAGAT TTGATTTA TCT
                                ||||||||| |||||||| |||
                                ATATGTCTA AACTAAAT AGA
                                     C       G
GAM2175  DYT1     3'  TCTATGTAATAATGATGAGAAC 52646          AAC  TT
                                TCTATGTAATAAT   GA  AC
                                ||||||||||||   ||  ||
                                AGATACATTATTA   CT  TG
                                      CTA  CT
GAM2175  XK       3'  TCTATGCACATATGTGATTACA 52647        ATAATAAC
            T                   TCTATGTA       GATTACAT
                                ||||||||       ||||||||
                                AGATACGT       CTAATGTA
                                    GTATACA_
GAM2175  LOC221288 3'  TATGTAATAATGGTGAACACAT 52648          AAC  T
                                TATGTAATAAT   GA TACAT
                                ||||||||||   || |||||
                                ATACATTATTA   CT GTGTA
                                      CCA  T
GAM2176  FGF2     3'  TCTAGGTAAGCTTCACTGGGT  39373          AGA  CA
                                TCTAGGTAAGTTT   GCT  GGT
                                ||||||||||||   |||  |||
                                AGATCCATTCGAA   TGA  CCA
                                      G__   C_
GAM2176  FLT1     3'  GGTTACTTAGAGCTCAGGT   39374     AAG
                                GGT   TTTAGAGCTCAGGT
                                |||   ||||||||||||||
                                CCA   GAATCTCGAGTCCA
                                  AT_
GAM2176  C12orf22  3'  CTGGGTAGCTTCGAGAGCTCAG 39375    A   A   __
            GT                    CT GGTA GTTT  AGAGCTCAGGT
                                || |||| ||||  ||||||||||
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                                GA CCAT CGAA  TCTCGAGTCCA
                                 C   _   GC
GAM2176 KIAA1915 3' TAGGGTAAGAGCTCAGG    39376     TAA  TT
                                TAGG  GT  AGAGCTCAGG
                                ||||  ||  ||||||||||
                                ATCC  CA  TCTCGAGTCC
                                  ___  T_
GAM2176 RNF13    3' TCTAGGTAACTTTATGGAGGT 39377       G   GAGCTC
                                TCTAGGTAA TTTA    AGGT
                                ||||||||| ||||    ||||
                                AGATCCATT AAAT    TCCA
                                     G   ACC___
GAM2177 ADAM10   5' CTGCCGCCGCCCATGG     52652       TCCC
                                CTGCCGCC   GCCTGTGG
                                ||||||||   ||||||||
                                GACGGCGG   CGGGTACC
                                    _____
GAM2177 ADAM10   5' CCGCCGCCTCCTCACGGGT   52653        _  CT T
                                CTGCCGCCTCC CGC  G GGT
                                |||||||||||  |||  | |||
                                GGCGGCGGAGG GTG  C CCA
                                     A  __ _
GAM2177 APLP2    3' GCCGCCTCCTTGGTGTGGT   52654       CGCC
                                GCCGCCTCC   TGTGGT
                                |||||||||   ||||||
                                CGGCGGAGG   ACACCA
                                     AACC
GAM2177 ATF4     5' CTGCCGCCGCCATCTTGGT   52655       TCCC  TG__
                                CTGCCGCC   GCC   TGGT
                                ||||||||   |||   ||||
                                GACGGCGG   CGG   ACCA
                                    _____  TAGA
GAM2177 BAX      5' CCGCCGCCTCTCGCCGGGT   52656        C   T T
                                CTGCCGCCTC CGCC G GGT
                                |||||||||| |||| | |||
                                GGCGGCGGAG GCGG C CCA
                                     A   _ _
GAM2177 BAX      5' CCGCCGCCTCTCGCCGGGT   52656        C   T T
                                CTGCCGCCTC CGCC G GGT
                                |||||||||| |||| | |||
                                GGCGGCGGAG GCGG C CCA
                                     A   _ _
GAM2177 BAX      5' CCGCCGCCTCTCGCCGGGT   52656        C   T T
                                CTGCCGCCTC CGCC G GGT
                                |||||||||| |||| | |||
                                GGCGGCGGAG GCGG C CCA
                                     A   _ _
GAM2177 BAX      5' CCGCCGCCTCTCGCCGGGT   52656        C   T T
                                CTGCCGCCTC CGCC G GGT
                                |||||||||| |||| | |||
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                                GGCGGCGGAG GCGG C CCA
                                     A   _ _
GAM2177 BAX      5' CCGCCGCCTCTCGCCGGGT   52656         C   T T
                                CTGCCGCCTC CGCC G GGT
                                |||||||||| |||| | |||
                                GGCGGCGGAG GCGG C CCA
                                     A   _ _
GAM2177 BTAF1    5' CTGCCGCCTACCCGAGCT    52657        _   C_
                                CTGCCGCCT CCCG  CT
                                ||||||||| ||||  ||
                                GACGGCGGA GGGC  GA
                                     T   TC
GAM2177 CAPS     3' CTGCCCCTCCCCGCTCTGTGGT 52658      G    _ _
                                CTGCC CCTCCC GC CTGTGGT
                                ||||| |||||| || |||||||
                                GACGG GGAGGG CG GACACCA
                                   _    G  A
GAM2177 CELSR3   5' CTGCCGCCTCCCGCCGC     52659           T
                                CTGCCGCCTCCCGCC GT
                                |||||||||||||| ||
                                GACGGCGGAGGGCGG CG
                                                _
GAM2177 CLCN7    3' CTGCCGCCTGCCCGCCCAGC   52660        _     _
                                CTGCCGCCT CCCGCCT GT
                                ||||||||| ||||||| ||
                                GACGGCGGA GGGCGGG CG
                                     C      T
GAM2177 EGLN2    3' CCGCTGCCTCCCACGG      52661     C       CTGT
                                CTGC GCCTCCCGC   GG
                                |||| |||||||||   ||
                                GGCG CGGAGGGTG   CC
                                  A       ____
GAM2177 EIF2AK3  5' CTGCCTCTCCCGCCGC      52662      GC       T
                                CTGCC  CTCCCGCC GT
                                |||||  |||||||| ||
                                GACGG  GAGGGCGG CG
                                   A_       _
GAM2177 EP300    5' CTGCCGCCTCTCTCCACCACAG 52663        _________  CCTG
            GCG                   TGCCGCCTC       CCG   TG
                                |||||||||       |||   ||
                                ACGGCGGAG       GGT   GC
                                     AGAGGIIIT   GTCC
GAM2177 FKBP2    5' CTGCCGCCTCTGCGCAGGCGCG 52664        C_  CT  _
            T                    CTGCCGCCTC  CGC  GTG GT
                                |||||||||  |||  ||| ||
                                GACGGCGGAG  GCG  CGC CA
                                     AC   TC   G
GAM2177 FOXO1A   3' CTGCCCCAAATACCTGTGGT   52665      G  TCCC
                                CTGCC CC    GCCTGTGGT
                                ||||| ||    |||||||||
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                                GACGG GG   TGGACACCA
                                  _ TTTA
GAM2177 FUS1    5' CCGCCGCCTTCCGCAGGC   10631       C   CTGT
                                CTGCCGCCT CCGC   GGT
                                ||||||||| ||||   |||
                                GGCGGCGGA GGCG   CCG
                                     A   T___
GAM2177 FUT5    3' CTGTGCCTCCCAGCGG     52666    CC     CCT
                                CTG  GCCTCCCG  GTGG
                                |||  ||||||||  ||||
                                GAC  CGGAGGGT  CGCC
                                 A_      ___
GAM2177 GRB14   5' CCGCCGCCTCCTCAGG     52667         _ CCTGT
                                CTGCCGCCTCC CG    GG
                                |||||||||| ||    ||
                                GGCGGCGGAGG GT    CC
                                     A _____
GAM2177 GRM1    5' GCCGCCTCTCCCGGAGTGGT  52668     __   CCT
                                GCCGCC  TCCCG  GTGGT
                                ||||||  |||||  |||||
                                CGGCGG  AGGGC  CACCA
                                   AG   CT_
GAM2177 HOXD1   5' CTGCCGCCGTCTGCGCCGC   52669       _ C_  T
                                CTGCCGCC TC  CGCC GT
                                |||||||| ||  |||| ||
                                GACGGCGG AG  GCGG CG
                                     C  AC   _
GAM2177 HSF2BP  5' CTGCCGCCTCCGCTCCGT    52670        C _
                                CTGCCGCCTCC GC CTGT
                                |||||||||| || ||||
                                GACGGCGGAGG CG GGCA
                                      _ A
GAM2177 IRS1    5' CTGCCGCCGCCCGCGGGCGCGT 52671       T   CT  _
                                CTGCCGCC CCCGC  GTG GT
                                |||||||| |||||  ||| ||
                                GACGGCGG GGGCG  CGC CA
                                     C   CC  G
GAM2177 JUN     5' CCGCCGCCTTCTGGTACCACAG 52672       _ _________  CCTG
           GCG                   TGCCGCCT C      CCG   TG
                                 |||||||| |      |||   ||
                                 GCGGCGGA G      GGT   GC
                                    A ACCAIIIT  GTCC
GAM2177 LDB1    5' CCGCCGCCTCTTGCTACCACAG 52673       __________  CCTG
           GCG                   TGCCGCCTC       CCG   TG
                                 |||||||||       |||   ||
                                 GCGGCGGAG       GGT   GC
                                    AACGAIIIT  GTCC
GAM2177 LIF     3' CTGCTGTCTCACCCTGTGGT  52674     CGC  CCG
                                CTGC  CTC  CCTGTGGT
                                ||||  |||  ||||||||
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                                GACG  GAG  GGACACCA
                                  ACA  TG_
GAM2177 LOH11CR2A 5' CTGCCGCCTTCGACCCAGGT  52675        CC  _   T
                                CTGCCGCCT  CG CCTG GGT
                                |||||||||  || |||| |||
                                GACGGCGGA  GC GGGT CCA
                                     A_  T   _
GAM2177 MAN2A1   5' CTGCCGCCCTCCCCGGGGT   52676       TC  G  T T
                                CTGCCGCC  CC CC G GGT
                                ||||||||  || || | |||
                                GACGGCGG  GG GG C CCA
                                     GA  _  _ C
GAM2177 MAP3K1   5' CTGCCCGCCTCCCGCAGCAGT  52677      _       CT TG
                                CTGCC GCCTCCCGC  G  GT
                                ||||| |||||||||  |  ||
                                GACGG CGGAGGGCG  C  CA
                                   G        T_ GT
GAM2177 MDS1     5' CTGCAGCCTCTGGTGTGTGGT  52678     C    CCGCC
                                CTGC GCCTC    TGTGGT
                                |||| |||||    ||||||
                                GACG CGGAG    ACACCA
                                  T    ACCAC
GAM2177 MTL5     5' CTGTCGCCCCCCGCGAGC    52679     C        CT
                                CTG CGCCTCCCGC  GT
                                ||| ||||||||||  ||
                                GAC GCGGGGGGCG  CG
                                  A        CT
GAM2177 NAGLU    5' CTGCCGCCTCCGGCCACGT   52680          C  _
                                CTGCCGCCTCC GCC TGT
                                |||||||||||| ||| |||
                                GACGGCGGAGG CGG GCA
                                      C  T
GAM2177 NUP98    5' CTGCTGCCACCCGCCGC     52681     C  T     T
                                CTGC GCC CCCGCC GT
                                |||| ||| |||||| ||
                                GACG CGG GGGCGG CG
                                  A  T    _
GAM2177 PITPN    5' CGTCGCCTCTCGCGCCGC    52682    C     C  _
                                TG CGCCTC CGC CTGT
                                || |||||| ||| ||||
                                GC GCGGAG GCG GGCG
                                 A     A  C
GAM2177 PPP1R12B 5' CTGCCGCCTCTCTCAACCACAG 52683         __________  CCTG
           GCG                    TGCCGCCTC       CCG   TG
                                |||||||||       |||   ||
                                ACGGCGGAG       GGT   GC
                                     AGAGTIIIT  GTCC
GAM2177 PTPRJ    5' CTGCCGTCTCCTTCGCCT    52684       C   __
                                CTGCCG CTCC  CGCCT
                                |||||| ||||  |||||
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                                GACGGC GAGG  GCGGA
                                   A   AA
GAM2177  RAB4A    5'  GCCGCCTCTCGCCGGGT    52685       C   T T
                                GCCGCCTC CGCC G GGT
                                |||||||| |||| | |||
                                CGGCGGAG GCGG C CCA
                                    A   _ _
GAM2177  RAB6A    5'  CCGCCGCCTCCCGGCAG    52686          CCT TG
                                CTGCCGCCTCCCG   G  G
                                ||||||||||||   |  |
                                GGCGGCGGAGGGC   C  C
                                       ___ GT
GAM2177  RAD23A   3'  CTGTCGCCTCCCAGTCCT    52687    C       __
                                CTG CGCCTCCCG  CCT
                                ||| |||||||||  |||
                                GAC GCGGAGGGT  GGA
                                  A       CA
GAM2177  RAD51L3  3'  GCATCCTCTTTCGCCTGTGGT  52688   CG   C__
                                GC  CCTC   CGCCTGTGGT
                                ||  ||||   ||||||||||
                                CG  GGAG   GCGGACACCA
                                 TA   AAA
GAM2177  RAD51L3  3'  GCATCCTCTTTCGCCTGTGGT  52688   CG   C__
                                GC  CCTC   CGCCTGTGGT
                                ||  ||||   ||||||||||
                                CG  GGAG   GCGGACACCA
                                 TA   AAA
GAM2177  RAD51L3  3'  GCATCCTCTTTCGCCTGTGGT  52688   CG   C__
                                GC  CCTC   CGCCTGTGGT
                                ||  ||||   ||||||||||
                                CG  GGAG   GCGGACACCA
                                 TA   AAA
GAM2177  RAD51L3  3'  GCATCCTCTTTCGCCTGTGGT  52688   CG   C__
                                GC  CCTC   CGCCTGTGGT
                                ||  ||||   ||||||||||
                                CG  GGAG   GCGGACACCA
                                 TA   AAA
GAM2177  RANBP3   3'  CCGCCTCCTCCCCGGT     52689       CG   G
                                CCGCCTCC  CCT TGGT
                                ||||||||  ||| ||||
                                GGCGGAGG  GGG GCCA
                                    A_  _
GAM2177  RNPEPL1  3'  GCCGCCTCTCCCAGCATGGT   52690        _  __  CT
                                GCCGCCTC CC  GC  GTGGT
                                |||||||| ||  ||  |||||
                                CGGCGGAG GG  CG  TACCA
                                    A  GT  __
GAM2177  SLC10A2  3'  CTGCCACCTCCCTGACCATGGT 52691           GC_
                                CTGCCGCCTCCC   CTGTGGT
                                ||||||||||||   |||||||
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                                GACGGTGGAGGG  GGTACCA
                                      ACT
GAM2177 SLC18A3  5' CTGTTGCCGCCCGCCCGC   52692    CC  T
                                CTG  GCC CCCGCCTGT
                                |||  ||| |||||||||
                                GAC  CGG GGGCGGGCG
                                  AA  C
GAM2177 SLC21A9  3' CTGCTGCCTCCCGAGCAGT   52693     C      CCT TG
                                CTGC GCCTCCCG  G  GT
                                |||| ||||||||  |  ||
                                GACG CGGAGGGC  C  CA
                                  A      T__ GT
GAM2177 SMURF1   3' CCGCCTCCCGCGGGT      52694         CT T
                                CCGCCTCCCGC  G GGT
                                ||||||||||  | |||
                                GGCGGAGGGCG  C CCA
                                      __ _
GAM2177 STARD5   3' CTGCCGCCTCTGGTACCACAGG 52695        _________  CCTG
             CG                   CTGCCGCCTC      CCG   TG
                                |||||||||       |||   ||
                                GACGGCGGAG      GGT   GC
                                     ACCAIIIT  GTCC
GAM2177 STXBP1   5' CCGCCGCCTCCTCAGG     52667         _ CCTGT
                                CTGCCGCCTCC CG    GG
                                |||||||||| ||    ||
                                GGCGGCGGAGG GT    CC
                                     A _____
GAM2177 TFG     5' CCGCCGCCTCTCCGCAGGT   52696        _   CTGT
                                CTGCCGCCTC CCGC   GGT
                                |||||||||| ||||   |||
                                GGCGGCGGAG GGCG   CCA
                                     A   T___
GAM2177 VARS2    3' TGCTGCCATCCCCATGGT    52697    C  TC  G  T
                                TGC GCC  CC CC GTGGT
                                ||| |||  || || |||||
                                ACG CGG  GG GG TACCA
                                  A  TA  _  _
GAM2177 WASF3    3' CCGCCGCCTCCTGTG      52698         CGCC
                                CTGCCGCCTCC   TGTG
                                ||||||||||   ||||
                                GGCGGCGGAGG   ACAC
                                      ____
GAM2177 ACTR3    5' CTGCCGCCGTCTGCTCCGT   52699       _ CC  _
                                CTGCCGCC TC  GC CTGT
                                |||||||| ||  || ||||
                                GACGGCGG AG  CG GGCA
                                     C  A_  A
GAM2177 ARFGAP3  3' CTGCCGCCTGAGATGTGGT   52700        CCCGCC
                                CTGCCGCCT     TGTGGT
                                |||||||||     ||||||
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                                GACGGCGGA     ACACCA
                                     CTCT__
GAM2177 BLOV1    3' CCGCCGCCTCCCGGG      52701          CCTGT
                                CTGCCGCCTCCCG    GG
                                ||||||||||||    ||
                                GGCGGCGGAGGGC    CC
                                      _____
GAM2177 C12orf22 5' CTGCCTCCTCCCGTGATGGT  52702      G      CCT
                                CTGCC CCTCCCG  GTGGT
                                ||||| |||||||  |||||
                                GACGG GGAGGGC  TACCA
                                   A      AC_
GAM2177 CHODL    5' CTGCCGCCTGCCGCGCCTGT  52703         _ _
                                CTGCCGCCT CC CGCCTGT
                                ||||||||| || |||||||
                                GACGGCGGA GG GCGGACA
                                     C  C
GAM2177 CHST8    3' CTGCTGCCTCCCACAGCGAT  52704     C       CT
                                CTGC GCCTCCCGC  GTGGT
                                |||| |||||||||  |||||
                                GACG CGGAGGGTG  CGCTA
                                  A        T_
GAM2177 DKFZP434B168 5' CCGCCGCCTTCTTGCTGGT   52705         _ CC  CTG
                                CTGCCGCCT C  GC   TGGT
                                ||||||||| |  ||   ||||
                                GGCGGCGGA G  CG   ACCA
                                     A AA  ___
GAM2177 EHM2     5' GCCGCCTCTCGCGGGC      52706        C   CT T
                                GCCGCCTC CGC  G GGT
                                |||||||| |||  | |||
                                CGGCGGAG GCG  C CCG
                                     A   __ _
GAM2177 FADS2    5' GCTGCCTCCCAGCCGGT     52707    C      _  TGT
                                GC GCCTCCC GCC   GGT
                                || ||||||| |||   |||
                                CG CGGAGGG CGG   CCA
                                 A      T  ___
GAM2177 FLJ00024 3' CTGCAGCCTCTCCAGGGT    52708     C    _  CCTGT
                                CTGC GCCTC CCG    GGT
                                |||| ||||| |||    |||
                                GACG CGGAG GGT    CCA
                                  T    A  C____
GAM2177 FLJ10970 3' CTGTTCTCTCCCACCATGGT  52709     CCGC      T
                                CTG   CTCCCGCC GTGGT
                                |||   |||||||| |||||
                                GAC   GAGGGTGG TACCA
                                  AAGA      _
GAM2177 FLJ11155 3' CTGCTGCCACCTGCTGGT    52710     C  TCCC    _
                                CTGC GCC   GCCTG TGGT
                                |||| |||   ||||| ||||
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                                GACG CGG   TGGAC ACCA
                                  A  ____    G
GAM2177  FLJ11506  3'  CTGTCCCCTCCCTGTGGT   52711    _ G    GCC
                                CTG CC CCTCCC  TGTGGT
                                ||| || ||||||  ||||||
                                GAC GG GGAGGG  ACACCA
                                  A _    ___
GAM2177  FLJ12484  3'  TGTCACCTCCCGCACAGT   52712   C       CT TG
                                TG CGCCTCCCGC  G  GT
                                || ||||||||||  |  ||
                                AC GTGGAGGGCG  T  CA
                                 A        __ GT
GAM2177  FLJ13089  5'  CTGCCACCTCCTGTG      52713         CGCC
                                CTGCCGCCTCC   TGTG
                                ||||||||||   ||||
                                GACGGTGGAGG   ACAC
                                      ____
GAM2177  FLJ13955  5'  CTGCGGCCTCCCGGGGCCGT  52714    C     CCT  G
                                CTGC GCCTCCCG  GT GT
                                |||| ||||||||  || ||
                                GACG CGGAGGGC  CG CA
                                  C      CC_  G
GAM2177  FLJ14327  3'  CTGCCGCCTCTCTCTACCACAG 52715       _________  CCTG
           GCG                   TGCCGCCTC      CCG   TG
                                |||||||||      |||   ||
                                ACGGCGGAG      GGT   GC
                                     AGAGAIIIT  GTCC
GAM2177  FLJ14451  5'  CTGCCGCCTGCCGGT     52716       CCC  TGT
                                CTGCCGCCT  GCC  GGT
                                |||||||||  |||  |||
                                GACGGCGGA  CGG  CCA
                                     ___  ___
GAM2177  FLJ20255  5'  CCGCCGTCTCCCGCCGGT   52717     C     TGT
                                CTGCCG CTCCCGCC  GGT
                                |||||| ||||||||  |||
                                GGCGGC GAGGGCGG  CCA
                                   A      ___
GAM2177  FLJ20371  5'  CTGTTGCCACCCGCGGCGAT  52718   CC  T   CT
                                CTG  GCC CCCGC  GTGGT
                                |||  ||| |||||  |||||
                                GAC  CGG GGGCG  CGCTA
                                  AA  T   C_
GAM2177  FLJ20464  5'  TGTCGCCTCCCGGAGCTGGT  52719   C      CCTG
                                TG CGCCTCCCG   TGGT
                                || |||||||||   ||||
                                AC GCGGAGGGC   ACCA
                                 A       CTCG
GAM2177  FLJ20811  5'  CTGTCATCTCTTCCTATGGT  52720    C  C  CCG
                                CTG CG CTC  CCTGTGGT
                                ||| || |||  ||||||||
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                                GAC GT GAG   GGATACCA
                                  A  A   AA_
GAM2177  FLJ22301  5'  CTGTCCCTCTCGCCCGCG    52721     CCG    C
                                CTG   CCTC CGCCTGTG
                                |||   |||| ||||||||
                                GAC   GGAG GCGGGCGC
                                  AG_    A
GAM2177  FLJ22795  3'  CTGCCTTTCCTGCCACGGAGT  52722      GCC   C  _  TG
                                CTGCC   TCC GCC TG  GT
                                |||||   ||| ||| ||  ||
                                GACGG   AGG CGG GC  CA
                                   AA_   A   T  CT
GAM2177  FLJ30927  5'  CTGCCGCCTCCTCGGG      52723          _  CCTGT
                                CTGCCGCCTCC CG     GG
                                ||||||||||| ||     ||
                                GACGGCGGAGG GC     CC
                                      A  _____
GAM2177  GABARAPL3 3'  CTGCCGCCCCTGGGGTGGT   52724         CCGCCT
                                CTGCCGCCTC     GTGGT
                                |||||||||      |||||
                                GACGGCGGGG     CACCA
                                     ACCC__
GAM2177  ICSBP1    5'  CTGCCGCCGTCCTGCCGCCGT  52725        _  C   T  G
                                CTGCCGCC TCC GCC GT GT
                                |||||||| ||| ||| || ||
                                GACGGCGG AGG CGG CG CA
                                     C   A   _  G
GAM2177  ICSBP1    5'  CTGCCGCCGTCTCGCCGCCCG  52726        ___  _
                                CTGCCGCC   TC CCGCCTG
                                ||||||||   || |||||||
                                GACGGCGG   AG GGCGGGC
                                     CAG  C
GAM2177  KCNJ9     5'  CTGCCACCTGCCGCGCGT    52727         C    C
                                CTGCCGCCT CCGC TGT
                                ||||||||| |||| |||
                                GACGGTGGA GGCG GCA
                                     C    C
GAM2177  KIAA0528  5'  CTGCCGCCCCTGCTTGT     52728        T  C  C
                                CTGCCGCC CC GC TGT
                                |||||||| || || |||
                                GACGGCGG GG CG ACA
                                     _  A  A
GAM2177  KIAA0652  3'  CTGCTGCCACCTGTAG      52729      C   TCCC
                                CTGC GCC    GCCTGTGG
                                ||||  |||    ||||||||
                                GACG CGG    TGGACATC
                                  A  _____
GAM2177  KIAA0826  5'  CTGCCGCCATCTGCTACCACAG 52730        _  _________   CCTG
            GCG                   TGCCGCC TC       CCG    TG
                                ||||||| ||       |||    ||
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                                ACGGCGG AG      GGT   GC
                                   T ACGAIIIT   GTCC
GAM2177 KIAA1068 5' TGTCGCCTCCCGCCCTAGGT  52731   C        GT
                                TG CGCCTCCCGCCT  GGT
                                || ||||||||||||  |||
                                AC GCGGAGGGCGGG  CCA
                                 A          AT
GAM2177 KIAA1237 3' CTGTCTCCTCCACTGTGGT   52732    CCG    CGC
                                CTG   CCTCC   CTGTGGT
                                |||   |||||   |||||||
                                GAC   GGAGG   GACACCA
                                  AGA    T__
GAM2177 KIAA1610 5' CTGCCGCTCCCGCCGC     52733       C      T
                                CTGCCGC TCCCGCC GT
                                ||||||| ||||||| ||
                                GACGGCG AGGGCGG CG
                                   _     _
GAM2177 KIAA1755 3' CTGTGGCTCCCTGCCTGTGGT 52734     CC  C   _
                                CTG  GC TCCC GCCTGTGGT
                                |||  || |||| |||||||||
                                GAC  CG AGGG CGGACACCA
                                  AC  _   A
GAM2177 LMOD1    3' CTGCCGCCTTCCTGGGCCTGT  52735         _  C__
                                CTGCCGCCT CC   GCCTGT
                                |||||||| ||   ||||||
                                GACGGCGGA GG   CGGACA
                                     A  ACC
GAM2177 MGC26684 5' CCGCCGCCTCCCGCTCAGGT   52736           CTGT
                                CTGCCGCCTCCCGC   GGT
                                ||||||||||||||   |||
                                GGCGGCGGAGGGCG   CCA
                                       AGT_
GAM2177 MIR      5' CTGCCGCCTTGTCACTGGT   52737        CC_  CTG
                                CTGCCGCCT   CGC   TGGT
                                |||||||||   |||   ||||
                                GACGGCGGA   GTG   ACCA
                                     ACA   ____
GAM2177 MYT1     5' GCTGCCTCCCGTACAGCGGT   52738    C      CCT_
                                GC GCCTCCCG    GTGGT
                                || ||||||||    |||||
                                CG CGGAGGGC    CGCCA
                                 A       ATGT
GAM2177 NBL1     3' CTGTCCCTCCCCCCAGGT    52739     CCG     G   T
                                CTG   CCTCCC CCTG GGT
                                |||   |||||| |||| |||
                                GAC   GGAGGG GGGT CCA
                                  AG_     _   _
GAM2177 OBSCN    3' CTCCCGCCTCCTCCATGGT   52740    G      CG  T
                                CT CCGCCTCC  CC GTGGT
                                || ||||||||  || |||||
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                                GA GGCGGAGG  GG TACCA
                                 G       A_ _
GAM2177  PCDH17   5'  CTGCTCGCCTCCCGTGAT    52741     _      GCCT
                                CTGC CGCCTCCC    GTGGT
                                |||| ||||||||    |||||
                                GACG GCGGAGGG    CACTA
                                  A      ____
GAM2177  PDE4DIP  5'  CTGTCTCCCGCCTCGGT     52742     CCGC       G
                                CTG    CTCCCGCCT TGGT
                                |||    ||||||||| ||||
                                GAC    GAGGGCGGA GCCA
                                  A___        _
GAM2177  PRDM15   3'  CTGCTGCCACCTGTGA      52743     C   TCCC
                                CTGC GCC    GCCTGTGG
                                |||| |||    ||||||||
                                GACG CGG    TGGACACT
                                  A  ____
GAM2177  PRDM8    3'  TGCCGCCGCCCGTGGC      52744       TCCC
                                TGCCGCC    GCCTGTGGT
                                |||||||    |||||||||
                                ACGGCGG    CGGGCACCG
                                           ____
GAM2177  RAB6C    5'  CCGCCGCCTCCCGGCAG     52686           CCT TG
                                CTGCCGCCTCCCG   G  G
                                ||||||||||||   |  |
                                GGCGGCGGAGGGC   C  C
                                      ___ GT
GAM2177  SAST     5'  GCCGCCTCCAGCAGGTGGT   52745         C  CT
                                GCCGCCTCC GC  GTGGT
                                |||||||| ||  |||||
                                CGGCGGAGG CG  CACCA
                                     T  TC
GAM2177  SEC14L2  3'  CTGCTGCCACCCTGTGGT    52746     C   T   GCC
                                CTGC GCC CCC   TGTGGT
                                |||| ||| |||   ||||||
                                GACG CGG GGG   ACACCA
                                  A   T   ___
GAM2177  SSH-3    3'  CTGCTGGCCTCCCTTGGT    52747     C_     GCCTG
                                CTGC  GCCTCCC    TGGT
                                ||||  |||||||    ||||
                                GACG  CGGAGGG    ACCA
                                  AC      A____
GAM2177  ST7L     3'  CTACTGCTCATGACCTGTGGT  52748     C  C  CC_
                                CTGC GC TC   GCCTGTGGT
                                |||| || ||   |||||||||
                                GATG CG AG   TGGACACCA
                                  A  _  TAC
GAM2177  ST7L     3'  CTACTGCTCATGACCTGTGGT  52748     C  C  CC_
                                CTGC GC TC   GCCTGTGGT
                                |||| || ||   |||||||||
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                                GATG CG AG   TGGACACCA
                                  A  _  TAC
GAM2177  ST7L     3'  CTACTGCTCATGACCTGTGGT  52748     C  C  CC_
                                CTGC GC TC   GCCTGTGGT
                                |||| || ||   |||||||||
                                GATG CG AG   TGGACACCA
                                  A  _  TAC
GAM2177  TLE4     3'  CTGCCGCCCCTCGCGCAGGT   52749         C   CTGT
                                CTGCCGCCTC CGC    GGT
                                |||||||||| |||    |||
                                GACGGCGGGG GCG    CCA
                                     A   CGT_
GAM2177  TPC2     3'  CTGCCGCCCCTGCTACCACAGG 52750          _________   CCTG
              CG                  CTGCCGCCTC      CCG    TG
                                |||||||||       |||    ||
                                GACGGCGGGG      GGT    GC
                                     ACGAIIIT   GTCC
GAM2177  ZDHHC5   5'  CCGCCGCCTCCCGGCAGT    52751           CCT TG
                                CTGCCGCCTCCCG   G  GT
                                ||||||||||||   |  ||
                                GGCGGCGGAGGGC   C  CA
                                       ___ GT
GAM2177  LOC116113 5'  TGCTGTCTGCACCCGTGGT    52752     CGC  CC
                                TGC   CT  CGCCTGTGGT
                                |||   ||  ||||||||||
                                ACG   GA  GTGGGCACCA
                                  ACA  C_
GAM2177  LOC116228 5'  CCGCCGCCTCCCGCCCTGT    52753             _
                                CTGCCGCCTCCCGCC TGT
                                |||||||||||||| |||
                                GGCGGCGGAGGGCGG ACA
                                         G
GAM2177  LOC121536 5'  CTGCTGCTCCCGCCGC      52754      C  C      T
                                CTGC GC TCCCGCC GT
                                |||| || ||||||| ||
                                GACG CG AGGGCGG CG
                                  A  _      _
GAM2177  LOC128402 3'  TGTCCACATGCCTGTGGT    52755    _   CTCCC
                                TG CCGC    GCCTGTGGT
                                || ||||    |||||||||
                                AC GGTG    CGGACACCA
                                 A   TA___
GAM2177  LOC132617 5'  CCGCCGCCTCCTCTCGGT    52756          CGC  G
                                CTGCCGCCTCC   CT TGGT
                                ||||||||||   || ||||
                                GGCGGCGGAGG   GA GCCA
                                       A__  _
GAM2177  LOC138150 3'  CTCCCGCCTCCCGTCCCAC    52757    G        _  TG
                                CT CCGCCTCCCG CC  T
                                || ||||||||| ||  |
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                                GA GGCGGAGGGC GG  G
                                 G        A  GT
GAM2177  LOC144347 3'  CCGCCTCCTGCCCGAGT     52758        C    T
                                CCGCCTCC GCCTG GGT
                                |||||||| ||||| |||
                                GGCGGAGG CGGGC TCA
                                     A    _
GAM2177  LOC145717 3'  CTGCCTTTCCTGCCACGGAGT  52722      GCC  C  _ TG
                                CTGCC   TCC GCC TG  GT
                                |||||   ||| ||| ||  ||
                                GACGG   AGG CGG GC  CA
                                   AA_   A   T  CT
GAM2177  LOC145990 5'  CTGCCGCCCCCCGCCGCCAT   52760            T  G
                                CTGCCGCCTCCCGCC GT GT
                                |||||||||||||| || ||
                                GACGGCGGGGGGCGG CG TA
                                        _  G
GAM2177  LOC145990 5'  CCGCCGCCTCCGTGCTGGT    52759          C_  CTG
                                CTGCCGCCTCC  GC   TGGT
                                ||||||||||  ||   ||||
                                GGCGGCGGAGG  CG   ACCA
                                      CA  ___
GAM2177  LOC146452 3'  CTGCCGCCATTCTGACCTGT   52761         __  CC
                                CTGCCGCC  TC  GCCTGT
                                ||||||||  ||  ||||||
                                GACGGCGG  AG  TGGACA
                                     TA  AC
GAM2177  LOC147118 5'  CTGGACTCCGCCTGTGGT    52762     CCGC   C
                                CTG   CTCC GCCTGTGGT
                                |||   |||| |||||||||
                                GAC   GAGG CGGACACCA
                                  CT__   _
GAM2177  LOC147229 5'  CTGCAGCCTCCCGGGGGT    52763      C       CCTGT
                                CTGC GCCTCCCG    GGT
                                |||| ||||||||    |||
                                GACG CGGAGGGC    CCA
                                   T       CC___
GAM2177  LOC147694 5'  CTCCCGCCTCTCCGTGGT    52764    G      CCGC
                                CT CCGCCTC   CTGTGGT
                                || |||||||   |||||||
                                GA GGCGGAG   GGCACCA
                                 G      A___
GAM2177  LOC152137 5'  CTGCCGCCTCGCTGT       52765         CC  C
                                CTGCCGCCTC  GC TGT
                                ||||||||||  || |||
                                GACGGCGGAG  CG ACA
                                      __  _
GAM2177  LOC152464 5'  CTGCCACCTGCTTGTGGT    52766         CCC  C
                                CTGCCGCCT   GC TGTGGT
                                |||||||||   || ||||||
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                                GACGGTGGA  CG ACACCA
                                     ___  A
GAM2177  LOC163126 5'  CTCCCGCCTCCCGCGGC    52767   G       CTGT
                                CT CCGCCTCCCGC   GGT
                                || ||||||||||   |||
                                GA GGCGGAGGGCG   CCG
                                 G       ____
GAM2177  LOC163682 5'  CTGTGGTCCTCCTTGCCTGTGG 52768    CCG_   C_
           T                     CTG   CCTCC  GCCTGTGGT
                                |||   |||||  |||||||||
                                GAC   GGAGG  CGGACACCA
                                  ACCA   AA
GAM2177  LOC170281 5'  CTGCCAGTTCCCTGTGGT   52769      CC   GCC
                                CTGCCG  TCCC   TGTGGT
                                ||||||  ||||   ||||||
                                GACGGT  AGGG   ACACCA
                                   CA   ___
GAM2177  LOC201102 3'  CTGCCCTCTCCTGTGGC    52770     GC   CCG
                                CTGCC  CTC   CCTGTGGT
                                |||||  |||   ||||||||
                                GACGG  GAG   GGACACCG
                                   __  A__
GAM2177  LOC220537 3'  CTGCCTTTCCTGCCGCGG   52771     GCC   C   T
                                CTGCC   TCC GCC GTGG
                                |||||   ||| ||| ||||
                                GACGG   AGG CGG CGCC
                                   AA_   A  _
GAM2177  LOC221250 5'  CTGCCGCCGCCGGCGGTGGT  52772       T  C  CT
                                CTGCCGCC CC GC  GTGGT
                                |||||||| || ||  |||||
                                GACGGCGG GG CG  CACCA
                                     C  C  C_
GAM2177  LOC254118 5'  CTGCGCCTCCTCGCGG     52773     C    _  CTGT
                                CTGC GCCTCC CGC   GG
                                |||| |||||| |||   ||
                                GACG CGGAGG GCG   CC
                                  _     A  _____
GAM2177  LOC255452 3'  CTACCGCCTTCCTGGG     52774       CCCG   T
                                CTGCCGCCT   CCTG GG
                                |||||||||   |||| ||
                                GATGGCGGA   GGAC CC
                                     A___   _
GAM2177  LOC51285  3'  CTGCCTTTCCCGTCCACCAGGT 52775     GCC    _  TGT_
                                CTGCC   TCCCG CC   GGT
                                |||||   ||||| ||   |||
                                GACGG   AGGGC GG   CCA
                                   AA_    A  TGGT
GAM2177  LOC90120  3'  CTCCCGCCTCCCGTCCCAC   52757   G       _  TG
                                CT CCGCCTCCCG CC  T
                                || ||||||||| ||  |
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                                GA GGCGGAGGGC GG  G
                                 G        A  GT
GAM2177  LOC90268  5'  CCGCCGCCTCCCGCGCCGGCG  52776            _  _
                                CTGCCGCCTCCCGC CTG TG
                                |||||||||||||| ||| ||
                                GGCGGCGGAGGGCG GGC GC
                                       C   C
GAM2177  LOC90393  5'  CTGCCTACTGTCCTGTGGT   52777      GC  CCCG
                                CTGCC  CT   CCTGTGGT
                                |||||  ||   ||||||||
                                GACGG  GA   GGACACCA
                                   AT  CA__
GAM2177  LOC90768  5'  CTGCCACCTCCTCGGG      52778          _  CCTGT
                                CTGCCGCCTCC CG    GG
                                |||||||||| ||    ||
                                GACGGTGGAGG GC    CC
                                      A  _____
GAM2178  SPRY4     3'  TACATTCAATTCATATAAGTG  52781       GAA    G
                                TACATT   CAATT ATATAAGTG
                                ||||||   ||||| |||||||||
                                ATGTAA   GTTAA TATATTCAC
                                    ___    G
GAM2179  ABIN-2    5'  GGCGTCCCCCTCCAGCGCG   52784       TCG  G     A
                                GGCGTCC   CC TCCAGC CG
                                |||||||   || ||||||  ||
                                CCGCAGG   GG AGGTCG GC
                                    ___  G     C
GAM2179  DCAMKL1   5'  GCTGTCCTCGCCGGGCTGGGCG 52785    _        TCCA__  A
            CG                    GC GTCCTCGCCG     GC CG
                                || ||||||||||     || ||
                                CG CAGGAGCGGC     CG GC
                                 A         CCGACC  C
GAM2179  FLJ20274  5'  TGGCGTCCTCGTCTATCGCCGG 52786          C____  T  A  A
            CGCGA                   GGCGTCCTCG    CG CC GC CGA
                                |||||||||     || || || |||
                                CCGCAGGAGC     GC GG CG GCT
                                      AGATA  _  C  C
GAM2179  SIMRP7    3'  TGGTGTCCACGCCGTCCA    52787     C    T
                                TGG GTCC CGCCGTCCA
                                ||| |||| |||||||||
                                ACC CAGG GCGGCAGGT
                                  A   T
GAM2179  LOC132617 5'  GGCGTCCTCGCGCACCGCGGCG 52788          _  T  A__  A
            CG                    GGCGTCCTCGC CG CC   GC CG
                                |||||||||| || ||   || ||
                                CCGCAGGAGCG GT GG   CG GC
                                      C  _  CGC  C
GAM2179  LOC152137 5'  TGGACCGGGGCCGTCCAGTACG 52789     CGT  TC_       C
                                TGG   CC   GCCGTCCAG ACG
                                |||   ||   ||||||||| |||
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                                ACC   GG   CGGCAGGTC TGC
                                  T__  CCC        A
GAM2180  FLJ23142  3'  TGTGTAAATCTAGACATTTTTC 52792        _   A   ACG
              T                   TGTGTAAA CTA ATA   TTTTCT
                                  |||||||| ||| |||   ||||||
                                  ACACATTT GAT TGT   AAAAGA
                                      A   C   A__
GAM2180  LOC147991 3'  TGTGTGAACTAAATAAACAT   52793      A        _
                                  TGTGT AACTAAATAA CGT
                                  ||||| |||||||||| |||
                                  ACACA TTGATTTATT GTA
                                     C         T
GAM2181  BAALC     3'  GGGAGGGCCAGATCATGTGC   52796       TG        C
                                  GGGAGG  CAGATCATG GC
                                  ||||||  ||||||||| ||
                                  CCCTCC  GTCTAGTAC CG
                                      CG        A
GAM2181  P53AIP1   3'  CAGGGAGGTGTAGGCG      52797          C  ATCAT
                                  CAGGGAGGTG AG     GCG
                                  |||||||||| ||     |||
                                  GTCCCTCCAC TC     CGC
                                       A  ______
GAM2181  STMN2     5'  AGGGATGTGCAGACGC      52798       G       CAT
                                  AGGGA GTGCAGAT   GC
                                  ||||| ||||||||   ||
                                  TCCCT CACGTCTG   CG
                                     A       ____
GAM2181  CNNM3     3'  GGGAGGTGTGGAGCAGGTGC   52799         CA  T  __
                                  GGGAGGTG  GA CA  TGC
                                  ||||||||  || ||  |||
                                  CCCTCCAC  CT GT  ACG
                                       AC  C  CC
GAM2181  CPSF2     3'  GGTGAGCCGAGATCGTGTGC   52800    _   G  C     A  C
                                  GG GAG TG AGATC TG GC
                                  || ||| || ||||| || ||
                                  CC CTC GC TCTAG AC CG
                                   A   G  _     C  A
GAM2181  FLJ20249  3'  TGAGGGGGGTGCAGAAGACCTG 52801    C    A       TCA__
              C                    A AGGG GGTGCAGA     TGC
                                   | |||| ||||||||     |||
                                   A TCCC CCACGTCT     ACG
                                   C   C       TCTGG
GAM2181  KIAA0014  3'  CAGGGACAGGAAGATCATG    52802       __  TGC
                                  CAGGGA  GG   AGATCATG
                                  ||||||  ||   ||||||||
                                  GTCCCT  CC   TCTAGTAC
                                     GT  T__
GAM2181  LOC112476 3'  CAGGGAGGTTGGAACCAGTGC  52803          GCA    _
                                  CAGGGAGGT   GATCA TGC
                                  |||||||||   ||||| |||
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                                GTCCCTCCA  TTGGT ACG
                                     ACC    C
GAM2181  LOC149422 3'  GGAGGTGCGCCTCGGTGCGC  52804       AGA  A_
                                GGAGGTGC  TC  TGCGC
                                ||||||||  ||  |||||
                                CCTCCACG  AG  ACGCG
                                    CGG  CC
GAM2181  LOC153883 5'  AGGGAGGTCAGATGC      52805       G   TCA
                                AGGGAGGT CAGA  TGC
                                |||||||| ||||  |||
                                TCCCTCCA GTCT  ACG
                                  _   ___
GAM2181  LOC219699 5'  CAGGGAGGTGCAGAGGGC   52806          TCAT
                                CAGGGAGGTGCAGA   GC
                                ||||||||||||||   ||
                                GTCCCTCCACGTCT   CG
                                       CC__
GAM2182  C17orf26  3'  TCAGATTATAAGTTACCAA   52809         A  TT
                                TCAGATTATAA TT  CTAA
                                |||||||||| ||  ||||
                                AGTCTAATATT AA  GGTT
                                      C  T_
GAM2182  C20orf26  5'  CAGGTAAATTTTCTAATAA   52810    ATTA
                                CAG   TAAATTTTCTAATAA
                                |||   ||||||||||||||
                                GTC   ATTTAAAAGATTATT
                                  C___
GAM2182  FBXO8    3'  TCAAATTATAAATTTATATTAT 52811           TCTA_
           AAA                   TCAGATTATAAATTT    ATAAA
                                 ||||||||||||||    |||||
                                 AGTTTAATATTTAAA    TATTT
                                       TATAA
GAM2182  KIAA0918  3'  TCAAATATTTTCTAATAA   52812      TATAA
                                 TCAGAT    ATTTTCTAATAA
                                 ||||||    ||||||||||||
                                 AGTTTA    TAAAAGATTATT
                                   _____
GAM2182  MRPS7    3'  TCAGCGTGAGAATTTTCTAATA 52813     ATTATA
           AA                    TCAG     AATTTTCTAATAAA
                                 ||||     |||||||||||||
                                 AGTC     TTAAAAGATTATTT
                                   GCACTC
GAM2182  TIEG2    3'  TCAGATTATCAAATTTTCTA   52814       _
                                 TCAGATTAT AAATTTTCTA
                                 ||||||||| ||||||||||
                                 AGTCTAATA TTTAAAAGAT
                                      G
GAM2182  TRAF3    3'  TCAGATTTATTTTCCTCTAATA 52815       ATAAA
           A                     TCAGATT    TTTTCTAATAA
                                 |||||||    ||||||||||
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                                AGTCTAA    AGGAGATTATT
                                   ATAAA
GAM2182 UNC5D    3' TCAGATTCTAAATTCTAA    52816       A    TT
                                TCAGATT TAAAT  TCTAA
                                ||||||| |||||  |||||
                                AGTCTAA ATTTA  AGATT
                                   G    __
GAM2183 DIO2     3' GTAATATTTGGGAATTTT    52819     GTTCCGC
                                GTAA     TTGGGAATTTT
                                ||||     ||||||||||
                                CATT     AACCCTTAAAA
                                  ATA____
GAM2183 DIO2     3' GTAATATTTGGGAATTTT    52819     GTTCCGC
                                GTAA     TTGGGAATTTT
                                ||||     ||||||||||
                                CATT     AACCCTTAAAA
                                  ATA____
GAM2183 KIAA0318 3' CGAAAGTTCATAAAGGGAATTT 52820    T     CGCTT
           T                     CG AAGTTC    GGGAATTTT
                                || ||||||    |||||||||
                                GC TTCAAG    CCCTTAAAA
                                 T     TATTT
GAM2183 KIAA0495 3' GTAAGTTCCACACAGAATTTT  52821          TTG
                                GTAAGTTCCGC   GGAATTTT
                                ||||||||||   ||||||||
                                CATTCAAGGTG   TCTTAAAA
                                      TG_
GAM2183 KIAA1615 3' GTAAGTTCAGTGGTCATTTT   52822        CGCT   GA
                                GTAAGTTC    TGG  ATTTT
                                ||||||||    |||  |||||
                                CATTCAAG    ACC  TAAAA
                                     TC__   AG
GAM2183 PRO2893  3' GTAATTTTCAGCGTGGAATTTT 52823     G_   C  TTG
                                GTAA  TTC GC   GGAATTTT
                                ||||  ||| ||   ||||||||
                                CATT  AAG CG   CCTTAAAA
                                   AA   T  CA_
GAM2184 AHR      3' TGAAGAAAGTAGGTAAGCAGTG 52826   A        A____
                                A AAGAAAGTAG     CAGTG
                                | ||||||||||     |||||
                                A TTCTTTCATC     GTCAC
                                 C         CATTC
GAM2184 CASP8    3' TAAGAGAAAGGAGACAGTG    52827     A     T
                                TAA AGAAAG AGACAGTG
                                ||| |||||| ||||||||
                                ATT TCTTTC TCTGTCAC
                                  C     C
GAM2184 CASP8    3' TAAGAGAAAGGAGACAGTG    52827     A     T
                                TAA AGAAAG AGACAGTG
                                ||| |||||| ||||||||
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                                ATT TCTTTC TCTGTCAC
                                  C     C
GAM2184  CASP8    3'  TAAGAGAAAGGAGACAGTG   52827    A     T
                                TAA AGAAAG AGACAGTG
                                ||| |||||| ||||||||
                                ATT TCTTTC TCTGTCAC
                                  C     C
GAM2184  CASP8    3'  TAAGAGAAAGGAGACAGTG   52827    A     T
                                TAA AGAAAG AGACAGTG
                                ||| |||||| ||||||||
                                ATT TCTTTC TCTGTCAC
                                  C     C
GAM2184  EMP1     3'  TAAAGAAAAGTAGGCAAGAT  52828     AG     A   T
                                TAAA  AAAGTAG CAG GAT
                                ||||  ||||||| ||| |||
                                ATTT  TTTCATC GTT CTA
                                   CT      C  _
GAM2184  PTPRG    3'  TAAAAAAAAGTAGCATGTA   52829          A  _
                                TAAAAGAAAGTAG CA GTG
                                |||||||||||| || |||
                                ATTTTTTTTCATC GT CAT
                                        _ A
GAM2184  SET      3'  CAAGAGAAAGTAGACAGATACA 52830    A         GT
                                TAA AGAAAGTAGACA  GATACG
                                ||| ||||||||||||  ||||||
                                GTT TCTTTCATCTGT  CTATGT
                                  C          __
GAM2184  FLJ12505 3'  TAAAAGAAAGTAGGTAAATG  52831          AC_
                                TAAAAGAAAGTAG   AGTG
                                ||||||||||||   ||||
                                ATTTTCTTTCATC   TTAC
                                        CAT
GAM2184  H_GS165L15.1 3'  TAAAAGAAAGGACGCATGGTAC 52832         TA   A_   A
           G                     TAAAAGAAAG  GAC  GTG TACG
                                ||||||||||  |||  ||| ||||
                                ATTTTCTTTC  CTG  TAC ATGC
                                      __  CG   C
GAM2184  KIAA1434  3'  TAAAAGGCAACAGCTAGTGATA 52833       AA    AC
           CG                     TAAAAG  AGTAG  AGTGATACG
                                ||||||  |||||  |||||||||
                                ATTTTC  TTGTC  TCACTATGC
                                   CG    GA
GAM2184  MGC10924  3'  TAAAAGCAAGTAGTACAGTA   52834       A    _
                                TAAAAG AAGTAG ACAGTG
                                |||||| |||||| ||||||
                                ATTTTC TTCATC TGTCAT
                                   G     A
GAM2184  LOC128346 3'  AAAAAAGTGAAAGTGAT     52835        A  C
                                AAGAAAGT GA AGTGAT
                                |||||||| || ||||||
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                                TTTTTTCA CT TCACTA
                                     _ T
GAM2184 LOC153525 5' TAAAAGCAAGTAGTACAGTA  52834      A    _
                                TAAAAG AAGTAG ACAGTG
                                |||||| |||||| ||||||
                                ATTTTC TTCATC TGTCAT
                                   G     A
GAM2184 LOC90268 3' GAAAGCAGGTGGATACA     52836       ACA  _
                                GAAAGTAG   GTG ATACG
                                ||||||||   ||| |||||
                                CTTTCGTC   CAC TATGT
                                     ___   C
GAM2184 LOC92465 5' GAATAGATAAACAGTGATACG 52837    _ _
                                GAA AG TAGACAGTGATACG
                                ||| || ||||||||||||||
                                CTT TC ATTTGTCACTATGC
                                  A  T
GAM2185 AKAP13   3' TCAACCCTTGCATGCACTA   52840       AG   AACA
                                TCAACCCT  GCA   CACTA
                                ||||||||  |||   |||||
                                AGTTGGGA  CGT   GTGAT
                                     A_   AC__
GAM2185 APMCF1   3' AACCACTAAGAACACACTA   52841     _    CA
                                AACC CTAGG  AACACACTA
                                |||| |||||  |||||||||
                                TTGG GATTC  TTGTGTGAT
                                  T    __
GAM2185 APOL4    5' AATCAAGCACAGCAAACACGCT 52842      CCCTA       A
                                AATCAA    GGCAAACAC CT
                                ||||||    ||||||||| ||
                                TTAGTT    TCGTTTGTG GA
                                   CGTG_       C
GAM2185 FLJ10193 3' TCAACCCTGGGGAAGCAC    52843       A  C  A
                                TCAACCCT GG AA CAC
                                |||||||| || || |||
                                AGTTGGGA CC TT GTG
                                     C  C  C
GAM2185 FLJ10232 3' AATCAACCCTGGTTGAGAGTCA 52844         A  CAAACA__
             CT                   AATCAACCCT GG       CACT
                                |||||||||| ||       ||||
                                TTAGTTGGGA CC       GTGA
                                     _  AACTCTCA
GAM2185 FLJ10759 3' CAACCCTAGGACCAGGTACTA  52845         _ AAACAC
                                CAACCCTAGG C     ACTA
                                |||||||||| |     ||||
                                GTTGGGATCC G     TGAT
                                     T GTCCA_
GAM2185 FLJ11149 3' CCCTAAACAACACACTA     52846         A
                                CCCTAGGCAA CACACTA
                                |||||||||| |||||||
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                                GGGATTTGTT GTGTGAT
                                       _
GAM2185  FLJ14624  3'  CCTTCAGATAAACACACTA   52847    __  GC
                                CCT  AG  AAACACACTA
                                |||  ||  ||||||||||
                                GGA  TC  TTTGTGTGAT
                                  AG  TA
GAM2185  FLJ23375  3'  AACCCTAAAAAACACACT    52848        C
                                AACCCTAGG AAACACACT
                                ||||||||| |||||||||
                                TTGGGATTT TTTGTGTGA
                                       _
GAM2185  KIAA1966  3'  AACTCTAGGATGAACACACTA  52849    C    CA_
                                AAC CTAGG   AACACACTA
                                ||| |||||   |||||||||
                                TTG GATCC   TTGTGTGAT
                                  A    TAC
GAM2185  PEG10    3'  TCACCACTTCAAAACACACTA  52850    A  _  AGGC
                                TCA CC CT    AAACACACTA
                                ||| || ||    ||||||||||
                                AGT GG GA    TTTGTGTGAT
                                  _  T  AGT_
GAM2185  PTR4     3'  AATCAATCCAGGCAACA     52851      CC      A
                                AATCAA  CTAGGCAA CA
                                ||||||  |||||||| ||
                                TTAGTT  GGTCCGTT GT
                                   A_      _
GAM2185  SLC11A2  3'  AACCATAGAAACACACT     52852     C   CA
                                AACC TAGG  AACACACT
                                |||| ||||  ||||||||
                                TTGG ATCT  TTGTGTGA
                                  T   __
GAM2185  LOC148824 3'  AATCAATCCTATGGCAGACA   52853      C   _   A
                                AATCAA CCTA GGCA ACA
                                |||||| |||| |||| |||
                                TTAGTT GGAT CCGT TGT
                                   A   A   C
GAM2185  LOC153579 3'  TCAACCCTGACATCTGTGCACT 52854        A   AACA__
            A                    TCAACCCT GGCA     CACTA
                                |||||||| ||||     |||||
                                AGTTGGGA CTGT     GTGAT
                                     _   AGACAC
GAM2185  LOC155061 3'  CCAACCTTCCAACACACTA   52855      CTAGGCA
                                TCAACC      AACACACTA
                                ||||||      |||||||||
                                GGTTGG      TTGTGTGAT
                                   AAGG___
GAM2185  LOC196743 3'  TCAACCCTGGCCAGACT     52856        A   AAA  C
                                TCAACCCT GGC   CA ACT
                                |||||||| |||   || |||
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                                AGTTGGGA CCG   GT TGA
                                   _  ___  C
GAM2185  LOC199678 3'  AATCAATAACTTAAAACACACT 52857       CCCTAGGC
             A                    AATCAA       AAACACACTA
                                  ||||||       ||||||||||
                                  TTAGTT       TTTGTGTGAT
                                     ATTGAAT_
GAM2185  LOC200933 3'  ATCAGTCTTCACAAACACACTA 52858      ACC  AG
                                  ATCA   CT  GCAAACACACTA
                                  ||||   ||  ||||||||||||
                                  TAGT   GA  TGTTTGTGTGAT
                                    CA_  AG
GAM2185  LOC202934 3'  ATCAGCCTGCCACACACACTA  52859     AC   AG  AA_
                                  ATCA  CCT  GC   ACACACTA
                                  ||||  |||  ||   ||||||||
                                  TAGT  GGA  CG   TGTGTGAT
                                    C_   __  GTG
GAM2186  SERPINB9  3'  AATGTGGAATGGTTCAACTGCT 52862     A    CATTCC
                                  AAT TGGAA     CAGCTGCT
                                  ||| |||||     ||||||||
                                  TTA ACCTT     GTTGACGA
                                    C    ACCAA_
GAM2186  ST7      3'  AATATGTGATGCATTTTTAGCT 52863       _ A_   CCC
             GCT                    AATATG GA  CATT   AGCTGCT
                                    ||||||  ||  ||||   |||||||
                                    TTATAC CT  GTAA   TCGACGA
                                       A  AC    AAA
GAM2186  SYT1     3'  AAATATGGAATATTGCACAGTG 52864         C  CC_  C
             CT                      AAATATGGAA ATT   CAG TGCT
                                     ||||||||||  |||   |||  ||||
                                     TTTATACCTT TAA   GTC ACGA
                                          A   CGT   _
GAM2186  TNFRSF11A 3'  AATATAGAACATTTTTCAG    52865          CC_
                                     AATATGGAACATT   CAG
                                     ||||||||||||   |||
                                     TTATATCTTGTAA   GTC
                                           AAA
GAM2186  TNFSF6   3'  TAGAACACCTGGTAGCTGCT   52866        CCC_
                                     TGGAACATT    AGCTGCT
                                     |||||||||    |||||||
                                     ATCTTGTGG    TCGACGA
                                          ACCA
GAM2186  TOX      3'  AAATATAGAACTATCAGTCAGT 52867          AT  C__  C
             TG                      AAATATGGAAC  TC   CAG TG
                                     ||||||||||  ||   ||| ||
                                     TTTATATCTTG  AG   GTC AC
                                           AT  TCA   A
GAM2186  C11orf24  3'  TGGAACCCCCAGCTGCT     52868       AT
                                     TGGAAC  TCCCAGCTGCT
                                     ||||||  ||||||||||
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                                ACCTTG  GGGGTCGACGA
                                  __
GAM2186  C20orf162 5'  TGGGATTCTACCAGCTGCT   52869    AAC   __
                                TGG   ATTC  CCAGCTGCT
                                |||   ||||  |||||||||
                                ACC   TAAG  GGTCGACGA
                                  C__    AT
GAM2186  DKFZP434J193 3'  AAATATTGGACATTCCCAG   52870      _  A
                                AAATAT GGA CATTCCCAG
                                |||||| ||| |||||||||
                                TTTATA CCT GTAAGGGTC
                                   A  _
GAM2186  KIAA0795  5'  AAATACGGGATCGAGGCTGCT  52871       AACAT  CCA
                                AAATATGG    TC   GCTGCT
                                ||||||||    ||   ||||||
                                TTTATGCC    AG   CGACGA
                                     CT___  CTC
GAM2186  KIAA1821  3'  AAATATGGGGCATTCAAACT   52872       AA    CC
                                AAATATGG  CATTC  AGCT
                                ||||||||  |||||  ||||
                                TTTATACC  GTAAG  TTGA
                                     CC    T_
GAM2186  MASA     3'  AAATATGAAATACAGCTG    52873        CATTCC
                                AAATATGGAA     CAGCTG
                                ||||||||||     ||||||
                                TTTATACTTT     GTCGAC
                                     AT____
GAM2186  P114-RHO-GEF 3'  AAATAGGAACATTTG      52874      T      CCCAGC
                                AAATA GGAACATT     TG
                                |||||  ||||||||     ||
                                TTTAT CCTTGTAA     AC
                                  _     _______
GAM2186  PRO1331   3'  AAATATGGTACATTTGACAG   52875       A    CC_
                                AAATATGG ACATT   CAG
                                |||||||| |||||   |||
                                TTTATACC TGTAA   GTC
                                     A    ACT
GAM2186  SCYA22    3'  ATGGAATTACCAGCTGCT    52876      AC   C
                                ATGGA  ATT CCAGCTGCT
                                |||||  ||| |||||||||
                                TACCT  TAA GGTCGACGA
                                   __  T
GAM2186  TIP120A   3'  AAAAGTGGAACATTTTGAAGCT 52877     TA       CCC_
                                AAA  TGGAACATT    AGCT
                                |||  |||||||||    ||||
                                TTT  ACCTTGTAA    TCGA
                                  TC        AACT
GAM2186  UBE3B     3'  TGCAATATTTCCAGCTGCT    52878    G  C   C
                                TG AA ATT CCAGCTGCT
                                || || ||| |||||||||
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                                AC TT TAA GGTCGACGA
                                 G  A   A
GAM2186  LOC152179 3'  AAATCTGGAACATTTG      52879      A       CCCAGC
                                AAAT TGGAACATT      TG
                                |||| |||||||||      ||
                                TTTA ACCTTGTAA      AC
                                  G       _______
GAM2186  LOC158629 5'  AAAAATGGAACATCTG      52880     T       TCCCAG
                                AAA ATGGAACAT     CTG
                                ||| |||||||||      |||
                                TTT TACCTTGTA     GAC
                                  T       _______
GAM2187  PTGER2    3'  CAGCTTAAATGTTTGTAT    52883       T     _
                                TAGCTT GATGTT GTAT
                                |||||| |||||| ||||
                                GTCGAA TTACAA CATA
                                    T      A
GAM2187  PC326     5'  TAGTTTTGATGCGTGTAT    52884     C       _
                                TAG TTTGATGT TGTAT
                                ||| |||||||| |||||
                                ATC AAACTACG ACATA
                                  A       C
GAM2187  LOC151996 3'  TAGCTTTGAAGGCAGCAT    52885         T_  T
                                TAGCTTTGA  GT GTAT
                                |||||||||  || ||||
                                ATCGAAACT  CG CGTA
                                      TC  T
GAM2187  LOC152110 3'  TAGCTCTGACATCCTGTAT    52886           __
                                TAGCTTTGATGT  TGTAT
                                ||||||||||||  |||||
                                ATCGAGACTGTA  ACATA
                                       GG
GAM2188  ADAM11    3'  TCTCAGCTGCCTGGT      52889     G    ATTGTC
                                TCT CAGC     TGCCTGGT
                                ||| ||||     ||||||||
                                AGA GTCG     ACGGACCA
                                  _   _______
GAM2188  ADAM11    3'  TCTCAGCTGCCTGGT      52889     G    ATTGTC
                                TCT CAGC     TGCCTGGT
                                ||| ||||     ||||||||
                                AGA GTCG     ACGGACCA
                                  _   _______
GAM2188  DBY       3'  CCTGTAGTGAGGCCTGGTC    52890     C  CAT  TCT
                                TCTG AG   TG   GCCTGGTC
                                |||| ||   ||   ||||||||
                                GGAC TC   AC   CGGACCAG
                                  A  ___  TC_
GAM2188  GRB10     5'  TCTGTAGCACTGTCTGCTG    52891      C         C
                                TCTG AGCATTGTCTGC TG
                                |||| |||||||||||| ||
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                                AGAC TCGTGACAGACG AC
                                  A         _
GAM2188 TLX1     3' CTGTGACCCTCTGTCTGGT   52892     CAGC  G   C
                                CTG   ATT TCTG CTGGT
                                |||   ||| |||| |||||
                                GAC   TGG AGAC GACCA
                                  AC__  G   A
GAM2188 DKFZp434M0331 5' TCTGCAGCAGTAACTGGT   52893        TT  CTGC
                                TCTGCAGCA  GT   CTGGT
                                |||||||||  ||   |||||
                                AGACGTCGT  CA   GACCA
                                     __ TT__
GAM2188 FLJ22593  5' TCTGCAGCGTTGTCTGCCC   52894        A
                                TCTGCAGC TTGTCTGCCT
                                |||||||| ||||||||||
                                AGACGTCG AACAGACGGG
                                     C
GAM2188 FLJ23056  3' TCAGCAGCATTGTGGT     52895    T       CTGCCT
                                TC GCAGCATTGT     GGT
                                || ||||||||||     |||
                                AG CGTCGTAACA     CCA
                                 T       _______
GAM2188 KIAA0792  3' CTGCAGCATCTCTTTGGT   52896         G   GCC
                                CTGCAGCATT TCT   TGGT
                                |||||||||| |||   ||||
                                GACGTCGTAG AGA   ACCA
                                     _  A__
GAM2188 KIAA1500  3' CGCAGCATCCTTGGTC     52897        TGTCTG  _
                                TGCAGCAT     CCT GGTC
                                ||||||||     ||| ||||
                                GCGTCGTA     GGA CCAG
                                     _______  A
GAM2188 KIAA1643  3' CCTGCGGTGTCAGTGCCTGGTC 52898      AGCAT   __
                                TCTGC    TGTC  TGCCTGGTC
                                |||||    ||||  |||||||||
                                GGACG    ACAG  ACGGACCAG
                                   CC___    TC
GAM2188 NTSR2    5' TCTGGGCGAGCTGCCTGGT   52899     CA  ATT T
                                TCTG  GC   G CTGCCTGGT
                                ||||  ||   | |||||||||
                                AGAC  CG   C GACGGACCA
                                  C_  CT_ _
GAM2188 PPP1R16B  3' TCTGGTTGACTTTGCCTGGT   52900     CAGCA   T __
                                TCTG    TTG CT  GCCTGGT
                                ||||    ||| ||  |||||||
                                AGAC    AAC GA  CGGACCA
                                  C_____  T  AA
GAM2188 RAB-R    3' TCTCAGGACTGTCTGGTC    52901     G   C      GCCT
                                TCT CAG ATTGTCT    GGTC
                                ||| ||| |||||||    ||||
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                                AGA GTC TGACAGA    CCAG
                                  _   C      _____
GAM2188  SLC17A6   3'  TACAGCAAGACTTGCCTGGT   52902        TT TC
                                TGCAGCA  G  TGCCTGGT
                                |||||||  |  ||||||||
                                ATGTCGT  T  ACGGACCA
                                    TC GA
GAM2188  SV2B      5'  TCTGCGACTGCCTGGT      52903       AGCATT T
                                TCTGC     G CTGCCTGGT
                                |||||     | |||||||||
                                AGACG     C GACGGACCA
                                   _______ T
GAM2188  LOC124460 3'  TGCAACATTGTGGGGTGGT    52904          CTGCC
                                TGCAGCATTGT     TGGT
                                ||||||||||     ||||
                                ACGTTGTAACA     ACCA
                                      CCCC_
GAM2188  LOC201562 3'  TCTGCAGCATTTTTTGATC    52905          GTCTGCC
                                TCTGCAGCATT      TGGTC
                                ||||||||||      |||||
                                AGACGTCGTAA      ACTAG
                                      AAA_____
GAM2188  LOC220522 3'  CTGCAGTCACTGCCTGGTCA   52906       _  TTGT
                                CTGCAG CA    CTGCCTGGTCA
                                |||||| ||    ||||||||||
                                GACGTC GT    GACGGACCAGT
                                   A _____
GAM2188  LOC255974 5'  TCTGCAGCGCTGTGGT      52907        ATT T   CC
                                TCTGCAGC   G CTG  TGGT
                                ||||||||   | |||  ||||
                                AGACGTCG   C GAC  ACCA
                                     ____ _   __
GAM2188  LOC91149  3'  TCTGTGGCGTTGCCTAGC    52908      CA  ATT  C
                                TCTG  GC   GT TGCCTGGT
                                ||||  ||   || ||||||||
                                AGAC  CG   CA ACGGATCG
                                  AC  ____  _
GAM2188  LOC91300  5'  TCTGAGTTCCGCACTGCCTGGT 52909      C  CA   _
                                TCTG AG  TTGT CTGCCTGGT
                                |||| ||  |||| |||||||||
                                AGAC TC  GGCG GACGGACCA
                                  _  AA    T
GAM2188  LOC91300  5'  TCTGAGTTCCGCACTGCCTGGT 52909      C  CA   _
                                TCTG AG  TTGT CTGCCTGGT
                                |||| ||  |||| |||||||||
                                AGAC TC  GGCG GACGGACCA
                                  _  AA    T
GAM2189  RPP20     3'  ATGCAGAGTCCTTTG       52912          GGCAAG
                                ATGCAGAGTC     CTTTG
                                ||||||||||     |||||
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                                TACGTCTCAG     GAAAC
                                       ______
GAM2189 SLC6A6   3' GCAGAGTAGATAGCTTTGGA  52913       C  CA
                                GCAGAGT GG  AGCTTTGGA
                                ||||||| ||  ||||||||
                                CGTCTCA TC  TCGAAACCT
                                    _  TA
GAM2189 WNT8B    3' TGGAAAGTGGCAAGCTTTGGA 52914    C    C
                                TG AGAGT GGCAAGCTTTGGA
                                || ||||| ||||||||||||
                                AC TTTCA CCGTTCGAAACCT
                                 C    _
GAM2189 ACTR2    3' GATGGGAACAAGCTTTGGA   52915    GTC_
                                GA   GGCAAGCTTTGGA
                                ||   ||||||||||||
                                CT   TTGTTCGAAACCT
                                 ACCC
GAM2189 C5orf6   3' TGCAGAGTCGGTGATGCTATGG 52916          CAA_  T
             A                   TGCAGAGTCGG   GCT TGGA
                                ||||||||||    ||| ||||
                                ACGTCTCAGCC   CGA ACCT
                                      ACTA  T
GAM2189 FIBL-6   3' TATGTGGAATAGGCTTTGGA  52917     CA   C  CAA
                                TATG  GAGT GG   GCTTTGGA
                                ||||  |||| ||   ||||||||
                                ATAC  CTTA TC   CGAAACCT
                                  AC   _ ___
GAM2189 KIAA1297 5' TGCAGAGCTCGGTGACAATGA  52918       _   CAA  TT
                                TGCAGAG TCGG   GC  TGG
                                ||||||| ||||   ||  |||
                                ACGTCTC AGCC   TG  ACT
                                    G   AC_  TT
GAM2189 LOC149345 3' TGCAGGGCCAGCTTTGG     52919      AGTC   A
                                TGCAG   GGC AGCTTTGG
                                |||||   ||| ||||||||
                                ACGTC   CCG TCGAAACC
                                   _____  G
GAM2189 LOC197196 5' TGCAGAGGCCCACTTTGGA   52920      GTC   AA
                                TGCAGA  GGC  GCTTTGGA
                                ||||||  |||  ||||||||
                                ACGTCT  CCG  TGAAACCT
                                   ___  GG
GAM2189 LOC254065 5' TATTAGAGGTATAAGCTTTGGA 52921    GC   TCGGC
                                TAT  AGAG    AAGCTTTGGA
                                |||  ||||    ||||||||||
                                ATA  TCTC    TTCGAAACCT
                                  A_   CATA_
GAM2189 LOC51754  5' TGCAGGGGTGGGGCTTTGG   52922      A_  C  CAA
                                TGCAG  GT GG   GCTTTGG
                                |||||  || ||   |||||||
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                                ACGTC  CA CC   CGAAACC
                                   CC  C ___
GAM2190  ANK1     3'  CAAGTGGAATGGAGGTATGTGG 52925        _     CTTAA
                                CAAGTGGA TGGAGG    GG
                                |||||||| ||||||    ||
                                GTTCACCT ACCTCC    CC
                                     T     ATACA
GAM2190  ANK1     3'  CAAGTGGAATGGAGGTATGTGG 52925        _     CTTAA
                                CAAGTGGA TGGAGG    GG
                                |||||||| ||||||    ||
                                GTTCACCT ACCTCC    CC
                                     T     ATACA
GAM2190  BICD1    5'  GTGGATGGAGGCAGGA      52926          TTA
                                GTGGATGGAGGC   AGGA
                                ||||||||||||   ||||
                                CACCTACCTCCG   TCCT

                                      ___
GAM2190  CETN1    3'  TGACTGGAATTTAAGGAA    52927    GA    GC
                                TG  TGGAG  TTAAGGAA
                                ||  |||||  ||||||||
                                AC  ACCTT  AATTCCTT
                                 TG    A_
GAM2190  JAK3     3'  AGGGGGCCAGGGCTTAAGG   52928    T  A_   A
                                AG GG  TGG GGCTTAAGG
                                || ||  ||| |||||||||
                                TC CC  GTC CCGAATTCC
                                 C  CG  _
GAM2190  MKI67    3'  GTGAATGGGGAGGAA       52929        A  CTTA
                                GTGGATGG GG    AGGAA
                                ||||||||  ||    |||||
                                CACTTACC CC    TCCTT

                                   _  _____
GAM2190  MMP19    3'  GTGGTGGAGCCTCAGGG     52930     A    G    A
                                GTGG TGGAG CTTA GG
                                |||| ||||| |||| ||
                                CACC ACCTC GAGT CC
                                   _    G    C
GAM2190  MMP19    3'  GTGGTGGAGCCTCAGGG     52930     A    G    A
                                GTGG TGGAG CTTA GG
                                |||| ||||| |||| ||
                                CACC ACCTC GAGT CC
                                   _    G    C
GAM2190  MMP19    3'  GTGGTGGAGCCTCAGGG     52930     A    G    A
                                GTGG TGGAG CTTA GG
                                |||| ||||| |||| ||
                                CACC ACCTC GAGT CC
                                   _    G    C
GAM2190  MMP19    3'  GTGGTGGAGCCTCAGGG     52930     A    G    A
                                GTGG TGGAG CTTA GG
                                |||| ||||| |||| ||
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                                CACC ACCTC GAGT CC
                                  _    G    C
GAM2190 POU2F2   3' CAAGTGGAGGAGGAGGAGGA  52931        T    CTTA
                                CAAGTGGA GGAGG    AGGA
                                |||||||| |||||    ||||
                                GTTCACCT CCTCC    TCCT
                                     _    TCC_
GAM2190 PRV1     3' TGAGTGGATGGTGGTCTTCTGG 52932   A       A _   AA_
           GAAT                   C AGTGGATGG GG CTT   GGAAT
                                | |||||||| || |||   |||||
                                A TCACCTACC CC GAA   CCTTA
                                 C        A A   GAC
GAM2190 PTGFRN   3' CAGGTGGGTGGAGGTCAA    52933    A    A     C
                                CA GTGG TGGAGG TTAA
                                || |||| |||||| ||||
                                GT CACC ACCTCC AGTT
                                 C    C     _
GAM2190 SDC2     3' AAGTGATGGGGCAGGAA     52934      G    A   TTA
                                AAGTG ATGG GGC   AGGAA
                                ||||| |||| |||   |||||
                                TTCAC TACC CCG   TCCTT
                                  _    _   ____
GAM2190 SSA1     5' AGTGTGGAGACCTTTAGG    52935     GA       A_
                                AGTG  TGGAGGCTT  AGG
                                ||||  |||||||||  |||
                                TCAC  ACCTCTGGA  TCC
                                  __        AA
GAM2190 BRD2     5' CAAGCGGATGGAGGTGGA    52936           CTTAA
                                CAAGTGGATGGAGG    GGA
                                ||||||||||||||    |||
                                GTTCGCCTACCTCC    CCT
                                        A_____
GAM2190 CTPS2    3' CAGGTGGAGGGGAAGATAGGGA 52937    A    T_    CT  A
                                CA GTGGA  GGAGG  TA GGA
                                || |||||  |||||  || |||
                                GT CACCT  CCTTC  AT CCT
                                 C    CC    T_  C
GAM2190 FLJ12387 3' AAGGGATGGAGCTGGA     52938     T      G  TAA
                                AAG GGATGGAG CT   GGA
                                ||| ||||||| ||   |||
                                TTC CCTACCTC GA   CCT
                                  _       _ ____
GAM2190 FLJ12650 3' GTGGATGGAGCCGTCAGG    52939         G  TA_
                                GTGGATGGAG CT   AGG
                                |||||||||| ||   |||
                                CACCTACCTC GG   TCC
                                     _ CAG
GAM2190 FLJ21156 3' TGAGTGGATGTGGGTTCTGA  52940   A      GA  C  AAG
                                C AGTGGATG  GG TT   GA
                                | ||||||||  || ||   ||
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                                A TCACCTAC  CC AA   CT
                                 C       AC  _  GA_
GAM2190  H-L(3)MBT 3'  TGAGTGGGTAGAGAGCAGAGGA 52941    A     A     _  TTA
                                C AGTGG TGGAG GC   AGGA
                                | ||||| ||||| ||   ||||
                                A TCACC ATCTC CG   TCCT
                                 C    C     T  TC_
GAM2190  KIAA0377  3'  CAGATGGATGCTGGGCTTGAGG 52942    AG     GA_    A
              AAT                   CA  TGGATG   GGCTT AGGAAT
                                ||  ||||||   ||||| ||||||
                                GT  ACCTAC   CCGAA TCCTTA
                                 CT     GAC    C
GAM2190  KIAA0711  3'  TGGGTGGATGACCAGGAA    52943     A   _   TA
                                TGG TGGA GGCT  AGGAA
                                ||| |||| ||||  |||||
                                ACC ACCT CTGG  TCCTT
                                  C   A   __
GAM2190  KIAA1529  3'  CAGGTAGATGGACAGGGAAGGA 52944    A       __  CTT
                                CA GTGGATGGA  GG   AAGGA
                                || |||||||||  ||   |||||
                                GT CATCTACCT  CC   TTCCT
                                 C       GT  C__
GAM2190  MGC12966  3'  CAAGTGGAAGGAAAGG      52945        T   GGCTT
                                CAAGTGGA GGA     AAGG
                                |||||||| |||    ||||
                                GTTCACCT CCT     TTCC
                                     T  _____
GAM2190  MGC15482  3'  AGTGGATGGGGGTAAGG     52946         A  CT
                                AGTGGATGG GG  TAAGG
                                ||||||||| ||  |||||
                                TCACCTACC CC  ATTCC
                                      _  C_
GAM2190  MGC2477   5'  TGAGGGGATGGAGAGGGA    52947    A  T       CTTAA
                                C AG GGATGGAGG    GGA
                                | || |||||||||    |||
                                A TC CCTACCTCT    CCT
                                 C  C       C____
GAM2190  MGC2541   5'  CAAATGGATGACAGCTGGGGAA 52948          GA    TAA
              T                  CAAGTGGATG  GGCT   GGAAT
                                |||||||||  ||||   |||||
                                GTTTACCTAC  TCGA   CCTTA
                                      TG    CC_
GAM2190  NSBP1     3'  CAAGGGATGGAGGTGGGGGA   52949      T       CTTAA
                                CAAG GGATGGAGG    GGA
                                |||| |||||||||    |||
                                GTTC CCTACCTCC    CCT
                                  _       ACCC_
GAM2190  PIP5K1C   3'  GTGGATGGAGGCAGA       52950           TTAA
                                GTGGATGGAGGC    GGA
                                ||||||||||||   |||
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                                CACCTACCTCCG   TCT
                                      ____
GAM2190  PRO1584  3'  AAGTGGATGGACTGGAAGG   52951         __ CTT
                                AAGTGGATGGA  GG   AAGG
                                ||||||||||  ||   ||||
                                TTCACCTACCT  CC   TTCC
                                     GA  ___
GAM2190  PSMD13   3'  CAGGTGGATGGGGATGGA    52952    A      A  CTTAA
                                CA GTGGATGG GG    GGA
                                || ||||||||  ||    |||
                                GT CACCTACC CC    CCT
                                 C       _  TA___
GAM2190  UBP1     3'  AATATTTGAGAGGCTTAAGG  52953     GA  _
                                AGTG  TG GAGGCTTAAGG
                                ||||  || ||||||||||
                                TTAT  AC CTCCGAATTCC
                                   AA  T
GAM2190  ZNF33A   3'  CAAGTGGATGCAAGGGA     52954         G   CTTAA
                                CAAGTGGATG AGG    GGA
                                |||||||||| |||    |||
                                GTTCACCTAC TTC    CCT
                                     G  _____
GAM2190  LOC133022 3'  CAAGTGGAATGGACAGGAA   52955        _   GGCTTA
                                CAAGTGGA TGGA     AGGAA
                                |||||||| ||||     |||||
                                GTTCACCT ACCT     TCCTT
                                     T   G_____
GAM2190  LOC146542 3'  CAAGTTGGAAACTTGAGG    52956      GGA       A
                                CAAGT   TGGAGGCTT AGG
                                |||||   ||||||||| |||
                                GTTCA   ACCTTTGAA TCC
                                   ___       C
GAM2190  LOC149506 3'  AAGTGGATGGCAGAAGG     52957         A  CTT
                                AAGTGGATGG GG   AAGG
                                ||||||||||  ||   ||||
                                TTCACCTACC TC   TTCC
                                     G  ___
GAM2190  LOC152048 3'  TGAGTGGATGGGGGTGGCTGGA 52958   A       A___   TAA
                                C AGTGGATGG   GGCT   GGA
                                | |||||||||   ||||   |||
                                A TCACCTACC   CCGA   CCT
                                 C       CCCA   ___
GAM2190  LOC197350 3'  GTGGATGGAGGCAAGAAT    52959          TTA
                                GTGGATGGAGGC   AGGAAT
                                ||||||||||||  ||||||
                                CACCTACCTCCG   TTCTTA
                                      ___
GAM2190  LOC200531 5'  AAGTGGTGACTTAAGGAA    52960       ATGGA
                                AAGTGG    GGCTTAAGGAA
                                ||||||    ||||||||||
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                                TTCACC    CTGAATTCCTT
                                   A____
GAM2190  LOC253980 3'  TGAGTGGTGGGGCCGGAA   52961   A   A  A   TAA
                                C AGTGG TGG GGCT  GGAA
                                | ||||| ||| ||||  ||||
                                A TCACC ACC CCGG  CCTT
                                 C   _  _  ___
GAM2190  LOC256073 5'  GTGGATGGAGGAAAGAAT   52962         CTT
                                GTGGATGGAGG  AAGGAAT
                                ||||||||||  |||||||
                                CACCTACCTCC  TTTCTTA
                                      ___
GAM2190  LOC256980 3'  TGGTTTGGGAGGCTTGAGGA  52963    AT__      A
                                TGG   GGAGGCTT AGGA
                                |||   |||||||| ||||
                                ACC   CCTCCGAA TCCT
                                  AAAC       C
GAM2190  LOC51312  3'  AAGTGGATGGACTGGAAGG   52951          __ CTT
                                AAGTGGATGGA  GG  AAGG
                                ||||||||||  ||  ||||
                                TTCACCTACCT  CC  TTCC
                                      GA  ___
GAM2190  LOC58486  5'  AAGGGATGGGGTGGGAAGG   52964    T    A  CTT_
                                AAG GGATGG GG   AAGG
                                ||| |||||| ||   ||||
                                TTC CCTACC CC   TTCC
                                  _    _ ACCC
GAM2191  BARHL1   3'  GGGAGAAAGGGGTTGCCTAG  52967   AG   AA  _
                                GG  GAAAG  GTT CCTGG
                                ||  |||||  ||| |||||
                                CC  CTTTC  CAA GGATC
                                 CT    CC  C
GAM2191  CENPB    3'  GGAGGAAAGAGGATTCTGA   52968        A_   C
                                GGAGGAAAGA  GTTC TGG
                                ||||||||||  |||| |||
                                CCTCCTTTCT  TAAG ACT
                                      CC   _
GAM2191  EN2      3'  GGAGGAGGGAGTTAGGTGCA  52969      AA  A   CCT  _
                                GGAGGA  GA GTT   GGT CA
                                ||||||  || |||   ||| ||
                                CCTCCT  CT CAA   CCA GT
                                   CC  _   T__   C
GAM2191  ETS2     3'  GGAGGCAGCCTGGTCA     52970      AA  AAGTT
                                GGAGG  AG    CCTGGTCA
                                |||||  ||    ||||||||
                                CCTCC  TC    GGACCAGT
                                  G_  ______
GAM2191  FUT3     3'  GGAGGGGAGAGGCTCCTGG   52971      AA   A
                                GGAGG  AGA GTTCCTGG
                                |||||  ||| ||||||||
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                                CCTCC  TCT CGAGGACC
                                  CC   C
GAM2191  GFRA2    3'  GGAGGAGACAGGTTCAGCGACA 52972       AAGAA   C_  T
                AG                  GGAGGA    GTTC  TGG CAAG
                                    ||||||    ||||  ||| ||||
                                    CCTCCT    CAAG  GCT GTTC
                                      CTGTC   TC  _
GAM2191  HEPH     5'  GGAGGGGAGTTCCCATCCA   52973      AAA  A     GT
                                    GGAGG   GA GTTCCTG  CA
                                    |||||   || |||||||  ||
                                    CCTCC   CT CAAGGGT  GT
                                      C__  _      AG
GAM2191  IGFBP4   3'  AGAGGAAGGACGATGGTCAAG  52974       A  AGTTCC
                                    GGAGGAA GA     TGGTCAAG
                                    |||||||  ||     ||||||||
                                    TCTCCTT CT     ACCAGTTC
                                       C  GCT___
GAM2191  IL24     3'  GGAGGGAGGTCCTGGTC     52975      AAA  A  T
                                    GGAGG   GA GT CCTGGTC
                                    |||||   || ||  |||||||
                                    CCTCC   CT CA GGACCAG
                                      ___  C  _
GAM2191  IL6R     3'  GGAGGAGAGAGCTTCTTCCCCC 52976       A   A  _______  TG
                AG                  GGAGGA AGA GT     TCC  G
                                    ||||||  |||  ||     |||  |
                                    CCTCCT TCT CG     GGG  C
                                      C   _  AAGAAG   GT
GAM2191  MAML1    3'  GGAGGAAGGGATTCCTGG    52977       A AA
                                    GGAGGAA G  GTTCCTGG
                                    |||||||  |  ||||||||
                                    CCTCCTT C  TAAGGACC
                                       _ CC
GAM2191  MGAT1    3'  GGAGAAGGGGTCTGGTCAAG   52978       AAGAA  TC
                                    GGAGGA    GT  CTGGTCAAG
                                    ||||||    ||  |||||||||
                                    CCTCTT    CA  GACCAGTTC
                                      CCC__  __
GAM2191  MYH11    3'  GGGGAAAGAATTCTCAA     52979    A      G   CTGG
                                    GG GGAAAGAA TTC    TCAA
                                    || ||||||| |||    ||||
                                    CC CCTTTCTT AAG    AGTT
                                      _      _  _____
GAM2191  MYH11    3'  GGGGAAAGAATTCTCAA     52979    A      G   CTGG
                                    GG GGAAAGAA TTC    TCAA
                                    || ||||||| |||    ||||
                                    CC CCTTTCTT AAG    AGTT
                                      _      _  _____
GAM2191  MYH11    3'  GGGGAAAGAATTCTCAA     52979    A      G   CTGG
                                    GG GGAAAGAA TTC    TCAA
                                    || ||||||| |||    ||||
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                                CC CCTTTCTT AAG    AGTT
                                 _      _  _____
GAM2191  OPCML    3'  AGAGGAAAGGGAAGGGTCAAG  52980         __    TTCCT
                                GGAGGAAA  GAAG    GGTCAAG
                                ||||||||  ||||    |||||||
                                TCTCCTTT  CTTC    CCAGTTC
                                    CC   ______
GAM2191  PFKFB2   3'  GGGGAAGAAAGCAGTCAA    52981    A    AG    TCCT
                                GG GGAA  AAGT    GGTCAA
                                || ||||  ||||    ||||||
                                CC CCTT  TTCG    TCAGTT
                                 _   CT   _____
GAM2191  PFN1     3'  GGAGGAAAGGGGTGCAA     52982         AAGTTCCT  _
                                GGAGGAAAG       GGT CAA
                                |||||||||       ||| |||
                                CCTCCTTTC       CCA GTT
                                     C________  C
GAM2191  PPARBP   5'  GGAGGAAACAAGTTGGC     52983        G    TCC
                                GGAGGAAA AAGT   TGGT
                                |||||||| ||||   ||||
                                CCTCCTTT TTCA   ACCG
                                     G   ___
GAM2191  SFRS2IP  5'  GGAGAGAGAAAATGGTCAA    52984      AA     TTCC
                                GGAGG  AGAAG    TGGTCAA
                                |||||  |||||    |||||||
                                CCTCT  TCTTT    ACCAGTT
                                   C_    T___
GAM2191  SLC18A1  3'  GGAGGAAAGAAGATTCCCAG   52985          _    TG
                                GGAGGAAAGAAG TTCC  G
                                |||||||||||| ||||  |
                                CCTCCTTTCTTC AAGG  C
                                       T    GT
GAM2191  SVIL     3'  GGTGGAAAGAAGTTTCCAAACA 52986    A         C TG T
                                GG GGAAAGAAGTT C  G CA
                                || |||||||||| |  | ||
                                CC CCTTTCTTCAA G  T GT
                                 A          A GT T
GAM2191  SVIL     3'  GGTGGAAAGAAGTTTCCAAACA 52986    A         C TG T
                                GG GGAAAGAAGTT C  G CA
                                || |||||||||| |  | ||
                                CC CCTTTCTTCAA G  T GT
                                 A          A GT T
GAM2191  TCFL1    3'  GCAGGAAAGAAGTTTCTGA    52987    G         C
                                G AGGAAAGAAGTT CTGG
                                | ||||||||||| ||||
                                C TCCTTTCTTCAA GACT
                                 G          A
GAM2191  WNT3A    3'  GAAGGGGCCTTGCCCTGGTCA  52988       AAAGAA  T
                                GGAGG     GT CCTGGTCA
                                |||||     || ||||||||
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                                CTTCC     CG GGACCAGT
                                   CCGGAA  _
GAM2191  ARL8     3'  GGAGGGAGTGCTGGTCAA    52989      AAA  A  TC
                                GGAGG   GA GT  CTGGTCAA
                                |||||   || ||  ||||||||
                                CCTCC   CT CA  GACCAGTT
                                   ____  _  C_
GAM2191  CNTNAP1  3'  GGAGGAAAGAGGGTTCCTCAT  52990         A_     G
                                GGAGGAAAGA  GTTCCT GT
                                ||||||||||  |||||| ||
                                CCTCCTTTCT  CAAGGA TA
                                      CC     G
GAM2191  CSEN     3'  GGAGGCAGACCCCTCCTGGT   52991      AA   AG_
                                GGAGG  AGA   TTCCTGGT
                                |||||  |||   ||||||||
                                CCTCC  TCT   GAGGACCA
                                   G_   GGG
GAM2191  DKFZP434J193 5'  GGAAGTTTAGTTTGGTCAAG   52992      AAAGA    CC
                                GGAGG    AGTT  TGGTCAAG
                                |||||    ||||  ||||||||
                                CCTTC    TCAA  ACCAGTTC
                                   AAA__   __
GAM2191  FLJ10276  3'  GGAGGAAAGGAAGGAGGTGGGT 52993         _   TTCCT_
            CA                    GGAGGAAAG AAG     GGTCA
                                |||||||| |||     |||||
                                CCTCCTTTC TTC     CCAGT
                                     C   CTCCAC
GAM2191  FLJ11608  3'  GGAGAGAGAGGTCACCTTGG   52994      AA   A   _   _
                                GGAGG  AGA GTT CCT GG
                                |||||  ||| ||| ||| ||
                                CCTCT  TCT CAG GGA CC
                                   C_   C   T   A
GAM2191  FLJ20048  3'  GAAGGAAGAAGTTCCCCAT    52995        A        G
                                GGAGGAA GAAGTTCCT GT
                                |||||||  |||||||| ||
                                CTTCCTT CTTCAAGGG TA
                                   _        G
GAM2191  FLJ20413  3'  GGAGGAAGGAGGCTCCCAG    52996        A  A     TG
                                GGAGGAA GA GTTCC  G
                                |||||||  || |||||  |
                                CCTCCTT CT CGAGG  C
                                     C  C     GT
GAM2191  FLJ20456  5'  GGAGGAAGGAAGTCCCGG     52997        A     T
                                GGAGGAA GAAGT CCTGG
                                |||||||  ||||| |||||
                                CCTCCTT CTTCA GGGCC
                                     C     _
GAM2191  GTPBP1   3'  GGAGGAAAGGAAAGGGTTGG   52998         _   TTCC
                                GGAGGAAAG AAG    TGG
                                |||||||| |||    |||
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                                CCTCCTTTC TTT   ACC
                                     C  CCCA
GAM2191 KIAA0447 3' GGGGAGAAGTTCTGA      52999    A  AA     C
                                GG GGA  GAAGTTC TGG
                                || |||  ||||||| |||
                                CC CCT  CTTCAAG ACT
                                 _  __     _
GAM2191 KIAA0553 3' GGAGGGTGGGAGGGCAGTCAAG 53000      AAA_  A_  TCCT
                                GGAGG   GA  GT   GGTCAAG
                                |||||   ||  ||   |||||||
                                CCTCC   CT  CG   TCAGTTC
                                   CACC  CC  ____
GAM2191 MARCKS   3'  GGGGAGAAAAGTTCTTCGCTTG 53001     A      ________  GGTCA
            ACA                   GGA AGAAGTTC      CT    A
                                ||| ||||||||      ||    |
                                CCT TTTTCAAG      GA    T
                                  C       AAGCIII  ACTGG
GAM2191 MGC16309 5' GGAGGAAAGGGGGTTGATTCA  53002        AA_   CCTGG
                                GGAGGAAAG   GTT    TCA
                                |||||||||   |||    |||
                                CCTCCTTTC   CAA    AGT
                                     CCC   CTA__
GAM2191 MGC4342  3' GGAGGGCAGGGGTTCCCGG   53003      AA  AA
                                GGAGG  AG  GTTCCTGG
                                |||||  ||  ||||||||
                                CCTCC  TC  CAAGGGCC
                                   CG  CC
GAM2191 MGC4504  3' GGGGGGAATCTGGTCAA    53004    A  AAA   GTTC
                                GG GG   GAA    CTGGTCAA
                                || ||   |||    ||||||||
                                CC CC   CTT    GACCAGTT
                                 _  C__   A___
GAM2191 moblak   3'  GGAGGAAAGAGGCTGCCTGG   53005         A  _
                                GGAGGAAAGA GTT CCTGG
                                |||||||||| ||| |||||
                                CCTCCTTTCT CGA GGACC
                                      C   C
GAM2191 NDUFA4   3'  GGAGAAATATTTCCTGGTTAAG 53006       AGAAG       C
                                GGAGGAA    TTCCTGGT AAG
                                |||||||    |||||||| |||
                                CCTCTTT    AAGGACCA TTC
                                    ATA__       A
GAM2191 PSKH1    3'  GGAGGAAAGGGGGTCCCAGA   53007        AA_    T
                                GGAGGAAAG   GTTCC GG
                                |||||||||   ||||| ||
                                CCTCCTTTC   CAGGG CT
                                      CCC    T
GAM2191 PTPRT    3'  GGAGCAGAGAAGTTCCCTGC   53008     GAA        G
                                GGAG   AGAAGTTCCT GT
                                ||||   |||||||||| ||
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                                CCTC   TCTTCAAGGG CG
                                  GTC         A
GAM2191  RAB9B    5'  GAAGGGAAGGAGTTTGTAACCA 53009      A   A    CC  GT
              AG                    GGAGG AAG AGTT  TG  CAAG
                                |||||| ||| ||||  ||  ||||
                                CTTCC TTC TCAA  AT  GTTC
                                   C   C    AC  TG
GAM2191  SHAPY    5'  GAGGAAGGAAGTTCCATG    53010       A       _
                                GAGGAA GAAGTTCC TG
                                |||||| |||||||| ||
                                CTCCTT CTTCAAGG AC
                                   C       T
GAM2191  STX5A    3'  GGAAGAAAGAGGTCAA      53011          AGTTCCT
                                GGAGGAAAGA      GGTCAA
                                ||||||||||      ||||||
                                CCTTCTTTCT      CCAGTT

                                   _______
GAM2191  LOC115129 5'  GAAGGAAGAAGTTCCAGA    53012        A       T
                                GGAGGAA GAAGTTCC GG
                                ||||||| |||||||| ||
                                CTTCCTT CTTCAAGG CT
                                   _       T
GAM2191  LOC149465 3'  GGAGGAGGCAGCTGTGGTCAAG 53013       AAGA    CC
                                GGAGGA    AGTT  TGGTCAAG
                                ||||||    ||||  ||||||||
                                CCTCCT    TCGA  ACCAGTTC
                                   CCG_    C_
GAM2191  LOC149773 5'  GGAGGAAAACCCGCCTGGTC   53014         AAGTT
                                GGAGGAAAG     CCTGGTC
                                |||||||||     |||||||
                                CCTCCTTTT     GGACCAG
                                     GGGC_
GAM2191  LOC150311 5'  GGAGGGAAGAGGCTTTTGG    53015      A   A   CC
                                GGAGG AAGA GTT  TGG
                                ||||| |||| |||  |||
                                CCTCC TTCT CGA  ACC
                                   C    C   AA
GAM2191  LOC151996 3'  GGCGGAAGGAGTTTTCCCCGG  53016    A    A  AG__
                                GG GGAA GA    TTCCTGG
                                || |||| ||    |||||||
                                CC CCTT CT    AGGGGCC
                                 G    C  CAAA
GAM2191  LOC153196 3'  GGAGGAAGATGGTCA       53017        A  AGTTCC
                                GGAGGAA GA     TGGTCA
                                ||||||| ||     ||||||
                                CCTCCTT CT     ACCAGT
                                   _ _______
GAM2191  LOC163556 5'  GGAGGGAGGAAGTCCCCCCAAG 53018       AAA       GG
                                GGAGG   GAAGTTCCT  TCAAG
                                |||||   |||||||||  |||||
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                                CCTCC  CTTCAGGGG  GGTTC
                                  CTC       __
GAM2191  LOC219899 3'  GGAGAGAGAAGTTCTGG     53019      AA      C
                                GGAGG  AGAAGTTC TGG
                                |||||  |||||||| |||
                                CCTCT  TCTTCAAG ACC
                                  C_       _
GAM2191  LOC219988 5'  GGAGGGAAGAGTTCGGG     53020      A   A   CT
                                GGAGG AAGA GTTC  GG
                                ||||| |||| ||||  ||
                                CCTCC TTCT CAAG  CC
                                  C   _   C_
GAM2191  LOC221632 5'  GGAGGAAAGAGAGTTCATCA  53021         _    CTG
                                GGAGGAAAGA AGTTC  GTCA
                                |||||||||| |||||  ||||
                                CCTCCTTTCT TCAAG  TAGT
                                     C   ____
GAM2191  LOC221687 3'  GGAGGAAAGAGTGTGTCTCAAG 53022         A  TCC  G_
                                GGAGGAAAGA GT  TG  TCAAG
                                |||||||||| ||  ||  |||||
                                CCTCCTTTCT CA  AC  AGTTC
                                     _  C__  AG
GAM2191  LOC253233 3'  GGGGAAGAGAAGTTCTTG    53023    A   _      C
                                GG GGAA AGAAGTTC TG
                                || |||| |||||||| ||
                                CC CCTT TCTTCAAG AC
                                 _   C       A
GAM2191  LOC91663  3'  GGAGGAAAGAAGTACTCC    53024          __
                                GGAGGAAAGAAGT  TCC
                                ||||||||||||  |||
                                CCTCCTTTCTTCA  AGG
                                       TG
GAM2191  LOC95633  3'  AGAGGAGAGAGGTTTGG     53025      A   A   CC
                                GGAGGA AGA GTT  TGG
                                |||||| ||| |||  |||
                                TCTCCT TCT CAA  ACC
                                  C   C   __
GAM2192  PACE4     3'  TCATTGATTTCTCTTTCA    53028    C    C
                                TCA TGATT CTTTTTCG
                                ||| ||||| ||||||||
                                AGT ACTAA GAGAAAGT
                                  A    A
GAM2192  PACE4     3'  TCATTGATTTCTCTTTCA    53028    C    C
                                TCA TGATT CTTTTTCG
                                ||| ||||| ||||||||
                                AGT ACTAA GAGAAAGT
                                  A    A
GAM2192  RAB30     3'  CTGATTCCTTTTCTTCTCCG  53029          CGATG
                                CTGATTCCTTTTT    CCG
                                ||||||||||||    |||
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                                GACTAAGGAAAAG    GGC
                                      AAGA_
GAM2192  AKAP7    3'  CTAATTCCTCACCAAATG    53030         T TC
                                CTGATTCCTT T  GATG
                                |||||||||| |  ||||
                                GATTAAGGAG G  TTAC
                                      T GT
GAM2192  AKAP7    3'  CTAATTCCTCACCAAATG    53030         T TC
                                CTGATTCCTT T  GATG
                                |||||||||| |  ||||
                                GATTAAGGAG G  TTAC
                                      T GT
GAM2192  AKAP7    3'  CTAATTCCTCACCAAATG    53030         T TC
                                CTGATTCCTT T  GATG
                                |||||||||| |  ||||
                                GATTAAGGAG G  TTAC
                                      T GT
GAM2192  C20orf172 5'  TCACTGGTCCTTTTTCA     53031       AT
                                TCACTG  TCCTTTTTCG
                                ||||||  ||||||||||
                                AGTGAC  AGGAAAAAGT
                                   C_
GAM2192  DKFZp761G0313 3'  CACTGGTTTTCTTTCGATG    53032       A  CC
                                CACTG TT  TTTTTCGATG
                                ||||| ||  ||||||||||
                                GTGAC AA  AGAAAGCTAC
                                   C  A_
GAM2192  FLJ20038  3'  TCAATGATTCCTTGCC      53033     C       TTTTCGA
                                TCA TGATTCCT      TGCC
                                ||| ||||||||      ||||
                                AGT ACTAAGGA      ACGG
                                  T      ________
GAM2192  FLJ20533  3'  TCACTGATTCTTTTCCTTTG   53034          C     GA
                                TCACTGATTC TTTTTC  TG
                                |||||||||| ||||||  ||
                                AGTGACTAAG AAAAGG  AC
                                      _     AA
GAM2192  KHDRBS1   3'  TGATTCCTTTTTTCATTCAGC   53035            AT__
                                TGATTCCTTTTTTCG   GC
                                ||||||||||||||   ||
                                ACTAAGGAAAAAGT   CG
                                      AAGT
GAM2192  KIAA0680  3'  TCACTGATTCTTTTGCATTG   53036          C   T  A
                                TCACTGATTC TTTT CG TG
                                |||||||||| |||| || ||
                                AGTGACTAAG AAAA GT AC
                                      _   C  A
GAM2192  LOC256310 5'  TGATTCCTCATCTGATGTCG   53037          T TC   C
                                TGATTCCTT T  GATG CG
                                |||||||||| |  |||| ||
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                                ACTAAGGAG A  CTAC GC
                                     T GA    A
GAM2192  LOC257465 3'  CTGATTCCTTATCATTG     53038          TT   A
                                CTGATTCCTT  TCG TG
                                ||||||||||  ||| ||
                                GACTAAGGAA  AGT AC
                                     T_   A
GAM2193  ACK1     5'  CGGGGCCGCTCCCAGGACC    53041     CAAGA      C  CA
                                CGG    CCGCTCCC GG  ACC
                                |||    |||||||| ||  |||
                                GCC    GGCGAGGG CC  TGG
                                  CC___       T __
GAM2193  ADAMTS8   5'  CGGCGGGAGCGCTCCCCCGGCG 53042      AA  C      _   AA
            GCC                    CGGC  GA CGCTCCCC GGC  CC
                                |||| || |||||||| |||  ||
                                GCCG  CT GCGAGGGG CCG  GG
                                  CC  C       G   CC
GAM2193  AP2B1    3'  GGGACCGCTCCCCACAA     53043    CAA          G
                                GG   GACCGCTCCCCG CAA
                                ||   ||||||||||||| |||
                                CC   CTGGCGAGGGGT GTT
                                  ___          _
GAM2193  ARHI     5'  CGGAGAGACTGCCGCGGCAACC 53044     CA    C   CCC
                                CGG  AGAC GCT   CGGCAACC
                                |||  |||| |||   ||||||||
                                GCC  TCTG CGG   GCCGTTGG
                                  TC    A   C__
GAM2193  ETV5     5'  CGGTGAACCGCTCCGCGCACC  53045     CAA        C  G  A
                                CGG   GACCGCTCC CG CA CC
                                |||   ||||||||| || || ||
                                GCC   TTGGCGAGG GC GT GG
                                  AC_        C  _  _
GAM2193  GAS11    5'  AGCCACGCCGTTTCCCGGCAAC 53046     AAGA   CTC
            C                     GGC    CCG   CCCGGCAACC
                                |||    |||   ||||||||||
                                TCG    GGC   GGGCCGTTGG
                                  GTGC   AAA
GAM2193  MAN2A1   5'  GGCGAGACTCGCCGGCAAC   53047     A   _   TCCC
                                GGC AGAC CGC    CGGCAAC
                                ||| |||| |||    |||||||
                                CCG TCTG GCG    GCCGTTG
                                  C   A  _____
GAM2193  MAP3K9   5'  GGCGAGCTGCTTTCACAGCAAC 53048     A  ACC   CCC_
            C                     GGC AG   GCT    CGGCAACC
                                ||| ||   |||    ||||||||
                                CCG TC   CGA    GTCGTTGG
                                  C  GA_   AAGT
GAM2193  PDE1B    3'  AGCTCCCCGCTCCCTGGCAGCC 53049     AAGA       C    A
                                GGC    CCGCTCCC GGCA CC
                                |||    |||||||| |||| ||
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                                TCG   GGCGAGGG CCGT GG
                                  AGG_      A   C
GAM2193 PDLIM1   5' GCAGGGCACCCCCGGCA    53050    A AC  T
                                GCA G  CGC CCCCGGCA
                                ||| |  ||| ||||||||
                                CGT C  GTG GGGGCCGT
                                  _ CC  _
GAM2193 RANBP3   5' GCAGCATCCCCGGCAGCC    53051    AGACC _      A
                                GCA    GC TCCCCGGCA CC
                                |||    || |||||||| ||
                                CGT    CG AGGGGCCGT GG
                                  _____ T       C
GAM2193 S100A10  5' CGGCAGGGCGCTCCCCCAGC  53052     A AC      _
                                CGGCA G  CGCTCCCC GGC
                                ||||| |  |||||||| |||
                                GCCGT C  GCGAGGGG TCG
                                   _ CC       G
GAM2193 AP3D1    3' GGCAAGACCGCTTTCCCAC   53053         CC  G
                                GGCAAGACCGCT  CC GC
                                ||||||||||||  || ||
                                CCGTTCTGGCGA  GG TG
                                      AA  G
GAM2193 B3GALT6  3' CGGCGCGCTGCCCCGGCAACC 53054     AAGAC   _
                                CGGC    CGCT CCCCGGCAACC
                                ||||    |||| ||||||||||
                                GCCG    GCGA GGGGCCGTTGG
                                  C____   C
GAM2193 C11orf24 5' CAGCAGGCCCCCGGCGC    53055     AGACC  T     AA
                                CGGCA    GC CCCCGGC  C
                                |||||    || |||||||  |
                                GTCGT    CG GGGGCCG  G
                                   C____ _      CC
GAM2193 CL683    3' GGCAAGACGTTCGTATCGGC  53056       C C  CC__
                                GGCAAGAC G TC    CGGC
                                |||||||| | ||    ||||
                                CCGTTCTG C AG    GCCG
                                     _ A  CATA
GAM2193 FLJ11939 3' GGCAAGACTGTCCCTGGC    53057       CGC   C
                                GGCAAGAC   TCCC GGC
                                ||||||||   |||| |||
                                CCGTTCTG   AGGG CCG
                                    AC_   A
GAM2193 MGC15438 3' CGGCGCGACCGCTCTCCAG   53058     AA      C
                                CGGC  GACCGCTC CCGG
                                ||||  |||||||| ||||
                                GCCG  CTGGCGAG GGTC
                                  CG       A
GAM2193 MGC2376  3' GGCAAGACTCTAGACCAAC   53059       CG  CC_
                                GGCAAGAC  CT   CCGGC
                                ||||||||  ||   |||||
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                                CCGTTCTG GA  GGTTG
                                    A_ TCT
GAM2193 SLC2A4RG 3' GGTGGGACCCCTCCCCGAC  53060   CAA  G
                                GG  GACC CTCCCCGGC
                                ||  |||| |||||||||
                                CC  CTGG GAGGGGCTG
                                 ACC  G
GAM2193 SLC37A1  3' GGGGAGACCGCTTCCCAAACC 53061   CA     C  GC
                                GG AGACCGCT CCCG AACC
                                || |||||||| ||||  ||||
                                CC TCTGGCGA GGGT TTGG
                                 CC      A  __
GAM2193 WSB1     3' GGTAAAGGTCGCCCCCAGC  53062   C_  AC  T
                                GG AAG CGC CCCCGGC
                                || ||| ||| |||||||
                                CC TTC GCG GGGGTCG
                                 AT  CA  _
GAM2193 LOC138046 3' GGCAAGACAGTCTTTTCCTTGG 53063       CG_ ___  CC
            CAA                   GGCAAGAC  C  TCC GGCAA
                                |||||||| |  ||| |||||
                                CCGTTCTG  G  AGG CCGTT
                                    TCA AAA  AA
GAM2193 LOC145581 5' CGGCAAGGTGGCTCCAGGTGGC 53064       ACC   CC__
                                CGGCAAG  GCTCC  GGC
                                |||||||  |||||  |||
                                GCCGTTC  CGAGG  CCG
                                   CAC   TCCA
GAM2193 LOC152485 3' GGAAGGGCCGCTCCCCGG  53065   C  A_
                                GG AAG CCGCTCCCCGG
                                || |||  ||||||||||
                                CC TTC GGCGAGGGGCC
                                 _  CC
GAM2193 LOC166129 5' CGGGGGACCGCTCTCAGC  53066    CAA     CC
                                CGG  GACCGCTC CGGC
                                |||  |||||||| ||||
                                GCC  CTGGCGAG GTCG
                                  CC_     A_
GAM2193 LOC196957 3' GGCTTAAGCTCCGGCAACC  53067    AAGACC   CC
                                GGC    GCTCC GGCAACC
                                |||    ||||| |||||||
                                CCG    CGAGG CCGTTGG
                                  AATT__   __
GAM2193 LOC196961 3' GGCTTAAGCTCCGGCAACC  53067    AAGACC   CC
                                GGC    GCTCC GGCAACC
                                |||    ||||| |||||||
                                CCG    CGAGG CCGTTGG
                                  AATT__   __
GAM2193 LOC197138 3' GGCTTAAGCTCCGGCAACC  53067    AAGACC   CC
                                GGC    GCTCC GGCAACC
                                |||    ||||| |||||||
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                                CCG     CGAGG  CCGTTGG
                                  AATT__    __
GAM2193  LOC221495 5'  CGGCCGAGGGCCCTTCTGGCAA 53068      AA  CC    CCC_
                                CGGC  GA  GCTC    GGCAA
                                ||||  ||  ||||    |||||
                                GCCG  CT  CGGG    CCGTT
                                  G_  CC    AAGA
GAM2193  LOC221914 5'  GCGGGACCGCTCCGCGGGC    53069    AA       C  _
                                GC  GACCGCTCC CGG C
                                ||  ||||||||| ||| |
                                CG  CTGGCGAGG GCC G
                                 CC        C   C
GAM2193  LOC245727 3'  GGCTTAAGCTCCGGCAACC    53067     AAGACC     CC
                                GGC     GCTCC  GGCAACC
                                |||     |||||  |||||||
                                CCG     CGAGG  CCGTTGG
                                  AATT__    __
GAM2193  LOC253868 5'  CGGCGAGGCTGCCCCCGGC    53070      A  ACC  T
                                CGGC AG   GC CCCCGGC
                                |||| ||   || |||||||
                                GCCG TC   CG GGGGCCG
                                  C  CGA  _
GAM2193  LOC90371  3'  CAGCAAGGTACTGGCAAC     53071        ACC   CCCC
                                CGGCAAG   GCT    GGCAAC
                                |||||||   |||    ||||||
                                GTCGTTC   TGA    CCGTTG
                                    CA_   ____
GAM2193  LOC91828  5'  CGGCCAGGTCGCTCCCCTAC   53072      A  AC       G
                                CGGC AG  CGCTCCCC GC
                                |||| ||  |||||||| ||
                                GCCG TC  GCGAGGGG TG
                                  G  CA       A
GAM2193  LOC92822  3'  GGCAGGGCCGCTCCCGGAC    53073      AGA       C
                                GGCA   CCGCTCCC GGC
                                ||||   |||||||| |||
                                CCGT   GGCGAGGG CTG
                                  CCC       C
GAM2194  CHRNA3    3'  TGGTGTACTAAGACAGTTATAT 53076     CA      TGT
           T                     TGG  TATTAAG   AGTTATATT
                                |||  |||||||   |||||||||
                                ACC  ATGATTC   TCAATATAA
                                  AC      TG_
GAM2194  ESRRBL1   3'  TGGCATATTTGTCATTGTATT  53077         AAG   A   A
                                TGGCATATT   TGT GTT TATT
                                |||||||||   ||| ||| ||||
                                ACCGTATAA   ACA TAA ATAA
                                     ___   G   C
GAM2194  SLT       3'  TAGCATATTAAGCTCATTGTAT 53078           GTA   A
           T                     TGGCATATTAAGT   GTT TATT
                                ||||||||||||   ||| ||||
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                                ATCGTATAATTCG   TAA ATAA
                                      AG_   C
GAM2194  CPR2     3'  TGGCATGTGAATTATA      53079       ATTAA   T
                                TGGCAT    GTG AGTTATA
                                ||||||    ||| |||||||
                                ACCGTA    CAC TTAATAT
                                   _____  _
GAM2194  DKFZP564A1164 3'  GGCATATTGGGTGGCCAT    53080        AA   TA
                                GGCATATT  GTG  GTTAT
                                ||||||||  |||  |||||
                                CCGTATAA  CAC  CGGTA
                                     CC  __
GAM2194  DSTN     3'  TAGTGTATTAGTGTTGTTATAT 53081     CA    A   A
              T                  TGG  TATTA GTGT GTTATATT
                                 |||  ||||| |||| ||||||||
                                 ATC  ATAAT CACA CAATATAA
                                   AC    _   A
GAM2194  KIAA1143  3'  TGACATATTAGGCTTATAT    53082         A  GTAG
                                TGGCATATTA GT    TTATAT
                                ||||||||||  ||   ||||||
                                ACTGTATAAT CG    AATATA
                                     C  ____
GAM2194  PRO2012   3'  TGGGTATTAAGTGTCATT    53083     CA        A
                                TGG  TATTAAGTGT GTT
                                |||  ||||||||||  |||
                                ACC  ATAATTCACA TAA
                                  C_        G
GAM2194  LOC221037 3'  TAGCATATTAAGTTTAAT    53084           G
                                TGGCATATTAAGT TAGT
                                ||||||||||||  ||||
                                ATCGTATAATTCA ATTA
                                      A
GAM2195  ABCB9    3'  GGAGAGGCCTAGTCTCTGGACA 53087     AA_   CTAC
              T                  GGA   GCTT    CTCTGGACAT
                                 |||   ||||    ||||||||||
                                 CCT   CGGA    GAGACCTGTA
                                   CTC    TCA_
GAM2195  EDNRA    3'  TGGAAAGCATTTCTTCTTGG   53088        __    ACC   _
                                TGGAAAGC  TTCT   TCT GG
                                ||||||||  ||||   ||| ||
                                ACCTTTCG  AAGA   AGA CC
                                     TA    ___   A
GAM2195  GAS11    3'  GGAAAGCTTCTACCCACA    53089            CTGG
                                GGAAAGCTTCTACCT    ACA
                                ||||||||||||||    |||
                                CCTTTCGAAGATGGG    TGT
                                      ____
GAM2195  LIF      3'  TGGAAACTTCTGCCAGA     53090       G    A  TCT
                                TGGAAA CTTCT CC   GGA
                                ||||||  ||||| ||   |||
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                                ACCTTT GAAGA GG   TCT
                                  _    C ____
GAM2195 ABCC13   3' TGGAAAACTTTTGTCGAGAAAC 53091          CTACCTCT
             AT                   TGGAAAGCTT       GGACAT
                                  ||||||||||       ||||||
                                  ACCTTTTGAA       TTTGTA
                                       AACAGCTC
GAM2195 BIRC3    5' TGGAAAGCTCTGCTGTCA    53092         T  ACCT   GA
                                  TGGAAAGCT CT    CTG  CA
                                  ||||||||| ||    |||  ||
                                  ACCTTTCGA GA    GAC  GT
                                       _ C___   A_
GAM2195 C6orf33  3' TGGAAAGCTTCAGTTGAA    53093          TACCTC
                                  TGGAAAGCTTC     TGGA
                                  ||||||||||      ||||
                                  ACCTTTCGAAG     ACTT
                                        TCA___
GAM2195 CCNB3    3' TGGAAGCCTTCTCCTGGACAT  53094      AG    ACC
                                  TGGAA  CTTCT   TCTGGACAT
                                  |||||  |||||   |||||||||
                                  ACCTT  GAAGA   GGACCTGTA
                                    CG    ___
GAM2195 DDX36    3' GAAGGCTTCTACCTTACACAT  53095     A        C  G
                                  GAA GCTTCTACCT TG ACAT
                                  ||| |||||||||| || ||||
                                  CTT CGAAGATGGA AT TGTA
                                    C         _ G
GAM2195 FLJ10468 3' TGGGAAGCTTCCATGGCA    53096     A       CCTC   A
                                  TGG AAGCTTCTA    TGG CA
                                  ||| |||||||||    ||| ||
                                  ACC TTCGAAGGT    ACC GT
                                    C       ____   _
GAM2195 FLJ11301 3' TGGAGATTTGCTTATTCTGGAC 53097      AA___    CTACC
             AT                   TGGA    GCTT    TCTGGACAT
                                  ||||    ||||    |||||||||
                                  ACCT    CGAA    AGACCTGTA
                                    CTAAA   TA___
GAM2195 FLJ11730 3' TGGAAGCTTCTGCACTAA    53098       A     ACCT
                                  TGGAA GCTTCT    CTGG
                                  ||||| ||||||    ||||
                                  ACCTT CGAAGA    GATT
                                    _     CGT_
GAM2195 HAND1    3' GGAAAGCTTTTATTTAGA    53099         C  CCTC
                                  GGAAAGCTT TA    TGGA
                                  ||||||||| ||    ||||
                                  CCTTTCGAA AT    ATCT
                                       A  AA__
GAM2195 KIAA1017 3' TGAAAAGCTTCTGCTCCCAACA 53100          AC    G
             T                    TGGAAAGCTTCT  CTCT GACAT
                                  ||||||||||||  |||| |||||
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                                ACTTTTCGAAGA  GAGG TTGTA
                                      C_   G
GAM2195  MGC12217  3'  TGGAAAGCTTTTCATAGCA   53101         CTACC  _  A
                                TGGAAAGCTT    TC TGG CA
                                ||||||||||    || ||| ||
                                ACCTTTCGAA    AG ATC GT
                                      A_____  T  _
GAM2195  MGC5521   3'  TGGGGAGCTTCTATTCCA    53102    AA      CC
                                TGG  AGCTTCTA  TCTG
                                |||  ||||||||  ||||
                                ACC  TCGAAGAT  AGGT
                                  CC       A_
GAM2195  PEG10     3'  TGGAGTGTACACATTCTGGACA 53103     AAGCTTC  C_
           T                     TGGA      TAC  TCTGGACAT
                                ||||      |||  |||||||||
                                ACCT      GTG  AGACCTGTA
                                   CACAT__   TA
GAM2195  PRO1575   5'  TGGAGAGAATTTCTGGACAT   53104     A  CTTCTACC
                                TGGA AG       TCTGGACAT
                                |||| ||       |||||||||
                                ACCT TC       AGACCTGTA
                                  C  TTAA_____
GAM2195  PRTD-NY3  3'  GGAGAGCTTCTACCTAGAGCA  53105     A        CT  A
                                GGA AGCTTCTACCT  GG CA
                                ||| ||||||||||  || ||
                                CCT TCGAAGATGGA  TC GT
                                  C         TC  _
GAM2195  SMCR8     3'  GGTGAGCATGCTCTGGACAT   53106    AA   TTCTAC
                                GG  AGC     CTCTGGACAT
                                ||  |||     ||||||||||
                                CC  TCG     GAGACCTGTA
                                 AC   TAC___
GAM2195  LOC149460 5'  TGGGGAGCTCCTACACTG    53107     AA       CT
                                TGG  AGCTTCTAC  CTG
                                |||  |||||||||  |||
                                ACC  TCGAGGATG  GAC
                                  CC       T_
GAM2195  LOC151473 3'  TGAAAAGCTTTTATTCCCTG   53108         C  C_
                                TGGAAAGCTT TA  CTCTG
                                |||||||||| ||  |||||
                                ACTTTTCGAA AT  GGGAC
                                      A  AA
GAM2195  LOC255975 5'  TGGAAAGCTTTACTTTAAGA   53109         C   CTCT
                                TGGAAAGCTT TAC    GGA
                                |||||||||| |||    |||
                                ACCTTTCGAA ATG    TCT
                                      _   AAAT
GAM2195  LOC256812 5'  TGGAAGGCTCTACCACTG     53110      A   T    T
                                TGGAA GCT CTACC CTG
                                ||||| ||| ||||| |||
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                                ACCTT CGA GATGG GAC
                                  C  _    T
GAM2196 AIM1     3'  TGTTAAGCAGTTTGTTTGCATT 53113        TGAGA  GC
                T                 TGTTAAGC    TG  TGCATTT
                                  ||||||||    ||  |||||||
                                  ACAATTCG    AC  ACGTAAA
                                      TCAA_  AA
GAM2196 ALB      3'  TGGTAGGCTGAGATGCT     53114    T  A       G
                                  TG TA GCTGAGATG CT
                                  || || |||||||||  ||
                                  AC AT CGACTCTAC GA
                                   C  C       _
GAM2196 KLK13    3'  TGTTAGCTGAGATTGAGCATTT 53115      A       GGCT
                                  TGTTA GCTGAGAT    GCATTT
                                  ||||| ||||||||    ||||||
                                  ACAAT CGACTCTA    CGTAAA
                                     _       ACT_
GAM2196 ALTE     3'  TGTTAAGTGTCTGCAT      53116        CTGAGA  G
                                  TGTTAAG     TG CTGCAT
                                  |||||||     || ||||||
                                  ACAATTC     AC GACGTA
                                      _______ A
GAM2196 ARSDR1   3'  TGTTAAGCTGAGGTTGCA    53117          GAT  C
                                  TGTTAAGCTGA   GG TGCA
                                  ||||||||||   || ||||
                                  ACAATTCGACT   CC ACGT
                                       ___ A
GAM2196 DNAH7    3'  TATTAAGTTTAGCTGCATT    53118        CTGAGA
                                  TGTTAAG     TGGCTGCATT
                                  |||||||     ||||||||||
                                  ATAATTC     ATCGACGTAA
                                     AA____
GAM2196 TRIM36   3'  TGTTAGCTGAGAACT       53119       A      TG
                                  TGTTA GCTGAGA  GCT
                                  ||||| |||||||  |||
                                  ACAAT CGACTCT  TGA
                                     _     __
GAM2196 LOC116211 3'  TGTAAGCTGAGGCAT       53120     T       ATGGCT
                                  TGT AAGCTGAG     GCAT
                                  ||| ||||||||     ||||
                                  ACA TTCGACTC     CGTA
                                    _      _______
GAM2196 LOC221474 5'  TGTTGAGTGAGGTGGTAC    53121      A  C    A   C
                                  TGTT AG TGAG TGG TGC
                                  |||| || |||| ||| |||
                                  ACAA TC ACTC ACC ATG
                                    C  _    C   _
GAM2197 TEX14    3'  TCTAGGCACAACCAAAAATTT  53124      A     TC
                                  TTTA GTACA  ACCAAAAATTT
                                  |||| |||||  ||||||||||
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                                AGAT CGTGT  TGGTTTTTAAA
                                  C    __
GAM2197  UBE2B    3'  TTTAAGTTACACCAAGATTTC  53125       ACAT     AA
                                TTTAAGT    CACCAA  ATTTC
                                |||||||    ||||||  |||||
                                AAATTCA    GTGGTT  TAAAG
                                   AT__     C_
GAM2197  GLYAT    5'  ATACACCACCTCCAGAAATTTC 53126         AA___
                                GTACATCACC     AAATTTC
                                ||||||||||     |||||||
                                TATGTGGTGG     TTTAAAG
                                     AGGTC
GAM2197  KIAA1145 3'  ATACTTTATCACCAAAGATTTC 53127      ___        A
                                GTAC   ATCACCAAA ATTTC
                                ||||   ||||||||| |||||
                                TATG   TAGTGGTTT TAAAG
                                  AAA        C
GAM2197  KIAA1598 3'  TTCAAGTACATTACCACTTATT 53128          C    AAA
           T                     TTTAAGTACAT ACCA   ATTT
                                |||||||||| ||||   ||||
                                AAGTTCATGTA TGGT   TAAA
                                     A    GAA
GAM2197  NTT73    3'  TTTAAGTATTCACAAAAATTT  53129        CA    C
                                TTTAAGTA  TCAC AAAAATTT
                                ||||||||  |||| ||||||||
                                AAATTCAT  AGTG TTTTTAAA
                                   A_    _
GAM2197  P15-2    3'  TTTAAGGGTGTCACCAAAA    53130       TACA
                                TTTAAG    TCACCAAAA
                                ||||||    |||||||||
                                AAATTC    AGTGGTTTT
                                   CCAC
GAM2197  PI4KII   3'  TTTAAATACATTACGTACAATT 53131          C  CAAA
           TC                     TTTAAGTACAT AC    AATTTC
                                |||||||||| ||    ||||||
                                AAATTTATGTA TG    TTAAAG
                                     A  CATG
GAM2197  SNRPB2   3'  TTTAAGTCCTTCACAAAAATTT 53132       ACA    C
           C                     TTTAAGT   TCAC AAAAATTTC
                                |||||||   |||| |||||||||
                                AAATTCA   AGTG TTTTTAAAG
                                   GGA   _
GAM2198  CALU     3'  CTCCTGAACATTTCTTAT     53135      C   GGGT
                                TTCC GAG    CATTTCTTAT
                                |||| |||    ||||||||||
                                GAGG CTT    GTAAAGAATA
                                  A  ____
GAM2198  PRPF18   3'  TTCCCTAAGTTTCTTAT      53136       G   GGTCA
                                TTCCC AGG     TTTCTTAT
                                ||||| |||     ||||||||
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                                AAGGG TTC    AAAGAATA
                                  A  _____
GAM2198 WHSC1    3' TTCTCAGGAGCACTTTCTTATC 53137    C G    CA
             A                    TTC C AGGGGT  TTTCTTATCA
                                  ||| | ||||||  ||||||||||
                                  AAG G TCCTCG  AAAGAATAGT
                                    A _    TG
GAM2198 KIAA1018 3' TTCTGAGGGGTCATTCCCT   53138    CC
                                  TTC  GAGGGGTCATTTCTT
                                  |||  ||||||||||||||
                                  AAG  CTCCCCAGTAAGGGA
                                    A_
GAM2198 KIAA1238 3' TTCCAGGGTAGTTTTCTTAT  53139    CG   GTCA
                                  TTCC  AGGG   TTTCTTAT
                                  ||||  ||||   ||||||||
                                  AAGG  TCCC   AAAGAATA
                                    __   ATCA
GAM2198 LOC146512 3' TTCTAAGGGGTCTCTTAT   53140    CC     ATT
                                  TTC  GAGGGGTC  TCTTAT
                                  |||  ||||||||  ||||||
                                  AAG  TTCCCCAG  AGAATA
                                    A_     ___
GAM2198 LOC255671 5' GAGGAGTCACCCTCTGTC   53141        TC  A
                                  GAGGGGTCATT  TT TC
                                  ||||||||||  || ||
                                  CTCCTCAGTGG  GA AG
                                        GA  C
GAM2199 SORCS1   3' TCTTTTGATTTTCCAACACT  53144        A   T
                                  TCTTTTGATTT TCCG ACACT
                                  |||||||||| |||| |||||
                                  AGAAAACTAAA AGGT TGTGA
                                        _   _
GAM2199 PGRMC2   3' TCTTGAGGAGATCTGTACACT 53145      TTT_  C
                                  TTTTGA   ATC GTACACT
                                  ||||||   ||| |||||||
                                  AGAACT   TAG CATGTGA
                                     CCTC  A
GAM2199 LOC130507 3' TCTTTTGACTTTCTGAATACA 53146        A  C__
                                  TCTTTTGATTT TC  GTACA
                                  |||||||||| ||  |||||
                                  AGAAAACTGAA AG  TATGT
                                        _ ACT
GAM2199 LOC137492 3' TCTTTTGATTTATTGTA    53147         CC
                                  TCTTTTGATTTAT  GTA
                                  ||||||||||||  |||
                                  AGAAAACTAAATA  CAT
                                        A_
GAM2200 KAL1     3' AATATCTATTATCAGGT     53150      CAAA
                                  AATATC   GTTATCAGGT
                                  ||||||   ||||||||||
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                                TTATAG   TAATAGTCCA
                                   A___
GAM2200 MEL     3' TCTGAATATACAACGTGTGGGT 53151        C  A TATCA
                                TCTGAATAT CAA GT    GGT
                                ||||||||| ||| ||    |||
                                AGACTTATA GTT CA    CCA
                                     T  G CAC__
GAM2200 MLC1    5' TCTGAATAGTCTGGGTTCAGG 53152       _ CAAA TA
                                TCTGAATA TC   GT TCAGG
                                |||||||| ||   || |||||
                                AGACTTAT AG   CA AGTCC
                                     C ACC_ __
GAM2200 KIAA1854 3' TCTGATATCCAATGCGGG   53153     A     A TATCA
                                TCTGA TATCCAA GT    GG
                                ||||| ||||||| ||    ||
                                AGACT ATAGGTT CG    CC
                                   _     A C_____
GAM2200 SS18L1   3' TGAATATTTAAAATTACC   53154       CC
                                TGAATAT  AAAGTTATC
                                |||||||  |||||||||
                                ACTTATA  TTTTAATGG
                                    AA
GAM2200 LOC120406 3' ATATCCAAGAATCAAGGT   53155       A TT   _
                                ATATCCAA G  ATCA GGT
                                |||||||| |  |||| |||
                                TATAGGTT C  TAGT CCA
                                     _ T_   T
GAM2200 LOC257117 5' TGACTATCCAAAAAAGG    53156    A       TTATC
                                TGA TATCCAAAG    AGG
                                ||| |||||||||    |||
                                ACT ATAGGTTTT    TCC
                                  G       T_____
GAM2200 LOC91947 3' TCTGAATATCCTGAGGTTA   53157         AAA_
                                TCTGAATATCC   GTTA
                                ||||||||||   ||||
                                AGACTTATAGG   CAAT
                                      ACTC
GAM2201 MTNR1A   3' AGATGGGATTTCATCATGTTG 53160   TC      T  _
                                AG  GGGATTTT TCG GTTG
                                ||  |||||||| ||| ||||
                                TC  CCCTAAAG AGT CAAC
                                 TA      T  A
GAM2201 NR1I2    5' GCTGGGATTTCCTAGGGGTTG 53161    C       C__
                                GT GGGATTTTTT  GGTTG
                                || ||||||||||  |||||
                                CG CCCTAAAGGA  CCAAC
                                 A        TCC
GAM2201 RNF12    5' GTCAGGATCCGACTCGGTTG  53162        T_
                                GTCGGGATTT  TTCGGTTG
                                |||||||||  ||||||||
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                                CAGTCCTAGG  GAGCCAAC
                                      CT
GAM2201  DSCAML1   3'  TCTGAGTTGGGATTTTGGTC  53163    AA  C      TTC
                                TC  AGT GGGATTTT   GGTT
                                ||  ||| ||||||||   ||||
                                AG  TCA CCCTAAAA   CCAG
                                 AC   A      ___
GAM2201  FLJ14735  3'  TCAAAGTCTGGGGTTTTTT   53164        _  A
                                TCAAAGTC GGG TTTTTT
                                |||||||| ||| ||||||
                                AGTTTCAG CCC AAAAAA
                                     A   C
GAM2201  PRDM5     3'  AAAGTAAGACTTTTTTTTGGTT 53165      C        C__
              G                   AAAGT GGGATTTTTT   GGTTG
                                |||||| ||||||||||   ||||||
                                TTTCA TTCTGAAAAA   CCAAC
                                  _        AAA
GAM2201  LOC51026  3'  TCAAAATTGGGGTTTCCT    53166       C   A
                                TCAAAGT GGG TTTTTT
                                ||||||| ||| ||||||
                                AGTTTTA CCC AAAGGA
                                     A   C
GAM2202  FLJ20055  3'  TAAGCATAATACATAAT     53169         TAGATG
                                TAAGCATA     ACATAAT
                                ||||||||     |||||||
                                ATTCGTAT     TGTATTA
                                     TA____
GAM2202  LOC133688 3'  GCTATTGATGACATGATG    53170    A  A      A
                                GC TAT GATGACAT ATG
                                || ||| |||||||| |||
                                CG ATA CTACTGTA TAC
                                 _  A       C
GAM2203  BAALC     3'  CAAAACATCCTTTTTCTGT    53173         AAC_
                                TAAAACAT    TTTCTGT
                                ||||||||    |||||||
                                GTTTTGTA    AAAGACA
                                     GGAA
GAM2203  COL17A1   3'  TCTAAAACATTGCAACTACTG  53174          ___   TT
                                TCTAAAACAT   AACT  CTG
                                ||||||||||   ||||  |||
                                AGATTTTGTA   TTGA  GAC
                                      ACG    T_
GAM2203  CRY1      3'  TAAAACATATACTGTCTGT    53175         _  T
                                TAAAACATA ACT TCTGT
                                ||||||||| ||| |||||
                                ATTTTGTAT TGA AGACA
                                      A   C
GAM2203  GRB10     3'  CAAAACTCTTTCTGTA      53176        ATAA
                                TAAAAC    CTTTCTGTA
                                ||||||    |||||||||
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                                GTTTTG   GAAAGACAT
                                   A___
GAM2203 HNRPA1   3' TCTAAAACATGTCTTCT    53177        AAC
                                TCTAAAACAT   TTTCT
                                ||||||||||  |||||
                                AGATTTTGTA   GAAGA
                                     CA_
GAM2203 ICOS     3' TAAGACATAGCTCTCTAT    53178    A    A
                                TAA ACATA CTTTCTGT
                                ||| ||||| ||||||||
                                ATT TGTAT GAGAGATA
                                  C    C
GAM2203 LIF      3' TCTAAGGCAGGAACATCTGTAC 53179      AA  T_   TT
             CA                   TCTAA  CA  AAC  TCTGTACCA
                                |||||  ||  |||  |||||||||
                                AGATT  GT  TTG  AGACATGGT
                                   CC  CC   T_
GAM2203 LPL      3' TCTAAAACATCATTCATAC    53180        AACT   T
                                TCTAAAACAT    TTC GTAC
                                ||||||||||    ||| ||||
                                AGATTTTGTA    AAG TATG
                                     GT__   _
GAM2203 PPEF2    3' TAAAAATAACTTTGCTTTACCA 53181      C      _  G
                                TAAAA ATAACTTT CT TACCA
                                ||||| |||||||| || |||||
                                ATTTT TATTGAAA GA ATGGT
                                   _      C  A
GAM2203 SPF30    3' TCCAAAACATGGTACCACTGC  53182        A__   TT
                                TCTAAAACAT   ACT  CTGT
                                ||||||||||   |||  ||||
                                AGGTTTTGTA   TGG  GACG
                                     CCA   T_
GAM2203 DKFZP434C1715 3' TCTAAACATAACTAGCTG    53183      A     TT
                                TCTAAA CATAACT  CTG
                                ||||||  |||||||  |||
                                AGATTT GTATTGA  GAC
                                   _      TC
GAM2203 KIAA0152  3' TCTAGACATAACTTCAGACC   53184     AA       CTGT
                                TCTA  ACATAACTTT    ACC
                                ||||  ||||||||||    |||
                                AGAT  TGTATTGAAG    TGG
                                  C_         TC__
GAM2203 KIAA0469  3' TCTAGGACAAGACTTCCTA    53185     AA   TA
                                TCTA  ACA  ACTTTCTG
                                ||||  |||  ||||||||
                                AGAT  TGT  TGAAGGAT
                                  CC   TC
GAM2203 KIAA0643  3' TCAGAAACATGAATCTGTACCA 53186    TA     AACTT
                                TC  AAACAT    TCTGTACCA
                                ||  ||||||    |||||||||
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                                AG  TTTGTA    AGACATGGT
                                 TC     CTT__
GAM2203  KIAA0979  3'  TAAAACATGCCTTTGTAC    53187        AA   TC
                                TAAAACAT  CTT  TGTAC
                                ||||||||  |||  |||||
                                ATTTTGTA  GAA  ACATG
                                    CG   __
GAM2203  KIAA1240  3'  TCTAAAACAGGTTTCAGTCCA  53188         TAAC    T  A
                                TCTAAAACA    TTTC GT CCA
                                |||||||||    |||| || |||
                                AGATTTTGT    AAAG CA GGT
                                     CC__    T  _
GAM2203  KIAA1437  3'  TCTAAAACGTGCCTTAGTGTCC 53189         ATAA   TC   A
            A                    TCTAAAAC    CTT  TGT CCA
                                |||||||||    |||  ||| |||
                                AGATTTTG    GAA  ACA GGT
                                     CACG   TC  _
GAM2203  KIAA1789  5'  TCTAAAACAAAACTACTA    53190         T    TT
                                TCTAAAACA AACT  CTG
                                |||||||||| ||||  |||
                                AGATTTTGT TTGA  GAT
                                     T    T_
GAM2203  NDP52     3'  TCTAGGGCATAACTCCCAACCA 53191      AAA      TT TGT
                                TCTA   CATAACT  C   ACCA
                                ||||   |||||||  |   ||||
                                AGAT   GTATTGA  G   TGGT
                                  CCC      GG T__
GAM2203  PCDH20    3'  TAAAACATTTCTCTGT      53192         AAC
                                TAAAACAT   TTTCTGT
                                ||||||||   |||||||
                                ATTTTGTA   AGAGACA
                                     A__
GAM2203  SEC22A    3'  TAAAACATAAACTTTCCA    53193          _
                                TAAAACATAA CTTTCTG
                                |||||||||| |||||||
                                ATTTTGTATT GAAAGGT
                                      T
GAM2203  SOX6      3'  TCTAAAACAGTAACTTAAACC  53194          _     TCTGT
                                TCTAAAACA TAACTT     ACC
                                |||||||||  ||||||     |||
                                AGATTTTGT ATTGAA     TGG
                                     C     TT____
GAM2203  SPTLC2    3'  TCTTGAAATAACTTTGTACCA  53195     AA  C      TC
                                TCT  AA ATAACTT  TGTACCA
                                |||  ||  |||||||  |||||||
                                AGA  TT TATTGAA  ACATGGT
                                  AC  _      __
GAM2203  TSGA14    3'  TCTAAAACAGAACTGGGCTG   53196         T    TT_
                                TCTAAAACA AACT   CTG
                                |||||||||  ||||   |||
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                                AGATTTTGT TTGA   GAC
                                     C    CCC
GAM2203  LOC129831 3'  CTAAGACATCTTTCTGT     53197      A    AA
                                CTAA ACAT  CTTTCTGT
                                |||| ||||  ||||||||
                                GATT TGTA  GAAAGACA
                                  C    __
GAM2203  LOC142973 3'  TCTAAAACATGTCTTCT     53177          AAC
                                TCTAAAACAT   TTTCT
                                ||||||||||   |||||
                                AGATTTTGTA   GAAGA
                                     CA_
GAM2203  LOC144983 3'  TCTAAAACATGTCTTCT     53177          AAC
                                TCTAAAACAT   TTTCT
                                ||||||||||   |||||
                                AGATTTTGTA   GAAGA
                                     CA_
GAM2203  LOC147398 3'  TCTAAAACATGTCTTCT     53177          AAC
                                TCTAAAACAT   TTTCT
                                ||||||||||   |||||
                                AGATTTTGTA   GAAGA
                                     CA_
GAM2203  LOC147852 3'  TCTAAAACATGTCTTCT     53177          AAC
                                TCTAAAACAT   TTTCT
                                ||||||||||   |||||
                                AGATTTTGTA   GAAGA
                                     CA_
GAM2203  LOC149332 5'  TCTAGTACATGTCCTGTAC    53198      AA    AACT
                                TCTA  ACAT    TTCTGTAC
                                ||||  ||||    ||||||||
                                AGAT  TGTA    AGGACATG
                                  CA    C___
GAM2203  LOC151249 3'  TCTAAAACATGTCTTCT     53177          AAC
                                TCTAAAACAT   TTTCT
                                ||||||||||   |||||
                                AGATTTTGTA   GAAGA
                                     CA_
GAM2203  LOC153817 3'  TCTAAAACATGTCTTCT     53177          AAC
                                TCTAAAACAT   TTTCT
                                ||||||||||   |||||
                                AGATTTTGTA   GAAGA
                                     CA_
GAM2203  LOC201562 3'  CTGAAACATAACTATACTG    53199    A        TT_
                                CT AAACATAACT   CTG
                                || ||||||||||   |||
                                GA TTTGTATTGA   GAC
                                 C         TAT
GAM2203  LOC220840 3'  TCTAAAACATGTCTTCT     53177          AAC
                                TCTAAAACAT   TTTCT
                                ||||||||||   |||||
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                                AGATTTTGTA  GAAGA
                                     CA_
GAM2204  LOC132332 3'  TAAAAAATATAAGCCACCTAAT 53202          ATAT
              AT                  TAAAAAATATAA   TCTAATAT
                                  ||||||||||||   ||||||||
                                  ATTTTTTATATT   GGATTATA
                                       CGGT
GAM2205  CAMP-GEFII 3'  AGTTAAAATTTTATCCAA    53205          _
                                  AGTTAAAATTTTA CCAG
                                  |||||||||||| ||||
                                  TCAATTTTAAAAT GGTT
                                        A
GAM2205  KCNS1    3'  TAAGTCAGAAGCCAGTATA   53206       AAATTTTA
                                  TAAGTTA      CCAGTATA
                                  |||||||      ||||||||
                                  ATTCAGT      GGTCATAT
                                     CTTC____
GAM2205  KIAA1257  3'  AGTTATGATTTACCAGTAT   53207      AAAT
                                  AGTTA   TTTACCAGTAT
                                  |||||   ||||||||||
                                  TCAAT   AAATGGTCATA
                                    ACT_
GAM2205  LOC151742 3'  TAAATTAAAAGAGACCAGT   53208         TTTT
                                  TAAGTTAAAA   ACCAGT
                                  |||||||||   ||||||
                                  ATTTAATTTT   TGGTCA
                                       CTC_
GAM2206  WHN      3'  TAATTTGTGTGTGTGCACGAGG 53211          T    TTT_
              GCT                   TAATTTGTGTGT TGCGC   GCT
                                  ||||||||||| |||||   |||
                                  ATTAAACACACA ACGTG   CGA
                                       C    CTCC
GAM2206  HSA250303 3'  TAATTTGTGTTTTTGTTTTTG  53212         G   CGC
                                  TAATTTGTGT TTTG  TTTG
                                  |||||||||| ||||  ||||
                                  ATTAAACACA AAAC  AAAC
                                       A   AA_
GAM2206  IMP-2    3'  TTTGTGTGTTTCGCTTT     53213          G
                                  TTTGTGTGTTT CGCTTT
                                  |||||||||| ||||||
                                  AAACACACAAA GCGAAA
                                             _
GAM2206  KIAA0429  5'  ATTTGTGTGTCTTTTGC     53214          GCGC
                                  ATTTGTGTGTTT   TTTGC
                                  ||||||||||||   |||||
                                  TAAACACACAGA   AAACG
                                             ____
GAM2206  KIAA1143  3'  TAATTTGTATGGCTTT      53215          TTTGC
                                  TAATTTGTGTG    GCTTT
                                  ||||||||||     |||||
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                                ATTAAACATAC    CGAAA
                                       _____
GAM2206  LOC152897 3'  TAATTTGTGTTTTGCGCTTT  53216         G
                                TAATTTGTGT TTTGCGCTTT
                                |||||||||| ||||||||||
                                ATTAAACACA AAACGCGAAA
                                         _
GAM2206  LOC257054 5'  TTTGCGTGGCTTTTGC     53217        TTT  GC
                                TTTGTGTG   GC  TTTGC
                                ||||||||   ||  |||||
                                AAACGCAC   CG  AAACG
                                     ___  A_
GAM2207  BAT1     5'  CAAGAGCGCAGGCGCAAGGGAC 53220     CA        ___
              CG                  CAAG  CGCAGGTGCAA   ACCG
                                ||||  ||||||||||  ||||
                                GTTC  GCGTCCGCGTT   TGGC
                                  TC         CCC
GAM2207  BAT1     5'  CAAGAGCGCAGGCGCAAGGGAC 53220     CA        ___
              CG                  CAAG  CGCAGGTGCAA   ACCG
                                ||||  ||||||||||  ||||
                                GTTC  GCGTCCGCGTT   TGGC
                                  TC         CCC
GAM2207  CTH      5'  TAAAGCACGCAGGTAGAGCCGA 53221   C         CAAA
                                A AAGCACGCAGGTG    CCGA
                                | ||||||||||||    ||||
                                A TTCGTGCGTCCAT    GGCT
                                 T          CTC_
GAM2207  LASS1    3'  CACGCAGCAGGGCAGGTCG   53222    A  C    T  AAC
                                CA GCA GCAGG GCA   CG
                                || ||| ||||| |||   ||
                                GT CGT CGTCC CGT   GC
                                 G  _    _  CCA
GAM2207  BCAA     3'  AAGCACACACTACAAGACTGA  53223        GG    _  C
                                AAGCACGCA  TGCAA AC GA
                                |||||||||  ||||| || ||
                                TTCGTGTGT  ATGTT TG CT
                                     G_    C  A
GAM2207  DKFZp761C121 3'  AAGTACCAATGCAAACTGA   53224    C  G  G     C
                                AAG AC CAG TGCAAAC GA
                                ||| || ||| ||||||| ||
                                TTC TG GTT ACGTTTG CT
                                  A  _  _      A
GAM2207  FLJ10661  3'  TACAAACACAGGCTGTGGGC   53225        __  A__  T
                                TACAAGCAC  GC   GG GC
                                |||||||||  ||   || ||
                                ATGTTTGTG  CG   CC CG
                                     TC  ACA  _
GAM2207  FLJ14146  3'  CAAACACGTGGCTGGGCCGA   53226        CA   GCAAA
                                CAAGCACG  GGT    CCGA
                                ||||||||  |||    ||||
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                                GTTTGTGC  CCG    GGCT
                                    A_   ACCC_
GAM2207  H2AFJ    3'  TACAAGTACTAACAGAAGC   53227       C  __    T
                                TACAAG AC  GCAGG GC
                                |||||| ||  ||||| ||
                                ATGTTC TG  TGTCT CG
                                   A  AT    T
GAM2207  HTMP10   3'  TACAAGCACCAGGATGAC    53228         G   _ _
                                TACAAGCAC CAGG TG C
                                ||||||||| |||| || |
                                ATGTTCGTG GTCC AC G
                                     _   T  T
GAM2207  MCJ      5'  CAAGCACGGGGTCACACTCCGA 53229        CA  _  AA
                                CAAGCACG  GGT GCA  CCGA
                                ||||||||  ||| |||  ||||
                                GTTCGTGC  CCA TGT  GGCT
                                    C_   G   GA
GAM2207  MGC10854 5'  CAGGCACGAAGCGGGCCG    53230    A    C    CAAA
                                CA GCACG AGGTG    CCG
                                || ||||| |||||    |||
                                GT CGTGC TTCGC    GGC
                                 C     _    CC__
GAM2207  MGC10992 3'  AGCGTCAGGTGCAGGCCGA    53231     ACG       AA
                                AGC   CAGGTGCA  CCGA
                                |||   ||||||||  ||||
                                TCG   GTCCACGT  GGCT
                                  CA_       CC
GAM2207  MGC16279 3'  TACAAACACAGGCTGTGGGC   53225         __  A__  T
                                TACAAGCAC  GC   GG GC
                                |||||||||  ||   || ||
                                ATGTTTGTG  CG   CC CG
                                     TC  ACA  _
GAM2207  SLC26A9  5'  TACAAGCAGTGGGTGAGCAAAG 53232        CGCA  __    _
            CCG                   TACAAGCA    GGT  GCAAA CCG
                                ||||||||    |||  ||||| |||
                                ATGTTCGT    CCA  CGTTT GGC
                                    CAC_   CT    C
GAM2207  SLC26A9  5'  TACAAGCAGTGGGTGAGCAAAG 53232        CGCA  __    _
            CCG                   TACAAGCA    GGT  GCAAA CCG
                                ||||||||    |||  ||||| |||
                                ATGTTCGT    CCA  CGTTT GGC
                                    CAC_   CT    C
GAM2207  TPARL    5'  CAAGCAGCGGGCGCCGAGCCG  53233       C  A    AAA_
                                CAAGCA GC GGTGC    CCG
                                |||||| || |||||    |||
                                GTTCGT CG CCGCG    GGC
                                   _ C    GCTC
GAM2207  LOC151781 3'  TACAAACACAGGCTGTGGGC   53225         __  A__  T
                                TACAAGCAC  GC   GG GC
                                |||||||||  ||   || ||
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                                ATGTTTGTG  CG   CC CG
                                     TC  ACA  _
GAM2207  LOC158490 3'  TACAAACACAGGCTGTGGGC   53225        __  A__  T
                                TACAAGCAC  GC   GG GC
                                |||||||||  ||   || ||
                                ATGTTTGTG  CG   CC CG
                                     TC  ACA  _
GAM2207  LOC196484 5'  TACAAACACAGGCTGTGGGC   53225        __  A__  T
                                TACAAGCAC  GC   GG GC
                                |||||||||  ||   || ||
                                ATGTTTGTG  CG   CC CG
                                     TC  ACA  _
GAM2207  LOC220073 5'  TACAAACACAGGCTGTGGGC   53225        __  A__  T
                                TACAAGCAC  GC   GG GC
                                |||||||||  ||   || ||
                                ATGTTTGTG  CG   CC CG
                                     TC  ACA  _
GAM2207  LOC220830 3'  TACAGGCACGGGGCGGCAAGGG 53234      A    CA   _  A__
           CCGA                    TACA GCACG  GGTG CAA   CCGA
                                |||| |||||  |||| |||   ||||
                                ATGT CGTGC  CCGC GTT   GGCT
                                  C    C_   C   CCC
GAM2207  LOC253070 5'  CAAGCACTGCGCGCGGGGGCCG 53235        _  AG   AAA__
                                CAAGCAC GC  GTGC    CCG
                                ||||||| ||  ||||    |||
                                GTTCGTG CG  CGCG    GGC
                                    A  __   CCCCC
GAM2207  LOC256379 3'  TACAGGCACGGGGCGGCAAGGG 53234      A    CA   _  A__
           CCGA                    TACA GCACG  GGTG CAA   CCGA
                                |||| |||||  |||| |||   ||||
                                ATGT CGTGC  CCGC GTT   GGCT
                                  C    C_   C   CCC
GAM2207  LOC90233  3'  TACAAGCATCATGTGAGACCGA 53236        CG  G   CAA
                                TACAAGCA  CA GTG   ACCGA
                                ||||||||  || |||   |||||
                                ATGTTCGT  GT CAC   TGGCT
                                    A_  A   TC_
GAM2207  LOC91069  3'  TACAAACACAGGCTGTGGGC   53225        __  A__  T
                                TACAAGCAC  GC   GG GC
                                |||||||||  ||   || ||
                                ATGTTTGTG  CG   CC CG
                                     TC  ACA  _
GAM2208  CASP10    3'  AACAAATTTACTGTACATG    53239        G
                                AACAAATT TATTGTACATG
                                |||||||| ||||||||||
                                TTGTTTAA ATGACATGTAC
                                         _
GAM2208  CASP10    3'  AACAAATTTACTGTACATG    53239        G
                                AACAAATT TATTGTACATG
                                |||||||| ||||||||||
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                                TTGTTTAA ATGACATGTAC
                                        _
GAM2208 KLRD1    3' TTAAAACACATTGTTTCACATA 53240        A    AT__
           CATG                  TTAAAACA ATTGT    TGTACATG
                                 |||||||| |||||    ||||||||
                                 AATTTTGT TAACA    GTATGTAC
                                      G    AAGT
GAM2208 KLRD1    3' TTAAAACACATTGTTTCACATA 53240        A    AT__
           CATG                  TTAAAACA ATTGT    TGTACATG
                                 |||||||| |||||    ||||||||
                                 AATTTTGT TAACA    GTATGTAC
                                      G    AAGT
GAM2208 SLC35A1  3' CTAGGACAAAATACTGTACATG 53241    AA    TT
                                 TTA  ACAAA  GTATTGTACATG
                                 |||  |||||  ||||||||||||
                                 GAT  TGTTT  TATGACATGTAC
                                   CC    __
GAM2208 FLJ21777 3' TTAAAACAAGATTAGCACTGTA 53242        _  _
                                 TTAAAACAA ATT GTATTGTA
                                 |||||||| ||| ||||||||
                                 AATTTTGTT TAA CGTGACAT
                                       C   T
GAM2208 RAB33B   3' TTAAAACAAATTGTTACA    53243           ATTG
                                 TTAAAACAAATTGT    TACA
                                 ||||||||||||||    ||||
                                 AATTTTGTTTAACA    ATGT
                                           _____
GAM2208 LOC253573 3' TTAAAACAAAATTGTAACCAGC 53244         _    TTGTA_
           CATG                  TTAAAACAAA TTGTA     CATG
                                 ||||||||||| |||||     ||||
                                 AATTTTGTTT AACAT     GTAC
                                       T    TGGTCG
GAM2209 MTR      3' GATGAGTGTATATTTTGCA   53247    C  C   AC
                                 GAT GA GTG  TATTTTGCA
                                 ||| || |||  |||||||||
                                 CTA CT CAC  ATAAAACGT
                                   _ _   AT
GAM2209 Nrap     3' CAAGATTGGGTGACTACC    53248       CGAC
                                 CAAGAT    GTGACTATT
                                 ||||||    |||||||||
                                 GTTCTA    CACTGATGG
                                     ACC_
GAM2209 ONECUT1  5' CAACATCGATGTGGCCAGGCA 53249    G    C   A   TTTT
                                 CAA ATCGA GTG CTA    GCA
                                 ||| ||||| ||| |||    |||
                                 GTT TAGCT CAC GGT    CGT
                                   G    A   C   C___
GAM2209 PHKG2    5' AGGGTCGACGCGAGCTGC    53250    A_       CTATT
                                 AG  TCGACGTGA     TTGC
                                 ||  |||||||||     ||||
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                                TC  AGCTGCGCT    GACG
                                 CC       C____
GAM2209  PIGR     3'  CAGGATCGACATGATTCTG   53251    A        CTA
                                CA GATCGACGTGA   TTTTG
                                || ||||||||||   |||||
                                GT CTAGCTGTACT   AAGAC
                                 C         ___
GAM2209  RRM1     3'  CAAGATGACTTATTTTGC    53252    C    _
                                CGA GTGACT ATTTTGC
                                ||| |||||| |||||||
                                GTT TACTGA TAAAACG
                                  C     A
GAM2209  SPTBN4   3'  GGAGATCGACGTTTTG     53253   A       GACTAT
                                C AGATCGACGT     TTTG
                                | ||||||||||     ||||
                                C TCTAGCTGCA     AAAC
                                 C        _______
GAM2209  C15orf5  5'  AAATCAATGGTTATTTTGCA  53254      AC   AC
                                AGATCG  GTG  TATTTTGCA
                                ||||||  |||  |||||||||
                                TTTAGT  TAC  ATAAAACGT
                                   __  CA
GAM2209  C5orf3   3'  CAAAATTGATAACATTTTGCA  53255      C  CG    T
                                CAAGAT GA  TGAC ATTTTGCA
                                |||||| ||  |||| ||||||||
                                GTTTTA CT  ATTG TAAAACGT
                                   A  __   _
GAM2209  DKFZp761K1423 3'  AAATCCTTCACTATTTTGC   53256      GACGTG
                                AGATC     ACTATTTTGC
                                |||||     ||||||||||
                                TTTAG     TGATAAAACG
                                  GAAG__
GAM2209  KIAA1486  3'  AAATCAACTATTTTG      53257      GACGT
                                AGATC    GACTATTTTG
                                |||||    ||||||||||
                                TTTAG    TTGATAAAAC
                                  _____
GAM2209  SLC2A13  3'  AAGATCTGGCACTATTTTGCA  53258      GAC  G
                                AAGATC   GT ACTATTTTGCA
                                ||||||   || ||||||||||
                                TTCTAG   CG TGATAAAACGT
                                   AC_  _
GAM2210  BCAS1    5'  TGGGAGTATCTTCAGT      53261          G   A
                                TGGGAGTATCT TCA GT
                                |||||||||| ||| ||
                                ACCCTCATAGA AGT CA
                                     _  _
GAM2210  IRTA1    3'  TGGGATATCTGTCACCTTAAAT 53262      G       AGT___
            ATTC                   TGGGA TATCTGTCA     ATATTC
                                |||||  |||||||||     ||||||
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                                ACCCT ATAGACAGT     TATAAG
                                  _       GGAATT
GAM2210 ARHGAP5  3' GAAATATGTCAAGTGTATT   53263       TC      A
                                GGAGTA  TGTCAAGT TATT
                                ||||||  |||||||| ||||
                                CTTTAT  ACAGTTCA ATAA
                                  __       C
GAM2210 KIAA0781 3' GGAGTCCTGAGTATATT     53264      A   TCA
                                GGAGT TCTG   AGTATATT
                                ||||| ||||   ||||||||
                                CCTCA GGAC   TCATATAA
                                  _   ____
GAM2210 LOC200609 5' TGGGATATACTTAAGTATATTC 53265      GTAT  GTC
                                TGGGA   CT   AAGTATATTC
                                |||||   ||   ||||||||||
                                ACCCT   GA   TTCATATAAG
                                   ATAT  A__
GAM2210 LOC221399 5' TGGAGAGTTTTGAGTATATTC  53266    _   ATC  TCA
                                TGG GAGT   TG   AGTATATTC
                                ||| ||||   ||   |||||||||
                                ACC CTCA   AC   TCATATAAG
                                  T   AA_ ____
GAM2211 TRRAP    3' TTTAAATTAGGAAGGTA     53269         AC
                                TTTAAATTAG  AAGGTG
                                ||||||||||  ||||||
                                AAATTTAATC  TTCCAT
                                      C_
GAM2211 MGC15435 5' TTTAAATTAGACAGTGGGTA   53270          A__
                                TTTAAATTAGACA   GGTG
                                ||||||||||||   ||||
                                AAATTTAATCTGT   CCAT
                                        CAC
GAM2211 POT1     3' TTTAAATTTGACAAACACTGTC 53271        A    GGT   _
                                TTTAAATT GACAA   GCGC GTC
                                |||||||| |||||   |||| |||
                                AAATTTAA CTGTT   TGTG CAG
                                     A    ___    A
GAM2211 WBP4     3' TTTAAATTGAGTAAGGTAAGC  53272        A  C_     C
                                TTTAAATT GA  AAGGTG GC
                                |||||||| ||  |||||| ||
                                AAATTTAA CT  TTCCAT CG
                                     _ CA     T
GAM2212 AMFR     3' GACCGCTGTGTAGGAAAA    53275           AGTTA
                                GACCGTTGTGTGG    GAAAA
                                ||||||||||||    |||||
                                CTGGCGACACATC    CTTTT
                                                 _____
GAM2212 RPL22    5' GCGGCAGCGGAGTTAGAAA   53276    T  _
                                GT GT GTGGAGTTAGAAA
                                || || ||||||||||||
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                                CG CG CGCCTCAATCTTT
                                 C  T
GAM2212  SLC25A17  5'  CGCAGCCAGTGGAGTTAGGAAA 53277     T __        A
              G                  CGT GT  GTGGAGTTAG AAAG
                                 ||| ||  |||||||||| ||||
                                 GCG CG  CACCTCAATC TTTC
                                   T  GT         C
GAM2212  ST7      3'  GACTGTGCAAGAGTTGGGAGA  53278     CGT     _    ___
                                 GAC   TGTGTG GAGTT   AGA
                                 |||   |||||| |||||   |||
                                 CTG   ACACGT CTCAA   TCT
                                   ___     T    CCC
GAM2212  AP3M2    3'  CTGTTTTGGGTTAGAAAAG   53279      G_   A
                                 TTGT  TGG GTTAGAAAAG
                                 ||||  ||| ||||||||||
                                 GACA  ACC CAATCTTTTC
                                   AA  _
GAM2212  C1orf22   3'  GTTGTTTTGATAACTTAGAAAA 53280       GTG___  G
              G                  GTTGT     GA TTAGAAAAG
                                 |||||      || |||||||||
                                 CAACA      TT AATCTTTTC
                                    AAACTA  G
GAM2212  D2S448    3'  GCTGTTGGAGCAGTTAGAAAAG 53281       G     ___
                                 GTTGT TGGAGT   TAGAAAAG
                                 ||||| ||||||   ||||||||
                                 CGACA ACCTCG   ATCTTTTC
                                    _      TCA
GAM2212  FKBP5    3'  GCTGTGTGTGGTAGAAA     53282         GA  T
                                 GTTGTGTG  GT AGAAA
                                 ||||||||  || |||||
                                 CGACACAC  CA TCTTT
                                       AC  _
GAM2212  FLJ14950  3'  GACTGTTGTGTGGGCAG     53283     C        A  T
                                 GAC GTTGTGTGG GT AG
                                 ||| |||||||| || ||
                                 CTG CAACACACC CG TC
                                   A        _  _
GAM2212  KIAA0792  3'  GTTGTGTGTGTGCTCAGAA    53284         GA_ _
                                 GTTGTGTG   G TTAGAA
                                 ||||||||   | ||||||
                                 CAACACAC   C AGTCTT
                                       ACA G
GAM2212  KIAA1881  5'  CCGTGTGTGGTGGCCAAAA    53285      T     A_
                                 CCGT GTGTGG  GTTAGAA
                                 |||| ||||||  |||||||
                                 GGCA CACACC  CGGTTTT
                                    _      AC
GAM2212  LBP-9    3'  GACTGCAGGAGTTAGGAAAG   53286     CGT    T       A
                                 GAC   TGTG GGAGTTAG AAAG
                                 |||   |||| |||||||| ||||
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                                CTG   ACGT CCTCAATC TTTC
                                  ___   _      C
GAM2212  NXN      3'  GACTGTGTTGCTTAGAAAA   53287    CGT    GGAG
                                GAC   TGTGT   TTAGAAAA
                                |||   |||||   ||||||||
                                CTG   ACACA   AATCTTTT
                                  ___    ACG_
GAM2212  PHF3     3'  GACCGTTGGTATGAAGAAG   53288       _     TT
                                GACCGTTG TGTGGAG  AG
                                |||||||| |||||||  ||
                                CTGGCAAC ATACTTC  TC
                                     C      T_
GAM2212  PPP1R9A  3'  GTTGGTAAGTTAGAGAAG   53289     T  G     A
                                GTTG GTG AGTTAGA AAG
                                |||| ||| ||||||| |||
                                CAAC CAT TCAATCT TTC
                                  _  _      C
GAM2212  LOC145725 5'  GCTGTTGACCAAGTTAGA    53290      _ _ G
                                GTTGT G T GAGTTAGA
                                ||||| | | ||||||||
                                CGACA C G TTCAATCT
                                   A T G
GAM2212  LOC145732 5'  GCTGTTGACCAAGTTAGA    53290      _ _ G
                                GTTGT G T GAGTTAGA
                                ||||| | | ||||||||
                                CGACA C G TTCAATCT
                                   A T G
GAM2212  LOC148638 3'  CCATTGTGTGCGTGGAAA    53291         GA  TA
                                CCGTTGTGTG  GT  GAAA
                                ||||||||||  ||  ||||
                                GGTAACACAC  CA  CTTT
                                      G_  C_
GAM2212  LOC151610 3'  GTTGTGTGCATGCTAGGAAAG  53292        GA_    A
                                GTTGTGTG   GTTAG AAAG
                                ||||||||   ||||| ||||
                                CAACACAC   CGATC TTTC
                                     GTA    C
GAM2212  LOC170347 5'  CGCTAATGGAGTTAGAA     53293      T
                                CGTTG GTGGAGTTAGAA
                                ||||| ||||||||||||
                                GCGAT TACCTCAATCTT
                                  _
GAM2212  LOC170353 5'  CGCTAATGGAGTTAGAA     53293      T
                                CGTTG GTGGAGTTAGAA
                                ||||| ||||||||||||
                                GCGAT TACCTCAATCTT
                                  _
GAM2212  LOC196337 5'  TTGTGTGGGGTCCATAAAG   53294        A   AGA
                                TTGTGTGG GTT   AAAG
                                |||||||| |||   ||||
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                                AACACACC CAG   TTTC
                                    C   GTA
GAM2212  LOC196957 5'  GCTGTTGACCAAGTTAGA    53290      _ _ G
                                GTTGT G T GAGTTAGA
                                |||||| | | ||||||||
                                CGACA C G TTCAATCT
                                   A T G
GAM2212  LOC196961 5'  GCTGTTGACCAAGTTAGA    53290      _ _ G
                                GTTGT G T GAGTTAGA
                                |||||| | | ||||||||
                                CGACA C G TTCAATCT
                                   A T G
GAM2212  LOC197138 5'  GCTGTTGACCAAGTTAGA    53290      _ _ G
                                GTTGT G T GAGTTAGA
                                |||||| | | ||||||||
                                CGACA C G TTCAATCT
                                   A T G
GAM2212  LOC51301  3'  GACTGTTATGTGGAGAACTTAA 53295     C        ___
             A                   GAC GTTGTGTGGAG   TTAGA
                                ||| ||||||||||   |||||
                                CTG CAATACACCTC   AATTT
                                  A         TTG
GAM2212  LOC91252  3'  GACTGTGTGTGTGCTGA     53296     C  T    GA   A
                                GAC GT GTGTG  GTT GA
                                ||| || |||||  ||| ||
                                CTG CA CACAC  CGA CT
                                  A  _    A_  _
GAM2213  FLJ20373  3'  TTAAGCCCAACAATGGA     53299      C    GTAG
                                TTAA GCCT    AACAATGGA
                                |||| ||||   |||||||||
                                AATT CGGG    TTGTTACCT
                                  _   _____
GAM2213  LOC145609 5'  CCTCAAGACAATGGACT     53300     GT   A
                                CCT  AGA CAATGGACT
                                |||  ||| |||||||||
                                GGA  TCT GTTACCTGA
                                  GT  _
GAM2214  BCL2L12   5'  TGCAGGAGGTAGAGGCTTA   53303      AA  A
                                TGCA  AG TAGAGGCTTA
                                ||||  || ||||||||||
                                ACGT  TC ATCTCCGAAT
                                   CC  C
GAM2214  KIAA0258  3'  TGTGAAAGATAAGGCTT     53304    CA     A
                                TG  AAAGAT GAGGCTT
                                ||  |||||| |||||||
                                AC  TTTCTA TTCCGAA
                                  AC     _
GAM2214  KIAA1145  3'  TGCAAAATATTGCACTTAATTT 53305        GATAGAG
             G                   TGCAAAA      GCTTAATTTG
                                |||||||      ||||||||||
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                                ACGTTTT      TGAATTAAAC
                                    ATAACG_
GAM2214  PIB5PA    3'  TGCAAAAGATTGAGGCAGAAT  53306          A    TT
                                TGCAAAAGAT GAGGC  AAT
                                |||||||||| |||||  |||
                                ACGTTTTCTA CTCCG  TTA
                                      A    TC
GAM2214  SLC26A10  5'  TGCAGGAGAAGAGGCCT     53307      AA   T
                                TGCA  AGA AGAGGCTT
                                ||||  ||| ||||||||
                                ACGT  TCT TCTCCGGA
                                  CC  _
GAM2214  LOC121441 3'  TGCAAAAGATATCATGTAATTT 53308           GAGGCT
           G                     TGCAAAAGATA     TAATTTG
                                ||||||||||      |||||||
                                ACGTTTTCTAT     ATTAAAC
                                      AGTAC_
GAM2214  LOC92181  3'  TGCAAAAGGCTCTTAATTTG   53309         ATAGAGG
                                TGCAAAAG      CTTAATTTG
                                ||||||||      |||||||||
                                ACGTTTTC      GAATTAAAC
                                    CGA____
GAM2215  GNAI1     3'  TTATGTTATTTCCAAAGCCATC 53312      A    A      T
                                TTAT TTATT TCCAAAG CTATC
                                |||| ||||| ||||||| |||||
                                AATA AATAA AGGTTTC GGTAG
                                  C    _     _
GAM2215  DKFZp434K2435 3'  TTATCTCCAAGTCTATC     53313      A    A
                                TTATT TCCAA GTCTATC
                                ||||| ||||| |||||||
                                AATAG AGGTT CAGATAG
                                   _    _
GAM2215  FLJ13194  3'  TTATATATCAAAGTCTAT    53314      _   C
                                TTAT TATC AAAGTCTAT
                                |||| |||| |||||||||
                                AATA ATAG TTTCAGATA
                                  T   _
GAM2215  FLJ22344  3'  TTATATTATTATCCACAGC    53315            A
                                TTATATTATTATCCA AGT
                                |||||||||||||| |||
                                AATATAATAATAGGT TCG
                                        G
GAM2215  MGC21854  3'  CTAATATCCAAAGTTTATC    53316     T        C
                                TTA TATCCAAAGT TATC
                                ||| |||||||||| ||||
                                GAT ATAGGTTTCA ATAG
                                  T        A
GAM2215  LOC222252 5'  TTATATTCTTATCCAAACTGTC 53317        A       __
                                TTATATT TTATCCAAA  GTC
                                ||||||| |||||||||  |||
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                                AATATAA AATAGGTTT  CAG
                                    G        GA
GAM2216  FGF23    3'  GTTACATTTTTATAAATATCTA 53320    GT__
                                GT    TTTTTATAAATATCTA
                                ||    ||||||||||||||||
                                CA    AAAAATATTTATAGAT
                                 ATGT
GAM2216  GASC1    3'  ATATATTTTATAAATATCTA   53321      T
                                GTGT TTTTATAAATATCTA
                                |||| ||||||||||||||
                                TATA AAAATATTTATAGAT
                                  T
GAM2216  MYBL1    3'  GTGTACGTATAAATATCT    53322      TTTT
                                GTGT    TATAAATATCT
                                ||||    ||||||||||
                                CACA    ATATTTATAGA
                                  TGC_
GAM2216  PRO1770  5'  TAGTGTAATATAAATAT     53323       TTTT
                                TAGTGT    TATAAATAT
                                ||||||    |||||||||
                                ATCACA    ATATTTATA
                                    TT__
GAM2216  TJP2     3'  ATAGTGTTTTCCTCAAGTATCT 53324          TA   A
                                ATAGTGTTTTT  TAA TATCT
                                ||||||||||  ||| |||||
                                TATCACAAAAG  GTT ATAGA
                                      GA   C
GAM2216  LOC150150 3'  TATTCTTTATAAGTATCTA    53325           A
                                TGTTTTTTATAA TATCTA
                                |||||||||||| ||||||
                                ATAAGAAATATT ATAGAT
                                      C
GAM2216  LOC91355  3'  TATAGTGCTTTAAGAAAAATGT 53326          TTAT_   A
            CT                    TATAGTGTTTT    AAAT TCT
                                ||||||||||    |||| |||
                                ATATCACGAAA    TTTA AGA
                                      TTCTT    C
GAM2217  CARPX    3'  TGATGGAGGTTGTAAGAGT    53329        TC_   AA
                                TGATGGAG   GTAA  AGT
                                ||||||||   ||||  |||
                                ACTACCTC   CATT  TCA
                                     CAA    C_
GAM2217  DAAM2    3'  TGATGGAGTTTTAGAAAAATTT 7469          CG  _
            T                    TGATGGAGT  TA AAAAGTTTT
                                |||||||||  || |||||||||
                                ACTACCTCA  AT TTTTTAAAA
                                      AA  C
GAM2217  TBXA2R   5'  ATGGACCTAAGAAGTTTTAT   53330      G  G   A
                                ATGGA TC TAA AAGTTTTAT
                                ||||| || ||| |||||||||
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                                TACCT GG ATT TTCAAAATA
                                  _ _  C
GAM2217 KIAA1979 3' TGATGGAGTCTCTTTTTA    53331         GTAAAAAG
                                TGATGGAGTC      TTTTA
                                ||||||||||      |||||
                                ACTACCTCAG      AAAAT
                                     AGA_____
GAM2217 LOC222671 5' TGGCGGAGTCGTAGAAGC    7472     A        AA
                                TG TGGAGTCGTA  AAGT
                                || ||||||||||  ||||
                                AC GCCTCAGCAT  TTCG
                                 C         C_
GAM2217 LOC257615 5' TGGCGGAGTCGTAGAAGC    7472     A        AA
                                TG TGGAGTCGTA  AAGT
                                || ||||||||||  ||||
                                AC GCCTCAGCAT  TTCG
                                 C         C_
GAM2218 PCTK3    3' TATATTATCTGTCTCTG     53334          C   C
                                TATATTATCT GTC TTG
                                |||||||||| ||| |||
                                ATATAATAGA CAG GAC
                                      _  A
GAM2218 FLJ20457 3' TTATCCCTTGGTTTA      53335       TCGT
                                TTATC   CCTTGGTTTA
                                |||||   ||||||||||
                                AATAG   GGAACCAAAT
                                  _____
GAM2218 KIAA0368 3' ATCTTGTCCTAATCTAC     53336      C    T
                                ATCT GTCCT GGTTTAC
                                |||| ||||| |||||||
                                TAGA CAGGA TTAGATG
                                  A    _
GAM2218 KIAA0711 3' TATTTTATCTCGTTCCAGATT  53337     A       _  TT
                                TAT TTATCTCGT CC  GGTT
                                ||| ||||||||| ||  ||||
                                ATA AATAGAGCA GG  CTAA
                                  A       A  T_
GAM2219 PPP4R1   3' GCATTTATTGGTAGACAT    53340          _
                                GCATTTATTGG AGACGT
                                |||||||||| ||||||
                                CGTAAATAACC TCTGTA
                                       A
GAM2219 RAB3A    3' TCGCTTTATTGGGTGCGT    53341      A      AGA
                                TCGC TTTATTGG   CGT
                                |||| ||||||||   |||
                                AGCG AAATAACC   GCA
                                  _       CAC
GAM2219 DKFZP761F241 3' TCGTATTTATTGGAAAAGCA  53342     C         C
                                TCG ATTTATTGGAGA GTA
                                ||| |||||||||||| |||
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                                AGC TAAATAACCTTT CGT
                                  A         T
GAM2219 ENDOFIN  3' CATTTATTGCTACATAA    53343       GAG
                                CATTTATTG  ACGTAA
                                |||||||||  ||||||
                                GTAAATAAC  TGTATT
                                     GA_
GAM2219 FLJ11767 3' TCCATTTATTAGTAACA    53344   G       A
                                TC CATTTATTGG GACG
                                || |||||||||| ||||
                                AG GTAAATAATC TTGT
                                 _       A
GAM2219 LSM3     3' TCATATTTATTGGAGAGC    53345   C       C
                                TCG ATTTATTGGAGA GT
                                ||| |||||||||||| ||
                                AGT TAAATAACCTCT CG
                                  A        _
GAM2219 Rpo1-2   3' ATTCATTAAATATGTAACAA  53346       GAC
                                ATTTATTGGA  GTAACAA
                                ||||||||||  |||||||
                                TAAGTAATTT  CATTGTT
                                     ATA
GAM2219 Rpo1-2   3' ATTCATTAAATATGTAACAA  53346       GAC
                                ATTTATTGGA  GTAACAA
                                ||||||||||  |||||||
                                TAAGTAATTT  CATTGTT
                                     ATA
GAM2219 LOC124491 3' GCATTTATTGTCACTAAGATGT 53347     _____  C  A  III
           AGCAAT                TTATTG   GAGA GTA CAA  T
                                ||||||   |||| ||| |||  |
                                AATAAC   TTCT CAT GTT  A
                                   AGTGA  A  C  III
GAM2219 LOC220936 3' TCTATTTTGGACGTAACA   53348     GGA
                                TTTATT  GACGTAACA
                                ||||||  |||||||||
                                AGATAA  CTGCATTGT
                                   AAC
GAM2220 MPP3     3' TAATTCATGTTGATGGT     53351      TATTA
                                TAATTC    ATGTTGATGGT
                                ||||||    ||||||||||
                                ATTAAG    TACAACTACCA
                                     _____
GAM2220 TEC      3' TAATTCCGTTGATGTCTTAGTA 53352      TA A   GA
                                TAATTC  TT ATGTT  TGGTA
                                ||||||  || |||||  |||||
                                ATTAAG  AA TACAG  ATCAT
                                   GC  C    A_
GAM2220 TOP2A    3' TTCTATCTGATGGTA      53353       AATGT
                                TTCTATT    TGATGGTA
                                |||||||    ||||||||
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                                AAGATAG    ACTACCAT
                                       _____
GAM2220  FLJ14281  3'  TAATTCAATTACTCAATGGTAA 53354       T   ATG TG
                                TAATTC ATTA   T  ATGGTAA
                                |||||| ||||  |  |||||||
                                ATTAAG TAAT   A  TACCATT
                                    T   G__ GT
GAM2220  KIAA1939  3'  ATTCTATTAATGGTCTGG    53355          TTGA
                                ATTCTATTAATG   TGG
                                ||||||||||||   |||
                                TAAGATAATTAC   ACC
                                       CAG_
GAM2220  LBP-9    3'  TAATTCTGTGAATTGATGGT   53356       ATTAAT
                                TAATTCT     GTTGATGGT
                                |||||||     |||||||||
                                ATTAAGA     TAACTACCA
                                    CACT__
GAM2220  RAB21    3'  TAATTCTATAATTCCATTGGTA 53357        T   GTTGA
              A                  TAATTCTAT AAT    TGGTAA
                                |||||||||  |||    ||||||
                                ATTAAGATA TTA    ACCATT
                                      _  AGGTA
GAM2220  ZMPSTE24  3'  TAATTTTACAACTTGATGGTAA 53358      C   T   G
                                TAATT TAT AAT TTGATGGTAA
                                ||||| ||| ||| ||||||||||
                                ATTAA ATG TTG AACTACCATT
                                   A  _  _
GAM2220  LOC220980 3'  TAACTCTACATTGATGGT    53359        TAAT
                                TAATTCTAT   GTTGATGGT
                                |||||||||   |||||||||
                                ATTGAGATG   TAACTACCA
                                       _____
GAM2220  LOC221448 3'  TTCCATGTTGATGGTAA     53360      ATTA
                                TTCT   ATGTTGATGGTAA
                                ||||   ||||||||||||
                                AAGG   TACAACTACCATT
                                      ____
GAM2221  NR3C2    3'  AAGAAATGGACGCTAACGAG   53363          CACT
                                AAGAAATGGACGT   TGAG
                                ||||||||||||   ||||
                                TTCTTTACCTGCG   GCTC
                                       ATT_
GAM2221  NR4A2    3'  TACAGAAATGGGGGGCAGCTTG 53364      A      AC_  CA
              AG                   TACA GAAATGG   GT  CTTGAG
                                |||| |||||||   ||  ||||||
                                ATGT CTTTACC   CG  GAACTC
                                   _      CCC  TC
GAM2221  AP3S2    3'  AGAACTGGGTGCACCCGAG    53365      A   AC T
                                AGAA TGG  G CACTTGAG
                                |||| |||  | ||||||||
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                                TCTT ACC  C GTGGGCTC
                                  G   CA _
GAM2221  FLJ11710  3'  CAAGAGGATCACTTGA     53366      AAT   CG
                                CAAGA   GGA  TCACTTGA
                                |||||   |||  ||||||||
                                GTTCT   CCT  AGTGAACT
                                  ____  __
GAM2221  FLJ13263  3'  AGAAATGGAAGTTTGAG     53367        C  CAC
                                AGAAATGGA GT   TTGAG
                                |||||||||  ||   |||||
                                TCTTTACCT CA   AACTC
                                     T ____
GAM2221  FLJ22028  3'  TACAAAAAATGTAAAATATTTG 53368          GACGTCAC
           AG                     TACAAGAAATG       TTGAG
                                ||||||||||        |||||
                                ATGTTTTTTAC       AACTC
                                      ATTTTATA
GAM2221  FLJ32499  3'  CAAGAGGATCACTTGA     53366      AAT   CG
                                CAAGA   GGA  TCACTTGA
                                |||||   |||  ||||||||
                                GTTCT   CCT  AGTGAACT
                                  ____  __
GAM2221  INDO      3'  TACAAGAAATGCACAGGTATTT 53369          G   TCAC__
           TGAG                    TACAAGAAATG ACG     TTGAG
                                ||||||||||| |||     |||||
                                ATGTTCTTTAC TGT     AACTC
                                      G   CCATAA
GAM2221  KIAA0205  3'  CACAAGAAGTGGGCAACATGAG 53370        A   AC  C  T
                                TACAAGAA TGG  GT AC TGAG
                                |||||||| |||  || || ||||
                                GTGTTCTT ACC  CG TG ACTC
                                     C   __  T  T
GAM2221  KIAA0527  3'  AAGGAGGGCAGATCACTTGAG  53371     AAAT  AC_
                                AAG   GG   GTCACTTGAG
                                |||   ||   ||||||||||
                                TTC   CC   TAGTGAACTC
                                  CTC_  GTC
GAM2221  KIAA1755  3'  CAAGAGGATCACTTGA     53366      AAT   CG
                                CAAGA   GGA  TCACTTGA
                                |||||   |||  ||||||||
                                GTTCT   CCT  AGTGAACT
                                  ____  __
GAM2221  KIAA1940  3'  GAAGTGGACGTCCCCCCAG   53372     A      A   G
                                GAA TGGACGTC CTT AG
                                ||| |||||||| ||| ||
                                CTT ACCTGCAG GGG TC
                                  C       G   G
GAM2221  MCLC      3'  ACAAGGGCGGGTCACTTGAG   53373      AAA   AC
                                ACAAG   TGG  GTCACTTGAG
                                |||||   |||  ||||||||||
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                                TGTTC  GCC  CAGTGAACTC
                                  CC_  __
GAM2221  MGC4342  3'  ACAAGGCAGTGGACGTCACTTG 53374      AAA_
                                ACAAG   TGGACGTCACTTG
                                |||||   ||||||||||||||
                                TGTTC   ACCTGCAGTGAAC
                                  CGTC
GAM2221  MGC5528  3'  AGAGGGGAACTCACTCACTTGA 53375    AAT   G___
           G                     AGA  GGAC   TCACTTGAG
                                |||  ||||   |||||||||
                                TCT  CTTG   AGTGAACTC
                                 CCC   AGTG
GAM2221  PI15     5'  TACAAAGACATCATTTG     53376      GAAAT      C
                                TACAA    GGACGTCA TTG
                                |||||    |||||||| |||
                                ATGTT    TCTGTAGT AAC
                                  _____       A
GAM2221  LOC148645 5'  TACAGGAAATGGAGGTGCA   53377     A      C  _
                                TACA GAAATGGA GT CA
                                |||| |||||||| || ||
                                ATGT CTTTACCT CA GT
                                  C      C  C
GAM2221  LOC150290 3'  AAGAGGATCACTTGA      53378     AAT  CG
                                AAGA  GGA  TCACTTGA
                                ||||  |||  ||||||||
                                TTCT  CCT  AGTGAACT
                                  ___  __
GAM2221  LOC56920  3'  TACAAGAAATGTGCTCTGA   53379         GACG  ACT
                                TACAAGAAATG   TC   TGA
                                ||||||||||   ||  |||
                                ATGTTCTTTAC   AG   ACT
                                      ACG_  ___
GAM2222  ATP6V1E1  3'  CTCAAGAGTGGGGACTGCAGGG 53382     TCTCG     CA
                                CTCG    GGGGAC  CAGGG
                                ||||    ||||||  |||||
                                GAGT    CCCCTG  GTCCC
                                  TCTCA     AC
GAM2222  CA3      5'  TCTCTCTCAAAACTGCAGGG   53383     G     GG   CA
                                TCTC TCTCGG  GAC  CAGGG
                                |||| ||||||  |||  |||||
                                AGAG AGAGTT  TTG  GTCCC
                                  _     __  AC
GAM2222  FUT7     3'  GTCTCGGGGACCACAGG     53384         G
                                GTCTCGGGG ACCACAGG
                                ||||||||| ||||||||
                                CAGAGCCCC TGGTGTCC
                                          _
GAM2222  JUP      3'  GCCAGGGCCACAGGG       53385     TCG   A
                                GTC   GGGG CCACAGGG
                                |||   |||| ||||||||
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                                CGG   TCCC GGTGTCCC
                                  ___   _
GAM2222 MTNR1A   5' TCGCGTCCCGGCCGCAGG    53386    T      GGGA  A
                                TC CGTCTCGG    CC CAGG
                                || ||||||||    || ||||
                                AG GCAGGGCC    GG GTCC
                                 C       _____  C
GAM2222 NONO     3' CTCCGTCTCGGGGGGCGGG    53387    T        ACCACA
                                CTC CGTCTCGGGGGG     GG
                                ||| ||||||||||||     ||
                                GAG GCAGAGCCCCC      CC
                                  _        GC_____
GAM2222 RENT1    3' TCTCGCCTCCTGGCCACAGGG  53388         GGG  A
                                TCTCGTCTC   GG CCACAGGG
                                |||||||||   || ||||||||
                                AGAGCGGAG   CC GGTGTCCC
                                     GA_ _
GAM2222 SLC19A1  3' CCCTCGAGGCAGGGGTCGTGGG 53389       TCT     ACCACA
             G                   CTCTCG   CGGGGG     GGG
                                ||||||   ||||||     |||
                                GGGAGC   GTCCCC     CCC
                                   TCC     AGCAC_
GAM2222 TNFRSF5  3' CTCCTGTCTCAAACTGCAGGG  53390    TC     GGG   CA
                                CTC  GTCTCG   GAC  CAGGG
                                |||  ||||||   |||  |||||
                                GAG  CAGAGT   TTG  GTCCC
                                  GA     ___   AC
GAM2222 VANGL2   3' GTCTAAGACCACAGGG     53391     CGG
                                GTCT   GGGACCACAGGG
                                ||||   ||||||||||||
                                CAGA   TTCTGGTGTCCC
                                  ___
GAM2222 CDK5RAP3 3' TCGCCTGGTAGACCACAGGG   53392       C  GG
                                TCGTCT GG  GACCACAGGG
                                |||||| ||  ||||||||||
                                AGCGGA CC  CTGGTGTCCC
                                   _ AT
GAM2222 DECR2    5' CTCCCGTCGGGGACTGCGGG   53393        TCG     CACA
                                CTCTCGTC   GGGGAC    GGG
                                ||||||||   ||||||    |||
                                GAGGGCAG   CCCCTG    CCC
                                     ___      ACG_
GAM2222 DKFZp761J1523 3'  CTCTCTGTCTGCCACAGG    53394      _    CGGGGGA
                                CTCTC GTCT      CCACAGG
                                ||||| ||||      |||||||
                                GAGAG CAGA      GGTGTCC
                                   A   C_______
GAM2222 FLJ10922 3' CTTTCGTCTGGGGACCAGTCAG 53395    C     CG       __
             GG                   CT TCGTCT  GGGGACCA  CAGGG
                                || ||||||  ||||||||  |||||
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                                GA AGCAGA  CCCCTGGT  GTCCC
                                 A     __       CA
GAM2222  FLJ20700  3'  TCTCATCTTGGGGGATCTGTAC 53396        C     CC___
                AGGG                  TCTCGTCT GGGGGA     ACAGGG
                                |||||||| ||||||    ||||||
                                AGAGTAGA CCCCCT    TGTCCC
                                    A     AGACA
GAM2222  KIAA0552  3'  CTCTTTGGTCTGGGGTTATGGG 53397     C__   C   GACCACA
                G                   CTCT   GTCT GGGG      GGG
                                ||||   |||| ||||      |||
                                GAGA   CAGA CCCC      CCC
                                  AAC    _   AATAC__
GAM2222  KIAA1956  3'  CTCTTCTTAGACCACAGG    53398      CGTC  GGG
                                CTCT    TC   GGACCACAGG
                                ||||    ||   ||||||||||
                                GAGA    AG   TCTGGTGTCC
                                  _____  AA_
GAM2222  NUDT3     3'  CTCTCTTCAGAGGACTGCAGGG 53399      GTC       CA
                                CTCTC   TCGGGGGAC  CAGGG
                                |||||   |||||||||  |||||
                                GAGAG   AGTCTCCTG  GTCCC
                                   A__        AC
GAM2222  RNF9      5'  CTCTCTCTGCTTGGCCACGGGG 53400      G   CGGG  A    A
                                CTCTC TCT    GG CCAC GGG
                                ||||| |||    || |||| |||
                                GAGAG AGA    CC GGTG CCC
                                   _  CGAA  _    C
GAM2222  RNF9      5'  CTCTCTCTGCTTGGCCACGGGG 53400      G   CGGG  A    A
                                CTCTC TCT    GG CCAC GGG
                                ||||| |||    || |||| |||
                                GAGAG AGA    CC GGTG CCC
                                   _  CGAA  _    C
GAM2222  LOC132241 5'  CTCATCAGGGGACCATAGG    53401       TC       C
                                CTCGTC  GGGGGACCA AGG
                                ||||||  |||||||| |||
                                GAGTAG  TCCCCTGGT TCC
                                   __        A
GAM2222  LOC257060 3'  CTCCCACCTCTCGGGGGACTGC 53402        __         CA
                AGGG                  CTCTCG  TCTCGGGGGAC  CAGGG
                                ||||||  ||||||||||  |||||
                                GAGGGT  AGAGCCCCCTG  GTCCC
                                   GG          AC
GAM2222  LOC257458 5'  CTCCGTGGGGGCCACAGGG    53403     T   CTC    A
                                CTC CGT   GGGGG CCACAGGG
                                ||| |||   ||||| ||||||||
                                GAG GCA   CCCCC GGTGTCCC
                                  _  ____    _
GAM2222  LOC257475 3'  TCTCTCCCAGGGTCACAGGG   53404      G       GAC
                                TCTC TCTCGGGG   CACAGGG
                                |||| ||||||||   |||||||
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                                AGAG AGGGTCCC   GTGTCCC
                                  _      A__
GAM2222 LOC90139 3' CTCTTGTCTGGGGGAACCGGG 53405     C   C      ACA
                                CTCT GTCT GGGGGACC   GGG
                                |||| |||| ||||||||   |||
                                GAGA CAGA CCCCTTGG   CCC
                                  A   C      ___
GAM2223 HCFC1    3' TGCAGCAGTTGGCAGTGCGGCC 53408         AA  TC  C
           T                     TGTAGCAGTT  CG  GC GGCCT
                                |||||||||| ||  || |||||
                                ACGTCGTCAA  GT  CG CCGGA
                                      CC  CA  _
GAM2223 LOC51001 5' TGTAACAGTGTTCTTGCTGGTC 53409        TAACGTC  C  C
           T                     TGTAGCAGT      GC GG CT
                                |||||||||      || || ||
                                ACATTGTCA      CG CC GA
                                      CAAGAA_  A  A
GAM2224 CDK5R2   3' AACAGCGGCGGTGGCTTTGT   53412         A  ATA_
                                AATAGCGGCG TG    TGT
                                |||||||||| ||    |||
                                TTGTCGCCGC AC    ACA
                                      C  CGAA
GAM2224 CPO      3' ACGATAATGATATGTATG    53413     GC
                                GCG  GATGATATGTATG
                                |||  ||||||||||||
                                TGC  TTACTATACATAC
                                  TA
GAM2224 PKHD1    3' TGATAGCTGCAAAATATGTATG 53414   A    G    T
           A                     C ATAGC GCGA GATATGTATGA
                                | ||||| |||| ||||||||||
                                A TATCG CGTT TTATACATACT
                                 C    A   _
GAM2224 STARD5   3' CAGTGGCGATGATGATTCTCTA 53415     C       ATG____
           TGA                     TAG GGCGATGAT      TATGA
                                ||| |||||||||      |||||
                                GTC CCGCTACTA      ATACT
                                  A       CTAAGAG
GAM2224 GNB4     3' GGAGAACAAATATGTATGA   53416    C  T__
                                GG GA   GATATGTATGA
                                || ||   ||||||||||||
                                CC CT   TTATACATACT
                                 T  TGT
GAM2224 KIAA0316 3' TAGAGGCGGTGATGCATG    53417     C   A   TA
                                TAG GGCG TGA  TGTATG
                                ||| |||| |||  ||||||
                                ATC CCGC ACT  ACGTAC
                                  T   C   __
GAM2224 KIAA1377 5' TAGCGGCGATGGCAGCTGA   53418          A  T  A
                                TAGCGGCGATG TA GT TGA
                                |||||||||| || || |||
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                                ATCGCCGCTAC GT CG ACT
                                      C  _  _
GAM2224  KIAA1416  3'  TGAGCAAGTATGATATGTATG  53419   T    CG
                                A AGCGG  ATGATATGTATG
                                | |||||  ||||||||||||
                                A TCGTT  TACTATACATAC
                                 C    CA
GAM2224  MEGF10   3'  CAAGTGGTGAATATGTATG   53420   T  C  C  TG
                                A AG GG GA  ATATGTATG
                                | || || ||  |||||||||
                                G TC CC CT  TATACATAC
                                 T  A  A  __
GAM2225  IL2RA    3'  TCTTTATACTACATATAGGGTG 53423      _  CA   CAA
            GA                    TCTTT TAC  ACA   AGGGTGGA
                                |||||| |||  |||   ||||||||
                                AGAAA ATG  TGT   TCCCACCT
                                   T   A_   ATA
GAM2225  INPP5D   3'  TCTTCTACCAGCACGATGG   53424         A   AAAG
                                TCTTTTACCA CAC    GGTGG
                                |||||||||| |||    |||||
                                AGAAGATGGT GTG    CTACC
                                      C   _____
GAM2225  PLXNA1   3'  TCTCTTGCTGAGGGCAAGGGTG 53425       ACCAACACA
            GA                    TCTTTT        AAGGGTGGA
                                ||||||        |||||||||
                                AGAGAA        TTCCCACCT
                                   CGACTCCCG
GAM2225  PRG4     3'  TCTTTTACAGGTGTGA      53426         CAACACAA  _
                                TCTTTTAC       AGG GTGG
                                ||||||||       ||| ||||
                                AGAAAATG       TCC CACT
                                     _________  A
GAM2225  PRKCN    3'  TCTTTTACAAACACGACTTAAA 53427         C     AAAGGGT
            GA                    TCTTTTAC AACAC      GGA
                                |||||||| |||||      |||
                                AGAAAATG TTGTG      TCT
                                     T    CTGAATT
GAM2225  BHMT     3'  TCTTTTACTGGTAGAAAAGTGG 53428         CAACACA
                                TCTTTTAC      AAGGGTGG
                                ||||||||      ||||||||
                                AGAAAATG      TTTTCACC
                                     ACCATC_
GAM2225  DKFZP434B044 3'  TTTTACCAACTCCTTAAAGGGG 53429          AC___     _
            TGG                   TTTTACCAAC    AAAGGG TGG
                                ||||||||||    |||||| |||
                                AAAATGGTTG    TTTCCC ACC
                                     AGGAA     C
GAM2225  FLJ10458  3'  TCTCTTACCAACACGGGG    53430             AAA
                                TCTTTTACCAACAC   GGG
                                ||||||||||||||   |||
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                                AGAGAATGGTTGTG  CCC
                                      C__
GAM2225  FLJ20272  3'  TCTTTTACCAGCAGGTG    53431        ACACAAA
                                TCTTTTACCA     GGGTG
                                ||||||||||     |||||
                                AGAAAATGGT     TCCAC
                                     CG_____
GAM2225  FLJ23598  3'  TCTTTTATTACCCAGGGTGGA  53432      CCAAC  AA
                                TCTTTTA    AC  AGGGTGGA
                                |||||||    ||  ||||||||
                                AGAAAAT    TG  TCCCACCT
                                    AA___  GG
GAM2225  KIAA1755  3'  CTCTGGCCAGTATGAAGGGTGG 53433    TA   ACACA
                                CTTT  CCA    AAGGGTGG
                                ||||  |||    ||||||||
                                GAGA  GGT    TTCCCACC
                                  CC   CATAC
GAM2225  MGC21621  3'  TCTTTTACCAACCAGCCTAGGG 53434         A  A___
                                TCTTTTACCAAC CA    AGGG
                                ||||||||||| ||    ||||
                                AGAAAATGGTTG GT    TCCC
                                      _ CGGA
GAM2225  MGC3077  3'  TCTTTTACCAGAGCAAGGA   53435        ACACA
                                TCTTTTACCA    AAGGG
                                ||||||||||    |||||
                                AGAAAATGGT    TTCCT
                                      CTCG_
GAM2225  MGC4707  3'  TTTTACCAGACATGAGGG    53436       _  CAA
                                TTTTACCA ACA   AGGG
                                |||||||| |||   ||||
                                AAAATGGT TGT   TCCC
                                    C   AC_
GAM2225  MGC5149  3'  TCTTTTACCAATGAGGA     53437        CACAA
                                TCTTTTACCAA    AGGG
                                ||||||||||    ||||
                                AGAAAATGGTT    TCCT
                                      AC___
GAM2225  RAB3IL1  3'  TTTTACCAACAAAGCCTG    53438        CA   GG
                                TTTTACCAACA  AAG  TG
                                ||||||||||  |||  ||
                                AAAATGGTTGT  TTC  AC
                                      __  GG
GAM2225  LOC119369 5'  TTTTTCCAGAAATAGGGTGGA  53439     A   ACACAA
                                TTTT CCA     AGGGTGGA
                                |||| |||     ||||||||
                                AAAA GGT     TCCCACCT
                                  A  CTTTA_
GAM2225  LOC150035 5'  TCTTTTACCAGTACTACAA   53440        __ _
                                TCTTTTACCA  AC ACAA
                                ||||||||||  || ||||
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                                AGAAAATGGT  TG TGTT
                                      CA  A
GAM2225  LOC219649 5'  ACCAAAGCACAAAGGGTGGA   53441      __
                                ACCAA  CACAAAGGGTGGA
                                |||||  ||||||||||||
                                TGGTT  GTGTTTCCCACCT
                                   TC
GAM2225  LOC221688 5'  TTTTACCAATGTGGTTGGA   53442        CACAAA  G
                                TTTTACCAA     GG TGGA
                                |||||||||     || ||||
                                AAAATGGTT     CC ACCT
                                      ACA___  A
GAM2226  COL4A3    3'  GTGTTATCATCAAGGTAT    53445     CGAT
                                GTGT   TCATCAAGGTAT
                                ||||   ||||||||||||
                                CACA   AGTAGTTCCATA
                                  AT__
GAM2226  COL4A3    3'  GTGTTATCATCAAGGTAT    53445     CGAT
                                GTGT   TCATCAAGGTAT
                                ||||   ||||||||||||
                                CACA   AGTAGTTCCATA
                                  AT__
GAM2226  COL4A3    3'  GTGTTATCATCAAGGTAT    53445     CGAT
                                GTGT   TCATCAAGGTAT
                                ||||   ||||||||||||
                                CACA   AGTAGTTCCATA
                                  AT__
GAM2226  FLJ14594  3'  CGCGTGTCGGTTCGTCGGC   53446        A   A  AA
                                CGCGTGTCG TTC TC  GGT
                                ||||||||| ||| ||  |||
                                GCGCACAGC AAG AG  CCG
                                      C   C  __
GAM2226  LOC150051 3'  CACGTGTGTATGGAATCAAGGT 53447       CGATTC_
                                CGCGTGT      ATCAAGGT
                                |||||||      ||||||||
                                GTGCACA      TAGTTCCA
                                    CATACCT
GAM2226  LOC153259 5'  ACGTGTGTTGACTTTATCAAG  53448     C   C   C_
                                ACG GTGT GATT  ATCAAG
                                ||| |||| ||||  ||||||
                                TGC CACA CTGA  TAGTTC
                                  A   A   AA
GAM2227  C5orf5    3'  TAAAACATTTAAATAGTG    53451           _
                                TAAAACATTTGAAT GTG
                                |||||||||||||| |||
                                ATTTTGTAAATTTA CAC
                                         T
GAM2227  FBXO21    3'  TAAAACACTTGAAATCTGTG   53452          ___
                                TAAAACATTTGAA   TGTG
                                ||||||||||||   ||||
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                                ATTTTGTGAACTT  ACAC
                                       TAG
GAM2227  PROL2    3'  CAAAACACCTGCAATGTG    53453          _
                                TAAAACATTTG AATGTG
                                |||||||||| ||||||
                                GTTTTGTGGAC TTACAC
                                       G
GAM2227  YAP1     3'  TAAAACATTTAAAATGTG    53454          _
                                TAAAACATTTGAA TGTG
                                |||||||||||| ||||
                                ATTTTGTAAATTT ACAC
                                       T
GAM2228  CEBPD    3'  TGCTTTATTCTTACAAATACTG 53457        _ CG_      A
            TAAA                   TGCTTTGT C   TAGATACT TAAA
                                |||||||| |   |||||||| ||||
                                ACGAAATA G   GTTTATGA ATTT
                                     A AAT       C
GAM2228  RAB27A   3'  TGCTTTATTCGTAGGTCTA   53458        C    ATA
                                TGCTTTGT CGTAG   CTA
                                |||||||| |||||   |||
                                ACGAAATA GCATC   GAT
                                     A    CA_
GAM2228  RORA     5'  TGCTTTGCCCCAGTGTACTAT  53459         G   A_
                                TGCTTTGTCC TAG  TACTAT
                                |||||||||| |||  ||||||
                                ACGAAACGGG GTC  ATGATA
                                       _  AC
GAM2228  RORA     5'  TGCTTTGCCCCAGTGTACTAT  53459         G   A_
                                TGCTTTGTCC TAG  TACTAT
                                |||||||||| |||  ||||||
                                ACGAAACGGG GTC  ATGATA
                                       _  AC
GAM2228  STK38    3'  TGCTTTATTTCCTTAGTACTAT 53460        __  G   A
                                TGCTTTG  TCC TAG TACTAT
                                |||||||  ||| ||| ||||||
                                ACGAAAT  AGG ATC ATGATA
                                     AA  A  _
GAM2228  KIAA0157 3'  TGCTTTGTCAGATATACA    53461         CGT    C
                                TGCTTTGTC   AGATA TATA
                                |||||||||   ||||| ||||
                                ACGAAACAG   TCTAT ATGT
                                       ___    _
GAM2228  MGC22014 3'  CTTTGTGAAAGGATACTATAAA 53462       CCGTA
                                CTTTGT    GATACTATAAA
                                ||||||    ||||||||||
                                GAAACA    CTATGATATTT
                                   CTTTC
GAM2228  RNAC     3'  TGCTTTGTCTGTAGGCACT   53463         C   A
                                TGCTTTGTC GTAG TACT
                                ||||||||| |||| ||||
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                                ACGAAACAG CATC GTGA
                                     A    C
GAM2228  LOC150208 3'  TGCCTTGTCTGTAAACAGCTGT 53464          C      _  A
              AAA                    TGCTTTGTC GTAGATA CT TAAA
                                |||||||||  |||||||  ||  ||||
                                ACGGAACAG CATTTGT GA ATTT
                                     A      C  C
GAM2228  LOC257484 3'  CTTTGTGAAAGGATACTATAAA 53462        CCGTA
                                CTTTGT    GATACTATAAA
                                ||||||    ||||||||||
                                GAAACA    CTATGATATTT
                                   CTTTC
GAM2228  LOC90410  3'  TGTTTTGCCTTCCTACTATAAA 53465    C    T  GTAGA
                                TG TTTG CC    TACTATAAA
                                || ||||  ||    |||||||||
                                AC AAAC GG    ATGATATTT
                                 A    _  AAGG_
GAM2229  NRXN2     3'  AGTCAGCCCCGGGACTGAC    53468        G  AAC   AATA
                                AGTCAGCC CG   GGA    AC
                                ||||||||  ||   |||    ||
                                TCAGTCGG GC   CCT    TG
                                     G  ____   GAC_
GAM2229  NRXN2     3'  AGTCAGCCCCGGGACTGAC    53468        G  AAC   AATA
                                AGTCAGCC CG   GGA    AC
                                ||||||||  ||   |||    ||
                                TCAGTCGG GC   CCT    TG
                                     G  ____   GAC_
GAM2229  NRXN2     3'  AGTCAGCCCCGGGACTGAC    53468        G  AAC   AATA
                                AGTCAGCC CG   GGA    AC
                                ||||||||  ||   |||    ||
                                TCAGTCGG GC   CCT    TG
                                     G  ____   GAC_
GAM2229  PCTP      3'  AGTCAGCTCTGAACGAAA     53469        CGC
                                AGTCAGC   GAACGGAA
                                |||||||   ||||||||
                                TCAGTCG   CTTGCTTT
                                     AGA
GAM2229  PSCD4     3'  AGTCAGCCTGGGCTCCGCAAAT 53470          ____  GAA  G
              AACG                   AGTCAGCC   GC   CG AAATAACG
                                |||||||   ||   ||  ||||||||
                                TCAGTCGG   CG   GC TTTATTGC
                                     ACC  AG_  G
GAM2229  KIAA1030  3'  AGTCAGCCTGAATGGGAAA    53471        GC   C_
                                AGTCAGCC  GAA  GGAAA
                                ||||||||  |||  |||||
                                TCAGTCGG  CTT  CCTTT
                                     A_   AC
GAM2230  GDF2      5'  TTAGCGGGCACGGGGAGGAGC  53474      AA       _  AC
                                TTAG  GGCACGGG AG  GC
                                ||||  ||||||||  ||  ||
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                                AATC  CCGTGCCC TC  CG
                                  GC       C  CT
GAM2230  MAP4     5'  AGGAGGTAGGAGACGTCG    53475    A   CAC       C
                                AG AGG   GGGAGACG CG
                                || |||   |||||||| ||
                                TC TCC   TCCTCTGC GC
                                 C   A__       A
GAM2230  MAP4     5'  AGGAGGTAGGAGACGTCG    53475    A   CAC       C
                                AG AGG   GGGAGACG CG
                                || |||   |||||||| ||
                                TC TCC   TCCTCTGC GC
                                 C   A__       A
GAM2230  PPP2R5E  5'  AGGGGCGGGAGACGGGCGAG   53476     CA       C_
                                AGG  CGGGAGACG  CGAG
                                |||  |||||||||  ||||
                                TCC  GCCCTCTGC  GCTC
                                  CC        CC
GAM2230  WHSC1L1  3'  TTAGAAGGCACATTGCTGA   53477           GGAGAC  C
                                TTAGAAGGCACG     GC GA
                                ||||||||||||     || ||
                                AATCTTCCGTGT     CG CT
                                       AA_____  A
GAM2230  LOC148894 5'  CTAGAAGGCAGAGGATGC    53478          C   A  C
                                TTAGAAGGCA GGG GA GC
                                |||||||||| ||| || ||
                                GATCTTCCGT CTC CT CG
                                       _  _  A
GAM2230  LOC150244 5'  AGAAGGCATCAGAGGCGCTGAG 53479         CG    A   C
                                AGAAGGCA  GGAG CGC GAG
                                ||||||||  |||| ||| |||
                                TCTTCCGT  TCTC GCG CTC
                                     AG    C   A
GAM2230  LOC256337 3'  TTAGAAGGTTTGCTGTGGGGTG 53480       CAC_____   AGAC
            CCGAG                  AGAAGG       GGG    GCCGAG
                                ||||||       |||    ||||||
                                TCTTCC       CCC    CGGCTC
                                   AAACGACA   CA__
GAM2230  LOC93052  5'  TTAGAAGGAGCGGAGCCGA   53481         CA    AGAC
                                TTAGAAGG  CGGG    GCCGA
                                ||||||||  ||||    |||||
                                AATCTTCC  GCCT    CGGCT
                                     TC   _____
GAM2231  HSJ001348 3'  GAACTTTTGAAGTCCCCTT    53484       C      AA
                                GAACT TTGAAG  CTTTT
                                ||||| ||||||  |||||
                                CTTGA AACTTC  GGGAA
                                   A     AG
GAM2231  VAV3     3'  CAGAACTCCAATTTTTCG     53485          TGAAG  C
                                TAGAACTCT     AA TTTTCG
                                |||||||||     || ||||||
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                                GTCTTGAGG    TT AAAAGC
                                     _____ A
GAM2232 NUP153   3' CAGCACAAAGTACAATCCAGTA 53488       _     T  C
             T                   CAGCACAA GTACAATT CA GTAT
                                 |||||||| |||||||| || ||||
                                 GTCGTGTT CATGTTAG GT CATA
                                    T      _ _
GAM2232 PCDH11X  3' CAGCATGAGTACAATCAACAT  53489     CA      TC
                                 CAGCA  AGTACAATT  ACGT
                                 |||||  |||||||||  ||||
                                 GTCGT  TCATGTTAG  TGTA
                                    AC       T_
GAM2232 PCDH11Y  3' CAGCATGAGTACAATCAACAT  53489     CA      TC
                                 CAGCA  AGTACAATT  ACGT
                                 |||||  |||||||||  ||||
                                 GTCGT  TCATGTTAG  TGTA
                                    AC       T_
GAM2232 PCDH11Y  3' CAGCATGAGTACAATCAACAT  53489     CA      TC
                                 CAGCA  AGTACAATT  ACGT
                                 |||||  |||||||||  ||||
                                 GTCGT  TCATGTTAG  TGTA
                                    AC       T_
GAM2232 PCDHA11  5' CACCACAGAATTTCACGT    53490    G   A TAC
                                 CA CACA G   AATTTCACGT
                                 || |||| |   ||||||||||
                                 GT GTGT C   TTAAAGTGCA
                                  G   _ ___
GAM2232 PCDHA11  5' CACCACAGAATTTCACGT    53490    G   A TAC
                                 CA CACA G   AATTTCACGT
                                 || |||| |   ||||||||||
                                 GT GTGT C   TTAAAGTGCA
                                  G   _ ___
GAM2232 SH3GL3   5' CAGCTTGAGTTTTCTTCACGT  53491     ACA   ACAA
                                 CAGC   AGT    TTTCACGT
                                 ||||   |||    ||||||||
                                 GTCG   TCA    GAAGTGCA
                                   AAC   AAA_
GAM2232 TNFSF11  3' AGCACAAATATAATTTACA    53492        C    C
                                 AGCACAAGTA AATTT ACG
                                 |||||||||| ||||| |||
                                 TCGTGTTTAT TTAAA TGT
                                      A    _
GAM2232 TNFSF11  3' AGCACAAATATAATTTACA    53492        C    C
                                 AGCACAAGTA AATTT ACG
                                 |||||||||| ||||| |||
                                 TCGTGTTTAT TTAAA TGT
                                      A    _
GAM2232 UBL3     3' CAGCTGAGTATTTCACGTA    53493     ACA    CAA
                                 CAGC   AGTA   TTTCACGTA
                                 ||||   ||||   |||||||||
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                                GTCG   TCAT   AAAGTGCAT
                                  AC_   ___
GAM2232  WSX1     3'  GCCACTCTCAATTTCATGTAT  53494    A  AGTA      C
                                GC CA    CAATTTCA GTAT
                                || ||    |||||||| ||||
                                CG GT    GTTAAAGT CATA
                                 _ GAGA       A
GAM2232  FLJ11186 3'  GCAAGTACAATTTTACAT    53495     CA        C
                                GCA  AGTACAATTT ACGT
                                |||  |||||||||| ||||
                                CGT  TCATGTTAAA TGTA
                                  __        A
GAM2232  GRP3     3'  GCACAAGTTGGTTTTAGCGTAT 53496         ACAA   CA
                                GCACAAGT    TTT  CGTAT
                                ||||||||    |||  |||||
                                CGTGTTCA    AAA  GCATA
                                     ACCA   TC
GAM2232  KIAA0663 3'  GCACAGTACAATTCAGT     53497      A       T  C
                                GCACA GTACAATT CA GT
                                ||||| |||||||| || ||
                                CGTGT CATGTTAA GT CA
                                  _       _ _
GAM2232  LOC219673 5'  CACAGGTACTTCACGTAT    53498      A    AAT
                                CACA GTAC   TTCACGTAT
                                |||| ||||   |||||||||
                                GTGT CATG   AAGTGCATA
                                  C   ___
GAM2232  LOC253019 3'  GCACAGTACAATTCAGT     53497      A       T  C
                                GCACA GTACAATT CA GT
                                ||||| |||||||| || ||
                                CGTGT CATGTTAA GT CA
                                  _       _ _
GAM2232  LOC253975 3'  GCACAGTACAATTCAGT     53497      A       T  C
                                GCACA GTACAATT CA GT
                                ||||| |||||||| || ||
                                CGTGT CATGTTAA GT CA
                                  _       _ _
GAM2233  BLAME    3'  CATGTGGCCTGACTGTAG     53501      A_      A
                                CATG  GCCTGACT TAG
                                ||||  |||||||| |||
                                GTAC  CGGACTGA ATC
                                  AC       C
GAM2233  CCR2     3'  CATGGGTGCCATAGATA      53502      AGCC  A
                                CATG    TG CTATAGATA
                                ||||    || |||||||||
                                GTAC    AC GGTATCTAT
                                  CC__  _
GAM2233  LPIN1    3'  TACCATGAGCTAGAT        53503          CTGACTA
                                TACCATGAGC      TAGAT
                                ||||||||||      |||||
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                                ATGGTACTCG      ATCTA
                                          ________
GAM2233  NPR2L    3'  TACCATGATGCTTCACAGAT   53504        _  CTGAC
                                TACCATGA GC    TATAGAT
                                |||||||| ||    |||||||
                                ATGGTACT CG    GTGTCTA
                                     A  AA___
GAM2233  PART1    3'  TACCATGAGCTTCTTAGATA   53505         CTGA  A
                                TACCATGAGC   CT TAGATA
                                ||||||||||   || ||||||
                                ATGGTACTCG   GA ATCTAT
                                      AA__  _
GAM2233  RECQL5   3'  TACCATGAGCTTCGTGACT    53506         C___
                                TACCATGAGC   TGACT
                                ||||||||||   |||||
                                ATGGTACTCG   ACTGA
                                      AAGC
GAM2233  SYBL1    3'  TACCATGAGCCAGATTAT     53507          T  C
                                TACCATGAGCC GA TAT
                                |||||||||| || |||
                                ATGGTACTCGG CT ATA
                                       T  A
GAM2233  FHOD2    3'  CCAGGGCCTGGTTATAGACAA  53508     TGA    AC
                                CCA   GCCTG  TATAGATAA
                                |||   |||||  |||||||||
                                GGT   CGGAC  ATATCTGTT
                                  CC_    CA
GAM2233  FLJ23518 3'  CCATGAAGATATAGATA      53509       CCT  C
                                CCATGAG   GA TATAGATA
                                |||||||   || ||||||||
                                GGTACTT   CT ATATCTAT
                                          ___  _
GAM2233  MGC19595 3'  CCTGAGCCTGGCCCACAG     53510    A      A_
                                CC TGAGCCTG  CTATAG
                                || ||||||||  ||||||
                                GG ACTCGGAC  GGTGTC
                                 _       CG
GAM2233  NPD009   3'  TACCATGAGCTTATATATAGAT 53511          C  AC
            A                    TACCATGAGC TG  TATAGATA
                                ||||||||||  ||  ||||||||
                                ATGGTACTCG AT  ATATCTAT
                                       A  AT
GAM2233  VRP      5'  CAGAGCCTGACACACAGA     53512    T      _
                                CA GAGCCTGAC TATAGA
                                || |||||||| ||||||
                                GT CTCGGACTG GTGTCT
                                 _       T
GAM2233  LOC145082 5'  CATGAGCCTGGCCTATAA     53513         A_
                                CATGAGCCTG  CTATAG
                                ||||||||||  ||||||
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                                GTACTCGGAC  GATATT
                                      CG
GAM2233  LOC146050 3'  TACCTGATTTACTATAGAT   53514     A   GCCTG
                                TACC TGA    ACTATAGAT
                                |||| |||    |||||||||
                                ATGG ACT    TGATATCTA
                                  _   AAA__
GAM2234  KIAA1172  3'  TAATATTTATTCATATTTT   53517          A
                                TAATATTTATTCA TATTTT
                                |||||||||||| ||||||
                                ATTATAAATAAGT ATAAAA
                                          _
GAM2234  PSIP2     3'  TATAACATTTATTCATATTT  53518          A
                                TATAATATTTATTCA TATTT
                                |||||||||||||| |||||
                                ATATTGTAAATAAGT ATAAA
                                          _
GAM2235  CENTD2    3'  GTTGGGCCAAGAGGTCT     53521        AACA   TA
                                GTTGGGCCA   AGA  TCT
                                |||||||||   |||  |||
                                CAACCCGGT   TCT  AGA
                                     ____   CC
GAM2235  CENTD2    3'  GTTGGGCCAAGAGGTCT     53521        AACA   TA
                                GTTGGGCCA   AGA  TCT
                                |||||||||   |||  |||
                                CAACCCGGT   TCT  AGA
                                     ____   CC
GAM2235  KCNH3     3'  GTTGGGCCGAACAGCAGAT   53522        A   __
                                GTTGGGCC AACA  AGAT
                                |||||||| ||||  ||||
                                CAACCCGG TTGT  TCTA
                                     C   CG
GAM2235  ORC5L     3'  GCTGGGCCAGCACCTG      53523        AACAA A
                                GTTGGGCCA    G TATCTG
                                |||||||||    | ||||||
                                CGACCCGGT    C GTGGAC
                                     _____ _
GAM2235  PRV1      3'  GTTGGGCCACACAGCCCTG   53524        A   AGATA
                                GTTGGGCCA ACA    TCTG
                                ||||||||| |||    ||||
                                CAACCCGGT TGT    GGAC
                                     G   CG___
GAM2235  CGI-85    3'  GTTGGGCTGAAAACATCTG   53525       CAAAC
                                GTTGGGC    AAGATATCTG
                                |||||||    ||||||||||
                                CAACCCG    TTTTGTAGAC
                                    AC___
GAM2235  EPI64     3'  GTTGGACCAGGCAGAATCTG  53526        AACA   T
                                GTTGGGCCA   AGA ATCTG
                                |||||||||   ||| |||||
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                                CAACCTGGT    TCT TAGAC
                                     CCG_  _
GAM2235  LOC197342 5'  GTTGGGCCAGAGATCT      53527         AACAA  T
                                GTTGGGCCA    GA ATCT
                                |||||||||    || ||||
                                CAACCCGGT    CT TAGA
                                     _____  C
GAM2236  ALS2      3'  TTAGTCCTGCTCGAAAACAC  53530         A   AAC
                                TTAGTCCTG CTC   AATAC
                                ||||||||| |||   |||||
                                AATCAGGAC GAG   TTGTG
                                     _  CTT
GAM2236  PHKB      3'  TTAGCATGACAATACC      53531       CC    TCAAC
                                TTAGT  TGAC    AATACC
                                |||||  ||||    ||||||
                                AATCG  ACTG    TTATGG
                                   T_   _____
GAM2236  CLSTN2    3'  TTAGTTCTGCCTCAACAA    53532       C   A
                                TTAGT CTG CTCAACAA
                                ||||| ||| ||||||||
                                AATCA GAC GAGTTGTT
                                   A   G
GAM2236  DKFZp761D221 3'  GTGCCATTCAACAATACTAC  53533    _  TGAC        C
                                GT CC    TCAACAATAC AC
                                || ||    |||||||||| ||
                                CA GG    AGTTGTTATG TG
                                 C  TA__         A
GAM2236  FLJ12800  3'  GTCCTGACTCAACCA       53534           ACAAT
                                GTCCTGACTCA     ACCA
                                ||||||||||     ||||
                                CAGGACTGAGT     TGGT
                                     _____
GAM2237  MYO10     3'  TGTGTACACCATTACACA     53537    C   G      TT
                                TG GTA CACCATT  CATA
                                || ||| |||||||  ||||
                                AC CAT GTGGTAA  GTGT
                                 A   _      T_
GAM2237  NAP1L3    3'  TGTGTAGCACCAAACTAACAT  53538    C       TTTTCA
                                TG GTAGCACCA     TAACAT
                                || |||||||||     ||||||
                                AC CATCGTGGT     ATTGTA
                                 A        TTG___
GAM2237  SOX11     3'  GTAGTCATTCATAACA      53539      _  CCATT
                                GTAG CA     TTCATAACA
                                |||| ||     |||||||||
                                CATC GT     AAGTATTGT
                                  A  _____
GAM2237  LOC199958 3'  TGTGTACATCATTTTCAC    53540    C   G  C
                                TG GTA CA CATTTTCAT
                                || ||| || |||||||||
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                                AC CAT GT GTAAAAGTG
                                 A  _  A
GAM2238 HD       3' CAAGATGTCAGCTGGA      53543          ATACTCC
                                CAAGATGTTAGC      GGA
                                ||||||||||||      |||
                                GTTCTACAGTCG      CCT
                                      A_______
GAM2238 NYX      3' TGAATGTTAGCATATGAAAGA 53544   A        CTCC
                                A GATGTTAGCATA    GGA
                                | ||||||||||||    |||
                                A TTACAATCGTAT    TCT
                                 C          ACTT
GAM2238 SYBL1    3' TGAGATGTTAGCAATACT    53545   A        _
                                C AGATGTTAGCA TACT
                                | |||||||||| ||||
                                A TCTACAATCGT ATGA
                                 C          T
GAM2238 TEK      3' AGATGTTAGCATCCTGGA    53546          TAC  _
                                AGATGTTAGCA   TCC GGA
                                ||||||||||   ||| |||
                                TCTACAATCGT   AGG CCT
                                      ___  A
GAM2238 TEM8     3' TGAATGTTAGACACTGGGA   53547   A      C    CC
                                A GATGTTAG ATACT  GGA
                                | ||||||| |||||  |||
                                A TTACAATC TGTGA  CCT
                                 C       _    C_
GAM2238 CLIC4    3' AAATGTTAGCATATCAAA    53548          CTC
                                AGATGTTAGCATA   CGGA
                                ||||||||||||   ||||
                                TTTACAATCGTAT   GTTT
                                       A__
GAM2238 DKFZp762K2015 3' GATGTTAGTATATGGAA     53549        C   CTCC
                                GATGTTAG ATA    GGAA
                                |||||||| |||    ||||
                                CTACAATC TAT    CCTT
                                     A   A___
GAM2238 FLJ14326 3' AGGGTGTTAGCAGGCTTGGA   53550    A_      TA  CC
                                AG  TGTTAGCA  CT  GGA
                                ||  ||||||||  ||  |||
                                TC  ACAATCGT  GA  CCT
                                 CC       CC  A_
GAM2238 KIAA0711 5' CAAGGTCGAGCCTTACTCCGG  53551     AT  _  A_
                                CAAG  GTT AGC  TACTCCGG
                                ||||  ||| |||  ||||||||
                                GTTC  CAG TCG  ATGAGGCC
                                   __  C  GA
GAM2238 KIAA1364 3' AGGGGTTAGCCTTCCTGGAA  53552    AT     ATAC  _
                                AG  GTTAGC    TCC GGAA
                                ||  ||||||    ||| ||||
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                                TC  CAATCG    AGG CCTT
                                 CC     GA__   A
GAM2238  KIAA1765  3'  CAAGATGTTTCCACTTTGG   53553        AGCA    CC
                                CAAGATGTT    TACT  GG
                                |||||||||    ||||  ||
                                GTTCTACAA    GTGA  CC
                                      AG__    AA
GAM2238  KIAA1908  5'  TGAGATGTGGCTCCGGAA    53554   A     TAGCATA
                                C AGATGT      CTCCGGAA
                                | ||||||      ||||||||
                                A TCTACA      GAGGCCTT
                                 C     CC_____
GAM2238  KIAA1944  3'  CAAGACACTGTACTCTGGAA   53555      TG  AGCA    C
                                CAAGA  TT    TACTC GGAA
                                |||||  ||    ||||| ||||
                                GTTCT  GA    ATGAG CCTT
                                   GT  C___     A
GAM2238  SEMA4G    5'  GATGTCAGGAATGCTCCGGAA  53556        C_  A
                                GATGTTAG  AT CTCCGGAA
                                ||||||||  || ||||||||
                                CTACAGTC  TA GAGGCCTT
                                     CT  C
GAM2238  SSFA2     3'  AAGATGTTAGTCTGAAGAA    53557         CATA  CC
                                AAGATGTTAG    CT  GGAA
                                ||||||||||    ||  ||||
                                TTCTACAATC    GA  TCTT
                                      A___  CT
GAM2238  LOC122830 3'  TGAAATGTTAGTATACTTAAAG 53558   A       C    CC_
            A                    C AGATGTTAG ATACT   GGA
                                | |||||||||  |||||   |||
                                A TTTACAATC TATGA   TCT
                                 C        A     ATT
GAM2238  LOC147160 5'  AAGATGTTACATCCGG      53559         G  TAC
                                AAGATGTTA CA   TCCGG
                                |||||||||  ||   |||||
                                TTCTACAAT GT   AGGCC
                                      _  ___
GAM2238  LOC155061 3'  GATGTTAGATGCTGGAA     53560         C  A  CC
                                GATGTTAG AT CT  GGAA
                                ||||||||  ||  ||  ||||
                                CTACAATC TA GA  CCTT
                                     _  C  __
GAM2238  LOC221002 3'  AAGATGTTATCATGGA      53561         G   ACTCC
                                AAGATGTTA CAT     GGA
                                |||||||||  |||     |||
                                TTCTACAAT GTA     CCT
                                      A  _____
GAM2238  LOC90639  5'  ATGTTGGCGACTCCGGA     53562       A  AT
                                ATGTT GC  ACTCCGGA
                                |||||  ||  ||||||||
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                                TACAA CG  TGAGGCCT
                                   C  C_
GAM2239  GAS41    3'  AATAGTACAAATTCCTATTGCT 53565          TTTA   C__
                                AATGGTACAAAT   TCCT   GCT
                                ||||||||||||   ||||  |||
                                TTATCATGTTTA   AGGA   CGA
                                      _____   TAA
GAM2239  TERF1    3'  AATAGTACAAATTTTGTCCC  53566            A
                                AATGGTACAAATTTT TCCT
                                |||||||||||||| ||||
                                TTATCATGTTTAAAA AGGG
                                          C
GAM2239  DKFZp761O17121 3'  ATGGACATGTTTATCCTTGCT  53567     T   AAT      C
                                ATGG ACA   TTTATCCT GCT
                                |||| |||   |||||||| |||
                                TACC TGT   AAATAGGA CGA
                                  _  AC_      A
GAM2239  FLJ20856  5'  TGGTTCAAATTTTGCCCT    53568     A      AT
                                TGGT CAAATTTT  CCT
                                |||| ||||||||  |||
                                ACCA GTTTAAAA  GGA
                                   A       CG
GAM2239  HS747E2A  5'  GCCTTAAATTTTATTTTCGCT  53569    AC_       CC
                                GT   AAATTTTAT  TCGCT
                                ||   |||||||||  |||||
                                CG   TTTAAAATA  AGCGA
                                 GAA        AA
GAM2239  KIAA0882  3'  TGGTATAGGATTTACCCTCGCT 53570      CAAAT
                                TGGTA    TTTATCCTCGCT
                                |||||    ||||||||||||
                                ACCAT    AAATGGGAGCGA
                                   ATCCT
GAM2239  PCDH20   3'  GGCAATGATTTTATCCTTGCT  53571     CAA        C
                                GGTA   ATTTTATCCT GCT
                                ||||   |||||||||| |||
                                CCGT   TAAAATAGGA CGA
                                  TAC         A
GAM2239  LOC152620 3'  AATAGTACAAATTTTGTCCC  53566            A
                                AATGGTACAAATTTT TCCT
                                |||||||||||||| ||||
                                TTATCATGTTTAAAA AGGG
                                          C
GAM2239  LOC158668 3'  AATAGTACAAATTTTGTCCC  53566            A
                                AATGGTACAAATTTT TCCT
                                |||||||||||||| ||||
                                TTATCATGTTTAAAA AGGG
                                          C
GAM2239  LOC254700 3'  TGGTATGGATTTCACCTC    53572      CAA     T
                                TGGTA   ATTTTA CCTC
                                |||||   |||||| ||||
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                                ACCAT   TAAAGT GGAG
                                   ACC     _
GAM2239  LOC51170  3'  ATGGTACAAATTTTGCAAAGCC 53573            ATCCTC
                                ATGGTACAAATTTT     GCT
                                ||||||||||||||     |||
                                TACCATGTTTAAAA     CGG
                                       CGTTT_
GAM2239  LOC90918  5'  AATGGTGTAAATCTTATC    53574       AC
                                AATGGT  AAATTTTATC
                                ||||||  ||||||||||
                                TTACCA  TTTAGAATAG
                                   CA
GAM2240  DKFZP434P211 3'  CCTGAGAAAGCACATG      53577       C  CTAC
                                CCTGA GA    GAGCACATG
                                |||||  ||    |||||||||
                                GGACT CT    TTCGTGTAC

                                  _  _____
GAM2240  EFA6R     3'  CCTGCAGACTGAGCACATGC   53578     AC    AC
                                CCTG  GACT  GAGCACATGC
                                ||||  ||||  ||||||||||
                                GGAC  CTGA  CTCGTGTACG
                                  GT    __
GAM2240  SRF       3'  TCCCTGACACACGCAT      53579         G  T   AGCA
                                TCCCTGAC AC ACG    CAT
                                ||||||||  ||  |||    |||
                                AGGGACTG TG TGC    GTA

                                    _  _   _____
GAM2240  ZNF281    3'  TCCCTGACGATCTATACATG   53580          _   CGAGC
                                TCCCTGACGA CTA     ACATG
                                ||||||||||  |||     |||||
                                AGGGACTGCT GAT     TGTAC
                                      A   A_____
GAM2240  LOC130814 3'  CCTTGCTAGAGCACATG     53581     GACGA   C
                                CCT     CTA GAGCACATG
                                |||     |||  |||||||||
                                GGA     GAT CTCGTGTAC
                                  AC___   _
GAM2240  LOC150174 3'  CCTGAGAAAGCACATG      53577       C  CTAC
                                CCTGA GA    GAGCACATG
                                |||||  ||    |||||||||
                                GGACT CT    TTCGTGTAC

                                  _  _____
GAM2240  LOC152698 5'  TCCCTGACCACACCCTCATG   53582         G  T  GAGCA
                                TCCCTGAC AC AC     CATG
                                ||||||||  ||  ||     ||||
                                AGGGACTG TG TG     GTAC
                                     G  _  GGA__
GAM2240  LOC203286 5'  TCCCTGACGATCTATAACCTAC 53583          _   CG   __
            ATG                    TCCCTGACGA CTA  AGC  ACATG
                                ||||||||||  |||  |||  |||||
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                                AGGGACTGCT GAT  TTG  TGTAC
                                     A  A_  GA
GAM2240 LOC91464 5' TCCCTGACGTCACTTTACATGC 53584        AC  GAGC
                                TCCCTGACG  TAC   ACATGC
                                |||||||||  |||   ||||||
                                AGGGACTGC  GTG   TGTACG
                                     A_  AAA_
GAM2241 ACP5    3' CACCCCGGAACTCAG      53587      TAC  A
                                TACCC  CG GAACTCAG
                                |||||  || ||||||||
                                GTGGG  GC CTTGAGTC
                                  ____ _
GAM2241 EFEMP1   3' TACCCTACAGAAACCAG    53588       CG   CT
                                TACCCTAC  AGAA  CAG
                                ||||||||  ||||  |||
                                ATGGGATG  TCTT  GTC
                                     __   TG
GAM2241 EFEMP1   3' TACCCTACAGAAACCAG    53588       CG   CT
                                TACCCTAC  AGAA  CAG
                                ||||||||  ||||  |||
                                ATGGGATG  TCTT  GTC
                                     __   TG
GAM2241 EIF4G2   5' ACCTTCACCGAGAACTCAG   53589    C_
                                ACC  TACCGAGAACTCAG
                                |||  ||||||||||||||
                                TGG  GTGGCTCTTGAGTC
                                  AA
GAM2241 FBXW1B   3' TACTCTACCAAATATCAG    53590    C      AAC
                                TAC CTACCGAG   TCAG
                                ||| ||||||||   ||||
                                ATG GATGGTTT   AGTC
                                  A       AT_
GAM2241 FBXW1B   3' TACTCTACCAAATATCAG    53590    C      AAC
                                TAC CTACCGAG   TCAG
                                ||| ||||||||   ||||
                                ATG GATGGTTT   AGTC
                                  A       AT_
GAM2241 FBXW1B   3' TACTCTACCAAATATCAG    53590    C      AAC
                                TAC CTACCGAG   TCAG
                                ||| ||||||||   ||||
                                ATG GATGGTTT   AGTC
                                  A       AT_
GAM2241 GSTM3    3' TACCCAAGAGAAACTCAG    53591      TACC   _
                                TACCC   GAGAA CTCAG
                                |||||   ||||| |||||
                                ATGGG   CTCTT GAGTC
                                   TT__    T
GAM2241 LSS      3' CCTCTCCCAAGAACTCAG    53592    _ A
                                CC CT CCGAGAACTCAG
                                || || ||||||||||||
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                                GG GA GGTTCTTGAGTC
                                 A  G
GAM2241  PCTP     3'  TACCCTACCAAAATTCAG    53593           AC
                                TACCCTACCGAGA  TCAG
                                |||||||||||||  ||||
                                ATGGGATGGTTTT  AGTC
                                       A_
GAM2241  SOX13    3'  CACCCACAGGAACTCAG     53594      T  CGA
                                TACCC AC   GAACTCAG
                                ||||| ||   ||||||||
                                GTGGG TG   CTTGAGTC
                                   _  TC_
GAM2241  ZNF134   3'  ACCCCCAATGAACTCAG     53595      TA   _
                                ACCC  CCGA GAACTCAG
                                ||||  |||| ||||||||
                                TGGG  GGTT CTTGAGTC
                                  __    A
GAM2241  AKR1D1   3'  ACCCTTAAAGAACTCAG     53596      ACC
                                ACCCT   GAGAACTCAG
                                |||||   ||||||||||
                                TGGGA   TTCTTGAGTC
                                  AT_
GAM2241  ALS2CR3  3'  TACCCCACCAACCCCTCAG   53597          GAA
                                TACCCTACCGA   CTCAG
                                ||||||||||   |||||
                                ATGGGGTGGTT   GAGTC
                                      GGG
GAM2241  CAP350   3'  TACCCTAGTCTAAACTCAG   53598       CCGA
                                TACCCTA    GAACTCAG
                                |||||||    ||||||||
                                ATGGGAT    TTTGAGTC
                                    CAGA
GAM2241  DKFZp586H0623 3'  CACCCTACCCCCACAACTCAG  53599         GAG__
                                TACCCTACC    AACTCAG
                                |||||||||    |||||||
                                GTGGGATGG    TTGAGTC
                                     GGGTG
GAM2241  KIAA1458 3'  TACTTTACCAAACTCAG     53600     CC     GA
                                TAC  TACCGA  ACTCAG
                                |||  ||||||  ||||||
                                ATG  ATGGTT  TGAGTC
                                  AA     __
GAM2241  KIAA1671 3'  CACCCTACCGAAACCAG     53601           A T
                                TACCCTACCGAGA C CAG
                                |||||||||||||| | |||
                                GTGGGATGGCTTT G GTC
                                          _ _
GAM2241  KIAA1679 3'  ACTCTAGAAAACTCAG      53602    C   CC
                                AC CTA  GAGAACTCAG
                                || |||  ||||||||||
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                                TG GAT  CTTTTGAGTC
                                 A  __
GAM2241  LASP1    3'  CACTCTCCCAAACTCAG     53603     C  A  GA
                                TAC CT CC  GAACTCAG
                                ||| || ||  ||||||||
                                GTG GA GG  TTTGAGTC
                                  A  _  G_
GAM2241  RAB40A   5'  TACCCTACAGGAGATTATTCAG 53604        C_   AC__
                                TACCCTAC  GAGA   TCAG
                                ||||||||  ||||   ||||
                                ATGGGATG  CTCT   AGTC
                                     TC   AATA
GAM2241  UST      3'  CACCTGCACAGAACTCAG    53605     C_  CG
                                TACC  TAC  AGAACTCAG
                                ||||  |||  |||||||||
                                GTGG  GTG  TCTTGAGTC
                                  AC  __
GAM2241  LOC133088 5'  ACCCTTCCAAACTCAG      53606      A   GA
                                ACCCT CCGA  ACTCAG
                                ||||| ||||  ||||||
                                TGGGA GGTT  TGAGTC
                                   A   __
GAM2241  LOC199718 5'  CACCCAGAGAACTCAG      53607      TACC
                                TACCC   GAGAACTCAG
                                |||||   ||||||||||
                                GTGGG   CTCTTGAGTC
                                   T___
GAM2241  LOC257443 3'  TACTTTACCAAACTCAG     53600     CC     GA
                                TAC  TACCGA  ACTCAG
                                |||  ||||||  ||||||
                                ATG  ATGGTT  TGAGTC
                                  AA    __
GAM2241  LOC92095  3'  CACCCTACTCCACCTGCTCAG  53608       __  AGAA
                                TACCCTA  CCG   CTCAG
                                |||||||  |||   |||||
                                GTGGGAT  GGT   GAGTC
                                    GA   GGAC
GAM2241  LOC92096  3'  CACCCTACTCCACCTGCTCAG  53608       __  AGAA
                                TACCCTA  CCG   CTCAG
                                |||||||  |||   |||||
                                GTGGGAT  GGT   GAGTC
                                    GA   GGAC
GAM2242  APPL     3'  ACTGTAAAATCTCTGTTCT   53611      A       CA
                                ATTG TAAAATCTC  TTCT
                                |||| |||||||||  ||||
                                TGAC ATTTTAGAG  AAGA
                                  _       AC
GAM2242  F8       3'  TATTGTATTCTCTCCATT    53612      A  AAA
                                TATTG TA   TCTCCATT
                                ||||| ||   ||||||||
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                                ATAAC AT   AGAGGTAA
                                  _ AAG
GAM2242  RAB6A    3'  TAATATTGAGTTTTATTTCCAT 53613         TAAA_  C
             TCT                   TAATATTGA     AT TCCATTCT
                                   |||||||||     || ||||||||
                                   ATTATAACT     TA AGGTAAGA
                                       CAAAA  A
GAM2242  RNF14    3'  ATATTATAAATTTCCATTCT   53614       ATA    C
                                   ATATTG   AAAT TCCATTCT
                                   ||||||   |||| ||||||||
                                   TATAAT   TTTA AGGTAAGA
                                      A__    A
GAM2242  SART2    3'  TAATATTAATAAAACCCAATTC 53615              CC
             T                     TAATATTGATAAAATCT  ATTCT
                                   ||||||||||||||||  |||||
                                   ATTATAATTATTTTGGG  TAAGA
                                            T_
GAM2242  EEA1     3'  TAATATTGTTAAAACAAAAACC 53616         A     CT___
             ATT                   TAATATTG TAAAAT     CCATT
                                   ||||||||| ||||||     |||||
                                   ATTATAAC ATTTTG     GGTAA
                                        A     TTTTT
GAM2242  FLJ10980 3'  TAATTTGGTACACTCCATTCT  53617      A   A  AAAT
                                   TAAT TTG TA    CTCCATTCT
                                   |||| ||| ||    |||||||||
                                   ATTA AAC AT    GAGGTAAGA
                                     _   C  GT__
GAM2242  FLJ22794 3'  TATTGATAAGATGACCATT    53618         A  CT
                                   TATTGATAA AT  CCATT
                                   |||||||||  ||  |||||
                                   ATAACTATT TA  GGTAA
                                        C  CT
GAM2242  KIAA1328 3'  TAATATTAGTGGGCTCCATTCT 53619         ATAAAAT
                                   TAATATTG      CTCCATTCT
                                   ||||||||      |||||||||
                                   ATTATAAT      GAGGTAAGA
                                        CACCC__
GAM2242  PRO0902  3'  TAAAATTGATCTCCATT     53620     T    TAAAA
                                   TAA ATTGA     TCTCCATT
                                   ||| |||||     ||||||||
                                   ATT TAACT     AGAGGTAA
                                     T    ______
GAM2242  RASGRP4  3'  ACATTGATAGAAATCCCTGTTC 53621          _      CA
             T                      ATATTGATA AAATCTC  TTCT
                                    |||||||||  |||||||  ||||
                                    TGTAACTAT TTTAGGG  AAGA
                                         C      AC
GAM2242  WBP4     3'  TGTATAAGTCTCCATTCT    53622    _    AA
                                    TG ATAA  TCTCCATTCT
                                    ||  ||||  ||||||||||
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                                AC TATT  AGAGGTAAGA
                                 A   C_
GAM2242  LOC116150 3'  TATTAAACTGCTCCATTCT   53623       TAAAAT
                                TATTGA     CTCCATTCT
                                ||||||     |||||||||
                                ATAATT     GAGGTAAGA
                                   TGAC__
GAM2242  LOC164200 5'  TATTGATAACAACCTCATT   53624         _     C
                                TATTGATAA AATCTC ATT
                                ||||||||| |||||| |||
                                ATAACTATT TTGGAG TAA
                                     G     _
GAM2242  LOC51320  3'  ATATTGATAATTTATCATTCT  53625         AATCTC
                                ATATTGATAA     CATTCT
                                ||||||||||     ||||||
                                TATAACTATT     GTAAGA
                                     AAATA_
GAM2243  BSN       3'  CATTGCATAGAACGTTAG    53628         AACT
                                CATTGCATA    CGTTAG
                                |||||||||    ||||||
                                GTAACGTAT    GCAATC
                                     CTT_
GAM2243  BTEB1     3'  TTGCTTGCATAAAGACA     53629      A       CT
                                TTGC TTGCATAAA  CG
                                |||| |||||||||  ||
                                AACG AACGTATTT  GT
                                  _       CT
GAM2243  TXNRD2    3'  TTGCATTGCAGAAATGCCAG   53630         T   CTC
                                TTGCATTGCA AAA   GTTAG
                                |||||||||| |||   |||||
                                AACGTAACGT TTT   CGGTC
                                     C   A__
GAM2243  C8orf7    3'  CTGCATTGCATAAGCCTGACTA 53631           A_  CG
              G                  TTGCATTGCATAA  CT  TTAG
                                ||||||||||||  ||  ||||
                                GACGTAACGTATT  GA  GATC
                                       CG  CT
GAM2243  CNOT4     3'  TCGCATTGCATCTGGGGTTAG  53632         AAACTC
                                TTGCATTGCAT     GTTAG
                                ||||||||||     |||||
                                AGCGTAACGTA     CAATC
                                     GACCC_
GAM2243  FLJ14906  3'  TTGCATTGCATAATTCA     53633          AC
                                TTGCATTGCATAA  TCG
                                ||||||||||||  |||
                                AACGTAACGTATT  AGT
                                     A_
GAM2243  FLJ20533  3'  TTACGTTGCAACTCGTTAG   53634      A    TAA
                                TTGC TTGCA   ACTCGTTAG
                                |||| |||||   |||||||||
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                                AATG AACGT   TGAGCAATC
                                  C    ___
GAM2243  KIAA0053  3'  TTGCTTGCATAAATACA     53635      A       CT
                                TTGC TTGCATAAA  CG
                                |||| |||||||||  ||
                                AACG AACGTATTT  GT
                                  _       AT
GAM2243  LOC115574 3'  TTGCATTGCAAATCTCTTAG   53636          TAAA   G
                                TTGCATTGCA    CTC TTAG
                                ||||||||||    ||| ||||
                                AACGTAACGT    GAG AATC
                                      TTA_  _
GAM2243  LOC146603 5'  TTGCATTATATAGGTTCGTT   53637        C   AAC
                                TTGCATTG ATA   TCGTT
                                |||||||| |||   |||||
                                AACGTAAT TAT   AGCAA
                                     A   CCA
GAM2244  B3GALT3   3'  TGTAGTAGGTTTGTTTACACCA 53640        A     C    G_
           GC                     TGTGGTAG TTTGTT TATA  AGC
                                |||||||| |||||| ||||  |||
                                ACATCATC AAACAA ATGT  TCG
                                     C      _    GG
GAM2244  KIAA1985  5'  TGGTGGATTTGTTTTAATACAG 53641      A       C___
           AGC                     TGGT GATTTGTT    TATAGAGC
                                |||| ||||||||    ||||||||
                                ACCA CTAAACAA    ATGTCTCG
                                  C       AATT
GAM2244  MCM10     3'  TGTGGTAATTTGCATAG     53642       A      TCT
                                TGTGGT GATTTGT   ATAG
                                ||||||| |||||||   ||||
                                ACACCA TTAAACG   TATC
                                   _      ____
GAM2244  LOC149707 5'  TGGTAGATGTTGTGGAG     53643         _    TCTATA
                                TGGTAGAT TTGT     GAG
                                |||||||| ||||      |||
                                ACCATCTA AACA     CTC
                                     C    C_____
GAM2244  LOC200227 5'  TGGTAGATGTTGTGGAG     53643         _    TCTATA
                                TGGTAGAT TTGT     GAG
                                |||||||| ||||      |||
                                ACCATCTA AACA     CTC
                                     C    C_____
GAM2244  LOC222234 3'  TGTGGTAATTTGTTACAGAGC  53644       A      TC
                                TGTGGT GATTTGT  TATAGAGC
                                ||||||| |||||||  ||||||||
                                ACACCA TTAAACA  ATGTCTCG
                                   _      __
GAM2244  LOC255718 5'  GTAGACATGTTCTATAGAGC   53645       T
                                GTAGAT TGTTCTATAGAGC
                                |||||| ||||||||||||
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                                CATCTG ACAAGATATCTCG
                                   T
GAM2245 DSG3     3' GTATGAACCCAAACATTTAA  53648     C_
                                GTAT  ATTTAAACATTTAA
                                ||||  ||||||||||||||
                                CATA  TGGGTTTGTAAATT
                                  CT
GAM2245 LPIN1    3' CAGTATCATTATCATTT     53649         TAAA
                                CAGTATCATT   CATTT
                                ||||||||||   |||||
                                GTCATAGTAA   GTAAA
                                      TA__
GAM2245 TRPM1    3' ACAGTATCATCACTTTCATTT 53650          TAAA_
                                ACAGTATCATT    CATTT
                                ||||||||||    |||||
                                TGTCATAGTAG    GTAAA
                                      TGAAA
GAM2245 C1QR1    3' AACAGTATCACATTTA      53651         ATTTAA
                                AACAGTATC     ACATTTA
                                |||||||||     |||||||
                                TTGTCATAG     TGTAAAT
                                              _______
GAM2245 DEPP     3' AACAGAAGACAGAAAACATTTA 53652      TAT_ TTT
          AC                      AACAG   CA  AAACATTTAAC
                                |||||   ||  ||||||||||
                                TTGTC   GT  TTTGTAAATTG
                                  TTCT  CT_
GAM2245 FLJ20668 3' AGTATCATGGTCCATTTAA   53653       TTAAA
                                AGTATCAT    CATTTAA
                                ||||||||    |||||||
                                TCATAGTA    GTAAATT
                                    CCAG_
GAM2245 KIAA1524  5' ACAGTAGGTTCTAAACATTTA  53654      TCA
                                ACAGTA   TTTAAACATTTA
                                ||||||   ||||||||||||
                                TGTCAT   AGATTTGTAAAT
                                   CCA
GAM2245 PRO1617   5' CAGTACCATTCACTGATTT   53655          AAC
                                CAGTATCATTTA   ATTT
                                ||||||||||||   ||||
                                GTCATGGTAAGT   TAAA
                                      GAC
GAM2245 SDF1     3' ACAGTATTCATCACATTTAAC  53656       _   TAA
                                ACAGTAT CATT   ACATTTAAC
                                ||||||| ||||   |||||||||
                                TGTCATA GTAG   TGTAAATTG
                                   A   ___
GAM2245 LOC130074 3' AGTATCAATTGACACCTAAC   53657       TTTAA
                                AGTATCA    ACATTTAAC
                                |||||||    |||||||||
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                                TCATAGT    TGTGGATTG
                                   TAAC_
GAM2245  LOC146952 5'  AACAGTACATAAAATTACATTT 53658       T  TT __
            A                   AACAGTA CAT  AA  ACATTTA
                                ||||||| |||  ||  |||||||
                                TTGTCAT GTA  TT  TGTAAAT
                                   _  TT  AA
GAM2245  LOC157983 3'  AGTATCATTTAACATGCAA   53659          A  T
                                AGTATCATTTAA CAT TAA
                                |||||||||||| ||| |||
                                TCATAGTAAATT GTA GTT
                                      _  C
GAM2245  LOC203289 3'  AGTATCATTTAACATGCAA   53659          A  T
                                AGTATCATTTAA CAT TAA
                                |||||||||||| ||| |||
                                TCATAGTAAATT GTA GTT
                                      _  C
GAM2245  LOC256544 3'  AGTATCATTTAACATGCAA   53659          A  T
                                AGTATCATTTAA CAT TAA
                                |||||||||||| ||| |||
                                TCATAGTAAATT GTA GTT
                                      _  C
GAM2246  NY-REN-60 3'  TAGGTCCCCATTGGTAGT    53662
                                TAGGTCCCTATTGGTAGT
                                ||||||||||||||||||
                                ATCCAGGGGTAACCATCA

GAM2246  LOC150208 5'  TAGGTCTGCTGTGTTCACT   53663       CCTATTG  A
                                TAGGTC      GT GTTCACT
                                ||||||      || |||||||
                                ATCCAG      CA CAAGTGA
                                   ACGA___  _
GAM2247  F7      3'  CACTTGGTGTGTGTGTGC    53666          AACCCATA
                                CATTTGGTGT      TGTGC
                                ||||||||||      |||||
                                GTGAACCACA      ACACG
                                      CAC_____
GAM2247  F7      3'  CACTTGGTGTGTGTGTGC    53666          AACCCATA
                                CATTTGGTGT      TGTGC
                                ||||||||||      |||||
                                GTGAACCACA      ACACG
                                      CAC_____
GAM2247  TLL2     5'  CATTTGGTGTACGTG       53667          AACCCAT
                                CATTTGGTGT      ATGTG
                                ||||||||||      |||||
                                GTAAACCACA      TGCAC
                                      _______
GAM2247  FLJ13544  5'  CATTTGGTGTCGTTCCCGGCC  53668          AA__  ATAT T
                                CATTTGGTGT   CCC   G GCC
                                ||||||||||   |||   | |||
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                                GTAAACCACA   GGG   C CGG
                                     GCAA  _____ _
GAM2247  FLJ20378  5'  CAATTGGTGTAATTTGTG   53669   T      CCCATA
                                CA TTGGTGTAA     TGTG
                                || |||||||||     ||||
                                GT AACCACATT     ACAC
                                 T       AA____
GAM2247  jdp2      3'  CATTCGGTGAGTATGTGC   53670        TAACCCA
                                CATTTGGTG      TATGTGC
                                |||||||||      |||||||
                                GTAAGCCAC      ATACACG
                                     TC_____
GAM2247  KIAA0884  3'  ATTTTGTGCATATATGTGC   53671     G    ACCC
                                ATTT GTGTA   ATATGTGC
                                |||| |||||   ||||||||
                                TAAA CACGT   TATACACG
                                  A    A___
GAM2247  KIAA1243  3'  ATTTGGTGCTAATTTAATAAGC 53672        AACCCAT   T
              C                  ATTTGGTGT      ATG GCC
                                |||||||||      ||| |||
                                TAAACCACG      TAT CGG
                                     ATTAAAT   T
GAM2247  KIAA1889  3'  CTGGTGTAACTTATGTG    53673        CCA
                                TTGGTGTAAC   TATGTG
                                ||||||||||   ||||||
                                GACCACATTG   ATACAC
                                     A__
GAM2247  LIPI      3'  TTTGGTGTACATGTG      53674        AACCC
                                TTTGGTGT    ATATGTG
                                ||||||||    |||||||
                                AAACCACA    TGTACAC
                                     _____
GAM2247  MGC35521  3'  CATCTGGTGTGGCTGTGC   53675        AACCCATA
                                CATTTGGTGT       TGTGC
                                ||||||||||       |||||
                                GTAGACCACA       ACACG
                                     CCG_____
GAM2247  PB1       3'  TTTGGTGTAATTCAAGGATGT  53676        CC  T__
                                TTTGGTGTAA  CA   ATGT
                                ||||||||||  ||   ||||
                                AAACCACATT  GT   TACA
                                     AA  TCC
GAM2247  RoXaN     3'  ATTTGCTGTGGCCCCCTGGCC  53677      G   AA   ATA  T
                                ATTTG TGT  CCC   TG GCC
                                ||||| |||  |||   || |||
                                TAAAC ACA  GGG   AC CGG
                                   G   CC   GG_ _
GAM2247  TPARL     3'  ATTTGGGTAATCCCACATGGCC 53678      T   _      T
                                ATTTGG GTAA CCCATATG GCC
                                |||||| |||| |||||||| |||
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                                TAAACC CATT GGGTGTAC CGG
                                  _   A      _
GAM2247  LOC148645 3'  TTTGATGCCCATGTGTGC    53679       TAA    A
                                TTTGGTG   CCCAT TGTGC
                                |||||||   ||||| |||||
                                AAACTAC   GGGTA ACACG
                                   ___    C
GAM2247  LOC149842 5'  CATTTGGAGTGACCTATG    53680       T  A   CA
                                CATTTGG GT ACC  TATG
                                ||||||| || |||  ||||
                                GTAAACC CA TGG  ATAC
                                   T  C   __
GAM2247  LOC253970 3'  CATCTGGTGTGGGAGATGTGCC 53681         AACCCAT
                                CATTTGGTGT      ATGTGCC
                                ||||||||||      |||||||
                                GTAGACCACA      TACACGG
                                      CCCTC__
GAM2247  LOC256667 3'  CATATTGTTTTCCATATGTG   53682    TTGG   AAC
                                CAT    TGT   CCATATGTG
                                |||    |||   |||||||||
                                GTA    ACA   GGTATACAC
                                  TA__   AAA
GAM2247  LOC55954  3'  CACTTGGTGTGGCCGTGT    53683        AA  CATA
                                CATTTGGTGT  CC    TGT
                                |||||||||  ||   |||
                                GTGAACCACA  GG    ACA
                                      CC  C___
GAM2248  CDH13     3'  TTAGTTTCCACCCACCTTGC   53686      C   G     GTCC
                                TTAGT TCC ACCCGCC    GC
                                ||||| ||| |||||||    ||
                                AATCA AGG TGGGTGG    CG
                                   A   _      AA__
GAM2248  EYA1      3'  TTAGTCTCCGATTCATGAACC  53687         CC  CCGT
                                TTAGTCTCCGA  CG    CC
                                ||||||||||  ||    ||
                                AATCAGAGGCT  GT    GG
                                      AA  ACTT
GAM2248  FLJ13162  5'  GTCTCATCCACCTGCTGTCTGC 53688      CG__   C  C   C
                                GTCTC    ACC GC GTC GC
                                |||||    ||| || ||| ||
                                CAGAG    TGG CG CAG CG
                                   TAGG   A  A   A
GAM2248  FLJ21195  5'  GTCTCCCGCCGCCGC      53689      CCGA      T
                                GTCT    CCCGCCG CCGC
                                ||||    ||||||| ||||
                                CAGA    GGGCGGC GGCG
                                  _____     _
GAM2248  KIAA0205  3'  TTAGTCTCTACCCTTCCTGC   53690        CG   GCCG   _
                                TTAGTCTC  ACCC    TCC GC
                                ||||||||  ||||    ||| ||
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                                AATCAGAG  TGGG   AGG CG
                                    A_   A___   A
GAM2248  RoXaN    3'  TCAGTCTCCGGAGTGTCTGCC  53691         ACCCGCC   C
                                TTAGTCTCCG      GTC GCC
                                ||||||||||      ||| |||
                                AGTCAGAGGC      CAG CGG
                                     CTCA___   A
GAM2248  LOC147791 3'  TTAGCCTCTGACTTGCACC   53692        C   C__
                                TTAGTCTC GAC   CGCC
                                |||||||| |||   ||||
                                AATCGGAG CTG   GTGG
                                    A   AAC
GAM2249  PSPHL    5'  TTGGAGCTGTATGACAATGGAT 53695     A      ATT    A_
              G                  TTG AGCTGTAT   ACGA  GATG
                                ||| ||||||||   ||||  ||||
                                AAC TCGACATA   TGTT  CTAC
                                  C       C__    AC
GAM2249  PSPH     3'  TTGGAGCTGTACGACAATGGAT 53696     A      ATT    A_
              G                  TTG AGCTGTAT   ACGA  GATG
                                ||| ||||||||   ||||  ||||
                                AAC TCGACATG   TGTT  CTAC
                                  C       C__    AC
GAM2249  LOC152185 3'  TTAAGGCTGTATATTTCACTTG 53697      A        A  AA_
              ATG                  TTGA GCTGTATATT CG   GATG
                                |||| |||||||||| ||   ||||
                                AATT CGACATATAA GT   CTAC
                                  C        A  GAA
GAM2250  CACNA1D  3'  GGCGGGGCCTGCTGTTTCCT   53700     A         AA
                                GGC GGGTCTGCTGTT  CT
                                ||| ||||||||||||  ||
                                CCG CCCGGACGACAA  GA
                                  C          AG
GAM2250  CHRNB4   3'  AGGCAGGGTAACGTGACTGT   53701         C___  _
                                AGGCAGGGT    TG CTGT
                                |||||||||    || ||||
                                TCCGTCCCA    AC GACA
                                     TTGC  T
GAM2250  DDEF2    3'  AGGCAGGATCTTGATTA     53702          GCT
                                AGGCAGGGTCT   GTTA
                                ||||||||||   ||||
                                TCCGTCCTAGA   TAAT
                                     AC_
GAM2250  HS2ST1   3'  GGCAGGGTTGACTAGCTGT    53703         ___  _
                                GGCAGGGT   CT GCTGT
                                ||||||||   || |||||
                                CCGTCCCA   GA CGACA
                                     ACT  T
GAM2250  INHBB    3'  AGGCAGGTCTGCAAGTGCTA   53704        G    ___
                                AGGCAGG TCTGC   TGTTA
                                ||||||| |||||   |||||
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                                TCCGTCC AGACG   ACGAT
                                   _    TTC
GAM2250  LZTS1    5'  GGCAGGGTCTTGGAAAGGCTGT 53705          _______
                                GGCAGGGTCT      GCTGT
                                ||||||||||      |||||
                                CCGTCCCAGA      CGACA
                                     ACCTTTC
GAM2250  PTGS1    3'  AGGCAGGAGTCGATGGCTAT   53706       _  T___
                                AGGCAGG GTC    GCTGT
                                ||||||| |||    |||||
                                TCCGTCC CAG    CGATA
                                   T   CTAC
GAM2250  PTGS1    3'  AGGCAGGAGTCGATGGCTAT   53706       _  T___
                                AGGCAGG GTC    GCTGT
                                ||||||| |||    |||||
                                TCCGTCC CAG    CGATA
                                   T   CTAC
GAM2250  VANGL2   3'  GGTCAGGGTCTGCAAGCCACTA 53707    _       T_   A
            T                    GG CAGGGTCTGC  GTTA CTAT
                                 || ||||||||||  |||| ||||
                                 CC GTCCCAGACG  CGGT GATA
                                  A         TT   _
GAM2250  CACNA2D1 3'  GGCAGGGTCTGGAGTTTAACTA 53708          CT   _
            T                    GGCAGGGTCTG  GTT AACTAT
                                 ||||||||||  ||| ||||||
                                 CCGTCCCAGAC  CAA TTGATA
                                       CT   A
GAM2250  DKFZP566N034 3'  AGGTGGGTCTGCTCAGTCCTAT 53709     CA       GTTAA
                                 AGG  GGGTCTGCT    CTAT
                                 |||  |||||||||    ||||
                                 TCC  CCCAGACGA    GATA
                                   A_       GTCAG
GAM2250  FLJ13224 3'  GGCAGGGTCGGGCGCCGTT   53710        ___
                                 GGCAGGGTC   TGCTGTT
                                 |||||||||   |||||||
                                 CCGTCCCAG   GCGGCAA
                                       CCC
GAM2250  FLJ13315 3'  AGACAGGGTCTCTGATAACT   53711          G   T
                                 AGGCAGGGTCT CTG TAACT
                                 |||||||||| ||| |||||
                                 TCTGTCCCAGA GAC ATTGA
                                       _   T
GAM2250  FLJ14440 3'  GGCTCTTTGTTGTTAACTAT   53712    G   GC__
                                 GG TCT    TGTTAACTAT
                                 || |||    ||||||||||
                                 CC AGA    ACAATTGATA
                                  G   AACA
GAM2250  INVS     3'  AGATTTTGCTGTTAATTAT    53713     GTC       C
                                 AGG   TGCTGTTAA TAT
                                 |||   ||||||||| |||
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                                TCT   ACGACAATT ATA
                                  AAA       A
GAM2250  KIAA0964  3'  GGGCGTTTGTTAACTATA    53714     CTGC
                                GGGT    TGTTAACTATA
                                ||||    ||||||||||
                                CCCG    ACAATTGATAT
                                  CAA_
GAM2250  MAPK6     3'  AGGCAAGGTTTGTTTCCTGT   53715        C ____
                                AGGCAGGGT TG    CTGT
                                ||||||||| ||    ||||
                                TCCGTTCCA AC    GACA
                                      A  AAAG
GAM2250  MCF2L     3'  GGCAGGGCTCTCTGAGCTAT   53716       _  G   TTAA
                                GGCAGGG TCT CTG    CTAT
                                ||||||| ||| |||    ||||
                                CCGTCCC AGA GAC    GATA
                                    G   _   TC__
GAM2250  PRO2389   3'  GGCAGGGCCTGCCCTAT     53717          GTTAA
                                GGCAGGGTCTGCT    CTAT
                                ||||||||||||     ||||
                                CCGTCCCGGACGG    GATA
                                          _____
GAM2250  SRCRB4D   3'  AGGCAGAGTCTGGTGCTA     53718          C
                                AGGCAGGGTCTG TGTTA
                                |||||||||||| |||||
                                TCCGTCTCAGAC ACGAT
                                       C
GAM2250  LOC147700 3'  AGGAGGGTCTGGGGGACTGT   53719     C      _____
                                AGG AGGGTCTG     CTGT
                                ||| ||||||||     ||||
                                TCC TCCCAGAC     GACA
                                  _       CCCCT
GAM2250  LOC149465 3'  AGGCAGGGTATTGTTCCAT    53720        CTGC    AA
                                AGGCAGGGT    TGTT  CTAT
                                |||||||||    ||||  ||||
                                TCCGTCCCA    ACAA  GGTA
                                      TA__    __
GAM2250  LOC158055 3'  GGCAGGGTTGGTTTCTGCAGCT 53721        _______    T
           A                     GGCAGGG      TCTGC GTTA
                                 |||||||      ||||| ||||
                                 CCGTCCC      AGACG CGAT
                                     AACCAA     T
GAM2250  LOC170372 3'  AGGCAAGGTTTGTTTCCTGT   53715        C ____
                                AGGCAGGGT TG    CTGT
                                ||||||||| ||    ||||
                                TCCGTTCCA AC    GACA
                                      A  AAAG
GAM2250  LOC91862  3'  AGCCAGGGTCTGTTGCATCCAT 53722    G       C   TAA
                                AG CAGGGTCTG TGT   CTAT
                                || |||||||| |||   ||||
```

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                                TC GTCCCAGAC ACG   GGTA
                                 G        A   TA_
GAM2251  DKFZP434A0225 3'  TGATTGAACATTTAGT      53725        TGAC
                                TGATTGA    ATATTTAGT
                                |||||||    |||||||||
                                ACTAACT    TGTAAATCA
                                    ____
GAM2251  LOC150481 5'  GATTGATGGCATATCCTGT    53726         A     TA
                                GATTGATG CATATT  GT
                                |||||||| ||||||  ||
                                CTAACTAC GTATAG  CA
                                     C      GA
GAM2252  PTPRM    3'  TCAGCTGTAACAATAACGA    53729        T GG
                                TCAGTTG T  TAATAACGA
                                ||||||| |  |||||||||
                                AGTCGAC A  GTTATTGCT
                                    _ TT
GAM2252  SRGAP1   3'  CAGTTATTGAATAACG      53730          TA
                                CAGTTGTTGG  ATAACG
                                ||||||||||  ||||||
                                GTCAATAACT  TATTGC
                                    __
GAM2252  GMFB     3'  TCAGTTGTTGGTTTTGTTAAAC 53731           AAT____
                GA                  TCAGTTGTTGGT      AACGA
                                ||||||||||||      |||||
                                AGTCAACAACCA      TTGCT
                                      AAACAAT
GAM2252  HTEX4    5'  TCAGCTGTCCACTTAACG    53732         G TAA
                                TCAGTTGTT G   TAACG
                                ||||||||| |   |||||
                                AGTCGACAG T   ATTGC
                                     G GA_
GAM2252  HTEX4    5'  TCAGCTGTCCACTTAACG    53732         G TAA
                                TCAGTTGTT G   TAACG
                                ||||||||| |   |||||
                                AGTCGACAG T   ATTGC
                                     G GA_
GAM2252  HTEX4    5'  TCAGCTGTCCACTTAACG    53732         G TAA
                                TCAGTTGTT G   TAACG
                                ||||||||| |   |||||
                                AGTCGACAG T   ATTGC
                                     G GA_
GAM2252  SEC15B   3'  CCAGTTAAGAAATAACGA    53733        TT  T
                                TCAGTTG  GG AATAACGA
                                |||||||  || ||||||||
                                GGTCAAT  TC TTATTGCT
                                    __  T
GAM2252  LOC130564 5'  TCAGTTGCTGGTGCCGA     53734           AATAA
                                TCAGTTGTTGGT    CGA
                                ||||||||||||    |||
```

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                                AGTCAACGACCA    GCT
                                      CG___
GAM2252  LOC253955 3'  TCAGTAATCTATTGGTAAT   53735     ____
                                TCAGT   TGTTGGTAAT
                                |||||   ||||||||||
                                AGTCA   ATAACCATTA
                                   TTAG
GAM2253  FLJ10697  3'  TATCATGCAAGTATCTATATAT 53738      A   GATTG
                                TATCAT CAAG    TTATATAT
                                |||||| ||||    ||||||||
                                ATAGTA GTTC    GATATATA
                                   C   ATA__
GAM2253  NTN4      3'  ATACAAGGAAATACTATAT   53739       T_
                                ATACAAGGA  TGTTATAT
                                |||||||||  ||||||||
                                TATGTTCCT  ATGATATA
                                      TT
GAM2253  SEMA3E    3'  TATGATACAAGGATTAACAT   53740    C         T
                                TAT ATACAAGGATTG TAT
                                ||| ||||||||||| |||
                                ATA TATGTTCCTAAT GTA
                                  C         T
GAM2254  ADAM12    3'  TTGGTTCATATCCTCTTATA   53743     TA      _
                                TTGGT  TTATATTC CTTATA
                                |||||  |||||||| ||||||
                                AACCA  AGTATAGG GAATAT
                                   __       A
GAM2254  C8orf2    3'  TTGGTTATTACCTGTTTTATA  53744         ATTCC
                                TTGGTTATTAT    TTATA
                                ||||||||||    |||||
                                AACCAATAATG    AATAT
                                      GACAA
GAM2254  FLJ13197  3'  CTTGGCTATTACCAGTAGTTCC 53745       A_____      III
              TTATAT                GTTATTAT    TTCCTTATA  T
                                ||||||||    |||||||||  |
                                CGATAATG    AAGGAATAT  A
                                     GTCATC       III
GAM2254  FLJ14107  5'  CCTTGGAGCGCATGTTCCTT   53746      TTAT  A
                                CCTTGG   TAT TTCCTT
                                ||||||   ||| ||||||
                                GGAACC   GTA AAGGAA
                                   TCGC  C
GAM2254  KIAA0825  3'  CTTGGTTGTTTGCTCCTTAT   53747      A  ATA
                                CTTGGTT TT   TTCCTTAT
                                ||||||| ||   ||||||||
                                GAACCAA AA   GAGGAATA
                                   C  AC_
GAM2254  LOC256950 3'  TCATGGCTATTATTTCTTATA  53748    CT       A  C
                                TC  TGGTTATTAT TTC TTATA
                                ||  |||||||||| ||| |||||
```

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                                AG  ACCGATAATA AAG AATAT
                                 T_        _  _
GAM2255  DKFZP564A1164 3'  TTGCCCCAACAGTGGTAAT   53751      A      TAAC
                                TTGT CCCGATA   GGTAAT
                                |||| |||||||   ||||||
                                AACG GGGTTGT   CCATTA
                                  _      CA__
GAM2256  ICAM1    3'  TAGACAGCAGTGCCATGTCTA  53754      AAA  CTATA
                                TAGA   CA    CCATGTCTA
                                ||||   ||    |||||||||
                                ATCT   GT    GGTACAGAT
                                  GTC  CAC__
GAM2256  L1CAM    3'  GAGGAGACCCCACCATGTCT   53755    AAAC   A
                                GA    ACT TACCATGTCT
                                ||    ||| ||||||||||
                                CT    TGG GTGGTACAGA
                                 CCTC   G
GAM2256  L1CAM    3'  GAGGAGACCCCACCATGTCT   53755    AAAC   A
                                GA    ACT TACCATGTCT
                                ||    ||| ||||||||||
                                CT    TGG GTGGTACAGA
                                 CCTC   G
GAM2256  MASP1    3'  GAAAACACTTATGGCCTTGC   53756         _ A_  A
                                GAAAACACT AT  CC TGT
                                ||||||||| ||  || |||
                                CTTTTGTGA TA  GG ACG
                                     A  CC  A
GAM2256  PPEF2    3'  GAAAACACTATACCTAAGTTCT 53757            ATG__
              AC                  GAAAACACTATACC    TCTAC
                                ||||||||||||||    |||||
                                CTTTTGTGATATGG    AGATG
                                       ATTCA
GAM2256  SIM2     3'  TAGAAAATGCTTAAAATGTCTA 53758        CA  A  CC
              C                  TAGAAAA  CT TA  ATGTCTAC
                                |||||||  || ||  ||||||||
                                ATCTTTT  GA AT  TACAGATG
                                    AC  _  TT
GAM2256  CAPS2    3'  AAAAACACTATATGCATAT    53759          C_
                                GAAAACACTATA  CATGT
                                ||||||||||||  |||||
                                TTTTTGTGATAT  GTATA
                                       AC
GAM2256  DKFZP564O0423 3'  TACAAAACACTGCCCAGTCT   53760    G      ATA   T
                                TA AAAACACT   CCA GTCT
                                || ||||||||   ||| ||||
                                AT TTTTGTGA   GGT CAGA
                                 G       CG_  _
GAM2256  HNRPA0   3'  TAGAAAACGCTGTAGCCAGGT  53761        A  A  _   T
                                TAGAAAAC CT TA CCA GT
                                |||||||| || || ||| ||
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                                ATCTTTTG GA AT GGT CA
                                    C  C  C   C
GAM2256  KIAA0895  3'  TAGAAAACACTACACAATGC   53762            C
                                TAGAAAACACTATAC ATGT
                                |||||||||||||| ||||
                                ATCTTTTGTGATGTG TACG
                                       T
GAM2256  KIAA0931  3'  TAGAAAACACAATGTCT     53763          TATACC
                                TAGAAAACAC     ATGTCT
                                ||||||||||     ||||||
                                ATCTTTTGTG     TACAGA
                                      T_____
GAM2256  KIAA1456  3'  AAAAACACTATACATGT     53764           C
                                GAAAACACTATAC ATGT
                                |||||||||||| ||||
                                TTTTTGTGATATG TACA
                                         _
GAM2256  MGC5370   3'  TAGGAAACCTCTGCCATGTCT  53765     A    A  ATA
                                TAG AAAC CT   CCATGTCT
                                ||| |||| ||   ||||||||
                                ATC TTTG GA   GGTACAGA
                                  C    _  GAC
GAM2256  Rpo1-2    3'  TAAAAAACACTGTACCTGT    53766          A    A
                                TAGAAAACACT TACC TGT
                                |||||||||| |||| |||
                                ATTTTTTGTGA ATGG ACA
                                       C    _
GAM2256  Rpo1-2    3'  TAAAAAACACTGTACCTGT    53766          A    A
                                TAGAAAACACT TACC TGT
                                |||||||||| |||| |||
                                ATTTTTTGTGA ATGG ACA
                                       C    _
GAM2256  RTP801    3'  AAACACTATTCCCCCAC      53767         A  ATG
                                AAACACTAT CC   TCTAC
                                |||||||| ||   |||||
                                TTTGTGATA GG   GGGTG
                                      A  ___
GAM2256  SEMA5A    3'  AAGAACACGTTTCCATGTCTAC 53768     A     TATA
                                GA AACAC    CCATGTCTAC
                                || |||||    ||||||||||
                                TT TTGTG    GGTACAGATG
                                  C     CAAA
GAM2256  SFRS12    3'  TAGAAAACAGTATACCACAT   53769          C
                                TAGAAAACA TATACCATGT
                                ||||||||| ||||||||||
                                ATCTTTTGT ATATGGTGTA
                                       C
GAM2256  ZNF396    3'  GAAAACACAATACATGT      53770         T    C
                                GAAAACAC ATAC ATGT
                                |||||||| |||| ||||
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                                CTTTTGTG TATG TACA
                                     T   _
GAM2256  LOC145826 5'  AGAAAACACTATGCT      53771          TACCA  T
                                AGAAAACACTA     TG CT
                                ||||||||||     || ||
                                TCTTTTGTGAT     AC GA
                                      _____ _
GAM2256  LOC201627 3'  AAAAAACCCATCATGTCTA   53772        A    AC
                                AGAAAAC CTAT  CATGTCTA
                                ||||||| ||||  ||||||||
                                TTTTTTG GGTA  GTACAGAT
                                   _   __
GAM2256  LOC219505 3'  TAGAAAACACTACATGT     53773           TAC
                                TAGAAAACACTA   CATGT
                                ||||||||||||   |||||
                                ATCTTTTGTGAT   GTACA
                                      ___
GAM2256  LOC91923  5'  GAAGCAACACACATGTCTA   53774     __    TATAC
                                GAA  AACAC     CATGTCTA
                                |||  |||||     ||||||||
                                CTT  TTGTG     GTACAGAT
                                  CG     T____
GAM2257  DSG1      3'  TTGTGGACTTGACTATGTAG   53777        GA   A
                                TTGTGGAT  TGA CTATGTAG
                                ||||||||  ||| ||||||||
                                AACACCTG  ACT GATACATC
                                     A_   _
GAM2257  AF9Q34    3'  CTTTGTGGCTGAGTGTGTA    53778        A   _  AACTA
                                CTTTGTGG TGA TG     TGTA
                                |||||||| ||| ||     ||||
                                GAAACACC ACT AC     ACAT
                                     G   C  _____
GAM2257  DKFZP434F1735 5'  CTTTGTGGAGGATGGACT    53779          T    A
                                CTTTGTGGA GATG ACT
                                ||||||||| |||| |||
                                GAAACACCT CTAC TGA
                                      C    C
GAM2257  LOC144509 5'  CTTTGTGGAGATGGGTGCA    53780          T    AACTA
                                CTTTGTGGA GATG     TGTA
                                ||||||||| ||||     ||||
                                GAAACACCT CTAC     ACGT
                                     _    CC___
GAM2257  LOC148195 5'  TTTGAGGATGATGACTCTG    53781      T        A  A
                                TTTG GGATGATGA CT TG
                                |||| ||||||||| || ||
                                AAAC CCTACTACT GA AC
                                  T        _  G
GAM2257  LOC199986 5'  CTTTGTGGATGAGTGGAGCAG  53782            _  AACTAT
                                CTTTGTGGATGA TG     GTAG
                                ||||||||||| ||     ||||
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                                GAAACACCTACT AC     CGTC
                                      C  CT____
GAM2257  LOC256113 5'  CTTTGTGGATTATTCCGTATGT 53783         G  GAAC
                                CTTTGTGGAT AT    TATGT
                                |||||||||| ||    |||||
                                GAAACACCTA TA    ATACA
                                     A  AGGC
GAM2257  LOC90841  5'  TTTGTGGATGAGGAAACC    53784          T_
                                TTTGTGGATGA  GAACT
                                |||||||||||  |||||
                                AAACACCTACT  TTTGG
                                      CC
GAM2258  XT3       3'  TGAGCAAAGGAATCTGTATCA  53787          ACCA  AC
                                TGAGCGAAGGAG   CT  ATCA
                                ||||||||||||   ||  ||||
                                ACTCGTTTCCTT   GA  TAGT
                                      A___  CA
GAM2258  KIAA0408  3'  TGGCTGAAGGAGATTTCAATAT 53788    A  _      CCACTAC
              CA                  TG GC GAAGGAGA      ATCA
                                || || ||||||||      ||||
                                AC CG CTTCCTCT      TAGT
                                 _ A       AAAGTTA
GAM2258  KIAA0668  3'  TGAGCGGACGACCCCTACATCA 53789      AA GA    A
                                TGAGCG  G  GACC CTACATCA
                                ||||||  |  |||| ||||||||
                                ACTCGC  C  CTGG GATGTAGT
                                   __ TG    G
GAM2258  LOC202458 5'  CGGGCGGGGGAGACCACC    53790    A   AA
                                TG GCG  GGAGACCACT
                                || |||  ||||||||||
                                GC CGC  CCTCTGGTGG
                                 C   CC
GAM2258  LOC204285 5'  TGACGAGGGAGACCACCA    53791    G   A
                                TGA CGA GGAGACCACTA
                                ||| ||| ||||||||||
                                ACT GCT CCTCTGGTGGT
                                  _  C
GAM2259  MID1      3'  ACAACTCTATTGTAAAC     53794          TTTT
                                ACAACTTTATTGT   GAAC
                                ||||||||||||   ||||
                                TGTTGAGATAACA   TTTG
                                      ____
GAM2259  TNFRSF11A 3'  CAACTTTATTCTTCCTTGAACT 53795         G_
                                CAACTTTATT  TTTTTGAACT
                                ||||||||||  ||||||||||
                                GTTGAAATAA  AGGAACTTGA
                                      GA
GAM2259  ZNF195    3'  AACTTTATTAAGTCTGAACT   53796         TT
                                AACTTTATTG  TTTGAACT
                                ||||||||||  ||||||||
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                                TTGAAATAAT  AGACTTGA
                                      TC
GAM2259  DKFZP434L187 3'  TCACAACCTTGTCATGA     53797        TTA    TT
                                TCACAACT   TTGTT  TGA
                                ||||||||   |||||  |||
                                AGTGTTGG   AACAG  ACT
                                     ___     T_
GAM2259  JDD1     3'  TCACAGCTTATTGCAGCCTGAA 53798      A   T    T_
           CT                     TCACA CTT ATTGT  TTTGAACT
                                ||||| ||| |||||  ||||||||
                                AGTGT GAA TAACG  GGACTTGA
                                  C   _    TC
GAM2259  KIAA0769  3'  TCACAACTTTGTTTTT      53799         TAT
                                TCACAACTT   TGTTTTT
                                |||||||||   |||||||
                                AGTGTTGAA   ACAAAAA
                                     ___
GAM2259  MO25     3'  TCACAACTATTGTACTG     53800        TT    TT
                                TCACAACT  ATTGT  TTG
                                ||||||||  |||||  |||
                                AGTGTTGA  TAACA  GAC
                                    __    T_
GAM2259  NAP1L2   3'  CAAATTAATTAGTTTTTGAACT 53801     C  T  _
                                CAA TT ATT GTTTTTGAACT
                                ||| || ||| ||||||||||
                                GTT AA TAA CAAAAACTTGA
                                  T  T   T
GAM2259  OSF-2    3'  TCACAACTCTTCGATTTGAA   53802          A   TT
                                TCACAACTTT TTG  TTTGAA
                                |||||||||| |||  ||||||
                                AGTGTTGAGA AGC  AAACTT
                                      _  T_
GAM2259  PTPRT    3'  TCACAGCTTTATTGTATAGA   53803       A       TTTT
                                TCACA CTTTATTGT    GA
                                ||||| |||||||||    ||
                                AGTGT GAAATAACA    CT
                                   C        TAT_
GAM2259  RPS27L   3'  TCAAAACTTTATTGAAAAACT  53804     C        TTTTT
                                TCA AACTTTATTG    GAACT
                                ||| ||||||||||    |||||
                                AGT TTGAAATAAC    TTTGA
                                  T         TT___
GAM2259  SIAT8A   3'  CTGTCTTGTTTTTGAACT    53805    TTA
                                CT   TTGTTTTTGAACT
                                ||   ||||||||||||
                                GA   AACAAAAACTTGA
                                 CAG
GAM2259  ZNF197   3'  TCCAACTTTATTGACAAC    53806    A        TTTTTG
                                TC CAACTTTATTG     AAC
                                || ||||||||||     |||
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                                AG GTTGAAATAAC      TTG
                                 _          TG_____
GAM2259  LOC120103 3'  TCAGAACTTAATTTTTTGAACT 53807      C     TATTG
                                TCA AACTT     TTTTTGAACT
                                ||| |||||     ||||||||||
                                AGT TTGAA     AAAAACTTGA
                                  C     TTA__
GAM2259  LOC91960  3'  TCACAACTGTTATTGAAGAACT 53808         _     TTTTT
                                TCACAACT TTATTG     GAACT
                                |||||||| ||||||     |||||
                                AGTGTTGA AATAAC     CTTGA
                                     C      TT___
GAM2260  BACH2     3'  TGAGAAATAAGTTTCCA      53811          C    AG
                                TGAGAAATA GTTT  CCG
                                ||||||||| ||||  |||
                                ACTCTTTAT CAAA  GGT
                                      T    __
GAM2260  CYP1B1    3'  TGGGAAAATGTTTAACCATCTT 53812     A    TAC        C
               T                 TG GAAA   GTTTAGCCG CTTT
                                || ||||   ||||||||| ||||
                                AC CTTT   CAAATTGGT GAAA
                                 C    TA_        A
GAM2260  ChGn      3'  GAGAAATATGCTTGCCTT     53813         C    AGCC
                                GAGAAATA GTTT    GCCTT
                                |||||||| ||||    |||||
                                CTCTTTAT CGAA    CGGAA
                                     A    _____
GAM2260  KIAA0781  3'  TGAAAAATATATTGCCTT     53814          CG  TAGCC
                                TGAGAAATA  TT    GCCTT
                                |||||||||  ||    |||||
                                ACTTTTTAT  AA    CGGAA
                                      AT  ______
GAM2260  KIAA1813  5'  TGAGAAATGCGTTTGTGGC    53815         A    A__
                                TGAGAAAT CGTTT   GC
                                |||||||| |||||   ||
                                ACTCTTTA GCAAA   CG
                                     C     CAC
GAM2261  AXIN1     3'  GCCTAGCCTGAGAAAT      53818     A   AT  G
                                GC TAG  CC TGAGAAAT
                                || |||  || ||||||||
                                CG ATC  GG ACTCTTTA
                                 G   __  _
GAM2261  BCL11A    3'  TAGCCATTGTTGTGAGAAATAC 53819      ATAGATCC
                                TAGC       GTGAGAAATAC
                                ||||       ||||||||||||
                                ATCG       CACTCTTTATG
                                  GTAACAA_
GAM2261  CDS1      3'  TAACATAGATCAAGTAAG     53820           C_
                                TAGCATAGATC  GTGAG
                                ||||||||||  |||||
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                                ATTGTATCTAG  CATTC
                                      TT
GAM2261  CREBL2   3'  ACATAGTGATGCTGAGAAATAC 53821       ATCCG_
                                GCATAG     TGAGAAATAC
                                ||||||     ||||||||||
                                TGTATC     ACTCTTTATG
                                   ACTACG
GAM2261  MSR1     3'  AGCATGGCGAGAAATA      53822       AGATCC
                                AGCAT     GTGAGAAATA
                                |||||     ||||||||||
                                TCGTA     CGCTCTTTAT
                                  C_____
GAM2261  PCDH9    5'  CAGCATTGATGTGAGAAAT    53823        A   CC
                                TAGCAT GAT  GTGAGAAAT
                                |||||| |||  |||||||||
                                GTCGTA CTA  CACTCTTTA
                                   A  __
GAM2261  PLOD2    3'  GCATAGGTGTTCAGAAATAC   53824       ATCC  ___
                                GCATAG   GTG   AGAAATAC
                                ||||||   |||   ||||||||
                                CGTATC   CAC   TCTTTATG
                                   ____  AAG
GAM2261  TNFSF4   3'  GCACATCTGTGAGAAATA    53825      AG   C
                                GCAT  ATC GTGAGAAATA
                                ||||  ||| ||||||||||
                                CGTG  TAG CACTCTTTAT
                                  __  A
GAM2261  ZNF175   3'  ACATAGATACAGAAATA     53826        C GTG
                                GCATAGAT C   AGAAATA
                                |||||||| |   |||||||
                                TGTATCTA G   TCTTTAT
                                     T ___
GAM2261  C20orf82 3'  TAGCGTAATGTATGAGAAATAC 53827      A   ATCC
                                TAGC TAG    GTGAGAAATAC
                                |||| |||    ||||||||||
                                ATCG ATT    TACTCTTTATG
                                  C   ACA_
GAM2261  FLJ10468 3'  AGCATAGAGAGCAGAAAT    53828        TCC  G
                                AGCATAGA   GT AGAAAT
                                ||||||||   || ||||||
                                TCGTATCT   CG TCTTTA
                                     CT_  _
GAM2261  FLJ21477 3'  TAGCATTAGGAGAAATA     53829       _ ATCCGT
                                TAGCAT AG     GAGAAATA
                                |||||| ||     ||||||||
                                ATCGTA TC     CTCTTTAT
                                   A _______
GAM2261  GOLGA1   3'  AGCATGATTGAGAAATAC    53830       A   CCG
                                AGCAT GAT   TGAGAAATAC
                                ||||| |||   ||||||||||
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                                TCGTA CTA   ACTCTTTATG
                                  _  ____
GAM2261  KIAA0495  3'  AGTATAGCGTGAGAAATAC   53831    C    ATC
                                AG ATAG   CGTGAGAAATAC
                                || ||||   ||||||||||||
                                TC TATC   GCACTCTTTATG
                                 A   ____
GAM2261  KIAA0530  3'  TAGATATGGTGAGAAATA    53832      CC_
                                TAGAT   GTGAGAAATA
                                |||||   ||||||||||
                                ATCTA   CACTCTTTAT
                                   TAC
GAM2261  PCDHB10   3'  AGCATAGTAGTAGAGAAATA   53833       ATCCGT
                                AGCATAG     GAGAAATA
                                |||||||     ||||||||
                                TCGTATC     CTCTTTAT
                                    ATCAT_
GAM2261  PRO0038   5'  TAGTATAAAGTGAGAAATA   53834    C    TCC
                                TAG ATAGA   GTGAGAAATA
                                ||| |||||   ||||||||||
                                ATC TATTT   CACTCTTTAT
                                  A    ____
GAM2261  PRO0456   3'  TAGCACAGATACATGTAG    53835        C   _
                                TAGCATAGAT CGTG AG
                                |||||||||| |||| ||
                                ATCGTGTCTA GTAC TC
                                      T    A
GAM2261  SYNCOILIN 3'  TAGAGTATAGTGAGAAATAC   53836     TCC__
                                TAGA    GTGAGAAATAC
                                ||||    ||||||||||||
                                ATCT    CACTCTTTATG
                                  CATAT
GAM2261  LOC145990 3'  GCATAAAGGAAAGAGAAATAC  53837       TCCGT
                                GCATAGA    GAGAAATAC
                                |||||||    |||||||||
                                CGTATTT    CTCTTTATG
                                    CCTTT
GAM2261  LOC152573 3'  TAGCATAGATTGAAA       53838         CCG
                                TAGCATAGAT   TGAGA
                                ||||||||||   |||||
                                ATCGTATCTA   ACTTT
                                             ____
GAM2261  LOC153727 5'  TAGCATAGATTCAGCTTCAAGA 53839         _ C  ___
           A                    TAGCATAGAT C GT   GAGAA
                                |||||||||| | ||   |||||
                                ATCGTATCTA G CG   TTCTT
                                      A T  AAG
GAM2261  LOC221490 5'  TAGATGAAAATGAGAAATA    53840      CC__
                                TAGAT    GTGAGAAATA
                                |||||    ||||||||||
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                                ATCTA   TACTCTTTAT
                                   CTTT
GAM2261 LOC90230 3' TAGCATAAGATGTGAGAA    53841       _  CC
                                TAGCATA GAT  GTGAGAA
                                ||||||| |||  |||||||
                                ATCGTAT CTA  CACTCTT
                                    T  __
GAM2262 ARHGEF12 3' TAATAAGCAGGAAGATGTC   53844          GAT   A
                                TAATAGGCAGGA  AGAT TC
                                ||||||||||||  |||| ||
                                ATTATTCGTCCT  TCTA AG
                                       ___   C
GAM2262 CASP8    5' TAAAAGGCAGGAGAATATAATC 53845    T       TAGAT
           CG                     TAA AGGCAGGAGA    ATCCG
                                ||| ||||||||||    |||||
                                ATT TCCGTCCTCT    TAGGC
                                  T        TATAT
GAM2262 CASP8    5' TAAAAGGCAGGAGAATATAATC 53845    T       TAGAT
           CG                     TAA AGGCAGGAGA    ATCCG
                                ||| ||||||||||    |||||
                                ATT TCCGTCCTCT    TAGGC
                                  T        TATAT
GAM2262 NDUFS2   3' ATAGGCAGGGGGGGATCAAAC  53846       A__  _
                                ATAGGCAGG   GAT AGAT
                                |||||||||   ||| ||||
                                TATCCGTCC   CTA TTTG
                                     CCC   G
GAM2262 PEX6     3' TAGGCAGGAGATATCTC     53847          GATA
                                TAGGCAGGAGATA   TC
                                ||||||||||||    ||
                                ATCCGTCCTCTAT   AG
                                       AG__
GAM2262 HSA249128 3' TAATAGGCAGGGAGAAAAC  53848         _  T
                                TAATAGGCAGG AGA AGAT
                                |||||||||| ||| ||||
                                ATTATCCGTCC TCT TTTG
                                       C  _
GAM2262 LYPLA2   3' AGGCAGGAGACACGATTATC  53849         _  _
                                AGGCAGGAGATA GAT ATC
                                |||||||||||| ||| |||
                                TCCGTCCTCTGT CTA TAG
                                       G   A
GAM2262 PRSS12   3' AATAGGTAGGGGATAGAT    53850      C   A
                                AATAGG AGG GATAGAT
                                |||||| ||| |||||||
                                TTATCC TCC CTATCTA
                                   A   C
GAM2262 LOC91308 3' TAATCAATGTAAGATAGATAT 53851     AGGCAG
                                TAAT     GAGATAGATAT
                                ||||     ||||||||||
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                                ATTA     TTCTATCTATA
                                  GTTACA
GAM2263  CHEK1     3'  TCAGGAACTACTATTT      53854       CAGAT
                                TTAGGA    ACTACTATTT
                                ||||||    ||||||||||
                                AGTCCT    TGATGATAAA
                                  _____
GAM2263  D12S2489E 3'  TAGGATGGATATTACTATTC   53855      CA   C
                                TAGGA  GATA TACTATTT
                                |||||  |||| ||||||||
                                ATCCT  CTAT ATGATAAG
                                   AC   A
GAM2263  SCN1A     3'  TTAGTGCAGGTACTACCA    53856     GA   A
                                TTAG  CAG TACTACTA
                                ||||  ||| ||||||||
                                AATC  GTC ATGATGGT
                                  AC   C
GAM2263  WASF3     3'  TTAGAATACCACTATTT     53857     GACA
                                TTAG   GATACTACTATTT
                                ||||   ||||||||||||
                                AATC   TTATGGTGATAAA
                                  ____
GAM2263  LOC91694  3'  TTAGGACAGATATATCT     53858          CTAC
                                TTAGGACAGATA   TATTT
                                ||||||||||||   |||||
                                AATCCTGTCTAT   ATAGA
                                  _____
GAM2264  BACH1     3'  TCCAAGTTAAAATGATTTGTGT 53861       G     CGT
                                TCCAAG TAAAAT   GTTTGTGT
                                |||||| ||||||   ||||||||
                                AGGTTC ATTTTA   TAAACACA
                                   A     C__
GAM2264  BMP6      3'  TCCAAGGCAGAATGTGT     53862         A   C
                                TCCAAGGTA AAT GTGT
                                ||||||||| ||| ||||
                                AGGTTCCGT TTA CACA
                                     C   _
GAM2264  FZD8      3'  TCCCAGGTGAAATCTGTGT   53863     A   A    _
                                TCC AGGT AAATC GTGT
                                ||| |||| ||||| ||||
                                AGG TCCA TTTAG CACA
                                  G   C    A
GAM2264  LANCL1    3'  CCAAACTCTAATTGTGTTTGTG 53864      GTAA   C
           T                     CCAAG    AAT GTGTTTGTGT
                                |||||    ||| ||||||||||
                                GGTTT    TTA CACAAACACA
                                   GAGA   A
GAM2264  MSR1      3'  TCCAAGGTAAGGTTTTGCCT   53865         AATCG
                                TCCAAGGTAA    TGTTT
                                ||||||||||    |||||
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                                AGGTTCCATT    ACGGA
                                      CCAAA
GAM2264  MSR1     3'  TCCAAGGTAAGGTTTTGCCT  53865         AATCG
                                TCCAAGGTAA    TGTTT
                                ||||||||||    |||||
                                AGGTTCCATT    ACGGA
                                      CCAAA
GAM2264  NFYA     3'  CAAGGTAAGTGCTTTGTGT   53866        AATC    _
                                CAAGGTAA   GTGTTT GTGT
                                ||||||||   |||||| ||||
                                GTTCCATT   CACGAA CACA
                                     ____     A
GAM2264  NFYA     3'  CAAGGTAAGTGCTTTGTGT   53866        AATC    _
                                CAAGGTAA   GTGTTT GTGT
                                ||||||||   |||||| ||||
                                GTTCCATT   CACGAA CACA
                                     ____     A
GAM2264  RARA     3'  TCCAGTGTGTGTGTGTTTGTGT 53867     AG  AAAATC
                                TCCA  GT     GTGTTTGTGT
                                ||||  ||     ||||||||||
                                AGGT  CA     CACAAACACA
                                  CA  CACA__
GAM2264  SEPX1    3'  TCCAAGGTGGAATGGCCAACGT 53868        AA   C  GTT
           GT                     TCCAAGGT  AAT GT   TGTGT
                                ||||||||  ||| ||   |||||
                                AGGTTCCA  TTA CG   GCACA
                                    CC   C  GTT
GAM2264  XT3      3'  TCCCAGGTGAGTGTTTGTG   53869     A   AAAATC
                                TCC AGGT     GTGTTTGTG
                                ||| ||||     |||||||||
                                AGG TCCA     CACAAACAC
                                  G   CT____
GAM2264  ATP6V1H  3'  TCCAAGTAAAATCAAACAGTGT 53870       G       TGTTT
                                TCCAAG TAAAATCG    GTGT
                                ||||||  ||||||||    ||||
                                AGGTTC ATTTTAGT    CACA
                                   _       TTGT_
GAM2264  FLJ21290 3'  AAGTAAAATCCTATGTGT    53871         G  TT
                                AGGTAAAATC TG  TGTGT
                                |||||||||| ||  |||||
                                TTCATTTTAG AT  ACACA
                                     G  __
GAM2264  FLJ21791 3'  AAGTAAAATCTTGTG       53872          GTGT
                                AGGTAAAATC    TTGTG
                                ||||||||||    |||||
                                TTCATTTTAG    AACAC
                                              ____
GAM2264  KIAA1656 3'  TCCAGGGCAAGTGGTTTGTGT  53873      A    AATC  _
                                TCCA GGTAA    GTG TTTGTGT
                                |||| |||||    ||| |||||||
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                                AGGT CCGTT    CAC AAACACA
                                  C     ____   C
GAM2264  LCHN     3'  CAGGGCAAAATCTATGCAGTGT 53874    A       _    TT
                                CA GGTAAAATC GTGT  GTGT
                                || ||||||||| ||||  ||||
                                GT CCGTTTTAG TACG  CACA
                                 C       A   T_
GAM2264  PLAGL2   3'  TCCAAGGTGAAACCCTCTGTGT 53875        A    GTG
                                TCCAAGGT AAATC   TTTGTGT
                                |||||||| |||||   |||||||
                                AGGTTCCA TTTGG   AGACACA
                                     C    G__
GAM2264  LOC254719 5'  CAGGGCAAAATCTATGCAGTGT 53874    A       _    TT
                                CA GGTAAAATC GTGT  GTGT
                                || ||||||||| ||||  ||||
                                GT CCGTTTTAG TACG  CACA
                                 C       A   T_
GAM2265  SNTB1    3'  TATATCAGATGACAATAT    53878       TAA
                                TATGTT   AGATGACAATAT
                                ||||||   ||||||||||||
                                ATATAG   TCTACTGTTATA
                                   ___
GAM2265  KIAA0062  3'  TATTATGTTTAAGGAATGA   53879          A_
                                TATTATGTTTAA  GATGA
                                ||||||||||||  |||||
                                ATAATACAAATT  TTACT
                                      CC
GAM2265  SLC26A7   3'  TATTTCCAAAGATGGCAATAT  53880     G        A
                                TAT TTTAAAGATG CAATAT
                                ||| |||||||||| ||||||
                                ATA AGGTTTCTAC GTTATA
                                  A        C
GAM2266  ITGBL1   3'  TGATATTCTACCTCCTGTGTGC 53883        _      ATA
            TTG                   TGATATTT ACTTTTT   TGCTTG
                                |||||||| |||||||   ||||||
                                ACTATAAG TGGAGGA   ACGAAC
                                     A      CAC
GAM2266  NRCAM    3'  ATATTTACTTTTTAAACT    53884           TAT
                                ATATTTACTTTTTA   GCT
                                ||||||||||||||   |||
                                TATAAATGAAAAAT   TGA
                                      T__
GAM2266  CSE-C    3'  TGCATTTTTTTTTATATGCTTG 53885    A    AC
                                TG TATTT  TTTTTATATGCTTG
                                || |||||  ||||||||||||||
                                AC GTAAA  AAAAATATACGAAC
                                 _    A_
GAM2266  KIAA0164  3'  ATACAGGCTTTTTATATGCTTG 53886     TTA
                                ATAT   CTTTTTATATGCTTG
                                ||||   ||||||||||||||
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                                TATG   GAAAAATATACGAAC
                                  TCC
GAM2266 KIAA0564 3' TGATTTTACTTTTTTTACTT   53887     A       ATA
                                TGAT TTTACTTTTT   TGCTT
                                |||| ||||||||||   |||||
                                ACTA AAATGAAAAA   ATGAA
                                  _       A__
GAM2266 MGC4308  3' TGATATTTACTGAGTGCTT    53888          TTTTATA
                                TGATATTTACT      TGCTT
                                ||||||||||       |||||
                                ACTATAAATGA      ACGAA
                                      CTC____
GAM2266 LOC221362 3' TGAGATTTGCCCTCCATATGTG 53889     T   A       __
            CTTG                   TGA ATTT CTTTTTATA  TGCTTG
                                ||| |||| |||||||||  ||||||
                                ACT TAAA GGGAGGTAT  ACGAAC
                                  C   C       AC
GAM2267 ACK1     3' AAGAAGCAGGACTGAATGC    53892         A  A_
                                AAGAAGCAG AC  GATGC
                                ||||||||| ||  |||||
                                TTCTTCGTC TG  TTACG
                                     C  AC
GAM2267 ADCY6    3' AAGAAGCAGAGACAAGCCAC   53893          ACA   C
                                AAGAAGCAGA   GATG GCCAC
                                ||||||||||   |||| |||||
                                TTCTTCGTCT   CTGT CGGTG
                                     ___   T
GAM2267 ADCY6    3' AAGAAGCAGAGACAAGCCAC   53893          ACA   C
                                AAGAAGCAGA   GATG GCCAC
                                ||||||||||   |||| |||||
                                TTCTTCGTCT   CTGT CGGTG
                                     ___   T
GAM2267 ADRA2B   3' AAGAAGCAGGGTGACCCCGGCG 53894         AACA  ____
            CCAC                   AAGAAGCAG   GAT   GCGCCAC
                                |||||||||   |||   |||||||
                                TTCTTCGTC   CTG   CGCGGTG
                                     CCA_  GGGC
GAM2267 ARHGDIA  3' AAGAAGCAGGGACAGGCGC   53895         A_   AT
                                AAGAAGCAG  ACAG  GCGC
                                |||||||||  ||||  ||||
                                TTCTTCGTC  TGTC  CGCG
                                     CC   __
GAM2267 ASB1     5' GAAGCAGAACGACCCGC     53896          A  G
                                GAAGCAGAAC GAT CGC
                                |||||||||| ||| |||
                                CTTCGTCTTG CTG GCG
                                     _  G
GAM2267 C18orf1  3' AAGAAGCAGAAGGGAAC     53897          CA  T
                                AAGAAGCAGAA  GA GC
                                ||||||||||  || ||
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                                TTCTTCGTCTT  CT TG
                                      CC  _
GAM2267  CALCA    3'  AGAAGCAGGACAGAGGAGC   53898        A    T__
                                AGAAGCAG ACAGA   GC
                                |||||||| |||||   ||
                                TCTTCGTC TGTCT   CG
                                     C    CCT
GAM2267  CARD10   3'  AGGAGCAGAACAGGCCCA    53899    A        AT  G
                                AG AGCAGAACAG  GC CCA
                                || ||||||||||  || |||
                                TC TCGTCTTGTC  CG GGT
                                 C        __ _
GAM2267  CARPX    3'  GAAGGAGAACAGACCAAAGC  53900      C        _____
                                GAAG AGAACAGAT    GC
                                |||| |||||||||    ||
                                CTTC TCTTGTCTG    CG
                                   C        GTTT
GAM2267  CCND2    3'  AAGAAGCAGGATGTCAC     53901         AACA   _
                                AAGAAGCAG    GATG CGC
                                |||||||||    |||| |||
                                TTCTTCGTC    CTAC GTG
                                      _____    A
GAM2267  CCND2    3'  AAGAGGCAGAACAGAGC     53902      A        T
                                AAGA GCAGAACAGA GC
                                |||| |||||||||| ||
                                TTCT CGTCTTGTCT CG
                                   C        _
GAM2267  CD3Z     3'  AAAAAGCAGAGCAGAGAGCG  53903          A    T_
                                AAGAAGCAGA CAGA  GCG
                                |||||||||| ||||  |||
                                TTTTTCGTCT GTCT  CGC
                                      C    CT
GAM2267  CD83     3'  AGAAGCAGCAGTGGCC      53904         AA   A  C
                                AGAAGCAG  CAG TG GCC
                                ||||||||  ||| || |||
                                TCTTCGTC  GTC AC CGG
                                      __   _  _
GAM2267  CDC6     3'  GAGCAGAGAACGCGCCA     53905    A    ACA
                                GA GCAGA   GATGCGCCA
                                || |||||   |||||||||
                                CT CGTCT   TTGCGCGGT
                                  _    C__
GAM2267  CHST6    3'  AAGAAGCAGAAAGTGC      53906          C  A
                                AAGAAGCAGAA AG TGC
                                |||||||||||| || |||
                                TTCTTCGTCTT TC ACG
                                      _ _
GAM2267  COL1A1   3'  AAGGAACAGAACAGAAC     53907     A        T
                                AAG AGCAGAACAGA GC
                                ||| ||||||||||| ||
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                                TTC TTGTCTTGTCT TG
                                  C         _
GAM2267 CRYBA4   3' AAGGAGAGAACACACCA     53908     A  C    AGAT
                                AAG AG AGAAC    GCGCCA
                                ||| || |||||    ||||||
                                TTC TC TCTTG    TGTGGT
                                  C  _    _____
GAM2267 CST6     3' AAGAAGCAGCACTGGCCA     53909         AACAGA  C
                                AAGAAGCAG     TG GCCA
                                |||||||||     || ||||
                                TTCTTCGTC     AC CGGT
                                     GTG___  _
GAM2267 CYP3A4   3' AGAAGCAGAGGAGCCA      53910         ACA  TGC
                                AGAAGCAGA   GA   GCCA
                                |||||||||   ||   ||||
                                TCTTCGTCT   CT   CGGT
                                     C__  ____
GAM2267 CYP4F3   3' AAGAAGCAGAATAGCCA     53911          ACAG   C
                                AAGAAGCAGA    ATG GCCA
                                ||||||||||    ||| ||||
                                TTCTTCGTCT    TAT CGGT
                                      _____  _
GAM2267 DLST     3' AAGAAGCAAAGCAGCAC     53912          A   A
                                AAGAAGCAGA CAG TGC
                                |||||||||| ||| |||
                                TTCTTCGTTT GTC GTG
                                     C  _
GAM2267 EIF4A2   3' AAGAAGCACAATGCAC      53913        GAACA
                                AAGAAGCA    GATGCGC
                                ||||||||    |||||||
                                TTCTTCGT    TTACGTG
                                     G____
GAM2267 ENAM     5' AAGAAGCAAGATACA       53914        GAAC
                                AAGAAGCA   AGATGCG
                                ||||||||   |||||||
                                TTCTTCGT   TCTATGT
                                      _____
GAM2267 ENPP1    3' AGAAGCAGAAAGGCA       53915         C  AT
                                AGAAGCAGAA AG  GCG
                                |||||||||| ||  |||
                                TCTTCGTCTT TC  CGT
                                      _  __
GAM2267 F8       3' GAAGCAGAAACAGACTTTAC  53916         _    GC_
                                GAAGCAGAA CAGAT   GC
                                ||||||||| |||||   ||
                                CTTCGTCTT GTCTG   TG
                                     T    AAA
GAM2267 FBXL7    3' AGAACAGAATGGATGAAC    53917     G    CA   C
                                AGAA CAGAA  GATG GC
                                |||| |||||  |||| ||
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                                TCTT GTCTT  CTAC TG
                                  _    AC    T
GAM2267  FCMD     3'  AAAAGCAGAATGATTTTCAC   53918          CA   GCGC
                                AGAAGCAGAA  GAT    CAC
                                ||||||||||  |||    |||
                                TTTTCGTCTT  CTA    GTG
                                     A_   AAA_
GAM2267  FLT1     3'  AAGAAGCAGCAATCCAC     53919          AACA   G
                                AAGAAGCAG    GAT CGC
                                |||||||||    ||| |||
                                TTCTTCGTC    TTA GTG
                                     G___   G
GAM2267  FOXD2    5'  AAGAAATAGAACAGAGTTGGGT 53920        C       ________
             TGC                   AAGAAG AGAACAGA      TGC
                                |||||| ||||||||       |||
                                TTCTTT TCTTGTCT       ACG
                                   A       CAACCCA
GAM2267  GAS7     3'  AAGAAGCAGAGTAGTACGCC   53921          AC  A
                                AAGAAGCAGA  AG TGCGCC
                                ||||||||||  || ||||||
                                TTCTTCGTCT  TC ATGCGG
                                     CA  _
GAM2267  GFPT2    3'  AGAAGTGGAGGGATGTGGGCCA 53922       CA  ACA    C__
             C                   AGAAG  GA   GATG   GCCAC
                                |||||  ||   ||||   |||||
                                TCTTC  CT   CTAC   CGGTG
                                   AC  CC_    ACC
GAM2267  GLS      3'  AAGCAGCAGAGTGTGCTCA    53923       AA    _  C  _
                                AAGCAG  CAGA TG GC CA
                                ||||||  |||| || || ||
                                TTCGTC  GTCT AC CG GT
                                   __    C  A  A
GAM2267  GRB7     3'  AAGAAGCAGAGGAGAAAAC    53924          AC   T_
                                AAGAAGCAGA  AGA  GC
                                ||||||||||  |||  ||
                                TTCTTCGTCT  TCT  TG
                                     CC   TT
GAM2267  IHPK1    3'  AAGCAGCAGATCTGTGCCA    53925        AA    __  C
                                AAGCAG  CAGA  TG GCCA
                                ||||||  ||||  || ||||
                                TTCGTC  GTCT  AC CGGT
                                   __    AG  A
GAM2267  IL1RAP   3'  GAAGCAGAATAGTCAGCCAC   53926         C  ATGC
                                GAAGCAGAA AG    GCCAC
                                |||||||||  ||    |||||
                                CTTCGTCTT TC    CGGTG
                                     A  AGT_
GAM2267  INPP5D   3'  GAAGCAGAGCTGAAAGCCAC   53927         ACA  TGC
                                GAAGCAGA   GA   GCCAC
                                ||||||||   ||   |||||
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                                CTTCGTCT  CT  CGGTG
                                    CGA  TT_
GAM2267  KCNA5    3'  GAAACAGAACAGCCCA     53928         GAT  G
                                GAAGCAGAACA  GC CCA
                                ||||||||||  || |||
                                CTTTGTCTTGT  CG GGT
                                    ___  _
GAM2267  KIF3C    3'  GAAGCAGAAATGACAGTGTCGC 53929       ____  A  _
                                GAAGCAGA   ACAG TG CGC
                                ||||||||   |||| || |||
                                CTTCGTCT   TGTC AC GCG
                                    TTAC   _  A
GAM2267  KRTHA8   5'  AAGAAGCAAAGTTATAGCCA  53930        ACAG  C
                                AAGAAGCAGA   ATG GCCA
                                ||||||||||   ||| ||||
                                TTCTTCGTTT   TAT CGGT
                                    CAA_  _
GAM2267  LETM1    5'  AGGGGCGGACCGCGCCAC    53931    AA  A  A AGA
                                AG  GC GA C  TGCGCCAC
                                ||  || || |  ||||||||
                                TC  CG CT G  GCGCGGTG
                                 CC  C  _ ___
GAM2267  MAP1A    3'  AGGAGCAGAACACAGCAGCAC 53932    A       GAT  C
                                AG AGCAGAACA  GCG CAC
                                || |||||||||  ||| |||
                                TC TCGTCTTGT  CGT GTG
                                 C       GT_  C
GAM2267  MAP3K7IP1 3'  AAGAAGCAAGGCAGGCAC    53933        AA  AT
                                AAGAAGCAG  CAG  GCGC
                                |||||||||  |||  ||||
                                TTCTTCGTT  GTC  CGTG
                                    CC  __
GAM2267  MAPRE2   5'  AGAAGGGGAACAAACCGC    53934      CA      G
                                AGAAG  GAACAGAT CGC
                                |||||  |||||||| |||
                                TCTTC  CTTGTTTG GCG
                                   CC      _
GAM2267  MBL2     3'  AAGAAGCAAGTATTGCCA    53935        AACAG  GC
                                AAGAAGCAG    AT  GCCA
                                |||||||||    ||  ||||
                                TTCTTCGTT    TA  CGGT
                                    CA___  A_
GAM2267  MECP2    3'  GAAGCAAAACAAGAATCCAC  53936         _  TGCG
                                GAAGCAGAACA GA   CCAC
                                |||||||||| ||   ||||
                                CTTCGTTTTGT CT   GGTG
                                    T  TA__
GAM2267  MEN1     5'  AAGGACAGAACAGTCCCA    53937     AA       ATGCG
                                AAG  GCAGAACAG    CCA
                                |||  |||||||||    |||
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                                TTC  TGTCTTGTC    GGT
                                  C_       AG___
GAM2267  NESH    3'  AAGGACAGAACACAGCTCAC   53938    AA      GAT  GC
                                AAG  GCAGAACA   GC  CAC
                                |||  ||||||||   ||  |||
                                TTC  TGTCTTGT   CG  GTG
                                  C_      GT_  A_
GAM2267  NPTX1   3'  AGAAGGAACACGCCAC     53939     CA   AGAT
                                AGAAG  GAAC   GCGCCAC
                                |||||  ||||   |||||||
                                TCTTC  CTTG   TGCGGTG
                                  __   _____
GAM2267  PIK3R3  3'  AAGGAGCAGACACATTAC    53940    A    _  GA
                                AAG AGCAGA ACA  TGC
                                ||| |||||| |||  |||
                                TTC TCGTCT TGT  ATG
                                  C     G   A_
GAM2267  RFP     3'  AGAAGCAGGACTGAGAACCA   53941       A  A  TGC
                                AGAAGCAG AC GA   GCCA
                                |||||||| || ||   ||||
                                TCTTCGTC TG CT   TGGT
                                     C  A  CT_
GAM2267  SH3BP2  3'  AAGAAGCAGACGGCAACGC   53942        ACA_
                                AAGAAGCAGA   GATGC
                                ||||||||||   |||||
                                TTCTTCGTCT   TTGCG
                                      GCCG
GAM2267  SLC4A4  3'  AGAAGCAGAGAGAGCGC    53943       AC   T
                                AGAAGCAGA  AGA GCGC
                                |||||||||  ||| ||||
                                TCTTCGTCT  TCT CGCG
                                     C_   _
GAM2267  SLC6A12 3'  AGAAGCAGGATGGCAAATGGTG 53944       AA___    _____
            TCGC                  AGAAGCAG    CAGATG   CGC
                                |||||||    ||||||   |||
                                TCTTCGTC    GTTTAC   GCG
                                     CTACC     CACA
GAM2267  SS18    3'  AGAACAGAACAGTGGAC     53945     G      A  C
                                AGAA CAGAACAG TG GC
                                |||| |||||||| || ||
                                TCTT GTCTTGTC AC TG
                                  _       _ C
GAM2267  TCF21   3'  GAAGCAGAGACAGAGAGCAC  53946       _    T_
                                GAAGCAGA ACAGA  GCGC
                                |||||||| |||||  ||||
                                CTTCGTCT TGTCT  CGTG
                                     C    CT
GAM2267  TGM3    3'  AGAAGCAGGAATGCCCC    53947       AACA    G
                                AGAAGCAG   GATGC CC
                                ||||||||   ||||| ||
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                                TCTTCGTC   TTACG GG
                                    C___    G
GAM2267 ZNF135   3' AGAACAGAGCAGCAAAAGCCA 53948     G   A  ATGC_
                                AGAA CAGA CAG    GCCA
                                |||| |||| |||    ||||
                                TCTT GTCT GTC    CGGT
                                  _   C  GTTTT
GAM2267 ZNF76    3' AGAAGGGGAACAGACTGAGGGC 53949     CA      GC___
                                AGAAG  GAACAGAT    GC
                                |||||  ||||||||    ||
                                TCTTC  CTTGTCTG    CG
                                   CC      ACTCC
GAM2267 ASB16    3' AGGGGCAGAACACACCA    53950    AA     AGAT
                                AG  GCAGAAC   GCGCCA
                                ||  |||||||   ||||||
                                TC  CGTCTTG   TGTGGT
                                 CC     _____
GAM2267 ATP10B   3' AAAAAGCAGAACCAACTCGC  53951          A  G
                                AAGAAGCAGAAC GAT CGC
                                |||||||||||| ||| |||
                                TTTTTCGTCTTG TTG GCG
                                      G  A
GAM2267 BRAG     3' AAGAAGCAGAATTACACCAC  53952          CAGA
                                AAGAAGCAGAA   TGCGCCAC
                                ||||||||||   ||||||||
                                TTCTTCGTCTT   ATGTGGTG
                                      A___
GAM2267 C11orf14 3' AAGAAGCAGAGAAATAGGCCAC 53953         AC   C
                                AAGAAGCAGA  AGATG GCCAC
                                ||||||||||  ||||| |||||
                                TTCTTCGTCT  TTTAT CGGTG
                                      C_    C
GAM2267 C21orf4  5' GAAGGAGACTGCTGCGCCAC  53954     C  ACAGA
                                GAAG AGA    TGCGCCAC
                                |||| |||    ||||||||
                                CTTC TCT    ACGCGGTG
                                  C  GACG_
GAM2267 C6orf5   3' AGAATGCAGAGCAGTCAC    53955     _    A  A
                                AGAA GCAGA CAG TGC
                                |||| ||||| ||| |||
                                TCTT CGTCT GTC GTG
                                  A    C  A
GAM2267 CD109    3' GAAGGGAACAGATGAAGC    53956     CA      C_
                                GAAG  GAACAGATG  GC
                                ||||  |||||||||  ||
                                CTTC  CTTGTCTAC  CG
                                  C_       TT
GAM2267 CDH26    3' AGAAGGTAGAACAGAGGACAC  53957      C_      T_
                                AGAAG  AGAACAGA  GCGC
                                |||||  ||||||||  ||||
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                                TCTTC  TCTTGTCT  TGTG
                                   CA       CC
GAM2267  CGGBP1    3'  AAAAAGCAGGGCAGTTCTTCCA 53958         AA   ATGCG
                                AAGAAGCAG  CAG    CCA
                                |||||||||  |||    |||
                                TTTTTCGTC  GTC    GGT
                                     CC   AAGAA
GAM2267  CNNM1     3'  GAAGGCAGAACATTCTGTCAC  53959      _     GA_ _
                                GAAG CAGAACA   TG CGC
                                |||| |||||||   || |||
                                CTTC GTCTTGT   AC GTG
                                  C      AAG  A
GAM2267  COLEC12   3'  AAGAAGCAGGGCAGGCAC    53960         AA   AT
                                AAGAAGCAG  CAG  GCGC
                                |||||||||  |||  ||||
                                TTCTTCGTC  GTC  CGTG
                                     CC  __
GAM2267  CPR2      3'  AGAGGGCAGAACAGATAGGGC  53961     A_         C_
                                AGA  GCAGAACAGATG  GC
                                |||  ||||||||||||  ||
                                TCT  CGTCTTGTCTAT  CG
                                  CC          CC
GAM2267  CXorf1    3'  AGAAGCAAAGTACACC      53962         AAC  A
                                AGAAGCAG   AG TGCGCC
                                ||||||||   || ||||||
                                TCTTCGTT   TC ATGTGG
                                     ____  _
GAM2267  CYP3A7    3'  AGAAGCAGAGAAGCCA      53963         ACA  TGC
                                AGAAGCAGA   GA   GCCA
                                |||||||||   ||   ||||
                                TCTTCGTCT   CT   CGGT
                                     ____  T__
GAM2267  DD96      5'  AGGAGCAAAACACAAGGCCA  53964    A       GATGC
                                AG AGCAGAACA    GCCA
                                || |||||||||    ||||
                                TC TCGTTTTGT    CGGT
                                 C        GTTC_
GAM2267  DKFZP434B044 3'  GAGCAGAGATCACGCCAC    53965    A    ACA  _
                                GA GCAGA   GAT GCGCCAC
                                || |||||   ||| |||||||
                                CT CGTCT   CTA TGCGGTG
                                 _    ____  G
GAM2267  DKFZP434D1335 5'  AGAGGCAGATCCCACGCCAC  53966     A    ACAGA
                                AGA GCAGA    TGCGCCAC
                                ||| |||||    ||||||||
                                TCT CGTCT    GTGCGGTG
                                  C    AGG__
GAM2267  DKFZp434K1210 3'  GAAGGAGAGCCCTGCGCCAC  53967      C   ACAGA
                                GAAG AGA    TGCGCCAC
                                |||| |||    ||||||||
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                                CTTC TCT    ACGCGGTG
                                  C  CGGG_
GAM2267  EFS2     3'  AAGAAGCAGAGTCAGGGAGGC  53968        A_  AT__
                                AAGAAGCAGA  CAG   GC
                                ||||||||||  |||   ||
                                TTCTTCGTCT  GTC   CG
                                     CA   CCTC
GAM2267  FLJ11210 3'  AGAAGCAGTGTAACACAGTCAC 53969       ___   GATG
                                AGAAGCAG   AACA   CGC
                                ||||||||   ||||   |||
                                TCTTCGTC   TTGT   GTG
                                    ACA    GTCA
GAM2267  FLJ12768 3'  AGAAGGCAGAACAGCTAACAGC 53971      _      AT_ _
            CA                    AGAAG CAGAACAG   GC GCCA
                                ||||| ||||||||   || ||||
                                TCTTC GTCTTGTC   TG CGGT
                                   C       GAT  T
GAM2267  FLJ12768 3'  AGGAACAGACAGGTGTCG    53970    A     A   A  _
                                AG AGCAGA CAG TG CG
                                || |||||| ||| || ||
                                TC TTGTCT GTC AC GC
                                 C     _   C  A
GAM2267  FLJ12788 3'  AGAAACAGAGTGGCCA      53972         ACA A  C
                                AGAAGCAGA   G TG GCCA
                                |||||||||   | || ||||
                                TCTTTGTCT   C AC CGGT
                                     ___ _ _
GAM2267  FLJ12892 3'  AGAAGCAGAGAGACCAACC   53973        AC    GC
                                AGAAGCAGA  AGAT  GCC
                                |||||||||  ||||  |||
                                TCTTCGTCT  TCTG  TGG
                                     C_    GT
GAM2267  FLJ12899 3'  AAGAAGCAAATGGAAGACTTGC 53974         AC__    GC
                                AAGAAGCAGA    AGAT  GC
                                ||||||||||    ||||  ||
                                TTCTTCGTTT    TCTG  CG
                                     ACCT    AA
GAM2267  FLJ13881 3'  AGAAGCAGAGGGAATGGGTTGC 53975         ACA   C___
                                AGAAGCAGA   GATG   GC
                                |||||||||   ||||   ||
                                TCTTCGTCT   TTAC   CG
                                     CCC    CCAA
GAM2267  FLJ14442 3'  GGAAAGCAGAATCTGCCAC   53976   A       CAGATGC
                                A GAAGCAGAA      GCCAC
                                | |||||||||      |||||
                                C TTTCGTCTT      CGGTG
                                 C       AGA____
GAM2267  FLJ14624 3'  AAAAAGCAGCTTACACAGATG  53977         A____
                                AAGAAGCAG    ACAGATG
                                |||||||||    |||||||
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                                TTTTTCGTC    TGTCTAC
                                     GAATG
GAM2267  FLJ14665  3'  GAAGCAGGAATGCACC     53978       AACA
                                GAAGCAG   GATGCGCC
                                |||||||   ||||||||
                                CTTCGTC   TTACGTGG
                                    C___
GAM2267  FLJ20132  5'  GAAGCAGAGCAGCTCTCGCCAC 53979       A  ATG_
                                GAAGCAGA CAG   CGCCAC
                                |||||||| |||   ||||||
                                CTTCGTCT GTC   GCGGTG
                                     C  GAGA
GAM2267  FLJ20694  5'  AAGAAGCAGAAAGACCCCTCCA 53980         C   GCG_
                                AAGAAGCAGAA AGAT   CCA
                                |||||||||| ||||   |||
                                TTCTTCGTCTT TCTG   GGT
                                      _   GGGA
GAM2267  FLJ22167  5'  AAGAAGCAGAGAGGTGAGAGC  53981        AC____  T
                                AAGAAGCAGA     AGA GC
                                ||||||||||     ||| ||
                                TTCTTCGTCT     TCT CG
                                     CTCCAC  _
GAM2267  FLJ23375  3'  GAAGCAGAGAGCCCA      53982       ACA  T  G
                                GAAGCAGA   GA GC CCA
                                ||||||||   || || |||
                                CTTCGTCT   CT CG GGT
                                     ___  _  _
GAM2267  GCMA      5'  AGAAGCAGACAGCAC      53983       A  GAT
                                AGAAGCAGA CA   GCGC
                                |||||||| ||   ||||
                                TCTTCGTCT GT   CGTG
                                     _  ___
GAM2267  H11       5'  AGAAGCAGAACCAACCA     53984         AGATGC
                                AGAAGCAGAAC     GCCA
                                ||||||||||     ||||
                                TCTTCGTCTTG     TGGT
                                     GT____
GAM2267  HN1L      3'  AGAAGGCAGGACAGATGC    53985      _  A
                                AGAAG CAG ACAGATGC
                                ||||| ||| ||||||||
                                TCTTC GTC TGTCTACG
                                   C  C
GAM2267  HPCAL4    3'  AGAAGCAGGACAGGTGGGC   53986       A   A  C
                                AGAAGCAG ACAG TG GC
                                |||||||| |||| || ||
                                TCTTCGTC TGTC AC CG
                                     C   C  C
GAM2267  JM11      3'  AAGAAGCAGGGTGTCAGACAC  53987       AA___
                                AAGAAGCAG    CAGATGC
                                |||||||||    |||||||
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                                TTCTTCGTC    GTCTGTG
                                     CCACA
GAM2267 KIAA0342 3' GAAGGCAGAAAAGTCGCCAC  53988     _    C  ATG
                                GAAG CAGAA AG   CGCCAC
                                |||| ||||| ||   ||||||
                                CTTC GTCTT TC   GCGGTG
                                  C    T  A__
GAM2267 KIAA0513 3' AGAGGCAGAGGCCACGCCAC  53989     A    ACAGA
                                AGA GCAGA    TGCGCCAC
                                ||| |||||    ||||||||
                                TCT CGTCT    GTGCGGTG
                                  C    CCG__
GAM2267 KIAA0562 5' AAGAAGCAGACCCGGCC     53990         ACAGA  C
                                AAGAAGCAGA    TG GCC
                                ||||||||||    || |||
                                TTCTTCGTCT    GC CGG
                                     GG___  _
GAM2267 KIAA1198 3' GAGGCAGAGGTTGCGCCAC   53991    A    ACAGA
                                GA GCAGA    TGCGCCAC
                                || |||||    ||||||||
                                CT CGTCT    ACGCGGTG
                                 C    CCA__
GAM2267 KIAA1200 3' AAAAAGCAGAGTGCATTTGC  53992         A__  GA
                                AAGAAGCAGA   CA  TGC
                                ||||||||||   ||  |||
                                TTTTTCGTCT   GT  ACG
                                     CAC  AA
GAM2267 KIAA1210 3' GAGCGGAGATCGCGCCAC    53993    A  A  ACA  _
                                GA GC GA   GAT GCGCCAC
                                || || ||   ||| |||||||
                                CT CG CT   CTA CGCGGTG
                                 _  C  ___   G
GAM2267 KIAA1922 3' AAGAAGCAGGAGAGGCA     53994         AAC   T
                                AAGAAGCAG   AGA GCG
                                |||||||||   ||| |||
                                TTCTTCGTC   TCT CGT
                                     C__   C
GAM2267 KIAA1940 3' GAAGCAAAGCAAGCCA      53995         A   ATGC
                                GAAGCAGA CAG    GCCA
                                |||||||| |||    ||||
                                CTTCGTTT GTT    CGGT
                                     C  ____
GAM2267 KIAA1977 5' GAAGCAGAAGTTATCTGCCAC 53996         CAG  GC
                                GAAGCAGAA   AT  GCCAC
                                |||||||||   ||  |||||
                                CTTCGTCTT   TA  CGGTG
                                     CAA  GA
GAM2267 LASP1    3' GAAACAGAATGCACCAGCGCCA 53997         __  GAT
             C                   GAAGCAGAA  CA   GCGCCAC
                                |||||||||  ||   |||||||
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                                CTTTGTCTT  GT   CGCGGTG
                                     AC  GGT
GAM2267 LGI2     3'  AGAAGCAGATGAGCCA      53998          ACAGA  C
                                AGAAGCAGA    TG GCCA
                                |||||||||    || ||||
                                TCTTCGTCT    AC CGGT
                                     _____  T
GAM2267 LNX      3'  AAGAAGCGGGCAGTGAGCC   53999        AGAA   A  C
                                AAGAAGC    CAG TG GCC
                                |||||||    ||| || |||
                                TTCTTCG    GTC AC CGG
                                   CCC_   _ T
GAM2267 MGC10500 3'  AGAGCAGAACACAGGCCA    54000     A       GATGC
                                AGA GCAGAACA     GCCA
                                ||| ||||||||     ||||
                                TCT CGTCTTGT     CGGT
                                  _      GTC__
GAM2267 MGC15631 3'  AGAAGCAGAGAGATTTAC    54001         AC    GC
                                AGAAGCAGA  AGAT  GC
                                |||||||||  ||||  ||
                                TCTTCGTCT  TCTA  TG
                                     C_    AA
GAM2267 MGC19570 3'  AGAAGTAGAACCAATGCTGC   54002      C     A    _
                                AGAAG AGAAC GATGC GC
                                ||||| ||||| ||||| ||
                                TCTTC TCTTG TTACG CG
                                   A    G    A
GAM2267 MGC2865  3'  GAAACGGGACAGATGCCGC    54003      AGA       _
                                GAAGC   ACAGATGC GC
                                |||||   |||||||| ||
                                CTTTG   TGTCTACG CG
                                   CCC       G
GAM2267 moblak   3'  AAGAAGCAGAGTGCA       54004          ACA A
                                AAGAAGCAGA   G TGCG
                                ||||||||||   | ||||
                                TTCTTCGTCT   C ACGT
                                     ____ _
GAM2267 MR       5'  GAAGCAGATACACTGCTGC    54005         _  GA  _
                                GAAGCAGA ACA  TGC GC
                                |||||||| |||  ||| ||
                                CTTCGTCT TGT  ACG CG
                                     A  G_  A
GAM2267 NEUROG3  3'  AGAAGCAGAAGGAACAAGTGC  54006          ____   A
                                AGAAGCAGA    ACAG TGC
                                |||||||||    |||| |||
                                TCTTCGTCT    TGTT ACG
                                     TCCT    C
GAM2267 PALMD    5'  AGAAGCAGGGAGAAATCCGC   54007         AAC_   G
                                AGAAGCAG    AGAT CGC
                                ||||||||    |||| |||
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                                TCTTCGTC   TTTA GCG
                                     CCTC   G
GAM2267  POLD3    3'  AAGGAACAGAACACAAGCCAC  54008    A       GATGC
                                AAG AGCAGAACA    GCCAC
                                ||| |||||||||    |||||
                                TTC TTGTCTTGT    CGGTG
                                  C       GTT__
GAM2267  PPIE     3'  GAAGCAGAGAGAGTGCCGC   54009       AC  _  _
                                GAAGCAGA  AGA TGC GC
                                ||||||||  ||| ||| ||
                                CTTCGTCT  TCT ACG CG
                                     C_  C  G
GAM2267  RHOBTB1  5'  AAGAACAGAACACTCTGC    54010     G     GA_
                                AAGAA CAGAACA   TGC
                                ||||| |||||||   |||
                                TTCTT GTCTTGT   ACG
                                   _     GAG
GAM2267  SAC2     5'  AGAAGCAGCGGCAGAGGGAACG 54011       AA_   T___
              C                  AGAAGCAG   CAGA   GCGC
                                 ||||||||   ||||   ||||
                                 TCTTCGTC   GTCT   TGCG
                                      GCC   CCCT
GAM2267  SAST     5'  AAGGAGCAGAACATGCCGACCA 54012    A       GA  __
              C                  AAG AGCAGAACA  TGC  GCCAC
                                 ||| |||||||||  |||  |||||
                                 TTC TCGTCTTGT  ACG  TGGTG
                                   C        __  GC
GAM2267  SEC14L1  3'  AAGAAGCAGGACTCCTACATGC 54013       A  AGA  __
              CAC                  AAGAAGCAG AC   TGC  GCCAC
                                   ||||||||| ||   |||  |||||
                                   TTCTTCGTC TG   ATG  CGGTG
                                        C  AGG   TA
GAM2267  SEC22C   3'  AGAAGCAGAAAGAGAAACA   54014        C_  T
                                AGAAGCAGAA  AGA GCG
                                ||||||||||  ||| |||
                                TCTTCGTCTT  TCT TGT
                                      TC   T
GAM2267  SERF1B   3'  GAGCAGAGATCACGCCAC    53965    A    ACA  _
                                GA GCAGA   GAT GCGCCAC
                                || |||||   ||| |||||||
                                CT CGTCT   CTA TGCGGTG
                                 _    ___  G
GAM2267  SLC2A13  3'  AGAAGCAGGGCAGTGAAGTCAC 54015       AA  A  CGC_
                                AGAAGCAG  CAG TG   CAC
                                ||||||||  ||| ||   |||
                                TCTTCGTC  GTC AC   GTG
                                     CC   _  TTCA
GAM2267  TBCC     3'  AAGAACAGAGTGACAACTGC   54016     G   ___   A
                                AAGAA CAGA   ACAG TGC
                                ||||| ||||   |||| |||
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                                TTCTT GTCT   TGTT ACG
                                  _   CAC    G
GAM2267  TRIM36    3'  AGAAACAGAAAATGCCA     54017         CA   GC
                                AGAAGCAGAA  GAT  GCCA
                                ||||||||||  |||  ||||
                                TCTTTGTCTT  TTA  CGGT
                                     __   __
GAM2267  WFDC3     3'  AGAAGCAGAGCAGAGAGGGCCA 54018         A    TGC_
                                AGAAGCAGA CAGA    GCCA
                                ||||||||| ||||    ||||
                                TCTTCGTCT GTCT    CGGT
                                     C    CTCC
GAM2267  LOC121219 3'  AGAAGCAGAGCAACCCA     54019         A  GAT  G
                                AGAAGCAGA CA   GC CCA
                                ||||||||| ||   || |||
                                TCTTCGTCT GT   TG GGT
                                     C  ___  _
GAM2267  LOC122553 3'  AGAAGCAGAAGAGGGATGC    54020         CA__
                                AGAAGCAGAA    GATGC
                                ||||||||||    |||||
                                TCTTCGTCTT    CTACG
                                     CTCC
GAM2267  LOC128708 5'  AGAAGCAAGAGATAAGTGCTGC 54021        _  AC__  A  _
                                AGAAGCA GA    AG TGC GC
                                ||||||| ||    || ||| ||
                                TCTTCGT CT    TC ACG CG
                                    T  CTAT  _   A
GAM2267  LOC130355 5'  AGAAGCAGGACGGCC       54022         AACA    C
                                AGAAGCAG    GATG GCC
                                ||||||||    |||| |||
                                TCTTCGTC    CTGC CGG
                                     ____   _
GAM2267  LOC135932 3'  AGAGGCACAGACACTGCTAC   54023     A  AGA      _  C
                                AGA GC   ACAGATGC GC AC
                                ||| ||   |||||||| || ||
                                TCT CG   TGTCTGTG CG TG
                                  C  ___       A  A
GAM2267  LOC143286 5'  AAGAAGCAGAGACATTGCC    54024          _  GATGC
                                AAGAAGCAGA ACA     GCC
                                |||||||||| |||     |||
                                TTCTTCGTCT TGT     CGG
                                     C   AA___
GAM2267  LOC144473 3'  AGAACCAGAATGTGACCGC    54025      G    CA_  G
                                AGAA CAGAA   GAT CGC
                                |||| |||||   ||| |||
                                TCTT GTCTT   CTG GCG
                                  G    ACA  _
GAM2267  LOC144563 5'  GAATGCAGGTGCGCGCCAC    54026     _   AACAGA
                                GAA GCAG     TGCGCCAC
                                ||| ||||     ||||||||
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                                CTT CGTC     GCGCGGTG
                                  A   CAC___
GAM2267  LOC145757 5'  AGGAGCAGAACAGGCAC     54027    A        AT
                                AG AGCAGAACAG  GCGC
                                || ||||||||||  ||||
                                TC TCGTCTTGTC  CGTG
                                 C        __
GAM2267  LOC145783 3'  AAGAGGCAAAACAATGGC     54028     A       A  C
                                AAGA GCAGAACAG TG GC
                                |||| ||||||||| || ||
                                TTCT CGTTTTGTT AC CG
                                  C       _ _
GAM2267  LOC145828 5'  AAGAAACAGAAGCTCGCCAC   54029          AC  ATG
                                AAGAAGCAGA  AG   CGCCAC
                                ||||||||||  ||   ||||||
                                TTCTTTGTCT  TC   GCGGTG
                                      __  GA_
GAM2267  LOC145864 5'  GAAGCAGAATACATCA      54030        ACAG    C
                                GAAGCAGA    ATGCG CA
                                ||||||||    ||||| ||
                                CTTCGTCT    TATGT GT
                                     _____    A
GAM2267  LOC145921 3'  AAGAAGCAGGAGAGACAGAGCC 54031         A____    TGC
           A                     AAGAAGCAG    ACAGA   GCCA
                                ||||||||     |||||   ||||
                                TTCTTCGTC    TGTCT   CGGT
                                     CTCTC    ___
GAM2267  LOC146562 5'  AGCAGGACAAACACCAC     54032      A    AT
                                AGCAG ACAG  GCGCCAC
                                ||||| ||||  |||||||
                                TCGTC TGTT  TGTGGTG
                                   C   __
GAM2267  LOC148229 5'  GAAGCAGAACTGGCC       54033          AGA  C
                                GAAGCAGAAC   TG GCC
                                ||||||||||   || |||
                                CTTCGTCTTG   AC CGG
                                     ___  _
GAM2267  LOC148508 3'  AGAAGCAGTGCACCAC      54034        AACAGA
                                AGAAGCAG     TGCGCCAC
                                ||||||||     ||||||||
                                TCTTCGTC     ACGTGGTG
                                     _______
GAM2267  LOC150166 5'  AGAAGCAGGCTGGTGCCAC    54035        AACAGA  C_
                                AGAAGCAG     TG  GCCAC
                                ||||||||     ||  |||||
                                TCTTCGTC     AC  CGGTG
                                     CG_____  CA
GAM2267  LOC151632 5'  GAATGCAGGTGTGCGCCAC    54036     _   AACAGA
                                GAA GCAG     TGCGCCAC
                                ||| ||||     ||||||||
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                                CTT CGTC     ACGCGGTG
                                  A   CAC___
GAM2267  LOC152313 5'  AAGAAGCAGGGAGACCGC    54037        AAC   G
                                AAGAAGCAG   AGAT CGC
                                |||||||||   |||| |||
                                TTCTTCGTC   TCTG GCG
                                     CC_   _
GAM2267  LOC153364 5'  AAGCAGAGGCTGCGCCAC    54038       ACAGA
                                AAGCAGA    TGCGCCAC
                                |||||||    ||||||||
                                TTCGTCT    ACGCGGTG
                                    CCG__
GAM2267  LOC153469 3'  AAGAAGCAGGTGGACGAGGC  54039        AACA   C_
                                AAGAAGCAG   GATG  GC
                                |||||||||   ||||  ||
                                TTCTTCGTC   CTGC  CG
                                     CAC_   TC
GAM2267  LOC157254 3'  AAAAGCAGAACACACC      54040         AGAT
                                AGAAGCAGAAC   GCGCC
                                ||||||||||   |||||
                                TTTTCGTCTTG   TGTGG
                                      ____
GAM2267  LOC157624 5'  AAGAAGCAGACAAGTGACTGC  54041         ACA__  _
                                AAGAAGCAGA    GA TGC
                                |||||||||    || |||
                                TTCTTCGTCT    CT ACG
                                     GTTCA  G
GAM2267  LOC157842 5'  AAGAGCAGGTGCCGCGCCAC   54042     A   AACAGA
                                AAGA GCAG     TGCGCCAC
                                |||| ||||     ||||||||
                                TTCT CGTC     GCGCGGTG
                                  _   CACG__
GAM2267  LOC158293 3'  AAAAAGCAGGCAGTGC      54043        AA   A
                                AAGAAGCAG  CAG TGC
                                |||||||||  ||| |||
                                TTTTTCGTC  GTC ACG
                                     C_   _
GAM2267  LOC196410 5'  AAGAAGCAGCACCAGCAGCTGC 54044        AA_   AT  _
                                AAGAAGCAG   CAG  GC GC
                                |||||||||   |||  || ||
                                TTCTTCGTC   GTC  CG CG
                                     GTG   GT  A
GAM2267  LOC196510 3'  AAGAAGCAGACATGGCCA    54045        A  GA  C
                                AAGAAGCAGA CA  TG GCCA
                                |||||||||| ||  || ||||
                                TTCTTCGTCT GT  AC CGGT
                                      _  __  _
GAM2267  LOC200301 5'  GAGCGGAGATCGCGCCAC    53993    A  A  ACA  _
                                GA GC GA   GAT GCGCCAC
                                || || ||   ||| |||||||
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                                CT CG CT   CTA CGCGGTG
                                 _ C ___  G
GAM2267  LOC202741 3'  AGAAGCAGAGTGAGAATCAC  54046        AC_  TG
                                AGAAGCAGA  AGA  CGC
                                |||||||||  |||  |||
                                TCTTCGTCT  TCT  GTG
                                     CAC  TA
GAM2267  LOC220032 3'  AAGAAGCAGGGGAGATGTGGC  54047        AAC   C_
                                AAGAAGCAG  AGATG  GC
                                |||||||||  |||||  ||
                                TTCTTCGTC  TCTAC  CG
                                     CCC   AC
GAM2267  LOC221044 5'  AAGACAGCAGGACGGCC    54048    _   AACA   C
                                AAGA AGCAG   GATG GCC
                                |||| |||||   |||| |||
                                TTCT TCGTC   CTGC CGG
                                  G   _____  _
GAM2267  LOC221061 3'  AGAAGCGGAACAGATGAAC   54049      A       C
                                AGAAGC GAACAGATG GC
                                |||||| ||||||||| ||
                                TCTTCG CTTGTCTAC TG
                                   C       T
GAM2267  LOC221241 3'  AAGAAACAGAAAACGTCA    54050         CA   _
                                AAGAAGCAGAA  GATG CG
                                ||||||||||  |||| ||
                                TTCTTTGTCTT  TTGC GT
                                      __   A
GAM2267  LOC221687 3'  AGAAGCAAAACACATCG     54051         G  G
                                AGAAGCAGAACA AT CG
                                |||||||||||| || ||
                                TCTTCGTTTTGT TA GC
                                       G  _
GAM2267  LOC253926 5'  GACTAGAACAGATGTCCA    54052    AGC       CG
                                GA  AGAACAGATG  CCA
                                ||  ||||||||||  |||
                                CT  TCTTGTCTAC  GGT
                                 GA_        A_
GAM2267  LOC254822 5'  AAAAAGCAGAACAAAGATCAC  54053           TG_
                                AAGAAGCAGAACAGA  CGC
                                ||||||||||||||  |||
                                TTTTTCGTCTTGTTT  GTG
                                       CTA
GAM2267  LOC256515 5'  GAATGCAGGGGCGCGCCAC   54054    _   AACAGA
                                GAA GCAG     TGCGCCAC
                                ||| ||||     ||||||||
                                CTT CGTC     GCGCGGTG
                                  A   CCC___
GAM2267  LOC256812 5'  GAAGCAGAAGCCGCCA      54055        CAGAT  _
                                GAAGCAGAA    GC GCCA
                                |||||||||    || ||||
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                                CTTCGTCTT    CG CGGT
                                     _____ G
GAM2267  LOC257476 3'  AAGCAGCAGATCTGTGCCA   53925      AA   __ C
                                AAGCAG  CAGA  TG GCCA
                                ||||||  ||||  || ||||
                                TTCGTC  GTCT  AC CGGT
                                   __   AG  A
GAM2267  LOC257486 3'  GAGCGGAGATCGCGCCAC    53993    A  A  ACA  _
                                GA GC GA   GAT GCGCCAC
                                || || ||   ||| |||||||
                                CT CG CT   CTA CGCGGTG
                                 _ C  ___  G
GAM2267  LOC51193  3'  AAGAAACAGGATGACAGTCAC  54056        A___   A
                                AAGAAGCAG    ACAG TGC
                                |||||||||    |||| |||
                                TTCTTTGTC    TGTC GTG
                                     CTAC    A
GAM2267  LOC55885  3'  AAGAAGCAAATGGAACAC    54057        ACA  T
                                AAGAAGCAGA   GA GCGC
                                ||||||||||   || ||||
                                TTCTTCGTTT   CT TGTG
                                     AC_  _
GAM2267  LOC93048  3'  AGAAGCAGGCCAGAGTGC    54058       AA   _
                                AGAAGCAG  CAGA TGC
                                ||||||||  |||| |||
                                TCTTCGTC  GTCT ACG
                                     CG   C
GAM2268  HEM1      5'  TGTATCACTTTGATGTGTC   54061        AC   AA
                                TGTATCACTT  GAT  TGTC
                                ||||||||||  |||  ||||
                                ACATAGTGAA  CTA  ACAG
                                     A_   C_
GAM2268  SPARC     3'  TAATGTATTCACTTAAATCTAT 54062       _    C   A_
            GT                    TAATGTAT CACTTA GAT  ATGT
                                ||||||||  ||||||  |||  ||||
                                ATTACATA GTGAAT TTA  TACA
                                     A    _   GA
GAM2268  FLJ13448  3'  TAATGCAGAACATGATAATGTC 54063       TC  TTAC
                                TAATGTA  AC   GATAATGTC
                                |||||||  ||   |||||||||
                                ATTACGT  TG   CTATTACAG
                                    CT  TA__
GAM2268  KIAA1586  5'  TAATGTATTACTTTTTAATGT  54064       C   ACGA
                                TAATGTAT ACTT   TAATGT
                                ||||||||  ||||   ||||||
                                ATTACATA TGAA   ATTACA
                                     A   AA__
GAM2268  PPP2R3A   3'  TAATGTATCATTATTCCTTTAT 54065        CTTACGATA_
            GTC                   TAATGTATCA       ATGTC
                                ||||||||||       |||||
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                                ATTACATAGT        TACAG
                                     AATAAGGAAA
GAM2268 SEC63L   3' TGTATCACTGCAAAATGTC   54066        TA  T
                                TGTATCACT  CGA AATGTC
                                |||||||||  ||| ||||||
                                ACATAGTGA  GTT TTACAG
                                     C_  _
GAM2269 BCL11A   3' CAGGTTTATTTTATACTCAAC  54069    C         G
                                CA GTTTATTTTATAT TCAAC
                                || |||||||||||| |||||
                                GT CAAATAAAATATG AGTTG
                                 C         _
GAM2269 GPR85    3' AACACATTTACCTCATGTCAAC 54070           AT
                                AACACGTTTATTTT  ATGTCAAC
                                ||||||||||||||  ||||||||
                                TTGTGTAAATGGAG  TACAGTTG
                                          __
GAM2269 PRKRA    3' CATTTTTATTTCATCATCAAC  54071    CG       A
                                CA  TTTATTTTAT TGTCAAC
                                ||  |||||||||| |||||||
                                GT  AAATAAAGTA GTAGTTG
                                 AA        _
GAM2269 CHCR     3' AACACGCTTATTGTTGTGT   54072          TTATA
                                AACACGTTTATT    TGT
                                ||||||||||||    |||
                                TTGTGCGAATAA    ACA
                                     CAAC_
GAM2269 FLJ13490 3' CGTTTATTTTTATATGCAA   54073         _   T
                                CGTTTATTTT ATATG CAA
                                |||||||||| ||||| |||
                                GCAAATAAAA TATAC GTT
                                     A    _
GAM2269 FLJ22940 3' AACAGGTTTATTTTATACA   54074     C
                                AACA GTTTATTTTATATG
                                |||| ||||||||||||||
                                TTGT CAAATAAAATATGT
                                  C
GAM2269 IMP-2    3' AACACGTTCACCTATGT     54075          TTA
                                AACACGTTTATT   TATGT
                                ||||||||||||   |||||
                                TTGTGCAAGTGG   ATACA
                                          ___
GAM2269 MGC3035  3' AACACTTTATTTTTCAAGTCAA 54076      G      A  T
           C                     AACAC TTTATTTT TA GTCAAC
                                 ||||| |||||||| || ||||||
                                 TTGTG AAATAAAA GT CAGTTG
                                    _      A  T
GAM2269 TSGA2    3' ACGTTTATTTGCATTTGTCAA  54077         _  A
                                ACGTTTATTT TAT TGTCAA
                                |||||||||| ||| ||||||
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                                TGCAAATAAA GTA ACAGTT
                                      C   A
GAM2269  LOC133686 3'  AACATATTTACCTATGTCAA  54078     CG     TTA
                                AACA  TTTATT   TATGTCAA
                                ||||  ||||||   ||||||||
                                TTGT  AAATGG   ATACAGTT
                                  AT     ___
GAM2269  LOC149018 3'  AACACGTTTACTTGTCA     54079          TTATA
                                AACACGTTTATT    TGTCA
                                ||||||||||||    |||||
                                TTGTGCAAATGA    ACAGT
                                          _____
GAM2269  LOC158476 5'  CACATACATCTTTATATGTTAA 54080      T     _     C
                C                CACGT TATTTT ATATGT AAC
                                 ||||| |||||| |||||| |||
                                 GTGTA GTAGAA TATACA TTG
                                    T     A     A
GAM2269  LOC220766 5'  CATGTTTATTTCCTTTCAAC   54081    C       ATATG
                                CA GTTTATTTT    TCAAC
                                || |||||||||    |||||
                                GT CAAATAAAG    AGTTG
                                 A       GAA__
GAM2269  LOC51205  3'  CACTTTATTTTAAAATCAAC   54082     G       TAT
                                CAC TTTATTTTA   GTCAAC
                                ||| |||||||||   ||||||
                                GTG AAATAAAAT   TAGTTG
                                  _       TT_
GAM2270  CAT       3'  GAGCGGGTTACACGGATGAACG 54085     T  A   TG    CA
                C                GAGC GG TTG  CGGA  AACGC
                                 |||| || |||  ||||  |||||
                                 CTCG CC AAT  GCCT  TTGCG
                                   C  _   GT    AC
GAM2270  TYK2      3'  GCTGGATTAGTGCCCCTACAAA 54086        _    GG__
                                GCTGGATT GTGC    ACAAA
                                |||||||| ||||    |||||
                                CGACCTAA CACG    TGTTT
                                     T    GGGA
GAM2270  FLJ22684  3'  AGCTGGATGTGGTGGCA     54087        T   C_  A
                                AGCTGGAT GTG  GG CA
                                |||||||| |||  || ||
                                TCGACCTA CAC  CC GT
                                     _   CA  _
GAM2270  MO25      5'  GCGGCTGCGCGGGCGGACG    54088    T  A       ACAA
                                GC GG TTGTGCGG    ACG
                                || || ||||||||    |||
                                CG CC GACGCGCC    TGC
                                 _ _       CGCC
GAM2270  LOC145719 5'  GAGCTGGTGAGGCAAGG     54089        ATTG  C  A   AC
                                GAGCTGG    TG GG CAA  G
                                |||||||    || || |||  |
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                                CTCGACC    AC CC GTT  C
                                    _____ T  _   CA
GAM2270  LOC145720 5'  GAGCTGGTGAGGCAAGG     54089       ATTG  C  A   AC
                                GAGCTGG    TG GG CAA  G
                                |||||||    || || |||  |
                                CTCGACC    AC CC GTT  C
                                    _____ T  _   CA
GAM2270  LOC197114 5'  GAGCTGGTGAGGCAAGG     54089       ATTG  C  A   AC
                                GAGCTGG    TG GG CAA  G
                                |||||||    || || |||  |
                                CTCGACC    AC CC GTT  C
                                    _____ T  _   CA
GAM2270  LOC203668 5'  GAGCTGGATGTATTCGGATAAA 54090         _  G   C   C
            TGC                    GAGCTGGAT TGT CGGA AAA GC
                                |||||||||| ||| |||| ||| ||
                                CTCGACCTA ATA GCCT TTT CG
                                      C   A   A   A
GAM2270  LOC220776 3'  GAGCTGGATACAGAC       54091         TGT
                                GAGCTGGAT   GCGGAC
                                |||||||||   ||||||
                                CTCGACCTA   TGTCTG
                                    ____
GAM2271  BCAR1     3'  CCCCTGGGCTTCGGCTCC     54094          C  A  AA
                                CCCCTGGGCT TC GG  CTCC
                                |||||||||| || ||  ||||
                                GGGGACCCGA AG CC  GAGG
                                    _  _  __
GAM2271  CASQ1     5'  CCCCTGGGTCCCAGATTCT    54095         C      AA
                                CCCCTGGG TCTCAGG  CT
                                |||||||| |||||||  ||
                                GGGGACCC AGGGTCT  GA
                                    _      AA
GAM2271  CHRNB2    5'  CCTGGGCCTCAGGGAGCCG    54096        T     AACT
                                CCTGGGC CTCAGG    CCG
                                ||||||| ||||||    |||
                                GGACCCG GAGTCC    GGC
                                    _     CTC_
GAM2271  DDX11     3'  CCTGGGCTGCAGGCTC      54097         CT    AA
                                CCTGGGCT  CAGG  CTC
                                ||||||||  ||||  |||
                                GGACCCGA  GTCC  GAG
                                     C_    __
GAM2271  EGR4      5'  CCCCGGGCTCCTGGCTTC     54098          CA  AAC
                                CCCTGGGCTCT  GG   TC
                                ||||||||||  ||   ||
                                GGGGCCCGAGG  CC   AG
                                      A_  GA_
GAM2271  EXTL1     5'  CCCCTGGGCACTGCTCTGCGGA 54099        T  CA_________  AACT
            GTTCC                  CTGGGC CT        GG    CC
                                |||||| ||         ||    ||
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                                GACCCG GA        CC   GG
                                   T  CGAGACIIIG  TCAA
GAM2271  GEMIN5   5'  CCCTGGACTCTCGCCTGCGGAG 54100         A_________  AACT
            TTCC                  CTGGGCTCTC       GG   CC
                                  ||||||||||       ||   ||
                                  GACCTGAGAG       CC   GG
                                     CGGACIIIG  TCAA
GAM2271  GPR62    3'  CCTGGCTCTCAGAAGTCCG   54101      G       AC
                                  CCTGG CTCTCAGGA  TCCG
                                  ||||| |||||||||  ||||
                                  GGACC GAGAGTCTT  AGGC
                                    _       C_
GAM2271  HIP1     3'  ACTCCTGGGCTGGGCTCTGCGG 54102        ___  A_____  AACT
            AGTTCC                  CTGGGCT   CTC     GG   CC
                                  |||||||   |||     ||   ||
                                  GACCCGA   GAG     CC   GG
                                     CCC   ACIIIG  TCAA
GAM2271  HYAL2    3'  CCTCCTGGGCTTCCTGGGGGCT 54103    _      _ CA  AA
            C                    CC CCTGGGCT CT  GG  CTC
                                 || |||||||| ||  ||  |||
                                 GG GGACCCGA GG  CC  GAG
                                  A       A  AC  CC
GAM2271  HYAL2    3'  CCTCCTGGGCTTCCTGGGGGCT 54103    _      _ CA  AA
            C                    CC CCTGGGCT CT  GG  CTC
                                 || |||||||| ||  ||  |||
                                 GG GGACCCGA GG  CC  GAG
                                  A       A  AC  CC
GAM2271  INPP5A   3'  CCCCGGTCCCAGGAACTC    54104       GC
                                  CCCTGG  TCTCAGGAACTC
                                  ||||||  ||||||||||||
                                  GGGGCC  AGGGTCCTTGAG
                                    __
GAM2271  KCNS2    3'  ACCCCTGGGTTCTATTGCGGAG 54105         C   CA_______  AACT
            TC                     CCCCTGGG TCT       GG   C
                                  |||||||| |||       ||   |
                                  GGGGACCC AGA       CC   G
                                     A   TAACIIIG  TCAA
GAM2271  KRTHA5   3'  CCTGGGCCTGGGCTCTGCGGAG 54106  _____        CA___  AACT
            TTCC                    CCTGGGCTCT    GG   CC
                                   ||||||||||    ||   ||
                                   GGACCCGAGA    CC   GG
                                  ACCC        CIIIG  TCAA
GAM2271  LZTS1    3'  ACCCTTGGATTCTCCCTCTGCG 54107     GC   A__________  AACT
            GAGTTCC                  TGG  TCTC        GG   CC
                                  |||  ||||        ||   ||
                                  ACC  AGAG        CC   GG
                                    TA   GGAGACIIIG  TCAA
GAM2271  MUC4     3'  CCTGGGCTCCTCACTCCTCCG  54108         _  GGAA
                                  CCTGGGCTC TCA    CTCCG
                                  ||||||||| |||    |||||
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                                GGACCCGAG AGT   GAGGC
                                     G  GAG_
GAM2271  NT5M    3'  CCCCTGGGCTTCTGGCAGCT  54109        C  A  AA_
                                CCCCTGGGCT TC GG  CT
                                |||||||||| || ||  ||
                                GGGGACCCGA AG CC  GA
                                     _  A  GTC
GAM2271  NTSR1   5'  CCGGGCTCCGGGCTCC     54111        CA  AA
                                CTGGGCTCT  GG  CTCC
                                |||||||||  ||  ||||
                                GGCCCGAGG  CC  GAGG
                                     __ C_
GAM2271  NTSR1   5'  CCCCGGGCTCCGGGCTCC   54110         CA  AA
                                CCCTGGGCTCT  GG  CTCC
                                ||||||||||  ||  ||||
                                GGGGCCCGAGG  CC  GAGG
                                     __ C_
GAM2271  PTPRJ   5'  CCCTGAGCGCGCAGGGGCTTCG 54112       TCT   AA  C
                                CCCTGGGC  CAGG  CT CG
                                ||||||||  ||||  || ||
                                GGGACTCG  GTCC  GA GC
                                     CGC   CC  A
GAM2271  RAP1GA1 5'  CCTGGGCTCGGCACTC     54113        TCA  A
                                CCTGGGCTC  GG ACTC
                                |||||||||  || ||||
                                GGACCCGAG  CC TGAG
                                     ___ G
GAM2271  SLC2A8  3'  CCCCTGGGGCAGGCAGGGGCTC 54114       _ TCT   AA
                                CCCCTGGG C  CAGG  CTC
                                |||||||| |  ||||  |||
                                GGGGACCC G  GTCC  GAG
                                     C TCC   CC
GAM2271  SULT2A1 3'  CCCTGGGCTTTGAACCC     54115        CTCAG
                                CCCTGGGCT   GAACTC
                                |||||||||   ||||||
                                GGGACCCGA   CTTGGG
                                     AA___
GAM2271  TACC2   3'  CCCTGATACAGGAACTC     54116      GCTCT
                                CCCTGG   CAGGAACTC
                                ||||||   |||||||||
                                GGGACT   GTCCTTGAG
                                   AT___
GAM2271  TNFAIP1 3'  ACCCCTGGGCTGCTTGGA    54117         _  CA
                                ACCCCTGGGCT CT  GGA
                                |||||||||| ||  |||
                                TGGGGACCCGA GA  CCT
                                     C  A_
GAM2271  A2BP1   5'  CCCCTGGGCTCCGTCCGCGGAG 54118         CA_______  AACT
            TC                  CCCTGGGCTCT       GG   C
                                ||||||||||        ||   |
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                                GGGACCCGAGG       CC    G
                                      CAGGCIIIG  TCAA
GAM2271  AD-017   5'  ACCCCTGGTTAGGGCTCC    54119        GCTCTC   AA
                                ACCCCTGG     AGG  CTCC
                                ||||||||     |||  ||||
                                TGGGGACC     TCC  GAGG
                                    AA_____   C_
GAM2271  ADIR     3'  ACCCCTGGGTCACAGAACTTCG 54120         C  TCA     C
                                ACCCCTGGG TC   GGAACT CG
                                ||||||||| ||   |||||| ||
                                TGGGGACCC AG   TCTTGA GC
                                    _ TG_     A
GAM2271  ALOXE3   5'  CCTGGGCTTTCTCTCTCCG   54121        __   AGGAA
                                CCTGGGC  TCTC    CTCCG
                                |||||||  ||||    |||||
                                GGACCCG  AGAG    GAGGC
                                    AA   A_____
GAM2271  APXL2    5'  CCCCGGGCTCTGACTCC     54122         CAG  A
                                CCCTGGGCTCT   GA CTCC
                                ||||||||||   || ||||
                                GGGGCCCGAGA   CT GAGG
                                      ___  _
GAM2271  BC008967 5'  ACTCCTGGGTTCGGCATGCTC  54123    C     C  TCA  AA__
                                AC CCTGGG TC   GG    CTC
                                || |||||| ||   ||    |||
                                TG GGACCC AG   CC    GAG
                                 A     A ___  GTAC
GAM2271  C11orf9  3'  CTCTGGCTCTCAGGTTCC    54124    G_       AAC
                                CT  GGCTCTCAGG   TCC
                                ||  ||||||||||   |||
                                GA  CCGAGAGTCC   AGG
                                 GA        A__
GAM2271  C20orf85 3'  ACCCCTGGGCAGAACTCC    54125         TCTCA
                                ACCCCTGGGC    GGAACTCC
                                ||||||||||    ||||||||
                                TGGGGACCCG    TCTTGAGG
                                      _____
GAM2271  C20orf98 5'  ACCCCTGGGACTGTGGGCTC   54126         CT  CA  AA
                                ACCCCTGGG  CT  GG  CTC
                                |||||||||  ||  ||  |||
                                TGGGGACCC  GA  CC  GAG
                                     T_  CA  C_
GAM2271  C5orf6   3'  ACTCCTGGGCTCACAGTTTCC  54127    C       T   GAAC
                                AC CCTGGGCTC CAG    TCC
                                || |||||||| |||    |||
                                TG GGACCCGAG GTC    AGG
                                 A       T   AA__
GAM2271  DNAL4    3'  CCCCTGGCTCTCAACTGCGGAG 54128      G    A_________  AACT
            TC                   CCTGG CTCTC       GG    C
                                |||||  |||||        ||    |
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                                GGACC GAGAG       CC   G
                                  _    TTGACIIIG  TCAA
GAM2271  FLJ00007  3'  CCTCCTGGACTGGGAGCTCCG  54129    _      CTCA  A
                                CC CCTGGGCT   GGA CTCCG
                                || ||||||||   ||| |||||
                                GG GGACCTGA   CCT GAGGC
                                 A      C___  C
GAM2271  FLJ12355  3'  CCCTGGGCTCTCGGCACCC   54130          A  A
                                CCCTGGGCTCTC GG ACTC
                                |||||||||||| || ||||
                                GGGACCCGAGAG CC TGGG
                                       _ G
GAM2271  FLJ14327  3'  ACTCCTGGGCTCCCATCTGCGG 54131         A_________  AACT
            AGTTCC                CTGGGCTCTC       GG   CC
                                |||||||||        ||   ||
                                GACCCGAGGG       CC   GG
                                      TAGACIIIG  TCAA
GAM2271  FLJ14346  5'  CCTCTGCACCCTGGGAGTTCCG 54132   C  G   CA  AC
                                CC CTG GCTCT  GGA  TCCG
                                || ||| |||||  |||  ||||
                                GG GAC TGGGA  CCT  AGGC
                                 A  G    C_   CA
GAM2271  FLJ21044  5'  CCTGGGCCGAGGGGCTTCG   54133       CTC  AA  C
                                CCTGGGCT   AGG  CT CG
                                ||||||||   |||  || ||
                                GGACCCGG   TCC  GA GC
                                     C__   CC  A
GAM2271  FLJ22612  3'  CTGGGCTCTTAAACACC    54134        CAG   T
                                CTGGGCTCT   GAAC CC
                                |||||||||   |||| ||
                                GACCCGAGA   TTTG GG
                                     A__    T
GAM2271  FLJ30663  5'  CCCCGGGCTCCGGCTC     54135         CA  AA
                                CCCTGGGCTCT  GG  CTC
                                ||||||||||  ||  |||
                                GGGGCCCGAGG  CC  GAG
                                       __ __
GAM2271  GAL3ST2   5'  ACGCCTGGGCTCTGCCTCTGCG 54136       CA__________  AACT
            GAGTTCC               TGGGCTCT        GG   CC
                                |||||||         ||   ||
                                ACCCGAGA        CC   GG
                                    CGGAGACIIIG  TCAA
GAM2271  GGA2     3'  CCCTCTGCCCAGGAACTC    54137     GG  T T
                                CCCT  GC C CAGGAACTC
                                ||||  || | |||||||||
                                GGGA  CG G GTCCTTGAG
                                  GA  _ _
GAM2271  GGA2     3'  CCCTCTGCCCAGGAACTC    54137     GG  T T
                                CCCT  GC C CAGGAACTC
                                ||||  || | |||||||||
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                                GGGA  CG G GTCCTTGAG
                                  GA  _ _
GAM2271  HDAC11   3'  ACCTATGGGCTGGTGACTTCG  54138    CC     CTCA  A_   C
                                ACC  TGGGCT    GG  ACT CG
                                |||  ||||||    ||  ||| ||
                                TGG  ACCCGA    CC  TGA GC
                                  AT     _____  AC   A
GAM2271  HSPC156  5'  CCGGGCTCCGGGCTCC      54111         CA  AA
                                CTGGGCTCT  GG  CTCC
                                |||||||||  ||  ||||
                                GGCCCGAGG  CC  GAGG
                                     __  C_
GAM2271  IMP-2    3'  CCCCTGGGGTTCTCAGGGCCTC 54139        C_      AA
                                CCCCTGGG  TCTCAGG  CTC
                                ||||||||  |||||||  |||
                                GGGGACCC  AGAGTCC  GAG
                                     CA      CG
GAM2271  KCND1    5'  CCTGGGCTTTGCAGGAAGCT   54140        CT_     _
                                CCTGGGCT   CAGGAA CT
                                ||||||||   ||||||  ||
                                GGACCCGA   GTCCTT GA
                                     AAC     C
GAM2271  KIAA0062  3'  CCCCTGGGCTCCAACTGCGGAG 54141          CA_______  AACT
            TC                   CCCTGGGCTCT       GG    C
                                ||||||||||        ||    |
                                GGGACCCGAGG       CC    G
                                     TTGACIIIG  TCAA
GAM2271  KIAA0326  3'  ACCCCTGGGCCTTCATCTGCGG 54142       TC  A_________  AACT
            AGTTCC                  CTGGGC  TC       GG    CC
                                ||||||  ||       ||    ||
                                GACCCG  AG       CC    GG
                                   GA  TAGACIIIG  TCAA
GAM2271  KIAA0352  3'  ACCCCTGGTTCTCCACATCTC  54143        GC    AGGAA
                                ACCCCTGG  TCTC    CTC
                                ||||||||  ||||    |||
                                TGGGGACC  AGAG    GAG
                                     A_    GTGTA
GAM2271  KIAA0444  3'  CTGGGCTCTGGCCCA       54144         CA  AAC
                                CTGGGCTCT  GG   TCCG
                                |||||||||  ||   ||||
                                GACCCGAGA  CC   GGGT
                                     __  ___
GAM2271  KIAA0596  3'  CCTCTGGGCTCCAGCAGCCG   54145    C       T   GAACT
                                CC CTGGGCTC CAG    CCG
                                || ||||||||| |||    |||
                                GG GACCCGAG GTC    GGC
                                 A       _  GTC__
GAM2271  KIAA0892  3'  CCCTGGGCTCCAGATCTC    54146          T    AA
                                CCCTGGGCTC CAGG  CTC
                                |||||||||| ||||  |||
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                                GGGACCCGAG GTCT  GAG
                                      _   A_
GAM2271  KIAA1007  5'  ACTCCTGGGTCCCCGACTCCG  54147    C     C    AG  A
                                AC CCTGGG TCTC  GA CTCCG
                                || |||||| ||||  || |||||
                                TG GGACCC AGGG  CT GAGGC
                                 A     _   G_ _
GAM2271  KIAA1086  3'  CCTCTGGGCTCCGGGTCTGCGG 54148        CA__________  AACT
            AGTTCC                TGGGCTCT        GG   CC
                                |||||||||         ||   ||
                                ACCCGAGG         CC   GG
                                    CCCAGACIIIG  TCAA
GAM2271  KIAA1372  5'  CCCCTGGGCCAGAAGCT     54149         TCT    A
                                CCCCTGGGC   CAGGA CT
                                |||||||||   ||||| ||
                                GGGGACCCG   GTCTT GA
                                     ___    C
GAM2271  KIAA1981  3'  ACCCCTGGGTTCTCCACACC   54150         C   AGGA
                                ACCCCTGGG TCTC    ACT
                                ||||||||| ||||    |||
                                TGGGGACCC AGAG    TGG
                                     A    GTG_
GAM2271  KIF13B   3'  CCTGCTCAAGTCAGGAACTC   54151     GG   ___
                                CCT  GCTC   TCAGGAACTC
                                |||  ||||   ||||||||||
                                GGA  CGAG   AGTCCTTGAG
                                  __    TTC
GAM2271  KIF13B   3'  CCTGCTCAAGTCAGGAACTC   54151     GG   ___
                                CCT  GCTC   TCAGGAACTC
                                |||  ||||   ||||||||||
                                GGA  CGAG   AGTCCTTGAG
                                  __    TTC
GAM2271  LGP1     5'  ACCCCTGGGTGACTCTGCGGAG 54152         CT_  A_____  AACT
            TC                    CCCCTGGG   CTC     GG   C
                                |||||||   |||     ||   |
                                GGGGACCC   GAG     CC   G
                                     ACT   ACIIIG  TCAA
GAM2271  LHFPL2   5'  ACCCCTGGGTTCCGGA      54153         C   CA
                                ACCCCTGGG TCT  GGA
                                ||||||||| |||  |||
                                TGGGGACCC AGG  CCT
                                     A  __
GAM2271  LMOD1    3'  CCCTGGGCTCCACTC       54154          CAGGA
                                CCCTGGGCTCT    ACTC
                                ||||||||||    ||||
                                GGGACCCGAGG    TGAG
                                              _____
GAM2271  MCF2L    3'  CCCCGGGCTCGACTC       54155          TCAG  A
                                CCCTGGGCTC    GA CTC
                                |||||||||    || |||
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                                GGGGCCCGAG   CT GAG
                                     _____  _
GAM2271  MGC21945  5'  ACCCCTGGTTCCCTGGCTCCG  54156        GC   A  AA
                                ACCCCTGG  TCTC GG  CTCCG
                                ||||||||  |||| ||  |||||
                                TGGGGACC  AGGG CC  GAGGC
                                    A_   A  __
GAM2271  phospho1  5'  CTGGGCTCCGGCTCACG     54157         CA  AA  _
                                CTGGGCTCT  GG  CTC CG
                                |||||||||  ||  ||| ||
                                GACCCGAGG  CC  GAG GC
                                     __ __  T
GAM2271  PTRF      3'  ACTCCTGGGCTCTGGCGCGGAG 54158   C        CA_______  AACT
            TC                    C CCTGGGCTCT       GG    C
                                | ||||||||||       ||    |
                                G GGACCCGAGA       CC    G
                                 A         CCGCIIIG  TCAA
GAM2271  RALY      3'  ACCCCTGTGCTCTACCCTC   54159        G    CAGGAA
                                ACCCCTG GCTCT     CTC
                                ||||||| |||||     |||
                                TGGGGAC CGAGA     GAG
                                    A    TGG___
GAM2271  SS18L1    3'  CCCTGGGCACAGAATGCTC   54160        TCT    A_
                                CCCTGGGC   CAGGA  CTC
                                ||||||||   |||||  |||
                                GGGACCCG   GTCTT  GAG
                                     T__    AC
GAM2271  WBSCR18   3'  ACTCCTGGGCTTTCGGGA    54161    C       C  A
                                AC CCTGGGCT TC GGA
                                || |||||||| || |||
                                TG GGACCCGA AG CCT
                                 A       A  C
GAM2271  LOC124220 5'  CCCAGGGCTCTCGCCTGCGGAG 54162    T       A_________  AACT
            TTCC                   C GGGCTCTC        GG    CC
                                | ||||||||        ||    ||
                                G CCCGAGAG        CC    GG
                                 T       CGGACIIIG  TCAA
GAM2271  LOC130940 5'  ACTCCTGGGCTCTCGCCGCGGA 54163   C        A________  AACT
            GTC                    CCTGGGCTCTC       GG    C
                                 ||||||||||        ||    |
                                 GGACCCGAGAG       CC    G
                                A         CGGCIIIG  TCAA
GAM2271  LOC149422 3'  ACCCCTGGGCTTCCAGAA    54164          CT
                                ACCCCTGGGCT  CAGGA
                                ||||||||||  |||||
                                TGGGGACCCGA  GTCTT
                                      AG
GAM2271  LOC150295 3'  CTGGGCTCCTCAGGCTCCG    54165        _    AA
                                CTGGGCTC TCAGG  CTCCG
                                |||||||| |||||  |||||
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                                GACCCGAG AGTCC  GAGGC
                                    G    __
GAM2271  LOC151040 5'  CCCTGGGCTGCGGCTCC     54166         CTCA  AA
                                CCCTGGGCT    GG  CTCC
                                |||||||||    ||  ||||
                                GGGACCCGA    CC  GAGG
                                     CG__  __
GAM2271  LOC152762 3'  CCTGGGTCCTCAGGACT     54167       CT      A
                                CCTGGG  CTCAGGA CT
                                ||||||  ||||||| ||
                                GGACCC  GAGTCCT GA
                                   AG      _
GAM2271  LOC152897 3'  ACTCCTGGGCTCCAGTGATCT  54168    C       T   _  A
                                AC CCTGGGCTC CAG GA CT
                                || |||||||| ||| || ||
                                TG GGACCCGAG GTC CT GA
                                 A        _   A  A
GAM2271  LOC155382 5'  CCCCGGGCTGCCGGGCTCCG   54169         C  A  AA
                                CCCTGGGCT TC GG  CTCCG
                                ||||||||| || ||  |||||
                                GGGGCCCGA GG CC  GAGGC
                                     C  C  __
GAM2271  LOC157697 5'  CCCCTGGGCTCCACCTGCGGAG 54170          CA_______  AACT
            TC                   CCCTGGGCTCT       GG    C
                                 ||||||||||        ||    |
                                 GGGACCCGAGG       CC    G
                                       TGGACIIIG  TCAA
GAM2271  LOC160942 5'  CCCCTGGATTTTCCTTCGCGGA 54171      C__   CA_______  AACT
            GTTCC                   CTGGG   TCT      GG    CC
                                    |||||   |||      ||    ||
                                    GACCT   AGG      CC    GG
                                      AAA   AAGCIIIG  TCAA
GAM2271  LOC197414 3'  CTGGGCTCCTGACACCCG    54172         CA GA  T
                                CTGGGCTCT  G  AC CCG
                                |||||||||  |  || |||
                                GACCCGAGG  C  TG GGC
                                     A_ TG  _
GAM2271  LOC200488 5'  ACCTCTGGGCTCCTTTTGGCTC 54173     C       CA__  AA
                                ACC CTGGGCTCT    GG  CTC
                                ||| |||||||||    ||  |||
                                TGG GACCCGAGG    CC  GAG
                                  A        AAAA  __
GAM2271  LOC200982 3'  CCCTGGGTTAAGAGCTTCG    54174       CTCTC    A  C
                                CCCTGGG     AGGA CT CG
                                |||||||     |||| || ||
                                GGGACCC     TTCT GA GC
                                    AA___    C  A
GAM2271  LOC203871 5'  CCCCGGGCTCTCAACTGCGGAG 54175          A_________  AACT
            TC                   CCTGGGCTCTC       GG    C
                                 ||||||||||        ||    |
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                                GGGCCCGAGAG       CC    G
                                     TTGACIIIG  TCAA
GAM2271  LOC220370 3'  ACTCCTGGGCTCCTTGCTGCGG 54176        CA_________  AACT
           AGTTCC                 CTGGGCTCT        GG    CC
                                ||||||||||        ||    ||
                                GACCCGAGG        CC    GG
                                     AACGACIIIG  TCAA
GAM2271  LOC253289 3'  CCCTGGGCTCTCCCTTTGCGGA 54177        A__________  AACT
           GTTCC                  TGGGCTCTC        GG    CC
                                ||||||||||        ||    ||
                                ACCCGAGAG        CC    GG
                                     GGAAACIIIG  TCAA
GAM2271  LOC254170 3'  CCTGAGCTCTGAACTC      54178          CAG
                                CCTGGGCTCT   GAACTC
                                ||||||||||   ||||||
                                GGACTCGAGA   CTTGAG

                                     ____
GAM2271  LOC51725  3'  CCTACTTCAGGAACTCCG    54179     GG   C
                                CCT  GCT TCAGGAACTCCG
                                |||  ||| ||||||||||||
                                GGA  TGA AGTCCTTGAGGC

                                  __  _
GAM2271  LOC90139  3'  CCCCTGGGCTTTGATGACTTCT 54180         CTCAG  A__
           C                     CCCCTGGGCT    GA   CTC
                                ||||||||||    ||   |||
                                GGGGACCCGA    CT   GAG
                                     AACTA  GAA
GAM2271  LOC93259  5'  CCCTTTGGGCTCTTGGCCACT  54181     C_      CA  A_
                                CCC  TGGGCTCT  GG  ACT
                                |||  ||||||||  ||  |||
                                GGG  ACCCGAGA  CC  TGA
                                  AA       A_  GG
GAM2272  FMR2     3'  TCCATGAGGCAATATGCTT    54184        A_   C
                                TCCATGAG  AATA GTTT
                                ||||||||  |||| ||||
                                AGGTACTC  TTAT CGAA
                                     CG    A
GAM2272  MYO10    3'  TCCATGAGAAAGGCTGCCCGC  54185          TAC   TAG
                                TCCATGAGAAA   GTT   CCGC
                                ||||||||||   |||   ||||
                                AGGTACTCTTT   CGA   GGCG
                                     C__   CG_
GAM2272  NKTR     3'  TCCATGAAGGAATGTTGTCCTG 54186       __  ATAC   TA
           C                     TCCATGA  GAA    GTT  GC
                                |||||||  |||    |||  ||
                                AGGTACT  CTT    CAG  CG
                                     TC   ACAA   GA
GAM2272  AD-017   3'  TCCTGAGAAATGCTTGC     54187     A       AC    A
                                TCC TGAGAAAT  GTTT GC
                                |||  ||||||||  |||| ||
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                                AGG ACTCTTTA  CGAA CG
                                  _      __   _
GAM2272 C12orf6   5' CCTGTGGGAAGGGGCTAGCCGC 54188    A_ A  ATAC  T
                                CC  TG GAA    GTT AGCCGC
                                ||  || |||    ||| |||||||
                                GG  AC CTT    CGA TCGGCG
                                 AC  C   CCC_  _
GAM2272 KIAA0326  3' TCCATGAGAACTGTCCAGGGC  54189         ATAC     CC
                                TCCATGAGAA    GTTTAG  GC
                                ||||||||||    ||||||  ||
                                AGGTACTCTT    CAGGTC  CG
                                      GA__     C_
GAM2272 KIAA1813  5' TGAGAAATGCGTTTGTGGC    53815        A    A__
                                TGAGAAAT CGTTT   GC
                                |||||||| |||||   ||
                                ACTCTTTA GCAAA   CG
                                     C    CAC
GAM2272 KIAA1906  3' CATGAGAAATAGTATCCA     54190          C  TTAG
                                CATGAGAAATA GT    CCG
                                |||||||||||  ||    |||
                                GTACTCTTTAT CA    GGT
                                      _  TA__
GAM2272 USP24     3'  TCCTTGAGAAATACACGATCCG 54191     A         TTTAG
          C                      TCC TGAGAAATACG     CCGC
                                ||| ||||||||||     ||||
                                AGG ACTCTTTATGT     GGCG
                                  A         GCTA_
GAM2272 LOC143310 5'  TCCATGAAAGTCAGGCG     54192         AATAC   TA  C
                                TCCATGAGA     GTT  GC G
                                |||||||||     |||  || |
                                AGGTACTTT     CAG  CG C
                                     _____   TC  A
GAM2272 LOC148418 3'  TCCATGAGGAAAACCAC     54193         A  TACGTTT
                                TCCATGAG AA      AGCCGC
                                |||||||| ||      ||||||
                                AGGTACTC TT      TTGGTG
                                     C  _______
GAM2272 LOC162605 5'  TGAGAAATGTTCACC       54194         AC    G
                                TGAGAAAT  GTTTA CC
                                ||||||||  ||||| ||
                                ACTCTTTA  CAAGT GG
                                     __    _
GAM2272 LOC164356 5'  TCCATGAGAAATGGCC      54195           ACGTTTA
                                TCCATGAGAAAT      GCC
                                ||||||||||||      |||
                                AGGTACTCTTTA      CGG
                                      C_______
GAM2272 LOC202134 5'  CCATGAGAAATCAGAGC     54196           A  TTT
                                CCATGAGAAAT CG   AGC
                                |||||||||| ||   |||
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                                GGTACTCTTTA GT   TCG
                                      _ C__
GAM2272 LOC89231 3' TCCATGAGGACTATGTAAAGC 54197       AAA  C  TT
                                TCCATGAG   TA GT  AGC
                                ||||||||   || ||  |||
                                AGGTACTC   AT CA  TCG
                                    CTG  A  TT
GAM2272 LOC92299 3' TCCATGAGTAAGTGCGTCAAGG 54198       AAATA_   T  CC
          GC                    TCCATGAG     CGTT AG  GC
                                ||||||||     |||| ||  ||
                                AGGTACTC     GCAG TC  CG
                                    ATTCAC    T  C_
GAM2273 AXIN1    3' GCCTAGCCTGAGAAAT     53818    A   AT  A
                                GC TAG  CC TGAGAAAT
                                || |||  || ||||||||
                                CG ATC  GG ACTCTTTA
                                 G  __ _
GAM2273 BAPX1    3' TAGCATGGATACCATGAA    54201       A  _
                                TAGCAT GAT CCATGAG
                                |||||| ||| |||||||
                                ATCGTA CTA GGTACTT
                                   C   T
GAM2273 CREBL2   3' ACATAGTGATGCTGAGAAATAC 53821       ATCCA_
                                GCATAG     TGAGAAATAC
                                ||||||     ||||||||||
                                TGTATC     ACTCTTTATG
                                   ACTACG
GAM2273 KCND2    3' AGCATCCCCATGAGAAATAC   54202      AGA
                                AGCAT   TCCATGAGAAATAC
                                |||||   ||||||||||||||
                                TCGTA   GGGTACTCTTTATG
                                  G__
GAM2273 PCDH9    5' CAGCATTGATGTGAGAAAT    53823      A   CCA
                                TAGCAT GAT   TGAGAAAT
                                |||||| |||   ||||||||
                                GTCGTA CTA   ACTCTTTA
                                   A   C__
GAM2273 TNFSF4   3' GCACATCTGTGAGAAATA    53825     AG   CA
                                GCAT  ATC  TGAGAAATA
                                ||||  |||  |||||||||
                                CGTG  TAG  ACTCTTTAT
                                  __   AC
GAM2273 ZNF175   3' ACATAGATACAGAAATA     53826        C  TGA
                                GCATAGAT CA   GAAATA
                                |||||||| ||   ||||||
                                TGTATCTA GT   CTTTAT
                                    T  ____
GAM2273 C20orf82 3' TAGCGTAATGTATGAGAAATAC 53827      A   ATCC
                                TAGC TAG    ATGAGAAATAC
                                |||| |||    ||||||||||
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                                ATCG ATT    TACTCTTTATG
                                  C   ACA_
GAM2273  FLJ12899  3'  AGCATTTCAATGAGAAATAC   54203      AGA  C
                                AGCAT   TC ATGAGAAATAC
                                |||||   || ||||||||||
                                TCGTA   AG TACTCTTTATG
                                  A__  T
GAM2273  FLJ21477  3'  TAGCATTAGGAGAAATA     53829       _  ATCCAT
                                TAGCAT AG     GAGAAATA
                                |||||| ||     ||||||||
                                ATCGTA TC     CTCTTTAT
                                  A _______
GAM2273  GOLGA1    3'  AGCATGATTGAGAAATAC    53830      A   CCA
                                AGCAT GAT   TGAGAAATAC
                                ||||| |||   ||||||||||
                                TCGTA CTA   ACTCTTTATG
                                  _   ____
GAM2273  KIAA0495  3'  AGTATAGCGTGAGAAATAC   53831    C    ATCCA
                                AG ATAG     TGAGAAATAC
                                || ||||     ||||||||||
                                TC TATC     ACTCTTTATG
                                 A   GC____
GAM2273  MEGF11    3'  ACATATGTATGAGAAATA     54204      GATCC
                                GCATA     ATGAGAAATA
                                |||||     ||||||||||
                                TGTAT     TACTCTTTAT
                                  ACA__
GAM2273  PCDHB10   3'  AGCATAGTAGTAGAGAAATA   53833       ATCCAT
                                AGCATAG     GAGAAATA
                                |||||||     ||||||||
                                TCGTATC     CTCTTTAT
                                   ATCAT_
GAM2273  PRO0456   3'  TAGCACAGATACATGTAG     53835         C   _
                                TAGCATAGAT CATG AG
                                |||||||||| |||| ||
                                ATCGTGTCTA GTAC TC
                                      T   A
GAM2273  PRRG1     3'  AGCATCTTAAAATGAGAAATA  54205      AGATCC
                                AGCAT     ATGAGAAATA
                                |||||     ||||||||||
                                TCGTA     TACTCTTTAT
                                  GAATTT
GAM2273  UMP-CMPK  3'  TAGCATAAATCTAGCCACATG  54206          _______
                                TAGCATAGATC     CATG
                                ||||||||||     ||||
                                ATCGTATTTAG     GTAC
                                      ATCGGT
GAM2273  LOC145990 3'  GCATAAAGGAAAGAGAAATAC  53837        TCCAT
                                GCATAGA    GAGAAATAC
                                |||||||    |||||||||
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                                CGTATTT    CTCTTTATG
                                    CCTTT
GAM2273  LOC152573 3'  TAGCATAGATTGAAA      53838         CCA
                                TAGCATAGAT   TGAGA
                                ||||||||||  |||||
                                ATCGTATCTA   ACTTT
                                     ___
GAM2273  LOC153727 5'  TAGCATAGATTCAGCTTCAAGA 53839         C ____
             A                   TAGCATAGAT CA    TGAGAA
                                ||||||||||| ||   ||||||
                                ATCGTATCTA GT    GTTCTT
                                      A  CGAA
GAM2273  LOC90230  3'  TAGCATAAGATGTGAGAA    53841       _  CCA
                                TAGCATA GAT   TGAGAA
                                ||||||| |||   ||||||
                                ATCGTAT CTA   ACTCTT
                                    T  C__
GAM2273  LOC93333  5'  TAGTCACCATGAGAGATAC    54207     AT_      A
                                TAG   CCATGAGA ATAC
                                |||   |||||||| ||||
                                ATC   GGTACTCT TATG
                                  AGT       C
GAM2274  CACNA1C   5'  CAGGACTCTACTGGGAAAATAT 54210      G  G_   TA
             TG                   CAGGA CT  ACT  GAAAATATTG
                                ||||| ||  |||  ||||||||||
                                GTCCT GA  TGA  CTTTTATAAC
                                  _ GA   CC
GAM2274  PRSS11    3'  GGTGCTGACTTGGAGAAAA   54211    A      __
                                GG GCTGACTT  AGAAAA
                                || ||||||||  ||||||
                                CC CGACTGAA  TCTTTT
                                 A       CC
GAM2274  FLJ20793  3'  AGTAGCTGAGAAAAATATTG   54212    G     CTTA
                                AG AGCTGA    GAAAATATTG
                                || ||||||    ||||||||||
                                TC TCGACT    TTTTTATAAC
                                 A     C___
GAM2274  LANCL2    3'  GGTGCTGTTAGAAAATGTTG   54213    A   AC       A
                                GG GCTG  TTAGAAAAT TTG
                                || ||||  ||||||||| |||
                                CC CGAC  AATCTTTTA AAC
                                 A   __        C
GAM2275  CCND2     3'  GAATAGGGTCTGATAGCCCAG  54216       AC_   AAC
                                GAATAG   CTGA   AGCCCAG
                                ||||||   ||||  |||||||
                                CTTATC   GACT   TCGGGTC
                                    CCA   A__
GAM2275  DUOX2     3'  GAATAGACCTGGAGACAG    54217          AA_
                                GAATAGACCTG   ACAG
                                ||||||||||   ||||
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                                CTTATCTGGAC  TGTC
                                     CTC
GAM2275 SCN4A    3' GACCTTGAAACAGTCCAG    54218      _     C
                                GACCT GAAACAG CCAG
                                ||||| ||||||| ||||
                                CTGGA CTTTGTC GGTC
                                   A      A
GAM2275 SLC2A1   3' TGAATAGATTTGAGCAACAG  54219        CC  __
                                TGAATAGA  TGA  AACAG
                                ||||||||  |||  |||||
                                ACTTATCT  ACT  TTGTC
                                    AA   CG
GAM2275 THBD     3' GAATAGAAGAAAACAGC     54220       CCT
                                GAATAGA   GAAACAGC
                                |||||||   ||||||||
                                CTTATCT   TTTTGTCG
                                    TC_
GAM2275 APBA2BP  3' TAAATAGAAAGCAAGCAGCCCA 54221        CCTGAAA
           G                     TGAATAGA      CAGCCCAG
                                ||||||||      ||||||||
                                ATTTATCT      GTCGGGTC
                                    TTCGTTC
GAM2275 APBA2BP  3' TAAATAGAAAGCAAGCAGCCCA 54221        CCTGAAA
           G                     TGAATAGA      CAGCCCAG
                                ||||||||      ||||||||
                                ATTTATCT      GTCGGGTC
                                    TTCGTTC
GAM2275 DKFZp434H2215 3' TGAGGGACCTAGACCCAGCCCA 54222     ATA    _ AA
           G                     TGA   GACCT GA  CAGCCCAG
                                |||   ||||| ||  ||||||||
                                ACT   CTGGA CT  GTCGGGTC
                                  CC_    T  GG
GAM2275 DKFZp434L0850 3' TGAATAGGAGAGGCAGCCCAG  54223       ACCT  AA
                                TGAATAG    GA  CAGCCCAG
                                |||||||    ||  ||||||||
                                ACTTATC    CT  GTCGGGTC
                                    CT__  CC
GAM2275 DRIL2    3' TGAATGGAGCCTGGACAG    54224      A  _   AA
                                TGAAT GA CCTG  ACAG
                                ||||| || ||||  ||||
                                ACTTA CT GGAC  TGTC
                                   C  C    C_
GAM2275 E2IG4    3' TGAAGACTAAGGAAACAGCCCA 54225     AT    CT__
           G                     TGA  AGAC    GAAACAGCCCAG
                                |||  ||||   ||||||||||||
                                ACT  TCTG   CTTTGTCGGGTC
                                  __   ATTC
GAM2275 E2IG5    3' TGGTAAGAAAAACAGCCCAG  54226    AAT   CCT
                                TG   AGA   GAAACAGCCCAG
                                ||   |||   ||||||||||||
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                                AC   TCT   TTTTGTCGGGTC
                                 CAT   ___
GAM2275  FLJ10101  3'  GATCCAGCTGGGGCAGCCCAG  54227    A_   AC   AAA
                                GA  TAG  CTG   CAGCCCAG
                                ||  |||  |||   ||||||||
                                CT  GTC  GAC   GTCGGGTC
                                 AG   __   CCC
GAM2275  FLJ10849  3'  TGAACAGACCCACAAGCTCAG  54228          AAAC   C
                                TGAATAGACCTG    AGC CAG
                                ||||||||||||    ||| |||
                                ACTTGTCTGGGT    TCG GTC
                                       GT__   A
GAM2275  FLJ12076  3'  TGAAGGGACTGAGCAGCCCAG  54229     TA   C   AA
                                TGAA  GAC TGA  CAGCCCAG
                                ||||  ||| |||  ||||||||
                                ACTT  CTG ACT  GTCGGGTC
                                  CC   _   C_
GAM2275  FLJ12998  3'  TGAGACCCGAGCAGCTCA    54230   T      AA    C
                                A AGACCTGA  CAGC CA
                                | ||||||||  |||| ||
                                A TCTGGGCT  GTCG GT
                                 C       C_    A
GAM2275  FLJ20128  5'  TGATAGACCTGGAACAG     54231     A       A
                                TGA TAGACCTG AACAG
                                ||| |||||||| |||||
                                ACT ATCTGGAC TTGTC
                                  _       C
GAM2275  FUT10     3'  TGGATAAACTTGAAACAGC    54232    A     C
                                TG ATAGAC TGAAACAGC
                                || |||||| |||||||||
                                AC TATTTG ACTTTGTCG
                                 C     A
GAM2275  ITGB5     3'  GAAGGGAGAGACAGCCCAG    54233     TA  CCT  A
                                GAA  GA   GA ACAGCCCAG
                                |||  ||   || |||||||||
                                CTT  CT   CT TGTCGGGTC
                                  CC  ___  C
GAM2275  KIAA0258  3'  TGGACAGACCTGATGCC     54234    A        AACA
                                TG ATAGACCTGA    GCC
                                || ||||||||||    |||
                                AC TGTCTGGACT    CGG
                                 C         A___
GAM2275  KIAA0469  3'  AGACATGACAGCCCAG      54235      C   AA
                                AGAC TGA  CAGCCCAG
                                |||| |||  ||||||||
                                TCTG ACT  GTCGGGTC
                                  T   __
GAM2275  KIAA1157  3'  TGAAGAGGCCCAGCCCA     54236      T  A  TGAAA
                                TGAA AG CC    CAGCCCA
                                |||| || ||    |||||||
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                                ACTT TC GG    GTCGGGT
                                  C  C _____
GAM2275 KIAA1946 3' TGAATAGGCCAGAAAAAG   54237       A  T   C
                                TGAATAG CC GAAA AG
                                ||||||| || |||| ||
                                ACTTATC GG CTTT TC
                                    C  T   T
GAM2275 LYPLA3   3' ACAGGACCACAGCCCAG    54238     _  TGAA
                                ATAG ACC   ACAGCCCAG
                                |||| |||   |||||||||
                                TGTC TGG   TGTCGGGTC
                                  C  ____
GAM2275 MGC3048  3' TGAAGACTGAGGCAGCCCAG  54239    AT   C   AA
                                TGA  AGAC TGA  CAGCCCAG
                                |||  |||| |||  ||||||||
                                ACT  TCTG ACT  GTCGGGTC
                                  __   _  CC
GAM2275 MGC35558 3' TGAGGGACTGAGGCAGCCCAG 54240    ATA   C   AA
                                TGA   GAC TGA  CAGCCCAG
                                |||   ||| |||  ||||||||
                                ACT   CTG ACT  GTCGGGTC
                                  CC_  _  CC
GAM2275 MRPL45   3' TGAAAAGACCTGAGCAG    54241     T      AA
                                TGAA AGACCTGA  CAG
                                |||| ||||||||  |||
                                ACTT TCTGGACT  GTC
                                  T      C_
GAM2275 MTHFD1   3' TGAATAGACACTGGCC     54242         _  AAACA
                                TGAATAGAC CTG    GCC
                                ||||||||| |||    |||
                                ACTTATCTG GAC    CGG
                                     T  _____
GAM2275 TIAF1    3' TGCGTAGGCTTGCTCAACCCAG 54243    AA   ACC  AAA
                                TG  TAG   TG   CAGCCCAG
                                ||  |||   ||   ||||||||
                                AC  ATC   AC   GTTGGGTC
                                 GC   CGA  GA_
GAM2275 VPS33B   5' TGAGAAGGCCGGCCGCAGCCCA 54244    AT  A  TGAAA
            G                    TGA  AG CC    CAGCCCAG
                                |||  || ||    ||||||||
                                ACT  TC GG    GTCGGGTC
                                  CT  C  CCGGC
GAM2275 LOC124976 3' GAAAGCTTTGGGGCAGCCCAG  54245    T  ACC  AAA
                                GAA AG   TG   CAGCCCAG
                                ||| ||   ||   ||||||||
                                CTT TC   AC   GTCGGGTC
                                  _  GAA  CCC
GAM2275 LOC149770 3' TAGATAGGAAAGGCAGCCCAG  54246     CCT   __
                                TAGA   GAAA  CAGCCCAG
                                ||||   ||||  ||||||||
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                                ATCT  CTTT  GTCGGGTC
                                  ATC   CC
GAM2275  LOC158263 3'  TGAATAGACTGTCCTTCCCAG  54247        C  AAACAG
                                TGAATAGAC TG     CCCAG
                                ||||||||| ||     |||||
                                ACTTATCTG AC     GGGTC
                                     _ AGGAA_
GAM2275  LOC159053 3'  GATCCTGGAAACAGTCCAG   54248   _   _    C
                                GA CCTG AAACAG CCAG
                                || |||| |||||| ||||
                                CT GGAC TTTGTC GGTC
                                 A   C     A
GAM2275  LOC203350 3'  TGAGTAGAGAACAGCCCAG   54249    A   CCT   A
                                TGA TAGA   GAA CAGCCCAG
                                ||| ||||   ||| ||||||||
                                ACT ATCT   CTT GTCGGGTC
                                  C   ___  _
GAM2275  LOC255330 5'  TAAATAGACTTGGAATGATCCC 54250        CT_  ACAG
                                TGAATAGAC   GAA   CCC
                                |||||||||   |||   |||
                                ATTTATCTG   CTT   GGG
                                     AAC   ACTA
GAM2275  LOC256789 3'  GAATAGGTTCCAGCAGCCCAG  54251      A__  TGAAA
                                GAATAG   CC    CAGCCCAG
                                ||||||   ||    ||||||||
                                CTTATC   GG    GTCGGGTC
                                   CAA  TC___
GAM2275  LOC256948 3'  TGAATAGACTTAAGGCC     54252        C   AACA
                                TGAATAGAC TGA    GCC
                                ||||||||| |||    |||
                                ACTTATCTG ATT    CGG
                                     A   C___
GAM2275  LOC54466  3'  CAGCCCACAGCCCAG      54253     A   GAA
                                TAG CCT   ACAGCCCAG
                                ||| |||   |||||||||
                                GTC GGG   TGTCGGGTC
                                  _  ___
GAM2275  LOC90148  3'  TGGGAAGACCTGAACCACCAG  54254    AAT      A  GC
                                TG   AGACCTGAA CA  CCAG
                                ||   ||||||||| ||  ||||
                                AC   TCTGGACTT GT  GGTC
                                 CCT       G  __
GAM2276  GRM1     3'  AATTGTACATATACGCAT    54257        TATTT
                                GATTGTAC    GTATACGCAT
                                ||||||||    ||||||||||
                                TTAACATG    TATATGCGTA
                                      _____
GAM2276  ELF2     3'  GATTGTTTTTGTATATGCAT   54258       ACTA      C
                                GATTGT    TTTGTATA GCAT
                                ||||||    |||||||| ||||
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                                CTAACA    AAACATAT CGTA
                                   A___       A
GAM2276  FACTP140  3'  ATTGTACCATGTGTGCAT    54259         T   ATAC
                                ATTGTACTAT TGT    GCAT
                                |||||||||| |||    ||||
                                TAACATGGTA ACA    CGTA
                                     C  _____
GAM2276  LOC151273 3'  GATTGTTTTCGTATATGCAT   54260       ACTA       C
                                GATTGT    TTTGTATA GCAT
                                ||||||    |||||||| ||||
                                CTAACA    AAGCATAT CGTA
                                   A___       A
GAM2277  FUS2      3'  CAGGAAACATGCCCAGGTTAAA 54263         _  G_
              GC                    TAGGAAACA GT  AGGTTAAAGC
                                |||||||||| ||  ||||||||||
                                GTCCTTTGT CG  TCCAATTTCG
                                     A  GG
GAM2277  GRLF1     3'  GGAGACAGTGAGCCAGCC     54264     A       GTTAA
                                GGA ACAGTGAG     AGCC
                                ||| ||||||||     ||||
                                CCT TGTCACTC     TCGG
                                  C       GG___
GAM2277  HTR1D     3'  GGGGGGTGGGCGTCTAAAGCCG 54265     AAACA   A   ___
                                GG     GTG GGT   TAAAGCCG
                                ||     ||| |||   ||||||||
                                CC     CAC CCG   ATTTCGGC
                                 CCC__   _   CAG
GAM2277  KPNA1     3'  TAGGAAACAATGAGGTTA     54266
                                TAGGAAACAGTGAGGTTA
                                ||||||||||||||||||
                                ATCCTTTGTTACTCCAAT

GAM2277  MYOC      3'  GGAAAGCAGTCAAAGC       54267      AC   GA
                                GGAA  AGT  GGTTAAAGC
                                ||||  |||  |||||||||
                                CCTT  TCG  TCAGTTTCG
                                   __  __
GAM2277  NID       3'  GGGAACAGTGAGGGAAAAG    54268     A        TT
                                GG AACAGTGAGG  AAAG
                                || ||||||||||  ||||
                                CC TTGTCACTCC  TTTC
                                  C         CT
GAM2277  RUNX3     3'  GGAGACAGTGAGGTCCTTCCG  54269      A         AAAG
                                GGA ACAGTGAGGTT    CCG
                                ||| ||||||||||    |||
                                CCT TGTCACTCCAG    GGC
                                  C         GAA_
GAM2277  ABCA9     3'  TAGGAAACATGGGATTTGGTT  54270         GT_  ___
                                TAGGAAACA   GA   GGTT
                                |||||||||   ||   ||||
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                                ATCCTTTGT  CT  CCAA
                                     ACC  AAA
GAM2277 ANKRD6   3' GGGAACAGTGGGGCCTAAG   54271   A     A  TA
                                GG AACAGTG GGT  AAG
                                || ||||||| |||  |||
                                CC TTGTCAC CCG  TTC
                                 C     C  GA
GAM2277 DKFZP586M1120 3' GGAAACAGTGGAGTGAGC    54272         AG  TAA
                                GGAAACAGTG  GT   AGC
                                ||||||||||  ||   |||
                                CCTTTGTCAC  CA   TCG
                                      CT  C__
GAM2277 KIAA0982  3' GGCAAACAGTGAAACTAAGGGC 54273    _      GG   A_
                                GG AAACAGTGA  TTAA  GC
                                || |||||||||  ||||  ||
                                CC TTTGTCACT  GATT  CG
                                 G       TT   CC
GAM2277 KIAA1655  3' TAGAAAACGGAATGAGGCT   54274        __
                                TAGGAAAC  AGTGAGGTT
                                ||||||||  |||||||||
                                ATCTTTTG  TTACTCCGA
                                     CC
GAM2277 KIAA1718  3' TAGGAAAAATATATTAAAGC   54275       C   AG
                                TAGGAAA AGTG  GTTAAAGC
                                ||||||| ||||  ||||||||
                                ATCCTTT TTAT  TAATTTCG
                                   _   A_
GAM2277 SART3    3' TAGGAAACATGAAACAAGGGC  54276        G   GG TAAA
                                TAGGAAACA TGA  T   GC
                                ||||||||| |||  |   ||
                                ATCCTTTGT ACT  G   CG
                                     _  TT TTCC
GAM2277 SMAP1    3' GGAAATATGAGCAAAGC    54277      CA    GT
                                GGAAA  GTGAG  TAAAGC
                                |||||  |||||  ||||||
                                CCTTT  TACTC  GTTTCG
                                  A_   __
GAM2277 LOC121642 5'  AGGAAACAGAAGATGTTAAAGC 54278        T_  G
            CG                    AGGAAACAG  GA GTTAAAGCCG
                                |||||||||  || ||||||||||
                                TCCTTTGTC  CT CAATTTCGGC
                                     TT  A
GAM2277 LOC151878 3'  GGAAACAGATGAGAAGCCG   54279        _    TTAA
                                GGAAACAG TGAGG   AGCCG
                                |||||||| |||||   |||||
                                CCTTTGTC ACTCT   TCGGC
                                     T   ____
GAM2277 LOC153338 5'  TAGTAAACAGTAAAAGTT    54280     G       _
                                TAG AAACAGTGAG GTT
                                ||| |||||||||| |||
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                                ATC TTTGTCATTT CAA
                                  A         T
GAM2277  LOC254428 3'  GGAGAATGAGGTGAGGTTAGAG 54281     AACA___        A
             C                     GGA       GTGAGGTTA AGC
                                   |||       ||||||||| |||
                                   CCT       CACTCCAAT TCG
                                     CTTACTC         C
GAM2277  LOC90120  5'  AGGAAGCGGATGAAGC      54282      AAC    A   TA
                                   AGGA   AGTG GGT  AAGC
                                   ||||   |||| |||  ||||
                                   TCCT   TCGC CTA  TTCG
                                     ___    _  C_
GAM2277  LOC90784  5'  TAGGAAACGCTGGCTGGC    54283         A  GA    AAA
                                   TAGGAAAC GT  GGTT   GC
                                   |||||||| ||  ||||   ||
                                   ATCCTTTG CG  CCGA   CG
                                        _ A_    C__
GAM2278  DIAPH2    3'  AAGGGAATTATCATGGGTAATC 54286         ACA    A
                                   AGGGGAAT   CATG GTAATC
                                   ||||||||   |||| ||||||
                                   TTCCCTTA   GTAC CATTAG
                                        ATA    C
GAM2278  EMP1      3'  AAGGGAATACATGGT       54287           CA  A
                                   AGGGGAATACA  TG GT
                                   ||||||||||  || ||
                                   TTCCCTTATGT  AC CA
                                          __ _
GAM2278  MEOX2     3'  TAAGGGTAATATATACAGAGT  54288       G    C__   T
                                   TAAGGG AATA   ACA GAGT
                                   |||||| ||||   ||| ||||
                                   ATTCCC TTAT   TGT CTCA
                                      A   ATA   _
GAM2278  PACE4     5'  TAAGGGGAAAGCATTCAGT    54289         TACA   G_
                                   TAAGGGGAA    CAT  AGT
                                   |||||||||    |||  |||
                                   ATTCCCCTT    GTA  TCA
                                        TC__   AG
GAM2278  PSMD9     3'  AGGGGAATACGTATGGC      54290          AC   A
                                   AGGGGAATAC  ATG GT
                                   ||||||||||  ||| ||
                                   TCCCCTTATG  TAC CG
                                         CA   _
GAM2278  SIP       3'  GGGGAATAGGAGTAAT       54291         CACAT
                                   GGGGAATA    GAGTAAT
                                   ||||||||    |||||||
                                   CCCCTTAT    CTCATTA
                                        C____
GAM2278  CRMP5     3'  CAAGGGGAGTGCTGGGAGTGAT 54292         ATACACAT    A
             C                     TAAGGGGA       GAGT ATC
                                   ||||||||       |||| |||
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                                GTTCCCCT       CTCA TAG
                                     CACGACC_    C
GAM2278  MAFB     3'  CAAGGGGAGTATGATCCATGA  54293        A  CA___
                                TAAGGGGA TA     CATGA
                                |||||||| ||     |||||
                                GTTCCCCT AT     GTACT
                                     C  ACTAG
GAM2278  ShrmL    3'  AGGGGGACACACACTGAT     54294       A       GA
                                AGGGG ATACACAT  GT
                                ||||| ||||||||  ||
                                TCCCC TGTGTGTG  TA
                                   C       AC
GAM2278  ZNF262   3'  TAAGGGGAAAACCTAAAAGT   54295        T  ACAT
                                TAAGGGGAA AC    GAGT
                                ||||||||| ||    ||||
                                ATTCCCCTT TG    TTCA
                                      T  GATT
GAM2278  LOC145828 3'  TAAGAGGAATGTTTGGTAATC  54296          ACACA  A
                                TAAGGGGAAT     TG GTAATC
                                ||||||||||     || ||||||
                                ATTCTCCTTA     AC CATTAG
                                     CAA__  _
GAM2278  LOC150384 3'  AGGGGAATGCAATGAGC     54297        A  C
                                AGGGGAAT CA ATGAGT
                                |||||||| || ||||||
                                TCCCCTTA GT TACTCG
                                     C  _
GAM2278  LOC90183  3'  CAAGGGGAGTATGATCCATGA  54293        A  CA___
                                TAAGGGGA TA     CATGA
                                |||||||| ||     |||||
                                GTTCCCCT AT     GTACT
                                     C  ACTAG
GAM2278  LOC91585  3'  AAGGGGAATACAGTTAAT     54298          CATGAG
                                AAGGGGAATACA      TAAT
                                ||||||||||||     ||||
                                TTCCCCTTATGT      ATTA
                                      CA____
GAM2279  CLECSF12  3'  TGAGTCGAGATTGTGCCACTG  54301        C  CCATC   T
                                TGAGTCGA GA     GCC ACTG
                                |||||||| ||     ||| ||||
                                ACTCAGCT CT     CGG TGAC
                                     _  AACA_   _
GAM2279  FCAR     3'  TGAGTCGAGATCGTGCCACTG  54302        C  CCA   C_
                                TGAGTCGA GA   TCG  CTACTG
                                |||||||| ||   |||  ||||||
                                ACTCAGCT CT   AGC  GGTGAC
                                     _  ____   AC
GAM2279  FCAR     3'  TGAGTCGAGATCGTGCCACTG  54302        C  CCA   C_
                                TGAGTCGA GA   TCG  CTACTG
                                |||||||| ||   |||  ||||||
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                                ACTCAGCT CT   AGC  GGTGAC
                                    _ ____   AC
GAM2279  INMT     3'  TGAGTCGAGATCGCGCCACTG  54303       C  CCA   _
                                TGAGTCGA GA   TCGC CTACTG
                                |||||||| ||   |||| ||||||
                                ACTCAGCT CT   AGCG GGTGAC
                                    _ ____   C
GAM2279  H-plk    5'  TGAGTCGAGATCATGCCACTG  54304       C  C   C   T
                                TGAGTCGA GA CAT GCC ACTG
                                |||||||| || ||| ||| ||||
                                ACTCAGCT CT GTA CGG TGAC
                                    _ A   _  _
GAM2279  MGC2474  3'  TGAGTCGAGATCGCACCA    54305       C  CCA   _
                                TGAGTCGA GA   TCGC CTA
                                |||||||| ||   |||| |||
                                ACTCAGCT CT   AGCG GGT
                                    _ ____   T
GAM2279  MYH10    3'  TGAGTGACGACCACGGCGCT   54306      C       C  _
                                TGAGT GACGACCAT GC CT
                                ||||| ||||||||| || ||
                                ACTCA CTGCTGGTG CG GA
                                   _       C  C
GAM2279  LOC152343 3'  TGAGTCGAGATCGCACCACTG  54307       C  CCA   _
                                TGAGTCGA GA   TCGC CTACTG
                                |||||||| ||   |||| ||||||
                                ACTCAGCT CT   AGCG GGTGAC
                                    _ ____   T
GAM2279  LOC197083 5'  TGAGTCGACGATCACTTGACT  54308         CCA   CT_
                                TGAGTCGACGA   TCGC   ACT
                                ||||||||||   ||||   |||
                                ACTCAGCTGCT   AGTG   TGA
                                      ____   AAC
GAM2280  ADCY6    3'  GGTAGGCATGGCAAGCTGCCA  54311      A       ATC_
                                GGTAG TATGGCAA    CCA
                                ||||| ||||||||    |||
                                CCATC GTACCGTT    GGT
                                   C       CGAC
GAM2280  ADCY6    3'  GGTAGGCATGGCAAGCTGCCA  54311      A       ATC_
                                GGTAG TATGGCAA    CCA
                                ||||| ||||||||    |||
                                CCATC GTACCGTT    GGT
                                   C       CGAC
GAM2280  AQP3     3'  GGTAGATAGGGAGCTCCTTAGC 54312        T  CAAA   CAA_
            C                    GGTAGATA GG    TCC    CC
                                ||||||||  ||    |||    ||
                                CCATCTAT CC    AGG    GG
                                     C  TCG_   AATC
GAM2280  BACH2    3'  GGTAGATATGTGTGAAAACTGT 54313         GC___    C__
            CC                    GGTAGATATG    AAAT   CC
                                ||||||||||    ||||   ||
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                                CCATCTATAC    TTTG  GG
                                     ACACT   ACA
GAM2280 HAS1    3' GGAGACCCAGAAGTCCCAGTCC 54314   T   A  C A   AC
                                GG AGAT TGG AA TCCCA  CC
                                || |||| ||| || |||||  ||
                                CC TCTG GTC TT AGGGT  GG
                                 _   G  _ C    CA
GAM2280 LDLR    3' GGAAGAAACCAAAATCCCAACC 54315   T  T GGC
           C                     GG AGA AT   AAATCCCAACCC
                                || ||| ||  ||||||||||||
                                CC TCT TG   TTTAGGGTTGGG
                                 T  T GT_
GAM2280 ARHGEF9  3' GGAGAGCAAATCCTGGCC   54316   T  TATG     CAA
                                GG AGA   GCAAATCC   CC
                                || |||   ||||||||   ||
                                CC TCT   CGTTTAGG   GG
                                 _  _____      ACC
GAM2280 CRA     3' TATAACGTAAATCCCAGTCC   54317      __      AC
                                TATGGC  AAATCCCA  CC
                                ||||||  ||||||||  ||
                                ATATTG  TTTAGGGT  GG
                                   CA      CA
GAM2280 GMEB2   3' GGCAGAAAAGGTCCCAACC   54318      TAT  CAAA
                                GGTAGA   GG   TCCCAACC
                                ||||||   ||   ||||||||
                                CCGTCT   CC   AGGGTTGG
                                   TTT  _____
GAM2280 KIAA0420 3' GTAGATATAAGTTTCCTGGCCC 54319        CAAA  CAA
                                GTAGATATGG   TCC  CCC
                                ||||||||||   |||  |||
                                CATCTATATT   AGG  GGG
                                     CAA_  ACC
GAM2280 KIAA0980 3' GGTGAACAAAGAATCCCAATCC 54320    AG  T CA     _
                                GGT  ATA GG  AATCCCAA CC
                                |||  ||| ||  |||||||| ||
                                CCA  TGT TC  TTAGGGTT GG
                                  CT  T __      A
GAM2280 RAB3-GAP150 3' GGCAAAAAGCAAATCTTAAC  54321      TAT     CC
                                GGTAGA  GGCAAATC  AAC
                                ||||||  ||||||||  |||
                                CCGTTT  TCGTTTAG  TTG
                                   T__      AA
GAM2280 SCYA22  3' GATAGACCCAAATCCCA    54322       ATGG
                                GGTAGAT   CAAATCCCA
                                |||||||   |||||||||
                                CTATCTG   GTTTAGGGT
                                   G___
GAM2280 TCEB1   3' GTAGCAAACAAATTTCAAC   54323     ATAT     CC
                                GTAG   GGCAAAT  CAAC
                                ||||   |||||||  ||||
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                                CATC   TTGTTTA  GTTG
                                  GT__     AA
GAM2280  TP53INP1  3'  GGTGTGGTAATCCCAACC   54324    AGATA  CA
                                GGT    TGG  AATCCCAACC
                                |||    |||  ||||||||||
                                CCA    ACC  TTAGGGTTGG
                                  C____  A_
GAM2280  TP53INP1  3'  GGTGTGGTAATCCCAACC   54324    AGATA  CA
                                GGT    TGG  AATCCCAACC
                                |||    |||  ||||||||||
                                CCA    ACC  TTAGGGTTGG
                                  C____  A_
GAM2280  LOC255520 3'  AGTAGACAAAAATCCCAA   54325       TGGC
                                GGTAGATA   AAATCCCAA
                                ||||||||   |||||||||
                                TCATCTGT   TTTAGGGTT
                                     T___
GAM2280  LOC257354 3'  GTAGATATAAGTTTCCTGGCCC 54319         CAAA  CAA
                                GTAGATATGG   TCC  CCC
                                ||||||||||   |||  |||
                                CATCTATATT   AGG  GGG
                                     CAA_  ACC
GAM2280  LOC91263  5'  GGTGGTGGGAATCCCAAC   54326    AGATA  CA
                                GGT    TGG  AATCCCAAC
                                |||    |||  |||||||||
                                CCA    ACC  TTAGGGTTG
                                  CC___  C_
GAM2281  C20orf150 3'  TAGCTGGAGCGCTGGACCA   54329    A      CAATC
                                TAG TGGAGCGC    GCCG
                                ||| ||||||||    ||||
                                ATC ACCTCGCG    TGGT
                                  G      ACC__
GAM2281  KIAA0620  3'  AGATGGAGCAGGCGTCGAT   54330        CCAAT  C
                                AGATGGAGCG    CG CGAT
                                ||||||||||    || ||||
                                TCTACCTCGT    GC GCTA
                                     CC___  A
GAM2281  LOC201514 5'  AGATGGAGCCACTCGCCG   54331       GC   A
                                AGATGGA  GCCA TCGCCG
                                |||||||  |||| ||||||
                                TCTACCT  CGGT AGCGGC
                                    __   G
GAM2282  ABCC5    3'  TCTGTGCAGTGGCCAGCCATAG 54334    CA  T      GC_
           GAA                    TC  TGC GTGGCCGGT  AGGAA
                                ||  ||| |||||||||  |||||
                                AG  ACG CACCGGTCG  TCCTT
                                 AC  T       GTA
GAM2282  BECN1    3'  CATATTGTTAAGTGCAGGAA  54335     C  GGCC
                                CATG TGT   GGTGCAGGAA
                                |||| |||   ||||||||||
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                                GTAT ACA    TCACGTCCTT
                                  A  AT__
GAM2282  DBN1     5'  TGCTGTGGCCGGGCCGG     54336          T  A
                                TGCTGTGGCCGG GC GG
                                |||||||||||| || ||
                                ACGACACCGGCC CG CC
                                       _  G
GAM2282  LETM1    3'  CCATGCTGCCGAGTGCGGG    54337       GTG   _    A
                                CCATGCT   GCCG GTGC GG
                                |||||||   |||| |||| ||
                                GGTACGA   CGGC CACG CC
                                    ___   T   C
GAM2282  MYO6     5'  TCCACTGTCACCGGTGCGGGA  54338     AT    G      A
                                TCC  GCTGT GCCGGTGC GGA
                                |||  ||||| |||||||| |||
                                AGG  TGACA TGGCCACG CCT
                                  __    G       C
GAM2282  RAMP3    3'  GCTGGGGCTGGTGCAGGA    54339     T   C
                                GCTG GGC GGTGCAGGA
                                |||| ||| |||||||||
                                CGAC CCG CCACGTCCT
                                  C   A
GAM2282  SHANK2   3'  TCCCTGAGTTTGCTGGTGCAGG 54340     A  CTGTG  C
                                TCC TG     GC GGTGCAGG
                                ||| ||     || ||||||||
                                AGG AC     CG CCACGTCC
                                  G  TCAAA  A
GAM2282  ST5      3'  TCCATGCTCTGGCAGGACAGGA 54341        G    C  T
            A                    TCCATGCT TGGC GG GCAGGAA
                                ||||||||| |||| || |||||||
                                AGGTACGA ACCG CC TGTCCTT
                                     G    T  _
GAM2282  ST5      3'  TCCATGCTCTGGCAGGACAGGA 54341        G    C  T
            A                    TCCATGCT TGGC GG GCAGGAA
                                ||||||||| |||| || |||||||
                                AGGTACGA ACCG CC TGTCCTT
                                     G    T  _
GAM2282  TLL1     3'  CTGTTTGATCATGTGCAGGAA  54342      __ GC  _
                                CTGT  G  CG GTGCAGGAA
                                ||||  |  || |||||||||
                                GACA  C  GT CACGTCCTT
                                  AA TA  A
GAM2282  DEPP     3'  CCTGTGTGGAAGTGGTGTAGG  54343    A  C    CC__   C
                                CC TG TGTGG    GGTG AGG
                                || || |||||    |||| |||
                                GG AC ACACC    CCAC TCC
                                 _  _     TTCA    A
GAM2282  DKFZp761D0614 3'  TGCTGGTTGGGTGCAGGAA    54344       TGGCC
                                TGCTG     GGTGCAGGAA
                                |||||     ||||||||||
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                                ACGAC    CCACGTCCTT
                                  CAAC_
GAM2282  FLJ13456  3'  ATACTGTGGTGCTTGGGGA   54345       GGCC    A___
                                ATGCTGT   GGTGC   GGA
                                |||||||   |||||   |||
                                TATGACA   CCACG   CCT
                                    _____   AACC
GAM2282  GTPBP1   3'  TCCGGCTGTGGCCTGAGCGGGA 54346     AT       GGT  A
                                TCC  GCTGTGGCC   GC GGA
                                |||  |||||||||  || |||
                                AGG  CGACACCGG   CG CCT
                                  C_       ACT  C
GAM2282  HA-1     3'  GCTATGCCGTGGTGCAGG    54347       G  __
                                GCTGTG CC  GGTGCAGG
                                ||||||  ||  ||||||||
                                CGATAC GG  CCACGTCC
                                   _ CA
GAM2282  KIAA0153  3'  ATGCCCAGGGCCGGTGTGGG   54348      GT_      CA
                                ATGCT   GGCCGGTG  GG
                                |||||   ||||||||  ||
                                TACGG   CCGGCCAC  CC
                                   GTC       AC
GAM2282  KIAA0420  3'  CCATGCTGGCCAAGTGCAGG   54349       GT    _
                                CCATGCT  GGCCG GTGCAGG
                                |||||||  ||||| |||||||
                                GGTACGA  CCGGT CACGTCC
                                    __    T
GAM2282  KIAA1701  3'  TCCTGCTGTGGGAATCTAGGAA 54350     A      CC   GC
                                TCC TGCTGTGG  GGT  AGGAA
                                ||| ||||||||  |||  |||||
                                AGG ACGACACC  TTA  TCCTT
                                  _      C_   GA
GAM2282  MGC22014  3'  TCTGTGCTGCGGTCTCTGCTCA 54351    CA      CCG__  G
            GG                    TC  TGCTGTGG    GT CAGG
                                ||  ||||||||    || ||||
                                AG  ACGACGCC    CG GTCC
                                 AC       AGAGA  A
GAM2282  MGC2541   3'  TGCTGTGGTTGTAGGAA     54352        CCG  GC
                                TGCTGTGG   GT  AGGAA
                                |||||||   ||  |||||
                                ACGACACC   CA  TCCTT
                                    AA_  __
GAM2282  MGC4832   5'  TCCATGCTGAGCACAGCGGGGA 54353         T  _    CA
                                TCCATGCTG GGC CGGTG  GGA
                                |||||||||| ||| |||||  |||
                                AGGTACGAC TCG GTCGC  CCT
                                    _  T    C_
GAM2282  PROL3    3'  CATATTTGGGGTGCAGGA    54354     CTG   CC
                                CATG   TGG  GGTGCAGGA
                                ||||   |||  |||||||||
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                                GTAT  ACC  CCACGTCCT
                                  AA_  __
GAM2282  SKIP    3'  TCCATGCCGTGAGTAGGGA   54355        GCC   CA
                                TCCATGCTGTG  GGTG  GGA
                                ||||||||||  ||||  |||
                                AGGTACGGCAC  TCAT  CCT
                                      ___   C_
GAM2282  SKIP    3'  TCCATGCCGTGAGTAGGGA   54355        GCC   CA
                                TCCATGCTGTG  GGTG  GGA
                                ||||||||||  ||||  |||
                                AGGTACGGCAC  TCAT  CCT
                                      ___   C_
GAM2282  SRPK1   3'  TCTCTGCTGTGGTGCTGGGCAG 54356   CA     CC__  T
           G                     TC  TGCTGTGG   GG GCAGG
                                ||  ||||||||   || |||||
                                AG  ACGACACC   CC CGTCC
                                 AG      ACGA  _
GAM2282  TIGD5   3'  TCCAGTGCATGTGACTGGTGCA 54357    _  _    C
           GG                    TCCA TGC TGTGGC GGTGCAGG
                                |||| ||| |||||| ||||||||
                                AGGT ACG ACACTG CCACGTCC
                                  C  T    A
GAM2282  TReP-132  5'  CATGCTGCTGGACAGGTGGGAA 54358      _  _ C   CA
                                CATGCTG TGG C GGTG  GGAA
                                ||||||| ||| | ||||  ||||
                                GTACGAC ACC G CCAC  CCTT
                                    G  T T   __
GAM2282  TReP-132  5'  CATGCTGCTGGACAGGTGGGAA 54358      _  _ C   CA
                                CATGCTG TGG C GGTG  GGAA
                                ||||||| ||| | ||||  ||||
                                GTACGAC ACC G CCAC  CCTT
                                    G  T T   __
GAM2282  TReP-132  5'  CATGCTGCTGGACAGGTGGGAA 54358      _  _ C   CA
                                CATGCTG TGG C GGTG  GGAA
                                ||||||| ||| | ||||  ||||
                                GTACGAC ACC G CCAC  CCTT
                                    G  T T   __
GAM2282  LOC125268 3'  CCTGTGCTGCTGGGTGCAGG  54359   A_    GGCC
                                CC  TGCTGT   GGTGCAGG
                                ||  ||||||   ||||||||
                                GG  ACGACG   CCACGTCC
                                 AC     AC__
GAM2282  LOC146445 3'  TCCTGCTGTGGCCGAGG    54360    A       GTGC
                                TCC TGCTGTGGCCG   AGG
                                ||| ||||||||||   |||
                                AGG ACGACACCGGC   TCC
                                  _       ____
GAM2282  LOC147077 3'  TCCCTGCTGTGGTCGCAGG   54361    A      CCGG
                                TCC TGCTGTGG   TGCAGG
                                ||| ||||||||   ||||||
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                                AGG ACGACACC    GCGTCC
                                  G       A___
GAM2282  LOC148760 3'  TCCTTGTCCTGTGGTGCAGG   54362     A __    GGCC
                                TCC TG  CTGT    GGTGCAGG
                                ||| ||  ||||    ||||||||
                                AGG AC  GACA    CCACGTCC
                                  A  AG   ____
GAM2282  LOC149830 3'  TGTCTGCTCCGTGCGGGA    54363    _   GG   G   A
                                TG CTGT  CCG TGC GGA
                                || ||||  ||| ||| |||
                                AC GACG  GGC ACG CCT
                                 A    A_  _   C
GAM2282  LOC149838 5'  TCCAAGGCCCGGTGCAGGA    54364      TGCTGT   _
                                TCCA     GGCC GGTGCAGGA
                                ||||     |||| |||||||||
                                AGGT     CCGG CCACGTCCT
                                  T_____    G
GAM2282  LOC151623 5'  CCCAGGCTGGTGCAGG      54365      TGCTGT   C
                                TCCA     GGC GGTGCAGG
                                ||||     ||| ||||||||
                                GGGT     CCG CCACGTCC
                                  _______  A
GAM2282  LOC153020 3'  CTGTCAGCTGCAGGAA      54366      _   CGG
                                CTGT GGC   TGCAGGAA
                                |||| |||   ||||||||
                                GACA TCG   ACGTCCTT
                                  G   ___
GAM2282  LOC158856 5'  TCCATGCTGTGCCTCTACTAGG 54367          G  GG   _
            AA                    TCCATGCTGTG CC  TGC AGGAA
                                ||||||||||| ||  ||| |||||
                                AGGTACGACAC GG  ATG TCCTT
                                      _  AG   A
GAM2282  LOC203504 5'  TCCATGCTGTGCCTCTACTAGG 54367          G  GG   _
            AA                    TCCATGCTGTG CC  TGC AGGAA
                                ||||||||||| ||  ||| |||||
                                AGGTACGACAC GG  ATG TCCTT
                                      _  AG   A
GAM2282  LOC253868 3'  CCGTCCTGCTGGTGCAGGAA   54368      G__  C
                                CTGT   GC GGTGCAGGAA
                                ||||   || ||||||||||
                                GGCA   CG CCACGTCCTT
                                  GGA  A
GAM2282  LOC255461 5'  CCCAGGCTGGTGCAGG      54365      TGCTGT   C
                                TCCA     GGC GGTGCAGG
                                ||||     ||| ||||||||
                                GGGT     CCG CCACGTCC
                                  _______  A
GAM2282  LOC255516 5'  CCCAGGCTGGTGCAGG      54365      TGCTGT   C
                                TCCA     GGC GGTGCAGG
                                ||||     ||| ||||||||
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                                GGGT     CCG CCACGTCC
                                  ______  A
GAM2282  LOC256306 5'  TCCATGCTGTGACCCACAGCAG 54369           GGT_
              G                   TCCATGCTGTGGCC   GCAGG
                                  ||||||||||||||   |||||
                                  AGGTACGACACTGG   CGTCC
                                        GTGT
GAM2282  LOC257354 3'  CCATGCTGGCCAAGTGCAGG  54349       GT   _
                                  CCATGCT  GGCCG GTGCAGG
                                  |||||||  ||||| |||||||
                                  GGTACGA  CCGGT CACGTCC
                                     __    T
GAM2282  LOC91812  5'  CATGCTGTGTGACCTCAGGAA  54370        __  GGTG
                                  CATGCTGTG  GCC   CAGGAA
                                  |||||||||  |||   ||||||
                                  GTACGACAC  TGG   GTCCTT
                                       AC   A___
GAM2282  LOC91813  5'  CATGCTGTGTGACCTCAGGAA  54370        __  GGTG
                                  CATGCTGTG  GCC   CAGGAA
                                  |||||||||  |||   ||||||
                                  GTACGACAC  TGG   GTCCTT
                                       AC   A___
GAM2283  ABCB10    3'  CATGAGATTATCGGAAT    54373        TTCA   C
                                  CATGAGATT   ATC GGAGT
                                  |||||||||   ||| |||||
                                  GTACTCTAA   TAG CCTTA
                                     _____  _
GAM2283  ATP11B    3'  CACGAGATTTTTCAGAG    54374         CAATC
                                  CATGAGATTTT   CGGAG
                                  ||||||||||||  |||||
                                  GTGCTCTAAAA   GTCTC
                                       A_____
GAM2283  HPGD      3'  TCCTGAGATTTTTGGAG    54375    A      CAATCC
                                  TCC TGAGATTTT    GGAG
                                  ||| |||||||||    ||||
                                  AGG ACTCTAAAA    CCTC
                                    _      A_____
GAM2283  NFKBIA    3'  TCCATGAAATTTTTGATAACC  54376          CAAT__
                                  TCCATGAGATTTT    CC
                                  ||||||||||||||   ||
                                  AGGTACTTTAAAA    GG
                                       ACTATT
GAM2283  FLJ10989  3'  CCATGAGATATAGAGAATCTGG 54377        TTTC__   C  A
              GGT                   CCATGAGAT    AATC GG GT
                                  |||||||||    |||| || ||
                                  GGTACTCTA    TTAG CC CA
                                       TATCTC   A  C
GAM2283  KIAA1102  3'  TCCATGGGCAAGGTCCGGAGT  54378      AGATTTT  __
                                  TCCATG     CAA  TCCGGAGT
                                  ||||||     |||  ||||||||
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                                AGGTAC      GTT  AGGCCTCA
                                   CC_____   CC
GAM2283  KIAA1157  3'  TCCATAGAGATATCTGGG    54379      _    TTTCA   C  A
                                TCCAT GAGAT    ATC GG G
                                ||||| |||||    ||| || |
                                AGGTA CTCTA    TAG CC C
                                   T    _____  A  C
GAM2283  LOC151361 3'  CCATGGATAGTCCGGAG     54380      A   TTTCAA
                                CCATG GAT     TCCGGAG
                                ||||| |||     |||||||
                                GGTAC CTA     AGGCCTC
                                   _  TC____
GAM2283  LOC154222 3'  TGAGAATTTTGCCCAGAGT   54381      T   CAA
                                TGAGA TTT   TCCGGAGT
                                ||||| |||   ||||||||
                                ACTCT AAA   GGGTCTCA
                                   T   AC_
GAM2283  LOC221692 3'  CATGAATTTTCAGGCAGAA   54382      A     ATC
                                CATGAG TTTTCA   CGGAG
                                ||||||| ||||||   |||||
                                GTACTT AAAAGT   GTCTT
                                   _     CC_
GAM2283  LOC92106  5'  TCCACGAGATTTTAGGAG    54383          CAATCC
                                TCCATGAGATTTT     GGAG
                                ||||||||||||      ||||
                                AGGTGCTCTAAAA     CCTC
                                      T_____
GAM2284  BCL11B    3'  TTGAAAGATTGTTATCCGC   54386      TA       GTAT
                                TTGAA  ATTGTTATT    CGC
                                |||||  |||||||||    |||
                                AACTT  TAACAATAG    GCG
                                   TC       _____
GAM2284  ITGA1     3'  TTGAATAATTGTTATTAT    54387
                                TTGAATAATTGTTATTGT
                                ||||||||||||||||||
                                AACTTATTAACAATAATA

GAM2284  FLJ20335  3'  TTGAATATTGTCATTGT     54388        A
                                TTGAATA TTGTTATTGT
                                ||||||| ||||||||||
                                AACTTAT AACAGTAACA
                                   _
GAM2284  KIAA1497  5'  AATAATTGTTATTCATCATCT  54389          G    _
                                AATAATTGTTATT TATCG CT
                                |||||||||||| ||||| ||
                                TTATTAACAATAA GTAGT GA
                                      _    A
GAM2284  LOC152225 3'  TTGAGTTATTGTTACTGT    54390      ATA
                                TTGA   ATTGTTATTGT
                                ||||   ||||||||||
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                                AACT   TAACAATGACA
                                  CAA
GAM2284  LOC92228  3'  TCGAGTAATTGTTGCTCGC   54391     A      TAT   A
                                TTGA TAATTGT   TGT TCGC
                                |||| |||||||   ||| ||||
                                AGCT ATTAACA   ACG AGCG
                                  C      ___   _
GAM2285  EFNA3     3'  ATTATATATAGAGATATAGAG  54394       CA      G
                                ATTGTA  TATAGAG ATATAGAG
                                ||||||  ||||||| ||||||||
                                TAATAT  ATATCTC TATATCTC
                                   __     _
GAM2285  SOX12     3'  TTATACATATGGAAAGA     54395          AGA   TAT
                                TTGTACATAT   GGA   AGA
                                ||||||||||   |||   |||
                                AATATGTATA   CCT   TCT
                                     ___   T__
GAM2285  DKFZP434N093 3'  TTGTACTGTAGAGAACA     54396       ATA
                                TTGTAC   TAGAGGATA
                                ||||||   |||||||||
                                AACATG   ATCTCTTGT
                                   AC_
GAM2285  FLJ23342  3'  TTGTAAATATTACTTATATAGA 54397      C    AGAGG
           G                     TTGTA ATAT     ATATAGAG
                                ||||| ||||     ||||||||
                                AACAT TATA     TATATCTC
                                   T    ATGAA
GAM2285  KIAA0563  3'  TTCTACATATAGAAAGCTAG   54398    G          ATA
                                TT TACATATAGAGG   TAG
                                || ||||||||||||   |||
                                AA ATGTATATCTTT   ATC
                                 G          CG_
GAM2285  KIAA1671  3'  ATTGTACATATAGAGGAT    54399
                                ATTGTACATATAGAGGAT
                                ||||||||||||||||||
                                TAACATGTATATCTCCTA

GAM2285  MEGF11   3'  ATTGTACATGCAGGATA     54400         ATAG
                                ATTGTACAT    AGGATA
                                |||||||||    ||||||
                                TAACATGTA    TCCTAT
                                     CG__
GAM2285  LOC146901 3'  ATTGATATCCAGGATATAGAG  54401     TAC    AG
                                ATTG   ATAT  AGGATATAGAG
                                ||||   ||||  ||||||||||
                                TAAC   TATA  TCCTATATCTC
                                   ___    GG
GAM2285  LOC147071 3'  TTCTACATATAGAAAGCTAG   54398    G          ATA
                                TT TACATATAGAGG   TAG
                                || ||||||||||||   |||
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                                AA ATGTATATCTTT   ATC
                                 G          CG_
GAM2285  LOC148195 5'  ATTGTAAGTGAAAATATAGAG  54402       CATATA
                                ATTGTA     GAGGATATAGAG
                                ||||||     ||||||||||||
                                TAACAT     CTTTTATATCTC
                                   TCA___
GAM2285  LOC150587 3'  TTGTACATATGAGGATA     54403          A
                                TTGTACATAT GAGGATA
                                |||||||||| |||||||
                                AACATGTATA CTCCTAT
                                          _
GAM2285  LOC154442 3'  ATTGTACATGTAGCAGGATA   54404         A  _
                                ATTGTACAT TAG AGGATA
                                ||||||||| ||| ||||||
                                TAACATGTA ATC TCCTAT
                                     C   G
GAM2285  LOC201173 3'  TTCTACATATAGAAAGCTAG   54398    G         ATA
                                TT TACATATAGAGG   TAG
                                || ||||||||||||   |||
                                AA ATGTATATCTTT   ATC
                                 G          CG_
GAM2285  LOC201220 3'  TTCTACATATAGAAAGCTAG   54398    G         ATA
                                TT TACATATAGAGG   TAG
                                || ||||||||||||   |||
                                AA ATGTATATCTTT   ATC
                                 G          CG_
GAM2286  OA1       3'  TTGGGAAGGTGAGAACACAGT  54407        AT__
                                TTGGGAAG    GAATATGGT
                                ||||||||    |||||||||
                                AACCCTTC    CTTGTGTCA
                                     CACT
GAM2286  POU4F1    3'  TTGGGGAGGTGGTAATAATGGT 54408      A  A  __   _
            GGT                    TTGGG AG TG  AATA TGGTGGT
                                |||||  ||  ||  ||||  |||||||
                                AACCC TC AC  TTAT ACCACCA
                                   C  C  CA    T
GAM2286  PUM2      3'  TATTGGGAAGATTGGGT     54409          GAATAT
                                TATTGGGAAGAT     GGT
                                ||||||||||||     |||
                                ATAACCCTTCTA     CCA
                                       AC_____
GAM2286  RBBP9     3'  TTGGGAAATGAAAAAGGGT    54410       A     TAT  T
                                TTGGGA GATGAA   GG GGT
                                ||||||  ||||||   ||  |||
                                AACCCT TTACTT   TC CCA
                                   _     TT_  _
GAM2286  ABCA5     5'  CATTGGGCCCTGGATATGGTGG 54411        AAGA  A
            T                    TATTGGG    TG ATATGGTGGT
                                |||||||    ||  ||||||||||
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                                GTAACCC    AC TATACCACCA
                                    GGG_  C
GAM2286  ANKRD6    3'  TATTGAGGAGATGAATAT     54412        A
                                TATTGGG AGATGAATAT
                                ||||||| ||||||||||
                                ATAACTC TCTACTTATA
                                    C
GAM2286  FLJ10738  3'  TATTGGGAGATGGAGTTTGTGG 54413        A    AATATG
           T                     TATTGGGA GATG     GTGGT
                                ||||||||| ||||     |||||
                                ATAACCCT CTAC     CACCA
                                    _   CTCAAA
GAM2286  HSPC155   5'  TGGGAAGATGAGACGTTGG    54414          AT   G
                                TGGGAAGATGA  ATG TGG
                                |||||||||||  ||| |||
                                ACCCTTCTACT  TGC ACC
                                      C_  A
GAM2286  KRTAP9-8  3'  TTGTTGTGTGAGTATGGTGGT  54415     GGAAGA   A
                                TTG     TGA TATGGTGGT
                                |||     ||| |||||||||
                                AAC     ACT ATACCACCA
                                  AACAC_  C
GAM2286  SLC34A1   3'  TTGGGAAGGGAATTAATTGTGG 54416        AT    A_____
           TGGT                    TTGGGAAG  GAAT     TGGTGGT
                                ||||||||  ||||     |||||||
                                AACCCTTC  CTTA     ACCACCA
                                    C_    ATTAAC
GAM2286  LOC170372 3'  TATTGTGAAGCACTATGGTGGT 54417      G    ATGAA
                                TATTG GAAG     TATGGTGGT
                                ||||| ||||     |||||||||
                                ATAAC CTTC     ATACCACCA
                                   A    GTG__
GAM2286  LOC201175 5'  TATTGGGAAGATTAAATGAGGT 54418           GAAT    T
                                TATTGGGAAGAT    ATGG GGT
                                ||||||||||||    |||| |||
                                ATAACCCTTCTA    TACT CCA
                                      ATT_    _
GAM2287  GA        3'  TGGTGGTTATGGATTACATGTG 54421    A    AAC  TG
                                TG TGGT   TG  TTACATGTG
                                || ||||   ||  |||||||||
                                AC ACCA   AC  AATGTACAC
                                 C    AT_  CT
GAM2287  LRRC2     3'  ATGGTAGCCACATGT      54422       ACTGT
                                ATGGTA    GTTACATGT
                                ||||||    |||||||||
                                TACCAT    CGGTGTACA
                                    _____
GAM2287  MUC3B     5'  TGATGGCAGTTGTGGATGTGC  54423        AC    TTAC
                                TGATGGTA  TGTG    ATGTGC
                                ||||||||  ||||    ||||||
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                                ACTACCGT  ACAC    TACACG
                                    CA    C___
GAM2287  PTPRA     5'  TGGTAACTGTGTCATGT     54424          TA
                                TGGTAACTGTGT  CATGT
                                ||||||||||||  |||||
                                ACCATTGACACA  GTACA
                                          __
GAM2287  FLJ00001  3'  TGGTGGCAACCCCCGGACATGT 54425    A      GTGTT
           GC                     TG TGGTAACT    ACATGTGC
                                || ||||||||    ||||||||
                                AC ACCGTTGG    TGTACACG
                                 C       GGGCC
GAM2287  FLJ20127  5'  GATGGTGGCTGTGCTATGTG   54426      AA       CA
                                GATGGT  CTGTGTTA  TGTG
                                ||||||  ||||||||  ||||
                                CTACCA  GACACGAT  ACAC
                                   CC       __
GAM2287  KIAA1100  3'  TGAGGTAACTGTAAAATGTGC  54427    T        TTAC
                                TGA GGTAACTGTG    ATGTGC
                                ||| ||||||||||    ||||||
                                ACT CCATTGACAT    TACACG
                                  _         TT__
GAM2287  KIAA1317  3'  TGATGGTATTGCCATGTG    54428        AC   GTTA
                                TGATGGTA  TGT    CATGTG
                                ||||||||  |||    ||||||
                                ACTACCAT  ACG    GTACAC
                                    A_  _____
GAM2287  PRO0082   3'  TGATGGTAACAGATCCATGTG  54429          TGT   A
                                TGATGGTAAC   GTT CATGTG
                                ||||||||||   ||| ||||||
                                ACTACCATTG   TAG GTACAC
                                      TC_  _
GAM2287  Rpo1-2    3'  TGATGGTATCAAAGGTGTGTGC 54430        ACT___    TACAT
                                TGATGGTA     GTGT    GTGC
                                ||||||||     ||||    ||||
                                ACTACCAT     CACA    CACG
                                    AGTTTC   ______
GAM2287  Rpo1-2    3'  TGATGGTATCAAAGGTGTGTGC 54430        ACT___    TACAT
                                TGATGGTA     GTGT    GTGC
                                ||||||||     ||||    ||||
                                ACTACCAT     CACA    CACG
                                    AGTTTC   ______
GAM2287  SEC15L    3'  TGTGGTAACTTCTGTGTG    54431    A      G_   TACAT
                                TG TGGTAACT  TGT     GTG
                                || ||||||||  |||     |||
                                AC ACCATTGA  ACA     CAC
                                  _      AG   ______
GAM2287  SMARCF1   3'  TGATGGTATCTAATGCCCATGT 54432         A   _    A
           GC                     TGATGGTA CTG TGTT CATGTGC
                                ||||||||  ||| |||| |||||||
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                                ACTACCAT GAT ACGG GTACACG
                                    A  T  _
GAM2287  TBL1Y   5'  ATGGTAACTTCATGTG     54433        GTGTTA
                                ATGGTAACT    CATGTG
                                |||||||||    ||||||
                                TACCATTGA    GTACAC
                                    A_____
GAM2287  TBL1Y   5'  ATGGTAACTTCATGTG     54433        GTGTTA
                                ATGGTAACT    CATGTG
                                |||||||||    ||||||
                                TACCATTGA    GTACAC
                                    A_____
GAM2287  TBL1Y   5'  ATGGTAACTTCATGTG     54433        GTGTTA
                                ATGGTAACT    CATGTG
                                |||||||||    ||||||
                                TACCATTGA    GTACAC
                                    A_____
GAM2288  ACADM   3'  TAAAATAGGAGAATAT     54436         AAAGAT
                                TAAAATGGGA   GAATAT
                                ||||||||||   ||||||
                                ATTTTATCCT   CTTATA
                                     ______
GAM2288  AF1Q    3'  TAAAATGGGAAAGGAGTG    54437          A  _
                                TAAAATGGGAAA GA TG
                                |||||||||||| || ||
                                ATTTTACCCTTT CT AC
                                      C  C
GAM2288  CLCN5   5'  AATGGGAAAGGATTTATGA   54438        A  GAA
                                AATGGGAAA GAT  TATGA
                                ||||||||| |||  |||||
                                TTACCCTTT CTA  ATACT
                                    C  A__
GAM2288  GPR48   3'  ATGGGGAAGATGTATG      54439      AA    AA
                                ATGGG  AAGATG  TATG
                                |||||  ||||||  ||||
                                TACCC  TTCTAC  ATAC
                                  C_    __
GAM2288  GRINL1A 3'  ATGGCCAATGAATATGA     54440     GAAAA
                                ATGG    GATGAATATGA
                                ||||    ||||||||||
                                TACC    TTACTTATACT
                                  GG___
GAM2288  IFNA14  3'  AAATGGAAGAACATGAAAGTG  54441        A  G    TA
                                AAATGGGA AA ATGAA  TG
                                |||||||| || |||||  ||
                                TTTACCTT TT TACTT  AC
                                     C  G    TC
GAM2288  PPT2    3'  AAAATGGGGGATAATATG    54442        AAAA    A
                                AAAATGGG   GATGA TATG
                                ||||||||   ||||| ||||
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                                TTTTACCC   CTATT ATAC
                                    C___   _
GAM2288 PPT2     3' AAAATGGGGGATAATATG    54442        AAAA    A
                                AAAATGGG   GATGA TATG
                                ||||||||   ||||| ||||
                                TTTTACCC   CTATT ATAC
                                    C___   _
GAM2288 STAM     3' TAAAATGAGAAATAAAGAATGT 54443          A T   A
           GA                    TAAAATGGGAAA GA GAAT TGA
                                ||||||||||||| || |||| |||
                                ATTTTACTCTTT TT CTTA ACT
                                      A T   C
GAM2288 STAU2    3' TAAGATGGAAAAGGAGATGA   54444     A      __
                                TAA ATGGGAAA  AGATGA
                                ||| ||||||||  ||||||
                                ATT TACCTTTT  TCTACT
                                  C       CC
GAM2288 CGGBP1   3' TAAAATGGGGGCGGGGGAAGTA 54445         AAAAGAT  _
           TG                    TAAAATGGG      GAA TATG
                                |||||||||      ||| ||||
                                ATTTTACCC      CTT ATAC
                                     CCGCCCC   C
GAM2288 DKFZP434G1415 3' TAAAATGGTGAAGGATGA    54446        GA  A
                                TAAAATGG  AA GATGA
                                ||||||||  || |||||
                                ATTTTACC  TT CTACT
                                     AC  C
GAM2288 FBXO21   3' TAAAATGGAGGAATTGTAGATG 54447       __  A___     A
           AGTATG                  AAAATGG  GAA   AGATGA TATG
                                ||||||| |||   |||||| ||||
                                TTTTACC  CTT   TCTACT ATAC
                                    TC   AACA     C
GAM2288 FLJ10738 3' TAAAATGGGAAGAGGTGA    54448          A  A
                                TAAAATGGGAA AG TGA
                                |||||||||| || |||
                                ATTTTACCCTT TC ACT
                                      C  C
GAM2288 FLJ30681 3' AAATGGGAAAGGACATG     54449          A   GAAT
                                AAATGGGAAA GAT    ATG
                                |||||||||| |||    |||
                                TTTACCCTTT CTG    TAC
                                     C  _____
GAM2288 GPR88    3' TAGTAAACCAAAGATGAATATG 54450     GA____
           A                     TGG     AAAGATGAATATGA
                                |||     ||||||||||||||
                                ATC     TTTCTACTTATACT
                                  ATTTGG
GAM2288 KIAA0648 3' TAAAATGAGGGGAAATCAAAAT 54451       ___     AGAT
           ATGA                    TAAAAT   GGGAAA    GAATATGA
                                ||||||   ||||||    ||||||||
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                                ATTTTA  CCCTTT   TTTATACT
                                   CTC     AGT_
GAM2288 KIAA0937 3' AAAATGGGAAGAGAATGA    54452         A  _
                                AAAATGGGAA AGA TGA
                                |||||||||| ||| |||
                                TTTTACCCTT TCT ACT
                                     C  T
GAM2288 KIAA1219 3' AAATGTGGAGAAAAAAATATGA 54453      _  A   T
                                AAATG GGA AAGA GAATATGA
                                ||||| ||| |||| ||||||||
                                TTTAC CCT TTTT TTTATACT
                                   A  C   _
GAM2288 KIAA1557 3' TGGAAGAATGGTGAATATG   54454      A  GA_
                                TGGGA AA   TGAATATG
                                ||||| ||   ||||||||
                                ACCTT TT   ACTTATAC
                                   C  ACC
GAM2288 KIAA1918 3' TAAGATGAGAAAAGAAAATGTG 54455     A        T   A
            A                    TAA ATGGGAAAAGA GAAT TGA
                                ||| |||||||||| |||| |||
                                ATT TACTCTTTTCT TTTA ACT
                                  C         _   C
GAM2288 LY6G6C   3' CAAAATGGAAAGAGGTGAGTAT 54456          A  A   A
            G                    TAAAATGGGAA AG TGA TATG
                                |||||||||| || ||| ||||
                                GTTTTACCTTT TC ACT ATAC
                                     C  C   C
GAM2288 MGC5457  3' ATGGGAAAGTAGGCAGAATGTG 54457        __ AT_   A
            A                    ATGGGAAA  AG   GAAT TGA
                                |||||||| ||   |||| |||
                                TACCCTTT  TC   CTTA ACT
                                    CA  CGT   C
GAM2288 MYNN     3' TGAATGGGAATTTAATATG   54458   A      AAGATG
                                A AATGGGAA     AATATG
                                | ||||||||     ||||||
                                A TTACCCTT     TTATAC
                                 C       AAA___
GAM2288 PMX2B    5' AAAATGAAATAAAAGATGGATA 54459       GG __      A
            TG                    AAAATG  A  AAAGATG ATATG
                                |||||| |  ||||||| |||||
                                TTTTAC  T  TTTCTAC TATAC
                                   TT AT      C
GAM2288 PSTPIP2  3' TAAAATGAGAAAGTATGA    54460          AG
                                TAAAATGGGAAA  ATGA
                                ||||||||||||  ||||
                                ATTTTACTCTTT  TACT
                                     CA
GAM2288 SSH2     3' TAAAATGAGGAGAGATGAATAT 54461        _  AA
                                TAAAATG GGA  AGATGAATAT
                                ||||||| |||  ||||||||||
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                                ATTTTAC CCT  TCTACTTATA
                                    T   C_
GAM2288  ZDHHC3    3'  TAAAATGAGAAGGGGATGA    54462          AA_
                                TAAAATGGGAA   GATGA
                                ||||||||||   |||||
                                ATTTTACTCTT   CTACT
                                      CCC
GAM2288  LOC146669 3'  TGGGAAGGAGATGGATGTGA   54463       A_    A  A
                                TGGGAA  AGATG AT TGA
                                ||||||  ||||| || |||
                                ACCCTT  TCTAC TA ACT
                                   CC    C  C
GAM2288  LOC153651 3'  TAAAATGGGGAAATGACATCTG 54464         AAA     ATA_
           A                     TAAAATGGG   AGATGA    TGA
                                |||||||||   ||||||    |||
                                ATTTTACCC   TTTACT    ACT
                                      C__      GTAG
GAM2288  LOC202025 5'  TAAAATGGGAGTGGACATG    54465          AAA A  A
                                TAAAATGGGA   G TG ATATG
                                ||||||||||   | || |||||
                                ATTTTACCCT   C AC TGTAC
                                      ____ _  C
GAM2288  LOC203411 3'  GGGATGCAAAGATGAATATGA  54466      ___
                                GGGA   AAAGATGAATATGA
                                ||||   ||||||||||||||
                                CCCT   TTTCTACTTATACT
                                  ACG
GAM2288  LOC221504 3'  ATGGGAAAGGAAGAGGTATG   54467        A  T  A_
                                ATGGGAAA GA GA  TATG
                                ||||||||| || ||  ||||
                                TACCCTTT CT CT  ATAC
                                     C  T  CC
GAM2288  LOC92568  3'  TGGGGGAAGGTGAACATGA    54468      AA   A
                                TGGG  AAG TGAATATGA
                                ||||  ||| |||||||||
                                ACCC  TTC ACTTGTACT
                                  CC   C
GAM2289  ARHGEF7   3'  GATTCATCAGTCATGGTTTGA  54471      G     TA TG
                                GAT CATCA  T  TGGTTTGA
                                ||| |||||  |  ||||||||
                                CTA GTAGT  A  ACCAAACT
                                  A    C_ GT
GAM2289  COG6      3'  TAGATCATTGTTTCTTTGGTTT 54472       G   CATATTG_
           GA                    TAGAT CAT       TGGTTTGA
                                |||||  |||       ||||||||
                                ATCTA GTA       ACCAAACT
                                  _   ACAAAGAA
GAM2289  PCDH7     3'  GAGCATCATATTAGAGTGG    54473    T        ___
                                GA GCATCATATT   GTGG
                                || ||||||||||   ||||
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                                CT CGTAGTATAA   CACC
                                 _        TCT
GAM2289  WIF1     3'  TAAATGCATTGTAATTT     54474         CATAT
                                TAGATGCAT    TGTGGTTT
                                |||||||||    ||||||||
                                ATTTACGTA    ACATTAAA
                                      _____
GAM2289  ZFP100   3'  TAGATGCATTTATTTGG     54475         CA   G
                                TAGATGCAT  TATT TGG
                                |||||||||  |||| |||
                                ATCTACGTA  ATAA ACC
                                     A_   _
GAM2289  LOC150622 3'  TAGATGTGCATATTTTGG    54476       CAT     G
                                TAGATG   CATATT TGG
                                ||||||   |||||| |||
                                ATCTAC   GTATAA ACC
                                   AC_     A
GAM2289  LOC155435 3'  TACATGCATTGTAAGCACTTTG 54477    G     CA  TT   G
            A                    TA ATGCAT  TA  GTG TTTGA
                                || ||||||  ||  ||| |||||
                                AT TACGTA  AT  CGT AAACT
                                 G     AC  T_   G
GAM2289  LOC197379 3'  TAGGTGCATCATGTTT      54478     A       ATTGTG
                                TAG TGCATCAT     GTTT
                                ||| ||||||||     ||||
                                ATC ACGTAGTA     CAAA
                                  C      _______
GAM2289  LOC220469 3'  AGATGCATCGGCCTGTGGTTTG 54479         ATA
            A                    AGATGCATC   TTGTGGTTTGA
                                |||||||||   ||||||||||
                                TCTACGTAG   GACACCAAACT
                                     CCG
GAM2290  PTGFR    3'  GCCAGTCTTCCCCTCTTAG   54482    T     GTTAG    C
                                GC CAGTCT    TCCTC TAG
                                || ||||||    ||||| |||
                                CG GTCAGA    GGGAG ATC
                                 _     AG___     A
GAM2290  RAD54B   3'  GCTCAATCTGTAGTGCTCCTGG 54483          T  C    A
            T                    GCTCAGTCTGT AGT CTCCT GT
                                ||||||||||| ||| ||||| ||
                                CGAGTTAGACA TCA GAGGA CA
                                      _  C    C
GAM2290  SDC1     3'  GCTTCCAGATTTGGTTCTCCTA 54484     __  TCTG  A  C
            GT                    GCT  CAG   TT GT CTCCTAGT
                                |||  |||   || || ||||||||
                                CGA  GTC   AA CA GAGGATCA
                                  AG   TA__  C  A
GAM2290  C1orf19  3'  GCTTGGTCTGTTATTTCAGCC  54485     CA      G_  CT
                                GCT  GTCTGTTA  TC  CC
                                |||  ||||||||  ||  ||
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                                CGA  CAGACAAT  AG  GG
                                  AC       AA  TC
GAM2290  FADS1    3'  GCTCTGTCTTTTCCTCCTAGT  54486     A   GTTAG
                                GCTC GTCT    TCCTCCTAGT
                                |||| ||||    ||||||||||
                                CGAG CAGA    AGGAGGATCA
                                  A   AA___
GAM2290  FLJ14397 3'  GCTAGGTCCCCTTCCTCCTAGT 54487     CA   G  AG
                                GCT  GTCT TT  TCCTCCTAGT
                                |||  |||| ||  ||||||||||
                                CGA  CAGG GA  AGGAGGATCA
                                  TC   G  __
GAM2290  KIAA1317 3'  GCTGAGTCTGTCATCCTAG   54488     C       GTCC
                                GCT AGTCTGTTA   TCCTAG
                                ||| |||||||||   ||||||
                                CGA TCAGACAGT   AGGATC
                                  C       _____
GAM2290  KIAA1500 3'  GCTCAGTCTTTAGTCCT     54489         G
                                GCTCAGTCT TTAGTCCT
                                ||||||||| ||||||||
                                CGAGTCAGA AATCAGGA
                                          _
GAM2290  KIAA1712 3'  CTTGAGACCATAGTCCTC    54490    C_  T   T
                                CT  AG CTGT AGTCCTC
                                ||  || |||| |||||||
                                GA  TC GGTA TCAGGAG
                                 AC  T   _
GAM2290  PGLYRP   3'  GCTGGGTCTGCCCTCCTG    54491     CA     TAGT     A
                                GCT  GTCTGT   CCTCCT G
                                |||  ||||||   |||||| |
                                CGA  CAGACG   GGAGGA C
                                  CC     _____     C
GAM2290  LOC150291 3'  ACTCAGTCTGTTTTCTTAG   54492          AGTCC  C
                                GCTCAGTCTGTT    TC TAG
                                ||||||||||||    || |||
                                TGAGTCAGACAA    AG ATC
                                       A____  A
GAM2291  MBD4     3'  TTTTTTGGATTGTTGTCAAAT  54495          A  _
                                TTTTTTGGGTT TTG CAAAT
                                |||||||||||| ||| |||||
                                AAAAAACCTAA AAC GTTTA
                                       C   A
GAM2291  DNAJC8   3'  TTTTTTGGGTATAAAAATTTAT 54496         TATTGC
                                TTTTTTGGGT     AAATTTAT
                                ||||||||||     ||||||||
                                AAAAAACCCA     TTTAAATA
                                       TATT__
GAM2291  FLJ20772 3'  TTTTTTGGGCTGTCAATTTTAT 54497          ATTG   A
                                TTTTTTGGGTT    CAA TTTAT
                                ||||||||||    ||| |||||
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                                AAAAAACCCGA   GTT AAATA
                                      CA__  A
GAM2291 KIAA0997 3' CTTTTTGGGTTGATGGAA   54498         AT  C
                                TTTTTTGGGTT  TG AA
                                |||||||||||  || ||
                                GAAAAACCCAA  AC TT
                                      CT  C
GAM2291 MGC14697 3' TTTTTTGGGTTCATAATTTAT  54499          ATTGCA
                                TTTTTTGGGTT     AATTTAT
                                |||||||||||     |||||||
                                AAAAAACCCAA     TTAAATA
                                      GTA___
GAM2291 pcnp     3' TTTTTTGAGTTTGACAAATTTA 54500          ATT
           T                    TTTTTTGGGTT   GCAAATTTAT
                                |||||||||||   ||||||||||
                                AAAAAACTCAA   TGTTTAAATA
                                      AC_
GAM2291 SPAG7    3' TTTTTTGGGTTAAACAGTATTT 54501          TT  A_
           AT                    TTTTTTGGGTTA  GCA  ATTTAT
                                ||||||||||||  |||  ||||||
                                AAAAAACCCAAT  TGT  TAAATA
                                      T_  CA
GAM2291 LOC149563 3' TTGGGTTACTTTATTTAT    54502         GCAA
                                TTGGGTTATT    ATTTAT
                                ||||||||||    ||||||
                                AACCCAATGA    TAAATA
                                      AA__
GAM2292 ALDH1A3  3' AAATATACCACCTCTGTG    54505         TG
                                AAATATGCC  TTTTGTG
                                |||||||||  |||||||
                                TTTATATGG  GAGACAC
                                     TG
GAM2292 CNTNAP2  3' TCAAATGTGTCCGTTTTA    54506       A  C
                                TCAAAT TG CTGTTTTG
                                |||||| || ||||||||
                                AGTTTA AC GGCAAAAT
                                   C  A
GAM2292 ENC1     3' GCCAAATGTGTTACTTGTGCA  54507    T    A  CCTGT
                                GC CAAAT TG    TTTGTGCA
                                || ||||| ||    ||||||||
                                CG GTTTA AC    GAACACGT
                                 _    C  AAT__
GAM2292 KIT      3' TCAAACTGTGCTTTGTG     54508       A  CC
                                TCAAAT TG  TGTTTTGTG
                                |||||| ||  |||||||||
                                AGTTTG AC  ACGAAACAC
                                     _ __
GAM2292 SIAT8E   3' GCTCAAGTGTCCTGTGAAGTG  54509       ATA _    TTT
                                GCTCAA   TG CCTGT   GTG
                                ||||||   || |||||   |||
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                                CGAGTT  AC GGACA  CAC
                                   C__  A   CTT
GAM2292 TEP1    5' GCTTGTATATGCCTGGGGCG  54510    CAA      TTTT
                                GCT  ATATGCCTG  GTG
                                |||  |||||||||  |||
                                CGA  TATACGGAC  CGC
                                  ACA       CC__
GAM2292 DKFZP761F241 3' ACTCAAATGTGCCTGAGC   54511       A    TTTTGT
                                GCTCAAAT TGCCTG    GC
                                |||||||| ||||||    ||
                                TGAGTTTA ACGGAC    CG
                                    C     T_____
GAM2292 FLJ12903 3' TCAGGTAATGCTTTTGTGCA  54512    AAT_  CTG
                                TCA   ATGC  TTTTGTGCA
                                |||   ||||  |||||||||
                                AGT   TACG  AAAACACGT
                                  CCAT   ___
GAM2292 FLJ21324 5' GCTCAGGTATCCTCCCCTGTG 54513     AA  G  G
                                GCTCA  TAT CCT TTTTGTG
                                |||||  ||| ||| |||||||
                                CGAGT  ATA GGA GGGACAC
                                   CC  _  G
GAM2292 KIAA0143 3' TCAAGTATGCTTGTCCTA   54514    A   C
                                TCAA TATGC TGTTTTG
                                |||| ||||| |||||||
                                AGTT ATACG ACAGGAT
                                  C    A
GAM2292 KIAA0469 3' GCTCAAATGTGTACTAAGCTGT 54515       A  C_  TT
            G                    GCTCAAAT TG  CTG  TTGTG
                                |||||||| ||  |||  |||||
                                CGAGTTTA AC  GAT  GACAC
                                    C  AT   TC
GAM2292 KIAA1655 5' GCTTGGAGATGCCTGTCCTG  54516    CAAAT
                                GCT    ATGCCTGTTTTG
                                |||    ||||||||||||
                                CGA    TACGGACAGGAC
                                  ACCTC
GAM2292 SFRS5   3' GCTCTAATGTGTCTGTCCAGCA 54517    A  A  C    TGT
                                GCTC AAT TG CTGTTT  GCA
                                |||| ||| || ||||||  |||
                                CGAG TTA AC GACAGG  CGT
                                  A  C  A    T__
GAM2292 TJP2    3' CTCAAGTATCTGCTTTTGTGCA 54518     A  GC     _
                                CTCAA TAT  CTGTTTT GTGCA
                                ||||| |||  ||||||| |||||
                                GAGTT ATA  GACGAAA CACGT
                                  C  __     A
GAM2292 TUCAN   3' ACTCAAATGTGCCAGGTGTA  54519       A   TGTTT
                                GCTCAAAT TGCC    TGTG
                                |||||||| ||||    ||||
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                                TGAGTTTA ACGG    ACAT
                                    C   TCC__
GAM2292  LOC128989 3'  GCTTGCATGTGTGTGCTTGTGC 54520    CAAA   CC  _
             A                   GCT   TATG  TGT TTTGTGCA
                                 |||   ||||  ||| ||||||||
                                 CGA   GTAC  ACA GAACACGT
                                   AC__   AC  C
GAM2292  LOC152317 5'  TCTAATATGCCAGGCAGTGTG  54521    A      T_  TT
                                 TC AATATGCC  GT  TGTG
                                 || ||||||||  ||  ||||
                                 AG TTATACGG  CG  ACAC
                                  A       TC  TC
GAM2292  LOC154860 3'  CTTGAATATGGTTGTTTTGTG  54522    CA     CC
                                 CT  AATATG  TGTTTTGTG
                                 ||  ||||||  |||||||||
                                 GA  TTATAC  ACAAAACAC
                                  AC     CA
GAM2292  LOC221336 3'  AAACATGACTTTGTGCA     54523       C  GTT
                                 AAATATG CT   TTGTGCA
                                 |||||||  ||   |||||||
                                 TTTGTAC GA   AACACGT
                                     T  ___
GAM2292  LOC91151  5'  GCTCAAATTGCTTTGTA     54524       ATGCC
                                 GCTCAAAT    TGTTTTGTG
                                 ||||||||    |||||||||
                                 CGAGTTTA    ACGAAACAT
                                             _____
GAM2293  C14orf1   3'  TAGCTGGATGTGGTGGTAC   54527        T  C_  _
                                 TAGCTGGAT GTG  GG AC
                                 |||||||||  |||  ||  ||
                                 ATCGACCTA CAC  CC TG
                                       _  CA  A
GAM2293  FLJ10650  3'  TAGCTGGGATTACAGACGAA  54528       ATTG
                                 TAGCTGG    TGCGGACGAA
                                 |||||||    ||||||||||
                                 ATCGACC    ATGTCTGCTT
                                     CTA_
GAM2293  FLJ20189  3'  CAGCTGGATTGTATCAGA    54529          _
                                 TAGCTGGATTGTG CGGA
                                 ||||||||||||| ||||
                                 GTCGACCTAACAT GTCT
                                         A
GAM2293  FLJ20695  3'  TAGCTGGGTGTGGCAGCAC   54530       AT   _  _
                                 TAGCTGG  TGTG CGG AC
                                 |||||||  |||| ||| ||
                                 ATCGACC  ACAC GTC TG
                                     C_   C   G
GAM2293  KIAA0014  3'  GCTGGGCCTGGGCGGACA    54531      A_   T
                                 GCTGG  TTG GCGGACG
                                 |||||  ||| |||||||
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                                CGACC  GAC CGCCTGT
                                   CG   C
GAM2293  KIAA1388  3'  TAGCTGGATGTTGTCCAGA   54532        __  G
                                TAGCTGGAT  TGT CGGA
                                |||||||||  ||| ||||
                                ATCGACCTA  ACA GTCT
                                     CA   G
GAM2293  MGC4840   3'  TAGCTGGACTACAGGCGG    54533         T__
                                TAGCTGGATTG   GCGG
                                ||||||||||   ||||
                                ATCGACCTGAT   CGCC
                                      GTC
GAM2293  PRO1386   3'  AGCTGGGACTATGGGTGA    54534       _    C  AC
                                AGCTGG ATTGTG GG  GA
                                ||||||  ||||||  ||  ||
                                TCGACC TGATAC CC  CT
                                   C     _  A_
GAM2293  PSPH      3'  TAGCCGGATGTGGTGGCGG   54535        T__  _
                                TAGCTGGAT   GTG CGG
                                |||||||||   ||| |||
                                ATCGGCCTA   CAC GCC
                                     CAC   C
GAM2293  LOC129676 5'  GCTTTGTGCGGATGAGCA    54536     GGA       C  A
                                GCT   TTGTGCGGA GA CA
                                |||   ||||||||| || ||
                                CGA   AACACGCCT CT GT
                                  ___        A  C
GAM2293  LOC148418 3'  TAGCTGAATATGGATGGA    54537        T   C__
                                TAGCTGGAT GTG   GGA
                                |||||||||  |||   |||
                                ATCGACTTA TAC   CCT
                                     _  CTA
GAM2294  INMT      3'  CCTATTCCTTGACCAAAGCAC  54540    G    CC_  A
                                CC ATTCC   GC CGGAGCAC
                                ||  |||||   ||  ||||||||
                                GG TAAGG   TG GTTTCGTG
                                 A    AAC  _
GAM2294  SRGAP2    3'  GATTTCCCACAAAGCAC     54541     C     CG
                                GATT CCCGCA  GAGCAC
                                ||||  ||||||  ||||||
                                CTAA GGGTGT  TTCGTG
                                  A     __
GAM2294  ABLIM     3'  TAACCGATTTTTCCCATGCGG  54542        C__   CA
                                TAACCGATT   CCCG  CGG
                                |||||||||   ||||  |||
                                ATTGGCTAA   GGGT  GCC
                                     AAA    AC
GAM2294  ABLIM     3'  TAACCGATTTTTCCCATGCGG  54542        C__   CA
                                TAACCGATT   CCCG  CGG
                                |||||||||   ||||  |||
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                                ATTGGCTAA  GGGT  GCC
                                     AAA   AC
GAM2294  DKFZP434K1772 5'  CCGCACCGCACGGAGCAC   54543    ATTCC
                                CCG    CCGCACGGAGCAC
                                |||    ||||||||||||
                                GGC    GGCGTGCCTCGTG
                                  GT___
GAM2294  DKFZP566J2046 3'  TAACCGATTATGTACAGGAG  54544        CCCC  C
                                TAACCGATT   GCA GGAG
                                |||||||||   ||| ||||
                                ATTGGCTAA   TGT CCTC
                                     TACA  _
GAM2294  FLJ22344  5'  CAACAGCCCTGCACGGAGCAC  54545     TC  _
                                CGAT  CCC GCACGGAGCAC
                                ||||  ||| ||||||||||
                                GTTG  GGG CGTGCCTCGTG
                                  TC  A
GAM2294  SEC14L1   3'  GATCCCTGCACGGGGCA    54546    T  C    A
                                GAT CCC GCACGG GCA
                                ||| ||| |||||| |||
                                CTA GGG CGTGCC CGT
                                  _  A    C
GAM2294  LOC151174 5'  CGAGCCTCCCCGCACGGAGC  54547    __
                                CGA  TTCCCCGCACGGAGC
                                |||  ||||||||||||||
                                GCT  GAGGGGCGTGCCTCG
                                  CG
GAM2295  ALDH3B2   3'  CCCTGGCAGGCAGGATGCA   54550    C   TTAA
                                CCC GGCG   CGGGATGCA
                                ||| ||||   |||||||||
                                GGG CCGT   GTCCTACGT
                                  A   CC__
GAM2295  CHRM1    3'  CCCTGGGGCTGAGGATGCAGCC 54551    C  C   AAC      A
                                CCC GG GTT   GGGATGCA CC
                                ||| || |||   |||||||| ||
                                GGG CC CGA   TCCTACGT GG
                                  A  C   C__       C
GAM2295  CRHR2    3'  GGCGTTAACCCACCCAAC    54552        GGG  G
                                GGCGTTAAC   AT CAAC
                                |||||||||   || ||||
                                CCGCAATTG   TG GTTG
                                     GG_  G
GAM2295  LIMD1    3'  GGTGCTATGATGCAACC    54553    C   ACGG
                                GG GTTA   GATGCAACC
                                || ||||   |||||||||
                                CC CGAT   CTACGTTGG
                                 A   A___
GAM2295  PLA2G2D   3'  GGCACCAGGGATGCAAC    54554     TT AC
                                GGCG  A  GGGATGCAAC
                                ||||  |  ||||||||||
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                                CCGT  T  CCCTACGTTG
                                  GG __
GAM2295  FLJ20542  3'  CCTGGCGTGGCAAACACAACC  54555    C    TAAC __
                                CC GGCGT   GG  GATGCAACC
                                || |||||   ||  |||||||||
                                GG CCGCA   CC  TTGTGTTGG
                                 A    _____  GT
GAM2295  HSA249128 3'  CCCTGGGTTAACAGCAAC    54556    C  C     GGAT
                                CCC GG GTTAACG   GCAAC
                                ||| || |||||||   |||||
                                GGG CC CAATTGT   CGTTG
                                  A  _     _____
GAM2295  KIAA0161  3'  AGCCCTGGGGATGCAGCC    54557    G  AAC      A
                                GGC TT   GGGATGCA CC
                                ||| ||   |||||||| ||
                                TCG GA   CCCTACGT GG
                                  G  C__       C
GAM2295  KIAA0632  3'  CCTCGGTGTCAACAGCAGC   54558   _  C      GAT
                                CC CGG GTTAACGG   GC
                                || ||| ||||||||   ||
                                GG GCC CAGTTGTC   CG
                                 A  A       GT_
GAM2295  KLK15    3'  GGCATTAAACAGGTGACC    54559        _   A  CA
                                GGCGTTAA CGGG TG  ACC
                                |||||||| |||| ||  |||
                                CCGTAATT GTCC AC  TGG
                                     T   _ __
GAM2295  KLK15    3'  GGCATTAAACAGGTGACC    54559        _   A  CA
                                GGCGTTAA CGGG TG  ACC
                                |||||||| |||| ||  |||
                                CCGTAATT GTCC AC  TGG
                                     T   _ __
GAM2295  KLK15    3'  GGCATTAAACAGGTGACC    54559        _   A  CA
                                GGCGTTAA CGGG TG  ACC
                                |||||||| |||| ||  |||
                                CCGTAATT GTCC AC  TGG
                                     T   _ __
GAM2295  KLK15    3'  GGCATTAAACAGGTGACC    54559        _   A  CA
                                GGCGTTAA CGGG TG  ACC
                                |||||||| |||| ||  |||
                                CCGTAATT GTCC AC  TGG
                                     T   _ __
GAM2295  MAPK13   5'  CCCCGGCGTGGCGGCTGC    54560        TAA  GA
                                CCCCGGCGT   CGG  TGC
                                |||||||||   |||  |||
                                GGGGCCGCA   GCC  ACG
                                     CC_   G_
GAM2295  PTK9     5'  CCGGCGCTGAGTGCAC      54561        AAC  A   A
                                CCGGCGTT   GGG TGCA C
                                ||||||||   ||| |||| |
```

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                                GGCCGCGA  CTC ACGT G
                                   ___  _   C
GAM2295 TAF6L    5' CCCCGGCGTGGCGAAGGC   54562       TAAC _ T_
                                CCCCGGCGT   GG GA  GC
                                |||||||||   || ||  ||
                                GGGGCCGCA   CC CT  CG
                                    ____  G  TC
GAM2295 TCF17    5' CCGCCGGCCGGGATGCAC   54563   _   GTTAA      A
                                CC CCGGC    CGGGATGCA C
                                || |||||    ||||||||| |
                                GG GGCCG    GCCCTACGT G
                                 C    _____       C
GAM2295 LOC123876 5' GGCCTTAGACATCTGCAACC  54564    G  _  GGA
                                GGC TTA ACG  TGCAACC
                                ||| ||| |||  |||||||
                                CCG AAT TGT  ACGTTGG
                                  G  C  AG_
GAM2295 LOC148397 5' CCTGACGTTAACGGTTAACC  54565   C       GATGC
                                CC GGCGTTAACGG    AACC
                                || ||||||||||    ||||
                                GG CTGCAATTGCC    TTGG
                                 A        AA___
GAM2295 LOC204820 5' CCCCGGCGCTGGCAGCTGGC  54566        AA  GAT
                                CCCCGGCGTT  CGG  GC
                                |||||||||  |||  ||
                                GGGGCCGCGA  GTC  CG
                                     CC  GAC
GAM2295 LOC254381 5' CCCGGCGTTGGGTGTGC    54567       AAC  A  CAA
                                CCCGGCGTT  GGG TG  C
                                |||||||||  ||| ||  |
                                GGGCCGCAA  CCC AC  G
                                   ___  _ ACC
GAM2295 LOC91300  5' CCAGCGTTTCCATGGGGATGC 54568       AA ___
                                CCGGCGTT  C  GGGATGC
                                ||||||||  |  |||||||
                                GGTCGCAA  G  CCCTACG
                                    AG TAC
GAM2295 LOC91300  5' CCAGCGTTTCCATGGGGATGC 54568       AA ___
                                CCGGCGTT  C  GGGATGC
                                ||||||||  |  |||||||
                                GGTCGCAA  G  CCCTACG
                                    AG TAC
GAM2296 RUNX1    3' GCTATTAGCTGTTTACAAAAGT 54571   ATGA  A_
           G                     GC   AGC  TTTACAAAAGTG
                                ||   |||  ||||||||||||
                                CG   TCG  AAATGTTTTCAC
                                 ATAA  AC
GAM2296 ARHGAP11A 3' TGGCATGAACCCAGGAAGT   54572       AGC   CAA
                                TGGCATGA  ATTTA  AAGT
                                ||||||||  |||||  ||||
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                                ACCGTACT  TGGGT  TTCA
                                    ___    CC_
GAM2296 FLJ12788 3' TGACATGAAGGATAATGCAAGA 54573        C TTA_  A
          GTG                    TGGCATGAAG AT   CAA AGTG
                                |||||||||| ||   ||| ||||
                                ACTGTACTTC TA   GTT TCAC
                                    C TTAC  C
GAM2296 FOXO3A  3' TGGCGTGGGATTCACAAAGGTG 54574     A AAGC      A
                                TGGC TG   ATTTACAAA GTG
                                |||| ||   ||||||||| |||
                                ACCG AC   TAAGTGTTT CAC
                                  C CC__      C
GAM2296 ODC-p   3' GCATTATATTTACAAAGGTG  54575     GAAGC      A
                                GCAT    ATTTACAAA GTG
                                ||||    ||||||||| |||
                                CGTA    TAAATGTTT CAC
                                  ATA__      C
GAM2296 PPIB    3' TGGTAGGAGTTTGTTACAAAAG 54576    CAT AGCAT
          TG                    TGG  GA   TTACAAAAGTG
                                |||  ||   ||||||||||
                                ACC  CT   AATGTTTTCAC
                                 ATC CAAAC
GAM2296 SDFR1   3' GCTGTACTTTACAAAAGT   54577   A AA A
                                GC TG GC TTTACAAAAGT
                                || ||  || ||||||||||
                                CG AC  TG AAATGTTTTCA
                                 _ A_ _
GAM2296 SDFR1   3' GCTGTACTTTACAAAAGT   54577   A AA A
                                GC TG GC TTTACAAAAGT
                                || ||  || ||||||||||
                                CG AC  TG AAATGTTTTCA
                                 _ A_ _
GAM2296 LOC157695 3' GCATGAAACAGCACAGGAGTG 54578        TT   AA
                                GCATGAAGCA TACA AGTG
                                |||||||||| |||| ||||
                                CGTACTTTGT GTGT TCAC
                                    C_   CC
GAM2296 LOC200488 5' TGGTATGAAGCATTTCAA   54579    C       A
                                TGG ATGAAGCATTT CAA
                                ||| |||||||||| |||
                                ACC TACTTCGTAAA GTT
                                  A        _
GAM2296 LOC255338 5' TGGCATGAGTCATGACTCAAGT 54580       AG  TT  AA
          G                     TGGCATGA CAT AC AAGTG
                                |||||||| ||| || |||||
                                ACCGTACT GTA TG TTCAC
                                    CA  C_ AG
GAM2297 NT5M    5' CGCCGTGCTGCCGGAT     54583       C    III
                                TGCCGTGC GCCGGA  T
                                |||||||| ||||||  |
```

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                                GCGGCACG CGGCCT   A
                                    A     III
GAM2297 DCTD     3'  TATGCCATGCTTCACTTGG    54584          __  C_
                                TATGCCGTGC  CGC  GG
                                ||||||||||  |||  ||
                                ATACGGTACG  GTG  CC
                                     AA   AA
GAM2297 FLJ23375 5'  CATGCCGCCCGCCCGCCGG   54585         __  _
                                TATGCCGT  GCC GCCGG
                                ||||||||  ||| |||||
                                GTACGGCG  CGG CGGCC
                                    GG   G
GAM2297 KIAA1372 3'  TATACCGTACAGCAGTCGGA   54586          C ___
                                TATGCCGTGC GC   CGGA
                                |||||||||| ||   ||||
                                ATATGGCATG CG   GCCT
                                     T  TCA
GAM2297 LOC164714 5'  ATGCCATGGTGCGCCGGA    54587        C__
                                ATGCCGTG   CGCCGGA
                                ||||||||   |||||||
                                TACGGTAC   GCGGCCT
                                    CAC
GAM2298 AICDA    3'  CCCGGCCCTCTCTCTTTCTTTT 54590     T  G  GC   CC
           T                     CCCG CT TC  CTCT  CTTTTT
                                 |||| || ||  ||||  ||||||
                                 GGGC GG AG  GAGA  GAAAAA
                                   C  G  A_   AA
GAM2298 ANKRA2   5'  TGTCCCTCTCTCCTTTTT    54591     G    _
                                 TGTC CCTCTC CCTTTTT
                                 |||| |||||| |||||||
                                 ACAG GGAGAG GGAAAAA
                                   _     A
GAM2298 CDH2     3'  CCCTTTCTTTCCTTTCCTTTTT 54592    G_  GTCG  C  C
           T                     CCC  TCT   CCT TCC TTTTT
                                 |||  |||   ||| ||| |||||
                                 GGG  AGA   GGA AGG AAAAA
                                   AA   AA__   A   A
GAM2298 CDKN2C   5'  CCGGTTTCTTCTCCCTTTT   54593    TCTG  GCC
                                 CCG   TC   TCTCCCTTTT
                                 |||   ||   ||||||||||
                                 GGC   AG   AGAGGGAAAA
                                   CAA_  A__
GAM2298 GPR17    3'  CCCTTTGTCAGTTCTTCCTTTT 54594    GTC    CC   C
           T                     CCC   TGTCG  TCT CCTTTTT
                                 |||   |||||  ||| |||||||
                                 GGG   ACAGT  AGA GGAAAAA
                                   AA_    CA   A
GAM2298 HMGA2    3'  GTTTGCTTACTTCCCTTTTT   54595    C   CGC  C
                                 GT TGT   CT TCCCTTTTT
                                 || |||   || |||||||||
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                                CA ACG   GA AGGGAAAAA
                                 A   AAT  _
GAM2298  MAP1A    3'  GTGGCTCAGCTTCTCCCTTTTT 54596    CTG  _  C
                                GT   TC GC TCTCCCTTTTT
                                ||   || || ||||||||||
                                CA   AG CG AGAGGGAAAAA
                                 CCG  T  A
GAM2298  RAB13    3'  CCCTTCCTCTCTCTTCCTTTTT 54597     G   G  GC    C
                                CCC TCT TC  CTCT CCTTTTT
                                ||| ||| ||  |||| |||||||
                                GGG AGG AG  GAGA GGAAAAA
                                 A   _  A_   A
GAM2298  RNF3     5'  CCCGTTTTTTGGGCCCCCCTTT 54598       CTGTC__   T T
            TT                   CCCGT      GCC C CCCTTTTT
                                |||||      ||| | ||||||||
                                GGGCA      CGG G GGGAAAAA
                                   AAAAACC  _ _
GAM2298  SOX4     3'  CGTCTGTCCTTTTCGTTTCTTT 54599         GCC_  TCC_
            TT                   CGTCTGTC   TC   CTTTTT
                                |||||||   ||   ||||||
                                GCAGACAG   AG   GAAAAA
                                    GAAA  CAAA
GAM2298  TEX15    3'  GCTTGACCTTCCCTTTTT    54600    TC  TC    C
                                G  TG  GCCT TCCCTTTTT
                                |  ||  |||| |||||||||
                                C  AC  TGGA AGGGAAAAA
                                 GA  __   _
GAM2298  ABCC13   3'  GTCCCCGCCCTCTCTTTTT   54601     G    T   C
                                GTCT TCGCC CTC CTTTTT
                                |||| ||||| ||| ||||||
                                CAGG GGCGG GAG GAAAAA
                                   _    _   A
GAM2298  ARPC1B   3'  CCCATCTGTCCCCTCCCTTTTT 54602          G  T
                                CCCGTCTGTC CC CTCCCTTTTT
                                |||||||||| || ||||||||||
                                GGGTAGACAG GG GAGGGAAAAA
                                      _ _
GAM2298  FHR5     3'  TCTGTCTCTCTCTCTCTTT   54603       GC    C
                                TCTGTC  CTCTC CTTTTT
                                ||||||  ||||| ||||||
                                AGACAG  GAGAG GAGAAA
                                   A_    A
GAM2298  FLJ13102 3'  GTCTCTCCCACCCCTTTTT   54604     G  G  T T
                                GTCT TC CC C CCCTTTTT
                                |||| || || | ||||||||
                                CAGA AG GG G GGGAAAAA
                                  G  _  T _
GAM2298  KIAA0268 3'  TCTGTTGTGCACCCTTTTT   54605      C__  CTCT
                                TCTGT   GC    CCCTTTTT
                                |||||   ||    ||||||||
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                                AGACA  CG   GGGAAAAA
                                  ACA  T___
GAM2298 KIAA1210 3' CCTCTTTCTCACTCTCCCTTTT 54606   G  G  GC_
          T                    CC TCT TC  CTCTCCCTTTTT
                               || ||| ||  ||||||||||||
                               GG AGA AG  GAGAGGGAAAAA
                                _  A  AGT
GAM2298 KIAA1828 5' CCCGTCTGTCAGCCCCTTTTCT 54607        _    CC_
          TTTT                   CCCGTCTGTC GCCTCT  CTTTTT
                               |||||||||| ||||||  ||||||
                               GGGCAGACAG CGGGGA  GAAAAA
                                     T    AAA
GAM2298 MAP3K2   3' TCTCCCCCATCTCTCTTTTT  54608    G  G  _  C
                               TCT TC CC TCTC CTTTTT
                               ||| || || |||| ||||||
                               AGA GG GG AGAG GAAAAA
                                 G  _  T   A
GAM2298 PRO1496  3' TCCCTCTCTCTCTCTTTTT   54609    G  GC   C
                               TCT TC  CTCTC CTTTTT
                               ||| ||  ||||| ||||||
                               AGG AG  GAGAG GAAAAA
                                 G  A_    A
GAM2298 PRO2214  5' CCCCTCAAGCTTTCCCTTTTT  54610    G  TGTC  CTC
                               CCC TC   GC   TCCCTTTTT
                               ||| ||   ||   |||||||||
                               GGG AG   CG   AGGGAAAAA
                                 G  TT__  AA_
GAM2298 RASAL2   5' CCTGCTCTCTCCCTTTTT   54611     CGC
                               TCTGT  CTCTCCCTTTTT
                               |||||  ||||||||||||
                               GGACG  GAGAGGGAAAAA
                                  A__
GAM2298 SEMA4G   5' CCGTCTGGTTGTTTTTCCCTTT 54612       TCGCCTC_
          TT                   CCGTCTG      TCCCTTTTT
                               |||||||      |||||||||
                               GGCAGAC      AGGGAAAAA
                                   CAACAAAA
GAM2298 TPD52    3' TCTATCACTTTTCCCTTTTT  54613       CTC
                               TCTGTCGC  TCCCTTTTT
                               ||||||||  |||||||||
                               AGATAGTG  AGGGAAAAA
                                    AAA
GAM2298 LOC150213 3' CCTGTTCCCCCCCTTTTT   54614     CG   T
                               TCTGT  CCTC CCCTTTTT
                               |||||  |||| ||||||||
                               GGACA  GGGG GGGAAAAA
                                  A_   _
GAM2298 LOC152273 3' TGTCAGCAAATTCCCTTTTT  54615    _  CTC_
                               TGTC GC   TCCCTTTTT
                               |||| ||   |||||||||
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                                ACAG CG    AGGGAAAAA
                                  T  TTTA
GAM2298  LOC164312 3'  CCGTCTGTGTCTTCCTTTTT   54616        CGCC   C
                                CCGTCTGT    TCT CCTTTTT
                                ||||||||    ||| |||||||
                                GGCAGACA    AGA GGAAAAA
                                    C___   A
GAM2298  LOC206324 5'  CCAGCATCGGCTTTTCCCTTTT 54617    C  CT    C  C_
           T                     CC GT  GTCG CT  TCCCTTTTT
                                || ||  |||| ||  |||||||||
                                GG CG  TAGC GA  AGGGAAAAA
                                 T  __    C  AA
GAM2298  LOC220739 3'  CCGCCAGGGCCTCTCCTTTTTT 54618      TGTC       C
                                CCGTC    GCCTCTCC TTTTT
                                |||||    |||||||| |||||
                                GGCGG    CGGAGAGG AAAAA
                                   TCC_       A
GAM2298  LOC221756 3'  CCCGTCTGTCTCCTTTCC    54619         G   C
                                CCCGTCTGTC CCT TCC
                                |||||||||| ||| |||
                                GGGCAGACAG GGA AGG
                                     A   A
GAM2298  LOC257486 3'  CCTCTTTCTCACTCTCCCTTTT 54606    G   G  GC_
           T                     CC TCT TC   CTCTCCCTTTTT
                                || ||| ||   ||||||||||||
                                GG AGA AG   GAGAGGGAAAAA
                                 _   A  AGT
GAM2298  LOC90538  3'  TCTGTTTTCCCCTTTCTTTTT  54620      CG_    CC
                                TCTGT   CCTCT  CTTTTT
                                |||||   |||||  ||||||
                                AGACA   GGGGA  GAAAAA
                                   AAA     AA
GAM2299  CPSF6     3'  TAGCATGAATCAATACGGTGCA 54623        _     AT  CAC
                                TAGCATGA TCAATG  GT   GCA
                                |||||||| ||||||  ||   |||
                                ATCGTACT AGTTAT  CA   CGT
                                     T     GC  ___
GAM2299  TACC1     3'  GCATGATCATGGCTCACTGCA  54624         A  ATG   _
                                GCATGATCA TG   TCAC GCA
                                |||||||||  ||   |||| |||
                                CGTACTAGT AC   AGTG CGT
                                     _  CG_    A
GAM2299  ZNF216    3'  TAGCATGATTATGTGC      54625         CA   A
                                TAGCATGAT  ATG TGT
                                |||||||||  ||| |||
                                ATCGTACTA  TAC ACG
                                     A_   _
GAM2299  AAK1      3'  GCATGATCAGGGCTCACTGCA  54626         ATGATG   _
                                GCATGATCA     TCAC GCA
                                |||||||||     |||| |||
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                                CGTACTAGT     AGTG CGT
                                     CCCG__    A
GAM2299 CYorf14   3'  GCATGATCATGGCTCACTGCA 54624        A  ATG   _
                                GCATGATCA TG   TCAC GCA
                                ||||||||| ||   |||| |||
                                CGTACTAGT AC   AGTG CGT
                                     _ CG_    A
GAM2299 DNAJC6    3'  TAGCATAATCAAAATCATGT   54627          __ G
                                TAGCATGATCA  AT ATGT
                                ||||||||||  || ||||
                                ATCGTATTAGT  TA TACA
                                      TT  G
GAM2299 FLJ12666  3'  GCATGATCTGTGCTCACTGCA  54628        AA  A  _   _
                                GCATGATC  TG TG TCAC GCA
                                ||||||||  || || |||| |||
                                CGTACTAG  AC AC AGTG CGT
                                     __ _ G    A
GAM2299 HUMAGCGB  5'  ACGTGATCAATGGTCCG     54629    A       AT   A
                                GC TGATCAATG  GTC CG
                                || |||||||||  ||| ||
                                TG ACTAGTTAC  CAG GC
                                 C       __   _
GAM2299 KIAA0433  3'  TAGTGTGATCAACTGATACA   54630     CA      _    T
                                TAG  TGATCAA TGATG CA
                                |||  ||||||| ||||| ||
                                ATC  ACTAGTT ACTAT GT
                                  AC      G    _
GAM2299 NRN1      3'  TAGCATGATTAATAT       54631          CAA
                                TAGCATGAT   TGATGT
                                |||||||||   ||||||
                                ATCGTACTA   ATTATA
                                     ___
GAM2299 PP5395    3'  TAGCATGAGTGGTGAAATGCTG 54632        TCAAT__    CAC
              CA                   TAGCATGA      GATGT   GCA
                                |||||||       |||||   |||
                                ATCGTACT      TTACG   CGT
                                     CACCACT     A__
GAM2299 LOC150933 3'  TAGATGATCAATGTGT      54633     C        A
                                TAG ATGATCAATG TGT
                                ||| |||||||||| |||
                                ATC TACTAGTTAC ACA
                                  _        _
GAM2299 LOC196337 3'  ACCCTAACAGTGATGTCA    54634    A_   T  A
                                GC  TGA CA TGATGTCA
                                ||  ||| || ||||||||
                                TG  ATT GT ACTACAGT
                                 GG   _  C
GAM2300 P2RY12    3'  TCAGTTAATATTTTTACT    54637          CC
                                TTAGTTAATA  TTTACT
                                ||||||||||  ||||||
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                                AGTCAATTAT  AAATGA
                                     AA
GAM2300  FLJ10244  3'  TAATACATGTTAGTACCTTTAC 54638       TTA   A
              T                   TAATAC   GTTA TACCTTTACT
                                  ||||||   |||| ||||||||||
                                  ATTATG   CAAT ATGGAAATGA
                                     TA_   C
GAM2300  FLJ11011  3'  TACTCATACCTTTACT     54639      AGTTA
                                  TACTT    ATACCTTTACT
                                  |||||    ||||||||||
                                  ATGAG    TATGGAAATGA
                                    _____
GAM2300  LOC56267  3'  TTAGGGACACCTTTACT     54640      TTA
                                  TTAG   ATACCTTTACT
                                  ||||   ||||||||||
                                  AATC   TGTGGAAATGA
                                    CC_
GAM2301  EGR3     3'  CGCGCGTGCGTGCGGCGG    54643    A A   C
                                  CG GC TGCG GCGGCGG
                                  || || |||| |||||||
                                  GC CG ACGC CGCCGCC
                                   G  C   A
GAM2301  LASS1    3'  CGGGCAGCGCGCACTGACCCT  54644    A  T     G G
                                  CG GCA GCGCGCG C GACCCT
                                  || ||| ||||||| | ||||||
                                  GC CGT CGCGCGT G CTGGGA
                                   C  _     _ A
GAM2301  NEURL    5'  CGAGTGTGCGCGCGCGG     54645     CA      G
                                  CGAG  TGCGCGCG CGG
                                  ||||  |||||||| |||
                                  GCTC  ACGCGCGC GCC
                                    AC      _
GAM2301  PPP1R3C  5'  GCAGAGAGGCGGCGGACCCTA  54646     TGCGC
                                  GCA    GCGGCGGACCCTA
                                  |||    ||||||||||||
                                  CGT    CGCCGCCTGGGAT
                                    CTCTC
GAM2301  ABHD3    5'  CGAGCGCGGCGCGCGGGTCCT  54647      AT  C  _   AC
                                  CGAGC  GCG GCG GCGG  CCT
                                  |||||  ||| ||| ||||  |||
                                  GCTCG  CGC CGC CGCC  GGA
                                     __  _  G   CA
GAM2301  CLSTN1   5'  CGAGGCGCGCGCGCGGCGGACC 54648     _ A
              CT                   CGAG C TGCGCGCGGCGGACCCT
                                   |||| | |||||||||||||||||
                                   GCTC G GCGCGCGCCGCCTGGGA
                                     C C
GAM2301  FLJ11280 5'  GCATGCGCTCCGGGCCCTA   54649       GCGG   A
                                  GCATGCGC    CGG CCCTA
                                  ||||||||    ||| |||||
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                                CGTACGCG   GCC GGGAT
                                    AG__   C
GAM2301  FLJ20514  5'  GCGCGCAGCTTGCGGATCCT   54650        ____   C
                                GCGCGCGGC   GGA CCT
                                |||||||||   ||| |||
                                CGCGCGTCG   CCT GGA
                                     AACG   A
GAM2301  SLC26A1   3'  CGGGCAGCGCCTGGATCCT   54651   A  T   GCGGC  C
                                CG GCA GCGC    GGA CCT
                                || ||| ||||    ||| |||
                                GC CGT CGCG    CCT GGA
                                 C  _   GA___  A
GAM2301  SLIT1     5'  CGGGCTTGCGCGCGGCGCCCCT 54652   A  A       GA
                                CG GC TGCGCGCGGCG  CCCT
                                || || ||||||||||  ||||
                                GC CG ACGCGCGCCGC  GGGA
                                 C  A        G_
GAM2301  STX1B2    3'  CGAGCATGTGCCGGCGG    54653       C  G
                                CGAGCATG GC CGGCGG
                                |||||||| || ||||||
                                GCTCGTAC CG GCCGCC
                                    A  _
GAM2301  LOC146506 3'  GAGCATGCAGTGGCACAGGG   54654       ____    C
                                GAGCATGC   GCGCGG GG
                                ||||||||   |||||| ||
                                CTCGTACG   CGTGTC CC
                                    TCAC    _
GAM2301  LOC221302 5'  CGAGTGCGTGCGCGGCGTCC   54655    CA  C     GA
                                CGAG  TG GCGCGGCG  CC
                                ||||  || ||||||||  ||
                                GCTC  GC CGCGCCGC  GG
                                  AC  A      A_
GAM2302  DDEF2     3'  TACCCTACGTTGTCATAA    54658     CAGAC  TG
                                TACCC    CGT  TGTTATAA
                                |||||    |||  ||||||||
                                ATGGG    GCA  ACAGTATT
                                   AT___  __
GAM2302  MYO10     3'  CAGACCACCATTATAAA     54659       TT  GT
                                CAGACCG  GT  TATAAA
                                |||||||  ||  ||||||
                                GTCTGGT  TA  ATATTT
                                    GG  __
GAM2302  SFRS7     3'  CAGGCTGTATCATAA      54660    ACC
                                CAG   GTTGTGTTATAA
                                |||   ||||||||||||
                                GTC   CGACATAGTATT
                                  ___
GAM2302  SOCS4     5'  CCAGATTCTAATGTTATAAA  54661      CCGTT
                                CCAGA    GTGTTATAAA
                                |||||    ||||||||||
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                                GGTCT    TACAATATTT
                                  AAGAT
GAM2302 AKR1D1   3' CCAGAGGTCAGTGTTATAA   54662      CC  _
                                CCAGA  GTT GTGTTATAA
                                |||||  ||| |||||||||
                                GGTCT  CAG CACAATATT
                                  C_   T
GAM2302 DKFZP434A043 5' TACATCAGACCACTTTATG   54663    CC     __
                                TAC  CAGACCG  TTGTG
                                |||  |||||||  |||||
                                ATG  GTCTGGT  AATAC
                                  TA      GA
GAM2302 DKFZP434N1817 5' TACTCCAGGTTGTGTTA    54664    C   ACC
                                TAC CCAG   GTTGTGTTA
                                ||| ||||   |||||||||
                                ATG GGTC   CAACACAAT
                                  A   ___
GAM2302 GIT2     3'  TACCCCAAACTTAGAGATTATG 54665         C_____
                                TACCCCAGAC     GTTGTG
                                ||||||||||     ||||||
                                ATGGGGTTTG     TAATAC
                                     AATCTC
GAM2302 GIT2     3'  TACCCCAAACTTAGAGATTATG 54665         C_____
                                TACCCCAGAC     GTTGTG
                                ||||||||||     ||||||
                                ATGGGGTTTG     TAATAC
                                     AATCTC
GAM2302 GIT2     3'  TACCCCAAACTTAGAGATTATG 54665         C_____
                                TACCCCAGAC     GTTGTG
                                ||||||||||     ||||||
                                ATGGGGTTTG     TAATAC
                                     AATCTC
GAM2302 LOC255714 5' CCCTGGGACAGTTGTTATAA   54666    CA_  C    GT
                                CCC   GAC GTTGT  TATAA
                                |||   ||| |||||  |||||
                                GGG   CTG CAACA  ATATT
                                  ACC   T    __
GAM2302 LOC51611  3'  TACCCGAGACTGGGTAATTATA 54667      C   CGTTGT
          AA                    TACCC AGAC     GTTATAAA
                                |||||| ||||     ||||||||
                                ATGGG TCTG     TAATATTT
                                  C    ACCCAT
GAM2303 DSP      3'  TAAAAGTTTATTGCCAGAATAG 54670         _      TC_
                                TAAAAGTTT TTGCCAG   AG
                                |||||||||| |||||||   ||
                                ATTTTCAAA AACGGTC   TC
                                     T      TTA
GAM2303 KCNE1L   3'  AGCAGCTGCCAGTTAGAC    54671     TT       C
                                AGT  TTGCCAGT AGAC
                                |||  |||||||| ||||
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                                TCG  GACGGTCA TCTG
                                  TC       A
GAM2303  MAGEA4   5'  AAGCTGCTGGTCAGACA     54672      TTT   CA
                                AAGT   TGC  GTCAGACA
                                ||||   |||  ||||||||
                                TTCG   ACG  CAGTCTGT
                                  ___   AC
GAM2303  MBNL     3'  AGTTTTTGTCAGTCATGA     54673        C     _
                                AGTTTTTG CAGTCA GA
                                |||||||| |||||| ||
                                TCAAAAAC GTCAGT CT
                                     A     A
GAM2303  TERF2    3'  TTTTTGCTAAAAAGACAG     54674       C  TC
                                TTTTTGC AG  AGACAG
                                ||||||| ||  ||||||
                                AAAAACG TT  TCTGTC
                                    A  TT
GAM2303  USP6     3'  AAAGTTCTCTATCAGACAG    54675         GCCA
                                AAAGTTTTT    GTCAGACAG
                                |||||||||    |||||||||
                                TTTCAAGAG    TAGTCTGTC
                                     A___
GAM2303  FLJ10901 3'  AGAGGCTGTCAGTCAGACAG   54676    TTT   C
                                AG   TTG CAGTCAGACAG
                                ||   ||| ||||||||||
                                TC   GAC GTCAGTCTGTC
                                 TCC   A
GAM2303  FLJ20051 3'  TAAAAGTTTTGTGCTGCTCAG  54677          _   CAG
                                TAAAAGTTTT TGC   TCAG
                                |||||||||| |||   ||||
                                ATTTTCAAAA ACG   AGTC
                                      C   ACG
GAM2303  HCA127   3'  TAAAATTTTTTGTCAGTCAG   54678      G     C
                                TAAAA TTTTTG CAGTCAG
                                ||||| |||||| |||||||
                                ATTTT AAAAAC GTCAGTC
                                   A     A
GAM2303  KIAA0625 3'  AAAGCTTTTGCAAATGACAG   54679          C   CA
                                AAAGTTTTTGC AGT  GACAG
                                |||||||||| |||  |||||
                                TTTCGAAAACG TTA  CTGTC
                                      T   __
GAM2303  KIAA0677 5'  GTCCCTTTAGTCAGACAG    54680       GCC
                                GTTTTT   AGTCAGACAG
                                ||||||   ||||||||||
                                CAGGGA   TCAGTCTGTC
                                   AA_
GAM2303  KIAA1405 3'  AAGTGGGGCCAGTCAGACAG   54681      TTTT
                                AAGT    GCCAGTCAGACAG
                                ||||    ||||||||||||
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                                TTCA   CGGTCAGTCTGTC
                                  CCC_
GAM2303 KIAA1948 3' AAAGTTTTTTGGTAGAGACAG 54682        GCCAGTC
                                AAAGTTTTT      AGACAG
                                |||||||||      ||||||
                                TTTCAAAAA      TCTGTC
                                    ACCATC_
GAM2303 LOC118851 3' AGTTTTGCCAGCCACAC     54683       T      G
                                AGTTTT GCCAGTCA AC
                                |||||| |||||||| ||
                                TCAAAA CGGTCGGT TG
                                   _       G
GAM2303 LOC132671 3' AAGTAGTTTTGGTCAGACAG   54684      __    CCA
                                AAGT  TTTTG   GTCAGACAG
                                ||||  |||||   |||||||||
                                TTCA  AAAAC   CAGTCTGTC
                                  TC    ____
GAM2303 LOC155036 5' GGAAGCCAGCGGCCAGTCAGGC 54685    A    TTT_       A
          AG                      A AAGTT    GCCAGTCAG CAG
                                | |||||    ||||||||| |||
                                C TTCGG    CGGTCAGTC GTC
                                 C     TCGC       C
GAM2303 LOC221814 5' TAAAAGTTTTTGTTGTC     54686          CCA
                                TAAAAGTTTTTG   GTC
                                ||||||||||||   |||
                                ATTTTCAAAAAC   CAG
                                     AA_
GAM2303 LOC245771 5' AGAGGCTGTCAGTCAGACAG   54676    TTT   C
                                AG   TTG CAGTCAGACAG
                                ||   ||| ||||||||||||
                                TC   GAC GTCAGTCTGTC
                                 TCC   A
GAM2304 CRYGA    5' ATAGGGACAAAGGGGCAAC    54689          AT
                                ATAGGGATAAAGG  TAAT
                                ||||||||||||  ||||
                                TATCCCTGTTTCC  GTTG
                                       CC
GAM2304 CRYGA    5' ATAGGGACAAAGGGGCAAC    54689          AT
                                ATAGGGATAAAGG  TAAT
                                ||||||||||||  ||||
                                TATCCCTGTTTCC  GTTG
                                       CC
GAM2304 MTAP     3' TAATAGGGGGAGAAGAGAATG  54690       ATAA   TT
                                TAATAGGG   AGGA  AATG
                                ||||||||   ||||  ||||
                                ATTATCCC   TTCT  TTAC
                                    CCTC   C_
GAM2304 LOC121457 3' TAATAGGTGAAATTAATGA   54691       _  TAAAG
                                TAATAGG GA    GATTAATGA
                                ||||||| ||    |||||||||
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                                ATTATCC CT     TTAATTACT
                                   A _____
GAM2304 LOC90777 3' AGACCCTGAGGATTAATGAT  54692      AA__
                                GGAT    AGGATTAATGAT
                                ||||    ||||||||||||
                                TCTG    TCCTAATTACTA
                                  GGAC
GAM2305 DKFZP434G072 3' ACAGGTATTTTTAGAT      54695      TCTTA
                                ACGG    GTATTTTTAGAT
                                ||||    ||||||||||||
                                TGTC    CATAAAAATCTA
                                  _____
GAM2305 MGC4342  3' TTCACAGATATTTTTAG     54696        TCTTA
                                TTCACGG    GTATTTTTAG
                                |||||||    ||||||||||
                                AAGTGTC    TATAAAAATC
                                  _____
GAM2306 ABHD3    3' TGGTTAAGTGCAATTTC     54699        TA  GCTA
                                TGGTTA  TG    CAATTTC
                                ||||||  ||    |||||||
                                ACCAAT  AC    GTTAAAG
                                   TC  ____
GAM2306 DKFZp761N0624 3' GTGTGAAATGGTTGCAATTTCA 54700     GTTAT    CTA
                                GTG    ATGG   CAATTTCA
                                |||    ||||   ||||||||
                                CAC    TACC   GTTAAAGT
                                  ACTT_   AAC
GAM2306 SH2D3A   3' GCTGTATGGCTATGATTT    54701     A       CA
                                GTT TATGGCTA  ATTT
                                ||| ||||||||  ||||
                                CGA ATACCGAT  TAAA
                                  C       AC
GAM2306 LOC158310 5' TGTGGTTGCAGAGTCAATTTCA 54702         A  T  CTA
                                TGTGGTT TA GG   CAATTTCA
                                ||||||| || ||   ||||||||
                                ACACCAA GT TC   GTTAAAGT
                                   C  C  A__
GAM2307 BCL2     3' CATTGCTTCTAACATGTTTTTA 54705      AATAA_
            A                    CATT     AACATGTTTTTAA
                                ||||     ||||||||||||||
                                GTAA     TTGTACAAAAATT
                                  CGAAGA
GAM2307 DIAPH2   3' TACATTGACAAAACAGGCT   54706       A       T
                                TACATT ATAAAACA GTT
                                |||||| |||||||| |||
                                ATGTAA TGTTTTGT CGA
                                   C       C
GAM2307 NPDC1    3' CACAGCATCAAAACATGTTTTT 54707      T  A
            A                    TACA TA TAAAACATGTTTTTA
                                |||| || ||||||||||||||||
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                                GTGT GT GTTTTGTACAAAAAT
                                  C  A
GAM2307  WHSC1    3'  TACATTAACAAAGTCTGTTTT  54708          ACA
                                TACATTAATAAA   TGTTTT
                                ||||||||||||   ||||||
                                ATGTAATTGTTT   ACAAAA
                                       CAG
GAM2307  IFI44    3'  ACATTAATAAAACACATCCCT  54709
                                ACATTAATAAAACATGTTTTT
                                ||||||||||||||||||||
                                TGTAATTATTTTGTGTAGGGA

GAM2307  KIAA1253 3'  CACATTAATAAATATTTTTAA  54710          AAC
                                TACATTAATAA   ATGTTTTTAA
                                ||||||||||||   ||||||||||
                                GTGTAATTATT   TATAAAAATT
                                       ___
GAM2307  KIAA1644 3'  ACATTGATAAGACATGTTCCCA 54711       A    A
              A                  ACATT ATAA ACATGTTTTTAA
                                ||||| |||| ||||||||||||
                                TGTAA TATT TGTACAAGGGTT
                                  C    C
GAM2307  PHF3     3'  ATTAATAAAACAAATCTTT    54712           T
                                ATTAATAAAACA GTTTTT
                                ||||||||||||| ||||||
                                TAATTATTTTGT TAGAAA
                                       T
GAM2307  SCDGF-B  3'  TACATTAATAAAATGTGATTTT 54713           CA  _
              T                  TACATTAATAAAA  TG TTTTT
                                ||||||||||||||  || |||||
                                ATGTAATTATTTT  AC AAAAA
                                       AC  T
GAM2307  SCDGF-B  3'  TACATTAATAAAATGTGATTTT 54713           CA  _
              T                  TACATTAATAAAA  TG TTTTT
                                ||||||||||||||  || |||||
                                ATGTAATTATTTT  AC AAAAA
                                       AC  T
GAM2307  STRIN    3'  TACATTAGTGAAACATCTTTTT 54714        ATA     G
                                TACATTA   AAACAT TTTTT
                                |||||||   |||||| |||||
                                ATGTAAT   TTTGTA AAAAA
                                    CAC     G
GAM2307  XRN2     3'  TACATTAATGAAATGTTTCCAA 54715         A  AC
                                TACATTAAT AA  ATGTTTTTAA
                                |||||||||  ||  ||||||||||
                                ATGTAATTA TT  TACAAAGGTT
                                       C  __
GAM2307  LOC151188 3'  TACATTAAAAAAACACAT    54716         T
                                TACATTAA AAAACATGT
                                ||||||||  |||||||||
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                                ATGTAATT TTTTGTGTA
                                     T
GAM2307  LOC199858 3'  TACATTCACAAACATGTTTTTA 54717       AATA
                                TACATT    AAACATGTTTTTA
                                ||||||    ||||||||||||
                                ATGTAA    TTTGTACAAAAAT
                                   GTG_
GAM2307  LOC84549  3'  TACATTAACACAGTTTTTA    54718        AAA   T
                                TACATTAAT   ACA GTTTTTA
                                |||||||||   ||| |||||||
                                ATGTAATTG   TGT CAAAAAT
                                      ___   _
GAM2308  CNTFR     3'  GTGGGTGGGTTAGCTGCA    54721      C       GG
                                GTGGG GGGTTAGT  GCG
                                ||||| ||||||||  |||
                                CACCC CCCAATCG  CGT
                                   A       A_
GAM2308  PPT2      3'  GTGGGCAGGGGGGTGGG      54722        TTAGT   C
                                GTGGGCGGG    GGG GGG
                                |||||||||    ||| |||
                                CACCCGTCC    CCC CCC
                                     _____   A
GAM2308  PPT2      3'  GTGGGCAGGGGGGTGGG      54722        TTAGT   C
                                GTGGGCGGG    GGG GGG
                                |||||||||    ||| |||
                                CACCCGTCC    CCC CCC
                                     _____   A
GAM2308  RANBP3    3'  GGGCGGGTGGGCGGG       54723        TAGT
                                GGGCGGGT   GGGCGGG
                                ||||||||   |||||||
                                CCCGCCCA   CCCGCCC
                                     ____
GAM2308  RANBP3    3'  GGGCGGGTGGGCGGG       54723        TAGT
                                GGGCGGGT   GGGCGGG
                                ||||||||   |||||||
                                CCCGCCCA   CCCGCCC
                                     ____
GAM2308  RANBP3    3'  GGGCGGGTGGGCGGG       54723        TAGT
                                GGGCGGGT   GGGCGGG
                                ||||||||   |||||||
                                CCCGCCCA   CCCGCCC
                                     ____
GAM2308  CX46.6    5'  TAGGGGCGGGCGGGCGGG    54724     T       TAGT
                                TAG GGGCGGGT   GGGCGGG
                                |||  ||||||||   |||||||
                                ATC CCCGCCCG   CCCGCCC
                                  _     ____
GAM2308  FLJ11467  3'  GTGGGGGGAGGGCGGG      54725       C   TTAGT
                                GTGGG GGG    GGGCGGG
                                ||||| |||    |||||||
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                                CACCC CCC    CCCGCCC
                                  _  T____
GAM2308  FLJ22215  5'  TAGTGGCGGTGGGCGG     54726      G  GTTAG
                                TAGTGG CGG    TGGGCGG
                                |||||| |||    |||||||
                                ATCACC GCC    ACCCGCC
                                  _  _____
GAM2308  FLJ22215  3'  TAGTGGCGGTGGGCGG     54726      G  GTTAG
                                TAGTGG CGG    TGGGCGG
                                |||||| |||    |||||||
                                ATCACC GCC    ACCCGCC
                                  _  _____
GAM2308  TIGD5     5'  GTGGCGCAGGCTGGGCGGGT  54727     _    TAG
                                GTGG GCGGGT   TGGGCGGGT
                                |||| ||||||   |||||||||
                                CACC CGTCCG   ACCCGCCCA
                                  G    ___
GAM2308  LOC157958 5'  TGGGGGGTGGCGGGCGGG    54728     C   TA
                                TGGG GGGT  GTGGGCGGG
                                |||| ||||  |||||||||
                                ACCC CCCA  CGCCCGCCC
                                  _   C_
GAM2309  CACNG3    5'  CCCCCGTTCCTTCCCGGGT    54731       G__  ACTAC A
                                CCCCCGTTC   CCC    G GGT
                                |||||||||   |||    | |||
                                GGGGGCAAG   GGG    C CCA
                                    GAA  _____ _
GAM2309  FGFR1     5'  CCCGTCCGCCACCCGGGGTC   54732       C  A  A
                                CCCGTTCGCC ACT CG GGTC
                                |||||||||| ||| || ||||
                                GGGCAGGCGG TGG GC CCAG
                                    _  _  C
GAM2309  FGFR1     5'  CCCGTCCGCCACCCGGGGTC   54732       C  A  A
                                CCCGTTCGCC ACT CG GGTC
                                |||||||||| ||| || ||||
                                GGGCAGGCGG TGG GC CCAG
                                    _  _  C
GAM2309  FGFR1     5'  CCCGTCCGCCACCCGGGGTC   54732       C  A  A
                                CCCGTTCGCC ACT CG GGTC
                                |||||||||| ||| || ||||
                                GGGCAGGCGG TGG GC CCAG
                                    _  _  C
GAM2309  FGFR1     5'  CCCGTCCGCCACCCGGGGTC   54732       C  A  A
                                CCCGTTCGCC ACT CG GGTC
                                |||||||||| ||| || ||||
                                GGGCAGGCGG TGG GC CCAG
                                    _  _  C
GAM2309  FGFR1     5'  CCCGTCCGCCACCCGGGGTC   54732       C  A  A
                                CCCGTTCGCC ACT CG GGTC
                                |||||||||| ||| || ||||
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                                GGGCAGGCGG TGG GC CCAG
                                      _  _  C
GAM2309  FGFR1    5'  CCCGTCCGCCACCCGGGGTC  54732        C  A  A
                                CCCGTTCGCC ACT CG GGTC
                                |||||||||| ||| || ||||
                                GGGCAGGCGG TGG GC CCAG
                                      _  _  C
GAM2309  PAFAH1B1 5'  CCTCCGCTCGCTCACTCG    54733   _     C   A
                                CC CCGTTCGC CACT CG
                                || |||||||| |||| ||
                                GG GGCGAGCG GTGA GC
                                 A      A   _
GAM2309  PCDH7    3'  CCCTTTGTTCACACAAAGTC  54734    CC_    CCACT
                                CCC  GTTCGC    ACGAGGTC
                                |||  ||||||    ||||||||
                                GGG  CAAGTG    TGTTTCAG
                                  AAA    _____
GAM2309  TEAD2    3'  CAGACACCCACTGTGAGGTC  54735    TT      AC
                                CG  CGCCCACT  GAGGTC
                                ||  ||||||||  ||||||
                                GT  GTGGGTGA  CTCCAG
                                 CT       CA
GAM2309  TFAP2C   3'  CCCCCGTTTGAACACGGGGT  54736       CGCCC  T   A
                                CCCCCGTT    AC ACG GGT
                                ||||||||    || ||| |||
                                GGGGGCAA    TG TGC CCA
                                     ACT__  _   C
GAM2309  ARHGAP11A 5'  CCCTCGTTCGCCACCAAGT   54737    _      CACT  G
                                CCC CGTTCGCC    AC AGGT
                                ||| ||||||||    || ||||
                                GGG GCAAGCGG    TG TTCA
                                  A       ____  G
GAM2309  FLJ10408 3'  CCCCCGTTTCCTATTGACGTC  54738       CG  CACTAC  G
                                CCCCCGTT  CC     GA GTC
                                ||||||||  ||     || |||
                                GGGGGCAA  GG     CT CAG
                                     A_  ATAA__  G
GAM2309  FLJ20445 5'  CCCGTCCGTCGGCCCGAGGT   54739    __    C   ACTAC
                                CCC  CCGTT GCCC    GAGGT
                                |||  ||||| ||||    |||||
                                GGG  GGCAG CGGG    CTCCA
                                  CA    C   _____
GAM2309  RoXaN    3'  CATCTCACACCCACTGTGGGGT 54740     ___      ACGA
                                CGTT   CGCCCACT    GGT
                                ||||   ||||||||    |||
                                GTAG   GTGGGTGA    CCA
                                  AGT       CACC
GAM2309  LOC221463 3'  CCCTGTTCCCTGGAGATGAGGT 54741     C   G  CACTAC_
             C                   CCC GTTC CC      GAGGTC
                                ||| |||| ||      ||||||
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                                GGG CAAG GG      CTCCAG
                                  A   _ ACCTCTA
GAM2310 CHD3     3' GCAAAAATGTCAGTTAGATAA 54744     T  T T
                                GCAA AAT TC GGTTAGATAA
                                |||| ||| || ||||||||||
                                CGTT TTA AG TCAATCTATT
                                  T  C  _
GAM2310 DNMT3B   3' GCAATAACTGTCTTGGATGA  54745        _  _ TTA
                                GCAATAATT TCT GG  GA
                                ||||||||| ||| ||  ||
                                CGTTATTGA AGA CC  CT
                                     C  A TA_
GAM2310 FLJ10948 3' TCGTGATTATTTCTAGCCAG  54746    CA A
                                TCG  AT ATTTCTGGTTAG
                                |||  || ||||||||||||
                                AGC  TA TAAAGATCGGTC
                                  AC  A
GAM2310 FLJ20637 5' GCAATAATTTAATTTTGGATAG 54747         C____  T
                                GCAATAATTT    TGG TAG
                                ||||||||||    ||| |||
                                CGTTATTAAA    ACC ATC
                                     TTAAA  T
GAM2310 OSBPL10  3' TCACAATAATTTTGAAATGATA 54748          C  TTA
             A                   TCGCAATAATTT TGG  GATAA
                                ||||||||||| |||  |||||
                                AGTGTTATTAAA ACT  CTATT
                                      _  TTA
GAM2311 HSF4     5' CTCCTCCAGCGCGGCGTT    54751    G_  CGTT
                                CTC  CCG   GCGCGGCGTT
                                |||  |||   ||||||||||
                                GAG  GGT   CGCGCCGCAA
                                  GA  ____
GAM2311 NPC1     5' GCTGACGCCGGCGGCGTT    54752    C_    C
                                GC  GCGTTG GCGGCGTT
                                ||  |||||| ||||||||
                                CG  TGCGGC CGCCGCAA
                                 AC    _
GAM2311 C11orf11 5' CTCGTCCAGCACGGCGTT    54753     _  CGTT
                                CTCG CCG   GCGCGGCGTT
                                |||| |||   ||||||||||
                                GAGC GGT   CGTGCCGCAA
                                  A  ____
GAM2311 FLJ10900 5' CTCGCCGCGTTAGCGGCGT   54754          C
                                CTCGCCGCGTTG GCGGCGT
                                |||||||||||| |||||||
                                GAGCGGCGCAAT CGCCGCA
                                          _
GAM2312 HAGH     5' ACGCCGCCCGGGTACCCG    54757      AT  TCGA  A
                                ACGCC  CT   GG GTACCCG
                                |||||  ||   || |||||||
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                                TGCGG  GG    CC CATGGGC
                                  CG  ____  _
GAM2312  MTR      5'  GCTTTCTTCCCGGGTACCCGG  54758    CA    GA  A
                                GC  TCTTC  GG GTACCCGG
                                ||  |||||  || ||||||||
                                CG  AGAAG  CC CATGGGCC
                                 AA    GG  _
GAM2312  PLXNA2   3'  GCCGTTTCCCCAGGGTGCCTGG 54759     A__    G   A  A  C
                                GCC   TCTTC AGG GT CC GG
                                |||   ||||| ||| || || ||
                                CGG   AGGGG TCC CA GG CC
                                  CAA    _  _  C  A
GAM2312  CDH22    5'  GCCCAGCCGCGGGGGTACCCGG 54760     AT_  T  A  A
                                GCC   CT CG GG GTACCCGG
                                |||   || || || ||||||||
                                CGG   GG GC CC CATGGGCC
                                  GTC  C  _  C
GAM2312  FLJ22021  5'  ACGCGTCTTCGAGGACCCCGG  54761     CA       GTA
                                ACGC  TCTTCGAGGA   CCCGG
                                ||||  ||||||||||   |||||
                                TGCG  AGAAGCTCCT   GGGCC
                                  C_        G__
GAM2312  FLJ22625  5'  CGCCATCTTGGAGTC      54762         CGA    ACC
                                CGCCATCTT   GGAGT   C
                                |||||||||   |||||   |
                                GCGGTAGAA   CCTCA   G
                                          ___    ___
GAM2312  FLJ22795  3'  GCCATCCCAGGGGGTGTCCGG  54763       T  A  A  AC
                                GCCATCT CG GG GT  CCGG
                                |||||||  || || ||  ||||
                                CGGTAGG GT CC CA  GGCC
                                    _  C  C  CA
GAM2312  FLJ22938  5'  CACCATCTTTGGGGCCTCGG   54764         CGA  A  ACC
                                CGCCATCTT   GG GT   CGG
                                |||||||||   || ||   |||
                                GTGGTAGAA   CC CG   GCC
                                     AC_  _  GA_
GAM2312  MGC12992  5'  CGCCATCTCCGGGGCCCG    54765          A  A TA
                                CGCCATCTTCG GG G  CCCG
                                ||||||||||| || |  ||||
                                GCGGTAGAGGC CC C  GGGC
                                          _  _ __
GAM2312  P125     5'  ACGTCTCCGGGTACCC      54766     CCA    GA  A
                                ACG   TCTTC  GG GTACCC
                                |||   |||||  || ||||||
                                TGC   AGAGG  CC CATGGG
                                  ____    __  _
GAM2312  LOC130471 3'  ACACCATCTTTGGTGCA     54767          CGA  A
                                ACGCCATCTT   GG GTA
                                |||||||||   || |||
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                                TGTGGTAGAA   CC CGT
                                    A__  A
GAM2312  LOC145717 3'  GCCATCCCAGGGGGTGTCCGG  54763       T  A  A  AC
                                GCCATCT CG GG GT  CCGG
                                ||||||| || || ||  ||||
                                CGGTAGG GT CC CA  GGCC
                                    _  C  C  CA
GAM2312  LOC145725 5'  GCCATCCCAGGGGGTGTCCGG  54763       T  A  A  AC
                                GCCATCT CG GG GT  CCGG
                                ||||||| || || ||  ||||
                                CGGTAGG GT CC CA  GGCC
                                    _  C  C  CA
GAM2312  LOC145732 5'  GCCATCCCAGGGGGTGTCCGG  54763       T  A  A  AC
                                GCCATCT CG GG GT  CCGG
                                ||||||| || || ||  ||||
                                CGGTAGG GT CC CA  GGCC
                                    _  C  C  CA
GAM2312  LOC155032 3'  CCATCTTCGTCCTGTGCCTGG  54768        AGGA  A  C
                                CCATCTTCG    GT CC GG
                                |||||||||    || || ||
                                GGTAGAAGC    CA GG CC
                                     AGGA  C  A
GAM2312  LOC161528 3'  GCCATCCCAGGGGGTGTCCGG  54763       T  A  A  AC
                                GCCATCT CG GG GT  CCGG
                                ||||||| || || ||  ||||
                                CGGTAGG GT CC CA  GGCC
                                    _  C  C  CA
GAM2312  LOC161734 3'  TCTCAGAGGAGTACTCGG    54769     C       C
                                TCTT GAGGAGTAC CGG
                                |||| ||||||||| |||
                                AGAG CTCCTCATG GCC
                                  T       A
GAM2312  LOC196957 5'  GCCATCCCAGGGGGTGTCCGG  54763       T  A  A  AC
                                GCCATCT CG GG GT  CCGG
                                ||||||| || || ||  ||||
                                CGGTAGG GT CC CA  GGCC
                                    _  C  C  CA
GAM2312  LOC196961 5'  GCCATCCCAGGGGGTGTCCGG  54763       T  A  A  AC
                                GCCATCT CG GG GT  CCGG
                                ||||||| || || ||  ||||
                                CGGTAGG GT CC CA  GGCC
                                    _  C  C  CA
GAM2312  LOC197138 5'  GCCATCCCAGGGGGTGTCCGG  54763       T  A  A  AC
                                GCCATCT CG GG GT  CCGG
                                ||||||| || || ||  ||||
                                CGGTAGG GT CC CA  GGCC
                                    _  C  C  CA
GAM2312  LOC220537 3'  GCCATCCCAGGGGGTGTCCGG  54763       T  A  A  AC
                                GCCATCT CG GG GT  CCGG
                                ||||||| || || ||  ||||
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                                CGGTAGG GT CC CA  GGCC
                                    _ C  C  CA
GAM2312  LOC245727 5'  GCCATCCCAGGGGGTGTCCGG  54763       T  A  A  AC
                                GCCATCT CG GG GT  CCGG
                                ||||||| || || ||  ||||
                                CGGTAGG GT CC CA  GGCC
                                    _ C  C  CA
GAM2313  MUC12    3'  CTTCAGGGCCTGACTTCG    54772    C       _
                                CT CAGGGCCTG CTTCG
                                || |||||||| |||||
                                GA GTCCCGGAC GAAGC
                                 A       T
GAM2313  PKLR     3'  CTTAGGGCCTGCTGAGCAGAT  54773    CC       TCGAC
                                CT  AGGGCCTGCT    GAT
                                ||  ||||||||||    |||
                                GA  TCCCGGACGA    CTA
                                 A_       CTCGT
GAM2313  SPTBN2   3'  CCCCCAGGGCCTGCTTCA    54774
                                CCTCCAGGGCCTGCTTCG
                                |||||||||||||||||
                                GGGGGTCCCGGACGAAGT

GAM2313  BAT8     3'  CCTCCAGGGCCTGGCTGGGATC 54775           _  TCGAC
                                CCTCCAGGGCCTG CT    GATC
                                |||||||||||| ||    ||||
                                GGAGGTCCCGGAC GA    CTAG
                                      C  CC___
GAM2313  C20orf106 3'  CCTCCAGGGTTCAAGTGAT   54776        CCTGC    C_
                                CCTCCAGGG    TTCGA  GAT
                                |||||||||    |||||  |||
                                GGAGGTCCC    AAGTT  CTA
                                     _____    CA
GAM2313  CAMKK1   3'  CCTCCAGGTTCTGTGTCTCGTG 54777       GC   C__   AC
            ATC                   CCTCCAGG  CTG   TTCG  GATC
                                |||||||||  |||   ||||  ||||
                                GGAGGTCC  GAC   GAGC  CTAG
                                    AA   ACA   A_
GAM2313  DKFZP434L1435 5'  CCGCCAGGGCCGCGGCGAT   54778    T      T  TTC A
                                CC CCAGGGCC GC   G CGAT
                                || |||||||| ||   | ||||
                                GG GGTCCCGG CG   C GCTA
                                 C       _ ___ C
GAM2313  DKFZP434L1435 5'  CCGCCAGGGCCGCGGCGAT   54778    T      T  TTC A
                                CC CCAGGGCC GC   G CGAT
                                || |||||||| ||   | ||||
                                GG GGTCCCGG CG   C GCTA
                                 C       _ ___ C
GAM2313  DKFZP434L1435 5'  CCGCCAGGGCCGCGGCGAT   54778    T      T  TTC A
                                CC CCAGGGCC GC   G CGAT
                                || |||||||| ||   | ||||
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                                GG GGTCCCGG CG   C GCTA
                                 C       _ ___ C
GAM2313  FLJ10989  3'  CCTCCAGGGTTCAAGTGAT   54776        CCTGC    C_
                                CCTCCAGGG    TTCGA  GAT
                                |||||||||    |||||  |||
                                GGAGGTCCC    AAGTT  CTA
                                     _____    CA
GAM2313  FLJ12190  3'  CCCCCAGGGTCTGCTGTC    54779        C    _
                                CCTCCAGGG CTGCT TC
                                ||||||||| ||||| ||
                                GGGGGTCCC GACGA AG
                                     A    C
GAM2313  FLJ12666  3'  CCTCCAGGGTTCAAGTGAT   54776        CCTGC    C_
                                CCTCCAGGG    TTCGA  GAT
                                |||||||||    |||||  |||
                                GGAGGTCCC    AAGTT  CTA
                                     _____    CA
GAM2313  KIAA0014  3'  CCCCGGGGCCCACAGATGATC  54780     A    TG TTC  C
                                CTCC GGGCC  C   GA GATC
                                |||| |||||  |   || ||||
                                GGGG CCCGG  G   CT CTAG
                                  C    GT T__  A
GAM2313  KIAA0596  3'  CCTCCAGGGTTCAAGCGAT   54781        CCTGC    _
                                CCTCCAGGG    TTCGA CGAT
                                |||||||||    ||||| ||||
                                GGAGGTCCC    AAGTT GCTA
                                     _____    C
GAM2313  MGC29762  3'  CCTCCAGGCTTCAAGCGAT   54782       GGCCT     _
                                CCTCCAG    GCTTCGA CGAT
                                |||||||    ||||||| ||||
                                GGAGGTC    CGAAGTT GCTA
                                     _____     C
GAM2313  N4BP3    3'  CCTTCGGGACCTTGGGGCTGGT 54783    CCA    ____   TCGAC
           GATC                  CT   GGGCCT    GCT    GATC
                                ||  ||||||   |||    ||||
                                GA  CCTGGA   CGA    CTAG
                                 AGC    ACCC   CCA__
GAM2313  WBSCR21   3'  CCTCCAGGGTTCAAGTGAT   54776        CCTGC    C_
                                CCTCCAGGG    TTCGA  GAT
                                |||||||||    |||||  |||
                                GGAGGTCCC    AAGTT  CTA
                                     _____    CA
GAM2313  WBSCR23   3'  CCTCCAGGGTTCAAGCGAT   54781        CCTGC    _
                                CCTCCAGGG    TTCGA CGAT
                                |||||||||    ||||| ||||
                                GGAGGTCCC    AAGTT GCTA
                                     _____    C
GAM2313  ZFP106    3'  CCTCCAGGGTTCAAGTGAT   54776        CCTGC    C_
                                CCTCCAGGG    TTCGA  GAT
                                |||||||||    |||||  |||
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                                GGAGGTCCC    AAGTT  CTA
                                     _____    CA
GAM2313  LOC122622 3'  CTGCCAGGGCCTGTTGGGATC  54784    _        CTTCGAC
                                CT CCAGGGCCTG      GATC
                                || ||||||||||      ||||
                                GA GGTCCCGGAC      CTAG
                                 C         AACC___
GAM2313  LOC148397 5'  CCCCAGAACAGCGCTTTGGCGA 54785         C_    CGA
                TC                  CTCCAGGGC  TGCTT   CGATC
                                |||||||||  |||||   |||||
                                GGGGTCTTG  GCGAA   GCTAG
                                      TC    ACC
GAM2313  LOC149073 5'  CCTCAGGGCCTGCTTTGAC   54786     C         C
                                CCTC AGGGCCTGCTT GAC
                                |||| |||||||||| |||
                                GGAG TCCCGGACGAA CTG
                                  _         A
GAM2313  LOC149302 5'  CCTTCAGAGCCTGCACG     54787     C         TT
                                CCT CAGGGCCTGC  CG
                                ||| ||||||||||  ||
                                GGA GTCTCGGACG  GC
                                  A         T_
GAM2313  LOC197201 3'  TCCAGGCCTAAATGAT      54788       G    CTTC  C
                                TCCAGG CCTG    GA GAT
                                |||||| ||||    || |||
                                AGGTCC GGAT    TT CTA
                                   _   _____ A
GAM2313  LOC199733 3'  CCTCCGGGGCTCAAGCGAT   54789      A    CTGCT   _
                                CCTCC GGGC    TCGA CGAT
                                ||||| ||||    |||| ||||
                                GGAGG CCCG    AGTT GCTA
                                   C    _____    C
GAM2313  LOC203248 3'  CCTCCAGGGCTTCTTCA     54790          CTG
                                CCTCCAGGGC   CTTCG
                                ||||||||||   |||||
                                GGAGGTCCCG   GAAGT
                                      AA_
GAM2313  LOC255231 3'  CCTCCAGAGCTCAGGTGAT   54791          CTGCT   AC_
                                CCTCCAGGGC    TCG   GAT
                                ||||||||||    |||   |||
                                GGAGGTCTCG    AGT   CTA
                                      _____  CCA
GAM2313  LOC256683 5'  CTCCAGGGGCTGCTTGCCG   54792        C     CGA
                                CTCCAGGG CTGCTT   CG
                                |||||||| ||||||   ||
                                GAGGTCCC GACGAA   GC
                                     C     CG_
GAM2313  LOC58492  5'  CTCCAGGGTTAGCGCCCCGCG  54793         CC__      A
                                CTCCAGGG    TGCTTCG CG
                                ||||||||    ||||||| ||
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                                GAGGTCCC    GCGGGGC GC
                                    AATC      _
GAM2313  LOC91355  5'  CCTCCAGGGCATGCGTTC    54794          C  _
                                CCTCCAGGGC TGC TTC
                                |||||||||| ||| |||
                                GGAGGTCCCG ACG AAG
                                     T   C
GAM2314  HOXC5     3'  TATTTGATATGACAAAATAT   54797     C     C
                                TAT TGATAT ACAAAATAT
                                ||| |||||| |||||||||
                                ATA ACTATA TGTTTTATA
                                  A     C
GAM2314  13CDNA73  3'  TCTGAACAGAATATCAA     54798      TATC   A
                                TCTGA    ACA AATATCAA
                                |||||    ||| ||||||||
                                AGACT    TGT TTATAGTT
                                   _____  C
GAM2314  EVI5      3'  TGACACAAAATATCA       54799     TAT
                                TGA   CACAAAATATCA
                                |||   ||||||||||||
                                ACT   GTGTTTTATAGT
                                   ___
GAM2314  EVI5      3'  TCAAATATCACAAAATGTCA   54800    T          A
                                TC GATATCACAAAAT TCA
                                || |||||||||||| |||
                                AG TTATAGTGTTTTA AGT
                                 T           C
GAM2314  SNAPC1    3'  TCAATACACAAAATATCAAT   54801    T    T
                                TC GATA CACAAAATATCAAT
                                || |||| ||||||||||||||
                                AG TTAT GTGTTTTATAGTTA
                                   _   _
GAM2314  LOC200059 3'  TATCCTGACAAAATATCA     54802      GATATC
                                TATCT      ACAAAATATCA
                                |||||      ||||||||||
                                ATAGG      TGTTTTATAGT
                                   AC_____
GAM2314  LOC219376 3'  TCTAATATTATACAGACTATCA 54803        C__   AAA
            AT                    TCTGATAT   ACA   TATCAAT
                                |||||||   |||   |||||||
                                AGATTATA   TGT   ATAGTTA
                                     ATA   CTG
GAM2314  LOC51133  3'  TATCTGGTATTCAATATCAAT  54804       A   CACAA
                                TATCTG TAT     AATATCAAT
                                |||||| |||    |||||||||
                                ATAGAC ATA     TTATAGTTA
                                   C   AG___
GAM2315  AMFR      3'  AAAAGGTACTTGAATCCGTCCT 54807       CG  A_
                                AGAAG  AC  GAATCCGTCCT
                                |||||  ||  ||||||||||
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                                TTTTC  TG  CTTAGGCAGGA
                                   CA  AA
GAM2315  ARF3     3'  AAGAATCCATCATCTGTCCT   54808      GCGA  GA   C
                                AAGAA    CA  ATC GTCCT
                                ||||||    ||  ||| |||||
                                TTCTT    GT  TAG CAGGA
                                   AG__  AG   A
GAM2315  ATP8A2   3'  AAGAGCGACAGGTGTGTTCCT  54809      A      AATCCG
                                AAGA GCGACAG     TCCT
                                |||| |||||||     ||||
                                TTCT CGCTGTC     AGGA
                                  _      CACACA
GAM2315  CLECSF5  3'  AAGAGTGACAGAATCTGT    54810      A C        C
                                AAGA G GACAGAATC GT
                                |||| | |||||||||  ||
                                TTCT C CTGTCTTAG CA
                                  _ A        A
GAM2315  KLRD1    5'  AAGAAGCAGTAGAATCACAAGC 54811         AC     _  T_
            CT                    AAGAAGCG  AGAATC CG  CCT
                                |||||||||  ||||||  ||  |||
                                TTCTTCGT  TCTTAG GT  GGA
                                    CA     T  TC
GAM2315  KLRD1    5'  AAGAAGCAGTAGAATCACAAGC 54811         AC     _  T_
            CT                    AAGAAGCG  AGAATC CG  CCT
                                |||||||||  ||||||  ||  |||
                                TTCTTCGT  TCTTAG GT  GGA
                                    CA     T  TC
GAM2315  TCF1     3'  AAGCAGCGACAGTCCCTCCT   54812     A       AA   G
                                AAG AGCGACAG  TCC TCCT
                                |||  ||||||||  |||  ||||
                                TTC TCGCTGTC  AGG AGGA
                                  G        __   G
GAM2315  UBE2H    3'  AAGAAGCAATTTTTTCCTGTTC 54813         CAGAA  _  C
            T                     AAGAAGCGA     TCC GT CT
                                |||||||||     |||  ||  ||
                                TTCTTCGTT     AGG CA GA
                                     AAAAA   A  A
GAM2315  XRCC5    3'  AGAAGTGAGTCCGTCCT     54814      C  CAGAA
                                AGAAG GA     TCCGTCCT
                                |||||  ||     ||||||||
                                TCTTC CT     AGGCAGGA
                                   A  C_____
GAM2315  AD034    3'  AAAACATTTGAATCCGTC     54815       ACA
                                GAAGCG   GAATCCGTC
                                ||||||   |||||||||
                                TTTTGT   CTTAGGCAG
                                   AAA
GAM2315  CAMKK2   3'  AGAGCGACAGGCCAGGCCT   54816     A      AAT   T_
                                AGA GCGACAG   CCG  CCT
                                |||  |||||||   |||  |||
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                                TCT CGCTGTC   GGT  GGA
                                  _     C__   CC
GAM2315  CSTF1    3'  AAGAAACGGCAAGTCC     54817       A   AATCC
                                AAGAAGCG CAG    GTCC
                                |||||||| |||    ||||
                                TTCTTTGC GTT    CAGG
                                    C  _____
GAM2315  DKFZp434K114 3'  AGAAGTAACCTCCCCGTCCT   54818      CG  AGAA
                                AGAAG  AC   TCCGTCCT
                                |||||  ||   ||||||||
                                TCTTC  TG   GGGCAGGA
                                   AT  GAG_
GAM2315  DKFZP566K0524 3'  AGAGGCAACAGAAGTC     54819     A       TCC
                                AGA GCGACAGAA   GTC
                                ||| |||||||||   |||
                                TCT CGTTGTCTT   CAG
                                  C       ___
GAM2315  FLJ20202  5'  GAGGCGACAGAGGCAGGTCCT  54820    A      ATCC_
                                GA GCGACAGA    GTCCT
                                || ||||||||    |||||
                                CT CGCTGTCT    CAGGA
                                 C       CCGTC
GAM2315  FLJ22635  3'  AAGGGGCCGAGTCCCCGTCCT  54821    AA  GAC  AA
                                AAG  GC   AG  TCCGTCCT
                                |||  ||   ||  ||||||||
                                TTC  CG   TC  GGGCAGGA
                                  CC  GC_  AG
GAM2315  GIT2     3'  AAAAAGCGGCAAAGTCC     54822       A   ATCC
                                AAGAAGCG CAGA   GTCC
                                |||||||| ||||   ||||
                                TTTTTCGC GTTT   CAGG
                                    C  _____
GAM2315  GIT2     3'  AAAAAGCGGCAAAGTCC     54822       A   ATCC
                                AAGAAGCG CAGA   GTCC
                                |||||||| ||||   ||||
                                TTTTTCGC GTTT   CAGG
                                    C  _____
GAM2315  GIT2     3'  AAAAAGCGGCAAAGTCC     54822       A   ATCC
                                AAGAAGCG CAGA   GTCC
                                |||||||| ||||   ||||
                                TTTTTCGC GTTT   CAGG
                                    C  _____
GAM2315  HBOA     3'  AGAAATGACAGACAGATCCC   54823     C     ATCC
                                AGAAG GACAGA   GTCCT
                                ||||| ||||||   |||||
                                TCTTT CTGTCT   TAGGG
                                   A     GTC_
GAM2315  IRX1     3'  AAAGCGACGGATGCGAGTCCT  54824       A  ATCC_
                                GAAGCGAC GA    GTCCT
                                |||||||| ||    |||||
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                                TTTCGCTG CT    CAGGA
                                    C  ACGCT
GAM2315 KIAA0303  5' AGAAGTACCCGTCCCGTCCT  54825      CG  AGAA
                                AGAAG  AC   TCCGTCCT
                                |||||  ||   ||||||||
                                TCTTC  TG   GGGCAGGA
                                   A_  GGCA
GAM2315 MGC10500  3' AGGAGCTAGATCCGTCCT   54826    A   GAC   A
                                AG AGC   AGA TCCGTCCT
                                || |||   ||| ||||||||
                                TC TCG   TCT AGGCAGGA
                                 C   A__   _
GAM2315 mPA-PLA1  3' GAGGCCTCCAGTCCGTCCT   54827    A  GA_   AA
                                GA GC   CAG  TCCGTCCT
                                || ||   |||  ||||||||
                                CT CG   GTC  AGGCAGGA
                                 C  GAG   __
GAM2315 PDK2      3' AGAGGCGGCAGTCCGTCCT   54828    A   A   AA
                                AGA GCG CAG  TCCGTCCT
                                ||| ||| |||  ||||||||
                                TCT CGC GTC  AGGCAGGA
                                  C   C   __
GAM2315 TA-KRP    3' AAAAAGCGGCAGGAAATC    54829       A   __
                                AAGAAGCG CAG  AATC
                                |||||||| |||  ||||
                                TTTTTCGC GTC  TTAG
                                    C   CT
GAM2315 TERA      3' AAAGCTCAGTCTGTCCT     54830      GA   AA  C
                                GAAGC  CAG  TC GTCCT
                                |||||  |||  || |||||
                                TTTCG  GTC  AG CAGGA
                                   A_   __  A
GAM2315 ZFP36L2   5' AGAAGCGAGGAGCGCTCCT   54831       CA  ATC  _
                                AGAAGCGA  GA   CG TCCT
                                ||||||||  ||   || ||||
                                TCTTCGCT  CT   GC AGGA
                                    C_  C__  G
GAM2315 LOC145828 5' AAGATAGCTCAAAATCTGTTCT 54832      _  GA     C  C
                                AAGA AGC  CAGAATC GT CT
                                |||| |||  ||||||| || ||
                                TTCT TCG  GTTTTAG CA GA
                                  A  A_     A  A
GAM2315 LOC149703 3' GAATGACAGAATCAGGGCCT  54833     GC       CGT_
                                GAA  GACAGAATC   CCT
                                |||  |||||||||   |||
                                CTT  CTGTCTTAG   GGA
                                  A_       TCCC
GAM2315 LOC150606 5' AGCGGAATCCGTCCT       54834      ACA
                                AGCG  GAATCCGTCCT
                                ||||  ||||||||||
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                                TCGC   CTTAGGCAGGA
                                  ___
GAM2315  LOC150848 3'  AAAAAGACAAAATCTGTC    54835      C       C
                                AGAAG GACAGAATC GTC
                                ||||| ||||||||| |||
                                TTTTT CTGTTTTAG CAG
                                  _       A
GAM2315  LOC152794 5'  AAGAGCTGACAGAATATC    54836     A  _      CC
                                AAGA GC GACAGAAT  GTC
                                |||| || ||||||||  |||
                                TTCT CG CTGTCTTA  TAG
                                  _ A      __
GAM2315  LOC204285 3'  AAGAAGCGTGGACTCTTGTCCT 54837        ACA  A  C_
                                AAGAAGCG   GA TC  GTCCT
                                ||||||||   || ||  |||||
                                TTCTTCGC   CT AG  CAGGA
                                     AC_  G  AA
GAM2315  LOC220954 3'  AGGGACAGAATGCCATTCT   54838    C      _   C
                                AG GACAGAAT CCGT CT
                                || |||||||| |||| ||
                                TC CTGTCTTA GGTA GA
                                 C       C    A
GAM2315  LOC253805 3'  AAGAAGCGATGCCCTTCCT   54839        CAGAA   G
                                AAGAAGCGA    TCC TCCT
                                |||||||||    ||| ||||
                                TTCTTCGCT    GGG AGGA
                                     AC___   A
GAM2315  LOC254700 3'  AGAAGCAAAGCATCTTTGTC  54840       C  A   C__
                                AGAAGCGA AG ATC   GTC
                                |||||||| || |||   |||
                                TCTTCGTT TC TAG   CAG
                                     _  G   AAA
GAM2315  LOC51076  3'  AAGAAGCACAGACCA      54841       G    AT
                                AAGAAGC ACAGA  CCG
                                ||||||| |||||  |||
                                TTCTTCG TGTCT  GGT
                                  _    __
GAM2315  LOC91547  5'  AGAGGCGGTGACCGCGTCCT  54842    A   ACA  A  _
                                AGA GCG   GA TC CGTCCT
                                ||| |||   || || ||||||
                                TCT CGC   CT GG GCAGGA
                                  C   CA_  _  C
GAM2316  DMC1      3'  TCTCTGCCTCCTGGGTTCAAG  54845     ATA   A   TAG
                                TCTC   CTT TGG   GTTCAAG
                                ||||   ||| |||   |||||||
                                AGAG   GAG ACC   CAAGTTC
                                  ACG   G   ___
GAM2316  E2F3      3'  TCATACTTTTGCATGACTTCAA 54846        ATG   _  _
              G                  TCATACTT   GTA GG TTCAAG
                                ||||||||   ||| || ||||||
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                                AGTATGAA  CGT CT AAGTTC
                                   AA_  A  G
GAM2316 MEN1    3' TCTCATACTTAGGTATGC   54847        T   G
                                TCTCATACTTA GGTA GT
                                |||||||||| |||| ||
                                AGAGTATGAAT CCAT CG
                                      _   A
GAM2316 NOV     3' TCATAATTATGGCCCAA    54848     C     AGGT
                                TCATA TTATGGT   TCAA
                                ||||| |||||||   ||||
                                AGTAT AATACCG   GGTT
                                  T     ____
GAM2316 SLC14A1  3' TCTTGAACTCCTGGGTTCAAG 54849   CAT   A  TAG
                                TCT  ACTT TGG  GTTCAAG
                                |||  |||| |||  |||||||
                                AGA  TGAG ACC  CAAGTTC
                                  ACT   G  ___
GAM2316 DKFZP564M182 3' TCTCGAACTCCTGGGTTCAAG 54850    AT   A  TAG
                                TCTC  ACTT TGG  GTTCAAG
                                ||||  |||| |||  |||||||
                                AGAG  TGAG ACC  CAAGTTC
                                  CT   G  ___
GAM2316 FLJ11267 3' TCTCGAACTGCTGGGTTCAAG 54851    AT  TA  TAG
                                TCTC  ACT  TGG  GTTCAAG
                                ||||  |||  |||  |||||||
                                AGAG  TGA  ACC  CAAGTTC
                                  CT  CG  ___
GAM2316 FLJ20972 3' TCTCTGCCTCCTGGGTTCAAG 54845    ATA  A  TAG
                                TCTC  CTT TGG  GTTCAAG
                                ||||  ||| |||  |||||||
                                AGAG  GAG ACC  CAAGTTC
                                  ACG  G  ___
GAM2316 KIAA1456 3' TCTTGAACTCCTGGGTTCAAG 54849   CAT   A  TAG
                                TCT  ACTT TGG  GTTCAAG
                                |||  |||| |||  |||||||
                                AGA  TGAG ACC  CAAGTTC
                                  ACT   G  ___
GAM2316 KIAA1954 3' TCTTGAACTCCTGGGTTCAAG 54849   CAT   A  TAG
                                TCT  ACTT TGG  GTTCAAG
                                |||  |||| |||  |||||||
                                AGA  TGAG ACC  CAAGTTC
                                  ACT   G  ___
GAM2316 MAWBP   3' TCTCGAACTCCTAGGTTCAAG 54852    AT   ATGG
                                TCTC  ACTT   TAGGTTCAAG
                                ||||  ||||   ||||||||||
                                AGAG  TGAG   ATCCAAGTTC
                                  CT   G___
GAM2316 MGC10854 3' TCTGTACTTATGGTACCCA   54853   CA       GG
                                TCT  TACTTATGGTA  TTCA
                                |||  ||||||||||  ||||
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                                AGA  ATGAATACCAT  GGGT
                                  C_         __
GAM2316  MGC16142  3'  TCTCTGCCTCCTGGGTTCAAG  54845     ATA   A   TAG
                                TCTC   CTT TGG   GTTCAAG
                                ||||   ||| |||   |||||||
                                AGAG   GAG ACC   CAAGTTC
                                  ACG   G   ___
GAM2316  MGC16386  3'  TCTTTACACAGGTGGGTTCAAG 54854     CA   TTAT   A
                                TCT  TAC    GGT GGTTCAAG
                                |||  |||    ||| ||||||||
                                AGA  ATG    CCA CCAAGTTC
                                  A_   TGT_   C
GAM2316  MGC32104  3'  TCATGTTTTATTTTAGGTTCAA 54855     AC_   GG
           G                     TCAT   TTAT  TAGGTTCAAG
                                ||||   ||||  ||||||||||
                                AGTA   AATA  ATCCAAGTTC
                                  CAA    AA
GAM2316  LOC146159 3'  TCTCAAACTCCTGGGTTCAAG  54856      T    A   TAG
                                TCTCA ACTT TGG   GTTCAAG
                                ||||| |||| |||   |||||||
                                AGAGT TGAG ACC   CAAGTTC
                                   T    G   ___
GAM2316  LOC146856 5'  TCATACTTTTGCATGACTTCAA 54846       ATG   _  _
           G                     TCATACTT   GTA GG TTCAAG
                                ||||||||   ||| || ||||||
                                AGTATGAA   CGT CT AAGTTC
                                    AA_   A  G
GAM2316  LOC150225 3'  TCTCGAACTCCTGGGTTCAAG  54850     AT    A   TAG
                                TCTC  ACTT TGG   GTTCAAG
                                ||||  |||| |||   |||||||
                                AGAG  TGAG ACC   CAAGTTC
                                  CT    G   ___
GAM2316  LOC151248 3'  TCTCTGCCTCCTGGGTTCAAG  54845     ATA   A   TAG
                                TCTC   CTT TGG   GTTCAAG
                                ||||   ||| |||   |||||||
                                AGAG   GAG ACC   CAAGTTC
                                  ACG   G   ___
GAM2316  LOC196027 3'  TCTCAAACTCCTGGGTTCAAG  54856      T    A   TAG
                                TCTCA ACTT TGG   GTTCAAG
                                ||||| |||| |||   |||||||
                                AGAGT TGAG ACC   CAAGTTC
                                   T    G   ___
GAM2316  LOC219627 3'  TCTCTGCCTCCTGGGTTCAAG  54845     ATA   A   TAG
                                TCTC   CTT TGG   GTTCAAG
                                ||||   ||| |||   |||||||
                                AGAG   GAG ACC   CAAGTTC
                                  ACG   G   ___
GAM2316  LOC220906 3'  TCTCTGCCTCCTGGGTTCAAG  54845     ATA   A   TAG
                                TCTC   CTT TGG   GTTCAAG
                                ||||   ||| |||   |||||||
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                                AGAG   GAG ACC   CAAGTTC
                                  ACG   G   ___
GAM2316  LOC221822 5'  TCATACTTGTGAAACTTCA   54857        A   T  G
                                TCATACTT TGG AG TTCA
                                |||||||| ||| || ||||
                                AGTATGAA ACT TT AAGT
                                     C   _  G
GAM2316  LOC254436 3'  TCATATTACTTAGGTTCAAG   54858      C    GG
                                TCATA TTAT  TAGGTTCAAG
                                ||||| ||||  ||||||||||
                                AGTAT AATG  ATCCAAGTTC
                                  _    A_
GAM2316  LOC90777  3'  TCTCAAACCCCTGGGTTCAAG  54859      T   TA   TAG
                                TCTCA ACT  TGG   GTTCAAG
                                ||||| |||  |||   |||||||
                                AGAGT TGG  ACC   CAAGTTC
                                  T   GG   ___
GAM2317  CLTC     3'  TATGCATAATGGGGAAACCTGC 54862     _   GC  A    A
                                TATG ATAA  GG GGAAA CCTGC
                                |||| ||||  || ||||| |||||
                                ATAC TATT  CC CCTTT GGACG
                                  G   A_ _    _
GAM2317  EMX2     3'  TGATAAACGGAATACCTGC    54863          GAAA
                                TGATAAGCGGAG    ACCTGC
                                ||||||||||||   ||||||
                                ACTATTTGCCTT    TGGACG
                                       A___
GAM2317  GYG2     3'  TGATGGGAGGAAATTTGC    54864      AAGC       ACC
                                TGAT   GGAGGAAA   TGC
                                ||||   ||||||||   |||
                                ACTA   CCTCCTTT   ACG
                                  C___       AA_
GAM2317  PXR1     3'  CATGATGAGCAGAGAGATCTG  54865       A      _  AAAC
                                TATGAT AGCGGAG GA   CTG
                                |||||| ||||||| ||   |||
                                GTACTA TCGTCTC CT   GAC
                                   C      T  A___
GAM2317  DJ167A19.1 5'  TATGAGGAAGAAAATTTG    54866      TAAGC       CC
                                TATGA    GGAGGAAAA  TG
                                |||||    |||||||||  ||
                                ATACT    CCTTCTTTT  AC
                                  _____        AA
GAM2317  EIF5     3'  TGATAATGGAGGAAAATTTGC  54867       GC       CC
                                TGATAA  GGAGGAAAA  TGC
                                ||||||  |||||||||  |||
                                ACTATT  CCTCCTTTT  ACG
                                   A_       AA
GAM2317  HSA249128 3'  TGACAAGCCCATAAAACCTGC  54868        GGAGG
                                TGATAAGC    AAAACCTGC
                                ||||||||    |||||||||
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                                ACTGTTCG    TTTTGGACG
                                    GGTA_
GAM2317 KIAA1041 3' GATGAGTGGGGAAACCTGC   54869    A C A   A
                                GAT AG GG GGAAA CCTGC
                                ||| || || ||||| |||||
                                CTA TC CC CCTTT GGACG
                                  C A _   _
GAM2317 SSH2    3' TGATAAGCCAAAAACCTG    54870       GGAG
                                TGATAAGC   GAAAACCTG
                                ||||||||   |||||||||
                                ACTATTCG   TTTTTGGAC
                                    G___
GAM2317 TIEG    3' TGATAAGAAATGAAACCTGC  54871      CG  GA
                                TGATAAG  GAG  AAACCTGC
                                |||||||  |||  ||||||||
                                ACTATTC  TTT  TTTGGACG
                                   __  AC
GAM2317 LOC148443 3' TATGCACCTAGAGGAAAACTTG 54872     A  AGC       C
                                TATG TA   GGAGGAAAAC TG
                                |||| ||   |||||||||| ||
                                ATAC GT   TCTCCTTTTG AC
                                  _ GGA        A
GAM2317 LOC152925 3' TATGATAAAGCTAATTAAGAAT 54873       _ GG___    AAC
          CTG                   TATGATAA GC    AGGAA   CTG
                                |||||||| ||    |||||  |||
                                ATACTATT CG    TTCTT   GAC
                                    T  ATTAA    A__
GAM2317 LOC91056 3' CATGGTAATGGAAACCTG   54874    A  GC  GGAA
                                TATG TAA  GGA   AACCTG
                                |||| |||  |||   ||||||
                                GTAC ATT  CCT   TTGGAC
                                  C  A_  _____
GAM2318 PRKWNK3  3' TGACAAAATTATTGTAATT   54877       TC_
                                TGACAAAATT   GTAGTT
                                ||||||||||   ||||||
                                ACTGTTTTAA   CATTAA
                                     TAA
GAM2318 ZNF136   3' TGACAGAATTTCATGCT    54878     A     A
                                TGACA AATTTCGT GTT
                                ||||| |||||||| |||
                                ACTGT TTAAAGTA CGA
                                  C      _
GAM2318 KIAA0441 3' TGACAAAAATTCAGAATT    54879       T   T
                                TGACAAAA TTCG AGTT
                                |||||||| |||| ||||
                                ACTGTTTT AAGT TTAA
                                    T   C
GAM2318 MRPL3    3' TGACAAAACTTTAATAAAAGTT 54880        CGT____
          AAATTT                GACAAAATTT     AGTTAAATTT
                                ||||||||||     ||||||||||
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                                CTGTTTTGAA      TCAATTTAAA
                                      ATTATTT
GAM2318  PCDH10    3'  TGACAAAATTTTGTAGCT    54881          C
                                TGACAAAATTT GTAGTT
                                |||||||||| ||||||
                                ACTGTTTTAAA CATCGA
                                      A
GAM2318  TRIM2     3'  TGACAAAATTTCATTTAAATTT 54882           AG
                                TGACAAAATTTCGT  TTAAATTT
                                |||||||||||||  ||||||||
                                ACTGTTTTAAAGTA  AATTTAAA
                                        __
GAM2318  LOC221810 3'  TGGCAAAATTCTGTAGCT    54883    A      TC
                                TG CAAAATT  GTAGTT
                                || |||||||  ||||||
                                AC GTTTTAA  CATCGA
                                 C      GA
GAM2319  CYLN2     3'  TGGCAGGGCGAGGGGTTG    54886      ___    AT
                                TGGCA   TGAGG  GGTTG
                                |||||   |||||  |||||
                                ACCGT   GCTCC  CCAAC
                                   CCC    __
GAM2319  G6PC      3'  TGTTATGAGCAGGATGGTTG   54887    GC   ___
                                TG  ATGA   GGATGGTTG
                                ||  ||||   |||||||||
                                AC  TACT   CCTACCAAC
                                 AA    CGT
GAM2319  SLC22A3   3'  TGTCATGAGAATCAGGTTG   54888    G       __
                                TG CATGAGGAT  GGTTG
                                || |||||||||  |||||
                                AC GTACTCTTA  CCAAC
                                 A        GT
GAM2319  UBE4A     3'  TGGCTGTGGACAAGGTTG    54889      A  A   __
                                TGGC TG GGAT  GGTTG
                                |||| || ||||  |||||
                                ACCG AC CCTG  CCAAC
                                  _ A    TT
GAM2319  XT3       3'  TGGAAGATGAGATGGTTG    54890     C__    G
                                TGG   ATGAG ATGGTTG
                                |||   ||||| |||||||
                                ACC   TACTC TACCAAC
                                  TTC    _
GAM2319  KIAA0087  3'  TGGGATGAGAATGAGTTG    54891     C       _
                                TGG ATGAGGATG GTTG
                                ||| ||||||||| ||||
                                ACC TACTCTTAC CAAC
                                  C        T
GAM2319  KIAA1332  3'  TGACATGAACCCTGGTTG    54892         GA_
                                TGGCATGAG   TGGTTG
                                |||||||||   ||||||
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                                ACTGTACTT  ACCAAC
                                     GGG
GAM2319 KRTAP9-9 3' TGGGTGAGAACATGGTTG   54893    CA    __
                                TGG  TGAGGA  TGGTTG
                                |||  ||||||  ||||||
                                ACC  ACTCTT  ACCAAC
                                  C_     GT
GAM2319 NS1-BP   5' GGTATGAAGACAGGTGGTTG  54894   C     ____
                                GG ATGAGGA   TGGTTG
                                || |||||||   ||||||
                                CC TACTTCT   ACCAAC
                                 A      GTCC
GAM2319 LOC118611 5' TGGCGTGACAATGAGTTG   54895     A  G   _
                                TGGC TGA GATG GTTG
                                |||| ||| |||| ||||
                                ACCG ACT TTAC CAAC
                                  C  G   T
GAM2319 LOC51725 3' TGGCATGACGCTGAGGTTG   54896       G___  T
                                TGGCATGA   GA GGTTG
                                ||||||||   || |||||
                                ACCGTACT   CT CCAAC
                                     GCGA  _
GAM2320 GAB2    3' TCCAGAGTTCTGGGGACCCA   54899    C     A
                                TCC GAGTTCT GGGACCTA
                                ||| ||||||| ||||||||
                                AGG CTCAAGA CCCTGGGT
                                  T      C
GAM2320 GAB2    3' TCCAGAGTTCTGGGGACCCA   54899    C     A
                                TCC GAGTTCT GGGACCTA
                                ||| ||||||| ||||||||
                                AGG CTCAAGA CCCTGGGT
                                  T      C
GAM2320 LRRC2   3' TCCTGGGCTCAAACAACCTGCT 54900    CGA   T  G    A
           TG                     TCC   GTTC AG GACCT CTTG
                                ||||  |||| || ||||| ||||
                                AGG   CGAG TT TTGGA GAAC
                                  ACC    T  G    C
GAM2320 KIAA1086 3' CCCCGAGTTTAGAATCTGCTTG 54901       CTA   C  A
                                TCCCGAGTT   GGGA CT CTTG
                                |||||||||   |||| || ||||
                                GGGGCTCAA   TCTT GA GAAC
                                     A__    A  C
GAM2320 MGC2562  3' TCCTGAGCTCAAGTGATTTGCT 54902    C     T  G  CCTA
           TG                     TCC GAGTTC AG GA    CTTG
                                ||| |||||| || ||    ||||
                                AGG CTCGAG TC CT    GAAC
                                  A     T  A  AAAC
GAM2320 LOC137492 5' CCCCGAGTTCTGGGGGAC    54903          A_
                                TCCCGAGTTCT  GGGAC
                                ||||||||||  |||||
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                                GGGGCTCAAGA  CCCTG
                                      CC
GAM2320  LOC152286 5'  TCCTGAGCTCCCTACT      54904     C     TAGGGA
                                TCC GAGTTC     CCTACT
                                ||| ||||||     ||||||
                                AGG CTCGAG     GGATGA
                                  A     _______
GAM2320  LOC84548  3'  AGCAAAGGACCTATTTG     54905     TCT       C
                                AGT   AGGGACCTA TTG
                                |||   ||||||||| |||
                                TCG   TTCCTGGAT AAC
                                  T__       A
GAM2321  ADD2      3'  GGCCATCAGACATTGTCCTC   54908       _   CCGC
                                GGCCGTC GACA    CCTC
                                ||||||| ||||    ||||
                                CCGGTAG CTGT    GGAG
                                    T    AACA
GAM2321  ADD2      3'  GGCCATCAGACATTGTCCTC   54908       _   CCGC
                                GGCCGTC GACA    CCTC
                                ||||||| ||||    ||||
                                CCGGTAG CTGT    GGAG
                                    T    AACA
GAM2321  ADD2      3'  GGCCATCAGACATTGTCCTC   54908       _   CCGC
                                GGCCGTC GACA    CCTC
                                ||||||| ||||    ||||
                                CCGGTAG CTGT    GGAG
                                    T    AACA
GAM2321  ALK       5'  GAGGCCGTTTACACTGCTCTC  54909       CG    C  C
                                GAGGCCGT  ACAC GC CTC
                                ||||||||  |||| || |||
                                CTCCGGCA  TGTG CG GAG
                                     AA    A  A
GAM2321  CSHL1     3'  GAAGCCACAGCTGCCCTC     54910       T  ACACC
                                GAGGCCG CG     GCCCTC
                                ||||||| ||     ||||||
                                CTTCGGT GT     CGGGAG
                                    _  CGA__
GAM2321  CSHL1     3'  GAAGCCACAGCTGCCCTC     54910       T  ACACC
                                GAGGCCG CG     GCCCTC
                                ||||||| ||     ||||||
                                CTTCGGT GT     CGGGAG
                                    _  CGA__
GAM2321  DDX5      3'  AAGGCCATGCATTGCCTTC    54911       CGA  CC   C
                                GAGGCCGT   CA  GCC TC
                                ||||||||   ||  ||| ||
                                TTCCGGTA   GT  CGG AG
                                    C__  AA   A
GAM2321  FKBP2     5'  AGGCCGGGCCACGCCGCCCTC  54912      __   G  A
                                AGGCC  GTC AC CCGCCCTC
                                |||||  ||| || ||||||||
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                                TCCGG  CGG TG GGCGGGAG
                                  CC   _  C
GAM2321  G6PD    5'  GGCCTCGGCCACCACCCC    54913     G   A_
                                GGCC TCG  CACCGCCCT
                                |||| |||  |||||||||
                                CCGG AGC  GTGGTGGGG
                                  _   CG
GAM2321  GH1     3'  GAAGCCACAGCTGCCCTC    54910       T  ACACC
                                GAGGCCG CG    GCCCTC
                                |||||||  ||    ||||||
                                CTTCGGT GT    CGGGAG
                                    _  CGA__
GAM2321  GH2     3'  GAAGCCACAGCTGCCCTC    54910       T  ACACC
                                GAGGCCG CG    GCCCTC
                                |||||||  ||    ||||||
                                CTTCGGT GT    CGGGAG
                                    _  CGA__
GAM2321  GNAS    3'  GGGTCCTCTTCGCCGCCCTC   54914   A  _  G  GACA
                                G GG CC TC    CCGCCCTC
                                |  ||  ||  ||    |||||||||
                                C CC GG AG    GGCGGGAG
                                 _  A  _  AAGC
GAM2321  HCFC1   5'  GAGGCCGCCATCTTAACTGCCC 54915          AC___  C
           TC                    GAGGCCGTCG    AC GCCCTC
                                |||||||||     ||  ||||||
                                CTCCGGCGGT    TG CGGGAG
                                     AGAAT  A
GAM2321  HSPA6   3'  GAGGATGAACCGCCCT     54916     CC  C  C
                                GAGG  GT GA ACCGCCCT
                                ||||  ||  ||  ||||||||
                                CTCC  TA CT TGGCGGGA
                                  __  _  _
GAM2321  IHPK1   3'  GAACCCAGGCGCCGCCCTC   54917    G   T_  ACA
                                GAG CCG  CG   CCGCCCTC
                                |||  |||  ||   ||||||||
                                CTT GGT  GC   GGCGGGAG
                                  G   CC  ___
GAM2321  IL17R   5'  GAGGCTTTCTTTTCCGCCCTC  54918      CG  GACA
                                GAGGC  TC    CCGCCCTC
                                |||||  ||    ||||||||
                                CTCCG  AG    GGCGGGAG
                                   AA  AAAA
GAM2321  MID2    5'  AGGCCGCCGCCCCGCCTTC    54919        ACA    C
                                AGGCCGTCG   CCGCC TC
                                |||||||||   |||||  ||
                                TCCGGCGGC   GGCGG AG
                                     G__     A
GAM2321  MID2    5'  AGGCCGCCGCCCCGCCTTC    54919        ACA    C
                                AGGCCGTCG   CCGCC TC
                                |||||||||   |||||  ||
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                                TCCGGCGGC  GGCGG AG
                                    G__    A
GAM2321  MTCP1   5'  GGCCGGCCACCGCCCTC    54920     TCGA
                                GGCCG   CACCGCCCTC
                                |||||   ||||||||||
                                CCGGC   GTGGCGGGAG
                                  CG__
GAM2321  MTMR1   5'  GGGCCCCCGCCGCCCTC    54921   A   G   ACA
                                G GGCC TCG  CCGCCCTC
                                | |||| |||  ||||||||
                                C CCGG GGC  GGCGGGAG
                                 _   G  ___
GAM2321  MUS81   5'  GAGAGCCTGCGGCCGCCCTC  54922    _  GT  ACA
                                GAG GCC  CG  CCGCCCTC
                                ||| |||  ||  ||||||||
                                CTC CGG  GC  GGCGGGAG
                                  T  AC  C__
GAM2321  NUP62   5'  GAGGCCGCCGCCGCCTCTC   54923        ACA   _
                                GAGGCCGTCG  CCGCC CTC
                                ||||||||||  ||||| |||
                                CTCCGGCGGC  GGCGG GAG
                                    ___    A
GAM2321  NUP62   5'  GAGGCCGCCGCCGCCTCTC   54923        ACA   _
                                GAGGCCGTCG  CCGCC CTC
                                ||||||||||  ||||| |||
                                CTCCGGCGGC  GGCGG GAG
                                    ___    A
GAM2321  NXT1    5'  GAGCGCCCCGGCGCCGCCCTC  54924    _  G  ACA
                                GAG GCC TCG  CCGCCCTC
                                ||| ||| |||  ||||||||
                                CTC CGG GGC  GGCGGGAG
                                  G  _  CGC
GAM2321  SDC1    3'  AGGCCCCTGCCGCCCTC    54925     G  GACA
                                AGGCC TC   CCGCCCTC
                                |||||  ||  ||||||||
                                TCCGG GG   GGCGGGAG
                                   _  AC__
GAM2321  SNX6    5'  GGGCCGTCGTCCAGGCCTTC  54926   A     A_  CC  C
                                G GGCCGTCG  CA  GCC TC
                                | ||||||||  ||  ||| ||
                                C CCGGCAGC  GT  CGG AG
                                _      AG  C_  A
GAM2321  TDG     5'  GAGGCCGCTGATGCGGCGGCTC 54927       C  CACC  C_
                                GAGGCCGT GA   GC  CTC
                                |||||||| ||   ||  |||
                                CTCCGGCG CT   CG  GAG
                                    A  ACGC  CC
GAM2321  TFG     5'  GAGGCCGCGGCCGCCGCC   54928      T  ACA   _
                                GAGGCCG CG  CCGCC CT
                                ||||||| ||  ||||| ||
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                                CTCCGGC GC   GGCGG GG
                                   _ C__     C
GAM2321  TOP3A    3'  AAGGCCAACACTGTCCTC    54929       GTC    CGC
                                GAGGCC   GACAC   CCTC
                                ||||||   |||||   ||||
                                TTCCGG   TTGTG   GGAG
                                   ___     ACA
GAM2321  BRAP     3'  AAGGCCGGCCTTCGTCCTC   54930       _  GACAC  C
                                GAGGCCG TC    CG CCTC
                                ||||||| ||    || ||||
                                TTCCGGC GG    GC GGAG
                                   C  AA___  A
GAM2321  C1orf2   5'  GAGGCCGCGGCGCCGCTGTCTC 54931       T  ACA   C__
                                GAGGCCG CG   CCGC   CTC
                                ||||||| ||   ||||   |||
                                CTCCGGC GC   GGCG   GAG
                                   _ CGC    ACA
GAM2321  C1orf2   5'  GAGGCCGCGGCGCCGCTGTCTC 54931       T  ACA   C__
                                GAGGCCG CG   CCGC   CTC
                                ||||||| ||   ||||   |||
                                CTCCGGC GC   GGCG   GAG
                                   _ CGC    ACA
GAM2321  C20orf172 5'  AAGGCCACGGGTCGCTCTC   54932       T  ACAC   C
                                GAGGCCG CG    CGC CTC
                                ||||||| ||    ||| |||
                                TTCCGGT GC    GCG GAG
                                   _ CCA_   A
GAM2321  CKLF1    5'  GGCGGAGCACCGCCCTC     54933     CGTC  _
                                GGC    GA CACCGCCCTC
                                |||    || ||||||||||
                                CCG    CT GTGGCGGGAG
                                  C___  C
GAM2321  CKLF1    5'  GGCGGAGCACCGCCCTC     54933     CGTC  _
                                GGC    GA CACCGCCCTC
                                |||    || ||||||||||
                                CCG    CT GTGGCGGGAG
                                  C___  C
GAM2321  CPLX1    3'  AGGCCCCGCCGCCCT       54934       G   ACA
                                AGGCC TCG   CCGCCCT
                                ||||| |||   |||||||
                                TCCGG GGC   GGCGGGA
                                   _  ___
GAM2321  DDX39    3'  GAGGCCGTCAGACACTGGGCTC 54935         _    CGCC
                                GAGGCCGTC GACAC    CTC
                                ||||||||| |||||    |||
                                CTCCGGCAG CTGTG    GAG
                                     T    ACCC
GAM2321  DKFZP434N093 3'  AAGGCCGCACTCGCACTGC   54936         ___  A   C
                                GAGGCCGT   CG CAC GC
                                ||||||||   || ||| ||
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                                TTCCGGCG   GC GTG CG
                                    TGA  _   A
GAM2321  DOC-1R   5'  GGCGGTGGCCACCGCCCTC   54937     C  CGA
                                GGC GT   CACCGCCCTC
                                ||| ||   ||||||||||
                                CCG CA   GTGGCGGGAG
                                  C  CCG
GAM2321  FLJ00001 3'  GGCCGTCAACCGTCCTC     54938        AC    C
                                GGCCGTCG  ACCG CCTC
                                ||||||||  |||| ||||
                                CCGGCAGT  TGGC GGAG
                                    __    A
GAM2321  FLJ12387 3'  GACCGTCGCCGCCCC       54939        ACA
                                GGCCGTCG   CCGCCCT
                                ||||||||   |||||||
                                CTGGCAGC   GGCGGGG
                                    ___
GAM2321  FLJ13072 5'  GGCCGTCACACAACACTC    54940       G    C  C
                                GGCCGTC ACAC GC CTC
                                ||||||| |||| || |||
                                CCGGCAG TGTG TG GAG
                                    _   T  T
GAM2321  FOXD4    5'  GGGCCGCCGCCGCCCTC     54941    A      ACA
                                G GGCCGTCG   CCGCCCTC
                                | ||||||||   ||||||||
                                C CCGGCGGC   GGCGGGAG
                                _      ___
GAM2321  GCHFR    3'  AAGGCCATTCACTGCCCT     54942        CGA   C
                                GAGGCCGT   CAC GCCCT
                                ||||||||   ||| |||||
                                TTCCGGTA   GTG CGGGA
                                    A__   A
GAM2321  GOLPH2   5'  GAGGCCGCCCGGGTCGCTCTC  54943         GACAC   C
                                GAGGCCGTC    CGC CTC
                                |||||||||    ||| |||
                                CTCCGGCGG    GCG GAG
                                     GCCCA   A
GAM2321  KCNG3    5'  GAGGCCGCGGTGCCCTC     54944       T  ACACC
                                GAGGCCG CG    GCCCTC
                                ||||||| ||    ||||||
                                CTCCGGC GC    CGGGAG
                                    _ CA___
GAM2321  KIAA0478 3'  GAGACCACACAAACACTGTCCT 54945       TC__    CGC
           C                     GAGGCCG   GACAC   CCTC
                                ||||||||   |||||  ||||
                                CTCTGGT    TTGTG   GGAG
                                    GTGT    ACA
GAM2321  KIAA0515 3'  GAGGCCGCATGGCGGCACCGTC 54946        _____ A    C
           CTC                    GAGGCCGT    CG CACCG CCTC
                                ||||||||    || ||||| ||||
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                                CTCCGGCG   GC GTGGC GGAG
                                    TACC  C    A
GAM2321  KIAA1431  5'  GAGGCCGCGCGACGCCCT   54947       _   ACC
                                GAGGCCGT CGAC   GCCCT
                                |||||||| ||||   |||||
                                CTCCGGCG GCTG   CGGGA
                                    C   ___
GAM2321  KIAA1766  5'  GGGTCCCCGTCGCCGCCCTC   54948   ____    ACA
                                GG   CCGTCG   CCGCCCTC
                                ||   ||||||   ||||||||
                                CC   GGCAGC   GGCGGGAG
                                 CAGG    ___
GAM2321  KIAA1950  3'  AGCTGTGACCCCGCCCTC   54949    C  C   A
                                GGC GT GAC CCGCCCTC
                                ||| || ||| ||||||||
                                TCG CA CTG GGCGGGAG
                                  A  _   G
GAM2321  KIAA1970  5'  GAGGCCGCCGAAGGCCTCTC   54950         CACC  _
                                GAGGCCGTCGA   GCC CTC
                                ||||||||||   ||| |||
                                CTCCGGCGGCT   CGG GAG
                                      TC__   A
GAM2321  MGC16386  5'  AAGGCCACTCGCTGCCCTC   54951       _   ACACC
                                GAGGCCG TCG    GCCCTC
                                ||||||| |||    ||||||
                                TTCCGGT AGC    CGGGAG
                                    G   GA___
GAM2321  MGC2744   5'  AGGCTGTCCCCCGCCCTC    54952     C   GACA
                                AGGC GTC    CCGCCCTC
                                |||| |||    ||||||||
                                TCCG CAG    GGCGGGAG
                                  A   GG__
GAM2321  MGC2865   5'  GGCGCCGTCACCGCCCTC    54953     C    A
                                GGC GTCG CACCGCCCTC
                                ||| |||| ||||||||||
                                CCG CGGC GTGGCGGGAG
                                  _    A
GAM2321  MGC3731   5'  GAGGCCGCCGGCTTCCTC    54954         ACACC  __
                                GAGGCCGTCG    GC  CCTC
                                |||||||||    ||  ||||
                                CTCCGGCGGC    CG  GGAG
                                      _____  AA
GAM2321  MGC4701   5'  GAGCCCGCCGCCACCGCCCTC  54955     G     A
                                GAG CCGTCG CACCGCCCTC
                                ||| |||||| ||||||||||
                                CTC GGCGGC GTGGCGGGAG
                                  G     G
GAM2321  MRPL34    5'  GAGCCCAGAGCCGCCCTC    54956     G   TC  CA
                                GAG CCG  GA  CCGCCCTC
                                ||| |||  ||  ||||||||
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                                CTC GGT  CT  GGCGGGAG
                                  G  __  C_
GAM2321  PIP5K2A   5'  GAGGCCGGGGACCCGCCCTC  54957       TC   A
                                GAGGCCG  GAC CCGCCCTC
                                |||||||  ||| ||||||||
                                CTCCGGC  CTG GGCGGGAG
                                    CC  _
GAM2321  RAB21     5'  GGCGCTGTCCCCACGCCCTC  54958     C__   GA   C
                                GGC   GTC  CAC GCCCTC
                                |||   |||  ||| ||||||
                                CCG   CAG  GTG CGGGAG
                                  CGA   GG  _
GAM2321  SC65      3'  GGCCATCGGCACCAGGCT    54959        A    CC
                                GGCCGTCG CACCG  CT
                                |||||||| |||||  ||
                                CCGGTAGC GTGGT  GA
                                     C    CC
GAM2321  SLC37A1   5'  GAGACCGTCCCCGGCTCTC   54960        GACA  _ C
                                GAGGCCGTC   CCG C CTC
                                |||||||||   ||| | |||
                                CTCTGGCAG   GGC G GAG
                                     G___   C A
GAM2321  TRAD      5'  GAGAGCCGGCTCCCGCCCTC  54961     _   TCGACA
                                GAG GCCG     CCGCCCTC
                                ||| ||||     ||||||||
                                CTC CGGC     GGCGGGAG
                                  T   CGAG__
GAM2321  TRAF3     3'  GCAGCGTCGACACTGCCCTC  54962   A  C      C
                                G GGC GTCGACAC GCCCTC
                                | ||| |||||||| ||||||
                                C TCG CAGCTGTG CGGGAG
                                 G  _       A
GAM2321  UBXD2     5'  GAAGCCGGCTCCGCCCTC    54963       TCGACA
                                GAGGCCG     CCGCCCTC
                                |||||||     ||||||||
                                CTTCGGC     GGCGGGAG
                                    CGA___
GAM2321  LOC114987 3'  GAAGGGTACCGCCCTC      54964     CC  CGAC
                                GAGG  GT   ACCGCCCTC
                                ||||  ||   |||||||||
                                CTTC  CA   TGGCGGGAG
                                  C_  _____
GAM2321  LOC126823 5'  GAGTGTGGATACCGCCCTC   54965     GCC  C  C
                                GAG   GT GA ACCGCCCTC
                                |||   || || |||||||||
                                CTC   CA CT TGGCGGGAG
                                  A__  C  A
GAM2321  LOC146823 5'  GGCGCCGACCGCCCT       54966     C    CA
                                GGC GTCGA  CCGCCCT
                                ||| |||||  |||||||
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                                CCG CGGCT  GGCGGGA
                                  _    __
GAM2321  LOC147895 5'  GAGGCCGTGGCCACCACC    54967        CGA
                                GAGGCCGT   CACCGCC
                                ||||||||   |||||||
                                CTCCGGCA   GTGGTGG
                                    CCG
GAM2321  LOC148696 5'  AGGACGAGCACCGCCCT     54968     CCGT  _
                                AGG    CGA CACCGCCCT
                                |||    ||| |||||||||
                                TCC    GCT GTGGCGGGA
                                  T___   C
GAM2321  LOC149076 3'  GAAGGTCCCACATTGCCCTC   54969     CCG  G   CC
                                GAGG   TC ACA  GCCCTC
                                ||||   || |||  ||||||
                                CTTC   GG TGT  CGGGAG
                                   CA_  G   AA
GAM2321  LOC149469 5'  GAGGCCATCACACAGCCCTC   54970        G    C
                                GAGGCCGTC ACAC GCCCTC
                                |||||||||| |||| ||||||
                                CTCCGGTAG TGTG CGGGAG
                                     _    T
GAM2321  LOC150271 3'  GAGGCCACAAGCTGCTCTC    54971        T   CACC  C
                                GAGGCCG CGA    GC CTC
                                ||||||| |||    || |||
                                CTCCGGT GTT    CG GAG
                                    _   CGA_  A
GAM2321  LOC152190 5'  GAGGCCGTGCGGCGCCGCT    54972         _  ACAC   _
                                GAGGCCGT CG    CGCC CT
                                |||||||| ||    |||| ||
                                CTCCGGCA GC    GCGG GA
                                     C  C___    C
GAM2321  LOC169436 3'  GAGGCCACTGCCGCCCTC     54973        TCGACA
                                GAGGCCG     CCGCCCTC
                                |||||||     ||||||||
                                CTCCGGT     GGCGGGAG
                                    GAC___
GAM2321  LOC219790 5'  GGGCCGTCGCCACTCCT     54974    A       ACA   _
                                G GGCCGTCG   CCGC CCT
                                | ||||||||   |||| |||
                                C CCGGCAGC   GGTG GGA
                                _       ___    A
GAM2321  LOC221184 5'  GGGCGCCACCGCCCTC      54975    C   CGA
                                GG CGT   CACCGCCCTC
                                || |||   ||||||||||
                                CC GCG   GTGGCGGGAG
                                 C   ___
GAM2321  LOC253039 3'  GGGTCAGATGCCGCCCTC    54976    CC   _  CA
                                GG  GTC GA  CCGCCCTC
                                ||  ||| ||  ||||||||
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                                CC  CAG CT  GGCGGGAG
                                 __   T  AC
GAM2321  LOC255328 3'  GAGGCCATTTGTCATTTGCCTT 54977        CGA_  CC_   C
              C                  GAGGCCGT    CA   GCC TC
                                 ||||||||    ||   ||| ||
                                 CTCCGGTA    GT   CGG AG
                                     AACA  AAA   A
GAM2321  LOC256855 3'  GAGGCTGCGGCACCGCCCTC   54978      C T  A
                                 GAGGC G CG CACCGCCCTC
                                 ||||| | || ||||||||||
                                 CTCCG C GC GTGGCGGGAG
                                    A _  C
GAM2321  LOC257476 3'  GAACCCAGGCGCCGCCCTC    54917     G   T_  ACA
                                 GAG CCG  CG   CCGCCCTC
                                 ||| |||  ||   ||||||||
                                 CTT GGT  GC   GGCGGGAG
                                   G   CC  ___
GAM2321  LOC51133  5'  GACGCGCTCGCCGCCCTC    54979    G  CG   ACA
                                 GA GC  TCG   CCGCCCTC
                                 || ||  |||   ||||||||
                                 CT CG  AGC   GGCGGGAG
                                  G  CG   ___
GAM2321  LOC51171  5'  GAGGCCGTCGCATCAAATCCTC 54980          A  C  C__
                                 GAGGCCGTCG CA CG   CCTC
                                 |||||||||| || ||   ||||
                                 CTCCGGCAGC GT GT   GGAG
                                       _  A  TTA
GAM2321  LOC57795  3'  GAGGCCGCTGCCTGCCCT    54981        CGACA  _
                                 GAGGCCGT    CC GCCCT
                                 ||||||||    || |||||
                                 CTCCGGCG    GG CGGGA
                                     AC___  A
GAM2321  LOC91759  5'  GGCGCTTGGTCAGCCGCCCTC  54982     C____    ACA
                                 GGC    GTCG   CCGCCCTC
                                 |||    ||||   ||||||||
                                 CCG    CAGT   GGCGGGAG
                                   CGAAC   C__
GAM2322  CLCN7    3'  CCCTGGTGCTACGAGTCCGTG  54985     C   CTT      C
                                 CCC GGT   CTACGAG CCGTG
                                 ||| |||   ||||||| |||||
                                 GGG CCA   GATGCTC GGCAC
                                   A   C__      A
GAM2322  DLG4     3'  CCCCCGGTGGGTCTGTGCACGG 54986      CT_  T________   AGCC
              GCTCG                 CCGGT   TC       ACG    CG
                                 |||||   ||       |||    ||
                                 GGCCA   AG       TGC    GC
                                    CCC  ACACIIIG   CCGA
GAM2322  LATS2    3'  CCCTCGGCTTCCCTATTGGCCT 54987     _   T    ACGA__   C
              GTG                   CCC CGG CTTCT     GCC GTG
                                 ||| ||| |||||     ||| |||
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                                GGG GCC GAAGG     CGG CAC
                                  A  _    GATAAC  A
GAM2322 SLC1A4   3' CCCCTGGTCTACCGACTCTGTG 54988     C    TCTA  GCCC
                                CCCC GGTCT   CGA   GTG
                                |||| |||||   |||   |||
                                GGGG CCAGA   GCT   CAC
                                  A    TG__  GAGA
GAM2322 TNFRSF6B 5' CCCGGTCTTCTCGGACCGTG  54989         A  AG  C
                                CCCGGTCTTCT CG  CC GTG
                                |||||||||| ||  || |||
                                GGGCCAGAAGA GC  GG CAC
                                       _ CT  _
GAM2322 FLJ20727 5' CGTTCTTCTACTACTTGTG   54990    G      GA  CC
                                CG TCTTCTAC  GC  GTG
                                || ||||||||  ||  |||
                                GC AGAAGATG  TG  CAC
                                 A       A_  AA
GAM2322 KIAA0982  3' CCCCGATCTTGTCTGTGCACGG 54991      __ T_______  AGCC
           GCTCG                  CGGTCT  TC      ACG   CG
                                |||||| ||      |||   ||
                                GCTAGA  AG      TGC   GC
                                   AC  ACACIIIG   CCGA
GAM2322 KIAA1058  3' CCCTTGGTCCTCCCTGTGCACG 54992  C     T_________  AGCC
           GGCTCG                  GGTCTTC       ACG   CG
                                 |||||||       |||   ||
                                 CCAGGAG       TGC   GC
                                A     GGACACIIIG   CCGA
GAM2322 KIAA1373  5' CCCTTGGTGTCCGCAGCCCGTG 54993    CC   CT  TA G
                                CCC  GGT  TC  C AGCCCGTG
                                |||  |||  ||  | ||||||||
                                GGG  CCA  AG  G TCGGGCAC
                                  AA   C_  GC _
GAM2322 KIAA1940  3' CCCTCAGTCCACGGGGCCCGTG 54994    _    TCT   A_
                                CCC CGGTCT   ACG  GCCCGTG
                                ||| ||||||   |||  |||||||
                                GGG GTCAGG   TGC  CGGGCAC
                                  A     ___   CC
GAM2322 MYT1L    5' CCTGGTCCTCTCCAGCTTGTG  54995    C      ACG   CC
                                CC GGTCTTCT   AGC  GTG
                                || ||||||||   |||  |||
                                GG CCAGGAGA   TCG  CAC
                                 A       GG_   AA
GAM2322 RPH3A    3' CCCTGGTCTTCTAAATGCCTCC 54996     C       CGA  __
           GTG                    CCC GGTCTTCTA   GCC  CGTG
                                ||| |||||||||   |||  ||||
                                GGG CCAGAAGAT   CGG  GCAC
                                  A        TTA   AG
GAM2322 LOC145693 5' CCAGTCTAGGAGCCTGTG    54997        TCTAC    C
                                CCGGTCT    GAGCC GTG
                                |||||||    ||||| |||
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                                GGTCAGA    CTCGG CAC
                                   TC___    A
GAM2322  LOC151174 5'  CCTGGTCTGTCTGTCCTGTG  54998    C    _  ACGAG  C
                                CC GGTCT TCT    CC GTG
                                || ||||| |||    || |||
                                GG CCAGA AGA    GG CAC
                                 A    C   CA___  A
GAM2322  LOC203441 5'  GCCTCCGCTACGAGCCTGTG  54999      __       C
                                GTCTT  CTACGAGCC GTG
                                |||||  ||||||||| |||
                                CGGAG  GATGCTCGG CAC
                                   GC       A
GAM2322  LOC254312 5'  CCTCGGTCTTCTGCACGC    55000    C       ACGA  C
                                CC CGGTCTTCT   GC CGT
                                || |||||||||   || |||
                                GG GCCAGAAGA   CG GCG
                                 A        _____  T
GAM2322  LOC51162  3'  CCTCCGGGCTGCCTGGCCTGTG 55001    _   T  T  ACGA   C
                                CC CCGG CT CT   GCC GTG
                                || |||| || ||   ||| |||
                                GG GGCC GA GG   CGG CAC
                                 A   C  C  AC__  A
GAM2322  LOC51162  3'  CCTCCGGGCTGCCTGGCCTGTG 55001    _   T  T  ACGA   C
                                CC CCGG CT CT   GCC GTG
                                || |||| || ||   ||| |||
                                GG GGCC GA GG   CGG CAC
                                 A   C  C  AC__  A
GAM2323  IRS2     5'  TCGGGGTCCGCGCCGCCGCCGG 55004     AC_     T  GA_
            G                    TCGG   CCGCGC CG   CCGGG
                                ||||   |||||| ||   |||||
                                AGCC   GGCGCG GC   GGCCC
                                  CCA     _ GGC
GAM2323  MUS81    5'  CCGGCCCAGGCGGACCGGG   55005     A   C  TC
                                TCGG CCCG GC  GGACCGGG
                                |||| |||| ||  ||||||||
                                GGCC GGGT CG  CCTGGCCC
                                  _   C  __
GAM2323  ARS2     5'  GGACTCGCGCTCGGACGGG   55006     C        C
                                GGAC CGCGCTCGGAC GGG
                                |||| |||||||||| |||
                                CCTG GCGCGAGCCTG CCC
                                  A        _
GAM2323  KIAA0339  3'  TCGGACCGGCGCTCGGAC    55007       C
                                TCGGACC GCGCTCGGAC
                                ||||||| ||||||||||
                                AGCCTGG CGCGAGCCTG
                                    C
GAM2323  KIAA0444  3'  GGACCCGCCCCCGCCGGG    55008        G   GA
                                GGACCCGC CTCG  CCGGG
                                |||||||| ||||  |||||
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                                CCTGGGCG GGGC  GGCCC
                                    G   __
GAM2323  MGC10992  5'  TCGGACCTCGGGCCGGGA    55009       CGCGC   A
                                TCGGACC    TCGG CCGGGA
                                |||||||    |||| ||||||
                                AGCCTGG    AGCC GGCCCT
                                    _____   C
GAM2323  WBP4     5'  TCAGACTCGCGCTTTCCCAGCG 55010      C     ____  AC
           GGAC                   CGGAC CGCGCT   CGG  CGGGAC
                                |||||  ||||||   |||  ||||||
                                GTCTG GCGCGA   GTC  GCCCTG
                                   A     AAGG  __
GAM2323  LOC112937 5'  GACGCCGCGCTCGGGCCGGGAC 55011     _       A
                                GAC CCGCGCTCGG CCGGGAC
                                ||| |||||||||| |||||||
                                CTG GGCGCGAGCC GGCCCTG
                                  C        C
GAM2323  LOC115073 5'  TCGGACCCCGCTGGGGG     55012       G   C  ACC
                                TCGGACCC CGCT GG   GGG
                                |||||||| |||| ||   |||
                                AGCCTGGG GCGA CC   CCC
                                    _   _ ___
GAM2323  LOC146325 5'  TCGGACCCCGCGGACGCGCTGG 55013       G   TC   _ ___
           G                    TCGGACCC CGC  GGAC C   GGG
                                |||||||| |||  |||| |   |||
                                AGCCTGGG GCG  CCTG G   CCC
                                    _   __    C CGA
GAM2323  LOC148114 5'  GGACCTGCTGCATCGGGAC    55014      C  _  TCGGAC
                                GGACC GC GC     CGGGAC
                                ||||| || ||     ||||||
                                CCTGG CG CG     GCCCTG
                                   A  A  TA____
GAM2323  LOC154834 5'  TCGGACCGACGCGGGCCGGG   55015       C   TC  A
                                TCGGACC GCGC  GG CCGGG
                                ||||||| ||||  || |||||
                                AGCCTGG TGCG  CC GGCCC
                                    C   C_  _
GAM2323  LOC221751 5'  TCCGACCCGCGCTCCTTGGAC  55016    G        ___
                                TC GACCCGCGCTC   GGAC
                                || ||||||||||   ||||
                                AG CTGGGCGCGAG   CCTG
                                  G         GAA
GAM2323  LOC255042 5'  TCTGACCTGCAGGATCGGGA   55017    G   C   CTC   C
                                TC GACC GCG   GGA CGGGA
                                || |||| |||   ||| |||||
                                AG CTGG CGT   CCT GCCCT
                                  A   A  ___  A
GAM2323  LOC255426 5'  TCGGCGCCGCGGACCGGG    55018     AC   GCTC
                                TCGG  CCGC   GGACCGGG
                                ||||  ||||   ||||||||
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                                AGCC  GGCG   CCTGGCCC
                                  GC   ____
GAM2323  LOC91748  3'  GGACTCGTGGCTCCGGAGGA  55019     C  C_   _  CCG
                                GGAC CG  GCTC GGA  GGA
                                |||| ||  |||| |||  |||
                                CCTG GC  CGAG CCT  CCT
                                  A  AC   G  ___
GAM2324  FLJ11222  3'  AATTTGTATCTGATAATT   55022     C       CG
                                GAT TGTATCTGG  GTT
                                ||| |||||||||  |||
                                TTA ACATAGACT  TAA
                                  A        AT
GAM2324  FLJ12688  3'  CTAGATTTGTTCTAACTCTC  55023      C  A     GG
                                CTAGAT TGT TCTGGC  TTC
                                |||||| ||| ||||||  |||
                                GATCTA ACA AGATTG  GAG
                                   A  _     A_
GAM2324  NEUROD6   5'  CTAGATCTGTGTATATCTG   55024         ____
                                CTAGATCTGT   ATCTG
                                ||||||||||   |||||
                                GATCTAGACA   TAGAC
                                     CATA
GAM2324  NTT73     3'  TAAATCTGTAAAATGGTTC   55025         TCTGGC
                                TAGATCTGTA     GGTTC
                                ||||||||||     |||||
                                ATTTAGACAT     CCAAG
                                     TTTA__
GAM2324  PPP1R1A   3'  TAGGTATGTATCTGGGCAAGCT 55026     ATC      _  _
                                TAG   TGTATCT GGC GGTT
                                |||   ||||||| ||| ||||
                                ATC   ACATAGA CCG TCGA
                                  CAT      C   T
GAM2324  UPB1      3'  CTAGATTAGTGTCTGATTGCGG 55027     CT  A   G_____  GTTC
            AAC                   AGAT  GT TCTG      CG   C
                                |||| || ||||      ||   |
                                TCTA  CA AGAC      GC   G
                                  AT  C   TAACIII  CTTG
GAM2324  LOC123031 5'  CTGGAACATGGCGGTTCC    55028     T_  C
                                CTG  AT TGGCGGTTCC
                                |||  || ||||||||||
                                GAC  TG ACCGCCAAGG
                                  CT  T
GAM2324  LOC147727 3'  GATTTGTATCTGAAAAGCT   55029     C       C_
                                GAT TGTATCTGG  GGTT
                                ||| |||||||||  ||||
                                CTA ACATAGACT  TCGA
                                  A        TT
GAM2324  LOC151176 5'  CTAGATCTGTGCTCC       55030          ATCTGGCG
                                CTAGATCTGT       GTTCC
                                ||||||||||       |||||
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                                GATCTAGACA       CGAGG
                                          ________
GAM2325  DDX15    3'  AGAAGCATTTTCAACCATTT   55033        CGGG
                                AGAGGCAT    GGCCATTT
                                ||||||||    ||||||||
                                TCTTCGTA    TTGGTAAA
                                    AAAG
GAM2325  PPP3CA   3'  TCAAAGGCATTAAGCATTT    55034         CG  GGC
                                TCAGAGGCAT  GG   CATTT
                                ||||||||||  ||   |||||
                                AGTTTCCGTA  TC   GTAAA
                                     AT  ___
GAM2325  RANBP3   5'  TCTTCAGAGGCATTGCTGGACT 55035     _       CGG_   _
            CATTT                   TCT CAGAGGCAT    GGGC CATTT
                                ||| |||||||||    |||| |||||
                                AGA GTCTCCGTA    CCTG GTAAA
                                  A        ACGA    A
GAM2325  SUV39H2  3'  TCAGAGGCATCGGTAATACATT 55036           GGGC_
            T                    TCAGAGGCATCGG     CATTT
                                ||||||||||||     |||||
                                AGTCTCCGTAGCC     GTAAA
                                      ATTAT
GAM2325  FLJ12960 5'  TCTCAGAGGTGTCGGCGAC    55037         CA    G
                                TCTCAGAGG  TCGG GGC
                                |||||||||  |||| |||
                                AGAGTCTCC  AGCC CTG
                                     AC    G
GAM2325  MED6     3'  TCTCAGAGGATCAAAAA     55038         C
                                TCTCAGAGG ATCGGGGG
                                ||||||||| ||||||||
                                AGAGTCTCC TAGTTTTT
                                          _
GAM2325  MGC27044 5'  TCAGAGGCATGACATT      55039         CGGG   C
                                TCAGAGGCAT    GGC ATT
                                ||||||||||    ||| |||
                                AGTCTCCGTA    CTG TAA
                                          _____   _
GAM2325  LOC145988 5'  TCTCAGGGCTACTGCCATT    55040       A   ATCGGGG
                                TCTCAG GGC      GCCATT
                                |||||| |||      ||||||
                                AGAGTC CCG      CGGTAA
                                   _   ATGA___
GAM2326  ENG      3'  CTGGGCGAGCGCGGGGGGCCG  55043        _   A__
                                TTGGGCG GCG   GGGGCCG
                                ||||||| |||   |||||||
                                GACCCGC CGC   CCCCGGC
                                    T   GCC
GAM2326  RAB26    5'  TTGGGCGGCGCGTCGGGGC    55044         A___
                                TTGGGCGGCG    GGGGC
                                ||||||||||    |||||
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                                AACCCGCCGC   CCCCG
                                     GCAG
GAM2326 SHMT2    3' TTGAGCAAGTTGGGGCCGAA  55045       CGA
                                TTGGGCGG  GGGGCCGAA
                                ||||||||  |||||||||
                                AACTCGTT  CCCCGGCTT
                                     CAA
GAM2326 CENTA2   3' TGGGCAGCCAGGGCCGA    55046       GA
                                TGGGCGGC  GGGGCCGA
                                ||||||||  ||||||||
                                ACCCGTCG  TCCCGGCT
                                     G_
GAM2326 DKFZP564D0478 3' TACTGGGCACTGGGCTGAGGC 55047       ____  GA
                                TATTGGGC   GGC  GGGGC
                                ||||||||   |||  |||||
                                ATGACCCG   CCG  CTCCG
                                     TGAC  A_
GAM2326 DMWD     5' TACTGGGGCGGGGCCGA    55048      CG  GA
                                TATTGGG  GC  GGGGCCGA
                                |||||||  ||  ||||||||
                                ATGACCC  CG  CCCCGGCT
                                     __  __
GAM2326 FLJ20171  3' TATTAGGCGAACCTGGGGGGC  55049        _ GA__
                                TATTGGGCGG C   GGGGC
                                |||||||||| |   |||||
                                ATAATCCGCT G   CCCCG
                                     T GACC
GAM2326 KIAA0215  5' TTGGGCGGCGGCGGCGGCTGA  55050        A_ _  C
                                TTGGGCGGCG  GG GGC GA
                                ||||||||||  || ||| ||
                                AACCCGCCGC  CC CCG CT
                                     CG  G   A
GAM2326 KIAA0415  3' ATTGGGGGCGGGGCCGA    55051      C   GA
                                ATTGGG GGC  GGGGCCGA
                                ||||||  |||  ||||||||
                                TAACCC CCG  CCCCGGCT
                                     _  __
GAM2326 LOC126917 3' GGCTGGCGAGGGAGGGAA    55052    _      CC
                                GGC GGCGAGGGG  GAA
                                ||| |||||||||  |||
                                CCG CCGCTCCCT  CTT
                                  A        CC
GAM2326 LOC144017 5' ATTGGGCGGCGAAGGAGC    55053          _
                                ATTGGGCGGCGAGGG GC
                                ||||||||||||||| ||
                                TAACCCGCCGCTTCC CG
                                          T
GAM2326 LOC152426 5' TTGGGCGAGACAGTCGAA    55054       C  G  GC
                                TTGGGCGG GA GG  CGAA
                                |||||||| || ||  ||||
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                                AACCCGCT CT TC  GCTT
                                    _ G  A_
GAM2326  LOC245744 3'  CTCAGGGCGAGGGGCTGA    55055    G  C        C
                                TT GG GGCGAGGGGC GA
                                || || |||||||||| ||
                                GA TC CCGCTCCCCG CT
                                 G  _        A
GAM2326  LOC51337  3'  TGGGCGGCGAGGGGTGCGA   55056             C_
                                TGGGCGGCGAGGGG  CGA
                                ||||||||||||||  |||
                                ACCCGCCGCTCCCC  GCT
                                       AC
GAM2327  APG5L    3'  CTTTAAACTTCAAAAGACTG   55059        C   TGT
                                CTTTAAAC TTA   AGACTG
                                |||||||| |||   ||||||
                                GAAATTTG AGT   TCTGAC
                                    A   TT_
GAM2327  GALR1    3'  CTTTAAAATGTAGACT      55060        CCTT
                                CTTTAAA    ATGTAGACT
                                |||||||    |||||||||
                                GAAATTT    TACATCTGA
                                    ____
GAM2327  MTMR6    3'  TACCTTTAAATCATATA     55061          CC
                                TACCTTTAAA  TTATGTA
                                ||||||||||  |||||||
                                ATGGAAATTT  AGTATAT
                                    __
GAM2327  TRPM7    3'  TACCTTTAAAATTTCTCAGCTG 55062          CC  ATG   A
                                TACCTTTAAA  TT   TAG CTG
                                ||||||||||  ||   ||| |||
                                ATGGAAATTT  AA   GTC GAC
                                     TA  GA_  _
GAM2327  USH2A    3'  CCTTTAAATTTTGTGACCG    55063        CC  A   A
                                CCTTTAAA  TT TGT GACTG
                                ||||||||  || ||| |||||
                                GGAAATTT  AA ACA CTGGC
                                    __  A  _
GAM2327  ZNF36    3'  CCTTTGGAACTGTAGACT     55064      A_   CTTA
                                CCTTT  AAC    TGTAGACT
                                |||||  |||    ||||||||
                                GGAAA  TTG    ACATCTGA
                                   CC  ____
GAM2327  DKFZP564C103 3'  CCTTTAAACTCAAGACT     55065         C   TGT
                                CCTTTAAAC TTA   AGACT
                                ||||||||| |||   |||||
                                GGAAATTTG AGT   TCTGA
                                    _  ___
GAM2327  KIAA1301 3'  CCTGTAAACCCATAGGCTG    55066     T      TAT    A
                                CCT TAAACCT   GTAG CTG
                                ||| |||||||   |||| |||
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                                GGA ATTTGGG   TATC GAC
                                  C      ___    C
GAM2327  PRDX2    3'  TACCTCTAGGCCTGTGTGCGGC 55067       AA   TA_  AGA
             TG                   TACCTTTA  CCT   TGT   CTG
                                  ||||||||  |||   |||   |||
                                  ATGGAGAT  GGA   ACG   GAC
                                      CC    CAC   CC_
GAM2327  LOC155081 3'  CCTTCAAATGCTCCTGGACTG  55068       C_   A  TA
                                  CCTTTAAA  CTT TG  GACTG
                                  ||||||||  ||| ||  |||||
                                  GGAAGTTT  GAG AC  CTGAC
                                      AC    G   __
GAM2327  LOC202802 3'  CCTTCAAATGCTCCTGGACTG  55068       C_   A  TA
                                  CCTTTAAA  CTT TG  GACTG
                                  ||||||||  ||| ||  |||||
                                  GGAAGTTT  GAG AC  CTGAC
                                      AC    G   __
GAM2327  LOC222228 3'  CCTTCAAATCCTCCTGGACTG  55069       _    A  TA
                                  CCTTTAAA CCTT TG  GACTG
                                  ||||||||  |||| ||  |||||
                                  GGAAGTTT GGAG AC  CTGAC
                                      A    G   __
GAM2327  LOC222233 3'  CCTTCAAATCCTCCTGGACTG  55069       _    A  TA
                                  CCTTTAAA CCTT TG  GACTG
                                  ||||||||  |||| ||  |||||
                                  GGAAGTTT GGAG AC  CTGAC
                                      A    G   __
GAM2328  CREBL2   3'  TCAGAGCCTGTCAGGAAATTCA 55072       ATG   TA
             T                    TCAGAGC   GTC  GAAATTCAT
                                  |||||||   |||  |||||||||
                                  AGTCTCG   CAG  CTTTAAGTA
                                     GA_    TC
GAM2328  GABRE    3'  GCATGTCCAAATTCAT     55073      G    GA
                                  GCATG TCTA  AATTCAT
                                  |||||  ||||  |||||||
                                  CGTAC AGGT  TTAAGTA
                                    _    __
GAM2328  GABRE    3'  GCATGTCCAAATTCAT     55073      G    GA
                                  GCATG TCTA  AATTCAT
                                  |||||  ||||  |||||||
                                  CGTAC AGGT  TTAAGTA
                                    _    __
GAM2328  GABRE    3'  GCATGTCCAAATTCAT     55073      G    GA
                                  GCATG TCTA  AATTCAT
                                  |||||  ||||  |||||||
                                  CGTAC AGGT  TTAAGTA
                                    _    __
GAM2328  GABRE    3'  GCATGTCCAAATTCAT     55073      G    GA
                                  GCATG TCTA  AATTCAT
                                  |||||  ||||  |||||||
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                              CGTAC AGGT  TTAAGTA
                                _   __
GAM2328 RAB11A   3' AGGCATTTTAGAAATTCAT   55074    A   GGTC
                              AG GCAT   TAGAAATTCAT
                              || ||||   ||||||||||
                              TC CGTA   ATCTTTAAGTA
                               _   AA__
GAM2328 RAB11A   3' AGGACATGGAAAAATTCAT   55075    AG   TCT
                              AG  CATGG   AGAAATTCAT
                              ||  |||||   ||||||||||
                              TC  GTACC   TTTTTAAGTA
                               CT    ___
GAM2328 KIAA0562 3' GATCAGGTGGAAATTCAT    55076    G  T   CTA
                              GA CA GGT   GAAATTCAT
                              || || |||   ||||||||
                              CT GT CCA   CTTTAAGTA
                               A  _  C__
GAM2328 KIAA1500 3' GAGAAATCAGAAATTCAT    55077    CAT   T
                              GAG   GGTC AGAAATTCAT
                              |||   |||| ||||||||||
                              CTC   TTAG TCTTTAAGTA
                                T__   _
GAM2328 PRO0641  3' GAGAGTATCATGAAATTCAT  55078    CATG  TA
                              GAG   GTC  GAAATTCAT
                              |||   |||  ||||||||
                              CTC   TAG  CTTTAAGTA
                                TCA_  TA
GAM2328 LOC152316 5' CCAGAGCATGGGAACCAAGTTC 55079          T__   AAA
            AT                  TCAGAGCATGG   CTAG   TTCAT
                              ||||||||||  ||||  |||||
                              GGTCTCGTACC   GGTT   AAGTA
                                    CTT   C__
GAM2328 LOC152793 3' GCCATCTGGAAATTCAT    55080    ATG   A
                              GC   GTCT GAAATTCAT
                              ||   |||| ||||||||
                              CG   TAGA CTTTAAGTA
                               G__   C
GAM2328 LOC255446 3' TCAGAACATGGTCTAGAA   55081
                              TCAGAGCATGGTCTAGAA
                              ||||||||||||||||||
                              AGTCTTGTACCAGATCTT

GAM2328 LOC255995 3' TCAGAGCAGGATAGAGAAATT  55082        T   CT
                              TCAGAGCA GGT  AGAAATT
                              |||||||| |||  |||||||
                              AGTCTCGT CTA  TCTTTAA
                                   C   TC
GAM2328 LOC90233  3' TCAGAATGTGGAAAAATTCAT  55083       CA   TCT
                              TCAGAG  TGG   AGAAATTCAT
                              ||||||  |||   ||||||||||
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                                AGTCTT  ACC   TTTTTAAGTA
                                   AC  ___
GAM2328 LOC91300 3' CCGGAGCACCAGAAATT     55085    A    TGGT
                                TC GAGCA    CTAGAAATT
                                || |||||    |||||||||
                                GG CTCGT    GGTCTTTAA
                                 C    ____
GAM2328 LOC91300 3' CCAGAGCACCAGAAATT     55084        TGGT
                                TCAGAGCA    CTAGAAATT
                                ||||||||    |||||||||
                                GGTCTCGT    GGTCTTTAA
                                      ____
GAM2329 DDB2     5' TACAAAACTGCGGGGCCA    55088        A    AGAT   G
                                TACAAGA CTGCG    GGT CA
                                ||||||| |||||    ||| ||
                                ATGTTTT GACGC    CCG GT
                                    _    C___   _
GAM2329 GNAS     3' ACAGGATCACAGAGATGGTGC  55089     A  ACT  _
                                ACA GA   GC GAGATGGTGC
                                ||| ||   || ||||||||||
                                TGT CT   TG CTCTACCACG
                                  C  AG_  T
GAM2329 SNX9     3' AAGAACCAAATGGTGCA      55090        GCG
                                AAGAACT   AGATGGTGCA
                                |||||||   ||||||||||
                                TTCTTGG   TTTACCACGT
                                     ___
GAM2329 AMOTL1   3' GAGCTGCAAGAGTGCA      55091    A       TG
                                GA CTGCGAGA  GTGCA
                                || ||||||||  |||||
                                CT GACGTTCT  CACGT
                                 C       __
GAM2329 BC022889 3' CAAGAACTGCAGAGGAC     55092          G   T  T
                                CAAGAACTGC AGA GG GC
                                |||||||||| ||| || ||
                                GTTCTTGACG TCT CC TG
                                      _  _  _
GAM2329 C20orf4  3' ACAGGGACTGTGATCATAGTAC 55093     AGA    C  G_
                                ACA   ACTG GA  ATGGTGC
                                |||   |||| ||  |||||||
                                TGT   TGAC CT  TATCATG
                                  CCC    A  AG
GAM2329 C20orf97 3' CAGGAACTGCATGTGTG     55094    A      GAG  _
                                CA GAACTGC   ATG GTG
                                || |||||||   ||| |||
                                GT CTTGACG   TAC CAC
                                 C       ___  A
GAM2329 DKFZp434A2417 3'  TACAAGAACTGTGTGCAAAGTG 55095           CGAGAT_
             C                    TACAAGAACTG      GGTGC
                                ||||||||||       |||||
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                                ATGTTCTTGAC      TCACG
                                      ACACGTT
GAM2329  FLJ11273  3'  TACAAGAACTGCAGGTCCA   55096          AGAT   G
                                TACAAGAACTGCG    GGT CA
                                ||||||||||||    ||| ||
                                ATGTTCTTGACGT    CCA GT
                                      ____  G
GAM2329  FLJ21841  3'  ACTGCAGTGAGATGGTGCAC   55097      ___
                                ACTGC   GAGATGGTGCAC
                                |||||   ||||||||||||
                                TGACG   CTCTACCACGTG
                                   TCA
GAM2329  KIAA0092  3'  AAGAACTGTGAAGGTA      55098        C   AT
                                AAGAACTG GAG  GGTG
                                |||||||| |||  ||||
                                TTCTTGAC CTT  CCAT
                                     A  __
GAM2329  KIAA0789  5'  TAAAGAACTGTGAGAATAGCAC 55099   C      C   _  TG
                                A AAGAACTG GAGA TGG  C
                                | |||||||| |||| |||  |
                                A TTCTTGAC CTCT ATC  G
                                 T       A    T   GT
GAM2329  KIAA0993  3'  GAACAACACTGAGGTGGTGC   55100     T  ___  A
                                GAAC GC   GAG TGGTGC
                                |||| ||   ||| ||||||
                                CTTG TG   CTC ACCACG
                                  T  TGA   C
GAM2329  KIAA1239  3'  TAAAGAAGCATACAGATGGTG  55101   C    C__   G
                                A AAGAA   TGC AGATGGTG
                                | |||||   ||| ||||||||
                                A TTCTT   ATG TCTACCAC
                                 T    CGT   _
GAM2329  RBBP4     5'  CAAGAGCTCGCTCTGTGCGC   55102      A  G  AGA  _
                                CAAGA CT CG   TG GTGC
                                ||||| || ||   || ||||
                                GTTCT GA GC   AC CGCG
                                   C  _  GAG  A
GAM2329  RGS7      5'  TACAAGAATTATCAGTGTGC   55103       C  CG  ATG
                                TACAAGAA TG  AG   GTGC
                                |||||||| ||  ||   ||||
                                ATGTTCTT AT  TC   CACG
                                     A  AG  A__
GAM2329  LOC118851 5'  AAGGGCTGCGAAAGGCGC    55104     AA       T
                                AAG  CTGCGAGA GGTGC
                                |||  |||||||| |||||
                                TTC  GACGCTTT CCGCG
                                  CC       _
GAM2329  LOC130497 3'  CAAGAGCTGGGAGGGGGC    55105      A   C   AT  T
                                CAAGA CTG GAG  GG GC
                                ||||| ||| |||  || ||
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                                GTTCT GAC CTC  CC CG
                                  C   C   C_ _
GAM2329  LOC138307 5'  CACGAGGACACCCAGGATGGTG 55106     A  A  TG_  A
             CAC                   TAC AG AC   CG GATGGTGCAC
                                |||  ||  ||   ||  ||||||||||
                                GTG TC TG   GT CTACCACGTG
                                  C  C  TGG  C
GAM2329  LOC146443 5'  TACAAGAATTGTAGTGC     55107         C  CGAGA
                                TACAAGAA TG     TGGTGC
                                ||||||||  ||    ||||||
                                ATGTTCTT AC     ATCACG
                                    A  _____
GAM2329  LOC150848 5'  TACAAGATTTGTGAGGTCCA   55108        AC  C  GAT   G
                                TACAAGA  TG GA   GGT CA
                                |||||||  ||  ||   |||  ||
                                ATGTTCT  AC CT   CCA GT
                                    AA  A  ___   G
GAM2329  LOC154222 3'  CACAAGAACTGTGAGAAATCCA 55109           C    T   G
                                TACAAGAACTG GAGA GGT CA
                                ||||||||||| ||||  |||  ||
                                GTGTTCTTGAC CTCT TTA GT
                                    A    _   G
GAM2329  LOC51014  3'  TACAGTGGCAATGGTGCA    55110      AGAACT  GA
                                TACA     GC  GATGGTGCA
                                ||||     ||  |||||||||
                                ATGT     CG  TTACCACGT
                                  CAC___  __
GAM2329  LOC51336  3'  CAAGAACTGTAGGTGTAC    55111         CG  ATG
                                CAAGAACTG  AG   GTGC
                                |||||||||  ||   ||||
                                GTTCTTGAC  TC   CATG
                                    A_  CA_
GAM2330  AICDA     3'  CATCCTACCTAAAAGTCATAGA 55114      AAGAAG       C
                                CATC     AAAAGTCA AGA
                                ||||     ||||||||  |||
                                GTAG     TTTTCAGT TCT
                                  GATGGA       A
GAM2330  BCAT1     3'  ACATCAGGAAGAAAACAG     55115       A      AGTC
                                ACATCA GAAGAAA    ACAG
                                ||||||  |||||||    ||||
                                TGTAGT CTTCTTT    TGTC
                                   C      _____
GAM2330  CLTB      3'  TACATCAGGAGGGACAGTCACA 55116        A  AGAAA
                                TACATCA GA     AGTCACA
                                |||||||  ||    |||||||
                                ATGTAGT CT     TCAGTGT
                                    C  CCCTG
GAM2330  CLTB      3'  TACATCAGGAGGGACAGTCACA 55116        A  AGAAA
                                TACATCA GA     AGTCACA
                                |||||||  ||    |||||||
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                                ATGTAGT CT    TCAGTGT
                                    C  CCCTG
GAM2330  DNM1    3'  TACAACAGATTAAGTCACAGA  55117     TCA   AGAA
                                TACA   AGA   AAGTCACAGA
                                ||||   |||   ||||||||||
                                ATGT   TCT   TTCAGTGTCT
                                  TG_   AA__
GAM2330  GRM1    3'  TACATCAAGGTGAAGAGT    55118        AA   A
                                TACATCAAG  GAA AGT
                                |||||||||  ||| |||
                                ATGTAGTTC  CTT TCA
                                     CA   C
GAM2330  KRT2A   5'  TCCAGGGAGGAAAGTCACAG   55119    A  A_  A
                                TC AG  AG AAAGTCACAG
                                || ||  || ||||||||||
                                AG TC  TC TTTCAGTGTC
                                 G  CC  C
GAM2330  MAN1A1  3'  CATAAGGAGGCTGTCACAGA   55120     C   A  AAAA
                                CAT AAG AG    GTCACAGA
                                |||| ||| ||   ||||||||
                                GTA TTC TC    CAGTGTCT
                                  _   C  CGA_
GAM2330  PCP4    3'  ACATCAAGGAAAATAGTTGCAG 55121        A    A   CA
                                ACATCAAG AGAA AGT  CAG
                                |||||||| |||| |||  |||
                                TGTAGTTC TTTT TCA  GTC
                                     C    A   AC
GAM2330  PEX1    3'  AAGAAGAAATTCATAGA     55122         AG   C
                                AAGAAGAAA  TCA AGA
                                |||||||||  ||| |||
                                TTCTTCTTT  AGT TCT
                                     A_   A
GAM2330  STX1A   3'  TCAAGAAGGCAACACGGA    55123        AAA  T   A
                                TCAAGAAG   AG CAC GA
                                ||||||||   || ||| ||
                                AGTTCTTC   TT GTG CT
                                     CG_  _   C
GAM2330  TLX1    5'  TCAAGAAGTAAAATCCTACAG  55124        A     __
                                TCAAGAAG AAAGTC  ACAG
                                |||||||| ||||||  ||||
                                AGTTCTTC TTTTAG  TGTC
                                     A     GA
GAM2330  ABCA9   3'  ATCTTTAAAAGAGTCACAG   55125    A__     AAA
                                ATC   AGAAGA   GTCACAG
                                |||   ||||||   |||||||
                                TAG   TTTTCT   CAGTGTC
                                  AAA     ____
GAM2330  C8orf13 3'  TACACAGGAAGAAGTCACAG   55126     T  A    AA
                                TACA CA GAAGA  AGTCACAG
                                |||| || |||||  ||||||||
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                                ATGT GT CTTCT  TCAGTGTC
                                  _ C    __
GAM2330  CCR8     3'  TACATGAGAAGAAACATCA    55127       CA       A
                                TACAT  AGAAGAAA GTCA
                                |||||  |||||||| ||||
                                ATGTA  TCTTCTTT TAGT
                                   C_       G
GAM2330  CXorf1   3'  ACATTAAGAAAAATTAAGTCAC 55128      C      __
              AGA                  ACAT AAGAAGAA  AAGTCACAGA
                                |||| ||||||||  ||||||||||
                                TGTA TTCTTTTT  TTCAGTGTCT
                                   A       AA
GAM2330  DKFZp566D234 3'  TACATGAAATCATTAAGTCACA 55129       C   AAGAA
              GA                   TACAT AAG     AAGTCACAGA
                                ||||| |||     ||||||||||
                                ATGTA TTT     TTCAGTGTCT
                                   C   AGTAA
GAM2330  ELKS     3'  ACATCAAGAAGGTTAGTGTAGA 55130           AAA   CAC
                                ACATCAAGAAG   AGT   AGA
                                ||||||||||   |||   |||
                                TGTAGTTCTTC   TCA   TCT
                                      CAA   CA_
GAM2330  FLJ10178 3'  AGCAAATGAAGTCACAGA    55131    _   AA
                                AG AAG  AAGTCACAGA
                                || |||  ||||||||||
                                TC TTT  TTCAGTGTCT
                                 G   AC
GAM2330  FLJ10420 3'  CACATCAAGAGGACAGA     55132          A  AAAGTCA
                                TACATCAAGA GA      CAGA
                                |||||||||| ||      ||||
                                GTGTAGTTCT CT      GTCT
                                      C  ________
GAM2330  FLJ10483 3'  CATCAGCTGAGTCACAGA    55133       A AAGAAA
                                CATCA G     AGTCACAGA
                                ||||| |     |||||||||
                                GTAGT C     TCAGTGTCT
                                   _ GAC____
GAM2330  FLJ11539 5'  TCAAGAAACCCACAGTCACAG  55134         AAA__
                                TCAAGAAG    AGTCACAG
                                ||||||||    ||||||||
                                AGTTCTTT    TCAGTGTC
                                     GGGTG
GAM2330  FLJ14249 3'  CATCAAGAGGAGGCTCAG    55135        A  AAA  CA
                                CATCAAGA GA   GT  CAG
                                |||||||| ||   ||  |||
                                GTAGTTCT CT   CG  GTC
                                     C  C__  A_
GAM2330  FLJ14249 3'  CATCAAGAGGAGGCTCAG    55135        A  AAA  CA
                                CATCAAGA GA   GT  CAG
                                |||||||| ||   ||  |||
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                                GTAGTTCT CT   CG  GTC
                                     C  C__  A_
GAM2330  FLJ14917  3'  CACCAGGAAAGTCACAGA    55136      A   GAAA
                                CATCA GAA    AGTCACAGA
                                ||||| |||    |||||||||
                                GTGGT CTT    TCAGTGTCT
                                   C  _____
GAM2330  FLJ20190  5'  CATCCAGAAGAAAGGCCA    55137     A       A
                                CATC AGAAGAAA GTCA
                                |||| |||||||| ||||
                                GTAG TCTTCTTT CGGT
                                  G       C
GAM2330  KIAA0843  3'  CCAAAAAGAGAAGTTGCAG   55138         A    CA
                                TCAAGAAGA AAGT  CAG
                                ||||||||| ||||  |||
                                GGTTTTTCT TTCA  GTC
                                      C    AC
GAM2330  KIAA1956  3'  TGATCAAGAAGATGCACAG   55139   C        AAA T
                                A ATCAAGAAGA   G CACAG
                                | ||||||||||   | |||||
                                A TAGTTCTTCT   C GTGTC
                                 C         A__ _
GAM2330  MGC24447  3'  TACATTAAGAAAAGCTTTCAC  55140      C      AAAG
                                TACAT AAGAAGA    TCAC
                                ||||| |||||||    ||||
                                ATGTA TTCTTTT    AGTG
                                   A      CGAA
GAM2330  NUDE1    3'  TCAAGAAGAAACCCGGCAGA   55141          AGTCA
                                TCAAGAAGAAA     CAGA
                                ||||||||||     ||||
                                AGTTCTTCTTT     GTCT
                                      GGGCC
GAM2330  NUDT9    5'  CATCGAGAAAAATCCAG     55142      AAGA       A
                                CATC    AGAAAAGTC CAG
                                ||||    ||||||||| |||
                                GTAG    TCTTTTTAG GTC
                                  C___        _
GAM2330  PRO1331  3'  CATCAAGAAGGAAAAGTCA   55143          _
                                CATCAAGAAG AAAAGTCA
                                |||||||||| ||||||||
                                GTAGTTCTTC TTTTCAGT
                                      C
GAM2330  SDF1     3'  CATCAAGACATTGGTCACAGA  55144        AGAAAA
                                CATCAAGA     GTCACAGA
                                ||||||||     ||||||||
                                GTAGTTCT     CAGTGTCT
                                     GTAAC_
GAM2330  ZMPSTE24 3'  ATCAGAGCATGAAGTCACAGA  55145     _  AAGAA
                                ATCA AG     AAGTCACAGA
                                |||| ||     ||||||||||
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                                TAGT TC    TTCAGTGTCT
                                  C  GTAC_
GAM2330  LOC129446 3'  ATCAAAAAAAGTTACAGA    55146      GAA     C
                                ATCAA   GAAAAGT ACAGA
                                |||||   ||||||| |||||
                                TAGTT   TTTTTCA TGTCT
                                   ___      A
GAM2330  LOC145719 5'  TACAACAGACTAAGTCACAGA  55147     TCA   AGAA
                                TACA   AGA    AAGTCACAGA
                                ||||   |||   ||||||||||
                                ATGT   TCT    TTCAGTGTCT
                                  TG_   GA__
GAM2330  LOC145720 5'  TACAACAGACTAAGTCACAGA  55147     TCA   AGAA
                                TACA   AGA    AAGTCACAGA
                                ||||   |||   ||||||||||
                                ATGT   TCT    TTCAGTGTCT
                                  TG_   GA__
GAM2330  LOC151470 3'  CATTAAGGTGAAAAGTCA    55148     C   AA
                                CAT AAG  GAAAAGTCA
                                ||| |||  |||||||||
                                GTA TTC  CTTTTCAGT
                                 A   CA
GAM2330  LOC197114 5'  TACAACAGACTAAGTCACAGA  55147     TCA   AGAA
                                TACA   AGA    AAGTCACAGA
                                ||||   |||   ||||||||||
                                ATGT   TCT    TTCAGTGTCT
                                  TG_   GA__
GAM2330  LOC197117 3'  TACAACAGACTAAGTCACAGA  55147     TCA   AGAA
                                TACA   AGA    AAGTCACAGA
                                ||||   |||   ||||||||||
                                ATGT   TCT    TTCAGTGTCT
                                  TG_   GA__
GAM2330  LOC253832 3'  CATCAACATTAAGTCACAG    55149      GAAGAA
                                CATCAA     AAGTCACAG
                                ||||||     |||||||||
                                GTAGTT     TTCAGTGTC
                                   GTAA__
GAM2330  LOC253955 3'  CATTTTACAGAAGAGTCACAGA 55150     CAAGA   A
                                CAT    AGAA AGTCACAGA
                                |||    |||| |||||||||
                                GTA    TCTT TCAGTGTCT
                                 AAATG   C
GAM2330  LOC256044 5'  CACATCATCAAAGGTCACAGA  55151       A_   AAAA
                                TACATCA  GAAG   GTCACAGA
                                |||||||  ||||   ||||||||
                                GTGTAGT  TTTC   CAGTGTCT
                                   AG   _____
GAM2330  LOC92568  3'  TCAAGAAGAGGGCCCAGA    55152        AAA   A
                                TCAAGAAGA   GTC CAGA
                                |||||||||   ||| ||||
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                                AGTTCTTCT   CGG GTCT
                                     CC_  _
GAM2331  PRY      3'  TTGTTGGAGGTTGTGATGT   55155    G   A  C   AACA
                                TTG TGGA GG TGT   ATGT
                                ||| |||| || |||   ||||
                                AAC ACCT CC ACA   TACA
                                  A   _ A  C___
GAM2331  PUNC     3'  TCGGTGGAGGGTGACAGTGTC  55156       A  C  TA  A
                                TTGGTGGA GG TG  ACA TGTC
                                |||||||| || ||  ||| ||||
                                AGCCACCT CC AC  TGT ACAG
                                     C  _  __   C
GAM2331  TSN      3'  CTGGTGGAAAACAAAATGATGT 55157          TGT  CA
                                TTGGTGGAAGGC   AA  ATGT
                                ||||||||||||   ||  ||||
                                GACCACCTTTTG   TT  TACA
                                       TT_  AC
GAM2331  FLJ10539 3'  TTGGTTGAAAAACAATGT    55158      G   GCTGT
                                TTGGT GAAG    AACAATGT
                                ||||| ||||    ||||||||
                                AACCA CTTT    TTGTTACA
                                   A   _____
GAM2331  KIAA0453  3'  CTGGTGACTGTAATAGTGT   55159      GAAG     CAA
                                TTGGTG   GCTGTAA   TGT
                                ||||||   |||||||  |||
                                GACCAC   TGACATT   ACA
                                    ____     ATC
GAM2331  KRTAP4-2  3'  TTGGTAGAGGGTAGCAACATAG 55160       A  CT    A__
            TGT                   TTGGTGGA GG  GTAACA   TGT
                                ||||||||  ||  ||||||   |||
                                AACCATCT CC  CGTTGT   ACA
                                     C  AT     ATC
GAM2331  LOC146958 3'  TTGGTCGAGGGCTGTAAC    55161      G  A
                                TTGGT GA GGCTGTAAC
                                ||||| ||  |||||||||
                                AACCA CT CCGACATTG
                                   G  C
GAM2331  LOC149995 5'  CTGGTGGACACTTGATAGTGTC 55162       AG   GTAACAA
                                TTGGTGGA  GCT      TGTC
                                ||||||||  |||      ||||
                                GACCACCT  TGA      ACAG
                                     G_   ACTATC_
GAM2331  LOC150157 3'  TTGGTGGAGAGTTCTGTAGATG 55163       AG __    ACA
            TC                   TTGGTGGA  G  CTGTA   ATGTC
                                ||||||||  |  |||||   |||||
                                AACCACCT  C  GACAT   TACAG
                                     CT AA    C__
GAM2331  LOC159160 3'  TTGTTGGAGGTTGCGATGT   55164    G   A  C   AACA
                                TTG TGGA GG TGT   ATGT
                                ||| |||| || |||   ||||
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                                AAC ACCT CC ACG    TACA
                                  A    _ A   C___
GAM2331  LOC160646 3'  TTGATGGAAAAGCAGTGATGT  55165          _  T  AACA
                                TTGGTGGAAG GC GT    ATGT
                                |||||||||| || ||    ||||
                                AACTACCTTT CG CA    TACA
                                      T  T  C___
GAM2331  LOC196890 3'  TTGGTGGAGAGTTCTGTAGATG 55163         AG __     ACA
              TC                  TTGGTGGA  G  CTGTA   ATGTC
                                |||||||| | |||||  |||||
                                AACCACCT  C  GACAT   TACAG
                                    CT AA    C__
GAM2331  LOC200488 5'  TTGGTGGAGGCTAATG      55166         A     TAACA
                                TTGGTGGA GGCTG     ATG
                                |||||||| |||||     |||
                                AACCACCT CCGAT     TAC
                                  _    _____
GAM2332  BARHL1    3'  TTCGACATTTAAAAAAGA     55169        CCA
                                TTCGACA   TTAAAAAAGA
                                |||||||   ||||||||||
                                AAGCTGT   AATTTTTTCT
                                   A__
GAM2332  TR2       5'  TACATTCGACTCCCAAAGAAGA 55170          A  AT    A
                                TACGTTCGAC CC  TAAA AAGA
                                |||||||||| ||  |||| ||||
                                ATGTAAGCTG GG  GTTT TTCT
                                      A __    C
GAM2332  FLJ21032  3'  GCTTCACACCGTTAAAAAAG   55171     CG     A
                                GTT  ACACC TTAAAAAAG
                                |||  ||||| |||||||||
                                CGA  TGTGG AATTTTTTC
                                  AG     C
GAM2332  KIAA0089  3'  TACATTCGACACCTTCAA     55172            A
                                TACGTTCGACACC TTAA
                                |||||||||||| ||||
                                ATGTAAGCTGTGG AGTT
                                       A
GAM2332  LHX9      3'  GTTAGACACCATAAAG       55173     C       TAAA
                                GTT GACACCAT    AAAG
                                ||| ||||||||    ||||
                                CAA CTGTGGTA    TTTC
                                  T       ____
GAM2332  LOC51336  3'  GTTACAAAACCATTAAAGGAG  55174     _   C        AA
                                GTT CGA ACCATTAAA  AG
                                ||| ||| |||||||||  ||
                                CAA GTT TGGTAATTT  TC
                                  T   T        CC
GAM2333  SMOH      3'  CACCGGCTATGCAGGTTG     55177       C   _
                                CACCG CTGT TAGGTTG
                                ||||| |||| |||||||
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                                GTGGC GATA GTCCAAC
                                  C    C
GAM2333  FLJ11939  3'  CACCAGGTCTGGTTAGGTTG   55178      C__  _
                                CACCG   CTG TTAGGTTG
                                |||||   ||| ||||||||
                                GTGGT   GAC AATCCAAC
                                  CCA   C
GAM2333  GTPBP1    3'  CACCAGCTGTCTTTGGGTTG   55179      C    A___
                                CACCG CTGTT    GGTTG
                                ||||| |||||    |||||
                                GTGGT GACAG    CCAAC
                                  C    AAAC
GAM2333  KIAA0350  3'  CACCTGCCCCTTAGGTTG    55180     _   G
                                CACC GCCT TTAGGTTG
                                |||| |||| ||||||||
                                GTGG CGGG AATCCAAC
                                  A   G
GAM2333  KIAA0356  3'  CACCTGCCTGCCACCGTTG   55181     _      G_
                                CACC GCCTGTTA  GTTG
                                |||| ||||||||  ||||
                                GTGG CGGACGGT  CAAC
                                  A       GG
GAM2333  KIAA0601  3'  CACCACCTTGTTAAGGTTG   55182        _   _
                                CACCGCCT GTTA GGTTG
                                |||||||| |||| |||||
                                GTGGTGGA CAAT CCAAC
                                    A   T
GAM2333  KIAA0869  3'  CACTGCCCGCTCCACGTTG   55183     C     __ G
                                CAC GCCTGT  TA GTTG
                                ||| ||||||  || ||||
                                GTG CGGGCG  GT CAAC
                                  A     AG  G
GAM2333  KIAA1610  3'  ACTGCCTGCCAACAGTTG    55184    C      __
                                AC GCCTGTTA  GGTTG
                                || ||||||||  |||||
                                TG CGGACGGT  TCAAC
                                 A       TG
GAM2333  ZNF-U69274 3'  CACTGCCATCAAATATTAGGTT 55185     C  ______        III
           GC                     CAC GCC     TGTTAGGTTG  C
                                ||| |||     ||||||||||  |
                                GTG CGG     ATAATCCAAC   G
                                  A   TAGTTT         III
GAM2333  LOC122728 3'  CACCACCTGGTACTGGTTG   55186        T __
                                CACCGCCTG TA  GGTTG
                                |||||||| ||  |||||
                                GTGGTGGAC AT  CCAAC
                                    C  GA
GAM2333  LOC145368 3'  CACCACCTGGTACTGGTTG   55186        T __
                                CACCGCCTG TA  GGTTG
                                |||||||| ||  |||||
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                                GTGGTGGAC AT  CCAAC
                                     C  GA
GAM2333  LOC150423 3'  CACCACCTGGTACTGGTTG   55186        T __
                                CACCGCCTG TA  GGTTG
                                ||||||||| ||  |||||
                                GTGGTGGAC AT  CCAAC
                                     C  GA
GAM2334  DGCR2    3'  AGTGCAACCGTTGTGACA    55189       ___
                                AGTGCGAT   TGTGACA
                                ||||||||   |||||||
                                TCACGTTG   ACACTGT
                                     GCA
GAM2334  JUN      3'  TGAATACATTTATTGTGACA   55190       ___
                                TGAGTGCG   ATTGTGACA
                                ||||||||   |||||||||
                                ACTTATGT   TAACACTGT
                                     AAA
GAM2334  LOXL3    3'  TGAGTGCGGTTGCTGACA    55191       A  _
                                TGAGTGCG TTG TGACA
                                |||||||| ||| |||||
                                ACTCACGC AAC ACTGT
                                     C   G
GAM2334  C9orf4   3'  TGACTGTGAACTTATGACA   55192     G  C __
                                TGA TG GA  TTGTGACA
                                ||| || ||  ||||||||
                                ACT AC CT  AATACTGT
                                  G  A  TG
GAM2334  RAI17    3'  TGAATGCATCTGTTGACA    55193       A   _
                                TGAGTGCG TTGT GACA
                                |||||||| |||| ||||
                                ACTTACGT GACA CTGT
                                     A   A
GAM2335  ADH5     3'  ATGTAGTTCACTATACTAGAAA 55196     A   CCTTTG
           T                     ATG AGT     ATACTAGAAAT
                                ||| |||     ||||||||||
                                TAC TCA     TATGATCTTTA
                                  A   AGTGA_
GAM2335  TPST2    3'  ATGAAGTCATTTGCGGAGA    55197       C   ATACT
                                ATGAAGTC TTTG    AGA
                                |||||||| ||||    |||
                                TACTTCAG AAAC    TCT
                                     T   GCC__
GAM2335  WIG1     3'  TGAAATCCACAACTGGAAAT   55198       TTTGAT  A
                                TGAAGTCC     ACT GAAAT
                                ||||||||     ||| |||||
                                ACTTTAGG     TGA CTTTA
                                     TGT___   C
GAM2335  DATF1    3'  GAAGTCCTGACAGACTAG    55199       TT  __
                                GAAGTCCT  GAT  ACTAG
                                ||||||||  |||  |||||
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                                CTTCAGGA  CTG  TGATC
                                    __   TC
GAM2335 DATF1    3' GAAGTCCTGACAGACTAG    55199       TT  __
                                GAAGTCCT  GAT  ACTAG
                                ||||||||  |||  |||||
                                CTTCAGGA  CTG  TGATC
                                    __   TC
GAM2335 FLJ13373 3' ATGAAGTCCTTTTACTGGAAAT 55200          GA   A
                                ATGAAGTCCTTT  TACT GAAAT
                                ||||||||||||  |||| |||||
                                TACTTCAGGAAA  ATGA CTTTA
                                      __   C
GAM2335 KIAA0125 3' ATGGAGCCCACTAGAA     55201     A    TTTGAT
                                ATG AGTCC     ACTAGAA
                                ||| |||||     |||||||
                                TAC TCGGG     TGATCTT
                                  C   _______
GAM2335 KIAA0350 3' TGGGGTCCTTTGAAGCCAAAA  55202    AA       TA
                                TG  GTCCTTTGA  CTAGAA
                                ||  |||||||||  ||||||
                                AC  CAGGAAACT  GGTTTT
                                 CC        TC
GAM2335 SH2D3A   3' TGAAGTCAACTGCTAGAAAT   55203       CT   ATA
                                TGAAGTC  TTG   CTAGAAAT
                                |||||||  |||   ||||||||
                                ACTTCAG  GAC   GATCTTTA
                                    TT  ____
GAM2335 SLC17A6  5' TGAGTCCTTTTCCTGGAA    55204     A     GATA  A
                                TGA GTCCTTT    CT GAA
                                ||| |||||||    || |||
                                ACT CAGGAAA    GA CTT
                                  _      AG__  C
GAM2336 EXT2     3' TGATGTAAATAACTAAAA    55207    A   GG
                                C GTG  AATAACTAAAA
                                | |||  ||||||||||
                                A TAC  TTATTGATTTT
                                 C   AT
GAM2336 PAFAH1B1 3' TACAGTGGGAAGATAAAAAG   55208          TAACT
                                TACAGTGGGAA    AAAAG
                                ||||||||||    |||||
                                ATGTCACCCTT    TTTTC
                                      CTAT_
GAM2336 PSAP     3' TATTACAGTGGGAATTAC    55209            A
                                TATTACAGTGGGAAT AC
                                |||||||||||||| ||
                                ATAATGTCACCCTTA TG
                                          A
GAM2336 LOC143879 3' TACATACATAATAACTAAAAG  55210     GTGGG
                                TACA    AATAACTAAAAG
                                ||||    ||||||||||||
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                                ATGT    TTATTGATTTTC
                                  ATGTA
GAM2337 ARHGAP6  3' AAGCGTATCGCCTTCTGCTGGT 55213    _   T   C
            C                   AAG GTAT CGCC TCTGCTGGTC
                                ||| |||| |||| ||||||||||
                                TTC CATA GCGG AGACGACCAG
                                  G   _   A
GAM2337 ARHGAP6  3' AAGCGTATCGCCTTCTGCTGGT 55213    _   T   C
            C                   AAG GTAT CGCC TCTGCTGGTC
                                ||| |||| |||| ||||||||||
                                TTC CATA GCGG AGACGACCAG
                                  G   _   A
GAM2337 CLECSF2  3' AAAAGTACTTTGCTGG     55214       TTCGCC  C
                                AAAGGTA     CT TGCTGG
                                |||||||     || ||||||
                                TTTTCAT     GA ACGACC
                                   _______  A
GAM2337 TEGT    3' TGAAGTTGGCGCCCTCTGCTGG 55215   A   ATT
            TC                    A AGGT   CGCCCTCTGCTGGTC
                                | ||||   ||||||||||||||
                                A TTCA   GCGGGAGACGACCAG
                                 C   ACC
GAM2337 BAG5    3' AAGGTATTATTGCTGGT     55216       CGCCCTC
                                AAGGTATT      TGCTGGT
                                ||||||||      |||||||
                                TTCCATAA      ACGACCA
                                    TA_____
GAM2337 DJ159A19.3 3' AAAAGTATTTACAATTGCTGGT 55217        CG CCTC
                                AAAGGTATT  C    TGCTGGT
                                |||||||||  |    |||||||
                                TTTTCATAA  G    ACGACCA
                                     AT TTA_
GAM2337 FLJ00058  5' AAAGGTATTTTCCACAGTGTGG 55218        CG  CTC_  C
            TC                    AAAGGTATT  CC    TG TGGTC
                                |||||||||  ||    || |||||
                                TTTCCATAA  GG    AC ACCAG
                                     AA  TGTC  _
GAM2337 FLJ20254  5' GGTGAGACACTTTGCTGGTC   55219     ATTC  C  C
                                GGT    GC CT TGCTGGTC
                                |||    || || ||||||||
                                CCA    TG GA ACGACCAG
                                  CTC_  T  A
GAM2337 FLJ20371  5' AAGGGACAGTGGCCTCTGCTGG 55220      T  TCGC_
            TC                    AAGG AT    CCTCTGCTGGTC
                                |||| ||    ||||||||||||
                                TTCC TG    GGAGACGACCAG
                                  C  TCACC
GAM2337 FLJ20695  3' GGAGGTGCTGTGCCTGCTGGTC 55221   A   ATTC_  CTC
                                A AGGT    GCC   TGCTGGTC
                                | ||||    |||   ||||||||
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                                C TCCA    CGG   ACGACCAG
                                 C    CGACA  ___
GAM2337  MGC10960  3'  AGGTTTTCGCCCTCTGAGGT   55222      A         CT
                                AGGT TTCGCCCTCTG  GGT
                                |||| ||||||||||  |||
                                TCCA AAGCGGGAGAC  CCA
                                   A         T_
GAM2337  MGC2776   5'  GGAGGTATTCCCTTTGCT    55223    A      CG    C
                                A AGGTATT  CCCT TGCT
                                | |||||||  |||| ||||
                                C TCCATAA  GGGA ACGA
                                 C       __    A
GAM2337  MST4      3'  AAAGGTATTCATCCTCGTAACT 55224           C    T__
                                AAAGGTATTCG CCTC   GCT
                                |||||||||| ||||   |||
                                TTTCCATAAGT GGAG   TGA
                                       A    CAT
GAM2337  SLC38A1   5'  GGAGGTGTCCGCCCTTCCGGGG 55225    A    A       _   CT
              T                 A AGGT TTCGCCCT CTG  GGT
                                | |||| |||||||| |||  |||
                                C TCCA AGGCGGGA GGC  CCA
                                 C    C       A   C_
GAM2337  LOC115343 5'  GGAGGTGGTCGCCCTCCG    55226    A    AT
                                A AGGT  TCGCCCTCTG
                                | ||||  ||||||||||
                                C TCCA  AGCGGGAGGC
                                 C    CC
GAM2337  LOC128553 5'  AGGTATTTGCCCTCTGATGTC  55227        C       CTG
                                AGGTATT GCCCTCTG   GTC
                                |||||||| ||||||||   |||
                                TCCATAA CGGGAGAC   CAG
                                    A       TA_
GAM2337  LOC201931 3'  AGGTATTTGCCCTCCATAAGTC 55228        C       CT
                                AGGTATT GCCCTCTG  GGTC
                                |||||||| ||||||||  ||||
                                TCCATAA CGGGAGGT  TCAG
                                    A       AT
GAM2337  LOC90268  3'  AAAAGTATTTGCCTTCTG    55229          C   C
                                AAAGGTATT GCC TCTG
                                |||||||||| ||| ||||
                                TTTTCATAA CGG AGAC
                                      A   A
GAM2337  LOC91351  3'  AGGTATTCATTTTTACTCTGGT 55230          CCCT__  G
                                AGGTATTCG     CT CTGGT
                                |||||||||     || |||||
                                TCCATAAGT     GA GACCA
                                      AAAAAT  _
GAM2338  BMP1      3'  TCAGGGAGTTTGGACCCGCAGA 55233     ATA        AAGA
              A                  TCA   AGTTTGGAC    GGAA
                                |||   |||||||||    ||||
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                                AGT  TCAAACCTG   TCTT
                                  CCC       GGCG
GAM2338  CLCN4    3'  ATAAGACCTGAGAGGAAA    55234      _   GACA
                                ATAAG TTTG   AGAGGAAA
                                ||||| ||||   ||||||||
                                TATTC GGAC   TCTCCTTT
                                  T  _____
GAM2338  F2R      3'  TCAATAAAGTTTGGGTGGGGA  55235       _    ACAAGA
                                TCAATAA GTTTGG     GGA
                                |||||||  ||||||     |||
                                AGTTATT CAAACC     CCT
                                    T     CACC__
GAM2338  GNA11    5'  TCAATAACTTAAAAAAGGGGAA 55236       G     C   A
             A                   TCAATAA TTTGGA AAG GGAAA
                                |||||||  ||||||  |||  |||||
                                AGTTATT GAATTT TTC CCTTT
                                    _     T   C
GAM2338  NESH     5'  ATTCCGGGACAAGAGGAA    55237     __
                                GTTT  GGACAAGAGGAA
                                ||||  ||||||||||||
                                TAAG  CCTGTTCTCCTT
                                  GC
GAM2338  NOTCH2   3'  TCAATAAATTTGGATAGG    55238           CAAG
                                TCAATAAGTTTGGA   AGG
                                ||||||||||||||   |||
                                AGTTATTTAAACCT   TCC
                                       A___
GAM2338  PCDHB4   3'  GTGGTGGTCACAAGAGGAAA  55239    T_  __
                                GT  TGG  ACAAGAGGAAA
                                ||  |||  ||||||||||
                                CA  ACC  TGTTCTCCTTT
                                 CC   AG
GAM2338  PDE4A    3'  TAAGGCAGAAACAAGAGGA   55240     _ TT
                                TAAG T  GGACAAGAGGA
                                ||||  |  ||||||||||
                                ATTC G  TTTGTTCTCCT
                                  C TC
GAM2338  SLC16A2  3'  AATGAGTTTGGAACACCTGGA  55241     A      _ AGA
                                AAT AGTTTGGA CA   GGA
                                |||  |||||||  ||   |||
                                TTA TCAAACCT GT   CCT
                                  C       T  GGA
GAM2338  STC1     3'  TCCATAAGTTTGGGGACCTGGG 55242    A      __   AAGA
             GA                   TC ATAAGTTT  GGAC   GGA
                                ||  ||||||||  ||||   |||
                                AG TATTCAAA  CCTG    CCT
                                 G       CC    GACC
GAM2338  ZNF10    3'  TCAGTAAGTTTGGCACAGAGA  55243     A       ACA
                                TCA TAAGTTTGG   AGAGG
                                |||  |||||||||   |||||
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                                AGT ATTCAAACC   TCTCT
                                  C       GTG
GAM2338 ARPP-21   3' TCAATTAAAGTAAGAGGAA   55244      __   TTGGAC
                                TCAAT  AAGT     AAGAGGAA
                                |||||  ||||     ||||||||
                                AGTTA  TTCA     TTCTCCTT
                                  AT   _______
GAM2338 FLJ23563  5' TCAATAAATTTGGAGAAG    55245           CAA
                                TCAATAAGTTTGGA   GAGG
                                ||||||||||||||   ||||
                                AGTTATTTAAACCT   CTTC
                                                 ___
GAM2338 H_GS165L15.1 3' CAAGTGGACCAAGAGGA     55246       TT   _
                                TAAGT  GGAC AAGAGGA
                                |||||  |||| |||||||
                                GTTCA  CCTG TTCTCCT
                                  __   G
GAM2338 HN1L      3' TAAGGCTGATGAGAGGAA    55247      T    ACA
                                TAAG TTGG   AGAGGAA
                                ||||| ||||   |||||||
                                ATTC GACT   TCTCCTT
                                  C    AC_
GAM2338 KIAA0321  3' TCAATGAGTTAGAGGAA     55248      A    TGGACA
                                TCAAT AGTT     AGAGGAA
                                |||||| ||||     |||||||
                                AGTTA TCAA     TCTCCTT
                                  C    _______
GAM2338 KIAA0475  3' AACAAGTTGGAGGAGG      55249        T   CAA
                                AATAAGTT GGA   GAGG
                                |||||||| |||   ||||
                                TTGTTCAA CCT   CTCC
                                     _   C__
GAM2338 KIAA0828  3' AGCCTGGACAAGAGGAAA    55250
                                AGTTTGGACAAGAGGAAA
                                ||||||||||||||||||
                                TCGGACCTGTTCTCCTTT

GAM2338 KIAA1598  3' AATAAGTTGTGGTGAGGA    55251        _  ACAA
                                AATAAGTT TGG    GAGGA
                                |||||||| |||    |||||
                                TTATTCAA ACC    CTCCT
                                     C   A___
GAM2338 PPIL2     3' TCAGTAAGTCTGGGGTCTGAAA 55252     A       ACAAGAG
                                TCA TAAGTTTGG      GAAA
                                ||| |||||||||      ||||
                                AGT ATTCAGACC      CTTT
                                  C       CCAGA__
GAM2338 PRO0618   3' TCAATGAGTTGGACAAGATGA  55253      A   T      G
                                TCAAT AGTT GGACAAGA GA
                                ||||| |||| |||||||| ||
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                                AGTTA TCAA CCTGTTCT CT
                                  C   _      A
GAM2338  RBM11    3'  AATATGTGAGAAGAGGAA    55254    T  _  C
                                AGT TG GA AAGAGGAA
                                ||| || || ||||||||
                                TTA AC CT TTCTCCTT
                                  T  A  C
GAM2338  TSGA14   3'  TCAGGGGTTCTGAAAAGAGGAA 55255    ATAAG    C
                                TCA    TTTGGA AAGAGGAA
                                |||    |||||| ||||||||
                                AGT    AGACTT TTCTCCTT
                                  CCCCA    _
GAM2338  LOC145676 5'  TCAAAAATGATGACAAGGGGAA 55256     T   TTG    A
                                TCAA AAGT   GACAAG GGAA
                                |||| ||||   |||||| ||||
                                AGTT TTTA   CTGTTC CCTT
                                  _   CTA    C
GAM2338  LOC146138 3'  TCAATCCGAGGGACAAGAGG   55257      AAGTTT
                                TCAAT     GGACAAGAGG
                                |||||     ||||||||||
                                AGTTA     CCTGTTCTCC
                                   GGCTC_
GAM2338  LOC146952 5'  TCAAGAAGCTTGAGAGG     55258     T     GACA
                                TCAA AAGTTTG    AGAGG
                                |||| |||||||    |||||
                                AGTT TTCGAAC    TCTCC
                                  C      ____
GAM2338  LOC148254 3'  TAAATTTGGACATGGAA     55259          AGA
                                TAAGTTTGGACA   GGAA
                                ||||||||||||   ||||
                                ATTTAAACCTGT   CCTT
                                       A__
GAM2338  LOC148438 3'  AGTGAAAAGCAAGAGGAA    55260    TT  _
                                AGT  GGA CAAGAGGAA
                                |||  ||| |||||||||
                                TCA  TTT GTTCTCCTT
                                  CT   C
GAM2338  LOC154792 5'  AAGTAACAAGAGGAA      55261     TTG
                                AAGT   GACAAGAGGAA
                                ||||   ||||||||||
                                TTCA   TTGTTCTCCTT
                                   ___
GAM2338  LOC155036 3'  GTAGGACTCAAGAGGAAA    55262    TT   __
                                GT  GGAC  AAGAGGAAA
                                ||  ||||  |||||||||
                                CA  CCTG  TTCTCCTTT
                                 T_    AG
GAM2338  LOC157931 3'  CAATAAAGTTACAAGAGGA   55263       _  TGG
                                CAATAA GTT   ACAAGAGGA
                                ||||||  |||   |||||||||
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                                GTTATT CAA   TGTTCTCCT
                                   T  ___
GAM2338  LOC158835 5'  TCAGAAGCTTGAGAGG      55264     AT      GACA
                                TCA  AAGTTTG    AGAGG
                                |||  |||||||    |||||
                                AGT  TTCGAAC    TCTCC
                                  C_      ____
GAM2338  LOC255645 3'  AGTTCTGGGCAAGAGGAA     55265     _   A
                                AGT TTGG CAAGAGGAA
                                ||| |||| |||||||||
                                TCA GACC GTTCTCCTT
                                  A   C
GAM2338  LOC256306 5'  AGCTTGGAGAATGAGGAA     55266        C  _
                                AGTTTGGA AA GAGGAA
                                |||||||| || ||||||
                                TCGAACCT TT CTCCTT
                                     C  A
GAM2338  LOC257273 5'  TAAGTTCTAGAAGAGGAAA    55267       GGAC
                                TAAGTTT    AAGAGGAAA
                                |||||||    |||||||||
                                ATTCAAG    TTCTCCTTT
                                    ATC_
GAM2338  LOC90408  5'  AATAAGTGTGAGAGGAA      55268       T  GACA
                                AATAAGT TG    AGAGGAA
                                ||||||| ||    |||||||
                                TTATTCA AC    TCTCCTT
                                    C  ____
GAM2338  LOC91445  3'  TCAATAAGATTCAGAGGAA    55269       TTTGGACA
                                TCAATAAG       AGAGGAA
                                ||||||||       |||||||
                                AGTTATTC       TCTCCTT
                                     TAAG____
GAM2339  A1BG      3'  AGGAACTAGATATTACTA     55272       _
                                AGGAACTA ATATTACTA
                                |||||||| |||||||||
                                TCCTTGAT TATAATGAT
                                    C
GAM2339  AGR2      3'  TAGAGGAATTCCATATATTA   55273       __  _
                                TAGAGGAA  CTA ATATTA
                                ||||||||  ||| ||||||
                                ATCTCCTT  GGT TATAAT
                                     AA   A
GAM2339  MDM1      3'  AGGACAGTATAATATTACTA   55274     AC___
                                AGGA     TAATATTACTA
                                ||||     ||||||||||||
                                TCCT     ATTATAATGAT
                                  GTCAT
GAM2339  BDG-29    3'  GAGGACTTTTATTACTA      55275      A  AA
                                GAGGA CT  TATTACTA
                                ||||| ||  ||||||||
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                                CTCCT GA  ATAATGAT
                                   _  AA
GAM2339  CNOT7     3'  GAGATTTGCTAATATTACT   55276     AA__
                                GAGG   CTAATATTACT
                                ||||   ||||||||||
                                CTCT   GATTATAATGA
                                  AAAC
GAM2339  FLJ10458  3'  GAGGAACTGCACTTCTA     55277       AA   A
                                GAGGAACT  TATT CTA
                                ||||||||  |||| |||
                                CTCCTTGA  GTGA GAT
                                     C_   A
GAM2339  FLJ10849  3'  CAGAGATACGATATTACT    55278      A  TA
                                TAGAGG AC  ATATTACT
                                ||||||  ||  ||||||||
                                GTCTCT TG  TATAATGA
                                   A  C_
GAM2339  FLJ13984  3'  AGAGGAACTAAAATTCTA    55279        T   A
                                AGAGGAACTAA ATT CTA
                                ||||||||||| ||| |||
                                TCTCCTTGATT TAA GAT
                                      T  _
GAM2339  FLJ22191  3'  AAAGAACTTTTGATATTACT  55280       A___
                                GAGGAACT   ATATTACT
                                ||||||||   ||||||||
                                TTTCTTGA   TATAATGA
                                     AAAC
GAM2339  KIAA0547  3'  TAAAGGAACAATTACT     55281       TAAT
                                TAGAGGAAC   ATTACT
                                |||||||||   ||||||
                                ATTTCCTTG   TAATGA
                                     T___
GAM2339  KIAA1128  3'  ATAGAGAAAAATAAATTACT  55282       CTAAT
                                ATAGAGGAA    ATTACT
                                |||||||||    ||||||
                                TATCTCTTT    TAATGA
                                     TTATT
GAM2339  KIAA1198  3'  ACAGAGGAAAATACTTACT   55283       CT    _
                                ATAGAGGAA  AATATT ACT
                                |||||||||  |||||| |||
                                TGTCTCCTT  TTATGA TGA
                                     __     A
GAM2339  MAP2K6    3'  ATAGAGGAGCCAGCTATT    55284       A  A_
                                ATAGAGGA CTA  TATT
                                ||||||||  |||  ||||
                                TATCTCCT GGT  ATAA
                                     C   CG
GAM2339  MAP2K6    3'  ATAGAGGAGCCAGCTATT    55284       A  A_
                                ATAGAGGA CTA  TATT
                                ||||||||  |||  ||||
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                                TATCTCCT GGT  ATAA
                                    C   CG
GAM2339  MGC3184   3'  ATAAAGGAATGCAACTAATATT 55285        _____
                                ATAGAGGA    ACTAATATT
                                ||||||||    |||||||||
                                TATTTCCT    TGATTATAA
                                    TACGT
GAM2339  RGS18     3'  TAGAGGTGATATTACTA     55286       AACTA
                                TAGAGG    ATATTACTA
                                ||||||    |||||||||
                                ATCTCC    TATAATGAT
                                   AC___
GAM2339  LOC147639 5'  ATAGTGGAACTAATTCTCACT  55287      A       A_
                                ATAG GGAACTAAT  TTACT
                                |||| |||||||||  |||||
                                TATC CCTTGATTA  AGTGA
                                  A        AG
GAM2339  LOC150297 3'  ACAGAGGAGTGACTACTA    55288        ACTAAT
                                ATAGAGGA     ATTACTA
                                ||||||||     |||||||
                                TGTCTCCT     TGATGAT
                                    CAC___
GAM2339  LOC154789 3'  TAGGGGGACTAATATTGCC    55289     A  A       A
                                TAG GG ACTAATATT CT
                                ||| || |||||||||| ||
                                ATC CC TGATTATAA GG
                                  C  C        C
GAM2339  LOC168448 3'  CAGAGTTAATATTACTA     55290      GAAC
                                TAGAG    TAATATTACTA
                                |||||    ||||||||||
                                GTCTC    ATTATAATGAT
                                   A___
GAM2339  LOC221060 3'  ATAGAGGAACATGTCTTCTA   55291          TAATA  A
                                ATAGAGGAAC     TT CTA
                                ||||||||||     || |||
                                TATCTCCTTG     AA GAT
                                      TACAG  _
GAM2339  LOC256401 3'  CAGAGTTAATATTACTA     55290      GAAC
                                TAGAG    TAATATTACTA
                                |||||    ||||||||||
                                GTCTC    ATTATAATGAT
                                   A___
GAM2339  LOC90786  5'  TAGAAGAACTGGTCCTCATACT 55292          AATAT___
             A                   TAGAGGAACT       TACTA
                                 ||||||||||       |||||
                                 ATCTTCTTGA       ATGAT
                                      CCAGGAGT
GAM2340  1D12A     3'  TAAAAGACATATTTACAGACAT 55295       A        CCT
             GT                    TAGAA ACATATTTAT   TGTGT
                                   ||||| ||||||||||   |||||
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                                ATTTT TGTATAAATG   GTACA
                                   C        TCT
GAM2340  GPR105    3'  TAGAAAACATATTTAGCATGT  55296            TCCT
                                TAGAAAACATATTTA    TGT
                                |||||||||||||||    |||
                                ATCTTTTGTATAAAT    ACA
                                       CGT_
GAM2340  JM11      3'  TAGAAAACACAACTTGTG    55297          TTTATC
                                TAGAAAACATA     CTTGTG
                                ||||||||||      ||||||
                                ATCTTTTGTGT     GAACAC
                                       T_____
GAM2340  STIM2     3'  CAGAAAACATAGTGTTTTTTGT 55298          TTTATCC
                 GT                  TAGAAAACATA      TTGTGT
                                ||||||||||      ||||||
                                GTCTTTTGTAT      AACACA
                                       CACAAAA
GAM2340  LOC134266 3'  TAGAGATTATTTTCCTTGTGT  55299      AAACA    A
                                TAGA    TATTT TCCTTGTGT
                                ||||    ||||| |||||||||
                                ATCT    ATAAA AGGAACACA
                                  CTA__    _
GAM2341  ABCC5     3'  TTCACATTTTCAGATTTT    55302        GC   C
                                TTCACATT  CAG TTTT
                                ||||||||  ||| ||||
                                AAGTGTAA  GTC AAAA
                                     AA   T
GAM2341  CASP2     3'  TTCACTTGTCAGGCTCTT    55303      A   C   _
                                TTCAC TTG CAG CTTTT
                                ||||| ||| ||| |||||
                                AAGTG AAC GTC GAGAA
                                   _   A   C
GAM2341  CASP2     3'  TTCACTTGTCAGGCTCTT    55303      A   C   _
                                TTCAC TTG CAG CTTTT
                                ||||| ||| ||| |||||
                                AAGTG AAC GTC GAGAA
                                   _   A   C
GAM2341  CASP2     3'  TTCACTTGTCAGGCTCTT    55303      A   C   _
                                TTCAC TTG CAG CTTTT
                                ||||| ||| ||| |||||
                                AAGTG AAC GTC GAGAA
                                   _   A   C
GAM2341  CASP2     3'  TTCACTTGTCAGGCTCTT    55303      A   C   _
                                TTCAC TTG CAG CTTTT
                                ||||| ||| ||| |||||
                                AAGTG AAC GTC GAGAA
                                   _   A   C
GAM2341  MYO5A     3'  CATATTGCCAGTTTATTTC    55304    C      CT    C
                                CA ATTGCCAG  TTTA TTC
                                || ||||||||  |||| |||
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                                GT TAACGGTC  AAAT AAG
                                 A       __    A
GAM2341  PCSK1    3'  TTACCAACCATACTTCA     55305         TT
                                TTGCCAGCT  TACTTCA
                                |||||||||  |||||||
                                AATGGTTGG  ATGAAGT
                                      T_
GAM2341  QDPR     3'  CTCGCATTGTCTTACTTC    55306     A    CCAGC
                                TTC CATTG    TTTTACTTC
                                ||| |||||    |||||||||
                                GAG GTAAC    AGAATGAAG
                                  C    _____
GAM2341  RNF18    3'  TTCCATTGATTTTTACTTC   55307     A    CCAGC
                                TTC CATTG    TTTTACTTC
                                ||| |||||    |||||||||
                                AAG GTAAC    AAAATGAAG
                                  _    TA___
GAM2341  SHOC2    3'  TTCACTTTGCCAGTTTTTTTTT 55308      A     C   AC_
              TCA                   TTCAC TTGCCAG TTTT   TTCA
                                |||||| ||||||| ||||   ||||
                                AAGTG AACGGTC AAAA   AAGT
                                   A      A    AAA
GAM2341  TMOD     3'  TTCATGCTGCCAGCATTTT   55309     CA      _
                                TTCA  TTGCCAGC TTTT
                                ||||  |||||||| ||||
                                AAGT  GACGGTCG AAAA
                                  AC       T
GAM2341  TPST1    3'  TTCACATTGAAAGCTTTTA   55310         CC
                                TTCACATTG  AGCTTTTA
                                |||||||||  ||||||||
                                AAGTGTAAC  TCGAAAAT
                                      TT
GAM2341  VIL2     3'  TTGCAAAGCTTTTATTTCA   55311     C_      C
                                TTGC  AGCTTTTA TTCA
                                ||||  |||||||| ||||
                                AACG  TCGAAAAT AAGT
                                   TT       A
GAM2341  ZHX1     3'  TTCACATTTTTGGTGCAGTATT 55312    GC_____   CT   C   III
              TATTTCAT                TT      CAG  TTTA TTCA   T
                                ||      |||  |||| ||||  |
                                AA      GTC  AAAT AAGT   A
                                 AAACCAC   AT    A   III
GAM2341  DKFZP434N093 3'  TTCACACTGTCAACACTT    55313         C    TTTT
                                TTCACATTG CAGC    ACTT
                                |||||||||  ||||   ||||
                                AAGTGTGAC GTTG    TGAA
                                      A   ____
GAM2341  EIF2S1   3'  TTCATGTTGCCAGCTTTC    55314      CA
                                TTCA  TTGCCAGCTTTT
                                ||||  ||||||||||||
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                                AAGT  AACGGTCGAAAG
                                  AC
GAM2341  FLJ20647  5'  TTCACATTTCCACACAGCTTC  55315        ___ _
                                TTCACATT   GC CAGCTTT
                                ||||||||   || |||||||
                                AAGTGTAA   TG GTCGAAG
                                     AGG  T
GAM2341  FLJ20668  3'  TTCACATTTCCATATCATACTT 55316        G   GCTTT
                                TTCACATT CCA     TACTT
                                |||||||| |||     |||||
                                AAGTGTAA GGT     ATGAA
                                     A   ATAGT
GAM2341  FLJ23233  3'  TTCAATTGCCAGCTCCCTC   55317      C         TTA
                                TTCA ATTGCCAGCTT   CTTC
                                |||| ||||||||||   ||||
                                AAGT TAACGGTCGAG   GGAG
                                  _        ___
GAM2341  HYPH      3'  TTCACATTGCTAGTATTTTCC  55318         C  CT   A
                                TTCACATTGC AG  TTT CT
                                |||||||||| ||  ||| ||
                                AAGTGTAACG TC  AAA GG
                                      A  AT   A
GAM2341  KIAA0218  5'  TTCACTTTGCCCAGCGCTACTT 55319      A    _  TT
           C                     TTCAC TTGCC AGC  TTACTTC
                                |||||| ||||| |||  |||||||
                                AAGTG AACGG TCG  GATGAAG
                                   A    G   C_
GAM2341  KIAA0530  3'  TTCACATTTCCATTGTATTTCA 55320        G   GCTTT  C
                                TTCACATT CCA     TA TTCA
                                |||||||| |||     || ||||
                                AAGTGTAA GGT     AT AAGT
                                     A   AAC__  A
GAM2341  KIAA0802  3'  ACATTGCCAGTTAATCTTTT   55321         _____
                                ACATTGCCAG     CTTTT
                                ||||||||||     |||||
                                TGTAACGGTC     GAAAA
                                      AATTA
GAM2341  KIAA1023  3'  TTCACATTTCAGCTTCCA     55322        GC
                                TTCACATT  CAGCTTTTA
                                ||||||||  |||||||||
                                AAGTGTAA  GTCGAAGGT
                                     A_
GAM2341  KIAA1677  3'  TTCACATTTCCATGACTTC    55323        G   GCTTTT
                                TTCACATT CCA     ACTTC
                                |||||||| |||     |||||
                                AAGTGTAA GGT     TGAAG
                                     A   AC____
GAM2341  LANO      3'  TTCACATTCCCCAACTGCTTCA 55324        _ G     TTTA
                                TTCACAT T CCAGCT    CTTCA
                                ||||||| | ||||||    |||||
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                                AAGTGTA G GGTTGA    GAAGT
                                    A G     C___
GAM2341  LANO     3'  TTCACATTCCCCAACTGCTTCA 55324       _ G     TTTA
                                TTCACAT T CCAGCT    CTTCA
                                ||||||| | ||||||    |||||
                                AAGTGTA G GGTTGA    GAAGT
                                    A G     C___
GAM2341  OSBPL11  3'  ATTGCCAGCAATTCTTCA    55325        TT  A
                                ATTGCCAGC  TT CTTCA
                                |||||||||  || |||||
                                TAACGGTCG  AA GAAGT
                                     TT  _
GAM2341  RPIA     3'  TTCACATTTCACAGCAGTGCTT 55326       GC_   TTTTA
                                TTCACATT   CAGC    CTT
                                ||||||||   ||||    |||
                                AAGTGTAA   GTCG    GAA
                                    AGT    TCAC_
GAM2341  ZNFN1A2  3'  CATGTGCAGTTCTTTACTTCA  55327    _   C  C_
                                CAT TGC AG  TTTTACTTCA
                                ||| ||| ||  ||||||||||
                                GTA ACG TC  GAAATGAAGT
                                  C   _  AA
GAM2341  LOC144144 3'  TTCCATTGATTTTTACTTC    55307     A    CCAGC
                                TTC CATTG    TTTTACTTC
                                ||| |||||    |||||||||
                                AAG GTAAC    AAAATGAAG
                                  _    TA___
GAM2341  LOC144248 5'  TTCACATTTTGCAGACTTC    55328       GC_   CTTTT
                                TTCACATT   CAG    ACTTC
                                ||||||||   |||    |||||
                                AAGTGTAA   GTC    TGAAG
                                    AAC   _____
GAM2341  LOC145082 5'  CTCACATTGCTGGCCAATTTCA 55329         CA   TTTAC
                                TTCACATTGC  GCT    TTCA
                                ||||||||||  |||    ||||
                                GAGTGTAACG  CGG    AAGT
                                     AC   TTA__
GAM2341  LOC151446 5'  TTCACATTGCAGCTACTC    55330         C    TTT
                                TTCACATTGC AGCT   ACTT
                                |||||||||| ||||   ||||
                                AAGTGTAACG TCGA   TGAG
                                      _   ___
GAM2341  LOC155179 3'  TTCACATTTCAGCTTCCA    55322       GC
                                TTCACATT  CAGCTTTTA
                                ||||||||  |||||||||
                                AAGTGTAA  GTCGAAGGT
                                    A_
GAM2341  LOC201249 3'  TTCACACTTGTTAGCTTGACC  55331       GCC_    TT
                                TTCACATT    AGCTT  ACT
                                ||||||||    |||||  |||
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                                AAGTGTGA   TCGAA  TGG
                                    ACAA    C_
GAM2341  LOC220486 3'  TTCCATTGATTTTTACTTC   55307    A    CCAGC
                                TTC CATTG    TTTTACTTC
                                ||| |||||    |||||||||
                                AAG GTAAC    AAAATGAAG
                                  _    TA___
GAM2342  F13A1    3'  TAATATACTAAGTTAAGCCAGT 55334        A      __
           TT                    TAATATAC TAAGTTAA  TAGTTT
                                ||||||||| ||||||||  ||||||
                                ATTATATG ATTCAATT  GTCAAA
                                    _      CG
GAM2342  FLJ12747  3'  AATATACATAAGTTGTCT    55335           AATA
                                AATATACATAAGTT    GTTT
                                ||||||||||||||    ||||
                                TTATATGTATTCAA    CAGA
                                          _____
GAM2342  H2AV     3'  TAACATACATAGTAATTTAGTT 55336          A  TAA_
           TT                    TAATATACATA GT    TAGTTTT
                                ||||||||||| ||    |||||||
                                ATTGTATGTAT CA    ATCAAAA
                                      _ TTAA
GAM2342  PRO2133   3'  TAATATTACAAGTCAGTTAATG 55337       _   TA__     A
           GTTTT                   TAATAT ACA    AGTTAAT GTTTT
                                |||||| |||    ||||||| |||||
                                ATTATA TGT    TCAATTA CAAAA
                                    A   TCAG      C
GAM2343  FLJ11896  3'  AGTATATAAAAACTGTCAAAAT 55340        CGTT
                                AGTATATA    ATTGTCAAAAT
                                ||||||||    ||||||||||||
                                TCATATAT    TGACAGTTTTA
                                     TTT_
GAM2343  FLJ20097  5'  GTATAATGGTTAATGTCAAAAT 55341       TAC    T
                                GTATA   GTTA TGTCAAAAT
                                |||||   |||| |||||||||
                                CATAT   CAAT ACAGTTTTA
                                   TAC    T
GAM2343  ZIM2     3'  ATATATACGTTACACAA     55342           TGT
                                GTATATACGTTAT   CAA
                                ||||||||||||   |||
                                TATATATGCAATG   GTT
                                       T__
GAM2344  ARSD     3'  TATAAAATACCCAGTCTC    55345        T    A
                                TATAAAAT CCCA TCTT
                                |||||||| |||| ||||
                                ATATTTTA GGGT AGAG
                                     T    C
GAM2344  FLJ10546  3'  ATAAAATTCCAAATCTTG    55346          C
                                ATAAAATTCC AATCTTG
                                |||||||||| |||||||
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                                TATTTTAAGG TTAGAAC
                                      T
GAM2344  LANO     3'  TAAAAATTCCCCTTCCTG    55347   T       AA
                                A AAAATTCCC  TCTTG
                                | |||||||||  |||||
                                A TTTTAAGGG  AGGAC
                                 T       GA
GAM2344  MRPL35   3'  TATGAAATTCCCTTTCCCG   55348    A       AA
                                TAT AAATTCCC  TCTTG
                                ||| ||||||||  |||||
                                ATA TTTAAGGG  AGGGC
                                  C       AA
GAM2345  ARHGEF12 3'  AAACTTGTTAAGTTGCAGT   55351           _
                                AAACTTGTTAAGT GCGGT
                                |||||||||||||| |||||
                                TTTGAACAATTCA CGTCA
                                         A
GAM2345  LNPEP    3'  CAAAATGAGGTGCGGTTGTG   55352     CT  TTAA
                                CAAA  TG   GTGCGGTTGTG
                                ||||  ||   ||||||||||
                                GTTT  AC   CACGCCAACAC
                                  T_  TC__
GAM2345  MDM1     3'  TCAAACTTTTTAAAAATTGTG  55353       G    TGC
                                TCAAACTT TTAAG   GGTTGTG
                                |||||||| |||||   |||||||
                                AGTTTGAA AATTT   TTAACAC
                                     A    ____
GAM2345  TEGT     3'  TCAAACTGTGCACTGGTTGTG  55354       T  TAA TG _
                                TCAAACT GT   G  C GGTTGTG
                                ||||||| ||   |  | |||||||
                                AGTTTGA CA   C  G CCAACAC
                                     _  ____ GT A
GAM2345  FLJ25132 5'  TCAAACTTGTTGGTGCG     55355          AA
                                TCAAACTTGTT  GTGCG
                                ||||||||||  |||||
                                AGTTTGAACAA  CACGC
                                       C_
GAM2345  KIAA0620 3'  TCAAACTTGTGCTGCAGTTGTG 55356         TAAG
                                TCAAACTTGT   TGCGGTTGTG
                                ||||||||||   ||||||||||
                                AGTTTGAACA   ACGTCAACAC
                                      CG__
GAM2345  RBBP1    3'  TCAAATTTGCTAAGTGCCCTTT 55357      C        GG_
              G                  TCAAA TTGTTAAGTGC   TTG
                                 |||||  ||||||||||   |||
                                 AGTTT AACGATTCACG   AAC
                                   A          GGA
GAM2345  RBBP1    3'  TCAAATTTGCTAAGTGCCCTTT 55357      C        GG_
              G                  TCAAA TTGTTAAGTGC   TTG
                                 |||||  ||||||||||   |||
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                                AGTTT AACGATTCACG   AAC
                                   A         GGA
GAM2345  LOC221474 5'  TCAAGCATGTTGAGTGAGGT   55358     ACT   A   C
                                TCAA   TGTT AGTG GGT
                                ||||   |||| |||| |||
                                AGTT   ACAA TCAC CCA
                                  CGT    C    T
GAM2346  ACVR1B    3'  TGCCATTAGGAGGTAAAT    55361        A  TC
                                TGCCATTAG AG  AAAT
                                ||||||||| ||  ||||
                                ACGGTAATC TC  TTTA
                                      C  CA
GAM2346  RB1CC1    3'  CATTAACTTGTCAAATTCAG   55362      AA_
                                CATTAG   GTCAAATTCAG
                                ||||||   ||||||||||
                                GTAATT   CAGTTTAAGTC
                                   GAA
GAM2346  C5orf3    3'  TGCCTTAGAAGTTAAATCC    55363     A      C
                                TGCC TTAGAAGT AAATTC
                                |||| |||||||| ||||||
                                ACGG AATCTTCA TTTAGG
                                  _       A
GAM2346  FLJ20487  3'  TGCCTTTGAAGGATTCAGC    55364     A  A    TCAA
                                TGCC TT GAAG    ATTCAGC
                                |||| || ||||    |||||||
                                ACGG AA CTTC    TAAGTCG
                                  _ A    C___
GAM2346  OLIG1     3'  TGCCAGTTAAATTCGGC     55365      TTAGAA  C     A
                                TGCCA     GT AAATTC GC
                                |||||     || |||||| ||
                                ACGGT     CA TTTAAG CG
                                  _______ A     C
GAM2346  POLD3     3'  TGTCATTAGAAGGTAACAGCT  55366    C       TCAAATT
                                TG CATTAGAAG      CAGCT
                                || |||||||||      |||||
                                AC GTAATCTTC      GTCGA
                                 A        CATT___
GAM2346  ShrmL     5'  TGCCATGCAGAATTCAGC     55367      _   AGTCAA
                                TGCCAT TAGA     ATTCAGC
                                |||||| ||||     |||||||
                                ACGGTA GTCT     TAAGTCG
                                   C   _______
GAM2347  ATP6V1G2  3'  TTACAATGGGAAAGTAA     55370          TA
                                TTACAGTGGGAA  AGTAA
                                ||||||||||||  |||||
                                AATGTTACCCTT  TCATT
                                              __
GAM2347  ATP6V1G2  3'  TTACAATGGGAAAGTAA     55370          TA
                                TTACAGTGGGAA  AGTAA
                                ||||||||||||  |||||
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                                AATGTTACCCTT  TCATT
                                      __
GAM2347  CPA3     3'  CTACTGAAAGTAAGTAAAAG   55371      AG  GG A
                                TTAC  TG  A TAAGTAAAAG
                                ||||  ||  | ||||||||||
                                GATG  AC  T ATTCATTTTC
                                  __  TT C
GAM2347  PAFAH1B1 3'  TACAGTGGGAAGATAAAAA    55372           TAA
                                TACAGTGGGAA   GTAAAAG
                                ||||||||||   |||||||
                                ATGTCACCCTT   TATTTTT
                                      C__
GAM2347  BC-2     3'  TATTACAGAGGGGTTGTGGTAA 55373         T   AATAA_
            AAG                   TATTACAG GGG     GTAAAAG
                                ||||||||| |||     |||||||
                                ATAATGTC CCC     CATTTTC
                                     T   CAACAC
GAM2347  FLJ23120 3'  TACTTGGGGAATAAGTAAAAG  55374     AGT
                                TAC   GGGAATAAGTAAAAG
                                |||   ||||||||||||||||
                                ATG   CCCTTATTCATTTTC
                                  AAC
GAM2347  SFRS4    3'  TACTGTGGGCCATGAGTAAAAG 55375     A     A_  A
                                TAC GTGGG  AT AGTAAAAG
                                ||| |||||  || ||||||||
                                ATG CACCC  TA TCATTTTC
                                  A    GG  C
GAM2347  SPEC1    3'  TATTCGGTGGGAAACAAG    55376      ACA      _
                                TATT   GTGGGAA TAAG
                                ||||   ||||||| ||||
                                ATAA   CACCCTT GTTC
                                  GC_      T
GAM2347  ULK2     3'  TATTCAAGCAGGTAAGTAAAAG 55377      AC  TG  AA
                                TATT  AG  GG  TAAGTAAAAG
                                ||||  ||  ||  ||||||||||
                                ATAA  TC  CC  ATTCATTTTC
                                  GT  GT  __
GAM2347  LOC146434 3'  TATTACATGGGAATGTGTGTAA 55378         G      AA__
            A                    TATTACA TGGGAAT    GTAAA
                                ||||||| |||||||    |||||
                                ATAATGT ACCCTTA    CATTT
                                     _      CACA
GAM2348  PLCB4    3'  TGAGTGAGTCTTTTGATG    55381         _   CCA
                                TGAGTGAG CTTT   GTG
                                |||||||| ||||   |||
                                ACTCACTC GAAA   TAC
                                     A   AC_
GAM2348  TRPS1    3'  TGAGGAGCTTTCCCTTCAT   55382      T       AGTGGA
                                TGAG GAGCTTTCC     CAT
                                |||| |||||||||     |||
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                                ACTC CTCGAAAGG     GTA
                                  _       GAA___
GAM2348 ZNF239   3' TGAGTGATTTTTCAGTG    55383       GC   C
                                TGAGTGA  TTTC AGTG
                                |||||||  |||| ||||
                                ACTCACT  AAAG TCAC
                                   AA   _
GAM2348 ZNF268   3' TGAATGAGTTTTCTGGTG    55384       C   CA
                                TGAGTGAG TTTC  GTG
                                |||||||| ||||  |||
                                ACTTACTC AAAG  CAC
                                     A   AC
GAM2348 DKFZP434A0131 3' TGAGTGAGTTTATCAGATG   55385       C  TC  _
                                TGAGTGAG TT  CAG TG
                                |||||||| ||  ||| ||
                                ACTCACTC AA  GTC AC
                                     A  TA   T
GAM2348 FLJ25415 3' TGGGTTGGCTTTCTGGACATG  55386    A  GA     CAG
                                TG GT  GCTTTC   TGGACATG
                                || ||  ||||||   ||||||||
                                AC CA  CGAAAG   ACCTGTAC
                                 C  AC    ___
GAM2348 GPR105   3' TGAGTGAGTTGTCTTTGATTAT 55387       CTT  CAG   AC
           G                     TGAGTGAG   TC   TGG  ATG
                                |||||||   ||   |||  |||
                                ACTCACTC   AG   ACT  TAC
                                     AAC  AA_   AA
GAM2348 KIAA0084 3' ATGACACCTTTCCAGTGGA   55388     G__
                                GTGA   CTTTCCAGTGGA
                                ||||   ||||||||||||
                                TACT   GAAAGGTCACCT
                                  GTG
GAM2348 KIAA1615 5' TGAGGAGCTCCATGGACAT   55389     T   TT   G
                                TGAG GAGC  TCCA TGGACAT
                                |||| ||||  |||| |||||||
                                ACTC CTCG  AGGT ACCTGTA
                                  _   __   _
GAM2348 ODZ2     3' TGAGTGAGGTAATTGGATATG  55390       CTTTCCAG   C
                                TGAGTGAG       TGGA ATG
                                ||||||||       |||| |||
                                ACTCACTC       ACCT TAC
                                     CATTA___    A
GAM2348 SMCR8    3' TGGGTGAGCATGCTCTGGACAT 55391    A     TTTCCAG
           G                     TG GTGAGC      TGGACATG
                                || ||||||      ||||||||
                                AC CACTCG      ACCTGTAC
                                 C     TACGAG_
GAM2348 LOC126528 5' TGAGTGAGTTTGGGATAT    55392       C  CCAGT  C
                                TGAGTGAG TTT    GGA AT
                                |||||||| |||    ||| ||
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                                ACTCACTC AAA    CCT TA
                                    _  C____   A
GAM2348 LOC202126 5' GAGTGGGCTTTCCAGCTCCA  55393      A       GGA
                                GAGTG GCTTTCCAGT  CA
                                ||||| ||||||||||  ||
                                CTCAC CGAAAGGTCG  GT
                                   C        AG_
GAM2349 ING1    3' TACTGAATTGTTATATGG    55396          TGT
                                TACTGAATTGTT  TGG
                                ||||||||||||  |||
                                ATGACTTAACAA  ACC
                                       TAT
GAM2349 TMEPAI  3' CATGTTGGGTTGTTTATTGG  55397    AC  AA
                                CAT  TG  TTGTTTGTTGG
                                |||  ||  ||||||||||
                                GTA  AC  AACAAATAACC
                                  CA  CC
GAM2349 FBXO9   3' TCCCATACTGAATTGTGG    55398    G         TTGTT
                                TC CATACTGAATTGT    GG
                                || ||||||||||||    ||
                                AG GTATGACTTAACA    CC
                                 G          _____
GAM2349 LOC91565 5' GCATACTGAGCTCTGG     55399        ATT   GT
                                GCATACTGA  GTTT  TGG
                                |||||||||  ||||  |||
                                CGTATGACT  CGAG  ACC
                                       ___   __
GAM2350 ADRA1B  5' TCCCCCGTGGTCTTCTTCC   55402    A  A  G   GAA
                                TCC CC CG GGT   CTTCC
                                ||| || || |||   |||||
                                AGG GG GC CCA   GAAGG
                                  _ _  A   GAA
GAM2350 ATP8B2  3' TCCCTGCCAAGACTTCCCC   55403    ACCA   GTGA
                                TCC   CGGG   ACTTCCCC
                                |||   ||||   ||||||||
                                AGG   GTTC   TGAAGGGG
                                  GACG   _____
GAM2350 COPA    3' TCCATCACAGAGTTTTCC    55404     C      GAAC
                                TCCA CACGGGGT   TTCC
                                |||| ||||||||   ||||
                                AGGT GTGTCTCA   AAGG
                                  A      A___
GAM2350 CTBP2   3' TCTACCACAGGCAAACAGTTTT 55405    C     G TG  _______
            TTCC                  TC ACCACGG G  AAC     TTCC
                                || ||||||| |  |||     ||||
                                AG TGGTGTC C  TTG     AAGG
                                 A      _ GT   TCAAAA
GAM2350 CTBP2   3' TCTACCACAGGCAAACAGTTTT 55406    C     G TG  _____  C
            CTCC                  TC ACCACGG G  AAC    TTC CC
                                || ||||||| |  |||    ||| ||
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                                AG TGGTGTC C  TTG   AAG GG
                                 A     _ GT   TCAA   A
GAM2350  DYRK1A   3'  TCCTGTCATGGGGGACTCTTC  55407    AC_  C   T  A_
                                TCC   CA GGGG GA  CTTC
                                |||   || |||| ||  ||||
                                AGG   GT CCCC CT  GAAG
                                  ACA  A   _  GA
GAM2350  EN2      5'  ACCGTGGGGCGAAATCCC    55408    AC      CT
                                ACC  GGGGTGAA  TCCC
                                |||  ||||||||  ||||
                                TGG  CCCCGCTT  AGGG
                                  CA       T_
GAM2350  GOLGA4   5'  CCAAGATGTGAACTTCCC    55409    C GG
                                CCA G  GTGAACTTCCC
                                ||| |  ||||||||||
                                GGT C  CACTTGAAGGG
                                  T TA
GAM2350  GRM1     5'  TCCACCACCGCCTCCTTCCCC  55410       GGG  GAA
                                TCCACCAC   GT   CTTCCCC
                                ||||||||   ||   |||||||
                                AGGTGGTG   CG   GAAGGGG
                                     G__  GAG
GAM2350  ISLR     3'  TCCACCACTGAGGCTTCTCCC  55411       _    GAA
                                TCCACCAC GGGGT   CTTCC
                                |||||||| |||||   |||||
                                AGGTGGTG CTCCG   GAGGG
                                     A    AA_
GAM2350  PLAUR    5'  TCCGCCACAAACTTCC      55412    A   GGGGT
                                TCC CCAC    GAACTTCC
                                ||| ||||    ||||||||
                                AGG GGTG    TTTGAAGG
                                  C   _____
GAM2350  PLOD     5'  TCGGCCGCGGGGGTGAACCT   55413    CA  A
                                TC  CC CGGGGGTGAACTT
                                ||  || ||||||||||||
                                AG  GG GCCCCACTTGGA
                                 CC  C
GAM2350  TADA2L   5'  TCCTTACGGGGGTGGGACCGGCC 55414    ACC      A_  TC
                                TCC   ACGGGGGTG  ACT  CC
                                |||   ||||||||  |||  ||
                                AGG   TGCCCCAC  TGG  GG
                                  AA_      CC   CC
GAM2350  TADA2L   5'  TCCTTACGGGGGTGGGACCGGCC 55414    ACC      A_  TC
                                TCC   ACGGGGGTG  ACT  CC
                                |||   ||||||||  |||  ||
                                AGG   TGCCCCAC  TGG  GG
                                  AA_      CC   CC
GAM2350  TCIRG1   5'  CCCGTCACGGGGGTGCTCC    55415    AC       AAC
                                TCC  CACGGGGGTG   TTCC
                                |||  |||||||||   ||||
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                                GGG  GTGCCCCAC   GAGG
                                  CA       ___
GAM2350  C20orf21  3'  CCACTGGACATCAAACTTCCCC 55416      G  ___
                                CCAC GGG   TGAACTTCCCC
                                |||| |||   ||||||||||
                                GGTG CCT   GTTTGAAGGGG
                                  A   GTA
GAM2350  DCNP1     3'  TCCACCATGGGCCTCCC     55417        C   GTGAA
                                TCCACCA GGG    CTTCCC
                                ||||||| |||    ||||||
                                AGGTGGT CCC    GGAGGG
                                   A  _____
GAM2350  DKFZP434F1735 3'  TCCCCATGGGGCCTCTTCC    55418     A   C    GAA
                                TCC CCA GGGGT   CTTCC
                                ||| ||| |||||   |||||
                                AGG GGT CCCCG   GAAGG
                                  _  A    GA_
GAM2350  DNAJB5    3'  CACAGGTTGTGAACTTTCCC   55419       __       C
                                CACGGG  GTGAACTT CCC
                                ||||||  |||||||| |||
                                GTGTCC  CACTTGAA GGG
                                   AA       A
GAM2350  FLJ11413  3'  TCTACCACGGGGGCCTTCC    55420    C        TGAA
                                TC ACCACGGGG    CTTCC
                                || |||||||||    |||||
                                AG TGGTGCCCC    GAAGG
                                 A        CG__
GAM2350  FLJ14327  3'  CACCGCGAGTGTGCTTCCCCC  55421      A   _   AA
                                CACC CGGG GTG  CTTCCCCC
                                |||| |||| |||  ||||||||
                                GTGG GCTC CAC  GAAGGGGG
                                  C   A   __
GAM2350  FLJ21616  5'  CCCATATGAACTTCCTCC     55422    A  GG        _
                                CC CG  GTGAACTTCC CC
                                || ||  ||||||||||| ||
                                GG GT  TACTTGAAGG GG
                                 _ A_         A
GAM2350  FLJ21841  3'  CACATGCTGTGACTTCCCC    55423      GG__    A
                                CACG    GTGA CTTCCCC
                                ||||    |||| |||||||
                                GTGT    CACT GAAGGGG
                                  ACGA   _
GAM2350  FLJ22578  3'  TCCACCGCAGTCCCCTTCCCCC 55424        A   GGTGAA
                                TCCACC CGG     CTTCCCCC
                                |||||| |||     ||||||||
                                AGGTGG GTC     GAAGGGGG
                                   C   AGGG__
GAM2350  FLJ23132  3'  TCCTCCACGGAATTTCCCC    55425     A        GAAC
                                TCC CCACGGGGT    TTCCCC
                                ||| |||||||||    ||||||
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                                AGG GGTGCCTTA    AAGGGG
                                  A       _____
GAM2350  FTSJ3    3'  TCCAACACCGAACTTCCC    55426     C   GGGG
                                TCCA CAC    TGAACTTCCC
                                |||| |||    ||||||||||
                                AGGT GTG    GCTTGAAGGG
                                  T  _____
GAM2350  HT002    3'  TCCCCACAGGACTTTCCTC    55427     A       GAA
                                TCC CCACGGGGT   CTTC
                                ||| |||||||||   ||||
                                AGG GGTGTCCTG   GGAG
                                  _       AAA
GAM2350  IGSF2    3'  TCCACACGGGGCTTTCC     55428      C      GAAC
                                TCCAC ACGGGGT    TTCC
                                ||||| |||||||    ||||
                                AGGTG TGCCCCG    AAGG
                                  _      A___
GAM2350  IMAP1    3'  CCGTTGGAATGAAGTTTTCCC  55429    AC_      C__
                                CC   GGGGTGAA   TTCCC
                                ||   |||||||   |||||
                                GG   CCTTACTT   AAGGG
                                 CAA       CAA
GAM2350  KIAA0350 3'  CCATGATGGTCTTCCCC     55430     C  _   GAA
                                CCA GG GGT   CTTCCCC
                                ||| || |||   |||||||
                                GGT CT CCA   GAAGGGG
                                  A  A  ___
GAM2350  KIAA0354 5'  TCCGTTACGGGACTTCCTCC   55431     ACC    GTGA    _
                                TCC   ACGGG    ACTTCC CC
                                |||   |||||    |||||| ||
                                AGG   TGCCC    TGAAGG GG
                                  CAA     _____      A
GAM2350  KIAA0450 5'  TCCACCACGCGGGTCTGCTCCC 55432          _    GAA
                                TCCACCACG GGGT   CTTCC
                                ||||||||| ||||   |||||
                                AGGTGGTGC CCCA   GAGGG
                                      G   GAC
GAM2350  KIAA1032 3'  CCACGCTGAACTTTCCCC    55433      GGG     _
                                CCACG   TGAACTT CCCC
                                |||||   ||||||| ||||
                                GGTGC   ACTTGAA GGGG
                                   G__      A
GAM2350  KIAA1957 5'  TCTGCCCGGGGTGATGGCCC   55434    CA  A      ACTT
                                TC  CC CGGGGTGA    CCC
                                ||  || ||||||||    |||
                                AG  GG GCCCCACT    GGG
                                 AC  _       ACC_
GAM2350  L3MBTL2  5'  CCTTCAGGAACTTCCCC     55435    A_    TGA
                                CC  CGGGG   ACTTCCCC
                                ||  |||||   ||||||||
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                                GG  GTCCT   TGAAGGGG
                                 AA    ___
GAM2350  MGC10715  3'  TCCCTACACATAAACTTC    55436     AC_   GGG
                                TCC   CAC   GTGAACTTC
                                |||   |||   |||||||||
                                AGG   GTG   TATTTGAAG
                                  GAT   ___
GAM2350  MGC4268   5'  TCCTCACGGGGCCAAATGGTTT 55437     AC       G  C____
              CCC                   TCC  CACGGGGT AA     TTCCC
                                |||  |||||||| ||    |||||
                                AGG  GTGCCCCG TT    AAGGG
                                  A_       G  TACCA
GAM2350  P2RX1     3'  TCCACCCGTCGCTTCCCC    55438       A  GG TGAA
                                TCCACC CG  G    CTTCCCC
                                ||||||  ||  |   |||||||
                                AGGTGG GC  C    GAAGGGG
                                   _  AG _____
GAM2350  PRO1880   3'  TCCACTACAGTGAAACTT    55439      C    GGT
                                TCCAC ACGG   GAACTT
                                |||||  ||||   ||||||
                                AGGTG TGTC   TTTGAA
                                   A    AC_
GAM2350  RAB40C    3'  TCCACCACGGGGGGTCC     55440           TGAACT
                                TCCACCACGGGG     TCC
                                ||||||||||||     |||
                                AGGTGGTGCCCC     AGG
                                      CC_____
GAM2350  SP192     3'  CCCACCACACAAACTTC     55441         GGG TG
                                TCCACCAC   G  AACTTC
                                ||||||||   |  ||||||
                                GGGTGGTG   T  TTGAAG
                                     ___ GT
GAM2350  LOC112840 3'  ACCAAGATAACTTCC       55442      CG     A
                                ACCA  GGGTGA CTTCC
                                ||||  |||||| |||||
                                TGGT  TCTATT GAAGG
                                  __    _
GAM2350  LOC113763 3'  TCCAAATAAGGGACTTCCCC   55443      CCAC    TGA
                                TCCA    GGGG   ACTTCCCC
                                ||||    ||||   ||||||||
                                AGGT    TCCC   TGAAGGGG
                                  TTAT    ___
GAM2350  LOC121838 5'  TCCAATTCCCTGTGAACTTTCT 55444      ___  ACGGG       _ C
              CC                    TCCA   CC     GTGAACTT C CC
                                ||||   ||     |||||||| | ||
                                AGGT   GG     CACTTGAA G GG
                                  TAA  GA___       A A
GAM2350  LOC146108 3'  TCCCCACAGAACTGGGTTTCCC 55445      A     GG GAAC_
                                TCC CCACGG  T     TTCCC
                                ||| ||||||  |     |||||
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                                AGG GGTGTC  G    AAGGG
                                  _     TT ACCCA
GAM2350  LOC153232 5'  CACCACGCAGGGCTTCCCCC  55446       __  TGAA
                                CACCACG  GGG   CTTCCCCC
                                |||||||  |||   ||||||||
                                GTGGTGC  CCC   GAAGGGGG
                                   GT  _____
GAM2350  LOC153810 5'  CCACTGGCTTGAATTTCTCCC  55447     _ GG   C  _
                                CCAC GG  TGAA TTC CCC
                                |||| ||  |||| ||| |||
                                GGTG CC  ACTT AAG GGG
                                  A  GA   A  A
GAM2350  LOC204084 5'  TCCATCACCAAACTTCC     55448     C  GGGG
                                TCCA CAC   TGAACTTCC
                                |||| |||   |||||||||
                                AGGT GTG   GTTTGAAGG
                                  A  _____
GAM2350  LOC254808 3'  CCGCACAAGGTTTTCCCC    55449   AC      GAAC
                                CC  CACGGGGT   TTCCCC
                                ||  ||||||||   ||||||
                                GG  GTGTTCCA   AAGGGG
                                 C_      A___
GAM2350  LOC51308  3'  CCATCTGGGCTAGGACTTCCCC 55450    CG_   GA__
           C                     CCA   GGGT   ACTTCCCCC
                                |||   ||||   |||||||||
                                GGT   CCCG   TGAAGGGGG
                                  AGA   ATCC
GAM2350  LOC90620  5'  CCACCACGGGGTGTGACACCTC 55451          A___
           C                     CCACCACGGGGTG   ACTTCC
                                ||||||||||||   ||||||
                                GGTGGTGCCCCAC   TGGAGG
                                       ACTG
GAM2350  LOC90826  5'  TCCGCCGCGGGTGAACTC   55452    A  A   G
                                TCC CC CGGG TGAACTT
                                ||| || |||| |||||||
                                AGG GG GCCC ACTTGAG
                                  C  C   _
GAM2351  DMP1      3'  TTACTGGTGTCACTCCACAG  55455     ACC   C
                                TTACT   GTCAC TCCACAG
                                |||||   ||||| |||||||
                                AATGA   CAGTG AGGTGTC
                                   CCA    _
GAM2351  EPHA3     3'  CTACGCCTTCCACAGC     55456     C  ACC
                                CTAC GTC   TCCACAGC
                                |||| |||   ||||||||
                                GATG CGG   AGGTGTCG
                                  _  A__
GAM2351  HKR3      5'  CTCCGTCGCCTCCACAGC   55457    A   A
                                CT CCGTC CCTCCACAGC
                                || ||||| ||||||||||
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                                GA GGCAG GGAGGTGTCG
                                 _    C
GAM2351  NDUFV1   5'  TCACGCTGTCACCTTCATAGC  55458     TACC     C  C
                                TTAC   GTCACCT CA AGC
                                ||||   ||||||| || |||
                                AGTG   CAGTGGA GT TCG
                                  CGA_     A  A
GAM2351  WASF3    3'  CATTCCTACCGTCACCTC    55459     A
                                CATT CTACCGTCACCTC
                                |||| ||||||||||||
                                GTAA GATGGCAGTGGAG
                                  G
GAM2351  CRSP3    3'  ATTTCTACTTTCTCCACAG   55460    A   CGTCAC
                                ATT CTAC    CTCCACAG
                                ||| ||||    ||||||||
                                TAA GATG    GAGGTGTC
                                 A   AAA___
GAM2351  FLJ12891 3'  CACTCCACCTCCACAG     55461     ACCG
                                TACT   TCACCTCCACAG
                                ||||   ||||||||||||
                                GTGA   GGTGGAGGTGTC
                                  ____
GAM2351  FLJ21148 3'  ATTACTACCGTATGTCCAC   55462         CACC
                                ATTACTACCGT   TCCAC
                                ||||||||||   |||||
                                TAATGATGGCA   AGGTG
                                      TAC_
GAM2351  FLJ21687 3'  CCTCCAGCATCTCCACAG    55463    A  T  C
                                CT CCG CA CTCCACAG
                                || ||| || ||||||||
                                GG GGT GT GAGGTGTC
                                 A  C  A
GAM2351  JAM1     3'  CACTACACACATCTCCACAGC  55464      _  T  C
                                TACTAC CG CA CTCCACAGC
                                |||||| || || |||||||||
                                GTGATG GT GT GAGGTGTCG
                                   T  _  A
GAM2351  JAM1     3'  CACTACACACATCTCCACAGC  55464      _  T  C
                                TACTAC CG CA CTCCACAGC
                                |||||| || || |||||||||
                                GTGATG GT GT GAGGTGTCG
                                   T  _  A
GAM2351  JAM1     3'  CACTACACACATCTCCACAGC  55464      _  T  C
                                TACTAC CG CA CTCCACAGC
                                |||||| || || |||||||||
                                GTGATG GT GT GAGGTGTCG
                                   T  _  A
GAM2351  JAM1     3'  CACTACACACATCTCCACAGC  55464      _  T  C
                                TACTAC CG CA CTCCACAGC
                                |||||| || || |||||||||
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                                GTGATG GT GT GAGGTGTCG
                                   T  _  A
GAM2351  KIAA0934  3'  TCACTGTTGTCCCACAGC    55465      ACC   ACCT
                                TTACT   GTC    CCACAGC
                                |||||   |||    |||||||
                                AGTGA   CAG    GGTGTCG
                                  CAA   ____
GAM2351  MEGF10    3'  CATTACTACTGTATCATAGGAC 55466        C__    CCTCC
           AGC                    CATTACTAC   GTCA    ACAGC
                                |||||||||   ||||    |||||
                                GTAATGATG   TAGT    TGTCG
                                     ACA    ATCC_
GAM2351  SLC26A9   3'  CCAATCTTACCTCCACAGC    55467     _  __
                                CCG TC  ACCTCCACAGC
                                |||  ||  ||||||||||
                                GGT AG  TGGAGGTGTCG
                                  T  AA
GAM2351  SLC26A9   3'  CCAATCTTACCTCCACAGC    55467     _  __
                                CCG TC  ACCTCCACAGC
                                |||  ||  ||||||||||
                                GGT AG  TGGAGGTGTCG
                                  T  AA
GAM2351  LOC150527 3'  CACTGCCTTCTCGCCTCCACAG 55468      A  G__  A
           C                     TACT CC   TC CCTCCACAGC
                                ||||  ||   ||  ||||||||||
                                GTGA GG   AG GGAGGTGTCG
                                  C  AAG  C
GAM2351  LOC154428 5'  CTGCCGCAGCCCACAGC     55469    A   T  C T
                                CT CCG CA C CCACAGC
                                ||  ||| ||  |  |||||||
                                GA GGC GT G GGTGTCG
                                 C   _  C _
GAM2351  LOC161742 3'  TACACAGTTCATTTCCACAGC  55470     T  CG_   CC
                                TAC AC   TCA  TCCACAGC
                                |||  ||   |||  ||||||||
                                ATG TG   AGT  AGGTGTCG
                                  _  TCA   AA
GAM2352  GALNT7    5'  TGCAACAGGTCATGTTCAA    55473        A    __
                                TGCAATAG TCAT  TCAG
                                |||||||| ||||  ||||
                                ACGTTGTC AGTA  AGTT
                                     C    CA
GAM2352  MAGEB3    3'  TGCAACAGATCACTAAATAA   55474            C
                                TGCAATAGATCATT AGTAA
                                |||||||||||||| |||||
                                ACGTTGTCTAGTGA TTATT
                                          T
GAM2352  MAP3K7    3'  TGCAATGAAACAGTAAAA     55475       A  TCATT
                                TGCAAT GA    CAGTAAAA
                                ||||||  ||    ||||||||
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                                ACGTTA CT    GTCATTTT
                                   _ TT___
GAM2352 MBNL    3' ACAGTACAATCAGTAAAA    55476     AT  T
                                ATAG  CA TCAGTAAAA
                                |||||  || |||||||||
                                TGTC  GT AGTCATTTT
                                  AT  T
GAM2352 MCCC1   3' GCATACAATCATTTAGTAAAAC 55477    ATA     C
                                GCA   GATCATT AGTAAAAC
                                |||   ||||||| ||||||||
                                CGT   TTAGTAA TCATTTTG
                                  ATG      A
GAM2352 PCDH11X 3' TAGATCATCAGAAAAC      55478        T   T
                                TAGATCAT CAG AAAAC
                                |||||||| ||| |||||
                                ATCTAGTA GTC TTTTG
                                   _  _
GAM2352 PCDH11X 3' TAGATCATCAGAAAAC      55478        T   T
                                TAGATCAT CAG AAAAC
                                |||||||| ||| |||||
                                ATCTAGTA GTC TTTTG
                                   _  _
GAM2352 PCDH11Y 3' TAGATCATCAGAAAAC      55478        T   T
                                TAGATCAT CAG AAAAC
                                |||||||| ||| |||||
                                ATCTAGTA GTC TTTTG
                                   _  _
GAM2352 PIK3R3  3' GCTTGGTATTATTCAGTAAAAC 55479    AATAG  C
                                GC    AT ATTCAGTAAAAC
                                ||    || ||||||||||||
                                CG    TA TAAGTCATTTTG
                                 AACCA  A
GAM2352 RP2     3' TGCAAAGATCATTTGTAAA   55480      T       CA
                                TGCAA AGATCATT  GTAAA
                                ||||| ||||||||  |||||
                                ACGTT TCTAGTAA  CATTT
                                   _       A_
GAM2352 BIKE    3' TGCAAAATCATTAGTAA     55481      TA      C
                                TGCAA  GATCATT AGTAA
                                |||||  ||||||| |||||
                                ACGTT  TTAGTAA TCATT
                                   __      _
GAM2352 C20orf28 3' TGCAGAGATCACCAGC     55482     AT      T
                                TGCA  AGATCAT CAGT
                                ||||  ||||||| ||||
                                ACGT  TCTAGTG GTCG
                                  C_      _
GAM2352 CHRNA6  3' TGCAATAGTTCACAAAGT    55483        A   TC
                                TGCAATAG TCAT  AGT
                                |||||||| ||||  |||
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                                ACGTTATC AGTG  TCA
                                    A    TT
GAM2352 CNOT8    3' TAGACAGATTCAGTAAAA    55484      C_
                                TAGAT  ATTCAGTAAAA
                                |||||  ||||||||||||
                                ATCTG  TAAGTCATTTT
                                   TC
GAM2352 ENPP4    3' TGCAATAATCCATAAAGC    55485        A    TC
                                TGCAATAG TCAT  AGT
                                |||||||| ||||  |||
                                ACGTTATT GGTA  TCG
                                    A    TT
GAM2352 FLJ13340 3' CAATAGTTCCAGTAAAA     55486       ATCA
                                CAATAG    TTCAGTAAAA
                                ||||||    ||||||||||
                                GTTATC    AGGTCATTTT
                                   A___
GAM2352 KIAA0924 3' TGCAGAGGACAGGGCAGTAAAA 55487      ATA   CATT
             C                   TGCA   GAT    CAGTAAAAC
                                ||||   |||    |||||||||
                                ACGT   CTG    GTCATTTTG
                                  CTC   TCCC
GAM2352 KIAA1804 3' TACAATAGATTGCAGCAAAA   55488         CATT
                                TGCAATAGAT    CAGTAAAA
                                ||||||||||    ||||||||
                                ATGTTATCTA    GTCGTTTT
                                      AC__
GAM2352 MGC14161 3' TGCAATAATCAGTAA       55489        ATCAT
                                TGCAATAG     TCAGTAA
                                ||||||||     |||||||
                                ACGTTATT     AGTCATT
                                      _____
GAM2352 PAIP1    3' TGGAATAAATCTTCAGT     55490    C       A
                                TG AATAGATC TTCAGT
                                || |||||||| ||||||
                                AC TTATTTAG AAGTCA
                                 C       _
GAM2352 PDE10A   3' TGCAAAGGGTTCAGTAAAAC   55491      T  ATCA
                                TGCAA AG    TTCAGTAAAAC
                                ||||| ||    ||||||||||||
                                ACGTT TC    AAGTCATTTTG
                                   _ CC__
GAM2352 RERG     3' CAATAGATCATTGAGAGAA    55492          C  TA
                                CAATAGATCATT AG  AA
                                |||||||||||| ||  ||
                                GTTATCTAGTAA TC  TT
                                       C  TC
GAM2352 STIM2    3' TGCAGTAAATCACAGT      55493      A      TT
                                TGCA TAGATCA  CAGT
                                |||| |||||||  ||||
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                                ACGT ATTTAGT  GTCA
                                  C      __
GAM2352  TBDN100   3'  CAATAGTTCCAGTAAAA     55486       ATCA
                                CAATAG    TTCAGTAAAA
                                ||||||    ||||||||||
                                GTTATC    AGGTCATTTT
                                   A___
GAM2352  UNC5D     3'  TGCAATAGGACAATAAAA     55494        ATCATT
                                TGCAATAG     CAGTAAAA
                                ||||||||     ||||||||
                                ACGTTATC     GTTATTTT
                                     CT____
GAM2352  LOC134266 3'  TGTAATAGACCATTAGAAAA   55495    C         C  T
                                TG AATAGATCATT AG AAAA
                                || |||||||||| || ||||
                                AC TTATCTGGTAA TC TTTT
                                 A         _ _
GAM2352  LOC152275 3'  TGCAGTGGGCATTCAGTAAA   55496      ATAGAT
                                TGCA     CATTCAGTAAA
                                ||||     ||||||||||
                                ACGT     GTAAGTCATTT
                                  CACCC_
GAM2352  LOC169008 5'  TAGATTCAGTAAAAC       55497       CAT
                                TAGAT   TCAGTAAAAC
                                |||||   ||||||||||
                                ATCTA   AGTCATTTTG
                                  ____
GAM2352  LOC51720  3'  TGCATAGATCATAAAAAA     55498      A       TCAGT
                                TGCA TAGATCAT     AAAA
                                |||| ||||||||     ||||
                                ACGT ATCTAGTA     TTTT
                                  _       TT____
GAM2352  LOC57822  3'  TACAATAGGTCACTGAAGC    55499         A    C_
                                TGCAATAG TCATT  AGT
                                |||||||| |||||  |||
                                ATGTTATC AGTGA  TCG
                                     C    CT
GAM2352  LOC90288  3'  TACAATGGGCCCCAGTAAAAC  55500       AGATCA
                                TGCAAT     TTCAGTAAAAC
                                ||||||     ||||||||||
                                ATGTTA     GGGTCATTTTG
                                   CCCG__
GAM2352  LOC92710  3'  TACGATAGATCATTTCAAT    55501     A        _
                                TGC ATAGATCATT CAGT
                                ||| |||||||||| ||||
                                ATG TATCTAGTAA GTTA
                                  C         A
GAM2353  ADAMTS4   3'  GAGGCCGAGGCAGGTCGAT    55504      AA    TA
                                GAGG  CCGG  TGGGTCGAT
                                ||||  ||||  |||||||||
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                                CTCC  GGCT  GTCCAGCTA
                                  __   CC
GAM2353  NTRK2    5'  TGGGGGTCCGGTATGCACCTCG 55505    A  AA      G __
                                TG GG  CCGGTATG G  TCG
                                || ||  |||||||| |  |||
                                AC CC  GGCCATAC T  AGC
                                 C  CA       G GG
GAM2353  KIAA0677  3'  TGAGAAGATGATGGGTCG    55506       ACC  _
                                TGAGGA   GGT ATGGGTCG
                                ||||||   ||| ||||||||
                                ACTCTT   CTA TACCCAGC
                                   ___  C
GAM2353  MGC16279  5'  TGAGGAACCGAGTGTGTCCAC  55507          TA  G   G
                                TGAGGAACCGG  TG GTC AT
                                ||||||||||  || ||| ||
                                ACTCCTTGGCT  AC CAG TG
                                      C_  A   G
GAM2353  MGC16279  3'  TGAGGAACCGAGTGTGTCCAC  55507          TA  G   G
                                TGAGGAACCGG  TG GTC AT
                                ||||||||||  || ||| ||
                                ACTCCTTGGCT  AC CAG TG
                                      C_  A   G
GAM2353  PME-1    3'  TGGGGAAGCCGATGTTGGTCA  55508    A   _    ATG
                                TG GGAA CCGGT   GGTCG
                                || |||| |||||   |||||
                                AC CCTT GGCTA   CCAGT
                                 C   C    CAA
GAM2353  LOC147669 5'  TGAGGAACTGGTGGGT      55509        C   AT
                                TGAGGAAC GGT  GGGT
                                ||||||||  |||  ||||
                                ACTCCTTG CCA  CCCA
                                    A  __
GAM2353  LOC150384 3'  TGGGGAGCCAGTATATCA    55510    A  A     GG
                                TG GGA CCGGTAT  GTCG
                                || ||| |||||||  ||||
                                AC CCT GGTCATA  TAGT
                                 C  C      __
GAM2353  LOC157450 3'  TGAGGAACCGAGTGTGTCCAC  55507          TA  G   G
                                TGAGGAACCGG  TG GTC AT
                                ||||||||||  || ||| ||
                                ACTCCTTGGCT  AC CAG TG
                                      C_  A   G
GAM2353  LOC158490 3'  TGAGGAACCGAGTGTGTCCAC  55507          TA  G   G
                                TGAGGAACCGG  TG GTC AT
                                ||||||||||  || ||| ||
                                ACTCCTTGGCT  AC CAG TG
                                      C_  A   G
GAM2353  LOC219917 3'  TGGGGAACCGAGTGTGTCCAC  55511    A      TA  G   G
                                TG GGAACCGG  TG GTC AT
                                || ||||||||  || ||| ||
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                                AC CCTTGGCT  AC CAG TG
                                 C       C_  A   G
GAM2353  LOC220073 5'  TGAGGAACCGAGTGTGTCCAC  55507          TA  G   G
                                TGAGGAACCGG  TG GTC AT
                                ||||||||||  || ||| ||
                                ACTCCTTGGCT  AC CAG TG
                                      C_  A   G
GAM2353  LOC93320  3'  TGAGGAACTGAGTGTGTCCAC  55512        C  TA  G   G
                                TGAGGAAC GG  TG GTC AT
                                ||||||||  ||  || ||| ||
                                ACTCCTTG CT  AC CAG TG
                                     A  C_  A   G
GAM2354  CANX     3'  CATGAAAAAACAAACCTAAGA  55515       CAAT
                                CATGA   GAACAAACCTAAGA
                                |||||   ||||||||||||||
                                GTACT   TTTGTTTGGATTCT
                                   TT__
GAM2354  CIT      3'  ATGAGAATGAACAGGAACAAG  55516      C       AACC
                                ATGA AATGAACA   TAAG
                                |||| ||||||||   ||||
                                TACT TTACTTGT   GTTC
                                  C       CCTT
GAM2354  GNAI3    3'  ATAACATAAAACCTAAG     55517        A    CAA
                                ATGACA TGAA   ACCTAAG
                                |||||| ||||   |||||||
                                TATTGT ATTT   TGGATTC
                                   _   ____
GAM2354  IL8RA    3'  CATACAGTGAACAAACC     55518      A  A
                                CATG CA TGAACAAACC
                                |||| || ||||||||||
                                GTAT GT ACTTGTTTGG
                                  _  C
GAM2354  JRK      3'  TGACTTACGTGCAAACCTAAGA 55519      A_   AA
              C                  TGAC  ATG  CAAACCTAAGAC
                                ||||  |||  ||||||||||||
                                ACTG  TGC  GTTTGGATTCTG
                                  AA   AC
GAM2354  MAN1A1   3'  ATGATAATAAACATAAAAGAC  55520      C       AACCT
                                ATGA AATGAACA    AAGAC
                                |||| ||||||||    |||||
                                TACT TTATTTGT    TTCTG
                                  A       ATT__
GAM2354  PRKWNK3  3'  TGAAAGGTAAACCTAAGAC   55521      C___
                                TGAA   AAACCTAAGAC
                                ||||   ||||||||||
                                ACTT   TTTGGATTCTG
                                  TCCA
GAM2354  PSCDBP   3'  TGGGCATAAGCAAACCTAAGA  55522    ACA   A
                                TG   ATGA CAAACCTAAGA
                                ||   |||| ||||||||||
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                                AC   TATT GTTTGGATTCT
                                 CCG    C
GAM2354  AP3D1     3'  TGACAATGGACAACGCCT     55523         A    A_
                                TGACAATG ACAA  CCT
                                |||||||| ||||  |||
                                ACTGTTAC TGTT  GGA
                                     C    GC
GAM2354  FLJ13263  3'  ATGATAATGAACAAGTGAAAG  55524      C        ACCT
                                ATGA AATGAACAA    AAG
                                |||| |||||||||    |||
                                TACT TTACTTGTT    TTC
                                  A        CACT
GAM2354  FLJ20208  3'  TGACAATGAGCAGACAATAG   55525          A  A  CTA
                                TGACAATGA CA AC   AG
                                ||||||||| || ||   ||
                                ACTGTTACT GT TG   TC
                                     C  C  TTA
GAM2354  FLJ21432  3'  ATGACAGTAACCTAAGAC     55526       ATGAACA
                                ATGACA      AACCTAAGAC
                                ||||||      ||||||||||
                                TACTGT      TTGGATTCTG
                                   CA_____
GAM2354  KIAA0731  3'  ATGGTGATGACAAACCCCAGA  55527     ACA    A      A
                                ATG   ATGA CAAACCT AGA
                                |||   |||| ||||||| |||
                                TAC   TACT GTTTGGG TCT
                                  CAC    _      G
GAM2354  KIAA1430  3'  CATGACAACTGAATAATTAGAA 55528         _    CAAACCT
              GA                   CATGACAA TGAA       AAGA
                                |||||||| ||||       ||||
                                GTACTGTT ACTT       TTCT
                                     G    ATTAATC
GAM2354  PEG10     3'  ATGATAATGAACATGTGAAAGA 55529      C       AACCT
                                ATGA AATGAACA     AAGA
                                |||| ||||||||     ||||
                                TACT TTACTTGT     TTCT
                                  A       ACACT
GAM2354  TBCC      3'  TGACAATAAGTAAACTTCGAGA 55530         AC    CTA_
              C                    TGACAATGA  AAAC    AGAC
                                |||||||||  ||||    ||||
                                ACTGTTATT  TTTG    TCTG
                                     CA    AAGC
GAM2354  LOC144519 5'  ATGACAATGATGACACAGAGA  55531          ACAA  CTA
                                ATGACAATGA    AC   AGA
                                ||||||||||    ||   |||
                                TACTGTTACT    TG   TCT
                                      ACTG  TC_
GAM2354  LOC147632 3'  ACACCGAAACCTAAGAC     55532     A    CAA
                                ACA TGAA   ACCTAAGAC
                                ||| ||||   |||||||||
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                                TGT GCTT   TGGATTCTG
                                  G   ___
GAM2354  LOC159089 5'  CATGACAATGTACCCCAAG   55533         A  AAA
                                CATGACAATG AC   CCTAAG
                                |||||||||| ||   ||||||
                                GTACTGTTAC TG   GGGTTC
                                     A  ___
GAM2354  LOC221683 5'  CATCACACCAAAACCTAAGAC  55534     G   ATGAAC
                                CAT ACA     AAACCTAAGAC
                                ||| |||     ||||||||||
                                GTA TGT     TTTGGATTCTG
                                  G   GGT___
GAM2354  LOC221814 5'  TGACAATGATGCTACAATCTGG 55535         _____   AC  AA
            GAC                    TGACAATGA    ACAA  CT  GAC
                                |||||||||    ||||  ||  |||
                                ACTGTTACT    TGTT  GA  CTG
                                     ACGA    A_  CC
GAM2354  LOC54505  5'  GACAATAAACCTGAGA      55536        ACAA    A
                                GACAATGA    ACCT AGA
                                ||||||||    |||| |||
                                CTGTTATT    TGGA TCT
                                     _____   C
GAM2355  ACHE     3'  AGAGGAGGGGCCCCTGTGGC   55539        C  G __  C
                                AGAGGAGG GG T  TG GGC
                                |||||||| || |  || |||
                                TCTCCTCC CC G  AC CCG
                                     _  G GG  A
GAM2355  ADAM19   3'  TGAGAGGACGCGTTGGG     55540        G  GG    C
                                TGAGAGGA GC  GTTG GG
                                |||||||| ||  |||| ||
                                ACTCTCCT CG  CAAC CC
                                     G  __   _
GAM2355  ASPH     3'  GAGAGGAGGGAAGGTGG     55541        C_    TGC
                                GAGAGGAGG  GGGT   GG
                                |||||||||  ||||   ||
                                CTCTCCTCC  TCCA   CC
                                     CT   ___
GAM2355  ASPH     3'  GAGAGGAGGGAAGGTGG     55541        C_    TGC
                                GAGAGGAGG  GGGT   GG
                                |||||||||  ||||   ||
                                CTCTCCTCC  TCCA   CC
                                     CT   ___
GAM2355  BAAT     3'  TGAGAGAAGGTCCCGG      55542        AGGC    G
                                TGAGAGG    GGGTT CGG
                                |||||||    ||||| |||
                                ACTCTCT    TCCAG GCC
                                     _____    G
GAM2355  BCL10    5'  GAGAGGAGGCGGAGCGG     55543           TT
                                GAGAGGAGGCGGG  GCGG
                                ||||||||||||  ||||
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                                CTCTCCTCCGCCT  CGCC
                                           __
GAM2355 BMP1    3' CGGGAGGAGGCAGGGTGGC   55544   A     _   T
                                TG GAGGAGGC GGGT GC
                                || |||||||| |||| ||
                                GC CTCCTCCG CCCA CG
                                 C      T   C
GAM2355 CDKN2A  3' AAGCGGGGTGGGTTGTGGC   55545    A A C    C
                                GAG GG GG GGGTTG GGC
                                ||| || || |||||| |||
                                TTC CC CC CCCAAC CCG
                                  G _ A    A
GAM2355 CDKN2A  3' AAGCGGGGTGGGTTGTGGC   55545    A A C    C
                                GAG GG GG GGGTTG GGC
                                ||| || || |||||| |||
                                TTC CC CC CCCAAC CCG
                                  G _ A    A
GAM2355 CDKN2A  3' AAGCGGGGTGGGTTGTGGC   55545    A A C    C
                                GAG GG GG GGGTTG GGC
                                ||| || || |||||| |||
                                TTC CC CC CCCAAC CCG
                                  G _ A    A
GAM2355 CDKN2A  3' AAGCGGGGTGGGTTGTGGC   55545    A A C    C
                                GAG GG GG GGGTTG GGC
                                ||| || || |||||| |||
                                TTC CC CC CCCAAC CCG
                                  G _ A    A
GAM2355 CELSR1  3' TGAGGGGAGGGGGTGG     55546    A   C   TGC
                                TGAG GGAGG GGGT  GG
                                |||| ||||| ||||  ||
                                ACTC CCTCC CCCA  CC
                                  C   _  ____
GAM2355 CLDN14  5' TGAGAGGAGGTGGCTTGGC   55547       CG  GC
                                TGAGAGGAGG  GGTT  GGC
                                ||||||||||  ||||  |||
                                ACTCTCCTCC  CCGA  CCG
                                     A_   A_
GAM2355 CLTB    3' TGAGAGGAGGCGTGAGGGGC  55548        GGTTGC
                                TGAGAGGAGGCG    GGC
                                ||||||||||||    |||
                                ACTCTCCTCCGC    CCG
                                      ACTCC_
GAM2355 CLTB    3' TGAGAGGAGGCGTGAGGGGC  55548        GGTTGC
                                TGAGAGGAGGCG    GGC
                                ||||||||||||    |||
                                ACTCTCCTCCGC    CCG
                                      ACTCC_
GAM2355 COL4A3  3' TGAGTGGAGGCCAGTGG    55549    A    G  TGC
                                TGAG GGAGGC GGT  GG
                                |||| |||||| |||  ||
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                                ACTC CCTCCG TCA   CC
                                  A     G  ___
GAM2355  COL4A3   3'  TGAGTGGAGGCCAGTGG     55549      A     G   TGC
                                TGAG GGAGGC GGT   GG
                                |||| |||||| |||   ||
                                ACTC CCTCCG TCA   CC
                                  A     G  ___
GAM2355  COL4A3   3'  TGAGTGGAGGCCAGTGG     55549      A     G   TGC
                                TGAG GGAGGC GGT   GG
                                |||| |||||| |||   ||
                                ACTC CCTCCG TCA   CC
                                  A     G  ___
GAM2355  COL5A3   3'  TGAGAGGAGGCTGGAC      55550          G  TT
                                TGAGAGGAGGC GG  GC
                                |||||||||| ||  ||
                                ACTCTCCTCCG CC  TG
                                       A  __
GAM2355  CTF1     3'  CGGGAGGAGGCGGGGC      55551    A         TT
                                TG GAGGAGGCGGG  GC
                                || ||||||||||  ||
                                GC CTCCTCCGCCC  CG
                                 C         __
GAM2355  CXCL1    5'  TGAGAGGAGCGGAAGAGC    55552         G    TT_
                                TGAGAGGAG CGGG   GC
                                ||||||||| ||||   ||
                                ACTCTCCTC GCCT   CG
                                      _   TCT
GAM2355  CYP8B1   3'  TGAGAGGAGGGTTCGG      55553        GGC    G
                                TGAGAGGA   GGGTT CGG
                                ||||||||   ||||| |||
                                ACTCTCCT   CCCAA GCC
                                     ___    _
GAM2355  DTR      5'  GAGAGGAGGCGGCGAGGC    55554           GT  C
                                GAGAGGAGGCGG  TG GGC
                                ||||||||||||  || |||
                                CTCTCCTCCGCC  GC CCG
                                      __  T
GAM2355  EPHA8    3'  TGAGAGGAGGGCAGAGGC    55555          _   TTGC
                                TGAGAGGAGG CGGG    GGC
                                |||||||||| ||||    |||
                                ACTCTCCTCC GTCT    CCG
                                      C   ____
GAM2355  EPS15    5'  GAGGAGGCGGAGGGAGCGGC  55556           TT__
                                GAGGAGGCGGG    GCGGC
                                ||||||||||    |||||
                                CTCCTCCGCCT    CGCCG
                                       CCCT
GAM2355  EXO1     5'  TGAGCGGAGCCGATTGCGG   55557      A    G G
                                TGAG GGAG C GGTTGCGG
                                |||| |||| | ||||||||
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                                ACTC CCTC G CTAACGCC
                                  G   _ G
GAM2355  F2RL3    3'  TGAGGGGATGAGGTTGCGG   55558     A  GGC
                                TGAG GGA  GGGTTGCGG
                                |||| |||  |||||||||
                                ACTC CCT  TCCAACGCC
                                  C  AC_
GAM2355  FHIT     3'  GAGAGGCGGGGGGGGCGG    55559      A  C  TT
                                GAGAGG GG GGG  GCGG
                                |||||| || |||  ||||
                                CTCTCC CC CCC  CGCC
                                   G  _  C_
GAM2355  FLOT2    3'  GAGGGAGGGCCGGGTGGC    55560    A   __   T
                                GAG GGAGG  CGGGT GC
                                ||| |||||  ||||| ||
                                CTC CCTCC  GCCCA CG
                                  _    CG    C
GAM2355  FOXD2    5'  GAGAGGTGAGATTGCGGC    55561      A GC
                                GAGAGG G  GGGTTGCGGC
                                |||||| |  ||||||||||
                                CTCTCC C  TCTAACGCCG
                                   A __
GAM2355  FZD3     3'  TGAGAGGAAGGTGTTAGGC   55562        CGG   C
                                TGAGAGGAGG  GTTG GGC
                                ||||||||||  |||| |||
                                ACTCTCCTTC  CAAT CCG
                                     CA_  _
GAM2355  GBF1     3'  TGGAGGAGGTGGCCCAGGGC  55563   A     C G  C
                                TG GAGGAGG GG TTG GGC
                                || ||||||| || ||| |||
                                AC CTCCTCC CC GGT CCG
                                  _     A G  C
GAM2355  GFRA2    5'  GAGAGGCGGGCGATGGGC    55564    G      __ C
                                GAG AGGCGGGT  TG GGC
                                ||| ||||||||  || |||
                                CTC TCCGCCCG  AC CCG
                                  _      CT  _
GAM2355  GGA1     3'  TGGAGGAGGCCTAAGCTG    55565   A      __
                                TG GAGGAGGC  GGGTTG
                                || ||||||||  ||||||
                                AC CTCCTCCG  TTCGAC
                                  _      GA
GAM2355  GPC1     3'  TGGGAGGAGGCGGGGAGGAAGG 55567   A        TTGC__
                C                TG GAGGAGGCGGG     GGC
                                || ||||||||||     |||
                                AC CTCCTCCGCCC     CCG
                                  C         CTCCTT
GAM2355  GPC1     3'  TGGGAGCAGGCGGGTCCTGGC  55566   A  G       GC
                                TG GAG AGGCGGGTT  GGC
                                || ||| |||||||||  |||
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                                AC CTC TCCGCCCAG  CCG
                                 C  G       GA
GAM2355  GSPT1    5'  TGAGGGAAGGCGGCGGGGC   55568     A      GT  C
                                TGAG GGAGGCGG  TG GGC
                                |||| ||||||||  || |||
                                ACTC CTTCCGCC  GC CCG
                                  C       __ C
GAM2355  HDAC5    5'  GAGGGGGTGGAGCTGCGG    55569     A  C  _
                                GAGG GG GG GTTGCGG
                                |||| || || |||||||
                                CTCC CC CC CGACGCC
                                  C  A  T
GAM2355  HDAC5    5'  GAGGGGGTGGAGCTGCGG    55569     A  C  _
                                GAGG GG GG GTTGCGG
                                |||| || || |||||||
                                CTCC CC CC CGACGCC
                                  C  A  T
GAM2355  IL21R    3'  GAGGGGAGGCGACTTGGC    55570     A      G  _
                                GAG GGAGGCGG TTG C
                                ||| |||||||| ||| |
                                CTC CCTCCGCT AAC G
                                  C       G  C
GAM2355  INSRR    3'  GAGAGGAGGCGGAAGGAGGGC  55571           TTGC_
                                GAGAGGAGGCGGG    GGC
                                ||||||||||||    |||
                                CTCTCCTCCGCCT    CCG
                                       TCCTC
GAM2355  KIFC3    3'  TGAGGGGAGACGGGGC      55572     A       TT
                                TGAG GGAGGCGGG  GC
                                |||| |||||||||  ||
                                ACTC CCTCTGCCC  CG
                                  C       __
GAM2355  LFG      3'  TGAGAGGATGTGGGTCTCGG  55573       GGC   TG
                                TGAGAGGA  GGGT  CGG
                                ||||||||  ||||  |||
                                ACTCTCCT  CCCA  GCC
                                     ACA   GA
GAM2355  MAD2L2   3'  GAGAAGTCGAGGTTGCGGC   55574      G  _
                                GAGGAG CG GGTTGCGGC
                                |||||| || |||||||||
                                CTCTTC GC CCAACGCCG
                                   A  T
GAM2355  MAP1B    5'  TGAGAGAGGGCGGGGAGGC   55575      GA    TTGC
                                TGAGAG  GGCGGG   GGC
                                ||||||  ||||||   |||
                                ACTCTC  CCGCCC   CCG
                                   TC    CT__
GAM2355  MAP4     3'  TGAGAGGAGGTGTGGGGC    55576        C__  TT
                                TGAGAGGAGG   GGG  GC
                                ||||||||||   |||  ||
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                                ACTCTCCTCC  CCC  CG
                                     ACA  __
GAM2355  MAP4    3'  TGAGAGGAGGTGTGGGGC   55576        C__  TT
                                TGAGAGGAGG  GGG  GC
                                ||||||||||  |||  ||
                                ACTCTCCTCC  CCC  CG
                                     ACA  __
GAM2355  MBP     3'  TGGGAGGAAGCCATGCCTGGC  55577   A     GG_  GC
                                TG GAGGAGGC  GTT  GGC
                                || ||||||||  |||  |||
                                AC CTCCTTCG  CGG  CCG
                                 C      GTA  A_
GAM2355  MSI1    3'  TGCAGGGGAGGGGGCGGC   55578   _ A   C   T
                                TG AG GGAGG GGGT GC
                                || || ||||| |||| ||
                                AC TC CCTCC CCCG CG
                                 G  C   _   C
GAM2355  MUS81   5'  GAGAGGAGAGCCTGCGGC   55579       GC  G
                                GAGAGGAG  GG TTGCGGC
                                ||||||||  || |||||||
                                CTCTCCTC  TC GACGCCG
                                     __  G
GAM2355  MYF5    5'  TGAGAGGCAGGCGGTGC    55580       _    GT
                                TGAGAGG AGGCGG  TGC
                                ||||||| ||||||  |||
                                ACTCTCC TCCGCC  ACG
                                    G    __
GAM2355  NFIA    5'  GAGGGGGCGGCTGCGGC    55581     A   G
                                GAGG GGCGG TTGCGGC
                                |||| ||||| |||||||
                                CTCC CCGCC GACGCCG
                                  C   _
GAM2355  OAS2    3'  GAGAGGAGGGCTAGTGGC    55582       _ G  T
                                GAGAGGAGG C GGT GC
                                ||||||||| | ||| ||
                                CTCTCCTCC G TCA CG
                                     C A  C
GAM2355  OTP     3'  GAGGGGAGGCGGCGGGC    55583    A     GT  C
                                GAG GGAGGCGG  TG GGC
                                |||  ||||||||  || |||
                                CTC CCTCCGCC  GC CCG
                                  C      __ _
GAM2355  PACSIN1 3'  TGGGAGGGGAGGGGCGGC   14758   A   A  C  TT
                                TG GAGG GG GGG  GCGGC
                                || |||| || |||  |||||
                                AC CTCC CC CCC  CGCCG
                                 C   _ T  __
GAM2355  PHKG2   5'  TGAAGGAGGCGGGGG      55584    G       TTGC
                                TGA AGGAGGCGGG   GG
                                |||  ||||||||||   ||
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                                ACT TCCTCCGCCC   CC
                                  _      ____
GAM2355 PPFIA3   5' CGGGAGGAGGCGGGGG     55585    A        TTGC
                                TG GAGGAGGCGGG   GG
                                || ||||||||||   ||
                                GC CTCCTCCGCCC   CC
                                 C        ____
GAM2355 PPP3R1   5' GAGAGGGGGCGAAGACGGC   55586      A     TT
                                GAGAGG GGCGGG  GCGGC
                                |||||| ||||||  |||||
                                CTCTCC CCGCTT  TGCCG
                                   C     C_
GAM2355 PRV1     3' GAGGGGCAGGAGGCGGC     55587     A     TT
                                GAGG GGCGGG  GCGGC
                                |||| ||||||  |||||
                                CTCC CCGTCC  CGCCG
                                  _     TC
GAM2355 RAD51L3  3' TGGAGGAGGCGGGAAGC     55588    A        TT
                                TG GAGGAGGCGGG  GC
                                || ||||||||||  ||
                                AC CTCCTCCGCCC  CG
                                 _         TT
GAM2355 RFNG     3' GAGGGGCACTGCGGC      55589     A   GG
                                GAGG GGCG  TTGCGGC
                                |||| ||||  |||||||
                                CTCC CCGT  GACGCCG
                                  _   __
GAM2355 RNH      5' GAGAGGAGGCTTGGATGGC   55590          __   T
                                GAGAGGAGGC  GGGT GC
                                ||||||||||  |||| ||
                                CTCTCCTCCG  CCTA CG
                                      AA   C
GAM2355 SIX1     5' AGGGAGGGGGGCGCGG     55591    A    C   T
                                AG GGAGG GGG TGCGG
                                || ||||| ||| |||||
                                TC CCTCC CCC GCGCC
                                 _    _  C
GAM2355 SLC21A9  3' AGAGGAGGTACTGCTGTGGC  55592        CGG_   C
                                AGAGGAGG   GTTG GGC
                                ||||||||   |||| |||
                                TCTCCTCC   CGAC CCG
                                     ATGA   A
GAM2355 SLC22A12 3' TGGGAGGAGGCAGGCTTGTGGC 55593    A          _ C
                                TG GAGGAGGCGGGTT G GGC
                                || |||||||||||| | |||
                                AC CTCCTCCGTCCGA C CCG
                                 C          A A
GAM2355 SMG1     5' TGAGAGAGGCGGATGAAGGC  55594       G       TGC
                                TGAGAG AGGCGGGT   GGC
                                |||||| ||||||||   |||
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                                ACTCTC TCCGCCTA   CCG
                                   _       CTT
GAM2355  SORCS2   3'  TGAGAGGGAGGCCACGG     55595        A GC    TG
                                TGAGAGG G  GGGT  CGG
                                ||||||| |  ||||  |||
                                ACTCTCC C  TCCG  GCC
                                   _ __    GT
GAM2355  SOX11    3'  GAGGGGAGGCGGGAAGGGC   55596     A        TTGC
                                GAG GGAGGCGGG    GGC
                                ||| |||||||||    |||
                                CTC CCTCCGCCC    CCG
                                  C        TTC_
GAM2355  TK1      3'  GAGAGGAGGGAGCATGCGGC   55597         C    _
                                GAGAGGAGG GGGT TGCGGC
                                ||||||||| |||| ||||||
                                CTCTCCTCC CTCG ACGCCG
                                   _   T
GAM2355  WHSC1L1  5'  GAGAGGAGCCTGCGG       55598        G GGG
                                GAGAGGAG C   TTGCGG
                                |||||||| |   ||||||
                                CTCTCCTC G   GACGCC
                                   _ ___
GAM2355  WHSC1L1  5'  GAGAGGAGCCTGCGG       55598        G GGG
                                GAGAGGAG C   TTGCGG
                                |||||||| |   ||||||
                                CTCTCCTC G   GACGCC
                                   _ ___
GAM2355  ZNF2     5'  GAGAGCGAGCCGTTGTGGC   55599      _  G GG    C
                                GAGAG GAG C  GTTG GGC
                                ||||| ||| |  |||| |||
                                CTCTC CTC G  CAAC CCG
                                   G   G __    A
GAM2355  A2BP1    5'  TGGAGGAGGCGGCGG       55600     A       GGTT
                                TG GAGGAGGCG    GCGG
                                || |||||||||    ||||
                                AC CTCCTCCGC    CGCC
                                  _       ____
GAM2355  AGPAT1   3'  TGAGAGGCAGGGAGTGGC    55601        _  C    T
                                TGAGAGG AGG GGGT GC
                                ||||||| ||| |||| ||
                                ACTCTCC TCC CTCA CG
                                   G   _    C
GAM2355  AGPAT1   3'  TGAGAGGCAGGGAGTGGC    55601        _  C    T
                                TGAGAGG AGG GGGT GC
                                ||||||| ||| |||| ||
                                ACTCTCC TCC CTCA CG
                                   G   _    C
GAM2355  C22orf4  3'  TGAGAAGAGCACTGTGG     55602         G  GG   C
                                TGAGAGGAG CG  TTG GG
                                |||||||||  ||  ||| ||
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                                ACTCTTCTC GT  GAC CC
                                      _ __  A
GAM2355 C3IP1    3' TGGGAGAGGCAATGTGG     55603    A  G     GT  C
                                TG GAG AGGCGG  TG GG
                                || ||| ||||||  || ||
                                AC CTC TCCGTT  AC CC
                                 C  _     __ A
GAM2355 CACNA1I  3' TGAGACGGGGCGGGCGG     55604      _ A    GTT
                                TGAGA GG GGCGG   GCGG
                                ||||| || |||||   ||||
                                ACTCT CC CCGCC   CGCC
                                   G  _    ____
GAM2355 CLIC5    5' CGGGAGGAGGCGGGGAAAGC  55605    A        TT__
                                TG GAGGAGGCGGG    GC
                                || ||||||||||    ||
                                GC CTCCTCCGCCC    CG
                                 C          CTTT
GAM2355 CLPTM1   3' GAGGGGAGGCGAGGGGGC    55606    A       TTGC
                                GAG GGAGGCGGG    GGC
                                ||| |||||||||    |||
                                CTC CCTCCGCTC    CCG
                                  C        CC__
GAM2355 CPLX1    3' TGAGGGAGGCGGCGGG      55607     A      GT  C
                                TGAG GGAGGCGG  TG GG
                                |||| ||||||||  || ||
                                ACTC CCTCCGCC  GC CC
                                   _       __ _
GAM2355 DJ37E16.5 3' GGAGGGGGTTGCAAGGGC    55608      C     ____
                                GGAGG GGGTTGC   GGC
                                ||||| |||||||   |||
                                CCTCC CCCAACG   CCG
                                   _      TTC
GAM2355 DKFZp434F142 3' TGGGAGGCAGGCGGGAACTTGG 55609    A   _     TTGC_
             C                   TG GAGG AGGCGGG     GGC
                                || |||| |||||||     |||
                                AC CTCC TCCGCCC     CCG
                                 C   G      TTGAA
GAM2355 DKFZP586B2420 3' GAGAGGAGGTGGGGTGGC    55610         C   TTGC
                                GAGAGGAGG GGG    GGC
                                ||||||||| |||    |||
                                CTCTCCTCC CCC    CCG
                                     A  CA__
GAM2355 DKFZp762K222 5' CGGGAGGAGGCGGGGAGGGGGC 55611    A        TTGC_
                                TG GAGGAGGCGGG     GGC
                                || ||||||||||     |||
                                GC CTCCTCCGCCC     CCG
                                 C          CTCCC
GAM2355 EDR2     3' CGGGAGGAGGCGCCCTGGGC   55612    A       GG  C
                                TG GAGGAGGCG  TTG GGC
                                || |||||||||  ||| |||
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                                GC CTCCTCCGC  GAC CCG
                                 C       GG  _
GAM2355  ELF2     5'  GAGGAGGCGGAACCCGCGGC  55613          __
                                GAGGAGGCGGG  TTGCGGC
                                ||||||||||  |||||||
                                CTCCTCCGCCT  GGCGCCG
                                      TG
GAM2355  FBP17    3'  TGAGAGGAGGGGCTGC     55614         CG
                                TGAGAGGAGG  GGTTGC
                                ||||||||||  ||||||
                                ACTCTCCTCC  CCGACG
                                     __
GAM2355  FLJ10706 5'  TGAGAGGAGTCGGGGC     55615         G   TT
                                TGAGAGGAG CGGG  GC
                                |||||||| ||||  ||
                                ACTCTCCTC GCCC  CG
                                      A  __
GAM2355  FLJ10922 3'  TGAAGGAGGCGGGGC      55616     G       TT
                                TGA AGGAGGCGGG  GC
                                ||| ||||||||||  ||
                                ACT TCCTCCGCCC  CG
                                 _       __
GAM2355  FLJ12800 3'  TGAAAGGAGGCTGGTGG    55617          G  TGC
                                TGAGAGGAGGC GGT  GG
                                |||||||||| |||  ||
                                ACTTTCCTCCG CCA  CC
                                      A  ___
GAM2355  FLJ12800 3'  TGAAAGGAGGCTGGTGG    55617          G  TGC
                                TGAGAGGAGGC GGT  GG
                                |||||||||| |||  ||
                                ACTTTCCTCCG CCA  CC
                                      A  ___
GAM2355  FLJ12875 3'  TGGGAGGAGACGCCACGGC  55618    A      GG  TG
                                TG GAGGAGGC  GT  CGGC
                                || ||||||||  ||  ||||
                                AC CTCCTCTG  CG  GCCG
                                 C       __  GT
GAM2355  FLJ14871 3'  TGAGAGAGGCAACGG      55619       G    GGTT
                                TGAGAG AGGCG   GCGG
                                |||||| |||||   ||||
                                ACTCTC TCCGT   TGCC
                                   _   ____
GAM2355  FLJ20257 5'  TGGAGGAGGTGGCCGCGGC  55620    A     CG
                                TG GAGGAGG  GGTTGCGGC
                                || |||||||  |||||||||
                                AC CTCCTCC  CCGGCGCCG
                                 _     A_
GAM2355  FLJ20300 3'  TGGAGGAGGCAGCAACTGTGG 55621    A       G__  C
                                TG GAGGAGGCGG  TTG GG
                                || ||||||||||  ||| ||
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                                AC CTCCTCCGTC   GAC CC
                                 _        GTT   A
GAM2355  FLJ20320  5'  TGGGAGGAGGCAGTGTAGGC   55622    A        GT  C
                                TG GAGGAGGCGG  TG GGC
                                || ||||||||||  || |||
                                AC CTCCTCCGTC  AT CCG
                                 C         AC  _
GAM2355  FLJ20445  5'  TGAGAGGCGGCGGAGTAGGC   55623        A    GT  C
                                TGAGAGG GGCGG  TG GGC
                                |||||||| |||||  || |||
                                ACTCTCC CCGCC  AT CCG
                                    G     TC  _
GAM2355  FLJ20580  3'  TGATGGGGGGATCGCGG     55624     GA  A  C
                                TGA  GG GG GGGTTGCGG
                                |||  || || |||||||||
                                ACT  CC CC CCTAGCGCC
                                  A_  _  _
GAM2355  FLJ20886  3'  TGAGGGAAGGCGGGGACAGGC  55625      A        TT  _
                                TGAG GGAGGCGGG  GC GGC
                                |||| |||||||||  || |||
                                ACTC CTTCCGCCC  TG CCG
                                   C        C_  T
GAM2355  FLJ21459  3'  TGACAGGAGGCGGAGC      55626     G         TT
                                TGA AGGAGGCGGG  GC
                                ||| ||||||||||  ||
                                ACT TCCTCCGCCT  CG
                                  G         ___
GAM2355  FLJ21478  3'  TGAGAGGAGGGGGGAGGC     55627          C   TT
                                TGAGAGGAGG GGG  GC
                                |||||||||| |||  ||
                                ACTCTCCTCC CCC  CG
                                      _  TC
GAM2355  FLJ22341  3'  TGGGAGCAGGCCCTGGGGTGGC 55628    A   G   _____   T
                                TG GAG AGGC    GGGT GC
                                || ||| ||||    |||| ||
                                AC CTC TCCG    CCCA CG
                                 C   G    GGAC    C
GAM2355  FLJ23519  5'  GAGAGGAGGCTTGGATGGC    55590          __    T
                                GAGAGGAGGC  GGGT GC
                                ||||||||||  |||| ||
                                CTCTCCTCCG  CCTA CG
                                      AA    C
GAM2355  FLJ23519  5'  GAGAGGAGGCTTGGATGGC    55590          __    T
                                GAGAGGAGGC  GGGT GC
                                ||||||||||  |||| ||
                                CTCTCCTCCG  CCTA CG
                                      AA    C
GAM2355  GGA2      3'  TGAAAGGACTTTATTGTGGC   55629        GGCGG    C
                                TGAGAGGA    GTTG GGC
                                ||||||||    |||| |||
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                                ACTTTCCT    TAAC CCG
                                    GAAA_   A
GAM2355 GGA2    3' TGAAAGGACTTTATTGTGGC  55629       GGCGG   C
                                TGAGAGGA    GTTG GGC
                                ||||||||    |||| |||
                                ACTTTCCT    TAAC CCG
                                    GAAA_   A
GAM2355 GPT2    3' TGAGGGAGGCGAGGG      55630     A       TTGC
                                TGAG GGAGGCGGG   GG
                                |||| |||||||||   ||
                                ACTC CCTCCGCTC   CC
                                  _      _____
GAM2355 HA-1    3' TGGGAGGAGGCGCCCGCTGG  55631    A       GG   _
                                TG GAGGAGGCG  TTGC GG
                                || |||||||||  |||| ||
                                AC CTCCTCCGC  GGCG CC
                                 C       G_   A
GAM2355 JAM1    5' TGGGAGGAGGAGGTTGC    55632    A     C
                                TG GAGGAGG GGGTTGC
                                || ||||||| |||||||
                                AC CTCCTCC TCCAACG
                                 C      _
GAM2355 KIAA0451 3' TGAGAGGAGGTGAGTGGC    55633         C   T
                                TGAGAGGAGG GGGT GC
                                |||||||||| |||| ||
                                ACTCTCCTCC CTCA CG
                                      A   C
GAM2355 KIAA0483 3' AGAGGCAAGCTGTTGCGG    55634      _   GG
                                AGAGG AGGC  GTTGCGG
                                ||||| ||||  |||||||
                                TCTCC TTCG  CAACGCC
                                   G   A_
GAM2355 KIAA1036 3' TGGGAGGAGACTCAGTGGC   55635    A      G_   T
                                TG GAGGAGGC  GGT GC
                                || ||||||||  ||| ||
                                AC CTCCTCTG  TCA CG
                                 C       AG   C
GAM2355 KIAA1257 5' TGAGAGGAGCGTCCGCCGG   55636        G  GG   _
                                TGAGAGGAG CG  TTGC GG
                                |||||||||  ||  |||| ||
                                ACTCTCCTC GC  GGCG CC
                                      _ A_   G
GAM2355 KIAA1287 5' TGAGAGGAAGGGTGGC      14836        GC   T
                                TGAGAGGAG  GGGT GC
                                |||||||||  |||| ||
                                ACTCTCCTT  CCCA CG
                                      __    C
GAM2355 KIAA1571 3' CGGGAGGTGGAGGTTGCGG   55637    A   A  C
                                TG GAGG GG GGGTTGCGG
                                || |||| || |||||||||
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                                GC CTCC CC TCCAACGCC
                                 C    A  _
GAM2355  KIAA1762  3'  TGGGAGGAGGCAGGAC      55638    A         TT
                                TG GAGGAGGCGGG  GC
                                || ||||||||||  ||
                                AC CTCCTCCGTCC  TG
                                 C          __
GAM2355  LHPP      3'  TGGAGGAGGCGGGGC       55639    A         TT
                                TG GAGGAGGCGGG  GC
                                || ||||||||||  ||
                                AC CTCCTCCGCCC  CG
                                 _          __
GAM2355  MAAT1     3'  TGAGAGGAGCCTCTGGGCGGC  55640          GCG__  TT
                                TGAGAGGAG    GG  GCGGC
                                |||||||||    ||  |||||
                                ACTCTCCTC    CC  CGCCG
                                     GGAGA  __
GAM2355  MAGE-E1   3'  TGAGAGGAGGCGCTCTGGC    55641           GG  GC
                                TGAGAGGAGGCG  TT  GGC
                                ||||||||||||  ||  |||
                                ACTCTCCTCCGC  AG  CCG
                                      G_  A_
GAM2355  MGC15827  3'  TGAGAGGAGGAGAGGAGGC    55642          C _  TT
                                TGAGAGGAGG G GG  GC
                                |||||||||| | ||  ||
                                ACTCTCCTCC C CC  CG
                                      T T  TC
GAM2355  MGC2452   5'  GAGAGGGGGTGCTGGGGGCGG  55643       AG__  _   TT
                                GAGAGG   GC GGG  GCGG
                                ||||||   || |||  ||||
                                CTCTCC   CG CCC  CGCC
                                   CCCA  A   C_
GAM2355  MGC3067   3'  TGAGAGGAGCGGCTGC      55644          G   G
                                TGAGAGGAG CGG TTGC
                                ||||||||| ||| ||||
                                ACTCTCCTC GCC GACG
                                          _  _
GAM2355  MGC4827   3'  TGAGAGGAGGTGAGAAGGAGC  55645          C   TTGC
                                TGAGAGGAGG GGG   GGC
                                |||||||||| |||   |||
                                ACTCTCCTCC CTC   TCG
                                      A   TTCC
GAM2355  NET-7     3'  TGAGAAGAGGCCAACCTGGC   55646          G GT GC
                                TGAGAGGAGGC G  T  GGC
                                |||||||||||| |  |  |||
                                ACTCTTCTCCG T  G  CCG
                                      G TG A_
GAM2355  NOR1      3'  AGGGAGGAGGCTGCGG      55647    A    C
                                AG GGAGG GGGTTGCGG
                                || ||||| |||||||||
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                                TC CCTCC TCCGACGCC
                                 _   _
GAM2355  OAZ2     5'  TGGGAGGAGGCGGCGC      55648    A        GT
                                TG GAGGAGGCGG  TGC
                                || ||||||||||  |||
                                AC CTCCTCCGCC  GCG
                                 C        __
GAM2355  P17.3    3'  TGAGAAGAGGTCAGAATGGC   55649          _   TTGC
                                TGAGAGGAGG CGGG   GGC
                                |||||||||| ||||   |||
                                ACTCTTCTCC GTCT   CCG
                                      A   TA__
GAM2355  PAK6     3'  TGAGAGGAGGAGGCAGGC    55650          C   TGC
                                TGAGAGGAGG GGGT   GGC
                                |||||||||| ||||   |||
                                ACTCTCCTCC TCCG   CCG
                                      _   T__
GAM2355  PDE10A   3'  TGAGAGGTGACTGCGG      55651        A   GGGT
                                TGAGAGG GGC   TGCGG
                                ||||||| |||   |||||
                                ACTCTCC CTG   ACGCC
                                    A  _____
GAM2355  PPI5PIV  3'  TGAGAGGAGGGGGAAGC      55652          C   TT
                                TGAGAGGAGG GGG  GC
                                |||||||||| |||  ||
                                ACTCTCCTCC CCT  CG
                                      _   T_
GAM2355  PPM1A    5'  GGAGGGGGTCACCGCGGC    55653      C    ____
                                GGAGG GGGTT   GCGGC
                                ||||| |||||   |||||
                                CCTCC CCCAG   CGCCG
                                   _    TGG
GAM2355  PRDM15   3'  TAAGGGGAGGCAGATGCGGC  55654      A        T
                                TGAG GGAGGCGGGT GCGGC
                                |||| |||||||||| |||||
                                ATTC CCTCCGTCTA CGCCG
                                  C        _
GAM2355  PYY2     5'  TGAGCAGGAGGTGGAAGGC   55655      _    C   TT
                                TGAG AGGAGG GGG  GC
                                |||| |||||| |||  ||
                                ACTC TCCTCC CCT  CG
                                  G     A   TC
GAM2355  RAB6B    5'  GAGGGGAGGCGGCCGGC     55656     A      GTTG
                                GAG GGAGGCGG    CGGC
                                ||| ||||||||    ||||
                                CTC CCTCCGCC    GCCG
                                  C       G___
GAM2355  RDHL     3'  TGGAGGAGACATTTGTGG    55657    A       GG   C
                                TG GAGGAGGCG  TTG GG
                                || |||||||||  ||| ||
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                                AC CTCCTCTGT  AAC CC
                                 _       A_   A
GAM2355  SCAMP5    3'  TGAAGGAGGCGAGGC      55658     G        TT
                                TGA AGGAGGCGGG  GC
                                ||| ||||||||||  ||
                                ACT TCCTCCGCTC  CG
                                  _        __
GAM2355  SEPT3     3'  TGAGAGGAAGAAGGTGG     55659          C    TGC
                                TGAGAGGAGG GGGT   GG
                                |||||||||| ||||   ||
                                ACTCTCCTTC TCCA   CC
                                      T   ___
GAM2355  SMCR8     5'  TGAGAGGAAGTGGGAAAGAATG 55660          C   T_____
              CGG                   TGAGAGGAGG GGG     TGCGG
                                |||||||||| |||     |||||
                                ACTCTCCTTC CCC     ACGCC
                                      A   TTTCTT
GAM2355  ZNF145    5'  AGAGGAGGCGAGAGCGGC    55661          TT
                                AGAGGAGGCGGG  GCGGC
                                ||||||||||||  |||||
                                TCTCCTCCGCTC  CGCCG
                                       T_
GAM2355  LOC112476 3'  TGGGAGGAGGCGGCCAGGG   55662    A       G   C
                                TG GAGGAGGCGG TTG GG
                                || ||||||||||  ||| ||
                                AC CTCCTCCGCC GGT CC
                                 C         _   C
GAM2355  LOC121838 5'  TGAGAGCAGCAAGTTGTGGC  55663      GA       C
                                TGAGAG  GGCGGGTTG GGC
                                ||||||  |||||||||  |||
                                ACTCTC  TCGTTCAAC CCG
                                   G_        A
GAM2355  LOC122955 5'  TGACAGCACTGGTTGCGG    55664     G  GAG  G
                                TGA AG   GC GGTTGCGG
                                |||  ||   ||  ||||||||
                                ACT TC   TG CCAACGCC
                                  G  G__  A
GAM2355  LOC124245 5'  GAGAGGAGGCCACGG       55665          GGGT
                                GAGAGGAGGC    TGCGG
                                ||||||||||    |||||
                                CTCTCCTCCG    GTGCC
                                       _____
GAM2355  LOC130497 3'  TGGGAGAGGCGCCGCTGCGGC  14877    A   G    G_
                                TG GAG AGGCG  GTTGCGGC
                                ||  |||  |||||  ||||||||
                                AC CTC TCCGC  CGACGCCG
                                 C   _     GG
GAM2355  LOC130813 3'  AGGAGGCGGAGGTTGCGG    55666          __
                                AGGAGGCGG  GTTGCGG
                                |||||||||  |||||||
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                                TCCTCCGCC  CAACGCC
                                     TC
GAM2355  LOC143720 3'  TGAGAGGAGGTGAGAAGGAGC  55645        C   TTGC
                                TGAGAGGAGG GGG   GGC
                                |||||||||| |||   |||
                                ACTCTCCTCC CTC   TCG
                                     A   TTCC
GAM2355  LOC144519 5'  TGAAAGGAGGTTTTATTGGC   55667        CGG_   _
                                TGAGAGGAGG   GTTG C
                                |||||||||   |||| |
                                ACTTTCCTCC   TAAC G
                                     AAAA   C
GAM2355  LOC145082 5'  TGGGATGAGGCGGAGTTTGG   55668    A  G     _  GC
                                TG GA GAGGCGG GTT  GG
                                || || ||||||| |||  ||
                                AC CT CTCCGCC CAA  CC
                                 C  A      T   A_
GAM2355  LOC145608 5'  TGGGAGGAAGCCTCATGGC   55669    A      GGG  GC
                                TG GAGGAGGC   TT  GGC
                                || ||||||||   ||  |||
                                AC CTCCTTCG   AG  CCG
                                 C       G__  TA
GAM2355  LOC146332 3'  TGGAGGAGGCGGTGC      55670    A       GT
                                TG GAGGAGGCGG  TGC
                                || ||||||||||  |||
                                AC CTCCTCCGCC  ACG
                                 _       __
GAM2355  LOC146336 3'  TGGAGGAGGCGGCCCAGC    55671    A       G TG
                                TG GAGGAGGCGG T  CGGC
                                || ||||||||||  |  ||||
                                AC CTCCTCCGCC G  GTCG
                                 _       G __
GAM2355  LOC147343 5'  TGATGGGAGGCGAGTCGG    55672    GA       TG
                                TGA  GGAGGCGGGT  CGG
                                |||  ||||||||||  |||
                                ACT  CCTCCGCTCA  GCC
                                  AC        __
GAM2355  LOC148397 5'  TGGAGGAGGCGCTGGG     55673    A     GG   C
                                TG GAGGAGGC  GTTG GG
                                || ||||||||  |||| ||
                                AC CTCCTCCG  CGAC CC
                                 _      __   _
GAM2355  LOC149664 5'  GAGAGGGGGGCCACGCGG    55674      A  C  GT_
                                GAGAGG GG GG   TGCGG
                                ||||||  || ||   |||||
                                CTCTCC CC CC   GCGCC
                                   _ _  GGT
GAM2355  LOC151176 5'  TGAGAGGAAGGGCCTGTGG   55675        C  G   C
                                TGAGAGGAGG GG TTG GG
                                |||||||||| || ||| ||
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                                ACTCTCCTTC CC GAC CC
                                      _ G   A
GAM2355  LOC151300 3'  GAGGGGAGGTGGACTAGGC   55676     A    C  GT  C
                                GAG GGAGG GG  TG GGC
                                ||| ||||| ||  || |||
                                CTC CCTCC CC  AT CCG
                                  C    A  TG  _
GAM2355  LOC151827 5'  TGAGGGAGGGCGTCCTGGC   55677     A    _  GG  GC
                                TGAG GGAGG CG  TT  GGC
                                |||| ||||| ||  ||  |||
                                ACTC CCTCC GC  GG  CCG
                                  _    C  A_  A_
GAM2355  LOC157450 3'  AGAGGGCAGATTGTGG     55678      AG       C
                                AGAGG  GCGGGTTG GG
                                |||||  |||||||| ||
                                TCTCC  CGTCTAAC CC
                                   __       A
GAM2355  LOC163682 5'  TGGCAGGAGGCGGCACCACG   55679    AG       _ TT
                                TG  AGGAGGCGG G  GCG
                                ||  |||||||||  |  |||
                                AC  TCCTCCGCC T  TGC
                                 CG        G GG
GAM2355  LOC196955 5'  TGAGAGAGGGAGCTGTGG    55680      G  C     C
                                TGAGAG AGG GGGTTG GG
                                |||||| ||| |||||| ||
                                ACTCTC TCC CTCGAC CC
                                   _  _     A
GAM2355  LOC201191 3'  TGAGAGGCAGACCTGTGTGG  55681       _   GG  T C
                                TGAGAGG AGGC  GT G GG
                                ||||||| ||||  || | ||
                                ACTCTCC TCTG  CA C CC
                                    G   GA  _ A
GAM2355  LOC220003 5'  TGAGACGGAGGAACGTGGC   55682      _    CGGGT  C
                                TGAGA GGAGG    TG GGC
                                ||||| |||||    || |||
                                ACTCT CCTCC    GC CCG
                                   G    TT___  A
GAM2355  LOC221833 3'  TGGGAGGAGGTCGGGGAGAGGG 55683    A     _   TTGC__
            GC                   TG GAGGAGG CGGG     GGC
                                || ||||||| ||||     |||
                                AC CTCCTCC GCCC     CCG
                                 C      A   CTCTCC
GAM2355  LOC222031 3'  TGAGAGGCAGGTGGATGC    55684       _  C   T
                                TGAGAGG AGG GGGT GC
                                ||||||| ||| |||| ||
                                ACTCTCC TCC CCTA CG
                                    G  A   _
GAM2355  LOC255758 5'  AGGCCTAGCGGGTTGCGG    55685    A__
                                AGG  GGCGGGTTGCGG
                                |||  ||||||||||||
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                                TCC   TCGCCCAACGCC
                                  GGA
GAM2355  LOC256789 3'  GAGGGGCAGGCCACCTTGGC   55686     A     TG ___
                                GAGG GGCGGGT  C   GGC
                                |||| |||||||  |   |||
                                CTCC CCGTCCG  G   CCG
                                  _     GT GAA
GAM2355  LOC51112  5'  GAGGGGAGGCGGGCTGGC    55687    A        _
                                GAG GGAGGCGGGTTG C
                                ||| ||||||||||||| |
                                CTC CCTCCGCCCGAC G
                                  C         C
GAM2355  LOC57333  3'  GAGAGGAGGTGTCCCAGGC   55688        CGG   G _
                                GAGAGGAGG   GTT C GGC
                                |||||||||   ||| | |||
                                CTCTCCTCC   CAG G CCG
                                     A__   G T
GAM2355  LOC89231  3'  GAGAGGAAGGTTGCGG     55689       GGC
                                GAGAGGA   GGGTTGCGG
                                |||||||   |||||||||
                                CTCTCCT   TCCAACGCC
                                   ___
GAM2355  LOC90333  3'  TGGGAGGAGGAGGTTGC    55632    A     C
                                TG GAGGAGG GGGTTGC
                                || ||||||| |||||||
                                AC CTCCTCC TCCAACG
                                 C     _
GAM2355  LOC91450  5'  TGAGAGGAAGTAACTGGC    55690         CGGGTT _
                                TGAGAGGAGG     GC GGC
                                ||||||||||     || |||
                                ACTCTCCTTC     TG CCG
                                     AT____  A
GAM2355  LOC91522  3'  TGCAGAGGCAGCTGGTTGTGG  55691   _   A  G   C
                                TG AGAGG GGC GGTTG GG
                                || ||||| ||| ||||| ||
                                AC TCTCC TCG CCAAC CC
                                 G    G  A    A
GAM2355  LOC92841  3'  CGGGAGGAGGAGGTTGCGG   55692    A     C
                                TG GAGGAGG GGGTTGCGG
                                || ||||||| |||||||||
                                GC CTCCTCC TCCAACGCC
                                 C     _
GAM2356  CAPS      3'  GTGGACCGGCAGGGACCTGG   55695         T  TACT
                                GTGGACCGGCA GG   CCTGG
                                |||||||||| ||   |||||
                                CACCTGGCCGT CC   GGACC
                                     _ CT__
GAM2356  MUCDHL    3'  GGCTGGGGACACTCCTGGC   55696    A  ___
                                GGC TGG   TACTCCTGGC
                                ||| |||   ||||||||||
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                                CCG ACC   GTGAGGACCG
                                  _  CCT
GAM2356 MUCDHL   3' GGCTGGGGACACTCCTGGC   55696    A  ___
                                GGC TGG   TACTCCTGGC
                                ||| |||   ||||||||||
                                CCG ACC   GTGAGGACCG
                                  _  CCT
GAM2356 XT3      3' GTGGAGTGGCATGATCTTGGC 55697      CC       A  CC
                                GTGGA  GGCATGGT CT  TGGC
                                |||||  |||||||| ||  ||||
                                CACCT  CCGTACTA GA  ACCG
                                   CA       _ __
GAM2356 C8orf2   3' GTGGGATGGCATGATCTTGGC 55698     ACC       A  CC
                                GTGG   GGCATGGT CT  TGGC
                                ||||   |||||||| ||  ||||
                                CACC   CCGTACTA GA  ACCG
                                   CTA       _ __
GAM2356 CGI-96   3' GTGGCCTGGTCCTTCCCTCCTG 55699     A  _  CATGGTA
             GC                   GTGG CC GG      CTCCTGGC
                                |||| || ||      ||||||||
                                CACC GG CC      GAGGACCG
                                  _  A  AGGAAGG
GAM2356 D4ST-1   3' GTGGACTGCATAATCCTGG   55700       CG     TAC
                                GTGGAC  GCATGG   TCCTGG
                                ||||||  ||||||   ||||||
                                CACCTG  CGTATT   AGGACC
                                   A_     ___
GAM2356 FBXO21   3' GTGGAGTGGCTTTCCTGG    55701      CCGGCA   AC
                                GTGGA     TGGT  TCCTGG
                                |||||     ||||  ||||||
                                CACCT     ACCG  AGGACC
                                   C_____    AA
GAM2356 FBXO9    3' GTGGAATGGCACGATCTTGGC 55702      CC       A  CC
                                GTGGA  GGCATGGT CT  TGGC
                                |||||  |||||||| ||  ||||
                                CACCT  CCGTGCTA GA  ACCG
                                   TA       _ __
GAM2356 FLJ14957 3' GTGGGTGGTGGCTCCTGG    55703     ACC  CA   TA
                                GTGG   GG  TGG  CTCCTGG
                                ||||   ||  |||  |||||||
                                CACC   CC  ACC  GAGGACC
                                   CA_  __   __
GAM2356 FLJ21709 3' GACTCTACGTGCTCCTGGC   55704     CG_  ATG  A
                                GAC   GC   GT CTCCTGGC
                                |||   ||   || ||||||||
                                CTG   TG   CA GAGGACCG
                                  AGA  ___  C
GAM2356 KIAA1866 3' GTGGGCTGCATGGTAGTGG   55705      ACCG       CTCC
                                GTGG   GCATGGTA   TGG
                                ||||   ||||||||   |||
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                                CACC   CGTACCAT   ACC
                                  CGA_      C___
GAM2356 KIAA1870 5' GTGGCCGAGTACTCCTGG   55706     A  GCAT
                                GTGG CCG   GGTACTCCTGG
                                |||| |||   ||||||||||
                                CACC GGC   TCATGAGGACC
                                  _  ____
GAM2356 KIAA1913 3' GGACTGAATTTGTACTCCTGG 55707     C  CATG
                                GGAC GG   GTACTCCTGG
                                |||| ||   ||||||||||
                                CCTG CT   CATGAGGACC
                                  A  TAAA
GAM2356 LAP1B    5' GTGGATCGCTCCCGCCTCCTGG 55708      C  G ATGGTA
             C                   GTGGA CG C     CTCCTGGC
                                ||||| || |     ||||||||
                                CACCT GC G     GAGGACCG
                                  A  _ AGGGCG
GAM2356 MGC5338  5' GTGGTTGGCATGGTTTGG    55709     ACC      ACTCC
                                GTGG  GGCATGGT    TGG
                                ||||  ||||||||    |||
                                CACC  CCGTACCA    ACC
                                  AA_      A____
GAM2356 PNMA1    5' GTGGCTCACCGTGCTCCTGGC  55710     ACCGG  G  A
                                GTGG    CAT GT CTCCTGGC
                                ||||    ||| || ||||||||
                                CACC    GTG CA GAGGACCG
                                  GA___   G  C
GAM2356 TOB2     3' GTGGTCTTGGGTGCTCCTGGC  55711     ACCGGCAT   A
                                GTGG      GGT CTCCTGGC
                                ||||      ||| ||||||||
                                CACC      CCA GAGGACCG
                                  AGAAC___   C
GAM2356 TOB2     3' GTGGTCTTGGGTGCTCCTGGC  55711     ACCGGCAT   A
                                GTGG      GGT CTCCTGGC
                                ||||      ||| ||||||||
                                CACC      CCA GAGGACCG
                                  AGAAC___   C
GAM2356 ZNF347   3' GCATTGGCACGATCTTGGC   55712      _    __ C
                                GCAT GGTAC  TC TGGC
                                |||| |||||  || ||||
                                CGTA CCGTG  AG ACCG
                                  A    CT  A
GAM2356 LOC118611 5' TGGTTGGCATGATCGCTGGC  55713    ACC      ACTC
                                TGG   GGCATGGT   CTGGC
                                |||   ||||||||   |||||
                                ACC   CCGTACTA   GACCG
                                  AA_      GC__
GAM2356 LOC147664 3' GTGGAATGGCACGATCTTGGC  55702      CC       A  CC
                                GTGGA  GGCATGGT CT  TGGC
                                |||||  |||||||| ||  ||||
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                                CACCT  CCGTGCTA GA  ACCG
                                  TA      _ __
GAM2356  LOC155081 3'  GTGGAACTGGAAACACTCCTGG 55714      CCG  A  ___
                                GTGGA   GC TGG   TACTCCTGG
                                |||||   || |||   |||||||||
                                CACCT   TG ACC   GTGAGGACC
                                  ___ _   TTT
GAM2356  LOC161158 5'  GGCGCCTGATGGTGCTCCTGGC 55715    A_ GGC    A
                                GG  CC   ATGGT CTCCTGGC
                                ||  ||   ||||| ||||||||
                                CC  GG   TACCA GAGGACCG
                                 GC  AC_    C
GAM2356  LOC162962 3'  GTGCACTGGCACGATCTTGGC  55716    G  C      A  CC
                                GTG AC GGCATGGT CT  TGGC
                                ||| || |||||||| ||  ||||
                                CAC TG CCGTGCTA GA  ACCG
                                 G  A      _ __
GAM2356  LOC202802 3'  GTGGAACTGGAAACACTCCTGG 55714      CCG  A  ___
                                GTGGA   GC TGG   TACTCCTGG
                                |||||   || |||   |||||||||
                                CACCT   TG ACC   GTGAGGACC
                                  ___ _   TTT
GAM2356  LOC204965 5'  GTGGCTCGGGGAGCTCCTGGC  55717     AC   CAT  TA
                                GTGG  CGG   GG  CTCCTGGC
                                ||||  |||   ||  ||||||||
                                CACC  GCC   CC  GAGGACCG
                                  GA  ___  TC
GAM2356  LOC91695  3'  GTGGCCTGGTCCTTCACTCCTG 55718     A  _  CATGG
           GC                     GTGG CC GG     TACTCCTGGC
                                ||||  ||  ||     ||||||||||
                                CACC GG CC     GTGAGGACCG
                                  _  A  AGGAA
GAM2357  AGTPBP1   3'  GAGTCAGCTCTGTATAAA    55721     CT  C  _
                                GAG  TC GC CTGTATAAA
                                |||  ||  ||  |||||||||
                                CTC  AG CG GACATATTT
                                  __  T  A
GAM2357  AVPR1A    5'  CTCCGAGCTTCCGGAAGCAC   55722           CCT
                                CTCCGAGCTTCCG   GTAT
                                ||||||||||||   ||||
                                GAGGCTCGAAGGC   CGTG
                                       CTT
GAM2357  IRF1      3'  CCGAGCAAGGCACTGTATAAA  55723       TTCC  _
                                CCGAGC    GC CTGTATAAA
                                ||||||    || |||||||||
                                GGCTCG    CG GACATATTT
                                   TTC_  T
GAM2357  TNFRSF11A 3'  CTTCGGGCTCCCAGCCATG    55724    C  A     _  _
                                CT CG GCTTCC GCC TG
                                || || |||||| ||| ||
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                                GA GC CGAGGG CGG AC
                                 A  C     T   T
GAM2357  ZHX1     3'  TCTGATCTGACACCTGTATAAA 55725    C  G  TC
                                TC GA CT  CGCCTGTATAAA
                                || || ||  ||||||||||||
                                AG CT GA  GTGGACATATTT
                                 A  A  CT
GAM2357  ZNF134   5'  ACCCCGAGCTTCTGCTCCG   55726          C  _
                                ACTCCGAGCTTC GC CTG
                                |||||||||||| || |||
                                TGGGGCTCGAAG CG GGC
                                       A  A
GAM2357  FLJ10701 3'  ACCCTGAGCACTGTATAA    55727     C   TTCCGC
                                ACTC GAGC     CTGTATAA
                                |||| ||||     ||||||||
                                TGGG CTCG     GACATATT
                                  A   T_____
GAM2357  FLJ20542 3'  CTCGAGCTTCCGCTGCCCGC   55728    C      ___
                                CTC GAGCTTCC   GCCTGT
                                ||| ||||||||   ||||||
                                GAG CTCGAAGG   CGGGCG
                                  _      CGA
GAM2357  KIAA1095 3'  GAACTTGCCTGTATAA      55729       CC
                                GAGCTT  GCCTGTATAA
                                ||||||  ||||||||||
                                CTTGAA  CGGACATATT
                                  __
GAM2357  LRG      3'  CCCCGAGTTTCACCTGTA    55730       C   C
                                CTCCGAG TTC GCCTGTA
                                ||||||| ||| |||||||
                                GGGGCTC AAG TGGACAT
                                   A  _
GAM2357  MGC2752  5'  CTCGAGCTTCACCTGTA     55731    C      C
                                CTC GAGCTTC GCCTGTA
                                ||| ||||||| |||||||
                                GAG CTCGAAG TGGACAT
                                  _     _
GAM2357  PRO0132  5'  ACTTTAGCTTTTGCTATATAA  55732    CCG    CC  C
                                ACT   AGCTT  GC TGTATAA
                                |||   |||||  || |||||||
                                TGA   TCGAA  CG ATATATT
                                  AA_    AA  _
GAM2357  TLN2     3'  ACTCCAGCTTCCGTCTTCTCCT 55733      G      _______
            G                    ACTCC AGCTTCCG     CCTG
                                |||||| ||||||||     ||||
                                TGAGG TCGAAGGC     GGAC
                                  _       AGAAGA
GAM2357  LOC154743 3'  ACTTTAAGCTTTCTATATAA  55734    CC     CCGC
                                ACT  GAGCTT    CTGTATAA
                                |||  ||||||    ||||||||
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                                TGA  TTCGAA    GATATATT
                                  AA     A___
GAM2357  LOC222166 3'  AAGCTTCAACGTATAAA     55735        C  CT
                                GAGCTTC GC  GTATAAA
                                ||||||| ||  |||||||
                                TTCGAAG TG  CATATTT
                                   T  __
GAM2357  LOC257054 5'  CTTCGAACTTCCATTGT     55736    C        CC
                                CT CGAGCTTCCG  TGT
                                || ||||||||||  |||
                                GA GCTTGAAGGT  ACA
                                 A        A_
GAM2357  LOC257487 5'  CTCCAGTGCCCTGTATAA    55737      A_  TTCCG
                                CTCCG  GC    CCTGTATAA
                                |||||  ||    |||||||||
                                GAGGT  CG    GGACATATT
                                   CA  _____
GAM2357  LOC90155  3'  CAAGATCCTGTCTGTATAAA  55738     CT   GC_
                                CGAG  TCC   CTGTATAAA
                                ||||  |||   |||||||||
                                GTTC  AGG   GACATATTT
                                  T_   ACA
GAM2357  LOC90381  3'  CTCTGAACTTCCTGAATGTA  55739     C      GCC_
                                CTC GAGCTTCC    TGTA
                                ||| ||||||||    ||||
                                GAG CTTGAAGG    ACAT
                                  A       ACTT
GAM2357  LOC92689  3'  TCCTTACTTTGCCTGTAT    55740     GA   CC
                                TCC  GCTT  GCCTGTAT
                                |||  ||||  ||||||||
                                AGG  TGAA  CGGACATA
                                  AA   A_
GAM2358  COL4A3    3'  TATACAGTTTGATACATTAAGA 55743        G   TCTGT
            T                    TATACAGT TTG    TTAAGAT
                                |||||||| |||    |||||||
                                ATATGTCA AAC    AATTCTA
                                     _   TATGT
GAM2358  COL4A3    3'  TATACAGTTTGATACATTAAGA 55743        G   TCTGT
            T                    TATACAGT TTG    TTAAGAT
                                |||||||| |||    |||||||
                                ATATGTCA AAC    AATTCTA
                                     _   TATGT
GAM2358  COL4A3    3'  TATACAGTTTGATACATTAAGA 55743        G   TCTGT
            T                    TATACAGT TTG    TTAAGAT
                                |||||||| |||    |||||||
                                ATATGTCA AAC    AATTCTA
                                     _   TATGT
GAM2358  NRXN1     3'  TATACAAGTGTCCATTTAAGAT 55744        T  T
                                TATACAG GT GTCTGTTTAAGAT
                                ||||||| || ||||||||||||
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                                ATATGTT CA CAGGTAAATTCTA
                                    _ _
GAM2358  NRXN1    3'  TATACAAGTGTCCATTTAAGAT 55744        T  T
                                TATACAG GT GTCTGTTTAAGAT
                                ||||||| || ||||||||||||
                                ATATGTT CA CAGGTAAATTCTA
                                    _ _
GAM2358  TGFBR1   3'  TATAAGTGTTAGTTTTAAGAT  55745      C      TCTG
                                TATA AGTGTTG    TTTAAGAT
                                |||| |||||||    ||||||||
                                ATAT TCACAAT    AAATTCTA
                                   _      CA__
GAM2358  TSGA10   5'  CATGATTTGTCTGTTTGAGAT  55746    GTG_        A
                                CA    TTGTCTGTTT AGAT
                                ||    |||||||||| ||||
                                GT    AACAGACAAA TCTA
                                 ACTA         C
GAM2358  FLJ14813 3'  TATACAGTTTTGAGGTTAAGAT 55747         G   TCT   T
                                TATACAGT TTG   GTT AAGAT
                                |||||||| |||   ||| |||||
                                ATATGTCA AAC   CAA TTCTA
                                     A   TC_  _
GAM2358  LOC158187 3'  TACAGGGCTTCTGTTTA     55748       T   G
                                TACAG GTT TCTGTTTA
                                ||||| ||| ||||||||
                                ATGTC CGA AGACAAAT
                                   C   _
GAM2358  LOC158230 3'  TATACAGTGTGTCACATAGAT  55749          T   TGTTTA
                                TATACAGTGT GTC      AGAT
                                |||||||||| |||      ||||
                                ATATGTCACA CAG      TCTA
                                      _   TGTA__
GAM2358  LOC221362 3'  CAGTGTTGTATATAAGAT    55750          CT  T
                                CAGTGTTGT  GT TAAGAT
                                |||||||||  || ||||||
                                GTCACAACA  TA ATTCTA
                                     __  T
GAM2359  CUL3     3'  ACTAAATTCATTATTTTTG    55753          C   GATG
                                GCTAAATTCA TAT    TTTTG
                                |||||||||| |||    |||||
                                TGATTTAAGT ATA    AAAAC
                                     A   _____
GAM2359  ITGA11   3'  GCAGAATTCAGATCTGTTTTGT 55754    TA     CTATGA
                                GC  AATTCA     TGTTTTGT
                                ||  ||||||     ||||||||
                                CG  TTAAGT     ACAAAACA
                                 TC     CTAG__
GAM2359  LOC115286 3'  GCTAGATTCCTGACATTTTGT  55755      A   A  AT
                                GCTA ATTC CT  GATGTTTTGT
                                |||| |||| ||  ||||||||||
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                                CGAT TAAG GA  CTGTAAAACA
                                  C   _ __
GAM2359  LOC144453 3'  GCTAAATCACTGTGGTCTG   55756       T   A  ATGT
                                GCTAAAT CACT TG   TTTG
                                ||||||| |||| ||   ||||
                                CGATTTA GTGA AC   AGAC
                                   _   C  C___
GAM2360  ETV5      3'  AGGTGCAAATGTTCCATCAGGT 55759         CGAC__  AC
           TGTC                   AGGTGCAAATG     CAG  TGTC
                                ||||||||||     |||  ||||
                                TCCACGTTTAC     GTC  ACAG
                                      AAGGTA   CA
GAM2360  MAPK1     3'  AAGTGCAAATAAGGGGCTGTC  55760         CGACCAGA
                                AGGTGCAAATG       CTGTC
                                ||||||||||       |||||
                                TTCACGTTTAT       GACAG
                                      TCCCC___
GAM2360  TNFRSF10B 3'  GGTGCAAATGAGACTG      55761         CGACC
                                GGTGCAAATG    AGACTG
                                |||||||||     ||||||
                                CCACGTTTAC    TCTGAC
                                   _____
GAM2360  DKFZP434C131 3'  AGGGCACTGGGTCAGACTGTC  55762     T   AATGCGAC
                                AGG GCA       CAGACTGTC
                                ||| |||       |||||||||
                                TCC CGT       GTCTGACAG
                                  _  GACCCA__
GAM2360  MGC13138  3'  GGCCCAAGATCAGACTGTC   55763     G   ATGC  C
                                GGT CAA    GA CAGACTGTC
                                ||| |||    || |||||||||
                                CCG GTT    CT GTCTGACAG
                                  G   ____  A
GAM2360  NCOA2     3'  GATGCGAGCTTCAGACTGTC   55764      AAAT  GAC
                                GGTGC    GC   CAGACTGTC
                                |||||    ||   |||||||||
                                CTACG    CG   GTCTGACAG
                                   CT__  AA_
GAM2360  NUDT13    3'  GTGCAAATGCCAGCAACTGT   55765         GACCA
                                GTGCAAATGC     GACTGT
                                |||||||||     ||||||
                                CACGTTTACG     TTGACA
                                      GTCG_
GAM2360  RPP14     3'  AGGTTCAGACAGACTG      55766      G  AATGC   C
                                AGGT CA     GAC AGACTG
                                |||| ||     ||| ||||||
                                TCCA GT     CTG TCTGAC
                                  A _____  _
GAM2360  WAC       3'  AGGTGCAAGTGTGGAAACAGTT 55767        A  C_  C_   AC
           GT                     AGGTGCAA TG  GA  CAG  TGT
                                ||||||| ||  ||  |||  |||
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                                TCCACGTT AC  CT  GTC  ACA
                                    C  AC  TT   A_
GAM2360  WAC      3'  AGGTGCAAGTGTGGAAACAGTT 55767        A  C_  C_  AC
              GT                    AGGTGCAA TG  GA  CAG  TGT
                                    |||||||| ||  ||  |||  |||
                                TCCACGTT AC  CT  GTC  ACA
                                    C  AC  TT   A_
GAM2360  WAC      3'  AGGTGCAAGTGTGGAAACAGTT 55767        A  C_  C_  AC
              GT                    AGGTGCAA TG  GA  CAG  TGT
                                    |||||||| ||  ||  |||  |||
                                TCCACGTT AC  CT  GTC  ACA
                                    C  AC  TT   A_
GAM2360  LOC220164 3'  GGTCCAGGACAGACTGT     55768     G  AATGC   C
                                GGT CA     GAC AGACTGT
                                ||| ||     ||| |||||||
                                CCA GT     CTG TCTGACA
                                  G  C____   _
GAM2360  LOC257445 3'  AGGGCACTGGGTCAGACTGTC  55762     T   AATGCGAC
                                AGG GCA       CAGACTGTC
                                ||| |||       |||||||||
                                TCC CGT       GTCTGACAG
                                  _   GACCCA__
GAM2361  BRF1     3'  CTCAGGAGGGGACGGTGCGGA  55771     C    AGC  CT
                                CTC GGAG   GG  TGGTGCGGA
                                ||| ||||   ||  |||||||||
                                GAG CCTC   CC  GCCACGCCT
                                  T   ___  CT
GAM2361  FOSL2    3'  CTCCGGAGGGAGGTGCA     55772        AGC  CTT
                                CTCCGGAG   GG   GGTGCG
                                ||||||||   ||   ||||||
                                GAGGCCTC   CC   CCACGT
                                     ___  T__
GAM2361  IGSF8    5'  CTCCGGGGGATGGCGCGG    55773       AGAGC  CT
                                CTCCGG    GG  TGGTGCGG
                                ||||||    ||  ||||||||
                                GAGGCC    CC  ACCGCGCC
                                   ______  CT
GAM2361  IL1RAPL2  5'  TCCGGAGAGCGCGGGCTGG   55774          GCT   T  _
                                TCCGGAGAGCG   TGG GC GG
                                ||||||||||   ||| || ||
                                AGGCCTCTCGC   GCC CG CC
                                     ___   _  A
GAM2361  ITM2B    5'  CTCCGGGAGCGGCTCCGG    55775       A       GGTG
                                CTCCGG GAGCGGCTT    CGG
                                |||||| |||||||||    |||
                                GAGGCC CTCGCCGAG    GCC
                                   _      ____
GAM2361  KLHL1    5'  CTCCGGAGGCGGCTGCAGCTGG 55776         A     _   GC
              A                   CTCCGGAG GCGGCT TGGT  GGA
                                  |||||||| |||||| ||||  |||
```

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                                GAGGCCTC CGCCGA GTCG  CCT
                                   _     C    A_
GAM2361  LRP1    5'  GGAGGGGGCTTGATGGA     55777      AGC        C
                                GGAG   GGCTTGGTG GG
                                ||||   ||||||||| ||
                                CCTC   CCGAACTAC CT
                                  CC_        _
GAM2361  NRG1     3'  GGGGAGCTTGGCGTGTGGA   55778    A   __   TTG   C
                                GG GAGC  GGC   GTG GGA
                                || ||||  |||   ||| |||
                                CC CTCG  CCG   CAC CCT
                                 C   AA  ___   A
GAM2361  NRGN     5'  CTCCGGCAGGGTGGGCGG    55779       AG  C  CT   T
                                CTCCGG  AG GG  TGG GCGG
                                ||||||  || ||  ||| ||||
                                GAGGCC  TC CC  ACC CGCC
                                   G_  _ __   _
GAM2361  SGT      3'  CTCTGAGAGCGGCCCGG     55780     CG
                                CTC  GAGAGCGGCTTGG
                                |||  |||||||||||||
                                GAG  CTCTCGCCGGGCC
                                  A_
GAM2361  SLIT3    5'  CCTGGGGAGCGGGCGGCGG   55781    _ A     CTTG   _
                                CC GG GAGCGG    GTG CGG
                                || || ||||||    ||| |||
                                GG CC CTCGCC    CGC GCC
                                 A  C     _____   C
GAM2361  SOLH     5'  CTCCGGAGAGCGGCGGG     55782            TT
                                CTCCGGAGAGCGGC  GG
                                ||||||||||||||  ||
                                GAGGCCTCTCGCCG  CC
                                        C_
GAM2361  SORD     5'  CTCTGGAGTGCGGCCTGG    55783     C    A
                                CTC GGAG GCGGCTTGG
                                ||| |||| |||||||||
                                GAG CCTC CGCCGGACC
                                  A   A
GAM2361  WT1      5'  CGGAGAGCCCCCGGGTGTGG   55784        GG  T   C
                                CGGAGAGC  CT GGTG GG
                                ||||||||  || |||| ||
                                GCCTCTCG  GG CCAC CC
                                     GG  C    A
GAM2361  WT1      5'  CGGAGAGCCCCCGGGTGTGG   55784        GG  T   C
                                CGGAGAGC  CT GGTG GG
                                ||||||||  || |||| ||
                                GCCTCTCG  GG CCAC CC
                                     GG  C    A
GAM2361  WT1      5'  CGGAGAGCCCCCGGGTGTGG   55784        GG  T   C
                                CGGAGAGC  CT GGTG GG
                                ||||||||  || |||| ||
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                                GCCTCTCG  GG CCAC CC
                                     GG  C    A
GAM2361  WT1      5'  CGGAGAGCCCCCGGGTGTGG   55784        GG  T    C
                                CGGAGAGC  CT GGTG GG
                                ||||||||  || |||| ||
                                GCCTCTCG  GG CCAC CC
                                     GG  C    A
GAM2361  AP3D1    3'  CTCCGCGGGGTGGTGCGG    55785     GGAGA    CT
                                CTCC    GCGG  TGGTGCGG
                                ||||    ||||  ||||||||
                                GAGG    CGCC  ACCACGCC
                                  _____   CC
GAM2361  CDV-1    5'  CTCCAGGGAGCGGCCTGG    55786       A
                                CTCCGG GAGCGGCTTGG
                                |||||| ||||||||||
                                GAGGTC CTCGCCGGACC
                                   C
GAM2361  DPYSL4   3'  CTCTGAGGAGCGGCTGCGG   55787     C GA      TGGT
                                CTC G  GAGCGGCT   GCGG
                                ||| |  ||||||||   ||||
                                GAG C  CTCGCCGA   CGCC
                                  A TC      ____
GAM2361  ERN1     5'  CTCCGGGGGCGGTACG      55788       AGAGC   TT
                                CTCCGG    GGC  GGTGCG
                                ||||||    |||  ||||||
                                GAGGCC    CCG  CCATGC
                                   C____  __
GAM2361  HSU79274 5'  TCGGGAGAGCGGGGCGGG    55790    C       CTT   C
                                TC GGAGAGCGG   GGTG GG
                                || |||||||||   |||| ||
                                AG CCTCTCGCC   CCGC CC
                                 C       ___   _
GAM2361  HSU79274 5'  TCCGGAGAGGCGGCTCGG    55789         _
                                TCCGGAGAG CGGCTTGG
                                |||||||||| ||||||||
                                AGGCCTCTC GCCGAGCC
                                     C
GAM2361  KIAA0444 3'  CGGAAGGTGGCTTTCACGG   55791      AGC    GG
                                CGGAG   GGCTT  TGCGG
                                |||||   |||||  |||||
                                GCCTT   CCGAA  GTGCC
                                   CCA    A_
GAM2361  KIAA1161 5'  TCCTGGGAGTACATGGTGCGG  55792    _ A   CG  T
                                TCC GG GAG  GC TGGTGCGG
                                ||| || |||  || ||||||||
                                AGG CC CTC  TG ACCACGCC
                                  A  _   A_  T
GAM2361  KIAA1600 5'  CTCCGGAGGGCGCCGGG     55793        A   G  T
                                CTCCGGAG GCG CT GG
                                |||||||| ||| || ||
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                                GAGGCCTC CGC GG CC
                                    C   _ C
GAM2361  MGC13007  5'  CTCCGGAGGTGGCTGTGG    55794        AGC   _
                                CTCCGGAG   GGCT TGG
                                ||||||||   |||| |||
                                GAGGCCTC   CCGA ACC
                                    CA_    C
GAM2361  Rab11-FIP3 5'  CTCCCGAGAGGCTAGTGGTGCG 55795     G   GC   __
           GA                     CTCC GAGA  GGCT  TGGTGCGGA
                                |||| ||||  ||||  |||||||||
                                GAGG CTCT  CCGA  ACCACGCCT
                                  G   __   TC
GAM2361  SAC2     5'  CTCGGGGAGCGGCCGGG     55796     C  A       T
                                CTC GG GAGCGGCT GG
                                ||| || |||||||| ||
                                GAG CC CTCGCCGG CC
                                  C _       C
GAM2361  SLC26A6   5'  CTCCGGAAGGCGGCGCCGG   55797        A    _
                                CTCCGGAG GCGGC TTGG
                                |||||||| ||||| ||||
                                GAGGCCTT CGCCG GGCC
                                    C    C
GAM2361  SLC26A6   5'  CTCCGGAAGGCGGCGCCGG   55797        A    _
                                CTCCGGAG GCGGC TTGG
                                |||||||| ||||| ||||
                                GAGGCCTT CGCCG GGCC
                                    C    C
GAM2361  SLC26A6   5'  CTCCGGAAGGCGGCGCCGG   55797        A    _
                                CTCCGGAG GCGGC TTGG
                                |||||||| ||||| ||||
                                GAGGCCTT CGCCG GGCC
                                    C    C
GAM2361  SNPH     3'  CTCTGAAGAGTGGGTGG     55798     C     C  CTTG   C
                                CTC GGAGAG GG    GTG G
                                ||| |||||| ||    ||| |
                                GAG CTTCTC CC    CAC C
                                  A     A _____  _
GAM2361  UBAP     3'  CTCCGGAGGGCTGAAGTGGG   55799        AGC   T_   C
                                CTCCGGAG   GGCT  GGTG GG
                                ||||||||   ||||  |||| ||
                                GAGGCCTC   CCGA  TCAC CC
                                    ___    CT   _
GAM2361  USP25    5'  CTCCAGGGAGCGGCGCGG    55800       A      TTGGT
                                CTCCGG GAGCGGC    GCGG
                                ||||||  |||||||    ||||
                                GAGGTC CTCGCCG    CGCC
                                   C      ______
GAM2361  LOC116349 5'  GGGGAGCGGCCATGGG      55801     A       TG   C
                                GG GAGCGGCT  GTG GG
                                || ||||||||  ||| ||
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                                CC CTCGCCGG  TAC CC
                                 C      __  _
GAM2361  LOC146774 3'  CTCCGGGGGCGGTACG      55788       AGAGC   TT
                                CTCCGG    GGC  GGTGCG
                                ||||||    |||  ||||||
                                GAGGCC    CCG  CCATGC
                                   C____   __
GAM2361  LOC148930 3'  CCTGGAGGGTGCAGGTGTGGA  55802    _   AGCG  TT   C
                                CC GGAG   GC  GGTG GGA
                                || ||||   ||  |||| |||
                                GG CCTC   CG  CCAC CCT
                                 A   CCA_  T_   A
GAM2361  LOC162461 3'  CTCCGAGGGCGGCCCATGG   55803      G  A    __
                                CTCCG AG GCGGCT  TGG
                                ||||| || ||||||  |||
                                GAGGC TC CGCCGG  ACC
                                   _ C     GT
GAM2361  LOC165246 5'  GGGACTGAGCTTGGTGTGGA   55804    A  GC_       C
                                GG GA   GGCTTGGTG GGA
                                || ||   ||||||||| |||
                                CC CT   TCGAACCAC CCT
                                 _ GAC        A
GAM2361  LOC220064 5'  TCCGGAAGCGGCGGCGCGG   55805      G     TT
                                TCCGGA AGCGGC  GGTGCGG
                                |||||| ||||||  |||||||
                                AGGCCT TCGCCG  CCGCGCC
                                   _    __
GAM2361  LOC51161  3'  GGAGGGTGGGGCCAGTGTGGA  55806     AGC__   T   C
                                GGAG    GGCT GGTG GGA
                                ||||    |||| |||| |||
                                CCTC    CCGG TCAC CCT
                                  CCACC   _   A
GAM2362  AMPD3    5'  CGCGGGGGCCGGGCGTTCAGAG 55809    AGCA  A  ____  CTC
           GG                   CGC   GCC GGC   AGA  GGG
                                |||   ||| |||   |||  |||
                                GCG   CGG CCG   TCT  CCC
                                 CCCC  C  CAAG  ___
GAM2362  CAPN7    5'  GCGGCGGCGAGGACTCGG    55810    A  A  C   CAG
                                GC GC GC AGG   ACTCGG
                                || || || |||  ||||||
                                CG CG CG TCC   TGAGCC
                                 C  C  C  ___
GAM2362  CDKN2A   3'  GCAGCAGCTCCGCCACTCGGG  55811       CAG  AG
                                GCAGCAGC   GC  ACTCGGG
                                ||||||||   ||  |||||||
                                CGTCGTCG   CG  TGAGCCC
                                    AGG  G_
GAM2362  CHRNA5   5'  AGCAGCTTCTGGCGGGCTCGGG 55812      CA__   AGA
                                AGCAGC   GGC   CTCGGG
                                ||||||   |||   ||||||
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                                TCGTCG   CCG  GAGCCC
                                   AAGA  CCC
GAM2362 CSNK2A1  3' GCAGCAGCCGGGATTGAGG   55813        A  CA_  CTC
                                GCAGCAGCC GG  GA  GG
                                ||||||||| ||  ||  ||
                                CGTCGTCGG CC  CT  CC
                                     C  TAA  ___
GAM2362 FASN     3' GCCGCAGCCAGCAGGCTTGGG 55814    A      G  A  C
                                GC GCAGCCAG CAG CT GGG
                                || |||||||| ||| || |||
                                CG CGTCGGTC GTC GA CCC
                                 G       _  C  A
GAM2362 FOXG1B   5' CGCAGTTGGACGCAGGCTCGGG 55815      CAGCCAG   A
                                CGCAG      GCAG CTCGGG
                                |||||      |||| ||||||
                                GCGTC      CGTC GAGCCC
                                   AACCTG_   C
GAM2362 HCFC1    3' GCAGCAGTTGGCAGTGCGG   55816       CCA    ACT
                                GCAGCAG  GGCAG  CGG
                                |||||||  |||||  |||
                                CGTCGTC  CCGTC  GCC
                                    AA_    AC_
GAM2362 HOXA3    3' CGCAGCAGCTGGGAACCGGG  55817        CA  CA  T
                                CGCAGCAGC  GG  GAC CGGG
                                |||||||||  ||  ||| ||||
                                GCGTCGTCG  CC  TTG GCCC
                                     AC  __  _
GAM2362 ITCH     5' GCATGGTACCGGGACTCGGG  55818    GCA_  A  CA
                                GCA   GCC GG  GACTCGGG
                                |||   ||| ||  ||||||||
                                CGT   TGG CC  CTGAGCCC
                                  ACCA  _ __
GAM2362 MAT1A    3' CAGCAGCCAGGCGTCTGGG   55819         AGA  C
                                CAGCAGCCAGGC   CT GGG
                                ||||||||||||  || |||
                                GTCGTCGGTCCG   GA CCC
                                      CA_  _
GAM2362 ORM1     5' ACGTGGAGCCAGGCAGTGCTGG 55820    CAGC       A_  C
                                ACG   AGCCAGGCAG  CT GG
                                |||   ||||||||||  || ||
                                TGC   TCGGTCCGTC  GA CC
                                  ACC_        AC  _
GAM2362 PKM2     3' GCAGCCAGGCTCTGGG     55821         AGA  C
                                GCAGCCAGGC   CT GGG
                                ||||||||||  || |||
                                CGTCGGTCCG   GA CCC
                                     A__  _
GAM2362 PTK2B    3' GCAGTGGCCAGGCAGCAG    55822     CA       ACT
                                GCAG  GCCAGGCAG   CGG
                                ||||  |||||||||   |||
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                                CGTC  CGGTCCGTC   GTC
                                  AC       ___
GAM2362  RARA     3'  ACCCAGTGGTCAGGCAGAGGG  55823    G   CAGC      CTC
                                AC CAG    CAGGCAGA   GGG
                                || |||    ||||||||   |||
                                TG GTC    GTCCGTCT   CCC
                                 G   ACCA      ___
GAM2362  SNCG     3'  GCAGCAGCACAGGTGGACAGG  55824        _   CA   TC
                                GCAGCAGC CAGG  GAC  GG
                                |||||||| ||||  |||  ||
                                CGTCGTCG GTCC  CTG  CC
                                     T   AC   T_
GAM2362  CDIPT    3'  GCAGCCAGGACCCGG      55825         CAG
                                GCAGCCAGG   ACTCGG
                                |||||||||   ||||||
                                CGTCGGTCC   TGGGCC
                                            ___
GAM2362  DKFZp434F1719 3'  GCAGCCAGGCAGACTTGGG    55826             C
                                GCAGCCAGGCAGACT GGG
                                |||||||||||||| |||
                                CGTCGGTCCGTCTGA CCC
                                          A
GAM2362  DKFZp434J0617 3'  GCAGACCGGGCACTCGGG    55827     _ A   AG
                                GCAG CC GGC  ACTCGGG
                                |||| || |||  |||||||
                                CGTC GG CCG  TGAGCCC
                                  T  C  __
GAM2362  EPI64    3'  CAGTGGCCAGGCAGCTTGG   55828     CA       A  C
                                CAG  GCCAGGCAG CT GG
                                |||  ||||||||| || ||
                                GTC  CGGTCCGTC GA CC
                                  AC        _  A
GAM2362  FARSL    3'  CGCAGCAGCAGGGACTCGGG   55829         C   CA
                                CGCAGCAGC AGG  GACTCGGG
                                |||||||| |||  ||||||||
                                GCGTCGTCG TCC  CTGAGCCC
                                            _  __
GAM2362  FBXO9    5'  GCGGCTGCCGGGGACTCGGG   55830    A  A   A  CA
                                GC GC GCC GG  GACTCGGG
                                || || ||| ||  ||||||||
                                CG CG CGG CC  CTGAGCCC
                                 C  A   C  __
GAM2362  FLJ10297 3'  ACGTGGCACCAGGTGCCAG   55831     CA   G    CAGAC
                                ACG  GCA CCAGG    TCGG
                                |||  ||| |||||    ||||
                                TGC  CGT GGTCC    GGTC
                                  AC   _    AC___
GAM2362  FLJ10851 3'  GCAGCAGCCAGGGCTGCCGGG  55832           CAGAC
                                GCAGCAGCCAGG    TCGGG
                                ||||||||||||    |||||
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                                CGTCGTCGGTCC    GGCCC
                                      CGAC_
GAM2362  FLJ13868  3'  GCAGCAGCCAGGCGGCTGG   55833          AGA  C
                                GCAGCAGCCAGGC   CT GG
                                |||||||||||||   || ||
                                CGTCGTCGGTCCG   GA CC
                                      CC_  _
GAM2362  FLJ22029  3'  ACGCAGCATCCATTTCGG    55834        G   GGCAGAC
                                ACGCAGCA CCA      TCGG
                                ||||||||  |||      ||||
                                TGCGTCGT GGT      AGCC
                                    A   AA_____
GAM2362  FLJ22169  3'  GCAGCAGCCCAAAGCCTCGGG  55835         __   AGA
                                GCAGCAGCC  AGGC   CTCGGG
                                |||||||||  ||||   ||||||
                                CGTCGTCGG  TTCG   GAGCCC
                                     GT   ___
GAM2362  FLJ31168  3'  GCAGCAGCCGGCCACACAGG   55836        A   AG  T
                                GCAGCAGCC GGC  AC CGGG
                                |||||||||  |||  ||  ||||
                                CGTCGTCGG CCG  TG GTCC
                                     _  G_  T
GAM2362  FLJ32784  3'  GCACAGCTGGGGACTCGGG    55837     G    CA  CA
                                GCA CAGC  GG  GACTCGGG
                                |||  ||||  ||  ||||||||
                                CGT GTCG  CC  CTGAGCCC
                                  _    AC  __
GAM2362  GBTS1     3'  CAGCAGCCAGGACAGGCTCGGG 55838          _  A
                                CAGCAGCCAGG CAG CTCGGG
                                ||||||||||| ||| ||||||
                                GTCGTCGGTCC GTC GAGCCC
                                      T   C
GAM2362  HSJ001348 5'  GCCGGCGGCCAGGCAGGAACGG 55839    A_  A       ACT
            G                    GC  GC GCCAGGCAG   CGGG
                                ||  ||  |||||||||   ||||
                                CG  CG CGGTCCGTC   GCCC
                                 GC  C        CTT
GAM2362  ITGB5     3'  AGCAGCCAGGTGACATGG     55840          CA   TC
                                AGCAGCCAGG  GAC  GG
                                ||||||||||  |||  ||
                                TCGTCGGTCC  CTG  CC
                                     A_   TA
GAM2362  KCNT1     3'  GCAGCAGCCGGGTGATGG     55841         A  CA  CTC
                                GCAGCAGCC GG  GA   GG
                                |||||||||  ||  ||   ||
                                CGTCGTCGG CC  CT   CC
                                     C  A_  A__
GAM2362  KIAA0125  3'  GCATGGTAGCCAGGCAGACTAG 55842     GC__          C
                                GCA    AGCCAGGCAGACT GG
                                |||    |||||||||||||  ||
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                                CGT    TCGGTCCGTCTGA TC
                                  ACCA          _
GAM2362  KIAA0222  5'  CGCAGCAGCTGGCAGCCAG    55843         CA     A T
                                CGCAGCAGC  GGCAG C CGG
                                |||||||||  ||||| | |||
                                GCGTCGTCG  CCGTC G GTC
                                     A_    _ _
GAM2362  KIAA0295  3'  GCAGCAGACCAAGGGCTTGGG  55844        _    CAGA  C
                                GCAGCAG CCAGG    CT GGG
                                |||||||  |||||    || |||
                                CGTCGTC GGTTC    GA CCC
                                    T    CC__  A
GAM2362  KIAA0527  5'  GCGCGGGCCAGCGGACTCGGG  55845    A  A_    G A
                                GC GC  GCCAG C GACTCGGG
                                || ||  ||||| | ||||||||
                                CG CG  CGGTC G CTGAGCCC
                                 _ CC    _ C
GAM2362  KIAA0711  5'  ACGCGCAGCCAGGCG      55846      A        AGACTC
                                ACGC GCAGCCAGGC     G
                                |||| ||||||||||     |
                                TGCG CGTCGGTCCG     C
                                  _        _______
GAM2362  KIAA1453  3'  GCGCAGCTGCTGGACTCGGG   55847    A    CAG  A_
                                GC GCAGC   GC  GACTCGGG
                                || |||||   ||  ||||||||
                                CG CGTCG   CG  CTGAGCCC
                                 _    A__  AC
GAM2362  KIAA1884  3'  GCGGCCAATGGACTCGGG    55848    A    GCA
                                GC GCCAG   GACTCGGG
                                || |||||   ||||||||
                                CG CGGTT   CTGAGCCC
                                 C    AC_
GAM2362  KRT6IRS   3'  GCTGGCAGCCAGGACCTGG    55849    A_       CAG  TC
                                GC  GCAGCCAGG   AC  GG
                                ||  |||||||||   ||  ||
                                CG  CGTCGGTCC   TG  CC
                                 AC         ___  GA
GAM2362  LHX6      3'  ACAGCAGGAAGGTGGACTTGGG 55850        CC   CA   C
                                GCAGCAG  AGG  GACT GGG
                                |||||||  |||  |||| |||
                                TGTCGTC  TCC  CTGA CCC
                                    CT   AC   A
GAM2362  LSM4      3'  CGCAGCAGCCGGTCTGG     55851          A  CAGA  C
                                CGCAGCAGCC GG    CT GG
                                |||||||||| ||    || ||
                                GCGTCGTCGG CC    GA CC
                                      _ A___  _
GAM2362  MAPKAPK5  5'  GCAGCAGCCGCCCCTCGGG   55852         AG  AGA
                                GCAGCAGCC  GC   CTCGGG
                                |||||||||  ||   ||||||
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                                CGTCGTCGG CG  GAGCCC
                                    __ GG_
GAM2362 MAPKAPK5 5' GCAGCAGCCGCCCCTCGGG  55852       AG AGA
                                GCAGCAGCC GC  CTCGGG
                                ||||||||| ||  ||||||
                                CGTCGTCGG CG  GAGCCC
                                    __ GG_
GAM2362 MRPS5   5' ACGCAGCAGCGCAGGCCGG  55853        _   AGACT
                                ACGCAGCAGC CAGGC   CGG
                                |||||||||| |||||   |||
                                TGCGTCGTCG GTCCG   GCC
                                     C  _____
GAM2362 PRDM12  3' ACAGCAGCAGGGAGACTCGGG 55854      C  C
                                GCAGCAGC AGG AGACTCGGG
                                |||||||| ||| |||||||||
                                TGTCGTCG TCC TCTGAGCCC
                                    _  C
GAM2362 TOLLIP  3' ACGCAGCGCCCAGGCAGTCAGA 55855     AG     AC
                                ACGCAGC  CCAGGCAG  TCGGG
                                |||||||  ||||||||  |||||
                                TGCGTCG  GGTCCGTC  AGTCT
                                   CG      __
GAM2362 TRIM11  3' GCAGCAGCTGGGACCCTGGG  55856      CA CA   _
                                GCAGCAGC  GG  GACTC GGG
                                ||||||||  ||  ||||| |||
                                CGTCGTCG  CC  CTGGG CCC
                                    A_ __    A
GAM2362 TSC22   3' ACGCAGCAGCCAGTTCTGCGGG 55857         GCAGA _
                                ACGCAGCAGCCAG    CT CGGG
                                ||||||||||||    || ||||
                                TGCGTCGTCGGTC    GA GCCC
                                      AA___  C
GAM2362 LOC116225 5' AGCAGCCAGGCGGGCTCCGGG  55858       AGA  _
                                AGCAGCCAGGC  CTC GGG
                                ||||||||||  ||| |||
                                TCGTCGGTCCG  GAG CCC
                                     CCC  G
GAM2362 LOC122970 5' CACAGCAGCCGTCCAGGCTCGG 55859       AGG  A
          G                      CGCAGCAGCC  CAG CTCGGG
                                ||||||||||  ||| ||||||
                                GTGTCGTCGG  GTC GAGCCC
                                     CAG  C
GAM2362 LOC124145 5' GCAGCAGCGACGGCTCGG   55860      CA_  AGAC
                                GCAGCAGC  GGC   TCGG
                                ||||||||  |||   ||||
                                CGTCGTCG  CCG   AGCC
                                    CTG  ____
GAM2362 LOC138399 5' AGCAGCCACAGCTTGG     55861      AG   A  C
                                AGCAGCC  GCAG CT GG
                                |||||||  |||| || ||
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                                TCGTCGG  TGTC GA CC
                                   __   _ A
GAM2362  LOC146315 5'  CGCAGCGCCAGGCAGTGG    55862       A       ACTC
                                CGCAGC GCCAGGCAG    GG
                                |||||| |||||||||    ||
                                GCGTCG CGGTCCGTC    CC
                                   _       A___
GAM2362  LOC147057 3'  ACGTGGAGCCAGGCTGAGG    55863     CAGC       A  CTC
                                ACG    AGCCAGGC GA   GG
                                |||    |||||||| ||   ||
                                TGC    TCGGTCCG CT   CC
                                  ACC_       A  ___
GAM2362  LOC147645 5'  GCAGCAGCACCTCTCGG     55864        CAG  AGA
                                GCAGCAGC   GC   CTCGG
                                ||||||||   ||   |||||
                                CGTCGTCG   TG   GAGCC
                                     ___  GA_
GAM2362  LOC148525 5'  ACGCAAGCAGAGCGGTAGGCTC 55865       _   CCA  C  A
            GGG                    ACGCA GCAG   GG AG CTCGGG
                                |||||| ||||   || || ||||||
                                TGCGT CGTC   CC TC GAGCCC
                                   T    TCG  A  C
GAM2362  LOC155036 5'  ACAGTGGCCTTGACTCGGG    55866     CA   AGGCA
                                GCAG  GCC    GACTCGGG
                                ||||  |||    ||||||||
                                TGTC  CGG    CTGAGCCC
                                  AC   AA___
GAM2362  LOC157918 3'  CAGCAGCCAGGCCCCCAGG    55867          AGA
                                CAGCAGCCAGGC   CTCGGG
                                ||||||||||||   ||||||
                                GTCGTCGGTCCG   GGGTCC
                                       G__
GAM2362  LOC161247 5'  GCGGCGGTCAGGCAGCTCG    55868    A  AGC      A
                                GC GC   CAGGCAG CTCG
                                || ||   ||||||| ||||
                                CG CG   GTCCGTC GAGC
                                 C  CCA      _
GAM2362  LOC162333 5'  GCACGGCGGGGGACTCGG     55869     G A  CA  CA
                                GCA C GC  GG  GACTCGG
                                ||| | ||  ||  |||||||
                                CGT G CG  CC  CTGAGCC
                                  _ C  __  CC
GAM2362  LOC200862 5'  GCGGCGGCGGCGGCGGCTCGGG 55870    A  A  CA_   AGA
                                GC GC GC   GGC   CTCGGG
                                || || ||   |||   ||||||
                                CG CG CG   CCG   GAGCCC
                                 C  C  CCG   CC_
GAM2362  LOC201546 5'  GCAGCCAAGTTCCCAGG     55871         CAGA
                                GCAGCCAGG    CTCGGG
                                |||||||||    ||||||
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                                CGTCGGTTC    GGGTCC
                                     AA__
GAM2362  LOC202152 5'  ACTCAGCAGCCAAGGACTTGGG 55872    G        CA   C
                                AC CAGCAGCCAGG  GACT GGG
                                || ||||||||||  |||| |||
                                TG GTCGTCGGTTC  CTGA CCC
                                 A         __   A
GAM2362  LOC202775 5'  GCCACCCCAGGCGGACTCGGG  55873    A  AG     A
                                GC GC  CCAGGC GACTCGGG
                                || ||  |||||| ||||||||
                                CG TG  GGTCCG CTGAGCCC
                                 G  G_     C
GAM2362  LOC203248 3'  GCGACAGCATAGGCTCGG    55874    A    C_   AGAC
                                GC GCAGC  AGGC    TCGG
                                || |||||  ||||    ||||
                                CG TGTCG  TCCG    AGCC
                                 C    TA   _____
GAM2362  LOC219513 5'  ACGGTGGCCAGGCAGCGCTGG  55875     CAGCA       A_  C
                                ACG    GCCAGGCAG  CT GG
                                |||    |||||||||  || ||
                                TGC    CGGTCCGTC  GA CC
                                  CAC__       GC  _
GAM2362  LOC222112 5'  CAGCAGCCAGGCACCCAGG    55876          AG
                                CAGCAGCCAGGC  ACTCGGG
                                ||||||||||||  |||||||
                                GTCGTCGGTCCG  TGGGTCC
                                              __
GAM2362  LOC222865 3'  GCAGCCAGGCCCACCTGGG    55877         AG  TC
                                GCAGCCAGGC  AC  GGG
                                ||||||||||  ||  |||
                                CGTCGGTCCG  TG  CCC
                                      GG  GA
GAM2362  LOC253805 3'  CGCAGCAGCAGGAGCCTCGGG  55878         C   C  A
                                CGCAGCAGC AGG AG CTCGGG
                                ||||||||| ||| || ||||||
                                GCGTCGTCG TCC TC GAGCCC
                                     _  _  G
GAM2362  LOC254485 3'  GCGGCAGCCAGGCACAG     55880    A        GACT
                                GC GCAGCCAGGCA    CGG
                                || ||||||||||    |||
                                CG CGTCGGTCCGT    GTC
                                 C          _____
GAM2362  LOC254485 3'  CACAGCAGCCGGGCAGAGG    55879         A     CTC
                                CGCAGCAGCC GGCAGA   GG
                                |||||||||| ||||||   ||
                                GTGTCGTCGG CCGTCT   CC
                                      C     ___
GAM2362  LOC254816 5'  AGCGGCGAAGGACTCGGG    55881     A  C   CA
                                AGC GC AGG  GACTCGGG
                                ||| || |||  ||||||||
```

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                                TCG CG TTC  CTGAGCCC
                                  C  C   __
GAM2362  LOC256295 3'  CGCACAGCCAGGCCTGG     55882      G        AGA  C
                                CGCA CAGCCAGGC   CT GG
                                |||| |||||||||   || ||
                                GCGT GTCGGTCCG   GA CC
                                  _       ___  _
GAM2363  ADCY6     3'  CACCCAAGGCTGAGGTCTTCC  55885          GGCCT
                                CACCCGAGGC    GGGTCTTCC
                                ||||||||||    |||||||||
                                GTGGGTTCCG    TCCAGAAGG
                                     AC___
GAM2363  ADCY6     3'  CACCCAAGGCTGAGGTCTTCC  55885          GGCCT
                                CACCCGAGGC    GGGTCTTCC
                                ||||||||||    |||||||||
                                GTGGGTTCCG    TCCAGAAGG
                                     AC___
GAM2363  BCL2      3'  CACTTGTGGCGGCCTGATGCTC 55886     CCGA        GT
                                CAC   GGCGGCCTGG  CTT
                                |||   ||||||||||  |||
                                GTG   CCGCCGGACT  GAG
                                  AACA        AC
GAM2363  CACNG3    5'  ACCCGGGGTGCTAAAGGGTCTT 55887      A  CG  CT__
                                ACCCG GG  GC    GGGTCTT
                                ||||| ||  ||    |||||||
                                TGGGC CC  CG    CCCAGAA
                                  _  CA  ATTT
GAM2363  CEACAM6   3'  CACCTCAGGCCTGAGGGTTTTC 55888     _ AGGC    __    C
            C                    CACC CG    GGCCT  GGGT TTCC
                                |||| ||    |||||  |||| ||||
                                GTGG GT    CCGGA  CCCA AAGG
                                  A _____     CT    A
GAM2363  CRHR1     3'  CACTTGGGCAGGGGTCTTC    55889     CCGA    CCT
                                CAC    GGCGG   GGGTCTTC
                                |||    |||||   ||||||||
                                GTG    CCGTC   CCCAGAAG
                                  AAC_    ____
GAM2363  DDX11     3'  GAGGCAGCTCTCTTTTGGAAGA 55890        _ T_________   TCT
            CCC                    AGGCGGC C        GGG   TCC
                                ||||||| |        |||   |||
                                TCCGTCG G        CCT   GGG
                                   A AGAAAAIII   TCT
GAM2363  DYRK1B    3'  GAGGGGGGGTCTTCC       55891      C  CCT
                                GAGG GG   GGGTCTTCC
                                |||| ||   |||||||||
                                CTCC CC   CCCAGAAGG
                                  _ ____
GAM2363  FMR2      3'  CCCTTGGGGAAAGGGTCTTCC  55892     GA  C  CCT
                                CCC  GG GG   GGGTCTTCC
                                |||  || ||   |||||||||
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                                GGG  CC CC   CCCAGAAGG
                                  AA  _  TTT
GAM2363  GRLF1    3'  CACCCAGCCTTGGGTCTTC    55893      GAGGC    _
                                CACCC    GGCCT GGGTCTTC
                                |||||    ||||| ||||||||
                                GTGGG    TCGGA CCCAGAAG
                                  _____    A
GAM2363  HMGA2    5'  CCCGGGCTGGAAGTTTTC    55894     A  _  CCT   C
                                CCCG GGC GG   GGGT TTC
                                |||| ||| ||   |||| |||
                                GGGC CCG CC   TTCA AAG
                                  _  A ___   A
GAM2363  PIGA     3'  ACCTGAGTGGCTTAAATGTTC  55895    C  GC  C   C
                                ACC GAG  GGC TGGGT TTC
                                ||| |||  ||| ||||| |||
                                TGG CTC  CCG ATTTA AAG
                                  A  A_  A    C
GAM2363  PIGA     3'  ACCTGAGTGGCTTAAATGTTC  55895    C  GC  C   C
                                ACC GAG  GGC TGGGT TTC
                                ||| |||  ||| ||||| |||
                                TGG CTC  CCG ATTTA AAG
                                  A  A_  A    C
GAM2363  PIGA     3'  ACCTGAGTGGCTTAAATGTTC  55895    C  GC  C   C
                                ACC GAG  GGC TGGGT TTC
                                ||| |||  ||| ||||| |||
                                TGG CTC  CCG ATTTA AAG
                                  A  A_  A    C
GAM2363  PK428    5'  CCCGGAGGCGGCTTTTCGGAAG 55896    _     CT_______  TCT
            ACC                   CCG AGGCGGC      GGG   TC
                                ||| |||||||       |||   ||
                                GGC TCCGCCG       CCT   GG
                                  C      AAAAGIII   TCT
GAM2363  PRX      3'  CACTCGGGGCAGCCTGAGT   55897    C  A
                                CAC CG GGCGGCCTGGGT
                                ||| || ||||||||||||
                                GTG GC CCGTCGGACTCA
                                  A  C
GAM2363  SLC13A4  3'  CACTTGAGGTGGCGGAATCTTC 55898    CC    C   CT
                                CAC  GAGG GGC  GGGTCTTC
                                |||  |||| |||  ||||||||
                                GTG  CTCC CCG  CTTAGAAG
                                  AA   A  C_
GAM2363  TACC1    3'  CACTAGGGGATGGGTCTTC   55899    CCG   C  CC
                                CAC   AGG GG  TGGGTCTTC
                                |||   ||| ||  |||||||||
                                GTG   TCC CC  ACCCAGAAG
                                  A__   _  T_
GAM2363  TNFRSF7  5'  CCCAGGCGGCTCCTTTCGGAAG 55900   G     _ T________  TCT
            ACC                   C AGGCGGC C      GGG   TC
                                | ||||||| |       |||   ||
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                                G TCCGCCG G       CCT   GG
                                _      A GAAAGIII   TCT
GAM2363  TNFSF12   3'  CCTGAAGTGGGGTCTTC     55901    C    C  CCTG
                                CC GAGG GG    GGTCTTC
                                || |||| ||    |||||||
                                GG CTTC CC    CCAGAAG
                                 A    A  ____
GAM2363  XPNPEP2   5'  CCCGAGGCGGACTGTGCAAGTT 55902          C   G  C__
              CC                   CCCGAGGCGG CTG GT   TTCC
                                |||||||||| ||| ||   ||||
                                GGGCTCCGCC GAC CG   AAGG
                                      T   A  TTC
GAM2363  YWHAG     5'  CACTGGGGCGGCCTGAAGGGC  55903     CCGA       ___
                                CAC    GGCGGCCT   GGGT
                                |||    ||||||||   ||||
                                GTG    CCGCCGGA   CCCG
                                  ACC_       CTT
GAM2363  ACVR2     5'  CCAGTTCCCTGGGTCTTCC    55904    G  GCGG
                                CC AG    CCTGGGTCTTCC
                                || ||    ||||||||||||
                                GG TC    GGACCCAGAAGG
                                 _  AAG_
GAM2363  C20orf50  5'  CCCTGAGGCGGCTTTCCGGAAG 55905     _       CT_______   TCT
              C                    CCC GAGGCGGC       GGG   T
                                ||| ||||||||       |||   |
                                GGG CTCCGCCG       CCT   G
                                  A       AAAGGIII   TCT
GAM2363  DDX21     5'  CCCAGGCCGACCGGTCTTC    55906     G    _    TG
                                CCC AGGC GGCC  GGTCTTC
                                ||| |||| ||||  |||||||
                                GGG TCCG CTGG  CCAGAAG
                                  _    G    __
GAM2363  FLJ10508  3'  AGCTTAGCTTGGGTCTTC     55907     __   C
                                GGC  GGC TGGGTCTTC
                                |||  ||| |||||||||
                                TCG  TCG ACCCAGAAG
                                  AA   A
GAM2363  HSA243666 3'  CCCAAGTCTGGGTTTTC      55908       GCGGC     C
                                CCCGAG     CTGGGT TTC
                                ||||||     |||||| |||
                                GGGTTC     GACCCA AAG
                                   A_____      A
GAM2363  JM5       5'  CCCGCGGCCCGGTTTTC      55909     GAG       GTC
                                CCC   GCGGCCTGG   TTC
                                |||   |||||||||   |||
                                GGG   CGCCGGGCC   AAG
                                  ____       AA_
GAM2363  KIAA0240  3'  CACCGGGGTATAGGTCTTC    55910      CGA  C  CC
                                CACC   GG GG  TGGGTCTTC
                                ||||   || ||  |||||||||
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                                GTGG  CC CC  ATCCAGAAG
                                  ___ _ AT
GAM2363 KIAA0444 3' CACCCCAGGCCCAGCTGGGT  55911     G  __  C
                                CACCC AGGC  GGC TGGGT
                                ||||| ||||  ||| |||||
                                GTGGG TCCG  TCG ACCCA
                                   G   GG  _
GAM2363 KIAA1671 3' CCTGGAGGTTGGGTCTTCC  55912   GA  C  CC
                                CC  GG GG  TGGGTCTTCC
                                ||  || ||  ||||||||||
                                GG  CC CC  ACCCAGAAGG
                                 A_  T  A_
GAM2363 KIAA1924 3' CACCCGGAGGTGGCTTTTCGGA 55913    _  C  CT_____  TCT
           AGACC                 CCG AGG GGC      GGG  TC
                                ||| ||| |||      |||  ||
                                GGC TCC CCG      CCT  GG
                                  C  A  AAAAGIII  TCT
GAM2363 NFKBIE   3' ACCTGGGGCTTTGGGGGTCTTC 55914    CGA  GGCCT
           C                    ACC  GGC   GGGTCTTCC
                                |||  |||   |||||||||
                                TGG  CCG   CCCAGAAGG
                                  ACC  AAACC
GAM2363 OAZIN    5' ACCCAAGGCGGCCTGGGCC   55915
                                ACCCGAGGCGGCCTGGGTC
                                |||||||||||||||||||
                                TGGGTTCCGCCGGACCCGG

GAM2363 RARRES2  3' CCCTGGGGGCTGGGGTCTTCC  55916    GA  C  CT
                                CCC  GG GGC  GGGTCTTCC
                                |||  || |||  |||||||||
                                GGG  CC CCG  CCCAGAAGG
                                  AC  _  AC
GAM2363 RDH-E2   3' CACTGGAGGCGGGCCTTTTCTG 55917      _ T_________  TCT
           GAAGACCC               AGGCGG CC       GGG  TCC
                                ||||||  ||       |||  |||
                                TCCGCC GG       CCT  GGG
                                   C  AAAAGAIII  TCT
GAM2363 RILP     3' CCGAGGCGGCCTTTTTTGGAAG 55918         T_________  TCT
           ACC                   CGAGGCGGCC       GGG  TC
                                ||||||||||       |||  ||
                                GCTCCGCCGG       CCT  GG
                                     AAAAAAIII   TCT
GAM2363 SEC3     5' CCGAGGCGGGTCTTC      55919       GGCCT
                                CCGAGGC    GGGTCTTC
                                |||||||    ||||||||
                                GGCTCCG    CCCAGAAG
                                  _____
GAM2363 LOC113523 3' CCCGGGCTGGTCTCTAAACTCC 55920     A  _  C__    T
                                CCCG GGC GG   CTGGG CTTC
                                |||| ||| ||   ||||| ||||
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                                GGGC CCG CC   GATTT GAGG
                                  _  A  AGA    _
GAM2363  LOC113828 5'  CGAGGCGGCAGCAGTTTC    55921         CTG   C
                                CGAGGCGGC   GGT TTC
                                |||||||||   ||| |||
                                GCTCCGCCG   TCA AAG
                                     TCG  _
GAM2363  LOC125268 3'  CACCCGGCGTGCAGTCTTC    55922      GA   _  CTG
                                CACCC  GGCG GC   GGTCTTC
                                |||||  |||| ||   |||||||
                                GTGGG  CCGC CG   TCAGAAG
                                   __    A  ___
GAM2363  LOC129607 3'  GAGTAAGACAGGTCTTCC    55923     GC_   CT
                                GAG   GGC  GGGTCTTCC
                                |||   |||  |||||||||
                                CTC   CTG  TCCAGAAGG
                                  ATT   __
GAM2363  LOC143724 3'  CACCCGAGGCAGCCTTTTGGAA 55924           T_______   TCT
            GC                    ACCCGAGGCGGCC      GGG   T
                                |||||||||||||      |||   |
                                TGGGCTCCGTCGG      CCT   G
                                       AAAAIII   TCT
GAM2363  LOC145815 5'  ACCTGGGGTGGTCTGGGTCTT  55925     CGA  C  C
                                ACC   GG GG CTGGGTCTT
                                |||   || || |||||||||
                                TGG   CC CC GACCCAGAA
                                  ACC  A  A
GAM2363  LOC146714 5'  CCTGGCGGGGCCTGGGTCTT   55926    GA   __
                                CC  GGC  GGCCTGGGTCTT
                                ||  |||  ||||||||||||
                                GG  CCG  CCGGACCCAGAA
                                 A_   CC
GAM2363  LOC149576 3'  CCCAGGCGCCCCGGTCTTCC   55927     G    G   G
                                CCC AGGCG CCT GGTCTTCC
                                ||| ||||| ||| |||||||||
                                GGG TCCGC GGG CCAGAAGG
                                  _    _  G
GAM2363  LOC151996 3'  ACCTGGGGCGGAAGGAGTTTTC 55928     CGA    CCT    C
            C                    ACC   GGCGG   GGGT TTCC
                                |||   |||||   |||| ||||
                                TGG   CCGCC   CTCA AAGG
                                  ACC    TTC    A
GAM2363  LOC152992 5'  CACTGAGGCGGCTTCCCTC    55929     CC       CTGGG
                                CAC  GAGGCGGC    TCTTC
                                |||  ||||||||    |||||
                                GTG  CTCCGCCG    GGGAG
                                  A_       AA___
GAM2363  LOC200321 5'  GAGGCGGCACTCTTTCGGAAGA 55930        _ T_________   TCT
            CCC                    AGGCGGC C       GGG   TCC
                                |||||||  |       |||   |||
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                                TCCGCCG G       CCT   GGG
                                   T AGAAAGIII   TCT
GAM2363  LOC220001 5'  CCCGGGCGGCTTCCTC      55931      A     CTGGG
                                CCCG GGCGGC    TCTTC
                                |||| ||||||    |||||
                                GGGC CCGCCG    AGGAG
                                  _     A____
GAM2363  LOC222681 5'  CCGGATCATTGGGTCTT     55932     A  _  GCC
                                CCG GG CG   TGGGTCTT
                                ||| || ||   ||||||||
                                GGC CT GT   ACCCAGAA
                                  _  A  A__
GAM2363  LOC255452 3'  CCCTTGGGAATCTTGGGTCTT  55933     GA  CG C  _
                                CCC  GG  G CT GGGTCTT
                                |||  ||  | || |||||||
                                GGG  CC  T GA CCCAGAA
                                  AA  CT A  A
GAM2363  LOC257068 3'  CACCAGCTGCTTGGGTCTTCC  55934      CGA   G  C
                                CACC   GGC GC TGGGTCTTCC
                                ||||   ||| || ||||||||||
                                GTGG   TCG CG ACCCAGAAGG
                                   ___   A  A
GAM2363  LOC257457 3'  CCAGACCCTGGGTCTT      55935    G    GG
                                CC AGGC  CCTGGGTCTT
                                || ||||  ||||||||||
                                GG TCTG  GGACCCAGAA
                                 _   __
GAM2363  LOC257507 5'  CCGGATCATTGGGTCTT     55932     A  _  GCC
                                CCG GG CG   TGGGTCTT
                                ||| || ||   ||||||||
                                GGC CT GT   ACCCAGAA
                                  _  A  A__
GAM2363  LOC257625 5'  CCGGATCATTGGGTCTT     55932     A  _  GCC
                                CCG GG CG   TGGGTCTT
                                ||| || ||   ||||||||
                                GGC CT GT   ACCCAGAA
                                  _  A  A__
GAM2363  LOC51619  5'  CCTGAGGCGGCCCGCTGG    55936    C        _____
                                CC GAGGCGGCCTG    GG
                                || ||||||||||     ||
                                GG CTCCGCCGGGC    CC
                                 A          GAIII
GAM2364  ADAM20    5'  AGAGAACAAGGTGTGAGGCACT 55939          CG_  ATA
            G                    AGAGAACAAGG   GA   CACTG
                                ||||||||||   ||   |||||
                                TCTCTTGTTCC   CT   GTGAC
                                       ACA  CC_
GAM2364  AIM1      3'  AGGAACAAGACAGATATGTTGG 55940    A          ATACAC
                                AG GAACAAGGCGGA     TGG
                                || ||||||||||||     |||
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                                TC CTTGTTCTGTCT     ACC
                                 _         ATACA_
GAM2364  BACE2    5'  GAGAAGGCGGAGGCCGG     55941      ACA      ATACA
                                GAGA   AGGCGGA    CTGG
                                ||||   |||||||    ||||
                                CTCT   TCCGCCT    GGCC
                                  ___      CC___
GAM2364  BACE2    5'  GAGAAGGCGGAGGCCGG     55941      ACA      ATACA
                                GAGA   AGGCGGA    CTGG
                                ||||   |||||||    ||||
                                CTCT   TCCGCCT    GGCC
                                  ___      CC___
GAM2364  BACE2    5'  GAGAAGGCGGAGGCCGG     55941      ACA      ATACA
                                GAGA   AGGCGGA    CTGG
                                ||||   |||||||    ||||
                                CTCT   TCCGCCT    GGCC
                                  ___      CC___
GAM2364  IL18     5'  GAGGGCAAAATGCACTG     55942      AACAA      A
                                GAG    GGCGGAAT CACTG
                                |||    |||||||| |||||
                                CTC    CCGTTTTA GTGAC
                                 _____       C
GAM2364  LYZ      3'  AAAGAACGGAATGTACTG     55943      ACAAG      AC
                                AGAGA    GCGGAAT  ACTG
                                |||||    |||||||  ||||
                                TTTCT    TGCCTTA  TGAC
                                  _____      CA
GAM2364  PABPN1   3'  AAGGGGAATTTACACTGG     55944      C   __
                                AAGG GGAA  TACACTGG
                                |||| ||||  ||||||||
                                TTCC CCTT  ATGTGACC
                                  _   AA
GAM2364  PLCB4    5'  GAGAACAAGGGGCAAGCGGCAC 55945          C  AATA___
            TGG                   GAGAACAAGG GG      CACTGG
                                ||||||||||  ||      ||||||
                                CTCTTGTTCC CC      GTGACC
                                      _  GTTCGCC
GAM2364  RAP1GDS1 3'  AGAGAATGAAGCGGAAGAAGCC 55946       CA       TACA___
            GCTGG                   AGAGAA  AGGCGGAA      CTGG
                                ||||||  ||||||||      ||||
                                TCTCTT  TTCGCCTT      GACC
                                   AC       CTTCGGC
GAM2364  SLC4A7   3'  AGAGAACAGAGTGGGAATCATT 55947         AG C_    A  C
            GG                    AGAGAACA  G  GGAAT CA TGG
                                ||||||||  |  ||||| || |||
                                TCTCTTGT  C  CCTTA GT ACC
                                     CT AC    _  A
GAM2364  SMARCA1  3'  AGAGTACCATGAATACACTGG  55948      A  AAGGCG
                                AGAG AC     GAATACACTGG
                                |||| ||     ||||||||||
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                                TCTC TG     CTTATGTGACC
                                  A  GTA___
GAM2364  SMARCA1   3'  AGAGTACCATGAATACACTGG  55948      A  AAGGCG
                                AGAG AC     GAATACACTGG
                                |||| ||     ||||||||||
                                TCTC TG     CTTATGTGACC
                                  A  GTA___
GAM2364  SPTBN4    3'  AGAGATCAAGGCAGCATTG    55949      A       AATA  C
                                AGAGA CAAGGCGG    CA TG
                                ||||| ||||||||    || ||
                                TCTCT GTTCCGTC    GT AC
                                  A       _____  A
GAM2364  TGM2      3'  AGAGGAGAAGGCAGTCGCTGG  55950      AAC      AATACA
                                AGAG   AAGGCGG     CTGG
                                ||||   |||||||     ||||
                                TCTC   TTCCGTC     GACC
                                  CTC      AGC___
GAM2364  THRA      5'  AGAGACTGGGGTGGGCACACTG 55951      ACAA  C  AA
           G                     AGAGA    GG GG  TACACTGG
                                |||||    || ||  ||||||||
                                TCTCT    CC CC  GTGTGACC
                                  GACC  A  C_
GAM2364  TPD52L2   3'  AGAGAAGCAGGTTTTGTACACT 55952       CA   CGGAA
           GG                    AGAGAA  AGG    TACACTGG
                                ||||||  |||    ||||||||
                                TCTCTT  TCC    ATGTGACC
                                   CG   AAAAC
GAM2364  ELF2      5'  GAGGAGGCGGAACCCGCGG    55953     AACA       ACAC
                                GAG    AGGCGGAAT    TGG
                                |||    |||||||||    |||
                                CTC    TCCGCCTTG    GCC
                                  C___        GGC_
GAM2364  ERF       3'  AGAGAACAGGGAGGGAGACAAG 55954        A  C  AAT   CT
           G                     AGAGAACA GG GG   ACA  GG
                                |||||||| || ||   |||  ||
                                TCTCTTGT CC CC   TGT  CC
                                     C  T  CTC   T_
GAM2364  FLJ10761  3'  AGGGAACAAGGCAGGAGACTGC 55955    A       _   ATACA
           TGG                   AG GAACAAGGC GGA     CTGG
                                || |||||||| |||     ||||
                                TC CTTGTTCCG CCT     GACC
                                 C        T   CTGAC
GAM2364  FLJ12747  3'  AAAGAACAAGGAATACATTGG  55956         GGC       C
                                AGAGAACAA   GGAATACA TGG
                                |||||||||   |||||||| |||
                                TTTCTTGTT   CCTTATGT ACC
                                      ___       A
GAM2364  FLJ20195  3'  AGAGAACAAGGCGGCGCTG    55957            AATACA
                                AGAGAACAAGGCGG     CTG
                                ||||||||||||||     |||
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                                TCTCTTGTTCCGCC     GAC
                                      GC_____
GAM2364  FLJ21687  3'  ACAGGACTGTGGATACACTGG  55958     A  ___  A
                                ACA GGC   GGA TACACTGG
                                ||| |||   ||| ||||||||
                                TGT CTG   CCT ATGTGACC
                                  C   ACA  _
GAM2364  KIAA1001  3'  GAGACCAGTGAGTACACTGG   55959     ACAA  CG  A
                                GAGA   GG  GA TACACTGG
                                ||||   ||  || ||||||||
                                CTCT   TC  CT ATGTGACC
                                  GG__  A_  C
GAM2364  KIAA1023  3'  AGAGAACAGGCTGGGCTG    55960        A  _  AATACA
                                AGAGAACA GGC GG     CTG
                                |||||||| ||| ||     |||
                                TCTCTTGT CCG CC     GAC
                                     _   A  C_____
GAM2364  KIAA1464  3'  GAGCAAGGCAGGCAGTGG    55961     AA       AATA  C
                                GAG  CAAGGCGG    CA TGG
                                |||  ||||||||    || |||
                                CTC  GTTCCGTC    GT ACC
                                  __       C___  C
GAM2364  KIAA1577  3'  AGGGAACAAGAGACACTG    55962    A       C GAAT
                                AG GAACAAGG G    ACACTG
                                || |||||||| |    ||||||
                                TC CTTGTTCT C    TGTGAC
                                 C       _ _____
GAM2364  LGALS8    3'  AGAGAACAGGGAACATACTGG  55963        AG C     C
                                AGAGAACA  G GGAATA ACTGG
                                ||||||||  | |||||| |||||
                                TCTCTTGT  C CCTTGT TGACC
                                     __ _     A
GAM2364  MGC955    3'  AGAGGAAGAAGGAAAGTACACT 55964      AAC   C   __
            GG                    AGAG   AAGG GGAA  TACACTGG
                                ||||   |||| ||||  ||||||||
                                TCTC   TTCT CCTT  ATGTGACC
                                  C__    T    TC
GAM2364  MIDORI    3'  GAGAGGTGGGGACACACTGG   55965     ACAA  C   A
                                GAGA   GG GGA TACACTGG
                                ||||   || ||| ||||||||
                                CTCT   CC CCT GTGTGACC
                                  CCA_ _  _
GAM2364  OR51E2    5'  GAGAGGGTGAGGTCACACTGG  55966     ACAA  CG  A__
                                GAGA   GG  GA   TACACTGG
                                ||||   ||  ||   ||||||||
                                CTCT   CC  CT   GTGTGACC
                                  _____  CA  CCA
GAM2364  PNMA5     3'  AGAGAACAAGCAGCCACTG    55967         G   AATA
                                AGAGAACAAG CGG    CACTG
                                |||||||||| |||    |||||
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                                TCTCTTGTTC GTC    GTGAC
                                      _   G___
GAM2364  STARD7    3'  AAGGCAAGACATACACTGG    55968       _ _
                                AAGGCG GA ATACACTGG
                                |||||| || |||||||||
                                TTCCGT CT TATGTGACC
                                   T  G
GAM2364  STARD7    3'  AAGGCAAGACATACACTGG    55968       _ _
                                AAGGCG GA ATACACTGG
                                |||||| || |||||||||
                                TTCCGT CT TATGTGACC
                                   T  G
GAM2364  TTTY9     3'  AGAAAACAGAAATATGCTG    55969        AGGC     CA
                                AGAGAACA   GGAATA  CTG
                                ||||||||   ||||||  |||
                                TCTTTTGT   CTTTAT  GAC
                                     _____     AC
GAM2364  LOC116411 5'  GAGGCCAAGGCGGGTTGCTGG  55970     AA       AATACA
                                GAG  CAAGGCGG     CTGG
                                |||  ||||||||     ||||
                                CTC  GTTCCGCC     GACC
                                  CG       CAAC__
GAM2364  LOC143196 5'  AGAAGTGCTGATACACTG    55971      CAAG  G  A
                                AGAA    GC GA TACACTG
                                ||||    || || |||||||
                                TCTT    CG CT ATGTGAC
                                  CA__  A  _
GAM2364  LOC144563 5'  AGAGGGGCAGGGCACACACTGG 55972      AACAA   _  A_
                                AGAG     GGC GG  ATACACTGG
                                ||||     ||| ||  |||||||||
                                TCTC     CCG CC  TGTGTGACC
                                  C_____   T  CG
GAM2364  LOC151632 5'  AGAGGGGCAGGGTACACACTGG 55973      AACAA     A__
                                AGAG     GGCGG   ATACACTGG
                                ||||     |||||   |||||||||
                                TCTC     CCGTC   TGTGTGACC
                                  C_____     CCA
GAM2364  LOC155179 3'  AGAGAACAGGCTGGGCTG     55960        A   _  AATACA
                                AGAGAACA GGC GG      CTG
                                |||||||| ||| ||      |||
                                TCTCTTGT CCG CC      GAC
                                     _   A  C______
GAM2364  LOC200904 5'  AGAGAGGCAGGGTACACACTGG 55974      ACAA     A__
                                AGAGA    GGCGG   ATACACTGG
                                |||||    |||||   |||||||||
                                TCTCT    CCGTC   TGTGTGACC
                                   _____     CCA
GAM2364  LOC203083 5'  AGAGGGGCAGGGTACACACTGG 55973      AACAA     A__
                                AGAG     GGCGG   ATACACTGG
                                ||||     |||||   |||||||||
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                                TCTC    CCGTC   TGTGTGACC
                                  C____    CCA
GAM2364  LOC219899 3'  AGAGAGGGCACATACACTG   55975     ACAA   GA
                                AGAGA   GGCG  ATACACTG
                                |||||   ||||  ||||||||
                                TCTCT   CCGT  TATGTGAC
                                  C___   G_
GAM2364  LOC219919 5'  AGAGGGGCAAGGTACACACTGG 55976     AA_    CGGA
                                AGAG   CAAGG   ATACACTGG
                                ||||   |||||   |||||||||
                                TCTC   GTTCC   TGTGTGACC
                                  CCC    A___
GAM2364  LOC221795 5'  AGAGGGGCAGGGTACACACTGG 55973     AACAA    A__
                                AGAG    GGCGG   ATACACTGG
                                ||||    |||||   |||||||||
                                TCTC    CCGTC   TGTGTGACC
                                  C____    CCA
GAM2364  LOC254176 5'  AGAGGGGCAGGGTACACACTGG 55973     AACAA    A__
                                AGAG    GGCGG   ATACACTGG
                                ||||    |||||   |||||||||
                                TCTC    CCGTC   TGTGTGACC
                                  C____    CCA
GAM2364  LOC256515 5'  AGAGGGGCAGGGTACACACTGG 55973     AACAA    A__
                                AGAG    GGCGG   ATACACTGG
                                ||||    |||||   |||||||||
                                TCTC    CCGTC   TGTGTGACC
                                  C____    CCA
GAM2364  LOC257206 3'  AAAGAATAAATAAAATACACTG 55977      C   GC
            G                    AGAGAA AAG  GGAATACACTGG
                                ||||||| |||  ||||||||||||
                                TTTCTT TTT  TTTTATGTGACC
                                   A  A_
GAM2364  LOC51125  3'  GAACAAGATAGAACACTGG   55978       GC   AT
                                GAACAAG  GGA  ACACTGG
                                |||||||  |||  |||||||
                                CTTGTTC  TCT  TGTGACC
                                    TA   __
GAM2364  LOC56181  5'  AAGGACAAGGCAGCCACTGG   55979    A       AATA
                                GAG ACAAGGCGG    CACTGG
                                ||| |||||||||    ||||||
                                TTC TGTTCCGTC    GTGACC
                                  C       G___
GAM2364  LOC91445  3'  AGAGAACAGAGCGGCACTG   55980       AG   AATA
                                AGAGAACA  GCGG    CACTG
                                ||||||||  ||||    |||||
                                TCTCTTGT  CGCC    GTGAC
                                    CT   _____
GAM2365  ACT     5'  TGAGTAGAATACTCAA     55983   C     AAGAA
                                A AGTAGA    ATACTCAA
                                | ||||||    ||||||||
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                                A TCATCT    TATGAGTT
                                 C    _____
GAM2365  AF1Q    3'  CACAGTAGGGAGAGAACA    55984        AA  _
                                TACAGTAG  AGA AATA
                                ||||||||  ||| ||||
                                GTGTCATC  TCT TTGT
                                    CC  C
GAM2365  ARCN1   3'  ATAGAAAGAAAAACCTAAAG  55985          T  TC
                                GTAGAAAGAAA AC  AAAG
                                ||||||||||| ||  ||||
                                TATCTTTCTTT TG  TTTC
                                      T  GA
GAM2365  BCL9    3'  CAGTTGAAAGAAAATAGTCCAA 55986      A       TAC__
            AG                    CAGT GAAAGAAA    TCAAAG
                                ||||| ||||||||    ||||||
                                GTCA CTTTCTTT    GGTTTC
                                  A       TATCA
GAM2365  CALB1   3'  TACATAGAAAGAAAATCCA   55987      G        TAC
                                TACA TAGAAAGAAA   TCA
                                |||| ||||||||||   |||
                                ATGT ATCTTTCTTT   GGT
                                  _        TA_
GAM2365  EIF2S3  3'  CAGCCTGGAGGTACTCAAAG  55988      AGAAA  AA
                                CAGT    GA  TACTCAAAG
                                ||||    ||  |||||||||
                                GTCG    CT  ATGAGTTTC
                                  GAC__  CC
GAM2365  NARS    3'  AGTAGAAAGAAAAACAGAAAG  55989          T  TC
                                AGTAGAAAGAAA AC  AAAG
                                |||||||||||| ||  ||||
                                TCATCTTTCTTT TG  TTTC
                                      T  TC
GAM2365  WNT1    3'  TACAGTGGAAGGAAATACT   55990       A   A
                                TACAGT GAA GAAATACT
                                |||||| ||| ||||||||
                                ATGTCA CTT CTTTATGA
                                    C   C
GAM2365  ZNF24   3'  TACAGTGGAAGAAATACC    55991       A   A
                                TACAGT GAA GAAATACT
                                |||||| ||| ||||||||
                                ATGTCA CTT CTTTATGG
                                    C   _
GAM2365  AFAP    3'  TACAGTAGAAAGAATAC     55992            A
                                TACAGTAGAAAGAA TAC
                                |||||||||||||| |||
                                ATGTCATCTTTCTT ATG
                                                _
GAM2365  CRMP5   3'  TACAGCAGGAGGAACACATCTC 55993        AAA  _  _
            AAAG                    TACAGTAG   GAA ATA CTCAAAG
                                ||||||||   ||| ||| |||||||
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                                ATGTCGTC  CTT TGT GAGTTTC
                                     CTC  G  A
GAM2365 DKFZP564O0423 3' GTGGAGGGAAGATACTCAAAG 55994    A AA  _
                                GT GA  GAA ATACTCAAAG
                                || ||  ||| ||||||||||
                                CA CT  CTT TATGAGTTTC
                                 C  CC  C
GAM2365 FLJ10482 3' AGCAGAAAGAGCACCTTCAA  55995        A_ AC
                                AGTAGAAAGA  AT  TCAA
                                ||||||||||  ||  ||||
                                TCGTCTTTCT  TG  AGTT
                                      CG  GA
GAM2365 FLJ10700 3' GTAAAGGAAGTACTCAAAG   55996     AA  A
                                GTAGA  GAA TACTCAAAG
                                |||||  ||| |||||||||
                                CATTT  CTT ATGAGTTTC
                                   C_  C
GAM2365 FLJ12969 5' GCAGAGGAAGCTCACTCAA   55997     __  AAA
                                GTAGA  AAG  TACTCAA
                                |||||  |||  |||||||
                                CGTCT  TTC  GTGAGTT
                                   CC  GA_
GAM2365 FLJ22344 3' TACAATAGAAGTATATATTCAA 55998        AGAA  C
           AG                     TACAGTAGAA   ATA TCAAAG
                                ||||||||||   ||| ||||||
                                ATGTTATCTT   TAT AGTTTC
                                     CATA  A
GAM2365 KIAA1764 3' ATAGAAAGAGACATTTCAAAG 55999        A  C_
                                GTAGAAAGA ATA  TCAAAG
                                ||||||||| |||  ||||||
                                TATCTTTCT TGT  AGTTTC
                                     C  AA
GAM2365 ZAP3    3' TACAGTGGAGGAAATACT    56000      A  AA
                                TACAGT GA  GAAATACT
                                |||||| ||  ||||||||
                                ATGTCA CT  CTTTATGA
                                   C  C_
GAM2365 LOC145845 3' ATAGAAAAAAATGCTTAAAG  56001         A  C
                                GTAGAAAGAAAT CT AAAG
                                |||||||||||| || ||||
                                TATCTTTTTTTA GA TTTC
                                      C  A
GAM2365 LOC149837 5' TACAGCAGAAACTCA      56002         AGAAAT
                                TACAGTAGAA    ACTCA
                                ||||||||||    |||||
                                ATGTCGTCTT    TGAGT
                                              _____
GAM2365 LOC196424 3' TACAGTAGAAATAAACCAA   56003         GAAAT  T
                                TACAGTAGAAA    AC CAA
                                ||||||||||    || |||
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                                ATGTCATCTTT    TG GTT
                                     ATT__  _
GAM2365  LOC200269 3'  TACAGCAGGAAGAATAGCCCAA 56004        A    ATA
           AG                     TACAGTAG AAGAA   CTCAAAG
                                  |||||||| |||||   |||||||
                                  ATGTCGTC TTCTT   GGGTTTC
                                      C    ATC
GAM2365  LOC253612 5'  TACAGTAGGAGAAACCAAA   56005        AA     ACT
                                  TACAGTAG  AGAAAT   CAAA
                                  ||||||||  ||||||   ||||
                                  ATGTCATC  TCTTTG   GTTT
                                      C_     ___
GAM2365  LOC255308 3'  CAGCCTGGAGGTACTCAAAG   55988     AGAAA  AA
                                  CAGT    GA  TACTCAAAG
                                  ||||    ||  |||||||||
                                  GTCG    CT  ATGAGTTTC
                                    GAC__  CC
GAM2365  LOC92710  5'  GTAGAAAGAGGTATTCAA    56006        AA  C
                                  GTAGAAAGA  TA TCAA
                                  |||||||||  || ||||
                                  CATCTTTCT  AT AGTT
                                       CC  A
GAM2366  CORO2A    3'  CTCCCAGAGTGCTGGGA     56009        C    A
                                  CTCCCAGAG TGCT GGA
                                  ||||||||| |||| |||
                                  GAGGGTCTC ACGA CCT
                                       _   C
GAM2366  CORO2A    3'  CTCCCAGAGTGCTGGGA     56009        C    A
                                  CTCCCAGAG TGCT GGA
                                  ||||||||| |||| |||
                                  GAGGGTCTC ACGA CCT
                                       _   C
GAM2366  EGFL5     5'  TCCCAGAACTGTTGCACGGT   56010         CTAGGAAC
                                  TCCCAGAGCTG       CGGT
                                  ||||||||||        ||||
                                  AGGGTCTTGAC       GCCA
                                       AACGT___
GAM2366  ITCH      3'  CTCCCAGAGTGCTAGGA     56011         C
                                  CTCCCAGAG TGCTAGGA
                                  ||||||||| ||||||||
                                  GAGGGTCTC ACGATCCT
                                       _
GAM2366  KDR       5'  CCCAGAACTCGGGAGCCGGT   56012        GCTA  A
                                  CCCAGAGCT   GGA CCGGT
                                  |||||||||   ||| |||||
                                  GGGTCTTGA   CCT GGCCA
                                       GC__   C
GAM2366  TBX6      3'  CTCCCAGAGTGCTGGGA     56009         C    A
                                  CTCCCAGAG TGCT GGA
                                  ||||||||| |||| |||
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                                GAGGGTCTC ACGA CCT
                                     _   C
GAM2366 ANKRD6   3' CCAGAGCTGTTAGCCAAT   56013       C  GAA
                                CCAGAGCTG TAG  CCGGT
                                ||||||||| |||  |||||
                                GGTCTCGAC ATC  GGTTA
                                    A  ____
GAM2366 ASB16    5' CTCCCAGAGCTGTGGAAGG   56014         CTA   CC
                                CTCCCAGAGCTG  GGAA  GG
                                ||||||||||||  ||||  ||
                                GAGGGTCTCGAC  CCTT  CC
                                      A__   __
GAM2366 ATP1B4   3' CCAGAGCTGTAGCTGCTGGT  56015       C  GAACC
                                CCAGAGCTG TAG    GGT
                                ||||||||| |||    |||
                                GGTCTCGAC ATC    CCA
                                     _  GACGA
GAM2366 DD96     5' CTCCTGGAGCTGCTGTGGA   56016     CA      A_
                                CTCC  GAGCTGCT  GGA
                                ||||  ||||||||  |||
                                GAGG  CTCGACGA  CCT
                                  AC       CA
GAM2366 DKFZP434C131 3' CCAGGGCAGCTAGGAGGCG   56017     A  T     AC
                                CCAG GC GCTAGGA  CG
                                |||| || |||||||  ||
                                GGTC CG CGATCCT  GC
                                  C  T      CC
GAM2366 DKFZP434C171 3' CTCCCAAGCTGCTGGGA    56018       G     A
                                CTCCCA AGCTGCT GGA
                                |||||| ||||||| |||
                                GAGGGT TCGACGA CCT
                                     _      C
GAM2366 DKFZP761C169 3' TCTAAAGCTGTTAGGAA    56019    CC     C
                                TC  AGAGCTG TAGGAA
                                ||  ||||||| ||||||
                                AG  TTTCGAC ATCCTT
                                 A_      A
GAM2366 FLJ13193  3' CTCCCAGAGTGCTGGGA    56009         C   A
                                CTCCCAGAG TGCT GGA
                                ||||||||| |||| |||
                                GAGGGTCTC ACGA CCT
                                     _   C
GAM2366 FLJ13441  3' CAGGGCTGCTAGGAAGCC   56020     A        _
                                CAG GCTGCTAGGAA CC
                                ||| |||||||||| ||
                                GTC CGACGATCCTT GG
                                  C         C
GAM2366 FLJ20150  3' CTCCTAAAGCTGCCCACTGGT  56021     C       AGGA  C
                                CTCC AGAGCTGCT   AC GGT
                                |||| |||||||||   || |||
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                                GAGG TTTCGACGG   TG CCA
                                  A       G___  A
GAM2366 KIAA1486 3' CTCCCAGAGTGCTGGGA    56009        C   A
                                CTCCCAGAG TGCT GGA
                                ||||||||| |||| |||
                                GAGGGTCTC ACGA CCT
                                      _   C
GAM2366 KIAA1872 3' CTCCCAGAGTGCTGGGA    56009        C   A
                                CTCCCAGAG TGCT GGA
                                ||||||||| |||| |||
                                GAGGGTCTC ACGA CCT
                                      _   C
GAM2366 KPNA6    3' CCAGAGCTGAAGGTTGGT    56022        CT  AACC
                                CCAGAGCTG  AGG   GGT
                                |||||||||  |||   |||
                                GGTCTCGAC  TCC   CCA
                                      T_  AA__
GAM2366 MDS028   3' TCTCAGGGTTGCTAGGAAC   56023    C   AGC
                                TC CAG   TGCTAGGAAC
                                || |||   ||||||||||
                                AG GTC   ACGATCCTTG
                                 A   CCA
GAM2366 MGC16037 3' CTCCCAGAGTGCTGGGA    56009        C   A
                                CTCCCAGAG TGCT GGA
                                ||||||||| |||| |||
                                GAGGGTCTC ACGA CCT
                                      _   C
GAM2366 RoXaN    3' CTCCCAGAGTGCTGGGA    56009        C   A
                                CTCCCAGAG TGCT GGA
                                ||||||||| |||| |||
                                GAGGGTCTC ACGA CCT
                                      _   C
GAM2366 TRIM11   3' TCCTGGAGTGCTAGAATTGGGG 56024    CA  C      ACC_
                T                TCC  GAG TGCTAGGA   GGT
                                ||| ||| ||||||||   |||
                                AGG  CTC ACGATCTT   CCA
                                  AC  _      AACC
GAM2366 UHRF2    5' CCTAGAGAGGAACCGG     56025    C   CTGCT
                                CC AGAG    AGGAACCGG
                                || ||||    |||||||||
                                GG TCTC    TCCTTGGCC
                                 A  _____
GAM2366 WBSCR23  3' CTCCCAGAGCGCTGGGA    56026        T   A
                                CTCCCAGAGC GCT GGA
                                |||||||||| ||| |||
                                GAGGGTCTCG CGA CCT
                                      _   C
GAM2366 LOC113763 3' CTCCTGGGGCTGCCAGCCAGT 56027    CAGA      GAA
                                CTCC   GCTGCTAG   CCGGT
                                ||||   ||||||||   |||||
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                                GAGG   CGACGGTC  GGTCA
                                  ACCC       ___
GAM2366  LOC123926 5'  CTCGGAGCTGCTCGGTCGGT  56028    CCA      A  AAC
                                CTC  GAGCTGCT GG  CGGT
                                |||  |||||||| ||  ||||
                                GAG  CTCGACGA CC  GCCA
                                  C__       G  A__
GAM2366  LOC146229 3'  CTCCCAGAGTGCTGGGA    56009        C   A
                                CTCCCAGAG TGCT GGA
                                ||||||||| |||| |||
                                GAGGGTCTC ACGA CCT
                                      _   C
GAM2366  LOC149345 3'  CTCTGGAGCTGCTGGCGCCGGC 56029    CCA      A  AA
                                CTC  GAGCTGCT GG  CCGGT
                                |||  |||||||| ||  |||||
                                GAG  CTCGACGA CC  GGCCG
                                  AC_       _  GC
GAM2366  LOC149506 3'  TCCCAGAGCTGTCGGGGGAA  56030         CTA__
                                TCCCAGAGCTG    GGAA
                                ||||||||||    ||||
                                AGGGTCTCGAC    CCTT
                                      AGCCC
GAM2366  LOC150225 3'  CCAGAGCATGGAACCGGT    56031       TGCTA
                                CCAGAGC    GGAACCGGT
                                |||||||    |||||||||
                                GGTCTCG    CCTTGGCCA
                                    TA___
GAM2366  LOC197335 3'  CTCCCAGAGTGCTGGGA    56009        C   A
                                CTCCCAGAG TGCT GGA
                                ||||||||| |||| |||
                                GAGGGTCTC ACGA CCT
                                      _   C
GAM2366  LOC201514 5'  TCCCGGAGCCGCTGGGAA    56032     A      A
                                TCCC GAGCTGCT GGAA
                                |||| |||||||| ||||
                                AGGG CTCGGCGA CCTT
                                  C       C
GAM2366  LOC221543 5'  CTCCCAGAGTGCTGGGA    56009        C   A
                                CTCCCAGAG TGCT GGA
                                ||||||||| |||| |||
                                GAGGGTCTC ACGA CCT
                                      _   C
GAM2366  LOC256980 3'  CTCCCAGAGTGCTGGGA    56009        C   A
                                CTCCCAGAG TGCT GGA
                                ||||||||| |||| |||
                                GAGGGTCTC ACGA CCT
                                      _   C
GAM2366  LOC257445 5'  CCAGGGCAGCTAGGAGGCG   56017     A  T     AC
                                CCAG GC GCTAGGA  CG
                                |||| || |||||||  ||
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                                GGTC CG CGATCCT  GC
                                  C T      CC
GAM2366  LOC257596 5'  CTCCCAGAGTGCTGGGA     56009         C    A
                                CTCCCAGAG TGCT GGA
                                ||||||||| |||| |||
                                GAGGGTCTC ACGA CCT
                                     _    C
GAM2366  LOC90573  3'  CTCCCAAGCTGCTAGGA     56033       G
                                CTCCCA AGCTGCTAGGA
                                |||||| ||||||||||
                                GAGGGT TCGACGATCCT
                                   _
GAM2367  CRY2      3'  CCTTCCCACTCTCAGATTTGC  56036          ATCATA
                                CCTTTCCACTCT     TTGC
                                ||||||||||||     ||||
                                GGAAGGGTGAGA     AACG
                                      GTCTA_
GAM2367  NBEA      3'  TTTCCACCAGAGATATTGC    56037        CTATC
                                TTTCCACT    ATATTGC
                                ||||||||    |||||||
                                AAAGGTGG    TATAACG
                                     TCTC_
GAM2367  SFPQ      3'  ACCTTTCCACTTTTCAAAAGC  56038          CTA   TATT
                                ACCTTTCCACT   TCA   GC
                                ||||||||||   |||   ||
                                TGGAAAGGTGA   AGT   CG
                                      AA_   TTT_
GAM2367  FEM-2     3'  CCTTGCCACTTTCAACTTTGC  56039      T    CTA   TA_
                                CCTT CCACT   TCA   TTGC
                                |||| |||||   |||   ||||
                                GGAA GGTGA   AGT   AACG
                                  C    A__   TGA
GAM2367  FLJ21016  5'  CCTTCCCATTCTGCTTTTGC  56040        C   ATCATA
                                CCTTTCCA TCT     TTGC
                                |||||||| |||     ||||
                                GGAAGGGT AGA     AACG
                                     A   CGAA__
GAM2367  FOXP1     3'  CCTTCCAAGGCCATATTG    56041        CTCTA
                                CTTTCCA    TCATATTG
                                |||||||    ||||||||
                                GGAAGGT    GGTATAAC
                                     TCC__
GAM2367  GDF11     3'  CCTCCCTCTGTTGTATTGC   56042      A   ATCA
                                TTTCC CTCT    TATTGC
                                ||||| ||||    ||||||
                                GGAGG GAGA    ATAACG
                                   _    CAAC
GAM2367  KIAA0010  3'  TTCCCACTTTAAAAGTATATTG 56043        C  TC___
              C                  TTTCCACT TA    ATATTGC
                                 |||||||| ||    |||||||
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                                AAGGGTGA AT    TATAACG
                                    A  TTTCA
GAM2367  KIAA1576  3'  ACTTTTCCACCTATGGTCTGC  56044    C     T   CATA
                                AC TTTCCAC CTAT   TTGC
                                || ||||||| ||||   ||||
                                TG AAAGGTG GATA   GACG
                                 A      _   CCA_
GAM2367  KIAA1954  5'  CCTTTCCACATACATTG     56045        TCTATC
                                CCTTTCCAC     ATATTG
                                |||||||||     ||||||
                                GGAAAGGTG     TGTAAC
                                      TA____
GAM2367  NCK1      3'  TTTCCACTTATTATTG      56046        C   CA
                                TTTCCACT TAT  TATTG
                                |||||||| |||  |||||
                                AAAGGTGA ATA  ATAAC

                                   _  __
GAM2367  OLFM3     5'  ACCTTTCCCTCGTCAGTTGC   56047        A   TA   TA
                                ACCTTTCC CTC  TCA  TTGC
                                |||||||| |||  |||  ||||
                                TGGAAAGG GAG  AGT  AACG
                                   _  C_  C_
GAM2367  RHOBTB2   3'  CCTTTCCACGTCTGGCCTTTTG 56048         _  ATCATA
           C                     CCTTTCCAC TCT     TTGC
                                |||||||| |||     ||||
                                GGAAAGGTG AGA     AACG
                                     C   CCGGAA
GAM2367  LOC115286 3'  ACCTTTCCATTTCATCCTGC   56049        CTCTA   A
                                ACCTTTCCA    TCAT TTGC
                                |||||||||    |||| ||||
                                TGGAAAGGT    AGTA GACG
                                     AA___    G
GAM2367  LOC146909 3'  CCTTTCCATTCCTCCGGTTGC  56050        C   A  ATA
                                CCTTTCCA TCT TC   TTGC
                                |||||||| ||| ||   ||||
                                GGAAAGGT AGG AG   AACG
                                   A  _  GCC
GAM2367  LOC148936 5'  TTTCTTTTCTATCACATTG    56051     CAC
                                TTTC   TCTATCATATTG
                                ||||   ||||||||||||
                                AAAG   AGATAGTGTAAC
                                  AAA
GAM2367  LOC148938 5'  TTTCTTTTCTATCACATTG    56051     CAC
                                TTTC   TCTATCATATTG
                                ||||   ||||||||||||
                                AAAG   AGATAGTGTAAC
                                  AAA
GAM2367  LOC220929 5'  AACCTTTCCTACTCTGTATTG  56052         _    ATCA
                                AACCTTTCC ACTCT    TATTG
                                |||||||| |||||    |||||
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                                TTGGAAAGG TGAGA    ATAAC
                                     A    C___
GAM2367  LOC252983 3'  CCTTTCCATTTCATCTG     56053        CTCTA    A
                                CCTTTCCA     TCAT TTG
                                ||||||||     |||| |||
                                GGAAAGGT     AGTA GAC
                                     AA___    _
GAM2367  LOC93538  3'  AACCTTTCTGTGTCTATCAT   56054        CAC_
                                AACCTTTC    TCTATCAT
                                ||||||||    ||||||||
                                TTGGAAAG    AGATAGTA
                                     ACAC
GAM2368  MORC      3'  TACTATGACTAAATAATAAAAT 56057        TGGCT
            TA                    TACTATG     ATAATAAAATTA
                                ||||||||    ||||||||||||
                                ATGATAC     TATTATTTTAAT
                                     TGATT
GAM2368  FLJ14957  3'  TATGTATATATAATAAAATTA  56058       GC
                                TATGTG  TATAATAAAATTA
                                ||||||  ||||||||||||
                                ATACAT  ATATTATTTTAAT
                                    AT
GAM2368  FLJ22944  3'  TACTATGTGGCTATACAAA    56059            A
                                TACTATGTGGCTATA TAAA
                                |||||||||||||| ||||
                                ATGATACACCGATAT GTTT
                                                _
GAM2368  KIAA0766  3'  CTATGTGAGCTTCTGCAAATT  56060        _   ATAATA
                                CTATGTG GCT      AAATT
                                ||||||| |||      |||||
                                GATACAC CGA      TTTAA
                                     T   AGACG_
GAM2368  KLF12     3'  CATGTTGTCCATAATAAAATTA 56061       GG_
                                TATGT   CTATAATAAAATTA
                                |||||   ||||||||||||||
                                GTACA   GGTATTATTTTAAT
                                   ACA
GAM2368  PPIL4     3'  TATGTATAACAATAAAATTA   56062       GCT
                                TATGTG   ATAATAAAATTA
                                ||||||   ||||||||||||
                                ATACAT   TGTTATTTTAAT
                                    AT_
GAM2368  LOC153443 3'  TACTTAAAACTATAATAAAATT 56063      A  TG
            A                    TACT TG  GCTATAATAAAATTA
                                ||||  ||  |||||||||||||||
                                ATGA AT  TGATATTATTTTAAT
                                  _  TT
GAM2368  LOC221154 3'  TACTAAGTTCTTTAATAAAATT 56064       T  GG  A
            A                    TACTA GT  CT TAATAAAATTA
                                |||||  ||  ||  ||||||||||
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                                ATGAT CA  GA ATTATTTTAAT
                                   T A_  A
GAM2369  CCND1    3'  TTAAAAATAAACTGTAT     56067          A
                                TTAAAAATAGA CTGTAT
                                |||||||||| ||||||
                                AATTTTTATTT GACATA
                                          _
GAM2369  P29      3'  TTAAAAAGGGAACTGTACA   56068        TA
                                TTAAAAA  GAACTGTATA
                                |||||||  ||||||||||
                                AATTTTT  CTTGACATGT
                                    CC
GAM2369  KIAA1718 3'  TTAAAAATGAACTGATAC    56069        A     T
                                TTAAAAAT GAACTG ATAC
                                |||||||| |||||| ||||
                                AATTTTTA CTTGAC TATG
                                         _     _
GAM2369  PRC1     3'  TTAAAAACAGGACACGTACTGT 56070          A _    AC
            AT                    TTAAAAATAG AC TGTAT  GTAT
                                |||||||||| || |||||  ||||
                                AATTTTTGTC TG GCATG  CATA
                                      C  T    A_
GAM2369  LOC203411 3'  CTAAAAATAGAACAAATACTGT 56071            TGT   _
            AT                    TTAAAAATAGAAC   ATAC GTAT
                                |||||||||||||   |||| ||||
                                GATTTTTATCTTG   TATG CATA
                                       TT_   A
GAM2370  HMOX1    3'  TGGTCATGGCCGTGTCAAC   56074     C   AT   A
                                TGG CATG  CGT TCAAT
                                ||| ||||  ||| |||||
                                ACC GTAC  GCA AGTTG
                                  A   CG   C
GAM2370  IGFBP4   3'  TGGCTGTGACCACAAATGGGGT 56075     CA     TAT   TAA_
                                TGGC  TGATCG   CAA   GGT
                                ||||  ||||||   |||   |||
                                ACCG  ACTGGT   GTT   CCA
                                  AC     ___   TACC
GAM2370  RASSF1   3'  TGGCTTTGATTAGCAAATAAGG 56076     CA   C_   TC
            T                     TGGC  TGAT  GTA  AATAAGGT
                                |||| ||||  |||  ||||||||
                                ACCG  ACTA  CGT  TTATTCCA
                                  AA   AT   __
GAM2370  FLJ10546 3'  TGGCCATAAACAATGAGG    56077         TCGTAT   A
                                TGGCCATGA     CAAT AGG
                                |||||||||     |||| |||
                                ACCGGTATT     GTTA TCC
                                      T_____    C
GAM2370  LOC143310 3'  TGGCCATGCTTTTCATAAGGT  56078         ATCGTA   A
                                TGGCCATG     TCA TAAGGT
                                ||||||||     ||| ||||||
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                                ACCGGTAC     AGT ATTCCA
                                    GAAA__  _
GAM2370  LOC220549 5'  TGGCCATGTCGTGTCGGGGAAG 56079        A   A  AAT_
             GT                   TGGCCATG TCGT TC    AAGGT
                                  |||||||| |||| ||   |||||
                                  ACCGGTAC AGCA AG    TTCCA
                                      _   C  CCCC
GAM2371  IDH3A    3'  TACATTTGTGTCTTTGTA    56082      C  C
                                  TACGT TG GTCTTTGTA
                                  ||||| || |||||||||
                                  ATGTA AC CAGAAACAT
                                    A  A
GAM2371  INHBB    3'  CGTCTCTGTCTTTGTGCTTT   56083      GC      AA
                                  CGTCT  GTCTTTGT  GTTTT
                                  |||||  ||||||||  |||||
                                  GCAGA  CAGAAACA  CGAAA
                                    GA      __
GAM2371  FLJ11726  3'  GTCTTTGTGTCTTTGTCAGT   56084     GC__      A
                                  GTCT    GTCTTTGT AGT
                                  ||||    |||||||| |||
                                  CAGA    CAGAAACA TCA
                                    AACA       G
GAM2371  FLJ20477  3'  TGCATATCTTTGTAAGTTTT   56085     __
                                  TGC  GTCTTTGTAAGTTTT
                                  |||  ||||||||||||||
                                  ACG  TAGAAACATTCAAAA
                                    TA
GAM2371  moblak    3'  ACGTCTGCGTCTGTAGTTTT   56086          TT   A
                                  ACGTCTGCGTCT  GTA GTTTT
                                  ||||||||||||  ||| |||||
                                  TGCAGACGCAGA  CAT CAAAA
                                        __  _
GAM2371  LOC196047 5'  TCTGTGTCTTTGGCTTT     56087      C      TAA
                                  TCTG GTCTTTG   GTTTT
                                  |||| |||||||   |||||
                                  AGAC CAGAAAC   CGAAA
                                    A      ___
GAM2372  GRSF1     3'  TCTGACATGTCACTTCAC     56090     GC       G GACC
                                  TC  GACATGTCG C    CAC
                                  ||  ||||||||| |    |||
                                  AG  CTGTACAGT G    GTG
                                   A_        _ AA__
GAM2372  LOC196326 5'  CATCGCGGTGTGTCGGCG     56091        ACA
                                  TATCGCG   TGTCGGCG
                                  |||||||   ||||||||
                                  GTAGCGC   ACAGCCGC
                                      CAC
GAM2373  BTG2      3'  TATTAAAGTAACAAAAAGGTGT 56094       T
                                  TGTTG GGTAACAAAAAGGTGT
                                  ||||| ||||||||||||||||
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                                ATAAT TCATTGTTTTTCCACA
                                  T
GAM2373 BICD2    3' AATGATTACTAACAAAAAGGTG 56095     TTG  G
             T                   AATG   TG TAACAAAAAGGTGT
                                 ||||   || ||||||||||||||
                                 TTAC   AT ATTGTTTTTCCACA
                                   TA_  G
GAM2373 KIAA0451  5' AATGTTGTGTTGATAACCCAGT 56096        ___    AAAAA
                                 AATGTTGTG   GTAAC    GGT
                                 |||||||||   |||||    |||
                                 TTACAACAC   TATTG    TCA
                                      AAC    GG___
GAM2373 LOC150622 3' TGTTTGGGAAAGAAAAGGTGT  56097     G   T  CA
                                 TGTT TGG AA  AAAAGGTGT
                                 |||| ||| ||  |||||||||
                                 ACAA ACC TT  TTTTCCACA
                                   _   C  TC
GAM2373 LOC152674 3' AATGATTTGCAGCAAGGAGGTG 56098     __  TG   CAAAA
             T                   AATG  TTG  GTAA    AGGTGT
                                 ||||  |||  ||||    ||||||
                                 TTAC  AAC  CGTT    TCCACA
                                   TA   GT   CC___
GAM2373 LOC201283 3' AATGTTGTGGTAGTGTAAGG   56099          ACAAA
                                 AATGTTGTGGTA    AAGG
                                 ||||||||||||    ||||
                                 TTACAACACCAT    TTCC
                                       CACA_
GAM2373 LOC257482 3' ATGTAGTGGTAACAGGT     56100      T       AAAA
                                 ATGT GTGGTAACA    GGT
                                 |||| |||||||||    |||
                                 TACA CACCATTGT    CCA
                                   T       ____
GAM2374 CDS2     3' TTAAGCAGGACTTTGTG     56103         A   CC  C
                                 TTAAGCAG ACT  TG TG
                                 |||||||| |||  || ||
                                 AATTCGTC TGA  AC AC
                                      C   A_  _
GAM2374 CELSR3   3' TGTTAAACGGGACTCAAGGCTG 56104        AGA    CT_
             ACC                   TGTTAAGC   ACTC   GCTGACC
                                   ||||||||   ||||   |||||||
                                   ACAATTTG   TGAG   CGACTGG
                                      CCC    TTC
GAM2374 ITCH     3' TGTTAAGCAAGGTTCTGAC   56105         AACTCCTG
                                 TGTTAAGCAG       CTGAC
                                 ||||||||||       |||||
                                 ACAATTCGTT       GACTG
                                       CCAA____
GAM2374 MEST     3' TTAGTCAGAGCTCCTGCTG   56106     AG    A
                                 TTA  CAGA CTCCTGCTG
                                 |||  |||| |||||||||
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                                AAT  GTCT GAGGACGAC
                                  CA    C
GAM2374  DKFZP434O047 3'  TGTTCATGTTTTCCTGCTGACC 56107      AAGCAGAAC
                                TGTT        TCCTGCTGACC
                                ||||        ||||||||||
                                ACAA        AGGACGACTGG
                                  GTACAAA__
GAM2374  DKFZp761G0313 3'  GTTAAGCAGGACTTGAC     56108          A   CCTGC
                                GTTAAGCAG ACT     TGAC
                                ||||||||| |||     ||||
                                CAATTCGTC TGA     ACTG
                                      C  _____
GAM2374  FLJ11618  3'  TGTTGGTCATCTCCTGCTGGCC 56109      AAG  GAA       A
                                TGTT   CA   CTCCTGCTG CC
                                ||||   ||   ||||||||| ||
                                ACAA   GT   GAGGACGAC GG
                                  CCA  A__        C
GAM2374  KIAA0806  3'  TGTTAAGCAGCAATGTGAC    56110          AACTCC  C
                                TGTTAAGCAG      TG TGAC
                                ||||||||||      || ||||
                                ACAATTCGTC      AC ACTG
                                      GTT___  _
GAM2374  KIAA0826  5'  TGTGAATCAGTGCTCCTGCTGA 56111     T  G   AA
                                TGT AA CAG  CTCCTGCTGA
                                ||| || |||  ||||||||||
                                ACA TT GTC  GAGGACGACT
                                  C  A   AC
GAM2374  TA-PP2C   3'  TGTTAAGCAGCACTCCAGCTGA 56112          A     T
            CC                    TGTTAAGCAG ACTCC GCTGACC
                                ||||||||||| ||||| |||||||
                                ACAATTCGTC TGAGG CGACTGG
                                      G     T
GAM2374  LOC124044 3'  TGGAAAGGCTCCTGCTGGCC   56113    TT   CAGAA       A
                                TG  AAG     CTCCTGCTG CC
                                ||  |||     ||||||||| ||
                                AC  TTC     GAGGACGAC GG
                                  CT   C____        C
GAM2374  LOC147790 5'  TGTAGAGTTCCTCCTGCTGACC 56114     TA  CAGAA
                                TGT  AG     CTCCTGCTGACC
                                |||  ||     ||||||||||||
                                ACA  TC     GAGGACGACTGG
                                  TC  AAG__
GAM2374  LOC149832 5'  TGTGGGCAGAACTTCTAGGCT  56115     TAA       C  __
                                TGT   GCAGAACT CT  GCT
                                |||   |||||||| ||  |||
                                ACA   CGTCTTGA GA  CGA
                                  CC_       A  TC
GAM2374  LOC159091 5'  GTTAGGCAGAACTGGCT     56116      A       CCT
                                GTTA GCAGAACT   GCT
                                ||||  ||||||||   |||
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                                CAAT CGTCTTGA   CGA
                                  C       C__
GAM2374  LOC200609 5'  TGTGGGCAGAACTTCATTGCTG 56117     TAA       _ C_
                                TGT   GCAGAACT C  TGCTG
                                |||   |||||||| |  |||||
                                ACA   CGTCTTGA G  ACGAC
                                  CC_       A TA
GAM2374  LOC256940 5'  TGTGGAGCAGAACCTGAC    56118     TA       TCCTG
                                TGT  AGCAGAAC    CTGAC
                                |||  ||||||||    |||||
                                ACA  TCGTCTTG    GACTG
                                  CC       _____
GAM2374  LOC257017 5'  TGTAAGCACTGCTGA       56119     T    GAACTC
                                TGT AAGCA     CTGCTGA
                                ||| |||||     |||||||
                                ACA TTCGT     GACGACT
                                  _    _______
GAM2374  LOC91807  5'  TGTTAAGCAGGTCTTGCC    56120          AAC  C
                                TGTTAAGCAG   TC TGCT
                                ||||||||||   || ||||
                                ACAATTCGTC   AG ACGG
                                      C__  A
GAM2375  CLASP1    5'  TCAATATCACTTCGAGA     56123       C       A
                                TCAATA CATTTCGA GA
                                |||||| |||||||| ||
                                AGTTAT GTGAAGCT CT
                                   A       _
GAM2375  HEPH      3'  TCAATACCTTCCAAGTGT    56124        AT   G   A
                                TCAATACC  TTC AAG GT
                                ||||||||  ||| ||| ||
                                AGTTATGG  AAG TTC CA
                                     __   G   A
GAM2375  HEPH      3'  TCAATACCTTCCAAGTGT    56124        AT   G   A
                                TCAATACC  TTC AAG GT
                                ||||||||  ||| ||| ||
                                AGTTATGG  AAG TTC CA
                                     __   G   A
GAM2375  ZNF215    3'  AATATCAACTCCAAGAGTAT   56125     C  T   G
                                AATA CA TTC AAGAGTAT
                                |||| || ||| ||||||||
                                TTAT GT GAG TTCTCATA
                                  A  T   G
GAM2375  FLJ12643  3'  TCAAAATCACATCCAAGAGTAT 56126     TAC   T  G
            CA                    TCAA   CAT TC AAGAGTATCA
                                ||||   ||| || ||||||||||
                                AGTT   GTG AG TTCTCATAGT
                                  TTA   T  G
GAM2375  STK38L    3'  TCAATACCATTTCAAGAATA   56127           G
                                TCAATACCATTTC AAGAGTA
                                |||||||||||| |||||||
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                                AGTTATGGTAAAG TTCTTAT
                                        _
GAM2375 LOC166647 5'  TCAGTGGCATCCTAAGAGTATC 56128    ATAC    CG
            A                   TCA   CATTT  AAGAGTATCA
                                |||   |||||  ||||||||||
                                AGT   GTAGG  TTCTCATAGT
                                  CACC    A_
GAM2376 ADRBK2   3'  AGCTGACCCCAAGCCGAAGGGT 56131    A_      AAGCT  _
            CC                  GGC  ACCCCAAGC    GG CC
                                |||  |||||||||    || ||
                                TCG  TGGGGTTCG    CC GG
                                  AC       GCTTC  A
GAM2376 B4GALT2  3'  AGGCAGTGCAGGGGCTGGCCC  56132     ACCCCAA   A__
                                AGGCA     GCA   GCTGGCCC
                                |||||     |||   ||||||||
                                TCCGT     CGT   CGACCGGG
                                   CA_____   CCC
GAM2376 B4GALT2  3'  AGGCAGTGCAGGGGCTGGCCC  56132     ACCCCAA   A__
                                AGGCA     GCA   GCTGGCCC
                                |||||     |||   ||||||||
                                TCCGT     CGT   CGACCGGG
                                   CA_____   CCC
GAM2376 CACNB1   3'  AGGCAACCCCTGGGCACCATCC 56133        AA_  AA   GG
                                AGGCAACCCC   GC  GCT  CC
                                ||||||||||   ||  |||  ||
                                TCCGTTGGGG   CG  TGG  GG
                                      ACC  __   TA
GAM2376 CHD2     3'  AGACAACTTCAAGCAAGCT    56134       CC
                                AGGCAAC  CAAGCAAGCT
                                |||||||  ||||||||||
                                TCTGTTG  GTTCGTTCGA
                                    AA
GAM2376 DGCR6    3'  AAGCAGACAGCAGCAGGCTGGC 56135      _  CCCA    A
            CC                    AGGCA AC    AGCA GCTGGCCC
                                  ||||| ||    |||| ||||||||
                                  TTCGT TG    TCGT CGACCGGG
                                    C  TCG_    C
GAM2376 EFNB1    3'  GCACAGCGGGCTGGCCC     56136     A CCCA   AA
                                GCA C    AGC  GCTGGCCC
                                ||| |    |||  ||||||||
                                CGT G    TCG  CGACCGGG
                                  _ ____   CC
GAM2376 EGFL4    3'  GGCTGACCCCAGGCAGGCGCC  56137     A_     A   A  TG
                                GGC  ACCCCA GCA GC  GCC
                                |||  |||||| ||| ||  |||
                                CCG  TGGGGT CGT CG  CGG
                                  AC     C   C  __
GAM2376 EIF4G1   3'  AGGCAGCCCCAAGCCATCCTGC 56138      A       AAG  G
            C                    AGGCA CCCCAAGC   CT GCC
                                 ||||| ||||||||   || |||
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                                TCCGT GGGGTTCG   GG CGG
                                  C       GTA  A
GAM2376  GFRA2    3'  AGCCAGCCTCAGGCACAGCCC  56139    G  A  C  A   AGC
                                AG CA CC CA GCA   TGGCCC
                                || || || || |||   ||||||
                                TC GT GG GT CGT   GTCGGG
                                 G  C  A  C  ___
GAM2376  GNA11    5'  GGCAGCCCCAAGCAGCCAGTGT 56140         A  _______    III
            TGGCCCG                  CCCAAGCA GCT     GGCCC   G
                                |||||||| |||     |||||  |
                                GGGTTCGT CGG     CCGGG   C
                                     _  TCACAA    III
GAM2376  GNA15    5'  GGCAACCCCCAGCCCAGCCGGC 56141         A  A_
            CC                    GGCAACCCC AGC  AGCTGGCCC
                                ||||||||| |||  |||||||||
                                CCGTTGGGG TCG  TCGGCCGGG
                                     G   GG
GAM2376  GNB2     5'  AGGCAGCTCCTGGCCGCTGGCC 56142      ACC  AA  AA
            C                     AGGCA   CC  GC  GCTGGCCC
                                |||||   ||  ||  ||||||||
                                TCCGT   GG  CG  CGACCGGG
                                  CGA  AC  G_
GAM2376  HIP12    3'  AGGGAGCCCCACGCTGGCC   56143     CAA    AGCAA
                                AGG   CCCCA    GCTGGCC
                                |||   |||||    |||||||
                                TCC   GGGGT    CGACCGG
                                  CTC    G____
GAM2376  HOXA3    3'  GGCAGCCCAGCTGGCC      56144      A   CAAGCA
                                GGCA CCC     AGCTGGCC
                                |||| |||     ||||||||
                                CCGT GGG     TCGACCGG
                                  C  _______
GAM2376  LCP1     3'  GGAAGCCACAACAAGCTGG   56145    C  C  CA
                                GG AA CC  AGCAAGCTGG
                                || || ||  ||||||||||
                                CC TT GG  TTGTTCGACC
                                 _  C  TG
GAM2376  LTK      3'  AGGCCAGCCCCGAGACAGGCCC 56146      AA_   A  CAA  T
                                AGGC   CCCC AG   GC GGCCC
                                ||||   |||| ||   || |||||
                                TCCG   GGGG TC   TG CCGGG
                                  GTC    C  ___  T
GAM2376  NDUFA10  3'  GGCTGCCGAGAGCTGGCC    41579     AACC  A  CA
                                GGC    CC AG  AGCTGGCC
                                |||    || ||  ||||||||
                                CCG    GG TC  TCGACCGG
                                  AC__  C  __
GAM2376  PCSK5    5'  GGCGCCCCCTCTGCTGGCCC   56147     AA   AAGCAA
                                GGC  CCCC     GCTGGCCC
                                |||  ||||     ||||||||
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                                CCG  GGGG     CGACCGGG
                                  CG   AGA___
GAM2376  PIK3R3   3'  AGCCAGCCCCAAGCTGCT    56148    G  A      AA
                                AG CA CCCCAAGC  GCT
                                || || ||||||||  |||
                                TC GT GGGGTTCG  CGA
                                 G  C       A_
GAM2376  PMP2     3'  GGAGCCCCTTCAAGCTGGC   56149    CAA   AAG
                                GG   CCCC   CAAGCTGGC
                                ||   ||||   |||||||||
                                CC   GGGG   GTTCGACCG
                                 TC_    AA_
GAM2376  POU5F1   5'  AGGCGCCCCAAGCCGGGGGCC  56150     AA      AAGCT
                                AGGC  CCCCAAGC    GGCC
                                ||||  ||||||||    ||||
                                TCCG  GGGGTTCG    CCGG
                                  C_      GCCC_
GAM2376  POU5F1   5'  AGGCGCCCCAAGCCGGGGGCC  56150     AA      AAGCT
                                AGGC  CCCCAAGC    GGCC
                                ||||  ||||||||    ||||
                                TCCG  GGGGTTCG    CCGG
                                  C_      GCCC_
GAM2376  PREB     3'  AGGCAACCTCAGCTGTGGACCC 56151        CCA   AAGC  _
                                AGGCAACC   AGC    TGG CCC
                                ||||||||   |||    ||| |||
                                TCCGTTGG   TCG    ACC GGG
                                     AG_   AC__   T
GAM2376  PRKCABP  3'  AGGCGCCCCAAGCCAGCAGGCC 56152     AA      A   T
                                AGGC  CCCCAAGC AGC GGCC
                                ||||  |||||||| ||| ||||
                                TCCG  GGGGTTCG TCG CCGG
                                  C_      G   T
GAM2376  PSEN1    3'  AAGCAACCTCAGGTTCAGACTG 56153        C  AG__  AG
            GCC                   AGGCAACC CA    CA  CTGGCC
                                ||||||||  ||    ||  ||||||
                                TTCGTTGG GT    GT  GACCGG
                                     A  CCAA  CT
GAM2376  PSEN1    3'  AAGCAACCTCAGGTTCAGACTG 56153        C  AG__  AG
            GCC                   AGGCAACC CA    CA  CTGGCC
                                ||||||||  ||    ||  ||||||
                                TTCGTTGG GT    GT  GACCGG
                                     A  CCAA  CT
GAM2376  RCN1     5'  GGCTAACCCCAGGCGGCC    56154    _      A  AAGCT
                                GGC AACCCCA GC    GGCC
                                ||| |||||||  ||    ||||
                                CCG TTGGGGT CG    CCGG
                                  A      C  _____
GAM2376  RXRA     3'  GGAGGCCCCAAGCCCCGCCC   56155    CAA      AAG  G
                                GG   CCCCAAGC   CT GCCC
                                ||   ||||||||   || ||||
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                                CC  GGGGTTCG  GG CGGG
                                 TCC      ___  G
GAM2376 SH3GL1   3' AGGCAGATCCCAGCTGGCC  56156     AC_   AGCAA
                                AGGCA  CCCA   GCTGGCC
                                |||||  ||||   |||||||
                                TCCGT  GGGT   CGACCGG
                                  CTA  _____
GAM2376 TFEB     5' GGCAGCCCCAAGCCAGGCCC  56157     A      AAGCT
                                GGCA CCCCAAGC   GGCCC
                                |||| ||||||||   |||||
                                CCGT GGGGTTCG   CCGGG
                                  C      GT___
GAM2376 TNFRSF8  3' AGGGGCCCCGGGAGCTGGCC  56158    CAA   AAGCA
                                AGG  CCCC   AGCTGGCC
                                |||  ||||   ||||||||
                                TCC  GGGG   TCGACCGG
                                 CC_   CCC__
GAM2376 UROS     3' AGGCCAGCCCCAGGTCAGGTCC 56159     AA_   AG_  AGCT  _
                                AGGC  CCCCA  CA   GG CC
                                ||||  |||||  ||   || ||
                                TCCG  GGGGT  GT   CC GG
                                  GTC   CCA  _____  A
GAM2376 USP6     5' AGGCAACCCAGGCAGAGCT   56160       CAA  _
                                AGGCAACCC  GCA AGCT
                                |||||||||  ||| ||||
                                TCCGTTGGG  CGT TCGA
                                     TC_  C
GAM2376 ZNF134   5' AGCAACCCCGAGCTTCTG    56161       A  AAG
                                GGCAACCCC AGC  CTG
                                ||||||||| |||  |||
                                TCGTTGGGG TCG  GAC
                                     C  AA_
GAM2376 ANGPTL4  3' GGCTGGCCCCAAGTGGTCC   56162    AA_     CAAGC  _
                                GGC  CCCCAAG   TGG CC
                                |||  |||||||   ||| ||
                                CCG  GGGGTTC   ACC GG
                                 ACC      _____  A
GAM2376 APELIN   5' GGCAGCGCCGCGAAGCTGGCC  56163    ACC  AA  _
                                GGCA  CC  GC AAGCTGGCC
                                ||||  ||  || |||||||||
                                CCGT  GG  CG TTCGACCGG
                                  CGC  __  C
GAM2376 C20orf161 3' GGCAACCCCAGCCAAAGCT   56164       A  __
                                GGCAACCCCA GC  AAGCT
                                |||||||||| ||  |||||
                                CCGTTGGGGT CG  TTCGA
                                      _  GT
GAM2376 C4orf6   3' AAGCAACCTCAGGCAAACT   56165       C  A
                                AGGCAACC CA GCAAGCT
                                |||||||| || |||||||
```

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                                TTCGTTGG GT CGTTTGA
                                    A  C
GAM2376 DGCR6L   3' AAGCAGACAGCAGCAGGCTGGC 56135      _ CCCA   A
           CC                    AGGCA AC   AGCA GCTGGCCC
                                 |||||  ||   ||||  ||||||||
                                 TTCGT TG   TCGT CGACCGGG
                                   C  TCG_   C
GAM2376 DKFZP564M182 5' GCAACCCCACTGCTGGC     56166         AGCAA
                                 GCAACCCCA    GCTGGC
                                 |||||||||    ||||||
                                 CGTTGGGGT    CGACCG
                                      GA___
GAM2376 DKFZP586J1624 3' GGCAGCCCGGCGACGCTGGCCC 56167     A   CAA  AA_
                                 GGCA CCC   GC   GCTGGCCC
                                 ||||  |||   ||   ||||||||
                                 CCGT GGG   CG   CGACCGGG
                                   C   C__  CTG
GAM2376 DKFZP762D096 5' GGCGGCCCCGGCGCTGGCCC   56168    AA   AA  AA
                                 GGC  CCCC  GC  GCTGGCCC
                                 |||  ||||  ||  ||||||||
                                 CCG  GGGG  CG  CGACCGGG
                                   CC   C_  __
GAM2376 FEM-2    3' AGGGGGCCCCATACTGGCC   56169    CAA    AGCAA
                                 AGG   CCCCA    GCTGGCC
                                 |||   |||||    |||||||
                                 TCC   GGGGT    TGACCGG
                                   CCC    A____
GAM2376 FLJ00001 3' AGGCAGCCCAAGCAGGGGC   56170      AC      AGCT
                                 AGGCA  CCCAAGCA   GGC
                                 |||||  ||||||||   |||
                                 TCCGT  GGGTTCGT   CCG
                                    C_      CC__
GAM2376 FLJ10140 3' GGCAGCAGCAAGCTGGCCC   56171     ACCCCA
                                 GGCA     AGCAAGCTGGCCC
                                 ||||     ||||||||||||
                                 CCGT     TCGTTCGACCGGG
                                   CG____
GAM2376 FLJ10251 3' AGCTTCCACAGCTGGCCC    56172    AA  CCAA   A
                                 GGC  CC    GCA GCTGGCCC
                                 |||  ||    ||| ||||||||
                                 TCG  GG    TGT CGACCGGG
                                   AA  ____   _
GAM2376 FLJ12132 3' AGGCTGGCCTCCTCCCGCTGGC 56173      AA_  _  AAGCAA
           CC                    AGGC   CC CC     GCTGGCCC
                                 ||||   || ||     ||||||||
                                 TCCG   GG GG     CGACCGGG
                                   ACC  A  AGGG__
GAM2376 FLJ12666 3' AGCCAACCCTGATGCTCCTGGC 56174    G     CAA_  AAG
                                 AG CAACCC    GC   CTGGC
                                 ||  ||||||    ||   |||||
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                                TC GTTGGG   CG  GACCG
                                 G     ACTA  AG_
GAM2376  FLJ13162  3'  AGCAACCCCGAGCTCTGCC   56175        A  AAG  G
                                GGCAACCCC AGC  CTG CC
                                ||||||||| |||  ||| ||
                                TCGTTGGGG TCG  GAC GG
                                     C  A__  _
GAM2376  FLJ13265  3'  AGGCGGCGGCAAGGCTGGCCC  56176     AACCCCAA   _
                                AGGC       GCAAG CTGGCCC
                                ||||       ||||| |||||||
                                TCCG       CGTTC GACCGGG
                                  CCGC____    C
GAM2376  FLJ14326  3'  AGGTAACCCCAAGCAGGC    56177     C        A
                                AGG AACCCCAAGCA GC
                                ||| ||||||||||| ||
                                TCC TTGGGGTTCGT CG
                                  A         C
GAM2376  FLJ14327  3'  AGGTGCTCCAAGAACACTGGCC 56178    CAACC    CAA
            C                    AGG    CCAAG   GCTGGCCC
                                |||    |||||  ||||||||
                                TCC    GGTTC   TGACCGGG
                                 ACGA_    TTG
GAM2376  FLJ21988  3'  AGGCAACCCCCGGGACAGGCT   56179        AA_  A
                                AGGCAACCCC   GCA GCT
                                ||||||||||  ||| |||
                                TCCGTTGGGG   TGT CGA
                                     CCC   C
GAM2376  FLJ30663  5'  GGCCGACCCCGGGCTCCGGC   56180    A_    AA  AAG
                                GGC  ACCCC  GC   CTGGC
                                |||  |||||  ||   |||||
                                CCG  TGGGG  CG   GGCCG
                                  GC    CC  A__
GAM2376  GIT1     3'  AGCCAGCCCCAGGCTCAGGTGC 56181    G  A    A  A_  CTG
                                AG CA CCCCA GC  AG   GC
                                || || ||||| ||  ||   ||
                                TC GT GGGGT CG  TC   CG
                                 G  C    C  AG  CA_
GAM2376  GPR88    3'  GCAACAAAGCAAGCTGG     56182      CCC
                                GCAAC   AAGCAAGCTGG
                                |||||   ||||||||||
                                CGTTG   TTCGTTCGACC
                                   T__
GAM2376  HSJ1     3'  AGACAACCCTAGGCCAAGTCC  56183        CAA  AAGCT  _
                                AGGCAACCC   GC    GG CC
                                |||||||||   ||    || ||
                                TCTGTTGGG   CG    TC GG
                                     ATC  GT___  A
GAM2376  KIAA0284  3'  GGCAGCCCCAAGCTCAATGG   56184     A       AAGC
                                GGCA CCCCAAGC    TGG
                                |||| ||||||||    |||
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                                CCGT GGGGTTCG    ACC
                                  C       AGTT
GAM2376 KIAA0582 5' AGCAGCCCCATGCGCTGGCCC 56185      A     A  AA
                                GGCA CCCCA GC  GCTGGCCC
                                |||| ||||| ||  ||||||||
                                TCGT GGGGT CG  CGACCGGG
                                  C    A  __
GAM2376 KIAA0870 3' AGACAGCTTGCCTCAGCTGGCC 56186      ACC__  AAGCA
              C                  AGGCA    CC    AGCTGGCCC
                                |||||    ||    |||||||||
                                TCTGT    GG    TCGACCGGG
                                  CGAAC  AG___
GAM2376 KIAA0872 3' GGCCAGTCCCAAGCATAGCCTG 56187     AAC_       _  _
              GCCC                  GGC    CCCAAGCA AGC TGGCCC
                                |||    |||||||| ||| ||||||
                                CCG    GGGTTCGT TCG ACCGGG
                                  GTCA       A   G
GAM2376 KIAA1271 3' AGGCATTCCCAAGCACCACATG 56188      AC       A_ _
                                AGGCA  CCCAAGCA  GC TG
                                |||||  ||||||||  || ||
                                TCCGT  GGGTTCGT  TG AC
                                  AA       GG  T
GAM2376 KIAA1649 3' GGCTAGCCTCAAGCAAATCT   56189     AAC _      _
                                GGC   CC CAAGCAAG CT
                                |||   || |||||||| ||
                                CCG   GG GTTCGTTT GA
                                  ATC  A       A
GAM2376 KIAA1649 3' GGCTAGCCTCAAGCAAATCT   56189     AAC _      _
                                GGC   CC CAAGCAAG CT
                                |||   || |||||||| ||
                                CCG   GG GTTCGTTT GA
                                  ATC  A       A
GAM2376 KIAA1655 5' AGGTGACCCAAGACTGGCC    56191     CAAC     CAA
                                AGG    CCCAAG   GCTGGCC
                                |||    ||||||   |||||||
                                TCC    GGGTTC   TGACCGG
                                  ACT_     ____
GAM2376 KIAA1655 3' AGGGACCCCAAGTCTGG      56190     CA       CAAG
                                AGG  ACCCCAAG    CTGG
                                |||  ||||||||    ||||
                                TCC  TGGGGTTC    GACC
                                  C_       A____
GAM2376 KIAA1754 3' AGGCAGGCCCAAGCACATG    56192       AC       AGC
                                AGGCA  CCCAAGCA   TG
                                |||||  ||||||||   ||
                                TCCGT  GGGTTCGT   AC
                                  CC       GT_
GAM2376 LGI2     3' GGCTCCAAAGCTGGCCC      56193     AACC    GCA
                                GGC    CCAA   AGCTGGCCC
                                |||    ||||   |||||||||
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                              CCG   GGTT   TCGACCGGG
                                A___   ___
GAM2376 MAAT1    3' GGGATCCCTGCCAAGCTGGCCC 56194    CAA   CAAG
                              GG   CCC    CAAGCTGGCCC
                              ||   |||    ||||||||||
                              CC   GGG    GTTCGACCGGG
                               CTA   ACG_
GAM2376 MARK2    3' GGCAGCCCGTCCAGCTGGCCC  56195     A   CAAGCA
                              GGCA CCC     AGCTGGCCC
                              |||| |||     |||||||||
                              CCGT GGG     TCGACCGGG
                                C   CAGG__
GAM2376 MARK2    3' GGCAGCCCGTCCAGCTGGCCC  56195     A   CAAGCA
                              GGCA CCC     AGCTGGCCC
                              |||| |||     |||||||||
                              CCGT GGG     TCGACCGGG
                                C   CAGG__
GAM2376 MGC15705 5' AAGCAACCCTAGAGGCAGTTGG 56196         CAA__   A C
             CC                 AGGCAACCC    GCA G TGGCC
                              |||||||||    ||| | |||||
                              TTCGTTGGG    CGT C ACCGG
                                   ATCTC   _ A
GAM2376 MGC1842  5' GGCCGCCCCAAGCGCCGCCC   56197    AA      AA   G
                              GGC  CCCCAAGC  GCTG CCC
                              |||  ||||||||  |||| |||
                              CCG  GGGGTTCG  CGGC GGG
                                GC       __   _
GAM2376 MGC21688 3' GGCAACCCCCGGCAAGCC    56198        AA
                              GGCAACCCC  GCAAGCT
                              |||||||||  |||||||
                              CCGTTGGGG  CGTTCGG
                                   GC
GAM2376 MGC2647  3' GGCGGCCTCGGCGGCTGGCCC  56199    AA  CCAA  AA
                              GGC  CC   GC  GCTGGCCC
                              |||  ||   ||  ||||||||
                              CCG  GG   CG  CGACCGGG
                                CC  AGC_  C_
GAM2376 MGC3279  5' GGCGTCCTGCCCGTCGCTGGCC 56200    AA __  AAGCAA
             C                  GGC  CC  CC     GCTGGCCC
                              |||  ||  ||     ||||||||
                              CCG  GG  GG     CGACCGGG
                                CA  AC  GCAG__
GAM2376 MGC8407  3' GGCCGGCCCTGCCACTGGCC   56201    AAC   AA  AA
                              GGC   CCC  GC  GCTGGCC
                              |||   |||  ||  |||||||
                              CCG   GGG  CG  TGACCGG
                                GCC   A_  G_
GAM2376 NFAT5    5' GGCCGGCCCCGAGCAGAGCT   56202    AA_   A   _
                              GGC   CCCC AGCA AGCT
                              |||   |||| |||| ||||
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                                CCG   GGGG TCGT TCGA
                                  GCC    C    C
GAM2376 PDZD2    5' AGATGACCCCAAACTTTCTGG 56203     CA       AAG
                                AGG  ACCCCAAGC   CTGG
                                |||  |||||||||   ||||
                                TCT  TGGGGTTTG   GACC
                                  AC        AAA
GAM2376 PI4KII   3' AGGCAACCTGAGCACAGGC   56204        CCA    AGCT
                                AGGCAACC   AGCA   GGC
                                ||||||||   ||||   |||
                                TCCGTTGG   TCGT   CCG
                                     AC_   GT__
GAM2376 PP5395   5' GCAGCCCCAAACTGGTCC    56205     A     GCAA    _
                                GCA CCCCAA    GCTGG CC
                                ||| ||||||    ||||| ||
                                CGT GGGGTT    TGACC GG
                                  C      ____     A
GAM2376 PRIC285  3' AGGCCAGGAGGCAGGCTGGCCC 56206      AACCCCAA   A
                                AGGC       GCA GCTGGCCC
                                ||||       ||| ||||||||
                                TCCG       CGT CGACCGGG
                                  GTCCTC__   C
GAM2376 RIP60    3' AGCAACTTCCCCTCAGCTGGCC 56207       __   AAG  A
              C                   GGCAAC  CCC   CA GCTGGCCC
                                ||||||  |||   || ||||||||
                                TCGTTG  GGG   GT CGACCGGG
                                   AA   GA_  _
GAM2376 SCAMP-4  3' AGGGGACCGGAAGCTGGCC   56208    CA   CCAAGC
                                AGG  ACC     AAGCTGGCC
                                |||  |||     |||||||||
                                TCC  TGG     TTCGACCGG
                                  CC   CC____
GAM2376 SEMA4B   3' GCAGCCCAAGCTGGTCC     56209     A   CAAGC      _
                                GCA CCC    AAGCTGG CC
                                ||| |||    ||||||| ||
                                CGT GGG    TTCGACC GG
                                  C  _____      A
GAM2376 SLC26A10 5' GACAACCCCAAGAGGCT     56210          CAA
                                GGCAACCCCAAG   GCT
                                ||||||||||||   |||
                                CTGTTGGGGTTC   CGA
                                       TC_
GAM2376 TAO1     3' AGGCATCTATCGCCAAGCTGGC 56211       ACCCCAA  _
              CC                   AGGCA      GC AAGCTGGCCC
                                |||||      || ||||||||||
                                TCCGT      CG TTCGACCGGG
                                   AGATAG_  G
GAM2376 TOB2     3' GGCCCAGACTGGGCTGGCCC   56212     AACC   AG AA_
                                GGC    CCA  C   GCTGGCCC
                                |||    |||  |   ||||||||
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                                CCG   GGT  G   CGACCGGG
                                  _____  CT ACC
GAM2376  TRPV6    3'  AGCGCCCAAGCAGGCTGGCC  56213    AAC      A
                                GGC   CCCAAGCA GCTGGCC
                                |||   |||||||| |||||||
                                TCG   GGGTTCGT CGACCGG
                                  C__       C
GAM2376  ZNF282   3'  AGGAACCCCAGGAGCTGGCC  56214    C      AGCA
                                AGG AACCCCA   AGCTGGCC
                                ||| |||||||   ||||||||
                                TCC TTGGGGT   TCGACCGG
                                  _      CC__
GAM2376  LOC118491 5'  GGTTCCAAGCAAGTAGC    56215    CAACC       C
                                GG    CCAAGCAAG TGGC
                                ||    ||||||||| ||||
                                CC    GGTTCGTTC ATCG
                                 AA___       _
GAM2376  LOC122700 5'  AGGTAACTAGCCTGGAGCTGGC 56216    C   CCCA   A___
              CC                  AGG AAC   AGC   AGCTGGCCC
                                ||| |||   |||   |||||||||
                                TCC TTG   TCG   TCGACCGGG
                                  A   A___   GACC
GAM2376  LOC126969 5'  GACGACCCCAAGTTTGCGCCC  56217    A      CAA  TG
                                GGC ACCCCAAG   GC  GCCC
                                ||| ||||||||   ||  ||||
                                CTG TGGGGTTC   CG  CGGG
                                  C       AAA  __
GAM2376  LOC143903 5'  GGCAGCCCCGCTGGCTGGCCC  56218     A   AA  AA
                                GGCA CCCC  GC  GCTGGCCC
                                |||| ||||  ||  ||||||||
                                CCGT GGGG  CG  CGACCGGG
                                  C   __  AC
GAM2376  LOC145826 5'  AGTTAACCCCAGGTAACTGGCC 56219    GC      AGCA
                                AG  AACCCCA   AGCTGGCC
                                ||  |||||||   ||||||||
                                TC  TTGGGGT   TTGACCGG
                                 AA      CCA_
GAM2376  LOC146220 3'  AGGAGTCCTGGGGCCAGCTGGC 56220    CAA  CCAA  A
              C                  AGG   CC   GC AGCTGGCC
                                |||   ||   || ||||||||
                                TCC   GG   CG TCGACCGG
                                  TCA  ACCC  G
GAM2376  LOC146226 5'  AGCAGCCCTTGTGCAAGCTGGC 56221     A   CAA_
                                GGCA CCC   GCAAGCTGGC
                                |||| |||   ||||||||||
                                TCGT GGG   CGTTCGACCG
                                  C   AACA
GAM2376  LOC154789 5'  GGCATCCAGGGAGCTGGCC   56222     A  CCA  CA
                                GGCA CC   AG  AGCTGGCC
                                |||| ||   ||  ||||||||
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                                CCGT GG   TC  TCGACCGG
                                  A ___  CC
GAM2376  LOC158046 5'  AGGCAACCTCAAGCCCTCAGG  56223        C    AAGCT
                                AGGCAACC CAAGC    GG
                                |||||||| |||||    ||
                                TCCGTTGG GTTCG    CC
                                    A    GGAGT
GAM2376  LOC159723 5'  AGCGGCCCCAAGCGAGTCC   56224    AA      A _
                                GGC  CCCCAAGC AG CT
                                |||  |||||||| || ||
                                TCG  GGGGTTCG TC GG
                                  CC       C  A
GAM2376  LOC196707 3'  AGGTGACCCCAAAAACCACTGG 56225    CA      CAA_
            CC                    AGG  ACCCCAAG   GCTGGCC
                                |||  ||||||||   |||||||
                                TCC  TGGGGTTT   TGACCGG
                                  AC       TTGG
GAM2376  LOC196746 3'  AGCCAACCCAGGCTGGC    56226   G    CA  CAA
                                AG CAACCC  AG   GCTGGC
                                || ||||||  ||   ||||||
                                TC GTTGGG  TC   CGACCG
                                 G     __ ___
GAM2376  LOC203317 3'  AAGTAACCCCAAGTAACAAG   56227    C       ___
                                AGG AACCCCAAG   CAAG
                                ||| |||||||||   ||||
                                TTC TTGGGGTTC   GTTC
                                  A       ATT
GAM2376  LOC221496 5'  AGCAGTAGCCCTAGGCTGGCCC 56228    AC__   A  CAA
                                GGCA   CCC AG   GCTGGCCC
                                ||||   ||| ||   ||||||||
                                TCGT   GGG TC   CGACCGGG
                                  CATC   A ___
GAM2376  LOC253695 3'  AGCCAGCCTTCCATGCTGGCC  56229   G  A  __   AGCAA
                                AG CA CC  CCA    GCTGGCC
                                || || ||  |||    |||||||
                                TC GT GG  GGT    CGACCGG
                                 G  C  AA   A____
GAM2376  LOC254532 5'  GGCGGGGTGGGGCAAGCTGGCC 56230    AACCCCAA
            C                    GGC       GCAAGCTGGCCC
                                |||       ||||||||||||
                                CCG       CGTTCGACCGGG
                                  CCCCACCC
GAM2376  LOC255028 5'  GGCTGGCCCTGGAGCCGCTGGC 56231    AA_  CA_  AA
            C                    GGC   CCC   AGC  GCTGGCC
                                |||   |||   |||  |||||||
                                CCG   GGG   TCG  CGACCGG
                                  ACC   ACC   G_
GAM2376  LOC255397 5'  GGCAGCCCTGGCCAGCTGGCC  56232    A   CAA  A
                                GGCA CCC   GC AGCTGGCC
                                |||| |||   || ||||||||
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                                CCGT GGG   CG TCGACCGG
                                  C   AC_  G
GAM2376  LOC256529 5'  GGAACCTCCTGCTGGCC     56233    C   _  AAGCAA
                                GG AACC CC     GCTGGCC
                                || |||| ||     |||||||
                                CC TTGG GG     CGACCGG
                                 _   A  A_____
GAM2376  LOC55901  5'  AGCAACCCCAGGCCGC      56234         AGCAA   G
                                GGCAACCCCA    GCTG C
                                ||||||||||    |||| |
                                TCGTTGGGGT    CGGC G
                                      C____   A
GAM2376  LOC90580  3'  AGCTGGCCTCAAACTCCTGGCC 56235     AAC  _    AAG
                                GGC   CC CAAGC   CTGGCC
                                |||   || |||||   ||||||
                                TCG   GG GTTTG   GACCGG
                                  ACC  A    AG_
GAM2376  LOC90631  3'  AGGAAACTGAGGCTGGCC    56236    C   CCCA  CAA
                                AGG AAC    AG   GCTGGCC
                                ||| |||    ||   |||||||
                                TCC TTG    TC   CGACCGG
                                  T   AC__  ___
GAM2376  LOC93273  3'  GGCTGCAGGCTAGGCTGGCCC  56237     AACCC  A  AA_
                                GGC    CA GC   GCTGGCCC
                                |||    || ||   ||||||||
                                CCG    GT CG   CGACCGGG
                                  AC___  C  ATC
GAM2377  EML1      3'  TGTGGCTATAATGTAAACG    56240         C_   C_
                                TGTGGCTA  ATG  AACG
                                ||||||||  |||  ||||
                                ACACCGAT  TAC  TTGC
                                     AT   AT
GAM2377  HIRA      3'  TGGGCTGGCGCTGGTGCAGGAC 56241    T    ACA   AAC_
              A                  TG GGCT   TGC    GCAGGACA
                                || ||||   |||    ||||||||
                                AC CCGA   GCG    CGTCCTGT
                                 _   CC_   ACCA
GAM2377  IFNAR1    3'  TGTGGCACATGCAGTAGCCAGC 56242       T      AC_  A  A
              A                  TGTGGC ACATGCA   GC GG CA
                                |||||| |||||||   || || ||
                                ACACCG TGTACGT   CG TC GT
                                   _      CAT  G  _
GAM2377  KIP2      3'  TGTGACTGCAGGGCAGGA    56243        ACAT   AC
                                TGTGGCT    GCA  GCAGGA
                                |||||||    |||  ||||||
                                ACACTGA    CGT  CGTCCT
                                    _____  CC
GAM2377  KRT6B     3'  TGTAGCTATAATGGGCAGGA  56244        C_   CAAC
                                TGTGGCTA  ATG   GCAGGA
                                ||||||||  |||   ||||||
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                                ACATCGAT  TAC    CGTCCT
                                    AT   C___
GAM2377  MCM4     3'  TGTGGCGTGCAGCAAGCAGGAC 56245       TACAT    C
             A                   TGTGGC    GCAA GCAGGACA
                                 ||||||    |||| ||||||||
                                 ACACCG    CGTT CGTCCTGT
                                    CACGT   _
GAM2377  FLJ21865 3'  GTGGCTACATGCGGCAG     56246          AAC
                                 GTGGCTACATGC   GCAG
                                 ||||||||||||   ||||
                                 CACCGATGTACG   CGTC
                                       C__
GAM2377  FLJ22282 3'  TGTGGCTAAATGGCAGGAC    56247        C   CAAC
                                 TGTGGCTA ATG    GCAGGAC
                                 ||||||||| |||    |||||||
                                 ACACCGAT TAC    CGTCCTG
                                    T  _____
GAM2377  FLJ23132 3'  TGTGGCTATATCACAAATGGCA 56248        C  _    C__
                                 TGTGGCTA AT GCAA   GCA
                                 |||||||| || ||||   |||
                                 ACACCGAT TA TGTT   CGT
                                    A  G    TAC
GAM2377  KIAA0450  5'  TGTGGCTACCGCAGCATGTGGG 56249        A    AC   _____
             ACA                   GTGGCTAC TGCA  GCA    GGACA
                                 |||||||| ||||  |||    |||||
                                 CACCGATG GCGT  CGT    CCTGT
                                    _   __   ACAC
GAM2377  KIAA0527  3'  TGGCTACATGCAGAAAGCA   56250          AC__
                                 TGGCTACATGCA    GCA
                                 ||||||||||||    |||
                                 ACCGATGTACGT    CGT
                                       CTTT
GAM2377  MGC16386  3'  GTGGCTATGTACAGGAC     56251        CA  CAAC
                                 GTGGCTA  TG    GCAGGAC
                                 |||||||  ||    |||||||
                                 CACCGAT  AC    TGTCCTG
                                    __  A___
GAM2377  MGC22776  3'  TGTGGCCACATGCCCGGA    56252           AACGCA
                                 TGTGGCTACATGC     GGA
                                 ||||||||||||      |||
                                 ACACCGGTGTACG     CCT
                                       GG_____
GAM2377  MGC2574   3'  TGTGCCTGTATGCAACAGGCA  56253     G  AC    AC    A
                                 TGTG CT  ATGCA  GCAGG CA
                                 |||| ||  |||||  ||||| ||
                                 ACAC GA  TACGT  TGTCC GT
                                   G  CA    __    _
GAM2377  WBSCR21   5'  TGTGGCCAACGACGACGCAGGG 56254        C   _ A      A
             CA                    TGTGGCTA ATG C ACGCAGG CA
                                 |||||||| ||| | ||||||| ||
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                                ACACCGGT TGC G TGCGTCC GT
                                    _  T C     C
GAM2377 ZNF333   3' TGTGGCTACATGAAACCA   56255         C  G
                                TGTGGCTACATG AAC CA
                                |||||||||||| ||| ||
                                ACACCGATGTAC TTG GT
                                       T  _
GAM2377 LOC146488 5' TGTGGCCACATGTGGCCCAGGG 56256          CAACG   A
          CA                   TGTGGCTACATG   CAGG CA
                               ||||||||||||    |||| ||
                               ACACCGGTGTAC    GTCC GT
                                     ACCGG   C
GAM2377 LOC159199 3' TGTGGCTGCAAGCAGGAC   56257       ACAT   C
                               TGTGGCT   GCAA GCAGGAC
                               |||||||   |||| |||||||
                               ACACCGA   CGTT CGTCCTG
                                  ____   _
GAM2378 CSH2     3' GGCACTGGAGTGGCACCT   56260   A     G A T  G
                               GG CACTGGAG TG G CAC CT
                               || |||||||| || | ||| ||
                               CC GTGACCTC AC C GTG GA
                                _     _ _ _  _
GAM2378 CSH2     3' GGCACTGGAGTGGCACCT   56260   A     G A T  G
                               GG CACTGGAG TG G CAC CT
                               || |||||||| || | ||| ||
                               CC GTGACCTC AC C GTG GA
                                _     _ _ _  _
GAM2378 CSH2     3' GGCACTGGAGTGGCACCT   56260   A     G A T  G
                               GG CACTGGAG TG G CAC CT
                               || |||||||| || | ||| ||
                               CC GTGACCTC AC C GTG GA
                                _     _ _ _  _
GAM2378 CSH2     3' GGCACTGGAGTGGCACCT   56260   A     G A T  G
                               GG CACTGGAG TG G CAC CT
                               || |||||||| || | ||| ||
                               CC GTGACCTC AC C GTG GA
                                _     _ _ _  _
GAM2378 CSHL1    3' GGCACTGGAGTGGCACCT   56260   A     G A T  G
                               GG CACTGGAG TG G CAC CT
                               || |||||||| || | ||| ||
                               CC GTGACCTC AC C GTG GA
                                _     _ _ _  _
GAM2378 CSHL1    3' GGCACTGGAGTGGCACCT   56260   A     G A T  G
                               GG CACTGGAG TG G CAC CT
                               || |||||||| || | ||| ||
                               CC GTGACCTC AC C GTG GA
                                _     _ _ _  _
GAM2378 CSHL1    3' GGCACTGGAGTGGCACCT   56260   A     G A T  G
                               GG CACTGGAG TG G CAC CT
                               || |||||||| || | ||| ||
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                                CC GTGACCTC AC C GTG GA
                                 _     _ _ _  _
GAM2378 CSHL1   3' GGCACTGGAGTGGCACCT   56260   A     G A T  G
                                GG CACTGGAG TG G CAC CT
                                || |||||||| || | ||| ||
                                CC GTGACCTC AC C GTG GA
                                 _     _ _ _  _
GAM2378 CSHL1   3' GGCACTGGAGTGGCACCT   56260   A     G A T  G
                                GG CACTGGAG TG G CAC CT
                                || |||||||| || | ||| ||
                                CC GTGACCTC AC C GTG GA
                                 _     _ _ _  _
GAM2378 GH1     3' GGCACTGGAGTGGCAAC    56261   A     G A  C
                                GG CACTGGAG TG GT AC
                                || |||||||| || || ||
                                CC GTGACCTC AC CG TG
                                 _     _ _ T
GAM2378 GH1     3' GGCACTGGAGTGGCAAC    56261   A     G A  C
                                GG CACTGGAG TG GT AC
                                || |||||||| || || ||
                                CC GTGACCTC AC CG TG
                                 _     _ _ T
GAM2378 GH1     3' GGCACTGGAGTGGCAAC    56261   A     G A  C
                                GG CACTGGAG TG GT AC
                                || |||||||| || || ||
                                CC GTGACCTC AC CG TG
                                 _     _ _ T
GAM2378 GH1     3' GGCACTGGAGTGGCAAC    56261   A     G A  C
                                GG CACTGGAG TG GT AC
                                || |||||||| || || ||
                                CC GTGACCTC AC CG TG
                                 _     _ _ T
GAM2378 GH1     3' GGCACTGGAGTGGCAAC    56261   A     G A  C
                                GG CACTGGAG TG GT AC
                                || |||||||| || || ||
                                CC GTGACCTC AC CG TG
                                 _     _ _ T
GAM2378 GPR61   3' GGGGACTGGAGGTGGGTCGCT 56262   AC      A  AC
                                GG  ACTGGAGGTG GTC  GCT
                                ||  |||||||||| |||  |||
                                CC  TGACCTCCAC CAG  CGA
                                 CC       C  __
GAM2378 HOXB5   5' GGCGTTAGGGAATCACGTGCTT 56263   ACACTGG  T    __
                                GG     AGG GAGTCAC  GCTT
                                ||     ||| |||||||  ||||
                                CC     TCC CTTAGTG  CGAA
                                 GCAA___  _     CA
GAM2378 FLJ20699 3' GGACGCTGGAGGTGCAGT   56264     A      _
                                GGAC CTGGAGGTG AGT
                                |||| ||||||||| |||
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                                CCTG GACCTCCAC TCA
                                  C       G
GAM2378 HT009    5' GGACACGAAAGTCACG      56265       T  GGTG
                                GGACAC GGA    AGTCACG
                                |||||| |||    |||||||
                                CCTGTG CTT    TCAGTGC
                                   _  _____
GAM2378 KIAA0469 3' GGACACTGGAGGGAGGGCGTCC 56266          T  TCA _
             T                   GGACACTGGAGG GAG   CG CTT
                                ||||||||||||| |||   || |||
                                CCTGTGACCTCC CTC   GC GGA
                                       _  CC_  A
GAM2378 RDH-E2   3' GGCACTGGAGGCGGGCC     56267    A        A
                                GG CACTGGAGGTG GTC
                                || ||||||||||| |||
                                CC GTGACCTCCGC CGG
                                 _         C
GAM2378 SCYA14   5' GGTGTTGGAGGTGGGTGGCT   56268    ACAC      A  CAC
                                GG    TGGAGGTG GT   GCT
                                ||    |||||||| ||   |||
                                CC    ACCTCCAC CA   CGA
                                 ACA_       C  C__
GAM2378 SCYA14   5' GGTGTTGGAGGTGGGTGGCT   56268    ACAC      A  CAC
                                GG    TGGAGGTG GT   GCT
                                ||    |||||||| ||   |||
                                CC    ACCTCCAC CA   CGA
                                 ACA_       C  C__
GAM2378 SCYA15   3' GGTGTTGGAGGTGGGTGGCT   56268    ACAC      A  CAC
                                GG    TGGAGGTG GT   GCT
                                ||    |||||||| ||   |||
                                CC    ACCTCCAC CA   CGA
                                 ACA_       C  C__
GAM2378 ZAK      3' GGCATTAGAAACACGTCACGCT 56269    A  C    GG GA
             T                   GG CA TGGA  T  GTCACGCTT
                                || || ||||  |  |||||||||
                                CC GT ATCT  G  CAGTGCGAA
                                 _  A    TT TG
GAM2378 LOC149483 3' GGACACCGGAGGTGGGTAC    56270            A  C
                                GGACACTGGAGGTG GT AC
                                |||||||||||||| || ||
                                CCTGTGGCCTCCAC CA TG
                                       C  _
GAM2378 LOC153811 3' GGATTTGGGGGCTCACGCT    56271     CAC   A   GAG
                                GGA   TGG GGT   TCACGCT
                                |||   ||| |||   |||||||
                                CCT   ACC CCG   AGTGCGA
                                  AA_   C   ___
GAM2378 LOC196214 3' GGACACTGGGGTTGGCC      56272         A   GA
                                GGACACTGG GGT  GTC
                                ||||||||| |||  |||
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                                CCTGTGACC CCA  CGG
                                     _  AC
GAM2379  EXTL3    3'  CGTATTCCAAGAAATAGAA   56275       ATTAA
                                CGTATTT    AAATAGAA
                                |||||||    ||||||||
                                GCATAAG    TTTATCTT
                                    GTTC_
GAM2379  FLJ11196 3'  GCTTGTATTAAAAATAGAA   56276    ATT
                                GT   TATTAAAAATAGAA
                                ||   ||||||||||||||
                                CG   ATAATTTTTATCTT
                                 AAC
GAM2379  FLJ20036 3'  GTATCATTAAAAATAGAA    56277      T
                                GTATT ATTAAAAATAGAA
                                ||||| ||||||||||||
                                CATAG TAATTTTTATCTT

                                  _
GAM2379  LOC145662 3'  AATCCTATCACAAAATAGAAA  56278     G    TATTA
                                AATC TATT    AAAATAGAAA
                                |||| ||||    ||||||||||
                                TTAG ATAG    TTTTATCTTT
                                  G    TG___
GAM2380  CDH17    3'  TTTGCAGAGTAGGTTGT     56281       GA  A
                                TTTGCGG  TA GGTTGT
                                |||||||  || ||||||
                                AAACGTC  AT CCAACA
                                    TC  _
GAM2380  FOSL1    5'  TCTGCGGGGTACACGGCT    56282        __  A
                                TTTGCGGG  ATA GGTT
                                ||||||||  ||| ||||
                                AGACGCCC  TGT CCGA
                                    CA   G
GAM2380  FPRL1    5'  TTTGCAAATAGGTTGT      56283       ATA
                                TTTGCGGG   AGGTTGT
                                ||||||||   |||||||
                                AAACGTTT   TCCAACA
                                    A__
GAM2380  FZD1     3'  TTTGCAGGAGCTGAGTTGT   56284        TAA_
                                TTTGCGGGA    GGTTGT
                                |||||||||    ||||||
                                AAACGTCCT    TCAACA
                                     CGAC
GAM2380  SLC1A3   3'  TTGTGGGATGAAAATTGT    56285     C    _
                                TTG GGGAT AAGGTTGT
                                ||| ||||| ||||||||
                                AAC CCCTA TTTTAACA
                                  A    C
GAM2380  FLJ10716 3'  TCTGGAAACAAGGGTTGT    56286     C GG    _
                                TTTG G  ATAAGG TTGT
                                |||| |  |||||| ||||
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                                AGAC C  TGTTCC AACA
                                  _ TT     C
GAM2380  FLJ13373  5'  CTTGCGGGAGAGTTGT     56287        TAA
                                TTTGCGGGA   GGTTGT
                                |||||||||   ||||||
                                GAACGCCCT   TCAACA
                                     C__
GAM2380  KIAA0125  5'  TCTGCGGGATCATTGT     56288        AAG
                                TTTGCGGGAT   GTTGT
                                ||||||||||   |||||
                                AGACGCCCTA   TAACA
                                     G__
GAM2380  NUDT12    3'  TTTGTGAGATAAAACTGT    56289     C      GG
                                TTTG GGGATAA  TTGT
                                |||| |||||||  ||||
                                AAAC CTCTATT  GACA
                                  A      TT
GAM2380  SV2B      3'  TTTGCAGATACCAGTTGT    56290       G   A_
                                TTTGCGG ATA  GGTTGT
                                ||||||| |||  ||||||
                                AAACGTC TAT  TCAACA
                                    _  GG
GAM2380  LOC148898 5'  TTTGCGGGACAGGAGGT     56291          A  TT
                                TTTGCGGGATA GG  GT
                                |||||||||||  ||  ||
                                AAACGCCCTGT CC  CA
                                      _ TC
GAM2380  LOC152445 5'  TTTGCGGGATGTTGT       56292        AAG
                                TTTGCGGGAT   GTTGT
                                ||||||||||   |||||
                                AAACGCCCTA   CAACA
                                      ___
GAM2380  LOC152503 3'  TTTGCAGAACTCCAGGTTGT   56293         A__
                                TTTGCGGGAT   AGGTTGT
                                ||||||||||   |||||||
                                AAACGTCTTG   TCCAACA
                                     AGG
GAM2380  LOC154092 3'  TTTGGGGAAGGTTGT       56294     C   TA
                                TTTG GGGA  AGGTTGT
                                |||| ||||  |||||||
                                AAAC CCCT  TCCAACA
                                  _   __
GAM2380  LOC222258 5'  TTTGCGGACATAGTTGT     56295       G   A
                                TTTGCGG ATA GGTTGT
                                ||||||| ||| ||||||
                                AAACGCC TGT TCAACA
                                    _  A
GAM2380  LOC256337 3'  CCTGAGGGTAAGGTTGT     56296     C   A
                                TTTG GGG TAAGGTTGT
                                |||| ||| |||||||||
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                                GGAC CCC ATTCCAACA
                                  T  _
GAM2381  TIGD4     3'  TATTACTCTTTAGATGTA    56299          _
                                TATTACTTTTT GATGTA
                                |||||||||||  ||||||
                                ATAATGAGAAA CTACAT
                                       T
GAM2381  LOC119467 3'  TACTACTCAGGGCTGATGTA   56300        T___
                                TATTACTT   TTGATGTA
                                ||||||||   ||||||||
                                ATGATGAG   GACTACAT
                                     TCCC
GAM2381  LOC196477 3'  TATTACTTTGAATGATGTA   56301         T__
                                TATTACTTT  TGATGTA
                                |||||||||  |||||||
                                ATAATGAAA  ACTACAT
                                      CTT
GAM2381  LOC221362 3'  TATTACTTAAAATTGATGTA   56302        T___
                                TATTACTT   TTGATGTA
                                ||||||||   ||||||||
                                ATAATGAA   AACTACAT
                                     TTTT
GAM2382  PCSK1     3'  TAATATAATTTATTATGCTCTT 56305             TCA
                                TAATATAGTTTATTAT  TTTT
                                ||||||||||||||||  ||||
                                ATTATATTAAATAATA  AGAA
                                        CG_
GAM2382  BCAR3     3'  ATAATAAATTATTCATTTTA  56306      TT
                                ATAGT  ATTATTCATTTTA
                                |||||  ||||||||||||
                                TATTA  TAATAAGTAAAAT
                                   TT
GAM2382  FLJ13188  3'  TAATATAATCATGATTCATTTT 56307         T  T
            A                    TAATATAGTT AT ATTCATTTTA
                                 |||||||||| || ||||||||||
                                 ATTATATTAG TA TAAGTAAAAT
                                       _  C
GAM2382  VEST1     3'  TAACATATCAATTATTCATTTT 56308       GTTT
            A                    TAATATA   ATTATTCATTTTA
                                 |||||||   ||||||||||||
                                 ATTGTAT   TAATAAGTAAAAT
                                     AGT_
GAM2383  ENTPD1    5'  TAATAGGAGAAAAGGCATA   56311          AA
                                TAATAGGAGAAAA  TATA
                                ||||||||||||  ||||
                                ATTATCCTCTTTT  GTAT
                                        CC
GAM2383  SCN3A     3'  ATAGGAGTTTATATAATG    56312       AAAAAA
                                ATAGGAG    TATATAATG
                                |||||||    |||||||||
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                                TATCCTC     ATATATTAC
                                   AA____
GAM2383  DKFZP434F1735 5'  CAATAGGAGGAAGCTAACATGT 56313         _  AA_    A
            AATG                    TAATAGGAG AA   AATAT TAATG
                                |||||||||  ||   |||||  |||||
                                GTTATCCTC TT   TTGTA ATTAC
                                     C  CGA    C
GAM2383  GPR74    3'  GGATTTAAATATATAATG    56314     GAAA
                                GGA   AAATATATAATG
                                |||   ||||||||||||
                                CCT   TTTATATATTAC
                                  AAA_
GAM2383  KIAA0478  3'  TAGGAGAAAAGGATAAAATG   56315          AAT   T
                                TAGGAGAAAA   ATA AATG
                                ||||||||||   ||| ||||
                                ATCCTCTTTT   TAT TTAC
                                      CC_   T
GAM2383  NPGPR    3'  GGATTTAAATATATAATG    56314     GAAA
                                GGA   AAATATATAATG
                                |||   ||||||||||||
                                CCT   TTTATATATTAC
                                  AAA_
GAM2384  CDKN2B   3'  TCCGCTTCTCTGTGTTTCG   56318     A  AG  AC
                                TCC GT  TT  GTGTTTCG
                                ||| ||  ||  ||||||||
                                AGG CG  GA  CACAAAGC
                                  _  AA  GA
GAM2384  GABRR2   3'  TCCAGTAGCTGCTGCATT    56319          AC_
                                TCCAGTAGTT   GTGTT
                                ||||||||||   |||||
                                AGGTCATCGA   CGTAA
                                      CGA
GAM2384  GPRC5B   3'  TCTGGTATTACGTGTCT     56320    CA   G
                                TC  GTA TTACGTGTTT
                                ||  ||| ||||||||||
                                AG  CAT AATGCACAGA
                                 AC  _
GAM2384  APOL6    3'  TCCAATAACAATGTTTCG    56321        TTAC
                                TCCAGTAG   GTGTTTCG
                                ||||||||   ||||||||
                                AGGTTATT   TACAAAGC
                                     GT__
GAM2384  DKFZP564B1162 3'  TCCAGCAGTTAAAGAGATTCG  56322          CGTGT_
                                TCCAGTAGTTA     TTCG
                                ||||||||||     ||||
                                AGGTCGTCAAT     AAGC
                                       TTCTCT
GAM2384  FLJ14075  3'  TCCAGTAAGTTTATGTTT    56323        _   AC
                                TCCAGTA GTT  GTGTTT
                                |||||||  |||  ||||||
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                                AGGTCAT CAA  TACAAA
                                    T  A_
GAM2384  FLJ22843  3'  TCCAGTAGTCAATGTATTTCG  56324          C_
                                TCCAGTAGTTA  GTGTTTCG
                                ||||||||||  ||||||||
                                AGGTCATCAGT  CATAAAGC
                                   TA
GAM2384  FOXD4     5'  TCCAGTAGTTGCCCTT      56325         AC  G
                                TCCAGTAGTT  GT TTT
                                ||||||||||  || |||
                                AGGTCATCAA  CG GAA
                                    __  G
GAM2384  KIAA1344  3'  TCCAGTAGTGCATCT       56326         TAC
                                TCCAGTAGT   GTGTTT
                                |||||||||   ||||||
                                AGGTCATCA   CGTAGA
                                    ___
GAM2384  LOC127534 5'  TCCAGTAGCTGCTTC       56327         TACG
                                TCCAGTAGT    TGTTTC
                                |||||||||    ||||||
                                AGGTCATCG    ACGAAG
                                    _____
GAM2384  LOC152816 3'  TCCAATAGTTTTAGTTTCG    56328          ACGT
                                TCCAGTAGTT    GTTTCG
                                ||||||||||    ||||||
                                AGGTTATCAA    CAAAGC
                                   AAT_
GAM2385  KIR2DL5   3'  TAAGTTTCACTGCTGACT     56331           _
                                TAAGTTTTATTGCT ACT
                                |||||||||||||| |||
                                ATTCAAAGTGACGA TGA
                                     C
GAM2385  ZNF141    3'  TATTAAGTATGAACATTGCTA  56332         TT___
                                TATTAAGT     TATTGCTA
                                ||||||||     ||||||||
                                ATAATTCA     GTAACGAT
                                   TACTT
GAM2385  DKFZp761G0313 3'  TATTAAGTTTTGCTCAAGGACC 56333          TAT   ACTA_
                                TATTAAGTTT   TGCT    ACC
                                ||||||||||   ||||    |||
                                ATAATTCAAA   ACGA    TGG
                                    ___   GTTCC
GAM2385  KIAA0997  3'  TATTAGGTTATATTGCCA     56334       A   T
                                TATTA GTT TATTGCTA
                                ||||| ||| ||||||||
                                ATAAT CAA ATAACGGT
                                  C   T
GAM2385  KIAA1354  3'  CATTAAGTTTTACTGACC     56335           _
                                TATTAAGTTTTATTG CT
                                |||||||||||||| ||
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                                GTAATTCAAAATGAC GG
                                        T
GAM2385  PTPN9    3'  ATTAAGAACACATTGCTACTGG 56336       TTT_        AA
            CC                   ATTAAG    TATTGCTACT  CC
                                 ||||||    ||||||||||  ||
                                 TAATTC    GTAACGATGA  GG
                                    TTGT         CC
GAM2385  LOC130250 5'  TTAAGTTTTATCTTTCTTGCTA 224           _______
                                 TTAAGTTTTAT     TGCTA
                                 ||||||||||      |||||
                                 AATTCAAAATA     ACGAT
                                       GAAAGA
GAM2386  ADCY6    5'  GGTAGGCAACAAGGGTA     56339      A    AAATC
                                 GGTA GCAG     CAAGGGTA
                                 |||| ||||     ||||||||
                                 CCAT CGTT     GTTCCCAT
                                   C   _____
GAM2386  BTAF1    5'  GGTAAGCAGGGGTCCAAGA    56340         AAA
                                 GGTAAGCAG   TCCAAGG
                                 |||||||||   |||||||
                                 CCATTCGTC   AGGTTCT
                                       CCC
GAM2386  CX3CR1   3'  TGGAAAGCAGAAGTCTAAGAGG 56341     T       A  C  _
            C                    TGG AAGCAGAA TC AAG GGT
                                 ||| |||||||| || ||| |||
                                 ACC TTCGTCTT AG TTC CCG
                                   T       C  A   T
GAM2386  NFE2L1   3'  TGGTAGGCAGAGGCCCGAG    56342       A     AA   A
                                 TGGTA GCAGA  TCC AG
                                 |||||| |||||  ||| ||
                                 ACCAT CGTCT  GGG TC
                                    C     CC   C
GAM2386  SCN8A    3'  TGGTAAGCAGACGACGTTTGGT 56343           AATCCAAG
            A                    TGGTAAGCAGA       GGTA
                                 ||||||||||        ||||
                                 ACCATTCGTCT       CCAT
                                       GCTGCAAA
GAM2386  C20orf59 3'  TGGGCAGGGCCCAAGGG     56344     TAA    AAA
                                 TGG   GCAG   TCCAAGGG
                                 |||   ||||   ||||||||
                                 ACC   CGTC   GGGTTCCC
                                   ___    CC_
GAM2386  FLJ11252 3'  TAGAATCAGAGGTCTAAGGGTA 56345     TAAG    AA  C
            C                    TGG    CAGA  TC AAGGGTAC
                                 |||    ||||  || ||||||||
                                 ATC    GTCT  AG TTCCCATG
                                   TTA_    CC  A
GAM2386  FLJ11800 3'  TGGTGAGCAGAAATGTCGGAGG 56346      A        CCAA_
            T                    TGGT AGCAGAAAT     GGGT
                                 |||| |||||||||     ||||
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                                ACCA TCGTCTTTA    TCCA
                                  C       CAGCC
GAM2386  HSPC054   5'  TGGTAAGCAGGGGTCCCTGTGC 56347         AAA   AAGG
                                TGGTAAGCAG   TCC    GT
                                ||||||||||  |||   ||
                                ACCATTCGTC   AGG    CG
                                     CCC   GACA
GAM2386  KIAA1458  3'  TGGTAAGCAGAGGGC      56348          AATCCAA
                                TGGTAAGCAGA     GGGT
                                ||||||||||      ||||
                                ACCATTCGTCT     CCCG
                                                _______
GAM2386  PEX11B    3'  GTAAGCAGAAATCTGAAGGT   56349           CA
                                GTAAGCAGAAATC  AGGGT
                                ||||||||||||  |||||
                                CATTCGTCTTTAG  TTCCA
                                       AC
GAM2386  PPP1R1B   3'  GGTAGAAAAGGATCTAAGGGTA 56350     A C   __   C
           C                     GGTA G AGAA  ATC AAGGGTAC
                                 |||| | ||||  ||| ||||||||
                                 CCAT C TTTT  TAG TTCCCATG
                                   _ _   CC   A
GAM2386  SMARCF1   3'  CAAACTGTGGGGATCCAAGGGT 56351      AGAA___
           A                     TAAGC      ATCCAAGGGTA
                                 |||||      ||||||||||
                                 GTTTG      TAGGTTCCCAT
                                    ACACCCC
GAM2386  SMARCF1   3'  CAAACTGTGGGGATCCAAGGGT 56351      AGAA___
           A                     TAAGC      ATCCAAGGGTA
                                 |||||      ||||||||||
                                 GTTTG      TAGGTTCCCAT
                                    ACACCCC
GAM2386  SMARCF1   3'  CAAACTGTGGGGATCCAAGGGT 56351      AGAA___
           A                     TAAGC      ATCCAAGGGTA
                                 |||||      ||||||||||
                                 GTTTG      TAGGTTCCCAT
                                    ACACCCC
GAM2386  LOC146667 5'  GGTAGAGTCCAAGGGT      56352      A C  AAA
                                GGTA G AG   TCCAAGGGT
                                |||| | ||   |||||||||
                                CCAT C TC   AGGTTCCCA
                                  _ _ ___
GAM2386  LOC150933 3'  TGGCAAGCAGAAATGAGGTA   56353           CCAA
                                TGGTAAGCAGAAAT    GGGTA
                                ||||||||||||||   |||||
                                ACCGTTCGTCTTTA    TCCAT
                                       C___
GAM2386  LOC158382 3'  GGAGAGGAATCCAAGGGT    56354    TA  C  A
                                GG  AG AG AATCCAAGGGT
                                ||  || || ||||||||||
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                                CC  TC TC TTAGGTTCCCA
                                 __ _ C
GAM2386  LOC200862 5'  GGTAGTGCATGATCCAAGGGT  56355      A_   GAA
                                GGTA  GCA   ATCCAAGGGT
                                ||||  |||   ||||||||||
                                CCAT  CGT   TAGGTTCCCA
                                  CA   AC_
GAM2386  LOC220575 3'  TGGTGAGCAGAAATGTCGGAGG 56346      A        CCAA_
           T                     TGGT AGCAGAAAT     GGGT
                                ||||  |||||||||     ||||
                                ACCA TCGTCTTTA     TCCA
                                  C        CAGCC
GAM2386  LOC257443 3'  TGGTAAGCAGAGGGC       56348           AATCCAA
                                TGGTAAGCAGA      GGGT
                                ||||||||||       ||||
                                ACCATTCGTCT      CCCG

                                        _______
GAM2387  BCAS2     3'  TTGAAAGCTTTAAATAAGGATC 56358         ATT_    A_
           CTT                    TTGAAAGC    GATGA  ATCCTT
                                ||||||||    |||||  ||||||
                                AACTTTCG    TTATT  TAGGAA
                                     AAAT    CC
GAM2387  DAPP1     3'  TTGAAAGAAAATCCT       56359        CATTGAT
                                TTGAAAG      GAAATCCT
                                |||||||      ||||||||
                                AACTTTC      TTTTAGGA

                                        _______
GAM2387  OCLN      3'  AAAGCATAAAATCCTT      56360        TGAT
                                AAAGCAT    GAAATCCTT
                                |||||||    |||||||||
                                TTTCGTA    TTTTAGGAA

                                         ____
GAM2387  KIAA1034  3'  TGAAAGCAGAAAATCCTT    56361         TTGAT
                                TGAAAGCA     GAAATCCTT
                                ||||||||     |||||||||
                                ACTTTCGT     TTTTAGGAA
                                     C____
GAM2387  KIAA1058  3'  GCAAAAGGATGAAATTCTTA   56362     TT__       C
                                GCA    GATGAAAT CTTA
                                |||    |||||||| ||||
                                CGT    CTACTTTA GAAT
                                  TTTC       A
GAM2387  SERPINB7  3'  TTGAAAGCATTAATGAAAT    56363
                                TTGAAAGCATTGATGAAAT
                                ||||||||||||||||||
                                AACTTTCGTAATTACTTTA

GAM2387  LOC157503 3'  TTGGTAGCAAAAATCCTT    56364      AA    TTGAT
                                TTG  AGCA    GAAATCCTT
                                |||  ||||    |||||||||
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                                AAC  TCGT    TTTTAGGAA
                                  CA  _____
GAM2388 KIF5A    3' CTTTGTGTGTGTGCATGCGTG  56367    A    CTAAA
                                CT TGTGT    GCATGCGTG
                                || |||||    |||||||||
                                GA ACACA    CGTACGCAC
                                 A    CACA_
GAM2388 MHC2TA   3' CTGGTGTGTGCACGCGTG    56368    A_    CTAAA
                                CT  TGTGT    GCATGCGTG
                                ||  |||||    |||||||||
                                GA  ACACA    CGTGCGCAC
                                 CC    _____
GAM2388 UC28     3' CTATGTGTCAGGCACTGTG    56369        TAAA    GC
                                CTATGTGTC    GCAT  GTG
                                |||||||||    ||||  |||
                                GATACACAG    CGTG  CAC
                                      TC__    A_
GAM2388 DKFZp761K1423 5'  TCACTGTGTGTGCATGTGT    56370    _ A    CTAAA    C
                                TC CT TGTGT    GCATG GT
                                || || |||||    ||||| ||
                                AG GA ACACA    CGTAC CA
                                 T  C    _____    A
GAM2388 FLJ21290  3'  TCCTATGTGTGCATGTGT    56371         CTAAA    C
                                TCCTATGTGT    GCATG GT
                                ||||||||||    ||||| ||
                                AGGATACACA    CGTAC CA
                                      _____    A
GAM2388 FLJ23120  3'  TATGTGCGTGCATGTGTG    56372       CTAAA    C
                                TATGTGT    GCATG GTG
                                |||||||    ||||| |||
                                ATACACG    CGTAC CAC
                                    CA___    A
GAM2388 HNRPAB    3'  TCCATATCCAAACAAAGCATGT 56373    _  G  TC       C
             GTG                   TCC TAT TG  TAAAGCATG GTG
                                ||| ||| ||  ||||||||| |||
                                AGG ATA GT  GTTTCGTAC CAC
                                  T   G  TT       A
GAM2388 KIAA1309  3'  TCCTGTGTGTCTAGGAAACTTT 56374     A      __    ATGC
             GTG                   TCCT TGTGTCTA  AAGC    GTG
                                |||| ||||||||  ||||    |||
                                AGGA ACACAGAT  TTTG    CAC
                                  C       CC    AAA_
GAM2388 KIAA1550  3'  CTATGTGTGCACGCATG     56375        CTAAA
                                CTATGTGT    GCATGCGTG
                                ||||||||    |||||||||
                                GATACACA    CGTGCGTAC
                                      _____
GAM2388 ZNF317    3'  TCCTGTGTCTCTAAAGCA    56376     A  G
                                TCCT TGT TCTAAAGCA
                                |||| ||| |||||||||
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                                AGGA ACA AGATTTCGT
                                  C  G
GAM2388 LOC255624 3' TCCTATGTATTTACAAGGCGTG 56377         CTAAA  T_
                                TCCTATGTGT   GCA  GCGTG
                                ||||||||||   |||  |||||
                                AGGATACATA   TGT  CGCAC
                                     AA___   TC
GAM2388 LOC256412 3' CTTCTGTGTCTAACAGGGGTG 56378   A_     AA  TGC
                                CT  TGTGTCTA  GCA  GTG
                                ||  ||||||||  |||  |||
                                GA  ACACAGAT  TGT  CAC
                                 AG       __  CCC
GAM2389 PPP3R1   3' TGGCACTTTTGTACTCTAT   56381        GTAATAA
                                TGGCATTTT     TGCTCTGT
                                |||||||||     ||||||||
                                ACCGTGAAA     ATGAGATA
                                     AC_____
GAM2389 DKFZP566I1024 3' TGGCCTTTCAGAGTGCTCTGT 56382     A   GTAATAA
                                TGGC TTTT     TGCTCTGT
                                |||| ||||     ||||||||
                                ACCG AAAG     ACGAGACA
                                  G   TCTC___
GAM2389 FLJ13189 3' TGGTGTTTTGTAAAACACT   56383    CA      T
                                TGG  TTTTGTAA AATGCT
                                |||  |||||||| ||||||
                                ACC  AAAACATT TTGTGA
                                  AC      _
GAM2389 FLJ20040 3' GGCATTTGTGATGCTCTG    56384       T  AATA
                                GGCATTT GT   ATGCTCTG
                                ||||||| ||   ||||||||
                                CCGTAAA CA   TACGAGAC
                                    _ C___
GAM2389 FLJ20152 3' TGGTGTTTTTTGTGCTCTGT  56385    CA   GTAATAA
                                TGG  TTTT     TGCTCTGT
                                |||  ||||     ||||||||
                                ACC  AAAA     ACGAGACA
                                  AC   AAC____
GAM2389 FLJ20716 3' TGTATTTTGTAATAATGCAACA 56386   GC          TC__
           TGT                   TG  ATTTTGTAATAATGC   TGT
                                ||  ||||||||||||||   |||
                                AC  TAAAACATTATTACG   ACA
                                 A_          TTGT
GAM2389 FLJ22386 3' TGGCACTGGCTGGTGCTCTGT 56387       TT  AATAA
                                TGGCATT  GT    TGCTCTGT
                                |||||||  ||    ||||||||
                                ACCGTGA  CG    ACGAGACA
                                    C_  ACC__
GAM2389 KLHL4    3' TAGCATTTTGTAGTAATG    56388          A
                                TGGCATTTTGTA TAATG
                                |||||||||||| |||||
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                                ATCGTAAAACAT ATTAC
                                       C
GAM2389 PRO0628  5' TGAGTATTTGTTAATGCTCTGT 56389    CAT    AA
                                TGG   TTTGT  TAATGCTCTGT
                                |||   |||||  ||||||||||
                                ACT   AAACA  ATTACGAGACA
                                  CAT    __
GAM2389 SLI     3' GGTGCTGATGATGCTCTG    56390    CATTT   A_  A
                                GG    TGT  AT ATGCTCTG
                                ||    |||  || ||||||||
                                CC    ACG  TA TACGAGAC
                                  _____  AC  C
GAM2389 LOC151195 3' TGGTTTTTGTAACTCT     56391     CA      ATAAT
                                TGG  TTTTGTA    GCTCT
                                |||  |||||||    |||||
                                ACC  AAAACAT    TGAGA
                                  A_     _____
GAM2389 LOC152018 3' TGGCATTTGTACATCTCTG    56392        T   ATAATG
                                TGGCATTT GTA     CTCTG
                                |||||||| |||     |||||
                                ACCGTAAA CAT     GAGAC
                                     _   GTA___
GAM2390 ADCY2    3' TGTAATAATTCTCTTGCTT    56395      A   CTC
                                TGTGA TAA   TCTCTTGTTT
                                ||||| |||   ||||||||||
                                ACATT ATT   AGAGAACGAA
                                   _   A__
GAM2390 BTAF1    3' TGAGAATAACTTGTTT      56396    T      CTCTCT
                                TG GAATAACT     TGTTT
                                || ||||||||     |||||
                                AC CTTATTGA     ACAAA
                                 T      _______
GAM2390 CEP1     5' TGTGGATAACCTCTGCCTC    56397     A    T   CTT
                                TGTG ATAAC CTCT   GTTTC
                                |||| ||||| ||||   |||||
                                ACAC TATTG GAGA   CGGAG
                                  C    _   ____
GAM2390 COL19A1  3' TGTGGATACAGCCTTGTTTC   56398     A   ACTCTC
                                TGTG ATA     TCTTGTTTC
                                |||| |||     |||||||||
                                ACAC TAT     GGAACAAAG
                                  C   GTC___
GAM2390 DLD      3' TGAATGACTGACTTGTTTCC   56399      A   CTCT
                                TGAAT ACT    CTTGTTTCC
                                ||||| |||    |||||||||
                                ACTTA TGA    GAACAAAGG
                                  C   CT__
GAM2390 IL1F8    3' TGAATAATTCTGCTGTTTC    56400        C   CTC
                                TGAATAA TCT   TTGTTTC
                                ||||||| |||   |||||||
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                              ACTTATT AGA   GACAAAG
                                  A  C__
GAM2390  NDUFV3   5'  GTGAATGAACACCCTTGTTTC  56401      _  TCT
                              GTGAAT AAC   CTCTTGTTTC
                              ||||||| |||   ||||||||||
                              CACTTA TTG   GGGAACAAAG
                                 C  T__
GAM2390  PARK2    3'  TGTGAGAACTCTCTCTC     56402      AT
                              TGTGA  AACTCTCTCTT
                              |||||  ||||||||||
                              ACACT  TTGAGAGAGAG
                                 C_
GAM2390  PARK2    3'  TGTGAGAACTCTCTCTC     56402      AT
                              TGTGA  AACTCTCTCTT
                              |||||  ||||||||||
                              ACACT  TTGAGAGAGAG
                                 C_
GAM2390  PARK2    3'  TGTGAGAACTCTCTCTC     56402      AT
                              TGTGA  AACTCTCTCTT
                              |||||  ||||||||||
                              ACACT  TTGAGAGAGAG
                                 C_
GAM2390  PCDH9    5'  TGTGAATGGCTGTCTCCT    56403       AA  C
                              TGTGAAT  CT TCTCTT
                              |||||||  || ||||||
                              ACACTTA  GA AGAGGA
                                  CC  C
GAM2390  SPI1     3'  TGAGAATAACTTTACTTGTTT  56404    T      CTCT
                              TG GAATAACT    CTTGTTT
                              || ||||||||    |||||||
                              AC CTTATTGA    GAACAAA
                               T       AAT_
GAM2390  STC1     3'  TGTGAATAACCTCTCCC     56405         T
                              TGTGAATAAC CTCTCTT
                              |||||||||| |||||||
                              ACACTTATTG GAGAGGG
                                        _
GAM2390  TRAM     3'  TGTAAATAGTTTTCTCTCC   56406        AC__
                              TGTGAATA    TCTCTCT
                              ||||||||    |||||||
                              ACATTTAT    AGAGAGG
                                   CAAA
GAM2390  VHL      3'  TGGAATTTCACTCTTGTTTCC  56407    T   AAC  T
                              TG GAAT   TC CTCTTGTTTCC
                              || ||||   || ||||||||||
                              AC CTTA   AG GAGAACAAAGG
                               _   A__  T
GAM2390  DNAJA2   3'  TGTGAAAGGGAGTCTTGTTTCC 56408       TAACTCTC
                              TGTGAA       TCTTGTTTCC
                              ||||||       ||||||||||
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                                ACACTT      AGAACAAAGG
                                   TCCCTC__
GAM2390  FLJ13615  3'  TGTGAATAATTTATAGCCTCTT 56409        CTCTCT_  G
             TCC                   TGTGAATAA      CTT TTTCC
                                |||||||||      ||| |||||
                                ACACTTATT      GGA AAAGG
                                    AAATATC   G
GAM2390  KIAA0481  5'  TGTGAACAGTTCTTTCGGCTTC 56410        AC   C  TT
                                TGTGAATA  TCT TC  GTTTC
                                ||||||||  ||| ||  |||||
                                ACACTTGT  AGA AG  CGAAG
                                    CA   A  C_
GAM2390  KIAA0937  3'  TGAAGGTTCTCTTGTTTCC    56411      TAACTC
                                TGAA     TCTCTTGTTTCC
                                ||||     ||||||||||||
                                ACTT     AGAGAACAAAGG
                                  CCA___
GAM2390  MGC16169  3'  TGTGAATAGTTTCTCAGTTTTC 56412        ACTC    TTG
                                TGTGAATA   TCTC   TTTC
                                ||||||||   ||||   ||||
                                ACACTTAT   AGAG   AAAG
                                    CAA_   TCA
GAM2390  SEMA3C    3'  TATGAATAACTCGTGTTT    56413          TCTCT
                                TGTGAATAACTC    TGTTT
                                ||||||||||||    |||||
                                ATACTTATTGAG    ACAAA
                                      C____
GAM2390  STAM2     3'  TGTAAATAACAGAAGATTTGTT 56414         TCTCTC_
             TCC                   TGTGAATAAC      TTGTTTCC
                                ||||||||||      ||||||||
                                ACATTTATTG      AACAAAGG
                                     TCTTCTA
GAM2390  LOC113251 3'  TGGACGTACTTTCTCTTGTTTC 56415    T  ATA   C
             C                     TG GA   ACT TCTCTTGTTTCC
                                || ||   ||| ||||||||||||
                                AC CT   TGA AGAGAACAAAGG
                                 _  GCA   A
GAM2390  LOC127702 3'  TGTGAAATAGCTCCCGTTT    56416       TAACTCT
                                TGTGAA      CTCTTGTTT
                                ||||||      |||||||||
                                ACACTT      GAGGGCAAA
                                   TATC___
GAM2390  LOC136345 3'  TGTGGGTAACTCCTGCTTC    56417      AA      CTCT
                                TGTG  TAACTCT    TGTTTC
                                ||||  |||||||    ||||||
                                ACAC  ATTGAGG    ACGAAG
                                  CC      _____
GAM2390  LOC149535 3'  TGTGAACAGAGCTTTTTGTTTC 56418        ACT  CTC
             C                     TGTGAATA   CT   TTGTTTCC
                                ||||||||   ||   ||||||||
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                                ACACTTGT  GA  AACAAAGG
                                    CTC  AA_
GAM2390  LOC149706 5'  TGTGAGTCACTTCCTGTTTC  56419     ATA  CTC
                                TGTGA  ACT  TCTTGTTTC
                                |||||  |||  |||||||||
                                ACACT  TGA  AGGACAAAG
                                   CAG  ___
GAM2390  LOC154641 5'  TGTGAATTGACTCTCTCAGTCT 56420      A_     TT
                                TGTGAAT  ACTCTCTC  GTTT
                                |||||||  ||||||||  ||||
                                ACACTTA  TGAGAGAG  CAGA
                                    AC      T_
GAM2390  LOC155032 5'  TGTGGGTAACTCCTGCTTC  56417     AA     CTCT
                                TGTG  TAACTCT   TGTTTC
                                ||||  |||||||   ||||||
                                ACAC  ATTGAGG   ACGAAG
                                  CC     _____
GAM2390  LOC222070 5'  TGTGAATAACCTCAGTATTC  56421        T  TCT
                                TGTGAATAAC CTC  TGTTT
                                |||||||||| |||  |||||
                                ACACTTATTG GAG  ATAAG
                                      _  TC_
GAM2390  LOC92379  3'  TATGAGTGACTCTCTCCTATCT 56422     ATA
                                TGTGA  ACTCTCTCTTGTTT
                                |||||  ||||||||||||||
                                ATACT  TGAGAGAGGATAGA
                                   CAC
GAM2391  KLRC1    3'  GATGTCTGTACTTTAGTAATT  56425    ACAA  _
                                GAT   TG ACTTTAGTAATT
                                |||   || ||||||||||||
                                CTA   AC TGAAATCATTAA
                                  CAG_  A
GAM2391  KLRC1    3'  GATGTCTGTACTTTAGTAATT  56425    ACAA  _
                                GAT   TG ACTTTAGTAATT
                                |||   || ||||||||||||
                                CTA   AC TGAAATCATTAA
                                  CAG_  A
GAM2391  KLRC2    3'  GATGTCTGTACTTTAGTAATT  56425    ACAA  _
                                GAT   TG ACTTTAGTAATT
                                |||   || ||||||||||||
                                CTA   AC TGAAATCATTAA
                                  CAG_  A
GAM2391  MMP8     3'  GAAACAATGACTTAATA     56426    T       T
                                GA ACAATGACTT AGTA
                                || |||||||||| ||||
                                CT TGTTACTGAA TTAT
                                 T       _
GAM2391  NEO1     3'  GATGCAATGACTCAGAATT   56427    A       T  T
                                GAT CAATGACTT AG AATT
                                ||| ||||||||| || ||||
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                                CTA GTTACTGAG TC TTAA
                                  C       _ _
GAM2391  KIAA1344  3'  AAGGTACAATGACTAAGCAATT 56428     A        TT
                                AAG TACAATGACT  AGTAATT
                                ||| ||||||||||  |||||||
                                TTC ATGTTACTGA  TCGTTAA
                                  C         T_
GAM2391  LOC147093 3'  TAAGATTGATGACTTTCAGT   56429       ACA      _
                                TAAGAT   ATGACTT TAGT
                                ||||||   ||||||| ||||
                                ATTCTA   TACTGAA GTCA
                                    AC_      A
GAM2392  KIAA1853  3'  TGAGCACCTTGTCAACCCCAAG 56432   T    ___
                                G GGCAC   GTCAACCCCAAG
                                | |||||   ||||||||||||
                                A TCGTG   CAGTTGGGGTTC
                                 C    GAA
GAM2393  EIF2AK3   3'  CCATTTTAGTTCTCACTATA   56435        A  G
                                CCATTTTA GT TTTCACTATA
                                |||||||| || ||||||||||
                                GGTAAAAT CA AGAGTGATAT
                                      _ _
GAM2393  ESR1      3'  AGCCACTTTAAATTCTTTGCT  56436           G   CA
                                AGCCATTTTAAGT TTT  CT
                                |||||||||||||| |||  ||
                                TCGGTGAAATTTA GAA  GA
                                       A   AC
GAM2393  GCA       3'  GCCATTTTAGGTGAACTAT    56437         A   TTTC
                                GCCATTTTA GTG    ACTAT
                                ||||||||| |||    |||||
                                CGGTAAAAT CAC    TGATA
                                     C   T___
GAM2393  PTPN18    3'  GCCATTTAAAGTGTTTCA     56438        T
                                GCCATTT AAGTGTTTCA
                                ||||||| ||||||||||
                                CGGTAAA TTCACAAAGT
                                    T
GAM2393  UBE3A     3'  AGCCATCTTTTTCATTAT     56439         AAGTG    C
                                AGCCATTTT     TTTCA TAT
                                |||||||||     ||||| |||
                                TCGGTAGAA     AAAGT ATA
                                      _____     A
GAM2393  UBE3A     3'  AGCCATCTTTTTCATTAT     56439         AAGTG    C
                                AGCCATTTT     TTTCA TAT
                                |||||||||     ||||| |||
                                TCGGTAGAA     AAAGT ATA
                                      _____     A
GAM2393  UBE3A     3'  AGCCATCTTTTTCATTAT     56439         AAGTG    C
                                AGCCATTTT     TTTCA TAT
                                |||||||||     ||||| |||
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                                TCGGTAGAA    AAAGT ATA
                                      _____   A
GAM2393 VCAM1    3' GCTATTTTAAGCAATCTTGCTA 56440   C       _  CA
           T                   GC ATTTTAAGTG TTT  CTAT
                               || |||||||||| |||  ||||
                               CG TAAAATTCGT AGA  GATA
                                A        T  AC
GAM2393 VCAM1    3' GCTATTTTAAGCAATCTTGCTA 56440   C       _  CA
           T                   GC ATTTTAAGTG TTT  CTAT
                               || |||||||||| |||  ||||
                               CG TAAAATTCGT AGA  GATA
                                A        T  AC
GAM2393 AF311304 3' ACCATTTTAAGTGTTACCAT  56441           TC
                               GCCATTTTAAGTGTT  ACTAT
                               ||||||||||||||  |||||
                               TGGTAAAATTCACAA  TGGTA

                                     __
GAM2393 FLJ12910 3' ACCATTTGTTTCACT      56442      TTAAG
                               GCCATT    TGTTTCACT
                               ||||||    |||||||||
                               TGGTAA    ACAAAGTGA

                                    _____
GAM2393 JWA      3' ACCATTTTTTTCACT      56443       AAGTG
                               GCCATTTT    TTTCACT
                               ||||||||    |||||||
                               TGGTAAAA    AAAGTGA

                                    _____
GAM2393 KIAA0226 3' GCTTTTTGAGTCTCACTAT   56444   CA   AAGT
                               GC  TTTT   GTTTCACTAT
                               ||  ||||   ||||||||||
                               CG  AAAA   CAGAGTGATA
                                A_   CT__
GAM2393 KIAA0354 3' GCATTTTGCATCACTATA    56445   C   TAAG  T
                               GC ATTT    TGT TCACTATA
                               || ||||    ||| ||||||||
                               CG TAAA    ACG AGTGATAT
                                _   _____  T
GAM2393 KIAA1393 3' GCCATTCTTGCATTGCTATA  56446       AAG  TTCA
                               GCCATTTT   TGT   CTATA
                               ||||||||   |||   |||||
                               CGGTAAGA   ACG   GATAT
                                    ___   TAAC
GAM2393 MGC10646 3' AGCCATTCTGGTCACT      56447       TAAG  TT
                               AGCCATTT    TG  TCACT
                               ||||||||    ||  |||||
                               TCGGTAAG    AC  AGTGA
                                    _____  C_
GAM2393 SEMA3C   3' AGCATTTTAACTATTTTTGCTA 56448    C     G    CA_
           TA                    AGC ATTTTAA TGTTT   CTATA
                               ||| ||||||| |||||   |||||
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                                TCG TAAAATT ATAAA   GATAT
                                  _     G    AAC
GAM2393  TSLRP    3'  AGCTATCTTAAGGATATTACTA 56449     C      TG TTC
                T                  AGC ATTTTAAG  T   ACTAT
                                   ||| |||||||| |   |||||
                                   TCG TAGAATTC  A   TGATA
                                     A       CT TAA
GAM2393  LOC126167 3'  GCACATTTGTTATTTTCACTAT 56450    _    TAAGTG
                                   GC CATTT     TTTCACTAT
                                   || |||||     |||||||||
                                   CG GTAAA     AAAGTGATA
                                    T    CAATA_
GAM2393  LOC147219 3'  AGCCATTCTGATGAGTTCACTA 56451         AA   T_
                T                  AGCCATTTT  GTG  TTCACTAT
                                   |||||||||  |||  ||||||||
                                   TCGGTAAGA  TAC  AAGTGATA
                                        C_   TC
GAM2394  ACPT     3'  CTGGACCCGGGAGAA      56454     T    GA
                                   CTG GACT  TGGGGGAG
                                   ||| ||||  ||||||||
                                   GAC CTGG  GCCCTCTT
                                     _   __
GAM2394  ACPT     3'  CTGGACCCGGGAGAA      56454     T    GA
                                   CTG GACT  TGGGGGAG
                                   ||| ||||  ||||||||
                                   GAC CTGG  GCCCTCTT
                                     _   __
GAM2394  AP2M1    3'  ACACTGATGTGTGGTGGGGGAG 56455       _  AC  A
                                   ACACTG TG  TG TGGGGGAG
                                   |||||| ||  || ||||||||
                                   TGTGAC AC  AC ACCCCCTC
                                      T  AC  C
GAM2394  ARF5     3'  CTGTGGCTATGGGGGAG     56456       A   A
                                   CTGTG CTG TGGGGGAG
                                   ||||| ||| ||||||||
                                   GACAC GAT ACCCCCTC
                                     C   _
GAM2394  ATP4A    3'  ACCTTGGGAATGGGGGAG    56457     G  ACT
                                   ACT TG   GATGGGGGAG
                                   ||| ||   ||||||||||
                                   TGG AC   TTACCCCCTC
                                     A  CC_
GAM2394  CAPN5    3'  ACACTGAGGCTGAGAGAG    56458       TGA    T
                                   ACACTG   CTGA GGGGG
                                   ||||||   |||| |||||
                                   TGTGAC   GACT CTCTC
                                      TCC   _
GAM2394  CD34     3'  ACACTGGATGGGAGAG      56459       TGACT
                                   ACACTG    GATGGGGGAG
                                   ||||||    ||||||||||
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                                TGTGAC    CTACCCTCTC
                                      _____
GAM2394  CUL4B    3'  AACACTGTTGTTGATGGTCCGG 56460        GAC     G__
                                AACACTGT   TGATGG   GG
                                ||||||||   ||||||   ||
                                TTGTGACA   ACTACC   CC
                                     ACA     AGG
GAM2394  DLEC1    3'  ACACGTGACAAGGGAG     56461     T    TGAT
                                ACAC GTGAC    GGGGGAG
                                |||| |||||    |||||||
                                TGTG CACTG    TTCCCTC
                                  _    ____
GAM2394  DLEC1    3'  ACACGTGACAAGGGAG     56461     T    TGAT
                                ACAC GTGAC    GGGGGAG
                                |||| |||||    |||||||
                                TGTG CACTG    TTCCCTC
                                  _    ____
GAM2394  DNLC2A   3'  CCGTTGGTGGGGGAGAA     56462     GAC  A
                                CTGT   TG TGGGGGAGAA
                                ||||   || ||||||||||
                                GGCA   AC ACCCCCTCTT
                                  ___  C
GAM2394  EGFL4    5'  TGCTGCTGTCGGGGGAGAA   56463     GA   A
                                TGT  CTG TGGGGGAGAA
                                |||  ||| ||||||||||
                                ACG  GAC GCCCCCTCTT
                                  AC   A
GAM2394  GOT2     3'  ACACTGTGGCTGAAAGAA    56464        A    T
                                ACACTGTG CTGA GGGG
                                |||||||| |||| ||||
                                TGTGACAC GACT TCTT
                                     C    T
GAM2394  HCK      3'  ACTGTGGCTGAAGCGAGGG   56465       A    __
                                ACTGTG CTGA  TGGGGG
                                |||||| ||||  ||||||
                                TGACAC GACT  GCTCCC
                                    C    TC
GAM2394  HOXC6    3'  TGTGTGATTAGGGGAGA     56466     AC   _
                                TGTG  TGAT GGGGGAGA
                                ||||  |||| ||||||||
                                ACAC  ACTA TCCCCTCT
                                  __    A
GAM2394  ITGA3    3'  ACACAGCCCATGGGGGAG    56467     TGTGA  G
                                ACAC    CT ATGGGGGAG
                                ||||    || |||||||||
                                TGTG    GG TACCCCCTC
                                  TC___  G
GAM2394  ITGA3    3'  ACACAGCCCATGGGGGAG    56467     TGTGA  G
                                ACAC    CT ATGGGGGAG
                                ||||    || |||||||||
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                                TGTG    GG TACCCCCTC
                                  TC___  G
GAM2394  KCNJ6    3'  TGTGTTGGGGGGAGAA     56468     AC  AT
                                TGTG  TG  GGGGGAGAA
                                ||||  ||  |||||||||
                                ACAC  AC  CCCCCTCTT
                                  A_  __
GAM2394  LAMP2    3'  CTGGGATTGATAAAAGAA    56469     T  C
                                CTG GA TGATGGGGGAG
                                |||  ||  ||||||||||
                                GAC CT ACTATTTTCTT
                                  C  A
GAM2394  LBR      3'  CACTGTATTGATAAAGG     56470       AC
                                CACTGTG  TGATGGGGG
                                |||||||  |||||||||
                                GTGACAT  ACTATTTCC
                                    A_
GAM2394  LEF1     5'  GTAACTCAAGGGTGGGGGAG  56471       _  ___
                                GTGACT GA   TGGGGGAG
                                ||||||  ||   ||||||||
                                CATTGA TT   ACCCCCTC
                                   G  CCC
GAM2394  LIFR     3'  CTGTGGATAGAGGAGAA     56472      ACT
                                CTGTG   GATGGGGGAGAA
                                |||||   ||||||||||||
                                GACAC   CTATCTCCTCTT
                                  ___
GAM2394  MECP2    3'  ACTCGTAGGATGGGGGAGAA  56473     _   ACT
                                ACT GTG   GATGGGGGAGAA
                                |||  |||   ||||||||||||
                                TGA CAT   CTACCCCCTCTT
                                  G   C__
GAM2394  NAV2     3'  CTGTGGGAAAGGGGAGAA    56474      ACT  T
                                CTGTG   GA GGGGGAGAA
                                |||||   ||  |||||||||
                                GACAC   CT TCCCCTCTT
                                   C__  T
GAM2394  NME1     3'  AACACTGTACAGGGAG      56475        A TGATG
                                AACACTGTG C    GGGGAG
                                |||||||||  |    ||||||
                                TTGTGACAT G    TCCCTC
                                   _ _____
GAM2394  NRIP1    3'  TGTGACTGTATTGGGGAA    56476       _  G
                                TGTGACTG AT GGGGAG
                                ||||||||  ||  ||||||
                                ACACTGAC TA CCCCTT
                                    A  A
GAM2394  NRXN1    3'  AACACTGTGGATGTTAGGGAA  56477        AC  A
                                AACACTGTG  TG TGGGGGA
                                |||||||||  ||  |||||||
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                                TTGTGACAC  AC ATCCCTT
                                     CT  A
GAM2394  NRXN1    3'  AACACTGTGGATGTTAGGGAA  56477        AC  A
                                AACACTGTG  TG TGGGGGA
                                |||||||||  || |||||||
                                TTGTGACAC  AC ATCCCTT
                                     CT  A
GAM2394  OFD1     3'  ACTATGACTGGAGAA      56478        GAT
                                ACTGTGACT   GGGGGA
                                |||||||||   ||||||
                                TGATACTGA   CCTCTT
                                      ___
GAM2394  OGG1     3'  ACTGTGGCCAGGGGAGA    56479      A  GAT
                                ACTGTG CT   GGGGGAGA
                                ||||||  ||  ||||||||
                                TGACAC GG   TCCCCTCT
                                   C  ___
GAM2394  OGG1     3'  ACTGTGGCCAGGGGAGA    56479      A  GAT
                                ACTGTG CT   GGGGGAGA
                                ||||||  ||  ||||||||
                                TGACAC GG   TCCCCTCT
                                   C  ___
GAM2394  PIK3R2   3'  CTGGAGAATGGGGGAG     56480    T  CT
                                CTG GA  GATGGGGGAG
                                |||  ||  ||||||||||
                                GAC CT  TTACCCCCTC
                                  _  C_
GAM2394  PPP2R5E  3'  CTGTGATGAGATATAGAA   56481      C   T  GGG
                                CTGTGA TGA GG   AGAA
                                ||||||  |||  ||   ||||
                                GACACT ACT CT   TCTT
                                   _   _  ATA
GAM2394  PRKCN    3'  AACACTGTGACAAAGGGAGAG  56482         TGAT
                                AACACTGTGAC    GGGGGAG
                                ||||||||||    |||||||
                                TTGTGACACTG    CCCTCTC
                                      TTT_
GAM2394  RAB36    3'  AACACTGTGACGGATCCTGGGG 56483         T   G__
            A                    AACACTGTGAC GAT   GGGGA
                                ||||||||||  |||   |||||
                                TTGTGACACTG CTA   CCCCT
                                      C   GGA
GAM2394  RAB38    3'  AACACTGTGATGATGGTGAG   56484        C     GG
                                AACACTGTGA TGATGG  GAG
                                ||||||||||  ||||||  |||
                                TTGTGACACT ACTACC  CTC
                                      _     A_
GAM2394  RANBP3   5'  AACACTGTGGTATGTGGGGG   56485        AC_  A
                                AACACTGTG   TG TGGGGG
                                |||||||||   || ||||||
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                                TTGTGACAC   AC ACCCCC
                                     CAT  _
GAM2394  RANBP3   3'  ACACCTGTGGCTGGGGAA    56486     _   ACTGA
                                ACAC TGTG    TGGGGGA
                                |||| ||||    |||||||
                                TGTG ACAC    ACCCCTT
                                  G   CG___
GAM2394  RELA     3'  CACTTGAGAAGAGGGGAGA   56487     G   CT  T_
                                CACT TGA  GA  GGGGGAGA
                                |||| |||  ||  ||||||||
                                GTGA ACT  CT  TCCCCTCT
                                  _  __ TC
GAM2394  RET      3'  ACATGTGGCTGGGACTGGGG  56488     C   A   A___
                                ACA TGTG CTG   TGGGG
                                ||| |||| |||   |||||
                                TGT ACAC GAC   ACCCC
                                  _   C  CCTG
GAM2394  RTN1     3'  ACTGGAGGGAGGGGGGAA    56489     T  CT  T
                                ACTG GA  GA GGGGGAG
                                |||| ||  || |||||||
                                TGAC CT  CT CCCCCTT
                                  _ CC  C
GAM2394  SERPINE1 3'  CAATGTGACTGGAACAGAA   56490    C      GAT   G
                                CA TGTGACT   GGGG AGAA
                                || |||||||   |||| ||||
                                GT ACACTGA   CCTT TCTT
                                 T      ___   G
GAM2394  SH3BP2   3'  ACACTGTGAGGGGAG       56491        CTGATG
                                ACACTGTGA     GGGGAG
                                |||||||||     ||||||
                                TGTGACACT     CCCCTC
                                      _______
GAM2394  SNX4     3'  CACTTTGATTGAAGAGAA    56492     G   C   T
                                CACT TGA TGA GGGGGA
                                |||| ||| ||| ||||||
                                GTGA ACT ACT TCTCTT
                                  A   A   _
GAM2394  SORCS2   3'  CACTGTGAGCTAAGGGGGAG  56493        _   T
                                CACTGTGA CTGA GGGGGAG
                                |||||||| |||| |||||||
                                GTGACACT GATT CCCCCTC
                                    C   _
GAM2394  SP110    3'  AACATGGTGACTGAGAGGG   56494     CT      T
                                AACA  GTGACTGA GGGGG
                                ||||  |||||||| |||||
                                TTGT  CACTGACT CTCCC
                                  AC       _
GAM2394  STXBP1   3'  CACTGTGACTTAGACTGGAGGA 56495         GA___
                                CACTGTGACT    TGGGGGA
                                |||||||||     |||||||
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                                GTGACACTGA    ACCTCCT
                                      ATCTG
GAM2394  TCFL4    3'  AACACTGAGACATGGGAGAG   56496       T   TG
                                AACACTG GAC  ATGGGGGAG
                                ||||||| |||  |||||||||
                                TTGTGAC CTG  TACCCTCTC
                                   T  __
GAM2394  UBE2H    3'  AACACTGTGGCTGCAGGG    56497        A   A
                                AACACTGTG CTG TGGGG
                                ||||||||| ||| |||||
                                TTGTGACAC GAC GTCCC
                                      C  _
GAM2394  XCL1     3'  ACTTGTGACTGATGTGTAAAGA 56498    _       GG_
              A                  ACT GTGACTGATG   GGAGAA
                                ||| ||||||||||   ||||||
                                TGA CACTGACTAC   TTTCTT
                                  A        ACA
GAM2394  AMOTL1   3'  AACACAGTGATCCCAGGGGAG  56499     T   CTGA
                                AACAC GTGA    TGGGGGAG
                                ||||| ||||    ||||||||
                                TTGTG CACT    GTCCCCTC
                                   T    AGG_
GAM2394  BA526D8.4 5'  CATGTGACTTCGGGGAGAA   56500    C     GATG
                                CA TGTGACT    GGGGAGAA
                                || |||||||    ||||||||
                                GT ACACTGA    CCCCTCTT
                                 _      AG__
GAM2394  C20orf55  3'  AACCTTGTATTGGGGGAG    56501     AC    ACTGA
                                AAC  TGTG    TGGGGGAG
                                |||  ||||    ||||||||
                                TTG  ACAT    ACCCCCTC
                                  GA    A____
GAM2394  DKFZP434J037 3'  CTGGGAGGTGGGGGAGAA    56502     T  CTGA
                                CTG GA    TGGGGGAGAA
                                ||| ||    ||||||||||
                                GAC CT    ACCCCCTCTT
                                  C  CC__
GAM2394  DKFZp547J036 3'  AACACCGGGAGGGGTGGGGGAG 56503        T  CTGA
              A                  AACACTG GA    TGGGGGAGA
                                ||||||| ||    |||||||||
                                TTGTGGC CT    ACCCCCTCT
                                   C  CCCC
GAM2394  DT1P1A10  3'  ACACTGTACTGGGGAA      56504         A  GAT
                                ACACTGTG CT   GGGGGA
                                |||||||| ||   ||||||
                                TGTGACAT GA   CCCCTT
                                      _  ____
GAM2394  FEM-2    3'  ACTGTGGCTGGAAGAGAA    56505       ACTGA
                                ACTGTG    TGGGGGAGAA
                                ||||||    ||||||||||
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                                TGACAC    ACCTTCTCTT
                                   CG___
GAM2394  FKSG17   5' CTGTAAAGAAGGGGGGAA    56506      CT  T    A
                                CTGTGA  GA GGGGG GAA
                                ||||||  || ||||| |||
                                GACATT  CT CCCCC CTT
                                   T_  T    _
GAM2394  FLJ10743 3' ACTGTGCTCTGGGAGAG     56507      A  GA
                                ACTGTG CT  TGGGGGAG
                                ||||||| ||  ||||||||
                                TGACAC GA  ACCCTCTC
                                   _ G_
GAM2394  FLJ10901 3' CTGGGAAATGGGGGAGA     56508     T  CT
                                CTG GA  GATGGGGGAGA
                                ||| ||  ||||||||||
                                GAC CT  TTACCCCCTCT
                                  C __
GAM2394  FLJ11807 3' CACTGTGCCCAGGGGAGA    56509       A  GA
                                CACTGTG CT  TGGGGGAGA
                                ||||||| ||  |||||||||
                                GTGACAC GG  GTCCCCTCT
                                   _ __
GAM2394  FLJ12287 3' AACACTGTGTTTCTGGAGG   56510        ACTGA
                                AACACTGTG    TGGGGG
                                |||||||||    ||||||
                                TTGTGACAC    ACCTCC
                                     AAAG_
GAM2394  FLJ12876 3' CTGTGACTGACTTTTGGAA   56511         GGG_
                                CTGTGACTGAT   GGAG
                                ||||||||||    ||||
                                GACACTGACTG   CCTT
                                      AAAA
GAM2394  FLJ13102 3' ACTGTGTGGTGGGAGAG     56512      AC  A
                                ACTGTG  TG TGGGGGAG
                                ||||||  || ||||||||
                                TGACAC  AC ACCCTCTC
                                   __  C
GAM2394  FLJ20154 5' CACTGTATGGTGGGGGAG    56513      AC  A
                                CACTGTG  TG TGGGGGAG
                                |||||||  || ||||||||
                                GTGACAT  AC ACCCCCTC
                                   __  C
GAM2394  FLJ20203 3' AACACTGTGATTAGACCACAGA 56514        CT_  GGG
           A                     AACACTGTGA  GAT  GGAG
                                ||||||||||  |||  ||||
                                TTGTGACACT  CTG  TCTT
                                     AAT  GTG
GAM2394  FLJ20464 5' CTGTGGTTTGGGGGAGAA    56515     ACTGA
                                CTGTG    TGGGGGAGAA
                                |||||    ||||||||||
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                                GACAC    ACCCCCTCTT
                                   CAA__
GAM2394  FLJ21034  3'  CTGTGACTGATTCTGGAA    56516          GGG
                                CTGTGACTGAT   GGAG
                                ||||||||||   ||||
                                GACACTGACTA   CCTT
                                      AGA
GAM2394  FLJ22035  3'  ACTGTGATGAGAGGGAGAA   56517       C   T
                                ACTGTGA TGA GGGGGAGAA
                                ||||||| ||| |||||||||
                                TGACACT ACT CTCCCTCTT
                                   _  _
GAM2394  FLJ23024  3'  AACAATGTGACTGGGAGAG   56518     C      GAT
                                AACA TGTGACT   GGGGGAG
                                |||| |||||||   |||||||
                                TTGT ACACTGA   CCCTCTC
                                  T     ___
GAM2394  FLJ23191  5'  CACTGTGACTGATAATGGAG   56519           G
                                CACTGTGACTGATGG GGAG
                                |||||||||||||| ||||
                                GTGACACTGACTATT CCTC
                                         A
GAM2394  FLJ23590  3'  ATAACTAGGGATGGGGGAG   56520       ___
                                GTGACT   GATGGGGGAG
                                ||||||   ||||||||||
                                TATTGA   CTACCCCCTC
                                    TCC
GAM2394  FLJ32865  3'  CACCGGGTGGTGGGGGAG    56521      TGAC  A
                                CACTG    TG TGGGGGAG
                                |||||    || ||||||||
                                GTGGC    AC ACCCCCTC
                                   CC__  C
GAM2394  FREQ     3'  CAGGATGTTGGTGGGGGAG   56522    CT   AC  A
                                CA  GTG  TG TGGGGGAG
                                ||  |||  || ||||||||
                                GT  TAC  AC ACCCCCTC
                                 CC   A_  C
GAM2394  FSCN3    5'  CATTGTGACTGTGAGGG     56523    C      A
                                CA TGTGACTG TGGGGG
                                || |||||||| ||||||
                                GT ACACTGAC ACTCCC
                                 A      _
GAM2394  H17      3'  ACACTGGGGAGGGGGAGA    56524       TGACT  T
                                ACACTG    GA GGGGGAGA
                                ||||||    || ||||||||
                                TGTGAC    CT CCCCCTCT
                                   CC___  _
GAM2394  HARS2    3'  ACACTGTGGCAGAGCAGAAGGG 56525        ACT  T___
             AG                   ACACTGTG   GA    GGGGGAG
                                ||||||||   ||   |||||||
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                              TGTGACAC  CT   TTCCCTC
                                  CGT  CGTC
GAM2394  HSPC152  3'  AACACTGTGTTTGGTGTCATTG 56526       AC  A _____
           GG                  AACACTGTG  TG TG   GGG
                               |||||||||  || ||   |||
                               TTGTGACAC  AC AC   CCC
                                  AA  C  AGTAA
GAM2394  HSPC152  3'  AACACTGTGTTTGGTGTCATTG 56526       AC  A _____
           GG                  AACACTGTG  TG TG   GGG
                               |||||||||  || ||   |||
                               TTGTGACAC  AC AC   CCC
                                  AA  C  AGTAA
GAM2394  KCNH4    3'  TGTTGTAATGGGGGAGA    56527    GAC
                               TGT   TGATGGGGGAGA
                               |||   ||||||||||||
                               ACA   ATTACCCCCTCT
                                 AC_
GAM2394  KIAA0016 3'  ACTGTGACTACGGAGAA    56528       G
                               ACTGTGACT ATGGGGGA
                               ||||||||| ||||||||
                               TGACACTGA TGCCTCTT
                                        _
GAM2394  KIAA0057 3'  TGTTCTCTAATGGGGGAG   56529    GA_
                               TGT   CTGATGGGGGAG
                               |||   ||||||||||||
                               ACA   GATTACCCCCTC
                                 AGA
GAM2394  KIAA0367 3'  AACACTGTGTTCTGGGAGAG  56530       ACTGA
                               AACACTGTG    TGGGGGAG
                               |||||||||    ||||||||
                               TTGTGACAC    ACCCTCTC
                                  AAG__
GAM2394  KIAA0637 3'  ACACTGTGGTGAGCTGGAGAG 56531       AC   TG_
                               ACACTGTG  TGA   GGGGAG
                               ||||||||  |||   ||||||
                               TGTGACAC  ACT   CCTCTC
                                  C_   CGA
GAM2394  KIAA0854 3'  CAGTGTGGGAGGGGGAG    56532    C   ACT  T
                               CA TGTG   GA GGGGGAG
                               || ||||   || |||||||
                               GT ACAC   CT CCCCCTC
                                C   C__  _
GAM2394  KIAA0953 3'  CACTGATGGCTGAGAGTGGAGA 56533     _  A   T  _
                               CACTG TG CTGA GGG GGAGA
                               ||||| || |||| ||| |||||
                               GTGAC AC GACT CTC CCTCT
                                  T  C   _   A
GAM2394  KIAA1128 3'  ACTGGAGATGGGGGAG     56534     T  CT
                               ACTG GA  GATGGGGGAG
                               |||| ||  ||||||||||
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                                TGAC CT  CTACCCCCTC
                                  _ __
GAM2394  KIAA1465  3'  AACACTGTGCTTGGCGGGGAA  56535        AC  A
                                AACACTGTG  TG TGGGGGA
                                |||||||||  || |||||||
                                TTGTGACAC  AC GCCCCTT
                                     GA  C
GAM2394  KIAA1550  3'  CTGTGACTGACTTCTTGGGAG  56536         GG___
                                CTGTGACTGAT    GGGAG
                                ||||||||||    |||||
                                GACACTGACTG    CCCTC
                                      AAGAA
GAM2394  KIAA1674  3'  AACACTGTAACTGAAACACAGA 56537           TGGG_
           A                     AACACTGTGACTGA    GGAG
                                ||||||||||||||    ||||
                                TTGTGACATTGACT    TCTT
                                       TTGTG
GAM2394  KIAA1884  3'  CACTGTGCTCAGGGGAG     56538       A  GA
                                CACTGTG CT  TGGGGGAG
                                |||||||  ||  ||||||||
                                GTGACAC GA  GTCCCCTC
                                  _ __
GAM2394  KIAA1893  3'  AACCTGTGACTCAGTGGGAGAG 56539     A      GA_
                                AAC CTGTGACT   TGGGGGAG
                                |||  ||||||||   ||||||||
                                TTG GACACTGA   ACCCTCTC
                                  _       GTC
GAM2394  KIAA1915  3'  GACTGTGGTGGTGGGAGAA   56540      A__   _
                                GACTG   TGG GGGAGAA
                                |||||   |||  |||||||
                                CTGAC   ACC CCCTCTT
                                   ACC   A
GAM2394  MGC10902  3'  TGTGCTGGTGGGGGGGAA    56541     A   A     A
                                TGTG CTG TGGGGG GAA
                                ||||  |||  ||||||  |||
                                ACAC GAC ACCCCC CTT
                                  _  C     C
GAM2394  MGC4643   3'  ACACTGTGGTTAAAGGA     56542       ACTGA
                                ACACTGTG    TGGGGGA
                                ||||||||    |||||||
                                TGTGACAC    ATTTCCT
                                     CA___
GAM2394  NEDD5     3'  AACATTAGTGGTTAGGGAGAA  56543     CT_   ACTGATG
                                AACA   GTG      GGGGAGAA
                                ||||   |||      ||||||||
                                TTGT   CAC      TCCCTCTT
                                  AAT   CAA____
GAM2394  NR4A3     5'  CTGTGACCAGGGGGGGAG     56544       GAT
                                CTGTGACT   GGGGGAG
                                ||||||||   |||||||
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                                GACACTGG   CCCCCTC
                                     TC_
GAM2394  OSBPL5   3'  ACACATCCCCAGATGGGGGAG  56545     T  GA  _
                                ACAC GT  CT GATGGGGGAG
                                |||| ||  || ||||||||||
                                TGTG TA  GG CTACCCCCTC
                                  _  GG  T
GAM2394  PFTK1    3'  ACGCTGTGCTGCAGAGGG    56546    A    A   AT
                                AC CTGTG CTG  GGGGG
                                || ||||| |||  |||||
                                TG GACAC GAC  CTCCC
                                 C    _  GT
GAM2394  PPY2     3'  AACAGTGTGGAGGGGAGA    56547     C    ACTGAT
                                AACA TGTG     GGGGGAGA
                                |||| ||||     ||||||||
                                TTGT ACAC     TCCCCTCT
                                  C   C_____
GAM2394  PRO0529  3'  CCGTTGGTGGGGGAGAA     56462     GAC  A
                                CTGT   TG TGGGGGAGAA
                                ||||   || ||||||||||
                                GGCA   AC ACCCCCTCTT
                                  ___  C
GAM2394  RBM7     3'  AACGTTTGACTGACAGAA    56548     ACTG
                                AAC    TGACTGATGGGG
                                |||    ||||||||||||
                                TTG    ACTGACTGTCTT
                                 CAA_
GAM2394  SLC39A3  3'  CACTGTGATGAGGGGGAG    56550        C   T
                                CACTGTGA TGA GGGGGAG
                                |||||||| ||| |||||||
                                GTGACACT ACT CCCCCTC
                                      _  _
GAM2394  SLC39A3  3'  ACACTGTGACTGCTGCCTTGTG 56549          A  GGG___
           AG                     ACACTGTGACTG TG     GAG
                                |||||||||||| ||     |||
                                TGTGACACTGAC AC     CTC
                                       G  GGAACA
GAM2394  SSH2     3'  AACACAGTGGAGGGGAGA    56551      T   ACTGAT
                                AACAC GTG     GGGGGAGA
                                ||||| |||     ||||||||
                                TTGTG CAC     TCCCCTCT
                                  T   C_____
GAM2394  SUI1     3'  AACCTGTGACAAGGGAGAG   56552     A      TGAT
                                AAC CTGTGAC    GGGGGAG
                                ||| |||||||    |||||||
                                TTG GACACTG    CCCTCTC
                                  _      TT__
GAM2394  UMP-CMPK 3'  CATTGTGACAGAAGAA      56553    C     TGAT
                                CA TGTGAC    GGGGGAG
                                || ||||||    |||||||
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                                GT ACACTG    TCTTCTT
                                 A    _____
GAM2394  ZNF197    3'  AACATTTGACTGACAGGA    56554      CTG
                                AACA   TGACTGATGGGG
                                ||||   ||||||||||||
                                TTGT   ACTGACTGTCCT
                                  AA_
GAM2394  ZNF313    3'  AACACTGGATGGGAGG      56555        TGACT       A
                                AACACTG    GATGGGGG G
                                |||||||    |||||||| |
                                TTGTGAC    CTACCCTC C
                                    _____      _
GAM2394  LOC121219 3'  CTGTGACTGGCTGGGGAG    56556          ATG
                                CTGTGACTG   GGGGAG
                                |||||||||   ||||||
                                GACACTGAC   CCCCTC
                                     CGA
GAM2394  LOC146268 3'  AACATGTGGCTGCAGGGAGAG  56557      C    A   AT
                                AACA TGTG CTG  GGGGGAG
                                |||| |||| |||  |||||||
                                TTGT ACAC GAC  CCCTCTC
                                  _   C   GT
GAM2394  LOC146988 3'  CACTAAGTCCTGGTGGGGGAGA 56558       TGA_   A
                                CACTG    CTG TGGGGGAGA
                                |||||    ||| |||||||||
                                GTGAT    GAC ACCCCCTCT
                                   TCAG   C
GAM2394  LOC147276 5'  ACACTGTGACTGGTGCAG    56559           A  G
                                ACACTGTGACTG TG GG
                                |||||||||||| || ||
                                TGTGACACTGAC AC TC
                                       C  G
GAM2394  LOC148443 3'  ACTGTGACATGAATTGGAG   56560         _   TGGG
                                ACTGTGAC TGA    GGAG
                                |||||||| |||    ||||
                                TGACACTG ACT    CCTC
                                     T   TAA_
GAM2394  LOC149703 3'  AACCTGTGGCTAGGGGAA    56561     A    ACTGA
                                AAC CTGTG    TGGGGGAG
                                ||| |||||    ||||||||
                                TTG GACAC    ATCCCCTT
                                  _    CG___
GAM2394  LOC164572 5'  CACTGTGATGCCGGGGG     56562         C  A
                                CACTGTGA TG TGGGGG
                                |||||||| || ||||||
                                GTGACACT AC GCCCCC
                                     _ G
GAM2394  LOC196527 3'  AACACTGTGGATGGCATGGGGA 56563          AC  __
            A                    AACACTGTG  TG  ATGGGGGA
                                ||||||||| ||  ||||||||
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                                TTGTGACAC  AC  TACCCCTT
                                     CT  CG
GAM2394  LOC200314 3'  AACATTGTGACTATGTAATGAA 56564      C       A  GGG_
                                AACA TGTGACTG TG    GAG
                                |||| |||||||| ||    |||
                                TTGT ACACTGAT AC    CTT
                                  A       _  ATTA
GAM2394  LOC220739 3'  CACAGTGGCGGCGGGGGAA    56565     T   AC  A
                                CAC GTG  TG TGGGGGAG
                                ||| |||  || ||||||||
                                GTG CAC  GC GCCCCCTT
                                  T   C_  C
GAM2394  LOC220980 3'  ACTGTGACTTGGGGAG      56566          GATG
                                ACTGTGACT    GGGGAG
                                |||||||||    ||||||
                                TGACACTGA    CCCCTC
                                     A___
GAM2394  LOC221463 3'  ACTGTGGTGTGGGGGAA     56567        AC  A
                                ACTGTG  TG TGGGGGAG
                                ||||||  || ||||||||
                                TGACAC  AC ACCCCCTT
                                   C_  _
GAM2394  LOC221763 3'  TGTAAATGGGGGAGAA      56568       CTG
                                TGTGA   ATGGGGGAGAA
                                |||||   ||||||||||||
                                ACATT   TACCCCCTCTT
                                  ___
GAM2394  LOC221773 3'  CATGTGACTGGAGAG       56569    C      GATG
                                CA TGTGACT    GGGGAG
                                || |||||||    ||||||
                                GT ACACTGA    CCTCTC
                                 _     _____
GAM2394  LOC222031 3'  CTGTGGCCCTGGGAGGA     56570       A  GA     A
                                CTGTG CT  TGGGGG GA
                                ||||| ||  |||||| ||
                                GACAC GG  ACCCTC CT
                                   C  G_     _
GAM2394  LOC245771 5'  CTGGGAAATGGGGGAGA     56508     T  CT
                                CTG GA  GATGGGGGAGA
                                ||| ||  ||||||||||||
                                GAC CT  TTACCCCCTCT
                                  C  __
GAM2394  LOC254302 5'  CACTGTGACGGGAGA       56571          TGATGG
                                CACTGTGAC     GGGAGA
                                |||||||||     ||||||
                                GTGACACTG     CCCTCT
                                     _______
GAM2394  LOC254874 5'  CACTGTGACGGGAGA       56571          TGATGG
                                CACTGTGAC     GGGAGA
                                |||||||||     ||||||
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                                GTGACACTG     CCCTCT
                                          ______
GAM2394  LOC255446 3'  CACTGTGAGCTGGGATAGGG  56572        _ __
                                CACTGTGA CT  GATGGGG
                                |||||||| ||  |||||||
                                GTGACACT GA  CTATCCC
                                     C  CC
GAM2394  LOC255702 5'  CTGTGGGCGAAGGGAGAA    56573      AC   TG
                                CTGTG  TGA  GGGGAGAA
                                |||||  |||  ||||||||
                                GACAC  GCT  TCCCTCTT
                                   CC  __
GAM2394  LOC64744  3'  CTGTGGAAAGGGGAGA      56574      ACT  T
                                CTGTG   GA GGGGGAGA
                                |||||   || ||||||||
                                GACAC   CT TCCCCTCT
                                   ___  T
GAM2394  LOC90927  3'  ACACTTTGACTGTAAGAGGA   56575      G     AT
                                ACACT TGACTG  GGGGGA
                                ||||| ||||||  ||||||
                                TGTGA ACTGAC  TCTCCT
                                   A     AT
GAM2394  LOC91445  3'  ACTGTGAAGAGGGGAG      56576       CT  TG
                                ACTGTGA  GA  GGGGAG
                                |||||||  ||  ||||||
                                TGACACT  CT  CCCCTC
                                     T_  __
GAM2394  LOC91947  3'  AACATGTGACCATGTGGGAG   56577     C      G   G
                                AACA TGTGACT ATG GGGAG
                                |||| ||||||| ||| |||||
                                TTGT ACACTGG TAC CCCTC
                                   _      _  A
GAM2395  AICDA     3'  CAGCGCATGATTGGATATTAAT 56580      A  AATCAA
                                CAGC CA     GGGTATTAAT
                                |||| ||     ||||||||||
                                GTCG GT     CCTATAATTA
                                   C  ACTAA_
GAM2395  G6PT1     3'  CAGCAGAAGTCAAGGGTCATTA 56581      C  A      _
                                CAGCA AA TCAAGGGT ATTA
                                ||||| || |||||||| ||||
                                GTCGT TT AGTTCCCA TAAT
                                   C  C       G
GAM2395  NOTCH2    3'  CAGACAAATCAGGTA      37025     C      AG
                                CAG ACAAATCA  GGTA
                                ||| ||||||||  ||||
                                GTC TGTTTAGT  CCAT
                                   _      __
GAM2395  PCDHB12   3'  GCAGATCAGAGCATTA      56582     CAA    A
                                GCA   ATCA GGGTATTA
                                |||   |||| ||||||||
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                                CGT   TAGT CTCGTAAT
                                  C__   _
GAM2395  USP6     3'  AACACAAATCACACAACATTA  37028          AGGG_
                                AGCACAAATCA     TATTA
                                ||||||||||     |||||
                                TTGTGTTTAGT     GTAAT
                                      GTGTT
GAM2395  ZNF146   3'  ACTACAAATCAAGCCACAGTA  56583    _       ____
                                GC ACAAATCAAG    GGTA
                                || ||||||||||    ||||
                                TG TGTTTAGTTC    TCAT
                                 A         GGTG
GAM2395  AFAP     3'  CAGCACAAATAATTAATTAATA 11631          C  GGGT
                                CAGCACAAAT AA    ATTAATA
                                |||||||||| ||    |||||||
                                GTCGTGTTTA TT    TAATTAT
                                      _ AAT_
GAM2395  C20orf27 3'  CAGCACAAATGAAGGCA     37029          CA
                                CAGCACAAAT  AGGGTA
                                ||||||||||  ||||||
                                GTCGTGTTTA  TTCCGT
                                      C_
GAM2395  FKSG14   3'  AGCAGAATCAAGAGTAGATTAA 56584      CA        __
           TA                    AGCA  AATCAAGGGTA  TTAATA
                                ||||  ||||||||||  ||||||
                                TCGT  TTAGTTCTCAT  AATTAT
                                  C_         CT
GAM2395  FLJ10483 3'  CACATAAGGAGTATTAAT    56585     AATC   _
                                CACA    AAGG GTATTAAT
                                ||||    |||| ||||||||
                                GTGT    TTCC CATAATTA
                                  A___    T
GAM2395  FLJ10701 3'  CAGCACACATTAGGAATACTAT 56586       AATCA   ____
           TAATA                   AGCACA    AGGG    TATTAATA
                                ||||||    ||||    ||||||||
                                TCGTGT    TCCT    ATAATTAT
                                   GTAA_    TATG
GAM2395  FLJ13114 3'  ACACAAATCAATTTTTAATA   56587          GGGTA
                                GCACAAATCAA     TTAATA
                                ||||||||||     ||||||
                                TGTGTTTAGTT     AATTAT
                                      AAA__
GAM2395  FLJ21478 5'  GCACAAACGAGCCAGCAATA   56588        CAA    AT_
                                GCACAAAT   GGGT   TAATA
                                ||||||||   ||||   |||||
                                CGTGTTTG   CTCG   GTTAT
                                     ___    GTC
GAM2395  HSPC228  3'  CAGCACAAATGCAGGTA     37030          CAA
                                CAGCACAAAT   GGGTA
                                ||||||||||   |||||
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                                GTCGTGTTTA  TCCAT
                                     CG_
GAM2395 KIAA0820 3' AACACAAATCAAGTAGTA   11635          _
                                AGCACAAATCAAG GGTA
                                |||||||||||| ||||
                                TTGTGTTTAGTTC TCAT
                                      A
GAM2395 KIAA1054 3' CAGCACAAATGCAATAAT   11636        _  GG
                                CAGCACAAAT CAA  GT
                                |||||||||| |||  ||
                                GTCGTGTTTA GTT  TA
                                     C   AT
GAM2395 KIAA1431 3' CAGCACAATCAAGGTGTA   56589       A    _
                                CAGCACAA TCAAGG GTA
                                |||||||| |||||| |||
                                GTCGTGTT AGTTCC CAT
                                    _     A
GAM2395 KIAA1530 3' CAGCACTGATCAAGGCACT  37033      AA     G
                                CAGCAC  ATCAAGG TATT
                                ||||||  ||||||| ||||
                                GTCGTG  TAGTTCC GTGA
                                   AC     _
GAM2395 MAP-1    3' CAGCACAAGGTAGGGATT   56590       ATCA   T
                                CAGCACAA   AGGG ATT
                                ||||||||   |||| |||
                                GTCGTGTT   TCCC TAA
                                    CCA_   _
GAM2395 MDN1     3' AGCACAGCATCAACTAGTA  11637      A_   G_
                                AGCACA  ATCAA  GGTA
                                ||||||  |||||  ||||
                                TCGTGT  TAGTT  TCAT
                                   CG    GA
GAM2395 RINZF    3' CAGCACAAAATCGAGAAATAAT 11638       TCAA  TAT
            A                    CAGCACAAA   GGG  TAATA
                                |||||||||   |||  |||||
                                GTCGTGTTT   CTC  ATTAT
                                     TAG_   TTT
GAM2395 LOC134111 3' AGCACAAATGAGGTCTAAAT  37034       CAA   ATT
                                AGCACAAAT  GGGT  AAT
                                |||||||||  ||||  |||
                                TCGTGTTTA  TCCA  TTA
                                     C__   GAT
GAM2395 LOC222223 5' CAGCATAGATCAAAGACACC  37036     CAA    GT
                                CAGCA  ATCAAGG  ATT
                                |||||  |||||||  |||
                                GTCGT  TAGTTTC  TGG
                                  ATC     TG
GAM2396 FOXO1A   3' AAATCTCCCCAATTTTTAA   56593      ATTA
                                AAATCT   CAATTTTTAA
                                ||||||   ||||||||||
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                                TTTAGA   GTTAAAAATT
                                   GGG_
GAM2396 C11orf25 3' AATGTATTACAATTTTTAAAT 56594    C
                                AAT TATTACAATTTTTAAAT
                                ||| ||||||||||||||||
                                TTA ATAATGTTAAAAATTTA
                                  C
GAM2396 MGC5149  3' AAATCTCCCAATTTTTAAAT  56595      ATTA
                                AAATCT   CAATTTTTAAAT
                                ||||||   ||||||||||||
                                TTTAGA   GTTAAAAATTTA
                                   GG__
GAM2396 SPIN    3' TAAGATCTATTACAATTTT   56596    A
                                TAA ATCTATTACAATTTT
                                ||| ||||||||||||||
                                ATT TAGATAATGTTAAAA
                                  C
GAM2397 ANGPT1   3' TATATATTTCCCTTACATATAA 56599           TC
             T                   TATATATTTCTCTT  TATATAAT
                                ||||||||||||||  ||||||||
                                ATATATAAAGGGAA  GTATATTA
                                        T_
GAM2397 DPYSL2   3' TATAGGGCCTCTTTCTAT    56600     TT_
                                TATA   TCTCTTTCTAT
                                ||||   ||||||||||
                                ATAT   GGAGAAAGATA
                                  CCC
GAM2397 MTAP    3' TATATATATTTCTTTCTA    56601       TTC
                                TATATAT   TCTTTCTA
                                |||||||   ||||||||
                                ATATATA   AGAAAGAT
                                    TAA
GAM2397 FLJ11896 3' TATATATTTCCCTGCCAT    56602          TT
                                TATATATTTCTCT  CTAT
                                ||||||||||||  ||||
                                ATATATAAAGGGA  GGTA
                                        C_
GAM2397 KIAA0976 3' TATAATGGTATCTTTCTATATA 56603     TATTTC
                                TATA     TCTTTCTATATA
                                ||||     ||||||||||||
                                ATAT     AGAAAGATATAT
                                  TACCAT
GAM2397 KIAA1856 3' TATATATTTATCTTTATATATA 56604        C    C
                                TATATATTT TCTTT TATATA
                                ||||||||| ||||| ||||||
                                ATATATAAA AGAAA ATATAT
                                      T    T
GAM2397 LOC196424 3' TATATATTTTTCTTTCCA    56605        C
                                TATATATTT TCTTTCTA
                                ||||||||| ||||||||
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                                ATATATAAA AGAAAGGT
                                     A
GAM2397  LOC200276 3'  TATATATTTCTCTTTTCT    56606            _
                                TATATATTTCTCTTT CT
                                ||||||||||||||| ||
                                ATATATAAAGAGAAA GA
                                        A
GAM2398  AQP6     3'  GAAGCCCTACAGAGAG      56609       AAA
                                GAAGCC  CTACAGAGAG
                                ||||||  ||||||||||
                                CTTCGG  GATGTCTCTC
                                  ___
GAM2398  AQP6     3'  GAAGCCCTACAGAGAG      56609       AAA
                                GAAGCC  CTACAGAGAG
                                ||||||  ||||||||||
                                CTTCGG  GATGTCTCTC
                                  ___
GAM2398  NQO1     3'  TGACCATAAACTACAGAGA   56610   A  __
                                A GCCA  AACTACAGAGA
                                | ||||  ||||||||||||
                                A TGGT  TTGATGTCTCT
                                 C   AT
GAM2398  TRPC6    3'  TAAATTAAGCCAAAGTTGGAG 56611     CG      CTACA
                                TAAA  AAGCCAAA    GAG
                                ||||  ||||||||    |||
                                ATTT  TTCGGTTT    CTC
                                  AA      CAAC_
GAM2398  BRD2     5'  AAACGAAGCCGTGCTGGGGGAG 56612         AAA  ACA_
                                AAACGAAGCC  CT   GAG
                                ||||||||||  ||   |||
                                TTTGCTTCGG  GA   CTC
                                     CAC  CCCC
GAM2398  DKFZP586I2223 3'  GAAGCCAAGACTGAGGGAG   56613        _  AC  A
                                GAAGCCAA ACT  AG GAG
                                |||||||| |||  || |||
                                CTTCGGTT TGA  TC CTC
                                     C   C_  C
GAM2398  DKFZP586I2223 3'  GAAGCCAAGACTGAGGGAG   56613        _  AC  A
                                GAAGCCAA ACT  AG GAG
                                |||||||| |||  || |||
                                CTTCGGTT TGA  TC CTC
                                     C   C_  C
GAM2398  DKFZP586I2223 3'  GAAGCCAAGACTGAGGGAG   56613        _  AC  A
                                GAAGCCAA ACT  AG GAG
                                |||||||| |||  || |||
                                CTTCGGTT TGA  TC CTC
                                     C   C_  C
GAM2398  KIAA0478  5'  GAAGCCAAGCACACCAGAG   56614         __  TA
                                GAAGCCAA  AC  CAGAG
                                ||||||||  ||  |||||
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                                CTTCGGTT  TG  GTCTC
                                     CG  TG
GAM2398  KIAA1254  3'  AACGAAGCTAAACTACAG    56615        C
                                AACGAAGC AAACTACAG
                                |||||||| |||||||||
                                TTGCTTCG TTTGATGTC
                                     A
GAM2398  PRO1584   3'  GAAGCCAAGCCATAAAGAG   56616        A  C
                                GAAGCCAA CTA AGAGAG
                                |||||||| ||| ||||||
                                CTTCGGTT GGT TTTCTC
                                     C  A
GAM2398  LOC146287 5'  TAAACGAAGCTACAG       56617         CAAAC
                                TAAACGAAGC    TACAG
                                ||||||||||    |||||
                                ATTTGCTTCG    ATGTC
                                              _____
GAM2398  LOC91035  5'  TAAATGAACCAAACTCAG    56618     C  G     A
                                TAAA GAA CCAAACT CAG
                                |||| ||| ||||||| |||
                                ATTT CTT GGTTTGA GTC
                                  A  _     _
GAM2399  FLJ10292  3'  GAACAACCAACAACTGT     56621       GCTAAA     C
                                GAGCAAC     CAACAAC GT
                                |||||||     ||||||| ||
                                CTTGTTG     GTTGTTG CA
                                     _______     A
GAM2399  KIAA1164  3'  TGATTGTAACTAAGTAACAACC 56622    GCAAC    AC
           GT                     TGA    GCTAA  AACAACCGT
                                |||    |||||  |||||||||
                                ACT    TGATT  TTGTTGGCA
                                  AACAT    CA
GAM2400  ATP2B2    5'  TGGCATCTACATGGT      56625     TTC
                                TGGC   GTTTATATGGT
                                ||||   ||||||||||
                                ACCG   TAGATGTACCA
                                     ___
GAM2400  B3GAT1    3'  TGGCCTCACTCCTGTGTGGT   56626         ATA__
                                TGGCTTCGTTT    TGGT
                                ||||||||||    ||||
                                ACCGGAGTGAG    ACCA
                                      GACAC
GAM2400  B3GAT1    3'  TGGCCTCACTCCTGTGTGGT   56626         ATA__
                                TGGCTTCGTTT    TGGT
                                ||||||||||    ||||
                                ACCGGAGTGAG    ACCA
                                      GACAC
GAM2400  BCL2      3'  TGGCTTCATACCACAGGT    56627         _    T
                                TGGCTTCGT TTATA GGT
                                ||||||||| ||||| |||
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                                ACCGAAGTA GGTGT CCA
                                     T    _
GAM2400 CD83     3' TGGCCTCATGCTATGTGGT   56628        _   A
                                TGGCTTCGT TTAT TGGT
                                ||||||||| |||| ||||
                                ACCGGAGTA GATA ACCA
                                     C   C
GAM2400 GPR4     3' TGGCTCACATTTGTGGT    56629       _    ATA
                                TGGCTT CGTTT  TGGT
                                |||||| |||||  ||||
                                ACCGAG GTAAA  ACCA
                                   T   C__
GAM2400 MEF2B    5' TGGCATTCATATGGT      56630     TTC
                                TGGC  GTTTATATGGT
                                ||||  ||||||||||
                                ACCG  TAAGTATACCA
                                  ___
GAM2400 OPTN     5' TGGCTTCGCTCAGGGT     56631          TAT
                                TGGCTTCGTTTA  GGT
                                ||||||||||||  |||
                                ACCGAAGCGAGT  CCA
                                      C__
GAM2400 PDGFRA   3' TGTTTCATTCATATGGT    56632    GC
                                TG  TTCGTTTATATGGT
                                ||  ||||||||||||||
                                AC  AAGTAAGTATACCA
                                 A_
GAM2400 SCN7A    5' TGGCATTCACATGGT      56633     TTC
                                TGGC  GTTTATATGGT
                                ||||  ||||||||||
                                ACCG  TAAGTGTACCA
                                  ___
GAM2400 TFAP4    3' TGGCTTCGTTCAAAGGT    56634          TAT
                                TGGCTTCGTTTA  GGT
                                ||||||||||||  |||
                                ACCGAAGCAAGT  CCA
                                      TT_
GAM2400 C20orf110 3' TGGCTTCACCCCATGGT   56635        TT A
                                TGGCTTCG  T TATGGT
                                ||||||||  | ||||||
                                ACCGAAGT  G GTACCA
                                    GG _
GAM2400 CLIC4    3' TAGCTTCTACATGGT      56636       GTT
                                TGGCTTC   TATATGGT
                                |||||||   ||||||||
                                ATCGAAG   ATGTACCA
                                  ___
GAM2400 FACTP140 3' TGGCTCAAGCTGTATGGT   56637       C_  TA
                                TGGCTT  GTT  TATGGT
                                ||||||  |||  ||||||
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                                ACCGAG  CGA  ATACCA
                                   TT   C_
GAM2400  FLJ11700  3'  TGGCCTTTTTATGTGGT     56638       CG    A
                                TGGCTT  TTTAT TGGT
                                ||||||  ||||| ||||
                                ACCGGA  AAATA ACCA
                                   A_    C
GAM2400  FLJ13195  3'  TGTTTTCCTTATATGGT     56639    GC   G
                                TG  TTC TTTATATGGT
                                ||  ||| ||||||||||
                                AC  AAG GAATATACCA
                                 AA  _
GAM2400  FLJ20174  3'  TGGCCTTCATATGGT       56640      TCG
                                TGGCT   TTTATATGGT
                                |||||   ||||||||||
                                ACCGG   AAGTATACCA
                                  ___
GAM2400  FLJ20671  3'  TGGCTCCATCAGCTATGGT   56641         TA_
                                TGGCTTCGTT   TATGGT
                                ||||||||||   ||||||
                                ACCGAGGTAG   ATACCA
                                     TCG
GAM2400  KIAA0323  3'  TGGCTTCATCGATTGGT     56642         T  A
                                TGGCTTCGTT AT TGGT
                                |||||||||| || ||||
                                ACCGAAGTAG TA ACCA
                                     C  _
GAM2400  KIAA1999  3'  TGGCTCTTGCATACAATGGT  56643       C_  T    _
                                TGGCTT  GT TATA TGGT
                                ||||||  || |||| ||||
                                ACCGAG  CG ATGT ACCA
                                   AA  T    T
GAM2400  TCF-3     3'  TGTCTTCTCACATGGT      56644    G    GT
                                TG CTTC  TTATATGGT
                                || ||||  |||||||||
                                AC GAAG  AGTGTACCA
                                 A   __
GAM2400  TCFL5     3'  TGGCTTCATCCCCAAATGGT  56645         AT__
                                TGGCTTCGTTT    ATGGT
                                ||||||||||    |||||
                                ACCGAAGTAGG    TACCA
                                     GGTT
GAM2400  TNK1      3'  TGGCTGTTCACATGGT      56646      TC
                                TGGCT  GTTTATATGGT
                                |||||  ||||||||||
                                ACCGA  CAAGTGTACCA
                                  __
GAM2400  LOC128209 3'  TGATCACATTTATATGGT    56647     CTT
                                TGG   CGTTTATATGGT
                                |||   ||||||||||||
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                                ACT   GTAAATATACCA
                                  AGT
GAM2400  LOC144583 3'  TGATCACATTTATATGGT    56647     CTT
                                TGG   CGTTTATATGGT
                                |||   ||||||||||||
                                ACT   GTAAATATACCA
                                  AGT
GAM2400  LOC147929 5'  TGGCTCCGTCCACGGT      56648         TA
                                TGGCTTCGTT  TATGGT
                                ||||||||||  ||||||
                                ACCGAGGCAG  GTGCCA
                                          __
GAM2400  LOC148809 5'  TGGCTTAGTACATGGT      56649       C  TT
                                TGGCTT GT  ATATGGT
                                ||||||  ||  |||||||
                                ACCGAA CA  TGTACCA
                                    T  __
GAM2400  LOC152263 5'  TGGCTTCGATGATACGGT    56650        TTT
                                TGGCTTCG   ATATGGT
                                ||||||||   |||||||
                                ACCGAAGC   TATGCCA
                                     TAC
GAM2400  LOC199720 3'  TGGCTCGCCCAGGTGGT     56651      T     TA
                                TGGCT CGTTTA  TGGT
                                |||||  ||||||  ||||
                                ACCGA GCGGGT  ACCA
                                   _     CC
GAM2400  LOC201245 3'  TGGCTGTTCACATGGT      56646      TC
                                TGGCT  GTTTATATGGT
                                |||||  ||||||||||
                                ACCGA  CAAGTGTACCA
                                     __
GAM2400  LOC253220 5'  TGGTCTTCACACATGGT     56652     _    TT
                                TGG CTTCG  TATATGGT
                                |||  |||||  ||||||||
                                ACC GAAGT  GTGTACCA
                                  A    __
GAM2401  B4GALT6   3'  AAAACTAAACTTAAAATTTGT  56655           TTACA
                                AAAACTAAACTTG    TTGT
                                ||||||||||||     ||||
                                TTTTGATTTGAAT    AACA
                                      TTTA_
GAM2401  CLCN3     3'  TTAAAACCAAGCTTCATTG    56656         ACTT   A
                                TTAAAACTAA    GTT CATTG
                                ||||||||||    |||  |||||
                                AATTTTGGTT    CGA GTAAC
                                      _____   A
GAM2401  JPH3      3'  ACTGAACAAGTTACATTGT    56657     A   TT
                                ACT AAC  GTTACATTGT
                                |||  |||  ||||||||||
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                                TGA TTG  CAATGTAACA
                                  C   TT
GAM2401  SLC38A2   3'  TTAAAACAAACATACATTG   56658       T   TTGT
                                TTAAAAC AAAC   TACATTG
                                ||||||| ||||   |||||||
                                AATTTTG TTTG   ATGTAAC
                                    _   T___
GAM2401  PCTAIRE2BP 3'  TTAAAACAAAACTTGTTA    56659       T
                                TTAAAAC AAACTTGTTA
                                ||||||| ||||||||||
                                AATTTTG TTTGAACAAT
                                    T
GAM2401  SGKL      3'  AACTTTTGTTACATTG      56660      AAAC
                                AACT   TTGTTACATTG
                                ||||   ||||||||||
                                TTGA   AACAATGTAAC
                                  A___
GAM2401  LOC124801 5'  ACTAAACTTGTCCACGGT    56661          A   T
                                ACTAAACTTGTT CAT GT
                                |||||||||||| ||| ||
                                TGATTTGAACAG GTG CA
                                      _  C
GAM2401  LOC148189 3'  TTAAAACTAAAATACTACCATT 56662          CTTGTTA
           GT                    TTAAAACTAAA      CATTGT
                                ||||||||||      ||||||
                                AATTTTGATTT      GTAACA
                                      TATGATG
GAM2402  MECP2     3'  ACAAATTTCCTTAATAAAT   56665      GG
                                GCGAG  TTCCTTAATAAAT
                                |||||  ||||||||||||
                                TGTTT  AAGGAATTATTTA
                                  A_
GAM2402  GS3955    3'  GACATTTTCCTTAATAAAT   56666    GGG_
                                GA   TTCCTTAATAAAT
                                ||   ||||||||||||
                                CT   AAGGAATTATTTA
                                 GTAA
GAM2402  MKP-7     3'  ACGCGAGGGTTTCCCCAAT   56667          _
                                ACGCGAGGGTT CCTTAAT
                                |||||||||| |||||||
                                TGCGCTCCCAA GGGGTTA
                                      A
GAM2403  FGFRL1    3'  GCGTGTGTATGTTCAGG     56670     ACAA   AC
                                GCGT   TGT  GTGTTCAGG
                                ||||   |||  |||||||||
                                CGCA   ACA  TACAAGTCC
                                  C___   __
GAM2403  DKFZp761N0624 3'  AAGCTGTGGTGTCCAG      56671      GTACAA   AC
                                AAGC     TGT  GTGTTCAG
                                ||||     |||  ||||||||
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                                TTCG     ACA  CACAGGTC
                                  _______  C_
GAM2403  FLJ10697  3'  AAGGTACAAAACATGTTCAGG  56672    C     TGT
                                AAG GTACAA   ACGTGTTCAGG
                                ||| ||||||   ||||||||||
                                TTC CATGTT   TGTACAAGTCC
                                  _     T__
GAM2403  LOC127428 5'  ACGTGCTTGCAGCGTGTTCAGG 56673      ACAA   _
                                GCGT    TGTA CGTGTTCAGG
                                ||||    |||| ||||||||||
                                TGCA    ACGT GCACAAGTCC
                                  CGA_   C
GAM2403  LOC152559 3'  GCTACAATGTATGATAG     56674    G      AC   TTC
                                GC TACAATGT  GTG   AG
                                || ||||||||  |||   ||
                                CG ATGTTACA  TAC   TC
                                 _      ___  TA_
GAM2403  LOC153894 5'  AAGCGGCGATGTGTCCAA    56675      TACAAT  AC_
                                AAGCG     GT   GTGTTCAG
                                |||||     ||   ||||||||
                                TTCGC     CG   CACAGGTT
                                  _______ CTA
GAM2403  LOC257206 5'  AAGCGGCAAATGTTCA      56676      TACAAT   C
                                AAGCG     GTA GTGTTCA
                                |||||     ||| |||||||
                                TTCGC     CGT TACAAGT
                                  _______  T
GAM2404  PCTK1    5'  TAGGTGAGCAGTGGCCA     56679     AC  C   ACG
                                TAG  GA GCA   GTGGCCA
                                |||  || |||   |||||||
                                ATC  CT CGT   CACCGGT
                                  CA  _  ___
GAM2404  TJP1     3'  TAGATAATGCACAAAAGCCATA 56680      CG C   A   T
            A                    TAGA  A GCA CGG GGCCATAA
                                ||||  | ||| ||| ||||||||
                                ATCT  T CGT GTT TCGGTATT
                                  AT A   _   T
GAM2404  C20orf178 3'  TAGACAGTGCAAACCATA    56681       AC    CGGTG
                                TAGACG  GCAA    GCCATA
                                ||||||  ||||    ||||||
                                ATCTGT  CGTT    TGGTAT
                                   CA   ______
GAM2404  KIAA0461  3'  TAGACGTGACCAACCATAG   56682      __   G    G
                                TAGAC  GAC CAAC GTGG
                                |||||  ||| |||| ||||
                                ATCTG  CTG GTTG TATC
                                  CA   _    G
GAM2404  KIAA0960  5'  TAGCGTCCGCGGTGGTGGCC   56683     A  A_   AAC
                                TAG CG  CGC   GGTGGCC
                                ||| ||  |||   |||||||
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                                ATC GC  GCG   CCACCGG
                                  _ AG   CCA
GAM2404  LOC148046 3'  GAGGAGCAAGTGGTGGCCATA  56684    C  C    C_
                                GA GA GCAA  GGTGGCCATA
                                || || ||||  ||||||||||
                                CT CT CGTT  CCACCGGTAT
                                 C  _    CA
GAM2404  LOC150279 3'  TAGACACGATGGCCAT      56685      GACGCA
                                TAGAC     ACGGTGGCCAT
                                |||||     ||||||||||
                                ATCTG     TGCTACCGGTA
                                   _______
GAM2404  LOC151031 3'  TAGACAGCTGGACGGTGGCCAT 56686       AC  A__
                                TAGACG  GC   ACGGTGGCCAT
                                ||||||  ||   ||||||||||
                                ATCTGT  CG   TGCCACCGGTA
                                   __  ACC
GAM2405  AQP6     5'  TCTTCTGGCTGACCC       56689          TGGTTTG
                                TCTTCTGGTT      GACCT
                                ||||||||||      |||||
                                AGAAGACCGA      CTGGG
                                   ________
GAM2405  EPAC     3'  TGGTGTGGAGACCTCT      56690      T   TTT
                                TGGT TGG   GGACCTCT
                                |||| |||   ||||||||
                                ACCA ACC   TCTGGAGA
                                  C  ___
GAM2405  EPHB2    3'  TCTTCTAGGTTGTAGGGTTT   56691       _   T___
                                TCTTCT GGTT    GGTTT
                                |||||| ||||    |||||
                                AGAAGA CCAA    CCAAA
                                   T    CATC
GAM2405  FTSJ2    3'  TCTTTTGGTTTGCTTTTTGG   56692      C      G__
                                TCTT TGGTTTG   TTTGG
                                |||| |||||||   |||||
                                AGAA ACCAAAC   AAACC
                                  A      GAA
GAM2405  GABPB1   3'  TTCTGGTTTTGGATCTCT    56693         GGTT   C
                                TTCTGGTTT    TGGA CTCT
                                |||||||||    |||| ||||
                                AAGACCAAA    ACCT GAGA
                                     _____    A
GAM2405  PIK4CB   3'  TCCTGGTTTGGGGTTTC     56694          TTT  ACC
                                TTCTGGTTTGG   GG   TC
                                ||||||||||   ||   ||
                                AGGACCAAACC   CC   AG
                                     ___  AA_
GAM2405  PMP22    3'  TCTGTTTGGTTTGGTTTGA   56695     TC_
                                TCT   TGGTTTGGTTTGG
                                |||   ||||||||||||
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                                AGA   ACCAAACCAAACT
                                  CAA
GAM2405  RAI14    3'  TCTGCTGGTTTGAAGTCTC    56696      GT        C_
                                TCTG  TTGGTTTGGA  CTC
                                ||||  ||||||||||  |||
                                AGAC  GACCAAACTT  GAG
                                  __         CA
GAM2405  TMOD     3'  TCTGCTGGTTTGGGGGCTTCT  56697     T       TTT  ACC
                                TCT CTGGTTTGG   GG   TCT
                                ||| |||||||||   ||   |||
                                AGA GACCAAACC   CC   AGA
                                  C        C__  GA_
GAM2405  VEGF     3'  TTCTTGTTTGGTTTGAAC    56698      G
                                TTCT GTTTGGTTTGGAC
                                |||| ||||||||||||
                                AAGA CAAACCAAACTTG
                                   A
GAM2405  ZFH4     5'  TTCGGGTTTGGTGGCCTCT    56699     T       TT  A
                                TTC GGTTTGGT  GG CCTCT
                                ||| ||||||||  || |||||
                                AAG CCAAACCA  CC GGAGA
                                  C       __ _
GAM2405  FLJ20712 5'  TTCTGGTTGTGGAACCTCT    56700         _  TTTG
                                TTCTGGTT TGG    GACCTCT
                                |||||||| |||    |||||||
                                AAGACCAA ACC    TTGGAGA
                                     C  _____
GAM2405  HSU79252 5'  CTTCTGGTTCTGAGGACTTCT  56701          GGTTT   C
                                CTTCTGGTTT     GGAC TCT
                                ||||||||||     |||| |||
                                GAAGACCAAG     CCTG AGA
                                     ACT__    A
GAM2405  KIAA0227 3'  TCGTTCTGGTTTTTGATCT    56702    _       __
                                TC TTCTGGTT  TGGTTT
                                || ||||||||  ||||||
                                AG AAGACCAA  ACTAGA
                                  C       AA
GAM2405  KIAA0266 5'  TTCTGATTTGGAGTCTC     56703          TTT  AC
                                TTCTGGTTTGG   GG  CTC
                                ||||||||||   ||  |||
                                AAGACTAAACC   TC  GAG
                                     ___  A_
GAM2405  KIAA1272 3'  CTCTGGTTTTTGGTGAC     56704         __   TTG
                                TTCTGGTT  TGGT   GAC
                                ||||||||  ||||   |||
                                GAGACCAA  ACCA   CTG
                                     AA   ___
GAM2405  KOC1     3'  TCTTTGGTTTGGCATCTGCCTC 56705      C        TTGGA
            T                    TCTT TGGTTTGGT    CCTCT
                                ||||  |||||||||     |||||
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                                AGAA ACCAAACCG    GGAGA
                                  _       TAGAC
GAM2405  SFXN5    3'  CTTCCCCCTGGTTTGGGCCT   56706     GG       A
                                CTTCT  TTTGGTTTGG CCT
                                |||||  |||||||||| |||
                                GAAGG  GGACCAAACC GGA
                                   G_       C
GAM2405  LOC144776 3'  TCTTCTGGCTTGTAGGGTTTCT 56707          GTTT  ACC
                                TCTTCTGGTTTG   GG   TCT
                                ||||||||||||   ||   |||
                                AGAAGACCGAAC   CC   AGA
                                       AT__  CAA
GAM2405  LOC206078 5'  TCTTCTGCTTTGGCCT     56708       G    TTTGGA
                                TCTTCTG TTTGG     CCT
                                ||||||| |||||     |||
                                AGAAGAC AAACC     GGA
                                   G    _______
GAM2405  LOC255862 3'  TTCTGGTATGGCCAGACCT   56709       T   T TG
                                TTCTGGT TGG T  GACCT
                                ||||||| ||| |  |||||
                                AAGACCA ACC G  CTGGA
                                   T   _ GT
GAM2405  LOC90133  5'  TTCTGGTTTTCCTGACTTCT   56710        GGTTTG   C
                                TTCTGGTTT     GAC TCT
                                |||||||||     ||| |||
                                AAGACCAAA     CTG AGA
                                      AGGA__   A
GAM2405  LOC91170  5'  CCTTCTGGGCATTGGGTCTCT  56711        TTTGGT    AC
                                TCTTCTGG     TTGG  CTCT
                                ||||||||     ||||  ||||
                                GGAAGACC     AACC  GAGA
                                     CGT___    CA
GAM2406  CLASP1    3'  GCTAAGGAGGAAGAACACA   56714     GT  T
                                GCTG  GG GAGGAAGAACACA
                                ||||  || ||||||||||||||
                                CGAT  TC CTCCTTCTTGTGT
                                  __ _
GAM2406  EXTL3     5'  TGGCTGTTGACCAAAGAACA   56715     GG_  G_
                                TGGT   TGA  GAAGAACA
                                ||||   |||  ||||||||
                                ACCG   ACT  TTTCTTGT
                                  ACA   GG
GAM2406  LDOC1     3'  TAGCTGGGGTTCAGGACAC   56716       T  G_   AGAA
                                TAGCTGG GGT  AGGA    CAC
                                ||||||| |||  ||||    |||
                                ATCGACC CCA  TCCT    GTG
                                   _  AG   _____
GAM2406  PSMB1     3'  TGATTGGTGATAAGAGCAC   56717      _    GG   A
                                TGGT GGTGA  AAGA CAC
                                |||| |||||  |||| |||
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                                ACTA CCACT  TTCT GTG
                                  A    A_   C
GAM2406 PTGFRN   3' TGGTGAGCCAGGAGGAGCACA 56718     _ G   A A
                                TGGTG GT AGGA GA CACA
                                ||||| || |||| || ||||
                                ACCAC CG TCCT CT GTGT
                                   T  G   C  C
GAM2406 SET      3' TGGTGGTGGCAGGCACA    56719       __  AAGAA
                                TGGTGGTG  AGG    CACA
                                ||||||||  |||    ||||
                                ACCACCAC  TCC    GTGT
                                     CG  _____
GAM2406 SLC22A1  3' GCAAGTATGAGGAAGAATACA 56720   T   G       C
                                GC GGTG TGAGGAAGAA ACA
                                || |||| |||||||||| |||
                                CG TCAT ACTCCTTCTT TGT
                                 T   _       A
GAM2406 TFDP2    3' GGTGGTGAGGGAACAC     56721        AA
                                GGTGGTGAGG  GAACAC
                                ||||||||||  ||||||
                                CCACCACTCC  CTTGTG
                                          __
GAM2406 20D7-FC4 3' GCTGGGGTGAGGAGACCCCA  56722     T      A  ACA
                                GCTGG GGTGAGGA GA   CA
                                ||||| |||||||| ||   ||
                                CGACC CCACTCCT CT   GT
                                   _      _  GGG
GAM2406 ANKRD2   3' TAGCTGGCTGGGCTGGGGCAC 56723       __  GA  AAGAA
                                TAGCTGGT  GGT  GG    CAC
                                ||||||||  |||  ||    |||
                                ATCGACCG  CCG  CC    GTG
                                     AC   AC  C____
GAM2406 ARFRP1   3' CAGCCAGACTGAGGAAGAACAC 56724     TG TGG
              A                  TAGC  G   TGAGGAAGAACACA
                                ||||  |   ||||||||||||||
                                GTCG  C   ACTCCTTCTTGTGT
                                  GT TG_
GAM2406 COLEC12  3' TAGCTGGCTGTGGGGGCAC   56725       G   A  AAGAA
                                TAGCTGGT GTG GG    CAC
                                ||||||||  ||| ||    |||
                                ATCGACCG CAC CC    GTG
                                     A   _  CC___
GAM2406 FLJ20450 3' AGCTGACAGGAAGAACAC    56726      TGGTG
                                AGCTGG    AGGAAGAACAC
                                ||||||    ||||||||||||
                                TCGACT    TCCTTCTTGTG
                                   G____
GAM2406 FLJ22944 3' TACCTGGCAGTGGGAGGAAGAA 56727    G   TG __
                                TA CTGG  GT  GAGGAAGAA
                                || ||||  ||  |||||||||
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                                AT GACC  CA  CTCCTTCTT
                                 G    GT  CC
GAM2406  FLJ32884  5'  TGGTGGGCCGGAAGAACAC   56728       TGA
                                TGGTGG   GGAAGAACAC
                                ||||||   ||||||||||
                                ACCACC   CCTTCTTGTG
                                   CGG
GAM2406  HS6ST     3'  TAGTTGGTGAGGGACAC     56729     _     AAGA
                                TGGT GGTGAGG    ACAC
                                |||| |||||||    ||||
                                ATCA CCACTCC    TGTG
                                  A      C___
GAM2406  HS6ST1    3'  TAGTTGGTGAGGGACAC     56729     _     AAGA
                                TGGT GGTGAGG    ACAC
                                |||| |||||||    ||||
                                ATCA CCACTCC    TGTG
                                  A      C___
GAM2406  JIK       3'  GGAGGTGGGGAAGAACAC    56730    T    A
                                GG GGTG GGAAGAACAC
                                || |||| ||||||||||
                                CC CCAC CCTTCTTGTG
                                 T    C
GAM2406  KIAA0469  3'  GCTGGTGTATCTAAGAACAC   56731       GTGAGG
                                GCTGGTG     AAGAACAC
                                |||||||     ||||||||
                                CGACCAC     TTCTTGTG
                                    ATAGA_
GAM2406  KIAA0494  5'  GGAGGTGAGGAAGGGCAC    56732    T       AA
                                GG GGTGAGGAAG  CAC
                                || ||||||||||  |||
                                CC CCACTCCTTC  GTG
                                 T        CC
GAM2406  KIAA1198  3'  TAGCTGGTTGTGGTGGCAC   56733       G   A_  AAGAA
                                TAGCTGGT GTG  GG    CAC
                                |||||||| |||  ||    |||
                                ATCGACCA CAC  CC    GTG
                                    A   CA  _____
GAM2406  KIAA1297  3'  GCTGGTGGTGCAGACAC     56734         A   AGAA
                                GCTGGTGGTG GGA    CAC
                                |||||||||| |||    |||
                                CGACCACCAC TCT    GTG
                                   G   _____
GAM2406  KIAA1453  3'  GCTGGTGGAGGAGACA      56735       TG    A  A
                                GCTGGTGG  AGGA GA CA
                                ||||||||  |||| || ||
                                CGACCACC  TCCT CT GT
                                    __    _ _
GAM2406  KIAA1673  3'  TAGCTGGTGCTGGGGAAG    56736         G  A
                                TAGCTGGTG TG GGAAG
                                ||||||||| || |||||
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                                ATCGACCAC AC CCTTC
                                     G  C
GAM2406  KRTHB3   3'  CAGCTGGTGGTGGGGCAGTGGC 56737          A  A  AA_
              AC                  TAGCTGGTGGTG GG AG   CAC
                                  |||||||||||| || ||   |||
                                  GTCGACCACCAC CC TC   GTG
                                        C  G  ACC
GAM2406  PEF      3'  GCCTGGTGAGGGAACAC     56738     GG      AA
                                  GCT  TGGTGAGG  GAACAC
                                  |||  ||||||||  ||||||
                                  CGG  ACCACTCC  CTTGTG
                                    __      __
GAM2406  PEG10    3'  TGGTGGTATTGGAGAATAC   56739        A_  A  C
                                  TGGTGGTG  GGA GAA AC
                                  ||||||||  ||| ||| ||
                                  ACCACCAT  CCT CTT TG
                                       AA  _  A
GAM2406  PQBP1    5'  TAGCTGGGTGGACAGAACA   56740        TG  A GA
                                  TAGCTGG  GTG G  AGAACA
                                  |||||||  |||  |  ||||||
                                  ATCGACC  CAC C  TCTTGT
                                      __  _ TG
GAM2406  LOC115051 3'  TAGTTGGTGAGGGACAC     56729      _      AAGA
                                  TGGT GGTGAGG    ACAC
                                  |||| |||||||    ||||
                                  ATCA CCACTCC    TGTG
                                    A      C___
GAM2406  LOC130951 3'  TGGTGGTGTAGTGGGAAGGGCA 56741         A____     AA
              CA                    TGGTGGTG     GGAAG  CACA
                                    ||||||||     |||||  ||||
                                    ACCACCAC     CCTTC  GTGT
                                         ATCAC     CC
GAM2406  LOC132864 3'  TAGCTGGGGTGAAAAGCAGAAG 56742         T    _____
              AA                    TAGCTGG GGTGA     GGAAGAA
                                    |||||||  |||||     |||||||
                                    ATCGACC CCACT     TCTTCTT
                                        _     TTTCG
GAM2406  LOC133418 3'  TAGTGGTGGTAAAATGGAAGAA 56743      C        ___
                                  TAG TGGTGGTGA   GGAAGAA
                                  |||  |||||||||   |||||||
                                  ATC ACCACCATT   CCTTCTT
                                    _        TTA
GAM2406  LOC138429 3'  AGCTGGTGGTTAAGAATACA   56744          G    GA
                                  AGCTGGTGGT AGGAA  ACA
                                  ||||||||||  |||||  |||
                                  TCGACCACCA TTCTT  TGT
                                        A     A_
GAM2406  LOC146108 5'  GGCCATGAGGAAGGACAC     56745      G        A
                                  GGT GTGAGGAAG ACAC
                                  |||  |||||||||  ||||
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                                CCG TACTCCTTC TGTG
                                  G       C
GAM2406  LOC150358 3'  GCTTGGTGAGGAAGGGCAC   56746    GG        AA
                                GCT  TGGTGAGGAAG  CAC
                                |||  ||||||||||  |||
                                CGA  ACCACTCCTTC  GTG
                                  __        CC
GAM2406  LOC169611 3'  GCTGGTGGCAAAGAACAC    56747        GAG
                                GCTGGTGGT   GAAGAACAC
                                |||||||||   |||||||||
                                CGACCACCG   TTTCTTGTG
                                     ___
GAM2406  LOC253980 3'  CAGCTGGAGAGGGAAGGACGCA 56748       T  TGA    A  A
                                TAGCTGG GG   GGAAG AC CA
                                |||||||  ||   ||||| || ||
                                GTCGACC CT   CCTTC TG GT
                                    T  C__    C  C
GAM2407  PCM1     5'  AGCGCAATGCGAGCTAGA    56751           CGCC
                                AGCGCAATGCGAGC    AGA
                                ||||||||||||||    |||
                                TCGCGTTACGCTCG    TCT
                                       A___
GAM2407  DKFZP761I2123 3'  ACGGCTGGGCTGCCAGAGC    56752     CAAT  GA_  C
                                GCG    GC   GC GCCAGAGC
                                |||    ||   || ||||||||
                                TGC    CG   CG CGGTCTCG
                                  _____  ACC  A
GAM2407  DKFZp761J139 5'  GCAACCTCTGCCGCCAGGGCT  56753      GCGA      A
                                GCAAT    GCCGCCAG GCT
                                |||||    |||||||| |||
                                CGTTG    CGGCGGTC CGA
                                   GAGA       C
GAM2407  FLJ22087  5'  GCAGTACACCAGAGCTGCCAGG 56754     A  _____   C    A
            GCT                    GCA TGC    GAGC GCCAG GCT
                                ||| |||    |||| ||||| |||
                                CGT ATG    CTCG CGGTC CGA
                                  C   TGGT    A    C
GAM2407  FLJ22169  3'  AGCGAGATGCGGGCCAGAGCT  56755     CA    AGCC
                                AGCG  ATGCG    GCCAGAGCT
                                ||||  |||||    |||||||||
                                TCGC  TACGC    CGGTCTCGA
                                  TC    C___
GAM2407  KIAA0537  5'  AGCGCGGGGCGAGCCGGGC    56756      AAT      CCAGA
                                AGCGC   GCGAGCCG     GC
                                |||||   ||||||||     ||
                                TCGCG   CGCTCGGC     CG
                                   CCC       C_____
GAM2407  KIAA0677  5'  AGCCCAAAGCCCCGCCAGGGCT 56757     G   T  GAG      A
                                AGC CAA GC   CCGCCAG GCT
                                ||| ||| ||   ||||||| |||
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                                TCG GTT CG   GGCGGTC CGA
                                  G   T G__      C
GAM2407  MGC10870  5'  AGCGCAATGCAGGCTGCC    56758          A  C
                                AGCGCAATGCG GC GCC
                                |||||||||| || |||
                                TCGCGTTACGT CG CGG
                                      C  A
GAM2407  MGC2752   5'  CGCAGTGCGAGCCGTCTGCT   56759     A       CCAGA
                                CGCA TGCGAGCCG    GCT
                                |||| |||||||||    |||
                                GCGT ACGCTCGGC    CGA
                                  C       AGA__
GAM2407  UBN1      3'  AGCGCAAGCCCCAGCCTAGAGC 56760       T  GAG  _  _
             T                   AGCGCAA GC   CC GCC AGAGCT
                                ||||||| ||   || ||| ||||||
                                TCGCGTT CG   GG CGG TCTCGA
                                    _ G__  T   A
GAM2407  USP3      5'  GCAATGCAGACGCTGGAGCT   56761       G  C   CA
                                GCAATGC AG CGC  GAGCT
                                ||||||| || |||  |||||
                                CGTTACG TC GCG  CTCGA
                                    _ T   AC
GAM2407  LOC161190 5'  GCCTGCGGGGAGCCGCCAGAGC 56762    AA  ___
             T                   GC  TGC   GAGCCGCCAGAGCT
                                ||  |||   ||||||||||||||
                                CG  ACG   CTCGGCGGTCTCGA
                                 G_  CCC
GAM2407  LOC222865 3'  GCCCAGAACCTGTCAGGGCT   56763    G  ATGC    GC_  A
                                GC CA    GAGCC   CAG GCT
                                || ||    |||||   ||| |||
                                CG GT    CTTGG   GTC CGA
                                 G _____    ACA   C
GAM2407  LOC256158 5'  AGCCAATGCGAGGGGTGGGGCT 56764     G       CCGCCAGA
                                AGC CAATGCGAG       GCT
                                ||| |||||||||       |||
                                TCG GTTACGCTC       CGA
                                  _       CCCACCC_
GAM2408  CALD1     3'  TGAGTTATCTAAAATGTG    56767    T     __
                                TG GTTATCT  GATGTG
                                || |||||||  ||||||
                                AC CAATAGA  TTACAC
                                 T      TT
GAM2408  CALD1     3'  TGAGTTATCTAAAATGTG    56767    T     __
                                TG GTTATCT  GATGTG
                                || |||||||  ||||||
                                AC CAATAGA  TTACAC
                                 T      TT
GAM2408  EMP2      3'  TGGTTATCTGAATGTGGATT   56768    T       _   C
                                TG GTTATCTGA TGTG GATT
                                || |||||||| |||| ||||
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                                AC CAATAGACT ACAC CTAA
                                 _       T   _
GAM2408 C1QTNF2  3' TGTGCTTGGGGTGCGATT    56769       ATC  AT
                                TGTGTT   TG  GTGCGATT
                                ||||||   ||  ||||||||
                                ACACGA   AC  CACGCTAA
                                   ___  CC
GAM2408 KIAA0914 3' GTGTTGTCTAATGTAGTGATT  56770       A       C_
                                GTGTT TCTGATGTG  GATT
                                ||||| |||||||||  ||||
                                CACAA AGATTACAT  CTAA
                                   C        CA
GAM2408 LOC138255 5' TGTGTTTCTGATGTCCAA    56771       A       G
                                TGTGTT TCTGATGT CGA
                                ||||||| |||||||| |||
                                ACACAA AGACTACA GTT
                                   _       G
GAM2408 LOC256112 3' TGTGTTTTCTGATGCACA    56772       A      TG
                                TGTGTT TCTGATG  CG
                                ||||||| |||||||  ||
                                ACACAA AGACTAC  GT
                                   A       GT
GAM2408 LOC91445  3' TGTGTTACTGATCCCACTGATT 56773        T     GT_ _
                                TGTGTTA CTGAT   GC GATT
                                ||||||| |||||   || ||||
                                ACACAAT GACTA   TG CTAA
                                   _    GGG  A
GAM2409 AF1Q     5' ACTGAGTCTGTCAGTT      56776       TCA
                                ATTGG   TCTGTCAGTT
                                |||||   ||||||||||
                                TGACT   AGACAGTCAA
                                  C__
GAM2409 ATP2B1   3' ACTGTTTATCTGTCAGTT    56777      GTC
                                ATTG   ATCTGTCAGTT
                                ||||   ||||||||||
                                TGAC   TAGACAGTCAA
                                  AAA
GAM2409 CEACAM5  3' TCATGAAGCTGTCAGTT     56778      T  TCAT
                                TCAT GG    CTGTCAGTT
                                |||| ||    |||||||||
                                AGTA CT    GACAGTCAA
                                  _ TC__
GAM2409 CHRNA3   3' TCATTGGCATCTAGTGAGTT   56779        T    _ C
                                TCATTGG CATCT GT AGTT
                                ||||||| ||||| || ||||
                                AGTAACC GTAGA CA TCAA
                                   _    T  C
GAM2409 CXCL13   5' TCATTAGCAGAGTCAGTT     56780        T  TCT
                                TCATTGG CA   GTCAGTT
                                ||||||| ||   |||||||
```

```
                                AGTAATC GT   CAGTCAA
                                   _ CT_
GAM2409  DDX10    3'  ATTGATCATCTCAATT     56781         TG
                                ATTGGTCATC  TCAGTT
                                ||||||||||  ||||||
                                TAACTAGTAG  AGTTAA
                                   __
GAM2409  DLG2     5'  CCGTTCCCTCTGTCAGTT    56782     G  A_
                                TTG TC  TCTGTCAGTT
                                ||| ||  ||||||||||
                                GGC AG  AGACAGTCAA
                                  A  GG
GAM2409  FACL3    3'  ACTAATCCTGTCAGTT      56783       AT
                                ATTGGTC  CTGTCAGTT
                                |||||||  |||||||||
                                TGATTAG  GACAGTCAA
                                   __
GAM2409  MAML1    3'  TCACTGGTGTTACTGTTGGTT 56784        CAT_   CA
                                TCATTGGT   CTGT  GTT
                                ||||||||   ||||  |||
                                AGTGACCA   GACA  CAA
                                     CAAT   AC
GAM2409  NEDD4L   3'  TCATTGGTAACAAAACTCAGTT 56785        __  TCTG
                                TCATTGGT  CA   TCAGTT
                                ||||||||  ||   ||||||
                                AGTAACCA  GT   AGTCAA
                                     TT  TTTG
GAM2409  NFIA     3'  ATTGATTCCTGTCAGTT     56786      CA
                                ATTGGT  TCTGTCAGTT
                                ||||||  ||||||||||
                                TAACTA  GGACAGTCAA
                                   A_
GAM2409  RCN2     3'  CATTGTCCTGTCAGTT      56787      G  AT
                                CATTG TC  CTGTCAGTT
                                |||||  ||  |||||||||
                                GTAAC AG  GACAGTCAA
                                   _  __
GAM2409  SOD3     5'  TCATTGTCATTGTCGTT     56788       G   C   A
                                TCATTG TCAT TGTC GTT
                                |||||| |||| |||| |||
                                AGTAAC AGTA ACAG CAA
                                   _   _   _
GAM2409  SOX12    3'  TCTTTGGTCATTCAGTT     56789    A      CTG
                                TC TTGGTCAT   TCAGTT
                                || ||||||||   ||||||
                                AG AACCAGTA   AGTCAA
                                  A      ____
GAM2409  USP7     3'  TCATTGGCATCCAAGCT     56790       T     TC
                                TCATTGG CATCTG  AGTT
                                |||||||  ||||||  ||||
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```
                                AGTAACC GTAGGT  TCGA
                                      _    __
GAM2409 WISP1    3' TCTTGGTCATTTCAGT     56791    A      CTG
                                TC TTGGTCAT   TCAGT
                                || ||||||||   |||||
                                AG AACCAGTA   AGTCA
                                 _      A__
GAM2409 YWHAG    3' CAAAAGCATCTGTCAGTT    56792    TT  T
                                CA  GG CATCTGTCAGTT
                                ||  || ||||||||||||
                                GT  TC GTAGACAGTCAA
                                 TT  _
GAM2409 CHRFAM7A 3' CATTGGTCAGGCTGGTCAGTT 56793         T_  _
                                CATTGGTCA  CTG TCAGTT
                                |||||||||  ||| ||||||
                                GTAACCAGT  GAC AGTCAA
                                      CC   C
GAM2409 COE2     3' TCATTGGTTTGTAAGTT     56794        CATC   C
                                TCATTGGT    TGT AGTT
                                ||||||||    ||| ||||
                                AGTAACCA    ACA TCAA
                                     A___   T
GAM2409 DKFZp547I224 3' TCATTAGTTCATGCAGTT    56795        _ TC  T
                                TCATTGGT CA  TG CAGTT
                                |||||||| ||  || |||||
                                AGTAATCA GT  AC GTCAA
                                     A  __  _
GAM2409 DSCAML1  3' TTGGTTTTTGTCTGTCAGTT  56796      CA___
                                TTGGT    TCTGTCAGTT
                                |||||    ||||||||||
                                AACCA    AGACAGTCAA
                                   AAAAC
GAM2409 EHM2     3' ATTGGCACCATTCAGTT     56797      T   TG
                                ATTGG CATC  TCAGTT
                                ||||| ||||  ||||||
                                TAACC GTGG  AGTCAA
                                   _   TA
GAM2409 FLJ10242 3' ATCTTCACACTGTCAGTT    56798    GG   _
                                ATT  TCAT CTGTCAGTT
                                |||  |||| |||||||||
                                TAG  AGTG GACAGTCAA
                                  A_   T
GAM2409 FLJ20208 3' TCATTTCCACCTGTCAGTT   56799      GG
                                TCATT  TCATCTGTCAGTT
                                |||||  ||||||||||||
                                AGTAA  GGTGGACAGTCAA
                                   A_
GAM2409 KIAA0022 3' TCATTGGTTATCAGTT     56800        CATC
                                TCATTGGT   TGTCAGTT
                                ||||||||   ||||||||
```

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                                AGTAACCA    ATAGTCAA
                                        ____
GAM2409 KOC1     3'  TCAGCGCCCATCTGTTGGTT  56801     T  G       CA
                                TCA TG TCATCTGT  GTT
                                ||| || ||||||||  |||
                                AGT GC GGTAGACA  CAA
                                  C  G       AC
GAM2409 MGC13523 3'  TCATTTCACTGTCAGTT     56802      GG   T
                                TCATT  TCA CTGTCAGTT
                                |||||  ||| |||||||||
                                AGTAA  AGT GACAGTCAA
                                    __  _
GAM2409 MRPS6    3'  CATTGGTCGTCAATT       56803         ATCT
                                CATTGGTC    GTCAGTT
                                ||||||||    |||||||
                                GTAACCAG    CAGTTAA
                                        ____
GAM2409 PRO1905  5'  TCATTGGTCATTCCTTTGGTT  56804          _ GTCA
                                TCATTGGTCAT CT    GTT
                                ||||||||||| ||    |||
                                AGTAACCAGTA GG    CAA
                                      A  AAAC
GAM2409 SEF      3'  TCATTAGTCAAAACCAGTT    56805          TCTG
                                TCATTGGTCA    TCAGTT
                                ||||||||||    ||||||
                                AGTAATCAGT    GGTCAA
                                      TTT_
GAM2409 SLC2A11  3'  ACTGATTTTCTGTCAGTT    56806       CA
                                ATTGGT  TCTGTCAGTT
                                ||||||  ||||||||||
                                TGACTA  AGACAGTCAA
                                   AA
GAM2409 ZNF220   3'  TCAATGGTTTGTCAGTT     56807     T   CATC
                                TCA TGGT    TGTCAGTT
                                ||| ||||    ||||||||
                                AGT ACCA    ACAGTCAA
                                  T   A___
GAM2409 LOC120856 3'  TCAATGGTTACATCAGTT    56808     T   C  CT
                                TCA TGGT AT  GTCAGTT
                                ||| |||| ||  |||||||
                                AGT ACCA TG  TAGTCAA
                                  T   A  __
GAM2409 LOC131870 3'  TCCTCAACATCTGTCGGTT   56809     A TG T       A
                                TC T  G CATCTGTC GTT
                                || |  | |||||||| |||
                                AG A  T GTAGACAG CAA
                                 G GT _       C
GAM2409 LOC142973 5'  TCATGGTCATCAAAAGTT    56810      T       TGTC
                                TCAT GGTCATC    AGTT
                                |||| |||||||    ||||
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                                AGTA CCAGTAG    TCAA
                                  _      TTT_
GAM2409  LOC144108 3'  TCACTGGTCGTCGAAGTT    56811        ATCT  __
                                TCATTGGTC    GTC  AGTT
                                |||||||||    |||  ||||
                                AGTGACCAG    CAG  TCAA
                                     ____   CT
GAM2409  LOC145773 3'  TTGTGTCTCACTGTCAGTT    56812     _  AT_
                                TTG GTC   CTGTCAGTT
                                |||  |||   |||||||||
                                AAC CAG   GACAGTCAA
                                  A   AGT
GAM2409  LOC148195 3'  CATTGGTTTATCAGTT      56813       CATC
                                CATTGGT    TGTCAGTT
                                |||||||    ||||||||
                                GTAACCA    ATAGTCAA
                                    A___
GAM2409  LOC149464 3'  TCATCTGCCTTTTGTCAGTT   56814      G   ATC
                                TCATT GTC   TGTCAGTT
                                |||||  |||   ||||||||
                                AGTAG CGG   ACAGTCAA
                                   A   AAA
GAM2409  LOC150577 5'  TCATTGGTCTTTCAGCT     56815        ATCTG
                                TCATTGGTC     TCAGTT
                                |||||||||     ||||||
                                AGTAACCAG     AGTCGA
                                     AA___
GAM2409  LOC152122 5'  TCATTTTCTGTCAGTT      56816      GGTCA
                                TCATT     TCTGTCAGTT
                                |||||     ||||||||||
                                AGTAA     AGACAGTCAA
                                   A____
GAM2409  LOC222681 3'  TCATTGGCCGACGTAGTT    56817        ATC   C
                                TCATTGGTC   TGT AGTT
                                |||||||||   ||| ||||
                                AGTAACCGG   GCA TCAA
                                     CT_  _
GAM2409  LOC257507 3'  TCATTGGCCGACGTAGTT    56817        ATC   C
                                TCATTGGTC   TGT AGTT
                                |||||||||   ||| ||||
                                AGTAACCGG   GCA TCAA
                                     CT_  _
GAM2409  LOC257625 3'  TCATTGGCCGACGTAGTT    56817        ATC   C
                                TCATTGGTC   TGT AGTT
                                |||||||||   ||| ||||
                                AGTAACCGG   GCA TCAA
                                     CT_  _
GAM2409  LOC92303  3'  TCAGTTAGGTCTGTCAGTT   56818     _   TCA
                                TCA TTGG   TCTGTCAGTT
                                |||  ||||   ||||||||||
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                                AGT AATC   AGACAGTCAA
                                  C    C__
GAM2410  PDE4B    3'  TCTAATGTGAGAATATTGTTT  56821        A  T   T
                                TCTAATGT GA AAT TTGTTT
                                |||||||| || ||| ||||||
                                AGATTACA CT TTA AACAAA
                                     _  C   T
GAM2410  RAD17    5'  TCTAATGTAGAAGGCCCATTT  56822          TAAT  TG
                                TCTAATGTAGA    TT  TTT
                                ||||||||||    ||  |||
                                AGATTACATCT    GG  AAA
                                      TCC_  GT
GAM2410  ARPP-21  3'  ATGAAATAATTTTGTTT     56823     T
                                ATG AGATAATTTTGTTT
                                ||| ||||||||||||||
                                TAC TTTATTAAAACAAA

                                 _
GAM2410  FLJ12505 3'  TCTCAATGTGATATTTTTGTTT 56824     _    A   A
                                TCT AATGT GATA TTTTGTTT
                                ||| ||||| |||| ||||||||
                                AGA TTACA CTAT AAAACAAA
                                  G    _   A
GAM2410  KIAA0981 3'  TCTAAGTAGATAACATGTT    56825      T       TT
                                TCTAA GTAGATAAT  TGTT
                                ||||| |||||||||  ||||
                                AGATT CATCTATTG  ACAA
                                   _       T_
GAM2410  KIAA1458 3'  TAATGTAGATAATTTGTTT    56826           T
                                TAATGTAGATAATTT GTTT
                                |||||||||||||| ||||
                                ATTACATCTATTAAA CAAA

                                        _
GAM2410  LOC257443 3'  TAATGTAGATAATTTGTTT    56826           T
                                TAATGTAGATAATTT GTTT
                                |||||||||||||| ||||
                                ATTACATCTATTAAA CAAA

                                        _
GAM2411  EPHA3    3'  TTAGTGCAGCATTCTATATAG  56829        A    AAGAT
                                TTAGTGTA CATTT    TAG
                                |||||||| |||||    |||
                                AATCACGT GTAAG    ATC
                                     C    ATAT_
GAM2411  INPP4A   3'  ATGTAACAGCTAATTAGA    56830        TTTAA
                                GTGTAACA    GATTAGA
                                ||||||||    |||||||
                                TACATTGT    TTAATCT
                                     CGA__
GAM2411  LOC150203 3'  GTGTAACATTAGTCCAG     56831         TA  A
                                GTGTAACATT  AG TTAG
                                ||||||||||  || ||||
```

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                                CACATTGTAA  TC GGTC
                                     __  A
GAM2412  LOC253296 5'  CAGCTGCGGACCGCGGTCGAG  56834      GTT       A
                                TAGC   CGGACCGC GTCGAG
                                ||||   |||||||| ||||||
                                GTCG   GCCTGGCG CAGCTC
                                  AC_       C
GAM2412  LOC257481 3'  CAGCGTTCGGGCTGGAGA    56835          ACC  AGTC
                                TAGCGTTCGG   GC    GAGA
                                ||||||||||   ||    ||||
                                GTCGCAAGCC   CG    CTCT
                                     ____  AC__
GAM2412  LOC257570 5'  CAGCTGCGGACCGCGGTCGAG  56834      GTT       A
                                TAGC   CGGACCGC GTCGAG
                                ||||   |||||||| ||||||
                                GTCG   GCCTGGCG CAGCTC
                                  AC_       C
GAM2413  GNRHR     5'  TTTGCATATACATCATGTCAGT 56838           _   _
            T                    TTTGCATATACAT ATG CGGTT
                                 |||||||||||| ||| |||||
                                 AAACGTATATGTA TAC GTCAA
                                       G   A
GAM2413  KL        3'  TTTGCATATAGTTTCTGTGTTT 56839           CATATGCG
            TA                    TTTGCATATA       GTTTTA
                                  ||||||||||       ||||||
                                  AAACGTATAT       CAAAAT
                                       CAAAGACA
GAM2413  SHOC2     3'  TTGTATATACATATATAG     56840     C         CG
                                TTG ATATACATATG  G
                                ||| ||||||||||  |
                                AAC TATATGTATAT  C
                                  A          AT
GAM2413  SRGAP2    3'  TTTGCATAAATGAAAACTGGTT 56841          TACATAT  _
            TTA                   TTTGCATA      GC GGTTTTA
                                  ||||||||      || |||||||
                                  AAACGTAT      TG CCAAAAT
                                       TTACTTT  A
GAM2413  AK5       3'  TTTGCATATGGGTATGACAAGG 56842          ACA   _ __
            TTT                   TTTGCATAT   TATG C  GGTTT
                                  |||||||||   |||| |  |||||
                                  AAACGTATA   ATAC G  CCAAA
                                       CCC    T TT
GAM2413  C5orf5    3'  TTTGTATATAGATATACAGTTT 56843      C     C
            T                     TTTG ATATA ATATGCGGTTTT
                                  |||| ||||| ||||||||||||
                                  AAAC TATAT TATATGTCAAAA
                                    A     C
GAM2413  DKFZp547I224 3'  TTTCCATGTAGTTGAGCGGTTT 56844      G   A  CATAT
            T                     TTT CAT TA     GCGGTTTT
                                  ||| ||| ||     ||||||||
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                                AAA GTA AT    CGCCAAAA
                                  G   C  CAACT
GAM2413  EPB41L1   3'  TTTGCAAATGCAGTTT     56845       TATACAT
                                TTTGCA      ATGCGGTTT
                                ||||||      |||||||||
                                AAACGT      TACGTCAAA
                                   T_______
GAM2413  KIAA0555  3'  TTTGACATATACATGTTTCA   56846     _       ATGCG
                                TTTG CATATACAT    GTTTTA
                                |||| |||||||||    ||||||
                                AAAC GTATATGTA    CAAAGT
                                  T       _____
GAM2413  LOC126669 3'  TTTGCATATGGGGCAGTTTT   56847         ACATAT
                                TTTGCATAT     GCGGTTTT
                                |||||||||     ||||||||
                                AAACGTATA     CGTCAAAA
                                     CCC___
GAM2413  LOC150157 3'  TTTCCATGTAGTTGAGCGGTTT 56844     G   A  CATAT
              T                  TTT CAT TA    GCGGTTTT
                                 ||| ||| ||    ||||||||
                                 AAA GTA AT    CGCCAAAA
                                   G   C  CAACT
GAM2413  LOC158014 5'  TGTATATACATATATGAAAGGT 56848    C         C____
              TTT                  TG ATATACATATG    GGTTTT
                                   || ||||||||||    ||||||
                                   AC TATATGTATAT    CCAAAA
                                    A         ACTTT
GAM2413  LOC196890 3'  TTTCCATGTAGTTGAGCGGTTT 56844     G   A  CATAT
              T                  TTT CAT TA    GCGGTTTT
                                 ||| ||| ||    ||||||||
                                 AAA GTA AT    CGCCAAAA
                                   G   C  CAACT
GAM2413  LOC255458 3'  TTTGCATGTGCTCGGTTTTA   56849       ATACATATG
                                TTTGCAT       CGGTTTTA
                                |||||||       ||||||||
                                AAACGTA       GCCAAAAT
                                    CACGA____
GAM2413  LOC257017 5'  TGCATATGTATATACAACTTTA 56850       AC     GG
                                TGCATAT  ATATGC  TTTTA
                                |||||||  ||||||  |||||
                                ACGTATA  TATATG  GAAAT
                                    CA     TT
GAM2414  SURF4     3'  TTTGATGTGTTTCCAAAAATCA 56853       C  A      AA
                                TTTGATG GT TTCAAAA  ATCA
                                ||||||| || |||||||  ||||
                                AAACTAC CA AGGTTTT  TAGT
                                    A  A      __
GAM2414  KIAA0429  3'  TTTGGCACCTTCAGAAAAATCA 56854     AT   TA   A
                                TTTG  GCG  TTCA AAAAATCA
                                ||||  |||  |||| ||||||||
```

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                                AAAC  CGT  AAGT TTTTTAGT
                                  __  GG   C
GAM2414  PC326    5'  TTTGATGCGTGTATCAAA    56855         AT_
                                TTTGATGCGT   TCAAA
                                ||||||||||  |||||
                                AAACTACGCA   AGTTT
                                     CAT
GAM2414  LOC145790 3'  TTTAATGTGTATGCAAAAATCA 56856       C   TCAA
                                TTTGATG GTAT   AAAAATCA
                                ||||||| ||||   ||||||||
                                AAATTAC CATA   TTTTTAGT
                                   A   CG__
GAM2414  LOC199777 3'  TTTGTGCGTCCCAAAAA     56857     A   A
                                TTTG TGCGT TTCAAAAA
                                |||| ||||| ||||||||
                                AAAC ACGCA GGGTTTTT
                                  _    _
GAM2414  LOC200301 5'  TGGTGCGTCCTCAAAAAATCA  56858    A   A      A
                                TG TGCGT TTCAAAAAA TCA
                                || ||||| ||||||||| |||
                                AC ACGCA GAGTTTTTT AGT
                                 C    G       _
GAM2415  AQP8     3'  GCAGCGTGTTCCCCAGG     56861     AA  A
                                GCA  TGT TTCCCCAGG
                                |||  ||| |||||||||
                                CGT  GCA AAGGGGTCC
                                  C_  C
GAM2415  BTNL3    3'  TGACTAGCAAATGAGGAGCCTG 56862      A      TATTC  CA
           GG                     TGAC AGCAAATG    CC  GG
                                |||| ||||||||    ||  ||
                                ACTG TCGTTTAC    GG  CC
                                  A      TCCTC  AC
GAM2415  CELSR2   3'  TGAGGGGCAGGCCCCCCAG   56863    CAA  AAT  AT
                                TGA   GCA   GT  TCCCCAG
                                |||   |||   ||  |||||||
                                ACT   CGT   CG  GGGGGTC
                                  CCC   C__  __
GAM2415  DSCR1    3'  TGCTGAGTGAATGCATTCCAGG 56864    ACA  CA       CC
                                TG   AG  AATGTATTCC  AGG
                                ||   ||  ||||||||||  |||
                                AC   TC  TTACGTAAGG  TCC
                                 GAC  AC        __
GAM2415  EMS1     3'  TGATGAGAAAATGCACCTCAGG 56865    CA  C     TT  C
                                TGA  AG AAATGTA  CC CAGG
                                |||  || |||||||  || ||||
                                ACT  TC TTTACGT  GG GTCC
                                  AC  T      __  A
GAM2415  EMS1     3'  TGATGAGAAAATGCACCTCAGG 56865    CA  C     TT  C
                                TGA  AG AAATGTA  CC CAGG
                                |||  || |||||||  || ||||
```

```
                                ACT  TC TTTACGT  GG GTCC
                                  AC  T      __  A
GAM2415  JAM3     3'  GACAAGCAGGGTTCCTCAGG   56866        AATGTA   C
                                GACAAGCA     TTCC CAGG
                                ||||||||     |||| ||||
                                CTGTTCGT     AAGG GTCC
                                     CCC___    A
GAM2415  NOTCH2   3'  TGACAGATGCTTTTTCCCCAGG 56867      A CAA   A__
                                TGACA G   ATGT   TTCCCCAGG
                                ||||| |   ||||   |||||||||
                                ACTGT C   TACG   AAGGGGTCC
                                   _ ___    AAA
GAM2415  PNOC     3'  TGGCAAGTCAAAACCCCAG    56868    A   _   TGTATT
                                TG CAAG CAAA     CCCCAG
                                || |||| ||||     ||||||
                                AC GTTC GTTT     GGGGTC
                                 C    A    T_____
GAM2415  SORCS1   3'  TGACAAACAAATGTGAAGACAG 56869           ATTCCC
             G                   TGACAAGCAAATGT     CAGG
                                ||||||||||||||     ||||
                                ACTGTTTGTTTACA     GTCC
                                       CTTCT_
GAM2415  WIF1     5'  GCAAATACATTTTCCAGG    56870          CC
                                GCAAATGTATT  CCAGG
                                ||||||||||  |||||
                                CGTTTATGTAA  GGTCC
                                      AA
GAM2415  APOL6    5'  AGCAAATCTGTGTCCCCAGG   56871       GTAT_
                                AGCAAAT    TCCCCAGG
                                |||||||    ||||||||
                                TCGTTTA    AGGGGTCC
                                    GACAC
GAM2415  ATP5D    3'  GCAGGCGCGGCTTCCCCAGG   56872     AA   A__
                                GCA  TGT   TTCCCCAGG
                                |||  |||   |||||||||
                                CGT  GCG   AAGGGGTCC
                                  CC   CCG
GAM2415  BTN3A1   3'  TGACAAGCACATGCCA      56873         A   TATTCC
                                TGACAAGCA ATG     CCA
                                ||||||||| |||     |||
                                ACTGTTCGT TAC     GGT
                                     G   _______
GAM2415  C14orf4  5'  GACAAGCGGGGCCCCCAG    56874        AAAT  ATT
                                GACAAGC   GT   CCCCAG
                                |||||||   ||   ||||||
                                CTGTTCG   CG   GGGGTC
                                    CCC_  ___
GAM2415  CNTNAP1  3'  AAGCAAATGGAAGATCTTCAGG 56875          TAT__  CC
                                AAGCAAATG    TC  CAGG
                                |||||||||    ||  ||||
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                                TTCGTTTAC    AG  GTCC
                                     CTTCT  AA
GAM2415  DDX31    3'  GCACGGTGGAAATTCCCCAGG  56876    AA_  T__
                                GCA   TG   ATTCCCCAGG
                                |||   ||   ||||||||||
                                CGT   AC   TAAGGGGTCC
                                  GCC  CTT
GAM2415  DKFZp434J0226 5'  GCAGTGCTTCCCCAGG     56877    AA   A
                                GCA  TGT TTCCCCAGG
                                |||  ||| |||||||||
                                CGT  ACG AAGGGGTCC
                                  C_  _
GAM2415  EML4     3'  TGAGAGCTGTATTCCCCAG   56878    CA   AAA
                                TGA  AGC   TGTATTCCCCAG
                                |||  |||   ||||||||||||
                                ACT  TCG   ACATAAGGGGTC
                                  C_  ____
GAM2415  FADS3    3'  CAGGCAGGGCACCCCCAGG   56879    A   AAT    T
                                CA GCA   GTAT CCCCAGG
                                || |||   |||| |||||||
                                GT CGT   CGTG GGGGTCC
                                 C   CC_   _
GAM2415  FLJ10483  3'  ACGGGCAAATGTTCTCCAGG   56880    AA      AT  C
                                AC  GCAAATGT  TC CCAGG
                                ||  ||||||||  || |||||
                                TG  CGTTTACA  AG GGTCC
                                 CC       __  A
GAM2415  GPA33    3'  GCAAAAGCTCCCCAGG     56881      T  AT
                                GCAAA GT  TCCCCAGG
                                ||||| ||  ||||||||
                                CGTTT CG  AGGGGTCC
                                   T  __
GAM2415  KIAA0326  3'  AGCAAATGCTTTGACCCCTGG  56882        ATT__    A
                                AGCAAATGT    CCCC GG
                                |||||||||    |||| ||
                                TCGTTTACG    GGGG CC
                                     AAACT    A
GAM2415  KIAA1708  3'  ACAAGCAAATATTTTCAGG   56883          A   CCC
                                ACAAGCAAATGT TTC   AGG
                                |||||||||||| |||   |||
                                TGTTCGTTTATA AAG   TCC
                                       A  ____
GAM2415  KIAA1940  3'  TGGGAAGTGGACGTCCCCCCAG 56884    AC   CAA    A
            G                    TG  AAG   ATGT TTCCCCAGG
                                ||  |||   |||| |||||||||
                                AC  TTC   TGCA GGGGGGTCC
                                 CC   ACC   _
GAM2415  MGC15634  3'  TGACAGCAAACAGAACTTCAGG 56885      A     GTATTCCC
                                TGACA GCAAAT       CAGG
                                ||||| ||||||       ||||
```

```
                                ACTGT CGTTTG      GTCC
                                  _     TCTTGAA_
GAM2415  OSBPL8   3'  TGAAAGGCAAATGTGGTCAGG  56886     CAA      ATTCCC
                                TGA   GCAAATGT     CAGG
                                |||   ||||||||     ||||
                                ACT   CGTTTACA     GTCC
                                  TTC       CCA___
GAM2415  PFDN1    3'  TGGGAAGCAAATGGGGCTCAGG 56887    AC       TATTCCC
                                TG  AAGCAAATG      CAGG
                                ||  |||||||||      ||||
                                AC  TTCGTTTAC      GTCC
                                 CC       CCCGA__
GAM2415  RAB4B    5'  TGACAAGCTGGTTCTCACCTCA 56888        AAAT  A   _  _
            GG                    TGACAAGC    GT TTC CC CAGG
                                ||||||||    || ||| || ||||
                                ACTGTTCG    CA GAG GG GTCC
                                     AC__  A   T  A
GAM2415  SHAPY    3'  GCAGATGTGTCCCCAGG     56889     A    AT
                                GCA ATGT  TCCCCAGG
                                ||| ||||  ||||||||
                                CGT TACA  AGGGGTCC
                                  C    C_
GAM2415  LOC145676 5'  TGACAAGCAATGCCTCAGA    56890         A  TATT  C
                                TGACAAGCAA TG    CC CAGG
                                |||||||||| ||    || ||||
                                ACTGTTCGTT AC    GG GTCT
                                     _  _____  A
GAM2415  LOC203378 5'  TGACAAGGGAGTACATTCCAGG 56891        CAAAT    TCC
                                TGACAAG    GTAT   CCAGG
                                |||||||    ||||   |||||
                                ACTGTTC    CATG   GGTCC
                                    CCT__    TAA
GAM2415  LOC221466 5'  TGACAAGCGGTGTGACACCCCC 56892        AAA   AT__
            AGG                   TGACAAGC   TGT    TCCCCAGG
                                ||||||||   |||   ||||||||
                                ACTGTTCG   ACA    GGGGGTCC
                                    CC_   CTGT
GAM2415  LOC222066 5'  TGACAAGCAGAGGCCTCCCAGG 56893         AAT  ATTC
                                TGACAAGCA   GT    CCCAGG
                                |||||||||   ||    ||||||
                                ACTGTTCGT   CG    GGGTCC
                                     CTC  GA__
GAM2415  LOC91308  3'  TGAAAGCAAATGACCTTAG    56894     C       TATT  CC
                                TGA AAGCAAATG    CC  AG
                                ||| |||||||||    ||  ||
                                ACT TTCGTTTAC    GG  TC
                                  _       T___  AA
GAM2415  LOC92661  3'  TGAGGGCAGCCACGTTCCCCAG 56895     CAA   AA  TA
            G                    TGA   GCA  TG  TTCCCCAGG
                                |||   |||  ||  |||||||||
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                                ACT  CGT  GT  AAGGGGTCC
                                  CC_  CG  GC
GAM2416 ESRRBL1  3' TAATTTCTTTATTAAACA   56898          T
                                TAATTTCTTTATT GATA
                                |||||||||||| ||||
                                ATTAAAGAAATAA TTGT
                                       T
GAM2416 SLC22A12 3' TCATTTGTTTCTTTATTCAAT 56899     AA       TG
                                TCATT  TTTCTTTATT  AT
                                |||||  ||||||||||  ||
                                AGTAA  AAAGAAATAA  TA
                                   AC        GT
GAM2416 FLJ32940 3' TCATTAATTTTTTCATCTA   56900        C
                                TCATTAATTT TTTATTTG
                                |||||||||| ||||||||
                                AGTAATTAAA AAGTAGAT
                                       A
GAM2416 LOC146420 3' TCATTAATTTCTGTAACTG   56901         T  T
                                TCATTAATTTCT TA TTG
                                |||||||||||| || |||
                                AGTAATTAAAGA AT GAC
                                       C  T
GAM2417 ELMO2    3' AAAAGGTGAGTGGCTGTT    56904        ATT  AT
                                AAAAGGTGA   TG  TGTT
                                |||||||||   ||  ||||
                                TTTTCCACT   AC  ACAA
                                     C__  CG
GAM2417 GYPA     3' TAAAAGGTAAATTTCTGTT   56905          GA
                                TAAAAGGTGAATTT  TTGTT
                                ||||||||||||||  |||||
                                ATTTTCCATTTAAA  GACAA
                                          __
GAM2417 MBTPS1   5' AAAAGTGAATTTTTGTT     56906          GA
                                AAAGGTGAATTT  TTGTT
                                ||||||||||||  |||||
                                TTTTCACTTAAA  AACAA
                                          __
GAM2417 SFRS7    3' TAAAGGGTGAACTTGAGAGCT  56907     A        TT
                                TAAA GGTGAATTTGA  GTT
                                ||||| ||||||||||  |||
                                ATTT CCACTTGAACT  CGA
                                   C         CT
GAM2417 KIAA0210 3' TAAAAGGTGAAATATAATTGTT 56908         TT_
                                TAAAAGGTGAA   TGATTGTT
                                ||||||||||   ||||||||
                                ATTTTCCACTT   ATTAACAA
                                       TAT
GAM2417 LNX      3' TAAAAGAGTGAATTTTTCATGT 56909       _      GAT_
             T                   TAAAAG GTGAATTT    TGTT
                                ||||||| ||||||||    ||||
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                                ATTTTC CACTTAAA    ACAA
                                   T       AAGT
GAM2417  MacGAP    3'  AAAAGGTGGAATGTTAT     56910        AATTT  T
                                AAAAGGTG     GA TGTTAT
                                ||||||||     || ||||||
                                TTTTCCAC     CT ACAATA
                                   ______  T
GAM2417  MGC12435  5'  AAGGCTTCTTTGATTGTT    56911       GAA
                                AAGGT   TTTGATTGTT
                                |||||   ||||||||||
                                TTCCG   AAACTAACAA
                                  AAG
GAM2417  MGC24447  3'  TAAAAGGTGAAATGTTCCTTAT 56912          TT  A  G
           T                     TAAAAGGTGAA  TG TT TTATT
                                ||||||||||  || || |||||
                                ATTTTCCACTT  AC AG AATAA
                                      T_  A  G
GAM2417  PLSCR2    5'  AGGTGAATTTGAAAAGGCT    56913          TT__
                                AGGTGAATTTGA    GTT
                                ||||||||||||    |||
                                TCCACTTAAACT    CGA
                                      TTTC
GAM2417  TERA      3'  TAAAAGGTGGCTTACTCCTTAT 56914         AA  TGA  G
           T                     TAAAAGGTG  TT   TT TTATT
                                |||||||||  ||   || |||||
                                ATTTTCCAC  AA   AG AATAA
                                     CG  TG_  G
GAM2417  UNC5D     3'  TGAAGGATGAATTTGATT    56915    A   _
                                A AAGG TGAATTTGATT
                                | |||| ||||||||||
                                A TTCC ACTTAAACTAA
                                 C    T
GAM2417  LOC146420 3'  TAAAAGGTGAGTTCTTATT    56916         A   GA
                                TAAAAGGTGA TTT  TTGTT
                                |||||||||| |||  |||||
                                ATTTTCCACT AAG  AATAA
                                      C   __
GAM2417  LOC158549 5'  AAAGGTAAATTTGATGTT     56917            T
                                AAAGGTGAATTTGAT GTT
                                ||||||||||||||| |||
                                TTTCCATTTAAACTA CAA
                                                _
GAM2417  LOC89890  3'  TAAAAGGTTGATTTGAGTGTT  56918         GA     T
                                TAAAAGGT  ATTTGA TGTT
                                ||||||||  |||||| ||||
                                ATTTTCCA  TAAACT ACAA
                                     AC     C
GAM2417  LOC90355  3'  AAAAGTAAATGGTTTGATTGTT 56919          ___
                                AAAGGTGAAT   TTGATTGTT
                                ||||||||||   |||||||||
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                                TTTTCATTTA  AACTAACAA
                                     CCA
GAM2418 EVI2A    3' TTGGTTGATAAGCTGGTGTACC 56922     GC_ A_________  AACC
           GGTTGG                TTGA  GC       ACC   GG
                                ||||  ||       |||   ||
                                AACT  CG       TGG   CC
                                  ATT  ACCACIIIA  CCAA
GAM2418 ABCA10   5' TTGGCTGAGCGCATCATTGGTA 56923          AC  ACC
                                TTGGTTGAGCGCA  CA  GGTA
                                ||||||||||||  ||  ||||
                                AACCGACTCGCGT  GT  CCAT
                                      A_  AA_
GAM2418 C1orf2   3' CTGGTCCCAACCAGC      56924       GAGCGCAA
                                TTGGTT      CCAACCGGT
                                ||||||      |||||||||
                                GACCAG      GGTTGGTCG
                                  _________
GAM2418 C1orf2   3' CTGGTCCCAACCAGC      56924       GAGCGCAA
                                TTGGTT      CCAACCGGT
                                ||||||      |||||||||
                                GACCAG      GGTTGGTCG
                                  _________
GAM2418 CSNK1G1  3' TTGGTTGAGCTAACCACC    56925         GC    A
                                TTGGTTGAGC  AACCA CC
                                ||||||||||  ||||| ||
                                AACCAACTCG  TTGGT GG
                                     A_    _
GAM2419 FLRT2    3' TGATAGGTGCTAGTAGAAAAT  56928        TAACT  A
                                TGGTAGGT    GTA AAAAT
                                ||||||||    ||| |||||
                                ACTATCCA    CAT TTTTA
                                    CGAT_  C
GAM2419 FLJ21791 3' AGGCTAATTGTAAAAAATA   56929        C
                                AGGTTAA TGTAAAAAATA
                                ||||||| ||||||||||
                                TCCGATT ACATTTTTTAT
                                    A
GAM2419 LOC150051 3' TGGGAGGTTAACAAAAAT    56930     T      TGTA
                                TGG AGGTTAAC    AAAAAT
                                ||| ||||||||    ||||||
                                ACC TCCAATTG    TTTTTA
                                  C      ____
GAM2419 LOC221184 3' TGGAGGTCCGGTTGTAAAAAAT 56931     T    AAC_
           AA                    TGG AGGTT    TGTAAAAAATAA
                                ||| |||||    ||||||||||||
                                ACC TCCAG    ACATTTTTTATT
                                  _    GCCA
GAM2420 EIF3S10  3' AAAAAAACTCAGCGATA     56934       T   AC
                                AAAAAG ACT  CAGCGATA
                                |||||| |||  ||||||||
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                                TTTTTT TGA  GTCGCTAT
                                      _  __
GAM2420 LFNG     3'  TAAAAAAATACTGTCACAATA  56935          ACCA
                                TAAAAAAGTACT    GCGATA
                                ||||||||||||   ||||||
                                ATTTTTTTTATGA   TGTTAT
                                      CAG_
GAM2420 MAGOH    3'  TAAAAAAATACTGCCCTGATA  56936          A  AGC
                                TAAAAAAGTACT CC   GATA
                                ||||||||||||| ||   ||||
                                ATTTTTTTTATGA GG   CTAT
                                      C  GA_
GAM2420 PCDHB11  3'  TAAAAAAGTACATGCAA     56937          TACCA
                                TAAAAAAGTAC    GCGA
                                ||||||||||     ||||
                                ATTTTTTCATG    CGTT
                                      TA___
GAM2420 FHR5     5'  AAAAATACTCCAGTGAT     56938         A   C
                                AAAAGTACT CCAG GAT
                                ||||||||| |||| |||
                                TTTTTATGA GGTC CTA
                                     _   A
GAM2420 KIAA1399 3'  TAAAAAAGTACTTGACAG    56939          AC_
                                TAAAAAAGTACT   CAG
                                ||||||||||||   |||
                                ATTTTTTCATGA   GTC
                                      ACT
GAM2420 KIAA1434 3'  AAAAAATACTACACAAT     56940          CA
                                AAAAAGTACTAC  GCGAT
                                ||||||||||||  |||||
                                TTTTTTATGATG  TGTTA
                                      __
GAM2420 MGC20460 5'  AAAGGAACTTTCAGCGATA   56941      T_  AC
                                AAAG  ACT  CAGCGATA
                                ||||  |||  ||||||||
                                TTTC  TGA  GTCGCTAT
                                  CT   AA
GAM2420 LOC130497 3'  AAAAAAAAACTCCAGTGATA  56942       T  A   C
                                AAAAAAG ACT CCAG GATA
                                ||||||| ||| |||| ||||
                                TTTTTTT TGA GGTC CTAT
                                    T   _   A
GAM2420 LOC146159 5'  AAAAGAGCAGGCACCAGCG   56943     A   C_
                                AAAA AGTA  TACCAGCG
                                |||| ||||  ||||||||
                                TTTT TCGT  GTGGTCGC
                                  C   CC
GAM2421 BRCA1    3'  TATTCACTACTTTTCTGTG   56946     A  ATAAT
                                TAT CA    CTTTTCTGTG
                                ||| ||    ||||||||||
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                                ATA GT    GAAAAGACAC
                                  A  GAT__
GAM2421  IMPDH1   3'  TAATACACAATGACGCAACTGT 56947          A  CTTTT
                 G                 TAATATACAAT AT    CTGTG
                                   |||||||||||  ||    ||||||
                                   ATTATGTGTTA TG    GACAC
                                         C  CGTT_
GAM2421  COL12A1  3'  TAATATACAGTACATGACATCT 56948        A  ATC____
                 TCTGTG                AATATACA TA      TTTTCTGTG
                                   ||||||||  ||      |||||||||
                                   TTATATGT AT      AGAAGACAC
                                        C  GTACTGT
GAM2421  COL12A1  3'  TAATATACAGTACATGACATCT 56948        A  ATC____
                 TCTGTG                AATATACA TA      TTTTCTGTG
                                   ||||||||  ||      |||||||||
                                   TTATATGT AT      AGAAGACAC
                                        C  GTACTGT
GAM2421  SEC15B   3'  AATATACAATAATTTAGTTTGT 56949          CTTTTC
                 G                  AATATACAATAAT     TGTG
                                    ||||||||||||      ||||
                                    TTATATGTTATTA     ACAC
                                          AATCAA
GAM2421  LOC116123 5'  ATATACAATAGTCCTTGTTCTG 56950         A    __
                 TG                  ATATACAATA TCTTT  TCTGTG
                                    ||||||||||  |||||  ||||||
                                    TATATGTTAT AGGAA  AGACAC
                                         C    CA
GAM2422  GLUL     3'  TACATTTAAATATAAAAAT   56953
                                    TACATTTAAATATAAAAAT
                                    ||||||||||||||||||
                                    ATGTAAATTTATATTTTTA

GAM2422  ZNF256   3'  TGTCCATTTAAACACAAAGAAT 56954     A          _
                 TTT                  TGT CATTTAAATATAAA AATTTT
                                    |||  ||||||||||||| ||||||
                                    ACA GTAAATTTGTGTTT TTAAAA
                                      G           C
GAM2422  CLSTN1   3'  TGTACATTTAAGCATAAA    56955          A
                                    TGTACATTTAA TATAAA
                                    ||||||||||  ||||||
                                    ACATGTAAATT GTATTT
                                          C
GAM2422  FLJ22174  3'  TGTACATTTACATACAAA    56956          A
                                    TGTACATTTA ATATAAA
                                    |||||||||  |||||||
                                    ACATGTAAAT TATGTTT
                                          G
GAM2422  LOC221751 3'  TGTACATTTACATACAAA    56956          A
                                    TGTACATTTA ATATAAA
                                    |||||||||  |||||||
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                                ACATGTAAAT TATGTTT
                                      G
GAM2423  GLUL     3'  TACATTTAAATATAAAAAT   56953
                                TACATTTAAATATAAAAAT
                                ||||||||||||||||||
                                ATGTAAATTTATATTTTTA

GAM2423  ZNF256   3'  TGTCCATTTAAACACAAAGAAT 56954     A          _
              TTT                  TGT CATTTAAATATAAA AATTTT
                                ||| |||||||||||||| ||||||
                                ACA GTAAATTTGTGTTT TTAAAA
                                  G           C
GAM2423  CLSTN1   3'  TGTACATTTAAGCATAAA    56955          A
                                TGTACATTTAA TATAAA
                                |||||||||||| ||||||
                                ACATGTAAATT GTATTT
                                      C
GAM2423  FLJ22174 3'  TGTACATTTACATACAAA    56956          A
                                TGTACATTTA ATATAAA
                                |||||||||| |||||||
                                ACATGTAAAT TATGTTT
                                      G
GAM2423  LOC221751 3'  TGTACATTTACATACAAA    56956          A
                                TGTACATTTA ATATAAA
                                |||||||||| |||||||
                                ACATGTAAAT TATGTTT
                                      G
GAM2424  BMP8     5'  CCCTGCCGTGCCACCTCC    56960       A_
                                TTTTGC  TGCCACCTCC
                                ||||||  ||||||||||
                                GGGACG  ACGGTGGAGG
                                   GC
GAM2424  CD3Z     5'  TATTCTGCAGCTACCTCCC   56961         T  C
                                TATTTTGCA GC ACCTCCC
                                ||||||||| || |||||||
                                ATAAGACGT CG TGGAGGG
                                      _  A
GAM2424  CRY2     3'  CATTTTGCCTGCAACCATC   56962         A  C  _
                                TATTTTGC TGC ACC TC
                                |||||||| ||| ||| ||
                                GTAAAACG ACG TGG AG
                                     G  T  T
GAM2424  DOK1     3'  ATCCCTAGTGCCACCTCCC   56963       GCA
                                ATTTT   TGCCACCTCCC
                                |||||   ||||||||||
                                TAGGG   ACGGTGGAGGG
                                   ATC
GAM2424  EGR1     3'  TATTTTGCTCCCAAAGCCTCCC 56964         ATG  ___
                                TATTTTGC   CCA   CCTCCC
                                ||||||||   |||   ||||||
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                                ATAAAACG  GGT  GGAGGG
                                   AG_  TTC
GAM2424  EPB49    3'  TATTTCCACCCCACCTCC    56965      G  G
                                TATTTT CAT CCACCTCC
                                |||||| ||| ||||||||
                                ATAAAG GTG GGTGGAGG
                                   _  G
GAM2424  EPHA1    3'  TTCTACCCCCACCTCCC     56966      ATG
                                TTTTGC  CCACCTCCC
                                ||||||  |||||||||
                                AAGATG  GGTGGAGGG
                                   GG_
GAM2424  GNB1     3'  TATCTTGCATCCAGCTTCC   56967        G  C  _
                                TATTTTGCAT CCA CT CC
                                |||||||||| ||| || ||
                                ATAGAACGTA GGT GA GG
                                      _  C  A
GAM2424  HLCS     3'  TATTCTGCAGATGCCCTCTC  56968        __  AC
                                TATTTTGCA  TGCC  CTC
                                |||||||||  ||||  |||
                                ATAAGACGT  ACGG  GAG
                                     CT   GA
GAM2424  IL18R1   3'  TATTTTGCATCACGTCC     56969        GC  C
                                TATTTTGCAT  CAC TCC
                                ||||||||||  ||| |||
                                ATAAAACGTA  GTG AGG
                                     __  C
GAM2424  MEIS1    3'  TACTTTGCAGCCTTCC      56970        T  ACC
                                TATTTTGCA GCC  TCC
                                |||||||||| |||  |||
                                ATGAAACGT CGG  AGG
                                     _  A__
GAM2424  MGAM     3'  ATTTTCCACACCTCCC      56971      G  TGC
                                ATTTT CA  CACCTCCC
                                ||||| ||  ||||||||
                                TAAAA GT  GTGGAGGG
                                   G  ___
GAM2424  MLLT2    3'  TATTCTGCCGTTACACCTCC  56972       ATGC_
                                TATTTTGC   CACCTCC
                                ||||||||   |||||||
                                ATAAGACG   GTGGAGG
                                     GCAAT
GAM2424  MSN      3'  TTTTGCACTCACTCCC      56973        GC  C
                                TTTTGCAT  CAC TCCC
                                ||||||||  ||| ||||
                                AAAACGTG  GTG AGGG
                                     A_  _
GAM2424  PCDH11X  3'  TATTCTGCATCCAATTTTCC  56974        G  CC__
                                TATTTTGCAT CCA   TCC
                                |||||||||| |||   |||
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                                ATAAGACGTA GGT   AGG
                                      _  TAAA
GAM2424  PCMT1    3'  TACTTTGCATCCTTCC     56975         G  ACC
                                TATTTTGCAT CC   TCC
                                |||||||||| ||   |||
                                ATGAAACGTA GG   AGG
                                      _ A__
GAM2424  RGS16    3'  CTTTGCAGAACCTGCCTCCC   56976       T_  A_
                                TTTTGCA  GCC  CCTCCC
                                |||||||  |||  ||||||
                                GAAACGT  TGG  GGAGGG
                                    CT   AC
GAM2424  RNF14    3'  TACTTTGCTACCAAGCCTCCC  56977        A   __
                                TATTTTGC TGCCA  CCTCCC
                                |||||||| |||||  ||||||
                                ATGAAACG ATGGT  GGAGGG
                                      _    TC
GAM2424  SIAH1    3'  TATTTTACAATGCTTCCT    56978         _  CA
                                TATTTTGCA TGC  CCT
                                ||||||||| |||  |||
                                ATAAAATGT ACG  GGA
                                     T   AA
GAM2424  SLC5A5   5'  TCTGTCCTGCCACCTCCC    56979     CA_
                                TTTG   TGCCACCTCCC
                                ||||   ||||||||||
                                AGAC   ACGGTGGAGGG
                                  AGG
GAM2424  SOX2     3'  TTTTGCACCCCTCCC      56980       AT   A
                                TTTTGC  GCC CCTCCC
                                ||||||  ||| ||||||
                                AAAACG  TGG GGAGGG
                                     __  _
GAM2424  STXBP1   3'  TATCCTGATTGTCACCTCCC  56981       CA  C
                                TATTTTG  TG CACCTCCC
                                |||||||  || ||||||||
                                ATAGGAC  AC GTGGAGGG
                                    TA  A
GAM2424  TRIM37   3'  TAAACTGTGCCACCTTCC    56982    TT   CA      _
                                TA  TTG  TGCCACCT CC
                                ||  |||  |||||||| ||
                                AT  GAC  ACGGTGGA GG
                                 TT  __       A
GAM2424  ACTR3    3'  TATCTCTTCCCCACCTCCC   56983       GCATG
                                TATTTT    CCACCTCCC
                                ||||||    |||||||||
                                ATAGAG    GGTGGAGGG
                                   AAGG_
GAM2424  C20orf142 3'  CACCATGGTGCCACCTCCC   56984     TT  CA
                                TAT  TG  TGCCACCTCCC
                                |||  ||  ||||||||||
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                                GTG  AC  ACGGTGGAGGG
                                  GT  C_
GAM2424  CNOT7    3'  TTTTGCACAACCAATTTTCC   56985          _   CC__
                                TTTTGCATG CCA    TCC
                                ||||||||| |||    |||
                                AAAACGTGT GGT    AGG
                                     T   TAAA
GAM2424  DKFZP566J091 3'  CTTTGCACATGCCCCACCTCCC 56986          ____
                                TTTTGCATG    CCACCTCCC
                                |||||||||    |||||||||
                                GAAACGTGT    GGTGGAGGG
                                     ACGG
GAM2424  DKFZP667C165 3'  ATTTTGCATCCATAGGCCATTT 56987          _______   CC
            CC                    ATTTTGCAT     GCCA  TCC
                                |||||||||     ||||  |||
                                TAAAACGTA     CGGT  AGG
                                     GGTATC    AA
GAM2424  DKFZp761K1824 3'  ATTTTAGTCTACCACCTCC    56988       CA_
                                ATTTTG   TGCCACCTCC
                                ||||||   ||||||||||
                                TAAAAT   ATGGTGGAGG
                                   CAG
GAM2424  FLJ10314  3'  CTTGGCTCTGCCACCTTCC    56989     T  A_      _
                                TTT GC  TGCCACCT CC
                                ||| ||  |||||||| ||
                                GAA CG  ACGGTGGA GG
                                  C  AG       A
GAM2424  FLJ10460  3'  TATTCTGCCTCAGCCTCCC    56990        ATGC  _
                                TATTTTGC    CA CCTCCC
                                ||||||||    || ||||||
                                ATAAGACG    GT GGAGGG
                                     GA__  C
GAM2424  FLJ11240  3'  ATTTTGCACAAACACTCCC    56991         GCC  _
                                ATTTTGCAT   AC CTCCC
                                |||||||||   || |||||
                                TAAAACGTG   TG GAGGG
                                     TT_  T
GAM2424  FLJ11506  3'  ATTCTGCAGCTGCCTCC     56992         T  CA
                                ATTTTGCA GC  CCTCC
                                |||||||| ||  |||||
                                TAAGACGT CG  GGAGG
                                     _  AC
GAM2424  FLJ12484  3'  CTCTGTTGTCACCTCCC     56993       CA  C
                                TTTTG  TG CACCTCCC
                                |||||  || ||||||||
                                GAGAC  AC GTGGAGGG
                                   A_  A
GAM2424  FLJ12895  3'  TATTTTGCTCACAACTTCCC   56994         A   C  C
                                TATTTTGC TGC AC TCCC
                                |||||||| ||| || ||||
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                                ATAAAACG GTG TG AGGG
                                    A   T  A
GAM2424  H2BFQ    3'  TCTACCATTGCCACCTCC    56995      A__
                                TTTGC   TGCCACCTCC
                                |||||   ||||||||||
                                AGATG   ACGGTGGAGG
                                   GTA
GAM2424  KIAA0164 3'  TATTCTGCAGGATAGACCTCC  56996         TGCC__
                                TATTTTGCA     ACCTCC
                                |||||||||     ||||||
                                ATAAGACGT     TGGAGG
                                     CCTATC
GAM2424  KIAA0293 3'  CATTTTGCTTCTGCCTCCT   56997        A__   A
                                TATTTTGC   TGCC CCT
                                ||||||||   |||| |||
                                GTAAAACG   ACGG GGA
                                     AAG   A
GAM2424  KIAA0981 3'  ATTTTCATGCCACTTCCC    56998      G      C
                                ATTTT CATGCCAC TCCC
                                ||||| |||||||| ||||
                                TAAAA GTACGGTG AGGG
                                  _       A
GAM2424  KIAA1244 3'  TATTTTACAACAGAAGTCACCT 56999         T _______
            C                    TATTTTGCA GC      CACCTC
                                |||||||||  ||     ||||||
                                ATAAAATGT TG      GTGGAG
                                     _  TCTTCA
GAM2424  KIAA1613 3'  CATTTTGCACTCCTATTTCTC  57000         G  AC___
                                TATTTTGCAT CC     CTC
                                ||||||||||  ||     |||
                                GTAAAACGTG GG     GAG
                                     A  ATAAA
GAM2424  KIAA1724 3'  TATTCTGCATCCATTTCTC    57001         G   C__
                                TATTTTGCAT CCA   CTC
                                ||||||||||  |||   |||
                                ATAAGACGTA GGT   GAG
                                     _   AAA
GAM2424  KIAA1795 3'  CATTTTCCACCACCTTCC     57002       G AT      _
                                TATTTT C  GCCACCT CC
                                ||||||  |  |||||||  ||
                                GTAAAA G  TGGTGGA GG
                                   G __       A
GAM2424  MGC10334 3'  TTTTGCACCCCAGCGTCTCCC  57003        G   C___
                                TTTTGCAT CCA    CTCCC
                                ||||||||  |||    |||||
                                AAAACGTG GGT    GAGGG
                                     G   CGCA
GAM2424  PLA2G3   3'  CATTACACATGCCATCTCC    57004      T       C
                                TATT TGCATGCCA CTCC
                                ||||  |||||||||  ||||
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                                GTAA GTGTACGGT GAGG
                                  T       A
GAM2424  PORIMIN   3'  TTTTGCATAACCATTTCCC   57005        _  CC
                                TTTTGCATG CCA  TCCC
                                ||||||||| |||  ||||
                                AAAACGTAT GGT  AGGG
                                     T  AA
GAM2424  SDS3      3'  TATTTTACATTCACCTC     57006        GC
                                TATTTTGCAT  CACCTC
                                ||||||||||  ||||||
                                ATAAAATGTA  GTGGAG
                                     A_
GAM2424  SEF       3'  TATTTCCTCCCTACCTCCC   57007       GCATG  _
                                TATTTT    CC ACCTCCC
                                ||||||    || |||||||
                                ATAAAG    GG TGGAGGG
                                   GAG__  A
GAM2424  WNT16     5'  TTTTGCACCCCCTCCC      57008        G  A
                                TTTTGCAT CC CCTCCC
                                |||||||| || ||||||
                                AAAACGTG GG GGAGGG
                                     _ _
GAM2424  LOC122792 3'  TACTTTGCATAGTACCTC    57009          CC
                                TATTTTGCATG  ACCTC
                                ||||||||||  |||||
                                ATGAAACGTAT  TGGAG
                                     CA
GAM2424  LOC132625 5'  TATTTCCAATGCCACCTCC    57010       GC
                                TATTTT  ATGCCACCTCC
                                ||||||  ||||||||||
                                ATAAAG  TACGGTGGAGG
                                   GT
GAM2424  LOC146177 5'  TATTTTGCCACCCACTC     57011        A   AC
                                TATTTTGC TGCC  CTC
                                |||||||| ||||  |||
                                ATAAAACG GTGG  GAG
                                     _   GT
GAM2424  LOC146895 5'  TTCTTCATCACCTCCC      57012      G  GC
                                TTTT CAT  CACCTCCC
                                |||| |||  ||||||||
                                AAGA GTA  GTGGAGGG
                                  A  __
GAM2424  LOC148354 3'  CATTACTGATGCCACCTCC    57013     _  C
                                TATT TTG ATGCCACCTCC
                                |||| ||| ||||||||||
                                GTAA GAC TACGGTGGAGG
                                  T  _
GAM2424  LOC148697 3'  CATTCTGCCTGCCACCTTCC   57014        A      _
                                TATTTTGC TGCCACCT CC
                                |||||||| |||||||| ||
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                                GTAAGACG ACGGTGGA GG
                                    G       A
GAM2424  LOC150343 5'  TATTCTGAACACCTCCC     57015        CATGC
                                TATTTTG    CACCTCCC
                                |||||||    ||||||||
                                ATAAGAC    GTGGAGGG
                                    TT___
GAM2424  LOC151361 5'  TTTTGCCACCATCTCCC     57016       A    C
                                TTTTGC TGCCA CTCCC
                                |||||| ||||| |||||
                                AAAACG GTGGT GAGGG
                                   _    A
GAM2424  LOC151361 5'  TATTTTGCAACCCATTCCC    57017         T   ACC
                                TATTTTGCA GCC   TCCC
                                ||||||||| |||   ||||
                                ATAAAACGT TGG   AGGG
                                     _  GTA
GAM2424  LOC151445 3'  CATTTTGCTATAATCCACCTCC 57018         ATG___
                                TATTTTGC     CCACCTCC
                                ||||||||     ||||||||
                                GTAAAACG     GGTGGAGG
                                     ATATTA
GAM2424  LOC151475 3'  TATTCTGGGCCACCTC      57019        CAT
                                TATTTTG   GCCACCTC
                                |||||||   ||||||||
                                ATAAGAC   CGGTGGAG
                                    C__
GAM2424  LOC152286 5'  TCTGCCCTGCCACTTCCC    57020      A_     C
                                TTTGC  TGCCAC TCCC
                                |||||  |||||| ||||
                                AGACG  ACGGTG AGGG
                                   GG     A
GAM2424  LOC152445 5'  CATTTCAAATGCCACCTCC    57021        C
                                TATTTTG ATGCCACCTCC
                                ||||||| ||||||||||
                                GTAAAGT TACGGTGGAGG
                                    T
GAM2424  LOC155063 3'  TATCTCCCAAGCTACCTC     57022       G  T  C
                                TATTTT CA GC ACCTC
                                |||||| || || |||||
                                ATAGAG GT CG TGGAG
                                    G  T  A
GAM2424  LOC157292 5'  TATTCTGCTTCAGCCTCC     57023         ATGC  _
                                TATTTTGC    CA CCTCC
                                ||||||||    || |||||
                                ATAAGACG    GT GGAGG
                                     AA__  C
GAM2424  LOC158382 5'  TCTTGCTATGTCACCTCCC    57024        _   C
                                TTTTGC ATG CACCTCCC
                                |||||| ||| ||||||||
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                                AGAACG TAC GTGGAGGG
                                   A   A
GAM2424  LOC166979 5'  TATTTCACCACCTCCC      57025       GCAT
                                TATTTT    GCCACCTCCC
                                ||||||    ||||||||||
                                ATAAAG    TGGTGGAGGG
                                  ____
GAM2424  LOC196214 5'  ATTTTGCATAAGCCCTTCC    57026         __   ACC
                                ATTTTGCAT  GCC   TCC
                                |||||||||  |||   |||
                                TAAAACGTA  CGG   AGG
                                     TT   GA_
GAM2424  LOC202052 3'  TATTTTACAATGTAACCTCCC  57027         _  CC
                                TATTTTGCA TG  ACCTCCC
                                |||||||||  ||  |||||||
                                ATAAAATGT AC  TGGAGGG
                                     T  AT
GAM2424  LOC219842 5'  CTTGGCTCTGCCACCTCC    57028     T  A_
                                TTT GC  TGCCACCTCC
                                |||  ||  ||||||||||
                                GAA CG  ACGGTGGAGG
                                  C  AG
GAM2424  LOC221456 3'  ACTTTGCATGCTGTCTCC    57029          CAC
                                ATTTTGCATGC   CTCC
                                ||||||||||   ||||
                                TGAAACGTACG   GAGG
                                      ACA
GAM2424  LOC222159 3'  TATTTTGCTGTGCAACTCC    57030        A_   CAC
                                TATTTTGC  TGC   CTCC
                                ||||||||  |||   ||||
                                ATAAAACG  ACG   GAGG
                                     AC   TT_
GAM2424  LOC254413 5'  TTTTACTCGCCACCTTCC    57031       A       _
                                TTTTGC TGCCACCT CC
                                |||||| |||||||| ||
                                AAAATG GCGGTGGA GG
                                   A       A
GAM2424  LOC51233  5'  TATTCTGCCGCCACCTCCC    57032        A
                                TATTTTGC TGCCACCTCCC
                                |||||||| ||||||||||
                                ATAAGACG GCGGTGGAGGG
                                   _
GAM2424  LOC57106  3'  TATTCTGCTCGGCCTCC     57033        A  CCA
                                TATTTTGC TG   CCTCC
                                |||||||| ||   |||||
                                ATAAGACG GC   GGAGG
                                     A  C__
GAM2424  LOC90768  5'  TCTTGCACTGCCACCTCC    57034        _
                                TTTTGCA TGCCACCTCC
                                |||||||  ||||||||||
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                                AGAACGT ACGGTGGAGG
                                    G
GAM2424 LOC91813 5' TTTTGCACTCGTGACCTCCC  57035       GCC__
                                TTTTGCAT    ACCTCCC
                                ||||||||    |||||||
                                AAAACGTG    TGGAGGG
                                    AGCAC
GAM2424 LOC92140 3' TATTCTGCTGACCTC      57036       A  CC
                                TATTTTGC TG  ACCTC
                                |||||||| ||  |||||
                                ATAAGACG AC  TGGAG
                                  _  __
GAM2424 LOC92270 5' TATTTTGCTACCTACTCCC   57037       A   AC
                                TATTTTGC TGCC  CTCCC
                                |||||||| ||||  |||||
                                ATAAAACG ATGG  GAGGG
                                    _   AT
GAM2425 CNTNAP2  3' TTGAAATTTTGGTGAGAGG   57040       C  A
                                TTGAGATT TG TGAGAGG
                                |||||||| || |||||||
                                AACTTTAA AC ACTCTCC
                                    A  C
GAM2425 THY1     3' AGATTCCAGAGGCTTG      57041       GATG
                                AGATTCT    AGAGGCTTG
                                |||||||    |||||||||
                                TCTAAGG    TCTCCGAAC
                                  _____
GAM2425 KIAA1755 3' TTGAGTTCAGGGAGGCTTG   57042      A   TGATGA
                                TTGAG TTC     GAGGCTTG
                                ||||| |||     |||||||||
                                AACTC AAG     CTCCGAAC
                                   _  TCC___
GAM2426 KIAA1030 3' ACCCACCTGCCTCCCTGCG   57045       _ TA
                                ACCCACCT T  CCCTGCG
                                |||||||| |  |||||||
                                TGGGTGGA G  GGGACGC
                                    C GA
GAM2426 LOC132740 5' CCTCACCCCCCTGCGA     57046    _    TTA
                                CC CACCT   CCCTGCGA
                                || |||||   |||||||||
                                GG GTGGG   GGGACGCT
                                 A    ___
GAM2426 LOC153688 3' CCCACCTTTATGCTTGGCG   57047         CC __
                                CCCACCTTTA  CT  GCG
                                ||||||||||  ||  |||
                                GGGTGGAAAT  GA  CGC
                                      AC  AC
GAM2426 LOC256530 5' ATAACCCATCTTACCCT     57048        CC
                                ATAACCCA  TTTACCCT
                                ||||||||  ||||||||
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                                TATTGGGT  GAATGGGA
                                    A_
GAM2427  DFFB     3'  AGCTGTTCAACAGACATTG   57051        TTTGA    C
                                AGCTGTTCA    AGACA TG
                                |||||||||    ||||| ||
                                TCGACAAGT    TCTGT AC
                                     TG___    A
GAM2427  LGALS3BP  3'  GAGCTGTTGGTGTCCAGGGCAC 57052        CATTTGA  A_
              TG                  GAGCTGTT      AG  CACTG
                                |||||||      ||  |||||
                                CTCGACAA      TC  GTGAC
                                    CCACAGG  CC
GAM2427  RBM3     3'  GAGCTGATGAAGATGCTG    57053       TTCATT     CA
                                GAGCTG     TGAAGA  CTG
                                ||||||     ||||||  |||
                                CTCGAC     ACTTCT  GAC
                                   T_____     AC
GAM2427  XT3      3'  GCTGCAAGGTGGGGACACTGA  57054      TCATT  AA
                                GCTGT    TG  GACACTGA
                                |||||    ||  ||||||||
                                CGACG    AC  CTGTGACT
                                  TTCC_  CC
GAM2427  C20orf12  3'  GAGCTGTCCATTTAGTACTGA  57055           AAGAC
                                GAGCTGTTCATTTG    ACTGA
                                ||||||||||||||    |||||
                                CTCGACAGGTAAAT    TGACT
                                       CA___
GAM2427  DKFZp434G179 3'  AGCTGTTTGTTTGAAGACA   57056       CA
                                AGCTGTT  TTTGAAGACA
                                |||||||  ||||||||||
                                TCGACAA  AAACTTCTGT
                                    AC
GAM2427  FARP1    3'  GCTGTTCATTCAAACGCTGA   57057         GA   A
                                GCTGTTCATTT  AGAC CTGA
                                ||||||||||  |||| ||||
                                CGACAAGTAAG  TTTG GACT
                                      __   C
GAM2427  FLJ10305  5'  GGCTGCAGTGAAGACACTGA   57058   A    TCATT
                                G GCTGT    TGAAGACACTGA
                                | |||||    ||||||||||||
                                C CGACG    ACTTCTGTGACT
                                 _    TC___
GAM2427  H2AV     3'  GAGCTGTTTGTCTTAACTG   57059       CA   GAAGAC
                                GAGCTGTT  TTT     ACTG
                                ||||||||  |||     ||||
                                CTCGACAA  AGA     TGAC
                                    AC   AT____
GAM2427  KIAA1579  3'  GGACTGTCAAAGGAGACACTGA 57060    AG    T  TTT  A
                                G  CTGT CA   GA GACACTGA
                                |  |||| ||   || ||||||||
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                                C  GACA GT   CT CTGTGACT
                                 CT    _ TTC  _
GAM2427  MCF2L    3'  GAGCTGCTCAGGCACT      57061          TTTGAA A
                                GAGCTGTTCA     G CACT
                                ||||||||||     | ||||
                                CTCGACGAGT     C GTGA
                                       _______ C
GAM2427  PDE2A    3'  GAGCTATTTTAGACATTG    57062        CATTTGA    C
                                GAGCTGTT      AGACA TG
                                ||||||||      ||||| ||
                                CTCGATAA      TCTGT AC
                                     AA_____     A
GAM2427  PNMA5    5'  GCCTGACACCTGGGGACACTGA 57063     GTT     AA
                                GCT   CATTTG  GACACTGA
                                |||   ||||||  ||||||||
                                CGG   GTGGAC  CTGTGACT
                                  ACT     CC
GAM2427  SMCR7    3'  GAGCAGTTCATTTTGGCACACT 57064      T       GAAG
              G                  GAGC GTTCATTT    ACACTG
                                ||||| ||||||||    ||||||
                                CTCG CAAGTAAA    TGTGAC
                                   T       ACCG
GAM2427  LOC143451 3'  GAGCAGTTGCTATGGAGACACT 57065      T   CATT  A
              G                  GAGC GTT    TG AGACACTG
                                ||||| |||    || ||||||||
                                CTCG CAA    AC TCTGTGAC
                                   T   CGAT  C
GAM2427  LOC145125 3'  GAGCAGTTGCTATGGAGACACT 57065      T   CATT  A
              G                  GAGC GTT    TG AGACACTG
                                ||||| |||    || ||||||||
                                CTCG CAA    AC TCTGTGAC
                                   T   CGAT  C
GAM2427  LOC146506 3'  GAGCTGCTCCAAGACGCTG    57066         ATTTG    A
                                GAGCTGTTC     AAGAC CTG
                                |||||||||     ||||| |||
                                CTCGACGAG     TTCTG GAC
                                     G_____     C
GAM2427  LOC160942 5'  GGCTGCATCCTGGGGACACTGA 57067    A    TCA    AA
                                G GCTGT   TTTG  GACACTGA
                                | |||||   ||||  ||||||||
                                C CGACG   GGAC  CTGTGACT
                                _     TA_    CC
GAM2427  LOC221405 5'  GAGCTGTCTGCGGAGGGCACTG 57068         CATT  A  A_
                                GAGCTGTT    TG AG  CACTG
                                ||||||||    || ||  |||||
                                CTCGACAG    GC TC  GTGAC
                                     AC__  C  CC
GAM2427  LOC221486 3'  GATTGTTCAGACACTG      57069    GC     TTTGAA
                                GA  TGTTCA     GACACTG
                                ||  ||||||     |||||||
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                                CT  ACAAGT     CTGTGAC
                                 A_    _______
GAM2427  LOC221832 3'  GAGCTGTCGAAGGGCGCTG   57070        CATTT   ACA_
                                GAGCTGTT    GAAG   CTG
                                ||||||||    ||||   |||
                                CTCGACAG    CTTC   GAC
                                     _____   CCGC
GAM2427  LOC254440 3'  GAGCAGTTGCTATGGAGACACT 57065     T  CATT  A
           G                     GAGC GTT    TG AGACACTG
                                |||| |||    || ||||||||
                                CTCG CAA    AC TCTGTGAC
                                  T  CGAT  C
GAM2427  LOC89919  3'  GAGCTCTTCATTTGAATACAAC 57071      G       G  _
           TG                    GAGCT TTCATTTGAA ACA CTG
                                ||||| |||||||||| ||| |||
                                CTCGA AAGTAAACTT TGT GAC
                                   G        A  T
GAM2427  LOC90538  3'  AGCTGTTTGGGCAGACACTGA  57072       CATTTGA
                                AGCTGTT      AGACACTGA
                                |||||||      |||||||||
                                TCGACAA      TCTGTGACT
                                   ACCCG__
GAM2427  LOC91689  3'  GAGCTGTCATGACTGGCACTGA 57073       T  TT   AGA_
                                GAGCTGT CA  TGA   CACTGA
                                ||||||| ||  |||   ||||||
                                CTCGACA GT  ACT   GTGACT
                                   _ __   GACC
GAM2427  LOC91759  5'  GAGCTGTTCATTAGCATTG   57074          TGA  A  C
                                GAGCTGTTCATT   AG CA TG
                                ||||||||||||   || || ||
                                CTCGACAAGTAA   TC GT AC
                                      ___  _  A
GAM2428  WSB1      5'  ATGGGGCACCGTCTGATTCCG  57077    AT    CGC     C
                                ATG  GTACC   GTCTGAT CCG
                                |||  |||||   ||||||| |||
                                TAC  CGTGG   CAGACTA GGC
                                  CC    ___      A
GAM2428  WSB1      5'  ATGGGGCACCGTCTGATTCCG  57077    AT    CGC     C
                                ATG  GTACC   GTCTGAT CCG
                                |||  |||||   ||||||| |||
                                TAC  CGTGG   CAGACTA GGC
                                  CC    ___      A
GAM2428  LOC120448 5'  ATGATGTATCCTTGCTCTG   57078        _  C_  G
                                ATGATGTA CC  GC TCTG
                                |||||||| ||  || ||||
                                TACTACAT GG  CG AGAC
                                    A  AA  _
GAM2428  LOC152991 5'  ATGGTGTACGCTAACATGATCC 57079     A    CC  GTC__
           CG                    ATG TGTAC  GC    TGATCCCG
                                ||| |||||  ||    ||||||||
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                                TAC ACATG  CG    ACTAGGGC
                                  C    __  ATTGT
GAM2428  LOC155438 3'  ATGTTGTCCAGTCTGATC    57080     A   AC   C
                                ATG TGT  CCG GTCTGATC
                                ||| |||  ||| ||||||||
                                TAC ACA  GGT CAGACTAG
                                  A  __  _
GAM2428  LOC253792 5'  TGATGTACCCTGAGGTCCG   57081         GC__
                                TGATGTACCC   GTCTG
                                ||||||||||   |||||
                                ACTACATGGG   CAGGC
                                      ACTC
GAM2429  PPP2CA    3'  CCTTGATTTTTATTTTACCTAC 57084   G      A   AC
              A                  C TTGATTTT TGT  TACCTACA
                                | |||||||| |||  ||||||||
                                G AACTAAAA ATA  ATGGATGT
                                 G       _  AA
GAM2429  FLJ20413  3'  GTTGATTTGTGTAAGCGTCCTA 57085       TA   CTA__
                                GTTGATTT  TGTA    CCTA
                                ||||||||  ||||    ||||
                                CAACTAAA  ACAT    GGAT
                                     C_   TCGCA
GAM2429  KIAA1042  3'  GTTGATTTTTGATGCATTAC   57086        __    C
                                GTTGATTTT  ATGTA TAC
                                |||||||||  ||||| |||
                                CAACTAAAA  TACGT ATG
                                      AC    A
GAM2429  PTBP2     3'  GTTAATTTTAACTAATGCCTAC 57087        TGT   ___
              A                  GTTGATTTTA   ACTA   CCTACA
                                ||||||||||   ||||   ||||||
                                CAATTAAAAT   TGAT   GGATGT
                                     ___    TAC
GAM2430  MCL1      3'  TGGTTGGTTAAAAGTCAAC    57090         CG_
                                TGGTTGGTTGAG   CAAC
                                ||||||||||||   ||||
                                ACCAACCAATTT   GTTG
                                       TCA
GAM2430  PLS1      3'  TGGTTGGCTGAATGACCAA    57091         CGCA
                                TGGTTGGTTGAG    ACCAA
                                ||||||||||||    |||||
                                ACCAACCGACTT    TGGTT
                                       AC__
GAM2430  SRM       3'  TGGTTGGTGGGCGAGAGCCA   57092       T A   CAA_
                                TGGTTGGT G GCG    CCA
                                |||||||| | |||    |||
                                ACCAACCA C CGC    GGT
                                     _ C   TCTC
GAM2430  TRPM1     5'  TGGTTGGTGAACTGGCCA     57093       T    GCAA
                                TGGTTGGT GAGC    CCA
                                |||||||| ||||    |||
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                                ACCAACCA CTTG    GGT
                                     _   ACC_
GAM2430  AGXT2    3'  TGGTTGGTAGGCAGTCAACCA  57094       TG  C   AC
                                TGGTTGGT  AG GCA  CAACCA
                                ||||||||  || |||  ||||||
                                ACCAACCA  TC CGT  GTTGGT
                                     __  _   CA
GAM2430  DKFZp547I014 5'  TGTTTGGTTGAGACTGACCA   57095    G       _ GCA
                                TG TTGGTTGAG C   ACCA
                                || |||||||| |   ||||
                                AC AACCAACTC G   TGGT
                                 A        T AC_
GAM2430  KIAA0316  3'  TGGTGGTTGAGTGTCGCGCC   57096     T      ___   AA
                                TGGT GGTTGAG   CGC  CC
                                |||| |||||||   |||  ||
                                ACCA CCAACTC   GCG  GG
                                  _      ACA   C_
GAM2430  MGC27382  3'  TGGTTGGTTGCGGAGGCA    57097         ___   C
                                TGGTTGGTT   GAG GCA
                                |||||||||   ||| |||
                                ACCAACCAA   CTC CGT
                                     CGC   _
GAM2430  LOC136288 5'  TGGCTGGCTGCAGCCAACCA   57098          _   G
                                TGGTTGGTTG AGC CAACCA
                                |||||||||| ||| ||||||
                                ACCGACCGAC TCG GTTGGT
                                      G   _
GAM2430  LOC197193 5'  TGGTTGGCTTTCAGTTGACCA  57099         GAG  CA__
                                TGGTTGGTT   CG    ACCA
                                |||||||||   ||    ||||
                                ACCAACCGA   GT    TGGT
                                     AA_  CAAC
GAM2430  LOC199720 3'  TGGTTGGTGGATGTGCTCAGCC 57100         T  ___  G  A
            A                    TGGTTGGT GA   GC CA CCA
                                |||||||| ||   || || |||
                                ACCAACCA CT   CG GT GGT
                                     C  ACA  A  C
GAM2430  LOC58525  3'  TGGTCGGCTTGGCGGCCAAC   57101         GA   CAA
                                TGGTTGGTT  GCG   CCAAC
                                |||||||||  |||   |||||
                                ACCAGCCGA  CGC   GGTTG
                                     AC   C__
GAM2430  LOC92299  5'  TGGTTGGTGGGAGCAGCCA   57102         T_    CAA
                                TGGTTGGT  GAGCG   CCA
                                ||||||||  |||||   |||
                                ACCAACCA  CTCGT   GGT
                                     CC    C__
GAM2431  CLK2     3'  CACTGCCAAAGTCTACC     57105          ATA  ACT
                                CACTGCCAAA   TC   TACC
                                ||||||||||   ||   ||||
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                                GTGACGGTTT  AG  ATGG
                                      C__ ___
GAM2431  GAP43    3'  TCATTACCAAAAACTTGCC   57106    C      TATC   A
                                TCA TGCCAAAA   ACTT CC
                                ||| ||||||||   |||| ||
                                AGT ATGGTTTT   TGAA GG
                                  A      ____   C
GAM2431  PCDH9    5'  TGTCATTTACATCACTTAC   57107    C  AA_
                                TG CA  ATATCACTTAC
                                || ||  ||||||||||
                                AC GT  TGTAGTGAATG
                                 A  AAA
GAM2431  RNGTT    3'  CCACTGCCAGAATGGACACACT 57108         A  AT___
                                TCACTGCCA AAT    CACT
                                ||||||||| |||    ||||
                                GGTGACGGT TTA    GTGA
                                      C  CCTGT
GAM2431  SLC9A5   3'  TCACTGCCAGGACACCACT   57109         AA
                                TCACTGCCA  ATATCACT
                                |||||||||  ||||||||
                                AGTGACGGT  TGTGGTGA
                                      CC
GAM2431  TDGF1    5'  TCATTGCCAAAACAGCCA    57110    C       _
                                TCA TGCCAAAATA TCA
                                ||| |||||||||| |||
                                AGT ACGGTTTTGT GGT
                                  A        C
GAM2431  BTN3A3   3'  CTGCACAATCACTTATCA    57111     _ AAAT      C
                                CTGC CA   ATCACTTA CA
                                |||| ||   |||||||| ||
                                GACG GT   TAGTGAAT GT
                                  T ____       A
GAM2431  C11orf21 3'  TCACTGCCGGTGCCAGTTGCCA 57112         AAAATA  C  A
                                TCACTGCC     TCA TT CCA
                                ||||||||     ||| || |||
                                AGTGACGG     GGT AA GGT
                                     CCAC__  C  C
GAM2431  DKFZP434O047 5'  TCACTGCCAGGAATACTCACT  57113         A_   _
                                TCACTGCCA  AATA TCACT
                                |||||||||  |||| |||||
                                AGTGACGGT  TTAT AGTGA
                                      CC   G
GAM2431  FLJ11193 3'  TGCCAAAAAATTTACCA    57114         T  CAC
                                TGCCAAAA AT   TTACCA
                                |||||||| ||   ||||||
                                ACGGTTTT TA   AATGGT
                                     T ___
GAM2431  FLJ12085 3'  ACTGCCAATCCACTTA     57115         AATA
                                ACTGCCAA   TCACTTA
                                ||||||||   |||||||
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                                TGACGGTT   GGTGAAT
                                    A___
GAM2431  KIAA0660  3'  CCACTGCCAAGACTTTGCC   57116        AATATC   A_
                                TCACTGCCAA     ACTT  CC
                                ||||||||||     ||||  ||
                                GGTGACGGTT     TGAA  GG
                                     C_____    AC
GAM2431  KIAA0752  5'  ACTGCCAACGTTCAGTTGCCA  57117       AATA   C  A
                                ACTGCCAA    TCA TT CCA
                                ||||||||    ||| || |||
                                TGACGGTT    AGT AA GGT
                                    GCA_   C  C
GAM2431  POLR3F    3'  TCCTGACCTATCACTTACC   57118    A  _  AAAA
                                TC CTG CC    TATCACTTACC
                                || ||| ||    ||||||||||
                                AG GAC GG    ATAGTGAATGG
                                 _   T  _____
GAM2431  LOC124245 3'  TCACAGCCAAAATAAGAC    57119     T       TC
                                TCAC GCCAAAATA  AC
                                |||| |||||||||  ||
                                AGTG CGGTTTTAT  TG
                                   T        TC
GAM2431  LOC149319 5'  TCACTGCCACGGGGCCAGGACT 57120        AAA___  TC
            TAC                   TCACTGCCA     TA  ACTTAC
                                |||||||||     ||  ||||||
                                AGTGACGGT     GT  TGAATG
                                     GCCCCG  CC
GAM2431  LOC155063 5'  TCACTGCCGGGATCACAGCCA  57121       AAAAT    TTA
                                TCACTGCC    ATCAC   CCA
                                ||||||||    |||||   |||
                                AGTGACGG    TAGTG   GGT
                                    CCC__    TC_
GAM2431  LOC157858 3'  CCACTGCCAAGATCCT      57122         AAT   A
                                TCACTGCCAA   ATC CT
                                ||||||||||   ||| ||
                                GGTGACGGTT   TAG GA
                                     C__   _
GAM2431  LOC158295 3'  ACTGCCAAGATATATCCTCA   57123       A__    A
                                ACTGCCAA   ATATC CTTA
                                ||||||||   ||||| ||||
                                TGACGGTT   TATAG GAGT
                                    CTA    _
GAM2431  LOC199982 3'  TCACTGACAAAATATTGAAACC 57124      C       CACTT
            A                    TCACTG CAAAATAT    ACCA
                                ||||||  ||||||||    ||||
                                AGTGAC GTTTTATA    TGGT
                                   T       ACTT_
GAM2431  LOC254756 3'  CACTGCCAGAGCCTGTCTGTTT 57125       AAATA__  AC_
            ACC                   CACTGCCA     TC   TTACC
                                ||||||||     ||   |||||
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                                GTGACGGT     AG  AATGG
                                    CTCGGAC  ACA
GAM2432 BBS4    3' AGCTGCAATACTCAGCAGGC  57128         _ _ CGAT
                                AGCTGCAATAC C GC   GGC
                                |||||||||||  | ||   |||
                                TCGACGTTATG G CG   CCG
                                     A T  T___
GAM2432 BNC     5' GCTGCGCAGCACGATGGCC   57129      AATACC _
                                GCTGC    GC CGATGGCC
                                |||||    || ||||||||
                                CGACG    CG GCTACCGG
                                   CGT___  T
GAM2432 CACNA1G  3' GCTGCAATGTGCTCGCGG   57130       ACC _ A
                                GCTGCAAT  GC CG TGG
                                ||||||||  || || |||
                                CGACGTTA  CG GC GCC
                                    CA_  A  _
GAM2432 CLCN6    3' AAGCTGCGACTGCGGCAATGGC 57131       A  AC  C
            C                    AAGCTGC AT  CG CGATGGCC
                                |||||||  ||  || ||||||||
                                TTCGACG TG  GC GTTACCGG
                                    C  AC  C
GAM2432 CLCN6    3' AAGCTGCGACTGCGGCAATGGC 57131       A  AC  C
            C                    AAGCTGC AT  CG CGATGGCC
                                |||||||  ||  || ||||||||
                                TTCGACG TG  GC GTTACCGG
                                    C  AC  C
GAM2432 CLCN6    3' AAGCTGCGACTGCGGCAATGGC 57131       A  AC  C
            C                    AAGCTGC AT  CG CGATGGCC
                                |||||||  ||  || ||||||||
                                TTCGACG TG  GC GTTACCGG
                                    C  AC  C
GAM2432 EPB49    3' AAGCTGCAGTGCAGGAAAGC  57132       ATACC  C_  T
                                AAGCTGCA    GC  GA GGC
                                ||||||||    ||  || |||
                                TTCGACGT    CG  CT TCG
                                    CA___  TC  T
GAM2432 RGS3     3' AGCTGCAAGCTCCAATGGCC  57133       TACCG
                                AGCTGCAA    CCGATGGCC
                                ||||||||    |||||||||
                                TCGACGTT    GGTTACCGG
                                    CGA__
GAM2432 RGS3     3' AGCTGCAAGCTCCAATGGCC  57133       TACCG
                                AGCTGCAA    CCGATGGCC
                                ||||||||    |||||||||
                                TCGACGTT    GGTTACCGG
                                    CGA__
GAM2432 RGS3     3' AGCTGCAAGCTCCAATGGCC  57133       TACCG
                                AGCTGCAA    CCGATGGCC
                                ||||||||    |||||||||
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                                TCGACGTT    GGTTACCGG
                                    CGA__
GAM2432  RGS3     3'  AGCTGCAAGCTCCAATGGCC  57133       TACCG
                                AGCTGCAA    CCGATGGCC
                                ||||||||    |||||||||
                                TCGACGTT    GGTTACCGG
                                    CGA__
GAM2432  RGS3     3'  AGCTGCAAGCTCCAATGGCC  57133       TACCG
                                AGCTGCAA    CCGATGGCC
                                ||||||||    |||||||||
                                TCGACGTT    GGTTACCGG
                                    CGA__
GAM2432  RGS3     3'  AGCTGCAAGCTCCAATGGCC  57133       TACCG
                                AGCTGCAA    CCGATGGCC
                                ||||||||    |||||||||
                                TCGACGTT    GGTTACCGG
                                    CGA__
GAM2432  RNF26    3'  AAGCTGCAAGCCCCTGGGCC  57134        TA  G  GAT
                                AAGCTGCAA  CC CC   GGCC
                                |||||||||  || ||   ||||
                                TTCGACGTT  GG GG   CCGG
                                    C_  _  AC_
GAM2432  SIP      3'  AAGCTGCAGTACAGTGGC    57135        A  CGCCGA
                                AAGCTGCA TAC     TGGC
                                |||||||| |||     ||||
                                TTCGACGT ATG     ACCG
                                    C   TC____
GAM2432  SPARC    3'  AAGCTGCAATGTGTGTTGGCCA 57136        ACC_________  GAT
            TCGG                    GCTGCAAT        GCC   GG
                                ||||||||         |||   ||
                                CGACGTTA         CGG   CC
                                    CACACAAIIIC   TAG
GAM2432  THBS1    3'  AAGGTGCAATACCAGCATTGG  57137     C        C  A
                                AAG TGCAATACCG CG TGG
                                ||| |||||||||| || |||
                                TTC ACGTTATGGT GT ACC
                                  C         C  A
GAM2432  CALN1    3'  AGCTGCAACACAGTGTGGC   57138         CGCCGA
                                AGCTGCAATAC     TGGC
                                ||||||||||      ||||
                                TCGACGTTGTG     ACCG
                                     TCAC__
GAM2432  CASKIN1  3'  AGCTGCAAGCCCGTGGC     57139        TACC   GA
                                AGCTGCAA    GCC  TGGC
                                ||||||||    |||  ||||
                                TCGACGTT    CGG  ACCG
                                    _____   GC
GAM2432  CHST8    3'  AAGCTGCAAACCACGTGG    57140        T    C A
                                AAGCTGCAA ACCGC G TGG
                                ||||||||| ||||| | |||
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                                TTCGACGTT TGGTG C ACC
                                      _    _ _
GAM2432 CLSTN2   3' AAGCTGCAATGATTGCAAATAT 57141         ACC_ C   _
           GC                  AAGCTGCAAT   GC GATG GC
                               ||||||||||   || |||| ||
                               TTCGACGTTA   CG TTAT CG
                                    CTAA  T   A
GAM2432 DKFZp547D155 3' GCTGCAATACTTCTGGCCATCG 57142         C_______  GAT
           G                   GCTGCAATAC      GCC   GG
                               ||||||||||      |||   ||
                               CGACGTTATG      CGG   CC
                                    AAGAIIIC   TAG
GAM2432 FLJ10201 3' GCTGTGATACCTGCAATAACC  57143     CA    GC
                               GCTG  ATACC  CGATGGCC
                               ||||  |||||  ||||||||
                               CGAC  TATGG  GTTATTGG
                                 AC    AC
GAM2432 FLJ10769 3' AAGCTGCAATATTCCAGAT    57144         CCG  _
                               AAGCTGCAATA   CC GAT
                               ||||||||||   || |||
                               TTCGACGTTAT   GG CTA
                                    AA_  T
GAM2432 FLJ14249 3' AGCTGCAATGACGAACATTGGC 57145         AC  C_  A
                               AGCTGCAAT  CG  CG TGGC
                               |||||||||  ||  || ||||
                               TCGACGTTA  GC  GT ACCG
                                    CT  TT  A
GAM2432 FLJ14249 3' AGCTGCAATGACGAACATTGGC 57145         AC  C_  A
                               AGCTGCAAT  CG  CG TGGC
                               |||||||||  ||  || ||||
                               TCGACGTTA  GC  GT ACCG
                                    CT  TT  A
GAM2432 FLJ22329 3' AGCCTGGGCCGCCGATGGC    57146     GCAATA
                               AGCT     CCGCCGATGGC
                               ||||     ||||||||||
                               TCGG     GGCGGCTACCG
                                 ACCC__
GAM2432 FLJ23153 3' AAGCTGCAATACTTCTGGCCAT 57147          C_______  GAT
           CGG                 AGCTGCAATAC      GCC   GG
                               ||||||||||       |||   ||
                               TCGACGTTATG      CGG   CC
                                    AAGAIIIC   TAG
GAM2432 FOXH1    5' GCTGCGATGACCCATGGC     57148      A  ACC   G
                               GCTGC AT   GCC ATGGC
                               ||||| ||   ||| |||||
                               CGACG TA   TGG TACCG
                                 C  C__   G
GAM2432 GC20     3' AAGCTGCAACGTACATGG     57149          ACC  CG
                               AAGCTGCAAT   GC  ATGG
                               ||||||||||   ||  ||||
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                                TTCGACGTTG   TG  TACC
                                     CA_  __
GAM2432  KIAA0607  3'  AACTGCGATATCAATGGCC    57150       A   CCGC
                                AGCTGC ATA    CGATGGCC
                                |||||| |||    ||||||||
                                TTGACG TAT    GTTACCGG
                                   C   A___
GAM2432  KIAA1045  3'  AAGCTGTGAAACCTGCAATGGC 57151       CAAT   GC
              C                  AAGCTG    ACC  CGATGGCC
                                |||||||   |||  ||||||||
                                TTCGAC    TGG  GTTACCGG
                                   ACTT   AC
GAM2432  KIAA1095  3'  GCTGCAATATTTGCAAACATGC 57152         CC_  C    _
                                GCTGCAATA   GC GATG GC
                                |||||||||   || |||| ||
                                CGACGTTAT   CG TTGT CG
                                     AAA  T    A
GAM2432  KIAA1372  5'  GCTGCAATGCCAGAACAAGGC  57153        A   C__   T
                                GCTGCAAT CCG   CGA GGC
                                |||||||| |||   ||| |||
                                CGACGTTA GGT   GTT CCG
                                     C   CTT   _
GAM2432  KIAA1701  3'  AAGCTGCAATTCTGGGTCGGCC 57154       ACC__________  GAT
              ATCGGC                TGCAAT          GCC   GGC
                                ||||||          |||   |||
                                ACGTTA          CGG   CCG
                                   AGACCCAGIIIC   TAG
GAM2432  MGC2452   3'  AAGCTGCAGCACAACTGGGTGG 57155         A   C  CGA_
                                AAGCTGCA TAC GC    TGG
                                |||||||| ||| ||    |||
                                TTCGACGT GTG TG    ACC
                                     C   T  ACCC
GAM2432  MGC3020   3'  AAGCTGCAAGTGCTGCCAATGA 57156         TACC_      _
              GCC                   AAGCTGCAA     GCCGATG GCC
                                |||||||||     ||||||| |||
                                TTCGACGTT     CGGTTAC CGG
                                     CACGA      T
GAM2432  MRPS33    5'  AAGCTACAGTGCCGAAGGCC   57157        ATACC    T
                                AAGCTGCA     GCCGA GGCC
                                ||||||||     ||||| ||||
                                TTCGATGT     CGGCT CCGG
                                     CA___     T
GAM2432  NICE-3    3'  AAGCTGCAACACATCTGG     57158           CGCCGA
                                AAGCTGCAATAC      TGG
                                ||||||||||||      |||
                                TTCGACGTTGTG      ACC
                                       TAG___
GAM2432  PRDM7     3'  GCTGCATGCACCGATGG      57159       ATAC
                                GCTGCA    CGCCGATGG
                                ||||||    |||||||||
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                                CGACGT   GTGGCTACC
                                   AC__
GAM2432 SERPING1 3' AAGCTGCAAAAAGTGGTTGGCC 57160     TACC_________ GAT
           ATCGGC                TGCAA         GCC  GGC
                                |||||         |||  |||
                                ACGTT         CGG  CCG
                                   TTTCACCAAIIIC  TAG
GAM2432 SUPT4H1  3' GCTGCAATCCCAGAGGC    57161       A  CC  T
                                GCTGCAAT CCG  GA GGC
                                |||||||| |||  || |||
                                CGACGTTA GGT  CT CCG
                                     G  __ _
GAM2432 TOMM70A  3' AAGCTGCAAGACTGCAAAC   57162       T  C  C
                                AAGCTGCAA AC GC GAT
                                ||||||||| || || |||
                                TTCGACGTT TG CG TTG
                                     C  A  T
GAM2432 UBCE7IP5 3' AAGCTGCAGTGACTGCACACAG 57163       AT_  C  CG
           C                     AAGCTGCA   AC GC  ATGGC
                                |||||||   || ||  |||||
                                TTCGACGT   TG CG  TGTCG
                                     CAC  A  TG
GAM2432 ZNF238   3' AAGCTGCAATATCCTTGGCCAT 57164        _ _______  GAT
           CGG                   AGCTGCAATA CC     GCC  GG
                                ||||||||||| ||     |||  ||
                                TCGACGTTAT GG     CGG  CC
                                     A  AAIIIC  TAG
GAM2432 LOC145622 5' AGCTTCAGCGCACCGATGGC  57165     G  ATAC
                                AGCT CA   CGCCGATGGC
                                |||| ||   ||||||||||
                                TCGA GT   GTGGCTACCG
                                  A  CGC_
GAM2432 LOC157567 3' AAGCTGCAATATAGTTTGGCCA 57166       CC_________  GAT
           TCGG                  GCTGCAATA       GCC  GG
                                |||||||||       |||  ||
                                CGACGTTAT       CGG  CC
                                     ATCAAAIIIC  TAG
GAM2432 LOC158722 5' AGCTGCACTACCACCAGGC   57167       A      AT
                                AGCTGCA TACCGCCG  GGC
                                ||||||| ||||||||  |||
                                TCGACGT ATGGTGGT  CCG
                                     G      __
GAM2432 LOC221463 5' AGCTGCAATGGCCACAGTGATG 57168       A_   C__
           GCC                   AGCTGCAAT  CCGC  GATGGCC
                                |||||||||  ||||  |||||||
                                TCGACGTTA  GGTG  CTACCGG
                                     CC   TCA
GAM2432 LOC254707 5' AGCTGCAAACTGCAGAGCC   57169       T  C  C  TG
                                AGCTGCAA AC GC GA  GCC
                                |||||||| || || ||  |||
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                                TCGACGTT TG CG CT  CGG
                                    _ A  T  __
GAM2432  LOC255189 5'  AAGCTGCAATTCTGCAAGAGC  57170         ACC  C  T
                                AAGCTGCAAT   GC GA GGC
                                ||||||||||   || || |||
                                TTCGACGTTA   CG TT TCG
                                     AGA  _  C
GAM2432  LOC51128  5'  AACTGCAAAGCGCGATGGC   57171        TAC   C
                                AGCTGCAA   CGC GATGGC
                                ||||||||   ||| ||||||
                                TTGACGTT   GCG CTACCG
                                    TC_  _
GAM2433  HFE     5'  GCCCAGTAAAACTTCCTGGTG  57174    _  C   TTTAAG
                                GCC AG AAA     TCCTGGTG
                                ||| || |||     ||||||||
                                CGG TC TTT     AGGACCAC
                                  G  A   TGA___
GAM2433  HFE     5'  GCCCAGTAAAACTTCCTGGTG  57174    _  C   TTTAAG
                                GCC AG AAA     TCCTGGTG
                                ||| || |||     ||||||||
                                CGG TC TTT     AGGACCAC
                                  G  A   TGA___
GAM2433  HFE     5'  GCCCAGTAAAACTTCCTGGTG  57174    _  C   TTTAAG
                                GCC AG AAA     TCCTGGTG
                                ||| || |||     ||||||||
                                CGG TC TTT     AGGACCAC
                                  G  A   TGA___
GAM2433  HFE     5'  GCCCAGTAAAACTTCCTGGTG  57174    _  C   TTTAAG
                                GCC AG AAA     TCCTGGTG
                                ||| || |||     ||||||||
                                CGG TC TTT     AGGACCAC
                                  G  A   TGA___
GAM2433  HFE     5'  GCCCAGTAAAACTTCCTGGTG  57174    _  C   TTTAAG
                                GCC AG AAA     TCCTGGTG
                                ||| || |||     ||||||||
                                CGG TC TTT     AGGACCAC
                                  G  A   TGA___
GAM2433  HFE     5'  GCCCAGTAAAACTTCCTGGTG  57174    _  C   TTTAAG
                                GCC AG AAA     TCCTGGTG
                                ||| || |||     ||||||||
                                CGG TC TTT     AGGACCAC
                                  G  A   TGA___
GAM2433  HFE     5'  GCCCAGTAAAACTTCCTGGTG  57174    _  C   TTTAAG
                                GCC AG AAA     TCCTGGTG
                                ||| || |||     ||||||||
                                CGG TC TTT     AGGACCAC
                                  G  A   TGA___
GAM2433  PCK1     5'  CGCCAGCAAGTTTGTGTTCCCA 57175        A   AAG_  TG
            GTG                  CGCCAGCAA TTT   TCC  GTG
                                ||||||||| |||   |||  |||
                                GCGGTCGTT AAA   AGG  CAC
                                     C   CACA   GT
GAM2433  C11orf21  5'  CAGCAAATGCCCTGGTG     57176        TTAA
                                CAGCAAAT   GTCCTGGTG
                                ||||||||   |||||||||
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                                GTCGTTTA   CGGGACCAC
                                    ____
GAM2433  FLJ12587  3'  CGCCAGGGTCAGTCCTGGT   57177      CAAATTTA
                                CGCCAG      AGTCCTGGT
                                ||||||      |||||||||
                                GCGGTC      TCAGGACCA
                                   CCAG____
GAM2433  FLJ23185  5'  ACAATCATCAAGTCCTGGTG  57178    AT_
                                GCAA  TTAAGTCCTGGTG
                                ||||  ||||||||||||
                                TGTT  AGTTCAGGACCAC
                                  AGT
GAM2433  HS6ST     3'  GCAGGTCTGGGGGTCCTGGTG 57179    AA  AA__
                                GCA  TTT   GTCCTGGTG
                                |||  |||   |||||||||
                                CGT  AGA   CAGGACCAC
                                  CC   CCCC
GAM2433  KIAA1939  3'  GCCGCAGATTTAAGTTAAGTG 57180    A  A      CCT
                                GCC GCA ATTTAAGT   GGTG
                                ||| ||| ||||||||   ||||
                                CGG CGT TAAATTCA   TCAC
                                  _  C       AT_
GAM2433  PHF5A     3'  CACTAGCAGGCACTCCTGGTG 57181    C   AATT  AG
                                CGC AGCA   TA  TCCTGGTG
                                ||| ||||   ||  ||||||||
                                GTG TCGT   GT  AGGACCAC
                                  A   CC__  G_
GAM2433  ZFP100    3'  CCTAGCAAATTGCCTGGT    57182    _      TAA T
                                CC AGCAAATT   G CCTGGT
                                || ||||||||   | ||||||
                                GG TCGTTTAA   C GGACCA
                                 A      ___ _
GAM2433  LOC115051 3'  GCAGGTCTGGGGGTCCTGGTG 57179    AA  AA__
                                GCA  TTT   GTCCTGGTG
                                |||  |||   |||||||||
                                CGT  AGA   CAGGACCAC
                                  CC   CCCC
GAM2433  LOC158714 3'  GCTACAAATTTAGGTCC    57183    CA       A
                                GC  GCAAATTTA GTCC
                                ||  ||||||||| ||||
                                CG  TGTTTAAAT CAGG
                                 A_       C
GAM2433  LOC163682 5'  GCCAGTGGTCCTCCTTCCTGGT 57184      CAAA_   AAG
           G                     GCCAG    TTT   TCCTGGTG
                                |||||    |||  ||||||||
                                CGGTC    GAG   AGGACCAC
                                   ACCAG   GA_
GAM2433  LOC204084 5'  GCCAACGGGTCCTGGTG    57185       AAATTTAA
                                GCCAGC      GTCCTGGTG
                                ||||||      |||||||||
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                                CGGTTG       CAGGACCAC
                                   CC_______
GAM2433  LOC221979 3'  GCTACAAATTTAGGTCC     57183    CA        A
                                GC  GCAAATTTA GTCC
                                ||  ||||||||| ||||
                                CG  TGTTTAAAT CAGG
                                 A_        C
GAM2433  LOC253150 3'  GCCCAGCAGCAGTCCTGGTG   57186     _    AATTTA
                                GCC AGCA     AGTCCTGGTG
                                ||| ||||     ||||||||||
                                CGG TCGT     TCAGGACCAC
                                  G    CG____
GAM2433  LOC51696  3'  AGCAAATTAGTTCTGGTG    57187         TA   C
                                AGCAAATT  AGT CTGGTG
                                ||||||||  ||| ||||||
                                TCGTTTAA  TCA GACCAC
                                     __   A
GAM2433  LOC90139  3'  GCATCAGGTCCTGGTG      57188     AAT   A
                                GCA   TTA GTCCTGGTG
                                |||   ||| |||||||||
                                CGT   AGT CAGGACCAC
                                  ___   C
GAM2434  C1QR1     3'  TATATGGAGAATTCGGAT     57191         T_
                                TATATGGA  ATTCGGAT
                                ||||||||  ||||||||
                                ATATACCT  TAAGCCTA
                                     CT
GAM2434  FLJ10980  3'  TACATGGAATATATGGAT     57192         _   TC
                                TATATGGA TAT  GGAT
                                |||||||| |||  ||||
                                ATGTACCT ATA  CCTA
                                     T   TA
GAM2435  CFTR      3'  TATCTACTTACACACCC      57195      A   CGCA
                                TATC TACT    TGCACACCC
                                |||| ||||    |||||||||
                                ATAG ATGA    ATGTGTGGG
                                  _   _____
GAM2435  PCDHB12   3'  CATTACACATGCACATTTCC   57196     ACT        CC_
                                CAT   CGCATGCACA   CC
                                |||   ||||||||||   ||
                                GTA   GTGTACGTGT   GG
                                  AT_         AAA
GAM2435  SAR1      3'  ATCATACTTCTCATGTCTCC   57197         _ G    CACA
                                ATCATACT C CATG    CC
                                |||||||| | ||||    ||
                                TAGTATGA G GTAC    GG
                                     A A    AGA_
GAM2435  ZNF146    5'  TATCATACTCAGTATATTCAAT 57198           ________  _
              GC                    TATCATACTCG      CA TGC
                                ||||||||||       || |||
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                                ATAGTATGAGT     GT ACG
                                      CATATAA  T
GAM2435 BOP     5' TCATACTCTCTGTGATACCCCC 57199       GCA  CAC_
                                TCATACTC  TG   ACCCCC
                                ||||||||  ||   ||||||
                                AGTATGAG  AC   TGGGGG
                                    AG_  ACTA
GAM2435 FLJ10661 3' TCATACTTGATACACAC    57200      CGC
                                TCATACT  ATGCACAC
                                |||||||  ||||||||
                                AGTATGA  TATGTGTG
                                   AC_
GAM2435 HSPC009  3' CACGGTCGCATGCACACC   57201    AC
                                CAT  TCGCATGCACACC
                                |||  ||||||||||||
                                GTG  AGCGTACGTGTGG
                                  CC
GAM2435 KIAA0630 5' TATCATACATGTGAACCC   57202     ACTC    CAC
                                TATCAT   GCATG   ACCC
                                ||||||   |||||   ||||
                                ATAGTA   TGTAC   TGGG
                                   ____    ACT
GAM2435 KIAA0711 5' TCATATCACCGCGCCCC    57203     C   A   ACA
                                TCATA TCGC TGC   CCCC
                                ||||| |||| |||   ||||
                                AGTAT AGTG GCG   GGGG
                                  _   _  C__
GAM2435 ZNF238   3' TCAAGTTCTTTGACACCCCC  57204    TAC  GCA  C
                                TCA   TC   TG ACACCCCC
                                |||   ||   || ||||||||
                                AGT   AG   AC TGTGGGGG
                                  TCA  AA_  _
GAM2435 LOC146515 3' TATCATACACACAAAACA   57205       T   T_
                                TATCATAC CGCA  GCA
                                |||||||| ||||  |||
                                ATAGTATG GTGT  TGT
                                     T   TT
GAM2435 LOC157450 3' CATCATACTTGATACACAC  57206       CGC
                                TATCATACT   ATGCACAC
                                |||||||||   ||||||||
                                GTAGTATGA   TATGTGTG
                                     AC_
GAM2435 LOC158490 3' CATCATACTTGATACACAC  57206       CGC
                                TATCATACT   ATGCACAC
                                |||||||||   ||||||||
                                GTAGTATGA   TATGTGTG
                                     AC_
GAM2435 LOC196484 5' TCATACTTGATACACAC    57200       CGC
                                TCATACT   ATGCACAC
                                |||||||   ||||||||
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                                AGTATGA   TATGTGTG
                                   AC_
GAM2435  LOC200014 3'  TACCAGTGACGCATGCATGCC  57207      TACT       CA
                                TATCA   CGCATGCA  CC
                                |||||   ||||||||  ||
                                ATGGT   GCGTACGT  GG
                                  CACT       AC
GAM2435  LOC219917 3'  CATCATACTTGATACACAC   57206        CGC
                                TATCATACT   ATGCACAC
                                |||||||||   ||||||||
                                GTAGTATGA   TATGTGTG
                                     AC_
GAM2435  LOC220073 5'  TCATACTTGATACACAC     57200        CGC
                                TCATACT   ATGCACAC
                                |||||||   ||||||||
                                AGTATGA   TATGTGTG
                                   AC_
GAM2435  LOC221632 3'  ATCATATACATGCACGCCC   57208       CTC       A
                                ATCATA   GCATGCAC CCC
                                ||||||   |||||||| |||
                                TAGTAT   TGTACGTG GGG
                                   A__       C
GAM2435  LOC90750  5'  CACACCATGCACACCTCC    57209       TCG        _
                                CATAC   CATGCACACC CC
                                |||||   ||||||||||  ||
                                GTGTG   GTACGTGTGG GG
                                  ___         A
GAM2435  LOC93320  3'  CATCATACTTGATACACAC   57206        CGC
                                TATCATACT   ATGCACAC
                                |||||||||   ||||||||
                                GTAGTATGA   TATGTGTG
                                     AC_
GAM2436  LAMB2     3'  TTCAGTGCATAGGCAGACATGC 57212      A      ATC
            AT                    TTCA TGTATAG   GATATGCAT
                                |||| |||||||   |||||||||
                                AAGT ACGTATC   CTGTACGTA
                                  C      CGT
GAM2436  MMP16     3'  TTCAATGTAGAGGTCATGCAC  57213         T  A  GAT
                                TTCAATGTA AG TC   ATGCAT
                                |||||||||  || ||   ||||||
                                AAGTTACAT TC AG   TACGTG
                                     C  C  ___
GAM2436  PLA2G4A   3'  TTCATGTATGTATATATATGCA 57214      A    AG  CG
            T                     TTCA TGTAT  AT  ATATGCAT
                                |||| |||||  ||  ||||||||
                                AAGT ACATA  TA  TATACGTA
                                  _    CA  TA
GAM2436  FLJ20073  3'  AATGTATAGATTCCCCAACAT  57215          ____
                                AATGTATAGAT    CGATAT
                                ||||||||||    ||||||
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                                TTACATATCTA   GTTGTA
                                      AGGG
GAM2436  OR7C1    3'  TTCAATGTATGATTGACA    57216         A  C
                                TTCAATGTAT GAT GATA
                                |||||||||| ||| ||||
                                AAGTTACATA CTA CTGT
                                      _  A
GAM2436  LOC145842 5'  AATGTATAGGTCATTTGCAT  57217        A  ATA
                                AATGTATAG TCG  TGCAT
                                ||||||||| |||  |||||
                                TTACATATC AGT  ACGTA
                                     C  AA_
GAM2436  LOC163590 3'  TTCATGTATAGATCTTTAT   57218     A       GA
                                TTCA TGTATAGATC  TAT
                                |||| ||||||||||  |||
                                AAGT ACATATCTAG  ATA
                                  _       AA
GAM2436  LOC81537  3'  TCAATGTATAGTAGCATATGCA 57219         ATCG
           T                     TCAATGTATAG   ATATGCAT
                                ||||||||||   ||||||||
                                AGTTACATATC   TATACGTA
                                      ATCG
GAM2436  LOC91149  3'  TTCAATGTGCATCTCTGTATG  57220       A  GA  GA
                                TTCAATGT TA  TC  TATG
                                |||||||| ||  ||  ||||
                                AAGTTACA GT  AG  ATAC
                                     C  AG  AC
GAM2436  LOC93206  5'  TGTACTTCCAATATGCAT    57221      AGA
                                TGTAT  TCGATATGCAT
                                |||||  ||||||||||
                                ACATG  GGTTATACGTA
                                   AA_
GAM2437  TDRD1     5'  TACTTGGCAATACAAACT    57224      A
                                TATTT GCAATACAAATT
                                ||||| ||||||||||
                                ATGAA CGTTATGTTTGA
                                   C
GAM2437  FLJ13841  3'  TATTTAGTTATACAAATCACAT 57225       CA       C
           TT                    TATTTAG  ATACAAATT TATTT
                                ||||||| |||||||| |||||
                                ATAAATC  TATGTTTAG GTAAA
                                     AA       T
GAM2437  LOC221400 3'  TTTAGCAAAATAAATCCT    57226        TAC
                                TTTAGCAA  AAATTCT
                                ||||||||  |||||||
                                AAATCGTT  TTTAGGA
                                     TTA
GAM2438  CLN2      3'  GTAGTAGCAGTGGGGATATAAG 57229     TG  __  A
                                GTA  AGC  TGG GATATAAG
                                |||  |||  ||| ||||||||
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                                CAT  TCG  ACC CTATATTC
                                  CA   TC   C
GAM2438  COL4A3    3'  AATTGTATAAGCTACTCATAAG 57230          GAGA
                                AATTGTATGAGCTG   TATAAG
                                |||||||||||||   ||||||
                                TTAACATATTCGAT   GTATTC
                                       GA__
GAM2438  COL4A3    3'  AATTGTATAAGCTACTCATAAG 57230          GAGA
                                AATTGTATGAGCTG   TATAAG
                                |||||||||||||   ||||||
                                TTAACATATTCGAT   GTATTC
                                       GA__
GAM2438  COL4A3    3'  AATTGTATAAGCTACTCATAAG 57230          GAGA
                                AATTGTATGAGCTG   TATAAG
                                |||||||||||||   ||||||
                                TTAACATATTCGAT   GTATTC
                                       GA__
GAM2438  IL1RAP    3'  TTGTGTTTGTGGAGATATAAG  57231     ATGAGC
                                TTGT     TGGAGATATAAG
                                ||||     ||||||||||||
                                AACA     ACCTCTATATTC
                                  CAAAC_
GAM2438  LOC149073 5'  AATTGTGTGGCTGGAAA     57232       A  A
                                AATTGT TG GCTGGAGA
                                |||||| || ||||||||
                                TTAACA AC CGACCTTT
                                   C  _
GAM2439  CGI-203   5'  CAAGGACCAAGAAACAA     57235         AA
                                TAAGGACCAA  AAACAA
                                ||||||||||  ||||||
                                GTTCCTGGTT  TTTGTT
                                      C_
GAM2439  DIS3      3'  CAAGGACCACTAATAAAA     57236         AAAAAAC
                                TAAGGACCA      AATAAAA
                                |||||||||      |||||||
                                GTTCCTGGT      TTATTTT
                                      GA_____
GAM2439  DKFZP434A043 5'  AAGGACCAGAAAGGCAACA   57237        A   AA
                                AAGGACCA AAA  CAATA
                                |||||||| |||  |||||
                                TTCCTGGT TTT  GTTGT
                                     C   CC
GAM2439  FAM3C     3'  TAAGCACCAAAAATCCCAA    57238      G       AA_
                                TAAG ACCAAAAA   CAA
                                |||| ||||||||   |||
                                ATTC TGGTTTTT   GTT
                                  G       AGG
GAM2439  FLJ31890  5'  AAGACCAAAAAAACGCCAA    57239            AA
                                AGGACCAAAAAAAC  TAA
                                ||||||||||||||  |||
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                                TTCTGGTTTTTTTG  GTT
                                        CG
GAM2439  SLK      5'  TAAGGACTAAAAACAATAAAA  57240        CAA
                                TAAGGAC   AAAAACAATAAAA
                                |||||||   ||||||||||||||
                                ATTCCTG   TTTTTGTTATTTT
                                    A__
GAM2439  ZDHHC9    3'  TAAAGACCAAAGAAAAACA   57241          __
                                TAAGGACCAAA  AAAACA
                                ||||||||||  ||||||
                                ATTTCTGGTTT  TTTTGT
                                       CT
GAM2439  ZTL1     3'  AGGCCAAAAAACCACAA     57242     A       ACA
                                AGG CCAAAAAA   ATAA
                                ||| ||||||||   ||||
                                TCC GGTTTTTT   TGTT
                                  _       GG_
GAM2439  LOC113730 5'  TAAGAACCATGGCAATAA    57243         AAAAAA
                                TAAGGACCA     CAATAA
                                |||||||||     ||||||
                                ATTCTTGGT     GTTATT
                                      ACC___
GAM2440  DKFZp761N1114 3'  TATTAAGCAGTTTGTGT     57246        T     A
                                TATTAAG CAGTTT TGT
                                ||||||| |||||| |||
                                ATAATTC GTCAAA ACA
                                    _     C
GAM2440  SIAT8A    3'  TATTAAGCCAGTTTGTGTT    57247            A
                                TATTAAGTCAGTTT TGTT
                                |||||||||||||| ||||
                                ATAATTCGGTCAAA ACAA
                                       C
GAM2441  COL15A1   3'  AGCAGTCCTGTTTCTGT     57250         TATATC
                                AGCAGTCTT     TTCTGT
                                |||||||||     ||||||
                                TCGTCAGGA     AAGACA
                                      CA____
GAM2441  DCX      5'  AAGCAGTCTTTGCATTTCAGT  57251          A  C  T
                                AAGCAGTCTTT TAT TTC GT
                                |||||||||| ||| ||| ||
                                TTCGTCAGAAA GTA AAG CA
                                      C  _  T
GAM2441  FANCC     3'  GCGCTCTCCGCCTCTTCTGTAT 57252    AG    ATA
                                GC  TCTTT   TCTTCTGTAT
                                ||  |||||   ||||||||||
                                CG  AGAGG   AGAAGACATA
                                 CG    CGG
GAM2441  MAPK1     3'  GCAGTCTTTATATAACCCAT   57253           CT
                                GCAGTCTTTATAT  TCTGT
                                ||||||||||||  |||||
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                                CGTCAGAAATATA  GGGTA
                                       TT
GAM2441  MELK     3'  AACAGTCTTTATGTAGGCTGTA 57254           ATCTT
              T                  AGCAGTCTTTAT    CTGTAT
                                 ||||||||||||    ||||||
                                 TTGTCAGAAATA    GACATA
                                       CATCC
GAM2441  BAG2     3'  AAGCAGACTTTATATCAGCAT  57255       T       TTCT
                                 AAGCAG CTTTATATC    GTAT
                                 |||||| |||||||||    ||||
                                 TTCGTC GAAATATAG    CGTA
                                    T       T___
GAM2441  TOR1B    3'  AAGCAGTCATTCCATTTTGTGT 57256        TTTA   C  C
                                 AAGCAGTC    TAT TT TGT
                                 ||||||||    ||| || |||
                                 TTCGTCAG    GTA AA ACA
                                      TAAG   A  C
GAM2442  CENPH    3'  TATGCTTTTCTAAAATTACGG  57259       GC  ATTA
                                 TATGCT  TC    GGAATTACGG
                                 ||||||  ||    ||||||||||
                                 ATACGA  AG    TTTTAATGCC
                                    AA  A___
GAM2442  TRIAD3   3'  TGCTGCTCAATGGGGATTCGG  57260         TTA  A   A
                                 TGCTGCTCA   GG ATT CGG
                                 |||||||||   || ||| |||
                                 ACGACGAGT   CC TAA GCC
                                       TAC  C   _
GAM2442  LOC157226 5'  TGCTGCTCATTGGTTGCG    57261          A  AATTA
                                 TGCTGCTCATT GG     CG
                                 |||||||||||| ||     ||
                                 ACGACGAGTAA CC     GC
                                       _  AAC__
GAM2443  CAPZB    3'  CTCTATGGAAATGTGGAGA    57264     GGAT
                                 CTT    TGGAAATGTGGAGA
                                 |||    ||||||||||||||
                                 GAG    ACCTTTACACCTCT
                                   AT__
GAM2443  CBFA2T1   5'  TGCACTTGGAGCAGAAATGTGG 57265    _      TT
              AG                   TG ACTTGGA  GGAAATGTGGAG
                                 || |||||||  ||||||||||||
                                 AC TGAACCT  TCTTTACACCTC
                                   G      CG
GAM2443  CHRM1    3'  TGGGTTGGATTGGGGAG     57266    AC       AAATGT
                                 TG  TTGGATTGG     GGAG
                                 ||  |||||||||     ||||
                                 AC  AACCTAACC     CCTC
                                   CC       _______
GAM2443  CMRF35   3'  GGATTCCAGGAGATGTGGAGA  57267       ___   A
                                 GGATT   GGA ATGTGGAGA
                                 |||||   ||| |||||||||
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                                CCTAA   CCT TACACCTCT
                                   GGT   C
GAM2443  DGKG     3'  CCTGTGGGAATGTGGAG     57268      GAT   A
                                CTTG   TGG AATGTGGAG
                                ||||   ||| |||||||||
                                GGAC   ACC TTACACCTC
                                  ___   C
GAM2443  MOCS1    3'  TGCTTGGATTGGCTGGTGGGGA 57269    A        AAAT    A
                                TG CTTGGATTGG    GTGG GA
                                || ||||||||||    |||| ||
                                AC GAACCTAACC    CACC CT
                                 _        GAC_    C
GAM2443  PGM1     3'  TGACTTGGATGGGTCCGGG    57270          T  AAA  T
                                TGACTTGGAT GG   TG GG
                                |||||||||| ||   || ||
                                ACTGAACCTA CC   GC CC
                                      C  AG_  _
GAM2443  PTPN1    3'  TGACTTGGAATGGCGGAG     57271         T   AAATG
                                TGACTTGGA TGG     TGGAG
                                ||||||||| |||     |||||
                                ACTGAACCT ACC     GCCTC
                                     T  ______
GAM2443  TKTL1    3'  TGACTTGAACAGTACAGTGTGG 57272          TGGAAA_
            AG                    TGACTTGGAT      TGTGGAG
                                ||||||||||      |||||||
                                ACTGAACTTG      ACACCTC
                                     TCATGTC
GAM2443  TNFSF4   3'  TGATTTGGATCGGGATTGGA   57273     C       AAATG
                                TGA TTGGATTGG     TGGA
                                ||| |||||||||     ||||
                                ACT AACCTAGCC     ACCT
                                  A        CTA__
GAM2443  C(27)-3BETA-HSD 3'  TGGATTGAAAATGTGGAG    57274
                                TGGATTGGAAATGTGGAG
                                ||||||||||||||||||
                                ACCTAACTTTTACACCTC

GAM2443  CAPN6    3'  ACTTGGATTGGGAGGTATGGGG 57275          AAA_    A
            A                    ACTTGGATTGG    TGTGG GA
                                ||||||||||    ||||| ||
                                TGAACCTAACC    ATACC CT
                                      CTCC     C
GAM2443  CASPR3   3'  TTGTTTGGAAATTGATGTGGAG 57276     GA     ____
                                TTG  TTGGAA    ATGTGGAG
                                |||  ||||||    ||||||||
                                AAC  AACCTT    TACACCTC
                                  A_     TAAC
GAM2443  COLEC12  3'  ACTTGAACCCGGGATGTGG   57277         _ AA
                                ACTTGGATT GG  ATGTGG
                                ||||||||| ||  ||||||
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                                TGAACTTGG CC  TACACC
                                     G  C_
GAM2443  DKFZP762D096 3'  TTGGATCTAAATGTGGAGA   57278       GG
                                TTGGATT  AAATGTGGAGA
                                |||||||  ||||||||||
                                AACCTAG  TTTACACCTCT
                                   A_
GAM2443  DZIP1    3'  ACTTTTTTGGGGTGTGGAG   57279     GGA   AAA
                                ACTT   TTGG   TGTGGAG
                                ||||   ||||   |||||||
                                TGAA   AACC   ACACCTC
                                  AA_   CC_
GAM2443  FLJ10101  5'  TGACCTGGATCTCCTGTGTGGG 57280          GGAAA    A
              GA                   TGACTTGGATT    TGTGG GA
                                |||||||||||    ||||| ||
                                ACTGGACCTAG    ACACC CT
                                      AGGAC    C
GAM2443  FLJ10849  3'  TGGCTTAGGACAAGTGTGGAGA 57281    A  _   T  AAA
                                TG CTT GGAT GG   TGTGGAGA
                                || ||| |||| ||   ||||||||
                                AC GAA CCTG TC   ACACCTCT
                                 C   T   T ___
GAM2443  JM4      3'  TGACCTGGGTTGGAAGGTAG   57282        A     AT
                                TGACTTGG TTGGAA  GTGG
                                |||||||| ||||||  ||||
                                ACTGGACC AACCTT  CATC
                                     C     C_
GAM2443  KIAA0759  3'  TGACTTAGGGAGATGTGTGGAG 57283        ATT   AA
                                TGACTTGG   GGA  TGTGGAG
                                ||||||||   |||  |||||||
                                ACTGAATC   TCT  ACACCTC
                                     CC_   AC
GAM2443  KIAA0774  5'  TTGGGGGTGGTGTGGAGA    57284     AT_   AAA
                                TTGG   TGG   TGTGGAGA
                                ||||   |||   ||||||||
                                AACC   ACC   ACACCTCT
                                  CCC   ___
GAM2443  KIAA1319  3'  TGGATTGGATTGGGAA      57285         AA  T
                                TGGATTGGA  TG GGAG
                                |||||||||  || ||||
                                ACCTAACCT  AC CCTT
                                     A_  _
GAM2443  KIAA1676  3'  TGACTTGGGGTTGGGGAG    57286        A_   AAATGT
                                TGACTTGG  TTGG     GGAG
                                ||||||||  ||||     ||||
                                ACTGAACC  AACC     CCTC
                                     CC   _______
GAM2443  PI4KII   3'  CTGGATCAAGACAATGTGGAGA 57287         _  _
                                TTGGATTG GA AATGTGGAGA
                                |||||||| || ||||||||||
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                                GACCTAGT CT TTACACCTCT
                                     T  G
GAM2443  PPP1R3B   3'  TGACTCGGGGTAAATGTGGGGA 57288        ATT  _      A
                                TGACTTGG   GG AAATGTGG GA
                                ||||||||   || |||||||| ||
                                ACTGAGCC   CC TTTACACC CT
                                     ___  A       C
GAM2443  WBSCR17   3'  CTGGGATGGGAGATGTGGAG   57289    T   T   A
                                CT GGAT GGA ATGTGGAG
                                || |||| ||| ||||||||
                                GA CCTA CCT TACACCTC
                                 C   C   C
GAM2443  LOC149448 3'  TGACTTGGGTGGAACCGGG    57290        AT    A  T
                                TGACTTGG  TGGAA TG GG
                                ||||||||  ||||| || ||
                                ACTGAACC  ACCTT GC CC
                                     C_    G  _
GAM2443  LOC151057 3'  CTGGATTGGAAGTTGCCTGAG  57291          A_   G_
                                TTGGATTGGAA  TGT  GAG
                                ||||||||||  |||  |||
                                GACCTAACCTT  ACG  CTC
                                      CA   GA
GAM2443  LOC201771 5'  GACTTGAGAAAATGTGGAGA   57292       ATT
                                GACTTGG   GGAAATGTGGAGA
                                |||||||   |||||||||||||
                                CTGAACT   CTTTTACACCTCT
                                     ___
GAM2443  LOC253626 5'  TTGGATTGGCGCATGGAG    57293        AAA
                                TTGGATTGG   TGTGGAG
                                |||||||||   |||||||
                                AACCTAACC   GTACCTC
                                     GC_
GAM2443  LOC254413 5'  CTTGGAGGATGTGGAG      57294       TT   AA
                                CTTGGA  GGA  TGTGGAG
                                ||||||  |||  |||||||
                                GAACCT  CCT  ACACCTC
                                    __   __
GAM2443  LOC93589  3'  TGAACTTTGAAGTGTGGAG   57295       G_   A
                                TGGATT  GAA TGTGGAG
                                ||||||  ||| |||||||
                                ACTTGA  CTT ACACCTC
                                   AA   C
GAM2444  CD5L     3'  TTCAAATGTTCCTTTC      57298          AA
                                TTCAAATGTT  TCTTTC
                                ||||||||||  ||||||
                                AAGTTTACAA  GGAAAG
                                     __
GAM2444  FHL1     3'  TTCAAATGTTAATTTTC     57299            C
                                TTCAAATGTTAAT TTTC
                                |||||||||||| ||||
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                                AAGTTTACAATTA AAAG
                                      _
GAM2444 JJAZ1    3' CTCAAATGCGTTCTTTC     57300        TAA
                                TTCAAATGT   TCTTTC
                                |||||||||   ||||||
                                GAGTTTACG   AGAAAG
                                     CA_
GAM2444 OPHN1    3' TTCAAATGTTTGCCTTTC    57301         AA
                                TTCAAATGTT  TCTTTC
                                ||||||||||  ||||||
                                AAGTTTACAA  GGAAAG
                                      AC
GAM2444 PCSK2    3' TTCAAACGTGCCCCTTTC    57302        TAA
                                TTCAAATGT   TCTTTC
                                |||||||||   ||||||
                                AAGTTTGCA   GGAAAG
                                     CGG
GAM2444 SNAI2    3' TTCAAAGCTAATCTTTC     57303       T
                                TTCAAA GTTAATCTTTC
                                ||||||| ||||||||||
                                AAGTTT CGATTAGAAAG
                                   _
GAM2444 BCDO     3' TTCAAATGTTTGACTTTC    57304         AAT
                                TTCAAATGTT  CTTTC
                                ||||||||||  |||||
                                AAGTTTACAA  GAAAG
                                      ACT
GAM2444 FLJ11710 5' CTCAAATGTTTTCTTTC     57305         AA
                                TTCAAATGTT  TCTTTC
                                ||||||||||  ||||||
                                GAGTTTACAA  AGAAAG
                                      A_
GAM2444 KIAA0449 3' TCCGCCTGTTAATCTTTC    57306     AAA
                                TTC  TGTTAATCTTTC
                                |||  ||||||||||||
                                AGG  ACAATTAGAAAG
                                  CGG
GAM2444 KIAA1323 3' CTCAAATGCTGACTTTC     57307         AAT
                                TTCAAATGTT  CTTTC
                                ||||||||||  |||||
                                GAGTTTACGA  GAAAG
                                      CT_
GAM2444 KIAA1560 3' TTCAAACGTACAATACTTTC  57308          _  _
                                TTCAAATGT TAAT CTTTC
                                ||||||||| |||| |||||
                                AAGTTTGCA GTTA GAAAG
                                      T   T
GAM2444 LOC122773 3' CTCAAATGTATGTAATCTTTC 57309         ___
                                TTCAAATGT   TAATCTTTC
                                |||||||||   |||||||||
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                                GAGTTTACA   ATTAGAAAG
                                     TAC
GAM2444  LOC154007 3'  TCCAAATCCAATCTTTC     57310        G
                                TTCAAAT TTAATCTTTC
                                ||||||| ||||||||||
                                AGGTTTA GGTTAGAAAG
                                      _
GAM2445  EBAG9     5'  AAAAATCGGCCTGGAGA     57313         GA  A
                                AAAAATCGGC  TG AGA
                                ||||||||||  || |||
                                TTTTTAGCCG  AC TCT
                                     G_  C
GAM2445  FBXL3A    3'  TAAAAAAAATTCGGAGAT    57314         A    C
                                TAAGAAAAA TCGG GAT
                                ||||||||| |||| |||
                                ATTTTTTTT AGCC CTA
                                     A    T
GAM2445  PTGFRN    3'  AGAAAAAAAATTAGATGAAG  57315         TCGGC
                                AGAAAAAA    GATGAAG
                                ||||||||    |||||||
                                TCTTTTTT    CTACTTC
                                     TTAAT
GAM2445  DNAM-1    3'  GAAAAAAATTGCATAAAGAT  57316        TCG  G
                                GAAAAAA   GC ATGAAGAT
                                |||||||   || ||||||||
                                CTTTTTT   CG TATTTCTA
                                     TAA  _
GAM2445  FHOD2     3'  TAAGAAAAAATTGCGAT     57317          CG
                                TAAGAAAAAAT  GCGAT
                                ||||||||||  |||||
                                ATTCTTTTTTA  CGCTA
                                     A_
GAM2445  FLJ20487  3'  AAGAAAGCCCAATGATGAAGAT 57318        AAA    C
                                AAGAAA   TCGG GATGAAGAT
                                ||||||   |||| |||||||||
                                TTCTTT   GGTT CTACTTCTA
                                   CG_    A
GAM2445  FLJ22644  3'  TAAAAAAAAATCCTGCCATGAA 57319           G_  G
            GAT                   TAAGAAAAAATC  GC ATGAAGAT
                                ||||||||||||  || ||||||||
                                ATTTTTTTTTAG  CG TACTTCTA
                                      GA  G
GAM2445  FLJ23132  3'  AGAAAATTTAGGATGAAGAT  57320       AATC  C
                                AGAAAA    GG GATGAAGAT
                                ||||||    || |||||||||
                                TCTTTT    TC CTACTTCTA
                                   AAA_  _
GAM2445  KIAA0063  3'  AGAGGAAACGACATGAAGAT  57321     AA   T    G
                                AGA  AAA CGGC ATGAAGAT
                                |||  ||| |||| ||||||||
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                                TCT  TTT GCTG TACTTCTA
                                  CC  _   _
GAM2445  KIAA0515  3'  GAAAAGGGACAAATGAAGAT  57322      AATC    _
                                GAAAA   GGCGA TGAAGAT
                                |||||   ||||| |||||||
                                CTTTT   CTGTT ACTTCTA
                                   CC__    T
GAM2445  KIAA1046  3'  TAAGACAAAGTGACAATGAAGA 57323      A  ATC
            T                    TAAGA AAA  GGCGATGAAGAT
                                |||||  |||  ||||||||||||
                                ATTCT TTT  CTGTTACTTCTA
                                   G  CA_
GAM2445  MAP2K3   3'  AAGAAAAAAATCAACAGAGGA  57324           _  T
                                AAGAAAAAAATCGGC GA GA
                                |||||||||||||| || ||
                                TTCTTTTTTTAGTTG CT CT
                                         T  C
GAM2445  MAP2K3   3'  AAGAAAAAAATCAACAGAGGA  57324           _  T
                                AAGAAAAAAATCGGC GA GA
                                |||||||||||||| || ||
                                TTCTTTTTTTAGTTG CT CT
                                         T  C
GAM2445  MGC10955  5'  TAAGAAATGAGGACATGAAGAT 57325       AAATC  G
                                TAAGAAA    GGC ATGAAGAT
                                |||||||    ||| ||||||||
                                ATTCTTT    CTG TACTTCTA
                                    ACTC_  _
GAM2445  MORF4    3'  GAAAAAATTTAATGAAGAT   57326       CGGC
                                GAAAAAAT   GATGAAGAT
                                ||||||||   |||||||||
                                CTTTTTTA   TTACTTCTA
                                    AA__
GAM2445  sdolf    3'  AGAAGAAACTTGCATGAAGAT  57327     A   CG  G
                                AGAA AAAT  GC ATGAAGAT
                                |||| ||||  || ||||||||
                                TCTT TTTG  CG TACTTCTA
                                  C   AA  _
GAM2445  LOC120973 5'  TAAGAGGGATACACCATGAAGA 57328      AAAAATCG  G
            T                    TAAGA       GC ATGAAGAT
                                |||||       || ||||||||
                                ATTCT       TG TACTTCTA
                                   CCCTATG_  G
GAM2445  LOC121190 3'  GAAAAAACAAACTGATGGGGAT 57329       CG  _   AA
                                GAAAAAAT  GC GATG  GAT
                                ||||||||  || ||||  |||
                                CTTTTTTG  TG CTAC  CTA
                                    TT  A   CC
GAM2445  LOC126037 5'  AATCGGCGGACGCGGGAAGATA 57330       _  ____     III
                                AATCGGCG AT   GAAGAT   A
                                |||||||| ||   ||||||  |
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                                TTAGCCGC TG   CTTCTA  T
                                    C  CGCC    III
GAM2445  LOC51014  3'  AAGAAAAGTCAATGAAGAT   57331       AATCGG
                                AAGAAAA    CGATGAAGAT
                                |||||||    ||||||||||
                                TTCTTTT    GTTACTTCTA
                                   CA____
GAM2446  MEN1    3'  TGAGAATTTCACATGG     57334     T     GTTT
                                TGAG AATTTCGC   ATGG
                                |||| ||||||||   ||||
                                ACTC TTAAAGTG   TACC
                                  _     _____
GAM2446  TPO     5'  TGAGTAATTTTCACGG     57335         CGCGT
                                TGAGTAATTT    TTATGG
                                ||||||||||    ||||||
                                ACTCATTAAA    AGTGCC
                                      ______
GAM2446  LOC115297 3'  TGAGTAACACAGTTTATGG   57336       TT  C
                                TGAGTAAT  CG GTTTATGG
                                ||||||||  || ||||||||
                                ACTCATTG  GT CAAATACC
                                    T_ _
GAM2446  LOC152674 5'  TGAGTAATTCACCTGTGGC   57337        T   GTTTA
                                TGAGTAATT CGC    TGGC
                                ||||||||| |||    ||||
                                ACTCATTAA GTG    ACCG
                                     _  GAC__
GAM2447  MUC4    3'  TGTGAAGTCCGATGCTTGCGT  57340    CA         TTA
                                TGT  AAGTCCGGTGTTT  CGT
                                |||  ||||||||||||  |||
                                ACA  TTCAGGCTACGAA  GCA
                                  C_         C__
GAM2447  FLJ11301  3'  TGTCAGAGCTGGTGTTT    57341      A  CC
                                TGTCA AGT  GGTGTTT
                                ||||| |||  |||||||
                                ACAGT TCG  CCACAAA
                                   C  A_
GAM2447  LOC203232 3'  TGTCACAGATGGCTGTTTTTAC 57342      A  TCC  _
            GT                   TGTCA AG   GG TGTTTTTACGT
                                ||||| ||   || ||||||||||
                                ACAGT TC   CC ACAAAAATGCA
                                   G  TA_  G
GAM2447  LOC253936 3'  TGTCACAGACGGCTGTTTTTAC 57343      A  TC  _
            GT                   TGTCA AG  CGG TGTTTTTACGT
                                ||||| ||  ||| ||||||||||
                                ACAGT TC  GCC ACAAAAATGCA
                                   G  T_  G
GAM2447  LOC51313  3'  GTTAAAGTCATTTATTTTACGT 57344    C     CGG     T
                                GT AAAGTC   TGTTTT ACGT
                                || ||||||   |||||| ||||
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                                CA TTTCAG   ATAAAA TGCA
                                 A     TAA     _
GAM2448  AGMAT    3'  TATACCTTTTAATCTGCTTGTG 57347         CA  _  T
                                TATACCTT  AA CT TTTGTG
                                ||||||||  || || ||||||
                                ATATGGAA  TT GA GAACAC
                                     AA  A  C
GAM2448  KIAA1407  3'  ATATACCTTTCAGCTATGTTTT 57348     _  AAC_____       III
            TTTGTGC                 CCTT CA       TTTTTGTG   C
                                ||||| ||       ||||||||   |
                                GGAA GT       AAAAACAC   G
                                  A  CGATACAA       III
GAM2448  MGC15397  3'  TAATACACCTTCAAGAGCAGAG 57349             ACTTTTT
            TG                    TAATATACCTTCAA      GTG
                                ||||||||||||||      |||
                                ATTATGTGGAAGTT      CAC
                                       CTCGTCT
GAM2449  CX3CR1   3'  TTAAACTTTTAGATTGTT    57352           TGCG
                                TTAAACTTTTGG    TGTT
                                ||||||||||||    ||||
                                AATTTGAAAATC    ACAA
                                       TA__
GAM2449  IL18R1   3'  TTAAACTTTTGTAGAACAT    57353          GT__
                                TTAAACTTTTG    GCGT
                                ||||||||||    ||||
                                AATTTGAAAAC    TGTA
                                       ATCT
GAM2449  FLJ14686  3'  TACCTTAAACTGTTGGATATT  57354          T    TGC
                                TACCTTAAACT TTGG   GTGTT
                                |||||||||||| ||||   |||||
                                ATGGAATTTGA AACC   TATAA
                                       C   ___
GAM2449  KIAA0513  3'  TTAAACCCAATGCGTGTT    57355       TT TG
                                TTAAAC  T  GTGCGTGTT
                                ||||||  |  |||||||||
                                AATTTG  G  TACGCACAA
                                    __ GT
GAM2449  UBE4B    3'  CCTTAAGCTTTTGACCGTGTT  57356       A       G
                                CCTTAA CTTTTGGT CGTGTT
                                |||||| |||||||| ||||||
                                GGAATT GAAAACTG GCACAA
                                    C       _
GAM2449  LOC201625 3'  TTAAACTTTTGGATGTT     57357          TGC
                                TTAAACTTTTGG   GTGTT
                                ||||||||||||   |||||
                                AATTTGAAAACC   TACAA
                                       ___
GAM2450  DKFZP434J1813 3'  TAAATGTAACATTCTAAATAGG 57360          TAAG
            T                    TGAATGTAAC    TAAATAGGT
                                ||||||||||    |||||||||
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                                ATTTACATTG   ATTTATCCA
                                     TAAG
GAM2450 FLJ20546 3' GAATGCAAGTAGATGGGT   57361       ACTA   A  A
                                GAATGTA   AGTA AT GGT
                                |||||||   |||| || |||
                                CTTACGT   TCAT TA CCA
                                    ____   C  C
GAM2450 KIAA0191 3' TGAATGTAACTGACATTGAGGT 57362          AAGTAAAT
          A                      TGAATGTAACT       AGGTA
                                 ||||||||||       |||||
                                 ACTTACATTGA       TCCAT
                                      CTGTAAC_
GAM2450 KIAA0240 3' GAATGTAACTGGTCCGGGGT  57363         AA  AAATA
                                GAATGTAACT  GT    GGT
                                |||||||||  ||    |||
                                CTTACATTGA  CA    CCA
                                     C_  GGCC_
GAM2450 KIAA0367 3' TGAAAGTAGCAAATAGGT    57364     T  AACTA
                                TGAA GT    AGTAAATAGGT
                                |||| ||    ||||||||||
                                ACTT CA    TCGTTTATCCA
                                  T _____
GAM2450 KIAA0923 3' TGAATGGACAACACAAATAGGT 57365       __   TAAG
                                TGAATG  TAAC   TAAATAGGT
                                ||||||  ||||   |||||||||
                                ACTTAC  GTTG   GTTTATCCA
                                   CT   T___
GAM2450 MGC10715 5' TGAATGTAACTGGTACCTA   57366         AA   AA
                                TGAATGTAACT  GTA  TA
                                ||||||||||  |||  ||
                                ACTTACATTGA  CAT  AT
                                      C_   GG
GAM2450 LOC149073 5' TGCATGTAACTAAAAGTGGGTA 57367    A         TAAATA
                                TG ATGTAACTAAG     GGTA
                                || ||||||||||     ||||
                                AC TACATTGATTT     CCAT
                                 G         TCAC__
GAM2450 LOC149711 3' TGAATAGTTAGTAAATAGGT   57368       TAACTA
                                TGAATG     AGTAAATAGGT
                                ||||||     ||||||||||
                                ACTTAT     TCATTTATCCA
                                   CAA___
GAM2450 LOC151437 3' TGAATTATATTTAAATAGGTA  57369      GTAACTAAG
                                TGAAT       TAAATAGGTA
                                |||||       ||||||||||
                                ACTTA       ATTTATCCAT
                                  ATATAA___
GAM2450 LOC90550 3' TGAGTGTAACCAAGAGGT    57370     A        TAAAT
                                TGA TGTAACTAAG    AGGT
                                ||| ||||||||||    ||||
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                                ACT ACATTGGTTC     TCCA
                                  C         _____
GAM2451  ADAM11    3'  TCCACATAGCTCAGGTCAGAGC 57373         A  CC___     A
              CGTC                    TCCACGTA GC     TCAGA CCGTC
                                ||||||||  ||     |||||  |||||
                                AGGTGTAT CG     AGTCT GGCAG
                                     _  AGTCC     C
GAM2451  DKFZp564O1278 3'  TCTGCGAAAGCCCTCAAA     57374     CA  T
                                TC  CG AAGCCCTCAGA
                                ||  ||  ||||||||||
                                AG  GC TTCGGGAGTTT
                                 AC  T
GAM2451  FLJ20232  3'  CACTAGGCCCTTAACCA      57375      G  A     CAG
                                CAC TA GCCCT   AACCG
                                |||  ||  |||||   |||||
                                GTG AT CGGGA   TTGGT
                                  _  C     A__
GAM2451  FLJ22774  3'  TCTGCGAAAGCCCTCAAA     57374     CA  T
                                TC  CG AAGCCCTCAGA
                                ||  ||  ||||||||||
                                AG  GC TTCGGGAGTTT
                                 AC  T
GAM2451  KIAA1037  3'  CACCTGGCCCTCAGAGCTGTC  57376      GTAA        ACC
                                CAC    GCCCTCAGA   GTC
                                |||    |||||||||   |||
                                GTG    CGGGAGTCT   CAG
                                  GAC_        CGA
GAM2451  MGC11316  3'  TCCACGTAGGCCTCAGAA     57377         A   C
                                TCCACGTA GCC TCAGAA
                                ||||||||  |||  ||||||
                                AGGTGCAT CGG AGTCTT
                                     C   _
GAM2451  LOC150407 3'  GTATGAGCCTCAGAACTGTC   57378      __    C      C
                                GTA  AGCC TCAGAAC GTC
                                |||  ||||  |||||||  |||
                                CAT  TCGG AGTCTTG CAG
                                  AC    _      A
GAM2451  LOC158301 3'  TCCACGAAGCCCTCGGCC     57379        T       AGAA
                                TCCACG AAGCCCTC    CC
                                ||||||  ||||||||    ||
                                AGGTGC TTCGGGAG    GG
                                     _       CC__
GAM2452  IRTA2     3'  CAACAGCAGCTGGTGGTGCT   57382       TAG TG
                                CGACA   G  GCTGGTGGTGCT
                                |||||   |  ||||||||||||
                                GTTGT   C  CGACCACCACGA
                                   ___ GT
GAM2452  MFGE8     3'  GACTGTGTGGTGGTGCT     57383     ATAG   GC
                                GAC    GTG  TGGTGGTGCT
                                |||    |||  ||||||||||
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                                CTG   CAC  ACCACCACGA
                                  A___  __
GAM2452 PLA2G10  5' CAGAGGTGGGACGGTGCT   57384   T    CT GT
                                CA AGGTGG  G  GGTGCT
                                || ||||||  |  ||||||
                                GT TCCACC  C  CCACGA
                                 C     __ TG
GAM2452 PNUTL1   3' GACCTGGGAGGGGGTGGTGCT 57385    ATA  T  CT
                                GAC   GG GG  GGTGGTGCT
                                |||   || ||  |||||||||
                                CTG   CC CC  CCACCACGA
                                  GAC  T  C_
GAM2452 SOX10    3' CATAGGTGGCATGGGC     57386         TG   T
                                CATAGGTGGC  GTGG GC
                                ||||||||||  |||| ||
                                GTATCCACCG  TACC CG
                                          __   _
GAM2452 CXorf2   5' CGACATGGGGGCTAGTGCTG  57387      A  T      G
                                CGACAT GG GGCTGGTG TG
                                |||||| || |||||||| ||
                                GCTGTA CC CCGATCAC AC
                                   C  _       G
GAM2452 DKFZp547I224 3' GAATAGGTGTGGTGTGGTGCT 57388   C     GCTG
                                GA ATAGGTG   GTGGTGCT
                                || |||||||   ||||||||
                                CT TATCCAC   CACCACGA
                                 _     ACCA
GAM2452 FLJ10853 3' ACATAGGTGGCTTGGGT    57389          GGT
                                ACATAGGTGGCT   GGT
                                ||||||||||||   |||
                                TGTATCCACCGA   CCA
                                       AC_
GAM2452 GP5      3' CACATCCACCTGGTGGTG    57390     GG  G
                                CATA  TG CTGGTGGTG
                                ||||  || |||||||||
                                GTGT  GT GACCACCAC
                                  AG  G
GAM2452 PRKWNK2  3' CAACGTAGGTGGCAGGAGGTGC 57391     A      T  T
            T                    CGAC TAGGTGGC GG GGTGCT
                                |||| |||||||| || ||||||
                                GTTG ATCCACCG CC CCACGA
                                  C       T  T
GAM2452 RP4-622L5 3' GACATAGGTTGGTCCCTGCT  57392        GGC   GG_
                                GACATAGGT   TGGT   TGCT
                                |||||||||   ||||   ||||
                                CTGTATCCA   ACCA   ACGA
                                      ___   GGG
GAM2452 ZNF282   3' CGGCAAGGTGGTTGGTG    57393    A  T    C
                                CG CA AGGTGG TGGTG
                                || || |||||| |||||
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                                GC GT TCCACC ACCAC
                                 C _     A
GAM2452  LOC126364 3'  CGGCATGGTGGCGGGTGCTG  57394    A  A    T   G
                                CG CAT GGTGGC GGTG TG
                                || ||| |||||| |||| ||
                                GC GTA CCACCG CCAC AC
                                 C  _     C   G
GAM2452  LOC132617 3'  GACATAGATGGTGCCTGCTG  57395          ___  G
                                GACATAGGTGG   CTG TG
                                ||||||||||   ||| ||
                                CTGTATCTACC   GAC AC
                                       ACG   G
GAM2452  LOC144952 5'  GATGTAGGTGGTTTAGTGCTA  57396    CA     CTGG
                                GA  TAGGTGG    TGGTGCTA
                                ||  |||||||    ||||||||
                                CT  ATCCACC    ATCACGAT
                                 AC      AA__
GAM2452  LOC149606 3'  GATGGCAGTGGTGGTGCT    57397       __
                                GGTGGC  TGGTGGTGCT
                                ||||||  ||||||||||
                                CTACCG  ACCACCACGA
                                    TC
GAM2452  LOC150157 3'  GAATAGGTGTGGTGTGGTGCT  57388    C      GCTG
                                GA ATAGGTG    GTGGTGCT
                                || |||||||    ||||||||
                                CT TATCCAC    CACCACGA
                                 _      ACCA
GAM2452  LOC159121 5'  GACATGGTGTGGCTGGGGTG   57398      AG_      T
                                GACAT   GTGGCTGG GGTG
                                |||||   |||||||| ||||
                                CTGTA   CACCGACC CCAC
                                   CCA      _
GAM2452  LOC196890 3'  GAATAGGTGTGGTGTGGTGCT  57388    C      GCTG
                                GA ATAGGTG    GTGGTGCT
                                || |||||||    ||||||||
                                CT TATCCAC    CACCACGA
                                 _      ACCA
GAM2452  LOC51720  3'  TAGGTGCTGGTGGTGCT     57399       G
                                TAGGTG CTGGTGGTGCT
                                |||||| ||||||||||
                                ATCCAC GACCACCACGA
                                       _
GAM2452  LOC57099  5'  GGCGCCGCTGGTGGTGCT    57400      __
                                GGTG  GCTGGTGGTGCT
                                ||||  ||||||||||||
                                CCGC  CGACCACCACGA
                                  GG
GAM2453  DCK      3'  AAAGAAACTTATATTAATATGA 57403      TTTAG   C
            AG                    AGAG    TATA TAATATGAAG
                                ||||    |||| ||||||||||
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                                TTTC    ATAT ATTATACTTC
                                  TTTGA   A
GAM2453  OTX1     3'  AGAGTTTAGTAGGGGCTGAAG  57404          TACTAATA
                                AGAGTTTAGTA      TGAAG
                                ||||||||||       |||||
                                TCTCAAATCAT      ACTTC
                                     CCCCG___
GAM2453  SART1    3'  GAGCTTTATTTAATATGAAG   57405       A  ATAC
                                GAGTTT GT    TAATATGAAG
                                |||||| ||    ||||||||||
                                CTCGAA TA    ATTATACTTC
                                   A  A___
GAM2453  LOC115265 3'  AGAGTTTAGTTTGTTAGAACAC 57406          _________
               T                  AGAGTTTAGT       ATACT
                                ||||||||||       |||||
                                TCTCAAATCA       TGTGA
                                     AACAATCT
GAM2454  ATP5J    5'  GGGCCTTTTCCCCCACAAG    57409      ACCC       C
                                GGGC    TCCCCCAC GAG
                                ||||    |||||||| |||
                                CCCG    AGGGGGTG TTC
                                  GAAA      _
GAM2454  CSPG4    3'  CAGGGTACTTCCTTCTCCTTGC 57410    __   _ C _______   CGA
               ACTCGGTG               AC  CCT C CC     CAC   GTG
                                ||  ||| | ||     |||   |||
                                TG  GGA G GG     GTG   CAC
                                 AA   A A  AACIII   AGC
GAM2454  EFNA4    3'  CAGGGCTTCTTCTTTGCCCTGC 57411   ACCC _____   ______   CGA
               ACTCGGTG                  TC    CCC     CAC   GTG
                                  ||    |||     |||   |||
                                  AG    GGG     GTG   CAC
                                AAGA  AAAC   ACIII   AGC
GAM2454  GRN      3'  AGGGCACCCTCCGAG       57412           CCCACC
                                AGGGCACCCTCC      GAG
                                ||||||||||||      |||
                                TCCCGTGGGAGG      CTC
                                      _______
GAM2454  MATK     3'  GGGCCAAGGGCCCCACCGGGTG 57413      ACCCTC       A
                                GGGC      CCCCACCG GTG
                                ||||      |||||||| |||
                                CCCG      GGGGTGGC CAC
                                  GTTCCC       C
GAM2454  MATK     3'  GGGCCAAGGGCCCCACCGGGTG 57413      ACCCTC       A
                                GGGC      CCCCACCG GTG
                                ||||      |||||||| |||
                                CCCG      GGGGTGGC CAC
                                  GTTCCC       C
GAM2454  MATK     3'  GGGCCAAGGGCCCCACCGGGTG 57413      ACCCTC       A
                                GGGC      CCCCACCG GTG
                                ||||      |||||||| |||
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                                CCCG     GGGGTGGC CAC
                                  GTTCCC       C
GAM2454  STAU    3'  AGGGACCGCCAGGTCACCGAGT 57414     C  _  CCCC
            G                    AGGG ACC CT    CACCGAGTG
                                 |||| ||| ||    |||||||||
                                 TCCC TGG GG    GTGGCTCAC
                                   _  C  TCCA
GAM2454  STAU    3'  AGGGACCGCCAGGTCACCGAGT 57414     C  _  CCCC
            G                    AGGG ACC CT    CACCGAGTG
                                 |||| ||| ||    |||||||||
                                 TCCC TGG GG    GTGGCTCAC
                                   _  C  TCCA
GAM2454  STAU    3'  AGGGACCGCCAGGTCACCGAGT 57414     C  _  CCCC
            G                    AGGG ACC CT    CACCGAGTG
                                 |||| ||| ||    |||||||||
                                 TCCC TGG GG    GTGGCTCAC
                                   _  C  TCCA
GAM2454  STAU    3'  AGGGACCGCCAGGTCACCGAGT 57414     C  _  CCCC
            G                    AGGG ACC CT    CACCGAGTG
                                 |||| ||| ||    |||||||||
                                 TCCC TGG GG    GTGGCTCAC
                                   _  C  TCCA
GAM2454  XPNPEP1  3'  GGGCATCTTCCTTTCACCAAGT 57415      CCC   CC_
            G                    GGGCA   TCC   CACCGAGTG
                                 |||||   |||   |||||||||
                                 CCCGT   AGG   GTGGTTCAC
                                   AGA   AAA
GAM2454  ZNF215   3'  CAGGGCACACTTCCTCAC    57416        C  C  C
                                 CAGGGCAC CT CC CAC
                                 |||||||| || || |||
                                 GTCCCGTG GA GG GTG
                                     T  A  A
GAM2454  DKFZP434H0820 3'  CAGGGTGCCCTCCCCAGCACTC 57417       CA       _____   CGA
            G                    CAGGG  CCCTCCCC    CAC   G
                                 |||||  ||||||||    |||   |
                                 GTCCC  GGGAGGGG    GTG   C
                                   AC       TCIII   AGC
GAM2454  DKFZP564D172 3'  CAGGGCGGCCTCCCCCGTCG   57418       AC       AC
                                 CAGGGC  CCTCCCCC  CG
                                 ||||||  ||||||||  ||
                                 GTCCCG  GGAGGGGG  GC
                                    CC       CA
GAM2454  FADS2    3'  CAGGGCAGCCTCCTCCTGCACT 57419       C    _  _____   CGA
            CG                     AGGGCA CCTCC CC    CAC   G
                                 ||||||  |||||  ||    |||   |
                                 TCCCGT  GGAGG  GG    GTG   C
                                   C    A  ACIII   AGC
GAM2454  FLJ20257  5'  TGAGGCGCCCTCCCCGTGCACT 57420   A    A       _______   CGA
            CG                     GGGC CCCTCCCC     CAC   G
                                  ||||  ||||||||     |||   |
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                                TCCG GGGAGGGG     GTG   C
                               C    C       CACIII   AGC
GAM2454  FLJ21742  3'  GGGCACCCTTCCCTGCAGCACT 57421       C  _________  CGA
            CGGT                  GCACCCT CCC       CAC   GT
                               ||||||| |||       |||   ||
                               CGTGGGA GGG       GTG   CA
                                  A   ACGTCIII   AGC
GAM2454  GT650    5'  GGTGCATCTGTCACCGAGTG   57422    _  CCC  CCC
                               GG GCA   TC   CACCGAGTG
                               || |||   ||   |||||||||
                               CC CGT   AG   GTGGCTCAC
                                A   ___  ACA
GAM2454  KIAA0363  5'  GGGCCGCCCTCCCCTGGCACTC 57423     A_      _______  CGA
            G                   GGGC  CCCTCCCC     CAC   G
                               ||||  ||||||||     |||   |
                               CCCG  GGGAGGGG     GTG   C
                                 GC       ACCIII   AGC
GAM2454  KIAA0700  3'  GGGGTCCCTCCCCTTGTGCACT 57424    CA      _________  CGA
            CGGT                  G  CCCTCCCC       CAC   GT
                               |  ||||||||       |||   ||
                               C  GGGAGGGG       GTG   CA
                                CA       AACACIII   AGC
GAM2454  KIAA1691  3'  CAGGGCCTCTCTCCTGGCACTC 57425      ACC   C  _______  CGA
            G                   AGGGC   CTC CC     CAC   G
                               |||||   ||| ||     |||   |
                               TCCCG   GAG GG     GTG   C
                                 GA_   A  ACCIII   AGC
GAM2454  KIAA1853  3'  GGGCACCTGCCCCTGTCCCAG  57426       CT    CA_  G
                               GGGCACC  CCCC   CC AG
                               |||||||  ||||   || ||
                               CCCGTGG  GGGG   GG TC
                                  AC    ACA  G
GAM2454  KIAA1957  3'  CAGGGCACCCTCGCCTGGCACT 57427          C  _______  CGA
            CG                    AGGGCACCCTC CC     CAC   G
                               |||||||||||  ||     |||   |
                               TCCCGTGGGAG GG     GTG   C
                                     C  ACCIII   AGC
GAM2454  LIPG     3'  CAGGTGCCTTTCCCCATGCACT 57428    _  ACCC    _______  CGA
            CG                    GG GC    TCCCC     CAC   G
                               ||  ||    |||||     |||   |
                               CC CG    AGGGG     GTG   C
                                A  GAA_     TACIII   AGC
GAM2454  MGC2628   3'  AGGGCACCTTCTCCTGTGCACT 57429       C  C  ________  CGA
            CGGT                  GGCACC TC CC      CAC   GT
                               ||||||  ||  ||      |||   ||
                               CCGTGG AG GG      GTG   CA
                                  A  A  ACACIII   AGC
GAM2454  N4BP3    3'  CAGGGCACCTTCTGACAGT   57430         C  CCCC  CG
                               CAGGGCACC TC    AC  AGT
                               |||||||||  ||    ||  |||
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                                GTCCCGTGG AG   TG  TCA
                                     A  AC__  __
GAM2454  TUBAL2   3'  AGGCACCCTCCTCCTGCACTCG 57431          _ _____  CGA
                                GGGCACCCTCC CC    CAC  G
                                |||||||||| ||    |||  |
                                TCCGTGGGAGG GG    GTG  C
                                     A  ACIII  AGC
GAM2454  WIRE     3'  CAAGGCACCTTTCCCCAAGCAC 57432       C_   _______  CGA
           TCGGT                 GGCACC  TCCCC    CAC  GT
                                ||||||  |||||     |||  ||
                                CCGTGG  AGGGG     GTG  CA
                                   AA    TTCIII  AGC
GAM2454  LOC148479 3'  CAGGGCACCCTGCCCTCGAG  57433          C  CAC
                                CAGGGCACCCT CCC  CGAG
                                |||||||||| |||  ||||
                                GTCCCGTGGGA GGG  GCTC
                                     C  A__
GAM2454  LOC150244 5'  CAGGGCACTCTCTCCAGCACTC 57434        C  C _____  CGA
           G                    CAGGGCAC CTC CC    CAC  G
                                |||||||| ||| ||    |||  |
                                GTCCCGTG GAG GG    GTG  C
                                     A  A  TCIII  AGC
GAM2454  LOC158301 3'  AGGGTTCCCTCCCCTGGCACTC 57435      CA      _______  CGA
           G                    AGGG  CCCTCCCC    CAC  G
                                ||||  ||||||||    |||  |
                                TCCC  GGGAGGGG    GTG  C
                                  AA      ACCIII  AGC
GAM2454  LOC158835 3'  CAGGGCACCTCTCCCCTAGCAC 57436       _    _______  CGA
           TCGGT                 GGCACC CTCCCC    CAC  GT
                                ||||||  ||||||    |||  ||
                                CCGTGG GAGGGG     GTG  CA
                                   A    ATCIII  AGC
GAM2454  LOC204285 3'  AGTGCACCCTCCCCTGGTGCAC 57437          _________  CGA
           TCGGT                 GCACCCTCCCC      CAC  GT
                                ||||||||||       |||  ||
                                CGTGGGAGGGG      GTG  CA
                                     ACCACIII  AGC
GAM2454  LOC206480 5'  CAGGGACCCTCCCCACTCGTG  57438      C       C  CGA
                                CAGGG ACCCTCCCC AC   GTG
                                |||||  |||||||| ||   |||
                                GTCCC TGGGAGGGG TG   CAC
                                  _       _ AG_
GAM2454  LOC91035  5'  GGGCACCCACCCCGGCCCGAGT 57439        T   CA_
           G                    GGGCACCC CCCC   CCGAGTG
                                ||||||||  ||||   |||||||
                                CCCGTGGG GGGG   GGCTCAC
                                     T   CCG
GAM2455  AHSG     3'  TCAGGCACTTTCATTAACA   57442     T  C  AA
                                TCAG GC AC  TTTCATTAACA
                                ||||  ||  ||  ||||||||||
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                                AGTC CG TG  AAAGTAATTGT
                                  _ _ __
GAM2455  GSTM3    3'  TCAGTACCACAGTTTTACT    57443          A   C
                                TCAGTGCCACA TTT ATT
                                |||||||||| ||| |||
                                AGTCATGGTGT AAA TGA
                                      C   A
GAM2455  RTN3     3'  GTACACACAGTTTCATTA     57444      _   A
                                GTGC CACA TTTCATTA
                                |||| |||| ||||||||
                                CATG GTGT AAAGTAAT
                                  T   C
GAM2455  TUFT1    3'  AGTGTCACTCTGACATTAACAA 57445      C   AATTT
                                AGTG CAC    CATTAACAA
                                |||| |||    |||||||||
                                TCAC GTG    GTAATTGTT
                                  A   AGACT
GAM2455  C6orf33  3'  ATGTCACAGGCCATTAACAA   57446     C    ATT
                                GTG CACA   TCATTAACAA
                                ||| ||||   ||||||||||
                                TAC GTGT   GGTAATTGTT
                                  A   CC_
GAM2455  FLJ23191 5'  TCAGTGCCTTCCTCATTAA    57447         ACAA
                                TCAGTGCC    TTTCATTAA
                                ||||||||    |||||||||
                                AGTCACGG    GGAGTAATT
                                     AA__
GAM2455  FLJ30213 3'  TCAGTGCCAAGATAAACTAACA 57448         CA  TTC
           A                     TCAGTGCCA  AT   ATTAACAA
                                |||||||||  ||   ||||||||
                                AGTCACGGT  TA   TGATTGTT
                                     TC  TT_
GAM2455  KIAA1184 3'  AGTGCCACAAGAGAAGCATTGA 57449          TTT___    A
           CAA                    AGTGCCACAA     CATT ACAA
                                ||||||||||     |||| ||||
                                TCACGGTGTT     GTAA TGTT
                                     CTCTTC    C
GAM2455  NDP52    3'  TCAGTGACATAACTCCACT    57450       C  C
                                TCAGTG CA AATTTCATT
                                |||||| || |||||||||
                                AGTCAC GT TTGAGGTGA
                                   T  A
GAM2455  TNRC6    3'  GTGCAACACTTTCATTAA    57451      C   A
                                GTGC ACA TTTCATTAA
                                |||| ||| |||||||||
                                CACG TGT AAAGTAATT
                                  T   G
GAM2455  LOC129676 5'  TCAGTGCCTGCAATTTGCAC   57452         A_     _
                                TCAGTGCC  CAATTT CAT
                                ||||||||  |||||| |||
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                                AGTCACGG  GTTAAA GTG
                                     AC      C
GAM2455  LOC148547 5'  TCAGTGCCAGAATCAGAACA   57453         C    TCATT
                                TCAGTGCCA AATT     AACA
                                ||||||||| ||||     ||||
                                AGTCACGGT TTAG     TTGT
                                     C    TC___
GAM2455  LOC152905 3'  GTACACACAGTTTCATTA    57444      _    A
                                GTGC CACA TTTCATTA
                                |||| |||| ||||||||
                                CATG GTGT AAAGTAAT
                                  T    C
GAM2455  LOC254402 5'  TCAGTGCCACAGCCACT     57454           ATT
                                TCAGTGCCACA   TCATT
                                ||||||||||   |||||
                                AGTCACGGTGT   GGTGA
                                      C__
GAM2455  LOC56267  3'  CAGTGCCATAATTACAACAA   57455         C    TCAT
                                CAGTGCCA AATT    TAACAA
                                |||||||| ||||    ||||||
                                GTCACGGT TTAA    GTTGTT
                                     A    T___
GAM2456  PAEP      3'  CTCCAAGGGTTTATTAATA   57458       TTATGTA
                                CTCCA      GTTTATTAATA
                                |||||      ||||||||||
                                GAGGT      CAAATAATTAT
                                   TCC____
GAM2456  RAP1GDS1  3'  ACATCATTATGTAGTTTA    57459    TC
                                AC  CATTATGTAGTTTA
                                ||  ||||||||||||||
                                TG  GTAATACATCAAAT
                                 TA
GAM2456  C20orf129 3'  ACATCATTATGTAGTGCAT    57460    TC         T
                                AC  CATTATGTAGT TAT
                                ||  |||||||||| |||
                                TG  GTAATACATCA GTA
                                 TA         C
GAM2456  FLJ14675  3'  TCCATTACATTTATTAATA    57461        GTA
                                TCCATTAT   GTTTATTAATA
                                ||||||||   ||||||||||
                                AGGTAATG   TAAATAATTAT
                                     ___
GAM2456  STXBP3    3'  ACTCCATTTCTATTAA      57462        ATGTAG
                                ACTCCATT     TTTATTAA
                                ||||||||     ||||||||
                                TGAGGTAA     AGATAATT
                                     _______
GAM2456  LOC220038 5'  ACTGCGTTATGTAGTTTA    57463     CCA
                                ACT   TTATGTAGTTTA
                                |||   ||||||||||||
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                                TGA  AATACATCAAAT
                                  CGC
GAM2457 TMEFF1   3' TTGCTGTGGTCATTGT    57466     CTTA  TA
                                TTGCT   GT  GTCATTGT
                                ||||||   ||  ||||||||
                                AACGA   CA  CAGTAACA
                                  _____  C_
GAM2457 KIAA0152 3' TTGTTCATTAATCATTGTG   57467    C  TTA
                                TTG TC   GTTAGTCATTGTG
                                ||| ||   ||||||||||||
                                AAC AG   TAATTAGTAACAC
                                  A  ___
GAM2458 LIMK1    3' TCCTGGATGGGGGTGGGT    57470    C  T  ATTTTT
                                TCC GG TG     GGGTGGGT
                                ||| || ||     ||||||||
                                AGG CC AC     CCCACCCA
                                  A  T  C_____
GAM2458 LIMK1    3' TCCTGGATGGGGGTGGGT    57470    C  T  ATTTTT
                                TCC GG TG     GGGTGGGT
                                ||| || ||     ||||||||
                                AGG CC AC     CCCACCCA
                                  A  T  C_____
GAM2458 OXTR     3' AGTTGATTTTTGCACATAGTG  57471          G TG_
                                GGTTGATTTTTG G   GGTG
                                ||||||||||| |   ||||
                                TCAACTAAAAAC T   TCAC
                                      G GTA
GAM2458 WT1      5' TCCCGGCTCTGGGTGGGT    57472       TGATT
                                TCCCGGT    TTTGGGTGGGT
                                |||||||    ||||||||||
                                AGGGCCG    AGACCCACCCA
                                   _____
GAM2458 WT1      5' TCCCGGCTCTGGGTGGGT    57472       TGATT
                                TCCCGGT    TTTGGGTGGGT
                                |||||||    ||||||||||
                                AGGGCCG    AGACCCACCCA
                                   _____
GAM2458 WT1      5' TCCCGGCTCTGGGTGGGT    57472       TGATT
                                TCCCGGT    TTTGGGTGGGT
                                |||||||    ||||||||||
                                AGGGCCG    AGACCCACCCA
                                   _____
GAM2458 WT1      5' TCCCGGCTCTGGGTGGGT    57472       TGATT
                                TCCCGGT    TTTGGGTGGGT
                                |||||||    ||||||||||
                                AGGGCCG    AGACCCACCCA
                                   _____
GAM2458 ANP32B   3' GGCTCTTTGGGTGGGTG     57473     TGA
                                GGT   TTTTTGGGTGGGTG
                                |||   ||||||||||||||
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                              CCG   AGAAACCCACCCAC
                                ___
GAM2458  FLJ10986  5'  TCCTGGTTGACTGGTAATGGGT 57474     C       TTTG
             G                   TCC GGTTGATT    GGTGGGTG
                                 ||| ||||||||    ||||||||
                                 AGG CCAACTGA    TTACCCAC
                                   A       CCA_
GAM2458  FLJ32934  3'  GGTTTATTTGGGGGGTGGGTG  57475     G    TT_
                                 GGTT ATTT   GGGTGGGTG
                                 |||| ||||   |||||||||
                                 CCAA TAAA   CCCACCCAC
                                   A   CCC
GAM2458  MGC32104  3'  AGTTGATTTTTGTATATCGTG  57476          GG  G_
                                 GGTTGATTTTTG  TG  GTG
                                 ||||||||||||  ||  |||
                                 TCAACTAAAAAC  AT  CAC
                                         AT  AG
GAM2458  LOC145801 3'  GGCTCTTTGGGTGGGTG     57473     TGA
                                 GGT   TTTTTGGGTGGGTG
                                 |||   ||||||||||||||
                                 CCG   AGAAACCCACCCAC
                                   ___
GAM2458  LOC201109 3'  CCTGTTGATTTGGGTG      57477     G      TT
                                 CC GTTGATT  TGGGTG
                                 || |||||||  ||||||
                                 GG CAACTAA  ACCCAC
                                   A      __
GAM2459  CUL3      3'  TGAGAATTTTAATTTTCCCACA 57480     A       A     T
             TT                    TGA AATTTTAAT TTTCT CATT
                                   ||| ||||||||| ||||| ||||
                                   ACT TTAAAATTA AAGGG GTAA
                                     C       A    T
GAM2459  IL1RAP    3'  TGAAAACTTTCATATTTTTCAT 57481          A     C
             T                     TGAAAATTTT ATATTT TTCATT
                                   |||||||||| |||||| ||||||
                                   ACTTTTGAAA TATAAA AAGTAA
                                         G     _
GAM2459  FLJ20967  3'  AAAAGTTTTCCATTTCTTCATT 57482      T   AA
                                   AAAA TTT  TATTTCTTCATT
                                   |||| |||  ||||||||||||
                                   TTTT AAA  GTAAAGAAGTAA
                                     C   AG
GAM2459  FLJ22004  3'  GAAATACATATTTCTTCATT   57483     ATTTTA
                                   GAAA     ATATTTCTTCATT
                                   ||||     ||||||||||||
                                   CTTT     TATAAAGAAGTAA
                                     ATG___
GAM2459  MGC15937  3'  TGAAAATTTTATTAAAATCCTT 57484          ATAT__
             CATT                    TGAAAATTTTA     TTCTTCATT
                                     ||||||||||      |||||||||
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                                ACTTTTAAAAT     AGGAAGTAA
                                      AATTTT
GAM2459  NRBF-2   3'  TGGAAATTTAAATATTTCTTC  57485    A     T
                                TG AAATTT AATATTTCTTC
                                || |||||| ||||||||||
                                AC TTTAAA TTATAAAGAAG
                                 C     T
GAM2459  LOC150596 3'  TGAAGTTTTAATATTTCTT   57486     AA
                                TGAA  TTTTAATATTTCTT
                                ||||  ||||||||||||||
                                ACTT  AAAATTATAAAGAA
                                  C_
GAM2460  ALS2     3'  ATAACACAAAGTCCTTTCCA   57489        TCT    C_
                                ATAACACAA   GGTCT  TCCA
                                |||||||||   |||||  ||||
                                TATTGTGTT   TCAGG  AGGT
                                      ___     AA
GAM2460  CD28     3'  TACATACACTTGGTCTCT    57490     _   AATC
                                TATA ACAC    TGGTCTCT
                                |||| ||||    ||||||||
                                ATGT TGTG    ACCAGAGA
                                  A    A___
GAM2460  CYBB     3'  ATAACACAGGGCAGATCTCTC  57491        ATCT_
                                ATAACACA     GGTCTCTC
                                ||||||||     ||||||||
                                TATTGTGT     CTAGAGAG
                                     CCCGT
GAM2460  EBF      3'  TAGCAGAATCCAACCTCTTCA  57492    A  C    GG    C
                                TA CA AATCT  TCTCT CA
                                || || |||||  ||||| ||
                                AT GT TTAGG  GGAGA GT
                                 C  C    TT    A
GAM2460  ESR1     3'  TATAACCAATGACCTCTC    57493       A   TC  GT
                                TATAAC CAA  TG  CTCTC
                                |||||| |||  ||  |||||
                                ATATTG GTT  AC  GAGAG
                                   _   __  TG
GAM2460  F12      3'  ACACAATCTTGCCTTCCA    57494        G    C
                                ACACAATCT GTCT TCCA
                                ||||||||| |||| ||||
                                TGTGTTAGA CGGA AGGT
                                     A    _
GAM2460  FMR2     3'  TATAACACTGTCTCATCT    57495        AA   G
                                TATAACAC  TCT GTCT
                                ||||||||  ||| ||||
                                ATATTGTG  AGA TAGA
                                     AC   G
GAM2460  GPC4     3'  ATAACACAAACAACCTCT    57496         TC GG
                                ATAACACAA  T  TCTCT
                                |||||||||  |  |||||
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                                TATTGTGTT  G  GGAGA
                                     T_ TT
GAM2460  GRIA2    3'  CATAACACGTCCATTTTCTCCA 57497        AA   GTC
                                TATAACAC  TCTG   TCTCCA
                                ||||||||  ||||   ||||||
                                GTATTGTG  AGGT   AGAGGT
                                     C_    AAA
GAM2460  JDP1     3'  TATAATACAATCTACTCT    57498      C      G
                                TATAA ACAATCTG TCT
                                ||||| |||||||| |||
                                ATATT TGTTAGAT AGA
                                   A       G
GAM2460  LEPR     3'  TATAACACAAATCTGAAGGTTT 57499         _  ___  C  C
               CTTCA                TATAACACAA TCT   GGT TCT CA
                                ||||||||||| |||   ||| ||| ||
                                ATATTGTGTT AGA   CCA AGA GT
                                      T   CTT   A   A
GAM2460  NPY2R    3'  AACACAATCTCTCTCTCTCTCC 57500         GG___
               A                  AACACAATCT    TCTCTCCA
                                ||||||||||    ||||||||
                                TTGTGTTAGA    AGAGAGGT
                                     GAGAG
GAM2460  PCDH11X  3'  TAAACACAATCTAAGTCT    57501   T        _
                                A AACACAATCTG GTCT
                                | ||||||||||| ||||
                                A TTGTGTTAGAT CAGA
                                 T         T
GAM2460  PCDH11X  3'  TAAACACAATCTAAGTCT    57501   T        _
                                A AACACAATCTG GTCT
                                | ||||||||||| ||||
                                A TTGTGTTAGAT CAGA
                                 T         T
GAM2460  PCDH11Y  3'  TAAACACAATCTAAGTCT    57501   T        _
                                A AACACAATCTG GTCT
                                | ||||||||||| ||||
                                A TTGTGTTAGAT CAGA
                                 T         T
GAM2460  RAD54B   3'  TAACACAATCTGAACTTTC   57502          GT  C
                                TAACACAATCTG  CT TC
                                ||||||||||||  || ||
                                ATTGTGTTAGAC  GA AG
                                      TT  A
GAM2460  RNF26    3'  CACAGTCTGCCCTCTCCA    57503      A   G
                                CACA TCTG TCTCTCCA
                                |||| |||| ||||||||
                                GTGT AGAC GGAGAGGT
                                  C   G
GAM2460  SMARCA3  3'  TATAACACAACATTGTCTCC  57504          CTG
                                TATAACACAAT   GTCTCT
                                ||||||||||   ||||||
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                                ATATTGTGTTG  CAGAGG
                                      TAA
GAM2460 SMARCA3  3' TATAACACAACATTGTCTCC  57504        CTG
                                TATAACACAAT  GTCTCT
                                ||||||||||  ||||||
                                ATATTGTGTTG  CAGAGG
                                      TAA
GAM2460 ANKRD6   3' TATATTGCAATCTAATGAGTCT 57505    ACA    ____
           CT                    TATA  CAATCT   GGTCTCT
                                ||||  ||||||  |||||||
                                ATAT  GTTAGA   TCAGAGA
                                  AAC    TTAC
GAM2460 BM045    3' TATCACACAATCCTATTCT   57506    A      GG_
                                TAT ACACAATCT  TCT
                                ||| |||||||||  |||
                                ATA TGTGTTAGG  AGA
                                  G       ATA
GAM2460 C6orf37  3' TAACAAATATAATCTCTC    57507     C  C
                                TAACA AAT TGGTCTCTC
                                ||||| ||| |||||||||
                                ATTGT TTA ATTAGAGAG
                                   _  T
GAM2460 CHK      3' TATAACACAGTCGCCATCT   57508       A  TG  _
                                TATAACACA TC  GTC TCT
                                ||||||||| ||  ||| |||
                                ATATTGTGT AG  CGG AGA
                                      C  __  T
GAM2460 DKFZp547A023 3' ATAACATAATCTGACTC    57509      C     T
                                ATAACA AATCTGG CTC
                                |||||| ||||||| |||
                                TATTGT TTAGACT GAG
                                   A     _
GAM2460 FLJ11996 3' TATAACATATTTGATCCCT   57510       CA  C
                                TATAACA  AT TGGTCTCT
                                |||||||  || ||||||||
                                ATATTGT  TA ACTAGGGA
                                     A_  A
GAM2460 FLJ20045 3' TAACACAAGCTCACAGCCTCT  57511       T  ___
                                TAACACAA CT   GGTCTCT
                                |||||||| ||   |||||||
                                ATTGTGTT GA   TCGGAGA
                                     C  GTG
GAM2460 FLJ20644 3' TATAAGACAGTCTAGTCTTTC  57512     C  A     C
                                TATAA ACA TCTGGTCT TC
                                ||||| ||| |||||||| ||
                                ATATT TGT AGATCAGA AG
                                   C  C      A
GAM2460 H2AV     3' TAACACAAGCCATAAATCTCT  57513       T  ___
                                TAACACAA CT   GGTCTCT
                                |||||||| ||   |||||||
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                                ATTGTGTT GG   TTAGAGA
                                     C  TAT
GAM2460 HSAJ1454 3' TAAACACAATTGAGGACTCT  57514   T      CT_  T
                                A AACACAAT   GG CTCT
                                | ||||||||   || ||||
                                A TTGTGTTA   CC GAGA
                                 T       ACT  T
GAM2460 KIAA0275 3' TGAACACAATTCCTAACTCT  57515   T      _ GGT
                                A AACACAAT CT   CTCT
                                | |||||||| ||   ||||
                                A TTGTGTTA GG   GAGA
                                 C       A  ATT
GAM2460 KIAA0863 3' TAACAGGGGTCTCTCCA     57516      CAATCT
                                TAACA     GGTCTCTCCA
                                |||||     ||||||||||
                                ATTGT     CCAGAGAGGT
                                   CC____
GAM2460 KIAA0863 3' TAACAGGGGTCTCTCCA     57516      CAATCT
                                TAACA     GGTCTCTCCA
                                |||||     ||||||||||
                                ATTGT     CCAGAGAGGT
                                   CC____
GAM2460 MGC2628  3' AACCTATGCCCTCTCTCCA   57517       _ ___
                                AATCTG GT   CTCTCCA
                                |||||| ||   |||||||
                                TTGGAT CG   GAGAGGT
                                    A  GGA
GAM2460 MGC32104 3' TATAATTGTGAAGTCTCTCCA 57518      CACAATCT
                                TATAA       GGTCTCTCCA
                                |||||       ||||||||||
                                ATATT       TCAGAGAGGT
                                   AACACT__
GAM2460 PRO2893  3' CACAATCTACAGTGTTCCA   57519        __  CTC
                                CACAATCT  GGT   TCCA
                                ||||||||  |||   ||||
                                GTGTTAGA  TCA   AGGT
                                     TG   CA_
GAM2460 SEC23B   3' TGAACACAATCTGACACC    57520   T        TC
                                A AACACAATCTGG  TC
                                | ||||||||||||  ||
                                A TTGTGTTAGACT  GG
                                 C          GT
GAM2460 SEC23B   3' TGAACACAATCTGACACC    57520   T        TC
                                A AACACAATCTGG  TC
                                | ||||||||||||  ||
                                A TTGTGTTAGACT  GG
                                 C          GT
GAM2460 SEC23B   3' TGAACACAATCTGACACC    57520   T        TC
                                A AACACAATCTGG  TC
                                | ||||||||||||  ||
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                                A TTGTGTTAGACT  GG
                                 C          GT
GAM2460  LOC123036 3'  TATAATGTCATCTGCCTCTCCA 57521      CACA    G
                                TATAA    ATCTG TCTCTCCA
                                |||||    ||||| ||||||||
                                ATATT    TAGAC GGAGAGGT
                                   ACAG    _
GAM2460  LOC125923 5'  TATAATCATAAAGTTTCTCTCC 57522      _  C  TCTGG
              A                  TATAA CA AA    TCTCTCCA
                                |||||  ||  ||    ||||||||
                                ATATT GT TT    AGAGAGGT
                                   A  A  TCAA_
GAM2460  LOC127428 3'  ATAACACAGCCTGCTTTCCA   57523        AT   GT  C
                                ATAACACA  CTG  CT TCCA
                                ||||||||  |||  ||  ||||
                                TATTGTGT  GAC  GA AGGT
                                     CG   __  A
GAM2460  LOC139065 5'  TAAGACACAATCTGACT     57524    TA         T
                                TA  ACACAATCTGG CT
                                ||  ||||||||||| ||
                                AT  TGTGTTAGACT GA
                                 TC         _
GAM2460  LOC145082 5'  TAACACAATCTCAAAATCT    57525          ___
                                TAACACAATCT   GGTCT
                                ||||||||||   |||||
                                ATTGTGTTAGA   TTAGA
                                      GTT
GAM2460  LOC150166 3'  TATTACACAGCCCCTCTC    57526     A    AT  GGT
                                TAT ACACA  CT   CTCTC
                                ||| |||||  ||   |||||
                                ATA TGTGT  GG   GAGAG
                                  A    CG  ___
GAM2460  LOC166765 3'  TAACCATTGGTCTCTC      57527      A  ATC
                                TAAC CA   TGGTCTCTC
                                |||| ||   |||||||||
                                ATTG GT   ACCAGAGAG
                                   _  A__
GAM2460  LOC196337 3'  TATGACACACTCACACACTCCA 57528     A    A  TGGTCT
                                TAT ACACA TC      CTCCA
                                ||| ||||| ||     |||||
                                ATA TGTGT AG     GAGGT
                                  C    G  TGTGT_
GAM2460  LOC254055 3'  TATAACACTGGACAGTCTTTC  57529        AATCT    C
                                TATAACAC     GGTCT TC
                                ||||||||     ||||| ||
                                ATATTGTG     TCAGA AG
                                     ACCTG    A
GAM2460  LOC255106 3'  TAACCAATCTGGTTCT      57530      A       C
                                TAAC CAATCTGGT TCT
                                |||| ||||||||| |||
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                                ATTG GTTAGACCA AGA
                                  _      _
GAM2460 LOC90670 3' AACACAATCATGCCTTTCCA  57531        TG   C
                                AACACAATC  GTCT TCCA
                                |||||||||  |||| ||||
                                TTGTGTTAG  CGGA AGGT
                                     TA    A
GAM2460 LOC92609 3' CATAACACATTCTCTCC     57532        ATCTGG
                                TATAACACA     TCTCTCC
                                |||||||||     |||||||
                                GTATTGTGT     AGAGAGG
                                     A_____
GAM2461 OGT      5' TTGCGCTACTGCAGGGTCACAG 57535        CGATTCT
                                TTGCGCTAC      TCACAG
                                |||||||||      ||||||
                                AACGCGATG      AGTGTC
                                     ACGTCCC
GAM2461 LOC162952 3' TTGCGTTATCCCTCACA     57536      CTACCG
                                TTGCG     ATTCTTCACA
                                |||||     ||||||||||
                                AACGC     TAGGGAGTGT
                                   AA____
GAM2461 LOC254700 5' TTGCTGCGACACTCTTCACAG  57537     _ T  CG
                                TTGC GC AC  ATTCTTCACAG
                                |||| || ||  ||||||||||
                                AACG CG TG  TGAGAAGTGTC
                                  A  C  __
GAM2462 DIM1     3' AATGTAATTAGTTAAGAT    57540          CAT
                                AATGTAATTAGT   GAT
                                ||||||||||||   |||
                                TTACATTAATCA   CTA
                                      ATT
GAM2462 KIAA0410 3' AATGTAATTAGTATGGT     57541          CATGATC
                                AATGTAATTAGT      ATGGT
                                ||||||||||||      |||||
                                TTACATTAATCA      TACCA
                                                 _______
GAM2463 ARHGEF12 3' TCTCTGACCACACCACCT    57544    C   G   C
                                TC CTGA CCAC ATCACCT
                                || |||| |||| |||||||
                                AG GACT GGTG TGGTGGA
                                 A   _   _
GAM2463 BAZ2A    5' TCCCTGAGCCTCAAG       57545         ACCA  CCT
                                TCCCTGAGCC    TCA   AG
                                ||||||||||    |||   ||
                                AGGGACTCGG    AGT   TC
                                              ____  ___
GAM2463 DDEF2    3' CTGAGCCATCATCCCAGA     57546        C   A  T
                                CTGAGCCA CATC CC AGA
                                |||||||| |||| || |||
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                                GACTCGGT GTAG GG TCT
                                   A   _ _
GAM2463  EDG8     3'  TCCCTGACCACCATCAC     57547        G
                                TCCCTGA CCACCATCAC
                                ||||||| ||||||||||
                                AGGGACT GGTGGTAGTG
                                   _
GAM2463  IL2RB    3'  TCCCTGAGCTGCAGAGGAGAC  57548         CAC  TCACCT
                                TCCCTGAGC   CA     AGAC
                                |||||||||   ||     ||||
                                AGGGACTCG   GT     TCTG
                                   AC_  CTCC__
GAM2463  LPIN2    3'  TCCCTGAGCCGTCACCC     57549          ACCA
                                TCCCTGAGCC    TCACCT
                                ||||||||||    ||||||
                                AGGGACTCGG    AGTGGG
                                   C___
GAM2463  ORC2L    3'  TCCCTGAGCACACTGTTCA    57550         _   CA_
                                TCCCTGAGC CAC   TCA
                                ||||||||| |||   |||
                                AGGGACTCG GTG   AGT
                                   T   ACA
GAM2463  PSMB8    3'  TCCCTGAGTCGGCCAAGA    57551         CCACCA  A_  T
                                TCCCTGAG     TC  CC AGA
                                ||||||||     ||  || |||
                                AGGGACTC     AG  GG TCT
                                   _______ CC  T
GAM2463  PSMB8    3'  TCCCTGAGTCGGCCAAGA    57551         CCACCA  A_  T
                                TCCCTGAG     TC  CC AGA
                                ||||||||     ||  || |||
                                AGGGACTC     AG  GG TCT
                                   _______ CC  T
GAM2463  PSMB8    3'  TCCCTGAGTCGGCCAAGA    57551         CCACCA  A_  T
                                TCCCTGAG     TC  CC AGA
                                ||||||||     ||  || |||
                                AGGGACTC     AG  GG TCT
                                   _______ CC  T
GAM2463  ZFHX1B   3'  TCTCTGAACCACACAGTTTTTA 57552    C        _  TCACC
            G                    TC CTGAGCCAC CA     TAG
                                || |||||||| ||     |||
                                AG GACTTGGTG GT     ATC
                                 A        T  CAAAA
GAM2463  BNIP2    3'  CCTGAGCCATCCCAGAC     57553          CCATCA
                                CCTGAGCCA     CCTAGAC
                                |||||||||     |||||||
                                GGACTCGGT     GGGTCTG
                                   A_____
GAM2463  C22orf19 3'  TCCCTGAGACACCAAGAC    57554         C    TC
                                TCCCTGAG CACCA  AC
                                |||||||| |||||  ||
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                                AGGGACTC GTGGT  TG
                                     T    TC
GAM2463  CGR11    3'  TCCCTGAGCTGCATAGAAAGAC 57555        CAC   CACCT
                                TCCCTGAGC   CAT    AGAC
                                |||||||||   |||    ||||
                                AGGGACTCG   GTA    TCTG
                                     AC_   TCTT_
GAM2463  DKFZp434C0923 3'  TCTCTGAGCCACCATCCC    57556    C          A
                                TC CTGAGCCACCATC CC
                                || ||||||||||||| ||
                                AG GACTCGGTGGTAG GG
                                 A          _
GAM2463  FLJ21144  3'  TCCCTGAGCCTTGGTCCTGGAC 57557         ACCATCA   A
                                TCCCTGAGCC      CCT GAC
                                ||||||||||      ||| |||
                                AGGGACTCGG      GGA CTG
                                      AACCA__   C
GAM2463  FLJ22938  3'  CCCCTGCATCACCTGGA     57558       AGCCAC       A
                                TCCCTG     CATCACCT GA
                                ||||||     |||||||| ||
                                GGGGAC     GTAGTGGA CT
                                   _______       C
GAM2463  FLJ23878  3'  TCCCTAAGTCCCGGCCTGGA   57559        _ ACCATCA   A
                                TCCCTGAG CC      CCT GA
                                |||||||| ||      ||| ||
                                AGGGATTC GG      GGA CT
                                     A  GCC____   C
GAM2463  KIAA0310  3'  CCCTGAGCCATCATGTCAGAC  57560         C   CACC
                                CCCTGAGCCA CAT    TAGAC
                                |||||||||| |||    |||||
                                GGGACTCGGT GTA    GTCTG
                                      A   CA__
GAM2463  KIAA1644  3'  CCTGAGCCAACCTGGA      57561         CCATC    A
                                CCTGAGCCA    ACCT GA
                                |||||||||    |||| ||
                                GGACTCGGT    TGGA CT
                                     _____    C
GAM2463  MGC13102  3'  TCCCTGAGGCGCTCTGCTTAGA 57562        CCACCA  AC  _
           C                     TCCCTGAG     TC  CT AGAC
                                 ||||||||     ||  || ||||
                                 AGGGACTC     AG  GA TCTG
                                      CGCG__  AC  A
GAM2463  MGC14161  5'  TCCCTGAGTCATAATCCCCAA  57563        C  CC   A
                                TCCCTGAG CA  ATC CCTAG
                                |||||||| ||  ||| |||||
                                AGGGACTC GT  TAG GGGTT
                                     A  AT   _
GAM2463  MGC2474   3'  CTCGGGCCGCCCACAATGTCTA 57564    _ A   A_    CAC__
           GA                    CT G GCC  CCAT     CTAGA
                                 || | |||  ||||     |||||
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                                GA C CGG  GGTG    GATCT
                                 G C   CG    TTACA
GAM2463  MGC2628   3'  TCCCTGAGCTGTGCATTCCAG  57565        CAC_   CAC
                                TCCCTGAGC    CAT   CTAG
                                |||||||||    |||   ||||
                                AGGGACTCG    GTA   GGTC
                                     ACAC   A__
GAM2463  RAB3GAP   3'  CCTGATCACCCAACTGGAC    57566      GC    AT  C  A
                                CCTGA  CACC  CA CT GAC
                                |||||  ||||  || || |||
                                GGACT  GTGG  GT GA CTG
                                   A_    __  T  C
GAM2463  LOC144509 3'  CCCTGAGCCACGACATCTGGAC 57567          CAT  C  A
                                CCCTGAGCCAC   CA CT GAC
                                ||||||||||   || || |||
                                GGGACTCGGTG   GT GA CTG
                                      CT_  A  C
GAM2463  LOC146512 3'  CCTGTCAACCCATCACCTAG   57568      AGCCA
                                CCTG    CCATCACCTAG
                                ||||    ||||||||||
                                GGAC    GGTAGTGGATC
                                  AGTTG
GAM2463  LOC151201 5'  TCCCAGAAGTCACCTAG     57569      T   CCACCA
                                TCCC GAG     TCACCTAG
                                |||| |||     ||||||||
                                AGGG CTT     AGTGGATC
                                  T   C_____
GAM2463  LOC196707 3'  TCCCAGTCATCACCTAGA    57570      TGAGCCAC
                                TCCC       CATCACCTAGA
                                ||||       ||||||||||
                                AGGG       GTAGTGGATCT
                                  TCA_____
GAM2463  LOC222234 3'  TCCCTGAGCGGAGAACCTAGAC 57571         CACCATC
                                TCCCTGAGC      ACCTAGAC
                                |||||||||      ||||||||
                                AGGGACTCG      TGGATCTG
                                     CCTCT__
GAM2463  LOC256236 3'  TCCCTAAGCCAGATGATCTTAG 57572          CC__   ACC
            AC                   TCCCTGAGCCA    ATC   TAGAC
                                ||||||||||    |||   |||||
                                AGGGATTCGGT    TAG   ATCTG
                                      CTAC   A__
GAM2463  LOC257359 5'  TCCCTGAGTCACCTTGCTGGAC 57573        C    ATCAC  A
                                TCCCTGAG CACC     CT GAC
                                |||||||| ||||     || |||
                                AGGGACTC GTGG     GA CTG
                                     A    AAC__  C
GAM2463  LOC91010  3'  TCCCTAAGCCTAGATACATCTA 57574         ACCAT_  C
            GAC                   TCCCTGAGCC     CA CTAGAC
                                ||||||||||      || ||||||
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                                AGGGATTCGG     GT GATCTG
                                     ATCTAT  A
GAM2464  GNAI3    3'  CATTGTGGGCACTGAATCAATC 57577      A  TT   CC
                                TATT TG  CAC  TGAATCAATC
                                |||| ||  |||  ||||||||||
                                GTAA AC  GTG  ACTTAGTTAG
                                  C  CC  __
GAM2464  TCF12    3'  TTATGTTCACCATAATC     57578          CTG
                                TTATGTTCACC   AATC
                                ||||||||||   ||||
                                AATACAAGTGG   TTAG
                                      TA_
GAM2464  WHSC1    3'  TATTTGTTCACCTAAA      57579      A       C
                                TATT TGTTCACC TGAA
                                |||| |||||||| ||||
                                ATAA ACAAGTGG ATTT
                                  _      _
GAM2464  AP1GBP1  3'  CATTTTCACCCTGAATTAAT   57580     G         C
                                TAT TTCACCCTGAAT AAT
                                ||| ||||||||||| |||
                                GTA AAGTGGGACTTA TTA
                                  A          A
GAM2464  AP1GBP1  3'  CATTTTCACCCTGAATTAAT   57580     G         C
                                TAT TTCACCCTGAAT AAT
                                ||| ||||||||||| |||
                                GTA AAGTGGGACTTA TTA
                                  A          A
GAM2464  BIA2     3'  TATCAGACCATTCTGAATCAAT 57581      TGT   CC
                                TATTA   TCA  CTGAATCAAT
                                |||||   |||  ||||||||||
                                ATAGT   GGT  GACTTAGTTA
                                   CT_   AA
GAM2464  GPA33    3'  TGTTCACTTTAAATCAAT    57582        CC
                                TGTTCAC  TGAATCAAT
                                |||||||  |||||||||
                                ACAAGTG  ATTTAGTTA
                                     AA
GAM2464  MGC15634 3'  TATTAATGTTTGAATCAAT   57583      _   CACCC
                                TATTA TGTT    TGAATCAAT
                                ||||| ||||    |||||||||
                                ATAAT ACAA    ACTTAGTTA
                                   T   _____
GAM2464  LOC222484 5'  TGTTCCCATTTTGAATCAAT  57584      A  C___
                                TGTTC CC    TGAATCAAT
                                ||||| ||    |||||||||
                                ACAAG GG    ACTTAGTTA
                                   _ TAAA
GAM2464  LOC92181 5'  TTATGTTTGCACCATCAAT   57585        __   CTGA
                                TTATGTT  CACC    ATCAAT
                                |||||||  ||||   ||||||
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                                AATACAA  GTGG   TAGTTA
                                   AC   ____
GAM2465  CACNA1B  3'  CATGCAGGCGTCTGAGC    57588   C      A  CAC
                                CA TGCAGGCGT TG   AGC
                                || |||||||| ||   |||
                                GT ACGTCCGCA AC   TCG
                                 _       G  ___
GAM2465  CENPB    3'  CACTCTGGCTCCATGCACAGCG 57589    GCA   G_
                                CACT   GGC  TATGCACAGCG
                                ||||   |||  ||||||||||
                                GTGA   CCG  GTACGTGTCGC
                                  GA_   AG
GAM2465  DNAJB9   3'  ACTGTAGAAAGGCACAGCG   57590    C   CGTAT
                                ACTG AGG    GCACAGCG
                                |||| |||    ||||||||
                                TGAC TCT    CGTGTCGC
                                  A   TTC__
GAM2465  MEF2B    5'  CTGCAGGCGTACTCCACAG   57591          G_
                                CTGCAGGCGTAT  CACAG
                                ||||||||||||  |||||
                                GACGTCCGCATG  GTGTC
                                      AG
GAM2465  PKP2     3'  TACACTGGAGGCCCAATGGCG  57592       C   G  TGCACA
                                TACACTG AGGC TA     GCG
                                ||||||| |||| ||     |||
                                ATGTGAC TCCG GT     CGC
                                   C   G  TAC___
GAM2465  DKFZp434N0650 3'  ACTGCAGGCAAGGCGGCG    57593         TAT  ACA
                                ACTGCAGGCG   GC   GCG
                                ||||||||||   ||   |||
                                TGACGTCCGT   CG   CGC
                                     TC_  C__
GAM2465  FLJ13193  5'  TGCGCTGCGCTGCACAGC    57594     AG_   A
                                TGC   GCGT TGCACAGC
                                |||   |||| ||||||||
                                ACG   CGCG ACGTGTCG
                                  CGA   _
GAM2465  FLJ13263  3'  CACACTGCAGAGCACAG     57595          CGTAT
                                TACACTGCAGG    GCACAG
                                ||||||||||    ||||||
                                GTGTGACGTCT    CGTGTC
                                      _____
GAM2465  HSPC009   3'  TACACAGCAAGTGTGCA     57596      T    C  AT
                                TACAC GCAGG GT  GCA
                                ||||| ||||| ||  |||
                                ATGTG CGTTC CA  CGT
                                   T    A  __
GAM2465  IRF7     5'  TGACTGCAGGTGTGGCCGGCG  57597   C      C  AT  ACA
                                A ACTGCAGG GT  GC   GCG
                                | |||||||| ||  ||   |||
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                                A TGACGTCC CA  CG   CGC
                                 C       A  C_  GC_
GAM2465  IRF7     5'  TGACTGCAGGTGTGGCCGGCG  57597   C      C  AT  ACA
                                A ACTGCAGG GT  GC   GCG
                                | |||||||| ||  ||   |||
                                A TGACGTCC CA  CG   CGC
                                 C       A  C_  GC_
GAM2465  IRF7     5'  TGACTGCAGGTGTGGCCGGCG  57597   C      C  AT  ACA
                                A ACTGCAGG GT  GC   GCG
                                | |||||||| ||  ||   |||
                                A TGACGTCC CA  CG   CGC
                                 C       A  C_  GC_
GAM2465  IRF7     5'  TGACTGCAGGTGTGGCCGGCG  57597   C      C  AT  ACA
                                A ACTGCAGG GT  GC   GCG
                                | |||||||| ||  ||   |||
                                A TGACGTCC CA  CG   CGC
                                 C       A  C_  GC_
GAM2465  KIAA0939 3'  ACACTGCAGGGCCTCAGCACAG 57598         C  AT__
                                ACACTGCAGG GT    GCACAG
                                |||||||||| ||    ||||||
                                TGTGACGTCC CG    CGTGTC
                                      _  GAGT
GAM2465  KIAA1814 3'  TACCTGCAGAAGGGCACAGCG  57599     A      CGTAT
                                TAC CTGCAGG     GCACAGCG
                                ||| |||||||     ||||||||
                                ATG GACGTCT     CGTGTCGC
                                  _       TCC__
GAM2465  LSM1     5'  TGCTGCAATGCACAGC      57600     AG   T
                                TGC  GCG ATGCACAGC
                                |||  ||| |||||||||
                                ACG  CGT TACGTGTCG
                                  A_  _
GAM2465  MGC15397 3'  ACACTGCACATTGATGCACAG  57601         GGCGT
                                ACACTGCA     ATGCACAG
                                ||||||||     ||||||||
                                TGTGACGT     TACGTGTC
                                     GTAAC
GAM2465  RAI1     3'  TGCGGGCGCACGACGCACGGCG 57602     A      ___    A
                                TGC GGCGTAT   GCAC GCG
                                ||| |||||||   |||| |||
                                ACG CCGCGTG   CGTG CGC
                                  C      CTG    C
GAM2465  LOC149951 3'  CAGTGCAGGCGGCCCATGGCG  57603    C       TAT  A  __
                                CA TGCAGGCG   GC CA  GCG
                                || ||||||||   || ||  |||
                                GT ACGTCCGC   CG GT  CGC
                                 C       ___  G  AC
GAM2465  LOC255481 3'  ACTGCAGGCCACCATGGCG   57604         G   G  CA
                                ACTGCAGGC TAT CA  GCG
                                ||||||||| ||| ||  |||
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                                TGACGTCCG GTG GT  CGC
                                     _  _ AC
GAM2466  CD1D     3'  TATACTTGACAACAAGCAG   57607       A  GCGA
                                TATATT GA   AACAAGCAG
                                |||||| ||   |||||||||
                                ATATGA CT   TTGTTCGTC
                                   A  G___
GAM2466  FGF2     3'  TCTATATTGGGCAAAAAGCAG  57608        AGA     CA
                                TCTATATT  GCGAAA  AGCAG
                                ||||||||  ||||||  |||||
                                AGATATAA  CGTTTT  TCGTC
                                     CC_    __
GAM2466  PCDH7    3'  TACAACAAGTGGAACAAGCAG  57609    G    ____
                                TA AGCGA   AACAAGCAG
                                || |||||   |||||||||
                                AT TTGTT   TTGTTCGTC
                                 G    CACC
GAM2466  RNMT     3'  TCTACATTGGAGTTTCTGGCAG 57610        A   CGAAACAA
                                TCTATATT GAG       GCAG
                                |||||||| |||       ||||
                                AGATGTAA CTC       CGTC
                                     C   AAAGAC__
GAM2466  RRAS2    3'  TCTATTTAGAGTAACAGTAGGC 57611      A     CG AACAA_
              AG                  TCTAT TTAGAG  A     GCAG
                                |||||  ||||||  |     ||||
                                AGATA AATCTC  T     CGTC
                                   _     AT GTCATC
GAM2466  FEZ2     3'  ACCAGTGGTGAAACAAGCAG   57612      AGC_
                                ATTAG    GAAACAAGCAG
                                |||||    ||||||||||||
                                TGGTC    CTTTGTTCGTC
                                   ACCA
GAM2466  FLJ23309 3'  TCATACACATGAGACAAGCAG  57613    _    TA   CGAA
                                TC TATAT  GAG    ACAAGCAG
                                || |||||  |||    ||||||||
                                AG ATGTG  CTC    TGTTCGTC
                                 T    TA  _____
GAM2466  KIAA0923 3'  TCTATGTACAGAGACAAGCAG  57614      AT_    CGAA
                                TCTAT   TAGAG    ACAAGCAG
                                |||||   |||||    ||||||||
                                AGATA   GTCTC    TGTTCGTC
                                   CAT    _____
GAM2466  KIAA1209 3'  TATATTAGAAACATGATGAGCA 57615          _  AAACA
              G                   TATATTAGAG CG     AGCAG
                                ||||||||||  ||     |||||
                                ATATAATCTT GT     TCGTC
                                      T  ACTAC
GAM2466  KIAA1431 3'  TCTATTTACAAAAACAAGCAG  57616      A   G GC
                                TCTAT TTA A  GAAACAAGCAG
                                ||||| ||| |  ||||||||||
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                                AGATA AAT T  TTTTGTTCGTC
                                  _  G __
GAM2466  LOC133418 3'  TCTAAATTAGGGCCTGAGCAG  57617     T    A  GAAACA
                                TCTA ATTAG GC     AGCAG
                                |||| ||||| ||     |||||
                                AGAT TAATC CG     TCGTC
                                  T    C  GAC___
GAM2466  LOC143916 3'  TCCATATTGGGCTGCAAGAATA 57618        AGA__   _  C
           AGCAG                   TCTATATT    GCGA AA AAGCAG
                                |||||||||    |||| || ||||||
                                AGGTATAA    CGTT TT TTCGTC
                                     CCCGA   C  A
GAM2466  LOC146420 3'  TCTAAATTAGAACTTGTGGGCA 57619     T      GAAACAA
           G                    TCTA ATTAGAGC      GCAG
                                |||| |||||||||      ||||
                                AGAT TAATCTTG      CGTC
                                  T       AACACC_
GAM2466  LOC253019 3'  TCCAAAAGCGAAATAAG     57620     TATT       C
                                TCTA    AGAGCGAAA AAG
                                ||||    ||||||||| |||
                                AGGT    TTTCGCTTT TTC
                                  ____        A
GAM2466  LOC253975 3'  TCCAAAAGCGAAATAAG     57620     TATT       C
                                TCTA    AGAGCGAAA AAG
                                ||||    ||||||||| |||
                                AGGT    TTTCGCTTT TTC
                                  ____        A
GAM2466  LOC55833  3'  TCTATATGAAGACAAACAG   57621       TAGAGC  _
                                TCTATAT     GAA ACAAGCAG
                                |||||||     ||| ||||||||
                                AGATATA     CTT TGTTTGTC
                                    ______  C
GAM2467  CLOCK    3'  TAATTTTTTCCCCCGAC     57624          GCACG   _
                                TAATTTTTTCC     CCCG C
                                ||||||||||     |||| |
                                ATTAAAAAAGG     GGGC G
                                     _____   T
GAM2467  LIG4     5'  TCTGATTTTTTCTGCACG    57625     A      C
                                TCT ATTTTTTC GCACG
                                ||| |||||||| |||||
                                AGA TAAAAAAG CGTGC
                                  C       A
GAM2468  ATP11A   3'  CGGGCGTGAGGGCCGGCTCCTC 57628      CAA  CT      C
           CT                    CGGGC   AG  CCGGCTCC CCT
                                |||||   ||  |||||||| |||
                                GCCCG   TC  GGCCGAGG GGA
                                   CAC  CC       A
GAM2468  ATP2B4   5'  GGGCTGGGTCTCCTCCCCCT   57629     CAAAG   GGC
                                GGGC    CTCC   TCCCCCT
                                ||||    ||||   |||||||
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                                CCCG    GAGG   AGGGGGA
                                  ACCCA   ___
GAM2468 BAZ1B    3' GGGCTGGGCTCCAACACCCC   57630     CAAA      T
                                GGGC    GCTCCGGC CCCC
                                ||||    |||||||| ||||
                                CCCG    CGAGGTTG GGGG
                                  ACC_      T
GAM2468 EIF2C1   5' CGGGCCGGGCTCGGCTCCCC   57631      AAA   C
                                CGGGCC   GCTC GGCTCCCC
                                ||||||   |||| ||||||||
                                GCCCGG   CGAG CCGAGGGG
                                   CC_   _
GAM2468 ENTPD1   5' GGGCCAAGGAAAACTTCCCCT  57632       AGCTCC    C
                                GGGCCAA     GGCT CCCCT
                                |||||||     |||| |||||
                                CCCGGTT     TTGA GGGGA
                                    CCTT__    A
GAM2468 ETV3     5' CGCGGCGTCTCCGGCTCCTCCT 57633    _  CAAAG        C
                                CG GGC     CTCCGGCTCC CCT
                                || |||     |||||||||| |||
                                GC CCG     GAGGCCGAGG GGA
                                 G   CA___        A
GAM2468 FZD1     5' GGCCGGCGGCGGCTCCCCCT   57634     AAA  TC
                                GGCC   GC  CGGCTCCCCCT
                                ||||   ||  ||||||||||
                                CCGG   CG  GCCGAGGGGGA
                                  C__  CC
GAM2468 GALNT7   3' GGGCCAAAGTGCTCTTGCATC  57635        __    CG  _
                                GGGCCAAA  GCTC  GC TC
                                ||||||||  ||||  || ||
                                CCCGGTTT  CGAG  CG AG
                                    CA    AA  T
GAM2468 GCN5L2   3' GGGCTGAACTTCCAACCCC    57636     CAA    _
                                GGGC   AGCT CCGGCTCC
                                ||||   |||| ||||||||
                                CCCG   TTGA GGTTGGGG
                                  AC_    A
GAM2468 GNA11    5' GGCCTGGCGGGCTCCCCC     57637     AAA  TCC
                                GGCC   GC   GGCTCCCCC
                                ||||   ||   |||||||||
                                CCGG   CG   CCGAGGGGG
                                  AC_  C__
GAM2468 HIRA     3' GGGCAGAGCTCCAGCCC      57638      CAA
                                GGGC   AGCTCCGGCTC
                                ||||   ||||||||||
                                CCCG   TCGAGGTCGGG
                                  TC_
GAM2468 MPZ      3' CAGGCCGGAGCTCCGGGCTC   57639       AA      _
                                CGGGCC  AGCTCCGG CTC
                                ||||||  |||||||| |||
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GTCCGG TCGAGGCC GAG
CC C
GAM2468 NFRKB 5' CGGGCCCGGCTCCCC 57640 AAAGCTC
CGGGCC CGGCTCCCC
GCCCGG GCCGAGGGG
GAM2468 OGDH 3' CAGGCCAAGGCTCTCTCC 57641 A CGG
CGGGCCAA GCTC CTCC
GTCCGGTT CGAG GAGG
C A__
GAM2468 PDE4C 3' GGGCTCAAGCGATCCCC 57642 CA TCC C
GGGC AAGC GG TCCCC
CCCG TTCG CT AGGGG
AG ___ _
GAM2468 PDXK 5' CGGGCTCCGGCCCCGGCTCCCC 57643 CAAA
CGGGC GCTCCGGCTCCCC
GCCCG CGGGGCCGAGGGG
AGGC
GAM2468 WHSC1 3' CGAGCCAAGGACTTTTCCC 57644 A CTCC CC_
CGGGCC AAG GGCT CCC
GCTCGG TTC CTGA GGG
_ ____ AAA
GAM2468 ARAP3 5' GGGTCAAAGCTCTGCTCC 57645 C CG
GGG CAAAGCTC GCTCC
CCC GTTTCGAG CGAGG
A A_
GAM2468 BCAA 5' AGGCAGAGGCTCCGGCTCCTCC 57646 CAAA C
T GGGC GCTCCGGCTCC CCT
TCCG CGAGGCCGAGG GGA
TCTC A
GAM2468 C11orf25 5' CGGTCTAGCGTCCGGCTCCCC 57647 GCCAA _
CGG AGC TCCGGCTCCCC
GCC TCG AGGCCGAGGGG
AGA__ C
GAM2468 CG1I 3' GGTCCAGGAAGAGCTCCCCCT 57648 G __ CTCC
GG CCA AAG GGCTCCCCCT
CC GGT TTC TCGAGGGGGA
A CC ____
GAM2468 DARS 5' CAGGCCAAAGGGGCTTCTCCCT 57649 CTCC _ C
CGGGCCAAAG GGCT C CCCT

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                                GTCCGGTTTC   CCGA G GGGA
                                     C___    A A
GAM2468 DKFZP434J193 3' GGGTTAAAGCTCCTTCCC    57650     CC       GGC
                                GGG  AAAGCTCC   TCCC
                                |||  ||||||||   ||||
                                CCC  TTTCGAGG   AGGG
                                  AA       A__
GAM2468 DKFZP434P0111 3' GCCGGGGCTCCAGCCACCTCT  57651     AAA       TC  C
                                GCC   GCTCCGGC  CC CT
                                |||   ||||||||  || ||
                                CGG   CGAGGTCG  GG GA
                                  CCC       GT  A
GAM2468 DNAJC5   3' CGTGGCCAGGCGCCGGCTCCTC 57652    _    AA  T       C
             CT                   CG GGCCA  GC CCGGCTCC CCT
                                || |||||  || |||||||| |||
                                GC CCGGT  CG GGCCGAGG GGA
                                 A    C_  C       A
GAM2468 DTX2     5'  CGGGCTGCAGCTCCGGCTCGGC 57653      CAA         CC
             CT                   CGGGC   AGCTCCGGCTC  CCT
                                |||||   ||||||||||  |||
                                GCCCG   TCGAGGCCGAG  GGA
                                   ACG         CC
GAM2468 FLJ10704  3' CGGGCCAAGCTCCTTCT     57654         A    GG
                                CGGGCCAA GCTCC  CT
                                |||||||| |||||  ||
                                GCCCGGTT CGAGG  GA
                                     _    AA
GAM2468 FLJ14566 5' GGCTGAGGGCCAGCTCCTCCT  57655     CAA  CT      C
                                GGC   AG  CCGGCTCC CCT
                                |||   ||  |||||||| |||
                                CCG   TC  GGTCGAGG GGA
                                  AC_  CC       A
GAM2468 HSPC228   3' GGGCCAAAGCTTGCTGACCCT  57656          CCG   CC
                                GGGCCAAAGCT   GCT  CCCT
                                ||||||||||   |||  ||||
                                CCCGGTTTCGA   CGA  GGGA
                                      A__   CT
GAM2468 HSPF2     5'  GGCTCAAAGTTCCTGCTCCCCC 57657     _    C   G
             T                    GGC CAAAG TCC GCTCCCCCT
                                ||| ||||| ||| |||||||||
                                CCG GTTTC AGG CGAGGGGGA
                                  A    A  A
GAM2468 KIAA0159  5'  CGGGCCAAGGCTCCGGCT    57658         A
                                CGGGCCAA GCTCCGGCT
                                |||||||| |||||||||
                                GCCCGGTT CGAGGCCGA
                                     C
GAM2468 KIAA0391  3' GGGCCTAAAGTGATCCTCCT   57659       _   CTCC  C   C
                                GGGCC AAAG    GG TCC CCT
                                ||||| ||||    || ||| |||
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                                CCCGG TTTC   CT AGG GGA
                                  A   A___ _  A
GAM2468 KIAA0444 3' CGGGCCAAGGCTTGGTCAGCTC 57660       A  C___
             C                   CGGGCCAA GCT   CGGCTCC
                                 |||||||| |||   |||||||
                                 GCCCGGTT CGA   GTCGAGG
                                     C  ACCA
GAM2468 KIAA0669 5' GGCTTCTCCGGCTCCTCCT   57661    CAAAG       C
                                 GGC    CTCCGGCTCC CCT
                                 |||    |||||||||| |||
                                 CCG    GAGGCCGAGG GGA
                                  AA___        A
GAM2468 KIAA1211 3' GGGCCAAATGCTTCACATGTCC 57662        _  _ _ GC
                                 GGGCCAAA GCT C CG  TCC
                                 |||||||| ||| | ||  |||
                                 CCCGGTTT CGA G GT  AGG
                                     A  A T  AC
GAM2468 KIAA1399 5' GGGCTCAGCAGCTCCCCC   57663    CAA  TCC
                                 GGGC  AGC  GGCTCCCCC
                                 ||||  |||  |||||||||
                                 CCCG  TCG  TCGAGGGGG
                                  AG_  ___
GAM2468 MGC13071 3' GGCTGGAGACCAGCTCCCTCT 57664    CAA CT      C
                                 GGC  AG  CCGGCTCCC CT
                                 |||  ||  ||||||||| ||
                                 CCG  TC  GGTCGAGGG GA
                                  ACC  T_      A
GAM2468 MGC15437 3' CGGGCCAGCAGCTCCCC    57665       AA  TCC     C
                                 CGGGCCA  GC  GGCTCCC C
                                 |||||||  ||  ||||||| |
                                 GCCCGGT  CG  TCGAGGG G
                                    __ ___     A
GAM2468 SOX30   5' CGGGTTTTCCGGCTCTTCCT  57666    CCAAAGC      CC
                                 CGGG     TCCGGCTC  CCT
                                 ||||     ||||||||  |||
                                 GCCC     AGGCCGAG  GGA
                                  AAA____      AA
GAM2468 LOC148114 5' CGTGGCTAAGGTTGGGCTCCCC 57667   _  CA  CTCC
                                 CG GGC  AAG   GGCTCCCC
                                 || |||  |||   ||||||||
                                 GC CCG  TTC   CCGAGGGG
                                  A  A_  CAAC
GAM2468 LOC149157 5' GGCTCTCTGGCTCCCCC    57668    CAAAG  C
                                 GGC    CTC GGCTCCCCC
                                 |||    ||| |||||||||
                                 CCG    GAG CCGAGGGGG
                                  A____  A
GAM2468 LOC149297 5' CGGGCCGGAGCCCCCCGCCCCT 57669      AA    GG  C
                                 CGGGCC  AGCTCC  CT CCCCT
                                 ||||||  ||||||  || |||||
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                                GCCCGG  TCGGGG  GG GGGGA
                                   CC      __  C
GAM2468  LOC155081 5'  CGAGCTCCTTCTCCGGCTCCTC 57670      CAAAG        C
                 CT                  CGGGC     CTCCGGCTCC CCT
                                     |||||     |||||||||| |||
                                     GCTCG     GAGGCCGAGG GGA
                                       AGGAA         A
GAM2468  LOC199927 5'  CGGCCCCTTCGGCTCCCTCT   57671     G  AAAG  C       C
                                     CGG CC    CT CGGCTCCC CT
                                     ||| ||    || |||||||| ||
                                     GCC GG    GA GCCGAGGG GA
                                       G  ____  A       A
GAM2468  LOC200058 3'  CGGATTGAGGCTCCTGCTCCCC 57672     CCAAA    G
                 CT                  CGGG     GCTCC GCTCCCCCT
                                     ||||     ||||| |||||||||
                                     GCCT     CGAGG CGAGGGGGA
                                       AACTC     A
GAM2468  LOC200084 5'  CGGGCTCGGGCTCCGGCTC    57673      CAAA
                                     CGGGC    GCTCCGGCTC
                                     |||||    ||||||||||
                                     GCCCG    CGAGGCCGAG
                                       AGCC
GAM2468  LOC222228 5'  CGAGCTCCTTCTCCGGCTCCTC 57670      CAAAG        C
                 CT                  CGGGC     CTCCGGCTCC CCT
                                     |||||     |||||||||| |||
                                     GCTCG     GAGGCCGAGG GGA
                                       AGGAA         A
GAM2468  LOC253181 5'  CGGGCCAAGCTGCCTCCCTCT  57674        A   CCG  TC  _
                                     CGGGCCAA GCT   GC  CCC CT
                                     |||||||| |||   ||  ||| ||
                                     GCCCGGTT CGA   CG  GGG GA
                                        _  ___  GA   A
GAM2468  LOC254266 5'  GGGCCGAAGCCCCGCCCC    57675      A       GCTC
                                     GGGCC AAGCTCCG    CCCC
                                     ||||| ||||||||    ||||
                                     CCCGG TTCGGGGC    GGGG
                                       C       ____
GAM2468  LOC255535 5'  CGAGGTCAGAGCCAGCTCCCTC 57676     CCAA  CT       C
                 T                    CGGG    AG  CCGGCTCCC CT
                                      ||||    ||  ||||||||| ||
                                      GCTC    TC  GGTCGAGGG GA
                                        CAG_  TC        A
GAM2468  LOC51055  5'  GGCCAAAGCTCCTTTCCC    57677          GGC
                                     GGCCAAAGCTCC   TCCC
                                     ||||||||||||   ||||
                                     CCGGTTTCGAGG   AGGG
                                           AA_
GAM2468  LOC89890  5'  GGACCCGGCTCTGGCTCCTCCT 57678      AAA   C     C
                                     GGGCC   GCTC GGCTCC CCT
                                     |||||   |||| |||||| |||
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                                CCTGG   CGAG CCGAGG GGA
                                   GC_   A     A
GAM2469  C18orf1   3'  TGGGATTTCTTGTGGCTTGGG  57681       ACTAC   CCC
                                TGGGATTT    GGC   TGGG
                                ||||||||    |||   ||||
                                ACCCTAAA    CCG   ACCC
                                    GAACA   A__
GAM2469  EMP1      3'  TGGGATTTTCGTATTTTCCTGG 57682       ACTACGGCC
           GA                     TGGGATTT       CCTGGGA
                                ||||||||       |||||||
                                ACCCTAAA       GGACCCT
                                    AGCATAAAA
GAM2469  IL17R     3'  TGGGATCTGGGCGGTCCCTGGG 57683        ACTA   C
                                TGGGATTT    CGG CCCTGGG
                                ||||||||    ||| |||||||
                                ACCCTAGA    GCC GGGACCC
                                    CCC_   A
GAM2469  SCG2      3'  TGGGATTTGCTTGGGGTGGGA  57684       A  AC  CCCC
                                TGGGATTT CT  GG    TGGGA
                                |||||||| ||  ||    |||||
                                ACCCTAAA GA  CC    ACCCT
                                    C  A_  CC__
GAM2469  STMN2     3'  GGGATTTACTATTGGTGGG   57685         C_  CCCC
                                GGGATTTACTA  GG    TGGG
                                ||||||||||  ||    ||||
                                CCCTAAATGAT  CC    ACCC
                                     AA  _____
GAM2469  FLJ12355  3'  TAGGAGGACCTGTGGCCCCTGG 57686      TTTA  AC
           G                     TGGGA    CT  GGCCCCTGGG
                                |||||    ||  ||||||||||
                                ATCCT    GA  CCGGGGACCC
                                   CCTG  CA
GAM2469  FLJ14803  3'  TGGAATTTACTAATTACTGGG  57687          CGGCCC
                                TGGGATTTACTA     CTGGG
                                ||||||||||||     |||||
                                ACCTTAAATGAT     GACCC
                                     TAAT__
GAM2469  FLJ32468  5'  TGGGATTCACTGCGGGGATCCC 57688        A  G_______  CCTG
           AGG                    GGATTTACT CG       CC    G
                                |||||||| ||       ||   |
                                CCTAAGTGA GC       GG    C
                                    C  CCCTIIIA  GTCC
GAM2469  KIAA0212  3'  GACAGCCTGTGGCCCCTGGGA  57689     TTA  AC
                                GAT   CT  GGCCCCTGGGA
                                |||   ||  ||||||||||
                                CTG   GA  CCGGGGACCCT
                                  TCG  CA
GAM2469  MGC15716  3'  TGGCATTTGTGCCCCCTGGGA  57690     G    ACTACG    _
                                TGG ATTT     GCCCC TGGGA
                                ||| ||||     ||||| |||||
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                                ACC TAAA     CGGGG ACCCT
                                  G   CA____    G
GAM2469  TTY7     3'  TGGGATTCACTGTCTGGG    57691          ACGGCCC
                                TGGGATTTACT      CTGGG
                                ||||||||||      |||||
                                ACCCTAAGTGA      GACCC
                                      CA_____
GAM2469  WDR7     3'  TGGGGTGGGCAGGCCCCTGGGA 57692      ATTTACTAC
                                TGGG       GGCCCCTGGGA
                                ||||       ||||||||||
                                ACCC       CCGGGGACCCT
                                  CACCCGT__
GAM2469  LOC115509 5'  CGGGCGCTGGCGGCCCCTGGGA 57693      ATTTACTA
                                TGGG       CGGCCCCTGGGA
                                ||||       ||||||||||
                                GCCC       GCCGGGGACCCT
                                  GCGACC__
GAM2469  LOC127534 3'  TGGGATTTGGTGCCAGTGGG   57694        ACTACG   CC
                                TGGGATTT     GCC  TGGG
                                ||||||||     |||  ||||
                                ACCCTAAA     CGG  ACCC
                                     CCA___   TC
GAM2469  LOC146337 5'  TGGGGTCTAGACCTCCCTGGGA 57695      A    CTAC   __
                                TGGG TTTA    GGCC  CCTGGGA
                                |||| ||||    ||||  |||||||
                                ACCC AGAT    CTGG  GGACCCT
                                  C   _____   AG
GAM2469  LOC147151 3'  TGGGATCTGCTGGCTGGG    57696        A  AC   CCC
                                TGGGATTT CT  GGC   TGGG
                                |||||||| ||  |||   ||||
                                ACCCTAGA GA  CCG   ACCC
                                     C  __   ____
GAM2469  LOC152485 3'  TGAGATCCAAGTGGTTCTTGGG 57697         CTAC  CCCC
                                TGGGATTTA    GG    TGGG
                                |||||||||    ||    ||||
                                ACTCTAGGT    CC    ACCC
                                     TCA_  AAGA
GAM2469  LOC256223 3'  TGGGATCTGCTGGCTGGG    57696        A  AC   CCC
                                TGGGATTT CT  GGC   TGGG
                                |||||||| ||  |||   ||||
                                ACCCTAGA GA  CCG   ACCC
                                     C  __   ____
GAM2470  IGF1     3'  GGGCCTCTGTCTTATCTG    57700           __
                                GGGCCTCTGTCT  TTTG
                                ||||||||||||  ||||
                                CCCGGAGACAGA  AGAC
                                       AT
GAM2470  LIFR     3'  GGGTCTCTAGTCTTAGAA    57701     C   _   TT
                                GGG CTCT GTCT  TGGAA
                                ||| |||| ||||  |||||
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                                CCC GAGA CAGA  ATCTT
                                  A   T   __
GAM2470 MERTK    3' GGCTTGATTTTTGGAATGT   57702    CTC  TC      C
                                GGC   TG  TTTTGGAA GT
                                |||   ||  |||||||| ||
                                CCG   AC  AAAACCTT CA
                                  A__  TA       A
GAM2470 PLXNA2   3' ACTGGCCTCTGTTTTTGCGAA 57703    G       C    _
                                AC GGCCTCTGT TTTTG GAA
                                || |||||||| ||||| |||
                                TG CCGGAGACA AAAAC CTT
                                 A        _    G
GAM2470 VIPR1    3' CAGGCCTCTGTCCCCGGCGT   57704            T  AA
                                CGGGCCTCTGTCTTT GG  CGT
                                |||||||||||||| ||  |||
                                GTCCGGAGACAGGGG CC  GCA

                                      _  __
GAM2470 ARHGEF3  5' CGGGCCTGCCCTTTGG     57705       CT
                                CGGGCCT  GTCTTTTGG
                                |||||||  |||||||||
                                GCCCGGA  CGGGAAACC

                                    __
GAM2470 DKFZp761G0313 3' GAGCCTACCACTTTGGAATGT  57706       _ TG CT     C
                                GGGCCT C  T  TTTGGAA GT
                                |||||| |  |  ||||||| ||
                                CTCGGA G  G  AAACCTT CA
                                    T GT __      A
GAM2470 FLJ14810 3' GGTCTCAGCCTTGGAGCGT   57707    GC   T    TT    A
                                GG  CTC GTCT  TGGA CGT
                                ||  ||| ||||  |||| |||
                                CC  GAG CGGA  ACCT GCA
                                 A_   T    __    C
GAM2470 RHOBTB2  3' GGGCCTCTGTTTATAGAA    57708         CTTT
                                GGGCCTCTGT    TGGAA
                                ||||||||||    |||||
                                CCCGGAGACA    ATCTT
                                      AAT_
GAM2470 LOC145868 3' AGGCCTCTGTCTTTAAAC    57709            TG
                                GGGCCTCTGTCTTT  GAAC
                                ||||||||||||||  ||||
                                TCCGGAGACAGAAA  TTTG

                                      __
GAM2470 LOC221495 5' CGTGCCTTCCATTTGGGGCGT  57710    G    CTG  _    AA
                                CG GCCT   TCT TTTGG  CGT
                                || ||||   ||| |||||  |||
                                GC CGGA   AGG AAACC  GCA
                                 A    ____   T    CC
GAM2471 SPAG11   3' TTTATCAGCTCTTCACCTTTGG 57713      G   _______      III
           TGCTAAAT                GCTC TTTA     GTGCTAAA   T
                                |||| ||||     ||||||||   |
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                                CGAG AAGT     CACGATTT   A
                                  _   GGAAAC       III
GAM2471  SPAG11   3'  TTTATCAGCTCTTCACCTTTGG 57713      G   _______      III
            TGCTAAAT                GCTC TTTA     GTGCTAAA   T
                                |||| ||||     ||||||||   |
                                CGAG AAGT     CACGATTT   A
                                  _   GGAAAC       III
GAM2471  SPAG11   3'  TTTATCAGCTCTTCACCTTTGG 57713      G   _______      III
            TGCTAAAT                GCTC TTTA     GTGCTAAA   T
                                |||| ||||     ||||||||   |
                                CGAG AAGT     CACGATTT   A
                                  _   GGAAAC       III
GAM2471  SPAG11   3'  TTTATCAGCTCTTCACCTTTGG 57713      G   _______      III
            TGCTAAAT                GCTC TTTA     GTGCTAAA   T
                                |||| ||||     ||||||||   |
                                CGAG AAGT     CACGATTT   A
                                  _   GGAAAC       III
GAM2471  DEGS     3'  TTTATTAGCTTTTTAATA    57714         CG
                                TTTATTAGCT  TTTAGTG
                                ||||||||||  |||||||
                                AAATAATCGA  AAATTAT
                                     A_
GAM2471  DEGS     3'  TTTATTAGCTTTTTAATA    57714         CG
                                TTTATTAGCT  TTTAGTG
                                ||||||||||  |||||||
                                AAATAATCGA  AAATTAT
                                     A_
GAM2471  MGC3251  3'  TTTATTAGCTGTTCAATA    57715         C
                                TTTATTAGCT GTTTAGTG
                                |||||||||| ||||||||
                                AAATAATCGA CAAGTTAT
                                     _
GAM2471  NSE1     3'  TTTATTAGCCTGTTGCTAA    57716         TC  TTAG
                                TTTATTAGC  GT    TGCTAA
                                |||||||||  ||    ||||||
                                AAATAATCG  CA    ACGATT
                                     GA  ____
GAM2471  NXPH3    3'  CTTATTAGCTTCACAGAGTGCT 57717          _   TT
            A                    TTTATTAGCT CGT  AGTGCTA
                                |||||||||| |||  |||||||
                                GAATAATCGA GTG  TCACGAT
                                     A   TC
GAM2471  SSB      3'  TTTATTAGTTAGTTTGTACTAA 57718         CTC    A
                                TTTATTAG   GTTT GTGCTAA
                                ||||||||   |||| |||||||
                                AAATAATC   CAAA CATGATT
                                     AAT    _
GAM2471  LOC221017 5'  TTTATCAGCTCCTGATGTGCTA 57719           GTTTA
                                TTTATTAGCTC    GTGCTA
                                ||||||||||     ||||||
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                                AAATAGTCGAG    CACGAT
                                     GACTA
GAM2472 SFRS12   3' TCAGTTTTTTAATCCACTTATT 57722       A    TTT
                                TCAGTTTT TAATCT   TTTATT
                                |||||||| ||||||   ||||||
                                AGTCAAAA ATTAGG   GAATAA
                                    A     T__
GAM2472 LOC157697 5' TCAGTTTCCTTTTTTTAT    57723       ATAAT
                                TCAGTTTT    CTTTTTTTAT
                                ||||||||    ||||||||||
                                AGTCAAAG    GAAAAAAATA
                                            _____
GAM2473 ANKH     3' GTCCAGGGGAGGAGGACAC    57726      A___
                                GTCCG   AGGAGGACAC
                                |||||   ||||||||||
                                CAGGT   TCCTCCTGTG
                                   CCCC
GAM2473 BACE     3' AGCTCTTGTGGTGGAGGACA   57727    A  C  CCGAA
                                AGC CT GT    GGAGGACA
                                ||| || ||    ||||||||
                                TCG GA CA    CCTCCTGT
                                  A  A  CCA__
GAM2473 BACE     3' AGCTCTTGTGGTGGAGGACA   57727    A  C  CCGAA
                                AGC CT GT    GGAGGACA
                                ||| || ||    ||||||||
                                TCG GA CA    CCTCCTGT
                                  A  A  CCA__
GAM2473 BFSP2    3' AAGCATTTATTTGAAGGAGGAC 57728      CTCGTCC
                                AAGCA      GAAGGAGGAC
                                |||||      ||||||||||
                                TTCGT      CTTCCTCCTG
                                   AAATAAA
GAM2473 IRS1     5' GCAGCTGAAGGAGGAC      57729     CTC  CC
                                GCA   GT  GAAGGAGGAC
                                |||   ||  ||||||||||
                                CGT   CG  CTTCCTCCTG
                                  ___  A_
GAM2473 NDRG1    3' GCACCCGTTTGAACCAGGA    57730       CC   GG
                                GCACTCGT  GAA  AGGA
                                ||||||||  |||  ||||
                                CGTGGGCA  CTT  TCCT
                                     AA   GG
GAM2473 13CDNA73 5' AGTGCTCATCTAAAGGACAC   57731    CA     CGAA
                                AG  CTCGTC    GGAGGACAC
                                ||  ||||||    |||||||||
                                TC  GAGTAG    TTTCCTGTG
                                 AC     A___
GAM2473 CASKIN1  3' AGCCACGCCAGGAGGAGGACAC 57732     ACT    CGA
                                AGC   CGTC   AGGAGGACAC
                                |||   ||||   ||||||||||
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                                TCG  GCGG  TCCTCCTGTG
                                  GT_   TCC
GAM2473 DRIL2    3' ACACTTGCTGCAGGAGGACA  57733      C  CCGA
                                GCACT GT   AGGAGGACA
                                |||||  ||  |||||||||
                                TGTGA CG   TCCTCCTGT
                                   A  ACG_
GAM2473 FLJ20150 3' GCAGGACATGGGGGAGGACAC  57734    CT_  CCGAA
                                GCA  CGT   GGAGGACAC
                                |||  |||   |||||||||
                                CGT  GTA   CCTCCTGTG
                                  CCT  CCC__
GAM2473 FLJ20436 3' AAGCAAAGGTGAAGGAGGACAC 57735      CTC  CC
                                AAGCA  GT  GAAGGAGGACAC
                                |||||  ||  ||||||||||||
                                TTCGT  CA  CTTCCTCCTGTG
                                   TTC  __
GAM2473 HSA250303 3' GCACTGGGGGATGGAGGACAC  57736      CGTCC  A
                                GCACT    GA GGAGGACAC
                                |||||    ||  |||||||||
                                CGTGA    CT CCTCCTGTG
                                   CCCC_  A
GAM2473 IL22R    3' GCACCCGTCTGAGGCCAGA   57737        C  A  A_
                                GCACTCGTC GA GG  GGA
                                |||||||||  ||  ||  |||
                                CGTGGGCAG CT CC  TCT
                                     A  _  GG
GAM2473 MTCH1    3' AGCATTAGATGAGGAGGACAC  57738     CTCGTCC  A
                                AGCA      GA GGAGGACAC
                                ||||      ||  |||||||||
                                TCGT      CT CCTCCTGTG
                                  AATCTA_  _
GAM2473 PTP4A1   3' AAGCACTCTAGAAGGGGGA   57739       GTCC    A
                                AAGCACTC   GAAGG GGA
                                ||||||||   |||||  |||
                                TTCGTGAG   CTTCC CCT
                                    AT__    C
GAM2473 SIVA     3' AGCGCTCGTCCAGGGAAGG   57740     A      AA
                                AGC CTCGTCCG  GGAGG
                                |||  ||||||||  |||||
                                TCG GAGCAGGT  CTTCC
                                  C       CC
GAM2473 SIVA     3' AGCGCTCGTCCAGGGAAGG   57740     A      AA
                                AGC CTCGTCCG  GGAGG
                                |||  ||||||||  |||||
                                TCG GAGCAGGT  CTTCC
                                  C       CC
GAM2473 TTLL1    5' GCGCTCGCAGGAGGAC      57741    A    CCGA
                                GC CTCGT   AGGAGGAC
                                ||  |||||   ||||||||
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                                CG GAGCG    TCCTCCTG
                                 C    _____
GAM2473  LOC145622 3'  AGCATTTTCATTAAAGGACAC  57742      CTCG  CGAA
                                AGCA    TC    GGAGGACAC
                                ||||    ||    |||||||||
                                TCGT    AG    TTTCCTGTG
                                  AAA_  TAA_
GAM2473  LOC151318 3'  AGCTGAGCTCCTGAGGGAGGAC 57743     ACTCG  _  A
            A                    AGC     TCC GA GGAGGACA
                                |||     ||| || ||||||||
                                TCG     AGG CT CCTCCTGT
                                  ACTCG   A  C
GAM2473  LOC152633 5'  AGTGCTCGTCCAGTGAGGA    57744    CA       AAG
                                AG  CTCGTCCG   GAGGA
                                ||  ||||||||   |||||
                                TC  GAGCAGGT   CTCCT
                                 AC       CA_
GAM2473  LOC158972 3'  CACTCCTGGGAGGGAGGACAC  57745       GTCC  A
                                CACTC    GA GGAGGACAC
                                |||||    || |||||||||
                                GTGAG    CT CCTCCTGTG
                                   GACC  C
GAM2473  LOC159963 5'  GCACTCGTGTGAATCTTCAGAC 57746         CC   GGA__
            AC                    GCACTCGT  GAA     GGACAC
                                ||||||||  |||     ||||||
                                CGTGAGCA  CTT     TCTGTG
                                     CA   AGAAG
GAM2473  LOC92822  3'  AAGGACTCGTCCGAAGACTGGG 57747     C          A_  A
            CA                    AAG ACTCGTCCGAAGG  GG CA
                                ||| ||||||||||||  || ||
                                TTC TGAGCAGGCTTCT  CC GT
                                  C          GA  C
GAM2474  EDG8     3'  TCTTTTCCGACTGCACCT    57750       CC    G
                                TCTTT  CTGAC GCATCT
                                |||||  ||||| ||||||
                                AGAAA  GGCTG CGTGGA
                                   A_     A
GAM2474  CKAP2     3'  TCTTTCCCTAACTCCATTCTAA 57751           GG  _
                                TCTTTCCCTGAC  CAT CTAA
                                ||||||||||||  ||| ||||
                                AGAAAGGGATTG  GTA GATT
                                       AG   A
GAM2474  DKFZP564G2022 3'  CTTCCCTGATGGTAGCCATCT  57752         C  ____
                                TTTCCCTGA GG    CATCT
                                |||||||||  ||    |||||
                                GAAGGGACT CC    GTAGA
                                     A  ATCG
GAM2474  TSPAN-5   3'  TCTTTTTTGGTAAGCATCTAAC 57753       CCCTGAC
                                TCTTT      GGCATCTAAC
                                |||||      ||||||||||
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                                AGAAA      TCGTAGATTG
                                  AAACCAT
GAM2474  LOC146520 5'  TCTTTCCCTGAGGTTTTCC    57754          C  CA_
                                TCTTTCCCTGA GG   TCT
                                |||||||||| ||   |||
                                AGAAAGGGACT CC   AGG
                                      _ AAA
GAM2474  LOC200982 3'  TCCTTCCCTGACCTTCC     57755          GGCA
                                TCTTTCCCTGAC    TCT
                                ||||||||||||    |||
                                AGGAAGGGACTG    AGG
                                      GA__
GAM2475  ADRA2B    3'  TCGGGGTAGGAATTCACACAC  57758     AACA_  GCA
                                TTGG    GAA   TTACACAC
                                ||||    |||   ||||||||
                                AGCC    CTT   AGTGTGTG
                                  CCATC   A__
GAM2475  CCND1     3'  TTGGAATAGAGCAGTAATCACA 57759       C   A   T  CA
                                TTGGAA AGA GCA TA  CACA
                                |||||| ||| ||| ||  ||||
                                AACCTT TCT CGT AT  GTGT
                                   A   _   C  TA
GAM2475  EMS1      3'  TTGGGGAAGAACACACAC    57760     AACA   CAT
                                TTGG   GAAG   TACACAC
                                ||||   ||||   |||||||
                                AACC   CTTC   GTGTGTG
                                  C___    TT_
GAM2475  EMS1      3'  TTGGGGAAGAACACACAC    57760     AACA   CAT
                                TTGG   GAAG   TACACAC
                                ||||   ||||   |||||||
                                AACC   CTTC   GTGTGTG
                                  C___    TT_
GAM2475  MME       3'  TTAGAAATTAAGCATTATGTAC 57761       CAG      C__
            AC                    TTGGAA   AAGCATTA   ACAC
                                ||||||   ||||||||   ||||
                                AATCTT   TTCGTAAT   TGTG
                                   TAA       ACA
GAM2475  MME       3'  TTAGAAATTAAGCATTATGTAC 57761       CAG      C__
            AC                    TTGGAA   AAGCATTA   ACAC
                                ||||||   ||||||||   ||||
                                AATCTT   TTCGTAAT   TGTG
                                   TAA       ACA
GAM2475  MME       3'  TTAGAAATTAAGCATTATGTAC 57761       CAG      C__
            AC                    TTGGAA   AAGCATTA   ACAC
                                ||||||   ||||||||   ||||
                                AATCTT   TTCGTAAT   TGTG
                                   TAA       ACA
GAM2475  MME       3'  TTAGAAATTAAGCATTATGTAC 57761       CAG      C__
            AC                    TTGGAA   AAGCATTA   ACAC
                                ||||||   ||||||||   ||||
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                                AATCTT  TTCGTAAT  TGTG
                                   TAA      ACA
GAM2475 MYLK    3' TTGGAATGTTACACACA    57762      CAGAAGCA
                                TTGGAA      TTACACACA
                                ||||||      |||||||||
                                AACCTT      AATGTGTGT
                                   AC_______
GAM2475 PDYN    3' TGGAGTAGAAGCATGATAC  57763    AC      __
                                TGGA  AGAAGCAT  TAC
                                ||||  ||||||||  |||
                                ACCT  TCTTCGTA  ATG
                                  CA      CT
GAM2475 SH3BP4  3' TTGGGTACAGAAAACACACAC 57764    A_     CATT
                                TTGG  ACAGAAG   ACACACAC
                                ||||  |||||||   ||||||||
                                AACC  TGTCTTT   TGTGTGTG
                                  CA     _____
GAM2475 SLBP    3' GAACAGAAAATCTGTACACA  57765       CAT__
                                GAACAGAAG    TACACA
                                |||||||||    ||||||
                                CTTGTCTTT    ATGTGT
                                     TAGAC
GAM2475 TCP1    3' TTGTGACCCTGTTACACACAC 57766    GA  AGAAGCA
                                TTG  AC      TTACACACAC
                                |||  ||      ||||||||||
                                AAC  TG      AATGTGTGTG
                                  AC  GGAC___
GAM2475 ABCC13  3' TTGTCAAAGTGTTACACACAC 57767    GAACA   CA
                                TTG    GAAG  TTACACACAC
                                |||    ||||  ||||||||||
                                AAC    TTTC  AATGTGTGTG
                                  AG___    AC
GAM2475 BLCAP   3' GGGACAGAACACACAC     57768    A     GCAT
                                GG ACAGAA    TACACAC
                                || ||||||    |||||||
                                CC TGTCTT    GTGTGTG
                                 C     _____
GAM2475 C12orf4 3' TTGGAATGGTTTCACACACA  57769      CAGAAGCA
                                TTGGAA      TTACACACA
                                ||||||      |||||||||
                                AACCTT      AGTGTGTGT
                                   ACCAA___
GAM2475 CCR5    3' TTGGAGGGGAAATCACACA   57770      ACA   GC
                                TTGGA   GAA  ATTACACA
                                |||||   |||  ||||||||
                                AACCT   CTT  TAGTGTGT
                                   CCC   __
GAM2475 DKFZP564C1940 3' TGGAATAGAAGCATTTGTTGCA 57771      C       ACA__
             C                   TGGAA AGAAGCATT    CAC
                                |||||| |||||||||    |||
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                                ACCTT TCTTCGTAA    GTG
                                   A       ACAAC
GAM2475 DNAJC5   3' TGGAACAGAACCCCATACA   57772        G ATTA  C
                                TGGAACAGAA C   CA ACA
                                |||||||||| |   || |||
                                ACCTTGTCTT G   GT TGT
                                      _ GG__  A
GAM2475 EAT2     3' GGAACAGAAATCACACA     57773        GC
                                GGAACAGAA  ATTACACA
                                |||||||||  ||||||||
                                CCTTGTCTT  TAGTGTGT
                                      __
GAM2475 FLJ14800 3' GGGGCAGAGTGACTACACAC  57774    AA   AGC
                                GG  CAGA   ATTACACAC
                                ||  ||||   |||||||||
                                CC  GTCT   TGATGTGTG
                                 CC    CAC
GAM2475 FLJ21817 3' TTGGACACAGACAATCACACA 57775     _    AGC
                                TTGGA ACAGA   ATTACACA
                                ||||| |||||   ||||||||
                                AACCT TGTCT   TAGTGTGT
                                   G    GT_
GAM2475 KIAA0982 3' TTAGAGTAGAAGCTGACTACAC 57776     AC    __
                                TTGGA  AGAAGC  ATTACAC
                                |||||  ||||||  |||||||
                                AATCT  TCTTCG  TGATGTG
                                   CA     AC
GAM2475 KIAA1100 3' TGGAATGGAAAAAACCACACA 57777     CA   CATTA
                                TGGAA  GAAG    CACACA
                                |||||  ||||    ||||||
                                ACCTT  CTTT    GTGTGT
                                   AC   TTTG_
GAM2475 KIAA1183 3' TTGGGACGAGGAAGCACACAC 57778     A  A__     T
                                TTGG AC   GAAGCAT ACAC
                                |||| ||   ||||||| ||||
                                AACC TG   CTTCGTG TGTG
                                  C  CTC     _
GAM2475 KIAA1257 3' TTGGAACAAAGCAACA     57779        A   TT
                                TTGGAACAGA GCA  ACA
                                |||||||||| |||  |||
                                AACCTTGTTT CGT  TGT
                                      _  __
GAM2475 MANBAL   3' TGGAGCAGAAGCAGGCAC    57780     A      TTA
                                TGGA CAGAAGCA   CAC
                                |||| ||||||||   |||
                                ACCT GTCTTCGT   GTG
                                  C       CC_
GAM2475 OCLM     3' GGAGCAGAATACACAC     57781     A    GCAT
                                GGA CAGAA    TACACAC
                                ||| |||||    |||||||
```

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                                CCT GTCTT    ATGTGTG
                                  C    _____
GAM2475  OS4      3'  TTGGAACAGAAGTCCTTGCAC  57782          CA_  A
                                TTGGAACAGAAG   TT CAC
                                ||||||||||||   || |||
                                AACCTTGTCTTC   AA GTG
                                       AGG  C
GAM2475  PIF1     5'  TTGGGCCAGGGCCACACAC   57783     AA   AA  AT
                                TTGG  CAG  GC  TACACAC
                                ||||  |||  ||  |||||||
                                AACC  GTC  CG  GTGTGTG
                                  CG   C_  __
GAM2475  PRO1048  3'  TTAGAACAGAAAAATGTACA  57784          C  _
                                TTGGAACAGAAG AT TACA
                                |||||||||||| || ||||
                                AATCTTGTCTTT TA ATGT
                                       T  C
GAM2475  RGS7     3'  TTGGAGATGGAATGTACACAC  57785      ACA_   GCAT
                                TTGGA    GAA    TACACAC
                                |||||    |||    |||||||
                                AACCT    CTT    ATGTGTG
                                   CTAC   AC__
GAM2475  LOC125476 3'  TTGGAGGGAAAACACACA    57786      ACA    CATT
                                TTGGA   GAAG    ACACACA
                                |||||   ||||    |||||||
                                AACCT   CTTT    TGTGTGT
                                   CC_    _____
GAM2475  LOC150142 5'  TTGGAACAGAGGCTCTGACTAC 57787          A  _____
                                TTGGAACAGA GC    ATTAC
                                |||||||||| ||    |||||
                                AACCTTGTCT CG    TGATG
                                      C  AGAC
GAM2475  LOC203530 3'  TGGGGCAGAAGCAACAC     57788     AA       TT
                                TGG  CAGAAGCA  ACAC
                                |||  ||||||||  ||||
                                ACC  GTCTTCGT  TGTG
                                  CC       __
GAM2475  LOC253461 3'  TTGGAACAGCAGCTACAATTGT 57789          A   _  ______
              ACAC                   TTGGAACAG AGC AT     TACAC
                                |||||||||| ||| ||    |||||
                                AACCTTGTC TCG TG     ATGTG
                                      G   A  TTAAC
GAM2476  ATF5     3'  TAGCGTAGTGTCCCAAGGTCAC 57792      ACGCG__  A GAG
                                TAGC      CC C   GAGGTCAC
                                ||||      || |   ||||||||
                                ATCG      GG G   TTCCAGTG
                                  CATCACA  _ ___
GAM2476  HAP1     3'  GCATGCGCCATAAAGGTCA    57793     C     CGA
                                GCA GCGCCA   GGAGGTCA
                                ||| ||||||   ||||||||
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                                CGT CGCGGT   TTTCCAGT
                                  A     A__
GAM2476 CAMKK1   3' ACGTGCGTGCGTGGAGGTCA  57794     C  CA_  A
                                ACG GC   CG GGAGGTCA
                                ||| ||   || ||||||||
                                TGC CG   GC CCTCCAGT
                                  A  CAC  A
GAM2476 FLJ23191 5' GCGCCCCAGTGAGGTCAC    57795      A  AG
                                GCGCC CG  GAGGTCAC
                                ||||| ||  ||||||||
                                CGCGG GT  CTCCAGTG
                                   G  CA
GAM2476 FYCO1    5' GCACGCGCTCGTGGGTCCAC  57796        CA  A  AGG
                                GCACGCGC  CG GG   TCAC
                                ||||||||  || ||   ||||
                                CGTGCGCG  GC CC   GGTG
                                     A_  A  CA_
GAM2476 MGC4796  3' GCCGTGTCCAAGGAGGTCA   57797    A  CGCCA
                                GC CG    CGAGGAGGTCA
                                || ||    ||||||||||
                                CG GC    GTTCCTCCAGT
                                 _  ACAG_
GAM2476 STAG3    5' CGCGCCACGTTTGAGTCAC   57798         AG_  G
                                CGCGCCACG   GAG TCAC
                                |||||||||   ||| ||||
                                GCGCGGTGC   CTC AGTG
                                     AAA  _
GAM2476 LOC149603 3' TAGCACGTGTCACGAGGAAGT  57799        CGC
                                TAGCACG   CACGAGGAGGT
                                |||||||   ||||||||||
                                ATCGTGC   GTGCTCCTTCA
                                    ACA
GAM2476 LOC153505 3' ACGCGTACAGGGAGGTCA    57800      CC   A
                                ACGCG  ACG GGAGGTCA
                                |||||  ||| ||||||||
                                TGCGC  TGT CCTCCAGT
                                   A_  C
GAM2476 LOC256797 5' GCTGACTAAGTGAGGAGGTCAC 57801    AC  GCCAC
                                GC  GC    GAGGAGGTCAC
                                ||  ||    ||||||||||
                                CG  TG    CTCCTCCAGTG
                                 AC  ATTCA
GAM2477 ADA      5' GCCAGCGGTGGCCGCGGCCG   57804     C   CGCAA
                                GCCG GCG    CCGCGGCCG
                                |||| |||    |||||||||
                                CGGT CGC    GGCGCCGGC
                                  _  CACC_
GAM2477 ADAM12   5' GCGTCGCGCGCGCCG     57805     C       AACCGCG
                                GCG CGCGCGCGC      GCCG
                                ||| |||||||||      ||||
```

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                                CGC GCGCGCGCG      CGGC
                                  A       _______
GAM2477 BRF1     5' CGCCGCGCGCGCCCGGGCCG  10910          AA  C
                                CGCCGCGCGCGC  CCG GGCCG
                                ||||||||||||  ||| |||||
                                GCGGCGCGCGCG  GGC CCGGC
                                              __  _
GAM2477 BTEB1    5' GCCTCGCGGTCCCGTGGCCG  57806    G   CGCAA  C
                                GCC CGCG    CCG GGCCG
                                ||| ||||    ||| |||||
                                CGG GCGC    GGC CCGGC
                                  A   CAG__  A
GAM2477 CCND1    3' GCGCCGCGGTGCAACCA     57807        CGC
                                GCGCCGCG   GCAACCG
                                ||||||||   |||||||
                                CGCGGCGC   CGTTGGT
                                     CA_
GAM2477 CCND3    5' GCCCGCGCGCGCGCGC      57808    G       AACC  G
                                GC CCGCGCGCGC   GCG C
                                || ||||||||||   ||| |
                                CG GGCGCGCGCG   CGC G
                                 _       _____  _
GAM2477 CDK2AP1  5' GCCCGCGCGCGTCCGGGCGGC 57809    G       CAA __
                                GC CCGCGCGCG   CC  GCGGC
                                || |||||||||   ||  |||||
                                CG GGCGCGCGC   GG  CGCCG
                                 _       A__  CC
GAM2477 CLCN4    5' GCCGCATCGCGCCCGCGGCCG 57810       _    AA
                                GCCGCG CGCGC  CCGCGGCCG
                                ||||||| |||||  |||||||||
                                CGGCGT GCGCG  GGCGCCGGC
                                   A    __
GAM2477 CYLN2    5' GCCTGCGCGCCCCGCGGCC   57811    GC     AA
                                GCC  GCGCGC  CCGCGGCC
                                |||  ||||||  ||||||||
                                CGG  CGCGCG  GGCGCCGG
                                  A_     G_
GAM2477 DAG1     5' GCGCCGCGCCGCAGCC      57812        GCGCAAC
                                GCGCCGCGC      CGCGGCC
                                |||||||||      |||||||
                                CGCGGCGCG      GCGTCGG
                                               _______
GAM2477 DSCAM    5' GCGCCGCGCCCCACGCTGCGGC 57813         ___   AACC
             CG                   GCGCCGCGC  GCGC   GCGGCCG
                                ||||||||||  ||||   |||||||
                                CGCGGCGCG  TGCG   CGCCGGC
                                     GGG   A___
GAM2477 FBXL5    5' CGCCTCAGCAGCCGCGGCCG  57814     G  CGC   A
                                CGCC CG   GCA CCGCGGCCG
                                ||||  ||   ||| |||||||||
```

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                                GCGG GT   CGT GGCGCCGGC
                                  A ___   C
GAM2477 FBXL5   5' CGCCTCAGCAGCCGCGGCCG  57814     G CGC  A
                                CGCC CG   GCA CCGCGGCCG
                                |||| ||   ||| |||||||||
                                GCGG GT   CGT GGCGCCGGC
                                  A ___   C
GAM2477 FOP     5' GCTCCGCGCGCGGGCTACGCGG 57815    G       CAAC_
            CCG                   GC CCGCGCGCG    CGCGGCCG
                                || |||||||||    ||||||||
                                CG GGCGCGCGC    GCGCCGGC
                                 A        CCGAT
GAM2477 G1P3    5' GCGCCGCGCGCGGGCTCC    57816          CAACC  GG
                                GCGCCGCGCGCG    GC  CC
                                ||||||||||||    ||  ||
                                CGCGGCGCGCGC    CG  GG
                                       C____  A_
GAM2477 G1P3    5' GCGCCGCGCGCGGGCTCC    57816          CAACC  GG
                                GCGCCGCGCGCG    GC  CC
                                ||||||||||||    ||  ||
                                CGCGGCGCGCGC    CG  GG
                                       C____  A_
GAM2477 G1P3    5' GCGCCGCGCGCGGGCTCC    57816          CAACC  GG
                                GCGCCGCGCGCG    GC  CC
                                ||||||||||||    ||  ||
                                CGCGGCGCGCGC    CG  GG
                                       C____  A_
GAM2477 GAD2    5' GCCCTGCGCGCGCGTGCGTGCC 57817    G _      AACC  _
            G                   GC CC GCGCGCGC    GCG GCCG
                                || || ||||||||    ||| ||||
                                CG GG CGCGCGCG    CGC CGGC
                                 _ A      CA__   A
GAM2477 GRIN2A  5' GCGCTGCGCGCACGAGCA    57818     C      AACC
                                GCGC GCGCGCGC   GCG
                                |||| ||||||||   |||
                                CGCG CGCGCGTG   CGT
                                  A      CT__
GAM2477 GTF2I   5' GCCGCGCGCGGGCTGCGGCCG  57819         CAACC
                                GCCGCGCGCG    GCGGCCG
                                ||||||||||    |||||||
                                CGGCGCGCGC    CGCCGGC
                                     CCGA_
GAM2477 GTF2I   5' GCCGCGCGCGGGCTGCGGCCG  57819         CAACC
                                GCCGCGCGCG    GCGGCCG
                                ||||||||||    |||||||
                                CGGCGCGCGC    CGCCGGC
                                     CCGA_
GAM2477 HBQ1    5' GCGCCGCGCCGCAGCTTCG   57820         G   ACCG
                                GCGCCGCGC CGCA   CG
                                |||||||| ||||   ||
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                                CGCGGCGCG GCGT   GC
                                      _   CGAA
GAM2477  HTR2C    5'  GCGCTGCGCGCCGCAACCTCG  57821     C    _    G
                                GCGC GCGCGC GCAACC CG
                                |||| |||||| |||||| ||
                                CGCG CGCGCG CGTTGG GC
                                  A    G    A
GAM2477  INPP4A   5'  GCGACGCGCGCGCCTGGC    57822    C      AACCGC
                                GCG CGCGCGCGC    GGC
                                ||| |||||||||     |||
                                CGC GCGCGCGCG    CCG
                                  T      GA____
GAM2477  INPP4A   5'  GCGACGCGCGCGCCTGGC    57822    C      AACCGC
                                GCG CGCGCGCGC    GGC
                                ||| |||||||||     |||
                                CGC GCGCGCGCG    CCG
                                  T      GA____
GAM2477  JAG1     5'  GCGCCGCGCGCCGCGG     57823          GCAAC
                                GCGCCGCGCGC   CGCGG
                                ||||||||||    |||||
                                CGCGGCGCGCG   GCGCC
                                      _____
GAM2477  JAG2     5'  GCGCCGCGGCGCGCGGGCC   57824       C   AAC  C
                                GCGCCGCG GCGC  CG GGCC
                                |||||||| ||||  || ||||
                                CGCGGCGC CGCG  GC CCGG
                                   _   C__  _
GAM2477  JUND     5'  GCGCCCGCCCCGGCCGCGGCCG 57825     G  G_  CAA
                                GCGCC CGC  CG  CCGCGGCCG
                                ||||| |||  ||  |||||||||
                                CGCGG GCG  GC  GGCGCCGGC
                                   _  GG  C__
GAM2477  NFRKB    5'  GCCCGCGGGGCGGTCGCGGCCG 57826   G   C_  CAAC
                                GC CCGCG  GCG   CGCGGCCG
                                || |||||  |||   ||||||||
                                CG GGCGC  CGC   GCGCCGGC
                                 _    CC   CA__
GAM2477  NPY2R    5'  GCGCCGCGCGGGCGGGCAGCCG 57827        C  AACC
                                GCGCCGCGCG GC   GCGGCCG
                                |||||||||| ||   |||||||
                                CGCGGCGCGC CG   CGTCGGC
                                      C  CC__
GAM2477  PDGFB    5'  GCTCCGCGCGCGCGGCGTGCC  57828   G       AACC  _
                                GC CCGCGCGCGC   GCG GCC
                                || ||||||||||   ||| |||
                                CG GGCGCGCGCG   CGC CGG
                                 A       C___  A
GAM2477  PFKFB3   5'  GCGCCGGCGCGCGGC      57829       C    AACCGC
                                GCGCCG GCGCGC    GGC
                                |||||| ||||||     |||
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                                CGCGGC CGCGCG     CCG
                                  _    ______
GAM2477 PK428    5' GCGCCGCGCGGGCAGAGAGCC 57830         C   ACCGC
                                GCGCCGCGCG GCA    GGCC
                                |||||||||| |||    ||||
                                CGCGGCGCGC CGT    TCGG
                                     C  CTC__
GAM2477 POU4F1   5' GCGCCGCGCGCCGGCC     57831          GCAACCG
                                GCGCCGCGCGC     CGGCC
                                ||||||||||      |||||
                                CGCGGCGCGCG     GCCGG
                                                _______
GAM2477 PPP1R7   3' GCGTCGCGCGCGCCAGC     57832     C       AACCG
                                GCG CGCGCGCGC    CGGC
                                ||| |||||||||    ||||
                                CGC GCGCGCGCG    GTCG
                                  A       _____
GAM2477 PRKCI    5' GCGCTTGCCGGAGAACCGCGGC 57833     C_  G  CGC
                CG                GCGC  GC CG   AACCGCGGCCG
                                ||||  || ||   ||||||||||
                                CGCG  CG GC   TTGGCGCCGGC
                                  AA  _  CTC
GAM2477 PTGER3   5' CCGCTGCTGGGACCGCGGCCG 57834     GC  GCA_
                                CCGC  GC   ACCGCGGCCG
                                ||||  ||   ||||||||||
                                GGCG  CG   TGGCGCCGGC
                                  A_  ACCC
GAM2477 PTPN18   5' GCCCCGCGCGCGCGGCGA    57835    G       AACC
                                GC CCGCGCGCGC   GCGG
                                || ||||||||||   ||||
                                CG GGCGCGCGCG   CGCT
                                 G       C___
GAM2477 RAD23A   5' GCGCCGCGCGCCGACCACTTCC 57836          GCA    GG
                G                 GCGCCGCGCGC   ACCGC  CCG
                                ||||||||||   |||||  |||
                                CGCGGCGCGCG   TGGTG  GGC
                                      GC_    AA
GAM2477 RAD23A   5' GCGCCGCGCCGCGCGC     57837        G   AACC   G
                                GCGCCGCGC CGC   GCG C
                                |||||||| |||   ||| |
                                CGCGGCGCG GCG   CGC G
                                  _   ____   _
GAM2477 RPS6KA2  5' GCCGCGCCGGCCACCGCGGCCG 57838       GC  A
                                GCCGCGC  GC ACCGCGGCCG
                                |||||||  || ||||||||||
                                CGGCGCG  CG TGGCGCCGGC
                                    GC  G
GAM2477 SFRP1    5' GCGTTGCCCGGCTCCGCGGCCG 57839     CC  G  C  AA
                                GCG  GC CG GC  CCGCGGCCG
                                |||  || || ||  |||||||||
```

```
                                CGC  CG GC CG  GGCGCCGGC
                                  AA  G  _  A_
GAM2477  SLC30A4   5'  GCGCTGCTCCACCCGCGGCCG  57840     C  GCG   AA
                                GCGC GC   CGC  CCGCGGCCG
                                |||| ||   |||  |||||||||
                                CGCG CG   GTG  GGCGCCGGC
                                  A  AG_  __
GAM2477  SMS       5'  GCGCGGCGTGTCAGGCTGCGGC 57841      C  ___  C  AACC
              CG                  GCGC GCG   CG GC    GCGGCCG
                                |||| |||   || ||    |||||||
                                CGCG CGC   GT CG    CGCCGGC
                                  C   ACA  C  A___
GAM2477  TBL1X     5'  GCGCCGCGCGCCCGGCCGCGCT 57842          GCAA    G_
              CCG                   GCGCCGCGCGC    CCGCG  CCG
                                ||||||||||    |||||  |||
                                CGCGGCGCGCG    GGCGC  GGC
                                      GGCC     GA
GAM2477  ZIC1      5'  GCGCCGCGCGGCGCTGGCC    57843          C  AACC  _
                                GCGCCGCGCG GC    GC GGCC
                                |||||||||| ||    || ||||
                                CGCGGCGCGC CG    CG CCGG
                                      _  _____  A
GAM2477  ZNF134    5'  GCGCCGGGCCCATCACCGCGGC 57844       C  G  CA
              CG                    GCGCCG GC CG  ACCGCGGCCG
                                |||||| || ||  ||||||||||
                                CGCGGC CG GT  TGGCGCCGGC
                                   C  G  AG
GAM2477  ZNF278    5'  GCGCCGGCGCGCAGCCA     57845       C      A
                                GCGCCG GCGCGCA CCG
                                |||||| ||||||| |||
                                CGCGGC CGCGCGT GGT
                                   _      C
GAM2477  ZNF278    5'  GCGCCGGCGCGCAGCCA     57845       C      A
                                GCGCCG GCGCGCA CCG
                                |||||| ||||||| |||
                                CGCGGC CGCGCGT GGT
                                   _      C
GAM2477  ZNF278    5'  GCGCCGGCGCGCAGCCA     57845       C      A
                                GCGCCG GCGCGCA CCG
                                |||||| ||||||| |||
                                CGCGGC CGCGCGT GGT
                                   _      C
GAM2477  ZNF278    5'  GCGCCGGCGCGCAGCCA     57845       C      A
                                GCGCCG GCGCGCA CCG
                                |||||| ||||||| |||
                                CGCGGC CGCGCGT GGT
                                   _      C
GAM2477  ZYX       5'  GCGCCGCGTCTCGGGTGGCCG  57846        CG_  CAACCGC
                                GCGCCGCG   CG      GGCCG
                                ||||||||   ||      |||||
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                              CGCGGCGC  GC     CCGGC
                                  AGA  CCA____
GAM2477 AKR7A3   5' GCCGCGCGCAGCGGC      57847        CAACC   C
                              GCCGCGCGCG    GCGG C
                              ||||||||||    |||| |
                              CGGCGCGCGT    CGCC G
                                  _____   A
GAM2477 ARF6     5' GCGCCGCGCGAGCGCCGCC   57848        C  AACC  G
                              GCGCCGCGCG GC   GC GCC
                              |||||||||| ||   || |||
                              CGCGGCGCGC CG   CG CGG
                                   T  ____  G
GAM2477 CENTG2   5' GCGCCGCGGCGGGTGCGGCCG 57849       C   CAACC
                              GCGCCGCG GCG    GCGGCCG
                              |||||||| |||    |||||||
                              CGCGGCGC CGC    CGCCGGC
                                  _  CCA__
GAM2477 COLEC12  5' GCGCCGCGCGCCGGCCG     57850        GCAACCG
                              GCGCCGCGCGC     CGGCCG
                              ||||||||||      ||||||
                              CGCGGCGCGCG     GCCGGC
                                  _______
GAM2477 COLEC12  5' GCGCCGCGCGCCGGCCG     57850        GCAACCG
                              GCGCCGCGCGC     CGGCCG
                              ||||||||||      ||||||
                              CGCGGCGCGCG     GCCGGC
                                  _______
GAM2477 ELKS     5' GCGCTGTCGCCGCCGCCGCGGC 57851     CG_  G  AA
           CG                   GCGC  CGC CGC  CCGCGGCCG
                              ||||  ||| |||  |||||||||
                              CGCG  GCG GCG  GGCGCCGGC
                                ACA  _  GC
GAM2477 FLJ10116 5' CCGCGCGCATCACGCCGCGGCC 57852        _ A_
           G                   CCGCGCGCG CA  CCGCGGCCG
                              |||||||| ||  |||||||||
                              GGCGCGCGT GT  GGCGCCGGC
                                   A  GC
GAM2477 FLJ11535 5' GCGCCGCAGGCCGTGGC     57853        C  GCAAC  C
                              GCGCCGCG GC     CG GGC
                              |||||||| ||     || |||
                              CGCGGCGT CG     GC CCG
                                  C  _____  A
GAM2477 FLJ12132 5' GCCGCGCGTGCGGCCACGCCG 57854       C  AA    G
                              GCCGCGCG GC  CCGCG CCG
                              |||||||| ||  ||||| |||
                              CGGCGCGC CG  GGTGC GGC
                                  A  CC    _
GAM2477 FLJ14124 3' GCCCGGCGCGGCCGCGGCCG  57855    G  C    CAA
                              GC CCG GCGCG   CCGCGGCCG
                              || ||| |||||   |||||||||
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                                CG GGC CGCGC   GGCGCCGGC
                                 _  _    C__
GAM2477 FLJ21019 5' GCGCGGGCAGCCGCGGCC    57856      C   A
                                GCGCG GCA CCGCGGCC
                                ||||| ||| ||||||||
                                CGCGC CGT GGCGCCGG
                                   C   C
GAM2477 FLJ21195 5' GCGCCGCGCGGTCCCAGGC   57857         CGCAA   C
                                GCGCCGCGCG    CCG GGC
                                ||||||||||    ||| |||
                                CGCGGCGCGC    GGT CCG
                                      CAG__  _
GAM2477 FLJ32784 3' GCACCGTGCTTCTCGCGGCCG 57858       C  GCGCAAC
                                GCGCCG GC      CGCGGCCG
                                |||||| ||      ||||||||
                                CGTGGC CG      GCGCCGGC
                                   A  AAGA___
GAM2477 HRD1    5' GCCCGCTCAATCCGCGCGACTG 57859    G   G_____    A  C
           CGGC                  GC CCGC     CGCGC AC GCGGC
                                || ||||     ||||| || |||||
                                CG GGCG     GCGCG TG CGCCG
                                 _   AGTTAG    C  A
GAM2477 HYA22    5' GCCGCGCGCGCGGGGGCC    57860          AACCGC
                                GCCGCGCGCGC     GGCC
                                ||||||||||     ||||
                                CGGCGCGCGCG     CCGG
                                      CCC___
GAM2477 KIAA1028 5' GCGCGCGCGCGCGCGC      57861      _       AACCGCG
                                GCGC CGCGCGCGC      GC
                                |||| |||||||||      ||
                                CGCG GCGCGCGCG      CG
                                  C       ________
GAM2477 KIAA1608 5' GCTGCCCGCCCGCCCGCGGCCG 57862    _  G   G   AA
                                GC GCC CGC CGC  CCGCGGCCG
                                || ||| ||| |||  |||||||||
                                CG CGG GCG GCG  GGCGCCGGC
                                 A   _   G   __
GAM2477 MAP2K5   5' GCGCGGCGCGCGCAGGC     57863      C       ACCGC
                                GCGC GCGCGCGCA     GGC
                                |||| |||||||||     |||
                                CGCG CGCGCGCGT     CCG
                                  C       _____
GAM2477 MGC20806 3' CGCCGCGCGCAGGCGGCC    57864          CAACC
                                CGCCGCGCGCG    GCGGCC
                                ||||||||||    ||||||
                                GCGGCGCGCGT    CGCCGG
                                      C____
GAM2477 MGC26684 5' GCGCCGCGCGCCCAGCTCACTC 57865          G  AC_  GG
           CG                   GCGCCGCGCGC CA   CGC  CCG
                                |||||||||| ||   |||  |||
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                                CGCGGCGCGCG GT  GTG  GGC
                                      G  CGA  A_
GAM2477 NET-6   5' GCGGCGCGCGCGCGGCGGC  57866    C      AACC
                                GCG CGCGCGCGC   GCGGC
                                ||| |||||||||   |||||
                                CGC GCGCGCGCG   CGCCG
                                  C       C___
GAM2477 OSBPL1A 5' GCGCCGCGCCCGCCCGGGCCG 57867       G  AA  C
                                GCGCCGCGC CGC  CCG GGCCG
                                ||||||||| |||  ||| |||||
                                CGCGGCGCG GCG  GGC CCGGC
                                      G  __  _
GAM2477 PCCX2   5' GCTCGCGCGCGCTGACATGGC 57868   _      AAC  C
                                GC CGCGCGCGC  CG GGC
                                || |||||||||  || |||
                                CG GCGCGCGCG  GT CCG
                                 A       ACT  A
GAM2477 PCDH17  5' GCGTGCGCGCGCGACGCG   57869    CC      AAC
                                GCG  GCGCGCGC  CGCG
                                |||  ||||||||  ||||
                                CGC  CGCGCGCG  GCGC
                                  A_      CT_
GAM2477 PKMYT1  5' GCTCCGCGCGCGTTCACGGGCC 57870   G      CAAC  C
            G                    GC CCGCGCGCG   CG GGCCG
                                || |||||||||   || |||||
                                CG GGCGCGCGC   GC CCGGC
                                 A       AAGT  _
GAM2477 PORIMIN 5' GCGTCGCGTGCGCAGCCG   57871    C  C   A
                                GCG CGCG GCGCA CCG
                                ||| |||| ||||| |||
                                CGC GCGC CGCGT GGC
                                  A  A   C
GAM2477 ROBO4   5' GCTCGTGCCGAATTCGCGGCCG 57872   _  C  G  CAAC
                                GC CG GC CG   CGCGGCCG
                                || || || ||   ||||||||
                                CG GC CG GC   GCGCCGGC
                                 A  A  _  TTAA
GAM2477 SEMA3C  5' GCGCCGCGGCGCGCGGCTCCGG 57873       _   AACCG
            C                    GCGCCGCG CGCGC    CGGC
                                |||||||| |||||    ||||
                                CGCGGCGC GCGCG    GCCG
                                     C    CCGAG
GAM2477 SMARCA4 5' CGCTGCGCGCGCGCTCGCCG  57874    C      AACC  G_
                                CGC GCGCGCGC   GC  GCCG
                                ||| ||||||||   ||  ||||
                                GCG CGCGCGCG   CG  CGGC
                                  A      ____  AG
GAM2477 SPS     5' GCGCCGCGCGCGGGCGGC   57875          CAACC
                                GCGCCGCGCGCG   GCGGC
                                ||||||||||||   |||||
```

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                                CGCGGCGCGCGC   CGCCG
                                      C____
GAM2477 STARD7   5' GCGCCGCACGCGCAGGCC   57876          ACCGC
                                GCGCCGCGCGCGCA   GGCC
                                ||||||||||||||   ||||
                                CGCGGCGTGCGCGT   CCGG
                                      _____
GAM2477 STARD7   5' GCGCCGCACGCGCAGGCC   57876          ACCGC
                                GCGCCGCGCGCGCA   GGCC
                                ||||||||||||||   ||||
                                CGCGGCGTGCGCGT   CCGG
                                      _____
GAM2477 TERE1    5' GCTCGTGCCGAATTCGCGGCCG 57872   _ C  G  CAAC
                                GC CG GC CG   CGCGGCCG
                                || || || ||   ||||||||
                                CG GC CG GC   GCGCCGGC
                                 A  A  _ TTAA
GAM2477 TNRC9    5' GCGCGTGGGACTCGCGGCCG  57877     CGCA  _
                                GCGCG   AC CGCGGCCG
                                |||||   || ||||||||
                                CGCGC   TG GCGCCGGC
                                   ACCC  A
GAM2477 LOC116064 5' GCGCCGCGCGCGGTCCAGAGGC 57878          CAA  C_
           CG                   GCGCCGCGCGCG  CCG  GGCCG
                                ||||||||||||  |||  |||||
                                CGCGGCGCGCGC  GGT  CCGGC
                                      CA_  CT
GAM2477 LOC123099 5' GCGCCGTTCGGAGCGCGGCCG  57879      CG  CGCAAC
                                GCGCCG  CG    CGCGGCCG
                                ||||||  ||    ||||||||
                                CGCGGC  GC    GCGCCGGC
                                   AA  CTC___
GAM2477 LOC132617 5' GCGCCGCGCAGTGCGGATGATG 57880         C_  AACCGCG
           CCG                  GCGCCGCGCG  GC     GCCG
                                ||||||||||  ||     ||||
                                CGCGGCGCGT  CG     CGGC
                                     CA  CCTACTA
GAM2477 LOC143173 5' GCGTCACGCGGCCGCGGCCG  57881    C    C  AAC
                                GCG CGCGCG GC   CGCGGCCG
                                ||| ||||||  ||   ||||||||
                                CGC GTGCGC CG   GCGCCGGC
                                  A    _ ___
GAM2477 LOC146108 5' GCGCCGCGCGTGTGGCAGTCG  57882         CGCAACC   C
                                GCGCCGCGCG     GCGG CG
                                ||||||||||     |||| ||
                                CGCGGCGCGC     CGTC GC
                                     ACAC___   A
GAM2477 LOC147670 5' GCGCCGCACTGACTGCGGC   57883         GCGCA  C
                                GCGCCGCGC    AC GCGGC
                                |||||||||    || |||||
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                                CGCGGCGTG    TG CGCCG
                                     AC___  A
GAM2477  LOC150465 5'  GCGCCGCGCGCCCGGGCC    57884         GCAA  C
                                GCGCCGCGCGC   CCG GGCC
                                ||||||||||   ||| ||||
                                CGCGGCGCGCG   GGC CCGG
                                      ____  _
GAM2477  LOC151647 5'  GCAGCCGCGCGCGCAGTCG   57885   _        AC
                                GC GCCGCGCGCGCA  CG
                                || ||||||||||||  ||
                                CG CGGCGCGCGCGT  GC
                                 T          CA
GAM2477  LOC152849 3'  GCGGCCGCCGCCGCAGCCGCGG 57886    _   _ G   A
           C                     GCG CCGC GC CGCA CCGCGGC
                                ||| |||| || |||| |||||||
                                CGC GGCG CG GCGT GGCGCCG
                                  C   G _   C
GAM2477  LOC219686 5'  GCGGCCCCGAGCAGCCGCGGCC 57887    _ G  CGC   A
           G                     GCG CC CG   GCA CCGCGGCCG
                                ||| || ||   ||| |||||||||
                                CGC GG GC   CGT GGCGCCGGC
                                  C  G  T__   C
GAM2477  LOC221184 5'  GCGCTGCCCGCGCGGCCACG   57888     C  G    AA
                                GCGC GC CGCGC  CCGCG
                                |||| || |||||  |||||
                                CGCG CG GCGCG  GGTGC
                                  A  G    CC
GAM2477  LOC221496 3'  CGCCGCCAAGAGCCGCGGCCG  57889      G  CGCAA
                                CGCCGC CG    CCGCGGCCG
                                ||||||  ||    |||||||||
                                GCGGCG GT    GGCGCCGGC
                                   _  TCTC_
GAM2477  LOC222183 5'  GCCGCGCGCGCGGGGGCCG   57890          AACCGC
                                GCCGCGCGCGC     GGCCG
                                ||||||||||     |||||
                                CGGCGCGCGCG     CCGGC
                                      CCC___
GAM2477  LOC253150 3'  GCGCCGGTGCGCGCCGGCGG   57891       C_     AACC
                                GCGCCG  GCGCGC   GCGG
                                ||||||  ||||||   ||||
                                CGCGGC  CGCGCG   CGCC
                                   CA     GC__
GAM2477  LOC254057 5'  GCCGCGGCACCGATCGCGGCCG 57892       C   AAC_
                                GCCGCG GCGC   CGCGGCCG
                                ||||||  ||||   ||||||||
                                CGGCGC CGTG   GCGCCGGC
                                   _   GCTA
GAM2477  LOC91828  5'  GCGTCGCGCGCGAGCTCC    57893     C      CAACC  GG
                                GCG CGCGCGCG    GC  CC
                                ||| ||||||||    ||  ||
```

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                                CGC GCGCGCGC    CG  GG
                                  A       T____  A_
GAM2478  SCA2     3'  AATTATGGAATAGCCCCCAA  57896          A_
                                AATTATGGAATA  CCTTAA
                                ||||||||||||  ||||||
                                TTAATACCTTAT  GGGGTT
                                      CG
GAM2478  DIS3     3'  TAGATTATGGAATAGAACTTA  57897    A        AC_
                                TA ATTATGGAATA   CTTA
                                || ||||||||||   ||||
                                AT TAATACCTTAT   GAAT
                                 C         CTT
GAM2478  LOC123036 3'  TAAATTATAGAATAATCT    57898            C
                                TAAATTATGGAATAA CT
                                |||||||||||||| ||
                                ATTTAATATCTTATT GA
                                          A
GAM2479  DKFZP564G0222 3'  GAAATGTACATTTAATT     57901          ATTG
                                GAAATGTACA    TAATT
                                ||||||||||    |||||
                                CTTTACATGT    ATTAA
                                      AA__
GAM2479  FLJ10970  3'  ATGAAATGTACAGTTGACTTTT 57902          A   TAA
                                ATGAAATGTACA TTG   TTTT
                                ||||||||||| |||   ||||
                                TACTTTACATGT AAC   AAAA
                                      C   TG_
GAM2479  KIAA0232  3'  GAAATGTACATGAGATTTT   57903         AT  TA
                                GAAATGTACA  TG  ATTTT
                                ||||||||||  ||  |||||
                                CTTTACATGT  AC  TAAAA
                                      __  TC
GAM2479  KRT20     3'  TGAAATGTATTGCAATTT    57904        CAA
                                TGAAATGTA   TTGTAATTT
                                |||||||||   |||||||||
                                ACTTTACAT   AACGTTAAA
                                      ___
GAM2479  MGC4730   3'  GAAATGAACTATGTAATTTT   57905       T  AAT
                                GAAATG AC   TGTAATTTT
                                |||||| ||   |||||||||
                                CTTTAC TG   ACATTAAAA
                                   T  AT_
GAM2479  SLC17A6   3'  GAAATGTATTATCATAATTTT  57906        CA  TG
                                GAAATGTA  AT  TAATTTT
                                ||||||||  ||  |||||||
                                CTTTACAT  TA  ATTAAAA
                                     AA  GT
GAM2479  LOC154930 3'  TGAAATGTATTACATTTGTA   57907         ___  A
                                TGAAATGT   ACA TTGTA
                                ||||||||   ||| |||||
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                                ACTTTACA  TGT AACAT
                                    TAA  A
GAM2479 LOC51320 3' TGAAATGTACGAGTATATTTT 57908        AATT  _
                                TGAAATGTAC   GTA ATTTT
                                ||||||||||   ||| |||||
                                ACTTTACATG   CAT TAAAA
                                     CT__  A
GAM2480 CDKN2B   3' TGGCAGGGTCTGCGCAGTTGG 57911     AAAATGA  _
                                TGGCA     TTG GCAGTTGG
                                |||||     ||| ||||||||
                                ACCGT     GAC CGTCAACC
                                  CCCA___  G
GAM2480 ESR1     3' TGGAAAGGAAATGCAGTTGGA 57912    C  AAT  TTG
                                TGG AAA  GA  GCAGTTGGA
                                ||| |||  ||  |||||||||
                                ACC TTT  CT  CGTCAACCT
                                  _  C__  TTA
GAM2480 NFYC     3' TGGCAAAAATTGTGTTGG    57913       AAT    GCA
                                TGGCAAA  GATTG  GTTGG
                                |||||||  |||||  |||||
                                ACCGTTT  TTAAC  CAACC
                                   ___    A__
GAM2480 SCGB1A1  3' GGCAGAGGCTGGAGCAGTTGG 57914     AAAA_ ATT
                                GGCA   TG  GGCAGTTGG
                                ||||   ||  |||||||||
                                CCGT   AC  TCGTCAACC
                                  CTCCG C__
GAM2480 TIAM1    3' TGTTGAAAATGACAAAGTTGG 57915   GCA      TGGC
                                TG  AAAATGAT   AGTTGG
                                ||  ||||||||   ||||||
                                AC  TTTTACTG   TCAACC
                                 AAC      TT__
GAM2480 FLJ10781 3' GCAAAGATGGTGACAGTTGG  57916      A  AT
                                GCAAA ATG  TGGCAGTTGG
                                ||||| |||  ||||||||||
                                CGTTT TAC  ACTGTCAACC
                                   C  C_
GAM2480 FLJ25348 5' GCAGATGTGGCAGTTGG    57917    AAAAT  _
                                GCA    GAT TGGCAGTTGG
                                |||    ||| ||||||||||
                                CGT    CTA ACCGTCAACC
                                  _____  C
GAM2480 KIAA1155 3' TGGCAAAAAGAGTTG      57918       ATGATT  C
                                TGGCAAAA     GG AGTTG
                                ||||||||     || |||||
                                ACCGTTTT     TC TCAAC
                                     ______ _
GAM2480 KIAA1271 3' GGCAGGAACTCAAGGCAGTTGG 57919     AA  GATT
                                GGCA  AAT   GGCAGTTGG
                                ||||  |||   |||||||||
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                                CCGT  TTG   CCGTCAACC
                                  CC  AGTT
GAM2480  PRO2730   5'  TGGCAAAAGTCATGAACTTGG  57920        ___   __
                                TGGCAAAA  ATGA  TTGG
                                ||||||||  ||||  ||||
                                ACCGTTTT  TACT  AACC
                                    CAG   TG
GAM2480  LOC162828 5'  GCAAAAATTTGCACGGTTGG  57921       GATTG  __
                                GCAAAAAT   GCA  GTTGG
                                ||||||||   |||  |||||
                                CGTTTTTA   CGT  CAACC
                                    AA___  GC
GAM2480  LOC254439 3'  TGACAAGAAGGGCAGTTGG   57922      AAAT  TT
                                TGGCAA   GA  GGCAGTTGG
                                ||||||   ||  |||||||||
                                ACTGTT   CT  CCGTCAACC
                                   ____  TC
GAM2480  LOC257000 3'  TGGAAATGGGGCACAGTTGGA  57923    CAA   ATTG
                                TGG  AAATG   GCAGTTGGA
                                |||  |||||   |||||||||
                                ACC  TTTAC   TGTCAACCT
                                  ___   CCCG
GAM2481  CDH5      3'  TGACAGGGTTATGTGG     57926       ATTA
                                TGATAGG   TTATGTGG
                                |||||||   ||||||||
                                ACTGTCC   AATACACC
                                    C___
GAM2481  FMR2      3'  GATGGTAGGATTAATGT    57927     A     TT
                                GATG TAGGATTA  ATGT
                                |||| ||||||||  ||||
                                CTAC ATCCTAAT  TACA
                                  C      __
GAM2481  TAPBP     3'  GATGATAGGGTATTATTTTAGG 57928        AT    GT__
                                GATGATAGG  TATTAT   GG
                                |||||||||  ||||||   ||
                                CTACTATCC  ATAATA   CC
                                     C_    AAAT
GAM2481  TITF1     3'  GATGGTGGTCTGTGTGGCGG  57929     ATA  A  ATTA
                                GATG   GG TT   TGTGGCGG
                                ||||   || ||   ||||||||
                                CTAC   CC AG   ACACCGCC
                                  CA_  _  AC__
GAM2481  SUN1      3'  TGACAGGCAGTGAGTGTGGCGG 57930       ATTATTA
                                TGATAGG     TGTGGCGG
                                |||||||     ||||||||
                                ACTGTCC     ACACCGCC
                                    GTCACTC
GAM2481  LOC132617 3'  GATCGTGAGCAGTTATGTGGTG 57931    AG_  T  _     C
            G                    GAT   GA TA TTATGTGG GG
                                |||   || || |||||||| ||
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                                CTA   CT GT AATACACC CC
                                  GCA  C  C       A
GAM2482  ATF7     3'  TAGAACAAAGGAACCTC     57934      TCA
                                TAGG   AAAGGAACCTC
                                ||||   ||||||||||
                                ATCT   TTTCCTTGGAG
                                  TG_
GAM2482  CNTNAP2  3'  TAAGTTAGGCACACTGAGAATC 57935          _  AAA    C
              T                  TAAGTTAGGT CA   GGAA CT
                                ||||||||||  ||   ||||  ||
                                ATTCAATCCG GT   TCTT GA
                                      T  GAC    A
GAM2482  GAB2     3'  AGTTTAAGAGAAGGAACCT    57936      _   TCAA
                                AGTT AGG    AAGGAACCT
                                ||||  |||    |||||||||
                                TCAA TTC    TTCCTTGGA
                                  A   TC__
GAM2482  GAB2     3'  AGTTTAAGAGAAGGAACCT    57936      _   TCAA
                                AGTT AGG    AAGGAACCT
                                ||||  |||    |||||||||
                                TCAA TTC    TTCCTTGGA
                                  A   TC__
GAM2482  IRAK4    3'  TGATTAGGTCAGGCCCT     57937    A       AAA  AA
                                A GTTAGGTCA   GG  CCT
                                |  |||||||||   ||  |||
                                A TAATCCAGT   CC  GGA
                                 C        ___  G_
GAM2482  PLEK     3'  TAAGCTAGGGGGACCT      57938          TCAAAA  A
                                TAAGTTAGG     GG ACCT
                                |||||||||      || ||||
                                ATTCGATCC     CC TGGA
                                      _______  C
GAM2482  SLC7A6   3'  TGATTGGGTCAAAAGGCTCCT  57939    A   A        AA
                                A GTT GGTCAAAAGG  CCT
                                |  |||  ||||||||||  |||
                                A TAA CCAGTTTTCC  GGA
                                 C   C         GA
GAM2482  TPK1     3'  TAGACTCCAAGAGGAACCTCA  57940      __    A
                                TAGG  TCAA AGGAACCTCA
                                ||||  ||||  ||||||||||
                                ATCT  GGTT TCCTTGGAGT
                                  GA    C
GAM2482  BHLHB2   3'  TAAGCTTGGTTAAAAGGA    57941       A   C
                                TAAGTT GGT AAAAGGA
                                ||||||  |||  |||||||
                                ATTCGA CCA TTTTCCT
                                    A   A
GAM2482  DKFZP586H2123 3'  AGCCTCAAAAGGGGCCTCA    57942      AGG       AA
                                AGTT   TCAAAAGG  CCTCA
                                ||||   ||||||||  |||||
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                                TCGG   AGTTTTCC  GGAGT
                                  ___       CC
GAM2482  FHOD2    3'  GTTATAGACAAAAGGAGTTTCA 57943      _  T       ACC
                                GTTA GG CAAAAGGA   TCA
                                |||| || ||||||||   |||
                                CAAT TC GTTTTCCT   AGT
                                  A  T       CAA
GAM2482  FLJ10514 3'  TAAGTAAAAAGGAACTTC    57944       C        C
                                TAGGT AAAAGGAAC TC
                                ||||| ||||||||| ||
                                ATTCA TTTTCCTTG AG
                                   T        A
GAM2482  FLJ13646 3'  TAAGTTGGTCAAAAGGAA    57945        A
                                TAAGTT GGTCAAAAGGAA
                                |||||| ||||||||||||
                                ATTCAA CCAGTTTTCCTT
                                  _
GAM2482  FLJ20354 3'  TAAGTTAGGCAAAGGA      57946          CA
                                TAAGTTAGGT  AAAGGA
                                ||||||||||  ||||||
                                ATTCAATCCG  TTTCCT
                                    __
GAM2482  KIAA0978 3'  AAGTACGTCAAAAGGAGCCTCA 57947      T G         A
                                AAGT A GTCAAAAGGA CCTCA
                                |||| | |||||||||| |||||
                                TTCA T CAGTTTTCCT GGAGT
                                  _ G         C
GAM2482  PSMD12   3'  AGGTCAAAGGGAGTCTCA    57948         A   AC
                                AGGTCAAA GGA  CTCA
                                |||||||| |||  ||||
                                TCCAGTTT CCT  GAGT
                                     C   CA
GAM2482  SE57-1   3'  AGTTAGGTCAGATCTC      57949          AAAG  AC
                                AGTTAGGTCA   GA  CTC
                                ||||||||||   ||  |||
                                TCAATCCAGT   CT  GAG
                                     _____  A_
GAM2482  SEC14L1  3'  TAAGTTAGGATCATGAGGTTCC 57950          _  AA___  GAAC
            T                    TAAGTTAGG TCA    AG   CT
                                |||||||| |||    ||   ||
                                ATTCAATCC AGT    TC   GA
                                     T  IIIAC  CAAG
GAM2482  SYTL4    3'  TAAGTTAAGTGAACCT      57951          CAAAAG
                                TAAGTTAGGT     GAACCT
                                ||||||||||     ||||||
                                ATTCAATTCA     CTTGGA
                                    _______
GAM2482  LOC151518 3'  GTTTTTGAAAGGAACCTCA   57952     AGGTCA
                                GTT     AAAGGAACCTCA
                                |||     ||||||||||||
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                                CAA     TTTCCTTGGAGT
                                  AAAC__
GAM2482  LOC154222 3'  TGATTAGGTCATGGGGGGCCT  57953   A       AAA  AA
                                A GTTAGGTCA   GG  CCT
                                | |||||||||   ||  |||
                                A TAATCCAGT   CC  GGA
                                 C        ACC  CC
GAM2482  LOC220047 3'  GTGTGTGAAAAGGAACCTCA   57954    TAG  C
                                GT   GT AAAAGGAACCTCA
                                ||   || ||||||||||||
                                CA   CA TTTTCCTTGGAGT
                                 CA_  C
GAM2482  LOC255045 3'  TAAGTTGGTCAAAAGGAA    57945       A
                                TAAGTT GGTCAAAAGGAA
                                |||||| ||||||||||||
                                ATTCAA CCAGTTTTCCTT
                                       _
GAM2482  LOC93589  3'  GTTAGGTCAGAAGTATGCTCA  57955         A   GAAC
                                GTTAGGTCA AAG    CTCA
                                ||||||||| |||    ||||
                                CAATCCAGT TTC    GAGT
                                     C   ATAC
GAM2483  ACPT      3'  CGACAGTCCCGTGAAGTTGGCT 57958         TGCC________   GAA
           TCGC                   GCAGTCCC         GGC   GC
                                ||||||||          |||   ||
                                TGTCAGGG          CCG   CG
                                    CACTTCAAIII   AAG
GAM2483  ACPT      3'  CGACAGTCCCGTGAAGTTGGCT 57958         TGCC________   GAA
           TCGC                   GCAGTCCC         GGC   GC
                                ||||||||          |||   ||
                                TGTCAGGG          CCG   CG
                                    CACTTCAAIII   AAG
GAM2483  ACTB      5'  CGGCGGATCGGCAAAGGCGAGG 57959      A_   CCT  C__    A
           C                     CGGC  GTC   GC   GGCGA GC
                                ||||  |||   ||   ||||| ||
                                GCCG  TAG   CG   CCGCT CG
                                  CC   C__  TTT    C
GAM2483  AQP6      5'  GGCAGCCCTTGTCCCCAGC    57960         C  ___
                                GGCAGTCC TG   CCGGC
                                |||||||| ||   |||||
                                CCGTCGGG AC   GGTCG
                                     A  AGG
GAM2483  BGN       3'  CGGCAGCCCTGGCAGAGC     57961        T   GCC   A
                                CGGCAG CCCT   GGCG AGC
                                |||||| ||||   |||| |||
                                GCCGTC GGGA   CCGT TCG
                                   _   ____   C
GAM2483  ENG       5'  ACGGCGTCCCTGCTCCAGC    57962       A       __
                                ACGGC GTCCCTGC  CGGC
                                ||||| ||||||||  ||||
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                                TGCCG CAGGGACG  GTCG
                                  _       AG
GAM2483  FOXE3    5'  CGGCAGCCCCTGCCCGCGCGGC 57963            G   AA
                                CGGCAGTCCCTGCC GCG  GC
                                |||||||||||||| |||  ||
                                GCCGTCGGGGACGG CGC  CG
                                       G   GC
GAM2483  FXR2     5'  ACGGCGGCCCTGCCACAGC   57964      A T      G GA
                                ACGGC G CCCTGCCG C  AGC
                                ||||| | |||||||| |  |||
                                TGCCG C GGGACGGT G  TCG
                                  C _      _ __
GAM2483  GEMIN5   5'  ACGGAGGTCCGCGCGGCGAAGC 57965     CA   CT  _
              C                  ACGG  GTCC  GC CGGCGAAGCC
                                ||||  ||||  || ||||||||||
                                TGCC  CAGG  CG GCCGCTTCGG
                                  TC   __  C
GAM2483  GNB1     5'  GCAGGTGCGCGCCGGCGAGGC  57966     TCCC_       A
                                GCAG    TGCCGGCGA GC
                                ||||    ||||||||| ||
                                CGTC    GCGGCCGCT CG
                                  CACGC       C
GAM2483  GPX3     3'  GGCATCCCTGCCCAGGGGC   57967     G      _____
                                GGCA TCCCTGCC   GGC
                                |||| ||||||||   |||
                                CCGT AGGGACGG   CCG
                                  _       GTCC
GAM2483  HRMT1L1  3'  ACGGCAGCTCCTGCCGAGC   57968       TC      GCGA
                                ACGGCAG  CCTGCCG   AGC
                                |||||||  |||||||   |||
                                TGCCGTC  GGACGGC   TCG
                                   GA     _____
GAM2483  IL1RN    3'  GGCAGTCCCTGCAGTCGGCTTG 57969          C_______   GAA
                                GGCAGTCCCTGC      GGC   G
                                ||||||||||||      |||   |
                                CCGTCAGGGACG      CCG   C
                                       TCAGIII   AAG
GAM2483  MBD3     3'  ACGTGGTCCCCACCTGGAGC   57970     GCA    TG  _  CGA
                                ACG   GTCCC  CC GG   AGC
                                |||   |||||  || ||   |||
                                TGC   CAGGG  GG CC   TCG
                                  AC_    GT  A  ___
GAM2483  MEN1     5'  CGGCGGCCCCTGCCCCGCAGAG 57971      A       G_   A
              CC                  CGGC GTCCCTGCC  GCG AGCC
                                |||| |||||||||  ||| ||||
                                GCCG CGGGGACGG  CGT TCGG
                                  C       GG   C
GAM2483  MEN1     5'  CGGCGGCCCCTGCCCCGCAGAG 57971      A       G_   A
              CC                  CGGC GTCCCTGCC  GCG AGCC
                                |||| |||||||||  ||| ||||
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                                GCCG CGGGGACGG  CGT TCGG
                                  C       GG   C
GAM2483  MPP5     3'  GGCAGTTTTTGCCAGATCAAG  57972       CCC     CG_
                                GGCAGT   TGCCGG   AAG
                                ||||||   ||||||   |||
                                CCGTCA   ACGGTC   TTC
                                   AAA     TAG
GAM2483  PTGS2    3'  AGCAGTCCTGAGCTGAG     57973        C  CC   GA
                                GGCAGTCC TG  GGC  AG
                                |||||||| ||  |||  ||
                                TCGTCAGG AC  TCG  TC
                                    _ __  AC
GAM2483  SOX18    5'  CGGTGGTCCCTGCAGCG     57974     CA       C
                                CGG  GTCCCTGC GGCG
                                |||  |||||||| ||||
                                GCC  CAGGGACG TCGC
                                  AC       _
GAM2483  SUFU     3'  GGCATCCCTGCTGGTGC     57975     G      C  CGAA
                                GGCA TCCCTGC GG    GC
                                |||| ||||||| ||    ||
                                CCGT AGGGACG CC    CG
                                  _      A  A___
GAM2483  TFDP1    5'  CGGGGTCCCTGCCCTGGGC    57976     CA       ___
                                CGG  GTCCCTGCC   GGC
                                |||  |||||||||   |||
                                GCC  CAGGGACGG   CCG
                                  C_        GAC
GAM2483  TIMP3    5'  GCGCGCCGCCGGCGGGGC    57977    A  C  T      AA
                                GC GT CC GCCGGCG  GC
                                || || || |||||||  ||
                                CG CG GG CGGCCGC  CG
                                 _ C  _      CC
GAM2483  TMEPAI   3'  ACGGCAGACCCCTGAAACGAAG 57978        _     CC
                C                ACGGCAG TCCCTG  GGCGAAGC
                                 |||||||  ||||||  ||||||||
                                 TGCCGTC GGGGAC  TTGCTTCG
                                    T     T_
GAM2483  APPD     3'  ACGGCAGTCTCTGGCTGGGC   57979         C   _ C_
                                 ACGGCAGTC CTG C  GGC
                                 |||||||||  ||| |  |||
                                 TGCCGTCAG GAC G  CCG
                                     A   C AC
GAM2483  ATP6V0A1 3'  ACGGCAGCCCTGCCAATGGC   57980        T      ___
                                 ACGGCAG CCCTGCC   GGC
                                 |||||||  |||||||   |||
                                 TGCCGTC GGGACGG   CCG
                                    _      TTA
GAM2483  CALCYON  5'  GGCAGTCCCTTGTCAGGCGGC  57981          GCC__    AA
                                 GGCAGTCCCT    GGCG  GC
                                 ||||||||||    ||||  ||
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                                CCGTCAGGGA    CCGC  CG
                                      ACAGT   __
GAM2483  CNOT8    5'  ACGGCAGCCCCTGGCCCGGAGC 57982          __   CGA
                                ACGGCAGTCCCTG  CCGG   AGC
                                ||||||||||||  ||||   |||
                                TGCCGTCGGGGAC  GGCC   TCG
                                   CG   ___
GAM2483  DKFZP434F0318 3'  GGAGTCCCTAGAGAAGC     57983    C      GCC  C
                                GG AGTCCCT   GG GAAGC
                                || |||||||   || |||||
                                CC TCAGGGA   TC CTTCG
                                 _      ___ T
GAM2483  DOK4     3'  ACGGCAGTCCTGCTGCGGC    57984         C   CG   AA
                                ACGGCAGTCC TGC  GCG  GC
                                |||||||||| |||  |||  ||
                                TGCCGTCAGG ACG  CGC  CG
                                      _   A_  __
GAM2483  FLJ14117  3'  GGCAGTCCCAGGTGAAG     57985         TGCC  C
                                GGCAGTCCC    GG GAAG
                                |||||||||    || ||||
                                CCGTCAGGG    CC CTTC
                                      T___  A
GAM2483  FLJ21140  3'  GGCAGTCCTGCCTAGTAAG    57986       C     GGCG
                                GGCAGT CCTGCC    AAG
                                |||||| ||||||    |||
                                CCGTCA GGACGG    TTC
                                   _     ATCA
GAM2483  FLJ22215  3'  CGGGGTCCCGCCAGGCGAGGCC 57987     CA    T  _    A
                                CGG  GTCCC GCC GGCGA GCC
                                |||  ||||| ||| ||||| |||
                                GCC  CAGGG CGG CCGCT CGG
                                  C_    _  T    C
GAM2483  FLJ32884  5'  CGTGCAGAGCTCGGCGAAG    57988    _   TCCCT  _
                                CG GCAG    GC CGGCGAAG
                                || ||||    || ||||||||
                                GC CGTC    CG GCCGCTTC
                                 A   T_____  A
GAM2483  HSH2     3'  GGCAGCCCCTGGCAGCGA    57989          C
                                GGCAGTCCCTG CGGCGA
                                |||||||||| ||||||
                                CCGTCGGGGAC GTCGCT
                                      C
GAM2483  KIAA0194  3'  AGTCCCTGTACAACAGCC    57990        CCG   _
                                AGTCCCTG   GCGA AGCC
                                ||||||||   |||| ||||
                                TCAGGGAC   TGTT TCGG
                                     A__    G
GAM2483  KIAA0514  3'  GGCAGTCCCTGTCACTGGGGCC 57991          C  G GAA_
                                GGCAGTCCCTG CG C    GCC
                                |||||||||| || |    |||
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                                CCGTCAGGGAC GT G   CGG
                                      A  _ ACCC
GAM2483 KIAA0607 3' GGTAGTCCCTGCTGGAGCC   57992   C       C  CGA
                                GG AGTCCCTGC GG   AGCC
                                || ||||||||| ||   ||||
                                CC TCAGGGACG CC   TCGG
                                 A       A  ___
GAM2483 KIAA0644 3' GGAGTCCCTGGCCAAGC     57993   C     GCC   G
                                GG AGTCCCT   GGC AAGC
                                || |||||||   ||| ||||
                                CC TCAGGGA   CCG TTCG
                                 _     ___  G
GAM2483 KIAA0663 3' ACAGCAGTTCCTTAGGAGC   57994       C   GCC  CGA
                                ACGGCAGT CCT   GG   AGC
                                |||||||| |||   ||   |||
                                TGTCGTCA GGA   CC   TCG
                                     A   AT_ ___
GAM2483 KIAA1322 3' GCAGTCCCACTGGAGC      57995       T  C  CGA
                                GCAGTCCC GC GG   AGC
                                |||||||| || ||   |||
                                CGTCAGGG TG CC   TCG
                                     _ A  ___
GAM2483 MTX2     5' CGGCGGCTGCAGTGAGGC    57996     A TCC   C  C  A
                                CGGC G   CTGC GG GA GC
                                |||| |   |||| || || ||
                                GCCG C   GACG TC CT CG
                                  C ___   _ A  C
GAM2483 NBR2     3' GGCAGCCCCTTCGGTGGAGC  57997         GC   CGA
                                GGCAGTCCCT  CGG   AGC
                                ||||||||||  |||   |||
                                CCGTCGGGGA  GCC   TCG
                                     A_   ACC
GAM2483 RIP60    3' CGGCAGTCCTTGCCGTGACATG 57998        C    GC  A__
              C                  CGGCAGTCC TGCCG  GA   GC
                                 ||||||||| |||||  ||   ||
                                 GCCGTCAGG ACGGC  CT   CG
                                      A    A_  GTA
GAM2483 SH3GLB1  5' CGGCAGCCGGGCGGAGC     57999       CCTGCC   A
                                CGGCAGTC     GGCG AGC
                                ||||||||     |||| |||
                                GCCGTCGG     CCGC TCG
                                     C_____    C
GAM2483 SSB-3    5' CGGCAGTCCCTGCCCCGGTGGG 58000           __ CGAA
              CC                   CGGCAGTCCCTGCC  GG   GCC
                                   ||||||||||||||  ||   |||
                                   GCCGTCAGGGACGG  CC   CGG
                                        GG  ACC_
GAM2483 VRP      5' GACAGTCCCTGCTCAGTGAGCC 58001          _  C  A
                                GGCAGTCCCTGC CGG GA GCC
                                |||||||||||| ||| || |||
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                                CTGTCAGGGACG GTC CT CGG
                                      A  A  _
GAM2483  ZNF213   3'  GGTAGTGCCGACGGAGC    58002   C  CCCT     A
                                GG AGT   GCCGGCG AGC
                                || |||   ||||||| |||
                                CC TCA   CGGCTGC TCG
                                 A  _____     C
GAM2483  LOC124976 3'  CAGTGGTCCCTGCATACCAGGC 58003    CA      CG  GAA
           C                     CGG  GTCCCTGC  GC   GCC
                                |||  ||||||||  ||   |||
                                GTC  CAGGGACG  TG   CGG
                                  AC       TA  GTC
GAM2483  LOC133308 5'  GGCAGTCTCCGGCGAAG    58004       CCTG
                                GGCAGTC   CCGGCGAAG
                                |||||||   |||||||||
                                CCGTCAG   GGCCGCTTC
                                    A___
GAM2483  LOC145216 3'  GGCACTGCCGGCGAGGC    58005     GTCC       A
                                GGCA   CTGCCGGCGA GC
                                ||||   |||||||||| ||
                                CCGT   GACGGCCGCT CG
                                  _____        C
GAM2483  LOC145748 3'  GCAGTCCCACCGGGGC     58006       T    CGAA
                                GCAGTCCC GCCGG   GC
                                |||||||| |||||   ||
                                CGTCAGGG TGGCC   CG
                                    _    C___
GAM2483  LOC146268 3'  GGCGGTCCCTGCCCACGAGGAG 58007    A       G   __
           C                     GGC GTCCCTGCC GCGA  AGC
                                ||| ||||||||| ||||  |||
                                CCG CAGGGACGG TGCT  TCG
                                  C       G   CC
GAM2483  LOC148490 5'  ACGCCAGTCCCTCAGAAGC   58008    G      GCCGGC
                                ACG CAGTCCCT     GAAGC
                                ||| ||||||||     |||||
                                TGC GTCAGGGA     CTTCG
                                  G       GT_____
GAM2483  LOC149566 3'  ACGGCAGTTTCTGGGGTCGGCT 58009       CC   CC_______  GAA
             TG                   CGGCAGT  CTG       GGC   G
                                |||||||  |||       |||  |
                                GCCGTCA  GAC       CCG   C
                                    AA   CCCAGIII   AAG
GAM2483  LOC150421 3'  CGGCCGTCTGTGTGCGGGGCC  58010     A   CC  CCG   AA
                                CGGC GTC  TG   GCG  GCC
                                |||| |||  ||   |||  |||
                                GCCG CAG  AC   CGC  CGG
                                  G   __  ACA   CC
GAM2483  LOC153196 3'  CAGTCCCTTAGGGAAGC     58011       GCC  C
                                CAGTCCCT   GG GAAGC
                                ||||||||   || |||||
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                                GTCAGGGA   CC CTTCG
                                    AT_  _
GAM2483  LOC158527 5'  GGCAGCCCCTGCCATTATAAGC 58012           GCG_
              C                  GGCAGTCCCTGCCG    AAGCC
                                 ||||||||||||||    |||||
                                 CCGTCGGGGACGGT    TTCGG
                                       AATA
GAM2483  LOC219731 5'  GGCAGCACCGGCGAAG      58013       CCCT
                                 GGCAGT    GCCGGCGAAG
                                 ||||||    ||||||||||
                                 CCGTCG    TGGCCGCTTC
                                   _____
GAM2483  LOC221463 3'  ACGGCAGTCCCCGGCA      58014          TGC
                                 ACGGCAGTCCC   CGGCG
                                 ||||||||||    |||||
                                 TGCCGTCAGGG   GCCGT
                                    ___
GAM2483  LOC253019 3'  ACAGCAGTTCCTTAGGAGC    57994        C   GCC  CGA
                                 ACGGCAGT CCT   GG   AGC
                                 ||||||| |||   ||   |||
                                 TGTCGTCA GGA   CC   TCG
                                     A   AT_  ___
GAM2483  LOC253946 3'  CGGCTGCACCGGCGGAG     58015      A  CCCT      A
                                 CGGC GT    GCCGGCG AG
                                 |||| ||    ||||||| ||
                                 GCCG CG    TGGCCGC TC
                                   A _____       C
GAM2483  LOC253975 3'  ACAGCAGTTCCTTAGGAGC    57994        C   GCC  CGA
                                 ACGGCAGT CCT   GG   AGC
                                 ||||||| |||   ||   |||
                                 TGTCGTCA GGA   CC   TCG
                                     A   AT_  ___
GAM2483  LOC256789 5'  GGCAGCCCTGTCGCCGGCTTG  58016       T   ___ C___   GAA
                                 GGCAG CCCT   GC    GGC   G
                                 ||||| ||||   ||    |||   |
                                 CCGTC GGGA   CG    CCG   C
                                    _    CAG  GIII   AAG
GAM2483  LOC51291  5'  GGGGTCGCGCGCCGGCGGGGCC 58017    CA   CC_      AA
                                 GG  GTC   TGCCGGCG  GCC
                                 ||  |||   ||||||||  |||
                                 CC  CAG   GCGGCCGC  CGG
                                  C_   CGC       CC
GAM2483  LOC92521  5'  GCAGCTGCCGGCGGAG      58018      TCC       A
                                 GCAG   CTGCCGGCG AG
                                 ||||   |||||||||  ||
                                 CGTC   GACGGCCGC TC
                                    ___        C
GAM2484  ARHGEF12  3'  CCTTCTGAGCTAAAATGC     58021           __
                                 CCTTCTGAGCT  GATGT
                                 ||||||||||  |||||
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                                GGAAGACTCGA  TTACG
                                      TT
GAM2484  CARKL    3'  CTTCTGAGCCTGCCTGCTG   58022        GA    A
                                CTTCTGAGCT  TGTCT CTG
                                ||||||||||  ||||| |||
                                GAAGACTCGG  ACGGA GAC
                                     __     C
GAM2484  PACE4    3'  GACTTTCTAAGCCACTGC    58023    C       GA
                                GAC TTCTGAGCT  TGT
                                ||| |||||||||  |||
                                CTG AAGATTCGG  ACG
                                  A        TG
GAM2484  PACE4    3'  GACTTTCTAAGCCACTGC    58023    C       GA
                                GAC TTCTGAGCT  TGT
                                ||| |||||||||  |||
                                CTG AAGATTCGG  ACG
                                  A        TG
GAM2484  ARG99    3'  GACCTTCTTGCCCTTGTTTGCT 58024       GA   GA   CTA
            G                    GACCTTCT  GCT  TGT   CTG
                                ||||||||  |||  |||   |||
                                CTGGAAGA  CGG  ACA   GAC
                                     A_   GA   AAC
GAM2484  DAPK2    3'  GACCTTCTGGGCTTAAGCAATG 58025        A  _____
            C                    GACCTTCTG GCT    GATGT
                                |||||||||  |||    |||||
                                CTGGAAGAC CGA    TTACG
                                     C   ATTCG
GAM2484  FLJ20573 5'  CTTCTGAGCAGGATTCAACTG  58026        T_   G  T
                                CTTCTGAGC  GAT TC ACTG
                                |||||||||  ||| || ||||
                                GAAGACTCG  CTA AG TGAC
                                     TC   _  T
GAM2484  FLJ23550 3'  GACCTTCTAGGACCTTCTACTG 58027        AGCT   G_
                                GACCTTCTG   GAT  TCTACTG
                                |||||||||   |||  |||||||
                                CTGGAAGAT   CTG  AGATGAC
                                     C___   GA
GAM2484  GABARAPL3 3'  TTCTGGGTTGGTGTCTACTG   58028      AGC  A
                                TTCTG   TG TGTCTACTG
                                |||||   || |||||||||
                                AAGAC   AC ACAGATGAC
                                   CCA  C
GAM2484  MGC10715 3'  GACCTTCTGGAGTTGTCCCCG  58029         _  CTGA    A
                                GACCTTCTG AG    TGTCT CTG
                                |||||||||  ||    ||||| |||
                                CTGGAAGAC TC    ACAGG GGC
                                     C  A___    _
GAM2484  PLAGL2   3'  CCTTTGAGCTGACACCT     58030      C       GT
                                CCTT TGAGCTGAT  CT
                                ||||  |||||||||  ||
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                                GGAA ACTCGACTG  GA
                                  _       TG
GAM2484  PRO1768   3'  GACCTTCCTGATTCGTCTACTG 58031       TGAG    __
                                GACCTTC   CTGAT  GTCTACTG
                                |||||||   |||||  ||||||||
                                CTGGAAG   GACTA  CAGATGAC
                                    ____    AG
GAM2484  LOC149912 5'  TCTGACAACTGATGTTTGCTG  58032      __      CTA
                                TCTGA  GCTGATGT   CTG
                                |||||  ||||||||   |||
                                AGACT  TGACTACA   GAC
                                   GT       AAC
GAM2484  LOC64744  5'  GACCCTCTGGCCGGCCTGTCTG 58033        A   A__    A
           CTG                    GACCTTCTG GCTG   TGTCT CTG
                                |||||||||| ||||   ||||| |||
                                CTGGGAGAC CGGC   ACAGA GAC
                                    _   CGG    C
GAM2485  CST4     3'  ACTACAGTGGGTGGGAGTGGGT 58036        A   TACACA_
           GG                     ATTACAGTG GGT      GGTGG
                                |||||||||| |||      |||||
                                TGATGTCAC CCA      CCACC
                                    _  CCCTCAC
GAM2485  HCS      3'  CAGTGAGATTGCACCACTG    58037         A   AGG
                                CAGTGAGGTT CAC   TG
                                |||||||||| |||   ||
                                GTCACTCTAA GTG   AC
                                     C   GTG
GAM2485  TEM8     3'  TTACAATGAGGTTACCCATGG  58038            ACAG
                                TTACAGTGAGGTTAC    GTGG
                                ||||||||||||||    ||||
                                AATGTTACTCCAATG    TACC
                                      GG__
GAM2485  CG012    5'  ATTACAGTAGGTAGGGTTAGGT 58039        G    TACAC_
           GG                     ATTACAGT AGGT     AGGTGG
                                |||||||| ||||     ||||||
                                TAATGTCA TCCA     TCCACC
                                    _   TCCCAA
GAM2485  DCNP1    3'  TACAGTGGAAGACAGGTGG    58040        A  TTAC
                                TACAGTG GG    ACAGGTGG
                                ||||||| ||    ||||||||
                                ATGTCAC CT    TGTCCACC
                                    _ TC__
GAM2485  FLJ21777  5'  ATTATGGCGAGGCTTCCGGGTG 58041      CA       ACACA
           G                      ATTA  GTGAGGTT     GGTGG
                                ||||  ||||||||    |||||
                                TAAT  CGCTCCGA    CCACC
                                  AC       AGGC_
GAM2485  KIAA0628  3'  GTGGTGGTTACACAGGTG    58042     A_
                                GTG  GGTTACACAGGTG
                                |||  ||||||||||||
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                                CAC  CCAATGTGTCCAC
                                  CA
GAM2485  KIAA1111  3'  AGTGGGTGGTACAGGTGG    58043     A   TAC
                                AGTG GGT   ACAGGTGG
                                |||| |||   ||||||||
                                TCAC CCA   TGTCCACC
                                  _   CCA
GAM2485  LOC128346 3'  CAGTTTCACACAGGTGG     58044     GAGG
                                CAGT    TTACACAGGTGG
                                ||||    ||||||||||||
                                GTCA    AGTGTGTCCACC
                                  A___
GAM2485  LOC132617 3'  TCACGAGCCCTTTATACAGGTG 58045     _   GAGG   C
              G                  TTAC AGT    TTA ACAGGTGG
                                |||| |||    ||| ||||||||
                                AGTG TCG    AAT TGTCCACC
                                  C   GGA_   A
GAM2485  LOC256273 3'  GTGGTGATCAGCACAGGTGG   58046     A_    _
                                GTG  GGTTA CACAGGTGG
                                |||  ||||| |||||||||
                                CAC  CTAGT GTGTCCACC
                                  CA    C
GAM2486  LETM1     3'  AAAGATGAGTGTGACACA    58049         CGCGA   CGT
                                GAAGATGAG    GAC   ACA
                                |||||||||    |||   |||
                                TTTCTACTC    CTG   TGT
                                     ACA__   ____
GAM2486  FLJ10483  3'  GAAGGGAGCGCGAGGCC     58050     AT        A
                                GAAG  GAGCGCGAG CC
                                ||||  ||||||||| ||
                                CTTC  CTCGCGCTC GG
                                  C_        C
GAM2486  FLJ12190  3'  AGATGAGCTGGGAGAACAG    58051         GC_   CCGT
                                AGATGAGC   GAGA    ACAG
                                ||||||||   ||||    ||||
                                TCTACTCG   CTCT    TGTC
                                     ACC   _____
GAM2486  HSPC166   3'  GAAGATGAGTGAGAAC      58052         CGC    CCGT
                                GAAGATGAG   GAGA    AC
                                |||||||||   ||||    ||
                                CTTCTACTC   CTCT    TG
                                     A__    _____
GAM2486  KIAA0495  5'  GAGGATGAGCGCTTCCGC    58053     A        GAGA
                                GA GATGAGCGC    CCGT
                                || |||||||||    ||||
                                CT CTACTCGCG    GGCG
                                  C        AA__
GAM2486  KIAA1656  3'  GAAGGTGAGCGCAGGGCG    58054     A      G  AC
                                GAAG TGAGCGC AG  CG
                                |||| |||||| ||  ||
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                                CTTC ACTCGCG TC  GC
                                  C      _ CC
GAM2486  SLC21A11  5'  GAGGATGAGCGCCAGGTTCCCG 58055    A       G  A___
                                GA GATGAGCGC AG   CCG
                                || ||||||||| ||   |||
                                CT CTACTCGCG TC   GGC
                                 C       G  CAAG
GAM2486  LOC147525 5'  GAGTGAGCGCACGCAACCGTGC 58056   _     GA__     A
           AG                     GA TGAGCGC   GACCGT CAG
                                || |||||||   |||||| |||
                                CT ACTCGCG   TTGGCA GTC
                                 C      TGCG     C
GAM2486  LOC197342 3'  GAAGACGAGTGTGAGCGT    58057         CGC   AC
                                GAAGATGAG   GAG  CGT
                                |||||||||   |||  |||
                                CTTCTGCTC   CTC  GCA
                                      ACA  __
GAM2486  LOC200918 3'  GAAGATGAGCATGAGGAGGTA  58058          C   ACC
                                GAAGATGAGCG GAG   GTA
                                |||||||||||| |||   |||
                                CTTCTACTCGT CTC   CAT
                                       A   CTC
GAM2487  FSCN3    5'  GACACCACAGGTGATGTCTCCG 58061     TG  ____
                                GGCG  AC   GATGTCTCCG
                                ||||  ||   ||||||||||
                                CTGT  TG   CTACAGAGGC
                                  GG  TCCA
GAM2487  KIAA0418  3'  TGGTAGGCGTGGCAATGC    58062    A      A
                                TG TAGGCGTG CGATGT
                                || |||||||| ||||||
                                AC ATCCGCAC GTTACG
                                 C       C
GAM2487  KIAA1210  3'  TGATAGGCAGTGATTTCT    58063        _   CGATG
                                TGATAGGC GTGA    TCT
                                |||||||| ||||    |||
                                ACTATCCG CACT    AGA
                                     T   AA___
GAM2487  LOC257486 3'  TGATAGGCAGTGATTTCT    58063        _   CGATG
                                TGATAGGC GTGA    TCT
                                |||||||| ||||    |||
                                ACTATCCG CACT    AGA
                                     T   AA___
GAM2488  APPBP2   3'  ACTGCAGTTTTCTGTCTGCA  58066       C_  GTG
                                ACTGCAGT  TC   CTGCA
                                ||||||||  ||   |||||
                                TGACGTCA  AG   GACGT
                                     AA  ACA
GAM2488  RAB7     5'  CTGTGTCCCATATCTGCAT   58067    CA      _
                                CTG  GTCTCGTG CTGCAT
                                |||  |||||||| ||||||
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                                GAC  CAGGGTAT GACGTA
                                  A_       A
GAM2488  TNXB     5'  CTGTGGCCTCGTGACTCCTGC  58068     CA       ____
                                CTG  GTCTCGTG    CTGC
                                |||  ||||||||    ||||
                                GAC  CGGAGCAC    GACG
                                  AC       TGAG
GAM2488  ABLIM    5'  TGCATCTGCTGCATCG      58069      GTC  G
                                TGCA   TC TGCTGCATCG
                                ||||   || ||||||||||
                                ACGT   AG ACGACGTAGC
                                   ___  _
GAM2488  BANK     3'  TGCAGTCTCGTAGTTGTCG    58070           CTGCA
                                TGCAGTCTCGTG    TCG
                                ||||||||||||    |||
                                ACGTCAGAGCAT    AGC
                                      CAAC_
GAM2488  KIAA0542 3'  CTGCAGTCTCTGCTGGGC    58071          G    CATC
                                CTGCAGTCTC TGCTG    GC
                                |||||||||| |||||    ||
                                GACGTCAGAG ACGAC    CG
                                     _    C___
GAM2488  KLK7     3'  TGCATCACTGCATTGC      58072      G  TCGT      C
                                TGCA TC    GCTGCAT GC
                                |||| ||    ||||||| ||
                                ACGT AG    TGACGTA CG
                                  _ _____       A
GAM2488  KLK7     3'  TGCATCACTGCATTGC      58072      G  TCGT      C
                                TGCA TC    GCTGCAT GC
                                |||| ||    ||||||| ||
                                ACGT AG    TGACGTA CG
                                  _ _____       A
GAM2488  LOC221814 3'  CTGCAGATTCAATTATGCATTG 58073       TC   TGC_    C
              CA                  CTGCAG  TCG    TGCAT GCA
                                |||||| |||    ||||| |||
                                GACGTC  AGT    ACGTA CGT
                                   TA   TAAT    A
GAM2488  LOC245726 3'  ACTGCAGTCTTGTGATCA    58074          C   CTG
                                ACTGCAGTCT GTG   CA
                                |||||||||| |||   ||
                                TGACGTCAGA CAC   GT
                                     A   TA_
GAM2489  ARPC2    3'  CTCGTTTCTGCAGATTATT    58077       G    A
                                CTTGTT TTGTA GATTATT
                                |||||| ||||| |||||||
                                GAGCAA GACGT CTAATAA
                                   A    _
GAM2489  CCR2     3'  TTGTTGTTATATACAGATT    58078           ___
                                TTGTTGTTGTA   AGATT
                                ||||||||||   |||||
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                                AACAACAATAT  TCTAA
                                     ATG
GAM2489 PTPRG    3' TTGCTGTTGTATAAGATT   58079        __
                                TTGTTGTTGTA AGATT
                                |||||||||| |||||
                                AACGACAACAT TCTAA
                                     AT
GAM2489 RPS17    3' TTGCTGTTGTCCCAGATT   58080       A__
                                TTGTTGTTGT  AGATT
                                |||||||||  |||||
                                AACGACAACA  TCTAA
                                     GGG
GAM2489 TRIM9    5' CTTGTTGTTGTTGGGGACT  58081        AA__
                                CTTGTTGTTGT  GATT
                                ||||||||||  ||||
                                GAACAACAACA  CTGA
                                     ACCC
GAM2489 XRCC2    3' CTCGTTGTTGTTTCGATT   58082        AA_
                                CTTGTTGTTGT  GATT
                                ||||||||||  ||||
                                GAGCAACAACA  CTAA
                                     AAG
GAM2489 24432    3' CCTGCCGCATGAGATTATT  58083       TGTA
                                CTTGTTGT  AGATTATT
                                ||||||||  ||||||||
                                GGACGGCG  TCTAATAA
                                    TAC_
GAM2489 ANKT     3' CTTGTTATTGTTCAAATT   58084       A_
                                CTTGTTGTTGT AGATT
                                |||||||||| |||||
                                GAACAATAACA TTTAA
                                     AG
GAM2489 EREG     3' TTGTTGTTGTTGTATTATT  58085        AAG
                                TTGTTGTTGT  ATTATT
                                ||||||||||  ||||||
                                AACAACAACA  TAATAA
                                     ACA
GAM2489 FLJ10099 3' TTGTTGTTACTATGATTATT 58086       _ A
                                TTGTTGTTG TA GATTATT
                                ||||||||| || |||||||
                                AACAACAAT AT CTAATAA
                                     G  A
GAM2489 KIAA0774 5' CTTGCTGTCAGTCAGATTATT 58087       _ A
                                CTTGTTGTT GT AGATTATT
                                ||||||||| || ||||||||
                                GAACGACAG CA TCTAATAA
                                     T  G
GAM2489 LOC147093 5' TTGTTGTTGTTGCATCATT  58088       AAG
                                TTGTTGTTGT  ATTATT
                                ||||||||||  ||||||
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                                AACAACAACA   TAGTAA
                                     ACG
GAM2489  LOC90625  3'  TTGTTGTTGCGCGAGCATT    58089          AA  T
                                TTGTTGTTGT  GA TATT
                                ||||||||||  || ||||
                                AACAACAACG  CT GTAA
                                     CG  C
GAM2490  TLR4      3'  TTGATGAGGTAAGAGTTGAAAT 58092         ___ CC  A
           GACTT                     TTGATGAG   AG  TT AAATGACTT
                                ||||||||   ||  || |||||||||
                                AACTACTC   TC  AA TTTACTGAA
                                     CAT  TC  C
GAM2490  TLR4      3'  TTGATGAGGTAAGAGTTGAAAT 58092         ___ CC  A
           GACTT                     TTGATGAG   AG  TT AAATGACTT
                                ||||||||   ||  || |||||||||
                                AACTACTC   TC  AA TTTACTGAA
                                     CAT  TC  C
GAM2490  TLR4      3'  TTGATGAGGTAAGAGTTGAAAT 58092         ___ CC  A
           GACTT                     TTGATGAG   AG  TT AAATGACTT
                                ||||||||   ||  || |||||||||
                                AACTACTC   TC  AA TTTACTGAA
                                     CAT  TC  C
GAM2490  TLR4      3'  TTGATGAGGTAAGAGTTGAAAT 58092         ___ CC  A
           GACTT                     TTGATGAG   AG  TT AAATGACTT
                                ||||||||   ||  || |||||||||
                                AACTACTC   TC  AA TTTACTGAA
                                     CAT  TC  C
GAM2490  DKFZP564D166 3'  TTGAGAGAGGTTAAGTGACTT  58093      T    CC    AA
                                TTGA GAGAG  TTAA  TGACTT
                                |||| |||||  ||||  ||||||
                                AACT CTCTC  AATT  ACTGAA
                                  _    C_   C_
GAM2490  DUSP14    3'  TTAATGAGGCCCCAAAGTGA   58094         A       A
                                TTGATGAG GCCTTAAA TGA
                                |||||||| |||||||| |||
                                AATTACTC CGGGGTTT ACT
                                     _       C
GAM2490  TCL6      3'  TGGTGAGAGCCCAAGGGGATGA 58095     A       TAAA__
           CTT                       TG TGAGAGCCT      ATGACTT
                                ||  |||||||||      |||||||
                                AC ACTCTCGGG      TACTGAA
                                  C        TTCCCC
GAM2490  TCL6      3'  TGGTGAGAGCCCAAGGGGATGA 58095     A       TAAA__
           CTT                       TG TGAGAGCCT      ATGACTT
                                ||  |||||||||      |||||||
                                AC ACTCTCGGG      TACTGAA
                                  C        TTCCCC
GAM2490  TED       3'  GATGGGGGCAGTCAAATGACTT 58096      AGA  CTTA
                                GATG   GC    AAATGACTT
                                ||||   ||   |||||||||
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                                CTAC   CG    TTTACTGAA
                                  CCC  TCAG
GAM2490  LOC138429 3'  CTGATGAGAAAAGTGACT    58097         GCCTT   A
                                TTGATGAGA     AAA TGACT
                                |||||||||     ||| |||||
                                GACTACTCT     TTT ACTGA
                                      _____   C
GAM2490  LOC93273  3'  TTAATGAGAGTTGACATGACTT 58098          CCTTAAA
                                TTGATGAGAG      ATGACTT
                                ||||||||||      |||||||
                                AATTACTCTC      TACTGAA
                                      AACTG__
GAM2491  RAB4B     5'  ATTGTGTGTTGTTGTGGG     58101      C  TGAGAG
                                ATTG GT      TGTTGTGGG
                                |||| ||      |||||||||
                                TAAC CA      ACAACACCC
                                  A  CA____
GAM2491  LOC158263 3'  TATTCGTCCTGTTGTGGG     58102      G    GAGAG
                                TATT CGTT     TGTTGTGGG
                                |||| ||||     |||||||||
                                ATAA GCAG     ACAACACCC
                                  _    G____
GAM2492  C18orf2   3'  AAAATTCTAGAGGAGAAAAAG  58105        A    A
                                AAAATTT AGAG AGAAAAAG
                                ||||||| |||| ||||||||
                                TTTTAAG TCTC TCTTTTTC
                                     A    C
GAM2492  CNGB3     3'  TAGAAAGATTTAAAAAGAAAAA 58106        _     GA
            G                    TAGAAA ATTTAA  GAAGAAAAAG
                                ||||||| |||||||  ||||||||||
                                ATCTTT TAAATT  TTTCTTTTTC
                                   C     __
GAM2492  CSN1      3'  GAAAATTTAGCTTAAGAAAAAG 58107          A AG_
                                GAAAATTTA G   AAGAAAAAG
                                ||||||||| |   |||||||||
                                CTTTTAAAT C   TTCTTTTTC
                                      _ GAA
GAM2492  F9        3'  TAGAAGATTCAAGATAGAA    58108       A      GA
                                TAGAA ATTTAAGA  AGAA
                                ||||| ||||||||  ||||
                                ATCTT TAAGTTCT  TCTT
                                   C       A_
GAM2492  HPSE      3'  AAAATTTAAGAGTATTGAAA   58109           AA__
                                AAAATTTAAGAG    GAAA
                                ||||||||||||    ||||
                                TTTTAAATTCTC    CTTT
                                      ATAA
GAM2492  ITGAM     3'  GAAAACTCGCGGGGGAGAAGAA 58110         AA____
                                GAAAATTT      GAGAAGAA
                                ||||||||      ||||||||
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                                CTTTTGAG     CTCTTCTT
                                     CGCCCC
GAM2492  KCNMB1   3'  TAGAGAATTCAAACAAAGAA  58111      A       A
                                TAGA AATTTAAG GAAGAA
                                |||| |||||||| ||||||
                                ATCT TTAAGTTT TTTCTT
                                  C       G
GAM2492  KRTHB6   3'  CAGAAGGTAGGAGGAAGAAAAA 58112       AATTTA  A
           G                     TAGAA     AG GAAGAAAAAG
                                ||||||     || ||||||||||
                                GTCTT     TC CTTCTTTTTC
                                   CCATCC  _
GAM2492  MAX      3'  AAAAATTTAAAAAAAAAA    58113
                                GAAAATTTAAGAGAAGAA
                                ||||||||||||||||||
                                TTTTTAAATTTTTTTTTT

GAM2492  MAX      3'  AAAAATTTAAAAAAAAAA    58113
                                GAAAATTTAAGAGAAGAA
                                ||||||||||||||||||
                                TTTTTAAATTTTTTTTTT

GAM2492  NTRK2    3'  AGAAAATTTAAAAAAAGAAAAA 58114
           G                     AGAAAATTTAAGAGAAGAAAAAG
                                |||||||||||||||||||||||
                                TCTTTTAAATTTTTTTCTTTTTC

GAM2492  PBX2     3'  AGAAAGACAGAGGAGAAAAAG  58115      ATTTA   A
                                AGAAA     AGAG AGAAAAAG
                                |||||     |||| ||||||||
                                TCTTT     TCTC TCTTTTTC
                                   CTG__    C
GAM2492  POLA     3'  TAGAAAACTTTATTCTTAAGAA 58116         AA_____
           GAA                     TAGAAAATTT      GAGAAGAA
                                ||||||||||      ||||||||
                                ATCTTTTGAA      TTCTTCTT
                                     ATAAGAA
GAM2492  SCD      3'  AGAAAACGTTCAGGGAAGAGAA 58117       TTA_  A    A
           AG                     AGAAAAT    AG GAAGA AAAG
                                |||||||    || ||||| ||||
                                TCTTTTG    TC CTTCT TTTC
                                    CAAG  C    C
GAM2492  SIX2     3'  CAGAAAAAAGAAAAGAGAAG   58118       TTT__
                                TAGAAAA    AAGAGAAG
                                |||||||    ||||||||
                                GTCTTTT    TTCTCTTC
                                     TTCTT
GAM2492  SIX3     5'  AGAAAATTCAGGGAGAGGAA   58119         A_   A
                                AGAAAATTTA  GAGA GAA
                                ||||||||||  |||| |||
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                                TCTTTTAAGT  CTCT CTT
                                      CC    C
GAM2492  TBR1     3'  AGAAAATTAAAAGAGAGA    58120        T_     A
                                AGAAAATT  AAGAGA GA
                                ||||||||  |||||| ||
                                TCTTTTAA  TTCTCT CT
                                     TT     _
GAM2492  TRIM37   3'  GAAAATAAAGAAGAAAA     58121       TTA
                                GAAAAT   AGAGAAGAAAA
                                ||||||   ||||||||||
                                CTTTTA   TTTCTTCTTTT
                                   ___
GAM2492  WIF1     3'  TAGAAAACTTAAAAGGAAGA   58122             _
                                TAGAAAATTTAAGAG AAGA
                                |||||||||||||| ||||
                                ATCTTTTGAATTTTC TTCT
                                          C
GAM2492  ZFHX1B   5'  CAGAAATGGTGAGAAGAAAAAG 58123       ATTTAA
                                TAGAAA     GAGAAGAAAAAG
                                ||||||     ||||||||||||
                                GTCTTT     CTCTTCTTTTTC
                                   ACCA__
GAM2492  1D12A    3'  AAAATTTAAAAGAGGGGAAAAA 58124           A__
            G                    AAAATTTAAGAGA   GAAAAAG
                                ||||||||||||   |||||||
                                TTTTAAATTTTCT   CTTTTTC
                                      CCC
GAM2492  ALS2CR2  3'  TAGAAATACAGAAGAAAAA   58125       ATT  AG
                                TAGAAA   TA  AGAAGAAAAA
                                ||||||   ||  ||||||||||
                                ATCTTT   AT  TCTTCTTTTT
                                   ___  G_
GAM2492  AMOT     5'  AGAGAACTAAGAGAAGA     58126     A    T
                                AGA AATT AAGAGAAGA
                                ||| |||| |||||||||
                                TCT TTGA TTCTCTTCT
                                  C    _
GAM2492  CAPS2    3'  TAGAAAATTTAAAATTATGAAG 58127             ____
                                TAGAAAATTTAAGA    GAAG
                                ||||||||||||||    ||||
                                ATCTTTTAAATTTT    CTTC
                                      AATA
GAM2492  CD109    3'  TAGAAGGCAAAGAAGAAA    58128       AATTTA
                                TAGAA     AGAGAAGAAA
                                |||||     ||||||||||
                                ATCTT     TTTCTTCTTT
                                   CCG___
GAM2492  DKFZp566H0824 5'  CAGAAAAGAGAAGGAAAA    58129       ATTTA      A
                                TAGAAA     AGAGAAG AAAA
                                ||||||     ||||||| ||||
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                                GTCTTT     TCTCTTC TTTT
                                   _____       C
GAM2492  DKFZp762E1511 5'  AAAAGCTCAAGGGGAAGAAAA  58130      A     A_
                                GAAA TTTAAG  GAAGAAAA
                                |||| ||||||  ||||||||
                                TTTT GAGTTC  CTTCTTTT
                                  C      CC
GAM2492  FLJ11565  3'  CAGAAGATAAGAGAAGA     58131       AATT
                                TAGAA    TAAGAGAAGA
                                |||||    ||||||||||
                                GTCTT    ATTCTCTTCT
                                   CT__
GAM2492  FLJ14001  3'  CAGAAAGGGAAGGAAGAAAA   58132       ATTT   A
                                TAGAAA    AAG GAAGAAAA
                                ||||||    ||| ||||||||
                                GTCTTT    TTC CTTCTTTT
                                    CCC_  _
GAM2492  FLJ23132  3'  AGAAAATTTAGGATGAAG    58133          A  _
                                AGAAAATTTA GA GAAG
                                |||||||||| || ||||
                                TCTTTTAAAT CT CTTC
                                      C  A
GAM2492  FLJ23186  3'  CAGAAAATAAAGAGGAAGAA   58134        TT    _
                                TAGAAAAT  AAGAG AAGAA
                                ||||||||  ||||| |||||
                                GTCTTTTA  TTCTC TTCTT
                                     T_    C
GAM2492  HNRNPG-T  3'  AGAAAATTTACAAGGGAAGAA  58135          __  A
                                AGAAAATTTA  AG GAAGAA
                                ||||||||||  || ||||||
                                TCTTTTAAAT  TC CTTCTT
                                      GT  C
GAM2492  KIAA0820  3'  TAGAGAATTCAAAGGAAGAA   58136     A       A
                                TAGA AATTTAAG GAAGAA
                                |||| |||||||| ||||||
                                ATCT TTAAGTTT CTTCTT
                                  C       C
GAM2492  KIAA1615  3'  TAGAAATTTAAAGAGAAG    58137       A  T
                                TAGAAA TT AAGAGAAG
                                |||||| || ||||||||
                                ATCTTT AA TTCTCTTC
                                   A  T
GAM2492  KIAA1718  3'  TAGAAAATTAAGAAATAAAAAA 58138          T     _
            AG                    TAGAAAATT AAGAGA AGAAAAAG
                                |||||||||| |||||| ||||||||
                                ATCTTTTAA TTCTTT TTTTTTTC
                                      _     A
GAM2492  LBP-9    3'  AGAAACAACGTAGAGAAGAAA  58139       ATTTA_
                                AGAAA      AGAGAAGAAA
                                |||||      ||||||||||
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                                TCTTT     TCTCTTCTTT
                                   GTTGCA
GAM2492  MGC20235  3'  TAGAAAACTTGAAAAGA     58140          AA
                                TAGAAAATTT  GAGAAGA
                                ||||||||||  |||||||
                                ATCTTTTGAA  CTTTTCT
                                          __
GAM2492  MGC21738  3'  TAGGAATTTAGGAGAAAAAAAA 58141     AA     A
            G                    TAG  AATTTA GAGAAGAAAAAG
                                |||  |||||| ||||||||||||
                                ATC  TTAAAT CTCTTTTTTTTC
                                  C_     C
GAM2492  P66       3'  GAAAATGGGGAGAAGAAA    58142       TTAA
                                GAAAAT    GAGAAGAAA
                                ||||||    |||||||||
                                CTTTTA    CTCTTCTTT
                                    CCC_
GAM2492  RABEX5    3'  TAGAAAATTAAACCAAAGAAG  58143         TA___
                                TAGAAAATT     AGAGAAG
                                |||||||||     |||||||
                                ATCTTTTAA     TTTCTTC
                                      TTTGG
GAM2492  SCDGF-B   3'  TAGAAAATGCTATGAGAGGAAA 58144         _  A    A
            AAG                    TAGAAAAT TTA GAGA GAAAAAG
                                |||||||| ||| |||| |||||||
                                ATCTTTTA GAT CTCT CTTTTTC
                                      C   A    C
GAM2492  SCDGF-B   3'  TAGAAAATGCTATGAGAGGAAA 58144         _  A    A
            AAG                    TAGAAAAT TTA GAGA GAAAAAG
                                |||||||| ||| |||| |||||||
                                ATCTTTTA GAT CTCT CTTTTTC
                                      C   A    C
GAM2492  ZNF342    3'  GAAAATTTACTTGGAGAAG    58145         A___
                                GAAAATTTA    GAGAAG
                                |||||||||    ||||||
                                CTTTTAAAT    CTCTTC
                                      GAAC
GAM2492  LOC130814 3'  TAGAGAACTTAAGAGTAAG    58146      A        _
                                TAGA AATTTAAGAG AAG
                                |||| |||||||||| |||
                                ATCT TTGAATTCTC TTC
                                   C         A
GAM2492  LOC144524 5'  TAGAAAATTTAAACATCGAGAA 58147           _____
            G                    TAGAAAATTTAA     GAGAAG
                                ||||||||||||     ||||||
                                ATCTTTTAAATT     CTCTTC
                                       TGTAG
GAM2492  LOC145624 5'  GAAAGAAACAAGAAGAAAAAG  58148      ATTTAA
                                GAAA     GAGAAGAAAAAG
                                ||||     ||||||||||||
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                                CTTT     TTCTTCTTTTTC
                                  CTTTG_
GAM2492  LOC145864 3'  AGAAAATTTAAATTGAGAAG  58149          ___
                                AGAAAATTTAA  GAGAAG
                                ||||||||||  ||||||
                                TCTTTTAAATT  CTCTTC
                                     TAA
GAM2492  LOC150468 3'  AGAAAATTTGAGAGTAAG    58150        A  _
                                AGAAAATTT AGAG AAG
                                ||||||||| |||| |||
                                TCTTTTAAA TCTC TTC
                                     C   A
GAM2492  LOC151057 3'  AGAAAGAAAGAAGAAAAA    58151      ATTTA
                                AGAAA    AGAGAAGAAAAA
                                |||||    ||||||||||||
                                TCTTT    TTTCTTCTTTTT
                                  C____
GAM2492  LOC151877 3'  AGAAAATTTAACAGAAAAA   58152         G
                                AGAAAATTTAA AGAAGAA
                                |||||||||| |||||||
                                TCTTTTAAATT TCTTTTT
                                     G
GAM2492  LOC203286 3'  CAGAAGGGAGAGAAGAAA    58153      AATTTA
                                TAGAA     AGAGAAGAAA
                                |||||     |||||||||
                                GTCTT     TCTCTTCTTT
                                  CCC___
GAM2492  LOC221773 3'  TAAAAAAACAAAGAAGAAGAA 58154       TTT  _
                                TAGAAAA   AAGA GAAGAA
                                |||||||   |||| ||||||
                                ATTTTTT   TTCT CTTCTT
                                    TGT   T
GAM2492  LOC51313  3'  GATTTATAAGAGAAGAAAA   58155    AAATT
                                GA    TAAGAGAAGAAAA
                                ||    ||||||||||||
                                CT    ATTCTCTTCTTTT
                                 AAAT_
GAM2492  LOC90925  3'  TAGAAAATAAAAGAAG      58156       TT
                                TAGAAAA  TAAGAGAAG
                                |||||||  |||||||||
                                ATCTTTT  ATTTTCTTC
                                  __
GAM2493  ADH7     5'  CAAACATAGACTTTTTCT    58159         C  GC
                                TAAACATAGAC TT  CT
                                |||||||||| ||  ||
                                GTTTGTATCTG AA  GA
                                     A  AA
GAM2493  DKFZP434P0721 3'  TATAAACATAGGCCCTGC    58160         A
                                TATAAACATAG CCTTGC
                                |||||||||| ||||||
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                                ATATTTGTATC GGGACG
                                      C
GAM2493  FLJ21615  3'  TATAAACATAGATCTTTCTATT 58161          C   GC
                                TATAAACATAGA CTT  CTATT
                                |||||||||||| |||  |||||
                                ATATTTGTATCT GAA  GATAA
                                       A   A_
GAM2493  LOC145663 5'  TATATGCATAGACCATTG    58162      AA      _
                                TATA  CATAGACC TTG
                                ||||  |||||||| |||
                                ATAT  GTATCTGG AAC
                                  AC       T
GAM2493  LOC253970 3'  ACGTAGACCTCCATTG      58163    A      TGC
                                AC TAGACCT   CTATTG
                                || |||||||   ||||||
                                TG ATCTGGA   GGTAAC
                                 C      ___
GAM2494  ITGA1     3'  TTTTGGATAATGCATGAC     58166         AT    G
                                TTTTGGATA  GTGCA GAC
                                |||||||||  ||||| |||
                                AAAACCTAT  TACGT CTG
                                      __    A
GAM2494  NPTX1     3'  TGCGTGTGCGTGTGCAGG     58167      TT  GATAA
                                TGCGT  TG    TGTGCAGG
                                |||||  ||    ||||||||
                                ACGCA  AC    ACACGTCC
                                   C_  GC___
GAM2494  PLAB      5'  TGCTTTTGGATGAGGTTGGGG  58168     G      AAT  GCA
                                TGC TTTTGGAT   GT   GG
                                ||| ||||||||   ||   ||
                                ACG AAAACCTA   CA   CC
                                  _      CTC  ACC
GAM2494  SRGAP1    5'  TGTGTTTTGGAAAATGAGA    58169    C      T   TGCA
                                TG GTTTTGGA AATG    GGA
                                || |||||||| ||||    |||
                                AC CAAAACCT TTAC    TCT
                                 A       T    _____
GAM2494  BRAG      3'  TGTGTTTTGGAATTGGGA     58170    C      TAATG  CA
                                TG GTTTTGGA     TG  GGA
                                || ||||||||     ||  |||
                                AC CAAAACCT     AC  CCT
                                 A       TA___  __
GAM2494  KIAA0339  3'  TGCGTTTTGGGGTGGTCAGG   58171         ATAA  TG
                                TGCGTTTTGG    TG  CAGG
                                ||||||||||    ||  ||||
                                ACGCAAAACC    AC  GTCC
                                      CC__  CA
GAM2494  PRO1048   3'  TGCGTTTTGATGATGGAGG    58172         ATAAT   C
                                TGCGTTTTGG     GTG AGG
                                ||||||||||     ||| |||
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                                ACGCAAAACT    TAC TCC
                                      AC___   C
GAM2494  LOC136120 3'  TGCGGTGATCCTGGTGTGCAGG 58173     ____     ATAA
                                TGCG   TTTTGG   TGTGCAGG
                                ||||   ||||||   ||||||||
                                ACGC   AGGACC   ACACGTCC
                                  CACT    ____
GAM2494  LOC202451 5'  TGTGTTTTGGAAATCTAAAGG  58174    C      T  G  C
                                TG GTTTTGGA AAT TG AGG
                                || |||||||| ||| || |||
                                AC CAAAACCT TTA AT TCC
                                 A       _  G  T
GAM2494  LOC255096 5'  TGGGTTCTGGATGTGCAGGA   58175    C      TAA
                                TG GTTTTGGA   TGTGCAGGA
                                || ||||||||   |||||||||
                                AC CAAGACCT   ACACGTCCT
                                 C      ___
GAM2494  LOC92305  3'  GTGTCTGTGTGTGCAGGA    58176    _   GATAA
                                GT TTTG    TGTGCAGGA
                                || ||||    |||||||||
                                CA AGAC    ACACGTCCT
                                 C   AC___
GAM2495  LOC170063 3'  TGGATGTAGGTAGAATCACGTA 58179      T   AGCGCT
           T                     TGGAT GTA     ATCACGTAT
                                |||||| |||     |||||||||
                                ACCTA CAT     TAGTGCATA
                                   _  CCATCT
GAM2496  M6PR     3'  TAACTCTGACTTACAAC     58182     G   A
                                TAAC TCT ACTTACAAC
                                |||| ||| |||||||||
                                ATTG AGA TGAATGTTG
                                   _  C
GAM2496  XK       3'  GCCTAGAAGAACACAACATGGT 58183      ACT___     C
                                GTCTA     TACAACA GGT
                                |||||     ||||||| |||
                                CGGAT     GTGTTGT CCA
                                   CTTCTT      A
GAM2496  DKFZp727G131 3'  TAACGTTTAACTACAAC     58184      C    T
                                TAACGT TAACT ACAAC
                                |||||| ||||| |||||
                                ATTGCA ATTGA TGTTG
                                   A    _
GAM2496  LOC146229 3'  GTCCAACTTGACTGGTC     58185        ACA  AC
                                GTCTAACTT   AC  GGTC
                                |||||||||   ||  ||||
                                CAGGTTGAA   TG  CCAG
                                     C__  A_
GAM2497  COG8     3'  TTCAGGTATTTGGGGACTACAT 58188         AAC  AT_
                                TTCAGGTATTT   GA   CAT
                                ||||||||||   ||   |||
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                                AAGTCCATAAA  CT  GTA
                                     CCC  GAT
GAM2497 DUSP5    3' TTCAAGTATGACTAAGAATCAT 58189       __   C
                                TTCAGGTAT  TTAA GAATCAT
                                |||||||||  |||| |||||||
                                AAGTTCATA  GATT CTTAGTA
                                     CT   _
GAM2497 SECTM1   3' TTCAGATATTCGAGTCAT    58190       TAA  A
                                TTCAGGTATT  CGA TCAT
                                ||||||||||  ||| ||||
                                AAGTCTATAA  GCT AGTA
                                     ___  C
GAM2497 SGK      3' AGGCATCTGAATACGAGTCAT 58191       A___  A
                                AGGTATTT   ACGA TCAT
                                ||||||||   |||| ||||
                                TCCGTAGA   TGCT AGTA
                                     CTTA   C
GAM2497 SMARCC1  3' TTCAGGTATTTTGTAGAAT   58192       AAC_
                                TTCAGGTATTT   GAAT
                                ||||||||||   ||||
                                AAGTCCATAAA   CTTA
                                      ACAT
GAM2497 CCR6     3' TTCAAGCATGAATCA      58193       TTAAC
                                TTCAGGTAT   GAATCA
                                |||||||||   ||||||
                                AAGTTCGTA   CTTAGT
                                     _____
GAM2497 CCR6     3' TTCAAGCATGAATCA      58193       TTAAC
                                TTCAGGTAT   GAATCA
                                |||||||||   ||||||
                                AAGTTCGTA   CTTAGT
                                     _____
GAM2497 CYLD     3' TTCAGGTATTAATAACTTCAT 58194       __   GAA
                                TTCAGGTATT  TAAC  TCAT
                                ||||||||||  ||||  ||||
                                AAGTCCATAA  ATTG  AGTA
                                      TT   A__
GAM2497 FLJ10388 3' TTCAGATATTTAACGAAT   58195
                                TTCAGGTATTTAACGAAT
                                ||||||||||||||||||
                                AAGTCTATAAATTGCTTA

GAM2497 FLJ21439 3' CAGGTATTCTTTAATCAT   58196       AACG
                                CAGGTATTT   AATCAT
                                |||||||||   ||||||
                                GTCCATAAG   TTAGTA
                                      AAA_
GAM2497 PINK1    3' TTCAGAGTATAAGAATCAT   58197      _   TTAAC
                                TTCAG GTAT   GAATCAT
                                ||||| ||||   |||||||
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                                AAGTC CATA    CTTAGTA
                                  T   TT___
GAM2497 STIP-1   3' TTCAAGTATTTTGAAATCAT  58198         AAC
                                TTCAGGTATTT  GAATCAT
                                ||||||||||  |||||||
                                AAGTTCATAAA  TTTAGTA
                                      AC_
GAM2497 UBE2G1   3' TTCAGTATTTGAACTAAATCAT 58199     G   _  _
                                TTCAG TATTT AAC GAATCAT
                                ||||| ||||| ||| |||||||
                                AAGTC ATAAA TTG TTTAGTA
                                  _   C  A
GAM2497 ZNF291   3' TTCAAGTATCTACAGTCAT   58200         ACGAA
                                TTCAGGTATTTA   TCAT
                                ||||||||||||   ||||
                                AAGTTCATAGAT   AGTA
                                      GTC__
GAM2497 LOC157285 3' TCCAGGTATCCCAGTCAT   58201         AACGAA
                                TTCAGGTATTT    TCAT
                                ||||||||||    ||||
                                AGGTCCATAGG    AGTA
                                      GTC___
GAM2497 LOC255423 5' TTCAAGTAGCCCCAGCGAGTCA 58202       __   A  A
          T                    TTCAGGTA  TTTA CGA TCAT
                               ||||||||  |||| ||| ||||
                               AAGTTCAT  GGGT GCT AGTA
                                    CG   C  C
GAM2497 LOC64146  3' TTCAGGTATTTGGGGACTACAT 58188         AAC  AT_
                                TTCAGGTATTT  GA  CAT
                                ||||||||||  ||  |||
                                AAGTCCATAAA  CT  GTA
                                      CCC  GAT
GAM2497 LOC93538  3' TTCAGGTACTTAGAAACC   58203         AC
                                TTCAGGTATTTA  GAATC
                                ||||||||||||  |||||
                                AAGTCCATGAAT  TTTGG
                                      C_
GAM2498 PTPN1    3' TAGTGCACTATGGATGCCTTTG 58206        CAAACAG  GA_
          G                     TAGTGTACTA     GC  TGG
                                ||||||||||     ||  |||
                                ATCACGTGAT     CG  ACC
                                     ACCTA__  GAA
GAM2498 CMG1     5' GTGTTACAGGGCGATGG    58207     AC   AACA
                                GTGT  TACA   GGCGATGG
                                ||||  ||||   ||||||||
                                CACA  ATGT   CCGCTACC
                                  __   C___
GAM2498 KIAA1253 3' TAGTATACTATAAGCAGG   58208         C  A
                                TAGTGTACTA AA CAGG
                                |||||||||| || ||||
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                                ATCATATGAT TT GTCC
                                      A  C
GAM2498 KIAA1643 3' TGCAGACGAACAGGCGGTG   58209     CT  A      A
                                TGTA  AC AACAGGCG TG
                                ||||  || |||||||| ||
                                ACGT  TG TTGTCCGC AC
                                  C_ C      C
GAM2498 MGC19556 3' TAATGTACTACGAGCGTAAGG 58210         AAACA   AT_
                                TAGTGTACTAC    GGCG  GG
                                ||||||||||    ||||  ||
                                ATTACATGATG    TCGC  CC
                                      C____   ATT
GAM2498 LOC151996 5' TAGTGTTTGCAAACAGCCCTCT 58211      ACTA     GCGA_
             GG                   TAGTGT   CAAACAG    TGG
                                ||||||   |||||||    |||
                                ATCACA   GTTTGTC    ACC
                                   AAC_     GGGAG
GAM2498 LOC166206 5' GTGAACTGCAGAGACAATGG  58212    T  A  AAC
                                GTG ACT CA   AGGCGATGG
                                ||| ||| ||   |||||||||
                                CAC TGA GT   TCTGTTACC
                                  T  C  C__
GAM2499 CYP1B1   3' GTCAGTTGTAATGGGAGTTCTG 58215       __  TA  CC
                                GTCAGTTG  GTG  AG  CTG
                                ||||||||  |||  ||  |||
                                CAGTCAAC  TAC  TC  GAC
                                     AT   CC  AA
GAM2499 EZH1    3' TCTTTCAGTTTGAGCCCTG   58216    G    GGTGTA
                                TCT TCAGTT     AGCCCTG
                                ||| ||||||     |||||||
                                AGA AGTCAA     TCGGGAC
                                  A     AC_____
GAM2499 GMNN    5' TCTGCAGTAAAGCCCT      58217      CAGTT   T
                                TCTGT    GGTG AAGCCCT
                                |||||    |||| |||||||
                                AGACG    TCAT TTCGGGA
                                  ______   _
GAM2499 KIAA0493 5' TCTGTCAGCTGGCTTCCTTG  58218          GTAAG  C
                                TCTGTCAGTTGGT    CC TG
                                ||||||||||||    || ||
                                AGACAGTCGACCG    GG AC
                                      AA___  A
GAM2499 KIAA1155 3' TCTTCAGTTTTAAAGCCCTG  58219    G    GGTGT
                                TCT TCAGTT    AAGCCCTG
                                ||| ||||||    ||||||||
                                AGA AGTCAA    TTCGGGAC
                                  _     AAT__
GAM2499 YAP     5' CTGTCAGTTGGCGGGCAGTCTT 58220          TA_  CCC
             GC                   CTGTCAGTTGGTG  AG  TGC
                                ||||||||||||  ||  |||
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                                GACAGTCAACCGC  TC  ACG
                                       CCG  AGA
GAM2499  LOC116349 3'  TGTCAGTTGGTGTGTCAAAGC  58221          ____
                                TGTCAGTTGGTGT   AAGC
                                |||||||||||||   ||||
                                ACAGTCAACCACA   TTCG
                                       CAGT
GAM2499  LOC121273 3'  TGGCAGTTGGTTTCCTTGC   58222   T      GTAAG  C
                                TG CAGTTGGT    CC TGC
                                || ||||||||    || |||
                                AC GTCAACCA    GG ACG
                                 C      AA___  A
GAM2499  LOC145748 3'  TCAGTCGGAGCCCTG      58223       TGTA
                                TCAGTTGG   AGCCCTG
                                ||||||||   |||||||
                                AGTCAGCC   TCGGGAC
                                      ____
GAM2499  LOC147639 5'  TGCAGTTGGTGAGATGGGCCCT 58224   T       TAA___
           GC                    TG CAGTTGGTG     GCCCTGC
                                || |||||||||     |||||||
                                AC GTCAACCAC     CGGGACG
                                 _       TCTACC
GAM2499  LOC203078 3'  TCCGCTGCTGGTGTGAGTCTTG 58225      CA      A  CCC
           C                     TCTGT  GTTGGTGT AG   TGC
                                ||||| ||||||| ||   |||
                                AGGCG  CGACCACA TC   ACG
                                   A_      C  AGA
GAM2500  HRMT1L2   3'  GGGAGCCCCGAAACCGCCTA   58228     AA      AAAAT
                                GGGA  CCTCGAAA    CCTA
                                ||||  ||||||||    ||||
                                CCCT  GGGGCTTT    GGAT
                                  C_      GGC__
GAM2500  LIMD1    3'  GGGCAAAAAAAAAAATCCT    58229     AAACCTC
                                GGG      GAAAAAAATCCT
                                |||      ||||||||||||
                                CCC      TTTTTTTTAGGA
                                  GTTT___
GAM2500  FLJ32312  3'  GGGAATGAGAAAAATCCTAA   58230      ACCTC  A
                                GGGAA    GA AAAAATCCTAA
                                |||||    || ||||||||||||
                                CCCTT    CT TTTTTAGGATT
                                   A____  C
GAM2500  KIAA0820  3'  AGGAAGAAGCAAAGGGAATCCT 58231      ACCT   AAA
           AA                    GGGAA   CGAA   AATCCTAA
                                |||||   ||||  ||||||||
                                TCCTT   GTTT   TTAGGATT
                                   CTTC   CCC
GAM2500  SGKL     3'  GGGAATACTTAAAAATCCTAA  58232      AC  CGAA
                                GGGAA  CT   AAAAATCCTAA
                                |||||  ||   ||||||||||
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                                CCCTT  GA    TTTTTAGGATT
                                   AT  A___
GAM2500  LOC133686 3'  GGGAAAAAAAAAAAGTCCTAA  58233       CCTC       _
                                GGGAAA    GAAAAAAA TCCTAA
                                ||||||    |||||||| ||||||
                                CCCTTT    TTTTTTTT AGGATT
                                   ____       C
GAM2500  LOC149276 5'  GAGAAACCTTGGGAACCCT    58234         CGAAAAA
                                GGGAAACCT      AATCCT
                                |||||||||      ||||||
                                CTCTTTGGA      TTGGGA
                                     ACCC___
GAM2500  LOC152674 3'  GGGAAACCTATGAACATCCTAA 58235         CGAAAAAA
                                GGGAAACCT       ATCCTAA
                                |||||||||       |||||||
                                CCCTTTGGA       TAGGATT
                                     TACTTG__
GAM2500  LOC200574 3'  AGGAAACCTAAATTCT      58236         CGAAAA    C
                                GGGAAACCT     AAAT CT
                                |||||||||     |||| ||
                                TCCTTTGGA     TTTA GA
                                   _______    A
GAM2501  ALDH2     3'  TTTTTCTTGGTTTTGTTGCTGA 58239           CGG  G
            T                   TTTTTCTTGGTTTT   GT TGAT
                                |||||||||||||   || ||||
                                AAAAAGAACCAAAA   CG ACTA
                                     CAA  _
GAM2501  GOLGA4    3'  TTTTTCTTGGTCTTTTGGC    58240           CG
                                TTTTTCTTGGTTTT  GGT
                                |||||||||||||  |||
                                AAAAAGAACCAGAA  CCG
                                     AA
GAM2501  CYP2C18   3'  TTTTTCTTTGTTTTCTAGTGAT 58241         G     GGGT
                                TTTTTCTT GTTTTC    GTGAT
                                |||||||| ||||||    |||||
                                AAAAAGAA CAAAAG    CACTA
                                     A     AT__
GAM2501  DKFZP434G2226 3'  TTTTGCTTGGTTTTGAAGTGAT 58242      T       C   T
                                TTTT CTTGGTTTT GGG GTGAT
                                |||| ||||||||| ||| |||||
                                AAAA GAACCAAAA CTT CACTA
                                   C       _   _
GAM2501  DKFZP434L1123 5'  TTTTTCTGGTTTTTGAGGT    58243        T     C   T
                                TTTTTCT GGTTTT GGG GT
                                ||||||| |||||| ||| ||
                                AAAAAGA CCAAAA CTC CA
                                   _     A   _
GAM2501  EBNA1BP2  3'  TTTTTCTTGGTTCTTTGTAT   58244           CGG
                                TTTTTCTTGGTTTT   GTGT
                                |||||||||||||   ||||
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                                AAAAAGAACCAAGA  CATA
                                      AA_
GAM2501 LAMB4    3' CTTTTTTTGGTTTTCATTCCTT 58245      C       GGTG_
           GAT                  TTTTT TTGGTTTTCG    TGAT
                                ||||| ||||||||||    ||||
                                GAAAA AACCAAAAGT    ACTA
                                   A        AAGGA
GAM2501 MGC20576 3' TTTTTCTTGGTTTCTGGAT   58246          TC
                                TTTTTCTTGGTTT  GGGT
                                ||||||||||||  ||||
                                AAAAAGAACCAAA  CCTA
                                      GA
GAM2501 MGC8407  3' TTTTTTTTGGCTTTGCAGGGTG 58247      C      _   T
           AT                   TTTTT TTGGTTTT CGGG GTGAT
                                ||||| |||||||| |||| |||||
                                AAAAA AACCGAAA GTCC CACTA
                                   A       C   _
GAM2501 OSF-2    3' TTTTTCTGGTTTTTGGAT    58248       T    C
                                TTTTTCT GGTTTT GGGT
                                ||||||| |||||| ||||
                                AAAAAGA CCAAAA CCTA
                                   _     A
GAM2501 PRO0245  5' TTCTTCTTTGGACTGGGTGTG  58249        _ TTTTC
                                TTTTTCTT GG    GGGTGTG
                                |||||||| ||    |||||||
                                AAGAAGAA CC    CCCACAC
                                     A  TGA__
GAM2501 LOC113179 3' TTTTTTTTGGTTTTGGGC    58250      C      C
                                TTTTT TTGGTTTT GGGT
                                ||||| |||||||| ||||
                                AAAAA AACCAAAA CCCG
                                   A       _
GAM2501 LOC144486 3' TTTTTCTTGGCTTTTTGTAT   58251          CGG
                                TTTTTCTTGGTTTT   GTGT
                                ||||||||||||||   ||||
                                AAAAAGAACCGAAA   CATA
                                      AA_
GAM2501 LOC84518  3' TTTTTTTTGGTTTTCAGGT    58252      C
                                TTTTT TTGGTTTTCGGGT
                                ||||| ||||||||||||
                                AAAAA AACCAAAAGTCCA
                                   A
GAM2502 CORO1C   3' TGTTTCTGCAAATTTG      58255       GT   C
                                TGTTTCT  GCA ATTTG
                                |||||||  ||| |||||
                                ACAAAGA  CGT TAAAC
                                     __  T
GAM2502 EIF3S10  3' TTCATGCTTTTTGTGTTATGGT 58256         C_   CACATT
           GAA                  TTCATGTTT  TGTG     TGAA
                                |||||||||  ||||     ||||
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                                AAGTACGAA ACAC     ACTT
                                     AA   AATACC
GAM2502 PRB4     3' ATGTTTCAAGGCATTTGAA   58257       TGT  CA
                                ATGTTTC  GCA TTTGAA
                                |||||||  |||  ||||||
                                TACAAAG  CGT AAACTT
                                   TTC  __
GAM2502 PRH2     3' ATGTTTCAAGGCATTTGAA   58257       TGT  CA
                                ATGTTTC  GCA TTTGAA
                                |||||||  |||  ||||||
                                TACAAAG  CGT AAACTT
                                   TTC  __
GAM2502 DKFZP762D096 3' CGTTTCTGTGTCAGCATTTTGA 58258          _ _   _
              A                  TGTTTCTGTG CA CATTT GAA
                                 |||||||||| || ||||| |||
                                 GCAAAGACAC GT GTAAA CTT
                                      A C    A
GAM2502 KIAA0852  5' ATGTTTCTGTGGAAATTTTG  58259          CACA_
                                ATGTTTCTGTG    TTTG
                                ||||||||||    ||||
                                TACAAAGACAC    AAAC
                                     CTTTA
GAM2502 PDE1C    3' TTCATGTTTTGTTTCTGTTTGA 58260         C  GCACA
                                TTCATGTTT TGT    TTTGA
                                ||||||||| |||    |||||
                                AAGTACAAA ACA    AAACT
                                    _  AAGAC
GAM2502 TLK1     3' TTCCTGTTTCTGTGTAACA   58261    A       C_
                                TTC TGTTTCTGTG  ACA
                                ||| ||||||||||  |||
                                AAG ACAAAGACAC  TGT
                                  G        AT
GAM2502 LOC143914 5' TTCTGAGGGCCTGTGCATTTGA 58262    A  TT__      CA
              A                  TTC TG   TCTGTGCA  TTTGAA
                                 ||| ||   ||||||||  ||||||
                                 AAG AC   GGACACGT  AAACTT
                                   _ TCCC      __
GAM2502 LOC145623 5' TTCATGTTTTATGTATGTTTGA 58263        C   CACA
              A                  TTCATGTTT TGTG   TTTGAA
                                 |||||||| ||||   ||||||
                                 AAGTACAAA ATAC   AAACTT
                                     _   ATAC
GAM2502 LOC151057 3' TGTTCACTAGCACATTTG    58264      _  T
                                TGTTT CTG GCACATTTG
                                ||||| ||| |||||||||
                                ACAAG GAT CGTGTAAAC
                                  T  _
GAM2502 LOC154089 3' ATATTTCTAAACATTTGAA   58265        TGC
                                ATGTTTCTG  ACATTTGAA
                                |||||||||  |||||||||
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                                TATAAAGAT   TGTAAACTT
                                     T__
GAM2502  LOC158431 3'  TTCATTTTCTGTGGCTCTTG   58266      G       CACA
                                TTCAT TTTCTGTG    TTTG
                                ||||| ||||||||    ||||
                                AAGTA AAAGACAC    GAAC
                                   _       CGA_
GAM2502  LOC164684 3'  TTCATATTTCTGTCATTTTG   58267           G  CA
                                TTCATGTTTCTGT CA  TTTG
                                |||||||||||| ||  ||||
                                AAGTATAAAGACA GT  AAAC
                                       _ A_
GAM2502  LOC201799 5'  TTCCTGTTTCCTGCTTGTTTG  58268     A      G   ACA
                                TTC TGTTTCT TGC   TTTG
                                ||| ||||||| |||   ||||
                                AAG ACAAAGG ACG   AAAC
                                  G      _   AAC
GAM2502  LOC91464  3'  TATTTTGCACATTTGA      58269       CTG
                                TGTTT   TGCACATTTGA
                                |||||   ||||||||||
                                ATAAA   ACGTGTAAACT
                                   ____
GAM2503  SMAC      5'  TTGAAGCCGGGAGGCACA     58272          A  TGTC
                                TTGAAGTCG GG    CACA
                                |||||||| ||    ||||
                                AACTTCGGC CC    GTGT
                                      _ TCC_
GAM2503  DKFZp434K114 5'  TTGGAGCGAAGCGTGCA     58273     A  T       C
                                TTG AG CGAGGTGT CA
                                ||| || |||||||| ||
                                AAC TC GCTTCGCA GT
                                  C _       C
GAM2503  MARK2     5'  TTGGAGTCAAGGTGTCCCA    58274     A           A
                                TTG AGTCGAGGTGTCC CA
                                ||| |||||||||||| ||
                                AAC TCAGTTCCACAGG GT
                                  C           _
GAM2503  THEA      3'  TTGAGGTTGAGGTGCCAC     58275      A  C      T
                                TTGA GT GAGGTG CCAC
                                |||| || |||||| ||||
                                AACT CA CTCCAC GGTG
                                   C  A     _
GAM2503  LOC145053 5'  TTAAAGTCAAAACTTCACACA  58276          GG GTC
                                TTGAAGTCGA  T   CACACA
                                ||||||||||  |   ||||||
                                AATTTCAGTT  G   GTGTGT
                                      TT AA_
GAM2503  LOC145748 3'  TTGTAGTCAACAGTTCACACAA 58277     A     GGT  C
              G                  TTG AGTCGA   GT CACACAAG
                                ||| ||||||   || ||||||||
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                                AAC TCAGTT   CA GTGTGTTC
                                  A     GT_  A
GAM2504  ACCN2    3'  GGAGGAGAGAGGGGCAGC    58280          ATA
                                GGAGGAGAGAGG   CGGC
                                ||||||||||||  ||||
                                CCTCCTCTCTCC   GTCG
                                      CC_
GAM2504  ADAR     3'  TGAAGAGGAGAGGGGCTGC    58281      G      A  ATACG
                                TGAAG AGGAGAG GG    GC
                                ||||| ||||||| ||    ||
                                ACTTC TCCTCTC CC    CG
                                   _      C  GA___
GAM2504  ADAR     3'  TGAAGAGGAGAGGGGCTGC    58281      G      A  ATACG
                                TGAAG AGGAGAG GG    GC
                                ||||| ||||||| ||    ||
                                ACTTC TCCTCTC CC    CG
                                   _      C  GA___
GAM2504  ADAR     3'  TGAAGAGGAGAGGGGCTGC    58281      G      A  ATACG
                                TGAAG AGGAGAG GG    GC
                                ||||| ||||||| ||    ||
                                ACTTC TCCTCTC CC    CG
                                   _      C  GA___
GAM2504  ADCY8    5'  AGGAGGAGGAGGGGGTCACGG  58283        A    A___
                                AGGAGGAG GAGG   TACGG
                                |||||||| ||||   |||||
                                TCCTCCTC CTCC   GTGCC
                                     _   CCCA
GAM2504  ADCY8    5'  GGAGGAGAAGGGAGGC      58282         A   TAC
                                GGAGGAGAG GGA   GGC
                                ||||||||| |||   |||
                                CCTCCTCTT CCT   CCG
                                     C   ___
GAM2504  BAT3     3'  TGAAGGAAGAGGGGGGAAACG  58284          AGA   T
                                TGAAGGAGGAG   GGA ACG
                                ||||||||||   ||| |||
                                ACTTCCTTCTC   CCT TGC
                                      CCC   T
GAM2504  BAT3     3'  TGAAGGAAGAGGGGGGAAACG  58284          AGA   T
                                TGAAGGAGGAG   GGA ACG
                                ||||||||||   ||| |||
                                ACTTCCTTCTC   CCT TGC
                                      CCC   T
GAM2504  BAT3     3'  TGAAGGAAGAGGGGGGAAACG  58284          AGA   T
                                TGAAGGAGGAG   GGA ACG
                                ||||||||||   ||| |||
                                ACTTCCTTCTC   CCT TGC
                                      CCC   T
GAM2504  C1orf6   5'  AGGAGGAGGAGGGGCGGGC    58285        A    ATAC
                                AGGAGGAG GAGG   GGC
                                |||||||| ||||   |||
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                                TCCTCCTC CTCC    CCG
                                     _   CCGC
GAM2504  CDC25B   5'  GAGGGAGGAGAGGGATGCG   58286    A       A   A
                                GA GGAGGAGAG GGAT CG
                                || ||||||||| ||||| ||
                                CT CCTCCTCTC CCTA GC
                                 C       _   C
GAM2504  CDC25B   5'  GAGGGAGGAGAGGGATGCG   58286    A       A   A
                                GA GGAGGAGAG GGAT CG
                                || ||||||||| ||||| ||
                                CT CCTCCTCTC CCTA GC
                                 C       _   C
GAM2504  EN2      3'  GAAGGAGGAGGGAGTTAGG   58287         A   GA  C
                                GAAGGAGGAG GAG  TA GG
                                |||||||||| |||  || ||
                                CTTCCTCCTC CTC  AT CC
                                      C   A_  _
GAM2504  HLF      3'  TGAAGGAGGGAGGGGAT     58288         A   A
                                TGAAGGAGG GAG GGAT
                                ||||||||| ||| ||||
                                ACTTCCTCC CTC CCTA
                                     _  C
GAM2504  HMGA1    3'  TGAAGGAGCAGAGAGGGC    58289        G      ATACG
                                TGAAGGAG AGAGAGG    GC
                                |||||||| |||||||    ||
                                ACTTCCTC TCTCTCC    CG
                                    G     _____
GAM2504  LASS1    3'  AGGAGGAGGAGGAGGTGG    58290        A    TAC
                                AGGAGGAG GAGGA   GG
                                |||||||| |||||   ||
                                TCCTCCTC CTCCT   CC
                                     _    CCA
GAM2504  MUC3B    3'  TGAGGAGAGGAGGGAGGAT   58291     A_     A
                                TGA  GGAGGAG GAGGAT
                                |||  ||||||| ||||||
                                ACT  TCTCCTC CTCCTA
                                  CC      C
GAM2504  NEDD4    5'  TGGAGGAGGAGGAGGAGAAGCG 58292    A      A    TAC
                                TG AGGAGGAG GAGGA   GGCG
                                || |||||||| |||||   ||||
                                AC TCCTCCTC CTCCT   TCGC
                                 C       _    CT_
GAM2504  NPEPPS   5'  AGGAGGAGGGGAGGAGGC    58293        A_    TAC
                                AGGAGGAG  GAGGA   GGC
                                ||||||||  |||||   |||
                                TCCTCCTC  CTCCT   CCG
                                     CC    ___
GAM2504  NPR1     3'  GGAGGGGAGGGGATCAG     58294       A   A   A
                                GGAGG GAG GGAT CGG
                                ||||| ||| |||| |||
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                                CCTCC CTC CCTA GTC
                                  C  C   _
GAM2504  PAFAH1B1  5'  GAAGGAGGGGGGAGGATGGCG  58295       AGA    AC
                                GAAGGAGG  GAGGAT  GGCG
                                ||||||||  ||||||  ||||
                                CTTCCTCC  CTCCTA  CCGC
                                    CCC    __
GAM2504  PCTK1   5'  AGGAGGAGGAGGCGGCGGC   58297       A   ATA
                                AGGAGGAG GAGG  CGGC
                                |||||||| ||||  ||||
                                TCCTCCTC CTCC  GCCG
                                    _  GCC
GAM2504  PCTK1   5'  AGGAGGAGGAGGCGGCGGC   58297       A   ATA
                                AGGAGGAG GAGG  CGGC
                                |||||||| ||||  ||||
                                TCCTCCTC CTCC  GCCG
                                    _  GCC
GAM2504  PCTK1   5'  TGAGGAGGAGGAGGCGGC   58296    A     A   ATA
                                TGA GGAGGAG GAGG  CGGC
                                ||| ||||||| ||||  ||||
                                ACT CCTCCTC CTCC  GCCG
                                  _     _   ___
GAM2504  PCTK1   5'  TGAGGAGGAGGAGGCGGC   58296    A     A   ATA
                                TGA GGAGGAG GAGG  CGGC
                                ||| ||||||| ||||  ||||
                                ACT CCTCCTC CTCC  GCCG
                                  _     _   ___
GAM2504  PIM1    3'  TGAAGGAGGGGGTGAGGGA   58298       A___  A
                                TGAAGGAGG   GAG GGA
                                |||||||||   ||| |||
                                ACTTCCTCC   CTC CCT
                                    CCCA  _
GAM2504  POU2F2  3'  TGGAGGAGGAGGAGGAT    58299    A     A
                                TG AGGAGGAG GAGGAT
                                || |||||||| ||||||
                                AC TCCTCCTC CTCCTA
                                 C      _
GAM2504  PPP3R1  5'  AGGAGGGGGAGAGGGGGC   58300      A_    ATAC
                                AGGAGG  GAGAGG   GGC
                                ||||||  ||||||   |||
                                TCCTCC  CTCTCC   CCG
                                   CC     C___
GAM2504  SEZ6L   5'  TGGAGGAGGAGAGGAGAT   58301    A       AG
                                TG AGGAGGAGAG  GAT
                                || ||||||||||  |||
                                AC TCCTCCTCTC  CTA
                                 C        CT
GAM2504  SF1     5'  GAGGGAGGAGAGAGGGCAC   58302    A        A
                                GA GGAGGAGAGAGG TAC
                                || ||||||||||| |||
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                                CT CCTCCTCTCTCC GTG
                                 C          C
GAM2504  SMG1     5'  AGGAGGAGGAGGCGGCGGC   58297        A   ATA
                                AGGAGGAG GAGG   CGGC
                                |||||||| ||||   ||||
                                TCCTCCTC CTCC   GCCG
                                     _   GCC
GAM2504  SMG1     5'  AGGAGGAGGAGGAGGCGGC   58303        A    TA
                                AGGAGGAG GAGGA  CGGC
                                |||||||| |||||  ||||
                                TCCTCCTC CTCCT  GCCG
                                     _   CC
GAM2504  SPTBN4   3'  GGAGGAGAGAGGAAAACAG   58304          T_
                                GGAGGAGAGAGGA  ACGG
                                ||||||||||||  ||||
                                CCTCCTCTCTCCT  TGTC
                                       TT
GAM2504  TCIRG1   5'  TGAAGGAGGAGGCGGGGC    58305         AGA  ATAC
                                TGAAGGAGGAG   GG   GGC
                                ||||||||||   ||   |||
                                ACTTCCTCCTC   CC   CCG
                                      CG_ ____
GAM2504  XYLB     3'  TGAAGGAGGGGGAGAGGA    58306        A_
                                TGAAGGAGG  GAGAGGA
                                |||||||||  |||||||
                                ACTTCCTCC  CTCTCCT
                                      CC
GAM2504  APELIN   5'  GGGGGAGGAGAGGTCGGGCG  58307   A   _    ATAC
                                GG GGAG AGAGG    GGCG
                                || |||| |||||    ||||
                                CC CCTC TCTCC    CCGC
                                 C   C    AGC_
GAM2504  ARHGEF11 3'  TGAAGGAGGAGTGGGGAC    58308         AGA
                                TGAAGGAGGAG   GGAT
                                ||||||||||   ||||
                                ACTTCCTCCTC   CCTG
                                      ACC
GAM2504  ARP3BETA 3'  AGGAGGAGGAGGGAGAGC    58309        A   ATAC
                                AGGAGGAG GAGG    GGC
                                |||||||| ||||    |||
                                TCCTCCTC CTCC    TCG
                                     _   CTC_
GAM2504  CECR7    5'  TGAAGGAAGAGACAGACGG   58310          G  GAT
                                TGAAGGAGGAGA AG   ACGG
                                |||||||||||| ||   ||||
                                ACTTCCTTCTCT TC   TGCC
                                       G ___
GAM2504  DKFZP434L0718 3'  TGAAGAGGAGAGAGATGG    58311      G        ATAC
                                TGAAG AGGAGAGAGG    GG
                                ||||| ||||||||||    ||
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                                ACTTC TCCTCTCTCT    CC
                                  _         A___
GAM2504  DKFZp547I224 5'  GGAGGAGGAGAGGCGCTCTGCG 58312         _     ATACG_
                                GGAGGAG AGAGG      GCG
                                ||||||| |||||      |||
                                CCTCCTC TCTCC      CGC
                                    C     GCGAGA
GAM2504  DKFZp762K222 5'  GAGGGAGGGGAGGCCACGGCG  58313    A     AGA    A
                                GA GGAGG   GAGG TACGGCG
                                || |||||   |||| |||||||
                                CT CCTCC   CTCC GTGCCGC
                                 C     C__    G
GAM2504  FLJ10815  3'  TGGAGGAGGAGAGGGAT     58314    A         A
                                TG AGGAGGAGAG GGAT
                                || |||||||||| ||||
                                AC TCCTCCTCTC CCTA
                                 C         _
GAM2504  FLJ14486  3'  TGAAGGGAGAGAGAGGAC     58315       AG
                                TGAAGG  GAGAGAGGAT
                                ||||||  ||||||||||
                                ACTTCC  CTCTCTCCTG
                                    CT
GAM2504  KIAA0326  3'  AAGGAGGAGAGGGGAGCCAA   58316          A   TA
                                AAGGAGGAGAG GGA  CGG
                                |||||||||| |||  |||
                                TTCCTCCTCTC CCT  GTT
                                      C   CG
GAM2504  KIAA0545  3'  AGGAGGAGAGAGTCGGC     58317           GATA
                                AGGAGGAGAGAG    CGGC
                                ||||||||||||    ||||
                                TCCTCCTCTCTC    GCCG
                                      A___
GAM2504  KIAA0652  3'  GGAGGAGGAGGAGGGAC     58318        A     TAC
                                GGAGGAG GAGGA   GGC
                                ||||||| |||||   |||
                                CCTCCTC CTCCT   CTG
                                   _     CC_
GAM2504  KIAA0669  5'  AGGAGGAGGAGGCGGTGGC    58320        A    ATAC
                                AGGAGGAG GAGG    GGC
                                |||||||| ||||    |||
                                TCCTCCTC CTCC    CCG
                                    _    GCCA
GAM2504  KIAA0669  5'  AGGAGGAGGAGGAGGC      58319        A     TAC
                                AGGAGGAG GAGGA   GGC
                                |||||||| |||||   |||
                                TCCTCCTC CTCCT   CCG
                                    _    ____
GAM2504  MAP2K5    5'  AGGAGGAGGAGGAAGGCGGCG  58321         A     TA_
                                AGGAGGAG GAGGA   CGGCG
                                |||||||| |||||   |||||
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                                TCCTCCTC CTCCT   GCCGC
                                     _    TCC
GAM2504  MGC10818  5'  TGAAGGAGGTGAGGGTGGC   58322        A   A  ATAC
                                TGAAGGAGG GAG GG   GGC
                                ||||||||| ||| ||   |||
                                ACTTCCTCC CTC CC   CCG
                                    A  _ A___
GAM2504  MGC16824  5'  GGAGGAGGAGGAGGAC      58323       A    TAC
                                GGAGGAG GAGGA  GGC
                                ||||||| |||||  |||
                                CCTCCTC CTCCT  CTG
                                     _    C__
GAM2504  MGC21854  3'  TGAAGAGGGGAGAGGATACAA  58324      GA  A
                                TGAAG  GG GAGAGGATACGG
                                |||||  || ||||||||||||
                                ACTTC  CC CTCTCCTATGTT
                                   TC  _
GAM2504  MGC2452   5'  TGAAGAGGAGAGGGGGTGC    58325      G      A  ATACG
                                TGAAG AGGAGAG GG    GC
                                ||||| ||||||| ||    ||
                                ACTTC TCCTCTC CC    CG
                                   _      _ CCA__
GAM2504  MGC4172   3'  AAGGGGGAGAGGGTGCAG     58326      A  A     ATA
                                AAGG GG GAGAGG   CGG
                                |||| || ||||||   |||
                                TTCC CC CTCTCC   GTC
                                  _ _     CAC
GAM2504  RAB6B     5'  AGGAGGAGAGAGAGGC       58327           ATAC
                                AGGAGGAGAGAGG    GGC
                                ||||||||||||    |||
                                TCCTCCTCTCTCT    CCG
                                          ____
GAM2504  SMARCF1   5'  GGAGGAGGAGGAGGCGGC     58328        A    TA
                                GGAGGAG GAGGA  CGGC
                                ||||||| |||||  ||||
                                CCTCCTC CTCCT  GCCG
                                     _    CC
GAM2504  SMARCF1   5'  AGGAGGAGGAGGCGGCGGC    58297        A   ATA
                                AGGAGGAG GAGG   CGGC
                                |||||||| ||||   ||||
                                TCCTCCTC CTCC   GCCG
                                     _   GCC
GAM2504  SMARCF1   5'  AGGAGGAGGAGGCGGCGGC    58297        A   ATA
                                AGGAGGAG GAGG   CGGC
                                |||||||| ||||   ||||
                                TCCTCCTC CTCC   GCCG
                                     _   GCC
GAM2504  SMARCF1   5'  AGGAGGAGGAGGCGGCGGC    58297        A   ATA
                                AGGAGGAG GAGG   CGGC
                                |||||||| ||||   ||||
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                                TCCTCCTC CTCC   GCCG
                                    _   GCC
GAM2504  SMARCF1   5'  GGAGGAGGAGGAGGCGGC    58328       A    TA
                                GGAGGAG GAGGA  CGGC
                                ||||||| |||||  ||||
                                CCTCCTC CTCCT  GCCG
                                    _   CC
GAM2504  SMARCF1   5'  GGAGGAGGAGGAGGCGGC    58328       A    TA
                                GGAGGAG GAGGA  CGGC
                                ||||||| |||||  ||||
                                CCTCCTC CTCCT  GCCG
                                    _   CC
GAM2504  TED       3'  TGAGGGGGAAGAGAGGAT    58329     A  A
                                TGA GG GGAGAGAGGAT
                                ||| || ||||||||||
                                ACT CC CTTCTCTCCTA
                                  C  C
GAM2504  TOB2      3'  TGAAGGAGGAAGGGAGGA    58330          A_
                                TGAAGGAGGAG  GAGGA
                                ||||||||||  |||||
                                ACTTCCTCCTT  CTCCT
                                      CC
GAM2504  ZIC4      3'  TGGGGGAGGGGAGAAGAT    58331    AA    A
                                TG  GGAGG GAGAGGAT
                                ||  ||||| ||||||||
                                AC  CCTCC CTCTTCTA
                                 CC    C
GAM2504  LOC116071 3'  TGAGGGAGGAGAGGCCCG    58332     A      GA  ATA
                                TGA GGAGGAGA  GG   CG
                                ||| ||||||||  ||   ||
                                ACT CCTCCTCT  CC   GC
                                  C       __  GG_
GAM2504  LOC124245 3'  GGAGGAGGAGGAAGAGAAGGCG 58333        A    TAC___
                                GGAGGAG GAGGA     GGCG
                                ||||||| |||||     ||||
                                CCTCCTC CTCCT     CCGC
                                    _    TCTCTT
GAM2504  LOC130813 3'  TGAGGCAGGAGAGAGCAAGCG  58334     A  _       GATAC
                                TGA GG AGGAGAGAG    GGCG
                                ||| || |||||||||    ||||
                                ACT CC TCCTCTCTC    TCGC
                                  _ G       GT___
GAM2504  LOC148709 5'  GGAGGAGGAGGACGC       58335        A     ACG
                                GGAGGAG GAGGAT   GC
                                ||||||| ||||||   ||
                                CCTCCTC CTCCTG   CG
                                    _    ___
GAM2504  LOC149153 3'  TGAGGAGGAGGGGGGACA    58336     A      AGA
                                TGA GGAGGAG   GGATA
                                ||| |||||||   |||||
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                                ACT CCTCCTC   CCTGT
                                  _     CCC
GAM2504  LOC149465 3'  GGAGGAGGAGGCAGC       58337        A   ATA
                                GGAGGAG GAGG   CGGC
                                ||||||| ||||   ||||
                                CCTCCTC CTCC   GTCG
                                   _   ___
GAM2504  LOC153785 3'  AGGAGGAAAGGATGCGGC    58338        GA     A
                                AGGAGGA  GAGGAT CGGC
                                |||||||  |||||| ||||
                                TCCTCCT  TTCCTA GCCG
                                    __     C
GAM2504  LOC158235 5'  TGAGGGGGCAGAGGGGACACAG 58339     A  A  _   A
                                TGA GG GG AGAG GGATACGG
                                ||| || || |||| ||||||||
                                ACT CC CC TCTC CCTGTGTC
                                  C  _  G   C
GAM2504  LOC197423 5'  AGGAGGAGGAGGCGGCGGC   58297        A   ATA
                                AGGAGGAG GAGG   CGGC
                                |||||||| ||||   ||||
                                TCCTCCTC CTCC   GCCG
                                    _   GCC
GAM2504  LOC197423 5'  AGGAGGAGGAGGAGGCGGC   58303        A    TA
                                AGGAGGAG GAGGA  CGGC
                                |||||||| |||||  ||||
                                TCCTCCTC CTCCT  GCCG
                                    _    CC
GAM2504  LOC200597 5'  GGAGGAGGAGAGGAGACAG   58340        _    T
                                GGAGGAG AGAGGA ACGG
                                ||||||| |||||| ||||
                                CCTCCTC TCTCCT TGTC
                                    C    C
GAM2504  LOC219688 5'  AGGAGGAGGAGGGGGGCAGCG  58341        A   ATA_
                                AGGAGGAG GAGG    CGGCG
                                |||||||| ||||    |||||
                                TCCTCCTC CTCC    GTCGC
                                    _   CCCC
GAM2504  LOC220565 5'  AGGAGGAGGAGGAGGCGGC   58303        A    TA
                                AGGAGGAG GAGGA  CGGC
                                |||||||| |||||  ||||
                                TCCTCCTC CTCCT  GCCG
                                    _    CC
GAM2504  LOC220565 5'  AGGAGGAGGAGGCGGCGGC   58297        A   ATA
                                AGGAGGAG GAGG   CGGC
                                |||||||| ||||   ||||
                                TCCTCCTC CTCC   GCCG
                                    _   GCC
GAM2504  LOC221641 5'  TGGAGGAGGGAGAGGATCAG  58342    A     A      A
                                TG AGGAGG GAGAGGAT CGG
                                || |||||| |||||||| |||
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                                AC TCCTCC CTCTCCTA GTC
                                 C     _       _
GAM2504  LOC222183 5'  GGAGGAGGAAGAGGGGC     58343        A     TAC
                                GGAGGAG GAGGA   GGC
                                ||||||| |||||   |||
                                CCTCCTC CTTCT   CCG
                                    _    CC_
GAM2504  LOC245787 3'  GAAGGAGGAGAGGAACCATTGG 58344           A    AC__
                                GAAGGAGGAGAG GGAT    GG
                                |||||||||||| ||||    ||
                                CTTCCTCCTCTC CTTG    CC
                                       _   GTAA
GAM2504  LOC257054 5'  GGAGGAGGAGGGACACGGCG   58345        _ A
                                GGAGGAG AG GGATACGGCG
                                ||||||| || ||||||||||
                                CCTCCTC TC CCTGTGCCGC
                                    C  _
GAM2504  LOC54466  5'  TGGGGGAGGAGAGAGGATA    58346    AA
                                TG  GGAGGAGAGAGGATA
                                ||  ||||||||||||||
                                AC  CCTCCTCTCTCCTAT
                                 CC
GAM2504  LOC58525  5'  AGGAGGAGGAGAGGCAGTTGG  58347         _    ATAC_
                                AGGAGGAG AGAGG     GG
                                |||||||| |||||     ||
                                TCCTCCTC TCTCC     CC
                                     C     GTCAA
GAM2504  LOC91397  5'  GAAGGGGGGGAGGGGCA     58348       A  AGA    ATAC
                                GAAGG GG   GAGG    GGCG
                                ||||| ||   ||||    ||||
                                CTTCC CC   CTCC    CCGT
                                   _ CC_   _____
GAM2504  LOC91960  3'  GGAGGAGGAGAGGTGGC     58349        _    ATAC
                                GGAGGAG AGAGG    GGC
                                ||||||| |||||    |||
                                CCTCCTC TCTCC    CCG
                                    C     A___
GAM2504  LOC92299  5'  GGAGGAGGAGGCGAGCCGCAGC 58350        A    ATA____
              G                  GGAGGAG GAGG       CGGCG
                                ||||||| ||||       |||||
                                CCTCCTC CTCC       GTCGC
                                    _    GCTCGGC
GAM2505  FBLN1     3'  TGATACATGTTGGCCTTATG   58353      _  GAT
                                TGATA ATG   TTGGCCTTATG
                                ||||| |||   ||||||||||
                                ACTAT TAC   AACCGGAATAC
                                   G  ___
GAM2505  DKFZp761H079 3'  TGATTAACCTGGCCTT      58354      AATG
                                TGAT    GATTTGGCCTT
                                ||||    ||||||||||
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                                ACTA    TTGGACCGGAA
                                  A___
GAM2505  LGALS8    3'  TGATAGTGCCTGCCTTATG    58355      A  GATTTG
                                TGATA TG     GCCTTATG
                                ||||| ||     ||||||||
                                ACTAT AC     CGGAATAC
                                   C  GGA___
GAM2505  LOC151277 5'  TGATAATGGCATTAAGGTTATG 58356         AT    CC
                                TGATAATGG  TTGG  TTATG
                                |||||||||  ||||  |||||
                                ACTATTACC  AATT  AATAC
                                      GT    CC
GAM2505  LOC196808 3'  ATGATTGATTTGGCCTT     58357      AATG
                                ATGAT    GATTTGGCCTT
                                |||||    ||||||||||
                                TACTA    CTAAACCGGAA
                                   A___
GAM2505  LOC221550 5'  TATGATAAGGAAACTTAT    58358        T   TTTGGC
                                TATGATAA GGA     CTTAT
                                |||||||| |||     |||||
                                ATACTATT CCT     GAATA
                                     _   TT_____
GAM2505  LOC257495 5'  TATGATAAGGAAACTTAT    58358        T   TTTGGC
                                TATGATAA GGA     CTTAT
                                |||||||| |||     |||||
                                ATACTATT CCT     GAATA
                                     _   TT_____
GAM2505  LOC257576 5'  TATGATAAGGAAACTTAT    58358        T   TTTGGC
                                TATGATAA GGA     CTTAT
                                |||||||| |||     |||||
                                ATACTATT CCT     GAATA
                                     _   TT_____
GAM2506  C7        3'  GTATCCACAGAATAGGGAAA   58361      ATTGT
                                GTATT    AATAGGGAAA
                                |||||    ||||||||||
                                CATAG    TTATCCCTTT
                                   GTGTC
GAM2506  ITGA11    3'  TCGTACTATGCACAGGG     58362        T   A
                                TCGTATTAT GTA TAGGG
                                ||||||||| ||| |||||
                                AGCATGATA CGT GTCCC
                                          _   _
GAM2506  FLJ21432  3'  GTATTATTGTCATAGAGA    58363         A
                                GTATTATTGT ATAGGGA
                                |||||||||| |||||||
                                CATAATAACA TATCTCT
                                      G
GAM2506  GMFB      3'  GTCTATTGAACAAATAGGGAAA 58364    A     T___
                                GT TTATTG    AATAGGGAAA
                                || ||||||    ||||||||||
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                                CA GATAAC    TTATCCCTTT
                                 _     TTGT
GAM2506 HSPC055  5' TCATATTACTAGGGAA      58365         TGTAA
                                TCGTATTAT    TAGGGAA
                                |||||||||    |||||||
                                AGTATAATG    ATCCCTT
                                      _____
GAM2506 KIAA0947 3' CGTATTAGATTTAGGGAAA   58366        TTGTAA
                                CGTATTA     TAGGGAAA
                                |||||||     ||||||||
                                GCATAAT     ATCCCTTT
                                    CTAA__
GAM2506 LOC91431 5' GTATGATTGTGATAGGGAA   58367      T     A
                                GTAT ATTGT ATAGGGAA
                                |||| ||||| ||||||||
                                CATA TAACA TATCCCTT
                                  C    C
GAM2507 SHOX     3' AGATGGATCTTCTCGGAGGT  58370      A  CCGCGA
                                AGAT GA     CTCGGAGGT
                                |||| ||     |||||||||
                                TCTA CT     GAGCCTCCA
                                  C  AGAA__
GAM2507 LOC205327 5' CGAGAGCGGTTCGGAGG    58371      TAGACC   AC
                                CGAGA     GCG  TCGGAGG
                                |||||     |||  |||||||
                                GCTCT     CGC  AGCCTCC
                                   _______  CA
GAM2507 LOC63928 3' GAGATAGACCTGGTGTGGGGT 58372          GCGACTC  A
                                GAGATAGACC      GG GGT
                                ||||||||||      || |||
                                CTCTATCTGG      CC CCA
                                     ACCACA_ _
GAM2508 AP3S1    3' AGAAGTCCAGTTACCTTGGA  58375        AGC  GTCG
                                AGAAGTCCA   GC    TGGA
                                |||||||||   ||    ||||
                                TCTTCAGGT   TG    ACCT
                                     CAA  GA__
GAM2508 F2RL3    3' TCAGACACCAGTGCGTCGTGG 58376      AGT   A C
                                TCAGA   CCA G GCGTCGTGG
                                |||||   ||| | |||||||||
                                AGTCT   GGT C CGCAGCACC
                                  GT_   _ A
GAM2508 PPP2R2B  3' TCAGAAGTTCAAGTCAACTATG 58377        C    _  C TC
           GA                   TCAGAAGT CAAG CG G  GTGGA
                                |||||||| |||| || |  |||||
                                AGTCTTCA GTTC GT T  TACCT
                                     A   A  _ GA
GAM2508 SLC9A1   5' CAGGGGTCCAGGCGCGCCG   58378     AA    A
                                CAG  GTCCA GCGCGTCG
                                |||  ||||| ||||||||
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                                GTC  CAGGT CGCGCGGC
                                  CC    C
GAM2508  UBE2V1   3'  CCAGAAGTTCAACTACGTGGA  58379       CCA  GCGT
                                TCAGAAGT  AGC   CGTGGA
                                ||||||||  |||   ||||||
                                GGTCTTCA  TTG   GCACCT
                                    AG_   AT__
GAM2508  UBE2V1   3'  CCAGAAGTTCAACTACGTGGA  58379       CCA  GCGT
                                TCAGAAGT  AGC   CGTGGA
                                ||||||||  |||   ||||||
                                GGTCTTCA  TTG   GCACCT
                                    AG_   AT__
GAM2508  UBE2V1   3'  CCAGAAGTTCAACTACGTGGA  58379       CCA  GCGT
                                TCAGAAGT  AGC   CGTGGA
                                ||||||||  |||   ||||||
                                GGTCTTCA  TTG   GCACCT
                                    AG_   AT__
GAM2508  C8orf2   3'  CCAGAAGTCTGGGCATGG   58380        CAA  GCGTC
                                TCAGAAGTC  GC   GTGG
                                |||||||||  ||   ||||
                                GGTCTTCAG  CG   TACC
                                     ACC  _____
GAM2508  CFP1     3'  GAAGTCTGCGCCATGG     58381       CAAGC
                                GAAGTC    GCGTCGTGG
                                ||||||    |||||||||
                                CTTCAG    CGCGGTACC
                                   A____
GAM2508  CLDN6    3'  TCAGAAGTTCCGGAGGTGG   58382        _ A_  CGCGTC
                                TCAGAAGT CC  AG    GTGG
                                |||||||| ||  ||    ||||
                                AGTCTTCA GG  TC    CACC
                                     A  CC  _______
GAM2508  DDX28    5'  GAAGGGCGCGTCGTGGA    58383     TCCAA
                                GAAG    GCGCGTCGTGGA
                                ||||    ||||||||||||
                                CTTC    CGCGCAGCACCT
                                  C____
GAM2508  FLJ10640 5'  TCAGAAATCCGAGTGTAGTGG  58384         A  CGC  C
                                TCAGAAGTCC AG   GT GTGG
                                |||||||||| ||   || ||||
                                AGTCTTTAGG TC   CA CACC
                                     C  A__  T
GAM2508  FLJ20811 3'  CAAACCAAGCGCGTTGTGG   58385     AGT        C
                                CAGA   CCAAGCGCGT GTGG
                                ||||   |||||||||| ||||
                                GTTT   GGTTCGCGCA CACC
                                  ___         A
GAM2508  HA-1     3'  GAAGTCCAGGCGCTCTCGG   58386        A   G  G
                                GAAGTCCA GCGC TC TGG
                                |||||||| |||| || |||
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                                CTTCAGGT CGCG AG GCC
                                     C   _ A
GAM2508 KIF13B   3' TCGGGAGTCCTAAGGCGGGTGG 58387   AGA   _  C  TC
                                TC  AGTCC AAG GCG  GTGG
                                ||  ||||| ||| |||  ||||
                                AG  TCAGG TTC CGC  CACC
                                 CCC    A  _  C_
GAM2508 KIF13B   3' TCGGGAGTCCTAAGGCGGGTGG 58387   AGA   _  C  TC
                                TC  AGTCC AAG GCG  GTGG
                                ||  ||||| ||| |||  ||||
                                AG  TCAGG TTC CGC  CACC
                                 CCC    A  _  C_
GAM2508 MGC15438 5' TCAGAAGCTCAGGTGTGTGCAA 58388      TC  AGC____  TC
          GTGGA                 CAGAAG  CA     GCG  GTGGA
                                ||||||  ||     |||  |||||
                                GTCTTC  GT     CGT  CACCT
                                   GA  CCACACA  T_
GAM2508 MGC20255 3' TCGGAGGTCAGGAACCGTGGA  58389   A  A   CA  CGCG
                                TC GA GTC  AG   TCGTGGA
                                || || |||  ||   |||||||
                                AG CT CAG  TC   GGCACCT
                                 C  C  __  CTT_
GAM2508 NEDD5    3' TCAGAAGTGTAGCAGTGTGG   58390      CCA   C  C
                                TCAGAAGT   AGCG GT GTGG
                                ||||||||   |||| || ||||
                                AGTCTTCA   TCGT CA CACC
                                     CA_   _ _
GAM2508 SHANK3   3' TCAGAAGCCCAAGGTG     58391          CGCGTC
                                TCAGAAGTCCAAG     GTG
                                ||||||||||||      |||
                                AGTCTTCGGGTTC     CAC
                                          _______
GAM2508 ZNF387   3' TCAGAAATTCAAGATTGTGG  58392       C   CGC  C
                                TCAGAAGT CAAG   GT GTGG
                                |||||||| ||||   || ||||
                                AGTCTTTA GTTC   TA CACC
                                     A   ___  A
GAM2508 LOC219972 3' TCAGAAGTCCAAGAGTG    58393          CGCGTC
                                TCAGAAGTCCAAG     GTG
                                ||||||||||||      |||
                                AGTCTTCAGGTTC     CAC
                                       T_____
GAM2508 LOC51161 3' TCAGAAGTCCAGGCTTGTC   58394         A  GC
                                TCAGAAGTCCA GC  GTC
                                |||||||||| ||  |||
                                AGTCTTCAGGT CG  CAG
                                      C  AA
GAM2509 GAGED2   5' GTGAGGTTCCCTCGTGCCTTA 58397     A  CT  ATAGA
                                GTGA GT  CC    GTGCCTTA
                                ||||  ||  ||    ||||||||
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                                CACT CA  GG    CACGGAAT
                                  C  AG  AG___
GAM2509  ITGA2    3'  GTGAAATCCTGAGAGTG     58398         CCAT
                                GTGAAGTCT    AGAGTG
                                |||||||||    ||||||
                                CACTTTAGG    TCTCAC
                                     AC__
GAM2509  JPH2     3'  TGGGGTCTCCATAGAATG    58399    AA
                                TG  GTCTCCATAGAGTG
                                ||  ||||||||||||||
                                AC  CAGAGGTATCTTAC
                                 CC
GAM2509  FLJ11320 3'  GTGAAGCCTTTGTGGCTT    58400         CCATAGA   C
                                GTGAAGTCT      GTG CTT
                                |||||||||      ||| |||
                                CACTTCGGA      CAC GAA
                                     AA_____   C
GAM2509  FLJ20203 3'  GTAAAGTCTTCATAAAAGACCT 58401         C      T
            T                    GTGAAGTCT CATAGAG GCCTT
                                |||||||||| ||||||| |||||
                                CATTTCAGA GTATTTT TGGAA
                                     A      C
GAM2509  FLJ21438 3'  GTGGTGTCTCCATTGAGGC    58402     AA       A   T
                                GTG  GTCTCCAT GAG GC
                                |||  |||||||| ||| ||
                                CAC  CAGAGGTA CTC CG
                                  CA       A  _
GAM2509  KIAA1550 3'  GTGAAGTCTTCAAGGAGACCCC 58403         C  TA   T
                                GTGAAGTCT CA  GAG GCCTT
                                ||||||||| ||  ||| |||||
                                CACTTCAGA GT  CTC TGGGG
                                     A  TC  _
GAM2509  KIAA1866 3'  ATGAAGTCTTCATAGGATG    58404         C    AG
                                GTGAAGTCT CATAG  TG
                                ||||||||| |||||  ||
                                TACTTCAGA GTATC  AC
                                     A    CT
GAM2509  ZNF17    3'  GTGAAGTCTTTCCCCATCTGCT 58405         ____    AGAG   C
            TTA                    TGAAGTCT    CCAT    TGC TTA
                                |||||||    ||||    ||| |||
                                ACTTCAGA    GGTA    ACG AAT
                                     AAGG    G___   A
GAM2509  LOC121504 3'  TGAAGTCTTTATGGAGTA    58406         CC  A
                                TGAAGTCT  AT GAGTG
                                ||||||||  || |||||
                                ACTTCAGA  TA CTCAT
                                     AA  C
GAM2509  LOC151429 3'  CGATCTCTATAGAGTGCCTT   58407    A    C
                                A GTCTC ATAGAGTGCCTT
                                | ||||| ||||||||||||
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                                G TAGAG TATCTCACGGAA
                                 C     A
GAM2509  LOC152580 5'  GTGAAGCCTCCATGGTG     58408            AGA
                                GTGAAGTCTCCAT   GTG
                                ||||||||||||   |||
                                CACTTCGGAGGTA   CAC
                                       C__
GAM2509  LOC199906 3'  GTGAAGCCTTCATAGAGC    58409         C
                                GTGAAGTCT CATAGAGT
                                ||||||||| ||||||||
                                CACTTCGGA GTATCTCG
                                      A
GAM2509  LOC200531 5'  GTGAGTCTCCACATGGTG    58410      A       GA
                                GTGA GTCTCCATA  GTG
                                |||| |||||||||  |||
                                CACT CAGAGGTGT  CAC
                                  _       AC
GAM2509  LOC254106 5'  TGAAGTCTTTATCGAGTGCCTT 58411         CCATA
              A                  TGAAGTCT    GAGTGCCTTA
                                |||||||||    ||||||||||
                                ACTTCAGA    CTCACGGAAT
                                     AATAG
GAM2509  LOC64744  3'  GTGGGATCTTCATAAAGT    58412     AA   C
                                GTG  GTCT CATAGAGT
                                |||  |||| ||||||||
                                CAC  TAGA GTATTTCA
                                  CC    A
GAM2509  LOC90529  3'  GTGAAGTCTCCAGGGAGCA   58413           TA
                                GTGAAGTCTCCA  GAGTG
                                ||||||||||||  |||||
                                CACTTCAGAGGT  CTCGT
                                       CC
GAM2510  LOC151171 5'  GCTTCGGTGTCTGGTGCG    58416        GCGG   C
                                GTTTCGGT    GTTT GGTGCG
                                ||||||||    |||| ||||||
                                CGAAGCCA    CAGA CCACGC
                                     _____   _
GAM2510  LOC164714 5'  GCTTTGGTGCGGGTGGGCTGTG 58417      C       TTCG_
              CGG                  GTTT GGTGCGGGT    GTGCGG
                                |||| |||||||||    ||||||
                                CGAA CCACGCCCA    CACGCC
                                  A       CCCGA
GAM2510  LOC90593  3'  CAGATGGGTTTTGGTGTGG   58418    TGC    C   C
                                CGG   GGGTTT GGTG GG
                                |||   |||||| |||| ||
                                GTC   CCCAAA CCAC CC
                                  TA_     A   A
GAM2511  ACADVL    3'  AAGGGGCTTCGGCTTTGGC   58421       AGC  GA
                                AGGGGG   CG  GCTTTGGC
                                ||||||   ||  ||||||||
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                                TTCCCC  GC  CGAAACCG
                                   GAA  __
GAM2511  BCL11B   5'  GGGGGAGCCGGGGGAGGGGGTC 58422          AGCTTT_  C
            CG                    GGGGGAGCCGG      GG CCG
                                  ||||||||||       || |||
                                  CCCCCTCGGCC      CC GGC
                                       CCCTCCC  A
GAM2511  BCL11B   5'  GGGGGAGCCGGGGGAGGGGGTC 58422          AGCTTT_  C
            CG                    GGGGGAGCCGG      GG CCG
                                  ||||||||||       || |||
                                  CCCCCTCGGCC      CC GGC
                                       CCCTCCC  A
GAM2511  CRHR1    3'  AGGGGAAGCTGGCCTGGCC   58423          C  AGC
                                  AGGGGGAGC GG   TTTGGCC
                                  |||||||||  ||   |||||||
                                  TCCCCTTCG CC   GGACCGG
                                       A  ___
GAM2511  DRD2     3'  GAGGGAGCTAAGGTTTTTGGC  58424        CG   C__
                                  GGGGGAGC  GAG   TTTGGC
                                  ||||||||  |||   ||||||
                                  CTCCCTCG  TTC   AAACCG
                                       A_   CAA
GAM2511  GALE     3'  AGGGGAGGCCTTGGC       58425        CCGGA
                                  GGGGGAG    GCTTTGGC
                                  |||||||    ||||||||
                                  TCCCCTC    CGGAACCG
                                             _____
GAM2511  MAPK7    3'  AGGGGGAGTTGGGGTCTCCCG  58426        CC_  AG  TTGG
                                  AGGGGGAG   GG  CT   CCCG
                                  ||||||||   ||  ||   ||||
                                  TCCCCCTC   CC  GA   GGGC
                                       AAC  CA  ____
GAM2511  MAPK7    3'  AGGGGGAGTTGGGGTCTCCCG  58426        CC_  AG  TTGG
                                  AGGGGGAG   GG  CT   CCCG
                                  ||||||||   ||  ||   ||||
                                  TCCCCCTC   CC  GA   GGGC
                                       AAC  CA  ____
GAM2511  MAPK7    3'  AGGGGGAGTTGGGGTCTCCCG  58426        CC_  AG  TTGG
                                  AGGGGGAG   GG  CT   CCCG
                                  ||||||||   ||  ||   ||||
                                  TCCCCCTC   CC  GA   GGGC
                                       AAC  CA  ____
GAM2511  MAPK7    3'  AGGGGGAGTTGGGGTCTCCCG  58426        CC_  AG  TTGG
                                  AGGGGGAG   GG  CT   CCCG
                                  ||||||||   ||  ||   ||||
                                  TCCCCCTC   CC  GA   GGGC
                                       AAC  CA  ____
GAM2511  MUC3B    3'  AGGGGGAGTCGGGGGCAGAACC 58427         C   A_  TTT
                                  AGGGGGAG CGG  GC   GGCC
                                  |||||||| |||  ||   ||||
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                                TCCCCCTC GCC  CG   TTGG
                                    A   CC  TC_
GAM2511  NR2C2    5'  GGCGGGAGCCGGGGGCCGCGGG 58428    _       A_   TT_   C
             CTCG                   GG GGGAGCCGG  GCT   GGC CG
                                || |||||||||  |||   ||| ||
                                CC CCCTCGGCC  CGG   CCG GC
                                 G       CC   CGC   A
GAM2511  PDE4A    5'  AGGGGGAGCCGCGGAGGGGCC  58429          __   CTTT
                                AGGGGGAGCC  GGAG   GGCC
                                ||||||||||  ||||   ||||
                                TCCCCCTCGG  CCTC   CCGG
                                     CG   C___
GAM2511  PIK3R2   3'  AGGGGAAGTTGGAGTCTG    58430        CC   C
                                AGGGGGAG  GGAG TTTG
                                ||||||||  |||| ||||
                                TCCCCTTC  CCTC AGAC
                                    AA   _
GAM2511  PKIA     5'  GGGGGAGCGGGGCCGCTCCCG  58431        C  A   TTGG
                                GGGGGAGC GG GCT   CCCG
                                ||||||||  || |||   ||||
                                CCCCCTCG CC CGG   GGGC
                                    C  _   CGA_
GAM2511  PLXNB2   3'  GAGGGAGCTGGGGCTGGGGC   58432        C  A   TT
                                GGGGGAGC GG GCT  GGC
                                ||||||||  || |||  |||
                                CTCCCTCG CC CGA  CCG
                                    A  C   CC
GAM2511  PRX      3'  AGGCGGAGCCGGGGCTCCG   58433     G       A
                                AGG GGAGCCGG GCTTTG
                                |||  ||||||||  ||||||
                                TCC CCTCGGCC CGAGGC
                                  G       C
GAM2511  PTGDS    3'  GGGGAGCCGGGGCAGGGGCTCG 58434          A  TTT   C
                                GGGGAGCCGG GC   GGC CG
                                ||||||||||  ||   ||| ||
                                CCCCTCGGCC CG   CCG GC
                                     C  TCC   A
GAM2511  RAPSN    5'  GGTGGGAGCCGGAATGGGGCC  58435    _        CTTT
                                GG GGGAGCCGGAG   GGCC
                                || ||||||||||    ||||
                                CC CCCTCGGCCTT   CCGG
                                 A         ACC_
GAM2511  RENT1    3'  AGGGGAAGCTGGAGGCC     58436         C   GCTTT
                                AGGGGGAGC GGA    GGCC
                                |||||||||  |||    ||||
                                TCCCCTTCG CCT    CCGG
                                    A  _____
GAM2511  RGS19IP1 3'  AGGGGGGCCGGGGACCC     58437       A    AGCTTT
                                AGGGGG GCCGG     GGCCC
                                ||||||  |||||     |||||
```

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                                TCCCCC CGGCC     CTGGG
                                  _    C_____
GAM2511  RPH3AL   3'  GGAGGAGCCGGGCAGGG     58438          A  TTT
                                GGGGGAGCCGG GC   GG
                                |||||||||| ||   ||
                                CCTCCTCGGCC CG   CC
                                      _ TC_
GAM2511  RXRA     3'  GGAGGGGCCGGGGCACTCTG   58439      A    A__
                                GGGGG GCCGG   GCTTTG
                                ||||| |||||   ||||||
                                CCTCC CGGCC   TGAGAC
                                  C    CCG
GAM2511  SIX2     5'  GGCGGGGCTGGCCCCCTGGCCC 58440    _  A  C  AG
           G                     GG GGG GC GG  CTTTGGCCCG
                                || ||| || ||  ||||||||||
                                CC CCC CG CC  GGGACCGGGC
                                 G  _ A  GG
GAM2511  WISP2    3'  AGGGGAAGTCGGAGAGAAAGCT 58441        C    CTTT   C
           CG                    AGGGGGAG CGGAG    GGC CG
                                |||||||| |||||    ||| ||
                                TCCCCTTC GCCTC    TCG GC
                                    A    TCTT   A
GAM2511  WSX1     5'  AGGGGGAGTGGGGAGGCGGCC  58442        CC_   CTT
                                AGGGGGAG   GGAG   TGGCC
                                ||||||||   ||||   |||||
                                TCCCCCTC   CCTC   GCCGG
                                    ACC    C__
GAM2511  ADMP     5'  AGGGGAAGCCGGGGCTCCG    58443          A
                                AGGGGGAGCCGG GCTTTG
                                |||||||||||| ||||||
                                TCCCCTTCGGCC CGAGGC
                                       C
GAM2511  AP1S2    5'  GGAGGAGCCGGGGCTGCG     58444          A   T
                                GGGGGAGCCGG GCT TG
                                |||||||||| ||| ||
                                CCTCCTCGGCC CGA GC
                                      C   C
GAM2511  C20orf102 3'  AGAGGGAGCTGGGGCATTG    58445        C  A  T
                                AGGGGGAGC GG GC TTG
                                ||||||||| || || |||
                                TCTCCCTCG CC CG AAC
                                    A  C  T
GAM2511  CECR6    5'  AGGGGAGCCGGGGCC       58446          AGCTTT
                                GGGGGAGCCGG     GGCC
                                ||||||||||     ||||
                                TCCCCTCGGCC     CCGG
                                                _____
GAM2511  DEPC-1   5'  GGGCGGAGCCGGGCGCGCCCG  58447     _      A  TTTG
                                GGG GGAGCCGG GC    GCCCG
                                ||| |||||||| ||    |||||
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                                CCC CCTCGGCC CG    CGGGC
                                  G       _ CG__
GAM2511  DKFZP434O047 5'  AGAGAAAGGGGGCTTTGG    58448      GG  CC  A
                                AGGG  AG  GG GCTTTGG
                                |||| ||  || |||||||
                                TCTC  TC  CC CGAAACC
                                  TT  C_  _
GAM2511  DKFZP564D0478 3'  AGGGGGAGCTGGAGTTAGG   58449          C    C  T
                                AGGGGGAGC GGAG TT GG
                                ||||||||| |||| || ||
                                TCCCCCTCG CCTC AA CC
                                     A    _ T
GAM2511  DKFZP762D096 5'  AGGGGGAGCCGGGGGTCGCT   58450           A_____
                                AGGGGGAGCCGG    GCT
                                ||||||||||||    |||
                                TCCCCCTCGGCC    CGA
                                       CCCAG
GAM2511  EFS2     5'  GGGCGGGCCGGGGCGTCG    58451     _ A    A  T
                                GGG GG GCCGG GC TTG
                                ||| || ||||| || |||
                                CCC CC CGGCC CG AGC
                                  G  _    C  C
GAM2511  FBXO2    5'  AGGAGGAGCCGGAGCGCTG    58452             T
                                AGGGGGAGCCGGAGC TTG
                                |||||||||||||| |||
                                TCCTCCTCGGCCTCG GAC
                                       C
GAM2511  FLJ22301  5'  GGGGGAGCGGGGAGGCGCCCG  58453        C_   CTTTG
                                GGGGGAGC  GGAG    GCCCG
                                ||||||||  ||||    |||||
                                CCCCCTCG  CCTC    CGGGC
                                     CC    CG___
GAM2511  FLJ22795  3'  GGGGGAGTTGAGCATTGG    58454        CCG    T
                                GGGGGAG   GAGC TTGG
                                |||||||   |||| ||||
                                CCCCCTC   CTCG AACC
                                     AA_    T
GAM2511  GAS2L1    5'  GGGGGCCGGAGCCGGGCC    58455      A       TT
                                GGGG GCCGGAGCT  GGCC
                                |||| |||||||||  ||||
                                CCCC CGGCCTCGG  CCGG
                                  _       C_
GAM2511  HSU24186  5'  AGGAGAAGGTGGGCTTTGGCTC 58456        CC  A      C
            G                    AGGGGGAG  GG GCTTTGGC CG
                                ||||||||  || ||||||| ||
                                TCCTCTTC  CC CGAAACCG GC
                                     CA  _       A
GAM2511  KCNH4    3'  AGGGGGAGGTTGGGGAAGGC   58457        CC___   CTTT
                                AGGGGGAG    GGAG    GGC
                                ||||||||    ||||    |||
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                                TCCCCCTC    CCTT   CCG
                                    CAACC   ____
GAM2511 KIAA0293 3' AAGGGGAGCTGGGGTCTCTAG 58458        C  AG_
                                AGGGGGAGC GG   CTTTGG
                                ||||||||| ||   ||||||
                                TTCCCCTCG CC   GAGATC
                                    A  CCA
GAM2511 KIAA0352 3' AAGGATGGAGCTTTGG     58459      GCC
                                GGGGA   GGAGCTTTGG
                                |||||   ||||||||||
                                TTCCT   CCTCGAAACC
                                  A__
GAM2511 KIAA1128 3' AGGGGGGGCGGAGCTTAGA   58460      A  C     T
                                AGGGGG GC GGAGCTT GG
                                |||||| || ||||||| ||
                                TCCCCC CG CCTCGAA CT
                                   C  _     T
GAM2511 KIAA1421 5' AGGGAGGAGCCGGAACCGCCCG 58461     _        TTG
                                AGGG GGAGCCGGAGCT   GCCCG
                                |||| ||||||||||||   |||||
                                TCCC CCTCGGCCTTGG   CGGGC
                                  T        ___
GAM2511 KIAA1655 5' AGGAGGAGTTGGAGCCCTG   58462        CC
                                AGGGGGAG  GGAGCTTTG
                                ||||||||  |||||||||
                                TCCTCCTC  CCTCGGGAC
                                    AA
GAM2511 LATS1    3' AGGGGGAGGTGGAGTTGTACC 58463       CC   CT   GC
                                AGGGGGAG  GGAG  TTG  CC
                                ||||||||  ||||  |||  ||
                                TCCCCCTC  CCTC  AAC  GG
                                    CA   __   AT
GAM2511 MGC10334 5' AGGGGGAGCCGTGGCTGAGGC 58464         GA   TT
                                AGGGGGAGCCG  GCT  GGC
                                ||||||||||  |||  |||
                                TCCCCCTCGGC  CGA  CCG
                                      AC   CT
GAM2511 PDZD2    5' GGGGGAACTGGGGCTCCCA   58465       C  A   TTGG
                                GGGGGAGC GG GCT   CCCG
                                |||||||| || |||   ||||
                                CCCCCTTG CC CGA   GGGT
                                    A  C   ____
GAM2511 PRAX-1   3' AGGGTGGGGCCCACTTTGGC  58466     _  A   GGA
                                AGGG GG GCC   GCTTTGGC
                                |||| || |||   ||||||||
                                TCCC CC CGG   TGAAACCG
                                  A  C   G__
GAM2511 QKI      5' AGGAGGAGCCGGGGCCGCC   58467          A   TTG
                                AGGGGGAGCCGG GCT   GCC
                                |||||||||||| |||   |||
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                                TCCTCCTCGGCC CGG   CGG
                                      C  ___
GAM2511  RHOBTB1   5'  GGGGGAGCGGGGGGGCCC    58468       C  AGCTTT
                                GGGGGAGC GG     GGCCC
                                |||||||| ||     |||||
                                CCCCCTCG CC     CCGGG
                                    C  CC____
GAM2511  SAE1      3'  AGGGGAGCTGGCAGGCCC    58469       C  AGCTTT
                                GGGGGAGC GG     GGCCC
                                |||||||| ||     |||||
                                TCCCCTCG CC     CCGGG
                                    A  GT____
GAM2511  SR-BP1    5'  GAGGGAGCCGGGGCC       58470         AGCTTT
                                GGGGGAGCCGG     GGCC
                                ||||||||||     ||||
                                CTCCCTCGGCC     CCGG

                                       _______
GAM2511  STRN3     3'  AGGGGGAACCACCTTGG     58471         GGA
                                AGGGGGAGCC   GCTTTGG
                                |||||||||   |||||||
                                TCCCCCTTGG   TGGAACC

                                       ___
GAM2511  TLK2      5'  GGGCGGAGCCGGGGCCTCTCC  58472    _      A    GG
                                GGG GGAGCCGG GCTTT  CC
                                ||| |||||||| |||||  ||
                                CCC CCTCGGCC CGGAG  GG
                                  G       C     A_
GAM2511  LOC115073 5'  GGGGGAGCGGGGCGGTGCCC   58473       C  A  TTTG
                                GGGGGAGC GG GC    GCCC
                                |||||||| || ||    ||||
                                CCCCCTCG CC CG    CGGG
                                    C  _  CCA_
GAM2511  LOC115574 3'  GGGGGAGCTGGGGGATCCCTG  58474       C___   G
                                GGGGGAGC    GGA CTTTG
                                ||||||||    ||| |||||
                                CCCCCTCG    CCT GGGAC
                                    ACCC   A
GAM2511  LOC126961 3'  GGGGGAGCCGGACCGCCAAAGC 58475          __   TT
            CCG                   GGGGGAGCCGGA  GCT  GGCCCG
                                ||||||||||||  |||  ||||||
                                CCCCCTCGGCCT  CGG  TCGGGC
                                      GG   TT
GAM2511  LOC148029 5'  AGGGGCAGCCCTTTGGCC    58476      G   GGAG
                                AGGGG AGCC    CTTTGGCC
                                ||||| ||||    ||||||||
                                TCCCC TCGG    GAAACCGG
                                  G   _____
GAM2511  LOC148137 3'  AGGGGGAGTGACCTTGG     58477        CCG  G
                                AGGGGGAG   GA CTTTGG
                                ||||||||   || ||||||
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                                TCCCCCTC   CT GGAACC
                                    A__  _
GAM2511  LOC153505 3'  AGGGGGAGCTGGGCCACCC    58478         C  A   TTG
                                AGGGGGAGC GG GCT   GCCC
                                ||||||||| || |||   ||||
                                TCCCCCTCG CC CGG   TGGG
                                    A  _  ___
GAM2511  LOC154101 5'  GGGGGCGCCGGAGCCGTGCC   58479      A        TTG
                                GGGGG GCCGGAGCT   GCC
                                ||||| |||||||||   |||
                                CCCCC CGGCCTCGG   CGG
                                   G        CA_
GAM2511  LOC200014 5'  AGGGGGAGCTGGAGGGTCTG   58480         C    C_
                                AGGGGGAGC GGAG  TTTG
                                ||||||||| ||||  ||||
                                TCCCCCTCG CCTC  AGAC
                                    A    CC
GAM2511  LOC201749 5'  GGGGGAGCTGGACAGCC     58481         C   GCTT
                                GGGGGAGC GGA    TGGCC
                                |||||||| |||    |||||
                                CCCCCTCG CCT    GTCGG
                                    A   _____
GAM2511  LOC207043 3'  GGGGGAGCTGGGCACTG     58483         C  A  T
                                GGGGGAGC GG GC TTG
                                |||||||| || || |||
                                CCCCCTCG CC CG GAC
                                    A  _  T
GAM2511  LOC207043 3'  GGGGGAGCCGGGCACTG     58482           A  T
                                GGGGGAGCCGG GC TTG
                                |||||||||||| || |||
                                CCCCCTCGGCC CG GAC
                                      _  T
GAM2511  LOC219333 5'  AGGGGAGCCGGGCCGCCC     58484          A   TTG
                                GGGGGAGCCGG GCT   GCCC
                                |||||||||||| |||   ||||
                                TCCCCTCGGCC CGG   CGGG
                                      _  ____
GAM2511  LOC220018 5'  AGGAGGGGCTGGATGCCT     58485       A  C   _
                                AGGGGG GC GGA GCTT
                                |||||| || ||| ||||
                                TCCTCC CG CCT CGGA
                                   C  A   A
GAM2511  LOC220537 3'  GGGGGAGTTGAGCATTGG     58454        CCG    T
                                GGGGGAG   GAGC TTGG
                                |||||||   |||| ||||
                                CCCCCTC   CTCG AACC
                                    AA_    T
GAM2511  LOC253216 3'  AGGGGGAGCCGTGGCTGGGC   58486           GA   TT
                                AGGGGGAGCCG  GCT  GGC
                                ||||||||||  |||  |||
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                                TCCCCCTCGGC  CGA  CCG
                                      AC   C_
GAM2511  LOC253430 5'  AGGGGGCGCCGGAGAACCC   58487       A      CTTT
                                AGGGGG GCCGGAG    GGCCC
                                |||||| |||||||    |||||
                                TCCCCC CGGCCTC    TTGGG
                                   G      _____
GAM2511  LOC255520 5'  AGGGGGAGCAGGAGCTGCCTCG 58488          C      TTG  _
                                AGGGGGAGC GGAGCT   GCC CG
                                ||||||||| ||||||   ||| ||
                                TCCCCCTCG CCTCGA   CGG GC
                                      T     ___   A
GAM2511  LOC257395 3'  GGGGGAGCCGGACCGCCAAAGC 58475           __   TT
            CCG                    GGGGGAGCCGGA  GCT  GGCCCG
                                ||||||||||||  |||  ||||||
                                CCCCCTCGGCCT  CGG  TCGGGC
                                       GG   TT
GAM2511  LOC56961  5'  GGGGGAGGGTTGGGGGCAGCTG 58489        CC___  A  T_
            GC                     GGGGGAG    GG GC  TTGGC
                                |||||||    || ||  |||||
                                CCCCCTC    CC CG  GACCG
                                    CCAAC  C  TC
GAM2511  LOC91040  5'  AGGGTGGAGTTGGGAGCCT    58490      _    CC_
                                AGGG GGAG   GGAGCTT
                                |||| ||||   |||||||
                                TCCC CCTC   CCTCGGA
                                  A    AAC
GAM2512  HYOU1    3'  TGAATGGGGAAAACAGAG    58493    T    TA
                                C AGTG  GAAAACAGAG
                                | ||||  ||||||||||
                                A TTAC  CTTTTGTCTC
                                 C    CC
GAM2512  ITGB1    3'  ACTAGTGTGAAACAAGAT    58494         A    A  G
                                ACTAGTGT GAAA CA AGAT
                                |||||||| |||| || ||||
                                TGATCACA CTTT GT TCTA
                                      _    _ _
GAM2512  MAGEA4   3'  TGTAAAAGGAAACAGAGATA   58495        ___
                                TGTAGAA   AACAGAGATA
                                |||||||   ||||||||||
                                ACATTTT   TTGTCTCTAT
                                    CCT
GAM2512  PTTG1IP  3'  ACTAAATCTAGAAACAGAGAT  58496       _ G     A
                                ACTAG T TAGAAA CAGAGAT
                                ||||| | |||||| |||||||
                                TGATT A ATCTTT GTCTCTA
                                  T G     _
GAM2512  RAB27A   3'  GCTGGTAAAGACAGAGAT    58497    __     AA
                                GT  GTAGA  ACAGAGAT
                                ||  |||||  ||||||||
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                                CG  CATTT  TGTCTCTA
                                 AC     C_
GAM2512  SALL2    5'  ACTGTGAAGCAGAGAT      58498     A   T  AAAA
                                ACT GTG AG    CAGAGAT
                                ||| ||| ||    |||||||
                                TGA CAC TC    GTCTCTA
                                  _   T  ____
GAM2512  SFRS7    3'  TAACTAATGTAGAAAGCA    58499             A
                                TAACTAGTGTAGAAA CA
                                |||||||||||||| ||
                                ATTGATTACATCTTT GT
                                          C
GAM2512  SLC19A2  3'  TAACTATGTAGAAAGAC     58500       G     AAACA
                                TAACTA TGTAGA    GAGAT
                                |||||| ||||||    |||||
                                ATTGAT ACATCT    TTCTG
                                  _     ______
GAM2512  C20orf97 3'  TAATCAAGAGGACAGAGAT   58501     GT   AA
                                TAGT  AGA  ACAGAGAT
                                ||||  |||  ||||||||
                                ATTA  TCT  TGTCTCTA
                                  GT   CC
GAM2512  CYB5-M   3'  CTAGGGTAGAAAAAACAGA   58502      T      __
                                CTAG GTAGAAA  ACAGA
                                |||| |||||||  |||||
                                GATC CATCTTT  TGTCT
                                  C      TT
GAM2512  CYB5-M   3'  CTAGGGTAGAAAAAACAGA   58502      T      __
                                CTAG GTAGAAA  ACAGA
                                |||| |||||||  |||||
                                GATC CATCTTT  TGTCT
                                  C      TT
GAM2512  FAM8A1   3'  TAGTGTAACCCAGGGATA    58503        AAAA   A
                                TAGTGTAG    CAG GATA
                                ||||||||    ||| ||||
                                ATCACATT    GTC CTAT
                                     GG__   C
GAM2512  FLJ10853 5'  TAAATAGTGTAGGCAGA     58504     C       AAAA
                                TAA TAGTGTAG    CAGA
                                ||| ||||||||    ||||
                                ATT ATCACATC    GTCT
                                  T       C___
GAM2512  FLJ14327 3'  CTAGTTTTGTAGACAGAGAT   58505       ___     AAA
                                CTAGT   GTAGA   CAGAGAT
                                |||||   |||||   |||||||
                                GATCA   CATCT   GTCTCTA
                                  AAA    ___
GAM2512  FLJ14681 5'  ATGCCTGGAAGGCAGAGATA   58506      A__   AA
                                GTGT   GAA  CAGAGATA
                                ||||   |||  ||||||||
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                                TACG   CTT  GTCTCTAT
                                  GAC   CC
GAM2512  HBOA     3'  TAAGTAGTGTACAGAGAT    58507     C     AGAAA
                                TAA TAGTGT    ACAGAGAT
                                ||| ||||||    ||||||||
                                ATT ATCACA    TGTCTCTA
                                  C     _____
GAM2512  HNRPA3   3'  TAAATGTAGAATAGAGAT    58508   T       AAC
                                C AGTGTAGAA   AGAGAT
                                | |||||||||   ||||||
                                A TTACATCTT   TCTCTA
                                 T       A__
GAM2512  KIAA0426 3'  ACCTGTCTCCCAAAACAGAGAT 58509     A  GTAG_
              A                  ACT GT     AAAACAGAGATA
                                ||| ||    ||||||||||||
                                TGG CA    TTTTGTCTCTAT
                                  A  GAGGG
GAM2512  KIAA0594 3'  TAATTAGTATAACTTAGAGATA 58510     C       AAAAC
                                TAA TAGTGTAG    AGAGATA
                                ||| ||||||||    |||||||
                                ATT ATCATATT    TCTCTAT
                                  A       GAA__
GAM2512  KIAA0635 5'  CTAGTGTAAATTGAGAT     58511          AAACA
                                CTAGTGTAGA    GAGAT
                                ||||||||||    |||||
                                GATCACATTT    CTCTA
                                      AA___
GAM2512  p25      3'  CTAGGTGACAGAGAT      58512      T  A  AAA
                                CTAG GT GA   CAGAGAT
                                |||| || ||   |||||||
                                GATC CA CT   GTCTCTA
                                  _ _ ____
GAM2512  PDZD2    5'  TAGTCCCCGAAAACAGGGAT   58513      GTA_      A
                                TAGT    GAAAACAG GAT
                                ||||    |||||||| |||
                                ATCA    CTTTTGTC CTA
                                  GGGG       C
GAM2512  PP1628   5'  ACTGGGGATGGGGAACAGAGAT 58514     A___   TA  AA
                                ACT    GTG  GA  ACAGAGAT
                                |||    |||  ||  ||||||||
                                TGA    TAC  CT  TGTCTCTA
                                  CCCC   CC  __
GAM2512  TIP120A  3'  TAGTGTGCGCAACAGGGATA   58515       AGAA    A
                                TAGTGT    AACAG GATA
                                ||||||    ||||| ||||
                                ATCACA    TTGTC CTAT
                                   CGCG    C
GAM2512  LOC220883 3'  TAAGTAGTGTACAGAGAT    58507     C     AGAAA
                                TAA TAGTGT    ACAGAGAT
                                ||| ||||||    ||||||||
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                                ATT ATCACA     TGTCTCTA
                                  C     _____
GAM2512  LOC220988 3'  TAAATGTAGAATAGAGAT    58508    T       AAC
                                C AGTGTAGAA   AGAGAT
                                | |||||||||   ||||||
                                A TTACATCTT   TCTCTA
                                 T       A__
GAM2512  LOC221337 5'  GTGCTTAGAGAACAGAGAT    58516     __  A
                                GTGT  AGA AACAGAGAT
                                ||||  ||| |||||||||
                                CACG  TCT TTGTCTCTA
                                  AA  C
GAM2512  LOC257017 5'  ATGCCAAAACAGAGATA     58517     AG
                                GTGT  AAAACAGAGATA
                                ||||  ||||||||||||
                                TACG  TTTTGTCTCTAT
                                  G_
GAM2512  LOC90829  5'  ACTGGTACCAAAACAGAGATA  58518    A   AG
                                ACT GTGT  AAAACAGAGATA
                                ||| ||||  ||||||||||||
                                TGA CATG  TTTTGTCTCTAT
                                  C   G_
GAM2513  DUT       3'  TAAGTTGCTGAAGGGAGAT    58521       _   A_
                                TAAGTTG TGAAG  AGAT
                                ||||||| |||||  ||||
                                ATTCAAC ACTTC  TCTA
                                    G    CC
GAM2513  XKRY      5'  TAAGCTGTGGAGTTCAAGTAAA 58522       A  AAGAT
            T                    TAAGTTGTG AG    AGTAAAT
                                |||||||||  ||    |||||||
                                ATTCGACAC TC    TCATTTA
                                     C  AAGT_
GAM2513  XKRY      5'  TAAGCTGTGGAGTTCAAGTAAA 58522       A  AAGAT
            T                    TAAGTTGTG AG    AGTAAAT
                                |||||||||  ||    |||||||
                                ATTCGACAC TC    TCATTTA
                                     C  AAGT_
GAM2513  FLJ20147  3'  TAAGCTGTGGAGAGGAAGCA   58523       A  A  T
                                TAAGTTGTG AGA GA AGTA
                                |||||||||  ||| ||  ||||
                                ATTCGACAC TCT CT TCGT
                                     C   C  _
GAM2513  KIAA1554  3'  AGTTGTGAAGATTTTCAGGTAA 58524         AGATA__
            AT                   AGTTGTGAAGA     GTAAAT
                                ||||||||||||     ||||||
                                TCAACACTTCT     CATTTA
                                      AAAAGTC
GAM2513  KIAA1598  3'  TAAGTTGTGGTGAGGAGAGT   58525       AA  A  T
                                TAAGTTGTG  GA GA AGT
                                |||||||||  || || |||
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                                ATTCAACAC  CT CT TCA
                                     CA  C  C
GAM2513  LOC120114 3'  TTGTGAAGAAGTTTCTAGT    58526          A___
                                TTGTGAAGAAG    TAGT
                                ||||||||||    ||||
                                AACACTTCTTC    ATCA
                                      AAAG
GAM2513  LOC153222 3'  TAAGTTTGAAGAAGCTAGT    58527       G       A
                                TAAGTT TGAAGAAG TAGT
                                ||||||| |||||||| ||||
                                ATTCAA ACTTCTTC ATCA
                                   _       G
GAM2513  LOC201696 3'  AGTTTGTGAAGAATGAAGT    58528      _       GAT
                                AGTT GTGAAGAA   AGT
                                |||| ||||||||   |||
                                TCAA CACTTCTT   TCA
                                  A       ACT
GAM2513  LOC56181  5'  TAAGTTGCGAGGGAGTAGGAAA 58529          AGA  A   T
           T                     TAAGTTGTGA   AG TAG AAAT
                                ||||||||||   || ||| ||||
                                ATTCAACGCT   TC ATC TTTA
                                      CCC  _   C
GAM2514  BTN2A1    3'  AGATGTGCGATCTGTCCCTCAT 58532           A_  __
           GTT                    AGATGTGCGATCTG  CC  ATGTT
                                ||||||||||||||  ||  |||||
                                TCTACACGCTAGAC  GG  TACAA
                                      AG  AG
GAM2514  LOC124491 3'  TGAGATGTGTTGTCCTTCATGT 58533         CGA   GAC
           T                     TGAGATGTG   TCT   CATGTT
                                |||||||||   |||   ||||||
                                ACTCTACAC   AGG   GTACAA
                                     AAC   AA_
GAM2515  COL4A4    5'  TAGTACTTAAAAAATATT    58536       C
                                TAGTAC TAAAGGATATT
                                |||||| ||||||||||
                                ATCATG ATTTTTTATAA
                                   A
GAM2515  PCDH15    3'  TATAGCACCTGAGATTTATT   58537          AAA    A
                                TATAGTACCT   GGAT TTATT
                                |||||||||   |||| |||||
                                ATATCGTGGA   TCTA AATAA
                                      C__   _
GAM2515  ZNF26     3'  AATACTGGGGGATATTATTC   58538       CTAAA
                                AGTAC    GGATATTATTC
                                |||||    ||||||||||
                                TTATG    CCTATAATAAG
                                   ACCC_
GAM2515  LOC151643 3'  TAGTACCTTCCCAGATATTGTT 58539         AAA_      A
           C                     TAGTACCT    GGATATT TTC
                                ||||||||    ||||||| |||
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                                ATCATGGA    TCTATAA AAG
                                    AGGG      C
GAM2516  BDNF     3'  TATAATCTAATCTATACAACA  58542        A
                                TATAAT TAATCTATATAATA
                                |||||| ||||||||||||||
                                ATATTA ATTAGATATGTTGT
                                   G
GAM2516  IRAK4    3'  TAACATAATCTAATAAT     58543           T
                                TAATATAATCTA ATAAT
                                |||||||||||| |||||
                                ATTGTATTAGAT TATTA
                                                _
GAM2516  MADH6    3'  TATAATATATATTTCCATATAA 58544         A___
              TA                  TATAATATA    TCTATATAATA
                                |||||||||    ||||||||||
                                ATATTATAT    AGGTATATTAT
                                     ATAA
GAM2516  RGS1     3'  TACAAACTATATAATAAT    58545       T
                                TATAA CTATATAATAAT
                                ||||| ||||||||||||
                                ATGTT GATATATTATTA
                                   T
GAM2516  MAIL     3'  TAATATAACCCACTATATAATA 58546          ___
                                TAATATAAT   CTATATAATA
                                |||||||||   ||||||||||
                                ATTATATTG   GATATATTAT
                                     GGT
GAM2516  LOC219920 3'  AATATAATTAATACAATAATA  58547         CT
                                AATATAAT  ATATAATAATA
                                ||||||||  ||||||||||||
                                TTATATTA  TATGTTATTAT
                                     AT
GAM2517  MSF      3'  TACATTTTCAACACTTTGTCAT 58550       CA_  T     T
              TT                  TACAT   CA CATTTT GTCATTT
                                |||||   || |||||| |||||||
                                ATGTA   GT GTGAAA CAGTAAA
                                   AAA  T     _
GAM2517  PAH      3'  ACTCATATCCTGTCATTT     58551     A   _
                                AC TCAT TTTTGTCATTT
                                || |||| ||||||||||||
                                TG AGTA AGGACAGTAAA
                                 _    T
GAM2517  PDC      3'  CATCAGTCATTTTTGTCA     58552       CA
                                CATCA  TCATTTTTGTCA
                                |||||  ||||||||||||
                                GTAGT  AGTAAAAACAGT
                                   C_
GAM2517  PDC      3'  CATCAGTCATTTTTGTCA     58552       CA
                                CATCA  TCATTTTTGTCA
                                |||||  ||||||||||||
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                                GTAGT  AGTAAAAACAGT
                                  C_
GAM2517  DKFZP434B172 3'  CATCACACATTTTTACA     58553        T       T
                                CATCACA CATTTTTG CA
                                ||||||| |||||||| ||
                                GTAGTGT GTAAAAAT GT
                                   _       _
GAM2517  FLJ21916  3'  TACATCCATCATGAATGT     58554        A      TTT
                                TACATC CATCAT   TGT
                                |||||| ||||||   |||
                                ATGTAG GTAGTA   ACA
                                   _     CTT
GAM2517  GS3955    3'  TACATCACAATGTGACATT    58555         TCATTTT  T
                                TACATCACA      TG CATT
                                |||||||||      || ||||
                                ATGTAGTGT      AC GTAA
                                     TAC____  T
GAM2517  KIAA1724  3'  TACATCACATTATCTGACACTT 58556          CATT    T
                                TACATCACAT    TTTG CATTT
                                ||||||||||    |||| |||||
                                ATGTAGTGTA    AGAC GTGAA
                                     AT__    T
GAM2517  KLF5      3'  ACATCGTTTGTCATCT      58557       ATT
                                ACATC   TTTGTCATTT
                                |||||   ||||||||||
                                TGTAG   AAACAGTAGA
                                  C__
GAM2517  MGC14136  3'  TACATTGCATCATTTTCTGT   58558       CA      _
                                TACAT  CATCATTT TTGT
                                |||||  |||||||| ||||
                                ATGTA  GTAGTAAA GACA
                                  AC       A
GAM2517  RASSF2    3'  ACATCACATATGTCTTTGTCAT 58559         CA_
              TT                  ACATCACAT   TTTTTGTCATTT
                                |||||||||   ||||||||||||
                                TGTAGTGTA   AGAAACAGTAAA
                                     TAC
GAM2517  SE57-1    3'  TACATTACATCATCTCATTT   58560       C       TTTG
                                TACAT ACATCATT    TCATTT
                                ||||| ||||||||    ||||||
                                ATGTA TGTAGTAG    AGTAAA
                                  A      _____
GAM2517  SE57-1    3'  TACATCATCTCATTTTTAT    58561        CA
                                TACATCA  TCATTTTTGT
                                |||||||  ||||||||||
                                ATGTAGT  AGTAAAAATA
                                    AG
GAM2517  TAF9L     3'  TACATCACATTAATTTGT     58562          CATT
                                TACATCACAT    TTTGT
                                ||||||||||    |||||
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                                ATGTAGTGTA  AAACA
                                    ATT_
GAM2517  LOC132720 3'  TACATCATATCATTTATGT  58563      C     T
                                TACATCA ATCATTT TGT
                                ||||||| ||||||| |||
                                ATGTAGT TAGTAAA ACA
                                    A     T
GAM2517  LOC143187 3'  TCAGTTCATTTTTGTCATTT  58564    CA
                                TCA  TCATTTTTGTCATTT
                                |||  |||||||||||||||
                                AGT  AGTAAAAACAGTAAA
                                  CA
GAM2517  LOC149182 3'  ACATCACCTTGCTTCATT   58565        TG_
                                ACATCATTTT  TCATT
                                ||||||||||  |||||
                                TGTAGTGGAA  AGTAA
                                    CGA
GAM2517  LOC196411 3'  ACATCATTAAAACTGTCATTT  58566       T___
                                ACATCATT   TTGTCATTT
                                ||||||||   |||||||||
                                TGTAGTAA   GACAGTAAA
                                    TTTT
GAM2517  LOC201824 3'  ATCTTTCATTTTTGTCATTT  58567    ACA
                                ATC  TCATTTTTGTCATTT
                                |||  ||||||||||||||
                                TAG  AGTAAAAACAGTAAA
                                  AA_
GAM2517  LOC203111 3'  TAATCACATCATTTTTAT   58568   C
                                A ATCACATCATTTTTGT
                                | ||||||||||||||||
                                A TAGTGTAGTAAAAATA
                                 T
GAM2518  GFR     3'  TGGAGGGTTTGCTCAGCCCA  58571     A      TA
                                TGGA GGTTTGCT  CGGTCCA
                                |||| ||||||||  |||||||
                                ACCT CCAAACGA  GTCGGGT
                                  C      __
GAM2518  OSBPL8   3'  GGAACCGTTTACGGTCCA   58572     GGT  C
                                GGAA  TTG TTACGGTCCA
                                ||||  ||| ||||||||||
                                CCTT  GGC AATGCCAGGT
                                  ___  A
GAM2518  LOC145608 5'  TGGGAGGTTTGCTTTGCC   58573    A       ACG
                                TGG AGGTTTGCTT  GTC
                                ||| ||||||||||  |||
                                ACC TCCAAACGAA  CGG
                                  C       A__
GAM2519  EIF4E   3'  GACATACTAATTCTAGTT   58576      GCAT
                                GACATA   ATTCTAGTT
                                ||||||   |||||||||
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                                CTGTAT   TAAGATCAA
                                   GAT_
GAM2519 KCNA3   3' ACAAGTCATTATTCTAGTT   58577    TAG  _
                                ACA  CAT ATTCTAGTT
                                |||  ||| |||||||||
                                TGT  GTA TAAGATCAA
                                  TCA  A
GAM2519 MTERF   3' TGGCATAACATATTCACAGTT  58578   A       _
                                TG CATAGCATATTC TAGTT
                                || ||||||||||| |||||
                                AC GTATTGTATAAG GTCAA
                                 C         T
GAM2519 NAPB    3' TGACATAACATAGGAAGTT   58579         TTCT
                                TGACATAGCATA   AGTT
                                ||||||||||||   ||||
                                ACTGTATTGTAT   TCAA
                                       CCT_
GAM2519 PKD2    3' TGCATTACAAATTCTAGTT   58580   A  A  T
                                TG CAT GCA ATTCTAGTT
                                || ||| ||| |||||||||
                                AC GTA TGT TAAGATCAA
                                 _  A  T
GAM2519 SFRP1   3' TGACACAGCAACCAGTT    58581        TATT
                                TGACATAGCA   CTAGTT
                                ||||||||||   ||||||
                                ACTGTGTCGT   GGTCAA
                                      T___
GAM2519 SMARCC1 3' GACATAGCATGCTAAAGTT   58582        A  CT
                                GACATAGCAT TT  AGTT
                                |||||||||| ||  ||||
                                CTGTATCGTA GA  TCAA
                                      C  TT
GAM2519 TIM3    3' TGACACAGCTCATAGTT    58583        ATAT  _
                                TGACATAGC   TC TAGTT
                                |||||||||   || |||||
                                ACTGTGTCG   AG ATCAA
                                     ____ T
GAM2519 TNFSF4  3' TGATATAGACCCTTCTAGTT  58584    C   _ ATA
                                TGA ATAG C   TTCTAGTT
                                ||| |||| |   ||||||||
                                ACT TATC G   AAGATCAA
                                  A   T GG_
GAM2519 CTCF    3' GACAGCAAGTTCTAGTT    58585    TA  TA
                                GACA  GCA  TTCTAGTT
                                ||||  |||  ||||||||
                                CTGT  CGT  AAGATCAA
                                   __  TC
GAM2519 DICER1  3' GACTACATATTCTGGTT    58586    ATA      A
                                GAC   GCATATTCT GTT
                                |||   ||||||||| |||
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                                CTG   TGTATAAGA CAA
                                  A__       C
GAM2519  DKFZP564F013 5'  GACATAGCACTCTGGTT     58587          AT   A
                                GACATAGCAT  TCT GTT
                                ||||||||||  ||| |||
                                CTGTATCGTG  AGA CAA
                                      __  C
GAM2519  FLJ22418  3'  TGACACAGTTGACTCTAGTT   58588        CAT
                                TGACATAG   ATTCTAGTT
                                ||||||||   |||||||||
                                ACTGTGTC   TGAGATCAA
                                     AAC
GAM2519  KIAA0527  3'  TGCACAGGTATTCTAGTT    58589    A    CA
                                TG CATAG  TATTCTAGTT
                                || |||||  ||||||||||
                                AC GTGTC  ATAAGATCAA
                                 _    C_
GAM2519  KIAA1950  3'  TGCATAGCCCTTCTAGTT    58590    A     ATA
                                TG CATAGC   TTCTAGTT
                                || ||||||   ||||||||
                                AC GTATCG   AAGATCAA
                                 _     GG_
GAM2519  PRO1635   3'  TGACACAGCATGAAACTGGTT  58591          ATT_  A
                                TGACATAGCAT    CT GTT
                                ||||||||||    || |||
                                ACTGTGTCGTA    GA CAA
                                       CTTT  C
GAM2519  SEMA3C    3'  GATGCAACAATTCTAGTT    58592    CA    T
                                GA  TAGCA ATTCTAGTT
                                ||  ||||| |||||||||
                                CT  GTTGT TAAGATCAA
                                 AC    _
GAM2519  SLC11A2   3'  GATGAAGCTATTCTAGTT    58593    CAT   A
                                GA   AGC TATTCTAGTT
                                ||   ||| ||||||||||
                                CT   TCG ATAAGATCAA
                                 ACT  _
GAM2519  TAF9L     3'  GATCTAGAATATTCTAGTT   58594    CA   C
                                GA  TAG ATATTCTAGTT
                                ||  ||| ||||||||||
                                CT  ATC TATAAGATCAA
                                 AG   T
GAM2519  UBA2      3'  GACATAACAATCTGGTT     58595        TAT   A
                                GACATAGCA   TCT GTT
                                |||||||||   ||| |||
                                CTGTATTGT   AGA CAA
                                      T__   C
GAM2519  USP24     3'  TGATACGGCACTCTAGTT    58596     C TA    AT
                                TGA A  GCAT  TCTAGTT
                                ||| |  ||||  |||||||
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                                ACT T  CGTG  AGATCAA
                                  A GC   __
GAM2519  LOC144715 5'  TAACATAGTGACCTCTAGTT   58597        CATA
                                TGACATAG    TTCTAGTT
                                ||||||||    ||||||||
                                ATTGTATC    GAGATCAA
                                     ACTG
GAM2519  LOC145790 3'  TGACTGCATTTCTAGTT     58598      ATA    A
                                TGAC   GCAT TTCTAGTT
                                ||||   |||| ||||||||
                                ACTG   CGTA AAGATCAA
                                  A__    _
GAM2519  LOC196283 3'  TGACAAGGCATCTTCTAGTT   58599       TA    A
                                TGACA  GCAT TTCTAGTT
                                |||||  |||| ||||||||
                                ACTGT  CGTA AAGATCAA
                                   TC    G
GAM2519  LOC219920 5'  TGACAACACATTTAGTT     58600       TA      C
                                TGACA  GCATATT TAGTT
                                |||||  ||||||| |||||
                                ACTGT  TGTGTAA ATCAA
                                   __      _
GAM2519  LOC221017 3'  TGACTAAACACTCTAGTT    58601      A   C
                                TGAC TAG ATATTCTAGTT
                                |||| ||| ||||||||||
                                ACTG ATT TGTGAGATCAA
                                  _  _
GAM2519  LOC221037 3'  ACATAGCATATTAAGTT     58602           CT
                                ACATAGCATATT  AGTT
                                ||||||||||||  ||||
                                TGTATCGTATAA  TCAA
                                       T_
GAM2519  LOC254158 3'  TGACATAGATTCCTTAGTT    58603        C  A TC
                                TGACATAG AT T  TAGTT
                                |||||||| || |  |||||
                                ACTGTATC TA G  ATCAA
                                     _  A GA
GAM2520  BCL2L2    3'  TCAGATCTGAAATGGTCA     58606        A  CTAC
                                TTAGATCT GG    TGGTCA
                                |||||||| ||    ||||||
                                AGTCTAGA CT    ACCAGT
                                     _  TT__
GAM2520  GAC1      3'  TCAGATCTGGCTGGGGTCA    58607        A    ACT
                                TTAGATCT GGCT   GGTCA
                                |||||||| ||||   |||||
                                AGTCTAGA CCGA   CCAGT
                                     _    CC_
GAM2520  GNRH1     5'  TTAGATCCAGACAAGGT      58608           TACT
                                TTAGATCTAGGC    GGT
                                ||||||||||||    |||
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                                AATCTAGGTCTG   CCA
                                      TT__
GAM2520 IFNA21   3' TTAGATCTATCAGCATGGTCA 58609       __  TAC
                                TTAGATCTA GGC  TGGTCA
                                ||||||||| |||  ||||||
                                AATCTAGAT TCG  ACCAGT
                                     AG  T__
GAM2520 LMO2     5' TCAGATCTAGGCTGCCTG   58610         A_
                                TTAGATCTAGGCT CTG
                                |||||||||||| |||
                                AGTCTAGATCCGA GAC
                                       CG
GAM2520 PPEF1    5' CTAGATCTTCACTTTGCTGGT 58611       AG  A__
                                TTAGATCT GCT  CTGGT
                                |||||||| |||  |||||
                                GATCTAGA TGA  GACCA
                                     AG  AAC
GAM2520 PXF      3' TCAGATCTGGGCTCTTCCA   58612       A   A GG
                                TTAGATCT GGCT CT  TCA
                                |||||||| |||| ||  |||
                                AGTCTAGA CCGA GA  GGT
                                     C   _ A_
GAM2520 FLJ14564 3' GATCTCTGCACTGGTCA    58613     AG  T
                                GATCT  GC ACTGGTCA
                                |||||  || ||||||||
                                CTAGA  CG TGACCAGT
                                   GA  _
GAM2520 HNK-1ST  3' TCAGATCTTCACCTGGT    58614      AG  TA
                                TTAGATCT  GC  CTGGT
                                ||||||||  ||  |||||
                                AGTCTAGA  TG  GACCA
                                     AG  __
GAM2520 KIAA1265 3' TTAAATTAGACTGGTC     58615     C   GCT
                                TTAGAT TAG   ACTGGTC
                                |||||| |||   |||||||
                                AATTTA ATC   TGACCAG
                                     _  ____
GAM2520 KIAA1466 5' GATAAATAGGCTACTGGTCA  58616    C__
                                GAT   TAGGCTACTGGTCA
                                |||   ||||||||||||||
                                CTA   ATCCGATGACCAGT
                                  TTT
GAM2520 MGC18257 3' TTAAATCTAGCAAGTGGT   58617        G TAC
                                TTAGATCTAG C   TGGT
                                |||||||||| |   ||||
                                AATTTAGATC G   ACCA
                                     _ TTC
GAM2520 UBA2     3' TTAGATCTAGGCTAAAAAT   58618          CT
                                TTAGATCTAGGCTA  GGT
                                |||||||||||||  |||
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                                AATCTAGATCCGAT  TTA
                                       TT
GAM2520  ZMPSTE24  3'  TTAAATCTGGGCTTTTCTG   58619        A   A__
                                TTAGATCT GGCT   CTG
                                |||||||| ||||   |||
                                AATTTAGA CCGA   GAC
                                     C    AAA
GAM2520  LOC51301  5'  TTAGATCCAGGTCTGAAGTCA  58620          _  ACT
                                TTAGATCTAGG CT   GGTCA
                                |||||||||||  ||   |||||
                                AATCTAGGTCC GA   TCAGT
                                      A  CT_
GAM2521  COL1A1   3'  TGGTTTTTGGTCATGTTCG   58623         ACT
                                TGGTTTTTGG   GTGTTCG
                                ||||||||||   |||||||
                                ACCAAAAACC   TACAAGC
                                      AG_
GAM2521  DKFZP434L1123 5'  TTTCTGGTTTTTGAGGTTAGTC 58624             ACTGT
           CG                     TTTCTGGTTTTTGG    GTTCG
                                |||||||||||||    |||||
                                AAAGACCAAAAACT    CAGGC
                                       CCAAT
GAM2522  PRM2     3'  TGTTTCGGGCGACTTTTTCTTA 58627        A  _   ACC
           AT                     TGTTTCGG TG TTT   CTTAAT
                                |||||||| || |||   ||||||
                                ACAAAGCC GC GAA   GAATTA
                                     C  T   AAA
GAM2522  FLJ14431  3'  GTTTGGATGTTTGTCCCCT   58628     C       A_
                                GTTT GGATGTTT  CCCTT
                                |||| ||||||||  |||||
                                CAAA CCTACAAA  GGGGA
                                  _       CA
GAM2522  LOC197125 3'  TATTTTGGATACCCTTA     58629      C   TGTT
                                TGTTT GGA    TACCCTTA
                                ||||| |||    ||||||||
                                ATAAA CCT    ATGGGAAT
                                   A  _____
GAM2523  DHCR7    5'  GCCTGCTTGCGCGCGCTGCT   58632       C    T__
                                GCCTGC TTGC   CGCTGCT
                                ||||||| ||||   |||||||
                                CGGACG AACG   GCGACGA
                                   _    CGC
GAM2523  RU2      5'  GCCGCCGCCTCAGCTCGCTGCT 58633       T    _
                                GCCGCC GCCTT GCTCGCTGCT
                                |||||| ||||| ||||||||||
                                CGGCGG CGGAG CGAGCGACGA
                                   _     T
GAM2523  STK24    5'  GCTCTCTGCCTTGGCAACATGC 58634    CGC       CTC  _
           T                     GC   CTGCCTTG   GC TGCT
                                ||   ||||||||   || ||||
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                                CG   GACGGAAC   TG ACGA
                                 AGA       CGT  T
GAM2523  TLX1     5'  CGGCTGCTCGCTCGCTG     58635    C    C
                                CG CTGC TTGCTCGCTG
                                || |||| ||||||||||
                                GC GACG AGCGAGCGAC
                                 C   _
GAM2523  FLJ20123 5'  AGCTGCCTGCCTGCTGC     58636     C       TGCTC
                                AGC GCCTGCCT    GCTGC
                                ||| ||||||||    |||||
                                TCG CGGACGGA    CGACG
                                 A      ______
GAM2523  FLJ20257 5'  TAGCCCCTGCCTCCGACTTGCT 58637       G       __   C
                                TAGCC CCTGCCTT  GCT GCT
                                ||||| ||||||||  ||| |||
                                ATCGG GGACGGAG  TGA CGA
                                   _       GC   A
GAM2523  FLJ20294 3'  CCAGGCCGCTCGCTGCT     58638    T_   TT
                                CC  GCC  GCTCGCTGCT
                                ||  |||  ||||||||||
                                GG  CGG  CGAGCGACGA
                                 TC   __
GAM2523  FLJ23186 3'  GCTGCCTGCCTCTCCGTGCT   58639    C       GC   C
                                GC GCCTGCCTT  TCG TGCT
                                || |||||||||  ||| ||||
                                CG CGGACGGAG  GGC ACGA
                                 A        A_   _
GAM2523  FLJ31547 5'  GCTGCCTGCCTGCACT      58640    C       T  TC
                                GC GCCTGCCT GC  GCT
                                || |||||||| ||  |||
                                CG CGGACGGA CG  TGA
                                 A       _ __
GAM2523  KIAA1138 3'  GCCGCCAGCTCATCCCGCTGCT 58641        T  CTTG
                                GCCGCC GC    CTCGCTGCT
                                |||||| ||    |||||||||
                                CGGCGG CG    GGGCGACGA
                                   T  AGTA
GAM2523  NIR3     3'  GCTGCCTGCCCTGAAGCT     58642    C        CTC
                                GC GCCTGCCTTG   GCT
                                || ||||||||||   |||
                                CG CGGACGGGAC   CGA
                                 A         TT_
GAM2523  PDZD2    5'  GCCGCCTGGCAGAGCCGCTGCT 58643         _ CTT  T
                                GCCGCCTG C   GC CGCTGCT
                                |||||||| |   || |||||||
                                CGGCGGAC G   CG GCGACGA
                                     C TCT  _
GAM2523  PPP1R16A 5'  GCTGCTTGCCCACAGGGCTGCT 58644    C  C    TGCTC
                                GC GC TGCCT     GCTGCT
                                || || |||||     ||||||
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                                CG CG ACGGG    CGACGA
                                 A  A    TGTCC
GAM2523  SEMA6A   5'  GCCGCTGCTACACGCTGCT   58645      C   CT   T
                                GCCGC TGC  TGC CGCTGCT
                                ||||| |||  ||| |||||||
                                CGGCG ACG  ATG GCGACGA
                                  _  __   T
GAM2523  LOC124842 3'  GCTGCCTGCCCTGTGC      58646    C        CTCGC
                                GC GCCTGCCTTG    TGC
                                || ||||||||||    |||
                                CG CGGACGGGAC    ACG
                                 A       _____
GAM2523  LOC149566 3'  TAACTGCCTGCCTGGGCACGTT 58648      C       T_  T  C
             GCT                   TAGC GCCTGCCT  GC CG TGCT
                                |||| ||||||||  || || ||||
                                ATTG CGGACGGA  CG GC ACGA
                                  A       CC  T  A
GAM2523  LOC149566 3'  GCCTGCCTGGGCACGTTGCT   58647        T_  T  C
                                GCCTGCCT  GC CG TGCT
                                ||||||||  || || ||||
                                CGGACGGA  CG GC ACGA
                                     CC  T  A
GAM2523  LOC153338 5'  CCTGCCTCTCACTGCT      58649        TG
                                CCTGCCT  CTCGCTGCT
                                |||||||  |||||||||
                                GGACGGA  GAGTGACGA
                                     __
GAM2523  LOC200471 5'  GCCGCCTGTTTCCCTGCT    58650         ___
                                GCCGCCTG   CCTTGCT
                                ||||||||   |||||||
                                CGGCGGAC   GGGACGA
                                     AAA
GAM2523  LOC255452 3'  GCCGCCTGCTTTGGGCT     58651         C   CTC
                                GCCGCCTGC TTG   GCT
                                ||||||||| |||   |||
                                CGGCGGACG AAC   CGA
                                     A  C__
GAM2524  ARCN1    3'  GGGCATTCTCTGGAGAGCTTGC 58654          AATTAT  _
             T                   GGGCATTCTT     GTT GCT
                                ||||||||||     ||| |||
                                CCCGTAAGAG     CGA CGA
                                      ACCTCT   A
GAM2524  CYP19    5'  GGGATTTCCAAATGTTGCT    58655     CA    TAATT
                                GGG  TTCT    ATGTTGCT
                                |||  ||||    ||||||||
                                CCC  AAGG    TACAACGA
                                  TA   TT___
GAM2524  IL18R1   3'  GGGCATTTTTAATATGT     58656        C    T
                                GGGCATT TTAAT ATGT
                                ||||||| ||||| ||||
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                                CCCGTAA AATTA TACA
                                   A    _
GAM2524  INPP5D    3'  GGGCTTCTTAATGCT      58657      A      TTATGT
                                GGGC TTCTTAA     TGCT
                                |||| |||||||     ||||
                                CCCG AAGAATT     ACGA
                                  _     _______
GAM2524  MCL1      3'  GGCATTCTTAGTGCT      58658          ATTAT  T
                                GGCATTCTTA    GT GCT
                                ||||||||||    || |||
                                CCGTAAGAAT    CA CGA
                                      ______ _
GAM2524  C8orf2    3'  GGGCATGTCATGTTGCTC    58659       TCTTAA
                                GGGCAT     TTATGTTGCTC
                                ||||||     ||||||||||
                                CCCGTA     AGTACAACGAG
                                   C_____
GAM2524  N4BP3     3'  GGCATTCCCTGGTGTTGTTCC  58660         AATTA    C
                                GGCATTCTT    TGTTG TCC
                                |||||||||    ||||| |||
                                CCGTAAGGG    ACAAC AGG
                                     ACC__    A
GAM2524  SCDGF-B   3'  GAGCGTTCTTAATTATTAGTGT 58661      A         GT_  C
           C                     GGGC TTCTTAATTAT   TG TC
                                |||| ||||||||||   || ||
                                CTCG AAGAATTAATA   AC AG
                                  C          ATC  _
GAM2524  SCDGF-B   3'  GAGCGTTCTTAATTATTAGTGT 58661      A         GT_  C
           C                     GGGC TTCTTAATTAT   TG TC
                                |||| ||||||||||   || ||
                                CTCG AAGAATTAATA   AC AG
                                  C          ATC  _
GAM2524  LOC153196 5'  GGGCATTCATAATTAAATGTT  58662         T     __
                                GGGCATTC TAATTA  TGTT
                                |||||||| ||||||  ||||
                                CCCGTAAG ATTAAT  ACAA
                                     T     TT
GAM2524  LOC197331 3'  GGTCATTCATGTTGCT      58663    G    TTAATT
                                GG CATTC     ATGTTGCT
                                || |||||     ||||||||
                                CC GTAAG     TACAACGA
                                 A    _______
GAM2524  LOC203232 3'  GGTCATTCATGTTGCT      58663    G    TTAATT
                                GG CATTC     ATGTTGCT
                                || |||||     ||||||||
                                CC GTAAG     TACAACGA
                                 A    _______
GAM2524  LOC51204  5'  GGGCATTCTTAGCTCTGCT    58664          ATTATG
                                GGGCATTCTTA     TTGCT
                                ||||||||||     |||||
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                                CCCGTAAGAAT     GACGA
                                      CGA___
GAM2525 CEACAM6  3' TGTACATTTGAACACACGGCTG 58667       CCA__   T
                                TGTACATT    ACAC GCTG
                                ||||||||    |||| ||||
                                ACATGTAA    TGTG CGAC
                                     ACTTG   C
GAM2525 CTBP2    3' TGTAGTTTCAACACTGCAAC  58668    CA  C      T
                                TGTA  TTC AACACTGC GC
                                ||||  ||| |||||||| ||
                                ACAT  AAG TTGTGACG TG
                                  CA  _      T
GAM2525 CTBP2    3' TGTAGTTTCAACACTGCAAC  58668    CA  C      T
                                TGTA  TTC AACACTGC GC
                                ||||  ||| |||||||| ||
                                ACAT  AAG TTGTGACG TG
                                  CA  _      T
GAM2525 CUL5     3' TGTACATTTACAGTATTTGCTG 58669       CCA  C____
             C                   TGTACATT  ACA    TGCTGC
                                 ||||||||  |||    ||||||
                                 ACATGTAA  TGT    ACGACG
                                      A__  CATAA
GAM2525 GAS1     3' TGTACATTTCTACAACGTCCAT 58670       CCA  CT  TG
                                TGTACATT  ACA  GC  CCAT
                                ||||||||  |||  ||  ||||
                                ACATGTAA  TGT  TG  GGTA
                                     AGA  __  CA
GAM2525 GPR81    3' TGCACATTCTGTCCCCTGCCAT 58671        CAACA  G
                                TGTACATTC    CT CTGCCAT
                                |||||||||    || |||||||
                                ACGTGTAAG    GG GACGGTA
                                      ACA__  G
GAM2525 MAX      3' TGTACATTTCCATGTGAATAAG 58672       _  ACACTGCT_
             CCAT                   TGTACATT CCA       GCCAT
                                    |||||||| |||       |||||
                                    ACATGTAA GGT       CGGTA
                                         A  ACACTTATT
GAM2525 PRKWNK3  3' TGTACATTTTGACATTGCC   58673       CCA  C
                                TGTACATT  ACA TGCT
                                ||||||||  ||| ||||
                                ACATGTAA  TGT ACGG
                                     AAC  A
GAM2525 PTGFRN   3' TGTAGATTCCAGGGCTGCCAT  58674     C    ACACT
                                TGTA ATTCCA    GCTGCCAT
                                |||| ||||||    ||||||||
                                ACAT TAAGGT    CGACGGTA
                                  C    CC___
GAM2525 DKFZp547D155 3' TGTACATTTCAGCATTTGCATC 58675       C  A  C_  TGC
             AT                   TGTACATT CA CA  TGC  CAT
                                  |||||||| || ||  |||  |||
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                                ACATGTAA GT GT  ACG   GTA
                                     A  C  AA   TA_
GAM2525  FLJ23047  3'  TGACATTCCAGCAGCT     58676    T      A  CT
                                TG ACATTCCA CA  GCT
                                || |||||||| ||  |||
                                AC TGTAAGGT GT  CGA
                                 _       C  __
GAM2525  KIAA0365  5'  TGTAATTCGTCTGGCTGCCAT  58677     C    CAACA  _
                                TGTA ATTC    CTG CTGCCAT
                                |||| ||||    ||| |||||||
                                ACAT TAAG    GAC GACGGTA
                                   _   CA___   C
GAM2525  KIAA0534  3'  TGTACACTCTAATGAAATCACT 58678         C _______
             GCTA                   TGTACATTC AA     CACTGCTG
                                |||||||||| ||     ||||||||
                                ACATGTGAG TT     GTGACGAT
                                      A  ACTTTA
GAM2525  KIAA1735  5'  TGTTGTTCCAACAGCTG     58679     ACA      CT
                                TGT   TTCCAACA  GCTG
                                |||   ||||||||  ||||
                                ACA   AAGGTTGT  CGAC
                                  AC_       __
GAM2525  LOC148438 3'  TGTACATTCCTATGTTCCA    58680          AACAC  CTG
                                TGTACATTCC    TG   CCA
                                ||||||||||    ||   |||
                                ACATGTAAGG    AC   GGT
                                      AT___  AA_
GAM2525  LOC150951 3'  TGTTATTTCCTAATTTGCTGCC 58681     ACA    AACAC
             AT                   TGT   TTCC    TGCTGCCAT
                                |||   ||||    |||||||||
                                ACA   AAGG    ACGACGGTA
                                  ATA    ATTAA
GAM2525  LOC203427 3'  TGTACATTTTATCACTGCT    58682         CCAA
                                TGTACATT    CACTGCT
                                ||||||||    |||||||
                                ACATGTAA    GTGACGA
                                     AATA
GAM2525  LOC221463 3'  TGTATTCCAACACAGGCC     58683      CA       TGCT
                                TGTA  TTCCAACAC    GCC
                                ||||  |||||||||    |||
                                ACAT  AAGGTTGTG    CGG
                                   __        TC__
GAM2525  LOC90826  5'  TGCACATTCTACTGCC      58684         CAACAC
                                TGTACATTC     TGCTGCC
                                |||||||||     |||||||
                                ACGTGTAAG     ATGACGG
                                              _______
GAM2526  PTPRB     3'  TAAATTATACATAGTATCAA   58687           _
                                TAAATTATACA AGTATTAA
                                |||||||||| ||||||||
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                                ATTTAATATGT TCATAGTT
                                      A
GAM2526 CTCF     3' AATTATACAAGGTTCAAA    58688          TA
                                AATTATACAAG  TTAAA
                                ||||||||||  |||||
                                TTAATATGTTC  AGTTT
                                      CA
GAM2526 POPX1    3' TAAATTACACAATGAATAAAAA 58689           GTAT
              TA                  TAAATTATACAA   TAAAAATA
                                ||||||||||||   ||||||||
                                ATTTAATGTGTT   ATTTTTAT
                                       ACTT
GAM2526 LOC157657 3' TAAATTTTACAAGTATGTAAA  58690       A       _
                                TAAATT TACAAGTAT TAAA
                                |||||| ||||||||| ||||
                                ATTTAA ATGTTCATA ATTT
                                    A        C
GAM2526 LOC254251 3' TAAATAATACAAGTACTAAAA  58691       T
                                TAAAT ATACAAGTATTAAAA
                                ||||| ||||||||||||||
                                ATTTA TATGTTCATGATTTT
                                   T
GAM2527 ACADSB   3' TCTGAACTATTATTCAGGATAA 58694    CA       C  CA
                                TC  AACTATTA TC  GGGATAA
                                ||  |||||||| ||  |||||||
                                AG  TTGATAAT AG  TCCTATT
                                 AC       A __
GAM2527 AP2B1    3' TCCAAATGACCAGGGATA    58695       CTATTACT
                                TCCAAA       CCAGGGATA
                                ||||||       |||||||||
                                AGGTTT       GGTCCCTAT
                                   ACT_____
GAM2527 BYSL     3' TCAGAACTAAACAGGGATA   58696    CA    TTACTC
                                TC  AACTA     CAGGGATA
                                ||  |||||     ||||||||
                                AG  TTGAT     GTCCCTAT
                                 TC    TT____
GAM2527 CDH19    5' TCCAACTATTACTCTTCAG    58697      A       __
                                TCCAA CTATTACTC  CAG
                                ||||| |||||||||  |||
                                AGGTT GATAATGAG  GTC
                                   _       AA
GAM2527 CR1      3' TCCAAACTATTTTCTATCTCC  58698          A_____
                                TCCAAACTATT     CTCC
                                ||||||||||     ||||
                                AGGTTTGATAA     GAGG
                                       AAGATA
GAM2527 DSC3     3' AAACTATCACTTAAAGTGA    58699          CC  _
                                AAACTATTACT  AGG GA
                                ||||||||||  ||| ||
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                                TTTGATAGTGA  TTC CT
                                      AT   A
GAM2527  DSC3     3'  AAACTATCACTTAAAGTGA   58699          CC  _
                                AAACTATTACT  AGG GA
                                ||||||||||  ||| ||
                                TTTGATAGTGA  TTC CT
                                      AT   A
GAM2527  EFG2     5'  TCCAAACTGTTACTGTCTCGG  58700        A    CCA__
                                TCCAAACT TTACT    GG
                                ||||||||  |||||    ||
                                AGGTTTGA AATGA    CC
                                     C    CAGAG
GAM2527  IL1R1    3'  TCCAGGTGACCTCAGGGATAA  58701     AACTATT  TC
                                TCCA      AC  CAGGGATAA
                                ||||      ||  ||||||||||
                                AGGT      TG  GTCCCTATT
                                  CCAC___  GA
GAM2527  PSCDBP   3'  CTCAATTATTCACAGGGATAA  58702    __    C  _
                                CT  ATTA TC CAGGGATAA
                                ||  |||| || ||||||||||
                                GA  TAAT AG GTCCCTATT
                                 GT    A  T
GAM2527  RFP      3'  TCCCAGAATCCTTCCAGGGAT  58703     AAACT   AC
                                TCC    ATT  TCCAGGGAT
                                |||    |||  ||||||||||
                                AGG    TAG  AGGTCCCTA
                                  GTCT_   GA
GAM2527  SRR      3'  CCAGTCAGTACTCCAGGGAT   58704     AAC  T
                                CCA   TA TACTCCAGGGAT
                                |||   || ||||||||||||
                                GGT   GT ATGAGGTCCCTA
                                  CA_  C
GAM2527  ZNF207   3'  TCCAAACCTATTAGACTGGAT  58705        _    CTCCAG
                                TCCAAAC TATTA     GGAT
                                |||||||  |||||     ||||
                                AGGTTTG ATAAT     CCTA
                                     G    CTGA__
GAM2527  DKFZP434L187 3'  TCCAAACTTATTACTTTTATGG 58706         _     CCAG_
                                TCCAAACT ATTACT    GG
                                ||||||||  ||||||    ||
                                AGGTTTGA TAATGA    CC
                                     A     AAATA
GAM2527  FLJ13154  3'  TCCTGGCTCGACCAGGGATAA  58707     AAA  ATTACT
                                TCC   CT     CCAGGGATAA
                                |||   ||     ||||||||||
                                AGG   GA     GGTCCCTATT
                                  ACC  GCT___
GAM2527  KIAA0009  3'  TCCAAATATTACTCCTGG    58708       C        A
                                TCCAAA TATTACTCC GG
                                ||||||  |||||||| ||
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                                AGGTTT ATAATGAGG CC
                                  _       A
GAM2527  KIAA1423  3'  TCCACACTATTACTTCCCCTTT 58709     A       _  AG___
             GG                   TCCA ACTATTACT CC    GG
                                  |||| ||||||||| ||    ||
                                  AGGT TGATAATGA GG    CC
                                    G       A  GGAAA
GAM2527  ZNF297B   3'  TCCAAACTTATTAGGAAGGATA 58710       _   CTCC
             A                    TCCAAACT ATTA   AGGGATAA
                                  |||||||| ||||   ||||||||
                                  AGGTTTGA TAAT   TTCCTATT
                                      A   CC__
GAM2527  LOC120227 3'  AAACCAAGTTCAGGGATAA   58711       TTACTC
                                  AAACTA     CAGGGATAA
                                  ||||||     |||||||||
                                  TTTGGT     GTCCCTATT
                                     TCAA__
GAM2527  LOC127133 3'  CAAACTATTACTGTTCCATAG  58712          ___   G
                                  CAAACTATTAC   TCCA GG
                                  ||||||||||   |||| ||
                                  GTTTGATAATG   AGGT TC
                                        ACA   A
GAM2527  LOC170082 3'  CCCAAACTGTAACTTTTAGGGA 58713        ATT   CC_
             T                    TCCAAACT   ACT   AGGGAT
                                  ||||||||   |||   ||||||
                                  GGGTTTGA   TGA   TCCCTA
                                       CAT   AAA
GAM2528  REGL     3'  CATTAGATGGCCATTAGT    58716      A   AT
                                  CATTA ATG  GTTATTAGT
                                  ||||| |||  |||||||||
                                  GTAAT TAC  CGGTAATCA
                                    C   __
GAM2528  RHO      3'  TTACATTAATTGATGTTATT   58717         A
                                  TTACATTAA TGATGTTATT
                                  ||||||||| ||||||||||
                                  AATGTAATT ACTACAATAA
                                        A
GAM2528  PRO1635   3'  TTACAATAAATGATGAAATAGT 58718      T       TTAT
                                  TTACA TAAATGATG    TAGT
                                  ||||| |||||||||    ||||
                                  AATGT ATTTACTAC    ATCA
                                     T       TTT_
GAM2528  LOC221830 3'  TTACATTAGATAACTTCTTAGT 58719        A    GTTA
             C                    TTACATTA ATGAT    TTAGTC
                                  |||||||| |||||    ||||||
                                  AATGTAAT TATTG    AATCAG
                                       C    AAG_
GAM2529  MFI2     3'  TTCCCACATAACAATATTTT   58722        TT_
                                  TTCCCAC   ATAATATTTT
                                  |||||||   ||||||||||
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                                AAGGGTG  TGTTATAAAA
                                   TAT
GAM2529 NEK2     3' TACTCTTCCTGCATAAATATTT 58723        CACTTAT
             T                  TACTCTTCC     AATATTTT
                                |||||||||     ||||||||
                                ATGAGAAGG     TTATAAAA
                                   ACGTAT_
GAM2529 PRKCN    3' TACTCTTCCTTTTGTAACAT  58724        CAC  A
                                TACTCTTCC  TT TAATAT
                                |||||||||  || ||||||
                                ATGAGAAGG  AA ATTGTA
                                   AA_  C
GAM2529 RAD51L1  3' ACTCTTTCCCAATATTT    58725      _   CTTATA
                                ACTCTT CCCA    ATATTT
                                |||||| ||||    ||||||
                                TGAGAA GGGT    TATAAA
                                   A  _______
GAM2529 SUSP1    3' TACTCTTTCCTCTTAAATATTT 58726      C  A   T
                                TACTCTT CC CTTA AATATTT
                                ||||||| || |||| |||||||
                                ATGAGAA GG GAAT TTATAAA
                                   A  A   _
GAM2529 C1orf9   3' CCTTTCCCATTAATATTTT   58727   TC    CTTA
                                C  TTCCCA   TAATATTTT
                                |  ||||||   |||||||||
                                G  AAGGGT   ATTATAAAA
                                 GA    A___
GAM2529 CHORDC1  3' CTCTTCCTTAAATATTT    58728      CAC   T
                                CTCTTCC   TTA AATATTT
                                |||||||   ||| |||||||
                                GAGAAGG   AAT TTATAAA
                                   ___  _
GAM2529 GPNMB    3' CTCTTCCCACACTTTATTTT  58729        TTATAA
                                CTCTTCCCAC     TATTTT
                                ||||||||||     ||||||
                                GAGAAGGGTG     ATAAAA
                                   TGAA__
GAM2529 RFX3     3' TTCCCACTTAAAATATTTT   58730        T
                                TTCCCACTTA AATATTTT
                                |||||||||| ||||||||
                                AAGGGTGAAT TTATAAAA
                                   T
GAM2529 Rpo1-2   3' CTCTTCCATTTATCAATATTT 58731      CAC   _
                                CTCTTCC   TTAT AATATTT
                                |||||||   |||| |||||||
                                GAGAAGG   AATA TTATAAA
                                   TA_   G
GAM2529 Rpo1-2   3' CTCTTCCATTTATCAATATTT 58731      CAC   _
                                CTCTTCC   TTAT AATATTT
                                |||||||   |||| |||||||
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                                GAGAAGG  AATA TTATAAA
                                   TA_   G
GAM2529 UNC5D    3' TACTCTTCCCTATTAACAT   58732        ACTTA
                                TACTCTTCCC    TAATAT
                                ||||||||||    ||||||
                                ATGAGAAGGG    ATTGTA
                                     ATA__
GAM2529 ZER6     3' TATCCTTCCCACTGATCCATTT 58733    CT       TATAA
           T                     TA  CTTCCCACT    TATTTT
                                ||  |||||||||    ||||||
                                AT  GAAGGGTGA    GTAAAA
                                 AG       CTAG_
GAM2530 FABP5    3' TATTTATTAACCAAAGGGATGA 58736        ATATA__  C
           TCC                    TATTTATTAA      GA GATCC
                                ||||||||||      || |||||
                                ATAAATAATT      CT CTAGG
                                     GGTTTCC  A
GAM2530 KIAA0669 3' TATCTATTAAATGCAATCC   58737         ATAGA
                                TATTTATTAAAT    CGATCC
                                ||||||||||||    ||||||
                                ATAGATAATTTA    GTTAGG
                                     C____
GAM2530 LOC131308 3' TTTATTAAATACAAATTCC   58738           CGA
                                TTTATTAAATATAGA   TCC
                                ||||||||||||||   |||
                                AAATAATTTATGTTT   AGG
                                       A__
GAM2531 E2F3     3' AGCCCAGTAACTGGAA      58741       ATA  TA   C
                                AGCCCA   GT  AGC GGAA
                                ||||||   ||  ||| ||||
                                TCGGGT   CA  TTG CCTT
                                   ___  __   A
GAM2531 MGEA5    3' TCAGCTCAAAGTTAAAC     58742       C   T
                                TCAGC CAA AGTTAAGC
                                ||||| ||| ||||||||
                                AGTCG GTT TCAATTTG
                                   A  _
GAM2531 NTRK3    3' GCTTCAGTCAAGGCTGGAA   58743    CCAA       _ C
                                GC    TAGTTAAG C GGAA
                                ||    |||||||| | ||||
                                CG    GTCAGTTC G CCTT
                                 AA__       C A
GAM2531 PCDH11X  5' CAATAGTTAAGGGAAA      58744          CC
                                CAATAGTTAAG  GGAAA
                                ||||||||||  |||||
                                GTTATCAATTC  CCTTT
                                       __
GAM2531 PCDH11X  5' CAATAGTTAAGGGAAA      58744          CC
                                CAATAGTTAAG  GGAAA
                                ||||||||||  |||||
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                              GTTATCAATTC  CCTTT
                                          __
GAM2531  PCDH11X  5'  CAATAGTTAAGGGAAA     58744          CC
                              CAATAGTTAAG  GGAAA
                              ||||||||||  |||||
                              GTTATCAATTC  CCTTT
                                          __
GAM2531  PCDH11Y  5'  CAATAGTTAAGGGAAA     58744          CC
                              CAATAGTTAAG  GGAAA
                              ||||||||||  |||||
                              GTTATCAATTC  CCTTT
                                          __
GAM2531  PCDH11Y  5'  CAATAGTTAAGGGAAA     58744          CC
                              CAATAGTTAAG  GGAAA
                              ||||||||||  |||||
                              GTTATCAATTC  CCTTT
                                          __
GAM2531  TEM7     3'  TCAGCCCAGGGCATGCTGGGA  58745        ATA  TAA  C_
                              TCAGCCCA   GT   GC  GGA
                              ||||||||   ||   ||  |||
                              AGTCGGGT   CG   CG  CCT
                                   CC_  TA_  AC
GAM2531  WNT2     3'  ACCCAATAGTTACAGA      58746          AGC
                              GCCCAATAGTTA   CGGA
                              ||||||||||||   ||||
                              TGGGTTATCAAT   GTCT
                                          ___
GAM2531  FLJ12331 3'  ACCCAATAGTTAGGA       58747          AGCC
                              GCCCAATAGTTA    GGA
                              ||||||||||||    |||
                              TGGGTTATCAAT    CCT
                                          ____
GAM2531  FLJ14346 5'  TCAGCCCAGTCACCACACTGGA 58748         ATA TT A  C
                              TCAGCCCA   G  A GC GGA
                              ||||||||   |  | || |||
                              AGTCGGGT   T  T TG CCT
                                   CAG GG G  A
GAM2531  GPT2     3'  CAGCCTGGGAGGGGAGCCGGAA 58749       CAAT  TTA
                              CAGCC    AG   AGCCGGAA
                              |||||    ||   ||||||||
                              GTCGG    TC   TCGGCCTT
                                 ACCC  CCC
GAM2531  KIAA0276 3'  CAGTATTTCAGTTAAGCTGGGA 58750     CCCAA       C_
                              CAG     TAGTTAAGC  GGA
                              |||     |||||||||  |||
                              GTC     GTCAATTCG  CCT
                                ATAAA        AC
GAM2531  KIAA0564 3'  TCAGCCCAAGAGTGTGTGGGAA 58751         T   TAAGCC
                              TCAGCCCAA AGT     GGAA
                              ||||||||| |||     ||||
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                                AGTCGGGTT TCA     CCTT
                                     C   CACAC_
GAM2531  MAP      3'  TCATCCACAGCTTTAAGCCGGA 58752     GC   A   __
              A                    TCA  CCA TAGT  TAAGCCGGAA
                                   |||  ||| ||||  ||||||||||
                                   AGT  GGT GTCG  ATTCGGCCTT
                                    A_  _   AA
GAM2531  MDN1     3'  TCAGCCCAGGCAAAGCCGG   58753        ATA  T
                                   TCAGCCCA   GT AAGCCGG
                                   ||||||||   || |||||||
                                   AGTCGGGT   CG TTCGGCC
                                        C__  T
GAM2531  POLA2    5'  GCCCAAGCCAGGGGCCGG   58754      AT    A__
                                   GCCCA  AGTTA   GCCGG
                                   |||||  |||||   |||||
                                   CGGGT  TCGGT   CGGCC
                                      __    CCC
GAM2531  POLR3F   5'  CAGCCCGGTAGCAAGCCGG   58755      AA   T
                                   CAGCCC  TAGT AAGCCGG
                                   ||||||  |||| |||||||
                                   GTCGGG  ATCG TTCGGCC
                                      CC   _
GAM2531  PPAP2C   3'  TCAGCCCAGGGTTCCTGGA   58756        ATA   AAG  _
                                   TCAGCCCA   GTT   CC GGA
                                   ||||||||   |||   || |||
                                   AGTCGGGT   CAA   GG CCT
                                        CC_   ___  A
GAM2531  RAB40C   3'  TCAAGCCCAGGCAGCTGG   58757    _    ATA  TA   C
                                   TCA GCCCA   GT  AGC GG
                                   ||| |||||   ||  ||| ||
                                   AGT CGGGT   CG  TCG CC
                                     T    C__  __   A
GAM2531  LOC146856 3'  AGCCCAGTAACTGGAA      58741       ATA  TA   C
                                   AGCCCA   GT  AGC GGAA
                                   ||||||   ||  ||| ||||
                                   TCGGGT   CA  TTG CCTT
                                      ___  __   A
GAM2531  LOC148887 3'  TCAGCCCAACTGGAGCGGCTGG 58758          ___   TAA  C
              AAA                    TCAGCCCAAT   AGT   GC GGAAA
                                   ||||||||||   |||   || |||||
                                   AGTCGGGTTG   TCG   CG CCTTT
                                        ACC   C__  A
GAM2531  LOC150150 5'  CCAGCCCAGTGCCTGGAA    58759        ATA  TAA  _
                                   TCAGCCCA   GT   GCC GGAA
                                   ||||||||   ||   ||| ||||
                                   GGTCGGGT   CA   CGG CCTT
                                        ___  ___   A
GAM2531  LOC220739 3'  CCAGCCCAGTTTTAAGGGCCGG 58760         ATAG   __
              AA                     TCAGCCCA    TTAA  GCCGGAA
                                   ||||||||    ||||  |||||||
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                                GGTCGGGT   AATT  CGGCCTT
                                    CAA_   CC
GAM2531  LOC256267 3'  TCAGCCCAGGAGGCGGA     58761        AT  TTAA  C
                                TCAGCCCA  AG   GC GGA
                                ||||||||  ||   || |||
                                AGTCGGGT  TC   CG CCT
                                    CC  ____  _
GAM2531  LOC92466  3'  TCAGCCCAGGAGGCGGA     58761        AT  TTAA  C
                                TCAGCCCA  AG   GC GGA
                                ||||||||  ||   || |||
                                AGTCGGGT  TC   CG CCT
                                    CC  ____  _
GAM2532  AGC1      3'  GCTCAGCGTCCTGGGTGCG   58764     GA  A   C
                                GCT  CAG GTCC TGGGTGCG
                                |||  ||| |||| ||||||||
                                CGA  GTC CAGG ACCCACGC
                                  __   G   _
GAM2532  AGC1      3'  GCTCAGCGTCCTGGGTGCG   58764     GA  A   C
                                GCT  CAG GTCC TGGGTGCG
                                |||  ||| |||| ||||||||
                                CGA  GTC CAGG ACCCACGC
                                  __   G   _
GAM2532  GAS7      3'  GCTGCAAAGGATTCTGGGTGCG 58765     A    TCC_
                                GCTG CAGAG   CTGGGTGCG
                                |||| |||||   |||||||||
                                CGAC GTTTC   GACCCACGC
                                  _    CTAA
GAM2532  GAS7      3'  GCTGCAAAGGATTCTGGGTGCG 58765     A    TCC_
                                GCTG CAGAG   CTGGGTGCG
                                |||| |||||   |||||||||
                                CGAC GTTTC   GACCCACGC
                                  _    CTAA
GAM2532  MYBL2     3'  AAGCTGACGGAGCTCCCTG   58766        A  _
                                AAGCTGAC GAG TCCCTG
                                |||||||| ||| ||||||
                                TTCGACTG CTC AGGGAC
                                    C   G
GAM2532  NRGN      3'  AGCTGCATGCTGGGTGC     58767      A  GAGTCC
                                AGCTG CA     CTGGGTGC
                                ||||| ||     ||||||||
                                TCGAC GT     GACCCACG
                                  _ AC_____
GAM2532  SERPIND1  3'  AGTGACAGAGTCAGGTG     58768    C       CCT
                                AG TGACAGAGTC   GGGTG
                                || ||||||||||   |||||
                                TC ACTGTCTCAG   TCCAC
                                  _       ____
GAM2532  SGCG      3'  AGCTGCTCCCTGGGTG      58769      ACAGAG
                                AGCTG     TCCCTGGGTG
                                |||||     ||||||||||
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                                TCGAC     AGGGACCCAC
                                  G_____
GAM2532 WWOX     3' GCTGTGCAGGGTCCCAGGTGCG 58770      A_  A    T
                                GCTG  CAG GTCCC GGGTGCG
                                ||||  ||| ||||| |||||||
                                CGAC  GTC CAGGG TCCACGC
                                  AC  C    _
GAM2532 ZNF274   5' AAGTGGGCAGAGTCCCGGCG  58771     C  A_       TG
                                AAG TG  CAGAGTCCC  GGTG
                                ||| ||  |||||||||  ||||
                                TTC AC  GTCTCAGGG  CCGC
                                  _ CC       __
GAM2532 DKFZP434N178 5' GCTGGCAGGGCCCCAGGTG   58772      A   A T   TG
                                GCTG CAG G CCC  GGTG
                                |||| ||| | |||  ||||
                                CGAC GTC C GGG  CCAC
                                  C   C _   GT
GAM2532 DKFZP761D0211 3' TGCAGGTCCCTGGGTG     58773    A   A
                                TG CAG GTCCCTGGGTG
                                || ||| ||||||||||
                                AC GTC CAGGGACCCAC
                                 _   _
GAM2532 FLJ13158  3' AAGCTGGTAAGTCCCTG     58774       ACA
                                AAGCTG   GAGTCCCTG
                                ||||||   |||||||||
                                TTCGAC   TTCAGGGAC
                                   CA_
GAM2532 FLJ13710  3' AAGCTGGCAGAGTCCTG     58775       A      C
                                AAGCTG CAGAGTCC TG
                                |||||| |||||||| ||
                                TTCGAC GTCTCAGG AC
                                   C       _
GAM2532 FLJ22578  3' AGCCGGCGGAGGCAGGTGCG  58776      ACA   TCCC
                                AGCTG   GAG   TGGGTGCG
                                |||||   |||   ||||||||
                                TCGGC   CTC   GTCCACGC
                                  CGC   C___
GAM2532 HES6     3' AGCTGCAGGGTCCCTAAA    58777      A   A
                                AGCTG CAG GTCCCTGGG
                                ||||| ||| |||||||||
                                TCGAC GTC CAGGGATTT
                                  _  C
GAM2532 KCNH8    3' AGTTGGCAGAGCCTAGATG   58778    C  A    TC
                                AG TG CAGAG  CCTGGGTG
                                || || |||||  ||||||||
                                TC AC GTCTC  GGATCTAC
                                 A  C    __
GAM2532 KIAA0635 3' AAGTTGACAGAGGTAGAAT   58779     C       TCCCT
                                AAG TGACAGAG    GGGT
                                ||| ||||||||    ||||
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                                TTC ACTGTCTC    CTTA
                                  A       CAT__
GAM2532  KIAA0759  3'  GCTGCAGAGTCCAGTG     58780     A      CTG
                                GCTG CAGAGTCC   GGTG
                                |||| ||||||||   ||||
                                CGAC GTCTCAGG   TCAC
                                  _       ___
GAM2532  KIAA0774  5'  GCTGACAGATTCTCTTCCTTGT 58781        G ____  GG
              G                  GCTGACAGA TC   CCT  GTG
                                |||||||| ||   |||  |||
                                CGACTGTCT AG   GGA  CAC
                                     A  AGAA   A_
GAM2532  KIAA1508  3'  AAGCTGACAGAGTCCTATTATG 58782            CTGG
                                AAGCTGACAGAGTCC   GTG
                                ||||||||||||||   |||
                                TTCGACTGTCTCAGG   TAC
                                         ATAA
GAM2532  N4BP3    3'  GCAGACAGGAGGTGGGTGCG   58783    T    _  TCCC
                                GC GACAG AG   TGGGTGCG
                                || ||||| ||   ||||||||
                                CG CTGTC TC   ACCCACGC
                                 T    C  C___
GAM2532  NEIL1    5'  TGGCAGAGTCCTGGCTG     58784    A      C   G
                                TG CAGAGTCC TGG TG
                                || |||||||| ||| ||
                                AC GTCTCAGG ACC AC
                                 C       _   G
GAM2532  TOR2A    3'  AGCCTGGCCCCTGGGTG     58785     GACAGA
                                AGCT     GTCCCTGGGTG
                                ||||     ||||||||||
                                TCGG     CGGGGACCCAC
                                  AC____
GAM2532  WDF2     3'  AAGTTGGAAGAGTCCCCTTGCG 58786     C  AC       GG
                                AAG TG  AGAGTCCCT  GTG
                                ||| ||  |||||||||  |||
                                TTC AC  TCTCAGGGG  CGC
                                  A  CT        AA
GAM2532  LOC115817 5'  GCTGACAACTGGGTGC      58787        AGTCC
                                GCTGACAG    CTGGGTGC
                                ||||||||    ||||||||
                                CGACTGTT    GACCCACG
                                          _____
GAM2532  LOC133688 3'  AAGTTGTCAGAGTCCTG     58788     C  A      C
                                AAG TG CAGAGTCC TG
                                ||| || |||||||| ||
                                TTC AC GTCTCAGG AC
                                  A  A       _
GAM2532  LOC145501 3'  GCTGGTAGATGTCCAGGCG   58789     AC  _   CT
                                GCTG  AGA GTCC  GGGTG
                                ||||  ||| ||||  |||||
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                                CGAC  TCT CAGG  TCCGC
                                  CA  A   __
GAM2532  LOC146853 3'  AGCGGACAGAGTCAGGTG    58790    T       CCT
                                AGC GACAGAGTC  GGGTG
                                ||| |||||||||  |||||
                                TCG CTGTCTCAG  TCCAC
                                  C       ___
GAM2532  LOC154092 3'  AAGCTGGCAGGTTCCCCG    58791       A  AG
                                AAGCTG CAG  TCCCTG
                                |||||| |||  ||||||
                                TTCGAC GTC  AGGGGC
                                   C  CA
GAM2532  LOC157623 5'  AAGTGAACTTGTCCTGGGTG  58792    C  CAGA   C
                                AAG TGA   GTCC TGGGTG
                                ||| |||   |||| ||||||
                                TTC ACT   CAGG ACCCAC
                                  _  TGAA  _
GAM2532  LOC168391 5'  AAGCTGACAGAGGCTCCTG   58793         _ TC
                                AAGCTGACAGA G  CCTG
                                |||||||||| |  ||||
                                TTCGACTGTCT C  GGAC
                                      C GA
GAM2532  LOC206360 5'  GCTGCATATCCTGGGTG    58794     A  GA   C
                                GCTG CA  GTCC TGGGTG
                                |||| ||  |||| ||||||
                                CGAC GT  TAGG ACCCAC
                                  _ A_  _
GAM2532  LOC221477 3'  GCTGGCAGAGTCCTAGCCAAGT 58795     A      ___ TG
            G                    GCTG CAGAGTCC  C  GGTG
                                |||| ||||||||  |  ||||
                                CGAC GTCTCAGG  G  TCAC
                                  C       ATC GT
GAM2532  LOC253216 3'  AGCGGCAGCACTGGGTGC    58796    T A  AGTCC
                                AGC G CAG    CTGGGTGC
                                ||| | |||    ||||||||
                                TCG C GTC    GACCCACG
                                  _ C  GT___
GAM2532  LOC253815 5'  AAGGTGATGGGGTCCCGGGCG  58797    C  CAGA   T
                                AAG TGA   GTCCC GGGTG
                                ||| |||   ||||| |||||
                                TTC ACT   CAGGG CCCGC
                                  C  ACCC   _
GAM2532  LOC90139  3'  AGCTGACAGAGTCCTGGATG  58798          C
                                AGCTGACAGAGTCC TGGGTG
                                |||||||||||||| ||||||
                                TCGACTGTCTCAGG ACCTAC
                                                _
GAM2533  GFI1     3'  TAACATGGTGCCTGGTAC    58801        AA   A
                                TAACATGGT  CTGG AT
                                |||||||||  |||| ||
```

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                                ATTGTACCA  GACC TG
                                     CG    A
GAM2533  SHMT2    3'  TAACATGGTGGGTTGGAGTTAG 58802        AAC_   A_  A
              GAT                   TAACATGGT   TGGA  TAG GAT
                                ||||||||||   ||||  ||| |||
                                ATTGTACCA    ACCT  ATC CTA
                                     CCCA    CA  _
GAM2533  SLC29A1  3'  TAACGTGGCAACTGTACAG   58803     A       GA
                                TAAC TGGTAACTG  ATAG
                                |||| |||||||||  ||||
                                ATTG ACCGTTGAC  TGTC
                                  C       A_
GAM2533  SP110    3'  CAACATGGTGACTGAGAG    58804         A   GAAT
                                TAACATGGT ACTG   AGAG
                                |||||||||| ||||   ||||
                                GTTGTACCA TGAC   TCTC
                                     C   _____
GAM2533  KIAA1987 3'  CATGGTAAGGTGTGGAGAT   58805        CT  AATA
                                CATGGTAA  GG   GAGAT
                                ||||||||  ||   |||||
                                GTACCATT  CC   CTCTA
                                     __  ACAC
GAM2533  PRO0478  3'  TAACATGATAAACATGGA    58806          _ _
                                TAACATGGTAA C TGGA
                                |||||||||||| | ||||
                                ATTGTACTATT G ACCT
                                       T T
GAM2533  SLC25A18 5'  TAACTGGCTAGAATAG     58807     A   TAA
                                TAAC TGG   CTGGAATAG
                                |||| |||   |||||||||
                                ATTG ACC   GATCTTATC
                                  _   ____
GAM2533  LOC143680 3'  ATGGTAACTATAGAGA     58808         GGA
                                ATGGTAACT   ATAGAGA
                                |||||||||   |||||||
                                TACCATTGA   TATCTCT
                                     ____
GAM2533  LOC151760 5'  AACATGTCTTGGGATAGAGAT  58809       GTAAC   A
                                AACATG     TGG ATAGAGAT
                                ||||||     ||| ||||||||
                                TTGTAC     ACC TATCTCTA
                                   AGA__   C
GAM2533  LOC158777 5'  ATAATTTGGGATAGAGAT    58810      C_   A
                                GTAA  TGG ATAGAGAT
                                ||||  ||| ||||||||
                                TATT  ACC TATCTCTA
                                  AA   C
GAM2533  LOC255328 3'  ATGACTACATTGGAATAGAGAT 58811      TA  __
                                ATGG  AC  TGGAATAGAGAT
                                ||||  ||  ||||||||||||
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                                TACT  TG  ACCTTATCTCTA
                                  GA  TA
GAM2534  BSN      3'  TAGAGCCTGAGACTAGGCCTGC 58814          TGTTC_
                T                  TAGAGCCTGGG     CCTGCT
                                   ||||||||||      ||||||
                                   ATCTCGGACTC     GGACGA
                                         TGATCC
GAM2534  DIAPH2   3'  TAGAACCTGTTTTCCCTGCTAG 58815         GGTG
                                   TAGAGCCTG    TTCCCTGCTAG
                                   |||||||||    ||||||||||
                                   ATCTTGGAC    AAGGGACGATC
                                         AA__
GAM2534  POLS     3'  TAAAGCTTGTCCTTGCT     58816       C  GGTGT   C
                                   TAGAGC TG    TCC TGCT
                                   |||||| ||    ||| ||||
                                   ATTTCG AC    AGG ACGA
                                      A _____   A
GAM2534  DKFZP434J193 3'  TAGGCCTGGGTACAAGCTGCT  58817     A       TTCC
                                   TAG GCCTGGGTG    CTGCT
                                   ||| |||||||||    |||||
                                   ATC CGGACCCAT    GACGA
                                     _       GTTC
GAM2534  FLJ20294  3'  GAGCCTGGCCCGATCCCTG    58818        G_  T
                                   GAGCCTGG  TG TCCCTG
                                   ||||||||  || ||||||
                                   CTCGGACC  GC AGGGAC
                                         GG  T
GAM2534  HS6ST    3'  CTGGGGCAGCCTGCTAG     58819      T  TC
                                   CTGGG GT  CCTGCTAG
                                   ||||| ||  ||||||||
                                   GACCC CG  GGACGATC
                                     _ TC
GAM2534  KIAA1550  3'  TACAGCCTTACCTTCCTGCTAG 58820    G    GGG G   C
                                   TA AGCCT   T TTCC TGCTAG
                                   || |||||   | |||| ||||||
                                   AT TCGGA   G AAGG ACGATC
                                    G    AT_ G   _
GAM2534  KIAA1822  5'  TAGAGCCTGCGGTTGTGCT    58821         _  GTTCCC
                                   TAGAGCCTG GGT     TGCT
                                   |||||||| |||     ||||
                                   ATCTCGGAC CCA     ACGA
                                         G   AC____
GAM2534  SLC38A1   5'  AAGCTTGACACCCCTGTTAG   58822     C   GTGT     C
                                   GAGC TGG    TCCCTG TAG
                                   |||| |||    |||||| |||
                                   TTCG ACT    GGGGAC ATC
                                     A  GT__     A
GAM2534  TReP-132  5'  GAGCCAGGTGTTCCTG      58823       T       C
                                   GAGCC GGGTGTTCC TG
                                   ||||| |||||||| ||
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                                CTCGG TCCACAAGG AC
                                  _     _
GAM2534  TReP-132  5'  GAGCCAGGTGTTCCTG     58823      T      C
                                GAGCC GGGTGTTCC TG
                                ||||| ||||||||| ||
                                CTCGG TCCACAAGG AC
                                  _     _
GAM2534  TReP-132  5'  GAGCCAGGTGTTCCTG     58823      T      C
                                GAGCC GGGTGTTCC TG
                                ||||| ||||||||| ||
                                CTCGG TCCACAAGG AC
                                  _     _
GAM2534  LOC115051 3'  CTGGGGCAGCCTGCTAG    58819      T  TC
                                CTGGG GT  CCTGCTAG
                                ||||| ||  ||||||||
                                GACCC CG  GGACGATC
                                  _ TC
GAM2534  LOC115708 3'  GCCAGGCCCCTGCTA      58824     T   GTT
                                GCC GGGT   CCCTGCTA
                                ||| ||||   ||||||||
                                CGG TCCG   GGGACGAT
                                  _   ___
GAM2534  LOC123435 3'  GAGCCCGGGTGTTTCTG    58825          CC
                                GAGCCTGGGTGTT  CTG
                                ||||||||||||  |||
                                CTCGGGCCCACAA  GAC
                                      A_
GAM2534  LOC148887 3'  TAGACTTGGGCCTAGATCTTGC 58826     _____      G TCCC
           T                    TAGA    GCCTGGGT T   TGCT
                                ||||    |||||||| |   ||||
                                ATCT    CGGATCTA A   ACGA
                                  GAACC      G ____
GAM2534  LOC222031 3'  GATCTGGGTGTTCTTGCT   58827    GC       CC
                                GA  CTGGGTGTTC  TGCT
                                ||  ||||||||||  ||||
                                CT  GACCCACAAG  ACGA
                                 A_        A_
GAM2534  LOC92017  5'  TAGGCCTGGGTGTTTCTG   58828    A        CC
                                TAG GCCTGGGTGTT  CTG
                                ||| ||||||||||  |||
                                ATC CGGACCCACAA  GAC
                                  _        A_
GAM2535  GPR62     3'  GCCCTTAGGGCCCTCTTC   58831    TG   AA
                                GCT  CTTA  GCCCTCTTC
                                |||  ||||  |||||||||
                                CGG  GAAT  CGGGAGAAG
                                  __   CC
GAM2535  NEBL      3'  ACTTGCTTGCTTGGTTTTCTT  58832          AAAGCCC
                                GCTTGCTTGCTT      TCTT
                                ||||||||||||      ||||
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                                TGAACGAACGAA      AGAA
                                      CCAAA__
GAM2535  PPP2R5E   3'  GCTGTTTGCTCAACTCTT    58833     T C       AGCC
                                GCT G TTGCTTAA    CTCTT
                                ||| | ||||||||    |||||
                                CGA C AACGAGTT    GAGAA
                                  _ A       _____
GAM2535  DCNP1     3'  GCTTGCTTGCCTCCGCACCTCT 58834           AAA  _
               T                   GCTTGCTTGCTT   GC CCTCTT
                                   ||||||||||||   || ||||||
                                   CGAACGAACGGA   CG GGAGAA
                                         GG_  T
GAM2535  GGTLA4    3'  GCCTGTCCCCCAAAGTCCTCTT 58835       C  G       C
               C                    GCTTG TT CTTAAAG CCTCTTC
                                    ||||| || ||||||| |||||||
                                    CGGAC AG GGGTTTC GGAGAAG
                                      _ G      A
GAM2535  KIAA0553  3'  TTGCCTGCCACTTTCTT     58836         TAAA  CC
                                    TTGCTTGCT    GC  TCTT
                                    |||||||||    ||  ||||
                                    AACGGACGG    TG  AGAA
                                         _____  AA
GAM2535  MGC12837  5'  GCTTGTTTCCTCCCCTCTT    58837       C  G   AAAG
                                    GCTTG TT CTT    CCCTCTT
                                    ||||| || |||    |||||||
                                    CGAAC AA GAG    GGGAGAA
                                      A  G  _____
GAM2535  MGC2628   3'  GCGTGCACAGGGGGCCCTCTTC 58838    T   TT  TTAAA
                                    GC TGC  GC     GCCCTCTTC
                                    || |||  ||     |||||||||
                                    CG ACG  TG     CGGGAGAAG
                                     C   __  TCCCC
GAM2535  MIG       3'  GCTTATTGAGAAAGCCCTTTTC 58839       C   CTT       C
                                    GCTTG TTG   AAAGCCCT TTC
                                    ||||| |||   |||||||| |||
                                    CGAAT AAC   TTTCGGGA AAG
                                      _   TC_       A
GAM2535  LOC151318 3'  GCTTGCTGTCTCCATCCTTTTC 58840        TG   AAAGC   C
                                    GCTTGCT  CTT     CCT TTC
                                    |||||||  |||     ||| |||
                                    CGAACGA  GAG     GGA AAG
                                        CA   GTA__   A
GAM2535  LOC160414 3'  GCCTGCTTGAAGCCCTCTTC   58841         A
                                    GCTTGCTT AAGCCCTCTTC
                                    |||||||| ||||||||||
                                    CGGACGAA TTCGGGAGAAG
                                        C
GAM2535  LOC54505  5'  GCTTACTCTTAGGGTCCTCTTC 58842        TG    AAGC
                                    GCTTGCT  CTTA    CCTCTTC
                                    |||||||  ||||    |||||||
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                                CGAATGA  GAAT   GGAGAAG
                                   __   CCCA
GAM2536  SLC10A2   3'  GGGGCCCTTCTGACTTTTGGG  58845    AC      _   _
                                GG  CCTTTCTG CTTT GGG
                                ||  |||||||| |||| |||
                                CC  GGGAAGAC GAAA CCC
                                 CC       T    A
GAM2536  C20orf28  3'  TGTTGGACACTGCTTTGG    58846     A   CCTTT
                                TGTT GGAC    CTGCTTTGG
                                |||| ||||    |||||||||
                                ACAA CCTG    GACGAAACC
                                  _   T_____
GAM2536  KIAA0090  3'  TGTAGGATCCTTTCTGC     58847     T   C
                                TGT AGGA CCTTTCTGC
                                ||| |||| |||||||||
                                ACA TCCT GGAAAGACG
                                  _   A
GAM2536  KIAA0831  3'  TGTTAGGACTCTTTCATAGG   58848        C    TGCTTT
                                TGTTAGGAC CTTTC     GG
                                ||||||||| |||||     ||
                                ACAATCCTG GAAAG     CC
                                     A    TAT___
GAM2536  LOC129138 3'  GTTGGAATTTTTTGCTTTGGG  58849    A   CCC   C
                                GTT GGA   TTT TGCTTTGGG
                                ||| |||   ||| |||||||||
                                CAA CCT   AAA ACGAAACCC
                                  _   TA_   A
GAM2536  LOC157657 3'  TATTAGGATTTTTGTGATTTTG 58850       CCC   C  C_
            GG                    TGTTAGGA   TTT TG  TTTGGG
                                ||||||||   ||| ||  ||||||
                                ATAATCCT   AAA AC  AAACCC
                                     AA_   C  TA
GAM2536  LOC96597  5'  TGTGGGGACCAAGCTTTGG   58851    TA    CTTTCT
                                TGT  GGACC     GCTTTGG
                                |||  |||||     |||||||
                                ACA  CCTGG     CGAAACC
                                  CC    TT_____
GAM2537  FOXE1     3'  CAGTGGACAAATGAACGAATGT 58854       C  TACG   _
                                CAGTGGAC AA    GGAT AATGT
                                |||||||| ||    |||| |||||
                                GTCACCTG TT    CTTG TTACA
                                     _  TA__    C
GAM2537  MLLT2     3'  CAGTGGAACAGAATATAATGT  58855       CCAAT      __
                                CAGTGGA    ACGGGATA  ATGT
                                |||||||    ||||||||  ||||
                                GTCACCT    TGTCTTAT  TACA
                                     ______       AT
GAM2537  SCD       3'  CAGTGGACTGAGTGTTTGGTAG 58856       CAATACG__  A  A
            TGT                    CAGTGGAC       GG TA TGT
                                ||||||||       || || |||
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                                GTCACCTG        CC AT ACA
                                    ACTCACAAA  _  C
GAM2537  MEGF10   3'  CAGTGATCAGAATAAT      58857       ACCAATA
                                CAGTGG      CGGGATAAT
                                ||||||      |||||||||
                                GTCACT      GTCTTATTA
                                   A_______
GAM2537  SEMA4B   3'  GTGGCAGCGGGATAATGT     58858      ACCAATA
                                GTGG      CGGGATAATGT
                                ||||      ||||||||||
                                CACC      GCCCTATTACA
                                  GTC____
GAM2538  GAD1     3'  TACTTCATATATAAATAAGAT  58861          CTATTT
                                TATTTCATATA     ATAAGAT
                                ||||||||||      |||||||
                                ATGAAGTATAT     TATTCTA
                                      ATT___
GAM2538  NUDT12   3'  ATTTCATATATTATCCTTAAG  58862          C    TA
                                ATTTCATATA TATT  TAAG
                                |||||||||| ||||  ||||
                                TAAAGTATAT ATAG  ATTC
                                      A   GA
GAM2538  ZNF334   3'  TTCATTACATTTATAAGAT    58863       A   T
                                TTCAT TAC ATTTATAAGAT
                                ||||| ||| ||||||||||
                                AAGTA ATG TAAATATTCTA
                                  _  _
GAM2538  LOC146723 3'  TATTTTATATACTATTTAC    58864       C
                                TATTT ATATACTATTTAT
                                ||||| ||||||||||||
                                ATAAA TATATGATAAATG
                                   A
GAM2538  LOC201283 3'  ACACACTATTTGTAAGAT     58865           A
                                ATATACTATTT TAAGAT
                                |||||||||| ||||||
                                TGTGTGATAAA ATTCTA
                                      C
GAM2539  ABL1     3'  GCACATCACGTTAACAA      58868       G     G
                                GCAC ATCGTG TTAACAA
                                |||| |||||| |||||||
                                CGTG TAGTGC AATTGTT
                                  _     _
GAM2539  ABL1     3'  GCACATCACGTTAACAA      58868       G     G
                                GCAC ATCGTG TTAACAA
                                |||| |||||| |||||||
                                CGTG TAGTGC AATTGTT
                                  _     _
GAM2539  DDX6     3'  TAGCATGAAAGTTAACA      58869       C  TCGT
                                TAGCA GA    GGTTAACA
                                ||||| ||    ||||||||
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                                ATCGT CT   TCAATTGT
                                  A  T___
GAM2539  GEM     3'  TAATAGTCACGATTCTGAT   58870      _    CG
                                TAATAG CACGAT  TGGT
                                |||||| ||||||  ||||
                                ATTATC GTGCTA  ACTA
                                   A     AG
GAM2539  GLS     3'  TAATAGCACAGTCAAC     58871        GATCGT
                                TAATAGCAC     GGTTAAC
                                |||||||||     |||||||
                                ATTATCGTG     TCAGTTG
                                              _______
GAM2539  WISP1   3'  TAATAGCCTGATATTCATTAAC 58872       AC   C  G_
            AA                    TAATAGC  GAT GT  GTTAACAA
                                |||||||  ||| ||  ||||||||
                                ATTATCG  CTA TA  TAATTGTT
                                    GA   _  AG
GAM2539  CNNM2   3'  TAGCAGCATCTTGGGTTAACAA 58873     CG   GT_
                                TAGCA  ATC   GGTTAACAA
                                |||||  |||   |||||||||
                                ATCGT  TAG   CCAATTGTT
                                  CG   AAC
GAM2539  HBP1    3'  TAATAGCACCATTACAGT    58874       G  CG
                                TAATAGCAC AT  TGGT
                                |||||||||  ||  ||||
                                ATTATCGTG TA  GTCA
                                     G  AT
GAM2539  HSNOV1  3'  TAATAGCATTGTCTTTTAACA  58875       CGA  GTGG
                                TAATAGCA   TC    TTAACA
                                ||||||||   ||    ||||||
                                ATTATCGT   AG    AATTGT
                                    AAC  AA__
GAM2539  KIAA0210 3'  TAATAGCACTGTAACTAA    58876       GATC  GG
                                TAATAGCAC    GT  TTAA
                                |||||||||    ||  ||||
                                ATTATCGTG    CA  GATT
                                     A___    TT
GAM2539  KIAA1243 3'  TGACGGTGTTCTGGTTAACA   58877   C   A___  G
                                G ACG    TC TGGTTAACA
                                | |||    || |||||||||
                                A TGC    AG ACCAATTGT
                                 C   CACA  _
GAM2539  MGC13053 3'  CAGCAGGATGGTTAAC      58878      C  TCG
                                TAGCA GA   TGGTTAAC
                                ||||| ||   ||||||||
                                GTCGT CT   ACCAATTG
                                  C  ___
GAM2539  RBBP4   3'  TAATAGCATTATCGGTGG    58879       CG   _
                                TAATAGCA  ATCG TGG
                                ||||||||  |||| |||
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                                ATTATCGT  TAGC ACC
                                     AA    C
GAM2539  LOC158267 3'  TAATAGCAAGATTGTAAT    58880        C   C
                                TAATAGCA GAT GTGGT
                                |||||||| ||| |||||
                                ATTATCGT CTA CATTA
                                     T   A
GAM2540  BTEB5     3'  TGGTGGATGGGTGAGACA    58883            T
                                TGGTGGATGGGTGA GACA
                                |||||||||||||| ||||
                                ACCACCTACCCACT CTGT

                                          _
GAM2540  CYP2A7    5'  TGGTGATGGGTGGGGT      58884      G      ATGACA
                                TGGTG ATGGGTG     GGGT
                                ||||| |||||||      ||||
                                ACCAC TACCCAC     CCCA

                                  _     _______
GAM2540  CYP2A7    5'  TGGTGATGGGTGGGGT      58884      G      ATGACA
                                TGGTG ATGGGTG     GGGT
                                ||||| |||||||      ||||
                                ACCAC TACCCAC     CCCA

                                  _     _______
GAM2540  DLAT      5'  GGTGGAAAGTGGTAGGGT     58885       T     ATGAC
                                GGTGGA GGGTG    AGGGT
                                |||||| |||||    |||||
                                CCACCT TTCAC    TCCCA
                                   _    CA___
GAM2540  FLJ20511  3'  TGGTGGATGGTGAAGG      58886          G   TGACA
                                TGGTGGATGG TGA    GGG
                                |||||||||| |||    |||
                                ACCACCTACC ACT    TCC

                                     _  _____
GAM2540  KIAA0053  3'  TGGTGGGGTGGCAGAATGGGGT 58887       ATG  __   ACA
              T                  TGGTGG   GGT  GATG   GGGTT
                                 ||||||   |||  ||||   |||||
                                 ACCACC   CCG  TTAC   CCCAA
                                    CCA   TC   ___
GAM2540  RFX4      3'  TGGGGGATGGGTGTTGGGT    58888     T       ATGACA
                                TGG GGATGGGTG     GGGT
                                ||| |||||||||     ||||
                                ACC CCTACCCAC     CCCA
                                  C        AA____
GAM2540  ZF5128    3'  TGGGGGTGAGACAGGG      58889     AT     T
                                TGG  GGGTGA GACAGGG
                                |||  |||||| |||||||
                                ACC  CCCACT CTGTCCC

                                  __     _
GAM2540  LOC123242 5'  GGTGGGTCATTGACAGGGTT   58890    A    G  _
                                GG TGGGT AT GACAGGGTT
                                || ||||| || |||||||||
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                                CC ACCCA TA CTGTCCCAA
                                 _    G  A
GAM2540  LOC199714 5'  TGGTGGATGGGTACTGGT    58891          ATGACAG
                                TGGTGGATGGGTG      GGT
                                ||||||||||||      |||
                                ACCACCTACCCAT      CCA
                                      GA_____
GAM2540  LOC200982 3'  TGGTGGGGGGGTGACATTTGGGT 58892       AT       ACA
           T                     TGGTGG  GGGTGATG   GGGTT
                                ||||||  ||||||||   |||||
                                ACCACC  CCCACTGT   CCCAA
                                   C_       AAA
GAM2540  LOC253001 5'  GGTGGGTCATTGACAGGGTT   58890    A    G  _
                                GG TGGGT AT GACAGGGTT
                                || ||||| || |||||||||
                                CC ACCCA TA CTGTCCCAA
                                 _    G  A
GAM2541  RAP1A    3'  TAAAGTATAATGGTTCAACT   58895          A   GT
                                TAGAGTATAATG TTTA  T
                                |||||||||||| ||||  |
                                ATTTCATATTAC AAGT  A
                                      C    TG
GAM2541  C21orf91  3'  AGAGTATAATGATCTGCT    58896           A
                                AGAGTATAATGATTT GTT
                                |||||||||||||| |||
                                TCTCATATTACTAGA CGA
                                                _
GAM2541  FBXO8    3'  TAGAGTATAATGTCAGTT    58897          AT
                                TAGAGTATAATG  TTAGTT
                                ||||||||||||  ||||||
                                ATCTCATATTAC  AGTCAA
                                                __
GAM2541  FLJ14721  3'  TAGAATATAATGGTCAATT    58898          AT
                                TAGAGTATAATG  TTAGTT
                                ||||||||||||  ||||||
                                ATCTTATATTAC  AGTTAA
                                      C_
GAM2541  LOC134553 3'  TAGGTATAATGGTTTCAGTT   58899    A      A_
                                TAG GTATAATG  TTTAGTT
                                ||| ||||||||  |||||||
                                ATC CATATTAC  AAGTCAA
                                  _       CA
GAM2542  CHES1     5'  TCGATCGCCTGCCCCCCCGCTG 58902    C_       G
           CT                     TCG  CGCCTGCCTT CTCGCTGCT
                                ||| ||||||||||| |||||||||
                                AGC  GCGGACGGGG GGGCGACGA
                                  TA        _
GAM2542  COG4      3'  TCGCTGCCTGCCGTGGCT    58903     C      T  CTC
                                TCGC GCCTGCC TG   GCT
                                |||| ||||||| ||   |||
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                                AGCG CGGACGG AC   CGA
                                  A      C ___
GAM2542  DYRK2    5'  TCGCCGCCGCCGGTCCTGCTGC 58904        T   TTG TC
                T                  TCGCCGCC GCC   C  GCTGCT
                                   |||||||| |||   |  ||||||
                                   AGCGGCGG CGG   G  CGACGA
                                       _  CCA GA
GAM2542  DYRK2    5'  TCGCCGCCGCCGGTCCTGCTGC 58904        T   TTG TC
                T                  TCGCCGCC GCC   C  GCTGCT
                                   |||||||| |||   |  ||||||
                                   AGCGGCGG CGG   G  CGACGA
                                       _  CCA GA
GAM2542  DYRK2    5'  TCGTCGCCGCCTCGCGTCTGCT 58905     C   T      TCG
                                   TCG CGCC GCCTTGC   CTGCT
                                   ||| |||| |||||||   |||||
                                   AGC GCGG CGGAGCG   GACGA
                                     A   _      CA_
GAM2542  DYRK2    5'  TCGTCGCCGCCTCGCGTCTGCT 58905     C   T      TCG
                                   TCG CGCC GCCTTGC   CTGCT
                                   ||| |||| |||||||   |||||
                                   AGC GCGG CGGAGCG   GACGA
                                     A   _      CA_
GAM2542  FAT2     3'  TCCCGCCTGCCTTGCTC     58906    G
                                   TC CCGCCTGCCTTGCTC
                                   || ||||||||||||||
                                   AG GGCGGACGGAACGAG
                                    _
GAM2542  GSPT1    5'  TCGCTGCTGCTGCTGCCGCTGC 58907      C __    CT   T
                T                  TCGC GC  CTGC  TGC CGCTGCT
                                   |||| ||  ||||  ||| |||||||
                                   AGCG CG  GACG  ACG GCGACGA
                                     A  AC   __  _
GAM2542  PTPN6    3'  CCTTGTCTGCTGACCGCTGCT  58908    GC__    CT  CT
                                   CC   CTGC  TG  CGCTGCT
                                   ||   ||||  ||  |||||||
                                   GG   GACG  AC  GCGACGA
                                    AACA   __  TG
GAM2542  RU2      5'  CCGCCGCCTCAGCTCGCTGCT  58909       T    _
                                   CCGCC GCCTT GCTCGCTGCT
                                   ||||| ||||| ||||||||||
                                   GGCGG CGGAG CGAGCGACGA
                                      _    T
GAM2542  TRIM34   5'  TCACTGCCTCCTTGTTGCT   58910      C   G    CTC
                                   TCGC GCCT CCTTG   GCT
                                   |||| |||| |||||   |||
                                   AGTG CGGA GGAAC   CGA
                                     A   _    AA_
GAM2542  TRIM9    5'  TCGCTCGCTTGCTTGCTTGCT  58911      _  C  C    C
                                   TCGC CGC TGC TTGCT GCT
                                   |||| ||| ||| ||||| |||
```

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                                AGCG GCG ACG AACGA CGA
                                  A  A  _   A
GAM2542 VEGF    5' GCCCCTGTCGCTTTCGCTGCT 58912    G   CC  __
                                GCC CCTG  TTGC  TCGCTGCT
                                ||| ||||  ||||  ||||||||
                                CGG GGAC  AGCG  AGCGACGA
                                  _   __   AA
GAM2542 CES2    5' TCGCTGCCGGCGGACACGCTGC 58913     C   T  CTT  T
             T                   TCGC GCC GC   GC CGCTGCT
                                ||||| ||| ||   || |||||||
                                AGCG CGG CG   TG GCGACGA
                                  A   C  CC_  T
GAM2542 ctm-1   3' GCCTCCTGCCTCTAATCTGCT 58914    G      GCTCG
                                GCC CCTGCCTT    CTGCT
                                ||| ||||||||    |||||
                                CGG GGACGGAG    GACGA
                                  A       ATTA_
GAM2542 HSAJ1454 5' CGCTGCTTTCTGGAGCTGCT  58915    C   C  G  C__
                                CGC TGC TT CT   GCTGCT
                                ||| ||| || ||   ||||||
                                GCG ACG AA GA   CGACGA
                                  _   A  _  CCT
GAM2542 LAP1B   5' CCGCCGCCTGCGTCGTCGCTGC 58916          C   C
             T                   TCGCCGCCTGC TTG TCGCTGCT
                                |||||||||||| ||| ||||||||
                                GGCGGCGGACG AGC AGCGACGA
                                       C  _
GAM2542 PRO1635  3' TCGCGCCTGCCTCCACACTG  58917     C       GCT
                                TCGC GCCTGCCTT   CGCTG
                                |||| |||||||||   |||||
                                AGCG CGGACGGAG   GTGAC
                                  _       GT_
GAM2542 SIAT8A   5' TCGCCGCCTCCCGCGCTGC   58918        G  TTGCT
                                TCGCCGCCT CC    CGCTGC
                                ||||||||| ||    ||||||
                                AGCGGCGGA GG    GCGACG
                                     G  C____
GAM2542 TIP120A  5' TCCCGCCTGCTGGCGCTGC   58919    G      CT  CT
                                TC CCGCCTGC  TG  CGCTGC
                                || ||||||||  ||  ||||||
                                AG GGCGGACG  AC  GCGACG
                                  _      __  C_
GAM2542 LOC121536 5' TCGCTGCTGCTCCCGCCGCTGC 58920     C  C  _   T
             T                   TCGC GC TGC CTTGC CGCTGCT
                                |||| || ||| ||||| |||||||
                                AGCG CG ACG GGGCG GCGACGA
                                  A  _   A    _
GAM2542 LOC133993 5' TCGCCTCTCCCTCTCGCTGCT  58921      GC  G   G
                                TCGCC  CT CCTT CTCGCTGCT
                                |||||  || |||| |||||||||
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                                AGCGG  GA GGGA GAGCGACGA
                                  A_ _   _
GAM2542  LOC143146 5'  CCGCTGCCTGCTTCTGCAATTG 58922     C     C_   TCGC
             CT                    TCGC GCCTGC  TTGC    TGCT
                                   |||| ||||||  ||||    ||||
                                   GGCG CGGACG  GACG    ACGA
                                     A     AA    TTA_
GAM2542  LOC200093 3'  GCTCCTGCTCCTTCTGCTGCT  58923    CG    _   G  C
                                   GC  CCTGC CTT CT GCTGCT
                                   ||  ||||| ||| || ||||||
                                   CG  GGACG GGA GA CGACGA
                                    A_    A  A  _
GAM2542  LOC200312 3'  GCTGTCCTGTCTATCCTGCT   58924    CG_   C  TGC  G
                                   GC   CCTG CT   TC CTGCT
                                   ||   |||| ||   || |||||
                                   CG   GGAC GA   AG GACGA
                                    ACA    A  T__  _
GAM2542  LOC254221 5'  GCTGCTTTCCCTGGGGCTGCT  58925    C  CTG    CTC
                                   GC GC   CCTTG   GCTGCT
                                   || ||   |||||   ||||||
                                   CG CG   GGGAC   CGACGA
                                    A  AAA    CC_
GAM2542  LOC255452 3'  TCGCCGCCTGCTTTGGGCT   58926          C   CTC
                                   TCGCCGCCTGC TTG   GCT
                                   ||||||||||| |||   |||
                                   AGCGGCGGACG AAC   CGA
                                         A   C__
GAM2543  KCNH1     3'  AGGTATCTGTCTCTGACTTTT  58929        A_  G_
                                   AGGTATCT  CT  GACTTTT
                                   ||||||||  ||  |||||||
                                   TCCATAGA  GA  CTGAAAA
                                       CA  GA
GAM2543  NFKBIA    3'  TGACAGGTAGTAACTTTT    58930         TCTACTG
                                   TGACAGGTA      GACTTTT
                                   |||||||||      |||||||
                                   ACTGTCCAT      TTGAAAA
                                       CA_____
GAM2543  TOP1      3'  TAACAGGTGCGCTGGGTTTTT  58931        ATCTA   AC
                                   TGACAGGT    CTGG  TTTT
                                   ||||||||    ||||  ||||
                                   ATTGTCCA    GACC  AAAA
                                       CGC__    CA
GAM2543  WISP3     3'  TGACAGGATTGACTAACTTTTC 58932        T  CT   G
                                   TGACAGG AT  ACTG ACTTTTC
                                   ||||||| ||  |||| |||||||
                                   ACTGTCC TA  TGAT TGAAAAG
                                       _ AC   _
GAM2543  WISP3     3'  TGACAGGATTGACTAACTTTTC 58932        T  CT   G
                                   TGACAGG AT  ACTG ACTTTTC
                                   ||||||| ||  |||| |||||||
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                                ACTGTCC TA  TGAT TGAAAAG
                                    _ AC   _
GAM2543  C6orf5    3'  TGACAAGTATTTGTCCTTTC   58933        CTAC  GA
                                TGACAGGTAT   TG  CTTTT
                                ||||||||||   ||  |||||
                                ACTGTTCATA   AC  GAAAG
                                     A___  AG
GAM2543  FLJ20081  3'  ACAGGTATTTTGAGACTTTT   58934       CTACT
                                ACAGGTAT    GGACTTTT
                                ||||||||    ||||||||
                                TGTCCATA    TCTGAAAA
                                    AAAC_
GAM2543  FLJ20967  3'  TGACAGGTACTTGCTGAA    58935        CTA
                                TGACAGGTAT  CTGGA
                                ||||||||||  |||||
                                ACTGTCCATG  GACTT
                                     AAC
GAM2543  KIAA0410  3'  GACAGAAACTGGACTTTT    58936      TATCT
                                GACAGG    ACTGGACTTTT
                                ||||||    ||||||||||
                                CTGTCT    TGACCTGAAAA
                                   T____
GAM2543  SEF       3'  TGCAGGTATCTTCCTGTTTTTC 58937    A       A_  GAC
                                TG CAGGTATCT  CTG   TTTTC
                                || |||||||||  |||   |||||
                                AC GTCCATAGA  GAC   AAAAG
                                 _       AG   A__
GAM2543  LOC150082 5'  TGACAGGTTTTGGTCTCTT   58938       ATCTAC  A
                                TGACAGGT     TGG CTTTT
                                ||||||||     ||| |||||
                                ACTGTCCA     ACC GAGAA
                                     AA____   A
GAM2543  LOC150960 5'  TGACAGGTGGTTTATCTCAGGC 58939      _____   ACT  A
            TTTTC                ACAGGT    ATCT   GG CTTTTC
                                ||||||    ||||  || ||||||
                                TGTCCA    TAGA   CC GAAAAG
                                   CCAAA   GT_  _
GAM2543  LOC153338 5'  GGTATTACTGGACTTTTC    58940      C
                                GGTAT TACTGGACTTTTC
                                ||||| ||||||||||||
                                CCATA ATGACCTGAAAAG
                                   _
GAM2543  LOC157740 3'  ACAGGTATTCCTGTTTTTC   58941       CTA   GAC
                                ACAGGTAT   CTG   TTTTC
                                ||||||||   |||   |||||
                                TGTCCATA   GAC   AAAAG
                                     AG_   A__
GAM2543  LOC221069 3'  TGACAGGGATCAGGCTTTT   58942       T   TACT  A
                                TGACAGG ATC    GG CTTTT
                                ||||||| |||    || |||||
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                                ACTGTCC TAG    CC GAAAA
                                    C  T___  _
GAM2544  KIAA1373  3'  TGGTGACAAACACAACATTGCA 58945     C       ATT     A
              T                  TGG GGCAAATG   ACATT CAT
                                 ||| ||||||||   ||||| |||
                                 ACC CTGTTTGT   TGTAA GTA
                                   A       GT_    C
GAM2544  MGC13130  5'  TGGTGCAAATGATTGCA     58946     CG        A
                                 TGG  GCAAATGATT CA
                                 |||  ||||||||||  ||
                                 ACC  CGTTTACTAA GT
                                   A_         C
GAM2544  LOC253933 3'  TGGCGGCAGGGAAATACAT    58947        AAT  T_
                                 TGGCGGCA   GA  TACAT
                                 ||||||||   ||  |||||
                                 ACCGCCGT   CT  ATGTA
                                      CC_  TT
GAM2545  EPHB6     5'  GTGGACCTGACGCTG       58950       AACGAG
                                 GTGGAC     CTGACGCTG
                                 ||||||     |||||||||
                                 CACCTG     GACTGCGAC
                                      _______
GAM2545  PCDH9     5'  TGTAGACAAGGCTGGCGCTG   58951         CGA    A
                                 TGTGGACAA   GCTG CGCTG
                                 |||||||||   |||| |||||
                                 ACATCTGTT   CGAC GCGAC
                                       C__    C
GAM2545  SQSTM1    3'  TGTGGACAGTGAGCAGCCAA   58952         AC    TGAC  TG
                                 TGTGGACA  GAGC    GC  A
                                 ||||||||  ||||    ||  |
                                 ACACCTGT  CTCG    CG  T
                                      CA    T___  GT
GAM2545  WHSC1     3'  TGAGGGTAGCGACGCTGA    58953     T  ACAACG   T
                                 TG GG      AGC GACGCTGA
                                 || ||      ||| ||||||||
                                 AC CC      TCG CTGCGACT
                                   T  CA____  _
GAM2545  FLJ10044  3'  TGTGGACAGCAGGACTTGCTG  58954         ACGA  T_  __
                                 TGTGGACA   GC  GAC  GCTG
                                 ||||||||   ||  |||  ||||
                                 ACACCTGT   CG  CTG  CGAC
                                      _____  TC   AA
GAM2545  FLJ23356  3'  TGTGGACAACGAACCACATG   58955            G   C
                                 TGTGGACAACGAGCT ACG TG
                                 ||||||||||||||| ||| ||
                                 ACACCTGTTGCTTGG TGT AC
                                          _  _
GAM2545  FLJ31300  3'  TGTGGACAGAGAGCTGCA     58956         AC     A
                                 TGTGGACA  GAGCTG CG
                                 ||||||||  ||||||  ||
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                                ACACCTGT  CTCGAC GT
                                    CT     _
GAM2545 KIAA1145  3'  TGTGGACACTGAGTACATGAC  58957       AC   CTG   C
                                TGTGGACA  GAG   ACG TGAC
                                ||||||||  |||   ||| ||||
                                ACACCTGT  CTC   TGT ACTG
                                    GA   A__   _
GAM2545 KIAA1297  5'  TGTGACGGTGACGCTG     58958     GACA   AGC
                                TGTG   ACG   TGACGCTG
                                ||||   |||   ||||||||
                                ACAC   TGC   ACTGCGAC
                                  _____  C__
GAM2545 MGC9753   5'  GTGGACAGGGATGGTGCTGA   58959       AC  GC  AC
                                GTGGACA  GA  TG  GCTGA
                                |||||||  ||  ||  |||||
                                CACCTGT  CT  AC  CGACT
                                    CC  __  CA
GAM2545 LOC222484 5'  TGTGGAAAGAGACGCTGA    58960      CAAC   CT
                                TGTGGA   GAG  GACGCTGA
                                ||||||   |||  ||||||||
                                ACACCT   TTC  CTGCGACT
                                    _____  T_
GAM2545 LOC90631  3'  TGTGGACAGCAGGGCTCGGC   58961        A  A_   GAC
                                TGTGGACA CG  GCT   GC
                                |||||||| ||  |||   ||
                                ACACCTGT GT  CGA   CG
                                    C  CC   GC_
GAM2546 RAP1A     3'  TAAAGTATAATGGTTCAACT   58895          A    GT
                                TAGAGTATAATG TTTA  T
                                ||||||||||| ||||  |
                                ATTTCATATTAC AAGT  A
                                      C    TG
GAM2546 C21orf91  3'  AGAGTATAATGATCTGCT    58896            A
                                AGAGTATAATGATTT GTT
                                ||||||||||||| |||
                                TCTCATATTACTAGA CGA
                                          _
GAM2546 FBXO8     3'  TAGAGTATAATGTCAGTT    58897          AT
                                TAGAGTATAATG  TTAGTT
                                ||||||||||  ||||||
                                ATCTCATATTAC  AGTCAA
                                          __
GAM2546 FLJ14721  3'  TAGAATATAATGGTCAATT    58898          AT
                                TAGAGTATAATG  TTAGTT
                                ||||||||||  ||||||
                                ATCTTATATTAC  AGTTAA
                                      C_
GAM2546 LOC134553 3'  TAGGTATAATGGTTTCAGTT   58899     A      A_
                                TAG GTATAATG  TTTAGTT
                                ||| ||||||||  |||||||
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                                ATC CATATTAC  AAGTCAA
                                  _      CA
GAM2547  FLT1     3'  CACAGGTGGTTTGCGTAT    58965         AAT  C
                                CACAGGTGGT   CG TAT
                                ||||||||||   || |||
                                GTGTCCACCA   GC ATA
                                     AAC  _
GAM2547  SDC4     3'  CCAGCACAGCTGAGGCT     58966         G   TAATC
                                CCAGCACAG TGG    GCT
                                ||||||||| |||    |||
                                GGTCGTGTC ACT    CGA
                                     G   C____
GAM2547  TNXB     5'  CAGACAATGAAGTCGCT     58967     C   G   TAA
                                CAG ACAG TGG   TCGCT
                                ||| |||| |||   |||||
                                GTC TGTT ACT   AGCGA
                                  _   _  TC_
GAM2547  LATS1    3'  GCACAGGTAAGTTCTGCTAT   58968         TAA  _
                                GCACAGGTGG   TC GCTAT
                                ||||||||||   || |||||
                                CGTGTCCATT   AG CGATA
                                     CA_  A
GAM2547  PRO2900  3'  CAGCACAGGTGGGTCA      58969          TAA
                                CAGCACAGGTGG   TCG
                                ||||||||||||   |||
                                GTCGTGTCCACC   AGT
                                     C__
GAM2547  SYNE-2   3'  CAGGCAGGTGGTGTAGCACT   58970     CA      AAT_
                                CAG  CAGGTGGT    CGCT
                                |||  ||||||||    ||||
                                GTC  GTCCACCA    GTGA
                                  C_       CATC
GAM2547  ZNF17    3'  CAGTACAGTAATATGCTATA   58971     C   G    ATC
                                CAG ACAG TGGTA   GCTATA
                                ||| |||| |||||   ||||||
                                GTC TGTC ATTAT   CGATAT
                                  A   _    A__
GAM2547  LOC128387 3'  CAGTTCAGGTGGTGGTTCTATA 58972     CA      AATCG
                                CAG  CAGGTGGT    CTATA
                                |||  ||||||||    |||||
                                GTC  GTCCACCA    GATAT
                                  AA       CCAA_
GAM2548  DUSP4    5'  CCTCCGGCGCTCAGCCCTCGT  58975         GAATA
                                CCTCCGGTGT    AGCCCTCGT
                                ||||||||||    |||||||||
                                GGAGGCCGCG    TCGGGAGCA
                                     AG___
GAM2548  AF020591 3'  CCTCCAGTGTGTGTCCTCTCGT 58976          AATAAG  _
                                CCTCCGGTGTG     CC CTCGT
                                ||||||||||     || |||||
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                                GGAGGTCACAC     GG GAGCA
                                      ACA___  A
GAM2548  CYP2S1    3'  CCTCCGGTCTGAGGGTCCTCGT 58977        G   ATAAGC
                                CCTCCGGT TGA     CCTCGT
                                |||||||| |||     ||||||
                                GGAGGCCA ACT     GGAGCA
                                     G   CCCA__
GAM2548  SYT12     3'  CCTCCAGTCCCCTGGGCCCTTG 58978        GTGAATAA    C
              T                  CCTCCGGT       GCCCT GT
                                 ||||||||       ||||| ||
                                 GGAGGTCA       CGGGA CA
                                      GGGGACC_     A
GAM2548  LOC146445 3'  CCTCCGTGTGCCCTC       58979       G   GAATAA
                                CCTCCG TGT     GCCCTC
                                |||||| |||     ||||||
                                GGAGGC ACA     CGGGAG
                                  _  _______
GAM2548  LOC158668 5'  CCTCGGCCACTAGGCCCTCGT  58980      C   GTGAA  A
                                CCTC GGT     TA GCCCTCGT
                                |||| |||     || ||||||||
                                GGAG CCG     AT CGGGAGCA
                                  _   GTG__  C
GAM2548  LOC204823 3'  CTCTGATGTGAATGGCCCT    58981     C        AA
                                CTC GGTGTGAAT  GCCCT
                                ||| |||||||||  |||||
                                GAG CTACACTTA  CGGGA
                                  A        C_
GAM2549  BTG1      3'  TATGGCACTGTCACTTAAAA   58984        ACGC
                                TATGGCA    CGCTTAAAA
                                |||||||    |||||||||
                                ATACCGT    GTGAATTTT
                                     GACA
GAM2549  CHAD      3'  GGCATGGGCTTTAAAACCCT   58985      ACGCC   _
                                GGCA     GCTT AAAACCCT
                                ||||     |||| ||||||||
                                CCGT     CGAA TTTTGGGA
                                   ACC__    A
GAM2549  CHST3     3'  CATGGCAATGTTGGACTCAGAT 58986        CGCC__     AAAC
              CCT                   TATGGCAA     GCTTA    CCT
                                    ||||||||     |||||    |||
                                    GTACCGTT     TGAGT    GGA
                                         ACAACC     CTA_
GAM2549  DKFZp762L0311 3'  TATGGCAACATTTTCTAAGTCC 58987          CCG_  TAAAAC
              T                   TATGGCAACG    CT     CCT
                                  ||||||||||    ||     |||
                                  ATACCGTTGT    GA     GGA
                                        AAAA  TTCA__
GAM2549  FLJ20273  3'  GCAACTCGATTAAAACC     58988       GC  C
                                GCAAC  CG TTAAAACC
                                |||||  || ||||||||
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                                CGTTG  GC AATTTTGG
                                   A_  T
GAM2549  MSC      3'  TATGGTAAGCCGCCCACCC    58989       C  C      AAA
                                TATGG AA GCCGCTT   ACCC
                                ||||| || |||||||   ||||
                                ATACC TT CGGCGGG   TGGG
                                   A  _      ___
GAM2549  PRO2176  3'  TATGGTAGTGTCTGTAAAACCC 58990       CAACGCCG  _
              T                  TATGG       CT TAAAACCCT
                                |||||       || |||||||||
                                ATACC       GA ATTTTGGGA
                                   ATCACA__  C
GAM2549  RBBP1    3'  TATGGCAGGCTGCTTAACC    58991        AC  C    AA
                                TATGGCA  GC GCTTA  ACC
                                |||||||  || |||||  |||
                                ATACCGT  CG CGAAT  TGG
                                    C_  A    __
GAM2549  RBBP1    3'  TATGGCAGGCTGCTTAACC    58991        AC  C    AA
                                TATGGCA  GC GCTTA  ACC
                                |||||||  || |||||  |||
                                ATACCGT  CG CGAAT  TGG
                                    C_  A    __
GAM2550  ACPT     3'  GTGACATTCCCTCCATCTTTGG 58994             __  A_
              C                  GTGGCATTCCCTCC  CTT  GC
                                |||||||||||||  |||  ||
                                CACTGTAAGGGAGG  GAA  CG
                                       TA   AC
GAM2550  ACPT     3'  GTGACATTCCCTCCATCTTTGG 58994             __  A_
              C                  GTGGCATTCCCTCC  CTT  GC
                                |||||||||||||  |||  ||
                                CACTGTAAGGGAGG  GAA  CG
                                       TA   AC
GAM2550  AKAP13   3'  GTGGTGTGCCCTCACCCAGCA  58995     CATT    C
                                GTGG   CCCTC CTTAGCA
                                ||||   ||||| |||||||
                                CACC   GGGAG GGGTCGT
                                  ACAC    T
GAM2550  ANGPT2   5'  GTGTTGTTCCCTCCCTCA    58996     GCA
                                GTG   TTCCCTCCCTTA
                                |||   ||||||||||||
                                CAC   AAGGGAGGGAGT
                                  AAC
GAM2550  BACE     3'  GTGGCATTTTCACTTCATGGTA 58997        CCC  C   AGC___
              GCA                  GTGGCATT   TC CTT     AGCA
                                |||||||   || |||     ||||
                                CACCGTAA   AG GAA     TCGT
                                    A__  T   GTACCA
GAM2550  BACE     3'  GTGGCATTTTCACTTCATGGTA 58997        CCC  C   AGC___
              GCA                  GTGGCATT   TC CTT     AGCA
                                |||||||   || |||     ||||
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                              CACCGTAA   AG GAA     TCGT
                                  A__  T   GTACCA
GAM2550  DMD     3'  GTGGCATTGCTAGCAG     58998        CCCTCCC
                              GTGGCATT     TTAGCAG
                              ||||||||     |||||||
                              CACCGTAA     GATCGTC
                                  C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG     58998        CCCTCCC
                              GTGGCATT     TTAGCAG
                              ||||||||     |||||||
                              CACCGTAA     GATCGTC
                                  C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG     58998        CCCTCCC
                              GTGGCATT     TTAGCAG
                              ||||||||     |||||||
                              CACCGTAA     GATCGTC
                                  C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG     58998        CCCTCCC
                              GTGGCATT     TTAGCAG
                              ||||||||     |||||||
                              CACCGTAA     GATCGTC
                                  C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG     58998        CCCTCCC
                              GTGGCATT     TTAGCAG
                              ||||||||     |||||||
                              CACCGTAA     GATCGTC
                                  C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG     58998        CCCTCCC
                              GTGGCATT     TTAGCAG
                              ||||||||     |||||||
                              CACCGTAA     GATCGTC
                                  C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG     58998        CCCTCCC
                              GTGGCATT     TTAGCAG
                              ||||||||     |||||||
                              CACCGTAA     GATCGTC
                                  C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG     58998        CCCTCCC
                              GTGGCATT     TTAGCAG
                              ||||||||     |||||||
                              CACCGTAA     GATCGTC
                                  C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG     58998        CCCTCCC
                              GTGGCATT     TTAGCAG
                              ||||||||     |||||||
                              CACCGTAA     GATCGTC
                                  C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG     58998        CCCTCCC
                              GTGGCATT     TTAGCAG
                              ||||||||     |||||||
                              CACCGTAA     GATCGTC
                                  C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG     58998        CCCTCCC
                              GTGGCATT     TTAGCAG
                              ||||||||     |||||||
                              CACCGTAA     GATCGTC
                                  C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG     58998        CCCTCCC
                              GTGGCATT     TTAGCAG
                              ||||||||     |||||||
                              CACCGTAA     GATCGTC
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                                CACCGTAA     GATCGTC
                                     C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG      58998        CCCTCCC
                                GTGGCATT     TTAGCAG
                                ||||||||     |||||||
                                CACCGTAA     GATCGTC
                                     C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG      58998        CCCTCCC
                                GTGGCATT     TTAGCAG
                                ||||||||     |||||||
                                CACCGTAA     GATCGTC
                                     C_______
GAM2550  DMD     3'  GTGGCATTGCTAGCAG      58998        CCCTCCC
                                GTGGCATT     TTAGCAG
                                ||||||||     |||||||
                                CACCGTAA     GATCGTC
                                     C_______
GAM2550  GARP    3'  GTGGCATTTTCACTTTCTCGCA 58999        __ C  CC   A
                                GTGGCAT  TC CT  CTT GCA
                                |||||||  || ||  ||| |||
                                CACCGTA  AG GA  GAG CGT
                                    AA  T  AA  _
GAM2550  HMGN1   3'  GTGGGATTCCCTCCTTCTTA   59000      C        __
                                GTGG ATTCCCTCC  CTTA
                                |||| |||||||||  |||||
                                CACC TAAGGGAGG  GAAT
                                  C        AA
GAM2550  INPP4A  5'  GTGGCATTTCTTCATAGAAGCA 59001         CC  CCCT   C
                                GTGGCATT  CT    TAG AGCA
                                ||||||||  ||    ||| ||||
                                CACCGTAA  GA    ATC TCGT
                                     A_  AGT_   T
GAM2550  INPP4A  5'  GTGGCATTTCTTCATAGAAGCA 59001         CC  CCCT   C
                                GTGGCATT  CT    TAG AGCA
                                |||||||  ||    ||| ||||
                                CACCGTAA  GA    ATC TCGT
                                     A_  AGT_   T
GAM2550  LASS1   3'  GTGGCATCTTCCTCCCAGGC   59002        C_     TTA
                                GTGGCATT  CCTCCC   GC
                                |||||||  ||||||   ||
                                CACCGTAG  GGAGGG   CG
                                     AA     TC_
GAM2550  PHKB    3'  GTGGCATTCACCTCCCCAGCA  59003         _      T
                                GTGGCATTC CCTCCCT AGCA
                                ||||||||| ||||||| ||||
                                CACCGTAAG GGAGGGG TCGT
                                      T      _
GAM2550  PRKAR1A  3'  TGGCATTTCTCCCTTTAGCAGC 59004        CC      _
            A                    TGGCATT  CTCCCTT AGCAGCA
                                 |||||||  ||||||| |||||||
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                                ACCGTAA  GAGGGAA TCGTCGT
                                   A_      A
GAM2550  ACAA2    5'  GGCGTTCGCTTAGCAGC     59005     A   CCTCC
                                GGC TTC     CTTAGCAGC
                                ||| |||     |||||||||
                                CCG AAG     GAATCGTCG
                                  C   C____
GAM2550  ANKRD6   3'  GTGGCATTTACTCGCTTTAGCA 59006        CC   C   _
                                GTGGCATT  CTC CTT AGCA
                                ||||||||  ||| ||| ||||
                                CACCGTAA  GAG GAA TCGT
                                     AT   C   A
GAM2550  C11orf11  5'  GTGACATTCTTGGCAG      59007         CCTCCC  A
                                GTGGCATTC     TT GCAG
                                |||||||||     || ||||
                                CACTGTAAG     AA CGTC
                                      _______ C
GAM2550  CAPN13   5'  TGGTATAAACTTTAGCAGCA   59008     C  TCC  CCC
                                TGG AT   CT   TTAGCAGCA
                                ||| ||   ||   |||||||||
                                ACC TA   GA   AATCGTCGT
                                  A  TTT  ___
GAM2550  D15Wsu75e 3'  GTGGCATTTTGTTCTGTTTCTT 59009     CCC_  C____        III
            AGCAGCAT                TT    TC     CTTAGCAGCA   T
                                ||   ||    ||||||||||  |
                                AA   AG    GAATCGTCGT   A
                                 AACA  ACAAA        III
GAM2550  DKFZp566D234 3'  GTGACATTCCCTTCAAGGCA   59010           CCCTTA
                                GTGGCATTCCCT     GCA
                                ||||||||||||     |||
                                CACTGTAAGGGA     CGT
                                      AGTTC_
GAM2550  EPSTI1   3'  GTAGCATTTCCCTGGCAG    59011        CCC     TA
                                GTGGCATT   TCCCT  GCAG
                                ||||||||   |||||  ||||
                                CATCGTAA   AGGGA  CGTC
                                     ___     C_
GAM2550  ERG-1    3'  GTAGCATTTCCTTTGGCA    59012        CCC   C  A
                                GTGGCATT   TCC TT GCA
                                ||||||||   ||| || |||
                                CATCGTAA   AGG AA CGT
                                     ___   A  C
GAM2550  FLJ10829 3'  GTGACATTCTCTCTGGGCA   59013         C   CCTTA
                                GTGGCATTC CTC    GCA
                                ||||||||| |||    |||
                                CACTGTAAG GAG    CGT
                                     A   ACC__
GAM2550  FLJ23074 3'  GTGGCATTCCTGCCCTGGC   59014         CT    TA
                                GTGGCATTCC  CCCT  GC
                                ||||||||||  ||||  ||
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                                CACCGTAAGG  GGGA  CG
                                     AC    C_
GAM2550  HSPCAL3   3'  GCGGCATTTCTTCAGTTACAGC 59015        CCC  CCT__
             AGCA                  GTGGCATT   TC    TAGCAGCA
                                |||||||||  ||    ||||||||
                                CGCCGTAA  AG    GTCGTCGT
                                    AGA  TCAAT
GAM2550  KIAA1297  3'  GTGGCATTCTCCCGGCA     59017        CC    TTA
                                GTGGCATTC  TCCC   GCA
                                |||||||||  ||||   |||
                                CACCGTAAG  AGGG   CGT
                                     __    C__
GAM2550  KIAA1297  5'  GTGTATTCCCTCTAGCA     59016     GC      CCT
                                GTG  ATTCCCTC   TAGCA
                                |||  ||||||||   |||||
                                CAC  TAAGGGAG   ATCGT
                                  A_       ___
GAM2550  LAMP3     3'  TGACTTAGTTCCTTTCTTTAGC 59018      A___    C_  CC
             AGCA                  TGGC    TTCC  TC  TTAGCAGCA
                                ||||    ||||  ||  |||||||||
                                ACTG    AAGG  AG  AATCGTCGT
                                  AATC    AA  A_
GAM2550  SNPH      3'  GTGGCTTCTCTAGCAG      59019       A   C  CCCTT
                                GTGGC TTC CT    AGCAG
                                ||||| ||| ||    |||||
                                CACCG AAG GA    TCGTC
                                  _  A  ______
GAM2550  LOC124145 5'  CTCCTCTCCCTTAGCGGC     59020      _        A
                                TTCC CTCCCTTAGC GC
                                |||| ||||||||| ||
                                GAGG GAGGGAATCG CG
                                  A        C
GAM2550  LOC143308 5'  GTGGCATCTCTTTTGCA     59021        TCC   CC  A
                                GTGGCAT   CTC  TT GCA
                                |||||||   |||  || |||
                                CACCGTA   GAG  AA CGT
                                     ___   AA  _
GAM2550  LOC144321 3'  ATGGCATTTATTAGCCCTTGGT 59022        CCCT__    AGCA
             GGCA                  GTGGCATT     CCCTT    GCA
                                ||||||||     |||||    |||
                                TACCGTAA     GGGAA    CGT
                                    ATAATC     CCAC
GAM2550  LOC144363 3'  ATGGCATTCTCTTGTCAG     59023         C  CCC
                                GTGGCATTC CT   TTAG
                                |||||||||  ||   ||||
                                TACCGTAAG GA   AGTC
                                     A  AC_
GAM2550  LOC150960 5'  TGGCATTCCCTCTTCATAGCA  59024          CCT_
                                TGGCATTCCCTC    TAGCA
                                ||||||||||||    |||||
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                                ACCGTAAGGGAG   ATCGT
                                      AAGT
GAM2550  LOC152485 3'  GTGGCACTCCATGGCAGC    59025        CTCCCTTA
                                GTGGCATTCC      GCAGC
                                ||||||||||      |||||
                                CACCGTGAGG      CGTCG
                                     TAC_____
GAM2550  LOC158147 3'  GTGACATTTTCTCCTCCAGCA  59026       CC   CT
                                GTGGCATT  CTCC  TAGCA
                                ||||||||  ||||  |||||
                                CACTGTAA  GAGG  GTCGT
                                    AA   AG
GAM2550  LOC158956 3'  GTGGGATTCCCTCCTTCTTA   59000     C       __
                                GTGG ATTCCCTCC  CTTA
                                |||| |||||||||  ||||
                                CACC TAAGGGAGG  GAAT
                                  C       AA
GAM2550  LOC202301 5'  TGGCGTTCTCTCCCTAGCA    59027     A  C     T
                                TGGC TTC CTCCCT AGCA
                                |||| ||| ||||||| ||||
                                ACCG AAG GAGGGA TCGT
                                  C  A    _
GAM2550  LOC203042 5'  GTGTATTCCCTCCCGCAG     59028     GC        TTA
                                GTG  ATTCCCTCCC   GCAG
                                |||  ||||||||||   ||||
                                CAC  TAAGGGAGGG   CGTC
                                 A_        ___
GAM2550  LOC220143 5'  GTGGCATTCTTCACCTTCAGCA 59029         CC  _   AG
                                GTGGCATTC  TC CCTT  CAGCA
                                |||||||||  || ||||  |||||
                                CACCGTAAG  AG GGAA  GTCGT
                                     A_  T   __
GAM2550  LOC91115  3'  GTGGTCTCCTCCCTTAGTGGC  59030     CAT  _       CA
                                GTGG   TC CCTCCCTTAG  GC
                                ||||   || ||||||||||  ||
                                CACC   AG GGAGGGAATC  CG
                                  ___  A         AC
GAM2550  LOC91351  3'  GTGGCATTCTCCTTCCTC    59031         _  C
                                GTGGCATTC CCT CCTT
                                ||||||||| ||| ||||
                                CACCGTAAG GGA GGAG
                                     A  A
GAM2550  LOC91960  3'  GTGGTTTTCCTCTTCAGCA   59032     CA   C  CC
                                GTGG  TTCC TC  TTAGCA
                                ||||  |||| ||  ||||||
                                CACC  AAGG AG  AGTCGT
                                  AA   _ A_
GAM2550  LOC93190  3'  GTGGTATTTTGTTCCAGCAGCA 59033     C  CCC_  CTT
                                GTGG ATT   TCC   AGCAGCA
                                |||| |||   |||  |||||||
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                                CACC TAA   AGG  TCGTCGT
                                  A  AACA  ___
GAM2551  INADL     5'  GGGAGCCCGGGTCGGGCG   59036       C   AA
                                GGGAGTTTG GGTC  GCG
                                ||||||||| ||||  |||
                                CCCTCGGGC CCAG  CGC
                                     _   CC
GAM2551  MGC10963  5'  CGGGAGTTAAGTCGCAAGCG  59037       TG__  GT
                                CGGGAGTT   CG  CAAGCG
                                ||||||||   ||  ||||||
                                GCCCTCAA   GC  GTTCGC
                                    TTCA  __
GAM2551  LOC143666 3'  GAGGGCTCCTTGGTCAAGCG  59038   C  AG  GC
                                GA GGG  TTT  GGTCAAGCG
                                || |||  |||  |||||||||
                                CT CCC  GGA  CCAGTTCGC
                                 _  GA  A_
GAM2551  LOC164395 5'  GACGGGAGTTTGTGGGCC   59039         C_
                                GACGGGAGTTTG  GGTC
                                ||||||||||||  ||||
                                CTGCCCTCAAAC  CCGG
                                      AC
GAM2551  LOC165254 3'  CGGGAGTTTGCGAGCG     59040         GTCA
                                CGGGAGTTTGCG   AGCG
                                ||||||||||||   ||||
                                GCCCTCAAACGC   TCGC
                                      _____
GAM2551  LOC253258 3'  GAGGGCTCCTTGGTCAAGCG  59038   C  AG  GC
                                GA GGG  TTT  GGTCAAGCG
                                || |||  |||  |||||||||
                                CT CCC  GGA  CCAGTTCGC
                                 _  GA  A_
GAM2551  LOC256980 3'  CAGGAGTTTGCGCTCAGCA   59041         G  A
                                CGGGAGTTTGCG TCA GCG
                                |||||||||||| ||| |||
                                GTCCTCAAACGC AGT CGT
                                      G  _
GAM2552  IL22RA2   3'  TGTTTTATTAAGTCAGGCT   59044     A       AT
                                TGTT TATTAAGTCA  CT
                                |||| ||||||||||  ||
                                ACAA ATAATTCAGT  GA
                                  A        CC
GAM2552  KIAA0391  3'  TGTTAAATTAAGTCAAACT   59045     T       T
                                TGTTA ATTAAGTCAA CT
                                ||||| |||||||||| ||
                                ACAAT TAATTCAGTT GA
                                  T        T
GAM2552  LOC220672 3'  TCAGAGTCAGTCTAATCA    59046    _    A
                                TTA AGTCA TCTAATCA
                                ||| ||||| ||||||||
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                                AGT TCAGT AGATTAGT
                                  C    C
GAM2553  IL22RA2   3'  ACCATAAATGAATTTTGTTTTA 59049        AATGTCG
                                ACCATAAAT      TTGTTTTA
                                |||||||||      ||||||||
                                TGGTATTTA      AACAAAAT
                                     CTTAA__
GAM2553  LYPLA1    3'  CCATAAATAATATCTTG     59050           G
                                CCATAAATAATGTC TTG
                                |||||||||||||| |||
                                GGTATTTATTATAG AAC
                                              _
GAM2553  NAPB      3'  ACCATAAATAATTATATTTT   59051          GTCGT
                                ACCATAAATAAT    TGTTTT
                                ||||||||||||    ||||||
                                TGGTATTTATTA    ATAAAA
                                       AT___
GAM2553  PMCHL1    3'  ATAAATAATAAGTCGTTTTA   59052         TC
                                ATAAATAATG  GTTGTTTTA
                                ||||||||||  |||||||||
                                TATTTATTAT  CAGCAAAAT
                                     T_
GAM2553  SGK       3'  CATAAATAATGCCCATTTTA   59053          GTT
                                CATAAATAATGTC   GTTTTA
                                ||||||||||||   ||||||
                                GTATTTATTACGG   TAAAAT
                                       G__
GAM2553  CLPX      3'  ACCAAAATAATGTACATT     59054      T       _
                                ACCA AAATAATGT CGTT
                                |||| ||||||||| ||||
                                TGGT TTTATTACA GTAA
                                  _       T
GAM2553  FLJ14936  3'  CCTGGATAATGTCAATGCTT   59055    ATAA       T
                                CC    ATAATGTCG TGTTT
                                ||    ||||||||| |||||
                                GG    TATTACAGT ACGAA
                                 ACC_       T
GAM2553  FLJ22969  3'  ACTATAAGCTAATGTGTTGTTT 59056    C    A_     C
            T                    AC ATAA  TAATGT GTTGTTTT
                                 || ||||  |||||| ||||||||
                                 TG TATT  ATTACA CAACAAAA
                                  A   CG     _
GAM2553  FLJ23053  3'  ACCATTAAATGGTGTCAGGTTT 59057      _    AA    TT
            TA                    ACCAT AAAT  TGTCG  GTTTTA
                                  ||||| ||||  |||||  ||||||
                                  TGGTA TTTA  ACAGT  CAAAAT
                                    A   CC    C_
GAM2553  KIAA0993  3'  ACCACAGATAATGTCTTTG   59058       A       G
                                ACCATA ATAATGTC TTG
                                |||||| |||||||| |||
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                                TGGTGT TATTACAG AAC
                                   C       A
GAM2553  KIAA1954  3'  ACCATAAACAAGGTGTT     59059          T  C
                                ACCATAAATAA GT GTT
                                |||||||||| || |||
                                TGGTATTTGTT CA CAA
                                      C  _
GAM2553  PGRMC2    3'  CATAAATAATGTCTAGTT    59060           GTT
                                CATAAATAATGTC   GTT
                                ||||||||||||   |||
                                GTATTTATTACAG   CAA
                                       AT_
GAM2553  LOC150587 3'  CATAAATAATGTTGGCTG    59061           C_
                                CATAAATAATGT  GTTG
                                ||||||||||||  ||||
                                GTATTTATTACA  CGAC
                                       AC
GAM2554  MBNL      3'  ACTGCAGTAATAATAAAATA   59064        A   AA
                                ACTGCAG TGA  AATAAAATA
                                ||||||| |||  |||||||||
                                TGACGTC ATT  TTATTTTAT
                                   _  A_
GAM2554  NPTX2     3'  AACATGTATGAAAAATAAAATA 59065     TGCAG
                                AAC    ATGAAAAATAAAATA
                                |||    ||||||||||||||
                                TTG    TACTTTTTATTTTAT
                                  TACA_
GAM2554  RNF4      3'  ACTGCAGATCAATGATAA    59066         G  AA
                                ACTGCAGAT AA  ATAA
                                ||||||||| ||  ||||
                                TGACGTCTA TT  TATT
                                     G  AC
GAM2554  RRM2      3'  TACAGTGAGAAATAAAAT    59067       A   A
                                TGCAG TGA AAATAAAAT
                                ||||| ||| |||||||||
                                ATGTC ACT TTTATTTTA
                                   _  C
GAM2554  SCN1A     3'  TGCTGAAAAATAAAATA     59068     AGA
                                TGC   TGAAAAATAAAATA
                                |||   ||||||||||||||
                                ACG   ACTTTTTATTTTAT
                                  ____
GAM2554  SMARCA2   3'  TGCCTGATGAAAAATAAAATA 59069     A_
                                TGC  GATGAAAAATAAAATA
                                |||  ||||||||||||||||
                                ACG  CTACTTTTTATTTTAT
                                  GA
GAM2554  C1orf8    3'  CTACAGATATTAGTAAAATA  59070         AAAAA
                                CTGCAGATG    TAAAATA
                                |||||||||    |||||||
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                                GATGTCTAT    ATTTTAT
                                     AATC_
GAM2554  C1QTNF7   5'  TAACTTGATGAAAAATAAA   59071      GCA
                                TAACT  GATGAAAAATAAA
                                |||||  ||||||||||||||
                                ATTGA  CTACTTTTTATTT
                                   A__
GAM2554  FENS-1    3'  AACTGCAGAAAATAGAAT    59072        TGAA    A
                                AACTGCAGA   AAATA AAT
                                |||||||||   ||||| |||
                                TTGACGTCT   TTTAT TTA
                                     ____   C
GAM2554  FLJ23462  3'  CACATGAAAGATAAAATA    59073    G     A
                                CA ATGAAA ATAAAATA
                                || |||||| ||||||||
                                GT TACTTT TATTTTAT
                                  G     C
GAM2554  KIAA1323  3'  TAACTACAGATTCCTTAAAATA 59074          GAAAAA
                                TAACTGCAGAT     TAAAATA
                                ||||||||||     |||||||
                                ATTGATGTCTA     ATTTTAT
                                     AGGA__
GAM2554  KLHL8     3'  ACTGCAAATACAAAATAAAATA 59075         A
                                ACTGCAGATG AAAATAAAATA
                                |||||||||| ||||||||||
                                TGACGTTTAT TTTTATTTTAT
                                     G
GAM2554  MEIS3     3'  AACTGCAGATATTAAAATA    59076         A_
                                AACTGCAGATG  AAAATA
                                ||||||||||  ||||||
                                TTGACGTCTAT  TTTTAT
                                     AA
GAM2554  NS1-BP    3'  TAACAGATGAGAGAAATAAA   59077    T      A__
                                C GCAGATGA   AAATAAA
                                | ||||||||   |||||||
                                A TGTCTACT   TTTATTT
                                 T       CTC
GAM2554  UNG2      3'  CTGCAAAATAAATAAAATA    59078       TGAA
                                CTGCAGA    AAATAAAATA
                                |||||||    ||||||||||
                                GACGTTT    TTTATTTTAT
                                     TA__
GAM2554  LOC152941 3'  CTGATTGATAAAAAATAAAATA 59079     CA_
                                CTG   GATGAAAAATAAAATA
                                |||   ||||||||||||||||
                                GAC   CTATTTTTTATTTTAT
                                  TAA
GAM2554  LOC154089 3'  GCAAATGAATGGGGAATAAAAT 59080         A_____
              A                  GCAGATGAA     AATAAAATA
                                 |||||||||     |||||||||
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                                CGTTTACTT    TTATTTTAT
                                     ACCCC
GAM2554  LOC254556 3'  ACTGCAGATCAATGATAA    59066        G  AA
                                ACTGCAGAT AA  ATAA
                                ||||||||| ||  ||||
                                TGACGTCTA TT  TATT
                                     G  AC
GAM2554  LOC257206 3'  TAACTGATGGCAAAATAAAATA 59081      GCA   A_
                                TAACT   GATG  AAAATAAAATA
                                |||||   ||||  ||||||||||
                                ATTGA   CTAC  TTTTATTTTAT
                                   ___   CG
GAM2555  PGLS     3'  CGGGTAGGGCTGCTGGCCGGAG 59084    A  _  AA       CT__
            GCTG                   CG GG AG  CTGCTGGCC    GCTG
                                || || ||  |||||||||    ||||
                                GC CC TC  GACGACCGG    CGAC
                                 _  A  CC        CCTC
GAM2555  PIST     5'  CGAAGGGAACTGCTGGGACTG  59085      A        CC
                                CGAGG GAACTGCTGG  CTG
                                ||||| ||||||||||  |||
                                GCTTC CTTGACGACC  GAC
                                   C         CT
GAM2555  PPP1R12B  3'  CGAGGAAAATTTTCTTGCTG   59086         _____  _
                                CGAGGAGAA    CT GCTG
                                |||||||||    || ||||
                                GCTCCTTTT    GA CGAC
                                     AAAA  A
GAM2555  TCF3     3'  CGAGGGGACACCCTGC      59087       A  A TGCTG
                                CGAGG GA C    GCCCTGC
                                ||||| || |    |||||||
                                GCTCC CT G    TGGGACG
                                   C  _ ______
GAM2555  TNFRSF6B  5'  GGGGGGTGGCCATAGCCCTGCT 59088    AGAACT  __
            G                   GG     GCT  GGCCCTGCTG
                                ||     |||  ||||||||||
                                CC     CGG  TCGGGACGAC
                                 CCCCAC   TA
GAM2555  VCL      3'  CGGGAGTGGCCCTGC       59089    A   AACTGC
                                CG GGAG     TGGCCCTGC
                                || ||||     |||||||||
                                GC CCTC     ACCGGGACG
                                  _   _______
GAM2555  VCL      3'  CGGGAGTGGCCCTGC       59089    A   AACTGC
                                CG GGAG     TGGCCCTGC
                                || ||||     |||||||||
                                GC CCTC     ACCGGGACG
                                  _   _______
GAM2555  ZNF147   3'  CAAGGAGAGTTCTGCCTGCTG  59090        ACTG   GC
                                CGAGGAGA   CTG  CCTGCTG
                                ||||||||   |||  |||||||
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                                GTTCCTCT   GAC  GGACGAC
                                    CAA_  __
GAM2555  ZNF278   3'  CGAGGAGAGACATGTTCTGCTG 59091        ACT  _  GCC
                                CGAGGAGA  GC TG  CTGCTG
                                ||||||||  || ||  ||||||
                                GCTCCTCT  TG AC  GACGAC
                                    C__  T  AA_
GAM2555  CIZ1     5'  GGGGACTGCTGGAGCAGCTG  59092    A  A     CCCT
                                GG GA CTGCTGG   GCTG
                                || || |||||||   ||||
                                CC CT GACGACC   CGAC
                                 C  _      TCGT
GAM2555  DKFZp564K142 3'  GAGGAGAAACAACTGTCTTGCT 59093        _ T   GCCC
             G                   GAGGAGAA C GCTG   TGCTG
                                ||||||||| | ||||   |||||
                                CTCCTCTT G TGAC   ACGAC
                                    T T   AGA_
GAM2555  FLJ21140  3'  CGGGGAAAACTGCAAATGCTG  59094    A        TGGCCC
                                CG GGAGAACTGC     TGCTG
                                || ||||||||||     |||||
                                GC CCTTTTGACG     ACGAC
                                 C         TTT___
GAM2555  HSPC195   5'  CCAGGACCTGGCCCTGCT    59095   G   GAACTG
                                C AGGA     CTGGCCCTGCT
                                | ||||     ||||||||||
                                G TCCT     GACCGGGACGA
                                 G   G_____
GAM2555  HUMZD58C02 3'  CGAGGGGGGAGCAGCCCTGCTG 59096      AGAACT  T
                                CGAGG     GC GGCCCTGCTG
                                |||||     || ||||||||||
                                GCTCC     CG TCGGGACGAC
                                   CCCCT_  _
GAM2555  KIAA0280  3'  GGAGATGCTGGTCTTGCT    59097      AC     CCC
                                GGAGA  TGCTGG   TGCT
                                |||||  ||||||   ||||
                                CCTCT  ACGACC   ACGA
                                   __      AGA
GAM2555  KIAA0789  3'  CAAGGGAAGCTGGCCCTG    59098      A   CT
                                CGAGG GAA  GCTGGCCCTG
                                ||||| |||  ||||||||||
                                GTTCC CTT  CGACCGGGAC
                                   _  __
GAM2555  KIAA1879  5'  GAGCAGAATGTCTTTGCT    59099    G   C  _  GGCCC
                                GAG AGAA TG CT    TGCT
                                ||| |||| || ||    ||||
                                CTC TCTT AC GA    ACGA
                                  G   _ A  A____
GAM2555  KLF12    3'  AAGGGGATTCAGCCCTGCTG   59100     A  ACTGCT
                                GAGG GA     GGCCCTGCTG
                                |||| ||     ||||||||||
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                                TTCC CT     TCGGGACGAC
                                  C  AAG___
GAM2555  TBC1D2   5'  GAGGGAATGAGCTCCCTGCTG  59101     A  CT_  GG
                                GAGG GAA   GCT  CCCTGCTG
                                |||| |||   |||  ||||||||
                                CTCC CTT   CGA  GGGACGAC
                                  _   ACT   __
GAM2555  VILL     3'  GACGGAGCTGCTGGTTCTGCTG 59102    _   AA      CC
                                GA GGAG  CTGCTGG  CTGCTG
                                || ||||  |||||||  ||||||
                                CT CCTC  GACGACC  GACGAC
                                 G   __      AA
GAM2555  VRP      5'  GAGGAGAATGGCTCAGCT    59103        CTGC    CCT
                                GAGGAGAA    TGGC   GCT
                                ||||||||    ||||   |||
                                CTCCTCTT    ACCG   CGA
                                     _____    AGT
GAM2555  LOC118920 5'  GGGACCCCTTCCCTGCTG    59104    A  A  G  GG
                                GG GA CT CT  CCCTGCTG
                                || || || ||  ||||||||
                                CC CT GG GA  GGGACGAC
                                 _ _  G  A_
GAM2555  LOC148343 5'  GAGGAGCTGGTGGCCCTG    59105       AA   C
                                GAGGAG  CTG TGGCCCTG
                                ||||||  ||| ||||||||
                                CTCCTC  GAC ACCGGGAC
                                   __   C
GAM2555  LOC155036 5'  GAGGAGTCCTTGCCCTGCTG   59106       AA  GCTG
                                GAGGAG  CT    GCCCTGCTG
                                ||||||  ||    |||||||||
                                CTCCTC  GA    CGGGACGAC
                                   AG  A___
GAM2555  LOC197342 3'  GGGGGGGCACAGCCCTGCTG   59107    AGAACT  _
                                GG     GC TGGCCCTGCTG
                                ||     || ||||||||||
                                CC     CG GTCGGGACGAC
                                 CCCC__  T
GAM2555  LOC253394 5'  GAGAATTCAGCCCTGCTG    59108      CTGC
                                GAGAA    TGGCCCTGCTG
                                |||||    ||||||||||
                                CTCTT    GTCGGGACGAC
                                  AA__
GAM2555  LOC255520 3'  AAGGAGAACTTAAACTTTGCTG 59109         GCT   CC
                                GAGGAGAACT   GGC  TGCTG
                                ||||||||||   |||  |||||
                                TTCCTCTTGA   TTG  ACGAC
                                     AT_   AA
GAM2555  LOC51184  3'  GAAGAGAAGAATGTTCTGCTG  59110        CTGC  GCC
                                GAGGAGAA    TG   CTGCTG
                                ||||||||    ||   ||||||
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                                CTTCTCTT   AC   GACGAC
                                    CTT_  AA_
GAM2555 LOC90750 3' GAGGGTGAGGCCCTGCT    59111     AGAAC  CT
                                GAGG    TG  GGCCCTGCT
                                ||||    ||  |||||||||
                                CTCC    AC  CCGGGACGA
                                  C____  T_
GAM2555 LOC91179 3' CGAGGGGGGAGCAGCCCTGCTG 59096      AGAACT  T
                                CGAGG     GC GGCCCTGCTG
                                |||||     || ||||||||||
                                GCTCC     CG TCGGGACGAC
                                  CCCCT_ _
GAM2556 ARF4L    5' ACCGCAGCCGCCCCGCG     59114          ATGACA
                                GCCGCAGCCGCC     GCG
                                ||||||||||||     |||
                                TGGCGTCGGCGG     CGC
                                      GG____
GAM2556 ARNT2    3' CAGCCGCGGCTGCAGGGGAGAG 59115       A  C  CAT_  C
                                CAGCCGC GC GC    GA AG
                                ||||||| || ||    || ||
                                GTCGGCG CG CG    CT TC
                                    C  A  TCCC  C
GAM2556 ATP5A1   5' CAGCCGCAGCCTCCGGAC    59116          G  AT
                                CAGCCGCAGCC CC  GAC
                                |||||||||||  ||  |||
                                GTCGGCGTCGG GG  CTG
                                      A  C_
GAM2556 CD47     5' CAGCCGCCGCCGCCGTTACAG  59117       A     ATG
                                CAGCCGC GCCGCC   ACAG
                                ||||||| ||||||   ||||
                                GTCGGCG CGGCGG   TGTC
                                    G     CAA
GAM2556 CYB561   3' AGCCACAGCCAGCAGCAGCG   59118          C  TGA
                                AGCCGCAGCCG CA   CAGCG
                                ||||||||||  ||   |||||
                                TCGGTGTCGGT GT   GTCGC
                                      C  C__
GAM2556 EGLN1    5' CAGCCGCAAGCGGGTAGCG    59119        C  CCATGAC
                                CAGCCGCAG CG      AGCG
                                |||||||| ||      ||||
                                GTCGGCGTT GC      TCGC
                                    C  CCA____
GAM2556 FOXD2    5' CAGCCGCAGCCAGGGAAGTGGC 59120          CCATGACA
              G                   CAGCCGCAGCCG       GCG
                                ||||||||||||       |||
                                GTCGGCGTCGGT       CGC
                                      CCCTTCAC
GAM2556 FZD1     5' ACCGCAGCCGCCGCCGCCGCG  59121          A_  ACA
                                GCCGCAGCCGCC  TG   GCG
                                ||||||||||||  ||   |||
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                                TGGCGTCGGCGG GC  CGC
                                      CG GG_
GAM2556 GCH1    5' GCCGCAGCCGCTGCCGTTCG 59122        CA ACAG_
                                GCCGCAGCCGC TG   CG
                                |||||||||| ||   ||
                                CGGCGTCGGCG AC   GC
                                     __ GGCAA
GAM2556 GRHPR   5' CAGTGCAGCCGCCGACCCG  59123   CC      AT  AG
                                CAG GCAGCCGCC GAC CG
                                ||| ||||||||| ||| ||
                                GTC CGTCGGCGG CTG GC
                                  A_       __  G_
GAM2556 HADHSC  5' GCAGCGGCGGCGACAGCGA  59124     C CA
                                GCAGC GC TGACAGCGA
                                ||||| || |||||||||
                                CGTCG CG GCTGTCGCT
                                   C CC
GAM2556 KCND2   5' CAGCCGCCGCCGCCGTGGCG  59125      A    A ACA
                                CAGCCGC GCCGCC TG  GCG
                                ||||||| |||||| ||  |||
                                GTCGGCG CGGCGG AC  CGC
                                    G    C ___
GAM2556 LRPAP1  3' CAGCCCCAGCCACCCTGACGGC 59126     G      A  A
          G                  CAGCC CAGCCGCC TGAC GCG
                             ||||| |||||||| |||| |||
                             GTCGG GTCGGTGG ACTG CGC
                                G      G  C
GAM2556 NME1    5' GCTGCAGCCGCCAGCACCCGA 59127   C       TG AG
                                GC GCAGCCGCCA AC CGA
                                || |||||||||| || |||
                                CG CGTCGGCGGT TG GCT
                                 A       CG G_
GAM2556 OTOF    3' AGCCGCAGCCTGGGGCAGTGA 59128        GCCATGA  C
                                AGCCGCAGCC     CAG GA
                                ||||||||||     ||| ||
                                TCGGCGTCGG     GTC CT
                                     ACCCC__  A
GAM2556 POLR2E  3' CAGCCACAGCGGCAGTGA   59129        C CA
                                CAGCCGCAGC GC TGA
                                |||||||||| || |||
                                GTCGGTGTCG CG ACT
                                     C TC
GAM2556 POU2F2  3' CAGCCGCAGCCGCTGCTGA  59130         CA_
                                CAGCCGCAGCCGC  TGA
                                |||||||||||||  |||
                                GTCGGCGTCGGCG  ACT
                                       ACG
GAM2556 POU4F1  5' CAGCCGCGGCGGTCGCGGCG  59131      A ___  CATGACA
                                CAGCCGC GC  CGC     GCG
                                ||||||| ||  |||     |||
```

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                                GTCGGCG CG   GCG      CGC
                                    C  CCA   C_______
GAM2556  PTBP1    3'  CAGCCGCGGCCGCCGCG     59132        A     ATGACA
                                CAGCCGC GCCGCC     GCG
                                ||||||| ||||||     |||
                                GTCGGCG CGGCGG     CGC
                                    C     _______
GAM2556  PTBP1    3'  CAGCCGCGGCCGCCGCG     59132        A     ATGACA
                                CAGCCGC GCCGCC     GCG
                                ||||||| ||||||     |||
                                GTCGGCG CGGCGG     CGC
                                    C     _______
GAM2556  SFRP5    5'  CAGCCGCCGCCGCCGCCGCCGC 59133        A     A_  ACA
              G                  CAGCCGC GCCGCC  TG   GCG
                                ||||||| ||||||  ||   |||
                                GTCGGCG CGGCGG  GC   CGC
                                    G     CG  GG_
GAM2556  SNL      3'  GCCGCAGCCGCTGACCCGA   59134          CA    AG
                                GCCGCAGCCGC  TGAC  CGA
                                ||||||||||  ||||  |||
                                CGGCGTCGGCG  ACTG  GCT
                                      __    G_
GAM2556  USP11    5'  CAGCAGCAGCTGTAGAAGCG   59135     C    CGCCAT  C
                                CAGC GCAGC     GA AGCG
                                |||| |||||     || ||||
                                GTCG CGTCG     CT TCGC
                                  T    ACAT__  _
GAM2556  ADAR3    5'  CAGCCGCCGCCGCCGCTGCTGC 59136        A     A_  ACA
              GA                   CAGCCGC GCCGCC  TG   GCGA
                                ||||||| ||||||  ||   ||||
                                GTCGGCG CGGCGG  AC   CGCT
                                    G     CG  GA_
GAM2556  C(27)-3BETA-HSD 5'  GCTGCAGCCGCTATCCCAG   59137    C       C  GA
                                GC GCAGCCGC AT  CAG
                                || |||||||| ||  |||
                                CG CGTCGGCG TA  GTC
                                 A       A  GG
GAM2556  C15orf12  5'  CAGCCGCAGCCGCAGGACCCGA 59138            CAT   AG
                                CAGCCGCAGCCGC   GAC  CGA
                                ||||||||||||   |||  |||
                                GTCGGCGTCGGCG   CTG  GCT
                                      TC_   G_
GAM2556  C4S-2    5'  CAGCCGCCGCCGCCGCCCCGCG 59139        A     ATGACA
              A                   CAGCCGC GCCGCC     GCGA
                                ||||||| ||||||     ||||
                                GTCGGCG CGGCGG     CGCT
                                    G     CGGGG_
GAM2556  COL4A3BP  5'  CAGCCGCCGCCGCCGTCGC   59140        A     ATGACA
                                CAGCCGC GCCGCC     GC
                                ||||||| ||||||     ||
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                                GTCGGCG CGGCGG     CG
                                   G     CAG___
GAM2556 DCTD     3' CAGCCCCAGCTGCCACCAC   59141      G   C    G
                                CAGCC CAGC GCCAT AC
                                ||||| |||| ||||| ||
                                GTCGG GTCG CGGTG TG
                                   G    A    G
GAM2556 Dlc2     5' CAGCCGCCGCCGCCGC      59142        A     ATGACA
                                CAGCCGC GCCGCC     GC
                                ||||||| ||||||     ||
                                GTCGGCG CGGCGG     CG
                                   G     _______
GAM2556 DXS9928E 5' GCGGCGGCGGCGACAGCGA   59143    C  A  C  CAT
                                GC GC GC GC   GACAGCGA
                                || || || ||   ||||||||
                                CG CG CG CG   CTGTCGCT
                                 C  C  C  ___
GAM2556 ENDO180  3' CAGCTCCGGCTCCCAACAGCGA 59144     CGCA  CG  A
                                CAGC   GC  CC TGACAGCGA
                                ||||   ||  || |||||||||
                                GTCG   CG  GG GTTGTCGCT
                                  AGGC  A_  _
GAM2556 FLJ10597 3' CAGCCGCAGCCCTAACGA    59145          GCC
                                CAGCCGCAGCC   ATGA
                                ||||||||||   ||||
                                GTCGGCGTCGG   TGCT
                                      GAT
GAM2556 FLJ13187 5' GCGGCGGCGGCGACAGCGA   59143    C  A  C  CAT
                                GC GC GC GC   GACAGCGA
                                || || || ||   ||||||||
                                CG CG CG CG   CTGTCGCT
                                 C  C  C  ___
GAM2556 FLJ13204 5' CAGCTGCAGCCGCCGTCGC   59146      C        ATGACA
                                CAGC GCAGCCGCC     GC
                                |||| |||||||||     ||
                                GTCG CGTCGGCGG     CG
                                  A       CAG___
GAM2556 FLJ23277 5' GCCGCAGCCGCCGCCGCG    59147           ATGACA
                                GCCGCAGCCGCC     GCG
                                ||||||||||||     |||
                                CGGCGTCGGCGG     CGC
                                      CGG___
GAM2556 FLJ30663 5' CAGCCGCAACCTAACGGCG   59148          GCCA   A
                                CAGCCGCAGCC    TGAC GCG
                                ||||||||||    |||| |||
                                GTCGGCGTTGG    ATTG CGC
                                      ____   C
GAM2556 KIAA0014 3' CAGCCGCGCCTGCTGGAGC   59149        A  GCCA  AC
                                CAGCCGC GCC    TG  AGC
                                ||||||| |||    ||  |||
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                              GTCGGCG CGG   AC  TCG
                                 _  ACG_  C_
GAM2556  KIAA0089  5'  GCCGCAGCTGACAGCG     59150       CGCCA
                              GCCGCAGC    TGACAGCG
                              ||||||||    ||||||||
                              CGGCGTCG    ACTGTCGC
                                 _____
GAM2556  KIAA0169  5'  GCAGCCACTGGCATGGCAG   59151       ___   A
                              GCAGCCGC   CATG CAG
                              ||||||||   |||| |||
                              CGTCGGTG   GTAC GTC
                                   ACC    C
GAM2556  KIAA0450  3'  CAGCCGCGGATGCTGGCCCGA  59152      A___  C_   A
                              CAGCCGC    GC  GCC TGA
                              |||||||    ||  ||| |||
                              GTCGGCG    CG  CGG GCT
                                   CCTA  AC   _
GAM2556  KIAA0459  3'  CAGCCGCAAGGACTGGCAGTGA 59153       CC  CA  A   C
                              CAGCCGCAG  GC  TG CAG GA
                              |||||||||  ||  || ||| ||
                              GTCGGCGTT  TG  AC GTC CT
                                   CC  __  C   A
GAM2556  KIAA0475  5'  CAGCCGCCGCCGCCGCCACAGC 59154      A     ATG
          G                    CAGCCGC GCCGCC   ACAGCG
                              |||||||  ||||||   ||||||
                              GTCGGCG CGGCGG   TGTCGC
                                   G     CGG
GAM2556  KIAA0731  5'  GCAGCCGCCGTAAATCCGA   59155       A   CAG
                              GCAGCCGCC TGA   CGA
                              |||||||||  |||   |||
                              CGTCGGCGG ATT   GCT
                                   C   TAG
GAM2556  KIAA0806  5'  CAGACGCAGCGCGACAGCG   59156    C     C  CAT
                              CAG CGCAGC GC   GACAGCG
                              |||  ||||||  ||   |||||||
                              GTC GCGTCG CG   CTGTCGC
                                T     _  ___
GAM2556  KIAA1012  5'  GCCGCAGCACAGGCAGCG    59157       C  CATGA
                              GCCGCAGC GC     CAGCG
                              ||||||||  ||    |||||
                              CGGCGTCG TG     GTCGC
                                   _  TCC__
GAM2556  KIAA1297  3'  GCCGCAGCCGCTGGGACAGTGA 59159         CAT    C
                              GCCGCAGCCGC   GACAG GA
                              ||||||||||   |||||  ||
                              CGGCGTCGGCG   CTGTC CT
                                     ACC    A
GAM2556  KIAA1297  3'  CAGCCGCTGGGACAGTGACAGC 59158       AGCC  CA
          GA                   CAGCCGC    GC  TGACAGCGA
                              |||||||    ||  |||||||||
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                                GTCGGCG   TG  ACTGTCGCT
                                    ACCC  TC
GAM2556 KIAA1416 3' GCCGCGGCTGCTCTGGCGA   59160      A  C  CA  ACA
                                GCCGC GC GC  TG   GCGA
                                ||||| || ||  ||   ||||
                                CGGCG CG CG  AC   CGCT
                                   C  A  AG  ___
GAM2556 KIAA1508 3' CAGCCGCAGAAACTGGCAGTGA 59161         CC  CA  A   C
                                CAGCCGCAG  GC  TG CAG GA
                                |||||||||  ||  || ||| ||
                                GTCGGCGTC  TG  AC GTC CT
                                     TT  __  C   A
GAM2556 KIAA1925 5' GCCGCAGCTCCCACCTCTGA   59162        ___    A_
                                GCCGCAGC   CGCC  TGA
                                ||||||||   ||||  |||
                                CGGCGTCG   GTGG  ACT
                                    AGG    AG
GAM2556 LANO     5' ACTCGCAGCCGCCGCGCG    59163    _       ATGACA
                                GC CGCAGCCGCC     GCG
                                || ||||||||||     |||
                                TG GCGTCGGCGG     CGC
                                 A        CG____
GAM2556 MCOLN3   5' GCCGCAGCTCCGGTGTCCGCG 59164        CG  A_  ACA
                                GCCGCAGC  CC  TG   GCG
                                ||||||||  ||  ||   |||
                                CGGCGTCG  GG  AC   CGC
                                    A_  CC  AGG
GAM2556 MGC2487  5' CAGCGGCAGCCGCTGGGCATG  59165     C      _____
                                CAGC GCAGCCGC    CATG
                                |||| ||||||||    ||||
                                GTCG CGTCGGCG    GTAC
                                  C       ACCC
GAM2556 MKNK1    3' CAGCCCCAGCCGCCACAGCTAC 59166      G        ___
            AGCG                  CAGCC CAGCCGCCATG   ACAGCG
                                |||||  ||||||||||   ||||||
                                GTCGG GTCGGCGGTGT   TGTCGC
                                   G          CGA
GAM2556 NCOR1    5' CAGCCGCCGCCGCCGCCGCG   59167       A     ATGACA
                                CAGCCGC GCCGCC     GCG
                                ||||||| ||||||     |||
                                GTCGGCG CGGCGG     CGC
                                    G     CGG___
GAM2556 NTN4     5' GCCCGCAGCCGCCGCTGA    59168    _       A_
                                GCC GCAGCCGCC  TGA
                                ||| |||||||||  |||
                                CGG CGTCGGCGG  ACT
                                  G        CG
GAM2556 PCSK7    5' CAGCTGCCGCCGCCTCCCTGCG 59169      C  A     ATGACA
                                CAGC GC GCCGCC     GCG
                                |||| || ||||||     |||
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                                GTCG CG CGGCGG     CGC
                                  A G     AGGGA_
GAM2556 PIP5K2A  5' CAGCCGCATCCCCCCGGCGGCG 59170        G  G  ATGACA
                                CAGCCGCA CC CC     GCG
                                |||||||| || ||     |||
                                GTCGGCGT GG GG     CGC
                                    A  G  GCCGC_
GAM2556 PTPN4    5' CAGCCGCCGCCGCAGC      59171        A    CATGAC
                                CAGCCGC GCCGC     AGC
                                ||||||| |||||     |||
                                GTCGGCG CGGCG     TCG
                                   G    _______
GAM2556 RNASE6PL 5' GCCGCAGCAGCCCTGGCGA   59172        C   A  ACA
                                GCCGCAGC GCC TG   GCGA
                                |||||||| ||| ||   ||||
                                CGGCGTCG CGG AC   CGCT
                                    T   G  ___
GAM2556 S164     5' CAGCCGCGCTGCGCGGCG    59173        A  C  CAT ACA
                                CAGCCGC GC GC   G   GCG
                                ||||||| || ||   |   |||
                                GTCGGCG CG CG   C   CGC
                                   _  A  ___ GC_
GAM2556 SDCCAG3  3' CAGCGGCAGCCACGCG      59174     C      CATGACA
                                CAGC GCAGCCGC      GCG
                                |||| ||||||||      |||
                                GTCG CGTCGGTG      CGC
                                  C       ________
GAM2556 SDOS     3' GCCCGGCCGCCACCTAGTGA  59175     GCA      GAC  C
                                GCC   GCCGCCAT   AG GA
                                |||   ||||||||   || ||
                                CGG   CGGCGGTG   TC CT
                                  GC_      GA_  A
GAM2556 SRF      5' GCCGCAGCCGCCGCCATCG   59176          ATGA  G
                                GCCGCAGCCGCC    CA CG
                                ||||||||||||    || ||
                                CGGCGTCGGCGG    GT GC
                                      CG__  A
GAM2556 TNRC5    5' CAGCCGCAGCCCGCCTTCAAAG 59177          _  ATGAC
             CG                   CAGCCGCAGCC GCC    AGCG
                                ||||||||||| |||    ||||
                                GTCGGCGTCGG CGG    TCGC
                                      G   AAGTT
GAM2556 ULK2     5' CAGCCGCAGCCCCGGGCCCGGG 59178          ____  ATGACA
             CG                   CAGCCGCAGCC    GCC     GCG
                                ||||||||||    |||     |||
                                GTCGGCGTCGG    CGG     CGC
                                      GGCC   GCC___
GAM2556 LOC119200 5' GCTGCCGCCGCCATAGCG    59179    C  A      GAC
                                GC GC GCCGCCAT   AGCG
                                || || ||||||||   ||||
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                                CG CG CGGCGGTA   TCGC
                                 A  G      ___
GAM2556  LOC126328 5'  CAGCCGCGGCTGGCTATCGCGA 59180        A  C_  CATGACA
                                CAGCCGC GC  GC      GCGA
                                ||||||| ||  ||      ||||
                                GTCGGCG CG  CG      CGCT
                                    C  AC  ATAG___
GAM2556  LOC145483 5'  GCAGCGACAGTGACAGCGA   59181      C  CA
                                GCAGC GC  TGACAGCGA
                                ||||| ||  |||||||||
                                CGTCG TG  ACTGTCGCT
                                   C  TC
GAM2556  LOC145989 3'  GCCGCAGCCGCTGACCCGA   59134          CA   AG
                                GCCGCAGCCGC  TGAC  CGA
                                ||||||||||  ||||  |||
                                CGGCGTCGGCG  ACTG  GCT
                                      __   G_
GAM2556  LOC147009 5'  CAGCTGCAGCCGCTGCTGCG   59182     C      CA  ACA
                                CAGC GCAGCCGC  TG   GCG
                                |||| ||||||||  ||   |||
                                GTCG CGTCGGCG  AC   CGC
                                  A       __  GA_
GAM2556  LOC147632 3'  CAGCGCAACGGTGACAGCG   59183     C    CGCCA
                                CAGC GCAGC    TGACAGCG
                                |||| |||||    ||||||||
                                GTCG CGTTG    ACTGTCGC
                                  _    CC___
GAM2556  LOC149069 3'  CAGCCACAGCTGAAGCCAGTGG 59184         C___   _  ACA
            CGA                   AGCCGCAGC   GCCA TG   GCGA
                                |||||||||   |||| ||   ||||
                                TCGGTGTCG   CGGT AC   CGCT
                                     ACTT   C  ___
GAM2556  LOC152849 3'  GCCGCAGCCGCGGCTGCAGCG  59185          CA_  A
                                GCCGCAGCCGC   TG CAGCG
                                ||||||||||   || |||||
                                CGGCGTCGGCG   AC GTCGC
                                      CCG  _
GAM2556  LOC154428 5'  GCCGCAGCCCACAGCG      59186         GCCATG
                                GCCGCAGCC     ACAGCG
                                |||||||||     ||||||
                                CGGCGTCGG     TGTCGC
                                     G_____
GAM2556  LOC164714 5'  GCTGCGCGTCCAACAGCGA   59187    C  A  CG   TG
                                GC GC GC  CCA  ACAGCGA
                                || || ||  |||  |||||||
                                CG CG CG  GGT  TGTCGCT
                                 A  _  CA   __
GAM2556  LOC169611 3'  GCCATGTCCTGTCATGACAGCG 59188     CAG  GC_
                                GCCG   CC   CATGACAGCG
                                ||||   ||   ||||||||||
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                                CGGT   GG   GTACTGTCGC
                                  ACA  ACA
GAM2556  LOC196761 3'  CAGCCGCTGCGCTGGTAGCG   59189       A  C  CA  AC
                                CAGCCGC GC GC  TG  AGCG
                                ||||||| || ||  ||  ||||
                                GTCGGCG CG CG  AC  TCGC
                                   A  _  __  CA
GAM2556  LOC199992 5'  CAGCCGCAGTCCGCGGGCG    59190         _   CATGACA
                                CAGCCGCAG CCGC      GCG
                                ||||||||| ||||      |||
                                GTCGGCGTC GGCG      CGC
                                    A   CC_____
GAM2556  LOC219686 5'  CAGCCGCGGCCGCCACGCTCG  59191        A       ACAG
                                CAGCCGC GCCGCCATG    CG
                                ||||||| |||||||||    ||
                                GTCGGCG CGGCGGTGC    GC
                                   C       GA__
GAM2556  LOC221341 5'  CAGCCGCGGCTGCTGCTGCA   59192       A  C  CA  ACA
                                CAGCCGC GC GC  TG   GCG
                                ||||||| || ||  ||   |||
                                GTCGGCG CG CG  AC   CGT
                                   C  A  __  GA_
GAM2556  LOC253489 5'  AGCCGCAGCAGAAGACAGCG   59193         CGCCAT
                                AGCCGCAGC     GACAGCG
                                |||||||||     |||||||
                                TCGGCGTCG     CTGTCGC
                                    TCTT__
GAM2556  LOC253727 5'  CAGCCGCAGTTCCACTGCTGCG 59194         CCG    GACA
            A                    CAGCCGCAG   CCAT    GCGA
                                |||||||||   ||||    ||||
                                GTCGGCGTC   GGTG    CGCT
                                    AA_    ACGA
GAM2556  LOC255069 5'  CAGCCGGGCCCACTGCGGCGA  59195       CA   GC   GACA
                                CAGCCG  GCC  CAT    GCGA
                                ||||||  |||  |||    ||||
                                GTCGGC  CGG  GTG    CGCT
                                   C_   __   ACGC
GAM2556  LOC256310 5'  CAGCTGCAGCCGCAGCACG    59196      C       __
                                CAGC GCAGCCGC  CATG
                                |||| ||||||||  ||||
                                GTCG CGTCGGCG  GTGC
                                  A       TC
GAM2556  LOC91828  5'  CAGCCGCGGGCGTCGCGCGCGA 59197        A_  __   CATGACA
                                CAGCCGC  GC  CGC      GCGA
                                |||||||  ||  |||      ||||
                                GTCGGCG  CG  GCG      CGCT
                                   CC  CA   CG_____
GAM2557  CANX     3'  AGGCATGACATATACT      59200        G    CTAA  T
                                AGGCATG ACATA    TA CT
                                ||||||| |||||    || ||
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                                TCCGTAC TGTAT    AT GA
                                  _    _____  _
GAM2557 VHL      3'  AGGGAGACTATACTAATGTTTG 59201     CAT    _       ATC
              T                   AGG   GGAC ATACTAAT   TGT
                                  |||   |||| ||||||||   |||
                                  TCC   TCTG TATGATTA   ACA
                                    C__    A       CAA
GAM2558 CSHL1    3'  TGTGGAGCAGCTCTAAGTTG   59204      AG ATCTAA
                                  TGTG  G     CTCTAAGTTG
                                  ||||  |     ||||||||||
                                  ACAC  C     GAGATTCAAC
                                    CT GTC___
GAM2558 FOXO1A   3'  TGTAAGAATTTTAAGTTG    59205         CTAACTC
                                  TGTGAGGAT      TAAGTTG
                                  |||||||||      |||||||
                                  ACATTCTTA      ATTCAAC
                                       AA_____
GAM2558 FLJ14351 3'  TGTGAAGATGGCCACTGGGTTG 59206         CTA_   CTAA
                                  TGTGAGGAT    ACT    GTTG
                                  |||||||||    |||    ||||
                                  ACACTTCTA    TGA    CAAC
                                       CCGG   CC__
GAM2558 KIAA1181 3'  TGAGGCCTGGGTTCTAGGTTG  59207       A   AAC_    A
                                  TGAGG TCT    TCTA GTTG
                                  ||||| |||    |||| ||||
                                  ACTCC GGA    AGAT CAAC
                                    _   CCCA    C
GAM2558 KIAA1354 3'  TGTTAGGATGACTAAGTTG    59208     G     CTAACT
                                  TGT AGGAT      CTAAGTTG
                                  ||| |||||      ||||||||
                                  ACA TCCTA      GATTCAAC
                                    A     CT_____
GAM2558 RAB35    3'  TGTGAGGAATTTAATTCACTTG 59209         TC_   C  TAAG
              A                    TGTGAGGA   TAA TC    TTGA
                                  ||||||||   ||| ||    ||||
                                  ACACTCCT   ATT AG    AACT
                                       TAA   A  TG__
GAM2558 LOC202025 5' TGTGAGGATCAGCTCCGTCTG  59210          TAA    AAG
                                  TGTGAGGATC   CTCT   TTG
                                  ||||||||||   ||||   |||
                                  ACACTCCTAG   GAGG   GAC
                                       TC_    CA_
GAM2558 LOC54499 3'  TGTACATAAAATTCTAAGTTGA 59211      AGGATCT  C
                                  TGTG       AA TCTAAGTTGA
                                  ||||       || ||||||||||
                                  ACAT       TT AGATTCAACT
                                    GTATT__  A
GAM2559 ADARB1   3'  TCCACCAGTCCCTGGAACCC   59214        AG       A
                                  TCCACCA  CCCTGGAA TCT
                                  |||||||  |||||||| |||
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                                AGGTGGT  GGGACCTT GGG
                                   CA       _
GAM2559  GARP     3'  CCTGCCGAGCTCTGGAGCCCT  59215    A_  A   C     AAT
                                CC  CC AGC CTGGA   CTCT
                                ||  || ||| |||||   ||||
                                GG  GG TCG GACCT   GGGA
                                 AC  C   A    C__
GAM2559  LPIN2    3'  AAACCCTGGAAGCTCTA     59216          AT
                                AAGCCCTGGAA  CTCTA
                                ||||||||||  |||||
                                TTTGGGACCTT  GAGAT
                                      C_
GAM2559  MANBA    3'  CCACCAAGAAATCTCT      59217       AGCCCT
                                CCACCA     GGAAATCTCT
                                ||||||     ||||||||||
                                GGTGGT     TCTTTAGAGA

                                _______
GAM2559  MAPK14   3'  TCCACCATGGAGGAAATCTCT  59218       AGCCCT
                                TCCACCA     GGAAATCTCT
                                |||||||     ||||||||||
                                AGGTGGT     CCTTTAGAGA
                                   ACCT__
GAM2559  MAPK14   3'  TCCACCATGGAGGAAATCTCT  59218       AGCCCT
                                TCCACCA     GGAAATCTCT
                                |||||||     ||||||||||
                                AGGTGGT     CCTTTAGAGA
                                   ACCT__
GAM2559  MAPK14   3'  TCCACCATGGAGGAAATCTCT  59218       AGCCCT
                                TCCACCA     GGAAATCTCT
                                |||||||     ||||||||||
                                AGGTGGT     CCTTTAGAGA
                                   ACCT__
GAM2559  NAPB     3'  CCAGCCCTGACCAAGATTTCTA 59219     A      AA___  C
                                CCA GCCCTGG     AT TCTA
                                ||| |||||||     || ||||
                                GGT CGGGACT     TA AGAT
                                  _      GGTTC  A
GAM2559  RXRA     3'  TCCATCAAACCCTGGCACCT   59220      C         AA
                                TCCA CAAGCCCTGG  ATCT
                                |||| ||||||||||  ||||
                                AGGT GTTTGGGACC  TGGA
                                   A         G_
GAM2559  TCF8     3'  TCCGCAGAGTCCTGGAAAACT  59221     AC  _  C       T
                                TCC  CA AG CCTGGAAA CT
                                |||  || || |||||||| ||
                                AGG  GT TC GGACCTTT GA
                                  C_  C  A       T
GAM2559  ASB16    5'  TCCCTCGGGCCCTGGAAGTCC  59222     ACCAA        A
                                TCC     GCCCTGGAA TCT
                                |||     ||||||||| |||
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                                AGG    CGGGACCTT AGG
                                  GAGCC       C
GAM2559 CAMKK2   3' TCCACCAAGCGCTGGAAA   59223         C
                                TCCACCAAGC CTGGAAA
                                |||||||||| |||||||
                                AGGTGGTTCG GACCTTT
                                      C
GAM2559 COVA1    3' TCCACCAAGCAGAAGTTTCT  59224        CCT   ATC
                                TCCACCAAGC  GGAA  TCT
                                ||||||||||  ||||  |||
                                AGGTGGTTCG  TCTT  AGA
                                      ___   CAA
GAM2559 ET       3' TCCACCAAGCTCTGTGTCC   59225        C  GAAA
                                TCCACCAAGC CTG   TCT
                                |||||||||| |||   |||
                                AGGTGGTTCG GAC   AGG
                                      A  AC__
GAM2559 FLJ10718 3' TCCACCAAGGCCCTGGAAA   59226        _
                                TCCACCAAG CCCTGGAAA
                                ||||||||| |||||||||
                                AGGTGGTTC GGGACCTTT
                                      C
GAM2559 FLJ13544 3' CCACCAAGCCTGACTCTCT   59227        C  AAA
                                CCACCAAGCC TGG  TCTCT
                                |||||||||| |||  |||||
                                GGTGGTTCGG ACT  AGAGA
                                      _  G__
GAM2559 KIAA0210 3' TCCACTAGTTCTGGTTCATTCT 59228     CA  CC   AAATC
            A                   TCCAC  AG  CTGG    TCTA
                                |||||  ||  ||||    ||||
                                AGGTG  TC  GACC    AGAT
                                   A_  AA   AAGTA
GAM2559 KIAA0447 3' CAAGCCCTGGAGCTCT     59229         AAT
                                CAAGCCCTGGA  CTCT
                                ||||||||||  ||||
                                GTTCGGGACCT  GAGA
                                      C__
GAM2559 KIAA0514 3' CACAGGCCTTGAGAAATCT   59230    CAA  C  _
                                CAC  GCC TG GAAATCT
                                |||  ||| || |||||||
                                GTG  CGG AC CTTTAGA
                                  TC_  A  T
GAM2559 KIAA0993 3' CCACCAAGCCTTTTCTCT    59231        CTGGAAA
                                CCACCAAGCC     TCTCT
                                ||||||||||     |||||
                                GGTGGTTCGG     AGAGA
                                      AAA____
GAM2559 KIAA1169 5' CCTGCTATGGAAATCTCT    59232    AA  CC
                                CC  GC  TGGAAATCTCT
                                ||  ||  ||||||||||
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                                GG  CG  ACCTTTAGAGA
                                 A_  AT
GAM2559 KIAA1509 3' TCTGCCAGGCCCTGGAGACCT 59233    CA   A      A
                                TC  CCA GCCCTGGA ATCT
                                ||  ||| |||||||| ||||
                                AG  GGT CGGGACCT TGGA
                                 AC   C       C
GAM2559 KIAA1878 3' CACCAGCCCTGATCT      59234      A     GAA
                                CACCA GCCCTG   ATCT
                                ||||| ||||||   ||||
                                GTGGT CGGGAC   TAGA
                                   _    ___
GAM2559 PPFIA4   3' CCAGGGCCTGGAATCTCTA   59235     AGC      A
                                CCA   CCTGGAA TCTCTA
                                |||   ||||||| ||||||
                                GGT   GGACCTT AGAGAT
                                  CCC      _
GAM2559 PPP1R13B 3' TCTACCTGGCCCTGGTCT    59236    C   AA      AAA
                                TC ACC  GCCCTGG   TCT
                                || |||  |||||||   |||
                                AG TGG  CGGGACC   AGA
                                 A   AC      ___
GAM2559 RALGPS1A 3' CACCAAGCCATTCAAATTTCTA 59237         CTGG    C
                                CACCAAGCC    AAAT TCTA
                                |||||||||    |||| ||||
                                GTGGTTCGG    TTTA AGAT
                                     TAAG    A
GAM2559 SYT13    3' CCACCTGGGCAATCTCT     59238     AGC    A_
                                CCA   CCTGG  AATCTCT
                                |||   |||||  |||||||
                                GGT   GGACC  TTAGAGA
                                  ___    CG
GAM2559 TNFRSF19L 3' TCTGCCAAGCCCAGCCTCT   59239    CA       T  AAA
                                TC  CCAAGCCC GG   TCTCT
                                ||  |||||||| ||   |||||
                                AG  GGTTCGGG TC   GGAGA
                                 AC       _ ___
GAM2559 TRAF2    3' TCTGCCAAGCCCCTCCGCAGTC 59240    CA       GGAAA__
            TCT                   TC  CCAAGCCCT      TCTCT
                                ||  |||||||||      |||||
                                AG  GGTTCGGGG      AGAGA
                                 AC        AGGCGTC
GAM2559 TSPAN-2  3' TCCATTAAGAAGAAATCTCT   59241     CC   CCCT
                                TCCA  AAG    GGAAATCTCT
                                ||||  |||    ||||||||||
                                AGGT  TTC    TCTTTAGAGA
                                  AA   T___
GAM2559 UMP-CMPK 3' TCTGCCAGGCTCTGAACCCCTA 59242    CA   A  C    AA
                                TC  CCA GC CTGG  ATCTCTA
                                ||  ||| || ||||  |||||||
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                                AG  GGT CG GACT  TGGGGAT
                                 AC   C  A   __
GAM2559  LOC144347 3'  TCCACGGAGCCCTGAGCCAAGT 59243       CA      _ AAATC
              CT                  TCCAC  AGCCCTG G     TCT
                                  |||||  ||||||| |     |||
                                  AGGTG  TCGGGAC C     AGA
                                    CC       T GGTTC
GAM2559  LOC151512 5'  CCTGCCAAGCCCAAGTCT    59244    A_      T  AAA
                                  CC  CCAAGCCC GG   TCT
                                  ||  |||||||| ||   |||
                                  GG  GGTTCGGG TC   AGA
                                   AC       T  ___
GAM2559  LOC90019  5'  TCCTGGGCCCTGGACCCT    59245    ACCAA       AAT
                                  TCC    GCCCTGGA   CTCT
                                  |||    ||||||||   ||||
                                  AGG    CGGGACCT   GGGA
                                    ACC__       ____
GAM2559  LOC91308  3'  TCTACTAAACCCCGTCTCT    59246    C  C       GAAA
                                  TC AC AAGCCCTG    TCTCT
                                  || || ||||||||    |||||
                                  AG TG TTTGGGGC    AGAGA
                                   A  A       _____
GAM2559  LOC93259  5'  CCAAGCCCTGGGTTGTTCTA   59247           AAATC
                                  CCAAGCCCTGG     TCTA
                                  ||||||||||     ||||
                                  GGTTCGGGACC     AGAT
                                         CAACA
GAM2560  MGA       3'  AGGCTTGAATTTGTTAAT    59250      CCTG   A
                                  AGGC    GAA TTGTTAAT
                                  ||||    ||| ||||||||
                                  TCCG    CTT AACAATTA
                                    AA__   A
GAM2560  NFE2L1    3'  ATAAGCCCAGTTGTT       59251         T  AAA
                                  ATAGGCCC GG   TTGTT
                                  |||||||| ||   |||||
                                  TATTCGGG TC   AACAA
                                       _  ____
GAM2560  SCG3      3'  AACAGGGGGAAATTGTTA    59252       CCCT
                                  AATAGG    GGAAATTGTTA
                                  ||||||    ||||||||||
                                  TTGTCC    CCTTTAACAAT
                                     C____
GAM2560  SLC17A7   3'  AGGTCCTGGAAACTGCCA    59253     C
                                  AGG CCTGGAAATTGTTA
                                  ||| ||||||||||||||
                                  TCC GGACCTTTGACGGT
                                    A
GAM2560  LOC153513 3'  ATAGGTCCTGGAAATGAGCT   59254       C        T_
                                  ATAGG CCTGGAAAT  GTT
                                  ||||| |||||||||  |||
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                                TATCC GGACCTTTA  CGA
                                  A       CT
GAM2560  LOC221964 3'  TAGGCCCTGATGTTA      59255         AAAT
                                TAGGCCCTGG   TGTTA
                                ||||||||||   |||||
                                ATCCGGGACT   ACAAT
                                     _____
GAM2561  KCND2    3'  TATGTAATAATCTTCATCATAG 59258          _    C  A
            CC                    TATGTAATAGTCT CATCA TA CC
                                ||||||||||||| ||||| || ||
                                ATACATTATTAGA GTAGT AT GG
                                      A    _ C
GAM2561  SRD5A2   5'  CATGTAACCTCATCATTAA   59259       AGT     C
                                TATGTAAT   CTCATCA TAA
                                ||||||||   ||||||| |||
                                GTACATTG   GAGTAGT ATT
                                     ___      A
GAM2561  TSG      3'  TATATAATTAAACACATCACT  59260       AGTCT_
                                TATGTAAT     CATCACT
                                ||||||||     |||||||
                                ATATATTA     GTAGTGA
                                     ATTTGT
GAM2561  FLJ22655  5'  TGTAATAGTCACAAAGACACT  59261         T  T___
                                TGTAATAGTC CA    CACT
                                |||||||||| ||    ||||
                                ACATTATCAG GT    GTGA
                                      T  TTCT
GAM2561  KIAA1102  3'  CATGTAATAAATAATCGCTAGC 59262         TCTC   A   A
            C                    TATGTAATAG    ATC CTA CC
                                ||||||||||    ||| ||| ||
                                GTACATTATT    TAG GAT GG
                                      TAT_   C   C
GAM2561  MGC14376  3'  ATGAACATCTTATCACTAAC   59263     T    G   C
                                ATG AATA TCT ATCACTAAC
                                ||| |||| ||| |||||||||
                                TAC TTGT AGA TAGTGATTG
                                  _   _   A
GAM2561  LOC143884 3'  ATGTACAGTTGTCACTGACC   59264      A    CTCA    A
                                ATGTA TAGT    TCACT ACC
                                ||||| ||||    ||||| |||
                                TACAT GTCA    AGTGA TGG
                                   _    AC__     C
GAM2562  BACH2    3'  CGTGGCTGGGGCCAACACGG   59267    CA  ACAA  AA_
                                CG  GC    TG   CCAACACGG
                                ||  ||    ||   |||||||||
                                GC  CG    AC   GGTTGTGCC
                                 AC  _____  CCC
GAM2562  NCL      3'  CAGTCAAAACCAACACG     59268     _  CAAT
                                CAG CA    GAACCAACACG
                                ||| ||    ||||||||||
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                                GTC GT    TTTGGTTGTGC
                                  A _____
GAM2562  NEO1     3'  CACAGCACAAAGACACG     59269          T  ACCAA
                                CGCAGCACAA GA     CACG
                                |||||||||| ||     ||||
                                GTGTCGTGTT CT     GTGC
                                      T ______
GAM2562  SLC21A3  3'  GCAGCACACCAACAG       59270        AATGA      C
                                GCAGCAC    ACCAACA G
                                |||||||    ||||||| |
                                CGTCGTG    TGGTTGT C
                                    ______      A
GAM2562  UGCG     5'  CCGCTGCGGCCGCCAACACGG  59271      A  ACAA  AA
                                CCGC GC    TG  CCAACACGG
                                |||| ||    ||  |||||||||
                                GGCG CG    GC  GGTTGTGCC
                                  A  CCG_  __
GAM2562  KIAA1975 5'  GCAGCACACCAACACG      59272        AATGA
                                GCAGCAC    ACCAACACG
                                |||||||    |||||||||
                                CGTCGTG    TGGTTGTGC
                                    ______
GAM2562  MGC3101  3'  GCAGCACAGGAAAACGCGG    59273         AT   CC   A
                                GCAGCACA  GAA  AAC CGG
                                ||||||||  |||  ||| |||
                                CGTCGTGT  CTT  TTG GCC
                                     C_   __   C
GAM2562  MGC3413  3'  GCACAATGTAGCACTAACATGG 59274         A___  C    C
                                GCACAATG    AC AACA GG
                                ||||||||    || |||| ||
                                CGTGTTAC    TG TTGT CC
                                     ATCG  A    A
GAM2562  LOC151568 5'  CCTAGCCAAGGCCAACACGG   59275    GC   A   TGAA
                                CC  AGC CAA    CCAACACGG
                                ||  ||| |||    |||||||||
                                GG  TCG GTT    GGTTGTGCC
                                  A_   _   CC__
GAM2562  LOC152765 5'  GCAGCACAAGACACAC       59276         T  ACCA
                                GCAGCACAA GA    ACAC
                                |||||||| ||    ||||
                                CGTCGTGTT CT    TGTG
                                     _ G___
GAM2562  LOC158314 5'  CCGCAGCACAGTGAAGGGTGG  59277          A    CCAACAC
                                CCGCAGCACA TGAA       GG
                                |||||||||| ||||       ||
                                GGCGTCGTGT ACTT       CC
                                     C    CCCA___
GAM2562  LOC256536 3'  CCGGTGGCAACCAACACG     59278     CA_   CAATGA
                                CCG   GCA     ACCAACACG
                                |||   |||     |||||||||
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                                GGC  CGT     TGGTTGTGC
                                  CAC  _______
GAM2562 LOC57086 3' GCAGCACACCAACAG      59270       AATGA     C
                                GCAGCAC    ACCAACA G
                                |||||||    ||||||| |
                                CGTCGTG    TGGTTGT C
                                    _____      A
GAM2562 LOC91531 5' CAGTACAATCAACACG     59279     C    GAAC
                                CAG ACAAT    CAACACG
                                ||| |||||    |||||||
                                GTC TGTTA    GTTGTGC
                                  A    _____
GAM2563 ABCE1    3' TGATGTTTATTTATCAAATGTC 59282    A   A      CATC
             AA                   C ATGT TATTTATC    GTCAA
                                | |||| ||||||||    |||||
                                A TACA ATAAATAG    CAGTT
                                 C    A       TTTA
GAM2563 DMC1     3' CAATGTATAGTTATCATAAATC 59283        T    CATC
             A                    CAATGTATA TTATC    GTCA
                                |||||||||| |||||    ||||
                                GTTACATAT AATAG    TAGT
                                      C     TATT
GAM2563 PHEMX    3' TGATGTATATTTGACCAC    59284    A       AT
                                C ATGTATATTT  CCAT
                                | ||||||||||  ||||
                                A TACATATAAA  GGTG
                                 C         CT
GAM2563 PHEMX    3' TGATGTATATTTGACCAC    59284    A       AT
                                C ATGTATATTT  CCAT
                                | ||||||||||  ||||
                                A TACATATAAA  GGTG
                                 C         CT
GAM2563 PHEMX    3' TGATGTATATTTGACCAC    59284    A       AT
                                C ATGTATATTT  CCAT
                                | ||||||||||  ||||
                                A TACATATAAA  GGTG
                                 C         CT
GAM2563 PHEMX    3' TGATGTATATTTGACCAC    59284    A       AT
                                C ATGTATATTT  CCAT
                                | ||||||||||  ||||
                                A TACATATAAA  GGTG
                                 C         CT
GAM2563 H-L(3)MBT 3' AATGTATCCCCATCGT      59285       ATTTA
                                AATGTAT    TCCATCGT
                                |||||||    ||||||||
                                TTACATA    GGGTAGCA
                                    G____
GAM2563 KIAA0979 3' CAATGTATGTTGATCCCACC   59286       A  T   _
                                CAATGTAT TT ATCC ATC
                                |||||||| || |||| |||
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                                GTTACATA AA TAGG TGG
                                     C C   G
GAM2563  LOC220672 3'  TGATGTTTATTTATCAAATGTC 59282   A   A      CATC
              AA                  C ATGT TATTTATC   GTCAA
                                  | |||| ||||||||   |||||
                                  A TACA ATAAATAG   CAGTT
                                   C   A      TTTA
GAM2563  LOC257336 5'  AATGTACATTTATTTTTTTCAA 59287           CCATCG
                                  AATGTATATTTAT     TCAA
                                  ||||||||||||     ||||
                                  TTACATGTAAATA     AGTT
                                        AAAAA_
GAM2564  ATP11A   3'  TCTCTCTGCTGTGCATACACGT 59290    C   ATAGAA  _
                                  TC CTC     TG ATACACGT
                                  || |||     || ||||||||
                                  AG GAG     AC TATGTGCA
                                   A  ACGAC_  G
GAM2564  MPHOSPH1  3'  TCATTCTCCATGATACACGTAT 59291     AGA__
                                  TCAT    ATGATACACGTAT
                                  ||||    ||||||||||||
                                  AGTA    TACTATGTGCATA
                                    AGAGG
GAM2564  STAT6    3'  CATAGTCTCATACACGTAT   59292      AATG
                                  CATAG   ATACACGTAT
                                  |||||   ||||||||||
                                  GTATC   TATGTGCATA
                                     AGAG
GAM2564  TLX1     3'  TCTCCCATAGATGCCCATGT   59293    C      A  ATA  C
                                  TC CTCATAGA TG   CA GT
                                  || |||||||| ||   || ||
                                  AG GGGTATCT AC   GT CA
                                   A       _  GG_  A
GAM2564  UBE4A    3'  TCATGGATATGATACCCGT    59294      A  _     A
                                  TCAT GA ATGATAC CGT
                                  |||| || ||||||| |||
                                  AGTA CT TACTATG GCA
                                    C  A      G
GAM2564  DKFZP434E2135 3'  TCCCTCACACCTGCCTATACGT 59295         GAA  A_  C
                                  TCCCTCATA   TG  TA ACGT
                                  |||||||||   ||  || ||||
                                  AGGGAGTGT   AC  AT TGCA
                                       GG_  GG  A
GAM2564  KIAA1344  3'  TCCCTCACAGAATGAGGCCGT  59296            TACA
                                  TCCCTCATAGAATGA    CGT
                                  ||||||||||||||    |||
                                  AGGGAGTGTCTTACT    GCA
                                           CCG_
GAM2564  LOC149703 3'  CTCTTAAAGGATGATACA    59297     A   __
                                  CTC TAGA  ATGATACA
                                  ||| ||||  ||||||||
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                                GAG ATTT  TACTATGT
                                  A   CC
GAM2564  LOC254251 3'  TCATAGAATGCACTGTCGT   59298         A  A__
                                TCATAGAATG TAC   CGT
                                |||||||||| |||   |||
                                AGTATCTTAC GTG   GCA
                                      _  ACA
GAM2565  BACH2    3'  CGTGGCTGGGGCCAACACGG   59267    CA  ACAA  AA_
                                CG  GC   TG   CCAACACGG
                                ||  ||   ||   |||||||||
                                GC  CG   AC   GGTTGTGCC
                                 AC  ____  CCC
GAM2565  NCL      3'  CAGTCAAAACCAACACG     59268     _  CAAT
                                CAG CA   GAACCAACACG
                                ||| ||   ||||||||||
                                GTC GT   TTTGGTTGTGC
                                  A  ____
GAM2565  NEO1     3'  CACAGCACAAAGACACG     59269         T  ACCAA
                                CGCAGCACAA GA    CACG
                                |||||||||| ||    ||||
                                GTGTCGTGTT CT    GTGC
                                      T  _____
GAM2565  SLC21A3  3'  GCAGCACACCAACAG      59270       AATGA     C
                                GCAGCAC    ACCAACA G
                                |||||||    ||||||| |
                                CGTCGTG    TGGTTGT C
                                   _____     A
GAM2565  UGCG     5'  CCGCTGCGGCCGCCAACACGG  59271     A  ACAA  AA
                                CCGC GC   TG  CCAACACGG
                                |||| ||   ||  |||||||||
                                GGCG CG   GC  GGTTGTGCC
                                  A  CCG_  __
GAM2565  KIAA1975 5'  GCAGCACACCAACACG      59272       AATGA
                                GCAGCAC    ACCAACACG
                                |||||||    |||||||||
                                CGTCGTG    TGGTTGTGC
                                   _____
GAM2565  MGC3101  3'  GCAGCACAGGAAAACGCGG   59273       AT   CC   A
                                GCAGCACA  GAA  AAC CGG
                                ||||||||  |||  ||| |||
                                CGTCGTGT  CTT  TTG GCC
                                     C_   __   C
GAM2565  MGC3413  3'  GCACAATGTAGCACTAACATGG 59274       A___  C    C
                                GCACAATG    AC AACA GG
                                ||||||||    || |||| ||
                                CGTGTTAC    TG TTGT CC
                                     ATCG  A    A
GAM2565  LOC151568 5'  CCTAGCCAAGGCCAACACGG   59275    GC   A   TGAA
                                CC  AGC CAA    CCAACACGG
                                ||  ||| |||    |||||||||
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                                GG  TCG GTT    GGTTGTGCC
                                 A_  _   CC__
GAM2565  LOC152765 5'  GCAGCACAAGACACAC      59276         T  ACCA
                                GCAGCACAA GA    ACAC
                                ||||||||| ||    ||||
                                CGTCGTGTT CT    TGTG
                                      _ G___
GAM2565  LOC158314 5'  CCGCAGCACAGTGAAGGGTGG  59277          A    CCAACAC
                                CCGCAGCACA TGAA      GG
                                |||||||||| ||||      ||
                                GGCGTCGTGT ACTT      CC
                                      C    CCCA___
GAM2565  LOC256536 3'  CCGGTGGCAACCAACACG    59278     CA_   CAATGA
                                CCG   GCA     ACCAACACG
                                |||   |||     |||||||||
                                GGC   CGT     TGGTTGTGC
                                  CAC   _______
GAM2565  LOC57086  3'  GCAGCACACCAACAG       59270        AATGA      C
                                GCAGCAC    ACCAACA G
                                |||||||    ||||||| |
                                CGTCGTG    TGGTTGT C
                                     _____      A
GAM2565  LOC91531  5'  CAGTACAATCAACACG      59279     C    GAAC
                                CAG ACAAT    CAACACG
                                ||| |||||    |||||||
                                GTC TGTTA    GTTGTGC
                                  A    _____
GAM2566  NCL       3'  CAGTCAAAACCAACAC      59302     _  CAAT
                                CAG CA    GAACCAACAC
                                ||| ||    ||||||||||
                                GTC GT    TTTGGTTGTG
                                  A  _____
GAM2566  NEO1      3'  CACAGCACAAAGACAC      59303          T  ACCAA
                                CGCAGCACAA GA     CAC
                                |||||||||| ||     |||
                                GTGTCGTGTT CT     GTG
                                      T  ______
GAM2566  POMZP3    5'  CCGCAGCAGGCACGAGGTACAG 59304         CA_    ACCAAC
                                CCGCAGCA   ATGA     ACAG
                                ||||||||   ||||     ||||
                                GGCGTCGT   TGCT     TGTC
                                     CCG    CCA___
GAM2566  SRM       5'  CCGCAGCACAACGGGACCA    59305           A_
                                CCGCAGCACAATG  ACCA
                                ||||||||||||  ||||
                                GGCGTCGTGTTGC  TGGT
                                        CC
GAM2566  USH3A     5'  GCAGGAATGAGCCAGTGCAG   59306      CAC    A   ACA
                                GCAG   AATGA CCA   CAG
                                ||||   ||||| |||   |||
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                                CGTC   TTACT GGT   GTC
                                  C__    C   CAC
GAM2566 ATP6V1B2 3' GCAGCACAGCCCAGCAATACAG 59307        ATGAAC   C
                                GCAGCACA     CAA ACAG
                                ||||||||     ||| ||||
                                CGTCGTGT     GTT TGTC
                                     CGGGTC   A
GAM2566 DKFZP434P1750 3' ACACAATTACAACACAG     59308       GAAC
                                GCACAAT    CAACACAG
                                |||||||    ||||||||
                                TGTGTTA    GTTGTGTC
                                   AT__
GAM2566 HEMK     3' CCACAGCAATTTCACCAACACA 59309        CAATGA
              G                  CCGCAGCA     ACCAACACAG
                                 ||||||||     ||||||||||
                                 GGTGTCGT     TGGTTGTGTC
                                      TAAAG_
GAM2566 ITPK1    3' CACAGCACAAATCCTCAGCACA 59310         TGAAC  A
              G                  CGCAGCACAA     CA CACAG
                                 ||||||||||     || |||||
                                 GTGTCGTGTT     GT GTGTC
                                       TAGGA  C
GAM2566 KIAA0229 3' CCGCAGCACAGTGTGGTTCCTC 59311          A  AACCAACA
              AG                   CCGCAGCACA TG       CAG
                                   |||||||||| ||       |||
                                   GGCGTCGTGT AC       GTC
                                        C  ACCAAGGA
GAM2566 KIAA0298 3' GCAGCACAAGGACAATACCA   59312        T  ____
                                GCAGCACAA GA    ACCA
                                |||||||||  ||    ||||
                                CGTCGTGTT CT    TGGT
                                     C  GTTA
GAM2566 KIAA0940 3' CACAGCACAGAAAACACA    59313        AT   CC
                                CGCAGCACA  GAA  AACACA
                                |||||||||  |||  ||||||
                                GTGTCGTGT  CTT  TTGTGT
                                     __  __
GAM2566 KIAA1975 5' GCAGCACACCAACAC       59314       AATGA
                                GCAGCAC    ACCAACAC
                                |||||||    ||||||||
                                CGTCGTG    TGGTTGTG
                                     _____
GAM2566 LGALS12  5' GCAGCACATGGCCATTGCAG   59315        A  AA   ACA
                                GCAGCACA TG  CCA   CAG
                                |||||||| ||  |||   |||
                                CGTCGTGT AC  GGT   GTC
                                     _ C_   AAC
GAM2566 NYD-SP11 3' CCTAGTGCACCAACACA     59316    GC  CACAA  A
                                CC  AG    TG ACCAACACA
                                ||  ||    || |||||||||
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                                GG  TC    AC TGGTTGTGT
                                 A_ _____  G
GAM2566  PELI1    5'  ACAGTACAATGAAATACA    59317     C      CCA
                                GCAG ACAATGAA   ACA
                                |||| ||||||||   |||
                                TGTC TGTTACTT   TGT
                                  A       TA_
GAM2566  PHYHIP   3'  CCACAGCAATGCTGTCAGCACA 59318        CA   AAC_  A
              G                  CCGCAGCA  ATG    CA CACAG
                                |||||||| |||    || |||||
                                GGTGTCGT  TAC    GT GTGTC
                                     __  GACA  C
GAM2566  PLU-1    3'  CAGCCACTGAAACCAACA    59319     A  A   _
                                CAGC CA TGAA CCAACA
                                |||| || |||| ||||||
                                GTCG GT ACTT GGTTGT
                                  _ G   T
GAM2566  PLU-1    3'  CAGCCACTGAAACCAACA    59319     A  A   _
                                CAGC CA TGAA CCAACA
                                |||| || |||| ||||||
                                GTCG GT ACTT GGTTGT
                                  _ G   T
GAM2566  SDF1     3'  CCACAGCACAAACACGTGGCAC 59320          TGA  CAA_
              AG                  CCGCAGCACAA   AC    CACAG
                                ||||||||||   ||   |||||
                                GGTGTCGTGTT   TG    GTGTC
                                      TG_  CACC
GAM2566  LOC150498 3'  GCACAGAGACAACACAG     59321      AT  AC
                                GCACA  GA  CAACACAG
                                |||||  ||  ||||||||
                                CGTGT  CT  GTTGTGTC
                                  __  CT
GAM2566  LOC152765 5'  GCAGCACAAGACACAC      59276         T  ACCA
                                GCAGCACAA GA    ACAC
                                ||||||||| ||    ||||
                                CGTCGTGTT CT    TGTG
                                     _ G___
GAM2566  LOC158308 3'  CCGCAGCACTGAGCAC      59322         AA   ACCAA
                                CCGCAGCAC  TGA    CAC
                                |||||||||  |||    |||
                                GGCGTCGTG  ACT    GTG
                                     __  C____
GAM2566  LOC164386 5'  CCCCAGCTCAGTCAACACA   59323    G   A  ATGAAC
                                CC CAGC CA     CAACACA
                                || |||| ||     |||||||
                                GG GTCG GT     GTTGTGT
                                 G   A  CA____
GAM2566  LOC201617 5'  GCACAATGCCTGGCACAG    59324        AA  AA_
                                GCACAATG  CC   CACAG
                                ||||||||  ||   |||||
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                                CGTGTTAC  GG   GTGTC
                                    __  ACC
GAM2566  LOC255096 5'  CCCCAGCAATGAACTGACACAG 59325    G    CA     CA
                                CC CAGCA  ATGAAC  ACACAG
                                || |||||  ||||||  ||||||
                                GG GTCGT  TACTTG  TGTGTC
                                 G    __     AC
GAM2566  LOC51279  3'  GCAGCACACTGGGAAGAGCACA 59326        AT__   CCAA
            G                    GCAGCACA   GAA   CACAG
                                ||||||||   |||   |||||
                                CGTCGTGT   CTT   GTGTC
                                    GACC   CTC_
GAM2567  BTG3     3'  CAACATGACACCAACAC     59329      CAA   _
                                CAACA   TGA ACCAACAC
                                |||||   ||| ||||||||
                                GTTGT   ACT TGGTTGTG
                                   ___  G
GAM2567  JPH3     5'  TCCCGCAAACGGTGAAAAC    59330        C  AA   CC
                                TCCCGCAA AC  TGAA  AAC
                                |||||||| ||  ||||  |||
                                AGGGCGTT TG  ACTT  TTG
                                    _ CC   __
GAM2567  DKFZP566I1024 3'  TCCCACAATGCAATGCTTCAC  59331        CA    AACCA
                                TCCCGCAA  CAATG    AC
                                ||||||||  |||||    ||
                                AGGGTGTT  GTTAC    TG
                                    AC    GAAG_
GAM2567  IMAGE:4907098 3'  TCCCGAACACAATTCTACA   59332      C      GAACCA
                                TCCCG AACACAAT     ACA
                                ||||| ||||||||     |||
                                AGGGC TTGTGTTA     TGT
                                   _      AGA___
GAM2567  LOC152100 5'  TCCCGCAACAGAAAC      59333         CAAT   CCA
                                TCCCGCAACA   GAA   AC
                                ||||||||||   |||   ||
                                AGGGCGTTGT   CTT   TG
                                     ____   ___
GAM2567  LOC160786 5'  TCTTCAACCACCTGACCAACAC 59334    CCG    A  A_   A
                                TC   CAAC CA  TGA CCAACAC
                                ||   |||| ||  ||| |||||||
                                AG   GTTG GT  ACT GGTTGTG
                                 AA_    _ GG   _
GAM2567  LOC255096 5'  CCCCCCAGCAATGAACTGACAC 59335     G  ACA      CA
                                TCCC CA   CAATGAAC  ACAC
                                |||| ||   ||||||||  ||||
                                GGGG GT   GTTACTTG  TGTG
                                  G  C__       AC
GAM2568  CDC7L1   3'  TACCTCATAACAGTAAAC    59338         AA   AAA
                                TACCTCATA  ACA   AAGC
                                |||||||||  |||   ||||
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                                ATGGAGTAT  TGT   TTTG
                                    __   CA_
GAM2568  DLG5     3'  TACCTGTAAAACAAAGGACAGC 59339      CA       AA__
                                TACCT  TAAAACAAA    AGC
                                |||||  |||||||||    |||
                                ATGGA  ATTTTGTTT    TCG
                                   C_       CCTG
GAM2568  PDCL     3'  TACCTTGTTAAAACAAAAA   59340      CA_
                                TACCT   TAAAACAAAAA
                                |||||   ||||||||||
                                ATGGA   ATTTTGTTTTT
                                   ACA
GAM2568  RP2      3'  TCATAAATTCAAAAGCTAT   59341       ACAA
                                TCATAAA    AAAAGCTAT
                                |||||||    |||||||||
                                AGTATTT    TTTTCGATA
                                    AAG_
GAM2568  AK5      3'  TACCATCATCTTGGGAAAGCTA 59342      _   AAAACAAA
              T                  TACC TCAT       AAAGCTAT
                                 |||| ||||       ||||||||
                                 ATGG AGTA       TTTCGATA
                                   T   GAACCC__
GAM2568  AND-1    3'  TACCTCAAAAAAATCCAGGCTA 59343       T    CAAAAAA
              T                  TACCTCA AAAA      GCTAT
                                 ||||||| ||||      |||||
                                 ATGGAGT TTTT      CGATA
                                    T   TAGGTC_
GAM2568  C22orf4  3'  CTCAGAAAACAAAGGCT     59344      T      AAA
                                CTCA AAAACAAA   GCT
                                |||| ||||||||   |||
                                GAGT TTTTGTTT   CGA
                                  C       C__
GAM2568  KIAA0161 3'  CACCTCCAGAAAAGCT      59345       ATAAAA  A
                                TACCTC     CA AAAAGCT
                                ||||||     || |||||||
                                GTGGAG     GT TTTTCGA
                                   _______ C
GAM2568  KIAA0476 3'  ACCTCATAAGCAAGGGGGCT  59346        AA   AAAA
                                ACCTCATAA  CAA    GCT
                                |||||||||  |||    |||
                                TGGAGTATT  GTT    CGA
                                    C_   CCCC
GAM2568  KIAA0789 5'  TACCTCATGGGAACAGAAGCT  59347       AA_   AAA
                                TACCTCAT   AACA   AAGCT
                                ||||||||   ||||   |||||
                                ATGGAGTA   TTGT   TTCGA
                                    CCC    C__
GAM2568  KIAA1795 3'  TCACAAAACAATAATGGCTAT  59348         AAAA_
                                TCATAAAACAA    GCTAT
                                ||||||||||     |||||
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                                AGTGTTTTGTT    CGATA
                                      ATTAC
GAM2568 LEPROTL1 3' ACTTCATAAAACAACAGACAGC 59349    C        AAA__
             T                   AC TCATAAAACAA    AGCT
                                 || |||||||||||    ||||
                                 TG AGTATTTTGTT    TCGA
                                  A         GTCTG
GAM2568 NEDD5    3' CACCTCTAAAAAAGCT      59350       ATAAAAC
                                 TACCTC      AAAAAAGCT
                                 ||||||      |||||||||
                                 GTGGAG      TTTTTTCGA
                                    A_______
GAM2568 pcnp     3' CCCATAAGGAAAAAAGCT    59351        AAC
                                 CTCATAA   AAAAAAGCT
                                 |||||||   |||||||||
                                 GGGTATT   TTTTTTCGA
                                     CC_
GAM2568 RYK      3' TCATAAAACCAAAGAACT    59352         A  A
                                 TCATAAAAC AAA AGCT
                                 ||||||||| ||| ||||
                                 AGTATTTTG TTT TTGA
                                       G  C
GAM2568 LOC139420 3' TACCTCTAGAACAAAACTAC  59353       A  A      AA
                                 TACCTC TA AACAAAA  GC
                                 |||||| || |||||||  ||
                                 ATGGAG AT TTGTTTT  TG
                                    _ C      GA
GAM2568 LOC145815 5' TACCTACATAAAACAAAAA   59354      _
                                 TACCT CATAAAACAAAAA
                                 ||||| ||||||||||||
                                 ATGGA GTATTTTGTTTTT
                                    T
GAM2568 LOC149721 5' CCTCATAAAACAGGCC      59355           AAAAA
                                 CCTCATAAAACA    GCT
                                 ||||||||||||    |||
                                 GGAGTATTTTGT    CGG
                                       C____
GAM2568 LOC151234 3' CCTCAAACAGGAAAGCTAT   59356      TAA   AA
                                 CCTCA   AACA  AAAGCTAT
                                 |||||   ||||  ||||||||
                                 GGAGT   TTGT  TTTCGATA
                                    ___   CC
GAM2569 KIAA1449  3' TGCGATCAGAGTATCTTAAATA 59359         _    GCT
                                 TGCGATCAGA TATTT   AATA
                                 |||||||||| |||||   ||||
                                 ACGCTAGTCT ATAGA   TTAT
                                       C    AT_
GAM2570 NDRG2    5' TTGGCTGGATGCAGTGGG    59362        C  A   AATATA
                                 TTGGCTGG AT CGG     GG
                                 |||||||| || |||     ||
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                                AACCGACC TA GTC     CC
                                     _ C   AC____
GAM2570 PLXNA2   3' TTGGCTGGCGTAGGGAGAGGA 59363        A C   ATAT
                                TTGGCTGGC TA GGA    AGGA
                                ||||||||| || |||    ||||
                                AACCGACCG AT CCT    TCCT
                                     C C   C___
GAM2570 DKFZP566J091 3' CTGGCTGGTATGACCCATGGGA 59364        CA  C  AA   A
                                TTGGCTGG  TA GG  TAT GGA
                                ||||||||  || ||  ||| |||
                                GACCGACC  AT CT  GTA CCT
                                     __ A  GG   C
GAM2570 GFR      3' TTGGCTGGTAGTTGGATTATAG 59365        CATAC   A
             GA                   TTGGCTGG    GGA TATAGGA
                                ||||||||    ||| |||||||
                                AACCGACC    CCT ATATCCT
                                     ATCAA   A
GAM2570 MGC12981 3' TTAGCTGGCGTGGGGTAGG   59366        ATAC  AATA
                                TTGGCTGGC   GG   TAGG
                                |||||||||   ||   ||||
                                AATCGACCG   CC   ATCC
                                     CACC  ____
GAM2570 MGC18257 3' TTGGCTGCCAAATATAGG    59367       G  TACGG
                                TTGGCTG CA    AATATAGG
                                ||||||| ||    ||||||||
                                AACCGAC GT    TTATATCC
                                     G _____
GAM2570 PTPRT    3' TTGGCTAGTAGAATGTAGG   59368        CATAC    A
                                TTGGCTGG    GGAAT TAGG
                                ||||||||    ||||| ||||
                                AACCGATC    TCTTA ATCC
                                     A____    C
GAM2570 UPLC1    3' TTGGCTGGGGAATATAGG    59369        CATAC
                                TTGGCTGG    GGAATATAGG
                                ||||||||    ||||||||||
                                AACCGACC    CCTTATATCC
                                     _____
GAM2570 LOC145195 3' TGGCTGGCCTAATGTAGG    59370        ATACGG   A
                                TGGCTGGC     AAT TAGG
                                ||||||||     ||| ||||
                                ACCGACCG     TTA ATCC
                                     GA____   C
GAM2570 LOC149606 3' TTGGCTGGCACATGGTGGTGGG 59371          C  AATATA
             A                    TTGGCTGGCATA GG     GGA
                                ||||||||||||| ||     |||
                                AACCGACCGTGT CC     CCT
                                       A  ACCAC_
GAM2571 C8orf6   3' TGTATGTGGTGAGGAAAGCGGG 59374      A_  C  __
                                TGTAT  GG GA  AAAGCGGG
                                |||||  || ||  ||||||||
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                                ACATA  CC CT  TTTCGCCC
                                   CA  A  CC
GAM2571  EIF4B    3'  ACATGTATTCAGGAGCGG    59375        __  CGAAA
                                GCATGTAT  AGG    AGCGG
                                ||||||||  |||    |||||
                                TGTACATA  TCC    TCGCC
                                    AG  _____
GAM2571  FLJ12800 3'  TAGCATGTAAGGTAGTGG    59376        T  CGAAA  C
                                TAGCATGTA AGG    AG GG
                                |||||||||  |||    || ||
                                ATCGTACAT TCC    TC CC
                                     _  A____  A
GAM2571  TNRC6    3'  TAGCATGTATGGCGCTATTTGG 59377         A   AAAAGC
           G                     TAGCATGTAT GGCG     GGG
                                ||||||||||  ||||     |||
                                ATCGTACATA CCGC     CCC
                                     _   GATAAA
GAM2571  UBE4B    3'  ATGTACAGGAAGCGG      59378        CGAA
                                ATGTATAGG   AAGCGG
                                |||||||||   ||||||
                                TACATGTCC   TTCGCC
                                     ____
GAM2571  LOC91010 3'  ACATGTACAAAAAAGTGG    59379        GGC    C
                                GCATGTATA   GAAAAG GG
                                |||||||||   |||||| ||
                                TGTACATGT   TTTTTC CC
                                     ___     A
GAM2572  CHC1L    3'  AATGACTCCAAGTAAAAAGA   59382      ATAA
                                AATGATT   GAGTAAAAAGA
                                |||||||   ||||||||||
                                TTACTGA   TTCATTTTTCT
                                    GG__
GAM2572  DMD      3'  AATGATTTAAAAATCAAAAAGA 59383      A    _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                     _     G
GAM2572  DMD      3'  AATGATTTAAAAATCAAAAAGA 59383      A    _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                     _     G
GAM2572  DMD      3'  AATGATTTAAAAATCAAAAAGA 59383      A    _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                     _     G
GAM2572  DMD      3'  AATGATTTAAAAATCAAAAAGA 59383      A    _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
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                                TTACTAA ATTTTTA TTTTTCT
                                   _     G
GAM2572  DMD     3'  AATGATTTAAAAATCAAAAAGA 59383       A     _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                   _     G
GAM2572  DMD     3'  AATGATTTAAAAATCAAAAAGA 59383       A     _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                   _     G
GAM2572  DMD     3'  AATGATTTAAAAATCAAAAAGA 59383       A     _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                   _     G
GAM2572  DMD     3'  AATGATTTAAAAATCAAAAAGA 59383       A     _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                   _     G
GAM2572  DMD     3'  AATGATTTAAAAATCAAAAAGA 59383       A     _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                   _     G
GAM2572  DMD     3'  AATGATTTAAAAATCAAAAAGA 59383       A     _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                   _     G
GAM2572  DMD     3'  AATGATTTAAAAATCAAAAAGA 59383       A     _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                   _     G
GAM2572  DMD     3'  AATGATTTAAAAATCAAAAAGA 59383       A     _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                   _     G
GAM2572  DMD     3'  AATGATTTAAAAATCAAAAAGA 59383       A     _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                   _     G
GAM2572  GABPB1  3'  AATGACCTACAGAGTAAA    59384       ATA
                                AATGATT   AGAGTAAA
                                |||||||   ||||||||
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                                TTACTGG   TCTCATTT
                                   ATG
GAM2572  HSPA8    5'  TAAATGATCATGAAACCAAAAA 59385          A   G
                GA                   TAAATGATTAT AGA TAAAAAGA
                                     |||||||||||  ||| ||||||||
                                     ATTTACTAGTA TTT GTTTTTCT
                                           C   G
GAM2572  CMAS     3'  TAAATAATTATCTTGCGTAAAG 59386          AAGA_    A
                AGA                    TAAATGATTAT    GTAAA AGA
                                     ||||||||||     ||||| |||
                                     ATTTATTAATA    CATTT TCT
                                           GAACG    C
GAM2572  FLJ23560 3'  GATACAGGAGAGTAAAAAG   59387    _ TA
                                     GAT TA  AGAGTAAAAAG
                                     ||| ||  ||||||||||
                                     CTA GT  TCTCATTTTTC
                                       T  CC
GAM2572  HEMK     3'  TGACTAAGAGTAAAGAG     59388     TA       A
                                     TGAT  TAAGAGTAAA AG
                                     ||||  |||||||||| ||
                                     ACTG  ATTCTCATTT TC
                                       __        C
GAM2572  KIAA1223 3'  TGATTTAAGAGTAAGGAG    59389      A       AA
                                     TGATT TAAGAGTAA  AG
                                     ||||| |||||||||  ||
                                     ACTAA ATTCTCATT  TC
                                       _       CC
GAM2572  KIAA1726 3'  AATGATTATAGCACAAAG    59390        AAG   A
                                     AATGATTAT   AGTA AAAG
                                     |||||||||   |||| ||||
                                     TTACTAATA   TCGT TTTC
                                           ___   G
GAM2572  NUP133   3'  GACCACGTGAGAGTAAAAAGA  59391       A__
                                     GATTAT   AGAGTAAAAAGA
                                     ||||||   ||||||||||||
                                     CTGGTG   TCTCATTTTTCT
                                        CAC
GAM2572  PRRG1    3'  AAATGATTAGAGTAAAAAGA   59392        ATA
                                     AAATGATT   AGAGTAAAAAGA
                                     ||||||||   ||||||||||||
                                     TTTACTAA   TCTCATTTTTCT
                                           ___
GAM2572  SSH2     3'  GATTATAAAAGTCTGAAGA   59393          AAA
                                     GATTATAAGAGT   AAGA
                                     ||||||||||||   ||||
                                     CTAATATTTTCA   TTCT
                                           GAC
GAM2572  LOC92096 3'  ATTATAAGATGTCAAAAAGA   59394         _ _
                                     ATTATAAGA GT AAAAAGA
                                     |||||||||  || |||||||
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                                TAATATTCT CA TTTTTCT
                                     A  G
GAM2573 ABH     3' TCTCTGTTTTTGGCTTGTCTG 59397    C   CTCTA
                                TC CTGT    GTTTGTCTG
                                || ||||    |||||||||
                                AG GACA    CGAACAGAC
                                 A   AAAAC
GAM2573 CBFA2T2  3' CCTTGTTTCTAGTTCAGTTC  59398    C  C      TCT
                                CC TGT TCTAGTTTG  GTTC
                                || ||| |||||||||  ||||
                                GG ACA AGATCAAGT  CAAG
                                 A  A      ___
GAM2573 COL4A3   3' CTGTCTCTGGGTCATGTT    59399       AGTTT  _
                                CTGTCTCT    GTC TGTT
                                ||||||||    ||| ||||
                                GACAGAGA    CAG ACAA
                                     CC___  T
GAM2573 COL4A3   3' CTGTCTCTGGGTCATGTT    59399       AGTTT  _
                                CTGTCTCT    GTC TGTT
                                ||||||||    ||| ||||
                                GACAGAGA    CAG ACAA
                                     CC___  T
GAM2573 COL4A3   3' CTGTCTCTGGGTCATGTT    59399       AGTTT  _
                                CTGTCTCT    GTC TGTT
                                ||||||||    ||| ||||
                                GACAGAGA    CAG ACAA
                                     CC___  T
GAM2573 F7      3' TCTCTGTCTCTGTCTCTCTCTG 59400    C      AG_  G
           TT                    TC CTGTCTCT   TTT TCTGTT
                                || ||||||||  ||| ||||||
                                AG GACAGAGA  AGA AGACAA
                                 A       CAG  G
GAM2573 F7      3' TCTCTGTCTCTGTCTCTCTCTG 59400    C      AG_  G
           TT                    TC CTGTCTCT   TTT TCTGTT
                                || ||||||||  ||| ||||||
                                AG GACAGAGA  AGA AGACAA
                                 A       CAG  G
GAM2573 HDAC4    3' CCTGTTTCTGTCCAGTTTTGTT 59401      C____      GTC
                                CCTGT    TCTAGTTT  TGTT
                                |||||    ||||||||  ||||
                                GGACA    AGGTCAAA  ACAA
                                   AAGAC      ___
GAM2573 MEN1     5' TGTTTGTTAGTTTGTCTGTT  59402     CTC_
                                TGT   TAGTTTGTCTGTT
                                |||   ||||||||||||
                                ACA   ATCAAACAGACAA
                                  AACA
GAM2573 NKX3A    3' TCACTGTCTCTGTTGT      59403    C      A  T
                                TC CTGTCTCT GTT GT
                                || |||||||| ||| ||
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                                AG GACAGAGA CAA CA
                                 T      _  _
GAM2573  PDCD2    3'  TCCCTGTCACTGGACACTTTTG 59404        T  AG_____
              T                   TCCCTGTC CT      TTTGT
                                  |||||||| ||      |||||
                                  AGGGACAG GA      AAACA
                                       T  CCTGTGA
GAM2573  PDE4D    3'  TCCTTGTCTGTAATTTGT    59405     C    C
                                  TCC TGTCT TAGTTTGT
                                  ||| ||||| ||||||||
                                  AGG ACAGA ATTAAACA
                                    A    C
GAM2573  SLC2A4   3'  TCTCTGCTCTGGTTTGTC    59406    C  T   A
                                  TC CTG CTCT GTTTGTC
                                  || ||| |||| |||||||
                                  AG GAC GAGA CAAACAG
                                   A  _   C
GAM2573  CLSTN3   3'  TCCCATGTCTGGAGTGTCTGTT 59407     _    CT   TT
                                  TCCC TGTCT  AGT  GTCTGTT
                                  |||| |||||  |||  |||||||
                                  AGGG ACAGA  TCA  CAGACAA
                                    T    CC  __
GAM2573  FLJ12684 3'  TGTCTGCAGCTGCTGTTTGTTC 59408      C    __  C
                                  TGTCT TAGTT  TGT TGTTC
                                  ||||| |||||  ||| |||||
                                  ACAGA GTCGA  ACA ACAAG
                                     C    CG   A
GAM2573  FLJ20208 3'  TCCCTGTCTTGGCTAGACCTGT 59409         ___   TTTG
              T                   TCCCTGTCT   CTAG   TCTGTT
                                  |||||||||   ||||   ||||||
                                  AGGGACAGA   GATC   GGACAA
                                       ACC   T___
GAM2573  FLJ33069 5'  TGTTCTCTTGTCTGTT     59410    _   AGTT
                                  TGT CTCT   TGTCTGTT
                                  ||| ||||   ||||||||
                                  ACA GAGA   ACAGACAA
                                    A   ____
GAM2573  FREQ     3'  TCTTTTAAAACGTCTGTTC   59411    C_  TT
                                  TCT  TAG  TGTCTGTTC
                                  |||  |||  |||||||||
                                  AGA  ATT  GCAGACAAG
                                    AA   TT
GAM2573  KIAA0143 3'  CCTTACTTTTGTCTGTT    59412    GTCT  AG
                                  CCT   CT  TTTGTCTGTT
                                  |||   ||  ||||||||||
                                  GGA   GA  AAACAGACAA
                                    AT__  __
GAM2573  KIAA0595 3'  CTCTCTCTAGTTGATGTT   59413    G       T TC
                                  CT TCTCTAGTT G  TGTT
                                  || |||||||| |  ||||
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                                GA AGAGATCAA C  ACAA
                                 G       _ T_
GAM2573 KIAA0935 3' TCCCTGTCCTGGGTCTGTT   59414       T  AGTTT
                                TCCCTGTC CT    GTCTGTT
                                |||||||| ||    |||||||
                                AGGGACAG GA    CAGACAA
                                     _ CC___
GAM2573 KIAA1904 3' CCGTCTCTGCACTTCTGTTC  59415       A  TTG
                                CTGTCTCT GT   TCTGTTC
                                |||||||| ||   |||||||
                                GGCAGAGA CG   AGACAAG
                                     _ TGA
GAM2573 LGI4    5' TCTCTCTTTCTGCCTGTT    59416      AG_
                                TCTCT   TTTGTCTGTT
                                |||||   ||||||||||
                                AGAGA   AGACGGACAA
                                   GAA
GAM2573 MGC12904 3' TCCCTGTCTCCAGGGTTTGTT 59417          TTT  C
                                TCCCTGTCTCTAG   GT TGTT
                                ||||||||||||   || ||||
                                AGGGACAGAGGTC   CA ACAA
                                       C__  A
GAM2573 PFTK1    3' TCCCTGTCTTTGTTCTTAACGT 59418        CTA   GTC_
             T                   TCCCTGTCT   GTTT   TGTT
                                |||||||||   ||||   ||||
                                AGGGACAGA   CAAG   GCAA
                                     AA_   AATT
GAM2573 PRO2949  5' TCCTTAGTTTTTGCCTGTT   59419    TC    __
                                TC  TAGTT  TGTCTGTT
                                ||  |||||  ||||||||
                                AG  ATCAA  ACGGACAA
                                 GA    AA
GAM2573 RIP60    5' TCCCTGTGTCTGCTGT     59420       CTCTA    T
                                TCCCTGT    GTTTG CTGT
                                |||||||    ||||| ||||
                                AGGGACA    CAGAC GACA
                                     _____   _
GAM2573 SERPINB7 5' CCTTTCTCTAGGTGATCTGTTC 59421    G     TTT
                                CCT TCTCTAG   GTCTGTTC
                                ||| |||||||   ||||||||
                                GGA AGAGATC   TAGACAAG
                                  A      CAC
GAM2573 SRPK2    5' CTTCTCTAATCCCTTTTGTTC  59422    G       GTC_
                                CT TCTCTAGTTT   TGTTC
                                || ||||||||||   |||||
                                GA AGAGATTAGG   ACAAG
                                 _       GAAA
GAM2573 ZNF-U69274 3' CCAAATCTAGTTTGTTTGTTC  59423    TGTC       C
                                CC   TCTAGTTTGT TGTTC
                                ||   |||||||||| |||||
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                                GG    AGATCAAACA ACAAG
                                 TTT_         A
GAM2573  LOC161357 3'  ATCTTTGGTAGTTTGTTTGTTC 59424      C___       C
                                GTCT    TAGTTTGT TGTTC
                                ||||    |||||||| |||||
                                TAGA    ATCAAACA ACAAG
                                  AACC       A
GAM2573  LOC199923 3'  TCCCTGCCGCTTTTTGTTTGTT 59425         T  AG    C
                                TCCCTGTC CT  TTTGT TGTT
                                |||||||| ||  ||||| ||||
                                AGGGACGG GA  AAACA ACAA
                                     C  A_    A
GAM2573  LOC221632 3'  CCTTCTTCTGTCTGTT      59426     G   CTAG
                                CCT TCT    TTTGTCTGTT
                                ||| |||    ||||||||||
                                GGA AGA    AGACAGACAA
                                 _  _____
GAM2573  LOC254873 3'  TCTCTGCTCTGGTTTGTC    59406    C   T    A
                                TC CTG CTCT GTTTGTC
                                || ||| |||| |||||||
                                AG GAC GAGA CAAACAG
                                 A   _    C
GAM2573  LOC256979 5'  TCCCAGTTTCTAAATTTGT    59427      T  C    _
                                TCCC GT TCTAG TTTGT
                                |||| || ||||| |||||
                                AGGG CA AGATT AAACA
                                  T  A    T
GAM2573  LOC54505  5'  TCTTTGCTCTAGTTTGT     59428    CC  T
                                TC  TG CTCTAGTTTGT
                                ||  || ||||||||||
                                AG  AC GAGATCAAACA
                                 AA  _
GAM2574  AXIN1     3'  GCTGGAGGCAGGTGCAGTGCT  59431     AAA_  __
                                GCT    GCA  TGCAGTGCT
                                |||    |||  |||||||||
                                CGA    CGT  ACGTCACGA
                                  CCTC   CC
GAM2574  B3GALT2   5'  GCCAGAGCTAAAATGTAGTGCT 59432      A      GC   C
                                GCTA AGCTAAA  ATG AGTGCT
                                |||| |||||||  ||| ||||||
                                CGGT TCGATTT  TAC TCACGA
                                  C       __   A
GAM2574  EGFL5     5'  AGCTAAAGCTGAAGTGCT     59433         A  C
                                AGCTAAAGC TG AGTGCT
                                ||||||||| || ||||||
                                TCGATTTCG AC TCACGA
                                      _ T
GAM2574  KCNAB1    5'  GCAAAGCTAATTGCACGGTGCT 59434    T       A_    CA
                                GC AAAGCTAA  GCATG  GTGCT
                                || ||||||||  |||||  |||||
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                                CG TTTCGATT  CGTGC  CACGA
                                 _      AA    __
GAM2574  MSN      5'  GCTAGGACTGTCGGGCAGTGCT 59435      AA   AAAGCAT
                                GCTA  GCT      GCAGTGCT
                                ||||  |||      ||||||||
                                CGAT  TGA      CGTCACGA
                                  CC   CAGCC__
GAM2574  NAV2     3'  GCTGAGACTAAAGCAGGGATAG 59436     AAA       TGC__
             TG                   GCT   GCTAAAGCA    AGTG
                                |||   |||||||||    ||||
                                CGA   TGATTTCGT    TCAC
                                  CTC       CCCTA
GAM2574  SLC2A6   3'  GCTGTGGCTGGACAGCAGTGCT 59437     AAA   AAA   T
                                GCT   GCT   GCA GCAGTGCT
                                |||   |||   ||| ||||||||
                                CGA   CGA   TGT CGTCACGA
                                  CAC   CC_   _
GAM2574  ATP9A    3'  GCTAAATTAAAGCATAC     59438       GC
                                GCTAAA  TAAAGCATGC
                                ||||||  ||||||||||
                                CGATTT  ATTTCGTATG
                                   A_
GAM2574  DKFZP434G1411 5'  GCTGGTAGCTGAGGCAGTGCT  59439     AA_   AA  CAT
                                GCT   AGCT  AG   GCAGTGCT
                                |||   ||||  ||   ||||||||
                                CGA   TCGA  TC   CGTCACGA
                                  CCA    C_  ____
GAM2574  FLJ20139  3'  ACTAAAGCTAAGGCTGGCTGT  59440          A  AT  A
                                GCTAAAGCTAA GC  GC GT
                                |||||||||||  ||  || ||
                                TGATTTCGATT CG  CG CA
                                      C  AC  A
GAM2574  KIAA1016  5'  GCTCGGGCTGAGTGCCGCAGTG 59441     AAA   AAA_  A
             CT                   GCT   GCT    GC TGCAGTGCT
                                |||   |||    || |||||||||
                                CGA   CGA    CG GCGTCACGA
                                  GCC   CTCA  _
GAM2574  PADI5    3'  GCAGAACTGAGTGTGCAGTGCT 59442    TAA    AA  CA
                                GC   AGCT  AG  TGCAGTGCT
                                ||   ||||  ||  |||||||||
                                CG   TTGA  TC  ACGTCACGA
                                 TC_    C_  AC
GAM2574  PTPNS1   3'  GCTAAAGCTAAAGCTATACA   59443           _
                                GCTAAAGCTAAAGC ATGCA
                                ||||||||||||| |||||
                                CGATTTCGATTTCG TATGT
                                         A
GAM2574  ZDHHC5   5'  GCTAAAGCTGGACAACAGC    59444         AAA   T
                                GCTAAAGCT   GCA GCAGT
                                |||||||||   ||| |||||
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                                CGATTTCGA   TGT TGTCG
                                     CC_  _
GAM2574  LOC150208 3'  GCTGAGCTGAGGCAGCAGTGCT 59445     AA   AAA  T
                                GCT  AGCT   GCA GCAGTGCT
                                |||  ||||   ||| ||||||||
                                CGA  TCGA   CGT CGTCACGA
                                  C_   CTC  _
GAM2574  LOC151516 5'  GCTGGGGCAGAGGCAGGCAGTG 59446     AAA  TAAA  T
             CT                   GCT   GC   GCA GCAGTGCT
                                |||   ||   ||| ||||||||
                                CGA   CG   CGT CGTCACGA
                                  CCC  TCTC  C
GAM2575  KIAA1340  3'  TATGTCAAGGGACCTAAA    59449        A__
                                TATGTCAG   ACCTAAA
                                ||||||||   |||||||
                                ATACAGTT   TGGATTT
                                     CCC
GAM2575  KIAA1450  3'  TATGTCAAGTAAACCTAA    59450        ___
                                TATGTCA   GAACCTAA
                                |||||||   ||||||||
                                ATACAGT   TTTGGATT
                                    TCA
GAM2576  ASTN     3'  TGCATTGTGTGTGCACACGTGT 59453         _ TTTGT
             G                   TGCATTGTG GT    TGTGTG
                                |||||||||  ||    ||||||
                                ACGTAACAC CA    GCACAC
                                     A  CGTGT
GAM2576  PCP4     3'  TATGCGTGTGTGGATTGTGTG  59454      AT_    TTTT
                                TATGC   TGTGG   GTTGTGTG
                                |||||   |||||   ||||||||
                                ATACG   ACACC   TAACACAC
                                   CAC    _____
GAM2576  BRAG     3'  TGCATTGTGTTTTGGAAT    59455        G    TT
                                TGCATTGTG TTTTG  GT
                                |||||||||  |||||  ||
                                ACGTAACAC AAAAC  TA
                                     _    CT
GAM2576  KIAA0329  3'  TGTGTTGTGGTGTGCATGTG   59456    CA     TT  _
                                TG  TTGTGGT  TGT TGTG
                                ||  |||||||  ||| ||||
                                AC  AACACCA  ACG ACAC
                                 AC      C_   T
GAM2576  KIAA0410  3'  GCATGCTTTTTGTTGTGTG    59457     T  GG
                                GCAT GT  TTTTGTTGTGTG
                                ||||  ||  ||||||||||||
                                CGTA CG  AAAACAACACAC
                                  _ A_
GAM2576  KIAA1813  5'  TGCATTTAGTTATTTGTTGTGT 59458       G   __
             G                   TGCATT TGGTT  TTGTTGTGTG
                                ||||||  |||||  ||||||||||
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                                ACGTAA ATCAA  AACAACACAC
                                   _    TA
GAM2576 SR-BP1   3' TGTGTGTATGTGTTGTGTG   59459     _ TT_
                                TGTG GT   TGTTGTGTG
                                |||| ||   |||||||||
                                ACAC CA   ACAACACAC
                                  A  TAC
GAM2576 TP53INP1 3' TGTGTTGTGGTTGGCCTTGTG 59460    CA      TT  TG
                                TG  TTGTGGTT  GT  TGTG
                                ||  ||||||||  ||  ||||
                                AC  AACACCAA  CG  ACAC
                                 AC       C_  GA
GAM2576 TP53INP1 3' TGTGTTGTGGTTGGCCTTGTG 59460    CA      TT  TG
                                TG  TTGTGGTT  GT  TGTG
                                ||  ||||||||  ||  ||||
                                AC  AACACCAA  CG  ACAC
                                 AC       C_  GA
GAM2576 LOC150112 3' TGCGTGTGTGTGTGTTGTGTG 59461     AT    GTTT
                                TGC  TGTG   TGTTGTGTG
                                |||  ||||   |||||||||
                                ACG  ACAC   ACAACACAC
                                  C_   ACAC
GAM2576 LOC150135 3' TGCGTTGTGCTTTTGTTCTG   59462     A    G      G
                                TGC TTGTG TTTTGTT TG
                                ||| ||||| ||||||| ||
                                ACG AACAC AAAACAA AC
                                  C    G      G
GAM2576 LOC151446 3' CATTCTGGTTTTGTTGTGTG   59463      G
                                CATT TGGTTTTGTTGTGTG
                                |||| ||||||||||||||
                                GTAA ACCAAAACAACACAC
                                  G
GAM2576 LOC92360  5' TGTCATTGTGATGTTGTGTG   59464    _      TTT
                                TG CATTGTGG   TGTTGTGTG
                                || ||||||||   |||||||||
                                AC GTAACACT   ACAACACAC
                                 A      ____
GAM2577 FLJ14486  3' CACGGGTCCCGCAGCGGGCGTG 59467        GA   CAAA_
            GCC                   TACGGGTC  GTA    CGTGGCC
                                |||||||  |||    |||||||
                                GTGCCCAG  CGT    GCACCGG
                                    GG   CGCCC
GAM2578 DAF      3' GTTCTATTTTCAAGAGGTGTA  59470         T   AC  A
                                GTTCTGTTTT CGA  AG TGTA
                                |||||||||| |||  || ||||
                                CAAGATAAAA GTT  TC ACAT
                                      _  C_  C
GAM2578 SLC11A3   3' GTTTTGTTTTTCCACATACATG 59471     C      GA   G__
            TAA                   GTT TGTTTTTC  ACA   ATGTAA
                                ||| ||||||||  |||   ||||||
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                                CAA ACAAAAAG  TGT   TACATT
                                  A       G_   ATG
GAM2578  FLJ21272  3'  GTTCTGTTTTGATGT       59472          TCGAACA
                                GTTCTGTTTT      GATGT
                                ||||||||||      |||||
                                CAAGACAAAA      CTACA
                                        _______
GAM2578  LOC143888 3'  GTTCTTCAGCAAGAATAGATGT 59473      GTTTTTC   C
           AA                     GTTCT      GAA AGATGTAA
                                |||||      ||| ||||||||
                                CAAGA      CTT TCTACATT
                                   AGTCGTT   A
GAM2578  LOC147299 3'  GTTTTGTTTTTCACCTTATGT  59474     C        AACAG
                                GTT TGTTTTTCG     ATGT
                                ||| |||||||||     ||||
                                CAA ACAAAAAGT     TACA
                                  A       GGAA_
GAM2579  TMEM1     3'  TACATCAGTTAGTCTG      59477          ACACC  G
                                TACATCAGTTG     GT TG
                                ||||||||||     || ||
                                ATGTAGTCAAT     CA AC
                                       _____ G
GAM2579  XRCC2     3'  CATCAGTCTACGTGTGT     59478         GACAC
                                CATCAGTT     CGTGTGT
                                ||||||||     |||||||
                                GTAGTCAG     GCACACA
                                     AT___
GAM2579  CNNM4     3'  TACAGCAGTTGACAACAGATGT 59479      T       C  T
                                TACA CAGTTGACA CG GTGT
                                |||| ||||||||| || ||||
                                ATGT GTCAACTGT GT TACA
                                  C       T  C
GAM2579  DKFZP761E2110 3'  CATCAGCTGAGAATGTGT    59480          CACC
                                CATCAGTTGA    GTGTGT
                                ||||||||||    ||||||
                                GTAGTCGACT    TACACA
                                     CT__
GAM2579  KIAA0513  3'  CATCAGATGACACCACGT    59481       T
                                CATCAG TGACACCGTGT
                                ||||||| ||||||||||
                                GTAGTC ACTGTGGTGCA
                                   T
GAM2579  LOC116437 3'  TACATTGGTTGCACCATGT    59482      CA    A
                                TACAT  GTTG CACCGTGT
                                |||||  |||| ||||||||
                                ATGTA  CAAC GTGGTACA
                                  AC    _
GAM2579  LOC120856 3'  TACATCAGTTACATCACAT    59483          A  C  TG
                                TACATCAGTTG CA CG  T
                                |||||||||| || ||  |
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                                ATGTAGTCAAT GT GT  A
                                      _ A  GT
GAM2579  LOC150587 3'  TCAGTTGAACTTGTGT      59484        C  CG
                                TCAGTTGA AC  TGTGT
                                |||||||| ||  |||||
                                AGTCAACT TG  ACACA
                                     _ A_
GAM2579  LOC151446 3'  TACACCAAGCTGTGTG      59485        _  GACACC
                                TACATCA GTT     GTGTG
                                ||||||| |||     |||||
                                ATGTGGT CGA     CACAC
                                   T  _______
GAM2579  LOC203257 5'  CATCAGCTGGTACTGTCTGT   59486         AC  C  G
                                CATCAGTTG  AC GT TGT
                                |||||||||  || || |||
                                GTAGTCGAC  TG CA ACA
                                      CA  A  G
GAM2579  LOC219988 3'  TACATCAGCTGGTTTGTGT    59487          ACACCG
                                TACATCAGTTG     TGTGT
                                ||||||||||      |||||
                                ATGTAGTCGAC     ACACA
                                      CAA___
GAM2579  LOC256895 3'  CATCAGTTAGACATTGCGC    59488         _   CC
                                CATCAGTT GACA  GTGT
                                |||||||| ||||  ||||
                                GTAGTCAA CTGT  CGCG
                                     T   AA
GAM2579  LOC57149  3'  CATCAGCTGGCATGTGT     59489         ACAC
                                CATCAGTTG   CGTGTGT
                                |||||||||   |||||||
                                GTAGTCGAC   GTACACA
                                      C___
GAM2580  REV3L    5'  TGAGAGAAATCTTCCTCAGATA 59492       C    GA__   A
            TAT                   TGAGAG AATCT   TGGA TATAT
                                |||||| |||||   |||| |||||
                                ACTCTC TTAGA   GTCT ATATA
                                   T    AGGA   _
GAM2580  FLJ13614  5'  TGATAGCATGGAATAT      59493     G   ATCTGA
                                TGA AGCA     TGGAATAT
                                ||| ||||     ||||||||
                                ACT TCGT     ACCTTATA
                                  A  _______
GAM2580  FLJ13782  3'  TGAGAGCAAATTGTACATATAT 59494         TC  A  GA
                                TGAGAGCAA  TG TG  ATATAT
                                |||||||||  || ||  ||||||
                                ACTCTCGTT  AC AT  TATATA
                                     TA  _  G_
GAM2580  FLJ21007  5'  TGAGAGCAATCAGGATGA    59495          T_
                                TGAGAGCAATC  GATGG
                                ||||||||||  |||||
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                                ACTCTCGTTAG  CTACT
                                      TC
GAM2580  OCT11    3'  TGAAGGCAATCTGTCTGTATAT 59496     A      A_  GA
                                TGAG GCAATCTG  TG  ATAT
                                |||| ||||||||  ||  ||||
                                ACTT CGTTAGAC  AC  TATA
                                  C       AG  A_
GAM2580  LOC154442 3'  TGAGGGTCAATCTCTGAATATA 59497     AG_     GATG
            T                    TGAG   CAATCT    GAATATAT
                                ||||   ||||||    ||||||||
                                ACTC   GTTAGA    CTTATATA
                                  CCA     GA__
GAM2580  LOC91963  3'  TGAGAGCAGCCTGGGCAATAT  59498        AT   AT  _
                                TGAGAGCA  CTG  GG AATAT
                                ||||||||  |||  || |||||
                                ACTCTCGT  GAC  CC TTATA
                                     CG   __  G
GAM2581  LPIN1    3'  CATCACATGTGACAAACA    59501     G    C__
                                CAT CACG   GACAAACA
                                ||| ||||   ||||||||
                                GTA GTGT   CTGTTTGT
                                  _    ACA
GAM2581  NFIB     3'  CTGTTGCATGCAGAGAGAACAC 59502     C       CGC  CA
                                TTG TGCATGCA   GA  AACAC
                                ||| ||||||||   ||  |||||
                                GAC ACGTACGT   CT  TTGTG
                                  A       CT_  C_
GAM2581  PCDH15   3'  TTACTGCATCCACATGATAGAC 59503        G    C  CAA
            A                    TTGCTGCAT CACG GA   ACA
                                |||||||||  |||| ||   |||
                                AATGACGTA GTGT CT   TGT
                                     G    A  ATC
GAM2581  PIGN     3'  TTGCTGCAGGTGCTCTCAACA  59504        __   ACG
                                TTGCTGCA  TGC   CGACA
                                ||||||||  |||   |||||
                                AACGACGT  ACG   GTTGT
                                     CC   AGA
GAM2581  PUM2     3'  TTGCTGCAGTGACTGGGACA   59505        _  C  GC_
                                TTGCTGCA TG AC   GACA
                                ||||||||  || ||   ||||
                                AACGACGT AC TG   CTGT
                                     C  _  ACC
GAM2581  C20orf150 3'  TTGCTTATGCACACTGACA    59506      GC       _
                                TTGCT  ATGCACGC GACA
                                |||||  |||||||| ||||
                                AACGA  TACGTGTG CTGT
                                  A_       A
GAM2581  CFP1     3'  TTGCTGCATGGGCGCTCA     59507         CA   GA
                                TTGCTGCATG  CGC  CA
                                ||||||||||  |||  ||
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                                AACGACGTAC  GCG  GT
                                      CC   A_
GAM2581  FLJ13181  5'  CTGCGCGCCACACGCGACAA   59508     _  A
                                TTGC TGC TGCACGCGACAA
                                |||| ||| ||||||||||||
                                GACG GCG GTGTGCGCTGTT
                                  C   _
GAM2581  MBLL39    3'  TTGCTGCAGAGACAGTGGCGGA 59509        T__   C__   _
           C                     TTGCTGCA   GCA   GCG AC
                                ||||||||   |||   ||| ||
                                AACGACGT   TGT   CGC TG
                                     CTC   CAC   C
GAM2581  MGC27434  3'  TTGCTGCACGTATTCAACA    59510         CACG
                                TTGCTGCATG    CGACA
                                ||||||||||    |||||
                                AACGACGTGC    GTTGT
                                      ATAA
GAM2581  LOC146136 5'  CTGCTGCATGCCTGCAGACA   59511          AC  _
                                TTGCTGCATGC  GC GACA
                                ||||||||||  || ||||
                                GACGACGTACG  CG CTGT
                                       GA  T
GAM2581  LOC149351 3'  CTGTATGAACACAAACA     59512     C   C     CAA
                                CTG ATG ACGCGA   ACA
                                ||| ||| ||||||   |||
                                GAC TAC TGTGTT   TGT
                                  A   T     ____
GAM2581  LOC152905 3'  TGTTGCATGCACAGACA     59513    C        C
                                TG TGCATGCACG GACA
                                || ||||||||| ||||
                                AC ACGTACGTGT CTGT
                                 A        _
GAM2581  LOC152917 5'  CTGCCGCACGTGGCAGACA    59514          CAC  _
                                TTGCTGCATG   GC GACA
                                ||||||||||   || ||||
                                GACGGCGTGC   CG CTGT
                                      AC_  T
GAM2581  LOC160335 5'  CTGCTGCATGCAACAGGACA   59515           _  C
                                TTGCTGCATGCA CG GACA
                                |||||||||||| || ||||
                                GACGACGTACGT GT CTGT
                                       T  C
GAM2581  LOC199704 3'  CTGCTGCATGCGTGCAACA    59516          AC
                                TTGCTGCATGC  GCGACA
                                ||||||||||  ||||||
                                GACGACGTACG  CGTTGT
                                       CA
GAM2581  LOC220565 3'  CTGCTGCATGCCTGCAGACA   59511          AC  _
                                TTGCTGCATGC  GC GACA
                                ||||||||||  || ||||
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                                GACGACGTACG  CG CTGT
                                      GA  T
GAM2581  LOC92285  3'  CTGCTGCATGCGTGCAACA   59516          AC
                                TTGCTGCATGC  GCGACA
                                ||||||||||  ||||||
                                GACGACGTACG  CGTTGT
                                      CA
GAM2582  HOXC11    3'  CAACGGTGTTCACTCGCCGT   59519        CCCC   _
                                CAACGGTG   TTTA TCGCCGT
                                ||||||||   |||| |||||||
                                GTTGCCAC   AAGT AGCGGCA
                                     ____   G
GAM2582  MEN1      5'  ACTGTGCCCCCGGGGCTGTA   59520    G      TTATC  C
                                AC GTGCCCCT    GC GTA
                                || ||||||||    || |||
                                TG CACGGGGG    CG CAT
                                 A       CCC__  A
GAM2582  MPO       3'  CAGCGGTGCCTTTATTATCA   59521    A      CCT_
                                CA CGGTGCC    TTATCG
                                || |||||||    ||||||
                                GT GCCACGG    AATAGT
                                 C      AAAT
GAM2582  C20orf122 3'  TGACAGTGCCTTCTAGCTGT   59522    A      CC    TC  C
                                C ACGGTGCC  TTTA  GC GT
                                | ||||||||  ||||  || ||
                                A TGTCACGG  AGAT  CG CA
                                 C       A_   __  A
GAM2582  FLJ11252  3'  CAGTGGTCTCTAGCACCTGT   59523      CCC    T   _
                                CGGTG   CTTTA CGCC GT
                                |||||   ||||| |||| ||
                                GTCAC   GAGAT GTGG CA
                                   CA_    C    A
GAM2583  ANKRA2    3'  TATACAGTAAAACATAGTTA   59526        T    ATT
                                TATACAGTA AATG   TAGTTA
                                |||||||||  ||||   ||||||
                                ATATGTCAT TTGT   ATCAAT
                                      T   ___
GAM2583  BACH2     3'  TATACAGTATACTTGAGTTA   59527          A_   T
                                TATACAGTATA  TGA TTA
                                ||||||||||  |||  |||
                                ATATGTCATAT  ACT AAT
                                      GA   C
GAM2583  CAV2      3'  TATACAGTAAAATGAAACATC  59528        T    TTTA
                                TATACAGTA AATGA    GTT
                                |||||||||  |||||    |||
                                ATATGTCAT TTACT    TAG
                                      T    TTG_
GAM2583  CNTN3     3'  TATACAGTATATGCGGACCT   59529          AT__
                                TATACAGTATA    GATTT
                                ||||||||||    |||||
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                                ATATGTCATAT   CTGGA
                                      ACGC
GAM2583  MYCN     3'  TATAAGTATCAAATTTAGTTA  59530     C    AAT
                                TATA AGTAT   GATTTAGTTA
                                |||| |||||   ||||||||||
                                ATAT TCATA   TTAAATCAAT
                                  _    GT_
GAM2583  MYO1E    3'  TATACAGTATATGATCCTGT   59531         A    TA
                                TATACAGTATA TGATT  GT
                                |||||||||||| |||||  ||
                                ATATGTCATAT ACTAG  CA
                                      _    GA
GAM2583  PPP4R1   3'  TACAGTATGTGAAGAAGTT   59532        AA   TTT
                                TACAGTAT  TGA   AGTT
                                ||||||||  |||   ||||
                                ATGTCATA  ACT   TCAA
                                     C_   TCT
GAM2583  ROCK2    3'  TACACAGTATAATGGTCA    59533          ATTTA
                                TATACAGTATAATG    GTTA
                                ||||||||||||||    ||||
                                ATGTGTCATATTAC    CAGT
                                                  _____
GAM2583  TNFSF11  3'  TACAGTATAAGATAACATTTAC 59534         T   TTAG_
                                TACAGTATAA GAT    TTAC
                                |||||||||| |||    ||||
                                ATGTCATATT CTA    AATG
                                      _   TTGTA
GAM2583  TNFSF11  3'  TACAGTATAAGATAACATTTAC 59534         T   TTAG_
                                TACAGTATAA GAT    TTAC
                                |||||||||| |||    ||||
                                ATGTCATATT CTA    AATG
                                      _   TTGTA
GAM2583  FBXO3    3'  TATGCAGAGAACAATTTAGTTA 59535    A   TAT  TG
                                TAT CAG   AA  ATTTAGTTA
                                ||| |||   ||  |||||||||
                                ATA GTC   TT  TAAATCAAT
                                  C   TC_  GT
GAM2583  MBLL39   3'  TACAGTAACAATGTTTAGTTA  59536       _    A
                                TACAGTA TAATG TTTAGTTA
                                ||||||| ||||| ||||||||
                                ATGTCAT GTTAC AAATCAAT
                                     T    _
GAM2583  MBLL39   3'  TACAGTAACAATGTTTAGTTA  59536       _    A
                                TACAGTA TAATG TTTAGTTA
                                ||||||| ||||| ||||||||
                                ATGTCAT GTTAC AAATCAAT
                                     T    _
GAM2583  PRO1914  5'  ATACAGTATAACAGTTA     59537          GATTT
                                ATACAGTATAAT    AGTTA
                                ||||||||||||    |||||
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                                TATGTCATATTG    TCAAT
                                      _____
GAM2583  LOC131873 3'  CAGCAGATTTAGTTA      59538      TAAT
                                CAGTA   GATTTAGTTA
                                |||||   ||||||||||
                                GTCGT   CTAAATCAAT
                                   ____
GAM2583  LOC143570 5'  TACAGTATAATCCAGTT     59539        ATG
                                TACAGTATA  ATTTAGTT
                                |||||||||  ||||||||
                                ATGTCATAT  TAGGTCAA
                                    ___
GAM2583  LOC150295 3'  TATACAGTAAGTTCAGTT    59540        TAATGA
                                TATACAGTA    TTTAGTT
                                |||||||||    |||||||
                                ATATGTCAT    AAGTCAA
                                     TC____
GAM2583  LOC221272 3'  GCCCCCATGATTTAGTTAC   59541    ATA_
                                GT   ATGATTTAGTTAC
                                ||   ||||||||||||||
                                CG   TACTAAATCAATG
                                 GGGG
GAM2584  ADD1     3'  GGGCCCACACAAGCTTGCCT   59544    A     __ C
                                GGG CCCGCGC  GC TGCCT
                                ||| |||||||  || |||||
                                CCC GGGTGTG  CG ACGGA
                                  _     TT  A
GAM2584  ADD1     3'  GGGCCCACACAAGCTTGCCT   59544    A     __ C
                                GGG CCCGCGC  GC TGCCT
                                ||| |||||||  || |||||
                                CCC GGGTGTG  CG ACGGA
                                  _     TT  A
GAM2584  ADRA2B   3'  CGGGACCGCGAGTGCCT     59545      CGC   CC
                                CGGGACC   GCG  TGCCT
                                |||||||   |||  |||||
                                GCCCTGG   CGC  ACGGA
                                    ___   TC
GAM2584  AXIN1    3'  GGGACCCCCTACCTGCCT    59546      GCGC
                                GGGACCC    GCCTGCCT
                                |||||||    ||||||||
                                CCCTGGG    TGGACGGA
                                   GGA_
GAM2584  C8orf1   5'  CGGGACCCGCCCACCACGC   59547        G   _
                                CGGGACCCGC CGCC TGC
                                |||||||||| |||| |||
                                GCCCTGGGCG GTGG GCG
                                     G   T
GAM2584  CACNA1C  3'  CGGGACCCTCGCCGCCT     59548      GCG   T
                                CGGGACCC   CGCC GCCT
                                ||||||||   |||| ||||
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                                GCCCTGGG  GCGG CGGA
                                    A__   _
GAM2584  CCND1    3'  CGGTGGCGCCCGCCTGCCT   59549    GACC  G
                                CGG   CGC CGCCTGCCT
                                |||   ||| |||||||||
                                GCC   GCG GCGGACGGA
                                  ACC_  G
GAM2584  CDC34    5'  CGGGGCCGCCGCCTGCCT   59550    AC   G
                                CGGG  CCGC CGCCTGCCT
                                ||||  |||| |||||||||
                                GCCC  GGCG GCGGACGGA
                                  C_   _
GAM2584  CDH20    3'  GGACGCGCGCCTGCCT     59551    CC
                                GGAC  GCGCGCCTGCCT
                                ||||  ||||||||||||
                                CCTG  CGCGCGGACGGA

                                  __
GAM2584  COL4A4   5'  GGATCCGCGCCCACCT     59552    C    G  T
                                GGA CCGCGC CC GCCT
                                ||| |||||| || ||||
                                CCT GGCGCG GG TGGA
                                  A     _ _
GAM2584  DNASE1   5'  CAGGACACGCCTGCC      59553      CCGC
                                CGGGAC   GCGCCTGCC
                                ||||||   |||||||||
                                GTCCTG   TGCGGACGG

                                  _____
GAM2584  DPH2L1   5'  CAGGACCCGGATTGCTGCCT  59554       CGCGC
                                CGGGACCCG    CTGCCT
                                |||||||||    ||||||
                                GTCCTGGGC    GACGGA
                                     CTAAC
GAM2584  DYT1     5'  GGACCCGCGCCACCCTGC    59555       G__
                                GGACCCGCGC   CCTGC
                                ||||||||||   |||||
                                CCTGGGCGCG   GGACG
                                     GTG
GAM2584  ENC1     5'  CAGGACCCGCAGAGCGTCT   59556        ___  C
                                CGGGACCCGC   GCG CT
                                ||||||||||   ||| ||
                                GTCCTGGGCG   CGC GA
                                     TCT   A
GAM2584  FASN     3'  CGGGACCCACACGCTGCCT   59557          C
                                CGGGACCCGCGCGC TGCCT
                                |||||||||||||| |||||
                                GCCCTGGGTGTGCG ACGGA
                                                _
GAM2584  GJA4     5'  CGGGCCTCCGTCGCCTGCCT  59558     A  CG  _
                                CGGG CC  CG CGCCTGCCT
                                |||| ||  || |||||||||
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                                GCCC GG  GC GCGGACGGA
                                  _ AG  A
GAM2584  HDAC4    3'  CGGGACCCGCCAGAGTGTGC   59559         G  CC___
                                CGGGACCCGC CG    TGC
                                |||||||||| ||    |||
                                GCCCTGGGCG GT    ACG
                                      _ CTCAC
GAM2584  HNRPA2B1 5'  CGGGACCCGGCGCTGC     59560         C   C
                                CGGGACCCG GCGC TGC
                                ||||||||| |||| |||
                                GCCCTGGGC CGCG ACG
                                      _   _
GAM2584  HNRPA2B1 5'  CGGGACCCGGCGCTGC     59560         C   C
                                CGGGACCCG GCGC TGC
                                ||||||||| |||| |||
                                GCCCTGGGC CGCG ACG
                                      _   _
GAM2584  HNRPDL   5'  CGGGCCCCGCGCGGCCT    59561      A       CCT
                                CGGG CCCGCGCG   GCCT
                                |||| ||||||||   ||||
                                GCCC GGGCGCGC   CGGA
                                  G      ___
GAM2584  HUNK     5'  CGCGGCCCGCGCGGCTCCT   59562    _ A       C  G
                                CG GG CCCGCGCG CT CCT
                                || || |||||||| || |||
                                GC CC GGGCGCGC GA GGA
                                 G _       C _
GAM2584  KCNN4    3'  GGGACCCAGGAGTCCTGCCT  59563        CGCG_
                                GGGACCCG    CCTGCCT
                                ||||||||    |||||||
                                CCCTGGGT    GGACGGA
                                    CCTCA
GAM2584  LASS1    3'  CGGGGTCCGCGCCCGCGCCC  59564      AC     G  _
                                CGGG  CCGCGC CC TGCCT
                                ||||  |||||| || |||||
                                GCCC  GGCGCG GG GCGGG
                                  CA     _  C
GAM2584  MDFI     5'  CGGGGCCCGCCATGCGCGCCT 59565      A    ___    CT
                                CGGG CCCGC   GCGC  GCCT
                                |||| |||||   ||||  ||||
                                GCCC GGGCG   CGCG  CGGA
                                  C    GTA   __
GAM2584  MMP19    3'  CAGGGCAGTGCCTGCCT     59566      ACCC   C_
                                CGGG   GCG  GCCTGCCT
                                ||||   |||  ||||||||
                                GTCC   CGT  CGGACGGA
                                  ____   CA
GAM2584  MMP19    3'  CAGGGCAGTGCCTGCCT     59566      ACCC   C_
                                CGGG   GCG  GCCTGCCT
                                ||||   |||  ||||||||
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                                GTCC   CGT  CGGACGGA
                                  ____  CA
GAM2584  MTA1L1   5'  GGGGCCCGCGCAGCCGGCACCT 59567     A     _  T__
                                GGG CCCGCGC GCC   GCCT
                                ||| ||||||| |||   ||||
                                CCC GGGCGCG CGG   TGGA
                                  C      T   CCG
GAM2584  P2RY2    5'  GGGGCCACGCCCAGCCT     59568     AC     G  T
                                GGG  CCGCGC CC GCCT
                                |||  |||||| || ||||
                                CCC  GGTGCG GG CGGA
                                  C_     _ T
GAM2584  PARN     5'  CGGGCCCGCGCCCGCCT     59569      A    GC
                                CGGG CCCGC  GCCTGCCT
                                |||| |||||  ||||||||
                                GCCC GGGCG  CGGGCGGA
                                  _    __
GAM2584  PITPN    5'  CGCGGCCCGCCCGGCCT     59570    _ A    G  CCT
                                CG GG CCCGC CG   GCCT
                                || || ||||| ||   ||||
                                GC CC GGGCG GC   CGGA
                                 G  _    G  ___
GAM2584  PPP2R2B  5'  AGGATGCTGCGCCTGCCT    59571      CCC  _
                                GGGA   GC GCGCCTGCCT
                                ||||   || ||||||||||
                                TCCT   CG CGCGGACGGA
                                  A__  A
GAM2584  PROK1    3'  GGGCTCCCTACACCTGCCT   59572     A_   GC
                                GGG  CCC  GCGCCTGCCT
                                |||  |||  ||||||||||
                                CCC  GGG  TGTGGACGGA
                                  GA   A_
GAM2584  PTPN14   5'  CGGACGCCGCCTGCCT      59573      ACC   G
                                CGGG   CGC CGCCTGCCT
                                ||||   ||| |||||||||
                                GCCT   GCG GCGGACGGA
                                  ___   _
GAM2584  RGS6     3'  GGAGCGCCGCCGCCTGCCT   59574     C__    G
                                GGA   CCGC CGCCTGCCT
                                |||   |||| |||||||||
                                CCT   GGCG GCGGACGGA
                                  CGC   _
GAM2584  ROCK2    5'  CGGGCCCACCGCCTGCCT    59575      A    G
                                CGGG CCCGC CGCCTGCCT
                                |||| ||||| |||||||||
                                GCCC GGGTG GCGGACGGA
                                  _    _
GAM2584  RPH3AL   3'  GGGGGCACTGCGCCTGCCT   59576     ACC   _
                                GGG   CGC GCGCCTGCCT
                                |||   ||| ||||||||||
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                                CCC   GTG CGCGGACGGA
                                  CC_   A
GAM2584  SCN4A    3'  CAGGACCCAGCCTGTCT     59577         CGC    C
                                CGGGACCCG   GCCTG CT
                                |||||||||   ||||| ||
                                GTCCTGGGT   CGGAC GA
                                     ___    A
GAM2584  SLC18A3  5'  CGGGACCCGCGGCTGC      59578          C  C
                                CGGGACCCGCG GC TGC
                                |||||||||||  || |||
                                GCCCTGGGCGC CG ACG
                                     _ _
GAM2584  SMARCD2  5'  CGGGAACCCGCCCGCGCCT   59579      _    G   CT
                                CGGGA CCCGC CGC  GCCT
                                ||||| ||||| |||  ||||
                                GCCCT GGGCG GCG  CGGA
                                   T    G  __
GAM2584  SORL1    5'  CGGGACCGCGCGCGCCGC    59580       _      T
                                CGGGACC CGCGCGCC GC
                                ||||||| |||||||| ||
                                GCCCTGG GCGCGCGG CG
                                    C      _
GAM2584  SURF5    3'  GGGACCCAGCACGGGGCCT   59581       _    CCT
                                GGGACCC GCGCG   GCCT
                                ||||||| |||||   ||||
                                CCCTGGG CGTGC   CGGA
                                    T    CC_
GAM2584  TAF1C    3'  CGGCACCTCCAGCCTGCCT   59582     G   CG  C
                                CGG ACC  CG GCCTGCCT
                                ||| |||  || ||||||||
                                GCC TGG  GT CGGACGGA
                                  G   AG  _
GAM2584  TEM7     5'  CGGACCTGCCCCCGGCCTGC  59583     A___   G  C
                                CGGG    CCC CG GCCTGC
                                ||||    ||| || ||||||
                                GCCT    GGG GC CGGACG
                                   GGAC   G  _
GAM2584  XRCC3    3'  AGGAGGAGCCGCCTGCCT    59584     CCC  G
                                GGGA   GC CGCCTGCCT
                                ||||   || |||||||||
                                TCCT   CG GCGGACGGA
                                   CCT  _
GAM2584  AFAP     3'  GGGACCCTGGCCTGCCT     59585       GCGC
                                GGGACCC    GCCTGCCT
                                |||||||    ||||||||
                                CCCTGGG    CGGACGGA
                                    AC__
GAM2584  C20orf80 5'  CGGGTCACCCGCCTGTCT    59586     ACC   G     C
                                CGGG   CGC CGCCTG CT
                                ||||   ||| |||||| ||
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                                GCCC   GTG GCGGAC GA
                                  A__  G     A
GAM2584  C22orf4   3'  GGGACCCCTGACCTGCCT    59587       GCGC
                                GGGACCC    GCCTGCCT
                                |||||||    ||||||||
                                CCCTGGG    TGGACGGA
                                   GAC_
GAM2584  CPR2      3'  AGGACTCCACCTGCCT      59588      _ GCGC
                                GGGAC CC    GCCTGCCT
                                ||||| ||    ||||||||
                                TCCTG GG    TGGACGGA
                                  A _____
GAM2584  DKFZP564L0864 5'  GGGCCCGGCCTGCCT      59589     A   CGC
                                GGG CCCG   GCCTGCCT
                                ||| ||||   ||||||||
                                CCC GGGC   CGGACGGA
                                  _    ____
GAM2584  DKFZP566J091 3'  GGAATCCCACCACTGCCT    59590      _    G   C
                                GGGA CCCGC CGC TGCCT
                                |||| ||||| ||| |||||
                                CCTT GGGTG GTG ACGGA
                                  A    _  _
GAM2584  DKFZP761G1913 3'  GAGCCATTGCGCCTGCCT    59591     A  CGC
                                GGG CC   GCGCCTGCCT
                                ||| ||   ||||||||||
                                CTC GG   CGCGGACGGA
                                  _ TAA
GAM2584  DOC-1R    5'  GGACCTCGCACCTGTCT     59592       CG       C
                                GGACC  CGCGCCTG CT
                                |||||  |||||||| ||
                                CCTGG  GCGTGGAC GA
                                   A_       A
GAM2584  DRIL2     3'  AGGACCCCAGCCTGCCT     59593        G  C
                                GGGACCC CG GCCTGCCT
                                ||||||| || ||||||||
                                TCCTGGG GT CGGACGGA
                                     _ _
GAM2584  EMILIN    3'  CGGCGCCCGCGCGGGGGAGCCT 59594     GA       CCT__
                                CGG  CCCGCGCG    GCCT
                                |||  ||||||||    ||||
                                GCC  GGGCGCGC    CGGA
                                  GC       CCCCT
GAM2584  FLJ13491  3'  CGGAGCCCTCACCTGCCT    59595     GA   GCG
                                CGG  CCC   CGCCTGCCT
                                |||  |||   |||||||||
                                GCC  GGG   GTGGACGGA
                                  TC   A__
GAM2584  FLJ20366  5'  CGGGACCCCGCGTCGC      59596         G    CC
                                CGGGACCC CGCG  TGC
                                |||||||| ||||  |||
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                                GCCCTGGG GCGC  GCG
                                    _   A_
GAM2584  FREQ     3'  GGGGCCGCACCTGCCT     59597     A  CGC
                                GGG CC   GCGCCTGCCT
                                ||| ||   ||||||||||
                                CCC GG   CGTGGACGGA
                                  C ___
GAM2584  GC20     5'  CGGGGCCCGCCCGGATCACCT  59598      A    G  CC_
                                CGGG CCCGC CG   TGCCT
                                |||| ||||| ||   |||||
                                GCCC GGGCG GC   GTGGA
                                  C    G  CTA
GAM2584  GGA2     3'  CAGGACAGCAGCCTGCCT    59600       CC   C
                                CGGGAC  GCG GCCTGCCT
                                ||||||  ||| ||||||||
                                GTCCTG  CGT CGGACGGA
                                   T_  _
GAM2584  GGA2     3'  CAGGACAGCAGCCTGCCT    59600       CC   C
                                CGGGAC  GCG GCCTGCCT
                                ||||||  ||| ||||||||
                                GTCCTG  CGT CGGACGGA
                                   T_  _
GAM2584  GGA2     3'  CGGGGCCTGCCCTGGCCT    59599      AC  GC  G   _
                                CGGG  CC  GC CCTG CCT
                                ||||  ||  || |||| |||
                                GCCC  GG  CG GGAC GGA
                                  C_  A_  _   C
GAM2584  H2BFQ    3'  GGGACCCGGCTGCGCGGCCT  59601         _ _   CT
                                GGGACCCG C GCGC  GCCT
                                |||||||| | ||||  ||||
                                CCCTGGGC G CGCG  CGGA
                                    C A   C_
GAM2584  HA-1     3'  CAGGGCAGGGCCTGCCT     59602      ACCC  C_
                                CGGG   GCG  GCCTGCCT
                                ||||   |||  ||||||||
                                GTCC   CGT  CGGACGGA
                                  ____  CC
GAM2584  HSU79303 3'  GGGGCACCCGCCTGCCT     59603     ACC  G
                                GGG  CGC CGCCTGCCT
                                |||  ||| |||||||||
                                CCC  GTG GCGGACGGA
                                  C__  G
GAM2584  KIAA0125 3'  GGGACCCGGCACCCCTGCCT  59604         _  G
                                GGGACCCG CGC CCTGCCT
                                |||||||| ||| |||||||
                                CCCTGGGC GTG GGACGGA
                                    C  G
GAM2584  KIAA0217 3'  CGAGGCCACACCTGCCT     59605      A  CGC
                                CGGG CC   GCGCCTGCCT
                                |||| ||   ||||||||||
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                                GCTC GG   TGTGGACGGA
                                  C ___
GAM2584 KIAA0415 3' CGGGAACTCGCGCCGCTGCCT 59606      _ C    GC
                                CGGGA C CGCGC  CTGCCT
                                ||||| | |||||  ||||||
                                GCCCT G GCGCG  GACGGA
                                   T A    GC
GAM2584 KIAA0427 3' GGGACCGTGCCTGCCT     59607       CGC C
                                GGGACC   G GCCTGCCT
                                ||||||   | ||||||||
                                CCCTGG   C CGGACGGA
                                   ___ A
GAM2584 KIAA0429 5' GGGACCCAGAAGCATGCCT   59608        CGC  C
                                GGGACCCG   GC TGCCT
                                ||||||||   || |||||
                                CCCTGGGT   CG ACGGA
                                     CTT  T
GAM2584 KIAA0469 3' GGGCACCCGCAGCTGTCTGC  59609    _    _ GC_
                                GGG ACCCGC GC   CTGC
                                ||| |||||| ||   ||||
                                CCC TGGGCG CG   GACG
                                  G     T  ACA
GAM2584 KIAA0596 3' GGGTGCCCAGCACTGCCT    59610    A_   C    C
                                GGG  CCCG GCGC TGCCT
                                |||  |||| |||| |||||
                                CCC  GGGT CGTG ACGGA
                                  AC   _   _
GAM2584 KIAA0603 5' CGGGCTCCCGCGCCTGCCT   59611     AC  G
                                CGGG  CC CGCGCCTGCCT
                                ||||  || ||||||||||
                                GCCC  GG GCGCGGACGGA
                                  GA  _
GAM2584 KIAA0876 3' GGGCCCCGAAGGCCTGCCT   59612    A   CGC
                                GGG CCCG   GCCTGCCT
                                ||| ||||   ||||||||
                                CCC GGGC   CGGACGGA
                                  G   TTC
GAM2584 KIAA1023 3' GGAACGGCGAGCCTGCCT    59613     CC   C
                                GGGAC  GCG GCCTGCCT
                                |||||  ||| ||||||||
                                CCTTG  CGC CGGACGGA
                                   C_   T
GAM2584 KIAA1303 3' CGGGACCCGGCAGTGCCT    59614        C   CC
                                CGGGACCCG GCG  TGCCT
                                ||||||||| |||  |||||
                                GCCCTGGGC CGT  ACGGA
                                     _  C_
GAM2584 KIAA1691 3' GGGGCAGCACCTGCCT     59615    ACCC  _
                                GGG   GC GCGCCTGCCT
                                |||   || ||||||||||
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                                CCC   CG CGTGGACGGA
                                  _____ T
GAM2584 MCLC    5' CGGGATCCCCTGCCTGCCT   59616     _  GCGC
                                CGGGA CCC   GCCTGCCT
                                ||||| |||   ||||||||
                                GCCCT GGG   CGGACGGA
                                   A  GA__
GAM2584 MGC13071 3' CGGGACCCTCTCACACCTGC  59617       G__
                                CGGGACCC  CGCGCCTGC
                                ||||||||  |||||||||
                                GCCCTGGG  GTGTGGACG
                                    AGA
GAM2584 MGC15737 5' CGGGACCCGGGACAGGCCT   59618       CGC  CT
                                CGGGACCCG  GC  GCCT
                                |||||||||  ||  ||||
                                GCCCTGGGC  TG  CGGA
                                     CC_  TC
GAM2584 MGC3036  3' GGGCCACTCAGCCTGCCT   59619    AC   GC_
                                GGG  CCGC  GCCTGCCT
                                |||  ||||  ||||||||
                                CCC  GGTG  CGGACGGA
                                  __   AGT
GAM2584 MGC8407  3' GGGACCTGCAGGGCCTGCCT  59620      C  C_
                                GGGACC GCG  GCCTGCCT
                                |||||| |||  ||||||||
                                CCCTGG CGT  CGGACGGA
                                   A  CC
GAM2584 MRPS18A  3' GGGACCCAACTGCCCTGCCT  59621       _ _ G
                                GGGACCCG C GC CCTGCCT
                                |||||||| | || |||||||
                                CCCTGGGT G CG GGACGGA
                                     T A  _
GAM2584 NEIL2    5' CGGGGCCCGCCCTCCCT    59622     A   GCG  G
                                CGGG CCCGC  CCT CCT
                                |||| |||||  ||| |||
                                GCCC GGGCG  GGA GGA
                                  C    ___  G
GAM2584 NPTXR    3' GGGGCTGGCCCACCCCCTGCCT 59623    A____   GCG
                                GGG   CCCGC  CCTGCCT
                                |||   |||||  |||||||
                                CCC   GGGTG  GGACGGA
                                  CGACC   GG_
GAM2584 NPTXR    3' GGGGCTGGCCCACCCCCTGCCT 59623    A____   GCG
                                GGG   CCCGC  CCTGCCT
                                |||   |||||  |||||||
                                CCC   GGGTG  GGACGGA
                                  CGACC   GG_
GAM2584 PIF1     3' GGGACACTGCCTGCCT     59624      CC  GC
                                GGGAC  GC  GCCTGCCT
                                |||||  ||  ||||||||
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                                CCCTG  TG  CGGACGGA
                                  __  A_
GAM2584  PTPN21   5'  CGGGGCCGCGCGCCCCGC    59625     AC        _
                                CGGG  CCGCGCGCCT GC
                                ||||  |||||||||| ||
                                GCCC  GGCGCGCGGG CG
                                  C_        G
GAM2584  QKI      5'  CGGGACCCGGCGTCCCGC    59626        C  _
                                CGGGACCCG GCG CCTGC
                                ||||||||| ||| |||||
                                GCCCTGGGC CGC GGGCG
                                      _  A
GAM2584  RAB35    3'  GGAACTGCAGGGCCTGCCT   59627      CC  C_
                                GGGAC  GCG  GCCTGCCT
                                |||||  |||  ||||||||
                                CCTTG  CGT  CGGACGGA
                                   A_  CC
GAM2584  RoXaN    3'  CAGGACCCCCAGCTCTGCCT  59628        G  C  _
                                CGGGACCC CG GC CTGCCT
                                |||||||| || || ||||||
                                GTCCTGGG GT CG GACGGA
                                     G  _  A
GAM2584  RPS6KB1  5'  GGACCCGCCGCAGCCT     59629        G   CT
                                GGACCCGC CGC  GCCT
                                |||||||| |||  ||||
                                CCTGGGCG GCG  CGGA
                                     _  T_
GAM2584  SDCCAG3  5'  CGGGGCACGACCTGCCT    59630     ACCC    _
                                CGGG   GCGCG CCTGCCT
                                ||||   ||||| |||||||
                                GCCC   CGTGC GGACGGA
                                  _____    T
GAM2584  SDS3     5'  CGGTACTCGCCGTCTGCCT   59631     G  C   G  C
                                CGG AC CGC CG CTGCCT
                                ||| || ||| || ||||||
                                GCC TG GCG GC GACGGA
                                  A  A  _  A
GAM2584  SEC23A   5'  CAGGACCCGTCGCAGCCT    59632         _  _
                                CGGGACCCG CGC GCCT
                                ||||||||| ||| ||||
                                GTCCTGGGC GCG CGGA
                                     A  T
GAM2584  SEC61A1  3'  GGGTACAGCTGCCTGCCT    59633     _  CC  GC
                                GGG AC  GC  GCCTGCCT
                                ||| ||  ||  ||||||||
                                CCC TG  CG  CGGACGGA
                                  A  T_  A_
GAM2584  SEMA7A   3'  GGGGCCCAGCAGCCGCCT    59634     A   C  _  T
                                GGG CCCG GC GCC GCCT
                                ||| |||| || ||| ||||
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                                CCC GGGT CG CGG CGGA
                                  C   _ T  _
GAM2584 SERHL   3' GGAACCCAGACTCTGTCT   59635       C GC  C
                                GGGACCCG GC  CTG CT
                                |||||||| ||  ||| ||
                                CCTTGGGT TG  GAC GA
                                    C A_  A
GAM2584 SMCR7   3' CAGGACCCTCAGCTGCCT   59636       G C C
                                CGGGACCC CG GC TGCCT
                                |||||||| || || |||||
                                GTCCTGGG GT CG ACGGA
                                    A _ _
GAM2584 SPS     5' CGGGGGCTCGCCTGCCT    59637     ACCC G
                                CGGG   GC CGCCTGCCT
                                ||||   || |||||||||
                                GCCC   CG GCGGACGGA
                                  C___ A
GAM2584 TCF6L1  5' GGAACCCGCGTGCGACCC   59638       C CT
                                GGGACCCGCG GC  GCCT
                                |||||||||| ||  ||||
                                CCTTGGGCGC CG  TGGG
                                    A C_
GAM2584 TOPK    5' CGAGACCCTGCAGCTGCCT  59639       GC  C
                                CGGGACCC  GCG CTGCCT
                                ||||||||  ||| ||||||
                                GCTCTGGG  CGT GACGGA
                                    A_  C
GAM2584 TRIM17  5' GGGCCCGCACAGCGCCT    59640    A    _ CT
                                GGG CCCGCGC GC  GCCT
                                ||| ||||||| ||  ||||
                                CCC GGGCGTG CG  CGGA
                                  _     T __
GAM2584 XT2     5' CGGGGCGCGCGCCCAGCCC  59641     ACC      _
                                CGGG  CGCGCGCCT GCCT
                                ||||  ||||||||| ||||
                                GCCC  GCGCGCGGG CGGG
                                  C__       T
GAM2584 ZER6    5' CGGGACTCACGCGGCC     59642      C    CCT
                                CGGGAC CGCGCG  GCC
                                |||||| ||||||  |||
                                GCCCTG GTGCGC  CGG
                                   A    ____
GAM2584 ZFP95   3' CAGGACCTCCTGCCTGCCT  59643      CGCGC
                                CGGGACC   GCCTGCCT
                                |||||||   ||||||||
                                GTCCTGG   CGGACGGA
                                   AGGA_
GAM2584 ZFP95   3' CAGGACCTCCTGCCTGCCT  59643      CGCGC
                                CGGGACC   GCCTGCCT
                                |||||||   ||||||||
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                                GTCCTGG    CGGACGGA
                                   AGGA_
GAM2584  LOC113146 5'  GGGACCCCAGCACCTGCCT   59644       GC
                                GGGACCC  GCGCCTGCCT
                                |||||||  ||||||||||
                                CCCTGGG  CGTGGACGGA
                                   GT
GAM2584  LOC133482 5'  GGGCCCGCGCGGCCT      59645    A      CCT
                                GGG CCCGCGCG   GCCT
                                ||| ||||||||   ||||
                                CCC GGGCGCGC   CGGA
                                  _      ____
GAM2584  LOC145693 5'  GGAATATACATGCCTGCCT   59646     CCC   C
                                GGGA   GCG GCCTGCCT
                                ||||   ||| ||||||||
                                CCTT   TGT CGGACGGA
                                  ATA   A
GAM2584  LOC146057 5'  CGGGACCCGAGCGCGGC    59647        C    CT
                                CGGGACCCG GCGC  GC
                                |||||||||| ||||  ||
                                GCCCTGGGC CGCG  CG
                                     T    C_
GAM2584  LOC146336 3'  AGGACACAGCCTGCCT     59648      CC   C
                                GGGAC  GCG GCCTGCCT
                                |||||  ||| ||||||||
                                TCCTG  TGT CGGACGGA
                                  __   _
GAM2584  LOC147040 5'  CGGGACCCGGCCGCGCCGCCT  59649         __     T
                                CGGGACCCG  CGCGCC GCCT
                                |||||||||  |||||| ||||
                                GCCCTGGGC  GCGCGG CGGA
                                     CG     _
GAM2584  LOC147599 3'  GGGACCCAGGCATGCCT     59650        C   CC
                                GGGACCCG GCG  TGCCT
                                |||||||| |||  |||||
                                CCCTGGGT CGT  ACGGA
                                     C   __
GAM2584  LOC149773 5'  CGGGTCCACACTTTGCCT    59651     AC     GCC
                                CGGG  CCGCGC   TGCCT
                                ||||  ||||||   |||||
                                GCCC  GGTGTG   ACGGA
                                  A_     AA_
GAM2584  LOC151361 3'  GGACCTCGTGCGCCTGCCT   59652      _  C
                                GGACC CG GCGCCTGCCT
                                ||||| || ||||||||||
                                CCTGG GC CGCGGACGGA
                                  A  A
GAM2584  LOC152048 3'  CGGGACCCGACATTGTGC    59653        C   CC_
                                CGGGACCCG GCG   TGC
                                ||||||||| |||   |||
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                                GCCCTGGGC TGT   ACG
                                      _  AAC
GAM2584  LOC155179 3'  GGAACGGCGAGCCTGCCT    59613      CC   C
                                GGGAC  GCG GCCTGCCT
                                |||||  ||| ||||||||
                                CCTTG  CGC CGGACGGA
                                   C_   T
GAM2584  LOC157562 5'  GGACTTGGACCACCTGCCT    59654     CC__  G
                                GGAC    GC CGCCTGCCT
                                ||||    || |||||||||
                                CCTG    TG GTGGACGGA
                                  AACC  _
GAM2584  LOC158292 5'  GGAGCAGCGCTGCCTGCCT    59655     CCC   _
                                GGA   GCGC GCCTGCCT
                                |||   |||| ||||||||
                                CCT   CGCG CGGACGGA
                                  CGT    A
GAM2584  LOC163682 5'  CGGGCCTGCGTGCCTGCCT    59656     A  C   C
                                CGGG CC GCG GCCTGCCT
                                |||| ||  ||| ||||||||
                                GCCC GG CGC CGGACGGA
                                  _ A   A
GAM2584  LOC197322 3'  GGGACCTGCCCTGGAGAGCCT  59657       CGC  G  _____
                                GGGACC   GC CCT    GCCT
                                ||||||   || |||    ||||
                                CCCTGG   CG GGA    CGGA
                                   A__  _   CCTCT
GAM2584  LOC219731 5'  CGGGCCCCGCCTGCCT     59658     A   GCG
                                CGGG CCC   CGCCTGCCT
                                |||| |||   |||||||||
                                GCCC GGG   GCGGACGGA
                                  _   ___
GAM2584  LOC222182 5'  GGGACCTCGCCTGCCT      59659       CGCG
                                GGGACC    CGCCTGCCT
                                ||||||    |||||||||
                                CCCTGG    GCGGACGGA
                                   A___
GAM2584  LOC253681 5'  CGGGACCCGGCCGCGCCGCCT  59649          __     T
                                CGGGACCCG  CGCGCC GCCT
                                |||||||||  |||||| ||||
                                GCCCTGGGC  GCGCGG CGGA
                                     CG     _
GAM2584  LOC254887 5'  CGGGACCCGGGCTCCGC     59660         C  GC
                                CGGGACCCG GC  CTGC
                                |||||||||  ||  ||||
                                GCCCTGGGC CG  GGCG
                                     C  A_
GAM2584  LOC257169 5'  CGGGCCCAGAGCCTGCCT    59661     A   CGC
                                CGGG CCCG   GCCTGCCT
                                |||| ||||   ||||||||
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                                GCCC GGGT   CGGACGGA
                                  _   CT_
GAM2584 LOC51074 5' GGGACCCGCGCGGCCT     59662          CCT
                                GGGACCCGCGCG   GCCT
                                ||||||||||||  ||||
                                CCCTGGGCGCGC   CGGA
                                      ____
GAM2584 LOC56996 3' CAGGATAGGCCGCCTGCCT   59663      CCC  G
                                CGGGA   GC CGCCTGCCT
                                |||||   || |||||||||
                                GTCCT   CG GCGGACGGA
                                   ATC  _
GAM2584 LOC90019 5' GGACTCGTCCACCTGCCT    59664     C  CG
                                GGAC CG  CGCCTGCCT
                                ||||  ||  |||||||||
                                CCTG GC  GTGGACGGA
                                  A  AG
GAM2584 LOC90835 5' CGGGGTCACACACCCCTGCCT  59665     ACC_    G
                                CGGG    CGCGC CCTGCCT
                                ||||    ||||| |||||||
                                GCCC    GTGTG GGACGGA
                                  CAGT    G
GAM2584 LOC91547 3' CGTGATCCGCCCACCTCTGCCT 59666    G  C    G    __
                                CG GA CCGC CGCCT  GCCT
                                ||  ||  |||| |||||  ||||
                                GC CT GGCG GTGGA  CGGA
                                 A  A    G     GA
GAM2585 ATP11B   3'  TTATATGCACGTTTTATAAG   59669          AGCAGC
                                TTATGTGCACG     ATAAG
                                ||||||||||||     |||||
                                AATATACGTGC     TATTC
                                      AAAA__
GAM2585 WHN      3'  TGTGCACGAGGGCTTAAG    59670          CA  A
                                TGTGCACGAG  GC TAAG
                                ||||||||||  ||  ||||
                                ACACGTGCTC  CG ATTC
                                      C_  A
GAM2585 FLJ11017 3'  TATGTGACAAGCAGCAT     59671        C
                                TATGTG ACGAGCAGCAT
                                ||||||  ||||||||||||
                                ATACAC TGTTCGTCGTA
                                   _
GAM2585 KIAA0429 3'  TTATGTGTTAAAGCATAAG   59672        CACG  C
                                TTATGTG    AG AGCATAAG
                                |||||||    ||  ||||||||
                                AATACAC    TT TCGTATTC
                                    AA__  _
GAM2585 KIAA0993 3'  TATGTGCATTTTAGTGCATAAG 59673         CG__  CA
                                TATGTGCA    AG  GCATAAG
                                ||||||||    ||  |||||||
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                                ATACACGT    TC  CGTATTC
                                     AAAA  A_
GAM2585  KIAA1673  3'  CATTATGTGCATGACAAAATAA 59674          C  G   C
              G                   TATTATGTGCA GA CAG ATAAG
                                  |||||||||||  ||  |||  |||||
                                  GTAATACACGT CT GTT TATTC
                                        A  _   T
GAM2585  LOC152263 3'  TTATATGCATTTTCATAAG   59675         CGAGCAG
                                  TTATGTGCA      CATAAG
                                  |||||||||      ||||||
                                  AATATACGT      GTATTC
                                       AAAA___
GAM2585  LOC56181  3'  TATGACGGAGCAGCATAAG   59676      C  _
                                  TGTG ACG AGCAGCATAAG
                                  ||||  |||  ||||||||||
                                  ATAC TGC TCGTCGTATTC
                                    _   C
GAM2586  ARHD      3'  TGTTGCAGTGGAGTTCGGC   59679      A       GTG
                                  TGTT CAGTGGAG   TGGT
                                  ||||  ||||||||   ||||
                                  ACAA GTCACCTC   GCCG
                                    C       AA_
GAM2586  ARHG      5'  TGCTGTAGTGGAGGCAGTG   59680      AC        _
                                  TGTT  AGTGGAGGT GTG
                                  ||||  |||||||||  |||
                                  ACGA  TCACCTCCG CAC
                                    CA        T
GAM2586  KIF5C     3'  TGTTACATGGACTATAGTAC  59681       G   GG
                                  TGTTACA TGGA  TGTGGTAC
                                  |||||||  ||||  ||||||||
                                  ACAATGT ACCT  ATATCATG
                                       _   G_
GAM2586  LY64      3'  TGCTGTAGTGGGGGTGGGT   59682      AC    A   T
                                  TGTT  AGTGG GGTG GGT
                                  ||||  |||||  ||||  |||
                                  ACGA  TCACC CCAC CCA
                                    CA    C   _
GAM2586  PARK2     3'  TTACAGTGGAGCCAAATG    59683          G___
                                  TTACAGTGGAG T  GTG
                                  ||||||||||| |  |||
                                  AATGTCACCTC G  TAC
                                         G TT
GAM2586  PARK2     3'  TTACAGTGGAGCCAAATG    59683          G___
                                  TTACAGTGGAG T  GTG
                                  ||||||||||| |  |||
                                  AATGTCACCTC G  TAC
                                         G TT
GAM2586  PARK2     3'  TTACAGTGGAGCCAAATG    59683          G___
                                  TTACAGTGGAG T  GTG
                                  ||||||||||| |  |||
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                                AATGTCACCTC G  TAC
                                      G TT
GAM2586  PML      3'  TGTGACAGTGGAGGCAGGGC   59684     T         T
                                TGT ACAGTGGAGGTG GGT
                                ||| |||||||||||| |||
                                ACA TGTCACCTCCGT CCG
                                  C          C
GAM2586  PTPRA    3'  TTACAGTGCATGGTGGTAC   59685        GAGGT
                                TTACAGTG    GTGGTAC
                                ||||||||    |||||||
                                AATGTCAC    CACCATG
                                     GTAC_
GAM2586  PTPRA    3'  TTACAGTGCATGGTGGTAC   59685        GAGGT
                                TTACAGTG    GTGGTAC
                                ||||||||    |||||||
                                AATGTCAC    CACCATG
                                     GTAC_
GAM2586  PTPRA    3'  TTACAGTGCATGGTGGTAC   59685        GAGGT
                                TTACAGTG    GTGGTAC
                                ||||||||    |||||||
                                AATGTCAC    CACCATG
                                     GTAC_
GAM2586  SOX10    3'  GTTGTAGTGGAGGAGGAC    59686     AC       TGT  T
                                GTT  AGTGGAGG   GG AC
                                |||  ||||||||   || ||
                                CAA  TCACCTCC   CC TG
                                  CA       T__  _
GAM2586  ZNF10    3'  TGTTGTATGTGGGCATGGT   59687      ACA   GA
                                TGTT   GTG  GGTGTGGT
                                ||||   |||  ||||||||
                                ACAA   TAC  CCGTACCA
                                  CA_   AC
GAM2586  DKFZP564F013 3'  TGTTCATTTCAGTGTGGTA   59688      A  GTGGA
                                TGTT CA    GGTGTGGTA
                                |||| ||    |||||||||
                                ACAA GT    TCACACCAT
                                  _  AAAG_
GAM2586  DKFZP572C163 3'  TGTTATGTGGTAAGGTAT    59689      CA   __
                                TGTTA  GTGG  AGGTGT
                                |||||  ||||  ||||||
                                ACAAT  CACC  TCCATA
                                   A_    AT
GAM2586  FLJ13102  3'  TGTTACAGGGGAGGCCTGTGC  59690         T     G  _
                                TGTTACAG GGAGGT TG GT
                                |||||||| |||||| || ||
                                ACAATGTC CCTCCG AC CG
                                     C     G  A
GAM2586  FLJ14621  3'  TTACAGTGGCCAGTGTGGT   59691         A_
                                TTACAGTGG  GGTGTGGT
                                |||||||||  ||||||||
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                                AATGTCACC  TCACACCA
                                     GG
GAM2586  FLJ14668  3'  TGTTACAGGGGAGAGCCTTAC  59692        T    T  GG
                                TGTTACAG GGAGG GT  TAC
                                |||||||| ||||| ||  |||
                                ACAATGTC CCTCT CG  ATG
                                     C    _ GA
GAM2586  KIAA0329  3'  TGTGGGCAGTGAGGTGTGGT   59693     TA_    G
                                TGT   CAGTG AGGTGTGGT
                                |||   ||||| |||||||||
                                ACA   GTCAC TCCACACCA
                                  CCC    _
GAM2586  KIAA0555  3'  TGTTTCCATGGGGTGTGGT    59694      ACA    A
                                TGTT   GTGG GGTGTGGT
                                ||||   |||| ||||||||
                                ACAA   TACC CCACACCA
                                   AGG   _
GAM2586  KIAA0979  3'  TGTTACAGGGAGTTAAATA    59695        T    GTGT
                                TGTTACAG GGAG    GGTA
                                |||||||| ||||    ||||
                                ACAATGTC CCTC    TTAT
                                     _   AAT_
GAM2586  KIAA1023  3'  TGTTGCAGTGACAATCAGTAC  59696      A     AG  G
                                TGTT CAGTGG  GT TGGTAC
                                |||| ||||||  || ||||||
                                ACAA GTCACT  TA GTCATG
                                   C     GT  _
GAM2586  KIAA1096  3'  TGTTACTGTTGTGGTA      59697       A  GGAGG
                                TGTTAC GT     TGTGGTA
                                ||||||  ||    |||||||
                                ACAATG CA     ACACCAT
                                   A  _____
GAM2586  KIAA1196  3'  TGTTGGGTGGAGGTGAGGC    59698      ACA        T
                                TGTT   GTGGAGGTG GGT
                                ||||   ||||||||| |||
                                ACAA   CACCTCCAC CCG
                                   CC_        T
GAM2586  KIAA1449  3'  TGCTATGGTGGAGGCAGGC    59699      CA        T
                                TGTTA  GTGGAGGTG GGT
                                |||||  ||||||||| |||
                                ACGAT  CACCTCCGT CCG
                                   AC        _
GAM2586  KIAA1938  3'  TGTTACAGGGTGGGGTGC     59700        __    A
                                TGTTACA  GTGG GGTGT
                                |||||||  |||| |||||
                                ACAATGT  CACC CCACG
                                     CC    _
GAM2586  NUDT11    3'  TGTGCAGCTACTGTGTGGTA   59701     TA    GGAG
                                TGT  CAGT    GTGTGGTA
                                |||  ||||    ||||||||
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                                ACA  GTCG    CACACCAT
                                  C_    ATGA
GAM2586  OASIS     3'  TGTACAGTGGGGGTGGGGT   59702     T      A    T
                                TGT ACAGTGG GGTG GGT
                                ||| ||||||| |||| |||
                                ACA TGTCACC CCAC CCA
                                  _      C    C
GAM2586  TIGD4     3'  TGTTTAAGTGGTGTGGTAC   59703      ACAGT  A
                                TGTT    GG GGTGTGGTAC
                                ||||    || ||||||||||
                                ACAA    TC CCACACCATG
                                  AT___  A
GAM2586  ZAP3      3'  TGTACAGTGGAGGAAATAC   59704     T        TGT
                                TGT ACAGTGGAGG   GGTAC
                                ||| ||||||||||   |||||
                                ACA TGTCACCTCC   TTATG
                                  _        T__
GAM2586  LOC152122 3'  TTATGGTGGAAGCTACGTGGT  59705     CA       ___
                                TTA  GTGGAGGT   GTGGT
                                |||  ||||||||   |||||
                                AAT  CACCTTCG   CACCA
                                  AC       ATG
GAM2586  LOC155038 3'  TGTCACAGGGGTGTGGT     59706        GT  A
                                TGTTACA  GG GGTGTGGT
                                |||||||  || ||||||||
                                ACAGTGT  CC CCACACCA
                                     __ _
GAM2586  LOC155179 3'  TGTTGCAGTGACAATCAGTAC  59696      A     AG  G
                                TGTT CAGTGG  GT TGGTAC
                                |||| ||||||  || ||||||
                                ACAA GTCACT  TA GTCATG
                                  C     GT  _
GAM2586  LOC158402 5'  GTTACAGTAGGTGGTA      59707          AGGT
                                GTTACAGTGG    GTGGTA
                                ||||||||||    ||||||
                                CAATGTCATC    CACCAT
                                     _____
GAM2586  LOC219914 3'  TGTTACAGCTCTTAAGGTGGT  59708         GG__   T
                                TGTTACAGT    AGG GTGGT
                                |||||||||    ||| |||||
                                ACAATGTCG    TTC CACCA
                                     AGAA  _
GAM2586  LOC221271 3'  TGTTCAATGTGTGGTA      59709      A   GGAG
                                TGTT CAGT    GTGTGGTA
                                |||| ||||    ||||||||
                                ACAA GTTA    CACACCAT
                                  _   _____
GAM2586  LOC51014  3'  TATTACAGTGGCAATGGT    59710          AGGT
                                TGTTACAGTGG    GTGGT
                                ||||||||||    |||||
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                                ATAATGTCACC   TACCA
                                      GT__
GAM2586 LOC92822 3' TGTTTGGTCATGTGGTA    59711    ACAG  AG
                                TGTT   TGG GTGTGGTA
                                ||||   ||| ||||||||
                                ACAA   ACC TACACCAT
                                  ____  AG
GAM2586 LOC96652 3' TGTTTGGTGGAGGTGGAGT   59712    ACA      TG
                                TGTT  GTGGAGGTG GT
                                ||||  ||||||||| ||
                                ACAA  CACCTCCAC CA
                                  AC_       CT
GAM2587 DOC1    5' CGCTGCGAGCCGACTGTG    59715       A _ _
                                CGCTGCGAG CG C GTG
                                ||||||||| || | |||
                                GCGACGCTC GC G CAC
                                     G  T A
GAM2587 HNRPDL   5' CCGCCGCGCGCACGCGTG    59716       AG_
                                CCGCTGCG  ACGCGTG
                                ||||||||  |||||||
                                GGCGGCGC  TGCGCAC
                                    GCG
GAM2587 MUS81    5' CCGCTGCGCAGCGGCAGTG    59717       _ AC _
                                CCGCTGCG AG  GC GTG
                                |||||||| ||  || |||
                                GGCGACGC TC  CG CAC
                                    G  GC  T
GAM2587 NCOR2    3' CCGCTGCGGCAACGATGTG   59718       A_   C_
                                CCGCTGCG  GACG  GTG
                                ||||||||  ||||  |||
                                GGCGACGC  TTGC  CAC
                                    CG    TA
GAM2587 DPYSL4   5' CGCGTGAGCCGGGACGCGTG  59719    _ ___ A
                                CGC TG   CG GACGCGTG
                                ||| ||   || ||||||||
                                GCG AC   GC CTGCGCAC
                                  C  TCG  C
GAM2587 FARP1    3' CCACTGCGGAAACGAGTG    59720       _    C
                                CCGCTGCG AGACG GTG
                                |||||||| ||||| |||
                                GGTGACGC TTTGC CAC
                                    C    T
GAM2587 LOC255031 5' CCGCTGCAGCCCACCGTG    59721       G  A_  _
                                CCGCTGC AG  CGC GTG
                                ||||||| ||  ||| |||
                                GGCGACG TC  GTG CAC
                                   _ GG  G
GAM2587 LOC257085 5' CCGCCGCGTGCGAACGTGTG  59722       A___   C
                                CCGCTGCG   GACG GTG
                                ||||||||   |||| |||
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                                GGCGGCGC   TTGC CAC
                                    ACGC   A
GAM2588 CLOCK    3' CAGTAAGAATCATAAA     59725      TTTTT
                                CAGTA    GGAATCATAAA
                                |||||    ||||||||||
                                GTCAT    TCTTAGTATTT
                                  _____
GAM2588 DIAPH2   3' CAGTATTTTCTAACATAA    59726        GGAAT
                                CAGTATTTTT    CATAA
                                ||||||||||    |||||
                                GTCATAAAAG    GTATT
                                    ATT__
GAM2588 GOCAP1   3' CAGTATTTTTCTCATAAAAA  59727        GGAA
                                CAGTATTTTT   TCATAAAAA
                                ||||||||||   |||||||||
                                GTCATAAAAA   AGTATTTTT
                                    G___
GAM2588 MTRR     3' TCATATTTCCCAGCATCATAAA 59728    GTA   TG A
          AA                      TCA   TTTT  G ATCATAAAAA
                                |||   ||||  | ||||||||||
                                AGT   AAGG  C TAGTATTTTT
                                  ATA   GT G
GAM2588 MTRR     3' TCATATTTCCCAGCATCATAAA 59728    GTA   TG A
          AA                      TCA   TTTT  G ATCATAAAAA
                                |||   ||||  | ||||||||||
                                AGT   AAGG  C TAGTATTTTT
                                  ATA   GT G
GAM2588 SLC38A2  3' AGTATTTTTGGTACAAAAA   59729        AATC
                                AGTATTTTTGG   ATAAAAA
                                ||||||||||   |||||||
                                TCATAAAAACC   TGTTTTT
                                    A___
GAM2588 TGFBR2   3' TCAGTATTTTTAGGAACTACA 59730        _   C
                                TCAGTATTTTT GGAAT ATA
                                |||||||||| ||||| |||
                                AGTCATAAAAA CCTTG TGT
                                    T   A
GAM2588 BHMT     3' CCAGTAGTGGGTCATAAAA   59731      TTTT  AA
                                TCAGTA   TGG  TCATAAAA
                                ||||||   |||  ||||||||
                                GGTCAT   ACC  AGTATTTT
                                  C___   C_
GAM2588 MGC10612 3' TCAGTATTCTATGTGGAA    59732        ___
                                TCAGTATTTT   TGGAA
                                ||||||||||   |||||
                                AGTCATAAGA   ACCTT
                                    TAC
GAM2588 LOC206426 3' AGTATTTTGGACTCATGAAA  59733       T  A   A
                                AGTATTTT GGA TCAT AAA
                                |||||||| ||| |||| |||
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                                TCATAAAA CCT AGTA TTT
                                    _  G   C
GAM2588 LOC92379 3' TCAGCATTTCTATTCATA    59734          GAA
                                TCAGTATTTTTG  TCATA
                                ||||||||||||  |||||
                                AGTCGTAAAGAT  AGTAT
                                      A__
GAM2589 FLJ10508 3' TATTAGTTACCTTATTCCT   59737         G
                                TATTAGTTAC CTTATTTTT
                                |||||||||| |||||||||
                                ATAATCAATG GAATAAGGA
                                    _
GAM2589 MGC19780 3' TAGTTACGTTTATCAATGT   59738        C    TTT
                                TAGTTACG TTATT  ATGT
                                |||||||| |||||  ||||
                                ATCAATGC AATAG  TACA
                                     A    T__
GAM2589 LOC91115 3' CATTAGTATAATTTATTTTTAT 59739       TACGC
           GT                    TATTAGT    TTATTTTTATGT
                                |||||||    ||||||||||||
                                GTAATCA    AATAAAAATACA
                                   TATTA
GAM2590 AXIN1    3' TGCCGGGGGATGGGGGGGGGTC 59742         CA  A  A
                                TGCTGGGGGA  GG GG GGGTT
                                ||||||||||  || || |||||
                                ACGGCCCCCT  CC CC CCCAG
                                      AC  _  C
GAM2590 BCL2L10  5' TGCTGGGGGGCCGGGCC     59743        ACAG AGGA
                                TGCTGGGGG   G   GGGTT
                                |||||||||   |   |||||
                                ACGACCCCC   C   CCCGG
                                    _____ GG__
GAM2590 CD68     3' TGCTGGGGGGGGGGGGGGC   59744         ACA  A  A
                                TGCTGGGGG   GG GG GGGT
                                |||||||||   || || ||||
                                ACGACCCCC   CC CC CCCG
                                     CCC  _  _
GAM2590 CDKN1A   3' GCTGGGGGGCAGGGGGC     59745        A   AGGA
                                GCTGGGGG CAGG   GGGT
                                |||||||| ||||   ||||
                                CGACCCCC GTCC   CCCG
                                     C   _____
GAM2590 CNTFR    3' TGCTGGGGGGAGGGGG      59746        ACAG   A
                                TGCTGGGGG   GAGG GGG
                                |||||||||   |||| |||
                                ACGACCCCC   CTCC CCC
                                    _____   _
GAM2590 DNAI2    5' TGCTGGGGGGCAGAGGGA    59747         A  GA
                                TGCTGGGGG CAG  GGA
                                ||||||||| |||  |||
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                                ACGACCCCC GTC  CCT
                                     C   TC
GAM2590  DNMT3L   5'  GCTGGGGGATTGGGGTT     59748         CA  AGGAG
                                GCTGGGGGA  GG    GGTT
                                |||||||||  ||    ||||
                                CGACCCCCT  CC    CCAA
                                     AA  _____
GAM2590  GADD45B  3'  TGCTGGGGGGGGAGGGGGTT   59749         ACA    A
                                TGCTGGGGG   GGAGG GGGTT
                                |||||||||   ||||| |||||
                                ACGACCCCC   CCTCC CCCAA
                                      ___    _
GAM2590  MAP4     3'  TGTGGGGGGCGGGAGACAATGT 59750    C     ACA    AGG_
           C                     TG TGGGGG   GGAGG    GTT
                                 || ||||||   |||||    |||
                                 AC ACCCCC   CCTCT    CAG
                                  _     CGC     GTTA
GAM2590  MAP4     3'  TGTGGGGGGCGGGAGACAATGT 59750    C     ACA    AGG_
           C                     TG TGGGGG   GGAGG    GTT
                                 || ||||||   |||||    |||
                                 AC ACCCCC   CCTCT    CAG
                                  _     CGC     GTTA
GAM2590  MIC2     3'  CTGGGGGACGGGGGGGT     59751         A  A  A
                                CTGGGGGAC GG GG GGGT
                                ||||||||| || || ||||
                                GACCCCCTG CC CC CCCA
                                      _  _  _
GAM2590  MNT      3'  TGTTGAGGGGATGGGAGGA   59752    C  _    CA
                                TG TG GGGGA  GGAGGA
                                || || |||||  ||||||
                                AC AC CCCCT  CCTCCT
                                 A  T    AC
GAM2590  PIAS3    3'  TGTTGGGGGACAGCGAAG    59753    C        _
                                TG TGGGGGACAG GAGG
                                || ||||||||| ||||
                                AC ACCCCCTGTC CTTC
                                 A         G
GAM2590  PRG3     3'  TGGGGGACGGGAGGGAGC    59754         A    A
                                TGGGGGAC GGAGG GGGT
                                |||||||| ||||| ||||
                                ACCCCCTG CCTCC CTCG
                                     C    _
GAM2590  SF3A2    3'  TGCTGGGGGGAGGGAGCAGCTTC 59755         CA   GA  G
                                TGCTGGGGGGA  GGAG  GG TTC
                                |||||||||  ||||  || |||
                                ACGACCCCCT  CCTC  TC AAG
                                      C_   G_  G
GAM2590  TFE3     3'  TGCTGGGGGGAAGGCTTCCAGTT 59756         C  AGGAG
                                TGCTGGGGGGA AGG    GGTT
                                |||||||||| |||    ||||
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                                ACGACCCCCT TCC    TCAA
                                      _  GAAGG
GAM2590 TWIST    3' TGCTGAGGGGGTGGGGGGCTC 59757        ACA  A  A
                                TGCTGGGGGG  GG GG GGGTTC
                                |||||||||  || || ||||||
                                ACGACTCCC  CC CC CCCGAG
                                     ___ A  C
GAM2590 ADAR3    3' TGTGGGGGACAGGGT      59758    C       GGAGGA
                                TG TGGGGGACA     GGGT
                                || |||||||||     ||||
                                AC ACCCCCTGT     CCCA
                                _      _______
GAM2590 DEFB118  3' TGGTGGGGGGGTGGGAGGGTC  59759    C     ACAGGA
                                TG TGGGGG     GGAGGGTT
                                || ||||||     ||||||||
                                AC ACCCCC     CCTCCCAG
                                 C     CAC___
GAM2590 DKFZP434K1772 5' GCTGGGGGACAGGGGGCT    59760           AGGA
                                GCTGGGGGACAGG   GGGTT
                                ||||||||||||   |||||
                                CGACCCCCTGTCC   CCCGA
                                      _____
GAM2590 DKFZp547O146 5' TGTTGGGGGATTGGGGGG    59761    C      CA  A  A
                                TG TGGGGGA  GG GG GG
                                || |||||||  || || ||
                                AC ACCCCCT  CC CC CC
                                 A      AA  _  _
GAM2590 FLJ21369  3' TGCTGGGGGTGGGGGGGGGGGG 59762         ACA_  A  A
           T                     TGCTGGGGG   GG GG GGGT
                                |||||||||   || || ||||
                                ACGACCCCC   CC CC CCCA
                                     ACCC  C  C
GAM2590 KCNH4    3' TGTTGGGGGGTAGAGGAG    59763    C     ACA
                                TG TGGGGG  GGAGGAG
                                || ||||||  |||||||
                                AC ACCCCC  TCTCCTC
                                 A     CA_
GAM2590 KIAA0773  3' TGCTGGGGGGAGGGAGGGT   59764         ACA GA
                                TGCTGGGGG  G  GGAGGGT
                                |||||||||  |  |||||||
                                ACGACCCCC  C  CCTCCCA
                                     ___ TC
GAM2590 KIAA1706  3' TGCGTGGGGACAGGAGGGTTC  59765     TG        GGA
                                TGC  GGGGACAGGA  GGGTTC
                                |||  ||||||||||  ||||||
                                ACG  CCCCTGTCCT  CCCAAG
                                  CA        ___
GAM2590 MGC11271  5' TGCTGGGGTACAGGGGA     59766        G    A
                                TGCTGGGG ACAGG GGA
                                |||||||| ||||| |||
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                                ACGACCCC TGTCC CCT
                                    A    _
GAM2590  MGC20235  3'  TGCTGAGGGGGTGGGAGG    59767        ACA  A_
                                TGCTGGGGG   GG  GGAGG
                                |||||||||   ||  |||||
                                ACGACTCCC   CC  CCTCC
                                    ___  AC
GAM2590  MGC2452   5'  TGCTGGGGGGCGGTGCGGGGAGG 59768        ACA_____    A
           GGGGTT                  GCTGGGGG       GGAGG GGGTT
                                |||||||||       ||||| |||||
                                CGACCCCC       CCTCC CCCAA
                                    GCCACGCC    C
GAM2590  RASD2     3'  TGCTGGGGGTGGGAGGGGGT   59769        ACA    A
                                TGCTGGGGG   GGAGG GGGT
                                |||||||||   ||||| ||||
                                ACGACCCCC   CCTCC CCCA
                                    AC_    _
GAM2590  RFX4      3'  CTGGGGGATGGGTGTTGGGTT  59770        CA  AGGA
                                CTGGGGGA  GG    GGGTT
                                ||||||||  ||    |||||
                                GACCCCCT  CC    CCCAA
                                    AC  ACAA
GAM2590  TNFAIP3   3'  TGCTGGGGGGAGGGGAGG     59771        CA  A
                                TGCTGGGGGGA  GG GGAGG
                                ||||||||||  || |||||
                                ACGACCCCCT  CC CCTCC
                                    __  _
GAM2590  LOC127841 5'  TGCTGGGGAGCAGTGCCTGGGT 59772        GA   GAGGA
           TC                    TGCTGGGG  CAG    GGGTTC
                                ||||||||  |||    ||||||
                                ACGACCCC  GTC    CCCAAG
                                    TC   ACGGA
GAM2590  LOC196955 5'  GCTGGGGTGAGGAGGGTT    59773        GACAG
                                GCTGGGG    GAGGAGGGTT
                                |||||||    ||||||||||
                                CGACCCC    CTCCTCCCAA
                                    A____
GAM2590  LOC253868 5'  TGGTGGGGGGGCAGGGATT    59774    C     A   AGGAG
                                TG TGGGGG CAGG    GGTT
                                || |||||| ||||    ||||
                                AC ACCCCC GTCC    CTAA
                                 C     C   _____
GAM2590  LOC257309 5'  TGCTGGGGGGGCAGAGGGA    59747        A   GA
                                TGCTGGGGG CAG  GGA
                                ||||||||| |||  |||
                                ACGACCCCC GTC  CCT
                                    C   TC
GAM2591  CNGB3     3'  TAAACAGCTATACATGTAGGTT 59777        CCCG  T  AC
                                TAAACAGC    AT TG  AGGTT
                                ||||||||    || ||  |||||
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                                ATTTGTCG   TG AC  TCCAA
                                    ATA_  T  A_
GAM2591  EFNA1    3'  GCCCCAAGACAGGTT      59778       TTT
                                GCCCCGA   GACAGGTT
                                |||||||   ||||||||
                                CGGGGTT   CTGTCCAA
                                   ___
GAM2591  STAU     5'  TAAACAGCTTTCAGTGCAGGTT 59779        CCCGATT  A
                                TAAACAGC      TG CAGGTT
                                ||||||||      || ||||||
                                ATTTGTCG      AC GTCCAA
                                    AAAGTC_  _
GAM2591  KIAA1237  3'  TAAACAGCTTTGAGTGGT    59780        CCCGA    CA
                                TAAACAGC    TTTGA  GGT
                                ||||||||    |||||  |||
                                ATTTGTCG    AAACT  CCA
                                   _____    CA
GAM2591  LOC145826 5'  AACAGCCTCATTATAGGTT    59781       C G   TGAC
                                AACAGCC C ATT    AGGTT
                                ||||||| | |||    |||||
                                TTGTCGG G TAA    TCCAA
                                    A _   TA__
GAM2591  LOC149010 5'  AAACAGTTTCCCAACAGGTT   59782       C__   GATTT
                                AAACAG   CCC    GACAGGTT
                                ||||||   |||    ||||||||
                                TTTGTC   GGG    TTGTCCAA
                                   AAA  _____
GAM2591  LOC150967 5'  TGACAGCCCTGAAAGTTAGGTT 59783    A      C  TTTGAC
                                A ACAGCCC GA     AGGTT
                                | ||||||| ||     |||||
                                A TGTCGGG CT     TCCAA
                                 C      A  TTCAA_
GAM2591  LOC255978 3'  TAAACAGCTATAGAGTACAGGT 59784        CCCGATTTG
            T                    TAAACAGC       ACAGGTT
                                ||||||||       |||||||
                                ATTTGTCG       TGTCCAA
                                    ATATCTCA_
GAM2592  SPTBN4   3'  TGCAGATCGGGGCTGGGGGCT  59787    T  A       TTTAT
                                TG CA ATCGGGGCTG     GCT
                                || || ||||||||||     |||
                                AC GT TAGCCCCGAC     CGA
                                 _  C        CCC__
GAM2592  KIAA1032  3'  TGTCAAATGGGTGTGTT     59788        C   GC
                                TGTCAAAT GGG  TGTT
                                |||||||| |||  ||||
                                ACAGTTTA CCC  ACAA
                                    _  AC
GAM2592  KLK15    3'  TGTCAGGCGGGGCTGCT     59789      AAT
                                TGTCA   CGGGGCTGTT
                                |||||   ||||||||||
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                                ACAGT  GCCCCGACGA
                                  CC_
GAM2592 KLK15    3' TGTCAGGCGGGGCTGCT    59789     AAT
                                TGTCA  CGGGGCTGTT
                                |||||  ||||||||||
                                ACAGT  GCCCCGACGA
                                  CC_
GAM2592 KLK15    3' TGTCAGGCGGGGCTGCT    59789     AAT
                                TGTCA  CGGGGCTGTT
                                |||||  ||||||||||
                                ACAGT  GCCCCGACGA
                                  CC_
GAM2592 KLK15    3' TGTCAGGCGGGGCTGCT    59789     AAT
                                TGTCA  CGGGGCTGTT
                                |||||  ||||||||||
                                ACAGT  GCCCCGACGA
                                  CC_
GAM2592 MGC4643  3' GGTCCAGCTGTTTATGCT   59790   ___
                                GG  GGCTGTTTATGCT
                                ||  ||||||||||||
                                CC  TCGACAAATACGA
                                 AGG
GAM2592 LOC220980 5' TCAAACTCCTGTTTATG    59791      CGGGG
                                TCAAAT   CTGTTTATG
                                ||||||   |||||||||
                                AGTTTG   GACAAATAC
                                   AG___
GAM2593 SPTBN4   3' TGCAGATCGGGGCTGGGGGCT 59787   T A      ATTTAT
                                TG CA ATCGGGGCT    GCT
                                || || |||||||||     |||
                                AC GT TAGCCCCGA    CGA
                                 _ C       CCCC__
GAM2593 DKFZP434D1335 3' TATCAAATCTTCATTTATG   59794        GGGGC
                                TGTCAAATC   TATTTATG
                                |||||||||   ||||||||
                                ATAGTTTAG   GTAAATAC
                                     AA___
GAM2593 FLJ20035 3' TGTAAATCATATTTATGC    59795    C    GGGC
                                TGT AAATCG   TATTTATGC
                                ||| ||||||   |||||||||
                                ACA TTTAGT   ATAAATACG
                                  _    _____
GAM2594 ADAM12   5' GCCCGGGGACTAGGAAGAGCG 59798       _ CAA  C  A
                                GCCCGGGG C   GAA AG TG
                                |||||||| |   ||| || ||
                                CGGGCCCC G   CTT TC GC
                                     T ATC   C  _
GAM2594 BCAT2    3' GCTGGGGGCCAAGATGCCTGGG 59799   CC       ACAGAT
            TC                   GC  GGGGCCAAGA    GGTC
                                ||  ||||||||||    ||||
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                                CG  CCCCGGTTCT     CCAG
                                 AC         ACGGAC
GAM2594  DUSP1    5'  CGGGGCCAAGGGCAGGGC    59800          AA   AT
                                CGGGGCCAAG  CAG  GGT
                                ||||||||||  |||  |||
                                GCCCCGGTTC  GTC  CCG
                                      CC   __
GAM2594  ENIGMA   3'  GCTCGGGCCAGGAGCCAGGGT  59801    C    G   A A_   AT
                                GC CGGG CCA GA  CAG  GGT
                                || |||| ||| ||  |||  |||
                                CG GCCC GGT CT  GTC  CCA
                                 A    _   C  CG   __
GAM2594  FMOD     3'  GGAGCCAAGAACGTAGTC    59802           AGA
                                GGGGCCAAGAAC   TGGTC
                                ||||||||||||   |||||
                                CCTCGGTTCTTG   ATCAG
                                       C__
GAM2594  GALNT2   3'  CCGGGGCCGAGGCCGGTGGTC  59803         A  AACAGA
                                CCGGGGCC AG     TGGTC
                                ||||||||  ||     |||||
                                GGCCCCGG TC     ACCAG
                                     C  CGGCC_
GAM2594  HS3ST3B1 5'  GCTCGGGGCCAGGAGGACG    59804    C       A  ACA
                                GC CGGGGCCA GA   GATG
                                || ||||||||  ||   ||||
                                CG GCCCCGGT CT   CTGC
                                 A       C  C__
GAM2594  KIF5C    5'  CCGGGGCCGGGAACGAC     59805         AA    A
                                CCGGGGCC  GAAC GAT
                                ||||||||  |||| |||
                                GGCCCCGG  CTTG CTG
                                     CC    _
GAM2594  NCOR2    3'  GCCCGGGGCGGGAGTCTTAGT  59806         CAA  ACAGA
                                GCCCGGGGC   GA    TGGT
                                |||||||||   ||    ||||
                                CGGGCCCCG   CT    ATCA
                                     CC_  CAGA_
GAM2594  OTX1     5'  GCCCGGGGCCAGGAGCGGT    59807          A  ACA A
                                GCCCGGGGCCA GA   G TGGT
                                |||||||||| ||   | ||||
                                CGGGCCCCGGT CT   C GCCA
                                      C  ____ _
GAM2594  PRKY     3'  GCTGGGGGCAAGGCAGATGGT  59808    CC    C   AA
                                GC  GGGGC AAG  CAGATGGT
                                ||  ||||| |||  ||||||||
                                CG  CCCCG TTC  GTCTACCA
                                 AC     _   C_
GAM2594  PTPRN    3'  GCCCGGGGCTGAGAAGCAG   59809         CA   _
                                GCCCGGGGC  AGAA CAG
                                |||||||||  |||| |||
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                                CGGGCCCCG  TCTT GTC
                                     AC    C
GAM2594  SMG1     5'  GCCCGGGGCTGAGGAGGAAGC  59810         CA  AAC  AT
                                GCCCGGGGC  AG   AG  GGT
                                |||||||||  ||   ||  |||
                                CGGGCCCCG  TC   TC  TCG
                                     AC  C__  CT
GAM2594  TP53BP1  5'  GCCCGGGGCAAGGACAG     59811         C   A
                                GCCCGGGGC AAG ACAG
                                ||||||||| ||| ||||
                                CGGGCCCCG TTC TGTC
                                     _  C
GAM2594  VGF      3'  GCCCGGGGACAGGGGC      59812         CCAAGA    AT
                                GCCCGGGG     ACAG  GGT
                                ||||||||     ||||  |||
                                CGGGCCCC     TGTC  CCG
                                     _______   C_
GAM2594  APCL     3'  GCCCGGGGTCAAGCAACGGC  59813         C    AACA
                                GCCCGGGG CAAG    GATGGT
                                |||||||| ||||    ||||||
                                CGGGCCCC GTTC    TTGCCG
                                     A   G___
GAM2594  FLJ23590 5'  GCCCGGGGCAGGGAATAGA   59814         CAA   C
                                GCCCGGGGC   GAA AGA
                                |||||||||   ||| |||
                                CGGGCCCCG   CTT TCT
                                     TCC   A
GAM2594  KIAA0408 3'  GCTGGGGGCCAAGGAAGTGGTC 59815    CC       AAC  A
                                GC  GGGGCCAAG   AG TGGTC
                                ||  |||||||||   || |||||
                                CG  CCCCGGTTC   TC ACCAG
                                 AC        CT_  _
GAM2594  KIAA1260 5'  GCCTGAGGTTAAGAACAA    59816     C    CC
                                GCC GGGG  AAGAACAG
                                ||| ||||  ||||||||
                                CGG CTCC  TTCTTGTT
                                  A   AA
GAM2594  MGC5442  3'  GCCCGGGGCCGAGGCAG     59817          A  AA
                                GCCCGGGGCC AG  CAG
                                |||||||||| ||  |||
                                CGGGCCCCGG TC  GTC
                                     C  C_
GAM2594  PIP5K2B  3'  CCTGGGGCCAAGGCAGTGGT   59818    C       AA   A
                                CC GGGGCCAAG  CAG TGGT
                                || |||||||||  ||| ||||
                                GG CCCCGGTTC  GTC ACCA
                                 A        C_  _
GAM2594  PIP5K2B  3'  CCTGGGGCCAAGGCAGTGGT   59818    C       AA   A
                                CC GGGGCCAAG  CAG TGGT
                                || |||||||||  ||| ||||
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                                GG CCCCGGTTC  GTC ACCA
                                 A       C_  _
GAM2594  PROZ     3'  CGTGGGCCAAGCGGGTGGTC  59819   _      AACAGA
                                CG GGGCCAAG     TGGTC
                                || ||||||||     |||||
                                GC CCCGGTTC     ACCAG
                                 A       GCCC__
GAM2594  ST7L     3'  GCCCAGGGTTGGGGGGCACCAGA 59820        CCAAGAA___   TG
              GTC                   GCCCGGGG        CAGA  GTC
                                ||||||||        ||||  |||
                                CGGGTCCC        GTCT  CAG
                                    AACCCCCGTG   __
GAM2594  USP22    5'  GCCCGGGCGCCGAGAACA    59821       _  A
                                GCCCGGG GCC AGAACA
                                ||||||| ||| ||||||
                                CGGGCCC CGG TCTTGT
                                    G   C
GAM2594  LOC145694 5'  GCCTCGGGGCTGGGGGCAGGCG 59822    _    CAAGAA   ATG
              TC                    GCC CGGGGC     CAG   GTC
                                ||| ||||||     |||   |||
                                CGG GCCCCG     GTC   CAG
                                 A     ACCCCC   CG_
GAM2594  LOC149478 5'  GCTCGGGGACAGGAACAGAC   59823    C    C  A
                                GC CGGGG CA GAACAGAT
                                || ||||| || ||||||||
                                CG GCCCC GT CTTGTCTG
                                 A    T  C
GAM2594  LOC220565 5'  GCCCGGGGCTGAGGAGGAAGC  59810        CA  AAC  AT
                                GCCCGGGGC  AG   AG  GGT
                                |||||||||  ||   ||  |||
                                CGGGCCCCG  TC   TC  TCG
                                     AC  C__  CT
GAM2594  LOC254105 3'  GCCCAGGGGCTGAGGTGGT    59824     _    CAAGAAC  A
                                GCCC GGGGC      AG TGGT
                                |||| |||||      || ||||
                                CGGG CCCCG      TC ACCA
                                  T    AC_____  C
GAM2594  LOC257458 5'  GCCCGGGGTTGGTGACGCTGTC 59825        CCAAGAACA   __
                                GCCCGGGG        GATG  GTC
                                ||||||||        ||||  |||
                                CGGGCCCC        CTGC  CAG
                                    AACCA____    GA
GAM2594  LOC257479 5'  GCCCGGGGCGCAGGAGCAG   59826        _  A  A
                                GCCCGGGGC CA GA CAG
                                ||||||||| || || |||
                                CGGGCCCCG GT CT GTC
                                     C  C  C
GAM2594  LOC257482 3'  GCAAAGAGGACAGATGGT    59827    C   __
                                GC AAGA  ACAGATGGT
                                || ||||  |||||||||
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                                CG TTCT  TGTCTACCA
                                 T   CC
GAM2594 LOC80298 5' GCCTGGAGCCGGGATTTCGGTC 59828    C    AA  ACAGA
                                GCC GGGGCC  GA    TGGTC
                                ||| ||||||  ||    |||||
                                CGG CCTCGG  CT    GCCAG
                                  A     CC  AAA__
GAM2594 LOC91286 3' GGGGAACAGATGGTC      59829     CCAAG
                                GGGG    AACAGATGGTC
                                ||||    ||||||||||
                                CCCC    TTGTCTACCAG

                                 _____
GAM2594 LOC93166 5' GCCCGGGGCCGGAGGTGGC   59830         AAGAAC  A
                                GCCCGGGGCC     AG TGGT
                                ||||||||||     || ||||
                                CGGGCCCCGG     TC ACCG
                                      CC____  C
GAM2595 FOXD2    5' CTTCGCCGCCGCTCCTGC    59833          GA  C
                                CTTCGCCGCCGC  CC GC
                                ||||||||||||  || ||
                                GAAGCGGCGGCG  GG CG
                                       A_  A
GAM2595 MYO1E    5' TACTCGCCGCTCGCCGC     59834     T    _  GACC
                                TACT CGCCGC CGC    CGC
                                |||| |||||| |||    |||
                                ATGA GCGGCG GCG    GCG
                                  _     A  _____
GAM2595 PKD1     5' CTGCGCGGCCGCGACCTGC   59835    T  C       C
                                CT CGC GCCGCGACC GC
                                || ||| |||||||| ||
                                GA GCG CGGCGCTGG CG
                                 C  C       A
GAM2595 REV3L    5' TTCGCCGCCGCCGCCA      59836          GACC
                                TTCGCCGCCGC    CGCCA
                                ||||||||||    |||||
                                AAGCGGCGGCG    GCGGT

                                 _____
GAM2595 RGS19IP1 5' CTCCGCCGCCGCCGCCGC    59837          GAC
                                CTTCGCCGCCGC   CCGC
                                ||||||||||||   ||||
                                GAGGCGGCGGCG   GGCG
                                       GC_
GAM2595 UBE3A    5' TTCGCTGCCGCCACCGC     59838      C    G   C
                                TTCGC GCCGC ACC GC
                                ||||| ||||| ||| ||
                                AAGCG CGGCG TGG CG
                                   A    G   _
GAM2595 ADPRTL2  5' CCGTCGCCGCCGCGCCGC    59839    _        AC
                                CT TCGCCGCCGCG  CCGC
                                || ||||||||||  ||||
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                                GG AGCGGCGGCGC  GGCG
                                 C        __
GAM2595  DKFZP566A1524 5'  CTCTGCCGCCCGCTCCGCC   59840    TC     G  AC
                                CT  GCCGCC CG  CCGCC
                                ||  |||||| ||  |||||
                                GA  CGGCGG GC  GGCGG
                                 GA     _  GA
GAM2595  HUMAGCGB  5'  TACTTCGCCGACTGCTCCCGCC 59841          _ C  GA
                                TACTTCGCCG C GC  CCCGCC
                                |||||||||| | ||  ||||||
                                ATGAAGCGGC G CG  GGGCGG
                                      T A  A_
GAM2595  MESDC1    5'  TTCGCCGCCGCCGCCGC     59842          GAC
                                TTCGCCGCCGC   CCGC
                                ||||||||||   ||||
                                AAGCGGCGGCG   GGCG
                                      GC_
GAM2595  NCOR1     5'  CTTCGCCACCTTGGCCGCCA   59843         GCGAC
                                CTTCGCCGCC    CCGCCA
                                ||||||||||    ||||||
                                GAAGCGGTGG    GGCGGT
                                      AACC_
GAM2595  LOC145581 5'  CACTTCGCTGCCCTTTGCCA   59844        C   GCGACCC
                                TACTTCGC GCC      GCCA
                                |||||||| |||      ||||
                                GTGAAGCG CGG      CGGT
                                     A   GAAA___
GAM2595  LOC145748 5'  CTCGCGACCCGCGACCCGCCAC 59845      CG_
                                TTCGC   CCGCGACCCGCCAC
                                |||||   ||||||||||||||
                                GAGCG   GGCGCTGGGCGGTG
                                   CTG
GAM2595  LOC256158 5'  CTCCAGCCGCGACTCG      59846      CC       C
                                CTTCG  GCCGCGAC CG
                                |||||  |||||||| ||
                                GAGGT  CGGCGCTG GC
                                   __       A
GAM2596  BRCA1     3'  TCTAATACCTGCCTCAGAATTT 59849    CG        ___    C
            CCT                   TC  AATACCTGTC   GAAT TCCT
                                ||  ||||||||||   |||| ||||
                                AG  TTATGGACGG   CTTA AGGA
                                 A_        AGT    A
GAM2596  BRCA1     3'  TCTAATACCTGCCTCAGAATTT 59849    CG        ___    C
            CCT                   TC  AATACCTGTC   GAAT TCCT
                                ||  ||||||||||   |||| ||||
                                AG  TTATGGACGG   CTTA AGGA
                                 A_        AGT    A
GAM2596  BRCA1     3'  TCTAATACCTGCCTCAGAATTT 59849    CG        ___    C
            CCT                   TC  AATACCTGTC   GAAT TCCT
                                ||  ||||||||||   |||| ||||
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                                AG  TTATGGACGG   CTTA AGGA
                                 A_       AGT    A
GAM2596  BRCA1    3'  TCTAATACCTGCCTCAGAATTT 59849    CG        ___    C
              CCT                  TC  AATACCTGTC   GAAT TCCT
                                ||  ||||||||||   ||||  ||||
                                AG  TTATGGACGG   CTTA AGGA
                                 A_       AGT    A
GAM2596  BRCA1    3'  TCTAATACCTGCCTCAGAATTT 59849    CG        ___    C
              CCT                  TC  AATACCTGTC   GAAT TCCT
                                ||  ||||||||||   ||||  ||||
                                AG  TTATGGACGG   CTTA AGGA
                                 A_       AGT    A
GAM2596  BRCA1    3'  TCTAATACCTGCCTCAGAATTT 59849    CG        ___    C
              CCT                  TC  AATACCTGTC   GAAT TCCT
                                ||  ||||||||||   ||||  ||||
                                AG  TTATGGACGG   CTTA AGGA
                                 A_       AGT    A
GAM2596  BRCA1    3'  TCTAATACCTGCCTCAGAATTT 59849    CG        ___    C
              CCT                  TC  AATACCTGTC   GAAT TCCT
                                ||  ||||||||||   ||||  ||||
                                AG  TTATGGACGG   CTTA AGGA
                                 A_       AGT    A
GAM2596  BRCA1    3'  TCTAATACCTGCCTCAGAATTT 59849    CG        ___    C
              CCT                  TC  AATACCTGTC   GAAT TCCT
                                ||  ||||||||||   ||||  ||||
                                AG  TTATGGACGG   CTTA AGGA
                                 A_       AGT    A
GAM2596  BRCA1    3'  TCTAATACCTGCCTCAGAATTT 59849    CG        ___    C
              CCT                  TC  AATACCTGTC   GAAT TCCT
                                ||  ||||||||||   ||||  ||||
                                AG  TTATGGACGG   CTTA AGGA
                                 A_       AGT    A
GAM2596  BRCA1    3'  TCTAATACCTGCCTCAGAATTT 59849    CG        ___    C
              CCT                  TC  AATACCTGTC   GAAT TCCT
                                ||  ||||||||||   ||||  ||||
                                AG  TTATGGACGG   CTTA AGGA
                                 A_       AGT    A
GAM2596  BRCA1    3'  TCTAATACCTGCCTCAGAATTT 59849    CG        ___    C
              CCT                  TC  AATACCTGTC   GAAT TCCT
                                ||  ||||||||||   ||||  ||||
                                AG  TTATGGACGG   CTTA AGGA
                                 A_       AGT    A
GAM2596  BRCA1    3'  TCTAATACCTGCCTCAGAATTT 59849    CG        ___    C
              CCT                  TC  AATACCTGTC   GAAT TCCT
                                ||  ||||||||||   ||||  ||||
                                AG  TTATGGACGG   CTTA AGGA
                                 A_       AGT    A
GAM2596  CD1D     5'  GAATACCTCTTGAATAAATTCC 59850        GTC    C___
              T                    GAATACCT   GAAT    TCCT
                                |||||||||   ||||    ||||
                                CTTATGGA   CTTA    AGGA
                                     GAA    TTTA
GAM2596  HOXA7    3'  TCTGAATACCTGTTCTGCCC   59851    C        CGAA   _
                                TC GAATACCTGT    TCT CCT
                                ||  ||||||||||    |||  |||
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                                AG CTTATGGACA   AGA GGG
                                 A       _____  C
GAM2596 NFE2L1   3' GAATATTGGGAATCTCCT   59852     CC  TC
                                GAATA  TG  GAATCTCCT
                                ||||||  ||  |||||||||
                                CTTAT  AC  CTTAGAGGA
                                   A_  C_
GAM2596 PRKACG   3' CTCCAAATATCTGGGCTTCCT  59853        C   TCGAATC
                                CTCCGAATA CTG     TCCT
                                ||||||||| |||     ||||
                                GAGGTTTAT GAC     AGGA
                                     A  CCGA___
GAM2596 CAMK2G   3' CTCCGGCTGGAATCTC     59854     AATAC   TC
                                CTCCG    CTG  GAATCTC
                                |||||    |||  |||||||
                                GAGGC    GAC  CTTAGAG
                                   C_____  __
GAM2596 KIAA0620 3' TCCGGTACTCAGGAATCTCCT  59855     AA   CTGTC
                                TCCG  TAC    GAATCTCCT
                                ||||  |||    |||||||||
                                AGGC  ATG    CTTAGAGGA
                                  C_   AGTC_
GAM2596 ZNF304   3' CTCTAGAATGTTCGAATCTCCT 59856     C_    ACCTG
                                CTC  GAAT    TCGAATCTCCT
                                |||  ||||    ||||||||||
                                GAG  CTTA    AGCTTAGAGGA
                                  AT   CA___
GAM2596 LOC146136 5' TCCAAATGCTTGTCGAAT    59857       ACC
                                TCCGAAT   TGTCGAAT
                                |||||||   ||||||||
                                AGGTTTA   ACAGCTTA
                                    CGA
GAM2596 LOC146443 5' CTCCGAATCTCTGCCTGGGTCT 59858        AC    GAA_
            CCT                   CTCCGAAT  CTGTC    TCTCCT
                                |||||||  |||||   ||||||
                                GAGGCTTA  GACGG    AGAGGA
                                     GA    ACCC
GAM2596 LOC151996 5' CTCCAGATATAATAAAATCTCC 59859      A   CCT  C
            T                    CTCCG ATA   GT GAATCTCCT
                                |||||  |||   ||  |||||||||
                                GAGGT TAT   TA TTTAGAGGA
                                   C   AT_  T
GAM2596 LOC152048 3' TCCGAATACCTCTTGAAC    59860          GTC
                                TCCGAATACCT   GAAT
                                ||||||||||   ||||
                                AGGCTTATGGA   CTTG
                                       GAA
GAM2596 LOC206426 5' CTCGGAATCGAATCTC      59861     C  ATACCT       C
                                CTC GA     GTCGAATCT C
                                |||  ||     ||||||||| |
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                                GAG CT     TAGCTTAGA G
                                  C _______        A
GAM2596  LOC220565 3'  TCCAAATGCTTGTCGAAT    59857        ACC
                                TCCGAAT   TGTCGAAT
                                |||||||   ||||||||
                                AGGTTTA   ACAGCTTA
                                    CGA
GAM2597  ACCN2     3'  GCACCCAGAAGGAGGA      59864        CGC
                                GCACCC   GAAGGAGGA
                                ||||||   |||||||||
                                CGTGGG   CTTCCTCCT
                                   T__
GAM2597  ADM       3'  AAGCCCCCAGAAGGAGG     59865      A    C
                                AAGC CCCCG GAAGGAGG
                                |||| ||||| ||||||||
                                TTCG GGGGT CTTCCTCC
                                  _    _
GAM2597  ADRA2B    3'  AAGCACCCACCTGGGGGGA    59866        C  GAA  A
                                AAGCACCC GC   GG GGA
                                |||||||| ||   || |||
                                TTCGTGGG TG   CC CCT
                                    _ GAC  C
GAM2597  AXIN1     3'  GCCCTCAGAAAGGAGGA     59867     A  C  C
                                GC CC CG GAAGGAGGA
                                || || || |||||||||
                                CG GG GT TTTCCTCCT
                                 _ A  C
GAM2597  BCL2      3'  AAGCCCCCGCGGAAGGAGG   59868      A      _
                                AAGC CCCCGCG AAGGAGG
                                |||| ||||||| |||||||
                                TTCG GGGGCGC TTCCTCC
                                  _      C
GAM2597  CA7       3'  AGCACCCCCCCAGGGAGGA    59869        G  AA
                                AGCACCCC CG  GGAGGA
                                |||||||| ||  ||||||
                                TCGTGGGG GT  CCTCCT
                                    G  C_
GAM2597  CARD15    3'  AAACACCGGAAAGGAGG     59870        CCGC
                                AAGCACC    GAAGGAGG
                                |||||||    ||||||||
                                TTTGTGG    TTTCCTCC
                                    CC__
GAM2597  CBL       5'  AAGCAGGGCGTGAAGGAGG   59871       CCC  C
                                AAGCA   CG GAAGGAGG
                                |||||   || ||||||||
                                TTCGT   GC CTTCCTCC
                                  CCC  A
GAM2597  ELL       3'  AGACCCTGCCCAAGGAGGA   59872     C    C  G_
                                AG ACCC GC  AAGGAGGA
                                || |||| ||  ||||||||
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                                TC TGGG CG  TTCCTCCT
                                 _   A  GG
GAM2597  HNF4A    3'  AGCAGCAGAAGGAGGA      59873      CCCC  _
                                AGCA   GC GAAGGAGGA
                                ||||   || |||||||||
                                TCGT   CG CTTCCTCCT
                                  ____  T
GAM2597  HOXA3    3'  AAGCATCCCCAGAGGA      59874      _   GCGAA
                                AAGCA CCCC    GGAGGA
                                ||||| ||||    ||||||
                                TTCGT GGGG    TCTCCT
                                  A   _____
GAM2597  ITPR3    3'  AACTACCCACAAGGAGGA    59875     AC    G
                                AGC  CCCGC AAGGAGGA
                                |||  ||||| |||||||||
                                TTG  GGGTG TTCCTCCT
                                  AT   _
GAM2597  MEN1     5'  AAGCACCCCAATGAGGA     59876         CGAAG
                                AAGCACCCCG    GAGGA
                                ||||||||||    |||||
                                TTCGTGGGGT    CTCCT
                                     TA___
GAM2597  MYO6     3'  AAGACACTGCAAAGGAGGA   59877    _  CCC
                                AAG CAC   GCGAAGGAGGA
                                ||| |||   ||||||||||
                                TTC GTG   CGTTTCCTCCT
                                  T   A__
GAM2597  NPC1     5'  AGCACCCCGCGCAGGAGGA   59878          A
                                AGCACCCCGCG AGGAGGA
                                |||||||||| |||||||
                                TCGTGGGGCGC TCCTCCT
                                     G
GAM2597  NR1I2    3'  AAGCAGCTCGGAAGAGGAGG  59879      CCC  C  __
                                AAGCA   CG GA  AGGAGG
                                |||||   || ||  ||||||
                                TTCGT   GC CT  TCCTCC
                                   CGA  _  TC
GAM2597  NR1I2    3'  AAGCAGCTCGGAAGAGGAGG  59879      CCC  C  __
                                AAGCA   CG GA  AGGAGG
                                |||||   || ||  ||||||
                                TTCGT   GC CT  TCCTCC
                                   CGA  _  TC
GAM2597  OSM      3'  AAACACGGAAAGGAGGA     59880       CCC C
                                AAGCAC   G GAAGGAGGA
                                ||||||   | |||||||||
                                TTTGTG   C TTTCCTCCT
                                   ___ C
GAM2597  OXTR     3'  AAGCCACCCCAAGGAGG     59881     _     CGA
                                AAGC ACCCCG   AGGAGG
                                |||| ||||||   ||||||
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                                TTCG TGGGGT   TCCTCC
                                  G    ___
GAM2597  PCDHA2   3'  AAGCACATTGGAAAAAAGGAGG 59882       CCCGC___
             A                    AAGCAC       GAAGGAGGA
                                  ||||||       |||||||||
                                  TTCGTG       TTTCCTCCT
                                     TAACCTTT
GAM2597  PRV1     3'  AAGCACCCCAGGAGG       59883         GCGA
                                  AAGCACCCC    AGGAGG
                                  |||||||||    ||||||
                                  TTCGTGGGG    TCCTCC
                                               _____
GAM2597  RASGRP1  3'  AAGTACCCCCAAAAAGGA    59884     C    G    G
                                  AAG ACCCC CGAAG AGGA
                                  ||| ||||| ||||| ||||
                                  TTC TGGGG GTTTT TCCT
                                    A    _    _
GAM2597  SERPINE1 3'  AGCACCCCTGTACTGGGGAGG  59885        ___  GAA
                                  AGCACCCC   GC   GGAGG
                                  ||||||||   ||   |||||
                                  TCGTGGGG   TG   CCTCC
                                       ACA  ACC
GAM2597  TACC1    3'  AAGACCCCAAAGAGG       59886     C     CGA
                                  AAG ACCCCG   AGGAGG
                                  ||| ||||||   ||||||
                                  TTC TGGGGT   TTCTCC
                                    _     ___
GAM2597  ZNF26    3'  AAGCACCCCAGAGAGG      59887          C  AG
                                  AAGCACCCCG GA  GAGG
                                  |||||||||| ||  ||||
                                  TTCGTGGGGT CT  CTCC
                                               _ __
GAM2597  BLCAP    3'  AAGCTCCTGGCGGGAGGA    59888      A  CC   AA
                                  AAGC CC  GCG  GGAGGA
                                  |||| ||  |||  ||||||
                                  TTCG GG  CGC  CCTCCT
                                    A  AC   __
GAM2597  BLCAP    3'  AGACCCTGACAAGGAGG     59889    C   C_  G
                                  AG ACCC  GC AAGGAGG
                                  || ||||  || |||||||
                                  TC TGGG  TG TTCCTCC
                                   _    AC  _
GAM2597  C20orf27 5'  GCACCCCGGGGCCGGGGAGG  59890        _____  AA
                                  GCACCCCG    CG  GGAGG
                                  ||||||||    ||  |||||
                                  CGTGGGGC    GC  CCTCC
                                       CCCG  C_
GAM2597  CACNG4   3'  AAACACCCTTTTTCGGGGAGG  59891        CG___  AA
                                  AAGCACCC    CG  GGAGG
                                  ||||||||    ||  |||||
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                                TTTGTGGG    GC  CCTCC
                                    AAAAA  C_
GAM2597 CDIPT    3' AGCACCGCCTGGATGGAGG   59892       _ GC  A
                                AGCACC CC  GA GGAGG
                                |||||| ||  || |||||
                                TCGTGG GG  CT CCTCC
                                   C  AC  A
GAM2597 DAPK3    3' GCACCCCACACCCGGGGGA   59893         AA_  A
                                GCACCCCGCG   GG GGA
                                ||||||||||   || |||
                                CGTGGGGTGT   CC CCT
                                     GGG  C
GAM2597 DKFZP434J193 3' AAGCACCTCCTCAAGGAGG   59894        _  G G
                                AAGCACC CC C AAGGAGG
                                ||||||| || | |||||||
                                TTCGTGG GG G TTCCTCC
                                    A  A _
GAM2597 FLJ00024 3' AGCCCCCAAAAGAGGA     59895     A   GC
                                AGC CCCC  GAAGGAGGA
                                ||| ||||  |||||||||
                                TCG GGGG  TTTTCTCCT
                                  _   __
GAM2597 FLJ12704 3' AGCACCCCATCCTTGAAGGA  59896         CGAA_
                                AGCACCCCG    GGAGGA
                                |||||||||    ||||||
                                TCGTGGGGT    CTTCCT
                                     AGGAA
GAM2597 FLJ21687 3' AAGCACGCCAGACTGAGGA   59897       C   C  AG
                                AAGCAC CCG GA  GAGGA
                                |||||| ||| ||  |||||
                                TTCGTG GGT CT  CTCCT
                                   C   _  GA
GAM2597 GNB1L    3' GCACTCCACAAAAGGA      59898      C     AG
                                GCAC CCGCGA  GAGGA
                                |||| ||||||  |||||
                                CGTG GGTGTT  TTCCT
                                  A     __
GAM2597 IMP13    3' AACCACCCCGCCCCAAGGA   59899    G       GAAG
                                AA CACCCCGC    GAGGA
                                || ||||||||    |||||
                                TT GTGGGGCG    TTCCT
                                 G       GGG_
GAM2597 KIAA0014 3' GCTGCCCCGCGAAGGGCGG   59900    A_         A_
                                GC  CCCCGCGAAGG  GG
                                ||  ||||||||||  ||
                                CG  GGGGCGCTTCC  CC
                                 AC          CG
GAM2597 KIAA0836 3' AAGCAACCACAAGGAGGA    59901       CC    G
                                AAGCA  CCGC AAGGAGGA
                                |||||  |||| ||||||||
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                                TTCGT  GGTG TTCCTCCT
                                  T_   _
GAM2597 KIAA1430 5' GCGCCCCGCGAGCAGGA     59902    A       A G
                                GC CCCCGCGA G AGGA
                                || |||||||| | ||||
                                CG GGGGCGCT C TCCT
                                 C       _ G
GAM2597 KIAA1509 3' AACACCCCGAGACCGGGGA   59903         C  A_  A
                                AGCACCCCG GA  GG GGA
                                ||||||||| ||  || |||
                                TTGTGGGGC CT  CC CCT
                                      T  GG  _
GAM2597 KIAA1549 3' AGCACCAGAAGAAGGAGGA   59904       CCGC
                                AGCACC   GAAGGAGGA
                                ||||||   |||||||||
                                TCGTGG   CTTCCTCCT
                                   TCTT
GAM2597 KIAA1750 3' GCTACCACAAAGGAGGA     59905    ACC
                                GC   CCGCGAAGGAGGA
                                ||   ||||||||||||
                                CG   GGTGTTTCCTCCT
                                 AT_
GAM2597 MGC16169 5' AAGCACAAAGACAAGGGGGA  59906       CCC_   A  A
                                AAGCAC   GCGA GG GGA
                                ||||||   |||| || |||
                                TTCGTG   TGTT CC CCT
                                   TTTC   C  _
GAM2597 MIC2L1   3' AAGCACCCGGGGCGGGGGG   59907        C__   AA  A
                                AAGCACCC   GCG  GG GG
                                ||||||||   |||  || ||
                                TTCGTGGG   CGC  CC CC
                                     CCC   C_  _
GAM2597 NPTXR    3' GGACACACAAAGGAGG      59908   A   CCC
                                A GCAC   GCGAAGGAGG
                                | ||||   ||||||||||
                                C TGTG   TGTTTCCTCC
                                 C   ___
GAM2597 NPTXR    3' GGACACACAAAGGAGG      59908   A   CCC
                                A GCAC   GCGAAGGAGG
                                | ||||   ||||||||||
                                C TGTG   TGTTTCCTCC
                                 C   ___
GAM2597 ODC-p    5' AACACCCCGAGGAGG       59909        CGA
                                AGCACCCCG   AGGAGG
                                |||||||||   ||||||
                                TTGTGGGGC   TCCTCC
                                      ___
GAM2597 ORCTL4   3' AGCTCCTGCAGAAGGAGG    59910     A  CC  _
                                AGC CC  GC GAAGGAGG
                                ||| ||  || ||||||||
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                                TCG GG  CG CTTCCTCC
                                  A  A_  T
GAM2597  OS4      3'  AGCACCCCAGCCTTGGGGA   59911        _  GAA  A
                                AGCACCCC GC   GG GGA
                                |||||||| ||   || |||
                                TCGTGGGG CG   CC CCT
                                     T  GAA  _
GAM2597  phospho1  3'  AAACACCAGAGGAAGGAGG   59912       CCGC
                                AAGCACC    GAAGGAGG
                                |||||||    ||||||||
                                TTTGTGG    CTTCCTCC
                                     TCTC
GAM2597  SCGF     3'  AAGACACTAACAAGGAGGA   59913     _   CCC  G
                                AAG CAC   GC AAGGAGGA
                                ||| |||   || ||||||||
                                TTC GTG   TG TTCCTCCT
                                  T   AT_  _
GAM2597  SFXN5    3'  AGCTCCACGAAGGGGGA     59914     ACC       A
                                AGC   CCGCGAAGG GGA
                                |||   ||||||||| |||
                                TCG   GGTGCTTCC CCT
                                  A__        C
GAM2597  TA-LRRP   3'  AAACACTGCAAGGAGGA     59915       CCC  G
                                AAGCAC   GC AAGGAGGA
                                ||||||   || ||||||||
                                TTTGTG   CG TTCCTCCT
                                    A__  _
GAM2597  TERE1    5'  ACCGCCCGGGAAGGAGGA    59916    AC    C
                                GC  CCCG GAAGGAGGA
                                ||  |||| |||||||||
                                TG  GGGC CTTCCTCCT
                                 GC    C
GAM2597  ZFP106    3'  AAACACCCCGTGAGCCCAGAGG 59917          C  A___
              A                  AAGCACCCCG GA    GGAGGA
                                ||||||||||| ||    ||||||
                                TTTGTGGGGC CT    TCTCCT
                                      A  CGGG
GAM2597  LOC115343 3'  AGACATCAGGAAGGAGGA    59918    C  CC  C
                                AG AC  CG GAAGGAGGA
                                || ||  || |||||||||
                                TC TG  GT CTTCCTCCT
                                 _  TA  C
GAM2597  LOC147160 5'  AAGCACCCGCAGGCTGAGGA   59919        C   AAG_
                                AAGCACCC GCG    GAGGA
                                |||||||| |||    |||||
                                TTCGTGGG CGT    CTCCT
                                     _  CCGA
GAM2597  LOC148223 3'  AGCACCCCAGACAGGGG     59920         C  _   A
                                AGCACCCCG GA AGG GG
                                ||||||||| || ||| ||
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                                TCGTGGGGT CT TCC CC
                                     _ G  _
GAM2597  LOC150311 5'  AAGTACCAGACAAGGAGGA   59921    C  CC  G
                                AAG ACC  GC AAGGAGGA
                                ||| |||  || ||||||||
                                TTC TGG  TG TTCCTCCT
                                  A  TC  _
GAM2597  LOC150372 5'  AGCACGCCAAGGAGGA     59922      CCC  G
                                AGCAC   GC AAGGAGGA
                                |||||   || ||||||||
                                TCGTG   CG TTCCTCCT
                                   ___  G
GAM2597  LOC150421 3'  AACACCTGCCAAGGAGGA    59923       CC  G
                                AGCACC  GC AAGGAGGA
                                ||||||  || ||||||||
                                TTGTGG  CG TTCCTCCT
                                    A_  G
GAM2597  LOC151512 5'  AAGCACCCCTACAACAGAGGA  59924         _   A
                                AAGCACCCC GCGA GGAGGA
                                ||||||||| |||| ||||||
                                TTCGTGGGG TGTT TCTCCT
                                     A   G
GAM2597  LOC152860 3'  AAGCACCCACGGGGG      59925        C   AA  A
                                AAGCACCC GCG  GG GG
                                |||||||| |||  || ||
                                TTCGTGGG TGC  CC CC
                                     _  __  _
GAM2597  LOC152897 5'  AGTCACAGACAAGAAGGAGGA  59926    _  CC_  C
                                AG CAC   CG GAAGGAGGA
                                || |||   || |||||||||
                                TC GTG   GT CTTCCTCCT
                                 A  TCT  T
GAM2597  LOC155063 3'  AAGTGCCCCACGACCGAGG   59927    CA      AG
                                AAG  CCCCGCGA  GAGG
                                |||  ||||||||  ||||
                                TTC  GGGGTGCT  CTCC
                                  AC       GG
GAM2597  LOC157543 3'  GCACCCCACGGCTATGGGGA  59928         AA___  A
                                GCACCCCGCG    GG GGA
                                ||||||||||    || |||
                                CGTGGGGTGC    CC CCT
                                     CGATA  _
GAM2597  LOC163397 5'  AAGCACCCTTGGCTGGAGG   59929        C__  GAA
                                AAGCACCC   GC   GGAGG
                                ||||||||   ||   |||||
                                TTCGTGGG   CG   CCTCC
                                    AAC  A__
GAM2597  LOC200261 5'  AAGACTCAGAAGGAGG     59930    C  CC  C
                                AAG AC  CG GAAGGAGG
                                ||| ||  || ||||||||
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                                TTC TG  GT CTTCCTCC
                                  _ A_  _
GAM2597  LOC201164 3'  AAGCACCCCGTGGCAGG     59931          CGAA  _
                                AAGCACCCCG    GG AGG
                                ||||||||||    || |||
                                TTCGTGGGGC    CC TCC
                                     A___  G
GAM2597  LOC221922 5'  AAGCACCCTCCGTGAGAGGA   59932        CG  AA
                                AAGCACCC  CG  GGAGGA
                                ||||||||  ||  ||||||
                                TTCGTGGG  GC  TCTCCT
                                     AG  AC
GAM2597  LOC221979 3'  AAGCACCACCAGAAGGAGGA   59933        _  C
                                AAGCACC CCG GAAGGAGGA
                                ||||||| ||| |||||||||
                                TTCGTGG GGT CTTCCTCCT
                                     T  _
GAM2597  LOC222031 3'  AAGTCAACAAAGGAGGA     59934     _ CCCC
                                AAG CA    GCGAAGGAGGA
                                ||| ||    ||||||||||
                                TTC GT    TGTTTCCTCCT
                                  A _____
GAM2597  LOC222133 5'  AGACCGTCCGCGAAGGAGG    59935    C  __
                                AG ACC  CCGCGAAGGAGG
                                || |||  ||||||||||||
                                TC TGG  GGCGCTTCCTCC
                                  _  CA
GAM2597  LOC222189 3'  AGACATCAGGAAGGAGGA    59918    C  CC  C
                                AG AC  CG GAAGGAGGA
                                || ||  || |||||||||
                                TC TG  GT CTTCCTCCT
                                  _ TA  C
GAM2597  LOC245787 3'  AGACATCAGGAAGGAGGA    59918    C  CC  C
                                AG AC  CG GAAGGAGGA
                                || ||  || |||||||||
                                TC TG  GT CTTCCTCCT
                                  _ TA  C
GAM2597  LOC252995 3'  GCACCCTGCAAAAGGA      59936       C    AG
                                GCACCC GCGA  GAGGA
                                |||||| ||||  |||||
                                CGTGGG CGTT  TTCCT
                                     A   __
GAM2597  LOC253805 3'  AAGCACCCTGTCCACACGGAGG 59937         ____    AA
              A                  AAGCACCC   CGCG  GGAGGA
                                 ||||||||   ||||  ||||||
                                 TTCGTGGG   GTGT  CCTCCT
                                      ACAG   G_
GAM2597  LOC255170 3'  AAGCACCCCCAACCTGGGG   59938         G   A__  A
                                AAGCACCCC CGA   GG GG
                                ||||||||| |||   || ||
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                                TTCGTGGGG GTT   CC CC
                                     _  GGA  _
GAM2597  LOC255696 5'  AAGCTCCCGAAGGAGGA     59939      A   CGC
                                AAGC CCC   GAAGGAGGA
                                |||| |||   |||||||||
                                TTCG GGG   CTTCCTCCT
                                  A  ___
GAM2597  LOC256158 5'  AAGCACGGAAGGAGG       59940       CCC C
                                AAGCAC   G GAAGGAGG
                                ||||||   | ||||||||
                                TTCGTG   C CTTCCTCC
                                   ___ _
GAM2597  LOC84570  5'  AAGCACCCTCCGTCCGGGGA   59941        CG  AA_  A
                                AAGCACCC  CG   GG GGA
                                ||||||||  ||   || |||
                                TTCGTGGG  GC   CC CCT
                                     AG  AGG  _
GAM2597  LOC91974  5'  AAACGTCCACCAAGGAGGA    59942     ACC    G
                                AAGC   CCGC AAGGAGGA
                                ||||   |||| ||||||||
                                TTTG   GGTG TTCCTCCT
                                  CA_    G
GAM2597  LOC93082  3'  AAGCACCCCATCAGAAGGA    59943         CGA
                                AAGCACCCCG   AGGAGGA
                                ||||||||||   |||||||
                                TTCGTGGGGT   TCTTCCT
                                     AG_
GAM2598  5T4      3'  GTATCTATAGTGGAGGATGA   59946        ATTCC
                                GTATCTA    GAGGATGA
                                |||||||    ||||||||
                                CATAGAT    CTCCTACT
                                    ATCAC
GAM2598  BIA2     3'  CCATGTCTAATTCTTATATG   59947      A       CGAGG
                                CCGT TCTAATTC     ATG
                                |||| ||||||||     |||
                                GGTA AGATTAAG     TAC
                                  C       AATA_
GAM2598  C11orf11  5'  GCAGACAACCATTCCGAGGGTG 59948     TCTA___        A
            A                    GTA      ATTCCGAGG TGA
                                |||      ||||||||| |||
                                CGT      TAAGGCTCC ACT
                                  CTGTTGG        C
GAM2598  KIAA0125  5'  TACCCTGCCATCTGAGGATGA  59949     GTAT   AT  C
                                TACC    CTA  TC GAGGATGA
                                ||||    |||  || ||||||||
                                ATGG    GGT  AG CTCCTACT
                                  GAC_   __  A
GAM2598  LOC149506 5'  CCGTGTCTAATTCCTCCCCGA  59950      A        GAGGA
                                CCGT TCTAATTCC     TGA
                                |||| |||||||||     |||
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                                GGCA AGATTAAGG    GCT
                                  C       AGGG_
GAM2598  LOC196337 5'  GCTGTAATCTGAGAGGATGA  59951    ATC    CC_
                                GT  TAATT  GAGGATGA
                                ||  |||||  ||||||||
                                CG  ATTAG  CTCCTACT
                                 AC_    ACT
GAM2598  LOC221398 3'  TACTGTATCTAATGAAAAATGA 59952    C       TCC
                                TAC GTATCTAAT  GAGGATGA
                                ||| |||||||||  ||||||||
                                ATG CATAGATTA  TTTTTACT
                                  A       C__
GAM2599  ABCC5    3'  GGAGGCGGCAGAGGGGGCTGTC 59955           A  ___
            GG                    GGAGGCGGCAGAGG GGC  CGG
                                |||||||||||||| |||  |||
                                CCTCCGCCGTCTCC CCG  GCC
                                        C  ACA
GAM2599  ACHE     3'  AGAGGGGACAGGAGGGGGAG  59956     C   GA    CC
                                GGAGG GGCA  GGAGG  GGAG
                                ||||| ||||  |||||  ||||
                                TCTCC CTGT  CCTCC  CCTC
                                   C    __    C_
GAM2599  AF5Q31   5'  GGAGGCGGCGGGGGTTCCGGAG 59957        AGA  A  __
                                GGAGGCGGC  GG GG  CCGGAG
                                |||||||||  || ||  ||||||
                                CCTCCGCCG  CC CC  GGCCTC
                                      C__  _  AA
GAM2599  AGRN     3'  GGGGTGTGGCAGAGGGATACGG 59958    A  C__      A  C_
                                GG GG  GGCAGAGG GG  CGG
                                || ||  |||||||| ||  |||
                                CC CC  CCGTCTCC CT  GCC
                                 _  ACA       _  AT
GAM2599  AKT1     3'  AGGAGGCGTGGAGGGGCC    59959        GCA   A
                                AGGAGGCG  GAGG GGCC
                                ||||||||  |||| ||||
                                TCCTCCGC  CTCC CCGG
                                     AC_   _
GAM2599  ALPP     3'  AGGAGGTGGGGAGCAGGA    59960       C  CAGA   G C
                                AGGAGG GG   GGAG C GGA
                                |||||| ||   |||| | |||
                                TCCTCC CC   CCTC G CCT
                                   A  ____   _ T
GAM2599  AP2B1    5'  GGTGGCGGCGGGAGCCGGAG  59961    A     AGA  AG
                                GG GGCGGC  GG  GCCGGAG
                                || ||||||  ||  |||||||
                                CC CCGCCG  CC  CGGCCTC
                                 A     ___  CT
GAM2599  AR       5'  AGGAGGTGGAGAGAGAGTGGG  59962       C  C   _  GCC
                                AGGAGG GG AGAG GAG  GG
                                |||||| || |||| |||  ||
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                                TCCTCC CC TCTC CTC   CC
                                   A  _   T   AC_
GAM2599 ATP5J    5' GGAGGCGGGAGGGGGGTTGG  59963       CA   A  CC_
                                GGAGGCGG  GAGG GG   GG
                                ||||||||  |||| ||   ||
                                CCTCCGCC  CTCC CC   CC
                                    __    C  CAA
GAM2599 ATP6V0D1 5' GGGAGCGGCGGGACCGGA   59964    AG    AGA  A
                                GG  GCGGC   GG GGCCGGA
                                ||  |||||   || |||||||
                                CC  CGCCG   CC CTGGCCT
                                 CT    ___  _
GAM2599 B4GALT6  5' GGAGGCGCGGAGGCCGA    59965       G AGA
                                GGAGGCG C   GGAGGCCGG
                                ||||||| |   |||||||||
                                CCTCCGC G   CCTCCGGCT
                                   _ ___
GAM2599 BACE2    5' AGAAGGCGGAGGCCGG     59966       GGCAGA
                                AGGAGGC     GGAGGCCGG
                                |||||||     |||||||||
                                TCTTCCG     CCTCCGGCC
                                   _______
GAM2599 BACE2    5' AGAAGGCGGAGGCCGG     59966       GGCAGA
                                AGGAGGC     GGAGGCCGG
                                |||||||     |||||||||
                                TCTTCCG     CCTCCGGCC
                                   _______
GAM2599 BACE2    5' AGAAGGCGGAGGCCGG     59966       GGCAGA
                                AGGAGGC     GGAGGCCGG
                                |||||||     |||||||||
                                TCTTCCG     CCTCCGGCC
                                   _______
GAM2599 BACH2    5' GAAGGGGCGAGGGGAGGCCGG 59967      C  _  A
                                GGAGG GGC AG GGAGGCCGG
                                ||||| ||| || |||||||||
                                CTTCC CCG TC CCTCCGGCC
                                   _  C  C
GAM2599 BARHL1   3' GGAGCCGGCAGAGGCTGGGG  59968     G       A_  CC
                                GGAG CGGCAGAGG  GG  GG
                                ||||  |||||||||  ||  ||
                                CCTC GCCGTCTCC  CC  CC
                                  G       GA  __
GAM2599 BTG1     5' AGGAGGCGGCAGGAGAGA    59969          AG
                                AGGAGGCGGCAG  GAGG
                                ||||||||||||  ||||
                                TCCTCCGCCGTC  CTCT
                                       CT
GAM2599 CACNG7   3' AGGAGGAGGCAGGGGGAG    59970       C    A_
                                AGGAGG GGCAG  GGAG
                                ||||||  |||||  ||||
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                                TCCTCC CCGTC  CCTC
                                   T    CC
GAM2599 CAPG    3' AGGCAGGTGGTGGGGGGCAGG 59971    _  C CAGA A  C
                                AGG AGG GG   GG GGC GG
                                ||| ||| ||   || ||| ||
                                TCC TCC CC   CC CCG CC
                                  G  A ACC_ _  T
GAM2599 CAPON   5' GGAGGGCGGCAGGGGAGG   59973     _    A
                                GGAGG CGGCAG GGAGG
                                ||||| |||||| |||||
                                CCTCC GCCGTC CCTCC
                                   C     C
GAM2599 CAPON   5' AGGAGGTGGCGGCGGGAGCGGG 59972      C  AGA AG C
                                AGGAGG GGC   GG  GC GG
                                |||||| |||   ||  || ||
                                TCCTCC CCG   CC  CG CC
                                   A   CCG  CT  C
GAM2599 CBFA2T2  3' AGGAGGCAGATGGGGTCGG   59974       CAGA A C
                                AGGAGGCGG   GG GG CGG
                                |||||||||   || || |||
                                TCCTCCGTC   CC CC GCC
                                     TA__ _ A
GAM2599 CD34    3' AGGAGGGGGTAGGGGAAGGG  59975      C C A   CC
                                AGGAGG GG AG GGAGG  GG
                                |||||| || || |||||  ||
                                TCCTCC CC TC CCTTC  CC
                                   C  A  C    __
GAM2599 CD7     3' AGGGGTGTGGCAGGGTGGGG  59976    A C__   A A CC
                                AGG GG   GGCAG GG GG  GG
                                ||| ||   ||||| || ||  ||
                                TCC CC   CCGTC CC CC  CC
                                  _ ACA    _ A __
GAM2599 CD97    5' AGGAGCGGCAGGGGAAAGA   59977     G    A   GCC
                                AGGAG CGGCAG GGAG   GGA
                                ||||| |||||| ||||   |||
                                TCCTC GCCGTC CCTT   TCT
                                   _    C   ____
GAM2599 CD97    5' AGGAGCGGCAGGGGAAAGA   59977     G    A   GCC
                                AGGAG CGGCAG GGAG   GGA
                                ||||| |||||| ||||   |||
                                TCCTC GCCGTC CCTT   TCT
                                   _    C   ____
GAM2599 CEP2    5' GGGGGCGGCAGAGCGCGG    59978   A       GAG C
                                GG GGCGGCAGAG   GC GG
                                || ||||||||||   || ||
                                CC CCGCCGTCTC   CG CC
                                 C        G__ _
GAM2599 CHIC2   5' GAGGCGGCGGAGGCTGAG    59979       AGA    CG
                                GAGGCGGC   GGAGGC  GAG
                                ||||||||   ||||||  |||
```

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                                CTCCGCCG  CCTCCG  CTC
                                   ___     A_
GAM2599  CLASP1   3'  GGAGGCAGCAGCTTGGAG    59980          A__
                                GGAGGCGGCAG  GGAG
                                ||||||||||  ||||
                                CCTCCGTCGTC  CCTC
                                    GAA
GAM2599  CLC      3'  GGAGGTGGGGAGGAGAC     59981      C  CA
                                GGAGG GG  GAGGAGGC
                                ||||| ||  ||||||||
                                CCTCC CC  CTCCTCTG
                                  A  C_
GAM2599  CLDN3    5'  GGAGACGAGGGGCCGG      59982       GGCA   A
                                GGAGGC   GAGG GGCCGG
                                ||||||   |||| ||||||
                                CCTCTG   CTCC CCGGCC
                                   ____   _
GAM2599  COL6A2   3'  AGGAGGCGTGGGGGCAGTGAG  59983        GCAGA  A  CG_
                                AGGAGGCG    GG GGC  GAG
                                ||||||||    || |||  |||
                                TCCTCCGC    CC CCG  CTC
                                    AC___  _  TCA
GAM2599  CSK      5'  AGGGGGCGGGAGGGAGTCGG  59984    A    C  A   GC
                                AGG GGCGG AG GGAG  CGG
                                ||| ||||| || ||||  |||
                                TCC CCGCC TC CCTC  GCC
                                  C    C  _   A_
GAM2599  CXCL16   5'  AGGAGACGGCGGCCGG      59985         AGAGGA
                                AGGAGGCGGC    GGCCGG
                                ||||||||||    ||||||
                                TCCTCTGCCG    CCGGCC
                                   _______
GAM2599  DDX26    5'  AGGAGATGGTAGAGGTGGA   59986     GC  C    AGGCC
                                AGGAG  GG AGAGG    GGA
                                |||||  || |||||    |||
                                TCCTC  CC TCTCC    CCT
                                   TA  A    A____
GAM2599  DES      5'  GGCAGGCGGCCGGCCGGA    59987   _     AGAGGA
                                GG AGGCGGC    GGCCGGA
                                || |||||||    |||||||
                                CC TCCGCCG    CCGGCCT
                                 G     G_____
GAM2599  DLG4     3'  AGGGGTGGGAGGGAGGCCGG  59988    A  C  C  A
                                AGG GG GG AG GGAGGCCGG
                                ||| || || || |||||||||
                                TCC CC CC TC CCTCCGGCC
                                  _  A  C  _
GAM2599  DPYSL3   3'  AGAGGCAATATGAGGAGGTTGG 59989       CA_     CC
                                GGAGGCGG  GAGGAGG  GG
                                ||||||||  |||||||  ||
```

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                                TCTCCGTT  CTCCTCC  CC
                                   ATA     AA
GAM2599  DUSP4    5'  GGAGGCGGCGAAGGCGCCTGCG 59990        AG  AG  ___
            G                   GGAGGCGGC  AGG  GCC  GG
                                |||||||||  |||  |||  ||
                                CCTCCGCCG  TCC  CGG  CC
                                   CT  G_  ACG
GAM2599  EIF4G1   3'  AGGGGTGGTACAGGGGCTGG  59991    A  C  CAG  A  C
                                AGG GG GG  AGG GGC GG
                                ||| || ||  ||| ||| ||
                                TCC CC CC  TCC CCG CC
                                  _ A ATG  _  A
GAM2599  ELL      3'  AGGAGGCAGTGGGCTTCCTGG  59992       CAGA  AGG  _
                                AGGAGGCGG   GG  CC GG
                                |||||||||   ||  || ||
                                TCCTCCGTC   CC  GG CC
                                   AC__  GAA  A
GAM2599  ESR1     3'  GGAGGCGGTAGGGAACGG   59993       C  A   GC
                                GGAGGCGG AG GGAG  CGG
                                |||||||| || ||||  |||
                                CCTCCGCC TC CCTT  GCC
                                   A  _   __
GAM2599  FAAH     5'  AGGAGGCGGCGGGGGGGCGGAG  59994        AGA  A  C
                                AGGAGGCGGC  GG GGC GGAG
                                ||||||||||  || ||| ||||
                                TCCTCCGCCG  CC CCG CCTC
                                   CC_  _  _
GAM2599  FASN     3'  GGAGGCGGCGGGTGGGTGG   59995       AGA  A  CC
                                GGAGGCGGC  GG GG  GG
                                |||||||||  || ||  ||
                                CCTCCGCCG  CC CC  CC
                                   C__  A  CA
GAM2599  FGD1     3'  AGGAGGCAGGGCTGGGTCGG  59996       CAGA  A__  C
                                AGGAGGCGG   GG  GG CGG
                                |||||||||   ||  || |||
                                TCCTCCGTC   CC  CC GCC
                                   ____  GAC  A
GAM2599  FHIT     5'  GGAGCGCGGGGCCGGA     59997    _   CAGAGGA
                                GGAG GCGG     GGCCGGA
                                |||| ||||     |||||||
                                CCTC CGCC     CCGGCCT
                                  G  _______
GAM2599  FKBP2    3'  AGAAGGTGGTGGGGTATGCTGG 59998      C  CAGA  AG_  C
            AG                  AGGAGG GG   GG  GC GGAG
                                ||||||  ||   ||  || ||||
                                TCTTCC CC   CC  CG CCTC
                                  A  ACC_  ATA  A
GAM2599  FKBP2    3'  AGAAGGTGGTGGGGTATGCTGG 59998      C  CAGA  AG_  C
            AG                  AGGAGG GG   GG  GC GGAG
                                ||||||  ||   ||  || ||||
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                                TCTTCC CC    CC   CG CCTC
                                   A  ACC_  ATA  A
GAM2599  FPGS     3'  AGGAGGCAGGCGGGGTGTTGG  59999        _   AGA  A  CC__
                                AGGAGGC GGC   GG GG    GG
                                ||||||| |||   || ||    ||
                                TCCTCCG CCG   CC CC    CC
                                   T  ___  _  ACAA
GAM2599  FSTL3    3'  GGGGGCTGGAGGAGGCTGGAG  60000    A   GGCA       C
                                GG GGC    GAGGAGGC GGAG
                                || |||    |||||||| ||||
                                CC CCG    CTCCTCCG CCTC
                                 C   AC__       A
GAM2599  GABPB1   5'  AGGAGGTGGTGCGGGGACCCGA 60001       C  CAGA  A    G
            G                    AGGAGG GG    GG GGCC GAG
                                ||||||  ||    || |||| |||
                                TCCTCC CC    CC CTGG CTC
                                   A  ACG_  C    G
GAM2599  GARS     5'  GGAGGCGGCGGCGGGCAAGGAG 60002         AGA  A_   C_
                                GGAGGCGGC   GG  GGC  GGAG
                                |||||||||   ||  |||  ||||
                                CCTCCGCCG   CC  CCG  CCTC
                                     ___  GC   TT
GAM2599  GAS1     5'  GGGAGCGGCGGACGCGGA    60003    AG    AGA   G  C
                                GG  GCGGC   GGA GC GGA
                                ||  |||||   ||| || |||
                                CC  CGCCG   CCT CG CCT
                                 CT    ____   G  _
GAM2599  GLRX2    5'  AGGATGGTGGCAGACATGCTGG 60004      _  C     GGAG  C
                                AGGA GG GGCAGA    GC GG
                                ||||  || ||||||    || ||
                                TCCT CC CCGTCT    CG CC
                                  A  A     GTA_  A
GAM2599  GLTSCR1  3'  AGCAGGCGGCAGGGAAGGA   60005    G       A    GCC
                                AG AGGCGGCAG GGAG   GGA
                                || |||||||| ||||   |||
                                TC TCCGCCGTC CCTT   CCT
                                 G       _   ___
GAM2599  GNA15    5'  AGGAGGTGGGGAGGCCAG    60006       C  CAGA
                                AGGAGG GG    GGAGGCCGG
                                ||||||  ||    |||||||||
                                TCCTCC CC    CCTCCGGTC
                                   A  _____
GAM2599  GPC1     3'  AGGAGGCGGGGAGGAAG     60007         CA
                                AGGAGGCGG  GAGGAGG
                                |||||||||  |||||||
                                TCCTCCGCC  CTCCTTC
                                     C_
GAM2599  GPC3     5'  GGAGAGTGGCAGCCGGA     60008      _ C   GAGGAG
                                GGAG G GGCA     GCCGGA
                                |||| | ||||     ||||||
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                                CCTC C CCGT     CGGCCT
                                  T A   ______
GAM2599  GRB14    5'  AGGGGGCGGAGGAGGAGG    60009    A    CA
                                AGG GGCGG  GAGGAGG
                                ||| |||||  |||||||
                                TCC CCGCC  CTCCTCC
                                  C    TC
GAM2599  GRB14    5'  GAGGCGGCGGGGGAGGGGAG  60010       AGA    CC
                                GAGGCGGC   GGAGG  GGAG
                                ||||||||   |||||  ||||
                                CTCCGCCG   CCTCC  CCTC
                                     CCC    __
GAM2599  GRIN2A   5'  GGGGGCGGCTATCCCAGCCGGA 60011    A     AGAGGA
              G                  GG GGCGGC     GGCCGGAG
                                || ||||||     ||||||||
                                CC CCGCCG     TCGGCCTC
                                 C     ATAGGG
GAM2599  HIF1A    5'  AGCGGGCGGCAATCGCCGG   60012    GA      AGGAG
                                AG  GGCGGCAG    GCCGG
                                ||  ||||||||    |||||
                                TC  CCGCCGTT    CGGCC
                                 GC       AG___
GAM2599  HNF4A    3'  GGAGGCAGCAGAGGTGGGG   60013           A  CC
                                GGAGGCGGCAGAGG GG  GG
                                |||||||||||||| ||  ||
                                CCTCCGTCGTCTCC CC  CC
                                        A  __
GAM2599  HOXB5    3'  GGCGGCGGCAGAGCGGGG    60014    A       GA  CC
                                GG GGCGGCAGAG  GG  GG
                                || ||||||||||  ||  ||
                                CC CCGCCGTCTC  CC  CC
                                 G        G_  __
GAM2599  HOXD3    3'  GGAGGCGGCGGCAGGGCAAGAG 60015         AGA  A   C
                                GGAGGCGGC   GG GGC GGAG
                                |||||||||   || ||| ||||
                                CCTCCGCCG   TC CCG TCTC
                                      CCG  _   T
GAM2599  HRB      5'  AGGAGGCCGGCAGGGCCGG    60016        _    AGGA
                                AGGAGGC GGCAG    GGCCGG
                                ||||||| |||||    ||||||
                                TCCTCCG CCGTC    CCGGCC
                                    G    _____
GAM2599  HS3ST3A1  5'  GGAGGCAGCGGCCGG       60017         AGAGGA
                                GGAGGCGGC     GGCCGG
                                |||||||||     ||||||
                                CCTCCGTCG     CCGGCC
                                              _______
GAM2599  IL2RB    3'  GGAGGGAAGGAGGAGGCTGG   60018      C  CA       C
                                GGAGG GG  GAGGAGGC GG
                                ||||| ||  |||||||| ||
```

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                                CCTCC CT  CTCCTCCG CC
                                  _ TC       A
GAM2599 IL6R    5' AGGGGTGGCAGGGGCGGG    60019    A C   GA A  C
                                AGG GG GGCA  GG GGC GG
                                ||| || ||||  || ||| ||
                                TCC CC CCGT  CC CCG CC
                                 _ A   __ _  C
GAM2599 INS     3' AGGAGGCGGCGGGTGGGG    60020         AGA A CC
                                AGGAGGCGGC  GG GG  GG
                                ||||||||||  || ||  ||
                                TCCTCCGCCG  CC CC  CC
                                     C__  A __
GAM2599 ITGBL1  5' GGAGGCGGCAGGAGGGA     60021         GA   CCG
                                GGAGGCGGCA  GGAGG  GA
                                ||||||||||  |||||  ||
                                CCTCCGCCGT  CCTCC  CT
                                  __   ___
GAM2599 JAM2    5' AGGAGCGCAGGAGGCCGG    60022      _ GGCAG
                                AGGAG GC    AGGAGGCCGG
                                ||||| ||    ||||||||||
                                TCCTC CG    TCCTCCGGCC
                                  G _____
GAM2599 KCNK4   5' AGGTGGGTGGCAGAGGAGCCGG 60023    A_ C       G
          AG                      AGG  GG GGCAGAGGAG CCGGAG
                                ||| || |||||||||| ||||||
                                TCC  CC CCGTCTCCTC GGCCTC
                                 AC  A       _
GAM2599 LAMB1   5' GGACGCGGCAGAGGAGTGGAG  60024    G         GCC
                                GGA GCGGCAGAGGAG  GGAG
                                ||| ||||||||||||  ||||
                                CCT CGCCGTCTCCTC  CCTC
                                 G         A__
GAM2599 LBX1    3' GGAGTGGCAGAGGAGGTCCCAG 60025    GC        __
                                GGAG  GGCAGAGGAGG  CCGG
                                ||||  ||||||||||  ||||
                                CCTC  CCGTCTCCTCC  GGTC
                                  A_        AG
GAM2599 LCN1    3' GGGGGTGGTAGGAAGGGG    60026   A C  C  A   CC
                                GG GG GG AG GGAGG  GG
                                || || || || |||||  ||
                                CC CC CC TC CTTCC  CC
                                 C  A  A  _   __
GAM2599 LCN1    3' GGGGGTGGTAGGAAGGGG    60026   A C  C  A   CC
                                GG GG GG AG GGAGG  GG
                                || || || || |||||  ||
                                CC CC CC TC CTTCC  CC
                                 C  A  A  _   __
GAM2599 LFG     3' AGGAGGTGGAGGAGGGTGG   60027     C  CAG    CC
                                AGGAGG GG  AGGAGG  GG
                                |||||| ||  ||||||  ||
```

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                                TCCTCC CC   TCCTCC  CC
                                   A ___     CA
GAM2599  LRP1    5'  AGGAGGCGGGGAGGGG      60029         CAGA    CC
                                AGGAGGCGG   GGAGG  GG
                                |||||||||   |||||  ||
                                TCCTCCGCC   CCTCC  CC
                                    ____    __
GAM2599  LRP1    5'  AGGAGGCGGGGAGGGGGGGTGG 60028          CA   A  CC_
                                AGGAGGCGG  GAGG GG   GG
                                |||||||||  ||||  ||   ||
                                TCCTCCGCC  CTCC CC   CC
                                     C_   C  CCA
GAM2599  LSP1    3'  GGGGGCGGCAAGCAGCGGG   60030    A      G  GA   C
                                GG GGCGGCA AG  GGC GG
                                || |||||||  ||  ||| ||
                                CC CCGCCGT TC  TCG CC
                                 C      _ G_   C
GAM2599  LSP1    3'  AGGAGGTGGCAGCGGATGG   60031       C    A  _
                                AGGAGG GGCAG GGA GG
                                ||||||  |||||  ||| ||
                                TCCTCC CCGTC CCT CC
                                   A    G  A
GAM2599  MAFF    3'  GGAGGGAGCTGAGGCCGGAG  60032      C  AGAG
                                GGAGG GGC   GAGGCCGGAG
                                |||||  |||   ||||||||||
                                CCTCC TCG   CTCCGGCCTC
                                  C  A___
GAM2599  MEN1    3'  AGGAGGCGGCAGGGGAGGCGGG 60033          A    C
                                AGGAGGCGGCAG GGAGGC GG
                                ||||||||||||  ||||||  ||
                                TCCTCCGCCGTC CCTCCG CC
                                      C     C
GAM2599  MLLT2   3'  GGGGGCGGCAGGAGCGG    60034    A     GA   GC
                                GG GGCGGCA  GGAG  CGG
                                || |||||||  ||||  |||
                                CC CCGCCGT  CCTC  GCC
                                 C      __   __
GAM2599  MMP14   3'  AGGAGGCTGCGGGGAGGGG   60035       G  AGA    CC
                                AGGAGGC GC   GGAGG  GG
                                |||||||  ||   |||||  ||
                                TCCTCCG CG   CCTCC  CC
                                    A  CC_    __
GAM2599  MN1     5'  GAGGCGGCAGGCGCCGGGGGCT 60036          A____  A  C
           GGAG                    GAGGCGGCAG    GG GGC GGAG
                                |||||||||||    || ||| ||||
                                CTCCGCCGTC    CC CCG CCTC
                                      CGCGG  C   A
GAM2599  MPDU1   3'  GGAAGCAGGGAGGCTGGA    60037        CAGA     C
                                GGAGGCGG    GGAGGC GGA
                                ||||||||    |||||| |||
```

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                                CCTTCGTC   CCTCCG CCT
                                     ____     A
GAM2599  NCK2     3'  GGAGGCGAGTGTGGGGCCGG   60038        CAGA  A
                                GGAGGCGG   GG GGCCGG
                                ||||||||   || ||||||
                                CCTCCGCT   CC CCGGCC
                                    CACA  _
GAM2599  NF1      5'  GGGGCGTTGGCAAGGAGGCTGG 60039    A  ___   G     C
                                GG GGC   GGCA AGGAGGC GG
                                || |||   |||| ||||||| ||
                                CC CCG   CCGT TCCTCCG CC
                                 _  CAA   _     A
GAM2599  NFKB1    5'  AAGAGGCGGCGGCAGGCCGGAG 60040          AGA  _
                                AGGAGGCGGC   GG AGGCCGGAG
                                ||||||||||   || |||||||||
                                TTCTCCGCCG   CC TCCGGCCTC
                                     ___  G
GAM2599  NPEPPS   5'  GGAGGAGGCGGAGGGCCGA   60041      C  A   AG
                                GGAGG GGC GAGG  GCCGG
                                ||||| ||| ||||  |||||
                                CCTCC CCG CTCC  CGGCT
                                   T  C   __
GAM2599  OTP      3'  GGAGGCGGCGGGCGAGGGG   60042        A___   A
                                GGAGGCGGC   GAGG GG
                                |||||||||   |||| ||
                                CCTCCGCCG   CTCC CC
                                     CCCG   _
GAM2599  OXCT     5'  AGGAGGAGGCTGCGGGTTGGAG 60043       C  AGA  AGGCC
                                AGGAGG GGC   GG    GGAG
                                |||||| |||   ||    ||||
                                TCCTCC CCG   CC    CCTC
                                   T  ACG  CAA__
GAM2599  P2RY1    5'  AGGAGGCGGCGAGAGGGC    60044         A  GA
                                AGGAGGCGGC GAG  GGC
                                |||||||||| |||  |||
                                TCCTCCGCCG CTC  CCG
                                      _  TC
GAM2599  PAX2     3'  AGGGGCGGCAGGCGGGGCTGG  60045    A      A_  A  C
                                AGG GGCGGCAG  GG GGC GG
                                ||| ||||||||  || ||| ||
                                TCC CCGCCGTC  CC CCG CC
                                  _      CG  _  A
GAM2599  PAX2     3'  AGGGGCGGCAGGCGGGGCTGG  60045    A      A_  A  C
                                AGG GGCGGCAG  GG GGC GG
                                ||| ||||||||  || ||| ||
                                TCC CCGCCGTC  CC CCG CC
                                  _      CG  _  A
GAM2599  PAX5     3'  GGATGAGCAGGAGGCTGG    60046    GGC   GA    C
                                GGA   GGCA  GGAGGC GG
                                |||   ||||  |||||| ||
```

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                                CCT   TCGT  CCTCCG CC
                                  AC_   __     A
GAM2599  PCTK1    5'  AGGATGCGGCGCCAAGCCGGAG 60047      G     AGAGG
                                AGGA GCGGC    AGGCCGGAG
                                |||| |||||    |||||||||
                                TCCT CGCCG    TTCGGCCTC
                                  A    CGG__
GAM2599  PDGFB    5'  GGAGGCAGCGGGGGAGGCTGCG 60048          AGA     __
                G                  GGAGGCGGC   GGAGGC  CGG
                                |||||||||   ||||||  |||
                                CCTCCGTCG   CCTCCG  GCC
                                     CCC     AC
GAM2599  PFN1     5'  GGAGGCGGAGAGCTCGG     60049         C   GGAG  _
                                GGAGGCGG AGA    GC CGG
                                |||||||| |||    || |||
                                CCTCCGCC TCT    CG GCC
                                   _  _____  A
GAM2599  PGAM1    3'  GGAGGGGCAGAGGGACAAG    60050       C       A   C
                                GGAGG GGCAGAGG GGC GG
                                ||||| |||||||| ||| ||
                                CCTCC CCGTCTCC CTG TC
                                  _       _  T
GAM2599  PHKG2    5'  AGGGGGCAGGCAGAGGAGCCAG 60051     A  _        G
                                AGG GGC GGCAGAGGAG CCGG
                                ||| ||| |||||||||| ||||
                                TCC CCG CCGTCTCCTC GGTC
                                  C   T        _
GAM2599  PIK3R3   5'  AGGAAGGCAAAAAAGGGGGCTG 60052      _    C    A   C
                GAG                  AGGA GGCGG AGAGG GGC GGAG
                                |||| ||||| ||||| ||| ||||
                                TCCT CCGTT TTTCC CCG CCTC
                                  T    T    C   A
GAM2599  PLA2G10  5'  GGAGGGTGGCAGAGGTGG     60053       C_       A
                                GGAGG  GGCAGAGG GG
                                |||||  |||||||| ||
                                CCTCC  CCGTCTCC CC
                                   CA       A
GAM2599  PLOD3    5'  GGAGGCGGGGGGAGGGGCGG    60054         CA    A   C
                                GGAGGCGG  GAGG GGC GG
                                ||||||||  |||| ||| ||
                                CCTCCGCC  CTCC CCG CC
                                     CC    _  _
GAM2599  PLTP     3'  AGGGGCTGAGAGGGGTTGG    60055     A   GGC     A  CC
                                AGG GGC   AGAGG GG  GG
                                ||| |||   ||||| ||  ||
                                TCC CCG   TCTCC CC  CC
                                  _   AC_    _  AA
GAM2599  POMC     3'  GGAGGCGGCAGCAGGGCAGG   60056           A  A   C
                                GGAGGCGGCAG GG GGC GG
                                |||||||||| || ||| ||
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                                CCTCCGCCGTC TC CCG CC
                                      G _  T
GAM2599  PPP1R11  3'  AGAGGGAAGGAGGGGGCTGGAG 60057      C  CA   A  C
                                GGAGG GG  GAGG GGC GGAG
                                ||||| ||  |||| ||| ||||
                                TCTCC CT  CTCC CCG CCTC
                                  _ TC   C  A
GAM2599  PPP1R11  3'  AGAGGGAAGGAGGGGGCTGGAG 60057      C  CA   A  C
                                GGAGG GG  GAGG GGC GGAG
                                ||||| ||  |||| ||| ||||
                                TCTCC CT  CTCC CCG CCTC
                                  _ TC   C  A
GAM2599  PTGIS    3'  AGGAGGCGGCAGTGGGG     60058          A  A
                                AGGAGGCGGCAG GG GG
                                |||||||||||| || ||
                                TCCTCCGCCGTC CC CC
                                      A _
GAM2599  PTMS     5'  AAGAGGCGGCAGAGGCGCGCGG 60059           AG  _
                                AGGAGGCGGCAGAGG  GC CGG
                                ||||||||||||||  || |||
                                TTCTCCGCCGTCTCC  CG GCC
                                      G_  C
GAM2599  PTPN6    5'  AGGGGGCGCAGGGAATGAGGAG 60060    A   G  A   GCC
                                AGG GGCG CAG GGAG   GGAG
                                ||| |||| ||| ||||   ||||
                                TCC CCGC GTC CCTT   CCTC
                                  C   _  _   ACT
GAM2599  PTPN6    5'  AGGGGGCGCAGGGAATGAGGAG 60060    A   G  A   GCC
                                AGG GGCG CAG GGAG   GGAG
                                ||| |||| ||| ||||   ||||
                                TCC CCGC GTC CCTT   CCTC
                                  C   _  _   ACT
GAM2599  PTPRS    3'  GGAGGGGCAGAGGCATCCGG   60061      C      AGG
                                GGAGG GGCAGAGG   CCGG
                                ||||| ||||||||   ||||
                                CCTCC CCGTCTCC   GGCC
                                  _       GTA
GAM2599  PTPRS    3'  GGAGGGGCAGAGGCATCCGG   60061      C      AGG
                                GGAGG GGCAGAGG   CCGG
                                ||||| ||||||||   ||||
                                CCTCC CCGTCTCC   GGCC
                                  _       GTA
GAM2599  PTPRS    3'  GGAGGGGCAGAGGCATCCGG   60061      C      AGG
                                GGAGG GGCAGAGG   CCGG
                                ||||| ||||||||   ||||
                                CCTCC CCGTCTCC   GGCC
                                  _       GTA
GAM2599  PTPRS    3'  GGAGGGGCAGAGGCATCCGG   60061      C      AGG
                                GGAGG GGCAGAGG   CCGG
                                ||||| ||||||||   ||||
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                                CCTCC CCGTCTCC  GGCC
                                  _      GTA
GAM2599  RAD1    5'  GGAGGCGGCACAGACCTGGAG  60062        GAGG   _
                                GGAGGCGGCA   AGGCC GGAG
                                ||||||||||   ||||| ||||
                                CCTCCGCCGT   TCTGG CCTC
                                     G___    A
GAM2599  RAX     5'  GGAGGCGGGAGGGCGCTTTGGA 60063       CA   AG  C__
           G                     GGAGGCGG  GAGG  GC  GGAG
                                ||||||||  ||||  ||  ||||
                                CCTCCGCC  CTCC  CG  CCTC
                                    __   CG  AAA
GAM2599  ROR2    3'  GGAGGCAGCAGAAATGGAG   60064         ___
                                GGAGGCGGCAGA  GGAG
                                ||||||||||||  ||||
                                CCTCCGTCGTCT  CCTC
                                      TTA
GAM2599  RXRA    3'  GGAGGGCGGCGGGGAGGAG   60065     _   A__
                                GGAGG CGGC  GAGGAG
                                ||||| ||||  ||||||
                                CCTCC GCCG  CTCCTC
                                   C   CCC
GAM2599  S100A10  5'  GGAGGCGGCGCGGGAGCGGG  60066       AGA  AG  C
                                GGAGGCGGC  GG  GC GG
                                |||||||||  ||  || ||
                                CCTCCGCCG  CC  CG CC
                                     CG_  CT  C
GAM2599  SIX3    3'  AGGAGGCGGAGGGGAAGGA   60067       CAG  A  CC
                                AGGAGGCGG  AGG GG  GGA
                                |||||||||  ||| ||  |||
                                TCCTCCGCC  TCC CC  CCT
                                     ___  _  TT
GAM2599  SLC29A1  3'  AGGAGGCGCAGGGGAGAATGGA 60068       G  A   CC
           G                     AGGAGGCG CAG GGAGG  GGAG
                                ||||||||  ||| |||||  ||||
                                TCCTCCGC GTC CCTCT  CCTC
                                     _  C    TA
GAM2599  SLC5A5   5'  GGAAGCGGCGAGAGGGGCCGG  60069       _   A
                                GGAGGCGGC AGAGG GGCCGG
                                |||||||||  ||||| ||||||
                                CCTTCGCCG TCTCC CCGGCC
                                     C   _
GAM2599  SMG1    5'  AGGCGGCGGCGGAGGGCGG   60071    A    AGA   C
                                AGG GGCGGC  GGAGG CGG
                                |||  ||||||  ||||| |||
                                TCC CCGCCG  CCTCC GCC
                                  G    ___   C
GAM2599  SMG1    5'  AGGAGGCGGCGGCGG      60070         AGAGGA  C
                                AGGAGGCGGC    GGC GG
                                ||||||||||    ||| ||
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                                TCCTCCGCCG     CCG CC
                                        _______  _
GAM2599  SMT3H1   5'  GGAGGCGGCGCGGGGGAA    60072         AGA  A  CC
                                GGAGGCGGC   GG GG  GGA
                                |||||||||   || ||  |||
                                CCTCCGCCG   CC CC  CTT
                                    CG_  _  __
GAM2599  SOX12    3'  AGGGGGGTGTGGGGAGGCCGGA 60073     A  C  CAGA_
            G                    AGG GG GG    GGAGGCCGGAG
                                |||  || ||    ||||||||||
                                TCC CC CC    CCTCCGGCCTC
                                  _  _  ACACC
GAM2599  SREBF1   3'  AGGGGTGCTGAGGCCGG     60074     A  CG  AGAG
                                AGG GG  GC   GAGGCCGG
                                |||  ||  ||   ||||||||
                                TCC CC  CG   CTCCGGCC
                                  _  A_  A___
GAM2599  STAU     5'  AGGAGGCGGGCGCCGCCGGGCC 60075         _ AGAGGA_
            GG                    AGGAGGCGG C      GGCCGG
                                |||||||||  |      ||||||
                                TCCTCCGCC G      CCGGCC
                                    C CGGCGGC
GAM2599  STAU     5'  AGGAGGCGGGCGCCGCCGGGCC 60075         _ AGAGGA_
            GG                    AGGAGGCGG C      GGCCGG
                                |||||||||  |      ||||||
                                TCCTCCGCC G      CCGGCC
                                    C CGGCGGC
GAM2599  STAU     5'  AGGAGGCGGGCGCCGCCGGGCC 60075         _ AGAGGA_
            GG                    AGGAGGCGG C      GGCCGG
                                |||||||||  |      ||||||
                                TCCTCCGCC G      CCGGCC
                                    C CGGCGGC
GAM2599  STAU     5'  AGGAGGCGGGCGCCGCCGGGCC 60075         _ AGAGGA_
            GG                    AGGAGGCGG C      GGCCGG
                                |||||||||  |      ||||||
                                TCCTCCGCC G      CCGGCC
                                    C CGGCGGC
GAM2599  STX1A    3'  AGGGGTTGCTCCTGGGGCCGGA 60076     A  CG  AGA_  A
            G                    AGG GG  GC   GG GGCCGGAG
                                |||  ||  ||   || ||||||||
                                TCC CC  CG   CC CCGGCCTC
                                  _  AA  AGGA  _
GAM2599  SUPT6H   3'  AGGAGGGGCAGGGAGGGA    60077       C    A    CCG
                                AGGAGG GGCAG GGAGG   GA
                                ||||||  |||||  |||||   ||
                                TCCTCC CCGTC CCTCC   CT
                                    _    _    ____
GAM2599  TBP      3'  AGGGGGTGGGGGAGGCAAGG   60078     A  C  CAGA     C_
                                AGG GG GG    GGAGGC  GG
                                |||  ||  ||   ||||||  ||
```

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                                TCC CC CC    CCTCCG  CC
                                  C  A  C___     TT
GAM2599  TCIRG1    5'  AGGAGGAGGCGGGGCCAG    60079       C   AGA  A
                                AGGAGG GGC   GG GGCCGG
                                |||||| |||   || ||||||
                                TCCTCC CCG   CC CCGGTC
                                   T  ___  _
GAM2599  TGFB1     3'  AGGAGGAGGCAGAGAGGGA   60080       C      G   CCG
                                AGGAGG GGCAGAG AGG   GA
                                |||||| ||||||| |||   ||
                                TCCTCC CCGTCTC TCC   CT
                                   T      _  ___
GAM2599  TLR9      3'  GGAGGCGAGCAGGGGAGG    60081        _    A
                                GGAGGCG GCAG GGAGG
                                ||||||| |||| |||||
                                CCTCCGC CGTC CCTCC
                                    T   C
GAM2599  UBE2A     5'  AGGAGGCCGAAGAGGCTGGAG  60082       GGCA       C
                                AGGAGGC    GAGGAGGC GGAG
                                |||||||    |||||||| ||||
                                TCCTCCG    CTTCTCCG CCTC
                                    G___       A
GAM2599  UBE2V1    3'  GGAGGCGGGAGGGTAAGGGG   60084        CA   ___   CC
                                GGAGGCGG  GAGG   AGG  GG
                                ||||||||  ||||   |||  ||
                                CCTCCGCC  CTCC   TCC  CC
                                    __    CAT   __
GAM2599  UBE2V1    3'  GGAGGCGGGAGGGTAAAGGGAG 60083        CA    AGGCC_
                                GGAGGCGG  GAGG     GGAG
                                ||||||||  ||||     ||||
                                CCTCCGCC  CTCC     CCTC
                                    __    CATTTC
GAM2599  UBE2V1    3'  GGAGGCGGGAGGGTAAAGGGAG 60083        CA    AGGCC_
                                GGAGGCGG  GAGG     GGAG
                                ||||||||  ||||     ||||
                                CCTCCGCC  CTCC     CCTC
                                    __    CATTTC
GAM2599  USP14     5'  GGAGGCGGCGGCGCAGGA    60085        AGA  AG  C
                                GGAGGCGGC   GG  GC GGA
                                |||||||||   ||  || |||
                                CCTCCGCCG   CC  CG CCT
                                     ___  G_  T
GAM2599  VASP      3'  AGGGGATGGCAGAGGGG     60086     A  C_      A
                                AGG GG  GGCAGAGG GG
                                ||| ||  |||||||| ||
                                TCC CC  CCGTCTCC CC
                                  _  TA       _
GAM2599  VDR       3'  GGAGGTGGCAGAGGAGGGG   60087      C         CC
                                GGAGG GGCAGAGGAGG  GG
                                ||||| ||||||||||  ||
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                                CCTCC CCGTCTCCTCC  CC
                                  A         __
GAM2599  WDR1     5'  AGTGGGCGGTCCGAGGCCGG  60088    GA    CAGAG
                                AG  GGCGG    GAGGCCGG
                                ||  |||||    ||||||||
                                TC  CCGCC    CTCCGGCC
                                 AC     AGG__
GAM2599  WDR1     5'  AGTGGGCGGTCCGAGGCCGG  60088    GA    CAGAG
                                AG  GGCGG    GAGGCCGG
                                ||  |||||    ||||||||
                                TC  CCGCC    CTCCGGCC
                                 AC     AGG__
GAM2599  WNT5A    5'  GGGGGGTGGAGGATGGGG    60089    A  C  CA    _  CC
                                GG GG GG  GAGGA GG  GG
                                || || ||  ||||| ||  ||
                                CC CC CC  CTCCT CC  CC
                                 _  _  AC     A  __
GAM2599  YY1      5'  AGGAGGCGGCCGGCCG      60090          AGAGGA
                                AGGAGGCGGC     GGCCG
                                ||||||||||     |||||
                                TCCTCCGCCG     CCGGC
                                      G_____
GAM2599  ZNF16    3'  GGAAGTGGCAGAGGCTGA    60091      C       AGGCCG
                                GGAGG GGCAGAGG     GA
                                ||||| ||||||||     ||
                                CCTTC CCGTCTCC     CT
                                   A       GA____
GAM2599  ZNF274   5'  AGGGGCGGCAGGCGAAGCCGG  60092     A       AG
                                AGG GGCGGCAG  GAGGCCGG
                                ||| ||||||||  ||||||||
                                TCC CCGCCGTC  CTTCGGCC
                                  _       CG
GAM2599  ZNF274   5'  AGGGGCGGCAGGCGAAGCCGG  60092     A       AG
                                AGG GGCGGCAG  GAGGCCGG
                                ||| ||||||||  ||||||||
                                TCC CCGCCGTC  CTTCGGCC
                                  _       CG
GAM2599  ZNFN2A1  5'  GGGGGCCGCAGGGCGCCAG   60093    A   G    A  AG
                                GG GGC GCAG GG  GCCGG
                                || ||| |||| ||  |||||
                                CC CCG CGTC CC  CGGTC
                                 C   G    _  G_
GAM2599  A2BP1    5'  GGAGACCAGGAAGGGGGCTGG  60094       __  C  A  A   C
                                GGAGGC  GG AG GG GGC GG
                                ||||||  || || || ||| ||
                                CCTCTG  CC TC CC CCG CC
                                    GT  T  _  _   A
GAM2599  AF9Q34   3'  AGGCAGCGGTGGGAGGGGGCTG 60095     A    CA_   A   C
              G                  AGG GGCGG   GAGG GGC GG
                                ||| |||||   |||| ||| ||
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                                TCC TCGCC   CTCC CCG CC
                                  G    ACC    C   A
GAM2599  ALS2CR19  3'  GGCAGGTGGCGGGAATCGG   60096    _  C   AGA   GC
                                GG AGG GGC   GGAG  CGG
                                || ||| |||   ||||  |||
                                CC TCC CCG   CCTT  GCC
                                 G   A   C__    A_
GAM2599  APBA2BP   3'  GGAGGCAGGCAGGGTCCCGG   60097       _    A  AGG
                                GGAGGC GGCAG GG   CCGG
                                |||||| ||||| ||   ||||
                                CCTCCG CCGTC CC   GGCC
                                    T    _ AG_
GAM2599  ATP6V0A1  3'  GGAGGCGGGGAGGGTAGCATGG 60098        CA   A_   C_
                                GGAGGCGG  GAGG  GGC  GG
                                ||||||||  ||||  |||  ||
                                CCTCCGCC  CTCC  TCG  CC
                                     C_   CA   TA
GAM2599  ATP6V1EL2 5'  AGGGGACGGCAGAGAGGGA   60099    A       G   CCG
                                AGG GGCGGCAGAG AGG   GA
                                ||| |||||||||| |||   ||
                                TCC CTGCCGTCTC TCC   CT
                                  C        _  ___
GAM2599  BCL2L12   5'  GGAGGCGGGCAGTCGGAG    60100        _  A_
                                GGAGGCGG CAG  GGAG
                                |||||||| |||  ||||
                                CCTCCGCC GTC  CCTC
                                     C   AG
GAM2599  C20orf175 3'  GGAGGCTGGCAGGAAACGTGGA 60101       _   GA    C_
            G                    GGAGGC GGCA  GGAGGC  GGAG
                                ||||||| ||||  ||||||  ||||
                                CCTCCG CCGT  CCTTTG  CCTC
                                   A   __     CA
GAM2599  C22orf4   3'  AGGAGGCGGCAGGAGGAGG   60102          _
                                AGGAGGCGGCAG AGGAGG
                                |||||||||||| ||||||
                                TCCTCCGCCGTC TCCTCC
                                        C
GAM2599  CDC37    3'  AGGTGGCGGTGGTAGCTGG   60103    A   CAGA  A   C
                                AGG GGCGG   GG GGC GG
                                ||| |||||   || ||| ||
                                TCC CCGCC   CC TCG CC
                                  A    A___  A   A
GAM2599  CDH24    3'  GGAGGCGGCCACACGGGAGGCT 60104         AGA___    C
            GGAG                   GGAGGCGGC     GGAGGC GGAG
                                |||||||||     |||||| ||||
                                CCTCCGCCG     CCTCCG CCTC
                                      GTGTGC     A
GAM2599  CHST3    3'  AGGAGGGAGCAGTGGGGAGGCT 60105       C    A__     C
            GG                     AGGAGG GGCAG   GGAGGC GG
                                |||||| |||||   |||||| ||
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                                TCCTCC TCGTC   CCTCCG CC
                                   C     ACC     A
GAM2599  CL25084   5'  AGGAGGAGGTGGAGGAGG    60106       C  CA
                                AGGAGG GG  GAGGAGG
                                |||||| ||  |||||||
                                TCCTCC CC  CTCCTCC
                                   T  AC
GAM2599  CL25084   5'  AGGAGGTGGAGGAGGAGG    60107       C  CA
                                AGGAGG GG  GAGGAGG
                                |||||| ||  |||||||
                                TCCTCC CC  CTCCTCC
                                   A  TC
GAM2599  CLSTN3    5'  GGAGGGGGCAGAGAGGGG    60108       C      G   CC
                                GGAGG GGCAGAG AGG  GG
                                ||||| ||||||| |||  ||
                                CCTCC CCGTCTC TCC  CC
                                   C      _  __
GAM2599  CPLX1     3'  GGAGGCGGCGGGCGCGG     60109         AGAGGA  _
                                GGAGGCGGC     GGC CGG
                                |||||||||     ||| |||
                                CCTCCGCCG     CCG GCC
                                     C_____   C
GAM2599  dJ309H15.1 3'  AGGAGGGGTGGAGAGGGG    60110       C  C__    A
                                AGGAGG GG   AGAGG GG
                                |||||| ||   ||||| ||
                                TCCTCC CC   TCTCC CC
                                   _  ACC    _
GAM2599  DKFZP434C128 3'  AGCCCCTGCAGAGGAGGCCGG  60111     G___
                                GGC    GCAGAGGAGGCCGG
                                |||    ||||||||||||||
                                TCG    CGTCTCCTCCGGCC
                                  GGGA
GAM2599  DKFZP434K028 3'  AGGGGGTTGGCATGGGGCCGG  60112     A  C_   GA  A
                                AGG GG  GGCA  GG GGCCGG
                                ||| ||  ||||  || ||||||
                                TCC CC  CCGT  CC CCGGCC
                                  C  AA   A_  _
GAM2599  DKFZP434N1511 5'  GGAGGCGGCGGGCGGGACACCG 60113          AGA__   G
            G                    GGAGGCGGC     GGA GCCGG
                                |||||||||     ||| |||||
                                CCTCCGCCG     CCT TGGCC
                                     CCCGC   G
GAM2599  DKFZp547M072 3'  AGGAGGCGGCGGAAGGGATGG  60114          A    A  CC
                                AGGAGGCGGC GAGG GG  GG
                                |||||||||| |||| ||  ||
                                TCCTCCGCCG CTTC CC  CC
                                     C    _  TA
GAM2599  DKFZP564O0423 3'  AGGTGGTGGCAGAGGGGCTGAG 60115     A  C       A   CG
                                AGG GG GGCAGAGG GGC  GAG
                                ||| || |||||||| |||  |||
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                                TCC CC CCGTCTCC CCG  CTC
                                  A  A       _   A_
GAM2599  DKFZP564O123 5'  AGAGACAGCAGGAGGAGGTCGG 60116           _     C
                                GGAGGCGGCAG AGGAGG CGG
                                |||||||||| |||||| |||
                                TCTCTGTCGTC TCCTCC GCC
                                      C     A
GAM2599  DKFZP761I2123 3'  GGAGGTGGCAAGGGCTGCCGG  60117      C    A  AG
                                GGAGG GGCAG GG  GCCGG
                                ||||| ||||| ||  |||||
                                CCTCC CCGTT CC  CGGCC
                                   A    C  GA
GAM2599  DKFZp762K222 5'  AGGAGGCGGGGAGGGGGCGGG  60118         CA   A  C
                                AGGAGGCGG  GAGG GGC GG
                                |||||||||  |||| ||| ||
                                TCCTCCGCC  CTCC CCG CC
                                      C_   C  C
GAM2599  DKFZp762K222 5'  AGGAGGCGGGGAGGGG      60029         CAGA    CC
                                AGGAGGCGG   GGAGG  GG
                                |||||||||   |||||  ||
                                TCCTCCGCC   CCTCC  CC
                                      ____   __
GAM2599  EFNA5    5'  AGAAGGCGGTGGGATGGGG   60119         CAGA  _ CC
                                AGGAGGCGG   GGA GG  GG
                                |||||||||   ||| ||  ||
                                TCTTCCGCC   CCT CC  CC
                                      AC__   A  __
GAM2599  EIF4B    3'  AGGGGCTGGCAGCCTCCTGGAG 60120     A  _    AGGAGG  _
                                AGG GGC GGCAG     CC GGAG
                                ||| ||| |||||     || ||||
                                TCC CCG CCGTC     GG CCTC
                                  _  A    GGA___  A
GAM2599  ELF2     5'  AGGAGGCGGAACCCGCGGCCGG 60121         CAGAGGA
            AG                    AGGAGGCGG      GGCCGGAG
                                |||||||||      ||||||||
                                TCCTCCGCC      CCGGCCTC
                                      TTGGGCG
GAM2599  ET       5'  AGCGGAGTCTGAGGGGGCCGG  60122      CA___   A
                                GGCGG    GAGG GGCCGG
                                |||||    |||| ||||||
                                TCGCC    CTCC CCGGCC
                                   TCAGA   C
GAM2599  FAM10A6  5'  GGAGGCGGTGGGCGAAGCTGG  60123        CAGAG    C
                                GGAGGCGG    GAGGC GG
                                ||||||||    ||||| ||
                                CCTCCGCC    CTTCG CC
                                      ACCCG    A
GAM2599  FASTK    5'  AGGAGGCGGCGGCGGCACAGAG 60124          AGA  A  _
                                AGGAGGCGGC   GG GGC CGGAG
                                ||||||||||   || ||| |||||
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                                TCCTCCGCCG  CC CCG GTCTC
                                      ___ G  T
GAM2599 FKBP8    3' AGGGGGCGGCAGGCGGGG   60125    A      A_ A
                                AGG GGCGGCAG  GG GG
                                ||| ||||||||  || ||
                                TCC CCGCCGTC  CC CC
                                  C       CG  _
GAM2599 FLJ00001 3' GGAGGCGGTGGGGACAG    60126        CAGA  A  C
                                GGAGGCGG    GG GG CGG
                                ||||||||    || || |||
                                CCTCCGCC    CC CC GTC
                                     A___  _  T
GAM2599 FLJ10110 5' AGGAGGCGACAGGACGCTGGAG 60127          GA  G  C
                                AGGAGGCGGCA  GGA GC GGAG
                                ||||||||||  ||| || ||||
                                TCCTCCGCTGT  CCT CG CCTC
                                      __  G  A
GAM2599 FLJ11078 3' GGAGTGGCAGGGCGCGGAG   60128     GC    AGGA  _
                                GGAG  GGCAG    GGC CGGAG
                                ||||  |||||    ||| |||||
                                CCTC  CCGTC    CCG GCCTC
                                  A_    _____  C
GAM2599 FLJ11939 3' AGGAGGGAGGGGCTGG      60129       CGGCA   A  C
                                AGGAGG     GAGG GGC GG
                                ||||||     |||| ||| ||
                                TCCTCC     CTCC CCG CC
                                     ______   _  A
GAM2599 FLJ12242 3' GGGTGCAGACAGAGGAGGCCGG 60130    AG   _
                                GG  GCGG CAGAGGAGGCCGG
                                ||  |||| ||||||||||||||
                                CC  CGTC GTCTCCTCCGGCC
                                 CA   T
GAM2599 FLJ12891 5' AGGAGGCGGCGGCAGGGCTGG  60131          AGA  A   C
                                AGGAGGCGGC   GG GGC GG
                                ||||||||||   || ||| ||
                                TCCTCCGCCG   TC CCG CC
                                      CCG  _   A
GAM2599 FLJ13111 3' GGGGGTGGGGAGGAGACCTGGA 60132    A  C  CA       _
           G                     GG GG GG  GAGGAGGCC GGAG
                                || || ||  ||||||||| ||||
                                CC CC CC  CTCCTCTGG CCTC
                                 C  A  C_       A
GAM2599 FLJ13154 3' AGGAGGGGTAGAGAGAGG    60133       C  C   _
                                AGGAGG GG AGAG GAGG
                                |||||| || |||| ||||
                                TCCTCC CC TCTC CTCC
                                   _  A   T
GAM2599 FLJ13576 5' GGAGGCGGCACGCCTTGG    60134          GAGGAG  __
                                GGAGGCGGCA     GCC  GG
                                ||||||||||     |||  ||
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                                CCTCCGCCGT     CGG  CC
                                     G_____   AA
GAM2599  FLJ13710  3'  GGAGGCGGCTGAGGCAGG    60135        AGAG    C
                                GGAGGCGGC    GAGGC GG
                                |||||||||    ||||| ||
                                CCTCCGCCG    CTCCG CC
                                     A___     T
GAM2599  FLJ13840  5'  AGGAGGTGGCAGAAGCGG    60136       C       A
                                AGGAGG GGCAGAGG GG
                                |||||| |||||||| ||
                                TCCTCC CCGTCTTC CC
                                   A       G
GAM2599  FLJ14126  3'  GGAGGAGAGGGGGCTGG     60137      CGGC    A   C
                                GGAGG    AGAGG GGC GG
                                |||||    ||||| ||| ||
                                CCTCC    TCTCC CCG CC
                                   _____    C   A
GAM2599  FLJ14146  3'  GGGGTTGGCAGAGGGGTATGG  60138    A  C_      A  CC_
                                GG GG  GGCAGAGG GG   GG
                                || ||  |||||||| ||   ||
                                CC CC  CCGTCTCC CC   CC
                                 _ AA       _ ATA
GAM2599  FLJ14249  3'  GGAGGCGGTGCAGGCTGGGAG  60139        CAGAGG   C_
                                GGAGGCGG     AGGC  GGAG
                                ||||||||     ||||  ||||
                                CCTCCGCC     TCCG  CCTC
                                     ACG___    AC
GAM2599  FLJ14249  3'  GGAGGCGGTGCAGGCTGGGAG  60139        CAGAGG   C_
                                GGAGGCGG     AGGC  GGAG
                                ||||||||     ||||  ||||
                                CCTCCGCC     TCCG  CCTC
                                     ACG___    AC
GAM2599  FLJ14299  5'  GGGGGCGGGGAGGGCGG     60140    A    CAGA    C
                                GG GGCGG    GGAGG CGG
                                || |||||    ||||| |||
                                CC CCGCC    CCTCC GCC
                                 C     _____     C
GAM2599  FLJ14594  3'  GGGGGCAGCAGGGGACGGAG   60141    A      A  A   C
                                GG GGCGGCAG GG GGC GGAG
                                || |||||||| || ||| ||||
                                CC CCGTCGTC CC CTG CCTC
                                 C       _  _   _
GAM2599  FLJ20079  3'  AGGGGGCGGGGAGGGG      60142    A    CAGA    CC
                                AGG GGCGG    GGAGG  GG
                                ||| |||||    |||||  ||
                                TCC CCGCC    CCTCC  CC
                                  C    _____    __
GAM2599  FLJ20232  3'  AGGGGGCGGCAGAGAGCACAG  60143     A        GA  _
                                AGG GGCGGCAGAG  GGC CGG
                                ||| ||||||||||  ||| |||
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                                TCC CCGCCGTCTC  TCG GTC
                                  C         __  T
GAM2599  FLJ20294  3'  AGGAGGTGGAAGAACGGA    60144       C  CAGAG   GC
                                AGGAGG GG    GAG  CGGA
                                |||||| ||    |||  ||||
                                TCCTCC CC    TTC  GCCT
                                   A ______  TT
GAM2599  FLJ20552  3'  GGAGGCGGCCGAGGGGGAGGCT 60145         A ___     C
              GG                  GGAGGCGGC GA   GGAGGC GG
                                |||||||||| ||   |||||| ||
                                CCTCCGCCG CT   CCTCCG CC
                                     G  CCC     A
GAM2599  FLJ20552  3'  AGAGGACGGGGAGGCTGG    60146      _  CAGA     C
                                GGAGG CGG    GGAGGC GG
                                ||||| |||    |||||| ||
                                TCTCC GCC    CCTCCG CC
                                   T  _____     A
GAM2599  FLJ21324  5'  AGGCAGGCGGCAGGGGAGA    60147     _       A
                                AGG AGGCGGCAG GGAGG
                                ||| ||||||||| |||||
                                TCC TCCGCCGTC CCTCT
                                  G        C
GAM2599  FLJ22215  3'  GGAGGTGGAGGAGACGCGG    60148       C  CAG      _
                                GGAGG GG   AGGAGGC CGG
                                ||||| ||   ||||||| |||
                                CCTCC CC   TCCTCTG GCC
                                   A ___       C
GAM2599  FLJ22390  5'  AGGTGGCGGCGGCAAGGCCGGA 60149     A     AGAG
              G                   AGG GGCGGC    GAGGCCGGAG
                                ||| ||||||    ||||||||||
                                TCC CCGCCG    TTCCGGCCTC
                                  A     CCG_
GAM2599  FLJ23436  3'  AGGAAGAAGAGGGAGGCTGG   60150       C  C  A     C
                                AGGAGG GG AG GGAGGC GG
                                |||||| || || |||||| ||
                                TCCTTC TC TC CCTCCG CC
                                   T  _  _     A
GAM2599  FLJ23841  5'  AGGAGGCGGCGGGAGGC     60151          AGA
                                AGGAGGCGGC   GGAGGC
                                ||||||||||   ||||||
                                TCCTCCGCCG   CCTCCG
                                     C__
GAM2599  FLJ32919  5'  GGAGGCGGCAGGGTCGG     60152          A  AGGC
                                GGAGGCGGCAG GG    CGG
                                |||||||||||| ||    |||
                                CCTCCGCCGTC CC    GCC
                                      _  A___
GAM2599  GABPB2    5'  AGGAGGTGGTGCGGGGACCCGA 60001       C  CAGA  A    G
              G                   AGGAGG GG    GG GGCC GAG
                                |||||| ||    || |||| |||
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                                TCCTCC CC    CC CTGG CTC
                                   A  ACG_  C    G
GAM2599  GBTS1     3'  GGAGGCAGCGGGGGTCAG    60153          AGA  A  C
                                GGAGGCGGC   GG GG CGG
                                |||||||||   || || |||
                                CCTCCGTCG   CC CC GTC
                                     C__  _  A
GAM2599  GC20      5'  AGGAGGAGGCGGAGGAAG    60154       C   A
                                AGGAGG GGC GAGGAGG
                                |||||| ||| |||||||
                                TCCTCC CCG CTCCTTC
                                   T   C
GAM2599  HES6      5'  GGGAGCGGCGGGGACCGGAG   60155    AG    AGA  A
                                GG  GCGGC   GG GGCCGGAG
                                ||  |||||   || ||||||||
                                CC  CGCCG   CC CTGGCCTC
                                 CT    C__  _
GAM2599  HGC6.1.1  5'  AGGAGGCGATGGCAGCTGGAG  60156          CAGA  A   C
                                AGGAGGCGG    GG GGC GGAG
                                |||||||||    || ||| ||||
                                TCCTCCGCT    CC TCG CCTC
                                     A___  G   A
GAM2599  HGC6.1.1  5'  GGGGCGGCCTGGCCGGAG    60157    A     AGAGGA
                                GG GGCGGC     GGCCGGAG
                                || ||||||     ||||||||
                                CC CCGCCG     CCGGCCTC
                                 _     GA_____
GAM2599  HNK-1ST   3'  AGGGGTGTGGTGGAGGAAGGG  60158    A  C__  CA      CC
                                AGG GG   GG  GAGGAGG  GG
                                ||| ||   ||  |||||||  ||
                                TCC CC   CC  CTCCTTC  CC
                                  _  ACA  AC      __
GAM2599  HRIHFB2122 3'  AGGAGGCTGTGGGGCCATGGAG 60159          GGCAGA  A   __
                                AGGAGGC     GG GGCC  GGAG
                                |||||||     || ||||  ||||
                                TCCTCCG     CC CCGG  CCTC
                                     ACA___  _    TA
GAM2599  HSPC031   3'  GGTAGGTGGCAGAAGTGGGG   60160    _  C       A  CC
                                GG AGG GGCAGAGG GG  GG
                                || ||| |||||||| ||  ||
                                CC TCC CCGTCTTC CC  CC
                                 A  A       A  __
GAM2599  HUMAGCGB  5'  GGCGGGCGGGCGGAGGCCGGAG 60161    A_    CAGA
                                GG  GGCGG    GGAGGCCGGAG
                                ||  |||||    ||||||||||
                                CC  CCGCC    CCTCCGGCCTC
                                 GC    CG__
GAM2599  KIAA0057  3'  AGGAGGAGGCAGGGAGGGG   60162       C    A    CC
                                AGGAGG GGCAG GGAGG  GG
                                |||||| ||||| |||||  ||
```

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                                TCCTCC CCGTC CCTCC  CC
                                   T    _    ___
GAM2599  KIAA0084  5'  AGGAGGCGGCGCGGGGAGG   60163          AGA_
                                AGGAGGCGGC   GGAGG
                                ||||||||||   |||||
                                TCCTCCGCCG   CCTCC
                                     CGCC
GAM2599  KIAA0125  5'  GGAGGCAGGCAGGGCTTGGG  60164      _    A  AGGCC
                                GGAGGC GGCAG GG    GG
                                ||||||| ||||| ||    ||
                                CCTCCG CCGTC CC    CC
                                   T    _  GAAC_
GAM2599  KIAA0125  3'  GGAGGCAGGCAGGGCTTGGG  60164      _    A  AGGCC
                                GGAGGC GGCAG GG    GG
                                ||||||| ||||| ||    ||
                                CCTCCG CCGTC CC    CC
                                   T    _  GAAC_
GAM2599  KIAA0210  3'  AGGAGGCGGTGAGCTTGCTGG  60165        CA   GAG  C
                                AGGAGGCGG  GAG   GC GG
                                |||||||||  |||   || ||
                                TCCTCCGCC  CTC   CG CC
                                     A_   GAA  A
GAM2599  KIAA0222  5'  GGAGGCGGCGGGCCTGG     60166         AGAGGA   _
                                GGAGGCGGC     GGCC GG
                                |||||||||     |||| ||
                                CCTCCGCCG     CCGG CC
                                     C_____    A
GAM2599  KIAA0255  3'  GGCAGCCCTGGAGGAGGCTGG  60167       A___       C
                                GGCGGC    GAGGAGGC GG
                                ||||||    |||||||| ||
                                CCGTCG    CTCCTCCG CC
                                   GGAC       A
GAM2599  KIAA0293  3'  GGGGGTGCAGAAAAGTGGAG   60168    A  CG       GCC
                                GG GG  GCAGAGGAG   GGAG
                                || ||  |||||||||   ||||
                                CC CC  CGTCTTTTC   CCTC
                                 _  CA        A__
GAM2599  KIAA0350  5'  GGAGGCGGTGGAGGAACCGCGA 60169        CA     G  _
            G                    GGAGGCGG  GAGGAG CCG GAG
                                ||||||||  |||||| ||| |||
                                CCTCCGCC  CTCCTT GGC CTC
                                     AC     _  G
GAM2599  KIAA0415  3'  GGGGGCGGGGCCGAGGCCGGAG 60170    A    CAGAG
                                GG GGCGG    GAGGCCGGAG
                                || |||||    ||||||||||
                                CC CCGCC    CTCCGGCCTC
                                 C    CCGG_
GAM2599  KIAA0543  3'  GGAAGCGGCAGACTATGGAG   60171          _____
                                GGAGGCGGCAGA   GGAG
                                ||||||||||||   ||||
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                                CCTTCGCCGTCT   CCTC
                                      GATA
GAM2599  KIAA0649  5' GGAGGCGGCGGGCCGG     60172        AGAGGA
                                GGAGGCGGC    GGCCGG
                                |||||||||    ||||||
                                CCTCCGCCG    CCGGCC
                                     C_____
GAM2599  KIAA0769  5' AGGAGGAGGAGGGCCGGA    60173      CGGCAG    _
                                AGGAGG    AGGAGG CCGGA
                                ||||||    |||||| |||||
                                TCCTCC    TCCTCC GGCCT
                                   _______    C
GAM2599  KIAA0819  3' GGAGGCGGCAGGCGGCTGGAG 60174         AGGA  C
                                GGAGGCGGCAG   GGC GGAG
                                ||||||||||   ||| ||||
                                CCTCCGCCGTC   CCG CCTC
                                      CG__  A
GAM2599  KIAA0995  5' AGGAGGCGGCGAGCGGCGGG  60175        A  GA  C
                                AGGAGGCGGC GAG  GGC GG
                                |||||||||| |||  ||| ||
                                TCCTCCGCCG CTC  CCG CC
                                      _  G_  C
GAM2599  KIAA1026  5' GGAGGAGGCGGAGGAGAAAAAA 60176     C  A     CC
          G                      GGAGG GGC GAGGAGG  GGAG
                                ||||| ||| |||||||  ||||
                                CCTCC CCG CTCCTCT  TTTC
                                   T  C      TT
GAM2599  KIAA1077  5' GGAGGAGGCAGAGGAGCAG   60177     C       GC
                                GGAGG GGCAGAGGAG  CGG
                                ||||| ||||||||||  |||
                                CCTCC CCGTCTCCTC  GTC
                                   T        __
GAM2599  KIAA1100  5' GGAGGCGGCGCAGGACGC    60178       AG   G
                                GGAGGCGGC  AGGA GC
                                |||||||||  |||| ||
                                CCTCCGCCG  TCCT CG
                                      CG   G
GAM2599  KIAA1157  5' AGGAGGCGGCGGGGGCCGG   60179        AGA  A
                                AGGAGGCGGC   GG GGCCGG
                                ||||||||||   || ||||||
                                TCCTCCGCCG   CC CCGGCC
                                      C__  _
GAM2599  KIAA1205  3' GGAGGGGCAGAGAGAGGGG   60180     C     _   CC
                                GGAGG GGCAGAG GAGG  GG
                                ||||| ||||||| ||||  ||
                                CCTCC CCGTCTC CTCC  CC
                                   _     T   __
GAM2599  KIAA1266  3' AGGAGGGGAGAGGCTGG     60181      C  CAGA    C
                                AGGAGG GG   GGAGGC GG
                                |||||| ||   |||||| ||
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                                TCCTCC CC    TCTCCG CC
                                  _ _____      A
GAM2599  KIAA1271  3'  GGAGGGAAAGAGGAGGCTGGAG 60182       C  C        C
                                GGAGG GG AGAGGAGGC GGAG
                                ||||| || ||||||||| ||||
                                CCTCC CT TCTCCTCCG CCTC
                                  _ T        A
GAM2599  KIAA1285  5'  GGAGGCGCGCGGGCGGA     60183        _ AGAGGA  C
                                GGAGGCG GC      GG CGGA
                                ||||||| ||      || ||||
                                CCTCCGC CG      CC GCCT
                                   G _______ C
GAM2599  KIAA1655  5'  AGAGGGGTGAAGGGAGGCCGG  60184       C  C__  A
                                GGAGG GG   AG GGAGGCCGG
                                ||||| ||   || |||||||||
                                TCTCC CC   TC CCTCCGGCC
                                  _ ACT  _
GAM2599  KIAA1819  5'  AGGGGGCGGTGGAGGGGC    60185     A    CA    A
                                AGG GGCGG  GAGG GGC
                                ||| |||||  |||| |||
                                TCC CCGCC  CTCC CCG
                                  C    AC   _
GAM2599  KIAA1831  5'  AGGAGGCAGGCAGAGAGGA    60186        _       AGGCC
                                AGGAGGC GGCAGAGG     GGA
                                ||||||| ||||||||     |||
                                TCCTCCG CCGTCTCT     CCT
                                   T       _____
GAM2599  KIAA1855  3'  AGGAGGCTGCAGCTGGGGTTGG 60187        G    A_  A  CC
                                AGGAGGC GCAG  GG GG  GG
                                ||||||| ||||  || ||  ||
                                TCCTCCG CGTC  CC CC  CC
                                   A   GA  _  AA
GAM2599  KIAA1862  3'  AGGAGGCGCAGCTTCCGGA   60188        G   AGGAGG
                                AGGAGGCG CAG     CCGGA
                                |||||||| |||     |||||
                                TCCTCCGC GTC     GGCCT
                                   _  GAA___
GAM2599  KIAA1870  3'  AGGAGTGTGGCAGGGGAGG   60189       GC_    A
                                AGGAG   GGCAG GGAGG
                                |||||   ||||| |||||
                                TCCTC   CCGTC CCTCC
                                  ACA    C
GAM2599  KIAA1870  3'  AGAGGGTGGCAGAGGAGTGTGG 60190       C_        GCC
                                GGAGG  GGCAGAGGAG   GG
                                |||||  ||||||||||   ||
                                TCTCC  CCGTCTCCTC   CC
                                  CA         ACA
GAM2599  KIAA1879  5'  AGAGGTGGCAGGGGAGGGAGGA 60191       C    A    CC
            G                    GGAGG GGCAG GGAGG  GGAG
                                ||||| ||||| |||||  ||||
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                                TCTCC CCGTC CCTCC  CCTC
                                  A    C    CT
GAM2599 KIAA1887 5' AGGAGGAGGCATGAGGGGCCGG 60192       C   _   A
             AG                    AGGAGG GGCA GAGG GGCCGGAG
                                |||||| |||| |||| ||||||||
                                TCCTCC CCGT CTCC CCGGCCTC
                                  T   A   _
GAM2599 KIAA1913 5' AGAAGGCGGCAGGGTCGG    60193          A AGGC
                                AGGAGGCGGCAG GG   CGG
                                |||||||||||| ||   |||
                                TCTTCCGCCGTC CC   GCC
                                      _ A___
GAM2599 LIMK2    5' AGGAGGCGGGGGGACACAG    60194        CAGA A  _
                                AGGAGGCGG   GG GGC CGG
                                |||||||||   || ||| |||
                                TCCTCCGCC   CC CTG GTC
                                    _____ _  T
GAM2599 MCF2L    3' AGGGGGCGCGTGGGGAGTGGAG 60195    A   GCAGA   GCC
                                AGG GGCG    GGAG  GGAG
                                ||| ||||    ||||  ||||
                                TCC CCGC    CCTC  CCTC
                                  C   GCACC   A__
GAM2599 MEIS3    3' GGAGGTGGGGGGGGACAGGAG  60196     C CAGA A  C
                                GGAGG GG   GG GGC GGAG
                                ||||| ||   || ||| ||||
                                CCTCC CC   CC CTG CCTC
                                   A CC__ _  T
GAM2599 MGC10772 5' GGAGGCGGCGGCGGCCCGG   33811       AGA A   _
                                GGAGGCGGC  GG GGCC GG
                                |||||||||  || |||| ||
                                CCTCCGCCG  CC CCGG CC
                                     ___ G  G
GAM2599 MGC10966 5' AGGAGGCGGCAGATGGC    60197         GGA
                                AGGAGGCGGCAGA  GGC
                                ||||||||||||  |||
                                TCCTCCGCCGTCT  CCG
                                      A__
GAM2599 MGC12945 5' AGGAGGCGGCGGAGGCTGAAG 60198        AGA    C
                                AGGAGGCGGC  GGAGGC GGAG
                                |||||||||  |||||| ||||
                                TCCTCCGCCG  CCTCCG CTTC
                                     ___    A
GAM2599 MGC14386 5' GGAGGCGGCGGGGATGGGG   60199       AGA  _ CC
                                GGAGGCGGC  GGA GG  GG
                                |||||||||  ||| ||  ||
                                CCTCCGCCG  CCT CC  CC
                                     CC_  A __
GAM2599 MGC15437 5' AGGAGGCGGCGGCAGCGGA   60200       AGA A  C
                                AGGAGGCGGC  GG GGC GGA
                                |||||||||  || ||| |||
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                                TCCTCCGCCG   CC TCG CCT
                                     ___  G   _
GAM2599  MGC20460  5'  AGGAGGCGGTGGTGGTGGA   60201        CAGA  A  CC
                                AGGAGGCGG   GG GG  GGA
                                |||||||||   || ||  |||
                                TCCTCCGCC   CC CC  CCT
                                     A___  A  A_
GAM2599  MGC2452   5'  AGGAGGTGGGAGAGGAGG    60202       C  C
                                AGGAGG GG AGAGGAGG
                                |||||| || ||||||||
                                TCCTCC CC TCTCCTCC
                                   A  C
GAM2599  MGC2817   5'  AGGAGGCGGCGGCGACTGAGGA 60204         AGA  A   C__
           G                    AGGAGGCGGC   GG GGC   GGAG
                                ||||||||||   || |||   ||||
                                TCCTCCGCCG   CC CTG   CCTC
                                     ___  G   ACT
GAM2599  MGC2817   5'  AGGCGGCGGCAGAGGAGGAGGA 60203     A          CC
           G                    AGG GGCGGCAGAGGAGG  GGAG
                                ||| ||||||||||||||  ||||
                                TCC CCGCCGTCTCCTCC  CCTC
                                  G           T_
GAM2599  MGC3329   3'  AGGAGGCGGGGGGGAGGTGGG   60205        CAGA    CC
                                AGGAGGCGG   GGAGG  GG
                                |||||||||   |||||  ||
                                TCCTCCGCC   CCTCC  CC
                                     CC__    AC
GAM2599  MGC3771   5'  AGGAGGCGGAGGTTGGGG    60206        C  A__  A
                                AGGAGGCGG AG   GG GG
                                |||||||||  ||   || ||
                                TCCTCCGCC TC   CC CC
                                     _  CAA  _
GAM2599  MGC4342   3'  GGCAGGCGGCAGGCACATGGGG 60207    _       A_____  A
                                GG AGGCGGCAG     GG GG
                                || |||||||||     || ||
                                CC TCCGCCGTC     CC CC
                                  G       CGTGTA  _
GAM2599  MGC4415   3'  GGGGGCGGCAGAAGCCTGTGAG 60208    A       GGA   G__
                                GG GGCGGCAGA   GGCC   GAG
                                || |||||||||   ||||   |||
                                CC CCGCCGTCT   TCGG   CTC
                                  C        ___    ACA
GAM2599  MSRA      5'  GGGGGCGGCAGGGGCGCGG   60209    A     GA  A  _
                                GG GGCGGCA  GG GGC CGG
                                || |||||||  || ||| |||
                                CC CCGCCGT  CC CCG GCC
                                  C      __  _  C
GAM2599  NBL1      3'  AGGAGGCAGGCAGAATTGGGG  60210        _     GA  CC
                                AGGAGGC GGCAGAG  GG  GG
                                |||||||  |||||||  ||  ||
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                                TCCTCCG CCGTCTT  CC  CC
                                    T      AA  __
GAM2599  NDRG4    3'  AGGGGACAGCAGGAGGCTGG   60211     A      GA     C
                                AGG GGCGGCA  GGAGGC GG
                                ||| |||||||  |||||| ||
                                TCC CTGTCGT  CCTCCG CC
                                  C      __      A
GAM2599  NDRG4    3'  AGGGGACAGCAGGAGGCTGG   60211     A      GA     C
                                AGG GGCGGCA  GGAGGC GG
                                ||| |||||||  |||||| ||
                                TCC CTGTCGT  CCTCCG CC
                                  C      __      A
GAM2599  NIR3     3'  AGGCAGGTGGTGGGGCGTGG   60212     _   C  CAGA  A   C_
                                AGG AGG GG    GG GGC  GG
                                ||| ||| ||    || |||  ||
                                TCC TCC CC    CC CCG  CC
                                  G   A  A___  _   CA
GAM2599  NME3     3'  GGCCCTGGAGGAGGCTGGAG   60213     GGCA       C
                                GGC    GAGGAGGC GGAG
                                |||    |||||||| ||||
                                CCG    CTCCTCCG CCTC
                                  GGAC       A
GAM2599  OAZ2     5'  AGGAGGCGGCGCAGGGAG    60214           __  A
                                AGGAGGCGGC  AG GGAG
                                ||||||||||  || ||||
                                TCCTCCGCCG  TC CCTC
                                      CG  _
GAM2599  PA26     3'  AGGAGGCAGGCAGAGGCAGAG  60215        _       AGGC
                                AGGAGGC GGCAGAGG    CGGAG
                                |||||||  ||||||||    |||||
                                TCCTCCG CCGTCTCC    GTCTC
                                    T       _____
GAM2599  PCSK7    3'  GGTGGTGGCAGGACTGGAG    60216    A  C    AGGA   C
                                GG GG GGCAG    GGC GGAG
                                || || |||||    ||| ||||
                                CC CC CCGTC    CTG CCTC
                                 A  A     _____   A
GAM2599  PLA2G3   5'  AGGAGGAGGAAAGAGGCTGGAG 60217       C  CA       C
                                AGGAGG GG  GAGGAGGC GGAG
                                ||||||  ||  |||||||| ||||
                                TCCTCC CC  TTTCTCCG CCTC
                                   T  __       A
GAM2599  PLA2G6   3'  GGCAGGCCCTCAGGGAGGCTGG 60218    _   GG_  A     C
                                GG AGGC   CAG GGAGGC GG
                                || ||||   ||| |||||| ||
                                CC TCCG   GTC CCTCCG CC
                                 G   GGA  _     A
GAM2599  PLAGL2   3'  GGAGGTGGCAGGGAAAGGGG   60219      C    A    CC
                                GGAGG GGCAG GGAGG  GG
                                ||||| ||||| |||||  ||
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                                CCTCC CCGTC CCTTT  CC
                                  A    _    CC
GAM2599  PPP1R1A  5'  GAAGGCGGCGGGACTCGGGGCT 60220         A_  ___  A   C
                GG                  GGAGGCGGC  GA   GG GGC GG
                                    |||||||||  ||   || ||| ||
                                    CTTCCGCCG  CT   CC CCG CC
                                         CC  GAG  _   A
GAM2599  PRO1635  3'  AGGAGGAGAGGGGCTGG     60221       CGGC    A   C
                                    AGGAGG    AGAGG GGC GG
                                    ||||||    ||||| ||| ||
                                    TCCTCC    TCTCC CCG CC
                                       ____     _  A
GAM2599  PROL3    3'  AGGAGGCTGTGGATAACTTGG  60222        GGCAGA  _   C_
                                    AGGAGGC     GGA GGC  GG
                                    |||||||      ||| |||  ||
                                    TCCTCCG     CCT TTG  CC
                                        ACA___   A   AA
GAM2599  PTGES2   3'  AGGGGCGGCAGAGCAGGGAG   60223     A        G   CCG
                                    AGG GGCGGCAGAG AGG   GAG
                                    ||| ||||||||| |||   |||
                                    TCC CCGCCGTCTC TCC   CTC
                                      _         G   ___
GAM2599  PTP4A1   5'  AGGAGGCGGCGGTGGTCGTGGC 60224          AGA  A___   C
                GGAG                  AGGAGGCGGC   GG    GGC GGAG
                                      |||||||||   ||    ||| ||||
                                      TCCTCCGCCG   CC    CCG CCTC
                                           CCA  AGCA  _
GAM2599  QKI      5'  GGAGGGGCGGGGGCGAG     60225       C   AGA  A   C
                                    GGAGG GGC   GG GGC GG
                                    |||||  |||   || ||| ||
                                    CCTCC CCG   CC CCG TC
                                       _  C__  _   C
GAM2599  Rab11-FIP3 5'  GGGGGCCGAGGAGGCCGGAG   60226    C   A
                                    GG GGC GAGGAGGCCGGAG
                                    || ||| ||||||||||||
                                    CC CCG CTCCTCCGGCCTC
                                     C   G
GAM2599  Rab11-FIP3 5'  GGGGGCCGAGGAGGCCGG    60227    C   A
                                    GG GGC GAGGAGGCCGG
                                    || ||| ||||||||||
                                    CC CCG CTCCTCCGGCC
                                     C   G
GAM2599  RASGRP4   5'  GGGGTGAGGAGGCCGG      60228    C  CA
                                    GG GG  GAGGAGGCCGG
                                    || ||  ||||||||||
                                    CC CC  CTCCTCCGGCC
                                     _ A_
GAM2599  SCAMP5   3'  GGAGGAGGCAGAGGGAC     60229       C       A
                                    GGAGG GGCAGAGG GGC
                                    ||||| ||||||| |||
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                                CCTCC CCGTCTCC CTG
                                  T      _
GAM2599 SDBCAG84 3' GGAGGGTGGCAGAGGCTGGGG 60230     C_     A_ CC
                                GGAGG GGCAGAGG GG GG
                                ||||| |||||||| || ||
                                CCTCC CCGTCTCC CC CC
                                  CA      GA __
GAM2599 SDCCAG43 3' GGAGGTGGAGGAGGCTGG   60231     C CAG     C
                                GGAGG GG  AGGAGGC GG
                                ||||| ||  ||||||| ||
                                CCTCC CC  TCCTCCG CC
                                  A ___     A
GAM2599 SEC14L1  5' GGAGGCGGGAGGGGGAAGG  60232       CA   A CC
                                GGAGGCGG GAGG GG GG
                                |||||||| |||| ||  ||
                                CCTCCGCC CTCC CC CC
                                    __   C TT
GAM2599 SIAT8C   5' GGAGGCCACCGGGGCCGG   60233      G AGA A
                                GGAGGC GC  GG GGCCGG
                                |||||| ||  || ||||||
                                CCTCCG TG  CC CCGGCC
                                  G G__ _
GAM2599 SLC26A10 5' GGAGGAGATGAGGTTGGA   60234     CGGC G   CC
                                GGAGG   AGA GAGG GGA
                                |||||   ||| |||| |||
                                CCTCC   TCT CTCC CCT
                                  _____ A   AA
GAM2599 SLC38A4  3' AGGAGACGGCAGGGGAAAGAG 60235         A   GCC
                                AGGAGGCGGCAG GGAG  GGAG
                                |||||||||||| ||||  ||||
                                TCCTCTGCCGTC CCTT  TCTC
                                      C   ___
GAM2599 SPRY4    3' GGGGGCGGAGGGAGGGA    60236   A   C A   CCG
                                GG GGCGG AG GGAGG  GA
                                || ||||| || |||||  ||
                                CC CCGCC TC CCTCC  CT
                                 C    _ _   ___
GAM2599 SUCLG2   5' AGGAGGCGGAGGAGGAGCAG  60237       CA    GC
                                AGGAGGCGG GAGGAG CGG
                                ||||||||| |||||| |||
                                TCCTCCGCC CTCCTC GTC
                                    TC    __
GAM2599 SYT13    3' AGGAGGTTGCAGAGGACGG   60238      CG     GGC
                                AGGAGG GCAGAGGA  CGG
                                |||||| |||||||| |||
                                TCCTCC CGTCTCCT  GCC
                                  AA      ___
GAM2599 TA-PP2C  5' AGGAGGCGGGGGGCCGG    60239       CAGA A
                                AGGAGGCGG   GG GGCCGG
                                |||||||||   || ||||||
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                                TCCTCCGCC   CC CCGGCC
                                      ____ _
GAM2599 TCF-3    3' GGCAGGCGGCAGGGGCGAG   60240   _     GA A  C
                                GG AGGCGGCA  GG GGC GG
                                || ||||||||  || ||| ||
                                CC TCCGCCGT  CC CCG TC
                                 G      __ _  C
GAM2599 TEX27    3' AGGAGGGGGCGGGGGGCCCTGG 60241      C  AGA A  __
                                AGGAGG GGC   GG GGCC  GG
                                |||||| |||   || ||||  ||
                                TCCTCC CCG   CC CCGG  CC
                                   C   CC_ _   GA
GAM2599 THG-1    5' GGAGGTGGCGGGAGGGG    60242     C  AGA   CC
                                GGAGG GGC   GGAGG  GG
                                ||||| |||   |||||  ||
                                CCTCC CCG   CCTCC  CC
                                   A  C__   __
GAM2599 TIAF1    3' AGAGGGTGGGGTGGGGGCTGGA 60243     C_ CAGA  A  C
             G                   GGAGG  GG   GG GGC GGAG
                                ||||| ||   || ||| ||||
                                TCTCC  CC   CC CCG CCTC
                                   CA  CCAC  _  A
GAM2599 TIAF1    3' GGGGGCGGCAGATGGGAG    60244   A      __
                                GG GGCGGCAGA  GGAG
                                || |||||||||  ||||
                                CC CCGCCGTCT  CCTC
                                 C       AC
GAM2599 TLN2     3' GGAGGCGGCAGAGGAGTTGTGG 60245           GCC_
                                GGAGGCGGCAGAGGAG   GG
                                ||||||||||||||||   ||
                                CCTCCGCCGTCTCCTC   CC
                                         AACA
GAM2599 TREX1    5' AGGAGGTGGCAAAGGCTTAGG  60246     C      AGGCC
                                AGGAGG GGCAGAGG    GG
                                |||||| ||||||||    ||
                                TCCTCC CCGTTTCC    CC
                                   A      GAAT_
GAM2599 TREX1    5' AGGAGGTGGCAAAGGCTTAGG  60246     C      AGGCC
                                AGGAGG GGCAGAGG    GG
                                |||||| ||||||||    ||
                                TCCTCC CCGTTTCC    CC
                                   A      GAAT_
GAM2599 TRIP-Br2 5' AGGAGGCGGGCGGAGGGG    60247       CAGA   CC
                                AGGAGGCGG   GGAGG  GG
                                |||||||||   |||||  ||
                                TCCTCCGCC   CCTCC  CC
                                     CG__   __
GAM2599 VIAAT    5' AGGAGGCGAGGGCTGG     60248       GCAGA  A  C
                                AGGAGGCG    GG GGC GG
                                ||||||||    || ||| ||
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                                TCCTCCGC    TC CCG CC
                                   _____ _   A
GAM2599  ZDHHC2   5'  AGGAGGCGGAGGGGGGCGG   60249       C  A  A   C
                                AGGAGGCGG AG GG GGC GG
                                ||||||||| || || ||| ||
                                TCCTCCGCC TC CC CCG CC
                                   _ _ C   _
GAM2599  ZIC4     5'  GGAGGCGGCGGTGAGCTGG   60250       AGA  A_   C
                                GGAGGCGGC   GG  GGC GG
                                |||||||||   ||  ||| ||
                                CCTCCGCCG   CC  TCG CC
                                   ___ AC   A
GAM2599  LOC112476 3'  AGGAGGCGGCCAGGGTGGA   60251        AG   AGGCC
                                AGGAGGCGGC  AGG    GGA
                                ||||||||||  |||    |||
                                TCCTCCGCCG  TCC    CCT
                                   G_   CA___
GAM2599  LOC113521 5'  AGGGGGCGGAGAGGCCGA    60252    A    CAGA
                                AGG GGCGG    GGAGGCCGG
                                ||| |||||    |||||||||
                                TCC CCGCC    TCTCCGGCT
                                  C    _____
GAM2599  LOC115574 3'  GGAGGCTGCAGGCCGGA     60253      G   GAGGA
                                GGAGGC GCA    GGCCGGA
                                |||||| |||    |||||||
                                CCTCCG CGT    CCGGCCT
                                   A  ______
GAM2599  LOC124402 3'  GGAGGAGGCAGGGCCCTGG   60254     C    AGGA   __
                                GGAGG GGCAG    GGCC  GG
                                ||||| |||||    ||||  ||
                                CCTCC CCGTC    CCGG  CC
                                   T    _____    GA
GAM2599  LOC124739 3'  GGAGGCGGAGAGAGCTGG    60255       C   GA   C
                                GGAGGCGG AGAG  GGC GG
                                |||||||| ||||  ||| ||
                                CCTCCGCC TCTC  TCG CC
                                   _   __   A
GAM2599  LOC126364 3'  AGGGGGCGGCAGAGCTTCCTGG 60256    A        GAGG  _
                                AGG GGCGGCAGAG    CC GG
                                ||| ||||||||||    || ||
                                TCC CCGCCGTCTC    GG CC
                                  C         GAA_  A
GAM2599  LOC126526 3'  AGGGGGCCGCTGGGAGGCCGGA 60257    A   G  AGA
            G                   AGG GGC GC   GGAGGCCGGAG
                                ||| ||| ||   ||||||||||
                                TCC CCG CG   CCTCCGGCCTC
                                  C   G  AC_
GAM2599  LOC128439 3'  AGGAGGCGGGAGGACACGGAG  60258        CA    G  C
                                AGGAGGCGG  GAGGA GC GGAG
                                |||||||||  ||||| || ||||
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                                TCCTCCGCC  CTCCT TG CCTC
                                     __    G  _
GAM2599  LOC129676 5'  GGGAGCGAGGAGGCTGG    60259    C   A      C
                                GG GGC GAGGAGGC GG
                                || ||| |||||||| ||
                                CC TCG CTCCTCCG CC
                                 C   _       A
GAM2599  LOC130612 5'  AGGGGGCTGCTGGGCCGGA   60260    A   G  AGAGGA
                                AGG GGC GC     GGCCGGA
                                ||| ||| ||     |||||||
                                TCC CCG CG     CCGGCCT
                                  C   A  AC____
GAM2599  LOC132112 3'  AGGAGGAGGTAGGAGTTGGAG  60261       C  CAG    GCC
                                AGGAGG GG   AGGAG   GGAG
                                |||||| ||   |||||   ||||
                                TCCTCC CC   TCCTC   CCTC
                                    T  A__     AA_
GAM2599  LOC132617 3'  GGCAGGTGGCAGAGAGTGGG   60262    _  C      G  GCC
                                GG AGG GGCAGAG AG   GG
                                || ||| ||||||| ||   ||
                                CC TCC CCGTCTC TC   CC
                                 G   A       _ AC_
GAM2599  LOC139673 3'  AGGGGCTGGCAGCCTCCTGGAG 60120     A  _    AGGAGG  _
                                AGG GGC GGCAG      CC GGAG
                                ||| ||| |||||      || ||||
                                TCC CCG CCGTC      GG CCTC
                                  _   A    GGA___  A
GAM2599  LOC144483 3'  GGAGGGGCAGAGGGACAAG    60050       C       A   C
                                GGAGG GGCAGAGG GGC GG
                                ||||| |||||||| ||| ||
                                CCTCC CCGTCTCC CTG TC
                                   _       _   T
GAM2599  LOC145719 5'  AGGGGGCTGGCTTTGGGGCTGG 60263     A  _  AGA  A   C
                                AGG GGC GGC   GG GGC GG
                                ||| ||| |||   || ||| ||
                                TCC CCG CCG   CC CCG CC
                                  C   A   AAA  _   A
GAM2599  LOC145720 5'  AGGGGGCTGGCTTTGGGGCTGG 60263     A  _  AGA  A   C
                                AGG GGC GGC   GG GGC GG
                                ||| ||| |||   || ||| ||
                                TCC CCG CCG   CC CCG CC
                                  C   A   AAA  _   A
GAM2599  LOC145988 5'  AGGAGGAGGCGGAGGAGGACTT 60264       C   A     _ C_
            GG                    AGGAGG GGC GAGGAGG C  GG
                                ||||||  ||| |||||||  |  ||
                                TCCTCC CCG CTCCTCC G  CC
                                   T   C      T AA
GAM2599  LOC146268 3'  GGAGGCAGGTAGGAGCTGG    60265        CAG    G C
                                GGAGGCGG   AGGAG C GG
                                ||||||||   ||||| | ||
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                                CCTCCGTC   TCCTC G CC
                                     CA_    _ A
GAM2599  LOC146332 3'  AGGAGGCGGTGCAGGAGG    60266        CAG
                                AGGAGGCGG   AGGAGG
                                |||||||||   ||||||
                                TCCTCCGCC   TCCTCC
                                     ACG
GAM2599  LOC147958 3'  GGAGGCGGCGTAAACGGG    60267        AGAGG   C
                                GGAGGCGGC    AGGC GG
                                |||||||||    |||| ||
                                CCTCCGCCG    TTTG CC
                                     CA___    C
GAM2599  LOC147965 5'  AGGAGGCGGGTGGCTTGGA    60268        CAGAG A   C_
                                AGGAGGCGG    G GGC  GGA
                                |||||||||    | |||  |||
                                TCCTCCGCC    C CCG  CCT
                                     _____ A   AA
GAM2599  LOC148078 5'  AGGAGCCCTGGAGGCCGG    60269     C   AGA
                                AGG GGC   GGAGGCCGG
                                ||| |||   |||||||||
                                TCC TCG   CCTCCGGCC
                                  _   GGA
GAM2599  LOC148137 3'  GGAGCTGGGGTGGAGGCCGG   60270     GC  CAGA
                                GGAG  GG   GGAGGCCGG
                                ||||  ||   |||||||||
                                CCTC  CC   CCTCCGGCC
                                  GA  CCA_
GAM2599  LOC149668 5'  GGGGGTGGCAGAGGACCAA    60271    A  C      AG
                                GG GG GGCAGAGG  GCCGG
                                || || ||||||||  |||||
                                CC CC CCGTCTCC  TGGTT
                                 C  A       __
GAM2599  LOC150067 5'  AGGAGGCGGCAGCGGGG     60272          A  A
                                AGGAGGCGGCAG GG GG
                                |||||||||||| || ||
                                TCCTCCGCCGTC CC CC
                                       G  _
GAM2599  LOC151512 5'  AGGAGGCGGCCGAGGCGCAGGC 60273         A   ___   C
            GGAG                   AGGAGGCGGC GAGG   AGGC GGAG
                                |||||||||| ||||   |||| ||||
                                TCCTCCGCCG CTCC   TCCG CCTC
                                     G   GCG   _
GAM2599  LOC152905 5'  AGGGGGCGGGAGAGAGGGA   60274    A    C   G   CCG
                                AGG GGCGG AGAG AGG   GA
                                ||| ||||| |||| |||   ||
                                TCC CCGCC TCTC TCC   CT
                                  C    C   _  ___
GAM2599  LOC153565 5'  AGAGGCGGCGGGGGCCTTGG   60275        AGA  A   __
                                GGAGGCGGC   GG GGCC  GG
                                |||||||||   || ||||  ||
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                                TCTCCGCCG  CC CCGG  CC
                                    C__ _   AA
GAM2599  LOC153688 3'  AGGAGGGGCAGAGGGGCCGG  60276      C      A
                                AGGAGG GGCAGAGG GGCCGG
                                |||||| |||||||| ||||||
                                TCCTCC CCGTCTCC CCGGCC
                                  _      _
GAM2599  LOC155434 3'  AGGAGGTGGAGGGAGAGGA   60277      C  C  A    CC
                                AGGAGG GG AG GGAGG  GGA
                                |||||| || || |||||  |||
                                TCCTCC CC TC CCTCT  CCT
                                   A  _ _   __
GAM2599  LOC158056 5'  GGCAGGGGCTGGGGGGCTGG  60278   _  C  AGA  A  C
                                GG AGG GGC  GG GGC GG
                                || ||| |||  || ||| ||
                                CC TCC CCG  CC CCG CC
                                 G  _  ACC  _  A
GAM2599  LOC159090 5'  AGGGGGCGGAGGAGGG     60279    A   CAG    CCG
                                AGG GGCGG  AGGAGG  G
                                ||| |||||  ||||||  |
                                TCC CCGCC  TCCTCC  C
                                 C   ____   ____
GAM2599  LOC163412 5'  AGGAGGCGGTGGTGGTGGG   60280       CAGA  A  CC
                                AGGAGGCGG   GG GG  GG
                                |||||||||   || ||  ||
                                TCCTCCGCC   CC CC  CC
                                     A___  A  AC
GAM2599  LOC164386 5'  GGAGGCGGGGGGTACCTGG   60281       CAGA  AG  _
                                GGAGGCGG   GG  GCC GG
                                ||||||||   ||  ||| ||
                                CCTCCGCC   CC  TGG CC
                                     _____  CA  A
GAM2599  LOC195977 3'  GGAGGTGGTGGAGGCGGAG   60282     C  CAGA    C
                                GGAGG GG   GGAGGC GGAG
                                ||||| ||   |||||| ||||
                                CCTCC CC   CCTCCG CCTC
                                   A  A___    _
GAM2599  LOC196214 5'  AGGAGGCGGAGGGGGTGG    60283       C  A  A  CC
                                AGGAGGCGG AG GG GG  GG
                                ||||||||| || || ||  ||
                                TCCTCCGCC TC CC CC  CC
                                     _ _ _  A_
GAM2599  LOC196743 5'  GGAGCTCTCGGAGGAGGCCGGA 60284     G GGCA_
           G                    GGAG C    GAGGAGGCCGGAG
                                |||| |    |||||||||||||
                                CCTC G    CTCCTCCGGCCTC
                                  _ AGAGC
GAM2599  LOC197114 3'  AGGAGGCGGGGATGGGG    60285       CAGA  _  CC
                                AGGAGGCGG   GGA GG  GG
                                |||||||||   ||| ||  ||
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                                TCCTCCGCC   CCT CC  CC
                                     ____  A  __
GAM2599  LOC197114 5'  AGGGGGCTGGCTTTGGGGCTGG 60263    A  _  AGA  A   C
                                AGG GGC GGC   GG GGC GG
                                ||| ||| |||   || ||| ||
                                TCC CCG CCG   CC CCG CC
                                  C   A   AAA  _   A
GAM2599  LOC197117 3'  AGGAGGCGGGGATGGGG     60285         CAGA  _  CC
                                AGGAGGCGG    GGA GG  GG
                                |||||||||    ||| ||  ||
                                TCCTCCGCC    CCT CC  CC
                                     ____  A  __
GAM2599  LOC197335 5'  GGAGGCGGGTGGAGGACACGAG 60286        CA_    G  C
                                GGAGGCGG   GAGGA GC GG
                                ||||||||   ||||| || ||
                                CCTCCGCC   CTCCT TG TC
                                     CAC    G  C
GAM2599  LOC197423 5'  AGGAGGCGGCGGCGGGCGG   60287         AGA  A  C
                                AGGAGGCGGC   GG GG CGG
                                ||||||||||   || || |||
                                TCCTCCGCCG   CC CC GCC
                                     ___  G  C
GAM2599  LOC199953 5'  AGGAGGCGGTGACGCCGG    60288        CAGAG  G
                                AGGAGGCGG    GA GCCGG
                                |||||||||    || |||||
                                TCCTCCGCC    CT CGGCC
                                     A____  G
GAM2599  LOC201294 3'  AGGAGGCTGGGGCGGGGCCGGA 60289       _  CAGA  A
           G                     AGGAGGC GG   GG GGCCGGAG
                                |||||||  ||   || ||||||||
                                TCCTCCG CC   CC CCGGCCTC
                                   A  CCG_  _
GAM2599  LOC201702 5'  GGAGCGCGGGGCCGGA     59997     _   CAGAGGA
                                GGAG GCGG      GGCCGGA
                                |||| ||||      |||||||
                                CCTC CGCC      CCGGCCT
                                  G   ________
GAM2599  LOC201911 3'  GGAGGCGGCGGGGGAGGAG   60290        A___
                                GGAGGCGGC   GAGGAG
                                |||||||||   ||||||
                                CCTCCGCCG   CTCCTC
                                     CCCC
GAM2599  LOC203069 5'  AGGAGCGCGGCAGGGGCCAGAG 60291      _    GA  A
                                AGGAG GCGGCA  GG GGCCGGAG
                                ||||| ||||||  || ||||||||
                                TCCTC CGCCGT  CC CCGGTCTC
                                  G    __  _
GAM2599  LOC219513 5'  AGGCGGCGGCGGGGAGGGA   60292    A    AGA    CCG
                                AGG GGCGGC   GGAGG   GA
                                ||| ||||||   |||||   ||
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                                TCC CCGCCG   CCTCC   CT
                                  G     CC_    ___
GAM2599  LOC220565 5'  AGGAGGCGGCGGCGG       60070         AGAGGA   C
                                AGGAGGCGGC     GGC GG
                                ||||||||||     ||| ||
                                TCCTCCGCCG     CCG CC
                                       _______  _
GAM2599  LOC220565 5'  AGGCGGCGGCGGAGGGCGG   60071    A     AGA    C
                                AGG GGCGGC   GGAGG CGG
                                ||| ||||||   ||||| |||
                                TCC CCGCCG   CCTCC GCC
                                  G     ___     C
GAM2599  LOC221641 5'  AAGGAGGCCTGGGGGCCGG   60293     C   AGA  A
                                GAGG GGC   GG GGCCGG
                                |||| |||   || ||||||
                                TTCC CCG   CC CCGGCC
                                  T   GAC  _
GAM2599  LOC221749 5'  AGGAGGCGCGCCCCGGCCGG   60294        _  AGAGGA
                                AGGAGGCG GC     GGCCGG
                                |||||||| ||     ||||||
                                TCCTCCGC CG     CCGGCC
                                     G  GGG___
GAM2599  LOC253758 5'  AGGAGGCGGCGGGAGGGG    60295         AGA    CC
                                AGGAGGCGGC   GGAGG  GG
                                ||||||||||   |||||  ||
                                TCCTCCGCCG   CCTCC  CC
                                     C__    __
GAM2599  LOC254100 5'  GGAGGCGGAGGCCAG       60296       GGCAGA
                                GGAGGC     GGAGGCCGG
                                ||||||     |||||||||
                                CCTCCG     CCTCCGGTC
                                       _______
GAM2599  LOC254532 5'  AGAGGTGGCGGGGCCTGGA   60297      C   AGA  A   _
                                GGAGG GGC   GG GGCC GGA
                                ||||| |||   || |||| |||
                                TCTCC CCG   CC CCGG CCT
                                   A   ___  _   A
GAM2599  LOC255043 3'  AGGGGGCGGGCAGGCTGTGGGG 60298     A    _  A____  A
                                AGG GGCGG CAG     GG GG
                                ||| ||||| |||     || ||
                                TCC CCGCC GTC     CC CC
                                  C    C   CGACA  _
GAM2599  LOC255057 3'  GGAGGGGTGCTGCTGGCCGGAG 60299       C  CAGAGGA
                                GGAGG GG      GGCCGGAG
                                ||||| ||      ||||||||
                                CCTCC CC      CCGGCCTC
                                   _  ACGACGA
GAM2599  LOC255259 5'  GGAGGAGGCGGGGGCCGG    60300       C   AGA  A
                                GGAGG GGC   GG GGCCGG
                                ||||| |||   || ||||||
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                                CCTCC CCG   CC CCGGCC
                                  T   C__  _
GAM2599  LOC256000 5'  AGGAAGCGGCGGGCTCGG    60301         AGAGGA  _
                                AGGAGGCGGC     GGC CGG
                                ||||||||||     ||| |||
                                TCCTTCGCCG     CCG GCC
                                     C_____   A
GAM2599  LOC257104 5'  AGGAGGCGCAGAGGGGCGTGG  60302        G     A  C_
                                AGGAGGCG CAGAGG GGC  GG
                                |||||||| |||||| |||  ||
                                TCCTCCGC GTCTCC CCG  CC
                                     _     _  CA
GAM2599  LOC51066  3'  AGGAGCTGTATAAGGGGTTGGA 60303      G GGCA_   A  CC
            G                    AGGAG C    GAGG GG  GGAG
                                ||||| |    |||| ||  ||||
                                TCCTC G    TTCC CC  CCTC
                                  _ ACATA   _  AA
GAM2599  LOC51072  5'  AGGAGGCGGCAGCGGGG     60272          A  A
                                AGGAGGCGGCAG GG GG
                                ||||||||||| || ||
                                TCCTCCGCCGTC CC CC
                                      G  _
GAM2599  LOC51112  5'  GGAGGCGGGCTGGCGGGGGCCG 60304        _ AGA_  A
            G                    GGAGGCGG C    GG GGCCGG
                                |||||||| |    || ||||||
                                CCTCCGCC G    CC CCGGCC
                                     C ACCG  C
GAM2599  LOC51133  5'  GGGGCGGCGGCGGCCGGAG   60305    A     AGA  A
                                GG GGCGGC   GG GGCCGGAG
                                || ||||||   || ||||||||
                                CC CCGCCG   CC CCGGCCTC
                                 _     ____  G
GAM2599  LOC51291  3'  AGGAGGCAGGCAGGTGTGGGG  60306       _    A___  A
                                AGGAGGC GGCAG    GG GG
                                ||||||| |||||    || ||
                                TCCTCCG CCGTC    CC CC
                                    T    CACA  _
GAM2599  LOC51762  5'  AGGAGGCGGTGGAGAGAG    60307         CA  _
                                AGGAGGCGG  GAG GAG
                                |||||||||  ||| |||
                                TCCTCCGCC  CTC CTC
                                     AC   T
GAM2599  LOC55954  3'  GGGGGGCAGGTGGAGGAGA   60308    A  C    A_    CC
                                GG GG GGCAG  GGAGG  GGA
                                || || |||||  |||||  |||
                                CC CC CCGTC  CCTCC  TCT
                                  _ _    CA    __
GAM2599  LOC56270  3'  GGAGACGGTGGACCTGG     60309        CAGA  AG  _
                                GGAGGCGG   GG  GCC GG
                                ||||||||   ||  ||| ||
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                                CCTCTGCC   CC  TGG CC
                                    A___  __  A
GAM2599  LOC56961  5'  AGGAGGCGACAGAGGAGGGAG  60311              CCG
                                AGGAGGCGGCAGAGGAGG  GAG
                                ||||||||||||||||||  |||
                                TCCTCCGCTGTCTCCTCC  CTC
                                                ___
GAM2599  LOC56961  5'  AGGAGGTGGAGAGGAAGGG   60310      C  C      CC
                                AGGAGG GG AGAGGAGG  GG
                                ||||||  || ||||||||  ||
                                TCCTCC CC TCTCCTTC  CC
                                   A  _      __
GAM2599  LOC57100  3'  GGAGGAGGCAGGGTGGGG   60312      C    A  A  CC
                                GGAGG GGCAG GG GG  GG
                                |||||  ||||| || ||  ||
                                CCTCC CCGTC CC CC  CC
                                   T    _  A  __
GAM2599  LOC57147  5'  GAAGGCGGCGGGGGAGGAG   60313        A___
                                GGAGGCGGC   GAGGAG
                                |||||||||   ||||||
                                CTTCCGCCG   CTCCTC
                                     CCCC
GAM2599  LOC57795  3'  AGGAGGCAGCAGAGGGAG   60314            _
                                AGGAGGCGGCAGAGG AG
                                ||||||||||||||  ||
                                TCCTCCGTCGTCTCC TC
                                          C
GAM2599  LOC63928  5'  GGAGGCGGAAGGGCCGGA   60315        CAG  A
                                GGAGGCGG  AGG GGCCGGA
                                ||||||||  ||| |||||||
                                CCTCCGCC  TTC CCGGCCT
                                     ___  _
GAM2599  LOC83985  5'  GAGGGGAGGAGGCTGGA    60316     C  CAG     C
                                GAGG GG  AGGAGGC GGA
                                ||||  ||  ||||||| |||
                                CTCC CC  TCCTCCG CCT
                                  _  ___      A
GAM2599  LOC90313  5'  AGGGGTGGTAGAGGAAG    60317    A  C  C
                                AGG GG GG AGAGGAGG
                                |||  ||  ||  ||||||||
                                TCC CC CC TCTCCTTC
                                  _  A  A
GAM2599  LOC91301  5'  AGGGGGCGGCAGCCGGGCCGG  60318    A      AGGA
                                AGG GGCGGCAG   GGCCGG
                                |||  ||||||||   ||||||
                                TCC CCGCCGTC   CCGGCC
                                  C       GGC_
GAM2599  LOC92714  3'  AGGAGCTGGCAGAGGCTGG   60319      GC      AGGCC
                                AGGAG  GGCAGAGG    GG
                                |||||  ||||||||    ||
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                                TCCTC  CCGTCTCC    CC
                                  GA      GA___
GAM2599 LOC92715 5' GGGGCGGCGAGGCCGG     60320    A     AGAG
                                GG GGCGGC   GAGGCCGG
                                || ||||||   ||||||||
                                CC CCGCCG   CTCCGGCC
                                 _    _____
GAM2600 AP1S2    5' GGAAGCCCCTGTCGCCGTGCT  60323     A  TG  G
                                GGAA CT  CC GTCGCCGTGCT
                                |||| ||  || ||||||||||
                                CCTT GG  GG CAGCGGCACGA
                                  C __ A
GAM2600 KIAA1909 5' TGGAGGCTGCCGCCGTCTGTGC 60324     AAC     G   CC_
             T                   TGGA   TTGCCG TCG   GTGCT
                                ||||   |||||| |||   |||||
                                ACCT   GACGGC GGC   CACGA
                                  CC_     _  AGA
GAM2600 SMARCF1  3' TGGAAACTTGCTGCTCTCC   60325         CGG  G
                                TGGAAACTTGC   TC CC
                                ||||||||||   || ||
                                ACCTTTGAACG   AG GG
                                      ACG  A
GAM2601 KITLG    3' GGTACATGCAGTCTGAGACACG 60328    _    A  CGCCCA
             T                   GG ACATG CG     AGACACGT
                                || ||||| ||     ||||||||
                                CC TGTAC GT     TCTGTGCA
                                 A    _  CAGAC_
GAM2601 KITLG    3' GGTACATGCAGTCTGAGACACG 60328    _    A  CGCCCA
             T                   GG ACATG CG     AGACACGT
                                || ||||| ||     ||||||||
                                CC TGTAC GT     TCTGTGCA
                                 A    _  CAGAC_
GAM2601 ATP6M8-9 5' GGAGGTGACGCGCTCGGACTCG 60329    CA      CCAA   A
             T                   GGA  TGACGCGC    GAC CGT
                                |||  ||||||||    ||| |||
                                CCT  ACTGCGCG    CTG GCA
                                  CC       AGC_   A
GAM2601 MGC22014 3' GGATGTGACCTGCCCAAGA   60330    CA   GC
                                GGA  TGAC  GCCCAAGA
                                |||  ||||  ||||||||
                                CCT  ACTG  CGGGTTCT
                                  AC    GA
GAM2602 KBRAS2   3' TGACTGGGAAAGACAGCTT   60333     GCGA   CCC
                                TGAC    GGA   GACAGCTT
                                ||||    |||   ||||||||
                                ACTG    CCT   CTGTCGAA
                                  AC__   TT_
GAM2602 LOC148918 5' GAGGGCCCCTGACAGCTTA   60334     A_  _
                                GAGG  CCC GACAGCTTA
                                ||||  ||| |||||||||
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                              CTCC  GGG CTGTCGAAT
                                CG  A
GAM2603  SDHD    3'  TATTATATAACATTTTAT    60337
                              TATTATATAATATTTTAT
                              ||||||||||||||||||
                              ATAATATATTGTAAAATA

GAM2604  ADAM11   3'  CTCCTGTAAATGTCAAAAC   60340        AGA_
                              TTCCTGTAAA   AAAAC
                              ||||||||||   |||||
                              GAGGACATTT   TTTTG
                                   ACAG
GAM2604  ADAM11   3'  CTCCTGTAAATGTCAAAAC   60340        AGA_
                              TTCCTGTAAA   AAAAC
                              ||||||||||   |||||
                              GAGGACATTT   TTTTG
                                   ACAG
GAM2604  AKAP2    3'  TCCCCCAAAAAAAGAAAAAC  60341     GT__
                              TTCCT   AAAAGAAAAAC
                              |||||   ||||||||||
                              AGGGG   TTTTCTTTTTG
                                 GTTT
GAM2604  GAB2     3'  CTCCTGCCAAGAAAAAC    60342       AA
                              TTCCTGT  AAGAAAAAC
                              |||||||  |||||||||
                              GAGGACG  TTCTTTTTG
                                   G_
GAM2604  GAB2     3'  CTCCTGCCAAGAAAAAC    60342       AA
                              TTCCTGT  AAGAAAAAC
                              |||||||  |||||||||
                              GAGGACG  TTCTTTTTG
                                   G_
GAM2604  KRT1     3'  TCTCCACAAAAGAAAAAC   60343    _ TG
                              TC C  TAAAAGAAAAAC
                              || |  ||||||||||||
                              AG G  GTTTTCTTTTTG
                                A GT
GAM2604  OTOF     3'  CTCCAAGAAAAGAAAAAC   60344     TGT
                              TTCC   AAAAGAAAAAC
                              ||||   ||||||||||
                              GAGG   TTTTCTTTTTG
                                TTC
GAM2604  TNFSF4   3'  TCCCTGTATACAAGAAAA   60345       A__
                              TTCCTGTA  AAGAAAA
                              ||||||||  |||||||
                              AGGGACAT  TTCTTTT
                                   ATG
GAM2604  CPEB1    5'  TTCCTGCTTAAAAAAAC    60346       AAA
                              TTCCTGT   AGAAAAAC
                              |||||||   ||||||||
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                                AAGGACG  TTTTTTTG
                                   AA_
GAM2604  EBF2     3'  TTCCTACAAAGAAAAAC     60347      GTA
                                TTCCT  AAAGAAAAAC
                                |||||  ||||||||||
                                AAGGA  TTTCTTTTTG
                                   TG_
GAM2604  ITGB8    3'  TCCTGTAAAAAAGAAAAC    60348          _
                                TCCTGTAAAAGA AAAAC
                                |||||||||||| |||||
                                AGGACATTTTTT TTTTG
                                       C
GAM2604  KIAA0339 3'  TTCTCCGCAAAGAAAAAC    60349    _      A
                                TTC CTGTAAA GAAAAAC
                                ||| ||||||| |||||||
                                AAG GGCGTTT CTTTTTG
                                  A     _
GAM2604  KIAA0373 5'  TTCCCATGTAAGAAAAAC    60350       AA
                                TTCCTGT  AAGAAAAAC
                                |||||||  |||||||||
                                AAGGGTA  TTCTTTTTG
                                   CA
GAM2604  KIAA0416 3'  TTCCTGTATTAGGAAAAC    60351        AA  A
                                TTCCTGTA  AG AAAAC
                                ||||||||  || |||||
                                AAGGACAT  TC TTTTG
                                     AA  C
GAM2604  KIAA0626 3'  CTCCTGCCTTAGAAAAAC    60352       AAA
                                TTCCTGT   AGAAAAAC
                                |||||||   ||||||||
                                GAGGACG   TCTTTTTG
                                   GAA
GAM2604  MMRN     3'  TTCCTGTAGAAAAAC      60353       AAA
                                TTCCTGT   AGAAAAAC
                                |||||||   ||||||||
                                AAGGACA   TCTTTTTG
                                   ___
GAM2604  PRO2893  5'  CTCCTGTATCTAAAGAAA    60354        ___
                                TTCCTGTA   AAAGAAA
                                ||||||||   |||||||
                                GAGGACAT   TTTCTTT
                                     AGA
GAM2604  PTP4A1   3'  TTCCTTTAAAAAAAAAAC    60355      G
                                TTCCT TAAAAGAAAAAC
                                ||||| ||||||||||||
                                AAGGA ATTTTTTTTTTG
                                   A
GAM2604  SIMRP7   3'  CTCCTATGCCAGAAAAAC    60356       AAA
                                TTCCTGT   AGAAAAAC
                                |||||||   ||||||||
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                                GAGGATA   TCTTTTTG
                                    CGG
GAM2604  SNIP1    3'  TCGCCCCAAAAGAAAAAC    60357    _ G
                                TC CT TAAAAGAAAAAC
                                || || ||||||||||||
                                AG GG GTTTTCTTTTTG
                                 C  G
GAM2604  LOC146856 3'  TTCCCATACAGGAAAAAC    60358        AAA
                                TTCCTGTA   GAAAAAC
                                ||||||||   |||||||
                                AAGGGTAT   CTTTTTG
                                    GTC
GAM2604  LOC149103 3'  TTCCTAAAAAAGAAAAAC    60359       T
                                TTCCTG AAAAGAAAAAC
                                |||||| ||||||||||
                                AAGGAT TTTTCTTTTTG
                                   T
GAM2604  LOC151414 3'  CTCCTGCAAAAAGGGAGAAAAA 60360          _____
                                TTCCTGTAAA    AGAAAAA
                                ||||||||||    |||||||
                                GAGGACGTTT    TCTTTTT
                                     TTCCC
GAM2604  LOC153469 3'  TCCCCGTAAAGGGAAAAAC   60361          A_
                                TTCCTGTAAA  GAAAAAC
                                ||||||||||  |||||||
                                AGGGGCATTT  CTTTTTG
                                     CC
GAM2604  LOC163882 3'  TTCCTGAAAGAAAAAC     60362       TA
                                TTCCTG  AAAGAAAAAC
                                ||||||  ||||||||||
                                AAGGAC  TTTCTTTTTG
                                   __
GAM2604  LOC219376 5'  TTCCTGTGGCAGAAAAAC    60363        AAA
                                TTCCTGT   AGAAAAAC
                                |||||||   ||||||||
                                AAGGACA   TCTTTTTG
                                    CCG
GAM2605  BAZ2A    3'  CTTTTCTACAGCTGCAC     60366       GATT
                                TTTTTT    TAGCTGCAC
                                ||||||    |||||||||
                                GAAAAG    GTCGACGTG
                                   AT__
GAM2605  CARD15   3'  TTTTTTAAAGCTGCA      60367        TTT
                                TTTTTTGA   AGCTGCA
                                ||||||||   |||||||
                                AAAAAATT   TCGACGT
                                    ___
GAM2605  CUGBP1   5'  TTCTTTGAGCAGCGGCTGCACC 60368         TTTA__
                                TTTTTTGA     GCTGCACC
                                ||||||||     ||||||||
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                                AAGAAACT     CGACGTGG
                                     CGTCGC
GAM2605  AKAP7    3'  TCTTTTGATTTAGCAACA    60369           T
                                TTTTTTGATTTAGC GCA
                                |||||||||||||| |||
                                AGAAAACTAAATCG TGT
                                       T
GAM2605  AKAP7    3'  TCTTTTGATTTAGCAACA    60369           T
                                TTTTTTGATTTAGC GCA
                                |||||||||||||| |||
                                AGAAAACTAAATCG TGT
                                       T
GAM2605  AKAP7    3'  TCTTTTGATTTAGCAACA    60369           T
                                TTTTTTGATTTAGC GCA
                                |||||||||||||| |||
                                AGAAAACTAAATCG TGT
                                       T
GAM2605  FLJ22635 3'  CTTTTTGGCAAAGCTGCACC  60370       ATTT
                                TTTTTTG   AGCTGCACC
                                |||||||   |||||||||
                                GAAAAAC   TCGACGTGG
                                     CGTT
GAM2605  KIAA1580 5'  TTTTTGATTTCAGCCACCCG  60371        _   TG
                                TTTTTGATT TAGC  CACCCG
                                ||||||||| ||||  ||||||
                                AAAAACTAA GTCG  GTGGGC
                                      A   __
GAM2605  STATI2   3'  TCTTTTACATAGCTGCATTCG 60372       ATT      CC
                                TTTTTTG   TAGCTGCA  CG
                                |||||||   ||||||||  ||
                                AGAAAAT   ATCGACGT  GC
                                     GT_      AA
GAM2605  STATI2   3'  TCTTTTACATAGCTGCATTCG 60372       ATT      CC
                                TTTTTTG   TAGCTGCA  CG
                                |||||||   ||||||||  ||
                                AGAAAAT   ATCGACGT  GC
                                     GT_      AA
GAM2606  ARHE     3'  TTTAGACTTCACCTTTTT    60375        TG  GA
                                TTTAGACTT  TC  TTTT
                                |||||||||  ||  ||||
                                AAATCTGAA  GG  AAAA
                                      GT  A_
GAM2606  BHC80    3'  GACTTGTCTTCTCTACC     60376      T   GA
                                GACTT GTC  TTTTCTACC
                                ||||| |||  |||||||||
                                CTGAA CAG  AAGAGATGG
                                     _  __
GAM2606  HSA250303 3'  TTTAGATTTATTTTCTAC    60377       C    CGAT
                                TTTAGA TTTGT    TTTCTAC
                                |||||| |||||    |||||||
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                                AAATCT AAATA    AAAGATG
                                  _    _____
GAM2606 KIAA0232 5' TAGATGTGATTTTCTAC     60378      CTT   C
                                TAGA   TGT GATTTTCTAC
                                ||||   ||| ||||||||||
                                ATCT   ACA CTAAAAGATG
                                  ___   _
GAM2606 TIEG2    3' TTCAGATTATCAAATTTTCTAC 60379       CT      _
             C                   TTTAGA  TTGTCGA TTTTCTACC
                                ||||||  ||||||| |||||||||
                                AAGTCT  AATAGTT AAAAGATGG
                                   __      T
GAM2606 LOC120856 3' TTTAGTATTCTCATTTTCTAC  60380       ACT  G  G
                                TTTAG   TT TC ATTTTCTAC
                                |||||   || || |||||||||
                                AAATC   AA AG TAAAAGATG
                                   AT_  G  _
GAM2606 LOC164971 5' TAGGCTTTGATGTTTTCTAC   60381     A     TCGA
                                TAG CTTTG    TTTTCTAC
                                ||| |||||    ||||||||
                                ATC GAAAC    AAAAGATG
                                  C    TAC_
GAM2607 BACH2    3' AGAGGAATGTTGGAACCTG    60384         CATC    G
                                AGAGGAAT    GGAA CTG
                                ||||||||    |||| |||
                                TCTCCTTA    CCTT GAC
                                     CAA_    G
GAM2607 KCNE1L   3' AAGGCAACTGGAAGCTGGACT  60385      AATC  C       A
                                GAGG    AT GGAAGCTG ACT
                                ||||    || |||||||| |||
                                TTCC    TG CCTTCGAC TGA
                                  GT__  A       C
GAM2607 PRKY     3' AGAGGGAGTGGGGCTGAACT   60386       AATCATC  AA
                                AGAGG      GG  GCTGAACT
                                |||||      ||  ||||||||
                                TCTCC      CC  CGACTTGA
                                   CTCA___  C_
GAM2607 PTTG1IP  3' AGAGCGGCTGGAAGCTGGACT  60387      GAATCATC       A
                                AGAG       GGAAGCTG ACT
                                ||||       |||||||| |||
                                TCTC       CCTTCGAC TGA
                                  GCCGA___       C
GAM2607 RAD23A   3' GAGGACAGGAAGCTGGACT    60388       ATCATC       A
                                GAGGA     GGAAGCTG ACT
                                |||||     |||||||| |||
                                CTCCT     CCTTCGAC TGA
                                   GT____       C
GAM2607 SLC9A3R1 3' GAGGAACCAGCTGAA       60389          TCGGAA
                                GAGGAATCA     GCTGAA
                                |||||||||     ||||||
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                              CTCCTTGGT     CGACTT
                                        _______
GAM2607 TRPM6    3' AGAGGCAATCATTGGCAAACT 60390      _     C _
                              AGAGG AATCAT GG AAGCT
                              ||||| |||||| || |||||
                              TCTCC TTAGTA CC TTTGA
                                 G     A G
GAM2607 BS69     3' AGAGTAATCATCGGGGTGA   60391     G       AAGC
                              AGAG AATCATCGG    TGA
                              |||| |||||||||    |||
                              TCTC TTAGTAGCC    ACT
                                A       CC__
GAM2607 CECR6    3' AGAGGGTGACTGGGGCTGAACT 60392      AATC  C  AA
                              AGAGG    AT GG  GCTGAACT
                              |||||    || ||  ||||||||
                              TCTCC    TG CC  CGACTTGA
                                 CAC_  A  C_
GAM2607 CLLD8    5' AGAGGAACTGTCGGGGGCC   60393       CA    AA
                              AGAGGAAT  TCGG  GCT
                              ||||||||  ||||  |||
                              TCTCCTTG  AGCC  CGG
                                   AC    CC
GAM2607 EPS8R3   3' AGAGGAATTCTCGGGGCT    60394       CA    AA
                              AGAGGAAT  TCGG  GCT
                              ||||||||  ||||  |||
                              TCTCCTTA  AGCC  CGA
                                   AG    C_
GAM2607 EPS8R3   3' AGAGGAATTCTCGGGGCT    60394       CA    AA
                              AGAGGAAT  TCGG  GCT
                              ||||||||  ||||  |||
                              TCTCCTTA  AGCC  CGA
                                   AG    C_
GAM2607 FLJ14950 3' AAGGAATGGAAAGAAGCTG   60395       CATC
                              GAGGAAT    GGAAGCTG
                              |||||||    ||||||||
                              TTCCTTA    TCTTCGAC
                                   CCTT
GAM2607 FLJ20203 3' AGAGAAAGGAGCTGAA      60396       TCATC   A
                              AGAGGAA     GGA GCTGAA
                              |||||||     ||| ||||||
                              TCTCTTT     CCT CGACTT
                                        _____  _
GAM2607 MGC13159 5' GAGGAATCGCCGCCGGAGCT  60397        A___     A
                              GAGGAATC    TCGGA GCT
                              ||||||||    ||||| |||
                              CTCCTTAG    GGCCT CGA
                                   CGGC    _
GAM2607 POFUT1   3' AGAAGACGGAGGCTGGAC    60398       ATCAT    A    A
                              AGAGGA     CGGA GCTG AC
                              ||||||     |||| |||| ||
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                                TCTTCT    GCCT CGAC TG
                                  _____   C    C
GAM2607  SS-56    3'  AGAGGAATCCTTGGATACTG  60399        ATC   A
                                AGAGGAATC   GGA GCTG
                                |||||||||   ||| ||||
                                TCTCCTTAG   CCT TGAC
                                     GAA   A
GAM2607  UBF-fl   3'  AGAAGAATCAGTTGAA     60400         TCGGAA C
                                AGAGGAATCA     G TGAA
                                ||||||||||     | ||||
                                TCTTCTTAGT     C ACTT
                                      ______ A
GAM2607  LOC152426 5'  GAGGAATCATCGGAAGTCC   60401             _
                                GAGGAATCATCGGAAG CT
                                |||||||||||||||| ||
                                CTCCTTAGTAGCCTTC GG
                                          A
GAM2607  LOC158863 3'  GAGGAATCAATGAAGGTGAACT 60402        TCG   C
                                GAGGAATCA   GAAG TGAACT
                                |||||||||   |||| ||||||
                                CTCCTTAGT   CTTC ACTTGA
                                     TA_   C
GAM2607  LOC169831 5'  AGGGAAGATGAAGAAGCTGGAC 60403    A   TCATC      A
           T                    AG GGAA    GGAAGCTG ACT
                                || ||||    |||||||| |||
                                TC CCTT    TCTTCGAC TGA
                                 _   CTACT      C
GAM2607  LOC220980 5'  AGAGGAATCTTGGAGGAGCT   60404        ATC   __
                                AGAGGAATC   GGA  AGCT
                                |||||||||   |||  ||||
                                TCTCCTTAG   CCT  TCGA
                                     AA_   CC
GAM2607  LOC64102  5'  AGAGGAGAAGCTGAA      60405      ATCATCG
                                AGAGGA      GAAGCTGAA
                                ||||||      |||||||||
                                TCTCCT      CTTCGACTT
                                  ________
GAM2608  AK1      3'  GAGACGGAGTCTTGCTCTGT   60408    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_       AAC  G_
GAM2608  DFFA     3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_       AGC  G_
GAM2608  DMC1     3'  GAGACGGAGTCTCACTCTGT   60410    AA      CA   AG
                                GA  ACGGAGTC  ACT  TGT
                                ||  ||||||||  |||  |||
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                                CT TGCCTCAG TGA ACA
                                 C_     AG  G_
GAM2608 GRAF    3' GAGACGGAGTCTGGCTCTGT 60411   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     ACC G_
GAM2608 IL1R1   3' GAGACGGAGTCTTGCTCTGT 60408   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AAC G_
GAM2608 ITGAL   3' GAGACGGAGTCTCGCTGTGT 60412   AA     CAA A
                                GA ACGGAGTC  CT GTGT
                                || ||||||||  || ||||
                                CT TGCCTCAG  GA CACA
                                 C_     AGC _
GAM2608 LDLR    3' GAGACGGAGTCTCGCTCTGT 60409   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 OGG1    5' GAGACGGAGTCTCACTCTGT 60410   AA     CA  AG
                                GA ACGGAGTC ACT TGT
                                || ||||||||  ||| |||
                                CT TGCCTCAG TGA ACA
                                 C_     AG  G_
GAM2608 OGG1    5' GAGACGGAGTCTCACTCTGT 60410   AA     CA  AG
                                GA ACGGAGTC ACT TGT
                                || ||||||||  ||| |||
                                CT TGCCTCAG TGA ACA
                                 C_     AG  G_
GAM2608 OGG1    5' GAGACGGAGTCTCACTCTGT 60410   AA     CA  AG
                                GA ACGGAGTC ACT TGT
                                || ||||||||  ||| |||
                                CT TGCCTCAG TGA ACA
                                 C_     AG  G_
GAM2608 PSMB2   3' GAGACGGAGTCTCACTCTGT 60410   AA     CA  AG
                                GA ACGGAGTC ACT TGT
                                || ||||||||  ||| |||
                                CT TGCCTCAG TGA ACA
                                 C_     AG  G_
GAM2608 RAB7L1  3' GAGACGGAGTCCTTCTCTGT 60413   AA      AA AG
                                GA ACGGAGTCC CT TGT
                                || |||||||||  || |||
                                CT TGCCTCAGG GA ACA
                                 C_      AA G_
GAM2608 SLC26A4 3' GAGACGGAGTCTTGCTCTGT 60408   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
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                                CT TGCCTCAG  GA ACA
                                 C_     AAC G_
GAM2608 SLC2A3   3' GAGACGGAGTCTCGCCCTGT 60414   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GG ACA
                                 C_     AGC G_
GAM2608 TEM7     3' GAGACGGAGTCTCGCTCTGT 60409   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 VHL      3' GAGACGGAGTCTCACTCTGT 60410   AA     CA  AG
                                GA ACGGAGTC ACT TGT
                                || ||||||||  ||| |||
                                CT TGCCTCAG TGA ACA
                                 C_     AG  G_
GAM2608 WRB      3' TCGAGGACGGTGTTCACTAGT 60415    AA   A CCA
                                TCGA ACGG GT  ACTAGT
                                ||||  |||| ||  ||||||
                                AGCT TGCC CA  TGATCA
                                  CC   A AG_
GAM2608 ZNF91    3' GAGACGGAGTCTCGCTCTGT 60409   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 APXL2    3' GAGACGGAGTCTTGCTCTGT 60408   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AAC G_
GAM2608 C20orf183 3' GAGACGGAGTCTCGCTCTGT 60409   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 C6orf5   3' GAGACGGAGTCTCGCTCTGT 60409   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 CAMKK2   5' TCTGAAACGGAGTCTCGCTCTG 60416   GA      CAA AG
             T                   TC AAACGGAGTC  CT TGT
                                 || ||||||||||  || |||
                                 AG TTTGCCTCAG  GA ACA
                                  AC       AGC G_
GAM2608 CDT1     3' GAGACGGAGTCTCGCTCTGT 60409   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
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                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  DDX34     3'  GAGACGGAGTCTTGCTCTGT   60408    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AAC  G_
GAM2608  DKFZP434B168 3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  DKFZp434E169 3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  DKFZp566H0824 5'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  DKFZp761J139 5'  GAGACGGAGTCTCACTCTGT   60410    AA      CA   AG
                                GA  ACGGAGTC  ACT  TGT
                                ||  ||||||||  |||  |||
                                CT  TGCCTCAG  TGA  ACA
                                 C_      AG   G_
GAM2608  DRF1      3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  FBXO27    3'  GAGACGGAGTCTCGCTGTGT   60412    AA      CAA  A
                                GA  ACGGAGTC   CT GTGT
                                ||  ||||||||   || ||||
                                CT  TGCCTCAG   GA CACA
                                 C_      AGC  _
GAM2608  FLJ10462  5'  CGAGGATGGGGTCCAACTAGT  60417     AAAC  A
                                CGA    GG GTCCAACTAGT
                                |||    || ||||||||||||
                                GCT    CC CAGGTTGATCA
                                  CCTA  C
GAM2608  FLJ13456  3'  GAGACGGAGTCTTACTCTGT   60418    AA      CA   AG
                                GA  ACGGAGTC  ACT  TGT
                                ||  ||||||||  |||  |||
                                CT  TGCCTCAG  TGA  ACA
                                 C_      AA   G_
GAM2608  FLJ14346  3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
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                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 FLJ20802 3' GAGACGGAGTCTCGCTCTGT  60409   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 FUSIP1   3' GAGACGGAGTCTCACTCTGT  60410   AA     CA  AG
                                GA ACGGAGTC ACT TGT
                                || ||||||||  ||| |||
                                CT TGCCTCAG TGA ACA
                                 C_     AG  G_
GAM2608 HES2     3' GAGACGGAGTCTCGCTCTGT  60409   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 HSPF2    5' TCAAAGTGGAGTCCAAAAACTT 60419     AAC      CTAG_
              GT                 TCGAA  GGAGTCCAA   TGT
                                |||||  |||||||||   |||
                                AGTTT  CCTCAGGTT   ACA
                                  CA_      TTTGA
GAM2608 KIAA0226 3' GAGACGGAGTCTCACTCTGT  60410   AA     CA  AG
                                GA ACGGAGTC ACT TGT
                                || ||||||||  ||| |||
                                CT TGCCTCAG TGA ACA
                                 C_     AG  G_
GAM2608 KIAA0441 3' GAGACGGAGTCTCGCTCTGT  60409   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 KIAA0562 3' TCGAGACGGAGTCTCGCTCTGT 60420    AA     CAA AG
                                TCGA ACGGAGTC  CT TGT
                                ||||  ||||||||  || |||
                                AGCT  TGCCTCAG  GA ACA
                                  C_     AGC G_
GAM2608 KIAA0872 3' GAGACGGAGTCTCACTCTGT  60410   AA     CA  AG
                                GA ACGGAGTC ACT TGT
                                || ||||||||  ||| |||
                                CT TGCCTCAG TGA ACA
                                 C_     AG  G_
GAM2608 KIAA1164 3' GAGACGGAGTCTCCCTCTGT  60421   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGG G_
GAM2608 KIAA1228 3' GAGACGGAGTCTCACTCTGT  60410   AA     CA  AG
                                GA ACGGAGTC ACT TGT
                                || ||||||||  ||| |||
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                                CT  TGCCTCAG  TGA  ACA
                                 C_      AG   G_
GAM2608 KIAA1462 3' TCAGAACGGAGTTCATATACAT 60422     AA      C  ACTA_
             GT                  TCG  AACGGAGT CA    GTGT
                                ||| |||||||| ||    ||||
                                AGT  TTGCCTCA GT    TACA
                                 C_      A  ATATG
GAM2608 KIAA1586 5' GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608 KIAA1674 3' GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608 KIAA1969 3' GAGACGGAGTCTCACTCTGT   60410    AA      CA   AG
                                GA  ACGGAGTC  ACT  TGT
                                ||  ||||||||  |||  |||
                                CT  TGCCTCAG  TGA  ACA
                                 C_      AG   G_
GAM2608 MCAM     3' TCGAGACGGAGTCTCGCTGTGT 60423     AA      CAA  A
                                TCGA  ACGGAGTC   CT GTGT
                                ||||  ||||||||   || ||||
                                AGCT  TGCCTCAG   GA CACA
                                  C_      AGC  _
GAM2608 MGC23244 3' GAGACGGAGTCTCACTCTGT   60410    AA      CA   AG
                                GA  ACGGAGTC  ACT  TGT
                                ||  ||||||||  |||  |||
                                CT  TGCCTCAG  TGA  ACA
                                 C_      AG   G_
GAM2608 MGC3207  3' GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608 MGC4663  3' GAGACGGAGTCTGGCTCTGT   60411    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      ACC  G_
GAM2608 MRPL48   5' GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608 PDCD7    3' GAGACGGAGTCTTGCTCTGT   60408    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
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                                CT TGCCTCAG  GA ACA
                                 C_     AAC G_
GAM2608 PRO0255  3' GAGACGGAGTCTCGCTCTGT 60409   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 PRO0478  3' GAGACGGAGTCTCGCTCTGT 60409   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 PRO2015  3' GAGACGGAGTCTCACTGTGT 60424   AA     CA  A
                                GA ACGGAGTC ACT GTGT
                                || ||||||||  ||| ||||
                                CT TGCCTCAG TGA CACA
                                 C_     AG  _
GAM2608 SCAND2   3' GAGACGGAGTCTCACTCTGT 60410   AA     CA  AG
                                GA ACGGAGTC ACT  TGT
                                || ||||||||  |||  |||
                                CT TGCCTCAG TGA  ACA
                                 C_     AG  G_
GAM2608 SCYA5    3' GAGACGGAGTCTCGCTCTGT 60409   AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 SPRY4    3' GAGACGGAGTCTCACTCTGT 60410   AA     CA  AG
                                GA ACGGAGTC ACT  TGT
                                || ||||||||  |||  |||
                                CT TGCCTCAG TGA  ACA
                                 C_     AG  G_
GAM2608 ZFP106   3' GAGACGGAGTCTCACTCTGT 60410   AA     CA  AG
                                GA ACGGAGTC ACT  TGT
                                || ||||||||  |||  |||
                                CT TGCCTCAG TGA  ACA
                                 C_     AG  G_
GAM2608 LOC122704 3' GAGACGGAGTCTCGCCCTGT 60414  AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GG ACA
                                 C_     AGC G_
GAM2608 LOC145299 3' GAGACGGAGTCTCGCTCTGT 60409  AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
                                CT TGCCTCAG  GA ACA
                                 C_     AGC G_
GAM2608 LOC145438 3' GAGACGGAGTCTCGCTCTGT 60409  AA     CAA AG
                                GA ACGGAGTC  CT TGT
                                || ||||||||  || |||
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                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  LOC145757 3'  TCGAGACGGAGTCTCGCTCTGT 60420     AA      CAA  AG
                                TCGA  ACGGAGTC   CT  TGT
                                ||||  ||||||||   ||  |||
                                AGCT  TGCCTCAG   GA  ACA
                                  C_      AGC  G_
GAM2608  LOC146756 3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  LOC146958 3'  GAGACGGAGTCTCGCTGTGT   60412    AA      CAA  A
                                GA  ACGGAGTC   CT GTGT
                                ||  ||||||||   || ||||
                                CT  TGCCTCAG   GA CACA
                                 C_      AGC  _
GAM2608  LOC149113 5'  AAAACGGAGTTTGGCTCTTGT  60425         CCAA  AG
                                AAAACGGAGT   CT  TGT
                                ||||||||||   ||  |||
                                TTTTGCCTCA   GA  ACA
                                      AACC  GA
GAM2608  LOC149672 5'  GAGACGGAGTCTCACTCTGT   60410    AA      CA   AG
                                GA  ACGGAGTC  ACT  TGT
                                ||  ||||||||  |||  |||
                                CT  TGCCTCAG  TGA  ACA
                                 C_      AG   G_
GAM2608  LOC150358 3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  LOC151248 3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  LOC153711 3'  GAAAACAGGAGTCTGTG     60426       _     CAACTA
                                GAAAAC GGAGTC     GTG
                                ||||||  ||||||     |||
                                CTTTTG CCTCAG     CAC
                                   T     A_____
GAM2608  LOC154403 5'  AAAACGGAGTTTGGCTCTTGT  60425         CCAA  AG
                                AAAACGGAGT   CT  TGT
                                ||||||||||   ||  |||
                                TTTTGCCTCA   GA  ACA
                                      AACC  GA
GAM2608  LOC158819 3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
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                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  LOC199858 3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  LOC201931 3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  LOC202868 3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  LOC203378 3'  GAGACGGAGTCTCGCTGTGT   60412    AA      CAA  A
                                GA  ACGGAGTC   CT GTGT
                                ||  ||||||||   || ||||
                                CT  TGCCTCAG   GA CACA
                                 C_      AGC  _
GAM2608  LOC221042 3'  GAGACGGAGTCTTGCTCTGT   60408    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AAC  G_
GAM2608  LOC221271 3'  GAGACGGAGTCTAGATGT    60427    AA      CAAC  _
                                GA  ACGGAGTC    TAG TGT
                                ||  ||||||||    ||| |||
                                CT  TGCCTCAG    ATC ACA
                                 C_      ____   T
GAM2608  LOC51320  5'  TCAAAATGGAGTCCACATAGT  60428       AC      AC
                                TCGAAA  GGAGTCCA  TAGT
                                ||||||  ||||||||  ||||
                                AGTTTT  CCTCAGGT  ATCA
                                   A_      GT
GAM2608  LOC90321  3'  GAGACGGAGTCTCGCTCTGT   60409    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2608  LOC90393  5'  GAGACGGAGTCTCACTCTGT   60410    AA      CA   AG
                                GA  ACGGAGTC  ACT  TGT
                                ||  ||||||||  |||  |||
                                CT  TGCCTCAG  TGA  ACA
                                 C_      AG   G_
GAM2608  LOC92421  3'  GAGACGGAGTCTCCCTCTGT   60421    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
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                                CT  TGCCTCAG   GA  ACA
                                 C_       AGG  G_
GAM2609  FADD     3'  TGTAGAATTGCAGGACCCA   60431         AC  T    A
                                TGTAGAATT  CG GGATC CA
                                |||||||||  || ||||| ||
                                ACATCTTAA  GT CCTGG GT
                                     C_ _    _
GAM2609  PPAT     3'  TGTAGAATTACTAAACTGTCAC 60432          CGTGGA_
              A                  TGTAGAATTAC      TCACA
                                 ||||||||||       |||||
                                 ACATCTTAATG      AGTGT
                                       ATTTGAC
GAM2609  DKFZp566D234 5'  TGTGGAAATATAAATCACAA   60433     A   TTACC
                                TGT GAA    GTGGATCACAA
                                ||| |||    ||||||||||
                                ACA CTT    TATTTAGTGTT
                                  C   TA___
GAM2609  KIAA1040  5'  GAATTAAAATTATCACAAC   60434       CC  GG
                                GAATTA  GT  ATCACAAC
                                ||||||  ||  ||||||||
                                CTTAAT  TA  TAGTGTTG
                                    TT  A_
GAM2609  RAP2B    3'  TAGAATTGGTACATCACAAC   60435        ACC   G
                                TAGAATT   GTG ATCACAAC
                                |||||||   ||| ||||||||
                                ATCTTAA   CAT TAGTGTTG
                                    C__   G
GAM2609  STK38L   3'  TGTAGAATTTCCTCTTGTAG   60436         A  _____
                                TGTAGAATT CC    GTGG
                                |||||||||  ||    ||||
                                ACATCTTAA GG    CATC
                                      A  AGAA
GAM2609  TRIP-Br2  3'  TGTAAGTTACTGTAAATCA    60437      AA    C
                                TGTAG  TTAC GTGGATCA
                                |||||  |||| ||||||||
                                ACATT  AATG CATTTAGT
                                   C_    A
GAM2609  LOC148013 3'  TGAGAATTACCAAAATGTGAC  60438     T       ___   _
                                TG AGAATTACC   GTG GAT
                                ||  |||||||||   ||| |||
                                AC TCTTAATGG   TAC CTG
                                 _       TTT   A
GAM2609  LOC153469 3'  TGAGGAATTAAGAGATCACA   60439     TA     CCGT
                                TG  GAATTA    GGATCACA
                                ||  ||||||    ||||||||
                                AC  CTTAAT    TCTAGTGT
                                 TC     TC__
GAM2609  LOC158654 5'  TGTAGCATCTGCTTGGATCAC  60440       A   ACCG
                                TGTAG ATT    TGGATCAC
                                ||||| |||    ||||||||
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                                ACATC TAG    ACCTAGTG
                                   G   ACGA
GAM2610  MATN3    3'  CAAGCATTAATACAGA      60443          TTCGT
                                CAAGTATTAA    TACAGA
                                ||||||||||    ||||||
                                GTTCGTAATT    ATGTCT
                                      _____
GAM2610  CHFR     3'  CAAGTATTATTCCAGA      60444          A   GTTA
                                CAAGTATTA TTC    CAGA
                                ||||||||| |||    ||||
                                GTTCATAAT AAG    GTCT
                                      _  ____
GAM2610  UCH37    3'  AAGTATTTAAATTACAGAT    60445        AATTC
                                AAGTATT    GTTACAGAT
                                |||||||    |||||||||
                                TTCATAA    TAATGTCTA
                                     ATT__
GAM2610  LOC132916 3'  CAGGTATTACATTTACAGAT   60446    A     ATTCG
                                CA GTATTA    TTACAGAT
                                || ||||||    ||||||||
                                GT CATAAT    AATGTCTA
                                 C     GTA__
GAM2610  LOC146733 5'  TCCAAGGATGTTACAG      60447       T  TAATTC
                                TCCAAG AT     GTTACAG
                                |||||| ||     |||||||
                                AGGTTC TA     CAATGTC
                                   C _______
GAM2610  LOC201562 3'  CAAGTACTTAGTGTTACAG    60448         AATTC
                                CAAGTATT    GTTACAG
                                ||||||||    |||||||
                                GTTCATGA    CAATGTC
                                     ATCA_
GAM2610  LOC253971 3'  TCCAAGTTTTAATTCAGCAAAG 60449        A      _  TA__
            CAGAT                   TCCAAGT TTAATTC GT    CAGAT
                                ||||||| ||||||| ||    |||||
                                AGGTTCA AATTAAG CG    GTCTA
                                     A      T  TTTC
GAM2610  LOC90231  3'  CAAGTATTTGCCATACAG    60450         AAT    T
                                CAAGTATT   TCGT ACAG
                                ||||||||   |||| ||||
                                GTTCATAA   GGTA TGTC
                                     AC_    _
GAM2611  ACCN2    3'  TACAGCACCAGGGCCGCA    60453           TTCT  A
                                TACAGCACCAGG    CC CA
                                ||||||||||||    || ||
                                ATGTCGTGGTCC    GG GT
                                       C___  C
GAM2611  ACVR1B   3'  GCACTGAGTTCTCCACAC    60454      CA
                                GCAC  GGTTCTCCACAC
                                ||||  ||||||||||||
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                                CGTG  TCAAGAGGTGTG
                                  AC
GAM2611  ADAMTS4   5'  GCACCAAGTCCTCCACAC    60455
                                GCACCAGGTTCTCCACAC
                                ||||||||||||||||||
                                CGTGGTTCAGGAGGTGTG

GAM2611  AK3       3'  CACAGCACCAATACTACAC   60456          GTT  C
                                TACAGCACCAG   CT CAC
                                ||||||||||   || |||
                                GTGTCGTGGTT   GA GTG
                                      AT_  T
GAM2611  C18orf1   3'  TACAGCACAGAGCCACCGCAC  60457        C   TT T  A
                                TACAGCAC AGG  C CC CAC
                                |||||||| |||  | || |||
                                ATGTCGTG TCT  G GG GTG
                                     _  CG T  C
GAM2611  CLK2      3'  GCAGCCTATACTCCACAC    60458     _ AG  T
                                GCA CC  GT CTCCACAC
                                ||| ||  || ||||||||
                                CGT GG  TA GAGGTGTG
                                  C  A_  T
GAM2611  CNTNAP2   3'  TACACACCAGGTGCCA      60459      G       TCT
                                TACA CACCAGGT   CCA
                                |||| ||||||||   |||
                                ATGT GTGGTCCA   GGT
                                   _       C__
GAM2611  DDX11     3'  CAGCACTCTGGACTCCACAC   60460       CA_  TT
                                CAGCAC   GG  CTCCACAC
                                ||||||   ||  ||||||||
                                GTCGTG   CC  GAGGTGTG
                                    AGA  T_
GAM2611  DUOX2     3'  TAAGCATCACAGCTTCTGCAC  60461    C   C__   G   C
                                A AGCA   CAG TTCT CAC
                                | ||||   ||| |||| |||
                                A TCGT   GTC AAGA GTG
                                 T    AGT   G    C
GAM2611  EPHA3     3'  TACACACCAAAACTGCAC     60462      G      TT  C
                                TACA CACCAGG  CT CAC
                                |||| |||||||  || |||
                                ATGT GTGGTTT  GA GTG
                                   _      T_  C
GAM2611  FLOT2     3'  TACAGCACTCGATTCTGTAC   60463        CA     CC
                                TACAGCAC  GGTTCT  AC
                                ||||||||  ||||||  ||
                                ATGTCGTG  CTAAGA  TG
                                     AG     CA
GAM2611  GRB10     5'  GCACCGCTTGGACTCCACAC   60464       A___  TT
                                GCACC   GG  CTCCACAC
                                |||||   ||  ||||||||
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                                CGTGG   CC  GAGGTGTG
                                   CGAA  T_
GAM2611  GSK3B    5'  CAGCATTAAGTTCTCCCAC   60465      CC       A
                                CAGCA  AGGTTCTCC CAC
                                |||||  ||||||||| |||
                                GTCGT  TTCAAGAGG GTG
                                   AA       _
GAM2611  HIF1A    5'  TAAGCGCTGGCTCCCTCCACAC 60466   C   ACCA  __
                                A AGC   GGT  TCTCCACAC
                                | |||   |||  |||||||||
                                A TCG   CCG  GGAGGTGTG
                                 T  CGA_  AG
GAM2611  IFNA4    3'  ACACCAAGCTTCTTCACAC   60467         _  C
                                GCACCAGGTT CT CACAC
                                |||||||||| || |||||
                                TGTGGTTCGA GA GTGTG
                                      A  A
GAM2611  MAP1B    5'  CACAGCACTGAAATTCTCTACA 60468        C_      C
                                TACAGCAC  AGGTTCTC ACA
                                ||||||||  |||||||| |||
                                GTGTCGTG  TTTAAGAG TGT
                                     AC       A
GAM2611  NOC4     3'  CAGCACCAGCACTCCAC     60469         GTT
                                CAGCACCAG   CTCCAC
                                |||||||||   ||||||
                                GTCGTGGTC   GAGGTG
                                      GT_
GAM2611  PCDHA11  5'  TACAGTACCAGATTCTTCA   60470      C       C
                                TACAG ACCAGGTTCT CA
                                ||||| |||||||||| ||
                                ATGTC TGGTCTAAGA GT
                                   A        A
GAM2611  PCDHA11  5'  TACAGTACCAGATTCTTCA   60470      C       C
                                TACAG ACCAGGTTCT CA
                                ||||| |||||||||| ||
                                ATGTC TGGTCTAAGA GT
                                   A        A
GAM2611  PHLDA3   3'  CAGCGCCTCCTCCACAC     60471     A  AGG
                                CAGC CC   TTCTCCACAC
                                |||| ||   ||||||||||
                                GTCG GG   AGGAGGTGTG
                                  C  ___
GAM2611  PIK3C2B  3'  TACAGCCCACCCCACA      60472       A   GGTT
                                TACAGC CCA    CTCCACA
                                |||||| |||    |||||||
                                ATGTCG GGT    GGGGTGT
                                   _  ____
GAM2611  PIK3R3   3'  ACGGCACCAAAGTCACA     60473    A      _  TCTC
                                AC GCACCAG GT    CACA
                                || ||||||| ||    ||||
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                                TG CGTGGTT CA   GTGT
                                 C      T ____
GAM2611  RXRA     3'  TACAGCACATACATGTTTACAC 60474        ___ G   CTC
                                TACAGCAC   CA GTT   CAC
                                ||||||||   || |||   |||
                                ATGTCGTG   GT CAA   GTG
                                     TAT  A   AT_
GAM2611  SLC12A2  5'  CAGCACGCCCTCCACAC     60475       CAG
                                CAGCAC   GTTCTCCACAC
                                ||||||   ||||||||||
                                GTCGTG   CGGGAGGTGTG
                                   ___
GAM2611  SLC17A1  3'  GCAAGTGCTCTGTTTCACAC   60476     CC  _    C___
                                GCA  AG GTTCT    CACAC
                                |||  || |||||    |||||
                                CGT  TC CGAGA    GTGTG
                                  __  A    CAAA
GAM2611  TARDBP   3'  CACCACCAAGTCTCTGCAC    60477    G       _  C
                                CA CACCAGGT TCT CAC
                                || |||||||| ||| |||
                                GT GTGGTTCA AGA GTG
                                 G       G   C
GAM2611  TRIM9    3'  TACACACCAGGGGCACA     60478      G      TTCTC
                                TACA CACCAGG     CACA
                                |||| |||||||     ||||
                                ATGT GTGGTCC     GTGT
                                  _      CC___
GAM2611  APMCF1   3'  CAGCACCTAAATCTCCACAC   60479        AG T
                                CAGCACC  G TCTCCACAC
                                |||||||  | |||||||||
                                GTCGTGG  T AGAGGTGTG
                                     AT T
GAM2611  ATP9A    3'  TACAGAGCCAGGTTCAGCA    60480      CA       TC
                                TACAG  CCAGGTTC  CA
                                |||||  ||||||||  ||
                                ATGTC  GGTCCAAG  GT
                                   TC       TC
GAM2611  C20orf110 3'  CAGCATCACTGCTCTGCAC    60481      C  G_    C
                                CAGCA CA  GTTCT CAC
                                |||||  ||  ||||| |||
                                GTCGT GT  CGAGA GTG
                                   A  GA    C
GAM2611  C20orf97  3'  CACAGCACACTCCACA      60482        CAGGTT
                                TACAGCAC     CTCCACA
                                ||||||||     |||||||
                                GTGTCGTG     GAGGTGT
                                     T_____
GAM2611  CART     3'  TACAGGCATTATTCTTCACAC  60483      _  CCAG    C
                                TACAG CA    GTTCT CACAC
                                |||||  ||    ||||| |||||
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                                ATGTC GT    TAAGA GTGTG
                                  C  AA__     A
GAM2611  CD200    5'  CAGTACTTTTCCTCCACAC    60484     C  CAGG
                                CAG AC    TTCTCCACAC
                                ||| ||    ||||||||||
                                GTC TG    AGGAGGTGTG
                                  A  AAA_
GAM2611  CDC2L5   3'  CAAGACCCTTCTCCACA     60485     C   AGG
                                CAG ACC   TTCTCCACA
                                ||| |||   |||||||||
                                GTT TGG   AAGAGGTGT
                                  C   G__
GAM2611  CDC2L5   3'  CAAGACCCTTCTCCACA     60485     C   AGG
                                CAG ACC   TTCTCCACA
                                ||| |||   |||||||||
                                GTT TGG   AAGAGGTGT
                                  C   G__
GAM2611  CXorf12  3'  CACAGCACTCCACCCCTCCACA 60486         CAGG_
              C                  TACAGCAC    TTCTCCACAC
                                |||||||     ||||||||||
                                GTGTCGTG    GGGAGGTGTG
                                    AGGTG
GAM2611  DKFZP434N014 3'  TACAGCACCAGTTCCTGAC    60487          G    CC
                                TACAGCACCAG TTCT  AC
                                |||||||||| ||||  ||
                                ATGTCGTGGTC AAGG  TG
                                      _   AC
GAM2611  ERp44    3'  TACAGCACCAAAAAACTTGCAC 60488           TT_  C_
                                TACAGCACCAGG   CT  CAC
                                ||||||||||||   ||  |||
                                ATGTCGTGGTTT   GA  GTG
                                      TTT  AC
GAM2611  FHOD2    5'  CACAGTACTCTCCACA      60489      C  CAGGT
                                TACAG AC    TCTCCACA
                                ||||| ||    ||||||||
                                GTGTC TG    AGAGGTGT
                                  A  _____
GAM2611  FLJ00001 3'  CAGCATCAAGCCTCCACA    60490      C    T
                                CAGCA CAGGT CTCCACA
                                ||||| ||||| |||||||
                                GTCGT GTTCG GAGGTGT
                                  A    _
GAM2611  FLJ10094 3'  GCGGGACCAACCCCACAC    60491    ___    GTT
                                GC   ACCAG   CTCCACAC
                                ||   |||||   ||||||||
                                CG   TGGTT   GGGGTGTG
                                 CCC    ___
GAM2611  FLJ13197 3'  TGAGCACATTTCCTCCAC    60492   C    C GG
                                A AGCAC A  TTCTCCAC
                                | ||||| |  ||||||||
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                                A TCGTG T  AGGAGGTG
                                 C    _ AA
GAM2611  FLJ13902  3'  CACAGCGCTTTCCACA     60493      ACCAG  C
                                TACAGC    GTT TCCACA
                                ||||||    ||| ||||||
                                GTGTCG    CGA AGGTGT
                                   _____  A
GAM2611  FLJ20643  3'  AGCAGCCTCTTCTCCACA    60494    _ AGG
                                AGCA CC   TTCTCCACA
                                |||| ||   |||||||||
                                TCGT GG   AAGAGGTGT
                                  C  AG_
GAM2611  FLJ21736  3'  ACACAAAGGTTCTCCACA    60495    C_
                                GCAC  AGGTTCTCCACA
                                ||||  ||||||||||||
                                TGTG  TCCAAGAGGTGT
                                  TT
GAM2611  KIAA0326  3'  GCAACATGGTTCTCCGCAC   60496    C _      A
                                GCA CA GGTTCTCC CAC
                                ||| || |||||||| |||
                                CGT GT CCAAGAGG GTG
                                  T A       C
GAM2611  KIAA1157  3'  ACGGCACTGTCTCCACAC    60497   A   CAG  T
                                AC GCAC   GT CTCCACAC
                                || ||||   || ||||||||
                                TG CGTG   CA GAGGTGTG
                                 C   A__  _
GAM2611  KIAA1229  5'  CACAGCGACTTCTCCACA    60498      _ CAGG
                                TACAGC AC    TTCTCCACA
                                |||||| ||    |||||||||
                                GTGTCG TG    AAGAGGTGT
                                   C  ____
GAM2611  KIAA1297  5'  CAGCACCATCCCACA       60499       GGT  T
                                CAGCACCA   TC CCACA
                                ||||||||   || |||||
                                GTCGTGGT   AG GGTGT
                                     ___  _
GAM2611  KIAA1505  5'  TACAGATGCTCCTCCACA    60500     CACCAG   _
                                TACAG     GTTC TCCACA
                                |||||     |||| ||||||
                                ATGTC     CGAG AGGTGT
                                   TA____    G
GAM2611  KIAA1814  3'  ACAGCACCAAGCCAC       60501         TTCT
                                ACAGCACCAGG    CCAC
                                ||||||||||    ||||
                                TGTCGTGGTTC    GGTG
                                     _____
GAM2611  KIAA1870  5'  CAGCACCAGTGCCAGCTC    60502        _  __
                                CAGCACCAG GTT  CTC
                                ||||||||| |||  |||
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                                GTCGTGGTC CGG  GAG
                                     A   TC
GAM2611  KIAA1881  3'  CACAGCACTGCCTGCAC     60503        CAG  T  C
                                TACAGCAC   GT CT CAC
                                ||||||||   || || |||
                                GTGTCGTG   CG GA GTG
                                    A__  _  C
GAM2611  KIAA1911  3'  TACAGTACCAAGCTACAC    60504      C       CTC
                                TACAG ACCAGGTT   CAC
                                ||||| ||||||||   |||
                                ATGTC TGGTTCGA   GTG
                                   A       T__
GAM2611  KIAA1954  3'  TACTGGCAGTTTTCTCCACAC  60505     A_   CCAGG
                                TAC  GCA    TTCTCCACAC
                                |||  |||    ||||||||||
                                ATG  CGT    AAGAGGTGTG
                                  AC   CAA__
GAM2611  KIAA1981  3'  ACCCCTGGGTTCTCCACAC    60506    A  A_
                                GC CC  GGTTCTCCACAC
                                || ||  ||||||||||||
                                TG GG  CCAAGAGGTGTG
                                 G  AC
GAM2611  L3MBTL2   3'  CACAGCACCGGGCAGAATTTAC 60507         A   TCTCC__
           AC                     TACAGCACC GGT      ACAC
                                |||||||| |||      ||||
                                GTGTCGTGG CCG      TGTG
                                     C   TCTTAAA
GAM2611  LASP1     3'  CAGCCCCAACTCCACAC     60508      A    GTT
                                CAGC CCAG   CTCCACAC
                                |||| ||||   ||||||||
                                GTCG GGTT   GAGGTGTG
                                  G   ___
GAM2611  MFN2      3'  CAGCACCGCCCCTCTCCAC   60509        AGG_
                                CAGCACC    TTCTCCAC
                                |||||||    ||||||||
                                GTCGTGG    GAGAGGTG
                                    CGGG
GAM2611  MGC11279  3'  CAGTGTCAGGCCCCAGCCACAC 60510     CAC       __
                                CAG   CAGGTTCT  CCACAC
                                |||   ||||||||  ||||||
                                GTC   GTCCGGGG  GGTGTG
                                  ACA       TC
GAM2611  MGC14436  5'  GCAGCCTGGACTCCTCCAC   60511     _  A  __
                                GCA CC GG  TTCTCCAC
                                ||| || ||  ||||||||
                                CGT GG CC  AGGAGGTG
                                  C  A  TG
GAM2611  MGC22014  3'  TACAGCACCAGGCTCCGCAC   60512              C
                                TACAGCACCAGGTTCT CAC
                                |||||||||||||||| |||
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                                ATGTCGTGGTCCGAGG GTG
                                        C
GAM2611 NMT2     3' CAGCAATTTCTCTCCACAC  60513      CCAGG
                                CAGCA    TTCTCCACAC
                                |||||    ||||||||||
                                GTCGT    GAGAGGTGTG
                                   TAAA_
GAM2611 OCLM     3' TACAGTCTATGCTCTTCACAC 60514      CACCAG    C
                                TACAG     GTTCT CACAC
                                |||||     ||||| |||||
                                ATGTC     CGAGA GTGTG
                                   AGATA_    A
GAM2611 OSBPL1A  3' TACAGTAGGTCTCCACAC   60515      CACC   T
                                TACAG   AGGT CTCCACAC
                                |||||   |||| ||||||||
                                ATGTC   TCCA GAGGTGTG
                                   A___   _
GAM2611 OSBPL1A  3' TACAGTAGGTCTCCACAC   60515      CACC   T
                                TACAG   AGGT CTCCACAC
                                |||||   |||| ||||||||
                                ATGTC   TCCA GAGGTGTG
                                   A___   _
GAM2611 OSBPL1A  3' TACAGTAGGTCTCCACAC   60515      CACC   T
                                TACAG   AGGT CTCCACAC
                                |||||   |||| ||||||||
                                ATGTC   TCCA GAGGTGTG
                                   A___   _
GAM2611 PPP1R16B 3' CAGAGCCAGGCCCCGCAC   60516    CA       C
                                CAG  CCAGGTTCT CAC
                                |||  ||||||||| |||
                                GTC  GGTCCGGGG GTG
                                  TC       C
GAM2611 RES4-22  3' CAGCACCAGCTCCGCAC    60517       GTT    A
                                CAGCACCAG   CTCC CAC
                                |||||||||   |||| |||
                                GTCGTGGTC   GAGG GTG
                                     ___    C
GAM2611 SLC1A7   5' CACAGCACCATTCCAC     60518       GGTTC
                                TACAGCACCA    TCCAC
                                ||||||||||    |||||
                                GTGTCGTGGT    AGGTG
                                     A____
GAM2611 TIAF1    3' CAGCACCAGGCACTGCAC   60519         T  C
                                CAGCACCAGGT CT CAC
                                |||||||||||| || |||
                                GTCGTGGTCCG GA GTG
                                      T  C
GAM2611 WBSCR17  3' CAGTACCAGGTCCACA     60520    C     TTC
                                CAG ACCAGG   TCCACA
                                ||| ||||||   ||||||
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                                GTC TGGTCC   AGGTGT
                                  A     ___
GAM2611  ZFP100    3'  TACAGACTGCCCCCACA     60521      C  CAG    T
                                TACAG AC   GTTC CCACA
                                ||||| ||   |||| |||||
                                ATGTC TG   CGGG GGTGT
                                  _  A__   _
GAM2611  ZID       3'  TACAACACTAATAGCTACAC   60522        C  GTT  C
                                TACAGCAC AG   CT CAC
                                |||||||| ||   || |||
                                ATGTTGTG TT   GA GTG
                                     A  ATC  T
GAM2611  LOC123876 5'  CAGCACCACTGCCACAC     60523        GGTT  _
                                CAGCACCA    CT CCACAC
                                ||||||||    || ||||||
                                GTCGTGGT    GA GGTGTG
                                     _____  C
GAM2611  LOC126123 5'  CAGCACCAAGGGGTCGCAC    60524         TTC  _
                                CAGCACCAGG   TC CAC
                                ||||||||||   || |||
                                GTCGTGGTTC   AG GTG
                                      CCC  C
GAM2611  LOC129563 3'  TACACACCAGATGGCACTCCAC 60525      G       T___
              AC                  TACA CACCAGGT    CTCCACAC
                                ||||| ||||||||    ||||||||
                                ATGT GTGGTCTA    GAGGTGTG
                                  _       CCGT
GAM2611  LOC146346 5'  CACAGCACCAGATGCTGCA    60526           T  C
                                TACAGCACCAGGT CT CA
                                |||||||||||||| || ||
                                GTGTCGTGGTCTA GA GT
                                       C  C
GAM2611  LOC151171 5'  ACAGCACCGGGGAGGGCCACAC 60527         A  TTCT_
                                ACAGCACC GG     CCACAC
                                |||||||| ||     ||||||
                                TGTCGTGG CC     GGTGTG
                                     C  CTCCC
GAM2611  LOC152286 3'  GCATGGCCTCTCCACAC     60528     CCA  _
                                GCA   GGT TCTCCACAC
                                |||   ||| |||||||||
                                CGT   CCG AGAGGTGTG
                                  A__   G
GAM2611  LOC152426 5'  CAGCACCAGTCTCCCTGCAC   60529         G    CA
                                CAGCACCAG TTCTC  CAC
                                ||||||||| |||||  |||
                                GTCGTGGTC GAGGG  GTG
                                      A    AC
GAM2611  LOC153454 5'  ACAGCACCATTTGCTTCACAC  60530         GGTT  C
                                ACAGCACCA    CT CACAC
                                |||||||||    || |||||
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                                TGTCGTGGT   GA GTGTG
                                     AAAC  A
GAM2611  LOC154739 5'  AGACATGTGCCTCCACAC    60531    C  CAG  _
                                AG AC   GT TCTCCACAC
                                || ||   || |||||||||
                                TC TG   CA GGAGGTGTG
                                 _  TA_  C
GAM2611  LOC169966 5'  CATCACCTGATCTCCACAC    60532    G    A   T
                                CA CACC GGT CTCCACAC
                                || |||| ||| |||||||||
                                GT GTGG CTA GAGGTGTG
                                 A   A  _
GAM2611  LOC200531 5'  CACAGTGTGAGTCTCCACA    60533      CACCA   T
                                TACAG    GGT CTCCACA
                                |||||    ||| |||||||
                                GTGTC    TCA GAGGTGT
                                   ACAC_  _
GAM2611  LOC203276 3'  AGACGTGTGCCTCCACAC    60534    C  CAG  _
                                AG AC   GT TCTCCACAC
                                || ||   || |||||||||
                                TC TG   CA GGAGGTGTG
                                 _  CA_  C
GAM2611  LOC203305 3'  AGACGTGTGCCTCCACAC    60534    C  CAG  _
                                AG AC   GT TCTCCACAC
                                || ||   || |||||||||
                                TC TG   CA GGAGGTGTG
                                 _  CA_  C
GAM2611  LOC221760 5'  CAGCACGCTGCCCCACAC    60535      CAG   _
                                CAGCAC   GTT CTCCACAC
                                ||||||   ||| ||||||||
                                GTCGTG   CGA GGGGTGTG
                                   ___   C
GAM2611  LOC221931 3'  ACATTAGGTGTCTCCACAC    60536     CC   _
                                GCA  AGGT TCTCCACAC
                                |||  |||| |||||||||
                                TGT  TCCA AGAGGTGTG
                                  AA    C
GAM2611  LOC254243 3'  AGACGTGTGCCTCCACAC    60534    C  CAG  _
                                AG AC   GT TCTCCACAC
                                || ||   || |||||||||
                                TC TG   CA GGAGGTGTG
                                 _  CA_  C
GAM2611  LOC256295 3'  ACAGCACCAGAGGCTGCA    60537          TT  C
                                ACAGCACCAGG  CT CA
                                ||||||||||  || ||
                                TGTCGTGGTCT  GA GT
                                       CC  C
GAM2611  LOC257180 3'  TACAGTGCACGCCTCCACAC   60538      CAC  G  T
                                TACAG   CA GT CTCCACAC
                                |||||   || || ||||||||
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                                ATGTC   GT CG GAGGTGTG
                                  AC_  G  _
GAM2611  LOC257460 3'  GCATTCAGATTCTCTACA    60539     C_       C
                                GCA  CAGGTTCTC ACA
                                |||  ||||||||| |||
                                CGT  GTCTAAGAG TGT
                                  AA        A
GAM2611  LOC51652  3'  TACAACACCAGAGTGAATCTTC 60540          _ ___   C
           A                     TACAGCACCAG GT   TCT CA
                                ||||||||||| ||   ||| ||
                                ATGTTGTGGTC CA   AGA GT
                                       T  CTT   A
GAM2611  LOC90038  3'  AGACGTGTGCCTCCACAC    60534    C  CAG  _
                                AG AC   GT TCTCCACAC
                                || ||   || |||||||||
                                TC TG   CA GGAGGTGTG
                                 _  CA_  C
GAM2611  LOC90355  5'  TAAGCACCAGTCTGCAC     60541   C       GT   C
                                A AGCACCAG  TCT CAC
                                | ||||||||  ||| |||
                                A TCGTGGTC  AGA GTG
                                 T       __   C
GAM2611  LOC92017  5'  GCACCAGGTTTCAGCCAC    60542          _ T_
                                GCACCAGGTT C  CCAC
                                |||||||||| |  ||||
                                CGTGGTCCAA G  GGTG
                                       A TC
GAM2612  ADAM19    3'  GGAGGAGGGTGGGAGGAGC    60545        C  G
                                GGAGGAG GG GGGAGGAGC
                                ||||||| || |||||||||
                                CCTCCTC CC CCCTCCTCG
                                    _  A
GAM2612  ADH5      5'  GGGGCGGGGCGTGGGGGGGGC  60546      A  A  _    A  A
                                GGGG GG GCG GGGGG GG GC
                                |||| || ||| ||||| || ||
                                CCCC CC CGC CCCCC CC CG
                                  G  C   A    _  _
GAM2612  AIPL1     3'  GGGGAGACAGGGAGGG      60547       GA       A
                                GGGGAG  GCGGGGGG GG
                                ||||||  |||||||| ||
                                CCCCTC  TGTCCCTC CC
                                    __       _
GAM2612  ANK1      3'  GGGAGGAGCGTCACCAGGGAG  60548          G____
                                GGGAGGAGCG     GGGGAG
                                ||||||||||     ||||||
                                CCCTCCTCGC     TCCCTC
                                       AGTGG
GAM2612  ANK1      3'  GGGGAGGATGGAGGGGGGC    60549        GC     A  A
                                GGGGAGGA  GGGGGG GG GC
                                ||||||||  |||||| || ||
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                                CCCCTCCT  CCTCCC CC CG
                                   A_     _ _
GAM2612  ANK1     3'  GGGGAGGATGGAGGGGGGC   60549        GC     A  A
                                GGGGAGGA  GGGGGG GG GC
                                ||||||||  |||||| || ||
                                CCCCTCCT  CCTCCC CC CG
                                   A_     _ _
GAM2612  ANK1     3'  GGGAGGAGCGTCACCAGGGAG  60548         G____
                                GGGAGGAGCG    GGGGAG
                                ||||||||||    ||||||
                                CCCTCCTCGC    TCCCTC
                                      AGTGG
GAM2612  ANKH     5'  GGCGAGGGGCGACGGGGG    60550    G    A    G   A
                                GG GAGG GCGG GGG GG
                                || |||| |||| ||| ||
                                CC CTCC CGCT CCC CC
                                 G   C    G  _
GAM2612  ANKH     5'  GGCGAGGGGCGACGGGGG    60550    G    A    G   A
                                GG GAGG GCGG GGG GG
                                || |||| |||| ||| ||
                                CC CTCC CGCT CCC CC
                                 G   C    G  _
GAM2612  ANP32A   3'  GGGGGGAGAGGGGATATGG    60551     A    C    GA_
                                GGGG GGAG GGGGG   GG
                                |||| |||| |||||   ||
                                CCCC CCTC CCCCT   CC
                                  _   T    ATA
GAM2612  AR       5'  GGGGAGGGGGGGAAGG      60553        AGC
                                GGGGAGG   GGGGGGAGG
                                |||||||   |||||||||
                                CCCCTCC   CCCCCTTCC

                                   ___
GAM2612  AR       5'  GGGGGGCGGGTGGGGAGAAG   60552     A  A    __
                                GGG GG GCGGG  GGGAGGAG
                                ||| || |||||  ||||||||
                                CCC CC CGCCC  CCCTCTTC
                                  _ _    AC
GAM2612  ARHGDIA  3'  GGGGAGGGGCTGGGGGGG    41614        A  G    A
                                GGGGAGG GC GGGGG GG
                                ||||||| || ||||| ||
                                CCCCTCC CG CCCCC CC
                                   C  A    _
GAM2612  ARHGDIA  3'  GGGGATGGGGCGGGGGAGG   60555      _  A      G
                                GGGGA GG GCGGGGG AGG
                                ||||| || ||||||| |||
                                CCCCT CC CGCCCCC TCC
                                  A  C      _
GAM2612  ARHGDIA  3'  GGGGAGGGCTGAGGAGG     60554        A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
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                                CCCCTCC CG  CTCCTCC
                                   _ A_
GAM2612 ARL2    3' GGGGTGGAGGAGGGGGAG    60556     A   C
                                GGGG GGAG GGGGGGAG
                                |||| |||| ||||||||
                                CCCC CCTC TCCCCCTC
                                  A   C
GAM2612 ARVCF   3' GGGGGGAGTGGGGTGGGGGGGC 60557     A   C   _ A A
                                GGGG GGAG GGGG GG GG GC
                                |||| |||| |||| || || ||
                                CCCC CCTC CCCC CC CC CG
                                  _   A   A C  C
GAM2612 ASGR1   5' GGAGGGGAGCGGGCAGGG    60558     A      G  A
                                GGGG GGAGCGGG GG GG
                                |||| |||||||| || ||
                                CCTC CCTCGCCC TC CC
                                  C       G  _
GAM2612 BAZ1B   3' GGGGGGGTGGGAGGAG      60560     AGGAGC  _
                                GGGG     GGG GGGAGGAG
                                ||||     ||| |||||||||
                                CCCC     CCC CCCTCCTC
                                  _______  A
GAM2612 BAZ1B   5' GGGGTGGGGTGGGGGAAGG   60559     A  AGC
                                GGGG GG   GGGGGGGAGG
                                |||| ||   |||||||||
                                CCCC CC   CCCCCTTCC
                                  A  CCA
GAM2612 BIN1    5' AGGGAGGGAGAGGGGAGGGGC  60562       AGC       A
                                GGGGAGG   GGGGGGAGG GC
                                |||||||   ||||||||| ||
                                TCCCTCC   CTCCCCTCC CG
                                   CT_       C
GAM2612 BIN1    5' GGGGAGGGGCCGGGCCTCAGG  60561       A  G   GG__
                                GGGGAGG GC GGG    AGG
                                ||||||| || |||    |||
                                CCCCTCC CG CCC    TCC
                                   C  G   GGAG
GAM2612 BIN1    5' AGGGAGGGAGAGGGGAGGGGC  60562       AGC       A
                                GGGGAGG   GGGGGGAGG GC
                                |||||||   ||||||||| ||
                                TCCCTCC   CTCCCCTCC CG
                                   CT_       C
GAM2612 BIN1    5' GGGGAGGGGCCGGGCCTCAGG  60561       A  G   GG__
                                GGGGAGG GC GGG    AGG
                                ||||||| || |||    |||
                                CCCCTCC CG CCC    TCC
                                   C  G   GGAG
GAM2612 BMP1    3' AGGGAGGAGTGGGGGAG     60563         CG
                                GGGGAGGAG  GGGGGAG
                                |||||||||  |||||||
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                                TCCCTCCTC  CCCCCTC
                                    A_
GAM2612  C1QG     3'  GGGGAGGGGGTGCAGTGGGG   60564       A___   _
                                GGGGAGG   GCGG GGGG
                                |||||||   |||| ||||
                                CCCCTCC   CGTC CCCC
                                    CCCA   A
GAM2612  CA12     3'  GGGAGGAAAATGGAGGAG    60565       CG_
                                GGGAGGAG  GGGGGAG
                                ||||||||  |||||||
                                CCCTCCTT  CCTCCTC
                                    TTA
GAM2612  CACNA1B  3'  AGGGAGGGGCCACAGGAGC   60567       A  GGGGGG
                                GGGGAGG GC    AGGAGC
                                ||||||| ||    ||||||
                                TCCCTCC CG    TCCTCG
                                    C  GTG___
GAM2612  CACNA1B  3'  GGGGAGGAGGGGGAGGGAGGGG 60566        C  _    A
              C                  GGGGAGGAG GGG GGGAGG GC
                                |||||||||  ||| |||||| ||
                                CCCCTCCTC CCC CCCTCC CG
                                    C  T    C
GAM2612  CACNG7   3'  GAGGAGGAGGCAGGGGGAG   60568        _
                                GGGGAGGAG CGGGGGGAG
                                |||||||||  |||||||||
                                CTCCTCCTC GTCCCCCTC
                                    C
GAM2612  CACNG7   3'  GGGGAGGAGTCATTTGGGAG  60569        _  GG_
                                GGGGAGGAG CG   GGGAG
                                |||||||||  ||   |||||
                                CCCCTCCTC GT   CCCTC
                                    A  AAA
GAM2612  CALM3    3'  GGGGTGGGGTGGGGAGG     41619      A  AGC  _
                                GGGG GG   GG GGGGAGG
                                ||||  ||   ||  |||||||
                                CCCC CC   CC CCCCTCC
                                  A  ___  A
GAM2612  CALR     3'  GGGGAGAAAGGGAGGGG     60571        C     A
                                GGGGAGGAG GGGGGG GG
                                |||||||||  ||||||  ||
                                CCCCTCTTT CCCTCC CC
                                    _     _
GAM2612  CALR     3'  GGGGAGGGGGTGGGGGAGA   60570       AGCG
                                GGGGAGG   GGGGGAGG
                                |||||||   ||||||||
                                CCCCTCC   CCCCCTCT
                                    CCCA
GAM2612  CAPON    5'  GGGGAGGGGAGACTGGAGC   60572       AGC    GA
                                GGGGAGG   GGGGG  GGAGC
                                |||||||   |||||  |||||
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                                CCCCTCC  CCTCT  CCTCG
                                   ___    GA
GAM2612  CAPON    5'  GGGGAGCGGTGGGGCTTGC   60573   A    _   AGGA
                                GG GGAGCGG GGGG   GC
                                || ||||||| ||||   ||
                                CC CCTCGCC CCCC   CG
                                 _     A   GAA_
GAM2612  CAPON    5'  GGGGAGGAGGTGGCGGCGGGAG 60574       CG  G  A_
             C                   GGGGAGGAG  GG GG  GGAGC
                                 |||||||||  || ||  |||||
                                 CCCCTCCTC  CC CC  CCTCG
                                      CA  G  GC
GAM2612  CARPX    5'  GGGGGGAAGGGGGGAG     60575     A   C
                                GGGG GGAG GGGGGGAG
                                |||| |||| ||||||||
                                CCCC CCTT CCCCCCTC

                                  _   _
GAM2612  CD74     3'  GGGTGGGACATGGGGGAGGGGC 60576    GA  GCG      A
                                GGG  GGA   GGGGGAGG GC
                                |||  |||   |||||||| ||
                                CCC  CCT   CCCCCTCC CG
                                  AC   GTA       C
GAM2612  CDC42    3'  GGGAGGGGGAAGGGGGGGGC   60577      AGC_    A  A
                                GGGAGG    GGGGGG GG GC
                                ||||||    |||||| || ||
                                CCCTCC    TCCCCC CC CG
                                   CCCT     _  _
GAM2612  CHST6    3'  GGGGAGGGGGAGGGG      60578       AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   CCCTCC CC

                                   ___     _
GAM2612  CKM      3'  GGGGGCGGGGCGAGGAG     60579     AGGA     G
                                GGGG    GCGGGG GAGGAG
                                ||||    |||||| ||||||
                                CCCC    CGCCCC CTCCTC
                                  _____     G
GAM2612  CKM      3'  GGGCGAGGAGTGAGGGAG    60580     _     CG
                                GGG GAGGAG  GGGGGAG
                                ||| ||||||  |||||||
                                CCC CTCCTC  CTCCCTC
                                  G     A_
GAM2612  CLTB     3'  GGGGAGGAGTGGAATAGG    60581        C    GG
                                GGGGAGGAG GGGG  AGG
                                ||||||||| ||||  |||
                                CCCCTCCTC CCTT  TCC
                                     A   A_
GAM2612  CLTB     3'  GGGGAGGAGTGGAATAGG    60581        C    GG
                                GGGGAGGAG GGGG  AGG
                                ||||||||| ||||  |||
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                                CCCCTCCTC CCTT  TCC
                                     A   A_
GAM2612  CNN2     3'  GGGGAGAGAGCGTGCTGGGAG  60582       _    GG__
                                GGGGAG GAGCG   GGGAG
                                ||||||| |||||   |||||
                                CCCCTC CTCGC   CCCTC
                                   T    ACGA
GAM2612  COL1A1   3'  GGGCAGGAGCGGGCTGAGG   41625     G       GG
                                GGG AGGAGCGGG  GAGG
                                ||| |||||||||  ||||
                                CCC TCCTCGCCC  CTCC
                                  G       GA
GAM2612  COL1A1   3'  GGGGAGGCCAAGGGGGGG     60583       AG      A
                                GGGGAGG  CGGGGGG GG
                                |||||||  ||||||| ||
                                CCCCTCC  GTTCCCC CC
                                   G_      _
GAM2612  CRHR2    3'  GGTGGAGGAGGACAGGGGAGC  60584    _     C  G   A
                                GG GGAGGAG GG GGG GGAGC
                                || ||||||| || ||| |||||
                                CC CCTCCTC CT TCC CCTCG
                                 A      _ G  _
GAM2612  CSH2     3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                |||||||  ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  CSH2     3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                |||||||  ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  CSH2     3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                |||||||  ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  CSH2     3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                |||||||  ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  CSHL1    3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                |||||||  ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  CSHL1    3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                |||||||  ||  |||||||
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                                CCTCTCC TG  CCCCTCC
                                    G  A_
GAM2612  CSHL1    3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                    G  A_
GAM2612  CSHL1    3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                    G  A_
GAM2612  CSHL1    3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                    G  A_
GAM2612  CSK      5'  GGGGGGAGGGGAGGGG      60586     A   C     A
                                GGGG GGAG GGGGGG GG
                                |||| |||| |||||| ||
                                CCCC CCTC CCCTCC CC
                                  _   _     _
GAM2612  CSNK1G2  3'  GGGGCAGGAGTGGGGTAGGGC  60587      _    C   GG   A
                                GGGG AGGAG GGGG  AGG GC
                                |||| ||||| ||||  ||| ||
                                CCCC TCCTC CCCC  TCC CG
                                  G    A   A_  _
GAM2612  CYP21A2  3'  GGGGGGAGGGGAGGGG     60586     A   C     A
                                GGGG GGAG GGGGGG GG
                                |||| |||| |||||| ||
                                CCCC CCTC CCCTCC CC
                                  _   _     _
GAM2612  DACH     5'  GGGGTGGGGCGGGGAGGG    60588     A  A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCTC CC
                                  A  C       _
GAM2612  DBH      3'  GGAGGAGGGGGAGGAG      60589       GCG
                                GGAGGA   GGGGGAGGAG
                                ||||||   ||||||||||
                                CCTCCT   CCCCCTCCTC
                                   ___
GAM2612  DBN1     3'  GGGGAGGGGGTCCCAGGGAGC  60590       AGC   G___  A
                                GGGGAGG   GGG    GG GGAGC
                                |||||||   |||    || |||||
                                CCCCTCC   CCC    TC CCTCG
                                    ___   AGGG  _
GAM2612  DBN1     3'  GGGGAGGGGGTCCCAGGGAGC  60590       AGC   G___  A
                                GGGGAGG   GGG    GG GGAGC
                                |||||||   |||    || |||||
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                                CCCCTCC  CCC   TC CCTCG
                                   ___  AGGG  _
GAM2612 DES     3' GGGGAGGGCGTGGGGAGG   41628       A  G
                                GGGGAGG GCG GGGGAGG
                                ||||||| ||| |||||||
                                CCCCTCC CGC CCCCTCC
                                   _  A
GAM2612 DLG4    3' AGGGAGGCCGGGGGGAG    60591       AG
                                GGGGAGG  CGGGGGGAG
                                |||||||  |||||||||
                                TCCCTCC  GCCCCCCTC
                                   G_
GAM2612 DNASE1L1 3' GAGGAGGATGGAAGGGAGG  60592        GC
                                GGGGAGGA  GGGGGGAGG
                                ||||||||  |||||||||
                                CTCCTCCT  CTTCCCTCC
                                    AC
GAM2612 DNMT3L   5' GGGGAGGGGCGGGGGCGGGGC 60595       A     GA  A
                                GGGGAGG GCGGGGG  GG GC
                                ||||||| |||||||  || ||
                                CCCCTCC CGCCCCC  CC CG
                                   C     G_  C
GAM2612 DNMT3L   5' GGGGGCGGGGAGGGG     60594     AGGA      A  A
                                GGGG   GCGGGGGG GG G
                                ||||   |||||||| || |
                                CCCC   CGCCCCTC CC C
                                  ____      _ _
GAM2612 DNMT3L   5' GGGCGAGGAGCTGCGGGGGG  60593    _     ___
                                GGG GAGGAGC   GGGGGG
                                ||| |||||||   ||||||
                                CCC CTCCTCG   CCCCCC
                                  G      ACG
GAM2612 DVL3    3' GGGTGGGAGCGGAATGGAGC  60596    GA       GGA
                                GGG  GGAGCGGGG   GGAGC
                                |||  |||||||||   |||||
                                CCC  CCTCGCCTT   CCTCG
                                  AC       A__
GAM2612 EFNB1    3' AGGGGGGCGAGGGAGGGGC   60597     A  A     GA  A
                                GGGG GG GCGGGGG  GG GC
                                |||| || |||||||  || ||
                                TCCC CC CGCTCCC  CC CG
                                  _ _      TC  _
GAM2612 EHD2    3' GGGAAGGGGCTGCGGAGGG   60598       A___
                                GGGGAGG   GCGGGGGG
                                |||||||   ||||||||
                                CCCTTCC   CGCCTCCC
                                   CCGA
GAM2612 EPS15    5' GGGGAGGAGGCGGAGGGAG   60599        _
                                GGGGAGGAG CGGGGGGAG
                                ||||||||| |||||||||
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                                CCCCTCCTC GCCTCCCTC
                                     C
GAM2612  ESRRA    3'  GGGGAGGAGAGGGCGTGGG   60600        C  ___
                                GGGGAGGAG GGG  GGG
                                ||||||||| |||  |||
                                CCCCTCCTC CCC  CCC
                                     T  GCA
GAM2612  ESRRA    3'  GAGGAGGAGCGAAGGGGG    60601           A
                                GGGGAGGAGCGGGGGG GG
                                |||||||||||||||| ||
                                CTCCTCCTCGCTTCCC CC
                                                _
GAM2612  F2RL3    3'  GGGGAGGCGGGGCTGGAGGAGC 60602      GA    __
                                GGGGAG  GCGGGG  GGAGGAGC
                                ||||||  ||||||  ||||||||
                                CCCCTC  CGCCCC  CCTCCTCG
                                   __     GA
GAM2612  F2RL3    3'  GGGGAGGGGCGTGGCTGGGGGA 60603      A  _____
            G                    GGGGAGG GCG    GGGGGAG
                                ||||||| |||    |||||||
                                CCCCTCC CGC    CCCCCTC
                                    C  ACCGA
GAM2612  FBXL11   3'  GGGGCGGGGTGGGGGGAAGAG  60605     A  AGC
                                GGGG GG  GGGGGGAGGAG
                                |||| ||  ||||||||||
                                CCCC CC  CCCCCCTTCTC
                                  G  CCA
GAM2612  FBXL11   3'  GGGGAGGAGGGGCACAGGGC  60604       C  GGG  A
                                GGGGAGGAG GGG  AGG GC
                                ||||||||| |||  ||| ||
                                CCCCTCCTC CCC  TCC CG
                                     _  GTG  _
GAM2612  FKBP10   3'  GGGGAGGAAGGCAGAGGG    60606       __
                                GGGGAGGA  GCGGGGGG
                                ||||||||  ||||||||
                                CCCCTCCT  CGTCTCCC
                                     TC
GAM2612  FLT1     5'  GGGGAGGAGCCGAGAGGAG   60607        _
                                GGGGAGGAGC GGGGGGAG
                                |||||||||| ||||||||
                                CCCCTCCTCG CTCTCCTC
                                     G
GAM2612  FMNL     5'  GGGGAGGGGAGGCCGGG     60608      AGC   GA  A
                                GGGGAGG  GGGGG  GG G
                                |||||||  |||||  || |
                                CCCCTCC  CCTCC  CC C
                                   ___    GG  _
GAM2612  FOS      5'  GGGCGAGGGGCCGAGGGG    60609    _   A  _
                                GGG GAGG GC GGGGGG
                                ||| |||| || ||||||
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                                CCC CTCC CG CTCCCC
                                  G   C G
GAM2612  FOXD2    5'  GGGGAGGGGGCGGGGGACTGAG 60610       A_      AG
                                GGGGAGG  GCGGGGGG  GAG
                                |||||||  ||||||||  |||
                                CCCCTCC  CGCCCCCT  CTC
                                    CC       GA
GAM2612  FOXG1B   5'  GGGGGGGCGGCGGGCGG    41641     A  A   G   A
                                GGGG GG GCGG GGG GG
                                |||| || |||| ||| ||
                                CCCC CC CGCC CCC CC
                                  _ _   G   G
GAM2612  FXR2     5'  GAGGAGGAGCCGGAGGGGGAGC 60611         _     A
                                GGGGAGGAGC GGGGGG GGAGC
                                |||||||||| |||||| |||||
                                CTCCTCCTCG CCTCCC CCTCG
                                      G     _
GAM2612  FXYD1    3'  GGGAAGGGGCGGCGGAGGGGGC 60612       A   G  GA  A
                                GGGGAGG GCGG GG  GG GC
                                |||||||  |||| ||  || ||
                                CCCTTCC CGCC CC  CC CG
                                    C   G  TC  C
GAM2612  FXYD1    3'  GGGAAGGGGCGGCGGAGGGGGC 60612       A   G  GA  A
                                GGGGAGG GCGG GG  GG GC
                                |||||||  |||| ||  || ||
                                CCCTTCC CGCC CC  CC CG
                                    C   G  TC  C
GAM2612  FZD7     3'  GGGTGGGAAAGGTGGGGAGGGG 60613    GA   C  _     A
            C                    GGG  GGAG GG GGGGAGG GC
                                |||  |||| || ||||||| ||
                                CCC  CCTT CC CCCCTCC CG
                                  AC   T  A     C
GAM2612  GAS1     5'  GGGGAGCGGCGGACGCGGAGC  60614    A     G   A__
                                GG GGAGCGG GGG   GGAGC
                                || ||||||| |||   |||||
                                CC CCTCGCC CCT   CCTCG
                                 _     G   GCG
GAM2612  GATA2    5'  GGGGAGGGGAGGGACTCGG   60615       AGC     ___
                                GGGGAGG   GGGGGGA   GG
                                |||||||   |||||||   ||
                                CCCCTCC   CCTCCCT   CC
                                    ___      GAG
GAM2612  GDF2     5'  GGGAAGGAGCGGGCCGG     60617          GGGA
                                GGGGAGGAGCGGG   GG
                                ||||||||||||   ||
                                CCCTTCCTCGCCC   CC
                                      GG__
GAM2612  GDF2     5'  GGGGAGGAGCTGGGAAGGAGC  60616         GG
                                GGGGAGGAGC  GGGGAGGAGC
                                ||||||||||  ||||||||||
```

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                                CCCCTCCTCG  CCCTTCCTCG
                                    A_
GAM2612  GH1     3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  GH1     3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  GH1     3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  GH1     3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  GH1     3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  GH2     3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  GH2     3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  GH2     3'  GGAGAGGCACTGGGGAGG    60585       A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2612  GPR30   3'  GGGGAGGAGCTGGGTGACAGG  60618          _  _  G
                                GGGGAGGAGC GGG GG AGG
                                |||||||||| ||| || |||
                                CCCCTCCTCG CCC CT TCC
                                     A  A  G
GAM2612  GRB14   5'  GGGGAGAGGGGAGGAGC     60619       GAGCG
                                GGGGAG    GGGGGAGGAGC
                                ||||||    ||||||||||
```

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                                CCCCTC    TCCCCTCCTCG
                                  _____
GAM2612 GRM7    5' GGGGGAATCCGGGGAGGGGC  60620     A  G_     A A
                                GGGG GGA  CGGGGGG GG GC
                                |||| |||  ||||||| || ||
                                CCCC CTT  GCCCCTC CC CG
                                  _  AG     _ _
GAM2612 HOXB2   5' GGGGAGGGGGCTGCTGGGGGGG 60621       A_ ____     A
            G                    GGGGAGG  GC   GGGGGG GG
                                |||||||  ||   |||||| ||
                                CCCCTCC  CG   CCCCCC CC
                                   CC  ACGA    _
GAM2612 HOXC10  3' GAGGAGGGGCGGGGAGAGGAA 60622       A
                                GGGGAGG GCGGGGGGAGGAG
                                ||||||| |||||||||||||
                                CTCCTCC CGCCCCTCTCCTT
                                   C
GAM2612 HOXC13  3' GGGGAGGCAGTGGGGCAAAGGC 60623       _ C   G   A
                                GGGGAGG AG GGGG GAGG GC
                                ||||||| || |||| |||| ||
                                CCCCTCC TC CCCC TTTC CG
                                   G A   G   _
GAM2612 HOXD4   3' GGGGTGGAGTGGGGGAGAA   60624     A   CG
                                GGGG GGAG  GGGGGAGGA
                                |||| ||||  |||||||||
                                CCCC CCTC  CCCCCTCTT
                                  A   A_
GAM2612 HPSE    5' GGGGAGGAGCGCCCGGGGAGGA 60626         G__
            GC                   GGGGAGGAGCG   GGGGAGGAGC
                                ||||||||||  ||||||||||
                                CCCCTCCTCGC   CCCCTCCTCG
                                      GGG
GAM2612 HPSE    5' GGGAGGCCTGGGGAGGAGC   60625      AGCGG
                                GGGAGG    GGGGAGGAGC
                                ||||||    ||||||||||
                                CCCTCC    CCCCTCCTCG
                                   GGA__
GAM2612 HPSE    5' GGGGAGGAGCGCCCGGGGAG  60627         G__
                                GGGGAGGAGCG   GGGGAG
                                ||||||||||  ||||||
                                CCCCTCCTCGC   CCCCTC
                                      GGG
GAM2612 HR      5' GGGGAGGGCCGGGCCGGGGC  60628       A G  GGA A
                                GGGGAGG GC GGG   GG GC
                                ||||||| || |||  || ||
                                CCCCTCC CG CCC   CC CG
                                   _ G  GG_  C
GAM2612 HRMT1L2  3' GGAGAGGAAGGGGGAG     60629        GC
                                GGGGAGGA  GGGGGGAG
                                ||||||||  ||||||||
```

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                                CCTCTCCT  TCCCCCTC
                                   __
GAM2612  HRY     3'  GGAGGAGGGGTGGCCTGAGC   60630       C   G  AG_
                                GGAGGAG GGG GG   GAGC
                                ||||||| ||| ||   ||||
                                CCTCCTC CCC CC   CTCG
                                   _  A  GGA
GAM2612  IFI35   5'  GGGGAGGGGAGTAGGAG     60631       AGC   GG
                                GGGGAGG   GGGG  AGGAG
                                |||||||   ||||  |||||
                                CCCCTCC   CCTC  TCCTC
                                   ____   A_
GAM2612  IGF2    5'  GGGGGGGACGGGAGGGAGC   60632     A  AG      AG
                                GGGG GG  CGGGGGG  GAGC
                                |||| ||  |||||||  ||||
                                CCCC CC  GCCCTCC  CTCG
                                  _ CT      __
GAM2612  IGFBP2  3'  GGAGAGGGGCGGGGGGCAGGGG 60633        A      _  A
            C                    GGGGAGG GCGGGGGG AGG GC
                                ||||||| |||||||| ||| ||
                                CCTCTCC CGCCCCCC TCC CG
                                   C       G   C
GAM2612  IKBKG   5'  GGAGGAGGAGGGAGGAG     60634       GC
                                GGAGGA  GGGGGGAGGAG
                                ||||||  ||||||||||
                                CCTCCT  CCTCCCTCCTC
                                   __
GAM2612  ILF1    5'  GGGGAGGAGGCGTGGGGGGGGG 60635        _ _    A  A
            GC                    GGGGAGGAG CG GGGGG GG GC
                                ||||||||| || ||||| || ||
                                CCCCTCCTC GC CCCCC CC CG
                                     C  A    C  C
GAM2612  IMPDH1  3'  GGGGAGCGGCCTGAGGAGC   60636    A     GGG
                                GG GGAGCGG   GAGGAGC
                                || |||||||   |||||||
                                CC CCTCGCC   CTCCTCG
                                  _      GGA
GAM2612  INSR    3'  GGGGGCGGGTGGGGGGAAC   60637     AGGA   _  A
                                GGGG   GCGGG GGG GGAGC
                                ||||   ||||| ||| |||||
                                CCCC   CGCCC CCC CCTTG
                                   ____    A  C
GAM2612  IRS2    5'  GGGCGAGGGGCGGAGGGGG   60638    _   A      A
                                GGG GAGG GCGGGGGG GG
                                ||| |||| |||||||| ||
                                CCC CTCC CGCCTCCC CC
                                  G   C      _
GAM2612  JAG2    3'  GAGGAGGGGCGGCCGGGG    60639       A   __
                                GGGGAGG GCGG  GGGG
                                ||||||| ||||  ||||
```

```
                                CTCCTCC CGCC  CCCC
                                    C    GG
GAM2612  KCNC3    5'  GAGGAGGGGCGGGGCGGGG   60641       A     _ A
                                GGGGAGG GCGGGG GG GG
                                ||||||| |||||| || ||
                                CTCCTCC CGCCCC CC CC
                                    C     G  _
GAM2612  KCNC3    5'  GGGGCGGGGCGGGAGGGG    60642     A  A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCTCC CC
                                  G  C      _
GAM2612  KCNC3    5'  GGGAGGGGCGGGGACGCAGGGG 60640       A      G__   A
              C                  GGGAGG GCGGGGG   AGG GC
                                |||||| |||||||   ||| ||
                                CCCTCC CGCCCCT   TCC CG
                                    C      GCG   C
GAM2612  KCNK3    3'  GGGGATGAGGAAGGGGAG    41660      G   CG
                                GGGGA GAG  GGGGGAG
                                ||||| |||  |||||||
                                CCCCT CTC  TCCCCTC
                                  A   CT
GAM2612  KCNMB4   5'  GGGGAGTGGGCGGCGAGGGGGA 60643       GA_   _   A
              GC                   GGGGAG   GCGG GGGG GGAGC
                                |||||||   |||| |||| |||||
                                CCCCTC   CGCC CTCC CCTCG
                                    ACC    G    C
GAM2612  KCNN4    5'  GGGGAGGGGCAGGGGAGG    60644       A      G
                                GGGGAGG GCGGGGGG AGG
                                ||||||| ||||||| |||
                                CCCCTCC CGTCCCC TCC
                                    C      _
GAM2612  KCNQ2    5'  GGGGCGGAGCGCGGGGGG    60645     A     G    A
                                GGGG GGAGCG GGGG GG
                                |||| |||||| |||| ||
                                CCCC CCTCGC CCCC CC
                                  G     G   _
GAM2612  KIAA0442 5'  GGGGAGGAGGGACGGGGAGC   60646         C   G  A
                                GGGGAGGAG GGG GG GGAGC
                                ||||||||| ||| || |||||
                                CCCCTCCTC CCT CC CCTCG
                                      _   G  _
GAM2612  KIFC3    3'  GGAGAGGGGCGGGGAGGG    60647       A      A
                                GGGGAGG GCGGGGGGG GG
                                ||||||| |||||||| ||
                                CCTCTCC CGCCCCTC CC
                                    C      _
GAM2612  KRT8     3'  GGGGTAGGCTGGGAGGGG    60648      _  AGC     A
                                GGGG AGG   GGGGGG GG
                                |||| |||   |||||| ||
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                                CCCC TCC   CCCTCC CC
                                  A  GA_     _
GAM2612  LRP1     3'  GGGAAGGGCTGGCTGGGGAGGG 60649        A  _ __      A
                GC                  GGGGAGG GC GG  GGGGAGG GC
                                    ||||||| || ||  ||||||| ||
                                    CCCTTCC CG CC  CCCCTCC CG
                                       _ A  GA      C
GAM2612  LRP1     5'  GGGGAGGGGGGGGTGGGGGGC   60650        AGC  _  A  A
                                    GGGGAGG   GGG GGG GG GC
                                    |||||||   ||| ||| || ||
                                    CCCCTCC   CCC CCC CC CG
                                       CC_  A  _ _
GAM2612  LY9      3'  GGGTGAGAAGGAGGGGGAGGGG 60651     _     C       A
                C                    GGG GAGGAG GGGGGGAGG GC
                                    ||| |||||| ||||||||| ||
                                    CCC CTCTTC TCCCCCTCC CG
                                      A     C        C
GAM2612  MAF      5'  GGAGAGGGAGGGGGGAG     60652        AGC
                                    GGGGAGG   GGGGGGAG
                                    |||||||   ||||||||
                                    CCTCTCC   CCCCCCTC
                                       CT_
GAM2612  MAML1    3'  GGGAGGGAGGAGGAGGAGC   60653       AGC
                                    GGGAGG   GGGGGGAGGAGC
                                    ||||||   ||||||||||||
                                    CCCTCC   TCCTCCTCCTCG
                                       C__
GAM2612  MAP1A    3'  GGGAAGCGTGGGGAGGAGC   60654    A     G
                                    GG GGAGCG GGGGAGGAGC
                                    || |||||| ||||||||||
                                    CC CTTCGC CCCCTCCTCG
                                      _     A
GAM2612  MAT1A    3'  GGGGAGGGAGGGGGAG      60655        AGC
                                    GGGGAGG   GGGGGGAG
                                    |||||||   ||||||||
                                    CCCCTCC   TCCCCCTC
                                       C__
GAM2612  MBD3     3'  GGGGAGGAGCTGGCCTCGAGC  60656          GG  GGAG
                                    GGGGAGGAGC  GG   GAGC
                                    ||||||||||  ||   ||||
                                    CCCCTCCTCG  CC   CTCG
                                          A_  GGAG
GAM2612  MECP2    3'  GGGGGGAGCTGGGGGAG     60658     A    G
                                    GGGG GGAGC GGGGGAG
                                    |||| ||||| |||||||
                                    CCCC CCTCG CCCCCTC
                                      _    A
GAM2612  MECP2    3'  GGGAAGGGGACTGGGGGAG   60657        A_  G
                                    GGGGAGG  GC GGGGGAG
                                    |||||||  || |||||||
```

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                                CCCTTCC  TG CCCCCTC
                                    CC  A
GAM2612  MECP2    3'  GGGGAGGTGGGGGGAG      60659        AGC
                                GGGGAGG   GGGGGGAG
                                |||||||   ||||||||
                                CCCCTCC   CCCCCCTC
                                    A__
GAM2612  MFAP4    3'  GGGGAGCAAGGAGGAG      60660    A     GG
                                GG GGAGCG  GGGAGGAG
                                || ||||||  ||||||||
                                CC CCTCGT  TCCTCCTC
                                 _     __
GAM2612  MIC2     5'  GGGGGCGGGTGAGGGGAGC    60661      AGGA    _  A
                                GGGG    GCGGG GGG GGAGC
                                ||||    ||||| ||| |||||
                                CCCC    CGCCC CTC CCTCG
                                  _____    A  C
GAM2612  MMP2     3'  GGGAAGGGGCGCCTGGGAGGAG 60662        A  GG_
                                GGGGAGG GCG   GGGAGGAG
                                ||||||| |||   ||||||||
                                CCCTTCC CGC   CCCTCCTC
                                    C   GGA
GAM2612  MNT      3'  GGGCAGGCTGAGGGGAGGGGC  60663     G   AGC       A
                                GGG AGG   GGGGGGAGG GC
                                ||| |||   ||||||||| ||
                                CCC TCC   CTCCCCTCC CG
                                  G   GA_       C
GAM2612  MPP2     3'  GGGGAGGGGTGGCAGGGGG    24563        A___
                                GGGGAGG    GCGGGGGG
                                |||||||    ||||||||
                                CCCCTCC    CGTCCCCC
                                    CCAC
GAM2612  MSL3L1   5'  GGGGAGGGCGGGCGGGGGC    60664        A    G  A  A
                                GGGGAGG GCGGG GG GG GC
                                ||||||| ||||| || || ||
                                CCCCTCC CGCCC CC CC CG
                                    _    G  _  _
GAM2612  MSL3L1   5'  GGGGAGGGCGGGCGGGGGC    60664        A    G  A  A
                                GGGGAGG GCGGG GG GG GC
                                ||||||| ||||| || || ||
                                CCCCTCC CGCCC CC CC CG
                                    _    G  _  _
GAM2612  MSL3L1   5'  GGGGAGGGCGGGCGGGGGC    60664        A    G  A  A
                                GGGGAGG GCGGG GG GG GC
                                ||||||| ||||| || || ||
                                CCCCTCC CGCCC CC CC CG
                                    _    G  _  _
GAM2612  MSN      3'  GGGGAGAGGAGGGGAG      60665        G  C
                                GGGGAG AG GGGGGGAG
                                |||||| || ||||||||
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                                CCCCTC TC CTCCCCTC
                                  _ _
GAM2612 MUCDHL   3' GGGGGAGAGGGTGGAGGGGC  60666    A   C  G   A
                                GGG GGAG GGG GGAGG GC
                                ||| |||| ||| ||||| ||
                                CCC CCTC CCC CCTCC CG
                                  _   T  A   C
GAM2612 MUCDHL   3' GGGGGAGAGGGTGGAGGGGC  60666    A   C  G   A
                                GGG GGAG GGG GGAGG GC
                                ||| |||| ||| ||||| ||
                                CCC CCTC CCC CCTCC CG
                                  _   T  A   C
GAM2612 MVK      3' AGGGAGGGGCGACAAGGGG   60667       A  ___
                                GGGGAGG GCG   GGGGG
                                ||||||| |||   |||||
                                TCCCTCC CGC   TCCCC
                                    C   TGT
GAM2612 NCALD    3' GGGGAAGAGAGGGGAG     60668        CG
                                GGGGAGGAG  GGGGGAG
                                |||||||||  |||||||
                                CCCCTTCTC  TCCCCTC
                                    __
GAM2612 NCOA6IP  5' GGGAAGGGGCGGGACCACGGGC 60669       A    GGA_ A
                                GGGGAGG GCGGGG   GG GC
                                ||||||| ||||||   || ||
                                CCCTTCC CGCCCT   CC CG
                                    C    GGTG _
GAM2612 NEUD4    3' GGGGAGAATTGAGGAGC    60670       GCGGGGG
                                GGGGAGGA     GAGGAGC
                                ||||||||     |||||||
                                CCCCTCTT     CTCCTCG
                                   AA_____
GAM2612 NEUROD2  3' GGGGAGGGGTGCCTCCAGGGAG 60671       A__  GG__
                                GGGGAGG   GC   GGGGAG
                                |||||||   ||   ||||||
                                CCCCTCC   CG   TCCCTC
                                    CCA  GAGG
GAM2612 NEUROD2  5' GGGGAGGGGAGGGGGGGAGGGG 60672     __   C      A_
          GC                  GGGGA  GGAG GGGGGGAGG  GC
                              |||||  |||| |||||||||  ||
                              CCCCT  CCTC CCCCCCTCC  CG
                                CC   _       CC
GAM2612 NGFR     3' GGGGGGCAAGAGGGG      60673    A  A     A
                                GGG GG GCGGGGGG GG
                                ||| || |||||||| ||
                                CCC CC CGTTCTCC CC
                                  _ _     _
GAM2612 NGFR     3' GGGGAGGATGGGGGAG     60674        GCG
                                GGGGAGGA  GGGGGAG
                                ||||||||  |||||||
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                                CCCCTCCT  CCCCCTC
                                   A__
GAM2612  NPC2    5'  GGGGCGGGCCCGGGGAGGAGC  60675     A  A  GG
                                GGGG GG GC  GGGGAGGAGC
                                |||| || ||  ||||||||||
                                CCCC CC CG  CCCCTCCTCG
                                  G  _  GG
GAM2612  NRXN1   5'  GGGGAGCGGGCGGCGCGGAG  60676    A      G  A__
                                GG GGAGCGGG GG  GGAG
                                || ||||||||  ||  ||||
                                CC CCTCGCCC CC  CCTC
                                 _      G  GCG
GAM2612  NT5M    5'  GGGGAGCGGGGCGGGGAGC   60677    A       _  A
                                GG GGAGCGGGG GG GGAGC
                                || |||||||||  || |||||
                                CC CCTCGCCCC CC CCTCG
                                 _       G  _
GAM2612  NTSR1   3'  GGGGAGGGGTGGGGAGGAG   41680       AGC  _
                                GGGGAGG  GG GGGGAGGAG
                                |||||||  ||  |||||||||
                                CCCCTCC  CC CCCCTCCTC
                                   ___  A
GAM2612  NTSR1   3'  GGGGAGGAGTTGGGGACAGG  60678        CG   _
                                GGGGAGGAG  GGGGG AGG
                                |||||||||  |||||  |||
                                CCCCTCCTC  CCCCT TCC
                                     AA    G
GAM2612  OGG1    3'  GGGGAGGAGGGTACACTGGGG  60679        C  _______
                                GGGGAGGAG GG     GGGG
                                |||||||||  ||     ||||
                                CCCCTCCTC CC     CCCC
                                   _  ATGTGA
GAM2612  OLR1    3'  GGGGAGGAGTCATCAGGAGGAG 60680        _  GG
            C                    GGGGAGGAG CG  GGGAGGAGC
                                |||||||||  ||  |||||||||
                                CCCCTCCTC GT  TCCTCCTCG
                                     A  AG
GAM2612  OTOF    3'  GGGGCAGGGGTGGGAAGA    60681     AGG  C  _
                                GGGG  AG GGG GGGAGGA
                                ||||  ||  ||| |||||||
                                CCCC  TC CCC CCCTTCT
                                  G__  _  A
GAM2612  OTP     3'  GGGGAGGCGGCGGGCGAGGG  60682       A_    G GA
                                GGGGAGG  GCGGG G  GG
                                |||||||  ||||| |  ||
                                CCCCTCC  CGCCC C  CC
                                    GC    G TC
GAM2612  OTP     3'  GGGGCGGAGCGGGCCGGG    60683     A      __
                                GGGG GGAGCGGG  GGG
                                |||| ||||||||  |||
```

```
                                CCCC CCTCGCCC  CCC
                                  G       GG
GAM2612  PACSIN1   3'  GGGGAGGAGTGACGGGAG    60686         C  G
                                GGGGAGGAG GG GGGAG
                                ||||||||| || |||||
                                CCCCTCCTC CT CCCTC
                                     A  G
GAM2612  PACSIN1   3'  GGGGAGGGGCGGCAGTGGGGAG 60684        A  ____
           GAG                    GGGGAGG GCGG   GGGGAGGAG
                                ||||||| ||||   |||||||||
                                CCCCTCC CGCC   CCCCTCCTC
                                    C   GTCA
GAM2612  PACSIN1   5'  GGGGAGGAGGGGGCTGG     60685         C   GGA
                                GGGGAGGAG GGGG   GG
                                ||||||||| ||||   ||
                                CCCCTCCTC CCCC   CC
                                     _   GA_
GAM2612  PAFAH1B1  5'  GGGGGAGGGGAGGGGAG     60687     A   C     A
                                GGG GGAG GGGGGG GGAG
                                ||| |||| |||||| ||||
                                CCC CCTC CCCTCC CCTC
                                  _   _     _
GAM2612  PAX2      3'  GGGAGGGGATGGGAGGAG    60689       AGC  _
                                GGGAGG   GGG GGGAGGAG
                                ||||||   ||| ||||||||
                                CCCTCC   CCT CCCTCCTC
                                   ___   A
GAM2612  PAX2      3'  GGGGCGGGGCGGAGGGGGAG   60688     A  A      A
                                GGGG GG GCGGGGGG GGAG
                                |||| || |||||||| ||||
                                CCCC CC CGCCTCCC CCTC
                                  G  C      _
GAM2612  PAX2      3'  GGGGCGGGGCGGAGGGGGAG   60688     A  A      A
                                GGGG GG GCGGGGGG GGAG
                                |||| || |||||||| ||||
                                CCCC CC CGCCTCCC CCTC
                                  G  C      _
GAM2612  PAX2      3'  GGGAGGGGATGGGAGGAG    60689       AGC  _
                                GGGAGG   GGG GGGAGGAG
                                ||||||   ||| ||||||||
                                CCCTCC   CCT CCCTCCTC
                                   ___   A
GAM2612  PBX2      3'  GGGGAAGGGAAAGTGGGGGAG  60690      __   CG_
                                GGGGA  GGAG   GGGGGAG
                                |||||  ||||   |||||||
                                CCCCT  CCTT   CCCCCTC
                                   TC   TCA
GAM2612  PCTK3     3'  GGGGAGGAGGGTAGAG      60691         C  GG
                                GGGGAGGAG GG  GGAG
                                ||||||||| ||  ||||
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                                CCCCTCCTC CC  TCTC
                                     _ A_
GAM2612  PDE4A    3'  GGGGGGCGGGGGGGTGAG    60694     A A      AG
                                GGG GG GCGGGGGG  GAG
                                ||| || ||||||||  |||
                                CCC CC CGCCCCCC  CTC
                                  _ _      CA
GAM2612  PDE4A    3'  GGGGGGCAGTGGGGGAAGG   60692      A _ C
                                GGGG GG AG GGGGGGAGG
                                |||| || || |||||||||
                                CCCC CC TC CCCCCTTCC
                                  _ G  A
GAM2612  PDE4A    3'  GGGGAGGAGTGGAGGGGAA   60693         C     A
                                GGGGAGGAG GGGGGG GGA
                                ||||||||| |||||| |||
                                CCCCTCCTC CCTCCC CTT
                                     A     _
GAM2612  PDE4A    3'  AGGGGAGTGAGGGGAGGAG   60695     A   C
                                GGG GGAG GGGGGGAGGAG
                                ||| |||| ||||||||||
                                TCC CCTC CTCCCCTCCTC
                                  _   A
GAM2612  PDE4A    3'  GGGGAGGAGGGAGAGAGGGGGC 60697         C       A_
                                GGGGAGGAG GGGGGGAGG  GC
                                ||||||||| |||||||||  ||
                                CCCCTCCTC CCTCTCTCC  CG
                                     _       CC
GAM2612  PDE4A    3'  GGGGGTGAGTGGATCAGAGC   60696     AG   C   GGGA
                                GGGG  GAG GGG   GGAGC
                                ||||  ||| |||   |||||
                                CCCC  CTC CCT   TCTCG
                                  CA   A   AG__
GAM2612  PEX14    3'  GGAGAGGGGGCTGGGGAGGGGC 60698        A_  GG      A
                                GGGGAGG  GC  GGGGAGG GC
                                |||||||  ||  ||||||| ||
                                CCTCTCC  CG  CCCCTCC CG
                                    CC  A_      C
GAM2612  PFKM     5'  GGGAAAGGGGGGAGG       60699       AGC
                                GGGAGG   GGGGGGAGG
                                ||||||   |||||||||
                                CCCTTT   CCCCCCTCC
                                     ___
GAM2612  PHF1     3'  GGGAAGGATGGGAGGGG     60700        GC     A
                                GGGGAGGA  GGGGGG GG
                                ||||||||  |||||| ||
                                CCCTTCCT  CCCTCC CC
                                    A_     _
GAM2612  PHF1     3'  GGGAAGGATGGGAGGGG     60700        GC     A
                                GGGGAGGA  GGGGGG GG
                                ||||||||  |||||| ||
```

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                                CCCTTCCT  CCCTCC CC
                                   A_     _
GAM2612  PIP5K1A   3'  GAGGAGGAGTTTAAAGAGGAGC 60701         CGG
                                GGGGAGGAG   GGGGAGGAGC
                                |||||||||   ||||||||||
                                CTCCTCCTC   TTTCTCCTCG
                                    AAA
GAM2612  PLCB2     3'  GGGGAGGGGAGGGCCCTCAGC  60702       AGC     AGG__
                                GGGGAGG   GGGGGG    AGC
                                |||||||   ||||||    |||
                                CCCCTCC   CCTCCC    TCG
                                   ___     GGGAG
GAM2612  PLEK      3'  GGGGAGGAGGAATGCAGGAG   60703        C   GGG
                                GGGGAGGAG GGG   AGGAG
                                |||||||||| |||   |||||
                                CCCCTCCTC CTT   TCCTC
                                    _  ACG
GAM2612  PLOD3     5'  GGGAGGCGGGGGAGGGGC    60704       AGCG      A
                                GGGAGG   GGGGGAGG GC
                                ||||||   |||||||| ||
                                CCCTCC   CCCCCTCC CG
                                   G___      C
GAM2612  PML       3'  GGCGAGGAGTGGGCTGGCGAGG 60705    G     C  __ _
            AG                    GG GAGGAG GGG  GG GAGGAG
                                || |||||| |||  || ||||||
                                CC CTCCTC CCC  CC CTCCTC
                                 G     A   GA  G
GAM2612  PML       3'  GGCGAGGAGTGGGCTGGCGAGG 60705    G     C  __ _
            AG                    GG GAGGAG GGG  GG GAGGAG
                                || |||||| |||  || ||||||
                                CC CTCCTC CCC  CC CTCCTC
                                 G     A   GA  G
GAM2612  PML       3'  GGCGAGGAGTGGGCTGGCGAGG 60705    G     C  __ _
            AG                    GG GAGGAG GGG  GG GAGGAG
                                || |||||| |||  || ||||||
                                CC CTCCTC CCC  CC CTCCTC
                                 G     A   GA  G
GAM2612  PMP22     3'  GGGAAGGGGCGACATGGAG    60706       A   GG_
                                GGGGAGG GCGG   GGAG
                                |||||||  ||||   ||||
                                CCCTTCC CGCT   CCTC
                                   C    GTA
GAM2612  POLA      3'  GGGGAGGGGAGCTTGGGGAGGG 60707      __    GG      A
            GC                    GGGGA  GGAGC  GGGGAGG GC
                                |||||  |||||  ||||||| ||
                                CCCCT  CCTCG  CCCCTCC CG
                                  CC     AA      C
GAM2612  POMZP3    5'  GGGGAGGGCGGTGTGGAG    60708       A   GG_
                                GGGGAGG GCGG   GGAG
                                |||||||  ||||   ||||
```

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                                CCCCTCC CGCC   CCTC
                                    _    ACA
GAM2612  PPGB     3'  GGGAGAGGCTGGGAGGGG    60709      GA _     A
                                GGGAG  GC GGGGGG GG
                                ||||||  || |||||| ||
                                CCCTC  CG CCCTCC CC
                                   TC  A     _
GAM2612  PPP2R4   3'  AGGGAGGGGATGGGGAGGGGC  60710       AGCGG      A
                                GGGGAGG     GGGGAGG GC
                                |||||||     ||||||| ||
                                TCCCTCC     CCCCTCC CG
                                    CCTA_      C
GAM2612  PPT2     5'  GGGAAGGGCGGGCTGCTTGGG  60711       A    _______
                                GGGGAGG GCGGG      GGG
                                ||||||| |||||      |||
                                CCCTTCC CGCCC      CCC
                                    _    GACGAA
GAM2612  PPT2     5'  GGGAAGGGCGGGCTGCTTGGG  60711       A    _______
                                GGGGAGG GCGGG      GGG
                                ||||||| |||||      |||
                                CCCTTCC CGCCC      CCC
                                    _    GACGAA
GAM2612  PRDM16   3'  GGGGAGGATGCTGAGGAG    60712        _ GG
                                GGGGAGGA GC  GGGGAG
                                |||||||| ||  ||||||
                                CCCCTCCT CG  CTCCTC
                                     A  A_
GAM2612  PRKACG   3'  GGGCGGGGGGGTGAGGGAGC   60713    A      A___
                                GG GCGGGGGGG    GGAGC
                                || ||||||||    |||||
                                CC CGCCCCCC    CCTCG
                                 _       ACTC
GAM2612  PRKCABP  3'  GGGGAGGGAGGGTGGAGGGGC  60714       AGC   _    A
                                GGGGAGG   GGGG GGAGG GC
                                |||||||   |||| ||||| ||
                                CCCCTCC   TCCC CCTCC CG
                                    C__    A    C
GAM2612  PRKCL1   5'  AGGGAGGGGCGGCCAGAGGAGC 60715       A   GG
                                GGGGAGG GCGG  GGAGGAGC
                                ||||||| ||||  ||||||||
                                TCCCTCC CGCC  TCTCCTCG
                                    C   GG
GAM2612  PROC     3'  GGGGGGGGGCGGGGGGGG    41696     A A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCCC CC
                                  C  C       _
GAM2612  PROK1    3'  GGGGAGGGGAGGGGGAA     60716       AGC     A
                                GGGGAGG   GGGGGG GGAG
                                |||||||   |||||| ||||
```

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                                CCCCTCC   CCTCCC CCTT
                                   ___    _
GAM2612  PTK2B    3'  GGGTAGGGGTGGGGAGAGGGC  60717    G  AGC       A
                                GGG AGG   GGGGGGAGG GC
                                ||| |||   ||||||||| ||
                                CCC TCC   CCCCTCTCC CG
                                  A  CCA       _
GAM2612  PTK2B    3'  GGGGAGAGAAAGAGGAGGAG   60718      G  CG
                                GGGGAG AG  GGGGGAGGAG
                                |||||| ||  ||||||||||
                                CCCCTC TC  TCTCCTCCTC
                                   _ TT
GAM2612  PTMS     3'  AGGGAGGGGAGGGGGG      60719       AGC     A  A
                                GGGGAGG   GGGGGG GG G
                                |||||||   |||||| || |
                                TCCCTCC   CCTCCC CC C
                                   ___    _ _
GAM2612  PTPRG    5'  GGGGAGAGGCAGGGGGAG    60720       GA
                                GGGGAG  GCGGGGGGAG
                                ||||||  ||||||||||
                                CCCCTC  CGTCCCCCTC
                                   TC
GAM2612  PTPRZ1   5'  GGAGAGGGAGGGGGAG      60721       AGC
                                GGGGAGG   GGGGGGAG
                                |||||||   ||||||||
                                CCTCTCC   TCCCCCTC
                                   C__
GAM2612  RAB13    5'  GGGGGAGCCGGGGGAGG     41701     A    G
                                GGG GGAGC GGGGGAGG
                                ||| ||||| ||||||||
                                CCC CCTCG CCCCCTCC
                                  _    G
GAM2612  RAB13    5'  GGGGAGGGGTGGGGAG      60722       AGC  _
                                GGGGAGG   GG GGGGAG
                                |||||||   || ||||||
                                CCCCTCC   CC CCCCTC
                                   ___ A
GAM2612  RAB3A    3'  GGGGGGGGGGGGGTCCCAGG   60723     A  AGC     _____
                                GGGG GG   GGGGGG   AGG
                                |||| ||   ||||||   |||
                                CCCC CC   CCCCCC   TCC
                                  _ ___     AGGG
GAM2612  RAB5C    3'  GGGGAGGAAGTGGGAAGAGC  60724        CGGG
                                GGGGAGGAG   GGGAGGAGC
                                |||||||||   |||||||||
                                CCCCTCCTT   CCCTTCTCG
                                   CA__
GAM2612  RAB7     3'  AGGGAGGGGAAAGGGGGGG   60725       AGC_    A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
```

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                                TCCCTCC   TCCCCC CC
                                   CCTT    _
GAM2612  RABL2A   3'  GGGGAGGGGGTGGGGAAGG   60726      AGCG
                                GGGGAGG   GGGGGAGG
                                |||||||   ||||||||
                                CCCCTCC   CCCCTTCC
                                   CCCA
GAM2612  RABL2B   3'  GGGGAGGGGGTGGGGAAGG   60726      AGCG
                                GGGGAGG   GGGGGAGG
                                |||||||   ||||||||
                                CCCCTCC   CCCCTTCC
                                   CCCA
GAM2612  RAD21    5'  GGGGAGGGGGTGGGGAAAGGGG 60727   AGC _   _______   III
            GGAGCG                G   GG GGGGA    GGAGC   G
                                |   || |||||     |||||   |
                                C   CC CCCCT     CCTCG   C
                                 C__  A    TTCCCC    III
GAM2612  RARA     3'  GAGGAGGAGAACTGGGGGG   60728       C___
                                GGGGAGGAG   GGGGGG
                                |||||||||   ||||||
                                CTCCTCCTC   CCCCCC
                                     TTGA
GAM2612  RARB     5'  GGGGAGGAAGTGGAGATGGGGG 60729       _ C ____   A
            G                    GGGGAGGA G GG   GGGG GG
                                |||||||| | ||   |||| ||
                                CCCCTCCT C CC   CCCC CC
                                     T A  TCTA   _
GAM2612  RCE1     3'  GGGGGGTGGGGAGAGG     60730     A  AGC
                                GGGG GG   GGGGGGAGG
                                ||||  ||   |||||||||
                                CCCC CC   CCCCTCTCC
                                  _  A__
GAM2612  RCV1     5'  GGAGGAGGGGCCCAGGAGC   60732      C   GGG
                                GGAGGAG GGG   AGGAGC
                                ||||||| |||   ||||||
                                CCTCCTC CCC   TCCTCG
                                    _   GGG
GAM2612  RCV1     3'  AGGGAGGGGTGGGACCGGGC   60731      AGC _   A_  A
                                GGGGAGG   GG GGGG  GG GC
                                |||||||   || ||||  || ||
                                TCCCTCC   CC CCCT  CC CG
                                    ___  A   GG  _
GAM2612  RERE     5'  GGGGAGGCGACGCGGAGGG   60733      A___
                                GGGGAGG   GCGGGGGG
                                |||||||   ||||||||
                                CCCCTCC   CGCCTCCC
                                    GCTG
GAM2612  REST     5'  GGGGAGAGGTGGGGGAGG   41705      G  CG
                                GGGGAG AG  GGGGGAGG
                                ||||||  ||  ||||||||
```

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                                CCCCTC TC  CCCCCTCC
                                   _ CA
GAM2612  RNPEPL1   3'  GGGAGAGCCCAGGGGAGGGGC  60734      G  G_      A
                                GGGAG AGC  GGGGGAGG GC
                                ||||| |||  |||||||| ||
                                CCCTC TCG  TCCCCTCC CG
                                   _  GG       C
GAM2612  RPA1      3'  GGGGATGGGGGGGGGGG      31322       _ AGC     A
                                GGGGA GG   GGGGGG GG
                                ||||| ||   |||||| ||
                                CCCCT CC   CCCCCC CC
                                  A ____     _
GAM2612  RTN4      5'  GGGGAGGACTGAGAGGGG    60735         GC     A
                                GGGGAGGA  GGGGGG GG
                                ||||||||  |||||| ||
                                CCCCTCCT  CTCTCC CC
                                     GA     _
GAM2612  RXRB      3'  GGGGGGGCGGCGGGAAG     60736      A  A    G
                                GGGG GG GCGG GGGAGG
                                |||| || |||| ||||||
                                CCCC CC CGCC CCCTTC
                                  _ _   G
GAM2612  SALL1     3'  GGGGCGGGGTGGGGGGCAAGGA 60738      A  AGC     __
            G                    GGGG GG   GGGGGG  AGGAG
                                |||| ||   ||||||  |||||
                                CCCC CC   CCCCCC  TCCTC
                                  G  CCA     GT
GAM2612  SALL1     3'  GGGGCGGGGCGGGGTGGGGGGC 60737      A  A     _  A  A
                                GGGG GG GCGGGG GG GG GC
                                |||| || |||||| || || ||
                                CCCC CC CGCCCC CC CC CG
                                  G  C     A  _  C
GAM2612  SCN4A     3'  GGGGAGGAGAGGGGAG      60739         CG
                                GGGGAGGAG  GGGGGAG
                                |||||||||  |||||||
                                CCCCTCCTC  TCCCCTC
                                              __
GAM2612  SDC1      3'  GGGCAGGAGCGACCAGAGGGGC 60740      G       GG     A
                                GGG AGGAGCGG  GGAGG GC
                                ||| ||||||||  ||||| ||
                                CCC TCCTCGCT  TCTCC CG
                                  G       GG    C
GAM2612  SET7      5'  GAGGAGGAGGAAGAGGAGGAGC 60741          CG
                                GGGGAGGAG  GGGGGAGGAGC
                                |||||||||  ||||||||||
                                CTCCTCCTC  TCTCCTCCTCG
                                     CT
GAM2612  SH3GL1    3'  GGGGCGGGGCGGGGACACGG   60742      A  A      GA_
                                GGGG GG GCGGGGG   GG
                                |||| || |||||||   ||
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                                CCCC CC CGCCCCT   CC
                                  G C      GTG
GAM2612 SIAT8E   5' GGGGAGGGGGAGGGG      60578       AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   CCCTCC CC
                                    ___     _
GAM2612 SIGLEC6  5' GGGGAGGAACGGGTGGCTGGGG 60743        _______       III
            AGGAGCG                 GGAGCGGG     GGGAGGAGC   G
                                |||||||||     |||||||||   |
                                CCTTGCCC     CCCTCCTCG   C
                                     ACCGAC        III
GAM2612 SLC7A8   3' GGGGAGGGGCAGGAAAGAGGGC 60744       A _ GG    A
                                GGGGAGG GC GG  GGAGG GC
                                ||||||| || ||  ||||| ||
                                CCCCTCC CG CC  TCTCC CG
                                    C  T  TT    _
GAM2612 SLC9A1   3' GGGAGGCGGCAGGGGAGGAGC  60745      A_     G
                                GGGAGG  GCGGGGG AGGAGC
                                ||||||  ||||||| ||||||
                                CCCTCC  CGTCCCC TCCTCG
                                   GC     _
GAM2612 SLC9A3R2 3' GGGGAGGGGAAGGGGGGGGG   60746       ___ C     A
                                GGGGAGG   AG GGGGGG GG
                                |||||||   || |||||| ||
                                CCCCTCC   TC CCCCCC CC
                                    CCT _     _
GAM2612 SLIT3    5' GGGGAGCGGGCGGCGGAG    60747    A      G  A
                                GG GGAGCGGG GG GGAG
                                || |||||||| || ||||
                                CC CCTCGCCC CC CCTC
                                 _      G  G
GAM2612 SMG1     3' GGGGAGGAGTAGGGAACGA   60748        CG     G
                                GGGGAGGAG  GGGGGA GA
                                |||||||||  |||||| ||
                                CCCCTCCTC  TCCCTT CT
                                     A_     G
GAM2612 SNRP70   3' GGGGAGGGGATGACAGCAAGGG 60749       ________
              G                  GGGGAGG      AGCGGGGGG
                                |||||||      |||||||||
                                CCCCTCC      TCGTTCCCC
                                    CCTACTG
GAM2612 SOX11    3' GGGGGGCCGGGGGAGG      41716     A  A  G
                                GGG GG GC GGGGGAGG
                                ||| || || ||||||||
                                CCC CC CG CCCCCTCC
                                  _ _  G
GAM2612 SOX12    3' GAGGGGGCGACGTGGGGAGGGG 60750      A  A   ___      A
              C                  GGGG GG GCGG   GGGGAGG GC
                                |||| || ||||   ||||||| ||
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                                CTCC CC CGCT   CCCCTCC CG
                                  _ _   GCA      C
GAM2612  SOX12    3'  GGGGTGGGCCCCAGCGGAGGG  60751      A _____
                                GGGG GG    AGCGGGGGG
                                |||| ||    |||||||||
                                CCCC CC    TCGCCTCCC
                                  A  CGGGG
GAM2612  SOX13    3'  GGGGAGGGGAGGGCAGG     60752        AGC    _
                                GGGGAGG   GGGGGG AGG
                                |||||||   |||||| |||
                                CCCCTCC   CCTCCC TCC
                                    ___      G
GAM2612  SPI1     3'  GGGGAGGGGCGGGTGACGGAGC 60753        A    G GA
                                GGGGAGG GCGGG G  GGAGC
                                ||||||| ||||| |  |||||
                                CCCCTCC CGCCC C  CCTCG
                                    C    A TG
GAM2612  SPTB     3'  GGGGAGGAGTGGAGGAGG    60754         CG
                                GGGGAGGAG  GGGGGAGG
                                |||||||||  ||||||||
                                CCCCTCCTC  CCTCCTCC
                                     A_
GAM2612  SRD5A1   5'  GAGGAGGGGCGGCTACCGGAGG 60755        A   GG___    A
            GGC                    GGGGAGG GCGG    GGAGG GC
                                |||||||  ||||    |||||  ||
                                CTCCTCC CGCC    CCTCC CG
                                    C   GATGG    C
GAM2612  SREBF2   3'  GGTGGAGGGGTGGGCTGAGC   60756    A   C   _   AG
                                GG GGAG GGG GGG  GAGC
                                ||  ||||  |||  |||  ||||
                                CC CCTC CCC CCC  CTCG
                                  A   _   A   GA
GAM2612  SSRP1    5'  GGGGGGACGCGGGGGGGG    60757      A  _       A
                                GGGG GGA GCGGGGGG GG
                                ||||  ||| ||||||||  ||
                                CCCC CCT CGCCCCCC CC
                                  _   G       _
GAM2612  SYN2     3'  GGGGGGAGGAGAGGAG      60758      A   C
                                GGGG GGAG GGGGGGAG
                                ||||  ||||  ||||||||
                                CCCC CCTC CTCTCCTC
                                  _    _
GAM2612  SYNGR1   3'  GGGGACAGATGGGGAGGGGC   60759       _   GC     A  A
                                GGGGA GGA  GGGGGG GG GC
                                |||||  |||  ||||||  ||  ||
                                CCCCT TCT  CCCCTC CC CG
                                  G   A_     _  _
GAM2612  TAF1C    3'  AGGGAGGAAAGAAAGGGGGGAG 60760         C____
                                GGGGAGGAG    GGGGGGAG
                                |||||||||    ||||||||
```

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                                TCCCTCCTT    CCCCCCTC
                                     TCTTT
GAM2612  TAGLN    3'  GGGGAGGGCCGGGCTCAGGGC  60761       A  G   GG_  A
                                GGGGAGG GC GGG   AGG GC
                                ||||||| || |||   ||| ||
                                CCCCTCC CG CCC   TCC CG
                                   _ G   GAG  _
GAM2612  TBR1     3'  GGGGAAGAGCTGTGAGGGG   60762         ___
                                GGGGAGGAGC   GGGGGG
                                ||||||||||   ||||||
                                CCCCTTCTCG   CTCCCC
                                      ACA
GAM2612  TFAP2A   3'  GGTGAGGCGTGGGAGGGGC   60763    GA  A   GG     A
                                GG  GG GCG  GGGAGG GC
                                ||  || |||  |||||| ||
                                CC  TC CGC  CCCTCC CG
                                 AC  _   A_     C
GAM2612  TFAP4    3'  GAGGAGGGCTGGGGGGG     60765       A  G    A
                                GGGGAGG GC GGGGG GG
                                ||||||| || ||||| ||
                                CTCCTCC CG CCCCC CC
                                   _ A    _
GAM2612  TFAP4    3'  GGGAAGGGGGAGGGGGGC    60764       AGC     A  A
                                GGGGAGG   GGGGGG GG GC
                                |||||||   |||||| || ||
                                CCCTTCC   CCTCCC CC CG
                                   C__     _ _
GAM2612  TFE3     3'  GGGAAGGGGTGGGGCCTGGC  60766       AGC  _   AGGA
                                GGGGAGG   GG GGGG   GC
                                |||||||   || ||||   ||
                                CCCTTCC   CC CCCC   CG
                                   ___  A   GGAC
GAM2612  TGFB1    3'  GGGGCGGGGCGGGGTGGGG   60768     A  A    _  A
                                GGGG GG GCGGGG GG GG
                                |||| || |||||| || ||
                                CCCC CC CGCCCC CC CC
                                  G  C     A  _
GAM2612  TGFB1    3'  GGGGCGGGGTGGGGCCGGGC  60767     A  AGC  _   A_  A
                                GGGG GG   GG GGGG  GG GC
                                |||| ||   || ||||  || ||
                                CCCC CC   CC CCCC  CC CG
                                  G  ___  A   GG  _
GAM2612  THY1     3'  GGTGGAGGCAGGGAGGGGC   60769   _   GA      A  A
                                GG GGAG  GCGGGGGG GG GC
                                || ||||  |||||||| || ||
                                CC CCTC  CGTCCCTC CC CG
                                 A   ___       _ _
GAM2612  TIMP3    3'  AGGGAGGAGGCTGGAGGAG   60770         _ G
                                GGGGAGGAG C GGGGGAG
                                ||||||||| | |||||||
```

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                                TCCCTCCTC G CCTCCTC
                                     C A
GAM2612  TLX1     5'  GGGGAGGGGAGGGAGAGAG   60771       AGC      _
                                GGGGAGG   GGGGGGAG GAG
                                |||||||   |||||||| |||
                                CCCCTCC   CCTCCCTC CTC
                                   ___       T
GAM2612  TMEPAI   5'  GGGGCGGCCGGGGGGGG    60772     A  AG     A
                                GGGG GG  CGGGGGG GG
                                |||| ||  ||||||| ||
                                CCCC CC  GCCCCCC CC
                                  G  G_     _
GAM2612  TNFRSF11A 3'  GGGGGGAGTCGGGGGGAGGAAG 60773     A   _        _
              C                  GGGG GGAG CGGGGGGAGGA GC
                                |||| |||| |||||||||| ||
                                CCCC CCTC GCCCCCCTCCT CG
                                  _   A        T
GAM2612  TSLP     5'  AGGGAGGAGCGGGGAACACAAG 60774             AG_
                                GGGGAGGAGCGGGGGG   GAG
                                ||||||||||||||   |||
                                TCCCTCCTCGCCCCTT   TTC
                                        GTG
GAM2612  TSLP     5'  GGGGAGGAAGGTCAGGGAGGAG 60775         C  __
              C                  GGGGAGGAG GG  GGGGAGGAGC
                                |||||||| ||  ||||||||||
                                CCCCTCCTT CC  TCCCTCCTCG
                                     _ AG
GAM2612  TULP1    3'  GGGGAGGAGGGGGGCACAGC   60776       GC     AGG
                                GGGGAGGA  GGGGGG   AGC
                                ||||||||  ||||||   |||
                                CCCCTCCT  CCCCCC   TCG
                                   __     GTG
GAM2612  UCP3     3'  GGGGGGGGGTGGGGAAGAG    60777     A  AGC  _
                                GGGG GG   GG GGGGAGGAG
                                |||| ||   || |||||||||
                                CCCC CC   CC CCCCTTCTC
                                  _ C__  A
GAM2612  UGCG     5'  GGGGTGGGGACGGAAGGGG   60778     A_  AG     A
                                GGGG  GG  CGGGGGG GG
                                ||||  ||  ||||||| ||
                                CCCC  CC  GCCTTCC CC
                                  AC  CT     _
GAM2612  UNC5C    5'  GGGGAGGGGAGGGGGA      60779       AGC     A
                                GGGGAGG   GGGGGG GGA
                                |||||||   |||||| |||
                                CCCCTCC   CCTCCC CCT
                                   ___    _
GAM2612  UNRIP    5'  AGGGAGGGGTGAGGGAGG    60780       AGCG
                                GGGGAGG   GGGGGAGG
                                |||||||   ||||||||
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                                TCCCTCC   CTCCCTCC
                                   CCA_
GAM2612  VAT1    3'  GGGGAGGGGCAGGGGAGAGC  60781       A     GA
                                GGGGAGG GCGGGGG  GGAGC
                                ||||||| |||||||  |||||
                                CCCCTCC CGTCCCC  TCTCG
                                   C     __
GAM2612  VDR     3'  GGGGAGGTGGCAGAGGAGGGGC 60782       A_     GA  A
                                GGGGAGG  GCGGGGG  GG GC
                                |||||||  |||||||  || ||
                                CCCCTCC  CGTCTCC  CC CG
                                   AC      TC  _
GAM2612  VEGF    5'  GGGGAGGAGGTGGTAACTGGGG 60783        CG  GG A_  A
            C                    GGGGAGGAG  GG  G  GG GC
                                |||||||||  ||  |  || ||
                                CCCCTCCTC  CC  T  CC CG
                                     CA  AT GA  C
GAM2612  VIPR1   3'  GGGAAGGGGCGGGAGGGG    60784       A      A
                                GGGGAGG GCGGGGGGG GG
                                ||||||| |||||||| ||
                                CCCTTCC CGCCCTCC CC
                                   C     _
GAM2612  VIPR2   3'  GGGGAGGAACAGCCGAGGGGC  60785         GGG   A
                                GGGGAGGAGCGG   GAGG GC
                                ||||||||||||   |||| ||
                                CCCCTCCTTGTC   CTCC CG
                                      GG_   C
GAM2612  WNT5A   5'  GGGCAGGGGGTGGGGGG    60786    G  AGC  _  A  A
                                GGG AGG   GGG GGG GG G
                                ||| |||   ||| ||| || |
                                CCC TCC   CCC CCC CC C
                                  G  ____  A  _ _
GAM2612  WNT7A   5'  GGGAGGAGGGAGGGAGGAGC  60787       C
                                GGGAGGAG GGGGGGAGGAGC
                                |||||||| ||||||||||||
                                CCCTCCTC CCTCCCTCCTCG
                                   _
GAM2612  WSX1    5'  AGGGGGAGTGGGGAGG     60788     A   CGG
                                GGGG GGAG   GGGGAGG
                                |||| ||||   |||||||
                                TCCC CCTC   CCCCTCC
                                  _   A__
GAM2612  YWHAE   3'  GGGGAGGAGTGAGGGGAAGGAG 60789        C _
                                GGGGAGGAG G GGGGGAGGAG
                                ||||||||| | ||||||||||
                                CCCCTCCTC C CCCCTTCCTC
                                     A T
GAM2612  ZNF278  5'  GGGGAGGAGAAGGAGGGG    60790        C     A
                                GGGGAGGAG GGGGGG GG
                                |||||||| |||||| ||
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                                CCCCTCCTC TCCTCC CC
                                     T     _
GAM2612 ZNF278   5' GGGGAGGAGAAGGAGGGG    60790        C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CCCCTCCTC TCCTCC CC
                                     T     _
GAM2612 ZNF278   5' GGGGAGGAGAAGGAGGGG    60790        C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CCCCTCCTC TCCTCC CC
                                     T     _
GAM2612 ZNF278   5' GGGGAGGAGAAGGAGGGG    60790        C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CCCCTCCTC TCCTCC CC
                                     T     _
GAM2612 20D7-FC4 3' GGGGGGAGAGGGGAGG      41731      A    CG
                                GGGG GGAG  GGGGGAGG
                                |||| ||||  ||||||||
                                CCCC CCTC  TCCCCTCC
                                  _   __
GAM2612 7h3      3' GGGGGGGGCAAGGGGGGGGC  60791      A A       A A
                                GGGG GG GCGGGGGG GG GC
                                |||| || |||||||| || ||
                                CCCC CC CGTTCCCC CC CG
                                  _ C       _ C
GAM2612 ARFGAP1  5' AGGGAGGGGCGGGCAGGG    60792        A    G A
                                GGGGAGG GCGGG GG GG
                                ||||||| ||||| || ||
                                TCCCTCC CGCCC TC CC
                                    C    G _
GAM2612 ARHGEF2  3' GGGGCAGGGGGGAGGGGC    60793      AGGAGC        A
                                GGGG     GGGGGGAGG GC
                                ||||     ||||||||| ||
                                CCCC     CCCCCCTCC CG
                                  GT____        C
GAM2612 ARHGEF9  5' GGGGAGGGGAGGGGGA      60779        AGC     A
                                GGGGAGG   GGGGGG GGA
                                |||||||   |||||| |||
                                CCCCTCC   CCTCCC CCT
                                    ___     _
GAM2612 ASB16    5' GGGGAGGAGGGACGAG      60794        GCGGG   G
                                GGGGAGGA    GGGA GAG
                                ||||||||    |||| |||
                                CCCCTCCT    CCCT CTC
                                     _____   G
GAM2612 ATPW     5' GGGGCGGGGGCGGGGCGAGGGC 60795      A A_     G   A
                                GGGG GG  GCGGGG GAGG GC
                                |||| ||  |||||| |||| ||
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                                CCCC CC  CGCCCC CTCC CG
                                  G  CC     G   _
GAM2612  BAG5     3'  GGTGACCCGGGGGAGGAG    60796    A  AG     G
                                GG GG  CGGGGG AGGAG
                                || ||  |||||| |||||
                                CC CT  GCCCCC TCCTC
                                 A  GG     _
GAM2612  BCL2L1   3'  GGGTGGGGGTTGGGGGAGGGGC 60797     GA  AGCG       A
                                GGG  GG    GGGGGAGG GC
                                |||  ||    |||||||| ||
                                CCC  CC    CCCCCTCC CG
                                  AC  CCAA       C
GAM2612  BDH      5'  GGGGAGAGCCGAGGGGGGGC   60798       G  _     A  A
                                GGGGAG AGC GGGGGG GG GC
                                |||||| ||| |||||| || ||
                                CCCCTC TCG CTCCCC CC CG
                                   _   G     _ _
GAM2612  BMF      3'  GGAGGTCGGGGGGGAGGGGC   60799       AGC       A
                                GGAGG   GGGGGGAGG GC
                                |||||   |||||||||  ||
                                CCTCC   CCCCCCTCC CG
                                   AGC        C
GAM2612  BRD2     3'  AGGGGGGCGGGGGGGGG      60800      A  A       A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                TCCC CC CGCCCCCC CC
                                  _  _       _
GAM2612  BTN3A1   3'  GGGAAGGAGTCAACAGGGG   60801          ____
                                GGGGAGGAG    CGGGGG
                                |||||||||    ||||||
                                CCCTTCCTC    GTCCCC
                                     AGTT
GAM2612  C12orf22  5'  GGGAAGGAGGGAGGAG      60802         GCGGG
                                GGGGAGGA    GGGAGGAG
                                ||||||||    ||||||||
                                CCCTTCCT    CCCTCCTC
                                  _____
GAM2612  C20orf149 3'  GGAGAGGGGCGGGGAGGGGC   60803         A       A  A
                                GGGGAGG GCGGGGGG GG GC
                                ||||||| |||||||| || ||
                                CCTCTCC CGCCCCTC CC CG
                                   C       _ _
GAM2612  C20orf178 3'  GGGTGAGGAGTGGGCCAGAG   60804     _     C   G_
                                GGG GAGGAG GGG  GGAG
                                ||| |||||| |||  ||||
                                CCC CTCCTC CCC  TCTC
                                  A     A  GG
GAM2612  C20orf27  3'  GGAGAGGAGGACGAGGGAGGGG 60805          CG_       A
            C                    GGGGAGGAG   GGGGGAGG GC
                                |||||||||   |||||||| ||
```

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                                CCTCTCCTC  CTCCCTCC CG
                                     CTG       C
GAM2612  C20orf55  3'  GGGGAGGAGGGGGTTCTCAGG  60806        C   GG___
                                GGGGAGGAG GGGG    AGG
                                ||||||||| ||||    |||
                                CCCCTCCTC CCCC    TCC
                                     _   AAGAG
GAM2612  C21orf57  5'  GGCGGGGTGCGGGGAGGGGC  60807   _ A A     A A
                                GG GG GG GCGGGGGG GG GC
                                || || || |||||||| || ||
                                CC CC CC CGCCCCTC CC CG
                                 G _ A      _ _
GAM2612  C22orf5   3'  GGGGATGGAGCGGTCGGG    60808     _     G_
                                GGGGA GGAGCGG  GGG
                                ||||| |||||||  |||
                                CCCCT CCTCGCC  CCC
                                   A      AG
GAM2612  C2orf9    3'  GGGGAGGGGCGGGGGGGCAG  41737       A      A_
                                GGGGAGG GCGGGGGG  GG
                                ||||||| ||||||||  ||
                                CCCCTCC CGCCCCCC  TC
                                    C       CG
GAM2612  C6orf28   3'  GGGGAAGAGGAGGAGGAGC   60809       GCG
                                GGGGAGGA   GGGGGAGGAGC
                                ||||||||   ||||||||||
                                CCCCTTCT   CCTCCTCCTCG
                                     ___
GAM2612  C8orf2    3'  AGGAGTTGGCGGGGGGGGG   60810     GA_      A
                                GGGAG   GCGGGGGG GG
                                |||||   |||||||| ||
                                TCCTC   CGCCCCCC CC
                                   AAC       C
GAM2612  C9orf7    3'  GAGGAGGGGCAGCCGAGGGGC  60811       A   GGG   A
                                GGGGAGG GCGG   GAGG GC
                                ||||||| ||||   |||| ||
                                CTCCTCC CGTC   CTCC CG
                                    C   GG_   C
GAM2612  CITED2    3'  GGGGGGCGGCGGGGGGGGACAGC 60812     A A_      A _
                                GGGG GG  GCGGGGGG GG AGC
                                |||| ||  |||||||| || |||
                                CCCC CC  CGCCCCCC CT TCG
                                  _ GC       _ G
GAM2612  CLSTN1    5'  GGGAGGGGCGGGGGAGAGGAGC 60813       A     _
                                GGGAGG GCGGGGG GAGGAGC
                                |||||| ||||||| |||||||
                                CCCTCC CGCCCCC CTCCTCG
                                   C      T
GAM2612  CLSTN1    5'  GGAGAGGAGCGGAGGGAG    60814
                                GGGGAGGAGCGGGGGGAG
                                ||||||||||||||||||
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                                CCTCTCCTCGCCTCCCTC

GAM2612 CLSTN1   5' GGGAGGGGCGGGGATGGGGAGC 60815       A     __ A
                                GGGAGG GCGGGG  GG GGAGC
                                |||||| ||||||  || |||||
                                CCCTCC CGCCCC  CC CCTCG
                                   C     TA  _
GAM2612 CLSTN3   5' GGGAGGGGGCAGAGAGGGGC  60816       A_      A A
                                GGGAGG  GCGGGGGG GG GC
                                ||||||  |||||||| || ||
                                CCCTCC  CGTCTCTC CC CG
                                   CC       _ _
GAM2612 CLSTN3   3' GGGGGGCCGGGGGAGGGGC   60817     A A G      A
                                GGG GG GC GGGGGAGG GC
                                ||| || || |||||||| ||
                                CCC CC CG CCCCCTCC CG
                                  _ _ G       C
GAM2612 CNIL     5' GGGGAGGAGGAGCGGGGAGC  60818         C  G A
                                GGGGAGGAG GGG GG GGAGC
                                ||||||||| ||| || |||||
                                CCCCTCCTC CTC CC CCTCG
                                     _  G  _
GAM2612 CNOT3    3' GGGGAGGAGGGGGCAG      60819         GC    G
                                GGGGAGGA  GGGGG AG
                                ||||||||  ||||| ||
                                CCCCTCCT  CCCCC TC
                                    __     G
GAM2612 CNOT3    3' GGGGTGGGTAGAGGGAGGGGC  60820      A  AGC       A
                                GGGG GG   GGGGGGAGG GC
                                |||| ||   ||||||||| ||
                                CCCC CC   TCTCCCTCC CG
                                  A  CA_       C
GAM2612 COX4I2   3' GGGCAGGGGAGGGGAGGGGC  60821     G   AGC       A
                                GGG AGG   GGGGGGAGG GC
                                ||| |||   ||||||||| ||
                                CCC TCC   CTCCCCTCC CG
                                  G   C__       C
GAM2612 CPLX1    3' GGAGGATCTGTAGGGGGAGGGG 60822       GC___       A
              C                  GGAGGA    GGGGGGAGG GC
                                 ||||||    ||||||||| ||
                                 CCTCCT    TCCCCCTCC CG
                                    AGACA       C
GAM2612 CREB-H   3' AGGGAGGCCGGGAGGGG     60823        AG      A
                                GGGGAGG  CGGGGGG GG
                                |||||||  ||||||| ||
                                TCCCTCC  GCCCTCC CC
                                   G_      _
GAM2612 CRELD1   5' GGAGAGGAGGCCAGAGGGG   60824         _ G    A
                                GGGGAGGAG C GGGGG GG
                                ||||||||| | ||||| ||
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                                CCTCTCCTC G TCTCC CC
                                     C G    _
GAM2612  CSEN     3'  GGGGAGGAGACCAGGGGAG   60825         _ G
                                GGGGAGGAG C GGGGGAG
                                ||||||||| | |||||||
                                CCCCTCCTC G TCCCCTC
                                     T G
GAM2612  CSTF1    3'  GGGGAGGAGGGTAGAG     60691         C  GG
                                GGGGAGGAG GG  GGAG
                                ||||||||| ||  ||||
                                CCCCTCCTC CC  TCTC
                                     _ A_
GAM2612  CX46.6   3'  GGGGAGGGCTGAAGAAGGAGC  60826        A  G
                                GGGGAGG GC GGGGGAGGAGC
                                ||||||| || ||||||||||
                                CCCCTCC CG CTTCTTCCTCG
                                    _ A
GAM2612  DDX39    3'  GGGAAGGGAGGTGGGAGGGGC  60827        AGC  _     A
                                GGGGAGG   GGG GGGAGG GC
                                |||||||   ||| |||||| ||
                                CCCTTCC   TCC CCCTCC CG
                                    C__   A     C
GAM2612  DEFCAP   5'  AGGGAGGAGCCCAGAGGGG   60828          ___
                                GGGGAGGAGC   GGGGGG
                                ||||||||||   ||||||
                                TCCCTCCTCG   CTCCCC
                                     GGT
GAM2612  DGKD     3'  GGGGGGAGGGAGGAG      60829      AGGAGC
                                GGGG     GGGGGGAGGAG
                                ||||     ||||||||||
                                CCCC     CCTCCCTCCTC

                                  _______
GAM2612  DKFZP434K2235 3'  GGGGAGGGGAGAGGAG      60830       GGAGC
                                GGGGA    GGGGGGAGGAG
                                |||||    ||||||||||
                                CCCCT    CCCCTCTCCTC

                                  ______
GAM2612  DKFZP434P0111 3'  GGGGAGGGGGGCAATGG     60831        AGC   G  _
                                GGGGAGG   GGGG GA GG
                                |||||||   |||| || ||
                                CCCCTCC   CCCC TT CC
                                    ___   G  A
GAM2612  DKFZp547F072 5'  GGGGAGGGGTGGGGAGAAA   41749        AGC  _
                                GGGGAGG   GG GGGGAGGAG
                                |||||||   || |||||||||
                                CCCCTCC   CC CCCCTCTTT
                                    ___ A
GAM2612  DKFZp547F072 5'  GGGGAGGAGTGTAGGGGG    60832         C__
                                GGGGAGGAG   GGGGGG
                                |||||||||   ||||||
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                                CCCCTCCTC   TCCCCC
                                     ACA
GAM2612  DKFZp547J036 3'  GGGAGGGGTGGGGGAGAGAGAG 60833       AGC_      _
             C                    GGGAGG    GGGGGGAG GAGC
                                  ||||||    |||||||| ||||
                                  CCCTCC    CCCCTCTC CTCG
                                      CCAC       T
GAM2612  DKFZp547J036 3'  AGGGAGGGGTGGAGGG      60834        AGC  GG    A
                                  GGGGAGG   GG  GGAGG G
                                  |||||||   ||  ||||| |
                                  TCCCTCC   CC  CCTCC C
                                      ___  A_    C
GAM2612  DKFZP564C196 3'  GGGGTGGATTTGGGGGAGG   60835     A   GCG
                                  GGGG GGA   GGGGGGAGG
                                  |||| |||   ||||||||
                                  CCCC CCT   CCCCCTCC
                                    A   AAA
GAM2612  DKFZP564D0478 3'  GGGGAGGAGGGGACAGG     60836        GC    G
                                  GGGGAGGA  GGGGG AGG
                                  ||||||||  ||||| |||
                                  CCCCTCCT  CCCCT TCC
                                      __     G
GAM2612  DKFZP564G092 5'  GGGGAGGGTAAAGAGGGAGGAG 60837        AGC_
             C                    GGGGAGG    GGGGGGAGGAGC
                                  |||||||    ||||||||||||
                                  CCCCTCC    TCTCCCTCCTCG
                                      CATT
GAM2612  DKFZP564I1171 3'  AGGGAGGAGCGATCGGGAG   41751          G_
                                  GGGGAGGAGCGG  GGGAG
                                  ||||||||||||  |||||
                                  TCCCTCCTCGCT  CCCTC
                                         AG
GAM2612  DKFZP566C243 3'  GGGGAGGGGTTCTCAAAGGAGC 60838        AGC  GG___
                                  GGGGAGG   GG    GGAGGAGC
                                  |||||||   ||    ||||||||
                                  CCCCTCC   CC    TTTCCTCG
                                      ___  AAGAG
GAM2612  DKFZP586G1122 3'  GAGGAGGGGCGGGCTGGGAG   60839       A    __
                                  GGGGAGG GCGGG  GGGAG
                                  ||||||| |||||  |||||
                                  CTCCTCC CGCCC  CCCTC
                                      C    GA
GAM2612  DKFZP586J1624 3'  GGGGGGTGGCAAGAGGAG    60840     A  A_
                                  GGGG GG  GCGGGGGGAG
                                  |||| ||  ||||||||||
                                  CCCC CC  CGTTCTCCTC
                                    _  AC
GAM2612  DKFZP761F241 5'  GGCGGGGAGCCCGGGGAG    60841    _  A    GG
                                  GG GG GGAGC  GGGGAG
                                  || || |||||  ||||||
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                                CC CC CCTCG  CCCCTC
                                 G  _    GG
GAM2612  DKFZp761G2113 3'  GGGAGGGGAGTGGGGAG     60842       AGC   _  A
                                GGGAGG  GGGG GG GGAG
                                ||||||  |||| || ||||
                                CCCTCC  CCTC CC CCTC
                                   ___   A  _
GAM2612  DKFZp762K222 5'  GGGGAGGGGGCGGGCGGGG   41752       A_   G  A
                                GGGGAGG  GCGGG GG GG
                                |||||||  ||||| || ||
                                CCCCTCC  CGCCC CC CC
                                    CC    G  _
GAM2612  DKFZp762K222 5'  GGGGCGGGCGGGGTGGGGGC   60843     A  A    _  A  A
                                GGGG GG GCGGGG GG GG GC
                                |||| || |||||| || || ||
                                CCCC CC CGCCCC CC CC CG
                                  G  _    A  _  _
GAM2612  DREV1    3'  GGGGGGGTGGGGGGAGG     60844     A  AGC
                                GGGG GG   GGGGGGAGG
                                ||||  ||   |||||||||
                                CCCC CC   CCCCCCTCC
                                  _  CA_
GAM2612  DRIL2    3'  GGGGAGGACTGGGGAGGGC    60845        G GG      A
                                GGGGAGGA C  GGGGAGG GC
                                ||||||||  |  ||||||| ||
                                CCCCTCCT G  CCCCTCC CG
                                    _ A_      _
GAM2612  DT1P1A10  3'  GGGGAGAGGGTGGAGATGG    60846       G  C  _    _
                                GGGGAG AG GG GGGGA GG
                                ||||||  || || |||||  ||
                                CCCCTC TC CC CCTCT CC
                                   _  _  A    A
GAM2612  E1B-AP5   5'  GGGGGAAAGGGGGGGGG     60847     AG   C     A
                                GGGG  GAG GGGGGG GG
                                ||||  |||  ||||||  ||
                                CCCC  TTC CCCCCC CC
                                  CT   _     _
GAM2612  ELOVL1    3'  GGGGAGGGGAGGGCCAG     60848       AGC     A_
                                GGGGAGG   GGGGGG  GG
                                |||||||   ||||||  ||
                                CCCCTCC   CCTCCC  TC
                                   ___      GG
GAM2612  ETR101    3'  GGAGGGGGAAGGGGAG      60849      AGC     A
                                GGAGG   GGGGGG GGAG
                                |||||   |||||| ||||
                                CCTCC   CCTTCC CCTC
                                  C__     _
GAM2612  FBP17     3'  GGGGTGGGGAGGGGGAG     60850      A  AGC     A
                                GGGG GG   GGGGGG GGAG
                                ||||  ||   |||||| ||||
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                                CCCC CC   CCTCCC CCTC
                                  A ____     _
GAM2612 FHX      5' GGGGGAGGAGGGGAGGAGC    60851     A    C
                                GGG GGAG GGGGGGAGGAGC
                                ||| |||| ||||||||||||
                                CCC CCTC CTCCCCTCCTCG
                                  _   _
GAM2612 FLJ00058 5' GGGGAGGGTGGGAGAGG     60852        AGCG
                                GGGGAGG    GGGGGAGG
                                |||||||    ||||||||
                                CCCCTCC    CCCTCTCC
                                   CA__
GAM2612 FLJ00060 5' GGTGGAGGTAGGGGAGGGG    60854    _    _ C     A
                                GG GGAGG AG GGGGGG GG
                                || ||||| || |||||| ||
                                CC CCTCC TC CCCTCC CC
                                 A    A _    _
GAM2612 FLJ00060 5' GGGGAGGGGTTGGGGTGATTGG 60853        AGCG   _ __
                                GGGGAGG    GGGG GA  GG
                                |||||||    |||| ||  ||
                                CCCCTCC    CCCC CT  CC
                                   CCAA    A  AA
GAM2612 FLJ10246 3' GGAGAGGGACAATGGGGAGG   41753        AG  _
                                GGGGAGG  CGG GGGGAGG
                                |||||||  ||| |||||||
                                CCTCTCC  GTT CCCCTCC
                                   CT   A
GAM2612 FLJ10330 5' GGGGGGAGGGGGCCAAGC    60855     A  GCG    AG
                                GGGG GGA   GGGGG  GAGC
                                |||| |||   |||||  ||||
                                CCCC CCT   CCCCC  TTCG
                                  _  ___    GG
GAM2612 FLJ10377 3' GGGGAGGAGCCCAGGAG     60856         GGG
                                GGGGAGGAGC   GGGAG
                                ||||||||||   |||||
                                CCCCTCCTCG   TCCTC
                                     GG_
GAM2612 FLJ10377 3' GGGGGATGGGGAGGAG      60857     A  GCGG
                                GGG GGA    GGGGAGGAG
                                ||| |||    |||||||||
                                CCC CCT    CCCCTCCTC
                                  _  A___
GAM2612 FLJ10748 5' GGGGAGGGGCCGGGAGAGG   60858       A  G
                                GGGGAGG GC GGGGGAGG
                                ||||||| || ||||||||
                                CCCCTCC CG CCCTCTCC
                                   C  G
GAM2612 FLJ10898 3' GGAGAGGAGCGGAGCAGGGGC 60859           G G   A
                                GGGGAGGAGCGGG G AGG GC
                                |||||||||||| | ||| ||
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                                CCTCTCCTCGCCT C TCC CG
                                       _ G   C
GAM2612  FLJ12287  3'  GGGGAGAGGTGAAGGGG     60860       G  CG    A
                                GGGGAG AG  GGGGG GG
                                |||||| ||  ||||| ||
                                CCCCTC TC  CTTCC CC
                                   _  CA    _
GAM2612  FLJ12455  3'  GGGGAGGGGACGGGAGGGGGC  60861        A_      A  A
                                GGGGAGG  GCGGGGGG GG GC
                                |||||||  |||||||| || ||
                                CCCCTCC  TGCCCTCC CC CG
                                    CC       _ _
GAM2612  FLJ12505  5'  GGGGAGCGGCGGCGGGAG    60862       GA   G
                                GGGGAG  GCGG GGGAG
                                ||||||  |||| |||||
                                CCCCTC  CGCC CCCTC
                                   GC    G
GAM2612  FLJ12587  3'  GAGGAGGGGAGGGGAGG     60863       AGC
                                GGGGAGG   GGGGGGAGG
                                |||||||   |||||||||
                                CTCCTCC   CTCCCCTCC
                                    C__
GAM2612  FLJ13055  3'  GGGGAGGAAGGCGAGGGG    60864        __
                                GGGGAGGA  GCGGGGGG
                                ||||||||  ||||||||
                                CCCCTCCT  CGCTCCCC
                                     TC
GAM2612  FLJ13102  3'  GGAGAGCCAAGGGGGAGGAGC  60865     G  __
                                GGAG AGC  GGGGGGAGGAGC
                                |||| |||  ||||||||||||
                                CCTC TCG  TCCCCCTCCTCG
                                  _  GT
GAM2612  FLJ13154  3'  GGGGAGGAGAGACAGGAGG   60866        C  G
                                GGGGAGGAG GG GGGAGG
                                ||||||||| || ||||||
                                CCCCTCCTC CT TCCTCC
                                     T  G
GAM2612  FLJ13189  5'  GGCGGGCGCGGGGAGGAG    60867    A  A   G
                                GG GG GCG GGGGAGGAG
                                || || ||| |||||||||
                                CC CC CGC CCCCTCCTC
                                 G  _   G
GAM2612  FLJ13189  5'  GGAGGGGAGAAGAGGAG     60868      AGC
                                GGAGG   GGGGGGAGGAG
                                |||||   ||||||||||
                                CCTCC   CTCTTCTCCTC
                                  C__
GAM2612  FLJ13265  3'  GGGGGGAGGTGAAGGAG     60869     A   CG
                                GGGG GGAG  GGGGGAG
                                |||| ||||  |||||||
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                                CCCC CCTC  CTTCCTC
                                  _   CA
GAM2612  FLJ13391  5'  GGGGAGAGGTGGGGTGTCAGGA 60870       G  CG   G___
              GC                  GGGGAG AG  GGGG   AGGAGC
                                  |||||| ||  ||||   ||||||
                                  CCCCTC TC  CCCC   TCCTCG
                                    _ CA   ACAG
GAM2612  FLJ14009  3'  GGGGGGGGATGAAAAGAGGAGC  60871      A   GC GG
                                  GGGG GGA  G  GGGAGGAGC
                                  |||| ||| | |||||||||
                                  CCCC CCT  C  TTCTCCTCG
                                    C   A_ TT
GAM2612  FLJ14154  3'  GGGGAGGACCCAAGGAG     60872         G GG
                                  GGGGAGGA C  GGGGAG
                                  |||||||| |  ||||||
                                  CCCCTCCT G  TTCCTC
                                      _ GG
GAM2612  FLJ14466  3'  GGGGAGGAGAGGGGACACAGC  60873          C     AGG
                                  GGGGAGGAG GGGGGG   AGC
                                  ||||||||| ||||||   |||
                                  CCCCTCCTC TCCCCT   TCG
                                       _     GTG
GAM2612  FLJ14596  3'  GGGAAGGGAGGAGGAG      60874       GAGC
                                  GGGAG   GGGGGGAGGAG
                                  |||||   ||||||||||
                                  CCCTT   CCCTCCTCCTC
                                    _____
GAM2612  FLJ14681  3'  GGGTGGGTTGGGGGGGAGC   60875     GA  AGCG    A
                                  GGG  GG   GGGGG GGAGC
                                  |||  ||   ||||| |||||
                                  CCC  CC   CCCCC CCTCG
                                    AC  AA__   _
GAM2612  FLJ14810  3'  GGGGAGAGGTGGGTTCTCTGGG 60876       G  CG   GGA___  A
              C                    GGGGAG AG  GGG     GG GC
                                  |||||| ||  |||     || ||
                                  CCCCTC TC  CCC     CC CG
                                     _ CA   AAGAGA  _
GAM2612  FLJ20254  3'  AGGGAGGGGACAGGGAGGGGC  60877        A_      A  A
                                  GGGGAGG  GCGGGGGG GG GC
                                  |||||||  |||||||| || ||
                                  TCCCTCC  TGTCCCTC CC CG
                                      CC       _ _
GAM2612  FLJ20273  3'  GGGGAGGAGGGGACAGG     60836         GC    G
                                  GGGGAGGA  GGGGG AGG
                                  ||||||||  ||||| |||
                                  CCCCTCCT  CCCCT TCC
                                       __    G
GAM2612  FLJ20337  3'  GGGGGCGGGGTGAAGAAA    60878      AGGA    _
                                  GGGG   GCGGGG GGAGGAG
                                  ||||   |||||| |||||||
```

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                                CCCC   CGCCCC CTTCTTT
                                  ____     A
GAM2612  FLJ20378  5'  GGGGAGGAGAGGGAAAAGG   60879        C   GG
                                GGGGAGGAG GGG  GAGG
                                ||||||||| |||  ||||
                                CCCCTCCTC CCC  TTCC
                                     T   TT
GAM2612  FLJ20406  3'  GGGGCGGGGCGGGGGACGGGC  60880     A  A     GA  A
                                GGGG GG GCGGGGG  GG GC
                                |||| || |||||||  || ||
                                CCCC CC CGCCCCC  CC CG
                                  G  C      TG  _
GAM2612  FLJ21135  5'  GGGGAGGGGGCGGTGAG     60881       AGC   G  AG
                                GGGGAGG   GGG GG  GAG
                                |||||||   ||| ||  |||
                                CCCCTCC   CCC CC  CTC
                                   ___   G  A_
GAM2612  FLJ21324  5'  GGGGAGGGGGTGGGGG      60882       AGC  _  A
                                GGGGAGG   GGG GGG GG
                                |||||||   ||| ||| ||
                                CCCCTCC   CCC CCC CC
                                   ___   A  _
GAM2612  FLJ21438  3'  GGGGGGGGGGGGGAGGG      60883     A  AGC       A
                                GGGG GG   GGGGGGAGG G
                                |||| ||   |||||||| |
                                CCCC CC   CCCCCCTCC C
                                  _  ___       _
GAM2612  FLJ22056  5'  GGGAAGGAGCTTAAGGAG    60884         GG
                                GGGGAGGAGC  GGGGAG
                                ||||||||||  ||||||
                                CCCTTCCTCG  TTCCTC
                                     AA
GAM2612  FLJ22242  5'  GGGGAAGGGTGGGTACAGC   60885       AGC  _  GAGG
                                GGGGAGG   GG GGG   AGC
                                |||||||   || |||   |||
                                CCCCTTC   CC CCC   TCG
                                   ___  A   ATG_
GAM2612  FLJ22393  3'  GGGAAGGGGGAAAGAGGAGC  60886       AGC  GG
                                GGGGAGG   GG  GGAGGAGC
                                |||||||   ||  ||||||||
                                CCCTTCC   CC  TCTCCTCG
                                   C__  TT
GAM2612  FLJ22678  3'  GGGGAGAAGTGGGGTGGGG   60887        C   _  A
                                GGGGAGGAG GGGG GG GG
                                ||||||||| |||| || ||
                                CCCCTCTTC CCCC CC CC
                                     A   A  _
GAM2612  FLJ22679  3'  GGGGTAGGGGAAGAGGGGC   60888     AGG  C       A
                                GGGG   AG GGGGGGAGG GC
                                ||||   || |||||||| ||
```

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                                CCCC   TC CCCTTCTCC CG
                                  A__ _       C
GAM2612  FLJ22679  3'  GGGGTAGGGGAAGAGGGGC   60888     AGG  C       A
                                GGGG   AG GGGGGGAGG GC
                                ||||   || ||||||||| ||
                                CCCC   TC CCCTTCTCC CG
                                  A__ _       C
GAM2612  FLJ23058  3'  GGGAGAAGGGGAGGGG      60889       C     A
                                GGGAGGAG GGGGGG GG
                                |||||||| |||||| ||
                                CCCTCTTC CCCTCC CC

                                   _     _
GAM2612  FLJ23416  3'  GGGGAGGAGAGGGGAGGAG   60890        CG
                                GGGGAGGAG  GGGGGAGGAG
                                |||||||||  ||||||||||
                                CCCCTCCTC  TCCCCTCCTC

                                    __
GAM2612  FLJ23598  5'  GGGTAGGAGCGGGGAAGGAG  60891    G        G
                                GGG AGGAGCGGGGG AGGAG
                                ||| |||||||||| |||||
                                CCC TCCTCGCCCCT TCCTC
                                  A         _
GAM2612  FLJ30213  5'  GGGGTGGGTGGGGGGAGG    41761     A  AGC
                                GGGG GG   GGGGGGAGG
                                |||| ||   |||||||||
                                CCCC CC   CCCCCCTCC
                                  A  CA_
GAM2612  FLJ30213  3'  GGTGGAGGCAGGGGAGGGG   60893   _    _ C     A
                                GG GGAGG AG GGGGGG GG
                                || ||||| || |||||| ||
                                CC CCTCC TC CCCTCC CC
                                 A    G _     _
GAM2612  FLJ30213  3'  GGGGAGGGGTTGGTTGGAGC  60892       AGC  GG  A_
                                GGGGAGG   GG  GG  GGAGC
                                |||||||   ||  ||  |||||
                                CCCCTCC   CC  CC  CCTCG
                                    ____  AA  AA
GAM2612  FLJ30567  3'  GGCGGAGGAGCTCCCCAGGGAG 60894    _      GG___
                                GG GGAGGAGC     GGGGAG
                                || ||||||||     ||||||
                                CC CCTCCTCG     TCCCTC
                                 G       AGGGG
GAM2612  FOXH1     3'  GGGTGGGAGCGGGAGGGAGGAG 60895     GA      _
           C                     GGG  GGAGCGGG GGGAGGAGC
                                |||  |||||||| |||||||||
                                CCC  CCTCGCCC CCCTCCTCG
                                  AC       T
GAM2612  FOXN4     3'  GGGGGAGCGGGCTGGGG     60896     A      G_  A
                                GGG GGAGCGGG  GG GG
                                ||| ||||||||  || ||
```

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                                CCC CCTCGCCC  CC CC
                                  _       GA  _
GAM2612  FOXO3A   5'  GGGGCGGGGAGAAGGGGGAGGG 60898      A__    C        A
                GC                  GGGG   GGAG GGGGGGAGG GC
                                    ||||   |||| ||||||||| ||
                                    CCCC   CCTC TCCCCCTCC CG
                                      GCC    T        C
GAM2612  FOXO3A   5'  GGGGAGGGGCGCCCGGGGGAGG 60897        A  ___       A
                GGC                   GGGGAGG GCG   GGGGGAGG GC
                                    |||||||  |||   |||||||| ||
                                    CCCCTCC CGC   CCCCCTCC CG
                                        C  GGG       C
GAM2612  GABBR1   5'  GGGGAGGAGGGGGGCGAGGGC   60899          C    G    A
                                    GGGGAGGAG GGGG GAGG GC
                                    |||||||||  |||| |||| ||
                                    CCCCTCCTC CCCC CTCC CG
                                        _   G   _
GAM2612  GBTS1    3'  GGGGAGGAAGTGGGTGGG    60900          _ C   _
                                    GGGGAGGA G GGG GGG
                                    ||||||||  | ||| |||
                                    CCCCTCCT C CCC CCC
                                         T A   A
GAM2612  GDF11    5'  GGGGAGGGGAGGGAGG      60901         AGC
                                    GGGGAGG   GGGGGGAGG
                                    |||||||   |||||||||
                                    CCCCTCC   CCTCCCTCC
                                              ___
GAM2612  GEMIN7   3'  GAGGGGAGCACTGGGGAG    60902      A     G_
                                    GGGG GGAGCG  GGGGAG
                                    |||| ||||||  ||||||
                                    CTCC CCTCGT  CCCCTC
                                      _     GA
GAM2612  GNG3     3'  GGAGAGGGAAAAGGGAGGAG   60903         AGC
                                    GGGGAGG   GGGGGGAGGAG
                                    |||||||   ||||||||||
                                    CCTCTCC   TTTCCCTCCTC
                                        CT_
GAM2612  GP5      3'  GGGGAGGGGAGGGAGAG     60904         AGC       G
                                    GGGGAGG   GGGGGGAG AG
                                    |||||||   ||||||||  ||
                                    CCCCTCC   CCTCCCTC TC
                                              ___       _
GAM2612  GS3955   5'  GGGGGGGTGCGGGAGAGGGC   60906      A  A      G   A
                                    GGGG GG GCGGGGG AGG GC
                                    |||| || ||||||| ||| ||
                                    CCCC CC CGCCCTC TCC CG
                                      C  A      _  _
GAM2612  GS3955   5'  GGGGAGGGGACAGAAGAGGGGC 60905         A_      GA  A
                                    GGGGAGG  GCGGGGG  GG GC
                                    |||||||  |||||||  || ||
```

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                                CCCCTCC  TGTCTTC  CC CG
                                    CC      TC  _
GAM2612  GSK3A    3'  GGGGAGGGGGCCAAGGGGG   60907       A_  G    A
                                GGGGAGG  GC GGGGG GG
                                |||||||  || ||||| ||
                                CCCCTCC  CG TTCCC CC
                                    CC  G    _
GAM2612  GTF2A1   5'  GAGGAGGAGGAGGGGGG    60908        C    A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CTCCTCCTC CTCCCC CC
                                  _    _
GAM2612  HAAO     3'  GGGCAGGAGCGGGGCCGGGG  60909    G        __  A
                                GGG AGGAGCGGGG  GG GG
                                ||| ||||||||||  || ||
                                CCC TCCTCGCCCC  CC CC
                                  G        GG  _
GAM2612  HES6     5'  GGGGAGCGGCGGGGACCGGAG  60910      GA     GA
                                GGGGAG  GCGGGGG  GGAG
                                ||||||  |||||||  ||||
                                CCCCTC  CGCCCCT  CCTC
                                    GC      GG
GAM2612  HEYL     3'  GGAGGAGGAGGAGGAGGAG   60911       C
                                GGAGGAG GGGGGGAGGAG
                                ||||||| ||||||||||
                                CCTCCTC TCCTCCTCCTC
                                    C
GAM2612  HNRPA0   5'  GGGGGAGGGAAGGGGAG    60912    A   C    A
                                GGG GGAG GGGGGG GGAG
                                ||| |||| |||||| ||||
                                CCC CCTC CCTTCC CCTC
                                  _   _    _
GAM2612  HRD1     3'  GGGGCCTGGGGGGAGGGGC   60914     AGGAGC       A
                                GGGG     GGGGGGAGG GC
                                ||||     ||||||||| ||
                                CCCC     CCCCCCTCC CG
                                  GGA___        C
GAM2612  HRD1     3'  GGGGAGGGGCGGGGCAGG    60913       A    G G
                                GGGGAGG GCGGG G AGG
                                ||||||| ||||| | |||
                                CCCCTCC CGCCC C TCC
                                    C    _ G
GAM2612  HS6ST1   5'  GGGGCGGGGCCTGGGAGGGGAG 60915   A  A  ____         III
            GAGCG                  G GG GC   GGGGGGAGGAGC   G
                                | || ||   ||||||||||||  |
                                C CC CG   CTCCCCTCCTCG   C
                                 G  C  GACC          III
GAM2612  HSA9947  3'  GGGGTGGTCTCGGGGGAGGAG  60916     A  AGCG
                                GGGG GG   GGGGGAGGAG
                                |||| ||   ||||||||||
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                                CCCC CC    CCCCCTCCTC
                                  A  AGAG
GAM2612  HSPC195   5'  GGGGAGGGGCGGGGCAGGGAGC 60918        A     _ A
                                GGGGAGG GCGGGG GG GGAGC
                                ||||||| |||||| || |||||
                                CCCCTCC CGCCCC TC CCTCG
                                    C     G _
GAM2612  HSPC195   5'  GGGGAGGGGGGGGGAG       60917        AGC
                                GGGGAGG   GGGGGGAG
                                |||||||   ||||||||
                                CCCCTCC   CCCCCCTC
                                          ___
GAM2612  HSRNAFEV  5'  GGGGGGGACGGGGAAGGGGGGC 60919      A  AG    __  A  A
                                GGGG GG  CGGGG  GG GG GC
                                |||| ||  |||||  || || ||
                                CCCC CC  GCCCC  CC CC CG
                                  _ CT    TT  _  C
GAM2612  HU-K4     3'  GGGGAGAGAGCCTGAGGAGC   60920       _   GGGGG
                                GGGGAG GAGC    GAGGAGC
                                |||||| ||||    |||||||
                                CCCCTC CTCG    CTCCTCG
                                   T   GA___
GAM2612  HYPK      5'  GGGGAGGAGGCGGGGCTGG    60921         _    GGA
                                GGGGAGGAG CGGGG   GG
                                ||||||||| |||||   ||
                                CCCCTCCTC GCCCC   CC
                                     C    GA_
GAM2612  ISYNA1    3'  GGGGGGCAGCGGGGAGGAAGAG 60922      A _      _
            C                    GGGG GG AGCGGGG GGAGGAGC
                                |||| || ||||||| ||||||||
                                CCCC CC TCGCCCC CCTTCTCG
                                  _ G      T
GAM2612  KHDRBS3   5'  GAGGAGGAGCGGGCGCGGG    60923          ___
                                GGGGAGGAGCGGG   GGG
                                ||||||||||||   |||
                                CTCCTCCTCGCCC   CCC
                                       GCG
GAM2612  KIAA0125  3'  GGGGAGGTGCACACTGAGGAGC 60924        A   GGGG
                                GGGGAGG GCG    GAGGAGC
                                ||||||| |||    |||||||
                                CCCCTCC CGT    CTCCTCG
                                    A   GTGA
GAM2612  KIAA0144  3'  GGGGAGAGGGAAATGGGGGAGG 60925      ___   CG      A
            GGC                   GGGGA   GGAG  GGGGGAGG GC
                                |||||   ||||  |||||||| ||
                                CCCCT   CCTT  CCCCCTCC CG
                                  CTC    TA      C
GAM2612  KIAA0232  3'  GGGGGTGAGATGGGGAGGAGC  60926     AG   CGG
                                GGGG  GAG   GGGGAGGAGC
                                ||||  |||   ||||||||||
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                                CCCC  CTC   CCCCTCCTCG
                                  CA  TA_
GAM2612 KIAA0275 3' GGAGAGGGCACTGGAGGGGC  60927       A  GGG    A
                                GGGGAGG GCG   GGAGG GC
                                ||||||| |||   ||||| ||
                                CCTCTCC CGT   CCTCC CG
                                   _  GA_    C
GAM2612 KIAA0284 3' GGGGAGGAACAAAGGAG     60928         GGGG
                                GGGGAGGAGCG   GAGGAG
                                ||||||||||    ||||||
                                CCCCTCCTTGT   TTCCTC
                                      ____
GAM2612 KIAA0290 3' GGGGAGGAGCGAATCTCGGGC 60929          GGGA  A
                                GGGGAGGAGCGGG   GG GC
                                ||||||||||||   || ||
                                CCCCTCCTCGCTT   CC CG
                                       AGAG  _
GAM2612 KIAA0450 5' GGAGGGGGATAGGAGGGGC   60930     C   ___    A
                                GGAG GGGG   GGAGG GC
                                |||| ||||   ||||| ||
                                CCTC CCCC   CCTCC CG
                                  _   TAT    C
GAM2612 KIAA0481 3' GGGGTGGGGTGGGGATGCTGAG 60931     A  AGC    GAG_
          C                      GGGG GG   GGGGG   GAGC
                                |||| ||   |||||   ||||
                                CCCC CC   CCCCT   CTCG
                                  A  CCA    ACGA
GAM2612 KIAA0537 5' GGGGAGGGGGAGCGAGGGG   60932      ___
                                GGGGA   GGAGCGGGGGG
                                |||||   ||||||||||
                                CCCCT   CCTCGCTCCCC
                                   CCC
GAM2612 KIAA0552 3' GGGGAGGGGCTGGGCAGG    60933       A  GG   G
                                GGGGAGG GC  GGG AGG
                                ||||||| ||  ||| |||
                                CCCCTCC CG  CCC TCC
                                    C  A_   G
GAM2612 KIAA0552 5' GGGGGGAGGGGAGGGGAGGGGC 60934     A   C  _     A
                                GGGG GGAG GG GGGGAGG GC
                                |||| |||| || ||||||| ||
                                CCCC CCTC CC CCCCTCC CG
                                  _   C  T      C
GAM2612 KIAA0649 5' GGGGAGGCGGCGGGCCGGGGG  60936       A_    __  A
                                GGGGAGG  GCGGG  GGG GG
                                |||||||  |||||  ||| ||
                                CCCCTCC  CGCCC  CCC CC
                                    GC    GG  _
GAM2612 KIAA0649 5' GGGGAGGGGCGCGCAGAGGGGC 60935       A  GGG    A
                                GGGGAGG GCG   GGAGG GC
                                ||||||| |||   ||||| ||
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                                CCCCTCC CGC   TCTCC CG
                                    C   GCG    C
GAM2612  KIAA0657  5'  GGGGGGGGCAGGGGGGG      60937      A  A       A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGTCCCCC CC
                                  _ _       _
GAM2612  KIAA0775  3'  GGAGAGGCCTGGGAGGGG     60938        AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCTCTCC   CCCTCC CC
                                    GGA     _
GAM2612  KIAA0918  3'  GGGGAGGAGAGAAGGAGAGGGG 60939          C    _    A
             C                   GGGGAGGAG GGGGG GAGG GC
                                |||||||| ||||| |||| ||
                                CCCCTCCTC CTTCC CTCC CG
                                     T    T    C
GAM2612  KIAA0930  3'  GGGGAGGAGGGCATCCCAGGAG 60940          C  GGGG__
                                GGGGAGGAG GG     AGGAG
                                ||||||||| ||     |||||
                                CCCCTCCTC CC     TCCTC
                                     _ GTAGGG
GAM2612  KIAA0993  3'  GGGGAGGGAGAGTGTGGGGGGA 60941        _  C____
             G                   GGGGAGG AG    GGGGGGAG
                                ||||||| ||    ||||||||
                                CCCCTCC TC    CCCCCCTC
                                    C  TCACA
GAM2612  KIAA1046  3'  GGGGGGGGGGGGGGGAGGAA   60943     A  AGC
                                GGGG GG   GGGGGGAGGAG
                                |||| ||   ||||||||||
                                CCCC CC   CCCCCCTCCTT
                                  _ CC_
GAM2612  KIAA1046  3'  GGGGGGGGGGGGGGGGGGA   60942     A  AGC     A
                                GGGG GG   GGGGGG GGA
                                |||| ||   |||||| |||
                                CCCC CC   CCCCCC CCT
                                  _ CCC     C
GAM2612  KIAA1075  5'  GGGGAGGATGTGGGGGAGG   60944        GCG
                                GGGGAGGA   GGGGGAGG
                                ||||||||   ||||||||
                                CCCCTCCT   CCCCCTCC
                                     ACA
GAM2612  KIAA1076  3'  GGTGAGGCCAGGGGGAGG    60946    G   AG
                                GG GAGG  CGGGGGGAGG
                                || ||||  ||||||||||
                                CC CTCC  GTCCCCCTCC
                                 A   G_
GAM2612  KIAA1076  3'  GGGGAGGGGTGAGGCAAGG   60945        AGC   G
                                GGGGAGG   GGGG GAGG
                                |||||||   |||| ||||
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                                CCCCTCC   CTCC TTCC
                                    CCA    G
GAM2612 KIAA1077 5' AGGGAGGAGGCAGAGGAGC   60947        GCG  G
                                GGGGAGGA   GG GGAGGAGC
                                ||||||||   || ||||||||
                                TCCCTCCT   CC TCTCCTCG
                                   ___  G
GAM2612 KIAA1100 5' GGGGGAGGGGGGGGGG      60949     A   C     A
                                GGG GGAG GGGGGG GG
                                ||| |||| |||||| ||
                                CCC CCTC CCCCCC CC
                                  _   _    _
GAM2612 KIAA1100 5' GGGGAGGGGGGGGGGG      60948       AGCG    A  A
                                GGGGAGG    GGGGG GG G
                                |||||||    ||||| || |
                                CCCCTCC    CCCCC CC C
                                   ____    _ A
GAM2612 KIAA1100 5' GGGGCAGGGGGGGTGGAGGGGC 60950     _  AGC   _    A
                                GGGG AGG   GGGG GGAGG GC
                                |||| |||   |||| ||||| ||
                                CCCC TCC   CCCC CCTCC CG
                                  G  ___   A    C
GAM2612 KIAA1205 3' GGGGAGGGAGTGGAGGGGG   60951       _ C     A
                                GGGGAGG AG GGGGGG GG
                                ||||||| || |||||| ||
                                CCCCTCC TC CCTCCC CC
                                    C  A    _
GAM2612 KIAA1266 3' AGGGAGGAGGTGGAGGGG    60952        CG    A
                                GGGGAGGAG  GGGGG GG
                                |||||||||  ||||| ||
                                TCCCTCCTC  CCTCC CC
                                     CA    _
GAM2612 KIAA1337 3' GGGGGGGCGGGGTTAGG     60954     A  A     GG
                                GGGG GG GCGGGG  AGG
                                |||| || ||||||  |||
                                CCCC CC CGCCCC  TCC
                                  _ _     AA
GAM2612 KIAA1337 3' GGGGAGGGTTGCGGGGGG    60953       A__
                                GGGGAGG   GCGGGGGG
                                |||||||   ||||||||
                                CCCCTCC   CGCCCCCC
                                   CAA
GAM2612 KIAA1388 5' GGGAGGGAGGAGAGGAG     60955       AGC
                                GGGAGG   GGGGGGAGGAG
                                ||||||   ||||||||||
                                CCCTCC   CTCCTCTCCTC
                                  ___
GAM2612 KIAA1434 3' GGAGAGGAGCAAAGGAG     60956          GGGG
                                GGGGAGGAGCG   GAGGAG
                                ||||||||||    ||||||
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                                CCTCTCCTCGT   TTCCTC
                                      ____
GAM2612 KIAA1437 3' GGGGAGGTGCGAATGGAG   60957       A   G
                                GGGGAGG GCGGG GGAG
                                ||||||| ||||| ||||
                                CCCCTCC CGCTT CCTC
                                    A   A
GAM2612 KIAA1443 5' GGGGGAAGTGGGGGAGAGGGC 60958    A   C   _   A
                                GGGG GGAG GGGGG GAGG GC
                                |||| |||| ||||| |||| ||
                                CCCC CTTC CCCCC CTCC CG
                                  _   A   T   _
GAM2612 KIAA1545 3' GGGGCAGGGCATGGGGGGG   60959    _  A  _   A
                                GGGG AGG GCG GGGGG GG
                                |||| ||| ||| ||||| ||
                                CCCC TCC CGT CCCCC CC
                                  G   _  A   _
GAM2612 KIAA1553 3' GGGGAGGTGGTGGGAGAGGGC 60960       AGCG      A
                                GGGGAGG   GGGGGAGG GC
                                |||||||   |||||||| ||
                                CCCCTCC   CCCTCTCC CG
                                    ACCA      _
GAM2612 KIAA1580 5' GGGGCGGGGGGCGGGGGCGGGGG 60961    A  A_    GA  A
          C                  GGGG GG  GCGGGGG  GG GC
                             |||| ||  |||||||  || ||
                             CCCC CC  CGCCCCC  CC CG
                               G  CC      GC  C
GAM2612 KIAA1580 5' GGGGGGGGGAGGGGAACAGC   60962    A  AGC      G
                                GGGG GG   GGGGGGGAG AGC
                                |||| ||   |||||||| |||
                                CCCC CC   CTCCCCTT TCG
                                  _ C__       G
GAM2612 KIAA1771 5' GGGGGGGGGCAGGAGGGG    60963    A  A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGTCCTCC CC
                                  _ C       _
GAM2612 KIAA1813 5' GGGGAGGGGTAGGCCAGGAGC 60964       AGCG   GG
                                GGGGAGG   GGG  AGGAGC
                                |||||||   |||  ||||||
                                CCCCTCC   TCC  TCCTCG
                                    CCA_   GG
GAM2612 KIAA1867 3' AGGGGGAGGGGAGGAG     60965    A   C
                                GGGG GGAG GGGGGGAG
                                |||| |||| ||||||||
                                TCCC CCTC CCCTCCTC
                                  _   _
GAM2612 KIAA1878 3' GGGCGGGGGGTGGGGAAGC   60966   A      A___
                                GG GCGGGGGG   GGAGC
                                || ||||||||   |||||
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                                CC CGCCCCCC   CTTCG
                                 _      ACCC
GAM2612 KIAA1884 3' GGGGGGCGGGAATAGG     60967    A A     G
                                GGG GG GCGGGGG AGG
                                ||| || ||||||| |||
                                CCC CC CGCCCTT TCC
                                  _ _     A
GAM2612 KIAA1887 5' GAGGAGGAGGCATGAGGGG   60968        _ __
                                GGGGAGGAG C  GGGGGG
                                ||||||||| |  ||||||
                                CTCCTCCTC G  CTCCCC
                                     C TA
GAM2612 KIAA1910 5' GGAGGGGGGCGGAGGG     60969     AGC   _    A
                                GGAGG   GGGG GGAGG G
                                |||||   |||| ||||| |
                                CCTCC   CCCC CCTCC C
                                  ___   G    _
GAM2612 KIAA1938 3' GGGGAGGGGGGGGCATAAGC  60970      AGC    AG_
                                GGGGAGG   GGGGGG   GAGC
                                |||||||   ||||||   ||||
                                CCCCTCC   CCCCCC   TTCG
                                   ___     GTA
GAM2612 KIAA1949 5' GGGGAGGCAAGGAGGGG    60971      AGC    A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   TCCTCC CC
                                   GT_    _
GAM2612 KIAA1949 5' GGGGAGAGGTGGGACACAAAGC 60973     G  CG   GA_
                                GGGGAG AG  GGGG   GGAGC
                                |||||| ||  ||||   |||||
                                CCCCTC TC  CCCT   TTTCG
                                   _ CA   GTG
GAM2612 KIAA1949 5' GGGGAGAGGTGGGACACAAAGC 60973     G  CG   GA_
                                GGGGAG AG  GGGG   GGAGC
                                |||||| ||  ||||   |||||
                                CCCCTC TC  CCCT   TTTCG
                                   _ CA   GTG
GAM2612 KIAA1949 5' GGGGAGGCAAGGAGGGG    60971      AGC    A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   TCCTCC CC
                                   GT_    _
GAM2612 KIAA1949 5' GGGGGAGGGGGTGCGGAGGAGC 60972    A   C   ___
                                GGG GGAG GGGG   GGAGGAGC
                                ||| |||| ||||   ||||||||
                                CCC CCTC CCCC   CCTCCTCG
                                  _   _   ACG
GAM2612 KIAA1949 5' GGGGGAGGGGGTGCGGAGGAGC 60972    A   C   ___
                                GGG GGAG GGGG   GGAGGAGC
                                ||| |||| ||||   ||||||||
```

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                                CCC CCTC CCCC   CCTCCTCG
                                  _   _    ACG
GAM2612  KIAA1949  5'  GGGGGAGGGGGTGCGGAGGAGC 60972     A    C   ___
                                GGG GGAG GGGG   GGAGGAGC
                                ||| |||| ||||   ||||||||
                                CCC CCTC CCCC   CCTCCTCG
                                  _   _    ACG
GAM2612  KIAA1949  5'  GGGGAGAGGTGGGACACAAAGC 60973       G  CG    GA_
                                GGGGAG AG  GGGG   GGAGC
                                |||||| ||  ||||   |||||
                                CCCCTC TC  CCCT   TTTCG
                                    _ CA    GTG
GAM2612  KIAA1949  5'  GGGGAGGCAAGGAGGGG     60971        AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   TCCTCC CC
                                    GT_     _
GAM2612  LANCL2    5'  GGGAGGAGCGGGGCGTCTGAGC 60974            GGAG_
                                GGGAGGAGCGGGG    GAGC
                                ||||||||||||    ||||
                                CCCTCCTCGCCCC    CTCG
                                       GCAGA
GAM2612  LGI4      3'  GGGTAGGAGCGGGTTGAGAGG  60975     G       __
                                GGG AGGAGCGGG  GGGAGG
                                ||| |||||||||  ||||||
                                CCC TCCTCGCCC  CTCTCC
                                  A        AA
GAM2612  MACMARCKS 5'  GGCGGAGGGGTGGGGCTGG   60976    _    AGC  _    A_
                                GG GGAGG   GG GGGG  GG
                                || |||||   || ||||  ||
                                CC CCTCC   CC CCCC  CC
                                 G    ___  A    GA
GAM2612  Magmas    3'  GGGGTGGGCGGGGGGAG     41839      A  A
                                GGGG GG GCGGGGGGAG
                                |||| || ||||||||||
                                CCCC CC CGCCCCCCTC
                                  A  _
GAM2612  MAP2K5    5'  GGGGAGGGAAGAGGGGAGG    60977        AGC
                                GGGGAGG   GGGGGGAGG
                                |||||||   |||||||||
                                CCCCTCC   CTCCCCTCC
                                    CTT
GAM2612  MAP4K3    5'  GGGCAGGGGAGGGGGG      60978     G   AGC     A  A
                                GGG AGG   GGGGGG GG G
                                ||| |||   |||||| || |
                                CCC TCC   CCTCCC CC C
                                  G  ____     _ _
GAM2612  MESDC1    5'  GGGGAGGAGCGCGGGAGG    60979          G   G
                                GGGGAGGAGCG GGG AGG
                                |||||||||| ||| |||
```

```
                                CCCCTCCTCGC CCC TCC
                                      G  _
GAM2612  MGC10433  3'  GGGGATGGGTGGACAGCTGGGG 60980      _ _______  G
              G                  GGGGA GG     AGC GGGGG
                                 ||||| ||     ||| |||||
                                 CCCCT CC     TCG CCCCC
                                    A  CACCTG   A
GAM2612  MGC10471  3'  GGGGAGGATGCGGCATCTGAGC 60981        _   GGGGAG
                                 GGGGAGGA GCGG     GAGC
                                 |||||||| ||||     ||||
                                 CCCCTCCT CGCC     CTCG
                                      A   GTAGA_
GAM2612  MGC10500  5'  GGGGAGCGGCCCACGGGGAG   60982    A     _____
                                 GG GGAGCGG    GGGGAG
                                 || |||||||    ||||||
                                 CC CCTCGCC    CCCCTC
                                  _     GGGTG
GAM2612  MGC10882  3'  GGGGAGGGAAGGGGAG     60983       AGC
                                 GGGGAGG   GGGGGGAG
                                 |||||||   ||||||||
                                 CCCCTCC   TTCCCCTC
                                     C__
GAM2612  MGC10966  5'  GGGGAGGGCACTAGGAG     60984       A   GG
                                 GGGGAGG GCG  GGGAG
                                 ||||||| |||  |||||
                                 CCCCTCC CGT  TCCTC
                                     _  GA
GAM2612  MGC1136   3'  GGGGAGGATGGGTGATCTGGGC 60985        GC  _ GA_  A
                                 GGGGAGGA  GGG GG   GG GC
                                 ||||||||  ||| ||   || ||
                                 CCCCTCCT  CCC CT   CC CG
                                      A_   A  AGA  _
GAM2612  MGC12679  3'  GGGAAGGGCCGGGGGGG     60986       A  G    A
                                 GGGGAGG GC GGGGG GG
                                 ||||||| || ||||| ||
                                 CCCTTCC CG CCCCC CC
                                     _  G    _
GAM2612  MGC14386  5'  GGCGGGGATGGGGGGAG     60988    _ A   GC
                                 GG GG GGA  GGGGGGGAG
                                 || || |||  ||||||||
                                 CC CC CCT  CCCCCCTC
                                  G  _   A_
GAM2612  MGC14386  5'  GGGGAGGCGACTGGGGAG    60987       A_  GG
                                 GGGGAGG  GC  GGGGAG
                                 |||||||  ||  ||||||
                                 CCCCTCC  TG  CCCCTC
                                     GC  A_
GAM2612  MGC15476  3'  GGGGAGAGTGAGGGGGG     60989       G  C     A
                                 GGGGAG AG GGGGGG GG
                                 |||||| || |||||| ||
```

```
                                CCCCTC TC CTCCCC CC
                                   _ A    _
GAM2612 MGC16703 5' GGGGAGGAGACGGGCCTGG   60990        _   G__
                                GGGGAGGAG CGGG   GG
                                ||||||||| ||||   ||
                                CCCCTCCTC GCCC   CC
                                     T   GGA
GAM2612 MGC2668  3' GGGAAGGGGAGGAGGG     60991      AGC      A
                                GGGAGG   GGGGGGAGG G
                                ||||||   ||||||||| |
                                CCCTTC   CCCTCCTCC C
                                   ___       C
GAM2612 MGC2668  3' GGGGAGGAGGGGCAAAG     60993        C  G
                                GGGGAGGAG GGG GGAG
                                ||||||||| ||| ||||
                                CCCCTCCTC CCC TTTC
                                     _  G
GAM2612 MGC2668  3' GGGGGGAGCAGGAGGGG     60992     A       A
                                GGGG GGAGCGGGGGG GG
                                |||| |||||||||| ||
                                CCCC CCTCGTCCTCC CC
                                  _        _
GAM2612 MGC2803  3' GGGCAGGTGGGGGAGGGGC   60994    G  AGCG     A
                                GGG AGG   GGGGGAGG GC
                                ||| |||   |||||||| ||
                                CCC TCC   CCCCCTCC CG
                                  G  A___      C
GAM2612 MGC35558 3' GGGGAGGGGGCTGGGGAG    60995      A_ GG
                                GGGGAGG  GC  GGGGAG
                                |||||||  ||  ||||||
                                CCCCTCC  CG  CCCCTC
                                    CC  A_
GAM2612 MGC35558 3' GGGAAGGGGTGTAAGGAG    60996      AGC  GGG
                                GGGGAGG   GG   GAGGAG
                                |||||||   ||   ||||||
                                CCCTTCC   CC   TTCCTC
                                    ___  ACA
GAM2612 MGC4172  3' GGTGGGGAGGGAAGGAGGAGC 60997   _ A   C
                                GG GG GGAG GGGGGGAGGAGC
                                || || |||| ||||||||||||
                                CC CC CCTC CCTTCCTCCTCG
                                 A  _   _
GAM2612 MGC4342  3' AGGGAGCGGGGAGGGG      60998   A       A  A
                                GG GGAGCGGGGGG GG G
                                || |||||||||| || |
                                TC CCTCGCCCCTC CC C
                                  _        _ _
GAM2612 MGC4415  3' GGGGAGGGTGGAGATGAGG   60999      AGC   _
                                GGGGAGG   GGGGG GAGG
                                |||||||   ||||| ||||
```

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                                CCCCTCC  CCTCT CTCC
                                   CA_    A
GAM2612  MGC4737  3'  GGAGAGGGCTGGGAGGGG   61000       A _    A
                                GGGGAGG GC GGGGGG GG
                                ||||||| || |||||| ||
                                CCTCTCC CG CCCTCC CC
                                   _ A    _
GAM2612  MIC2L1   5'  GGCGGAGGGCCCCGGAGGAGC  61001   _   A GGGG
                                GG GGAGG GC   GGAGGAGC
                                || ||||| ||   ||||||||
                                CC CCTCC CG   CCTCCTCG
                                 G    _ GGG_
GAM2612  MIC2L1   5'  GAGGAGGAGCGGGAGGAGGAGC 61002
                                GGGGAGGAGCGGGGGGAGGAGC
                                |||||||||||||||||||||
                                CTCCTCCTCGCCCTCCTCCTCG

GAM2612  MOST2    5'  GGGGAGGTGGGGGGAGGAG   61003       AGC
                                GGGGAGG  GGGGGGAGGAG
                                |||||||  ||||||||||
                                CCCCTCC  CCCCCCTCCTC
                                   A__
GAM2612  MSTP033  3'  GGGGAGGGGTGGAGAA     61004       AGC  GG
                                GGGGAGG  GG  GGAGGA
                                |||||||  ||  ||||||
                                CCCCTCC  CC  CCTCTT
                                   ___  A_
GAM2612  MYT1     5'  GGGGAGGAGAGGGAAGG     61005       CG
                                GGGGAGGAG  GGGGGAGG
                                |||||||||  ||||||||
                                CCCCTCCTC  TCCCTTCC
                                    __
GAM2612  NAV1     3'  GGAGAGGGGAGAGGAGGAGC  61006       AGC
                                GGGGAGG  GGGGGGAGGAGC
                                |||||||  ||||||||||||
                                CCTCTCC  CTCTCCTCCTCG
                                   C__
GAM2612  NBL1     3'  GAGGAAGAGTTGGGGGGG    61007       CG    A
                                GGGGAGGAG  GGGGG GG
                                |||||||||  ||||| ||
                                CTCCTTCTC  CCCCC CC
                                    AA    _
GAM2612  NDRG4    5'  GGCGGGGAGCGGGGCTTCGG  61008   _ A      GGA_
                                GG GG GGAGCGGGGG   GG
                                || || |||||||||   ||
                                CC CC CCTCGCCCC    CC
                                 G _       GAAG
GAM2612  NECL1    3'  GGGGAGCAAGCGGGAGGGG   61010      _       A
                                GGGGAG GAGCGGGGGG GG
                                |||||| |||||||||| ||
```

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                                CCCCTC TTCGCCCTCC CC
                                   G        _
GAM2612 NECL1    3' GGGGTGGGTGGGCTGGGGAGC 61009     A AGC  G_ A
                                GGGG GG  GGG  GG GGAGC
                                |||| ||  |||  || |||||
                                CCCC CC  CCC  CC CCTCG
                                  A CA_  GA  _
GAM2612 nexilin  3' GGGAGAGGGGAGGGGAG    61011      G C    A
                                GGGAG AG GGGGGG GGAG
                                ||||| || |||||| ||||
                                CCCTC TC CCCTCC CCTC
                                  _ _    _
GAM2612 NIN283   5' GGGGAGGGCTGGGCGAG    61012       A G  G
                                GGGGAGG GC GGG GAG
                                ||||||| || ||| |||
                                CCCCTCC CG CCC CTC
                                   _ A  G
GAM2612 NLI-IF   5' GGGGAGGGGTGGGAGGGAGG  41804       AGC_
                                GGGGAGG   GGGGGGAGG
                                |||||||   |||||||||
                                CCCCTCC   CCTCCCTCC
                                   CCAC
GAM2612 NLI-IF   5' GGGGGGGAGGGGAGGGG    41803     A  C    A
                                GGGG GGAG GGGGGG GG
                                |||| |||| |||||| ||
                                CCCC CCTC CCCTCC CC
                                  C  _    _
GAM2612 NLI-IF   3' GGTGGGGCAGGGGGAGGGGC  61013   GA A       A
                                GG  GG GCGGGGGGAGG GC
                                ||  || |||||||||| ||
                                CC  CC CGTCCCCCTCC CG
                                 AC _        C
GAM2612 NR4A3    5' GGGGAGCGGAGGAGGAG    61014   A       G
                                GG GGAGCGGGGG AGGAG
                                || |||||||||| |||||
                                CC CCTCGCCTCC TCCTC
                                  _       _
GAM2612 NR6A1    5' GGGGAGGAGGTTGTCAGGAGC 61015       CGGGGGG
                                GGGGAGGAG     AGGAGC
                                |||||||||     ||||||
                                CCCCTCCTC     TCCTCG
                                   CAACAG_
GAM2612 NR6A1    5' GGGGAGGAGGTTGTCAGGAGC 61015       CGGGGGG
                                GGGGAGGAG     AGGAGC
                                |||||||||     ||||||
                                CCCCTCCTC     TCCTCG
                                   CAACAG_
GAM2612 NR6A1    5' GGGGAGGAGGTTGTCAGGAGC 61015       CGGGGGG
                                GGGGAGGAG     AGGAGC
                                |||||||||     ||||||
```

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                                CCCCTCCTC      TCCTCG
                                     CAACAG_
GAM2612 OBTP     3' GGGGAGGAGCGCGGCCCGG   61016          G  GGA
                                GGGGAGGAGCG GG   GG
                                |||||||||| ||   ||
                                CCCCTCCTCGC CC   CC
                                      G  GGG
GAM2612 OCIA     5' GGGGAGGGGGAGGGG      60578       AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   CCCTCC CC
                                   ___    _
GAM2612 OLIG1    3' GGGTGGGGGCGGGGAAGG    61017     GA  A      G
                                GGG  GG GCGGGGG AGG
                                |||  || ||||||| |||
                                CCC  CC CGCCCCT TCC
                                  AC  C      _
GAM2612 OSBPL7   3' GGGGTGGAGGCAGGAGGAG   61018      A   _
                                GGGG GGAG CGGGGGGAG
                                |||| |||| |||||||||
                                CCCC CCTC GTCCTCCTC
                                  A   C
GAM2612 OSMR     5' GGGGACGGGCGGGTCGGGGG  61019       _ A    __  A
                                GGGGA GG GCGGG  GGG GG
                                ||||| || |||||  ||| ||
                                CCCCT CC CGCCC  CCC CC
                                   G  _    AG  _
GAM2612 P66      3' GGGGGGCAGTGGGAAG      61020     A  A   G
                                GGG GG GCGG GGGAGG
                                ||| || |||| ||||||
                                CCC CC CGTC CCCTTC
                                  _ _   A
GAM2612 PAK7     5' GGGTAGGGGCAAGGGGGG    61021     G   A      A
                                GGG AGG GCGGGGGGG GG
                                ||| ||| |||||||| ||
                                CCC TCC CGTTCCCC CC
                                  A   C      _
GAM2612 PALM     5' GGGGAGGGGAGGGGGACGC   61022        AGC     A  _
                                GGGGAGG   GGGGGG GGA GC
                                |||||||   |||||| ||| ||
                                CCCCTCC   CCTCCC CCT CG
                                   ___    _  G
GAM2612 PCANAP7  5' GGAGGCTCTGTGGGGGAGGGGC 61023       AGCG__      A
                                GGAGG     GGGGGAGG GC
                                |||||     |||||||| ||
                                CCTCC     CCCCCTCC CG
                                   GAGACA       C
GAM2612 PCYT2    3' GGGGAGGGCCGGCCAGGGC   61024        A  G  GGG   A
                                GGGGAGG GC GG   AGG GC
                                ||||||| || ||   ||| ||
```

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                                CCCCTCC CG CC   TCC CG
                                    _ G GG_  _
GAM2612 PDGFC    5' GGGGTGGGGACGCGGGGGAG  61025     A_ AG _
                                GGGG GG CG GGGGGAG
                                |||| || || |||||||
                                CCCC CC GC CCCCCTC
                                  AC CT G
GAM2612 PDZD2    3' GAGGAGGAGTGGCCAGAG    61026        C GG
                                GGGGAGGAG GG GGAG
                                ||||||||| || ||||
                                CTCCTCCTC CC TCTC
                                     A GG
GAM2612 PFTK1    3' GGGAGGGAGTGAGAGGGG    61027    GA  C    A
                                GGG GGAG GGGGGG GG
                                ||| |||| |||||| ||
                                CCC CCTC CTCTCC CC
                                  TC  A    _
GAM2612 PI15     5' GGGGGGGGGGGGGGAA      61028     A AGC    A
                                GGGG GG  GGGGGG GGAG
                                |||| ||  |||||| ||||
                                CCCC CC  CCCCCC CCTT
                                  _ ___    _
GAM2612 PILR(ALPHA) 5' GGAGAGGGGCCCTGTGGAGGGG 61029       A GGGG_   A
          C                      GGGGAGG GC    GGAGG GC
                                ||||||| ||    ||||| ||
                                CCTCTCC CG    CCTCC CG
                                    C GGACA   C
GAM2612 PILR(BETA) 5' GGAGAGGGGCCCTGTGGAGGGG 61029       A GGGG_   A
          C                      GGGGAGG GC    GGAGG GC
                                ||||||| ||    ||||| ||
                                CCTCTCC CG    CCTCC CG
                                    C GGACA   C
GAM2612 PISD     3' GGTGATGGGGGGAGGAG     61030   AG GC
                                GG GA GGGGGGAGGAG
                                || || ||||||||||
                                CC CT CCCCCCTCCTC
                                 A_ A_
GAM2612 PMF1     3' GGAGGGGGGCGGAGGG      60969     AGC  _   A
                                GGAGG  GGGG GGAGG G
                                |||||  |||| ||||| |
                                CCTCC  CCCC CCTCC C
                                   ___  G   C
GAM2612 PP2447   3' GGGTGGGCTGGGGGAGG     61031    A A G
                                GGG GG GC GGGGGAGG
                                ||| || || ||||||||
                                CCC CC CG CCCCCTCC
                                  A _ A
GAM2612 PPM1A    5' GGGGCGGAGGAGGGGAGGAGCG 61032     A  C        III
                                GGGG GGAG GGGGGGAGGAGC  G
                                |||| |||| ||||||||||||  |
```

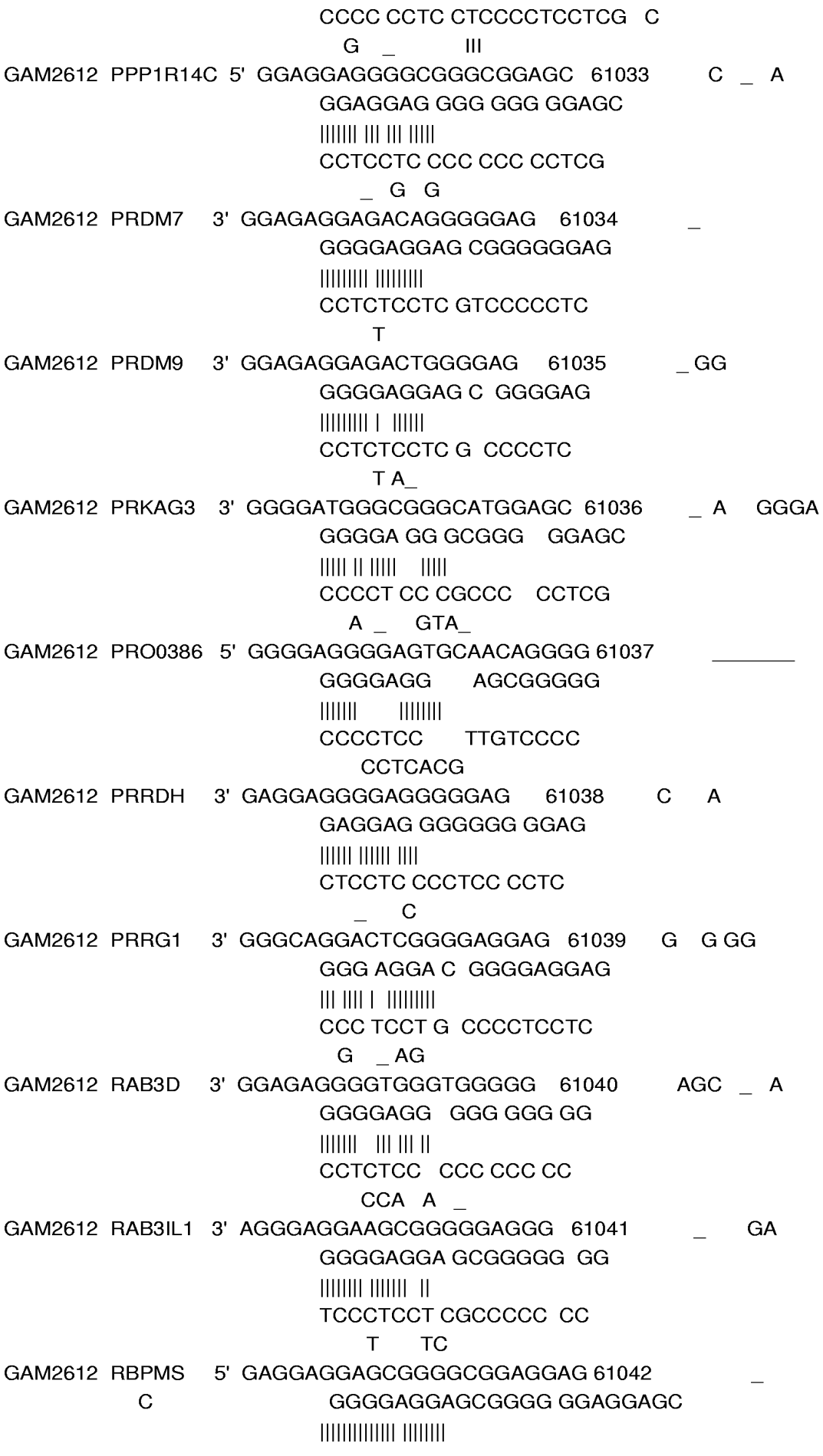
CCCC CCTC CTCCCCTCCTCG C
G _ III
GAM2612 PPP1R14C 5' GGAGGAGGGGCGGGCGGAGC 61033 C _ A
GGAGGAG GGG GGG GGAGC
||||||| ||| ||| |||||
CCTCCTC CCC CCC CCTCG
_ G G
GAM2612 PRDM7 3' GGAGAGGAGACAGGGGGAG 61034 _
GGGGAGGAG CGGGGGGAG
||||||||| |||||||||
CCTCTCCTC GTCCCCCTC
T
GAM2612 PRDM9 3' GGAGAGGAGACTGGGGAG 61035 _ GG
GGGGAGGAG C GGGGAG
||||||||| | ||||||
CCTCTCCTC G CCCCTC
T A_
GAM2612 PRKAG3 3' GGGGATGGGCGGGCATGGAGC 61036 _ A GGGA
GGGGA GG GCGGG GGAGC
||||| || ||||| |||||
CCCCT CC CGCCC CCTCG
A _ GTA_
GAM2612 PRO0386 5' GGGGAGGGGAGTGCAACAGGGG 61037 _____
GGGGAGG AGCGGGGG
||||||| ||||||||
CCCCTCC TTGTCCCC
CCTCACG
GAM2612 PRRDH 3' GAGGAGGGGAGGGGGAG 61038 C A
GAGGAG GGGGGG GGAG
|||||| |||||| ||||
CTCCTC CCCTCC CCTC
_ C
GAM2612 PRRG1 3' GGGCAGGACTCGGGGAGGAG 61039 G G GG
GGG AGGA C GGGGAGGAG
||| |||| | |||||||||
CCC TCCT G CCCCTCCTC
G _ AG
GAM2612 RAB3D 3' GGAGAGGGGTGGGTGGGGG 61040 AGC _ A
GGGGAGG GGG GGG GG
||||||| ||| ||| ||
CCTCTCC CCC CCC CC
CCA A _
GAM2612 RAB3IL1 3' AGGGAGGAAGCGGGGGAGGG 61041 _ GA
GGGGAGGA GCGGGGG GG
|||||||| ||||||| ||
TCCCTCCT CGCCCCC CC
T TC
GAM2612 RBPMS 5' GAGGAGGAGCGGGGCGGAGGAG 61042 _
C GGGGAGGAGCGGGG GGAGGAGC
|||||||||||||| ||||||||

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                                CTCCTCCTCGCCCC CCTCCTCG
                                       G
GAM2612  REPRIMO   3'  GGGGGGAGCAGGAGAAGA    61043      A
                                GGGG GGAGCGGGGGGAGG
                                |||| ||||||||||||||
                                CCCC CCTCGTCCTCTTCT
                                  _
GAM2612  RFX3      5'  GGAGGAGGAGGAGAGGAG    61044        C
                                GGAGGAG GGGGGGAGGAG
                                ||||||| ||||||||||
                                CCTCCTC CTCCTCTCCTC
                                   _
GAM2612  RFX3      5'  GGAGGAGGAGGAGAGGAG    61044        C
                                GGAGGAG GGGGGGAGGAG
                                ||||||| ||||||||||
                                CCTCCTC CTCCTCTCCTC
                                   _
GAM2612  RGS19     5'  GGGTGGGGGCAGGAGGGG    61045     GA  A       A
                                GGG  GG GCGGGGGG GG
                                |||  || ||||||| ||
                                CCC  CC CGTCCTCC CC
                                  AC  C       _
GAM2612  RHOBTB2   3'  GGGGAGGGCCCTGAGGAGC   61046        A  GGGGG
                                GGGGAGG GC    GAGGAGC
                                ||||||| ||    |||||||
                                CCCCTCC CG    CTCCTCG
                                   _  GGA__
GAM2612  RLUCL     5'  GGTGGGGGCGGGGAGGGGC   61047    _  A  A      A  A
                                GG GG GG GCGGGGGG GG GC
                                || || || |||||||| || ||
                                CC CC CC CGCCCCTC CC CG
                                 A  _ _       _ _
GAM2612  RNF2      5'  GGGGAGGGCGGGAAGGAGC   61048        A    GG
                                GGGGAGG GCGGG  GAGGAGC
                                ||||||| |||||  |||||||
                                CCCCTCC CGCCC  TTCCTCG
                                   _    ___
GAM2612  RPL36     3'  GGAGAGGGCAGGGGAGGGGC  61049        A     GA  A
                                GGGGAGG GCGGGGG  GG GC
                                ||||||| |||||||  || ||
                                CCTCTCC CGTCCCC  CC CG
                                   _      TC  _
GAM2612  RPL36     3'  GGAGAGGGCAGGGGAGGGGC  61049        A     GA  A
                                GGGGAGG GCGGGGG  GG GC
                                ||||||| |||||||  || ||
                                CCTCTCC CGTCCCC  CC CG
                                   _      TC  _
GAM2612  SAST      5'  GGGGAGAAGTTTCGGGGG    61050          ____
                                GGGGAGGAG   CGGGGG
                                |||||||||   ||||||
```

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                                CCCCTCTTC  GCCCCC
                                     AAA
GAM2612 SCAMP-4  3' GGGGAGGGGTGGGGTGGGG  41818      AGC  _ A
                                GGGGAGG  GGGG GG GG
                                |||||||  |||| || ||
                                CCCCTCC  CCCC CC CC
                                   CCA  A _
GAM2612 SCOP     5' GGGGAAGCGGGAGGGG     61051    A       A
                                GGG GGAGCGGGGGG GG
                                ||| ||||||||||| ||
                                CCC CTTCGCCCTCC CC
                                  _       _
GAM2612 SCYA22   3' GGGGGGGGGTGGGGAGA     61052    A AGC _
                                GGGG GG  GG GGGGAGG
                                |||| ||  || |||||||
                                CCCC CC  CC CCCCTCT
                                  _ ___ A
GAM2612 SCYA4    5' GGGGGGGGGGGGGGGGGGGA   60942    A AGC    A
                                GGGG GG  GGGGGG GGA
                                |||| ||  |||||| |||
                                CCCC CC  CCCCCC CCT
                                  _ CCC    C
GAM2612 SCYA4    5' GGGGGGGGGGGGGGGGGGAA   61053    A AGC    A
                                GGGG GG  GGGGGG GGAG
                                |||| ||  |||||| ||||
                                CCCC CC  CCCCCC CCTT
                                  _ CCC    _
GAM2612 SCYB5    5' GGTGGAGGAGCGGAGATTGGAG 61054   _        ___
           GAGC                    GG GGAGGAGCGGGG  GGAGGAGC
                                || ||||||||||||  ||||||||
                                CC CCTCCTCGCCTC  CCTCCTCG
                                 A         TAA
GAM2612 SDC3     5' AGGGGGAGCACCGAGGGG    61055    A   ___
                                GGGG GGAGC  GGGGGG
                                |||| |||||  ||||||
                                TCCC CCTCG  CTCCCC
                                  _   TGG
GAM2612 SE70-2   5' GGTGGAGGTGGGGGGAG    61056   _   AGC
                                GG GGAGG  GGGGGGAG
                                || |||||  ||||||||
                                CC CCTCC  CCCCCCTC
                                 A   A__
GAM2612 SEMA3B   5' GGGAGGCTAGGGGGGGAG   61057     AGC    A
                                GGGAGG  GGGGGG GGAG
                                ||||||  |||||| ||||
                                CCCTCC  TCCCCC CCTC
                                   GA_    _
GAM2612 SEMA6A   5' GGGGGGCGGGGTGGGGGC   61058    A A    _ A A
                                GGG GG GCGGGG GG GG GC
                                ||| || |||||| || || ||
```

```
                                CCC CC CGCCCC CC CC CG
                                  _ _     A _ _
GAM2612 SENP8    3' GGGAAGGGCAGAAAGAGGAGC 61059       A    GG
                                GGGGAGG GCGG  GGAGGAGC
                                ||||||| ||||  ||||||||
                                CCCTTCC CGTC  TCTCCTCG
                                   _    TT
GAM2612 SEPT6    5' GGGGAGGTGCAAGGGAGGGGC 61060       A      GA A
                                GGGGAGG GCGGGGG  GG GC
                                ||||||| |||||||  || ||
                                CCCCTCC CGTTCCC  CC CG
                                    A      TC _
GAM2612 SERPINA1 3' AGGGGAGGGGTTGAGGAGC   61061     A   C   GG
                                GGG GGAG GGG  GAGGAGC
                                ||| |||| |||  |||||||
                                TCC CCTC CCC  CTCCTCG
                                  _   _  AA
GAM2612 SFXN5    3' GGGAAGGGGTGGGTAGG     61062       AGC _   G
                                GGGGAGG   GG GGG AGG
                                |||||||   || ||| |||
                                CCCTTCC   CC CCC TCC
                                    ___ A   A
GAM2612 SFXN5    3' GGGGAGGGCGGGAAGGG     41822       A       A
                                GGGGAGG GCGGGGGG GG
                                ||||||| |||||||| ||
                                CCCCTCC CGCCCTTC CC
                                   _      _
GAM2612 SLC2A12  3' GGGGAGGAGGGGGATTAAAGG 61063        C    ___
                                GGGGAGGAG GGGGG   GAGG
                                ||||||||| |||||   ||||
                                CCCCTCCTC CCCCT   TTCC
                                    _    AAT
GAM2612 SNRPD1   5' GGGGGGGGGGGGGGAA      61028     A AGC     A
                                GGGG GG   GGGGGG GGAG
                                |||| ||   |||||| ||||
                                CCCC CC   CCCCCC CCTT
                                  _ ___     _
GAM2612 SNTA1    5' GGGGAGGAGCTCTGGGGG    61064         G__
                                GGGGAGGAGC   GGGGG
                                ||||||||||   |||||
                                CCCCTCCTCG   CCCCC
                                     AGA
GAM2612 SOX17    5' GGGGAGGGGGTGGGGAATGAG 61065       AGC _    _
                                GGGGAGG   GG GGGGAG GAG
                                |||||||   || |||||| |||
                                CCCCTCC   CC CCCCTT CTC
                                    C__ A     A
GAM2612 SPATA6   5' GGGGAGGGGCGGCGGGGAG   41824       A   _
                                GGGGAGG GCGG GGGGAG
                                ||||||| |||| ||||||
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                                CCCCTCC CGCC CCCCTC
                                    C   G
GAM2612  SPRY4    3'  AGGGAGGGAGAAGGAGGGGC  10464       AGC       A
                                GGGGAGG  GGGGGGAGG GC
                                |||||||  ||||||||| ||
                                TCCCTCC  TCTTCCTCC CG
                                    C__       C
GAM2612  SR-BP1   3'  GGGGAGGAGGTGGGAAG    61066        CGG
                                GGGGAGGAG  GGGGAG
                                |||||||||  ||||||
                                CCCCTCCTC  CCCTTC
                                     CA_
GAM2612  SRF      3'  GGGGAGGAGGGGGGGTGGGGC  61067        C    GA  A
                                GGGGAGGAG GGGGG  GG GC
                                ||||||||| |||||  || ||
                                CCCCTCCTC CCCCC  CC CG
                                    _    AC  _
GAM2612  SSH-3    3'  GGGGCGGGGGGTGGGAGG    61068     A  AGC  _
                                GGGG GG  GGG GGGAGG
                                |||| ||  ||| ||||||
                                CCCC CC  CCC CCCTCC
                                  G ___  A
GAM2612  STRN3    5'  GGAGAGGGGCGGGGAAGG    61069       A     G
                                GGGGAGG GCGGGGG AGG
                                ||||||| ||||||| |||
                                CCTCTCC CGCCCCT TCC
                                    C     _
GAM2612  STX1B2   3'  GGGGATGGAGTGAAAGGGG   41828      _   C GG  A
                                GGGGA GGAG G  GGG GG
                                ||||| |||| |  ||| ||
                                CCCCT CCTC C  TCC CC
                                  A   A TT  _
GAM2612  SV2      5'  GGGAAGGGACAGGGGGAG    61071       AG
                                GGGGAGG  CGGGGGGAG
                                |||||||  |||||||||
                                CCCTTCC  GTCCCCCTC
                                    CT
GAM2612  SV2      5'  GGGAAGGGGAAGGGGAG     61070       AGC     A
                                GGGGAGG  GGGGGG GGAG
                                |||||||  |||||| ||||
                                CCCTTCC  CCTTCC CCTC
                                   ___     _
GAM2612  SYT12    3'  GGAGAGGGCAGGGGGGGAG   61072       A      A
                                GGGGAGG GCGGGGGG GGAG
                                ||||||| |||||||| ||||
                                CCTCTCC CGTCCCCC CCTC
                                   _     _
GAM2612  T1A-2    5'  GGGGGGGCCGGAGGGG      61073     A  A  G    A
                                GGGG GG GC GGGGG GG
                                |||| || || ||||| ||
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                                CCCC CC CG CCTCC CC
                                  _ _ G    _
GAM2612 TEKT3    5' GGCGAGGGGCGGGAAGGGGC  61074    G   A      A A
                                GG GAGG GCGGGGGG GG GC
                                || |||| |||||||| || ||
                                CC CTCC CGCCCTTC CC CG
                                 G   C      _ _
GAM2612 THG-1    5' GGGGAGGTGGCGGGAGGGGGGA 61075       A_    _  A
             GC                   GGGGAGG  GCGGG GGG GGAGC
                                |||||||  ||||| ||| |||||
                                CCCCTCC  CGCCC CCC CCTCG
                                   AC    T  C
GAM2612 TLN2     3' GGGGAGGCGGCAGAGGAG    61076       AGCG  G
                                GGGGAGG   GG GGAGGAG
                                |||||||   || |||||||
                                CCCCTCC   CC TCTCCTC
                                   G___  G
GAM2612 TNKS1BP1 3' GGGAAGGTGTGGGGGGAG    61077       AGC
                                GGGGAGG   GGGGGGAG
                                |||||||   ||||||||
                                CCCTTCC   CCCCCCTC
                                   ACA
GAM2612 TNRC6    3' AAAAAGGGGCGGGGGGGGG   61078       A      A
                                GGGGAGG GCGGGGGG GG
                                ||||||| |||||||| ||
                                TTTTTCC CGCCCCCC CC
                                   C      C
GAM2612 TRIAD3   3' GGGGATGCGAGGGGAGGGGC  61079     GGA        A
                                GGGGA  GCGGGGGGAGG GC
                                |||||  |||||||||| ||
                                CCCCT  CGCTCCCCTCC CG
                                  A__         C
GAM2612 TRIM28   5' GGGGAGGAGGGGCGCGGGG   61080       ___  G
                                GGGGAGGA  GCG GGGG
                                ||||||||  ||| ||||
                                CCCCTCCT  CGC CCCC
                                    CCC  G
GAM2612 TUB      3' GGGGGGAAGTGGGGAGGGC   61081     A  CGG     A
                                GGGG GGAG  GGGGAGG GC
                                |||| ||||  ||||||| ||
                                CCCC CCTT  CCCCTCC CG
                                  _   CA_     _
GAM2612 U2AF65   3' GGGGCGGGAGTGGGGAGAAG  61082     A_   C
                                GGGG  GGAG GGGGGGAGG
                                ||||  |||| |||||||||
                                CCCC  CCTC CCCCTCTTC
                                  GC   A
GAM2612 UNC93B1  3' GGGGAGGGGAGACAGGGGC   61083       AGC    G  A
                                GGGGAGG   GGGGG AGG GC
                                |||||||   ||||| ||| ||
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                                CCCCTCC  CCTCT TCC CG
                                   ___   G  C
GAM2612 VPS4A    3' GGGGGGAGGCAGAAGGAGC  61084    A  GC  G
                                GGGG GGA  GG GGGAGGAGC
                                |||| |||  || |||||||||
                                CCCC CCT  CC TCTTCCTCG
                                  _  __ G
GAM2612 WAC      5' GGGGAGGGGGGGAGAG     61085      AGC
                                GGGGAGG  GGGGGGAG
                                |||||||  ||||||||
                                CCCCTCC  CCCCTCTC
                                   ___
GAM2612 WAC      5' GGGGAGGGGGGGAGAG     61085      AGC
                                GGGGAGG  GGGGGGAG
                                |||||||  ||||||||
                                CCCCTCC  CCCCTCTC
                                   ___
GAM2612 WBSCR18  3' GGGGAGGGCAGGGGGAG    61086      A
                                GGGGAGG GCGGGGGGAG
                                ||||||| |||||||||
                                CCCCTCC CGTCCCCCTC
                                   _
GAM2612 ZD52F10  3' GGGGGCCAAGGGGAGGAGC  61087    A AG
                                GGG GG  CGGGGGGAGGAGC
                                ||| ||  |||||||||||||
                                CCC CC  GTTCCCCTCCTCG
                                  _ G_
GAM2612 ZFP36L2  5' GGGCGAGGGGCGGGGAGGGGC 61088   _  A     A A
                                GGG GAGG GCGGGGGG GG GC
                                ||| |||| |||||||| || ||
                                CCC CTCC CGCCCCTC CC CG
                                  G   C     _ _
GAM2612 ZNF304   3' GGGGGGGGGGGGAAG      61089    A AGC
                                GGGG GG  GGGGGGAGG
                                |||| ||  |||||||||
                                CCCC CC  CCCCCCTTC
                                   _ ___
GAM2612 LOC115110 5' GGGGAGGAGGTGGGGAAAG  61090       CG
                                GGGGAGGAG  GGGGGAGG
                                |||||||||  ||||||||
                                CCCCTCCTC  CCCCTTTC
                                     CA
GAM2612 LOC115110 5' GGGGAGGCGGGGGGAG    61091      GA
                                GGGGAG  GCGGGGGGAG
                                ||||||  ||||||||||
                                CCCCTC  CGCCCCCCTC
                                   __
GAM2612 LOC115129 3' GGGGAGGAGGGATCTGAG  61092       C  GG_
                                GGGGAGGAG GGG  GAG
                                ||||||||| |||  |||
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                                CCCCTCCTC CCT   CTC
                                     _  AGA
GAM2612  LOC115207 3'  GGCGAGGGGGTCTGGGGAGC  61093   G   AGC  G__  A
                                GG GAGG  GGG  GG GGAGC
                                || ||||  |||  || |||||
                                CC CTCC  CCC  CC CCTCG
                                 G   ___  AGA  _
GAM2612  LOC116113 3'  GGGCAGGAGCGGAAGGGAGG  61095    G      _
                                GGG AGGAGCGGG GGGAGG
                                ||| ||||||||| ||||||
                                CCC TCCTCGCCT CCCTCC
                                  G       T
GAM2612  LOC116113 3'  GGGAGGGGGCGGAGGG     61094      AGC  G   A
                                GGGAGG  GGG GGAGG G
                                ||||||  ||| ||||| |
                                CCCTCC  CCC CCTCC C
                                   ___  G   _
GAM2612  LOC116113 3'  GGGGGCGGCTGGAGGAG    61096    AGGA   GG
                                GGGG   GCGG  GGAGGAG
                                ||||   ||||  |||||||
                                CCCC   CGCC  CCTCCTC
                                   _____  GA
GAM2612  LOC118611 3'  GGGGCGGGGCAGGAGGAG   61097    A  A
                                GGGG GG GCGGGGGGAG
                                |||| || ||||||||||
                                CCCC CC CGTCCTCCTC
                                  G  C
GAM2612  LOC118672 5'  GGGGAGACCGGAGGAG     61098      GA  G
                                GGGGAG  GC GGGGGAG
                                ||||||  || |||||||
                                CCCCTC  TG CCTCCTC
                                   __  G
GAM2612  LOC123591 5'  GGGGCGGGGTGGGGAGGA   61100    A  AGC  _
                                GGGG GG  GG GGGGAGGA
                                |||| ||  || ||||||||
                                CCCC CC  CC CCCCTCCT
                                  G  ___  A
GAM2612  LOC123591 5'  GGGGAGGACTGGGCTGAGC   61099       GCGGG  AG
                                GGGGAGGA   GGG  GAGC
                                ||||||||   |||  ||||
                                CCCCTCCT   CCC  CTCG
                                    GA___  GA
GAM2612  LOC124044 3'  GGGGAGGAGGGGGTGGGG   61101       C   _  A
                                GGGGAGGAG GGGG GG GG
                                ||||||||| |||| || ||
                                CCCCTCCTC CCCC CC CC
                                     _   A  _
GAM2612  LOC124976 3'  GGGAAGGAGTGGGGTCCTGG  61102       C   GGA_
                                GGGGAGGAG GGGG   GG
                                ||||||||| ||||   ||
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                                CCCTTCCTC CCCC   CC
                                     A   AGGA
GAM2612  LOC126364 3'  GGGAGGGGGCGGCAGAG    61103      AGC  G  A
                                GGGAGG  GGG GG GGAG
                                ||||||  ||| || ||||
                                CCCTCC  CCC CC TCTC
                                   ___  G  G
GAM2612  LOC127262 3'  GGGGAGGGGGAGGAG      61104      GGAGCG
                                GGGGA    GGGGGAGGAG
                                |||||    ||||||||||
                                CCCCT    CCCCCTCCTC
                                  _______
GAM2612  LOC131034 5'  GGGAGGGAGTGGAGTGGAG   61105    GA   C  _
                                GGG  GGAG GGGG GGAG
                                |||  |||| |||| ||||
                                CCC  CCTC CCTC CCTC
                                  TC   A   A
GAM2612  LOC135138 5'  GGGGCGGGGCGGGAAGAGGGC  61106     A  A       A
                                GGGG GG GCGGGGGGAGG GC
                                |||| || ||||||||||| ||
                                CCCC CC CGCCCTTCTCC CG
                                  G  C       _
GAM2612  LOC142927 5'  GGGCAGGGGTGGTAAAAGGAGC 61107    G  AGC  GG
                                GGG AGG  GG  GGAGGAGC
                                ||| |||  ||  ||||||||
                                CCC TCC  CC  TTTCCTCG
                                  G  CCA  AT
GAM2612  LOC143451 3'  GGGGAGGAGTGGCTGGGG    61108       C  __
                                GGGGAGGAG GG  GGGG
                                |||||||| ||  ||||
                                CCCCTCCTC CC  CCCC
                                     A  GA
GAM2612  LOC144017 3'  GGGGTGGGCCAATAAGGAGC  61109     A  A  G  GG
                                GGGG GG GC GG  GAGGAGC
                                |||| || || ||  |||||||
                                CCCC CC CG TT  TTCCTCG
                                  A  _  G  A_
GAM2612  LOC144110 3'  GGGGAGGAGTGGGTGAACCCAG 61110       C  _  AGG
           C                     GGGGAGGAG GGG GGG  AGC
                                |||||||| ||| |||  |||
                                CCCCTCCTC CCC CTT  TCG
                                     A  A  GGG
GAM2612  LOC144347 3'  GGGGAGGAAGGCTCAGAGGGGC 61111       C  GG_   A
                                GGGGAGGAG GG  GGAGG GC
                                |||||||| ||  ||||| ||
                                CCCCTCCTT CC  TCTCC CG
                                     _ GAG   C
GAM2612  LOC144404 3'  GGGAAGGAGCCCGGGAG    61112        GGG
                                GGGGAGGAGC  GGGAG
                                |||||||||  |||||
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                                CCCTTCCTCG   CCCTC
                                     GG_
GAM2612  LOC144501 3'  GAGGAGGAGCCTCAGAGGAGC  61113          GGGG
                                GGGGAGGAGC    GGAGGAGC
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                                CTCCTCCTCG    TCTCCTCG
                                     GAG_
GAM2612  LOC145125 3'  GGGGAGGAGTGGCTGGGG    61108         C __
                                GGGGAGGAG GG  GGGG
                                ||||||||| ||  ||||
                                CCCCTCCTC CC  CCCC
                                     A  GA
GAM2612  LOC145371 3'  GGGGACGGGGTTTGAGGAGC  61114     AGGA     G__
                                GGGG   GCGGGG   GAGGAGC
                                ||||   ||||||   |||||||
                                CCCC   TGCCCC   CTCCTCG
                                  _____     AAA
GAM2612  LOC145717 3'  GGGAGGGGGGGTGGGAATCTGAG 61115       AGC  _    ___
            C                    GGGAGGG   GGG GGGAG   GAGC
                                ||||||   ||| |||||   ||||
                                CCCTCC   CCC CCCTT   CTCG
                                   C__   A     AGA
GAM2612  LOC145820 3'  GGGTGAGGAGTGGGGAGAAA  61116     _     C
                                GGG GAGGAG GGGGGGAGG
                                ||| |||||| |||||||||
                                CCC CTCCTC CCCCTCTTT
                                  A     A
GAM2612  LOC145989 3'  GGGAGGAGGTGGCTGGGAGGGG 61117         CG __     A
            C                    GGGAGGAG  GG  GGGAGG GC
                                ||||||||  ||  |||||| ||
                                CCCTCCTC  CC  CCCTCC CG
                                     CA  GA     C
GAM2612  LOC146268 3'  GGGGAGGGCGGGGAGAAGAG  61118        A
                                GGGGAGG GCGGGGGGAGGAG
                                ||||||| ||||||||||||
                                CCCCTCC CGCCCCTCTTCTC
                                     _
GAM2612  LOC146445 3'  GGTGAGGAGCGGGAGGGG    61119    G          A
                                GG GAGGAGCGGGGGG GG
                                || ||||||||||||| ||
                                CC CTCCTCGCCCTCC CC
                                  A          _
GAM2612  LOC146515 3'  GGGGTGGGCGGGGGGAGA    61120     A  A
                                GGGG GG GCGGGGGGAGG
                                |||| || ||||||||||
                                CCCC CC CGCCCCCCTCT
                                  A  _
GAM2612  LOC146894 3'  GGGGAGGGTGGGGAGAG     61121        AGC
                                GGGGAGG   GGGGGGAG
                                |||||||   ||||||||
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                                CCCCTCC   CCCCTCTC
                                   CA_
GAM2612  LOC147077 3'  GAGGGGAGGGGAGGAG      61122      A    C
                                GGGG GGAG GGGGGGAG
                                |||| |||| ||||||||
                                CTCC CCTC CCCTCCTC
                                  _   _
GAM2612  LOC147779 3'  GGGGAGGGAGTCCCAGGAG    61123        _ ___
                                GGGGAGG AG   CGGGGG
                                ||||||| ||   ||||||
                                CCCCTCC TC   GTCCTC
                                   C  AGG
GAM2612  LOC148193 5'  GGCGGGGCGGGGAGGGG     47010    A  A      A  A
                                GG GG GCGGGGGG GG G
                                || || |||||||| || |
                                CC CC CGCCCCTC CC C
                                 G  C       _ _
GAM2612  LOC148195 5'  GAGGAGGAGGAGAAGGAGGAG  61124          C
                                GGGGAGGAG GGGGGGAGGAG
                                ||||||||| ||||||||||
                                CTCCTCCTC TCTTCCTCCTC
                                   C
GAM2612  LOC148696 5'  GAGGAGGGGAAGGGGGGG     61125        AGC     A
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                                CTCCTCC   TCCCCC CC
                                   CCT     _
GAM2612  LOC149501 3'  GGGGCAGGCTGGGAGGGG     61126     _  AGC     A
                                GGGG AGG   GGGGGG GG
                                |||| |||   |||||| ||
                                CCCC TCC   CCCTCC CC
                                  G   GA_     _
GAM2612  LOC149773 5'  GGGAGGGGGGCAGGAGGAGGAG 61127        A__
                                GGGAGG   GCGGGGGGAGGAG
                                ||||||   |||||||||||||
                                CCCTCC   CGTCCTCCTCCTC
                                   CCC
GAM2612  LOC150005 3'  GGGGAGGGAGTGGGGAGG     61128        AGC  _
                                GGGGAGG   GG GGGGAGG
                                |||||||   || |||||||
                                CCCCTCC   TC CCCCTCC
                                   C__  A
GAM2612  LOC150319 3'  GGGGGGTGGGGGAGAGAGC    61129      A  AGCG      _
                                GGGG GG    GGGGGAG GAGC
                                |||| ||    ||||||| ||||
                                CCCC CC    CCCCCTC CTCG
                                  _ A___       T
GAM2612  LOC150481 5'  GGTGGAGGGCAGGGGGAGG    61130    _    A
                                GG GGAGG GCGGGGGGAGG
                                || ||||| ||||||||||
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                                CC CCTCC CGTCCCCCTCC
                                 A    _
GAM2612  LOC150605 5'  GGGGAGGGTTGGGAAGGAG   61131       AGCGG
                                GGGGAGG    GGGGAGGAG
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                                CCCCTCC    CCCTTCCTC
                                    CAA__
GAM2612  LOC151056 3'  GGGGAGGGGCGGTGAAG    61133       A   GG
                                GGGGAGG GCGG  GGAG
                                ||||||| ||||  ||||
                                CCCCTCC CGCC  CTTC
                                    C   A_
GAM2612  LOC151056 3'  AGGGTGGGGTGGGGGGAGGGGC 61132     A  AGC       A
                                GGGG GG   GGGGGGAGG GC
                                |||| ||   ||||||||| ||
                                TCCC CC   CCCCCCTCC CG
                                  A  CCA       C
GAM2612  LOC151361 3'  GGGAGGAATGTGGGGGGAG   61134       C__
                                GGGAGGAG   GGGGGGAG
                                ||||||||   ||||||||
                                CCCTCCTT   CCCCCCTC
                                    ACA
GAM2612  LOC151878 5'  GGGGAGGGGTGGAGGGGC    61135       AGC  GG    A
                                GGGGAGG   GG  GGAGG GC
                                |||||||   ||  ||||| ||
                                CCCCTCC   CC  CCTCC CG
                                    ___ A_    C
GAM2612  LOC152048 3'  GGGGGGAGTGGGGAAG     61136     A   CG
                                GGGG GGAG  GGGGGAG
                                |||| ||||  |||||||
                                CCCC CCTC  CCCCTTC
                                  _   A_
GAM2612  LOC152100 5'  GGGGAGTGGAGGGGAGGGGC   61137       GAGC       A
                                GGGGAG    GGGGGGAGG GC
                                ||||||    ||||||||| ||
                                CCCCTC    CTCCCCTCC CG
                                   AC__       C
GAM2612  LOC152926 5'  GGAGGACGGGGGAGGAG     61138       G     G
                                GGAGGA CGGGGG AGGAG
                                |||||| |||||| |||||
                                CCTCCT GCCCCC TCCTC
                                   _     _
GAM2612  LOC153232 3'  GGGGGGGGGGGGGCGGG      61139     A  AGC     A  A
                                GGGG GG   GGGGGG GG G
                                |||| ||   |||||| || |
                                CCCC CC   CCCCCC CC C
                                  _ ___     G  _
GAM2612  LOC153232 3'  GGGGGGGGGGCGGGCAGGG    61140     A  A    G  A
                                GGGG GG GCGGG GG GG
                                |||| || ||||| || ||
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                                CCCC CC CGCCC TC CC
                                  C C    G _
GAM2612  LOC153243 3'  GGGGTAGGCTGGGAGGGG   60648     _  AGC    A
                                GGGG AGG   GGGGGG GG
                                |||| |||   |||||| ||
                                CCCC TCC   CCCTCC CC
                                  A  GA_    _
GAM2612  LOC153260 5'  GGGCGAGGAGGTGGGGGG   61141    _    C_
                                GGG GAGGAG  GGGGGG
                                ||| ||||||  ||||||
                                CCC CTCCTC  CCCCCC
                                  G    CA
GAM2612  LOC153474 3'  AGGGAGGAGCGATCGGGAG   41751          G_
                                GGGGAGGAGCGG  GGGAG
                                ||||||||||||  |||||
                                TCCCTCCTCGCT  CCCTC
                                       AG
GAM2612  LOC155179 3'  GGGGAGGAGTTGGGGACAGG   60678        CG   _
                                GGGGAGGAG  GGGGG AGG
                                |||||||||  ||||| |||
                                CCCCTCCTC  CCCCT TCC
                                     AA    G
GAM2612  LOC155382 3'  GGGGGAGGAGGAGGAGC    61142    A  GCG
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                                ||| |||   ||||||||||
                                CCC CCT   CCTCCTCCTCG
                                  _  ___
GAM2612  LOC157226 5'  GGGGGGCGGTGGGGGGAA    61143    A A   _   A
                                GGG GG GCGG GGGG GGAG
                                ||| || |||| |||| ||||
                                CCC CC CGCC CCCC CCTT
                                  _ _   A   _
GAM2612  LOC158236 5'  AGGGGGAGGGGGAGGGGC    61144    A   C    A A
                                GGGG GGAG GGGGGG GG GC
                                |||| |||| |||||| || ||
                                TCCC CCTC CCCCTC CC CG
                                  _   _    _ _
GAM2612  LOC158308 5'  GGGGAGAGTGGGGAGAGG    61145      G  C
                                GGGGAG AG GGGGGGAGG
                                |||||| || |||||||||
                                CCCCTC TC CCCCTCTCC
                                   _ A
GAM2612  LOC158819 5'  GGGGAGGAAAGAGGAGG     41853        CG
                                GGGGAGGAG  GGGGGAGG
                                |||||||||  ||||||||
                                CCCCTCCTT  TCTCCTCC
                                     __
GAM2612  LOC158972 3'  AGGGAGGAAGAGGAGGGGC   61146        GCG      A
                                GGGGAGGA   GGGGGAGG GC
                                ||||||||   |||||||| ||
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                                TCCCTCCT   TCTCCTCC CG
                                   ___       C
GAM2612  LOC161158 5'  GGGGAGGGGAGGGCCTCCGGGA 61147        AGC     A_____
                G                   GGGGAGG   GGGGGG     GGAG
                                    |||||||   ||||||     ||||
                                    CCCCTCC   CCTCCC     CCTC
                                       ___     GGAGGC
GAM2612  LOC163724 5'  GGTGGAGGGAGGGGGAG     61148    A   C     A
                                    GG GGAG GGGGGG GGAG
                                    || |||| |||||| ||||
                                    CC CCTC CCTCCC CCTC
                                     A   _     _
GAM2612  LOC164572 5'  GGGTGGGCGGGGAGGGG     61149     A  A       A  A
                                    GGG GG GCGGGGGG GG G
                                    ||| || |||||||| || |
                                    CCC CC CGCCCCTC CC C
                                      A  _       _  _
GAM2612  LOC195977 3'  GGGGAGGCGGCACCTGGAGGAG 61150        A_   GGG
                C                   GGGGAGG  GCG   GGAGGAGC
                                    |||||||  |||   ||||||||
                                    CCCCTCC  CGT   CCTCCTCG
                                        GC   GGA
GAM2612  LOC195977 3'  GGGGAGTGACAAAGGGGG    61151       GA       A
                                    GGGGAG  GCGGGGGG GG
                                    ||||||  |||||||| ||
                                    CCCCTC  TGTTTCCC CC
                                       AC       _
GAM2612  LOC196500 3'  GGGGAGAGGGTGCAGGAGC   61152       AGC   GGG
                                    GGGGAGG   GGG   AGGAGC
                                    |||||||   |||   ||||||
                                    CCCCTCT   CCC   TCCTCG
                                       ___   ACG
GAM2612  LOC196746 3'  GGGGAGGAGGGGCACTGGG   61153         C   ____
                                    GGGGAGGAG GGG    GGG
                                    ||||||||| |||    |||
                                    CCCCTCCTC CCC    CCC
                                          _   GTGA
GAM2612  LOC196955 3'  AGGGATAGAGGGGGAGG     61154      GG  C
                                    GGGGA  AG GGGGGGAGG
                                    |||||  || |||||||||
                                    TCCCT  TC TCCCCCTCC
                                      A_  _
GAM2612  LOC197136 3'  GGGGAGGAGGGGGTGGGG    61101         C   _  A
                                    GGGGAGGAG GGGG GG GG
                                    ||||||||| |||| || ||
                                    CCCCTCCTC CCCC CC CC
                                          _    A  _
GAM2612  LOC197419 3'  AGGGAGGAAGGGGGGGGG     61155         C     A
                                    GGGGAGGAG GGGGGG GG
                                    ||||||||| |||||| ||
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                                TCCCTCCTT CCCCCC CC
                                      _    _
GAM2612  LOC200186 3'  GGGGAAGAGTGGTGAGGAGGGG 61156         C _      A
                C                    GGGGAGGAG GG GGGGAGG GC
                                     ||||||||| || ||||||| ||
                                     CCCCTTCTC CC CTCCTCC CG
                                           A  A      C
GAM2612  LOC200854 5'  GGGGGGAACGAAGGGAG     61157      A
                                     GGGG GGAGCGGGGGGAG
                                     |||| ||||||||||||
                                     CCCC CCTTGCTTCCCTC
                                       _
GAM2612  LOC201191 3'  GGGAGGAGCTGGAGGGG     61158          G    A
                                     GGGAGGAGC GGGGG GG
                                     ||||||||| ||||| ||
                                     CCCTCCTCG CCTCC CC
                                           A    _
GAM2612  LOC201911 3'  GGGGAGGCGGCGGGGGAGGAGC 61159         A_      G
                                     GGGGAGG  GCGGGGG AGGAGC
                                     |||||||  ||||||| ||||||
                                     CCCCTCC  CGCCCCC TCCTCG
                                        GC      _
GAM2612  LOC202347 3'  GGGGGCGGGGGGGGGGGC    61160      AGGA       A  A
                                     GGGG    GCGGGGGG GG GC
                                     ||||    |||||||| || ||
                                     CCCC    CGCCCCCC CC CG
                                       _____       C  C
GAM2612  LOC204161 5'  GAGGAGGGGCCCAGCAGAGGGG 61161         A  G_  G    A
                C                    GGGGAGG GC  GG GGAGG GC
                                     ||||||| ||  || ||||| ||
                                     CTCCTCC CG  TC TCTCC CG
                                        C  GG  G    C
GAM2612  LOC204820 3'  GAGGGGAGCGGGCACCGTGGG  61162      A       _______
                                     GGGG GGAGCGGG      GGG
                                     |||| ||||||||      |||
                                     CTCC CCTCGCCC      CCC
                                       _       GTGGCA
GAM2612  LOC206389 5'  GGAGAGGAGCGGGAGAGGGGC  61163              GA  A
                                     GGGGAGGAGCGGGGG  GG GC
                                     ||||||||||||||  || ||
                                     CCTCTCCTCGCCCTC  CC CG
                                              TC  _
GAM2612  LOC219513 5'  GGGGAAGCGGGGGGGGGGGC   61164     A         A  A
                                     GGG GGAGCGGGGGG GG GC
                                     ||| |||||||||| || ||
                                     CCC CTTCGCCCCCC CC CG
                                       _         C  C
GAM2612  LOC219654 5'  GGAGGGGCGGGCACCGGGGAGC 61165       A    G___  A
                                     GGAGG GCGGG    GG GGAGC
                                     ||||| |||||    || |||||
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                                CCTCC CGCCC    CC CCTCG
                                  C     GTGG  _
GAM2612  LOC219688 5'  GAGGAGGAGGAGGGGGG     60908         C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CTCCTCCTC CTCCCC CC
                                          _     _
GAM2612  LOC221296 3'  GGGAAGAAGGGGAGGGG     61167         C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CCCTTCTTC CCCTCC CC
                                          _     _
GAM2612  LOC221296 3'  GGGGAGGGGCGTAAGAG     61166         A   GG
                                GGGGAGG GCG  GGGAG
                                ||||||| |||  |||||
                                CCCCTCC CGC  TTCTC
                                    C   A_
GAM2612  LOC221656 3'  GGGGGGGGCGGGGGGCGGGC   61168      A  A       A  A
                                GGGG GG GCGGGGGG GG GC
                                |||| || |||||||| || ||
                                CCCC CC CGCCCCCC CC CG
                                  _ C       G  _
GAM2612  LOC221833 3'  GGAGAGGGGCGGGCGCAGG    61169         A    GGG
                                GGGGAGG GCGGG   AGG
                                ||||||| |||||   |||
                                CCTCTCC CGCCC   TCC
                                    C    GCG
GAM2612  LOC221914 3'  GGGGAGGAGGGGAAAGGGC    61170         GC   GG   A
                                GGGGAGGA  GGGG  AGG GC
                                ||||||||  ||||  ||| ||
                                CCCCTCCT  CCCC  TCC CG
                                    __    TT   _
GAM2612  LOC221975 5'  AGGGAGGGGTGGGGTGG      61171         AGC  _   A
                                GGGGAGG   GG GGGG GG
                                |||||||   || |||| ||
                                TCCCTCC   CC CCCC CC
                                    ___  A    A
GAM2612  LOC222865 3'  GGGGTGGGGAGGGGGAG      60850      A  AGC     A
                                GGGG GG   GGGGGG GGAG
                                |||| ||   |||||| ||||
                                CCCC CC   CCTCCC CCTC
                                  A ____     _
GAM2612  LOC222962 3'  GGGGACAGGGGAGGGGC      61172      AGGA      GA  A
                                GGGG    GCGGGGG  GG GC
                                ||||    |||||||  || ||
                                CCCC    TGTCCCC  CC CG
                                  _____       TC  _
GAM2612  LOC253367 3'  GGGAGGGAGAGGGGAG       61173         AGC     A
                                GGGAGG   GGGGGG GGAG
                                ||||||   |||||| ||||
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                                CCCTCC   CTCTCC CCTC
                                   ___    _
GAM2612  LOC253866 5'  GGGGAGGGGAGGGGAGGGC   61174       AGC       A
                                GGGGAGG   GGGGGGAGG GC
                                |||||||   ||||||||| ||
                                CCCCTCC   CTCCCCTCC CG
                                   C__       _
GAM2612  LOC254440 3'  GGGGAGGAGTGGCTGGGG    61108        C  __
                                GGGGAGGAG GG  GGGG
                                ||||||||| ||  ||||
                                CCCCTCCTC CC  CCCC
                                     A  GA
GAM2612  LOC254532 5'  GGGGAGGGGCGGGGTGGGG   41863       A    _ A
                                GGGGAGG GCGGGG GG GG
                                ||||||| |||||| || ||
                                CCCCTCC CGCCCC CC CC
                                   C     A _
GAM2612  LOC254532 5'  GGGGCGGGGTGGGGCAAGC   61175     A  AGC  _   AG
                                GGGG GG   GG GGGG  GAGC
                                |||| ||   || ||||  ||||
                                CCCC CC   CC CCCC  TTCG
                                  G ___ A   G_
GAM2612  LOC255031 5'  GGGCGAGGGGCGGGCGAAGAGC 61176    _   A    G G
                                GGG GAGG GCGGG G AGGAGC
                                ||| |||| ||||| | ||||||
                                CCC CTCC CGCCC C TTCTCG
                                  G   C    G _
GAM2612  LOC255031 5'  GGGGAGGGGGCTGCCAGGAGC  61177       AGC   GGG__
                                GGGGAGG   GGG    AGGAGC
                                |||||||   |||    ||||||
                                CCCCTCC   CCC    TCCTCG
                                   ___  GACGG
GAM2612  LOC255057 3'  GGGGCGGGGGTGGGAGAGGGC  61178     A  AGCG      A
                                GGGG GG   GGGGGGAGG GC
                                |||| ||   |||||||| ||
                                CCCC CC   CCCTCTCC CG
                                  G  CCCA      _
GAM2612  LOC256050 5'  GGGGGGCAGCGGGCTGGG    61179     A  _    __
                                GGGG GG AGCGGG  GGG
                                |||| || ||||||  |||
                                CCCC CC TCGCCC  CCC
                                  _ G     GA
GAM2612  LOC256866 5'  GGGAAGGAGTGGGTCTGGG   61180        C  ___
                                GGGGAGGAG GGG   GGG
                                ||||||||| |||   |||
                                CCCTTCCTC CCC   CCC
                                     A  AGA
GAM2612  LOC51195  3'  GGGAGGGGGCAGGGAG     61181       AGC  G  A
                                GGGAGG   GGG GG GGAG
                                ||||||   ||| || ||||
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                                CCCTCC   CCC TC CCTC
                                   ___   G  _
GAM2612  LOC51720  5'  GGGGGGGAGGGGGAGGGGC    61182     A   C     A  A
                                GGGG GGAG GGGGGG GG GC
                                |||| |||| |||||| || ||
                                CCCC CCTC CCCCTC CC CG
                                  _   _     _ _
GAM2612  LOC57795  3'  GAGGAGGCAGCAGAGGGAGGAG 61183        _
                                GGGGAGG AGCGGGGGGAGGAG
                                ||||||| ||||||||||||||
                                CTCCTCC TCGTCTCCCTCCTC
                                    G
GAM2612  LOC58512  3'  GGGGAGGAGGTGGGGACAAAGC 61184         CG    AG
                                GGGGAGGAG  GGGGG  GAGC
                                |||||||||  |||||  ||||
                                CCCCTCCTC  CCCCT  TTCG
                                     CA    GT
GAM2612  LOC58512  3'  GGGGAGGGGGGGGACGCAGAGC  61185       AGCG    ___
                                GGGGAGG   GGGGGA   GGAGC
                                |||||||   ||||||   |||||
                                CCCCTCC   CCCCCT   TCTCG
                                   _____     GCG
GAM2612  LOC64744  3'  GGGGAGAGGGTGGGAGG     61186       AGC  _
                                GGGGAGG   GGG GGGAGG
                                |||||||   ||| ||||||
                                CCCCTCT   CCC CCCTCC
                                   ___   A
GAM2612  LOC84548  3'  GGGGGGGGGGGGGGGAG      61187     A  AGC     A
                                GGGG GG   GGGGGG GGAG
                                |||| ||   |||||| ||||
                                CCCC CC   CCCCCC CCTC
                                  _ ___     _
GAM2612  LOC90133  3'  GGGAGGGGCAGACTAGGAGGAG 61188       A    __
            C                    GGGAGG GCGGG  GGGAGGAGC
                                |||||| |||||  |||||||||
                                CCCTCC CGTCT  TCCTCCTCG
                                   C    GA
GAM2612  LOC90249  3'  GGGGCAGGGGCAGGGAGGAGC  61189     _  A  GG
                                GGGG AGG GC  GGGGAGGAGC
                                |||| ||| ||  ||||||||||
                                CCCC TCC CG  TCCCTCCTCG
                                  G  C __
GAM2612  LOC90768  5'  GGGGCGGGAGCTAGGGAG    61190     A_    GG
                                GGGG  GGAGC  GGGGAG
                                ||||  |||||  ||||||
                                CCCC  CCTCG  TCCCTC
                                  GC    A_
GAM2612  LOC90917  5'  GGGAGGAGTGGGAAAGAGC   61191        CGG
                                GGGAGGAG   GGGGAGGAGC
                                ||||||||   ||||||||||
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                                CCCTCCTC  CCCTTTCTCG
                                    A__
GAM2612 LOC91397 5' GAGGAAGGGGGGGGAGGGGC  61192      C       A
                                GAGGAG GGGGGGAGG GC
                                |||||| ||||||||| ||
                                CTCCTT CCCCCCTCC CG
                                   C       C
GAM2612 LOC91661 3' GGGGAGGATGTGGGGGACACGC 61193       GCG     GGA
                                GGGGAGGA  GGGGGA  GC
                                ||||||||  ||||||  ||
                                CCCCTCCT  CCCCCT  CG
                                    ACA     GTG
GAM2612 LOC92017 5' GAGGAGGAGCCCTGGGGG   61194        G__
                                GGGGAGGAGC  GGGGG
                                ||||||||||  |||||
                                CTCCTCCTCG  CCCCC
                                      GGA
GAM2612 LOC92080 5' GGGGAGGGTGGTGGAGGAGC  61195      AGCG  G
                                GGGGAGG   GG GGAGGAGC
                                |||||||   || ||||||||
                                CCCCTCC   CC CCTCCTCG
                                    CA__  A
GAM2612 LOC92148 5' GGGTGGGGCTGGGGGGAG   61196    GA  A  _
                                GGG  GG GC GGGGGGAG
                                |||  || || ||||||||
                                CCC  CC CG CCCCCCTC
                                  AC  _  A
GAM2612 LOC92299 5' AGGGAGGAGTGGGAGGTTGG  61197       C     A_
                                GGGGAGGAG GGGGGG  GG
                                ||||||||| ||||||  ||
                                TCCCTCCTC CCCTCC  CC
                                     A     AA
GAM2612 LOC92840 3' GGGAGGGCTGACTGGGAGGGGC 61198      A  GGG__     A
                                GGGAGG GC    GGGAGG GC
                                |||||| ||    |||||| ||
                                CCCTCC CG    CCCTCC CG
                                   _ ACTGA     C
GAM2612 LOC92912 5' GGGAGGGGCGCGGAAGGGGAGC 61199      A__      A
                                GGGAGG  GCGGGGGG GGAGC
                                ||||||  |||||||| |||||
                                CCCTCC  CGCCTTCC CCTCG
                                   CCG      _
GAM2613 DAAM2    3' AGAGGCTGGAACAGACCCTTCC 61202    C  CGAA       CC
            C                    AGA GC   AACGGGCCC  CCC
                                ||| ||   |||||||||  |||
                                TCT CG   TTGTCTGGG  GGG
                                  C  ACC_       AA
GAM2613 EPAS1    5' AGACGCCGAGCACCTGGGCTCC 61203        AA  __   C
            C                    AGACGCCGA  AC  GGGC CCC
                                |||||||||  ||  |||| |||
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                                TCTGCGGCT  TG  CCCG GGG
                                     CG  GA   A
GAM2613  GCN5L1   5'  ACGCCGGGCCCCCTCC     61204      GAAAAC      _
                                ACGCC     GGGCCCCC CC
                                |||||     |||||||| ||
                                TGCGG     CCCGGGGG GG
                                  _______      A
GAM2613  GNA11    5'  CGACCGAGGGAGCCCCCC    61205    _   AAAC
                                CG CCGA    GGGCCCCCC
                                || ||||    |||||||||
                                GC GGCT    CTCGGGGGG
                                 T   CC__
GAM2613  MADH6    5'  GCCGAGGTCGCCCCCCC     61206      AAAC __
                                GCCGA   GG  GCCCCCCC
                                |||||   ||  ||||||||
                                CGGCT   CC  CGGGGGGG
                                  _____ AG
GAM2613  MAGEA8   5'  AGACCCTGAGCCCGCTTCCC   61207     G  GAAAAC     C___
                                AGAC CC     GGGCCC    CCC
                                |||| ||     ||||||    |||
                                TCTG GG     CTCGGG    GGG
                                  _ A_____     CGAA
GAM2613  MSX1     5'  AGAGCCGGGCCCCCC       61208     C   GAAAAC
                                AGA GCC     GGGCCCCCC
                                ||| |||     |||||||||
                                TCT CGG     CCCGGGGGG
                                  _  _______
GAM2613  NFRKB    5'  AGACGCCGAGGCTTCCGCGCCC 61209          AAA___  G
              CC                  AGACGCCGA     CG GCCCCC
                                |||||||||     || ||||||
                                TCTGCGGCT     GC CGGGGG
                                     CCGAAG  G
GAM2613  NGFR     3'  GCCAGGCGGGCCCCCCCC    61210      AAAA
                                GCCG    CGGGCCCCCCCC
                                ||||    ||||||||||||
                                CGGT    GCCCGGGGGGGG
                                  CC__
GAM2613  RAB7L1   3'  AGATGCCCAGACCCCTCC     61211     C   GAAAA      C
                                AGA GCC     CGGGCCCC CC
                                ||| |||     |||||||| ||
                                TCT CGG     GTCTGGGG GG
                                  A  _____       A
GAM2613  SNX9     3'  AGACGCCGGGGTGCTGGGTGCC 61212          AAAAC___ _   C
              CTCC                  AGACGCCG       GG GCCC CC
                                |||||||||       || |||| ||
                                TCTGCGGC       CC CGGG GG
                                     CCCACGAC  A    A
GAM2613  THBD     5'  GACGCCGATGGCGACAGCCTCT 61213          AAA __    CCC
              CC                  GACGCCGA   CG  GGCC   CC
                                |||||||||   ||  ||||   ||
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                                CTGCGGCT  GC TCGG  GG
                                    ACC TG   AGA
GAM2613 VANGL2   3' GCCTGAGAACCAAGCCCCCTCC 61214    _ AAA_      _
                                GCC GA   CGGGCCCCC CC
                                ||| ||   ||||||||| ||
                                CGG CT   GTTCGGGGG GG
                                  A CTTG       A
GAM2613 ALTE     3' AGACACCGAAGACATAACCTCC 61215        A _   C
                                AGACGCCGAA ACG GGCC CC
                                |||||||||| ||| |||| ||
                                TCTGTGGCTT TGT TTGG GG
                                     C  A   A
GAM2613 BLR1     3' GACTCCCACGGGCCCCTTCC  61216    G GAAA      CC
                                GAC CC   ACGGGCCCC CC
                                ||| ||   ||||||||| ||
                                CTG GG   TGCCCGGGG GG
                                  A G___       AA
GAM2613 BLR1     3' GACTCCCACGGGCCCCTTCC  61216    G GAAA      CC
                                GAC CC   ACGGGCCCC CC
                                ||| ||   ||||||||| ||
                                CTG GG   TGCCCGGGG GG
                                  A G___       AA
GAM2613 C20orf18 5' GACGCCGAGTGCGGGGTCCC  61217       AAA   CC
                                GACGCCGA  CGGG CCC
                                ||||||||  |||| |||
                                CTGCGGCT  GCCC GGG
                                    CAC   CA
GAM2613 C20orf18 5' GACGCCGAGTGCGGGGTCCC  61217       AAA   CC
                                GACGCCGA  CGGG CCC
                                ||||||||  |||| |||
                                CTGCGGCT  GCCC GGG
                                    CAC   CA
GAM2613 CENTA1   3' GACGCCAGAGCCCCCC     61218       AAAAC
                                GACGCCG    GGGCCCCCC
                                |||||||    |||||||||
                                CTGCGGT    CTCGGGGGG
                                           _____
GAM2613 CGI-142  5' AGATGCCGGGAGGCCGCCCCCC 61219    C   AAAAC   _
                                AGA GCCG    GGGCC CCCCCC
                                ||| ||||    ||||| ||||||
                                TCT CGGC    TCCGG GGGGGG
                                  A  CC___    C
GAM2613 DKFZP434K1772 5' CACCGAGGAGCCACCCCCC   61220      AAAC   _
                                CGCCGA   GGGCC CCCCCC
                                ||||||   ||||| ||||||
                                GTGGCT   CTCGG GGGGGG
                                   C___    T
GAM2613 DKFZp761G2113 3' GCCGAGGCAGGCCCCCTCC   61221      AAA      _
                                GCCGA  CGGGCCCCC CC
                                |||||  ||||||||| ||
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                                CGGCT   GTCCGGGGG GG
                                  CC_       A
GAM2613  DOC2B    3'  AGAGCTGAGAGCCCCCC     61222     C  C  AAAC
                                AGA GC GA    GGGCCCCCC
                                ||| || ||    |||||||||
                                TCT CG CT    CTCGGGGGG
                                 _  A  ____
GAM2613  FLJ13162 3'  GAGCCCCGGGCCCCCCC     61223    C   GAAAA
                                GA GCC    CGGGCCCCCCC
                                || |||    ||||||||||
                                CT CGG    GCCCGGGGGGG
                                 _  G____
GAM2613  FLJ21562 5'  AAACGCCGCGCGTCGGGTCCTC 61224        AAAA_   _  C
            CC                    AGACGCCG    CGGG CC CCC
                                ||||||||    |||| || |||
                                TTTGCGGC    GCCC GG GGG
                                     GCGCA   A  A
GAM2613  FLJ22029 3'  AGATGCTGAAAACAGCTCACC  61225     C  C      ___
                                AGA GC GAAAACGG   GCC
                                ||| || ||||||||   |||
                                TCT CG CTTTTGTC   TGG
                                  A  A       GAG
GAM2613  GRWD     3'  AGACCTGAATGAACCCCTTCC  61226     GCC   AAC      CC
                                AGAC   GAA   GGGCCCC  CC
                                ||||   |||   |||||||  ||
                                TCTG   CTT   CTTGGGG  GG
                                  GA_   A__      AA
GAM2613  KIAA0329 3'  AGACGCCGGGCCCCC      61227       GAAAAC      C
                                AGACGCC     GGGCCCC C
                                |||||||     ||||||| |
                                TCTGCGG     CCCGGGG G
                                    _______      A
GAM2613  KIAA0375 3'  AGACGCCTGGGCTCCTCC    61228       GAAAAC   C  C
                                AGACGCC     GGGC CC CC
                                |||||||     |||| || ||
                                TCTGCGG     CCCG GG GG
                                    A_____    A  A
GAM2613  KIAA0513 3'  AGGCGCAGAAGGCAGGCCCCC 61229    A   C   AA
                                AG CGC GAA  CGGGCCCCC
                                || ||| |||  |||||||||
                                TC GCG CTT  GTCCGGGGG
                                 C   T   CC
GAM2613  KIAA0876 3'  AGACCCCCGGGCTTCCCC    61230     G  GAAAA    CC
                                AGAC CC    CGGGC  CCCC
                                |||| ||    |||||  ||||
                                TCTG GG    GCCCG  GGGG
                                  G  _____    AA
GAM2613  KIAA0953 3'  AACGCTGAGGGCGAACCCC   61231      C  AAA
                                GACGC GA   CGGGCCCC
                                ||||| ||   ||||||||
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                                TTGCG CT   GCTTGGGG
                                  A  CCC
GAM2613  KIAA1548  5'  AGACGCCGAGAAATGGCGCCC  61232        AAACG  _
                                AGACGCCGA    GGC CCC
                                |||||||||    ||| |||
                                TCTGCGGCT    CCG GGG
                                     CTTTA   C
GAM2613  MGC10960  3'  AGACCCAGGGCCCCCC     61233     G   AAAAC
                                AGAC CCG    GGGCCCCCC
                                ||||  |||    |||||||||
                                TCTG GGT    CCCGGGGGG
                                  _  _____
GAM2613  MGC23940  5'  AGACGCCGGGTCGCCCCC    61234        AAAAC  __
                                AGACGCCG    GG  GCCCCC
                                ||||||||    ||  ||||||
                                TCTGCGGC    CC  CGGGGG
                                     _____  AG
GAM2613  MGC3121   5'  AGACGCCGGGCGAGGCTTTTCC 61235        AAAA  _  CCCC
                                AGACGCCG    CG GGC    CC
                                ||||||||    || |||    ||
                                TCTGCGGC    GC CCG    GG
                                     CC__   T   AAAA
GAM2613  OGFR     3'  AGACGCCGACGGGCACTCC   61236        AAA    CCC
                                AGACGCCGA   CGGGC   CC
                                |||||||||   |||||   ||
                                TCTGCGGCT   GCCCG   GG
                                     ___    TGA
GAM2613  PCBP4    3'  AGCTACCCAACGGGCCCTCC   61237    AC   GAA       C
                                AG  GCC   AACGGGCCC CC
                                ||  |||   ||||||||| ||
                                TC  TGG   TTGCCCGGG GG
                                 GA   G__       A
GAM2613  PCBP4    3'  AGCTACCCAACGGGCCCTCC   61237    AC   GAA       C
                                AG  GCC   AACGGGCCC CC
                                ||  |||   ||||||||| ||
                                TC  TGG   TTGCCCGGG GG
                                 GA   G__       A
GAM2613  PCBP4    3'  AGCTACCCAACGGGCCCTCC   61237    AC   GAA       C
                                AG  GCC   AACGGGCCC CC
                                ||  |||   ||||||||| ||
                                TC  TGG   TTGCCCGGG GG
                                 GA   G__       A
GAM2613  Rab11-FIP3 3'  AGACCCCGAGAAGCACAGGCCC 61238      G    AA___        _
            CCTCC                   AGAC CCGA    ACGGGCCCCC CC
                                ||||  ||||    |||||||||| ||
                                TCTG GGCT    TGTCCGGGGG GG
                                  G   CTTCG        A
GAM2613  TNFRSF19L 3'  GACGGGCACAGGCCCCTCCC   61239     CCGAAA       _
                                GACG     ACGGGCCCC CCC
                                ||||     ||||||||| |||
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                                CTGC     TGTCCGGGG GGG
                                  CCG___       A
GAM2613  ZFP36L2   5'  GCCCGGCCCGCCCCCCCC   61240    GAAAA  ___
                                GCC    CGG   GCCCCCCCC
                                |||    |||   |||||||||
                                CGG    GCC   CGGGGGGGG
                                 _____  GGG
GAM2613  ZNF297    5'  CGCCCCCGGGCCCCCCCC   61241     GAAAA
                                CGCC    CGGGCCCCCCCC
                                ||||    ||||||||||||
                                GCGG    GCCCGGGGGGGG
                                  GG___
GAM2613  LOC146733 3'  CGCCGGGCCCCGCCCC     61242     GAAAAC     _
                                CGCC     GGGCCCC CCCC
                                ||||     ||||||| ||||
                                GCGG     CCCGGGG GGGG
                                  _______      C
GAM2613  LOC159121 5'  AGACGCCAGAATGGAGGATCCC 61243       _  AAC_ GC
                                AGACGCC GAA   GG  CCC
                                ||||||| |||   ||  |||
                                TCTGCGG CTT   CC  GGG
                                    T   ACCT  TA
GAM2613  LOC163404 5'  GACGCGGTGGGCCCCCTCC   61244      CGAAAAC      _
                                GACGC      GGGCCCCC CC
                                |||||      |||||||| ||
                                CTGCG      CCCGGGGG GG
                                   CCA____       A
GAM2613  LOC195977 5'  AGAGGCTGAGCACAGGCCCC   61245    C  C  AA
                                AGA GC GA  ACGGGCCCC
                                ||| || ||  |||||||||
                                TCT CG CT  TGTCCGGGG
                                  C  A  CG
GAM2613  LOC200473 5'  AGAGCGACGGGCCCTCCC    61246    C  CGAAA      C
                                AGA GC    ACGGGCCC CCC
                                ||| ||    |||||||| |||
                                TCT CG    TGCCCGGG GGG
                                  _ C____       A
GAM2613  LOC201931 5'  GGACCTGCCAGGCCCCTCCC  61247   C   GAAAA      _
                                A GCC    CGGGCCCC CCC
                                | |||    |||||||| |||
                                C TGG    GTCCGGGG GGG
                                 C   ACG__       A
GAM2613  LOC221550 5'  GAGCCGAAAATTTAGGCC    61248    C       C__
                                GA GCCGAAAA   GGGCC
                                || ||||||||   |||||
                                CT CGGCTTTT   TCCGG
                                  _       AAA
GAM2613  LOC254617 5'  AGACCCGGCGAGGCCCCCC   61249     G   AAAA  _
                                AGAC CCG    CG GGCCCCCC
                                |||| |||    || ||||||||
```

```
                                TCTG GGC    GC CCGGGGGG
                                  _  C___  T
GAM2613  LOC255057 3'  AGACGGCGGGGCCCCCTCC    61250      C  AAAAC      _
                                AGACG CG    GGGCCCCC CC
                                ||||| ||    |||||||| ||
                                TCTGC GC    CCCGGGGG GG
                                  C _____       A
GAM2613  LOC257495 5'  GAGCCGAAAATTTAGGCC    61248    C       C__
                                GA GCCGAAAA   GGGCC
                                || ||||||||   |||||
                                CT CGGCTTTT   TCCGG
                                 _       AAA
GAM2613  LOC257576 5'  GAGCCGAAAATTTAGGCC    61248    C       C__
                                GA GCCGAAAA   GGGCC
                                || ||||||||   |||||
                                CT CGGCTTTT   TCCGG
                                 _       AAA
GAM2613  LOC91064  5'  GACACCGGGACCCCCTCC    61251       AAAAC      _
                                GACGCCG    GGGCCCCC CC
                                |||||||    |||||||| ||
                                CTGTGGC    CCTGGGGG GG
                                   _____       A
GAM2614  ACTN2     5'  CGGGCGGCGGGCGCGGGG    61254        TGCGC    C
                                CGGGCGGCG    GCGCG GG
                                |||||||||    ||||| ||
                                GCCCGCCGC    CGCGC CC
                                     C____    C
GAM2614  ATOX1     5'  GGCGGTGTGGCGGCGGTGTGGC 61255      C  C  C  C___
           G                     GGCGG GTG GCG GCG   GGCG
                                ||||| ||| ||| |||   ||||
                                CCGCC CAC CGC CGC   CCGC
                                  A  _  _  CACA
GAM2614  B3GNT4    5'  CGGGCGGCGGCGGCGGCG    61256        T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                      _  _  _
GAM2614  BCL11A    5'  CGGGCGGCGGCGGCGGCG    61256        T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                      _  _  _
GAM2614  BCL11A    5'  CGGGCGGCGGCGGCGGCG    61256        T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                      _  _  _
GAM2614  BCL11A    5'  CGGGCGGCGGCGGCGGCG    61256        T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
```

```
                                GCCCGCCGC CGC CGC CGC
                                    _  _  _
GAM2614 BDNF     5' CGGGCGGGTGCGCCCGGGCGCG 61257       C     G __
              GCG                   CGGGCGG GTGCGC C  GCGCGGCG
                                |||||||| |||||| |  ||||||||
                                GCCCGCC CACGCG G  CGCGCCGC
                                    _     G CC
GAM2614 CACNA1A  5' CGGGCGGCGGCGGCTCGGC   61258        T   CGC  G
                                CGGGCGGCG GCG   GC CGGC
                                ||||||||| |||   || ||||
                                GCCCGCCGC CGC   CG GCCG
                                    _  ____ A
GAM2614 CACNA1A  5' CGGGCGGCGGCGGCTCGGC   61258        T   CGC  G
                                CGGGCGGCG GCG   GC CGGC
                                ||||||||| |||   || ||||
                                GCCCGCCGC CGC   CG GCCG
                                    _  ____ A
GAM2614 CAPON    5' GGGCGCGGCGACGCGTGGCG   61259      G  T   C    C
                                GGGCG CG GCG GCGCG GGCG
                                ||||| || ||| ||||| ||||
                                CCCGC GC CGC TGCGC CCGC
                                  _  _  _    A
GAM2614 CDK2AP1  5' CGGGCGGCGGGCGCGCCGGGCG 61260         T     ___
              CGGCG                 CGGGCGGCG GCGCGC   GCGCGGCG
                                |||||||| ||||||   ||||||||
                                GCCCGCCGC CGCGCG   CGCGCCGC
                                    C     GCC
GAM2614 COPEB    5' GGGCGGCGAGGCGCGCGG    61261        TGCGC
                                GGGCGGCG    GCGCGCGG
                                ||||||||    ||||||||
                                CCCGCCGC    CGCGCGCC
                                    TC___
GAM2614 DVL3     5' GGCGGCGGCGCGCGGCG     61262       T     C
                                GGCGGCG GCGCGCG GCG
                                ||||||| ||||||| |||
                                CCGCCGC CGCGCGC CGC
                                    _     _
GAM2614 EGR3     3' GGCGCGCGTGCGTGCGGCG   61263        C  C
                                GGCGTGCG GCG GCGGCG
                                |||||||| ||| ||||||
                                CCGCGCGC CGC CGCCGC
                                    A  A
GAM2614 EXT1     5' GGGTGGCGGCGGCGGCG     61264     C   T  C  C
                                GGG GGCG GCG GCG GCG
                                ||| |||| ||| ||| |||
                                CCC CCGC CGC CGC CGC
                                  A   _  _  _
GAM2614 FASN     5' CGGGCGGCGGTGCGGGCGGCG  61265        _   C  C
                                CGGGCGGCG TGCG GCG GCG
                                ||||||||| |||| ||| |||
```

```
                                GCCCGCCGC ACGC CGC CGC
                                     C   C  _
GAM2614  FTH1    5'  GGCGGCGGTGGCTGCGCGGCG  61266       _  C  GC
                                GGCGGCG TG GC  GCGCGGCG
                                ||||||| || ||  ||||||||
                                CCGCCGC AC CG  CGCGCCGC
                                    C  _  A_
GAM2614  HDAC4   5'  CGGGCGGCGGCGGCGGCG    61256        T   C   C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                     _   _   _
GAM2614  HDAC4   5'  CGGGCGGCGGCGGGGACGG   61267         T   CGCGC
                                CGGGCGGCG GCG    GCGG
                                ||||||||| |||    ||||
                                GCCCGCCGC CGC    TGCC
                                     _   CCC__
GAM2614  HDAC5   5'  CGGGCGGCGGCGGCAGCAGCGG 61268         T   C  _  _
           CG                     CGGGCGGCG GCG GC GC GCGGCG
                                ||||||||| ||| || || ||||||
                                GCCCGCCGC CGC CG CG CGCCGC
                                     _   _  T  T
GAM2614  HDAC5   5'  CGGGCGGCGGCGGCAGCAGCGG 61268         T   C  _  _
           CG                     CGGGCGGCG GCG GC GC GCGGCG
                                ||||||||| ||| || || ||||||
                                GCCCGCCGC CGC CG CG CGCCGC
                                     _   _  T  T
GAM2614  JAG2    5'  GGGCGGCGGGCGTGCAGGGGCG 61269         T   C   C__
           GCG                    GGGCGGCG GCG GCG   GCGGCG
                                |||||||| ||| |||   ||||||
                                CCCGCCGC CGC CGT   CGCCGC
                                     C   A   CCC
GAM2614  KIF3B   5'  CGGGCGGCGGCGGCGGCG    61256        T   C   C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                     _   _   _
GAM2614  LATS2   5'  CGGGCGGCGGCGGTGGCG    61270        T   CGC
                                CGGGCGGCG GCG   GCG
                                ||||||||| |||   |||
                                GCCCGCCGC CGC   CGC
                                     _   CAC
GAM2614  LEF1    5'  CGGGGGCGTCTGCGCGGCG   61271     C    GC    C
                                CGGG GGCGT  GCGCG GCG
                                |||| |||||  ||||| |||
                                GCCC CCGCA  CGCGC CGC
                                   _    GA    _
GAM2614  MAML1   5'  CGGAGCGGGCTCGCGCGCGGCG 61272     _   CGT  G
                                CGG GCGG   GC CGCGCGCGGCG
                                ||| ||||   || ||||||||||
```

```
                                GCC CGCC   CG GCGCGCGCCGC
                                  T   ___  A
GAM2614  MSL3L1   5'  GGGCGGGCGGAGCGCGCGCGG  61273      C   C_
                                GGGCGG GTG  GCGCGCGCGG
                                |||||| |||  ||||||||||
                                CCCGCC CGC  CGCGCGCGCC
                                   _  CT
GAM2614  MSL3L1   5'  GGGCGGGCGGAGCGCGCGCGG  61273      C   C_
                                GGGCGG GTG  GCGCGCGCGG
                                |||||| |||  ||||||||||
                                CCCGCC CGC  CGCGCGCGCC
                                   _  CT
GAM2614  MSL3L1   5'  GGGCGGGCGGAGCGCGCGCGG  61273      C   C_
                                GGGCGG GTG  GCGCGCGCGG
                                |||||| |||  ||||||||||
                                CCCGCC CGC  CGCGCGCGCC
                                   _  CT
GAM2614  NFATC1   5'  AGGGGCGTGTGCGCGCGTGGCG 61274    C     C     C
                                GGG GGCGTG GCGCGCG GGCG
                                ||| |||||| ||||||| ||||
                                TCC CCGCAC CGCGCGC CCGC
                                  _    A      A
GAM2614  NFKB1    5'  CGGGCGGCTGCGGCCTCGGCG  61275       G   C  GCG
                                CGGGCGGC TGCG GC   CGGCG
                                |||||||| |||| ||   |||||
                                GCCCGCCG ACGC CG   GCCGC
                                   _   _  GA_
GAM2614  NR2F2    5'  CGGGCGGCGGCGGGGCGGC   61276        T   CGCGC
                                CGGGCGGCG GCG    GCGGC
                                ||||||||| |||    |||||
                                GCCCGCCGC CGC    CGCCG
                                     _  CC___
GAM2614  ODC1     5'  CGGGCGGCGGCGGCGGCG    61256        T   C   C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                     _  _  _
GAM2614  OPTN     5'  CGGGCGGCGGCGGTGGCG    61270        T   CGC
                                CGGGCGGCG GCG   GCG
                                ||||||||| |||   |||
                                GCCCGCCGC CGC   CGC
                                     _  CAC
GAM2614  PDGFB    5'  GGCTGCTCCGCGCGCGCGGCG  61277     G  GTG
                                GGC GC   CGCGCGCGCGGCG
                                ||| ||   |||||||||||||
                                CCG CG   GCGCGCGCGCCGC
                                  A  AG_
GAM2614  POMZP3   5'  GGGCGGTGTGGAGCGCGGCG  61278      C   CGCGC
                                GGGCGG GTG    GCGCGGCG
                                |||||| |||    ||||||||
```

```
                                CCCGCC CAC    CGCGCCGC
                                   A  CT___
GAM2614  PTGER3   5'  CGGGCGGCGGCGGAGGTCGGCG 61279        T  CGCGCG
                                CGGGCGGCG GCG     CGGCG
                                ||||||||| |||     |||||
                                GCCCGCCGC CGC     GCCGC
                                     _  CTCCA_
GAM2614  PTMA     5'  GGCGGCGGAGGAGGCGCGCGGC 61280       TGCGC_
            G                    GGCGGCG     GCGCGCGGCG
                                |||||||     ||||||||||
                                CCGCCGC     CGCGCGCCGC
                                   CTCCTC
GAM2614  PTPN18   5'  CGGCCCCGCGCGCGCGGC    61281     GTG
                                CGGC  CGCGCGCGCGGC
                                ||||  ||||||||||||
                                GCCG  GCGCGCGCGCCG
                                  GG_
GAM2614  PYGL     5'  GGGCGGCGGGCTGCGCGGCG  61282       TGC  GC
                                GGGCGGCG  GC  GCGCGGCG
                                ||||||||  ||  ||||||||
                                CCCGCCGC  CG  CGCGCCGC
                                    C__  A_
GAM2614  SLC6A8   5'  CGGGCGGCGGCGGCGGCG    61256       T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                     _  _  _
GAM2614  SLC6A8   5'  CGGGCGGCGGCGGCTGCGGCG  61283       T  C  GC
                                CGGGCGGCG GCG GC  GCGGCG
                                ||||||||| ||| ||  ||||||
                                GCCCGCCGC CGC CG  CGCCGC
                                     _  _  A_
GAM2614  SORCS3   5'  CGGGGGGTGTGCGCGCGCCGGC 61284     C  C       G
            G                    CGGG GG GTGCGCGCGC CGGCG
                                |||| || |||||||||| |||||
                                GCCC CC CACGCGCGCG GCCGC
                                  C  A        _
GAM2614  TLE1     5'  CGGCGATCCGCGTGCGCGGCG  61285      _ G   C
                                CGGCG T CGCG GCGCGGCG
                                ||||| | |||| ||||||||
                                GCCGC A GCGC CGCGCCGC
                                   T G   A
GAM2614  USF2     3'  GGGCGGCGGCGGCTGCGTGG  61286       T  C  _  C
                                GGGCGGCG GCG GC GCG GG
                                |||||||| ||| || ||| ||
                                CCCGCCGC CGC CG CGC CC
                                     _  _  A  A
GAM2614  VGF      3'  GGGCGCCGGCGCGCGCGCGCGG 61287      G  _
            CG                   GGGCG CG TGCGCGCGCGCGGCG
                                ||||| || ||||||||||||||||
```

```
                                CCCGC GC GCGCGCGCGCCGC
                                   G  C
GAM2614  ZNF219   5'  CGGGCGGCGGCGGAGCGGGCGG 61289         T   C_   C
                CG                  CGGGCGGCG GCG  GCG GCGGCG
                                    ||||||||| |||  ||| ||||||
                                    GCCCGCCGC CGC  CGC CGCCGC
                                         _  CT   C
GAM2614  ZNF219   5'  CGGGCGGCGGGCCGGCGGC   61288         TGC  G  C
                                    CGGGCGGCG   GC CG GCGGC
                                    |||||||||   || || |||||
                                    GCCCGCCGC   CG GC CGCCG
                                         C__  _  _
GAM2614  ZNF219   5'  CGGGCGGCGGCGGCGGCG    61256         T   C   C
                                    CGGGCGGCG GCG GCG GCG
                                    ||||||||| ||| ||| |||
                                    GCCCGCCGC CGC CGC CGC

                                         _  _  _
GAM2614  ALK7     5'  GGCTGGCGGTGCGCGGCG    61290     _   _     C
                                    GGC GGCG TGCGCG GCG
                                    ||| |||| |||||| |||
                                    CCG CCGC ACGCGC CGC
                                      A   C     _
GAM2614  ASTN2    5'  CGGGCGGCGGCGGCGG      61291         T   CGCGC
                                    CGGGCGGCG GCG     GCGG
                                    ||||||||| |||     ||||
                                    GCCCGCCGC CGC     CGCC

                                         _  ______
GAM2614  C20orf28 3'  GGGTGGGTCCGGCGCGGC    61292     C  C  G  CGC
                                    GGG GG GT CG   GCGCGGC
                                    ||| || || ||   |||||||
                                    CCC CC CA GC   CGCGCCG
                                      A  _  G  ___
GAM2614  CAMP-GEFII 5'  GAGCGGCGGCGCGCGG      61293         TGCGC
                                    GGGCGGCG    GCGCGCGG
                                    ||||||||    ||||||||
                                    CTCGCCGC    CGCGCGCC

                                         ______
GAM2614  CEGP1    5'  CGGGCGGTGGCGGCGG       61294        CG  C   CGC
                                    CGGGCGG  TG GCG   GCGG
                                    |||||||  || |||   ||||
                                    GCCCGCC  AC CGC   CGCC

                                         __  _   ___
GAM2614  cerk     5'  CGGGCGGCGGGCGGCGGGCGGC 61295         T   C   C
                G                    CGGGCGGCG GCG GCG GCGGCG
                                     ||||||||| ||| ||| ||||||
                                     GCCCGCCGC CGC CGC CGCCGC
                                          C   _   C
GAM2614  CLSTN1   5'  GCGAGGCGCGCGCGCGGC    61296     T_
                                    GCG  GCGCGCGCGCGGC
                                    |||  ||||||||||||
```

```
                                CGC  CGCGCGCGCGCCG
                                  TC
GAM2614  DKFZP564D172 3'  CGGGTGGGTGCGCCAGGGC   61297     C  C     G  CGC
                                CGGG GG GTGCGC CG   GGC
                                |||| || |||||| ||   |||
                                GCCC CC CACGCG GT   CCG
                                  A _     _ C__
GAM2614  DKFZp762K222 5'  CGGGCGCTGTGCGTGCGCGCGG 61298       GC    C
                                CGGGCG  GTGCG GCGCGCGG
                                ||||||  ||||| ||||||||
                                GCCCGC  CACGC CGCGCGCC
                                   GA    A
GAM2614  DXS9928E  5'  CGGGCGGCGGCGGCGGCG    61256         T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                      _  _  _
GAM2614  FLJ10493  5'  GGTTCCCCGCGCGCGCGCGG   61299    GCGGCG
                                GG     TGCGCGCGCGCGG
                                ||     |||||||||||||
                                CC     GCGCGCGCGCGCC
                                 AAGGG_
GAM2614  FLJ13187  5'  CGGGCGGCGGCGGCGGCG    61256         T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                      _  _  _
GAM2614  KIAA0997  5'  GGCGGCGGCGCGCGGCG     61262        T     C
                                GGCGGCG GCGCGCG GCG
                                ||||||| ||||||| |||
                                CCGCCGC CGCGCGC CGC
                                      _     _
GAM2614  KIAA1855  3'  CGGGTGGCGCGCGTCGGGCG   61300     C      _ C
                                CGGG GGCGTGCG CG GCG
                                |||| |||||||| || |||
                                GCCC CCGCGCGC GC CGC
                                  A       A  C
GAM2614  KIAA1957  5'  CGGGCGGCGGCGGCGGCG    61256         T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                      _  _  _
GAM2614  LRP15    5'  GGCGGCGTTGGTGCGCGGCG  61301        GCGCGC
                                GGCGGCGT     GCGCGGCG
                                ||||||||     ||||||||
                                CCGCCGCA     CGCGCCGC
                                    ACCA__
GAM2614  MAP      5'  GGGCGGCGGCGGCGGCG     61302         T  C  C
                                GGGCGGCG GCG GCG GCG
                                |||||||| ||| ||| |||
```

```
                                CCCGCCGC CGC CGC CGC
                                      _  _  _
GAM2614 MGC3413  5' CGGGCGGCGGGCAGAGGCGG  61303        T  CGCGC
                                CGGGCGGCG GCG    GCGG
                                ||||||||| |||    ||||
                                GCCCGCCGC CGT    CGCC
                                     C  CTC__
GAM2614 NET-6    5' GCGCGGCGCGCGCGCGGC    61304    G  T
                                GCG CG GCGCGCGCGCGGC
                                ||| || ||||||||||||
                                CGC GC CGCGCGCGCGCCG
                                  _ _
GAM2614 OSBP2    5' GGGCGCAGTCACGTGCGCGCGG 61305      GC  _  C
                CG                GGGCG  GT GCG GCGCGCGGCG
                                  |||||  || ||| ||||||||||
                                  CCCGC  CA TGC CGCGCGCCGC
                                     GT  G   A
GAM2614 OSBPL1A  5' CGGGCGGCTCCCTGCGCGCGGC 61306        GTGCGC
                G                 CGGGCGGC     GCGCGCGGCG
                                  ||||||||     ||||||||||
                                  GCCCGCCG     CGCGCGCCGC
                                      AGGGA_
GAM2614 P5CR2    5' CGGGCGGCGTGCCGAGGACCGG 61307          G  C__  G
                CG                CGGGCGGCGTGC CG   GC CGGCG
                                  |||||||||||| ||   || |||||
                                  GCCCGCCGCACG GC   TG GCCGC
                                        _  TCC  _
GAM2614 PIP5K1C  3' CGGGTGGCGTGGCGTCATACG  61308     C     C  _  CG
                                  CGGG GGCGTG GCG CG  CG
                                  |||| |||||| ||| ||  ||
                                  GCCC CCGCAC CGC GT  GC
                                    A     _   A  AT
GAM2614 PLXNC1   5' CGGGCGGCGGCGGCGGCG    61256        T  C  C
                                  CGGGCGGCG GCG GCG GCG
                                  ||||||||| ||| ||| |||
                                  GCCCGCCGC CGC CGC CGC
                                        _  _  _
GAM2614 PPP1R1B  5' CAGGCGGCGGGCTGTGCGGCG  61309        T  GCGCGC
                                  CGGGCGGCG GC     GCGGCG
                                  ||||||||| ||     ||||||
                                  GTCCGCCGC CG     CGCCGC
                                       C  ACA___
GAM2614 SIAT8C   5' AGCGCGCGCGCGTGTGGCG   61310          CGC
                                  GGCGTGCGCGCG   GGCG
                                  ||||||||||||   ||||
                                  TCGCGCGCGCGC   CCGC
                                         ACA
GAM2614 TIEG2    5' CGGGCGGCGGCGGCGGCG    61256        T  C  C
                                  CGGGCGGCG GCG GCG GCG
                                  ||||||||| ||| ||| |||
```

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                                GCCCGCCGC CGC CGC CGC
                                      _  _  _
GAM2614  TLE4     5'  CGGGCGGCAGGAACGCGCGGCG 61311         TGCGC
                                CGGGCGGCG    GCGCGCGGCG
                                |||||||||    ||||||||||
                                GCCCGCCGT    TGCGCGCCGC
                                   CCT__
GAM2614  LOC115574 5'  CGGGCGGCGGGCGGGTGCTGCG 61312         T  C__  GC
            GCG                    CGGGCGGCG GCG  GC  GCGGCG
                                |||||||||| |||  ||  ||||||
                                GCCCGCCGC CGC  CG  CGCCGC
                                   C  CCA  A_
GAM2614  LOC131583 5'  GGGCGGCGGCGGCGGCG     61302        T  C  C
                                GGGCGGCG GCG GCG GCG
                                |||||||| ||| ||| |||
                                CCCGCCGC CGC CGC CGC
                                      _  _  _
GAM2614  LOC138855 5'  GGCGGCGGCTGCTGCGCGGCG  61313        T  _  GC
                                GGCGGCG GC GC  GCGCGGCG
                                ||||||| || ||  ||||||||
                                CCGCCGC CG CG  CGCGCCGC
                                   _  A  A_
GAM2614  LOC144596 3'  GGGCGGCGGCGGCTGCGTGG   61286        T  C  _  C
                                GGGCGGCG GCG GC GCG GG
                                |||||||| ||| || ||| ||
                                CCCGCCGC CGC CG CGC CC
                                   _  _ A  A
GAM2614  LOC145123 5'  GGCGGCGGAGGAGGCGCGCGGC 61280        TGCGC_
            G                   GGCGGCG     GCGCGCGGCG
                                |||||||     ||||||||||
                                CCGCCGC     CGCGCGCCGC
                                   CTCCTC
GAM2614  LOC145870 5'  CGGGCGGCGTTGCGTCGCGCCG 61314         _  _ G___  GCG
            G                   CGGGCGGCGT GCG C   CGC  G
                                |||||||||| ||| |   |||  |
                                GCCCGCCGCA CGC G   GCG  C
                                   A  A CIII  GCG
GAM2614  LOC148479 5'  CGGGCGGCTGCGCAGGGC    61315        G    CGCGC
                                CGGGCGGC TGCGCG    GGC
                                |||||||| ||||||    |||
                                GCCCGCCG ACGCGT    CCG
                                   _    C____
GAM2614  LOC153546 5'  CGGGCGGCGGGCGGCGGCG   61316        T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                   C  _  _
GAM2614  LOC196694 5'  GCGCGCGGCGCGTGCGTGGCG  61317    _  T   C  C
                                GCG GCG GCGCG GCG GGCG
                                ||| ||| ||||| ||| ||||
```

```
                                CGC CGC CGCGC CGC CCGC
                                  G  _    A  A
GAM2614  LOC221710 5'  CGGGCGGCGGCGCGTCCTGCG  61318        T    CGC_
                                CGGGCGGCG GCGCG   GCG
                                ||||||||| |||||   |||
                                GCCCGCCGC CGCGC   CGC
                                      _    AGGA
GAM2614  LOC255057 5'  GGGCGGCGGGCTGGCGGC    61319       T  GCGCGC
                                GGGCGGCG GC     GCGGC
                                |||||||| ||     |||||
                                CCCGCCGC CG     CGCCG
                                    C  AC____
GAM2614  LOC255152 5'  GGGCGGCGGTGGAGATAGCGGC 61320       _  CGCGCGC
             G                   GGGCGGC GTG      GCGGCG
                                |||||||  |||      ||||||
                                CCCGCCG CAC      CGCCGC
                                    C  CTCTAT_
GAM2614  LOC57801  5'  CGGGCGAGCGGCGAGCGCGCGG 61321       _  T  C
             CG                   CGGGCG GCG GCG GCGCGCGGCG
                                |||||| ||| ||| ||||||||||
                                GCCCGC CGC CGC CGCGCGCCGC
                                   T  _  T
GAM2615  ADCY8    5'  GGGGCGGAGCTGGGGGCGG   41610     A   G   A
                                GGGG GGAGC GGGGG GG
                                |||| ||||| ||||| ||
                                CCCC CCTCG CCCCC CC
                                  G   A   G
GAM2615  AQP5     5'  GGGGGGGCAGGGGGCGG    41611     A  A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGTCCCCC CC
                                  _ _      G
GAM2615  AR       5'  GGGGGGCGGGTGGGGAGAAGGG 41612    A  A   __      C
                                GGG GG GCGGG  GGGAGGAG GG
                                ||| || |||||  |||||||| ||
                                CCC CC CGCCC  CCCTCTTC CC
                                  _ _   AC      _
GAM2615  ARHG     5'  GGGGGAGCTGGGGGCGG    41613    A   G   A
                                GGG GGAGC GGGGG GG
                                ||| ||||| ||||| ||
                                CCC CCTCG CCCCC CC
                                  _   A   G
GAM2615  ARHGDIA  3'  GGGGAGGGGCTGGGGGGG   41614       A  G   A
                                GGGGAGG GC GGGGG GG
                                ||||||| || ||||| ||
                                CCCCTCC CG CCCCC CC
                                    C  A   _
GAM2615  B3GAT1   5'  GGAGAGGGGCGGCCACGGGCGG 41615       A   GGGGA  A
                                GGGGAGG GCGG    GG GCGG
                                ||||||| ||||    || ||||
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                                CCTCTCC CGCC    CC CGCC
                                    C   GGTG_ _
GAM2615 BSN     3' GGGGTGGGGTGGGGAGG    41619     A AGC _
                                GGGG GG  GG GGGGAGG
                                |||| ||  || |||||||
                                CCCC CC  CC CCCCTCC
                                  A ___ A
GAM2615 C1orf6  5' GAGGAGGAGGAGGGGCGG   41616        C    A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CTCCTCCTC CTCCCC CC
                                     _    G
GAM2615 C1QG    3' GGGGAGGGGGTGCAGTGGGGGT 41617       A___  __   A
            GG                   GGGGAGG   GCG  GGGGG GG
                                |||||||   |||  ||||| ||
                                CCCCTCC   CGT  CCCCC CC
                                    CCCA  CA   A
GAM2615 CACNG6  5' GGGCGGGAGCGAGGAGCG   41618   A    _
                                GG GCGGGGG GAGGAGCG
                                || ||||||| ||||||||
                                CC CGCCCTC CTCCTCGC
                                 _     G
GAM2615 CALM3   3' GGGGTGGGGTGGGGAGG    41619     A AGC _
                                GGGG GG  GG GGGGAGG
                                |||| ||  || |||||||
                                CCCC CC  CC CCCCTCC
                                  A ___ A
GAM2615 CALR    3' GGGGAGGGGGTGGGGGAGAGTG 41620       AGCG     G C
            G                    GGGGAGG   GGGGGAG AG GG
                                |||||||   ||||||| || ||
                                CCCCTCC   CCCCCTC TC CC
                                    CCCA     _ A
GAM2615 CAPON   5' GGGGAGGAGGTGGCGGCGGGAG 41622        CG  G  A_
            CGG                   GGGGAGGAG  GG GG  GGAGCGG
                                |||||||||  || ||  |||||||
                                CCCCTCCTC  CC CC  CCTCGCC
                                     CA  G  GC
GAM2615 CAPON   5' GGGGAGCGGTGGGGCTTGCGG  41621   A    _   AGGA
                                GG GGAGCGG GGGG   GCGG
                                || ||||||| ||||   ||||
                                CC CCTCGCC CCCC   CGCC
                                 _     A   GAA_
GAM2615 CDC25B  5' GGGCGAGGGGTGGGGGGGG   41623   _   AGC    A
                                GGG GAGG  GGGGGG GG
                                ||| ||||  |||||| ||
                                CCC CTCC  CCCCCC CC
                                  G   CCA   _
GAM2615 CDC25B  5' GGGCGAGGGGTGGGGGGGG   41623   _   AGC    A
                                GGG GAGG  GGGGGG GG
                                ||| ||||  |||||| ||
```

```
                                CCC CTCC   CCCCCC CC
                                  G    CCA     _
GAM2615  COL11A2   3'  GGGGAGGACAGGGGTGG     41624         G     GA
                                GGGGAGGA CGGGGG  GG
                                |||||||| ||||||  ||
                                CCCCTCCT GTCCCC  CC
                                     _     A_
GAM2615  COL11A2   3'  GGGGAGGACAGGGGTGG     41624         G     GA
                                GGGGAGGA CGGGGG  GG
                                |||||||| ||||||  ||
                                CCCCTCCT GTCCCC  CC
                                     _     A_
GAM2615  COL1A1    3'  GGGCAGGAGCGGGCTGAGG    41625     G        GG
                                GGG AGGAGCGGG  GAGG
                                ||| |||||||||  ||||
                                CCC TCCTCGCCC  CTCC
                                  G        GA
GAM2615  CSNK1G2   3'  GGGGCAGGAGTGGGGTAGGGCG 41626      _    C    GG   A
              G                   GGGG AGGAG GGGG  AGG GCGG
                                ||||| ||||| ||||  ||| ||||
                                CCCC TCCTC CCCC  TCC CGCC
                                  G    A    A_  _
GAM2615  CTRL      3'  GGAGGAGGGGTGGGGGCCCCGG 41627        C   _   A  AG_
                                GGAGGAG GGG GGG GG   CGG
                                ||||||| ||| ||| ||   |||
                                CCTCCTC CCC CCC CC   GCC
                                     _   A   _  GGG
GAM2615  DES       3'  GGGGAGGGCGTGGGGAGG     41628        A   G
                                GGGGAGG GCG GGGGAGG
                                ||||||| ||| |||||||
                                CCCCTCC CGC CCCCTCC
                                     _   A
GAM2615  DLX2      3'  GGGGAGGGCGGGCAGGCG     41629         A    G  AGGA
                                GGGGAGG GCGGG GG    GCG
                                ||||||| ||||| ||    |||
                                CCCCTCC CGCCC TC    CGC
                                     _     G  ____
GAM2615  DNMT3L    5'  GGGGAGGGGCGGGGGCGG    41630         A      GA
                                GGGGAGG GCGGGGG  GG
                                ||||||| |||||||  ||
                                CCCCTCC CGCCCCC  CC
                                     C      G_
GAM2615  DNMT3L    5'  GGGGGCGGGGAGGGGCG     41631      AGGA       A  A
                                GGGG    GCGGGGGG GG GCG
                                ||||    |||||||| || |||
                                CCCC    CGCCCCTC CC CGC
                                      ____       _ _
GAM2615  ED1       5'  AGGGAGGAGGAGGGGCGG     41632          C      A
                                GGGGAGGAG GGGGGG GG
                                |||||||| |||||| ||
```

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                                TCCCTCCTC CTCCCC CC
                                   _     G
GAM2615  EGFL5    3'  GGGGGGGGGCAGGGGGCGG    41633      A  A       A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGTCCCCC CC
                                  _ C       G
GAM2615  EGLN1    5'  GGGGAGGGCCGAGGGGCGG   41634         A  G    AGGA
                                GGGGAGG GC GGGGG   GCGG
                                ||||||| || |||||   ||||
                                CCCCTCC CG CTCCC   CGCC
                                   _ G   _____
GAM2615  EIF4G1   3'  GGGGAGGAGAGGGACACCTGGC 41635          C   GGAGGA
            GG                    GGGGAGGAG GGGG     GCGG
                                |||||||| ||||     ||||
                                CCCCTCCTC CCCT     CGCC
                                     T   GTGGAC
GAM2615  EPS15    5'  GGGGAGGAGGCGGAGGGAGCGG 41636          _       GGA
                                GGGGAGGAG CGGGGGGA   GCGG
                                |||||||| ||||||||   ||||
                                CCCCTCCTC GCCTCCCT   CGCC
                                     C      ___
GAM2615  F2RL3    3'  GGGGAGGGGCGTGGCTGGGGGA 61324        A  _ __  A   C
            GTGG                  GGGGAGG GCG GG  GGG GGAG GG
                                ||||||| ||| ||  ||| |||| ||
                                CCCCTCC CGC CC  CCC CCTC CC
                                   C  A  GA  _   A
GAM2615  F2RL3    3'  GGGGAGGCGGGGCTGGAGGAGC 61323       GA    __
            GG                    GGGGAG  GCGGGG  GGAGGAGCGG
                                ||||||  ||||||  ||||||||||
                                CCCCTC  CGCCCC  CCTCCTCGCC
                                   __     GA
GAM2615  FBXL11   3'  GGGGCGGGGTGGGGGGAAG   41637      A  AGC
                                GGGG GG   GGGGGGAGG
                                |||| ||   |||||||||
                                CCCC CC   CCCCCCTTC
                                  G  CCA
GAM2615  FCN2     3'  GGGAGGAGTGTGGGGGTGG   41638         CG_    A
                                GGGAGGAG   GGGGG GG
                                |||||||   ||||| ||
                                CCCTCCTC   CCCCC CC
                                     ACA    A
GAM2615  FHIT     3'  GGGGAGAGGCGGGGGGGCG   41639       GA      AGGA
                                GGGGAG  GCGGGGGG   GCG
                                ||||||  ||||||||   |||
                                CCCCTC  CGCCCCCC   CGC
                                   TC      _____
GAM2615  FOS      5'  GGGCGAGGGGCCGAGGGGCGG  41640    _   A  G    AGGA
                                GGG GAGG GC GGGGG   GCGG
                                ||| |||| || |||||   ||||
```

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                                CCC CTCC CG CTCCC    CGCC
                                  G   C G    ____
GAM2615 FOXG1B   5' GGGGGGGCGGCGGGCGG     41641      A A   G   A
                                GGGG GG GCGG GGG GG
                                |||| || |||| ||| ||
                                CCCC CC CGCC CCC CC
                                  _ _   G  G
GAM2615 FXR2     5' GGGGAGCCGCGGGGGGCGG   41642       GA      A
                                GGGGAG  GCGGGGGG GG
                                ||||||  |||||||| ||
                                CCCCTC  CGCCCCCC CC
                                   GG       G
GAM2615 FXYD1    3' GGGAAGGGGCGGCGGAGGGGGC 41643        A   G  GA  A
           GG                     GGGGAGG GCGG GG  GG GCGG
                                |||||||  |||| ||  || ||||
                                CCCTTCC CGCC CC  CC CGCC
                                   C   G  TC  C
GAM2615 FXYD1    3' GGGAAGGGGCGGCGGAGGGGGC 41643        A   G  GA  A
           GG                     GGGGAGG GCGG GG  GG GCGG
                                |||||||  |||| ||  || ||||
                                CCCTTCC CGCC CC  CC CGCC
                                   C   G  TC  C
GAM2615 GDF2     5' GGGGAGGAGCTGGGAAGGAGCG 41644          GG
           G                     GGGGAGGAGC  GGGGAGGAGCGG
                                ||||||||||  ||||||||||||
                                CCCCTCCTCG  CCCTTCCTCGCC
                                     A_
GAM2615 GNA15    3' GGGCAGGAGTACCCTGGGGGGC 41645    G    C_____     A
           GG                     GGG AGGAG     GGGGGG GG
                                |||  |||||     |||||| ||
                                CCC TCCTC     CCCCCC CC
                                  G    ATGGGA     G
GAM2615 GRB14    5' GGGGAGAGGGGAGGAGCGG   41646       GAGCG
                                GGGGAG    GGGGGAGGAGCGG
                                ||||||    ||||||||||||
                                CCCCTC    TCCCCTCCTCGCC
                                     _____
GAM2615 GRB14    5' GGGGAGGAGCGGCCGGTGG   41647          GG  A
                                GGGGAGGAGCGG  GG GG
                                ||||||||||||  || ||
                                CCCCTCCTCGCC  CC CC
                                      GG  A
GAM2615 GTF2IRD1 5' GGAGAGGAGCGGAGAGCGG   41648             A
                                GGGGAGGAGCGGGGGG GG
                                |||||||||||||||| ||
                                CCTCTCCTCGCCTCTC CC
                                        G
GAM2615 HNRPDL   5' GAGGAGGGGCGGGGGCTGG   41649       A      GA
                                GGGGAGG GCGGGGG  GG
                                |||||||  |||||||  ||
```

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                                CTCCTCC CGCCCCC  CC
                                    C       GA
GAM2615  HOXC10    3'  GAGGAGGGGCGGGGAGAGGAAG 41650     A          ____    III
              GAGCGGC                  GG GCGGGGGGAGGA    GCGG   C
                                || ||||||||||||    ||||   |
                                CC CGCCCCTCTCCT    CGCC   G
                                 C           TCCT    III
GAM2615  IGFBP2    3'  GGAGAGGGGCGGGGGGGCAGG   41651         A      _
                                GGGGAGG GCGGGGGGG AGG
                                ||||||| |||||||| |||
                                CCTCTCC CGCCCCCC TCC
                                    C       G
GAM2615  INSR      3'  GGGGGCGGGTGGGGGGAACG   41652      AGGA    _  A
                                GGGG    GCGGG GGG GGAGCG
                                ||||    ||||| ||| ||||||
                                CCCC    CGCCC CCC CCTTGC
                                  ____     A   C
GAM2615  ITGA6     5'  GGAGGGGAGCGGGGACCTGCAG 41653      A         GAGG_
              CGG                    GGGG GGAGCGGGGG     AGCGG
                                |||| ||||||||||     |||||
                                CCTC CCTCGCCCCT     TCGCC
                                  C         GGACG
GAM2615  JAM2      5'  GGGCGAGGAGCTGGGGGCGG   41654     _      G     A
                                GGG GAGGAGC GGGGG GG
                                ||| ||||||| ||||| ||
                                CCC CTCCTCG CCCCC CC
                                  G       A    G
GAM2615  JUNB      3'  GGGGAGGGCAGGGGGCGG     41655         A       A
                                GGGGAGG GCGGGGGG GG
                                ||||||| |||||||| ||
                                CCCCTCC CGTCCCCC CC
                                    _       G
GAM2615  KCNC3     3'  GGGAAGGGGCGGGGGGGACCG  41657         A       AG  G
                                GGGGAGG GCGGGGGG  GA CG
                                ||||||| ||||||||  || ||
                                CCCTTCC CGCCCCCC  CT GC
                                    C       __  G
GAM2615  KCNC3     5'  GGGAGGGGCGGGGACGCAGGGG 41656       A      G__   A
              CGG                    GGGAGG GCGGGGG   AGG GCGG
                                |||||| |||||||   ||| ||||
                                CCCTCC CGCCCCT   TCC CGCC
                                    C       GCG   C
GAM2615  KCNC3     5'  GGGGGGCGGGGCGGGAGGGGCG 41658     A  A     __     A
              G                     GGG GG GCGGGG  GGAGG GCGG
                                ||| || ||||||  ||||| ||||
                                CCC CC CGCCCC  CCTCC CGCC
                                  _ _      GC     C
GAM2615  KCNF1     3'  GGGGAGGGTTGGGGGGGACACAG 41659         AGC       GGA
                                GGGGAGG   GGGGGGA   GCGG
                                |||||||   |||||||   ||||
```

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                                CCCCTCC  CCCCCCT  TGTC
                                   CAA     G__
GAM2615 KCNK3   3' GGGGATGAGGAAGGGGAG   41660     G  CG
                                GGGGA GAG  GGGGGAG
                                ||||| |||  |||||||
                                CCCCT CTC  TCCCCTC
                                  A  CT
GAM2615 KCNQ2   5' GGGGCGGAGCGCGGGGGGCGG 41661    A    _   AGGA
                                GGGG GGAGCG GGGGG   GCGG
                                |||| |||||| |||||   ||||
                                CCCC CCTCGC CCCCC   CGCC
                                  G    G   ____
GAM2615 LASS1   3' GGAGGGGGTGGAGGGGCG   41662     C  _   A
                                GGAG GGGG GGAGG GCG
                                |||| |||| ||||| |||
                                CCTC CCCC CCTCC CGC
                                  _  A   C
GAM2615 LBX1    3' GGGGAGGAGGCGGGAGTGG   41663       _    GA
                                GGGGAGGAG CGGGGG  GG
                                |||||||| ||||||  ||
                                CCCCTCCTC GCCCTC  CC
                                     C    A_
GAM2615 LRP1    5' GGCGGGGAGGGGGGGTGG   41665   _ A  C    A
                                GG GG GGAG GGGGGG GG
                                || || |||| |||||| ||
                                CC CC CCTC CCCCCC CC
                                 G _  _    A
GAM2615 LRP1    5' GGAGGGGGGGTGGGGGGCG   41664    C    A__ A
                                GGAG GGGGGG  GG GCG
                                |||| ||||||  || |||
                                CCTC CCCCCC  CC CGC
                                  _    ACC  C
GAM2615 LSP1    3' GGGGAGGGCGGGGGCGG    41666      A     GA
                                GGGGAGG GCGGGGG  GG
                                ||||||| |||||||  ||
                                CCCCTCC CGCCCCC  CC
                                   _     G_
GAM2615 MAP3K10  5' GGGGAGGGGCCGGGGGCTGCGG 41667       A  G   AGGA
                                GGGGAGG GC GGGGG   GCGG
                                ||||||| || |||||   ||||
                                CCCCTCC CG CCCCC   CGCC
                                   C  G   GA__
GAM2615 MGMT    5' GGGGGGGGCGGGGGGGG    41669    A  A     A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCCC CC
                                  _ C      _
GAM2615 MGMT    5' GGGGCGGCGGGGGGGGCG   41668     AGGA      A GA
                                GGGG   GCGGGGGG G  GCG
                                ||||   |||||||| |  |||
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                                CCCC   CGCCCCCC C  CGC
                                  GC__      _ __
GAM2615 MIC2    5' GGGGGCGGGTGAGGGGAGCGG 41670     AGGA   _  A
                                GGGG   GCGGG GGG GGAGCGG
                                ||||   ||||| ||| |||||||
                                CCCC   CGCCC CTC CCTCGCC
                                  ____    A  C
GAM2615 MKPX    5' GAGGAGGAGCGGCGGGGCGG  41671          _   A
                                GGGGAGGAGCGG GGGG GG
                                |||||||||||| |||| ||
                                CTCCTCCTCGCC CCCC CC
                                      G   G
GAM2615 MNT     3' GGGGAGGGGCAGCGGGTGG   41672       A   G   A
                                GGGGAGG GCGG GGG GG
                                ||||||| |||| ||| ||
                                CCCCTCC CGTC CCC CC
                                   C   G   A
GAM2615 MSL3L1  5' GGGGAGGGCGGGCGGGGGCGG 41673       A   G A A
                                GGGGAGG GCGGG GG GG GCGG
                                ||||||| ||||| || || ||||
                                CCCCTCC CGCCC CC CC CGCC
                                   _    G  _ _
GAM2615 MSL3L1  5' GGCGGGGGCGGGGAGGCG   41674   _ A A     AGGA
                                GG GG GG GCGGGGGGG   GCG
                                || || || ||||||||   |||
                                CC CC CC CGCCCCTC   CGC
                                 G  _ _     ____
GAM2615 MSL3L1  5' GGGGAGGGCGGGCGGGGGCGG 41673       A   G A A
                                GGGGAGG GCGGG GG GG GCGG
                                ||||||| ||||| || || ||||
                                CCCCTCC CGCCC CC CC CGCC
                                   _    G  _ _
GAM2615 MSL3L1  5' GGCGGGGGCGGGGAGGCG   41674   _ A A     AGGA
                                GG GG GG GCGGGGGGG   GCG
                                || || || ||||||||   |||
                                CC CC CC CGCCCCTC   CGC
                                 G  _ _     ____
GAM2615 MSL3L1  5' GGGGAGGGCGGGCGGGGGCGG 41673       A   G A A
                                GGGGAGG GCGGG GG GG GCGG
                                ||||||| ||||| || || ||||
                                CCCCTCC CGCCC CC CC CGCC
                                   _    G  _ _
GAM2615 MSL3L1  5' GGCGGGGGCGGGGAGGCG   41674   _ A A     AGGA
                                GG GG GG GCGGGGGGG   GCG
                                || || || ||||||||   |||
                                CC CC CC CGCCCCTC   CGC
                                 G  _ _     ____
GAM2615 NCALD   3' GGGGAAGAGAGGGGAGTGG   41675       C    A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
```

```
                                CCCCTTCTC CCCCTC CC
                                     T     A
GAM2615 NCOA6IP  5' GGGAAGGGGCGGGACCACGGGC 41676       A     GGA_ A
             GG                   GGGGAGG GCGGGG    GG GCGG
                                  ||||||| ||||||    || ||||
                                  CCCTTCC CGCCCT    CC CGCC
                                     C     GGTG _
GAM2615 NEUROD2  5' GGGGAGGGGAGGGGGGGAGG  41677      __   C
                                  GGGGA  GGAG GGGGGGAGG
                                  |||||  |||| |||||||||
                                  CCCCT  CCTC CCCCCCTCC
                                    CC   _
GAM2615 NPR1     5' GGGAAGGAGCAGGAGC      41678          GGGGGG
                                  GGGGAGGAGC     AGGAGC
                                  ||||||||||     ||||||
                                  CCCTTCCTCG     TCCTCG

                                          _______
GAM2615 NRXN1    5' GGGGAGCGGGCGGCGCGGAGTG 41679    A      G  A__   C
             G                    GG GGAGCGGG GG   GGAG GG
                                  || |||||||| ||   |||| ||
                                  CC CCTCGCCC CC   CCTC CC
                                   _      G  GCG   A
GAM2615 NTSR1    3' GGGGAGGGGTGGGGAGGAG   41680       AGC  _
                                  GGGGAGG   GG GGGGAGGAG
                                  |||||||   || |||||||||
                                  CCCCTCC   CC CCCCTCCTC
                                     ___ A
GAM2615 PACSIN1  3' GGGGAGGGGCGGCAGTGG    41681       A   G  GA
                                  GGGGAGG GCGG GG  GG
                                  ||||||| |||| ||  ||
                                  CCCCTCC CGCC TC  CC
                                     C   G  A_
GAM2615 PAFAH1B1 5' GGGGGAGGGGAGGGGAGCG   41682     A   C     A
                                  GGG GGAG GGGGGG GGAGCG
                                  ||| |||| |||||| ||||||
                                  CCC CCTC CCCTCC CCTCGC
                                    _   _    _
GAM2615 PAX2     3' GGGAGGGGATGGGAGGAGTGG  41683       AGC  _      C
                                  GGGAGG   GGG GGGAGGAG GG
                                  ||||||   ||| ||||||| ||
                                  CCCTCC   CCT CCCTCCTC CC
                                     ___  A       A
GAM2615 PAX2     3' GGGGAGGGGCGGCAGGCGG   41684       A   G   A
                                  GGGGAGG GCGG GGG GG
                                  ||||||| |||| ||| ||
                                  CCCCTCC CGCC TCC CC
                                     C   G   G
GAM2615 PAX2     3' GGGAGGGGATGGGAGGAGTGG  41683       AGC  _      C
                                  GGGAGG   GGG GGGAGGAG GG
                                  ||||||   ||| ||||||| ||
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                                CCCTCC   CCT CCCTCCTC CC
                                   ___  A       A
GAM2615  PAX2     3'  GGGGAGGGGCGGCAGGCGG   41684        A   G  A
                                GGGGAGG GCGG GGG GG
                                ||||||| |||| ||| ||
                                CCCCTCC CGCC TCC CC
                                    C   G  G
GAM2615  PCTK3    3'  GGGGAGGAGTGGAGGGTGG   41685         C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CCCCTCCTC CCTCCC CC
                                     A     A
GAM2615  PDE4A    3'  AGGGGAGTGAGGGGAGGAGTGG 41688     A   C         C
                                GGG GGAG GGGGGGAGGAG GG
                                ||| |||| |||||||||| ||
                                TCC CCTC CTCCCCTCCTC CC
                                  _   A         A
GAM2615  PDE4A    3'  GGGGGGCGGGGGGGGTGAGTGG  41686     A  A      AG   C
                                GGG GG GCGGGGGG  GAG GG
                                ||| || ||||||||  ||| ||
                                CCC CC CGCCCCCC  CTC CC
                                  _ _      CA   A
GAM2615  PDE4A    3'  GGGGAGGAGTGGAGGGGAACAG 41687          CG     A
                                GGGGAGGAG  GGGGG GGAGCGG
                                |||||||||  ||||| |||||||
                                CCCCTCCTC  CCTCC CCTTGTC
                                     A_    _
GAM2615  PLOD3    5'  GGGAGGCGGGGGAGGGGCGG   41690       AGCG       A
                                GGGAGG    GGGGGAGG GCGG
                                ||||||    |||||||| ||||
                                CCCTCC    CCCCCTCC CGCC
                                   G___       C
GAM2615  PLOD3    5'  GGGGAGGGGCGGCGGCTCGG   41689        A   G  GA_
                                GGGGAGG GCGG GG   GG
                                ||||||| |||| ||   ||
                                CCCCTCC CGCC CC   CC
                                    C   G  GAG
GAM2615  PML      3'  GGCGAGGAGTGGGCTGGCGAGG 41691    G     C  __ _     C
            AGTGG                 GG GAGGAG GGG  GG GAGGAG GG
                                || |||||| |||  || |||||| ||
                                CC CTCCTC CCC  CC CTCCTC CC
                                 G     A  GA G     A
GAM2615  PML      3'  GGCGAGGAGTGGGCTGGCGAGG 41691    G     C  __ _     C
            AGTGG                 GG GAGGAG GGG  GG GAGGAG GG
                                || |||||| |||  || |||||| ||
                                CC CTCCTC CCC  CC CTCCTC CC
                                 G     A  GA G     A
GAM2615  PML      3'  GGCGAGGAGTGGGCTGGCGAGG 41691    G     C  __ _     C
            AGTGG                 GG GAGGAG GGG  GG GAGGAG GG
                                || |||||| |||  || |||||| ||
```

```
                                CC CTCCTC CCC  CC CTCCTC CC
                                 G     A  GA G     A
GAM2615  PPP2R1A  3'  GGGGAGGACGGGAGGTGG    41692         G      A
                                GGGGAGGA CGGGGGG GG
                                |||||||| ||||||| ||
                                CCCCTCCT GCCCTCC CC
                                     _      A
GAM2615  PRDM16   3'  GGGGAGGATGCTGAGGAGTGG  41693          _ _     A
                                GGGGAGGA GC GGGGGG GG
                                |||||||| || |||||| ||
                                CCCCTCCT CG CTCCTC CC
                                     A A     A
GAM2615  PRDM2    3'  GGGGAGAGAGGGGTGG      41694         AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCT   CTCCCC CC
                                     ___     A
GAM2615  PRKCA    3'  GGGGAGGGCTGGGGGCTGG   41695         A _    GA
                                GGGGAGG GC GGGGG  GG
                                ||||||| || |||||  ||
                                CCCCTCC CG CCCCC  CC
                                     _ A    GA
GAM2615  PROC     3'  GGGGGGGGGCGGGGGGGG    41696      A A       A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCCC CC
                                  C  C       _
GAM2615  PRODH    3'  GGCGGGGGCGGGGGGTGCTGG 41697    _ A A       AGGA _
                                GG GG GG GCGGGGGG   GC GG
                                || || || ||||||||   || ||
                                CC CC CC CGCCCCCC   CG CC
                                 G  _ _      A___  A
GAM2615  PRX      3'  GGGGAGGAGCGGCGGCGG    61325          G  GA
                                GGGGAGGAGCGG GG  GG
                                ||||||||||| ||  ||
                                CCCCTCCTCGCC CC  CC
                                       G  G_
GAM2615  PTPRF    3'  GGCGGAGGAGAGGGGAGCG   41698    A   C     A
                                GG GGAG GGGGGG GGAGCG
                                || |||| |||||| ||||||
                                CC CCTC CTCTCC CCTCGC
                                 G   _     _
GAM2615  PTPRF    3'  GGCGGAGGAGAGGGGAGCG   41698    A   C     A
                                GG GGAG GGGGGG GGAGCG
                                || |||| |||||| ||||||
                                CC CCTC CTCTCC CCTCGC
                                 G   _     _
GAM2615  PTPRG    5'  GGGGAGAGGCAGGGGGAGCGG 41699       GA       GGA
                                GGGGAG  GCGGGGGGA   GCGG
                                ||||||  |||||||||   ||||
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                                CCCCTC  CGTCCCCCT   CGCC
                                   TC       ___
GAM2615  PXN     3'  GGGGAGGATGGAGAGTGG    41700        GC     A
                                GGGGAGGA  GGGGGG GG
                                ||||||||  |||||| ||
                                CCCCTCCT  CCTCTC CC
                                     A_     A
GAM2615  RAB13   5'  GGGGGAGCCGGGGGAGG     41701     A    G
                                GGG GGAGC GGGGGAGG
                                |||  ||||| ||||||||
                                CCC CCTCG CCCCCTCC
                                  _    G
GAM2615  RAB13   5'  GGGGAGGGGTGGGGAGCGC   41702        AGC  _     GA
                                GGGGAGG   GG GGGGAG  GC
                                |||||||   || ||||||  ||
                                CCCCTCC   CC CCCCTC  CG
                                    ___  A     G_
GAM2615  RAB3A   3'  GGGGGGGGGGGGGGGTCCCAG   41703     A  AGC     A  AG_
                                GGGG GG   GGGGGG GG   CGG
                                ||||  ||   ||||||  ||   |||
                                CCCC CC   CCCCCC CC   GTC
                                  _  ___     _  AGG
GAM2615  RANBP3  3'  GGGAGGGGGGTTTGGGGGGCGG 41704       AGC  ___   A  A
                                GGGAGG   GGG   GGG GG GCGG
                                ||||||   |||   ||| || ||||
                                CCCTCC   CCC   CCC CC CGCC
                                   C__   AAA   _  _
GAM2615  REST    5'  GGGGAGAGGTGGGGGAGG    41705       G  CG
                                GGGGAG AG  GGGGGAGG
                                ||||||  ||  ||||||||
                                CCCCTC TC  CCCCCTCC
                                   _  CA
GAM2615  RHCG    3'  GGGGAGGGCAGGGGTGG     41706        A      GA
                                GGGGAGG GCGGGGG  GG
                                |||||||  |||||||  ||
                                CCCCTCC CGTCCCC  CC
                                   _      A_
GAM2615  RNH     5'  GGGGAGGGGTGGGTGGGGTGG  41707        AGC_  _    A
                                GGGGAGG    GG GGGG GG
                                |||||||    ||  |||| ||
                                CCCCTCC    CC CCCC CC
                                    CCAC  A    A
GAM2615  RNH     5'  GGGGAGGGGTGGGTGGGGTGG  41707        AGC_  _    A
                                GGGGAGG    GG GGGG GG
                                |||||||    ||  |||| ||
                                CCCCTCC    CC CCCC CC
                                    CCAC  A    A
GAM2615  RPA1    3'  GGGGATGGGGGGGGGGTGG    41708       _  AGC     A
                                GGGGA GG   GGGGGG GG
                                |||||  ||   ||||||  ||
```

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                                CCCCT CC   CCCCCC CC
                                  A  CC_     A
GAM2615  SALL1    3'  GGGGCGGGGTGGGGGGCAAGG  41709      A  AGC     __
                                GGGG GG   GGGGGG  AGG
                                |||| ||   ||||||  |||
                                CCCC CC   CCCCCC  TCC
                                  G  CCA     GT
GAM2615  SCRT1    3'  GGGGAGGGGAGGGGGCTCGG   41710        AGC     A  AG
                                GGGGAGG   GGGGGG GG  CGG
                                |||||||   ||||||  ||  |||
                                CCCCTCC   CCTCCC CC  GCC
                                   ___     _  GA
GAM2615  SF1      5'  GGGGCGGGCCGGGGGCGG    41711      A  A  G    A
                                GGGG GG GC GGGGG GG
                                |||| || || ||||| ||
                                CCCC CC CG CCCCC CC
                                  G  _  G    G
GAM2615  SIAT8E   5'  GGGGAGGGGGAGGGGCG     41712      GGAGCG       A
                                GGGGA     GGGGGAGG GCG
                                |||||     |||||||| |||
                                CCCCT     CCCCCTCC CGC
                                  _______       C
GAM2615  SLC9A1   3'  GGGGAGGAGCTGTGCTGGGGTG 41713          GG____    A
            G                    GGGGAGGAGC     GGGG GG
                                ||||||||||     |||| ||
                                CCCCTCCTCG     CCCC CC
                                     ACACGA    A
GAM2615  SLC9A3R2 5'  GGGGGAGCTCGGGGGCGG    41714     A    G_    A
                                GGG GGAGC  GGGGG GG
                                ||| |||||  ||||| ||
                                CCC CCTCG  CCCCC CC
                                  _    AG    G
GAM2615  SMG1     3'  GGGGAGGAGTAGGGAACGATGG 41715         CG     G  GC
                                GGGGAGGAG  GGGGGA GA  GG
                                |||||||||  ||||||  ||  ||
                                CCCCTCCTC  TCCCTT CT  CC
                                     A_     G  A_
GAM2615  SOX11    3'  GGGGGGCCGGGGGAGG      41716     A  A  G
                                GGG GG GC GGGGGAGG
                                ||| || || ||||||||
                                CCC CC CG CCCCCTCC
                                  _  _  G
GAM2615  SOX12    3'  GGGGTGGGCCCCAGCGGAGGGG 61326      A  A  G__  G    A
            CGG                    GGGG GG GC   GG GGAGG GCGG
                                |||| || ||   || ||||| ||||
                                CCCC CC CG   TC CCTCC CGCC
                                  A  _  GGG  G    C
GAM2615  SOX12    3'  GGGGAGGCCGGAGGGGCG    61327        AG      AGGA
                                GGGGAGG  CGGGGGG    GCG
                                |||||||  |||||||    |||
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                                CCCCTCC  GCCTCCC    CGC
                                   G_      _____
GAM2615  SPI1     3'  GGAGTGGGGGGAGGGGCGG    41718      C        A
                                GGAG GGGGGGAGG GCGG
                                |||| ||||||||| ||||
                                CCTC CCCCCCTCC CGCC
                                  A        C
GAM2615  SPI1     3'  GGGGAGGGGCGGGTGACGG    41717        A     G GA
                                GGGGAGG GCGGG G  GG
                                ||||||| ||||| |  ||
                                CCCCTCC CGCCC C  CC
                                   C     A TG
GAM2615  SPTB     3'  GGGGAGGATGGAGGGCGG     41719         GC      A
                                GGGGAGGA  GGGGGG GG
                                ||||||||  |||||| ||
                                CCCCTCCT  CCTCCC CC
                                    A_     G
GAM2615  SRD5A1   5'  GAGGAGGGGCGGCTACCGGAGG 41720         A    GG___     A
              GGCGG                  GGGGAGG GCGG     GGAGG GCGG
                                ||||||| ||||     ||||| ||||
                                CTCCTCC CGCC     CCTCC CGCC
                                   C    GATGG     C
GAM2615  SYNGR1   3'  GGGGACAGATGGGGAGGGGCGG 61328       _   GC      A  A
                                GGGGA GGA  GGGGGG GG GCGG
                                ||||| |||  |||||| || ||||
                                CCCCT TCT  CCCCTC CC CGCC
                                  G   A_     _ _
GAM2615  TCF3     3'  GGGGGGGACGGGGGGGCTCAGG 41721      A  AG      _____
                                GGGG GG  CGGGGGG    AGG
                                |||| ||  |||||||    |||
                                CCCC CC  GCCCCCC    TCC
                                  _ CT      CGAG
GAM2615  TFAP2A   3'  GGTGAGGCGTGGGAGGGGCGG  41722    GA  A   GG     A
                                GG  GG GCG  GGGAGG GCGG
                                ||  || |||  |||||| ||||
                                CC  TC CGC  CCCTCC CGCC
                                 AC  _   A_     C
GAM2615  TNFRSF11A 3'  GGGGGGAGTCGGGGGGAGG    41723      A    _
                                GGGG GGAG CGGGGGGAGG
                                |||| |||| ||||||||||
                                CCCC CCTC GCCCCCCTCC
                                  _    A
GAM2615  TNFSF5   3'  GGGGGGGGGGGGGGGGTTTCGG  41724      A  AGC     A  AG_
                                GGGG GG   GGGGGG GG   CGG
                                |||| ||   |||||| ||   |||
                                CCCC CC   CCCCCC CC   GCC
                                  _ C__      _ AAA
GAM2615  TSLP     5'  GGGGAGGAAGGTCAGGGAGGAG 41725         C  __
              CGG                   GGGGAGGAG GG  GGGGAGGAGCGG
                                ||||||||| ||  ||||||||||||
```

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                                CCCCTCCTT CC  TCCCTCCTCGCC
                                     _ AG
GAM2615  TULP1    3'  GGGGAGGAGGGGGGGCACAGCGG 41726        GC     AGG
                                GGGGAGGA  GGGGGG   AGCGG
                                ||||||||  ||||||   |||||
                                CCCCTCCT  CCCCCC   TCGCC
                                     __     GTG
GAM2615  UGCG     5'  GGGGGGTGGGGACGGAAGGGGC 41727      A  AGC  __     A
           GG                     GGGG GG   GGG  GGGAGG GCGG
                                ||||  ||   |||  |||||| ||||
                                CCCC CC   CCC  CCTTCC CGCC
                                  _ AC_   TG     C
GAM2615  VAT1     3'  GGGGAGGGGCAGGGGAGAGCGG 41728        A      GA
                                GGGGAGG GCGGGGG  GGAGCGG
                                |||||||  |||||||  |||||||
                                CCCCTCC CGTCCCC  TCTCGCC
                                    C      __
GAM2615  WSX1     5'  AGGGGGAGTGGGGAGGCG    41729      A   C     AGGA
                                GGGG GGAG GGGGGG    GCG
                                ||||  ||||  ||||||    |||
                                TCCC CCTC CCCCTC    CGC
                                  _    A     _____
GAM2615  YWHAE    3'  GGGGAGGAGTGAGGGGAAG    41730         C
                                GGGGAGGAG GGGGGGAGG
                                |||||||||  |||||||||
                                CCCCTCCTC CTCCCCTTC
                                     A
GAM2615  20D7-FC4  3'  GGGGGGAGAGGGGAGG      41731      A   CG
                                GGGG GGAG  GGGGGAGG
                                ||||  ||||  ||||||||
                                CCCC CCTC  TCCCCTCC
                                  _    __
GAM2615  ARHGEF9   5'  GGGGAGGGGAGGGGGATG    41732        AGC     A  GC
                                GGGGAGG   GGGGGG GGA  G
                                |||||||   ||||||  |||  |
                                CCCCTCC   CCTCCC CCT  C
                                     ____     _  A_
GAM2615  ATPW     5'  GGGGCGGGGGCGGGGCGAGGGC 41733      A  A_     G    A
           GG                     GGGG GG  GCGGGG GAGG GCGG
                                ||||  ||  ||||||  ||||  ||||
                                CCCC CC  CGCCCC CTCC CGCC
                                  G  CC     G   _
GAM2615  BCL2L1    3'  GGGGAGAGTGGGGGGGAAAA    41734        G  C
                                GGGGAG AG GGGGGGAGGA
                                ||||||  ||  ||||||||||
                                CCCCTC TC CCCCCCTTTT
                                     _ A
GAM2615  C20orf178 3'  GGGTGAGGAGTGGGCCAGAGTG 41735     _     C   GGGA    C
           G                      GGG GAGGAG GGG    GGAG GG
                                |||  ||||||  |||    ||||  ||
```

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                                CCC CTCCTC CCC    TCTC CC
                                  A     A  GG__    A
GAM2615  C20orf46  3'  GGGCGGGAGCAGGGGGTGG   41736     GA         A
                                GGG  GGAGCGGGGGG GG
                                |||  |||||||||||  ||
                                CCC  CCTCGTCCCCC CC
                                  GC          A
GAM2615  C2orf9    3'  GGGGAGGGGCGGGGGGGCAG   41737        A       AGGA
                                GGGGAGG GCGGGGGG    GCGG
                                |||||||  ||||||||    ||||
                                CCCCTCC CGCCCCCC    CGTC
                                    C       _____
GAM2615  C8orf2    3'  AGGAGTTGGCGGGGGGGGG    60810       GA_       A
                                GGGAG   GCGGGGGG GG
                                |||||   |||||||| ||
                                TCCTC   CGCCCCCC CC
                                   AAC       C
GAM2615  CACNG4    3'  GGGTGGGGGGCGAGGGGGCG    41738     GA  A       AGGA
                                GGG  GG GCGGGGGG    GCG
                                |||  ||  ||||||||    |||
                                CCC  CC CGCTCCCC    CGC
                                  AC  C       _____
GAM2615  CAMKK1    3'  GGGGAGGGGCGGGAGTGG     41739         A      GA
                                GGGGAGG GCGGGGG  GG
                                |||||||  |||||||  ||
                                CCCCTCC CGCCCTC  CC
                                    C       A_
GAM2615  CARM1     3'  GGGGGGGCGGGGGGGGG      41740      A  A       A
                                GGGG GG GCGGGGGG GG
                                ||||  ||  |||||||| ||
                                CCCC CC CGCCCCCC CC

                                  _  _        _
GAM2615  CITED2    3'  GGGGGGCGGCGGGGGGGACAG  41741      A  A    _    A  AG
                                GGG GG GCGG GGGG GG  CGG
                                |||  ||  ||||  ||||  ||  |||
                                CCC CC CGCC CCCC CC  GTC
                                  _  _    G    _  CT
GAM2615  CLSTN1    5'  GGGAGGGGCGGGGGAGAGGAGC 41742        A       _
              GG                    GGGAGG GCGGGGG GAGGAGCGG
                                |||||| ||||||| |||||||||
                                CCCTCC CGCCCCC CTCCTCGCC
                                   C       T
GAM2615  CNIL      5'  GGGGAGGAGGAGCGGGGAGCGG 41743          C   G  A
                                GGGGAGGAG GGG GG GGAGCGG
                                |||||||||  |||  ||  |||||||
                                CCCCTCCTC CTC CC CCTCGCC
                                      _   G  _
GAM2615  CPLX1     3'  GGAGGATCTGTAGGGGGAGGGG 41744        GC___        A
              CGG                   GGAGGA     GGGGGGAGG GCGG
                                ||||||     |||||||||  ||||
```

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                                CCTCCT    TCCCCCTCC CGCC
                                   AGACA       C
GAM2615  CPLX1    3'  GGGGAGGGGCGGGGGCTCCGCG 41745       A     GAGGA
              G                    GGGGAGG GCGGGGG    GCGG
                                   ||||||| |||||||    ||||
                                   CCCCTCC CGCCCCC    CGCC
                                      C      GAGG_
GAM2615  DDX39    3'  GGGAAGGGAGGTGGGAGGGGCG 41746       AGC  _    A
              G                    GGGGAGG   GGG GGGAGG GCGG
                                   |||||||   ||| |||||| ||||
                                   CCCTTCC   TCC CCCTCC CGCC
                                      C__   A     C
GAM2615  DGKD     3'  GGGGGGAGGGAGGAGCG     61329     AGGAGC
                                   GGGG     GGGGGGAGGAGCG
                                   ||||     |||||||||||||
                                   CCCC     CCTCCCTCCTCGC
                                     _______
GAM2615  DGKZ     3'  GGGGAGGGTCGCCGGAGCG    41748       AG  GGGGGA
                                   GGGGAGG  CG     GGAGCG
                                   |||||||  ||     ||||||
                                   CCCCTCC  GC     CCTCGC
                                      CA  GG____
GAM2615  DGKZ     3'  GGGGCAGGAGCGGGGGCTGG   41747     _        GA
                                   GGGG AGGAGCGGGGG  GG
                                   |||| ||||||||||  ||
                                   CCCC TCCTCGCCCCC  CC
                                     G          GA
GAM2615  DKFZp547F072 5'  GGGGAGGGGTGGGGAGAAA    41749       AGC  _
                                   GGGGAGG   GG GGGGAGGAG
                                   |||||||   || |||||||||
                                   CCCCTCC   CC CCCCTCTTT
                                      ___  A
GAM2615  DKFZp547O146 5'  GGGGTGGGGAGAGGGGCG    41750     AGGAGC       A
                                   GGGG     GGGGGGAGG GCG
                                   ||||     ||||||||| |||
                                   CCCC     CCCCTCTCC CGC
                                     A_____        C
GAM2615  DKFZP564I1171 3'  AGGGAGGAGCGATCGGGAG    41751          G_
                                   GGGGAGGAGCGG  GGGAG
                                   ||||||||||||  |||||
                                   TCCCTCCTCGCT  CCCTC
                                         AG
GAM2615  DKFZp762K222 5'  GGGGAGGGGGCGGGCGGGG    41752       A_    G  A
                                   GGGGAGG  GCGGG GG GG
                                   |||||||  ||||| || ||
                                   CCCCTCC  CGCCC CC CC
                                      CC    G  _
GAM2615  FLJ10246  3'  GGAGAGGGACAATGGGGAGG   41753       AG  _
                                   GGGGAGG  CGG GGGGAGG
                                   |||||||  ||| |||||||
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                                CCTCTCC  GTT CCCCTCC
                                    CT   A
GAM2615  FLJ13224  5'  GGGGAGGGTCGGGGGGCCAGG  41754       AG     __
                                GGGGAGG  CGGGGGG  AGG
                                |||||||  |||||||  |||
                                CCCCTCC  GCCCCCC  TCC
                                    CA      GG
GAM2615  FLJ13322  3'  GGGGAGAAGCAGGGGTGG    41755           GA
                                GGGGAGGAGCGGGGG  GG
                                ||||||||||||||  ||
                                CCCCTCTTCGTCCCC  CC
                                       A_
GAM2615  FLJ14280  3'  GGGGAGCGGTGGGAAAGGGGGG 41756      _______   C     A
           TGG                    GGGGA     GGAG GGGGGG GG
                                |||||     |||| |||||| ||
                                CCCCT     CCTT CCCCCC CC
                                   CGCCAC    T     A
GAM2615  FLJ14681  3'  GGGTGGGTTGGGGGGGAGCGG  41757     GA  AGCG    A
                                GGG  GG   GGGGG GGAGCGG
                                |||  ||   ||||| |||||||
                                CCC  CC   CCCCC CCTCGCC
                                  AC  AA__   _
GAM2615  FLJ20406  3'  GGGGCGGGGCGGGGGACGG   41758     A  A     GA
                                GGGG GG GCGGGGG  GG
                                |||| || |||||||  ||
                                CCCC CC CGCCCCC  CC
                                   G  C      TG
GAM2615  FLJ23058  3'  GGGTGGGAGCGGGGGGCTGG  41759     GA        A_
                                GGG  GGAGCGGGGGG  GG
                                |||  ||||||||||  ||
                                CCC  CCTCGCCCCCC  CC
                                  AC         GA
GAM2615  FLJ23416  3'  GGGGAGGGCTGGGAGCGG    41760       A  G    A
                                GGGGAGG GC GGGGG GG
                                ||||||| || ||||| ||
                                CCCCTCC CG CCCTC CC
                                    _ A    G
GAM2615  FLJ23519  5'  GGGGAGGGGTGGGTGGGGTGG  41707       AGC_ _   A
                                GGGGAGG   GG GGGG GG
                                |||||||   || |||| ||
                                CCCCTCC   CC CCCC CC
                                    CCAC  A   A
GAM2615  FLJ30213  5'  GGGGTGGGTGGGGGGAGG    41761     A  AGC
                                GGGG GG   GGGGGGGAGG
                                |||| ||   |||||||||
                                CCCC CC   CCCCCCTCC
                                  A  CA_
GAM2615  FLJ30567  3'  GGCGGAGGAGCTCCCCAGGGAG 41762    _      _____     A
           TGG                    GG GGAGGAGC    GGGGGG GG
                                || ||||||||    |||||| ||
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                                CC CCTCCTCG    TCCCTC CC
                                 G      AGGGG    A
GAM2615  FOXH1    3'  GGGTGGGAGCGGGAGGGAGGAG 41763    GA      _
            CGG                   GGG  GGAGCGGG GGGAGGAGCGG
                                ||| |||||||| ||||||||||
                                CCC  CCTCGCCC CCCTCCTCGCC
                                  AC      T
GAM2615  FOXO3A   5'  GGGGAGGGGCGCCCGGGGGAGG 41764       A  ___      A
            GGCGG                   GGGGAGG GCG   GGGGGAGG GCGG
                                ||||||| |||   |||||||| ||||
                                CCCCTCC CGC   CCCCCTCC CGCC
                                    C  GGG      C
GAM2615  GBTS1    3'  GGGGAGGCAGCGGGGGTCAG   41765       _      GA
                                GGGGAGG AGCGGGGG  GG
                                ||||||| ||||||||  ||
                                CCCCTCC TCGCCCCC  TC
                                    G       AG
GAM2615  GDF11    5'  AGGGAGGTACTGGGGGGCGG   41766       A _    A
                                GGGGAGG GC GGGGGG GG
                                ||||||| || |||||| ||
                                TCCCTCC TG CCCCCC CC
                                    A A     G
GAM2615  HNRPA0   5'  GGGGGAGGGAAGGGGAGCG   41767    A   C    A
                                GGG GGAG GGGGGG GGAGCG
                                ||| |||| |||||| ||||||
                                CCC CCTC CCTTCC CCTCGC
                                  _  _    _
GAM2615  HRD1     3'  GGGGCCTGGGGGGGAGGGGCGG  41768     AGGAGC       A
                                GGGG     GGGGGGGAGG GCGG
                                ||||     ||||||||| ||||
                                CCCC     CCCCCCTCC CGCC
                                  GGA___       C
GAM2615  HSJ1     3'  GGGGAGAGAGCAGGGGCGG   41769       _       GA
                                GGGGAG GAGCGGGGG  GG
                                |||||| |||||||||  ||
                                CCCCTC CTCGTCCCC  CC
                                    T       G_
GAM2615  ILF3     5'  GGGGCGAGCGGGCGGGCGG   41770     AG     _  A
                                GGGG  GAGCGGG GGG GG
                                ||||  ||||||| ||| ||
                                CCCC  CTCGCCC CCC CC
                                  G_     G  G
GAM2615  KHDRBS3  5'  GAGGAGGAGCGGGCGCGGGCGG 41771            GGGA  A
                                GGGGAGGAGCGGG   GG GCGG
                                ||||||||||||   || ||||
                                CTCCTCCTCGCCC   CC CGCC
                                       GCG_ _
GAM2615  KIAA0189 3'  GGGGTGAAGGGGGAGTGG   41772     A   C    A
                                GGGG GGAG GGGGGG GG
                                |||| |||| |||||| ||
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```
                                CCCC CTTC CCCCTC CC
                                  A   _     A
GAM2615 KIAA0211 5' GGGGCGGAGCGGGGGCGG    41773      A        GA
                                GGGG GGAGCGGGGG  GG
                                |||| ||||||||||  ||
                                CCCC CCTCGCCCCC  CC
                                  G        G_
GAM2615 KIAA0237 5' GGGGCGGGGAGGGGCG      41774    A      A  A
                                GG GCGGGGGG GG GCG
                                || |||||||| || |||
                                CC CGCCCCTC CC CGC
                                 C      _ _
GAM2615 KIAA0339 3' GGGTGGGGGCGGAGGGCG    41775     A  AGC   G    A
                                GGG GG   GGG GGAGG GCG
                                ||| ||   ||| ||||| |||
                                CCC CC   CCC CCTCC CGC
                                  A ____  G    _
GAM2615 KIAA0444 5' GGGGAGGAGGGGAGGTGG    41776         C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| ||||||  ||
                                CCCCTCCTC CCCTCC CC
                                     _     A
GAM2615 KIAA0447 3' GGGGAGAGTGGGACAGGGTGG  61330       G  C  ___   A
                                GGGGAG AG GGG   GGG GG
                                |||||| || |||   ||| ||
                                CCCCTC TC CCC   CCC CC
                                   _ A   TGT   A
GAM2615 KIAA0537 5' GGGGAGGGGGAGCGAGGGGCGG 41777         AGC    _    A
                                GGGGAGG   GGGGG GAGG GCGG
                                |||||||   ||||| |||| ||||
                                CCCCTCC   CCCTC CTCC CGCC
                                   ___    G   C
GAM2615 KIAA0649 5' GGGGAGGCGGCGGGCCGGGGGC 41778        A_    G_  A  A
             GG                   GGGGAGG  GCGGG  GG GG GCGG
                                |||||||  |||||  || || ||||
                                CCCCTCC  CGCCC  CC CC CGCC
                                   GC    GG  _ _
GAM2615 KIAA0918 3' GGGGAGGAGAGAAGGAGAGGGG 41779         C    _    A
             CGG                   GGGGAGGAG GGGGG GAGG GCGG
                                |||||||| ||||| |||| ||||
                                CCCCTCCTC CTTCC CTCC CGCC
                                     T    T   C
GAM2615 KIAA1016 5' GGGGCGGGCGGGGAGGCG    41780     A  A      AGGA
                                GGGG GG GCGGGGGG   GCG
                                |||| || ||||||||   |||
                                CCCC CC CGCCCCTC   CGC
                                  G _      _____
GAM2615 KIAA1046 3' GGGGGGGGGGGGGGGGGAGG   61331     A  AGC
                                GGGG GG   GGGGGGAGG
                                |||| ||   |||||||||
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                                CCCC CC   CCCCCCTCC
                                  C  CCC
GAM2615  KIAA1183  3'  GGGGAGGGCGGGGGCCACAGGC 41781       A     GA__  A
                GG                  GGGGAGG GCGGGGG   GG GCGG
                                    ||||||| |||||||   || ||||
                                    CCCCTCC CGCCCCC   TC CGCC
                                       _     GGTG  _
GAM2615  KIAA1321  3'  AGGGAGGAGTGGGGGGAAAA  41782        C
                                    GGGGAGGAG GGGGGGAGGA
                                    ||||||||| ||||||||||
                                    TCCCTCCTC CCCCCCTTTT
                                         A
GAM2615  KIAA1337  3'  GGGGAGGGTTGCGGGGGGGCGG 41783       A__      AGGA
                                    GGGGAGG   GCGGGGGG   GCGG
                                    |||||||   ||||||||   ||||
                                    CCCCTCC   CGCCCCCC   CGCC
                                       CAA       _____
GAM2615  KIAA1388  5'  GGGAGGGAGGAGAGGAGCG   41784      AGC
                                    GGGAGG   GGGGGGAGGAGCG
                                    ||||||   ||||||||||||
                                    CCCTCC   CTCCTCTCCTCGC
                                       ___
GAM2615  KIAA1580  5'  GGGGCGGGGGCGGGGGCGGGGG 41785     A  A_     GA  A
                CGG                   GGGG GG  GCGGGGG  GG GCGG
                                      |||| ||  |||||||  || ||||
                                      CCCC CC  CGCCCCC  CC CGCC
                                        G  CC      GC  C
GAM2615  KIAA1884  3'  GGGGAGGGGTGGGGGGCGG   61332       AGC     A
                                    GGGGAGG   GGGGGG GG
                                    |||||||   |||||| ||
                                    CCCCTCC   CCCCCC CC
                                       CCA     G
GAM2615  KIAA1910  5'  GGAGGGGGGCGGAGGGCG    41786      AGC   _    A
                                    GGAGG   GGGG GGAGG GCG
                                    |||||   |||| ||||| |||
                                    CCTCC   CCCC CCTCC CGC
                                       ___    G    _
GAM2615  KIAA1949  5'  GGGGAGGCAAGGAGGGGCG   41787      GA      A  A
                                    GGGGAG  GCGGGGGG GG GCG
                                    ||||||  |||||||| || |||
                                    CCCCTC  CGTTCCTC CC CGC
                                       __       _ _
GAM2615  KIAA1949  5'  GGGGAGGCAAGGAGGGGCG   41787      GA      A  A
                                    GGGGAG  GCGGGGGG GG GCG
                                    ||||||  |||||||| || |||
                                    CCCCTC  CGTTCCTC CC CGC
                                       __       _ _
GAM2615  KIAA1949  5'  GGGGAGGCAAGGAGGGGCG   41787      GA      A  A
                                    GGGGAG  GCGGGGGG GG GCG
                                    ||||||  |||||||| || |||
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                                CCCCTC  CGTTCCTC CC CGC
                                  __      _ _
GAM2615 MAGEF1   5' GGGGAGGGGTTGGACAGCG   41788       AGC  GG   GG
                                GGGGAGG   GG  GGA  AGCG
                                |||||||   ||  |||  ||||
                                CCCCTCC   CC  CCT  TCGC
                                   ___  AA   G_
GAM2615 MASA     5' GGGGAGGGCGGAGGGCGG    41789       A       A
                                GGGGAGG GCGGGGGG GG
                                ||||||| |||||||| ||
                                CCCCTCC CGCCTCCC CC
                                   _       G
GAM2615 MGC:5244 5' GGGGAGGGGTGGGGGTGC    41790       AGC  G   A  A
                                GGGGAGG   GG GGG GG GC
                                |||||||   || ||| || ||
                                CCCCTCC   CC CCC CC CG
                                   ___  A   _  A
GAM2615 MGC10882 3' GGGGAGGGAAGGGGAGTGG   41791       AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   CCCCTC CC
                                   CTT     A
GAM2615 MGC21688 3' GGGGAGGGTGGGGGGTTGCTGG 41792       AGC     AGGA  _
                                GGGGAGG   GGGGGG   GC GG
                                |||||||   ||||||   || ||
                                CCCCTCC   CCCCCC   CG CC
                                   CA_     AA__  A
GAM2615 MGC22014 3' GGGGGTAAGGGAGGGGCGG   41793     AGGAGCG      A
                                GGGG      GGGGGAGG GCGG
                                ||||      |||||||| ||||
                                CCCC      TTCCCTCC CGCC
                                  CA_____       C
GAM2615 MGC25056 5' GGGGAGGGCTGGGGGCTGG   41695       A  _    GA
                                GGGGAGG GC GGGGG  GG
                                ||||||| || |||||  ||
                                CCCCTCC CG CCCCC  CC
                                   _  A    GA
GAM2615 MGC2865  3' GGGGGGCGAGGGGCGG     41794     A  A      A
                                GGG GG GCGGGGGG GG
                                ||| || |||||||| ||
                                CCC CC CGCTCCCC CC
                                  _  _      G
GAM2615 MGC3047  3' GGGGAGGGGTGTGGAGGCG   41795       AGC  GG_   GA
                                GGGGAGG   GG   GGAG  GCG
                                |||||||   ||   ||||  |||
                                CCCCTCC   CC   CCTC  CGC
                                   ___  ACA   __
GAM2615 MGC35558 3' GGGAAGGGGTGTAAGGAGTGG 41796       AGC  GGG     C
                                GGGGAGG   GG   GAGGAG GG
                                |||||||   ||   |||||| ||
```

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                                CCCTTCC  CC  TTCCTC CC
                                   ___ ACA    A
GAM2615 MGC4415  3' GGGGAGGGTGGAGATGAGGGGG 41797    ____   CG   A A
            GCGG                  GGGA   GGAG  GGGGG GG GCGG
                                ||||   ||||  ||||| || ||||
                                CCCT   CCTC  CTCCC CC CGCC
                                  CCCA   TA   _ _
GAM2615 MMPL1    3' GGGGAGGAGCTGGGTGTGG   41798        G  GGA
                                GGGGAGGAGC GGG  GG
                                |||||||||| |||  ||
                                CCCCTCCTCG CCC  CC
                                     A  ACA
GAM2615 N4BP3    3' GGGGTGGGGCGGGGGGTGG   61333    A A     A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCCC CC
                                  A C      A
GAM2615 NECL1    3' GGGGAGCAAGCGGGAGGGGCGG 41799   A     _    A
                                GG GGAGCGGG GGGAGG GCGG
                                || |||||||| |||||| ||||
                                CC CCTCGTTC CCCTCC CGCC
                                 _      G    C
GAM2615 NFAT5    5' GGGGGGAGCGGCGGTGG    41800    A     G  GA
                                GGGG GGAGCGG GG  GG
                                |||| ||||||| ||  ||
                                CCCC CCTCGCC CC  CC
                                  _     G  A_
GAM2615 NFAT5    5' GGGGGGAGCGGCGGTGG    41800    A     G  GA
                                GGGG GGAGCGG GG  GG
                                |||| ||||||| ||  ||
                                CCCC CCTCGCC CC  CC
                                  _     G  A_
GAM2615 NKX2B    5' GGGGAGGGGGGAGTGG     41801      AGC    A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   CCCCTC CC
                                   ___    A
GAM2615 NKX2B    5' GGGGGGAGTGGGGGGAGG   41802    A   C
                                GGGG GGAG GGGGGGAGG
                                |||| |||| |||||||||
                                CCCC CCTC CCCCCCTCC
                                  _   A
GAM2615 NLI-IF   5' GGGGGGGAGGGGAGGGG    41803    A   C    A
                                GGGG GGAG GGGGGG GG
                                |||| |||| |||||| ||
                                CCCC CCTC CCCTCC CC
                                  C   _    _
GAM2615 NLI-IF   5' GGGGAGGGGTGGGAGGGAGG  41804      AGC_
                                GGGGAGG   GGGGGGAGG
                                |||||||   |||||||||
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                                CCCCTCC   CCTCCCTCC
                                   CCAC
GAM2615 NR5A1   3' GGGAGGGGGCGGGGCGGGTGG 41805      A_    _ A_
                                GGGAGG GCGGGG GG GG
                                |||||| |||||| || ||
                                CCCTCC CGCCCC CC CC
                                   CC     G CA
GAM2615 NXPH3   3' GGTGGGGAGCGGAGGGTGG   61334   _ A       A
                                GG GG GGAGCGGGGGG GG
                                || || |||||||||| ||
                                CC CC CCTCGCCTCCC CC
                                 A _        A
GAM2615 NXPH3   3' GGGCAGGGGCGAAAGGTGGGGG 61335    G  A _______    A
            GTGG                   GGG AGG GC      GGGGGG GG
                                ||| ||| ||      |||||| ||
                                CCC TCC CG      CCCCCC CC
                                  G  C CTTTCCA     A
GAM2615 P5CR2   3' GGGGGGTGGCAGGGGCGG   41806     A A_     GA
                                GGGG GG GCGGGGG GG
                                |||| || ||||||| ||
                                CCCC CC CGTCCCC CC
                                  _ AC      G_
GAM2615 P66     3' GGGGCGGGCGGGGGGCAGTGG 61336     A A      AGG C
                                GGGG GG GCGGGGGG  AG GG
                                |||| || |||||||  || ||
                                CCCC CC CGCCCCCC  TC CC
                                  G _      G__ A
GAM2615 PAK7    5' GGGTAGGGGCAAGGGGGGCGG 41807    G  A      A GA
                                GGG AGG GCGGGGGG G GCGG
                                ||| ||| |||||||| |  ||||
                                CCC TCC CGTTCCCC C CGCC
                                 A  C      _ __
GAM2615 PALM    5' GGGGAGGGGAGGGGGACGCGG 41808       AGC    A _
                                GGGGAGG  GGGGGG GGA GCGG
                                |||||||  |||||| ||| ||||
                                CCCCTCC  CCTCCC CCT CGCC
                                   ___    _ G
GAM2615 PCDH19  3' GGGGTGGGGCGGGGGGGA   61337     A A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCCC CT
                                  A C      _
GAM2615 PDGFC   5' GGGGTGGGGACGCGGGGGAGCG 41809     A_ AG G   AG
            G                    GGGG GG CG GGGG GAGCGG
                                |||| || || |||| ||||||
                                CCCC CC GC CCCC CTCGCC
                                  AC CT G  __
GAM2615 PF1     5' GGGGAGGGTGATGGGGGGTGG 41810       AGC__    A
                                GGGGAGG    GGGGGG GG
                                |||||||    |||||| ||
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                                CCCCTCC    CCCCCC CC
                                    CACTA     A
GAM2615 PGLYRP   3' GGGGAGGAATGGGGTGCGG   41811        C   GGA
                                GGGGAGGAG GGGG  GG
                                ||||||||| ||||  ||
                                CCCCTCCTT CCCC  CC
                                     A   ACG
GAM2615 PPP1R12C 3' GGGGAGGGGTGACGGGGTGG  41812       A___    _
                                GGGGAGG   GCGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   TGCCCC CC
                                    CCAC     A
GAM2615 PPP1R1B  5' GGGGAGGGCGCGGGAGCG    41813       A  G  GAGG
                                GGGGAGG GCG GGG   AGCG
                                ||||||| ||| |||   ||||
                                CCCCTCC CGC CCC   TCGC
                                    _  G  ____
GAM2615 QKI      5' GGAGAGGAGGGAGGGGCG    41814     C       A
                                GGAG GGGGGGAGG GCG
                                |||| ||||||||| |||
                                CCTC CCTCCCTCC CGC
                                  T       C
GAM2615 RAB5EP   5' GGGGATGGGCGGGGAAGCG   41815     _ A     GGAG
                                GGGGA GG GCGGGG   GAGCG
                                ||||| || ||||||   |||||
                                CCCCT CC CGCCCC   TTCGC
                                  A _    ____
GAM2615 RBPMS    5' GAGGAGGAGGAGGAGC      41816      GCG
                                GAGGA  GGGGGAGGAGC
                                |||||  ||||||||||
                                CTCCT  CCTCCTCCTCG
                                   ___
GAM2615 REPRIMO  3' GGGGGGAGCAGGAGAAGAGTGG 41817     A       G    C
                                GGGG GGAGCGGGGG AGGAG GG
                                |||| |||||||||| ||||| ||
                                CCCC CCTCGTCCTC TTCTC CC
                                  _       _    A
GAM2615 SCAMP-4  3' GGGGAGGGGTGGGGTGGGG   41818       AGC   _ A
                                GGGGAGG   GGGG GG GG
                                |||||||   |||| || ||
                                CCCCTCC   CCCC CC CC
                                    CCA   A _
GAM2615 SCAMP-4  3' GGGGAGGAGGTGGTGGGCGG  41819        CG  _  A
                                GGGGAGGAG  GG GGG GG
                                |||||||||  || ||| ||
                                CCCCTCCTC  CC CCC CC
                                     CA  A  G
GAM2615 SCYA22   3' GGGGGGGGTGGGGAGAGG    41820     A  AGC
                                GGGG GG   GGGGGGAGG
                                |||| ||   |||||||||
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                                CCCC CC   CCCCTCTCC
                                  _ CCA
GAM2615 SEMA6A   5' GGGGGCGGGGTGGGGGCG    41821     AGGA    _ A A _
                                GGGG   GCGGGG GG GG GC G
                                ||||   |||||| || || || |
                                CCCC   CGCCCC CC CC CG C
                                  ____     A _ _ A
GAM2615 SFXN5    3' GGGGAGGGCGGGAAGGG     41822       A      A
                                GGGGAGG GCGGGGGG GG
                                ||||||| |||||||| ||
                                CCCCTCC CGCCCTTC CC
                                   _      _
GAM2615 SNTA1    5' GGGGAGGAGCTCTGGGGGCGG 41823         GG_   AGGA
                                GGGGAGGAGC   GGGG   GCGG
                                ||||||||||   ||||   ||||
                                CCCCTCCTCG   CCCC   CGCC
                                     AGA   ____
GAM2615 SPATA6   5' GGGGAGGGGCGGCGGGGAG   41824       A   _
                                GGGGAGG GCGG GGGGAG
                                ||||||| |||| ||||||
                                CCCCTCC CGCC CCCCTC
                                   C   G
GAM2615 SSH-3    3' GGGAGGGGGCGGGGGTGG    41825      A_     GA
                                GGGAGG  GCGGGGG  GG
                                ||||||  |||||||  ||
                                CCCTCC  CGCCCCC  CC
                                   CC      A_
GAM2615 STIM2    3' GGTGGGGAGTGGAGGGTGG   41826   _ A   C     A
                                GG GG GGAG GGGGGG GG
                                || || |||| |||||| ||
                                CC CC CCTC CCTCCC CC
                                 A _   A     A
GAM2615 STX1B2   3' GGGGTGGAGGAGGGGTGG    41827     A   C     A
                                GGGG GGAG GGGGGG GG
                                |||| |||| |||||| ||
                                CCCC CCTC CTCCCC CC
                                  A   _     A
GAM2615 STX1B2   3' GGGGATGGAGTGAAAGGGG   41828      _   C GG   A
                                GGGGA GGAG G  GGG GG
                                ||||| |||| |  ||| ||
                                CCCCT CCTC C  TCC CC
                                  A   A TT   _
GAM2615 T1A-2    5' GGGGGGGCCGGAGGGGTGG   41829     A AG   _   A
                                GGGG GG  CGG GGGG GG
                                |||| ||  ||| |||| ||
                                CCCC CC  GCC CCCC CC
                                  C  G_   T   A
GAM2615 TETRAN   3' GGGGGGTGGGGGTCAGGCAG  41830     A AGC    GA  A
                                GGGG GG   GGGGG  GG GCGG
                                |||| ||   |||||  || ||||
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                                CCCC CC   CCCCC  TC CGTC
                                  _ A__     AG  _
GAM2615  TGIF2    5'  GGCGGGGAGCGGGGGGCGCCGG 41831    _ A         AGGAG
                                GG GG GGAGCGGGGGG     CGG
                                || || ||||||||||     |||
                                CC CC CCTCGCCCCCC     GCC
                                 G  _         GCG__
GAM2615  WAC      5'  GGGGAGGGGGGGAGAGC      41832       GGAGC       G
                                GGGGA    GGGGGGAG AGC
                                |||||    |||||||| |||
                                CCCCT    CCCCCCTC TCG
                                  _____      _
GAM2615  WAC      5'  GGGGAGGGGGGGAGAGC      41832       GGAGC       G
                                GGGGA    GGGGGGAG AGC
                                |||||    |||||||| |||
                                CCCCT    CCCCCCTC TCG
                                  _____      _
GAM2615  WNT10A   5'  GGGGGGGGCGGGGGGGTGAAGAG 41833      A  A       __
            CGG                    GGGG GG GCGGGGGG  AGGAGCGG
                                |||| || ||||||||  ||||||||
                                CCCC CC CGCCCCCC  TTCTCGCC
                                  _ C       AC
GAM2615  LOC124044 3'  GGGGAGGAGGGGGTGGGGCGG  41834         GC    GA  A
                                GGGGAGGA  GGGGG  GG GCGG
                                ||||||||  |||||  || ||||
                                CCCCTCCT  CCCCC  CC CGCC
                                    __    AC  _
GAM2615  LOC124783 5'  GGCGGGGAGCGGGCTGGTGG   41835    _ A       G_  A
                                GG GG GGAGCGGG  GG GG
                                || || ||||||||  || ||
                                CC CC CCTCGCCC  CC CC
                                 G  _       GA  A
GAM2615  LOC131034 5'  GGGGACGAGCGGGTGGCGG    41836       G      G  A
                                GGGGA GAGCGGG GG GG
                                ||||| ||||||| || ||
                                CCCCT CTCGCCC CC CC
                                   G      A  G
GAM2615  LOC131583 3'  GGGCGGGAGCGGGGGCCGG    41837     GA         GA
                                GGG  GGAGCGGGGG  GG
                                |||  ||||||||||  ||
                                CCC  CCTCGCCCCC  CC
                                  GC         GG
GAM2615  LOC143677 3'  GGGAAGGGGTAGGGGGGTGG   41838         AGC_     A
                                GGGGAGG    GGGGGG GG
                                |||||||    |||||| ||
                                CCCTTCC    CCCCCC CC
                                    CCAT     A
GAM2615  LOC146515 3'  GGGGTGGGCGGGGGGAG     41839      A  A
                                GGGG GG GCGGGGGGAG
                                |||| || ||||||||||
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                                CCCC CC CGCCCCCCTC
                                  A  _
GAM2615  LOC146988 5'  GGGGAGGGATAGGGAGTGG   41840       AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   TCCCTC CC
                                    CTA     A
GAM2615  LOC147160 5'  GGGGAAGGGGGGGGTGG     41841       AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTTC   CCCCCC CC
                                    C__     A
GAM2615  LOC148343 5'  GGGGAGTGGGCCCGGGGGGCGG 41842      ___  AG      A
                                GGGGA   GG  CGGGGGG GG
                                |||||   ||  ||||||| ||
                                CCCCT   CC  GCCCCCC CC
                                   CAC  GG      G
GAM2615  LOC151056 3'  AGGGTGGGGTGGGGGGAGGGGC 41843     A  AGC       A
             GG                   GGGG GG   GGGGGGAGG GCGG
                                |||| ||   |||||||| ||||
                                TCCC CC   CCCCCCTCC CGCC
                                  A  CCA        C
GAM2615  LOC151648 5'  GGGGGGAGGTGGGGCTGGCGG  41844     A   CG   GAGGA
                                GGGG GGAG  GGGG    GCGG
                                |||| ||||  ||||    ||||
                                CCCC CCTC  CCCC    CGCC
                                  _   CA   GAC__
GAM2615  LOC151878 5'  GGGGAGGGGTGGAGGGGCTGG  41845       AGC  GG    A  _
                                GGGGAGG   GG  GGAGG GC GG
                                |||||||   ||  ||||| || ||
                                CCCCTCC   CC  CCTCC CG CC
                                    ___  A_    C  A
GAM2615  LOC151878 5'  GGGGTAGGGGAGGGGTGG    41846     _  AGC     A
                                GGGG AGG   GGGGGG GG
                                |||| |||   |||||| ||
                                CCCC TCC   CTCCCC CC
                                  A  C__     A
GAM2615  LOC153232 3'  GGGGGGGGGGGGGCGGGCAG   41847     A  AGC     A  A
                                GGGG GG   GGGGGG GG GCGG
                                |||| ||   |||||| || ||||
                                CCCC CC   CCCCCC CC CGTC
                                  _ ___     G  _
GAM2615  LOC153474 3'  AGGGAGGAGCGATCGGGAG   41751          G_
                                GGGGAGGAGCGG  GGGAG
                                ||||||||||||  |||||
                                TCCCTCCTCGCT  CCCTC
                                       AG
GAM2615  LOC153688 5'  GGGGGAAGTGGGGGCGG     41848     A   C    GA
                                GGGG GGAG GGGGG  GG
                                |||| |||| |||||  ||
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                                CCCC CTTC CCCCC  CC
                                  _   A    G_
GAM2615  LOC154427 3'  GGGAGGGGCCGGGGGAGCGG  41849      A  G    GGA
                                GGGAGG GC GGGGGA  GCGG
                                |||||| || ||||||  ||||
                                CCCTCC CG CCCCCT  CGCC
                                   C  G    ___
GAM2615  LOC157226 5'  GGGGCGGTGGGGGGAAAGGCGG 41851     A  AGC      GA
                                GGGG GG  GGGGGGAG  GCGG
                                |||| ||  ||||||||  ||||
                                CCCC CC  CCCCCCTT  CGCC
                                  G  A__      TC
GAM2615  LOC157226 5'  GGGGACGGGAGGGGGGCG   41850     AGGA      A  A
                                GGGG   GCGGGGGG GG GCG
                                ||||   |||||||| || |||
                                CCCC   TGCCCTCC CC CGC
                                  _____      _  C
GAM2615  LOC158236 5'  AGGGGGAGGGGGAGGGGCGG  41852    A   C    A  A
                                GGGG GGAG GGGGGG GG GCGG
                                |||| |||| |||||| || ||||
                                TCCC CCTC CCCCTC CC CGCC
                                  _   _    _ _
GAM2615  LOC158819 5'  GGGGAGGAAAGAGGAGG    41853        CG
                                GGGGAGGAG  GGGGGAGG
                                |||||||||  ||||||||
                                CCCCTCCTT  TCTCCTCC
                                     __
GAM2615  LOC158972 3'  AGGGAGGAAGAGGAGGGGCGG  41854       GCG      A
                                GGGGAGGA   GGGGGAGG GCGG
                                ||||||||   |||||||| ||||
                                TCCCTCCT   TCTCCTCC CGCC
                                     ___      C
GAM2615  LOC162333 5'  GGGGAGGGTTGGTGATGGGGTG 41855       AGC  ____   A
          G                      GGGGAGG   GG   GGGG GG
                                |||||||   ||   |||| ||
                                CCCCTCC   CC   CCCC CC
                                    CAA  ACTA   A
GAM2615  LOC197136 3'  GGGGAGGAGGGGGTGGGGCGG  41834       GC    GA  A
                                GGGGAGGA  GGGGG  GG GCGG
                                ||||||||  |||||  || ||||
                                CCCCTCCT  CCCCC  CC CGCC
                                     __    AC  _
GAM2615  LOC200862 5'  GGGAGGGAGCCCGGGAGCG   41856    GA    GG   GAGG
                                GGG  GGAGC  GGG   AGCG
                                |||  |||||  |||   ||||
                                CCC  CCTCG  CCC   TCGC
                                  TC    GG  _____
GAM2615  LOC203530 3'  GGGGGGTGGGGGGGAAG    41857     A  AGC
                                GGGG GG   GGGGGGAGG
                                |||| ||   |||||||||
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                                CCCC CC   CCCCCCTTC
                                  _  AC_
GAM2615  LOC221656 3'  GGGGGGGGCGGGGGGCGGGCGG 41858      A  A       A  A
                                GGGG GG GCGGGGGG GG GCGG
                                |||| || |||||||| || ||||
                                CCCC CC CGCCCCCC CC CGCC
                                  _  C       G  _
GAM2615  LOC221656 3'  GGGCGGGGGGGCGGGCG      41859    A       A  A
                                GG GCGGGGGG GG GCG
                                || |||||||| || |||
                                CC CGCCCCCC CC CGC
                                 _       G  _
GAM2615  LOC221692 3'  GGGGCGGGGCGGGGGGGCCGG  61338      A  A       AG AG
                                GGGG GG GCGGGGGG  G  CGG
                                |||| || ||||||||  |  |||
                                CCCC CC CGCCCCCC  C  GCC
                                  G  C       __ G_
GAM2615  LOC221833 3'  GGAGAGGGGCGGGCGCAGGGTG 41860        A    _____   A
               G                   GGGGAGG GCGGG   GGG GG
                                |||||||| |||||    ||| ||
                                CCTCTCC CGCCC    CCC CC
                                    C    GCGT   A
GAM2615  LOC221876 3'  GGGGAGGGGTGTGGGGAAAG   41861        AGCG_
                                GGGGAGG    GGGGGAGG
                                |||||||    ||||||||
                                CCCCTCC    CCCCTTTC
                                    CCACA
GAM2615  LOC222166 5'  GGGCGGCGGGAGGAGCG     41862    A   G
                                GG GCGG GGGAGGAGCG
                                || |||| ||||||||||
                                CC CGCC CCCTCCTCGC
                                 _   G
GAM2615  LOC254532 5'  GGGGGGAGTGAGGGGCCGG    41864      A   C     A_
                                GGGG GGAG GGGGGG  GG
                                |||| |||| ||||||  ||
                                CCCC CCTC CTCCCC  CC
                                  _   A     GG
GAM2615  LOC254532 5'  GGGGAGGGGCGGGGTGGGG    41863        A     _ A
                                GGGGAGG GCGGGG GG GG
                                ||||||| |||||| || ||
                                CCCCTCC CGCCCC CC CC
                                    C     A  _
GAM2615  LOC255031 5'  GGGCGAGGGGCGGGCGAAGAGC 41865     _   A    G G
               GG                   GGG GAGG GCGGG G AGGAGCGG
                                ||| |||| ||||| | ||||||||
                                CCC CTCC CGCCC C TTCTCGCC
                                  G   C    G _
GAM2615  LOC255259 5'  GGGGAGGAGGCGGGGGCCGG   41866         _     GA
                                GGGGAGGAG CGGGGG  GG
                                |||||||| ||||||  ||
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                                CCCCTCCTC GCCCCC  CC
                                     C     GG
GAM2615  LOC257200 3'  GGGAAGGGGTGGGGGGTGG   41867       AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCTTCC   CCCCCC CC
                                    CCA     A
GAM2615  LOC257484 3'  GGGGGTAAGGGAGGGGCGG   41793     AGGAGCG      A
                                GGGG      GGGGGAGG GCGG
                                ||||      |||||||| ||||
                                CCCC      TTCCCTCC CGCC
                                  CA_____       C
GAM2615  LOC64744  3'  GGGGAGAGGGTGGGAGGCG   41868       AGC  _    GA
                                GGGGAGG   GGG GGGAG  GCG
                                |||||||   ||| |||||  |||
                                CCCCTCT   CCC CCCTC  CGC
                                   ___  A    __
GAM2615  LOC90233  5'  GGGGAGCGGCGGCCGACCGGGG 41869      GA   GG  A_  A
            CGG                   GGGGAG  GCGG  GG  GG GCGG
                                ||||||  ||||  ||  || ||||
                                CCCCTC  CGCC  CT  CC CGCC
                                   GC    GG  GG  C
GAM2615  LOC92080  5'  GGGGAGGGTGGTGGAGGAGCGG 41870       AGCG  G
                                GGGGAGG    GG GGAGGAGCGG
                                |||||||    || ||||||||||
                                CCCCTCC    CC CCTCCTCGCC
                                    CA__  A
GAM2616  ABCC1    5'  CACCGGGCGGCGGGTGAT    61341         CCTTA
                                CACCGGGCGGC    GTGAT
                                ||||||||||     |||||
                                GTGGCCCGCCG    CACTA
                                      CC___
GAM2616  ABCC1    5'  CACCGGGCGGCGGGTGAT    61341         CCTTA
                                CACCGGGCGGC    GTGAT
                                ||||||||||     |||||
                                GTGGCCCGCCG    CACTA
                                      CC___
GAM2616  ABCC1    5'  CACCGGGCGGCGGGTGAT    61341         CCTTA
                                CACCGGGCGGC    GTGAT
                                ||||||||||     |||||
                                GTGGCCCGCCG    CACTA
                                      CC___
GAM2616  ABCC1    5'  CACCGGGCGGCGGGTGAT    61341         CCTTA
                                CACCGGGCGGC    GTGAT
                                ||||||||||     |||||
                                GTGGCCCGCCG    CACTA
                                      CC___
GAM2616  ABCC1    5'  CACCGGGCGGCGGGTGAT    61341         CCTTA
                                CACCGGGCGGC    GTGAT
                                ||||||||||     |||||
                                GTGGCCCGCCG    CACTA
                                      CC___
GAM2616  ABCC1    5'  CACCGGGCGGCGGGTGAT    61341         CCTTA
                                CACCGGGCGGC    GTGAT
                                ||||||||||     |||||
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                                GTGGCCCGCCG    CACTA
                                      CC___
GAM2616 ABCC1    5' CACCGGGCGGCGGGTGAT    61341         CCTTA
                                CACCGGGCGGC    GTGAT
                                ||||||||||    |||||
                                GTGGCCCGCCG    CACTA
                                      CC___
GAM2616 ADAMTS13 3' TGGCACTGGGTGTCCAACAGGA 61342    A  C  CGG  CT  T
             T                   TG CAC GGG   CC  TAG GAT
                                || ||| |||   ||  ||| |||
                                AC GTG CCC   GG  GTC CTA
                                 C  A  ACA  TT  _
GAM2616 GOLGA4   5' CATACTGCTTTCTTAGTGAT  61343    G  G  C__
                                CG GC GC   CTTAGTGAT
                                || || ||   |||||||||
                                GT TG CG   GAATCACTA
                                 A  A  AAA
GAM2616 FLJ14621 3' TGAACCGGCTTAGTG      61344     C    GCGGCC
                                TGA ACCGG     CTTAGTG
                                ||| |||||     |||||||
                                ACT TGGCC     GAATCAC
                                  _    _______
GAM2616 FLJ20452 3' TGCACCTGGCCTTTAGTGA   61345    A   GGGC   C
                                TG CACC    GGCC TTAGTGA
                                || ||||    |||| |||||||
                                AC GTGG    CCGG AATCACT
                                 _   A___   A
GAM2616 KIAA1940 3' TGACACCAGGCGCTGGTG    61346          G CCTTA
                                TGACACCGGGCG C     GTG
                                ||||||||||||  |    |||
                                ACTGTGGTCCGC G     CAC
                                      _ AC___
GAM2616 PTPRN2   3' CCGGGCGGCCTCACTGA     61347         C  G
                                CCGGGCGGCC TTA TGA
                                |||||||||| ||| |||
                                GGCCCGCCGG AGT ACT
                                      _  G
GAM2616 PTPRN2   3' CCGGGCGGCCTCACTGA     61347         C  G
                                CCGGGCGGCC TTA TGA
                                |||||||||| ||| |||
                                GGCCCGCCGG AGT ACT
                                      _  G
GAM2616 LOC144519 3' GGGATTCTGCCCTTAGTGAT  61348     CG___
                                GGG    GCCCTTAGTGAT
                                |||    ||||||||||||
                                CCC    CGGGAATCACTA
                                  TAAGA
GAM2616 LOC164584 5' CCTGGGCGGCCTCCTTGTTAGT 61349    _      _ ____
             GAT                   CC GGGCGGCC CT    TAGTGAT
                                || |||||||| ||    |||||||
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                                GG CCCGCCGG GG    ATCACTA
                                 A       A  AACA
GAM2617  DKFZp586I021 3'  TATTATTGATTCTATAGA    61352      CA
                                TATTA  GATTCTATAGA
                                |||||  ||||||||||
                                ATAAT  CTAAGATATCT
                                   AA
GAM2617  LXN      3'  TATTATGGACTCTATAAA    61353      CA
                                TATTA  GATTCTATAGA
                                |||||  ||||||||||
                                ATAAT  CTGAGATATTT
                                   AC
GAM2617  LOC151193 3'  TATTACAGATTCTAGGGA    61354            TA
                                TATTACAGATTCTA  GA
                                ||||||||||||||  ||
                                ATAATGTCTAAGAT  CT
                                         CC
GAM2618  ALDH3A2   3'  GGAGTGAAGGATTCAGTGAGGT 61357      CC  __________  CAAG
             GCCTTGGC                AAGGA  CGG       GC   GC
                                |||||  |||       ||   ||
                                TTCCT  GTC       CG   CG
                                   AA   ACTCCAIII  GAAC
GAM2618  C14orf1   3'  AAGGAAGAAGATGGCCAAGG   61358     T     CCCG
                                AAG GAAGGA    GGCCAAGG
                                ||| ||||||    ||||||||
                                TTC CTTCTT    CCGGTTCC
                                  _     CTA_
GAM2618  C20orf1   3'  AGTGAAGACCCATATAAAAGGC 61359       G     GGCC_
                                AGTGAAG ACCCG     AAGGC
                                ||||||| |||||     |||||
                                TCACTTC TGGGT     TTCCG
                                    _     ATATT
GAM2618  CACNB1    3'  AAGTGAAGGGGCTCAGGG    61360         ACCCG  _  A
                                AAGTGAAGG     GGC CA GG
                                |||||||||     ||| || ||
                                TTCACTTCC     CCG GT CC
                                     _____   A  C
GAM2618  COL6A1    3'  GTGGGGAACCCAGGTGAGGC   61361     AA       CCA
                                GTG  GGACCCGGG   AGGC
                                |||  |||||||||   ||||
                                CAC  CTTGGGTCC   TCCG
                                  CC        AC_
GAM2618  CPLX2     5'  GAGGGCGCCCGGGCCGAGG    61362    A  A_      A
                                GA GG  CCCGGGCC AGG
                                || ||  |||||||| |||
                                CT CC  GGGCCCGG TCC
                                 C  GC       C
GAM2618  CYLN2     3'  GTGGAGGCTGCAGGGCCAAGGC 61363     A   ACCC_
                                GTG AGG     GGGCCAAGGC
                                ||| |||     ||||||||||
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                                CAC TCC    CCCGGTTCCG
                                  C   GACGT
GAM2618  DCTN1    3'  AGTGGGGGAACCCGGGTCAAGG 61364     AA  _    C
                                AGTG  GGA CCCGGG CAAGG
                                ||||  ||| |||||| |||||
                                TCAC  CCT GGGCCC GTTCC
                                  CC   T     A
GAM2618  DCTN1    3'  AGTGGGGGAACCCGGGTCAAGG 61364     AA  _    C
                                AGTG  GGA CCCGGG CAAGG
                                ||||  ||| |||||| |||||
                                TCAC  CCT GGGCCC GTTCC
                                  CC   T     A
GAM2618  DDX6     3'  AGGAAAGAGGGCCAAGG     61365    T     CCC
                                AG GAAGGA   GGGCCAAGG
                                || ||||||   |||||||||
                                TC CTTTCT   CCCGGTTCC
                                 _    ____
GAM2618  DOK1     3'  GGAGTAAGGATCCAGGC     61366    A    A   C
                                A AGTGA GGA CCGGGC
                                | ||||| ||| ||||||
                                C TCATT CCT GGTCCG
                                 C    _   A
GAM2618  EGR1     3'  GTGAAGAACTTGGACATGGC   61367        CC    CAA
                                GTGAAGGAC  GGGC   GGC
                                |||||||||  ||||   |||
                                CACTTCTTG  CCTG   CCG
                                     AA    TA_
GAM2618  EMP1     5'  GAAGGACCCGCCTCCCGAGG   61368         GG_  A_
                                GAAGGACCCG   CC  AGG
                                ||||||||||   ||  |||
                                CTTCCTGGGC   GG  TCC
                                     GGA  GC
GAM2618  FPGS     3'  AGGAAGGAGAGACCAAGGC    61369    T     CCC
                                AG GAAGGA   GGGCCAAGGC
                                || ||||||   ||||||||||
                                TC CTTCCT   TCTGGTTCCG
                                 _     C__
GAM2618  HAS3     3'  ATGAAGGAAAGCACCAGGG    61371        CCC  _   A
                                GTGAAGGA   GG GCCA GG
                                ||||||||   || |||| ||
                                TACTTCCT   TC TGGT CC
                                    T__  G    C
GAM2618  HAS3     5'  GAAGGGGGCGCCAAGGC     61370       ACCC  _
                                GAAGG    GG GCCAAGGC
                                |||||    || ||||||||
                                CTTCC    CC CGGTTCCG
                                   C___  G
GAM2618  HLCS     5'  GGAGTGAAAGACCCCAGGTGCC 61372           __  _____  CAAG
            TTG                   AGTGAAGGACCC  GG    GC    G
                                ||||||||||||  ||    ||    |
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                                TCACTTTCTGGG CC   CG   C
                                      GT  AIII  GAAC
GAM2618 IFNGR1   3' AAAGTGAAGTGGCTACAAAGG 61373        GACCCGG C
                                AAAGTGAAG      GC AAGG
                                |||||||||      || ||||
                                TTTCACTTC      TG TTCC
                                     ACCGA__  T
GAM2618 IL1R1    3' AAAGGAGGAGGAAGGGTCGAGG 61374     T  A  CCC_  CCA
             C                   AAAG GA GGA   GGG  AGGC
                                |||| || |||   |||  ||||
                                TTTC CT CCT   CCC  TCCG
                                  _ _  CCTT  AGC
GAM2618 LPIN2    3' AAAGGAGGGATCCCAGGC    61375     T  A  _
                                AAAG GA GGA CCCGGGC
                                |||| || ||| |||||||
                                TTTC CT CCT GGGTCCG
                                  _ C  A
GAM2618 LZTS1    3' AAATGAAGGAACTGAGGGCTGA 61376         _ CC_   CA
             GGC                   AAGTGAAGGA C  GGGC  AGGC
                                |||||||||| |  ||||  ||||
                                TTTACTTCCT G  CCCG  TCCG
                                     T ACT   AC
GAM2618 MASP1    3' AGGAAGGATTAGGCCAAGGC  61377    T    CCC
                                AG GAAGGA  GGGCCAAGGC
                                || ||||||  ||||||||||
                                TC CTTCCT  TCCGGTTCCG
                                 _    AA_
GAM2618 MSF      3' AAAGTGAAGCATCTCAAGG   61378       GACC  GGC
                                AAAGTGAAG   CG   CAAGG
                                |||||||||   ||   |||||
                                TTTCACTTC   GT   GTTCC
                                     ____  AGA
GAM2618 MUC3B    3' TGGAGGATCCGAGAGAGGC   61379    A   C    CCA
                                TG AGGA CCGGG   AGGC
                                || |||| |||||   ||||
                                AC TCCT GGCTC   TCCG
                                 C   A    TC_
GAM2618 MUC5B    3' AGGGAGGGGCAAGGCCAAGG  61380    T  A  ACCC
                                AG GA GG   GGGCCAAGG
                                || || ||   |||||||||
                                TC CT CC   TCCGGTTCC
                                 C  C  CGT_
GAM2618 MYH7     5' ATGAGGAAAGGGGCCAAGGC  61381     A  CCC
                                GTGA GGA   GGGCCAAGGC
                                |||| |||   ||||||||||
                                TACT CCT   CCCGGTTCCG
                                  _  TTC
GAM2618 NGFR     3' AAGTGAAGGGGCCACACGGGC 61382        A_ ___
                                AAGTGAAGG  CC   CGGGC
                                |||||||||  ||   |||||
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                                TTCACTTCC  GG   GCCCG
                                     CC  TGT
GAM2618  PACE4    5'  AAGTAAAGGGCCTGCGGG    61383         A  __
                                AAGTGAAGG CC  CGGG
                                ||||||||| ||  ||||
                                TTCATTTCC GG  GCCC
                                     C  AC
GAM2618  PPP1R8   5'  GCGTAAGTTCGGGCCAAGGC   61384    _  GACC
                                GTG AAG   CGGGCCAAGGC
                                ||| |||   ||||||||||
                                CGC TTC   GCCCGGTTCCG
                                  A  AA__
GAM2618  PPP1R8   5'  GCGTAAGTTCGGGCCAAGGC   61384    _  GACC
                                GTG AAG   CGGGCCAAGGC
                                ||| |||   ||||||||||
                                CGC TTC   GCCCGGTTCCG
                                  A  AA__
GAM2618  PRG2     5'  ATGAAGGAGGCCCTGAGGC   61385       CCCG   A__
                                GTGAAGGA   GGCC   AGGC
                                ||||||||   ||||  ||||
                                TACTTCCT   CCGG   TCCG
                                     _____   GAC
GAM2618  PYGO2    5'  GGAGTGGGGGACCCGGGTTAGC 61386   A   AA       CCAA
                                A AGTG  GGACCCGGG   GGC
                                | ||||  |||||||||   |||
                                C TCAC  CCTGGGCCC   TCG
                                 C   CC       AA__
GAM2618  TGFB3    3'  AGGAGGGACCCAGAGGG    61387    T  A       CCAA
                                AG GA GGACCCGGG   GG
                                || || |||||||||   ||
                                TC CT CCTGGGTCT   CC
                                  _ C       C___
GAM2618  TNFAIP1  3'  GGAGTGAAGGCCTTCAGG    61388   A      A  __
                                A AGTGAAGG CC  CGGG
                                | ||||||| ||  ||||
                                C TCACTTCC GG  GTCC
                                 C       _ AA
GAM2618  BNIP-S   3'  AAGTGAAGATCCGGTGGTGCCT 61389       AC   ________  CAAG
            TG                   GTGAAGG  CCGG     GC   G
                                |||||||  ||||     ||   |
                                CACTTCT  GGCC     CG   C
                                    A_   ACCAIII  GAAC
GAM2618  BRUNOL6  5'  GCGGGGCGGGCCCGGGCCGAGG 61390    AA__  A      A
                                GTG   GG CCCGGGCC AGG
                                |||   || |||||||| |||
                                CGC   CC GGGCCCGG TCC
                                  CCCG  C       C
GAM2618  CBX6     3'  AAGTGAAGGTCCGACAGGTGCC 61391       AC   G_________  CAAG
            TTG                   TGAAGG  CCG       GC   G
                                ||||||  |||       ||   |
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                                ACTTCC  GGC       CG   C
                                   A_   TGTCCAIII  GAAC
GAM2618  CDH22    3'  AAGTGAAGTGACTTGCCCGAGG 61392        _   CCGG   A_
              C                    AAGTGAAG GAC    GCC  AGGC
                                   |||||||| |||    |||  ||||
                                   TTCACTTC CTG    CGG  TCCG
                                      A   AA__   GC
GAM2618  DKFZP434B205 3'  GAAGGTGCCCCGGGCCGAGGC  61393      A__      A
                                   GAAGG   CCCGGGCC AGGC
                                   |||||   |||||||| ||||
                                   CTTCC   GGGCCCGG TCCG
                                      ACG       C
GAM2618  DKFZp434C0328 3'  AAGTGAAAGGATGGATTATTAA 61394        _   CCC   CC___
              GGC                     AAGTGAA GGA   GGG    AAGGC
                                   |||||||| |||   |||    |||||
                                   TTCACTT CCT   CCT    TTCCG
                                      T   A__   AATAA
GAM2618  DKFZP547L112 5'  GCGAGCCGGGGCCAAGG     61395      AG A  C
                                   GTGA  G CC GGGCCAAGG
                                   ||||  | || |||||||||
                                   CGCT  C GG CCCGGTTCC
                                     __ _  C
GAM2618  DKFZp547M072 3'  GGAGTGAAGGGTGAAGGAGG   61396   A       ACCC   CCA
                                   A AGTGAAGG    GGG   AGG
                                   | ||||||||    |||   |||
                                   C TCACTTCC    TCC   TCC
                                    C       CACT   ___
GAM2618  DKFZp761A132 3'  GGAGTGAAGGACCTCGCGGC   61397   A         _ _
                                   A AGTGAAGGACC CG GGC
                                   | ||||||||||| || |||
                                   C TCACTTCCTGG GC CCG
                                    C          A  G
GAM2618  DKFZp762A227 3'  GGAGTCAAGGGTCTGCCAAGGC 61398   A   G    ACCCGG
                                   A AGT AAGG      GCCAAGGC
                                   | ||| ||||     ||||||||
                                   C TCA TTCC      CGGTTCCG
                                    C   G    CAGA__
GAM2618  EFNA5    3'  GTGAGAGAAGCCAAGGGCCAGG 61399      _   _  C_     A
              GC                     GTGA AGGA CC  GGGCCA GGC
                                   |||| |||| ||  |||||| |||
                                   CACT TCTT GG  CCCGGT CCG
                                     C    C  TT     C
GAM2618  ERMAP    3'  TGAAGGTCTGGGCCAAGG    61400       ACCC
                                   TGAAGG    GGGCCAAGG
                                   ||||||    |||||||||
                                   ACTTCC    CCCGGTTCC
                                      AGA_
GAM2618  ESPL1    5'  AAAGTGAGGAACCTCACAAGG  61401        A   C  GGGC
                                   AAAGTGA GGA CC    CAAGG
                                   ||||||| ||| ||    |||||
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                                TTTCACT CCT GG    GTTCC
                                   _  T  AGT_
GAM2618  FBXL9    3'  AAAGCAACCCGGGTCAAGGC  61402     _      C
                                GAAG GACCCGGG CAAGGC
                                |||| |||||||| ||||||
                                TTTC TTGGGCCC GTTCCG
                                  G       A
GAM2618  FKSG43   3'  AGGACAATGCCGGGCCAGGGC  61403      ____      A
                                AGGAC    CCGGGCCA GGC
                                |||||    |||||||| |||
                                TCCTG    GGCCCGGT CCG
                                   TTAC       C
GAM2618  FLJ00007 3'  GGAGGGAGGGGCCCAAGCCCAG 61404   A  T  A  A      AA_
            GGC                    A AG GA GG CCCGGGCC   GGC
                                | || || || ||||||||   |||
                                C TC CT CC GGGTTCGG   CCG
                                 C  C  C  C       GTC
GAM2618  FLJ12541 3'  GTGAAGGCCAAGGCTGAGG   61405       A  C    CA
                                GTGAAGG CC GGGC  AGG
                                ||||||| || ||||  |||
                                CACTTCC GG TCCG  TCC
                                   _ T    AC
GAM2618  FLJ14524 3'  GGAGTGAGGGCCCCAGGC    61406   A    A  A
                                A AGTGA GG CCCGGGC
                                | ||||| || |||||||
                                C TCACT CC GGGTCCG
                                 C    C  G
GAM2618  FLJ14596 3'  AGTGGGCGGGGCCAAGGC    61407     AA  ACCC
                                AGTG  GG   GGGCCAAGGC
                                ||||  ||   ||||||||||
                                TCAC  CC   CCCGGTTCCG
                                  __ GC__
GAM2618  FLJ20452 3'  GCCAGAGTCCGGGCCAGGGC  61408    GA   AC      A
                                GT  AGG  CCGGGCCA GGC
                                ||  |||  |||||||| |||
                                CG  TCT  GGCCCGGT CCG
                                 G_  CA       C
GAM2618  FLJ20695 3'  AAGTGAAAGGCCAAGG      61409       GGACCC
                                AAGTGAA     GGGCCAAGG
                                |||||||     |||||||||
                                TTCACTT     TCCGGTTCC
                                   _______
GAM2618  FLJ21736 3'  GGAGGGAGGACCCGGCACTGGG 61410   A  T  A      _  CAA
            GC                   A AG GA GGACCCGG GC   GGC
                                | || || |||||||| ||   |||
                                C TC CT CCTGGGCC TG   CCG
                                 C  C  _       G  ACC
GAM2618  G3BP     3'  AAGTGAAAGACTAAAGGTGCCT 61411          CC__ _____  CAAG
            TG                   AGTGAAGGAC    GG    GC    G
                                ||||||||||   ||   ||   |
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                                TCACTTTCTG   CC   CG   C
                                     ATTT  AIII  GAAC
GAM2618  GR6      5'  AGTGAAGGCTCCCAGGGC    61412        A_  _
                                AGTGAAGG  CCC GGGC
                                ||||||||  ||| ||||
                                TCACTTCC  GGG CCCG
                                    GA   T
GAM2618  GSPT2    5'  AGCGAAGGGCCAAGG      61413       GGACCC
                                AGTGAA     GGGCCAAGG
                                ||||||     |||||||||
                                TCGCTT     CCCGGTTCC
                                     _______
GAM2618  GTPBP1   3'  AAAGCTGAGGGCAGCCAGGGC  61414      GA   ACCCG    A
                                AAAGT  AGG    GGCCA GGC
                                |||||  |||    ||||| |||
                                TTTCG  TCC    TCGGT CCG
                                   AC   CG___    C
GAM2618  H6PD     5'  GAAGGCGCGAGGCCAAGGC   61415      ACC  _
                                GAAGG   CG GGCCAAGGC
                                |||||   || |||||||||
                                CTTCC   GC CCGGTTCCG
                                   GC_  T
GAM2618  HUMNPIIY20 3'  GGAGTGAAGAGGTCCAGGAAGG 61416   A      _ AC    CC
            C                    A AGTGAAG G  CCGGG  AAGGC
                                | |||||||  |  |||||  |||||
                                C TCACTTC C  GGTCC  TTCCG
                                 C      T CA    __
GAM2618  KIAA0212 3'  AAAGTGAAGAGACTTAGGTGCC 61417        _  CC_  _____  CAAG
            TTG                    AGTGAAG GAC   GG    GC    G
                                ||||||| |||   ||    ||    |
                                TCACTTC CTG   CC    CG    C
                                    T   AAT  AIII  GAAC
GAM2618  KIAA0275 3'  GTAGAAACCAAGGGGTCAGGGC 61418     AA    C__   C  A
                                GTG  GGACC   GGG CA GGC
                                |||  |||||   ||| || |||
                                CAT  TTTGG   CCC GT CCG
                                  C_    TTC   A  C
GAM2618  KIAA0296 3'  GTGAAGGATCCAGGAGTGGG   61419        C    CCAA
                                GTGAAGGA CCGGG    GG
                                |||||||| |||||    ||
                                CACTTCCT GGTCC    CC
                                     A     TCAC
GAM2618  KIAA0303 5'  AAATGAAAAATGGGCTGAGGC  61420         CCC    CA
                                AAGTGAAGGA   GGGC  AGGC
                                ||||||||||   ||||  ||||
                                TTTACTTTTT   CCCG  TCCG
                                     A__    AC
GAM2618  KIAA0444 3'  AGGTGTCACCGGGCCAAGGC   61421     AC___
                                AGG    CCGGGCCAAGGC
                                |||    ||||||||||||
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                                TCC    GGCCCGGTTCCG
                                  ACAGT
GAM2618 KIAA0552 5' GGAATGAAGGACCTACCTTGCG 61422   A       C_________
            GGGC                  A AGTGAAGGACC       GGGC
                                | ||||||||||        ||||
                                C TTACTTCCTGG       CCCG
                                 C          ATGGAACGC
GAM2618 KIAA0673 3' AAGTGAAAGGCTGCAGAGAGGC 61423       _ ACC   CCA
                                AAGTGAA GG   CGGG   AGGC
                                ||||||| ||   ||||   ||||
                                TTCACTT CC   GTCT   TCCG
                                    T  GAC    C__
GAM2618 KIAA0892 3' GGAGTGGGGGGGACCAAGA    61424   A   AA  ACCC
                                A AGTG  GG    GGGCCAAGG
                                | ||||  ||    |||||||||
                                C TCAC  CC    CCTGGTTCT
                                 C    C_ _____
GAM2618 KIAA1140 5' AAGTGGAGACCCGGCCGGGGGC 61425      AA      G  AA_
                                AAGTG  GGACCCGG CC   GGC
                                |||||  |||||||| ||   |||
                                TTCAC  TCTGGGCC GG   CCG
                                   C_       _ CCC
GAM2618 KIAA1600 5' AGTGAAGGCCGGTGCGGGGC   61426       AC   _ CAA
                                AGTGAAGG  CCGG GC   GGC
                                ||||||||  |||| ||   |||
                                TCACTTCC  GGCC CG   CCG
                                    __    A  CC_
GAM2618 MGC1842   3' AGCCCCAAGCCTGGGCCAGGGC 61427    GA_   A  C     A
                                AGT   AGG CC GGGCCA GGC
                                |||   ||| || |||||| |||
                                TCG   TTC GG CCCGGT CCG
                                  GGG   _  A     C
GAM2618 MGC2647   3' GAAGGTGACAGCGGGCCAAGGC 61428      __  C_
                                GAAGG  AC  CGGGCCAAGGC
                                |||||  ||  ||||||||||
                                CTTCC  TG  GCCCGGTTCCG
                                   AC  TC
GAM2618 MGC8407   3' GTAAGGACCCAGTAAGGC    61429     A      GCC
                                GTGA GGACCCGG   AAGGC
                                |||| ||||||||   |||||
                                CATT CCTGGGTC   TTCCG
                                   _       A__
GAM2618 N4BP3    3' TGAGTGAAGGACTGGAGGC   61430   A       CC_
                                A AGTGAAGGAC   GGGC
                                | ||||||||||   ||||
                                A TCACTTCCTG   TCCG
                                 C         ACC
GAM2618 OLIG1    3' GAAGGGAGGCCGGGCCGAGG   61431      AC__      A
                                GAAGG    CCGGGCC AGG
                                |||||    ||||||| |||
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                                CTTCC    GGCCCGG TCC
                                   CTCC      C
GAM2618  PIGQ     3'  GGAGTGAGGGCCCGGGC     61432    A     A  A
                                A AGTGA GG CCCGGGC
                                | ||||| || |||||||
                                C TCACT CC GGGCCCG
                                 C     C  _
GAM2618  RAI17    3'  AAAGGAAGAAAAGGGGCCGGGG 61433      T     CCC     AA
              C                  AAAG GAAGGA   GGGCC  GGC
                                 |||| ||||||   |||||  |||
                                 TTTC CTTCTT   CCCGG  CCG
                                   _     TTC     CC
GAM2618  RoXaN    3'  AAAGAGAAGGAAGCCAAGG    61435      T     CCCG
                                 AAAG GAAGGA    GGCCAAGG
                                 |||| ||||||    ||||||||
                                 TTTC CTTCCT    TCGGTTCC
                                   T     _____
GAM2618  RoXaN    3'  AAACTGAAGGACCTGTCCAAGG 61434     G        CGGG
              C                  AAA TGAAGGACC    CCAAGGC
                                 ||| |||||||||    |||||||
                                 TTT ACTTCCTGG    GGTTCCG
                                   G        ACA_
GAM2618  SNPH     5'  AGTGAAGGCCGTGCCCAAGG   61436         AC   G   _
                                 AGTGAAGG  CCG GCC AAGG
                                 ||||||||  ||| ||| ||||
                                 TCACTTCC  GGC CGG TTCC
                                      __   A   G
GAM2618  SP2      3'  GTGAGGGGAAGGGCCAAGGC   61437      A_   CCC
                                 GTGA  GGA   GGGCCAAGGC
                                 ||||  |||   ||||||||||
                                 CACT  CCT   CCCGGTTCCG
                                   CC   T__
GAM2618  SPRY1    3'  AGTGAAGATGGGCAAGG     61438         ACCC    C
                                 AGTGAAGG    GGGC AAGG
                                 ||||||||    |||| ||||
                                 TCACTTCT    CCCG TTCC
                                      A___    _
GAM2618  TOR1B    3'  GTGAAGGATTCCACAGCCAGGG 61439         C_   _    A
              C                  GTGAAGGA  CCG GGCCA GGC
                                 ||||||||  ||| ||||| |||
                                 CACTTCCT  GGT TCGGT CCG
                                      AA   G    C
GAM2618  UBE2M    3'  GAAGGGGAGGCAAGGCCAAGGC 61440       ACCC___
                                 GAAGG      GGGCCAAGGC
                                 |||||      ||||||||||
                                 CTTCC      TCCGGTTCCG
                                    CCTCCGT
GAM2618  ZD52F10  3'  GTGTGGCAGCCGGGCCAGGGC  61441     AA  AC_      A
                                 GTG  GG   CCGGGCCA GGC
                                 |||  ||   |||||||| |||
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                                CAC  CC   GGCCCGGT CCG
                                  A_  GTC       C
GAM2618  LOC127262 3'  AGTGGTAGGAACCAAGG     61442      A_    CCCGG
                                AGTG  AGGA    GCCAAGG
                                ||||  ||||    |||||||
                                TCAC  TCCT    TGGTTCC
                                  CA   _____
GAM2618  LOC143287 3'  GGAGGAAGGACCAGGCTGGGTC 61443     T       C    _____  A
            AGGGC                   AG GAAGGACC GGGC    CA GGC
                                || ||||||| ||||    || |||
                                TC CTTCCTGG TCCG    GT CCG
                                 _       _   ACCCA  C
GAM2618  LOC145216 3'  GGAGTGAGCGGGCGCTTAGG   61444    A    A GACC    CA__
                                A AGTGA G    CGGGC    AGG
                                | ||||| |    |||||    |||
                                C TCACT C    GCCCG    TCC
                                 C    _ ____     CGAA
GAM2618  LOC146332 3'  AAAGTGGAGGTTGTCCAAGG   61445       A   ACCCGGG
                                AAAGTG AGG       CCAAGG
                                |||||| |||       ||||||
                                TTTCAC TCC       GGTTCC
                                   C   AACA___
GAM2618  LOC147949 5'  GCCAGGGCCCGGGCCAGGGC   61446    GA   A       A
                                GT  AGG CCCGGGCCA GGC
                                ||  ||| |||||||| |||
                                CG  TCC GGGCCCGGT CCG
                                 G_   C        C
GAM2618  LOC149194 3'  GTCCAGACTTGGGCCAAGGC   61447    GAA    CC
                                GT   GGAC  GGGCCAAGGC
                                ||   ||||  ||||||||||
                                CA   TCTG  CCCGGTTCCG
                                 GG_    AA
GAM2618  LOC149276 3'  GAAAGCTGGTCTGGGCCAAGGC 61448       ACCC___
                                GAAGG      GGGCCAAGGC
                                |||||      ||||||||||
                                CTTTC      CCCGGTTCCG
                                   GACCAGA
GAM2618  LOC149706 3'  AAAGTGAAAGGGCTCCAGAGGT 61449    __  AC    ________  CAAG
              GCCTTGGC                AA  GG  CCGG      GC    GC
                                ||  ||  ||||      ||    ||
                                TT  CC  GGTC      CG    CG
                                 TC  GA    TCCAIII  GAAC
GAM2618  LOC150606 3'  AAAGTGAAGACCTCCCTGGG   61450          A__   _
                                AAAGTGAAGG   CCC GGG
                                ||||||||||   ||| |||
                                TTTCACTTCT   GGG CCC
                                      GGA   A
GAM2618  LOC152283 3'  AAAGTGAAGGCCCTGGGC    61451          A   _
                                AAAGTGAAGG CCC GGGC
                                |||||||||| ||| ||||
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                                TTTCACTTCC GGG CCCG
                                      _  A
GAM2618  LOC152762 3'  AAAGTGCAAGGACCAAAAAGGG 61452       _      C____
                                AAAGTG AAGGACC    GGG
                                |||||| |||||||    |||
                                TTTCAC TTCCTGG    CCC
                                   G      TTTTT
GAM2618  LOC197329 5'  AGGAAGGACCCGGCGCGC    61453    T        _______
                                AG GAAGGACCCGG    GC
                                || ||||||||||     ||
                                TC CTTCCTGGGCC    CG
                                 _         GCGIII
GAM2618  LOC219654 3'  AAGTGAAGGGTCACGATGCGGG 61454         ACC_  _  CAA
              G                  AAGTGAAGG   CGG GC   GG
                                |||||||||   ||| ||   ||
                                TTCACTTCC   GCT CG   CC
                                     CAGT   A  CC_
GAM2618  LOC221486 3'  AGCACCAGACCCGGGTCGGGGC 61455      AA       CCAA
                                AGTG  GGACCCGGG   GGC
                                ||||  |||||||||   |||
                                TCGT  TCTGGGCCC   CCG
                                  GG        AGCC
GAM2618  LOC222865 3'  AAAGGGAGGGCCCGGGC     61456      T  A  A
                                AAAG GA GG CCCGGGC
                                |||| || || |||||||
                                TTTC CT CC GGGCCCG
                                  C  C  _
GAM2618  LOC255328 3'  AAAGTGGAGCAGCCCAAGG   61457       A  GACC   G
                                AAAGTG AG   CGG CCAAGG
                                |||||| ||   ||| ||||||
                                TTTCAC TC   GTC GGTTCC
                                   C  ____   G
GAM2618  LOC257451 5'  GGAGTGGGGGACCCGGGTTAGC 61386   A   AA       CCAA
                                A AGTG  GGACCCGGG   GGC
                                | ||||  |||||||||   |||
                                C TCAC  CCTGGGCCC   TCG
                                 C   CC        AA__
GAM2618  LOC58512  3'  ATGAGGGACCCGGCCCGGC   61458     A      G  AA
                                GTGA GGACCCGG CC  GGC
                                |||| |||||||| ||  |||
                                TACT CCTGGGCC GG  CCG
                                  C       G  __
GAM2618  LOC91049  5'  AAGTGAAGGAGCAAAGG     61459         CCCGG  C
                                AAGTGAAGGA    GC AAGG
                                ||||||||||    || ||||
                                TTCACTTCCT    CG TTCC
                                      _____  T
GAM2618  LOC91960  3'  AAAGTGAAGGAGCAGGGGC   61460          CCC_
                                AAAGTGAAGGA   GGGC
                                ||||||||||    ||||
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                                TTTCACTTCCT   CCCG
                                      CGTC
GAM2619  FLJ20707  3'  TGTTTGTATTTTGGTTTCTTTG 61463        GTAG  C
                                TGTTTGTAT   TG TTTCTTTG
                                |||||||||   || ||||||||
                                ACAAACATA   AC AAAGAAAC
                                     AA__  C
GAM2619  KIAA0865  3'  TGTCTGTGTCCTGTGCTTTTTT 61464       ATGTA     C
           TG                    TGTTTGT    GTGCTTT TTTG
                                |||||||    ||||||| ||||
                                ACAGACA    CACGAAA AAAC
                                    CAGGA      A
GAM2619  KIAA1086  3'  TGTTTGTTTGTTTGTTTCTTTG 61465       A   AG  C
                                TGTTTGT TGT  TG TTTCTTTG
                                ||||||| |||  || ||||||||
                                ACAAACA ACA  AC AAAGAAAC
                                    A   A_  _
GAM2619  LOC136895 5'  TTTGTATGTTGGCTTCTTTG   61466        AGT   T
                                TTTGTATGT   GCTT CTTTG
                                |||||||||   |||| |||||
                                AAACATACA   CGAA GAAAC
                                     AC_   _
GAM2619  LOC144997 3'  TTTGTATGTGTGGGCTTTTTTG 61467        A  __    C
                                TTTGTATGT GT  GCTTT TTTG
                                ||||||||| ||  ||||| ||||
                                AAACATACA CA  CGAAA AAAC
                                     _  CC    _
GAM2619  LOC154215 3'  TGTTGTATGTAGAGGCTTT   61468     T      T_
                                TGTT GTATGTAG  GCTTT
                                |||| ||||||||  |||||
                                ACAA CATACATC  CGAAA
                                   _      TC
GAM2620  MJD     3'  CATCTTTCAAAAGAATTG    61471     GTAA
                                CATC   TCAAAAGAATTG
                                ||||   ||||||||||||
                                GTAG   AGTTTTCTTAAC
                                   AA__
GAM2620  MJD     3'  CATCTTTCAAAAGAATTG    61471     GTAA
                                CATC   TCAAAAGAATTG
                                ||||   ||||||||||||
                                GTAG   AGTTTTCTTAAC
                                   AA__
GAM2620  SOX11    3'  AACATCTCTGCCCAAAAGAGTT 61472      GTAA_      A
           G                     AACATC    TCAAAAGA TTG
                                ||||||    |||||||| |||
                                TTGTAG    GGTTTTCT AAC
                                   AGACG       C
GAM2620  HSPC014   3'  GTAATCAATTTGAGAGTTGC   61473       A___   A
                                GTAATCAA    AGA TTGC
                                ||||||||    ||| ||||
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                                CATTAGTT   TCT AACG
                                    AAAC  C
GAM2620 KIAA0372 3' CATCATAATTGAAGGAATTGC 61474        CA  A
                                CATCGTAAT  AA GAATTGC
                                ||||||||| || |||||||
                                GTAGTATTA  TT CTTAACG
                                    AC  C
GAM2620 LSM4    3' TAACATTTCTAACCGGAGAATT 61475      CG_   AAA
          GC                  TAACAT  TAATC  AGAATTGC
                              |||||| ||||| ||||||||
                              ATTGTA  ATTGG  TCTTAACG
                                 AAG   CC_
GAM2621 CLOCK   3' CAGTAAGAATCATAAA     59725      TTTTT
                              CAGTA   GGAATCATAAA
                              |||||   ||||||||||
                              GTCAT   TCTTAGTATTT
                                 _____
GAM2621 DIAPH2  3' CAGTATTTTCTAACATAA   59726        GGAAT
                              CAGTATTTTT   CATAA
                              ||||||||||   |||||
                              GTCATAAAAG   GTATT
                                   ATT__
GAM2621 GOCAP1  3' CAGTATTTTTCTCATAAAAA 59727        GGAA
                              CAGTATTTTT   TCATAAAAA
                              ||||||||||  |||||||||
                              GTCATAAAAA   AGTATTTTT
                                   G___
GAM2621 MTRR    3' TCATATTTCCCAGCATCATAAA 59728   GTA   TG A
          AA                  TCA  TTTT  G ATCATAAAAA
                              |||  ||||  | ||||||||||
                              AGT  AAGG  C TAGTATTTTT
                                ATA   GT G
GAM2621 MTRR    3' TCATATTTCCCAGCATCATAAA 59728   GTA   TG A
          AA                  TCA  TTTT  G ATCATAAAAA
                              |||  ||||  | ||||||||||
                              AGT  AAGG  C TAGTATTTTT
                                ATA   GT G
GAM2621 SLC38A2 3' AGTATTTTTGGTACAAAAA  59729        AATC
                              AGTATTTTTGG   ATAAAAA
                              ||||||||||   |||||||
                              TCATAAAAACC   TGTTTTT
                                   A___
GAM2621 TGFBR2  3' TCAGTATTTTTAGGAACTACA 59730        _   C
                              TCAGTATTTTT GGAAT ATA
                              |||||||||| ||||| |||
                              AGTCATAAAAA CCTTG TGT
                                   T   A
GAM2621 BHMT    3' CCAGTAGTGGGTCATAAAA  59731      TTTT  AA
                              TCAGTA   TGG  TCATAAAA
                              ||||||   |||  ||||||||
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                                GGTCAT   ACC  AGTATTTT
                                   C___  C_
GAM2621  MGC10612  3'  TCAGTATTCTATGTGGAA    59732          ___
                                TCAGTATTTT  TGGAA
                                ||||||||||  |||||
                                AGTCATAAGA  ACCTT
                                     TAC
GAM2621  LOC206426 3'  AGTATTTTGGACTCATGAAA  59733       T  A  A
                                AGTATTTT GGA TCAT AAA
                                |||||||| ||| |||| |||
                                TCATAAAA CCT AGTA TTT
                                   _  G   C
GAM2621  LOC92379  3'  TCAGCATTTCTATTCATA    59734          GAA
                                TCAGTATTTTTG  TCATA
                                ||||||||||||  |||||
                                AGTCGTAAAGAT  AGTAT
                                      A__
GAM2622  CSNK1D    3'  TCTGCTTTTCTTCCCAGCCCCG 61479        C  AG  G
            T                    TCTGCTTTTC TCC  AG TCTGT
                                 ||||||||||| |||  || |||||
                                 AGACGAAAAG AGG  TC GGGCA
                                      A  G_  G
GAM2622  CSNK1D    3'  TCTGCTTTTCTTCCCAGCCCCG 61479        C  AG  G
            T                    TCTGCTTTTC TCC  AG TCTGT
                                 ||||||||||| |||  || |||||
                                 AGACGAAAAG AGG  TC GGGCA
                                      A  G_  G
GAM2622  CYP19     3'  TCTGCTTTTTCTCTTGTACAGA 61480      C  _________  AGGT
            CCTCT                  GCTTTT CTC      CAG   CT
                                   |||||| |||      |||   ||
                                   CGAAAA GAG      GTC   GA
                                      A  AACAIIIT  TGGA
GAM2622  CYP19     3'  TCTGCTTTTTCTCTTGTACAGA 61480      C  _________  AGGT
            CCTCT                  GCTTTT CTC      CAG   CT
                                   |||||| |||      |||   ||
                                   CGAAAA GAG      GTC   GA
                                      A  AACAIIIT  TGGA
GAM2622  EFNA1     3'  TGCTTTTCCTTCAGTCAGT   61481        C  A_
                                TGCTTTTCCT CAG  GGT
                                |||||||||| |||  |||
                                ACGAAAAGGA GTC  TCA
                                      A  AG
GAM2622  FBXW7     3'  TCTTCTTTTCCTTCTTAGTCTG 61482    G      CCAGA
            T                   TCT CTTTTCCT    GGTCTGT
                                ||| ||||||||    |||||||
                                AGA GAAAAGGA    TCAGACA
                                  A       AGAA_
GAM2622  FBXW7     3'  TCTTCTTTTCCTTCTTAGTCTG 61482    G      CCAGA
            T                   TCT CTTTTCCT    GGTCTGT
                                ||| ||||||||    |||||||
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                                AGA GAAAAGGA    TCAGACA
                                  A       AGAA_
GAM2622  FUT4     3'  TCTGCTTTATTTTCACATCTGT 61483        TCCTC  GAG
                                TCTGCTTT    CA   GTCTGT
                                ||||||||    ||   ||||||
                                AGACGAAA    GT   TAGACA
                                    TAAAA  G__
GAM2622  IFIT4    3'  TCTGTTTTCCTCCTCT      61484      C       AGAGG
                                TCTG TTTTCCTCC    TCT
                                |||| |||||||||    |||
                                AGAC AAAAGGAGG    AGA
                                  _       _____
GAM2622  LAMC1    3'  TGCTTCTCTTTAAACTCTGT   61485        CTCCA   G
                                TGCTTTTC    GAG TCTGT
                                ||||||||    ||| |||||
                                ACGAAGAG    TTT AGACA
                                    AAA__   G
GAM2622  MS4A6A   3'  TCTGCTTTTCTTCTCTGTACAG 61486       __  ________  AGGT
            ACCTCT                CTTTTC  CTC      CAG    CT
                                ||||||  |||      |||    ||
                                GAAAAG  GAG      GTC    GA
                                   AA   ACAIIIT   TGGA
GAM2622  MTAP     3'  TGCTTTTCTTCTGTATACAGAC 61487       C  __________  AGGT
            CTCT                  CTTTTC TC        CAG    CT
                                ||||||  ||       |||    ||
                                GAAAAG AG        GTC    GA
                                   A  ACATAIIIT   TGGA
GAM2622  PDE4B    5'  TGCTTTTCTTCTAAATACAGAC 61488       C  __________  AGGT
            CTCT                  CTTTTC TC        CAG    CT
                                ||||||  ||       |||    ||
                                GAAAAG AG        GTC    GA
                                   A  ATTTAIIIT   TGGA
GAM2622  POU2F2   3'  CCTGGACCTCCAGGGGTCTGT  61489     CTTTT      A
                                TCTG    CCTCCAG GGTCTGT
                                ||||    ||||||| |||||||
                                GGAC    GGAGGTC CCAGACA
                                  CT___      C
GAM2622  PPP1R12B 5'  TCTGCTTCTTGAAGGTCTG    61490         CCTCCA
                                TCTGCTTTT     GAGGTCTG
                                |||||||||     ||||||||
                                AGACGAAGA     TTCCAGAC
                                     AC_____
GAM2622  PPP2R5E  3'  TGTTTTTTCCCAGAGGC     61491    C    CC
                                TG TTTT  TCCAGAGGT
                                ||  ||||  |||||||||
                                AC AAAA  GGGTCTCCG
                                 _   AA
GAM2622  PRCP     3'  TCTGCTTTTACTTTGTGTACAG 61492      C  C__________  AGGT
            ACCTCT                CTTTT CT        CAG    CT
                                |||||  ||        |||    ||
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                                GAAAA GA        GTC    GA
                                  T  AACACAIIIT   TGGA
GAM2622  PTMA     3'  TCTTTTTTCCTCCCCT     61493     GC       AGAGG
                                TCT  TTTTCCTCC    TCT
                                |||  |||||||||    |||
                                AGA  AAAAGGAGG    GGA
                                  A_       _____
GAM2622  SLC4A1   3'  TCTGCTTTTCCTTGGAAGGT   61494          CCA
                                TCTGCTTTTCCT   GAGGT
                                ||||||||||||  |||||
                                AGACGAAAAGGA   TTCCA
                                       ACC
GAM2622  SMARCA1  3'  TCTGCTTTTCTTTTCTGTACAG 61495       C__ ________  AGGT
            ACCTCT                CTTTTC   TC     CAG    CT
                                ||||||  ||     |||   ||
                                GAAAAG   AG     GTC    GA
                                   AAA  ACAIIIT   TGGA
GAM2622  SMARCA1  3'  TCTGCTTTTCTTTTCTGTACAG 61495       C__ ________  AGGT
            ACCTCT                CTTTTC   TC     CAG    CT
                                ||||||  ||     |||   ||
                                GAAAAG   AG     GTC    GA
                                   AAA  ACAIIIT   TGGA
GAM2622  SNX6     3'  TGCTTTTCTTCAGAAAT     61496        CTC
                                TGCTTTTC   CAGAGGT
                                ||||||||   |||||||
                                ACGAAAAG   GTCTTTA
                                     AA_
GAM2622  SPAG11   3'  TCTCTTTTCCTTCTTCATCTGT 61497     G       CCAGAG
                                TCT CTTTTCCT     GTCTGT
                                ||| ||||||||     ||||||
                                AGA GAAAAGGA     TAGACA
                                  _       AGAAG_
GAM2622  SPAG11   3'  TCTCTTTTCCTTCTTCATCTGT 61497     G       CCAGAG
                                TCT CTTTTCCT     GTCTGT
                                ||| ||||||||     ||||||
                                AGA GAAAAGGA     TAGACA
                                  _       AGAAG_
GAM2622  SPON1    3'  TCTGTTTTTCCCCAGGAACT   61498     C     T    A GT
                                TCTG TTTTCC CCAG G  CT
                                |||| |||||| |||| |  ||
                                AGAC AAAAGG GGTC C  GA
                                  A     _    _ TT
GAM2622  TRIM14   3'  TCTGCTTTCTTTCAGGACCT   61499         CCTC   A GT
                                TCTGCTTTT    CAG G  CT
                                |||||||||    ||| |  ||
                                AGACGAAAG    GTC C  GA
                                     AAA_   _ TG
GAM2622  WBSCR14  3'  TCTGCTCAGGAACAGAGGTCTG 61500        TTCCTC
            T                  TCTGCTT     CAGAGGTCTGT
                                |||||||     ||||||||||
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                                AGACGAG     GTCTCCAGACA
                                    TCCTT_
GAM2622 WBSCR14   3'  TCTGCTCAGGAACAGAGGTCTG 61500       TTCCTC
              T                  TCTGCTT     CAGAGGTCTGT
                                 |||||||     ||||||||||
                                 AGACGAG     GTCTCCAGACA
                                    TCCTT_
GAM2622 ADNP      3'  TCTGCTTTTCCTCGTGTACAGA 61501         _________  AGGT
              CCTCT                 GCTTTTCCTC      CAG   CT
                                 ||||||||||      |||   ||
                                 CGAAAAGGAG      GTC   GA
                                      CACAIIIT   TGGA
GAM2622 COLEC12   3'  TCTGTTTTTTTATCCATTGCTG 61502     C   CC_   GAG T
              T                  TCTG TTTT   TCCA   G CTGT
                                 |||| ||||   ||||   | ||||
                                 AGAC AAAA   AGGT   C GACA
                                   A    AAT    AA_ _
GAM2622 DKFZP434P211 3'  TCTGCTTTATTCTCTGCCTG   61503       TC_   CAGAG
                                 TCTGCTTT   CTC    GTCTG
                                 ||||||||   |||    |||||
                                 AGACGAAA   GAG    CGGAC
                                      TAA   A____
GAM2622 FLJ20060  5'  CTTTTCCTTCAGAGAGCTGT   61504       C    GT
                                 CTTTTCCT CAGAG  CTGT
                                 |||||||| |||||  ||||
                                 GAAAAGGA GTCTC  GACA
                                      A     TC
GAM2622 KIAA0326  3'  TCTGGCTTTGCGAGAGGTTTGT 61505     _   TCCTCC     C
                                 TCTG CTTT     AGAGGT TGT
                                 |||| ||||     |||||| |||
                                 AGAC GAAA     TCTCCA ACA
                                   C    CGC___      A
GAM2622 KIAA1634  3'  TCTGCTTTTTCTGCACTGATCT 61506        C  C  GA
                                 TCTGCTTTT CT CA  GGTCT
                                 ||||||||| || ||  |||||
                                 AGACGAAAA GA GT  CTAGA
                                      A  C  GA
GAM2622 KIAA1673  3'  TGCATTCTGCAGAGGTCTGT   61507     TT   CTC
                                 TGC  TTC   CAGAGGTCTGT
                                 |||  |||   ||||||||||
                                 ACG  AAG   GTCTCCAGACA
                                   T_   AC_
GAM2622 KIAA1678  3'  TGCTTTTCCTCTGACTTATTCT 61508         CAGAGG__
              GT                   TGCTTTTCCTC       TCTGT
                                 ||||||||||       |||||
                                 ACGAAAAGGAG       AGACA
                                      ACTGAATA
GAM2622 LANCL2    3'  TCTGCTTCTCTTTCAGGAT    61509         CTC   A
                                 TCTGCTTTTC   CAG GGT
                                 |||||||||   ||| |||
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                                AGACGAAGAG  GTC CTA
                                     AAA  _
GAM2622  MAL2     3'  TGTTTTTCCTCATGTCTTCTGT 61510    C      CAGAGG
                                TG TTTTCCTC     TCTGT
                                || ||||||||     |||||
                                AC AAAAGGAG     AGACA
                                 A       TACAGA
GAM2622  MGC15631 5'  TCTGCTCTTCCTTCTCTCTGT  61511          CCAGAGG
                                TCTGCTTTTCCT      TCTGT
                                ||||||||||||      |||||
                                AGACGAGAAGGA      AGACA
                                      AGAG___
GAM2622  OSMR     3'  TCTGCTCTTCTTAATGTCTGT  61512         CTCCAGAG
                                TCTGCTTTTC       GTCTGT
                                ||||||||||       ||||||
                                AGACGAGAAG       CAGACA
                                     AATTA___
GAM2622  SCAND2   3'  TCTCTTTTTCTCCAGAA     61513     G    C
                                TCT CTTTT CTCCAGAG
                                ||| ||||| ||||||||
                                AGA GAAAA GAGGTCTT
                                  _     A
GAM2622  SCAND2   3'  TCTCTTTTTCTCCAGAA     61513     G    C
                                TCT CTTTT CTCCAGAG
                                ||| ||||| ||||||||
                                AGA GAAAA GAGGTCTT
                                  _     A
GAM2622  SCAND2   3'  TCTCTTTTTCTCCAGAA     61513     G    C
                                TCT CTTTT CTCCAGAG
                                ||| ||||| ||||||||
                                AGA GAAAA GAGGTCTT
                                  _     A
GAM2622  SCAND2   3'  TCTCTTTTTCTCCAGAA     61513     G    C
                                TCT CTTTT CTCCAGAG
                                ||| ||||| ||||||||
                                AGA GAAAA GAGGTCTT
                                  _     A
GAM2622  SLC26A7  3'  TCTGCTTTTCCTTGGAAGAG  61514          CC__
                                TCTGCTTTTCCT    AGAG
                                ||||||||||||    ||||
                                AGACGAAAAGGA    TCTC
                                      ACCT
GAM2622  TCL6     5'  TCTGTCTCCATGCCAGAGGTCT 61515     CT    T__
              GT                  TCTG  TTTCC   CCAGAGGTCTGT
                                  ||||  |||||   ||||||||||||
                                  AGAC  AGAGG   GGTCTCCAGACA
                                    __     TAC
GAM2622  TCL6     5'  TCTGTCTCCATGCCAGAGGTCT 61515     CT    T__
              GT                  TCTG  TTTCC   CCAGAGGTCTGT
                                  ||||  |||||   ||||||||||||
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                                AGAC  AGAGG   GGTCTCCAGACA
                                  __    TAC
GAM2622  TCL6     5'  TCTGTCTCCATGCCAGAGGTCT 61515     CT    T__
              GT                  TCTG  TTTCC   CCAGAGGTCTGT
                                  ||||  |||||   ||||||||||||
                                  AGAC  AGAGG   GGTCTCCAGACA
                                  __    TAC
GAM2622  TCL6     5'  TCTGTCTCCATGCCAGAGGTCT 61515     CT    T__
              GT                  TCTG  TTTCC   CCAGAGGTCTGT
                                  ||||  |||||   ||||||||||||
                                  AGAC  AGAGG   GGTCTCCAGACA
                                  __    TAC
GAM2622  WSB1     3'  TCTCTTTTTTTTCCAGAAACT  61516    G    CC_      T
                                  TCT CTTTT   TCCAGAGG CT
                                  ||| |||||   |||||||| ||
                                  AGA GAAAA   AGGTCTTT GA
                                    _    AAA      _
GAM2622  LOC131827 3'  TGCTCTTCCTCCAGTTGT    61517            AG
                                  TGCTTTTCCTCCAG  GT
                                  ||||||||||||||  ||
                                  ACGAGAAGGAGGTC  CA
                                         AA
GAM2622  LOC132617 3'  CTTTTCCTTCAGGCCT      61518        C  GA
                                  CTTTTCCT CA  GGTCT
                                  |||||||| ||  |||||
                                  GAAAAGGA GT  CCGGA
                                     A  __
GAM2622  LOC142941 5'  TGCTTTTCCTTTAAGCAACTGT 61519          CCAG   __
                                  TGCTTTTCCT    AGGT  CTGT
                                  ||||||||||    ||||  ||||
                                  ACGAAAAGGA    TTCG  GACA
                                       AA__    TT
GAM2622  LOC145123 3'  TCTTTTTTCCTCCCCT     61493     GC       AGAGG
                                  TCT  TTTTCCTCC    TCT
                                  |||  |||||||||    |||
                                  AGA  AAAAGGAGG    GGA
                                    A_       ______
GAM2622  LOC150174 3'  TCTGCTTTATTCTCTGCCTG   61503        TC_   CAGAG
                                  TCTGCTTT   CTC    GTCTG
                                  ||||||||   |||    |||||
                                  AGACGAAA   GAG    CGGAC
                                      TAA   A_____
GAM2622  LOC150213 3'  TCTGCTTTATTCTCTGCCTG   61503        TC_   CAGAG
                                  TCTGCTTT   CTC    GTCTG
                                  ||||||||   |||    |||||
                                  AGACGAAA   GAG    CGGAC
                                      TAA   A_____
GAM2622  LOC150343 5'  TCTGCTTCTGAAATAGGGGTCT 61520          CCTCC  A
              GT                  TCTGCTTTT    AG GGTCTGT
                                  |||||||||    || |||||||
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                                AGACGAAGA    TC CCAGACA
                                     CTTTA  C
GAM2622  LOC150504 5'  TCTGCTTTCTTCTGCGATTTCT 61521        CC  CA_  GG
              GT                   TCTGCTTTT  TC   GA  TCTGT
                                   |||||||||  ||   ||  |||||
                                   AGACGAAAG  AG   CT  AGACA
                                        A_  ACG  AA
GAM2622  LOC153769 3'  CTGACTTTCTCCGGAGGTCTGT 61522     _    TC    A
                                   CTG CTTT  CTCC GAGGTCTGT
                                   |||  ||||  |||| |||||||||
                                   GAC GAAA  GAGG CTCCAGACA
                                     T    __    C
GAM2622  LOC158434 3'  TCTGCTTTTTTTCAGGT     61523         CC  CAG
                                   TCTGCTTTT  TC   AGGT
                                   |||||||||  ||   ||||
                                   AGACGAAAA  AG   TCCA
                                        AA  ____
GAM2622  LOC165246 5'  CCTGCCTCCTTCAGAGGTCTGT 61524       TT    C
                                   TCTGCT  TCCT CAGAGGTCTGT
                                   ||||||  |||| ||||||||||
                                   GGACGG  AGGA GTCTCCAGACA
                                      __    A
GAM2622  LOC169436 5'  TCTGCTTCTCCTCCATTGT    61525            GAG
                                   TCTGCTTTTCCTCCA   GT
                                   ||||||||||||||   ||
                                   AGACGAAGAGGAGGT   CA
                                         AA_
GAM2622  LOC196510 3'  CCTGCTTTTCAGGTT       61526          CTCCAG    C
                                   TCTGCTTTTC     AGGT T
                                   ||||||||||     |||| |
                                   GGACGAAAAG     TCCA A
                                        _______    A
GAM2622  LOC200220 3'  CCTGCTTTTCAGGTT       61526          CTCCAG    C
                                   TCTGCTTTTC     AGGT T
                                   ||||||||||     |||| |
                                   GGACGAAAAG     TCCA A
                                        _______    A
GAM2622  LOC200261 3'  GCTGGGCCTCCAGAGGTTTGT  61527     TTT         C
                                   GCT   CCTCCAGAGGT TGT
                                   |||   |||||||||||| |||
                                   CGA   GGAGGTCTCCA ACA
                                     CCC          A
GAM2622  LOC201626 3'  TGTTTCTCCTCCAATTGT    61528    C         AG
                                   TG TTTTCCTCCAG  GT
                                   ||  ||||||||||  ||
                                   AC AAGAGGAGGTT  CA
                                    A          AA
GAM2622  LOC219529 5'  TGCTTTTCTGCTGTTAATCTGT 61529         CTCCAGA
                                   TGCTTTTC      GGTCTGT
                                   ||||||||      |||||||
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                                ACGAAAAG      TTAGACA
                                    ACGACAA
GAM2622  LOC221550 5'  TCTACTTTTTTTCTAACTTCTG 61530        CC  C  AGG
             T                   TCTGCTTTT  TC AG   TCTGT
                                 |||||||||  || ||   |||||
                                 AGATGAAAA  AG TT   AGACA
                                      AA  A  GA_
GAM2622  LOC257495 5'  TCTACTTTTTTTCTAACTTCTG 61530        CC  C  AGG
             T                   TCTGCTTTT  TC AG   TCTGT
                                 |||||||||  || ||   |||||
                                 AGATGAAAA  AG TT   AGACA
                                      AA  A  GA_
GAM2622  LOC257576 5'  TCTACTTTTTTTCTAACTTCTG 61530        CC  C  AGG
             T                   TCTGCTTTT  TC AG   TCTGT
                                 |||||||||  || ||   |||||
                                 AGATGAAAA  AG TT   AGACA
                                      AA  A  GA_
GAM2622  LOC92078  3'  TCTGCTTCTCCTTCTTGTACAG 61531        _ _________   AGGT
             ACCTCT                CTTTTCCT C       CAG    CT
                                 ||||||||  |       |||    ||
                                 GAAGAGGA G       GTC    GA
                                      A AACAIIIT   TGGA
GAM2622  LOC92597  3'  TCTGCTTTTGTCTTCAGAAAT  61532        C_  C
                                 TCTGCTTTT  CT CAGAGGT
                                 |||||||||  || |||||||
                                 AGACGAAAA  GA GTCTTTA
                                      CA  A
GAM2623  CD1D     5'  CCCTTTCCGCTGGGTGCCAGC  61535     GC  GG      A
                                 CCCT  TC  GCTGGGT CCAGC
                                 ||||  ||  ||||||| |||||
                                 GGGA  AG  CGACCCA GGTCG
                                   A_  G_      C
GAM2623  CENPA    5'  CCTGCTCGGGCTGCCGGGT   61536          ___
                                 CCTGCTCGGGCT   GGGT
                                 ||||||||||||   ||||
                                 GGACGAGCCCGA   CCCA
                                        CGG
GAM2623  CRABP2    3'  ACCCTGCTCTGGGCTGGTTTGG 61537         _      GTACCA
             GGC                   ACCCTGCTC GGGCTGG     GC
                                 |||||||||  |||||||     ||
                                 TGGGACGAG CCCGACC     CG
                                      A      AAACCC
GAM2623  CRY2     3'  CCCTGGCTGGGTGTCAGC    61538     GCTCG       AC
                                 CCCT    GGCTGGGT  CAGC
                                 ||||    ||||||||  ||||
                                 GGGA    CCGACCCA  GTCG
                                   _____       CA
GAM2623  DUOX1    5'  ACCCTGCTTTGGCCCAGC    61539        CG    G
                                 ACCCTGCT  GGCT GGT
                                 ||||||||  |||| |||
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                                TGGGACGA  CCGG TCG
                                    AA    G
GAM2623  HMG20A   3'  CCTTGCTGGGGCTGGGAC    61540    C   C      T
                                CC TGCT GGGCTGGG AC
                                || |||| |||||||| ||
                                GG ACGA CCCGACCC TG
                                 A   C      _
GAM2623  HUNK     5'  CCCTGCTCGGGCGCGCGGG   61541           ___
                                CCCTGCTCGGGC   TGGG
                                ||||||||||||  ||||
                                GGGACGAGCCCG   GCCC
                                      CGC
GAM2623  KIF5A    5'  ACTCTTCTTGGGCTGCAGGGGT 61542    C  G  C    ____
                                AC CT CT GGGCT    GGGT
                                || || || |||||    ||||
                                TG GA GA CCCGA    CCCA
                                 A  A  A    CGTC
GAM2623  LASS1    3'  CCCGGCTCGGGCGCTCAG    61543    T      TGG  AC
                                CCC GCTCGGGC   GT  CAG
                                ||| ||||||||   ||  |||
                                GGG CGAGCCCG   CG  GTC
                                  C       ___  A_
GAM2623  MEN1     5'  CCGCTTTAGCTGGGTATCAG   61544      CG       C
                                CTGCT  GGCTGGGTA CAG
                                |||||  ||||||||| |||
                                GGCGA  TCGACCCAT GTC
                                   AA        A
GAM2623  MYLK2    3'  CCCTGTCTGGGGAGGTGCTAGC 61545      _  C   CT    ACC
                                CCCTG CT GGG  GGGT   AGC
                                ||||| || |||  ||||   |||
                                GGGAC GA CCC  TCCA   TCG
                                   A  C  __    CGA
GAM2623  SCN4A    3'  GCTCGGGCCTGGGTGTCAG   61546        _    AC
                                GCTCGGGC TGGGT  CAG
                                |||||||| |||||  |||
                                CGAGCCCG ACCCA  GTC
                                     G    CA
GAM2623  SDS      3'  ACCCTGCTCTGGGTACC     61547         GGGC
                                ACCCTGCTC    TGGGTACC
                                |||||||||    ||||||||
                                TGGGACGAG    ACCCATGG
                                             ____
GAM2623  SIAH2    5'  CCTGCTCGGGCTGCGGGC    61548           __
                                CCTGCTCGGGCT  GGGT
                                ||||||||||||  ||||
                                GGACGAGCCCGA  CCCG
                                      CG
GAM2623  SKP2     5'  CTGCTCGGGCCCCCAG      61549          GGGTA
                                CTGCTCGGGCT    CCAG
                                ||||||||||     ||||
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                                GACGAGCCCGG    GGTC
                                      G____
GAM2623 SKP2     5' CTGCTCGGGCCCCCAG     61549         GGGTA
                                CTGCTCGGGCT    CCAG
                                ||||||||||    ||||
                                GACGAGCCCGG    GGTC
                                      G____
GAM2623 SLC25A19 3' ACCCCGCTTGGGGCAGCTGGC 61550       C_   TG__
                                ACCCTGCT  GGGC   GGT
                                ||||||||  ||||   |||
                                TGGGGCGA  CCCG   CCG
                                    AC    TCGA
GAM2623 SOX12    3' CCTGCTGTGGGTGCCAG    61551      CGGGC    A
                                CCTGCT    TGGGT CCAG
                                ||||||    ||||| ||||
                                GGACGA    ACCCA GGTC
                                   C____    C
GAM2623 TRAP100  3' ACTCTCCTCAGGTGCCAG   61552   C  G    C  GGTA
                                AC CT CTCGGG TG   CCAG
                                || || |||||| ||   ||||
                                TG GA GAGTCC AC   GGTC
                                 A  G    _ ____
GAM2623 YY1      5' ACTCTGCTCGGGCCCGGC   61553   C       G
                                AC CTGCTCGGGCT GGT
                                || ||||||||||| |||
                                TG GACGAGCCCGG CCG
                                 A         G
GAM2623 COL12A1  3' CCGCTCGGGCTCCACCGGC  61554         GGG   A
                                CTGCTCGGGCT   TACC GC
                                ||||||||||   |||| ||
                                GGCGAGCCCGA   GTGG CG
                                      G__    C
GAM2623 COL12A1  3' CCGCTCGGGCTCCACCGGC  61554         GGG   A
                                CTGCTCGGGCT   TACC GC
                                ||||||||||   |||| ||
                                GGCGAGCCCGA   GTGG CG
                                      G__    C
GAM2623 DKFZP434C128 3' CTGCTGGTGGCTATACCAGC  61555     CG_   GG
                                CTGCT   GGCT  GTACCAGC
                                |||||   ||||  ||||||||
                                GACGA   CCGA  TATGGTCG
                                   CCA   __
GAM2623 DOC2B    3' CTTGGGCTGGAGCAGCCAG   61556   C     _  _
                                CT GGGCTGG GTA CCAG
                                || ||||||| ||| ||||
                                GA CCCGACC CGT GGTC
                                 A      T  C
GAM2623 FJX1     3' CCCTGCTCCGGGGCCACCAGC 61557       G  CT  G
                                CCCTGCTC GG  GG TACCAGC
                                |||||||| ||  || |||||||
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                                GGGACGAG CC  CC GTGGTCG
                                    G __  G
GAM2623  FLJ10432  3'  CCCTGCACGGGCCGTCCGGC   61558      T     GGTA  A
                                CCCTGC CGGGCTG   CC GC
                                |||||| |||||||   || ||
                                GGGACG GCCCGGC   GG CG
                                   T      A___  C
GAM2623  FLJ22056  3'  ACCTTGCTGGGCTGAAGGGC   61559    C   C   ___
                                ACC TGCT GGGCT   GGGT
                                ||| |||| |||||   ||||
                                TGG ACGA CCCGA   CCCG
                                  A   _    CTT
GAM2623  FLJ22341  3'  CCCTGTCTTGGGTCTCTGGC   61560     _ C  _ G_
                                CCCTG CT GGG CT  GGT
                                ||||| || ||| ||  |||
                                GGGAC GA CCC GA  CCG
                                   A  A   A  GA
GAM2623  GAL3ST2   5'  CCCTGCGCGCCGAGTGCC    61561      TC G     A
                                CCCTGC  G GCTGGGT CC
                                ||||||  | ||||||| ||
                                GGGACG  C CGGCTCA GG
                                   __ G      C
GAM2623  KIAA0450  3'  CCCTCCTTGGGCTGGGACAGC  61562    G  C      TAC
                                CCCT CT GGGCTGGG   CAGC
                                |||| || ||||||||   ||||
                                GGGA GA CCCGACCC   GTCG
                                  G  A       T__
GAM2623  KIAA0669  5'  CCCCGCTCGGGCTCCTCAGGC  61563          ____
                                CCCTGCTCGGGCT    GGGT
                                ||||||||||||    ||||
                                GGGGCGAGCCCGA    TCCG
                                       GGAG
GAM2623  KIAA0673  3'  ACCCAGGCCTGCTGGGTGTCAG 61564     T_  T GG     AC
            C                   ACCC  GC C  GCTGGGT  CAGC
                                ||||  || |  |||||||  ||||
                                TGGG  CG G  CGACCCA  GTCG
                                  TC  _ A_      CA
GAM2623  KIAA0683  3'  ACCCTGCCTGGGCTGTGA    61565      TC    _
                                ACCCTGC  GGGCTG GG
                                |||||||  |||||| ||
                                TGGGACG  CCCGAC CT
                                   GA     A
GAM2623  KIAA1075  5'  ACCCTGCTGGGAGTGTCAG   61566       C  CTG  AC
                                ACCCTGCT GGG   GGT  CAG
                                |||||||| |||   |||  |||
                                TGGGACGA CCC   TCA  GTC
                                   _  ___   CA
GAM2623  KIAA1613  3'  CCCTGCTTGGGCTTCAACCAGC 61567      C    GGGT
                                CCCTGCT GGGCT    ACCAGC
                                ||||||| |||||    ||||||
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                                GGGACGA CCCGA   TGGTCG
                                   A    AGT_
GAM2623 KR19    5' CCCTGCTCTGGCTGAAGGT  61568       G   __
                                CCCTGCTC GGCTG  GGT
                                |||||||| |||||  |||
                                GGGACGAG CCGAC  CCA
                                   A    TT
GAM2623 P5CR2   3' ACCCTGCCTCGGGCTTCAGC  61569      _    G_
                                ACCCTGC TCGGGCT  GGT
                                ||||||| |||||||  |||
                                TGGGACG AGCCCGA  TCG
                                   G      AG
GAM2623 PRDM15  3' ACCCTGTGTCGGGCGAACAC  61570      C_    T GG
                                ACCCTG  TCGGGC G  TAC
                                ||||||  |||||| |  |||
                                TGGGAC  AGCCCG C  GTG
                                   AC    _ TT
GAM2623 PTPRT   5' CCGCTCGGGCTCCCGGAGCCGG 61571         G__  TA  A
            C                   CTGCTCGGGCT  GG  CC GC
                                |||||||||||  ||  || ||
                                GGCGAGCCCGA  CC  GG CG
                                      GGG  TC  C
GAM2623 RC3     5' ACCCTCCTCGGGCTGCGA   61572      G      _
                                ACCCT CTCGGGCTG GG
                                ||||| |||||||| ||
                                TGGGA GAGCCCGAC CT
                                  G       G
GAM2623 RYK     5' ACTCTGTTAGGCACTGTACCAG 61573   C  CTC   TGG
            C                    AC CTG  GGGC  GTACCAGC
                                || |||  ||||  ||||||||
                                TG GAC  TCCG  CATGGTCG
                                 A  AA_   TGA
GAM2623 SLC21A12 3' CCTTCCTCGGGCTGCAGGC  61574    G_      __
                                CCT  CTCGGGCTG  GGT
                                |||  |||||||||  |||
                                GGA  GAGCCCGAC  CCG
                                  AG       GT
GAM2623 TIP-1   5' ACCCTGCTCTGGTCGCCCAGC  61575       GGGC  GTA_
                                ACCCTGCTC   TGG   CCAGC
                                |||||||||   |||   |||||
                                TGGGACGAG   ACC   GGTCG
                                     ____  AGCG
GAM2623 LOC120196 5' TGCTCCTTCTTCTGGGTACCAG 61576     GGG___
            C                    TGCTC    CTGGGTACCAGC
                                |||||    ||||||||||||
                                ACGAG    GACCCATGGTCG
                                  GAAGAA
GAM2623 LOC144110 5' ACCCTGCTCCGGGCTGCAG   61577        _    GGTAC
                                ACCCTGCTC GGGCTG    CAG
                                ||||||||| ||||||    |||
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                                TGGGACGAG CCCGAC    GTC
                                     G    _____
GAM2623  LOC149506 3'  CCCTGCACACTGGTGTCAG   61578      TC G   _  AC
                                CCCTGC  G GCTGG GT  CAG
                                ||||||  | ||||| ||  |||
                                GGGACG  T TGACC CA  GTC
                                   __ G    A __
GAM2623  LOC150135 3'  CCCTGCTCCTGGTGTCAG    61579      GGG   _  AC
                                CCCTGCTC   CTGG GT  CAG
                                ||||||||   |||| ||  |||
                                GGGACGAG   GACC CA  GTC
                                     ___    A __
GAM2623  LOC150135 3'  CCCTGCTCCTGGTGTCAG    61579      GGG   _  AC
                                CCCTGCTC   CTGG GT  CAG
                                ||||||||   |||| ||  |||
                                GGGACGAG   GACC CA  GTC
                                     ___    A __
GAM2623  LOC153684 5'  CCTGTGGAAATCTGGGTACCAG 61580     CTC  ___
              C                  CCTG   GGG   CTGGGTACCAGC
                                 ||||   |||   ||||||||||||
                                 GGAC   CCT   GACCCATGGTCG
                                   A__   TTA
GAM2623  LOC158158 3'  ACCCTGCCGTGTGAGGTGTCAG 61581       T  GGCT   AC
                                ACCCTGC CG    GGGT  CAG
                                ||||||| ||    ||||  |||
                                TGGGACG GC    TCCA  GTC
                                   _ ACAC    CA
GAM2623  LOC163812 5'  CTGCTCAGGGTATAGGTGTCAG 61582        C__    AC
                                CTGCTCGGG   TGGGT  CAG
                                |||||||||   |||||  |||
                                GACGAGTCC   ATCCA  GTC
                                     CAT    CA
GAM2623  LOC169330 5'  CCCGCTCGGCTGCCA      61583        G   GGTA
                                CCTGCTCGG CTG    CCA
                                ||||||||| |||    |||
                                GGGCGAGCC GAC    GGT
                                     _  _____
GAM2623  LOC197342 3'  CCTTCTTGGGCTGGGACAGC   61584     G  C      TAC
                                CCT CT GGGCTGGG   CAGC
                                ||| || ||||||||   ||||
                                GGA GA CCCGACCC   GTCG
                                  A  A       T__
GAM2623  LOC200197 3'  CTGAACAGGGCTGGGTACTGGC 61585     CT _        CA
                                CTG  C GGGCTGGGTAC  GC
                                |||  | ||||||||||  ||
                                GAC  G CCCGACCCATG  CG
                                  TT T         AC
GAM2623  LOC200862 5'  GCTCGGCTCGGGCTTCAG    61586      G  _   AC
                                GCTCGG CT GGGT  CAG
                                |||||| || ||||  |||
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                                CGAGCC GA CCCG  GTC
                                   _ G   AA
GAM2623  LOC202759 5'  CCCTGCTCTGGCTGAAGGT   61568        G    __
                                CCCTGCTC GGCTG  GGT
                                |||||||| |||||  |||
                                GGGACGAG CCGAC  CCA
                                     A    TT
GAM2623  LOC257206 3'  ACTCGGGCATTGGGTACCAGC  61587        __
                                GCTCGGGC  TGGGTACCAGC
                                ||||||||  ||||||||||
                                TGAGCCCG  ACCCATGGTCG
                                     TA
GAM2623  LOC90019  3'  CCTGCTCGGGCTGTGGGC    61588          __
                                CCTGCTCGGGCT  GGGT
                                ||||||||||||  ||||
                                GGACGAGCCCGA  CCCG
                                      CA
GAM2624  CENPF     3'  TGTGCACATTTTCCTTAAAAAC 61591        CC    GC_  TT
              AC                   TGTGCACA  TTTCC   GG  CAC
                                |||||||  |||||   ||  |||
                                ACACGTGT  AAAGG   TT  GTG
                                     A_    AAT  TT
GAM2624  LPIN2     3'  TGGCACACCTTTCCCTGGT    61592    T         GC
                                TG GCACACCTTTCC  GGT
                                || ||||||||||||  |||
                                AC CGTGTGGAAAGG  CCA
                                 _          GA
GAM2624  C2orf6    3'  TGTGTACACCTTCATGGTT    61593     C       CCGC
                                TGTG ACACCTTT    GGTT
                                |||| ||||||||    ||||
                                ACAC TGTGGAAG    CCAA
                                   A       TA__
GAM2624  DKFZp761F2014 3'  TGTGCACATCTGTCAGGATT   61594         C  T  CGC
                                TGTGCACA CT TC   GGTT
                                |||||||| || ||   ||||
                                ACACGTGT GA AG   CTAA
                                     A  C  TC_
GAM2624  FLJ20727  3'  TGTGCACATTTGTCCGCAAT   61595        CCTT
                                TGTGCACA    TCCGCGGT
                                ||||||||    ||||||||
                                ACACGTGT    AGGCGTTA
                                     AAAC
GAM2624  HSGT1     5'  TGTGGCACCTTTCCTTAGCC   61596      CA       GC
                                TGTG  CACCTTTCC  GGTT
                                ||||  |||||||||  ||||
                                ACAC  GTGGAAAGG  TCGG
                                   C_        AA
GAM2624  IRO039700 3'  TGTGCGCCCTTCCAGAT     61597       ACA       C
                                TGTGC   CCTTTCCG GGT
                                |||||   |||||||| |||
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                                ACACG   GGGAAGGT CTA
                                  C__       _
GAM2624  KCNS1     3'  TGTTCACACCTTTTTGAGGT   61598     G        CCGC
                                TGT CACACCTTT    GGT
                                ||| |||||||||    |||
                                ACA GTGTGGAAA    CCA
                                  A        AACT
GAM2624  PRO2289   3'  TGTGCACACCTTTCAGTT    61599            CGC
                                TGTGCACACCTTTC   GGTT
                                ||||||||||||||   ||||
                                ACACGTGTGGAAAG   TCAA
                                                 ___
GAM2624  LOC222134 5'  TGTGCACAATTTTCCCCCA    61600         CC_    G
                                TGTGCACA   TTTCC CG
                                ||||||||   ||||| ||
                                ACACGTGT   AAGGG GT
                                     TAA     G
GAM2624  LOC64744  3'  TGTGCACACTTCTCCCAC     61601         C_
                                TGTGCACAC  TTTCCGC
                                |||||||||  |||||||
                                ACACGTGTG  GAGGGTG
                                     AA
GAM2625  MAT2A     3'  TATCTGGTACCAAAGTGTGCAA 61604       A  TCG TG    A
                                TATCT GT   T  AAGT TGCAA
                                ||||| ||   |  |||| |||||
                                ATAGA CA   G  TTCA ACGTT
                                   C  T__ GT    C
GAM2625  NRL       3'  TATCTAGTTGTTGGATAT     61605         C    AA
                                TATCTAGTT GTTG  GTAT
                                ||||||||| ||||  ||||
                                ATAGATCAA CAAC  TATA
                                     _    C_
GAM2625  DKFZP566N034 3'  TATTTAATTCGTCCATGCA    61606     C        GAAG
                                TAT TAGTTCGTT    TATGCA
                                ||| |||||||||    ||||||
                                ATA ATTAAGCAG    GTACGT
                                  A        _____
GAM2625  LEC3      3'  TAGCTGGTAGTAAGTATGCA   61607       C  TG_
                                TAGTT GT   AAGTATGCA
                                ||||| ||   |||||||||
                                ATCGA CA   TTCATACGT
                                   C  TCA
GAM2625  SEMA3E    3'  TATCCAGTCAAATGAGTATG   61608         CGT   A
                                TATCTAGTT   TGA GTATG
                                |||||||||   ||| |||||
                                ATAGGTCAG   ACT CATAC
                                     TTT   _
GAM2625  LOC153525 3'  CAGTTCGTTGAATATACAA    61609           G
                                TAGTTCGTTGAA TATGCAA
                                |||||||||||| |||||||
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                                GTCAAGCAACTT ATATGTT
                                             _
GAM2625  LOC257397 3'  CTAGTCAAAAGTATGCA     61610       CGTT
                                CTAGTT    GAAGTATGCA
                                ||||||    ||||||||||
                                GATCAG    TTTCATACGT
                                   T___
GAM2626  BRCA2     3'  CCCTTTTTTTTTTTTCTTCGTAA 61613     GCG_
              A                  CCCT    TTTTTTCTTCGTAAA
                                 ||||    ||||||||||||||
                                 GGGA    AAAAAAGAAGCATTT
                                   AAAA
GAM2626  CLOCK     3'  ACCCCTTCTTTTTTTCTTTGTA  61614      GCG       C
                                 ACCCT   TTTTTTCTT GTA
                                 |||||   ||||||||| |||
                                 TGGGG   AAAAAAGAA CAT
                                    AAG        A
GAM2626  MAD2L1    3'  TGGTTTTCTCCATGTAAAA   61615    C       TC
                                 TG GTTTTTTCT  GTAAAA
                                 || |||||||||  ||||||
                                 AC CAAAAGAGG  CATTTT
                                  _        TA
GAM2626  NRXN2     3'  TGCGTTTCCTCTTCGTAA    61616
                                 TGCGTTTTTTCTTCGTAA
                                 ||||||||||||||||||
                                 ACGCAAAGGAGAAGCATT

GAM2626  NRXN2     3'  TGCGTTTCCTCTTCGTAA    61616
                                 TGCGTTTTTTCTTCGTAA
                                 ||||||||||||||||||
                                 ACGCAAAGGAGAAGCATT

GAM2626  NRXN2     3'  TGCGTTTCCTCTTCGTAA    61616
                                 TGCGTTTTTTCTTCGTAA
                                 ||||||||||||||||||
                                 ACGCAAAGGAGAAGCATT

GAM2626  PPP1R12A  3'  TGCGCTTTTTTTTCCTTAAAA  61617          C   G_
                                 TGCGTTTTTT TTC  TAAAA
                                 |||||||||| |||  |||||
                                 ACGCGAAAAA AAG  ATTTT
                                       A   GA
GAM2626  ST7       3'  ACCCTGCATTTTTTCTTTTTAA 61618             CG
              A                   ACCCTGCGTTTTTTCTT  TAAA
                                  |||||||||||||||||  ||||
                                  TGGGACGTAAAAAAGAA  ATTT
                                             AA
GAM2626  USP6      5'  CCTTGTTAGTTTCTTCGTA   61619     GC   T_
                                 CCT  GTT  TTTCTTCGTA
                                 |||  |||  ||||||||||
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                                GGA  CAA  AAAGAAGCAT
                                  A_   TC
GAM2626  FLJ14345  3'  CCCGGCGTCCTTTGTAA     61620     T       CTTC
                                CCC GCGTTTTTT    GTAA
                                ||| |||||||||    ||||
                                GGG CGCAGGAAA    CATT
                                  C       ____
GAM2626  MCF2L     3'  CCCTGCATTTTTTTTGTA     61621           C  C
                                CCCTGCGTTTTTT TT GTA
                                |||||||||||| || |||
                                GGGACGTAAAAAA AA CAT
                                          _ _
GAM2626  MGC11082  5'  CCCTCCGCCTTTTTTTTTGTAA 61622      G       CTTC_
              A                  CCCT CGTTTTTT     GTAAA
                                ||||| ||||||||     |||||
                                GGGA GCGGAAAA     CATTT
                                  G       AAAAA
GAM2626  SEMA3C    5'  CCTCTGAGTTTCTTTGTAAA   61623    _  C   TTT    C
                                CC CTG GTT   TCTT GTAAA
                                || ||| |||   |||| |||||
                                GG GAC CAA   AGAA CATTT
                                 A   T   ___    A
GAM2626  LOC130470 3'  GTTTTTTCAACCATAAAA     61624         T_
                                GTTTTTTC  TCGTAAAA
                                ||||||||  ||||||||
                                CAAAAAAG  GGTATTTT
                                     TT
GAM2626  LOC150166 5'  CCCTGCTGCCTCTTCTTTGTAA 61625        _        C
                                CCCTGC GTTTTTTCTT GTAA
                                |||||| |||||||||| ||||
                                GGGACG CGGAGAAGAA CATT
                                   A         A
GAM2627  NFIA      3'  CACCATATGAGAAATTAC     61628          T_
                                CACTATGTG  AAATTAC
                                |||||||||  |||||||
                                GTGGTATAC  TTTAATG
                                     TC
GAM2628  KRTHA8    3'  AAGAGGCTGTGTTGCCACA    61631      A     CTA
                                AAGA GCTGTG   CTATA
                                |||| ||||||   |||||
                                TTCT CGACAC   GGTGT
                                  C     AAC
GAM2628  TAF1C     3'  AAGAAACTACTACTGTATTTTG 61632         GT     A
                                AAGAAGCT  GCTACT TATTTTG
                                ||||||||  |||||| |||||||
                                TTCTTTGA  TGATGA ATAAAAC
                                     __     C
GAM2628  TEM5      3'  GAAGCTGGTTTGACATTTTG   61633        TGCTACT
                                GAAGCTG      ATATTTTG
                                |||||||      ||||||||
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                                CTTCGAC      TGTAAAAC
                                    CAAAC__
GAM2628  DKFZp762E1312 5'  AAGAAGCTGCTGCTACTGGTCT 61634         _      ATA_
           CTTG                   AAGAAGCTG TGCTACT    TTTTG
                                  ||||||||| |||||||    |||||
                                  TTCTTCGAC ACGATGA    AGAAC
                                     G      CCAG
GAM2628  EIF2S1    3'  AAGAAGCACCTGTTATATTTTG 61635       TGT   AC_
                                  AAGAAGC   GCT   TATATTTTG
                                  |||||||   |||   |||||||||
                                  TTCTTCG   TGG   ATATAAAAC
                                     ___   ACA
GAM2628  FLJ20297  3'  AGAATCTGTAGTTGTATATTTT 61636     G    CTAC
           G                       AGAA CTGTG    TATATTTTG
                                  |||| |||||    |||||||||
                                  TCTT GACAT    ATATAAAAC
                                    A     CAAC
GAM2628  FLJ20297  3'  AGAATCTGTAGTTGTATATTTT 61636     G    CTAC
           G                       AGAA CTGTG    TATATTTTG
                                  |||| |||||    |||||||||
                                  TCTT GACAT    ATATAAAAC
                                    A     CAAC
GAM2628  KIAA0999  3'  AAGCAGCTGTGATATTTT    61637     A      CTACT
                                  AAG AGCTGTG     ATATTTT
                                  ||| |||||||     |||||||
                                  TTC TCGACAC     TATAAAA
                                    G      _____
GAM2628  MGC2463   3'  AGAAACTGTGTTGCTGACT    61638         ___   _
                                  AGAAGCTGT   GCT ACT
                                  |||||||||   ||| |||
                                  TCTTTGACA   CGA TGA
                                       CAA   C
GAM2628  PRO2032   5'  AAGAAGCTAGTGCTGCTAT    61639         _     A
                                  AAGAAGCT GTGCT CTAT
                                  |||||||| ||||| ||||
                                  TTCTTCGA CACGA GATA
                                     T     C
GAM2628  LOC150538 5'  AGAAGCTGTGCTGTTACA     61640           AC
                                  AGAAGCTGTGCT  TATA
                                  ||||||||||||  ||||
                                  TCTTCGACACGA  ATGT
                                        CA
GAM2628  LOC150776 3'  AGAATCTGTAGTTGTATATTTT 61636     G    CTAC
           G                       AGAA CTGTG    TATATTTTG
                                  |||| |||||    |||||||||
                                  TCTT GACAT    ATATAAAAC
                                    A     CAAC
GAM2628  LOC153711 3'  AAGAAGCTGTTTTATTCT     61641          GCTACTA
                                  AAGAAGCTGT      TATTTT
                                  ||||||||||      ||||||
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                                TTCTTCGACA      ATAAGA
                                      AA_____
GAM2628  LOC166929 5'  AAGAAGCTTGTGATTT      61642        _  CTACTAT
                                AAGAAGCT GTG      ATTT
                                |||||||| |||      ||||
                                TTCTTCGA CAC      TAAA
                                     A  ________
GAM2629  FCMD      3'  CTGTATTAGGTTGGGTTAGAAG 61645        C_  T  C
                                CTGTATTAG  TG GT AGAAG
                                |||||||||  || || |||||
                                GACATAATC  AC CA TCTTC
                                      CA  C  A
GAM2629  LDHB      5'  TGTCTGTGTGTGGTCAGAA   61646   C   ATTAGC   _
                                TG CTGT     TGTG TCAGAA
                                || ||||     |||| ||||||
                                AC GACA     ACAC AGTCTT
                                 A   C_____   C
GAM2629  DRIM      3'  TGCTTGTATCAGCACAG     61647    C       TGTGT
                                TGC TGTATTAGC     CAG
                                ||| |||||||||     |||
                                ACG ACATAGTCG     GTC
                                  A        T____
GAM2629  FLJ13340  3'  TGCTTTGTTAGCTGTAACAG   61648    C_  AT      T
                                TGC  TGT  TAGCTGTG CAG
                                |||  |||  |||||||| |||
                                ACG  ACA  ATCGACAT GTC
                                  AA  __       T
GAM2629  FLJ20499  3'  TGCCTGCATTAGGCTGGAA   61649          _  TGTCA
                                TGCCTGTATTAG CTG    GAA
                                |||||||||||| |||    |||
                                ACGGACGTAATC GAC    CTT
                                       C  _____
GAM2629  FLJ20793  3'  CCTGTATTAGTTTATAGAAG   61650        CTG   C
                                CCTGTATTAG   TGT AGAAG
                                ||||||||||   ||| |||||
                                GGACATAATC   ATA TCTTC
                                      AA_  _
GAM2629  KIAA0040  5'  TGTCTGTGTGTGGTCAGAA   61646   C   ATTAGC   _
                                TG CTGT     TGTG TCAGAA
                                || ||||     |||| ||||||
                                AC GACA     ACAC AGTCTT
                                 A   C_____   C
GAM2629  KIAA0618  3'  TGTCTGTGTCAGCTGTGACAG  61651   C   A       T
                                TG CTGT TTAGCTGTG CAG
                                || |||| ||||||||| |||
                                AC GACA AGTCGACAC GTC
                                 A   C       T
GAM2629  KIAA1822  3'  TGCCTCTGTTAGCACAGCCAG  61652     GTA    TGT
                                TGCCT   TTAGC   GTCAG
                                |||||   |||||   |||||
```

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                                ACGGA   AATCG   CGGTC
                                  GAC     TGT
GAM2629  MMP24    3'  GCTTGTTGCTCACTGTGTCAGA 61653    C   ATTA_
             AG                   GC TGT     GCTGTGTCAGAAG
                                || |||    ||||||||||||
                                CG ACA    TGACACAGTCTTC
                                 A   ACGAG
GAM2629  TBDN100  3'  TGCTTTGTTAGCTGTAACAG   61648    C_   AT      T
                                TGC  TGT  TAGCTGTG CAG
                                |||  |||  |||||||| |||
                                ACG  ACA  ATCGACAT GTC
                                 AA   __       T
GAM2629  TCL6     3'  TGCCTGATAAATGTCAGAA    61654       T  TAGCT
                                TGCCTG AT    GTGTCAGAA
                                |||||| ||    |||||||||
                                ACGGAC TA    TACAGTCTT
                                   _  TT___
GAM2629  TCL6     3'  TGCCTGATAAATGTCAGAA    61654       T  TAGCT
                                TGCCTG AT    GTGTCAGAA
                                |||||| ||    |||||||||
                                ACGGAC TA    TACAGTCTT
                                   _  TT___
GAM2629  ZDHHC8   3'  GCCCACAGGCTGTGTCAGAAG  61655     TG  TTA
                                GCC  TA   GCTGTGTCAGAAG
                                |||  ||   ||||||||||||
                                CGG  GT   CGACACAGTCTTC
                                 GT  C__
GAM2629  ZNF387   5'  TGCCCTGCTGTGTCAG      61656      GTATTA
                                TGCCT     GCTGTGTCAG
                                |||||     ||||||||||
                                ACGGG     CGACACAGTC
                                  A_____
GAM2629  LOC149319 5'  TGCCCTGCCTGTGTCAG     61657     _   ATTAG
                                TGCC TGT     CTGTGTCAG
                                |||| |||    |||||||||
                                ACGG ACG     GACACAGTC
                                  G  _____
GAM2629  LOC51281  3'  TGCCTGCATTAGGCTGGAA    61649          _   TGTCA
                                TGCCTGTATTAG CTG     GAA
                                |||||||||||| |||    |||
                                ACGGACGTAATC GAC     CTT
                                       C  _____
GAM2630  ACADL    3'  ACCTTATATTGGAAAACTAG   61660        C   ___
                                ACCTTATA TGGA   CTAG
                                |||||||| ||||   ||||
                                TGGAATAT ACCT   GATC
                                    A    TTT
GAM2630  CALU     3'  TACCCTATATTGGGGCTAA    61661         C   A_
                                TACCTTATA TGG  CTAG
                                ||||||||| |||  ||||
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                                ATGGGATAT ACC  GATT
                                     A   CC
GAM2630 IDH3A    3'  CTTATACTGGTACTGC      61662          AC  G
                                CTTATACTGG  TA TGC
                                ||||||||||  || |||
                                GAATATGACC  AT ACG
                                      __  G
GAM2630 TP63     3'  CCTCGCTTTGGCTAGTGCCAA 61663     ATAC   A
                                CCTT    TGG CTAGTGCCAA
                                ||||    ||| ||||||||||
                                GGAG    ACC GATCACGGTT
                                  CGAA   _
GAM2630 FLJ12529 3'  TACCTGCCTACTAGTGCCA   61664      TATA  GG
                                TACCT    CT  ACTAGTGCCA
                                |||||    ||  ||||||||||
                                ATGGA    GG  TGATCACGGT
                                   C___  A_
GAM2630 HCGIV.9  3'  TACCTTATGTGGGTCTGCC   61665        AC   ACTAG
                                TACCTTAT  TGG    TGCC
                                ||||||||  |||    ||||
                                ATGGAATA  ACC    ACGG
                                     C_   CAG__
GAM2630 MGC10911 3'  CTCCAAGGGCTAGTGCCAA   61666     ATACT  A
                                CTT    GG CTAGTGCCAA
                                |||    || ||||||||||
                                GAG    CC GATCACGGTT
                                  GTT__  C
GAM2630 MKRN4    3'  CCTATACTGGAAAGGC      61667          CT  T
                                CTTATACTGGA  AG GC
                                ||||||||||  || ||
                                GGATATGACCT  TC CG
                                       T_  _
GAM2630 SLC5A7   3'  CTTATGTGAAAAAGTGCCAA  61668      AC    CT
                                CTTAT  TGGA  AGTGCCAA
                                |||||  ||||  ||||||||
                                GAATA  ACTT  TCACGGTT
                                   C_    TT
GAM2630 ZFR      3'  CTTACAACTAGTGTCA      61669       ACTG       C
                                CTTAT    GACTAGTG CA
                                |||||    |||||||| ||
                                GAATG    TTGATCAC GT
                                   _____       A
GAM2631 ATP6V0C  3'  AGGGGGTGGGGCGCCGG     61672     AA       GGCG
                                AGG  GTGGGGCGC    TGG
                                |||  |||||||||    |||
                                TCC  CACCCCGCG    GCC
                                  CC        _____
GAM2631 BTAF1    5'  GGGAGCGGCCGGTGCGGCGTGG 61673    A    __  C
             G                   GG AGTGG  GG GCGGCGTGGG
                                 || |||||  || ||||||||||
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                                CC TCGCC  CC CGCCGCACCC
                                 C    GG  A
GAM2631  CCND1    3'  GAGGGGTGGGGCGGGGTGGG  61674     AA      C  C
                                GAGG  GTGGGGCG GG GTGGG
                                ||||  |||||||| || |||||
                                CTCC  CACCCCGC CC CACCC
                                  C_      _ _
GAM2631  DMPK     3'  TGAGGAGGGGGGGCGCGG     61675       A T
                                TGAGGA G GGGGCGCGG
                                |||||| | |||||||||
                                ACTCCT C CCCCGCGCC
                                   _ C
GAM2631  DSC2     5'  GAGGAGGTGGGGCGCGCG    61676      A        G
                                GAGGA GTGGGGCGCG CG
                                ||||| |||||||||| ||
                                CTCCT CACCCCGCGC GC
                                  C        _
GAM2631  DSC2     5'  GAGGAGGTGGGGCGCGCG    61676      A        G
                                GAGGA GTGGGGCGCG CG
                                ||||| |||||||||| ||
                                CTCCT CACCCCGCGC GC
                                  C        _
GAM2631  GAN      3'  TGAGAAGTGGGGTAAAGTGGG  61677      G       CGCGGC
                                TGAG AAGTGGGG     GTGGG
                                |||| ||||||||     |||||
                                ACTC TTCACCCC     CACCC
                                  _       ATTT__
GAM2631  ITGA11   3'  TGAGGGAGGCCTTGGCGTGGG  61678      AAGT    GC_
                                TGAGG   GGGGC   GGCGTGGG
                                |||||   |||||   ||||||||
                                ACTCC   CTCCG   CCGCACCC
                                  _____     GAA
GAM2631  OGDH     3'  GAGGAGGGCGGTGGTGTGGG   61679      AGTG    C_  C
                                GAGGA   GGGCG  GG GTGGG
                                |||||   |||||  || |||||
                                CTCCT   CCCGC  CC CACCC
                                  _____     CA  A
GAM2631  RCE1     3'  TGGGGGGTGGGGGGGTGG     61680    A  AA     CGCG C
                                TG GG  GTGGGG    G GTGG
                                || ||  ||||||    | ||||
                                AC CC  CACCCC    C CACC
                                 _  CC     _____ _
GAM2631  SPTAN1   5'  CGGGGGGGTGAGGGGCGTGGG   61681    A  AA     CGC
                                TG GG  GTGGGG   GGCGTGGG
                                || ||  ||||||   ||||||||
                                GC CC  CACTCC   CCGCACCC
                                 _  CC     ____
GAM2631  WNT7A    5'  GAGGAGCGAGCGCGGCGTGGG  61682       A    G
                                GAGGA GTGGG CGCGGCGTGGG
                                ||||| ||||| ||||||||||
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                                CTCCT CGCTC GCGCCGCACCC
                                  _    _
GAM2631  DKFZP434H204 5'  TGAGGCGGGTGAAGGGCGTGGG 61683      AA_     CGC
                                TGAGG   GTGGGG   GGCGTGGG
                                |||||   ||||||   ||||||||
                                ACTCC   CACTTC   CCGCACCC
                                   GCC     ___
GAM2631  DKFZP434N1511 5'  TAAGGGAGTGGGGCGCGCCG   61684      A        G
                                TGAGG AGTGGGGCGCG CG
                                ||||| |||||||||| ||
                                ATTCC TCACCCCGCGC GC
                                   C         G
GAM2631  FLJ12132  3'  GGGGTGGGGTGGTGGCGTGGG  61685    AA     CGC_
                                GG  GTGGGG    GGCGTGGG
                                ||  ||||||    ||||||||
                                CC  CACCCC    CCGCACCC
                                 C_     ACCA
GAM2631  FLJ14642  3'  TGGGAGGTGGGGCGGG      61686    A  A      C
                                TG GGA GTGGGGCG GG
                                || ||| ||||||| ||
                                AC CCT CACCCCGC CC
                                 _  C      _
GAM2631  KIAA0514  3'  TAAGGAAGTGGGATGTGG     61687           CGCGGC
                                TGAGGAAGTGGGGG     GTGG
                                ||||||||||||      ||||
                                ATTCCTTCACCCT     CACC
                                        A_____
GAM2631  KIAA0802  3'  TGAGGCAGTGGGGGAATGTGGG 61688      A      CGCGGC
                                TGAGG AGTGGGG     GTGGG
                                ||||| |||||||     |||||
                                ACTCC TCACCCC     CACCC
                                   G      CTTA__
GAM2631  KIAA1462  3'  TGGGGAAGTGGGGCTGATAG   61689    A        GCGGC
                                TG GGAAGTGGGGC    GTGG
                                || ||||||||||     ||||
                                AC CCTTCACCCCG    TATC
                                 C         AC___
GAM2631  KIAA1817  3'  TGCGGGGGTGGGGGGCGTGGG  61690    A  AA     CGC
                                TG GG  GTGGGG   GGCGTGGG
                                || ||  ||||||   ||||||||
                                AC CC  CACCCC   CCGCACCC
                                 G  CC     ___
GAM2631  PDGFC     5'  TGAGGGGGTGGGGACGCGG    61691      AA     _
                                TGAGG  GTGGGG CGCGG
                                |||||  |||||| |||||
                                ACTCC  CACCCC GCGCC
                                   CC     T
GAM2631  PMX2B     3'  TGAGGAAGGGGGGTAGGAGTGGG 61692        T    CGC  C
                                TGAGGAAG GGGG   GG GTGGG
                                |||||||| ||||   || |||||
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                                ACTCCTTC CCCC   CC CACCC
                                     _    AT_  T
GAM2631  SRF      3'  TGGGGAGGTGGGGCACGG    61693    A   A
                                TG GGA GTGGGGCGCGG
                                || ||| ||||||||||
                                AC CCT CACCCCGTGCC
                                  C   C
GAM2631  ZNF213    3'  TGATGGAGTGGGGCGCCGAGTG 61694     _  A       _  C
           GG                     TGA GGA GTGGGGCGC GG GTGGG
                                ||| ||| ||||||||| || |||||
                                ACT CCT CACCCCGCG CT CACCC
                                  A  _       G  _
GAM2631  LOC113828 3'  GGGTGGGGAGTGGCGTGG    61695    AA     CGC
                                GG  GTGGGG   GGCGTGG
                                ||  ||||||   |||||||
                                CC  CACCCC   CCGCACC
                                 __     TCA
GAM2631  LOC118611 3'  TGAGGAATGGGGCGGG      61696       G      C
                                TGAGGAA TGGGGCG GG
                                ||||||| ||||||| ||
                                ACTCCTT ACCCCGC CC
                                     _      _
GAM2631  LOC124044 3'  GAGGGGGTGGGGCGGAGG    61697      AA       C  CGT
                                GAGG  GTGGGGCG GG   GG
                                ||||  |||||||| ||   ||
                                CTCC  CACCCCGC CT   CC
                                   CC       _ ____
GAM2631  LOC129303 5'  TGGGGAAGTGGGGGCGG     61698    A        C
                                TG GGAAGTGGGG GCGG
                                || ||||||||| ||||
                                AC CCTTCACCCC CGCC
                                  C        _
GAM2631  LOC151602 3'  TGAGGGGGTGGGCGCGG     61699       AA    G
                                TGAGG  GTGGG CGCGG
                                |||||  ||||| |||||
                                ACTCC  CACCC GCGCC
                                   CC    _
GAM2631  LOC152641 5'  GAGGGGCTCGGGGCGCGGCGTG 61700      AAG_
           GG                     GAGG   TGGGGCGCGGCGTGGG
                                ||||   ||||||||||||||||
                                CTCC   GCCCCGCGCCGCACCC
                                   CCGA
GAM2631  LOC157638 5'  GGAGGTGGGGCGCGAGG     61701     A         CGT
                                GGA GTGGGGCGCGG   GG
                                ||| ||||||||||   ||
                                CCT CACCCCGCGCT   CC
                                  C         ____
GAM2631  LOC158373 5'  TGAGGGCGGGGGCGGCGTGGG  61702       AA     C
                                TGAGG  GTGGGG GCGGCGTGGG
                                |||||  |||||| ||||||||||
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                                ACTCC  CGCCCC CGCCGCACCC
                                  __    _
GAM2631  LOC197136 3'  GAGGGGGTGGGGCGGAGG    61697     AA      C  CGT
                                GAGG  GTGGGGCG GG   GG
                                ||||  |||||||| ||   ||
                                CTCC  CACCCCGC CT   CC
                                  CC       _ ____
GAM2631  LOC197342 3'  GAGGGGTGGGGGTCCCTGTGGG 61703     AA     CGCGGC
                                GAGG  GTGGGG     GTGGG
                                ||||  ||||||     |||||
                                CTCC  CACCCC     CACCC
                                  C_     CAGGGA
GAM2631  LOC199800 5'  TGGGGAAATGGGGCGGG     61704    A         C
                                TG GGAAGTGGGGCG GG
                                || ||||||||||| ||
                                AC CCTTTACCCCGC CC
                                 C         _
GAM2631  LOC199923 5'  TGAGGAAGTGGGAGTGTGCAGT 61705           CGCG _
           GGG                    TGAGGAAGTGGGG    GC GTGGG
                                |||||||||||||    || |||||
                                ACTCCTTCACCCT    CG CACCC
                                       CACA  T
GAM2631  LOC221692 3'  TGAGGAAGTGGCGGCTGGCGTG 61706          _  GC
           GG                     TGAGGAAGTGG GGC  GGCGTGGG
                                |||||||||| |||  ||||||||
                                ACTCCTTCACC CCG  CCGCACCC
                                      G   A_
GAM2631  LOC222008 5'  CGGGAAGTGGGGAGTGG     61707    A       CGCGGC
                                TG GGAAGTGGGG     GTGG
                                || ||||||||||     ||||
                                GC CCTTCACCCC     CACC
                                 _        T_____
GAM2631  LOC222962 3'  TGAGGGAGTGGGGCTGCTGG   61708      A      GCG  G
                                TGAGG AGTGGGGC   GC TGG
                                ||||| ||||||||   || |||
                                ACTCC TCACCCCG   CG ACC
                                   C       A__  _
GAM2631  LOC254219 5'  TGGGGGGTGGGGGCGTGG    61709    A  AA     CGCG
                                TG GG  GTGGGG    GCGTGG
                                || ||  ||||||    ||||||
                                AC CC  CACCCC    CGCACC
                                 _  CC     ____
GAM2631  LOC56961  5'  TGGGGAGGGGGGGCGCGCAGG   61710    A  A  T      G  T
                                TG GG AG GGGGCGCG CG GG
                                || || || |||||||| || ||
                                AC CC TC CCCCGCGC GT CC
                                 _  C  C       _  _
GAM2631  LOC92360  3'  TGAGGAAGGGGGGGTG       61711         T    CGCGGC
                                TGAGGAAG GGGG     GTG
                                |||||||| ||||     |||
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                                ACTCCTTC CCCC     CAC
                                   _   _______
GAM2632 GPR85    3' TAATGCTTTTACAGATAATA  61714        ACTAAA
                                TAGTGCTTT     AGATAATA
                                |||||||||     ||||||||
                                ATTACGAAA     TCTATTAT
                                    ATG___
GAM2632 LEPR     5' GCCCCACTGAAGGATAAT    61715        A  A
                                GCTTTACT AA GATAAT
                                |||||||| || ||||||
                                CGGGGTGA TT CTATTA
                                    C  C
GAM2632 TUBG1    3' CAGTGCTTTATTAAAGAT    61716         CTA
                                TAGTGCTTTA   AAAGAT
                                ||||||||||   ||||||
                                GTCACGAAAT   TTTCTA
                                    AA_
GAM2632 FLJ10989 3' TAGTGCTTTAGTTACACAGAT 61717         C_  AA_
                                TAGTGCTTTA  TA   AGAT
                                ||||||||||  ||   ||||
                                ATCACGAAAT  AT   TCTA
                                    CA  GTG
GAM2632 FLJ11726 3' GCGCTTAAGAGATAATA     61718      TTAC   A
                                GTGCT    TAA AGATAATA
                                |||||    ||| ||||||||
                                CGCGA    ATT TCTATTAT
                                   _____  C
GAM2632 FLJ22843 5' TAGGCATCAAAAGATAATA   61719     T  TTTAC
                                TAG GC    TAAAAGATAATA
                                ||| ||    ||||||||||||
                                ATC CG    GTTTTCTATTAT
                                  _  TA___
GAM2632 KIAA1128 3' TAGTGCTTTAATGGAAAAG   61720         CT__
                                TAGTGCTTTA    AAAAG
                                ||||||||||    |||||
                                ATCACGAAAT    TTTTC
                                    TACC
GAM2632 NEDD5    3' TAGTGCTTTATTGATAAAAG  61721         C___
                                TAGTGCTTTA    TAAAAG
                                ||||||||||    ||||||
                                ATCACGAAAT    ATTTTC
                                    AACT
GAM2632 LOC149420 3' TAGTGCTTTATAAAGAT     61722         CTA
                                TAGTGCTTTA   AAAGAT
                                ||||||||||   ||||||
                                ATCACGAAAT   TTTCTA
                                    A__
GAM2632 LOC153397 3' CAGTGCTTTCGAGATAAT    61723         ACTAAA
                                TAGTGCTTT     AGATAAT
                                |||||||||     |||||||
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                                GTCACGAAA     TCTATTA
                                     GC____
GAM2632  LOC154792 5'  TAGTGCTCTGTTATAAAATA  61724        AC  A
                                TAGTGCTTT  TA AAGATA
                                |||||||||  || ||||||
                                ATCACGAGA  AT TTTTAT
                                     CA  A
GAM2632  LOC157922 3'  TAGTGCTTTCTTAAAATAAATA 61725        AC    GAT
           C                     TAGTGCTTT  TAAAA   AATAC
                                |||||||||  |||||   |||||
                                ATCACGAAA  ATTTT   TTATG
                                     GA    AT_
GAM2632  LOC169831 3'  TAGTGCTTCACTGAACAGAT   61726          AAA_
                                TAGTGCTTTACT    AGAT
                                ||||||||||||    ||||
                                ATCACGAAGTGA    TCTA
                                       CTTG
GAM2633  CHES1    3'  ACGTTGACATCCCTGCG     61729        AT   GA
                                ACGTTGACG  TCTC  TGCG
                                |||||||||  ||||  ||||
                                TGCAACTGT  AGGG  ACGC
                                     __   __
GAM2633  HYAL3    5'  CAACGTTGGCCCCCAGCGGTGC 61730        ACGA   __  A
           GG                     TAACGTTG    TTCT  CG TGCGG
                                |||||||||    ||||  || |||||
                                GTTGCAAC    GGGG  GC ACGCC
                                     CG__    TC  C
GAM2633  MGC20253  3'  ACATTGACCTCAGTGATGTGG  61731        GA   TC_   C
                                ACGTTGAC  TTC   GATG GG
                                ||||||||  |||   |||| ||
                                TGTAACTG  GAG   CTAC CC
                                     __  TCA   A
GAM2634  SLC14A1   3'  CCAAGAATATCAATAAATAC   61734      A        TCT
                                TCAA AATATCAATA   AATAC
                                |||| ||||||||||   |||||
                                GGTT TTATAGTTAT   TTATG
                                  C         ___
GAM2634  FBP17    5'  TCAAGAATATCAATTCCC    61735      A       A
                                TCAA AATATCAAT TCT
                                |||| ||||||||| |||
                                AGTT TTATAGTTA GGG
                                  C       A
GAM2634  OMD      3'  TCAAAAATATCATTCTA     61736           ATA
                                TCAAAAATATCA   TCTA
                                ||||||||||||   ||||
                                AGTTTTTATAGT   AGAT
                                       A__
GAM2634  PDE8A    3'  TCAAAAATATCAAAGTCC    61737            TA
                                TCAAAAATATCAA  TCT
                                ||||||||||||  |||
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                                AGTTTTTATAGTT  AGG
                                       TC
GAM2635  ZNF10    3'  TGATATGTTCAAATGCCCAAT  61740        A    A_
                                TGATATGTT AAAT  TCAAT
                                ||||||||| ||||  |||||
                                ACTATACAA TTTA  GGTTA
                                     G    CG
GAM2635  MEGF10   3'  TGATATGTTATGAATCTCAA   61741        A_   A
                                TGATATGTTA  AAT TCAA
                                ||||||||||  ||| ||||
                                ACTATACAAT  TTA AGTT
                                      AC   G
GAM2635  LOC54103 5'  TGATATGTTAAATCAA      61742         AAT
                                TGATATGTTAA   ATCAA
                                ||||||||||   |||||
                                ACTATACAATT   TAGTT
                                      ___
GAM2636  ACTN2    3'  TGATGAACCAGTCAGTACT    61745        A    TTTTT
                                TGATGAAC AGTT    TACT
                                |||||||| ||||    ||||
                                ACTACTTG TCAG    ATGA
                                     G    TC___
GAM2636  CXCL6    3'  TATGATGCATGGTCTTTTTT   61746        AACAA
                                TATGATG    GTTTTTTTT
                                |||||||    |||||||||
                                ATACTAC    CAGAAAAAA
                                     GTAC_
GAM2636  PDGFB    3'  TATGATGAGCAGGTCCCTT    61747        A  A
                                TATGATGA CA GTTTTTT
                                |||||||| || |||||||
                                ATACTACT GT CAGGGAA
                                     C  C
GAM2636  RNF12    5'  TGATGAACAAGTGGAAAATACT 61748          TTTTTT
                                TGATGAACAAGT     TACT
                                ||||||||||||     ||||
                                ACTACTTGTTCA     ATGA
                                       CCTTTT
GAM2636  FLJ20457 3'  ATGATGGGTAAATTATTTTTAC 61749        AAC    T
           T                    ATGATG   AAGTT TTTTTACT
                                ||||||   ||||| ||||||||
                                TACTAC   TTTAA AAAAATGA
                                   CCA    T
GAM2636  GIT2     3'  TATGATCAACAAGTTTTT    61750        G
                                TATGAT AACAAGTTTTT
                                |||||| ||||||||||
                                ATACTA TTGTTCAAAAA
                                   G
GAM2636  KIAA0769 3'  TGATGAACAAGATGTGGCTACT 61751          TTTTTT
                                TGATGAACAAG     TTACT
                                ||||||||||      |||||
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                                ACTACTTGTTC     GATGA
                                      TACACC
GAM2636  LOC148766 3'  TATGATGAAGACAAGAGTTT  61752        __    TT
                                TATGATGA  ACAAG  TTT
                                ||||||||  |||||  |||
                                ATACTACT  TGTTC  AAA
                                     TC    TC
GAM2637  B4GALT2   3'  CCAGCATAGGGAAGCCGGAAGC 61755        AAACTT TA
                                CCAGTATAG     T  GAAGC
                                |||||||||     |  |||||
                                GGTCGTATC     G  CTTCG
                                     CCTTC_ GC
GAM2637  CALB1     3'  ACCAGTATAGGATATTCTAG  61756         AAAC
                                ACCAGTATAG    TTTTAG
                                ||||||||||    ||||||
                                TGGTCATATC    AAGATC
                                      CTAT
GAM2637  HS2ST1    3'  AGTTAGGAGCTTTTAGAAG   61757     A   AAA
                                AGT TAG   CTTTTAGAAG
                                ||| |||   ||||||||||
                                TCA ATC   GAAAATCTTC
                                  _   CTC
GAM2637  KPNA1     3'  ACCAGTATCACATTTAGGAG  61758        AGAA  T    A
                                ACCAGTAT    AC TTTAG AG
                                ||||||||    || ||||| ||
                                TGGTCATA    TG AAATC TC
                                     G___  T    C
GAM2637  SLC21A3   3'  ACAGAAAATTTTTAGAAG    61759       C_
                                ATAGAAA  TTTTAGAAG
                                |||||||  |||||||||
                                TGTCTTT  AAAATCTTC
                                    TA
GAM2637  SLC21A3   3'  ACAGAAAATTTTTAGAAG    61759       C_
                                ATAGAAA  TTTTAGAAG
                                |||||||  |||||||||
                                TGTCTTT  AAAATCTTC
                                    TA
GAM2637  SLC4A7    3'  ACCAGTAACATTTAGAAG    61760       TAGAA  T
                                ACCAGTA    AC TTTAGAAG
                                |||||||    || ||||||||
                                TGGTCAT    TG AAATCTTC
                                     _____  T
GAM2637  SMARCC1   3'  CAGTGTGGAGGCCCTCAGAGGC 61761     ATA  AA      A
                                CAGT   GA  CTTTTAGA GC
                                ||||   ||  |||||||| ||
                                GTCA   CT  GGGAGTCT CG
                                  CAC  CC       C
GAM2637  BART1     3'  CAGTACAGAAACACAGAGC   61762          TTT    A
                                CAGTATAGAAAC   TAGA GC
                                ||||||||||||   |||| ||
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                                GTCATGTCTTTG  GTCT CG
                                      T__   _
GAM2637 C20orf21 3' GTATAAAAACTTAAGACGGC  61763          TT  A_
                                GTATAGAAACTT  AGA  GC
                                ||||||||||||  |||  ||
                                CATATTTTTGAA  TCT  CG
                                      T_  GC
GAM2637 CFP1     3' ACCAGTACTATTTATTTGGAAG 61764        AGAAACT  A
                                ACCAGTAT      TTT GAAG
                                ||||||||      ||| ||||
                                TGGTCATG      AAA CTTC
                                    ATAAAT_   C
GAM2637 DJ473B4  3' AGACATAGAAGTTTTTAGAAGC 61765   _     AC
                                AG TATAGAA  TTTTAGAAGC
                                || |||||||  ||||||||||
                                TC GTATCTT  AAAATCTTCG
                                 T      CA
GAM2637 FLJ11795 5' CAGTATAGAAATAGTAAG    61766          CTTT  _
                                CAGTATAGAAA    TAG AAG
                                ||||||||||    ||| |||
                                GTCATATCTTT    ATC TTC
                                      ____  A
GAM2637 KIAA0275 3' CCAGGGTAGAAACCAAGGGGAG 61767     TA      TTTAGA
          C                      CCAG  TAGAAACT     AGC
                                ||||  ||||||||     |||
                                GGTC  ATCTTTGG     TCG
                                  CC       TTCCCC
GAM2637 KIAA0836 3' ACCAGTATGCAAACAAAG    61768        AG    TTTTA
                                ACCAGTAT  AAAC    GAAG
                                ||||||||  ||||    ||||
                                TGGTCATA  TTTG    TTTC
                                    CG   _____
GAM2637 KIAA1904 3' CCGGCATAGGGGTCAAAAGC  61769    A     AAACTT
                                CC GTATAG     TTAGAAGC
                                || ||||||     ||||||||
                                GG CGTATC     AGTTTTCG
                                 C     CCC___
GAM2637 KLHL4    3' GTATAGAAGTTTTGTAGAAG  61770        AC  _
                                GTATAGAA  TTT TAGAAG
                                ||||||||  ||| ||||||
                                CATATCTT  AAA ATCTTC
                                    CA  C
GAM2637 PIR      3' AGTGTGGAATTCTTTAGAAGC 61771     ATA  AC
                                AGT  GAA  TTTTAGAAGC
                                |||  |||  ||||||||||
                                TCA  CTT  GAAATCTTCG
                                  CAC  AA
GAM2637 PJA1     5' CAGTATAGAATAAAGGAGC   61772         ACTTTT  A
                                CAGTATAGAA     AG AGC
                                ||||||||||     || |||
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                                GTCATATCTT     TC TCG
                                     ATT___  C
GAM2637  PRO0038   5'  CCAGTATAGCAGTTCCTCAG  61773        AAAC_
                                CCAGTATAG    TTTTAG
                                |||||||||    ||||||
                                GGTCATATC    GGAGTC
                                     GTCAA
GAM2637  UBE2G1    3'  CAGTATAGAAGAATAGAGGC  61774         ACTTT   A
                                CAGTATAGAA    TAGA GC
                                ||||||||||    |||| ||
                                GTCATATCTT    ATCT CG
                                     CTT__    C
GAM2637  LOC142927 3'  CAGTATCAGAGACACAAAAGC  61775       _  A  TTT
                                CAGTAT AGA AC   TAGAAGC
                                |||||| ||| ||   |||||||
                                GTCATA TCT TG   GTTTTCG
                                   G   C  T__
GAM2637  LOC90133  5'  ACCAGGTGGAGATTCCAGAAG  61776      TAT_  AAC
                                ACCAG   AGA   TTTTAGAAG
                                |||||   |||   |||||||||
                                TGGTC   TCT   AAGGTCTTC
                                  CACC  ___
GAM2637  LOC90470  3'  ACTAGTACTAGAAACTTT    61777    C    _
                                AC AGTAT AGAAACTTT
                                || ||||| |||||||||
                                TG TCATG TCTTTGAAA
                                 A    A
GAM2638  CENTD2    3'  TATATTATCAAAAAGTCCCCAA 61780        A        TG
                                TATATTAT AAAAAGTTTT  A
                                |||||||| ||||||||||  |
                                ATATAATA TTTTTCAGGG  T
                                     G         GT
GAM2638  CENTD2    3'  TATATTATCAAAAAGTCCCCAA 61780        A        TG
                                TATATTAT AAAAAGTTTT  A
                                |||||||| ||||||||||  |
                                ATATAATA TTTTTCAGGG  T
                                     G         GT
GAM2638  ODZ2      3'  TATATTACAAAAAAGTTCCT   61781
                                TATATTATAAAAAAGTTTTT
                                ||||||||||||||||||||
                                ATATAATGTTTTTTCAAGGA

GAM2638  Rab11-FIP2 3'  TATATTATATAAAAATTCTGAT 61782         A        T
           T                     TATATTATA AAAAGTTTT GATT
                                 |||||||||  |||||||||  ||||
                                 ATATAATAT TTTTTAAGA CTAA
                                      A        _
GAM2638  TRPC4     3'  TACAAAACAAAAAGGTTTTTGA 61783      TT       A
           TT                      TATA  ATAAAAA GTTTTTGATT
                                   ||||  |||||||  ||||||||||
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                                ATGT  TGTTTTT CAAAAACTAA
                                  TT      C
GAM2639  CD244    3'  GCTGTTTCTTCTTCCCCTG   61786    CATC       A
                                GCT   TCTTCTTC CTTG
                                |||   |||||||| ||||
                                CGA   AGAAGAAG GGAC
                                  CAA_       G
GAM2639  GRIN2B   3'  AAGCTCATTTCTCTTAACT   61787        C   T   C
                                AAGCTCAT TCT CTT ACT
                                |||||||| ||| ||| |||
                                TTCGAGTA AGA GAA TGA
                                     A   _   T
GAM2639  NR2E1    3'  AAGCTCTTCTCTTTTTGACATG 61788       A     C  C  T
                                AAGCTC TCTCTT TT AC TG
                                |||||| |||||| || || ||
                                TTCGAG AGAGAA AA TG AC
                                    A     A  C  T
GAM2639  PCMT1    3'  AAGCTCATCTCTATTTTC    61789           TC_
                                AAGCTCATCTCT   TTC
                                ||||||||||||   |||
                                TTCGAGTAGAGA   AAG
                                       TAA
GAM2639  ATPAF1   3'  GCTCATCTCTGTGACTGCTTGC 61790          TCTTCA_
           G                     GCTCATCTCT      CTTGCG
                                ||||||||||      ||||||
                                CGAGTAGAGA      GAACGC
                                      CACTGAC
GAM2639  DKFZp434J0617 3'  GCTCGCTCTTCTCACAGATGCG 61791      AT       _  CT
                                GCTC  CTCTTCTT CA  TGCG
                                ||||  |||||||| ||  ||||
                                CGAG  GAGAAGAG GT  ACGC
                                  C_       T  CT
GAM2639  MDS028   3'  AACTTGTCTCTTCTTTCACC   61792      CA       _
                                AGCT  TCTCTTCTT CACT
                                ||||  ||||||||| ||||
                                TTGA  AGAGAAGAA GTGG
                                  AC        A
GAM2639  MRF-1    3'  GCCTTCTTCTTCACTTG     61793     CATC
                                GCT   TCTTCTTCACTTG
                                |||   ||||||||||||
                                CGG   AGAAGAAGTGAAC
                                  A___
GAM2639  SYNCOILIN 3'  GCTCATCTTTCCTTTCCTTG   61794        C    CA
                                GCTCATCT TTCTT  CTTG
                                |||||||| |||||  ||||
                                CGAGTAGA AGGAA  GAAC
                                     A    AG
GAM2639  VIAAT    3'  GCCTTTGTCTCTTCTTTATTTG 61795     CA__       CAC
           CG                     GCT   TCTCTTCTT   TTGCG
                                |||   |||||||||  |||||
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                                CGG   AGAGAAGAA  AACGC
                                  AAAC       ATA
GAM2639  LOC145725 5'  AAGCTCATTTCTTCTCCAC   61796       C
                                AAGCTCAT TCTTCTTCAC
                                |||||||| ||||||||||
                                TTCGAGTA AGAAGAGGTG
                                     A
GAM2639  LOC145732 5'  AAGCTCATTTCTTCTCCAC   61796       C
                                AAGCTCAT TCTTCTTCAC
                                |||||||| ||||||||||
                                TTCGAGTA AGAAGAGGTG
                                     A
GAM2639  LOC147515 3'  AAGCTCATCTCTTCTCCA    61797
                                AAGCTCATCTCTTCTTCA
                                ||||||||||||||||||
                                TTCGAGTAGAGAAGAGGT

GAM2639  LOC147671 3'  CTCCTCTCCAGGCTTGCG    61798         __
                                CTCTTCTTCA  CTTGCG
                                ||||||||||  ||||||
                                GAGGAGAGGT  GAACGC
                                      CC
GAM2639  LOC149995 3'  AAGCTCATCTCTTCTCCA    61797
                                AAGCTCATCTCTTCTTCA
                                ||||||||||||||||||
                                TTCGAGTAGAGAAGAGGT

GAM2639  LOC163590 3'  AAGCTCATCTTTGTTTTTCA  61799        C__  C
                                AAGCTCATCT   TT TTCA
                                ||||||||||   || ||||
                                TTCGAGTAGA   AA AAGT
                                      AAC  A
GAM2639  LOC196957 5'  AAGCTCATTTCTTCTCCAC   61796       C
                                AAGCTCAT TCTTCTTCAC
                                |||||||| ||||||||||
                                TTCGAGTA AGAAGAGGTG
                                     A
GAM2639  LOC196961 5'  AAGCTCATTTCTTCTCCAC   61796       C
                                AAGCTCAT TCTTCTTCAC
                                |||||||| ||||||||||
                                TTCGAGTA AGAAGAGGTG
                                     A
GAM2639  LOC197138 5'  AAGCTCATTTCTTCTCCAC   61796       C
                                AAGCTCAT TCTTCTTCAC
                                |||||||| ||||||||||
                                TTCGAGTA AGAAGAGGTG
                                     A
GAM2639  LOC200597 3'  GCTTGTTCTTCTTCACCCA   61800    CATC
                                GCT   TCTTCTTCACTTG
                                |||   ||||||||||||
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                                CGA   AGAAGAAGTGGGT
                                  ACA_
GAM2639 LOC93380 5' AGCTGTTTCTTCTTCCACC   61801     CATC      _
                                AGCT   TCTTCTTC ACT
                                ||||   |||||||| |||
                                TCGA   AGAAGAAG TGG
                                  CAA_      G
GAM2640 LOC123872 5' TCAATGGTCTTGATGTAATTGT 61804         C      C
                                TTAATGGTCT GATGTAAT GT
                                |||||||||| |||||||| ||
                                AGTTACCAGA CTACATTA CA
                                      A      A
GAM2640 LOC50999 3' TTAATGGTCTTGACTGTAAC  61805         C  _
                                TTAATGGTCT GA TGTAAT
                                |||||||||| || ||||||
                                AATTACCAGA CT ACATTG
                                      A  G
GAM2641 ABR     3' GGAGGAAATGAAAGAACA    61808        C_
                                GGAGGAAA  GAAGAATG
                                ||||||||  ||||||||
                                CCTCCTTT  TTTCTTGT
                                     AC
GAM2641 ABR     3' GGAGGAAATGAAAGAACA    61808        C_
                                GGAGGAAA  GAAGAATG
                                ||||||||  ||||||||
                                CCTCCTTT  TTTCTTGT
                                     AC
GAM2641 BAZ1B   3' ACGGAGGAAGCAGAGGCCACA 61809        ACGA   AT  A
                                ACGGAGGAA    AGA  GC ACA
                                |||||||||    |||  || |||
                                TGCCTCCTT    TCT  CG TGT
                                     CG__   C_  G
GAM2641 CEP1    5' GGGGAAAAAAATGCA      61810    A   AAC
                                GG GGA   GAAGAATGCA
                                || |||   ||||||||||
                                CC CCT   TTTTTTACGT
                                  _  ____
GAM2641 COL5A3  3' ACGGAGGAGTGAGGAGGCA   61811        AAC  A  AT
                                ACGGAGGA   GA GA  GCA
                                ||||||||   || ||  |||
                                TGCCTCCT   CT CT  CGT
                                     CA_  C  C_
GAM2641 CTSK    3' GGAAGAAATGGAAGAGCA    61812        C_    AT
                                GGAGGAAA  GAAGA  GCA
                                ||||||||  |||||  |||
                                CCTTCTTT  CTTCT  CGT
                                     AC    __
GAM2641 CYB561  3' CGGAGAAACGAGAAGCA     61813      G     A   T
                                CGGAG AAACGA GAA GCA
                                ||||| |||||| ||| |||
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                                GCCTC TTTGCT CTT CGT
                                  _    _  _
GAM2641  GALC     3'  GAGGAAACGACTACAACA    61814         AGAA
                                GAGGAAACGA   TGCAACA
                                ||||||||||   |||||||
                                CTCCTTTGCT   ATGTTGT
                                   G___
GAM2641  INSR     3'  GGGGGGAACGAAAAAACA    61815    A  A       T
                                GG GG AACGAAGAA GCA
                                || || ||||||||| |||
                                CC CC TTGCTTTTT TGT
                                 C  C       _
GAM2641  LDOC1    3'  ACGGAGAAATGAAGAGAGAGAG 61816         AC     AT____
              CA                  ACGGAGGAA  GAAGA     GCA
                                |||||||||  |||||     |||
                                TGCCTCTTT  CTTCT     CGT
                                   A_    CTCTCT
GAM2641  MAP3K4   3'  ACGGAGGAGACAGAGGC     61817        A   A  AAT
                                ACGGAGGA ACG AG   GC
                                |||||||| ||| ||   ||
                                TGCCTCCT TGT TC   CG
                                   C   C  ___
GAM2641  MAP3K4   3'  ACGGAGGAGACAGAGGC     61817        A   A  AAT
                                ACGGAGGA ACG AG   GC
                                |||||||| ||| ||   ||
                                TGCCTCCT TGT TC   CG
                                   C   C  ___
GAM2641  MAPK14   3'  GGAGGAAATCTCTGCAACA   61818        CGAAGAA
                                GGAGGAAA      TGCAACA
                                ||||||||      |||||||
                                CCTCCTTT      ACGTTGT
                                   AGAG___
GAM2641  MAPK14   3'  GGAGGAAATCTCTGCAACA   61818        CGAAGAA
                                GGAGGAAA      TGCAACA
                                ||||||||      |||||||
                                CCTCCTTT      ACGTTGT
                                   AGAG___
GAM2641  MAPK14   3'  GGAGGAAATCTCTGCAACA   61818        CGAAGAA
                                GGAGGAAA      TGCAACA
                                ||||||||      |||||||
                                CCTCCTTT      ACGTTGT
                                   AGAG___
GAM2641  MECP2    3'  ACGGAGGAAGGGAAAGAA    61819        AC_
                                ACGGAGGAA   GAAGAA
                                |||||||||   ||||||
                                TGCCTCCTT   TTTCTT
                                   CCC
GAM2641  PTPRG    5'  CGGAGGAAACGGAGGAAAACA  61820          AA_   T
                                CGGAGGAAACG   GAA GCA
                                ||||||||||   ||| |||
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                                GCCTCCTTTGC  CTT TGT
                                     CTC  T
GAM2641  TAZ      5'  GGAGGAAACGGGAAGGC    61821        AA  T
                                GGAGGAAACG  GAA GC
                                ||||||||||  ||| ||
                                CCTCCTTTGC  CTT CG
                                     C_  C
GAM2641  UBE2L3   3'  ACGGAGGAAGTGGAGAGCA   61822       ACGA  AT
                                ACGGAGGAA   AGA  GCA
                                |||||||||   |||  |||
                                TGCCTCCTT   TCT  CGT
                                     CACC  __
GAM2641  ZNF239   5'  GGAGGAAAGCTCATGTAACA  61823       CGAAGA  C
                                GGAGGAAA    ATG AACA
                                ||||||||    ||| ||||
                                CCTCCTTT    TAC TTGT
                                    CGAG__  A
GAM2641  ZNF278   5'  CGGAGGAAACAAAAGGC    61824          AAT
                                CGGAGGAAACGAAG  GC
                                ||||||||||||||  ||
                                GCCTCCTTTGTTTT  CG
                                       C__
GAM2641  ZNF278   5'  CGGAGGAAACAAAAGGC    61824          AAT
                                CGGAGGAAACGAAG  GC
                                ||||||||||||||  ||
                                GCCTCCTTTGTTTT  CG
                                       C__
GAM2641  ZNF278   5'  CGGAGGAAACAAAAGGC    61824          AAT
                                CGGAGGAAACGAAG  GC
                                ||||||||||||||  ||
                                GCCTCCTTTGTTTT  CG
                                       C__
GAM2641  ZNF278   5'  CGGAGGAAACAAAAGGC    61824          AAT
                                CGGAGGAAACGAAG  GC
                                ||||||||||||||  ||
                                GCCTCCTTTGTTTT  CG
                                       C__
GAM2641  DDX31    3'  ACGGAGAAGGTGGAGGAAAGCA 61825       AAC_  A  T
                                ACGGAGGA   GA GAA GCA
                                ||||||||   || ||| |||
                                TGCCTCTT   CT CTT CGT
                                    CCAC  C  T
GAM2641  FLJ10597 3'  CGGGGAAGGGAGAATGCA   61826    A   AC  A
                                CGG GGAA  GA GAATGCA
                                ||| ||||  || |||||||
                                GCC CCTT  CT CTTACGT
                                  _   CC  _
GAM2641  FLJ13491 3'  GAGGAAACGAAGGCA      61827          AAT
                                GAGGAAACGAAG  GCA
                                ||||||||||||  |||
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                                CTCCTTTGCTTC  CGT
                                    ___
GAM2641  FLJ14351  3'  ACGGAGGAAGGAACGGGCA  61828       AC  GAAT
                                ACGGAGGAA GAA  GCA
                                ||||||||| |||  |||
                                TGCCTCCTT CTT  CGT
                                    C_  GCC_
GAM2641  FLJ20371  3'  GGAGGAAAAGAGGGAAGGCA  61829      C A_  T
                                GGAGGAAA GA GAA GCA
                                |||||||| ||  ||| |||
                                CCTCCTTT CT  CTT CGT
                                    T  CC  C
GAM2641  FLJ21916  3'  GGGGGAAACAAGGGCAA    61830   A    G  AAT
                                GG GGAAAC AAG  GCAA
                                || |||||| |||  ||||
                                CC CCTTTG TTC  CGTT
                                 C    _  C__
GAM2641  HABP4    3'  CGGAAGAAAAGGATGC     61831      AAC  A
                                CGGAGGA  GAAG ATGC
                                |||||||  |||| ||||
                                GCCTTCT  TTTC TACG
                                   ___  C
GAM2641  HN1      3'  GGAGGAAACAGACAGAACG  61832       _ _
                                GGAGGAAAC GA AGAATG
                                ||||||||| || ||||||
                                CCTCCTTTG CT TCTTGC
                                    T  G
GAM2641  KIAA0014  3'  ACGGAGAAGTGATCTGTAACA  61833      AAC  AGAA  C
                                ACGGAGGA  GA   TG AACA
                                ||||||||  ||   || ||||
                                TGCCTCTT  CT   AC TTGT
                                    CA_  AG__  A
GAM2641  KIAA0157  3'  ACAGAGGAGACGGTAATG   61834       A  AAG
                                ACGGAGGA ACG  AATG
                                |||||||| |||  ||||
                                TGTCTCCT TGC  TTAC
                                    C  CA_
GAM2641  KIAA0557  3'  GGAGGAAACGGGCAGCTGGCA  61835       A__  AAT
                                GGAGGAAACG  AG  GCA
                                |||||||||  ||  |||
                                CCTCCTTTGC  TC  CGT
                                   CCG  GAC
GAM2641  KIAA1084  3'  GGAGGAAAAGAGGCATGGCA  61836      C  AGA  _
                                GGAGGAAA GA  ATG CA
                                |||||||| ||  ||| ||
                                CCTCCTTT CT  TAC GT
                                    T  CCG  C
GAM2641  KIAA1305  3'  CGGAGGAAAGAGAGCA     61837       C  A  AT
                                CGGAGGAAA GA GA  GCA
                                ||||||||| || ||  |||
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                                GCCTCCTTT CT CT  CGT
                                      _ _ __
GAM2641 KIAA1796 3' ACGGGGGGAAGAATACAAC   61838     A  AAAC
                                ACGG GG   GAAGAATGCAAC
                                |||| ||   ||||||||||||
                                TGCC CC   CTTCTTATGTTG
                                  _ C___
GAM2641 KIAA1877 3' CAGAGATGAAGAATGCAAC   61839      AAAC
                                CGGAGG   GAAGAATGCAAC
                                ||||||   ||||||||||||
                                GTCTCT   CTTCTTACGTTG
                                   A___
GAM2641 MGC10955 3' ACAGAGAGAGAATGCA     61840       AAAC  A
                                ACGGAGG   GA GAATGCA
                                |||||||   || |||||||
                                TGTCTCT   CT CTTACGT
                                      ____ _
GAM2641 MGC23284 5' ACGGAGGAAAGATGGCAGCA  61841         C  AGAAT
                                ACGGAGGAAA GA    GCA
                                |||||||||| ||    |||
                                TGCCTCCTTT CT    CGT
                                     _ ACCGT
GAM2641 MGC3048  3' ACGGAGGAAGGAATGGGCA   61842        AC   GAAT
                                ACGGAGGAA  GAA   GCA
                                |||||||||  |||   |||
                                TGCCTCCTT  CTT   CGT
                                     C_  ACC_
GAM2641 PIP5K2B  3' GGAGGAATAATGCAAC     61843       ACGAAG
                                GGAGGAA    AATGCAAC
                                |||||||    ||||||||
                                CCTCCTT    TTACGTTG
                                   A_____
GAM2641 RNPC1    3' GGAGAAAATGGGACTCCAACA 61844       CGAA  ATG
                                GGAGGAAA   GA   CAACA
                                ||||||||   ||   |||||
                                CCTCTTTT   CT   GTTGT
                                     ACC_  GAG
GAM2641 SEMA4B   3' ACGGAGGAAGGCAGGCGAC   61845        ACGA  AAT  A
                                ACGGAGGAA   AG   GC AC
                                |||||||||   ||   || ||
                                TGCCTCCTT   TC   CG TG
                                     CCG_  ___  C
GAM2641 SKIP     3' CGGGGGAGAGTATGCAACA   61846     A   AAC  A A
                                CGG GGA   GA G ATGCAACA
                                ||| |||   || | ||||||||
                                GCC CCT   CT C TACGTTGT
                                  C  ___  _ A
GAM2641 SKIP     3' CGGGGGAGAGTATGCAACA   61846     A   AAC  A A
                                CGG GGA   GA G ATGCAACA
                                ||| |||   || | ||||||||
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                                GCC CCT   CT C TACGTTGT
                                  C  ___  _ A
GAM2641  SMT3H2   3'  GGGGGAAATGAAAGAATA    61847    A    C_
                                GG GGAAA  GAAGAATG
                                || |||||  ||||||||
                                CC CCTTT  TTTCTTAT
                                 C    AC
GAM2641  SPBPBP   3'  GGAGGAAATGAATGCA      61848        CGAA
                                GGAGGAAA   GAATGCA
                                ||||||||   |||||||
                                CCTCCTTT   CTTACGT
                                     A___
GAM2641  STX6     3'  ACGGAGAAAAGTCAGTGCA   61849         CGA  AA
                                ACGGAGGAAA  AG  TGCA
                                ||||||||||  ||  ||||
                                TGCCTCTTTT  TC  ACGT
                                      CAG  __
GAM2641  TERA     3'  GGAGGCACAGGATGCAACA   61850      AAACGA  A
                                GGAGG     AG ATGCAACA
                                |||||     || ||||||||
                                CCTCC     TC TACGTTGT
                                   GTG___  C
GAM2641  TTY7     3'  GGGGGAAAGAATGCAACA    61851    A   ACGA
                                GG GGAA    AGAATGCAACA
                                || ||||    ||||||||||
                                CC CCTT    TCTTACGTTGT
                                 C   _____
GAM2641  LOC145371 3'  GGAAGAGAGAAAAAGCA     61852       AAC     T
                                GGAGGA   GAAGAA GCA
                                ||||||   |||||| |||
                                CCTTCT   CTTTTT CGT
                                   CT_     _
GAM2641  LOC145547 3'  CGGAGGAAAGAGAGCA      61837         C  A  AT
                                CGGAGGAAA GA GA  GCA
                                ||||||||| || ||  |||
                                GCCTCCTTT CT CT  CGT
                                      _  _  __
GAM2641  LOC148696 5'  ACGGAGGAGGGGAAGGGGGGGC 61853         AAC    AAT__
            A                    ACGGAGGA   GAAG    GCA
                                ||||||||   ||||    |||
                                TGCCTCCT   CTTC    CGT
                                     CCC    CCCCC
GAM2641  LOC153277 3'  ACGAAGGAAAGAGGTGTGGCA  61854          C  AGAAT_
                                ACGGAGGAAA GA     GCA
                                |||||||||| ||     |||
                                TGCTTCCTTT CT     CGT
                                      _  CCACAC
GAM2641  LOC153937 5'  CGGTGGAACAAATGCAA     61855     A   A   AGA
                                CGG GGAA CGA   ATGCAA
                                ||| |||| |||   ||||||
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                                GCC CCTT GTT   TACGTT
                                  A   _  ____
GAM2641  LOC154547 3'  GGGGGAAATGAAAGAATA    61847    A    C_
                                GG GGAAA  GAAGAATG
                                || |||||  ||||||||
                                CC CCTTT  TTTCTTAT
                                 C     AC
GAM2641  LOC154789 3'  ACGGAGAAGATGAAACA     61856        AAC  A   T
                                ACGGAGGA   GA GAA GCA
                                ||||||||   || ||| |||
                                TGCCTCTT   CT CTT TGT
                                     ___  A   _
GAM2641  LOC158997 3'  GGGGGAAATGAAAGAATA    61847    A    C_
                                GG GGAAA  GAAGAATG
                                || |||||  ||||||||
                                CC CCTTT  TTTCTTAT
                                 C     AC
GAM2641  LOC202868 5'  CGGAGGAAAAGAAAGCA     61857       AAC     T
                                CGGAGGA   GAAGAA GCA
                                |||||||   |||||| |||
                                GCCTCCT   TTTCTT CGT
                                    ____     T
GAM2641  LOC221561 3'  GGGGGAAATGAAAGAATA    61847    A    C_
                                GG GGAAA  GAAGAATG
                                || |||||  ||||||||
                                CC CCTTT  TTTCTTAT
                                 C     AC
GAM2641  LOC257458 5'  CGGAGGAAGGAGAGGCA     61858        AC  A  AT
                                CGGAGGAA  GA GA  GCA
                                ||||||||  || ||  |||
                                GCCTCCTT  CT CT  CGT
                                     C_  _  C_
GAM2641  LOC257591 3'  GGGGGAAATGAAAGAATA    61847    A    C_
                                GG GGAAA  GAAGAATG
                                || |||||  ||||||||
                                CC CCTTT  TTTCTTAT
                                 C     AC
GAM2641  LOC51093  5'  CGGGGAGCGAGAACGCA     61859    A   AA   A
                                CGG GGA  CGA GAATGCA
                                ||| |||  ||| |||||||
                                GCC CCT  GCT CTTGCGT
                                  _   C_   _
GAM2641  LOC91145  3'  GGGGAAATAAGAATGCAACA   61860    A    CG
                                GG GGAAA  AAGAATGCAACA
                                || |||||  ||||||||||||
                                CC CCTTT  TTCTTACGTTGT
                                 _    A_
GAM2642  COL19A1   3'  TGTTTTGATGGTGGCTTCT    61863        CT    GC
                                TGTTTTGA  GTGGT  CT
                                ||||||||  |||||  ||
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                                ACAAAACT  CACCG  GA
                                    AC    AA
GAM2642  CRYGS    3'  TGTTTTATTGATGATGCCTA  61864       ACT
                                TGTTTTG  GTGGTGCCTA
                                |||||||  ||||||||||
                                ACAAAAT  TACTACGGAT
                                   AAC
GAM2642  PROCR    3'  TATTTTGATTGTGGATGACT  61865       C   _ C
                                TGTTTTGA TGTGG TG CT
                                |||||||| ||||| || ||
                                ATAAAACT ACACC AC GA
                                    A   T T
GAM2642  DKFZP547E2110 3'  TGTTTTGACTATGTACTT   61866          GTGCC
                                TGTTTTGACTGTG    TACTT
                                ||||||||||||    |||||
                                ACAAAACTGATAC    ATGAA

                                      _____
GAM2642  FLJ10922  3'  TGCTTTGATTGGCTGCTTTGC  61867       ____   GG
                                TGTTTTGA   CTGT  TGC
                                ||||||||   ||||  |||
                                ACGAAACT   GACG  ACG
                                    AACC   AA
GAM2642  KIAA0475  3'  TGTTTTACTGCAACTACTT   61868       A   TG TGC
                                TGTTTTG CTG  G   CTACTT
                                ||||||| |||  |  ||||||
                                ACAAAAT GAC  T   GATGAA
                                   _  GT ___
GAM2642  NRF      5'  TGTTTTGATTGTGGTCTCTA  61869       C    GC
                                TGTTTTGA TGTGGT  CTA
                                |||||||| ||||||  |||
                                ACAAAACT ACACCA  GAT
                                    A     GA
GAM2642  LOC154860 3'  TGTTTTGTGTGTGTGTCTGCTT 61870       AC   _  C  A
                                TGTTTTG  TGTG GTG CT CTT
                                |||||||  |||| ||| || |||
                                ACAAAAC  ACAC CAC GA GAA
                                   __   A  A  C
GAM2643  FDX1     3'  TCTGTTATAGGCAGAGATT   61873       CGA  TG   A
                                TCTGTTAT   AG  GGA GATT
                                ||||||||   ||  ||| ||||
                                AGACAATA   TC  TCT CTAA
                                    ___ CG  _
GAM2643  MECP2    3'  TGTTTTGAAGTGGGAACAT   61874     ATC       G
                                TGTT   GAAGTGGGAA AT
                                ||||   |||||||||| ||
                                ACAA   CTTCACCCTT TA
                                  AA_        G
GAM2644  TACSTD1  5'  CGTCGGGAGGACAGCGACG   61877    _ CAC
                                CG CG   AGGACAGCGACG
                                || ||   ||||||||||||
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                                GC GC   TCCTGTCGCTGC
                                 A  CC_
GAM2645  ACO1     3'  CACCCGACCTATCCATG     61880        GCACC
                                CACCCGAC    ATCCATG
                                ||||||||    |||||||
                                GTGGGCTG    TAGGTAC
                                    GA___
GAM2645  AIRE     5'  CCCGGCCCACCCACG       61881      AC  A
                                CCCG  GC CCATCCATG
                                ||||  || |||||||||
                                GGGC  CG GGTGGGTGC
                                  __ _
GAM2645  ANXA8    3'  CACCCAACCTGCGTCCATG   61882         __ ACCA
                                CACCCGAC  GC    TCCATG
                                ||||||||  ||    ||||||
                                GTGGGTTG  CG    AGGTAC
                                    GA  C___
GAM2645  BCL11A   3'  CCCTATGACAGCCATCCATG  61883     GAC_  _
                                CCC    GCA CCATCCATG
                                |||    ||| |||||||||
                                GGG    TGT GGTAGGTAC
                                  ATAC   C
GAM2645  YWHAG    3'  CACCCGACCCCCAACTCATG  61884        GCA   TC_
                                CACCCGAC   CCA   CATG
                                ||||||||   |||   ||||
                                GTGGGCTG   GGT   GTAC
                                    GG_   TGA
GAM2645  AK5      3'  CACCGCACCACTGTTCATG   61885      CGAC      C___
                                CACC    GCACCAT    CATG
                                ||||    |||||||    ||||
                                GTGG    CGTGGTG    GTAC
                                  ____      ACAA
GAM2645  BITE     5'  CACCCAACGAGTCTCATG    61886        CACCA  _
                                CACCCGACG    TC CATG
                                |||||||||    || ||||
                                GTGGGTTGC    AG GTAC
                                    TC___  A
GAM2645  DIO2     3'  CAACTGGGCTCCATCCATG   61887      ___  A
                                CGAC   GC CCATCCATG
                                ||||   || |||||||||
                                GTTG   CG GGTAGGTAC
                                  ACC  A
GAM2645  DIO2     3'  CAACTGGGCTCCATCCATG   61887      ___  A
                                CGAC   GC CCATCCATG
                                ||||   || |||||||||
                                GTTG   CG GGTAGGTAC
                                  ACC  A
GAM2645  DKFZP566M1046 3'  CACCCATGGCCCTGATTGTCCA 61888       AC  A  A_____
            TG                  CACCCG  GC CC     TCCATG
                                ||||||  || ||     ||||||
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                                GTGGGT  CG GG     AGGTAC
                                   AC  _  ACTAAC
GAM2645  FLJ11101  3'  CACCACCACCCCGTCCATG   61889     CGA   A  A
                                CACC   CGC CC TCCATG
                                ||||   ||| || ||||||
                                GTGG   GTG GG AGGTAC
                                  TG_   G  C
GAM2645  FLJ13055  3'  CACCCATGCCCCCCATG    61890      AC  A  A
                                CACCCG  GC CC TCCATG
                                ||||||  || || ||||||
                                GTGGGT  CG GG GGGTAC
                                   A_  _  _
GAM2645  FLJ20034  3'  CACCCATGCACATACATG   61891      AC   C  C
                                CACCCG  GCAC AT CATG
                                ||||||  |||| || ||||
                                GTGGGT  CGTG TA GTAC
                                   A_   _  T
GAM2645  FLJ20378  3'  ACTCCTCACCCATCCATG   61892   _  GA   A
                                AC CC  CGC CCATCCATG
                                || ||  ||| |||||||||
                                TG GG  GTG GGTAGGTAC
                                 A  A_  _
GAM2645  KIAA0285  3'  CCTCCCACACCATCCATG   61893   GA_
                                CC   CGCACCATCCATG
                                ||   ||||||||||||
                                GG   GTGTGGTAGGTAC
                                 AGG
GAM2645  KIAA0355  3'  CACCCACGCCCAACCATG   61894     G   A   T
                                CACCC ACGC CCA CCATG
                                |||||  |||| ||| |||||
                                GTGGG TGCG GGT GGTAC
                                   _   _   T
GAM2645  KIAA0892  3'  CACCCGTGTGCATCCACATG  61895      AC_  _  TC
                                CACCCG   GCA CCA  CATG
                                ||||||   ||| |||  ||||
                                GTGGGC   CGT GGT  GTAC
                                   ACA   A  __
GAM2645  KIAA1831  5'  CCCGGCACAGCATCCATG   61896    A   C
                                CCCG CGCA CATCCATG
                                |||| |||| ||||||||
                                GGGC GTGT GTAGGTAC
                                  C   C
GAM2645  KIAA1856  3'  CACCCGGGCATCCACG     61897      AC   CCA
                                CACCCG  GCA   TCCATG
                                ||||||  |||   ||||||
                                GTGGGC  CGT   AGGTGC
                                   C_  ____
GAM2645  KOC1     3'  CACTGTCACACCATCTATG   61898    CCGA      C
                                CAC   CGCACCATC ATG
                                |||   ||||||||| |||
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                                GTG   GTGTGGTAG TAC
                                  ACA_       A
GAM2645 MAST205  5' CACCCGCGGCCACCATG    61899      A  CA   T
                                CACCCG CG  CCA CCATG
                                |||||| ||  ||| |||||
                                GTGGGC GC  GGT GGTAC
                                   _ C_  _
GAM2645 PSMA7    3' CACATCGAGACTCATCCATG   61900    C_  C  AC
                                CAC  CGA GC  CATCCATG
                                |||  ||| ||  ||||||||
                                GTG  GCT TG  GTAGGTAC
                                  TA   C  A_
GAM2645 UBCE7IP5 3' CGGCACAGGCCATCCATG    61901    A   __
                                CG CGCA  CCATCCATG
                                || ||||  |||||||||
                                GC GTGT  GGTAGGTAC
                                 C    CC
GAM2645 ZFP95    3' CGACCATGTCCATCCATG    61902     G ____
                                CGAC CA   CCATCCATG
                                |||| ||   |||||||||
                                GCTG GT   GGTAGGTAC
                                  _ ACA
GAM2645 ZFP95    3' CGACCATGTCCATCCATG    61902     G ____
                                CGAC CA   CCATCCATG
                                |||| ||   |||||||||
                                GCTG GT   GGTAGGTAC
                                  _ ACA
GAM2645 LOC142972 3' CACCCAACCTGCGTCCATG   61882        __ ACCA
                                CACCCGAC  GC    TCCATG
                                ||||||||  ||    ||||||
                                GTGGGTTG  CG    AGGTAC
                                    GA  C___
GAM2645 LOC144231 5' CCTGAGACACATCCATG     61903    C  C    C
                                CC GA GCAC ATCCATG
                                || || |||| |||||||
                                GG CT TGTG TAGGTAC
                                 A  C   _
GAM2645 LOC151318 3' CACTGACAAGGCATCCATG   61904    CC    CAC
                                CAC  GACG   CATCCATG
                                |||  ||||   ||||||||
                                GTG  CTGT   GTAGGTAC
                                  A_   TCC
GAM2645 LOC253974 3' CACCCATGGCAAATTCCATG  61905       AC   CCA
                                CACCCG  GCA   TCCATG
                                ||||||  |||   ||||||
                                GTGGGT  CGT   AGGTAC
                                   AC   TTA
GAM2645 LOC256221 5' CCCGACGCCACGCATG      61906        AC   C
                                CCCGACGC  CAT CATG
                                ||||||||  ||| ||||
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                                GGGCTGCG  GTG GTAC
                                   __  C
GAM2646 ADAMTS5  3' TGACAAGGGGGAGACAGT   36902       A  T   T
                                TGACAAGG GG GATG GT
                                |||||||| || |||| ||
                                ACTGTTCC CC CTGT CA
                                    C  T   _
GAM2646 BACE     3' TGATAGGGAGGTAATGAACT  36903    CAA       TGT
                                TGA  GGAGGTGATG  GACT
                                |||  ||||||||||  ||||
                                ACT  CCTCCATTAC  TTGA
                                  ATC       ___
GAM2646 BACE     3' TGATAGGGAGGTAATGAACT  36903    CAA       TGT
                                TGA  GGAGGTGATG  GACT
                                |||  ||||||||||  ||||
                                ACT  CCTCCATTAC  TTGA
                                  ATC       ___
GAM2646 CBFB     3' AAGGAGGTGCCAAATGACT   36904       ATGT
                                AAGGAGGTG   GTGACT
                                |||||||||   ||||||
                                TTCCTCCAC   TACTGA
                                     GGTT
GAM2646 CBFB     3' AAGGAGGTGCCAAATGACT   36904       ATGT
                                AAGGAGGTG   GTGACT
                                |||||||||   ||||||
                                TTCCTCCAC   TACTGA
                                     GGTT
GAM2646 CHST6    3' TGCAGGGAGGATGTGACT    36905    A  A    TGAT
                                TG CA GGAGG   GTGTGACT
                                || || |||||   ||||||||
                                AC GT CCTCC   TACACTGA
                                 _  C    ____
GAM2646 CPT2     3' TGATGAGGAAGTGATGGTAGCT 36906    CA        T   A
                                TGA  AGGAGGTGATG GTG CT
                                |||  |||||||||| ||| ||
                                ACT  TCCTTCACTAC CAT GA
                                  AC         _  C
GAM2646 PYCR1    5' TGAAGGGGATGATGTGTGGCT  36907   C   A        A
                                A AAGG GGTGATGTGTG CT
                                | |||| |||||||||| ||
                                A TTCC CTACTACACAC GA
                                 C   C         C
GAM2646 C11orf21 3' GGCAGTGTGTGTGACTC     36908    A   A
                                GG GGTG TGTGTGACTC
                                || |||| ||||||||||
                                CC TCAC ACACACTGAG
                                 G   _
GAM2646 COLEC12  3' TGATGAGAAGGTGATGCA    36909     CA
                                TGA  AGGAGGTGATGTG
                                |||  ||||||||||||
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                                ACT  TCTTCCACTACGT
                                  AC
GAM2646  COLEC12   3'  TGATGAGAAGGTGATGCA    36909     CA
                                TGA  AGGAGGTGATGTG
                                |||  ||||||||||||
                                ACT  TCTTCCACTACGT
                                  AC
GAM2646  FBXO2     3'  GGAGGAGGATGTGTGGCT    36910      T_      A
                                GGAGG  GATGTGTG CT
                                |||||  |||||||| ||
                                CCTCC  CTACACAC GA
                                   TC       C
GAM2646  FLJ10241  3'  TGACAAGGTGAGTGTGGCT   36911      AGG     T    A
                                TGACA   AGGTGA GTGTG CT
                                |||||   |||||| ||||| ||
                                ACTGT   TCCACT CACAC GA
                                  ____     _    C
GAM2646  FLJ10743  3'  ACAAGGAGGGAGGTGACT    36912        T  TGT
                                ACAAGGAGG GA   GTGACT
                                |||||||||  ||   ||||||
                                TGTTCCTCC CT   CACTGA
                                     _ C__
GAM2646  FLJ10829  3'  GAAAGGAGGTGACGTCACTC   36913    C          GTG
                                GA AAGGAGGTGATGT   ACTC
                                || ||||||||||||   ||||
                                CT TTCCTCCACTGCA   TGAG
                                 _          G__
GAM2646  FLJ12816  3'  GACAGGGAGGTAAGAGTGACTC 36914      A       TGT
                                GACA GGAGGTGA   GTGACTC
                                ||||  ||||||||   |||||||
                                CTGT CCTCCATT   CACTGAG
                                  C       CT_
GAM2646  FLJ21777  3'  TGACAGGTGGGCGCAGTGACTC 36915       A  A_   ATGT
                                TGACA GG  GGTG    GTGACTC
                                |||||  ||  ||||    |||||||
                                ACTGT CC  CCGC    CACTGAG
                                   _  AC    GT__
GAM2646  HTMP10    3'  GGTCAGGGAATGTGTGGCTC   36916    __   TG      A
                                GG  AGG  ATGTGTG CTC
                                ||  |||  ||||||| |||
                                CC  TCC  TACACAC GAG
                                 AG   CT      C
GAM2646  KIAA0140  3'  GGAGGTGGCTGTGACTC     36917       ATG
                                GGAGGTG   TGTGACTC
                                |||||||   ||||||||
                                CCTCCAC   ACACTGAG
                                    CG_
GAM2646  KIAA1613  3'  GGAGGTGATTTATCAACT    36918        G  _
                                GGAGGTGAT TGT GACT
                                ||||||||| ||| ||||
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                                CCTCCACTA ATA TTGA
                                     A  G
GAM2646 MRPL3    3' TGACAAAGATGACATGTGTGA 36919        GGTG
                                TGACAAGGA   ATGTGTGA
                                |||||||||   ||||||||
                                ACTGTTTCT   TACACACT
                                     ACTG
GAM2646 SAST     5' TGATAAGGAGGCTGTA     36920    C      GA
                                TGA AAGGAGGT  TGTG
                                ||| ||||||||  ||||
                                ACT TTCCTCCG  ACAT
                                  A      __
GAM2646 SC4MOL   3' GACAAGGAGACAGAGTGTGGCT 36921        GT AT    A
                                GACAAGGAG  G  GTGTG CT
                                |||||||||  |  ||||| ||
                                CTGTTCCTC  T  CACAC GA
                                     TG CT    C
GAM2646 SLC34A1  3' TGGCAAGGAGGTGTGCA    36922    A       A
                                TG CAAGGAGGTG TGTG
                                || ||||||||||| ||||
                                AC GTTCCTCCAC ACGT
                                 C       _
GAM2646 STHM     3' TGACAAGGTGGTGATACAT   36923        A      TG
                                TGACAAGG GGTGATG  T
                                |||||||| |||||||  |
                                ACTGTTCC CCACTAT  A
                                     A      GT
GAM2646 STX12    5' TGACGAGGAGCTGAGACCTGCT 36924     A    G   TG G  A
            C                    TGAC AGGAG TGA  T TG CTC
                                |||| ||||| |||  | || |||
                                ACTG TCCTC ACT  G AC GAG
                                  C    G   CT G  _
GAM2646 LOC112687 3' CAAGGAGGTGAGCCACTC    36925          TGT  G
                                CAAGGAGGTGA   GT ACTC
                                ||||||||||   || ||||
                                GTTCCTCCACT   CG TGAG
                                      ___  G
GAM2646 LOC124538 3' TGAAAAGGAAGGTGTG      36926    C      TGAT
                                TGA AAGGAGG    GTGTG
                                ||| |||||||    |||||
                                ACT TTCCTTC    CACAC
                                  T      ____
GAM2646 LOC134266 3' TGACAAGGAGGCTGAAAATAA  36927          _   TGT
                                TGACAAGGAGG TGA   GTGA
                                |||||||||| |||   ||||
                                ACTGTTCCTCC ACT   TATT
                                       G   TT_
GAM2646 LOC144519 5' TGAAAGGAGGTTTTATTGGCT  36928    C       GA   G  A
                                TGA AAGGAGGT  TGT TG CT
                                ||| ||||||||  ||| || ||
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                                ACT TTCCTCCA  ATA AC GA
                                  _       AA  _ C
GAM2646  LOC146227 3'  TGGCAGGGTGGTGATGTTGTGG 36929    A  A  A      _  A
              CTC                  TG CA GG GGTGATGT GTG CTC
                                || || || |||||||| ||| |||
                                AC GT CC CCACTACA CAC GAG
                                 C  C  A       A   C
GAM2646  LOC163081 5'  TGACGAATGAGGTGTGACT   36930     AAG   G   T
                                TGAC   GAG TGA GTGTGACT
                                ||||   ||| ||| ||||||||
                                ACTG   CTT ACT CACACTGA
                                  ____  _  C
GAM2646  LOC256942 3'  GGCAGGGAGATGTGTGGCTC  36931    _  T_      A
                                GG AGG  GATGTGTG CTC
                                || |||  |||||||| |||
                                CC TCC  CTACACAC GAG
                                 G   CT       C
GAM2647  ABCB9    3'  TGAGGCCCCTCCAGACC     61910          G   TA
                                TGAGGCCCTT TAG  ACC
                                |||||||||| |||  |||
                                ACTCCGGGGA GTC  TGG
                                      G  __
GAM2647  ABL1     3'  TGGGCCCTTGCAGACC      61911    A         TA
                                TG GGCCCTTGTAG  ACC
                                || ||||||||||  |||
                                AC CCGGGAACGTC  TGG
                                _        __
GAM2647  ABL1     3'  TGGGCCCTTGCAGACC      61911    A         TA
                                TG GGCCCTTGTAG  ACC
                                || ||||||||||  |||
                                AC CCGGGAACGTC  TGG
                                _        __
GAM2647  ANPEP    3'  GAGGCCCTGCACCAGCC     61912         T  G  A
                                GAGGCCCT GTA TA CC
                                |||||||| ||| || ||
                                CTCCGGGA CGT GT GG
                                     _  G  C
GAM2647  CML66    5'  GAGGCCCTAGCAACC       61913         TGT
                                GAGGCCCT   AGTAACC
                                ||||||||   |||||||
                                CTCCGGGA   TCGTTGG
                                     ____
GAM2647  DGCR2    3'  TGGGCCCCCAGTGACC      61914    A     TG   A
                                TG GGCCCT  TAGT ACC
                                || ||||||  |||| |||
                                AC CCGGGG  GTCA TGG
                                 _    __   C
GAM2647  EGFL5    5'  TGAAGCCCCTGATAACC     61915          TA
                                TGAGGCCCTTG  GTAACC
                                ||||||||||  ||||||
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                                ACTTCGGGGAC  TATTGG
                                          __
GAM2647  EPHB4    3'  TGGGCCCCTGTTTCAAC     61916    A       AG
                                TG GGCCCTTGT  TAAC
                                || |||||||||  ||||
                                AC CCGGGGACA  GTTG
                                  _       AA
GAM2647  EXTL1    5'  TGAGGCCCATCGAGACC     61917        _  T  TA
                                TGAGGCCC TTG AG  ACC
                                |||||||| ||| ||  |||
                                ACTCCGGG AGC TC  TGG
                                     T  _ __
GAM2647  FACL3    3'  TGATGCCTACAGTAAC      61918     G   CT
                                TGA GCC  TGTAGTAAC
                                ||| |||  |||||||||
                                ACT CGG  ATGTCATTG
                                  A  __
GAM2647  GNAZ     3'  TGGGCTTGTAGTGACC      61919    A   CC      A
                                TG GGC  TTGTAGT ACC
                                || |||  ||||||| |||
                                AC CCG  AACATCA TGG
                                  _  __      C
GAM2647  HOXC6    3'  TGAGGCCCTGGAGCAGAGGCC  61920         T__    TAA
                                TGAGGCCCT   GTAG   CC
                                |||||||||   ||||   ||
                                ACTCCGGGA   CGTC   GG
                                     CCT    TCC
GAM2647  IHPK1    3'  TGAGACCCTGAGCGGACC     61921         T T   A_
                                TGAGGCCCT G AGT  ACC
                                ||||||||| | |||  |||
                                ACTCTGGGA C TCG  TGG
                                     _ _  CC
GAM2647  LENG4    5'  TGAGTCCTTTAGCAACC      61922      GC    G
                                TGAG  CCTT TAGTAACC
                                ||||  |||| ||||||||
                                ACTC  GGAA ATCGTTGG
                                  A_   _
GAM2647  LPIN1    3'  TAAGGCCCTTTCGATAGT     61923          ___
                                TGAGGCCCTT   GTAGT
                                |||||||||   |||||
                                ATTCCGGGAA   TATCA
                                     AGC
GAM2647  MTNR1B   3'  TGAGGCCCTTGTAGTTACC   61924            A
                                TGAGGCCCTTGTAGT ACC
                                |||||||||||||| |||
                                ACTCCGGGAACATCA TGG
                                       A
GAM2647  PSD      3'  GAGGCCCTCGTGGGTGGCC   61925          A_  AA
                                GAGGCCCTTGT  GT  CC
                                ||||||||||  ||  ||
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                                CTCCGGGAGCA  CA  GG
                                      CC  CC
GAM2647  RFNG     3'  TGAGCCCTTGCAATGGCC    61926     G        AA
                                TGAG CCCTTGTAGT  CC
                                |||| ||||||||||  ||
                                ACTC GGGAACGTTA  GG
                                  _        CC
GAM2647  RUNX3    3'  TGAGACCCTAATAACC      61927         TGT
                                TGAGGCCCT   AGTAACC
                                |||||||||   |||||||
                                ACTCTGGGA   TTATTGG
                                     ___
GAM2647  SIGLEC6  3'  TGGCAGCCCTAGTAACC     61928    A_     TGT
                                TG  GGCCCT   AGTAACC
                                ||  ||||||   |||||||
                                AC  TCGGGA   TCATTGG
                                 CG     ___
GAM2647  SLC4A1   5'  TGAGCCCCCAGCATAACC    61929     G   T   G
                                TGAG CCCT GTA TAACC
                                |||| |||| ||| |||||
                                ACTC GGGG CGT ATTGG
                                  G   T   _
GAM2647  SORBS1   3'  AACCTTTTTTGTAGTAACC   61930     C___
                                GGCC   TTGTAGTAACC
                                ||||   ||||||||||
                                TTGG   AACATCATTGG
                                  AAAA
GAM2647  STK24    5'  TAAGGCTTCGTCAGTAACC   61931      CC   _
                                TGAGGC  TTGT AGTAACC
                                ||||||  |||| |||||||
                                ATTCCG  AGCA TCATTGG
                                   A_   G
GAM2647  TAF5     3'  TGAGTGCCATACAGTAAC    61932     _  CT
                                TGAG GCC  TGTAGTAAC
                                |||| |||  |||||||||
                                ACTC CGG  ATGTCATTG
                                  A  T_
GAM2647  TAF5     3'  TGAGTGCCATACAGTAAC    61932     _  CT
                                TGAG GCC  TGTAGTAAC
                                |||| |||  |||||||||
                                ACTC CGG  ATGTCATTG
                                  A  T_
GAM2647  TCP10    3'  TGGGTGTCCTTGTAGTGAC   61933    A  C__      A
                                TG GG   CCTTGTAGT AC
                                || ||   ||||||||| ||
                                AC CC   GGAACATCA TG
                                 _ ACA       C
GAM2647  WISP3    5'  TGGGACTCTTCTAATAACC   61934    A   C   G
                                TG GGC CTT TAGTAACC
                                || ||| ||| ||||||||
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                                AC CTG GAA ATTATTGG
                                 C  A  G
GAM2647 C19orf7  3' TGAGGCCCCTCAAGTGGCC  61935       GT  AA
                                TGAGGCCCTT  AGT  CC
                                ||||||||||  |||  ||
                                ACTCCGGGGA  TCA  GG
                                      GT  CC
GAM2647 C20orf18 3' TGGGCCCTTGGTGACC     61936   A     TA  A
                                TG GGCCCTTG  GT ACC
                                || ||||||||  || |||
                                AC CCGGGAAC  CA TGG
                                 _     __ C
GAM2647 FLJ10803 3' TGAAGCCTGCAGTGAC     61937      CT    A
                                TGAGGCC  TGTAGT AC
                                |||||||  |||||| ||
                                ACTTCGG  ACGTCA TG
                                   __    C
GAM2647 FLJ14346 5' GAGGCCCTTCAGACC      61938       G  TA
                                GAGGCCCTT TAG  ACC
                                ||||||||| |||  |||
                                CTCCGGGAA GTC  TGG
                                      _  __
GAM2647 FLJ22555 5' GAGGCCCTTCGGCAACC    61939       GTA
                                GAGGCCCTT  GTAACC
                                |||||||||  ||||||
                                CTCCGGGAA  CGTTGG
                                     GC_
GAM2647 FLJ23093 5' TGAGGCCCTCGGGCACC    32044        TA  A
                                TGAGGCCCTTG  GTA CC
                                ||||||||||  ||| ||
                                ACTCCGGGAGC  CGT GG
                                      C_  _
GAM2647 HARS2    3' TGGGGCCCTCGGTGAGAACC  61940   A     T__ T
                                TG GGCCCTTG  AG AACC
                                || ||||||||  || ||||
                                AC CCGGGAGC  TC TTGG
                                 C      CAC  _
GAM2647 KIAA0350 3' GAGGCCCCTGAGAGTGACC  61941       T_  A
                                GAGGCCCTTG  AGT ACC
                                |||||||||  ||| |||
                                CTCCGGGGAC  TCA TGG
                                      TC  C
GAM2647 KIAA0855 5' TGGGGGCCTTGCAGTGAC   61942   A C      A
                                TG GG CCTTGTAGT AC
                                || || |||||||| ||
                                AC CC GGAACGTCA TG
                                 C C       C
GAM2647 KIAA0888 3' TGAAGCCCTTGTAACC     61943         GTA
                                TGAGGCCCTTGTA  ACC
                                ||||||||||||  |||
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                                ACTTCGGGAACAT   TGG
                                        ___
GAM2647 KIAA1328 3' TGAGGCTCTGTAACAACC    61944      CC
                                TGAGGC  TTGTAGTAACC
                                ||||||  ||||||||||
                                ACTCCG  GACATTGTTGG
                                   A_
GAM2647 Kv6.3    3' TGAAGCTTTCCAATAACC    61945      CC  G
                                TGAGGC  TT TAGTAACC
                                ||||||  || ||||||||
                                ACTTCG  AA GTTATTGG
                                   A_  G
GAM2647 LIPG     3' TGGGTCCTCAGCAGTAAC    61946    A  C   _
                                TG GG CCTT GTAGTAAC
                                || || |||| ||||||||
                                AC CC GGAG CGTCATTG
                                 _ A   T
GAM2647 MGC12518 3' GAGGTTGCAGTAACC      61947     CCC
                                GAGG   TTGTAGTAACC
                                ||||   ||||||||||
                                CTCC   AACGTCATTGG
                                  ___
GAM2647 MGC16491 3' TGAGAGCCCTGTAACC      61948     _    TGTA
                                TGAG GCCCT    GTAACC
                                |||| |||||    ||||||
                                ACTC CGGGA    CATTGG
                                  T    _____
GAM2647 OSBPL8   3' TGAGGCTCTCAGACAAC     61949      C   GT  _
                                TGAGGC CTT  AG TAAC
                                |||||| |||  || ||||
                                ACTCCG GAG  TC GTTG
                                   A   __  T
GAM2647 RALGPS1A 3' TGAGGCCCTGGTGACAAC    61950        T  AG
                                TGAGGCCCT GT  TAAC
                                ||||||||| ||  ||||
                                ACTCCGGGA CA  GTTG
                                     C  CT
GAM2647 RoXaN    3' TGAAGCCCTTTCCAACC     61951         GTAG
                                TGAGGCCCTT    TAACC
                                ||||||||||    |||||
                                ACTTCGGGAA    GTTGG
                                      AG__
GAM2647 SEC24C   3' TGAGCCCCCTGTAGTAACC   61952     G
                                TGAG CCCTTGTAGTAACC
                                |||| ||||||||||||||
                                ACTC GGGGACATCATTGG
                                  G
GAM2647 SLC16A3  3' TGAGGATGCCTTGTAACC    61953      C__      GTA
                                TGAGG   CCTTGTA   ACC
                                |||||   |||||||   |||
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                                ACTCC  GGAACAT  TGG
                                  TAC     ___
GAM2647  SPINLW1   3'  TGAGCCACAGTAGTAACC    61954     G  CTT
                                TGAG CC  GTAGTAACC
                                |||| ||  |||||||||
                                ACTC GG  CATCATTGG
                                  _ TGT
GAM2647  TFEC      5'  TGAGGCCTTGCAGAAC     61955       C     T
                                TGAGGCC TTGTAG AAC
                                ||||||| |||||| |||
                                ACTCCGG AACGTC TTG
                                     _    _
GAM2647  LOC126964 3'  TGAGTTTTATAGTAACC     61956     GCCC
                                TGAG   TTGTAGTAACC
                                ||||   ||||||||||
                                ACTC   AATATCATTGG
                                  AA__
GAM2647  LOC127534 3'  GAGGCCCCTGGAGTAGCC    61957         T   A
                                GAGGCCCTTG AGTA CC
                                |||||||||| |||| ||
                                CTCCGGGGAC TCAT GG
                                      C   C
GAM2647  LOC142893 5'  TAAGGCCCTAATGTAAC     61958        T  A
                                TGAGGCCCT GT GTAAC
                                ||||||||| || |||||
                                ATTCCGGGA TA CATTG
                                      T  _
GAM2647  LOC143196 3'  TAAGTTTTTTGTAGTAACC   61959     GCCC
                                TGAG   TTGTAGTAACC
                                ||||   ||||||||||
                                ATTC   AACATCATTGG
                                  AAAA
GAM2647  LOC145601 3'  TGAGGCCCAGGTCGTGACC   61960       TT  A  A
                                TGAGGCCC  GT GT ACC
                                ||||||||  || || |||
                                ACTCCGGG  CA CA TGG
                                     TC  G  C
GAM2647  LOC145988 5'  TGGGGGCCTTGCAGTGAC    61942    A  C       A
                                TG GG CCTTGTAGT AC
                                || || ||||||||| ||
                                AC CC GGAACGTCA TG
                                 C  C       C
GAM2647  LOC151405 5'  GAGGCCTTGTAGATAGCC    61961       C    _  A
                                GAGGCC TTGTAG TA CC
                                |||||| |||||| || ||
                                CTCCGG AACATC AT GG
                                    _    T  C
GAM2647  LOC153232 5'  TGAGGCCCCCCAGGAAGTGAC  61962         GT___   A
                                TGAGGCCCTT    AGT AC
                                ||||||||||    ||| ||
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                                ACTCCGGGGG    TCA TG
                                      GTCCT   C
GAM2647  LOC158056 5'  GAGGCCCCGTGGTAACC     61963        T  A
                                GAGGCCCT GT GTAACC
                                |||||||| || ||||||
                                CTCCGGGG CA CATTGG
                                     _  C
GAM2647  LOC168451 5'  TGAGGCCCCTGGAGACC     61964          T  TA
                                TGAGGCCCTTG AG  ACC
                                |||||||||||| ||  |||
                                ACTCCGGGGAC TC  TGG
                                      C  __
GAM2647  LOC169981 5'  TGAGTGCCTGCAGTAACC    61965     _   CT
                                TGAG GCC  TGTAGTAACC
                                |||| |||  ||||||||||
                                ACTC CGG  ACGTCATTGG
                                  A  __
GAM2647  LOC170384 3'  GAGGCCCTATGTTAGACC    61966        _  _  TA
                                GAGGCCCT TGT AG  ACC
                                |||||||| ||| ||  |||
                                CTCCGGGA ACA TC  TGG
                                     T  A  __
GAM2647  LOC202347 3'  TGAAGCCCCACAATAACC    61967         TGT
                                TGAGGCCCT   AGTAACC
                                |||||||||   |||||||
                                ACTTCGGGG   TTATTGG
                                      TG_
GAM2647  LOC202459 5'  GAGGCTCCTACAGTGGCC    61968      C       AA
                                GAGGC CTTGTAGT  CC
                                ||||| ||||||||  ||
                                CTCCG GGATGTCA  GG
                                   A       CC
GAM2647  LOC203769 5'  TAAGGCCCTTGAGCAGCC    61969          T    A
                                TGAGGCCCTTG AGTA CC
                                |||||||||| |||| ||
                                ATTCCGGGAAC TCGT GG
                                      _   C
GAM2647  LOC219627 5'  TGAGGTCCCGCTAACC      61970      _  TT  AG
                                TGAGG CCC  GT  TAACC
                                ||||| |||  ||  |||||
                                ACTCC GGG  CG  ATTGG
                                   A  __  __
GAM2647  LOC255045 5'  TGGGGCCCTCAGCAAACC    61971    A      GT    _
                                TG GGCCCTT  AGTAA CC
                                || |||||||  ||||| ||
                                AC CCGGGAG  TCGTT GG
                                 C      __    T
GAM2647  LOC257408 3'  TGGGGCCTCTGTCCTAACC   61972    A   C   AG
                                TG GGCC TTGT  TAACC
                                || |||| ||||  |||||
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                                AC CCGG GACA  ATTGG
                                 C   A   GG
GAM2647  LOC257476 3'  TGAGACCCTGAGCGGACC    61921        T T   A_
                                TGAGGCCCT G AGT  ACC
                                ||||||||| | |||  |||
                                ACTCTGGGA C TCG  TGG
                                     _ _  CC
GAM2647  LOC51194  3'  TGAGGCCCTGATGCACC     61973        T  A   A
                                TGAGGCCCT GT GTA CC
                                ||||||||| || ||| ||
                                ACTCCGGGA TA CGT GG
                                     C  _  _
GAM2647  LOC90190  3'  GAGGCCCTGCACCAACC     61974        T   G
                                GAGGCCCT GTA TAACC
                                |||||||| ||| |||||
                                CTCCGGGA CGT GTTGG
                                     _  G
GAM2648  ABCB9     3'  TGGTGAAAGTGCCCGCCAT    61977       AAC  A   A__
                                TGGTGAA   GG TGT   CCAT
                                |||||||   || |||   ||||
                                ACCACTT   TC ACG   GGTA
                                   ___ _  GGC
GAM2648  FUT9      3'  TATGGTAAAATAAGACCAT    61978        AC   TGTA
                                TATGGTGAAA  GGA   CCAT
                                ||||||||||  |||   ||||
                                ATACCATTTT  TCT   GGTA
                                     AT  _____
GAM2648  MADH1     5'  TATGGTGAAATAAAGCTGT    61979        AC_  A
                                TATGGTGAAA   GG TGT
                                ||||||||||   || |||
                                ATACCACTTT   TC ACA
                                     ATT  G
GAM2648  PCDH11X   3'  TGATGAAAAAGATATCATC    61980        C     AC
                                TGGTGAAAA GGATGT  CATC
                                ||||||||| ||||||  ||||
                                ACTACTTTT TCTATA  GTAG
                                     _    __
GAM2648  PCDH11X   3'  TGATGAAAAAGATATCATC    61980        C     AC
                                TGGTGAAAA GGATGT  CATC
                                ||||||||| ||||||  ||||
                                ACTACTTTT TCTATA  GTAG
                                     _    __
GAM2648  PCDH11Y   3'  TGATGAAAAAGATATCATC    61980        C     AC
                                TGGTGAAAA GGATGT  CATC
                                ||||||||| ||||||  ||||
                                ACTACTTTT TCTATA  GTAG
                                     _    __
GAM2648  PLXNA1    3'  TGGTGTGGCAGGTACCATC    61981       AAAAC  AT_
                                TGGTG    GG  GTACCATC
                                |||||    ||  ||||||||
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                                ACCAC    CC  CATGGTAG
                                  A____ GTC
GAM2648 TCF7    3' TATGGTGAAAACCTGTTGT   61982          GGA_
                                TATGGTGAAAAC   TGT
                                ||||||||||||  |||
                                ATACCACTTTTG   ACA
                                     GACA
GAM2648 WASF3   3' TGGTGAAAGGTGCCAT     61983        AC  A  TA
                                TGGTGAAA  GG TG  CCAT
                                ||||||||  || ||  ||||
                                ACCACTTT  CC AC  GGTA
                                     __  _  __
GAM2648 AKAP9   3' TGGTGAAAATGGTGAAGTCAT 61984         C  A  TAC_
                                TGGTGAAAA GG TG   CAT
                                ||||||||| || ||   |||
                                ACCACTTTT CC AC   GTA
                                     A  _  TTCA
GAM2648 FADS2   3' TGGTGAAAGGCAGATTGT    61985        A_    _
                                TGGTGAAA  CGGAT GT
                                ||||||||  ||||| ||
                                ACCACTTT  GTCTA CA
                                     CC    A
GAM2648 FLJ11806 5' TACGGTGAATCGAATTGT   61986         AA    _
                                TATGGTGAA  CGGAT GT
                                |||||||||  ||||| ||
                                ATGCCACTT  GCTTA CA
                                     A_    A
GAM2648 KIAA0276 3' GGTGAAAACATGTCAT     61987         GG   AC
                                GGTGAAAAC  ATGT  CAT
                                |||||||||  ||||  |||
                                CCACTTTTG  TACA  GTA
                                     __   __
GAM2648 KIAA0720 3' TATGGTGAAATGCCGTCGATGG 61988        A__ _____   TAC
          TACA                    TGGTGAAA   CG    GATG   CA
                                ||||||||   ||    ||||   ||
                                ACCACTTT   GC    CTAC   GT
                                     ACG  AGIII   CAT
GAM2648 LENEP   3' TATGGTAAGATCAACCAT    61989       AAAAC   GT
                                TATGGTG    GGAT  ACCAT
                                |||||||    ||||  |||||
                                ATACCAT    TCTA  TGGTA
                                     _____   GT
GAM2648 ST7L    3' TGGTGAAGAATTACCAT     61990       AAC   G
                                TGGTGAA   GGAT TACCAT
                                |||||||   |||| ||||||
                                ACCACTT   CTTA ATGGTA
                                     ___   _
GAM2648 ST7L    3' TGGTGAAGAATTACCAT     61990       AAC   G
                                TGGTGAA   GGAT TACCAT
                                |||||||   |||| ||||||
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                                ACCACTT   CTTA ATGGTA
                                   ___   _
GAM2648 ST7L     3'  TGGTGAAGAATTACCAT     61990       AAC   G
                                TGGTGAA   GGAT TACCAT
                                |||||||   |||| ||||||
                                ACCACTT   CTTA ATGGTA
                                   ___   _
GAM2648 LOC146229 3'  TATGGCGAGGATGGCA      61991       AAAC    TAC
                                TATGGTGA   GGATG   CA
                                ||||||||   |||||  ||
                                ATACCGCT   CCTAC   GT
                                    _____   C__
GAM2648 LOC163882 3'  TATGATGAGGATGTCCAT    61992       AAAC     A
                                TATGGTGA   GGATGT CCAT
                                ||||||||   |||||| ||||
                                ATACTACT   CCTACA GGTA
                                   _____    _
GAM2648 LOC256790 5'  CATGGTGAAAATGTACTCCAT  61993       AACG    __
                                TATGGTGAA   GATGTA  CCAT
                                |||||||||   ||||||  ||||
                                GTACCACTT   TTACAT  GGTA
                                    _____    GA
GAM2649 APPBP2   3'  GTTGTTTTATCACTGAGTGTG  61996     CTCCTG   TT
                                GTTG     CAT  TGAGTGTG
                                ||||     |||  ||||||||
                                CAAC     GTG  ACTCACAC
                                  AAAATA  __
GAM2649 NR2C2    3'  GTTGCTCCTTGGCAGGTGTG   61997       __  TTTTGA
                                GTTGCTCCT  GCA     GTGTG
                                |||||||||  |||     |||||
                                CAACGAGGA  CGT     CACAC
                                     AC   C_____
GAM2649 SLC16A2  3'  GTTGCTCCAGTATTTTCAGTG  61998       TGC    G
                                GTTGCTCC   ATTTT AGTG
                                ||||||||   ||||| ||||
                                CAACGAGG   TAAAA TCAC
                                     TCA    G
GAM2649 FLJ23403  3'  GTTGCATTTTCTGAGTGT    61999      TCCTGCA
                                GTTGC      TTTTGAGTGT
                                |||||      ||||||||||
                                CAACG      AAGACTCACA
                                   TAA_____
GAM2649 KIAA1045  3'  GTGGCTCCTGCCAGTGT     62000    T      ATTTTG
                                GT GCTCCTGC     AGTGT
                                || ||||||||     |||||
                                CA CGAGGACG     TCACA
                                 C       G_____
GAM2649 MGC861    5'  CGTTGCTCCTGCGGTGC     62001          ATTTT A
                                CGTTGCTCCTGC    G GTGT
                                ||||||||||||    | ||||
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                                GCAACGAGGACG    C CACG
                                      _____ _
GAM2649  LOC254479 5'  GCTGCTTCTGCATTCAGGGCGG 62002       C      ____  A
            GTGTG                   GTTGCT CTGCATTT    TG GTGTG
                                |||||| ||||||||   || |||||
                                CGACGA GACGTAAG   GC CACAC
                                   A       TCCC  C
GAM2650  GHR      3'  AAGTATTCTTCACTGAGA    62005             T
                                AAGTATTCTTCACTG AGA
                                ||||||||||||||| |||
                                TTCATAAGAAGTGAC TCT
                                                _
GAM2650  IDS      3'  AAGTATTCTTTGTGTATAATGT 62006         CAC   GAC
                                AAGTATTCTT   TGTA   ATGT
                                ||||||||||   ||||   ||||
                                TTCATAAGAA   ACAT   TACA
                                      AC_    AT_
GAM2650  PSMB2    3'  AAATATTTTTCACTACATG    62007       C     GTAG
                                AAGTATT TTCACT    ACATG
                                ||||||| ||||||    |||||
                                TTTATAA AAGTGA    TGTAC
                                   A     ____
GAM2650  KIAA0981  3'  AAGTATTCATCATACTGT    62008        T  __
                                AAGTATTC TC  ACTGT
                                |||||||| ||  |||||
                                TTCATAAG AG  TGACA
                                     T  TA
GAM2650  KIAA1765  3'  AAGTGTCCTTCACATCTATATG 62009     A       TGTAGAC
            T                    AAGT TTCTTCAC       ATGT
                                |||| ||||||||       ||||
                                TTCA AGGAAGTG       TACA
                                  C       TAGATA_
GAM2650  TRAF6    3'  AAGTATTATTCAACAGACATGT 62010       C    CTG
                                AAGTATT TTCA   TAGACATGT
                                ||||||| ||||   |||||||||
                                TTCATAA AAGT   GTCTGTACA
                                   T   T__
GAM2651  RECQL    5'  GTCCGGTGTCCGACTGTCCTGT 62013     A  A   G GT
                                GTTC GT TCC G  TGTCCTGT
                                |||| || ||| |  ||||||||
                                CAGG CA AGG C  ACAGGACA
                                  C  C   _ TG
GAM2651  RECQL    5'  GTCCGGTGTCCGACTGTCCTGT 62013     A  A   G GT
                                GTTC GT TCC G  TGTCCTGT
                                |||| || ||| |  ||||||||
                                CAGG CA AGG C  ACAGGACA
                                  C  C   _ TG
GAM2651  DKFZP434C128 3'  GTTCAGGATCCAAGTCCTGT   62014       T     GTT
                                GTTCAG ATCCGG   GTCCTGT
                                |||||| ||||||   |||||||
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                                CAAGTC TAGGTT   CAGGACA
                                   C     ___
GAM2651  FLJ21313  3'  ATTCAGTGTTTTTCATCCTGTA 62015       ATCCGGG TG
                                GTTCAGT      T  TCCTGTA
                                |||||||      |  |||||||
                                TAAGTCA      A  AGGACAT
                                    CAAAA__ GT
GAM2651  KIAA0865  3'  ATTTAGTGTCTGTGTCCTGT   62016     C   A  CGG  T
                                GTT AGT TC   GT GTCCTGT
                                ||| ||| ||   || |||||||
                                TAA TCA AG   CA CAGGACA
                                  A   C  A__  _
GAM2651  MYH10    3'  GTTTAATATATGTGTCCTGT   62017     C    CCGG  T
                                GTT AGTAT    GT GTCCTGT
                                ||| |||||    || |||||||
                                CAA TTATA    CA CAGGACA
                                  A    TA__  _
GAM2651  LOC257101 5'  GTTCAGGTCCAGGTCCTGT    62018       TA     TTG
                                GTTCAG  TCCGGG   TCCTGT
                                ||||||  ||||||   ||||||
                                CAAGTC  AGGTCC   AGGACA
                                   C_     ___
GAM2651  LOC92293  3'  GTTCAGCATCAGTTATGTCTTG 62019          C  GT_   C
            T                    GTTCAGTATC GG   TGTC TGT
                                ||||||||||  ||   |||| |||
                                CAAGTCGTAG TC   ACAG ACA
                                      _  AAT    A
GAM2652  MANBA    3'  TGCTAAAGCTGAGAG       62022       AATTTT       A
                                TGTTAA      AGCTGAGA G
                                ||||||      |||||||| |
                                ACGATT      TCGACTCT C
                                   _______       C
GAM2652  RNMT     3'  TGCTAAAATTTTAGCTAAG    62023
                                TGTTAAAATTTTAGCTGAG
                                ||||||||||||||||||
                                ACGATTTTAAAATCGATTC

GAM2652  LOC157909 5'  TGTGGAATTTTAAGTCTGAGAA 62024     TAA      _ _
            GT                    TGT   AATTTTA G CTGAGAAGT
                                |||   ||||||| | |||||||||
                                ACA   TTAAAAT C GACTCTTCA
                                  CC_      T A
GAM2653  DUSP12   3'  TAGTTTCCAGGTTACATCAA   62027     G    TCGAT
                                TAG TTCC     TTACATCAA
                                ||| ||||     |||||||||
                                ATC AAGG     AATGTAGTT
                                  A    TCC__
GAM2653  MGC13114  3'  GGTTCCTGCATCTGAGCATCA  62028        CG    A__
                                GGTTCCT  ATTT   CATCA
                                |||||||  ||||   |||||
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                                CCAAGGA  TAGA   GTAGT
                                   CG    CTC
GAM2653  MRPL35   3'  GGTACAATTTACATCAA     62029     TCCT
                                GGT    CGATTTACATCAA
                                |||    ||||||||||||||
                                CCA    GTTAAATGTAGTT
                                  T___
GAM2654  ADAM19   3'  CAGTGGCTGGCTTGACCC    62032        GC   GAC
                                CAGTGGCT  GGC   GACCC
                                ||||||||  |||   |||||
                                GTCACCGA  CCG   CTGGG
                                    __   AA_
GAM2654  AKAP13   3'  GTGGCTGCGCACCTAGACGGTC 62033         _ ___    AC
           C                     GTGGCTGCG GC   GACG  CC
                                |||||||| ||   ||||  ||
                                CACCGACGC TG   CTGC  GG
                                     G  GAT    CA
GAM2654  ATP1B1   5'  GTGGCTGCGGCGCGCCCC    62034          A  A
                                GTGGCTGCGGCG CG CCCC
                                |||||||||||| || ||||
                                CACCGACGCCGC GC GGGG
                                      _  _
GAM2654  CLCA3    3'  AATGGCTGTTACATTGATTCC  62035        CG   AC  CC
                                AGTGGCTG  GCG  GA  CC
                                ||||||||  |||  ||  ||
                                TTACCGAC  TGT  CT  GG
                                     AA   AA  AA
GAM2654  CREBL2   3'  GCGGTGCTGTGCACAACTCC   62036     C   G__  G    _
                                GTGG TGC   GC ACGAC CC
                                |||| |||   || ||||| ||
                                CGCC ACG   CG TGTTG GG
                                  _   ACA  _    A
GAM2654  DSCR3    5'  CAGTGGCTCACGTGACC     62037        G  G  AC
                                CAGTGGCT CG CG  GACC
                                |||||||| || ||  ||||
                                GTCACCGA GT GC  CTGG
                                   _  _  A_
GAM2654  GALNT2   3'  CAGTGGCTAACTGACGA     62038         CG  _
                                CAGTGGCTG  GC GACGA
                                |||||||||  || |||||
                                GTCACCGAT  TG CTGCT
                                     __  A
GAM2654  GRIK3    3'  CAGGGCTGCGGCAGAAAC    62039     T        AC
                                CAG GGCTGCGGCG  GAC
                                ||| ||||||||||  |||
                                GTC CCGACGCCGT  TTG
                                  _        CT
GAM2654  HDAC4    5'  ACGGTGCTCCGCGGCGGCGGCC 62040    A   G_      A  A
           CC                     AC GTG  CTGCGGCG CG CCCC
                                || |||  |||||||| || ||||
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                                TG CAC  GGCGCCGC GC GGGG
                                 C  GA       C  C
GAM2654  HS3ST4   3'  TACAGTGCTTGGGAGAGA    62041       GC  C  C  C
                                TACAGTG  TG GG GA GA
                                |||||||  || || || ||
                                ATGTCAC  AC CC CT CT
                                    GA  _  T  _
GAM2654  KLHL2    5'  CACCACCTGCGGCGGCGGCCCC 62042    G  G      A  A
                                CA TG CTGCGGCG CG CCCC
                                || || |||||||| || ||||
                                GT GT GACGCCGC GC GGGG
                                 G  G       C  C
GAM2654  KPNB1    5'  GTGGCGGCGGCGGCGACTCC   62043      T     A   _
                                GTGGC GCGGCG CGAC CC
                                ||||| |||||| |||| ||
                                CACCG CGCCGC GCTG GG
                                   C     C   A
GAM2654  NAP1L4   5'  GCGGCAGTGGCGGCGACCC    62044      TGC   A
                                GTGGC   GGCG CGACCC
                                |||||   |||| ||||||
                                CGCCG   CCGC GCTGGG
                                   TCA   C
GAM2654  NPY2R    5'  CAGAGGCTGCGGGCGATGGTCC 62045     T      _  CGAC
                                CAG GGCTGCGG CGA    CC
                                ||| |||||||| |||    ||
                                GTC CCGACGCC GCT    GG
                                  T       C   ACCA
GAM2654  NR2F2    5'  GCGGCGGGGCGGCGGCGGCTCC 62046      T__     A  AC_
                                GTGGC   GCGGCG CG   CC
                                |||||   |||||| ||   ||
                                CGCCG   CGCCGC GC   GG
                                   CCC     C  CGA
GAM2654  PLXNB3   3'  CAGTGGCTGGCTCGGTTCC   62047       GC   GA  AC_
                                CAGTGGCT  GGC  CG   CC
                                ||||||||  |||  ||   ||
                                GTCACCGA  CCG  GC   GG
                                    __   A_  CAA
GAM2654  POU4F1   5'  GCGGCGGCTGGCGGCGGCCCC  62048      T  _   A  A
                                GTGGC GC GGCG CG CCCC
                                ||||| || |||| || ||||
                                CGCCG CG CCGC GC GGGG
                                   C  A    C  C
GAM2654  PTP4A2   5'  GCGGCGGCGGCGACGACTCC   62049      T         _
                                GTGGC GCGGCGACGAC CC
                                ||||| |||||||||| ||
                                CGCCG CGCCGCTGCTG GG
                                   C          A
GAM2654  PTP4A2   5'  GCGGCGGCGGCGACGACTCC   62049      T         _
                                GTGGC GCGGCGACGAC CC
                                ||||| |||||||||| ||
```

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                                CGCCG CGCCGCTGCTG GG
                                   C         A
GAM2654  PTPRA    5'  GCGGCGGCGGCGGCGGCC    62050      T     A  A
                                GTGGC GCGGCG CG CC
                                ||||| |||||| || ||
                                CGCCG CGCCGC GC GG
                                   C     C  C
GAM2654  PYGB     3'  CAGGGCTGGCCACGACCC    62052     T   GC   G
                                CAG GGCT  GGC ACGACCC
                                ||| ||||  ||| |||||||
                                GTC CCGA  CCG TGCTGGG
                                  _   __  G
GAM2654  PYGB     3'  CACAGTGGTGGTCAGGGTGGTG 62051        CTG_   CGACGA__
              GCCCC                  TACAGTGG   CGG      CCCC
                                |||||||||   |||       ||||
                                GTGTCACC   GTC       GGGG
                                     ACCA   CCACCACC
GAM2654  SGT      3'  CAGGGCCGCGGCGGCCC     62053     T        ACGA
                                CAG GGCTGCGGCG   CCC
                                ||| ||||||||||   |||
                                GTC CCGGCGCCGC   GGG
                                  _        C___
GAM2654  SNRPN    5'  TACAGTGGCTGCGGCCAGCCC  62054             GA  A
                                TACAGTGGCTGCGGC  CG CCC
                                ||||||||||||||  || |||
                                ATGTCACCGACGCCG  GT GGG
                                      __ C
GAM2654  SNRPN    5'  TACAGTGGCTGCGGCCAGCCC  62054             GA  A
                                TACAGTGGCTGCGGC  CG CCC
                                ||||||||||||||  || |||
                                ATGTCACCGACGCCG  GT GGG
                                      __ C
GAM2654  SNRPN    5'  TACAGTGGCTGCGGCCAGCCC  62054             GA  A
                                TACAGTGGCTGCGGC  CG CCC
                                ||||||||||||||  || |||
                                ATGTCACCGACGCCG  GT GGG
                                      __ C
GAM2654  TEM7     3'  TACAGTGGCATGATTATGACCC 62055          TGCGGCGAC
              C                   TACAGTGGC        GACCCC
                                |||||||||        ||||||
                                ATGTCACCG        CTGGGG
                                     TACTAATA_
GAM2654  TWIST    3'  CAGTGGCTGATTGGCACGACC  62056          C__   G
                                CAGTGGCTG   GGC ACGACC
                                |||||||||   ||| ||||||
                                GTCACCGAC   CCG TGCTGG
                                     TAA   _
GAM2654  AQP10    3'  TAAGTGGCTGTGCCAACAGTGG 62057    C       CG  _    A___
              CCCC                  A AGTGGCTG  GC GACG    CCCC
                                | ||||||||  || ||||    ||||
```

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                                A TCACCGAC  CG TTGT    GGGG
                                 T       A_  G    CACC
GAM2654  C20orf81  5'  ATGGCCGCGGCGGCGGCC    62058          A  A
                                GTGGCTGCGGCG CG CC
                                |||||||||||| || ||
                                TACCGGCGCCGC GC GG
                                      C  C
GAM2654  FLJ23120  3'  TACAGTGGTGCAGTGGTGCGA  62059        C   _____
                                TACAGTGG TGCG    GCGA
                                |||||||| ||||    ||||
                                ATGTCACC ACGT    CGCT
                                     _   CACCA
GAM2654  FLJ30791  5'  CAGTGGCCTCAGATGACTCC   62060        G   C_   GA
                                CAGTGGCT CGG  GAC  CC
                                |||||||| |||  |||  ||
                                GTCACCGG GTC  CTG  GG
                                     A   TA   A_
GAM2654  ING4      3'  AGTGGCTGCGGCACCC      62061          GACG
                                AGTGGCTGCGGC    ACCC
                                ||||||||||||    ||||
                                TCACCGACGCCG    TGGG
                                          _____
GAM2654  KIAA0089  5'  CAGCGGCTGGCGGCGGCCCC   62062         _    ACGA
                                CAGTGGCTG CGGCG    CCCC
                                ||||||||| |||||    ||||
                                GTCGCCGAC GCCGC    GGGG
                                     C    C___
GAM2654  KIAA0193  3'  AGTGACTGCTAGGATTCC     62063         _  C  CGA
                                AGTGGCTGC GG GA   CC
                                ||||||||| || ||   ||
                                TCACTGACG TC CT   GG
                                     A  _  AA_
GAM2654  KIAA0237  3'  TGAGTGGCTGTGAGAAGCTCC  62064   C       C  C  CGAC
                                A AGTGGCTG GG GA    CC
                                | |||||||| || ||    ||
                                A TCACCGAC CT CT    GG
                                 C       A  _  TCGA
GAM2654  KIAA1061  5'  GTGGCGGCGGCGGCGACCCC   62065      T     A
                                GTGGC GCGGCG CGACCCC
                                ||||| |||||| |||||||
                                CACCG CGCCGC GCTGGGG
                                   C     C
GAM2654  MGC13016  3'  CACAGTGGCTGTGGTCC     62066          C  CGACGA
                                TACAGTGGCTG GG     CC
                                |||||||||||| ||     ||
                                GTGTCACCGAC CC     GG
                                      A  A_____
GAM2654  MGC16386  3'  TGAGTGGCTGGGCCAGGCGGCC 62067   C       C   GA__  A
              CC                  A AGTGGCTG GGC    CG CCCC
                                | |||||||| |||    || ||||
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                                A TCACCGAC CCG    GC GGGG
                                 C       _  GTCC  C
GAM2654  MGC17303  3'  GTGGCTGCAGCAGGCCCC    62068          ACGA
                                GTGGCTGCGGCG   CCCC
                                ||||||||||||   ||||
                                CACCGACGTCGT   GGGG
                                      CC__
GAM2654  PRO1048   3'  AGTGGCTGCGGCGCGGGCC   62069           A  AC
                                AGTGGCTGCGGCG CG  CC
                                |||||||||||| ||  ||
                                TCACCGACGCCGC GC  GG
                                      _ CC
GAM2654  TCL6      5'  CACAGTGGCTGCCTGGTCCC  62070          __ CGACGA
                                TACAGTGGCTGC  GG    CCC
                                ||||||||||||  ||    |||
                                GTGTCACCGACG  CC    GGG
                                      GA  A_____
GAM2654  TCL6      5'  CACAGTGGCTGCCTGGTCCC  62070          __ CGACGA
                                TACAGTGGCTGC  GG    CCC
                                ||||||||||||  ||    |||
                                GTGTCACCGACG  CC    GGG
                                      GA  A_____
GAM2654  TCL6      5'  CACAGTGGCTGCCTGGTCCC  62070          __ CGACGA
                                TACAGTGGCTGC  GG    CCC
                                ||||||||||||  ||    |||
                                GTGTCACCGACG  CC    GGG
                                      GA  A_____
GAM2654  TCL6      5'  CACAGTGGCTGCCTGGTCCC  62070          __ CGACGA
                                TACAGTGGCTGC  GG    CCC
                                ||||||||||||  ||    |||
                                GTGTCACCGACG  CC    GGG
                                      GA  A_____
GAM2654  LOC115330 3'  GTGACTGCGGCACACCC    62071          G  G
                                GTGGCTGCGGC AC ACCC
                                |||||||||||  || ||||
                                CACTGACGCCG TG TGGG
                                      _  _
GAM2654  LOC116071 5'  AGTGGCTGCAGCTCAGACC   62072           GAC
                                AGTGGCTGCGGC   GACC
                                ||||||||||||   ||||
                                TCACCGACGTCG   CTGG
                                      AGT
GAM2654  LOC148479 5'  GGCTCCGCGGCGGCGGCCCC  62073      __     A  A
                                GGCT  GCGGCG CG CCCC
                                ||||  ||||||  ||  ||||
                                CCGA  CGCCGC GC GGGG
                                  GG     C  C
GAM2654  LOC149773 3'  CACGGTGGCTGCACCTGGCCCC 62074     A        G GACGA
                                TAC GTGGCTGCG C     CCCC
                                |||  |||||||||  |     ||||
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                                GTG CACCGACGT G    GGGG
                                  C       _ GACC_
GAM2654  LOC151009 5'  TACAGTGGTGTGGGAGA    62075       C  C  C  C
                                TACAGTGG TG GG GA GA
                                |||||||| || || || ||
                                ATGTCACC AC CC CT CT
                                     _  A  _  _
GAM2654  LOC154386 5'  TACAGTGGTGAAGATGATCCC  62076       C  CGGC  C  _
                                TACAGTGG TG   GA GA CCC
                                |||||||| ||   || || |||
                                ATGTCACC AC   CT CT GGG
                                     _  TT__  A  A
GAM2654  LOC159199 5'  CACAGTGGTGGAGACGGCTCC  62077       CTGC  C   AC_
                                TACAGTGG   GG GACG   CC
                                ||||||||   || ||||   ||
                                GTGTCACC   CC CTGC   GG
                                     A___  T   CGA
GAM2654  LOC221583 3'  CACAGTGGGCTACGGTGAC   62078       _    C
                                TACAGTGG CTGCGG GAC
                                |||||||| |||||| |||
                                GTGTCACC GATGCC CTG
                                     C     A
GAM2654  LOC253960 3'  CAGTGGCTTGGGAACC     62079       GC  C  CG
                                CAGTGGCT  GG GA  ACC
                                ||||||||  || ||  |||
                                GTCACCGA  CC CT  TGG
                                     A_  _  __
GAM2654  LOC255104 5'  CAGTAGCCGTTGATGATCC   62080       CGGC  C  C
                                CAGTGGCTG   GA GA CC
                                |||||||||   || || ||
                                GTCATCGGC   CT CT GG
                                     AA__  A  A
GAM2654  LOC257449 3'  AGTGGCTAAGTGACCC     62081       C  CGAC
                                AGTGGCTG GG   GACCC
                                |||||||| ||   |||||
                                TCACCGAT TC   CTGGG
                                     _  A___
GAM2655  KCNJ6    3'  TACAGTATTTAGCAGTGCTGT  62084       CCATTC  A
                                TACAGTGTT     GT CTGT
                                |||||||||     || ||||
                                ATGTCATAA     CA GACA
                                     ATCGT_  C
GAM2655  MEN1     3'  TACAATGTTCTGCTCCCTGT   62085       CA   GTA
                                TACAGTGTTC  TTC   CTGT
                                ||||||||||  |||   ||||
                                ATGTTACAAG  GAG   GACA
                                     AC   G__
GAM2655  NRIP1    5'  CAGTGTTCTTCTGGCTGT    62086       CA   GTA
                                CAGTGTTC  TTC   CTGT
                                ||||||||  |||   ||||
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                                GTCACAAG  AAG   GACA
                                   __  ACC
GAM2655  UBQLN1   3'  TACAGTGTTCCTTCAGTCTGC  62087          A  _  A
                                TACAGTGTTCC TTC GT CTGT
                                |||||||||||| ||| || ||||
                                ATGTCACAAGG AAG CA GACG
                                      _  T  _
GAM2655  FLJ12994  5'  CAGTGCTCCGTCTGTA     62088         ATTC  A
                                CAGTGTTCC   GT CTGTA
                                |||||||||   || |||||
                                GTCACGAGG   CA GACAT
                                    ____ _
GAM2655  GK001    3'  TACAGTGTTCTAATTTTTAC  62089         C_  CG
                                TACAGTGTTC  ATT  TAC
                                ||||||||||  |||  |||
                                ATGTCACAAG  TAA  ATG
                                      AT   AA
GAM2655  IL22R    3'  TACAGTGTGTTATTGTAC    62090        TCC   C
                                TACAGTGT   ATT GTAC
                                ||||||||   ||| ||||
                                ATGTCACA   TAA CATG
                                   CAA  _
GAM2655  PRO1596  3'  AGTGTTCCATTATAATGTAC  62091          C   C
                                AGTGTTCCATT GTA TGTAC
                                |||||||||| ||| |||||
                                TCACAAGGTAA TAT ACATG
                                      _  T
GAM2655  SFRS10   3'  AGTGTTCCCTTATCATGTAC  62092        AT__   TAC
                                AGTGTTCC   TCG   TGTAC
                                ||||||||   |||   |||||
                                TCACAAGG   AGT   ACATG
                                   GAAT  ___
GAM2655  LOC122773 3'  TACAGTGTTCCATTTCTGTA  62093           CGTA
                                TACAGTGTTCCATT   CTGTA
                                ||||||||||||||   |||||
                                ATGTCACAAGGTAA   GACAT
                                      A___
GAM2655  LOC147711 3'  CACAGTGTGTGTACTGT    62094        TCCATTC
                                TACAGTGT     GTACTGT
                                ||||||||     |||||||
                                GTGTCACA     CATGACA
                                   CA_____
GAM2655  LOC151103 3'  AGTGCTCCAACTGTA      62095        TTCGT
                                AGTGTTCCA    ACTGTA
                                |||||||||    ||||||
                                TCACGAGGT    TGACAT
                                    _____
GAM2655  LOC153914 5'  CAGTGTTCCATTTCTTTGC   62096          _ GTAC
                                CAGTGTTCCATT C   TGT
                                |||||||||||| |   |||
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                                GTCACAAGGTAA G    ACG
                                      A AA__
GAM2655  LOC163231 5'  TACATGTTCCGTTCACATGC   62097      G     A     C
                                TACA TGTTCC TTCGTA TGT
                                |||| |||||| |||||| |||
                                ATGT ACAAGG AAGTGT ACG
                                  _     C     _
GAM2655  LOC200728 3'  TGTTTCATATACTGTAC     62098      C   TC
                                TGTT CAT  GTACTGTAC
                                |||| |||  |||||||||
                                ACAA GTA  TATGACATG
                                  A  __
GAM2656  TLX1      3'  TGTGACCCTCTGTCTGGT    62101          C_  C
                                TGTGATCCTC  TC GGT
                                ||||||||||  || |||
                                ACACTGGGAG  AG CCA
                                      AC  A
GAM2656  CENPH     3'  TGTAATCCTAGCACTTCGGT   62102         C___  C
                                TGTGATCCT    CT CGGT
                                |||||||||    || ||||
                                ACATTAGGA    GA GCCA
                                      TCGT  A
GAM2656  FLJ13902  3'  TGTGACCCAGCCCCTGGT    62103         TC   _
                                TGTGATCC  CTCC GGT
                                ||||||||  |||| |||
                                ACACTGGG  GGGG CCA
                                      TC    A
GAM2656  IMP-1     3'  TGTGATCCACCCTCTTGGT    62104         _    C_
                                TGTGATCC TCCTC  GGT
                                ||||||||  |||||  |||
                                ACACTAGG GGGAG  CCA
                                      T     AA
GAM2656  PSMD12    3'  TGTAATCCCAGCCTTTTTTGGT 62105          __  CC___  III
              A                  TGTGATCCT  CCT    GGT   A
                                |||||||||  |||    |||   |
                                ACATTAGGG  GGA    CCA   T
                                      TC   AAAAA   III
GAM2656  TCL6      3'  TGTCCTCCTCCTCCTCTGGTA  62106     GA       ___  III
                                TGT  TCCTCCTCC   GGT   A
                                |||  |||||||||   |||   |
                                ACA  AGGAGGAGG   CCA   T
                                  GG        AGA   III
GAM2656  TCL6      3'  TGTCCTCCTCCTCCTCTGGTA  62106     GA       ___  III
                                TGT  TCCTCCTCC   GGT   A
                                |||  |||||||||   |||   |
                                ACA  AGGAGGAGG   CCA   T
                                  GG        AGA   III
GAM2656  LOC145988 5'  TGTGATCCACCTGCCTCGGT   62107         T  _  __
                                TGTGATCC CCT CC  GGT
                                |||||||| ||| ||  |||
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                                ACACTAGG GGA GG  CCA
                                    T  C  AG
GAM2657  CD2AP    3'  TAAATTAAACATTATGTT    62110       _
                                TAAATTAA CATTATGTT
                                |||||||| |||||||||
                                ATTTAATT GTAATACAA
                                    T
GAM2657  INPP1    3'  AAATTAACATTATTATGAATAC 62111          GTTT
           A                     AAATTAACATTAT   AATACA
                                |||||||||||||   ||||||
                                TTTAATTGTAATA   TTATGT
                                      ATAC
GAM2657  MSR1     3'  TAACATTGATATCTAATAC   62112       _
                                TAACATT ATGTTTAATAC
                                ||||||| ||||||||||
                                ATTGTAA TATAGATTATG
                                    C
GAM2657  MSR1     3'  TAACATTGATATCTAATAC   62112       _
                                TAACATT ATGTTTAATAC
                                ||||||| ||||||||||
                                ATTGTAA TATAGATTATG
                                    C
GAM2657  BLZF1    3'  TAAATTAACACTGTTCA     62113         TA
                                TAAATTAACAT  TGTTTA
                                |||||||||||  ||||||
                                ATTTAATTGTG  ACAAGT
                                      __
GAM2658  ADCY7    3'  TGGAAATAAAAATGCAT     62116         AACTC
                                TGGAAATAAAGA   GCAT
                                ||||||||||||   ||||
                                ACCTTTATTTTT   CGTA
                                      A____
GAM2658  AGTR1    3'  TGGAAATAAAAAATAACA    62117          ACTC
                                TGGAAATAAAGAA   GCA
                                ||||||||||||   |||
                                ACCTTTATTTTTT   TGT
                                      AT__
GAM2658  AGTR1    3'  TGGAAATAAAAAATAACA    62117          ACTC
                                TGGAAATAAAGAA   GCA
                                ||||||||||||   |||
                                ACCTTTATTTTTT   TGT
                                      AT__
GAM2658  AGTR1    3'  TGGAAATAAAAAATAACA    62117          ACTC
                                TGGAAATAAAGAA   GCA
                                ||||||||||||   |||
                                ACCTTTATTTTTT   TGT
                                      AT__
GAM2658  AGTR1    3'  TGGAAATAAAAAATAACA    62117          ACTC
                                TGGAAATAAAGAA   GCA
                                ||||||||||||   |||
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                                ACCTTTATTTTTT   TGT
                                      AT__
GAM2658 AGTR1    3' TGGAAATAAAAAATAACA    62117          ACTC
                                TGGAAATAAAGAA   GCA
                                ||||||||||||   |||
                                ACCTTTATTTTTT   TGT
                                      AT__
GAM2658 BID      3' TGGAAATAAAGGCACCG     62118         AA  T
                                TGGAAATAAAG  AC CG
                                ||||||||||  || ||
                                ACCTTTATTTC  TG GC
                                      CG  _
GAM2658 GABRA1   3' TATGAAAATAAGGAAACT    62119          A
                                TATGGAAATAA GAAACT
                                |||||||||| ||||||
                                ATACTTTTATT CTTTGA
                                      C
GAM2658 FLJ10140 3' TATGGAAATAAAGTGACC    62120          AA
                                TATGGAAATAAAG  ACT
                                ||||||||||||  |||
                                ATACCTTTATTTC  TGG
                                      AC
GAM2658 FLJ14855 3' GGAAATAAAGGGAAAACT    62121          ___
                                GGAAATAAAG   AAACT
                                |||||||||   |||||
                                CCTTTATTTC   TTTGA
                                      CCT
GAM2658 KIAA0532 3' TATGGAACTAGAGAAACTCAC 62122        A  A
                                TATGGAA TA AGAAACTCGC
                                ||||||| || ||||||||||
                                ATACCTT AT TCTTTGAGTG
                                    G  C
GAM2658 KIAA1155 3' TGGTGTGCAGGAAACTCGCATG 62123     AAATAAA
                                TGG      GAAACTCGCATG
                                |||      ||||||||||||
                                ACC      CTTTGAGCGTAC
                                  ACACGTC
GAM2658 LOC130355 5' TGGAAACAGAGAAGCA      62124        A   ACTC
                                TGGAAATA AGAA   GCA
                                |||||||| ||||   |||
                                ACCTTTGT TCTT   CGT
                                     C   ____
GAM2658 LOC145371 3' TATGGGGTTAAAGAAACT    62125       AAA
                                TATGG   TAAAGAAACT
                                |||||   ||||||||||
                                ATACC   ATTTCTTTGA
                                   CCA
GAM2658 LOC145845 3' TATGGCAATGAAGAAACCAAAC 62126      A  A      C_
              A                  TATGG AAT AAGAAACT  GCA
                                |||||| ||| ||||||||  |||
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                                ATACC TTA TTCTTTGG  TGT
                                   G  C      TT
GAM2658  LOC148231 5'  GGAAATAAAGAGCGAACATG  62127          AACTC
                                GGAAATAAAGA    GCATG
                                ||||||||||    |||||
                                CCTTTATTTCT    TGTAC
                                     CGCT_
GAM2658  LOC220370 3'  TATGGAAAAGGAGAAAGGGCA  62128        TAA    CTC
                                TATGGAAA  AGAAA  GCA
                                ||||||||  |||||  |||
                                ATACCTTT  TCTTT  CGT
                                    TCC    CC_
GAM2658  LOC254778 3'  TATGGAAATAGGGAACTCA   62129         AA  A
                                TATGGAAATA  GAA CTCG
                                ||||||||||  ||| ||||
                                ATACCTTTAT  CTT GAGT
                                     CC  _
GAM2659  PRKCG    3'  GCTGTAGAGGCTGTATGGAGT  62132    A   CC    __
                                GT GTAG  GTTGTA  GAGT
                                || ||||  ||||||  ||||
                                CG CATC  CGACAT  CTCA
                                 A   TC    AC
GAM2660  AVPR1A   5'  TCAAGTATTTATGCGGTGCACT 62135        A_________  GTTGA
           CAAG                  AGTATTTAT       CAC    G
                                |||||||||       |||    |
                                TCATAAATA       GTG    C
                                    CGCCACIII   AGTTG
GAM2660  DNMT2    3'  TCAAGTATTTATAGTTGGT   62136          CAC   A
                                TCAAGTATTTATA  GTTG GT
                                ||||||||||||  |||| ||
                                AGTTCATAAATAT  CAAC CA
                                       ___   _
GAM2660  EEF2     3'  TCAAGTGTTATGGTTGAGT   62137      AT   ACAC
                                TCAAGT  TTAT   GTTGAGT
                                ||||||  ||||   |||||||
                                AGTTCA  AATA   CAACTCA
                                   C_   C___
GAM2660  PX19     3'  CAAGTATTTATTGAG      62138         ACACGT
                                CAAGTATTTAT     TGAG
                                ||||||||||     ||||
                                GTTCATAAATA     ACTC
                                      _______
GAM2660  DKFZP434I1735 3'  TCAAGTATTTATTATATTAAG  62139          ACAC
                                TCAAGTATTTAT   GTTGAG
                                ||||||||||||   ||||||
                                AGTTCATAAATA   TAATTC
                                      ATA_
GAM2660  FLJ11110  3'  AAGTATTCAAAGTGTTGAGTG  62140        TACAC
                                AAGTATTTA    GTTGAGTG
                                |||||||||    ||||||||
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                                TTCATAAGT    CAACTCAC
                                     TTCA_
GAM2660 FLJ21615 3' GTACATATGTACGTTGAGTG  62141     T  AC
                                GTAT TAT  ACGTTGAGTG
                                |||| |||  ||||||||||
                                CATG ATA  TGCAACTCAC
                                  T  CA
GAM2660 IRX3     3' GTATTTATACACGGACATG   62142          TTGA
                                GTATTTATACACG   GTG
                                ||||||||||||    |||
                                CATAAATATGTGC   TAC
                                       CTG_
GAM2660 MGC16202 3' CCAAGTATTTGTATGTGTGAGT 62143        A  CAC  _
             G                   TCAAGTATTT TA   GT TGAGTG
                                |||||||||| ||   || ||||||
                                GGTTCATAAA AT   CA ACTCAC
                                      C  A__  C
GAM2660 POF1B    3' TCAAGTATTTATTTGTGTTCAC 62144       AC_________  GTTGA
             TCAACGT                TATTTAT         AC    GT
                                |||||||         ||    ||
                                ATAAATA         TG    CA
                                    AACACAAIIIG  AGTTG
GAM2660 ZNF286   3' TCAAGTATTTAATACAGT    62145         _   C
                                TCAAGTATTTA TACA GT
                                |||||||||| |||| ||
                                AGTTCATAAAT ATGT CA
                                      T   _
GAM2660 LOC150568 5' TCAAGTATTTAGGCATCGGTG  62146         TACA    A
                                TCAAGTATTTA   CGTTG GTG
                                ||||||||||    ||||| |||
                                AGTTCATAAAT   GTAGC CAC
                                      CC__    _
GAM2660 LOC154562 3' CAAGTATTTATTGAG      62138          ACACGT
                                CAAGTATTTAT     TGAG
                                ||||||||||     ||||
                                GTTCATAAATA     ACTC
                                      _______
GAM2660 LOC220097 3' TCAAATATTTATAGAAGGAGTG 62147           CACGTT
                                TCAAGTATTTATA     GAGTG
                                ||||||||||||     |||||
                                AGTTTATAAATAT     CTCAC
                                       CTTC__
GAM2660 LOC90557  3' TCAAGTACTTTATCTATCTTGA 62148         _ ACACG
             GTG                   TCAAGTATTT AT    TTGAGTG
                                |||||||||| ||    |||||||
                                AGTTCATGAA TA    AACTCAC
                                      A  GATAG
GAM2660 LOC91409  3' TCAAGTACTTTATCTATCTTGA 62148         _ ACACG
             GTG                   TCAAGTATTT AT    TTGAGTG
                                |||||||||| ||    |||||||
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                                AGTTCATGAA TA    AACTCAC
                                     A  GATAG
GAM2660  LOC92755  3'  CAAGTATTTATTGAG      62138          ACACGT
                                CAAGTATTTAT    TGAG
                                ||||||||||     ||||
                                GTTCATAAATA    ACTC
                                       _____
GAM2661  CROT      3'  GAGCATGATTCTACTAATTTC  62151    A  CA       C
                                GA CA  ATTCTACTAA TTC
                                || ||  |||||||||| |||
                                CT GT  TAAGATGATT AAG
                                 C  AC        A
GAM2661  CX3CR1    3'  TTGAGCACAATTCTCAAC    62152     A       AC
                                TTGA CACAATTCT  TAAC
                                |||| |||||||||  ||||
                                AACT GTGTTAAGA  GTTG
                                  C       __
GAM2661  HCS       3'  CCTGAATACCACTAACTT    62153      CACAATT
                                CTTGAA      CTACTAACTT
                                ||||||      ||||||||||
                                GGACTT      GGTGATTGAA
                                   AT_____
GAM2661  AKAP6     3'  TGAATATTCCACTAACTT    62154     CACA
                                TGAA    ATTCTACTAACTT
                                ||||    ||||||||||||
                                ACTT    TAAGGTGATTGAA
                                  A___
GAM2661  C20orf28  3'  GAACACAACACTGACTT     62155        TCT   A
                                GAACACAAT   ACT ACTT
                                |||||||||   ||| ||||
                                CTTGTGTTG   TGA TGAA
                                     ___  C
GAM2661  FLJ21908  3'  CTTGAATACAATTCTCACTA   62156      C      _
                                CTTGAA ACAATTCT ACTA
                                |||||| |||||||| ||||
                                GAACTT TGTTAAGA TGAT
                                   A       G
GAM2661  HEY1      3'  CTTGAACAAAATTTAACAACT  62157       C   CT  T
                                CTTGAACA AATT  AC AACT
                                |||||||| ||||  || ||||
                                GAACTTGT TTAA  TG TTGA
                                     T   AT  _
GAM2661  KIAA0275  3'  CTTGAACACAATTCCTAACTC  62158          TA
                                CTTGAACACAATTC  CTAACTT
                                ||||||||||||||  |||||||
                                GAACTTGTGTTAAG  GATTGAG
                                       __
GAM2661  KIAA0844  3'  CTTGAACATAGTTTCCCAGAAA 62159       CAA__    CT
            CTT                   CTTGAACA    TTCTA  AACTT
                                ||||||||    |||||  |||||
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                                GAACTTGT    AGGGT  TTGAA
                                    ATCAA    CT
GAM2661  KIAA1128  3'  CTGAATACTCTACTAATTTC  62160      CACA        C
                                TTGAA    ATTCTACTAA TTC
                                |||||    |||||||||| |||
                                GACTT    TGAGATGATT AAG
                                   A___        A
GAM2661  KIAA1157  3'  CCTGAACACAAACTTGACTT  62161          TTCT  A_
                                CTTGAACACAA    ACT  ACTT
                                ||||||||||    |||  ||||
                                GGACTTGTGTT    TGA  TGAA
                                      ____  AC
GAM2661  KIAA1649  5'  CTTGAACACAGTTTAAGAACTT 62162          A  C  CT
                                CTTGAACACA TT TA  AACTT
                                |||||||||| || ||  |||||
                                GAACTTGTGT AA AT  TTGAA
                                      C  _  TC
GAM2661  TRABID    3'  CTTGGAGCACCACACTAACTT  62163     AA_   AATTC
                                CTTG   CAC    TACTAACTT
                                ||||   |||    |||||||||
                                GAAC   GTG    GTGATTGAA
                                  CTC   GT___
GAM2661  LOC51202  3'  CTGGACACAATTCTGACCAATT 62164     A        _    C
            TC                    TTG ACACAATTCT ACTAA TTC
                                |||  |||||||||| ||||| |||
                                GAC TGTGTTAAGA TGGTT AAG
                                  C         C    A
GAM2662  ATP7A     3'  TAAAACTAGATGTTTTATACAC 62167          AATC
                                TAAAACTAGGT    TATACAC
                                ||||||||||    |||||||
                                ATTTTGATCTA    ATATGTG
                                      CAAA
GAM2662  CALU      3'  TATAAAACTTGGTTTACAC    62168         A   AATC
                                TATAAAACT GGT    TATAC
                                |||||||| |||    |||||
                                ATATTTTGA CCA    ATGTG
                                      A   A___
GAM2662  EFNB2     3'  TACAAGACTAGGTAAGCT     62169      A       T
                                TATAA ACTAGGTAA CT
                                ||||| |||||||| ||
                                ATGTT TGATCCATT GA
                                   C        C
GAM2662  MPHOSPH1  3'  TATAAAACAGCAATCTATA    62170        TA
                                TATAAAAC  GGTAATCTATA
                                ||||||||  ||||||||||
                                ATATTTTG  TCGTTAGATAT
                                          __
GAM2662  POLR2J    3'  TATAAAACCTAATCTAT     62171         AGG
                                TATAAAACT   TAATCTAT
                                |||||||||   ||||||||
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                                ATATTTTGG  ATTAGATA
                                    ___
GAM2662  PRPS2    3'  TAAAACTAGCTCTATACA    62172        GTAA
                                TAAAACTAG   TCTATACA
                                |||||||||   ||||||||
                                ATTTTGATC   AGATATGT
                                     G___
GAM2662  SLC2A1   3'  TATAAATATCTTGCATCTATAC 62173       ACTAG_  A
              AC                  TATAAA    GTA TCTATACAC
                                |||||||     ||| |||||||||
                                ATATTT     CGT AGATATGTG
                                   ATAGAA  _
GAM2662  STC1     3'  TACAAAACTAAATCTATA    62174         GGT
                                TATAAAACTA  AATCTATA
                                ||||||||||  ||||||||
                                ATGTTTTGAT  TTAGATAT
                                    ___
GAM2662  TFRC     3'  TAAATCTAGGTAAGTGACAC  62175     A      TCT
                                TAAA CTAGGTAA  ATAC
                                |||| ||||||||  ||||
                                ATTT GATCCATT  TGTG
                                  A       CAC
GAM2662  FLJ10292 3'  TATAAAACTAGTATTATAC   62176         GTAATC
                                TATAAAACTAG     TATAC
                                ||||||||||     |||||
                                ATATTTTGATC     ATATG
                                      ATA___
GAM2662  KIAA0007 3'  ACTTCTAATCTATACAC     62177     AGG
                                ACT   TAATCTATACAC
                                |||   ||||||||||||
                                TGA   ATTAGATATGTG
                                  AG_
GAM2662  KIAA0196 3'  CATAAAACTAAATGGATTTATA 62178          A_  C
              CA                  TATAAAACTAGGT  AT TATACA
                                |||||||||||||  || ||||||
                                GTATTTTGATTTA  TA ATATGT
                                       CC  A
GAM2662  KIAA1240 3'  TAAAACTAGTAACCCAT     62179         G
                                TAAAACTAG TAATCTAT
                                ||||||||| ||||||||
                                ATTTTGATC ATTGGGTA
                                    _
GAM2662  KIAA1677 3'  AAACTAGAAAATTTATACA   62180        T   C
                                AAACTAGG AAT TATACA
                                |||||||| ||| ||||||
                                TTTGATCT TTA ATATGT
                                     T   A
GAM2662  PDK2     3'  TATAAAACTAACTATATAC   62181          G  ATC
                                TATAAAACTAG TA   TATAC
                                |||||||||| ||   |||||
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                                ATATTTTGATT AT   ATATG
                                      G ___
GAM2662  RDC1     3'  TATAAAACTATGGTAAATAAAA 62182         _    TCTAT
                CA                    TATAAAACTA GGTAA    ACA
                                ||||||||||  |||||    |||
                                ATATTTTGAT CCATT    TGT
                                     A    TATTT
GAM2662  SPC12    3'  AACTAAATCTATACAC      62183      GGT
                                AACTA   AATCTATACAC
                                |||||   ||||||||||
                                TTGAT   TTAGATATGTG
                                  ___
GAM2662  LOC200933 3'  TAAAACCAGGTAATTAAAAC   62184           CTAT
                                TAAAACTAGGTAAT    AC
                                ||||||||||||||   ||
                                ATTTTGGTCCATTA    TG
                                       ATTT
GAM2662  LOC92305  3'  TATAAAACTAAGTAACTTAT   62185           TC
                                TATAAAACTAGGTAA  TAT
                                ||||||||||||||  |||
                                ATATTTTGATTCATT  ATA
                                       GA
GAM2663  ACRC     3'  TATAATACTTCTGCACATACAC 62188        C   A   C_
                A                    TATAATAC TTT CAC  ACGCA
                                ||||||||  ||| |||  |||||
                                ATATTATG AGA GTG  TGTGT
                                     A   C   TA
GAM2663  KIAA0830 3'  TAGTACCTTTACTGCAGC    62189    A       AC  C
                                TA TACCTTTAC  CA GC
                                || |||||||||  || ||
                                AT ATGGAAATG  GT CG
                                 C        AC  _
GAM2663  KIAA1024 3'  TGAATACCTTGGCCCATCATGC 62190    T       TA__  C  C
                A                    A AATACCTT    CA CA GCA
                                | ||||||||    || || |||
                                A TTATGGAA    GT GT CGT
                                 C       CCGG  A  A
GAM2663  KIAA1391 3'  TATAATACTTTACAGCAA    62191        C     CCAC
                                TATAATAC TTTACA    GCAA
                                ||||||||  ||||||    ||||
                                ATATTATG AAATGT    CGTT
                                     _     _____
GAM2663  MRPS21   5'  CATAATACAAACTACACCGCGC 62192        CT_      A
                                TATAATAC   TTACACC CGC
                                ||||||||   |||||||  |||
                                GTATTATG   GATGTGG GCG
                                     TTT      C
GAM2663  USP25    3'  TAATACCTTTACAAACAGC    62193           C_  C
                                TAATACCTTTACA  CA GC
                                ||||||||||||||  || ||
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                                ATTATGGAAATGT  GT CG
                                       TT  _
GAM2663  WSB1     3'  TATAATACTTTATACCAC    62194        C    C
                                TATAATAC TTTA ACCAC
                                |||||||| |||| |||||
                                ATATTATG AAAT TGGTG
                                     _    A
GAM2663  WSB1     3'  TATAATACTTTATACCAC    62194        C    C
                                TATAATAC TTTA ACCAC
                                |||||||| |||| |||||
                                ATATTATG AAAT TGGTG
                                     _    A
GAM2663  XLKD1    3'  TAATACCTTGCACAGC      62195         _   CCAC
                                TAATACCTT TACA   GC
                                ||||||||| ||||   ||
                                ATTATGGAA GTGT   CG
                                     C   ____
GAM2664  ABR      3'  AGGAAGACTGAGGGGAGGC   62198         A  AAAA
                                AGGAAGATT AG   AGGC
                                ||||||||| ||   ||||
                                TCCTTCTGA TC   TCCG
                                     C  CCC_
GAM2664  ABR      3'  AGGAAGACTGAGGGGAGGC   62198         A  AAAA
                                AGGAAGATT AG   AGGC
                                ||||||||| ||   ||||
                                TCCTTCTGA TC   TCCG
                                     C  CCC_
GAM2664  ADRB3    3'  GAAGATTAGGAAGAAAAGAG  62199         ___     AG
                                GAAGATTA   AGAAAA  G
                                ||||||||   ||||||  |
                                CTTCTAAT   TCTTTT  C
                                     CCT     CT
GAM2664  CDC27    3'  AGGGAGATTAAAGAAAAA    44128     A     _
                                AGG AGATTAA GAAAAA
                                ||| ||||||| ||||||
                                TCC TCTAATT CTTTTT
                                  C      T
GAM2664  DDB2     5'  GGAGGATTGAGAGGCCTC    62200     A   A   AAAA
                                GGA GATT AGA   GGCCTC
                                ||| |||| |||   ||||||
                                CCT CTAA TCT   CCGGAG
                                  C   C  ____
GAM2664  HHLA1    5'  GGAGAGATTAAGCTGAAGG   62201     _      AAA
                                GGA AGATTAAG   AAGG
                                ||| ||||||||   ||||
                                CCT TCTAATTC   TTCC
                                  C       GAC
GAM2664  KCNK5    3'  GGAAGGTTAGGAAGGCCCC   62202      A   A  AAA
                                GGAAG TTA GA   AGGCCTC
                                ||||| ||| ||   |||||||
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                                CCTTC AAT CT   TCCGGGG
                                  C   C ___
GAM2664  NR2E1    5'  AGGAAGACTGAGGAAGAAG   62203        AA_  A
                                AGGAAGATT   GAA AAG
                                |||||||||   ||| |||
                                TCCTTCTGA   CTT TTC
                                    CTC   C
GAM2664  PTK2B    3'  AGGAGGAGTAAGAAAAGAG   62204     A  T      AG
                                AGGA GA TAAGAAAA  G
                                |||| || ||||||||  |
                                TCCT CT ATTCTTTT  C
                                  C  C       CT
GAM2664  SGPL1    3'  AGGAAGATAAGAGGAAG     62205        T   AA
                                AGGAAGAT AAGA  AAG
                                |||||||| ||||  |||
                                TCCTTCTA TTCT  TTC
                                    _   CC
GAM2664  TAF1     3'  AGGAAGATTAGGAGAGG     62206         A  AAA
                                AGGAAGATTA GA   AGG
                                |||||||||| ||   |||
                                TCCTTCTAAT CT   TCC
                                     C  C__
GAM2664  TAF1     3'  AGGAAGATTAGGAGAGG     62206         A  AAA
                                AGGAAGATTA GA   AGG
                                |||||||||| ||   |||
                                TCCTTCTAAT CT   TCC
                                     C  C__
GAM2664  TNFRSF6  5'  AGGAGGATGGGAAGGAAGCCTC 62207     A   TAA   AA
           G                     AGGA GAT   GAA  AGGCCTCG
                                |||| |||   |||  ||||||||
                                TCCT CTA   CTT  TTCGGAGC
                                  C   CC_   CC
GAM2664  ZFP36L1  3'  AGATCGGGAAGAAAAAGG    62208      ___
                                AGATT   AAGAAAAAGG
                                |||||   ||||||||||
                                TCTAG   TTCTTTTTCC
                                   CCC
GAM2664  DKFZP434B205 3'  AGGAAGATGAAGAAGCACTCG  62209        T   AAAA  _
                                AGGAAGAT AAGA    GGC CTCG
                                |||||||| ||||    ||| ||||
                                TCCTTCTA TTCT    TCG GAGC
                                    C    ____   T
GAM2664  DKFZp566H0824 5'  AGGAAGGTTAAGGAACCTCCTC 62210       A    A  AAGG
           G                     AGGAAG TTAAG AA    CCTCG
                                ||||||| ||||| ||    |||||
                                TCCTTC AATTC TT    GGAGC
                                   C    C  GGA_
GAM2664  EIF2S1   3'  AGAAAGATTGGGATTGTTTGCC 62211         AA  AAAAG_
           T                     AGGAAGATT  GA     GCCT
                                |||||||||  ||     ||||
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                                TCTTTCTAA CT     CGGA
                                     CC  AACAAA
GAM2664 FLJ12505 3' AGAAAGATTAAGAAGGAAG   62212           A_
                                AGGAAGATTAAGAA AAG
                                |||||||||||||| |||
                                TCTTTCTAATTCTT TTC
                                      CC
GAM2664 FLJ20291 5' GGAGGATCAAGAGAAAAC    62213    A      AA
                                GGA GATTAAGA AAGGC
                                ||| |||||||| |||||
                                CCT CTAGTTCT TTTTG
                                  C       C_
GAM2664 FLJ20424 3' AGGAAGATTAGGAGGC      62214         A AAAA
                                AGGAAGATTA GA   GGC
                                |||||||||| ||   |||
                                TCCTTCTAAT CT   CCG
                                      C ____
GAM2664 FLJ22865 3' GGCAGGGGGCAGGAAAAGGCCT 62215   A ATTA_ A
                                GG AG    AG AAAAGGCCT
                                || ||    || |||||||||
                                CC TC    TC TTTTCCGGA
                                 G CCCCG C
GAM2664 H2BFQ    3' GGGAGAGTAAGAAAAGG     62216   A T      A
                                GG AGA TAAGAAAA GG
                                || ||| |||||||| ||
                                CC TCT ATTCTTTT CC
                                 C  C       _
GAM2664 JIK      3' AGGGAGATAAAGAAAAAG    44146    A   T
                                AGG AGAT AAGAAAAAG
                                ||| |||| |||||||||
                                TCC TCTA TTCTTTTTC
                                  C   T
GAM2664 KIAA0295 3' AGGAAGATCAGGAGAGC     62217         A AAAA
                                AGGAAGATTA GA   GGC
                                |||||||||| ||   |||
                                TCCTTCTAGT CT   TCG
                                      C  C___
GAM2664 KIAA0426 5' GAAGGCAAGAGGCCTC      62218    AT    AAAA
                                GAAG  TAAGA   GGCCTC
                                ||||  |||||   ||||||
                                CTTC  GTTCT   CCGGAG
                                  C_    ____
GAM2664 KIAA1900 3' AGGAAGTTAGGAAAAAAG    62219      A  A
                                AGGAAG TTA GAAAAAGG
                                |||||| ||| ||||||||
                                TCCTTC AAT CTTTTTTC
                                   _  C
GAM2664 PSR      3' AGGAAGGTAAGGAAAAAG    62220      AT  _
                                AGGAAG  TAAG AAAAAG
                                ||||||  |||| ||||||
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                                TCCTTC  ATTC TTTTTC
                                   C_   C
GAM2664  SSH2     3'  AGGAAGATTAAGGAAGG     62221          AAA
                                AGGAAGATTAAG   AAGG
                                ||||||||||||  ||||
                                TCCTTCTAATTC   TTCC
                                       C__
GAM2664  ZDHHC5   5'  GGAAGATTAAGAAACACAAC   62222           AA_
                                GGAAGATTAAGAAA   GGC
                                ||||||||||||||  |||
                                CCTTCTAATTCTTT   TTG
                                       GTG
GAM2664  LOC149076 3'  GGAAGATTGGGAAGGTC     62223        AA  AAA   CC
                                GGAAGATT  GA   AGG  TC
                                ||||||||  ||   |||  ||
                                CCTTCTAA  CT   TCC  AG
                                     CC  ___   __
GAM2664  LOC149420 3'  AGGAAGATAAGGGAAGG     62224        T   AAA
                                AGGAAGAT AAG   AAGG
                                ||||||||| |||   ||||
                                TCCTTCTA TTC   TTCC
                                     _  CC_
GAM2664  LOC158809 5'  AGGAAGACTAGGAAGGC     62225         A  AAA
                                AGGAAGATTA GA   AGGC
                                |||||||||| ||   ||||
                                TCCTTCTGAT CT   TCCG
                                      C  ___
GAM2664  LOC163682 3'  AGGGAGACCAAAGGGGCCT   62226     A      AAAAA
                                AGG AGATTAAG    GGCCT
                                ||| ||||||||    |||||
                                TCC TCTGGTTT    CCGGA
                                  C      CC___
GAM2664  LOC197114 5'  AGGAAGATGGAGGGAGAAGCC  62227        TA  AAAA
                                AGGAAGAT  AG    AGGCC
                                ||||||||  ||   |||||
                                TCCTTCTA  TC   TTCGG
                                     CC  CCTC
GAM2664  LOC202451 5'  GGAAGATTGAGCAAGAC     62228        AA  AA
                                GGAAGATT  GA  AAGGC
                                ||||||||  ||  |||||
                                CCTTCTAA  CT  TTCTG
                                     __  CG
GAM2664  LOC219392 5'  GGAAGATTAAGGGAAGC     62229          AAAA
                                GGAAGATTAAG   AGGC
                                ||||||||||   ||||
                                CCTTCTAATTC   TTCG
                                      CC__
GAM2664  LOC220846 3'  GAAGATTAGGAAGAAAAGAG   62199         ___     AG
                                GAAGATTA   AGAAAA  G
                                ||||||||   ||||||  |
```

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                                CTTCTAAT  TCTTTT C
                                    CCT    CT
GAM2664 LOC221738 5' AGGAAGACTGGGAATACCTCG 62230       AA  AAAG
                                AGGAAGATT GAA   GCCTCG
                                ||||||||| |||   ||||||
                                TCCTTCTGA CTT   TGGAGC
                                    CC  A___
GAM2664 LOC255862 3' AGGAAGATATAAGGGAAAAAG 62231       TAA___
                                AGGAAGAT    GAAAAAG
                                ||||||||    |||||||
                                TCCTTCTA    CTTTTTC
                                    TATTCC
GAM2664 LOC90371  5' AGAAAAAGGAGGAAGGAGGCCT 62232      TTAA  AA
                                AGGAAGA   GAA AGGCCT
                                |||||||   ||| ||||||
                                TCTTTTT   CTT TCCGGA
                                    CCTC  CC
GAM2664 LOC91355  3' GAAGACCAAGAAGGCCT    62233        AAA
                                GAAGATTAAGA  AGGCCT
                                ||||||||||  ||||||
                                CTTCTGGTTCT  TCCGGA
                                      ___
GAM2664 LOC91966  5' AGGAAGATAAAGAGGAAAG  62234      T   A_
                                AGGAAGAT AAGA AAAG
                                |||||||| |||| ||||
                                TCCTTCTA TTCT TTTC
                                    T   CC
GAM2664 LOC93356  3' AGGAAGATTGAGAACATCCT  62235       A   AAAGG
                                AGGAAGATT AGAA   CCT
                                ||||||||| ||||   |||
                                TCCTTCTAA TCTT   GGA
                                    C   GTA__
GAM2665 PPP1R12B  3' TTGTGTGGACTCTGGGTT   62238     CA   AAACT
                                TTGTG GATTT   TGGGTT
                                ||||| |||||   ||||||
                                AACAC CTGAG   ACCCAA
                                  AC   _____
GAM2665 C12orf2   3' TTGTGCAGGAGTTTTGGGTTT 62239       ATTTAAAC
                                TTGTGCAG      TTGGGTTT
                                ||||||||      ||||||||
                                AACACGTC      AACCCAAA
                                    CTCAA___
GAM2665 FLJ23604  3' TGTGCCAAGAACTTGGGTTT  62240     AGATTTA
                                TGTGC     AACTTGGGTTT
                                |||||     ||||||||||
                                ACACG     TTGAACCCAAA
                                  GTTC___
GAM2665 KIAA0210  3' GTGGGAATGAACTTGGGTTT  62241    CA  TTA
                                GTG GAT   AACTTGGGTTT
                                ||| |||   ||||||||||
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                                CAC  TTA   TTGAACCCAAA
                                  CC   C__
GAM2665  KIAA0255  3'  TTGTAGCAACTAAGACTTGGGT 62242     _   ATTTAA
                TT                  TTGT GCAG     ACTTGGGTTT
                                    |||| ||||     ||||||||||
                                    AACA CGTT     TGAACCCAAA
                                      T    GATTC_
GAM2665  KIAA0889  3'  TTGTCAGGTTCCTACTCTTGGG 62243     G   A   AAA__
                TTT                 TTGT CAG TTT     CTTGGGTTT
                                    |||| ||| |||     |||||||||
                                    AACA GTC AAG     GAACCCAAA
                                      _   C   GATGA
GAM2665  KIAA1889  3'  TGTGTAGACAACATTTGGGTTT 62244     C    TTAAAC
                                    TGTG AGAT     TTGGGTTT
                                    |||| ||||     ||||||||
                                    ACAC TCTG     AACCCAAA
                                      A    TTGTA_
GAM2665  MGC20481  3'  TTGTGGAGTGGAAATTTGGGTT 62245      C  ATTT   C
                T                   TTGTG AG    AAA TTGGGTTT
                                    |||||  ||    ||| ||||||||
                                    AACAC TC    TTT AACCCAAA
                                      C  ACC_   A
GAM2665  NAG73    3'  TTGTGTGGAATTAAGACTGGGT 62246      CA  T    AC
                TT                  TTGTG  GA TTAA  TTGGGTTT
                                    |||||  ||  ||||  ||||||||
                                    AACAC  CT AATT  GACCCAAA
                                       AC  T    CT
GAM2665  TJP2     3'  TTGTGCAGCACTTGGGTT    62247        ATTTAA
                                    TTGTGCAG     ACTTGGGTT
                                    ||||||||     |||||||||
                                    AACACGTC     TGAACCCAA
                                         G_____
GAM2665  LOC127702 3'  TTGGGCAGATTTGGGTT     62248     T      TAAACT
                                    TTG GCAGATT     TGGGTT
                                    ||| |||||||     ||||||
                                    AAC CGTCTAA     ACCCAA
                                      C     _______
GAM2665  LOC90072  3'  TTGTCAGGTTCCTACTCTTGGG 62243     G   A   AAA__
                TTT                 TTGT CAG TTT     CTTGGGTTT
                                    |||| ||| |||     |||||||||
                                    AACA GTC AAG     GAACCCAAA
                                      _   C   GATGA
GAM2666  SPARC    3'  TCATTTTTAGCACCGTTA    62251        AATC   C
                                    TCATTTTT    AGC CCGTTA
                                    ||||||||    ||| ||||||
                                    AGTAAAAA    TCG GGCAAT
                                         _____   T
GAM2666  LOC145624 5'  GCCATTTTTAATTGCAGTTAA  62252          CA  CCC
                                    GTCATTTTTAAT  GC   GTTAA
                                    ||||||||||||  ||   |||||
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                                CGGTAAAAATTA CG  CAATT
                                      A_ T__
GAM2667 BMPR1B   3' ACAAGTTACCCAACGGTTT  62255    TC_   TCCG
                                ACAA  ACCCG   TGGTTT
                                ||||  |||||   ||||||
                                TGTT  TGGGT   GCCAAA
                                  CAA   T___
GAM2667 GALNT2   3' CACAGTCGTCCGTGCCTT   62256    ATCACC     G
                                CACA    CGTCCGTG TTT
                                ||||    |||||||| |||
                                GTGT    GCAGGCAC GAA
                                  CA____      G
GAM2667 PTTG1IP  3' ACACAGACGCTGTCCGTGGTTT 62257     ATCACCC
                                ACACA     GTCCGTGGTTT
                                |||||     ||||||||||
                                TGTGT     CAGGCACCAAA
                                   CTGCGA_
GAM2667 ZNF236   5' ACACAATCCTTTGTAGTTT   62258      ACCCGTCC
                                ACACAATC      GTGGTTT
                                ||||||||      |||||||
                                TGTGTTAG      CATCAAA
                                    GAAA____
GAM2667 BTN3A3   3' CACAATCACTTATCACAT    62259       CC  _
                                CACAATCAC  GTC CGT
                                |||||||||  ||| |||
                                GTGTTAGTG  TAG GTA
                                     AA  T
GAM2667 FLJ20551 3' ACACAATTTCTGCCTGGTTT  62260      CACCC T  G
                                ACACAAT   G CC TGGTTT
                                |||||||   | || ||||||
                                TGTGTTA   C GG ACCAAA
                                   AAGA_ _  _
GAM2667 FLJ22794 5' CACAGTGCATCCTTGATGGTTT 62261    ATCACC   ___
            C                    CACA    CGTCC  GTGGTTTC
                                ||||    |||||  ||||||||
                                GTGT    GTAGG  TACCAAAG
                                  CAC___    AAC
GAM2667 KIAA0976 3' ACAATCACGTTTGATGGTTT  62262      CCGTCC
                                ACAATCAC    GTGGTTT
                                ||||||||    |||||||
                                TGTTAGTG    TACCAAA
                                    CAAAC_
GAM2667 NSBP1    3' ACACAATCATCGTCAGAGTCT 62263       CC   CGT
                                ACACAATCA  CGTC  GGTTT
                                |||||||||  ||||  |||||
                                TGTGTTAGT  GCAG  TCAGA
                                     A_   TC_
GAM2667 OSBPL6   3' GAACAATCGTGTGGTT    62264   C    ACCC  CC
                                A ACAATC   GT  GTGGTT
                                | ||||||   ||  ||||||
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                              C TGTTAG   CA  CACCAA
                               T    ____ __
GAM2667 LOC51162 3' CAGTCACCCCGAGGTGGTTTC 62265   A    GTCC
                              CA TCACCC   GTGGTTTC
                              || ||||||   ||||||||
                              GT AGTGGG   CACCAAAG
                               C    GCTC
GAM2667 LOC90321 3' ACACAATCCATTTGTGTGGTTT 62266       ACCCGTCC
           C                   ACACAATC      GTGGTTTC
                              ||||||||      ||||||||
                              TGTGTTAG      CACCAAAG
                                  GTAAACA_
GAM2667 LOC91960 3' ACACAATTTCCGAGGGAATGGT 62267      CAC  TCC__
           TT                  ACACAAT  CCG   GTGGTTT
                              |||||||  |||   |||||||
                              TGTGTTA  GGC   TACCAAA
                                  AA_  TCCCT
GAM2668 FLJ11715 3' CTGGTTGGATACTTTCTGTCTC 62270      C__ GG  CC
           CTG                   TTGGTTG  GC  TC  GTCTCCTG
                              |||||||  ||  ||  ||||||||
                              GACCAAC  TG  AG  CAGAGGAC
                                  CTA  AA  A_
GAM2668 LOC221301 3' TTGGTTTGTATTTGTCTCCTG 62271      GCGCG  CCC
                              TTGGTT   GT   GTCTCCTG
                              ||||||   ||   ||||||||
                              AACCAA   TA   CAGAGGAC
                                 ACA__  AA_
GAM2669 ENO2    5' TCGGGACTGCAGACTCAGACGG 14137   A   C      TTA__
           TG                   TC GGAC TGCAGACTC    GTG
                              || |||| |||||||||    |||
                              AG CCTG ACGTCTGAG    CAC
                               C   _       TCTGC
GAM2669 TCF1    3' TCAGGACCTCAGACTCCT    62274        G
                              TCAGGACCT CAGACTCTT
                              ||||||||| |||||||||
                              AGTCCTGGA GTCTGAGGA
                                        _
GAM2669 TRIM14   3' TCAGGACCTCAGACTCCCCAGA 62275        G       AGT
                              TCAGGACCT CAGACTCTT   GA
                              ||||||||| |||||||||   ||
                              AGTCCTGGA GTCTGAGGG   CT
                                   _       GT_
GAM2669 ABLIM   3' TCAGAGCTTTTGTTCTTAGTG 62276     AC  GCAGAC
                              TCAGG  CT    TCTTAGTG
                              |||||  ||    ||||||||
                              AGTCT  GA    AGAATCAC
                                C_  AAACA_
GAM2669 ABLIM   3' TCAGAGCTTTTGTTCTTAGTG 62276     AC  GCAGAC
                              TCAGG  CT    TCTTAGTG
                              |||||  ||    ||||||||
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                                AGTCT  GA     AGAATCAC
                                  C_  AAACA_
GAM2669  C20orf110 3'  TCAGGGCCTGCAGAAGGGTG   14144      A      CTCTTA
                                TCAGG CCTGCAGA     GTG
                                ||||| ||||||||     |||
                                AGTCC GGACGTCT     CAC
                                  C       TCC___
GAM2669  C21orf93  3'  CCAGGACCTGCAGAGGTG    14145           CTCTTA
                                TCAGGACCTGCAGA     GTG
                                ||||||||||||||     |||
                                GGTCCTGGACGTCT     CAC
                                        C_____
GAM2669  CRA       3'  TCAGACCTTCTTAGT      62277      G   GCAGAC
                                TCAG ACCT     TCTTAGT
                                |||| ||||     |||||||
                                AGTC TGGA     AGAATCA
                                  _   _______
GAM2669  DKFZP762D096 3'  CCAGGACCTGCAGGGGGGTG   14146           ACTCTTA
                                TCAGGACCTGCAG      GTG
                                ||||||||||||      |||
                                GGTCCTGGACGTC      CAC
                                      CCCC___
GAM2669  EIF4ENIF1 3'  AGGTGCCACCTCTTGGTGA   62278     ACC   AGA    A
                                AGG   TGC   CTCTT GTGA
                                |||   |||   ||||| ||||
                                TCC   ACG   GAGAA CACT
                                  ___   GTG    C
GAM2669  FLJ14082  3'  TCAGACCCACTTCTTAGTG   62279     G   TG AGAC
                                TCAG ACC  C    TCTTAGTG
                                |||| |||  |    ||||||||
                                AGTC TGG  G    AGAATCAC
                                  _   GT A___
GAM2669  FLJ14827  3'  AGGGCTTGCAGACTTAGC    62280     ACC       CT
                                AGG   TGCAGACT  TAGT
                                |||   ||||||||  ||||
                                TCC   ACGTCTGA  ATCG
                                  CGA       __
GAM2669  KIAA0318  5'  TCAGCACCTGCAGGCTTCAG   62281      G       A  C
                                TCAG ACCTGCAG CT TTAG
                                |||| |||||||| || ||||
                                AGTC TGGACGTC GA AGTC
                                  G       C  _
GAM2669  KIAA1855  3'  TCAGGACCTGGAGGCCTGGTG  14151          C  ACT   A
                                TCAGGACCTG AG   CTT GTG
                                |||||||||| ||   ||| |||
                                AGTCCTGGAC TC   GGA CAC
                                      C  C__   C
GAM2669  MAPK11    3'  AGACCTGTGGGTCTCAGCAGTG 62282        CAGA_   T_
            A                    GGACCTG    CTC  TAGTGA
                                |||||||    |||  ||||||
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                                TCTGGAC    GAG  GTCACT
                                    ACCCA   TC
GAM2669  MGC34923  5'  TCAGGACCTTCAGTGAGTG   14152        G   ACTCTT
                                TCAGGACCT CAG     AGTG
                                ||||||||| |||     ||||
                                AGTCCTGGA GTC     TCAC
                                    A   AC____
GAM2669  PPP1R16B  3'  GGGTCTGCAGACTTTTCCTG   62283    AC       C  AG
                                GG  CTGCAGACT TT  TG
                                ||  ||||||||| ||  ||
                                CC  GACGTCTGA AA  AC
                                 CA        A  GG
GAM2669  LOC143308 5'  TCAGGGCCTGCAAACTCAAAG  14158      A         TT
                                TCAGG CCTGCAGACTC  AG
                                ||||| ||||||||||  ||
                                AGTCC GGACGTTTGAG  TC
                                   C          TT
GAM2669  LOC153592 3'  TCAGGACCTGGGACGGTGTGA  14160         CA   TCTTA
                                TCAGGACCTG  GAC    GTGA
                                ||||||||||  |||    ||||
                                AGTCCTGGAC  CTG    CACT
                                    C_   CCA__
GAM2669  LOC203504 3'  TCAGGACCTGGGTCCAGTG    14162         CAGAC   T
                                TCAGGACCTG    TCT AGTG
                                ||||||||||    ||| ||||
                                AGTCCTGGAC    AGG TCAC
                                    CC___   _
GAM2669  LOC254268 3'  CCAGGACCTGCAGCGGTG     14163           ACTCTTA
                                TCAGGACCTGCAG      GTG
                                ||||||||||||       |||
                                GGTCCTGGACGTC      CAC
                                     GC_____
GAM2669  LOC256447 5'  TCAGCACCTGTGGGTTCCCAG  62284      G    CAGAC
                                TCAG ACCTG    TCTTAG
                                |||| |||||    ||||||
                                AGTC TGGAC    AGGGTC
                                  G    ACCCA
GAM2670  SHOX     3'  TATGATCGCACCAGT       62287         A AATAGA
                                TATGATCG C     GCCAGT
                                |||||||| |     ||||||
                                ATACTAGC G     TGGTCA
                                    _ _______
GAM2670  FLJ11088  3'  TATGATTTATCCAATGCCAGTG 62288       CGA__   AGA
           T                    TATGAT    CAAT   GCCAGTGT
                                ||||||    ||||   ||||||||
                                ATACTA    GTTA   CGGTCACA
                                   AATAG   ___
GAM2670  LOC203245 3'  TGGTCACAATAGAGGAGT    62289    A  G       CC
                                TG TC ACAATAGAG  AGT
                                || || |||||||||  |||
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                                AC AG TGTTATCTC  TCA
                                 C  _       C_
GAM2670  LOC91974  5'  ATCGGTGGCAATAGAGCTGGTG 62290      A___       CA
             T                   ATCG   CAATAGAGC  GTGT
                                 ||||   |||||||||  ||||
                                 TAGC   GTTATCTCG  CACA
                                   CACC       AC
GAM2671  PRKAG2   3'  AGACTTTGTTCAAGTTCTAGAG 62293       AT__________   AAA
             TTTCTC                TTTGTT        GGAG   CTC
                                 ||||||        ||||  |||
                                 AAACAA        TCTC   GAG
                                    GTTCAAGAIII   AAA
GAM2671  SPG4     3'  TAGATTTATGAAGAAGAAACTC 62294      C     TAT
             T                   TAGA TTTGT   GGAGAAACTCT
                                 |||| |||||  ||||||||||
                                 ATCT AAATA   CTTCTTTGAGA
                                   _    CTT
GAM2671  CG018    3'  GACTTTGCTCAGAAACT     62295         ATGG
                                 GACTTTGTT    AGAAACT
                                 |||||||||    |||||||
                                 CTGAAACGA    TCTTTGA
                                      G___
GAM2671  HSPC228  3'  TAGGCTTGTTTCAAAGAAACT  62296     A   T   A GG
                                 TAG CTT GTT T  AGAAACT
                                 ||| ||| ||| |  |||||||
                                 ATC GAA CAA G  TCTTTGA
                                   C  _   A TT
GAM2671  KIAA1026 3'  TAGACTTTGTCACTAGGA    62297           __
                                 TAGACTTTGTTAT  GGA
                                 ||||||||||||  |||
                                 ATCTGAAACAGTG  CCT
                                        AT
GAM2671  KIAA1040 3'  TAGACTTTTTTATGCCTTTAGA 62298     G    __________   AAA
             GTTTCTC               TTT TTATG       GAG   CTC
                                 |||  |||||       |||   |||
                                 AAA AATAC       CTC   GAG
                                   A    GGAAAIIIT   AAA
GAM2671  SV2B     3'  GACTCTGTTTCAAAAGCTCT   62299        AT_   AAA
                                 GACTTTGTT   GGAG   CTCT
                                 |||||||||   ||||   ||||
                                 CTGAGACAA   TTTC   GAGA
                                      AGT   ___
GAM2671  LOC145609 5'  GACCGATGGAGAAGCTC     62300      TTGTT      A
                                 GACT    ATGGAGAA CTC
                                 ||||    |||||||| |||
                                 CTGG    TACCTCTT GAG
                                   C____       C
GAM2671  LOC200225 5'  GACTTTGCCCTGGGGACTCT   62301        TA   A  AA
                                 GACTTTGT  TGG GA  CTCT
                                 ||||||||  ||| ||  ||||
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                                CTGAAACG  ACC CT  GAGA
                                    GG   C  __
GAM2672  DIO1     3'  ACCGTGTGCAGGGAATGT    62304      C  T  T
                                ACCG GT GT GGGAATGT
                                |||| || || ||||||||
                                TGGC CA CG CCCTTACA
                                  A  _  T
GAM2672  FCMD     3'  TACCTGTTAGAAGGTGGGAATG 62305      GC    T____
              T                  TACC  GTTG    TGGGAATGT
                                ||||  ||||    |||||||||
                                ATGG  CAAT    ACCCTTACA
                                  A_    CTTCC
GAM2672  LASS1    3'  CACCGCGGTCCGGGATGT    62306        TTG     A
                                TACCGCG   TTGGGA TGT
                                |||||||   |||||| |||
                                GTGGCGC   GGCCCT ACA
                                    CA_     _
GAM2672  FLJ20485 3'  GCTGTCTTTTGAGAATGT    62307    _   G_
                                GC GTT  TTGGGAATGT
                                || |||  ||||||||||
                                CG CAG  AACTCTTACA
                                 A   AA
GAM2672  KIAA0319 3'  GCTTTGTGGGTGGGAATGT    62308    G    ___
                                GC TTGT   TGGGAATGT
                                || ||||   |||||||||
                                CG AACA   ACCCTTACA
                                 A    CCC
GAM2672  KIAA0451 3'  CACTAAGTGTGTTGGGGGTGT  62309     ___  _      AA
                                CGC   GT TGTTGGG  TGT
                                |||   || |||||||  |||
                                GTG   CA ACAACCC  ACA
                                  ATT  C      CC
GAM2672  KIAA1243 3'  TACTCATCATGGGAATGT    62310     CG   TG T
                                TAC  CGT  T GGGAATGT
                                |||  |||  | ||||||||
                                ATG  GTA  A CCCTTACA
                                  A_   GT _
GAM2672  KIAA1751 3'  CACTGTTGGTGGGAGTGT    62311     _   T    A
                                CGC GTTG TGGGA TGT
                                ||| |||| ||||| |||
                                GTG CAAC ACCCT ACA
                                  A   C    C
GAM2672  RP4-622L5 3'  CCTGCTGTTGTTGGGGATGT   62312    _ _       A
                                CC GC GTTGTTGGG ATGT
                                || || ||||||||| ||||
                                GG CG CAACAACCC TACA
                                 A  A        C
GAM2672  SIMRP7   3'  CCGCGTTGGCCAGGAGGATGT  62313         _ TG   __
                                CCGCGTTG T  GGA  ATGT
                                |||||||| |  |||  ||||
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                                GGCGCAAC G  CCT  TACA
                                    C GT   CC
GAM2672  Spir-1   5'  CACCGTGTTGGCCATGT    62314      CGT     GA
                                TACCG   TGTTGG  ATGT
                                |||||   ||||||  ||||
                                GTGGC   ACAACC  TACA
                                  ___     GG
GAM2672  LOC138307 5'  GCGCCCACCCGGGAATGT    62315      G__
                                GCGTT   TTGGGAATGT
                                |||||   ||||||||||
                                CGCGG   GGCCCTTACA
                                  GTG
GAM2672  LOC146745 5'  CCACGTTGATGCCAATGT    62316        T  GG
                                CCGCGTTG TG  AATGT
                                |||||||| ||  |||||
                                GGTGCAAC AC  TTACA
                                     T  GG
GAM2672  LOC147694 3'  CACTGCTGGTGGGAATGT    62317     _    T
                                CGC GTTG TGGGAATGT
                                ||| |||| |||||||||
                                GTG CGAC ACCCTTACA
                                  A   C
GAM2672  LOC157807 5'  GCCTTGCTTTGGGAATGT    62318    G    __
                                GC TTGT  TGGGAATGT
                                || ||||  |||||||||
                                CG AACG  ACCCTTACA
                                 G   AA
GAM2672  LOC197053 3'  GCATTGTAATTGGGAATGT    62319        ___
                                GCGTTGT   TGGGAATGT
                                |||||||   |||||||||
                                CGTAACA   ACCCTTACA
                                    TTA
GAM2672  LOC201243 5'  CCACGTTGATGCCAATGT    62316        T  GG
                                CCGCGTTG TG  AATGT
                                |||||||| ||  |||||
                                GGTGCAAC AC  TTACA
                                     T  GG
GAM2672  LOC205069 5'  GCTGAGGCCGTGGGGAATGT   62320    ____    T
                                GC    GTTGT GGGAATGT
                                ||    ||||| |||||||||
                                CG    CGGCA CCCTTACA
                                 ACTC    C
GAM2672  LOC205669 5'  GCTGTGGTGCAGGAATGT    62321    _ T _
                                GC GT GT TGGGAATGT
                                || || || |||||||||
                                CG CA CA GTCCTTACA
                                 A  C  C
GAM2672  LOC91145  3'  GCCCTGTCCAGGGAATGT    62322    G    __
                                GC TTGTT  GGGAATGT
                                || |||||  ||||||||
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                                CG GACAG  CCCTTACA
                                 G    GT
GAM2673  NAPB     3'  GTAGGATATATTATTA     62325     TATA
                                GTAG   GATATATTATTA
                                ||||   ||||||||||||
                                CATC   CTATATAATAAT
                                  ____
GAM2674  ICK      3'  TGATATAAAATAATTAGTAT  62328      AT  T
                                TGATA  TAG ATAATTAGTAT
                                |||||  ||| ||||||||||
                                ACTAT  ATT TATTAATCATA
                                   __  T
GAM2674  SLC11A2  3'  TTGATAATTTGGTATAATTA  62329        A_
                                TTGATAATT  GTATAATTA
                                |||||||||  |||||||||
                                AACTATTAA  CATATTAAT
                                      AC
GAM2674  LOC158576 3'  TTGATAATGAGTATCATTA   62330        T    A
                                TTGATAAT AGTAT ATTA
                                |||||||| ||||| ||||
                                AACTATTA TCATA TAAT
                                     C    G
GAM2675  HNRPD    3'  GCTACATAAGGAAGTATTATT  62333    A      TGTA
                                GC TACATAAG   TATTATT
                                || ||||||||   |||||||
                                CG ATGTATTC   ATAATAA
                                 _      CTTC
GAM2675  HNRPD    3'  GCTACATAAGGAAGTATTATT  62333    A      TGTA
                                GC TACATAAG   TATTATT
                                || ||||||||   |||||||
                                CG ATGTATTC   ATAATAA
                                 _      CTTC
GAM2675  C20orf7  3'  TACATATGTGAACATTAT    62334       A  T
                                TACATA GTG ATATTAT
                                ||||||| ||| |||||||
                                ATGTAT CAC TGTAATA
                                   A  T
GAM2675  DIO2     3'  AGCATATGACAAATATAT    62335       C_
                                AGCATA  ATAAGTGTAT
                                ||||||  ||||||||||
                                TCGTAT  TGTTTATATA
                                   AC
GAM2675  DIO2     3'  AGCATATGACAAATATAT    62335       C_
                                AGCATA  ATAAGTGTAT
                                ||||||  ||||||||||
                                TCGTAT  TGTTTATATA
                                   AC
GAM2675  FKBP14   3'  GCATACATATTTATATGTTATT 62336         AG    A
                                GCATACATA  TGTAT TTATT
                                |||||||||  ||||| |||||
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                                CGTATGTAT  ATATA AATAA
                                     AA    C
GAM2675  GDAP2    3'  AGCATACATTGGTTCTGTATAT 62337        AAG___
              T                   AGCATACAT     TGTATATT
                                  |||||||||     ||||||||
                                  TCGTATGTA     ACATATAA
                                     ACCAAG
GAM2675  UBE1C    3'  AGCATCCACAAAGTATATTATT 62338      A     T
                                  AGCAT CATAAG GTATATTATT
                                  ||||| |||||| ||||||||||
                                  TCGTA GTGTTT CATATAATAA
                                    G     _
GAM2675  VDU1     3'  AGCAGTGCATACTAT       62339      TACATAA
                                  AGCA      GTGTATATTAT
                                  ||||      ||||||||||||
                                  TCGT      CACGTATGATA
                                   ________
GAM2675  LOC219333 3'  ATACATATACTGTATATTATT  62340       AG_
                                  ATACATA   TGTATATTATT
                                  |||||||   ||||||||||||
                                  TATGTAT   ACATATAATAA
                                     ATG
GAM2675  LOC219401 3'  CATTATACATAAGTCATATT   62341    GC        G
                                  CA  ATACATAAGT TATATT
                                  ||  |||||||||| ||||||
                                  GT  TATGTATTCA GTATAA
                                   AA         _
GAM2675  LOC254700 3'  ATACATATACTGTATATTATT  62340       AG_
                                  ATACATA   TGTATATTATT
                                  |||||||   ||||||||||||
                                  TATGTAT   ACATATAATAA
                                     ATG
GAM2676  ADRBK1   3'  AGCAGCACCTGCTGCCA     62344       AGGA  G   C
                                  AGCAGC    GC TGC GCCA
                                  ||||||    || ||| ||||
                                  TCGTCG    TG ACG CGGT
                                     ____  G   A
GAM2676  BAI2     5'  TCAGCAGCAGGAGCGGGGGCCG 62345             T__
                                  TCAGCAGCAGGAGCG   GCCG
                                  ||||||||||||||||   ||||
                                  AGTCGTCGTCCTCGC   CGGC
                                           CCC
GAM2676  BCL9     5'  GCAGCAGAAACAGCTGC     62346           T  C
                                  GCAGCAGGAGCG GC GC
                                  |||||||||||| || ||
                                  CGTCGTCTTTGT CG CG
                                           _  A
GAM2676  CRYGS    3'  CAGCAGTGGGATGCATGCCA  62347       CA  _
                                  CAGCAG  GGA GCGTGCCG
                                  ||||||  ||| ||||||||
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                                GTCGTC  CCT CGTACGGT
                                   AC   A
GAM2676  EGFL4    3'  TCAGCAGCAGGGGTGCCA    62348          AGC
                                TCAGCAGCAGG   GTGCCG
                                ||||||||||   ||||||
                                AGTCGTCGTCC   CACGGT
                                      C__
GAM2676  EVA1     3'  AGTAGCAGAAGTGCTGC     62349    C     GC   C
                                AG AGCAGGA  GTGC GC
                                || |||||||  |||| ||
                                TC TCGTCTT  CACG CG
                                 A      __   A
GAM2676  FACL6    5'  TCAGCAGCGGGGCACTGCC   62350        A  A  _
                                TCAGCAGC GG GCG TGCC
                                |||||||| || ||| ||||
                                AGTCGTCG CC CGT ACGG
                                     C  _  G
GAM2676  FGFR3    3'  CCAGCAGCAGGGAGGGCTGC  62351          _  CGT  C
                                TCAGCAGCAGG AG   GC GC
                                |||||||||| ||   || ||
                                GGTCGTCGTCC TC   CG CG
                                      C  C__  A
GAM2676  FSTL3    3'  CAGCAGCAGGGGAGACGC    62352        __   _
                                CAGCAGCA  GGAG CGT
                                ||||||||  |||| |||
                                GTCGTCGT  CCTC GCG
                                     CC    T
GAM2676  HSD17B8  3'  TCATCAGCAGGAGGCCA     62353     G       CGT
                                TCA CAGCAGGAG   GCCG
                                ||| |||||||||   ||||
                                AGT GTCGTCCTC   CGGT
                                  A       ____
GAM2676  IHPK1    3'  CCAGCAGCAGCACAGCTGCCG  62354         G__   G
                                TCAGCAGCAG   AGC TGCCG
                                ||||||||||   ||| |||||
                                GGTCGTCGTC   TCG ACGGC
                                      GTG   _
GAM2676  LDB3     3'  CCAGCAGCAGGAGCAGCTCCG  62355           _  G
                                TCAGCAGCAGGAGC GT CCG
                                |||||||||||||| || |||
                                GGTCGTCGTCCTCG CG GGC
                                         T  A
GAM2676  MADH7    5'  CAGCAGCAGGGGCCCG       62356         A  GTG
                                CAGCAGCAGG GC   CCG
                                |||||||||| ||   |||
                                GTCGTCGTCC CG   GGC
                                      C  ____
GAM2676  MAK      3'  TCAGCAGCATGAGCTGGC     62357         G   GT
                                TCAGCAGCA GAGC  GC
                                |||||||| ||||  ||
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                                AGTCGTCGT CTCG  CG
                                     A    AC
GAM2676 MAPK8IP1 3' TCAGTGGCAGGAGCCACC    62358     CA     GCGT
                                TCAG  GCAGGA    GCCGCC
                                ||||  ||||||    ||||||
                                AGTC  CGTCCT    CGGTGG
                                  AC     ____
GAM2676 MEN1     3' TCAGCACAGGAGCAGAGGCC   62359       G      T__
                                TCAGCA CAGGAGCG   GCC
                                |||||| ||||||||   |||
                                AGTCGT GTCCTCGT   CGG
                                   _       CTC
GAM2676 NDUFS8   3' GCAGCAGGGGCTGCAGGCC   62360         A  G   C_
                                GCAGCAGG GC TGC  GCC
                                |||||||| || |||  |||
                                CGTCGTCC CG ACG  CGG
                                     C  _   TC
GAM2676 NRXN3    5' TCATAGCAGGAGGAAGAGTTGC 62361     GC       CG_____
              CA                  TCA  AGCAGGAG      TGCCG
                                ||| ||||||||      |||||
                                AGT  TCGTCCTC      ACGGT
                                  A_       CTTCTCA
GAM2676 PAM      5' GCAGCGGCGCCGCCA       62362       A  AGCG
                                GCAGC GG    TGCCGCCA
                                ||||| ||    ||||||||
                                CGTCG CC    GCGGCGGT
                                  _ ____
GAM2676 PAM      5' GCAGCGGCGCCGCCA       62362       A  AGCG
                                GCAGC GG    TGCCGCCA
                                ||||| ||    ||||||||
                                CGTCG CC    GCGGCGGT
                                  _ ____
GAM2676 PAM      5' GCAGCGGCGCCGCCA       62362       A  AGCG
                                GCAGC GG    TGCCGCCA
                                ||||| ||    ||||||||
                                CGTCG CC    GCGGCGGT
                                  _ ____
GAM2676 POLS     3' TCAGCGGCGGGCGTGCCGC    62363      A  A  A
                                TCAGC GC GG GCGTGCCGC
                                ||||| || || |||||||||
                                AGTCG CG CC CGCACGGCG
                                   C  _  _
GAM2676 PPP1R8   3' CAGCAGGAGGAGTGCTCA    62364         C_   _
                                CAGCAGGAG  GTGC CG
                                |||||||||  |||| ||
                                GTCGTCCTC  CACG GT
                                     CT    A
GAM2676 PPP1R8   3' CAGCAGGAGGAGTGCTCA    62364         C_   _
                                CAGCAGGAG  GTGC CG
                                |||||||||  |||| ||
```

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                                GTCGTCCTC  CACG GT
                                     CT    A
GAM2676  PPP1R8   3'  CAGCAGGAGGAGTGCTCA    62364         C_   _
                                CAGCAGGAG  GTGC CG
                                |||||||||  |||| ||
                                GTCGTCCTC  CACG GT
                                     CT    A
GAM2676  PRG2     5'  GCAGCAAGGAGTTGAGAGTGCC 62365       _   C_____
           A                     GCAGCA GGAG     GTGCCG
                                |||||| ||||     ||||||
                                CGTCGT CCTC     CACGGT
                                   T    AACTCT
GAM2676  RAB23    5'  TCAGCAGCAGCTCCGCC     62366          GAGCGTG
                                TCAGCAGCAG      CCGCC
                                ||||||||||      |||||
                                AGTCGTCGTC      GGCGG
                                     GA_____
GAM2676  REPS2    5'  TCAGCAGCAGCGGCGGCGGCC  62367          GA   T  C
                                TCAGCAGCAG  GCG GC GCC
                                ||||||||||  ||| || |||
                                AGTCGTCGTC  CGC CG CGG
                                     GC   _  C
GAM2676  RERE     5'  TCAGAAGCAGGAGCCCA     62368      C       GTG
                                TCAG AGCAGGAGC   CCG
                                ||||  |||||||||   |||
                                AGTC TCGTCCTCG   GGT
                                  T       ___
GAM2676  RPS20    5'  TCAGGAGCAGGAGCGTGC     62369      C
                                TCAG AGCAGGAGCGTGC
                                ||||  ||||||||||||
                                AGTC TCGTCCTCGCACG
                                  C
GAM2676  TFAP2A   3'  CAGCAGCAGGAAGGGTTGC    62370          CG__
                                CAGCAGCAGGAG    TGC
                                ||||||||||||    |||
                                GTCGTCGTCCTT    ACG
                                      CCCA
GAM2676  TNFSF9   3'  TCAGCAGCAGGGACCCCTGCCA 62371          AG GTG  _
           A                     TCAGCAGCAGG  C   CC GCCAA
                                ||||||||||  |   || |||||
                                AGTCGTCGTCC  G   GG CGGTT
                                     CT G__  A
GAM2676  TRPM7    5'  GCAGCAGAGGCCGCC       62372        G  CGT
                                GCAGCAG AG   GCCGCC
                                |||||||  ||   ||||||
                                CGTCGTC TC   CGGCGG
                                   _  ___
GAM2676  TYRO3    3'  AGCAGCAGGGGCAGCTCA    62373          A   T  _
                                AGCAGCAGG GCG GC CG
                                ||||||||| ||| || ||
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                                TCGTCGTCC CGT CG GT
                                     C  _ A
GAM2676 ARFGAP3  3' TCAGGAGCAGGAGGAGCCG  62374     C      CGT
                                TCAG AGCAGGAG  GCCG
                                |||| ||||||||  ||||
                                AGTC TCGTCCTC  CGGC
                                  C       CT_
GAM2676 ARL8     5' TCGGCAGCAGGTGCCGCTGCGC 62375    A      A  G  __
             C                   TC GCAGCAGG GC TGC  CGCC
                                || ||||||| || |||  ||||
                                AG CGTCGTCC CG GCG  GCGG
                                 C       A  _  AC
GAM2676 BRAP     5' TCAGCAGCAGCAGCTCC     62376          G  GTG
                                TCAGCAGCAG AGC  CC
                                |||||||||| |||  ||
                                AGTCGTCGTC TCG  GG
                                      G  A__
GAM2676 C21orf25 3' GCAGCAGGGTTTACGCCA    62377        AGCG  C
                                GCAGCAGG   TGC GCCA
                                ||||||||   ||| ||||
                                CGTCGTCC   ATG CGGT
                                     CAA_  _
GAM2676 COX4I2   5' TCGGCAGTGGGAGCGCGACC  62378    A   CA      _
                                TC GCAG  GGAGCGTG CC
                                || ||||  |||||||| ||
                                AG CGTC  CCTCGCGC GG
                                 C   AC       T
GAM2676 CPR2     3' CAGCAGCAGGGAGGCTGCCA  62379         _ CGT  C
                                CAGCAGCAGG AG  GC GCCA
                                |||||||||| ||  || ||||
                                GTCGTCGTCC TC  CG CGGT
                                      C  ___  A
GAM2676 CPSF2    3' GCAGCAGGAAGAAGTGCCA   62380         C__
                                GCAGCAGGAG  GTGCCG
                                ||||||||||  ||||||
                                CGTCGTCCTT  CACGGT
                                      CTT
GAM2676 DKFZP564I1171 5' TCAGCAGCGCGGGGCGGC    62381        A_  A  T
                                TCAGCAGC  GG GCG GC
                                ||||||||  || ||| ||
                                AGTCGTCG  CC CGC CG
                                     CG  C  _
GAM2676 DLAT     5' GCAGCGGCGTTGCCGTCA    62382      AGGA  _  C
                                GCAGC   GCGT GCCG CA
                                |||||   |||| |||| ||
                                CGTCG   CGCA CGGC GT
                                  C___   A  A
GAM2676 DZIP1    5' TCAGGAGCGGGAGAAGGCCG  62383     C  A   CGT
                                TCAG AGC GGAG  GCCG
                                |||| ||| ||||  ||||
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                                AGTC TCG CCTC   CGGC
                                  C   C    TTC
GAM2676 EPB41L1   3' TCAGCAGCAGAGTCCCA     62384          AGC  G
                                TCAGCAGCAGG   GT CCG
                                ||||||||||   || |||
                                AGTCGTCGTCT   CA GGT
                                      ___  G
GAM2676 FLJ12057  3' TCAGGAGCAGGGGCTCCA    62385     C     A  GTG
                                TCAG AGCAGG GC   CCG
                                |||| |||||| ||   |||
                                AGTC TCGTCC CG   GGT
                                  C     C  A__
GAM2676 FLJ20288  5' CAGCACGGCAGCCGCCA     62386      GGA   T
                                CAGCA   GCG GCCGCCA
                                |||||   ||| |||||||
                                GTCGT   CGT CGGCGGT
                                   GC_  _
GAM2676 FLJ20548  3' AGCAGAAGTCATGGTCGC    62387        _   C_
                                AGCAGGAG CGTG  CGC
                                |||||||| ||||  |||
                                TCGTCTTC GTAC  GCG
                                     A   CA
GAM2676 FLJ22596  5' TCAGCGTGGGATTACCGCCAA 62388      AGCA   GCG
                                TCAGC   GGA   TGCCGCCAA
                                |||||   |||   |||||||||
                                AGTCG   CCT   ATGGCGGTT
                                   CAC_  A__
GAM2676 FLJ23537  3' CAGCAGCAGGGGGGCAGAGC   62389        A_   T_
                                CAGCAGCAGG  GCG  GC
                                ||||||||||  |||  ||
                                GTCGTCGTCC  CGT  CG
                                      CC   CT
GAM2676 FLJ23537  3' CAGCAGCAGGGGGGCAGAGC   62389        A_   T_
                                CAGCAGCAGG  GCG  GC
                                ||||||||||  |||  ||
                                GTCGTCGTCC  CGT  CG
                                      CC   CT
GAM2676 FLJ25082  5' GCAGCAGGCGCCCCCCAA    62390       GA   G  G
                                GCAGCAG  GCGT CC CCAA
                                |||||||  |||| || ||||
                                CGTCGTC  CGCG GG GGTT
                                   __    G  _
GAM2676 GPR88     5' TCAGAAGCAGGAGTGGTGGC   62391     C      C_   CC
                                TCAG AGCAGGAG  GTG  GC
                                |||| ||||||||  |||  ||
                                AGTC TCGTCCTC  CAC  CG
                                  T       AC   __
GAM2676 HSD-3.1   5' CAGCAGCAGGGAAACCGTCGCC 62392          __   G  C
            A                    CAGCAGCAGG  AGC TG CGCCA
                                ||||||||||  ||| || |||||
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                                GTCGTCGTCC  TTG GC GCGGT
                                      CT   _  A
GAM2676 KIAA0494 3' CAGCAGTAGGAGCTGCCA    62393       C     G
                                CAGCAG AGGAGC TGCCG
                                |||||| |||||| |||||
                                GTCGTC TCCTCG ACGGT
                                   A     _
GAM2676 KIAA0775 5' CCGGCAGCAGGGGCAGGCTCCT 62394    A      A   TG__  _
           GCCA                    TC GCAGCAGG GCG    CC GCCA
                                || |||||||| |||    || ||||
                                GG CGTCGTCC CGT    GG CGGT
                                 C       C   CCGA  A
GAM2676 KIAA1026 3' CCAGCAGCATTTCTGCTGCCA  62395         GGAGCG   C
                                TCAGCAGCA     TGC GCCA
                                |||||||||      ||| ||||
                                GGTCGTCGT     ACG CGGT
                                      AAAG__   A
GAM2676 KIAA1163 5' TCAGCAGCAGGGAGTGC     62396          AGC
                                TCAGCAGCAGG   GTGC
                                ||||||||||   ||||
                                AGTCGTCGTCC   CACG
                                       CT_
GAM2676 KIAA1822 3' CCAGCAGCGGGGGCACCTGCCA 62397        A  A  GT   _
                                TCAGCAGC GG GC  GCC GCCA
                                |||||||| || ||  ||| ||||
                                GGTCGTCG CC CG  TGG CGGT
                                     C  C  __   A
GAM2676 LGALS8   5' TCAGCAGCTAAGTGCCGTCA   62398        AG AGC     C
                                TCAGCAGC  G   GTGCCG CA
                                ||||||||  |   |||||| ||
                                AGTCGTCG  T   CACGGC GT
                                     AT ____     A
GAM2676 MCPR     3' TCAGGGTAGGTTCACCGCCA   62399     CAGC   AGCG
                                TCAG    AGG    TGCCGCCA
                                ||||    |||    ||||||||
                                AGTC    TCC    GTGGCGGT
                                  CCA_   AA__
GAM2676 MGC18079 3' GCAGCAGGGGCTGGTGCCA    62400        A  __
                                GCAGCAGG GC  GTGCCG
                                |||||||| ||  ||||||
                                CGTCGTCC CG  CACGGT
                                     C  AC
GAM2676 MGC2835  3' CAGCAGCAGCTGAGTTGCCA   62401         __  CG
                                CAGCAGCAG  GAG  TGCCG
                                |||||||||  |||  |||||
                                GTCGTCGTC  CTC  ACGGT
                                     GA   A_
GAM2676 MLN64    5' TCAGCAGCAGGGCTGCTCCA   62402          A  G   CG
                                TCAGCAGCAGG GC TGC  CCA
                                |||||||||| || |||  |||
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                                AGTCGTCGTCC CG ACG  GGT
                                      _ _  A_
GAM2676  NISCH    3'  AGCAGCAAGATGCCA      62403         GCG
                                AGCAGCAGGA  TGCCG
                                ||||||||||  |||||
                                TCGTCGTTCT  ACGGT
                                     ____
GAM2676  OASIS    3'  CAGCAGCAGGGGGGTGCCA   62404         AGC
                                CAGCAGCAGG  GTGCCG
                                ||||||||||  ||||||
                                GTCGTCGTCC  CACGGT
                                      CCC
GAM2676  PAPSS2   5'  CAGCAGCAGCAGCGGCTGCC  62405        G   T  C
                                CAGCAGCAG AGCG GC GCC
                                ||||||||| |||| || |||
                                GTCGTCGTC TCGC CG CGG
                                     G   _ A
GAM2676  SIMRP7   3'  GCAGCAGGAGCAGCAGCCA   62406          T  C
                                GCAGCAGGAGCG GC GCCA
                                |||||||||||| || ||||
                                CGTCGTCCTCGT CG CGGT
                                      _ T
GAM2676  SSH2     3'  TCATAGCAGGAGCCAGGGCCA 62407     GC       GTGCC
                                TCA  AGCAGGAGC    GCCA
                                |||  |||||||||    ||||
                                AGT  TCGTCCTCG    CGGT
                                  A_       GTCC_
GAM2676  TIGA1    5'  CAGCGGCAGGAGCCCA     62408      A      GTG
                                CAGC GCAGGAGC  CCG
                                |||| ||||||||  |||
                                GTCG CGTCCTCG  GGT
                                  C      ____
GAM2676  LOC129563 3'  TCAGCAGCGAGGGGTGAAGCC  62409        _  AGC  CC
                                TCAGCAGC AGG  GTG  GCC
                                |||||||| |||  |||  |||
                                AGTCGTCG TCC  CAC  CGG
                                     C  C__  TT
GAM2676  LOC146774 3'  TCAGCAGCAGCAGCAGCCGCC  62410         G   T
                                TCAGCAGCAG AGCG GCCGCC
                                |||||||||| |||| ||||||
                                AGTCGTCGTC TCGT CGGCGG
                                      G   _
GAM2676  LOC147804 5'  TCAGCAACGGGACTCTGCCA  62411        A  AG G_
                                TCAGCAGC GG  C  TGCCG
                                |||||||| ||  |  |||||
                                AGTCGTTG CC  G  ACGGT
                                     _ CT AG
GAM2676  LOC148894 3'  AGCAGCAGATGTTGGTGCTGC  62412         AGC__   C
                                AGCAGCAGG    GTGC GC
                                |||||||||    |||| ||
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                                TCGTCGTCT    CACG CG
                                     ACAAC   A
GAM2676  LOC150319 3'  TCAGCAGCAAGAATGC      62413          GC
                                TCAGCAGCAGGA  GTGC
                                ||||||||||||  ||||
                                AGTCGTCGTTCT  TACG
                                      __
GAM2676  LOC153346 5'  TCAGCAGCTGGGCTGCCA    62414        A  A  G
                                TCAGCAGC GG GC TGCCG
                                |||||||| || || |||||
                                AGTCGTCG CC CG ACGGT
                                     A  _  _
GAM2676  LOC153474 5'  TCAGCAGCGCGGGGCGGC    62381         A_  A   T
                                TCAGCAGC  GG GCG GC
                                ||||||||  || ||| ||
                                AGTCGTCG  CC CGC CG
                                     CG  C   _
GAM2676  LOC155100 5'  CAGCAGCAGGGGCACC      62415         A  GT
                                CAGCAGCAGG GC  GCC
                                ||||||||||  ||  |||
                                GTCGTCGTCC CG  TGG
                                      C  __
GAM2676  LOC158046 3'  CCAGCAGCAGGATTGC      62416          GCG
                                TCAGCAGCAGGA   TGC
                                ||||||||||||   |||
                                GGTCGTCGTCCT   ACG
                                       A__
GAM2676  LOC163412 5'  TCAGCAGCGGGGTGGGCTCA  62417        A  AGC   CC  _
                                TCAGCAGC GG   GTG  GC CA
                                ||||||||  ||   |||  || ||
                                AGTCGTCG CC   CAC  CG GT
                                     C  ____   C_  A
GAM2676  LOC164121 5'  CCAGCAGCAGGGGCAGCC    62418          A   T
                                TCAGCAGCAGG GCG GCC
                                ||||||||||| ||| |||
                                GGTCGTCGTCC CGT CGG
                                       C  _
GAM2676  LOC197342 3'  TCAGCACAGGAACCGCCA    62419       G    GCGT
                                TCAGCA CAGGA    GCCGCCA
                                ||||||  |||||    |||||||
                                AGTCGT GTCCT    TGGCGGT
                                     _    _____
GAM2676  LOC199676 3'  AGTAGCAGGAGCCCCC      62420    C       GTG  G
                                AG AGCAGGAGC   CC CC
                                ||  |||||||||   || ||
                                TC TCGTCCTCG   GG GG
                                 A        ____  _
GAM2676  LOC201475 5'  TCAGCAACAGGAATGC      62421          GC
                                TCAGCAGCAGGA  GTGC
                                ||||||||||||  ||||
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                                AGTCGTTGTCCT  TACG
                                      __
GAM2676  LOC221122 3'  CCAGCAGCAGGGGTGACA    62422          AGC   C
                                TCAGCAGCAGG   GTG CG
                                ||||||||||   ||| ||
                                GGTCGTCGTCC   CAC GT
                                    C__   T
GAM2676  LOC222178 3'  ACAGCAGGAGACGCCA      62423         CGTGC
                                GCAGCAGGAG    CGCCA
                                ||||||||||    |||||
                                TGTCGTCCTC    GCGGT
                                    T_____
GAM2676  LOC255215 3'  TCAGCAGCAGGAGGCCCA    62424           C  G
                                TCAGCAGCAGGAG GT CCG
                                |||||||||||| || |||
                                AGTCGTCGTCCTC CG GGT
                                      _ _
GAM2676  LOC255536 3'  TCAGCAGCAGGGCGGCGGCC   62425          A   T  C
                                TCAGCAGCAGG GCG GC GCC
                                |||||||||| ||| || |||
                                AGTCGTCGTCC CGC CG CGG
                                      _  _ C
GAM2676  LOC257054 3'  CAGCAGCAGGAGTGGCCGTCA  62426           CGT    C
                                CAGCAGCAGGAG   GCCG CA
                                ||||||||||   |||| ||
                                GTCGTCGTCCTC   CGGC GT
                                    AC_   A
GAM2676  LOC257476 3'  CCAGCAGCAGCACAGCTGCCG  62354         G__   G
                                TCAGCAGCAG   AGC TGCCG
                                ||||||||||   ||| |||||
                                GGTCGTCGTC   TCG ACGGC
                                    GTG  _
GAM2676  LOC93259  5'  TCAGCAGGAGGGGCACACCCC  62427       C   A   TG  G
                                TCAGCAG AGG GCG  CC CC
                                ||||||| ||| |||  || ||
                                AGTCGTC TCC CGT  GG GG
                                   C   C   GT  _
GAM2677  APPBP2    3'  GGAACCCGGGAGGCGGA     62430        ACCA
                                GGAACCC    GAGGCGGA
                                |||||||    ||||||||
                                CCTTGGG    CTCCGCCT
                                   CC__
GAM2677  ARCN1     3'  GAACCCAGGAGGCGGA      62431        CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                   C__
GAM2677  ATP6V0E   5'  CGGATCCCACCAGGAAGTGCTT 62432    A      A ________  GGAA
            CG                   GA CCCACCAG G      GC    G
                                || |||||||| |      ||    |
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                                CT GGGTGGTC C      CG    C
                                 A       _ TTCAIII  AAGG
GAM2677  BAP1     3'  GGGCCCACCAGGACAG      62433    AA       A
                                GG  CCCACCAG GGCGG
                                ||  |||||||| |||||
                                CC  GGGTGGTC CTGTC
                                 C_       _
GAM2677  CRTAP    3'  GAACCCAAGAGGCGGA      62434        CC
                                GAACCCA  AGAGGCGGA
                                |||||||  |||||||||
                                CTTGGGT  TCTCCGCCT
                                   __
GAM2677  CYP4F3   3'  CCCGAACGCAGGAGGCGGA   62435    G    C  CCA
                                CC GAAC CA   GAGGCGGA
                                || |||| ||   ||||||||
                                GG CTTG GT   CTCCGCCT
                                 G    C  C__
GAM2677  DSCR1L2  3'  CCAGAGCCCACCAGGGCAG   62436       A       A
                                CCGGA CCCACCAG GGCGG
                                ||||| |||||||| |||||
                                GGTCT GGGTGGTC CCGTC
                                   C       _
GAM2677  EPB72    3'  GAACCCAGGAGGCGGA      62431        CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2677  FBXW1B   5'  CGGAGGCGGGCAGAGGCGGAGG 62437      ACCCAC        A
            C                    CGGA      CAGAGGCGGA GC
                                ||||      |||||||||| ||
                                GCCT      GTCTCCGCCT CG
                                  CCGCCC         C
GAM2677  FBXW1B   5'  CGGAGGCGGGCAGAGGCGGAGG 62437      ACCCAC        A
            C                    CGGA      CAGAGGCGGA GC
                                ||||      |||||||||| ||
                                GCCT      GTCTCCGCCT CG
                                  CCGCCC         C
GAM2677  FBXW1B   5'  CGGAGGCGGGCAGAGGCGGAGG 62437      ACCCAC        A
            C                    CGGA      CAGAGGCGGA GC
                                ||||      |||||||||| ||
                                GCCT      GTCTCCGCCT CG
                                  CCGCCC         C
GAM2677  FUT1     3'  GAACACAGGAGGCGGAAG     62438      C  CCA
                                GAAC CA   GAGGCGGAAG
                                |||| ||   ||||||||||
                                CTTG GT   CTCCGCCTTC
                                  T  C__
GAM2677  GATA3    5'  CCGGAACCCGCGCGGGGAGGGA 62439          ACCAGA  C_
            AG                   CCGGAACCC      GG  GGAAG
                                |||||||||      ||  |||||
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                              GGCCTTGGG    CC  CCTTC
                                   CGCGCC  TC
GAM2677  GM2A     3'  GAACCCAGGAGGCGGA     62431       CCA
                              GAACCCA  GAGGCGGA
                              |||||||  ||||||||
                              CTTGGGT  CTCCGCCT
                                 C__
GAM2677  HLCS     5'  GGAACCCAGTAGGCAGA     62440       CCAG
                              GGAACCCA   AGGCGGA
                              ||||||||   |||||||
                              CCTTGGGT   TCCGTCT
                                   CA__
GAM2677  HTR1E    5'  CCGCGAACCCGGGAGGCGGA  62441    _     ACCA
                              CCG GAACCC   GAGGCGGA
                              ||| ||||||   ||||||||
                              GGC CTTGGG   CTCCGCCT
                                G     CC__
GAM2677  LILRA3   3'  GAACCCGAGAGGCGGA     62442       ACC
                              GAACCC  AGAGGCGGA
                              ||||||  |||||||||
                              CTTGGG  TCTCCGCCT
                                 C__
GAM2677  MAFF     3'  CCAGGCCCAACCAGAGGTGGGG 62443     AA  C      C  AA
           GC                   CCGG  CC ACCAGAGG GG  GC
                              ||||  || |||||||| ||  ||
                              GGTC  GG TGGTCTCC CC  CG
                                CG  T      A  CC
GAM2677  MHC2TA   3'  GAACCCAAGAGGCGGA     62434       CC
                              GAACCCA  AGAGGCGGA
                              |||||||  |||||||||
                              CTTGGGT  TCTCCGCCT
                                   __
GAM2677  MRPL23   5'  CCGGGGTCCGCGAGGCGGAGGA 62444     AAC  ACCA      __
           GC                   CCGG   CC   GAGGCGGA  AGC
                              ||||   ||   |||||||| |||
                              GGCC   GG   CTCCGCCT  TCG
                                CCA  CG__      CC
GAM2677  NDUFB3   5'  CCGGAGCCAACCGGAAACGGA  62445      A  C   A
                              CCGGA CC ACC GAGGCGGA
                              ||||| || ||| ||||||||
                              GGCCT GG TGG CTTTGCCT
                                C  T   C
GAM2677  PABPC4   5'  CGGAAACGGGAGGCGGGGGC   62446      CCC  CA     AA
                              CGGAA   AC  GAGGCGG  GC
                              |||||   ||  |||||||  ||
                              GCCTT   TG  CTCCGCC  CG
                                 ___  CC     CC
GAM2677  PK428    5'  CCGCGCACAGAGGCGGAG    62447     GAACC   C       A
                              CCG    CAC AGAGGCGGA G
                              |||    ||| ||||||||| |
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                                GGC    GTG TCTCCGCCT C
                                  GC___  _       C
GAM2677 PRKACA   3' CCAGGATGGGGGAGGCGGAAGC 62448     AACCCACCA
                                CCGG       GAGGCGGAAGC
                                ||||       ||||||||||
                                GGTC       CTCCGCCTTCG
                                  CTACCCC__
GAM2677 PTGES    3' GAACCCGGGAGGCGGAGGC   62449      ACCA      A
                                GAACCC   GAGGCGGA GC
                                ||||||   |||||||| ||
                                CTTGGG   CTCCGCCT CG
                                   CC__      C
GAM2677 SEDL     3' CCTGAACCTGGGAGGCGGA   62450   G    CACCA
                                CC GAACC    GAGGCGGA
                                || |||||    ||||||||
                                GG CTTGG    CTCCGCCT
                                 A    ACC__
GAM2677 SIRT6    3' CCGGAACCGCACCAGAGGC   62451       _
                                CCGGAACC CACCAGAGGC
                                |||||||| ||||||||||
                                GGCCTTGG GTGGTCTCCG
                                     C
GAM2677 SULT2B1  5' GAACCCAGGAGGCGGA     62431       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                   C__
GAM2677 TACSTD2  3' GGGACACACCAGAGTAGCGCTT 62452   A  C      ________ GGAA
            CG                    G AC CACCAGAG      GC   G
                                | || ||||||||      ||   |
                                C TG GTGGTCTC      CG   C
                                 C  T       ATCGIII  AAGG
GAM2677 TAL1     5' CCGGAAAGGGGCGGAAG     62453       CCCACC  A
                                CCGGAA     AG GGCGGAAG
                                ||||||     || ||||||||
                                GGCCTT     TC CCGCCTTC
                                   _______  C
GAM2677 TAPBP    3' GAACCCAGGAGGCGGA      62431       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                   C__
GAM2677 TCOF1    3' CGGGATCAGCCAGAGACCGAGC 62454     AACC  _      G  A
                                CGG    CA CCAGAGGC GA GC
                                |||    || |||||||| || ||
                                GCC    GT GGTCTCTG CT CG
                                  CTA_  C       G  _
GAM2677 TFG      5' GGAAGAACAGAGGCGGGAGC   62455      CCCAC       A
                                GGAA     CAGAGGCGG AGC
                                ||||     ||||||||| |||
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                                CCTT    GTCTCCGCC TCG
                                  CTT__       C
GAM2677  TNFRSF10B 3'  GAACCCAGGAGGCGGA     62431       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                   C__
GAM2677  TRPV1    3'  GGAATCCAGGAGGCGGA     62456     C   CCA
                                GGAA CCA   GAGGCGGA
                                ||||  |||   ||||||||
                                CCTT GGT   CTCCGCCT
                                  A   C__
GAM2677  TRPV1    3'  GGAATCCAGGAGGCGGA     62456     C   CCA
                                GGAA CCA   GAGGCGGA
                                ||||  |||   ||||||||
                                CCTT GGT   CTCCGCCT
                                  A   C__
GAM2677  TRPV1    3'  GGAATCCAGGAGGCGGA     62456     C   CCA
                                GGAA CCA   GAGGCGGA
                                ||||  |||   ||||||||
                                CCTT GGT   CTCCGCCT
                                  A   C__
GAM2677  TRPV1    3'  GGAATCCAGGAGGCGGA     62456     C   CCA
                                GGAA CCA   GAGGCGGA
                                ||||  |||   ||||||||
                                CCTT GGT   CTCCGCCT
                                  A   C__
GAM2677  VENTX2   3'  GAACCCAGGAGGCGGA      62431       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                   C__
GAM2677  WWOX     3'  CCGAGGCCCACCAAGGGGG   62457      AA      A  C
                                CCGG  CCCACCAG GG GG
                                ||||  |||||||| || ||
                                GGCT  GGGTGGTT CC CC
                                  CC       C  _
GAM2677  ZNF264   3'  GAACCCAGGAGGCGGA      62431       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                   C__
GAM2677  ZNF42    5'  CAGGGCCTGGAGAAGGCGGAAG 62458     AA  CACCA
              C                  CGG  CC    GAGGCGGAAGC
                                 |||  ||    ||||||||||
                                 GTC  GG    TTCCGCCTTCG
                                   CC  ACCTC
GAM2677  13CDNA73  3'  GGAACCCAGTGGGGACAGGAGG 62459         CCAGA  _  A
              C                  GGAACCCA    GGC GGA GC
                                 ||||||||    ||| ||| ||
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                                CCTTGGGT    CTG CCT CG
                                    CACCC   T   C
GAM2677  APXL2    5'  GAACCCGGGAGGCGGAAG    62460       ACCA
                                GAACCC   GAGGCGGAAG
                                ||||||   ||||||||||
                                CTTGGG   CTCCGCCTTC
                                   CC__
GAM2677  ASE-1    3'  GGAACCCAGGAGGCGGA     62461        CCA
                                GGAACCCA  GAGGCGGA
                                ||||||||  ||||||||
                                CCTTGGGT  CTCCGCCT
                                    C__
GAM2677  BCL2L1   3'  CCTGAACCCACCATGAGGAGCG 62462        _  ________  GGAA
              CTTCCGC                ACCCACCA GAG      GC   GC
                                |||||||| |||      ||   ||
                                TGGGTGGT CTC      CG   CG
                                    A  CTCGIII  AAGG
GAM2677  BRD1     5'  GGACCCCACCAGGCACAGAGGC 62463     A       AG    A
                                GGA CCCACCAG  GCGGA GC
                                ||| ||||||||  ||||| ||
                                CCT GGGTGGTC  TGTCT CG
                                  G       CG    C
GAM2677  C1orf24  3'  CCTGAACCCAGGAGGCGGA   62464    G      CCA
                                CC GAACCCA   GAGGCGGA
                                || |||||||   ||||||||
                                GG CTTGGGT   CTCCGCCT
                                 A      C__
GAM2677  C8orf13  3'  CCAGAATCCACCAGGAGGC   62465       C     _
                                CCGGAA CCACCAG AGGC
                                |||||| ||||||| ||||
                                GGTCTT GGTGGTC TCCG
                                   A      C
GAM2677  CUGBP2   3'  GGGGCCCACCAGAGCAAGCGCT 62466   A       _________  GGAA
              TCCGC                  CCCACCAGAG       GC   GC
                                 ||||||||||       ||   ||
                                 GGGTGGTCTC       CG   CG
                                C         GTTCGIII  AAGG
GAM2677  DIRC2    5'  CCGGAGCAGCAGGAGGCGGAGG 62467      ACC  C  _      A
              C                   CCGGA   CA CAG AGGCGGA GC
                                |||||   || ||| ||||||| ||
                                GGCCT   GT GTC TCCGCCT CG
                                   C__  C   C      C
GAM2677  DKFZp434C0923 3'  GAGCCCAGGAGGCGGAGGC   62468    A   CCA      A
                                GA CCCA   GAGGCGGA GC
                                || ||||   |||||||| ||
                                CT GGGT   CTCCGCCT CG
                                 C   C__       C
GAM2677  DKFZp434F054 5'  CCGGAACCGCCGCGCCGGAAGC 62469        CA  AGAGG
                                CCGGAACC  CC    CGGAAGC
                                ||||||||  ||    |||||||
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                                GGCCTTGG  GG    GCCTTCG
                                    C_  CGCG_
GAM2677  DKFZP564K0822 3'  CAGAACCCACCACTGGAGCGCT 62470          ___  ____  GGAA
           TCG                   GAACCCACCA  GAG   GC   G
                                 ||||||||||  |||   ||   |
                                 CTTGGGTGGT  CTC   CG   C
                                     GAC  GIII  AAGG
GAM2677  DKFZP586J1624 3'  CCGGAACCCACAGGGGGAA   62471          C  A  C
                                 CCGGAACCCAC AG GG GGAA
                                 ||||||||||| || || ||||
                                 GGCCTTGGGTG TC CC CCTT
                                           _ _ _
GAM2677  DKFZp762P2111 3'  CCTGAACCCGAGAGGCGGA   62472    G     ACC
                                 CC GAACCC   AGAGGCGGA
                                 || ||||||   |||||||||
                                 GG CTTGGG   TCTCCGCCT
                                  A     C__
GAM2677  EIF5     5'  CCGAGTCCGAGGAGGCGGAGGC 62473      AA  CACCA      A
                                 CCGG  CC    GAGGCGGA GC
                                 ||||  ||    |||||||| ||
                                 GGCT  GG    CTCCGCCT CG
                                   CA  CTC__       C
GAM2677  ERN1     3'  GGGGCCACCAGAACAGA     62474    AAC       G
                                 GG   CCACCAGAG CGGA
                                 ||   ||||||||| ||||
                                 CC   GGTGGTCTT GTCT
                                  CC_        _
GAM2677  EVI5     3'  GAACCTGGGAAGCGGAAG    62475      CACCA
                                 GAACC    GAGGCGGAAG
                                 |||||    ||||||||||
                                 CTTGG    CTTCGCCTTC
                                    ACC__
GAM2677  FBP17    3'  GGAACCCAGGAGGTGGA     62476        CCA   C
                                 GGAACCCA   GAGG GGA
                                 ||||||||   |||| |||
                                 CCTTGGGT   CTCC CCT
                                      C__    A
GAM2677  FLJ10922  3'  CCCGAACCCAGGAGGCGGA   62477    G     CCA
                                 CC GAACCCA   GAGGCGGA
                                 || |||||||   ||||||||
                                 GG CTTGGGT   CTCCGCCT
                                  G      C__
GAM2677  FLJ11235  3'  CGGGACCCACCAGGGGTGC   62478     A       A _____
                                 CGG ACCCACCAG G    GC
                                 ||| ||||||||| |    ||
                                 GCC TGGGTGGTC C    CG
                                   C        C CAIII
GAM2677  FLJ12903  3'  GAACCCAGGAGGCGGA      62431        CCA
                                 GAACCCA   GAGGCGGA
                                 |||||||   ||||||||
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                              CTTGGGT  CTCCGCCT
                                 C__
GAM2677 FLJ13114 3' GAACCCAGGAAGCGGAGGC  62479      CCA      A
                              GAACCCA  GAGGCGGA GC
                              |||||||  |||||||| ||
                              CTTGGGT  CTTCGCCT CG
                                 C__      C
GAM2677 FLJ20296 3' GAACCCACCAGGTTGAGCGCTT 62480       ____  ____ GGAA
           CG                   AACCCACCA  GAG  GC  G
                              |||||||||  |||  ||  |
                              TTGGGTGGT  CTC  CG  C
                                  CCAA  GIII AAGG
GAM2677 FLJ20344 3' GAACCCAAGAGGCGGA    62434      CC
                              GAACCCA AGAGGCGGA
                              |||||||  |||||||||
                              CTTGGGT  TCTCCGCCT
                                 __
GAM2677 FLJ21302 3' GAACCCAGGAGGCGGA    62431      CCA
                              GAACCCA  GAGGCGGA
                              |||||||  ||||||||
                              CTTGGGT  CTCCGCCT
                                 C__
GAM2677 FLJ22055 3' GGGCCCACCAGGAGGGAAGC  62481   AA      AG C
                              GG  CCCACCAG  G GGAAGC
                              ||  ||||||||  | ||||||
                              CC  GGGTGGTC  C CCTTCG
                               C_      CT _
GAM2677 FLJ22965 3' CCCGAACCCGGGAGGCGGA  62482   G    ACCA
                              CC GAACCC   GAGGCGGA
                              || ||||||   ||||||||
                              GG CTTGGG   CTCCGCCT
                               G    CC__
GAM2677 GR6     5' CCGGGGCCCACCAGGCTGG  62483    AA     GA  _
                              CCGG  CCCACCA  GGC GG
                              ||||  |||||||  ||| ||
                              GGCC  GGGTGGT  CCG CC
                                CC     __  A
GAM2677 HIC2    3' GGGACCCACCAGAGTCGACAGA 62484   A       ___    A
           GC                   GG ACCCACCAGAG  GCGGA GC
                              || ||||||||||  ||||| ||
                              CC TGGGTGGTCTC  TGTCT CG
                               C         AGC   _
GAM2677 HN1L    3' CCCTGCCAGGGGCGGAAG   62485    A_  A
                              CCC  CCAG GGCGGAAG
                              |||  |||| ||||||||
                              GGG  GGTC CCGCCTTC
                                AC   C
GAM2677 HNK-1ST  3' AACCCACCAGTGATGGGTGCTT 62486       A __________ GGAA
           CCGC                   CCCACCAG G       GC   GC
                              |||||||| |       ||   ||
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                              GGGTGGTC C       CG   CG
                                  A TACCCAIII  AAGG
GAM2677 KIAA0194 3' CGGAACCCACCAGCTACGA   62487          AG
                              CGGAACCCACCAG  GCGG
                              ||||||||||||  ||||
                              GCCTTGGGTGGTC  TGCT
                                  GA
GAM2677 KIAA0544 3' GGGGCCTGCCAAACAGAAGC  62488   AA  CA   AG
                              GG  CC  CCAG  GCGGAAGC
                              ||  ||  ||||  ||||||||
                              CC  GG  GGTT  TGTCTTCG
                               CC  AC   __
GAM2677 KIAA0789 3' GGAACCCAGAGTGGTGGGGGC 62489       CC  A  C  AA
                              GGAACCCA  AG GG GG  GC
                              ||||||||  || || ||  ||
                              CCTTGGGT  TC CC CC  CG
                                  C_  A  A  CC
GAM2677 KIAA0889 3' GAACCCAGGAGGCGGA     62431       CCA
                              GAACCCA   GAGGCGGA
                              |||||||   ||||||||
                              CTTGGGT   CTCCGCCT
                                  C__
GAM2677 KIAA1161 5' CGCGATCCACCAGGCGGAAG  62490   _  AC     GA
                              CG GA  CCACCA  GGCGGAAG
                              || ||  ||||||  ||||||||
                              GC CT  GGTGGT  CCGCCTTC
                               G  A_     __
GAM2677 KIAA1303 3' CCGGAACCTTCTTCTGGTGGGA 62491       CACCAGA  C  A
           GC                  CCGGAACC      GG GG AGC
                              ||||||||      || || |||
                              GGCCTTGG      CC CC TCG
                                  AAGAAGA  A  C
GAM2677 KIAA1357 3' CCGGGGCCCACAGCACAGAAGC 62492     AA    C  AG
                              CCGG  CCCAC AG  GCGGAAGC
                              ||||  ||||| ||  ||||||||
                              GGCC  GGGTG TC  TGTCTTCG
                                CC    _  G_
GAM2677 KIAA1543 5' GGGGGCCACCAGATGACAGAAG 62493    AAC      _
           C                   GG   CCACCAGA GGCGGAAGC
                              ||   |||||||| |||||||||
                              CC   GGTGGTCT CTGTCTTCG
                               CCC       A
GAM2677 KIAA1737 3' GAACCCAGGAGGCGGA     62431       CCA
                              GAACCCA   GAGGCGGA
                              |||||||   ||||||||
                              CTTGGGT   CTCCGCCT
                                  C__
GAM2677 KIAA1814 3' GGAACCCATCAGCCCCCAGGC  62494       C  _____
                              GGAACCCA CAG    AGGC
                              |||||||| |||    ||||
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                                CCTTGGGT GTC    TCCG
                                    A  GGGGG
GAM2677 KLK7    3' GAACCCAGGAGGCGGA     62431       CCA
                                GAACCCA  GAGGCGGA
                                |||||||  ||||||||
                                CTTGGGT  CTCCGCCT
                                    C__
GAM2677 KLK7    3' GAACCCAGGAGGCGGA     62431       CCA
                                GAACCCA  GAGGCGGA
                                |||||||  ||||||||
                                CTTGGGT  CTCCGCCT
                                    C__
GAM2677 LC27    3' GGGGCCCAGCAGGTACAAAAGC 62495   AA   C  AG
                                GG  CCCA CAG  GCGGAAGC
                                ||  |||| |||  ||||||||
                                CC  GGGT GTC  TGTTTTCG
                                 CC   C  CA
GAM2677 MGC14836 3' CCCGAACCCTGGAGGCGGA   62496   G    ACCA
                                CC GAACCC   GAGGCGGA
                                || ||||||   ||||||||
                                GG CTTGGG   CTCCGCCT
                                 G    AC__
GAM2677 MGC1842  3' GAACCCAGGAGGCGGA     62431       CCA
                                GAACCCA  GAGGCGGA
                                |||||||  ||||||||
                                CTTGGGT  CTCCGCCT
                                    C__
GAM2677 MGC3771  5' CCTGAACCCAGGAGGCGGA   62464   G    CCA
                                CC GAACCCA  GAGGCGGA
                                || |||||||  ||||||||
                                GG CTTGGGT  CTCCGCCT
                                 A     C__
GAM2677 MYO5C    3' GAACCCAGGAAGCGGA     62497       CCA
                                GAACCCA  GAGGCGGA
                                |||||||  ||||||||
                                CTTGGGT  CTTCGCCT
                                    C__
GAM2677 OR2C3    3' CCGGAGCCTGCAAGGCGGA   62498     A  CACCA
                                CCGGA CC    GAGGCGGA
                                |||||  ||    ||||||||
                                GGCCT GG    TTCCGCCT
                                   C  ACG__
GAM2677 OSBPL2   3' CCGGGACGCCTCTGAGGCGGAA 62499     A  _  ACCA
            GC                    CCGG AC CC    GAGGCGGAAGC
                                ||||  ||  ||    ||||||||||
                                GGCC TG GG    CTCCGCCTTCG
                                  C  C  AGA_
GAM2677 OSBPL2   3' CCGGGACGCCTCTGAGGCGGAA 62499     A  _  ACCA
            GC                    CCGG AC CC    GAGGCGGAAGC
                                ||||  ||  ||    ||||||||||
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                                GGCC TG GG    CTCCGCCTTCG
                                  C  C  AGA_
GAM2677  P2RX1    3'  GGGACCCACCAGGGCTCCAG   62500    A       A   GGA
                                GG ACCCACCAG GGC   AG
                                || ||||||||| |||   ||
                                CC TGGGTGGTC CCG   TC
                                 C       _  AGG
GAM2677  PTK6     5'  GGAACCCACTGGGCAAG     62501         CAGA    GA
                                GGAACCCAC   GGCG  AG
                                |||||||||   ||||  ||
                                CCTTGGGTG   CCGT  TC
                                     AC__   __
GAM2677  RAI      5'  GAACCCAGGAGGCGGA      62431        CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2677  RNF30    5'  GAAACCCACTGTGAAGTGCTTC 62502         CA__  ____  GGAA
              G                  GGAACCCAC   GAG   GC   G
                                 |||||||||   |||   ||   |
                                 CTTTGGGTG   TTC   CG   C
                                      ACAC   AIII  AAGG
GAM2677  SMCR8    5'  CCGGAACCCACTGCGACAG   62503          CAGAG   GA
                                CCGGAACCCAC    GCG  AG
                                ||||||||||    |||  ||
                                GGCCTTGGGTG    CGC  TC
                                      A____   TG
GAM2677  TEX27    3'  CGGGACCAGAGCTTGGCGGAAG 62504     AACCC     ____
              C                  CGG    ACCAGA   GGCGGAAGC
                                 |||    ||||||   |||||||||
                                 GCC    TGGTCT   CCGCCTTCG
                                   C____     CGAA
GAM2677  TU12B1-TY 3'  GAACCCAGGAGGCGGA      62431        CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2677  LOC115219 5'  GAACCCAGGAGGCGGA      62431        CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2677  LOC116437 3'  GGCACCCACCAGTGTGGGTGCT 62505         AG_________  GGAA
              TCCGC                ACCCACCAG        GC   GC
                                   |||||||||        ||   ||
                                   TGGGTGGTC        CG   CG
                                      ACACCCAIII  AAGG
GAM2677  LOC121504 3'  GAACCCGGGAGGCGGAGGC   62449       ACCA      A
                                GAACCC   GAGGCGGA GC
                                ||||||   |||||||| ||
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                                CTTGGG    CTCCGCCT CG
                                   CC__       C
GAM2677  LOC126364 3'  GAACCCAGGAGGCGGA      62431        CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                   C__
GAM2677  LOC128977 3'  GGGACCCACCAGACTGTGTAGG 62506     A        ________
                C                   GG ACCCACCAGA       GGC
                                || ||||||||||       |||
                                CC TGGGTGGTCT       CCG
                                 C         GACACAT
GAM2677  LOC135763 3'  GAACCCAGGAGGCGGA      62431        CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                   C__
GAM2677  LOC143384 5'  CGGAGCCAAAAGGGGCGGGAGC 62507      AC   CC  A    A
                                CGGA  CCA  AG GGCGG AGC
                                ||||  |||  || ||||| |||
                                GCCT  GGT  TC CCGCC TCG
                                  C_   TT  C    C
GAM2677  LOC146909 3'  GAACCCAGGAGGCGGA      62431        CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                   C__
GAM2677  LOC147054 3'  GAACCCAGGAGGCGGAAG     62508        CCA
                                GAACCCA   GAGGCGGAAG
                                |||||||   ||||||||||
                                CTTGGGT   CTCCGCCTTC
                                   C__
GAM2677  LOC147057 5'  CCGGAGCCACCGAGGCGGAGGC 62509       AC     A       A
                                CCGGA  CCACC GAGGCGGA GC
                                |||||  ||||| |||||||| ||
                                GGCCT  GGTGG CTCCGCCT CG
                                  C_     _       C
GAM2677  LOC147165 3'  CCAGGAGTCCCGGGCGGGGGC  62510    _   A_   ACCAGA     AA
                                CC GGA  CCC      GGCGG  GC
                                || |||  |||      |||||  ||
                                GG CCT  GGG      CCGCC  CG
                                 T   CA   C_____     CC
GAM2677  LOC147660 3'  GAACCCAGGAGGCGGA      62431        CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                   C__
GAM2677  LOC148709 3'  GGACCCAGGAGGCGGA      62511     A    CCA
                                GGA CCCA   GAGGCGGA
                                ||| ||||   ||||||||
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                                CCT GGGT   CTCCGCCT
                                  _   C__
GAM2677  LOC150197 3'  CCTGAGCCCACCAGGTGGC   62512    G  A      A_
                                CC GA CCCACCAG  GGC
                                || || ||||||||  |||
                                GG CT GGGTGGTC  CCG
                                 A  C       CA
GAM2677  LOC151826 3'  GAACCTCAGGAGGCGGA     62513      _  CCA
                                GAACC CA   GAGGCGGA
                                ||||| ||   ||||||||
                                CTTGG GT   CTCCGCCT
                                   A  C__
GAM2677  LOC152220 3'  GAACCCAGGAAGCGGA      62497       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTTCGCCT
                                    C__
GAM2677  LOC153077 3'  GAACCCAGGAGGCGGA      62431       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2677  LOC154075 3'  GAACCCAGGAGGCGGA      62431       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2677  LOC154467 3'  CCGGAACCCCCCAGCAGGC   62514         A   _
                                CCGGAACCC CCAG AGGC
                                ||||||||| |||| ||||
                                GGCCTTGGG GGTC TCCG
                                     G   G
GAM2677  LOC158314 3'  GGAACCCACCACGGGAGCGCTT 62515          ___  ____  GGAA
            CG                    GAACCCACCA   GAG   GC   G
                                ||||||||||  |||   ||   |
                                CTTGGGTGGT   CTC   CG   C
                                      GCC   GIII  AAGG
GAM2677  LOC158549 5'  GAACCCAGGAGGCGGA      62431       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2677  LOC197358 3'  GGAACCCATGAGGTAGAGC   62516       CCA   CG  A
                                GGAACCCA   GAGG  GA GC
                                ||||||||   ||||  || ||
                                CCTTGGGT   CTCC  CT CG
                                    A__    AT  _
GAM2677  LOC199786 3'  GGAACCCACTCCGGAAG     62517        CAGAGG
                                GGAACCCAC     CGGAAG
                                |||||||||     ||||||
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                                CCTTGGGTG     GCCTTC
                                      AG____
GAM2677  LOC199858 5'  GGAACCCACTAAAAACTGG   62518         C     _
                                GGAACCCAC AGAGGC GG
                                ||||||||| |||||| ||
                                CCTTGGGTG TTTTTG CC
                                      A     A
GAM2677  LOC200845 5'  GAACCCGAGAGGCGGA     62442       ACC
                                GAACCC   AGAGGCGGA
                                ||||||   |||||||||
                                CTTGGG   TCTCCGCCT
                                   C__
GAM2677  LOC201294 3'  GAACCCAGGAGGCGGA     62431       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2677  LOC219445 5'  GAACCAGGGAGGCGGAGGC   62519      CACCA      A
                                GAACC    GAGGCGGA GC
                                |||||    |||||||| ||
                                CTTGG    CTCCGCCT CG
                                   TCC__       C
GAM2677  LOC220469 5'  GGAACCCATGAAGTGAGGTGCT 62520      CCA___  _____  GGAA
            TCCGC                 ACCCA     GAG    GC   GC
                                |||||     |||    ||   ||
                                TGGGT     CTC    CG   CG
                                   ACTTCA   CAIII  AAGG
GAM2677  LOC221773 3'  GAACCCAGGAGGCGGA     62431       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2677  LOC222031 3'  GAACCCAGGAGGCGGA     62431       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2677  LOC222865 3'  CCAGAACCTGTCAGGGCTGCTT 62521        CAC   A  _____
            GGA                   CCGGAACC   CAG GGC    GGA
                                |||||||   ||| |||    |||
                                GGTCTTGG   GTC CCG    CCT
                                     ACA   _   ACGAA
GAM2677  LOC253263 3'  GGAGTCACCAGAAAAAAAGAAG 62522     ACC       C__
                                GGA   CACCAGAGG   GGAAG
                                |||   |||||||||   |||||
                                CCT   GTGGTCTTT   TCTTC
                                  CA_       TTT
GAM2677  LOC253443 5'  GGAACCTATTGCACAAAAGCGC 62523    _____  C   ____  GGAA
            TTCCGC                CC    CAC AGAG    GC   GC
                                ||    ||| ||||    ||   ||
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                                GG    GTG TTTC   CG   CG
                                 ATAAC  T   GIII  AAGG
GAM2677  LOC255057 3'  CGGACTCCACCAGCAAGC    62524     AC     _
                                CGGA  CCACCAG AGGC
                                ||||  ||||||| ||||
                                GCCT  GGTGGTC TTCG
                                  GA      G
GAM2677  LOC256506 3'  GGAACCCACCAGGTCATTAGGC 62525          ______
                                GGAACCCACCAG     AGGC
                                ||||||||||||     ||||
                                CCTTGGGTGGTC     TCCG
                                       CAGTAA
GAM2677  LOC51193  5'  CCTGAATCCGGGAGGCGGA   62526   G  C  ACCA
                                CC GAA CC   GAGGCGGA
                                || ||| ||   ||||||||
                                GG CTT GG   CTCCGCCT
                                 A  A  CC__
GAM2677  LOC57107  3'  GAACCCAGGAGGCGGA     62431       CCA
                                GAACCCA  GAGGCGGA
                                |||||||  ||||||||
                                CTTGGGT  CTCCGCCT
                                   C__
GAM2677  LOC57805  3'  CCGGAACCTAGCAGAGCCTGTG 62527    CAC    _________ GGAA
           CTTCCGC               ACC  CAGAG      GC   GC
                                |||  |||||      ||   ||
                                TGG  GTCTC      CG   CG
                                 ATC    GGACAIII  AAGG
GAM2677  LOC90459  3'  CCTGAGCCCAGGAGGCGGA   62528   G  A   CCA
                                CC GA CCCA   GAGGCGGA
                                || || ||||   ||||||||
                                GG CT GGGT   CTCCGCCT
                                 A  C   C__
GAM2677  LOC92689  3'  GAACCCAGGAGGCGGA     62431       CCA
                                GAACCCA  GAGGCGGA
                                |||||||  ||||||||
                                CTTGGGT  CTCCGCCT
                                   C__
GAM2677  LOC95076  5'  GGATCCGCCGCAGAAGC    62529    AC  A  AGAG
                                GGA  CC CC   GCGGAAGC
                                |||  || ||   ||||||||
                                CCT  GG GG   CGTCTTCG
                                 A_  C  _____
GAM2678  ATP10C   5'  TAGGTTATCATCACTCGC    62532       TGATGA  C
                                TAGGTTATT    CAC CGC
                                |||||||||    ||| |||
                                ATCCAATAG    GTG GCG
                                     TA_____  A
GAM2678  CX3CR1   3'  AAGTTCTGATGACATTTGCAG  62533    TA       CCC
                                AGGT  TTTGATGACA  GCAG
                                ||||  ||||||||||  ||||
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                                TTCA  AGACTACTGT   CGTC
                                  __         AAA
GAM2678  TRPM1    3'  TAGGCTATTTGGTGGCCCTCAG 62534          A  ACA   G
                                TAGGTTATTTG TG   CCC CAG
                                |||||||||| ||   ||| |||
                                ATCCGATAAAC AC   GGG GTC
                                      C  C__   A
GAM2678  ALS2CR3  5'  AGTCAAATGACATCCG      62535       TTT      C
                                GGTTA   GATGACA CCG
                                |||||   ||||||| |||
                                TCAGT   TTACTGT GGC
                                  ___      A
GAM2678  C22orf2  3'  GGTTTTCAGACTGGCACCCGCA 62536      A  T   GA_
            G                    GGTT TT GAT   CACCCGCAG
                                |||| || |||   |||||||||
                                CCAA AG CTG   GTGGGCGTC
                                  A  T   ACC
GAM2678  FN5      5'  AGTTATTCCTGCCCGC      62537         GA  ACA
                                GGTTATTT  TG   CCCGC
                                ||||||||  ||   |||||
                                TCAATAAG  AC   GGGCG
                                    G_  ___
GAM2678  LOC201230 3'  TAGGTCACTCTTGGTGACACCT 62538          GA__      C
            GC                    TAGGTTATTT    TGACACC GC
                                ||||||||||    ||||||| ||
                                ATCCAGTGAG    ACTGTGG CG
                                      AACC      A
GAM2679  AXUD1    5'  GGTGCCGGACGTGCTCTGGG   62541    A   AGCTT      A
                                GG TGC     CGTGCTCT GG
                                || |||     |||||||| ||
                                CC ACG     GCACGAGA CC
                                 _   GCCT_       C
GAM2679  CRY2     3'  AAGGATTGGCTTCTCTG      62542       GCA    GTGC   A
                                AAGGAT   GCTTC    TCT G
                                ||||||   |||||    ||| |
                                TTCCTA   CGAAG    AGA C
                                   AC_    ____   C
GAM2679  FANCE    3'  GGAGGCAGTTGCAATCTGGG   62543     T   C  C  GC   A
                                GGA GCAG TT GT  TCT GG
                                ||| |||| || ||  ||| ||
                                CCT CGTC AA CG  AGA CC
                                  C    _ _ TT   C
GAM2679  IL6R     3'  AGGGTGCAGCTTGTGCAGAGG  62544     A       C    TCT
                                AGG TGCAGCTT GTGC   AGG
                                ||| |||||||| ||||   |||
                                TCC ACGTCGAA CACG   TCC
                                  C       _   TC_
GAM2679  MOCS1    3'  AGGGCTGCGGCTTCACAGACTT 62545     A_  A     T__   C
            AGG                    AGG  TGC GCTTCG   GCT TAGG
                                |||  ||| ||||||   ||| ||||
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                                TCC  ACG CGAAGT   TGA ATCC
                                  CG   C     GTC  _
GAM2679  SHMT2    3'  AGGATTTCGTGCTCTAG     62546       GCAGC
                                AGGAT    TTCGTGCTCTAG
                                |||||    ||||||||||||
                                TCCTA    AAGCACGAGATC
                                  ______
GAM2679  TCF8     3'  GGATGCAGCCTCCTGCACTGGG 62547           G   T  A
                                GGATGCAGCTTC TGC CT GG
                                |||||||||||| ||| || ||
                                CCTACGTCGGAG ACG GA CC
                                       G   T  C
GAM2679  TCP10    3'  AGGGTGCAGCCTTGCT      62548     A       CG
                                AGG TGCAGCTT  TGCT
                                ||| ||||||||  ||||
                                TCC ACGTCGGA  ACGA
                                  C       __
GAM2679  WNT8B    3'  AGGATTCAGACAGAGCTCTAGG 62549       G  _ TTCGT
                                AGGAT CAG C    GCTCTAGG
                                ||||| ||| |    ||||||||
                                TCCTA GTC G    CGAGATCC
                                   A   T TCT__
GAM2679  DKFZP434M131 3'  GGATACAGCTTTCTG       62550          CGTGC   A
                                GGATGCAGCTT    TCT G
                                ||||||||||    ||| |
                                CCTATGTCGAA    AGA C
                                      _____  A
GAM2679  KIAA0329 3'  AGGATGCATCTGGTTTTAGG   62551        G  TC  GCTC
                                AGGATGCA CT  GT   TAGG
                                |||||||| ||  ||   ||||
                                TCCTACGT GA  CA   ATCC
                                    A  C_  AA__
GAM2679  KIAA1573 3'  AAGGATGCGGTTCTAACATTAG 62552        AGC   GT  TC
            G                    AAGGATGC   TTC  GC  TAGG
                                ||||||||   |||  ||  ||||
                                TTCCTACG   AAG  TG  ATCC
                                    CC_   AT  TA
GAM2679  LYPLA3   3'  GGAGGCAGCTTCAGTCCT    62553     T      _  G
                                GGA GCAGCTTC GT CT
                                ||| |||||||| || ||
                                CCT CGTCGAAG CA GA
                                  C       T  G
GAM2679  TIAF1    3'  GGATGCAGCTGTGATGGAGAGG 62554          TC   CTCT__
                                GGATGCAGCT  GTG     AGG
                                ||||||||||  |||     |||
                                CCTACGTCGA  CAC     TCC
                                      __  TACCTC
GAM2679  ZFP106   3'  AAGGGTGCTGGAGCAGCTCTAG 62555      A  ____  TTCGT
            G                    AAGG TGC   AGC    GCTCTAGG
                                |||| |||   |||    ||||||||
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                                TTCC ACG   TCG    CGAGATCC
                                  C   ACC   T____
GAM2679  LOC122614 5'  AGGAGCTGTGCTCTA      62556     TGCA   TC
                                AGGA    GCT  GTGCTCTA
                                ||||    |||  ||||||||
                                TCCT    CGA  CACGAGAT
                                  ____   __
GAM2679  LOC126549 5'  AGGGCTGCAGCCAGTTCTAGG  62557     A_      TC  GC
                                AGG  TGCAGCT  GT  TCTAGG
                                |||  |||||||  ||  ||||||
                                TCC  ACGTCGG  CA  AGATCC
                                  CG      T_  __
GAM2679  LOC143915 3'  GGATGCAGCTCTGGGGCTTTAG 62558          CGT_   C
             G                   GGATGCAGCTT    GCT TAGG
                                ||||||||||    ||| ||||
                                CCTACGTCGAG    CGA ATCC
                                      ACCC   A
GAM2679  LOC145757 5'  GGAGTGCAGCTTTGATGTAGG  62559     _      C_   CTC
                                GGA TGCAGCTT  GTG   TAGG
                                ||| ||||||||  |||   ||||
                                CCT ACGTCGAA  TAC   ATCC
                                  C       AC  ___
GAM2679  LOC158147 3'  GGATACAGCTTTCTG       62550          CGTGC   A
                                GGATGCAGCTT    TCT G
                                ||||||||||    ||| |
                                CCTATGTCGAA    AGA C
                                      _____  A
GAM2679  LOC202025 5'  AGGATCAGCTCCGTCT      62560      G       G
                                AGGAT CAGCTTCGT CT
                                ||||| |||||||| ||
                                TCCTA GTCGAGGCA GA
                                  _       _
GAM2679  LOC255743 5'  AAGCGTGCAGCTTTTCCCCCTG 62561     GA      CGTG    A
             GG                   AAG  TGCAGCTT    CTCT GG
                                |||  ||||||||   |||| ||
                                TTC  ACGTCGAA    GGGA CC
                                  GC       AAGG   C
GAM2680  NAT1     3'  TATTATTATTATTTGAAA    62564
                                TGTTATTATTATTTGAAG
                                ||||||||||||||||||
                                ATAATAATAATAAACTTT

GAM2681  DPYSL2    3'  TGTATGAGCTTGGTGGGT    62567          A   ATT
                                TGTATGAGCT GGT   GGT
                                |||||||||| |||   |||
                                ACATACTCGA CCA   CCA
                                      A   C__
GAM2681  ETF1     3'  TGTAGGGCTGGGTCTGGT    62568      TGA   A   A
                                TGTA   GCT GGT TTGGT
                                ||||   ||| ||| |||||
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                                ACAT   CGA CCA GACCA
                                  CC_   C  _
GAM2681  NHLH1    3'  TGTAGAGCTAGGAGTTTGGT   62569      T       TA_
                                TGTA GAGCTAGG   TTGGT
                                |||| ||||||||   |||||
                                ACAT CTCGATCC   AACCA
                                  _       TCA
GAM2681  DKFZP564I052 3'  TGTATAGCTGTGGGGTTAA    62570      G    A_  TATT
                                TGTAT AGCT  GG    GGTTAA
                                ||||| ||||  ||    ||||||
                                ACATA TCGA  CC    CCAATT
                                  _    CA  ____
GAM2681  LOC133418 3'  TGTATGAGCCTCAATGGTTA   62571          AGGTAT
                                TGTATGAGCT     TGGTTA
                                ||||||||||     ||||||
                                ACATACTCGG     ACCAAT
                                      AGTT__
GAM2681  LOC153711 3'  TGTTTGGGCTAGGTAAGTAGT  62572     A  A       T_
                                TGT TG GCTAGGTA  TGGT
                                ||| || ||||||||  ||||
                                ACA AC CGATCCAT  ATCA
                                  A  C       TC
GAM2682  CLECSF6   5'  AGAAAATCTGTTTCAGATCTTT 62575       A   C  A TG
                                AGAAAA CTG TT T  GGTCTTT
                                |||||| ||| || |  |||||||
                                TCTTTT GAC AA A  CTAGAAA
                                   A   _  _ GT
GAM2682  COL1A1    3'  GAAAAACTGCTTTGTGCTTT   62576          AT  G T
                                GAAAAACTGCTT  TG G CTTT
                                ||||||||||||  || | ||||
                                CTTTTTGACGAA  AC C GAAA
                                      __  A _
GAM2682  DDX26     5'  GAAAACACTGTCTGGGTCTTT  62577      _   CTTA
                                GAAAA ACTG    TTGGGTCTTT
                                ||||| ||||    ||||||||||
                                CTTTT TGAC    GACCCAGAAA
                                   G    A___
GAM2682  MSL3L1    5'  AGAGGAACTGCTTAATGAGT   62578     AA       T
                                AGA  AACTGCTTA TGGGT
                                |||  ||||||||| |||||
                                TCT  TTGACGAAT ACTCA
                                  CC        T
GAM2682  TXK       3'  GAAGACTGCTGCGAAGTCTTT  62579     AA     TATT
                                GAA  ACTGCT    GGGTCTTT
                                |||  ||||||    ||||||||
                                CTT  TGACGA    TTCAGAAA
                                  C_     CGC_
GAM2682  XPR1      3'  AGAAATGGCTGCCAAGGTCTTT 62580       AA_    TATT
                                AGAAA   CTGCT    GGGTCTTT
                                |||||   |||||    ||||||||
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                                TCTTT  GACGG   TCCAGAAA
                                  ACC    T___
GAM2682 BRDG1    3' AGAGAAACTGCTGTTGGA    62581    A      TA
                                AGA AAACTGCT  TTGGG
                                ||| ||||||||  |||||
                                TCT TTTGACGA  AACCT
                                  C       C_
GAM2682 C20orf82 3' AAAAACTGCTTATAACGT    62582          TGG
                                AAAAACTGCTTAT  GT
                                ||||||||||||  ||
                                TTTTTGACGAATA  CA
                                       TTG
GAM2682 DCAMKL1  5' AGACGCCGCCGGGGGTCTTT  62583    AAAA   TATT
                                AGA   CTGCT   GGGTCTTT
                                |||   |||||   ||||||||
                                TCT   GGCGG   CCCAGAAA
                                  GC__    CC__
GAM2682 DSCAML1  3' AAAAAAATTGCTGAGTCTT   62584      C   TATT
                                AGAAAAA TGCT   GGGTCTT
                                ||||||| ||||   |||||||
                                TTTTTTT ACGA   CTCAGAA
                                   A   _____
GAM2682 FLJ00026 3' AGAAGCTGCTTATGCCTT    62585     AAA      TGG
                                AGAA  CTGCTTAT  GTCTT
                                ||||  ||||||||  |||||
                                TCTT  GACGAATA  CGGAA
                                  C__      ___
GAM2682 FLJ12969 3' AAAAAACTGTTTGAGGCTT   62586       CTTA   T
                                GAAAAACTG   TTGGG CTT
                                |||||||||   ||||| |||
                                TTTTTTGAC   AACTC GAA
                                     A___    C
GAM2682 KALI     3' GAAATGCTTATTGGAGC     62587     AAC       _
                                GAAA  TGCTTATTGG GT
                                ||||  |||||||||| ||
                                CTTT  ACGAATAACC CG
                                  ___        T
GAM2682 KIAA0215 3' AGGAAAACTGCTGAGT     62588    A      TATT
                                AG AAAACTGCT   GGGT
                                || |||||||||   ||||
                                TC TTTTGACGA   CTCA
                                 C       _____
GAM2682 KIAA0831 3' AGAAAAACTCTTATTAAAGAGC 62589        G    ___  T
            TTT                  AGAAAAACT CTTATT  GGG CTTT
                                |||||||| ||||||  ||| ||||
                                TCTTTTTGA GAATAA  CTC GAAA
                                     _    TTT  _
GAM2682 KIAA1560 3' AGGAAAACTGCTATTTGG    62590    A      TA
                                AG AAAACTGCT  TTGG
                                || |||||||||  ||||
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                                TC TTTTGACGA  AACC
                                 C        TA
GAM2682  MGC2647   3'  AGAGTAACTGCTCTGTCTT   62591     AA       ATTGG
                                AGA  AACTGCTT    GTCTT
                                |||  ||||||||    |||||
                                TCT  TTGACGAG    CAGAA
                                  CA       A____
GAM2682  MGC5149   5'  AGAAAGGCTTCTTGAACCTCT  62592      AACT   A   GG
                                AGAAA   GCTT TTG  TCTTT
                                |||||   |||| |||  |||||
                                TCTTT   CGAA AAC  GGAGA
                                  C___   G   TT
GAM2682  PARVA     3'  AAAGAAACTGCTTGGCTT    62593     A       ATTG  T
                                AGA AAACTGCTT    GG CTT
                                ||| |||||||||    || |||
                                TTT TTTGACGAA    CC GAA
                                  C       ____ _
GAM2682  PRO2198   3'  AACTGCTTAGCATCCTT     62594         TTGG
                                AACTGCTTA    GTCTTT
                                |||||||||    ||||||
                                TTGACGAAT    TAGGAA
                                     CG__
GAM2682  SPARCL1   5'  AGAAAAACTCTTTAAATCCCT  62595         G   AT
                                AGAAAAACT CTT  TGGGTCTTT
                                |||||||||| |||  |||||||||
                                TCTTTTTGA GAA  ATTTAGGGA
                                      _  __
GAM2682  SYNCOILIN 3'  GAAAAGGTGCTTGAACCTTT   62596      AC    TAT  GG
                                GAAAA  TGCT   TG  TCTTT
                                |||||  ||||   ||  |||||
                                CTTTT  ACGA   AC  GGAAA
                                  CC    ___  TT
GAM2682  LOC149420 3'  GAACAATTGCTTATTGAGT    62597     A  C
                                GAA AA TGCTTATTGGGT
                                ||| || ||||||||||||
                                CTT TT ACGAATAACTCA
                                  G  A
GAM2682  LOC151507 5'  AGAGGAACTGCTTAATGAGT   62578     AA       T
                                AGA  AACTGCTTA TGGGT
                                |||  ||||||||| |||||
                                TCT  TTGACGAAT ACTCA
                                  CC        T
GAM2682  LOC152215 3'  AAAAAAACTTCAGTGGGT     62598         GC   T
                                AGAAAAACT  TTA TGGGT
                                |||||||||  ||| |||||
                                TTTTTTTGA  AGT ACCCA
                                     __  C
GAM2682  LOC220469 3'  AGAGAAACTGCTTTTTGAA    62599     A       A
                                AGA AAACTGCTT TTGGG
                                ||| ||||||||| |||||
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                                TCT TTTGACGAA AACTT
                                  C        A
GAM2682  LOC254808 3'  AGAGAAACTGCTAGTTGAGACT 62600     A       TA     T
                                AGA AAACTGCT  TTGGG CT
                                ||| ||||||||  ||||| ||
                                TCT TTTGACGA  AACTC GA
                                  C       TC     T
GAM2682  LOC57107  3'  GAAAACTGCTTGACCTTT    62601      A     ATTG GT
                                GAAAA CTGCTT    G  CTTT
                                ||||| ||||||    |  ||||
                                CTTTT GACGAA    C  GAAA
                                   _     ____ TG
GAM2683  MMP13     3'  CTGTGTGAAGAAGGGCACATA  62604    A  _   CT
                                CT TGT AAG  GGGGGGCACATA
                                || ||| |||  ||||||||||
                                GA ACA TTC  TTCCCGTGTAT
                                 C  C  __
GAM2683  XK        3'  GACTGGTAAGTACTGGCACATA 62605      AT     C  GG
                                GACT  GTAAG TG  GGCACATA
                                ||||  ||||| ||  ||||||||
                                CTGA  CATTC AT  CCGTGTAT
                                  C_    _ GA
GAM2683  C20orf72  3'  TGCACACAGCTGGGGGCA    62606      ___
                                TGTA   AGCTGGGGGCA
                                ||||   ||||||||||
                                ACGT   TCGACCCCCGT
                                  GTG
GAM2683  DNM1L     3'  CTATGTAACTACACA       62607         G  GGGG
                                CTATGTAA CT    GCACA
                                |||||||| ||    |||||
                                GATACATT GA    TGTGT
                                   _ ____
GAM2683  KIAA0266  3'  GACTATGTGAGGCAA       62608         AAGCTG     C
                                GACTATGT     GGGGCA A
                                ||||||||     |||||| |
                                CTGATACA     CTCCGT T
                                   _______     A
GAM2684  DAG1      3'  ACTTGGCGTGAGCCAGGGC   62611    C   ATAA  T   C
                                AC TGGC    GG GCC GGGC
                                || ||||    || ||| ||||
                                TG ACCG    CT CGG CCCG
                                 A   CA__ _   T
GAM2684  EGLN2     5'  TACCTGGCCTAAGGAAGGGC  62612         A    TGCCC
                                TACCTGGC TAAGG     GGGC
                                |||||||| |||||     ||||
                                ATGGACCG ATTCC     CCCG
                                    G    TT___
GAM2684  EMD       5'  CCTGGCGGCGGCCCGGGC    62613       ATAA   _
                                CCTGGC    GGTG CCCGGGC
                                ||||||    |||| |||||||
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                                GGACCG   CCGC GGGCCCG
                                   ____   C
GAM2684 KCNQ2   5' CCTGGCGGGAGGCGCCCCGGG 62614      ATA     _
                                CCTGGC  AGGTGCCC GGG
                                ||||||  |||||||| |||
                                GGACCG  TCCGCGGG CCC
                                   CCC      G
GAM2684 MAGEC1  5' CCTGGCACTGCCTGGG     62615       AAGG   C
                                CCTGGCAT   TGCC GGG
                                ||||||||   |||| |||
                                GGACCGTG   ACGG CCC
                                   ____   A
GAM2684 PPID    5' TACCTAGTGGCCGCCCGGGC  62616       CATAA  _
                                TACCTGG    GGT GCCCGGGC
                                |||||||    ||| ||||||||
                                ATGGATC    CCG CGGGCCCG
                                   A____   G
GAM2684 RANBP3  3' CCTGGTGTGCAGCCGGGC   62617     CATAAG   __
                                CCTGG    GTGC  CCGGGC
                                |||||    ||||  ||||||
                                GGACC    CACG  GGCCCG
                                  A_____   TC
GAM2684 RANBP3  3' CCTGGTGTGCAGCCGGGC   62617     CATAAG   __
                                CCTGG    GTGC  CCGGGC
                                |||||    ||||  ||||||
                                GGACC    CACG  GGCCCG
                                  A_____   TC
GAM2684 RANBP3  3' CCTGGTGTGCAGCCGGGC   62617     CATAAG   __
                                CCTGG    GTGC  CCGGGC
                                |||||    ||||  ||||||
                                GGACC    CACG  GGCCCG
                                  A_____   TC
GAM2684 VIPR2   3' CCCGACACGGTGCTCGGGC  62618       AA    C
                                CCTGGCAT  GGTGC CGGGC
                                ||||||||  ||||| |||||
                                GGGCTGTG  CCACG GCCCG
                                   __     A
GAM2684 C17orf31 3' CTGGCATAGTCCTGGG    62619       AA   G  C
                                CTGGCAT  GGT CC GGG
                                |||||||  ||| || |||
                                GACCGTA  TCA GG CCC
                                   __  _ A
GAM2684 C20orf85 3' CCTGGCATGGCCCTGGG   62620       AAGGT   _
                                CCTGGCAT    GCCC GGG
                                ||||||||    |||| |||
                                GGACCGTA    CGGG CCC
                                   C____    A
GAM2684 CGB7    5' TACCTGGCTTTATACCTCGGG 62621       ATAAG    _
                                TACCTGGC    GTGCC CGGG
                                ||||||||    ||||| ||||
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                                ATGGACCG    TATGG GCCC
                                    AAA__    A
GAM2684 CGI-51   5' CCTCGCAGAGCTGCCCGGGC  62622    G  TA  G
                                CCT GCA  AG TGCCCGGGC
                                ||| |||  || |||||||||
                                GGA CGT  TC ACGGGCCCG
                                  G  C_  G
GAM2684 COL12A1  3' CTGGTTCACTGCCCGGG    62623    __  AAGG
                                CTGG  CAT   TGCCCGGG
                                ||||  |||   ||||||||
                                GACC  GTG   ACGGGCCC
                                  AA  ____
GAM2684 COL12A1  3' CTGGTTCACTGCCCGGG    62623    __  AAGG
                                CTGG  CAT   TGCCCGGG
                                ||||  |||   ||||||||
                                GACC  GTG   ACGGGCCC
                                  AA  ____
GAM2684 CRR9     3' CTGGCGGCAGCCCGGGC    62624     ATAA  _
                                CTGGC   GGT GCCCGGGC
                                |||||   ||| ||||||||
                                GACCG   CCG CGGGCCCG
                                   ____  T
GAM2684 EDG2     5' TACCTGGCGCGGGACAGGAGGG 62625       ATAA  TG CC__
          C                      TACCTGGC   GG  C   GGGC
                                ||||||||   ||  |   ||||
                                ATGGACCG   CC  G   CCCG
                                    CG__  CT TCCT
GAM2684 FLJ13955 5' CCTGCTCGGTGCCCGGGC   62626    G ATAA
                                CCTG C   GGTGCCCGGGC
                                ||||  |   ||||||||||
                                GGAC G   CCACGGGCCCG
                                  _ AG__
GAM2684 MAGEE1   5' CCTGGCACTGCCTGGG     62615      AAGG   C
                                CCTGGCAT   TGCC GGG
                                ||||||||   |||| |||
                                GGACCGTG   ACGG CCC
                                   ____   A
GAM2684 MGC15416 3' ACCTGGCAGGGCCTGGG    62627      TAA  T   C
                                ACCTGGCA   GG GCC GGG
                                ||||||||   || ||| |||
                                TGGACCGT   CC CGG CCC
                                   ___  _   A
GAM2684 MGC16186 5' CTGGCACCCCTGCCCGGG   62628      AAGG
                                CTGGCAT   TGCCCGGG
                                |||||||   ||||||||
                                GACCGTG   ACGGGCCC
                                   GGG_
GAM2684 MGC4504  5' CCTGGCACAGGGATAGGC   62629       A  TGCCC
                                CCTGGCATA GG    GGGC
                                ||||||||| ||    ||||
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                                GGACCGTGT CC    TCCG
                                    C  TA___
GAM2684  TCL6     5' CCTGGCATGGTGGTGGGC    62630       AA   CCC
                                CCTGGCAT  GGTG  GGGC
                                ||||||||  ||||  ||||
                                GGACCGTA  CCAC  CCCG
                                    __   CA_
GAM2684  TCL6     5' CCTGGCATGGTGGTGGGC    62630       AA   CCC
                                CCTGGCAT  GGTG  GGGC
                                ||||||||  ||||  ||||
                                GGACCGTA  CCAC  CCCG
                                    __   CA_
GAM2684  TCL6     5' CCTGGCATGGTGGTGGGC    62630       AA   CCC
                                CCTGGCAT  GGTG  GGGC
                                ||||||||  ||||  ||||
                                GGACCGTA  CCAC  CCCG
                                    __   CA_
GAM2684  TCL6     5' CCTGGCATGGTGGTGGGC    62630       AA   CCC
                                CCTGGCAT  GGTG  GGGC
                                ||||||||  ||||  ||||
                                GGACCGTA  CCAC  CCCG
                                    __   CA_
GAM2684  LOC112868 3' TACCTGGCATGTGGAGGG    62631        AAG  CCC
                                TACCTGGCAT  GTG  GGG
                                ||||||||||  |||  |||
                                ATGGACCGTA  CAC  CCC
                                    ____  CT_
GAM2684  LOC121036 3' CTGGTATGAAAATACCCTGGG  62632     C  _      _
                                CTGG AT AAGGTGCCC GGG
                                ||||  ||  |||||||||  |||
                                GACC TA TTTTATGGG CCC
                                  A  C       A
GAM2684  LOC145934 5' CCTGGCATGGTCCGCCGGG    62633       AA  GC_
                                CCTGGCAT  GGT  CCGGG
                                ||||||||  |||  |||||
                                GGACCGTA  CCA  GGCCC
                                    __  GGC
GAM2684  LOC148397 3' CCTGGCACTGAGGACAGGGC   62634       A_  T  CC
                                CCTGGCAT  AGG GC  GGGC
                                ||||||||  ||| ||  ||||
                                GGACCGTG  TCC TG  CCCG
                                    AC   _  T_
GAM2684  LOC151438 3' CACCTGGCATGGGAGGGG    62635        AA  TGCCC
                                TACCTGGCAT  GG    GGG
                                ||||||||||  ||    |||
                                GTGGACCGTA  CC    CCC
                                     C_  TC___
GAM2684  LOC151516 3' TGGCATAAGGCACAATGGGC   62636        TG CC_
                                TGGCATAAGG  C   GGGC
                                ||||||||||  |   ||||
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                                ACCGTATTCC  G   CCCG
                                     GT TTA
GAM2684  LOC157254 3'  CTGGCACCCGCCTGGGC     62637       AAGG   C
                                CTGGCAT    TGCC GGGC
                                |||||||    |||| ||||
                                GACCGTG    GCGG CCCG
                                    G___    A
GAM2684  LOC166341 3'  TGGATATAGGCCCGGGC     62638     C  A  T
                                TGG ATA GG GCCCGGGC
                                ||| ||| || ||||||||
                                ACC TAT TC CGGGCCCG
                                  _  A  _
GAM2684  LOC201220 5'  CCTGGCATAGGCATAGGG    62639        A   CCC
                                CCTGGCATA GGTG   GGG
                                ||||||||| ||||   |||
                                GGACCGTAT CCGT   CCC
                                     _   AT_
GAM2684  LOC256444 5'  CCTGGCATGGTCCGCCGGG   62633       AA  GC_
                                CCTGGCAT  GGT   CCGGG
                                ||||||||  |||   |||||
                                GGACCGTA  CCA   GGCCC
                                    __  GGC
GAM2684  LOC256790 5'  CCTGGCACAGGGCTGGGC    62640        A  T  CC
                                CCTGGCATA GG GC  GGGC
                                ||||||||| || ||  ||||
                                GGACCGTGT CC CG  CCCG
                                    _ _ A_
GAM2684  LOC54550  3'  TACCTGGCTAGGTTGGG     62641       ATA   GCCC
                                TACCTGGC   AGGT   GGG
                                ||||||||   ||||   |||
                                ATGGACCG   TCCA   CCC
                                    A__    A___
GAM2685  ANGPT4    3'  TCACAGACGGAGGGGAG     62644       TA   ACAT
                                TCACAGAC  AGGG   GAG
                                ||||||||  ||||   |||
                                AGTGTCTG  TCCC   CTC
                                    CC   _____
GAM2685  HTR1E     3'  TATCACAGATAAGACCAGAGG  62645       C    GA  T
                                TATCACAGA TAAGG  CA GAGG
                                ||||||||| |||||  || ||||
                                ATAGTGTCT ATTCT  GT CTCC
                                    _    G_ _
GAM2685  NT5C2     3'  TATCACAGATAAGAAGGAG   62646       C     ACAT
                                TATCACAGA TAAGGG   GAG
                                ||||||||| ||||||   |||
                                ATAGTGTCT ATTCTT   CTC
                                    _    C___
GAM2685  ROCK2     3'  TCACAGACTAATACTGAGG   62647         GGGACA
                                TCACAGACTAA     TGAGG
                                ||||||||||     |||||
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                                AGTGTCTGATT     ACTCC
                                      ATG___
GAM2685 BCL2L1   5' TATCACAGGTCGGGAGAG    62648        ACTAA   CAT
                                TATCACAG    GGGA   GAG
                                ||||||||    ||||  |||
                                ATAGTGTC    CCCT   CTC
                                    CAG__   ___
GAM2685 FLJ13852 3' TATCCAGACTAAGCCAGGG   62649     A     ____
                                TATC CAGACTA    AGGG
                                |||| |||||||    ||||
                                ATAG GTCTGAT    TCCC
                                  _     TCGG
GAM2685 FLJ23563 5' CAGAGGCGAGGACATGAGG   62650     CTAA
                                CAGA   GGGACATGAGG
                                ||||   ||||||||||
                                GTCT   TCCTGTACTCC
                                  CCGC
GAM2685 HSU47926 3' CACAGACTGGGAGAGAG     62651        AA   CAT
                                CACAGACT  GGGA   GAG
                                ||||||||  ||||   |||
                                GTGTCTGA  CCCT   CTC
                                    __   CT_
GAM2685 KIAA0161 3' TATCACAGGCTGAGGGCTCAAG 62652        A  A   ACA
                                TATCACAG CT AGGG   TGAG
                                |||||||| || ||||   ||||
                                ATAGTGTC GA TCCC   GTTC
                                    C  C   GA_
GAM2685 LANCL2   3' TCACATGTTACAGACATGAGG  62653     GAC  AG
                                TCACA   TA  GGACATGAGG
                                |||||   ||  ||||||||||
                                AGTGT   AT  TCTGTACTCC
                                  ACA  G_
GAM2685 MAP      3' TATCACAGGTTGAACCTGAGG  62654        ACTAAG   A
                                TATCACAG     GGAC TGAGG
                                ||||||||     |||| |||||
                                ATAGTGTC     CTTG ACTCC
                                    CAA___   G
GAM2685 PM5      3' TCACAGTGACAAGGGACATGGG 62655      AC_        A
                                TCACAG   TAAGGGACATG GG
                                ||||||   |||||||||||| ||
                                AGTGTC   GTTCCCTGTAC CC
                                  ACT         _
GAM2685 TRIM11   3' TCACAGACAGGCATGG      62656        TAA  A   A
                                TCACAGAC   GGG CATG G
                                ||||||||   ||| |||| |
                                AGTGTCTG   TCC GTAC C
                                    ___  _   _
GAM2685 LOC221421 3' CATCACAGGTTGGGTGAG    62657        ACTAA  ACA
                                TATCACAG    GGG   TGAG
                                ||||||||    |||   ||||
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                                GTAGTGTC    CCC   ACTC
                                    CAA__   ___
GAM2686  GPM6A    3'  TATAACACATGGGAAGTG    62660        GAAAA   ATA
                                TATAACACA    GGAA   TG
                                |||||||||    ||||   ||
                                ATATTGTGT    CCTT   AC
                                    AC___    C__
GAM2686  DDX37    3'  CATAACACAGGAAAGGCGTTGG 62661         A    AAATA
                                TATAACACAG AAAGG    TGG
                                |||||||||| |||||    |||
                                GTATTGTGTC TTTCC    ACC
                                    C    GCA__
GAM2686  FLJ10159 3'  TAACACTGAAAATATG     62662       AGAAAA
                                TAACAC     GGAAATATG
                                ||||||     |||||||||
                                ATTGTG     CTTTTATAC
                                   A_____
GAM2686  FLJ20343 3'  TATAACCAGATAAATATG    62663       A   AAAGG
                                TATAAC CAGA    AAATATG
                                |||||| ||||    |||||||
                                ATATTG GTCT    TTTATAC
                                   _   A____
GAM2686  ICK      3'  TATAATACAGAAAATGAAA   62664      C      G
                                TATAA ACAGAAAA GAAA
                                ||||| |||||||| ||||
                                ATATT TGTCTTTT CTTT
                                   A       A
GAM2686  KIAA1718 3'  TATAACACGAAAAGGAAA    62665        A
                                TATAACAC GAAAAGGAAA
                                |||||||| ||||||||||
                                ATATTGTG CTTTTCCTTT
                                    _
GAM2686  RBX1     3'  ACACAGAATACAATATGG    62666        AAGGA
                                ACACAGAA    AATATGG
                                ||||||||    |||||||
                                TGTGTCTT    TTATACC
                                    ATG__
GAM2686  LOC126917 3'  TAACACAGGTGGGGGAAACA  62667        AAAA_
                                TAACACAG    GGAAATA
                                ||||||||    |||||||
                                ATTGTGTC    CCTTTGT
                                    CACCC
GAM2686  LOC158865 5'  CACAGAAAAGACATGTTATGG  62668         AAA__
                                CACAGAAAAGG    TATGG
                                ||||||||||    |||||
                                GTGTCTTTTCT    ATACC
                                    GTACA
GAM2686  LOC254532 3'  AACACAGAAAAGATCTGG    62669          AAATA
                                AACACAGAAAAGG    TGG
                                ||||||||||||    |||
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                                TTGTGTCTTTTCT    ACC
                                      AG___
GAM2687 HNRPF    5' TTGGGTGTGGCTTTTTTGCGGA 62672  A      T_________  GCT
            GCCC                  GGTGTGGCT      CGG  CC
                                  |||||||||       |||  ||
                                  CCACACCGA       GCC  GG
                                  C       AAAAACIII  TCG
GAM2687 NAKAP95  3' TATTAGGTTTGGTTTCCAGCTT 62673       G  C  G  C
            CG                    TATTAGGT TGG TTC GGCT CG
                                  |||||||| ||| ||| |||| ||
                                  ATAATCCA ACC AAG TCGA GC
                                       A  A  G  A
GAM2687 TSC22    3' TTAGGTGTGGTTTTTGCGGAGC 62674        C T________  GCT
                                  TTAGGTGTGG T      CGG  C
                                  |||||||||| |      |||  |
                                  AATCCACACC A      GCC  G
                                        _ AAAACIII  TCG
GAM2687 LOC152110 5' TATCAGGTGTGGCAAATTCT  62675          TTCGGG
                                  TATTAGGTGTGGC    CT
                                  ||||||||||||     ||
                                  ATAGTCCACACCG    GA
                                        TTTAA_
GAM2687 LOC203369 3' TATTAGGTGGTGGAGCT    62676       _  CTTCG
                                  TATTAGGTG TGG    GGCT
                                  ||||||||| |||    ||||
                                  ATAATCCAC ACC    TCGA
                                       C  _____
GAM2688 CENTD2   3' GTTGGGCCAAGAGGTCT    53521        AC  ATA
                                  GTTGGGCCAA  AGG  TCT
                                  ||||||||||  |||  |||
                                  CAACCCGGTT  TCC  AGA
                                       C_  ___
GAM2688 CENTD2   3' GTTGGGCCAAGAGGTCT    53521        AC  ATA
                                  GTTGGGCCAA  AGG  TCT
                                  ||||||||||  |||  |||
                                  CAACCCGGTT  TCC  AGA
                                       C_  ___
GAM2688 CLCN7    3' GCTGGGCCAGGTGTCCTCTG  62679       AACA  ATA__
                                  GTTGGGCCA   GG   TCTG
                                  |||||||||   ||   ||||
                                  CGACCCGGT   CC   AGAC
                                       ____  ACAGG
GAM2688 KCNH3    3' GTTGGGCCGAACAGCAGAT   53522       A   __
                                  GTTGGGCC AACAG  GAT
                                  |||||||| |||||  |||
                                  CAACCCGG TTGTC  CTA
                                       C    GT
GAM2688 ORC5L    3' GCTGGGCCAGCACCTG      53523       AACAG A
                                  GTTGGGCCA    G TATCTG
                                  |||||||||    | ||||||
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                                CGACCCGGT    C GTGGAC
                                      _____ _
GAM2688 PRV1    3' GTTGGGCCACACAGCCCTG   53524        A   GATA
                                GTTGGGCCA ACAG   TCTG
                                ||||||||| ||||   ||||
                                CAACCCGGT TGTC   GGAC
                                     G   G___
GAM2688 TCFL4   3' ACTTGGGCCAAATGTTGCAGAT 62680       A_________  GATAT
           ATC                    TTGGGCCAA       CAG    C
                                ||||||||        |||    |
                                AACCCGGTT       GTC    G
                                     TACAACIII  TATAG
GAM2688 CDC14B  3' ACGTTAGGGTCAGTTAAGGAT  62681     _  C  AAC_
                                ACGTT GGG CA   AGGAT
                                ||||| ||| ||   |||||
                                TGCAA CCC GT   TCCTA
                                   T  A  CAAT
GAM2688 CGI-85  3' GTTGGGCTGAAAACATCTG   53525      CAAAC
                                GTTGGGC    AGGATATCTG
                                |||||||    ||||||||||
                                CAACCCG    TTTTGTAGAC
                                    AC___
GAM2688 EPI64   3' GTTGGACCAGGCAGAATCTG  53526        AA    TA
                                GTTGGGCCA  CAGGA  TCTG
                                |||||||||  |||||  ||||
                                CAACCTGGT  GTCTT  AGAC
                                     CC    __
GAM2688 KIAA1169 5' CGCTGGGCTAGGTAACGGTCTG 62682       CA___  A  ATA
                                CGTTGGGC    AAC GG   TCTG
                                ||||||||    ||| ||   ||||
                                GCGACCCG    TTG CC   AGAC
                                    ATCCA  _ ___
GAM2688 MGC10812 3' TTGGGCCAGACGCTGGTCTG  62683       A  A__  ATA
                                TTGGGCCA AC   GG   TCTG
                                |||||||| ||   ||   ||||
                                AACCCGGT TG   CC   AGAC
                                    C  CGA  ___
GAM2688 POLE3   3' TTGGGCCAAGTGGGTCTA    62684        ACA  ATA
                                TTGGGCCAA   GG   TCTG
                                |||||||||   ||   ||||
                                AACCCGGTT   CC   AGAT
                                     CA_  C__
GAM2688 PROZ    3' CGTGGGCCAAGCGGGTGGTCTG 62685    T     ACA  ATA_
                                CGT GGGCCAA   GG    TCTG
                                ||| |||||||   ||    ||||
                                GCA CCCGGTT   CC    AGAC
                                  _     CG_  CACC
GAM2688 SLC17A3 5' GTTGGGCAGGACACC      62686       CAAAC
                                GTTGGGC    AGGATATC
                                |||||||    ||||||||
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                                CAACCCG    TCCTGTGG
                                       _____
GAM2688 LOC197342 5' GTTGGGCCAGAGATCT     53527        AACAG  T
                                GTTGGGCCA    GA ATCT
                                |||||||||    || ||||
                                CAACCCGGT    CT TAGA
                                      _____ C
GAM2689 ABCD2    3' TAACATACTTCATGCAGTATAA 62689       ATAA__    C
           CA                    TAACATAT    CAGTA AACA
                                |||||||||    ||||| ||||
                                ATTGTATG    GTCAT TTGT
                                     AAGTAC    A
GAM2689 BARD1    3' TGAACATTAAAAACAGTACAA  62690    T    ATAT
                                TG AACAT    AACAGTACAA
                                || |||||    ||||||||||
                                AC TTGTA    TTGTCATGTT
                                 _    ATTT
GAM2689 EML1     3' TGTGTCATATATTGTACAACA  62691    AA     AACA
                                TGT  CATATAT    GTACAACA
                                |||  |||||||    ||||||||
                                ACA  GTATATA    CATGTTGT
                                  CA      A___
GAM2689 F11      5' TGTAACATTCTCTCTCAGTACA 62692       ATATAA_
                                TGTAACAT      CAGTACA
                                ||||||||      |||||||
                                ACATTGTA      GTCATGT
                                     AGAGAGA
GAM2689 F11      5' TGTAACATTCTCTCTCAGTACA 62692       ATATAA_
                                TGTAACAT      CAGTACA
                                ||||||||      |||||||
                                ACATTGTA      GTCATGT
                                     AGAGAGA
GAM2689 FBXL3A   3' TAACATATACTTTACAGTA    62693        A__
                                TAACATATAT   ACAGTA
                                ||||||||||   ||||||
                                ATTGTATATG   TGTCAT
                                      AAA
GAM2689 GOLGA5   3' TGTAACATGTACAAAGTA     62694       A    C
                                TGTAACAT TATAA AGTA
                                |||||||| ||||| ||||
                                ACATTGTA ATGTT TCAT
                                     C    _
GAM2689 MEN1     5' TGTAACATAGCAATACAAC    62695       TATAA
                                TGTAACATA    CAGTACAAC
                                |||||||||    |||||||||
                                ACATTGTAT    GTTATGTTG
                                      C____
GAM2689 RNF6     3' GTAACATATATATAGCA      62696         AC
                                GTAACATATATA  AGTA
                                ||||||||||||  ||||
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                                CATTGTATATAT  TCGT
                                      A_
GAM2689  SLC25A14  3'  TGTAACACATATAGCAATA   62697          A
                                TGTAACATATATA CAGTA
                                |||||||||||| |||||
                                ACATTGTGTATAT GTTAT
                                      C
GAM2689  SLC25A14  3'  TGTAACACATATAGCAATA   62697          A
                                TGTAACATATATA CAGTA
                                |||||||||||| |||||
                                ACATTGTGTATAT GTTAT
                                      C
GAM2689  TRHDE    3'  TGTAACACATATTCACACACAA 62698          A_  G
            CA                    TGTAACATATAT  ACA TACAACA
                                |||||||||||  ||| |||||||
                                ACATTGTGTATA  TGT GTGTTGT
                                      AG  _
GAM2689  B7-H1    3'  TGTAACATCTACTACAATA   62699        A  A
                                TGTAACAT TAT ACAGTA
                                |||||||| ||| ||||||
                                ACATTGTA ATG TGTTAT
                                     G  A
GAM2689  DKFZP434C1715 3'  TGTAACATACAACTTCTACAGT 62700          TA____
                                TGTAACATATA     ACAGT
                                ||||||||||     |||||
                                ACATTGTATGT     TGTCA
                                      TGAAGA
GAM2689  KIAA1046  3'  TGTCAACATAACAGTATGACA  62701    AACAT        CA
                                TGT    ATATAACAGTA  ACA
                                |||    ||||||||||  |||
                                ACA    TGTATTGTCAT  TGT
                                  GT___         AC
GAM2689  KIAA1548  3'  TGTAACATTTATAAAAGTA   62702        A    C
                                TGTAACAT TATAA AGTA
                                |||||||| ||||| ||||
                                ACATTGTA ATATT TCAT
                                     A    T
GAM2689  KIAA1577  3'  TATAATATATATACAGTACAA  62703      C      A
                                TGTAA ATATATA CAGTACAA
                                ||||| ||||||| ||||||||
                                ATATT TATATAT GTCATGTT
                                   A     _
GAM2689  MEGF10   3'  TGTAACACGTAGTTTTACAACA 62704        TA  TAACAG
                                TGTAACA  TA     TACAACA
                                |||||||  ||     |||||||
                                ACATTGT  AT     ATGTTGT
                                    GC  CAAA__
GAM2689  LOC146733 3'  TGTGGCATATATACACCAC   62705     AA       A  G
                                TGT  CATATATA CA TAC
                                |||  |||||||| || |||
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                                ACA  GTATATAT GT GTG
                                  CC       _ G
GAM2689  LOC203411 3'  TGAACATATATTTACAGTA   62706    T       A_
                                TG AACATATAT  ACAGTA
                                || |||||||||  ||||||
                                AC TTGTATATA  TGTCAT
                                  _       AA
GAM2689  LOC221312 3'  TGTAACACATACATTACAAT   62707           __
                                TGTAACATATATA  ACAGT
                                ||||||||||||  |||||
                                ACATTGTGTATGT  TGTTA
                                        AA
GAM2690  MHC2TA   3'  CAAGATGTGGTTCATTCCG   62710        AA_  GAGCTC
                                CAGGATGT   TCA     TCCG
                                ||||||||   |||     ||||
                                GTTCTACA   AGT     AGGC
                                     CCA   A_____
GAM2690  RGS16    3'  CAGGATGCAATCAGAGTC    62711             C
                                CAGGATGTAATCAGAG TC
                                |||||||||||||||  ||
                                GTCCTACGTTAGTCTC AG
                                                _
GAM2690  SNX15    3'  CAGGTGTAATCAGGGAGC    62712      A      __
                                CAGG TGTAATCA  GAGC
                                ||||  ||||||||  ||||
                                GTCC ACATTAGT  CTCG
                                  _       CC
GAM2690  TPST1    3'  CGGGATCAAGAGCTCTTTGC   62713    TA   _     CC
                                TG  ATCA GAGCTCT  GC
                                ||  ||||  |||||||  ||
                                GC  TAGT CTCGAGA  CG
                                 CC    T      AA
GAM2690  DKFZP434F091 3'  AAGATGTAATTATGTTCTCTGC 62714          CAGAGC    C
                                AGGATGTAAT     TCTC GC
                                ||||||||||     ||||  ||
                                TTCTACATTA     AGAG CG
                                      ATACA_    A
GAM2690  FLJ13204  3'  CAGGATGTAGTACAGAATGC   62715         AT_   __
                                CAGGATGTA   CAGA  GC
                                |||||||||   ||||  ||
                                GTCCTACAT   GTCT  CG
                                     CAT    TA
GAM2690  KIAA0495  5'  CAGGATGCGGTCCCTCCG    62716        AATCAGAG
                                CAGGATGT       CTCTCCG
                                ||||||||       |||||||
                                GTCCTACG       GGGAGGC
                                    CCA_____
GAM2690  KIAA0544  3'  CAGGATGTGGTCGATAGCCGC  62717         AA  A  GCTCT
                                CAGGATGT  TC GA    CCGC
                                ||||||||  || ||    ||||
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                                GTCCTACA  AG CT    GGCG
                                    CC  _  ATC__
GAM2690  KIAA1211  3'  AGGATGTAATTCCCTCG    62718        CAGAG    C
                                AGGATGTAAT    CTCTC G
                                ||||||||||    |||||  |
                                TCCTACATTA    GGGAG C
                                    A____    A
GAM2690  KLF12     3'  GGATGTAATTACAAAATTCT   62719        __    C
                                GGATGTAAT  CAGAG TCT
                                |||||||||  |||||  |||
                                CCTACATTA  GTTTT AGA
                                    AT    A
GAM2690  MGC26877  5'  AGATGTAATCGTTCCCTCCG   62720        AGAG
                                GGATGTAATC    CTCTCCG
                                ||||||||||    |||||||
                                TCTACATTAG    GGGAGGC
                                    CAA_
GAM2690  MGC32124  3'  CAGGTGCTTGGCAGAGCTCTC  62721     A   AAT_
                                CAGG TGT    CAGAGCTCTC
                                ||||  |||    ||||||||||
                                GTCC ACG    GTCTCGAGAG
                                  _  AACC
GAM2690  OVCOV1    5'  CAGGCTGGAGGAGCTCTCTGC  62722     A  TAATCA      C
                                CAGG TG     GAGCTCTC GC
                                ||||  ||     ||||||||  ||
                                GTCC AC     CTCGAGAG CG
                                  G  CTC___      A
GAM2690  STIM2     3'  CAGGATGTAAATAGCTCT    62723         TCAG
                                CAGGATGTAA    AGCTCT
                                ||||||||||    ||||||
                                GTCCTACATT    TCGAGA
                                    TA__
GAM2690  TCL6      3'  GGATGTAAATCTGTTGTCTCTC 62724        _  AGAG__    C
           TGC                    GGATGTAA TC     CTCTC GC
                                ||||||||  ||     |||||  ||
                                CCTACATT AG     GAGAG CG
                                    T  ACAACA    A
GAM2690  TCL6      3'  GGATGTAAATCTGTTGTCTCTC 62724        _  AGAG__    C
           TGC                    GGATGTAA TC     CTCTC GC
                                ||||||||  ||     |||||  ||
                                CCTACATT AG     GAGAG CG
                                    T  ACAACA    A
GAM2690  LOC113763 3'  CAGGATGCAACACCCAGCTCTC 62725          CAG_     C
           TGC                    CAGGATGTAAT    AGCTCTC GC
                                ||||||||||    |||||||  ||
                                GTCCTACGTTG    TCGAGAG CG
                                    TGGG      A
GAM2690  LOC148837 3'  AGGGGCACTCCAGAGCTCT    62726     AT   A_
                                AGG  GTA  TCAGAGCTCT
                                |||  |||  ||||||||||
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                                TCC  CGT  GGTCTCGAGA
                                  C_   GA
GAM2690  LOC149464 3'  GGAGTAATCAATCACTCT    62727     T       A_
                                GGA GTAATCAG  GCTCT
                                ||| ||||||||  |||||
                                CCT CATTAGTT  TGAGA
                                  _       AG
GAM2690  LOC149566 3'  CAGGATGTAGCTGGTCAC    62728         AATCAG    CTC
                                CAGGATGT     AGCT   CGC
                                ||||||||     ||||   |||
                                GTCCTACA     TCGA   GTG
                                    _______   CCA
GAM2690  LOC150297 5'  CAGAATGTAGTCGGAGCT    62729         A  A
                                CAGGATGTA TC GAGCT
                                ||||||||| || |||||
                                GTCTTACAT AG CTCGA
                                     C  C
GAM2690  LOC221501 3'  CAGGCGTAGTGGGGAGCTCTCC 62730      A    ATCA_
            GC                    CAGG TGTA     GAGCTCTCCGC
                                ||||| ||||     ||||||||||
                                GTCC GCAT     CTCGAGAGGCG
                                  _    CACCC
GAM2691  DKFZp547I224 3'  GATGGGTCATGACTC       62733         GGTC
                                GATGGGTC    GTGACTC
                                ||||||||    |||||||
                                CTACCCAG    TACTGAG
                                     _____
GAM2691  FLJ12476  5'  TCCGACAGGGTCGTG       62734         TCG
                                TCCGATGGG   GTCGTG
                                |||||||||   ||||||
                                AGGCTGTCC   CAGCAC
                                     ___
GAM2691  KIAA1719  3'  TGGGTCGGCAGAGATGGTTCC  62735         C___   AC
                                TGGGTCGGT    GTG  TCC
                                |||||||||    |||  |||
                                ACCCAGCCG    TAC  AGG
                                     TCTC   CA
GAM2691  MGC21688  3'  TCCAGGTGGGGGTGATTC    62736     GAT    C  TC    C
                                TCC   GGGT GG  GTGA TC
                                |||   |||| ||  |||| ||
                                AGG   TCCA CC  CACT AG
                                  ___   _ CC    A
GAM2691  LOC145333 3'  TCCTATGGGTCGGTATATGA   62737     G        C_
                                TCC ATGGGTCGGT  GTGA
                                ||| ||||||||||  ||||
                                AGG TACCCAGCCA  TACT
                                  A         TA
GAM2691  LOC221975 5'  TCCGGCGGCCGCGGTGGTCGTG 62738      ATG    _____
                                TCCG   GGTC    GGTCGTG
                                ||||   ||||    |||||||
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                                AGGC  CCGG   CCAGCAC
                                  CG_   CGCCA
GAM2691 LOC256307 3' TCCAATGACTTGTGACTC   62739       GTCGGTC
                                TCCGATGG     GTGACTC
                                ||||||||     |||||||
                                AGGTTACT     CACTGAG
                                    GAA____
GAM2692 FUT8    3' CGAACTGAGTTTGGTCGTTT  62742   T  CAC  CC
                                CG AC   AG  TGGTCGTTT
                                || ||   ||  |||||||||
                                GC TG   TC  ACCAGCAAA
                                 T  AC_  AA
GAM2692 FLJ11127 3' GTACCACAGTTTAATAGTTT  62743       CC   C
                                GTACCACAG  TGGT GTTT
                                |||||||||  |||| ||||
                                CATGGTGTC  ATTA CAAA
                                     AA   T
GAM2692 KIAA1396 3' GTGCCCACAGCCACCCCTTT  62744   A_     T G  G
                                GT  CCACAGCC G TC TTT
                                ||  |||||||| | || |||
                                CA  GGTGTCGG T GG AAA
                                 CG       _ G  G
GAM2692 LOC113828 5' CCGACTGCAGCTTGGACGT  62745    T  CA   C   T
                                CCG AC  CAGC TGG CGT
                                ||| ||  |||| ||| |||
                                GGC TG  GTCG ACC GCA
                                  _ AC   A   T
GAM2693 FGF2    3' TCTATATTTTTACCTTTTGGG  62748      ATTTT      C__
                                TCTATG    TTTTTACCT   GGG
                                ||||||    |||||||||   |||
                                AGATAT    AAAAATGGA   CCC
                                   _____       AAA
GAM2693 ARHGEF9  5' TCTGTGATTTTTTTTTTTTCTC 62749    A         AC_
           GG                    TCT TGATTTTTTTTT   CTCGG
                                |||  ||||||||||||   |||||
                                AGA ACTAAAAAAAAA   GAGCC
                                  C          AAA
GAM2693 FLJ21302 3' TCTATGATTTTATTCTGG    62750          T   ACCTC
                                TCTATGATTTT TTTT    GG
                                ||||||||||| ||||    ||
                                AGATACTAAAA AAGA    CC
                                      T   _____
GAM2694 ADCY7    3' TGACTTGCCAGGAGAGCCCC   62753        AAAA  C   TT
                                TGATTTGCCA   AG GGT  C
                                ||||||||||   || |||  |
                                ACTGAACGGT   TC TCG  G
                                     CC__  _   GG
GAM2694 CELSR1   3' TGATCTGCTGGGGCACCAGTTT 62754       CAAAAAAG
           C                     TGATTTGC      CGGTTTC
                                |||||||       |||||||
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                                ACTAGACG       GTCAAAG
                                    ACCCCGTG
GAM2694  LRAT     3'  ATTTGCCAATATTGGTTTCA   62755         AAAAGC
                                ATTTGCCAA     GGTTTCA
                                |||||||||     |||||||
                                TAAACGGTT     CCAAAGT
                                    ATAA__
GAM2694  PER2     3'  TGGTTTGCCAAACAACGCTTCA 62756    A       AA    G
                                TG TTTGCCAAA  AGCG TTTCA
                                || |||||||||  |||| |||||
                                AC AAACGGTTT  TTGC GAAGT
                                 C        G_   _
GAM2694  PODXL    3'  TGATTTGCAGAGGCCT      62757        CAAAAA  C
                                TGATTTGC      AG GGTTT
                                ||||||||      || |||||
                                ACTAAACG      TC CCGGA
                                    _______  T
GAM2694  TCEA1    3'  TGATTTGCAGGAAAACTAGTT  62758        CAAA    _
                                TGATTTGC    AAAGC GGTT
                                ||||||||    ||||| ||||
                                ACTAAACG    TTTTG TCAA
                                    TCC_    A
GAM2694  C5orf4   3'  TGATTTGCCAGGGTGTC     62759         AAAAA C   T
                                TGATTTGCCA    G GGT TC
                                ||||||||||    | ||| ||
                                ACTAAACGGT    C CCA AG
                                    ______ _   C
GAM2694  C5orf4   3'  TGATTTGCCAGGGTGTC     62759         AAAAA C   T
                                TGATTTGCCA    G GGT TC
                                ||||||||||    | ||| ||
                                ACTAAACGGT    C CCA AG
                                    ______ _   C
GAM2694  DKFZP564F013 3'  TGATTTACCAAAGAAAATGTTT 62760           A   CG
                                TGATTTGCCAAA AAG  GTTT
                                |||||||||||| |||  ||||
                                ACTAAATGGTTT TTT  CAAA
                                      C   TA
GAM2694  FHR5     3'  TGATTTGCCCAGGAACAATTT  62761         AAAAA
                                TGATTTGCC    AGCGGTTT
                                |||||||||    ||||||||
                                ACTAAACGG    TTGTTAAA
                                    GTCC_
GAM2694  FLJ20527 3'  GATTTGCCAGAAAAGTCA    62762         A    _
                                GATTTGCCA AAAAG CG
                                ||||||||| ||||| ||
                                CTAAACGGT TTTTC GT
                                    C    A
GAM2694  KIAA0009 3'  ATTTGCCAAGTCAATGTTTCA  62763         AAAAGCG
                                ATTTGCCAA      GTTTCA
                                |||||||||      ||||||
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                                TAAACGGTT      CAAAGT
                                     CAGTTA_
GAM2694  MGC29898  3'  TGATTGCCAAAAAAGTGTT   62764      T       CG
                                TGATT GCCAAAAAAG  GTT
                                ||||| ||||||||||  |||
                                ACTAA CGGTTTTTTC  CAA
                                   _       A_
GAM2694  PAK7      3'  TGATTTGCTGGATGAAGGGCT  62765       CAAAA_  C
                                TGATTTGC     AAG GGTT
                                ||||||||     ||| ||||
                                ACTAAACG     TTC CCGA
                                     ACCTAC  _
GAM2694  SPTLC2    3'  TGATCTGCTGAAAGAGGTCT   62766       CAAA   C
                                TGATTTGC    AAAG GGTTT
                                ||||||||    |||| |||||
                                ACTAGACG    TTTC CCAGA
                                     AC__    T
GAM2694  LOC145482 5'  TGATTTGCCGGAAAGAGGCT   62767       AAA    C
                                TGATTTGCC   AAAG GGTT
                                |||||||||   |||| ||||
                                ACTAAACGG   TTTC CCGA
                                     CC_    T
GAM2694  LOC158402 5'  TGATTTCCCAAAAAAGGCC    62768      G      GC
                                TGATTT CCAAAAAA  GGTT
                                ||||||  ||||||||  ||||
                                ACTAAA GGTTTTTT  CCGG
                                   G       __
GAM2694  LOC202986 5'  GATTGCTTAGGGGCGGTTTCA  62769     T  CAAAAAA
                                GATT GC      GCGGTTTCA
                                |||| ||      |||||||||
                                CTAA CG      CGCCAAAGT
                                  _  AATCCC_
GAM2694  LOC203084 3'  TGATTTGCAGGAAAACTAGTT  62758       CAAA    _
                                TGATTTGC    AAAGC GGTT
                                ||||||||    ||||| ||||
                                ACTAAACG    TTTTG TCAA
                                     TCC_    A
GAM2694  LOC204285 3'  TGATTTGCTGAAAGTCTTTTC  62770       CAAA   CGG
                                TGATTTGC    AAAG   TTTC
                                ||||||||    ||||   ||||
                                ACTAAACG    TTTC   AAAG
                                     AC__    AGA
GAM2694  LOC253795 5'  TGATTGCCAAAAACATCTTC   62771      T      AGCGG
                                TGATT GCCAAAAA    TTTC
                                ||||| ||||||||    ||||
                                ACTAA CGGTTTTT    GAAG
                                   _      GTA__
GAM2694  LOC255458 5'  TGATTTGCTGAGGACAGTCT   62772       CAAAAAA
                                TGATTTGC     GCGGTTT
                                ||||||||     |||||||
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                                ACTAAACG      TGTCAGA
                                    ACTCC__
GAM2694 LOC63920 5' TGATTTGCCAGCAAGTT     62773         AAAAA  _
                                TGATTTGCCA    GCG GTT
                                ||||||||||    ||| |||
                                ACTAAACGGT    CGT CAA
                                     _____  T
GAM2695 AP2B1    3' CTTTTCCGCTCCACACAT    62776          AC
                                CTTTTCCGCTTCA  CGT
                                ||||||||||||  |||
                                GAAAAGGCGAGGT  GTA
                                       GT
GAM2695 CXorf6   5' CTTTTCCAGTCATCCATT    62777        CT   A
                                CTTTTCCG  TCA CCGTT
                                ||||||||  ||| |||||
                                GAAAAGGT  AGT GGTAA
                                    C_   A
GAM2695 DKFZP586M1120 3' TTTTCCGCTTCTCCTGCT    62778          AA  _
                                TTTTCCGCTTC  CC GTT
                                ||||||||||  || |||
                                AAAAGGCGAAG  GG CGA
                                      A_  A
GAM2695 FLJ20010 3' CCTTTCCTGTTCCAATCGTT   62779       GC_    C
                                CTTTTCC   TTCAA CGTT
                                |||||||   ||||| ||||
                                GGAAAGG   AGGTT GCAA
                                    ACA     A
GAM2695 FLJ21596 3' CTTTCCCACCCACTGTT     62780          CA  C
                                CTTTTCCGCTT  AC GTT
                                ||||||||||  || |||
                                GAAAGGGTGGG  TG CAA
                                      __  A
GAM2695 KIAA0664 5' TCTTCCGCTTCCCGCT      62781          AA
                                TTTTCCGCTTC  CCGTT
                                ||||||||||  |||||
                                AGAAGGCGAAG  GGCGA
                                      __
GAM2695 KIAA0939 3' CTCTTCCGCCACAGCATCGTT  62782          T  AC__
                                CTTTTCCGCT CA    CGTT
                                |||||||||| ||    ||||
                                GAGAAGGCGG GT    GCAA
                                      T  CGTA
GAM2695 KIAA1819 5' CTTTCCCGCTTACGTT      62783          CAAC
                                CTTTTCCGCTT    CGTT
                                ||||||||||    ||||
                                GAAAGGGCGAA    GCAA
                                      T___
GAM2695 POLA2    3' CTTTCCCACCCAACTGTT    62784          T    C
                                CTTTTCCGCT CAAC GTT
                                |||||||||| |||| |||
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                                GAAAGGGTGG GTTG CAA
                                      _   A
GAM2695  S164     5'  CTTTCCCGCTCTCGTT      62785          CAAC
                                CTTTTCCGCTT   CGTT
                                ||||||||||   ||||
                                GAAAGGGCGAG   GCAA
                                     A___
GAM2695  SCAMP-4  3'  CTTTTTGGCCCAACCGTT    62786      CC  T
                                CTTTT  GCT CAACCGTT
                                |||||  ||| ||||||||
                                GAAAA  CGG GTTGGCAA
                                  AC  _
GAM2695  LOC150174 3'  CTTCTCCGCTTTCGTT      62787          CAAC
                                CTTTTCCGCTT   CGTT
                                ||||||||||   ||||
                                GAAGAGGCGAA   GCAA
                                     A___
GAM2695  LOC150213 3'  CTTCTCCGCTTTCGTT      62787          CAAC
                                CTTTTCCGCTT   CGTT
                                ||||||||||   ||||
                                GAAGAGGCGAA   GCAA
                                     A___
GAM2695  LOC157784 3'  CTTTTCCAGTTTTGCAACCGTT 62788        C ___
                                CTTTTCCG TT   CAACCGTT
                                |||||||| ||  ||||||||
                                GAAAAGGT AA   GTTGGCAA
                                     C  AAC
GAM2695  LOC219513 5'  CTTTCCCGCCCCTCTCGTT   62789          AAC
                                CTTTTCCGCTTC   CGTT
                                ||||||||||||  ||||
                                GAAAGGGCGGGG   GCAA
                                      AGA
GAM2695  LOC256118 5'  CTTCTCCGCGAAATAACTGTT  62790        TTC__  C
                                CTTTTCCGC    AAC GTT
                                |||||||||    ||| |||
                                GAAGAGGCG    TTG CAA
                                     CTTTA   A
GAM2695  LOC94431  5'  CTCTTCCACTACTGTT     62791         TCA  C
                                CTTTTCCGCT   AC GTT
                                ||||||||||  || |||
                                GAGAAGGTGA   TG CAA
                                     ___  A
GAM2696  CRI1     3'  TGGCACAAAACTATTTGG    62794          AAG
                                TGGCACAAGACTG   GG
                                ||||||||||||  ||
                                ACCGTGTTTTGAT   CC
                                      AAA
GAM2696  CYLN2    3'  TGGCAAGACCAGGAAGGG    62795      CA   __
                                TGGCA  AGACT  GAAGGG
                                |||||  |||||  ||||||
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                                ACCGT  TCTGG  CTTCCC
                                   __    TC
GAM2696  DLX4    3'  TGGCAAGACCAAGGG      62796      CA    G
                                TGGCA  AGACT AAGGG
                                |||||  ||||| |||||
                                ACCGT  TCTGG TTCCC
                                   __    _
GAM2696  DLX4    3'  TGGCAAGACCAAGGG      62796      CA    G
                                TGGCA  AGACT AAGGG
                                |||||  ||||| |||||
                                ACCGT  TCTGG TTCCC
                                   __    _
GAM2696  FLOT2   3'  TGGCACAAGGGCTCTGGGG   62797        A___   AA
                                TGGCACAAG   CTG  GGG
                                |||||||||   |||  |||
                                ACCGTGTTC   GAC  CCC
                                     CCGA  __
GAM2696  GPRK7   5'  AGCACAAGAGGGCTGGAGGG  62798         ___   A
                                GGCACAAGA   CTG AGGG
                                |||||||||   ||| ||||
                                TCGTGTTCT   GAC TCCC
                                     CCC   C
GAM2696  KCNS3   5'  TGGCCAAAAAGAAGGG     62799     A    CT
                                TGGC CAAGA  GAAGGG
                                ||||  |||||  ||||||
                                ACCG GTTTT  CTTCCC
                                  _     T_
GAM2696  KIF3C   3'  TGTCAAAGCTGAAGGG     62800    G  C   A
                                TG CA AAG CTGAAGGG
                                ||  ||  |||  ||||||||
                                AC GT TTC GACTTCCC
                                 A  _   _
GAM2696  MAL     3'  TGGCACAAGATGGGG      62801         C  AA
                                TGGCACAAGA TG  GGG
                                ||||||||||  ||  |||
                                ACCGTGTTCT AC  CCC
                                      _  __
GAM2696  MAL     3'  TGGCACAAGATGGGG      62801         C  AA
                                TGGCACAAGA TG  GGG
                                ||||||||||  ||  |||
                                ACCGTGTTCT AC  CCC
                                      _  __
GAM2696  MAL     3'  TGGCACAAGATGGGG      62801         C  AA
                                TGGCACAAGA TG  GGG
                                ||||||||||  ||  |||
                                ACCGTGTTCT AC  CCC
                                      _  __
GAM2696  MAL     3'  TGGCACAAGATGGGG      62801         C  AA
                                TGGCACAAGA TG  GGG
                                ||||||||||  ||  |||
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                                ACCGTGTTCT AC  CCC
                                      _  __
GAM2696  MLH3    3'  TGAAGAAGACTGAAGGG    62802    CAC
                                TGG  AAGACTGAAGGG
                                |||  ||||||||||||
                                ACT  TTCTGACTTCCC
                                  TC_
GAM2696  OTX1    3'  TGGCACAAAAATGGGGG    62803        C  AA
                                TGGCACAAGA TG  GGG
                                |||||||||| ||  |||
                                ACCGTGTTTT AC  CCC
                                     T  C_
GAM2696  PAK1    3'  TGGCACAATGAGGCTGGGG   62804       _  __  AA
                                TGGCACAA GA  CTG  GGG
                                |||||||| ||  |||  |||
                                ACCGTGTT CT  GAC  CCC
                                    A  CC  __
GAM2696  PARK2   3'  TGGACAAACTGAAAGG     62805    C  A
                                TGG ACA GACTGAAGGG
                                ||| ||| ||||||||||
                                ACC TGT TTGACTTTCC
                                  _  _
GAM2696  PARK2   3'  TGGACAAACTGAAAGG     62805    C  A
                                TGG ACA GACTGAAGGG
                                ||| ||| ||||||||||
                                ACC TGT TTGACTTTCC
                                  _  _
GAM2696  PARK2   3'  TGGACAAACTGAAAGG     62805    C  A
                                TGG ACA GACTGAAGGG
                                ||| ||| ||||||||||
                                ACC TGT TTGACTTTCC
                                  _  _
GAM2696  PNUTL2  3'  TGGCAGTAGCTGAAGGG    62806     CA  A
                                TGGCA  AG CTGAAGGG
                                |||||  || ||||||||
                                ACCGT  TC GACTTCCC
                                   CA  _
GAM2696  PNUTL2  3'  TGGCAGTAGCTGAAGGG    62806     CA  A
                                TGGCA  AG CTGAAGGG
                                |||||  || ||||||||
                                ACCGT  TC GACTTCCC
                                   CA  _
GAM2696  PNUTL2  3'  TGGCAGTAGCTGAAGGG    62806     CA  A
                                TGGCA  AG CTGAAGGG
                                |||||  || ||||||||
                                ACCGT  TC GACTTCCC
                                   CA  _
GAM2696  PNUTL2  3'  TGGCAGTAGCTGAAGGG    62806     CA  A
                                TGGCA  AG CTGAAGGG
                                |||||  || ||||||||
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                                ACCGT  TC GACTTCCC
                                  CA  _
GAM2696  RPL10    5'  TGGCACACCGAAGGG      62807       AAG
                                TGGCAC  ACTGAAGGG
                                ||||||  |||||||||
                                ACCGTG  TGGCTTCCC
                                  ___
GAM2696  RRAS2    3'  TAGCTAAAACTGAAGGG     62808      AC
                                TGGC  AAGACTGAAGGG
                                ||||  ||||||||||||
                                ATCG  TTTTGACTTCCC
                                  A_
GAM2696  TRIM9    3'  TAGCCAAGACTGAAGGG     62809      A
                                TGGC CAAGACTGAAGGG
                                |||| ||||||||||||
                                ATCG GTTCTGACTTCCC
                                  _
GAM2696  3-PAP    3'  TGACACAAATCCAGGG      62810         A  GA
                                TGGCACAAG CT  AGGG
                                ||||||||| ||  ||||
                                ACTGTGTTT GG  TCCC
                                     A  __
GAM2696  ALDRL6   3'  GGCACAAGTTGCCGTGAGGG  62811         A__   A_
                                GGCACAAG   CTG  AGGG
                                ||||||||   |||  ||||
                                CCGTGTTC   GGC  TCCC
                                     AAC   AC
GAM2696  ARFGAP1  3'  TGGCCAAGACTGAGGG      62812      A       A
                                TGGC CAAGACTGA GGG
                                |||| ||||||||| |||
                                ACCG GTTCTGACT CCC
                                  _       _
GAM2696  C20orf150 3'  TGGGACATAACTGAAGGG    62813     C   A
                                TGG ACA GACTGAAGGG
                                ||| ||| ||||||||||
                                ACC TGT TTGACTTCCC
                                  C   A
GAM2696  CBX6     3'  TGGTCAAGAACTGAAGGG    62814     CA    _
                                TGG  CAAGA CTGAAGGG
                                |||  ||||| ||||||||
                                ACC  GTTCT GACTTCCC
                                  A_    T
GAM2696  CNNM4    3'  TGTACAAGACTAAGGG      62815    GC       A
                                TG  ACAAGACTGA GGG
                                ||  |||||||||| |||
                                AC  TGTTCTGATT CCC
                                  A_        _
GAM2696  DKFZP434C171 3'  GGCACCAAGACTGAAGGG    62816      _
                                GGCAC AAGACTGAAGGG
                                ||||| ||||||||||||
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                                CCGTG TTCTGACTTCCC
                                   G
GAM2696  DKFZp547I014 5'  TAGCACAAGCCAGGG       62817          A  GA
                                TGGCACAAG CT  AGGG
                                ||||||||| ||  ||||
                                ATCGTGTTC GG  TCCC
                                      _  __
GAM2696  FLJ10101  3'  TGACACAAGCACCAGGG     62818          _  GA
                                TGGCACAAG ACT  AGGG
                                ||||||||| |||  ||||
                                ACTGTGTTC TGG  TCCC
                                     G  __
GAM2696  FLJ11193  3'  GCACAAGAGACCCTGAAGGG   62819         ____
                                GCACAAGA   CTGAAGGG
                                ||||||||   ||||||||
                                CGTGTTCT   GACTTCCC
                                    CTGG
GAM2696  FLJ20514  5'  TGGCACAAGCCTTCAGGG    62820          A  GA
                                TGGCACAAG CT  AGGG
                                ||||||||| ||  ||||
                                ACCGTGTTC GA  TCCC
                                     G  AG
GAM2696  FLJ21126  3'  TGGCAAAGGCCTGAAGGG    62821       C  A_
                                TGGCA AAG  CTGAAGGG
                                ||||| |||  ||||||||
                                ACCGT TTC  GACTTCCC
                                   _  CG
GAM2696  FLJ22055  3'  TGGCCACACACCCACTGAAGGG 62822      _  AG___
                                TGGC ACA    ACTGAAGGG
                                |||| |||    |||||||||
                                ACCG TGT    TGACTTCCC
                                  G  GTGGG
GAM2696  GALNT11   5'  TAGCATAGCTGAAGGG      62823       CA  A
                                TGGCA  AG CTGAAGGG
                                |||||  || ||||||||
                                ATCGT  TC GACTTCCC
                                   A_  _
GAM2696  KIAA0321  3'  TGGTCCTGAAGAGACTGAAGGG 62824     CACA____          III
            C                    TGG       AGACTGAAGGG  C
                                |||       ||||||||||  |
                                ACC       TCTGACTTCCC  G
                                  AGGACTTC          III
GAM2696  KIAA0472  3'  TGGCCAAAAGGTGAGGGG    62825      A    C_  A
                                TGGC CAAGA  TGA GGG
                                |||| |||||  ||| |||
                                ACCG GTTTT  ACT CCC
                                   _    CC  C
GAM2696  KIAA0710  3'  CGGTACAGCTGAAGGG      62826     C  A A
                                TGG ACA G CTGAAGGG
                                ||| ||| | ||||||||
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                                GCC TGT C GACTTCCC
                                  A  _ _
GAM2696  KIAA0937  3'  TGGCACAAGACAAAGGG     62827          T
                                TGGCACAAGAC GAAGGG
                                |||||||||| ||||||
                                ACCGTGTTCTG TTTCCC
                                          _
GAM2696  KIAA0976  3'  TGACACAAGCCTGTGAGGG   62828         A  A_
                                TGGCACAAG CTG  AGGG
                                ||||||||| |||  ||||
                                ACTGTGTTC GAC  TCCC
                                     G  AC
GAM2696  KIAA1054  3'  TGGCAAGACCAAGGG      62796      CA    G
                                TGGCA  AGACT AAGGG
                                |||||  ||||| |||||
                                ACCGT  TCTGG TTCCC
                                  __   _
GAM2696  KIAA1853  3'  TGGCTTAAGCTGAAGGG    62829     AC   A
                                TGGC  AAG CTGAAGGG
                                ||||  ||| ||||||||
                                ACCG  TTC GACTTCCC
                                  AA  _
GAM2696  KIAA1944  3'  TGACACAAAACCCAGGG    62830          GA
                                TGGCACAAGACT  AGGG
                                ||||||||||||  ||||
                                ACTGTGTTTTGG  TCCC
                                     G_
GAM2696  LW-1      5'  GCACAAGAGTGCCGAGGGG   62831        ___   A
                                GCACAAGA   CTGA GGG
                                ||||||||   |||| |||
                                CGTGTTCT   GGCT CCC
                                     CAC   C
GAM2696  LW-1      5'  GCACAAGAGTGCCGAGGGG   62831        ___   A
                                GCACAAGA   CTGA GGG
                                ||||||||   |||| |||
                                CGTGTTCT   GGCT CCC
                                     CAC   C
GAM2696  MAPK8IP3  3'  TGGCAGCAAGCGACCTGGGG  62832      _  __   GAA
                                TGGCA CAA  GACT   GGG
                                ||||| |||  ||||   |||
                                ACCGT GTT  CTGG   CCC
                                  C  CG   AC_
GAM2696  MGC2654   3'  TGACCAACTGAAGGG      62833     A  AG
                                TGGC CA  ACTGAAGGG
                                |||| ||  |||||||||
                                ACTG GT  TGACTTCCC
                                  _ __
GAM2696  My015     3'  TGGCACAAGATACTCTAGG   62834         __ GA
                                TGGCACAAGA  CT  AGG
                                ||||||||||  ||  |||
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                                ACCGTGTTCT  GA  TCC
                                      AT  GA
GAM2696  PASK     3'  TGGCCACAAACTAAAGGG    62835      ACA
                                TGGC   AGACTGAAGGG
                                ||||   ||||||||||
                                ACCG   TTTGATTTCCC
                                  GTG
GAM2696  PRDM10   3'  TGGCAAAAACCGAGGG      62836      C       A
                                TGGCA AAGACTGA GGG
                                ||||| |||||||| |||
                                ACCGT TTTTGGCT CCC
                                   _       _
GAM2696  PRDM12   3'  TGTCACAGCTGAAGGG      62837    G    A A
                                TG CACA G CTGAAGGG
                                || |||| | ||||||||
                                AC GTGT C GACTTCCC
                                 A   _ _
GAM2696  PSR      3'  TGACACAAGCTAGTGGG     62838         A   AA
                                TGGCACAAG CTG  GGG
                                ||||||||| |||  |||
                                ACTGTGTTC GAT  CCC
                                      _  CA
GAM2696  RGPR     3'  TAGCACAAACCTCTTGAAGGG  62839         AC___
                                TGGCACAAG    TGAAGGG
                                |||||||||    |||||||
                                ATCGTGTTT    ACTTCCC
                                     GGAGA
GAM2696  SKIP     3'  TGGGCAAGACTAGAAGAG    62840     CA      _
                                TGG  CAAGACT GAAGGG
                                |||  ||||||| ||||||
                                ACC  GTTCTGA CTTCTC
                                  C_      T
GAM2696  SKIP     3'  TGGGCAAGACTAGAAGAG    62840     CA      _
                                TGG  CAAGACT GAAGGG
                                |||  ||||||| ||||||
                                ACC  GTTCTGA CTTCTC
                                  C_      T
GAM2696  SOX7     3'  GGCACAAGAAGGAGAGGG    62841         CT  _
                                GGCACAAGA  GA AGGG
                                |||||||||  || ||||
                                CCGTGTTCT  CT TCCC
                                     TC  C
GAM2696  TREX1    5'  TGGCACAATGCACCGGGG    62842        G__    AA
                                TGGCACAA   ACTG  GGG
                                ||||||||   ||||  |||
                                ACCGTGTT   TGGC  CCC
                                    ACG    __
GAM2696  TREX1    5'  TGGCACAATGCACCGGGG    62842        G__    AA
                                TGGCACAA   ACTG  GGG
                                ||||||||   ||||  |||
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                                ACCGTGTT  TGGC  CCC
                                    ACG   __
GAM2696  TREX1    5'  TGGCACAATGCACCGGGG    62842       G__   AA
                                TGGCACAA  ACTG  GGG
                                ||||||||  ||||  |||
                                ACCGTGTT  TGGC  CCC
                                    ACG   __
GAM2696  XPO5     3'  TGGCACAAGTAGTTGAGGG   62843       AC__  A
                                TGGCACAAG   TGA GGG
                                |||||||||   ||| |||
                                ACCGTGTTC   ACT CCC
                                     ATCA  _
GAM2696  ZNF282   3'  TGACACAAACAAGGG      62844       A  TG
                                TGGCACA GAC  AAGGG
                                ||||||| |||  |||||
                                ACTGTGT TTG  TTCCC
                                   _  __
GAM2696  LOC144262 5'  GGAACGCAGACTGAAGGG   62845    C  A_
                                GG AC  AGACTGAAGGG
                                || ||  ||||||||||
                                CC TG  TCTGACTTCCC
                                 T  CG
GAM2696  LOC148147 3'  TGGCCAAAAGAAAGGG     62846     A    CT
                                TGGC CAAGA  GAAGGG
                                |||| |||||  ||||||
                                ACCG GTTTT  TTTCCC
                                  _    C_
GAM2696  LOC148183 5'  TGGCACAAAAGAGGG      62847         CT  A
                                TGGCACAAGA  GA GGG
                                ||||||||||  || |||
                                ACCGTGTTTT  CT CCC
                                     __  _
GAM2696  LOC149194 3'  TAGCACACTGAAGGG      62848       AAG
                                TGGCAC   ACTGAAGGG
                                ||||||   |||||||||
                                ATCGTG   TGACTTCCC
                                    ___
GAM2696  LOC150759 3'  TGTGCAAAACTGGAAGGG   62849    GCA      _
                                TG   CAAGACTG AAGGG
                                ||   |||||||| |||||
                                AC   GTTTTGAC TTCCC
                                 AC_       C
GAM2696  LOC151451 3'  TGGTAGACCAAACTGAGGGG  62850    C__  A     A
                                TGG   AC AGACTGA GGG
                                |||   || ||||||| |||
                                ACC   TG TTTGACT CCC
                                  ATC  G      C
GAM2696  LOC157506 3'  TGGCACAAAAATGGGG     62851         C  AA
                                TGGCACAAGA TG  GGG
                                |||||||||| ||  |||
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                                ACCGTGTTTT AC  CCC
                                      T  __
GAM2696  LOC158267 5'  TGGCACAAGCCACAAAGGG   62852        A  __
                                TGGCACAAG CT  GAAGGG
                                ||||||||| ||  ||||||
                                ACCGTGTTC GG  TTTCCC
                                      _ TG
GAM2696  LOC162333 5'  TGGCAAAACTGGCCGAGGG   62853      CA    A___
                                TGGCA  AGACTG   AGGG
                                |||||  ||||||   ||||
                                ACCGT  TTTGAC   TCCC
                                   __    CGGC
GAM2696  LOC222136 3'  GGCACAAGCTGTGGGAGGG   62854        A  A___
                                GGCACAAG CTG   AGGG
                                |||||||| |||   ||||
                                CCGTGTTC GAC   TCCC
                                      _  ACCC
GAM2696  LOC222682 5'  TGGCACAAACTCCAAAAGG   62855        A_ TG
                                TGGCACAAG  C  AAGGG
                                |||||||||  |  |||||
                                ACCGTGTTT  G  TTTCC
                                      GA GT
GAM2696  LOC257506 5'  TGGCACAAACTCCAAAAGG   62855        A_ TG
                                TGGCACAAG  C  AAGGG
                                |||||||||  |  |||||
                                ACCGTGTTT  G  TTTCC
                                      GA GT
GAM2696  LOC257624 5'  TGGCACAAACTCCAAAAGG   62855        A_ TG
                                TGGCACAAG  C  AAGGG
                                |||||||||  |  |||||
                                ACCGTGTTT  G  TTTCC
                                      GA GT
GAM2696  LOC51285  3'  TGGCACAAGGACCCCAGG    62856        _  GA
                                TGGCACAAG ACT  AGG
                                ||||||||| |||  |||
                                ACCGTGTTC TGG  TCC
                                      C  GG
GAM2696  LOC90050  3'  GGCTGCAAGGCTGAAGGG    62857    A_   A
                                GGC  CAAG CTGAAGGG
                                |||  |||| ||||||||
                                CCG  GTTC GACTTCCC
                                  AC   C
GAM2696  LOC90678  3'  TGGCACAAGGCTGAGCAGG   62858        A  A_
                                TGGCACAAG CTGA  GGG
                                ||||||||| ||||  |||
                                ACCGTGTTC GACT  TCC
                                      C   CG
GAM2696  LOC91496  5'  TGGCACAACGTGAAAAAGGG  62859        ___  CT
                                TGGCACAA  GA  GAAGGG
                                ||||||||  ||  ||||||
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                                ACCGTGTT  CT  TTTCCC
                                    GCA  T_
GAM2697  FLJ20275  3'  TGTTGGCTTTTTCTTTTGTG  62862     C     T   C
                                TGTT GCTTTTT CTTT GTG
                                |||| ||||||| |||| |||
                                ACAA CGAAAAA GAAA CAC
                                  C      _   A
GAM2697  KIAA1348  3'  CTGTTTGTTTTTTTCCTCC   62863     CGC
                                CTGTT  TTTTTTCTTTC
                                |||||  ||||||||||
                                GACAA  AAAAAAGGAGG
                                   ACA
GAM2697  LOC256021 3'  TGTTCACTGCTTTTTTTTGTG  62864       T   C  C
                                TGTTCGCT TTTT TTT GTG
                                |||||||| |||| ||| |||
                                ACAAGTGA GAAA AAA CAC
                                    C   A  A
GAM2697  LOC257302 5'  TGTTTGCTTTCTTTTCCA    62865     C      C
                                TGTT GCTTTTTT TTTCG
                                |||| |||||||| |||||
                                ACAA CGAAAGAA AAGGT
                                  A      _
GAM2697  LOC91138  5'  CTGTTTGCTGATGAACTTTTGT 62866     C  TTTTT_   C
          G                      CTGTT GCT     CTTT GTG
                                ||||| |||     |||| |||
                                GACAA CGA     GAAA CAC
                                   A  CTACTT   A
GAM2698  EVA1     3'  TGAATATTTATTAGTAGTA   62869     TAGAC
                                TGA    TTATTAGTAGTA
                                |||    ||||||||||||
                                ACT    AATAATCATCAT
                                  TATA_
GAM2698  EXTL1    3'  ACATGATAGGTTTTACCGGT   62870       AC_   TA
                                ACATGATAG  TTAT  GT
                                |||||||||  ||||  ||
                                TGTACTATC  AATG  CA
                                    CAA   GC
GAM2698  TFDP1    3'  ATGATAGACTTATAAGTA    62871         T
                                ATGATAGACTTAT AGTA
                                |||||||||||| ||||
                                TACTATCTGAATA TCAT
                                       T
GAM2698  LOC131368 3'  ACAGGGTCACATTAGTAGTA  62872     ACT__
                                ATAG    TATTAGTAGTA
                                ||||    ||||||||||
                                TGTC    GTAATCATCAT
                                  CCAGT
GAM2698  LOC154860 5'  TGATAGAAATAAGTAGT     62873       CT  TT
                                TGATAGA  TA  AGTAGT
                                |||||||  ||  ||||||
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                                ACTATCT  AT  TCATCA
                                   TT  __
GAM2699  ABCD4    3'  TACACAACACTGGCAAGT    62876        CAATT  T
                                TACACAATAC    TG CAAGT
                                ||||||||||    || |||||
                                ATGTGTTGTG    AC GTTCA
                                      _____ C
GAM2699  ABCD4    3'  TACACAACACTGGCAAGT    62876        CAATT  T
                                TACACAATAC    TG CAAGT
                                ||||||||||    || |||||
                                ATGTGTTGTG    AC GTTCA
                                      _____ C
GAM2699  ABCD4    3'  TACACAACACTGGCAAGT    62876        CAATT  T
                                TACACAATAC    TG CAAGT
                                ||||||||||    || |||||
                                ATGTGTTGTG    AC GTTCA
                                      _____ C
GAM2699  ABCD4    3'  TACACAACACTGGCAAGT    62876        CAATT  T
                                TACACAATAC    TG CAAGT
                                ||||||||||    || |||||
                                ATGTGTTGTG    AC GTTCA
                                      _____ C
GAM2699  CNR1     3'  ACACAATACTATTCAAGT    62877        CAATTTG
                                ACACAATAC     TCAAGT
                                |||||||||     ||||||
                                TGTGTTATG     AGTTCA
                                    ATA____
GAM2699  CPNE3    3'  TACACATGTATTGTCAAGT    62878      ATACCAAT
                                TACACA      TTGTCAAGT
                                ||||||      |||||||||
                                ATGTGT      AACAGTTCA
                                   ACAT____
GAM2699  HAO1     3'  CACAGTGTCTCTTTGTCAAGTA 62879     ATACCAA
                                CACA     TTTGTCAAGTA
                                ||||     ||||||||||
                                GTGT     AAACAGTTCAT
                                  CACAGAG
GAM2699  SIAH2    3'  CAACAGCCTGTCAAGT      62880      _ AATT
                                CAATA CC   TGTCAAGT
                                ||||| ||   ||||||||
                                GTTGT GG   ACAGTTCA
                                  C ____
GAM2699  SULT2A1  3'  TACACAATGACCCCAGTCAGGT 62881       _  AATTT   A
           A                     TACACAAT ACC    GTCA GTA
                                 ||||||||| |||    |||| |||
                                 ATGTGTTA TGG    CAGT CAT
                                     C  GGT__   C
GAM2699  KIAA0865 3'  AATACCAATAAAACACAAGTA  62882       TTGT__
                                AATACCAAT     CAAGTA
                                |||||||||     ||||||
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                                TTATGGTTA     GTTCAT
                                     TTTTGT
GAM2699  KIAA1096  3'  ACAATGCCAACTCAACACAGTA 62883      A      T  _
                                ACAAT CCAATTTG CA AGTA
                                ||||| |||||||| || ||||
                                TGTTA GGTTGAGT GT TCAT
                                   C       T  G
GAM2699  KIAA1374  3'  TACACAGTACAACTTGTAAGTA 62884      A  C      C
                                TACACA TAC AATTTGT AAGTA
                                |||||| ||| ||||||| |||||
                                ATGTGT ATG TTGAACA TTCAT
                                   C  _     _
GAM2699  LOC152215 3'  TACAGAATTACAAAGTCAAGTA 62885     C  AC  TTT
                                TACA AAT  CAA   GTCAAGTA
                                |||| |||  |||   ||||||||
                                ATGT TTA  GTT   CAGTTCAT
                                  C  AT  T__
GAM2699  LOC51031  3'  TACACAATATAATTCCATTTCG 62886        _____  A   TCA
            AGT                   ACACAATA    CCA TTTG   AGT
                                |||||||||    ||| ||||   |||
                                TGTGTTAT    GGT AAGC   TCA
                                    ATTAA   A   ___
GAM2699  LOC92344  3'  CACAATGTATTGGTCAAGTA   62887      ACCA   T
                                CACAAT    ATT GTCAAGTA
                                ||||||    ||| ||||||||
                                GTGTTA    TAA CAGTTCAT
                                   CA__   C
GAM2700  BFSP2    5'  GGCTGCTTTGTCTGCTGTCT   62890     ACA   G
                                GGCT   TTG CTGCTGTCT
                                ||||   ||| |||||||||
                                CCGA   AAC GACGACAGA
                                  CGA   A
GAM2700  CYP1B1   3'  TAAAGGCTACATATAAATGTTG 62891   T       _  C  C
            T                    C AAGGCTACAT TGG TG TGT
                                | ||||||||| ||| || |||
                                A TTCCGATGTA ATT AC ACA
                                 T        T   T  A
GAM2700  DTNA     3'  AGGCTGCTGCCAGGCTGCTGTC 62892      ACATT__
            T                    AGGCT      GGCTGCTGTCT
                                |||||      ||||||||||
                                TCCGA      CCGACGACAGA
                                   CGACGGT
GAM2700  DTNA     3'  AGGCTGCTGCCAGGCTGCTGTC 62892      ACATT__
            T                    AGGCT      GGCTGCTGTCT
                                |||||      ||||||||||
                                TCCGA      CCGACGACAGA
                                   CGACGGT
GAM2700  ELAVL3   3'  GGCTGCCTGTGCTGTCT    62893     ACA   GC
                                GGCT   TTG  TGCTGTCT
                                ||||   |||  ||||||||
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                                CCGA   GAC  ACGACAGA
                                  CG_  __
GAM2700 IL10RA   3' GGCTGTGTCTGATACTGTCT  62894     ACA_   C
                                GGCT    TTGG TGCTGTCT
                                ||||    |||| ||||||||
                                CCGA    GACT ATGACAGA
                                  CACA   _
GAM2700 MEST     3' AGCTACATTGGAAAGCCTCT  62895         CT_   G
                                GGCTACATTGG   GCT TCT
                                ||||||||||   ||| |||
                                TCGATGTAACC   CGG AGA
                                      TTT  _
GAM2700 MN1      3' TAAGGCTATTTTTAAAGCTGT  62896       CA  GGCT
                                TAAGGCTA  TT   GCTGT
                                ||||||||  ||   |||||
                                ATTCCGAT  AA   CGACA
                                     AA  ATTT
GAM2700 S100B    3' AGGCTGCAAGCCCTTGCTGTCT 62897      A  TT   ___
                                AGGCT CA  GGCT   GCTGTCT
                                ||||| ||  ||||   |||||||
                                TCCGA GT  TCGG   CGACAGA
                                  C  __   GAA
GAM2700 SCD      3' AGGCTACAGAAAGGTTGTCT   62898       TT__  CTGC
                                AGGCTACA   GG   TGTCT
                                ||||||||   ||   |||||
                                TCCGATGT   CC   ACAGA
                                     CTTT  A___
GAM2700 SLC21A2  3' CTGAGGTTACATTGAGCC    62899    A  C     _
                                CT AGG TACATTG GCT
                                || ||| ||||||| |||
                                GA TCC ATGTAAC CGG
                                 C  A     T
GAM2700 TGFA     3' AGGGTTGGCTGCTGTCT     62900    CTACA
                                AGG    TTGGCTGCTGTCT
                                |||    ||||||||||||
                                TCC    AACCGACGACAGA
                                  C____
GAM2700 C20orf177 3' TAGAGCTACATAATCTTGTCT  62901    AG     TGG  GC
                                TA  GCTACAT   CT  TGTCT
                                ||  |||||||   ||  |||||
                                AT  CGATGTA   GA  ACAGA
                                 CT      TTA  __
GAM2700 CALN1    3' GGCTACATGGCATCC       62902        T   TGCT
                                GGCTACAT GGC    GTCT
                                |||||||| |||    ||||
                                CCGATGTA CCG    TAGG
                                      _  ____
GAM2700 FLJ21126 3' TAAGATTTTTGTTGCTGTCT  62903      CTACA   GC
                                TAAGG    TTG  TGCTGTCT
                                |||||    |||  ||||||||
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                              ATTCT    AAC  ACGACAGA
                                 AAA__   A_
GAM2700  FLJ22679  3'  CTAAGCCTGCTGCTGT     62904      G  ACATTG
                              CTAAG CT     GCTGCTGT
                              ||||| ||     ||||||||
                              GATTC GA     CGACGACA
                                 G _______
GAM2700  FLJ22679  3'  CTAAGCCTGCTGCTGT     62904      G  ACATTG
                              CTAAG CT     GCTGCTGT
                              ||||| ||     ||||||||
                              GATTC GA     CGACGACA
                                 G _______
GAM2700  GALNT6    3'  GGGGTGCAATGGTGCTGTCT   62905    CTA_  T   C
                              GG    CA TGG TGCTGTCT
                              ||    || ||| ||||||||
                              CC    GT ACC ACGACAGA
                               CCAC  T  _
GAM2700  GBA2      5'  CTACAGGCAGGCTGCTGTC    62906      TT__
                              CTACA    GGCTGCTGTC
                              |||||    ||||||||||
                              GATGT    CCGACGACAG
                                 CCGT
GAM2700  KIAA0152  3'  CTGAAGCTAATCCTGCTGTCT  62907    A     C   GG
                              CT AGGCTA ATT  CTGCTGTCT
                              || |||||| |||  |||||||||
                              GA TTCGAT TAG  GACGACAGA
                               C     _  __
GAM2700  KIAA1054  3'  GGGTTGTTTGACTGCTGTCT   62908    CTACA
                              GG    TTGGCTGCTGTCT
                              ||    ||||||||||||
                              CC    AACTGACGACAGA
                               CAACA
GAM2700  MGC12928  5'  CTAAGGCTGTTCATTCTGTCT  62909        A__    GGCTG
                              CTAAGGCT   CATT    CTGTCT
                              ||||||||   ||||    ||||||
                              GATTCCGA   GTAA    GACAGA
                                   CAA   ______
GAM2700  PLPL      3'  TAAGGCATGACTGCTGTC    62910      TACAT
                              TAAGGC    TGGCTGCTGTC
                              ||||||    ||||||||||
                              ATTCCG    ACTGACGACAG
                                 T_____
GAM2700  PRO1866   5'  CTGAGGCTACAATGGTTCAACC 62911    A      T   CT__
                              CT AGGCTACA TGG    GCT
                              || |||||||| |||    |||
                              GA TCCGATGT ACC    TGG
                               C       T   AAGT
GAM2700  STX3A     3'  CTAGCGGCTGCTGCTGCTGT   62912     A_   ACATTG
                              CTA  GGCT     GCTGCTGT
                              |||  ||||     ||||||||
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                                GAT  CCGA     CGACGACA
                                  CG    CGA___
GAM2700  LOC149448 3'  GGCTGCCAATATGCTGTCT    62913      A_  T  GC
                                GGCT  CA TG  TGCTGTCT
                                ||||  || ||  ||||||||
                                CCGA  GT AT  ACGACAGA
                                  CG  T  __
GAM2700  LOC152445 3'  CAAGGTTGTAACTGCTGTC    62914       CTACAT
                                TAAGG     TGGCTGCTGTC
                                |||||     ||||||||||
                                GTTCC     ATTGACGACAG
                                   AAC___
GAM2700  LOC152687 5'  GGGGGTTTGGCTGCTGTCT    62915    CTACA
                                GG     TTGGCTGCTGTCT
                                ||     ||||||||||||
                                CC     AACCGACGACAGA
                                 CCCA_
GAM2700  LOC153139 5'  GCTGCATTGATGCTGTCT     62916     A     C
                                GCT CATTGG TGCTGTCT
                                ||| |||||| ||||||||
                                CGA GTAACT ACGACAGA
                                  C     _
GAM2700  LOC154184 5'  GCTGCATTGACGCTGTCT     62917     A      T
                                GCT CATTGGC GCTGTCT
                                ||| ||||||| |||||||
                                CGA GTAACTG CGACAGA
                                  C     _
GAM2700  LOC157273 3'  AGGCTACAATAGCATGTCT    62918        T    TGC
                                AGGCTACA TGGC   TGTCT
                                |||||||| ||||   |||||
                                TCCGATGT ATCG   ACAGA
                                     T   T__
GAM2700  LOC157503 3'  GGCTCATTGGTTGCTGTCT    62919      A     C
                                GGCT CATTGG TGCTGTCT
                                |||| |||||| ||||||||
                                CCGA GTAACC ACGACAGA
                                  _     A
GAM2700  LOC158147 3'  GGCTTGAAACTGCTGTCT     62920      ACATT
                                GGCT    GGCTGCTGTCT
                                ||||    ||||||||||
                                CCGA    TTGACGACAGA
                                  ACT__
GAM2700  LOC221122 3'  CTAGGGCAGTTGTGTGCTGTCT 62921     A   TACA   GC
                                CTA GGC    TTG  TGCTGTCT
                                ||| |||    |||  ||||||||
                                GAT CCG    AAC  ACGACAGA
                                  C   TC__   AC
GAM2700  LOC221601 5'  GCTGCATTGACGCTGTCT     62917     A      T
                                GCT CATTGGC GCTGTCT
                                ||| ||||||| |||||||
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                                CGA GTAACTG CGACAGA
                                  C      _
GAM2700  LOC253612 5'  CCAAGGCTGTAGATGCTGT   62922        ACAT   C
                                CTAAGGCT   TGG TGCTGT
                                ||||||||   ||| ||||||
                                GGTTCCGA   ATC ACGACA
                                    C___   T
GAM2700  LOC254048 3'  GGGGTCAAGAACTGCTGTCT  62923    CTA  TT
                                GG  CA  GGCTGCTGTCT
                                ||  ||  ||||||||||
                                CC  GT  TTGACGACAGA
                                 CCA  TC
GAM2701  FMOD      3'  TGGTGTTCACATGCAGATGCT  62926     AATCG   __
                                TGG    TCAC  GCAGATGCT
                                |||    ||||  |||||||||
                                ACC    AGTG  CGTCTACGA
                                  ACA__    TA
GAM2701  GNL1      5'  GGCCGCCGCAGATGTTCTC   62927    AA   CA      C
                                GG  TCGT  CGCAGATG TCTC
                                ||  ||||  |||||||| ||||
                                CC  GGCG  GCGTCTAC AGAG
                                 __   __       A
GAM2701  GNL1      5'  GGCCGCCGCAGATGTTCTC   62927    AA   CA      C
                                GG  TCGT  CGCAGATG TCTC
                                ||  ||||  |||||||| ||||
                                CC  GGCG  GCGTCTAC AGAG
                                 __   __       A
GAM2701  ARTS-1    3'  TGGAATCGTCATGTTTGAGCT  62928          CGCA_  T
                                TGGAATCGTCA     GA GCT
                                ||||||||||     || |||
                                ACCTTAGCAGT     CT CGA
                                      ACAAA  _
GAM2701  BCCIP     3'  TGGAATCATCATGTCAGA    62929          CG_
                                TGGAATCGTCA   CAGA
                                ||||||||||   ||||
                                ACCTTAGTAGT   GTCT
                                      ACA
GAM2701  GDAP2     3'  TGGAGTCTTGGAAGATGCTCT  62930      A  GTCACGC
                                TGGA TC      AGATGCTCT
                                |||| ||      |||||||||
                                ACCT AG      TCTACGAGA
                                  C  AACCT__
GAM2701  THEA      3'  GGAATCGTTGTGCAGCATCTC  62931        CAC   ATG
                                GGAATCGT   GCAG   CTC
                                ||||||||   ||||   |||
                                CCTTAGCA   CGTC   GAG
                                    ACA    GTA
GAM2701  LOC148188 5'  TGGATCAGGTTTGGATGCTCT  62932      A   TCACGCA
                                TGGA TCG      GATGCTCT
                                |||| |||      ||||||||
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                                ACCT AGT      CTACGAGA
                                  _  CCAAAC_
GAM2701  LOC153937 5'  TGTGATCATCCAGATGCT    62933    GA     ACG
                                TG  ATCGTC   CAGATGCT
                                ||  ||||||   ||||||||
                                AC  TAGTAG   GTCTACGA
                                 AC     ___
GAM2701  LOC196794 5'  TGGAATTGTACGTGGCCCT    62934       C  C   CAGAT
                                TGGAAT GT ACG    GCTCT
                                |||||| || |||    |||||
                                ACCTTA CA TGC    CGGGA
                                   A  _   AC___
GAM2701  LOC203392 5'  TGGGATCGTCACCAAGCGCTC  62935     A      G   A
                                TGG ATCGTCAC CAG TGCTC
                                ||| |||||||| ||| |||||
                                ACC TAGCAGTG GTT GCGAG
                                  C       _  C
GAM2701  LOC256950 3'  TGGATCACAGATGCTC      62936     ATCGTCA
                                TGGA      CGCAGATGCTC
                                ||||      ||||||||||
                                ACCT      GTGTCTACGAG
                                  A_______
GAM2701  LOC257541 5'  GGCCGCCGCAGATGTTCTC   62927    AA   CA      C
                                GG  TCGT  CGCAGATG TCTC
                                ||  ||||  |||||||| ||||
                                CC  GGCG  GCGTCTAC AGAG
                                  __   __       A
GAM2701  LOC51086  3'  TGGAATCGTTGCTGTC      62937        CACGCAGA   C
                                TGGAATCGT       TGCT TC
                                |||||||||       |||| ||
                                ACCTTAGCA       ACGA AG
                                     _________   C
GAM2702  FLJ14675  3'  TACAAAAAAAAAATCCATT   62940        CT_
                                TACAAAAA   AATCCATT
                                ||||||||   ||||||||
                                ATGTTTTT   TTAGGTAA
                                     TTT
GAM2702  FLJ22729  5'  TTCATCACAAAAAGTAAC    62941       T     C
                                TTCATC ACAAAAA TAAT
                                |||||| ||||||| ||||
                                AAGTAG TGTTTTT ATTG
                                   _      C
GAM2702  POF1B     3'  TCATCTACAGAACTAATTCATT 62942         AA     C
                                TCATCTACA  AACTAAT CATT
                                |||||||||  ||||||| ||||
                                AGTAGATGT  TTGATTA GTAA
                                     C_      A
GAM2702  ZNF33A    3'  TTCTCTACAAAGACAATC    62943     A       A  T
                                TTC TCTACAAA AC AATC
                                ||| |||||||| || ||||
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                                AAG AGATGTTT TG TTAG
                                  _       C  _
GAM2702  LOC120224 3'  TTCATCCATGAGGCCACTTCCA 62944        CAAAA__   AA
              TT                  TTCATCTA      ACT  TCCATT
                                  ||||||||      |||  ||||||
                                  AAGTAGGT      TGA  AGGTAA
                                     ACTCCGG  __
GAM2702  LOC196477 3'  ATCTAAAAAAAAAAATCCATT  62945      C     CT
                                  ATCTA AAAAA  AATCCATT
                                  ||||| |||||  ||||||||
                                  TAGAT TTTTT  TTAGGTAA
                                    T     TT
GAM2703  DGKI     3'  TCTGACAGACATTTCTGACTAG 62948     A      GCC
              A                    TCT ATAGATA   CTGACTAGA
                                  ||| |||||||   |||||||||
                                  AGA TGTCTGT   GACTGATCT
                                    C       AAA
GAM2703  IFNA21    3'  CAATAGATAGATAATTAGA    62949         CCC   C
                                  TAATAGATAG   TGA TAGA
                                  ||||||||||   ||| ||||
                                  GTTATCTATC   ATT ATCT
                                        T__   A
GAM2703  KIAA0594  3'  TAATAGGAAGAAATGACTAGA  62950       AT  CCC
                                  TAATAG  AG   TGACTAGA
                                  ||||||  ||   ||||||||
                                  ATTATC  TC   ACTGATCT
                                      CT  TTT
GAM2703  LOC143524 3'  TCTGATAGATAGCATTCCT    62951     A       ___
                                  TCT ATAGATAGC   CCT
                                  ||| |||||||||   |||
                                  AGA TATCTATCG   GGA
                                    C         TAA
GAM2703  LOC255515 3'  TCTGATAGATAGCATTCCT    62951     A       ___
                                  TCT ATAGATAGC   CCT
                                  ||| |||||||||   |||
                                  AGA TATCTATCG   GGA
                                    C         TAA
GAM2703  LOC90906  3'  TCTGATAGATAGCATTCCT    62951     A       ___
                                  TCT ATAGATAGC   CCT
                                  ||| |||||||||   |||
                                  AGA TATCTATCG   GGA
                                    C         TAA
GAM2704  CHD2      3'  ACAGAATACAAGTGAGCTGTGA 62954      T       CATTTTA
                                  ACAG ATACAAGT       TGA
                                  |||| ||||||||       |||
                                  TGTC TATGTTCA       ACT
                                    T       CTCGAC_
GAM2704  HS2ST1    3'  ACAGTAAGCAAGTCATCT    62955       TA
                                  ACAGTA  CAAGTCATTT
                                  ||||||  ||||||||||
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                                TGTCAT  GTTCAGTAGA
                                   TC
GAM2704  PBX3     3'  ACAATGTACATTACATTTTATG 62956      A    AGT
              AA                    ACAGT TACA   CATTTTATGAA
                                |||||| ||||   ||||||||||
                                TGTTA ATGT   GTAAAATACTT
                                  C    AAT
GAM2704  ATP10D   3'  CAGTATACATTATTTATGAA   62957         AGTCAT
                                CAGTATACA     TTTATGAA
                                |||||||||     ||||||||
                                GTCATATGT     AAATACTT
                                     AAT___
GAM2704  C20orf129 3'  ACAGTATTATAATCTTATGA   62958        ACAA  C
                                ACAGTAT    GT ATTTTATGA
                                |||||||    || |||||||||
                                TGTCATA    TA TAGAATACT
                                    A___  T
GAM2704  DKFZp761G0313 3'  AGTATTCAAGTTTCATGA    62959      A    CAT
                                AGTAT CAAGT   TTTATGA
                                ||||| |||||   |||||||
                                TCATA GTTCA   AAGTACT
                                  A    ___
GAM2704  KIAA1237  3'  ACAGAACACTTCATTTTGTG   62960      TAT   AG      A
                                ACAG   ACA  TCATTTT TG
                                ||||   |||  ||||||| ||
                                TGTC   TGT  AGTAAAA AC
                                  T__   GA      C
GAM2704  KIAA1348  3'  AGTCTACAAGTCCATGA     62961     A       ATTT
                                AGT TACAAGTC    TATGA
                                ||| ||||||||    |||||
                                TCA ATGTTCAG    GTACT
                                  G      _____
GAM2704  MGC22014  3'  AGTGTACAAATCAGCATG    62962     A        TTT
                                AGT TACAAGTCA   TATG
                                ||| |||||||||   ||||
                                TCA ATGTTTAGT   GTAC
                                  C        C__
GAM2704  MIC2L1    3'  ACAGTTTACAAGTCACACCTG  62963      A         TTTA
                                ACAGT TACAAGTCAT    TG
                                ||||| ||||||||||    ||
                                TGTCA ATGTTCAGTG    AC
                                  A         TGG_
GAM2704  PB1       3'  ATATACAACCAATTATGAA    62964         G   TT
                                GTATACAA TCA  TTATGAA
                                |||||||| |||  |||||||
                                TATATGTT GGT  AATACTT
                                     _   T_
GAM2704  WDR9      3'  CAGTATGCATGTATTTATGAA  62965       A  A  CAT
                                CAGTAT CA GT   TTTATGAA
                                |||||| || ||   ||||||||
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                                GTCATA GT CA   AAATACTT
                                   C  A  T__
GAM2704  LOC122553 3'  ACAGTATTGTAATCTTATG   62966       ACAA  C
                                ACAGTAT    GT ATTTTATG
                                |||||||    || ||||||||
                                TGTCATA    CA TAGAATAC
                                   A___  T
GAM2704  LOC145333 5'  GTATGCAAAGCATTTTATGAA  62967     A    T
                                GTAT CAAG CATTTTATGAA
                                |||| |||| ||||||||||
                                CATA GTTT GTAAAATACTT
                                  C    C
GAM2704  LOC157278 3'  ACAGTATATAGTCTATATG   62968       CA    ATTT
                                ACAGTATA  AGTC    TATG
                                ||||||||  ||||    ||||
                                TGTCATAT  TCAG    ATAC
                                   A_    AT__
GAM2704  LOC222160 5'  ATATACAAATACTTATGAA   62969        CAT
                                GTATACAAGT   TTTATGAA
                                ||||||||||   ||||||||
                                TATATGTTTA   GAATACTT
                                      T__
GAM2705  ADAM12    3'  GGAACACCGGGAAAGTGAAA   62972          TCCGC
                                GGAACACTGGG    TGAAA
                                ||||||||||     |||||
                                CCTTGTGGCCC    ACTTT
                                      TTTC_
GAM2705  ADD2      3'  AAGGAGCACTGGACTG      62973       A     GTCC
                                AAGGA CACTGG   GCTG
                                ||||| ||||||   ||||
                                TTCCT GTGACC   TGAC
                                   C     _____
GAM2705  ADD2      3'  AAGGAGCACTGGACTG      62973       A     GTCC
                                AAGGA CACTGG   GCTG
                                ||||| ||||||   ||||
                                TTCCT GTGACC   TGAC
                                   C     _____
GAM2705  ADD2      3'  AAGGAGCACTGGACTG      62973       A     GTCC
                                AAGGA CACTGG   GCTG
                                ||||| ||||||   ||||
                                TTCCT GTGACC   TGAC
                                   C     _____
GAM2705  ADD2      3'  AAGGAGCACTGGACTG      62973       A     GTCC
                                AAGGA CACTGG   GCTG
                                ||||| ||||||   ||||
                                TTCCT GTGACC   TGAC
                                   C     _____
GAM2705  DNMT3L    5'  GGAGGACTGGGCCATGGAA   62974     AC     T   CT
                                GGA  ACTGGG CCG  GAA
                                |||  |||||| |||  |||
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                                CCT  TGACCC GGT  CTT
                                  CC     _   AC
GAM2705  HCK     3'  TGAGGAAACTGTGGCTGAA   62975   A    C   GGTCC
                                C AGGAA ACTG    GCTGAA
                                | ||||| ||||    ||||||
                                A TCCTT TGAC    CGACTT
                                 C    _   AC___
GAM2705  IGFBP4   3'  AGGGGACGCTGAGTCCCTG   62976    A_ A      G
                                AGG  AC CTGGGTCC CTG
                                |||  || |||||||| |||
                                TCC  TG GACTCAGG GAC
                                  CC  C       _
GAM2705  JAM3     3'  CAGGGAGCACTGAGCCACTG   62977    A   A     T
                                CA GGA CACTGGG CCGCTG
                                || ||| ||||||| ||||||
                                GT CCT GTGACTC GGTGAC
                                 C   C      _
GAM2705  LEF1     5'  AAGGGCACTGGGCGGCGA    62978     AA      CC  T
                                AAGG  CACTGGGT  GC GA
                                ||||  ||||||||  || ||
                                TTCC  GTGACCCG  CG CT
                                  C_       C_ _
GAM2705  MEIS2    3'  TGAGGAACACGTGCTGA     62979   A      TGG  CC
                                C AGGAACAC   GT  GCTGA
                                | ||||||||   ||  |||||
                                A TCCTTGTG   CA  CGACT
                                 C       ___  __
GAM2705  MKPX     3'  CAAGGGCTATTTCCCAAGCTG  62980      AACA   GG  ___
                                CAAGG   CTG  TCC   GCTG
                                |||||   |||  |||   ||||
                                GTTCC   GAT  AGG   CGAC
                                   C___   AA   GTT
GAM2705  OGDH     3'  GGACACTGCAGAGACTGAA   62981    A    _  TCC
                                GGA CACTG GG   GCTGAA
                                ||| ||||| ||   ||||||
                                CCT GTGAC TC   TGACTT
                                  _    G  TC_
GAM2705  PON1     3'  AAGAACACTGGGTCCTCGGAA  62982            GCT
                                AGGAACACTGGGTCC   GAA
                                ||||||||||||||   |||
                                TTCTTGTGACCCAGG   CTT
                                         AGC
GAM2705  PTHLH    3'  TGAGAGCACCCCGCTGA     62983   A   A   GGGT
                                A GGA CACT    CCGCTGA
                                | ||| ||||    |||||||
                                A TCT GTGG    GGCGACT
                                 C   C    _____
GAM2705  TRPM2    3'  TGAGGGGCACTGGGTCCACCAA 62984   A   AA         TG
             A                   C AGG  CACTGGGTCCGC  AA
                                | |||  ||||||||||||  ||
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                                A TCC  GTGACCCAGGTG  TT
                                 C   CC          GT
GAM2705  AMOTL1    3'  TGAGGAGACAGGCTTTCGCTGA 62985    A    AC  T    C__
              AA                  C AGGA  AC GGGT   CGCTGAAA
                                | ||||  || ||||   ||||||||
                                A TCCT  TG TCCG   GCGACTTT
                                 C   C_ _   AAA
GAM2705  C1orf17   3'  CAAGGAACCTCTGGATTGCTGA 62986         A_     CC
              A                   CAAGGAAC  CTGGGT  GCTGAA
                                |||||||||  ||||||  ||||||
                                GTTCCTTG  GACCTA  CGACTT
                                     GA     A_
GAM2705  CABP4     3'  TGAGGAACGGTGGGCAGCTGA  62987    A     AC     CC
                                C AGGAAC  TGGGT  GCTGA
                                | ||||||  |||||  |||||
                                A TCCTTG  ACCCG  CGACT
                                 C     CC    T_
GAM2705  CDCA4     3'  AGGAACACTGCCTTGA      62988          GGT  GC
                                AGGAACACTG   CC  TGA
                                ||||||||||   ||  |||
                                TCCTTGTGAC   GG  ACT
                                      ____  A_
GAM2705  cerk      3'  GAGCAGCTGCATCCGCTGA    62989     A  _   G
                                GA CA CTG GTCCGCTGA
                                || || ||| |||||||||
                                CT GT GAC TAGGCGACT
                                 C  C   G
GAM2705  DMWD      3'  AAGGGGACAGACCCGCTGA    62990      AAC  T  GT
                                AAGG   AC GG  CCGCTGA
                                ||||   || ||  |||||||
                                TTCC   TG TC  GGCGACT
                                  CC_  _  TG
GAM2705  DXS9928E  3'  GGCACACTGAGGGAGCTGA    62991     A       TCC
                                GG ACACTGGG   GCTGA
                                || ||||||||   |||||
                                CC TGTGACTC   CGACT
                                 G       CCT
GAM2705  FHX       5'  GGAACTGGGTCCCCTGA     62992     AC       G
                                GGA  ACTGGGTCC CTGA
                                |||  |||||||| ||||
                                CCT  TGACCCAGG GACT
                                  __        G
GAM2705  FLJ11767  3'  GGAGGAACACTGGGTGCCA    62993    A          _
                                C AGGAACACTGGGT CCG
                                | ||||||||||||| |||
                                C TCCTTGTGACCCA GGT
                                 C           C
GAM2705  FLJ12577  3'  GGAGCACTGGATCCTGGGA    62994     A        GCT
                                GGA CACTGGGTCC   GA
                                ||| ||||||||||   ||
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                                CCT GTGACCTAGG   CT
                                  C         ACC
GAM2705  FLJ14708  3'  CAAGGGACACTGAGAACTG    62995       A       TCC
                                CAAGG ACACTGGG   GCTG
                                ||||| ||||||||   ||||
                                GTTCC TGTGACTC   TGAC
                                   C       T__
GAM2705  FLJ21709  3'  AAGAACACTGGGTAACATGTGA 62996            CC  ___
              A                  AGGAACACTGGGT  GC   TGAA
                                ||||||||||||  ||   ||||
                                TTCTTGTGACCCA  TG   ACTT
                                       T_  TAC
GAM2705  FLJ23042  3'  TGAGAAATGCTGGGTCCACAGA 62997    A    CA        T
                                C AGGAA  CTGGGTCCGC GA
                                | |||||  |||||||||| ||
                                A TCTTT  GACCCAGGTG CT
                                 C     AC         T
GAM2705  FLJ32430  3'  AGGAACACTGACCCCTGAA    62998          GT  G
                                AGGAACACTGG  CC CTGAA
                                ||||||||||  || |||||
                                TCCTTGTGACT  GG GACTT
                                      __ G
GAM2705  GAGED3    5'  CAAGGAACATGCACACTGAA   62999         CTGG TC
                                CAAGGAACA    G  CGCTGAA
                                |||||||||    |  |||||||
                                GTTCCTTGT    C  GTGACTT
                                     A___ GT
GAM2705  HT002     3'  TGAGGGGGCTGGGTCCTGCT   63000    A   AACA      _
                                C AGG    CTGGGTCC GCT
                                | |||    |||||||| |||
                                A TCC    GACCCAGG CGA
                                 C   CCC_       A
GAM2705  KIAA0599  3'  CAAGGGCACTGGACAGTGTGA  63001       AA      TCCGC
                                CAAGG  CACTGGG     TGA
                                |||||  |||||||     |||
                                GTTCC  GTGACCT     ACT
                                   C_      GTCAC
GAM2705  KIAA0729  3'  CAGAGAGCACTGGACAAACTGA 63002    AG  A      TCC
              A                  CA  GA CACTGGG   GCTGAA
                                ||  || |||||||   ||||||
                                GT  CT GTGACCT   TGACTT
                                 CT  C      GTT
GAM2705  KIAA1131  3'  AGTGAACACTGAAGATCTGA   63003    _        TCCG
                                AG GAACACTGGG    CTGA
                                || ||||||||||    ||||
                                TC CTTGTGACTT    GACT
                                 A         CTA_
GAM2705  KIAA1244  3'  AGGAAACACTGTTCTCTGA    63004       _    GG  CG
                                AGGAA CACTG  TC  CTGA
                                ||||| |||||  ||  ||||
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                                TCCTT GTGAC  AG  GACT
                                  T    A_  A_
GAM2705  KIAA1643  3'  TGAGGAGGTGTCCGCTG    63005   A   ACACT  _
                                C AGGA    GG GTCCGCTG
                                | ||||    || ||||||||
                                A TCCT    CC CAGGCGAC
                                 C   _____  A
GAM2705  KIAA1656  3'  GGCACACTGGGCATGAA    63006   A      CCGC
                                GG ACACTGGGT   TGAA
                                || |||||||||   ||||
                                CC TGTGACCCG   ACTT
                                 G       T___
GAM2705  Kv6.3     5'  AGGAAGCGCTGGGTTTACCA  63007     CA_    CC
                                AGGAA  CTGGGT  GCTG
                                |||||  ||||||  ||||
                                TCCTT  GACCCA  TGGT
                                   CGC    AA
GAM2705  MGC35558  3'  AGGGACACTGAGTGACTCTG  63008    A      CCG_
                                AGG ACACTGGGT   CTG
                                ||| |||||||||   |||
                                TCC TGTGACTCA   GAC
                                  C       CTGA
GAM2705  NR6A1     3'  AAGGAACACGTCCTGGGA    63009       TGG   GCT
                                AAGGAACAC  GTCC  GA
                                |||||||||  ||||  ||
                                TTCCTTGTG  CAGG  CT
                                     ___   ACC
GAM2705  NR6A1     3'  AAGGAACACGTCCTGGGA    63009       TGG   GCT
                                AAGGAACAC  GTCC  GA
                                |||||||||  ||||  ||
                                TTCCTTGTG  CAGG  CT
                                     ___   ACC
GAM2705  NR6A1     3'  AAGGAACACGTCCTGGGA    63009       TGG   GCT
                                AAGGAACAC  GTCC  GA
                                |||||||||  ||||  ||
                                TTCCTTGTG  CAGG  CT
                                     ___   ACC
GAM2705  XYLT1     3'  CAAGGAACCTGTAGGACTTGA 63010       A  GGTCC  _
                                CAAGGAAC CTG    GCT GA
                                |||||||| |||    ||| ||
                                GTTCCTTG GAC    TGA CT
                                     _  ATCC_   A
GAM2705  LOC124987 5'  CAAGGAACTTGCCATCTGCTG 63011       ACTGG  C
                                CAAGGAAC    GTC GCTG
                                ||||||||    ||| ||||
                                GTTCCTTG    TAG CGAC
                                     AACGG  A
GAM2705  LOC143158 5'  GGAGGAACACTGAACTGA    4093    A       GTCC
                                C AGGAACACTGG   GCTGA
                                | ||||||||||   |||||
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                                C TCCTTGTGACT    TGACT
                                 C         ____
GAM2705  LOC145082 5'  AGGAACACACAGGCCGTTGAA  63012         _   T   C
                                AGGAACAC TGGG CCG TGAA
                                |||||||| |||| ||| ||||
                                TCCTTGTG GTCC GGC ACTT
                                     T   _  A
GAM2705  LOC145761 5'  GGAGACAGAGCCGCTGAA    63013    _  CT   T
                                GGA ACA  GGG CCGCTGAA
                                ||| |||  ||| ||||||||
                                CCT TGT  CTC GGCGACTT
                                  C  __  _
GAM2705  LOC147057 3'  GGATGCTGGGCCGCATGA    63014    ACA    T   _
                                GGA   CTGGG CCGC TGA
                                |||   ||||| |||| |||
                                CCT   GACCC GGCG ACT
                                  AC_    _   T
GAM2705  LOC149722 5'  CAAGGAACACATGGGCACTGAA 63015          _    CC
               A                 CAAGGAACAC TGGGT  GCTGAAA
                                |||||||||| |||||  |||||||
                                GTTCCTTGTG ACCCG  TGACTTT
                                      T    __
GAM2705  LOC150197 3'  AAGGGGACACTGGGCCACC   63016     A_      T
                                AAGG  ACACTGGG CCGCT
                                ||||  |||||||| |||||
                                TTCC  TGTGACCC GGTGG
                                  CC       _
GAM2705  LOC153769 3'  CAAGGACGCTGCTTCAGGCTG  63017       A A   GG  C_
                                CAAGGA C CTG  TC  GCTG
                                |||||| | |||  ||  ||||
                                GTTCCT G GAC  AG  CGAC
                                   _ C   GA  TC
GAM2705  LOC162333 5'  AGAGAACAAGCCGCTGAA    63018   _    CTG  T
                                AG GAACA   GG CCGCTGAA
                                || |||||   || ||||||||
                                TC CTTGT   TC GGCGACTT
                                 T    ___  _
GAM2705  LOC197342 3'  AGGGGACACTGAGGTTTTCTGA 63019    A_    _  CCG
               AA                 AGG  ACACTG GGT   CTGAAA
                                |||  |||||| |||   ||||||
                                TCC  TGTGAC CCA   GACTTT
                                  CC     T   AAA
GAM2705  LOC255652 3'  CAAAGAACACTGGGAGTGAA   63020           TCCGC
                                CAAGGAACACTGGG    TGAA
                                ||||||||||||||    ||||
                                GTTTCTTGTGACCC    ACTT
                                         TC___
GAM2705  LOC92492  5'  AAGGATACTGGGTCTCTG    63021      AC       CG
                                AAGGA  ACTGGGTC  CTG
                                |||||  ||||||||  |||
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                                TTCCT  TGACCCAG  GAC
                                  A_       A_
GAM2706  WHSC1    3'  CTAATTACAGTCAATTTGACA  63024     TTGAT_  A
                                CTA     GT CAATTTGACA
                                |||     || ||||||||||
                                GAT     CA GTTAAACTGT
                                  TAATGT  _
GAM2706  ZFP36L1  3'  TATTGATGTGCAGTGAC     63025         A  ATT
                                TATTGATGT CA   TGAC
                                |||||||||  ||   ||||
                                ATAACTACA GT   ACTG
                                     C  C__
GAM2706  AGXT2L1  3'  TACTTTGCTCTCTAATTTGACA 63026      A   ATGTAC
              C                  TACT TTG     AATTTGACAC
                                |||| |||     ||||||||||
                                ATGA AAC     TTAAACTGTG
                                  _   GAGAGA
GAM2706  CLGN     3'  CACTGTAACTATAATTTGACAC 63027      AT    GTAC
                                TACT  TGAT    AATTTGACAC
                                ||||  ||||    ||||||||||
                                GTGA  ATTG    TTAAACTGTG
                                  C_    ATA_
GAM2706  CTCF     3'  TACTACTGGTGTGCAGCTGAC  63028        A   A  AT
                                TACTATTG TGT CA  TTGAC
                                |||||||| ||| ||  |||||
                                ATGATGAC ACA GT  GACTG
                                     C   C  C_
GAM2706  FLJ12377 3'  TACTATTGAAGTAGACATTGA  63029         T   CAAT
                                TACTATTGA GTA    TTGA
                                |||||||||  |||    ||||
                                ATGATAACT CAT    AACT
                                     T   CTGT
GAM2706  KIAA0426 3'  TACTATTGTGTATACTTG    63030         A    CA
                                TACTATTG TGTA  ATTTG
                                |||||||| ||||  |||||
                                ATGATAAC ACAT  TGAAC
                                     _    A_
GAM2706  LANO     3'  TACTGATGATCATTCTTTGACA 63031         TACAA__
                                TATTGATG      TTTGACA
                                ||||||||      |||||||
                                ATGACTAC      AAACTGT
                                     TAGTAAG
GAM2706  phorbolin-1 3'  TACTATTGTGTACTTGGAACA  63032         A    AATTT
                                TACTATTG TGTAC     GACA
                                |||||||| |||||     ||||
                                ATGATAAC ACATG     TTGT
                                     _     AACC_
GAM2706  LOC143465 5'  TACATTGACATGTTTGACA    63033     T       ACAA
                                TAC ATTGATGT    TTTGACA
                                ||| ||||||||    |||||||
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                                ATG TAACTGTA    AAACTGT
                                  _      C___
GAM2706 LOC51131 3' TATTGATGTAGAACTTGACA  63034         C
                                TATTGATGTA AATTTGACA
                                |||||||||| |||||||||
                                ATAACTACAT TTGAACTGT
                                      C
GAM2707 CARPX    5' GACGATAGCCCCCCGCCGGGCT 63037    G    TGA       A
            G                    GA GATA   CCCCCGCCG GCTG
                                || ||||   ||||||||| ||||
                                CT CTAT   GGGGGCGGC CGAC
                                 G   CG_       C
GAM2707 DUSP7    5' GGCGCCCGCCTCCCGCCGAGCT 63038    ATA_  A  _
            G                    GG    TG CC CCCGCCGAGCTG
                                ||    || || ||||||||||||
                                CC    GC GG GGGCGGCTCGAC
                                 GCGG  _  A
GAM2707 GADD45G  3' AGACCAAGGTCCCCGCCGGGCT 63039     ATGAC_      A
            G                    GGAT     CCCCGCCG GCTG
                                ||||     |||||||| ||||
                                TCTG     GGGGCGGC CGAC
                                  GTTCCA       C
GAM2707 SLC6A6   3' GAGGATACGACTCAAAAGCTG  63040          CCCCGCC
                                GAGGATATGAC      GAGCTG
                                ||||||||||      ||||||
                                CTCCTATGCTG      TTCGAC
                                      AGTT___
GAM2707 FLJ20308 3' GAGGATGAGGCCCAAGCT    63041      TA   CC   GCC
                                GAGGA  TGA  CCC   GAGCT
                                |||||  |||  |||   |||||
                                CTCCT  ACT  GGG   TTCGA
                                  __   CC   ___
GAM2707 FLJ22457 3' GAGGATATGGATTTTGGGAGCT 63042         ACCCCCGCC
            G                    GAGGATATG       GAGCTG
                                |||||||||       ||||||
                                CTCCTATAC       CTCGAC
                                     CTAAAACC_
GAM2707 MAP3K3   3' GAGGGTGGGGCCCACGGCT   63043     ATA  ACC    C A
                                GAGG   TG   CCCGC G GCT
                                ||||   ||   ||||| | |||
                                CTCC   AC   GGGTG C CGA
                                  C__  CCC    _ _
GAM2707 N4BP3    3' GGGGAACTGTTCTGCCGAGCTG 63044   A   TA  ACCCCC
                                G GGA  TG     GCCGAGCTG
                                | |||  ||     |||||||||
                                C CCT  AC     CGGCTCGAC
                                 C   TG  AAGA__
GAM2707 SIAT4A   5' GGGGATGACCCCCAACT     63045    AT       CCGA
                                GG  ATGACCCCCG    GCT
                                ||  ||||||||||    |||
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                                CC  TACTGGGGGT   TGA
                                 CC       ____
GAM2707  LOC150213 3'  GAGGTGTGGGAACCCGAGCTG  63046     ATAT__    CCGCC
                                GAGG     GACCC    GAGCTG
                                ||||     |||||    ||||||
                                CTCC     TTGGG    CTCGAC
                                  ACACCC    _____
GAM2707  LOC150236 5'  GAGGTGTGGGAACCCGAGCTG  63046     ATAT__    CCGCC
                                GAGG     GACCC    GAGCTG
                                ||||     |||||    ||||||
                                CTCC     TTGGG    CTCGAC
                                  ACACCC    _____
GAM2707  LOC151057 3'  GAGGCTGTGATCCCCACCACTG 63047     ATA  C     GA
                                GAGG   TGA CCCCGCC  GCTG
                                ||||   ||| |||||||  ||||
                                CTCC   ACT GGGGTGG  TGAC
                                  GAC   A     __
GAM2708  ADCY7    3'  CAGCATTTGTGAGGGGGCGGG  63050        C  TTGTAA
                                CAGCATTTG TG     CGGG
                                |||||||||  ||     ||||
                                GTCGTAAAC AC     GCCC
                                     _  TCCCCC
GAM2708  ASTN     3'  CAGCATTTGCCACAGG      63051          GTTGTA
                                CAGCATTTGCT     ACGGG
                                ||||||||||     |||||
                                GTCGTAAACGG     TGTCC
                                               _______
GAM2708  CUL5     3'  TACAGTATTTGCTGCTGT    63052      C
                                TACAG ATTTGCTGTTGT
                                ||||| ||||||||||||
                                ATGTC TAAACGACGACA
                                   A
GAM2708  MPV17    3'  GCATTTGCTGGGATATGGG   63053         TT   AC
                                GCATTTGCTG  GTA  GGG
                                ||||||||||  |||  |||
                                CGTAAACGAC  TAT  CCC
                                      CC   A_
GAM2708  RAI14    3'  CAGCATTTCTGTGCGG      63054        G    TGTAA
                                CAGCATTT CTGT    CGG
                                |||||||| ||||    |||
                                GTCGTAAA GACA    GCC
                                     _    C____
GAM2708  SLC7A5   3'  GCACTTGCTTGTTGTGGTGGG 63055         _    AAC
                                GCATTTGCT GTTGT   GGG
                                ||||||||| |||||   |||
                                CGTGAACGA CAACA   CCC
                                      A    CCA
GAM2708  FOXJ1    3'  AGCATTTGTTGTACCTGGG   63056       TGC      AC_
                                AGCATT   TGTTGTA   GGG
                                ||||||   |||||||   |||
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                                TCGTAA  ACAACAT  CCC
                                   ___     GGA
GAM2708 KIAA1257 3' TACAGCATTGTACATGACGGG 63057       _  _ TTGTA
                                TACAGCATT TGC TG    ACGGG
                                ||||||||| ||| ||    |||||
                                ATGTCGTAA ATG AC    TGCCC
                                    C  T _____
GAM2708 P11      3' TACAGCATTTAGTTCTCAGTGG 63058         CTG  GTAAC
           G                     TACAGCATTTG  TT    GGG
                                ||||||||||  ||    |||
                                ATGTCGTAAAT  AG    CCC
                                     CA_  AGTCA
GAM2708 LOC116228 3' TAAGTATTTGCTGTTTTTTAAT 63059   C  C       G__  C
           GGG                    A AG ATTTGCTGTT  TAA GGG
                                | || ||||||||||  ||| |||
                                A TC TAAACGACAA  ATT CCC
                                 T  A        AAA  A
GAM2708 LOC126751 3' ACAGCATTTGTGCAGTGATGGG 63060         C  T  AAC
                                ACAGCATTTG TGT GT  GGG
                                |||||||||| ||| ||  |||
                                TGTCGTAAAC ACG CA  CCC
                                     _  T  CTA
GAM2708 LOC139331 5' CAGCAGATGTTGTAATGGG   63061      TTTGC      C
                                CAGCA    TGTTGTAA GGG
                                |||||    |||||||| |||
                                GTCGT    ACAACATT CCC
                                   CT___      A
GAM2708 LOC145815 5' AGCATTTGCTATGATGGG    63062          T TAAC
                                AGCATTTGCTGT G   GGG
                                |||||||||||| |   |||
                                TCGTAAACGATA C   CCC
                                     _ TA__
GAM2708 LOC93496  3' TACAGCATTTACCAAGGCGGG 63063           TTGTAA
                                TACAGCATTTGCTG     CGGG
                                ||||||||||||||     ||||
                                ATGTCGTAAATGGT     GCCC
                                      TCC___
GAM2709 JAM3     3' AATACTCTTAATTATTGATATT 63066       GATTGA
                                AATACTC     TATTGATATT
                                |||||||     ||||||||||
                                TTATGAG     ATAACTATAA
                                    AATTA_
GAM2710 AXIN1    3' TATCTGTAGCTGCCCTT     63069       ATA  A_
                                TATCTGT  AGT  CCCTT
                                |||||||  |||  |||||
                                ATAGACA  TCG  GGGAA
                                    ___  AC
GAM2710 KERA     3' TACGGTATCTGCATAAGTA   63070     AA
                                TAC  TATCTGTATAAGTA
                                |||  ||||||||||||||
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                                ATG  ATAGACGTATTCAT
                                  CC
GAM2710  MTMR1    3'  TACAATACTGTACCAGT     63071        T     A
                                TACAATA CTGTAT AGT
                                ||||||| |||||| |||
                                ATGTTAT GACATG TCA
                                    _     G
GAM2710  C3IP1    3'  AATATCTGTTACCCACCCTT   63072         A  AG
                                AATATCTGT TA  TACCCTT
                                ||||||||| ||  |||||||
                                TTATAGACA AT  GTGGGAA
                                     _ GG
GAM2710  FLJ14084 3'  CACAATAATAAGTACTCT    63073        TCTGT      C
                                TACAATA    ATAAGTAC CT
                                |||||||    |||||||| ||
                                GTGTTAT    TATTCATG GA
                                   _____       A
GAM2710  SLC17A6  3'  TACAATATCTCTATGAAGT    63074         G  _
                                TACAATATCT TAT AAGT
                                |||||||||| ||| ||||
                                ATGTTATAGA ATA TTCA
                                     G   C
GAM2710  LOC120892 3'  CAAAAAATGTGAGTACCCTT   63075     TATC   ATA
                                CAA   TGT   AGTACCCTT
                                |||   |||   |||||||||
                                GTT   ACA   TCATGGGAA
                                  TTTT   C__
GAM2710  LOC220766 5'  CAATGGTATAAGTACCCT    63076     ATCT
                                CAAT   GTATAAGTACCCT
                                ||||   ||||||||||||
                                GTTA   CATATTCATGGGA
                                  C___
GAM2711  ITGA5    3'  CCTCTGTCCCTGGATCTGAG   63079      GTTAGA  A_
                                TCTCTG     CC  GATCTGAG
                                ||||||     ||  ||||||||
                                GGAGAC     GG  CTAGACTC
                                   AG____  AC
GAM2711  SCD      3'  CTCTTGATCAGATCTGAG    63080     _  TAGAC
                                CTCT GGT    CAGATCTGAG
                                |||| |||    ||||||||||
                                GAGA CTA    GTCTAGACTC
                                  A  _____
GAM2711  SF3B3    3'  TCTGGTTAGATTCTAGAGC   63081         CCAGA  _
                                TCTGGTTAGA    TCT GAGC
                                ||||||||||    ||| ||||
                                AGACCAATCT    AGA CTCG
                                     A____   T
GAM2711  SLC4A4   3'  TCTGGTTAACAACTCTGAGC  63082         AC   A
                                TCTGGTTAG  CAG TCTGAGC
                                |||||||||  ||| |||||||
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                                AGACCAATT  GTT AGACTCG
                                    __   G
GAM2711  ZNF180   3'  TCTCTGATTCAGGTCTGAG   63083        AGAC   A
                                TCTCTGGTT   CAG TCTGAG
                                |||||||||   ||| ||||||
                                AGAGACTAA   GTC AGACTC
                                    ____   C
GAM2711  AP1G2    5'  TCTCTGGTCGGGCGTGCCTGGG 63084        AGACCAGA   A
           C                     TCTCTGGTT      TCTG GC
                                 |||||||||      |||| ||
                                 AGAGACCAG      GGAC CG
                                     CCCGCAC_   C
GAM2711  BCL2L1   3'  CTGCAAGGGACCAGATCTGGGC 63085     GTTA_        A
                                CTG    GACCAGATCTG GC
                                |||    |||||||||||  ||
                                GAC    CTGGTCTAGAC CG
                                  GTTCC         C
GAM2711  DKFZP434D146 3'  TCTCTGGTGGATCACTTGAG   63086        TAGACCA   ___
                                TCTCTGGT     GATC   TGAG
                                ||||||||     ||||   ||||
                                AGAGACCA     CTAG   ACTC
                                    C_______   TGA
GAM2711  FLJ25012  5'  TCTTGTGCTTTTCAGATCTGAG 63087     C  _   AGAC
                                TCT TG GTT    CAGATCTGAG
                                ||| || |||    ||||||||||
                                AGA AC CGA    GTCTAGACTC
                                  _  A   AAA_
GAM2711  FLJ31952  3'  CTTTCAGAACCAGATTTG    63088    GG    _     C
                                CT  TTAGA CCAGAT TG
                                ||  ||||| |||||| ||
                                GA  AGTCT GGTCTA AC
                                 A_    T     A
GAM2711  MDS025   3'  TCTATCTCAAACCAGGTCTGAG 63089      G_       A
                                TCTG  TTAGACCAG TCTGAG
                                ||||  ||||||||| ||||||
                                AGAT  AGTTTGGTC AGACTC
                                  AG       C
GAM2711  MGC32043  3'  TCTTGAAGCATCAGATCTGAGC 63090     GGTT  AC_
                                TCT    AG   CAGATCTGAGC
                                |||    ||   ||||||||||
                                AGA    TC   GTCTAGACTCG
                                  ACT_  GTA
GAM2711  MSI2     3'  TCTCTGGTTGGGATGGGGAG   63091        AGACCA   CT_
                                TCTCTGGTT     GAT   GAG
                                |||||||||     |||   |||
                                AGAGACCAA     CTA   CTC
                                    CC____   CCC
GAM2711  ZNF271   5'  TCTCTGATGTTTAACCAGATCT 63092       __   A
             GAGC                   TCTCTG  GTT GACCAGATCTGAGC
                                    ||||||  ||| ||||||||||||||
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                                AGAGAC  CAA TTGGTCTAGACTCG
                                   TA   A
GAM2711  LOC144508 5'  TCCCTGGCACATGGATCTGAGC 63093        TAGACCA
                                TCTCTGGT      GATCTGAGC
                                ||||||||      |||||||||
                                AGGGACCG      CTAGACTCG
                                    TGTAC__
GAM2711  LOC145845 3'  TCTCTGGTGGGATTTGAG    63094        TAGACCA   C
                                TCTCTGGT      GAT TGAG
                                ||||||||      ||| ||||
                                AGAGACCA      CTA ACTC
                                    CC_____   A
GAM2711  LOC146227 3'  TCTTGGTCAAGATCTGAGC   63095    C     GACC
                                TCT TGGTTA    AGATCTGAGC
                                ||| ||||||    ||||||||||
                                AGA ACCAGT    TCTAGACTCG
                                  _     _____
GAM2712  ARHGEF7   3'  AGTCTGTCAGCCAGCAAGTT   63098    _  C    AGA
                                AG CTG CAGTT   AGCAAGTT
                                || ||| |||||   ||||||||
                                TC GAC GTCGG   TCGTTCAA
                                 A   A    ___
GAM2712  CSN1      5'  AAGTCTGGAGAGAAGCAAGTT  63099    _  CC  TT
                                AAG CTG  AG  AGAAGCAAGTT
                                ||| |||  ||  ||||||||||
                                TTC GAC  TC  TCTTCGTTCAA
                                  A  C_  __
GAM2712  FGF1      3'  AACTGGGCATTTAGAAGCAAGT 63100      C_  G
            T                    AGCTG  CA TTAGAAGCAAGTT
                                 |||||  || ||||||||||||
                                 TTGAC  GT AATCTTCGTTCAA
                                    CC  A
GAM2712  FGF1      3'  AACTGGGCATTTAGAAGCAAGT 63100      C_  G
            T                    AGCTG  CA TTAGAAGCAAGTT
                                 |||||  || ||||||||||||
                                 TTGAC  GT AATCTTCGTTCAA
                                    CC  A
GAM2712  FGF1      3'  AACTGGGCATTTAGAAGCAAGT 63100      C_  G
            T                    AGCTG  CA TTAGAAGCAAGTT
                                 |||||  || ||||||||||||
                                 TTGAC  GT AATCTTCGTTCAA
                                    CC  A
GAM2712  MBL2      3'  AAGTTGCCAGTTCTGCATAAGT 63101     C      AGAA  __
            T                    AAG TGCCAGTT   GCA  AGTT
                                 ||| ||||||||   |||  ||||
                                 TTC ACGGTCAA   CGT  TCAA
                                   A       GA__   AT
GAM2712  NBS1      3'  AAGCAGCCAGAACTTGGAAGTA 63102     T    TTA___   C
            AGTTA                   AAGC GCCAG     GAAG AAGTTA
                                 |||| |||||     |||| ||||||
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                                TTCG CGGTC     CTTC TTCAAT
                                  T    TTGAAC   A
GAM2712  SLC7A7   5'  AAGCTGTCCCAGAGCAAGTTA  63103       _ AGT   A
                                AAGCTG CC   TAGA GCAAGTTA
                                |||||| ||   |||| ||||||||
                                TTCGAC GG   GTCT CGTTCAAT
                                   A ____   _
GAM2712  YWHAH    3'  AAGCTGATGGAAAGGAGCAAGT 63104       CCAGTT  A
             T                   AAGCTG     AG AGCAAGTT
                                 ||||||     || ||||||||
                                 TTCGAC     TC TCGTTCAA
                                    TACCTT  C
GAM2712  BM-002   3'  AAGCTTCCAGTTAACAGTT   63105      G      GAA   A
                                AAGCT CCAGTTA   GCA GTT
                                ||||| |||||||   ||| |||
                                TTCGA GGTCAAT   TGT CAA
                                   A     ____  _
GAM2712  FLJ12604 3'  CTGTTGGTTAGAAGCAGGTTA  63106     CCA        A
                                CTG   GTTAGAAGCA GTTA
                                |||   |||||||||| ||||
                                GAC   CAATCTTCGT CAAT
                                  AAC         C
GAM2712  FLJ14681 3'  AGCTTGCCAGTTAGGAAG    63107     _       _
                                AGCT GCCAGTTAG AAG
                                |||| ||||||||| |||
                                TCGA CGGTCAATC TTC
                                  A        C
GAM2712  FLJ20559 3'  AGCTCCAGTTAGAAAAGTT   63108     G        GC
                                AGCT CCAGTTAGAA  AAGTT
                                |||| ||||||||||  |||||
                                TCGA GGTCAATCTT  TTCAA
                                  _        __
GAM2712  IL14     5'  AGCTGCCATCACAGTGAGTT   63109       G   GA  CA
                                AGCTGCCA TTA  AG  AGTT
                                |||||||| |||  ||  ||||
                                TCGACGGT AGT  TC  TCAA
                                     _  G_  AC
GAM2712  KIAA1034 3'  AAGCTGCCAGATAGGAAGC   63110         T  _
                                AAGCTGCCAG TAG AAGC
                                |||||||||| ||| ||||
                                TTCGACGGTC ATC TTCG
                                      T   C
GAM2712  KIAA1239 3'  AGCTATCAGTTGCAAACAAGTT 63111      C    AG
             A                   AGCTG CAGTT  AAGCAAGTTA
                                 ||||| |||||  ||||||||||
                                 TCGAT GTCAA  TTTGTTCAAT
                                    A    CG
GAM2712  KIAA1243 3'  ACTGCTGAATGAGCAAGTTA  63112      CAGTTA  A
                                GCTGC     GA GCAAGTTA
                                |||||     || ||||||||
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                                TGACG     CT CGTTCAAT
                                  ACTTA_  _
GAM2712 KIAA1884 3' AGCTGCTGTTGGAAGCAAA   63113       CA   A
                                AGCTGC  GTT GAAGCAAG
                                |||||||  ||| ||||||||
                                TCGACG  CAA CTTCGTTT
                                   A_   C
GAM2712 MGC34869 5' AAGCTGCCGTGGGCAAGTTA  63114        A  TAGAA
                                AAGCTGCC GT    GCAAGTTA
                                |||||||| ||    ||||||||
                                TTCGACGG CA    CGTTCAAT
                                     _ CC___
GAM2712 NIR3     3' AAGCTGACAAAGCAAGTT    63115       CCAGTTA
                                AAGCTG      GAAGCAAGTT
                                ||||||      ||||||||||
                                TTCGAC      TTTCGTTCAA
                                   TG_____
GAM2712 PASK     3' AAGCTGTCATTAGAAATCGAGT 63116       CCA       CA_
              T                  AAGCTG   GTTAGAAG   AGTT
                                ||||||   ||||||||   ||||
                                TTCGAC   TAATCTTT   TCAA
                                   AG_      AGC
GAM2712 PLSCR4   3' AAGTGCAACAGAAGCAAGTTA 63117     C   CAGT
                                AAG TGC    TAGAAGCAAGTTA
                                ||| |||    ||||||||||||
                                TTC ACG    GTCTTCGTTCAAT
                                  _   TT__
GAM2712 PRO1855  3' AACCTGCAGAAGCAGGTT    63118    G    CAGTT      A
                                AA CTGC     AGAAGCA GTT
                                || ||||     ||||||| |||
                                TT GACG     TCTTCGT CAA
                                 G   _____      C
GAM2712 SMUG1    3' AAACTGCCATGGCAGGTT     63119        GTTAGAA   A
                                AAGCTGCCA      GCA GTT
                                |||||||||      ||| |||
                                TTTGACGGT      CGT CAA
                                     AC_____   C
GAM2712 SSR1     3' GCTGATATGTAAGGCAAGTTA 63120     CCA_  T  AA
                                GCTG    GT AG  GCAAGTTA
                                ||||    || ||  ||||||||
                                CGAC    CA TC  CGTTCAAT
                                  TATA  T  __
GAM2712 LOC147343 5' AGCTGCCACTTGGGAGCAA   63121        G  AGA
                                AGCTGCCA TT   AGCAA
                                |||||||| ||   |||||
                                TCGACGGT AA   TCGTT
                                     G  CCC
GAM2712 LOC149837 3' GCGTGCCAGCAGCAAGTT    63122    _      TAGA
                                GC TGCCAGT    AGCAAGTT
                                || |||||||    ||||||||
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                                CG ACGGTCG    TCGTTCAA
                                 C      ____
GAM2712  LOC153346 5'  GCTGCCAGTATTGCAGTTA   63123        TAGAA   A
                                GCTGCCAGT     GCA GTTA
                                |||||||||     ||| ||||
                                CGACGGTCA     CGT CAAT
                                     TAA__   _
GAM2712  LOC220883 3'  AAGTTGCCCGAAGATAGCAGGT 63124     C    AGTT  _   A
           TA                    AAG TGCC    AGA AGCA GTTA
                                |||  ||||    |||  |||| ||||
                                TTC ACGG    TCT TCGT CAAT
                                  A    GCT_   A    C
GAM2712  LOC91151  5'  AAGCTGCCAGTTGCAAAGTC   63125          AGAA   _
                                AAGCTGCCAGTT    GCAA GTT
                                ||||||||||||    |||| |||
                                TTCGACGGTCAA    CGTT CAG
                                      ____    T
GAM2712  LOC93589  3'  GCCTACTCTAGAGGCAAGTTA  63126     AG__     A
                                GCC    TTAGA GCAAGTTA
                                |||    ||||| ||||||||
                                CGG    GATCT CGTTCAAT
                                  ATGA     C
GAM2712  LOC94468  5'  AAGCTGCCCAGTCAAGTT     63127        _  TAGAAG
                                AAGCTGCC AGT      CAAGTT
                                ||||||||  |||     ||||||
                                TTCGACGG TCA      GTTCAA
                                     G  _______
GAM2713  AASS      5'  AAGGCTGGCAGATCAGTTCTG  63130           G  CC
                                GAGGCTGGCAGATC AG  CTG
                                ||||||||||||||  ||  |||
                                TTCCGACCGTCTAG TC  GAC
                                      _  AA
GAM2713  ARHC      5'  GAAGCTGGCGGCCTCCTG     63131        AGATC A   __
                                GAGGCTGGC     G GCC  CTG
                                |||||||||     | |||  |||
                                CTTCGACCG     C CGG  GAC
                                     ______ _   AG
GAM2713  CENTD2    5'  GAGGCTGGGGAGGCCCCTG   63132        CAGATC   __
                                GAGGCTGG      GAG  CCCTG
                                ||||||||      |||  |||||
                                CTCCGACC      CTC  GGGAC
                                     C_____   CG
GAM2713  COL11A2   3'  GAGGTGGGTTCAGCCCTG    63133      C   CAGA  G
                                GAGG TGG    TC AGCCCTG
                                ||||  |||    ||  |||||||
                                CTCC ACC    AG TCGGGAC
                                  _   CA__  _
GAM2713  COL11A2   3'  GAGGTGGGTTCAGCCCTG    63133      C   CAGA  G
                                GAGG TGG    TC AGCCCTG
                                ||||  |||    ||  |||||||
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                                CTCC ACC    AG TCGGGAC
                                  _   CA__  _
GAM2713  COX10     3'  AGGGGCTGGCAGTCCAGCTTGA 63134    A       A  G   CC
                                AG GGCTGGCAG TC AGC  TGA
                                || ||||||||| || |||  |||
                                TC CCGACCGTC AG TCG  ACT
                                 C       _  G   A_
GAM2713  DNASE1L1  5'  AGCTGGCAGTCCAACGTCCTG  63135        A  G  __
                                GGCTGGCAG TC AGC  CCTG
                                ||||||||| || |||  ||||
                                TCGACCGTC AG TTG  GGAC
                                      _  G   CA
GAM2713  EMP1      5'  AGGTGCTGGCAGCAGCCCTG   63136    AG      ATCG
                                AG  GCTGGCAG    AGCCCTG
                                ||  ||||||||    |||||||
                                TC  CGACCGTC    TCGGGAC
                                 CA       G___
GAM2713  GBF1      3'  AGAGGCTGCAGATGACAGCTGA 63137        G    C  GCC
                                AGAGGCTG CAGAT GA   CTGA
                                |||||||| ||||| ||   ||||
                                TCTCCGAC GTCTA CT   GACT
                                     _    _  GTC
GAM2713  HOXB6     5'  AGAGGCTGGAGCCCT      63138         CAGATCG
                                AGAGGCTGG      AGCCCT
                                |||||||||      ||||||
                                TCTCCGACC      TCGGGA
                                               _______
GAM2713  ITGAL     3'  AGAGGCTGGTGAACCGTCTG   63139         CA    AGCC
                                AGAGGCTGG  GATCG    CTG
                                |||||||||  |||||    |||
                                TCTCCGACC  TTGGC    GAC
                                     AC     A___
GAM2713  JAG1      3'  GGCTGGGCAGGCTCCTG     63140       _  ATCGA  _
                                GGCTGG CAG     GC CCTG
                                |||||| |||     || ||||
                                CCGACC GTC     CG GGAC
                                   C  _____  A
GAM2713  KIR2DL3   3'  AGCTGGCAACCCAGTTTTGA   63141        G   G  CCC
                                GGCTGGCA ATC AG   TGA
                                |||||||| ||| ||   |||
                                TCGACCGT TGG TC   ACT
                                     _   G  AAA
GAM2713  LANGERIN  3'  GAGGCTGGGTGCCAGCCGAGCT 63142         ____  A     C
              CTGA                  GAGGCTGG    CAG TCGAGC CTGA
                                ||||||||    ||| |||||| ||||
                                CTCCGACC    GTC GGCTCG GACT
                                     CACG   _     A
GAM2713  LSP1      5'  GCTGGCAGATCCCTG       63143          CGAG
                                GCTGGCAGAT    CCCTG
                                ||||||||||    |||||
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                                CGACCGTCTA   GGGAC
                                     ____
GAM2713  MECP2    3'  AGAGGCTGCCCCAGCCCTG   63144       G AGA  G
                                AGAGGCTG C   TC AGCCCTG
                                |||||||| |   || |||||||
                                TCTCCGAC G   GG TCGGGAC
                                     _ ___  G
GAM2713  NUCB1    3'  AGGGGCTGGGCCTAGGTCCTG  63145    A    _ AGATCG  C_
                                AG GGCTGG C     AG  CCTG
                                || |||||| |     ||  ||||
                                TC CCGACC G     TC  GGAC
                                 C     C GA____  CA
GAM2713  PTTG1IP  3'  AAGGCTGGCAGGTTCACTG   63146         A_  AGCC
                                GAGGCTGGCAG  TCG   CTG
                                ||||||||||  |||   |||
                                TTCCGACCGTC  AGT   GAC
                                      CA  ____
GAM2713  RAB3A    3'  AGGGGCTGGCAGGCCT     63147    A       ATCGA  C
                                AG GGCTGGCAG    GCC T
                                || |||||||||    ||| |
                                TC CCGACCGTC    CGG A
                                 C       _____  _
GAM2713  RFC1     3'  GAGGCTGGGAATCCGAGTTCTG 63148        C  A    CC
                A                GAGGCTGG AG TCGAG  CTGA
                                |||||||| || |||||  ||||
                                CTCCGACC TT GGCTC  GACT
                                     C  A    AA
GAM2713  SCN4A    3'  GGCTGGCAGTGCCCTG     63149        ATCGA
                                GGCTGGCAG    GCCCTG
                                |||||||||    ||||||
                                CCGACCGTC    CGGGAC
                                     A____
GAM2713  SURF5    3'  AAAGGCTGGCCCAGCCTTG   63150        AGAT G   C
                                AGAGGCTGGC   C AGCC TG
                                ||||||||||   | |||| ||
                                TTTCCGACCG   G TCGG AC
                                     ____ G   A
GAM2713  TCF3     3'  GAGGCTGGCCAGGCCCC     63151        AGAT  A
                                GAGGCTGGC    CG GCCCT
                                |||||||||    || |||||
                                CTCCGACCG    GT CGGGG
                                     ____  C
GAM2713  TNNC1    3'  GAGGCTGGGCATAGGCAGCTCT 63152        _  GATCG   C
                G                GAGGCTGG CA    AGC CTG
                                |||||||| ||    ||| |||
                                CTCCGACC GT    TCG GAC
                                     C  ATCCG   A
GAM2713  UCP3     5'  AGAGGCTGCTCCACAGCCCTG  63153        G AGA  _
                                AGAGGCTG C   TCG AGCCCTG
                                |||||||| |   ||| |||||||
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                                TCTCCGAC G   GGT TCGGGAC
                                    _ A__   G
GAM2713  UCP3     5'  AGAGGCTGCTCCACAGCCCTG  63153        G AGA  _
                                AGAGGCTG C   TCG AGCCCTG
                                |||||||| |   ||| |||||||
                                TCTCCGAC G   GGT TCGGGAC
                                    _ A__   G
GAM2713  WNT11    3'  GAGGCTGGTCTCTGTGGCCCTG 63154        CAGA  GA__
           A                     GAGGCTGG   TC   GCCCTGA
                                |||||||   ||   |||||||
                                CTCCGACC   AG   CGGGACT
                                    AG__  ACAC
GAM2713  WNT14    3'  AGGGCTGGCAGGGCCT     63155    A       ATCGA  C
                                AG GGCTGGCAG    GCC T
                                || |||||||||    ||| |
                                TC CCGACCGTC    CGG A
                                 _       C_____  _
GAM2713  ANP32B   5'  GAGGCCGGCGGCGCGGTCCTG  63156        AGAT  AGC_
                                GAGGCTGGC   CG   CCTG
                                |||||||||   ||   ||||
                                CTCCGGCCG   GC   GGAC
                                     CC__  GCCA
GAM2713  BCCIP    3'  GAGGCTGGCAGGCTCCACCTG  63157         A_  GA  C
                                GAGGCTGGCAG  TC  GCC TG
                                ||||||||||  ||  ||| ||
                                CTCCGACCGTC  AG  TGG AC
                                     CG  G_  _
GAM2713  C11orf21 3'  GAGGCTGGTGAAGCCTG    63158       CAGATC    C
                                GAGGCTGG    GAGCC TG
                                ||||||||    ||||| ||
                                CTCCGACC    TTCGG AC
                                    AC_____   _
GAM2713  C1orf33  3'  AGGGGCGGCAGCAGTCCTG   63159   A  T   ATCG  C
                                AG GGC GGCAG   AG CCTG
                                || ||| |||||   || ||||
                                TC CCG CCGTC   TC GGAC
                                 C  _    G___  A
GAM2713  C21orf67 5'  GAGGATCGCTCGAGTCCTG   63160    CTG  AGA   C
                                GAGG  GC  TCGAG CCTG
                                ||||  ||  ||||| ||||
                                CTCC  CG  AGCTC GGAC
                                  TAG  ___    A
GAM2713  CDH24    3'  GAGGCTGGAGCTCTTGCCCTG  63161        C  A  GA
                                GAGGCTGG AG TC  GCCCTG
                                |||||||| || ||  ||||||
                                CTCCGACC TC AG  CGGGAC
                                    _ G  AA
GAM2713  CHST8    5'  GCTGGTCTCTGAGCCCTG    63162      CAGA  _
                                GCTGG   TC GAGCCCTG
                                |||||   || ||||||||
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                                CGACC   AG CTCGGGAC
                                   AG__ A
GAM2713 CINP     3' GGCTGGTGACAAGCTCTG    63163       CA T    C
                                GGCTGG  GA CGAGC CTG
                                ||||||  || ||||| |||
                                CCGACC  CT GTTCG GAC
                                   A_ _    A
GAM2713 DKFZp761G2113 3' AGAGGCTGGAGGCCCT      63164         C ATCGA
                                AGAGGCTGG AG    GCCCT
                                ||||||||| ||    |||||
                                TCTCCGACC TC    CGGGA
                                   _ _____
GAM2713 EIF4B    3' AGGGGCTGGCAGCCTCCTG   63165    A       A GAGC
                                AG GGCTGGCAG TC   CCTG
                                || |||||||| ||    ||||
                                TC CCGACCGTC GG   GGAC
                                 C        _ A___
GAM2713 FGD3     5' GAGGCTGGCCAGGGGCTTCCTG 63166         AGATCGA __
              A                  GAGGCTGGC      GC  CCTGA
                                |||||||||      ||  |||||
                                CTCCGACCG      CG  GGACT
                                     GTCCC__  AA
GAM2713 FLJ10898 5' GAGACTGGAAAACGAGCCCTG  63167        C   T
                                GAGGCTGG AGA CGAGCCCTG
                                |||||||| ||| |||||||||
                                CTCTGACC TTT GCTCGGGAC
                                     _  T
GAM2713 FLJ13693 3' AGAGGCTGAGTCTGAGCCCTGA 63168        GC  A  _
                                AGAGGCTG  AG TC GAGCCCTGA
                                ||||||||  || || |||||||||
                                TCTCCGAC  TC AG CTCGGGACT
                                     __  _  A
GAM2713 FLJ13881 3' AAGGCTGGTGGAGGCCTG    63169        CAGATC   C
                                GAGGCTGG     GAG CCTG
                                ||||||||     ||| ||||
                                TTCCGACC     CTC GGAC
                                     AC_____   C
GAM2713 FLJ20297 3' AGAGCGTAGCTGTTGAGCCCTG 63170     G _   AGATC
                                AGAG C TGGC    GAGCCCTG
                                |||| | ||||    ||||||||
                                TCTC G ATCG    CTCGGGAC
                                  _ C   ACAA_
GAM2713 FLJ20297 3' AGAGCGTAGCTGTTGAGCCCTG 63170     G _   AGATC
                                AGAG C TGGC    GAGCCCTG
                                |||| | ||||    ||||||||
                                TCTC G ATCG    CTCGGGAC
                                  _ C   ACAA_
GAM2713 FLJ20811 3' GGTCCTGGATTGAGCCCTG   63171    _ GGCA   C
                                GG CT    GAT GAGCCCTG
                                || ||    ||| ||||||||
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                                CC GG    CTA CTCGGGAC
                                 A  AC__   A
GAM2713  FLJ22678  3'  GAGGCTGGCAGGTGGCTCTG   63172          ATCGA  C
                                GAGGCTGGCAG     GC CTG
                                ||||||||||     || |||
                                CTCCGACCGTC     CG GAC
                                      CAC__  A
GAM2713  FLJ30532  3'  GAGGCTGGTAGATCATCTGA   63173        C     AGCC
                                GAGGCTGG AGATCG    CTGA
                                |||||||| ||||||    ||||
                                CTCCGACC TCTAGT    GACT
                                     A     A___
GAM2713  FYCO1     3'  AGAGGCTGATGGTCTCCTG    63174         CAGA  GAGC
                                AGAGGCTGG    TC    CCTG
                                |||||||||    ||    ||||
                                TCTCCGACT    AG    GGAC
                                      ACC_  A___
GAM2713  HSNOV1    3'  GAGGCTGGCTCAGTCCTG     63175         AGA  G  C
                                GAGGCTGGC   TC AG CCTG
                                |||||||||   || || ||||
                                CTCCGACCG   AG TC GGAC
                                     ___  _  A
GAM2713  KIAA0125  5'  AGAGGCTGGGGATCCAGGCTGA 63176         CA    G  CC
                                AGAGGCTGG  GATC AG  CTGA
                                |||||||||  ||||  ||  ||||
                                TCTCCGACC  CTAG TC  GACT
                                     C_    G  C_
GAM2713  KIAA0140  3'  AGGGGCGGGCAGACCCTG    63177    A   T    ATCGA
                                AG GGC GGCAG     GCCCTG
                                || ||| |||||     ||||||
                                TC CCG CCGTC     TGGGAC
                                 C   C    ______
GAM2713  KIAA0218  3'  GAGGCTGGCAGCCCCTG     63178          ATCGAG
                                GAGGCTGGCAG     CCCTG
                                ||||||||||     |||||
                                CTCCGACCGTC     GGGAC
                                      G_____
GAM2713  KIAA0258  3'  GAGGCTGGGGGATCATCTG    63179         CA    AGCC
                                GAGGCTGG  GATCG    CTG
                                ||||||||  |||||    |||
                                CTCCGACC  CTAGT    GAC
                                     CC    A___
GAM2713  KIAA0420  3'  AAGGCTGGGGTTTGAGTCCTG  63180         CAGATC   C
                                GAGGCTGG     GAG CCTG
                                ||||||||     ||| ||||
                                TTCCGACC     CTC GGAC
                                     CCAAA_   A
GAM2713  KIAA0515  3'  GAGGCTGCGCAGGCCCT     63181         _    ATCGA
                                GAGGCTG GCAG     GCCCT
                                |||||||  ||||     |||||
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                                CTCCGAC CGTC    CGGGA
                                   G  _____
GAM2713 KIAA0775 3' GAGGCTGGCAGACAGTCCCCTG 63182          CGAG
                                GAGGCTGGCAGAT   CCCTG
                                ||||||||||||   |||||
                                CTCCGACCGTCTG   GGGAC
                                     TCAG
GAM2713 KIAA0889 3' GATGCTGGCAGTCTCTG    63183   G      A  GAGCC
                                GA GCTGGCAG TC    CTG
                                || ||||||||| ||    |||
                                CT CGACCGTC AG    GAC
                                 A      _ A____
GAM2713 KIAA0892 3' AGGGGGTGGTGTCTTGAGCCCT 63184   A  C   CAGATC
             GA                   AG GG TGG     GAGCCCTGA
                                || || |||     |||||||||
                                TC CC ACC     CTCGGGACT
                                 C  C   ACAGAA
GAM2713 KIAA1543 3' GACTGAGCTGAGCCCTGA    63185      _ AGATC
                                GGCTG GC    GAGCCCTGA
                                ||||| ||    |||||||||
                                CTGAC CG    CTCGGGACT
                                   T  A____
GAM2713 KIAA1755 3' GAGGGTTGGCAGATAAATGCTC 63186     C_      C  _  C
             TG                   GAGG  TGGCAGAT GA GC CTG
                                ||||  |||||||| || || |||
                                CTCC  ACCGTCTA TT CG GAC
                                   CA       T  A  A
GAM2713 KIAA1924 3' GAGGACTGCTTGAGCCCTG   63187     _   G AGATC
                                GAGG CTG C    GAGCCCTG
                                |||| ||| |    ||||||||
                                CTCC GAC G    CTCGGGAC
                                   T   _ AA___
GAM2713 MAGE-E1  3' AGAAGCTGGCGCCAGCTCTG  63188        AGA  G   C
                                AGAGGCTGGC   TC AGC CTG
                                ||||||||||   || ||| |||
                                TCTTCGACCG   GG TCG GAC
                                     C__  _   A
GAM2713 MGC13114 3' GAGGCTGGCAGATGACCC    63189          C  G
                                GAGGCTGGCAGAT GA CCC
                                |||||||||||| || |||
                                CTCCGACCGTCTA CT GGG
                                          _ _
GAM2713 MGC16386 3' GAGGCTGGCAGAGCCCC     63190          TCGA
                                GAGGCTGGCAGA   GCCCT
                                ||||||||||||   |||||
                                CTCCGACCGTCT   CGGGG
                                          _____
GAM2713 MGC20398 3' AGAGGCTGTTAGAAACCTTG  63191       GC   TCG   C
                                AGAGGCTG  AGA   AGCC TG
                                ||||||||  |||   |||| ||
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                                TCTCCGAC  TCT   TTGG AC
                                    AA  ___   A
GAM2713  MGC33182  5'  GAGGCTGGGCTCAGCCCTGA  63192       CAGA  G
                                GAGGCTGG   TC AGCCCTGA
                                ||||||||   || ||||||||
                                CTCCGACC   AG TCGGGACT
                                    CG__  _
GAM2713  MGC4607   3'  AGGGCTTGGCTGAGCCCTG   63193   A   _   AGATC
                                AG GGCT GGC    GAGCCCTG
                                || |||| |||    ||||||||
                                TC CCGA CCG    CTCGGGAC
                                 _   A  A____
GAM2713  NBL1      3'  GGCTGGCAGCCACCCTG     63194        ATCGA
                                GGCTGGCAG    GCCCTG
                                |||||||||    ||||||
                                CCGACCGTC    TGGGAC
                                     GG___
GAM2713  NGEF      3'  AGAGGCTGGCAGAGGCCTG   63195          TCGA  C
                                AGAGGCTGGCAGA   GCC TG
                                ||||||||||||   ||| ||
                                TCTCCGACCGTCT   CGG AC
                                       C___  _
GAM2713  OPRL1     3'  AGAGGCTGTGAGGGGAGCCTTG 63196       GC  ATC    C
                                AGAGGCTG  AG   GAGCC TG
                                ||||||||  ||   ||||| ||
                                TCTCCGAC  TC   CTCGG AC
                                    AC  CC_    A
GAM2713  PHRET1    3'  GAGACTGGTGGACCACCTGA  63197       CA    AGC
                                GAGGCTGG  GATCG   CCTGA
                                ||||||||  |||||   |||||
                                CTCTGACC  CTGGT   GGACT
                                    AC    ___
GAM2713  PIG7      3'  AAAGGCTGGTTCAGCCGAGCTC 63198        __  A    C
            TG                   AGAGGCTGG  CAG TCGAGC CTG
                                |||||||||  ||| |||||| |||
                                TTTCCGACC  GTC GGCTCG GAC
                                    AA  _     A
GAM2713  PIP3-E    3'  AGAGGCAGGCAGATCACCTGA  63199      T       AGC
                                AGAGGC GGCAGATCG   CCTGA
                                ||||||  |||||||||  |||||
                                TCTCCG CCGTCTAGT   GGACT
                                   T       ___
GAM2713  PSKH1     5'  GAGGCTGGCAGGACCTGCTCTG 63200          _  GA  C
            A                    GAGGCTGGCAG ATC  GC CTGA
                                ||||||||||| |||  || ||||
                                CTCCGACCGTC TGG  CG GACT
                                       C  A_  A
GAM2713  RAB35     3'  AGCTGGCACAGGCCCTG     63201        GAT  A
                                GGCTGGCA   CG GCCCTG
                                ||||||||   || ||||||
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                                TCGACCGT   GT CGGGAC
                                   ___  C
GAM2713  RBPMS    3'  AGAGGCTGTGACAAAGTCTTGA 63202        GCA   C   CCC
                                AGAGGCTG   GAT GAG   TGA
                                ||||||||   ||| |||   |||
                                TCTCCGAC   CTG TTC   ACT
                                     A__   T   AGA
GAM2713  RPH3A    3'  AGAGACTGGAGGGGGTTCTGA  63203         C  ATCGAGCC
                                AGAGGCTGG AG       CTGA
                                ||||||||| ||       ||||
                                TCTCTGACC TC       GACT
                                     _  CCCCAA__
GAM2713  SNX11    3'  AGACGCTGGTGGCGGAAGCCCT 63204     G    CAGATC
              G                  AGA GCTGG     GAGCCCTG
                                 ||| |||||     ||||||||
                                 TCT CGACC     TTCGGGAC
                                   G    ACCGCC
GAM2713  TOLLIP   3'  AGAGGCTGGCAAGGCCTG    63205          GATCG  C
                                AGAGGCTGGCA    AG CCTG
                                ||||||||||     || ||||
                                TCTCCGACCGT    TC GGAC
                                      _____  C
GAM2713  TRIM26   3'  AGGGGCTGGCAGAGCACT    63206    A        TCGA  C
                                AG GGCTGGCAGA    GC CT
                                || ||||||||||    || ||
                                TC CCGACCGTCT    CG GA
                                 C         _____  T
GAM2713  LOC118920 5'  AGGGGTCGGTAGAGCCCTG    63207    A  C   CAGATC
                                AG GG TGG     GAGCCCTG
                                || || |||     ||||||||
                                TC CC GCC     CTCGGGAC
                                 C  A   AT_____
GAM2713  LOC124987 5'  GAAGCTGGCAGGGGCTTG    63208          ATCGA  CC
                                GAGGCTGGCAG    GC  TG
                                ||||||||||    ||  ||
                                CTTCGACCGTC    CG  AC
                                      CC___  A_
GAM2713  LOC139673 3'  AGGGGCTGGCAGCCTCCTG    63165    A       A  GAGC
                                AG GGCTGGCAG TC    CCTG
                                || ||||||||| ||    ||||
                                TC CCGACCGTC GG    GGAC
                                 C        _  A___
GAM2713  LOC144317 5'  GAGGCTGGTGGATCACCTGA   63209        CA    AGC
                                GAGGCTGG  GATCG   CCTGA
                                ||||||||  |||||   |||||
                                CTCCGACC  CTAGT   GGACT
                                     AC    ___
GAM2713  LOC144667 3'  AAGGCTGCAGTGAGCCCTG    63210        G   ATC
                                GAGGCTG CAG   GAGCCCTG
                                ||||||| |||   ||||||||
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                                TTCCGAC GTC   CTCGGGAC
                                   _  A__
GAM2713  LOC145801 5'  AGAGGCCGGCGGCGCGGTCCTG 63211          AGAT  AGC_
                                AGAGGCTGGC   CG   CCTG
                                ||||||||||   ||   ||||
                                TCTCCGGCCG   GC   GGAC
                                     CC__  GCCA
GAM2713  LOC145989 3'  GAGACTGGCAGCAGGGGGGCCC 63212          ATCGA__
              TG                  GAGGCTGGCAG      GCCCTG
                                ||||||||||       ||||||
                                CTCTGACCGTC      CGGGAC
                                     GTCCCCC
GAM2713  LOC146894 3'  GAGGGTGGGGAGAGCCCTG   63213     C   CA  TC
                                GAGG TGG  GA  GAGCCCTG
                                |||| |||  ||  ||||||||
                                CTCC ACC  CT  CTCGGGAC
                                  C   C_  __
GAM2713  LOC146909 3'  AGGGGCCGGTAGGTTAGGACAC 63214    A     C  ATC__  GC
              CT                  AG GGCTGG AG     GA  CCT
                                || |||||| ||     ||  |||
                                TC CCGGCC TC     CT  GGA
                                 C      A  CAATC  GT
GAM2713  LOC147958 5'  AGAGGCTGGCGGCTTCCTG   63215         AGATC A  __
                                AGAGGCTGGC    G GC  CCTG
                                ||||||||||    | ||  ||||
                                TCTCCGACCG    C CG  GGAC
                                      _____ _  AA
GAM2713  LOC148397 3'  AGGCTGGCAGCACCTGGCTCTG 63216          _   GA  C
                                AGGCTGGCAG ATC  GC CTG
                                |||||||||| |||  || |||
                                TCCGACCGTC TGG  CG GAC
                                     G   AC  A
GAM2713  LOC149672 5'  AGAGGCTGGAGTGAGATGCTTT 63217         C  ATC  _  CC
              GA                  AGAGGCTGG AG   GA GC  TGA
                                ||||||||| ||   || ||  |||
                                TCTCCGACC TC   CT CG  ACT
                                     _  ACT  A  AA
GAM2713  LOC150776 3'  AGAGCGTGGCTGTTGAGCCCTG 63218      G _   AGATC
                                AGAG C TGGC     GAGCCCTG
                                |||| | ||||     ||||||||
                                TCTC G ACCG     CTCGGGAC
                                  _ C    ACAA_
GAM2713  LOC150886 5'  AGATGCTGGCAGGTCCAGCGTC 63219     G       A  G   C_
              TG                  AGA GCTGGCAG TC AGC  CTG
                                ||| |||||||| || |||  |||
                                TCT CGACCGTC AG TCG  GAC
                                  A       C  G   CA
GAM2713  LOC150889 5'  AGGGCTGGCAGTCTCCCTG   63220    A       A  GAG
                                AG GGCTGGCAG TC   CCCTG
                                || |||||||| ||   |||||
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                                TC CCGACCGTC AG   GGGAC
                                 _       _ A__
GAM2713  LOC151959 5'  AGACGCTGGGAGCCCT      63221     G    CAGATC
                                AGA GCTGG     GAGCCCT
                                ||| |||||     |||||||
                                TCT CGACC     CTCGGGA
                                  G    _______
GAM2713  LOC152065 5'  GAGGCTGGCAGGGCCCTG    63222          ATCGA
                                GAGGCTGGCAG    GCCCTG
                                ||||||||||    ||||||
                                CTCCGACCGTC    CGGGAC
                                      C____
GAM2713  LOC155372 3'  GAGGCGGGCAGATCACCTGA   63223      T       AGC
                                GAGGC GGCAGATCG   CCTGA
                                ||||| |||||||||   |||||
                                CTCCG CCGTCTAGT   GGACT
                                   C       ___
GAM2713  LOC158656 5'  AGAGGCTGGTGGTCAGCCCTG  63224         CAGA  G
                                AGAGGCTGG    TC AGCCCTG
                                |||||||||    || |||||||
                                TCTCCGACC    AG TCGGGAC
                                     ACC_  _
GAM2713  LOC159199 5'  AGAGGCGGTGGGCCGTCCTTG  63225       T  CAGA   AG  C
                                AGAGGC GG    TCG  CC TG
                                |||||| ||    |||  || ||
                                TCTCCG CC    GGC  GG AC
                                   _  ACCC   A_  A
GAM2713  LOC196500 3'  GAGGACTGGCTCAGGGGGCTCT 63226      _    AGATCGA  C
            GA                   GAGG CTGGC      GC CTGA
                                |||| |||||      || ||||
                                CTCC GACCG      CG GACT
                                  T    AGTCCCC  A
GAM2713  LOC196759 3'  GGCTGGCATGTCAGCACTGCCC 63227        GA   A____
            TGA                  GGCTGGCA  TCG    GCCCTGA
                                |||||||  |||    |||||||
                                CCGACCGT  AGT    CGGGACT
                                     AC   CGTGA
GAM2713  LOC197285 3'  AGCTGGCAGGAGGTCCTG    63228         ATC   C_
                                GGCTGGCAG   GAG  CCTG
                                |||||||||   |||  ||||
                                TCGACCGTC   CTC  GGAC
                                     ___   CA
GAM2713  LOC197320 5'  GAGGCTGACGGAAGCGTCTGA  63229         A  TCG   C_
                                GAGGCTGGC GA   AGC  CTGA
                                ||||||||| ||   |||  ||||
                                CTCCGACTG CT   TCG  GACT
                                     C  ___   CA
GAM2713  LOC200222 5'  AGAGACTGGTGATGCCCTG   63230         CA   CGA
                                AGAGGCTGG  GAT   GCCCTG
                                |||||||||  |||   ||||||
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                                TCTCTGACC  CTA   CGGGAC
                                     A_  ___
GAM2713  LOC200488 5'  GAGGCTGGCGGCTGTCCTG   63231        AGATC A ___
                                GAGGCTGGC    G GC   CCTG
                                |||||||||    | ||   ||||
                                CTCCGACCG    C CG   GGAC
                                     _____ _  ACA
GAM2713  LOC201736 5'  AGGTGAAGGTTGAGCCCTG   63232     C   C  ATC
                                AGG TGG AG   GAGCCCTG
                                ||| ||| ||   ||||||||
                                TCC ACT TC   CTCGGGAC
                                  _  _  CAA
GAM2713  LOC202181 5'  AGAGGCTGGCACATGTCTG   63233          G  CGAGCC
                                AGAGGCTGGCA AT     CTG
                                |||||||||| ||     |||
                                TCTCCGACCGT TA     GAC
                                      G  CA____
GAM2713  LOC204084 5'  GATGCTGCCAACGGGTCCTG   63234    G   G   AT  AGC
                                GA GCTG CAG  CG   CCTG
                                || |||| |||  ||   ||||
                                CT CGAC GTT  GC   GGAC
                                 A   G   __ CCA
GAM2713  LOC221495 3'  GAGGCTGGAAGTCCTTGCTCTG 63235        C  A  GA  C
           A                     GAGGCTGG AG TC  GC CTGA
                                |||||||| || ||  || ||||
                                CTCCGACC TC GG  CG GACT
                                     T  A  AA  A
GAM2713  LOC253143 5'  GAGGCTGGGGAGGAGCCTGA   63236        CA  TC    C
                                GAGGCTGG  GA  GAGCC TGA
                                ||||||||  ||  ||||| |||
                                CTCCGACC  CT  CTCGG ACT
                                     C_  C_    _
GAM2713  LOC255031 5'  GGCTGCCAGGAGCCCTG     63237      G   ATC
                                GGCTG CAG   GAGCCCTG
                                ||||| |||   ||||||||
                                CCGAC GTC   CTCGGGAC
                                   G  ___
GAM2713  LOC257354 3'  AAGGCTGGGGTTTGAGTCCTG  63180        CAGATC   C
                                GAGGCTGG     GAG CCTG
                                ||||||||     ||| ||||
                                TTCCGACC     CTC GGAC
                                     CCAAA_   A
GAM2713  LOC257494 3'  AGGGGCTGGCAGAGCACT    63206    A       TCGA  C
                                AG GGCTGGCAGA    GC CT
                                || ||||||||||    || ||
                                TC CCGACCGTCT    CG GA
                                 C         _____ T
GAM2713  LOC90668  3'  AGGGGCTGGCAGGGGGCCCTG  63238    A       ATCGA
                                AG GGCTGGCAG     GCCCTG
                                || |||||||||     ||||||
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                                TC CCGACCGTC    CGGGAC
                                 C       CCC__
GAM2713 LOC91517 3' AGGGGCTGGCAGGCCTGCTCT 63239    A       AT GA  C
                                AG GGCTGGCAG  C  GC CT
                                || |||||||||  |  || ||
                                TC CCGACCGTC  G  CG GA
                                 C       CG A_  A
GAM2713 LOC92714 3' AGAGGCTGGGCAGGTCCTG   63240        _  ATCGAGC
                                AGAGGCTGG CAG      CCTG
                                ||||||||| |||      ||||
                                TCTCCGACC GTC      GGAC
                                     C   CA_____
GAM2714 BCR     3' CCCAGACCTGGGCAGATCTGCC 63243        A  A  TAT   A
                                TCCAGACCT GG GC   TCT CC
                                ||||||||| || ||   ||| ||
                                GGGTCTGGA CC CG   AGA GG
                                     _ _  TCT   C
GAM2714 CORO2A   3' TCCAGCTCTAGTTTTCTAC   63244      AC   GAGCTA
                                TCCAG  CTAG     TTCTAC
                                |||||  ||||     ||||||
                                AGGTC  GATC     AAGATG
                                   GA   AA____
GAM2714 CORO2A   3' TCCAGCTCTAGTTTTCTAC   63244      AC   GAGCTA
                                TCCAG  CTAG     TTCTAC
                                |||||  ||||     ||||||
                                AGGTC  GATC     AAGATG
                                   GA   AA____
GAM2714 FSHPRH1  5' AACCTAGGAGTTCAAGACC   63245        CTA   T__
                                GACCTAGGAG   TTC   ACC
                                ||||||||||   |||   |||
                                TTGGATCCTC   AAG   TGG
                                     ___   TTC
GAM2714 GYS1     3' TCCAGATCTAGAAGCCAGGACC 63246       C        TTCT
                                TCCAGA CTAGGAGCTA    ACC
                                |||||| ||||||||||    |||
                                AGGTCT GATCTTCGGT    TGG
                                   A        CC__
GAM2714 HIVEP3   5' CAGGGCCCACGCTATTCTA   63247     A_   GGA
                                CAG  CCTA   GCTATTCTA
                                |||  ||||   |||||||||
                                GTC  GGGT   CGATAAGAT
                                  CC   G__
GAM2714 HUNK     3' TCCACATAAAGCTATTCTA   63248      GACCTA
                                TCCA     GGAGCTATTCTA
                                ||||     ||||||||||||
                                AGGT     TTTCGATAAGAT
                                  GTA___
GAM2714 MYOC     3' CCAGAGGAGCTATTCT      63249       CCTA
                                CCAGA    GGAGCTATTCT
                                |||||    ||||||||||
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                                GGTCT   CCTCGATAAGA
                                  ____
GAM2714 RARA    3' CCAGGTCTGGGAAAACTCT   63250     AC A   CT
                                CCAG  CT GGAG  ATTCT
                                ||||  || ||||  |||||
                                GGTC  GA CCTT  TGAGA
                                  CA  C   T_
GAM2714 SLC25A19 3' TCCAGACCAGGAGTGTGTTCT 63251       T   CTA_
                                TCCAGACC AGGAG   TTCT
                                |||||||| |||||   ||||
                                AGGTCTGG TCCTC   AAGA
                                    _   ACAC
GAM2714 SULT1C1  3' TCCATGCCTGGGAGCCATGCC 63252     GA  A     T
                                TCCA  CCT GGAGCTAT CT
                                ||||  ||| |||||||| ||
                                AGGT  GGA CCTCGGTA GG
                                  AC  C       C
GAM2714 UBE2B   3' CCTAGGCATAAGCTATTCTGCC 63253      ____      A
                                CCTAGG   AGCTATTCT CC
                                ||||||   ||||||||| ||
                                GGATCC   TCGATAAGA GG
                                   GTAT       C
GAM2714 ALS2CR8  5' TCCAGGCCTCAAGCATTCTAC 63254     A  AG   T
                                TCCAG CCT  GAGC ATTCTAC
                                ||||| |||  |||| |||||||
                                AGGTC GGA  TTCG TAAGATG
                                  C  G_  _
GAM2714 API5    3' AACCTAAAAATTCTA      63255         GCT
                                GACCTAGGA   ATTCTA
                                |||||||||   ||||||
                                TTGGATTTT   TAAGAT
                                   ___
GAM2714 DKFZP586M0622 5' CAAATGAAAAGCTATTTTACC 63256     CCT       C
                                CAGA   AGGAGCTATT TACC
                                ||||   |||||||||| ||||
                                GTTT   TTTTCGATAA ATGG
                                  AC_        A
GAM2714 EPN2    3' CCAGACCTGGTAAATTCTA   63257       A  AGCT
                                CCAGACCT GG   ATTCTA
                                |||||||| ||   ||||||
                                GGTCTGGA CC   TAAGAT
                                   _ ATT_
GAM2714 FLJ22644 3' CCCAGACTGTCTTCTATTCTA 63258       CTAGGAG
                                TCCAGAC      CTATTCTA
                                |||||||      ||||||||
                                GGGTCTG      GATAAGAT
                                   ACAGAA_
GAM2714 KIAA0125 3' GATCCAGGAGCCCCTGCC   63259   C       AT  A
                                GA CTAGGAGCT  TCT CC
                                || |||||||||  ||| ||
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                                CT GGTCCTCGG  GGA GG
                                 A        __  C
GAM2714  KIAA1238  3'  TCTATACCCCACCTATTCTGCC 63260    CAG   AGGAG     A
                                TC   ACCT    CTATTCT CC
                                ||   ||||    ||||||| ||
                                AG   TGGG    GATAAGA GG
                                 ATA   GTG__      C
GAM2714  KIAA1271  3'  TCCAGACCTCAGGCGATCTGCC 63261        A  A  TAT   A
                                TCCAGACCT GG GC   TCT CC
                                ||||||||| || ||   ||| ||
                                AGGTCTGGA TC CG   AGA GG
                                     G  _  CT_   C
GAM2714  KIAA1582  5'  CAGACCTAGGGGATTCT     63262          AGCT
                                CAGACCTAGG    ATTCT
                                ||||||||||    |||||
                                GTCTGGATCC    TAAGA
                                      CC__
GAM2714  MGC12981  5'  TCCAGATCTGGAGCCACC     63263       C  A
                                TCCAGA CT GGAGCTATT
                                |||||| || |||||||||
                                AGGTCT GA CCTCGGTGG
                                   A  _
GAM2714  NIFU      3'  CAGACCAAGGCATTCTAC     63264       T   A  T
                                CAGACC AGG GC ATTCTAC
                                |||||| ||| || |||||||
                                GTCTGG TTC CG TAAGATG
                                    _   _  _
GAM2714  WIT-1     5'  CAGACCAGGAACCTCT      63265       T      AT
                                CAGACC AGGAGCT  TCT
                                |||||| |||||||  |||
                                GTCTGG TCCTTGG  AGA
                                    _      __
GAM2714  LOC120892 5'  CAAACCCTCTACTATTCTACC  63266        AGGA
                                CAGACCT    GCTATTCTACC
                                |||||||    ||||||||||
                                GTTTGGG    TGATAAGATGG
                                   AGA_
GAM2714  LOC138835 3'  TCCAGACCTGGGGGCACCCTGC 63267         A  A  T    A
            C                    TCCAGACCT GG GC ATTCT CC
                                ||||||||| || || ||||| ||
                                AGGTCTGGA CC CG TGGGA GG
                                     C  C  _    C
GAM2714  LOC149073 5'  TCCAGACCTGGGGTCATAGCC  63268         A  _____
                                TCCAGACCT GG    AGCT
                                ||||||||| ||    ||||
                                AGGTCTGGA CC    TCGG
                                     C  CAGTA
GAM2714  LOC150271 5'  TCCTGACCTAGGACCATCTGCC 63269     A       G   T  A
                                TCC GACCTAGGA CTAT CT CC
                                ||| ||||||||| |||| || ||
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                                AGG CTGGATCCT GGTA GA GG
                                  A       _   _ C
GAM2714  LOC159089 3'  TCCTGACCTAATTCTATC    63270     A      GAG
                                TCC GACCTAG   CTATT
                                ||| |||||||   |||||
                                AGG CTGGATT   GATAG
                                  A      AA_
GAM2715  CL25084   3'  TACTAGAATTTACATATT    63273      A
                                TATTA AATTTACATATT
                                ||||| ||||||||||||
                                ATGAT TTAAATGTATAA
                                   C
GAM2715  CSEN      3'  TATTTTATTAAAATATAC    63274            T
                                TATTTTATTAAAAT TAC
                                |||||||||||||| |||
                                ATAAAATAATTTTA ATG
                                        T
GAM2715  DC6       3'  TTTATTAAAATAACACATT    63275          TT
                                TTTATTAAAAT  ACATATT
                                ||||||||||  |||||||
                                AAATAATTTTA  TGTGTAA
                                       T_
GAM2715  KIAA1164  3'  TATTTTACTAACGTATACATAT 63276          AATT
              TC                  TATTTTATTAA    TACATATTC
                                ||||||||||    |||||||||
                                ATAAAATGATT    ATGTATAAG
                                       GCAT
GAM2715  LOC255621 3'  TTTTATTAAAATTATACAT    63277           _
                                TTTTATTAAAATT TACAT
                                |||||||||||| |||||
                                AAAATAATTTTAA ATGTA
                                        T
GAM2716  CRADD     3'  ATGACATGAGATATATATATG  63280        ATTTTA
                                ATGGCAT     ATATATATG
                                |||||||     |||||||||
                                TACTGTA     TATATATAC
                                    CTCTA_
GAM2716  ELOVL4    3'  GGTATATTTCCACATATGA    63281    C      AA
                                GG ATATTTT  TATATATGA
                                || |||||||  |||||||||
                                CC TATAAAG  GTGTATACT
                                  A     __
GAM2716  GRINL1A   3'  AATGACATGAACGTTTATATAT 63282        ATTTTAA
              G                   AATGGCAT      TATATATG
                                |||||||||     |||||||||
                                TTACTGTA      ATATATAC
                                    CTTGCAA
GAM2716  CKAP2     3'  AATGGCATATTTTGGGTCAAAG 63283           AATATA___
              TATGA                  AATGGCATATTTT       TATGA
                                ||||||||||||        |||||
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                                TTACCGTATAAAA       ATACT
                                      CCCAGTTTC
GAM2716 DIS3     3' TGACATATGACTATATATGA  63284        TTTAA
                                TGGCATAT    TATATATGA
                                ||||||||    |||||||||
                                ACTGTATA    ATATATACT
                                    CTG__
GAM2716 KIAA0737 3' TGGCATATTTGATATG     63285         TAATAT
                                TGGCATATTT     ATATG
                                ||||||||||     |||||
                                ACCGTATAAA     TATAC
                                     C_____
GAM2716 POT1     3' CGGCATATTTTACATG     63286         TAATA
                                TGGCATATTT     TATATG
                                ||||||||||     ||||||
                                GCCGTATAAA     ATGTAC

                                      _____
GAM2716 LOC116064 3' ATGGCATATAATATATATG   63287        TTT
                                ATGGCATA   TAATATATATG
                                ||||||||   ||||||||||
                                TACCGTAT   ATTATATATAC

                                      ___
GAM2716 LOC150538 3' ATGGCATACGTATATATATG   63288         TTTA
                                ATGGCATAT    ATATATATG
                                |||||||||    |||||||||
                                TACCGTATG    TATATATAC
                                     CA__
GAM2717 EHF      3' GCAACAATGTTCACCT      63291         CCTAACA
                                GCAACAGT      TTCACCT
                                ||||||||      |||||||
                                CGTTGTTA      AAGTGGA
                                     C_______
GAM2717 KCNS2    3' GCAACCCAACAACGTTCACCTC 63292      CAGT      ___
                                GCAA    CCTAACA   TTCACCTC
                                ||||    |||||||   |||||||||
                                CGTT    GGGTTGT   AAGTGGAG
                                  _____      TGC
GAM2717 LILRB4   3' TGCTGACAGTTTTCTTTCACCT 63293     A_    CCTAACA
             C                   TGC  ACAGT      TTCACCTC
                                 |||  |||||      |||||||||
                                 ACG  TGTCA      AAGTGGAG
                                   AC    AAAGA__
GAM2717 PKD2     3' GCATAGTATTTAACATTCATCT 63294     AC   CC_       C
                                 GCA  AGT   TAACATTCA CT
                                 |||  |||   ||||||||| ||
                                 CGT  TCA   ATTGTAAGT GA
                                   A_   TAA       A
GAM2717 DKFZp761G2113 3' GCGGCAGTTCTGGACGCCCACC 63295    AA    C  A_  A
             TC                    GC  CAGT CT  AC TTCACCTC
                                   ||  |||| ||  || ||||||||
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                                CG  GTCA GA  TG GGGTGGAG
                                 CC    A  CC  C
GAM2717  FIGN     3'  TGCAACAGTTTTGTTACTGCAT 63296         CCTAAC  _  C
              CTC                    TGCAACAGT     ATT CA CTC
                                |||||||||     ||| || |||
                                ACGTTGTCA     TGA GT GAG
                                     AAACAA   C  A
GAM2717  FLJ20105  5'  TGCAAGGTGGTAACATTCACCT 63297      CA  CC
                                TGCAA  GT  TAACATTCACCT
                                |||||  ||  ||||||||||||
                                ACGTT  CA  ATTGTAAGTGGA
                                   C_  CC
GAM2717  FLJ23878  3'  TGCAACAGTTTAAACACCATCA 63298         CCT    __
                                TGCAACAGT   AACAT  TCA
                                |||||||||   |||||  |||
                                ACGTTGTCA   TTGTG  AGT
                                     AAT    GT
GAM2717  KIAA0276  3'  TGTAACAATCCTCTCATT    63299    C       AA
                                TG AACAGTCCT  CATT
                                || |||||||||  ||||
                                AC TTGTTAGGA  GTAA
                                 A        GA
GAM2717  KIAA1000  5'  CAACTCAAAACATTCATCT    63300      AG  CT      C
                                CAAC  TC  AACATTCA CT
                                ||||  ||  |||||||| ||
                                GTTG  AG  TTGTAAGT GA
                                   __ TT       A
GAM2717  KIAA1786  3'  TGCAACAGTCCTGGAATCCCCT 63301           AAC    A
                                TGCAACAGTCCT   ATTC CCT
                                ||||||||||||   |||| |||
                                ACGTTGTCAGGA   TAGG GGA
                                       CCT   _
GAM2717  MAPK6    3'  GCACACAAGTCTAACATT    63302     _    TC
                                GCA ACAG  CTAACATT
                                ||| ||||  ||||||||
                                CGT TGTT  GATTGTAA
                                  G    CA
GAM2717  MGC21688  5'  GTCTCCAACATTCACCTC    63303     _
                                GTC CTAACATTCACCTC
                                ||| ||||||||||||||
                                CAG GGTTGTAAGTGGAG
                                  A
GAM2717  MGC23445  5'  TGCAACAGGCCTGACGTTTC   63304        T   A  A_
                                TGCAACAG CCT AC  TTC
                                |||||||| ||| ||  |||
                                ACGTTGTC GGA TG  AAG
                                     C   C  CA
GAM2717  ORC6L    3'  GCAACAGTCTTAGGATCC    63305         C  AC
                                GCAACAGTC TA  ATTC
                                |||||||||  ||  ||||
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                                CGTTGTCAG AT  TAGG
                                     A  CC
GAM2717  SCYA13   3'  CAGCAGTCCTACTATTGCATTC 63306    A      A_____     C
             ATCT                   CA CAGTCCTA     CATTCA CT
                                || ||||||||     ||||||| ||
                                GT GTCAGGAT     GTAAGT GA
                                 C       GATAAC     A
GAM2717  ZNF339   3'  TGTCACAGTCCTGGCTCACTC  63307    CA      AA__
                                TG  ACAGTCCT    CATTC
                                ||  ||||||||    |||||
                                AC  TGTCAGGA    GTGAG
                                 AG       CCGA
GAM2717  LOC145757 3'  TGCAACAGTCTAACATAACA   63308         C     T_
                                TGCAACAGTC TAACAT  CA
                                |||||||||| ||||||  ||
                                ACGTTGTCAG ATTGTA  GT
                                      _     TT
GAM2717  LOC151277 5'  TGCAACATTCTATAGATACCTC 63309       GTC   ACATTC
                                TGCAACA   CTA     ACCTC
                                |||||||   |||     |||||
                                ACGTTGT   GAT     TGGAG
                                    AA_   ATCTA_
GAM2717  LOC151584 5'  TACAACAGTAGAATTTACCT   63310        CCTAAC   C
                                TGCAACAGT     ATT ACCT
                                |||||||||     ||| ||||
                                ATGTTGTCA     TAA TGGA
                                     TCT___   A
GAM2717  LOC256158 5'  TGCAGCCAGTCCTCGCCCACCT 63311     A_      AACA
             C                   TGCA  CAGTCCT    TTCACCTC
                                ||||  |||||||   ||||||||
                                ACGT  GTCAGGA    GGGTGGAG
                                  CG      GC__
GAM2717  LOC91145  3'  TGCAACATTCCTGACATC    63312       G    A
                                TGCAACA TCCT ACATT
                                ||||||| |||| |||||
                                ACGTTGT AGGA TGTAG
                                    A    C
GAM2718  GAC1     5'  TGGAGGTTTGTATACCGCTGTA 63315       ________    TT_
             TCT                   TGGAGGT      TCGCT   TCT
                                |||||||      |||||   |||
                                ACCTCCA      GGCGA   AGA
                                    AACATAT     CAT
GAM2718  C20orf38  3'  TTGGAGGCTTTGTTCATAT    63316        CGCTT   T
                                TTGGAGGTT     TTC ATAT
                                |||||||||     ||| ||||
                                AACCTCCGA     AAG TATA
                                     AAC__   _
GAM2718  COLEC10   3'  TTGGGGTTAAAGCATTTCTATG 63317     A   C__  T      A
             TCT                   TTGG GGTT   GC TTTCTAT TCT
                                |||| ||||   || ||||||| |||
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                                AACC CCAA   CG AAAGATA AGA
                                  _   TTT  T      C
GAM2718  FLJ20457  3'  TTGGAGGTTTTTTTTTTAC   63318         CGC    C
                                TTGGAGGTT   TTTT TAT
                                |||||||||   |||| |||
                                AACCTCCAA   AAAA ATG
                                     AA_    A
GAM2718  FLJ22601  3'  TTGGAGGTTCTTTTTCT     63319          GC
                                TTGGAGGTTC  TTTTCT
                                ||||||||||  ||||||
                                AACCTCCAAG  AAAAGA
                                     A_
GAM2718  LOC139188 5'  GGTTTTGCTTTTCTATGTCT   63320      C_        A
                                GGTT  GCTTTTCTAT TCT
                                ||||  |||||||||| |||
                                CCAA  CGAAAAGATA AGA
                                  AA         C
GAM2718  LOC153792 3'  TTGGCAAGCCTTTTCTATGTCT 63321      _   TCG        A
                                TTGG AGGT   CTTTTCTAT TCT
                                |||| ||||   ||||||||| |||
                                AACC TTCG   GAAAAGATA AGA
                                  G   ___        C
GAM2719  DKFZp761B0514 3'  TGAGTGGGCCTGTAAAGTT    63324      AGC    TAGC
                                TGAG   GGCTT    GTAAAGTT
                                ||||   |||||    ||||||||
                                ACTC   CCGGA    CATTTCAA
                                  AC_    _____
GAM2719  LOC154386 3'  TGAGAGCAGTTTTAGGT     63325          C    C
                                TGAGAGCGG TTTAG GT
                                ||||||||| ||||| ||
                                ACTCTCGTC AAATC CA
                                     A    _
GAM2720  ANKTM1    3'  TGATTTTCCACCCTTTCTGT   63328      G   TG   C_
                                TGAT TTT  TCC  TCTGT
                                |||| |||  |||  |||||
                                ACTA AAG  GGG  AGACA
                                  A   GT   AA
GAM2720  DXF68S1E  3'  TGATGTTCCATTTTGTCTT   63329         TG CCCTC
                                TGATGTTT  T    TGTCTT
                                ||||||||  |    ||||||
                                ACTACAAG  A    ACAGAA
                                     GT AA____
GAM2720  PTEN      3'  ATGGTGTTTTATCCCTCT    63330     A
                                ATG TGTTTTGTCCCTCT
                                ||| ||||||||||||||
                                TAC ACAAAATAGGGAGA
                                  C
GAM2720  SS18      3'  ATGACGCCCCTTCTGT      63331       GTTTT     _
                                ATGAT    GTCCCT CTGT
                                |||||    |||||| ||||
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                                TACTG    CGGGGA GACA
                                  _____     A
GAM2720 STAR    3' ATGAGTTTTGTCTTTTTCC   63332     T      CCTCTG
                                ATGA GTTTTGTC     TCT
                                |||| ||||||||     |||
                                TACT CAAAACAG     AGG
                                  _       AAAA__
GAM2720 WBSCR1  3' ATGTGTTTTGTTCTTTATCTTA 63333     A      CC  C
                                ATG TGTTTTGT  CT TGTCTTA
                                ||| ||||||||  || |||||||
                                TAC ACAAAACA  GA ATAGAAT
                                  _       A_  A
GAM2720 WBSCR1  3' ATGTGTTTTGTTCTTTATCTTA 63333     A      CC  C
                                ATG TGTTTTGT  CT TGTCTTA
                                ||| ||||||||  || |||||||
                                TAC ACAAAACA  GA ATAGAAT
                                  _       A_  A
GAM2720 DDX35   3' ATGGTGTTTTGGCCTTCAGT  63334     A     T  C  T
                                ATG TGTTTTG CC TC GT
                                ||| ||||||| || || ||
                                TAC ACAAAAC GG AG CA
                                  C      C  A  T
GAM2720 GC20    3' ATGAGGTTTTGTTACCATCTTA 63335      T     CCCT
                                ATGA GTTTTGT    CTGTCTTA
                                |||| |||||||    ||||||||
                                TACT CAAAACA    GGTAGAAT
                                  C      AT__
GAM2720 JDD1    3' ATGGTGTTTTGTTCTTCGGTC  63336     A      CCC  T
                                ATG TGTTTTGT   TC GTC
                                ||| ||||||||   || |||
                                TAC ACAAAACA   AG CAG
                                  C       AGA  C
GAM2720 KIAA0280 3' TGCTGTTTTGTCCCTTTCT   63337    A        CTG
                                TG TGTTTTGTCCCT   TCT
                                || ||||||||||||   |||
                                AC ACAAAACAGGGA   AGA
                                 G          A__
GAM2720 KIAA1559 3' ATGATGTTTTGTTTCTTTCCCA 63338          CCC   G
                                ATGATGTTTTGT   TCT TCTTA
                                ||||||||||||   ||| |||||
                                TACTACAAAACA   AGA AGGGT
                                       A__   A
GAM2720 RAI     5' ATGATTTCTTCTCTGTCTT   63339      G   GTCC
                                ATGAT TTTT    CTCTGTCTT
                                ||||| ||||    |||||||||
                                TACTA AGAA    GAGACAGAA
                                  A   _____
GAM2720 SSH2    3' GTTTTGTCCCATCTT      63340          TCT
                                GTTTTGTCCC   GTCTT
                                ||||||||||   |||||
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                                CAAAACAGGG   TAGAA
                                     ___
GAM2720  LOC146092 5'  ATGCTGTTTTGTGCCCGTCTGT 63341     A       _  _
              CTTA                    ATG TGTTTTGT CCC TCTGTCTTA
                                      ||| |||||||| ||| |||||||||
                                      TAC ACAAAACA GGG AGACAGAAT
                                        G       C  C
GAM2720  LOC158046 3'  TGATGTTTGTCTTTCTG     63342         T   CC
                                      TGATGTTT GTC  TCTG
                                      |||||||| |||  ||||
                                      ACTACAAA CAG  AGAC
                                           _  AA
GAM2720  LOC200531 5'  ATGGTGTTTTGTCCATCCAT   63343     A         C
                                      ATG TGTTTTGTCC TCTGT
                                      ||| ||||||||| |||||
                                      TAC ACAAAACAGG AGGTA
                                        C         T
GAM2720  LOC200845 3'  ATGATGTTTTGATTTTTCTCA  63344           TCCCTCTG
                                      ATGATGTTTTG       TCTTA
                                      ||||||||||        |||||
                                      TACTACAAAAC       AGAGT
                                            TAAAA___
GAM2720  LOC221103 3'  ATGGTGTTTTGCTTTCCTC    63345     A       C__
                                      ATG TGTTTTGT   CCTC
                                      ||| ||||||||   ||||
                                      TAC ACAAAACG   GGAG
                                        C       AAA
GAM2720  LOC254504 5'  TGTTGTCCTTCTGTCTT     63346     TT    C
                                      TGT  TGTCC TCTGTCTT
                                      |||  ||||| ||||||||
                                      ACA  ACAGG AGACAGAA
                                        __     A
GAM2720  LOC257428 5'  ATGAGTGGAAAGTTCTCTGTCT 63347      _  TTTT  CC
              TA                      ATGA TG    GT  CTCTGTCTTA
                                      |||| ||    ||  ||||||||||
                                      TACT AC    CA  GAGACAGAAT
                                        C  CTTT  A_
GAM2721  CYP27B1   3'  AGTGCATACTTCACACATTGGT 63350         ATG       CA
              C                        GGTGCATA   TCACACAT  GTC
                                       ||||||||   ||||||||  |||
                                       TCACGTAT   AGTGTGTA  CAG
                                            GA_       AC
GAM2721  MAT1A    3'  GGTGCTTAGGAGACATCAGTC  63351       A  ATGTCAC
                                      GGTGC TA       ACATCAGTC
                                      ||||| ||       |||||||||
                                      CCACG AT       TGTAGTCAG
                                         A  CCTC___
GAM2721  RAD21    3'  GGTGCATAATTTCCCATCAGTC 63352          G  ACA
                                      GGTGCATAAT TC   CATCAGTC
                                      |||||||||| ||   ||||||||
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                                CCACGTATTA AG   GTAGTCAG
                                      A  G__
GAM2721  SLC16A2   3'  GGGCATAAGGAGGCATCAGTC  63353    T     TGTCACA
                                GG GCATAA       CATCAGTC
                                || ||||||       ||||||||
                                CC CGTATT       GTAGTCAG
                                 _      CCTCC__
GAM2721  SOX11     3'  GATGCATAGAAGACATCAGT   63354         ATGTCAC
                                GGTGCATA      ACATCAGT
                                ||||||||      ||||||||
                                CTACGTAT      TGTAGTCA
                                     CTTC___
GAM2721  TLL2      3'  GTGGGCCACACATTAGTC    63355     CATAAT        C
                                GTG     GTCACACAT AGTC
                                |||     ||||||||| ||||
                                CAC     CGGTGTGTA TCAG
                                  C_____        A
GAM2721  AFAP      3'  GGTGTCTAATGACATCAGT    63356      CA     TCAC
                                GGTG  TAATG    ACATCAGT
                                ||||  |||||    ||||||||
                                CCAC  ATTAC    TGTAGTCA
                                   AG    _____
GAM2721  LOC221035 3'  GGTTCATAATGCATAGTTATCA 63357     G       CACAC_
            GT                    GGT CATAATGT      ATCAGT
                                ||| ||||||||      ||||||
                                CCA GTATTACG      TAGTCA
                                  A       TATCAA
GAM2722  PON1      3'  AGAATTTTAAGATTTTCCT    63360          A
                                AGAATTTTAA ATTTTCTT
                                |||||||||| ||||||||
                                TCTTAAAATT TAAAAGGA
                                      C
GAM2722  PSMA5     3'  ATTTTAAAATTTTCTTTATT   63361
                                ATTTTAAAATTTTCTTTATT
                                ||||||||||||||||||||
                                TAAAATTTTAAAAGAAATAA

GAM2722  DIRC2     3'  TAGAGTTTTAAAATCCCCT    63362      A        TT
                                TAGA TTTTAAAATT  CT
                                |||| ||||||||||  ||
                                ATCT AAAATTTTAG  GA
                                   C         GG
GAM2722  DKFZP434I092 3'  AGACAAGCCAAATTTTCTTTAT 63363     ATTTTA
            T                     AGA      AAATTTTCTTTATT
                                |||      ||||||||||||||
                                TCT      TTTAAAAGAAATAA
                                  GTTCGG
GAM2722  FLJ13150  3'  GAACACAATTTTCTTTATT    63364      TTTAA
                                GAAT     AATTTTCTTTATT
                                ||||     ||||||||||||
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                                CTTG    TTAAAAGAAATAA
                                  TG___
GAM2722 P5-1    3' TAGAATATTAAATTCCTTTATT 63365      T    AT
                                TAGAAT TTAAA  TTTCTTTATT
                                |||||| |||||  ||||||||||
                                ATCTTA AATTT  AAGGAAATAA
                                   T    __
GAM2722 RMP     3' AAATTTTAAAATTTTCTTTA  63366
                                GAATTTTAAAATTTTCTTTA
                                ||||||||||||||||||||
                                TTTAAAATTTTAAAAGAAAT

GAM2722 RMP     3' AAATTTTAAAATTTTCTTTA  63366
                                GAATTTTAAAATTTTCTTTA
                                ||||||||||||||||||||
                                TTTAAAATTTTAAAAGAAAT

GAM2723 APS     5' GCAGGACAATAGCTTGGAT   63369      TAACAA  A_
                                GCAGGACA    GGT  GGAT
                                ||||||||    |||  ||||
                                CGTCCTGT    TCG  CCTA
                                    TA____   AA
GAM2723 ATP6IP1  3' AAGCAGGACAGACAGTTAAG  63370       TA  AGG
                                AAGCAGGACA  ACA  TAGG
                                |||||||||  |||  ||||
                                TTCGTCCTGT  TGT  ATTC
                                     C_  CA_
GAM2723 BCL11A   3' AACTAGGACATAATGGGT    63371    _      CAA
                                AGC AGGACATAA   GGT
                                ||| |||||||||   |||
                                TTG TCCTGTATT   CCA
                                  A       AC_
GAM2723 GYS1    3' GCAGGGCACAGTTTGGGGAT  63372     A   ACAA  TA
                                GCAGG CATA   GG  GGAT
                                ||||| ||||   ||  ||||
                                CGTCC GTGT   CC  CCTA
                                   C   CAAA __
GAM2723 HMGN2   3' GCAGGACATGGGCAGA     63373       AACAA
                                GCAGGACAT    GGTAGG
                                |||||||||    ||||||
                                CGTCCTGTA    CCGTCT
                                     C____
GAM2723 LCP1    3' AAGCAAAAGCAAGGTAGGAT  63374       CATAA
                                AAGCAGGA    CAAGGTAGGAT
                                ||||||||    ||||||||||
                                TTCGTTTT    GTTCCATCCTA
                                     C____
GAM2723 LLGL1   3' GCGGGACAGGACAGCAGG    63375    A   TA  AG
                                GC GGACA  ACA  GTAGG
                                || |||||  |||  |||||
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                                CG CCTGT  TGT  CGTCC
                                 C    CC  __
GAM2723  MAP1A    5'  AAGCAGGACACGGTAAG     63376          AACAA
                                AAGCAGGACAT    GGTAGG
                                ||||||||||    ||||||
                                TTCGTCCTGTG    CCATTC
                                      _____
GAM2723  MCM4     3'  AAGCAGGACATGCAGG      63377          AACAAG
                                AAGCAGGACAT    GTAGG
                                ||||||||||     |||||
                                TTCGTCCTGTA    CGTCC
                                      ______
GAM2723  P23      3'  GCAGGATATGGCAAGGA     63378       C  AACAA   _
                                GCAGGA AT    GGTA GGA
                                |||||| ||    |||| |||
                                CGTCCT TA    CCGT CCT
                                   A _____   T
GAM2723  PAFAH1B1 3'  AGGGGGACATAACGGAAGTGAT 63379    CA       AA  T  _
                                AG  GGACATAAC  GG AG GAT
                                ||  |||||||||  || || |||
                                TC  CCTGTATTG  CC TC CTA
                                 CC        __  T  A
GAM2723  PPP2R5C  3'  AAGCAGGATAAATAAG      63380        CATAACA
                                AAGCAGGA      AGGTAGG
                                ||||||||      |||||||
                                TTCGTCCT      TTTATTC
                                   A_______
GAM2723  PPP2R5D  3'  AAGACAGGGCACGGGGTAGG   63381     _   A   AACAA
                                AAG CAGG CAT     GGTAGG
                                ||| |||| |||     ||||||
                                TTC GTCC GTG     CCATCC
                                  T   C   CC___
GAM2723  PTGER3   3'  AAACAGGACATAACAGCTTCTG 63382             AGGTA_
            GAT                   AAGCAGGACATAACA     GGAT
                                ||||||||||||||     ||||
                                TTTGTCCTGTATTGT     CCTA
                                       CGAAGA
GAM2723  PTMS     3'  GCAGGACATGACGCTGGGGGAT 63383         A  AA_  TA
                                GCAGGACAT AC   GG  GGAT
                                |||||||| ||   ||  ||||
                                CGTCCTGTA TG   CC  CCTA
                                     C  CGA  C_
GAM2723  RGS16    5'  GCAGCACGTAGTAGGCAGGAT  63384     G  A  ACA
                                GCAG AC TA   AGGTAGGAT
                                |||| || ||   |||||||||
                                CGTC TG AT   TCCGTCCTA
                                  G  C  CA_
GAM2723  SLC7A5   3'  GCAGAGACATAAGCCCACAGG  63385     _      CAAGG
                                GCAG GACATAA     TAGG
                                |||| |||||||     ||||
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                                CGTC CTGTATT    GTCC
                                  T      CGGGT
GAM2723  AOP2     3'  AGAGGACGTGATAGGAC     63386    C    ATAACAA
                                AG AGGAC      GGTAGGAT
                                || |||||      ||||||||
                                TC TCCTG      CTATCCTG
                                 _    CA_____
GAM2723  BRD4     3'  GCAGGACATCACGAACGT     63387         A  _  G
                                GCAGGACAT AC AA GT
                                ||||||||| || || ||
                                CGTCCTGTA TG TT CA
                                      G  C  G
GAM2723  CDCA4    3'  GCAGGACATAATGAAGAAG    63388          CA   T
                                GCAGGACATAA  AGG AG
                                ||||||||||  ||| ||
                                CGTCCTGTATT  TTC TC
                                       AC   T
GAM2723  CEP3     3'  AAACAGGGCATAACAGGT     63389        A      A
                                AAGCAGG CATAACA GGT
                                ||||||| ||||||| |||
                                TTTGTCC GTATTGT CCA
                                    C      _
GAM2723  CKAP2    3'  GAAACTGACAAGGTAGGAT    63390     CATA
                                GGA    ACAAGGTAGGAT
                                |||    ||||||||||||
                                CTT    TGTTCCATCCTA
                                  TGAC
GAM2723  COLEC12  3'  AAGCAGGGCAGGCACAGA     63391        ACATAACA    _
                                AAGCAGG       AGGTA GGA
                                |||||||       ||||| |||
                                TTCGTCC       TCCGT TCT
                                    CG_______     G
GAM2723  CPLX1    3'  AGCAGGACGGACAGCGAC     63392        ATAACAA  _  _
                                AGCAGGAC      GG TAG GAT
                                ||||||||      || ||| |||
                                TCGTCCTG      CC GTC CTG
                                    ________ T   G
GAM2723  EPLIN    3'  AGCAGGACATAAAGTAG      63393          CAA
                                AGCAGGACATAA   GGTAG
                                ||||||||||||   |||||
                                TCGTCCTGTATT   TCATC
                                               ___
GAM2723  FENS-1   3'  AGCTAGGACATAGTAAAGAGA  63394     _       AC    T
                                AGC AGGACATA  AAGG AGG
                                ||| ||||||||  |||| |||
                                TCG TCCTGTAT  TTTC TCT
                                  A       CA   _
GAM2723  FLJ10604 3'  AGCAGGACAGAAATGGGA     63395         TAACA    A
                                AGCAGGACA     AGGT GGA
                                |||||||||     |||| |||
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                                TCGTCCTGT    TTTA CCT
                                    C____    C
GAM2723  FLJ14753  3'  AAGCAGGACATGGAAGA     63396          AACAA  T
                                AAGCAGGACAT    GG AGGA
                                ||||||||||    || ||||
                                TTCGTCCTGTA    CC TTCT
                                      _____ _
GAM2723  FLJ22490  3'  AAGTAGGACATATTAAAGGT   63397     C       AC_
                                AAG AGGACATA   AAGGT
                                ||| ||||||||   |||||
                                TTC TCCTGTAT   TTCCA
                                  A       AAT
GAM2723  HPCAL4    3'  AAGCAGGACAGGTGGG      63398          TAACAA   A
                                AAGCAGGACA     GGT GG
                                ||||||||||     ||| ||
                                TTCGTCCTGT     CCA CC
                                      _______  C
GAM2723  KIAA1056  3'  AAGCAGGACAAGCAGCCAG    63399          TAACA  G
                                AAGCAGGACA     AG TAG
                                ||||||||||     || |||
                                TTCGTCCTGT     TC GTC
                                     TCG__  G
GAM2723  KIAA1210  3'  AGTGGGTCACTGGAAGGTAGG  63400    CA  A   AAC
                                AG  GG CAT   AAGGTAGG
                                ||  || |||   ||||||||
                                TC  CC GTG   TTCCATCC
                                 AC  A   ACC
GAM2723  KIAA1393  3'  GCAGGACATGGGCAGA      63373          AACAA
                                GCAGGACAT    GGTAGG
                                |||||||||    ||||||
                                CGTCCTGTA    CCGTCT
                                    C____
GAM2723  LBP-9     3'  AAGCAGGAGTGACAGACCAAGG 63401          ____  TAA
                                AAGCAGGA   CA   CAAGG
                                ||||||||   ||   |||||
                                TTCGTCCT   GT   GTTCC
                                     CACT  CTG
GAM2723  N4BP3     3'  GCAGGACAGAGGCAAGGTGGG  63402          TAA_     A
                                GCAGGACA    CAAGGT GG
                                ||||||||    |||||| ||
                                CGTCCTGT    GTTCCA CC
                                     CTCC     C
GAM2723  P66       3'  AAGCAGGGTGGGGTGAGGGAGA 63403         ACATAACA   T
            AT                   AAGCAGG       AGG AGGAT
                                 |||||||       ||| |||||
                                 TTCGTCC       TCC TCTTA
                                    CACCCCAC   C
GAM2723  RASSF2    3'  GCAGGACAAAATGGA       63404          TAACA    A
                                GCAGGACA     AGGT GGA
                                ||||||||     |||| |||
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                                CGTCCTGT    TTTA CCT
                                       _____   _
GAM2723  RODH-4   3'  AAGCAGGAGGTAATGGCA    63405        CA   CAA
                                AAGCAGGA  TAA   GGTA
                                ||||||||  |||   ||||
                                TTCGTCCT  ATT   CCGT
                                    CC   A__
GAM2723  SEC24C   3'  AGCAGGACATGACAGAGT    63406         A   AG
                                AGCAGGACAT ACA  GT
                                |||||||||| |||  ||
                                TCGTCCTGTA TGT  CA
                                      C   CT
GAM2723  SNX11    3'  AAGAGCCCACAGACAGGGTAGG 63407     C  GA   _   A
            AT                    AAG AG  CATA ACA GGTAGGAT
                                ||| ||  |||| ||| ||||||||
                                TTC TC  GTGT TGT CCATCCTA
                                  _ GG    C   C
GAM2723  TRIAD3   3'  GCAGGGCATGAGGAGGA     63408      A   AACA   T
                                GCAGG CAT    AGG AGGA
                                ||||| |||    ||| ||||
                                CGTCC GTA    TCC TCCT
                                   C   C___   _
GAM2723  TUBB4    3'  AAGCAGGGTGTCGGCAGCAAGA 63409        ACATAACAA
            T                    AAGCAGG        GGTAGGAT
                                |||||||        ||||||||
                                TTCGTCC        TCGTTCTA
                                    CACAGCCG_
GAM2723  LOC124801 3'  AACAGGACATATAGG       63410          AACAAG
                                AGCAGGACAT     GTAGG
                                ||||||||||     |||||
                                TTGTCCTGTA     TATCC
                                       _______
GAM2723  LOC144289 3'  GCAGGACATACCACTGGAT    63411          A  AGGTA
                                GCAGGACATA CA     GGAT
                                |||||||||| ||     ||||
                                CGTCCTGTAT GT     CCTA
                                      G  GA___
GAM2723  LOC144583 3'  AAGTAGGACAGGGTCAGG     63412     C     TAACAA  _
                                AAG AGGACA     GGT AGG
                                ||| ||||||     ||| |||
                                TTC TCCTGT     CCA TCC
                                  A     C_____   G
GAM2723  LOC144747 5'  AGCAGGGCAAGGTAAG       63413       ACATAA
                                AGCAGG     CAAGGTAGG
                                ||||||     |||||||||
                                TCGTCC     GTTCCATTC
                                   C_____
GAM2723  LOC145540 3'  GCAGGACATGGGCAGA       63373         AACAA
                                GCAGGACAT     GGTAGG
                                |||||||||     ||||||
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                                CGTCCTGTA    CCGTCT
                                     C____
GAM2723  LOC146013 3'  AAGCAGGACATAGCCAGGA   63414         AACA  G
                                AAGCAGGACAT   AG TAGGA
                                ||||||||||   || |||||
                                TTCGTCCTGTA   TC GTCCT
                                     ____  G
GAM2723  LOC147817 3'  AAGCAGACATGACAATAGA   63415      G   A   AG
                                AAGCAG ACAT ACA  GTAGG
                                |||||| |||| |||  |||||
                                TTCGTC TGTA TGT  TATCT
                                   _   C  __
GAM2723  LOC148915 3'  GCAGGACATGGGCAGA     63373        AACAA
                                GCAGGACAT    GGTAGG
                                |||||||||    ||||||
                                CGTCCTGTA    CCGTCT
                                     C____
GAM2723  LOC150580 3'  GCAGGACATGGGCAGA     63373        AACAA
                                GCAGGACAT    GGTAGG
                                |||||||||    ||||||
                                CGTCCTGTA    CCGTCT
                                     C____
GAM2723  LOC152212 3'  GCAGGACATGGGCAGA     63373        AACAA
                                GCAGGACAT    GGTAGG
                                |||||||||    ||||||
                                CGTCCTGTA    CCGTCT
                                     C____
GAM2723  LOC158314 3'  GCAGGACATGCAGAA      63416        AACAAG
                                GCAGGACAT     GTAGGA
                                |||||||||     ||||||
                                CGTCCTGTA     CGTCTT
                                     _______
GAM2723  LOC170396 3'  AGTGGGACAAAACATGAGGGG  63417    CA    T   __   TA
                                AG  GGACA AACA  AGG  GG
                                ||  ||||| ||||  |||  ||
                                TC  CCTGT TTGT  TCC  CC
                                  AC    T   AC  __
GAM2723  LOC203292 3'  GCAGGATATGGCAAGGA     63378      C  AACAA   _
                                GCAGGA AT    GGTA GGA
                                |||||| ||    |||| |||
                                CGTCCT TA    CCGT CCT
                                   A _____   T
GAM2723  LOC219988 3'  AAGTAGGACATGCAGAAC    63418    C      AACAAG
                                AAG AGGACAT     GTAGGAT
                                ||| |||||||     |||||||
                                TTC TCCTGTA     CGTCTTG
                                  A     _______
GAM2723  LOC254000 3'  GCAGGACATGGGCAGA      63373        AACAA
                                GCAGGACAT    GGTAGG
                                |||||||||    ||||||
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                                CGTCCTGTA    CCGTCT
                                     C____
GAM2723 LOC256925 5' AGCAGGACTTAGGTCCAAGGAT 63419        ATAACA   ___
                                AGCAGGAC     AGGT   AGGAT
                                ||||||||     ||||   |||||
                                TCGTCCTG     TCCA   TCCTA
                                    AA____    GGT
GAM2723 LOC257481 3' AAGCAGGACATGACATGGT    63420          A   A
                                AAGCAGGACAT ACA GGT
                                |||||||||||| ||| |||
                                TTCGTCCTGTA TGT CCA
                                      C   A
GAM2723 LOC257486 3' AGTGGGTCACTGGAAGGTAGG  63400    CA  A   AAC
                                AG  GG CAT   AAGGTAGG
                                ||  || |||   ||||||||
                                TC  CC GTG   TTCCATCC
                                 AC  A   ACC
GAM2723 LOC88584  3' GCAGGACATGGGCAGA      63373         AACAA
                                GCAGGACAT    GGTAGG
                                |||||||||    ||||||
                                CGTCCTGTA    CCGTCT
                                     C____
GAM2723 LOC90499  3' GCAGGATATGGCAAGGA     63378       C  AACAA   _
                                GCAGGA AT    GGTA GGA
                                |||||| ||    |||| |||
                                CGTCCT TA    CCGT CCT
                                   A _____   T
GAM2723 LOC91523  3' GCAGGAATAACGCTGG      63421       C    AAG  A
                                GCAGGA ATAAC   GT GG
                                |||||| |||||   || ||
                                CGTCCT TATTG   CG CC
                                   _    ___  A
GAM2723 LOC92497  3' AAGTAGGAATGCCCAAGGTGGG 63422     C    CATAA     A
                                AAG AGGA     CAAGGT GG
                                ||| ||||     |||||| ||
                                TTC TCCT     GTTCCA CC
                                  A    TACGG     C
GAM2724 DISC1     3' CACTGTGTTACTGAGTACC    63425      A       __
                                TACT TGTTACTGA  ACC
                                |||| |||||||||  |||
                                GTGA ACAATGACT  TGG
                                  C        CA
GAM2724 SRGAP1    3' TGTTTAAAGGAACCTAGGTG   63426      ACT__
                                TGTT    GAACCTAGGTG
                                ||||    ||||||||||
                                ACAA    CTTGGATCCAC
                                  ATTTC
GAM2724 VPS41     3' CTAATGTTATTCCCAGGTG    63427     _    CTGAA
                                CTA TGTTA    CCTAGGTG
                                ||| |||||    ||||||||
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                                GAT ACAAT    GGGTCCAC
                                  T    AA___
GAM2724  VPS41    3'  CTAATGTTATTCCCAGGTG   63427    _    CTGAA
                                CTA TGTTA    CCTAGGTG
                                ||| |||||    ||||||||
                                GAT ACAAT    GGGTCCAC
                                  T    AA___
GAM2724  ABCA10   5'  TATGTTACTGACTGGTG     63428         AC  A
                                TATGTTACTGA  CT GGTG
                                ||||||||||  || ||||
                                ATACAATGACT  GA CCAC
                                          __ _
GAM2724  DKFZp761A132 3'  TGCTAAGCCAAACCTAGGTG   63429      __ TG
                                TGTTA  C  AACCTAGGTG
                                |||||  |  ||||||||||
                                ACGAT  G  TTGGATCCAC
                                   TC GT
GAM2724  GPS1     3'  TGCCACTGGGCCTGGGTG    63430        AA   A
                                TGTTACTG  CCT GGTG
                                ||||||||  ||| ||||
                                ACGGTGAC  GGA CCAC
                                     CC   C
GAM2724  KIAA0261  3'  TACTATGTTCTTAAAAGGTG   63431         A  GAACCT
                                TACTATGTT CT     AGGTG
                                |||||||||  ||     |||||
                                ATGATACAA GA     TCCAC
                                      _  ATTT__
GAM2724  LY75     3'  TACTAAGACTATAATCTAGGTG 63432      TGTT   _  C
                                TACTA    ACTG AA CTAGGTG
                                |||||    |||| || |||||||
                                ATGAT    TGAT TT GATCCAC
                                   TC__    A  A
GAM2724  LOC221415 5'  ACCACAGGTTGAACCTAGGTG  63433      GTTAC
                                ACTAT    TGAACCTAGGTG
                                |||||    ||||||||||||
                                TGGTG    ACTTGGATCCAC
                                   TCCA_
GAM2724  LOC255308 3'  TACATGCCAGCCTAGGT     63434     T     CTGAA
                                TAC ATGTTA    CCTAGGT
                                ||| ||||||    |||||||
                                ATG TACGGT    GGATCCA
                                  _     C_____
GAM2724  LOC255925 3'  ACTATGTTATTGGTGAAGGTG  63435         C  AACCT
                                ACTATGTTA TG    AGGTG
                                |||||||||  ||    |||||
                                TGATACAAT AC    TCCAC
                                      A  CACT_
GAM2724  LOC256447 3'  TACTATGTTCACTACTTGGGTG 63436         _    AACCTA
                                TACTATGT TACTG     GGTG
                                |||||||| |||||     ||||
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                                ATGATACA GTGAT     CCAC
                                    A    GAAC__
GAM2725 ANK3     5' TGGAATGGTGTTTTGTCA    63439         CTG   AA
                                TGGAATGGTG   TTG  TCA
                                ||||||||||   |||  |||
                                ACCTTACCAC   AAC  AGT
                                     AA_   __
GAM2725 IL13RA2  3' TGGAAACTGTTGAGTCAA    63440      TGGT      A
                                TGGAA    GCTGTTGA TCAA
                                |||||    |||||||| ||||
                                ACCTT    TGACAACT AGTT
                                  _____       C
GAM2725 MX1      5' TGGAATGGTGGCTGGATG    63441          _   T_
                                TGGAATGGTG CTG  TG
                                |||||||||| |||  ||
                                ACCTTACCAC GAC  AC
                                     C   CT
GAM2725 DKFZP434B044 3' TGGGATGCTGTTGCTTCA    63442     AAT        AA
                                TGG   GGTGCTGTTG  TCA
                                |||   ||||||||||  |||
                                ACC   CTACGACAAC  AGT
                                  ___         GA
GAM2725 DKFZP566D193 3' TGGAAGGTGTTAAAC       63443      T   GCT
                                TGGAA GGT   GTTGAAT
                                ||||| |||   |||||||
                                ACCTT CCA   CAATTTG
                                  _  ___
GAM2725 FLJ20309  3' TGGAATGGGTTTTTGGGGTCGA 63444         _____  CT
                                TGGAATGG     TG  GTTGA
                                ||||||||     ||  |||||
                                ACCTTACC     AC  CAGCT
                                     CAAAA  CC
GAM2725 FLJ21276  3' TGGAATGTGTTTGTCTTTGACA 63445        _ GC    GAAT_
                                TGGAATG GT  TGTT    CA
                                ||||||| ||  ||||    ||
                                ACCTTAC CA  ACAG    GT
                                    A  A_    AAACT
GAM2725 NUCB2    3' TGAAATAGATGTTGAGTTAACA 63446        TGC     ATC
                                TGGAATGG   TGTTGA   AACA
                                ||||||||   ||||||   ||||
                                ACTTTATC   ACAACT   TTGT
                                     T__     CAA
GAM2725 LOC149113 5' TGGGATGCTGTTGAGCTAACA  63447     AAT        ATC
                                TGG   GGTGCTGTTGA   AACA
                                |||   ||||||||||   ||||
                                ACC   CTACGACAACT   TTGT
                                  ___         CGA
GAM2725 LOC151318 3' GAAGTTTGTGTTGAATCGACA  63448     TGG  C       A
                                GAA   TG TGTTGAATC ACA
                                |||   || |||||||| |||
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                                CTT   AC ACAACTTAG TGT
                                  CAA _       C
GAM2725  LOC153328 3'  TGGAGGGCTTGAATCA     63449     AT  T   GT
                                TGGA  GG GCT  TGAATCA
                                ||||  || |||  |||||||
                                ACCT  CC CGA  ACTTAGT
                                  __  _  __
GAM2725  LOC154403 5'  TGGGATGCTGTTGAGCTAACA  63447    AAT        ATC
                                TGG   GGTGCTGTTGA   AACA
                                |||   ||||||||||   ||||
                                ACC   CTACGACAACT   TTGT
                                  ___         CGA
GAM2725  LOC154992 5'  TGGGATGCTGTTGAGCTAACA  63447    AAT        ATC
                                TGG   GGTGCTGTTGA   AACA
                                |||   ||||||||||   ||||
                                ACC   CTACGACAACT   TTGT
                                  ___         CGA
GAM2725  LOC158572 3'  TGGGGTGCTGCTGCCCA    63450    AAT       AA
                                TGG   GGTGCTGTTG  TCA
                                |||   ||||||||||  |||
                                ACC   CCACGACGAC  GGT
                                  ___         G_
GAM2725  LOC164397 5'  TGGAATGGCTGTTTATCAA   63451       GT    GA
                                TGGAATG  GCTGTT  ATCAA
                                |||||||  ||||||  |||||
                                ACCTTAC  CGACAA  TAGTT
                                   __     A_
GAM2725  LOC201868 5'  TGGGATGCTGTTGAGCTAACA  63447    AAT        ATC
                                TGG   GGTGCTGTTGA   AACA
                                |||   ||||||||||   ||||
                                ACC   CTACGACAACT   TTGT
                                  ___         CGA
GAM2725  LOC205095 3'  TGGAAGGTGCTGTTTTTCCAC  63452      T       GAA  A
                                TGGAA GGTGCTGTT   TC AC
                                |||||  |||||||||   || ||
                                ACCTT CCACGACAA   AG TG
                                  _       AA_  G
GAM2726  DHFR     3'  TAGCAATGTCTTCTGTTTT   63455      C     GCA
                                TAGCA ATGTCT   TTTGTTTT
                                |||||  ||||||   ||||||||
                                ATCGT TACAGA   AGACAAAA
                                  _     ___
GAM2726  EFNB2    3'  TAGCTGTCCAATTTGTTTT   63456     ACA     C
                                TAGC   TGTCTG ATTTGTTTT
                                ||||   ||||||  |||||||||
                                ATCG   ACAGGT TAAACAAAA
                                  ___     _
GAM2726  LOH11CR2A 3'  TAGTTCATGTCACCTGTTTTT  63457     CA     TGC
                                TAG  CATGTC   ATTTGTTTTT
                                |||  ||||||   ||||||||||
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                                ATC  GTACAG   TGGACAAAAA
                                  AA     ___
GAM2726  MAP2K1    3'  GCACATGCTGTGTTCT      63458        T   CATT
                                GCACATG CTG    TGTTTT
                                ||||||| |||    ||||||
                                CGTGTAC GAC    ACAAGA
                                   _  _____
GAM2726  PPP1R12B  3'  GCCATGTCTGCAGCTATTT    63459    A        T
                                GC CATGTCTGCA TTGTTT
                                || ||||||||||| ||||||
                                CG GTACAGACGT GATAAA
                                  _        C
GAM2726  DKFZp434A171 3'  CAGCATATTAACATTTGTTTTT 63461       CA   CT
                                TAGCA  TGT  GCATTTGTTTTT
                                |||||  |||  ||||||||||||
                                GTCGT  ATA  TGTAAACAAAAA
                                   __   AT
GAM2726  DKFZp434A171 5'  GCATGTGTACTTGCTTTGTTTT 63460     CA  _  _  A
            T                    GCA  TGT CT GC TTTGTTTTT
                                |||  ||| || || |||||||||
                                CGT  ACA GA CG AAACAAAAA
                                  AC   T  A  _
GAM2726  HSD17B12  3'  TAGCAGATGGCTATTTGTTTTT 63462       C   TCT  _
                                TAGCA ATG   GC ATTTGTTTTT
                                ||||| |||   || ||||||||||
                                ATCGT TAC   CG TAAACAAAAA
                                   C  ___  A
GAM2726  KIAA1257  3'  TAGCGCATGCCTGTATTC    63463      A       C
                                TAGC CATGTCTG ATTT
                                |||| |||||||| ||||
                                ATCG GTACGGAC TAAG
                                  C       A
GAM2726  LOC113523 3'  TAGCATAAACATTTGTTTTT   63464       CATGTCT
                                TAGCA      GCATTTGTTTTT
                                |||||      ||||||||||||
                                ATCGT      TGTAAACAAAAA
                                   ATT____
GAM2726  LOC121536 3'  GCACATGTTGTAATTGTTTTT  63465         C  CAT
                                GCACATGT TG   TTGTTTTT
                                |||||||| ||   ||||||||
                                CGTGTACA AC   AACAAAAA
                                     _  ATT
GAM2726  LOC90509  5'  TAGTATATGTCTACATATGTTT 63466     CAC         T
                                TAG   ATGTCTGCAT TGTTT
                                |||   |||||||||| |||||
                                ATC   TACAGATGTA ACAAA
                                  ATA         T
GAM2727  ADD2      5'  TAGCTCCACTCTCAAGGG    63469         _  A    A
                                TAGCTCC CT TTTAA GG
                                ||||||| || ||||| ||
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                                ATCGAGG GA GAGTT CC
                                   T _    C
GAM2727  ADD2    5'  TAGCTCCACTCTCAAGGG    63469       _ A    A
                                TAGCTCC CT TTTAA GG
                                ||||||| || ||||| ||
                                ATCGAGG GA GAGTT CC
                                   T _    C
GAM2727  ADD2    5'  TAGCTCCACTCTCAAGGG    63469       _ A    A
                                TAGCTCC CT TTTAA GG
                                ||||||| || ||||| ||
                                ATCGAGG GA GAGTT CC
                                   T _    C
GAM2727  ADD2    5'  TAGCTCCACTCTCAAGGG    63469       _ A    A
                                TAGCTCC CT TTTAA GG
                                ||||||| || ||||| ||
                                ATCGAGG GA GAGTT CC
                                   T _    C
GAM2727  ADD2    5'  TAGCTCCACTCTCAAGGG    63469       _ A    A
                                TAGCTCC CT TTTAA GG
                                ||||||| || ||||| ||
                                ATCGAGG GA GAGTT CC
                                   T _    C
GAM2727  ADD2    5'  TAGCTCCACTCTCAAGGG    63469       _ A    A
                                TAGCTCC CT TTTAA GG
                                ||||||| || ||||| ||
                                ATCGAGG GA GAGTT CC
                                   T _    C
GAM2727  ADD2    5'  TAGCTCCACTCTCAAGGG    63469       _ A    A
                                TAGCTCC CT TTTAA GG
                                ||||||| || ||||| ||
                                ATCGAGG GA GAGTT CC
                                   T _    C
GAM2727  ANK1    3'  GCTCGCCTCTCCAAGAGGC   63470       _ A    _
                                GCTC CCT TTTAA AGGC
                                |||| ||| ||||| ||||
                                CGAG GGA AGGTT TCCG
                                  C  G    C
GAM2727  ANK1    3'  GCTCGCCTCTCCAAGAGGC   63470       _ A    _
                                GCTC CCT TTTAA AGGC
                                |||| ||| ||||| ||||
                                CGAG GGA AGGTT TCCG
                                  C  G    C
GAM2727  CD79A   3'  CAGCTCCCCTAGAGGC      63471        ATT  A
                                TAGCTCCCT   TA AGGC
                                |||||||||   || ||||
                                GTCGAGGGG   AT TCCG
                                     ___ C
GAM2727  CD79A   3'  CAGCTCCCCTAGAGGC      63471        ATT  A
                                TAGCTCCCT   TA AGGC
                                |||||||||   || ||||
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                                GTCGAGGGG  AT TCCG
                                    ___  C
GAM2727  CHRNB4   3'  AGCTCCCTCCTACTGGGGC   63472        A   AA__
                                AGCTCCCT TTTA   GGC
                                |||||||| ||||   |||
                                TCGAGGGA GGAT   CCG
                                   _   GACC
GAM2727  DHFR     3'  CAGCTTCCCTAAAAAGGGC   63473     _   TTT  A
                                TAGCT CCCTA  AA GGC
                                ||||| |||||  || |||
                                GTCGA GGGAT  TT CCG
                                  A    TT_  C
GAM2727  EDAR     3'  TAGCTCCCTAAAAATGGC    63474         TTT  A
                                TAGCTCCCTA  AA GGC
                                ||||||||||  || |||
                                ATCGAGGGAT  TT CCG
                                     TT_  A
GAM2727  IER3     3'  TAGCCACCCTAAAGGC      63475     _   TTTA
                                TAGCT CCCTA   AAGGC
                                ||||| |||||   |||||
                                ATCGG GGGAT   TTCCG
                                  T   _____
GAM2727  LIM2     3'  CAGCTCCCTCCCATGGGC    18916         A   AA
                                TAGCTCCCT TTTA  GGC
                                |||||||| ||||  |||
                                GTCGAGGGA GGGT  CCG
                                   _   AC
GAM2727  MCM2     3'  CAGCTCTCTGGCCAAAGGC   63476      C  AT
                                TAGCTC CT  TTAAAGGC
                                |||||| ||  ||||||||
                                GTCGAG GA  GGTTTCCG
                                  A  CC
GAM2727  NRBP     3'  TAGCCCCCAACTAGAAGGC   63477       T   TA
                                TAGCTCCC ATT  AAGGC
                                |||||||| |||  |||||
                                ATCGGGGG TGA  TTCCG
                                     T   TC
GAM2727  RAB36    3'  CAGCTCCCTAGGAAGGC     63478         TTTA
                                TAGCTCCCTA   AAGGC
                                ||||||||||   |||||
                                GTCGAGGGAT   TTCCG
                                     CC__
GAM2727  SLC29A1  5'  CAGCTCCCTCCCTCAGGGGC  63479        A_   AA
                                TAGCTCCCT  TTTA  GGC
                                |||||||||  ||||  |||
                                GTCGAGGGA  GAGT  CCG
                                     GG   CC
GAM2727  AP3S2    3'  ACTCCCTACTGAGGAAGGC   63480         TA__
                                GCTCCCTATT   AAGGC
                                ||||||||||   |||||
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                                TGAGGGATGA   TTCCG
                                     CTCC
GAM2727 BAG5    3' CAGCTCCCCACGAAGGC    63481        TTA
                                TAGCTCCCTAT  AAGGC
                                ||||||||||  |||||
                                GTCGAGGGGTG  TTCCG
                                      C__
GAM2727 FLJ11539 3' CAGCTCTATTTAAAGGC    63482      CC
                                TAGCTC TATTTAAAGGC
                                ||||||  ||||||||||
                                GTCGAG ATAAATTTCCG
                                   __
GAM2727 FLJ11838 3' AGCTCTTCTTTTTAAAGG   63483     C_ A
                                AGCTC CT TTTAAAGG
                                |||||  || ||||||||
                                TCGAG GA AAATTTCC
                                   AA A
GAM2727 FLJ20254 5' TAGCTCCCGGCTCACCAGGC 63484       TA  A_
                                TAGCTCCC TTTA AGGC
                                ||||||||  ||||  ||||
                                ATCGAGGG GAGT TCCG
                                     CC   GG
GAM2727 FLJ21916 3' AGCTCCTACTAAAGGC     63485      C   T
                                AGCTCC TATT AAAGGC
                                |||||| |||| ||||||
                                TCGAGG ATGA TTTCCG
                                   _  _
GAM2727 FLJ22318 5' CAGCTCCCGGCCCAGGGC   63486       TA  AA
                                TAGCTCCC TTTA GGC
                                ||||||||  ||||  |||
                                GTCGAGGG GGGT CCG
                                     CC   C_
GAM2727 FLJ23191 5' CAGCTTCCACTCCAAAGGC  63487     C TA
                                TAGCT CC  TTTAAAGGC
                                |||||  ||  |||||||||
                                GTCGA GG  AGGTTTCCG
                                   A  TG
GAM2727 FLJ23233 3' CAGCTCCCTCATAAAGGC   63488       ATT
                                TAGCTCCCT  TAAAGGC
                                |||||||||  |||||||
                                GTCGAGGGA  ATTTCCG
                                     GT_
GAM2727 FYCO1   3' AACTCTCCTGTTTAAAGG    63489     _  A
                                AGCTC CCT TTTAAAGG
                                |||||  |||  ||||||||
                                TTGAG GGA AAATTTCC
                                   A  C
GAM2727 HPCAL4  3' TAGCTCCTTTAAAGG       63490       CTA
                                TAGCTCC  TTTAAAGG
                                |||||||  ||||||||
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                                ATCGAGG   AAATTTCC
                                   ___
GAM2727 KIAA0161 3' ACTCCCCAGGATTAAAGGC   63491       T__
                                GCTCCCTA   TTAAAGGC
                                ||||||||   ||||||||
                                TGAGGGGT   AATTTCCG
                                    CCT
GAM2727 KIAA0185 3' TAGCCTCCCCTAAAGG     63492     _    ATT
                                TAGC TCCCT   TAAAGG
                                |||| |||||   ||||||
                                ATCG AGGGG   ATTTCC
                                  G    ___
GAM2727 KIAA0227 3' TAGCTATGCCACTAAAGGC   63493     CC_    T
                                TAGCT   CTATT AAAGGC
                                |||||   ||||| ||||||
                                ATCGA   GGTGA TTTCCG
                                   TAC    _
GAM2727 KIAA0431 3' TAACTCCCTGTTCCCAAGG   63494       A   A_
                                TAGCTCCCT TTT  AAGG
                                ||||||||| |||  ||||
                                ATTGAGGGA AAG  TTCC
                                     C   GG
GAM2727 KIAA0450 3' CAGCTCCCACCCCGAGGC    63495       T    AA
                                TAGCTCCC ATTT  AGGC
                                |||||||| ||||  ||||
                                GTCGAGGG TGGG  TCCG
                                    _   GC
GAM2727 KIAA0888 3' CAGCTCCCCCAAAGGC      63496       ATT
                                TAGCTCCCT   TAAAGGC
                                |||||||||   |||||||
                                GTCGAGGGG   GTTTCCG
                                     ___
GAM2727 KIAA1219 3' TAGTCCTTTCAAAGGC      63497     C   CTA
                                TAG TCC   TTTAAAGGC
                                ||| |||   |||||||||
                                ATC AGG   AAGTTTCCG
                                  _   A__
GAM2727 KIAA1260 3' TAGCCCCACCAAAGGC      63498       CTAT
                                TAGCTCC    TTAAAGGC
                                |||||||    ||||||||
                                ATCGGGG    GGTTTCCG
                                    T___
GAM2727 KIAA1904 3' CAGCTCCCACCCAGAGG     63499       T    A
                                TAGCTCCC ATTTA AGG
                                |||||||| ||||| |||
                                GTCGAGGG TGGGT TCC
                                    _    C
GAM2727 MGC2705  3' CAGCTCCCTCCCAGAGG     63500       A    A
                                TAGCTCCCT TTTA AGG
                                ||||||||| |||| |||
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                                GTCGAGGGA GGGT TCC
                                     _   C
GAM2727 MRPS34   3' AGCTCCCTGCTCCGAGAGGC  63501       A  AA__
                                AGCTCCCT TTT   AGGC
                                |||||||| |||   ||||
                                TCGAGGGA GAG   TCCG
                                    C  GCTC
GAM2727 ORC6L    3' GCTTTGCTATTTAAAGGC    63502    CC_
                                GCT  CTATTTAAAGGC
                                |||  ||||||||||||
                                CGA  GATAAATTTCCG
                                  AAC
GAM2727 PPAP2C   3' CAGCTCCCTGCCTGGGC     63503        A  AAA
                                TAGCTCCCT TTT  GGC
                                ||||||||| |||  |||
                                GTCGAGGGA GGA  CCG
                                     C  C__
GAM2727 TAF2     3' AGCTCACCTTTTTAAAGG    63504     _  A
                                AGCTC CCT TTTAAAGG
                                ||||| ||| ||||||||
                                TCGAG GGA AAATTTCC
                                   T  A
GAM2727 UNC5D    3' TACCTCCCTACTGCAAGG    63505   G      TA
                                TA CTCCCTATT  AAGG
                                || |||||||||  ||||
                                AT GAGGGATGA  TTCC
                                 G       CG
GAM2727 LOC112609 3' CAGCTCTCTTCTAAAGG    63506      C  A
                                TAGCTC CT TTTAAAGG
                                |||||| || ||||||||
                                GTCGAG GA AGATTTCC
                                   A  _
GAM2727 LOC128439 3' CAGCTACTTTTTAAAGG    63507     CC  A
                                TAGCT  CT TTTAAAGG
                                |||||  || ||||||||
                                GTCGA  GA AAATTTCC
                                   T_  A
GAM2727 LOC144698 5' CAGCTCCCCTCAGGGC     63508       AT  AA
                                TAGCTCCCT  TTA  GGC
                                |||||||||  |||  |||
                                GTCGAGGGG  AGT  CCG
                                     __   C_
GAM2727 LOC147180 5' TAGCTCATTTAAAAAC     63509      CCT
                                TAGCTC   ATTTAAAGGC
                                ||||||   ||||||||||
                                ATCGAG   TAAATTTTTG
                                    ___
GAM2727 LOC149421 5' TAGTTCCCTACCATCAAGGC  63510    C      TA_
                                TAG TCCCTATT   AAGGC
                                ||| ||||||||   |||||
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                                ATC AGGGATGG   TTCCG
                                  A       TAG
GAM2727  LOC150319 5'  CAGCTCCCTGTCTGCCAAGGC  63511         A  TA__
                                TAGCTCCCT TT    AAGGC
                                |||||||||  ||    |||||
                                GTCGAGGGA AG    TTCCG
                                     C  ACGG
GAM2727  LOC151178 5'  AGCTCCTGTCCTCAAAGGC    63512       CTA_
                                AGCTCC    TTTAAAGGC
                                ||||||    |||||||||
                                TCGAGG    GAGTTTCCG
                                   ACAG
GAM2727  LOC152286 5'  AGCTCCCTACTTGGC       63513           AAA
                                AGCTCCCTATTT   GGC
                                ||||||||||||   |||
                                TCGAGGGATGAA   CCG
                                       ___
GAM2727  LOC153338 3'  TAGCTTCTTTCCAAAGG     63514       CC  A
                                TAGCT  CT TTTAAAGG
                                |||||  ||  ||||||||
                                ATCGA  GA AGGTTTCC
                                   A_  A
GAM2727  LOC154877 3'  CAGCTCCCTTTTGGGC      63515         A   AAA
                                TAGCTCCCT TTT   GGC
                                |||||||||  |||   |||
                                GTCGAGGGA AAA   CCG
                                     _   C__
GAM2727  LOC158819 3'  TAACCAAAATTTAAAGGC    63516       CCCT
                                TAGCT    ATTTAAAGGC
                                |||||    ||||||||||
                                ATTGG    TAAATTTCCG
                                   TTT_
GAM2727  LOC202459 3'  TAGCCCTTCTCAAAGGC     63517      TC   A
                                TAGC  CCT TTTAAAGGC
                                ||||  |||  |||||||||
                                ATCG  GGA GAGTTTCCG
                                   __   A
GAM2727  LOC219654 3'  TAGCTTCCCTTAAAAAAGGC   63518       _   ATTT
                                TAGCT CCCT    AAAGGC
                                |||||  ||||    ||||||
                                ATCGA GGGA    TTTCCG
                                   A    ATTT
GAM2727  LOC220370 3'  AGCTCCCTACTCACAGGGC    63519           AA_
                                AGCTCCCTATTTA   GGC
                                ||||||||||||   |||
                                TCGAGGGATGAGT   CCG
                                       GTC
GAM2727  LOC221103 5'  CAGCTCCCACACCCAGGG     63520         _     AA
                                TAGCTCCC TATTTA  GG
                                ||||||||  ||||||  ||
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                                GTCGAGGG GTGGGT  CC
                                     T     C_
GAM2727  LOC221474 5'  TAACTCCCGTCTAAGGGC    63521        TA    A
                                TAGCTCCC  TTTAA GGC
                                ||||||||  ||||| |||
                                ATTGAGGG  AGATT CCG
                                     C_    C
GAM2727  LOC221935 3'  GCTCCCTAAACCAGAAGG    63522        T_  _
                                GCTCCCTA  TTA AAGG
                                ||||||||  ||| ||||
                                CGAGGGAT  GGT TTCC
                                     TT   C
GAM2727  LOC91409  3'  TAGTGCCCTCCAAAGGC     63523     CT    AT
                                TAG  CCCT  TTAAAGGC
                                |||  ||||  ||||||||
                                ATC  GGGA  GGTTTCCG
                                  AC   __
GAM2727  LOC91585  3'  AGTTCCCTATCTGAAGGC    63524    C       A
                                AG TCCCTATTT AAGGC
                                || |||||||| |||||
                                TC AGGGATAGA TTCCG
                                 A        C
GAM2728  GRIK5     3'  AGTGGGTCTTAAGAGCCATT   63527           AAG
                                GGTGGGTCTTAAGAG   GTT
                                ||||||||||||||   |||
                                TCACCCAGAATTCTC   TAA
                                       GG_
GAM2728  PCDHA1    3'  AGTTGGTTAGAGAAGGTT    63528    G   CTTA
                                GGT GGT    AGAGAAGGTT
                                ||| |||    ||||||||||
                                TCA CCA    TCTCTTCCAA
                                  A   A___
GAM2728  PCDHA1    3'  AGTTGGTTAGAGAAGGTT    63528    G   CTTA
                                GGT GGT    AGAGAAGGTT
                                ||| |||    ||||||||||
                                TCA CCA    TCTCTTCCAA
                                  A   A___
GAM2728  PCDHA10   3'  AGTTGGTTAGAGAAGGTT    63528     G   CTTA
                                GGT GGT    AGAGAAGGTT
                                ||| |||    ||||||||||
                                TCA CCA    TCTCTTCCAA
                                  A   A___
GAM2728  PCDHA10   3'  AGTTGGTTAGAGAAGGTT    63528     G   CTTA
                                GGT GGT    AGAGAAGGTT
                                ||| |||    ||||||||||
                                TCA CCA    TCTCTTCCAA
                                  A   A___
GAM2728  PCDHA11   3'  AGTTGGTTAGAGAAGGTT    63528     G   CTTA
                                GGT GGT    AGAGAAGGTT
                                ||| |||    ||||||||||
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                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHA12  3' AGTTGGTTAGAGAAGGTT   63528   G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHA13  3' AGTTGGTTAGAGAAGGTT   63528   G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHA2   3' AGTTGGTTAGAGAAGGTT   63528   G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHA3   3' AGTTGGTTAGAGAAGGTT   63528   G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHA4   3' AGTTGGTTAGAGAAGGTT   63528   G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHA5   3' AGTTGGTTAGAGAAGGTT   63528   G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHA6   3' AGTTGGTTAGAGAAGGTT   63528   G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHA6   3' AGTTGGTTAGAGAAGGTT   63528   G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHA7   3' AGTTGGTTAGAGAAGGTT   63528   G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHA8   3' AGTTGGTTAGAGAAGGTT   63528   G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
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                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHA9   3' AGTTGGTTAGAGAAGGTT   63528    G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHAC1  3' AGTTGGTTAGAGAAGGTT   63528    G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 PCDHAC2  3' AGTTGGTTAGAGAAGGTT   63528    G  CTTA
                              GGT GGT   AGAGAAGGTT
                              ||| |||   ||||||||||
                              TCA CCA   TCTCTTCCAA
                                A  A___
GAM2728 TA-KRP   3' TAGATGGAAGAGAAGGTT   63529       TCTTA
                              TAGGTGGG   AGAGAAGGTT
                              ||||||||   ||||||||||
                              ATCTACCT   TCTCTTCCAA
                                   _____
GAM2728 TRPC3    5' TAGGTTGAAGACTAAGAGAAGG 63530     _  TC
          TTA                   TAGGT GGG  TTAAGAGAAGGTTA
                              ||||| |||  ||||||||||||||
                              ATCCA CTT  GATTCTCTTCCAAT
                                 A  CT
GAM2728 LOC152286 3' GGGGGTCTGGGGAGGGTT   63531   T    TAA  AA
                              GG GGGTCT  GAG  GGTT
                              || ||||||  |||  ||||
                              CC CCCAGA  CTC  CCAA
                               _    CCC  __
GAM2728 LOC221543 3' GGTGGCAAGGAGAGAAGGTT  63532     GTCTTA
                              GGTGG    AGAGAAGGTT
                              |||||    ||||||||||
                              CCACC    TCTCTTCCAA
                                 GTTCC_
GAM2728 LOC257596 3' GGTGGCAAGGAGAGAAGGTT  63532     GTCTTA
                              GGTGG    AGAGAAGGTT
                              |||||    ||||||||||
                              CCACC    TCTCTTCCAA
                                 GTTCC_
GAM2729 KIAA0009 3' TCAGTACTGGATGGCAAT   63535       A_  _
                              TCAGTACT  GTGG AAT
                              ||||||||  |||| |||
                              AGTCATGA  TACC TTA
                                   CC   G
GAM2730 FYCO1    3' TATCAAAGACTTTTGTTA    63538        C_
                              TATCAAAGAT  TTGTTA
                              ||||||||||  ||||||
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                                ATAGTTTCTG  AACAAT
                                      AA
GAM2731  BMF      3'  TGACTGGCTATTCGGCTCATCC 63541        GTACATA  _
               G                   TGACTGGC      GC CATCCG
                                   ||||||||      || ||||||
                                   ACTGACCG      CG GTAGGC
                                        ATAAGC_  A
GAM2731  FLJ22283  5'  GACCCCAGCATAGCCATCCGC  63542      GGCGTA
                                   GACT     CATAGCCATCCGC
                                   ||||     ||||||||||||||
                                   CTGG     GTATCGGTAGGCG
                                     GGTC__
GAM2731  LOC115574 3'  TGACTGGCTACAGATCG     63543        G    TAGCC   C
                                   TGACTGGC TACA     ATC G
                                   |||||||| ||||     ||| |
                                   ACTGACCG ATGT     TAG C
                                        _    C_____   A
GAM2731  LOC169436 5'  TGACTGGCGTAATGGTCATCC  63544          CATAGC
                                   TGACTGGCGTA      CATCC
                                   ||||||||||||     |||||
                                   ACTGACCGCAT      GTAGG
                                         TACCA_
GAM2732  HDAC4     3'  ATGCATTGCTGACATGC     63547          _  CT
                                   ATGCATTGCT ACA  TGC
                                   |||||||||| |||  |||
                                   TACGTAACGA TGT  ACG
                                         C  __
GAM2732  SLC23A1   5'  CGCTGAGTTACATTTGCTTATG 63548     ATTGC    C
               C                    TGC     TACA TTGCTTATGC
                                    |||     |||| ||||||||||
                                    GCG     ATGT AACGAATACG
                                      ACTCA    A
GAM2732  UBE4A     3'  GCTACACACTTGCTTGTGC    63549     AT   T        A
                                   GC  TGC ACACTTGCTT TGC
                                   ||  ||| |||||||||| |||
                                   CG  ATG TGTGAACGAA ACG
                                    __  _         C
GAM2732  APOBEC3G  3'  TGCATTGCTTTGCTGGTG    63550         ACAC     TA
                                   TGCATTGCT    TTGCT  TG
                                   |||||||||    |||||  ||
                                   ACGTAACGA    AACGA  AC
                                         _____     CC
GAM2732  FLJ20033  3'  ATGCATTACATCTGTTTATG   63551         TACAC   C
                                   ATGCATTGC     TTG TTATG
                                   |||||||||     ||| |||||
                                   TACGTAATG     GAC AATAC
                                         TA___   A
GAM2732  KIAA0893  3'  ATGCTTGCTACATACAGTG   63552      A       CT   TTA
                                   ATGC TTGCTACA  TGC   TG
                                   |||| ||||||||  |||   ||
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                                TACG AACGATGT  ATG   AC
                                  _      __   TC_
GAM2732  KIAA1948  5'  ATGCATCTGCCACTGCTTATGC 63553      _     ACT
                                ATGCAT TGCTAC   TGCTTATGC
                                |||||| ||||||   |||||||||
                                TACGTA ACGGTG   ACGAATACG
                                   G     ___
GAM2732  SPRY2     3'  TGTGTTGCTTTAGCTTATGC   63554    CA    ACACTT
                                TG  TTGCT     GCTTATGC
                                ||  |||||     ||||||||
                                AC  AACGA     CGAATACG
                                 AC    AAT___
GAM2732  LOC126272 3'  ATGCATTGCTAACAAAGTGC   63555          _ CT_
                                ATGCATTGCTA CA   TGC
                                |||||||||||  ||   |||
                                TACGTAACGAT GT   ACG
                                       T  TTC
GAM2732  LOC143680 5'  ATGCATTACTAATAATCTTATG 63556          CACTTG
                                ATGCATTGCTA     CTTATG
                                ||||||||||      ||||||
                                TACGTAATGAT     GAATAC
                                       TATTA_
GAM2732  LOC149699 3'  ATGCATTGCACGTTCTTCCATG 63557        T  AC  GC
           C                     ATGCATTGC AC  TT  TTATGC
                                |||||||||  ||  ||  ||||||
                                TACGTAACG TG  AG  GGTACG
                                     _  CA  AA
GAM2732  LOC255631 5'  ATGCATTGTTCACCCGATG    63558        CTA     CTT
                                ATGCATTG   CACTTG   ATG
                                ||||||||   ||||||   |||
                                TACGTAAC   GTGGGC   TAC
                                    AA_     ____
GAM2732  LOC84524  3'  TACATTGCTACCTTTTTATG   63559          A   GC
                                TGCATTGCTAC CTT  TTATG
                                ||||||||||| |||  |||||
                                ATGTAACGATG GAA  AATAC
                                      _   A_
GAM2732  LOC92293  3'  TGCTGCTACACAATTATGC    63560     AT      TTGC
                                TGC  TGCTACAC    TTATGC
                                |||  ||||||||    ||||||
                                ACG  ACGATGTG    AATACG
                                  __       TT__
GAM2732  LOC93550  3'  ATGCATTGTATGCTTTTG     63561        C  CACT    A
                                ATGCATTG TA    TGCTT TG
                                ||||||||  ||    |||||  ||
                                TACGTAAC AT    ACGAA AC
                                     _  _____     A
GAM2733  GCH1      3'  CTTATCAAGGCACAGAGAGT   63564    CG_   A
                                CT   CAG GCACAGAGAGT
                                ||   ||| ||||||||||
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                                GA   GTT CGTGTCTCTCA
                                 ATA   C
GAM2733  SREBF1    5'  TCCACTCGCAGAGCACAG    63565
                                TTCACTCGCAGAGCACAG
                                ||||||||||||||||||
                                AGGTGAGCGTCTCGTGTC

GAM2733  STAU      3'  ACTCGCAGGGCTACCAGGT   63566        A  _  AG  A
                                ACTCGCAG GC AC  AG GT
                                |||||||| || ||  || ||
                                TGAGCGTC CG TG  TC CA
                                     C  A  G_  _
GAM2733  STAU      3'  ACTCGCAGGGCTACCAGGT   63566        A  _  AG  A
                                ACTCGCAG GC AC  AG GT
                                |||||||| || ||  || ||
                                TGAGCGTC CG TG  TC CA
                                     C  A  G_  _
GAM2733  STAU      3'  ACTCGCAGGGCTACCAGGT   63566        A  _  AG  A
                                ACTCGCAG GC AC  AG GT
                                |||||||| || ||  || ||
                                TGAGCGTC CG TG  TC CA
                                     C  A  G_  _
GAM2733  STAU      3'  ACTCGCAGGGCTACCAGGT   63566        A  _  AG  A
                                ACTCGCAG GC AC  AG GT
                                |||||||| || ||  || ||
                                TGAGCGTC CG TG  TC CA
                                     C  A  G_  _
GAM2733  FLJ10540  3'  TTCGTGCGCAGAACAGAGT   63567     ACT       CAGA
                                TTC   CGCAGAGCA   GAGT
                                |||   |||||||||   ||||
                                AAG   GCGTCTTGT   CTCA
                                  CAC       _____
GAM2733  KIAA1615  5'  TTCACTTGCAGAACACCATCGT 63568       C        AGAGA
              C                  TTCACT GCAGAGCAC    GTC
                                |||||| |||||||||    |||
                                AAGTGA CGTCTTGTG    CAG
                                   A        GTAG_
GAM2733  KIAA1656  3'  ACTCACCTTTACAGAGAGTC   63569       AGAGC
                                ACTCGC    ACAGAGAGTC
                                ||||||    ||||||||||
                                TGAGTG    TGTCTCTCAG
                                   GAAA_
GAM2733  WDR7      3'  TTCACTCGCTGTACACAGGGAG 63570         AGA     A
              T                  TTCACTCGC   GCACAG GAGT
                                |||||||||   |||||| ||||
                                AAGTGAGCG   TGTGTC CTCA
                                     ACA     C
GAM2733  LOC118611 5'  CACTTGGGGCACAGAGAGTC   63571     CGCAGA
                                CACT     GCACAGAGAGTC
                                ||||     ||||||||||||
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                                GTGA     CGTGTCTCTCAG
                                  ACCC__
GAM2733  LOC147299 5'  TTCCTCGCCAGAGAG      63572     A    AGAGCA
                                TTC CTCGC     CAGAGAG
                                ||| |||||     |||||||
                                AAG GAGCG     GTCTCTC
                                 _    _______
GAM2733  LOC150150 5'  TTCACCCACACAGGGAGT    63573       GCAGA     A
                                TTCACTC    GCACAG GAGT
                                |||||||    |||||| ||||
                                AAGTGGG    TGTGTC CTCA
                                    _____     C
GAM2733  LOC157697 5'  TCATTCGCAGAGCACAAGA   63574     C         G
                                TCA TCGCAGAGCACA AGA
                                ||| ||||||||||| |||
                                AGT AGCGTCTCGTGT TCT
                                  A         _
GAM2734  FLJ20366  5'  CCCGCGTCGCTGCTG       63577    A  TCTT
                                CC CG    CGTCGCTGCTG
                                || ||    ||||||||||
                                GG GC    GCAGCGACGAC
                                 _ _____
GAM2734  FLJ20507  5'  CGCTCCGCAGTCGCTGCTG   63578     CA   CTTC
                                CGC  CGT    GTCGCTGCTG
                                |||  |||    ||||||||||
                                GCG  GCG    CAGCGACGAC
                                  AG   T___
GAM2734  FLJ20507  5'  CGCTCCGCAGTCGCTGCTG   63578     CA   CTTC
                                CGC  CGT    GTCGCTGCTG
                                |||  |||    ||||||||||
                                GCG  GCG    CAGCGACGAC
                                  AG   T___
GAM2734  TLR10     5'  GCCATGTCTCCGTTGTTGA   63579      C       CGC  C
                                GCCA GTCTTCGT   TG TGA
                                |||| ||||||||   || |||
                                CGGT CAGAGGCA   AC ACT
                                  A       ___  A
GAM2734  LOC127841 5'  CCACAGTTGCTGCTGA      63580       TCTTC  C
                                CCACG     GT GCTGCTGA
                                |||||     || ||||||||
                                GGTGT     CA CGACGACT
                                    _____  A
GAM2734  LOC199676 3'  CGCCACGTTTCCCATGCTG   63581         C   G   C
                                CGCCACGT TTC TCG TGCTG
                                |||||||| ||| ||| |||||
                                GCGGTGCA AAG GGT ACGAC
                                     _   _   _
GAM2734  LOC221431 3'  CCACCCAGGGTTGCTGCTGAT  63582      G  TTC  C
                                CCAC TC   GT GCTGCTGAT
                                |||| ||   || |||||||||
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                                GGTG GG   CA CGACGACTA
                                  _ TCC  A
GAM2734  LOC254890 3'  GTCTTCGTTGCCTTCCTTGAT  63583        C   GC___
                                GTCTTCGT GCT     TGAT
                                |||||||| |||     ||||
                                CAGAAGCA CGG     ACTA
                                    A   AAGGA
GAM2735  DLG5     5'  GGAGGTGAGGTCCTCATCACA  63586     A_  TAAAA  G
                                GGA  TG    TT TTATCACA
                                |||  ||    || ||||||||
                                CCT  AC    AG AGTAGTGT
                                  CC  TCC__  G
GAM2735  FBP1     3'  AGGAATGTAAGGTGCACA    63587          AAT  TTAT
                                AGGAATGTAA   TG   CACA
                                ||||||||||   ||   ||||
                                TCCTTACATT   AC   GTGT
                                     CC_  ____
GAM2735  PTEN     3'  AGGATGTGAACCAGTATATCAC 63588      A   A  ATT  _
             AA                   AGGA TGT AA   GT TATCACAA
                                ||||| ||| ||   || ||||||||
                                TCCT ACA TT   CA ATAGTGTT
                                  _  C  GGT  T
GAM2735  PYGO2    3'  AGGAATGAGAATTGCTA     63589        TAA
                                AGGAATG   AATTGTTA
                                |||||||   ||||||||
                                TCCTTAC   TTAACGAT
                                    TC_
GAM2735  SHANK2   3'  GGAATGTAGAACAAGTTAC    63590         A   T_
                                GGAATGTA AAT  GTTAT
                                |||||||| |||  |||||
                                CCTTACAT TTG  CAATG
                                     C   TT
GAM2735  SNX6     3'  AGGAAGTGTGGAATCATCAC   63591       _   AAAATT
                                AGGAA TGT     GTTATCAC
                                ||||| |||     ||||||||
                                TCCTT ACA     TAGTAGTG
                                   C   CCT___
GAM2735  SYT4     3'  GGCAATGTAAAAAATCTTCACA 63592     _       TT   A
                                GG AATGTAAAA  GTT TCACA
                                || |||||||||  ||| |||||
                                CC TTACATTTT  TAG AGTGT
                                 G        T_   A
GAM2735  VBP1     3'  AGAAATGTGGAAAAAAAAATCA 63593         A_   TTGTT
             CAA                   AGGAATGT  AAA    ATCACAA
                                ||||||||  |||    |||||||
                                TCTTTACA  TTT    TAGTGTT
                                     CC   TTTTT
GAM2735  ARFGAP3  3'  AGGAACGTGAAACAGAAATCAC 63594         A    TGTT
             A                     AGGAATGT AAAT    ATCACA
                                ||||||||  ||||    ||||||
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                                TCCTTGCA TTTG   TAGTGT
                                    C   TCTT
GAM2735 CFP1     3' AGGAATGCAAGAAGTCTTACA 63595        AATT  ATC
                                AGGAATGTAA   GTT  ACA
                                ||||||||||   |||  |||
                                TCCTTACGTT   CAG  TGT
                                     CTT_  AA_
GAM2735 COASTER  3' AGGAATGGAAATTGTTTCA   63596      TA     A
                                AGGAATG  AAATTGTT TCA
                                |||||||  |||||||| |||
                                TCCTTAC  TTTAACAA AGT
                                   C_     _
GAM2735 GMFB     3' GGAATGTAAAAACTGGAAT   63597        _  TT
                                GGAATGTAAAA TTG  AT
                                |||||||||||| |||  ||
                                CCTTACATTTT GAC  TA
                                      T  CT
GAM2735 HNRPR    3' AGGAATGCAAAACATACAATCA 63598         TGTT_
                                AGGAATGTAAAAT    ATCA
                                ||||||||||||    ||||
                                TCCTTACGTTTTG    TAGT
                                       TATGT
GAM2735 KIAA0022 3' AGAAATGTAAAGCTCTTAC   63599        A  G
                                AGGAATGTAAA TT TTAT
                                |||||||||| || ||||
                                TCTTTACATTT GA AATG
                                      C  G
GAM2735 KIAA0222 3' AGAATGTAGCCCTGTTAC    63600       AAA
                                GGAATGTA   TTGTTAT
                                ||||||||   |||||||
                                TCTTACAT   GACAATG
                                    CGG
GAM2735 KIAA1033 3' AGCAATGTAAACTAGTTAT   63601    G     ATT
                                AG AATGTAAA   GTTAT
                                || ||||||||   |||||
                                TC TTACATTT   CAATA
                                 G       GAT
GAM2735 KIAA1040 5' GGAATTAAAATTATCACA    63602     G   ATT
                                GGAAT TAAA   GTTATCACA
                                ||||| ||||   |||||||||
                                CCTTA ATTT   TAATAGTGT
                                  _   ___
GAM2735 KIAA1677 3' GGAATGTAAGTTAATCA     63603       AATT  _
                                GGAATGTAA    GTTA TCA
                                |||||||||    |||| |||
                                CCTTACATT    CAAT AGT
                                     ____    T
GAM2735 KIAA1894 3' GAATGAATCATTGTTATTGCA 63604     TAAA     CA
                                GAATG   ATTGTTAT  CA
                                |||||   ||||||||  ||
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                                CTTAC    TAACAATA  GT
                                   TTAG       AC
GAM2735  LBP-9    3'  GGAATGTAAAATGGTACA    63605          T  TATC
                                GGAATGTAAAAT GT    ACA
                                |||||||||||| ||    |||
                                CCTTACATTTTA CA    TGT
                                       C  ____
GAM2735  SLC26A9  3'  GGAATTATATTATCACA     63606      GTAAAAT
                                GGAAT      TGTTATCACA
                                |||||      ||||||||||
                                CCTTA      ATAATAGTGT
                                   AT_____
GAM2735  SLC26A9  3'  GGAATTATATTATCACA     63606      GTAAAAT
                                GGAAT      TGTTATCACA
                                |||||      ||||||||||
                                CCTTA      ATAATAGTGT
                                   AT_____
GAM2735  SPINLW1  3'  GGAATGTAAATTGGTTCA    63607         A   TTA
                                GGAATGTAAA TTG   TCA
                                |||||||||| |||   |||
                                CCTTACATTT AAC   AGT
                                      _  CA_
GAM2735  LOC143437 3'  AGAGTGTAAAATCATTAT    63608     A       TG
                                GGA TGTAAAAT  TTAT
                                ||| ||||||||  ||||
                                TCT ACATTTTA  AATA
                                  C       GT
GAM2735  LOC147694 3'  GGAATGTAAAATGGCACA    63609          T TTAT
                                GGAATGTAAAAT G    CACA
                                |||||||||||| |    ||||
                                CCTTACATTTTA C    GTGT
                                       C ____
GAM2735  LOC151171 5'  AGGAATGTGTGGCTCACA    63610        AAAAT  TTA
                                AGGAATGT    TG   TCACA
                                ||||||||    ||   |||||
                                TCCTTACA    AC   AGTGT
                                     C____  CG_
GAM2735  LOC152715 3'  AGGAATGTGAGTATCACA    63611        AAAATT  T
                                AGGAATGT     GT ATCACA
                                ||||||||     || ||||||
                                TCCTTACA     CA TAGTGT
                                     CT____  _
GAM2735  LOC158267 3'  AGGCATGTGGTGCCTATCACAA 63612     A    AAAAT  _
                                AGG ATGT     TGT TATCACAA
                                ||| ||||     ||| ||||||||
                                TCC TACA     ACG ATAGTGTT
                                  G   CC___   G
GAM2735  LOC220177 5'  AGGAGTGTAAAATCTGACCCCA 63613     A       GTT   A
            A                   AGGA TGTAAAATT   ATC CAA
                                |||| |||||||||   ||| |||
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                                TCCT ACATTTTAG   TGG GTT
                                  C       AC_   G
GAM2735  LOC253531 3'  AGAGTGTAAAATCATTAT    63608     A      TG
                                GGA TGTAAAAT  TTAT
                                ||| ||||||||  ||||
                                TCT ACATTTTA  AATA
                                  C       GT
GAM2735  LOC257451 3'  AGGAATGAGAATTGCTA     63589       TAA
                                AGGAATG   AATTGTTA
                                |||||||   ||||||||
                                TCCTTAC   TTAACGAT
                                    TC_
GAM2736  STC1      3'  CGTTACTGGTTTTAAAGGCT   63616       T A      A
                                CGTTACT G TTTTAAAG CT
                                ||||||| | |||||||| ||
                                GCAATGA C AAAATTTC GA
                                    _ C       C
GAM2736  VPS41     3'  AATCAGTTACTTAAAAATGAAG 63617     _       TTTTA
             ACT                  AATC GTTACTTGA     AAGACT
                                |||| |||||||||     ||||||
                                TTAG CAATGAATT     TTCTGA
                                  T       TTTAC
GAM2737  GYPC      3'  AGTGCTCTCTCTCTCTGTCTGG 63620         A    CTA
                                AGTGCTCTC CTCTC   TCTGG
                                ||||||||| |||||   |||||
                                TCACGAGAG GAGAG   AGACC
                                    A    AC_
GAM2737  GYPC      3'  AGTGCTCTCTCTCTCTGTCTGG 63620         A    CTA
                                AGTGCTCTC CTCTC   TCTGG
                                ||||||||| |||||   |||||
                                TCACGAGAG GAGAG   AGACC
                                    A    AC_
GAM2737  HLF       3'  TAGTACTCTTACTTATCTG    63621         C   CTCC
                                TAGTGCTCT ACT    TATCTG
                                ||||||||| |||    ||||||
                                ATCATGAGA TGA    ATAGAC
                                    A  _____
GAM2737  NTSR1     3'  TAGAGGCCCTTTTCCTATCTGG 63622     T_    CACTC
                                TAG  GCTCT    TCCTATCTGG
                                |||  |||||    ||||||||||
                                ATC  CGGGA    AGGATAGACC
                                  TC    AA___
GAM2737  C20orf18  5'  TGGTCTTCTCGTCCATCTG    63623    C   CA   _   T
                                TG TCT  CTC TCC ATCTG
                                || |||  ||| ||| |||||
                                AC AGA  GAG AGG TAGAC
                                 C  A_   C   _
GAM2737  C20orf18  5'  TGGTCTTCTCGTCCATCTG    63623    C   CA   _   T
                                TG TCT  CTC TCC ATCTG
                                || |||  ||| ||| |||||
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                                AC AGA  GAG AGG TAGAC
                                 C  A_  C  _
GAM2737  LOC221421 3'  TAGTGCTCCACTCTCCCAC   63624        T
                                TAGTGCTC CACTCTCCTAT
                                |||||||| ||||||||||
                                ATCACGAG GTGAGAGGGTG
                                        _
GAM2738  COL8A1    5'  CCTCTGGGGCTGGTTTCTGTCT 63627    _      AGCAGAAA_
           CTT                   CC CTGGGGCT       CTCTT
                                || ||||||||       |||||
                                GG GACCCCGA       GAGAA
                                 A       CCAAAGACA
GAM2738  PCSK5     5'  TCCCTGGGGCTGCCGGGACC  63628          A  AGAA
                                TCCCTGGGGCT GC    ACT
                                |||||||||| ||    |||
                                AGGGACCCCGA CG    TGG
                                       _ GCCC
GAM2738  CSEN      3'  CCCTGGGGCTAGCCTCT     63629           AGAAA
                                CCCTGGGGCTAGC     CTCT
                                ||||||||||||     ||||
                                GGGACCCCGATCG     GAGA
                                          _____
GAM2738  FLJ10922  3'  CTGGGGACCAGTCAGGGGCTCT 63630       _   _  AAA
           T                    CTGGGG CTAG CAG   CTCTT
                                |||||| |||| |||   |||||
                                GACCCC GGTC GTC   GAGAA
                                   T   A   CCC
GAM2738  FLJ20359  3'  CCTGGGGGCTGGCAGGGACT   63631       _ A   AA
                                CCTGGGG CT GCAG  ACT
                                ||||||| || ||||  |||
                                GGACCCC GA CGTC  TGA
                                    C  C   CC
GAM2738  KIAA1719  3'  CCTGGAAAGAAGCTCT      63632       CTAGC   A
                                CCTGGGG    AGAA CTCT
                                |||||||    |||| ||||
                                GGACCTT    TCTT GAGA
                                     _____   C
GAM2738  PP1201    3'  TCCCTGGGTTAGCAGAA     63633        GC
                                TCCCTGGG  TAGCAGAA
                                ||||||||  ||||||||
                                AGGGACCC  ATCGTCTT
                                    A_
GAM2738  SAE1      3'  TCTCTGGGGCTGCCAAATCTT  63634    C      A  AG   C
                                TC CTGGGGCT GC  AAA TCTT
                                || |||||||| ||  ||| ||||
                                AG GACCCCGA CG  TTT AGAA
                                 A       _ G_  _
GAM2738  SCAM-1    3'  CCTTGGGGCCAGAGCTCT    63635    C       C  AAA
                                CC TGGGGCTAG AG   CTCT
                                || |||||||| ||   ||||
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                                GG ACCCCGGTC TC   GAGA
                                 A       _ ____
GAM2738  STX5A    3'  TCCCTGGGGCTGCTTCCTCTC  63636          A  AGAAA
                                TCCCTGGGGCT GC    CTCTT
                                |||||||||||  ||    |||||
                                AGGGACCCCGA CG    GAGAG
                                      _  AAG__
GAM2738  UBE3B    3'  TCCCTGGAGCTAAAGTTCT   63637           C  AAAC
                                TCCCTGGGGCTAG AG   TCT
                                |||||||||||||  ||   |||
                                AGGGACCTCGATT TC   AGA
                                      _  A___
GAM2738  ZNF297B  3'  CTTGGCTGAACAGAAACTCTT  63638    GG   _
                                CT  GGCT AGCAGAAACTCTT
                                ||  |||| ||||||||||||
                                GA  CCGA TTGTCTTTGAGAA
                                 A_   C
GAM2738  LOC144583 3'  TCCCTGGGGCTAGTGAA     63639           CA
                                TCCCTGGGGCTAG  GAA
                                ||||||||||||  |||
                                AGGGACCCCGATC  CTT
                                       A_
GAM2738  LOC145824 5'  TCCCTGGGGTTGGTCAGAAA   63640         CTAG_
                                TCCCTGGGG    CAGAAA
                                |||||||||    ||||||
                                AGGGACCCC    GTCTTT
                                      AACCA
GAM2738  LOC146062 3'  CCTGAGGCACCAGGACTCTT   63641         T G   AA
                                CCTGGGGC A CAG  ACTCTT
                                ||||||||  | |||  ||||||
                                GGACTCCG T GTC  TGAGAA
                                     _ G   C_
GAM2738  LOC148824 3'  TCCCTGGGTTAGTTTCTGAATT 63642         GC   CA___   AC
            CTT                   TCCCTGGG  TAG    GAA  TCTT
                                ||||||||  |||    |||  ||||
                                AGGGACCC  ATC    CTT  AGAA
                                     A_   AAAGA   A_
GAM2738  LOC150468 3'  TCTCTGGGGCTTGCACTGCCT  63643    C       A   GAAA
                                TC CTGGGGCT GCA    CT
                                || ||||||||  |||    ||
                                AG GACCCCGA CGT    GA
                                 A       A   GACG
GAM2738  LOC153727 3'  TCCCTAGGTTCAAGGGATTCTT 63644         GC   CA  AAC
                                TCCCTGGG  TAG  GA   TCTT
                                ||||||||  |||  ||   ||||
                                AGGGATCC  GTT  CT   AGAA
                                     AA   CC  A__
GAM2738  LOC154789 5'  TCCCTGGGGCTGGAATGTCTT  63645          AGCA   AC
                                TCCCTGGGGCT    GAA  TCTT
                                ||||||||||    |||  ||||
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                                AGGGACCCCGA   CTT  AGAA
                                      C___   AC
GAM2738  LOC196485 5'  TGGGATTATGTGGAAACTCTT  63646     GC  GCA_
                                TGGG  TA   GAAACTCTT
                                ||||  ||   |||||||||
                                ACCC  AT   CTTTGAGAA
                                  TA  ACAC
GAM2738  LOC202986 5'  TGGGATTATGTGGAAACTCTT  63646     GC  GCA_
                                TGGG  TA   GAAACTCTT
                                ||||  ||   |||||||||
                                ACCC  AT   CTTTGAGAA
                                  TA  ACAC
GAM2738  LOC254221 5'  TCCCTGGGGCTGCTGGTTTCTT 63647          A  AGAAAC
                                TCCCTGGGGCT GC     TCTT
                                |||||||||| ||     ||||
                                AGGGACCCCGA CG     AGAA
                                      _  ACCAA_
GAM2738  LOC254975 3'  CCTCTGGAATCAGAAACTCTT  63648    _    GCTAG
                                CC CTGGG    CAGAAACTCTT
                                || |||||    ||||||||||
                                GG GACCT    GTCTTTGAGAA
                                 A    TA___
GAM2738  LOC91170  3'  TCTGTGGGGCCAGGGACTCTT  63649    CC       CAGAA
                                TC  TGGGGCTAG    ACTCTT
                                ||  |||||||||    ||||||
                                AG  ACCCCGGTC    TGAGAA
                                 AC       CC___
GAM2739  MMP25    5'  GGGGTCCCGGGAAGTGCGC   63652    A  A   TT_
                                GG GT CTC   GAGTGCGC
                                || || |||   ||||||||
                                CC CA GGG   TTCACGCG
                                 C  _   CCC
GAM2739  ODC1     3'  AGGGGCACTCTTGAGTAGCG   63653     A         _
                                AGG GTACTCTTGAGT GCG
                                ||| ||||||||||| |||
                                TCC CGTGAGAACTCA CGC
                                  C          T
GAM2739  FLJ23420  5'  AGGAGTACTCCTTGAGGGGC   63654         _    T_
                                AGGAGTACTC TTGAG  GC
                                |||||||||| |||||  ||
                                TCCTCATGAG AACTC  CG
                                      G    CC
GAM2739  MGC12837  3'  GGGGACTTTGAGTGCTGTGCAG 63655    AGT   C      ___
                                GG   ACT TTGAGTGC   GCAG
                                ||   ||| ||||||||   ||||
                                CC   TGA AACTCACG   CGTC
                                 CC_  _       ACA
GAM2739  LOC145623 3'  AGGAGTACTCTTTAGTTAAC   63656          G   GC
                                AGGAGTACTCTT AGT  GC
                                |||||||||||| |||  ||
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                                TCCTCATGAGAA TCA  TG
                                      A   AT
GAM2739  LOC150527 5'  GGAGGCGGCCAGTGCGCAG   63657     TACT  TG
                                GGAG   CT  AGTGCGCAG
                                ||||   ||  |||||||||
                                CCTC   GG  TCACGCGTC
                                  CGCC  __
GAM2739  LOC92267  5'  GGAGTGTTCGTTGAGGGCACAG 63658      AC  _    T
            CG                    GGAGT  TC TTGAG GCGCAGCG
                                ||||||  || ||||| ||||||||
                                CCTCA  AG AACTC CGTGTCGC
                                  CA  C    C
GAM2740  AGM1     3'  TTAGTGTTTAAGAAAAACA   63661          T
                                TTAGTGTTTAA AAAAATA
                                |||||||||||| |||||||
                                AATCACAAATT TTTTTGT
                                      C
GAM2740  CLECSF5   3'  TTAGTGTTGTAATAAAAAATAT 63662        _       _
            G                    TTAGTGTT TAATAAAAA TATG
                                |||||||| ||||||||| ||||
                                AATCACAA ATTATTTTT ATAC
                                     C        T
GAM2740  IL21R    3'  GTGTTTAATAAATATCTCTTGG 63663          A  A___
            G                    GTGTTTAATAAA AT    TGGG
                                |||||||||||| ||    ||||
                                CACAAATTATTT TA    ACCC
                                      A  GAGA
GAM2740  YES1     3'  TTAGAGTTTAATACTTGGG    63664      T       AAAATA
                                TTAG GTTTAATA     TGGG
                                |||| ||||||||      ||||
                                AATC CAAATTAT     ACCC
                                  T       GA_____
GAM2740  HSBP1    3'  TTAGTGTTTAATAATGAATAG  63665           AAAT
                                TTAGTGTTTAATAA    ATGG
                                ||||||||||||||    ||||
                                AATCACAAATTATT    TATC
                                      ACT_
GAM2740  LOC200059 3'  TTAGTGTTTAAAAAAAT     63666          T
                                TTAGTGTTTAA AAAAAT
                                |||||||||| ||||||
                                AATCACAAATT TTTTTA
                                      _
GAM2741  C1D      3'  TTACATATTAATGTACTTTTTG 63669     G        CGTA
            AA                    TTA ATATTAATGT    TTTGAA
                                ||| ||||||||||    ||||||
                                AAT TATAATTACA    AAACTT
                                  G         TGAA
GAM2741  FLJ10546  5'  TTACATACGTCAATCGTATTTG 63670     G    TAAT
            AA                    TTA ATAT    GTCGTATTTGAA
                                ||| ||||    ||||||||||||
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                                AAT TATG    TAGCATAAACTT
                                  G    CAGT
GAM2742  DGKE     3'  TATACCCATTATACTACTA    63673       AA   C
                                TATACT  CAT TATACTACTA
                                ||||||  ||| ||||||||||
                                ATATGG  GTA ATATGATGAT
                                   __   _
GAM2742  TIAL1    3'  CATATACTGTCCATACT     63674        AACA
                                TATATACT    TCTATACT
                                ||||||||    ||||||||
                                GTATATGA    AGGTATGA
                                     C___
GAM2742  FLJ23191 3'  TATATCCTAGCATCTATA    63675       A   A
                                TATAT CTA CATCTATA
                                ||||| ||| ||||||||
                                ATATA GAT GTAGATAT
                                   G   C
GAM2742  KIAA0408 5'  TACACTAACATTTAACT     63676          C  T
                                TATACTAACAT TA ACT
                                |||||||||||| || |||
                                ATGTGATTGTA AT TGA
                                      A  _
GAM2742  STIP-1   3'  TATATACTAACTTTTTAACTA  63677          ATCTAT
                                TATATACTAAC     ACTA
                                ||||||||||      ||||
                                ATATATGATTG     TGAT
                                      AAAAAT
GAM2742  LOC166968 3'  TACATACTGACATCACT     63678        A    TAT
                                TATATACT ACATC   ACT
                                |||||||| |||||   |||
                                ATGTATGA TGTAG   TGA
                                     C    ____
GAM2743  BAALC    3'  TGCCAGTGGGGACATAT     63681    A  A  A
                                TG CAG TG GGACATAT
                                || ||| || ||||||||
                                AC GTC AC CCTGTATA
                                 G   _  C
GAM2743  NEDD4    3'  TGACAGATGAAGAAATATG   63682           C
                                TGACAGATGAGGA ATATG
                                |||||||||||| |||||
                                ACTGTCTACTTCT TATAC
                                       T
GAM2743  ERO1L    3'  TACCTGATAAGACATAT     63683        CAGATG
                                TACCTGA     AGGACATAT
                                |||||||     |||||||||
                                ATGGACT     TTCTGTATA
                                    A_____
GAM2743  FLJ13273 3'  TTACCTGACATGATGGCAGCAT 63684          _   A_  A
                                TTACCTGACA GATG  GG CAT
                                |||||||||| ||||  || |||
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                                AATGGACTGT CTAC  TC GTA
                                     A    CG  _
GAM2743  HBP1     3'  TTACCTGATAGACATATA    63685        CAGATGA
                                TTACCTGA      GGACATATG
                                ||||||||      |||||||||
                                AATGGACT      TCTGTATAT
                                     A_______
GAM2743  KIAA1766 3'  TTACCTGGAGATGAAAA     63686        AC
                                TTACCTG  AGATGAGGA
                                |||||||  |||||||||
                                AATGGAC  TCTACTTTT
                                    C_
GAM2743  SCAP     3'  CCTGACAGATGATGATATG    63687           GGAC
                                CCTGACAGATGA    ATATG
                                ||||||||||||    |||||
                                GGACTGTCTACT    TATAC
                                      AC__
GAM2743  LOC115294 3'  CTGACAGATGACAACAGTATG  63688           G   _
                                CTGACAGATGA GACA TATG
                                |||||||||||| |||| ||||
                                GACTGTCTACT TTGT ATAC
                                      G   C
GAM2744  COG4     3'  CTTTATTCAGGGATCATA     63691          T_
                                CTTTATTCAG  ATCATA
                                |||||||||  ||||||
                                GAAATAAGTC  TAGTAT
                                      CC
GAM2744  CYP4F3   3'  TCTTTCATTCAGTATCAT     63692      _
                                TCTT TATTCAGTATCAT
                                |||| ||||||||||||
                                AGAA GTAAGTCATAGTA
                                  A
GAM2744  DSPG3    3'  CAATCTCAAAGTATCAT      63693        TATTC
                                TAATCTT     AGTATCAT
                                |||||||     ||||||||
                                GTTAGAG     TCATAGTA
                                    TT___
GAM2744  FLJ20366 3'  TAATCTTTATTTTCATCAT    63694           CAG
                                TAATCTTTATT   TATCAT
                                ||||||||||   ||||||
                                ATTAGAAATAA   GTAGTA
                                      AA_
GAM2744  FLJ23594 3'  TAATCTTTAATTCAGCAT     63695         _
                                TAATCTTTA TTCAGTAT
                                ||||||||| ||||||||
                                ATTAGAAAT AAGTCGTA
                                      T
GAM2744  KIAA0042 3'  TAATCTTCATCAAATCATA    63696          T   T
                                TAATCTTTAT CAG ATCATA
                                |||||||||| ||| ||||||
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                                ATTAGAAGTA GTT TAGTAT
                                      _  _
GAM2744  KIAA1371  3'  TAATCCTTAGTATCATA     63697        ATTC
                                TAATCTTT   AGTATCATA
                                ||||||||   |||||||||
                                ATTAGGAA   TCATAGTAT
                                     _____
GAM2744  PIGM      3'  ACCTTTATTCCCACCAT     63698         AG
                                ATCTTTATTC  TATCAT
                                ||||||||||  ||||||
                                TGGAAATAAG  GTGGTA
                                      G_
GAM2744  PRO0800   3'  ATCCTGATTCAGTATCATA   63699       T
                                ATCTT ATTCAGTATCATA
                                ||||| ||||||||||||
                                TAGGA TAAGTCATAGTAT
                                   C
GAM2744  UMP-CMPK  3'  TCTTTACTCTTGCTTCATA   63700         A_  A
                                TCTTTATTC  GT TCATA
                                |||||||||  || |||||
                                AGAAATGAG  CG AGTAT
                                     AA  A
GAM2744  LOC153222 3'  ACATTCATACAGTATCAT    63701    C    T
                                AT TTTAT CAGTATCAT
                                || ||||| |||||||||
                                TG AAGTA GTCATAGTA
                                 T    T
GAM2745  TCEA1     3'  AGATTATTTTATTCTGAAACAT 63704           AATT__
           TAT                    AGATTATTTTGTT     CATTAT
                                ||||||||||||      ||||||
                                TCTAATAAAATAA     GTAATA
                                      GACTTT
GAM2745  DKFZP434A043 3'  AAGATTGTCTCAGCAATTCATT 63705       A   GT
           AT                     AAGATT TTTT  TAATTCATTAT
                                ||||||| ||||  ||||||||||
                                TTCTAA AGAG  GTTAAGTAATA
                                   C   TC
GAM2745  DKFZP434P0721 3'  AAGATTAATTTGTAATCATT   63706       T    TAAT
                                AAGATTA TTTGT    TCATT
                                ||||||| |||||    |||||
                                TTCTAAT AAACA    AGTAA
                                    T    TT__
GAM2745  FLJ10900  3'  AAGATTATTTTATTAATTCA   63707
                                AAGATTATTTTGTTAATTCA
                                ||||||||||||||||||||
                                TTCTAATAAAATAATTAAGT

GAM2745  KIAA1320  3'  AAGATATATTTTGTTAAC    63708      _
                                AAGAT TATTTTGTTAAT
                                ||||| ||||||||||||
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                                TTCTA ATAAAACAATTG
                                   T
GAM2745  LOC203084 3'  AGATTATTTTATTCTGAAACAT 63704          AATT__
             TAT                  AGATTATTTTGTT     CATTAT
                                  ||||||||||||     ||||||
                                  TCTAATAAAATAA     GTAATA
                                        GACTTT
GAM2745  LOC255621 3'  AGATTATTTCTGCTTCATTAT  63709        GTTAA
                                  AGATTATTTT    TTCATTAT
                                  ||||||||||    ||||||||
                                  TCTAATAAAG    AAGTAATA
                                       ACG__
GAM2746  ACADM     3'  TACAATATTTTCTAAATGTAA  63712         A  A
                                  TACAATATTT TT AAATGTAA
                                  |||||||||| || ||||||||
                                  ATGTTATAAA AG TTTACATT
                                       _  A
GAM2746  ORC2L     3'  AACAATTACTAAAATGTAA    63713     T
                                  AATA TTATTAAAATGTAA
                                  |||| ||||||||||||||
                                  TTGT AATGATTTTACATT
                                     T
GAM2746  RRAS2     3'  CATCTCTATTAAAATGTAA    63714    ATA
                                  CA   TTTATTAAAATGTAA
                                  ||   ||||||||||||||
                                  GT   AGATAATTTTACATT
                                   AG_
GAM2746  ZNF140    3'  TACAAGAGTATTAAAATGTAA  63715      TATT
                                  TACAA    TATTAAAATGTAA
                                  |||||    ||||||||||||
                                  ATGTT    ATAATTTTACATT
                                     CTC_
GAM2746  DNAJC6    3'  CACAATATCTACAAATGT     63716          TA
                                  TACAATATTTAT  AAATGT
                                  ||||||||||||  ||||||
                                  GTGTTATAGATG  TTTACA
                                                __
GAM2746  FBXO22    3'  ACAATATATATAAAAATGTAA  63717       T   T
                                  ACAATAT TAT AAAATGTAA
                                  ||||||| ||| |||||||||
                                  TGTTATA ATA TTTTACATT
                                      T   T
GAM2746  KIAA1320  3'  TACAATATATATTAAAATAT   63718        T
                                  TACAATAT TATTAAAATGT
                                  |||||||| ||||||||||
                                  ATGTTATA ATAATTTTATA
                                       T
GAM2746  LAPTM4A   3'  CAAAAACTATTAAAATGTAA   63719     TAT
                                  CAA   TTATTAAAATGTAA
                                  |||   ||||||||||||||
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                                GTT  GATAATTTTACATT
                                  TTT
GAM2746 PRO0659  3' CAACATTTACATACATGTA  63720        TAAA
                                CAATATTTAT   ATGTA
                                ||||||||||   |||||
                                GTTGTAAATG   TACAT
                                     TATG
GAM2746 LOC132617 3' CAACAATACTAAAATGTAA  63721     TT
                                CAATA  TATTAAAATGTAA
                                |||||  ||||||||||||
                                GTTGT  ATGATTTTACATT
                                   T_
GAM2746 LOC51103  5' TACAAAAAAATCAAAATGTAA 63722     TATTT
                                TACAA    ATTAAAATGTAA
                                |||||    ||||||||||||
                                ATGTT    TAGTTTTACATT
                                   TTTT_
GAM2747 ADRA2A   3' TCATATTTATTTCACATTT   63725         A
                                TCATATTTATTT ATATTT
                                |||||||||||| ||||||
                                AGTATAAATAAA TGTAAA
                                       G
GAM2747 ERBB4    3' TCACATTTATTTACAACTTTT 63726          AT
                                TCATATTTATTTA  ATTTTT
                                |||||||||||||  ||||||
                                AGTGTAAATAAAT  TGAAAA
                                      GT
GAM2747 STAT1    3' TCATTTTATTTATACTTTTTCA 63727     A      A
                                TCAT TTTATTTA TATTTTTTCA
                                |||| |||||||| ||||||||||
                                AGTA AAATAAAT ATGAAAAAGT
                                  _      _
GAM2747 KIAA1878 3' TATTTTTGTTTAATATTTCTTC 63728     A__
            A                    TATTT   TTTAATATTTTTTCA
                                |||||   ||||||||||||||||
                                ATAAA   AAATTATAAAGAAGT
                                   AAC
GAM2747 LOC90509 5' TCATATTTATTAAACACATTTT 63729         T    T
                                TCATATTTATT AATAT TTTT
                                |||||||||| ||||| ||||
                                AGTATAAATAA TTGTG AAAA
                                      T    T
GAM2748 ALDH1B1  3' TTGTACATCTCTCTGG     63732        CCC
                                TTGTACATT   TTCTGG
                                |||||||||   ||||||
                                AACATGTAG   GAGACC
                                     A__
GAM2748 CDH13    3' TTGTACATTTACTGAGGAGG  63733        CC  TCT
                                TTGTACATT  CT   GGGGG
                                |||||||||  ||   |||||
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                                AACATGTAA  GA   CCTCC
                                     AT  CT_
GAM2748  DEC1     3'  TTGTGCATGTCTCTGAGG    63734      A   TCCC
                                TTGT CAT    TTCTGGGG
                                |||| |||    ||||||||
                                AACA GTA    GAGACTCC
                                  C   CA__
GAM2748  F7       5'  TTGACATTCCCCATGGG     63735     T       TC
                                TTG ACATTCCCT  TGGG
                                ||| |||||||||  ||||
                                AAC TGTAAGGGG  ACCC
                                  _       T_
GAM2748  F7       5'  TTGACATTCCCCATGGG     63735     T       TC
                                TTG ACATTCCCT  TGGG
                                ||| |||||||||  ||||
                                AAC TGTAAGGGG  ACCC
                                  _       T_
GAM2748  KNSL1    3'  TTGTACATATTCCTTCTG    63736        TC_
                                TTGTACAT   CCTTCTG
                                ||||||||   |||||||
                                AACATGTA   GGAAGAC
                                     TAA
GAM2748  PABPN1   3'  TGCATTTCCCCAGGGGG     63737      CA     TCT
                                TGTA  TTCCCT   GGGGG
                                ||||  ||||||   |||||
                                ACGT  AAGGGG   CCCCC
                                  A_     T__
GAM2748  PDGFRA   3'  TTGTACATGCCTTTCCTTGG  63738        T  C    GG
                                TTGTACAT CC TTCT  GG
                                |||||||| || ||||  ||
                                AACATGTA GG AAGG  CC
                                     C  A    AA
GAM2748  PDGFRA   3'  TTGTGCTTTCTCTGGAGG    63739      ACA   CCT
                                TTGT   TTC   TCTGGGGG
                                ||||   |||   ||||||||
                                AACA   AAG   AGACCTCC
                                  CGA   ___
GAM2748  RAD51C   3'  CTGTGCATTCCTTCTGG     63740      A     C
                                TTGT CATTCC TTCTGG
                                |||| |||||| ||||||
                                GACA GTAAGG AAGACC
                                  C     _
GAM2748  SLC38A2  3'  TTGTCCATTCTCTGGAATGGG 63741      A    CCT    ___
                                TTGT CATTC   TCTGG   GGG
                                |||| |||||   |||||   |||
                                AACA GTAAG   AGACC   CCC
                                  G     ___     TTA
GAM2748  SPOCK    3'  TTGTACATTTTCCTAAG     63742        CCC
                                TTGTACATT   TTCTGGG
                                |||||||||   |||||||
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                                AACATGTAA  AGGATTC
                                     A__
GAM2748 SPRR1B   3' GCACATTCTTTTTTGGGGG  63743       CC  C
                                GTACATTC  TT TGGGGG
                                ||||||||  || ||||||
                                CGTGTAAG  AA ACCCCC
                                     AA  A
GAM2748 TRPC5    3' CACTCTCCTTTCTGGGGG   63744     _   _
                                CATTC CCTT CTGGGGG
                                ||||| |||| |||||||
                                GTGAG GGAA GACCCCC
                                   A   A
GAM2748 VEGF     3' TTGCACATTCTTGGGCAGGGG 63745        CCTTCT
                                TTGTACATTC     GGGGG
                                ||||||||||     |||||
                                AACGTGTAAG     TCCCC
                                     AACCCG
GAM2748 ZNF83    5' TGTACATTTTTCTGGG     63746       CCC
                                TGTACATT   TTCTGGG
                                ||||||||   |||||||
                                ACATGTAA   AAGACCC
                                     A__
GAM2748 AP3M1    3' CTGTAAACTTCTGGGGG    63747      CATTCC
                                TTGTA     CTTCTGGGGG
                                |||||     ||||||||||
                                GACAT     GAAGACCCCC
                                   TT____
GAM2748 C20orf172 3' TTGCACATTCCTGGG      63748         CTTC
                                TTGTACATTCC   TGGG
                                ||||||||||   ||||
                                AACGTGTAAGG   ACCC
                                      ____
GAM2748 DKFZp434G179 3' CTGCATTTCTCCCTAGGGG  63749     CA_    TCT
                                TTGTA  TTCCCT  GGGGG
                                |||||  ||||||  |||||
                                GACGT  GAGGGA  TCCCC
                                   AAA    ___
GAM2748 DLAT     3' TCGTACATTTCCTAGAGG   63750       CCC
                                TTGTACATT  TTCTGGGGG
                                |||||||||  |||||||||
                                AGCATGTAA  AGGATCTCC
                                      ___
GAM2748 FLJ00024 3' TTGTACATCTTCTTCAAG   63751       CC   T
                                TTGTACATT  CTTC GG
                                |||||||||  |||| ||
                                AACATGTAG  GAAG TC
                                     AA   T
GAM2748 FLJ10120 3' TGTAATTCTTCCGGG     63752     C   CC
                                TGTA ATTC  TTCTGGG
                                ||||  ||||  |||||||
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                              ACAT TAAG  AAGGCCC
                                _   __
GAM2748 FLJ11259 3' CTGTACATTCTCTAGG      63753         CCT
                              TTGTACATTC   TCTGGG
                              ||||||||||   ||||||
                              GACATGTAAG   AGATCC
                                   ___
GAM2748 FLJ22969 3' TTGTCGTTTTCATCCTGGGG  63754     ACA_  CC
                              TTGT   TTC  TTCTGGGG
                              ||||   |||  ||||||||
                              AACA   AAG  AGGACCCC
                                GCAA   T_
GAM2748 FLJ31709 3' TTGTATTATTTCCCCAAGGGG 63755      CA__     TCT
                              TTGTA   TTCCCT   GGGG
                              |||||   ||||||   ||||
                              AACAT   AAGGGG   CCCC
                                 AATA     TT_
GAM2748 HEY1     3' TTGTACATTCACCTTTCTG   63756         _   _
                              TTGTACATTC CCTT CTG
                              |||||||||| |||| |||
                              AACATGTAAG GGAA GAC
                                    T   A
GAM2748 HSPC055  5' CTGTACATTTCCTCCCTTGG  63757         C     GG
                              TTGTACATT CCTTCT  GG
                              |||||||| ||||||  ||
                              GACATGTAA GGAGGG  CC
                                   A     AA
GAM2748 KIAA0255 3' TTGTCCATTCCTGGGG      63758     A     CTTC
                              TTGT CATTCC    TGGGG
                              |||| ||||||    |||||
                              AACA GTAAGG    ACCCC
                                G     ____
GAM2748 KIAA0440 3' TTGTGCACTCCCCGAAAGGGGG 63759      A       TCT_
                              TTGT CATTCCCT    GGGGG
                              |||| ||||||||    |||||
                              AACA GTGAGGGG    CCCCC
                                C       CTTT
GAM2748 KIAA0924 3' TTGTTCATTCCCTTGG      63760     A      TC
                              TTGT CATTCCCT  TGG
                              |||| ||||||||  |||
                              AACA GTAAGGGA  ACC
                                A      __
GAM2748 KIAA1130 3' CTGTACATTCTCTGG       63761         CCT
                              TTGTACATTC   TCTGG
                              ||||||||||   |||||
                              GACATGTAAG   AGACC
                                   ___
GAM2748 KIAA1819 5' TTGTACATTCCATCCCCGG   63762          C   G
                              TTGTACATTCC TTCT GG
                              |||||||||| |||| ||
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                                AACATGTAAGG AGGG CC
                                      T   G
GAM2748 KIAA1908 5' TGCAGCCTTTCTGGGGG    63763     CATT  C
                                TGTA   CC TTCTGGGGG
                                ||||   || |||||||||
                                ACGT   GG AAGACCCCC
                                  C___  A
GAM2748 MGC18079 3' CTGTGCATTCCCTTGGG    63764     A      TC
                                TTGT CATTCCCT  TGGG
                                |||| ||||||||  ||||
                                GACA GTAAGGGA  ACCC
                                  C      __
GAM2748 MGC20460 5' TGTGCATTCCCTGAGGCGGGG 63765    A      TC__
                                TGT CATTCCCT   TGGGG
                                ||| ||||||||   |||||
                                ACA GTAAGGGA   GCCCC
                                  C      CTCC
GAM2748 MUC13    3' TTGTACATTGGTTGGGGG    63766       CCCTTC
                                TTGTACATT     TGGGGG
                                |||||||||     ||||||
                                AACATGTAA     ACCCCC
                                     CCA___
GAM2748 NECL1    3' TTGTTCATTTCCGGGG      63767     A   CCCT
                                TTGT CATT    TCTGGGG
                                |||| ||||   |||||||
                                AACA GTAA    AGGCCCC
                                  A   _____
GAM2748 P8       3' TGTAGCTTTCTTTTCTGGGGG 63768     CA_  CC
                                TGTA   TTC  TTCTGGGGG
                                ||||   |||  |||||||||
                                ACAT   AAG  AAGACCCCC
                                  CGA   AA
GAM2748 SCAM-1   3' TACATTCTCTTCCAGAGG    63769       C    TG
                                TACATTC CTTC  GGGG
                                ||||||| ||||  ||||
                                ATGTAAG GAAG  CTCC
                                    A    GT
GAM2748 SGP28    3' TTGTACATTTTGTTCTAGG    63770       CCC
                                TTGTACATT   TTCTGGG
                                |||||||||   |||||||
                                AACATGTAA   AAGATCC
                                     AAC
GAM2748 SLI      3' CTGCCAGCCTTTCTGGGGG   63771     ACATT  C
                                TTGT    CC TTCTGGGGG
                                ||||    || |||||||||
                                GACG    GG AAGACCCCC
                                  GTC__  A
GAM2748 ZFP100   3' TTGTACACTCTTTTGGCCCCCA 63772       __________   TCTGG
            GAAG                 GTACATTC       CCT    GG
                                ||||||||       |||    ||
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                                CATGTGAG       GGG    TC
                                    AAAACCIII  GGTCT
GAM2748  LOC124944 5'  TTGTATATGTTCTGGGGG    63773      C  TCCC
                                TTGTA AT    TTCTGGGGG
                                ||||| ||    |||||||||
                                AACAT TA    AAGACCCCC
                                   A  C___
GAM2748  LOC143524 3'  CTGTATGATCCTTTCTGGGGG  63774      CAT   C
                                TTGTA   TCC TTCTGGGGG
                                |||||   ||| |||||||||
                                GACAT   AGG AAGACCCCC
                                   ACT   A
GAM2748  LOC144695 3'  TTATACATTTCTTCTGG     63775         CC
                                TTGTACATT  CTTCTGG
                                |||||||||  |||||||
                                AATATGTAA  GAAGACC
                                     A_
GAM2748  LOC152195 5'  TTGTACATATGCATGCCTGGGG 63776        TCCCT__
              G                  TTGTACAT      TCTGGGGG
                                 ||||||||      ||||||||
                                 AACATGTA      GGACCCCC
                                     TACGTAC
GAM2748  LOC158428 5'  TGTACATTTTCTATGG      63777        CCC    G
                                TGTACATT   TTCTG GG
                                ||||||||   ||||| ||
                                ACATGTAA   AAGAT CC
                                    ___     A
GAM2748  LOC165693 5'  TTGTACATTCCAAAAGGG    63778          CTTCT
                                TTGTACATTCC    GGGG
                                ||||||||||     ||||
                                AACATGTAAGG    TCCC
                                     TTT__
GAM2748  LOC200985 3'  GCATATTCCCTTTTGGGGG   63779     C      C
                                GTA ATTCCCTT TGGGGG
                                ||| |||||||| ||||||
                                CGT TAAGGGAA ACCCCC
                                  A       A
GAM2748  LOC253776 3'  CTGTACATTTCCTGAGG     63780         CCC
                                TTGTACATT   TTCTGGGG
                                |||||||||   ||||||||
                                GACATGTAA   AGGACTCC
                                    ___
GAM2748  LOC253933 3'  CTGCACCCTTTCTGGGGG    63781       ATT  C
                                TTGTAC   CC TTCTGGGGG
                                ||||||   || |||||||||
                                GACGTG   GG AAGACCCCC
                                   ___  A
GAM2748  LOC255105 3'  CTGCACCCTTTCTGGGGG    63781       ATT  C
                                TTGTAC   CC TTCTGGGGG
                                ||||||   || |||||||||
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                                GACGTG   GG AAGACCCCC
                                   ___  A
GAM2748  LOC255328 3'  TTGTGTTTCCCCTGGGGG    63782     ACA    TT
                                TTGT   TTCCC  CTGGGGG
                                ||||   |||||  |||||||
                                AACA   AAGGG  GACCCCC
                                  CA_    __
GAM2748  LOC255718 5'  TTGTACATCTCTCTGG      63732         CCC
                                TTGTACATT   TTCTGG
                                |||||||||   ||||||
                                AACATGTAG   GAGACC
                                     A__
GAM2748  LOC256369 3'  TTGGACATTTCCTGAAGGG   63783     T    C   TCT
                                TTG ACATT CCT   GGGG
                                ||| ||||| |||   ||||
                                AAC TGTAA GGA   TCCC
                                  C    A   CT_
GAM2748  LOC257239 5'  TTGTTCGTTCCTCCCTGGGG   63784     ACA    CT
                                TTGT   TTCC  TCTGGGG
                                ||||   ||||  |||||||
                                AACA   AAGG  GGACCCC
                                  AGC    AG
GAM2748  LOC257358 3'  TTGTGCATTTCCTAGGG     63785     A   CCC
                                TTGT CATT   TTCTGGGG
                                |||| ||||   ||||||||
                                AACA GTAA   AGGATCCC
                                  C   ____
GAM2749  RAD51L3   3'  GCCAGACACGCCATGCGCCGGC 63788     CA  T   ATA_   A
                                GCC  AC ACGC    CGCC GC
                                |||  || ||||    |||| ||
                                CGG  TG TGCG    GCGG CG
                                  TC  _   GTAC    C
GAM2749  RAD51L3   3'  GCCAGACACGCCATGCGCCGGC 63788     CA  T   ATA_   A
                                GCC  AC ACGC    CGCC GC
                                |||  || ||||    |||| ||
                                CGG  TG TGCG    GCGG CG
                                  TC  _   GTAC    C
GAM2749  DKFZP564C186 3'  TCCCCCAACTGCACAGACGCCA 63789    G      A   T
            GC                    TC CCCAACT CGCA ACGCCAGC
                                || ||||||| |||| ||||||||
                                AG GGGTTGA GTGT TGCGGTCG
                                 G      C   C
GAM2749  OR2C3     3'  TCGCCCAACTGCGACAGAGC   63790          A  _  TAC
                                TCGCCCAACT CG CA   GC
                                |||||||||| || ||   ||
                                AGCGGGTTGA GC GT   CG
                                      C  T  CT_
GAM2749  PP35      5'  CCTTGGCTAGGCACGACGCCAG 63791    CAA_   C    _
            C                    CC    CTA GCAT ACGCCAGC
                                ||    ||| |||| ||||||||
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                                GG    GAT CGTG TGCGGTCG
                                 AACC   C    C
GAM2749  PSMD10    5'  TCGCCGGCTCCGGCTACGCCAG 63792      CAA  AC_  A
                                TCGCC   CT   GC TACGCCAG
                                |||||   ||   || ||||||||
                                AGCGG   GA   CG ATGCGGTC
                                   CC_  GGC  _
GAM2749  LOC144308 5'  CCGCCCAGGGATTTATACGCCA 63793       ACTACGC
           GC                     TCGCCCA      ATACGCCAGC
                                |||||||      ||||||||||
                                GGCGGGT      TATGCGGTCG
                                    CCCTAAA
GAM2750  DJ159A19.3 3'  TTGTACATTTTTAAAAAGTAT  63796          CTATT
                                TTGTACATTTTT    AGTAT
                                ||||||||||||    |||||
                                AACATGTAAAAA    TCATA
                                       TTTT_
GAM2750  KIAA0408  3'  TATTGTACATTGTTTCAACT   63797          _   T
                                TATTGTACATT TTTC ATT
                                |||||||||| |||| |||
                                ATAACATGTAA AAAG TGA
                                       C    T
GAM2750  KIAA0555  3'  TATTGTACATTCTTCAGTTA   63798           TA
                                TATTGTACATTTTTC  TTA
                                |||||||||||||||  |||
                                ATAACATGTAAGAAG  AAT
                                       TC
GAM2750  LOC157507 3'  TATTGTACATTTATTTTTAGTA 63799          TTCTA
           T                    TATTGTACATTT    TTAGTAT
                                ||||||||||||    |||||||
                                ATAACATGTAAA    AATCATA
                                       TAAA_
GAM2751  ADCY7     3'  TTTGTTAGATACGTGTG     63802        A   C
                                TTTGTTAGA TAT TGTG
                                ||||||||| ||| ||||
                                AAACAATCT ATG ACAC
                                      _   C
GAM2751  CBFB      3'  TTTGTCAGAAGGCTGTG     63803         TAT
                                TTTGTTAGAA   CTGTG
                                |||||||||   |||||
                                AAACAGTCTT   GACAC
                                      CC_
GAM2751  CBFB      3'  TTTGTCAGAAGGCTGTG     63803         TAT
                                TTTGTTAGAA   CTGTG
                                |||||||||   |||||
                                AAACAGTCTT   GACAC
                                      CC_
GAM2751  DUSP4     3'  TTTGCTAGGATCTGTG      63804        AAT
                                TTTGTTAG   ATCTGTG
                                ||||||||   |||||||
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                                AAACGATC  TAGACAC
                                    C__
GAM2751  DUSP4    3'  TTTGCTAGGATCTGTG     63804       AAT
                                TTTGTTAG  ATCTGTG
                                ||||||||  |||||||
                                AAACGATC  TAGACAC
                                    C__
GAM2751  HIP1     3'  TTTGCTAGAGTCACACCTG   63805        ___
                                TTTGTTAGA  ATATCTG
                                |||||||||  |||||||
                                AAACGATCT  TGTGGAC
                                    CAG
GAM2751  LRP1     3'  TTTATAAGAATATCTGTG    63806     T
                                TTTGT AGAATATCTGTG
                                ||||| ||||||||||||
                                AAATA TCTTATAGACAC
                                   T
GAM2751  OGN      3'  TTGTTAGAATAATAATTGTG  63807         TC___
                                TTGTTAGAATA    TGTG
                                ||||||||||    ||||
                                AACAATCTTAT    ACAC
                                      TATTA
GAM2751  OGN      3'  TTGTTAGAATAATAATTGTG  63807         TC___
                                TTGTTAGAATA    TGTG
                                ||||||||||    ||||
                                AACAATCTTAT    ACAC
                                      TATTA
GAM2751  OGN      3'  TTGTTAGAATAATAATTGTG  63807         TC___
                                TTGTTAGAATA    TGTG
                                ||||||||||    ||||
                                AACAATCTTAT    ACAC
                                      TATTA
GAM2751  OGT      5'  TTTATTAGAATACTATG     63808          T
                                TTTGTTAGAATA CTGTG
                                |||||||||||| |||||
                                AAATAATCTTAT GATAC
                                      _
GAM2751  PLAG1    3'  CTTGTTAGAACATTGTG     63809          C
                                TTTGTTAGAATAT TGTG
                                |||||||||||| ||||
                                GAACAATCTTGTA ACAC
                                      _
GAM2751  RIMS1    3'  TTTGTTAGAAGCATCAGTG   63810        _   T
                                TTTGTTAGAA TATC GTG
                                |||||||||| |||| |||
                                AAACAATCTT GTAG CAC
                                      C   T
GAM2751  SLC2A2   3'  TCTGTTTAATCATCTGTG    63811       A  A
                                TTTGTT GA TATCTGTG
                                |||||| || ||||||||
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                                AGACAA TT GTAGACAC
                                   A  A
GAM2751  SRGAP1    5'  TTTGTTAGAATACTGTG     63812           T
                                TTTGTTAGAATA CTGTG
                                |||||||||||| |||||
                                AAACAATCTTAT GACAC
                                          _
GAM2751  C20orf106 3'  TTTGTCCCAATATCTGTG     63813        AG
                                TTTGTT  AATATCTGTG
                                ||||||  ||||||||||
                                AAACAG  TTATAGACAC
                                   GG
GAM2751  COL12A1   3'  TTCGTTAACCATTATCTGTG   63814         AA__
                                TTTGTTAG    TATCTGTG
                                ||||||||    ||||||||
                                AAGCAATT    ATAGACAC
                                     GGTA
GAM2751  COL12A1   3'  TTCGTTAACCATTATCTGTG   63814         AA__
                                TTTGTTAG    TATCTGTG
                                ||||||||    ||||||||
                                AAGCAATT    ATAGACAC
                                     GGTA
GAM2751  DKFZP434G1415 3'  TTGTCTCCAATATCTGTG    63815       AG_
                                TTGTT   AATATCTGTG
                                |||||   ||||||||||
                                AACAG   TTATAGACAC
                                  AGG
GAM2751  KIAA0676  3'  TTTGTTATTATCTGTG      63816        GAA
                                TTTGTTA   TATCTGTG
                                |||||||   ||||||||
                                AAACAAT   ATAGACAC
                                    A__
GAM2751  KIAA1040  3'  TTTGTCTACATCTGTG      63817        AGA
                                TTTGTT   ATATCTGTG
                                ||||||   |||||||||
                                AAACAG   TGTAGACAC
                                   A__
GAM2751  KIAA1107  5'  TCTGTTGATCATCTGTG     63818        A  A
                                TTTGTT GA TATCTGTG
                                |||||| || ||||||||
                                AGACAA CT GTAGACAC
                                   _  A
GAM2751  LOC138639 3'  TTTCTTAGTTCATCTGTG    63819     G    AA
                                TTT TTAG  TATCTGTG
                                ||| ||||  ||||||||
                                AAA AATC  GTAGACAC
                                  G    AA
GAM2751  LOC145371 3'  TTTGTAAACATCTGTG      63820      TA
                                TTTGT  GAATATCTGTG
                                |||||  ||||||||||
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                                AAACA  TTTGTAGACAC
                                   __
GAM2751  LOC146136 5'  TCTGTTAGAAACTGTG     63821        TAT
                                TTTGTTAGAA  CTGTG
                                ||||||||||  |||||
                                AGACAATCTT  GACAC
                                     T__
GAM2751  LOC146181 3'  TCTGTTAGAAACTGTG     63821        TAT
                                TTTGTTAGAA  CTGTG
                                ||||||||||  |||||
                                AGACAATCTT  GACAC
                                     T__
GAM2751  LOC146449 3'  TCTGTTAGAAACTGTG     63821        TAT
                                TTTGTTAGAA  CTGTG
                                ||||||||||  |||||
                                AGACAATCTT  GACAC
                                     T__
GAM2751  LOC160897 3'  TCTGTTAATTTAATCTGTG   63822       AAT_
                                TTTGTTAG   ATCTGTG
                                ||||||||   |||||||
                                AGACAATT   TAGACAC
                                    AAAT
GAM2751  LOC197423 3'  TCTGTTAGAAACTGTG     63821        TAT
                                TTTGTTAGAA  CTGTG
                                ||||||||||  |||||
                                AGACAATCTT  GACAC
                                     T__
GAM2751  LOC220565 3'  TCTGTTAGAAACTGTG     63821        TAT
                                TTTGTTAGAA  CTGTG
                                ||||||||||  |||||
                                AGACAATCTT  GACAC
                                     T__
GAM2752  ACADL    3'  TCACAGAGATGTTCTGCA    63825        AC  A
                                TCACGGAGAT  TCT CA
                                ||||||||||  ||| ||
                                AGTGTCTCTA  AGA GT
                                     CA  C
GAM2752  FPGS     3'  TCACGGAGTATGCTGGCCCCAC 63826       _ A __ TA
           T                     TCACGGAG AT CT  C  CACT
                                |||||||| || ||  |  ||||
                                AGTGCCTC TA GA  G  GTGA
                                    A  C  CC GG
GAM2752  LOH11CR2A 5'  TCACAGAGATACTCTTCA    63827          A
                                TCACGGAGATACTCT CA
                                |||||||||||||| ||
                                AGTGTCTCTATGAGA GT
                                       A
GAM2752  KIAA0318  5'  TCAGGAGATACTCTCCCT    63828    C       ACA
                                TCA GGAGATACTCT  CT
                                ||| ||||||||||  ||
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                                AGT CCTCTATGAGA  GA
                                  _       GG_
GAM2753 ATP6V0C  3' GCGCATGTACAAGACC    63831   AC     TCTT
                                GC CATGTACG  AGACC
                                || |||||||  |||||
                                CG GTACATGT  TCTGG
                                 C_     ____
GAM2753 GRM1    3' CACCAAAAGTCTTAGACCA  63832     TGTAC
                                CACCA   GTCTTAGACCA
                                |||||   ||||||||||
                                GTGGT   CAGAATCTGGT
                                  TTT__
GAM2753 RXRA    3' CCGCATCATTCCTAGAC    63833     C  GTACG
                                CCGCA CAT   TCTTAGAC
                                ||||| |||   ||||||||
                                GGCGT GTA   AGGATCTG
                                  A  _____
GAM2753 SRC     3' CACCATGTGTGTCCTGCCA  63834      AC   AGA
                                CACCATGT GTCTT  CCA
                                |||||||| |||||  |||
                                GTGGTACA CAGGA  GGT
                                    CA   C__
GAM2753 WEE1    3' GCAAACATGTTTTAGACCA  63835    C_   ACGTC
                                GCA CATGT   TTAGACCA
                                ||| |||||   ||||||||
                                CGT GTACA   AATCTGGT
                                 TT   A____
GAM2753 C1orf19  3' CCTCACTATGTACGTCAACC  63836   G  C      TTA
                                CC CAC ATGTACGTC  GACC
                                || ||| |||||||||  ||||
                                GG GTG TACATGCAG  TTGG
                                 A  A      ___
GAM2753 FLJ22644 3' GCACCATGAGAGGTAGACCA  63837       TACGTCT
                                GCACCATG     TAGACCA
                                ||||||||     |||||||
                                CGTGGTAC     ATCTGGT
                                    TCTCC__
GAM2753 KIAA1614 3' CACCATGTGGGCCAGAC    63838      AC  TT
                                CACCATGT GTC AGAC
                                |||||||| ||| ||||
                                GTGGTACA CGG TCTG
                                    CC  __
GAM2753 TNFRSF19L 3' CCGCAGTGTCCTTAGAC    63839     CCA  ACG
                                CCGCA  TGT  TCTTAGAC
                                |||||  |||  ||||||||
                                GGCGT  ACA  GGAATCTG
                                  C__  ___
GAM2753 TONDU   3' GCTGCCGTGTCTTAGACCA  63840   ACCA  AC_
                                GC   TGT  GTCTTAGACCA
                                ||   |||  ||||||||||
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                                CG   ACG  CAGAATCTGGT
                                 ____  GCA
GAM2753  LOC145828 3'  CAGGCCATACGTCTTGGGCCA  63841    CA  TG      AGA
                                CG  CCA  TACGTCTT   CCA
                                ||  |||  ||||||||   |||
                                GT  GGT  ATGCAGAA   GGT
                                 CC  __      CCC
GAM2753  LOC148758 5'  CACCATGTGGGCCAGAC     63838        AC  TT
                                CACCATGT  GTC  AGAC
                                ||||||||  |||  ||||
                                GTGGTACA  CGG  TCTG
                                     CC  __
GAM2753  LOC155036 5'  GCTGTGTTAGCTTAGACCA   63842    ACCA  AC T
                                GC   TGT  G CTTAGACCA
                                ||   |||  | |||||||||
                                CG   ACA  C GAATCTGGT
                                 AC__  AT _
GAM2754  RTN1     3'  TACCATAAGTGCGGTCGACTGC 63845        AC   _  T  A
                                TACCATAG  GCGG CG AT GT
                                ||||||||  |||| || || ||
                                ATGGTATT  CGCC GC TG CG
                                     CA   A  _  A
GAM2755  CDH12    5'  TGAATGGGGTGGGGAGATAGCA 63848        AA__________  GCTA
            TAGCTG                TGGGGTG        GCA   TG
                                |||||||        |||   ||
                                ACCCCAC        CGT   AC
                                   CCCTCTAIIIT  ATCG
GAM2755  CLK2     3'  TGGATGGGGTAGGGCAGGTA  63849    A      AA   C
                                TG ATGGGGTG  GCAG TA
                                || ||||||||  |||| ||
                                AC TACCCCAT  CGTC AT
                                 C      CC   C
GAM2755  DKK1     3'  TAAATGGGGTAAAGGGTTATGC 63850           CAGC
            T                   TGAATGGGGTGAAG   TATGCT
                                ||||||||||||||   ||||||
                                ATTTACCCCATTTC   ATACGA
                                      CCA_
GAM2755  EGFR     3'  TGGATGGGGTGGATATTAGCAT 63851        AA_________  GCTA
            AGCTG                 ATGGGGTG        GCA   TG
                                |||||||        |||   ||
                                TACCCCAC       CGT   AC
                                   CTATAAIIIT  ATCG
GAM2755  ENPP3    3'  TGAATGGGTGGGGCAGGGAGCC 63852        G  AA   CTAT
                                TGAATGGG TG  GCAG   GCT
                                |||||||| ||  ||||   |||
                                ACTTACCC AC  CGTC   CGG
                                   _ CC   CCT_
GAM2755  PCLO     3'  TGAATGGGGAGGACTCCTGCTA 63853        T_  AGCA_
            TGCT                  TGAATGGGG  GA    GCTATGCT
                                |||||||||  ||    ||||||||
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                                ACTTACCCC CT    CGATACGA
                                    TC GAGGA
GAM2755 PRKY    3' AAACAGGGTGGCTATG     63854         AAGCA
                                GAATGGGGTG    GCTATG
                                ||||||||||    ||||||
                                TTTGTCCCAC    CGATAC
                                    _____
GAM2755 SMAC    3' GAGTGGGGTGAAATGTTAGCAT 63855       A__________   GCTA
           AGCTG                TGGGGTG       AGCA   TG
                                |||||||       ||||   ||
                                ACCCCAC       TCGT   AC
                                    TTTACAAIII   ATCG
GAM2755 SMAC    3' GAGTGGGGTGAAATGTTAGCAT 63855       A__________   GCTA
           AGCTG                TGGGGTG       AGCA   TG
                                |||||||       ||||   ||
                                ACCCCAC       TCGT   AC
                                    TTTACAAIII   ATCG
GAM2755 SMAC    3' GAGTGGGGTGAAATGTTAGCAT 63855       A__________   GCTA
           AGCTG                TGGGGTG       AGCA   TG
                                |||||||       ||||   ||
                                ACCCCAC       TCGT   AC
                                    TTTACAAIII   ATCG
GAM2755 TCF7    3' TGAATGGGGAGGGGTGCACACT 63856        TGAAGCA  T
                                TGAATGGGG     GC ATGCT
                                |||||||||     || |||||
                                ACTTACCCC     CG TGTGA
                                    TCCCCA_  _
GAM2755 TPP2    3' TGAAGATTTATTGAAGCAGTTA 63857     T  GG___      C
           TGCT                   TGAA GG    TGAAGCAG TATGCT
                                |||| ||    |||||||| ||||||
                                ACTT CT    ACTTCGTC ATACGA
                                  _ AAATA      A
GAM2755 VDAC1   3' TAAATTCTGAAGGTAGCTATGC 63858      GGGG    C_
           T                    TGAAT   TGAAG  AGCTATGCT
                                |||||   |||||  |||||||||
                                ATTTA   ACTTC  TCGATACGA
                                   AG__    CA
GAM2755 ARHGEF15 3' TGGATGGGGTTGGGCAGCC   63859    A     GAA
                                TG ATGGGGT   GCAGCT
                                || |||||||   ||||||
                                AC TACCCCA   CGTCGG
                                 C      ACC
GAM2755 CASPR3   5' TGAGTGGGGAGAAGCAGCAGCA 63860    A    T      TA
           CC                     TGA TGGGG GAAGCAGC  TGCT
                                ||| ||||| ||||||||  ||||
                                ACT ACCCC CTTCGTCG  GTGG
                                  C    T       TC
GAM2755 FLJ32468 3' GAGATGGAAGCAGCTATGCT  63861       _
                                GGGGTG AAGCAGCTATGCT
                                |||||| ||||||||||||
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                                CTCTAC TTCGTCGATACGA
                                   C
GAM2755 KIAA0628 3' TGAATGGGGTAAGCTTGC    63862          AAGC   A
                                TGAATGGGGTG   AGCT TGC
                                ||||||||||   |||| |||
                                ACTTACCCCAT   TCGA ACG
                                          ____  _
GAM2755 MR       5' GAAGGGGAGTGGCTGTGC    63863    T   TGA  CA   A
                                GAA GGGG   AG  GCT TGC
                                ||| ||||   ||  ||| |||
                                CTT CCCC   TC  CGA ACG
                                  _   ___ AC   C
GAM2755 PLA2G12  3' AAATGGGAGTGGCTATGCT   63864       _  AAGCA
                                GAATGGG GTG    GCTATGCT
                                ||||||| |||    ||||||||
                                TTTACCC CAC    CGATACGA
                                    T  _____
GAM2755 TRIM29   3' TGAATGGGAGATGGGTGGCTGT 63865        T  AGCA__   A
             GCT                   TGAATGGGG GA     GCT TGCT
                                |||||||| ||     ||| ||||
                                ACTTACCCT CT     CGA ACGA
                                      _ ACCCAC   C
GAM2755 LOC115708 3' GAGTGGGGTGAGGCCCAGCT  63866    A      A __
                                GA TGGGGTGA GC  AGCT
                                || |||||||| ||  ||||
                                CT ACCCCACT CG  TCGA
                                 C       C  GG
GAM2755 LOC126917 3' GAATGGGGTGAAGTGGGACC  63867          CA__
                                GAATGGGGTGAAG   GCT
                                ||||||||||||   |||
                                CTTACCCCACTTC   TGG
                                       ACCC
GAM2755 LOC127534 3' TGAGATGGGGTGGGGCATCT  63868    _      AA   G
                                TGA ATGGGGTG  GCA CT
                                ||| ||||||||  ||| ||
                                ACT TACCCCAC  CGT GA
                                  C       CC   A
GAM2755 LOC165552 3' AGAGTGATGGCAGCTATG    63869       A_
                                GGGGTGA  GCAGCTATG
                                |||||||  |||||||||
                                TCTCACT  CGTCGATAC
                                    AC
GAM2756 EDG1     3' TCAATGGTGTTAACACGG    63872          __ T
                                TCAATGGTGT  AC CGG
                                ||||||||||  || |||
                                AGTTACCACA  TG GCC
                                      AT  T
GAM2756 SAD1     5' AATGGTGTCCAGGTACG     63873        A  C   TC
                                AATGGTGT CT GGT  ACG
                                |||||||| || |||  |||
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                                TTACCACA GG CCA  TGC
                                   _ T  __
GAM2756  LOC158301 3'  TCAATGGTGCATTTCAGAGCTG 63874          C_   TTCAC
           AG                    TCAATGGTGTA  TCGG    GAG
                                 ||||||||||  ||||    |||
                                 AGTTACCACGT  AGTC    CTC
                                      AA   TCGA_
GAM2757  DKFZP434N093 3'  TAGAGAACAGGGCGTGTG    63877        ___
                                 TAGAGGAC   GTGTGTG
                                 ||||||||   |||||||
                                 ATCTCTTG   CGCACAC
                                     TCC
GAM2757  KIAA1550  3'  GACTGCATGTGTGTGTGTATGT 63878     _____      C   CA
           CA                    GAC    GTGTGTG GTA  TCA
                                 |||    ||||||| |||  |||
                                 CTG    CACACAC CAT  AGT
                                   ACGTA      A   AC
GAM2757  KIAA1553  3'  TAGGGTGCGTGTGTGTGCA   63879     A  A_      C
                                 TAG GG  CGTGTGTG GTA
                                 ||| ||  ||||||||| |||
                                 ATC CC  GCACACAC CGT
                                   _ AC       A
GAM2757  KIAA1970  3'  TAGAGATGTGTGTGCAT     63880       AC
                                 TAGAGG  GTGTGTGCGT
                                 ||||||  ||||||||||
                                 ATCTCT  CACACACGTA
                                    A_
GAM2757  PP1665    3'  GAGGACGTGTCTCCACAT    63881          GTGCG
                                 GAGGACGTGT    TACAT
                                 ||||||||||    |||||
                                 CTCCTGCACA    GTGTA
                                      GAG__
GAM2757  STK33     5'  TAGAGTGTGTGTGTGCGT    63882      GAC
                                 TAGAG   GTGTGTGCGT
                                 |||||   ||||||||||
                                 ATCTC   CACACACGCA
                                    ACA
GAM2757  LOC200812 3'  GGGGGTGACCACCGTGTACATC 63883    AC   TG___  C
           A                     GG  GTG    TG GTACATCA
                                 ||  |||    || ||||||||
                                 CC  CAC    GC CATGTAGT
                                  CC   TGGTG  A
GAM2757  LOC253933 3'  GACAACCGCGTACATCA     63884      TGTG
                                 GACG    TGCGTACATCA
                                 ||||    ||||||||||
                                 CTGT    GCGCATGTAGT
                                   TG__
GAM2757  LOC255105 3'  GGGGGTGACCAGTGTGTACATC 63885    AC   T___   C
           A                     GG  GTG    GTG GTACATCA
                                 ||  |||    ||| ||||||||
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                                CC  CAC    CAC CATGTAGT
                                 CC   TGGT   A
GAM2758  GRIA3     3'  TTGAAGCAGCCACGTTTTCGG  63888        _  TG AACATC
                                TTGAAGC GT  C      TTCGG
                                ||||||| ||  |      |||||
                                AACTTCG CG  G      AAGCC
                                    T  GT CAA___
GAM2758  DKFZP434M131 3'  GAGGCACTGGGTGTCTTCGGC  63889    A     CAACA
                                GA GCGTTG    TCTTCGGC
                                || ||||||    ||||||||
                                CT CGTGAC    AGAAGCCG
                                 C     CCAC_
GAM2758  DUSP10    3'  TTAAAGTGTGTAGTATCTTCGG 63890       C  TGCAAC
                                TTGAAG GT     ATCTTCGG
                                ||||||| ||     ||||||||
                                AATTTC CA     TAGAAGCC
                                    A  CATCA_
GAM2758  DUSP10    3'  TTAAAGTGTGTAGTATCTTCGG 63890       C  TGCAAC
                                TTGAAG GT     ATCTTCGG
                                ||||||| ||     ||||||||
                                AATTTC CA     TAGAAGCC
                                    A  CATCA_
GAM2758  FLJ14437  3'  TGGCAACTGTGTGACATCTTTG 63891    A_   GT  CA      C
           G                     TG  AGC  TG  ACATCTT GG
                                ||  |||  ||  ||||||| ||
                                AC  TTG  AC  TGTAGAA CC
                                 CG   AC  AC      A
GAM2758  KIAA1649  3'  AGCTCTTGAGTATCTTCGGC   63892    G_   CAAC
                                AGC  TTG    ATCTTCGGC
                                |||  |||    |||||||||
                                TCG  AAC    TAGAAGCCG
                                  AG   TCA_
GAM2758  KIAA1649  3'  AGCTCTTGAGTATCTTCGGC   63892    G_   CAAC
                                AGC  TTG    ATCTTCGGC
                                |||  |||    |||||||||
                                TCG  AAC    TAGAAGCCG
                                  AG   TCA_
GAM2758  LOC119710 5'  TGAGGCCACAGTATCTTCGGC  63893    A C  TG  AC
                                TGA G GT  CA  ATCTTCGGC
                                ||| | ||  ||  |||||||||
                                ACT C CG  GT  TAGAAGCCG
                                  _ _  GT  CA
GAM2759  ATP11A    3'  AGAGGATGTCTGCTCATCACA  63896       C         ATAT
                                AGAGGA GTCTGTTCGT    CA
                                |||||| ||||||||||    ||
                                TCTCCT CAGACGAGTA    GT
                                    A         GT__
GAM2759  KIAA1040  5'  GAGGATGATGGATATATCAA   63897      CGTC  TTC_
                                GAGGA    TG    GTATATCAA
                                |||||    ||    |||||||||
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                                CTCCT   AC   TATATAGTT
                                  ____ TACC
GAM2759 SLC19A3  5' AGGGAGTGTCTGTTCACCA  63898   A  C_     GTAT
                                AG GGA  GTCTGTTC   ATCA
                                || |||  ||||||||   ||||
                                TC CCT  CAGACAAG   TGGT
                                 _  CA      ____
GAM2759 LOC122886 3' GAAGATGTCTGTTCTTCTAGTC 63899      C      GTA _
                                GAGGA GTCTGTTC   TA TC
                                ||||| ||||||||   || ||
                                CTTCT CAGACAAG   AT AG
                                   A       AAG  C
GAM2759 LOC222484 5' GAGGAGGTCTGTTCCACA   63900      C      G
                                GAGGA GTCTGTTC TATA
                                ||||| |||||||| ||||
                                CTCCT CAGACAAG GTGT
                                   C       _
GAM2760 FLJ10737  3' TAATAATATAAAATAAAAACAT 63903           TCCCA_
             CT                   TAATAATATAAAAT     ATCT
                                |||||||||||||      ||||
                                ATTATTATATTTTA     TAGA
                                       TTTTTG
GAM2761 IGF1     3' TCAGTGAGGTTCCTTTAATTC  63906        A    ___
                                TTAGTGAG TTCCT   ATTC
                                |||||||| |||||   ||||
                                AGTCACTC AAGGA   TAAG
                                     C     AAT
GAM2761 STAT6    3' TTAGTGAGGTCCTGTTC     63907        AT   A
                                TTAGTGAG  TCCT TTC
                                ||||||||  |||| |||
                                AATCACTC  AGGA AAG
                                     C_    C
GAM2761 TAPBP    3' GTGAGATTTTATAACAAAAT   63908        CC   TC
                                GTGAGATT  TAT  CAAAAT
                                ||||||||  |||  ||||||
                                CACTCTAA  ATA  GTTTTA
                                     A_   TT
GAM2761 TRIM14   3' TAGTGAGATTCTTGTTCC    63909          CTA
                                TAGTGAGATTC   TTCC
                                ||||||||||   ||||
                                ATCACTCTAAG   AAGG
                                      AAC
GAM2761 KIAA1718 3' TTAGTGAGATATTTCTCCA   63910         TCCTA
                                TTAGTGAGAT    TTCCA
                                ||||||||||    |||||
                                AATCACTCTA    GAGGT
                                      TAAA_
GAM2761 LEAP-2   5' CTAGCCACATTTCTATTCCAAA 63911      GAG   C
             AT                   TTAGT   ATT CTATTCCAAAAT
                                |||||   ||| ||||||||||||
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                                GATCG   TAA GATAAGGTTTTA
                                  GTG   A
GAM2761  ZNF238    3'  TTAGTGAGATTCTCATGCTATT 63912          _____     C
           CTAAA                  TTAGTGAGATTC    CTATTC AAA
                                  ||||||||||||    |||||| |||
                                  AATCACTCTAAG    GATAAG TTT
                                        AGTAC     A
GAM2761  LOC144970 3'  GTGGAAATATTCCAAAAT    63913    A  TTCC
                                  GTG GA    TATTCCAAAAT
                                  ||| ||    ||||||||||
                                  CAC CT    ATAAGGTTTTA
                                    _  TT__
GAM2761  LOC148171 3'  GTGGAAATATTCCAAAAT    63913    A  TTCC
                                  GTG GA    TATTCCAAAAT
                                  ||| ||    ||||||||||
                                  CAC CT    ATAAGGTTTTA
                                    _  TT__
GAM2761  LOC148172 3'  GTGGAAATATTCCAAAAT    63913    A  TTCC
                                  GTG GA    TATTCCAAAAT
                                  ||| ||    ||||||||||
                                  CAC CT    ATAAGGTTTTA
                                    _  TT__
GAM2761  LOC154405 3'  GTGGAAATATTCCAAAAT    63913    A  TTCC
                                  GTG GA    TATTCCAAAAT
                                  ||| ||    ||||||||||
                                  CAC CT    ATAAGGTTTTA
                                    _  TT__
GAM2761  LOC222057 3'  GTGGAAATATTCCAAAAT    63913    A  TTCC
                                  GTG GA    TATTCCAAAAT
                                  ||| ||    ||||||||||
                                  CAC CT    ATAAGGTTTTA
                                    _  TT__
GAM2761  LOC255975 3'  GTGGAAATATTCCAAAAT    63913    A  TTCC
                                  GTG GA    TATTCCAAAAT
                                  ||| ||    ||||||||||
                                  CAC CT    ATAAGGTTTTA
                                    _  TT__
GAM2761  LOC255987 3'  GTGGAAATATTCCAAAAT    63913    A  TTCC
                                  GTG GA    TATTCCAAAAT
                                  ||| ||    ||||||||||
                                  CAC CT    ATAAGGTTTTA
                                    _  TT__
GAM2761  LOC256019 3'  GTGGAAATATTCCAAAAT    63913    A  TTCC
                                  GTG GA    TATTCCAAAAT
                                  ||| ||    ||||||||||
                                  CAC CT    ATAAGGTTTTA
                                    _  TT__
GAM2761  LOC257069 3'  GTGGAAATATTCCAAAAT    63913    A  TTCC
                                  GTG GA    TATTCCAAAAT
                                  ||| ||    ||||||||||
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                                CAC CT    ATAAGGTTTTA
                                  _  TT__
GAM2762 AGRN     3'  GGGGTGGGGATGGGATGGGGGT 63916    AC       ACGC__    C
              GG                   GG  GGTGGGGG     GGGGG GG
                                ||  ||||||||     |||||  ||
                                CC  CCACCCCT     CCCCC CC
                                  __       ACCCTA     A
GAM2762 AQP5     5'  GGAGGTGGATGCGGCGGGGGCG 63917     C     GGAC
              G                    GGA GGTGGG    GCGGGGGCGG
                                ||| ||||||    ||||||||||
                                CCT CCACCT    CGCCCCCGCC
                                  _     ACGC
GAM2762 AR       5'  GGTGGGGGGAGGCGGGGTGG   63918        AC_     GC
                                GGTGGGGGG   GCGGGG  GG
                                ||||||||   ||||||  ||
                                CCACCCCC   CGCCCC  CC
                                     CTC     A_
GAM2762 ARHGEF1   3'  GGGGTGGGGGGTGGAGGGGTGG  63919    AC       ACGC    C
                                GG  GGTGGGGG    GGGGG GG
                                ||  ||||||||    |||||  ||
                                CC  CCACCCCC    TCCCC CC
                                  __       ACC_    A
GAM2762 BMP8     5'  GGCGGCGGGGGCGGGGCG     63920    A       GACGCG
                                GG CGGTGGGG     GGGGCG
                                || ||||||||     ||||||
                                CC GCCGCCCC     CCCCGC
                                  _       G_____
GAM2762 BTG1     5'  GGGGCGGCGTGCGGGGGCG    63921    T  G  AC_
                                GG GG GG   GCGGGGGCG
                                || || ||   |||||||||
                                CC CC CC   CGCCCCCGC
                                  _  G  GCA
GAM2762 C5R1     3'  GGACACGGCTGGGGTGTGGGGG 63922      __   G    ACGC    C
              TGG                    GGAC  GGT GGGG    GGGGG GG
                                ||||  ||| ||||    ||||| ||
                                CCTG  CCG CCCC    CCCCC CC
                                  TG   A    ACA_    A
GAM2762 CACNA1D   5'  GGCGTTGAGGCGGGGGCG    63923      GGG  C
                                GGTG   GA GCGGGGGCG
                                ||||   || |||||||||
                                CCGC   CT CGCCCCCGC
                                  AA_  C
GAM2762 CALM3     3'  GGGGTGGGGGGGTGGGGG     63924    AC       ACGCG    C
                                GG  GGTGGGGG    GGGG G
                                ||  ||||||||    |||| |
                                CC  CCACCCCC    CCCC C
                                  __       CA___    A
GAM2762 CHAT     5'  GGCGTGTCGCAGCGCGGGGGTG 63925    A  _  _ G  GA       C
              G                    GG CG GT G GG  CGCGGGGG GG
                                || || || | ||  |||||||| ||
```

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                                CC GC CA C TC  GCGCCCCC CC
                                 _ A  G G  __       A
GAM2762  CSNK2A1   3'  GGACGGTGGAGGAACAATGGTG 63926           C    G  C
              G                  GGACGGTGGGGGA GCGG GG GG
                                 |||||||||||| |||| || ||
                                 CCTGCCACCTCCT TGTT CC CC
                                        _    A  A
GAM2762  DACH     5'  GGGGTGGGGGGTGGGGCG     63927    AC       ACGCG
                                 GG  GGTGGGGG    GGGGCG
                                 ||  ||||||||    ||||||
                                 CC  CCACCCCC    CCCCGC
                                  __       A____
GAM2762  DIA1     3'  GGCGTGGGGTGCGCGGGGGCGG 63928    A  G    GA
                                 GG CG TGGGG  CGCGGGGGCGG
                                 || || |||||  ||||||||||
                                 CC GC ACCCC  GCGCCCCCGCC
                                  _ _    AC
GAM2762  DMPK     5'  GGAGGTGGGGAAGGGGG     63929     C       ACGC    C
                                 GGA GGTGGGGG   GGGGG G
                                 ||| ||||||||   ||||| |
                                 CCT CCACCCCT   TCCCC C
                                  _      ____    A
GAM2762  DNMT3L   5'  GGCGTGTCCCGCGGGGGCGG   63930      GGGGA
                                 GGTG    CGCGGGGGCGG
                                 ||||    ||||||||||
                                 CCGC    GCGCCCCCGCC
                                   ACAGG
GAM2762  DRIL1    5'  GGTGGGCGGCGGGGGCG     63931       GGAC
                                 GGTGGG   GCGGGGGCG
                                 ||||||   |||||||||
                                 CCACCC   CGCCCCCGC
                                    GC__
GAM2762  DRPLA    3'  GGCACGGTGGGGGGAGGGTGG  63932    _       ACGC    C
                                 GG ACGGTGGGGG   GGGGG GG
                                 || ||||||||||   ||||| ||
                                 CC TGCCACCCCC   CTCCC CC
                                  G        ____    A
GAM2762  EGFL4    3'  GGTGGTGGGGCTGGGGGTGG   63933      _  AC  _    C
                                 GGTGG GGG  GC GGGGG GG
                                 ||||| |||  || ||||| ||
                                 CCACC CCC  CG CCCCC CC
                                   A  __ A    A
GAM2762  FBXL4    5'  GGCCTGGGTGCGGGGGCG    63934     GG   AC
                                 GGT  GGG  GCGGGGGCG
                                 |||  |||  |||||||||
                                 CCG  CCC  CGCCCCCGC
                                  GA  A_
GAM2762  FHL2     5'  GGCGTGGGGCGCGGGGGGCGG  63935     _   A      _
                                 GGTG GGGG CGCGGGGG CGG
                                 |||| |||| |||||||| |||
```

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                                CCGC CCCC GCGCCCCC GCC
                                  A  _      C
GAM2762  G6PD    3'  GGAGGGTGGCCGTGGCGGGGGT 63936    C    GGGAC     C
             GG                   GGA GGTGG    GCGGGGG GG
                                  ||| |||||    ||||||| ||
                                  CCT CCACC    CGCCCCC CC
                                    C    GGCAC      A
GAM2762  GAS7    3'  GGTGGTGCGGGGGCAG      63937      GGGAC
                                  GGTGG    GCGGGGGCGG
                                  |||||    ||||||||||
                                  CCACC    CGCCCCCGTC
                                    A____
GAM2762  GRLF1   3'  GGACGGTGGGGATGAAGCG   63938          ACGCG
                                  GGACGGTGGGGG    GGGGCG
                                  ||||||||||||    ||||||
                                  CCTGCCACCCCT    CTTCGC
                                        A____
GAM2762  HDAC4   3'  GGACGCTGGGGAGGGGCG    63939      G    GACGC
                                  GGACG TGGGG    GGGGGCG
                                  ||||| |||||    |||||||
                                  CCTGC ACCCC    TCCCCGC
                                    G   _____
GAM2762  HOXC4   3'  GGAGGGTGGGGGCATGGGGTGG 63940    C      A  C   GC
                                  GGA GGTGGGGG CG GGGG  GG
                                  ||| |||||||| || ||||  ||
                                  CCT CCACCCCC GT CCCC  CC
                                    C       _ A   A_
GAM2762  HYOU1   3'  GGGGTGGGGTGAGGGGG    63941    AC     GACGC    C
                                  GG  GGTGGGG    GGGGG G
                                  ||  |||||||    ||||| |
                                  CC  CCACCCC    TCCCC C
                                   __      AC___    A
GAM2762  IHH     3'  GGGGTGGGGGACGCTGG     63942    AC         G
                                  GG  GGTGGGGGACGC GG
                                  ||  ||||||||||| ||
                                  CC  CCACCCCCTGCG CC
                                   __          A
GAM2762  IL6R    5'  GGCGGTGGGCGGGCAGGCGG   63943    A    GGGAC   __
                                  GG CGGTGG    GCGGG  GGCGG
                                  || ||||||    |||||  |||||
                                  CC GCCACC    CGCCC  CCGCC
                                   _    _____    GT
GAM2762  IRS2    5'  GGCGGAGGGGGCGCGGGCGGGG 63944    A  T    AC___
             GCGG                   GG CGG GGGGG    GCGGGGGCGG
                                  || ||| |||||    ||||||||||
                                  CC GCC CCCCC    CGCCCCCGCC
                                   _  T    GCGCC
GAM2762  KCNC3   5'  GGACGGGGGGCGGGGC      63945       T   GACGCG
                                  GGACGG GGGG     GGGGC
                                  |||||| ||||     |||||
```

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                                CCTGCC CCCC     CCCCG
                                   _   G_____
GAM2762  KCNC3    3'  GGGGTGGGGGGGCGGTGAGGCGG 63946    AC       A  CG
                                GG  GGTGGGGG CG  GGGGCGG
                                ||  |||||||| ||  |||||||
                                CC  CCACCCCC GC  CTCCGCC
                                 __       C  CA
GAM2762  KPNB1    5'  GGAGGGTGGGGTGGGGGGCGG  63947     C      GACGC
                                GGA GGTGGGG    GGGGGCGG
                                ||| |||||||    ||||||||
                                CCT CCACCCC    CCCCCGCC
                                  C      AC___
GAM2762  LHX5     3'  GGCCGAGCGCGGGGGCG     63948     G   GA
                                GGT GGG  CGCGGGGGCG
                                ||| |||  ||||||||||
                                CCG CTC  GCGCCCCCGC
                                  G  __
GAM2762  LHX5     5'  GGGTGGTGGGGGGCGGGTGG   63949    AC       AC    _
                                GG  GGTGGGGG  GCGGG GG
                                ||  ||||||||  ||||| ||
                                CC  CCACCCCC  CGCCC CC
                                 CA       __    A
GAM2762  LSP1     3'  GGTGGGGAGGGCGGGGGCGG  63950         AC
                                GGTGGGGG  GCGGGGGCGG
                                ||||||||  ||||||||||
                                CCACCCCT  CGCCCCCGCC
                                     CC
GAM2762  MGMT     5'  GGCGGCGGGGGGGGC       63951    A       ACGCGG
                                GG CGGTGGGGG     GGGC
                                || |||||||||     ||||
                                CC GCCGCCCCC     CCCG
                                  _      _______
GAM2762  MSL3L1   5'  CGGTGGGGGAGGGCG       63952          CGCGG
                                CGGTGGGGGA    GGGCG
                                ||||||||||    |||||
                                GCCACCCCCT    CCCGC
                                     ______
GAM2762  MSL3L1   5'  CGGTGGGGGAGGGCG       63952          CGCGG
                                CGGTGGGGGA    GGGCG
                                ||||||||||    |||||
                                GCCACCCCCT    CCCGC
                                     ______
GAM2762  MSL3L1   5'  CGGTGGGGGAGGGCG       63952          CGCGG
                                CGGTGGGGGA    GGGCG
                                ||||||||||    |||||
                                GCCACCCCCT    CCCGC
                                     ______
GAM2762  MSX2     3'  GGTGGGGCGGTGGGGGGCGG  63953         GACGC
                                GGTGGGG    GGGGGCGG
                                |||||||    ||||||||
```

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                                CCACCCC    CCCCCGCC
                                    GCCAC
GAM2762 NFIA    5' GGGTGTGGGGGAGGGGGCG   63954    ACG      CGC
                                GG  GTGGGGGA  GGGGGCG
                                ||  ||||||||  |||||||
                                CC  CACCCCCT  CCCCCGC
                                 CA_      ___
GAM2762 NTSR1   3' AGATGGTGGGAGTGGGGGTGG 63955    C      ACGC    C
                                GGA GGTGGGGGG   GGGGG GG
                                ||| ||||||||   ||||| ||
                                TCT CCACCCTC    CCCCC CC
                                  A      A___    A
GAM2762 PAH     5' GGGTGTGGGGGACGCAGG    63956    ACG
                                GG  GTGGGGGACGCGGG
                                ||  ||||||||||||||
                                CC  CACCCCCTGCGTCC
                                 CA_
GAM2762 PAX5    3' GGATGCTGGGGGACGGTCTCAT 63957    CGG      ____ G
            GG                    GGA  TGGGGGACG   CG GG
                                |||  |||||||||   || ||
                                CCT  ACCCCCTGC   GT CC
                                  ACG       CAGA  A
GAM2762 PRDM2   3' GGAAGGTGGGGAGAGAGGGGTG 63958    C     _ CGC    C
            G                    GGA GGTGGGG GA  GGGGG GG
                                ||| ||||||| ||  ||||| ||
                                CCT CCACCCC CT  TCCCC CC
                                  T     T C__    A
GAM2762 PTBP1   3' GGACAGGACGCGGGGGCG    63959     GGTGG
                                GGAC    GGGACGCGGGGGCG
                                ||||    ||||||||||||||
                                CCTG    TCCTGCGCCCCCGC
                                  _____
GAM2762 PTBP1   3' GGACAGGACGCGGGGGCG    63959     GGTGG
                                GGAC    GGGACGCGGGGGCG
                                ||||    ||||||||||||||
                                CCTG    TCCTGCGCCCCCGC
                                  _____
GAM2762 S100A1  3' GGGGTGGGGGTGGGGG     63960    AC      ACGCG   C
                                GG  GGTGGGGG    GGGG G
                                ||  ||||||||    |||| |
                                CC  CCACCCCC    CCCC C
                                 __      A____   A
GAM2762 SH3GL1  3' GGACGGAGGGGCGGGGCG    63961      T    A GCG
                                GGACGG GGGGG C  GGGGCG
                                |||||| ||||| |  ||||||
                                CCTGCC TCCCC G  CCCCGC
                                  _   _ ___
GAM2762 TFE3    3' GGAGGGTGGGGGAAAAGGCGG 63962    C       CGC
                                GGA GGTGGGGGA  GGGGGCGG
                                ||| |||||||||  ||||||||
```

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                                CCT CCACCCCCT   TTTCCGCC
                                  C       ___
GAM2762 YY1      5'  GGCGGCGGGGGAAGGGGCGG   63964    A       CGC
                                GG CGGTGGGGGA   GGGGGCGG
                                || ||||||||||   ||||||||
                                CC GCCGCCCCCT   TCCCCGCC
                                  _       ____
GAM2762 YY1      5'  GGCGGGGGGAGAGGGGGCGG   63963        ACGC
                                GGTGGGGG    GGGGGCGG
                                ||||||||    ||||||||
                                CCGCCCCC    CCCCCGCC
                                     CTCT
GAM2762 ZFP36L1  3'  GGTGGGGGGGGGTGGGGGGGCGG 63965        ACGC__
                                GGTGGGGG     GGGGGCGG
                                ||||||||     ||||||||
                                CCACCCCC     CCCCCGCC
                                     CCCACC
GAM2762 ACTR1A   3'  GGGGTGGGGGGTGAGGGG     63966    AC      ACGC    C
                                GG  GGTGGGGG    GGGGG G
                                ||  ||||||||    ||||| |
                                CC  CCACCCCC    CTCCC C
                                  __       A___    A
GAM2762 C8orf2   3'  GGGGGGTGGGGGGGTGGGGGGTGG 63967    AC      ACGC    C
                                GG  GGTGGGGG    GGGGG GG
                                ||  ||||||||    ||||| ||
                                CC  CCACCCCC    CCCCC CC
                                  C_       CAC_    A
GAM2762 CACNG4   3'  GGTGGGGGGCGAGGGGGCG    63968        A  C
                                GGTGGGGGG CG GGGGGCG
                                ||||||||| || |||||||
                                CCACCCCC GC CCCCCGC
                                     _ T
GAM2762 CARM1    3'  GGAGGTGGGGGGTTAGGGTGG   63969     C      ACGCG   C
                                GGA GGTGGGGG     GGGG GG
                                ||| ||||||||     |||| ||
                                CCT CCACCCCC     TCCC CC
                                  _       AA___    A
GAM2762 CDK5RAP3 5'  AGAATGGGGGTGCGGGGGTGG  63970    CG      AC      C
                                GGA  GTGGGGG  GCGGGGG GG
                                |||  |||||||  ||||||| ||
                                TCT  TACCCCC  CGCCCCC CC
                                  __       A_      A
GAM2762 CENTA1   3'  GGAGGTGGGGGGGAGGGCG    63971     C      ACGC
                                GGA GGTGGGGG    GGGGGCG
                                ||| ||||||||    |||||||
                                CCT CCACCCCC    CTCCCGC
                                  _       _____
GAM2762 CSEN     3'  GATGGAGGTTTCTTGGGGGTGG 63972        ACGC__    C
                                GGTGGGGG     GGGGG GG
                                ||||||||     ||||| ||
```

```
                                CTACCTCC     CCCCC CC
                                    AAAGAA    A
GAM2762  CXYorf1   3'  GGTGGTGGGGGGCGGTGGGGGTG 63973    AC      A C_    C
             G                   GG  GGTGGGGG CG  GGGGG GG
                                 ||  |||||||| ||  ||||| ||
                                 CC  CCACCCCC GC  CCCCC CC
                                  A_       _ CA    A
GAM2762  CXYorf1   3'  GGGGTGGTGGTGGGGGGCG    63974    AC    G  ACGC
                                 GG  GGTGG GG    GGGGGCG
                                 ||  ||||| ||    |||||||
                                 CC  CCACC CC    CCCCCGC
                                  __     A  A___
GAM2762  CYP2S1    3'  GGACTGTGCCTCTGTGGGGGCG 63975      G   GGGGACGC
             G                   GGAC GTG       GGGGGCGG
                                 ||||  |||       ||||||||
                                 CCTG CAC       CCCCCGCC
                                   A   GGAGACA_
GAM2762  DMWD      3'  GGAGGTGGGGAAGGGGG     63929     C       ACGC    C
                                 GGA GGTGGGGG    GGGGG G
                                 |||  ||||||||    ||||| |
                                 CCT CCACCCCT    TCCCC C
                                  _       _____     A
GAM2762  FLJ12242  5'  GGCGCTGGGGGCGGGCG     63976    A  G     A GCGG
                                 GG CG TGGGGG C    GGGCG
                                 || || |||||| |    |||||
                                 CC GC ACCCCC G    CCCGC
                                  _  G     _ _____
GAM2762  FLJ13063  5'  GGCGGGGCCCGACGCGGGGGCG 63977         ___
             G                   GGTGGGGG   GACGCGGGGGCGG
                                 |||||||   ||||||||||||||
                                 CCGCCCC   CTGCGCCCCCGCC
                                     GGG
GAM2762  FLJ14280  3'  GGAGCGGTGGGAAAGGGGGGTG 63978     _      GG CGC     C
             G                   GGA CGGTGGG  A   GGGGG GG
                                 |||  |||||||  |   ||||| ||
                                 CCT GCCACCC  T   CCCCC CC
                                   C       TT C__     A
GAM2762  FLJ14708  3'  GGACGGGGGCCCATGGGGGTGG 63979       T   GGA  C     C
                                 GGACGG GGG   CG GGGGG GG
                                 ||||||  |||   ||  ||||| ||
                                 CCTGCC CCC   GT CCCCC CC
                                     _   GG_  A     A
GAM2762  FLJ14950  3'  GGTGGGGGGTGGGGTGGGGGGTGG 63980         ACGC__     C
                                 GGTGGGGGG      GGGGG GG
                                 ||||||||       ||||| ||
                                 CCACCCCCC      CCCCC CC
                                      ACCCCA     A
GAM2762  FLJ20359  3'  GGGGTGGGGGGTGAGGGG     63966    AC       ACGC    C
                                 GG  GGTGGGGG    GGGGG G
                                 ||  ||||||||    ||||| |
```

```
                                CC  CCACCCCC    CTCCC C
                                 __       A___     A
GAM2762  FLJ21916  5'  GGACCTCGAGGGCGTGGGGGCG 63981      GG     A  C
              G                   GGAC  TGGGGG CG GGGGGCGG
                                  ||||  |||||| || ||||||||
                                  CCTG  GCTCCC GC CCCCCGCC
                                    GA     _  A
GAM2762  HCGIV.9   5'  GGCGGGGCTGGCCGCGGGGGCG 63982        GA___
              G                   GGTGGGG    CGCGGGGGCGG
                                  |||||||    ||||||||||
                                  CCGCCCC    GCGCCCCCGCC
                                      GACCG
GAM2762  ISYNA1    3'  GGTCGTGGGGGGCAGCGG    63983    A  G     AC    G
                                  GG CG TGGGGG  GCGG GG
                                  || || ||||||  ||||| ||
                                  CC GC ACCCCC  CGTC CC
                                   A  _     __    G
GAM2762  KIAA0256  3'  GGGTGGGGGGGGACAGTTGGGGG 63984    AC  T      C__     C
              TGG                   GG  GG GGGGGACG   GGGGG GG
                                  ||  || ||||||||   ||||| ||
                                  CC  CC CCCCCTGT   CCCCC CC
                                   CA  _       CAA     A
GAM2762  KIAA0339  3'  GGGGTGGGGGGCGGAGGGCGG   63985    AC       A  C
                                  GG  GGTGGGGG CG GGGGGCGG
                                  ||  |||||||| || ||||||||
                                  CC  CCACCCCC GC CTCCCGCC
                                   __       _ _
GAM2762  KIAA0545  3'  GGGGTGGGGGGACGGGTGG    63986    AC         C  _
                                  GG  GGTGGGGGGACG GG GG
                                  ||  |||||||||||| || ||
                                  CC  CCACCCCCTGC CC CC
                                   __         _  A
GAM2762  KIAA0616  3'  GGAGGTGGACAACCGGGGGCGG 63987     C     G   G
                                  GGA GGTGGG GAC CGGGGGCGG
                                  ||| |||||| ||| |||||||||
                                  CCT CCACCT TTG GCCCCCGCC
                                    _     G   _
GAM2762  KIAA0678  3'  GGATGGTGGGGGGGAGGAG    63988     C       ACGC    GC
                                  GGA GGTGGGGGG    GGGG  G
                                  ||| ||||||||    ||||  |
                                  CCT CCACCCCC    CTCC  C
                                    A       _____    TA
GAM2762  KIAA1138  3'  GGACGTGAGCGGGGGG       63989       G   GGGAC
                                  GGACG TGG     GCGGGGGG
                                  ||||| |||     |||||||
                                  CCTGC ACT     CGCCCCC
                                     _  ______
GAM2762  KIAA1205  3'  GGTAGTGGGAGCAGGGGGTGG  63990       _    C  _     C
                                  GGTGG GGGA GC GGGGG GG
                                  ||||| |||| || ||||| ||
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                                CCATC CCCT CG CCCCC CC
                                  A   _ T   A
GAM2762 KIAA1237 3' GGATGGTGAGGGGTGTGCCAGG 63991    C     AC__ G
                                GGA GGTGGGGGG   GC GGG
                                ||| ||||||||   || |||
                                CCT CCACTCCC   CG TCC
                                 A      CACA  G
GAM2762 KIAA1441 3' GGCGGGGGCGGGGGC      63992      GAC
                                GGTGGGG  GCGGGGGC
                                |||||||  ||||||||
                                CCGCCCC  CGCCCCCG
                                   ___
GAM2762 KIAA1453 3' GGATGGTGAGGGGGGAGGTGG 63993    C     ACGC   C
                                GGA GGTGGGGGG   GGGGG GG
                                ||| ||||||||   ||||| ||
                                CCT CCACTCCC   CCTCC CC
                                 A      C___   A
GAM2762 KIAA1580 5' GGCGGGGGCGGGGGC      63992      GAC
                                GGTGGGG  GCGGGGGC
                                |||||||  ||||||||
                                CCGCCCC  CGCCCCCG
                                   ___
GAM2762 KIAA1580 5' GGCGGGGGCGGGGGC      63992      GAC
                                GGTGGGG  GCGGGGGC
                                |||||||  ||||||||
                                CCGCCCC  CGCCCCCG
                                   ___
GAM2762 KIAA1706 3' GGCGGGGGAAGGGGGCG    63994       CGC
                                GGTGGGGGA  GGGGGCG
                                |||||||||  |||||||
                                CCGCCCCCT  CCCCCGC
                                     T__
GAM2762 KIAA1775 3' GGGTGGTGGGGGTCAGGGGCGG 63995   AC     ACG
                                GG GGTGGGGG  CGGGGGCGG
                                ||  ||||||||  |||||||||
                                CC  CCACCCCC  GTCCCCGCC
                                 CA      A__
GAM2762 KIAA1817 3' GGGGTGGGGGGCGTGGGGG   63996   AC     A  C
                                GG  GGTGGGGG CG GGGGG
                                ||  |||||||| || |||||
                                CC  CCACCCCC GC CCCCC
                                 __      C  A
GAM2762 KIAA1819 5' GGCGGTGGAGGGGCTGTAGTGG 63997   A      AC  GGG  C
                                GG CGGTGGGGG  GC   GG GG
                                || |||||||||  ||   || ||
                                CC GCCACCTCC  CG   TC CC
                                 _      C_  ACA  A
GAM2762 KIAA1866 3' GGGAGTGGTGGGTGTGGGGGTG 63998   AC   _  ACGC   C
          G                      GG  GGTGG GGG   GGGGG GG
                                ||  ||||| |||   ||||| ||
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                                CC  TCACC CCC    CCCCC CC
                                 C_     A   ACA_     A
GAM2762 KIAA1878 3' GGCAGTGAGTGGGGGCG     63999    A      GGACGC
                                GG CGGTGGG     GGGGGCG
                                || |||||||     |||||||
                                CC GTCACTC     CCCCCGC
                                 _      A_____
GAM2762 LMOD1    3' GGCAGTGGGGCTGGGGG     64000    A      GACGCG    C
                                GG CGGTGGGG     GGGG G
                                || ||||||||     |||| |
                                CC GTCACCCC     CCCC C
                                 _      GA____    A
GAM2762 MGC10924 3' GGGGGTGGGGGGTGGGGGTGG   64001    AC       ACGC    C
                                GG  GGTGGGGG    GGGGG GG
                                ||  ||||||||    ||||| ||
                                CC  CCACCCCC    CCCCC CC
                                 C_      A___     A
GAM2762 MGC2749  3' AGTGGGTGCGGGGGTGG     64002       GGAC      C
                                GGTGGG    GCGGGGG GG
                                ||||||    ||||||| ||
                                TCACCC    CGCCCCC CC
                                   A___      A
GAM2762 MGC2865  3' GGAGGTGGGGGGGCGAGGGGCGG 64003     C       AC  _
                                GGA GGTGGGGG  GCG GGGGCGG
                                ||| ||||||||  ||| |||||||
                                CCT CCACCCCC  CGC CCCCGCC
                                 _      __  T
GAM2762 MICAL    5' GGCGGGGGCGGGGGC       63992        GAC
                                GGTGGGG   GCGGGGGC
                                |||||||   ||||||||
                                CCGCCCC   CGCCCCCG
                                   ___
GAM2762 MICAL    5' GGCGGGGGCGGGGGC       63992        GAC
                                GGTGGGG   GCGGGGGC
                                |||||||   ||||||||
                                CCGCCCC   CGCCCCCG
                                   ___
GAM2762 NPTXR    3' GGAGGTGGGGGTCTGGGGTGG  64004     C      ACGCG   C
                                GGA GGTGGGGG    GGGG GG
                                ||| ||||||||    |||| ||
                                CCT CCACCCCC    CCCC CC
                                 _      AGA__    A
GAM2762 NPTXR    3' GGAGGTGGGGGGTCTGGGGTGG  64004     C      ACGCG   C
                                GGA GGTGGGGG    GGGG GG
                                ||| ||||||||    |||| ||
                                CCT CCACCCCC    CCCC CC
                                 _      AGA__    A
GAM2762 ODC-p    3' GGTGGAGCGCGGGGGGG      64005        GA       C
                                GGTGGGG  CGCGGGGG G
                                |||||||  |||||||| |
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                                CCACCTC  GCGCCCCC C
                                   __       A
GAM2762  OLFM2    3'  GGGGTGGGGGGTGGGGGG     64006    AC       ACGC    C
                                GG  GGTGGGGG    GGGGG G
                                ||  ||||||||    ||||| |
                                CC  CCACCCCC    CCCCC C
                                 __       A___     A
GAM2762  OSBP2    5'  GGCGGGGGGGCAGGCCGGGGGGCG 64007         A ___
              G                  GGTGGGGG CG   CGGGGGCGG
                                 |||||||| ||   |||||||||
                                 CCGCCCCC GT   GCCCCCGCC
                                     C  CCG
GAM2762  PDK2     3'  GGATGGTGAGGGGCACCACGGT 64008     C       A___    _
              GG                   GGA GGTGGGGG    CGCGG GG
                                 ||| ||||||||    ||||| ||
                                 CCT CCACTCCC    GTGCC CC
                                   A       CGTG    A
GAM2762  PPP1R14A 5'  GGCGGGGCTAGCCGGGGGCGG  64009       GAC  _
                                 GGTGGGG   GC GGGGGCGG
                                 |||||||   || ||||||||
                                 CCGCCCC   CG CCCCCGCC
                                     GAT  G
GAM2762  PRKWNK2  5'  CGCTGCGGGCGCGGGGGCGG   64010    G  G   A
                                 CG TG GGG CGCGGGGGCGG
                                 || || ||| ||||||||||
                                 GC AC CCC GCGCCCCCGCC
                                  G  G  _
GAM2762  RAGD     5'  GGACGGCGGGGGTCCCGGGGTG 64011           ACG    GC
              G                   GGACGGTGGGGG   CGGGG  GG
                                 ||||||||||||   |||||  ||
                                 CCTGCCGCCCCC   GCCCC  CC
                                        AGG    A_
GAM2762  SBBI54   3'  GGTGTGGGGAGGGGGCG     64012     _    CGC
                                 GGTG GGGGA   GGGGGCG
                                 ||||  |||||   |||||||
                                 CCAC CCCCT   CCCCCGC
                                   A    ___
GAM2762  SCAMP5   3'  GGCAGGTGGAGGGTGGGGGTGG 64013    AC       ACGC    C
                                 GG  GGTGGGGG    GGGGG GG
                                 ||  ||||||||    ||||| ||
                                 CC  CCACCTCC    CCCCC CC
                                  GT       CA__     A
GAM2762  SCOP     5'  GGTGGGCGGCGGGGGGCG     63931       GGAC
                                 GGTGGG    GCGGGGGCG
                                 ||||||    |||||||||
                                 CCACCC    CGCCCCCGC
                                    GC__
GAM2762  SEMA4G   5'  GGCGGTGGGGGCGGTGGGGGTG 64014    A       A  C_    C
              G                   GG CGGTGGGGG CG  GGGGG GG
                                 || |||||||| ||  ||||| ||
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                                CC GCCACCCCC GC  CCCCC CC
                                 _       _ CA    A
GAM2762  SMURF2   5'  GGCGGCGGGGGCGGCGGGCGG  64015    A      GAC   _
                                GG CGGTGGGG   GCGG GGGCGG
                                || ||||||||   |||| ||||||
                                CC GCCGCCCC   CGCC CCCGCC
                                 _      ____   G
GAM2762  STX5A    3'  GGGTGGTGGGGGGGAGGACAGGG 64016    AC      AC__     GC
            TGG                   GG  GGTGGGGGG   GCGGGG  GG
                                || ||||||||   ||||||  ||
                                CC  CCACCCCC   TGTCCC  CC
                                 CA      CTCC     A_
GAM2762  T1A-2    5'  GACGGTGGGGGGGGCCGGAGGGG 64017          A__  C    C
            TGG                   GACGGTGGGGG   CG GGGGG GG
                                ||||||||||   || ||||| ||
                                CTGCCACCCCC   GC TCCCC CC
                                       CCG  C    A
GAM2762  TEB4     3'  GGTGTGGGGTGGGGGCG     64018     _   ACGC
                                GGTG GGGG   GGGGGCG
                                |||| ||||   |||||||
                                CCAC CCCC   CCCCCGC
                                  A   A___
GAM2762  UBP1     3'  GGTGGGGGGTTAGGGTGGGGGT 64019        ACGC____    C
            GG                    GGTGGGGG       GGGGG GG
                                ||||||||       ||||| ||
                                CCACCCCC       CCCCC CC
                                     CAATCCCA    A
GAM2762  UBP1     3'  GGGGTGGGGGGGTTAGGGTGG   64020    AC      ACGCG   C
                                GG  GGTGGGGG    GGGG GG
                                ||  ||||||||    |||| ||
                                CC  CCACCCCC    TCCC CC
                                 __       CAA__   A
GAM2762  LOC116113 3'  GGCGGCGGGGGGGAGAGGCGG   49978    A       ACGC
                                GG CGGTGGGGG   GGGGGCGG
                                || |||||||||   ||||||||
                                CC GCCGCCCCC   TCTCCGCC
                                 _       C___
GAM2762  LOC123096 5'  GGATGGTGGGGATGGCGG    64021     C       AC
                                GGA GGTGGGGG  GCGG
                                ||| ||||||||  ||||
                                CCT CCACCCCT  CGCC
                                  A       AC
GAM2762  LOC124987 5'  GGGCGGTGGGGCCAATGGGGCG 64022    A       GA  CG
            G                     GG CGGTGGGG  CG  GGGGCGG
                                || ||||||||  ||  |||||||
                                CC GCCACCCC  GT  CCCCGCC
                                 C       G_  TA
GAM2762  LOC130497 3'  GGGGTGGGGGCAGGGGCG    64023    AC      GAC
                                GG  GGTGGGG   GCGGGGGCG
                                ||  |||||||   |||||||||
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                                CC  CCACCCC   CGTCCCCGC
                                 __     ____
GAM2762  LOC130644 5'  GACGGTGGGGGGACCGCATGGTG 64024           _   GG  C
                  G                 GACGGTGGGGGGAC GCG  GG GG
                                    |||||||||||| |||  || ||
                                    CTGCCACCCCCTG CGT  CC CC
                                           G   A_  A
GAM2762  LOC136555 5'  GGCGGTGGGGACCGGGGCGG   64025    A       GAC  G
                                    GG CGGTGGGG   GC GGGGCGG
                                    || ||||||||   || |||||||
                                    CC GCCACCCC   TG CCCCGCC
                                     _      ____ G
GAM2762  LOC147160 5'  GGACGTGGGTGCGGGGGCGG   64026      G    GGAC
                                    GGACG TGGG    GCGGGGGCGG
                                    ||||| ||||    ||||||||||
                                    CCTGC ACCC    CGCCCCCGCC
                                      _    A____
GAM2762  LOC151361 3'  GGTGGTGGGGAGATGGGGTGG  64027    AC       ACGCG    C
                                    GG  GGTGGGGG     GGGG GG
                                    ||  ||||||||     |||| ||
                                    CC  CCACCCCT     CCCC CC
                                     A_       CTA__    A
GAM2762  LOC151521 3'  GGAGTGGAAGTGTGGGGGTGG  64028     CG      ACGC     C
                                    GGA  GTGGGGG    GGGGG GG
                                    |||  |||||||    ||||| ||
                                    CCT  CACCTTC    CCCCC CC
                                      __       ACA_     A
GAM2762  LOC151602 3'  GGGGTGGGCGCGGGGGCG    64029    T  _   A
                                    GG GG GGG CGCGGGGGCG
                                    || || ||| ||||||||||
                                    CC CC CCC GCGCCCCCGC
                                     _ A   _
GAM2762  LOC153260 5'  GGCGCGTGGGGGACGCGG     64030     A  _
                                    GG CG GTGGGGGACGCGG
                                    || || ||||||||||||
                                    CC GC CACCCCCTGCGCC
                                     _ G
GAM2762  LOC153525 5'  GGGGGTGGGGGGTGGGGGTGG   64001    AC       ACGC     C
                                    GG  GGTGGGGG    GGGGG GG
                                    ||  ||||||||    ||||| ||
                                    CC  CCACCCCC    CCCCC CC
                                     C_       A___     A
GAM2762  LOC155060 5'  GACGGTGGCTGGCGGGGGGTGG  64031          GGGAC       C
                                    GACGGTGG     GCGGGGG GG
                                    ||||||||     ||||||| ||
                                    CTGCCACC     CGCCCCC CC
                                         GAC__       A
GAM2762  LOC157226 5'  GGCGGTGGGGGGGAAAGGCGGGG 64032    A        AC___
                  GCGG                   GG CGGTGGGGGG     GCGGGGGCGG
                                    || |||||||||     ||||||||||
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                                CC GCCACCCCC    CGCCCCCGCC
                                 _       CTTTC
GAM2762  LOC157931 3'  GGGTGATGGGGGATGGTGG   64033    AC       CGC  _
                                GG  GGTGGGGGA   GG GG
                                ||  |||||||||   || ||
                                CC  CTACCCCCT   CC CC
                                 CA       A__  A
GAM2762  LOC159090 5'  GGCGGGGGGCTGGGGGGCG     64034        ACGC
                                GGTGGGGGG    GGGGGGCG
                                ||||||||    |||||||
                                CCGCCCCC    CCCCCGC
                                     GA__
GAM2762  LOC164537 5'  GGCGGTCGGGGTCAGGGGGCGG 64036    A    G    A  C
                                GG CGGT GGGG CG GGGGGCGG
                                || |||| |||| || ||||||||
                                CC GCCA CCCC GT CCCCCGCC
                                 _   G    A  _
GAM2762  LOC164537 5'  GGGGTGGGGGGCCCGAGGGGCGG 64035    AC       A_  C
                                GG  GGTGGGGG  CG GGGGGCGG
                                ||  ||||||||  || ||||||||
                                CC  CCACCCCC  GC TCCCCGCC
                                 __       GG  _
GAM2762  LOC165476 5'  GGTGGCTGGGCGGGGGCG    64037      G_  AC
                                GGTGG  GG  GCGGGGGCG
                                |||||  ||  |||||||||
                                CCACC  CC  CGCCCCCGC
                                   GA  __
GAM2762  LOC166879 5'  GGCGGTCCGCGTGCGGGGGCGG 64038      GGGAC__
                                GGTGG      GCGGGGGCGG
                                |||||      ||||||||||
                                CCGCC      CGCCCCCGCC
                                   AGGCGCA
GAM2762  LOC200093 3'  GGGGTGGTGGTGGGGGCG    63974    AC    G  ACGC
                                GG  GGTGG GG    GGGGGCG
                                ||  ||||| ||    |||||||
                                CC  CCACC CC    CCCCCGC
                                 __     A  A___
GAM2762  LOC200093 3'  GGTGGTGGGGGCGGTGGGGGTG 63973    AC       A  C_    C
            G                    GG  GGTGGGGG CG  GGGGG GG
                                ||  |||||||| ||  ||||| ||
                                CC  CCACCCCC GC  CCCCC CC
                                 A_       _ CA    A
GAM2762  LOC219920 5'  GATGAGTGCCGCGGGGGTGG   64039       GGA       C
                                GGTGGG   CGCGGGGG GG
                                ||||||   |||||||| ||
                                CTACTC   GCGCCCCC CC
                                   ACG       A
GAM2762  LOC221415 5'  GGGGTGAGGGGTGTGGGGGTGG 64040    AC       ACGC    C
                                GG  GGTGGGGG    GGGGG GG
                                ||  ||||||||    ||||| ||
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                                CC  CCACTCCC    CCCCC CC
                                 __       CACA    A
GAM2762  LOC221463 3'  AGACGGTGGGGGGCGGGGGGTGG 64041          A  C    C
                                GGACGGTGGGGG CG GGGGG GG
                                |||||||||||| || ||||| ||
                                TCTGCCACCCCC GC CCCCC CC
                                       _ _    A
GAM2762  LOC221712 5'  GGCAGGTGGGGGGATGGTGG   64042    AC       CGC  _
                                GG  GGTGGGGGGA   GG GG
                                ||  |||||||||   || ||
                                CC  CCACCCCCT   CC CC
                                 GT       A__  A
GAM2762  LOC253980 3'  GGATGGTGGGGAGGAGGGGGCG 64043     C       ACGC
            G                    GGA GGTGGGGGG    GGGGGCGG
                                ||| ||||||||    ||||||||
                                CCT CCACCCCT    CCCCCGCC
                                  A       CCT_
GAM2762  LOC254245 5'  GGGGGTGGGGGGGCGCCGGCGG  64044    AC       A   GGG
                                GG  GGTGGGGG CGC   GGCGG
                                ||  |||||||| |||   |||||
                                CC  CCACCCCC GCG   CCGCC
                                 C_       C   G__
GAM2762  LOC255941 5'  GGCCGTGGGGGGATGGGGGCGG  64045    ACG      CGC
                                GG   GTGGGGGA   GGGGGCGG
                                ||   ||||||||   ||||||||
                                CC   CACCCCCT   CCCCCGCC
                                 GG_       A__
GAM2762  LOC256848 5'  GGGTGGTGGGGGGATTCCAGG   64046    AC       CG_
                                GG  GGTGGGGGGA   CGGG
                                ||  |||||||||   ||||
                                CC  CCACCCCCT   GTCC
                                 CA        AAG
GAM2762  LOC57115  3'  GGGTGGTGGGGGGCTGCCAGG   64047    AC       AC  G
                                GG  GGTGGGGGG  GC GGG
                                ||  ||||||||  || |||
                                CC  CCACCCCC  CG TCC
                                 CA       GA  G
GAM2762  LOC89944  3'  GGCGTGGGGGGGTGGGGGGCGG  64048    A  G     ACGC
                                GG CG TGGGGG    GGGGGCGG
                                || || ||||||    ||||||||
                                CC GC ACCCCC    CCCCCGCC
                                  _ _      CAC_
GAM2762  LOC91040  3'  GGGGTGGTGGTGGGGGGCG    63974    AC    G  ACGC
                                GG  GGTGG GG    GGGGGCG
                                ||  ||||| ||    |||||||
                                CC  CCACC CC    CCCCCGC
                                 __     A  A____
GAM2762  LOC91040  3'  GGTGGTGGGGGGCGGTGGGGGTG 63973    AC       A  C_    C
            G                    GG  GGTGGGGG CG  GGGGG GG
                                ||  |||||||| ||  ||||| ||
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                                CC  CCACCCCC GC  CCCCC CC
                                 A_      _ CA    A
GAM2762 LOC91272 5' GGCGGTGGTGGGGGGCG     64049    A    GGGACGC
                                GG CGGTGG      GGGGGCG
                                || ||||||      |||||||
                                CC GCCACC      CCCCCGC
                                 _     A_______
GAM2762 LOC91813 5' GGGGGTGGGGGTGGGGGTGG  64001    AC      ACGC    C
                                GG  GGTGGGGG   GGGGG GG
                                ||  ||||||||   ||||| ||
                                CC  CCACCCCC   CCCCC CC
                                 C_      A___    A
GAM2762 LOC92154 3' GGATGGTGTGGAGGGGGCG   64050    C   GG   CGC
                                GGA GGTG  GGA   GGGGGCG
                                ||| ||||  |||   |||||||
                                CCT CCAC  CCT   CCCCCGC
                                  A   A_  ___
GAM2762 LOC92689 3' GGGGTGGGGGGATGGTTTCGG  64051    AC      CGC  GGG
                                GG  GGTGGGGGA  GG   CGG
                                ||  |||||||||  ||   |||
                                CC  CCACCCCCT  CC   GCC
                                 __       A__  AAA
GAM2763 DDX9    3' CTATTACAAGTAGTATCA    64054    AG   _
                                CTA  TATA GTAGTATCA
                                |||  |||| |||||||||
                                GAT  ATGT CATCATAGT
                                  A_   T
GAM2763 SYT5    5' TCATGCTGGGAGTTGTAGTATC 64055     A  A__   ATA
           A                     TCAT CT   AGT   GTAGTATCA
                                ||||  ||   |||   |||||||||
                                AGTA GA   TCA   CATCATAGT
                                  C  CCC   A__
GAM2763 BIRC1   3' TACCAACTTATAGTAGTATCA  64056      G_
                                TACTAA  TATAGTAGTATCA
                                ||||||  ||||||||||||
                                ATGGTT  ATATCATCATAGT
                                   GA
GAM2763 FLJ11996 3' ATCATACTAAGTATAGTA    64057
                                ATCATACTAAGTATAGTA
                                ||||||||||||||||||
                                TAGTATGATTCATATCAT

GAM2763 IFI44   5' TACTGTCTGTAGTATCA     64058     AA  ATA
                                TACT  GT   GTAGTATCA
                                ||||  ||   |||||||||
                                ATGA  CA   CATCATAGT
                                  __  GA_
GAM2763 STIM2   3' ATCTATTAAGTATATAAATATC 64059     A  C      GT
           A                     ATC TA TAAGTATA  AGTATCA
                                ||| || ||||||||  |||||||
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                                TAG AT ATTCATAT  TTATAGT
                                  _ A       AT
GAM2763  LOC200059 3'  ATCATACAAGTATAAAGT    64060        T       T
                                ATCATAC AAGTATAG AGT
                                ||||||| |||||||| |||
                                TAGTATG TTCATATT TCA
                                     _       _
GAM2763  LOC92078  5'  TCATTATGGTTAGTAGTATCA  64061      ACTAA  A
                                TCAT    GT TAGTAGTATCA
                                ||||    || ||||||||||
                                AGTA    CA ATCATCATAGT
                                  ATAC_ _
GAM2764  HEMK      3'  TTAGGTGATTAAGACACT    64064         CAAAACC  T
                                TTAGGTGAT      GG CATT
                                |||||||||      || ||||
                                AATCCACTA      TC GTGA
                                     AT_____  T
GAM2765  SERPINB6  5'  TGGCAGACCTCCAAGCTTGTTG 64067       ATA  AGATGA
           T                     TGGCA  CT     CTTGTTGT
                                |||||  ||     ||||||||
                                ACCGT  GA     GAACAACA
                                   CTG  GGTTC_
GAM2765  CDW92     3'  TGGTGATACTAGATATTAGATG 64068     CA         ACTTGT
           T                     TGG  ATACTAGATG     TGT
                                |||  ||||||||||     |||
                                ACC  TATGATCTAT     ACA
                                  AC         AATCT_
GAM2765  MGC4825   3'  GGCAAACACGATGGCTTGTTGT 64069       TACTA    A
                                GGCAA     GATG CTTGTTGT
                                |||||     |||| ||||||||
                                CCGTT     CTAC GAACAACA
                                   TGTG_    C
GAM2765  LOC158427 3'  TGGCAGTGCTGGATGACCT    64070       ATA  A
                                TGGCA   CT GATGACTT
                                |||||   || ||||||||
                                ACCGT   GA CTACTGGA
                                   CAC  C
GAM2766  KIAA1345  3'  TAAGTGTAGTTTTTACAT    64073         ACC
                                TAAGTGTAG   TTTACGT
                                |||||||||   |||||||
                                ATTCACATC   AAATGTA
                                     AA_
GAM2766  LOC115294 3'  TAAGTATAGACTTTGTTTTAAT 64074           C   ACG
           A                     TAAGTGTAGAC TTT   TTAATA
                                |||||||||| |||   ||||||
                                ATTCATATCTG AAA   AATTAT
                                     _  CAA
GAM2767  ARHGAP6   5'  CTGCGGGGTGCTGGGTGTGGAG 64077          ATAGATAAA_
           AAG                     CTGCGGGGTG        AGAAG
                                |||||||||         |||||
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                                GACGCCCCAC        TCTTC
                                     GACCCACACC
GAM2767 ILK      5' CTGTGGAGTGATCCAGGGAAG 64078    C      AGATAAAA
                                CTG GGGGTGAT      GAAG
                                ||| ||||||||      ||||
                                GAC CCTCACTA      CTTC
                                  A       GGTCC___
GAM2767 UBE2B    5' GCGGGGTGGAGAAAGA     64079       AT   TAA
                                GCGGGGTG  AGA   AAGA
                                ||||||||  |||   ||||
                                CGCCCCAC  TCT   TTCT
                                     C_   ___
GAM2767 ATP6V0A1 3' CGGGGTGACAAGGAGGAAG   64080         ATAAAA
                                CGGGGTGATAG     GAAG
                                ||||||||||      ||||
                                GCCCCACTGTT     CTTC
                                      CCTC__
GAM2767 C20orf52 5' CTGCGGGGGATAGGAAAG    64081       T    ATA
                                CTGCGGGG GATAG   AAAG
                                |||||||| |||||   ||||
                                GACGCCCC CTATC   TTTC
                                     _    C__
GAM2767 CBX6     3' TGCAGGGTGAGAACAAAGA   64082        TA  TA
                                TGCGGGGTGA  GA  AAAGA
                                ||||||||||  ||  |||||
                                ACGTCCCACT  CT  TTTCT
                                      __  TG
GAM2767 DKFZP434N014 3' CTGGGGGTGCAGAGGGAA    64083    C     A    TAAAA
                                CTG GGGGTG TAGA     GAA
                                ||| |||||| ||||     |||
                                GAC CCCCAC GTCT     CTT
                                  _     _    CC___
GAM2767 FLJ10724 3' CTGCAGGATGTGATGAAG    64084        ATA   AAAA
                                CTGCGGGGTG   GAT    GAAG
                                ||||||||||   |||    ||||
                                GACGTCCTAC   CTA    CTTC
                                      A__   _____
GAM2767 FLJ14721 3' CTGCCAGCTTAGATAAAGGAAG 64085     G  GTGA      A
                                CTGC GG    TAGATAAA GAAG
                                |||| ||    |||||||| ||||
                                GACG TC    ATCTATTT CTTC
                                   G  GA__       C
GAM2767 FLJ20257 5' CTGCAGAGCAGATGGAAG    64086       GAT    AA
                                CTGCGGGGT   AGAT  AAG
                                |||||||||   ||||  |||
                                GACGTCTCG   TCTA  TTC
                                      ___    CC
GAM2767 KIAA0476 5' GCGGGGCGCAGTGGAAG     64087       A   ATAAAA
                                GCGGGGTG TAG     GAAG
                                |||||||| |||     ||||
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                                CGCCCCGC GTC     CTTC
                                     _  AC____
GAM2767  PEX12    5'  CTGTGGGGGACAGGTATGGGGG 64088    C   T    A  AAA__
             AAG                   CTG GGGG GATAG TA    GAAG
                                ||| |||| ||||| ||    ||||
                                GAC CCCC CTGTC AT    CTTC
                                  A   _    C  ACCCC
GAM2767  LOC132671 5'  CCGTGGGGTGATATGGCGGGAA 64089    C       GATAAAA
             G                   CTG GGGGTGATA      GAAG
                                ||| |||||||||      ||||
                                GGC CCCCACTAT      CTTC
                                  A       ACCGCC_
GAM2767  LOC221922 5'  TGCGGGGTGGACGGAGA    64090        ATA   AAA
                                TGCGGGGTG   GAT   AGA
                                |||||||||   |||   |||
                                ACGCCCCAC   CTG   TCT
                                     ____  CC_
GAM2767  LOC254085 5'  CTGCAGGGGGGGTAGGAGAA   64091       TGA   ATAAA
                                CTGCGGGG   TAG    AGAA
                                ||||||||   |||    ||||
                                GACGTCCC   ATC    TCTT
                                     CCC   C____
GAM2767  LOC255040 3'  TGCGGGGTGTGAGCGCCGAAG  64092        AT  ATAAAA
                                TGCGGGGTG  AG     GAAG
                                |||||||||  ||     ||||
                                ACGCCCCAC  TC     CTTC
                                     AC  GCGG__
GAM2767  LOC255041 3'  TGCGGGGTGTGAGCGCCGAAG  64092        AT  ATAAAA
                                TGCGGGGTG  AG     GAAG
                                |||||||||  ||     ||||
                                ACGCCCCAC  TC     CTTC
                                     AC  GCGG__
GAM2768  PIK3R1   3'  TGTGAGTGGACGTGCCTT    64095     C   A  GT
                                TGTG AGT GA  TGTGCCTT
                                |||| ||| ||  ||||||||
                                ACAC TCA CT  GCACGGAA
                                  _   C  __
GAM2768  CSR1     3'  TGTGCAGAGAGAACCTTC    64096       T   TTGT
                                TGTGCAG AGAG    GCCTTC
                                ||||||| ||||    ||||||
                                ACACGTC TCTC    TGGAAG
                                     _    T___
GAM2768  DKFZP586G1122 3'  TGTGCAGTGGAGGTGACT    64097       A   TT   C
                                TGTGCAGT GAG  GTG CT
                                |||||||| |||  ||| ||
                                ACACGTCA CTC  CAC GA
                                     C   __   T
GAM2768  FLJ10737  3'  TGTGGTGAGTGCCTTC     64098     CA  A   TGT
                                TGTG  GT GAGT   GCCTTC
                                ||||  || ||||   ||||||
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                                ACAC  CA CTCA   CGGAAG
                                  __ _   ____
GAM2768 JM11     3'  TGTGCAGTAGAGTGACCCT   64099          T T
                                TGTGCAGTAGAGT G GCCTT
                                |||||||||||| | |||||
                                ACACGTCATCTCA C TGGGA
                                    _ _
GAM2768 KIAA0637  5'  TGTGCAGCAGAGACGTGCTTC  64100         T    C
                                TGTGCAGTAGAG TGTGC TTC
                                |||||||||||| ||||| |||
                                ACACGTCGTCTC GCACG AAG
                                      T    _
GAM2768 KIAA1679  3'  TGTACAGTAGGAGAAAGGTTTT 64101         _ TTGTGCC
              C                  TGTGCAGTAG AG      TTC
                                |||||||||| ||      |||
                                ACATGTCATC TC      AAG
                                     C  TTTCCAA
GAM2768 LOC219347 3'  TGTGCAGAGCCTCTGTCTTC   64102       T  AG  G  C
                                TGTGCAG AG  TT TG CTTC
                                ||||||| ||  || || ||||
                                ACACGTC TC  GA AC GAAG
                                   _ G_  G  A
GAM2768 LOC90317  3'  TGTGCAGTGAGGTTTGAGCTCC 64103        A  __  T  CT
              G                  TGTGCAGT GAG  TTG GC  TCCG
                                ||||||| |||  ||| ||  ||||
                                ACACGTCA CTC  AAC CG  AGGC
                                   _  CA  T  __
GAM2769 MGC35558  3'  TCCAAGGATGGAGTTAAAATG  64106         TAATT_
                                TCCAAGGATG     AAATG
                                ||||||||||     |||||
                                AGGTTCCTAC     TTTAC
                                     CTCAAT
GAM2769 SLC38A4   3'  TCTGAGAATGCAAATGTTT   64107    CA       TTAA
                                TC  AGGATGTAA   ATGTTT
                                ||  |||||||||   ||||||
                                AG  TCTTACGTT   TACAAA
                                 AC       ____
GAM2770 DDX11     3'  ATCATGCTCTTCTCACAGTATC 64110          T
              G                  ATCATGTTTTT CTCACAGTATCG
                                |||||||||| ||||||||||
                                TAGTACGAGAA GAGTGTCATAGC
                                    _
GAM2770 HSD17B12  3'  CATATTTCACAGTAT      64111       TTTTC
                                CATGTT    TCACAGTAT
                                ||||||    |||||||||
                                GTATAA    AGTGTCATA
                                   _____
GAM2771 BACE      5'  GGGTCCGGGCTGTGGAGAGC   64114    C  AGAT T      A
                                GG GT   G GCTGTGGA AGC
                                || ||   | |||||||| |||
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                                CC CA    C CGACACCT TCG
                                 _ GG__ C       C
GAM2771 BACE     5' GGGTCCGGGCTGTGGAGAGC  64114    C  AGAT T      A
                                GG GT    G GCTGTGGA AGC
                                || ||    | |||||||| |||
                                CC CA    C CGACACCT TCG
                                 _ GG__ C       C
GAM2771 LAMC1    3' GGCTGGGTGTGGAGGAAAGCA 64115     GTAGA    CTGT
                                GGC    TGTG    GGAAAGCA
                                |||    ||||    ||||||||
                                CCG    ACAC    CCTTTCGT
                                  ACCC_   CT__
GAM2771 MUC3B    5' GTGGATGTGCTGACTGTGGA   64116    A      _____
                                GT GATGTGCT    GTGGA
                                || ||||||||    |||||
                                CA CTACACGA    CACCT
                                 C       CTGA
GAM2771 TNFAIP1  3' GGAGTAGATGTGTGGCCAAGCA 64117    C       GCT    A_
                                GG GTAGATGT   GTGG  AAGCA
                                || ||||||||   ||||  |||||
                                CC CATCTACA   CACC  TTCGT
                                 T       ___    GG
GAM2771 TNFRSF1B 3' GGCTGCGGCTGTGGAGGGC    64118     GTAGA   _      AA
                                GGC    TGTG CTGTGGA  GC
                                |||    |||| |||||||  ||
                                CCG    ACGC GACACCT  CG
                                  _____   C      CC
GAM2771 BIRC1    3' GGCAGTGGATAAATGGAAAG   64119     _ A    TGCT
                                GGC GT GATG    GTGGAAAG
                                ||| || ||||    ||||||||
                                CCG CA CTAT    TACCTTTC
                                  T  C    T___
GAM2771 KIAA0169 5' GCCGTAGGTTGGAGGCTGTGG  64120   G    A_  T__
                                G CGTAG  TG   GCTGTGG
                                | |||||  ||   |||||||
                                C GCATC  AC   CGACACC
                                 G    CA  CTC
GAM2771 KIAA1453 3' GATGTGCTGTGGGGGGCA    64121          AAA
                                GATGTGCTGTGG   GCA
                                ||||||||||||  |||
                                CTACACGACACC   CGT
                                       CCC
GAM2771 KIAA1775 3' GCTGTATTCCCTGTGGAGGGCA 64122    _  GATGTG      AA
                                GC GTA     CTGTGGA  GCA
                                || |||     |||||||  |||
                                CG CAT     GACACCT  CGT
                                 A  AAGG__      CC
GAM2771 MGC11102 3' GGTGAAGATGTGCAGAGC    64123    CGT      TGT   AA
                                GG   AGATGTGC   GGA  GC
                                ||   ||||||||   |||  ||
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                                CC  TCTACACG  TCT  CG
                                 ACT      ___  __
GAM2771  LOC202333 3'  GACATTTTGTGGAAAGCA    64124      GC
                                GATGT  TGTGGAAAGCA
                                |||||  ||||||||||
                                CTGTA  ACACCTTTCGT
                                   AA
GAM2771  LOC51200  3'  GGCTAGATGTGAATGAGG    64125    G      C_  T
                                GGC TAGATGTG  TG GG
                                ||| ||||||||  || ||
                                CCG ATCTACAC  AC CC
                                  _      TT  T
GAM2771  LOC92340  3'  GGCCTTCAAAGCTGTGGAAAGC 64126    GTAGATGT
           A                     GGC       GCTGTGGAAAGCA
                                |||       ||||||||||||
                                CCG       CGACACCTTTCGT
                                  GAAGTTT_
GAM2772  MBNL     3'  TGATTATATATTTATAAGA    64129     A
                                TGAT GTATATTTATAAGA
                                |||| ||||||||||||
                                ACTA TATATAAATATTCT
                                   A
GAM2772  LOC196527 3'  TGACAGTTTATAAGA       64130       ATAT
                                TGATAGT    TTATAAGA
                                |||||||    ||||||||
                                ACTGTCA    AATATTCT
                                           ____
GAM2773  DCN      3'  GTTAGGTTTCCAGTATCTAGCT 64133     AAAAA      C
           T                     GTTA     TCAGTATC AGCTT
                                ||||     |||||||| |||||
                                CAAT     GGTCATAG TCGAA
                                  CCAAA       A
GAM2773  DCN      3'  GTTAGGTTTCCAGTATCTAGCT 64133     AAAAA      C
           T                     GTTA     TCAGTATC AGCTT
                                ||||     |||||||| |||||
                                CAAT     GGTCATAG TCGAA
                                  CCAAA       A
GAM2773  DCN      3'  GTTAGGTTTCCAGTATCTAGCT 64133     AAAAA      C
           T                     GTTA     TCAGTATC AGCTT
                                ||||     |||||||| |||||
                                CAAT     GGTCATAG TCGAA
                                  CCAAA       A
GAM2773  DCN      3'  GTTAGGTTTCCAGTATCTAGCT 64133     AAAAA      C
           T                     GTTA     TCAGTATC AGCTT
                                ||||     |||||||| |||||
                                CAAT     GGTCATAG TCGAA
                                  CCAAA       A
GAM2773  DCN      3'  GTTAGGTTTCCAGTATCTAGCT 64133     AAAAA      C
           T                     GTTA     TCAGTATC AGCTT
                                ||||     |||||||| |||||
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                                CAAT    GGTCATAG TCGAA
                                  CCAAA       A
GAM2773 DCN      3' GTTAGGTTTCCAGTATCTAGCT 64133     AAAAA      C
             T                    GTTA    TCAGTATC AGCTT
                                  ||||    |||||||| |||||
                                CAAT    GGTCATAG TCGAA
                                  CCAAA       A
GAM2773 NLGN1    3' TGCTAAAAATATCCAG      64134        AATCA
                                TGTTAAAA    GTATCCAG
                                ||||||||    ||||||||
                                ACGATTTT    TATAGGTC
                                  _____
GAM2773 DNAM-1   3' TGTTGGTAAACTCTCCAGCTT  64135     AAA   CAGTA
                                TGTT   AAAT    TCCAGCTT
                                ||||   ||||    ||||||||
                                ACAA   TTTG    AGGTCGAA
                                  CCA    AG___
GAM2773 KIAA0317 3' TGCTAAAGGATCCCCAGCT   64136       AA   AGTA
                                TGTTAAA  ATC    TCCAGCT
                                |||||||  |||    |||||||
                                ACGATTT  TAG    GGGTCGA
                                   CC   ____
GAM2773 NEK1     3' TATTAAAAAATCAAGTATTTAG 64137          _    CC
                                TGTTAAAAAAATCA GTAT  AG
                                |||||||||||||| ||||  ||
                                ATAATTTTTTAGT CATA  TC
                                      T    AA
GAM2773 PIGM     3' TGTTAAAAGTTAAGACACAGCT 64138        AATC  T TC
             T                    TGTTAAAA    AG A  CAGCTT
                                  ||||||||    || |  ||||||
                                  ACAATTTT    TC T  GTCGAA
                                     CAAT  _ GT
GAM2773 SLC25A18 5' TTAAAAATTCTGTCCAGCTT   64139       A  AGTA
                                TTAAAAA TC    TCCAGCTT
                                ||||||| ||    ||||||||
                                AATTTTT AG    AGGTCGAA
                                   A  AC__
GAM2773 LOC145463 3' GTTAAAAAAAAAATCCAG    64140        TCAGT
                                GTTAAAAAA     ATCCAG
                                |||||||||     ||||||
                                CAATTTTTT     TAGGTC
                                     TTT__
GAM2773 LOC151007 3' TGTCAAAAATCTTATATTCAGC 64141         A  A_   C
             TT                    TGTTAAAAA TC  GTAT CAGCTT
                                   ||||||||| ||  |||| ||||||
                                   ACAGTTTTT AG  TATA GTCGAA
                                      _ AA   A
GAM2773 LOC196411 3' TTAAAAAATCACTCAGCTT   64142          GTATC
                                TTAAAAAATCA     CAGCTT
                                ||||||||||     ||||||
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                                AATTTTTTAGT    GTCGAA
                                      GA___
GAM2773  LOC200138 3'  GTTAAAAAATCTAAAGCAGCTT 64143          AGTATC
                                GTTAAAAAATC     CAGCTT
                                ||||||||||     ||||||
                                CAATTTTTTAG     GTCGAA
                                      ATTTC_
GAM2773  LOC256073 3'  TGTTAAAAAATTGTATC     64144          CA
                                TGTTAAAAAAT  GTATC
                                ||||||||||  |||||
                                ACAATTTTTTA  CATAG
                                      A_
GAM2774  ACK1     3'  GGGGCACCGGGACTGAACCAAA 64147     A   AAA
                                GGGG ACCG   ACTGAACCAAA
                                |||| ||||   ||||||||||
                                CCCC TGGC   TGACTTGGTTT
                                  G   CC_
GAM2774  ARHGAP6  5'  GGGAACCGAAAGGGACTCA   64148          ACT  AC
                                GGGAACCGAAA   GA  CA
                                ||||||||||   ||  ||
                                CCCTTGGCTTT   CT  GT
                                      CC_  GA
GAM2774  ARHGAP6  5'  GGGAACCGAAAGGGACTCA   64148          ACT  AC
                                GGGAACCGAAA   GA  CA
                                ||||||||||   ||  ||
                                CCCTTGGCTTT   CT  GT
                                      CC_  GA
GAM2774  CISH     3'  TGGGGATTGAAAAACCA     64149       ACC   AACT
                                TGGGGA   GAA   GAACCA
                                ||||||   |||   ||||||
                                ACCCCT   CTT   TTTGGT
                                   AA_   _____
GAM2774  CISH     3'  TGGGGATTGAAAAACCA     64149       ACC   AACT
                                TGGGGA   GAA   GAACCA
                                ||||||   |||   ||||||
                                ACCCCT   CTT   TTTGGT
                                   AA_   _____
GAM2774  CLASP1   5'  TGGGGAACTTGACCGGCTGCCA 64150        C_  AAA_   AA
                                TGGGGAAC  GA   CTG  CCA
                                ||||||||  ||   |||  |||
                                ACCCCTTG  CT   GAC  GGT
                                     AA  GGCC   __
GAM2774  DUSP4    5'  TGGGGAACTGAAGACAGA    64151        C   A  T
                                TGGGGAAC GAA AC GA
                                |||||||| ||| || ||
                                ACCCCTTG CTT TG CT
                                     A   C  T
GAM2774  EGLN2    5'  TGGAGAACTGGAGCACAGGCTG 64152        _____  AAAA
            AA                    TGGGGAAC    CG   CTGAA
                                ||||||||    ||   |||||
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                                ACCTCTTG    GT   GACTT
                                    ACCTC  GTCC
GAM2774  ELL      3'  TGGGAAACCGAGGACATCGCAA 64153          AA  TGAAC
             A                   TGGGGAACCGA  AC    CAAA
                                 ||||||||||  ||    ||||
                                 ACCCTTTGGCT  TG    GTTT
                                      CC  TAGC_
GAM2774  FIGF     3'  TGGGGAACTTGGAACGCTGAA  64154        C__   AA
                                 TGGGGAAC   GAA  CTGAA
                                 ||||||||   |||  |||||
                                 ACCCCTTG   CTT  GACTT
                                     AAC   GC
GAM2774  GLRA3    5'  TGGGGAACCAGAAAGACAGA   64155         _   _  T
                                 TGGGGAACC GAAA AC GA
                                 ||||||||| |||| || ||
                                 ACCCCTTGG CTTT TG CT
                                      T    C  T
GAM2774  GPC1     3'  TGGGGACCTGACCAGCAACCG  64156        _____   AA
                                 TGGGGA    ACCG  AACTG
                                 ||||||    ||||  |||||
                                 ACCCCT    TGGT  TTGGC
                                    GGAC    CG
GAM2774  KCNAB1   3'  TGGGGAACTTGCTGACCA    64157        CGAAAA   A
                                 TGGGGAAC     CTGA CCA
                                 ||||||||     |||| |||
                                 ACCCCTTG     GACT GGT
                                     AAC___    _
GAM2774  MTMR7    3'  GGAACTGAGCCACAAACCA    64158      C  AA_  T
                                 GGAAC GA   AC GAACCA
                                 ||||| ||   || ||||||
                                 CCTTG CT   TG TTTGGT
                                    A  CGG  _
GAM2774  NORE1    3'  TGGGGAACCCAAGTAGCCCA   64159         G  AAC  AA
                                 TGGGGAACC AA   TG  CCA
                                 ||||||||| ||   ||  |||
                                 ACCCCTTGG TT   AT  GGT
                                      G  C__  CG
GAM2774  SURF6    3'  TGGGGAACAGAAAGGAATGA   64160        C    AC__
                                 TGGGGAAC GAAA    TGA
                                 |||||||| ||||    |||
                                 ACCCCTTG CTTT    ACT
                                     T    CCTT
GAM2774  AMOT     3'  CGGGGATTGGAAACTGAA     64161       ACC    A
                                 TGGGGA   GAAA CTGAA
                                 ||||||   |||| |||||
                                 GCCCCT   CTTT GACTT
                                    AAC    _
GAM2774  AQP9     3'  GGGGAAAAGACTGAGCCA     64162       ACC   A    A
                                 GGGGA   GAA ACTGA CCA
                                 |||||   ||| ||||| |||
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                                CCCCT   TTT TGACT GGT
                                   ___  C    C
GAM2774  DKFZp564A176 5'  TGAGGAACTGGAAGAACCA   64163        C_  AACT
                                TGGGGAAC  GAA   GAACCA
                                ||||||||  |||   ||||||
                                ACTCCTTG  CTT   CTTGGT
                                     AC  ____
GAM2774  ERAL1    3'  AGGAACCACCTGGAAACTGA   64164        A____
                                GGGAACCG    AAACTGA
                                ||||||||    |||||||
                                TCCTTGGT    TTTGACT
                                     GGACC
GAM2774  FLJ11618 3'  GGGGAACCGGGGCTGTCAGCCA 64165         AAAA  AA__
              A                  GGGGAACCG   CTG   CCAA
                                 |||||||||   |||   ||||
                                 CCCCTTGGC   GAC   GGTT
                                      CCC_  AGTC
GAM2774  FLJ13188 3'  TGGGGAATGGGAGGAAAACCAA 64166       CCGAAAACT
              A                  TGGGGAA       GAACCAAA
                                 |||||||       ||||||||
                                 ACCCCTT       TTTGGTTT
                                    ACCCTCCT_
GAM2774  FLJ21742 3'  GGGAACACTGAACCAA     64167       CGAAA
                                GGGAAC    ACTGAACCAA
                                ||||||    ||||||||||
                                CCCTTG    TGACTTGGTT
                                    _____
GAM2774  FLJ22969 3'  TGGGAAACCGGGGCCTCTACTG 64168         AAA_____
              AACCA                TGGGGAACCG       ACTGAACCA
                                   ||||||||||       |||||||||
                                   ACCCTTTGGC       TGACTTGGT
                                       CCCGGAGA
GAM2774  KIAA0042 5'  TGAGGAACTGAATGGGGGACTG 64169        C   A_____
                                TGGGGAAC GAA     ACTG
                                |||||||| |||     ||||
                                ACTCCTTG CTT     TGAC
                                     A   ACCCCC
GAM2774  KIAA0064 3'  TGGGGAACTGGGCCAGACCAAA 64170        CGAAAA  GA
                                TGGGGAAC     CT  ACCAAA
                                ||||||||     ||  ||||||
                                ACCCCTTG     GG  TGGTTT
                                     ACCC__  TC
GAM2774  KIAA1719 3'  TGGGGAACAGAGACCA      64171        C  AAACT  A
                                TGGGGAAC GA    GA CCA
                                |||||||| ||    || |||
                                ACCCCTTG CT    CT GGT
                                     T  _____  _
GAM2774  KIAA1949 5'  TGGGGAAATGGAAAAAGTGAA  64172        CC_    C_
                                TGGGGAA   GAAAA  TGAA
                                |||||||   |||||  ||||
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                                ACCCCTT  CTTTT  ACTT
                                    TAC    TC
GAM2774  KIAA1949  5'  TGGGGAAATGGAAAAAGTGAA  64172       CC_    C_
                                TGGGGAA  GAAAA  TGAA
                                |||||||  |||||  ||||
                                ACCCCTT  CTTTT  ACTT
                                    TAC    TC
GAM2774  KIAA1949  5'  TGGGGAAATGGAAAAAGTGAA  64172       CC_    C_
                                TGGGGAA  GAAAA  TGAA
                                |||||||  |||||  ||||
                                ACCCCTT  CTTTT  ACTT
                                    TAC    TC
GAM2774  MAD4      3'  TGGGGAACCCAAGCCTGA    64173        G  AA
                                TGGGGAACC AA  CTGA
                                ||||||||| ||  ||||
                                ACCCCTTGG TT  GACT
                                     G  CG
GAM2774  MAP3K3    3'  TGGGGAACAAAGGCTGGGCCA  64174        C   AA   AA
                                TGGGGAAC GAA  CTG  CCA
                                |||||||| |||  |||  |||
                                ACCCCTTG TTT  GAC  GGT
                                    _  CC   CC
GAM2774  MOST2     5'  TGAGGAACTGAAAGAAGTGA   64175        C    AC__
                                TGGGGAAC GAAA    TGA
                                |||||||| ||||    |||
                                ACTCCTTG CTTT    ACT
                                    A    CTTC
GAM2774  NKX2B     3'  TGGGGAACCGCGCCGAA      64176         AAAA
                                TGGGGAACCG    CTGAA
                                ||||||||||    |||||
                                ACCCCTTGGC    GGCTT
                                     GC__
GAM2774  NXPH3     3'  GAGGAACTGGGAGGCCTTGAAC 64177        C__  AAA  _
                                GGGGAAC   GA   CT GAAC
                                |||||||   ||   || ||||
                                CTCCTTG   CT   GA CTTG
                                    ACC  CCG  A
GAM2774  P5-1      3'  TGGGGTGGAGCTGAACCAA    64178      AACC  AAA
                                TGGGG    GA   CTGAACCAA
                                |||||    ||   |||||||||
                                ACCCC    CT   GACTTGGTT
                                   AC__  C__
GAM2774  PCDH19    3'  TGGGAAACACTGAATCA      64179        CGAAA     C
                                TGGGGAAC     ACTGAA CA
                                ||||||||     |||||| ||
                                ACCCTTTG     TGACTT GT
                                     _____      A
GAM2774  PHRET1    3'  TGGGGAACTCGAAGCCAAA    64180         _   AA TG
                                TGGGGAAC CGAA  C  AA
                                |||||||| ||||  |  ||
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                                ACCCCTTG GCTT  G  TT
                                    A   C_ GT
GAM2774  PSKH1    3'  TGGGGAACTGGGGGGAAATTCT 64181        C_____   A_
             GA                   TGGGGAAC     GAAA  CTGA
                                  ||||||||     ||||  ||||
                                  ACCCCTTG     CTTT  GACT
                                      ACCCCC    AA
GAM2774  SMCR5    3'  TGGGGAAACTGAAGCC      64182        CCGAAA    _
                                  TGGGGAA     ACTGAA CC
                                  |||||||     |||||| ||
                                  ACCCCTT     TGACTT GG
                                      _______     C
GAM2774  STARD7   3'  TGGAGAACTGAAGGAAATCCAA 64183        C  AACT  A
             A                    TGGGGAAC GAA    GA CCAAA
                                  |||||||| |||    || |||||
                                  ACCTCTTG CTT    TT GGTTT
                                      A   CCT_  A
GAM2774  STARD7   3'  TGGAGAACTGAAGGAAATCCAA 64183        C  AACT  A
             A                    TGGGGAAC GAA    GA CCAAA
                                  |||||||| |||    || |||||
                                  ACCTCTTG CTT    TT GGTTT
                                      A   CCT_  A
GAM2774  VDU1     3'  TGGAGAACTGAAAGACTG    64184        C   _
                                  TGGGGAAC GAAA ACTG
                                  |||||||| |||| ||||
                                  ACCTCTTG CTTT TGAC
                                      A   C
GAM2774  LOC113828 3'  TGGGGAACCAGAAGCACCA    64185         _  AACTGA
                                  TGGGGAACC GAA     ACCA
                                  ||||||||| |||     ||||
                                  ACCCCTTGG CTT     TGGT
                                       T  CG____
GAM2774  LOC122525 5'  TGGGGACCGAAAACTGCC     64186       A        AA
                                  TGGGGA CCGAAAACTG  CC
                                  |||||| ||||||||||  ||
                                  ACCCCT GGCTTTTGAC  GG
                                      _       __
GAM2774  LOC126661 5'  TGGGGAACTGGGGGAAAAGCG  64187        C____    C
                                  TGGGGAAC    GAAAA TG
                                  ||||||||    ||||| ||
                                  ACCCCTTG    CTTTT GC
                                      ACCCC    C
GAM2774  LOC149194 5'  TGGGGAACTTGCACTGAGCCA  64188        CGAAA    A
                                  TGGGGAAC    ACTGA CCA
                                  ||||||||    ||||| |||
                                  ACCCCTTG    TGACT GGT
                                      AACG_    C
GAM2774  LOC220739 3'  TAGGGAAGAGAAACTGAA    64189        CC   A
                                  TGGGGAA  GAAA CTGAA
                                  |||||||  |||| |||||
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                                ATCCCTT  CTTT GACTT
                                    CT   _
GAM2774  LOC254722 5'  TGGGGAACTGAAGAAGCC    64190        C   AACT  _
                                TGGGGAAC GAA    GAA CC
                                |||||||| |||    ||| ||
                                ACCCCTTG CTT    CTT GG
                                    A   ____   C
GAM2774  LOC55885  3'  TGGGGAACATGGAACTTGAA   64191        CGAA   _
                                TGGGGAAC    AACT GAA
                                ||||||||    |||| |||
                                ACCCCTTG    TTGA CTT
                                    TACC    A
GAM2774  LOC57406  3'  TGGGGAACCGTGGATACCA    64192         AAAACT  _
                                TGGGGAACCG     GA ACCA
                                ||||||||||     || ||||
                                ACCCCTTGGC     CT TGGT
                                    AC____  A
GAM2774  LOC85414  3'  GGGGAACCAGGCTGGGCCAA   64193        AAAA   AA
                                GGGGAACCG    CTG  CCAA
                                |||||||||    |||  ||||
                                CCCCTTGGT    GAC  GGTT
                                    CC__   CC
GAM2775  DSC2      3'  ACAGACCCAGCCACCGATC    64196      TTA  _
                                ACGG   CA CCACCGATC
                                ||||   || |||||||||
                                TGTC   GT GGTGGCTAG
                                  TGG  C
GAM2775  KPNB3     3'  CACACAACACTACCGATC     64197       GTT    C
                                TACACG   ACAC ACCGATC
                                ||||||   |||| |||||||
                                GTGTGT   TGTG TGGCTAG
                                   ___    A
GAM2775  LOC158237 5'  CACAGTCAAGCACTGATC     64198        CAC   C
                                CACGGTTA   CAC GATC
                                ||||||||   ||| ||||
                                GTGTCAGT   GTG CTAG
                                    TC_   A
GAM2775  LOC158293 3'  TACACAGGTCACACTGATC    64199       _      CACC
                                TACAC GGTTACAC    GATC
                                ||||| ||||||||    ||||
                                ATGTG CCAGTGTG    CTAG
                                   T       A___
GAM2775  LOC219333 3'  TACATAGTTACACGGCAATC   64200      CG      CAC
                                TACA  GTTACAC   CGATC
                                ||||  |||||||   |||||
                                ATGT  CAATGTG   GTTAG
                                  AT      CC_
GAM2776  BCL7A     5'  CCAGGCAGACCACAGAG     64203     CC  C
                                CCA  CA GACCACAGAG
                                |||  || ||||||||||
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                                GGT  GT CTGGTGTCTC
                                  CC  _
GAM2776  CABC1    5'  CGCACCACGCACCTTGCAGAG  64204        C   GACCA
                                CGCACCAC CAC    CAGAG
                                |||||||| |||    |||||
                                GCGTGGTG GTG    GTCTC
                                    C   GAAC_
GAM2776  DHCR7    3'  GCCCCACCCACGACTGCAGAG  64205    A        CA
                                GC CCACCCACGAC  CAGAG
                                || ||||||||||  |||||
                                CG GGTGGGTGCTG  GTCTC
                                 G         AC
GAM2776  FECH     3'  TCACACTGCCAGCCCACAGAG  64206      CAC   CGA
                                TCGCAC   CCA   CCACAGAG
                                ||||||   |||  ||||||||
                                AGTGTG   GGT   GGTGTCTC
                                   AC_   CG_
GAM2776  HPS1     3'  CTCACACCACCCTGGGACGGAG 64207          AC_   CACA
                                CTCGCACCACCC   GAC   GAG
                                ||||||||||||  |||   |||
                                GAGTGTGGTGGG   CTG   CTC
                                      ACC   C___
GAM2776  NOLA1    5'  CTCGGTTACCGTACCGCCACAG 64208     C__   ACCCA  A
            AG                    CTCG   ACC    CG CCACAGAG
                                ||||   |||    || ||||||||
                                GAGC   TGG    GC GGTGTCTC
                                  CAA   CATG_  _
GAM2776  RAD1     5'  CTCGGCCACCGTCACCACAGAG 64209     CA    CACG
                                CTCG  CCACC   ACCACAGAG
                                ||||  |||||   |||||||||
                                GAGC  GGTGG   TGGTGTCTC
                                  C_    CAG_
GAM2776  RAD1     5'  CTCGGCCACCGTCACCACAGAG 64209     CA    CACG
                                CTCG  CCACC   ACCACAGAG
                                ||||  |||||   |||||||||
                                GAGC  GGTGG   TGGTGTCTC
                                  C_    CAG_
GAM2776  RAD1     5'  CTCGGCCACCGTCACCACAGAG 64209     CA    CACG
                                CTCG  CCACC   ACCACAGAG
                                ||||  |||||   |||||||||
                                GAGC  GGTGG   TGGTGTCTC
                                  C_    CAG_
GAM2776  TARBP2   3'  GCACCACCAGCTCCTGCAGAG  64210       CACGA  A_
                                GCACCACC    CC  CAGAG
                                ||||||||    ||  |||||
                                CGTGGTGG    GG  GTCTC
                                    TCGA_  AC
GAM2776  WHSC1    3'  TCCATCACCAGACCCACAGAG  64211    G  C   CACGA
                                TC CA CACC    CCACAGAG
                                || || ||||    ||||||||
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                                AG GT GTGG    GGTGTCTC
                                 _ A   TCTG_
GAM2776 WHSC1    3' TCCATCACCAGACCCACAGAG 64211   G C   CACGA
                                TC CA CACC    CCACAGAG
                                || || ||||    ||||||||
                                AG GT GTGG    GGTGTCTC
                                 _ A   TCTG_
GAM2776 WHSC1    3' TCCATCACCAGACCCACAGAG 64211   G C   CACGA
                                TC CA CACC    CCACAGAG
                                || || ||||    ||||||||
                                AG GT GTGG    GGTGTCTC
                                 _ A   TCTG_
GAM2776 ACAS2L   3' TCTCACCGCCCCAACCACAGAG 64212   G   A  A
                                TC CACC CCC CGACCACAGAG
                                || |||| ||| ||||||||||
                                AG GTGG GGG GTTGGTGTCTC
                                 A   C  _
GAM2776 FLJ20040 3' CTCTCACCACCCACCTCAGAG 64213    G      ACG  A
                                CTC CACCACCC  ACC CAGAG
                                ||| ||||||||  ||| |||||
                                GAG GTGGTGGG  TGG GTCTC
                                 A       ___  A
GAM2776 LGI3     3' CCCGCACCACTCGTGCATGAG 64214         CCA  AC  CA
                                CTCGCACCAC  CG  CA  GAG
                                ||||||||||  ||  ||  |||
                                GGGCGTGGTG  GC  GT  CTC
                                      A__  AC  A_
GAM2776 PP2447   3' CCCACGACGCCCACGACCACGG 64215      _ CA        A
             AG                   CTCGC AC  CCCACGACCAC GAG
                                ||||| ||  |||||||||| |||
                                GGGTG TG  GGGTGCTGGTG CTC
                                   C  C_         C
GAM2776 RCD-8    5' CTCGCTCACCCGCCAC     64216      AC    AC A
                                CTCGC  CACCC  G CCAC
                                |||||  |||||  | ||||
                                GAGCG  GTGGG  C GGTG
                                   A_    __ _
GAM2776 SDF1     3' CTCCACCATCCCATCCCACAGA 64217    G    _   CGA
             G                   CTC CACCA CCCA   CCACAGAG
                                ||| ||||| ||||   ||||||||
                                GAG GTGGT GGGT   GGTGTCTC
                                 _    A   AG_
GAM2776 ZNF340   3' CACGTGAACCCACGGCCACAGA 64218    ACC_     A
             G                   CGC    ACCCACG CCACAGAG
                                |||   ||||||| ||||||||
                                GTG   TGGGTGC GGTGTCTC
                                  CACT      C
GAM2776 LOC138389 3' GCACCACCCACGTCCCACCGGA 64219          A_   A_
             G                   GCACCACCCACG  CCAC  GAG
                                ||||||||||||  ||||  |||
```

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                                CGTGGTGGGTGC  GGTG  CTC
                                      AG    GC
GAM2776  LOC152316 3'  GCACCACCCACATAAGCACAGA 64220          AC__
              G                  GCACCACCCACG    CACAGAG
                                 ||||||||||||    |||||||
                                 CGTGGTGGGTGT    GTGTCTC
                                       ATTC
GAM2776  LOC254173 3'  GCACCACCCGCGCCTGAG    64221         A  A  ACA
                                 GCACCACCC CG CC   GAG
                                 |||||||||  || ||   |||
                                 CGTGGTGGG GC GG   CTC
                                       C  _  A__
GAM2776  LOC257358 3'  GCACCACCTAGGCCAACTGAG  64222        CACGA   _ A
                                 GCACCACC     CCA C GAG
                                 ||||||||     ||| | |||
                                 CGTGGTGG     GGT G CTC
                                      ATCC_   T A
GAM2776  LOC51195  3'  CCCGCACCATCCAGGGGCAGAG 64223         C   CGACCA
                                 CTCGCACCA CCA      CAGAG
                                 |||||||||  |||      |||||
                                 GGGCGTGGT GGT      GTCTC
                                       A   CCCC__
GAM2776  LOC91301  5'  CTCGACCACCCAGGGCAGA    64224      C       CGACCA
                                 CTCG ACCACCCA      CAGA
                                 ||||  ||||||||      ||||
                                 GAGC TGGTGGGT      GTCT
                                    _       CCC___
GAM2777  ANK3      5'  TGGAATGGTGTTTTGTCA    63439          CTG   AA
                                 TGGAATGGTG   TTG  TCA
                                 ||||||||||   |||  |||
                                 ACCTTACCAC   AAC  AGT
                                       AA_   __
GAM2777  IL13RA2   3'  TGGAAACTGTTGAGTCAA    63440       TGGT       A
                                 TGGAA    GCTGTTGA TCAA
                                 |||||    |||||||| ||||
                                 ACCTT    TGACAACT AGTT
                                    _____       C
GAM2777  MX1       5'  TGGAATGGTGGCTGGATG    63441           _   T_
                                 TGGAATGGTG CTG  TG
                                 |||||||||| |||  ||
                                 ACCTTACCAC GAC  AC
                                       C   CT
GAM2777  DKFZP434B044 3'  TGGGATGCTGTTGCTTCA    63442      AAT        AA
                                 TGG   GGTGCTGTTG  TCA
                                 |||   ||||||||||  |||
                                 ACC   CTACGACAAC  AGT
                                    ___         GA
GAM2777  DKFZP566D193 3'  TGGAAGGTGTTAAAC       63443       T   GCT
                                 TGGAA GGT   GTTGAAT
                                 ||||| |||   |||||||
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                                ACCTT CCA   CAATTTG
                                  _  ___
GAM2777  FLJ20309  3'  TGGAATGGGTTTTTGGGGTCGA 63444        _____  CT
                                TGGAATGG    TG  GTTGA
                                ||||||||    ||  |||||
                                ACCTTACC    AC  CAGCT
                                    CAAAA  CC
GAM2777  FLJ21276  3'  TGGAATGTGTTTGTCTTTGACA 63445       _ GC   GAAT_
                                TGGAATG GT  TGTT    CA
                                |||||||  ||  ||||    ||
                                ACCTTAC CA  ACAG    GT
                                   A  A_   AAACT
GAM2777  NUCB2     3'  TGAAATAGATGTTGAGTTAACA 63446       TGC    ATC
                                TGGAATGG   TGTTGA   AACA
                                ||||||||   ||||||   ||||
                                ACTTTATC   ACAACT   TTGT
                                    T__     CAA
GAM2777  LOC149113 5'  TGGGATGCTGTTGAGCTAACA  63447    AAT       ATC
                                TGG   GGTGCTGTTGA   AACA
                                |||   ||||||||||   ||||
                                ACC   CTACGACAACT   TTGT
                                  ___         CGA
GAM2777  LOC151318 3'  GAAGTTTGTGTTGAATCGACA  63448    TGG  C       A
                                GAA   TG TGTTGAATC ACA
                                |||   || |||||||| |||
                                CTT   AC ACAACTTAG TGT
                                  CAA  _       C
GAM2777  LOC153328 3'  TGGAGGGCTTGAATCA     63449     AT  T   GT
                                TGGA  GG GCT  TGAATCA
                                ||||  || |||  |||||||
                                ACCT  CC CGA  ACTTAGT
                                   __  _  __
GAM2777  LOC154403 5'  TGGGATGCTGTTGAGCTAACA  63447    AAT       ATC
                                TGG   GGTGCTGTTGA   AACA
                                |||   ||||||||||   ||||
                                ACC   CTACGACAACT   TTGT
                                  ___         CGA
GAM2777  LOC154992 5'  TGGGATGCTGTTGAGCTAACA  63447    AAT       ATC
                                TGG   GGTGCTGTTGA   AACA
                                |||   ||||||||||   ||||
                                ACC   CTACGACAACT   TTGT
                                  ___         CGA
GAM2777  LOC158572 3'  TGGGGTGCTGCTGCCCA     63450     AAT       AA
                                TGG   GGTGCTGTTG  TCA
                                |||   ||||||||||  |||
                                ACC   CCACGACGAC  GGT
                                  ___         G_
GAM2777  LOC164397 5'  TGGAATGGCTGTTTATCAA   63451       GT    GA
                                TGGAATG  GCTGTT  ATCAA
                                |||||||  ||||||  |||||
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                                ACCTTAC  CGACAA  TAGTT
                                  __     A_
GAM2777  LOC201868 5'  TGGGATGCTGTTGAGCTAACA  63447     AAT        ATC
                                TGG   GGTGCTGTTGA   AACA
                                |||   ||||||||||   ||||
                                ACC   CTACGACAACT   TTGT
                                 ___         CGA
GAM2777  LOC205095 3'  TGGAAGGTGCTGTTTTTCCAC  63452       T       GAA  A
                                TGGAA GGTGCTGTT   TC AC
                                ||||| |||||||||   || ||
                                ACCTT CCACGACAA   AG TG
                                  _       AA_  G
GAM2778  DMD       3'  TCCAAATTAATTATGC     64228         AATTAC
                                TCTAAATTA    ATTATGC
                                |||||||||    |||||||
                                AGGTTTAAT    TAATACG
                                  _______
GAM2778  DMD       3'  TCCAAATTAATTATGC     64228         AATTAC
                                TCTAAATTA    ATTATGC
                                |||||||||    |||||||
                                AGGTTTAAT    TAATACG
                                  _______
GAM2778  DMD       3'  TCCAAATTAATTATGC     64228         AATTAC
                                TCTAAATTA    ATTATGC
                                |||||||||    |||||||
                                AGGTTTAAT    TAATACG
                                  _______
GAM2778  DMD       3'  TCCAAATTAATTATGC     64228         AATTAC
                                TCTAAATTA    ATTATGC
                                |||||||||    |||||||
                                AGGTTTAAT    TAATACG
                                  _______
GAM2778  DMD       3'  TCCAAATTAATTATGC     64228         AATTAC
                                TCTAAATTA    ATTATGC
                                |||||||||    |||||||
                                AGGTTTAAT    TAATACG
                                  _______
GAM2778  DMD       3'  TCCAAATTAATTATGC     64228         AATTAC
                                TCTAAATTA    ATTATGC
                                |||||||||    |||||||
                                AGGTTTAAT    TAATACG
                                  _______
GAM2778  DMD       3'  TCCAAATTAATTATGC     64228         AATTAC
                                TCTAAATTA    ATTATGC
                                |||||||||    |||||||
                                AGGTTTAAT    TAATACG
                                  _______
GAM2778  DMD       3'  TCCAAATTAATTATGC     64228         AATTAC
                                TCTAAATTA    ATTATGC
                                |||||||||    |||||||
                                AGGTTTAAT    TAATACG
                                  _______
GAM2778  DMD       3'  TCCAAATTAATTATGC     64228         AATTAC
                                TCTAAATTA    ATTATGC
                                |||||||||    |||||||
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                                AGGTTTAAT     TAATACG
                                          _______
GAM2778  DMD      3'  TCCAAATTAATTATGC      64228         AATTAC
                                TCTAAATTA     ATTATGC
                                |||||||||     |||||||
                                AGGTTTAAT     TAATACG
                                          _______
GAM2778  DMD      3'  TCCAAATTAATTATGC      64228         AATTAC
                                TCTAAATTA     ATTATGC
                                |||||||||     |||||||
                                AGGTTTAAT     TAATACG
                                          _______
GAM2778  DMD      3'  TCCAAATTAATTATGC      64228         AATTAC
                                TCTAAATTA     ATTATGC
                                |||||||||     |||||||
                                AGGTTTAAT     TAATACG
                                          _______
GAM2778  DMD      3'  TCCAAATTAATTATGC      64228         AATTAC
                                TCTAAATTA     ATTATGC
                                |||||||||     |||||||
                                AGGTTTAAT     TAATACG
                                          _______
GAM2778  DMD      3'  TCCAAATTAATTATGC      64228         AATTAC
                                TCTAAATTA     ATTATGC
                                |||||||||     |||||||
                                AGGTTTAAT     TAATACG
                                          _______
GAM2778  MGEA5    3'  TCTAAATTAAAATACATGAAGC 64229           T     TAT
                TT                  TCTAAATTAAA TACAT   GCTT
                                ||||||||||| |||||   ||||
                                AGATTTAATTT ATGTA   CGAA
                                      T     CTT
GAM2778  CYorf15B 3'  TCTGAATCAAATATGCCATGCT 64230      A        TACA
                T                   TCT AATTAAAT    TTATGCTT
                                ||| ||||||||    ||||||||
                                AGA TTAGTTTA    GGTACGAA
                                  C       TAC_
GAM2778  HYPH     3'  CAAATTAAATTCTAATTTATGC 64231           ACA__
                TT                  TAAATTAAATT     TTATGCTT
                                ||||||||||     ||||||||
                                GTTTAATTTAA     AATACGAA
                                      GATTA
GAM2778  KIAA1434 3'  TCTAAATAAATTACATGC    64232        T       TTA
                                TCTAAAT AAATTACA   TGC
                                |||||||| ||||||||   |||
                                AGATTTA TTTAATGT   ACG
                                          _      ____
GAM2779  CLCN4    3'  TAGTAACATTGGGTAGCC    64235     C       AA
                                TAG TAACATT  GTAGTC
                                ||| |||||||  ||||||
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                                ATC ATTGTAA  CATCGG
                                  _     CC
GAM2779  DYRK1B   3'  TAGCAGCAATTCCAGTCAAGGA 64236     TAA  TTAAG
                                TAGC   CA    TAGTCAAGGA
                                ||||   ||    ||||||||||
                                ATCG   GT    GTCAGTTCCT
                                  TC_  TAAG_
GAM2779  MADH4    5'  CAGCTAACGTTGCAAG      64237        ATTAA  A T
                                TAGCTAAC    GT G CAAG
                                ||||||||    || | ||||
                                GTCGATTG    CA C GTTC
                                     _____  A _
GAM2779  PDE4B    3'  TAGCTGGCATGCTCATCAAGGA 64238      AA   TAA  A_
                                TAGCT  CAT   GT  GTCAAGGA
                                |||||  |||   ||  ||||||||
                                ATCGA  GTA   CG  TAGTTCCT
                                   CC   ___  AG
GAM2779  VSNL1    3'  ACTAACATTATGTAATCAAGGA 64239         A
                                GCTAACATTA GTAGTCAAGGA
                                |||||||||| ||||||||||
                                TGATTGTAAT CATTAGTTCCT
                                      A
GAM2779  WIG1     3'  TAACATTAAGCAGAGG      64240          TCA
                                TAACATTAAGTAG   AGG
                                ||||||||||||   |||
                                ATTGTAATTCGTC   TCC
                                         ___
GAM2779  IMPACT   3'  GCTGACTTAAGCAGTCAAGGA  64241    A  A
                                GCT AC TTAAGTAGTCAAGGA
                                ||| || ||||||||||||||
                                CGA TG AATTCGTCAGTTCCT
                                  C  _
GAM2779  KIAA1553 3'  TAGCTAACACTGAGGTCTGGG  64242         A  TA   AA
                                TAGCTAACATT AG  GTC  GG
                                |||||||||| ||  |||  ||
                                ATCGATTGTGA TC  CAG  CC
                                      C  __   AC
GAM2779  MGC16491 3'  GCTGGCATTAAGCCCACAGGG  64243     AA      AGT  A
                                GCT  CATTAAGT   CA GG
                                |||  ||||||||   || ||
                                CGA  GTAATTCG   GT CC
                                  CC       GGT  C
GAM2779  MGC21621 3'  GCTGGGACACAGTCAAGGA   64244     A__   TAAGT
                                GCT   ACAT    AGTCAAGGA
                                |||   ||||    |||||||||
                                CGA   TGTG    TCAGTTCCT
                                  CCC   _____
GAM2779  LOC153139 5'  GCTGACATTAAGCTAGG     64245     A       AGTCA
                                GCT ACATTAAGT    AGG
                                ||| |||||||||    |||
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                                CGA TGTAATTCG    TCC
                                  C       A____
GAM2779  LOC154184 5'  GCTGACATTAAGCTAGG    64245    A      AGTCA
                                GCT ACATTAAGT    AGG
                                ||| |||||||||    |||
                                CGA TGTAATTCG    TCC
                                  C       A____
GAM2779  LOC221601 5'  GCTGACATTAAGCTAGG    64245    A      AGTCA
                                GCT ACATTAAGT    AGG
                                ||| |||||||||    |||
                                CGA TGTAATTCG    TCC
                                  C       A____
GAM2779  LOC254848 5'  AGCTGACGGAGGTCAAGG    64246     A  ATTA  TA
                                AGCT AC   AG  GTCAAGG
                                |||| ||   ||  |||||||
                                TCGA TG   TC  CAGTTCC
                                  C  CC__  __
GAM2780  CYP4F3    3'  CGTCTTTCTGTTTGAACAC   64249    C      ATTT
                                CG CTTTTTGTTT   ACGC
                                || ||||||||||   ||||
                                GC GAAAGACAAA   TGTG
                                 A        CT__
GAM2780  MAB21L1   5'  ACCCCTTTCCGTATTTATTTGC 64250    G      __     A
            GC                   AC CCTTTTTGT  TTATTT CGC
                                || |||||||||  |||||| |||
                                TG GGAAAGGCA  AATAAA GCG
                                 G       TA     C
GAM2780  SHOX      5'  CGCTGTTATTTACGC      64251    CTTTT   T
                                CGC    TGTT ATTTACGC
                                |||    |||| ||||||||
                                GCG    ACAA TAAATGCG
                                 ______   _
GAM2780  SHOX      5'  CGCTGTTATTTACGC      64251    CTTTT   T
                                CGC    TGTT ATTTACGC
                                |||    |||| ||||||||
                                GCG    ACAA TAAATGCG
                                 ______   _
GAM2780  SLC4A7    3'  CTCCTGATTATTTACGCC    64252      T
                                TTTTTG TTATTTACGCC
                                |||||| ||||||||||
                                GAGGAC AATAAATGCGG
                                   T
GAM2780  CYP4F2    3'  CGTCTTTCTGTTTGAACAC   64249    C      ATTT
                                CG CTTTTTGTTT   ACGC
                                || ||||||||||   ||||
                                GC GAAAGACAAA   TGTG
                                 A        CT__
GAM2780  FLJ23309  3'  ACCCTTTTTTGTTAACTGTGCC 64253    G    _  T  TAC
            T                    AC CCTTTTT GTT ATT   GCCT
                                || ||||||| ||| |||   ||||
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                                TG GGAAAAA CAA TGA   CGGA
                                 _      A   T   CA_
GAM2780  KIAA0205  3'  ACCTTTTTTTTGTTTTATAGCCT 64254        __     ATT  C
                                GCCTTTT  TGTTT   TA GCCT
                                |||||||  |||||   || ||||
                                TGGAAAA  ACAAA   AT CGGA
                                   AA     AT_  _
GAM2780  KIAA0215  3'  GCCTTTTTTGTTTGGGAAACTGC 64255           ATTT_  _
              CT                  GCCTTTTTGTTT    AC GCCT
                                  ||||||||||||    || ||||
                                  CGGAAAAAACAAA    TG CGGA
                                        CCCTT  A
GAM2780  KIAA0376  3'  CCTTTTTGTTTGGTGCCC    64256          ATTTAC
                                  CCTTTTTGTTT     GCCT
                                  ||||||||||      ||||
                                  GGAAAAACAAA     CGGG
                                        CCA___
GAM2780  MGC14799  3'  GCCTGGCTGTTTATGCC     64257      TT       TTAC
                                  GCCT  TTGTTTAT    GCC
                                  ||||  ||||||||    |||
                                  CGGA  GACAAATA    CGG
                                    CC       _____
GAM2780  MGC2629   5'  CGCCTTTTTTGTTTGCTC    64258         _   A
                                  CGCCTTTTT GTTT TTT
                                  |||||||| |||| |||
                                  GCGGAAAAA CAAA GAG
                                       A    C
GAM2780  LOC124930 3'  GCCTCTTTTATTTGTGCCT    64259        GTT     AC
                                  GCCTTTTT   TATTT  GCCT
                                  ||||||||   |||||  ||||
                                  CGGAGAAA   ATAAA  CGGA
                                       ___     CA
GAM2780  LOC167555 5'  GCCTCATTTGTTTGTGCCT    64260       _      ATTTAC
                                  GCCTT TTTGTTT     GCCT
                                  ||||| |||||||     ||||
                                  CGGAG AAACAAA     CGGA
                                     T      CA_____
GAM2780  LOC256113 5'  GCCAATTTATTTACGC      64261     TTTTT
                                  GCC    GTTTATTTACGC
                                  |||    ||||||||||||
                                  CGG    TAAATAAATGCG
                                    T_____
GAM2781  BRCA1     3'  ACCATAATTTTGTGCTCATG   64264        CA__
                                  ATCGTAGT    TGCTCATG
                                  ||||||||    ||||||||
                                  TGGTATTA    ACGAGTAC
                                       AAAC
GAM2781  BRCA1     3'  ACCATAATTTTGTGCTCATG   64264        CA__
                                  ATCGTAGT    TGCTCATG
                                  ||||||||    ||||||||
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                              TGGTATTA  ACGAGTAC
                                  AAAC
GAM2781 BRCA1   3' ACCATAATTTTGTGCTCATG  64264      CA__
                              ATCGTAGT  TGCTCATG
                              ||||||||  ||||||||
                              TGGTATTA  ACGAGTAC
                                  AAAC
GAM2781 BRCA1   3' ACCATAATTTTGTGCTCATG  64264      CA__
                              ATCGTAGT  TGCTCATG
                              ||||||||  ||||||||
                              TGGTATTA  ACGAGTAC
                                  AAAC
GAM2781 BRCA1   3' ACCATAATTTTGTGCTCATG  64264      CA__
                              ATCGTAGT  TGCTCATG
                              ||||||||  ||||||||
                              TGGTATTA  ACGAGTAC
                                  AAAC
GAM2781 BRCA1   3' ACCATAATTTTGTGCTCATG  64264      CA__
                              ATCGTAGT  TGCTCATG
                              ||||||||  ||||||||
                              TGGTATTA  ACGAGTAC
                                  AAAC
GAM2781 BRCA1   3' ACCATAATTTTGTGCTCATG  64264      CA__
                              ATCGTAGT  TGCTCATG
                              ||||||||  ||||||||
                              TGGTATTA  ACGAGTAC
                                  AAAC
GAM2781 BRCA1   3' ACCATAATTTTGTGCTCATG  64264      CA__
                              ATCGTAGT  TGCTCATG
                              ||||||||  ||||||||
                              TGGTATTA  ACGAGTAC
                                  AAAC
GAM2781 BRCA1   3' ACCATAATTTTGTGCTCATG  64264      CA__
                              ATCGTAGT  TGCTCATG
                              ||||||||  ||||||||
                              TGGTATTA  ACGAGTAC
                                  AAAC
GAM2781 BRCA1   3' ACCATAATTTTGTGCTCATG  64264      CA__
                              ATCGTAGT  TGCTCATG
                              ||||||||  ||||||||
                              TGGTATTA  ACGAGTAC
                                  AAAC
GAM2781 BRCA1   3' ACCATAATTTTGTGCTCATG  64264      CA__
                              ATCGTAGT  TGCTCATG
                              ||||||||  ||||||||
                              TGGTATTA  ACGAGTAC
                                  AAAC
GAM2781 FBXL5   5' CATTTTCAATCTGCTCATG  64265    CG_   A
                              CAT  TAGTC TGCTCATG
                              |||  ||||| ||||||||
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                                GTA   GTTAG ACGAGTAC
                                  AAA    _
GAM2781  FGF12    3'  CATCGCAGCATTATCATG    64266        T   GC
                                CATCGTAG CAT  TCATG
                                |||||||| |||  |||||
                                GTAGCGTC GTA  AGTAC
                                     _  AT
GAM2781  IL1F9    3'  CATCGTGGGTAACGCGCATG   64267       A_  C    T
                                CATCGT  GT ATGC CATG
                                ||||||  || |||| ||||
                                GTAGCA  CA TGCG GTAC
                                   CC  T    C
GAM2781  KCND2    3'  CATCATAGCCAATGTTCATG   64268          _  C
                                CATCGTAGTCA TG TCATG
                                |||||||||||  || |||||
                                GTAGTATCGGT AC AGTAC
                                       T  A
GAM2781  NKTR     3'  CACTGTGCCAGACTCATG    64269     C  A    T
                                CAT GT GTCA GCTCATG
                                |||  ||  |||| |||||||
                                GTG CA CGGT TGAGTAC
                                  A  _    C
GAM2781  UBE2B    3'  CATCAGTTCTCTGCTCATG    64270      TAG  A_
                                CATCG   TC  TGCTCATG
                                |||||   ||  ||||||||
                                GTAGT   AG  ACGAGTAC
                                   CA_  AG
GAM2781  AP4E1    3'  ATCCAGCATGCTCATG      64271     G   T
                                ATC TAG CATGCTCATG
                                |||  ||| ||||||||||
                                TAG GTC GTACGAGTAC
                                  _  _
GAM2781  C1orf24  3'  CATCGTAGAACAATTCATG    64272        T_  TGC
                                CATCGTAG  CA   TCATG
                                ||||||||  ||   |||||
                                GTAGCATC  GT   AGTAC
                                     TT  TA_
GAM2781  C20orf160 3'  CATCGTAGCTGCGCAC      64273         CA   T
                                CATCGTAGT  TGC CAT
                                |||||||||  ||| |||
                                GTAGCATCG  ACG GTG
                                     __  C
GAM2781  DKFZP434B172 3'  CATGCAATCATGTTCATG    64274     C       C
                                CAT GTAGTCATG TCATG
                                |||  ||||||||| |||||
                                GTA CGTTAGTAC AGTAC
                                  _       A
GAM2781  DKFZP566F2124 3'  ATCCCATTTCATGCTCATG   64275     G  G_
                                ATC TA  TCATGCTCATG
                                |||  ||  ||||||||||
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                                TAG GT  AGTACGAGTAC
                                  G  AA
GAM2781  FLJ14106  5'  CACCGTGGTCACCCATG     64276       A   AT
                                CATCGT GTC  GCTCATG
                                |||||| |||  |||||||
                                GTGGCA CAG  TGGGTAC
                                   C   __
GAM2781  MGC4473   5'  CATCACATGCTCATG       64277       TAGT
                                CATCG   CATGCTCATG
                                |||||   ||||||||||
                                GTAGT   GTACGAGTAC
                                  _____
GAM2781  NIBAN     3'  CATCGTAGAACAATTCATG   64272        T_  TGC
                                CATCGTAG  CA   TCATG
                                ||||||||  ||   |||||
                                GTAGCATC  GT   AGTAC
                                     TT  TA_
GAM2781  PRO1257   5'  TCATTGCCTCTGCTCATG    64278      A   A_
                                TCGT GTC  TGCTCATG
                                |||| |||  ||||||||
                                AGTA CGG  ACGAGTAC
                                  A   AG
GAM2781  SEMA5A    3'  CATGGCATTAATGCTCATG   64279     C   GTC
                                CAT GTA   ATGCTCATG
                                ||| |||   |||||||||
                                GTA CGT   TACGAGTAC
                                  C   AAT
GAM2781  LOC146745 5'  CATCATAGTTGCCACG      64280         CA   T
                                CATCGTAGT  TGC CATG
                                |||||||||  ||| ||||
                                GTAGTATCA  ACG GTGC
                                     __  _
GAM2781  LOC152633 5'  CACGCGTGTACATGCTTATG   64281     _  A _     C
                                CAT CGT GT CATGCT ATG
                                ||| ||| || |||||| |||
                                GTG GCA CA GTACGA TAC
                                  C  _ T     A
GAM2781  LOC197003 5'  CACCAGTCATGCTTATG      64282      GT       C
                                CATC  AGTCATGCT ATG
                                ||||  ||||||||| |||
                                GTGG  TCAGTACGA TAC
                                   __        A
GAM2781  LOC200933 3'  ACCCAGATGCTCATG        64283      G   TC
                                ATC TAG  ATGCTCATG
                                ||| |||  |||||||||
                                TGG GTC  TACGAGTAC
                                  _  __
GAM2781  LOC201243 5'  CATCATAGTTGCCACG      64280         CA   T
                                CATCGTAGT  TGC CATG
                                |||||||||  ||| ||||
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                                GTAGTATCA  ACG GTGC
                                   __  _
GAM2781  LOC204285 5'  CATCTCCTCAATGCTCATG    64284      GTAG  _
                                CATC    TCA TGCTCATG
                                ||||    ||| ||||||||
                                GTAG    AGT ACGAGTAC
                                  AGG_   T
GAM2781  LOC257060 3'  CATCGCTCTGCTCATG      64285       AG  A
                                CATCGT  TC TGCTCATG
                                ||||||  || ||||||||
                                GTAGCG  AG ACGAGTAC
                                   __  _
GAM2781  LOC51031  3'  ACCAAAGTCATGTTCATG    64286      T      C
                                ATCG AGTCATG TCATG
                                |||| ||||||| |||||
                                TGGT TCAGTAC AGTAC
                                  T      A
GAM2781  LOC90495  3'  CATCCAATTAATGCTCATG    64287      G    C_
                                CATC TAGT  ATGCTCATG
                                |||| ||||  |||||||||
                                GTAG GTTA  TACGAGTAC
                                  _    AT
GAM2782  INMT      3'  TGAGTCATGCAGGCATGGA    64290       C_  T     AGCAC
                                TGAGTT  GC AGGCA    GGA
                                ||||||  || |||||    |||
                                ACTCAG  CG TCCGT    CCT
                                   TA  _    A_____
GAM2782  TCP11     5'  TGAGTTGTTGCACACGGA    64291       CGCTAG  AA
                                TGAGTT     GC  GCACGGA
                                ||||||     ||  |||||||
                                ACTCAA     CG  TGTGCCT
                                   CAA___  __
GAM2782  DKFZP761F241 3'  TGGTTCTCCAAGCACGG     64292     A    GCTAGG
                                TG GTTC     CAAGCACGG
                                || ||||     |||||||||
                                AC CAAG     GTTCGTGCC
                                 _    AG_____
GAM2782  FLJ11773  5'  GAGTTTGGAGCACGGA      64293       CGCTA  CA
                                GAGTT    GG  AGCACGGA
                                |||||    ||  ||||||||
                                CTCAA    CC  TCGTGCCT
                                  A_____  __
GAM2782  SFXN2     3'  TGAGTTCAGCTAGAATTACATG 64294        _     CAA   C
            G                    TGAGTTC GCTAGG   GCA GG
                                |||||||  ||||||   ||| ||
                                ACTCAAG CGATCT   TGT CC
                                   T     TAA   A
GAM2782  LOC165693 5'  TGAGTTCGTAGGTAAAC     64295         C    C
                                TGAGTTCG TAGG AAGC
                                |||||||| |||| ||||
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                                ACTCAAGC ATCC TTTG
                                     _   A
GAM2782  LOC205401 5'  TGAGTGTGCTCCAAGCACGG  64296     TC  AGG
                                TGAGT  GCT   CAAGCACGG
                                |||||  |||   |||||||||
                                ACTCA  CGA   GTTCGTGCC
                                   CA   G__
GAM2782  LOC254230 5'  CGGGTTCGCTAGTCCACGG   64297   A      GCAAG
                                TG GTTCGCTAG    CACGG
                                || |||||||||    |||||
                                GC CAAGCGATC    GTGCC
                                 C       AG___
GAM2783  ACCN2     3'  CCCCCACACTAGCCCTCCCCC  64300    G  TT  __   _
                                CCC CC  CGC  GCCC CCCCC
                                ||| ||  |||  |||| |||||
                                GGG GG  GTG  CGGG GGGGG
                                  _ T_  AT   A
GAM2783  ACK1      5'  CCGCCTTCCGCTGCCTCCCC  64301       _ _  C
                                CCGCCTTC GC GCC CCCC
                                |||||||| || ||| ||||
                                GGCGGAAG CG CGG GGGG
                                     G  A   A
GAM2783  ACK1      5'  CACCCCCAGGCGCCCCTCCCC  64302       __     _
                                CGCCTTC  GCGCCCC CCCC
                                |||||||  ||||||| ||||
                                GTGGGGG  CGCGGGG GGGG
                                     TC      A
GAM2783  ADAMTS4   3'  CGCCCACAGCCCCTCCCC    64303     T  C    _
                                CGCCT CG GCCCC CCCC
                                ||||| || ||||| ||||
                                GCGGG GT CGGGG GGGG
                                   T  _    A
GAM2783  ADAMTS8   5'  CCGCCTCCTGCCTCCTCCC   64304       GC  _  C
                                CCGCCTTC  GCC CC CCC
                                ||||||||  ||| || |||
                                GGCGGAGG  CGG GG GGG
                                     A_   A  A
GAM2783  ADORA1    3'  CCCGCCTCGCCCTCCC     64305      TCG    C
                                CCCGCCT   CGCCC CCC
                                |||||||   ||||| |||
                                GGGCGGA   GCGGG GGG
                                     ___     A
GAM2783  ADORA1    3'  CCCGCCTCGCCCTCCC     64305      TCG    C
                                CCCGCCT   CGCCC CCC
                                |||||||   ||||| |||
                                GGGCGGA   GCGGG GGG
                                     ___     A
GAM2783  AES       3'  CGTCCCTCGTGCCCCCCC   64306   _    C
                                CG CCTTCG GCCCCCCC
                                || |||||| ||||||||
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                                GC GGGAGC CGGGGGGG
                                 A     A
GAM2783  ANXA6    3'  CCCACCCCTGCCCCTTCC    64307       CGC    CC
                                CCCGCCTT  GCCCC  CC
                                ||||||||  |||||  ||
                                GGGTGGGG  CGGGG  GG
                                    A__    AA
GAM2783  AP2A1    5'  CCGCCCCCTGCCCCTCCCC   64308       GC    _
                                CCGCCTTC  GCCCC CCCC
                                ||||||||  ||||| ||||
                                GGCGGGGG  CGGGG GGGG
                                    A_    A
GAM2783  AP2A1    5'  CCGCCCCCTGCCCCTCCCC   64308       GC    _
                                CCGCCTTC  GCCCC CCCC
                                ||||||||  ||||| ||||
                                GGCGGGGG  CGGGG GGGG
                                    A_    A
GAM2783  APPBP2   5'  CCGCCTCCTCCGCCTCCTCC  64309       G_   C  C
                                CCGCCTTC  CGCC CC CC
                                ||||||||  |||| || ||
                                GGCGGAGG  GCGG GG GG
                                    AG    A  A
GAM2783  ARNT     5'  CCGCGCCACCCCCCCCC     64310    _   TTCGC
                                CC CGCC    GCCCCCCCC
                                || ||||    |||||||||
                                GG GCGG    TGGGGGGGG
                                 C   _____
GAM2783  ASB1     5'  CCGCCTCCGCGGCCGCCCC   64311         _ _
                                CCGCCTTCGCG CC CCCC
                                |||||||||| || ||||
                                GGCGGAGGCGC GG GGGG
                                      C  C
GAM2783  ASB2     5'  CCCACCCCCCGGTCCCCCTCC 64312        G  CC    _
                                CCCGCCTTC CG  CCCCC CC
                                |||||||| ||  ||||| ||
                                GGGTGGGGG GC  GGGGG GG
                                    _ CA    A
GAM2783  ATRN     3'  CCCGCCACGCCCTTCCC     64313       TTC     CC
                                CCCGCC   GCGCCC  CCC
                                ||||||   ||||||  |||
                                GGGCGG   TGCGGG  GGG
                                   ___     AA
GAM2783  AVPR1A   5'  CCTCGCGGCGCGCTCCCTCCC  64314    _  CTT    _  C
                                CC CGC   CGCGC CCC CCC
                                || |||   ||||| ||| |||
                                GG GCG   GCGCG GGG GGG
                                 A  CC_    A  A
GAM2783  BACE     3'  CCCACCTTGCCAGCCTTTTCC  64315       C __   CCCC
                                CCCGCCTT GC  GCC    CC
                                ||||||||  ||  |||    ||
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                                GGGTGGAA CG  CGG   GG
                                    _ GT   AAAA
GAM2783  BACE    3'  CCCACCTTGCCAGCCTTTTCC  64315       C __  CCCC
                                CCCGCCTT GC  GCC   CC
                                |||||||| ||  |||   ||
                                GGGTGGAA CG  CGG   GG
                                    _ GT   AAAA
GAM2783  BCAR1   3'  CCCTCCCCTGCCTCCCTCC   64317    GC   GC  _  C
                                CCC  CTTC  GCC CCC CC
                                |||  ||||  ||| ||| ||
                                GGG  GGGG  CGG GGG GG
                                  A_   A_  A  A
GAM2783  BCAR1   3'  CCGCCGCACCCCTCCCC     64316     TTC     _
                                CCGCC   GCGCCCC CCCC
                                |||||   ||||||| ||||
                                GGCGG   CGTGGGG GGGG
                                  ____     A
GAM2783  BHMT2   3'  CCCGCCTCGGCCTCCC      64318      T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _  A
GAM2783  BMP4    5'  CCGGGCTCCGCGCTCCTTCCC  64319    C_      _ CC
                                CCG  CTTCGCGC CC  CCC
                                |||  |||||||| ||  |||
                                GGC  GAGGCGCG GG  GGG
                                  CC       A  AA
GAM2783  BMP4    5'  CCGGGCTCCGCGCTCCTTCCC  64319    C_      _ CC
                                CCG  CTTCGCGC CC  CCC
                                |||  |||||||| ||  |||
                                GGC  GAGGCGCG GG  GGG
                                  CC       A  AA
GAM2783  BMP7    3'  CCCTTGCCACGCCCCCTTCC   64320    GCCT       CC
                                CCC   TCGCGCCCCC  CC
                                |||   ||||||||||  ||
                                GGG   GGTGCGGGGG  GG
                                  AAC_        AA
GAM2783  CACNG2  3'  CCCGGGGACCGCGCCCTCCTCC 64321     CCT_      _ C
                                CCCG   TCGCGCCC CC CC
                                ||||   |||||||| || ||
                                GGGC   GGCGCGGG GG GG
                                  CCCT       A  A
GAM2783  CALR    3'  CCCCCTTCTGCTGCCCTCC   64322    G   _ _   C
                                CCC CCTTC GC GCCC CC
                                ||| ||||| || |||| ||
                                GGG GGAAG CG CGGG GG
                                  _    A A   A
GAM2783  CAPN1   5'  CCGCCCTCCGCCCTCCC     64323       G    C
                                CCGCCTTC CGCCC CCC
                                |||||||| ||||| |||
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                                GGCGGGAG GCGGG GGG
                                   _    A
GAM2783  CAV2     5'  CCCGGCCCCGCCCCCCC     64324      _  TCG
                                CCCG CCT   CGCCCCCCC
                                |||| |||   |||||||||
                                GGGC GGG   GCGGGGGGG
                                  C  ___
GAM2783  CCND1    3'  CCTCCTCCCGCCTGTCCTCCC  64326    G    G   C__ _
                                CC CCTTC CGCC   CC CCC
                                || ||||| ||||   || |||
                                GG GGAGG GCGG   GG GGG
                                 A    _    ACA  A
GAM2783  CCND1    3'  CCTCCTCACACCTCCTCCC    64325    GC       _ C
                                CC  CTTCGCGCC CC CCC
                                ||  ||||||||| || |||
                                GG  GGAGTGTGG GG GGG
                                 A_       A  A
GAM2783  CDKN2B   3'  CCCACCTCGGCCCTCCTCC    64327       T  C   _  C
                                CCCGCCT CG GCCC CC CC
                                ||||||| || |||| || ||
                                GGGTGGA GC CGGG GG GG
                                   _ _    A  A
GAM2783  CEBPA    3'  CCACGGGCCTGCTCCCCTCC   64328    _ __   TC  G   C
                                CC C  GCCT  GC CCCC CC
                                || |  ||||  || |||| ||
                                GG G  CGGA  CG GGGG GG
                                 T CC   __ A   A
GAM2783  CHAC     5'  CCGCCTTCCCCACGCCCCTCCC 64329         ___      C
                                CCGCCTTC   GCGCCCC CCC
                                ||||||||   ||||||| |||
                                GGCGGAAG   TGCGGGG GGG
                                     GGG      A
GAM2783  CHAC     5'  CCGCCTTCCCCACGCCCCTCCC 64329         ___      C
                                CCGCCTTC   GCGCCCC CCC
                                ||||||||   ||||||| |||
                                GGCGGAAG   TGCGGGG GGG
                                     GGG      A
GAM2783  CHST1    5'  CCGCCTCCCGCGCCCTCCCC   64330        _     C
                                CCGCCTTC GCGCCC CCCC
                                |||||||| |||||| ||||
                                GGCGGAGG CGCGGG GGGG
                                     G     A
GAM2783  COPA     5'  CCACGTCAGCGACCCTCTCCC  64331      C  C   _   CC_
                                CCGC TT GCG CCC   CCC
                                |||| || ||| |||   |||
                                GGTG AG CGC GGG   GGG
                                  C  T   T   AGA
GAM2783  CREBL1   3'  CCCACCCCACCCTCCC      64332        TCG    C
                                CCCGCCT   CGCCC CCC
                                |||||||   ||||| |||
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                                GGGTGGG  GTGGG GGG
                                   ___    A
GAM2783 CRHR2    3' CCCATCCCACGCCTCCCTCC  64333     _ TT    _  C
                                CCCG CC  CGCGCC CCC CC
                                |||| ||  |||||| ||| ||
                                GGGT GG  GTGCGG GGG GG
                                  A __    A  A
GAM2783 CRYAA    3' CCCGCCCTCAGGGTGCTCCCCC 64334         C___  C
             C                   CCCGCCTTCG   GC CCCCCC
                                 ||||||||||   || ||||||
                                 GGGCGGGAGT   CG GGGGGG
                                      CCCA  A
GAM2783 CSNK1G2  3' CCCACCCCTGCCTTCCCC    64335       CGC  CC
                                CCCGCCTT  GCC  CCCC
                                ||||||||  |||  ||||
                                GGGTGGGG  CGG  GGGG
                                    A__  AA
GAM2783 CYLN2    5' CCGGCTGCACCCCCTCC     64336    C  TC      C
                                CCG CT  GCGCCCCC CC
                                ||| ||  |||||||| ||
                                GGC GA  CGTGGGGG GG
                                  C __      A
GAM2783 CYP11A   3' CCCACCCCTGGGCCTTCCTCC 64337       CGC  CC _
                                CCCGCCTT  GCC  CC CC
                                ||||||||  |||  || ||
                                GGGTGGGG  CGG  GG GG
                                    ACC  AA  A
GAM2783 CYP21A2  5' CCCACCTTCAGGTACCCTCCC 64338        C__   C
                                CCCGCCTTCG  GCCC CCC
                                ||||||||||  |||| |||
                                GGGTGGAAGT  TGGG GGG
                                     CCA   A
GAM2783 DDX1     5' CGCCTGCTCGCTCCCTCCC   64339     __   G  C
                                CGCCT  TCGC CCC CCC
                                |||||  |||| ||| |||
                                GCGGA  AGCG GGG GGG
                                  CG   A  A
GAM2783 DDX26    5' CCCGCCTCCGCCTCCTCC    64340        G_  C
                                CCCGCCTTCGC  CC CC
                                ||||||||||  || ||
                                GGGCGGAGGCG  GG GG
                                     GA  A
GAM2783 DHCR24   3' CCCATCTCCACCCCTCCC    64341     C    G  C
                                CCCG CTTCGC CCC CCC
                                |||| |||||| ||| |||
                                GGGT GAGGTG GGG GGG
                                  A     _  A
GAM2783 DLG3     5' CCCGCACCCACGGCTCCCCC  64342     C    _ C
                                CCCGC TTCGCG C CCCCC
                                ||||| |||||| | |||||
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                                GGGCG GGGTGC G GGGGG
                                  T     C A
GAM2783  DMPK     5'  CCCTTGGTCCAGCCCCCCTCC  64343     GCC_   C      _
                                CCC    TTCG GCCCCCC CC
                                |||    |||| ||||||| ||
                                GGG    AGGT CGGGGGG GG
                                 AACC    _      A
GAM2783  DNASE2   3'  CCCGTCCCCCGCCCCCCC    64344      _      G
                                CCCG CCTTCGC CCCCCC
                                |||| ||||||| ||||||
                                GGGC GGGGGCG GGGGGG
                                  A      _
GAM2783  DPEP1    5'  CCCGCCTCCTGCCTCCC     64345         GC   C
                                CCCGCCTTC  GCC CCC
                                |||||||||  ||| |||
                                GGGCGGAGG  CGG GGG
                                     A_   A
GAM2783  DUSP4    5'  CCCCCTTTCCAGCTCCCTTCC  64346     G    CG _ _   CC
                                CCC CCTT  C GC CCC  CC
                                ||| ||||  | || |||  ||
                                GGG GGAA  G CG GGG  GG
                                 _    AG T  A   AA
GAM2783  DYRK1B   3'  CCTGCCCCCACCCCCTCC    64347    C       G    C
                                CC GCCTTCGC CCCC CC
                                || |||||||| |||| ||
                                GG CGGGGGTG GGGG GG
                                 A       _    A
GAM2783  EDARADD  5'  CTGCGCGCCCCTGCCCTCC    64349    T       __   _
                                CT CGCGCCCC  CCC CC
                                || ||||||||  ||| ||
                                GA GCGCGGGG  GGG GG
                                 C       AC   A
GAM2783  EDARADD  5'  CCTGCCCTCCTCCGCCTTCCCC 64348    C     G__    CC
                                CC GCCTTC   CGCC  CCCC
                                || ||||||   ||||  ||||
                                GG CGGGAG   GCGG  GGGG
                                 A     GAG    AA
GAM2783  EGFL5    3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _   A
GAM2783  ELK4     5'  CCGCCCTCAGCCTCCTCC    64350         C   C  C
                                CCGCCTTCG GCC CC CC
                                ||||||||| ||| || ||
                                GGCGGGAGT CGG GG GG
                                     _   A  A
GAM2783  ELK4     5'  CCGCCCTCAGCCTCCTCC    64350         C   C  C
                                CCGCCTTCG GCC CC CC
                                ||||||||| ||| || ||
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                                GGCGGGAGT CGG GG GG
                                     _  A  A
GAM2783  EMP3     5'  CCCTCCTTTCACCCTCCC    64352     G   CG    C
                                CCC CCTT  CGCCC CCC
                                ||| ||||  ||||| |||
                                GGG GGAA  GTGGG GGG
                                  A   A_    A
GAM2783  EMP3     5'  CCCGCCTCTCTCACCGCCTTCC 64351        _  G   _  __  _
            TCC                   CCCGCCT TC CGCC CC  CC CC
                                ||||||| || |||| ||  || ||
                                GGGCGGA AG GTGG GG  GG GG
                                    G  A    C  AA  A
GAM2783  EN1      5'  CCGCGCCGCACCCGCGTCCCTC 64353      ____     _  C    CIII
            CCCG                  CGCC   TTCGCG CCC CCCC   G
                                ||||   |||||| ||| ||||   |
                                GCGG   GGGCGC GGG GGGG   C
                                  CGT     A   A    IIIC
GAM2783  ENC1     3'  CCCCCCTCCCTCGCCCCTTTCC 64354     G    G_     CC_
                                CCC CCTTC  CGCCCC   CC
                                ||| |||||  ||||||   ||
                                GGG GGAGG  GCGGGG   GG
                                  G    GA     AAA
GAM2783  EP300    5'  CCTCGCGCCGGCGCTCCCCTCC 64355    _  _ TC   _   C
                                CC CGC CT  GCGC CCCC CC
                                || ||| ||  |||| |||| ||
                                GG GCG GG  CGCG GGGG GG
                                 A  C  C_   A   A
GAM2783  EPB49    3'  CCCACCTCCTGCCCCTCCC    64356         GC    C
                                CCCGCCTTC  GCCCC CCC
                                |||||||||  ||||| |||
                                GGGTGGAGG  CGGGG GGG
                                     A_    A
GAM2783  ESPN     5'  CCGCACTCAGCGCCTTCCCC   64357     _  C    CC
                                CCGC CTT GCGCC  CCCC
                                |||| ||| |||||  ||||
                                GGCG GAG CGCGG  GGGG
                                  T  T    AA
GAM2783  EXT1     5'  CCCACCTTCTCTGGATGCCTTT 64358      GC_____  CC_   CIII
            CCCCG                 CCTTC     GCC  CCCC   G
                                |||||     |||  ||||   |
                                GGAAG     CGG  GGGG   C
                                  AGACCTA   AAA   IIIC
GAM2783  F2R      5'  CCGCTCGGCGCCCCCTCCC   64360     C  C      _
                                CCGC TT GCGCCCCC CCC
                                |||| || |||||||| |||
                                GGCG AG CGCGGGGG GGG
                                  _ C       A
GAM2783  F2R      3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
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                                GGGCGGA GT CGG GGG
                                  _ _  A
GAM2783  FAT     5'  CCGCTCCCGCGCCCTCTCCC  64361     CT      CC_
                                CCGC  TCGCGCCC   CCC
                                ||||  ||||||||   |||
                                GGCG  GGCGCGGG   GGG
                                  AG       AGA
GAM2783  FZD8    3'  CCCTCCTGGGCGCCCCCTCCC  64362    G   TC      _
                                CCC CCT  GCGCCCCC CCC
                                ||| |||  |||||||| |||
                                GGG GGA  CGCGGGGG GGG
                                  A  CC       A
GAM2783  GAS1    3'  CCCACATGCTTGCTTCCTCCC  64363      ___   C  GC  C
                                CCCGC   CTT GC  CC CCC
                                |||||   ||| ||  || |||
                                GGGTG   GAA CG  GG GGG
                                   TAC  _  AA  A
GAM2783  GCNT2   5'  CCCGCCTCTCTCAAACCTCC   64364       _  G  CC  C
                                CCCGCCT TC CG  CC CC
                                ||||||| || ||  || ||
                                GGGCGGA AG GT  GG GG
                                    G  A  TT  A
GAM2783  GNB2    3'  CCTGCCTCCGGCCCTCC     64365    C      C    C
                                CC GCCTTCG GCCC CC
                                || ||||||| |||| ||
                                GG CGGAGGC CGGG GG
                                 A      _    A
GAM2783  GNE     3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                  _ _   A
GAM2783  GRAF    3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                  _ _   A
GAM2783  GRAP2   5'  CCCACCTCTTACTCCCTCC   64366       C_  G   C
                                CCCGCCTT  GC CCC CC
                                ||||||||  || ||| ||
                                GGGTGGAG  TG GGG GG
                                    AA  A   A
GAM2783  GRIA3   5'  CTCCGCGCCGCCGCCTCC    64367        _  _  _
                                CTTCGCGCC CC CC CC
                                ||||||||| || || ||
                                GAGGCGCGG GG GG GG
                                    C  C  A
GAM2783  GYG2    5'  CCCGCCTCCGCCCAGCCCCC   64368          G  CC
                                CCCGCCTTCGC CC  CCCCC
                                |||||||||| ||  |||||
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                                GGGCGGAGGCG GG  GGGGG
                                      _ TC
GAM2783  GYS1    3'  CCCCTCCTGCCCTCCCC    64369    G    GC   C
                                CC CCTTC  GCCC CCCC
                                || |||||  |||| ||||
                                GG GGAGG  CGGG GGGG
                                 _    A_   A
GAM2783  HAGH    5'  CCCGCCTCGCGCTGCCC    64370       T    CC
                                CCCGCCT CGCGC  CCC
                                ||||||| |||||  |||
                                GGGCGGA GCGCG  GGG
                                    _    AC
GAM2783  HIPK2   3'  CCCTGCCCTCTGCCCCCCCCC  64371    _     GC
                                CCC GCCTTC  GCCCCCCCCC
                                ||| ||||||  ||||||||||
                                GGG CGGGAG  CGGGGGGGGG
                                  A     A_
GAM2783  HIRA    5'  CGCCGGCCCGCGCCCCCCTCC  64372     __         _
                                CGCC  TTCGCGCCCCCC CC
                                ||||  ||||||||||| ||
                                GCGG  GGGCGCGGGGGG GG
                                   CC          A
GAM2783  HMGA2   3'  CCCACCCCACCCCCCCC    64373       TCG
                                CCCGCCT   CGCCCCCCCC
                                |||||||   ||||||||||
                                GGGTGGG   GTGGGGGGGG
                                          ___
GAM2783  HNF4A   5'  CCGCCCTCCCACTGCCTCCTCC 64375        G  __ _ _
            C                    CCGCCTTC CGC  CC CC CCC
                                ||||||| |||  || || |||
                                GGCGGGAG GTG  GG GG GGG
                                     G   AC  A  A
GAM2783  HNF4A   5'  CCCGCCCTCCGCCCTCCC    64374         G    C
                                CCCGCCTTC CGCCC CCC
                                ||||||||| ||||| |||
                                GGGCGGGAG GCGGG GGG
                                     _    A
GAM2783  HOXB13  3'  CCCACTTTCGCTCCTCCC    64376      C    G  C
                                CCCGC TTCGC CC CCC
                                ||||| ||||| || |||
                                GGGTG AAGCG GG GGG
                                   A    A  A
GAM2783  HOXB3   5'  CGCCGGACCCCCCCCCC      64377      TTC C
                                CGCC   G GCCCCCCCCC
                                ||||   | ||||||||||
                                GCGG   C TGGGGGGGGG
                                  ___ C
GAM2783  HOXB3   5'  CCTCCCCTCTCTGCCCCCCTCC 64378    G_    GC_     _
                                CC  CCTTC   GCCCCCC CC
                                ||  |||||   ||||||| ||
```

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                                GG  GGGAG   CGGGGGG GG
                                 AG    AGA      A
GAM2783  HS2ST1   5'  GCCTGCTTGCCCGCCTCCC   64379     TC __   _ _
                                GCCT  GC  GCCC CC CCC
                                ||||  ||  |||| || |||
                                CGGA  CG  CGGG GG GGG
                                  __ AA   C  A
GAM2783  HSF4     5'  CCCGGCCCGCGCCCGTGCCCTC 64380     _ TT     ___  _
             CC                   CCCG CC  CGCGCCC   CCC CCC
                                ||||  ||  |||||||   ||| |||
                                GGGC GG  GCGCGGG   GGG GGG
                                  C __      CAC   A
GAM2783  HSPA1L   5'  CCCACCCCGTCCCTCCC     64381       T  CG   C
                                CCCGCCT CG  CCC CCC
                                |||||||  ||  ||| |||
                                GGGTGGG GC  GGG GGG
                                   _ A_   A
GAM2783  HSPA1L   5'  CCCACCCCGTCCCTCCC     64381       T  CG   C
                                CCCGCCT CG  CCC CCC
                                |||||||  ||  ||| |||
                                GGGTGGG GC  GGG GGG
                                   _ A_   A
GAM2783  IFRD1    3'  CCCGCCTCAGCCTCCCC     64382       T  C   C
                                CCCGCCT CG GCC CCCC
                                |||||||  || ||| ||||
                                GGGCGGA GT CGG GGGG
                                   _ _   A
GAM2783  IGF2R    3'  CCCGCCCAGCCTCCCTCC    64384       TCGC  _  C
                                CCCGCCT    GCC CCC CC
                                |||||||    ||| ||| ||
                                GGGCGGG    CGG GGG GG
                                   T___   A   A
GAM2783  IGF2R    3'  CCCGCCTGGCCTCCCTCC    64383       TCGC  _  C
                                CCCGCCT    GCC CCC CC
                                |||||||    ||| ||| ||
                                GGGCGGA    CGG GGG GG
                                   C___   A   A
GAM2783  IL10     3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                |||||||  || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  IL18     3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                |||||||  || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  IQGAP2   5'  CCCGCCTCTCGCCGATTTCCCC 64385       CG   CC___
                                CCCGCCTT  CGCC    CCCC
                                ||||||||  ||||    ||||
```

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                                GGGCGGAG  GCGG    GGGG
                                   A_    CTAAA
GAM2783  KAI1     3'  CCGCGCCCGGCCCCCTCC    64386      C   C     C
                                CCGC TTCG GCCCCC CC
                                |||| |||| |||||| ||
                                GGCG GGGC CGGGGG GG
                                  C   _     A
GAM2783  KAI1     3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  KCNJ5    3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  KCNQ3    5'  CCGCGCGCCCCTCCCC      64387      CTTC      _
                                CCGC   GCGCCCC CCCC
                                ||||   ||||||| ||||
                                GGCG   CGCGGGG GGGG
                                  _____      A
GAM2783  KIAA0442 5'  CCCCCTTCACGGCTTCCCTCC  64388     G       _ CC  _
                                CCC CCTTCGCG C  CCC CC
                                ||| |||||||| |  ||| ||
                                GGG GGAAGTGC G  GGG GG
                                  _      C AA   A
GAM2783  KIF1B    3'  CCCGCCTCGGCCTCCCC     64389        T  C   C
                                CCCGCCT CG GCC CCCC
                                ||||||| || ||| ||||
                                GGGCGGA GC CGG GGGG
                                   _ _   A
GAM2783  KIFC3    5'  CCCGCTCGCGCCCCTCCC    64390       CT       C
                                CCCGC  TCGCGCCCC CCC
                                |||||  ||||||||| |||
                                GGGCG  AGCGCGGGG GGG
                                  __       A
GAM2783  KIP2     3'  CCTTCACAGGCCCCCTTCC   64391         __     CC
                                CCTTCGC  GCCCCC  CC
                                |||||||  ||||||  ||
                                GGAAGTG  CGGGGG  GG
                                   TC     AA
GAM2783  KNSL1    3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  LAMC1    5'  CCCGCCTCCGCGCTTCCC    64392            CC
                                CCCGCCTTCGCGC  CCC
                                ||||||||||||  |||
```

```
                                GGGCGGAGGCGCG GGG
                                      AA
GAM2783 LASS2   5' CCCGCCCTCGCCCTCCC    64393          G C
                                CCCGCCTTCGC CC CCC
                                |||||||||| || |||
                                GGGCGGGAGCG GG GGG
                                      _ A
GAM2783 LDLR    3' CCCGCCTCGGCCTCCC     64318       T C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 LILRB1  3' CCCGCCTCGGCCTCCC     64318       T C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 LMO4    5' CCGCGCTCCTCCCGCTCCTCC 64394   _ _  G  C C
                                CC CGC CTTC CGC CC CC
                                || ||| |||| ||| || ||
                                GG GCG GGAG GCG GG GG
                                 C  A   G  A A
GAM2783 LNK     5' CCCGCCCTGGGCGCGTCCTCTC 64395       ___  _ CCC
          CC                     CCCGCCTT  CGCG CC  CCC
                                ||||||||  |||| ||  |||
                                GGGCGGGA  GCGC GG  GGG
                                    CCC   A AGA
GAM2783 LTBP2   5' CACCTTCGCGCCTCCTCCC   64397          _ C
                                CGCCTTCGCGCC CC CCC
                                |||||||||||| || |||
                                GTGGAAGCGCGG GG GGG
                                      A A
GAM2783 LTBP2   5' CCACACCAGGCCCCCTCC    64396     CT  C    C
                                CCGC  TCG GCCCCC CC
                                ||||  ||| |||||| ||
                                GGTG  GGT CGGGGG GG
                                  T_  C    A
GAM2783 MAF     5' CCCCCGCGCCCGCCCTCCC   64398         _ _
                                CCTTCGCGCCC CCC CCC
                                |||||||||| ||| |||
                                GGGGGCGCGGG GGG GGG
                                      C  A
GAM2783 MAN2A1  5' CCTGGCCTGCCGCCCTCCCC  64399   C_  TCG   C
                                CC  GCCT  CGCCC CCCC
                                ||  ||||  ||||| ||||
                                GG  CGGA  GCGGG GGGG
                                 AC   CG_   A
GAM2783 MAP1B   5' CCGCCCCCTGCGTCCCCCC   64401       _ _
                                CCGCCTTC GCG CCCCCC
                                |||||||| ||| ||||||
```

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                                GGCGGGGG CGC GGGGGG
                                    A   A
GAM2783  MAP1B    5'  CCCCCTCCGCCCTCTCCC    64400    G    G    CC_
                                CC CCTTC CGCCC   CCC
                                || ||||| |||||   |||
                                GG GGGAG GCGGG   GGG
                                 _    _    AGA
GAM2783  MAP3K5   5'  CCTCTCCGGCGCCCTCTCCC  64402    GC    _    CC_
                                CC  CTTCG CGCCC   CCC
                                ||  ||||| |||||   |||
                                GG  GAGGC GCGGG   GGG
                                 A_    C    AGA
GAM2783  MAP3K5   5'  CGCCGCGCCGCCGCCTCC    64403     TTC    _ _ _
                                CGCC   GCGCC CC CC CC
                                ||||   ||||| || || ||
                                GCGG   CGCGG GG GG GG
                                  ___    C  C  A
GAM2783  MAP4K5   5'  CCGCACCCGCGTCCTCCTCC   64404     C     _ C  C
                                CCGC TTCGCG CC CC CC
                                |||| |||||| || || ||
                                GGCG GGGCGC GG GG GG
                                  T     A  A  A
GAM2783  MAPK12   5'  CCCGCCCTCCGGCCCCTCC    64405        GC    C
                                CCCGCCTTC  GCCCC CC
                                |||||||||  ||||| ||
                                GGGCGGGAG  CGGGG GG
                                     GC    A
GAM2783  MAPK14   5'  CCTGCACCCGCACCCTCTCCC  64406    C  C       CC_
                                CC GC TTCGCGCCC   CCC
                                || || |||||||||   |||
                                GG CG GGGCGTGGG   GGG
                                 A  T       AGA
GAM2783  MAPK14   5'  CCTGCACCCGCACCCTCTCCC  64406    C  C       CC_
                                CC GC TTCGCGCCC   CCC
                                || || |||||||||   |||
                                GG CG GGGCGTGGG   GGG
                                 A  T       AGA
GAM2783  MAPK14   5'  CCTGCACCCGCACCCTCTCCC  64406    C  C       CC_
                                CC GC TTCGCGCCC   CCC
                                || || |||||||||   |||
                                GG CG GGGCGTGGG   GGG
                                 A  T       AGA
GAM2783  MAPK14   5'  CCTGCACCCGCACCCTCTCCC  64406    C  C       CC_
                                CC GC TTCGCGCCC   CCC
                                || || |||||||||   |||
                                GG CG GGGCGTGGG   GGG
                                 A  T       AGA
GAM2783  MAPRE3   3'  CCCTCACATGCCCCCCTCC    64407        __     _
                                CCTTCGC  GCCCCCC CC
                                |||||||  ||||||| ||
```

```
                                GGGAGTG  CGGGGGG GG
                                   TA      A
GAM2783  MBD1    5'  CCCGCCTCGCCCTCCTCC    64408       TCG    _  C
                                CCCGCCT   CGCCC CC CC
                                |||||||   ||||| || ||
                                GGGCGGA   GCGGG GG GG
                                   ___     A  A
GAM2783  MBD1    5'  CCCGCCTCGCCCTCCTCC    64408       TCG    _  C
                                CCCGCCT   CGCCC CC CC
                                |||||||   ||||| || ||
                                GGGCGGA   GCGGG GG GG
                                   ___     A  A
GAM2783  MBD1    5'  CCCGCCTCGCCCTCCTCC    64408       TCG    _  C
                                CCCGCCT   CGCCC CC CC
                                |||||||   ||||| || ||
                                GGGCGGA   GCGGG GG GG
                                   ___     A  A
GAM2783  MBD1    5'  CCCGCCTCGCCCTCCTCC    64408       TCG    _  C
                                CCCGCCT   CGCCC CC CC
                                |||||||   ||||| || ||
                                GGGCGGA   GCGGG GG GG
                                   ___     A  A
GAM2783  MBD1    5'  CCCGCCTCGCCCTCCTCC    64408       TCG    _  C
                                CCCGCCT   CGCCC CC CC
                                |||||||   ||||| || ||
                                GGGCGGA   GCGGG GG GG
                                   ___     A  A
GAM2783  MECP2   3'  CCTGCCTCACACCTCCC     64409    C   T     C
                                CC GCCT CGCGCC CCC
                                || |||| |||||| |||
                                GG CGGA GTGTGG GGG
                                 A   _     A
GAM2783  MEF2D   3'  CCCATCCTGCCCCTCCC     64410     _  TCGC    C
                                CCCG CCT    GCCCC CCC
                                ||||  |||    ||||| |||
                                GGGT GGA    CGGGG GGG
                                  A  _____     A
GAM2783  MET     5'  CCGCGCCTCCCCGCCTCC    64411    _     G   C
                                CC CGCCTTC CGCC CC
                                || ||||||| |||| ||
                                GG GCGGAGG GCGG GG
                                 C      G   A
GAM2783  MGAT5   5'  CCCATCACACCCCTCTCC    64412     CCT       CC_
                                CCCG   TCGCGCCCC   CC
                                ||||   |||||||||   ||
                                GGGT   AGTGTGGGG   GG
                                   ___        AGA
GAM2783  MIC2    5'  CCCGCCCCGGCCTCCCC     64413       T  C   C
                                CCCGCCT CG GCC CCCC
                                ||||||| || ||| ||||
```

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                                GGGCGGG GC CGG GGGG
                                  _ _  A
GAM2783  MKPX    5'  CCCGCCTTGCCGGTCCCC   64414       CGC  CC_
                                CCCGCCTT  GCC  CCCC
                                ||||||||  |||  ||||
                                GGGCGGAA  CGG  GGGG
                                   ___  CCA
GAM2783  MLF2    5'  CCTTCCACGCCGCCTCCTCCC  64415     _   _ _ _
                                CCTTC GCGCC CC CC CCC
                                ||||| ||||| || || |||
                                GGAAG TGCGG GG GG GGG
                                  G   C A A
GAM2783  MLLT3   5'  CCCCCCTCCTCCGCCCCCCC  64416    G   G_
                                CCC CCTTC  CGCCCCCCC
                                ||| |||||  |||||||||
                                GGG GGAGG  GCGGGGGGG
                                  G    AG
GAM2783  MLLT7   3'  CCTGATCCACATCCCCCCCC  64417    GCC    _
                                CC  TTCGCG CCCCCCCC
                                ||  ||||||  ||||||||
                                GG  AGGTGT GGGGGGGG
                                 ACT    A
GAM2783  MMP25   3'  CCTTGTCCTCCCCGCCCCTCCC 64418    CG__   G    _
           C                     CC   CCTTC CGCCCC CCCC
                                ||   ||||| |||||| ||||
                                GG   GGAGG GCGGGG GGGG
                                 AACA   G    A
GAM2783  MMP8    3'  CTTCACACGGCCTCCTCCC   64419       __ _ _
                                CTTCGCGC  CC CC CCC
                                ||||||||  || || |||
                                GAAGTGTG  GG GG GGG
                                    CC  A  A
GAM2783  MMP9    3'  CCCACCTCCACTCCTCCC    64420         G  C
                                CCCGCCTTCGC CC CCC
                                |||||||||||  || |||
                                GGGTGGAGGTG GG GGG
                                     A  A
GAM2783  MOG     3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                  _ _  A
GAM2783  MPST    5'  CCCGCGGCGCGGCGCCCCCTCC 64422      CTTC__     _
           C                     CCCGC    GCGCCCCC CCC
                                |||||     |||||||| |||
                                GGGCG     CGCGGGGG GGG
                                  CCGCGC      A
GAM2783  MPST    5'  CCGCGCCCGCAGCTGTCCCCTC 64421     C   _ C__   _
           C                     CCGC TTCGC GC   CCCC CC
                                |||| ||||| ||   |||| ||
```

```
                                GGCG GGGCG CG   GGGG GG
                                  C    T ACA   A
GAM2783  MTA1L1   5'  CCCGCCTCAGGGTTCGCCTCCT 64423        CG____   _ CC
             TCC                   CCCGCCTT     CGCC CC  CC
                                |||||||||     |||| ||  ||
                                GGGCGGAG     GCGG GG  GG
                                    TCCCAA    A  AA
GAM2783  MUC4     3'  CCAGCCTTCACGAAACTCTCCC 64424    C       CCCC___
             C                    CC GCCTTCGCG      CCCC
                                || |||||||||      ||||
                                GG CGGAAGTGC      GGGG
                                 T       TTTGAGA
GAM2783  NCOR2    3'  CCGCCCGCCCCCCCCCC      64425      TTCG
                                CCGCC   CGCCCCCCCCC
                                |||||   ||||||||||
                                GGCGG   GCGGGGGGGGG
                                  ____
GAM2783  NEURL    3'  CCAGCCCCCGCTCCCTCCC   64426    C      G   C
                                CC GCCTTCGC CCC CCC
                                || |||||||| ||| |||
                                GG CGGGGGCG GGG GGG
                                 T       A   A
GAM2783  NFRKB    5'  CCCCTTCCGCGCCCCTCC    64428    G    _      C
                                CC CCTTC GCGCCCC CC
                                || ||||| ||||||| ||
                                GG GGAAG CGCGGGG GG
                                 _    G      A
GAM2783  NFRKB    5'  CCCCTTCCGCGCCCCTCCC   64427    G    _      C
                                CC CCTTC GCGCCCC CCC
                                || ||||| ||||||| |||
                                GG GGAAG CGCGGGG GGG
                                 _    G      A
GAM2783  NLGN1    5'  CCCAGTTTTGCACCCCCCCCC  64429      CC  C
                                CCCG  TT GCGCCCCCCCCC
                                ||||  || ||||||||||||
                                GGGT  AA CGTGGGGGGGGG
                                  CA  A
GAM2783  NMB      5'  CCCGCCGTCCCCACCCTCCC   64430       _  G    C
                                CCCGCC TTC CGCCC CCC
                                |||||| ||| ||||| |||
                                GGGCGG AGG GTGGG GGG
                                   C   G    A
GAM2783  NPHS1    3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  NRXN2    3'  CCCACCCTCCCGCCCTTCTCC  64431         G    CCC_
                                CCCGCCTTC CGCCC   CC
                                ||||||||| |||||   ||
```

```
                                GGGTGGGAG GCGGG   GG
                                    G    AAGA
GAM2783 NRXN2   3' CCCACCCTCCCGCCCTTCTCC 64431       G   CCC_
                                CCCGCCTTC CGCCC   CC
                                ||||||||| |||||   ||
                                GGGTGGGAG GCGGG   GG
                                    G    AAGA
GAM2783 NRXN2   3' CCCACCCTCCCGCCCTTCTCC 64431       G   CCC_
                                CCCGCCTTC CGCCC   CC
                                ||||||||| |||||   ||
                                GGGTGGGAG GCGGG   GG
                                    G    AAGA
GAM2783 OIP2    5' CCCGCCCTCGCATCGACTTTCC 64432        ____ CCC
           CC                  CCCGCCTTCGC   GC  CCCC
                               ||||||||||   ||  ||||
                               GGGCGGGAGCG   TG  GGGG
                                    TAGC  AAA
GAM2783 OPA3    3' CCCGCCTCGGCCTCCC     64318      T C  C
                               CCCGCCT CG GCC CCC
                               ||||||| || ||| |||
                               GGGCGGA GC CGG GGG
                                  _ _  A
GAM2783 PA2G4   3' CCCGCCTCAGCCTCCC     64359      T C  C
                               CCCGCCT CG GCC CCC
                               ||||||| || ||| |||
                               GGGCGGA GT CGG GGG
                                  _ _  A
GAM2783 PAFAH1B1 5' CGCCCGAGCGCTCCCCTCC  64433     TC  _  C
                               CGCCT  GCGC CCCC CC
                               |||||  |||| |||| ||
                               GCGGG  CGCG GGGG GG
                                  CT   A   A
GAM2783 PCDH11X  3' CCCGCCTCGGCCTCCC     64318      T C  C
                               CCCGCCT CG GCC CCC
                               ||||||| || ||| |||
                               GGGCGGA GC CGG GGG
                                  _ _  A
GAM2783 PCDH11Y  3' CCCGCCTCGGCCTCCC     64318      T C  C
                               CCCGCCT CG GCC CCC
                               ||||||| || ||| |||
                               GGGCGGA GC CGG GGG
                                  _ _  A
GAM2783 PCDH11Y  3' CCCGCCTCGGCCTCCC     64318      T C  C
                               CCCGCCT CG GCC CCC
                               ||||||| || ||| |||
                               GGGCGGA GC CGG GGG
                                  _ _  A
GAM2783 PCDH11Y  3' CCCGCCTCGGCCTCCC     64318      T C  C
                               CCCGCCT CG GCC CCC
                               ||||||| || ||| |||
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```
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 PCDH11Y  3' CCCGCCTCGGCCTCCC     64318      T C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 PCDH7    5' CCCCCTCGGCGCCCCCCTCC  64434    G  C      _
                                CCC CCTT GCGCCCCCC CC
                                ||| |||| ||||||||| ||
                                GGG GGAG CGCGGGGGG GG
                                  _  C       A
GAM2783 PCDH7    5' CCCCCTCGGCGCCCCCCTCC  64434    G  C      _
                                CCC CCTT GCGCCCCCC CC
                                ||| |||| ||||||||| ||
                                GGG GGAG CGCGGGGGG GG
                                  _  C       A
GAM2783 PCDH7    5' CCCCCTCGGCGCCCCCCTCC  64434    G  C      _
                                CCC CCTT GCGCCCCCC CC
                                ||| |||| ||||||||| ||
                                GGG GGAG CGCGGGGGG GG
                                  _  C       A
GAM2783 PCDHGA11 3' CCGCCCCACCCCCCCCC    64435      TCG
                                CCGCCT  CGCCCCCCCCC
                                ||||||  ||||||||||
                                GGCGGG  GTGGGGGGGGG
                                  ___
GAM2783 PDAP1    3' CCCTCCCCCAGTCCCCCCCC  64436    G    CG
                                CCC CCTTCG  CCCCCCCC
                                ||| ||||||  ||||||||
                                GGG GGGGGT  GGGGGGGG
                                  A    CA
GAM2783 PDGFRB   3' CCCCCTTCCCAACCCTCCCC  64437    G   G _  C
                                CCC CCTTC CG CCC CCCC
                                ||| ||||| || ||| ||||
                                GGG GGAAG GT GGG GGGG
                                  _   G T  A
GAM2783 PFKFB2   3' CCCGCCCTCCATCCCCC     64438      G  C
                                CCCGCCTTC CG CCCCC
                                ||||||||| || |||||
                                GGGCGGGAG GT GGGGG
                                     _ A
GAM2783 PHF1     3' CCCACCTCGGACTCCTCCCC  64439      T  C  _  C
                                CCCGCCT CG GC CC CCCC
                                ||||||| || || || ||||
                                GGGTGGA GC TG GG GGGG
                                   _ C  A  A
GAM2783 PIK3C2B  3' CCCACCCCATGCCCCTTTCC  64440      T  C   CC_
                                CCCGCCT CG GCCCC  CC
                                ||||||| || |||||  ||
```

```
                                GGGTGGG GT CGGGG   GG
                                   _ A     AAA
GAM2783  PITX1    3'  CCGCGCCCGCGCCCTTCCCC   64441      C        CC
                                CCGC TTCGCGCCC  CCCC
                                |||| |||||||||  ||||
                                GGCG GGGCGCGGG  GGGG
                                  C        AA
GAM2783  PITX2    5'  CGCTCTGCCCGCCCCCCCCC   64442     _ _ G
                                CGC CT TC CGCCCCCCCCC
                                ||| || || ||||||||||
                                GCG GA GG GCGGGGGGGGG
                                 A  C  _
GAM2783  PNOC     5'  CCCACGCACAGCCCTCCCC    64443      CTT  _   C
                                CCCGC   CGC GCCC CCCC
                                |||||   ||| |||| ||||
                                GGGTG   GTG CGGG GGGG
                                  C__   T   A
GAM2783  POU3F2   3'  CCCGCGCTCTGCCCCTCCCC   64444      C   GC    _
                                CCCGC TTC  GCCCC CCCC
                                ||||| |||  ||||| ||||
                                GGGCG GAG  CGGGG GGGG
                                  C  A_    A
GAM2783  PPP2R2B  5'  CCTGCCTCCGCTGCCTCC    64445    C       _  C
                                CC GCCTTCGC GCC CC
                                || |||||||| ||| ||
                                GG CGGAGGCG CGG GG
                                 A       A  A
GAM2783  PRH1     5'  CCAACTTTGTGCTCCCCCCC   64446    C   CGC  _
                                CCG CTT   GC CCCCCCC
                                ||| |||   || |||||||
                                GGT GAA   CG GGGGGGG
                                  T   ACA  A
GAM2783  PRKAR2B  5'  CCGCCCTCGCCCCCTCCC    64447         G    C
                                CCGCCTTCGC CCCC CCC
                                |||||||||| |||| |||
                                GGCGGGAGCG GGGG GGG
                                     _   A
GAM2783  PROC     5'  CCGCCATGACAGCCCCCCCCC  64448      TTC  _
                                CCGCC   GC GCCCCCCCCC
                                |||||   || ||||||||||
                                GGCGG   TG CGGGGGGGGG
                                  TAC  T
GAM2783  PSCD4    3'  CCCTCCTGAGCTCTGCCTTCCC 64449     G   TC  ___   CC
              C                  CCC CCT  GC   GCC  CCCC
                                ||| |||  ||   |||  ||||
                                GGG GGA  CG   CGG  GGGG
                                  A   CT  AGA   AA
GAM2783  PSMB2    3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
```

```
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  PTGS1    3'  CCACCCTCAAAGCCCTTCCCC  64450        C_   CC
                                CCGCCTTCG  GCCC  CCCC
                                |||||||||  ||||  ||||
                                GGTGGGAGT  CGGG  GGGG
                                     TT    AA
GAM2783  PTGS1    3'  CCACCCTCAAAGCCCTTCCCC  64450        C_   CC
                                CCGCCTTCG  GCCC  CCCC
                                |||||||||  ||||  ||||
                                GGTGGGAGT  CGGG  GGGG
                                     TT    AA
GAM2783  PTPRJ    5'  CCGTCTCCTTCGCCTCCTCC   64451     C   G_   C C
                                CCG CTTC  CGCC CC CC
                                ||| ||||  |||| || ||
                                GGC GAGG  GCGG GG GG
                                  A   AA   A A
GAM2783  PYGO2    3'  CCTGCCTTCCCCACCCC     64452    C     GCG  _
                                CC GCCTTC   CCC CCCC
                                || ||||||   ||| ||||
                                GG CGGAAG   GGG GGGG
                                 A     ___   T
GAM2783  RAB1A    5'  CCCTCCCTGCTCCCCTCC    64454     G   C  G   C
                                CCC CCTT GC CCCC CC
                                ||| |||| || |||| ||
                                GGG GGGA CG GGGG GG
                                  A   _ A   A
GAM2783  RAB1A    5'  CCCACCCTCGGCCCCTCCC   64453         C    C
                                CCCGCCTTCG GCCCC CCC
                                |||||||||| ||||| |||
                                GGGTGGGAGC CGGGG GGG
                                     _    A
GAM2783  RAB3B    3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  RBM6     5'  CCTCCACGGCCCGCTCCTCC   64455         _  C__  _
                                CCTTCGCG CCC   CC CC
                                |||||||| |||   || ||
                                GGAGGTGC GGG   GG GG
                                     C   CGA  A
GAM2783  RENBP    5'  CCCGGCTCACCCTCCCCC    64456     C  TCG    _
                                CCCG CT   CGCCC CCCCC
                                |||| ||   ||||| |||||
                                GGGC GA   GTGGG GGGGG
                                  C ___     A
GAM2783  RHEB2    5'  CCCTCTTCGCGCCGTGGCCC  64457     GC       CCC_
                                CCC  CTTCGCGCC    CCC
                                |||  |||||||||    |||
```

```
                                GGG  GAAGCGCGG   GGG
                                  A_       CACC
GAM2783  RHO     3'  GCCTTCACCGTCCCCCTCC   64458        _ _    C
                                GCCTTCGC G CCCCC CC
                                |||||||| | ||||| ||
                                CGGAAGTG C GGGGG GG
                                     G A    A
GAM2783  SCA7    5'  CCCACTTTCAACTTCCCC    64459      C   C  CC
                                CCCGC TTCG GC  CCCC
                                ||||| |||| ||  ||||
                                GGGTG AAGT TG  GGGG
                                   A   _ AA
GAM2783  SCRT1   3'  CCCGCCCTCCGGCCCCTCC   64405        GC    C
                                CCCGCCTTC  GCCCC CC
                                |||||||||  ||||| ||
                                GGGCGGGAG  CGGGG GG
                                     GC    A
GAM2783  SDC2    5'  CCCGCGCCGCGCCTCCCTCC   64460      CT     _  C
                                CCCGC  TCGCGCC CCC CC
                                |||||  ||||||| ||| ||
                                GGGCG  GGCGCGG GGG GG
                                   C_     A  A
GAM2783  SDC4    3'  CCCTCCCCCATTCCCCCCC   64461    G     CG
                                CCC CCTTCG  CCCCCCC
                                ||| ||||||  |||||||
                                GGG GGGGGT  GGGGGGG
                                  A     AA
GAM2783  SERPINF2  3'  CCCAGCCGCGCCCCCCCCC   64462    _  TTC
                                CCC GCC   GCGCCCCCCCCC
                                ||| |||   ||||||||||||
                                GGG CGG   CGCGGGGGGGGG
                                  T  ____
GAM2783  SFRP1   3'  CCCACCCGAGGCTCCCTCCC   64463       TC_  G   C
                                CCCGCCT   GC CCC CCC
                                |||||||   || ||| |||
                                GGGTGGG   CG GGG GGG
                                     CTC  A   A
GAM2783  SHH     3'  CCCCCTCCCGCGCCCCTCCCC  64464    G    _     _
                                CCC CCTTC GCGCCCC CCCC
                                ||| ||||| ||||||| ||||
                                GGG GGAGG CGCGGGG GGGG
                                  _    G      A
GAM2783  SHOX    3'  CCGCCTTCTGCACCATCTCC   64465       _    CCCC
                                CCGCCTTC GCGCC   CC
                                |||||||| |||||   ||
                                GGCGGAAG CGTGG   GG
                                     A    TAGA
GAM2783  SIAH2   5'  CCCGCGCGGTGCCCTCCTCC   64466      CTT  C_   _  C
                                CCCGC   CG  GCCC CC CC
                                |||||   ||  |||| || ||
```

```
                                GGGCG  GC  CGGG GG GG
                                  C__  CA   A  A
GAM2783  SLC14A2  3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _  _   A
GAM2783  SLC26A4  3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _  _   A
GAM2783  SLC28A2  3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _  _   A
GAM2783  SLC9A5   3'  CCACCTCCTGCTCCTCCCC   64467        GC  _  C
                                CCGCCTTC  GC CC CCCC
                                ||||||||  || || ||||
                                GGTGGAGG  CG GG GGGG
                                    A_  A  A
GAM2783  SLC9A5   3'  CCACCTCCTGCTCCTCCCC   64467        GC  _  C
                                CCGCCTTC  GC CC CCCC
                                ||||||||  || || ||||
                                GGTGGAGG  CG GG GGGG
                                    A_  A  A
GAM2783  SMG1     3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _  _   A
GAM2783  SNX15    5'  CGCCGTCCCCACCCCTCC    64468     _  G     C
                                CGCC TTC CGCCCC CC
                                |||| ||| |||||| ||
                                GCGG AGG GTGGGG GG
                                  C  G     A
GAM2783  SOX4     3'  CCTCTCCTACCCCCCCC     64469    GC   GC
                                CC  CTTC  GCCCCCCCC
                                ||  ||||  |||||||||
                                GG  GAGG  TGGGGGGGG
                                 A_   A_
GAM2783  SRC      3'  CCCGGCCCCAGCCCTTCTCC  64470     C    C   CCC_
                                CCCG CTTCG GCCC   CC
                                |||| ||||| ||||   ||
                                GGGC GGGGT CGGG   GG
                                  C    _   AAGA
GAM2783  SURF6    3'  CCCACCCCCCACCGTTCCTCC  64471         _ CC  C
                                CCCGCCTTCGC G  CC CC
                                |||||||||| |  || ||
```

```
                                GGGTGGGGGTG C  GG GG
                                      G AA  A
GAM2783  SWAP70   3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  TACSTD2  5'  CCCGCCCTCGCGGCCTCC    64472           _  C
                                CCCGCCTTCGCG CC CC
                                |||||||||||| || ||
                                GGGCGGGAGCGC GG GG
                                      C  A
GAM2783  TARBP2   5'  CCTTCCTTCCGCGCCCCC    64473    CG    _
                                CC  CCTTC GCGCCCCC
                                ||  ||||| ||||||||
                                GG  GGAAG CGCGGGGG
                                 AA    G
GAM2783  TARBP2   5'  CCTTCCTTCCGCGCCCCC    64473    CG    _
                                CC  CCTTC GCGCCCCC
                                ||  ||||| ||||||||
                                GG  GGAAG CGCGGGGG
                                 AA    G
GAM2783  TBX6     3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  TK1      3'  CCACGCCTCCCGACTTCCTCC  64474    _      G  _ CC  C
                                CC CGCCTTC CG C  CC CC
                                || ||||||| || |  || ||
                                GG GCGGAGG GC G  GG GG
                                 T      _ T AA  A
GAM2783  TMEPAI   5'  CCCCCCCGGCCTCCCC      64475    G     C   C
                                CC CCTTCG GCC CCCC
                                || |||||| ||| ||||
                                GG GGGGGC CGG GGGG
                                 _     _  A
GAM2783  TNFRSF10A 3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  TNFRSF1B 3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  TPMT     3'  CCCGCCTCAGCCCCCC      64476        T  C
                                CCCGCCT CG GCCCCCC
                                ||||||| || |||||||
```

```
                                GGGCGGA GT CGGGGGG
                                    _ _
GAM2783 UMPK     5' CCCGCGTCGGACTCCCTCC   64477      CT  C C  C
                                CCCGC  TCG GC CCC CC
                                ||||||  ||| || ||| ||
                                GGGCG  AGC TG GGG GG
                                   C_  C A  A
GAM2783 WHSC1    3' CCCACCACACCCCCTCCC    64478      TTC     _
                                CCCGCC  GCGCCCCC CCC
                                ||||||  |||||||| |||
                                GGGTGG  TGTGGGGG GGG
                                   ___      A
GAM2783 WNT7A    5' CCAGCCCCCGCCCCTCCC    64479    C     G  C
                                CC GCCTTCGC CCC CCC
                                || |||||||| ||| |||
                                GG CGGGGGCG GGG GGG
                                 T      _  A
GAM2783 WRN      5' CGCTCTCCCCGCCTCCCC    64480    _   G   C
                                CGC CTTC CGCC CCCC
                                ||| |||| |||| ||||
                                GCG GAGG GCGG GGGG
                                  A   G   A
GAM2783 YWHAG    3' CCCACCTACCCTGCCCCCCCCC 64481       _ GC
                                CCCGCCT TC  GCCCCCCCCC
                                ||||||| ||  ||||||||||
                                GGGTGGA GG  CGGGGGGGGG
                                    T  GA
GAM2783 YY1      5' CCGGCGCTCCGCTTCCCCC   64482    C _    GC
                                CC GC CTTCGC  CCCCC
                                || || ||||||  |||||
                                GG CG GAGGCG  GGGGG
                                 C  C     AA
GAM2783 YY1      5' CCCGCCCTGGCCGCGCCTCCTC 64483       ___     _ C
             CC                   CCCGCCT   TCGCGCC CC CCC
                                |||||||   ||||||| || |||
                                GGGCGGG   GGCGCGG GG GGG
                                    ACC      A  A
GAM2783 ZIC1     5' CCGCCTCGCGCAGCCGCCCCTC 64484       _  _  _  _
             C                   CCGCCTT CGC GCC CCCC CC
                                ||||||| ||| ||| |||| ||
                                GGCGGAG GCG CGG GGGG GG
                                    C  T  C   A
GAM2783 ZNF205   3' CGCCCTCGCCCTCCCCC     6007         G  C
                                CGCCTTCGC CC CCCCC
                                |||||||||  || |||||
                                GCGGGAGCG GG GGGGG
                                     _ A
GAM2783 ZNF219   5' CCCGGCCCCCGCCCCCTCCC  64485     _     G   C
                                CCCG CCTTCGC CCCC CCC
                                |||| ||||||| |||| |||
```

```
                                GGGC GGGGGCG GGGG GGG
                                  C      _   A
GAM2783  ZNF79    5'  CCCGCCTCGCGCCACAGCCTCC 64486       T     C___ _
              C                   CCCGCCT CGCGCC   CC CCC
                                  ||||||| ||||||   || |||
                                  GGGCGGA GCGCGG   GG GGG
                                     _     TGTC  A
GAM2783  ABIN-2   5'  CCTGCCTTCGCAGCTGCTCCC  64487    C      _ CCCC
                                  CC GCCTTCGC GC   CCC
                                  || |||||||| ||   |||
                                  GG CGGAAGCG CG   GGG
                                   A       T  ACGA
GAM2783  ACP33    5'  CCGCCCCCACGTCCCTTCCC   64488          _  CC
                                  CCGCCTTCGCG CCC  CCC
                                  |||||||||| |||  |||
                                  GGCGGGGGTGC GGG  GGG
                                        A   AA
GAM2783  AP1G2    5'  CCCACGGGCGCCCCTTCCC   64489      CTTC      CC
                                  CCCGC   GCGCCCC  CCC
                                  |||||   |||||||  |||
                                  GGGTG   CGCGGGG  GGG
                                     CC__      AA
GAM2783  APEG1    3'  CCCTCGCAGCCGCCCCTTCCC  64490       _  _   __
                                  CCTTCGC GCC CCCC  CCC
                                  ||||||| ||| ||||  |||
                                  GGGAGCG CGG GGGG  GGG
                                       T  C   AA
GAM2783  APELIN   5'  CCGCTCTTCTGCAGCCTCC   64491     _   _ _  C
                                  CCGC CTTC GC GCC CC
                                  |||| |||| || ||| ||
                                  GGCG GAAG CG CGG GG
                                    A   A T  A
GAM2783  APOF     3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                  CCCGCCT CG GCC CCC
                                  ||||||| || ||| |||
                                  GGGCGGA GT CGG GGG
                                     _ _   A
GAM2783  APOF     3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                  CCCGCCT CG GCC CCC
                                  ||||||| || ||| |||
                                  GGGCGGA GT CGG GGG
                                     _ _   A
GAM2783  APXL2    3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                  CCCGCCT CG GCC CCC
                                  ||||||| || ||| |||
                                  GGGCGGA GC CGG GGG
                                     _ _   A
GAM2783  ARHU     5'  CCAGCCTCCGCAGCCTCCTCCC 64492    C      _  _ C
                                  CC GCCTTCGC GCC CC CCC
                                  || |||||||| ||| || |||
```

```
                                GG CGGAGGCG CGG GG GGG
                                 T      T  A  A
GAM2783  BIA2     3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  BIRC1    3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  BRD2     5'  CCCACCCCCCGCCTTTCCCC  64493         G    CC_
                                CCCGCCTTC CGCC   CCCC
                                ||||||||| ||||   ||||
                                GGGTGGGGG GCGG   GGGG
                                    _   AAA
GAM2783  BRPF3    5'  GCCTCCGCCGTGCCCCCTCCC  64494         ___     _
                                GCCTTCGC   GCCCCC CCC
                                ||||||||   |||||| |||
                                CGGAGGCG   CGGGGG GGG
                                    GCA     A
GAM2783  BRUNOL6  5'  CCCGCCCTGTCAGCCCTCCC  64495        __  C    C
                                CCCGCCT  TCG GCCC CCC
                                |||||||  ||| |||| |||
                                GGGCGGG  AGT CGGG GGG
                                   AC   _   A
GAM2783  C11orf11 3'  CCCACTCCACACCCTTCCCC  64496      C       CC
                                CCCGC TTCGCGCCC  CCCC
                                ||||| |||||||||  ||||
                                GGGTG AGGTGTGGG  GGGG
                                  _       AA
GAM2783  C13orf1  3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  C1orf25  3'  CCCCCTCCACCCCCTTCC    64497     G     G   CC
                                CCC CCTTCGC CCCC  CC
                                ||| ||||||| ||||  ||
                                GGG GGAGGTG GGGG  GG
                                  _     _   AA
GAM2783  C1orf34  3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  C1QTNF2  3'  CCCGCCTCAGCCTCCCC     64382        T  C   C
                                CCCGCCT CG GCC CCCC
                                ||||||| || ||| ||||
```

```
                                GGGCGGA GT CGG GGGG
                                   _ _  A
GAM2783  C20orf106 3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  C20orf178 3'  CCCACCCCGCCCGCCCCCC   64498       TCG   _
                                CCCGCCT   CGCCC CCCCCC
                                |||||||   ||||| ||||||
                                GGGTGGG   GCGGG GGGGGG
                                   ___   C
GAM2783  C20orf183 3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  C20orf27  3'  CCCACCCCAGGCCCTCCC   64499       T  C   C
                                CCCGCCT CG GCCC CCC
                                ||||||| || |||| |||
                                GGGTGGG GT CGGG GGG
                                   _ C  A
GAM2783  C20orf28  3'  CCACGCCTCACCCCTTCC   64500   _   TCG    CC
                                CC CGCCT   CGCCCC  CC
                                || |||||   ||||||  ||
                                GG GCGGA   GTGGGG  GG
                                 T    ___     AA
GAM2783  C20orf39  5'  GCTCCCCACGCCTCTCCCC  64501   _      CC_
                                GC CTTCGCGCC   CCCC
                                || |||||||||   ||||
                                CG GGGGTGCGG   GGGG
                                 A       AGA
GAM2783  C20orf67  5'  CCGCCTCGCCCTCCCC     64502      TCG   C
                                CCGCCT   CGCCC CCCC
                                ||||||   ||||| ||||
                                GGCGGA   GCGGG GGGG
                                   ___    A
GAM2783  C20orf72  3'  CCTGGGACCACGCCCCCCCCC  64503   GCCT_
                                CC    TCGCGCCCCCCCCC
                                ||    ||||||||||||||
                                GG    GGTGCGGGGGGGGG
                                 ACCCT
GAM2783  C5orf7    5'  CCCGCGGCCGCCGTTCCCCCCC 64504     CT   GC__
                                CCCGC  TCGC   CCCCCCC
                                |||||  ||||   |||||||
                                GGGCG  GGCG   GGGGGGG
                                  CC   GCAA
GAM2783  C8orf13   5'  CCCGCCTCGCCTCCCC     64505      TCG   C
                                CCCGCCT   CGCC CCCC
                                |||||||   |||| ||||
```

```
                                GGGCGGA  GCGG GGGG
                                   ___   A
GAM2783 C9orf7   3' CCCGCTTCTGCCAAGCCCC   64506     C  GC  CC_
                                CCCGC TTC  GCC  CCCC
                                ||||| |||  |||  ||||
                                GGGCG AAG  CGG  GGGG
                                  _  A_  TTC
GAM2783 CARD9    3' CCGCCTTCTCGCCCAGCTCCC 64507       G   CC__
                                CCGCCTTC CGCCC   CCC
                                |||||||| |||||   |||
                                GGCGGAAG GCGGG   GGG
                                    A    TCGA
GAM2783 CBCIP2   3' CCCGCCTCAGCCTCCC     64359       T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783 CBLN1    3' CCTGCCTTCGCCCTCTCCC   64508   C      G  CCC
                                CC GCCTTCGC CC  CCC
                                || ||||||||  ||  |||
                                GG CGGAAGCG GG  GGG
                                 A       _ AGA
GAM2783 CBX6     3' CCCCCCCAAGCCCCCCTCC   64509   G    C    _
                                CC CCTTCG GCCCCCC CC
                                || |||||| ||||||| ||
                                GG GGGGGT CGGGGGG GG
                                 _     T      A
GAM2783 CDH24    3' GCCCGCTGCCCCCCCCC     64510    TT  _
                                GCC  CGC GCCCCCCCCC
                                |||  ||| ||||||||||
                                CGG  GCG CGGGGGGGGG
                                  __  A
GAM2783 cerk     3' CCCGCCTCGGCCTCCC      64318       T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 CHST3    3' CCCACCTTGGCCTCCCC     64511       CGC  C
                                CCCGCCTT   GCC CCCC
                                ||||||||   ||| ||||
                                GGGTGGAA   CGG GGGG
                                    C__   A
GAM2783 CLDN4    3' CCCTGTCACTTCCGTCCCTCCC 64512    GC___   G  _  C
           C                     CCC    CTTC CG CCC CCCC
                                |||    |||| || ||| ||||
                                GGG    GAAG GC GGG GGGG
                                  ACAGT   _ A  A
GAM2783 CSAD     3' CCCGCCTCGGCCTCCC      64318       T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
```

```
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 CTRP5    5' CCAGCCCCCGCGCTTCTCCCC 64513   C       CCC_
                                CC GCCTTCGCGC   CCCC
                                || ||||||||||   ||||
                                GG CGGGGGCGCG   GGGG
                                 T       AAGA
GAM2783 CYP2A7   3' CCCGCCCTGACCCCGCCTTTCC 64514       CGC   _ ___
           C                     CCCGCCTT  GCCCC CC  CCC
                                ||||||||  ||||| ||  |||
                                GGGCGGGA  TGGGG GG  GGG
                                   C__    C  AAA
GAM2783 CYP2A7   3' CCCGCCCTGACCCCGCCTTTCC 64514       CGC   _ ___
           C                     CCCGCCTT  GCCCC CC  CCC
                                ||||||||  ||||| ||  |||
                                GGGCGGGA  TGGGG GG  GGG
                                   C__    C  AAA
GAM2783 DAPK3    3' CCCGTCCCACGACCTCCTCC  64515    _  T C  C C
                                CCCG CCT CG GCC CC CC
                                |||| ||| || ||| || ||
                                GGGC GGG GC TGG GG GG
                                  A  T  _  A A
GAM2783 DAZAP1   3' CCCTCCCCCCGCCCCCCCCC  64516    G   G
                                CCC CCTTC CGCCCCCCCCC
                                ||| ||||| ||||||||||
                                GGG GGGGG GCGGGGGGGGG
                                  A   _
GAM2783 DCAMKL1  3' CCTACCCCCACCTCCCCCC   64517   CG    G_
                                CC  CCTTCGC  CCCCCC
                                ||  |||||||  ||||||
                                GG  GGGGGTG  GGGGGG
                                 AT     GA
GAM2783 DDX34    3' CCCACCTCCTGAGCGTCTCCCC 64518       ___  CCC
                                CCCGCCTTC  GCG  CCCC
                                |||||||||  |||  ||||
                                GGGTGGAGG  CGC  GGGG
                                     ACT  AGA
GAM2783 DDX34    3' CCCGCCTCGGCCTCCC     64318      T C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 DF       3' CCCACCTCGGCCTCCCC    64519      T C  C
                                CCCGCCT CG GCC CCCC
                                ||||||| || ||| ||||
                                GGGTGGA GC CGG GGGG
                                   _ _  A
GAM2783 DF       3' CCCACCTCGGCCTCCCC    64519      T C  C
                                CCCGCCT CG GCC CCCC
                                ||||||| || ||| ||||
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```
                                GGGTGGA GC CGG GGGG
                                    _ _  A
GAM2783  DKFZp434C0923 3'  CCCGCCTGACTGCCTCCTCCC  64520       TC _  _ C
                                CCCGCCT  GC GCC CC CCC
                                |||||||  || ||| || |||
                                GGGCGGA  TG CGG GG GGG
                                   C_  A   A  A
GAM2783  DKFZp434E2220 5'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _  A
GAM2783  DKFZP434F1735 3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _  A
GAM2783  DKFZP434H0820 5'  CCCGCCCTGCTTCCCCC    64521        C  GC
                                CCCGCCTT GC  CCCCC
                                |||||||| ||  |||||
                                GGGCGGGA CG  GGGGG
                                    _ AA
GAM2783  DKFZp434I1117 3'  CCTCCCTTCCTGCCCTCCCC  64522    G_    GC    C
                                CC  CCTTC  GCCC CCCC
                                ||  |||||  |||| ||||
                                GG  GGAAG  CGGG GGGG
                                  AG    GA   A
GAM2783  DKFZP434J193 3'  CCTCCCTCACACCTTCCC    64523    G        CC
                                CC CCTTCGCGCC  CCC
                                || ||||||||||  |||
                                GG GGGAGTGTGG  GGG
                                  A         AA
GAM2783  DKFZp434M0331 5'  CCGCCTTCAGCATCCCCC    64524        _  C
                                CCGCCTTC GCG CCCCC
                                |||||||| ||| |||||
                                GGCGGAAG CGT GGGGG
                                    T  A
GAM2783  DKFZp434N035 3'  CGCCTCCGCAGCAGCCTCC   64526        _ CC  C
                                CGCCTTCGC GC  CC CC
                                ||||||||| ||  || ||
                                GCGGAGGCG CG  GG GG
                                   T  TC  A
GAM2783  DKFZp434N035 3'  CCGCCTCGCGCACCTCCCC   64525       T    _ C
                                CCGCCT CGCGC CC CCCC
                                |||||| ||||| || ||||
                                GGCGGA GCGCG GG GGGG
                                    _    T  A
GAM2783  DKFZP434N1511 3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
```

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                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  DKFZP434N178 3'  CCCGCTGCACGCCCCCTCC   64528      CTT       C
                                CCCGC  CGCGCCCCC CC
                                |||||  ||||||||| ||
                                GGGCG  GTGCGGGGG GG
                                  AC_       A
GAM2783  DKFZP434N178 3'  CCCCTCCGCATCCTCCCCC   64527    G      _ C
                                CC CCTTCGCG CC CCCCC
                                || |||||||| || |||||
                                GG GGAGGCGT GG GGGGG
                                 _      A  A
GAM2783  DKFZP434P0111 3'  CCCCTTGCCAGGCCCTCCCC  64529    G   C ___   C
                                CC CCTT GC   GCCC CCCC
                                || |||| ||   |||| ||||
                                GG GGAA CG   CGGG GGGG
                                 _   _ GTC    A
GAM2783  DKFZp434P0531 3'  CCCACTCAGCACCCCCTCCC  64530      C  C      _
                                CCCGC TT GCGCCCCC CCC
                                ||||| || |||||||| |||
                                GGGTG AG CGTGGGGG GGG
                                  _ T       A
GAM2783  DKFZP564A022 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  DKFZP564O0423 3'  CCTGCCCTCACTGCTCCCCC  64531    C      _ C
                                CC GCCTTCGC GC CCCCC
                                || |||||||| || |||||
                                GG CGGGAGTG CG GGGGG
                                 A       A  A
GAM2783  DKFZP566J2046 3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  DKFZP586I2223 3'  CCCGCTTCCGCCCCCCC     64532      C   G
                                CCCGC TTC CGCCCCCCC
                                ||||| ||| |||||||||
                                GGGCG AAG GCGGGGGGG
                                  _  _
GAM2783  DKFZP586J1624 3'  CCCGCCCCAGCCCTCCC     64533       T  C   C
                                CCCGCCT CG GCCC CCC
                                ||||||| || |||| |||
                                GGGCGGG GT CGGG GGG
                                   _ _   A
GAM2783  DKFZP761E1824 5'  CGCGCCCGCGCCTCCTCCC   64534    C      _ C
                                CGC TTCGCGCC CC CCC
                                ||| |||||||| || |||
```

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                                GCG GGGCGCGG GG GGG
                                  C       A  A
GAM2783  DKFZp761J139 5'  CCCGCCTCGACCTCCC      64535        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC TGG GGG
                                   _ _   A
GAM2783  DKFZP762D096 5'  CGCTGCTGGGCACCCCCTCCC  64536     __ TC       _
                                CGC  CT  GCGCCCCC CCC
                                |||  ||  |||||||| |||
                                GCG  GA  CGTGGGGG GGG
                                  AC  CC       A
GAM2783  DKFZp762E1511 5'  CCCCCCTATCAGCCTCCTCC   64537     G  _  C  C  C
                                CCC CCT TCG GCC CC CC
                                ||| ||| ||| ||| || ||
                                GGG GGA AGT CGG GG GG
                                  G   T   _   A  A
GAM2783  DNAJB5   3'  CCTCCCTCCCACTCCCCCC   64538    G    G   C
                                CC CCTTC CGC CCCCCC
                                || ||||| ||| ||||||
                                GG GGGAG GTG GGGGGG
                                 A    G   A
GAM2783  DZIP1    5'  CCCCCCTCCCGCCCCCTCCC   64539     G    G      _
                                CCC CCTTC CGCCCCC CCC
                                ||| ||||| ||||||| |||
                                GGG GGGAG GCGGGGG GGG
                                  _    G      A
GAM2783  DZIP1    5'  CCCCTCCGCGATCTCCCTCC   64540    G      CCC_  _
                                CC CCTTCGCG    CCC CC
                                || ||||||||    ||| ||
                                GG GGAGGCGC    GGG GG
                                  _       TAGA   A
GAM2783  EDR2     3'  CGCCCTTTCTGCCCTGCCTCCT 64541       __ GC   __ _ _
              CC                  CGCCT  TC  GCCC  CC CC CC
                                ||||| ||  ||||  || || ||
                                GCGGG  AG  CGGG  GG GG GG
                                   AA  A_   AC  A  A
GAM2783  ERF      3'  CCCCCTTCCCATCCCCCC    64542     G    G  C
                                CCC CCTTC CG CCCCCC
                                ||| ||||| || ||||||
                                GGG GGAAG GT GGGGGG
                                  _    G  A
GAM2783  ERO1L    5'  CCCGCCTCGGCCCTCC      64543        T  C    C
                                CCCGCCT CG GCCC CC
                                ||||||| || |||| ||
                                GGGCGGA GC CGGG GG
                                   _ _    A
GAM2783  FAF1     5'  CCGCCTCCTCCGCTTCCTCCC  64544        G_   CC  _
                                CCGCCTTC  CGC  CC CCC
                                ||||||||  |||  || |||
```

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                                GGCGGAGG  GCG  GG GGG
                                    AG   AA  A
GAM2783  FAM3C    5'  CCCGCCTTCCGGCCTCCC    64545         GC   C
                                CCCGCCTTC  GCC CCC
                                |||||||||  ||| |||
                                GGGCGGAAG  CGG GGG
                                     GC   A
GAM2783  FBXO24   3'  CCCCCTAGCAACCCCTTCCC   64546    G   TC  _   CC
                                CCC CCT  GCG CCCC  CCC
                                ||| |||  ||| ||||  |||
                                GGG GGA  CGT GGGG  GGG
                                  _  T_  T   AA
GAM2783  FBXO24   3'  CCCCCTAGCAACCCCTTCCC   64546    G   TC  _   CC
                                CCC CCT  GCG CCCC  CCC
                                ||| |||  ||| ||||  |||
                                GGG GGA  CGT GGGG  GGG
                                  _  T_  T   AA
GAM2783  FGF19    5'  CCCAGCCCCAGCCCCCTCCC   64547    _   T  C    _
                                CCC GCCT CG GCCCCC CCC
                                ||| |||| || |||||| |||
                                GGG CGGG GT CGGGGG GGG
                                  T   _ _    A
GAM2783  FKBP14   3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _  A
GAM2783  FKBP4    3'  CCCAGCCTACACCTTTCCCC   64548    _   TC    CC_
                                CCC GCCT  GCGCC   CCCC
                                ||| ||||  |||||   ||||
                                GGG CGGA  TGTGG   GGGG
                                  T   __    AAA
GAM2783  FKSG28   5'  CGACTTCGCGCACCCGCCTTCC 64549    C      _  _ __
            C                    CG CTTCGCGC CCC CC  CCC
                                || |||||||| ||| ||  |||
                                GC GAAGCGCG GGG GG  GGG
                                 T       T  C  AA
GAM2783  FLJ10157 3'  CCTACATCCACGCCCCTCC   64550    CG C        C
                                CC  C TTCGCGCCCC CC
                                ||  | ||||||||||  ||
                                GG  G AGGTGCGGGG GG
                                 AT T         A
GAM2783  FLJ10211 5'  CCCGCCTTCCAGCACATCC   64551         __   CC
                                CCCGCCTTC  GCGC  CC
                                |||||||||  ||||  ||
                                GGGCGGAAG  CGTG  GG
                                     GT   TA
GAM2783  FLJ10244 3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
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                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  FLJ10460  3' CCCGCCTCAGCCTCCCC    64382       T  C   C
                                CCCGCCT CG GCC CCCC
                                ||||||| || ||| ||||
                                GGGCGGA GT CGG GGGG
                                   _ _  A
GAM2783  FLJ10462  5' CCTCCCTCCGACCTTCCCC   64552    G    G  _  CC
                                CC CCTTC CG CC  CCCC
                                || ||||| || ||  ||||
                                GG GGGAG GC GG  GGGG
                                 A    _  T  AA
GAM2783  FLJ10525  3' CCCCCACAACTCCTCCCC    64553        _ _  C
                                CCTTCGCG C CC CCCC
                                |||||||| | || ||||
                                GGGGGTGT G GG GGGG
                                     T A  A
GAM2783  FLJ11126  3' CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  FLJ11362  3' CCACCTCACCCCCTCCC     64554       TCG     _
                                CCGCCT   CGCCCCC CCC
                                ||||||   ||||||| |||
                                GGTGGA   GTGGGGG GGG
                                   ___      A
GAM2783  FLJ11526  5' CCGCCTCCGGAAGCCCCCTTCC 64555         C__     CC
                                CCGCCTTCG   GCCCCC  CC
                                |||||||||   ||||||  ||
                                GGCGGAGGC   CGGGGG  GG
                                     CTT     AA
GAM2783  FLJ11539  3' CCCCCCGCGCGCGTCCCCC   64557    G   T    CC
                                CCC CCT CGCGC  CCCCC
                                ||| ||| |||||  |||||
                                GGG GGG GCGCG  GGGGG
                                  _  C    CA
GAM2783  FLJ11539  3' CCGCCCTCCGCCGCCTCCCCCC 64556         _ _  _
                                CCGCCTTC GC GCC CCCCCC
                                |||||||| || ||| ||||||
                                GGCGGGAG CG CGG GGGGGG
                                     G  G   A
GAM2783  FLJ11618  3' GCCCCGACCCCCCCCCC     64558     T  C
                                GCCT CG GCCCCCCCCC
                                |||| || ||||||||||
                                CGGG GC TGGGGGGGGG
                                  _ _
GAM2783  FLJ12132  5' CCCGCCTACATTCCCCCCC   64559       T  CG
                                CCCGCCT CG  CCCCCCC
                                ||||||| ||  |||||||
```

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                                GGGCGGA GT  GGGGGGG
                                   T  AA
GAM2783  FLJ12242  5'  CCCGCCCCGCTTCGCCCTTCCC 64560       CG__    CC
              C                   CCCGCCTT   CGCCC  CCCC
                                  ||||||||   |||||  ||||
                                  GGGCGGGG   GCGGG  GGGG
                                     CGAA    AA
GAM2783  FLJ12606  3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                  CCCGCCT CG GCC CCC
                                  ||||||| || ||| |||
                                  GGGCGGA GC CGG GGG
                                     _ _  A
GAM2783  FLJ12671  3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                  CCCGCCT CG GCC CCC
                                  ||||||| || ||| |||
                                  GGGCGGA GC CGG GGG
                                     _ _  A
GAM2783  FLJ12921  3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                  CCCGCCT CG GCC CCC
                                  ||||||| || ||| |||
                                  GGGCGGA GC CGG GGG
                                     _ _  A
GAM2783  FLJ13117  3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                  CCCGCCT CG GCC CCC
                                  ||||||| || ||| |||
                                  GGGCGGA GT CGG GGG
                                     _ _  A
GAM2783  FLJ13224  3'  CCACCCACCTCCCCCC     64561      TTCG   _
                                  CCGCC   CGCC CCCCCC
                                  |||||   |||| ||||||
                                  GGTGG   GTGG GGGGGG
                                     ____  A
GAM2783  FLJ13456  3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                  CCCGCCT CG GCC CCC
                                  ||||||| || ||| |||
                                  GGGCGGA GC CGG GGG
                                     _ _  A
GAM2783  FLJ13621  3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                  CCCGCCT CG GCC CCC
                                  ||||||| || ||| |||
                                  GGGCGGA GC CGG GGG
                                     _ _  A
GAM2783  FLJ13855  3'  CCCACCCCAAGCTCCCTTCC  64562       C_  G   CC
                                  CCCGCCTT  GC CCC  CC
                                  ||||||||  || |||  ||
                                  GGGTGGGG  CG GGG  GG
                                     TT  A   AA
GAM2783  FLJ14100  3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                  CCCGCCT CG GCC CCC
                                  ||||||| || ||| |||
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                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  FLJ14124  3' CCTGCCTCGCGCGGCCCC   64563   C   T   CC
                                CC GCCT CGCGC  CCCC
                                || |||| |||||  ||||
                                GG CGGA GCGCG  GGGG
                                 A   _    CC
GAM2783  FLJ14129  3' CCCGCCTCGGCCTCCC     64318      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  FLJ14225  3' CCCGCCTCGGCCTCCC     64318      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  FLJ14280  3' CCCGCCTCGGCCTCCC     64318      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  FLJ14326  3' CCCGCCTCACCCTCCC     64564      TCG   C
                                CCCGCCT   CGCCC CCC
                                |||||||   ||||| |||
                                GGGCGGA   GTGGG GGG
                                   ___    A
GAM2783  FLJ14346  3' CCCGCCTCGGCCTCCC     64318      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  FLJ14621  3' CCCGCCTCAGCCTCCC     64359      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  FLJ14827  5' CCCGTCCCCGCACCTTCTTCC  64565    C      CCCC_
                                CCCG CTTCGCGCC    CC
                                |||| |||||||||    ||
                                GGGC GGGGCGTGG    GG
                                  A       AAGAA
GAM2783  FLJ14834  3' CCCACCTCCTACCCTCCCCC  64566       GC   _
                                CCCGCCTTC  GCCC CCCCC
                                |||||||||  |||| |||||
                                GGGTGGAGG  TGGG GGGGG
                                     A_   A
GAM2783  FLJ14840  5' CCCAGCTCCGCCCTTCCC   64567    C    G  CC
                                CCCG CTTCGC CC  CCC
                                |||| |||||| ||  |||
```

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                                GGGT GAGGCG GG  GGG
                                  C     _ AA
GAM2783  FLJ20004  3' CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  FLJ20257  5' CCCTCCCCGGCGCTCCTCCCC  64568     G   TC   _ C
                                CCC CCT  GCGC CC CCCC
                                ||| |||  |||| || ||||
                                GGG GGG  CGCG GG GGGG
                                  A  GC   A A
GAM2783  FLJ20280  3' CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  FLJ20320  3' CACTGTCCACACCTCCTCC    64569     C_      C  C
                                CGC  TTCGCGCC CC CC
                                |||  |||||||| || ||
                                GTG  AGGTGTGG GG GG
                                  AC       A  A
GAM2783  FLJ20337  3' CCCGCCTCTGCAGTCCCTTCC  64570       TC   CC   CC
                                CCCGCCT  GCG  CCC  CC
                                |||||||  |||  |||  ||
                                GGGCGGA  CGT  GGG  GG
                                    GA   CA   AA
GAM2783  FLJ20374  5' CCCTGCCGCCAGGCCCCTCCCC 64571     _  T   C    _
                                CCC GCC TCG GCCCC CCCC
                                ||| ||| ||| ||||| ||||
                                GGG CGG GGT CGGGG GGGG
                                  A  C   C    A
GAM2783  FLJ20464  3' CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  FLJ20700  3' CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  FLJ21032  5' CCGCACGTCCAGTCCCCTCC  64572     CTTC  _ ___   _
                                CCGC   GCG CC   CCCC CC
                                ||||   ||| ||   |||| ||
                                GGCG   TGC GG   GGGG GG
                                  ____  A TCA   A
GAM2783  FLJ21839  5' CCCACCTCCTACCCCTTCCC  64573        GC    CC
                                CCCGCCTTC  GCCCC  CCC
                                |||||||||  |||||  |||
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                                GGGTGGAGG  TGGGG  GGG
                                    A_     AA
GAM2783  FLJ22313  3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  FLJ22386  3'  CCCGCCTCCCTGACCTCCCC   64574         GC_   C
                                CCCGCCTTC   GCC CCCC
                                |||||||||   ||| ||||
                                GGGCGGAGG   TGG GGGG
                                    GAC   A
GAM2783  FLJ22578  3'  CCCGCCCTCCACCCCCC     64575         G
                                CCCGCCTTC CGCCCCCC
                                ||||||||| ||||||||
                                GGGCGGGAG GTGGGGGG
                                   _
GAM2783  FLJ22593  5'  CGCCCTCAGCAGCCCCTTCC   64576        _ _    CC
                                CGCCTTC GC GCCCC  CC
                                ||||||| || |||||  ||
                                GCGGGAG CG CGGGG  GG
                                    T T    AA
GAM2783  FLJ22679  5'  CCCCCACAACCCCCCTCC    64577         _     _
                                CCTTCGCG CCCCCC CC
                                |||||||| |||||| ||
                                GGGGGTGT GGGGGG GG
                                    T     A
GAM2783  FLJ22688  3'  CCCCTCCTACCCCCTCCC    64578    G    GC     _
                                CC CCTTC  GCCCCC CCC
                                || |||||  |||||| |||
                                GG GGAGG  TGGGGG GGG
                                  _    A_     A
GAM2783  FLJ22795  3'  CCCACACCTACGCCTTCCCC   64579      _  C    CC
                                CCCGC CTT GCGCC  CCCC
                                ||||| ||| |||||  ||||
                                GGGTG GGA TGCGG  GGGG
                                   T   _    AA
GAM2783  FLJ23042  3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  FLJ23112  3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  FLJ23120  3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
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                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  FLJ23598  5'  CCGCCTTCGCGCCCCGGCCC  64580            CC
                                CCGCCTTCGCGCCCC  CCC
                                |||||||||||||||  |||
                                GGCGGAAGCGCGGGG  GGG
                                      CC
GAM2783  FLJ23878  3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  FLJ30567  3'  CACCTTCAGTTGCCCTCCTCC  64581        C__   _  C
                                CGCCTTCG   GCCC CC CC
                                ||||||||   |||| || ||
                                GTGGAAGT   CGGG GG GG
                                     CAA    A  A
GAM2783  FLJ30681  3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  FLJ31564  5'  CCTCCGGCCGCCCCCTCCC   64582       __     _
                                CCTTCG  CGCCCCC CCC
                                ||||||  ||||||| |||
                                GGAGGC  GCGGGGG GGG
                                   CG      A
GAM2783  FLJ32449  3'  CACCTTTCAGCCCTTCCC    64583       _  C   CC
                                CGCCTT CG GCCC  CCC
                                ||||||  || ||||  |||
                                GTGGAA GT CGGG  GGG
                                   A  _   AA
GAM2783  FLJ32915  5'  CCCGCCTTGGCCTCCCTCC   64584        CGC  _  C
                                CCCGCCTT   GCC CCC CC
                                ||||||||   ||| ||| ||
                                GGGCGGAA   CGG GGG GG
                                     C__   A  A
GAM2783  FN5       3'  CCCCCTCCCGCGCCTTCC    64585     G    _    CC
                                CCC CCTTC GCGCC  CC
                                ||| ||||| |||||  ||
                                GGG GGAGG CGCGG  GG
                                  _    G    AA
GAM2783  FUSIP1    3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  GAGED3    5'  CCCGCGTCATGCAGTCCTCCC  64586      CT   C  CC_ _
                                CCCGC  TCG GC   CC CCC
                                |||||  ||| ||   || |||
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```
                                GGGCG  AGT CG   GG GGG
                                  C_   A  TCA  A
GAM2783  GLTP     3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  GPR      5'  CCCCCTTTCTTAGCCCCCC   64587     G   _ GC_
                                CCC CCTT C   GCCCCCC
                                ||| |||| |   |||||||
                                GGG GGAA G   CGGGGGG
                                  _    A AAT
GAM2783  GREB1    3'  CCCGCCAACTCCCCCCC     64588       TTC  G
                                CCCGCC   GC CCCCCCC
                                ||||||   || |||||||
                                GGGCGG   TG GGGGGGG
                                   T__  A
GAM2783  HEMK     3'  CCCCCTTCGCCCTCCCC     64589     G     G  C
                                CCC CCTTCGC CC CCCC
                                ||| ||||||| || ||||
                                GGG GGAAGCG GG GGGG
                                  _     _ A
GAM2783  HES2     3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  HIG2     3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  HOOK1    5'  CCCTCCTACCGGCTCTCCTCC  64591     G  _  C  CCC  _
                                CCC CCT TCG GC   CC CC
                                ||| ||| ||| ||   || ||
                                GGG GGA GGC CG   GG GG
                                  A   T   _ AGA  A
GAM2783  HOOK1    5'  CCAGCGTTCGCCCCCTCCC   64590    C  C    G   C
                                CC GC TTCGC CCCC CCC
                                || || ||||| |||| |||
                                GG CG AAGCG GGGG GGG
                                  T  C    _   A
GAM2783  HSJ001348 5'  GCCTCCGCGCGCCTCTCCCC  64592          _  C__
                                GCCTTCGCGC CC   CCCC
                                |||||||||| ||   ||||
                                CGGAGGCGCG GG   GGGG
                                      C  AGA
GAM2783  HSPC134  5'  CCGCCCTCAGCGTCCTCC    64593         _  _  C
                                CCGCCTTC GCG CC CC
                                |||||||| ||| || ||
```

```
                                GGCGGGAG CGC GG GG
                                     T  A A
GAM2783  IL-17RC   5'  CCTGTGCTGCCCCCCCCC    64594     TC  _
                                CCT  GC GCCCCCCCCC
                                |||  || ||||||||||
                                GGA  CG CGGGGGGGGG
                                  CA  A
GAM2783  IMAGE:4215339 3'  CCCACCCCCATTCCCTCCC   64595          CG   C
                                CCCGCCTTCG  CCC CCC
                                ||||||||||  ||| |||
                                GGGTGGGGGT  GGG GGG
                                     AA   A
GAM2783  IMAGE:4907098 3'  CCTGCCTCCACAGGCTCCCC   64596    C       __  C
                                CC GCCTTCGC  GC CCCC
                                || ||||||||  || ||||
                                GG CGGAGGTG  CG GGGG
                                 A       TC  A
GAM2783  jdp2     3'  CCCGCAGCACGCCCCTCTCC   64597      CTT       CC_
                                CCCGC   CGCGCCCC   CC
                                |||||   ||||||||   ||
                                GGGCG   GTGCGGGG   GG
                                   TC_       AGA
GAM2783  KATII    5'  GCCTCGCCGCGCCCCCTCCC   64598       __        _
                                GCCTT  CGCGCCCCC CCC
                                |||||  ||||||||| |||
                                CGGAG  GCGCGGGGG GGG
                                   CG        A
GAM2783  KCNH4    5'  CCCTCTGGGCAGCCCTCCTCC  64599     GC  TC  _   _  C
                                CCC  CT  GC GCCC CC CC
                                |||  ||  || |||| || ||
                                GGG  GA  CG CGGG GG GG
                                  A_  CC  T   A  A
GAM2783  KCNH6    3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                     _  _   A
GAM2783  KIAA0057  3'  CCCTCTAACCACCCCCCCC   64600     GC  TCG
                                CCC  CT   CGCCCCCCCC
                                |||  ||   ||||||||||
                                GGG  GA   GTGGGGGGGG
                                  A_  TTG
GAM2783  KIAA0074  3'  CCCCCTCTGCCCTCCCC     64601    G    GC    C
                                CC CCTTC  GCCC CCCC
                                || |||||  |||| ||||
                                GG GGGAG  CGGG GGGG
                                 _    A_   A
GAM2783  KIAA0159  5'  CCCGCCTGCGAATCCCTCC   64602        TC   CCC  _
                                CCCGCCT  GCG   CCC CC
                                |||||||  |||   ||| ||
```

```
                                GGGCGGA  CGC   GGG GG
                                   __  TTA   A
GAM2783  KIAA0193  3'  CCCTCCTCCACGTGCTTCCTTC 64603     G     __  CC  CC
              C                     CCC CCTTCGC  GC  CC  CC
                                    ||| |||||||  ||  ||  ||
                                    GGG GGAGGTG  CG  GG  GG
                                      A      CA  AA  AA
GAM2783  KIAA0211  5'  CCCGCCTCCCGCCTCCC     64604         G   C
                                    CCCGCCTTC CGCC CCC
                                    ||||||||| |||| |||
                                    GGGCGGAGG GCGG GGG
                                         _   A
GAM2783  KIAA0227  5'  CCCGCACTCCCATTCTCCCC  64605      _   G  CCCC
                                    CCCGC CTTC CG    CCCC
                                    ||||| |||| ||    ||||
                                    GGGCG GAGG GT    GGGG
                                       T   _  AAGA
GAM2783  KIAA0227  5'  CCCGCTCCCGCCCTCCTCC   64606      CT  G    _  C
                                    CCCGC  TC CGCCC CC CC
                                    |||||  || ||||| || ||
                                    GGGCG  AG GCGGG GG GG
                                       __  G    A  A
GAM2783  KIAA0280  3'  CCTGGCCTTACCCCCCC     64607    C_    CGC
                                    CC  GCCTT   GCCCCCCC
                                    ||  |||||   ||||||||
                                    GG  CGGAA   TGGGGGGG
                                     AC    ____
GAM2783  KIAA0446  5'  CCCCCCTCAACCTCCCC     64608     G     C   C
                                    CCC CCTTCG GCC CCCC
                                    ||| |||||| ||| ||||
                                    GGG GGGAGT TGG GGGG
                                      _     _   A
GAM2783  KIAA0455  5'  CCCGCCTTCTCCCCGCCCC   64609         GCG   _
                                    CCCGCCTTC   CCCC CCCC
                                    |||||||||   |||| ||||
                                    GGGCGGAAG   GGGG GGGG
                                         A__    C
GAM2783  KIAA0469  3'  CCTTCACGCGTCCCTCCC    64610         C_  _
                                    CCTTCGCGC  CCC CCC
                                    |||||||||  ||| |||
                                    GGAAGTGCG  GGG GGG
                                         CA   A
GAM2783  KIAA0472  3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                    CCCGCCT CG GCC CCC
                                    ||||||| || ||| |||
                                    GGGCGGA GT CGG GGG
                                       _  _   A
GAM2783  KIAA0476  5'  CCTCCGCCATGGCCCCCCCC  64611        _____
                                    CCTTCGC    GCCCCCCCC
                                    |||||||    |||||||||
```

```
                                GGAGGCG   CGGGGGGGG
                                   GTAC
GAM2783 KIAA0476 5' CCCGCTTTCTCTACTCCCCC  64612     C  GC_ C
                                CCCGC TTC  GC CCCCC
                                ||||| |||  || |||||
                                GGGCG AAG  TG GGGGG
                                  A  AGA  A
GAM2783 KIAA0514 3' CCCACCTCAGAACCCCTTCC  64613       CGC   CC
                                CCCGCCTT  GCCCC  CC
                                ||||||||  |||||  ||
                                GGGTGGAG  TGGGG  GG
                                    TCT   AA
GAM2783 KIAA0552 3' CCCACTCACCCTGCCCTCCTCC 64614     CT  ___  _ C
                                CCCGC  TCGC  GCCC CC CC
                                |||||  ||||  |||| || ||
                                GGGTG  AGTG  CGGG GG GG
                                  __  GGA  A  A
GAM2783 KIAA0563 3' CCCGCCTCGGCCTCCC     64318      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 KIAA0596 3' CCCGCCTCGGCCTCCC     64318      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 KIAA0599 3' CCCGCCCTCACATCCTCC   64615        C  C
                                CCCGCCTTCGCG CC CC
                                |||||||||||| || ||
                                GGGCGGGAGTGT GG GG
                                      A  A
GAM2783 KIAA0616 3' CCCGCGCTCTGGCGCCTCCTCC 64616     _  C_  _ C
          C                      CCCGC CTT  GCGCC CC CCC
                                |||||  |||  ||||| || |||
                                GGGCG GAG  CGCGG GG GGG
                                  C  AC   A  A
GAM2783 KIAA0616 3' ACCATGCGCGCCCCTCCCC  64617   TT_     _
                                GCC  CGCGCCCC CCCC
                                |||  |||||||| ||||
                                TGG  GCGCGGGG GGGG
                                  TAC      A
GAM2783 KIAA0618 5' CGCCTCCGCCACCACCTCCC  64618       _  _ C
                                CGCCTTCGC GCC CC CCC
                                ||||||||| ||| || |||
                                GCGGAGGCG TGG GG GGG
                                    G  T  A
GAM2783 KIAA0628 3' CCCGCCTCGGCCTCCC     64318      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
```

```
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 KIAA0649 5' CCCGCCTCCCCGCCTCCCC  64619       G  C
                                CCCGCCTTC CGCC CCCC
                                ||||||||| |||| ||||
                                GGGCGGAGG GCGG GGGG
                                    G   A
GAM2783 KIAA0668 3' CCCGCCTTCTTGCCCCTTCCC 64620       GC   CC
                                CCCGCCTTC  GCCCC  CCC
                                |||||||||  |||||  |||
                                GGGCGGAAG  CGGGG  GGG
                                    AA    AA
GAM2783 KIAA0711 5' CCCGCCTCGCCTTTGCCCTCTC 64621      T  ____  CCC
          C                      CCCGCCT CGC   GCCC  CC
                                ||||||| |||   ||||  ||
                                GGGCGGA GCG   CGGG  GG
                                   _  GAAA   AGA
GAM2783 KIAA0731 3' CCCACCCTACCCCTTTCC   64622       CGC   CC_
                                CCCGCCTT  GCCCC  CC
                                ||||||||  |||||  ||
                                GGGTGGGA  TGGGG  GG
                                    ___   AAA
GAM2783 KIAA0800 5' CCGCCGCTGCCCCCCCCC   64623     TTC  _
                                CCGCC  GC GCCCCCCCCC
                                |||||  || ||||||||||
                                GGCGG  CG CGGGGGGGGG
                                  ___ A
GAM2783 KIAA0872 3' CCCGCCTCGGCCTCCC     64318      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 KIAA0889 3' CCCGCCTCGGCCTCCC     64318      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 KIAA0995 5' CCCCCTCCAGCTCCTCC    64624    G    C  C  C
                                CCC CCTTCG GC CC CC
                                ||| |||||| || || ||
                                GGG GGAGGT CG GG GG
                                  _   _ A  A
GAM2783 KIAA1091 5' CCGCCCTCAGGCCGCCCCTCCC 64625       C  _  _
                                CCGCCTTCG GCC CCCC CCC
                                ||||||||| ||| |||| |||
                                GGCGGGAGT CGG GGGG GGG
                                    C  C   A
GAM2783 KIAA1160 3' CCCGCCTCGGCCTCCC     64318      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
```

```
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 KIAA1194 5' CCGCCGCTGCCGCCTCCTCC  64626     TTC _  _ _ _
                                CCGCC  GC GCC CC CC CC
                                |||||  || ||| || || ||
                                GGCGG  CG CGG GG GG GG
                                   ___ A  C A A
GAM2783 KIAA1196 3' CCCGCCCAGTGCCTGCTCCCCT 64627      TC_ __ _  C
           CC                    CCCGCCT  GC  GC CCCC CC
                                |||||||  ||  || |||| ||
                                GGGCGGG  CG  CG GGGG GG
                                   TCA  GA  A   A
GAM2783 KIAA1204 5' CCCGCCCTCACGCCTTCC   64628          CC
                                CCCGCCTTCGCGCC  CC
                                ||||||||||||||  ||
                                GGGCGGGAGTGCGG  GG
                                      AA
GAM2783 KIAA1228 3' CCCGCCTCGGCCTCCC     64318      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 KIAA1257 3' CCCGCCTCGGCCTCCC     64318      T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 KIAA1277 3' CCTTCTCCACACCCTCCC   64629   GC       C
                                CC  CTTCGCGCCC CCC
                                ||  ||||||||| |||
                                GG  GAGGTGTGGG GGG
                                 AA        A
GAM2783 KIAA1340 5' CCAGCCTTCGCGGGCCCC   64630   C       CC
                                CC GCCTTCGCG  CCCC
                                || |||||||||  ||||
                                GG CGGAAGCGC  GGGG
                                 T        CC
GAM2783 KIAA1372 3' GCCCCCCGCCCCCCCCC    64632      G
                                GCCTTC CGCCCCCCCCC
                                |||||| ||||||||||
                                CGGGGG GCGGGGGGGGG
                                   _
GAM2783 KIAA1372 3' CCTGCCTCCACAGCTTCCC  64631   C      _ CC
                                CC GCCTTCGC GC  CCC
                                || |||||||| ||  |||
                                GG CGGAGGTG CG  GGG
                                 A       T  AA
GAM2783 KIAA1373 5' CCGCCTCTGCCTCCGCCCCCTC 64633      TC  G_ _   _
           C                     CCGCCT  GC  CC CCCCC CC
                                ||||||  ||  || ||||| ||
```

```
                                GGCGGA  CG  GG GGGGG GG
                                   GA  GA  C    A
GAM2783  KIAA1465  5'  CCCGGTTTCCGCCCCCC    64634     CC   G
                                CCCG  TTC CGCCCCCC
                                ||||  ||| ||||||||
                                GGGC  AAG GCGGGGGG
                                  CA  _
GAM2783  KIAA1465  3'  CGCCGCGCCGCGCCCCTCCCC  64635     T__      _
                                CGCC   TCGCGCCCC CCCC
                                ||||   ||||||||| ||||
                                GCGG   GGCGCGGGG GGGG
                                  CGC       A
GAM2783  KIAA1715  3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  KIAA1719  5'  CCCACCTTCAGGGAGCCCTCCC 64636         C___   C
                                CCCGCCTTCG    GCCC CCC
                                ||||||||||    |||| |||
                                GGGTGGAAGT    CGGG GGG
                                     CCCT    A
GAM2783  KIAA1737  5'  CCCACACGCAGCCCCCTCC   64638     CTT  _    C
                                CCCGC   CGC GCCCCC CC
                                |||||   ||| ||||||  ||
                                GGGTG   GCG CGGGGG GG
                                  T__   T     A
GAM2783  KIAA1737  5'  CCCTCACACAAGCCTCCTCCC  64637        ___  _  _
                                CCTTCGCGC   CC CC CCC
                                |||||||||   || || |||
                                GGGAGTGTG   GG GG GGG
                                     TTC  A  A
GAM2783  KIAA1813  5'  CCACCCGGAACCCCCTCCC   64639      TCGC    _
                                CCGCCT    GCCCCC CCC
                                ||||||    |||||| |||
                                GGTGGG    TGGGGG GGG
                                   CCT_     A
GAM2783  KIAA1813  5'  CCGCCTCCGCGGCGCCCCC   51554          _ _
                                CCGCCTTCGCG C CCCCC
                                |||||||||||  | |||||
                                GGCGGAGGCGC G GGGGG
                                     C C
GAM2783  KIAA1817  3'  CCTCCCCCCACCCCCCTCC   64640   G    G      _
                                CC CCTTC CGCCCCCC CC
                                ||  ||||| |||||||| ||
                                GG GGGGG GTGGGGGG GG
                                 A    _       A
GAM2783  KIAA1821  3'  CCTCTCTTTCTGCAACTCCCCC 64641    GC_  _ _  _ C
                                CC   CTT C GCG C CCCCC
                                ||   ||| | ||| | |||||
```

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                                GG   GAA G CGT G GGGGG
                                 AGA   A A   T A
GAM2783  KIAA1841  3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _   A
GAM2783  KIAA1870  3'  CCACGCCTGGCTGCTCCTTCCC 64642    _    TC _ _ CC
                                CC CGCCT  GC GC CC  CCC
                                || |||||  || || ||  |||
                                GG GCGGA  CG CG GG  GGG
                                 T    C_  A  A  AA
GAM2783  KIAA1879  3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _   A
GAM2783  KIAA1951  3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _   A
GAM2783  LIP8      5'  CCCCCTCTCACGCCTCCCCC   64643     G  _     C
                                CCC CCT TCGCGCC CCCCC
                                ||| ||| ||||||| |||||
                                GGG GGA AGTGCGG GGGGG
                                  _  G      A
GAM2783  LIPG      5'  CCCGCCACACCCCCTCCC    64644       TTC      _
                                CCCGCC   GCGCCCCC CCC
                                ||||||   |||||||| |||
                                GGGCGG   TGTGGGGG GGG
                                    ___       A
GAM2783  LMOD1     3'  CCCTCCCCACGCTCCCC     64645     GC       C
                                CCC  CTTCGCGC CCCC
                                |||  |||||||| ||||
                                GGG  GGGGTGCG GGGG
                                  A_       A
GAM2783  LSR68     3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _   A
GAM2783  LYSAL1    3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _   A
GAM2783  MAD4      3'  CCCGCCCTTCACAGACCCC   64646       _     CC
                                CCCGCC TTCGCG  CCCC
                                |||||| ||||||  ||||
```

```
                                GGGCGG AAGTGT  GGGG
                                   G     CT
GAM2783  MAP2K1IP1 5'  CCGGCGGCCGCGCCCCTCCCC  64647    C  CT       _
                                CC GC  TCGCGCCCC CCCC
                                || ||  ||||||||| ||||
                                GG CG  GGCGCGGGG GGGG
                                 C  CC        A
GAM2783  MAPK8IP3  3'  CCTGCCCCACGTTCCTCCCC   64648    C    T    CC  _
                                CC GCCT CGCG  CC CCCC
                                || |||| ||||  || ||||
                                GG CGGG GTGC  GG GGGG
                                 A   _   AA  A
GAM2783  MAPKAPK2  5'  CCGGCTCCGGGCCCCCTCCC   64649    C    C    _
                                CCG CTTCG GCCCCC CCC
                                ||| ||||| |||||| |||
                                GGC GAGGC CGGGGG GGG
                                  C    C     A
GAM2783  MAPKAPK2  5'  CCGGCTCCGGGCCCCCTCCC   64649    C    C    _
                                CCG CTTCG GCCCCC CCC
                                ||| ||||| |||||| |||
                                GGC GAGGC CGGGGG GGG
                                  C    C     A
GAM2783  MARK2    3'  CCCATCCACCCTCCCC     64650     CCT  G    C
                                CCCG   TC CGCCC CCCC
                                ||||   || ||||| ||||
                                GGGT   AG GTGGG GGGG
                                  ____  _    A
GAM2783  MARK2    3'  CCCATCCACCCTCCCC     64650     CCT  G    C
                                CCCG   TC CGCCC CCCC
                                ||||   || ||||| ||||
                                GGGT   AG GTGGG GGGG
                                  ____  _    A
GAM2783  MCAM     3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _  _   A
GAM2783  MGC10963  5'  CCAGCCGCCGCTCCTCCCC   64651    C   T    G  C
                                CC GCC TCGC CC CCCC
                                || ||| |||| || ||||
                                GG CGG GGCG GG GGGG
                                 T   C    A  A
GAM2783  MGC10986  3'  CCCAGCTCGACCTCCTTCC   64652     _  CT   C   _  CC
                                CCC GC  TCG GCC CC  CC
                                ||| ||  ||| ||| ||  ||
                                GGG CG  AGC TGG GG  GG
                                  T  __   _   A  AA
GAM2783  MGC10999  3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
```

```
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  MGC11316  3'  CACCCCCACTGTCCCCTCCC  64653        GC_  _
                                CGCCTTCGC  CCCC CCC
                                |||||||||  |||| |||
                                GTGGGGGTG  GGGG GGG
                                     ACA   A
GAM2783  MGC1203   3'  CCATTCAACGCCCCCCTCC   64654   _  _     _
                                CC TTCG CGCCCCCC CC
                                || |||| |||||||| ||
                                GG AAGT GCGGGGGG GG
                                 T  T      A
GAM2783  MGC1203   5'  CCGCCCTCCGCCCTCTCC    64655       G    CCC
                                CCGCCTTC CGCCC  CC
                                |||||||| |||||  ||
                                GGCGGGAG GCGGG  GG
                                   _   AGA
GAM2783  MGC13114  3'  CCCGCCTTTCCGACGCCCCC  64656       __  _
                                CCCGCCT  TCG CGCCCCC
                                |||||||  ||| |||||||
                                GGGCGGA  GGC GCGGGGG
                                    AA  T
GAM2783  MGC14126  3'  CCCGCCTCAGCCTCCC     64359       T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  MGC14799  3'  CCCGCCTCGGCCTCCC     64318       T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  MGC14839  3'  CCACGCCTCAGCCCCCTTCC  64657   _   T  C    CC
                                CC CGCCT CG GCCCCC  CC
                                || ||||| || ||||||  ||
                                GG GCGGA GT CGGGGG  GG
                                 T   _ _    AA
GAM2783  MGC15416  5'  CCATCTCCACGATGTTTCCCTC 64658    C     CCC___  _
           C                     CCG CTTCGCG     CCC CC
                                ||| |||||||     ||| ||
                                GGT GAGGTGC     GGG GG
                                  A      TACAAA   A
GAM2783  MGC20258  3'  CCGCCCTCCCCGCTCCTCCCC  64659       _ G  _ C
                                CCGCCTT C CGC CC CCCC
                                ||||||| | ||| || ||||
                                GGCGGGA G GCG GG GGGG
                                    G G   A  A
GAM2783  MGC20647  3'  CCCCCCTCACTCGTCCCCCCCC 64660    G     GC__
                                CCC CCTTCGC   CCCCCCCC
                                ||| |||||||   ||||||||
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```
                                GGG GGGAGTG    GGGGGGGG
                                  _      AGCA
GAM2783 MGC20781 5' CCCACTCCGGACGCTTCCTCCC 64661      _ TC    CC _
                                CCCGC CT  GCGC  CC CCC
                                ||||| ||  ||||  || |||
                                GGGTG GG  TGCG  GG GGG
                                   A  CC    AA  A
GAM2783 MGC2562  3' CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _  A
GAM2783 MGC2601  3' CCCTCCTACCAGCCCCTCCCC  64662     G  _  C    _
                                CCC CCT TCG GCCCC CCCC
                                ||| ||| ||| ||||| ||||
                                GGG GGA GGT CGGGG GGGG
                                  A  T  _    A
GAM2783 MGC2835  3' CCTACCTTTCGGCCTCCCCC  64663    CG   _ C   C
                                CC  CCTT CG GCC CCCCC
                                ||  |||| || ||| |||||
                                GG  GGAA GC CGG GGGGG
                                 AT    A _  A
GAM2783 MGC2941  5' CCCGGTCCGGCGCCCCCCTCC  64664      CC   _      _
                                CCCG  TTCG CGCCCCCC CC
                                ||||  |||| |||||||| ||
                                GGGC  AGGC GCGGGGGG GG
                                  C_   C       A
GAM2783 MGC29891 3' CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _  A
GAM2783 MGC3169  3' CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _  A
GAM2783 MGC31963 3' CCCGCCTCCAAAGTCCCCC   64665         CG__
                                CCCGCCTTCG   CCCCC
                                ||||||||||   |||||
                                GGGCGGAGGT   GGGGG
                                     TTCA
GAM2783 MGC35558 3' CCGCCTTCCCAGCAGCTCCCTT 64666        ___ _ _  CC
           CC                   CCGCCTTC   GC GC CCC  CC
                                ||||||||   || || |||  ||
                                GGCGGAAG   CG CG GGG  GG
                                    GGT  T  A   AA
GAM2783 MGC4562  3' CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
```

```
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  MGC4655   5'  CCGCGCGGCCTGCGCCCTCCC  64667    _  __  C    C
                                CC CGC  CTT GCGCCC CCC
                                || |||  ||| |||||| |||
                                GG GCG  GGA CGCGGG GGG
                                 C  CC  _    A
GAM2783  MGC8407   3'  CCCATCCCCTGCCCCCCC    64668    C   GC
                                CCCG CTTC  GCCCCCCC
                                |||| ||||  ||||||||
                                GGGT GGGG  CGGGGGGG
                                  A   A_
GAM2783  MIG2      5'  CCCGCGCTCCACCCTCTCCC   64669     C  G   CC_
                                CCCGC TTC CGCCC   CCC
                                ||||| ||| |||||   |||
                                GGGCG GAG GTGGG   GGG
                                   C  _    AGA
GAM2783  MLLT10    5'  CCGCCTCCTCCGCCTCCTCC   64309       G_   C  C
                                CCGCCTTC  CGCC CC CC
                                ||||||||  |||| || ||
                                GGCGGAGG  GCGG GG GG
                                    AG   A  A
GAM2783  MYH7B     3'  CCCGCCCTGCCTGCTCCTCC   64670       C  __  C  C
                                CCCGCCTT GC  GC CC CC
                                |||||||| ||  || || ||
                                GGGCGGGA CG  CG GG GG
                                   _ GA  A  A
GAM2783  N4BP3     3'  CCCACCCCAGCCTCCTTCC    64671       T  C   _  CC
                                CCCGCCT CG GCC CC  CC
                                ||||||| || ||| ||  ||
                                GGGTGGG GT CGG GG  GG
                                   _ _   A  AA
GAM2783  NEIL2     5'  CCCTCCCTTCCTGTCCCCTCCC 64672     G_    GCG_   C
                                CCC  CCTTC   CCCC CCC
                                |||  |||||   |||| |||
                                GGG  GGAAG   GGGG GGG
                                  AG    GACA   A
GAM2783  NOPAR     5'  CCTGCCTCCTCTGCTCCCCCC  64673    C     GC_  C
                                CC GCCTTC   GC CCCCCC
                                || ||||||   || ||||||
                                GG CGGAGG   CG GGGGGG
                                 A     AGA  A
GAM2783  NTN4      5'  CCTCCTCCTGGGCGTCCTCCTC 64674    G    ___   _  C  C
              C                  CC CCTTC   GCG CC CC CC
                                || |||||   ||| || || ||
                                GG GGAGG   CGC GG GG GG
                                 A    ACC   A  A  A
GAM2783  NXPH3     3'  CCTCGTCTCCACCCCCCTCC   64675    _  C     G    C
                                CC CG CTTCGC CCCCC CC
                                || || |||||| ||||| ||
```

```
                                GG GC GAGGTG GGGGG GG
                                 A  A     _    A
GAM2783  NYD-SP15  5'  GCCCTAGCGCCCCCCCCC    64676      C
                                GCCTT GCGCCCCCCCCC
                                ||||| ||||||||||||
                                CGGGA CGCGGGGGGGGG
                                   T
GAM2783  NYD-SP22  5'  CCCACACTGATGCCCCCCCCC  64677      _  TCGC
                                CCCGC CT   GCCCCCCCCC
                                ||||| ||   ||||||||||
                                GGGTG GA   CGGGGGGGGG
                                   T  CTA_
GAM2783  OBSCN    3'  CCCGCCTCCTCCATGGTGCCCT 64678     GC_______   _  C  CIII
            CCTCCG                 CTTC       GCCC CC CC   G
                                ||||       |||| || ||   |
                                GAGG       CGGG GG GG   C
                                  AGGTACCA   A  A  IIIC
GAM2783  P66      3'  CCCACCCTGCGCCCTCCTCC   64679        C     _  C
                                CCCGCCTT GCGCCC CC CC
                                |||||||| |||||| || ||
                                GGGTGGGA CGCGGG GG GG
                                     _     A  A
GAM2783  PARVA    3'  CCCCCCTCCGCCCTTCCC    64680     G    G    CC
                                CCC CCTTC CGCCC  CCC
                                ||| ||||| |||||  |||
                                GGG GGGAG GCGGG  GGG
                                  _    _     AA
GAM2783  PCAF     5'  CCCCCTTCGCCCACCCCCC   64682     G      G  _
                                CCC CCTTCGC CC CCCCCC
                                ||| ||||||| || ||||||
                                GGG GGAAGCG GG GGGGGG
                                  _      _  T
GAM2783  PCAF     5'  CCCGCCCCCGCCCTCCCCC   64681          G  C
                                CCCGCCTTCGC CC CCCCC
                                |||||||||| || |||||
                                GGGCGGGGGCG GG GGGGG
                                      _  A
GAM2783  PDCD7    3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                     _ _   A
GAM2783  PEX16    3'  CCCTCCCCACACCCTCC     64683     GC        C
                                CCC  CTTCGCGCCC CC
                                |||  |||||||||| ||
                                GGG  GGGGTGTGGG GG
                                  A_         A
GAM2783  PGS1     3'  CCTTCCTGCCAGCCCCTCCC  64684      GC  __   _
                                CCTTC  GCC  CCCC CCC
                                |||||  |||  |||| |||
```

```
                                GGAAG  CGG  GGGG GGG
                                  GA   TC    A
GAM2783  PHYHIP   3'  CCTTCTCCACACCTCTCCCC  64685    GC       CC_
                                CC  CTTCGCGCC   CCCC
                                ||  |||||||||   ||||
                                GG  GAGGTGTGG   GGGG
                                 AA        AGA
GAM2783  PITPNM   3'  CCCATGCCCACGCCCTCCTCC  64686     CC       _  C
                                CCCG  TTCGCGCCC CC CC
                                ||||  |||||||||  ||  ||
                                GGGT  GGGTGCGGG GG GG
                                  AC        A  A
GAM2783  PIWIL2   3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                |||||||  ||  |||  |||
                                GGGCGGA GC CGG GGG
                                   _  _   A
GAM2783  PLA2G12  5'  CCATATCCACGCCTCCTTCC   64687     CC       _  CC
                                CCG  TTCGCGCC CC  CC
                                |||  ||||||||  ||   ||
                                GGT  AGGTGCGG GG  GG
                                  AT       A  AA
GAM2783  PRDM8    3'  CCGCGCCGTCGGCTGTCCCCTC 64688    _    T   C  C__    _
            C                    CC CGCC TCG GC   CCCC CC
                                ||  ||||  |||  ||   ||||  ||
                                GG GCGG AGC CG   GGGG GG
                                 C    C   _  ACA    A
GAM2783  PRO0478  3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                |||||||  ||  |||  |||
                                GGGCGGA GC CGG GGG
                                   _  _   A
GAM2783  PRO1048  3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                |||||||  ||  |||  |||
                                GGGCGGA GC CGG GGG
                                   _  _   A
GAM2783  PRO2730  3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                |||||||  ||  |||  |||
                                GGGCGGA GC CGG GGG
                                   _  _   A
GAM2783  PRO2893  3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                |||||||  ||  |||  |||
                                GGGCGGA GT CGG GGG
                                   _  _   A
GAM2783  PSK      5'  CCGCTTCCGCCTGGGGTCCTCC 64689      C   G   _______  C
                                CCGC TTC CGCC     CC CC
                                ||||  |||  ||||     ||  ||
```

```
                                GGCG AAG GCGG     GG GG
                                  _  _   ACCCCA  A
GAM2783  PSK     5'  CCCGCCCCGGCCTCCTCCC   64690       T  C  _  C
                                CCCGCCT CG GCC CC CCC
                                ||||||| || ||| || |||
                                GGGCGGG GC CGG GG GGG
                                   _  _  A  A
GAM2783  PTRF    3'  CCCGCCTCAGCCTCCC     64359       T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _  _  A
GAM2783  PTRF    5'  CCCAGCTCCTCGCCCTCC   64691     C   G   C
                                CCCG CTTC CGCCC CC
                                |||| |||| ||||| ||
                                GGGT GAGG GCGGG GG
                                  C   A   A
GAM2783  RAB20   5'  CCAGCGCCCCCGCGCCCTCTCC 64692   __         CC_
            C                    CC  CGCCTTCGCGCCC   CCC
                                 ||  ||||||||||||   |||
                                 GG  GCGGGGGCGCGGG   GGG
                                  TC          AGA
GAM2783  RAB40C  3'  GCCCAGCCGCGCCCCCTCC   64693     __       C
                                GCCT  TCGCGCCCCC CC
                                ||||  |||||||||| ||
                                CGGG  GGCGCGGGGG GG
                                  TC        A
GAM2783  RAI17   3'  CCCAGAAACACGCCCCCCTCC  64694     CCTT       _
                                CCCG   CGCGCCCCCC CC
                                ||||   |||||||||| ||
                                GGGT   GTGCGGGGGG GG
                                  CTTT        A
GAM2783  RAP2B   3'  CCTCCTTTTCATCCACCCTTCC 64695   G   CG  _  _  __
            CC                   CC CCTT  CG CC CCC  CCCC
                                 || ||||  || || |||  ||||
                                 GG GGAA  GT GG GGG  GGGG
                                  A   AA  A  T   AA
GAM2783  RHOBTB2 3'  CCTCCAGCCCCGCCCTCC    64696      C    _  _
                                CCTTCG GCCCC CCC CC
                                |||||| ||||| ||| ||
                                GGAGGT CGGGG GGG GG
                                   _    C   A
GAM2783  RHOBTB2 3'  CCCGCCCCCCAACCTCCCC   64697        GC   C
                                CCCGCCTTC  GCC CCCC
                                |||||||||  ||| ||||
                                GGGCGGGGG  TGG GGGG
                                     GT   A
GAM2783  RLUCL   3'  CCCACCTCAGCCCTTCC     64698       T  C   CC
                                CCCGCCT CG GCCC  CC
                                ||||||| || ||||  ||
```

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                                GGGTGGA GT CGGG  GG
                                   _ _    AA
GAM2783  RNF24    5'  CCCTCCTCCGCGTCCCTCC   64699     G       _  C
                                CCC CCTTCGCG CCC CC
                                ||| |||||||| ||| ||
                                GGG GGAGGCGC GGG GG
                                  A       A  A
GAM2783  RNO2     5'  CCCGCCTCAACCCCCC      64700         CGC
                                CCCGCCTT   GCCCCCC
                                ||||||||   |||||||
                                GGGCGGAG   TGGGGGG
                                     T__
GAM2783  ROBO4    3'  CCTTCCTCCACAGCCCTCTCCC 64701    CG      _    CC_
                                CC  CCTTCGC GCCC   CCC
                                ||  ||||||| ||||   |||
                                GG  GGAGGTG CGGG   GGG
                                 AA      T    AGA
GAM2783  RoXaN    3'  CCCTGCCTCACCCCCCC     64702     _    TCG
                                CCC GCCT   CGCCCCCCC
                                ||| ||||   |||||||||
                                GGG CGGA   GTGGGGGGG
                                  A   ____
GAM2783  RoXaN    3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  RTP801   5'  CCACGCTCGCACCTCCCCC   64703     C       C
                                CCGC TTCGCGCC CCCCC
                                |||| |||||||| |||||
                                GGTG GAGCGTGG GGGGG
                                  C       A
GAM2783  SCAM-1   3'  CCCGCCTTGCTCCGCCCCCCC  64704         C  G  _
                                CCCGCCTT GC CC CCCCCCC
                                |||||||| || || |||||||
                                GGGCGGAA CG GG GGGGGGG
                                   _ A  C
GAM2783  SEC14L2  3'  CCCGCCTTTGGGCGGCCTCC   64705         C__   _  C
                                CCCGCCTT   GCG CC CC
                                ||||||||   ||| || ||
                                GGGCGGAA   CGC GG GG
                                     ACC   C  A
GAM2783  SEMA3E   3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  SEMA5A   3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
```

```
                                GGGCGGA GT CGG GGG
                                  _ _   A
GAM2783  SEMA6B   3'  CCCACCTTCGCCGCCCCCC   64706          _
                                CCCGCCTTCGC GCCCCCC
                                |||||||||| |||||||
                                GGGTGGAAGCG CGGGGGG
                                    G
GAM2783  SEMA6B   3'  CCCACCTTCGCCGCCCCCC   64706          _
                                CCCGCCTTCGC GCCCCCC
                                |||||||||| |||||||
                                GGGTGGAAGCG CGGGGGG
                                    G
GAM2783  SEMA6B   3'  CCCACCTTCGCCGCCCCCC   64706          _
                                CCCGCCTTCGC GCCCCCC
                                |||||||||| |||||||
                                GGGTGGAAGCG CGGGGGG
                                    G
GAM2783  Sfmbt    5'  CCCGCTCGCGCCCTCC     64707     CT      C
                                CCCGC  TCGCGCCC CC
                                |||||  |||||||| ||
                                GGGCG  AGCGCGGG GG
                                  __      A
GAM2783  SFXN2    5'  CCCGCCCCACGCCCCTCC   64708       T      C
                                CCCGCCT CGCGCCCC CC
                                ||||||| |||||||| ||
                                GGGCGGG GTGCGGGG GG
                                  _       A
GAM2783  SGKL     3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                  _ _   A
GAM2783  SIAT4A   3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                  _ _   A
GAM2783  SLC37A1  5'  CCAGCCCCCACCTCCCCCC  64709   C      G_
                                CC GCCTTCGC  CCCCCC
                                || ||||||||  ||||||
                                GG CGGGGGTG  GGGGGG
                                 T       GA
GAM2783  SMAP-5   3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                  _ _   A
GAM2783  SMARCA4  5'  CCCGCCTCGGCCACCGCCCCCC 64710       C  _  _
            C                    CCCGCCTT GC GCC CCCCCCC
                                ||||||||| || ||| |||||||
```

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                                GGGCGGAG CG TGG GGGGGGG
                                    C G   C
GAM2783  SNPH     3'  CCCGCCTCCCCACTTCCC    64711         G   CC
                                CCCGCCTTC CGC  CCC
                                ||||||||| |||  |||
                                GGGCGGAGG GTG  GGG
                                     G   AA
GAM2783  STMN3    3'  CCCTCCCCCGTCGCCCCTCCC  64712     G    _     C
                                CCC CCTTCG CGCCCC CCC
                                ||| |||||| |||||| |||
                                GGG GGGGGC GCGGGG GGG
                                  A     A     A
GAM2783  STMN4    3'  CCCCTTGGCCACCCCCCTCC   64713    G   C _      _
                                CC CCTT GC GCCCCCC CC
                                || |||| || ||||||| ||
                                GG GGAA CG TGGGGGG GG
                                 _   C  G      A
GAM2783  STRAIT11499 5'  CCCGCCTTCACGCGCTCTCC   64714           CCCCC
                                CCCGCCTTCGCGC    CC
                                ||||||||||||    ||
                                GGGCGGAAGTGCG    GG
                                       CGAGA
GAM2783  SUN1     3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _   A
GAM2783  SYT6     5'  CCCGCCTCTGGCAGCCCC    64715        C_ _
                                CCCGCCTT  GC GCCCC
                                ||||||||  || |||||
                                GGGCGGAG  CG CGGGG
                                     AC  T
GAM2783  TAO1     3'  CCCAGCTCATCTGCTCCTCCCC 64716     _ CT_  GC  _  C
                                CCC GC   TC  GC CC CCCC
                                ||| ||   ||  || || ||||
                                GGG CG   AG  CG GG GGGG
                                  T  AGT  A_  A  A
GAM2783  TAO1     5'  CCGCTTCCGCCTGGGGTCCTCC 64689      C   G   _______  C
                                CCGC TTC CGCC     CC CC
                                |||| ||| ||||     || ||
                                GGCG AAG GCGG     GG GG
                                  _  _   ACCCCA  A
GAM2783  TED      3'  CCAGCCCCCACTTCCTCCC   64717    C      GC  C
                                CC GCCTTCGC  CC CCC
                                || ||||||||  || |||
                                GG CGGGGGTG  GG GGG
                                 T       AA  A
GAM2783  TEX27    3'  CCCACCCCCCACCCTTCCCC   64718          G  CC
                                CCCGCCTTCGC CC  CCCC
                                |||||||||| ||  ||||
```

```
                                GGGTGGGGGTG GG  GGGG
                                      _ AA
GAM2783  TIP47    3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  TRAF3    5'  CCGCCTTCTGCCGCTTCCTCC  64719         _ _ CC  C
                                CCGCCTTC GC GC  CC CC
                                |||||||| || ||  || ||
                                GGCGGAAG CG CG  GG GG
                                     A  G  AA  A
GAM2783  TRAF3    3'  CCGCCTTCTGCCGCTTCCTCC  64719         _ _ CC  C
                                CCGCCTTC GC GC  CC CC
                                |||||||| || ||  || ||
                                GGCGGAAG CG CG  GG GG
                                     A  G  AA  A
GAM2783  TRIAD3   3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  TSGA     5'  CCCGCCTCCCGCCTCCC     64604         G    C
                                CCCGCCTTC CGCC CCC
                                ||||||||| |||| |||
                                GGGCGGAGG GCGG GGG
                                      _   A
GAM2783  TTC2     3'  CCACCCCCGCCTCCCTCC    64720         G_   C
                                CCGCCTTCGC  CCC CC
                                ||||||||||  ||| ||
                                GGTGGGGGCG  GGG GG
                                     GA   A
GAM2783  TTLL1    5'  CCCGCCTCCAGCCCCTCTCC  64721          C    CC_
                                CCCGCCTTCG GCCCC   CC
                                |||||||||| |||||   ||
                                GGGCGGAGGT CGGGG   GG
                                      _    AGA
GAM2783  U2AF65   3'  CCTGCCCCCACCCTCCCCC   64722    C      G  C
                                CC GCCTTCGC CC CCCCC
                                || |||||||| || |||||
                                GG CGGGGGTG GG GGGGG
                                 A       _ A
GAM2783  USP19    5'  CCGGCGCGCCCCTCCCC     64723     CCTT      _
                                CCG   CGCGCCCC CCCC
                                |||   |||||||| ||||
                                GGC   GCGCGGGG GGGG
                                  C___       A
GAM2783  ust3     3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
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                                GGGCGGA GT CGG GGG
                                    _ _  A
GAM2783 WBSCR20A 5' CCCCCTCGAAAGCCCTTTCCC 64724   G    C__   CC_
                                CC CCTTCG  GCCC  CCC
                                || ||||||  ||||  |||
                                GG GGGAGC  CGGG  GGG
                                 _    TTT   AAA
GAM2783 WDR13   5' CCGCCCTCCGCCTTCCC    64725       G   CC
                                CCGCCTTC CGCC  CCC
                                |||||||| ||||  |||
                                GGCGGGAG GCGG  GGG
                                    _   AA
GAM2783 WIT-1   3' CCCTCCCTTGCCCCCCCC   64726    G   CGC
                                CCC CCTT  GCCCCCCCC
                                ||| ||||  |||||||||
                                GGG GGGA  CGGGGGGGG
                                  A   A__
GAM2783 WNT16   5' CCTCTTTTGCACCCCCTCCC  64727   GC  C_     _
                                CC  CTT  GCGCCCCC CCC
                                ||  |||  |||||||| |||
                                GG  GAA  CGTGGGGG GGG
                                 A_  AA      A
GAM2783 ZDHHC1  5' CCTGGCCTTCCACCCTCCCC  64728   C_    G   C
                                CC  GCCTTC CGCCC CCCC
                                ||  |||||| ||||| ||||
                                GG  CGGAAG GTGGG GGGG
                                 AC    _   A
GAM2783 ZDHHC8  3' CCCGCCTGCCCCCCC     64729       TCGC
                                CCCGCCT   GCCCCCCC
                                |||||||   ||||||||
                                GGGCGGA   CGGGGGGG
                                   ____
GAM2783 ZFP106  3' CCCGCCTCGGCCTCCC     64318       T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783 ZIC4    5' CCCCCTCACACACCTCTCCCC  64730   G      _ C__
                                CC CCTTCGCGC CC  CCCC
                                || |||||||| ||  ||||
                                GG GGGAGTGTG GG  GGGG
                                 _       T  AGA
GAM2783 ZMPSTE24 5' CCCGCCCCCATCCCTCCC   64731        CG  C
                                CCCGCCTTCG  CCC CCC
                                ||||||||||  ||| |||
                                GGGCGGGGGT  GGG GGG
                                    A_  A
GAM2783 ZNF339  5' CCCGCCTCGCCTGCCCTCTTCC 64732       T  __   CCC_
                                CCCGCCT CGC  GCCC   CC
                                ||||||| |||  ||||   ||
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                                GGGCGGA GCG  CGGG   GG
                                   _  GA   AGAA
GAM2783  ZNF33A   3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC115110 5'  CCCCCTCGGCCTCCCC     64734    G     C   C
                                CC CCTTCG GCC CCCC
                                || |||||| ||| ||||
                                GG GGGAGC CGG GGGG
                                 _    _  A
GAM2783  LOC115110 5'  CCGCCCTCCTGCCCTCCCCC  64733        GC   _
                                CCGCCTTC  GCCC CCCCC
                                ||||||||  |||| |||||
                                GGCGGGAG  CGGG GGGGG
                                     GA   A
GAM2783  LOC115219 5'  CGCTTTAGCAGCCCCCCC    64735     C  C  _
                                CGC TT GC GCCCCCCC
                                ||| || || ||||||||
                                GCG AA CG CGGGGGGG
                                  A  T  T
GAM2783  LOC115557 5'  CCCCCTTACCCCCCC      64736     G   CGC
                                CCC CCTT   GCCCCCCC
                                ||| ||||   ||||||||
                                GGG GGAA   TGGGGGGG
                                  _   ____
GAM2783  LOC115861 3'  CCCGCCTTGGCCTCCCC    64737        CGC   C
                                CCCGCCTT   GCC CCCC
                                ||||||||   ||| ||||
                                GGGCGGAA   CGG GGGG
                                     C__   A
GAM2783  LOC116143 3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC116143 3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC121344 5'  CCACGCCACAGCCCCCCC    64738    _   TT  C
                                CC CGCC  CG GCCCCCCC
                                || ||||  || ||||||||
                                GG GCGG  GT CGGGGGGG
                                 T   T_ _
GAM2783  LOC121344 5'  CCCGCCTTAGCCCCTCC     64739        CGC    C
                                CCCGCCTT   GCCCC CC
                                ||||||||   ||||| ||
```

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                                GGGCGGAA   CGGGG GG
                                    T__     A
GAM2783  LOC122704 3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _   A
GAM2783  LOC125058 3'  CCCAGCCCCACCCCCTCCC    64740     _    TCG      _
                                CCC GCCT   CGCCCCC CCC
                                ||| ||||   ||||||| |||
                                GGG CGGG   GTGGGGG GGG
                                  T   ___      A
GAM2783  LOC126031 5'  CCTGCCTCCCCACCCCCC     64741    C      G
                                CC GCCTTC CGCCCCCC
                                || |||||| ||||||||
                                GG CGGAGG GTGGGGGG
                                 A     G
GAM2783  LOC126208 3'  CCCTGCCCGCCCCCCCCC     64742     _   TTCG
                                CCC GCC    CGCCCCCCCCC
                                ||| |||    ||||||||||
                                GGG CGG    GCGGGGGGGGG
                                  A  _____
GAM2783  LOC126282 3'  CCCGCCTCAGCCTCCC      64359        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _   A
GAM2783  LOC126520 3'  GCCCCCCAGCCCTCCCCC     64743       GC   _
                                GCCTTC  GCCC CCCCC
                                ||||||  |||| |||||
                                CGGGGG  CGGG GGGGG
                                   GT    A
GAM2783  LOC127687 5'  CCCCCCTTTCGGCCGCCCCCC  64744     G   _ C   _
                                CCC CCTT CG GCC CCCCCC
                                ||| |||| || ||| ||||||
                                GGG GGAA GC CGG GGGGGG
                                  G   A _   C
GAM2783  LOC127703 5'  CCCTCCCACACGCCCCTTTCC  64745     G   T      CC_
                                CCC CCT CGCGCCCC   CC
                                ||| ||| ||||||||   ||
                                GGG GGG GTGCGGGG   GG
                                  A   T       AAA
GAM2783  LOC131583 5'  CCCGCCTTTGCAGTGCGCCCTC 64746         C_____     CCC
            TCC                  CCCGCCTT     GCGCCC   CC
                                ||||||||     ||||||   ||
                                GGGCGGAA     CGCGGG   GG
                                    ACGTCA     AGA
GAM2783  LOC132927 5'  CCCGCCTTCCCCCCCC       64747         GCG
                                CCCGCCTTC   CCCCCC
                                |||||||||   ||||||
```

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                                GGGCGGAAG   GGGGGG
                                    ___
GAM2783  LOC133308 5'  CCCGCCTTTCGCACGAACCC   64748        _    CCC
                                CCCGCCTT CGCGC   CCC
                                |||||||| |||||   |||
                                GGGCGGAA GCGTG   GGG
                                     A    CTT
GAM2783  LOC142901 5'  CACGTCTCGCACCCCCTCC    64749     C_        C
                                CGC  TTCGCGCCCCC CC
                                |||  |||||||||| ||
                                GTG  GAGCGTGGGGG GG
                                  CA         A
GAM2783  LOC142927 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _   A
GAM2783  LOC143196 3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _   A
GAM2783  LOC143286 5'  CCCCTCCCCGCCCCCCCCC    64750    G    G
                                CC CCTTC CGCCCCCCCCC
                                || ||||| ||||||||||
                                GG GGAGG GCGGGGGGGGG
                                  _    G
GAM2783  LOC143287 3'  CCCGCCTTTCAGGACCCC     64752        _ C_
                                CCCGCCTT CG  GCCCC
                                |||||||| ||  |||||
                                GGGCGGAA GT  TGGGG
                                     A  CC
GAM2783  LOC143287 3'  CCGCCTCCACCACCCCCCCCC  64751          _
                                CCGCCTTCGC GCCCCCCCCC
                                |||||||||| ||||||||||
                                GGCGGAGGTG TGGGGGGGGG
                                      G
GAM2783  LOC144465 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _   A
GAM2783  LOC144543 5'  CCCCCTCGCGTCGCCCCTTCCC 64753     G   _ _    CC
                                CCC CCTT CG CGCCCC  CCC
                                ||| |||| || ||||||  |||
                                GGG GGAG GC GCGGGG  GGG
                                  _   C A     AA
GAM2783  LOC144817 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
```

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                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC145231 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC145299 3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC145333 3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC145387 3'  CCCGCCTCAGCCTCCCC     64382       T  C   C
                                CCCGCCT CG GCC CCCC
                                ||||||| || ||| ||||
                                GGGCGGA GT CGG GGGG
                                   _ _  A
GAM2783  LOC145438 3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC145663 3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC145717 3'  CCCACACCTACGCCTTCCCC   64579      _  C    CC
                                CCCGC CTT GCGCC  CCCC
                                ||||| ||| |||||  ||||
                                GGGTG GGA TGCGG  GGGG
                                   T  _    AA
GAM2783  LOC145748 3'  CCCCCACTGGCCTCCCCC    64754       __  C
                                CCTTCGC  GCC CCCCC
                                |||||||  ||| |||||
                                GGGGGTG  CGG GGGGG
                                    AC  A
GAM2783  LOC146229 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC146272 5'  CACCTCCCTGTGCCCCTCCCC  64755       GC__   _
                                CGCCTTC   GCCCC CCCC
                                |||||||   ||||| ||||
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                                GTGGAGG   CGGGG GGGG
                                   GACA    A
GAM2783  LOC146336 5'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  LOC146562 5'  CCTGCCTCTCCTGCCCCCCCC  64756    C   _  GC
                                CC GCCT TC  GCCCCCCCC
                                || |||| ||  |||||||||
                                GG CGGA AG  CGGGGGGGG
                                 A   G  GA
GAM2783  LOC146756 3'  CCCGCTTCGGCCTCCC     64757      C   C   C
                                CCCGC TTCG GCC CCC
                                ||||| |||| ||| |||
                                GGGCG AAGC CGG GGG
                                   _   _   A
GAM2783  LOC146756 3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  LOC146923 3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  LOC146950 5'  CCCGCGGCGCCCCCTCCC    64758      CTTC      _
                                CCCGC    GCGCCCCC CCC
                                |||||    |||||||| |||
                                GGGCG    CGCGGGGG GGG
                                   C___       A
GAM2783  LOC147057 5'  CCTCGCCTTCCTCGCCTTCCC  64759    _     G_   CC
                                CC CGCCTTC  CGCC  CCC
                                || |||||||  ||||  |||
                                GG GCGGAAG  GCGG  GGG
                                 A      GA    AA
GAM2783  LOC147071 3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  LOC147180 5'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  LOC147515 5'  CCCTAACCTGCCCCCCC    64760     __   TCGC
                                CCC  GCCT   GCCCCCCC
                                |||  ||||   ||||||||
```

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                                GGG  TGGA   CGGGGGGG
                                  AT   ____
GAM2783  LOC147687 5'  CACCGCGGTCCCCCCCC    64761     TTC  __
                                CGCC   GCG  CCCCCCCC
                                ||||   |||  ||||||||
                                GTGG   CGC  GGGGGGGG
                                  ___   CA
GAM2783  LOC147727 5'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC147990 3'  CCCGCCTCGACCTCCC     64535       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC TGG GGG
                                   _ _  A
GAM2783  LOC148022 5'  CCCGCCTTCTGCACGCCC    64762         _   _
                                CCCGCCTTC GCGC CCC
                                ||||||||| |||| |||
                                GGGCGGAAG CGTG GGG
                                    A   C
GAM2783  LOC148046 3'  CCCCCTCCAACTCCCCCCC   64763     G     _ G
                                CCC CCTTCG C CCCCCCC
                                ||| |||||| | |||||||
                                GGG GGAGGT G GGGGGGG
                                  _     T A
GAM2783  LOC148223 3'  CCGCACTAACGCCCCCTCCC  64764      _ TC      _
                                CCGC CT  GCGCCCCC CCC
                                |||| ||  |||||||| |||
                                GGCG GA  TGCGGGGG GGG
                                  T  T_       A
GAM2783  LOC148490 5'  GCTCCTCACGCTCCCTCC    64765    _      C   C
                                GC CTTCGCGC CCC CC
                                || |||||||| ||| ||
                                CG GGAGTGCG GGG GG
                                 A       A   A
GAM2783  LOC148734 3'  CCTGCCTCAGCCTCCCC     64766    C    T  C   C
                                CC GCCT CG GCC CCCC
                                || |||| || ||| ||||
                                GG CGGA GT CGG GGGG
                                 A   _ _  A
GAM2783  LOC148809 5'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC148946 5'  CCCAGCCGGACACCCCCCC   64767     _  TTC
                                CCC GCC   GCGCCCCCCC
                                ||| |||   ||||||||||
```

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                                GGG CGG   TGTGGGGGGG
                                  T   CC_
GAM2783  LOC149194 3'  CCCAGACCGGCGTCCTCCTCC  64768     __   TTC   _  C  C
                                CCC  GCC   GCG CC CC CC
                                |||  |||   ||| || || ||
                                GGG  TGG   CGC GG GG GG
                                  TC   C__   A  A  A
GAM2783  LOC149705 3'  CCCCCCTTCAGCCTCCC     64769     G     C   C
                                CCC CCTTCG GCC CCC
                                ||| |||||| ||| |||
                                GGG GGAAGT CGG GGG
                                  G     _   A
GAM2783  LOC150067 5'  CCGCCCCCACGGCCCCCTCCC  64770           _    _
                                CCGCCTTCGCG CCCCC CCC
                                |||||||||||| ||||| |||
                                GGCGGGGGTGC GGGGG GGG
                                       C    A
GAM2783  LOC150113 5'  CCTGTCTCCACGCTTCCCTCC  64771    GC_      CC   _
                                CC   CTTCGCGC  CCC CC
                                ||   ||||||||  ||| ||
                                GG   GAGGTGCG  GGG GG
                                 ACA       AA   A
GAM2783  LOC150185 3'  CCCGCCCCATCCCTCCCC    64772        CGCG   C
                                CCCGCCTT    CCC CCCC
                                ||||||||    ||| ||||
                                GGGCGGGG    GGG GGGG
                                     TA__   A
GAM2783  LOC150271 5'  CGTCCGCAGCCTCCCTCC    64773    CC    _  _   C
                                CG  TTCGC GCC CCC CC
                                ||  ||||| ||| ||| ||
                                GC  AGGCG CGG GGG GG
                                  __    T   A   A
GAM2783  LOC150279 5'  CCCACCCCACATCTCCTTCC   64774        T    CC_  CC
                                CCCGCCT CGCG   CC  CC
                                |||||||  ||||   ||  ||
                                GGGTGGG GTGT   GG  GG
                                    _    AGA  AA
GAM2783  LOC150372 3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _   A
GAM2783  LOC150517 5'  CGCCCCCGGCCCCCTCCC    64775        C     _
                                CGCCTTCG GCCCCC CCC
                                |||||||| |||||| |||
                                GCGGGGGC CGGGGG GGG
                                    _     A
GAM2783  LOC150886 5'  CCCATCTTCGCACGGTGGCCCC 64776      C       _____   _
              TCCC                  CCCG CTTCGCGC     CCCC CCC
                                |||| ||||||||     |||| |||
```

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                                GGGT GAAGCGTG    GGGG GGG
                                  A      CCACC   A
GAM2783  LOC151248 3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  LOC151429 5'  CCAGCCTGGGACCCCCCCC   64777    C   TCGC
                                CC GCCT   GCCCCCCCC
                                || ||||   |||||||||
                                GG CGGA   TGGGGGGGG
                                 T   CCC_
GAM2783  LOC151429 3'  CCCGCCTCGGCCTCCC     64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  LOC151438 5'  CCTCCTGGCACACCCCTTCC  64778    G  T_     CC
                                CC CCT  CGCGCCCC  CC
                                || |||  ||||||||  ||
                                GG GGA  GTGTGGGG  GG
                                 A  CC       AA
GAM2783  LOC151647 3'  CCGCCTCCTGCTGCCCCTCC  64779       _ _    C
                                CCGCCTTC GC GCCCC CC
                                |||||||| || ||||| ||
                                GGCGGAGG CG CGGGG GG
                                    A A    A
GAM2783  LOC151904 3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  LOC151987 5'  CCCCCCCGACGCCCTCCCCC  64780    G  TC    _
                                CCC CCT  GCGCCC CCCCC
                                ||| |||  |||||| |||||
                                GGG GGG  TGCGGG GGGGG
                                  _  GC    A
GAM2783  LOC152137 5'  CCCGGGCCCTGCCCCCCTCC  64781    __    CGC     _
                                CCC  GCCTT   GCCCCCC CC
                                |||  |||||   ||||||| ||
                                GGG  CGGGA   CGGGGGG GG
                                  CC    ___      A
GAM2783  LOC152274 3'  CCCACACCTGCTCCCCTCC   64782     _  C  G   C
                                CCCGC CTT GC CCCC CC
                                ||||| ||| || |||| ||
                                GGGTG GGA CG GGGG GG
                                   T  _ A   A
GAM2783  LOC152313 3'  CCCGCCTCAGCCTCCC     64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
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                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC152453 3'  CCCGCCTCGGCCTCCC     64318      T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC152633 5'  CCCGCCTTCCACGCCCCCC   64783        _
                                CCCGCCTTC GCGCCCCCC
                                ||||||||| |||||||||
                                GGGCGGAAG TGCGGGGGG
                                    G
GAM2783  LOC152917 5'  CCGCCTTCCGCTCCTCC     64784       G   C  C
                                CCGCCTTC CGC CC CC
                                |||||||| ||| || ||
                                GGCGGAAG GCG GG GG
                                   _  A  A
GAM2783  LOC153579 3'  CCCGCCTCGGCCTCCC      64318      T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC155072 3'  CCCGCCTCAGCCTCCC      64359      T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC157292 5'  CCCGCCTCAGCCTCCC      64359      T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC157464 5'  CCCGCCTCAGCCTCCC      64359      T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC157653 5'  CCACCTGCACTGCCCCTCC   64785       T  _    C
                                CCGCCT CGC GCCCC CC
                                |||||| ||| ||||| ||
                                GGTGGA GTG CGGGG GG
                                   C  A    A
GAM2783  LOC157983 3'  CCCGCCTCGGCCTCCC      64318      T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC158055 3'  CCCGCCTCACCCCTCC      64786      TCG    C
                                CCCGCCT   CGCCCC CC
                                |||||||   |||||| ||
```

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                                GGGCGGA  GTGGGG GG
                                   ___     A
GAM2783  LOC158308 3'  CCCTCCTTGCCCCCCC     64787    G   CGC
                                CCC CCTT  GCCCCCCC
                                ||| ||||  ||||||||
                                GGG GGAA  CGGGGGGG
                                  A  ___
GAM2783  LOC158337 3'  CCCGCCTCGGCCTCCC     64318       T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC158819 3'  CCCGCCTCAGCCTCCC     64359       T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC160418 5'  CCCGCCTCTCGGTCCTTCCCC  64788       _  CG  CC
                                CCCGCCT TCG  CC  CCCC
                                ||||||| |||  ||  ||||
                                GGGCGGA AGC  GG  GGGG
                                    G  CA  AA
GAM2783  LOC160507 5'  CCGGCCTCGCACGTCCTCCC  64789    C      CC  _
                                CCG CTTCGCGC  CC CCC
                                ||| ||||||||  || |||
                                GGC GGAGCGTG  GG GGG
                                  C       CA  A
GAM2783  LOC165257 3'  CCCGCCTCGCACCCCCC     64790       T
                                CCCGCCT CGCGCCCCCC
                                ||||||| ||||||||||
                                GGGCGGA GCGTGGGGGG
                                   _
GAM2783  LOC196051 3'  CCCACCTTCACAGCCTCTTCC  64791         _  CCCC
                                CCCGCCTTCGC GCC   CC
                                |||||||||| |||   ||
                                GGGTGGAAGTG CGG   GG
                                      T  AGAA
GAM2783  LOC196214 5'  CCCCCTTCCGTCCCCCC     64792    G   G  _
                                CCC CCTTC CG CCCCCC
                                ||| ||||| || ||||||
                                GGG GGAAG GC GGGGGG
                                  _   _ A
GAM2783  LOC196989 3'  CCGCCCCCGGCCCCCTCCC   64793        C    _
                                CCGCCTTCG GCCCCC CCC
                                ||||||||| |||||| |||
                                GGCGGGGGC CGGGGG GGG
                                      _    A
GAM2783  LOC197342 3'  CCTGCCTTCCCGCCCGCCTCC  64794   C    G   _  C
                                CC GCCTTC CGCCC CC CC
                                || |||||| ||||| || ||
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                                GG CGGAAG GCGGG GG GG
                                 A     G    C A
GAM2783  LOC197363 3'  CCTCCTTGGCATCCCCTTCC  64795    G   C  _   CC
                                CC CCTT GCG CCCC  CC
                                || |||| ||| ||||  ||
                                GG GGAA CGT GGGG  GG
                                 A   C  A   AA
GAM2783  LOC199786 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _  A
GAM2783  LOC199858 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _  A
GAM2783  LOC200314 3'  CCCACCTTCACCCCTTCC    64796         G   CC
                                CCCGCCTTCGC CCC  CC
                                |||||||||||| |||  ||
                                GGGTGGAAGTG GGG  GG
                                      _  AA
GAM2783  LOC200470 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _  A
GAM2783  LOC200862 5'  CCCGCCCTCGCCCCTCC     64797         G   C
                                CCCGCCTTCGC CCC CC
                                |||||||||||| ||| ||
                                GGGCGGGAGCG GGG GG
                                      _  A
GAM2783  LOC201173 3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _  A
GAM2783  LOC201294 3'  CCCACCCCCAACCTCCCCC   64798         C   C
                                CCCGCCTTCG GCC CCCCC
                                |||||||||| ||| |||||
                                GGGTGGGGGT TGG GGGGG
                                      _  A
GAM2783  LOC201514 5'  CCGTGGCCCGCGCCTCCCC   64799    CC_      C
                                CCG   TTCGCGCC CCCC
                                |||   |||||||| ||||
                                GGC   GGGCGCGG GGGG
                                  ACC       A
GAM2783  LOC201689 3'  CCTTCCTTCGCGAACCCTCC  64800    CG      CC  C
                                CC  CCTTCGCG  CCC CC
                                ||  ||||||||  ||| ||
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                                GG  GGAAGCGC  GGG GG
                                 AA       TT   A
GAM2783  LOC201689 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _   A
GAM2783  LOC201911 3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _   A
GAM2783  LOC202868 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                    _ _   A
GAM2783  LOC203246 3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _   A
GAM2783  LOC203289 3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _   A
GAM2783  LOC203392 5'  CGCCTTCTGCGCCCCCTCCC   64801        _      _
                                CGCCTTC GCGCCCCC CCC
                                ||||||| |||||||| |||
                                GCGGAAG CGCGGGGG GGG
                                    A       A
GAM2783  LOC203427 5'  CGCCCCCGCCGCCCCTCCC    64802         _    C
                                CGCCTTCGC GCCCC CCC
                                ||||||||| ||||| |||
                                GCGGGGGCG CGGGG GGG
                                     G    A
GAM2783  LOC204084 5'  CCTCCACACCTGTCCCTTCC   64803          ___   CC
                                CCTTCGCGCC   CCC  CC
                                ||||||||||   |||  ||
                                GGAGGTGTGG   GGG  GG
                                      ACA   AA
GAM2783  LOC219513 5'  CCCGCGCCGCGGCTCCTCC    64804      CT    _ C  C
                                CCCGC  TCGCG C CC CC
                                |||||  ||||| | || ||
                                GGGCG  GGCGC G GG GG
                                   C_    C A  A
GAM2783  LOC219649 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
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                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC219686 5'  CGACCTCCAACGCCTCCTCC  64806   _    _   C  C
                                CG CCTTCG CGCC CC CC
                                || |||||| |||| || ||
                                GC GGAGGT GCGG GG GG
                                 T    T   A  A
GAM2783  LOC219686 5'  CCTCCGGCCGGCCTCCTCC   64805      C  __ _ _
                                CCTTCG GCC  CC CC CC
                                |||||| |||  || || ||
                                GGAGGC CGG  GG GG GG
                                   _  CC  A  A
GAM2783  LOC220018 5'  CCCATCTCTGAGCGCCCCCC  64807    C  C__
                                CCCG CTT  GCGCCCCCC
                                |||| |||  |||||||||
                                GGGT GAG  CGCGGGGGG
                                  A  ACT
GAM2783  LOC220018 5'  CCCCCCTTCGGGAACCCTCC  64808    G    C__   C
                                CCC CCTTCG  GCCC CC
                                ||| ||||||  |||| ||
                                GGG GGAAGC  TGGG GG
                                  G    CCT   A
GAM2783  LOC220370 3'  CCCGCCTCGGCCTCCC     64318       T  C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC220370 5'  CCTGCCCTCGCTCTGCAGCCTC 64809   C      _______  CCC
           TCCC                  CC GCCTTCGC    GCC  CCC
                                || ||||||||     |||  |||
                                GG CGGGAGCG    CGG  GGG
                                 A      AGACGT  AGA
GAM2783  LOC220537 3'  CCCACACCTACGCCTTCCCC  64579     _  C   CC
                                CCCGC CTT GCGCC  CCCC
                                ||||| ||| |||||  ||||
                                GGGTG GGA TGCGG  GGGG
                                  T  _    AA
GAM2783  LOC220558 5'  CCCGCCTCGCTCATGCCTCCTC 64810      T  ____  C  C
           C                   CCCGCCT CGC   GCC CC CC
                                ||||||| |||   ||| || ||
                                GGGCGGA GCG   CGG GG GG
                                   _  AGTA  A  A
GAM2783  LOC220739 3'  CCCACCTCCCTCTGCTTCCCCC 64811       ____  GC
           C                   CCCGCCTTC   GC  CCCCCC
                                |||||||||   ||  ||||||
                                GGGTGGAGG   CG  GGGGGG
                                     GAGA  AA
GAM2783  LOC221002 5'  CCCGCCTCCACGCTCCCCC   64812          C
                                CCCGCCTTCGCGC CCCCC
                                |||||||||||| |||||
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                                GGGCGGAGGTGCG GGGGG
                                      A
GAM2783  LOC221092 3'  CCCTGCTTGAGCACCCTCCCCC 64814     _ CTTC     _
                                CCC GC    GCGCCC CCCCC
                                ||| ||    |||||| |||||
                                GGG CG    CGTGGG GGGGG
                                  A  AACT     A
GAM2783  LOC221092 3'  CCCCCCACCACCCCTCCCC    64813     G  TTCG     _
                                CCC CC    CGCCCC CCCC
                                ||| ||    |||||| ||||
                                GGG GG    GTGGGG GGGG
                                  G  TG__     A
GAM2783  LOC221474 5'  CACTCTAACCTGCCCCTCCCC  64815     _ __  GC    _
                                CGC CT  TC  GCCCC CCCC
                                ||| ||  ||  ||||| ||||
                                GTG GA  GG  CGGGG GGGG
                                  A  TT  A_    A
GAM2783  LOC221490 3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _   A
GAM2783  LOC221749 5'  CCCGCCTCGCGCCCCCC     64816        T
                                CCCGCCT CGCGCCCCCC
                                ||||||| ||||||||||
                                GGGCGGA GCGCGGGGGG
                                    _
GAM2783  LOC221849 5'  CCCGCCCCGTTCCCTCCC    64817        T  CG   C
                                CCCGCCT CG  CCC CCC
                                ||||||| ||  ||| |||
                                GGGCGGG GC  GGG GGG
                                    _ AA   A
GAM2783  LOC221922 5'  CCTGCCTCCACGCTCCCCC    64819    C         C
                                CC GCCTTCGCGC CCCCC
                                || |||||||||| |||||
                                GG CGGAGGTGCG GGGGG
                                  A         A
GAM2783  LOC221922 5'  CCCTGCCTTCCTGCCCCCCC   64818     _     GC
                                CCC GCCTTC  GCCCCCCC
                                ||| ||||||  ||||||||
                                GGG CGGAAG  CGGGGGGG
                                  A     GA
GAM2783  LOC222166 5'  CCCGCTCCTAGGCGCCCTCCTC 64820       _  C_     _  C
              C                   CCCGC CTT  GCGCCC CC CC
                                ||||| |||  |||||| || ||
                                GGGCG GGA  CGCGGG GG GG
                                   A   TC     A  A
GAM2783  LOC222166 5'  CCGCGCCCGCGGCTCCTCC    64821    _    T  C  C  C
                                CC CGCCT CG GC CC CC
                                || ||||| || || || ||
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                                GG GCGGG GC CG GG GG
                                 C    C _ A A
GAM2783  LOC222488 3'  CCCGCTCGGCCTCCTCC     64822      CT  C  C C
                                CCCGC  TCG GCC CC CC
                                |||||  ||| ||| || ||
                                GGGCG  AGC CGG GG GG
                                  __  _  A A
GAM2783  LOC222865 3'  CCCGCCTCGGCCTCCC      64318       T C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC253639 3'  CCCGCCTCAGCCTCCC      64359       T C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _  A
GAM2783  LOC253664 3'  CCCGCCTCGGCCTCCC      64318       T C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _  A
GAM2783  LOC253767 3'  CGCCTGGACACCCCCCCC    64823      TC
                                CGCCT  GCGCCCCCCCC
                                |||||  ||||||||||
                                GCGGA  TGTGGGGGGGG
                                   CC
GAM2783  LOC253767 3'  CCCGGCCCGCGCCCGTGCCCTC 64380     _ TT     ___  _
            CC                   CCCG CC  CGCGCCC   CCC CCC
                                ||||  ||  |||||||   ||| |||
                                GGGC GG  GCGCGGG   GGG GGG
                                  C __      CAC   A
GAM2783  LOC253815 3'  CCCGTCTTCCGCAGCCCC    64824     C   G  CC
                                CCCG CTTC CGC  CCCC
                                ||||  |||| |||  ||||
                                GGGC GAAG GCG  GGGG
                                  A   _  TC
GAM2783  LOC253866 5'  CCACACCCCTGCCCTTCCCC   64825     _   GC   CC
                                CCGC CTTC  GCCC  CCCC
                                ||||  ||||  ||||  ||||
                                GGTG GGGG  CGGG  GGGG
                                  T   A_   AA
GAM2783  LOC253955 5'  CCCACCTTCAGACCCTCCTCC  64826         C   _ C
                                CCCGCCTTCG GCCC CC CC
                                ||||||||||  |||| || ||
                                GGGTGGAAGT TGGG GG GG
                                      C   A A
GAM2783  LOC254020 5'  CACTCGCGCCCCTTCCC     64827     CT       CC
                                CGC  TCGCGCCCC  CCC
                                |||  |||||||||  |||
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                                GTG  AGCGCGGGG  GGG
                                  __       AA
GAM2783  LOC254099 5'  CCCGCCCTGGGCTCCCCC    64828        C_  G
                                CCCGCCTT  GC CCCCC
                                ||||||||  || |||||
                                GGGCGGGA  CG GGGGG
                                    CC  A
GAM2783  LOC254100 3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _  A
GAM2783  LOC254120 3'  CGCCTTCGGCCCTCGCCCTCC  64829        C   ___  _
                                CGCCTTCG GCCC   CCC CC
                                |||||||| ||||   ||| ||
                                GCGGAAGC CGGG   GGG GG
                                    _   AGC   A
GAM2783  LOC254173 3'  CCTGGCCTGGACCCCCCCC    64830    C_   TCGC
                                CC  GCCT    GCCCCCCCC
                                ||  ||||    |||||||||
                                GG  CGGA    TGGGGGGGG
                                 AC    CC__
GAM2783  LOC254266 3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _  A
GAM2783  LOC254381 5'  CCGGCCCCACGCGTCCCCCTCC 64831    C    _   _    C
                                CC GCCTT CGCG CCCCC CC
                                || ||||| |||| ||||| ||
                                GG CGGGG GCGC GGGGG GG
                                 C    T   A    A
GAM2783  LOC254531 5'  CCCGCCTTCGGACCTCCTCC   64832         C   C  C
                                CCCGCCTTCG GCC CC CC
                                |||||||||| ||| || ||
                                GGGCGGAAGC TGG GG GG
                                      C   A  A
GAM2783  LOC254808 3'  CCCGCCTCGGCCTCCC      64318        T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _  A
GAM2783  LOC254826 3'  CCCAGCCTCCAAGCCTCTCTCC 64833     _      C   CCCC_
                                CCC GCCTTCG GCC    CC
                                ||| ||||||| |||    ||
                                GGG CGGAGGT CGG    GG
                                  T      T  AGAGA
GAM2783  LOC255031 3'  GCCCCGCACCCCCCCCC     64834      T
                                GCCT CGCGCCCCCCCCC
                                |||| ||||||||||||
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                                CGGG GCGTGGGGGGGGG
                                  _
GAM2783  LOC255042 3'  CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _ _   A
GAM2783  LOC255452 3'  CCGCCTTCGGGGGCCTCCTCC  64835        C__   C  C
                                CCGCCTTCG   GCC CC CC
                                |||||||||   ||| || ||
                                GGCGGAAGC   CGG GG GG
                                     CCC   A  A
GAM2783  LOC255941 5'  CCCACCCTACTCCTCCCC    64836        C  G  C
                                CCCGCCTT GC CC CCCC
                                |||||||| || || ||||
                                GGGTGGGA TG GG GGGG
                                   _  A  A
GAM2783  LOC255971 3'  CCAGCCCCCCGCCCCTCCCC  64837    C     G     _
                                CC GCCTTC CGCCCC CCCC
                                || |||||| |||||| ||||
                                GG CGGGGG GCGGGG GGGG
                                 T     _     A
GAM2783  LOC255971 3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  LOC256329 3'  CCCGCCCGCGCCCTCCC     64838       TT      C
                                CCCGCC  CGCGCCC CCC
                                ||||||  ||||||| |||
                                GGGCGG  GCGCGGG GGG
                                   __      A
GAM2783  LOC256544 3'  CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783  LOC256867 5'  CCCTGCCCAACCCCCCCC    64839     _   TCGC
                                CCC GCCT    GCCCCCCCC
                                ||| ||||    |||||||||
                                GGG CGGG    TGGGGGGGG
                                  A   T___
GAM2783  LOC256880 5'  CGCTACCGCGCGCCCCTCCCC  64840     CT     _   _
                                CGC  TCGCGC CCCC CCCC
                                |||  |||||| |||| ||||
                                GCG  GGCGCG GGGG GGGG
                                  AT     C    A
GAM2783  LOC256982 5'  CCCGCCTCCCCCGCCTTCCTCC 64841         _ G    CC  _
                                CCCGCCTT C CGCC  CC CC
                                |||||||| | ||||  || ||
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                                GGGCGGAG G GCGG  GG GG
                                    G G    AA  A
GAM2783  LOC257451 3'  CCTGCCTTCCCCACCCC     64452    C     GCG  _
                                CC GCCTTC   CCC CCCC
                                || ||||||   ||| ||||
                                GG CGGAAG   GGG GGGG
                                 A     ___   T
GAM2783  LOC257460 5'  CCCGCCTCGAGCCACCCCC    64842       T  C  _
                                CCCGCCT CG GCC CCCCC
                                ||||||| || ||| |||||
                                GGGCGGA GC CGG GGGGG
                                    _ T  T
GAM2783  LOC257618 5'  CCCACCCCGTCCCTCCC     64381       T  CG   C
                                CCCGCCT CG  CCC CCC
                                ||||||| ||  ||| |||
                                GGGTGGG GC  GGG GGG
                                    _ A_  A
GAM2783  LOC51016  5'  CCCGCCTTCCCGCGCCCC     64843       G  _
                                CCCGCCTTC CGC CCCC
                                ||||||||| ||| ||||
                                GGGCGGAAG GCG GGGG
                                     G  C
GAM2783  LOC51072  5'  CCGCCCCCACGGCCCCCTCCC  64770          _    _
                                CCGCCTTCGCG CCCCC CCC
                                |||||||||| ||||| |||
                                GGCGGGGGGTGC GGGGG GGG
                                      C    A
GAM2783  LOC51093  5'  CCCACCCACGCCGCCCCCTCC  64844       T  _    C
                                CCCGCCT CGC GCCCCC CC
                                ||||||| ||| |||||| ||
                                GGGTGGG GCG CGGGGG GG
                                    T  G     A
GAM2783  LOC51313  5'  CGCCAGGTGCGCCCCCCTCC   64845     TTC_      _
                                CGCC   GCGCCCCCC CC
                                ||||   ||||||||| ||
                                GCGG   CGCGGGGGG GG
                                  TCCA       A
GAM2783  LOC51651  5'  CCTCACTCGCGCCTTCCC    64846   _  CT     CC
                                CC CGC  TCGCGCC  CCC
                                || |||  |||||||  |||
                                GG GTG  AGCGCGG  GGG
                                 A  __      AA
GAM2783  LOC56834  5'  CCCGCCCCACCCTCCCCC    64847       TCG   _
                                CCCGCCT   CGCCC CCCCC
                                |||||||   ||||| |||||
                                GGGCGGG   GTGGG GGGGG
                                    ___    A
GAM2783  LOC56961  5'  CCGCGTCCCCCGCCCCTCCCC  64848     __   G    _
                                CCGC  CTTC CGCCCC CCCC
                                ||||  |||| |||||| ||||
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                                GGCG  GGGG GCGGGG GGGG
                                  CA   _     A
GAM2783  LOC56961  5' CCCTTCTCCGGGCCCCTTTCC  64849    GC    C    CC_
                                CCC  CTTCG GCCCC   CC
                                |||  ||||| |||||   ||
                                GGG  GAGGC CGGGG   GG
                                  AA    C    AAA
GAM2783  LOC63928  5' CGCGTTTCCACGCCTCCCCC   64850    C__      C
                                CGC   TTCGCGCC CCCCC
                                |||   |||||||| |||||
                                GCG   AGGTGCGG GGGGG
                                  CAA       A
GAM2783  LOC90133  3' CCCACACAGCAGCCTCCCTCC  64851      CTTC  _  _  C
                                CCCGC    GC GCC CCC CC
                                |||||    || ||| ||| ||
                                GGGTG    CG CGG GGG GG
                                   TGT_  T   A   A
GAM2783  LOC90326  3' CCCCCTCACATGGCTTCCTCCC 64852    G     ___  CC  _
                                CC CCTTCGC   GC  CC CCC
                                || |||||||   ||  || |||
                                GG GGGAGTG   CG  GG GGG
                                 _      TAC  AA  A
GAM2783  LOC90529  3' CCCACCCAGCTCCCCTCC    64853       TC  G    C
                                CCCGCCT  GC CCCC CC
                                |||||||  || |||| ||
                                GGGTGGG  CG GGGG GG
                                    T_  A    A
GAM2783  LOC90624  3' CCCGCCTCAGCCTCCC      64359       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GT CGG GGG
                                   _  _   A
GAM2783  LOC90639  5' CCCACGCTCGCCTCCCTCC   64854      C    G_   C
                                CCCGC TTCGC  CCC CC
                                ||||| |||||  ||| ||
                                GGGTG GAGCG  GGG GG
                                  C    GA   A
GAM2783  LOC90678  5' CCCTCTTGCACCCCCTTCC   64855    GC   C      CC
                                CCC  CTT GCGCCCCC  CC
                                |||  ||| ||||||||  ||
                                GGG  GAA CGTGGGGG  GG
                                  A_   _       AA
GAM2783  LOC90719  3' CCCGTCCCCACCCCCCCC    64856     _  TCG
                                CCCG CCT   CGCCCCCCCC
                                |||| |||   ||||||||||
                                GGGC GGG   GTGGGGGGGG
                                  A   ___
GAM2783  LOC91064  5' CCCGCCTCGGGAGCCCCTCTCC 64857       T  C__    CC_
                                CCCGCCT CG   GCCCC   CC
                                ||||||| ||   |||||   ||
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                                GGGCGGA GC   CGGGG   GG
                                   _ CCT     AGA
GAM2783 LOC91301 5' CCCCCCCAGCCCCTTCCC    64858    G     C    CC
                                CC CCTTCG GCCCC  CCC
                                || |||||| |||||  |||
                                GG GGGGGT CGGGG  GGG
                                 _     _     AA
GAM2783 LOC91574 3' CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783 LOC91782 5' CCGCCCTCGTTCCCTCCC    64859         CG   C
                                CCGCCTTCG  CCC CCC
                                |||||||||  ||| |||
                                GGCGGGAGC  GGG GGG
                                     AA   A
GAM2783 LOC91828 3' CCAGCGGCCGGCCCCCCC    64860    C  CT   C
                                CC GC  TCG GCCCCCCC
                                || ||  ||| ||||||||
                                GG CG  GGC CGGGGGGG
                                 T  CC  _
GAM2783 LOC91960 3' CCCTACCCTGCCCCCC      64861     _    CGC
                                CCC GCCTT   GCCCCCC
                                ||| |||||   |||||||
                                GGG TGGGA   CGGGGGG
                                  A    ____
GAM2783 LOC92002 5' CCCGCGCTGCAGGCCCCCCTCC 64862       _ T  C      _
                                CCCGC CT CG GCCCCCC CC
                                ||||| || || ||||||| ||
                                GGGCG GA GT CGGGGGG GG
                                   C  C  C      A
GAM2783 LOC92228 3' CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783 LOC92283 3' CCCGCCTCGGCCTCCC      64318       T  C   C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                   _ _   A
GAM2783 LOC92303 3' CCCCTCCACATCCCTCCCC   64863    G      _  C
                                CC CCTTCGCG CCC CCCC
                                || |||||||| ||| ||||
                                GG GGAGGTGT GGG GGGG
                                 _       A  A
GAM2783 LOC92876 3' CCCTCCCCCATCTCCCCCC   64864     G     CG_
                                CCC CCTTCG   CCCCCC
                                ||| ||||||   ||||||
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                                GGG GGGGGT   GGGGGG
                                  A     AGA
GAM2783 LOC93132 5' GCCATCAGTTACCCTCCCCC  64865    T  C__   _
                                GCC TCG   GCCC CCCCC
                                ||| |||   |||| |||||
                                CGG AGT   TGGG GGGGG
                                  T  CAA   A
GAM2783 LOC93613 3' CCCGCCTCGGCCTCCC      64318       T C  C
                                CCCGCCT CG GCC CCC
                                ||||||| || ||| |||
                                GGGCGGA GC CGG GGG
                                    _ _  A
GAM2784 LOC120227 5' TTCACGCGTTCACAATCG    64868     A         A
                                TTCA CGCGTTCACAGT CG
                                |||| |||||||||||| ||
                                AAGT GCGCAAGTGTTA GC
                                  _         _
GAM2785 KIF3B    3' TGAAGAGTAAAGTGACATGGT  64871          AATAATT  _
                                TGAAGAGTAGA      ACG GGT
                                ||||||||||       ||| |||
                                ACTTCTCATTT      TGT CCA
                                      CAC____   A
GAM2785 LOH11CR2A 3' TAAAGGGTAGAAATAGTCA   64872      A       A
                                TGAAG GTAGAAATA TTA
                                ||||| ||||||||| |||
                                ATTTC CATCTTTAT AGT
                                   C        C
GAM2785 PRKAB1   3' TGAAGAGTGTGAAATGAGC   64873        A_    AATTAC
                                TGAAGAGT  GAAAT     GGGT
                                ||||||||  |||||     ||||
                                ACTTCTCA  CTTTA     CTCG
                                     CA    _______
GAM2785 SUSP1    3' TGAAAGTAGAAATGACAAG   64874     A        AATT
                                TGA GAGTAGAAAT    ACGGG
                                ||| ||||||||||    |||||
                                ACT TTCATCTTTA    TGTTC
                                  _        C___
GAM2785 UTY      3' TGAAGAGCAGAAATAATC    64875
                                TGAAGAGTAGAAATAATT
                                ||||||||||||||||||
                                ACTTCTCGTCTTTATTAG

GAM2785 DKFZp762K2015 3' TGGAGGTAGAAATAATT     64876    A  A
                                TG AG GTAGAAATAATT
                                || || ||||||||||||
                                AC TC CATCTTTATTAA
                                 C  _
GAM2785 KIAA1416  3' TGGAGGTAGAAACATGGATGGG 64877    A  A       ATTAC
             T                   TG AG GTAGAAATA    GGGT
                                || || |||||||||    ||||
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                                AC TC CATCTTTGT    CCCA
                                 C  _       ACCTA
GAM2785  MGC4248   3'  TGAGAGTAGAGTATAAATGGGT 64878    A     A_   TTAC
                                TGA GAGTAGA  ATAA   GGGT
                                ||| |||||||  ||||   ||||
                                ACT CTCATCT  TATT   CCCA
                                  _     CA   TA__
GAM2785  PPP4R1L   5'  TGAAGAGCGGGAAGAGCTGGGT 64879       A_   ATAATTAC
                                TGAAGAGT  GAA      GGGT
                                ||||||||  |||      ||||
                                ACTTCTCG  CTT      CCCA
                                     CC   CTCGA___
GAM2785  PRO1866   3'  TGAAGAGTATAGATAATC    64880        GAA
                                TGAAGAGTA   ATAATT
                                |||||||||   ||||||
                                ACTTCTCAT   TATTAG
                                      ATC
GAM2785  LOC145231 3'  TGGAGAATAGAGACCCAAAATG 64881    A      A  AATTAC_
           GGT                    TG AGAGTAGA AT      GGGT
                                || ||||||||  ||      ||||
                                AC TCTTATCT TG      CCCA
                                 C       C  GGTTTTA
GAM2785  LOC149300 3'  GAAGAGTAGGGCTGCTCCTTGG 64882        AAATAA  AC_
           GT                     GAAGAGTAG     TT   GGGT
                                |||||||||     ||   ||||
                                CTTCTCATC     AG   CCCA
                                      CCGACG  GAA
GAM2785  LOC254778 3'  TGAAGAGCAGAGATAGCAAGGT 64883          A   ATTAC
                                TGAAGAGTAGA ATA    GGGT
                                ||||||||||| |||    ||||
                                ACTTCTCGTCT TAT    TCCA
                                       C   CGT__
GAM2786  ABCG5    5'  CCCCAGAGTGGCTTCA      64886        CGTC  T  A
                                CCCCAGAG    TG GT TTCA
                                ||||||||    || || ||||
                                GGGGTCTC    AC CG AAGT
                                     _____  _  _
GAM2786  ARHGEF12  3'  AAGTGCCTGCTATTTAGT    64887     C     G    C
                                GAG GTCTGT TATT AGT
                                ||| |||||| |||| |||
                                TTC CGGACG ATAA TCA
                                  A     _    A
GAM2786  CANX     3'  GAGTGTTTATATATTCAGT    64888     C  C
                                GAG GT TGTGTATTCAGT
                                ||| || ||||||||||||
                                CTC CA ATATATAAGTCA
                                  A  A
GAM2786  HMGB1    3'  CAGAGTGGTATTCAG       64889       CGTC  T
                                CAGAG    TG GTATTCAG
                                |||||    || ||||||||
```

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                                GTCTC    AC CATAAGTC
                                  _____ _
GAM2786 HS3ST4   3' CCCCAGAGCTCTGACCTCGGT 64890        G   TGTA  A
                                CCCCAGAGC TCTG    TTC GT
                                ||||||||| ||||    ||| ||
                                GGGGTCTCG AGAC    GAG CA
                                     _   TG__   C
GAM2786 INPP5A   3' AGAGTGCGTATTCGGT     64891     CGTC       A
                                AGAG    TGTGTATTC GT
                                ||||    ||||||||| ||
                                TCTC    ACGCATAAG CA
                                  _____       C
GAM2786 LCP1     3' CCCTGGAGCATCTGTGCCGGGC 64892     CA         ATT_
            AGT                   CCC  GAGCGTCTGTGT    CAGT
                                ||| ||||||||||||   ||||
                                GGG  CTCGTAGACACG    GTCA
                                  AC          GCCC
GAM2786 NKX3A    3' CAGAGTTGATATTCAG      64893      CGTC  T
                                CAGAG    TG GTATTCAG
                                |||||    || ||||||||
                                GTCTC    AC TATAAGTC
                                   A___ _
GAM2786 CD84-H1  5' CCCCAGAGGTGTGATTCAG    64894        C  CT   T
                                CCCCAGAG GT  GTG ATTCAG
                                |||||||| ||  ||| ||||||
                                GGGGTCTC CA  CAC TAAGTC
                                  _ ___  _
GAM2786 DC-TM4F2 3' CCCCAGGGGAGTTATTCAG   64895       AGCGTCT  G
                                CCCCAG      GT TATTCAG
                                ||||||      || |||||||
                                GGGGTC      CA ATAAGTC
                                   CCCT____ _
GAM2786 KIAA0831 5' CCTAAGTGTAAAGTCATTCAGT 64896    A  C  CT_  G
                                CC GAG GT   GT TATTCAGT
                                || ||| ||   || ||||||||
                                GG TTC CA   CA GTAAGTCA
                                 A   A  TTT  _
GAM2786 MGC11352 5' CCCCAGGGGAGTTATTCAG   64895       AGCGTCT  G
                                CCCCAG      GT TATTCAG
                                ||||||      || |||||||
                                GGGGTC      CA ATAAGTC
                                   CCCT____ _
GAM2786 NUDC     5' CCCGGAGCTCTGCACTCTAGT  64897     A   G    GT   _
                                CCC GAGC TCTGT  ATTC AGT
                                ||| |||| |||||  |||| |||
                                GGG CTCG AGACG  TGAG TCA
                                  C   _    __   A
GAM2786 RA-GEF-2 3' GAGGTAAACTTGTATTCAGT   64898     C  CTG__
                                GAG GT    TGTATTCAGT
                                ||| ||    ||||||||||
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                                CTC CA    ACATAAGTCA
                                  _ TTTGA
GAM2786  LOC128344 3'  CCTGGAGAGTCTGTGTAT    64899    CA  C
                                CC  GAG GTCTGTGTAT
                                ||  ||| ||||||||||
                                GG  CTC CAGACACATA
                                 AC   T
GAM2786  LOC143680 5'  CCCTAGAATGAATATTCAG    64900     C    CGTC  T
                                CCC AGAG    TG GTATTCAG
                                ||| ||||    || ||||||||
                                GGG TCTT    AC TATAAGTC
                                  A    ____  T
GAM2786  LOC149276 3'  CCCATGGCACTGTATTCAGT   64901      GA   T     AT
                                CCCA  GCG CTGTGT  TCAGT
                                ||||  ||| ||||||  |||||
                                GGGT  CGT GACATA  AGTCA
                                   AC  _     __
GAM2786  LOC149767 3'  CAGAGTGGTATTCAG       64889       CGTC  T
                                CAGAG    TG GTATTCAG
                                |||||    || ||||||||
                                GTCTC    AC CATAAGTC
                                   ____  _
GAM2786  LOC164538 5'  CCACGGCGTCTGTCATTGTCAG 64902     GA       G  __
          T                      CCA  GCGTCTGT TAT  TCAGT
                                |||  |||||||| |||  |||||
                                GGT  CGCAGACA GTA  AGTCA
                                  GC       _  AC
GAM2787  MOG      3'  TTCAGAGTGTTCCTGAAAGT   64905         C
                                TTCAGAGT TTCCTGAAAGT
                                |||||||| ||||||||||
                                AAGTCTCA AAGGACTTTCA
                                     C
GAM2787  PTPRG    5'  TCCATGCTCCTGAAAGTT    64906     GA  CT
                                TTCA  GT  TCCTGAAAGTT
                                ||||  ||  ||||||||||
                                AGGT  CG  AGGACTTTCAA
                                  A_  __
GAM2787  KIAA1944  5'  CTCAGAGTTACCCGGGAGTTA  64907         CTT    AA
                                TTCAGAGT   CCTG  AGTTA
                                ||||||||   ||||  |||||
                                GAGTCTCA   GGGC  TCAAT
                                     AT_    CC
GAM2787  TOR1B    3'  TTCAGGGTTCTTCTGAAAG   64908      A  _   C
                                TTCAG GT CTTC TGAAAG
                                ||||| || |||| ||||||
                                AAGTC CA GAAG ACTTTC
                                   C  A   _
GAM2787  LOC152024 5'  TTCAGAGTCTCTTATCTCTG   64909          ____  _
                                TTCAGAGTCT    TC CTG
                                ||||||||||    || |||
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                                AAGTCTCAGA    AG GAC
                                      GAAT  A
GAM2787  LOC162891 5'  TTCAGAGTCTGCCTGACCATT  64910          T    AA
                                TTCAGAGTCT CCTGA  GTT
                                |||||||||| |||||  |||
                                AAGTCTCAGA GGACT  TAA
                                      C    GG
GAM2788  GPM6A     3'  TGCATATATCAGAAAAAT    64913      C
                                TGTA ATATCAGAAGGAT
                                |||| ||||||||||||
                                ACGT TATAGTCTTTTTA
                                  A
GAM2788  HUNK      3'  TGTATGTCAGAAAGACT     64914      CATA
                                TGTA    TCAGAAGGATT
                                ||||    ||||||||||
                                ACAT    AGTCTTTCTGA
                                  AC__
GAM2788  SLC1A3    3'  TGTATATCAGAGGATCTAT    64915      CA      A
                                TGTA  TATCAGA GGATTTAT
                                ||||  ||||||| ||||||||
                                ACAT  ATAGTCT CCTAGATA
                                  __      _
GAM2788  DKFZP434P0721 5'  TGTGTATATCAGACAGGA    64916     AC       _
                                TGT  ATATCAGA AGGA
                                |||  |||||||| ||||
                                ACA  TATAGTCT TCCT
                                  CA       G
GAM2788  LOC135154 3'  TGTACATATTCAGAAAACAATA 64917          _      ATT
           T                     TGTACATAT CAGAAGG   TAT
                                |||||||| |||||||   |||
                                ACATGTATA GTCTTTT   ATA
                                      A      GTT
GAM2789  DKFZP434G072 3'  ACAGGTATTTTTAGAT      54695      TCTTA
                                ACGG    GTATTTTTAGAT
                                ||||    ||||||||||||
                                TGTC    CATAAAAATCTA
                                  _____
GAM2789  MGC4342   3'  TTCACAGATATTTTTAG     54696        TCTTA
                                TTCACGG    GTATTTTTAG
                                |||||||    ||||||||||
                                AAGTGTC    TATAAAAATC
                                  _____
GAM2790  DKFZP434G072 3'  ACAGGTATTTTTAGAT      54695      TCTTA
                                ACGG    GTATTTTTAGAT
                                ||||    ||||||||||||
                                TGTC    CATAAAAATCTA
                                  _____
GAM2790  MGC4342   3'  TTCACAGATATTTTTAG     54696        TCTTA
                                TTCACGG    GTATTTTTAG
                                |||||||    ||||||||||
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                                AAGTGTC    TATAAAAATC
                                  _____
GAM2791 DLG5    5' AGCTGTGGGCCATCAGCT    64922          _
                                AGCTGTGGGTCATT GTT
                                ||||||||||||| |||
                                TCGACACCCGGTAG CGA
                                        T
GAM2791 ELK1    3' GAAGCTGTGTGTTTTCTGT   64923        G  CA_
                                GAAGCTGTG GT   TTGT
                                ||||||||| ||   ||||
                                CTTCGACAC CA   GACA
                                     A  AAA
GAM2791 FLJ13158 3' AGCTGTGGAAGGATGTTATG 64924        TCAT
                                AGCTGTGGG   TGTTATG
                                |||||||||   |||||||
                                TCGACACCT   ACAATAC
                                     TCCT
GAM2791 NAG73   5' TAGAAGCTGTGGTCTGT    64925         G  AT
                                TAGAAGCTGTGG TC  TGT
                                |||||||||||| ||  |||
                                ATCTTCGACACC AG  ACA
                                  _ __
GAM2791 LOC221518 3' CAGAGGCTGTGGGTCAGTG   64926     A        T
                                TAGA GCTGTGGGTCA TG
                                |||| |||||||||| ||
                                GTCT CGACACCCAGT AC
                                  C         C
GAM2791 LOC257566 3' CAGAGGCTGTGGGTCAGTG   64926     A        T
                                TAGA GCTGTGGGTCA TG
                                |||| |||||||||| ||
                                GTCT CGACACCCAGT AC
                                  C         C
GAM2792 ITGA6   3' ACAGCTAACGTGATGG     64929    TTTT
                                GCA   CTAACGTGATGG
                                |||   ||||||||||||
                                TGT   GATTGCACTACC
                                  C___
GAM2792 MAPK3   3' TCCATTTTCTAACAGTCTGG  64930   G        TGA
                                TC CATTTTCTAACG   TGG
                                || ||||||||||||   |||
                                AG GTAAAAGATTGT   ACC
                                 _         CAG
GAM2792 FLJ12903 3' TCACATTTTCTAGTTAAC   64931         ACG
                                TCGCATTTTCTA   TGAT
                                ||||||||||||   ||||
                                AGTGTAAAAGAT   ATTG
                                       CA_
GAM2792 UCH37   3' GCATTTTCTAGCTTCATATGG 64932        A___   A
                                GCATTTTCTA   CGTG TGG
                                ||||||||||   |||| |||
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                                CGTAAAAGAT    GTAT ACC
                                      CGAA    _
GAM2792  LOC132321 3'  TATCCATTTTCCTATGGATGG  64933      G       AACGT
                                TATC CATTTTCT     GATGG
                                |||| ||||||||     |||||
                                ATAG GTAAAAGG     CTACC
                                  _       ATAC_
GAM2792  LOC146435 3'  TATCCCATTTTCTGAT      64934      G       AACGT
                                TATC CATTTTCT     GAT
                                |||| ||||||||     |||
                                ATAG GTAAAAGA     CTA
                                  G       _____
GAM2792  LOC222066 3'  TCGCATCTTTTTAAATGTTGG  64935         CTAAC   A
                                TCGCATTTT     GTG TGG
                                |||||||||     ||| |||
                                AGCGTAGAA     TAC ACC
                                      AAATT   A
GAM2793  C21orf108 3'  CAGTAAATCGTGGCCATAGC   64938         CGATG
                                CAGTAAATCG     CGTAGC
                                ||||||||||     ||||||
                                GTCATTTAGC     GTATCG
                                      ACCG_
GAM2793  WBP11     3'  GCAGTAAATTCTGAACAAGGC  64939         _ ___    T
                                GCAGTAAAT C   GCGA GC
                                ||||||||| |   |||| ||
                                CGTCATTTA G   TGTT CG
                                      A ACT    C
GAM2794  FLJ12747  3'  GGTCTTTACAAAATCTCTTT   64942      A   TTAT
                                GGTC TTG    GAATCTCTTT
                                |||| |||    ||||||||||
                                CCAG AAT    TTTAGAGAAA
                                  A   GT__
GAM2794  LOC154215 3'  GTTATTGTTACTTGTCTCTTT  64943     C       GAA
                                GT ATTGTTAT   TCTCTTT
                                || ||||||||   |||||||
                                CA TAACAATG   AGAGAAA
                                 A       AAC
GAM2794  LOC157247 5'  GGCATTGGAGTCTCTTTC     64944     T     TTAT  A
                                GG CATTG    GA TCTCTTTC
                                || |||||    || ||||||||
                                CC GTAAC    CT AGAGAAAG
                                 _     _____  C
GAM2794  LOC221421 3'  TTGTCTAGAATCTCTTTCA    64945       AT
                                TTGTT  GAATCTCTTTCA
                                |||||  ||||||||||||
                                AACAG  CTTAGAGAAAGT
                                   AT
GAM2794  LOC256021 3'  GTCATTGTTCTCGTTTC      64946         TATGAA    _
                                GTCATTGT     TCTC TTTC
                                ||||||||     |||| ||||
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                                CAGTAACA     AGAG AAAG
                                       _______   C
GAM2795 DIAPH2   3'  TGTGTATGTGTGTTTTCAGATC 64949        ATAAC_  TCC
             GGA                  TGTGTATGT     TCA  CGGA
                                  |||||||||     |||  ||||
                                  ACACATACA     AGT  GCCT
                                       CACAAA   CTA
GAM2795 GPM6A    3'  TGTTATGTATAACACATGG   64950    G       T  CCC
                                  TGT TATGTATAAC CAT  GG
                                  ||| |||||||||| |||  ||
                                  ACA ATACATATTG GTA  CC
                                    _       T  ___
GAM2795 INHBC    3'  TGTGTCAACTCATCTTGG    64951     ATGTA      CC
                                  TGTGT    TAACTCATC  GG
                                  |||||    |||||||||  ||
                                  ACACA    GTTGAGTAG  CC
                                       _____       AA
GAM2795 PCDH11X  3'  TGTGTGTGTGTAGATCATC   64952     A  A  AC
                                  TGTGT TGT TA  TCATC
                                  ||||| ||| ||  |||||
                                  ACACA ACA AT  AGTAG
                                     C  C  CT
GAM2795 PCDH11X  3'  TGTGTGTGTGTAGATCATC   64952     A  A  AC
                                  TGTGT TGT TA  TCATC
                                  ||||| ||| ||  |||||
                                  ACACA ACA AT  AGTAG
                                     C  C  CT
GAM2795 PCDH11Y  3'  TGTGTGTGTGTAGATCATC   64952     A  A  AC
                                  TGTGT TGT TA  TCATC
                                  ||||| ||| ||  |||||
                                  ACACA ACA AT  AGTAG
                                     C  C  CT
GAM2795 ARHGEF9  3'  TGTGTATGTGTACTCAAGGG  64953       ATA    TCCC
                                  TGTGTATGT   ACTCA   GG
                                  |||||||||   |||||   ||
                                  ACACATACA   TGAGT   CC
                                       CA_    TC__
GAM2795 AXOT     3'  TGTGTATGTATATATTCAT   64954         AC_
                                  TGTGTATGTATA   TCAT
                                  ||||||||||||   ||||
                                  ACACATACATAT   AGTA
                                         ATA
GAM2795 DDX30    5'  TGCGTCAAACAACTCATTCCGG 64955     ATGT       C
                                  TGTGT    ATAACTCAT CCGG
                                  |||||    ||||||||| ||||
                                  ACGCA    TGTTGAGTA GGCC
                                     GTT_       A
GAM2795 JDD1     3'  TGTGTATGTGTGAGCTCATC  64956       ATAA_
                                  TGTGTATGT    CTCATC
                                  |||||||||    ||||||
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                                ACACATACA    GAGTAG
                                     CACTC
GAM2795 MGC15482 3' TGTGTATGTATGTGTGGCTCTG 64957          AACTCA_ CC
            G                    TGTGTATGTAT      TC  GG
                                 ||||||||||       ||  ||
                                 ACACATACATA      AG  CC
                                      CACACCG  A_
GAM2795 SLC5A7   3' TGTGTATGTGTAACACCAG   64958         A   TCATC
                                 TGTGTATGT TAAC    CCGG
                                 |||||||| ||||    ||||
                                 ACACATACA ATTG    GGTC
                                     C    T____
GAM2795 TNFAIP3  3' TATGTATGTATACCTTGG    64959          ACTCAT  C_
                                 TGTGTATGTATA     CC  GG
                                 ||||||||||||     ||  ||
                                 ATACATACATAT     GG  CC
                                        _______  AA
GAM2796 ABR      3' TGGCTGCAGCCTACCTGCCTGG 64962      A        __ _
            ACAC                    TGGC TGCAGCCTGCT  CC GGACAC
                                 |||| ||||||||||  || ||||||
                                 ACCG ACGTCGGATGG  GG CCTGTG
                                   _         AC  A
GAM2796 ABR      3' TGGCTGCAGCCTACCTGCCTGG 64962      A        __ _
            ACAC                    TGGC TGCAGCCTGCT  CC GGACAC
                                 |||| ||||||||||  || ||||||
                                 ACCG ACGTCGGATGG  GG CCTGTG
                                   _         AC  A
GAM2796 FCAR     3' TGTGTGCAGCCTGGCCAG    64963    GCA       CT
                                 TG   TGCAGCCTG  CCGG
                                 ||   |||||||||  ||||
                                 AC   ACGTCGGAC  GGTC
                                  AC_       C_
GAM2796 GLI4     3' TGGCATGCGGTGCTGGGCA   64964        AGCC    CC  A
                                 TGGCATGC    TGCT  GG CA
                                 ||||||||    ||||  || ||
                                 ACCGTACG    ACGA  CC GT
                                     CC__    __  C
GAM2796 NCALD    3' GGCATGCAGTCCTCTGG     64965         _  G  CC
                                 GGCATGCAG CCT CT  GG
                                 ||||||||| ||| ||  ||
                                 CCGTACGTC GGA GA  CC
                                      A  _ __
GAM2796 CACNA2D1 3' TGACATGCAGCCAGTGGGTGC  64966           _______
                                 TGGCATGCAGCC     TGC
                                 ||||||||||||     |||
                                 ACTGTACGTCGG     ACG
                                       TCACCC
GAM2796 DKFZP434P211 3' TGTGTGCAGCCCCAGAC     64967    GCA      TGCT
                                 TG   TGCAGCC    CCGGAC
                                 ||   |||||||    ||||||
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                                AC   ACGTCGG   GGTCTG
                                 AC_     ____
GAM2796 DKFZp761N1114 3' TGGCATGCGCCTGTAGTCA   64968       A    CTCC  A
                                TGGCATGC GCCTG   GG CA
                                |||||||| |||||   || ||
                                ACCGTACG CGGAC   TC GT
                                     _    A___  A
GAM2796 FRAT1    3' TGGCGCTGTGGCCACCCCGG  64969     A_  CA   T
                                TGGC  TG  GCC GCTCCGG
                                ||||  ||  ||| |||||||
                                ACCG  AC  CGG TGGGGCC
                                  CG  AC  _
GAM2796 KIAA0365 3' TGGCATGCCAGGAACTGGGCA 64970       AGCCT   CC  A
                                TGGCATGC    GCT  GG CA
                                ||||||||    |||  || ||
                                ACCGTACG    TGA  CC GT
                                     GTCCT   __  C
GAM2796 KIAA0748 3' GCATGCAGCTTGTGGCAGCA  64971       C  CTC   A
                                GCATGCAGC TG   CGG CA
                                ||||||||| ||   ||| ||
                                CGTACGTCG AC   GTC GT
                                     A  ACC   _
GAM2796 KIAA1641 3' GCTGTGCAGCCTGCTTCCTAAC 64972    A_        _  G
                                GC  TGCAGCCTGCT CC GAC
                                ||  |||||||||||| || |||
                                CG  ACGTCGGACGA GG TTG
                                 AC          A  A
GAM2796 MGC3036  3' TGGCAGCAGCTGCGGACA    64973      T    C   TCC
                                TGGCA GCAGC TGC   GGACA
                                ||||| ||||| |||   |||||
                                ACCGT CGTCG ACG   CCTGT
                                  _    _  ____
GAM2796 THEA     3' TGGCATGCAGACTGAGAGG   64974         C   CTCC
                                TGGCATGCAG CTG    GG
                                |||||||||| |||    ||
                                ACCGTACGTC GAC    CC
                                     T   TCT_
GAM2796 LOC144481 3' TGGTTTGCAGCCTGCTGGGA  64975    CA        CC
                                TGG  TGCAGCCTGCT  GGA
                                |||  ||||||||||  |||
                                ACC  ACGTCGGACGA  CCT
                                  AA         C_
GAM2796 LOC145748 3' TGGCTGCAGCCTGCTCGG    64976     A         C
                                TGGC TGCAGCCTGCTC GG
                                |||| ||||||||||| ||
                                ACCG ACGTCGGACGAG CC
                                  _         _
GAM2796 LOC150174 3' TGTGTGCAGCCCCAGAC     64967    GCA      TGCT
                                TG   TGCAGCC    CCGGAC
                                ||   |||||||    ||||||
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                                AC   ACGTCGG    GGTCTG
                                 AC_      _____
GAM2796  LOC150213 3'  TGTGTGCAGCCCCAGAC     64967    GCA      TGCT
                                TG   TGCAGCC    CCGGAC
                                ||   |||||||    ||||||
                                AC   ACGTCGG    GGTCTG
                                 AC_      _____
GAM2796  LOC150236 3'  TGTGTGCAGCCCCAGAC     64967    GCA      TGCT
                                TG   TGCAGCC    CCGGAC
                                ||   |||||||    ||||||
                                AC   ACGTCGG    GGTCTG
                                 AC_      _____
GAM2796  LOC201952 5'  TGGCATGGCTGCAGCTCCGGA  64977        _ A  CT
                                TGGCATG C GC  GCTCCGGA
                                |||||||  | ||  ||||||||
                                ACCGTAC G CG  CGAGGCCT
                                     C A  T_
GAM2796  LOC219445 3'  GCTGTGCAGCCTCCACAGGGCA 64978    A_       G TC   A_
              C                   GC  TGCAGCCT C  CGG  CAC
                                ||  ||||||||  |  |||  |||
                                CG  ACGTCGGA G  GTC  GTG
                                 AC       _ GT   CC
GAM2796  LOC254045 3'  TGGTTTGCAGCCTGCTGGGA   64975     CA         CC
                                TGG  TGCAGCCTGCT  GGA
                                |||  ||||||||||  |||
                                ACC  ACGTCGGACGA  CCT
                                  AA          C_
GAM2796  LOC256158 5'  TGGGTGCAGGGACCCCGGACAC 64979     CA    CCT
                                TGG  TGCAG   GCTCCGGACAC
                                |||  |||||   ||||||||||
                                ACC  ACGTC   TGGGGCCTGTG
                                  C_    CC_
GAM2796  LOC92492  5'  TGGCAGGCAGCCTGCTGGGAGG 64980       T        CC__  A
              CAC                    TGGCA GCAGCCTGCT    GG CAC
                                ||||| ||||||||||    || |||
                                ACCGT CGTCGGACGA    CC GTG
                                   C         CCCT  _
GAM2797  KIAA0257  3'  TACAGGTCTTATTAGAGTTT   64983      CG  AG
                                TACAG  CT  TATTAGAGTTT
                                |||||  ||  ||||||||||
                                ATGTC  GA  ATAATCTCAAA
                                   CA  __
GAM2798  FACL5    3'  TAGAGACTGTTGGCAAGTTATG 64986      AG      T  TT
                                TAGA  CTGTTGG CA  GTTATG
                                ||||  ||||||| ||  ||||||
                                ATCT  GACAACC GT  CAATAC
                                   CT       _  T_
GAM2798  NAG73    5'  TAGAAGCTGTGGTCTGT     64925          T    AT
                                TAGAAGCTGT GGTC  TGT
                                |||||||||| ||||  |||
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                                ATCTTCGACA CCAG  ACA
                                      _   __
GAM2798  SV2      3'  AGGAGTTGTTGGTCTCACAGTG 64987    A  C       A TG TA
                                AG AG TGTTGGTC T  T  TG
                                || || |||||||| |  |  ||
                                TC TC ACAACCAG A  G  AC
                                 C  A       _ GT TC
GAM2798  LOC150468 5'  AAAGCCATTATTGTTAT     64988         GGTC
                                GAAGCTGTT    ATTGTTAT
                                |||||||||    ||||||||
                                TTTCGGTAA    TAACAATA
                                     _____
GAM2799  IL13RA2   3'  CAATACCATGTCTCTTGATAT  64991         ATAA    A
                                TAATACCA    TCTT ATAT
                                ||||||||    |||| ||||
                                GTTATGGT    AGAA TATA
                                      ACAG    C
GAM2799  DKFZP762D096 3'  TAATACCAAATACAATATAAA  64992         TAATCT
                                TAATACCAA     TAATATAAA
                                |||||||||     |||||||||
                                ATTATGGTT     GTTATATTT
                                      TAT___
GAM2799  KIAA0836  3'  TAATACCTATAATCTTAA     64993        A
                                TAATACC ATAATCTTAA
                                ||||||| ||||||||||
                                ATTATGG TATTAGAATT
                                     A
GAM2799  LOC115297 3'  TAATACCAAATAGTTCTTAA   64994         TAA__
                                TAATACCAA     TCTTAA
                                |||||||||     ||||||
                                ATTATGGTT     AGAATT
                                      TATCA
GAM2799  LOC158116 3'  TAATACTAATAATCTAGTATA  64995       C       TAA
                                TAATAC AATAATCT   TATA
                                |||||| ||||||||   ||||
                                ATTATG TTATTAGA   ATAT
                                    A       TC_
GAM2799  LOC203107 3'  ATACCAATAAAATATAAA     64996         TCTT
                                ATACCAATAA    AATATAAA
                                ||||||||||    ||||||||
                                TATGGTTATT    TTATATTT
                                     _____
GAM2800  MECP2     3'  CGTGGATAAGTGTCCTTTGG   64999         GGATA
                                CGTGGATAAG     TTTGG
                                ||||||||||     |||||
                                GCACCTATTC     AAACC
                                      ACAGG
GAM2800  DKFZp547A023 3'  GTGGATAGTCTTATTTGGCA   65000        A GGA
                                GTGGATA G   TATTTGGCA
                                ||||||| |   |||||||||
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                                CACCTAT C   ATAAACCGT
                                    _ AGA
GAM2801  ICB-1    3'  AGGGAGTCACGTGCGAGAT   65003     A      A  T
                                AGG AGTTACGT CG AGAT
                                ||| |||||||| || ||||
                                TCC TCAGTGCA GC TCTA
                                  C       C  _
GAM2801  LOC126917 3'  AGGAAGTCGTGTGCTCC     65004       TA   AC  AGA
                                AGGAAGT  CGT  GT   TCC
                                |||||||  |||  ||   |||
                                TCCTTCA  GCA  CA   AGG
                                    __   __  CG_
GAM2802  LFNG     3'  ACAGACACGCCCACTGTG    65007     _  G
                                ATAG TG GCCCACTGTG
                                |||| || ||||||||||
                                TGTC GT CGGGTGACAC
                                  T  G
GAM2802  NDUFA9   3'  TGTTTTAATAGTGGAACTGTG  65008     AC       CCC
                                TGTT  AATAGTGGG   ACTGTG
                                ||||  |||||||||   ||||||
                                ACAA  TTATCACCT   TGACAC
                                  AA       ___
GAM2802  DKFZP564G092 5'  TGCTACAATAAAGCTACTGTG  65009          TG   CC
                                TGTTACAATAG  GGC  ACTGTG
                                ||||||||||  |||  ||||||
                                ACGATGTTATT  TCG  TGACAC
                                     __   A_
GAM2802  FLJ22557  3'  TATTACAATTCATGTTCACTGT 65010         A_  GGCC
           G                    TGTTACAAT  GTG   CACTGTG
                                |||||||||  |||   |||||||
                                ATAATGTTA  TAC   GTGACAC
                                    AG   AA__
GAM2802  ZNF397   3'  TGTTGGAGAGGCCCACTGT   65011     ACAAT  T
                                TGTT    AG GGGCCCACTGT
                                ||||    || ||||||||||
                                ACAA    TC TCCGGGTGACA
                                  CC___  _
GAM2802  LOC145919 3'  TGTTCAAGGGTCCACTGTG   65012     A   TAGT   C
                                TGTT CAA   GGG CCACTGTG
                                |||| |||   ||| ||||||||
                                ACAA GTT   CCC GGTGACAC
                                  _  ____   A
GAM2802  LOC146713 3'  TGTTACACACGGCCCACTGTG  65013       ATAGTG
                                TGTTACA     GGCCCACTGTG
                                |||||||     ||||||||||
                                ACAATGT     CCGGGTGACAC
                                    GTG___
GAM2802  LOC149832 5'  TGTTAGAGTCTGCCCTCCACTG 65014      CAAT   GG   ___
           TG                     TGTTA   AGT  GCCC   ACTGTG
                                |||||   |||  ||||   ||||||
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                                ACAAT   TCA  CGGG   TGACAC
                                  C___   GA   AGG
GAM2802  LOC151121 5'  TGTCACAATCCCCACTGT    65015        AGTGGG
                                TGTTACAAT     CCCACTGT
                                |||||||||     ||||||||
                                ACAGTGTTA     GGGTGACA
                                   G_____
GAM2802  LOC202108 5'  TGTTCTGGTGGCAAACCCATTG 65016     ACAATA TG     C
           TG                     TGTT     G  GGCCCA TGTG
                                ||||     |  |||||| ||||
                                ACAA     C  TTGGGT ACAC
                                  GACCAC GT     A
GAM2802  LOC245811 3'  TGTTACATTTATGAGCCCACTG 65017       ATA
           TG                     TGTTACA   GTGGGCCCACTGTG
                                |||||||   ||||||||||||||
                                ACAATGT   TACTCGGGTGACAC
                                   AAA
GAM2803  SMT3H1    3'  GTTGCACTTGAAGTACA     65020        CATA
                                GTTGCACT    GAAGTACA
                                ||||||||    ||||||||
                                CAACGTGA    CTTCATGT
                                   A___
GAM2803  C1QR1     3'  TGTTGCATCATGATGC      65021        C    A  A
                                TGTTGCA TCAT GA GT
                                ||||||| |||| || ||
                                ACAACGT AGTA CT CG
                                   _   _ A
GAM2803  CNK2      3'  TGTTGCACCTGAATACA     65022        CATA   G
                                TGTTGCACT    GAA TACA
                                |||||||||    ||| ||||
                                ACAACGTGG    CTT ATGT
                                   A___   _
GAM2803  FLJ10898  3'  TATGTTGCATTAACATTTGTAC 65023        CTC   GAA
                                TATGTTGCA   ATA   GTAC
                                |||||||||   |||   ||||
                                ATACAACGT   TGT   CATG
                                    AAT   AAA
GAM2803  FLJ20274  3'  TGTTGCACTAGTATAC      65024        CAT  AA
                                TGTTGCACT   AG  GTAC
                                |||||||||   ||  ||||
                                ACAACGTGA   TC  TATG
                                   ___ A_
GAM2803  LC27      3'  CATGTTGTTAGGCAGAAGTA   65025       CACTCA
                                TATGTTG     TAGAAGTA
                                |||||||     ||||||||
                                GTACAAC     GTCTTCAT
                                   AATCC_
GAM2803  PCCX2     3'  GTTGTGTCGATGAAGTACAC   65026     CAC  ATA
                                GTTG   TC   GAAGTACAC
                                ||||   ||   |||||||||
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                                CAAC  AG  CTTCATGTG
                                  AC_ CTA
GAM2803 PRO2032  5' TATGTTGCACATAGCCTATAC 65027        TC   AA_
                                TATGTTGCAC ATAG  GTAC
                                |||||||||| |||| ||||
                                ATACAACGTG TATC  TATG
                                     __   GGA
GAM2803 PSTPIP2  3' TGTTGTACAAAAAGTACA   65028     C TCAT
                                TGTTG AC   AGAAGTACA
                                ||||| ||   |||||||||
                                ACAAC TG   TTTTCATGT
                                  A T___
GAM2803 RTVP1    3' ATGTTTTAAAATAGAAGTACAC 65029     GCACTC
                                ATGTT    ATAGAAGTACAC
                                |||||    ||||||||||||
                                TACAA    TATCTTCATGTG
                                  AATTT_
GAM2803 SEMA4G   5' TATGTTGCGCTTGAGCAGC   65030       A CAT A
                                TATGTTGC CT  AG AGT
                                |||||||| ||  || |||
                                ATACAACG GA  TC TCG
                                    C AC_ G
GAM2803 LOC222008 3' ATGTTGATAGAAGTA      65031      CACTC
                                ATGTTG   ATAGAAGTA
                                ||||||   |||||||||
                                TACAAC   TATCTTCAT
                                  _____
GAM2803 LOC255338 5' TATGTTGCACTTGAGGGGAAG 65032        CATA__
                                TATGTTGCACT    GAAG
                                ||||||||||    ||||
                                ATACAACGTGA    CTTC
                                      ACTCCC
GAM2804 ERBB2IP  3' TCTTGCTGTCTTCCCCGCTT  65035    C G   G  T
                                TCT GC GTCTT CTC CTT
                                ||| || ||||| ||| |||
                                AGA CG CAGAA GGG GAA
                                  A A   G  C
GAM2804 HOXD3    3' GCGGTCTTAATCCTTTAT    65036       C TC
                                GCGGTCTTG TC  TTAT
                                ||||||||| ||  ||||
                                CGCCAGAAT AG  AATA
                                     T  GA
GAM2804 RFXANK   5' TCTGCGGTCTCAAAGGCTTAT 65037    C      GCTCT
                                TCT GCGGTCTT   CTTAT
                                ||| ||||||||   |||||
                                AGA CGCCAGAG   GAATA
                                  _     TTTCC
GAM2804 RFXANK   5' TCTGCGGTCTCAAAGGCTTAT 65037    C      GCTCT
                                TCT GCGGTCTT   CTTAT
                                ||| ||||||||   |||||
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                                AGA CGCCAGAG    GAATA
                                  _      TTTCC
GAM2804  ZNF141   3'  TCTCCGGTATGAATTCTCTTAT 65039     G   CT  C__
                                TCTC CGGT  TG   TCTCTTAT
                                |||| ||||  ||   ||||||||
                                AGAG GCCA  AC   AGAGAATA
                                  _   T_  TTA
GAM2804  ZNF141   3'  TCTCTGGTATAAATTCTCTTAT 65038     GC   CTTGC_
                                TCTC  GGT     TCTCTTAT
                                ||||  |||     ||||||||
                                AGAG  CCA     AGAGAATA
                                  A_   TATTTA
GAM2804  FLJ20079 3'  TCTGCGGTATTCTCTTA     65040     C    CTTGC
                                TCT GCGGT    TCTCTTA
                                ||| |||||    |||||||
                                AGA CGCCA    AGAGAAT
                                  _    TA___
GAM2804  FLJ33069 5'  TCGGCAGCCTCTTGTTCTCTT  65041    _     GC__
                                TCG CGGTCTT   TCTCTT
                                ||| |||||||   ||||||
                                AGC GTCGGAG   AGAGAA
                                  C      AACA
GAM2804  KIAA0100 3'  TCCCTGGGTCTTGCTCTCTT   65042     GC
                                TCTC  GGTCTTGCTCTCTT
                                ||||  ||||||||||||||
                                AGGG  CCAGAACGAGAGAA
                                  AC
GAM2804  LOC256112 3'  TCCTGTGTAAGCTCTCTTAT   65043    CGCG  CTT
                                TCT   GT   GCTCTCTTAT
                                |||   ||   ||||||||||
                                AGG   CA   CGAGAGAATA
                                  ACA_  TT_
GAM2805  BAALC    3'  ATACAATCTGCCAATGGAA    65046      TTTGT       A
                                ATGCA    TCTGCCAAT GAA
                                |||||    ||||||||| |||
                                TATGT    AGACGGTTA CTT
                                   T_____       C
GAM2805  C14orf1  3'  ATGCATCTGTAGATAGAA     65047         TCTGCCA
                                ATGCATTTGT     ATAGAA
                                ||||||||||     ||||||
                                TACGTAGACA     TATCTT
                                     TC_____
GAM2805  DNMT2    3'  ATGCATTTGTTTAGA       65048          CTGCCAA
                                ATGCATTTGTT     TAGA
                                ||||||||||     ||||
                                TACGTAAACAA     ATCT
                                               _______
GAM2805  FZD10    3'  CATTTGTTTAACAATAGAAA   65049        CT  C
                                CATTTGTT  GC AATAGAAA
                                ||||||||  || ||||||||
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                                GTAAACAA  TG TTATCTTT
                                    AT  _
GAM2805  GPR85    3'  ATGTATTTATTCTGCATTATTA 65050     C         CAA__
                GA                   ATG ATTTGTTCTGC     TAGA
                                    ||| ||||||||||     ||||
                                    TAC TAAATAAGACG     ATCT
                                      A          TAATA
GAM2805  M11S1    3'  ATGCAGTTGTTCTGCCAA     65051       T
                                    ATGCA TTGTTCTGCCAA
                                    ||||| ||||||||||||
                                    TACGT AACAAGACGGTT
                                      C
GAM2805  MTMR2    3'  GCATTTGCCTTTTAATAGAAA  65052         T  GCC
                                    GCATTTGT CT   AATAGAAA
                                    |||||||| ||   ||||||||
                                    CGTAAACG GA   TTATCTTT
                                        _  AAA
GAM2805  RET      3'  CATTTGTTCTGCACTGAA     65053           CA  A
                                    CATTTGTTCTGC  AT GAA
                                    ||||||||||||  || |||
                                    GTAAACAAGACG  TG CTT
                                          __  A
GAM2805  SIAT8E   5'  GCCTCCGGTTCTGCCGATAG   65054     A   _      A
                                    GC TTTG TTCTGCC ATAG
                                    || |||| ||||||| ||||
                                    CG AGGC AAGACGG TATC
                                     G   C       C
GAM2805  SNX6     3'  ATGCATTTGCTTTTCTTCAGAA 65055           CTGCCAA
                A                    ATGCATTTGTT       TAGAAA
                                    ||||||||||||       ||||||
                                    TACGTAAACGA       GTCTTT
                                          AAAGAA_
GAM2805  STAU     5'  TGCATTTAGTTCTACAGTAG   65056        _      CAA
                                    TGCATTT GTTCTGC   TAG
                                    ||||||| |||||||   |||
                                    ACGTAAA CAAGATG   ATC
                                        T       TC_
GAM2805  STAU     5'  TGCATTTAGTTCTACAGTAG   65056        _      CAA
                                    TGCATTT GTTCTGC   TAG
                                    ||||||| |||||||   |||
                                    ACGTAAA CAAGATG   ATC
                                        T       TC_
GAM2805  STAU     5'  TGCATTTAGTTCTACAGTAG   65056        _      CAA
                                    TGCATTT GTTCTGC   TAG
                                    ||||||| |||||||   |||
                                    ACGTAAA CAAGATG   ATC
                                        T       TC_
GAM2805  AD022    3'  ATGCATTTATTTTTGTTAGAAA 65057           CTGCCAA
                                    ATGCATTTGTT       TAGAAA
                                    ||||||||||||       ||||||
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                                TACGTAAATAA      ATCTTT
                                      AAACA__
GAM2805  DKFZp434C0328 3'  ATGCATTTGATCTGTCACTAAA 65058         T   C  A
                                ATGCATTTG TCTG CA TAGA
                                ||||||||| |||| || ||||
                                TACGTAAAC AGAC GT ATTT
                                     T   A  G
GAM2805  DKFZP434J214 3'  ATACATTTTAGTACTGCTGATA 65059        __  T   CA
           GAAA                   ATGCATTT  GT CTGC  ATAGAAA
                                ||||||||  || ||||  |||||||
                                TATGTAAA  CA GACG  TATCTTT
                                     AT  T   AC
GAM2805  GK001    3'  ATGCATTTGTTACTCAAGAAA  65060         TC  _  AT
                                ATGCATTTGT  TGC CA  AGAAA
                                ||||||||||  ||| ||  |||||
                                TACGTAAACA  ATG GT  TCTTT
                                      __   A  __
GAM2805  HSPC031   3'  TGCATTTGTCAGTGATAGA   65061         CTGCCA
                                TGCATTTGTT     ATAGA
                                ||||||||||     |||||
                                ACGTAAACAG     TATCT
                                      TCAC__
GAM2805  KIAA0319  3'  TGCTTTGTTCTGATGAGAAA   65062     A       CCAAT
                                TGC TTTGTTCTG     AGAAA
                                ||| |||||||||     |||||
                                ACG AAACAAGAC     TCTTT
                                  _       TAC__
GAM2805  KIAA1191  3'  TTTGTTCTGTGGCATAGAAA   65063         CCA_
                                TTTGTTCTG    ATAGAAA
                                |||||||||    |||||||
                                AAACAAGAC    TATCTTT
                                      ACCG
GAM2805  KIAA1458  3'  CATGAAAACCTGCTAATAGAAA 65064     TTGT_    C
                                CAT     TCTGC AATAGAAA
                                |||     ||||| ||||||||
                                GTA     GGACG TTATCTTT
                                  CTTTT     A
GAM2805  SPRY4     3'  GCGGTCATTCTGCCAATGGGA  65065    AT TG        A_
                                GC  T  TTCTGCCAAT  GA
                                ||  |  ||||||||||  ||
                                CG  A  AAGACGGTTA  CT
                                 CC GT         CC
GAM2805  LOC144997 3'  ATGCATTTTTCTGCTCCAG    65066         G     CAA
                                ATGCATTT TTCTGC   TAG
                                |||||||| ||||||   |||
                                TACGTAAA AAGACG   GTC
                                     _     AG_
GAM2805  LOC148811 3'  TCTGTGTTGCCAATAGAA     65067       TC
                                TTTGT  TGCCAATAGAA
                                |||||  ||||||||||
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                                AGACA  ACGGTTATCTT
                                   CA
GAM2805  LOC221968 3'  GCATATTTTTGTCAATAGAAA  65068      TTG  C  C
                                GCAT   TT TG CAATAGAAA
                                ||||   || || |||||||||
                                CGTA   AA AC GTTATCTTT
                                  TA_  A  A
GAM2805  LOC257443 3'  CATGAAAACCTGCTAATAGAAA 65064     TTGT_    C
                                CAT    TCTGC AATAGAAA
                                |||    ||||| ||||||||
                                GTA    GGACG TTATCTTT
                                 CTTTT    A
GAM2805  LOC90750  3'  ATGCATTTGTTTAGA       65048          CTGCCAA
                                ATGCATTTGTT      TAGA
                                ||||||||||       ||||
                                TACGTAAACAA      ATCT

                                        ________
GAM2806  DKFZP564I0422 3'  CAATATTATAAAGTCTACTTA  65071           CC
                                TAATATTATAAAG  TTTATTTA
                                ||||||||||||  ||||||||
                                GTTATAATATTTC  AGATGAAT
                                          __
GAM2806  OSBPL1A   3'  CATTCTAAAGCCTTTATTTA   65072      A
                                TATT TAAAGCCTTTATTTA
                                |||| ||||||||||||||
                                GTAA ATTTCGGAAATAAAT
                                  G
GAM2806  OSBPL1A   3'  CATTCTAAAGCCTTTATTTA   65072      A
                                TATT TAAAGCCTTTATTTA
                                |||| ||||||||||||||
                                GTAA ATTTCGGAAATAAAT
                                  G
GAM2806  OSBPL1A   3'  CATTCTAAAGCCTTTATTTA   65072      A
                                TATT TAAAGCCTTTATTTA
                                |||| ||||||||||||||
                                GTAA ATTTCGGAAATAAAT
                                  G
GAM2806  PRO1048   3'  TAATTTTATAAAGCCTTC     65073      A
                                TAAT TTATAAAGCCTTT
                                |||| ||||||||||||
                                ATTA AATATTTCGGAAG
                                  A
GAM2806  SAP30     3'  TAATAGTAATAACCTTTATTTA 65074       T  TAA
            A                    TAATA TA   AGCCTTTATTTAA
                                 |||||  ||   ||||||||||||
                                 ATTAT AT   TTGGAAATAAATT
                                   C  TA_
GAM2806  SLC11A2   3'  TAATATTATAAAATGCCATTTA 65075           __   _
                                TAATATTATAAA  GCC TTTA
                                ||||||||||||  ||| ||||
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                                ATTATAATATTT  CGG AAAT
                                      TA   T
GAM2806  LOC257407 3'  TAATATCATAGAGCCCCT    65076         A
                                TAATATTATA AGCCTTT
                                |||||||||| |||||||
                                ATTATAGTAT TCGGGGA
                                      C
GAM2806  LOC92997  3'  TAATATCATAGAGCCCCT    65076         A
                                TAATATTATA AGCCTTT
                                |||||||||| |||||||
                                ATTATAGTAT TCGGGGA
                                      C
GAM2807  ADAM10    3'  TGCAAGTGAAGAAAATGCA    65079      AAA      ATGA
                                TGCAA   AAGAAAAT   GCA
                                |||||   ||||||||   |||
                                ACGTT   TTCTTTTA   CGT
                                   CAC      ____
GAM2807  BSN       3'  AAAAAAGCTGATGAGCAG     65080       AAAAT
                                AAAAAAG    ATGAGCAG
                                |||||||    ||||||||
                                TTTTTTC    TACTCGTC
                                    GAC__
GAM2807  CASP10    3'  TGCAAAAGAAAAAGAAAAT    65081       ___
                                TGCAAAA   AAAGAAAAT
                                |||||||   |||||||||
                                ACGTTTT   TTTCTTTTA
                                    CTT
GAM2807  CASP10    3'  TGCAAAAGAAAAAGAAAAT    65081       ___
                                TGCAAAA   AAAGAAAAT
                                |||||||   |||||||||
                                ACGTTTT   TTTCTTTTA
                                    CTT
GAM2807  CCNDBP1   3'  TGCAAAAAGAGAATAAGGCAG  65082        A   AAAT   _
                                TGCAAAAA AGA   ATGAG CAG
                                |||||||| |||   ||||| |||
                                ACGTTTTT TCT   TATTC GTC
                                    C  ____    C
GAM2807  CCNDBP1   3'  TGCAAAAAGAGAATAAGGCAG  65082        A   AAAT   _
                                TGCAAAAA AGA   ATGAG CAG
                                |||||||| |||   ||||| |||
                                ACGTTTTT TCT   TATTC GTC
                                    C  ____    C
GAM2807  CELSR1    3'  TGCAAGAAAAGAAAACTGAA   65083      A       A
                                TGCAA AAAAGAAAAT TGAG
                                ||||| |||||||||| ||||
                                ACGTT TTTTCTTTTG ACTT
                                   C       _
GAM2807  COL1A1    3'  TGCAAAGGAAAAAAATAT     65084       AA
                                TGCAAA  AAGAAAATAT
                                ||||||  ||||||||||
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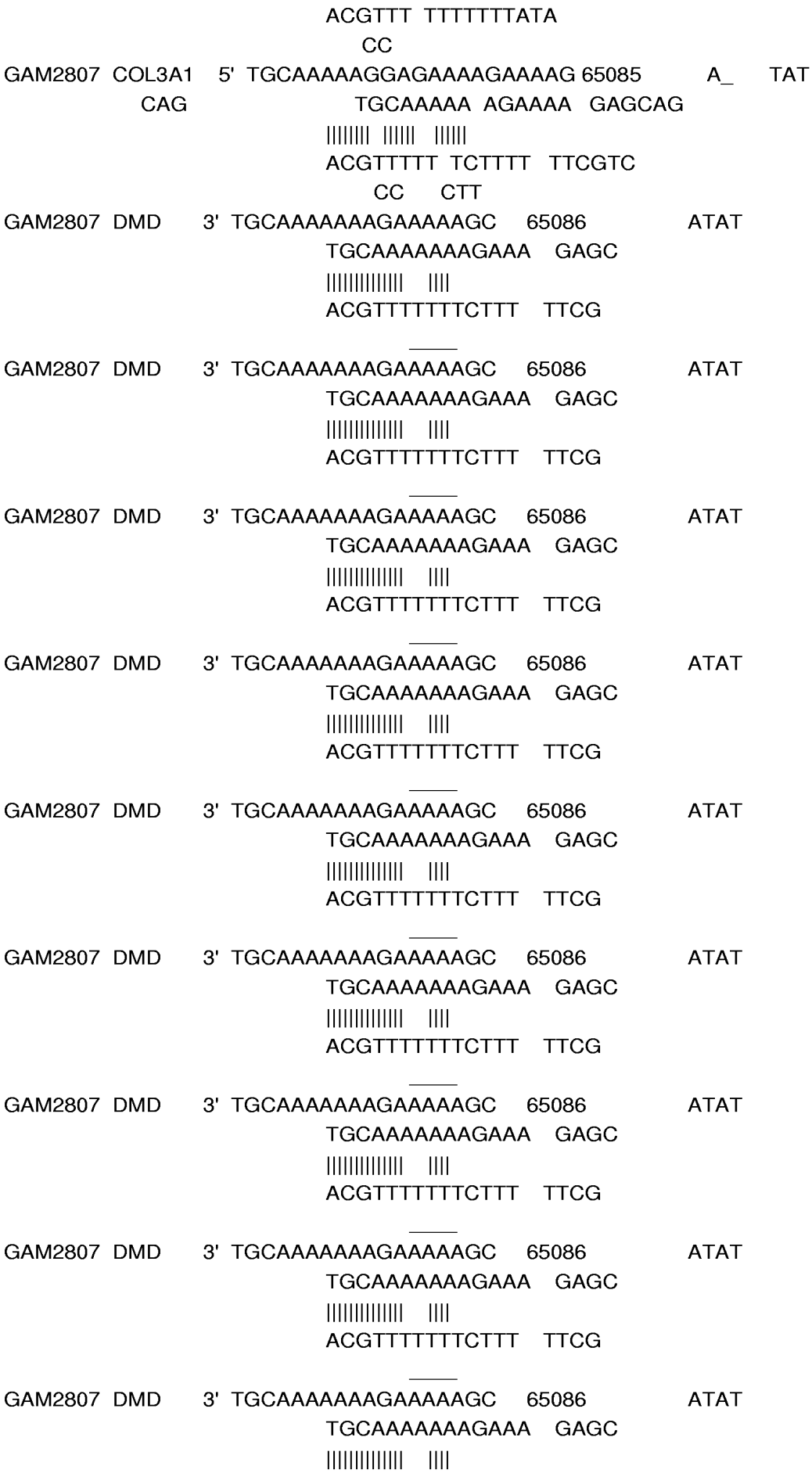
ACGTTT TTTTTTTATA
CC
GAM2807 COL3A1 5' TGCAAAAAGGAGAAAAGAAAAG 65085 A_ TAT
CAG TGCAAAAA AGAAAA GAGCAG
ACGTTTTT TCTTTT TTCGTC
CC CTT
GAM2807 DMD 3' TGCAAAAAAAGAAAAAGC 65086 ATAT
TGCAAAAAAAGAAA GAGC
ACGTTTTTTTCTTT TTCG
GAM2807 DMD 3' TGCAAAAAAAGAAAAAGC 65086 ATAT
TGCAAAAAAAGAAA GAGC
ACGTTTTTTTCTTT TTCG
GAM2807 DMD 3' TGCAAAAAAAGAAAAAGC 65086 ATAT
TGCAAAAAAAGAAA GAGC
ACGTTTTTTTCTTT TTCG
GAM2807 DMD 3' TGCAAAAAAAGAAAAAGC 65086 ATAT
TGCAAAAAAAGAAA GAGC
ACGTTTTTTTCTTT TTCG
GAM2807 DMD 3' TGCAAAAAAAGAAAAAGC 65086 ATAT
TGCAAAAAAAGAAA GAGC
ACGTTTTTTTCTTT TTCG
GAM2807 DMD 3' TGCAAAAAAAGAAAAAGC 65086 ATAT
TGCAAAAAAAGAAA GAGC
ACGTTTTTTTCTTT TTCG
GAM2807 DMD 3' TGCAAAAAAAGAAAAAGC 65086 ATAT
TGCAAAAAAAGAAA GAGC
ACGTTTTTTTCTTT TTCG
GAM2807 DMD 3' TGCAAAAAAAGAAAAAGC 65086 ATAT
TGCAAAAAAAGAAA GAGC
ACGTTTTTTTCTTT TTCG
GAM2807 DMD 3' TGCAAAAAAAGAAAAAGC 65086 ATAT
TGCAAAAAAAGAAA GAGC

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                              ACGTTTTTTTCTTT  TTCG
                                          ____
GAM2807 DMD     3' TGCAAAAAAAGAAAAAGC  65086        ATAT
                              TGCAAAAAAAGAAA  GAGC
                              ||||||||||||||  ||||
                              ACGTTTTTTTCTTT  TTCG
                                          ____
GAM2807 DMD     3' TGCAAAAAAAGAAAAAGC  65086        ATAT
                              TGCAAAAAAAGAAA  GAGC
                              ||||||||||||||  ||||
                              ACGTTTTTTTCTTT  TTCG
                                          ____
GAM2807 DMD     3' TGCAAAAAAAGAAAAAGC  65086        ATAT
                              TGCAAAAAAAGAAA  GAGC
                              ||||||||||||||  ||||
                              ACGTTTTTTTCTTT  TTCG
                                          ____
GAM2807 DMD     3' TGCAAAAAAAGAAAAAGC  65086        ATAT
                              TGCAAAAAAAGAAA  GAGC
                              ||||||||||||||  ||||
                              ACGTTTTTTTCTTT  TTCG
                                          ____
GAM2807 MDM4    3' TGCAAAAAAAAAAAAAAC  65087          TAT
                              TGCAAAAAAAGAAAA  GAGC
                              ||||||||||||||  ||||
                              ACGTTTTTTTTTTTT  TTTG
                                          ___
GAM2807 PFKM    3' CAAAGGAAGAAAACAAGCAG  65088    AA     AT
                              CAAA  AAGAAAAT  GAGCAG
                              ||||  ||||||||  ||||||
                              GTTT  TTCTTTTG  TTCGTC
                                CC      __
GAM2807 PPP2R2B  3' TACAAAAAAAGAGCATAGCAG 65089        AAATATG
                              TGCAAAAAAAGA     AGCAG
                              ||||||||||||     |||||
                              ATGTTTTTTTCT     TCGTC
                                     CGTA___
GAM2807 PSMB3   3' CAAAAAAAGAAAAAAAAG   65090         TAT
                              CAAAAAAAGAAAA  GAG
                              ||||||||||||||  |||
                              GTTTTTTTCTTTT  TTC
                                      TT_
GAM2807 SLC19A2  3' GCAAAAAAAGAAAAACA    65091        AATAT
                              GCAAAAAAAGAA   GAGCA
                              ||||||||||||   |||||
                              CGTTTTTTTCTT   TTTGT
                                          _____
GAM2807 SLC9A6   3' TGTAAAAAAAAAATGCATGGCA 65092   C       AA   A
            G                   TG AAAAAAAGAA  TATG GCAG
                              ||  ||||||||||  |||| ||||
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                                AC TTTTTTTTTT  GTAC CGTC
                                 A        AC   _
GAM2807  WIG1     3'  TGCAAAAGAAAATGGC      65093       AAA    AT   A
                                TGCAAA   AGAAA  ATG GC
                                ||||||   |||||  ||| ||
                                ACGTTT   TCTTT  TAC CG
                                   ____    __  _
GAM2807  ATP9B    3'  TACAAAAAAAGAAAGAAAAGCA 65094            ATAT
              G                  TGCAAAAAAAGAAA   GAGCAG
                                 ||||||||||||||   ||||||
                                 ATGTTTTTTTCTTT   TTCGTC
                                         CTT_
GAM2807  BANP     5'  TACAAAAAAAGAAAATGTAAA  65095             A
                                 TGCAAAAAAAGAAAAT TGAG
                                 |||||||||||||||| ||||
                                 ATGTTTTTTTCTTTTA ATTT
                                          C
GAM2807  C11orf11 3'  TGCAGAATGAAGGCACGAGCAG 65096     A  AAA   AA
                                 TGCA AA   GAA  TATGAGCAG
                                 |||| ||   |||  |||||||||
                                 ACGT TT   CTT  GTGCTCGTC
                                   C  A__   CC
GAM2807  C13orf1  3'  AGAAAATAGGATGAGCAG    65097        ___
                                 AGAAAATA   TGAGCAG
                                 ||||||||   |||||||
                                 TCTTTTAT   ACTCGTC
                                      CCT
GAM2807  C8orf14  5'  TGCAGTGGAGATTCTTATGAGC 65098     AAAAA   AAA_
              AG                   TGCA    AGA    TATGAGCAG
                                   ||||    |||    |||||||||
                                   ACGT    TCT    ATACTCGTC
                                     CACC_   AAGA
GAM2807  DKFZP434B172 3'  TGCAGAAAAGAAAATACAAA   65099      AA         TG
                                 TGCA  AAAAGAAAATA  AG
                                 ||||  ||||||||||  ||
                                 ACGT  TTTTCTTTTAT  TT
                                   C_         GT
GAM2807  DKFZP434D146 3'  TGTAAAAAAAGAAAAAAAAAGG 65100    C          TAT   _
              CAG                   TG AAAAAAAGAAAA   GAG CAG
                                    || ||||||||||||   ||| |||
                                    AC TTTTTTTCTTTT   TTC GTC
                                     A          TTT   C
GAM2807  FLJ12171 3'  GCGGAAAGGTACCTATGAGCAG 65101    AAAA    AAAA_
                                 GC    AAAG    TATGAGCAG
                                 ||    ||||    |||||||||
                                 CG    TTTC    ATACTCGTC
                                  CC__    CATGG
GAM2807  FLJ14327 3'  GCAAAAAAAGGAGAGCA     65102          AAAATAT
                                 GCAAAAAAAG      GAGCA
                                 ||||||||||      |||||
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                                CGTTTTTTTC      CTCGT
                                      CT_____
GAM2807  FLJ20984  3'  AAAAAAAGAAAAAGAAAGCAG  65103          TAT
                                AAAAAAAGAAAA   GAGCAG
                                ||||||||||||   ||||||
                                TTTTTTTCTTTT   TTCGTC
                                     TCT
GAM2807  FLJ21916  3'  TGCAAAAAGGGGAAAAGCA   65104        AA_  AATAT
                                TGCAAAAA   GAA    GAGCA
                                ||||||||   |||    |||||
                                ACGTTTTT   CTT    TTCGT
                                    CCC  _____
GAM2807  FLJ23053  3'  AAAAAGAAAATGAACAA     65105         AT
                                AAAAAGAAA  ATGAGCAG
                                |||||||||  ||||||||
                                TTTTTCTTT  TACTTGTT

                                    __
GAM2807  KIAA0871  5'  TGCAGAAAAAAAAATATAAA   65106      AA
                                TGCA  AAAAGAAAATATGAG
                                ||||  ||||||||||||||||
                                ACGT  TTTTTTTTTATATTT
                                  C_
GAM2807  KIAA0903  3'  TGCTAAAGAAGAAAATAT    65107      A   A
                                TGC AAA AAGAAAATAT
                                ||| ||| ||||||||||
                                ACG TTT TTCTTTTATA
                                  A   C
GAM2807  KIAA1170  3'  TGCAGAAAAAGAAAAATG    65108      A        T
                                TGCA AAAAAGAAAA ATG
                                |||| |||||||||| |||
                                ACGT TTTTTCTTTT TAC
                                  C        _
GAM2807  KIAA1550  3'  TGCGGAGAAAAAAAATTAAGCAG 65109     AAAAA       A
                                TGC    AAGAAAAT TGAGCAG
                                |||    |||||||| |||||||
                                ACG    TTTTTTTA ATTCGTC
                                  CCTC_      _
GAM2807  MDN1     3'  TGCAAAAGAAAACAGGCA    65110       AAA       TGA
                                TGCAAA   AGAAAATA   GCA
                                ||||||   ||||||||   |||
                                ACGTTT   TCTTTTGT   CGT
                                    ___       C__
GAM2807  OAZ2     3'  GCAAAGAAAGAAAATACACAA  65111       A         GA
                                GCAAA AAAGAAAATAT  GCAG
                                ||||| ||||||||||  ||||
                                CGTTT TTTCTTTTATG  TGTT
                                  C         __
GAM2807  PARVA    3'  TGCAAGAGACAGGAATAAGCAG 65112       AAAA   AAAT_
                                TGCAA    AGA    ATGAGCAG
                                |||||    |||    ||||||||
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                                ACGTT   TCT    TATTCGTC
                                  C___  GTCCT
GAM2807 PPP1R15B 3' TGCAAAAAAAAAAATTAAAC 65113          ATA
                                TGCAAAAAAAGAAA  TGAGC
                                |||||||||||||  |||||
                                ACGTTTTTTTTTTT  ATTTG
                                       A__
GAM2807 PRO2958  3' TGCAAAAAGAAGCTAGCA   65114      AA   AATATG
                                TGCAAAA  AGAA    AGCA
                                |||||||  ||||    ||||
                                ACGTTTT  TCTT    TCGT
                                   __   CGA___
GAM2807 RAB14    3' TACAAAAAGAGAAAAGCA   65115      A   AATAT
                                TGCAAAAA AGAA    GAGCA
                                |||||||| ||||    |||||
                                ATGTTTTT TCTT    TTCGT
                                    C   _____
GAM2807 SLC2A13  3' TGCAAAAAAAGGAAGTATG  65116        A  A
                                TGCAAAAAAAG AA TATG
                                |||||||||| || ||||
                                ACGTTTTTTTC TT ATAC
                                       C  C
GAM2807 TNFRSF19 3' TGCAAAAAAAAAAACTCATCCA 65117          ATATGAG
           G                     TGCAAAAAAAGAAA      CAG
                                 |||||||||||||      |||
                                 ACGTTTTTTTTTTT      GTC
                                       GAGTAG_
GAM2807 TSC22    5' TGGAAAAAAAGAGGGAACACCA 65118   C      A__    G
           GCAG                    TG AAAAAAAGA   AATAT AGCAG
                                   || |||||||||   ||||| |||||
                                   AC TTTTTTTCT   TTGTG TCGTC
                                    C       CCC    G
GAM2807 UBN1     3' TGTAAAAAAAGGAGTCAGAGCA 65119   C      AAAATAT
           G                     TG AAAAAAAG      GAGCAG
                                 || ||||||||      ||||||
                                 AC TTTTTTTC      CTCGTC
                                  A       CTCAGT_
GAM2807 LOC133418 3' TACAGAAGAAGAAAATATCAG  65120     A  A       G
                                TGCA AA AAGAAAATAT AG
                                |||| || |||||||||| ||
                                ATGT TT TTCTTTTATA TC
                                  C  C        G
GAM2807 LOC147165 3' AAGAAAGGACACCGAGCAG   65121       __   _
                                AAGAAA  ATAT GAGCAG
                                ||||||  |||| ||||||
                                TTCTTT  TGTG CTCGTC
                                   CC   G
GAM2807 LOC161784 3' AAAGAAAGAAAATAATGGCAG  65122     A       _  A
                                AAA AAAGAAAATA TG GCAG
                                ||| |||||||||| || ||||
```

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                                TTT TTTCTTTTAT AC CGTC
                                  C        T _
GAM2807  LOC165183 5'  GCAAAAGAAGAAAAATACCAG  65123       A     _  G
                                GCAAAA AAGAAAA TAT AG
                                |||||| ||||||| ||| ||
                                CGTTTT TTCTTTT ATG TC
                                   C      T  G
GAM2807  LOC202108 3'  TGCAAAAAAGAAAACCAAAG   65124         A     AT
                                TGCAAAAAA GAAAAT  GAG
                                ||||||||| ||||||  |||
                                ACGTTTTTT CTTTTG  TTC
                                      _     GT
GAM2807  LOC206426 3'  AAAAAAGAACATGGCA      65125         AA    A
                                AAAAAAGA  ATATG GCA
                                ||||||||  ||||| |||
                                TTTTTTCT  TGTAC CGT
                                     __    _
GAM2807  LOC221140 3'  GCAAAAAAACCAGAAGGAAATG 65126   ___   ___  A      III
            TGAGCAGC                AA   AGAA   AAT TGAGCAG   C
                                ||   ||||   ||| |||||||   |
                                TT   TCTT   TTA ACTCGTC   G
                                 TGG    CCT   C      III
GAM2807  LOC221354 3'  GCAAAAAAGGAATGTAGCAG   65127        A  AAAT  _
                                GCAAAAAA GA    ATG AGCAG
                                |||||||| ||    ||| |||||
                                CGTTTTTT CT    TAC TCGTC
                                     C _____   A
GAM2807  LOC254655 3'  GCAGGAAAAGAAAAAGCA    65128     AA       ATAT
                                GCA  AAAAGAAA    GAGCA
                                |||  ||||||||    |||||
                                CGT  TTTTCTTT    TTCGT
                                  CC       _____
GAM2807  LOC255229 3'  AAAGAAAGAAAATAATGGCAG  65122     A        _  A
                                AAA AAAGAAAATA TG GCAG
                                ||| |||||||||| || ||||
                                TTT TTTCTTTTAT AC CGTC
                                  C        T _
GAM2807  LOC256021 3'  TGAAAAGAAGAAAATATGTCAG 65129    C    A         AG
                                TG AAAA AAGAAAATATG  CAG
                                || |||| ||||||||||  |||
                                AC TTTT TTCTTTTATAC  GTC
                                  _   C         A_
GAM2807  LOC51312  3'  TGCAAAAAAAAAAATGA     65130           AAT
                                TGCAAAAAAAGAA   ATGA
                                ||||||||||||   ||||
                                ACGTTTTTTTTTT   TACT
                                        ___
GAM2807  LOC93512  3'  AAGAAAGGACACCGAGCAG   65121       __   _
                                AAGAAA  ATAT GAGCAG
                                ||||||  |||| ||||||
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                                TTCTTT  TGTG CTCGTC
                                   CC    G
GAM2808  PTPN11    3'  AATGCCAGTGCAAAGGTC    65133        C     AA
                                AATGTCAG TGCAAA  GTC
                                |||||||| ||||||  |||
                                TTACGGTC ACGTTT  CAG
                                     _     C_
GAM2808  SCG3      3'  CTCAATGTCTGAAAAGT     65134         AGC  CA
                                CTCAATGTC   TG  AAAAGT
                                |||||||||   ||  ||||||
                                GAGTTACAG   AC  TTTTCA
                                     ____ __
GAM2808  TCEB1L    3'  TCAATGCCAACTTTTAAAAGGT 65135          GC_   A
              C                  TCAATGTCAGCT   AAAA GTC
                                |||||||||||   |||| |||
                                AGTTACGGTTGA   TTTT CAG
                                      AAA    C
GAM2808  WIF1      3'  TCAAGCCAATGCAAAAAGT   65136     T    C
                                TCAA GTCAG TGCAAAAAGT
                                |||| ||||| ||||||||||
                                AGTT CGGTT ACGTTTTTCA
                                  _    _
GAM2808  CHST3     3'  TCAATGTCCTGAGAAGT     65137        AG   CAAA
                                TCAATGTC  CTG    AAGT
                                ||||||||  |||    ||||
                                AGTTACAG  GAC    TTCA
                                     __   TC__
GAM2808  DKFZP434D193 3'  TATCAACTTTGCAAAGAGTC   65138         __    A
                                TGTCAGCT  GCAAA AGTC
                                ||||||||  ||||| ||||
                                ATAGTTGA  CGTTT TCAG
                                     AA    C
GAM2808  FLJ12132  3'  CCTCAGTGCACAACTGAAGGTC 65139       A  _     C  AAA
                                CCTCA TGT CAGCTG AA   GTC
                                ||||| ||| |||||| ||   |||
                                GGAGT ACG GTTGAC TT   CAG
                                   C   T     _  C__
GAM2808  FLJ13215  3'  CTCAATATCCATGAAAAGTC   65140         AGC  CA
                                CTCAATGTC   TG  AAAAGTC
                                |||||||||   ||  |||||||
                                GAGTTATAG   AC  TTTTCAG
                                     GT_  __
GAM2808  FLJ14054  5'  TCAATGTCAGCTGAAGT     65141           CAAA
                                TCAATGTCAGCTG    AAGT
                                ||||||||||||    ||||
                                AGTTACAGTCGAC    TTCA
                                     _____
GAM2808  FLJ20039  3'  TCAACGTCCTGTGTGGAAAGT  65142         AGC  CAA
                                TCAATGTC   TG   AAAGT
                                ||||||||   ||   |||||
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                                AGTTGCAG  AC   TTTCA
                                    GAC  ACC
GAM2808  FLJ20396  3'  TCACTGTCTTGGGCAAAAAGTC 65143    A   AGCT
                                TCA TGTC   GCAAAAAGTC
                                ||| ||||   ||||||||||
                                AGT ACAG   CGTTTTTCAG
                                  G   AACC
GAM2808  FLJ22056  5'  CCCGGGGCAGCTGCAGGAGGTC 65144    CAAT T      AAAA
                                CCT   G CAGCTGCA   GTC
                                |||   | ||||||||   |||
                                GGG   C GTCGACGT   CAG
                                  CCC_ _      CCTC
GAM2808  HSP105B   3'  AATATCAAAGCAAAAAGTC   65145       CT
                                AATGTCAG  GCAAAAAGTC
                                ||||||||  ||||||||||
                                TTATAGTT  CGTTTTTCAG
                                    T_
GAM2808  MGC23280  3'  CTCAATGTTGGCAGTGCA    65146       ___   C
                                CTCAATGT   CAG TGCA
                                ||||||||   ||| ||||
                                GAGTTACA   GTC ACGT
                                    ACC   _
GAM2808  MLZE     5'  CTCAAGTCCTCAGCAAAAAGTC 65147      T   AGCT
                                CTCAA GTC    GCAAAAAGTC
                                ||||| |||    ||||||||||
                                GAGTT CAG    CGTTTTTCAG
                                  _  GAGT
GAM2808  TIEG2    3'  TGAAACTGCAAAAGGTC     65148    TC       A
                                TG  AGCTGCAAAA GTC
                                ||  |||||||||| |||
                                AC  TTGACGTTTT CAG
                                 T_        C
GAM2808  LOC154791 3'  TCAGTCTAGTGCAAAAAGT    65149    AT   _  C
                                TCA  GTC AG TGCAAAAAGT
                                |||  ||| || ||||||||||
                                AGT  CAG TC ACGTTTTTCA
                                  __   A  _
GAM2808  LOC197201 3'  ATCAGATCTGCAAAAGGTC    65150      __      A
                                GTCAG  CTGCAAAA GTC
                                |||||  |||||||| |||
                                TAGTC  GACGTTTT CAG
                                   TA       C
GAM2808  LOC200558 3'  TCAATGTCTCATTTGTAAAGAG 65151       AGC__  C   A
            TC                    TCAATGTC    TG AAA AGTC
                                |||||||||    || ||| ||||
                                AGTTACAG    AC TTT TCAG
                                    AGTAA  A   C
GAM2808  LOC256337 3'  CTCAGAGTCAGCAAAAAG    65152     AT     TGC
                                CTCA  GTCAGC   AAAAAG
                                ||||  ||||||   ||||||
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                                GAGT  CAGTCG   TTTTTC
                                  CT     ___
GAM2809  XYLT1    3'  CATCGCGTTGCCTTGTGA    65155       CCA
                                TATCGCG   CCTTGTGG
                                |||||||   ||||||||
                                GTAGCGC   GGAACACT
                                    AAC
GAM2809  LOC146272 3'  GCAGACACCTTGTGGTTGCAT  65156     C_       CTA
                                GCG  CACCTTGTGG   CAT
                                |||  ||||||||||   |||
                                CGT  GTGGAACACC   GTA
                                  CT        AAC
GAM2810  ENTPD5   3'  CTAAATCTCTAGGCTCAAGTC  65159       GCGCGC
                                CTAAATC     GGGCTCAAGTC
                                |||||||     ||||||||||||
                                GATTTAG     TCCGAGTTCAG
                                    AGA___
GAM2810  SCG3     5'  GCGCGCGGGAGTCAAGTC    65160        C_
                                GCGCGCGGG  TCAAGTC
                                |||||||||  |||||||
                                CGCGCGCCC  AGTTCAG
                                     TC
GAM2810  TNFRSF10B 3'  GCCCAAACAGGGCTCAAGT    65161    G __  _
                                GC C  GC GGGCTCAAGT
                                || |  || ||||||||||
                                CG G  TG CCCGAGTTCA
                                 G TT  T
GAM2810  FLJ10769  3'  TCTGCGCGGGCTCAGGT     65162    GC        A
                                TC  GCGCGGGCTCA GT
                                ||  ||||||||||| ||
                                AG  CGCGCCCGAGT CA
                                 A_         C
GAM2810  KIAA1877  3'  TAAATGTCATTAGCTCAAGT   65163      CGCG  CG
                                TAAAT    CG  GGCTCAAGT
                                |||||    ||  |||||||||
                                ATTTA    GT  TCGAGTTCA
                                   CA__  AA
GAM2811  C18orf1   3'  TCTATGCCATTTCTGTTAAAA  65166      AT      ATA
                                TCTAT  CATTTCT   TAAAA
                                |||||  |||||||  |||||
                                AGATA  GTAAAGA   ATTTT
                                   CG      CA_
GAM2811  IDE      3'  TATAATATTTCTACATAA    65167      TC
                                TATA  ATTTCTATATAA
                                ||||  ||||||||||||
                                ATAT  TAAAGATGTATT
                                  TA
GAM2811  FLJ14855  3'  CTATGTCATTTCTCTCAAAA  65168      A       ATA
                                CTAT TCATTTCT   TAAAA
                                |||| ||||||||   |||||
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                                GATA AGTAAAGA   GTTTT
                                  C       GA_
GAM2811  PRDM5    3'  TATACCATTTCTTGTTAAAA   65169          ATA
                                TATATCATTTCT   TAAAA
                                ||||||||||||   |||||
                                ATATGGTAAAGA   ATTTT
                                       ACA
GAM2811  LOC157574 3'  TCTTGTCATTTCTATAATAAAA 65170     ATA        _
                                TCT   TCATTTCTATA TAAAA
                                |||   |||||||||||| |||||
                                AGA   AGTAAAGATAT ATTTT
                                  AC_         T
GAM2812  HRK      3'  TTTTTTTATATATATAGAGC   65173      C    C
                                TTTTT TATAT TATAGGGC
                                ||||| ||||| ||||||||
                                AAAAA ATATA ATATCTCG
                                   A    T
GAM2812  KIAA1287  3'  TTTTTCTGAACTCCTAGGGCAT 65174       ATA_   A
              AT                  TTTTTCT    TCT TAGGGCATAT
                                  |||||||    ||| ||||||||||
                                  AAAAAGA    AGG ATCCCGTATA
                                     CTTG   _
GAM2812  LOC164832 3'  TTTTTCTATATCCAAGG     65175           T
                                TTTTTCTATATCTA AGG
                                |||||||||||||| |||
                                AAAAAGATATAGGT TCC
                                              _
GAM2812  LOC257436 3'  TATATCTATACTGCTATAT    65176          GG  _
                                TATATCTATA  GC ATAT
                                ||||||||||  || ||||
                                ATATAGATAT  CG TATA
                                      GA  A
GAM2812  LOC90075  5'  TTTTTCATATTTATAGGG    65177       T   C
                                TTTTTC ATAT TATAGGG
                                |||||| |||| |||||||
                                AAAAAG TATA ATATCCC
                                   _    A
GAM2813  COX11    3'  TCCAGAGATGTTAGAGGAG    65180        CTTCAG  C
                                TCTAGAG     GT AGAGGAG
                                |||||||     || |||||||
                                AGGTCTC     CA TCTCCTC
                                    TA____  A
GAM2813  RFX2     5'  TCTGGAGTTCGGGCCGGGAGT  65181     A   C   A   AGA
                                TCT GAG TTC GGTC   GGAGT
                                ||| ||| ||| ||||   |||||
                                AGA CTC AAG CCGG   CCTCA
                                  C   _   C    C__
GAM2813  DKFZP586J0619 3'  TCTCGGCCGCGGTCAGAGGGGT 65182     AGA   TCA        A
                                TCT   GCT   GGTCAGAGG GT
                                |||   |||   ||||||||| ||
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                                AGA   CGG   CCAGTCTCC CA
                                  GC_   CG_       C
GAM2813  FLJ23168  3'  TCTGGGGCTCAGGTCTGCTGAG 65183     AGA   T     AGA__
              AGT                   TCT   GCT CAGGTC     GGAGT
                                |||   ||| ||||||    |||||
                                AGA   CGA GTCCAG     TCTCA
                                  CCC   _     ACGAC
GAM2813  GDAP1L1   3'  CAGAGGTACCGGTTAGAGGAGT 65184      CTTCA   C
                                TAGAG     GGT AGAGGAGT
                                |||||     ||| ||||||||
                                GTCTC     CCA TCTCCTCA
                                   CATGG   A
GAM2813  KIAA1100  3'  TCCAGAGCTTCAGGCAGGG    65185           T   A
                                TCTAGAGCTTCAGG CAG GG
                                |||||||||||||| ||| ||
                                AGGTCTCGAAGTCC GTC CC
                                                _  _
GAM2813  LOC157729 5'  TCTAGAGCATTAGGCAGGG    65186        TTC   T   A
                                TCTAGAGC   AGG CAG GG
                                ||||||||   ||| ||| ||
                                AGATCTCG   TCC GTC CC
                                     TAA   _   _
GAM2813  LOC220177 5'  CCTGGAGCTTCAGGGCAAGGAG 65187     A        TCA
              T                  TCT GAGCTTCAGG   GAGGAGT
                                ||| ||||||||||   |||||||
                                GGA CTCGAAGTCC   TTCCTCA
                                  C         CG_
GAM2813  LOC51605  3'  TAGAAGTACTTAGAGGAGT    65188      ____   CAGGTC
                                TAGA   GCTT     AGAGGAGT
                                ||||   ||||     ||||||||
                                ATCT   TGAA     TCTCCTCA
                                  TCA   _______
GAM2813  LOC90936  5'  TCTAGGGGCTTCTCCAGAGGAG 65189      A_    AGG
                                TCTAG  GCTTC   TCAGAGGAG
                                |||||  |||||   |||||||||
                                AGATC  CGAAG   GGTCTCCTC
                                   CC     A__
GAM2813  LOC92661  3'  TCCAGGGCTGCCTCAGAGGGGT 65190      A   _  AGG      A
                                TCTAG GCT TC   TCAGAGG GT
                                ||||| ||| ||   ||||||| ||
                                AGGTC CGA GG   AGTCTCC CA
                                   C   C  ___      C
GAM2814  CEP2     5'  CTGGCTACAGTGTGGGGGCACG 65193         CACCCAAA
                                CTGGCTACA       GGCACG
                                |||||||||       ||||||
                                GACCGATGT       CCGTGC
                                     CACACCC_
GAM2814  CLN6     3'  CTGGTTACACACCCACAC     65194      C       AAAG
                                CTGG TACACACCC    GCAC
                                |||| |||||||||    ||||
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                                GACC ATGTGTGGG   TGTG
                                  A      ____
GAM2814  FAT2     3'  CCTGGCTACATACACTCTACAC 65195         C  CCAAAG
             A                    CCTGGCTACA AC     GCACG
                                  |||||||||| ||     |||||
                                  GGACCGATGT TG     TGTGT
                                       A  TGAGA_
GAM2814  SLC35A3  3'  CTGGCTACCATCTAGCACA   65196        A  CCCAAA
                                  CTGGCTAC CA     GGCACG
                                  |||||||| ||     ||||||
                                  GACCGATG GT     TCGTGT
                                     _  AGA___
GAM2814  TNFRSF1B 3'  TGGCTACACACACCCAC     65197          _  AAAGG
                                  TGGCTACACAC CC    CAC
                                  |||||||||| ||    |||
                                  ACCGATGTGTG GG    GTG
                                       T  _____
GAM2814  ASB10    5'  CCTGGCCACGCATCCAGCA   65198        A  C   AAG
                                  CCTGGCTAC CA CCA   GCA
                                  ||||||||| || |||   |||
                                  GGACCGGTG GT GGT   CGT
                                     C  A   ___
GAM2814  dJ383J4.3 3'  TGGCAACTCCAAAGGCA     65199      T  ACAC
                                  TGGC AC    CCAAAGGCA
                                  |||| ||    |||||||||
                                  ACCG TG    GGTTTCCGT
                                    T  A___
GAM2814  FIGN     5'  CCTGGCCACAAGAAAAGAGGCA 65200          CACCCAA
                                  CCTGGCTACA      AGGCA
                                  ||||||||||      |||||
                                  GGACCGGTGT      TCCGT
                                       TCTTTTC
GAM2814  FLJ13441 3'  CCTGGCCACACACCCTTCGC   65201             AAAG
                                  CCTGGCTACACACCC    GC
                                  ||||||||||||||    ||
                                  GGACCGGTGTGTGGG    CG
                                          AAG_
GAM2814  FLJ14146 3'  CTGCTGCACACCCACAC      65202     G  A      AAAG
                                  CTG CT CACACCC    GCAC
                                  ||| || |||||||    ||||
                                  GAC GA GTGTGGG    TGTG
                                    _  C      ____
GAM2814  KIAA1058 5'  CCTGGCCGTGCAAGGCACA    65203       ACACACCCA
                                  CCTGGCT        AAGGCACG
                                  |||||||        ||||||||
                                  GGACCGG        TTCCGTGT
                                     CACG_____
GAM2814  KIAA1742 3'  CCTGCTGCACACCCAGCA     65204      G  A       AAG
                                  CCTG CT CACACCCA   GCA
                                  |||| || ||||||||   |||
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                                GGAC GA GTGTGGGT   CGT
                                  _ C      ___
GAM2814  MAD4     3'  TGGCTACAGATGTACCAGAGGC 65205        CAC___   A
             ACG                   TGGCTACA     CCA AGGCACG
                                   ||||||||     ||| |||||||
                                   ACCGATGT     GGT TCCGTGC
                                      CTACAT   C
GAM2814  OBTP     3'  TGGCTACACCCCTGGC      65206         A   AAA
                                   TGGCTACAC CCC   GGC
                                   |||||||||| |||   |||
                                   ACCGATGTG GGG   CCG
                                         _  A__
GAM2814  USP24    3'  CCTGGCCACATGCCCACACA   65207         CA   AAAG
                                   CCTGGCTACA  CCC    GCACG
                                   ||||||||||  |||    |||||
                                   GGACCGGTGT  GGG    TGTGT
                                         AC  _____
GAM2814  LOC124801 3'  CCAGGAGACTGCCTGAAGGCAC 65208    T  CT  ACA  CA
             G                      CC GG  AC   CC  AAGGCACG
                                    || ||  ||   ||  ||||||||
                                    GG CC  TG   GG  TTCCGTGC
                                     T  TC  AC_  AC
GAM2814  LOC152274 5'  CCTGCTTTAACCCAAAGG    65209      G  ACAC
                                   CCTG CT    ACCCAAAGG
                                   |||| ||    |||||||||
                                   GGAC GA    TGGGTTTCC
                                     _ AAT_
GAM2814  LOC200301 5'  CTGGGTATACACCCAAAAG    65210      C  C
                                   CTGG TA ACACCCAAAGG
                                   |||| || ||||||||||
                                   GACC AT TGTGGGTTTTC
                                     C  A
GAM2814  LOC256158 5'  CTGGCCACGCACTCCAGC     65211         A  _  AAG
                                   CTGGCTAC CAC CCA   GC
                                   |||||||| ||| |||   ||
                                   GACCGGTG GTG GGT   CG
                                        C   A  ___
GAM2814  LOC257449 3'  CCTGCTGCACACCCAGCA     65204      G  A       AAG
                                   CCTG CT CACACCCA   GCA
                                   |||| || ||||||||   |||
                                   GGAC GA GTGTGGGT   CGT
                                     _ C      ___
GAM2814  LOC91923  5'  CTGGGTATATACCCAAAAG    65212      C  CAC
                                   CTGG TA   ACCCAAAGG
                                   |||| ||   |||||||||
                                   GACC AT   TGGGTTTTC
                                     C  ATA
GAM2815  SALL1    3'  TAAGCTTTCTTAGAACTCTAAA 65215       G     TACG
             G                      TAAGC TTCTTA    TTCTAAAG
                                    ||||| ||||||    ||||||||
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                                ATTCG AAGAAT    GAGATTTC
                                   A     CTT_
GAM2815 AP3M2    3' TAAGCTTTCTCTTTTTCTA   65216      G    ATACG
                                TAAGC TTCTT     TTCTA
                                ||||| |||||     |||||
                                ATTCG AAGAG     AAGAT
                                   A     AAA__
GAM2815 KIAA0776 3' AGCGTTCTTGTGCACCTGTAAA 65217         A__   G  C
             G                   AGCGTTCTT   TAC TT TAAAG
                                |||||||||   ||| || |||||
                                TCGCAAGAA   GTG GA ATTTC
                                     CAC   _  C
GAM2815 KIAA1726 3' GCTGTTCTTATGCTCTAAAG   65218    _      AC
                                GC GTTCTTAT  GTTCTAAAG
                                || ||||||||  |||||||||
                                CG CAAGAATA  CGAGATTTC
                                 A       __
GAM2815 MGC13007 5' TGACGTTCTTATATTCC     65219    A        AC
                                A GCGTTCTTAT  GTTCT
                                | ||||||||||  |||||
                                A TGCAAGAATA  TAAGG
                                 C         __
GAM2815 LOC134266 3' TAAGTGTTCTTATCGCAAAAAG 65220      C       A   TCT
                                TAAG GTTCTTAT CGT   AAAG
                                |||| |||||||| |||   ||||
                                ATTC CAAGAATA GCG   TTTC
                                   A       _   TT_
GAM2816 MCF2L    3' TTAATTGTTTAAATTATAGTT  65223          TGAT
                                TTAGTTGTTTAG    TTATAGTT
                                ||||||||||||    ||||||||
                                AATTAACAAATT    AATATCAA
                                       T___
GAM2816 MGC27044 3' TTAGTTGTTTATGAAATA    65224          G   TT
                                TTAGTTGTTTA TGA  TA
                                |||||||||| |||  ||
                                AATCAACAAAT ACT  AT
                                      _   TT
GAM2816 PRO0943  5' TTAGTTATTTAGTAGTAGT    65225           ATTTA
                                TTAGTTGTTTAGTG    TAGT
                                ||||||||||||||    ||||
                                AATCAATAAATCAT    ATCA
                                       C____
GAM2816 LOC206012 5' GTTGTTTAGTAGTAGTAGTT   65226          ATTTA
                                GTTGTTTAGTG    TAGTT
                                ||||||||||     |||||
                                CAACAAATCAT    ATCAA
                                      CATC_
GAM2817 FLJ20555 3' TGGGTGTTGTTATCTTCT    65229    T      GATTCC
                                TG GGTGTTGT     TCTTCT
                                || ||||||||     ||||||
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                                AC CCACAACA     AGAAGA
                                 _      AT____
GAM2817 LHX6    3'  TGTGTGTGTTTTCCCCTT    65230     _    GTGA
                                TGTG GTGTT    TTCCTCTT
                                |||| |||||    ||||||||
                                ACAC CACAA    AAGGGGAA
                                  A    ____
GAM2818 CASP2   3'  AAAGATCAATAAGGTACA    65233       A
                                AGAGAT AATAAGGTACA
                                |||||| ||||||||||
                                TTTCTA TTATTCCATGT
                                   G
GAM2818 CASP2   3'  AAAGATCAATAAGGTACA    65233       A
                                AGAGAT AATAAGGTACA
                                |||||| ||||||||||
                                TTTCTA TTATTCCATGT
                                   G
GAM2818 CASP2   3'  AAAGATCAATAAGGTACA    65233       A
                                AGAGAT AATAAGGTACA
                                |||||| ||||||||||
                                TTTCTA TTATTCCATGT
                                   G
GAM2818 CASP2   3'  AAAGATCAATAAGGTACA    65233       A
                                AGAGAT AATAAGGTACA
                                |||||| ||||||||||
                                TTTCTA TTATTCCATGT
                                   G
GAM2818 CD69    3'  TAAAAAGAGAGAAATATTACAA 65234         T    AGG
                                TAAAAAGAGA AAATA   TACAA
                                |||||||||| |||||   |||||
                                ATTTTTCTCT TTTAT   ATGTT
                                      C    A__
GAM2818 CISH    3'  AAAGAGGTAATAAAGGTA    65235       A   AT
                                AAAGAG TAA  AAGGTA
                                |||||| |||  ||||||
                                TTTCTC ATT  TTCCAT
                                   C   AT
GAM2818 CISH    3'  AAAGAGGTAATAAAGGTA    65235       A   AT
                                AAAGAG TAA  AAGGTA
                                |||||| |||  ||||||
                                TTTCTC ATT  TTCCAT
                                   C   AT
GAM2818 EHHADH  3'  TAAAAAGAGAAGAACTCTTACA 65236         TA   AAGG
            A                    TAAAAAGAGA  AAT    TACAA
                                ||||||||||  |||   |||||
                                ATTTTTCTCT  TTG    ATGTT
                                      TC   AGA_
GAM2818 FGF12   3'  AAGACTGTGGTAAGGTACAA  65237      AAA__
                                GAGAT    TAAGGTACAA
                                |||||    ||||||||||
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                                TTCTG    ATTCCATGTT
                                   ACACC
GAM2818 GMPR     3' AAAAAGAGAAAGGTGCA     65238        TAAAT    A
                                AAAAAGAGA    AAGGT CA
                                |||||||||    ||||| ||
                                TTTTTCTCT    TTCCA GT
                                     _____    C
GAM2818 HUS1     3' AGGGACAAATAAGTACA     65239    A       G
                                AG GATAAATAAG TACA
                                || ||||||||||| ||||
                                TC CTGTTTATTC ATGT
                                 C        _
GAM2818 ITGA2    3' AGAGAAAATAAGGTGCA     65240      T       A
                                AGAGA AAATAAGGT CA
                                ||||| ||||||||| ||
                                TCTCT TTTATTCCA GT
                                   _       C
GAM2818 PRKWNK3  3' TAAAAAGAGCTAAGGACA    65241        ATAAA    T
                                TAAAAAGAG    TAAGG ACA
                                |||||||||    ||||| |||
                                ATTTTTCTC    ATTCC TGT
                                     G____    _
GAM2818 SLC19A2  3' TAAAAAGAGAAAATATACTGTA 65242         TAA_  AG
                                TAAAAAGAGA   ATA  GTA
                                ||||||||||   |||  |||
                                ATTTTTCTCT   TAT  CAT
                                      TTTA   GA
GAM2818 SLC19A2  3' TAAAAAGAGATAAGAGCA    65243          ATAA
                                TAAAAAGAGATAA    GGTA
                                ||||||||||||    ||||
                                ATTTTTCTCTATT    TCGT
                                       C___
GAM2818 SLC7A6   3' TAAAAGGAGAAAGGTACA    65244      A   TAAAT
                                TAAAA GAGA    AAGGTACA
                                ||||| ||||    ||||||||
                                ATTTT CTCT    TTCCATGT
                                   C   _____
GAM2818 ZIC1     3' AAGAATCTTTAATAAGGTAC   65245      ATA__
                                AAGAG    AATAAGGTAC
                                |||||    ||||||||||
                                TTCTT    TTATTCCATG
                                   AGAAA
GAM2818 DKFZP434J214 3' AAGTAGTGTAAGTAAGGTACA  65246    _ A_  A
                                AAG AG  TAA TAAGGTACA
                                ||| ||  ||| |||||||||
                                TTC TC  ATT ATTCCATGT
                                  A  AC   C
GAM2818 DKFZP434L187 3' TAAAAAGAGAAGGTA      65247         TAAATA
                                TAAAAAGAGA    AGGTA
                                ||||||||||    |||||
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                                ATTTTTCTCT     TCCAT
                                       _______
GAM2818 E2F6     3' AGAGAGGGCAAGGTACAA    65248      TAAA
                                AGAGA    TAAGGTACAA
                                |||||    ||||||||||
                                TCTCT    GTTCCATGTT
                                   CCC_
GAM2818 FLJ12598 3' AAAAGAGATAATGTGGTACA  65249          ATAA
                                AAAAGAGATAA    GGTACA
                                ||||||||||    ||||||
                                TTTTCTCTATT    CCATGT
                                      ACA_
GAM2818 FLJ30046 3' TAAAAAGAAATAGGCACA    65250          AAATA
                                TAAAAAGAGAT    AGGTACA
                                ||||||||||    |||||||
                                ATTTTTCTTTA    TCCGTGT
                                       ______
GAM2818 GFR      3' TGAAAGAGATGAACAGGCA    65251    A      A    A
                                A AAAGAGAT AATA GGTA
                                | ||||||||| |||| ||||
                                A TTTCTCTA TTGT CCGT
                                 C       C    _
GAM2818 KDELR2   3' TAAAAAAAGATAAGGCA     65252          AATA
                                TAAAAAGAGATA    AGGTA
                                ||||||||||||    |||||
                                ATTTTTTTCTAT    TCCGT
                                       _____
GAM2818 KIAA0825 3' TAAAAAGAGATCATTATTACA 65253          AAATAAGG
                                TAAAAAGAGAT       TACA
                                ||||||||||        ||||
                                ATTTTTCTCTA       ATGT
                                      GTAATA__
GAM2818 KIAA0828 3' GATATAAGATAAGGTACAA   65254    G    _
                                GA ATAA ATAAGGTACAA
                                || |||| ||||||||||
                                CT TATT TATTCCATGTT
                                 A    C
GAM2818 KIAA1068 3' TAAAAAGAGAAAACAGGCA   65255          T    A
                                TAAAAAGAGA AAATA GGTA
                                |||||||||| ||||| ||||
                                ATTTTTCTCT TTTGT CCGT
                                      _    _
GAM2818 KIAA1817 3' AGAGAAGAGATAAAATACA   65256      TAA_
                                AGAGA    ATAAGGTACA
                                |||||    ||||||||||
                                TCTCT    TATTTTATGT
                                   TCTC
GAM2818 PTP4A1   3' TAAAAAGAGATGGCA       65257          AAATAA
                                TAAAAAGAGAT     GGTA
                                ||||||||||      ||||
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                                ATTTTTCTCTA     CCGT
                                           _______
GAM2818  TOPK     3'  GAAATGCTTAAGGTACAA    65258      AAA
                                GAGAT   TAAGGTACAA
                                |||||   ||||||||||
                                CTTTA   ATTCCATGTT
                                   CGA
GAM2818  TTTY9    3'  AAAGAAATAAATTTCTTACA  65259          AAGG
                                AAAGAGATAAAT    TACA
                                ||||||||||||    ||||
                                TTTCTTTATTTA    ATGT
                                      AAGA
GAM2818  LOC149705 3'  TAAAAAGAGAGAGTAC      65260          TAAATAA
                                TAAAAAGAGA      GGTAC
                                ||||||||||      |||||
                                ATTTTTCTCT      TCATG
                                      C_______
GAM2818  LOC152348 3'  TAAAAAAAGATGAATAAGGC   65261           A
                                TAAAAAGAGAT AATAAGGT
                                |||||||||||| ||||||||
                                ATTTTTTTCTA TTATTCCG
                                      C
GAM2818  LOC158156 3'  AGAGAATAAATAAAGGCA     65262       _     _
                                AGAGA TAAATAA GGTA
                                ||||| ||||||| ||||
                                TCTCT ATTTATT CCGT
                                   T      T
GAM2818  LOC158235 3'  TGAAGAGAAATAAAGCA      65263    A     TA
                                A AAGAGA  AATAAGGTA
                                | ||||||  |||||||||
                                A TTCTCT  TTATTTCGT
                                 C     __
GAM2818  LOC159319 5'  AAGAGGGGATAAACAAAGCA   65264      ___
                                AAGA   GATAAATAAGGTA
                                ||||   ||||||||||||
                                TTCT   CTATTTGTTTCGT
                                   CCC
GAM2818  LOC92360  3'  TGAAAAAGATAAATGGTA     65265    A         AA
                                A AAAGAGATAAAT  GGTA
                                | ||||||||||||  ||||
                                A TTTTTCTATTTA  CCAT
                                 C          __
GAM2819  DOCK1     3'  TACGATGGCACATCCCGGA    65268          A__
                                TATGATGGTG   TCCGGA
                                ||||||||||   ||||||
                                ATGCTACCGT   GGGCCT
                                      GTA
GAM2819  H4F2      3'  TGATGGTAAGCTCCTGGA     65269          __  _
                                TGATGGTGA  TCC GGA
                                |||||||||  ||| |||
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                                ACTACCATT  AGG CCT
                                     CG   A
GAM2819  MYL1     3'  ATGATGGTAAACAGATCTGGAT 65270        _____   C   III
                                ATGATGGT    GATC GGA   T
                                ||||||||    |||| |||   |
                                TACTACCA    CTAG CCT   A
                                    TTTGT    A   III
GAM2819  TFRC     3'  TATGATGGTTCACTCACGGA   65271        GA__  _
                                TATGATGGT    TC CGGA
                                |||||||||    || ||||
                                ATACTACCA    AG GCCT
                                     AGTG  T
GAM2819  LOC149506 3'  CATAATAAGTGATCTGGA    65272        _     C
                                TATGATG GTGATC GGA
                                ||||||| ||||||  |||
                                GTATTAT CACTAG CCT
                                    T     A
GAM2819  LOC197358 3'  CATGATGGTTCCTGTCCGGA   65273         GA___
                                TATGATGGT    TCCGGA
                                |||||||||    ||||||
                                GTACTACCA    AGGCCT
                                     AGGAC
GAM2819  LOC201695 5'  TATGATAGGTAATTTCTGGA   65274       _    __  C
                                TATGAT GGTGA  TC GGA
                                ||||||  |||||  ||  |||
                                ATACTA CCATT  AG CCT
                                    T    AA  A
GAM2819  LOC90784  5'  TGATGGTGGCATCCTTTGGA   65275        __   ___
                                TGATGGTG  ATCC   GGA
                                ||||||||  ||||   |||
                                ACTACCAC  TAGG   CCT
                                     CG    AAA
GAM2820  LTB4R    3'  GCCAGGCTGGAGCACGCTCTC  65278      TA    AAAA
                                GTCA  GGCT    CACGCTCTC
                                ||||  ||||    |||||||||
                                CGGT  CCGA    GTGCGAGAG
                                  __    CCTC
GAM2820  NDUFA5    3'  TGTCAGTAATAAGAACACGCTC 65279      _  GCTAA
              T                  TGTCA TAG     AACACGCTCT
                                 |||||  |||    ||||||||||
                                 ACAGT ATT     TTGTGCGAGA
                                   C   ATTC_
GAM2820  PTPN13    3'  TATCATAGGTTAAAGTAGC    65280        C    ACAC
                                TGTCATAGG TAAA    GC
                                |||||||||  ||||    ||
                                ATAGTATCC ATTT    CG
                                     A    CAT_
GAM2820  PTPN13    3'  TATCATAGGTTAAAGTAGC    65280        C    ACAC
                                TGTCATAGG TAAA    GC
                                |||||||||  ||||    ||
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                                ATAGTATCC ATTT    CG
                                     A    CAT_
GAM2820  PTPN13    3'  TATCATAGGTTAAAGTAGC    65280         C    ACAC
                                TGTCATAGG TAAA    GC
                                ||||||||| ||||    ||
                                ATAGTATCC ATTT    CG
                                     A    CAT_
GAM2820  C6orf37   3'  TGTCACAGGCTATGTGTTCTC  65281           AAACACG
                                TGTCATAGGCTA      CTC
                                ||||||||||||      |||
                                ACAGTGTCCGAT      GAG
                                      ACACAA_
GAM2820  DKFZP586G1517 3'  TGTCACAGGCTGCCCGCT    65282           AAAACA
                                TGTCATAGGCT     CGCT
                                ||||||||||      ||||
                                ACAGTGTCCGA     GCGA
                                      CGG___
GAM2820  FLJ10534  3'  TGTCAAGGCTAAAAAAAAGTCT 65283       T       CACGC
                                TGTCA AGGCTAAAA     TCT
                                ||||| |||||||||     |||
                                ACAGT TCCGATTTT     AGA
                                  _       TTTTC
GAM2820  FLJ21870  3'  TATCATAGGCTGCTAAGTGTTC 65284           AAAACACGC
            TC                    TGTCATAGGCT        TCTC
                                ||||||||||        ||||
                                ATAGTATCCGA        AGAG
                                      CGATTCACA
GAM2820  NFASC     3'  TGCATAGGCTGCCCTGCTCTC  65285    T      AAAACAC
                                TG CATAGGCT       GCTCTC
                                || ||||||||       ||||||
                                AC GTATCCGA       CGAGAG
                                 _       CGGGA__
GAM2820  REG-IV    3'  TCATAGGCTGGAGATGCACTCT 65286         AAAACA_
                                TCATAGGCT       CGCTCT
                                |||||||||       ||||||
                                AGTATCCGA       GTGAGA
                                      CCTCTAC
GAM2820  LOC143465 5'  TGTCATAGCTGGAACGAAAGC  65287         G  AA   AC__
                                TGTCATAG CT  AAC    GC
                                ||||||| ||  |||    ||
                                ACAGTATC GA  TTG    CG
                                     _ CC   CTTT
GAM2820  LOC152179 5'  AAACTAAAATACGCTCTC     65288         C
                                AGGCTAAAA ACGCTCTC
                                ||||||||| ||||||||
                                TTTGATTTT TGCGAGAG
                                      A
GAM2820  LOC200597 3'  TGTCATAGGCTAGAAGGATGCT 65289           AAACAC_
            CT                    TGTCATAGGCTA      GCTCT
                                ||||||||||||      |||||
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                              ACAGTATCCGAT     CGAGA
                                    CTTCCTA
GAM2820 LOC51716 3' TGTCATAGGTGACACTTTC   65290       CTAAA   GC
                              TGTCATAGG    ACAC  TC
                              |||||||||    ||||  ||
                              ACAGTATCC    TGTG  AG
                                   AC___   AA
GAM2820 LOC92017 3' TGTCATAGGCTCAACTATCT  65291        AA  ACG
                              TGTCATAGGCT  AAC   CT
                              ||||||||||  |||   ||
                              ACAGTATCCGA  TTG   GA
                                    G_   ATA
GAM2820 LOC92181 5' TGTCATAGGATAATCGCT    65292       C   AACA
                              TGTCATAGG TAA    CGCT
                              ||||||||| |||    ||||
                              ACAGTATCC ATT    GCGA
                                   T   A___
GAM2820 LOC92609 3' TGTTGTAAGCTAAGATCACATC 65293    CA      AA_   C
                              TGT  TAGGCTAA   CACG TC
                              |||  ||||||||   |||| ||
                              ACA  ATTCGATT   GTGT AG
                                AC       CTA   _
GAM2821 CAT56   3' AGATTCACAGAATTCAAA    65296       A   TC_
                              AGATTCA CAGG   CAAA
                              ||||||| ||||   ||||
                              TCTAAGT GTCT   GTTT
                                  _   TAA
GAM2822 B3GALT5  3' GAGTACCGAGCCGATAACAT  65299   ATC   A
                              GA   ACC GAGCCGATAACAT
                              ||   ||| ||||||||||||
                              CT   TGG CTCGGCTATTGTA
                               CA_  _
GAM2822 B3GALT5  3' GAGTACCGAGCCGATAACAT  65299   ATC   A
                              GA   ACC GAGCCGATAACAT
                              ||   ||| ||||||||||||
                              CT   TGG CTCGGCTATTGTA
                               CA_  _
GAM2822 B3GALT5  3' GAGTACCGAGCCGATAACAT  65299   ATC   A
                              GA   ACC GAGCCGATAACAT
                              ||   ||| ||||||||||||
                              CT   TGG CTCGGCTATTGTA
                               CA_  _
GAM2822 B3GALT5  3' GAGTACCGAGCCGATAACAT  65299   ATC   A
                              GA   ACC GAGCCGATAACAT
                              ||   ||| ||||||||||||
                              CT   TGG CTCGGCTATTGTA
                               CA_  _
GAM2822 B3GALT5  3' GAGTACCGAGCCGATAACAT  65299   ATC   A
                              GA   ACC GAGCCGATAACAT
                              ||   ||| ||||||||||||
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                                CT   TGG CTCGGCTATTGTA
                                 CA_  _
GAM2822  FXYD6    3'  TAGGGTCCCAGAGCCCAT    65300     AA  A       G
                                TAG  TC CCAGAGCC AT
                                |||  || |||||||| ||
                                ATC  AG GGTCTCGG TA
                                  CC  _       G
GAM2822  HS2ST1   3'  TAAAATCATTAGAAACCAAT   65301         CC   _
                                TAGAATCA  AGAG CCGAT
                                ||||||||  |||| |||||
                                ATTTTAGT  TCTT GGTTA
                                     AA    T
GAM2822  IGF2R    3'  TAGAACACCAGAGTCTATA    65302       T       CCG
                                TAGAA CACCAGAG   ATA
                                ||||| ||||||||   |||
                                ATCTT GTGGTCTC   TAT
                                  _       AGA
GAM2822  MSL3L1   3'  TAGATCACCAAAAATAACA    65303      A       GCC
                                TAGA TCACCAGA   GATAACA
                                |||| ||||||||   |||||||
                                ATCT AGTGGTTT   TTATTGT
                                  _       ____
GAM2822  MSL3L1   3'  TAGATCACCAAAAATAACA    65303      A       GCC
                                TAGA TCACCAGA   GATAACA
                                |||| ||||||||   |||||||
                                ATCT AGTGGTTT   TTATTGT
                                  _       ____
GAM2822  MSL3L1   3'  TAGATCACCAAAAATAACA    65303      A       GCC
                                TAGA TCACCAGA   GATAACA
                                |||| ||||||||   |||||||
                                ATCT AGTGGTTT   TTATTGT
                                  _       ____
GAM2822  NRAS     3'  AGAATAGAGCCGATAACAT    65304       CACC
                                AGAAT    AGAGCCGATAACAT
                                |||||    ||||||||||||||
                                TCTTA    TCTCGGCTATTGTA
                                  _____
GAM2822  PART1    3'  GATCACCAGAAAACA       65305    A       CCGAT
                                GA TCACCAGAG     AACA
                                || |||||||||     ||||
                                CT AGTGGTCTT     TTGT
                                  _       ______
GAM2822  PPP1CB   3'  TAGAATCACATCCAATA     65306         CAGAG
                                TAGAATCAC     CCGATA
                                |||||||||     ||||||
                                ATCTTAGTG     GGTTAT
                                     TA___
GAM2822  SLIT3    3'  GAATCACCAGGGGGTCCCACA  65307          AG___  G
                                GAATCACCAG     CC ATA
                                ||||||||||     || |||
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                                CTTAGTGGTC    GG TGT
                                     CCCCA  G
GAM2822  ADAM9    3'  AGAATCACTGCAATAACAT   65308       CAGA  C
                                AGAATCAC   GC GATAACAT
                                ||||||||   || ||||||||
                                TCTTAGTG   CG TTATTGTA
                                    A___  _
GAM2822  FLJ14547 3'  GAATCACCCGAGTCGGGAACAT 65309       A   C  AT
                                GAATCACC GAG CG  AACAT
                                |||||||| ||| ||  |||||
                                CTTAGTGG CTC GC  TTGTA
                                    G   A  CC
GAM2822  FLJ23537 5'  CAGAATCACTGGAAGCAATGAT 65310       CA_   C__
           A                     TAGAATCAC   GAGC   GATA
                                |||||||||   ||||   ||||
                                GTCTTAGTG   TTCG   CTAT
                                     ACC    TTA
GAM2822  KIAA0406 3'  TAGAGCCACCAGACAAT    65311     AT     GC
                                TAGA  CACCAGA  CGAT
                                ||||  |||||||  ||||
                                ATCT  GTGGTCT  GTTA
                                  CG      __
GAM2822  NPTXR    3'  CAGGGTCACCAGAGCTTTCCCC 65312     AA       CGATA__
           ACAT                   TAG  TCACCAGAGC      ACAT
                                |||  ||||||||||      ||||
                                GTC  AGTGGTCTCG      TGTA
                                  CC        AAAGGGG
GAM2822  NPTXR    3'  CAGGGTCACCAGAGCTTTCCCC 65312     AA       CGATA__
           ACAT                   TAG  TCACCAGAGC      ACAT
                                |||  ||||||||||      ||||
                                GTC  AGTGGTCTCG      TGTA
                                  CC        AAAGGGG
GAM2822  LOC148936 3'  CAGAATCAGGAAAGCTGAT   65313       CC    C
                                TAGAATCA  AGAGC GAT
                                ||||||||  ||||| |||
                                GTCTTAGT  TTTCG CTA
                                     CC    A
GAM2822  LOC148938 3'  CAGAATCAGGAAAGCTGAT   65313       CC    C
                                TAGAATCA  AGAGC GAT
                                ||||||||  ||||| |||
                                GTCTTAGT  TTTCG CTA
                                     CC    A
GAM2822  LOC151584 5'  TAGAATCACAATGATAAC    65314       CAGAGCC
                                TAGAATCAC      GATAAC
                                |||||||||      ||||||
                                ATCTTAGTG      CTATTG
                                     TTA_____
GAM2822  LOC202134 5'  AGAATCACCGTGATGGGCTGGT 65315        A_  ___  C___
           GACA                   AGAATCACC  GA   GC    GATA
                                |||||||||  ||   ||    ||||
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                                TCTTAGTGG CT  CG   CTGT
                                     CA ACC ACCA
GAM2823 8D6A    3' TGAGGGCTGGTGTGCCCG   65318   A  ACACC G C
                                C AGG    GC GG GTGCCCG
                                | |||    || || |||||||
                                A TCC    CG CC CACGGGC
                                 C  _____ A A
GAM2823 ADRA1A  5' AGGGGCGCGCGGGGCTGCCGG 65319    ACAC    C GC
                                AGG   CGCGGG GT CCGG
                                |||   |||||| ||  ||||
                                TCC   GCGCCC CG GGCC
                                  CCGC    _ AC
GAM2823 ADRA1A  5' AGGGGCGCGCGGGGCTGCCGG 65319    ACAC    C GC
                                AGG   CGCGGG GT CCGG
                                |||   |||||| ||  ||||
                                TCC   GCGCCC CG GGCC
                                  CCGC    _ AC
GAM2823 ADRA1A  5' AGGGGCGCGCGGGGCTGCCGG 65319    ACAC    C GC
                                AGG   CGCGGG GT CCGG
                                |||   |||||| ||  ||||
                                TCC   GCGCCC CG GGCC
                                  CCGC    _ AC
GAM2823 CDKN1A  5' CAGGGACACACGCGGGCACGCT 65320   A   _       CC
           TGG                   CA GGACAC CGCGGGCGTGC GG
                                || |||||| |||||||||| ||
                                GT CCTGTG GCGCCCGTGCG CC
                                 C    T        AA
GAM2823 CTSS    3' AGGCATGCACCACCGTGCTCGG 65321    A___    GGG   C
                                AGG   CACCGC  CGTGC CGG
                                |||   ||||||  ||||| |||
                                TCC   GTGGTG  GCACG GCC
                                  GTAC    ___   A
GAM2823 DDX26   5' GGACACCGGGGCCCGA     65322       C   GTGC
                                GGACACCG GGGC   CCGG
                                |||||||| ||||   ||||
                                CCTGTGGC CCCG   GGCT
                                      _  ____
GAM2823 E2F2    5' AGGGCACCGCGACCCG     65323    A     GGCGT
                                AGG CACCGCG    GCCCG
                                ||| |||||||    |||||
                                TCC GTGGCGC    TGGGC
                                  C     _____
GAM2823 EHD3    3' CAAGGACACTGCAGAGTCCCTG 65324        C   C G C
           G                    CAAGGACAC GCGGG GT CC GG
                                ||||||||| ||||| || || ||
                                GTTCCTGTG CGTCT CA GG CC
                                     A   _ G A
GAM2823 FBN2    3' TGAGGACGCAGCGCACCCTGG 65325   A   ACC   G TG  _
                                C AGGAC  GCGG CG  CCC GG
                                | |||||  |||| ||  ||| ||
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                                A TCCTG   CGTC GC  GGG CC
                                 C    ___   _ GT   A
GAM2823  FCGRT    5'  GGACACCGCGGGCACG     65326          TGCC
                                GGACACCGCGGGCG   CG
                                ||||||||||||||   ||
                                CCTGTGGCGCCCGT   GC
                                      ____
GAM2823  GUCY1A2  5'  GGCGCTGCGGTCGCGCCCGG  65327   ACACC   G
                                GG    GCGG CGTGCCCGG
                                ||    |||| |||||||||
                                CC    CGCC GCGCGGGCC
                                 GCGA_   A
GAM2823  HCN4     5'  AGGGGCGCGGCGCGCCGCCCGG 65328    ACAC    _   _
                                AGG   CGCGG GCGT GCCCGG
                                |||   ||||| |||| ||||||
                                TCC   GCGCC CGCG CGGGCC
                                  CC__    G   G
GAM2823  HIP1     3'  AGGCATGCGCCACTGTGCCCGG 65329    A  CC   G_ _
                                AGG CA  GCG  GC GTGCCCGG
                                ||| ||  |||  || ||||||||
                                TCC GT  CGC  TG CACGGGCC
                                  _ A_   GG  A
GAM2823  ICMT     3'  GGATTACAGGCGTGCCCGG   65330    CACC
                                GGA   GCGGGCGTGCCCGG
                                |||   ||||||||||||||
                                CCT   TGTCCGCACGGGCC
                                  AA__
GAM2823  ILVBL    5'  GGAGCGTGGCCGTGCCCGG   65331    CAC  C  G
                                GGA   CG GG CGTGCCCGG
                                |||   || || |||||||||
                                CCT   GC CC GCACGGGCC
                                  C__  A  G
GAM2823  MAP3K5   5'  AGGGCACGCCGCTGCCCGG   65332    A   C  GG  G
                                AGG CAC GC  GC TGCCCGG
                                ||| ||| ||  || |||||||
                                TCC GTG CG  CG ACGGGCC
                                  C   _  G_  _
GAM2823  MGEA5    5'  CAGGGACCCGAATGCCCG    65333   A   A  CGGGC
                                CA GGAC CCG    GTGCCCG
                                || |||| |||    |||||||
                                GT CCTG GGC    TACGGGC
                                 C    _   T_____
GAM2823  NCAM2    3'  CAAAGACACTGCGACGATTTGG 65334         C   G  TGCCC
                                CAAGGACAC GCGG CG    GG
                                ||||||||| |||| ||    ||
                                GTTTCTGTG CGCT GC    CC
                                      A   _  TAAA_
GAM2823  NFATC2   5'  GGACGCACGCCGGGTCCGG   65335    AC_   G  C  GC
                                GGAC   CGC GG GT  CCGG
                                ||||   ||| || ||  ||||
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                                CCTG  GCG CC CA  GGCC
                                  CGT  G _ __
GAM2823 NLGN2   3' GGGGGCCGGCGTGTGCCCGG  65336   ACACC  G  __
                                GG    GC GGC  GTGCCCGG
                                ||    || |||  ||||||||
                                CC    CG CCG  CACGGGCC
                                 CC___  G  CA
GAM2823 NTSR1   5' AGGACAGCGCCCAGCCCGG  65337      C  GGG  T
                                AGGACA CGC  CG GCCCGG
                                |||||| |||  || ||||||
                                TCCTGT GCG  GT CGGGCC
                                   C  G__ _
GAM2823 OTOF    3' GGAAGACAGGGTGTGCCCGG  65338  A    CCGC  C
                                C AGGACA   GGG GTGCCCGG
                                | ||||||   ||| ||||||||
                                C TTCTGT   CCC CACGGGCC
                                 C     ____  A
GAM2823 RAB26   3' CAAGGTGGAGCGTGCTCG   65339     ACACCGC     C
                                CAAGG     GGGCGTGC CG
                                |||||     |||||||| ||
                                GTTCC     CTCGCACG GC
                                  AC_____      A
GAM2823 RB1CC1  5' GGACACCGCCGCGGCTTGG  65340       GG  T  CC
                                GGACACCGC  GCG GC  GG
                                |||||||||  ||| ||  ||
                                CCTGTGGCG  CGC CG  CC
                                     G_  _ AA
GAM2823 RNF4    3' GGACAAAAGGTGGTGTGCCCGG 65341     CCGCG_  C
                                GGACA     GG GTGCCCGG
                                |||||     || ||||||||
                                CCTGT     CC CACGGGCC
                                  TTTCCA  A
GAM2823 SLC22A2 5' AGGCTGCCCGACGTGCCCGG  65342    ACA  G  G
                                AGG  CC CGG CGTGCCCGG
                                |||  || ||| |||||||||
                                TCC  GG GCT GCACGGGCC
                                 GAC  _  _
GAM2823 TXNRD2  3' GGCGCACCGTGTGCCCTGG  65343   A_   CGGGC    _
                                GG  CACCG   GTGCCC GG
                                ||  |||||   |||||| ||
                                CC  GTGGC   CACGGG CC
                                 GC   A____     A
GAM2823 USP6    5' TGAGGACGTGCACAGGGCCTGG 65344  A   AC_    CGT  C
                                C AGGAC  CGCGGG  GCC GG
                                | |||||  ||||||  ||| ||
                                A TCCTG  GTGTCC  CGG CC
                                 C    CAC     ___  A
GAM2823 ARNTL2  5' GGACGCCGCCCCGCAGCCCGG 65345    A  GG_  T
                                GGAC CCGC  GCG GCCCGG
                                |||| ||||  ||| ||||||
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                                CCTG GGCG   CGT CGGGCC
                                  C    GGG  _
GAM2823  C9orf12   3'  GGCACACTGCCCAGCCCGG   65346    A   C  GG  G _
                                GG CAC GC  GC T GCCCGG
                                || ||| ||  || | ||||||
                                CC GTG TG  CG G CGGGCC
                                 _  _ A_  G T
GAM2823  DKFZp434N0650 3'  GGAGGCACCGCGGCCCCGG   65347   A   A      G GTG
                                C AGG CACCGCGG C   CCCGG
                                | ||| |||||||| |   |||||
                                C TCC GTGGCGCC G   GGGCC
                                 C  _       _ ___
GAM2823  DOK4      5'  AAGGATGCCCAGGTGCCTGG   65348      CA  G    CG    C
                                AAGGA  CC CGGG  TGCC GG
                                |||||  || ||||  |||| ||
                                TTCCT  GG GTCC  ACGG CC
                                   AC  _    __    A
GAM2823  FADS1     5'  AGGGGCTGTCAGGCGCGTGCTC 65349     ACACCG      __ C
              GG                   AGG     CGGGCGT  GC CGG
                                |||     |||||||  || |||
                                TCC     GTCCGCG  CG GCC
                                  CCGACA      CA  A
GAM2823  FLJ11856  5'  GGACACCGCCGTCCG       65350         GGG   GC
                                GGACACCGC   CGT  CCG
                                |||||||||   |||  |||
                                CCTGTGGCG   GCA  GGC
                                      ___   __
GAM2823  FLJ12949  3'  GGATTACAGGCGTGCCTGG    65351     CACC         C
                                GGA    GCGGGCGTGCC GG
                                |||    |||||||||||| ||
                                CCT    TGTCCGCACGG CC
                                  AA__         A
GAM2823  FLJ22393  3'  CAGAGACATACTTGTGCCTGG  65352    AG    CC  GGGC    C
                                CA  GACA  GC    GTGCC GG
                                ||  ||||  ||    ||||| ||
                                GT  CTGT  TG    CACGG CC
                                 CT    A_  AA__     A
GAM2823  KIAA0417  3'  CAAAGACACCTTTGTGCCTGG  65353          GCGGGC    C
                                CAAGGACACC      GTGCC GG
                                ||||||||||      ||||| ||
                                GTTTCTGTGG      CACGG CC
                                      AAA___     A
GAM2823  KIAA0431  3'  AGGCGCATGCCACTGTGCCTGG 65354     ACAC    G ____     C
                                AGG    CGCG GC    GTGCC GG
                                |||    |||| ||    ||||| ||
                                TCC    GCGT CG    CACGG CC
                                  _____    A  GTGA     A
GAM2823  KIAA0603  5'  AGGGCACCGCGGAGGCCGG   65355     A        CGT   C
                                AGG CACCGCGGG   GCC GG
                                ||| |||||||||   ||| ||
```

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                                TCC GTGGCGCCT   CGG CC
                                  C       C__  _
GAM2823 KIAA0961 5' AGGATGCGCGGGGCCTCGG   65356     CAC     CGT  _
                                AGGA  CGCGGG  GCC CGG
                                ||||  ||||||  ||| |||
                                TCCT  GCGCCC  CGG GCC
                                  AC_     ___  A
GAM2823 KIAA1530 5' GAGCACCGCGGCGTGCCTGG  65357   GA      G     C
                                G  CACCGCGG CGTGCC GG
                                |  |||||||| |||||| ||
                                C  GTGGCGCC GCACGG CC
                                 TC       _     A
GAM2823 KIAA1879 3' AGGGGCCCAGGTGCCCG    65358    ACA  G   CG
                                AGG   CC CGGG  TGCCCG
                                |||   || ||||  ||||||
                                TCC   GG GTCC  ACGGGC
                                  CC_ _   __
GAM2823 MARK2    5' GGCACTGCTCCGCGCCCGG   65359    A   C  GGG
                                GG CAC GC   CGTGCCCGG
                                || ||| ||   |||||||||
                                CC GTG CG   GCGCGGGCC
                                 _  A  AG_
GAM2823 MGC15631 3' GGACATGCACAGGGCCTGG   65360      C_     CGT   C
                                GGACA  CGCGGG   GCC GG
                                |||||  ||||||   ||| ||
                                CCTGT  GTGTCC   CGG CC
                                   AC     ___   A
GAM2823 MGC20496 3' CAAGGACACTGCTGGCACTG  65361         C  G   _
                                CAAGGACAC GC GGCG TG
                                ||||||||| || |||| ||
                                GTTCCTGTG CG CCGT AC
                                      A  A   G
GAM2823 NYD-SP11 3' AAGGACACTGTAGGTTACATCC 65362        CGC   CG  __
                                AAGGACAC   GGG  TGC  CC
                                ||||||||   |||  |||  ||
                                TTCCTGTG   TCC  ATG  GG
                                     ACA   A_   TA
GAM2823 PDE8A    5' GGCGCCGCGGACACGCTGG   65363    ACA         CC
                                GG   CCGCGGGCGTGC  GG
                                ||   ||||||||||||  ||
                                CC   GGCGCCTGTGCG  CC
                                 GC_          A_
GAM2823 PLA2G6   3' AGGGGTACGGTTGTGCCCGG  65364    ACACC   GC
                                AGG    GCGG  GTGCCCGG
                                |||    ||||  ||||||||
                                TCC    TGCC  CACGGGCC
                                  CCA__    AA
GAM2823 STMN3    3' CAAGGACATCTGCAAAGCCCTG 65365        CCGCGG  T_   _
             G                   CAAGGACA     GCG  GCCC GG
                                 ||||||||     |||  |||| ||
```

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                                GTTCCTGT     CGT  CGGG CC
                                     AGA___   TT    A
GAM2823  LOC124512 5'  GGGGACCGCGGAAGGCTCCGG  65366    AC       CGT  _
                                GG  ACCGCGGG   GC CCGG
                                ||  ||||||||   || ||||
                                CC  TGGCGCCT   CG GGCC
                                 CC       TC_  A
GAM2823  LOC126382 5'  CAGGGAAACCGCCAATGCCCGG 65367    A   C     G GC
                                CA GGA ACCGC G  GTGCCCGG
                                || ||| ||||| |  ||||||||
                                GT CCT TGGCG T  TACGGGCC
                                 C   T     G __
GAM2823  LOC145371 3'  AGGAGCAGGTGGCGTGCCTGG  65368      _  CCGCG       C
                                AGGA CA     GGCGTGCC GG
                                |||| ||     |||||||| ||
                                TCCT GT     CCGCACGG CC
                                  C  CCA__       A
GAM2823  LOC152453 3'  AGGCATGTGCCACTGTGCCTGG 65369     A ____    GGGC     C
                                AGG CA    CCGC    GTGCC GG
                                ||| ||    ||||    ||||| ||
                                TCC GT    GGTG    CACGG CC
                                  _  ACAC    A___     A
GAM2823  LOC164584 5'  AGCGATGCCGCGGGCGGCGTCC 65370    _  CA       T  __
           GG                     AG GA  CCGCGGGCG GC  CCGG
                                || ||  |||||||| ||  ||||
                                TC CT  GGCGCCCGC CG  GGCC
                                 G  AC        _  CA
GAM2823  LOC197320 5'  AGGACACGCGCGGAACTCTCCG 65371        _     _ GTGC
           G                     AGGACAC CGCGGG C    CCGG
                                ||||||| |||||| |    ||||
                                TCCTGTG GCGCCT G    GGCC
                                    C     T AGA_
GAM2823  LOC199782 3'  CAAGGGCGCGCGGCACCCG    65372      ACACC   G  _ TG
                                CAAGG    GCG GC G  CCCG
                                |||||    ||| || |  ||||
                                GTTCC    CGC CG C  GGGC
                                  _____  G  C GT
GAM2823  LOC206962 5'  AGGACACCGCGGGCCGC     65373            G
                                AGGACACCGCGGGC TGC
                                |||||||||||||| |||
                                TCCTGTGGCGCCCG GCG
                                          _
GAM2823  LOC253070 5'  CAAAGACACCGTGCCC      65374          GCGGGC
                                CAAGGACACC     GTGCCC
                                ||||||||||     ||||||
                                GTTTCTGTGG     CACGGG
                                          _____
GAM2823  LOC254556 3'  GGACAAAAGGTGGTGTGCCCGG 65341       CCGCG_  C
                                GGACA     GG GTGCCCGG
                                |||||     || ||||||||
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                                CCTGT     CC CACGGGCC
                                   TTTCCA  A
GAM2823  LOC257000 3'  AGGACATGCGTAGCCTCGG   65375       CC   GGCGT  _
                                AGGACA  GCG    GCC CGG
                                ||||||  |||    ||| |||
                                TCCTGT  CGC    CGG GCC
                                   A_   AT___   A
GAM2824  LNK      5'  CCAGCGCTTGACAGTTGCGGGA 65378        CC  __   A  A
           GGAT                  CTAGCGCT  GCG  TGCG GA GAT
                                ||||||||  |||  |||| || |||
                                GGTCGCGA  TGT  ACGC CT CTA
                                    AC   CA   C  C
GAM2824  MLLT2    3'  CAGCGCTCTAGGCAATGGGGAG 65379        C__  _  C_
           A                    TAGCGCTC   GCG TG  GAGA
                                ||||||||   ||| ||  ||||
                                GTCGCGAG   CGT AC  CTCT
                                    ATC   T  CC
GAM2824  HH114    5'  ACTCCTGGGAGAAGAT     65380      GCG  C
                                GCTCC   TG GAGAAGAT
                                |||||   || ||||||||
                                TGAGG   AC CTCTTCTA
                                   ___  C
GAM2824  LHFPL2   3'  TAGCCCTTAATCTGTGAGAAGA 65381     G  CCGCG  C
           T                    TAGC CT    TG GAGAAGAT
                                |||| ||    || ||||||||
                                ATCG GA    AC CTCTTCTA
                                  G  ATTAG  A
GAM2824  RALGPS1A  3'  CTAGTCTTTGCTCAAAAAGAAG 65382     CG  CC  GTGC_
           AT                    CTAG  CT  GC    GAGAAGAT
                                ||||  ||  ||    ||||||||
                                GATC  GA  CG    TTCTTCTA
                                  A_  AA  AGTTT
GAM2824  LOC148188 5'  TCCTGCTAGCGAGAAGAT    65383     _  GT
                                TCC GC  GCGAGAAGAT
                                ||| ||  ||||||||||
                                AGG CG  CGCTCTTCTA
                                  A  AT
GAM2824  LOC90719  5'  GCGCTCTGCGGAGAGAAGAT   65384       C   TGC
                                GCGCTC GCG   GAGAAGAT
                                |||||| |||   ||||||||
                                CGCGAG CGC   CTCTTCTA
                                   A   CT_
GAM2825  B4GALT1   3'  CCTCTGCCTCTCTGATCTTTCC 65387       _   GGGCCC  C
                                CTTCTG CTC     GA CTTTCC
                                |||||| |||     || ||||||
                                GGAGAC GAG     CT GAAAGG
                                   G   AGA___  A
GAM2825  DPYSL3    5'  CTTCTGCTCCGGCTCGCC    65388         G   C  A
                                CTTCTGCTC GGC CG CC
                                ||||||||| ||| || ||
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                                GAAGACGAG CCG GC GG
                                     G   A  _
GAM2825 GDI1     3'  CTTCTGCTTGGCTCACTTTTC  65389        CG   C G  C
                                CTTCTGCT  GGC C AC TTTC
                                ||||||||  ||| | || ||||
                                GAAGACGA  CCG G TG AAAG
                                    A_   A _  A
GAM2825 HSPA4    5'  CTACTGCTCGGGCTCGGGCC   65390    T        C  A_
                                CT CTGCTCGGGC CG  CC
                                || ||||||||||  ||  ||
                                GA GACGAGCCCG GC  GG
                                 T         A  CC
GAM2825 MTNR1B   3'  CTTCTGCCCCAGGCCTTTC    65391         _    CGACC
                                CTTCTGCTC GGGCC     TTTC
                                |||||||||  |||||     ||||
                                GAAGACGGG TCCGG     AAAG
                                     G    ______
GAM2825 ODF2     3'  CTGCTGCTTTTGGGACTTTTC  65392    T    CG_  CCC   C
                                CT CTGCT   GG   GAC TTTC
                                || |||||   ||   ||| ||||
                                GA GACGA   CC   CTG AAAG
                                 C    AAA  ____  A
GAM2825 OSBP     5'  TTCTCTCGGGCCTGTCATTC   65393      G       CGACCT
                                TTCT CTCGGGCC     TTC
                                ||||  ||||||||     |||
                                AAGA GAGCCCGG     AAG
                                  _       ACAGT_
GAM2825 SERPINB6 5'  CTTCTGCTGGGAACGACCTTTC 65394        C   CC
                                CTTCTGCT GGG  CGACCTTTC
                                ||||||||  |||  |||||||||
                                GAAGACGA CCC  GCTGGAAAG
                                     _  TT
GAM2825 SLC1A4   3'  TTCTGCTCAGGCTCATGTCC   65395          C  A__
                                TTCTGCTCGGGC CG   CC
                                ||||||||||||  ||   ||
                                AAGACGAGTCCG GT   GG
                                       A  ACA
GAM2825 TRIM9    5'  CTTCCGCTCGGGTTTGAC    65396          CCC
                                CTTCTGCTCGGG   GAC
                                ||||||||||||   |||
                                GAAGGCGAGCCC   CTG
                                       AAA
GAM2825 B3GNT5   3'  TTCTCTCCTATGCTGACCTTTC 65397     G   GG__  CC
              C                  TTCT CTC    GC  GACCTTTCC
                                 ||||  |||    ||  |||||||||
                                 AAGA GAG    CG  CTGGAAAGG
                                   _  GATA  A_
GAM2825 C21orf42 3'  CTTCTGCTGGGTTTAGATTTTT 65398        C   CCC_  CC
              C                  CTTCTGCT GGG    GA  TTTC
                                 ||||||||  |||    ||  ||||
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```
                                GAAGACGA CCC   CT  AAAG
                                    _  AAAT  AA
GAM2825  C8orf14   5'  TCCACAGGCCCGGCCTTTC   65399    TG TC     A
                                TC  C  GGGCCCG CCTTTC
                                ||  |  ||||||| ||||||
                                AG  G  TCCGGGC GGAAAG
                                 GT __      C
GAM2825  DNAJB11   5'  CTTCTGCTCGTGCCGAATTCC  65400         G   C  CCT
                                CTTCTGCTCG GCC GA   TTCC
                                |||||||||| ||| ||   ||||
                                GAAGACGAGC CGG CT   AAGG
                                     A   _  T__
GAM2825  ELF4      3'  CTTCTGCCTGGCTCAAGGCTTT 65401        CG   C   C_
                                CTTCTGCT  GGC CGA  CTTT
                                ||||||||  ||| |||  ||||
                                GAAGACGG  CCG GTT  GAAA
                                    A_   A   CC
GAM2825  FLJ20330  5'  CTTCTGCTCGGATCTCCAGTCC 65402          CCCGA  TT
                                CTTCTGCTCGGG    CC  TCC
                                ||||||||||||    ||  |||
                                GAAGACGAGCCT    GG  AGG
                                     AGA__  TC
GAM2825  FLJ21709  3'  CTTCTGCTCTGAGCCCCTTTCC 65403         _     GAC
                                CTTCTGCTC GGGCCC   CTTTCC
                                |||||||| ||||||   ||||||
                                GAAGACGAG CTCGGG   GAAAGG
                                     A     ___
GAM2825  FOXO3A    5'  TTCGCTCGGGCCCGCTCT    65404     T        AC
                                TTC GCTCGGGCCCG  CT
                                ||| ||||||||||  ||
                                AAG CGAGCCCGGGC  GA
                                  _         GA
GAM2825  FTHFD     3'  TTCTTCTCACAAAGACCTTTC  65405      G    GGCCC
                                TTCT CTCG    GACCTTTC
                                |||| ||||    ||||||||
                                AAGA GAGT    CTGGAAAG
                                  A   GTTT_
GAM2825  JAM1      3'  CCTCTGCTTCCCCATGACCTTT 65406        CGGG  __
                                CTTCTGCT   CCC  GACCTTT
                                ||||||||   |||  |||||||
                                GGAGACGA   GGG  CTGGAAA
                                     AG__   TA
GAM2825  JAM1      3'  CCTCTGCTTCCCCATGACCTTT 65406        CGGG  __
                                CTTCTGCT   CCC  GACCTTT
                                ||||||||   |||  |||||||
                                GGAGACGA   GGG  CTGGAAA
                                     AG__   TA
GAM2825  JAM1      3'  CCTCTGCTTCCCCATGACCTTT 65406        CGGG  __
                                CTTCTGCT   CCC  GACCTTT
                                ||||||||   |||  |||||||
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                                GGAGACGA   GGG  CTGGAAA
                                    AG__   TA
GAM2825  JAM1     3'  CCTCTGCTTCCCCATGACCTTT 65406       CGGG  __
                                CTTCTGCT   CCC  GACCTTT
                                ||||||||   |||  |||||||
                                GGAGACGA   GGG  CTGGAAA
                                    AG__   TA
GAM2825  JAM1     3'  CCTCTGCTTCCCCATGACCTTT 65406       CGGG  __
                                CTTCTGCT   CCC  GACCTTT
                                ||||||||   |||  |||||||
                                GGAGACGA   GGG  CTGGAAA
                                    AG__   TA
GAM2825  MGC20255 3'  CTTCGCTCGGGCCTGAC     65407     T       C
                                CTTC GCTCGGGCC GAC
                                |||| ||||||||| |||
                                GAAG CGAGCCCGG CTG
                                  _       A
GAM2825  PEG10    3'  TTCTGCCCAGGTCTTTC     65408          CCCGAC
                                TTCTGCTCGGG     CTTTC
                                ||||||||||      |||||
                                AAGACGGGTCC     GAAAG
                                    A_____
GAM2825  RAI17    3'  TTCTGCACCTCCCCGGCCTTTC 65409       _ GGG   A
           C                     TTCTGC TC   CCCG CCTTTCC
                                ||||||  ||   |||| |||||||
                                AAGACG GG   GGGC GGAAAGG
                                   T  AG_   C
GAM2825  SCAMP5   3'  CTTCTGCTTGGGCCCTGA    65410        C     _
                                CTTCTGCT GGGCCC GA
                                |||||||| |||||| ||
                                GAAGACGA CCCGGG CT
                                    A     A
GAM2825  LOC204845 5'  TCTGCCGATTTGACCTTTC    65411      T   GCCC
                                TCTGC CGG    GACCTTTC
                                ||||| |||    ||||||||
                                AGACG GCT    CTGGAAAG
                                  _  AAA_
GAM2825  LOC221122 3'  CTTCTGCTTTGGGCTGAACCCT 65412        C_   CC
           T                     CTTCTGCT  GGGC  GACCTTT
                                |||||||  ||||  |||||||
                                GAAGACGA  CCCG  TTGGGAA
                                    AA    AC
GAM2825  LOC221415 5'  CCTCTGCGCCACTCGACCTTTC 65413       TCGG  ___
                                CTTCTGC    GCC   CGACCTTTC
                                |||||||    |||   |||||||||
                                GGAGACG    CGG   GCTGGAAAG
                                    _____  TGA
GAM2825  LOC254065 5'  CTTCTGCCTCGGCATTTGACCT 65414       CG   CC__
           TTC                     CTTCTGCT  GGC    GACCTTTC
                                |||||||  |||    ||||||||
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                                GAAGACGG CCG   CTGGAAAG
                                    AG  TAAA
GAM2825 LOC90982 5' CTTCTGCCATTAATGATTTTTC 65415      T GGCCC CC
            C                    CTTCTGC CG    GA TTTCC
                                 ||||||| ||    || |||||
                                 GAAGACG GT    CT AAAGG
                                    _ AATTA AA
GAM2826 ECGF1   5' TCGCGCACAGCGGTCCACTGC 65418       C C ACA
                                 TCGCGCACA GC GT  CACTGC
                                 ||||||||| || ||  ||||||
                                 AGCGCGTGT CG CA  GTGACG
                                     _ C G__
GAM2826 ITGA5   3' ACACAGCCTCACACTGC    65419     C  GTA
                                 GCACA GCC  CACACTGC
                                 ||||| |||  ||||||||
                                 TGTGT CGG  GTGTGACG
                                   _  A__
GAM2826 ITGAM   3' CGCACACATGCACACACTGC  65420      CC
                                 CGCACACG GTACACACTGC
                                 |||||||| ||||||||||
                                 GCGTGTGT CGTGTGTGACG
                                    A_
GAM2826 PTGS1   5' GCGTGCGCCTCGCACACTGC  65421    CACA  GTA
                                 GCG  CGCC  CACACTGC
                                 |||  ||||  ||||||||
                                 CGC  GCGG  GTGTGACG
                                   AC__   AGC
GAM2826 PTGS1   5' GCGTGCGCCTCGCACACTGC  65421    CACA  GTA
                                 GCG  CGCC  CACACTGC
                                 |||  ||||  ||||||||
                                 CGC  GCGG  GTGTGACG
                                   AC__   AGC
GAM2826 STX1A   3' GCTCCTCGCTGTGCACACTGC 65422    GCACA  C A
                                 GC   CGC GT CACACTGC
                                 ||   ||| || ||||||||
                                 CG   GCG CA GTGTGACG
                                  AGGA_  A  C
GAM2826 TCF12   3' GCAGAAGCGACACACTGC    65423    CAC  C T
                                 GCA  GC G ACACACTGC
                                 |||  || | |||||||||
                                 CGT  CG C TGTGTGACG
                                   CTT  _ _
GAM2826 GBTS1   3' GCGCACACACACACGTTGC   65424       CGT  AC
                                 GCGCACACGC  ACAC  TGC
                                 ||||||||||  ||||  |||
                                 CGCGTGTGTG  TGTG  ACG
                                       ____  CA
GAM2826 HIRIP3  5' TCGCGCACGCGCAGTGCTG   65425       A  C  ACACA
                                 TCGCGCAC CGC GT   CTG
                                 |||||||| ||| ||   |||
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                                AGCGCGTG GCG CA    GAC
                                    C   T  C____
GAM2826  MGC10871  5'  TCACGCACGCGCGAGTGCGCGC 65426        A   C_  ACACA
              TGC                   TCGCGCAC CGC  GT    CTGC
                                |||||||| |||  ||    ||||
                                AGTGCGTG GCG  CA    GACG
                                    C   CT  CGCGC
GAM2826  STK25    3'  CGTGCACAACAGCACACTGC   65427    C    C  CGTA
                                CG GCACA GC    CACACTGC
                                || ||||| ||    ||||||||
                                GC CGTGT TG    GTGTGACG
                                 A    _  TC__
GAM2826  STX1B2   3'  TCACGCACGCACACACACTG   65428        A   CGT
                                TCGCGCAC CGC   ACACACTG
                                |||||||| |||   ||||||||
                                AGTGCGTG GTG   TGTGTGAC
                                    C   ___
GAM2826  LOC127703 3'  GCGCATATACACACACTGC    65429      CACGCCG
                                GCGCA      TACACACTGC
                                |||||      ||||||||||
                                CGCGT      GTGTGTGACG
                                   ATAT___
GAM2826  LOC221705 3'  GCCAACACTGCACACTGC    65430    G  C    CGTA
                                GC CA ACGC    CACACTGC
                                || || ||||    ||||||||
                                CG GT TGTG    GTGTGACG
                                 _  _    AC__
GAM2827  KAL1     3'  TAATCTTAGTTGATTTTTC    65433      AC
                                TAAT  TAGTTGATTTTTC
                                ||||  ||||||||||||
                                ATTA  ATCAACTAAAAAG
                                  GA
GAM2827  NAT2     3'  CAATATTAAATGTTTTCTAGCA 65434      C   T  AT
                                TAATA TAG TG  TTTTCTAGCA
                                ||||| ||| ||  ||||||||||
                                GTTAT ATT AC  AAAAGATCGT
                                   A   T  __
GAM2827  KIAA1462  3'  TAATTCTAGTTGATACGGC    65435      A       TTTTCTA
                                TAAT CTAGTTGAT      GC
                                |||| |||||||||      ||
                                ATTA GATCAACTA      CG
                                  A       TGC_____
GAM2827  LOC125228 3'  TAACACTGATTTTTCTAG     65436        AGTT
                                TAATACT    GATTTTTCTAG
                                |||||||    ||||||||||
                                ATTGTGA    CTAAAAAGATC
                                     _____
GAM2827  LOC152348 5'  ATACTATTCTTTTCTAGCA    65437       GTTGA
                                ATACTA     TTTTTCTAGCA
                                ||||||     ||||||||||
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                                TATGAT    GAAAAGATCGT
                                   AA___
GAM2827  LOC169966 3'  CTGGTAGATTTTTCTAGC    65438    A  T
                                CT GT GATTTTTCTAGC
                                || || ||||||||||||
                                GA CA CTAAAAAGATCG
                                 C  T
GAM2827  LOC200339 3'  TAATCTAGTTGAATGCTTAGCA 65439      A       TTTTTC
                                TAAT CTAGTTGA     TAGCA
                                |||| ||||||||     |||||
                                ATTA GATCAACT     ATCGT
                                   _      TACGA_
GAM2828  IHPK3    3'  TCTGCCATATATAGAGAT    65442         _  C
                                TTTGTCGT TA AGAGAT
                                |||||||| || ||||||
                                AGACGGTA AT TCTCTA
                                     T  A
GAM2828  TLE4     3'  TTTGTCGTCCACGGAGAT    65443         _  A
                                TTTGTCGTT AC GAGAT
                                ||||||||| || |||||
                                AAACAGCAG TG CTCTA
                                     G  C
GAM2829  EGLN2    5'  TCACCACTGCCACTGCTGCAGC 65446       C_   AGCA
           T                     TTACCAC  CCG    CTGCAGCT
                                |||||||  |||   ||||||||
                                AGTGGTG  GGT    GACGTCGA
                                    AC   GAC_
GAM2829  PSCD4    3'  TCACCACCTCGCAAGGCAGCTA 65447        CCGA   CT
                                TTACCACC    GCA  GCAGCTA
                                ||||||||    |||  |||||||
                                AGTGGTGG    CGT  CGTCGAT
                                    AG__    TC
GAM2829  PTGFRN   3'  TTACCACCATCGAGTGTCTG   65448       C_   CA_
                                TTACCACC  CGAG   CTG
                                ||||||||  ||||   |||
                                AATGGTGG  GCTC   GAC
                                     TA    ACA
GAM2829  SHC1     3'  CCACCCCGGGCCTAGGCT    65449        A  A   CA
                                CCACCCCG GC CTG  GCT
                                |||||||| || |||  |||
                                GGTGGGGC CG GAT  CGA
                                     C  _   C_
GAM2829  DKFZP434K1772 5'  CCTGCCGGCACTGCAGCT    65450    ACC   A
                                CC   CCG GCACTGCAGCT
                                ||   ||| ||||||||||||
                                GG   GGC CGTGACGTCGA
                                 AC_  _
GAM2829  KIAA0445  5'  CCCGCAGGCGCTGCAGCT    65451     _  A  A
                                CCC CG GC CTGCAGCT
                                ||| || || ||||||||
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                                GGG GT CG GACGTCGA
                                  C  C  C
GAM2829  KIAA1681  3'  CACTGCAGCAGTACTGCAGCTA 65452     CC G  ___
                                CAC  C AGC   ACTGCAGCTA
                                |||  | |||   ||||||||||
                                GTG  G TCG   TGACGTCGAT
                                  AC _   TCA
GAM2829  MARCO    5'  CCCATCGAACCACTGCAGCT   65453     __    _
                                CCC  CGAGC ACTGCAGCT
                                |||  ||||| |||||||||
                                GGG  GCTTG TGACGTCGA
                                  TA    G
GAM2829  MCF2L    3'  CCGCCCTCGCTGCAGCT     65454    A  _ AGCA
                                CC CCC CG    CTGCAGCT
                                || ||| ||    ||||||||
                                GG GGG GC    GACGTCGA
                                 C   A _____
GAM2829  PAFAH2   3'  CTACTGTCCAGGCTGCAGCT   65455     CACC   A  AC
                                TTAC    CCG GC  TGCAGCT
                                ||||    ||| ||  |||||||
                                GATG    GGT CG  ACGTCGA
                                  ACA_   C  __
GAM2829  LOC115761 5'  TTACTATTAGACTGCAGCT    65456     CACCCCG  C
                                TTAC      AG ACTGCAGCT
                                ||||      || |||||||||
                                AATG      TC TGACGTCGA
                                  ATAA___  _
GAM2829  LOC125875 5'  CCTACCCCGAGGCCCCCAGCT  65457    _      CA  G
                                CC ACCCCGAG  CT CAGCT
                                || ||||||||  || |||||
                                GG TGGGGCTC  GG GTCGA
                                 A       CG  G
GAM2829  LOC149506 3'  CCACTCCCCTACTGCAGCT    65458     _  GAGC
                                CCAC CCC    ACTGCAGCT
                                |||| |||    |||||||||
                                GGTG GGG    TGACGTCGA
                                  A   GA__
GAM2829  LOC149579 5'  CCCGCAGGCGCTGCAGCT     65451     _  A  A
                                CCC CG GC CTGCAGCT
                                ||| || || ||||||||
                                GGG GT CG GACGTCGA
                                  C  C  C
GAM2829  LOC151827 5'  TTACAGTCCGCCTGCAGCT    65459     CAC  CGA  A
                                TTAC   CC   GC CTGCAGCT
                                ||||   ||   || ||||||||
                                AATG   GG   CG GACGTCGA
                                  TCA  ___  _
GAM2829  LOC157931 3'  CACCCACACCTGCAGCT     65460      CGA  A
                                CACCC   GC CTGCAGCT
                                |||||   || ||||||||
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                                GTGGG   TG GACGTCGA
                                  TG_ _
GAM2829  LOC221954 5'  CCGCAGCTCACTGCAGCT    65461     _  __
                                CCG AGC  ACTGCAGCT
                                ||| |||  |||||||||
                                GGC TCG  TGACGTCGA
                                  G   AG
GAM2829  LOC253044 3'  TTACCACCCTCTCCCTGTGGCT 65462         CGAGCA   CA
                                TTACCACCC     CTG  GCT
                                |||||||||     |||  |||
                                AATGGTGGG     GAC  CGA
                                     AGAGG_   AC
GAM2829  LOC257438 5'  TTACTCCTCCAAAGCTGCAGCT 65463      CA  _    CA
            A                    TTAC  CC CCGAG  CTGCAGCTA
                                ||||  || |||||  |||||||||
                                AATG  GG GGTTT  GACGTCGAT
                                  A_ A    C_
GAM2830  COL15A1   3'  TTCTAAACACTGACTTTATAAG 65466         G   T    C
            A                    TTCTGAACA TGG CTTTA AAGA
                                ||||||||| ||| ||||| ||||
                                AAGATTTGT ACT GAAAT TTCT
                                     G   _    A
GAM2830  HRH1     3'  TTCTGAACAATGGTTTCT    65467             C
                                TTCTGAACAGTGGT TTT
                                |||||||||||||| |||
                                AAGACTTGTTACCA AGA
                                       A
GAM2830  RXRB     3'  CTCTGGACAGTGACAGGGTCTT 65468    A     G_________    TAC
            GTAAA                  TG ACAGTG       TCTT   AA
                                || ||||||       ||||   ||
                                AC TGTCAC       AGAA   TT
                                 C     TGTCCCIII    CAT
GAM2830  TRPM8    3'  TTCTGAGTAGCTGGGATTACAG 65469       AC  _   TCT    A
            GA                   TTCTGA  AG TGG   TTACA GA
                                ||||||  || |||   ||||| ||
                                AAGACT  TC ACC   AATGT CT
                                   CA  G   CT_    C
GAM2830  KIAA1940  3'  CTCTGGAGGACTCTTTACAAG  65470      AAC  T  _
                                TTCTG   AG GG TCTTTACAAG
                                |||||   || || ||||||||||
                                GAGAC   TC CT AGAAATGTTC
                                   C__  _  G
GAM2830  PSR      3'  TTCTGAACAAGTGGTCTCT    65471          _
                                TTCTGAACA GTGGTCTTT
                                ||||||||| |||||||||
                                AAGACTTGT CACCAGAGA
                                      T
GAM2830  SERPINB1  3'  TTCTGGACAGTGGTTTTA    65472       A       C
                                TTCTG ACAGTGGT TTTA
                                ||||| |||||||| ||||
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                                AAGAC TGTCACCA AAAT
                                  C       _
GAM2830  LOC219529 3'  TTCTGAATAGTCACTTTACAAG 65473        C   G T
                                TTCTGAA AGT G CTTTACAAG
                                ||||||| ||| | |||||||||
                                AAGACTT TCA T GAAATGTTC
                                   A   G _
GAM2830  LOC253039 3'  TTCTGGGTGTGATTACAAG   65474      AACA   GTCT
                                TTCTG   GTG   TTACAAG
                                |||||   |||   |||||||
                                AAGAC   CAC   AATGTTC
                                  C___   ACT_
GAM2830  LOC253747 5'  TTCTAGCAGTGGCCTTAAG   65475      AA        TAC
                                TTCTG  CAGTGGTCTT   AAG
                                |||||  ||||||||||   |||
                                AAGAT  GTCACCGGAA   TTC
                                  C_        ____
GAM2830  LOC257206 3'  TTCTGTACAATTTTACAAG   65476      A    GGTC
                                TTCTG ACAGT   TTTACAAG
                                ||||| |||||   ||||||||
                                AAGAC TGTTA   AAATGTTC
                                  A    _____
GAM2830  LOC93624  5'  TTCTGGAGGTGGTCTTTA    65477      AACA
                                TTCTG   GTGGTCTTTA
                                |||||   ||||||||||
                                AAGAC   CACCAGAAAT
                                  CTC_
GAM2831  COL4A1    3'  TAAATTACTAATATATATA   65480         _
                                TAAATTACTA TATATATA
                                |||||||||| ||||||||
                                ATTTAATGAT ATATATAT
                                      T
GAM2831  HK3       3'  TAAATTATATATATATATT   65481        C
                                TAAATTA TATATATATATT
                                ||||||| ||||||||||||
                                ATTTAAT ATATATATATAA
                                     _
GAM2831  IFNGR2    3'  TAAATTACTAGGAGTATATTTA 65482          TATA
              CA                  TAAATTACTA   TATATTTACA
                                |||||||||   ||||||||||
                                ATTTAATGAT   ATATAAATGT
                                    CCTC
GAM2831  IGFBP1    3'  TTACTATATATATATACA    65483           TT
                                TTACTATATATATA  TACA
                                ||||||||||||| ||||
                                AATGATATATATAT  ATGT
                                      __
GAM2831  NCSTN     3'  TCATTATATATATATTTACA  65484     C
                                TTA TATATATATATTTACA
                                ||| ||||||||||||||||
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                                AGT ATATATATATAAATGT
                                  A
GAM2831  FLJ12078  5'  AATTATCTATATATATAT    65485      _
                                AATTA CTATATATATAT
                                ||||| ||||||||||||
                                TTAAT GATATATATATA
                                   A
GAM2831  KIAA0431  3'  ATCACTGCATTTATATTTACA  65486      A   A
                                ATTACT TAT TATATTTACA
                                |||||| ||| ||||||||||
                                TAGTGA GTA ATATAAATGT
                                   C   A
GAM2831  KIAA1321  3'  TAAATAACTATATATATAT    65487      T
                                TAAAT ACTATATATATAT
                                ||||| ||||||||||||
                                ATTTA TGATATATATATA
                                   T
GAM2831  KIAA1468  3'  TCACTATATATATATTTA     65488
                                TTACTATATATATATTTA
                                ||||||||||||||||||
                                AGTGATATATATATAAAT

GAM2831  LOC145474 5'  TAAATTATATATATATATTT   65489       C
                                TAAATTA TATATATATATTT
                                ||||||| ||||||||||||
                                ATTTAAT ATATATATATAAA
                                        _
GAM2831  LOC157503 3'  AATTTGAATATATATATTTACA 65490     ACT
                                AATT   ATATATATATTTACA
                                ||||   ||||||||||||||||
                                TTAA   TATATATATAAATGT
                                  ACT
GAM2831  LOC221763 5'  TAAATTACTATGTTGCAATTTA 65491          ATATAT
            CA                    TAAATTACTAT     ATTTACA
                                ||||||||||     |||||||
                                ATTTAATGATA     TAAATGT
                                      CAACGT
GAM2831  LOC51701  3'  TAAATATATATATATATATTTA 65492      TAC
                                TAAAT   TATATATATATTTA
                                |||||   ||||||||||||||
                                ATTTA   ATATATATATAAAT
                                   TAT
GAM2832  BBOX1     5'  TCAGGAGTAGATGCTGTCA    65495       C  C  _
                                TCAGGAGTA AT TTG CA
                                ||||||||| || ||| ||
                                AGTCCTCAT TA GAC GT
                                      C  C   A
GAM2832  FCRH3     5'  TCAGGAGTAATGTCTCCAAGAC 65496        CA_   G  CA
            T                    TCAGGAGTA   TCTT CA  ACT
                                |||||||||   |||| ||  |||
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                                AGTCCTCAT  AGAG GT  TGA
                                     TAC   _ TC
GAM2832  FGFR2   3'  GCATTCATCTTGCACGGCTA  65497    __       AA
                                GTA  CATCTTGCAC  CTA
                                |||  ||||||||||  |||
                                CGT  GTAGAACGTG  GAT
                                  AA        CC
GAM2832  FGFR2   3'  GCATTCATCTTGCACGGCTA  65497    __       AA
                                GTA  CATCTTGCAC  CTA
                                |||  ||||||||||  |||
                                CGT  GTAGAACGTG  GAT
                                  AA        CC
GAM2832  FGFR2   3'  GCATTCATCTTGCACGGCTA  65497    __       AA
                                GTA  CATCTTGCAC  CTA
                                |||  ||||||||||  |||
                                CGT  GTAGAACGTG  GAT
                                  AA        CC
GAM2832  FGFR2   3'  GCATTCATCTTGCACGGCTA  65497    __       AA
                                GTA  CATCTTGCAC  CTA
                                |||  ||||||||||  |||
                                CGT  GTAGAACGTG  GAT
                                  AA        CC
GAM2832  FGFR2   3'  GCATTCATCTTGCACGGCTA  65497    __       AA
                                GTA  CATCTTGCAC  CTA
                                |||  ||||||||||  |||
                                CGT  GTAGAACGTG  GAT
                                  AA        CC
GAM2832  FGFR2   3'  GCATTCATCTTGCACGGCTA  65497    __       AA
                                GTA  CATCTTGCAC  CTA
                                |||  ||||||||||  |||
                                CGT  GTAGAACGTG  GAT
                                  AA        CC
GAM2832  PRKCM   3'  AAGAGCACTAGGTCTTGCACAG 65498        A___       A
           CTA                    AGGAGTAC    TCTTGCACA CTA
                                |||||||||    |||||||||  |||
                                TTCTCGTG    AGAACGTGT GAT
                                     ATCC        C
GAM2832  CHODL   3'  AAGGCACATGTCTTGCACAA   65499     A    __
                                AGG GTACA  TCTTGCACAA
                                |||  |||||  ||||||||||
                                TTC CGTGT  AGAACGTGTT
                                  _     AC
GAM2832  KIAA1317  3'  AGGAGTGCTTGGCACACAACTA 65500       ACATCTT
                                AGGAGT      GCACAACTA
                                ||||||      |||||||||
                                TCCTCA      TGTGTTGAT
                                   CGAACCG
GAM2832  MGC5560   5'  TCAGAGTACATTTTTCAC    65501      G      C  G
                                TCAG AGTACAT TT CAC
                                ||||  |||||||  ||  |||
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                                AGTC TCATGTA AA GTG
                                  _      A  A
GAM2832  RFX4     3'  CCATTCATATCTTGCACAACT  65502     GGAG  C
                                TCA    TA ATCTTGCACAACT
                                |||    || ||||||||||||
                                GGT    GT TAGAACGTGTTGA
                                  AA__  A
GAM2832  SV2B     3'  TCAGGAGATGACACAATACA   65503        T__    CT
                                TCAGGAG   ACAT  TGCA
                                |||||||   ||||  ||||
                                AGTCCTC   TGTG  ATGT
                                    TAC    TT
GAM2832  TRF4-2   3'  CCAGGAGTCCCTGCGCAACT   65504         ACA     A
                                TCAGGAGT   TCTTGC CAACT
                                ||||||||   |||||| |||||
                                GGTCCTCA   GGGACG GTTGA
                                    ___     C
GAM2832  LOC152992 5'  GAGGACATCTTGCACGACTA   65505     T         A
                                GAG ACATCTTGCAC ACTA
                                ||| ||||||||||| ||||
                                CTC TGTAGAACGTG TGAT
                                  C         C
GAM2832  LOC257428 5'  TCGGAAGTACAAAACACA    65506    A       TCTT
                                TC GGAGTACA    GCACA
                                || ||||||||    |||||
                                AG CTTCATGT    TGTGT
                                 C       TT__
GAM2832  LOC51219  5'  TCAGAAGTACACACGGCA    65507           CTT
                                TCAGGAGTACAT   GCA
                                ||||||||||||   |||
                                AGTCTTCATGTG   CGT
                                       TGC
GAM2833  DNASE1L1  3'  GCATATCTGCTGCACAAGTG   65510     CAAG    T
                                GCA    TGCT GCACAAGTG
                                |||    |||| |||||||||
                                CGT    ACGA CGTGTTCAC
                                  ATAG   _
GAM2833  IL1A     3'  TGCACAAGTGAGACAAGT    65511          CTTGC
                                TGCACAAGTG    ACAAGT
                                ||||||||||    ||||||
                                ACGTGTTCAC    TGTTCA
                                      TC___
GAM2833  AP3M1    3'  CTTGCTTAATGGCACAAGT    65512      ACA    CTT
                                CTTGC   AGTG   GCACAAGT
                                |||||   ||||   ||||||||
                                GAACG   TTAC   CGTGTTCA
                                  AA_   ____
GAM2833  FLJ10159  3'  TGTACAAGTGCACACAAGTG   65513    C       TT
                                TG ACAAGTGC  GCACAAGTG
                                || ||||||||  |||||||||
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                                AC TGTTCACG  TGTGTTCAC
                                 A      __
GAM2833  FLJ22282  3'  CTTGCAGAAGGGGGCGCAGGTG 65514       C   TGCTT  A  A
                                CTTGCA AAG    GC CA GTG
                                ||||||| |||    || || |||
                                GAACGT TTC    CG GT CAC
                                   C   CCC__  C  C
GAM2833  KIAA0232  3'  CTTGCACAGATGTTACCAGTG  65515        AG  C    A  A
                                CTTGCACA  TG TTGC CA GTG
                                ||||||||  || |||| || |||
                                GAACGTGT  AC AATG GT CAC
                                     CT  _   _ _
GAM2833  KIAA1204  3'  TTGAGTGAGTGCCTGGAGTG   65516     CACA       CACA
                                TTG   AGTGCTTG   AGTG
                                |||   ||||||||   ||||
                                AAC   TCACGGAC   TCAC
                                  TCAC       C___
GAM2833  LOC124152 3'  TTGCAAAGGCGGCCACAAGTG  65517      C   T  TTG
                                TTGCA AAG GC   CACAAGTG
                                ||||| ||| ||   ||||||||
                                AACGT TTC CG   GTGTTCAC
                                   _  _  CCG
GAM2834  C6       5'  TAGTACTTATCTACTACTATTT 65520        C    TCA
                                TAGTATT ATCT   TGCTATTT
                                ||||||| ||||   ||||||||
                                ATCATGA TAGA   ATGATAAA
                                    A   TG_
GAM2834  FGF5     3'  TAGCATTTCATTTTATGCTATT 65521        _  C  C
            TA                    TAGTATT CAT TT ATGCTATTTA
                                ||||||| ||| || ||||||||||
                                ATCGTAA GTA AA TACGATAAAT
                                    A  A  _
GAM2834  FGF5     3'  TAGCATTTCATTTTATGCTATT 65521        _  C  C
            TA                    TAGTATT CAT TT ATGCTATTTA
                                ||||||| ||| || ||||||||||
                                ATCGTAA GTA AA TACGATAAAT
                                    A  A  _
GAM2834  PRKAB1   3'  TAGCATTCATTTTTGGCT    65522          C  CAT
                                TAGTATTCAT TT   GCT
                                |||||||||| ||   |||
                                ATCGTAAGTA AA   CGA
                                     A  AC_
GAM2834  PTTG1IP  3'  TAGCTATTCCCCAATGCTATTT 65523     _   A   TC
            A                     TAGT ATTC TCT  ATGCTATTTA
                                |||| |||| |||  ||||||||||
                                ATCG TAAG GGG  TACGATAAAT
                                  A   _  T_
GAM2834  FLJ10058 3'  TAGTTTCATCTTTATAGTATTT 65524     A      C   C
            A                     TAGT TTCATCTT ATG TATTTA
                                |||| |||||||| ||| ||||||
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                                ATCA AAGTAGAA TAT ATAAAT
                                  _      A  C
GAM2834  MATR3    3'  GTATTCACTTCAGTAACT    65525       T    T__
                                GTATTCA CTTCA  GCT
                                ||||||| |||||  |||
                                CATAAGT GAAGT  TGA
                                   _    CAT
GAM2834  NUCKS    3'  TAGTGTTCATCTCAAATCT   65526     A     T  TG_
                                TAGT TTCATCT CA  CT
                                |||| ||||||| ||  ||
                                ATCA AAGTAGA GT  GA
                                  C      _ TTA
GAM2834  RAN      3'  TAGTGGTTTCCAAATGCTATTT 65527     ATTCA  TC
            A                    TAGT    TCT  ATGCTATTTA
                                ||||    |||  ||||||||||
                                ATCA    AGG  TACGATAAAT
                                  CCAA_  TT
GAM2834  LOC158450 5'  ATATTCATTTTCACCATTTA  65528       C  AT
                                GTATTCAT TTC  GCTATTTA
                                |||||||| |||  ||||||||
                                TATAAGTA AAG  TGGTAAAT
                                   A  __
GAM2834  LOC158504 5'  ATATTCATTTTCACCATTTA  65528       C  AT
                                GTATTCAT TTC  GCTATTTA
                                |||||||| |||  ||||||||
                                TATAAGTA AAG  TGGTAAAT
                                   A  __
GAM2834  LOC93333  5'  TAGTATTCTCTGATGGCTGTTT 65529       A  TCAT  A
                                TAGTATTC TCT   GCT TTT
                                |||||||| |||   ||| |||
                                ATCATAAG AGA   CGA AAA
                                   _  CTAC  C
GAM2835  OVOL1    3'  AGGCAGCTGGGAGGCAATCCTG 65532       ATACATTT
            G                    AGGCAGC       CAATCCTGG
                                |||||||       |||||||||
                                TCCGTCG       GTTAGGACC
                                   ACCCTCC_
GAM2835  TEAD3    3'  AGGTAGATGAATCCTCAATCCT 65533    C  CATACA
            GG                   AGG AG     TTTCAATCCTGG
                                ||| ||     ||||||||||||
                                TCC TC     GGAGTTAGGACC
                                  A  TACTTA
GAM2835  FLJ20234 3'  GGTCAGAGTTTTAATCCTGG  65534   _  CATACA  C
                                GG CAG     TTT AATCCTGG
                                || |||     ||| ||||||||
                                CC GTC     AAA TTAGGACC
                                 A  TC_____  A
GAM2835  FLJ21125 3'  GGCAGCATTGTTCCCACCTGG  65535       ACA   AAT
                                GGCAGCAT   TTTC   CCTGG
                                ||||||||   ||||   |||||
```

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                                CCGTCGTA  AAGG  GGACC
                                   AC_   GT_
GAM2835 FLJ22393 3' GGTAATGTACATTTCTCACCCA 65536   C CA     AAT TG
           G                    GG AG  TACATTTC  CC  G
                                || ||  ||||||||  ||  |
                                CC TT  ATGTAAAG  GG  C
                                 A  AC      AGT  GT
GAM2835 HGC6.1.1 3' AGGCAGCATGAAAACAGTCCTG 65537       ACATTT  A
           G                    AGGCAGCAT    CA TCCTGG
                                |||||||||    || ||||||
                                TCCGTCGTA    GT AGGACC
                                     CTTTT_  C
GAM2835 HSPC128  3' AGGCAGCAGATATTTTAACCTG 65538       TAC   C  T
                                AGGCAGCA  ATTT AA CCTG
                                ||||||||  |||| || ||||
                                TCCGTCGT  TAAA TT GGAC
                                     CTA   A  _
GAM2835 KCNS1    3' GACAGCATGAGTGATCCTGG  65539       ACATTTCA
                                GGCAGCAT      ATCCTGG
                                ||||||||      |||||||
                                CTGTCGTA      TAGGACC
                                     CTCAC___
GAM2835 KIAA1297 3' GGCAGCATAGGGCACGATCTTG 65540       CATTTCA  C
           G                    GGCAGCATA     ATC TGG
                                |||||||||     ||| |||
                                CCGTCGTAT     TAG ACC
                                     CCCGTGC  A
GAM2835 KIAA1323 3' AAGCAGCATGCATTTCAAT   65541        A
                                AGGCAGCAT CATTTCAAT
                                ||||||||| |||||||||
                                TTCGTCGTA GTAAAGTTA
                                     C
GAM2835 MAPKAPK3 3' AGGCAGCAACGTGGTCCCTGG 65542       T ATTTCAA
                                AGGCAGCA AC     TCCTGG
                                |||||||| ||     ||||||
                                TCCGTCGT TG     GGGACC
                                    _ CACCA__
GAM2835 NPD009   5' GGAGGCATACATCACCACTTGG 65543   CA      _  ATCC
                                GG  GCATACATT TCA   TGG
                                ||  ||||||||| |||   |||
                                CC  CGTATGTAG GGT   ACC
                                 TC       T  GA__
GAM2835 POLM     3' GGCAGCATATCTGCCTG    65544       CATT  AAT
                                GGCAGCATA   TC  CCTG
                                |||||||||   ||  ||||
                                CCGTCGTAT   AG  GGAC
                                     _____ AC_
GAM2835 USP15    3' AGACAGCAAAAATTTTAATTTT 65545       TAC   C  CC
           GG                     AGGCAGCA  ATTT AAT  TGG
                                  ||||||||  |||| |||  |||
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                                TCTGTCGT   TAAA TTA  ACC
                                     TTT    A   AA
GAM2835  LOC144438 3'  AGGAGTATGCATTTCAATATGG 65546     C  C  A       CC
                                AGG AG AT CATTTCAAT  TGG
                                ||| || || |||||||||  |||
                                TCC TC TA GTAAAGTTA  ACC
                                  _  A  C        T_
GAM2835  LOC199718 5'  AGGCAGCATATGATCCTG    65547          CATTTCA
                                AGGCAGCATA      ATCCTG
                                ||||||||||      ||||||
                                TCCGTCGTAT      TAGGAC
                                      AC_____
GAM2835  LOC92997  5'  AGGCAGCAACATCCT      65548         T   TTTCAA
                                AGGCAGCA ACA     TCCT
                                ||||||||| |||     ||||
                                TCCGTCGT TGT     AGGA
                                   _  _______
GAM2836  BHLHB3    3'  TGCGGGATGAGCAAAACAGGAA 65551     TA      __   AA
                CTC                   TGC  GATGAGCG  GCA  GAACTC
                                ||| |||||||| |||  ||||||
                                ACG  CTACTCGT  TGT  CTTGAG
                                  CC       TT   C_
GAM2836  SMARCD2   3'  TGTAGGAATGGCAAAGAACT   65552    C   AT   C
                                TG TAG  GAG GGCAAAGAACT
                                || |||  ||| ||||||||||
                                AC ATC  CTT CCGTTTCTTGA
                                 _  __   A
GAM2836  CKAP4     3'  TGCAGAAGCAGAGAAC      65553     T   TG    CAA
                                TGC AGA  AGCGG   AGAAC
                                ||| |||  |||||   |||||
                                ACG TCT  TCGTC   TCTTG
                                  _  __    ___
GAM2836  DKKL1-pending 3'  TAGATGTAAGAAAGAACT    65554       AGC  C
                                TAGATG   GG AAAGAACT
                                ||||||   || ||||||||
                                ATCTAC   TC TTTCTTGA
                                    AT_  _
GAM2836  FLJ12455  3'  TGGTAGATGAGGCCAGGGCAGA 65555    C       _ ___    A
                G                    TG TAGATGAG C   GGCA AG
                                || |||||||| |   |||| ||
                                AC ATCTACTC G   CCGT TC
                                 C       C GTC    C
GAM2836  FLJ13614  3'  TGCTAAATTTCATGCAAAGGAC 65556        GAGCG     A
                TC                    TGCTAGAT    GCAAAG ACTC
                                ||||||||    |||||| ||||
                                ACGATTTA    CGTTTC TGAG
                                     AAGTA     C
GAM2836  GNG11     5'  TGCTAGATGAGGGTTAAG    65557          C  CA
                                TGCTAGATGAG GG  AAG
                                |||||||||| ||  |||
```

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                                ACGATCTACTC CC  TTC
                                      _ AA
GAM2836 KIAA1940 3' TAGATGTTCGAAAGAACT    65558      AG   CA
                                TAGATG  CGG  AAGAACT
                                ||||||  |||  |||||||
                                ATCTAC  GCT  TTCTTGA
                                   AA  __
GAM2836 LOC154094 3' TGCTAGATATTTACTGAAGA  65559        AGCG  A_
                                TGCTAGATG   GC  AAGA
                                |||||||||   ||  ||||
                                ACGATCTAT   TG  TTCT
                                     AAA_  AC
GAM2836 LOC220021 3' TGCTGGAGAGTGGCAAA     65560     A  T   C
                                TGCT GA GAG GGCAAA
                                |||| || ||| ||||||
                                ACGA CT CTC CCGTTT
                                  C _  A
GAM2836 LOC220522 3' AGCTGGGCAGCGAAGAACT   65561    A  A    A
                                AG TG GCGGC AAGAACT
                                || || ||||| |||||||
                                TC AC CGTCG TTCTTGA
                                 G  C    C
GAM2836 LOC254816 5' GCCAGTGAGCGGCGAAGGACTC 65562      A      A  A
                                GCTAG TGAGCGGC AAG ACTC
                                ||||| |||||||| ||| ||||
                                CGGTC ACTCGCCG TTC TGAG
                                   _      C  C
GAM2837 ACATN    5' TAGGTGCCCCCTGGAACGGC   65565          TAGA_
                                TAGGTGCCCCCT    GGT
                                ||||||||||||    |||
                                ATCCACGGGGGA    CCG
                                       CCTTG
GAM2837 FCGR2A   3' TAGGTATCTTCTTAGAAAGT   65566      CCCC     _
                                TAGGTG   CTTAGAG GT
                                ||||||   ||||||| ||
                                ATCCAT   GAATCTT CA
                                   AGAA      T
GAM2837 IL8RA    3' AGGTGCCTTCTTAGGAGGT    65567       CC    _
                                AGGTGCC  CTTAG AGGT
                                |||||||  ||||| ||||
                                TCCACGG  GAATC TCCA
                                    AA    C
GAM2837 ITGA6    3' TAGGTGCCTCCTCAGCTACAC  65568        C     AGG
                                TAGGTGCC CCTTAG   TACAC
                                |||||||| ||||||   |||||
                                ATCCACGG GGAGTC   ATGTG
                                    A     G__
GAM2837 MGAT5    5' GATGCCCCCTTGGGGGTA    65569          AGA
                                GGTGCCCCCTT   GGTA
                                ||||||||||   ||||
```

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                                CTACGGGGGAA  CCAT
                                     CCC
GAM2837 TIF1     3' TAAGTGCCTTCTTAATAGCA  65570       CC    A
                                TAGGTGCC CTTAG GGTA
                                |||||||| ||||| ||||
                                ATTCACGG GAATT TCGT
                                    AA    A
GAM2837 XPC      3' GGTGCCCCTCTAGTGGGC    65571       C   A_
                                GGTGCCCC TTAG GGT
                                |||||||| |||| |||
                                CCACGGGG GATC CCG
                                    A   AC
GAM2837 ABLIM    3' GGTAGTTCCCTTAAAGTACA  65572     CC_      G
                                GGTG  CCCTTAGAG TACA
                                ||||  ||||||||| ||||
                                CCAT  GGGAATTTC ATGT
                                  CAA       _
GAM2837 ABLIM    3' GGTAGTTCCCTTAAAGTACA  65572     CC_      G
                                GGTG  CCCTTAGAG TACA
                                ||||  ||||||||| ||||
                                CCAT  GGGAATTTC ATGT
                                  CAA       _
GAM2837 C20orf139 5' GATGCTCCCAGGTACAC    65573     C  TTAG
                                GGTGC CCC   AGGTACAC
                                ||||| |||   ||||||||
                                CTACG GGG   TCCATGTG
                                  A  _____
GAM2837 DKFZp547C176 3' TAGGTTGCTCTCTTGAAACACA 65574      _ CCC  A  GG
                                TAGGT GC  CTT GA  TACA
                                ||||| ||  ||| ||  ||||
                                ATCCA CG  GAA CT  GTGT
                                  A  AGA  _ TT
GAM2837 FLJ00001 3' TAGGTGCCCCCTGTGGGT    65575          TAGA
                                TAGGTGCCCCCT   GGT
                                ||||||||||||   |||
                                ATCCACGGGGGA   CCA
                                       CAC_
GAM2837 FLJ10815 3' AGGTGTCGGGGAGGTACACC  65576     CCCCCTTA
                                AGGTG      GAGGTACACC
                                |||||      ||||||||||
                                TCCAC      CTCCATGTGG
                                  AGCCC____
GAM2837 FLJ13855 3' TAGGTGCTCCTGTAAAGGTAC 65577       C  CT
                                TAGGTGC CC  TAGAGGTAC
                                ||||||| ||  |||||||||
                                ATCCACG GG  ATTTCCATG
                                    A  AC
GAM2837 PRO1596  5' GGTGCCCCCTTAATTTTGTAC 65578          AG__
                                GGTGCCCCCTTAG   GTAC
                                ||||||||||||   ||||
```

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                                CCACGGGGGAATT   CATG
                                      AAAA
GAM2837 SHANK3   3' GGTGCTCTCACAGGTACACC  65579     CCC   G
                                GGTGC  CTTA AGGTACACC
                                |||||  |||| |||||||||
                                CCACG  GAGT TCCATGTGG
                                   A__   G
GAM2837 ZDHHC1   3' TAGGGGCCCCTAAAGTGCAC  65580    T   CT   _
                                TAGG GCCCC  TAGAG GTAC
                                |||| |||||  ||||| ||||
                                ATCC CGGGG  ATTTC CGTG
                                  C    __    A
GAM2837 LOC147043 5' CAGGTGCCCTCTGTACAC   65581       C  TAGAG
                                TAGGTGCCC CT    GTACAC
                                ||||||||| ||    ||||||
                                GTCCACGGG GA    CATGTG
                                     A _____
GAM2837 LOC149837 3' TAGGTGCCCTTTAGAGGC   65582       CC
                                TAGGTGCCC  TTAGAGGT
                                |||||||||  ||||||||
                                ATCCACGGG  AATCTCCG
                                     A_
GAM2837 LOC257473 3' TAGGGGCCCCTAAAGTGCAC  65580    T   CT   _
                                TAGG GCCCC  TAGAG GTAC
                                |||| |||||  ||||| ||||
                                ATCC CGGGG  ATTTC CGTG
                                  C    __    A
GAM2837 LOC58486  5' GGTGCTCTCAGGTATGGTACAC 65583     CCC   A___
           C                     GGTGC  CTTAG   GGTACACC
                                |||||  |||||   ||||||||
                                CCACG  GAGTC   CCATGTGG
                                   A__    CATA
GAM2837 LOC92181  3' TAAGTGCCTTCTTGTCTGTAC  65584       CC  AGAG
                                TAGGTGCC  CTT   GTAC
                                ||||||||  |||   ||||
                                ATTCACGG  GAA   CATG
                                     AA  CAGA
GAM2838 AMFR     3' TAGAAAGTATTACAAAGA    65587       _  TG
                                TAGAAAGT TTA  AAGA
                                |||||||| |||  ||||
                                ATCTTTCA AAT  TTCT
                                     T  GT
GAM2838 AMFR     3' TAGAAAGTATTACAAAGA    65587       _  TG
                                TAGAAAGT TTA  AAGA
                                |||||||| |||  ||||
                                ATCTTTCA AAT  TTCT
                                     T  GT
GAM2838 CHST1    3' CAGGAAGGACACGAAGAT    65588    A  TT
                                TAG AAG  TATGAAGAT
                                ||| |||  |||||||||
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                                GTC TTC  GTGCTTCTA
                                  C   CT
GAM2838  ESRRBL1   3'  TAGAAAGTTGCTCAGGAAGAT  65589        ___  T
                                TAGAAAGT   TTA GAAGAT
                                ||||||||   ||| ||||||
                                ATCTTTCA   AGT CTTCTA
                                     ACG   C
GAM2838  FSTL1     3'  GAAAGTTTTTTATGAAGAT   65590       ___
                                GAAAGTT   TATGAAGAT
                                |||||||   |||||||||
                                CTTTCAA   ATACTTCTA
                                    AAA
GAM2838  KIF5C     3'  TAGAAGTCCTATAAAGAT    65591      AG
                                TAGAA  TTTATGAAGAT
                                |||||  ||||||||||
                                ATCTT  GGATATTTCTA
                                   CA
GAM2838  SACM2L    3'  CAGAAGTCCATGGAGAT     65592      A     A
                                TAGAA GTTTATG AGAT
                                ||||| ||||||| ||||
                                GTCTT CAGGTAC TCTA
                                   _     C
GAM2838  SACM2L    3'  CAGAAGTCCATGGAGAT     65592      A     A
                                TAGAA GTTTATG AGAT
                                ||||| ||||||| ||||
                                GTCTT CAGGTAC TCTA
                                   _     C
GAM2838  SLC2A3    3'  TAAAAAGCCATTGAAGAT    65593        TA
                                TAGAAAGTT  TGAAGAT
                                |||||||||  |||||||
                                ATTTTTCGG  ACTTCTA
                                     TA
GAM2838  DKFZp434C0328 5'  TAAAAAGTCTTCCATGAAGAT  65594        ___
                                TAGAAAGTT   TATGAAGAT
                                |||||||||   |||||||||
                                ATTTTTCAG   GTACTTCTA
                                     AAG
GAM2838  FLJ12994  3'  CAGAAAGTCCTACAGAGAT   65595        _  GA
                                TAGAAAGTT TAT  AGAT
                                ||||||||| |||  ||||
                                GTCTTTCAG ATG  TCTA
                                     G   TC
GAM2838  FLJ12994  3'  CAGAAAGTCCTACAGAGAT   65595        _  GA
                                TAGAAAGTT TAT  AGAT
                                ||||||||| |||  ||||
                                GTCTTTCAG ATG  TCTA
                                     G   TC
GAM2838  KIAA0009  3'  TAGAAAAACCATGAAGAT    65596       T
                                TAGAAAG TTATGAAGAT
                                ||||||| ||||||||||
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                                ATCTTTT GGTACTTCTA
                                    T
GAM2838  KIAA0368  3'  CAGAAAGCCTCTGAGAT     65597          A  A
                                TAGAAAGTTT TGA GAT
                                |||||||||| ||| |||
                                GTCTTTCGGA ACT CTA
                                     G  _
GAM2838  KIAA0625  3'  CAGAAAATACTGAAGAT     65598        TTA
                                TAGAAAGT  TGAAGAT
                                ||||||||  |||||||
                                GTCTTTTA  ACTTCTA
                                    TG_
GAM2838  KIAA1260  3'  TAGAACTCTATGAAGAT     65599       AG
                                TAGAA  TTTATGAAGAT
                                |||||  ||||||||||
                                ATCTT  AGATACTTCTA
                                   G_
GAM2838  KIAA1317  3'  TAGAAAGTGTTGTGAAGA    65600         _  A
                                TAGAAAGT TT TGAAGA
                                |||||||| || ||||||
                                ATCTTTCA AA ACTTCT
                                    C  C
GAM2838  KIAA1354  3'  TAGAAAGTATGAAAAT      65601         TT
                                TAGAAAGT  ATGAAGAT
                                ||||||||  ||||||||
                                ATCTTTCA  TACTTTTA
                                    __
GAM2838  MGC2747   5'  CAGAACATCATGAAGAT     65602       AGT
                                TAGAA   TTATGAAGAT
                                |||||   ||||||||||
                                GTCTT   AGTACTTCTA
                                   GT_
GAM2838  sdolf     3'  AGAAACTTGCATGAAGAT     65603       G  _
                                AGAAA TT TATGAAGAT
                                ||||| || |||||||||
                                TCTTT AA GTACTTCTA
                                   G  C
GAM2838  LOC144195 3'  TAAAAAGCCATTGAAGAT     65593         TA
                                TAGAAAGTT  TGAAGAT
                                |||||||||  |||||||
                                ATTTTTCGG  ACTTCTA
                                     TA
GAM2838  LOC145314 3'  TAGAAAGTTGAAGAC       65604         TTA
                                TAGAAAGT   TGAAGAT
                                ||||||||   |||||||
                                ATCTTTCA   ACTTCTG
                                    ___
GAM2838  LOC149628 3'  CAGAACACCATGAAGAT     65605       AGT
                                TAGAA   TTATGAAGAT
                                |||||   ||||||||||
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                                GTCTT  GGTACTTCTA
                                  GT_
GAM2838  LOC151098 5'  TAGAAAGTTCTGTAGAT    65606         A  A
                                TAGAAAGTTT TG AGAT
                                |||||||||| || ||||
                                ATCTTTCAAG AC TCTA
                                      _  A
GAM2838  LOC154313 3'  TAGAAAGTGCAATGAAGAT   65607        TT_
                                TAGAAAGT  ATGAAGAT
                                ||||||||  ||||||||
                                ATCTTTCA  TACTTCTA
                                    CGT
GAM2838  LOC157798 5'  CAGGAAGTTATGAAGAT    65608    A    T
                                TAG AAGTT ATGAAGAT
                                ||| ||||| ||||||||
                                GTC TTCAA TACTTCTA
                                  C   _
GAM2838  LOC157867 5'  TAGAAAATTCACCAGAT    65609          GA
                                TAGAAAGTTTAT  AGAT
                                ||||||||||||  ||||
                                ATCTTTTAAGTG  TCTA
                                      G_
GAM2838  LOC199692 3'  AGAAATTACTATGAAGAT   65610      GT_
                                AGAAA  TTATGAAGAT
                                |||||  ||||||||||
                                TCTTT  GATACTTCTA
                                  AAT
GAM2838  LOC219376 3'  AGAATAGCTTATGAGGAT   65611     _      A
                                AGAA AGTTTATGA GAT
                                |||| ||||||||| |||
                                TCTT TCGAATACT CTA
                                  A       C
GAM2838  LOC51270  3'  TAAAAAGTAAATAAAGAT   65612        TT
                                TAGAAAGT  ATGAAGAT
                                ||||||||  ||||||||
                                ATTTTTCA  TATTTCTA
                                    TT
GAM2839  ADCY7    3'  AATGTGTTTCTATGTTAT    65615       A  G
                                AATGTG TT TATGTTGT
                                |||||| || ||||||||
                                TTACAC AA ATACAATA
                                   A  G
GAM2839  EIF4E    3'  AATGTAATTATGATGTTACATT 65616        TG   T
                                AATGTGAT  TATG TGTTACATT
                                ||||||||  |||| |||||||||
                                TTACATTA  ATAC ACAATGTAA
                                    __   T
GAM2839  HAO1     3'  ATGTGATTGGAAATCTACATT  65617         TATGTTG
                                ATGTGATTG      TTACATT
                                |||||||||      |||||||
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                                TACACTAAC      GATGTAA
                                     CTTTA__
GAM2839  FLJ12619  3'  AATGTTATTTATACCTGTTACA 65618      GA_     G
              TT                   AATGT   TTGTAT TTGTTACATT
                                   |||||   |||||| ||||||||||
                                   TTACA   AATATG GACAATGTAA
                                     ATA     _
GAM2839  KIAA1900  3'  AATGTGATTATTAAGTTGTT   65619          AT_
                                   AATGTGATTGT   GTTGTT
                                   ||||||||||   ||||||
                                   TTACACTAATA   CAACAA
                                         ATT
GAM2839  KLF12     3'  AATGTGGTTTATGTTGCT    65620       ATTG
                                   AATGTG    TATGTTGTT
                                   ||||||    |||||||||
                                   TTACAC    ATACAACGA
                                      CAA_
GAM2839  KRTAP4-5  3'  AATGTGATTGTCTGTCATT   65621          A   TG
                                   AATGTGATTGT TGT  TT
                                   |||||||||| |||  ||
                                   TTACACTAACA ACA  AA
                                         G   GT
GAM2839  SFRS12    3'  AATCTGATTGTATTAGATTGC  65622     G       ___
                                   AAT TGATTGTAT   GTTGT
                                   ||| |||||||||   |||||
                                   TTA ACTAACATA   TAACG
                                     G        ATC
GAM2839  LOC153733 3'  AATGTCATTGTATGATTGTT   65623      G      _
                                   AATGT ATTGTATG TTGTT
                                   ||||| |||||||| |||||
                                   TTACA TAACATAC AACAA
                                      G       T
GAM2839  LOC221547 3'  ATGTGACTGTAGCAGTC     65624          T  T
                                   ATGTGATTGTA GT GTT
                                   |||||||||| || |||
                                   TACACTGACAT CG CAG
                                         _ T
GAM2839  LOC221895 3'  AATGTGATTTCATTTACAT   65625         GTATGTTG
                                   AATGTGATT       TTACAT
                                   |||||||||       ||||||
                                   TTACACTAA       AATGTA
                                        AGTA____
GAM2839  LOC257577 3'  ATGTGACTGTAGCAGTC     65624          T  T
                                   ATGTGATTGTA GT GTT
                                   |||||||||| || |||
                                   TACACTGACAT CG CAG
                                         _ T
GAM2840  UTY       3'  CCAGTTGCTTGACATA      65628       _  ATTT
                                   CTAGT GCT    TGACATA
                                   ||||| |||    |||||||
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                                GGTCA CGA    ACTGTAT
                                  A  _____
GAM2840  C20orf165 3'  CATATCTGGTGCTATTTCA    65629      C  A
                                TATA CT GTGCTATTTTG
                                |||| || ||||||||||
                                GTAT GA CACGATAAAGT
                                  A  C
GAM2840  FLJ13114  3'  TATACCAGTGCTGTTTG     65630       T     AT
                                TATACC AGTGCT  TTTG
                                |||||| ||||||  ||||
                                ATATGG TCACGA  AAAC
                                   _     C_
GAM2840  KIAA1466  3'  CTAGTGCCAGCCTGTTTTGATA 65631          _____     C
            TA                    CTAGTGCTA    TTTTGA ATA
                                |||||||||    |||||| |||
                                GATCACGGT    AAAACT TAT
                                     CGGAC     A
GAM2840  LOC122773 3'  TATATGTAGTGTTTTGACATA  65632     CC    CTA
                                TATA  TAGTG   TTTTGACATA
                                ||||  |||||   ||||||||||
                                ATAT  ATCAC   AAAACTGTAT
                                  AC    ___
GAM2840  LOC130026 3'  TAGCCGTTATTTTGACAT    65633      _ C
                                TAGT G TATTTTGACAT
                                |||| | ||||||||||
                                ATCG C ATAAAACTGTA
                                  G A
GAM2841  LAMC1     3'  TAAGGTATCATCTTGTAAA    65636     A      C
                                TAA GTATTATC TGTAAA
                                ||| |||||||| ||||||
                                ATT CATAGTAG ACATTT
                                  C       A
GAM2841  KIAA0227  3'  AGTTTATCCTAAGGAAATCGT  65637     A      T__
                                AGT TTATCCTG   AAATCGT
                                ||| ||||||||   |||||||
                                TCA AATAGGAT   TTTAGCA
                                  _       TCC
GAM2841  LOC133418 3'  TAAAGTATTTCTTGTCAAATC  65638         A  C  _
                                TAAAGTATT TC TGT AAATC
                                ||||||||| || ||| |||||
                                ATTTCATAA AG ACA TTTAG
                                     _ A   G
GAM2841  LOC138399 3'  TAAAGTATATATCCATGT     65639         _    _
                                TAAAGTAT TATCC TGT
                                |||||||| ||||| |||
                                ATTTCATA ATAGG ACA
                                     T    T
GAM2842  BPHL      3'  TTTCAATATGTCATTATT     65642       TA
                                TTTCA  ATGTCATTATT
                                |||||  ||||||||||
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                                AAAGT  TACAGTAATAA
                                   TA
GAM2842  HTR7     3'  TGTTTATTTCATCTCCATT   65643          AATG
                                TGTTTATTTCAT   TCATT
                                ||||||||||||  |||||
                                ACAAATAAAGTA   GGTAA
                                       GA__
GAM2842  HTR7     3'  TGTTTATTTCATCTCCATT   65643          AATG
                                TGTTTATTTCAT   TCATT
                                ||||||||||||  |||||
                                ACAAATAAAGTA   GGTAA
                                       GA__
GAM2842  PDGFRA   3'  TGTTTGTTTCTAATCCCATTAT 65644      A   A   G
              T                  TGTTT TTTC TAAT TCATTATT
                                ||||| |||| |||| ||||||||
                                ACAAA AAAG ATTA GGTAATAA
                                   C   _   G
GAM2842  PUM2     3'  GTTTATTTCATACAATGT    65645          __
                                GTTTATTTCATA  ATGT
                                ||||||||||||  ||||
                                CAAATAAAGTAT  TACA
                                       GT
GAM2842  FLJ11116 3'  TGTTTATTTTAAATGCCATT   65646        CAT
                                TGTTTATTT   AATGTCATT
                                |||||||||   |||||||||
                                ACAAATAAA   TTACGGTAA
                                      AT_
GAM2842  SFRS8    3'  TTTATTTCATAATACATT    65647          T
                                TTTATTTCATAATG CATT
                                |||||||||||||| ||||
                                AAATAAAGTATTAT GTAA
                                         _
GAM2842  LOC220477 5'  GCCCATTATAATGTCATTATT  65648       TC
                                GTTTATT  ATAATGTCATTATT
                                |||||||  ||||||||||||||
                                CGGGTAA  TATTACAGTAATAA
                                      __
GAM2843  ABL2     5'  TCCGCACCCGGCCTCCTCAC   65651     A  A    GC
                                TCCG AC CTGGC  CTCCTCAC
                                |||| || |||||  ||||||||
                                AGGC TG GGCCG  GAGGAGTG
                                  G  _    __
GAM2843  CNN1     5'  TCTGCACACTCTTCCCTCCTCA 65652    CGA    GGCG
              CA                   TC   ACACT    CCTCCTCACA
                                ||   |||||   ||||||||||
                                AG   TGTGA    GGAGGAGTGT
                                 ACG    GAAG
GAM2843  GABRE    3'  GAACACTGAGCATCAC      65653        _   CCTCC
                                GAACACTG GCG    TCAC
                                |||||||| |||    ||||
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                                CTTGTGAC CGT    AGTG
                                     T  _____
GAM2843  GABRE    3'  GAACACTGAGCATCAC     65653        _  CCTCC
                                GAACACTG GCG    TCAC
                                |||||||| |||    ||||
                                CTTGTGAC CGT    AGTG
                                     T  _____
GAM2843  GABRE    3'  GAACACTGAGCATCAC     65653        _  CCTCC
                                GAACACTG GCG    TCAC
                                |||||||| |||    ||||
                                CTTGTGAC CGT    AGTG
                                     T  _____
GAM2843  GABRE    3'  GAACACTGAGCATCAC     65653        _  CCTCC
                                GAACACTG GCG    TCAC
                                |||||||| |||    ||||
                                CTTGTGAC CGT    AGTG
                                     T  _____
GAM2843  HR       3'  TCCTGATGCCACCCTCTCCTCA 65654     GAACAC  G   ___
              CA                   TCC     TG CGCC   TCCTCACA
                                |||     || ||||  ||||||||
                                AGG     AC GTGG   AGGAGTGT
                                  ACT___  G    GAG
GAM2843  HYAL2    5'  CCCGGCTCAGCGCCTCCTC    65655      AACA  _
                                TCCG    CT GGCGCCTCCTC
                                ||||    || ||||||||||
                                GGGC    GA TCGCGGAGGAG
                                  C___  G
GAM2843  IL1F5    3'  TCTGACATCACCACCTCCTCA  65656    C  A  CT G
                                TC GA CA  G CGCCTCCTCA
                                || || ||  | ||||||||||
                                AG CT GT  T GTGGAGGAGT
                                 A  _  AG G
GAM2843  MAGEA12  5'  TCAGAACCTTGCCTCCTCAC   65657    C    A  GGC
                                TC GAAC CT   GCCTCCTCAC
                                || |||| ||   ||||||||||
                                AG CTTG GA   CGGAGGAGTG
                                 T    _  A__
GAM2843  MAGEA8   5'  CGAACCTTGCCTCCTCACA    65658      A  GGC
                                CGAAC CT   GCCTCCTCACA
                                ||||| ||   ||||||||||
                                GCTTG GA   CGGAGGAGTGT
                                   _  A__
GAM2843  PMCHL1   3'  GACACTGACGCTATTTCTTACA 65659    A       CTC__  C
                                GA CACTGGCGC    CT ACA
                                || |||||||||    || |||
                                CT GTGACTGCG    GA TGT
                                 _       ATAAA  A
GAM2843  D2S448   3'  TCCAATGACCTTCCTCAC    65660      ACAC   GCC
                                TCCGA   TGGC   TCCTCAC
                                |||||   ||||  |||||||
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                                AGGTT   ACTG  AGGAGTG
                                  _____   GA_
GAM2843  FLJ21125  3'  TCCAGGCAGCCTTCCTCAC   65661     AACACT  _   _
                                TCCG     GGC GCCT CCTCAC
                                ||||     ||| |||| ||||||
                                AGGT     CCG CGGA GGAGTG
                                  _______  T   A
GAM2843  FLJ22283  5'  CGAAGGCTGTTTCCTCACA   65662     CACT  GCC_
                                CGAA   GGC   TCCTCACA
                                ||||   |||   ||||||||
                                GCTT   CCG   AGGAGTGT
                                  ____  ACAA
GAM2843  HAAO     5'  CCCGGGCGCCTCCTCC      65663     AACACT        A
                                TCCG     GGCGCCTCCTC C
                                ||||     |||||||||||
                                GGGC     CCGCGGAGGAG G
                                  _______         C
GAM2843  HUMAGCGB  5'  CGGGCATCAGGTCCTCCTCACA 65664    AA  CT  CG
                                CG  CA  GG  CCTCCTCACA
                                ||  ||  ||  ||||||||||
                                GC  GT  TC  GGAGGAGTGT
                                 CC  AG  CA
GAM2843  KIAA0285  5'  TCCGGGGAGAGCCCTCCTCA   65665     AACACT  G
                                TCCG     GGC CCTCCTCA
                                ||||     ||| ||||||||
                                AGGC     TCG GGAGGAGT
                                  CCCTC_  _
GAM2843  KIAA0930  3'  TCCAGCACTGGCGTGCCATCGC 65666     AA      CCT  _  A
            A                    TCCG  CACTGGCG   CC TC CA
                                ||||  ||||||||  || || ||
                                AGGT  GTGACCGC   GG AG GT
                                  C_      AC_  T  C
GAM2843  MAGEA1   5'  CCTGAAAACCTTGCCTCCTCAC 65667   _  C  GGC
            A                    CC GAA ACT   GCCTCCTCACA
                                || ||| |||   ||||||||||
                                GG CTT TGG   CGGAGGAGTGT
                                 A  T  AA_
GAM2843  MAN1C1   3'  TCCAAGTCTTGTCTCCTCACA  65668     ACA  GGCGC
                                TCCGA  CT    CTCCTCACA
                                |||||  ||    |||||||||
                                AGGTT  GA    GAGGAGTGT
                                  CA_  ACA__
GAM2843  RNF40    3'  TCCGGGCACTGCCCTCAC    65669     AACACT    C_
                                TCCG     GGCGC  TCCTCAC
                                ||||     |||||  |||||||
                                AGGC     CCGTG  GGGAGTG
                                  _______    AC
GAM2843  TUBAL2   3'  TCCTGATTAGGCCTCCTCGCA  65670    GAACAC  C      A
                                TCC     TGG GCCTCCTC CA
                                |||     ||| |||||||| ||
```

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                                AGG      ATC CGGAGGAG GT
                                  ACTA__  _       C
GAM2843  LOC144571 5'  TCCGGTGGCGCCTCCT      65671      AACAC
                                TCCG     TGGCGCCTCCT
                                ||||     ||||||||||
                                AGGC     ACCGCGGAGGA
                                  C____
GAM2843  LOC144600 5'  TCCAGCACTGGCGTGCCATCGC 65666      AA       CCT  _  A
            A                    TCCG  CACTGGCG   CC TC CA
                                ||||  ||||||||   || || ||
                                AGGT  GTGACCGC   GG AG GT
                                  C_       AC_  T  C
GAM2843  LOC148137 3'  TCCAAACAACCCCTTTCTCACA 65672        CTG  G   C_
                                TCCGAACA   GC CCT  CTCACA
                                ||||||||   || |||  ||||||
                                AGGTTTGT   TG GGA  GAGTGT
                                     ___  G   AA
GAM2843  LOC168667 5'  TCCTGGCACTGGCGTAGAACAC 65673     GAA       CCTCCT
            A                    TCC   CACTGGCG     CACA
                                |||   ||||||||     ||||
                                AGG   GTGACCGC     GTGT
                                  ACC       ATCTT_
GAM2843  LOC200213 5'  TCCAGACCAGGGCCTCCTC    65674      A  ACT  C
                                TCCG AC   GG GCCTCCTC
                                |||| ||   || ||||||||
                                AGGT TG   CC CGGAGGAG
                                  C  GT_  _
GAM2843  LOC219401 3'  GAAGGCTGCCTCCTCA      65675     CACT  _
                                GAA    GGC GCCTCCTCA
                                |||    ||| |||||||||
                                CTT    CCG CGGAGGAGT
                                  _____  A
GAM2843  LOC221337 3'  CTGAGCACCCTTCCTCACA    65676     _    __
                                CTG GCGCC  TCCTCACA
                                ||| |||||  ||||||||
                                GAC CGTGG  AGGAGTGT
                                  T     GA
GAM2843  LOC254672 3'  GACACTGACGCTATTTCTTACA 65659     A       CTC__  C
                                GA CACTGGCGC     CT ACA
                                || |||||||||     || |||
                                CT GTGACTGCG     GA TGT
                                  _        ATAAA  A
GAM2843  LOC51125  5'  TCCGGACACCGGCGCCTGCT   65677      A         C
                                TCCG ACACTGGCGCCT CT
                                |||| |||||||||||| ||
                                AGGC TGTGGCCGCGGA GA
                                  C          C
GAM2843  LOC85415  3'  CCTGAACATGTTTGTTTCCTCA 65678    _    C  GCGCC_
            CA                    CC GAACA TG      TCCTCACA
                                || ||||| ||      ||||||||
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                                GG CTTGT AC      AGGAGTGT
                                 A    _ AAACAA
GAM2844  AXIN1    5'  GGGCGCCGCAGGGGCCCA    65681    T       A    G
                                GG GCGCCGCA GGGT CG
                                || |||||||| |||| ||
                                CC CGCGGCGT CCCG GT
                                 _       C    G
GAM2844  DFNA5    3'  AGGGTCCCAAGCAGGGGTGTGT 65682     TGCG ___  A    C
              TA                  AGG    CC   GCA GGGTG GTTA
                                |||    ||   ||| ||||| ||||
                                TCC    GG   CGT CCCAC CAAT
                                 CA__  GTT   C    A
GAM2844  BEX1     5'  AGGTGCGCCGCCGGGACAC    65683          AA   TG
                                AGGTGCGCCGC  GGG  C
                                ||||||||||  |||  |
                                TCCACGCGGCG  CCT  G
                                      GC   GT
GAM2844  HGC6.1.1  5'  AGGGCGCCGCAGGCTGATT    65684     T       A  G  C
                                AGG GCGCCGCA GG TG GTT
                                ||| |||||||| || || |||
                                TCC CGCGGCGT CC AC TAA
                                 _       _ G  _
GAM2844  LOC152860 5'  AAGGTGCGGCCGCGGGGTG    65685         _    AA
                                AAGGTGCG CCGC  GGGTG
                                |||||||| ||||  |||||
                                TTCCACGC GGCG  CCCAC
                                     C    C_
GAM2844  LOC161158 5'  AGGTGCGCCTGGGGTCCA     65686         GCAA    G
                                AGGTGCGCC    GGGT CG
                                |||||||||    |||| ||
                                TCCACGCGG    CCCA GT
                                      AC__    G
GAM2844  LOC222057 3'  AAAGTGTGCTGTGAGGCATTA  65687       C  CGCAA   T
                                AAGGTG GC     GGG GCGTTA
                                |||||| ||     ||| ||||||
                                TTTCAC CG     CTC CGTAAT
                                   A  ACA__   _
GAM2844  LOC257127 5'  GGTGCACCGTGAGGGGCCCTA  65688         CA    T  G
                                GGTGCGCCG  AGGG GC TTA
                                |||||||||  |||| || |||
                                CCACGTGGC  TCCC CG GAT
                                      AC    _ G
GAM2845  C20orf21  3'  TTCGCCCTCATTGTTTGT     65691       G    GTAAAA
                                TTCGC CTCA     TGTTTGT
                                ||||| ||||     |||||||
                                AAGCG GAGT     ACAAACA
                                  G    A_____
GAM2845  LEC3     3'  GCTTTGCTCTTATGTTTGTT   65692     ___    AGTAAA
                                GC   GCTC     ATGTTTGTT
                                ||   ||||     |||||||||
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                                CG  CGAG    TACAAACAA
                                 AAA   AA____
GAM2846 ADAM23   5' CGGCGCCCCCTTTCCCGGCTCG 65695   A     __   T
                                CG CGCCCCC  TCCC GTTTG
                                || |||||||  |||| |||||
                                GC GCGGGGG  AGGG CGAGC
                                 C      AA   C
GAM2846 FGF4     5' CCGGCGCCCCCTCCTACTCG   65696    A       C
                                TCG CGCCCCCTCC TGTTTG
                                ||| |||||||||| ||||||
                                GGC GCGGGGGAGG ATGAGC
                                  C       _
GAM2846 GTF2E2   5' TCGCCGCCCCCCTTCCTGC    65697    A      C
                                TCG CGCCCCCT CCTGT
                                ||| |||||||| |||||
                                AGC GCGGGGGA GGACG
                                  G       A
GAM2846 IFNAR2   3' TCGATGGCTCTTCCCTGTTT   65698    C_  CCCC
                                TCGA  GC   TCCCTGTTT
                                ||||  ||   |||||||||
                                AGCT  CG   AGGGACAAA
                                  AC  AGA_
GAM2846 LTBP2    5' TCGCGCCTCCTCCCTGT     65699    A   C
                                TCG CGCC CCTCCCTGT
                                ||| |||| |||||||||
                                AGC GCGG GGAGGGACA
                                  _   A
GAM2846 MAP3K14  3' TCGGCGTCCCCTGCCCCA    65700    A  C   _
                                TCG CG CCCCT CCCTG
                                ||| || ||||| |||||
                                AGC GC GGGGA GGGGT
                                  C  A    C
GAM2846 SMARCA3  5' TCGACGCCGTCTCCTTCTG   65701       CC   __
                                TCGACGCC  CTCC  CTG
                                ||||||||  ||||  |||
                                AGCTGCGG  GAGG  GAC
                                     CA    AA
GAM2846 SMARCA3  5' TCGACGCCGTCTCCTTCTG   65701       CC   __
                                TCGACGCC  CTCC  CTG
                                ||||||||  ||||  |||
                                AGCTGCGG  GAGG  GAC
                                     CA    AA
GAM2846 TARBP2   5' CCGCGCCCCCTCTCTCCCG   65702    A      ___
                                TCG CGCCCCCTC   CCTG
                                ||| |||||||||   ||||
                                GGC GCGGGGGAG   GGGC
                                  _       AGA
GAM2846 TARBP2   5' CCGCGCCCCCTCTCTCCCG   65702    A      ___
                                TCG CGCCCCCTC   CCTG
                                ||| |||||||||   ||||
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                                GGC GCGGGGGAG   GGGC
                                  _       AGA
GAM2846 CPVL     5' TCGGTGCTCCTCCCTGAGCCG 65703    AC  CC      TTT
                                TCG  GC  CCTCCCTG   GTCG
                                |||  ||  ||||||||   ||||
                                AGC  CG  GGAGGGAC   CGGC
                                  CA  A_      T__
GAM2846 KIAA1277 3' TCGGCGCCCCTCCCTTTTG   65704    A    C    G
                                TCG CGCCCC TCCCT TTTG
                                ||| |||||| ||||| ||||
                                AGC GCGGGG AGGGA AAAC
                                  C     _    _
GAM2846 LGI4     5' TCGGCCTTCCTCCCTGTTCG   65705    AC   C_
                                TCG  GCC  CCTCCCTGTTTG
                                |||  |||  ||||||||||||
                                AGC  CGG  GGAGGGACAAGC
                                  __   AA
GAM2846 PRO2389   5' TCGACGCCCCCACCTTATC    65706         T  CTGT
                                TCGACGCCCCC CC    TTGTC
                                |||||||||| ||    |||||
                                AGCTGCGGGGG GG    AATAG
                                       T _____
GAM2846 TAPBP-R   5' TCGAGTTCCCTCCTTGCCCACC 65707     CGCC     C    TG
              G                  TCGA    CCCTCC TGTT  TCG
                                ||||    ||||||  ||||  |||
                                AGCT    GGGAGG ACGG  GGC
                                  CAA_     A    GT
GAM2846 LOC152829 5' TCGGCGCATCCTCCCTGGGCG  65708     A   CC      TT
                                TCG CGC  CCTCCCTG  TG
                                ||| |||  ||||||||  ||
                                AGC GCG  GGAGGGAC  GC
                                  C   TA       CC
GAM2846 LOC157858 3' GCCTCCTCCCTGAGCTAT    65709     C       T_
                                GCC CCTCCCTG  TTGT
                                ||| ||||||||  ||||
                                CGG GGAGGGAC  GATA
                                  A       TC
GAM2846 LOC201911 3' TCGCGCTCCCTCCCTCCCT    65710     A  C      G
                                TCG CGC CCCTCCCT TTT
                                ||| ||| |||||||| |||
                                AGC GCG GGGAGGGA GGA
                                  _  A       G
GAM2846 LOC222488 3' TCGGCCGCCTCCTCCCGCTCG  65711     A_   C     T
                                TCG  CGCC CCTCCC GTTTG
                                |||  |||| |||||| |||||
                                AGC  GCGG GGAGGG CGAGC
                                  CG   A     _
GAM2846 LOC255759 5' TCGATGCCCCTTCCCCGCC    65712      C    C
                                TCGA GCCCC TCCCTGTT
                                |||| ||||| ||||||||
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                                AGCT CGGGG AGGGGCGG
                                  A    A
GAM2846 LOC91149 3' GATGCTCCTTCCCTGTCT    65713    C  C  C
                                GA GC CC TCCCTGTTT
                                || || || |||||||||
                                CT CG GG AGGGACAGA
                                 A  A  A
GAM2847 ATP2A3   3' CGGGACCCGGTGGGCAAG    65716        AATGAC   A
                                CGGGACCC     TGG TAAG
                                ||||||||     ||| ||||
                                GCCCTGGG     ACC GTTC
                                     CC_____   C
GAM2847 MX2      3' TACGGGACCCAAGGACTGGA   65717           T
                                TACGGGACCCAA GACTGGA
                                |||||||||||| |||||||
                                ATGCCCTGGGTT CTGACCT
                                       C
GAM2847 FLJ10932 3' TACGGGACCTATGAAGG     65718         CA    CT
                                TACGGGACC  ATGA  GG
                                |||||||||  ||||  ||
                                ATGCCCTGG  TACT  CC
                                     A_   T_
GAM2847 LOC147817 5' GGGACCCAGACTGTGGATAAG  65719         AT   __
                                GGGACCCA  GACT  GGATAAG
                                ||||||||  ||||  |||||||
                                CCCTGGGT  CTGA  CCTATTC
                                    __   CA
GAM2847 LOC91801 3' GGGACCAAATGGCTCAACA   65720       C   A  G
                                GGGACC AATG CT GATA
                                |||||| |||| || ||||
                                CCCTGG TTAC GA TTGT
                                   T   C  G
GAM2847 LOC92223 5' TACAGGACTCAGTGAATAAAT  65721         C  A   C
                                TACGGGAC CA TGA TGGAT
                                |||||||| || ||| |||||
                                ATGTCCTG GT ACT ATTTA
                                     A  C   T
GAM2848 RNF28    3' TCAGTTACCACCCCGTATG    65724        A      TGAA
                                TCAGTTA CCACTCT    TATG
                                ||||||| |||||||    ||||
                                AGTCAAT GGTGGGG    ATAC
                                    _      C___
GAM2848 RRM1     3' TTAACCACTCCCTGTATGC    65725           GAA
                                TTAACCACTCTT   TATGC
                                ||||||||||||   |||||
                                AATTGGTGAGGG   ATACG
                                       AC_
GAM2848 DKFZp761B1514 3' TCAGATAACTTTGTGAATATGC 65726      T    CACTCT
                                TCAG TAAC     TGAATATGC
                                |||| ||||     |||||||||
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                                AGTC ATTG     ACTTATACG
                                  T    AAAC__
GAM2848  FLJ12085  3'  TCAGTTAATGAAAATATG    65727        CCACTCTT
                                TCAGTTAA       GAATATG
                                ||||||||       |||||||
                                AGTCAATT       TTTATAC
                                     ACT_____
GAM2848  KIAA0472  3'  TCAGTGAGCTGCTGAATATGC  65728      TAACCA  C
                                TCAGT     CT TTGAATATGC
                                |||||     || ||||||||||
                                AGTCA     GA GACTTATACG
                                   CTC___  C
GAM2848  KIAA0766  3'  TCAGCTTGACCATTCTTGA   65729       A_   C
                                TCAGTT  ACCA TCTTGA
                                ||||||  |||| ||||||
                                AGTCGA  TGGT AGAACT
                                    AC    A
GAM2848  PAI-RBP1  3'  CCAGTTGACCATGTGTGAATAT 65730       A    CTCT
              GC                  TCAGTT ACCA    TGAATATGC
                                  ||||||| ||||    |||||||||
                                  GGTCAA TGGT    ACTTATACG
                                     C    ACAC
GAM2848  LOC152502 3'  CCAGTTGATCATGTGTGAATAT 65731       AAC  CTCT
              GC                  TCAGTT   CA    TGAATATGC
                                  ||||||   ||    |||||||||
                                  GGTCAA   GT    ACTTATACG
                                     CTA  ACAC
GAM2848  LOC221755 3'  TCAGTTAATTGCATTCTTGATG 65732        C__  C     ATA
              TGC                   TCAGTTAA   CA TCTTGA   TGC
                                    ||||||||   || ||||||   |||
                                    AGTCAATT   GT AGAACT   ACG
                                       AAC  A     AC_
GAM2849  LOC161003 3'  ACTGTTACATGAACAGT     65735         TCGC
                                GCTGTTATAT    GAACAGT
                                ||||||||||    |||||||
                                TGACAATGTA    CTTGTCA
                                      _____
GAM2849  LOC255231 3'  TCGCTGTTATATTGCACTAATG 65736           C   AAC
                                TCGCTGTTATATT GCG   AGTG
                                |||||||||||| |||   ||||
                                AGCGACAATATAA CGT   TTAC
                                      _   GA_
GAM2850  COLQ     3'  AGGTCTCAGGTTGGGCATGT   65739         CGA    A  C
                                AGGTCTCAG   GTTGG CA GT
                                |||||||||   ||||| || ||
                                TCCAGAGTC   CAACC GT CA
                                     ___    C  A
GAM2850  COLQ     3'  AGGTCTCAGGTTGGGCATGT   65739         CGA    A  C
                                AGGTCTCAG   GTTGG CA GT
                                |||||||||   ||||| || ||
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                                TCCAGAGTC  CAACC GT CA
                                     ___   C  A
GAM2850  COLQ    3'  AGGTCTCAGGTTGGGCATGT  65739       CGA   A  C
                                AGGTCTCAG  GTTGG CA GT
                                |||||||||  ||||| || ||
                                TCCAGAGTC  CAACC GT CA
                                     ___   C  A
GAM2850  COLQ    3'  AGGTCTCAGGTTGGGCATGT  65739       CGA   A  C
                                AGGTCTCAG  GTTGG CA GT
                                |||||||||  ||||| || ||
                                TCCAGAGTC  CAACC GT CA
                                     ___   C  A
GAM2850  COLQ    3'  AGGTCTCAGGTTGGGCATGT  65739       CGA   A  C
                                AGGTCTCAG  GTTGG CA GT
                                |||||||||  ||||| || ||
                                TCCAGAGTC  CAACC GT CA
                                     ___   C  A
GAM2850  COLQ    3'  AGGTCTCAGGTTGGGCATGT  65739       CGA   A  C
                                AGGTCTCAG  GTTGG CA GT
                                |||||||||  ||||| || ||
                                TCCAGAGTC  CAACC GT CA
                                     ___   C  A
GAM2850  KIAA1870  5'  AGGTCCCAGTGGGGACTGGTAC 65740        CGAGTT  ____
           GT                    AGGTCTCAG    GGAC   ACGT
                                 |||||||||    ||||   ||||
                                 TCCAGGGTC    CCTG   TGCA
                                      ACC___   ACCA
GAM2850  MY038   5'  AAGGTTCAGCGAGGAGAC   65741     C      TT
                                AAGGT TCAGCGAG  GGAC
                                |||||  ||||||||  ||||
                                TTCCA AGTCGCTC  TCTG
                                   _      C_
GAM2850  PARVA   3'  AAGGTCTCAGTCAGTTGA   65742       CG
                                AAGGTCTCAG  AGTTGG
                                ||||||||||  ||||||
                                TTCCAGAGTC  TCAACT
                                      AG
GAM2850  TRAF4   3'  AAGGTCTCAGTGACGTGCTG  65743       C  ___
                                AAGGTCTCAG GA   GTTG
                                |||||||||| ||   ||||
                                TTCCAGAGTC CT   CGAC
                                      A  GCA
GAM2850  LOC51093  5'  AAGGTGTCAGCGTCAGAGACAC 65744     C    AGTT
           GT                    AAGGT TCAGCG   GGACACGT
                                 |||||  ||||||   ||||||||
                                 TTCCA AGTCGC    TCTGTGCA
                                    C     AGTC
GAM2850  LOC93624  5'  GTCTCAGCTTCAAGACGCGT  65745       GAGTT   A
                                GTCTCAGC    GGAC CGT
                                ||||||||    |||| |||
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                                CAGAGTCG    TCTG GCA
                                    AAGT_   C
GAM2851  GPR34    3'  TGCTTGATTTTAATAACTACTT 65748        AC   TGA
                                TGCTTGATTT  AATA  TATTT
                                ||||||||||  ||||  |||||
                                ACGAACTAAA  TTAT  ATGAA
                                    A_   TG_
GAM2851  RNGTT    3'  TGTCTTGATTTCCTTGATATTT 65749   _     ACAATA
                                TG CTTGATTT    TGATATTT
                                || ||||||||    ||||||||
                                AC GAACTAAA    ACTATAAA
                                 A      GGA___
GAM2851  KLF12    3'  TGCTTGATTTGGCCAAAGATGA 65750        A__  T_
            TATTT                   TGCTTGATTT  CAA  ATGATATTT
                                ||||||||||  |||  |||||||||
                                ACGAACTAAA  GTT  TACTATAAA
                                    CCG   TC
GAM2851  mPA-PLA1 3'  TGTTTGATGTACAATGTGACAT 65751    C    T    A
                                TG TTGAT TACAAT TGATAT
                                || ||||| |||||| ||||||
                                AC AACTA ATGTTA ACTGTA
                                 A    C    C
GAM2851  TU12B1-TY 3'  TGTTTGCTTTACAACACAAT  65752    C  A      TG
                                TG TTG TTTACAATA  AT
                                || ||| |||||||||  ||
                                AC AAC AAATGTTGT  TA
                                 A  G       GT
GAM2852  BMP2     5'  GGCACCGGCGCAAAGTGG    65755      GTATA      C
                                GGCAT    GGCGCAAAG GG
                                |||||    ||||||||| ||
                                CCGTG    CCGCGTTTC CC
                                   G____       A
GAM2852  CELSR2   3'  TGGCCTGCCCGGGGCGCGGGGC 65756     A  ATA_    AAA
            GGG                   TGGC TGT   GGCGC   GCGGG
                                |||| |||   |||||  |||||
                                ACCG ACG   CCGCG   CGCCC
                                  G  GGCC    CCC
GAM2852  DRD3     3'  TGGCATGTCTGGCAGTGG    65757       ATA  GCAA  C
                                TGGCATGT   GGC   AG GG
                                ||||||||   |||   || ||
                                ACCGTACA   CCG   TC CC
                                    GA_   ____  A
GAM2852  WISP2    3'  TGTGTGTGTAGGCAGGGAGTGG 65758    GCA  A    CAA  C
            G                    TG   TGT TAGGCG   AG GGG
                                ||   ||| ||||||   || |||
                                AC   ACA ATCCGT   TC CCC
                                 AC_  C     CCC  A
GAM2852  STK25    3'  TGGCATGTGAGGCCCACGG   65759       AT   G AAA
                                TGGCATGT  AGGC C   GCGG
                                ||||||||  |||| |   ||||
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                                ACCGTACA  TCCG G   TGCC
                                    C_    G ___
GAM2852  STRAIT11499 5'  TGGCATGTGGGGGCTGGGCGGG 65760        ATA   GCAAA
                                TGGCATGT   GGC    GCGGG
                                ||||||||   |||    |||||
                                ACCGTACA   CCG    CGCCC
                                    CCC   ACC__
GAM2852  ZNF306    3'  TGGCATGTATGGCATG      65761          A    CAAAGC
                                TGGCATGTAT GGCG     G
                                |||||||||| ||||     |
                                ACCGTACATA CCGT     C
                                     _   A_____
GAM2853  LOC120864 5'  TTATATCAGTTTGGACCTTG   65764           CGTAG
                                TTGTATCAGTTT    TCTTG
                                ||||||||||||    |||||
                                AATATAGTCAAA    GGAAC
                                       CCT__
GAM2853  LOC199897 3'  GATTTGCAATTGTAGTCTT    65765     GTAT    TC
                                GATT    CAGTT  GTAGTCTT
                                ||||    |||||  ||||||||
                                CTAA    GTTAA  CATCAGAA
                                  AC__    __
GAM2854  AMD1      3'  GACAAGAAATATAAAATTTAG  65768           TAG__
                                GACAAGAAATATA    TAG
                                ||||||||||||    |||
                                CTGTTCTTTATAT    ATC
                                       TTTAA
GAM2854  CHRNA10   3'  GACAGGAAATGCAGCAG     65769     A    ATATA
                                GACA GAAAT    GTAGCAG
                                |||| |||||    |||||||
                                CTGT CTTTA    CGTCGTC
                                  C    _____
GAM2854  RRAS      3'  AGAAGGCACACAGTGGCAGT   65770     A_      A
                                AGAA  TATATAGT GCAGT
                                ||||  |||||||| |||||
                                TCTT  GTGTGTCA CGTCA
                                  CC       C
GAM2854  TRDN      3'  ACAAGAAATTTATAGCAG    65771         A
                                ACAAGAAAT TATAGTAG
                                ||||||||| ||||||||
                                TGTTCTTTA ATATCGTC
                                      A
GAM2854  ARSDR1    3'  TGACAAGAAGTACTGTGTAG   65772        A   ATA
                                TGACAAGAA TAT   GTAG
                                ||||||||| |||   ||||
                                ACTGTTCTT ATG   CATC
                                      C   ACA
GAM2854  KIAA0515  3'  TGGCAAGAAACATATAAAAG   65773    A          T
                                TG CAAGAAATATATAG AG
                                || ||||||||||||| ||
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                                AC GTTCTTTGTATATT TC
                                 C           T
GAM2854  KIAA0783  3'  TGACAAGACATGTATCCAG   65774       AATA  A  G_
                                TGACAAGA   TAT GTA  CAG
                                ||||||||   ||| |||  |||
                                ACTGTTCT   GTA CAT  GTC
                                     _____  _  AG
GAM2854  KIAA0802  3'  TGATGGCGAGGACACAGTAGCG 65775    CAA_  AAT       A
            GT                   TGA   GA  ATATAGTAGC GT
                                |||   ||  |||||||||| ||
                                ACT   CT  TGTGTCATCG CA
                                 ACCG  CC_       C
GAM2854  KIAA1643  3'  TGACATGGAACATGTAGCAGT  65776     AGAAAT   A
                                TGACA     ATAT GTAGCAGT
                                |||||     |||| ||||||||
                                ACTGT     TGTA CATCGTCA
                                   ACCT__   _
GAM2854  PDZD2    3'  TGGCAAGATGTAGTAGCAGT   65777    A    AATATA
                                TG CAAGA     TAGTAGCAGT
                                || |||||     ||||||||||
                                AC GTTCT     ATCATCGTCA
                                 C    AC____
GAM2855  ELMO2    3'  CCTATAGTAATGAAAATATATA 65780    _       CTT_
                                CC ATAGTAATG    TATATA
                                || |||||||||    ||||||
                                GG TATCATTAC    ATATAT
                                 A        TTTT
GAM2855  FLJ12903 3'  AGATCAGGTAATGCTTT     65781     C  TA
                                AGA CA  GTAATGCTTT
                                ||| ||  ||||||||||
                                TCT GT  CATTACGAAA
                                 A  C_
GAM2855  FLJ13940 3'  AGGCCACAGCACTTTAT     65782    A     AAT
                                AG CCATAGT   GCTTTAT
                                || |||||||   |||||||
                                TC GGTGTCG   TGAAATA
                                 C      ___
GAM2855  GPR64    3'  CAACAGTTGCTTTATAT     65783    _   AA
                                CA TAGT  TGCTTTATAT
                                || ||||  ||||||||||
                                GT GTCA  ACGAAATATA
                                 T   __
GAM2856  ADCY6    3'  GGTACGGGGATCCAGGGT    65786         CA   C
                                GGTACGGGGA  CGG GT
                                ||||||||||  ||| ||
                                CCATGCCCCT  GTC CA
                                      AG   C
GAM2856  ADCY6    3'  GGTACGGGGATCCAGGGT    65786         CA   C
                                GGTACGGGGA  CGG GT
                                ||||||||||  ||| ||
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                                CCATGCCCCT  GTC CA
                                      AG   C
GAM2856  AP2B1    3'  GGGTGAGGGGACAGCAT     65787      AC       CG
                                GGGT  GGGGACA  GCGT
                                ||||  |||||||  ||||
                                CCCA  CCCCTGT  CGTA
                                  CT       __
GAM2856  APOE     3'  GGGCGGGGACAGGGT       65788     TA       C  C
                                GGG  CGGGGACA GG GT
                                |||  |||||||| || ||
                                CCC  GCCCCTGT CC CA
                                  __       _ _
GAM2856  BMP1     3'  GGGCACGGGGAAGGGT       65789           CAC  C
                                GGGTACGGGGA   GG GT
                                ||||||||||   || ||
                                CCCGTGCCCCT   CC CA
                                      T__  _
GAM2856  BMP1     3'  GGGCACGGGGAAGGGT       65789           CAC  C
                                GGGTACGGGGA   GG GT
                                ||||||||||   || ||
                                CCCGTGCCCCT   CC CA
                                      T__  _
GAM2856  C1QG     5'  AGGCAAGAGGACACGGTGT    65790       C         C
                                GGGTA GGGGACACGG GT
                                |||||  |||||||||| ||
                                TCCGT CTCCTGTGCC CA
                                   T         A
GAM2856  CALM1    5'  GAGTAACGGCACGGCGT      65791       _   GGA
                                GGGTA CGG   CACGGCGT
                                |||||  |||   ||||||||
                                CTCAT GCC   GTGCCGCA
                                   T  ____
GAM2856  FXYD6    3'  GGGTGGGGGACACACA       65792      AC        G
                                GGGT  GGGGACACG CG
                                ||||  ||||||||| ||
                                CCCA  CCCCTGTGT GT
                                  C_         _
GAM2856  IGF2     3'  GGGCACGGGGACTGGGT      65793           AC  C
                                GGGTACGGGGAC  GG GT
                                ||||||||||||  || ||
                                CCCGTGCCCCTG  CC CA
                                      A_  _
GAM2856  KIF5C    5'  GGGCACGGGGATGGGT       65794           CAC  C
                                GGGTACGGGGA   GG GT
                                ||||||||||   || ||
                                CCCGTGCCCCT   CC CA
                                      A__  _
GAM2856  LASS1    3'  GGGCACGGGGGCGCGGGT     65795          ACA   C
                                GGGTACGGGG   CGG GT
                                |||||||||   ||| ||
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                                CCCGTGCCCC  GCC CA
                                     CGC  _
GAM2856 NONO     5' GGGTACAAAATGGCGT     65796        ACAC
                                GGGTACGGGG  GGCGT
                                ||||||||||  |||||
                                CCCATGTTTT  CCGCA
                                     A___
GAM2856 POLG     5' AGGCCCACGGCACGGCGT   65797    TA  G  A
                                GGG  CG GG CACGGCGT
                                |||  || || ||||||||
                                TCC  GT CC GTGCCGCA
                                  GG  G  _
GAM2856 PPP2R5A  5' GGGCACGGGGGTGCGGGT   65798        ACA  C
                                GGGTACGGGG  CGG GT
                                ||||||||||  ||| ||
                                CCCGTGCCCC  GCC CA
                                     CAC  _
GAM2856 SH3GL1   3' GGGCGGGGACACGGGT     65799    TA       C
                                GGG  CGGGGACACGG GT
                                |||  ||||||||||| ||
                                CCC  GCCCCTGTGCC CA
                                  __        _
GAM2856 C20orf80 5' GGGTACGGGGCCACGGGT   65800        A    C
                                GGGTACGGGG CACGG GT
                                |||||||||| ||||| ||
                                CCCATGCCCC GTGCC CA
                                     G   _
GAM2856 FLJ20320 5' GGGTTCCTAAGCACGGCGT  65801    ACG_  A
                                GGGT   GGG CACGGCGT
                                ||||   ||| ||||||||
                                CCCA   TTC GTGCCGCA
                                  AGGA  _
GAM2856 FLJ20699 3' GGGACGGGGACAGGCA     65802    T       C
                                GGG ACGGGGACA GGCG
                                ||| |||||||| ||||
                                CCC TGCCCCTGT CCGT
                                  _       _
GAM2856 FLJ30791 5' GGGACGGGGCCCAGCGT    65803    T    ACA
                                GGG ACGGGG  CGGCGT
                                ||| ||||||  ||||||
                                CCC TGCCCC  GTCGCA
                                  _    GG_
GAM2856 HSA243666 3' GGGTAAGGACACAGGT    65804     CG       C
                                GGGTA  GGGACACGG GT
                                |||||  |||||||| ||
                                CCCAT  TCCTGTGTC CA
                                  __       _
GAM2856 HU-K4    3' GGGTGCGGGGACAGGGACCGT 65805     A      C __
                                GGGT CGGGGACA GG  CGT
                                |||| |||||||| ||  |||
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                                CCCA GCCCCTGT CC  GCA
                                  C       C  TG
GAM2856 KIAA1056 3' GGGTAGGAACACCGGTGT    65806      AC       _  C
                                GGGT  GGGGACAC GG GT
                                ||||  |||||||| || ||
                                CCCA  TCCTTGTG CC CA
                                  __       G  A
GAM2856 KIAA1924 3' GGGCACGGGGGGCGGCAT     65807          ACA
                                GGGTACGGGG   CGGCGT
                                ||||||||||   ||||||
                                CCCGTGCCCC   GCCGTA
                                     C__
GAM2856 MGC11271 5' GGGTACAGGGGACACCGT    65808       _       GG
                                GGGTAC GGGGACAC  CGT
                                |||||| ||||||||  |||
                                CCCATG CCCCTGTG  GCA
                                   T      __
GAM2856 RNPS1    3' GAGTACAGTGGTGGGGTGCGGT 65809      _______   ACA   C  III
             GTA                  GTAC     GGGG   CGG GT   A
                                ||||     ||||   ||| ||   |
                                CATG     CCCC   GCC CA   T
                                  TCACCA    AC_   A  III
GAM2856 RNPS1    3' GAGTACAGTGGTGGGGTGCGGT 65809      _______   ACA   C  III
             GTA                  GTAC     GGGG   CGG GT   A
                                ||||     ||||   ||| ||   |
                                CATG     CCCC   GCC CA   T
                                  TCACCA    AC_   A  III
GAM2856 SIAT4B   5' GGGCCAGCCACGGCGT      65810      A   GGA
                                GGGT CGG   CACGGCGT
                                |||| |||   ||||||||
                                CCCG GTC   GTGCCGCA
                                  _   G__
GAM2856 SSB-4    3' AGGAGGGGCACGGCGT      65811      TAC    A
                                GGG   GGGG CACGGCGT
                                |||   |||| ||||||||
                                TCC   CCCC GTGCCGCA
                                  T__    _
GAM2856 TED      3' GGGACGGGGACAGGGT      65812      T       C  C
                                GGG ACGGGGACA GG GT
                                ||| ||||||||| || ||
                                CCC TGCCCCTGT CC CA
                                  _        _ _
GAM2856 LOC147958 3' GAGTACGGGGGCGGACCGT    65813          ACA  __
                                GGGTACGGGG   CGG  CGT
                                ||||||||||   |||  |||
                                CTCATGCCCC   GCC  GCA
                                     ____  TG
GAM2856 LOC164714 5' GGCTACGGGGACACCGGTGT   65814    G         _  C
                                GG TACGGGGACAC GG GT
                                || ||||||||||| || ||
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                                CC ATGCCCCTGTG CC CA
                                 G         G  A
GAM2856  LOC200942 5'  GGGTACGGGGTCCGCCGT    65815          ACA  G
                                GGGTACGGGG   CG CGT
                                ||||||||||   || |||
                                CCCATGCCCC   GC GCA
                                     AG_  G
GAM2856  LOC254057 5'  GGGCACGGGGAGCCCGCGT    65816          CACG
                                GGGTACGGGGA    GCGT
                                ||||||||||    ||||
                                CCCGTGCCCCT    CGCA
                                      CGGG
GAM2856  LOC254722 5'  GAGTGCGGGGACAGCCAGGTGT 65817      A       C___  C
                                GGGT CGGGGACA    GG GT
                                |||| ||||||||    || ||
                                CTCA GCCCCTGT    CC CA
                                  C       CGGT  A
GAM2856  LOC92421  3'  GGGTACAGGGATACACGT    65818          C   G
                                GGGTACGGGGA ACG CGT
                                |||||||||| ||| |||
                                CCCATGTCCCT TGT GCA
                                      A  _
GAM2857  AVPR1A    5'  GAAAGGACCTGCCTTTCCTG   65821      __   TTATA
                                GAGA  ATCT    CCTTTCCTG
                                ||||  ||||    |||||||||
                                CTTT  TGGA    GGAAAGGAC
                                  CC    C____
GAM2857  BMX       3'  GAATCTTTTGTTTCCTG     65822         ATACC
                                GAATCTTT    TTTCCTG
                                ||||||||    |||||||
                                CTTAGAAA    AAAGGAC
                                     AC___
GAM2857  CAPON     3'  AGAATCTCAATACTTTCCTG   65823         T   C
                                AGAATCTT ATAC TTTCCTG
                                |||||||| |||| |||||||
                                TCTTAGAG TATG AAAGGAC
                                     T   _
GAM2857  NP        3'  ACAGGAATCTTTTCCTTTC    65824     A       ATA
                                ACG GAATCTTT   CCTTTC
                                ||| ||||||||   ||||||
                                TGT CTTAGAAA   GGAAAG
                                  C       A__
GAM2857  AUTL1     3'  GAGAATCTAGTGACATCTTTC  65825         TT__   C
                                GAGAATCT    ATA CTTTC
                                ||||||||    ||| |||||
                                CTCTTAGA    TGT GAAAG
                                     TCAC   A
GAM2857  KIAA1463  3'  AGAATTCCCCTTTCCT      65826       _  TTATA
                                AGAAT CT    CCTTTCCT
                                ||||| ||    ||||||||
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                                TCTTA GG    GGAAAGGA
                                  A _____
GAM2857 KNTC1    5' CAGGAACCACTGTCTTTCCTG 65827    A    TTTATAC
                                CG GAATC     CTTTCCTG
                                || |||||     ||||||||
                                GT CTTGG     GAAAGGAC
                                 C    TGACA__
GAM2857 ZNF263   3' GAATCTCTCTTTCCT      65828        ATAC
                                GAATCTTT   CTTTCCT
                                ||||||||   |||||||
                                CTTAGAGA   GAAAGGA
                                     ____
GAM2857 LOC152348 3' GAGGGCTCCACTTTCCT    65829    AAT    TAC
                                GAG  CTTTA  CTTTCCT
                                |||  |||||  |||||||
                                CTC  GAGGT  GAAAGGA
                                  CC_   ___
GAM2857 LOC205418 5' CAAGGACCCTGTCTTTCCTG  65830    A    TATAC
                                CGAG ATCTT    CTTTCCTG
                                |||| |||||    ||||||||
                                GTTC TGGGA    GAAAGGAC
                                  C    CA___
GAM2857 LOC221393 3' ACAAGAATTTTTTTTTCCT   65831       C   ATACC
                                ACGAGAAT TTT    TTTCCT
                                |||||||| |||    ||||||
                                TGTTCTTA AAA    AAAGGA
                                    A  A____
GAM2858 BMP4     3' TGTAGTGTGTGGGTGA     65834       TACA  TA
                                TGTGGTGT   GT  GGTGA
                                ||||||||   ||  |||||
                                ACATCACA   CA  CCACT
                                    _____ C_
GAM2858 BMP4     3' TGTAGTGTGTGGGTGA     65834       TACA  TA
                                TGTGGTGT   GT  GGTGA
                                ||||||||   ||  |||||
                                ACATCACA   CA  CCACT
                                    _____ C_
GAM2858 BMP4     3' TGTAGTGTGTGGGTGA     65834       TACA  TA
                                TGTGGTGT   GT  GGTGA
                                ||||||||   ||  |||||
                                ACATCACA   CA  CCACT
                                    _____ C_
GAM2858 FLJ20127 5' GTGGTGTTCACGTGGGTGAA  65835       ACA  TA
                                GTGGTGTT   GT  GGTGAA
                                ||||||||   ||  ||||||
                                CACCACAA   CA  CCACTT
                                    GTG  C_
GAM2858 FLJ21870 3' GTGGTGTTAGAGATAGGTG   65836       C  T
                                GTGGTGTTA AG TAGGTG
                                ||||||||| || ||||||
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                                CACCACAAT TC ATCCAC
                                     C  T
GAM2858  FLJ22002  3'  TGTGGTGTTGCATGCCTGTAA  65837        A  GTTAG
                                TGTGGTGTT CA    GTGA
                                ||||||||| ||    ||||
                                ACACCACAA GT    CATT
                                     C  ACGGA
GAM2858  KIAA1577  3'  TGTGGTGTAGTGGTG      65838        TAC   TA
                                TGTGGTGT   AGT  GGTG
                                ||||||||   |||  ||||
                                ACACCACA   TCA  CCAC
                                     ___   __
GAM2858  KIAA1615  3'  TGTGTGTGTGTTATGGTG    65839     _   TACA   _
                                TGTG GTGT    GTTA GGTG
                                |||| ||||    |||| ||||
                                ACAC CACA    CAAT CCAC
                                  A   ____    A
GAM2858  MGC14801  3'  TATGTGGTTTACAGAGCATCTG 65840        G     T_  GG
            AA                    TATGTGGT TTACAG  TA  TGAA
                                |||||||| ||||||  ||  ||||
                                ATACACCA AATGTC  GT  ACTT
                                     _     TC  AG
GAM2858  MGC26641  3'  GTGGTGTTACAGGTTAGA    65841          _
                                GTGGTGTTACAG TTAGG
                                |||||||||||| |||||
                                CACCACAATGTC AATCT
                                       C
GAM2858  MRAS     3'  TGGTTTCAGTGCAGTTAGGTG  65842     G  ___
                                TGGT TTA   CAGTTAGGTG
                                |||| |||   ||||||||||
                                ACCA AGT   GTCAATCCAC
                                  A   CAC
GAM2858  P101-PI3K 3'  TGTGGTGTTTGCAGGGA     65843        ACA  T   T
                                TGTGGTGTT   GT AGG GA
                                |||||||||   || ||| ||
                                ACACCACAA   CG TCC CT
                                     A__  _   _
GAM2858  RFX3     5'  TGTGGTGTTGTTGGTG      65844        ACA   A
                                TGTGGTGTT   GTT GGTG
                                |||||||||   ||| ||||
                                ACACCACAA   CAA CCAC
                                     ___   _
GAM2858  RFX3     5'  TGTGGTGTTGTTGGTG      65844        ACA   A
                                TGTGGTGTT   GTT GGTG
                                |||||||||   ||| ||||
                                ACACCACAA   CAA CCAC
                                     ___   _
GAM2858  LOC120400 5'  GTGGTGTTCACATGGGTGAA  65845        _   GTTA
                                GTGGTGT TACA    GGTGAA
                                ||||||| ||||    ||||||
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                                CACCACA GTGT   CCACTT
                                    A   AC__
GAM2858 LOC144571 3' TGTGGTGCTTATAGAATAGA  65846       AC_ T_
                                TGTGGTGTT  AG  TAGG
                                |||||||||  ||  ||||
                                ACACCACGA  TC  ATCT
                                    ATA  TT
GAM2858 LOC253639 3' TGTAGTGTTGCACATATGA   65847       A  GTTAG
                                TGTGGTGTT CA   GTGA
                                ||||||||| ||   ||||
                                ACATCACAA GT   TACT
                                    C  GTA__
GAM2858 LOC92609  5' TGTGGGTGTTTCTCGTTAGGTG 65848     _   ACA_
                                TGTGG TGTT   GTTAGGTG
                                ||||| ||||   ||||||||
                                ACACC ACAA   CAATCCAC
                                  C   AGAG
GAM2859 DLX4    3' ATATAAGGCTGAGGTCCTTGAT 65851       CA   A__
          TT                    GTATAAGGC  AGGTT  GATTT
                                |||||||||  |||||  |||||
                                TATATTCCG  TCCAG  CTAAA
                                    AC    GAA
GAM2859 DLX4    3' ATATAAGGCTGAGGTCCTTGAT 65851       CA   A__
          TT                    GTATAAGGC  AGGTT  GATTT
                                |||||||||  |||||  |||||
                                TATATTCCG  TCCAG  CTAAA
                                    AC    GAA
GAM2859 N33     3' TAGTATAAAGTCAGGAACAG  65852       CCA  T_
                                TAGTATAAGG  AGG  TAG
                                ||||||||||  |||  |||
                                ATCATATTTC  TCC  GTC
                                     AG_  TT
GAM2859 FLJ12488 3' TAGTAAAGGCCAAGGTC    65853     T
                                TAGTA AAGGCCAAGGTT
                                ||||| ||||||||||||
                                ATCAT TTCCGGTTCCAG
                                  _
GAM2859 KIAA0470 3' TAGTAAAAGGCCAAATGTT   65854     T      _
                                TAGTA AAGGCCAAG GTT
                                ||||| ||||||||| |||
                                ATCAT TTCCGGTTT CAA
                                  T       A
GAM2859 KIAA0781 3' TAGTGTAAGGTCAAAGTAG   65855    A   C    T
                                TAGT TAAGG CAAGGT AG
                                |||| ||||| |||||| ||
                                ATCA ATTCC GTTTCA TC
                                  C   A    _
GAM2859 LOC220766 3' TAGTAAAAGGCCAAATGTT  65854     T      _
                                TAGTA AAGGCCAAG GTT
                                ||||| ||||||||| |||
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                                ATCAT TTCCGGTTT CAA
                                   T       A
GAM2860 ABCB10   3' TCAATCTTTAACAGCAGGCAA 65858       A       CA
                                TCAATC TTTAATGGC  AGGCAA
                                |||||| |||||||||  ||||||
                                AGTTAG AAATTGTCG  TCCGTT
                                   _       __
GAM2860 EHHADH   3' TTTAACTACACAAGGCAA    65859       G  _
                                TTTAAT GC CAAGGCAA
                                |||||| || ||||||||
                                AAATTG TG GTTCCGTT
                                   A  T
GAM2860 LENG4    3' TCCGTCACGAAGGCCAAGGCAA 65860    AA   TTAAT
                                TC  TCAT    GGCCAAGGCAA
                                ||  ||||    ||||||||||
                                AG  AGTG    CCGGTTCCGTT
                                 GC    CTT__
GAM2860 PPP1R2   3' ATCATTTAATTCTTGGCAA   65861         GGCCAA
                                ATCATTTAAT     GGCAA
                                ||||||||||     |||||
                                TAGTAAATTA     CCGTT
                                     AGAA__
GAM2860 SDHD     3' CCATTATTCCCAAGGCA     65862      TA  GG
                                TCATT  AT  CCAAGGCA
                                |||||  ||  ||||||||
                                GGTAA  TA  GGTTCCGT
                                   __  AG
GAM2860 SLC12A7  3' TCATGCTTAGCCAAGGCA    65863     TTAA
                                TCAT    TGGCCAAGGCA
                                ||||    ||||||||||
                                AGTA    ATCGGTTCCGT
                                  CGA_
GAM2860 DCOHM    3' TCAATATATTAACCGAGGCA   65864     TT_  A    A
                                TCA   TA TGGCC AGGCA
                                |||   || ||||| |||||
                                AGT   AT ATTGG TCCGT
                                  TAT  A    C
GAM2860 FLJ20502 3' TCAAATATTTAATAAATGAGGC 65865     TC       CCA
           AA                     TCAA  ATTTAATGG   AGGCAA
                                ||||  |||||||||   ||||||
                                AGTT  TAAATTATT   TCCGTT
                                   TA       TAC
GAM2860 FLJ23467 3' TCAACCATTTTGTCAAGG    65866         AA  GC
                                TCAATCATTT  TG  CAAGG
                                ||||||||||  ||  |||||
                                AGTTGGTAAA  AC  GTTCC
                                     __  A_
GAM2860 FLJ32894 3' TCAATCATTAGATGGAAGTGG 65867         TA   CCAA
                                TCAATCATT  ATGG   GG
                                |||||||||  ||||   ||
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                                AGTTAGTAA  TACC   CC
                                     TC   TTCA
GAM2860  HCA127    3'  TCAATGACTCTGGTCAAGG   65868     C   AA  C
                                TCAAT ATTT  TGG CAAGG
                                ||||| ||||  ||| |||||
                                AGTTA TGAG  ACC GTTCC
                                   C   __  A
GAM2860  KIAA0252  3'  TCAATGGGTGGGCCAAGGCA  65869     CATTTAAT
                                TCAAT      GGCCAAGGCA
                                |||||      ||||||||||
                                AGTTA      CCGGTTCCGT
                                   CCCAC___
GAM2860  KIAA1319  3'  TCAATCAATCACTGGGGCA   65870      T  A  CCAA
                                TCAATCA TTA TGG   GGCA
                                ||||||| ||| |||   ||||
                                AGTTAGT AGT ACC   CCGT
                                    T  G  ____
GAM2860  LRRC5     3'  AATCATTTACTTTAGCAGGCAA 65871       A__   CA
                                AATCATTTA  TGGC  AGGCAA
                                |||||||||  ||||  ||||||
                                TTAGTAAAT  ATCG  TCCGTT
                                     GAA   __
GAM2860  SMARCF1   3'  CCACCTTGGCCAAGGCAA    65872      AA
                                TCATTT  TGGCCAAGGCAA
                                ||||||  ||||||||||||
                                GGTGGA  ACCGGTTCCGTT
                                  __
GAM2860  LOC124801 3'  TCAATCATTCAGAAGGCA    65873        ATGGCC
                                TCAATCATTTA     AAGGCA
                                ||||||||||     ||||||
                                AGTTAGTAAGT     TTCCGT
                                      C_____
GAM2860  LOC145623 3'  TCAATCATTTAGGTGGCA    65874        AT  CCAA
                                TCAATCATTTA  GG   GGCA
                                ||||||||||  ||   ||||
                                AGTTAGTAAAT  CC   CCGT
                                     __ A___
GAM2860  LOC153743 3'  ATCATTTAATTCTTGGCAA   65861        GGCCAA
                                ATCATTTAAT     GGCAA
                                |||||||||     |||||
                                TAGTAAATTA     CCGTT
                                     AGAA__
GAM2860  LOC154813 5'  CAATTGTTAATCCCAAGGCAA  65875     CAT    GG
                                CAAT   TTAAT  CCAAGGCAA
                                ||||   |||||  |||||||||
                                GTTA   AATTA  GGTTCCGTT
                                  AC_    G_
GAM2860  LOC157531 3'  CCAATCAGGCCCTGGCCAAGG 65876       TTTAA
                                TCAATCA    TGGCCAAGG
                                |||||||    |||||||||
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                                GGTTAGT    ACCGGTTCC
                                    CCGGG
GAM2860  LOC203080 5'  TCAGATCACCGGCCAAGG    65877    _    TTAA
                                TCA ATCAT   TGGCCAAGG
                                ||| |||||   |||||||||
                                AGT TAGTG   GCCGGTTCC
                                  C   ____
GAM2861  FLJ23342  3'  GTAAATATTACTTATAT    65880    TT
                                GT  GATATTACTTATAT
                                ||  ||||||||||||||
                                CA  TTATAATGAATATA
                                 T_
GAM2861  KIAA1383  3'  TGATTCTGATATTGCTTATAT  65881      GTT     A
                                TGATTC   TGATATT CTTATAT
                                ||||||   ||||||| |||||||
                                ACTAAG   ACTATAA GAATATA
                                   ___      C
GAM2862  GABRP     3'  TAAAAACTCATCTTGGTATTG  65884       A   CAA
                                TAAAAACT ATCT   GTATTG
                                |||||||| ||||   ||||||
                                ATTTTTGA TAGA   CATAAC
                                     G   AC_
GAM2862  STXBP1    3'  TCTGACGACTAATCTCAGT    65885    AAAA       A
                                TCT    ACTAATCTCA GT
                                |||    |||||||||| ||
                                AGA    TGATTAGAGT CA
                                  CTGC       _
GAM2862  KIAA1340  3'  AAACTAATCTCCAACTG     65886         AAGT
                                AAACTAATCTC    ATTG
                                ||||||||||    ||||
                                TTTGATTAGAG    TGAC
                                      GT__
GAM2862  MKP-7     3'  TCTAAAAACTAACTCAAAT    65887         T
                                TCTAAAAACTAA CTCAAGT
                                |||||||||||| |||||||
                                AGATTTTTGATT GAGTTTA
                                           _
GAM2862  PPP1R16B  3'  TCTAGACACTGATCTCAAGC   65888     AAA   A
                                TCTA   ACT ATCTCAAGT
                                ||||   ||| |||||||||
                                AGAT   TGA TAGAGTTCG
                                  CTG   C
GAM2862  LOC144266 5'  TCTAGAGACTCATCTCAAAGT  65889     AAA   A     _
                                TCTA   ACT ATCTCAA GT
                                ||||   ||| ||||||| ||
                                AGAT   TGA TAGAGTT CA
                                  CTC   G      T
GAM2863  KCNJ8     3'  TGTTACTTTTTATTACTACAGA 65892         ACTTT
                                TGTTACTTTT     TTACAGA
                                ||||||||||     |||||||
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                                ACAATGAAAA    GATGTCT
                                      ATAAT
GAM2863  MS4A2    3'  TATGCTGTTTTTACAAAAAACA 65893       AC     TTTTT
              GA                    TATGTT  TTTTAC    ACAGA
                                    ||||||  ||||||    |||||
                                    ATACGA  AAAATG    TGTCT
                                       CA     TTTTT
GAM2863  NDP      3'  TATGCTGCTTTTACTTTC    65894       A
                                    TATGTT CTTTTACTTTT
                                    |||||| ||||||||||
                                    ATACGA GAAAATGAAAG
                                       C
GAM2863  ARPC5    3'  TATGTAATTTTTTTCTTTACAG 65895      TAC    AC
              A                     TATGT   TTTT  TTTTTACAGA
                                    |||||   ||||  ||||||||||
                                    ATACA   AAAA  AGAAATGTCT
                                       TT_   AA
GAM2863  D6S2654E  3'  TGTTATTTCCTTTTACAG    65896      CT   A
                                    TGTTA  TTT CTTTTTACAG
                                    ||||||  ||| ||||||||||
                                    ACAAT  AAA GGAAAATGTC
                                      __  _
GAM2863  DKFZP564D166 3'  GTTATTTTCTTTTTTACAGA   65897     C    AC
                                    GTTA TTTT  TTTTTACAGA
                                    |||| ||||  ||||||||||
                                    CAAT AAAA  AAAAATGTCT
                                      _   GA
GAM2863  EIF2C2   3'  TGTTGCTTTCACTCTCAGA    65898     A        TTA
                                    TGTT CTTTTACTTT   CAGA
                                    |||| ||||||||||   ||||
                                    ACAA GAAAGTGAGA   GTCT
                                      C        ___
GAM2863  HIP-55   3'  TGTTACTTTTCCTGAAGTCAGA 65899          A  TTTTA
                                    TGTTACTTTT CT     CAGA
                                    |||||||||| ||     ||||
                                    ACAATGAAAA GA     GTCT
                                          G  CTTCA
GAM2863  KIAA1170  3'  TGATGCTTTTACTTTTCA    65900    TTA
                                    TG   CTTTTACTTTTTA
                                    ||   ||||||||||||
                                    AC   GAAAATGAAAAGT
                                     TAC
GAM2863  KIAA1371  3'  TATGTTACTTTTCCTTT     65901           A
                                    TATGTTACTTTT CTTTT
                                    |||||||||||| |||||
                                    ATACAATGAAAA GGAAA
                                                 _
GAM2863  MADP-1   3'  TATGTTACTTTATATTTTATAG 65902           TACT    C
                                    TATGTTACTTT    TTTTA AG
                                    ||||||||||    ||||| ||
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                                ATACAATGAAA   AAAAT TC
                                      TAT_    A
GAM2863  ZNF291   3'  GTTACTTTTATTACAA     65903        CTTT
                                GTTACTTTTA   TTACAG
                                ||||||||||   ||||||
                                CAATGAAAAT   AATGTT
                                     ____
GAM2863  LOC256979 3'  ATGCATTTACTTTTTACAG   65904     TACT
                                ATGT   TTTACTTTTTACAG
                                ||||   ||||||||||||||
                                TACG   AAATGAAAAATGTC
                                  T___
GAM2864  CISH     3'  CTTTGCTATAATTATTATTTCA 65907       A  C    C
                                TTTTGCTA AA TATTA TTCA
                                |||||||| || ||||| ||||
                                GAAACGAT TT ATAAT AAGT
                                     A  A    A
GAM2864  CISH     3'  CTTTGCTATAATTATTATTTCA 65907       A  C    C
                                TTTTGCTA AA TATTA TTCA
                                |||||||| || ||||| ||||
                                GAAACGAT TT ATAAT AAGT
                                     A  A    A
GAM2864  ENPP3    3'  TATTTTGCCAAAATTACTT   65908         ACT
                                TATTTTGCTAAA  ATTACTT
                                ||||||||||||  |||||||
                                ATAAAACGGTTT  TAATGAA
                                     ___
GAM2864  ENPP3    3'  TATTTTGCCAAAATTACTT   65908         ACT
                                TATTTTGCTAAA  ATTACTT
                                ||||||||||||  |||||||
                                ATAAAACGGTTT  TAATGAA
                                     ___
GAM2864  FBN2     3'  TATTTTGCTACAGTGGTTGTGC 65909        AAACTATTA__
            TTCA                   TATTTTGCTA        CTTCA
                                ||||||||||        |||||
                                ATAAAACGAT        GAAGT
                                     GTCACCAACAC
GAM2864  GCSH     3'  TATTTTGCTGCAAAGCTGTTGC 65910       A_  _  A  A
            TTCA                   TATTTTGCT  AAA CT TT CTTCA
                                |||||||||  ||| || || |||||
                                ATAAAACGA  TTT GA AA GAAGT
                                     CG   C  C  C
GAM2864  CDH26    3'  TATTTTTTAAAAAATCACTTCA 65911      GC    CT
                                TATTTT  TAAAA  ATTACTTCA
                                ||||||  |||||  |||||||||
                                ATAAAA  ATTTT  TAGTGAAGT
                                   A_    T_
GAM2864  FLJ20668 3'  TACTTTACGCTATTACTTC   65912       TAAAA
                                TATTTTGC    CTATTACTTC
                                ||||||||    ||||||||||
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                                ATGAAATG    GATAATGAAG
                                    C____
GAM2864  PRO0159  5'  TATTCTGCTGAAGCTTTACTT  65913        A  A  A
                                TATTTTGCT AA CT TTACTT
                                ||||||||| || || ||||||
                                ATAAGACGA TT GA AATGAA
                                    C  C  _
GAM2864  TP53TG1  3'  TATTTTGCCAAAATTAGGACTC 65914          C  TT
                                TATTTTGCTAAAA TA  ACTT
                                |||||||||||| ||  ||||
                                ATAAAACGGTTTT AT  TGAG
                                      A  CC
GAM2864  LOC148193 3'  TATTTTGCTGCAAAGCTGTTGC 65910        A_  _  A  A
           TTCA                   TATTTTGCT  AAA CT TT CTTCA
                                ||||||||  ||| || || |||||
                                ATAAAACGA  TTT GA AA GAAGT
                                    CG   C  C  C
GAM2864  LOC81569  3'  CATTTTGCTAAAATTAATCC   65915          ACT   C
                                TATTTTGCTAAA   ATTA TTC
                                ||||||||||||   |||| |||
                                GTAAAACGATTT   TAAT AGG
                                      ___   T
GAM2865  BRCA1    5'  AGTGTCCCCCTCAAGGCA    65918     _       T
                                AGTG CCCCCTTAG GGCA
                                |||| ||||||||| ||||
                                TCAC GGGGGAGTT CCGT
                                  A       _
GAM2865  CDK7     3'  TAAGTTTTCCCTAATGCA    65919      GCCC      G
                                TAAGT   CCTTAGTG CA
                                |||||   |||||||| ||
                                ATTCA   GGGATTAC GT
                                   AAA_      _
GAM2865  CTPS     3'  TAAGTCCATGTGGCACAC    65920      G  CCCTTA
                                TAAGT CC     GTGGCACAC
                                ||||| ||     |||||||||
                                ATTCA GG     CACCGTGTG
                                   _ TA____
GAM2865  PLOD2    3'  GTGTTCCCTTAGTAACAC    65921     CC
                                GTG  CCCTTAGTGGCAC
                                |||  ||||||||||||
                                CAC  GGGAATCATTGTG
                                  AA
GAM2865  PTGS1    3'  GTGCCCCCTCTGTTGTATGC  65922         A___  _
                                GTGCCCCCTT   GTG GC
                                ||||||||||   ||| ||
                                CACGGGGGAG   CAT CG
                                      ACAA  A
GAM2865  PTGS1    3'  GTGCCCCCTCTGTTGTATGC  65922         A___  _
                                GTGCCCCCTT   GTG GC
                                ||||||||||   ||| ||
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                                CACGGGGGAG   CAT CG
                                     ACAA  A
GAM2865 PTPRG    3' TAAGTGCCCTTTCAGGA    65923       CC   T
                                TAAGTGCCC  TTAG GG
                                |||||||||  |||| ||
                                ATTCACGGG  AGTC CT
                                     AA   _
GAM2865 TIF1     3' TAAGTGCCTTCTTAATAGCA  65570       CC
                                TAAGTGCC  CTTAGTGGCA
                                ||||||||  ||||||||||
                                ATTCACGG  GAATTATCGT
                                     AA
GAM2865 CHL1     5' TAAGTTCCCCTTAGTTCCAC  65924      GC       GG
                                TAAGT  CCCCTTAGT  CAC
                                |||||  |||||||||  |||
                                ATTCA  GGGGAATCA  GTG
                                   A_       AG
GAM2865 FLJ10276 3' TAAGTGCCTCTTACCCAC    65925       CC   AGTG  A
                                TAAGTGCC  CTT   GC CAC
                                ||||||||  |||   || |||
                                ATTCACGG  GAA   TG GTG
                                     A_  ____  G
GAM2865 FLJ14351 3' TAAGTGTCCCATGGCACA    65926      C   CTTA
                                TAAGTG CCC   GTGGCACA
                                ||||||| |||   ||||||||
                                ATTCAC GGG   TACCGTGT
                                   A  ____
GAM2865 KIAA1332 3' GCTCTCAAAAGGCACACT    65927    CCC    T_
                                GC   CTTAG  GGCACACT
                                ||   |||||  ||||||||
                                CG   GAGTT  CCGTGTGA
                                 A__    TT
GAM2865 KR18     3' TAAGAGCCTAGTGGTGTAC    65928     T   CCCT     CAC
                                TAAG GCC   TAGTGG   AC
                                |||| |||   ||||||   ||
                                ATTC CGG   ATCACC   TG
                                  T  ____     ACA
GAM2865 OSBPL11  3' GTGCCCTAGTAGGTACA     65929      CCT   _  C
                                GTGCCC   TAGT GG ACA
                                ||||||   |||| || |||
                                CACGGG   ATCA CC TGT
                                   ___   T  A
GAM2865 QKI      3' TAAGTTTTTCTCTCATGGCACA 65930      GCCCC   A_
           CT                    TAAGT    CTT  GTGGCACACT
                                 |||||    |||  ||||||||||
                                 ATTCA    GAG  TACCGTGTGA
                                   AAAA_   AG
GAM2865 LOC124626 3'  TAAATGCCTTCTTAGAAATGCC 65931        CC    TG__  A
           A                     TAAGTGCC  CTTAG   GC CA
                                 ||||||||  |||||   || ||
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                                ATTTACGG  GAATC   CG GT
                                    AA    TTTA  _
GAM2865  LOC132671 3'  AGTGCTCCTTCCAGCACACT   65932      CC   AG
                                AGTGC  CCTT  TGGCACACT
                                |||||  ||||  |||||||||
                                TCACG  GGAA  GTCGTGTGA
                                  A_   G_
GAM2865  LOC157623 5'  TAAGTGCCCTGCTCTGCAC   65933        CC  AGTG
                                TAAGTGCCC  TT   GCAC
                                |||||||||  ||   ||||
                                ATTCACGGG  GA   CGTG
                                     AC  GA__
GAM2865  LOC200558 3'  TAAGTACCTCCTTAGTTCA   65934        C     GG
                                TAAGTGCC CCTTAGT  CA
                                |||||||| |||||||  ||
                                ATTCATGG GGAATCA  GT
                                     A     A_
GAM2865  LOC253650 3'  GTGCCCTCTGAGCACACT    65935       C  TAGT
                                GTGCCC CT   GGCACACT
                                |||||| ||   ||||||||
                                CACGGG GA   TCGTGTGA
                                   A  C___
GAM2865  LOC255565 3'  AAATGCACCTTGGTGGCACACT 65936       CC   A
                                AAGTGC  CCTT GTGGCACACT
                                ||||||  |||| ||||||||||
                                TTTACG  GGAA CACCGTGTGA
                                   T_   C
GAM2865  LOC90750  3'  TAAGTGCCCCCTTCATGTAGTC 65937          A__   _
           AC                    TAAGTGCCCCCTT   GTGG CAC
                                ||||||||||||   |||| |||
                                ATTCACGGGGGAA   CATC GTG
                                       GTA   A
GAM2866  C5orf7   3'  TGGCTGATTTTGTGCTATAATG 65940        CTATCT  CGT
           G                     TGGCTGATT     CT   GTGG
                                |||||||||     ||   ||||
                                ACCGACTAA     GA   TACC
                                     AACAC_  TAT
GAM2866  COQ7     3'  TGGCTGATTTTGCTTGTGAAGG 65941        CTATCT  C   T_
                                TGGCTGATT     CT GTG  GG
                                |||||||||     || |||  ||
                                ACCGACTAA     GA CAC  CC
                                     AAC___  A   TT
GAM2866  KIAA0557  3'  TGGCTAATTTTTTTTTTTTTTG 65942        CTATCTCTC___
           TGTGG                   TGGCTGATT         GTGTGG
                                |||||||||          ||||||
                                ACCGATTAA          CACACC
                                     AAAAAAAAAAAA
GAM2866  SSBP4    3'  TGGTAAGAGTCTTTCGTGTGG  65943     C   TTCTA   C
                                TGG TGA    TCT TCGTGTGG
                                ||| |||    ||| ||||||||
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                                ACC ATT     AGA AGCACACC
                                  _  CTC__   A
GAM2867  FAAH     3'  AGCGCCCGAGTAGGGGCCTGAG 65946         AC    A
                                GGCGCCCGA  AGGG CCTGAG
                                |||||||||  |||| ||||||
                                TCGCGGGCT  TCCC GGACTC
                                     CA   C
GAM2867  FOXD2    5'  TTGGCGCCCGCAGCCTTGGGCC 65947          AACA___   A
              TG                  TTGGCGCCCG      GGG CCTG
                                |||||||||||      ||| ||||
                                AACCGCGGGC      CCC GGAC
                                     GTCGGAA  _
GAM2867  IL1RN    3'  TTGGCCCTGCAGGGACCTGAG  65948      G  CGAA
                                TTGGC CC    CAGGGACCTGAG
                                ||||| ||    ||||||||||||
                                AACCG GG    GTCCCTGGACTC
                                  _ AC__
GAM2867  RFX2     3'  TGGCTGCGCAGGGACCTG    65949     GCC  AA
                                TGGC   CG  CAGGGACCTG
                                ||||   ||  ||||||||||
                                ACCG   GC  GTCCCTGGAC
                                  AC_  __
GAM2867  TIA1     3'  TTGTGTTTGAAACAAGGATCTG 65950     GCGCCC       C
              AG                  TTG     GAACAGGGA CTGAG
                                |||     ||||||||| |||||
                                AAC     TTTGTTCCT GACTC
                                  ACAAAC        A
GAM2867  TIA1     3'  TTGTGTTTGAAACAAGGATCTG 65950     GCGCCC       C
              AG                  TTG     GAACAGGGA CTGAG
                                |||     ||||||||| |||||
                                AAC     TTTGTTCCT GACTC
                                  ACAAAC        A
GAM2867  DDX31    3'  TTGGCGCCCAGGGCGGGCTG   65951         AACA   AC
                                TTGGCGCCCG    GGG  CTG
                                ||||||||||    |||  |||
                                AACCGCGGGT    CCC  GAC
                                     CCCG   __
GAM2867  FLJ22415 5'  CTGGCGCCCGGACGGGA     65952          A  A
                                TTGGCGCCCG AC GGGA
                                |||||||||| || ||||
                                GACCGCGGGC TG CCCT
                                     C  _
GAM2867  KIAA0222 3'  TGGCCGTTACGGGGACCTG    65953     GCC  A_  A
                                TGGC   CG  AC GGGACCTG
                                ||||   ||  || ||||||||
                                ACCG   GC  TG CCCTGGAC
                                  ___  AA  C
GAM2867  KIAA0285 3'  CTGGTCTGAGTGGGGACCTGAG 65954      CGCCC  ACA
                                TTGG    GA   GGGACCTGAG
                                ||||    ||   ||||||||||
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                                GACC    CT   CCCTGGACTC
                                  AGA__  CAC
GAM2867 KIAA1655  5' TTGGAGCCCTGGGGACCTG   65955     C   GAACA
                                TTGG GCCC    GGGACCTG
                                |||| ||||    ||||||||
                                AACC CGGG    CCCTGGAC
                                  T   AC___
GAM2867 PSK       5' TTGGGACCCAGGGGCCTGA   65956     C   GAAC   A
                                TTGG GCCC    AGGG CCTGA
                                |||| ||||   |||| |||||
                                AACC TGGG    TCCC GGACT
                                  C   _____   C
GAM2867 LOC147841 5' TTGGCGCCCAGCAGGCTGA   65957         AA   GAC
                                TTGGCGCCCG  CAGG   CTGA
                                ||||||||||  ||||   ||||
                                AACCGCGGGT  GTCC   GACT
                                     C_   ___
GAM2867 LOC221474 5' TTGGTGCTGAACAGGACGA   65958     C  CC      ACC
                                TTGG GC  GAACAGGG   TGA
                                |||| ||  ||||||||   |||
                                AACC CG  CTTGTCCT   GCT
                                  A  A_      ___
GAM2867 LOC221749 3' CTGGCGTCAGTGGGGCCTG   65959      CC  AACA   A
                                TTGGCG  CG    GGG CCTG
                                ||||||  ||    ||| ||||
                                GACCGC  GT    CCC GGAC
                                   A_  CAC_  _
GAM2868 CLCN6     3' CTGATACCATGTAGAAGG    65962         TGC   CAA
                                TTGATACCAT   GTG   AAGG
                                ||||||||||   |||   ||||
                                GACTATGGTA   CAT   TTCC
                                     ___   C__
GAM2868 CLCN6     3' CTGATACCATGTAGAAGG    65962         TGC   CAA
                                TTGATACCAT   GTG   AAGG
                                ||||||||||   |||   ||||
                                GACTATGGTA   CAT   TTCC
                                     ___   C__
GAM2868 CLCN6     3' CTGATACCATGTAGAAGG    65962         TGC   CAA
                                TTGATACCAT   GTG   AAGG
                                ||||||||||   |||   ||||
                                GACTATGGTA   CAT   TTCC
                                     ___   C__
GAM2868 PPP1R12B  3' ATACCATTGAGTGAGGGGGT  65963         C   CAAAA
                                ATACCATTG GTG    GGT
                                ||||||||| |||    |||
                                TATGGTAAC CAC    CCA
                                     T   TCCC_
GAM2868 dA141H5.1 5' TTGGACCACTGCAAAAGG    65964     AT    TGCG
                                TTG  ACCAT   TGCAAAAGG
                                |||  |||||   |||||||||
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                                AAC  TGGTG   ACGTTTTCC
                                  C_   _____
GAM2868  FLJ20005  5'  TTAATCCGCGTGCGGAAGG   65965      A  ATT     AA
                                TTGAT CC   GCGTGC  AAGG
                                |||||| ||   ||||||  ||||
                                AATTA GG   CGCACG  TTCC
                                  _ ___      CC
GAM2868  KIAA1277  3'  TTGTTACCATCAGCCGCAAAAG 65966     A      _  G
              GT                  TTG TACCATT GC TGCAAAAGGT
                                ||| ||||||| || ||||||||||
                                AAC ATGGTAG CG GCGTTTTCCA
                                  A      T  _
GAM2868  KIAA1775  3'  ATACCATTGTGCAAAACAGG   65967        GC      __
                                ATACCATT  GTGCAAA  AGG
                                ||||||||  |||||||  |||
                                TATGGTAA  CACGTTT  TCC
                                    __       TG
GAM2868  POPX1     3'  GATACCATTAGTTAGAGG    65968          C  GCAAA
                                GATACCATTG GT     AGG
                                |||||||||| ||     |||
                                CTATGGTAAT CA     TCC
                                     _  ATC__
GAM2868  UNC5D     3'  TTGATACCTCCCTACTGCAAGG 65969         A__    G     AA
              GGT                   TTGATACC   TTGC TGCAA  GGT
                                ||||||||   |||| |||||  |||
                                AACTATGG   GATG ACGTT  CCA
                                    AGG    _    CC
GAM2868  LOC131873 3'  TTAATACCAATGAATGCAGGGG 65970          T  C     AAA
              GT                    TTGATACCA TG GTGCA   GGT
                                |||||||||| || |||||   |||
                                AATTATGGT AC TACGT   CCA
                                     T  T    CCC
GAM2868  LOC158402 5'  TTGACACCACGTGGTAGAGG   65971         ATT     CAAA
                                TTGATACC   GCGTG    AGG
                                ||||||||   |||||    |||
                                AACTGTGG   TGCAC    TCC
                                    ___      CATC
GAM2869  LLT1      3'  TAATATTTTACTATGATTTT   65974       A    CG
                                TAATAT TTTAC  TGATTTT
                                |||||| |||||  |||||||
                                ATTATA AAATG  ACTAAAA
                                   _     AT
GAM2870  CLN2      3'  TATAGCCCTAAACTAAGGTAG  65977      T   _
                                TATA GCTC AAACTAAGGTAG
                                |||| |||| ||||||||||||
                                ATAT CGGG TTTGATTCCATC
                                  _    A
GAM2870  ICMT      3'  TATATGCTCAAATCCCTTTGG  65978           _  AA__
                                TATATGCTCAAA CT    GG
                                ||||||||||| ||    ||
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                                ATATACGAGTTT GG   CC
                                       A  GAAA
GAM2870 KIAA0853 3' TGCAAAATAAACTAAGGTAG  65979    TC___
                                TGC    AAACTAAGGTAG
                                |||    ||||||||||||
                                ACG    TTTGATTCCATC
                                  TTTTA
GAM2870 LOC55885 3' TATGCTATCACGTAAGGTAG  65980      CAA _
                                TATGCT   AC TAAGGTAG
                                ||||||   || ||||||||
                                ATACGA   TG ATTCCATC
                                    TAG  C
GAM2871 ADSS     3' TTGAACATTTCACTAAAT    65983          A
                                TTGAACATTTCAC AAAT
                                |||||||||||| ||||
                                AACTTGTAAAGTG TTTA
                                       A
GAM2871 LARS2    3' TTGAACATTTCCTAAATG    65984          ACA
                                TTGAACATTTC   AAATG
                                ||||||||||   |||||
                                AACTTGTAAAG   TTTAC
                                       GA_
GAM2871 SVIL     3' CTTGAACATTTACAAAATA   65985          C
                                CTTGAACATTT ACAAAATG
                                |||||||||| ||||||||
                                GAACTTGTAAA TGTTTTAT
                                          _
GAM2871 SVIL     3' CTTGAACATTTACAAAATA   65985          C
                                CTTGAACATTT ACAAAATG
                                |||||||||| ||||||||
                                GAACTTGTAAA TGTTTTAT
                                          _
GAM2871 DKFZp434A2417 3' TGGGCAGCCCACAAAGTGAATA 65986    AA  T      A
                                TG  CA TTCACAAA TGAATA
                                ||  || |||||||| ||||||
                                AC  GT GGGTGTTT ACTTAT
                                 CC  C       C
GAM2871 FLJ21415 3' CTTGAACATATTCAACTAGAAT 65987         TTCA   AAT
                                CTTGAACAT    CAA   GAAT
                                |||||||||    |||   ||||
                                GAACTTGTA    GTT   CTTA
                                      TAA_   GAT
GAM2871 FLJ22028 3' TTGACATTTCACAAAGAAT   65988      A        AT
                                TTGA CATTTCACAAA  GAAT
                                |||| ||||||||||  ||||
                                AACT GTAAAGTGTTT  CTTA
                                  _       __
GAM2871 FLJ22625 5' TTGAATTTCACATAATGAATA 65989      AC       A
                                TTGA  ATTTCACA AATGAATA
                                ||||  |||||||| ||||||||
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                                AACT  TAAAGTGT TTACTTAT
                                  __      A
GAM2871  FPGT     3'  TTGAACATTTAATGAAT     65990          CACAA
                                TTGAACATTT    AATGAAT
                                ||||||||||    |||||||
                                AACTTGTAAA    TTACTTA
                                      _____
GAM2871  KIAA0084 3'  CTTGAACATTCTGCAAAA    65991          CA
                                CTTGAACATTT  CAAAA
                                ||||||||||  |||||
                                GAACTTGTAAG  GTTTT
                                      AC
GAM2871  KIAA0265 3'  ACACACACAAAATGAAT     65992      TT
                                ACAT  CACAAAATGAAT
                                ||||  ||||||||||||
                                TGTG  GTGTTTTACTTA
                                  T_
GAM2871  KIAA1913 3'  TGGACATTTCATTTTATGAATA 65993    A       CAAA
                                TG ACATTTCA    ATGAATA
                                || ||||||||    |||||||
                                AC TGTAAAGT    TACTTAT
                                 C       AAAA
GAM2871  LHFP     3'  TTAAATTTTTTACAAAATGAAT 65994      CA   C
            A                    TTGAA  TTT ACAAAATGAATA
                                ||||||  ||| ||||||||||||
                                AATTT  AAA TGTTTTACTTAT
                                   AA   A
GAM2871  VIT      5'  CACCACACAGAATGAATA    65995     TT   A
                                CAT  CACA AATGAATA
                                |||  |||| ||||||||
                                GTG  GTGT TTACTTAT
                                  GT   C
GAM2871  VPS35    3'  CTTGAACACTTACCAAGTGAAT 65996          CA   AA
            A                    CTTGAACATTT  CAA  TGAATA
                                ||||||||||  |||  ||||||
                                GAACTTGTGAA  GTT  ACTTAT
                                      TG   C_
GAM2871  LOC153525 3'  TGAACATTTTCATCCTGAATA  65997         _  CAAAA
                                TGAACATTT CA    TGAATA
                                |||||||| ||    ||||||
                                ACTTGTAAA GT    ACTTAT
                                     A  AGG__
GAM2871  LOC169026 3'  CTTGATATTTCACAGGAATG   65998      AC      A_
                                CTTGA  ATTTCACA  AATG
                                |||||  ||||||||  ||||
                                GAACT  TAAAGTGT  TTAC
                                   A_       CC
GAM2871  LOC202934 5'  CCTGAACTGACCCAAAATGAAT 65999        ATT  A
            A                    CTTGAAC   TC CAAAATGAATA
                                |||||||   || ||||||||||
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                                GGACTTG   GG GTTTTACTTAT
                                   ACT  _
GAM2871  LOC255465 5'  TGAACTGACCCAAAATGAATA  66000      ATT  A
                                TGAAC   TC CAAAATGAATA
                                |||||   || ||||||||||
                                ACTTG   GG GTTTTACTTAT
                                  ACT  _
GAM2871  LOC51141  3'  CTTGAACTATTCACTAATG    66001       AT    AA
                                CTTGAAC  TTCAC  AATG
                                |||||||  |||||  ||||
                                GAACTTG  AAGTG  TTAC
                                   AT    A_
GAM2872  ACCN2     3'  CCTCCGGGAGAGGGACCAGT   66004    _    _  A  GTG
                                CC CCGGG GAG GGA   TTAGT
                                || ||||| ||| |||   |||||
                                GG GGCCC CTC CCT   GGTCA
                                 A    T  _  ____
GAM2872  BSND      5'  CCCCCGGGAGAGGGGGTG    66005     G      A_
                                CCCC GGGAGAGG  GTG
                                |||| ||||||||  |||
                                GGGG CCCTCTCC  CAC
                                  G       CC
GAM2872  C1QG      3'  CCCATGGGGAGGGGGTGCAGT  66006    C_     A  A    T
                                CCC  GGGGAG GG GTGT AGT
                                |||  |||||| || |||| |||
                                GGG  CCCCTC CC CACG TCA
                                 TA     _ C   _
GAM2872  DAXX      5'  CCCCGGAGGGAGGAAGTG    66007       A    _
                                CCCCGGGG GAGGA GTG
                                |||||||| ||||| |||
                                GGGGCCTC CTCCT CAC
                                   C    T
GAM2872  GNL1      5'  CCTAGGGGAGAGGGGGCGT    66008    CC       A_
                                CC  GGGGAGAGG  GTGT
                                ||  |||||||||  ||||
                                GG  CCCCTCTCC  CGCA
                                 AT       CC
GAM2872  GNL1      5'  CCTAGGGGAGAGGGGGCGT    66008    CC       A_
                                CC  GGGGAGAGG  GTGT
                                ||  |||||||||  ||||
                                GG  CCCCTCTCC  CGCA
                                 AT       CC
GAM2872  HDAC5     3'  CCCCGGGGAAGGGGAAGTA    66009        A_  _
                                CCCCGGGGAG  GGA GTG
                                ||||||||||  ||| |||
                                GGGGCCCCTT  CCT CAT
                                      CC   T
GAM2872  HM13      3'  CCCGGGGAGGGGGGGAAGCT    66010        A__    T
                                CCCGGGGAG   GGAG GTT
                                |||||||||   |||| |||
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                                GGGCCCCTC  CCTT CGA
                                     CCC   _
GAM2872 HTR6    5' CCCCGGGGGAGGTGAGTG   66011       _ AG
                                CCCCGGGG AG  GAGTG
                                |||||||| ||  |||||
                                GGGGCCCC TC  CTCAC
                                    C  CA
GAM2872 INPP5D  3' CCCGGGAGAGGGTCCAGT   66012      G   A G
                                CCCGGG AGAGG GT TTAGT
                                |||||| ||||| || |||||
                                GGGCCC TCTCC CA GGTCA
                                  _   _ _
GAM2872 KIF3B   3' CCCTGGGAGAGGAGAAGCT  66013    G       T_
                                CCC GGGAGAGGAG  GTT
                                ||| ||||||||||  |||
                                GGG CCCTCTCCTC  CGA
                                  A        TT
GAM2872 LFG     3' CCCAGGGAGAGGAGAACT   66014          TG
                                CCCGGGGAGAGGAG  TT
                                ||||||||||||||  ||
                                GGGTCCCTCTCCTC  GA
                                       TT
GAM2872 LRP1    3' CCCCAGGGGAGGGGAGGCT  66015    _    A   T
                                CCCC GGGGAG GGAG GTT
                                |||| |||||| |||| |||
                                GGGG CCCCTC CCTC CGA
                                  T    C   _
GAM2872 MECP2   3' CGGGGAGAGGGGCTATCAGT  66016        A _
                                CGGGGAGAGG G TGTTAGT
                                |||||||||| | |||||||
                                GCCCCTCTCC C ATAGTCA
                                     C G
GAM2872 MMP15   3' CCCTGGGGAGAGGGGCCCT  66017    C       A  G
                                CCC GGGGAGAGG GT TT
                                ||| ||||||||| || ||
                                GGG CCCCTCTCC CG GA
                                  A       C  G
GAM2872 MSN     3' CCCTGGGGAGAAGACAAACAGT 66018    C       GTGT
            AA                    CCC GGGGAGAGGA   TAGTAA
                                ||| ||||||||||   ||||||
                                GGG CCCCTCTTCT   GTCATT
                                  A        GTTT
GAM2872 SCN4A   3' CCTGGGGAGAGGCCAGTG   66019   C       __
                                CC GGGGAGAGG  AGTG
                                || |||||||||  ||||
                                GG CCCCTCTCC  TCAC
                                 A       GG
GAM2872 SIRT2   3' CCCCGGGGGCAGGAGACAGAGT 66020        AG    TGTT
                                CCCCGGGG  AGGAG   AGT
                                ||||||||  |||||   |||
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                                GGGGCCCC  TCCTC   TCA
                                    CG    TGTC
GAM2872  SIRT2    3'  CCCCGGGGGCAGGAGACAGAGT 66020       AG    TGTT
                                CCCCGGGG  AGGAG   AGT
                                ||||||||  |||||   |||
                                GGGGCCCC  TCCTC   TCA
                                    CG    TGTC
GAM2872  TIRAP    3'  GGGAAGAGGAACAGAGTA    66021         TGTT
                                GGGGAGAGGAG   AGTA
                                ||||||||||   ||||
                                CCCTTCTCCTT   TCAT
                                     GTC_
GAM2872  TTYH1    3'  CCATGGCCAAGAGTGTTAGT   66022    G  AG
                                CCG GG  AGGAGTGTTAGT
                                ||| ||  ||||||||||||
                                GGT CC  TTCTCACAATCA
                                  A  GG
GAM2872  TULP1    3'  CCCGGGGAGAGGGGAGGTTAA  66023         __   T
                                CCCGGGGAGA  GGAG GTTAG
                                ||||||||||  |||| |||||
                                GGGCCCCTCT  CCTC CAATT
                                     CC   _
GAM2872  APELIN   3'  CCCGGGGAGAGGGTGCTA    66024          A
                                CCCGGGGAGAGG GTGTTA
                                |||||||||||| ||||||
                                GGGCCCCTCTCC CACGAT
                                            _
GAM2872  C20orf98 3'  GGGAAGAGGGTGTGGGTA    66025        A   TA
                                GGGGAGAGG GTGT  GTA
                                ||||||||| ||||  |||
                                CCCTTCTCC CACA  CAT
                                     _   CC
GAM2872  CBX6     3'  CCCGGGGAGGGGAGGGCTAG  66026        A   T
                                CCCGGGGAG GGAG GTTAG
                                ||||||||| |||| |||||
                                GGGCCCCTC CCTC CGATC
                                     C   C
GAM2872  DKFZP564C1940 3'  CCCCAGGGGAGAGGCCTCAGTA 66027        A   GA  G
                                CCCCGGGG GAG  GT TTAGTA
                                |||||||| |||  || ||||||
                                GGGGTCCC CTC  CG AGTCAT
                                     _  TC  G
GAM2872  DKFZP762D096 3'  CCCCGGGGGGAGGATGAAGTGT 66028        A   ____
                                CCCCGGGG GAGGA   GTGT
                                |||||||| |||||   ||||
                                GGGGCCCC CTCCT   CACA
                                     C    ACTT
GAM2872  FLJ10157  5'  CCGGGGAGAGGCATTCGTAGT  66029          AG__  T
                                CCGGGGAGAGG   TGT AGT
                                ||||||||||   ||| |||
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                                GGCCCCTCTCC   GCA TCA
                                      GTAA  _
GAM2872  FLJ22494  3' CCCTGGGGAGAGGCGTCAG   66030    C       AG
                                CCC GGGGAGAGG  TGTTAG
                                ||| |||||||||  ||||||
                                GGG CCCCTCTCC  GCAGTC
                                  A       __
GAM2872  HCNGP     3' CCCCGGGGGGGAGCCCAGT    66031       AGA    G
                                CCCCGGGG   GGAGT TTAGT
                                ||||||||   ||||| |||||
                                GGGGCCCC   CCTCG GGTCA
                                     ____    _
GAM2872  HSPBP1    3' CCCTTGGGAGAGGGCCTTGTA  66032    CG      A  G  A
                                CCC  GGGAGAGG GT TT GTA
                                |||  |||||||| || || |||
                                GGG  CCCTCTCC CG AA CAT
                                  AA       _  G  _
GAM2872  KIAA0426  3' GGGGAGAGGATGCTACTAA   66033        G    G
                                GGGGAGAGGA TGTTA TAA
                                |||||||||| ||||| |||
                                CCCCTCTCCT ACGAT ATT
                                      _    G
GAM2872  KIAA0494  5' CCTTGGGTGCAGAGTGTTAGTA 66034    CG   AGA
                                CC  GGG   GGAGTGTTAGTA
                                ||  |||   ||||||||||||
                                GG  CCC   TCTCACAATCAT
                                 AA   ACG
GAM2872  KIAA0720  3' CCTGGGGAGAGGCTCTGATGGT 66035    C       AG_  TTA
                                CC GGGGAGAGG   TG   GT
                                || |||||||||   ||   ||
                                GG CCCCTCTCC   AC   CA
                                 A        GAG  TAC
GAM2872  KIAA0767  3' CCCTGGGGAGAGAGGTGT    66036    C       GA
                                CCC GGGGAGAG  GTGT
                                ||| ||||||||  ||||
                                GGG CCCCTCTC  CACA
                                  A       TC
GAM2872  KIAA1076  3' CCTGGGGAGAGGGAGGTC    66037    C       _  T
                                CC GGGGAGAGG AG GTT
                                || |||||||||  || |||
                                GG CCCCTCTCC TC CAG
                                 A        C  _
GAM2872  KIAA1576  3' CCCCGGGGGGAAGGAGAGCC   66038        AG    T
                                CCCCGGGG  AGGAG GTT
                                ||||||||  |||||  |||
                                GGGGCCCC  TCCTC CGG
                                     CT    T
GAM2872  KIAA1949  5' CCCCGGGGGGAGGGGGTGC    66039        A   A_
                                CCCCGGGG GAGG  GTGT
                                |||||||| ||||  ||||
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                                GGGGCCCC CTCC  CACG
                                     _   CC
GAM2872 KIAA1949 5' CCCCGGGGGAGGGGGTGC   66039       A   A_
                                CCCCGGGG GAGG  GTGT
                                |||||||| ||||  ||||
                                GGGGCCCC CTCC  CACG
                                     _   CC
GAM2872 KIAA1949 5' CCCCGGGGGAGGGGGTGC   66039       A   A_
                                CCCCGGGG GAGG  GTGT
                                |||||||| ||||  ||||
                                GGGGCCCC CTCC  CACG
                                     _   CC
GAM2872 MGC2721  5' CCCCGGGGAGGAGGGTCAG  66040        GA   T
                                CCCCGGGGA  GGAG GTTAG
                                |||||||||  |||| |||||
                                GGGGCCCCT  CCTC CAGTC
                                     __   C
GAM2872 NOPAR    5' CCAGGGGGAGGAGCAGCT    66041      A     _
                                CCGGGG GAGGAGT GTT
                                |||||| ||||||| |||
                                GGTCCC CTCCTCG CGA
                                   C      T
GAM2872 RAI16    3' CCCCGCGGGGAGGAATGT    66042      _  A
                                CCCCG GGG GAGGAGTGT
                                ||||| ||| |||||||||
                                GGGGC CCC CTCCTTACA
                                  G  _
GAM2872 SCAM-1   3' CCCTGGGAAGAGGAGGCC    66043    C        T
                                CCC GGGGAGAGGAG GTT
                                ||| ||||||||||| |||
                                GGG CCCTTCTCCTC CGG
                                  A        _
GAM2872 SFXN5    3' CCCCGGGGGAGGGAGGCC    66044       _ A   T
                                CCCCGGGG AG GGAG GTT
                                |||||||| || |||| |||
                                GGGGCCCC TC CCTC CGG
                                     C _   _
GAM2872 SRF      5' CCCCGGGGGGCAGGGGCTGCT 66045       AG_  A _
                                CCCCGGGG   AGG G TGTT
                                ||||||||   ||| | ||||
                                GGGGCCCC   TCC C ACGA
                                     CCG   C G
GAM2872 THEA     3' CCCTTGGGGGACCAATTAGTAA 66046    CG   AGA   GT_
                                CCC  GGG   GGA   GTTAGTAA
                                |||  |||   |||   ||||||||
                                GGG  CCC   CCT   TAATCATT
                                  AA   ____   GGT
GAM2872 WIT-1    3' CCCCGGGGAGAGGCGCTAG   66047          AG
                                CCCCGGGGAGAGG  TGTTAG
                                ||||||||||||  ||||||
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                                GGGGCCCCTCTCC  GCGATC
                                      __
GAM2872  LOC126823 5'  CCCCGGGGAGAGGGAGGGC   66048          _  T
                                CCCCGGGGAGAGG AG GT
                                |||||||||||| || ||
                                GGGGCCCCTCTCC TC CG
                                      C  C
GAM2872  LOC148078 5'  CCCGGGAGAGGAGCCCT    66049      G      G
                                CCCGGG AGAGGAGT TT
                                |||||| |||||||| ||
                                GGGCCC TCTCCTCG GA
                                   _      G
GAM2872  LOC148223 3'  CCCCGGGAGAGGAAGGAGGT  66050       _  __    T
                                CCCCGGG GAG  AGGAG GT
                                ||||||| |||  ||||| ||
                                GGGGCCC CTC  TCCTC CA
                                    T  CT   _
GAM2872  LOC150225 3'  CAGGGAGAGGGCCAGT     66051         AGT
                                CGGGGAGAGG   GTTAGT
                                ||||||||||   ||||||
                                GTCCCTCTCC   CGGTCA
                                      ___
GAM2872  LOC254122 3'  CCTTGGGAAGGGCACTAGT   66052   CG   G   A TG
                                CC  GGGA AGG G  TTAGT
                                ||  |||| ||| |  |||||
                                GG  CCCT TCC C  GATCA
                                 AA   _  _ GT
GAM2872  LOC257396 5'  CCTGGGGAGAAGGACATGCATG 66053   C     _  _   TA_
            GTAA                   CC GGGGAGA GGA GTGT   GTAA
                                || ||||||| ||| ||||   ||||
                                GG CCCCTCT CCT TACG   CATT
                                 A      T  G   TAC
GAM2872  LOC257541 5'  CCTAGGGGAGAGGGGGCGT   66008   CC       A_
                                CC  GGGGAGAGG  GTGT
                                ||  |||||||||  ||||
                                GG  CCCCTCTCC  CGCA
                                 AT        CC
GAM2872  LOC51107  3'  GGGGAGAGGAGGGATGCTGGT  66054          ___   A
                                GGGGAGAGGAG   TGTT GT
                                ||||||||||   |||| ||
                                CCCCTCTCCTC   ACGA CA
                                      CCT   C
GAM2872  LOC51279  3'  CCCAGGGAGGGAAAATGGTAA  66055        A   TGTTA
                                CCCGGGGAG GGAG    GTAA
                                |||||||| ||||    ||||
                                GGGTCCCTC CCTT    CATT
                                      _   TTAC_
GAM2872  LOC92771  3'  CCCCGGGGAGAGGAGGTGT   66056           _
                                CCCCGGGGAGAGGAG TGT
                                |||||||||||||| |||
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                                GGGGCCCCTCTCCTC ACA
                                        C
GAM2873  CLOCK    5'  TTCTTCAGGAAACTATAGGTTC 66059        A    CA  T
              A                  TTTTTCAG AAACT  AG GTTCA
                                 |||||||| |||||  || |||||
                                 AAGAAGTC TTTGA  TC CAAGT
                                     C    TA  _
GAM2873  COX7A1   3'  TTTTTCAGAGGCCAGCGTT   66060         AAACTCA
                                 TTTTTCAGA      AGTGTT
                                 |||||||||      ||||||
                                 AAAAAGTCT      TCGCAA
                                      CCGG___
GAM2873  DEC1     5'  TTTCTCAGAGAAGCCGCAGAGT 66061         A  _  _  _
              GTTCA                 TTTTTCAGA AA CT CA AGTGTTCA
                                 ||||||||| || || || ||||||||
                                 AAAGAGTCT TT GG GT TCACAAGT
                                      C  C  C  C
GAM2873  KIF5C    3'  TTTCGGAAAAGTGTTC      66062      A    ACTCA
                                 TTTC GAAA    AGTGTTC
                                 |||| ||||    |||||||
                                 AAAG CTTT    TCACAAG
                                   C   _____
GAM2873  MGAT1    3'  TTTTTCAGACAATTCAGCCTT  66063         A  C   A  G
                                 TTTTTCAGA AA TCA GT TT
                                 ||||||||| || ||| || ||
                                 AAAAAGTCT TT AGT CG AA
                                      G  A   _  G
GAM2873  PTGS1    3'  TTTTCCAGGAAACTGCAGTGTT 66064         A    CA
                                 TTTTTCAG AAACT  AGTGTT
                                 |||||||| |||||  ||||||
                                 AAAAGGTC TTTGA  TCACAA
                                     C    CG
GAM2873  PTGS1    3'  TTTTCCAGGAAACTGCAGTGTT 66064         A    CA
                                 TTTTTCAG AAACT  AGTGTT
                                 |||||||| |||||  ||||||
                                 AAAAGGTC TTTGA  TCACAA
                                     C    CG
GAM2873  PTPRD    5'  TTCTTTAGATCCCACGGGTGTT 66065      C   AAA   A__
              CA                   TTTTT AGA   CTCA   GTGTTCA
                                   |||||  |||   ||||   |||||||
                                   AAGAA TCT   GGGT   CACAAGT
                                     A   A__    GCC
GAM2873  PTPRD    5'  TTCTTTAGATCCCACGGGTGTT 66065      C   AAA   A__
              CA                   TTTTT AGA   CTCA   GTGTTCA
                                   |||||  |||   ||||   |||||||
                                   AAGAA TCT   GGGT   CACAAGT
                                     A   A__    GCC
GAM2873  PTPRD    5'  TTCTTTAGATCCCACGGGTGTT 66065      C   AAA   A__
              CA                   TTTTT AGA   CTCA   GTGTTCA
                                   |||||  |||   ||||   |||||||
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                                AAGAA TCT   GGGT   CACAAGT
                                  A  A__    GCC
GAM2873  PTPRD    5'  TTCTTTAGATCCCACGGGTGTT 66065      C   AAA    A__
             CA                    TTTTT AGA   CTCA   GTGTTCA
                                |||||| |||   ||||   |||||||
                                AAGAA TCT   GGGT   CACAAGT
                                  A  A__    GCC
GAM2873  RAI3     3'  TTTCTCAGAAGACTCAAGATTT 66066          A      TG
             C                     TTTTTCAGAA ACTCAAG  TTC
                                |||||||||| |||||||  |||
                                AAAGAGTCTT TGAGTTC  AAG
                                      C      TA
GAM2873  TOX      5'  TTTTTTAAAAAAAAGTGTTCA  66067      C     CTC
                                TTTTT AGAAAA   AAGTGTTCA
                                ||||| ||||||   |||||||||
                                AAAAA TTTTTT   TTCACAAGT
                                  A     ___
GAM2873  ALS2CR3   3'  TTCTTCAGAAAACTGCCTT    66068           CAA  G
                                TTTTTCAGAAAACT   GT TT
                                ||||||||||||||   || ||
                                AAGAAGTCTTTTGA   CG AA
                                       ___  G
GAM2873  CSMD1    3'  TTTTTCAGAGTATTCGTGTTCA 66069         AAACTCAA
                                TTTTTCAGA       GTGTTCA
                                |||||||||       |||||||
                                AAAAAGTCT       CACAAGT
                                     CATAAG__
GAM2873  DKFZP586A0522 3'  TTTTTCAGAAACTTGAGC     66070          A  CA
                                TTTTTCAGAAA CT  AGT
                                |||||||||||  ||  |||
                                AAAAAGTCTTT GA  TCG
                                      _  AC
GAM2873  FLJ21615  3'  TCTTTCATTAAGTGTTC      66071        GAAAACTC
                                TTTTTCA       AAGTGTTC
                                |||||||       ||||||||
                                AGAAAGT       TTCACAAG
                                   AA_______
GAM2873  KIAA0895  3'  TTTTTCAGAGCATGGTCAAGT  66072         AAAC__
                                TTTTTCAGA     TCAAGT
                                |||||||||     ||||||
                                AAAAAGTCT     AGTTCA
                                     CGTACC
GAM2873  MAP3K6   3'  TTTTTCAAAAGTGTTC      66073          AAACTCA
                                TTTTTCAGA      AGTGTTC
                                |||||||||      |||||||
                                AAAAAGTTT      TCACAAG
                                               _______
GAM2873  NDUFB6   3'  TTTTCCAGAAAATTCAGTA    66074           C   A
                                TTTTTCAGAAAA TCA GTG
                                |||||||||||| ||| |||
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                                AAAAGGTCTTTT AGT CAT
                                      A  _
GAM2873  LOC157489 3'  TTTTTCAGAATGATGGTGTGTT 66075          AACTCAA
                                TTTTTCAGAA      GTGTT
                                ||||||||||      |||||
                                AAAAAGTCTT      CACAA
                                     ACTACCA
GAM2873  LOC196529 3'  TTTTTCAGAAACTTGAGC    66070          A  CA
                                TTTTTCAGAAA CT  AGT
                                |||||||||||  ||  |||
                                AAAAAGTCTTT GA  TCG
                                      _  AC
GAM2873  LOC221773 3'  TTTTCCAGAAAATTCAGCTC   66076           C   AGT
                                TTTTTCAGAAAA TCA   GTTC
                                ||||||||||||  |||   ||||
                                AAAAGGTCTTTT AGT   CGAG
                                      A  ___
GAM2873  LOC93082  3'  TTTTTCAGGAAACACAAACTTT 66077         A    T    TG
                                TTTTTCAG AAAC CAAG  TT
                                ||||||||  ||||  ||||  ||
                                AAAAAGTC TTTG GTTT  AA
                                     C    T    GA
GAM2874  IMPA1    3'  GTATGGTAATGTGAAATG    66080          C   AT_
                                GTATGGTAA TGT   ATG
                                |||||||||  |||   |||
                                CATACCATT ACA   TAC
                                      _   CTT
GAM2874  TTC4     3'  GCTGTGGTAACTGCAGCAGATG 66081    A_         TAT  C
              G                  GT  TGGTAACTGTA   GA GG
                                ||  ||||||||||   || ||
                                CG  ACCATTGACGT   CT CC
                                 AC         CGT  A
GAM2875  CD28     3'  ACTTGGATTGAAGAACTCTGT  66084          AT____
                                ACTTGGATT     TTCTGT
                                |||||||||     ||||||
                                TGAACCTAA     GAGACA
                                     CTTCTT
GAM2875  NCOA1    3'  TAATATATTTGTATATCTCTGT 66085        C   GAT
              A                  TAATATA TTG   TATTTCTGTA
                                |||||||  |||   ||||||||||
                                ATTATAT AAC   ATAGAGACAT
                                     A  AT_
GAM2875  PUM2     3'  ATATACAATATTTCTGTA    66086        TTGGAT
                                ATATAC     TATTTCTGTA
                                ||||||     ||||||||||
                                TATATG     ATAAAGACAT
                                   TT_____
GAM2875  SWAP70   3'  ATATACTTAGTTCATTTCTGT  66087          A
                                ATATACTTGG TTATTTCTGT
                                |||||||||| ||||||||||
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                                TATATGAATC AGTAAAGACA
                                     A
GAM2875  FLJ10697  3'  ATATTCTTAGCTGTGTTTCTGT 66088      A    ATTA_
             A                    ATAT CTTGG    TTTCTGTA
                                  |||| |||||    ||||||||
                                  TATA GAATC    AAAGACAT
                                    A    GACAC
GAM2875  KIAA0336  3'  TAATATACGTGAACCATTTTTG 66089        T       C
             TA                   TAATATAC TGGATTATTT TGTA
                                  |||||||| |||||||||| ||||
                                  ATTATATG ACTTGGTAAA ACAT
                                       C        A
GAM2875  KIAA0527  3'  TAACATGTTTCATTTCTGT   66090   T  T  GA
                                  A AC TG  TTATTTCTGT
                                  | || ||  ||||||||||
                                  A TG AC  AGTAAAGACA
                                   T  T  AA
GAM2875  MAP2K1IP1 3'  ATAGACTGAACCATTTCTGT   66091    T   T
                                  ATA ACT GGATTATTTCTGT
                                  ||| ||| ||||||||||||
                                  TAT TGA CTTGGTAAAGACA
                                    C  _
GAM2875  LOC199982 3'  TAATATATACCATTTCTGT   66092       CTTGG
                                  TAATATA    ATTATTTCTGT
                                  |||||||    ||||||||||
                                  ATTATAT    TGGTAAAGACA
                                       A____
GAM2875  LOC255995 5'  TAATATATTTGTATATCTCTGT 66085       C   GAT
             A                    TAATATA TTG   TATTTCTGTA
                                  ||||||| |||   ||||||||||
                                  ATTATAT AAC   ATAGAGACAT
                                       A   AT_
GAM2876  BMP1     3'  TTTCTGCACTCGGAATTTGA   66095        _  C   CCCG
                                  TTTCTGCAC CG AAT    TGA
                                  ||||||||| || |||    |||
                                  AAAGACGTG GC TTA    ACT
                                       A  C   A___
GAM2876  BMP1     3'  TTTCTGCACTCGGAATTTGA   66095        _  C   CCCG
                                  TTTCTGCAC CG AAT    TGA
                                  ||||||||| || |||    |||
                                  AAAGACGTG GC TTA    ACT
                                       A  C   A___
GAM2876  BMP1     3'  TTTCTGCACTCGGAATTTGA   66095        _  C   CCCG
                                  TTTCTGCAC CG AAT    TGA
                                  ||||||||| || |||    |||
                                  AAAGACGTG GC TTA    ACT
                                       A  C   A___
GAM2876  BMP1     3'  TTTCTGCACTCGGAATTTGA   66095        _  C   CCCG
                                  TTTCTGCAC CG AAT    TGA
                                  ||||||||| || |||    |||
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                                AAAGACGTG GC TTA   ACT
                                    A  C   A___
GAM2876  MLANA    3'  CTTCTGCACATTCTTGTGA   66096       CGCAA  CC
                                TTTCTGCAC    TC  GTGA
                                |||||||||    ||  ||||
                                GAAGACGTG    AG  CACT
                                    TA___  AA
GAM2876  PMX1     5'  CTCTCTGCACTCCTGTG     66097       CGCAA   C
                                CTTTCTGCAC    TCC GTG
                                ||||||||||    ||| |||
                                GAGAGACGTG    AGG CAC
                                    _____  A
GAM2876  PMX1     5'  CTCTCTGCACTCCTGTG     66097       CGCAA   C
                                CTTTCTGCAC    TCC GTG
                                ||||||||||    ||| |||
                                GAGAGACGTG    AGG CAC
                                    _____  A
GAM2876  BTN3A1   3'  TTTCTGCACCCCAGTTTCC   66098       G  A__
                                TTTCTGCACC CA   TCC
                                |||||||||| ||   |||
                                AAAGACGTGG GT   AGG
                                    G  CAA
GAM2876  BTN3A3   3'  CTTTCTGCACCCCAGTTTCC   66099       G  A__
                                CTTTCTGCACC CA   TCC
                                |||||||||| ||   |||
                                GAAAGACGTGG GT   AGG
                                    G  CAA
GAM2876  DKFZP564D206 5'  TTCTGCACTGTAACTGTGAA  66100       CGC   CCC
                                TTCTGCAC   AAT   GTGAA
                                ||||||||   |||   |||||
                                AAGACGTG   TTG   CACTT
                                    ACA   A__
GAM2876  ILF3     3'  CTTTCTGCTTGCCCTGTG    66101       ACC  AAT  C
                                CTTTCTGC   GC   CC GTG
                                ||||||||   ||   || |||
                                GAAAGACG   CG   GG CAC
                                    AA_  ___  A
GAM2876  KIAA1143 3'  TTTCTGCATTGCAGATGA    66102       CC   ATCCC
                                TTTCTGCA  GCA    GTGA
                                ||||||||  |||    ||||
                                AAAGACGT  CGT    TACT
                                    AA   C____
GAM2876  KIAA1183 3'  TTCTGCACTGCCCAGGTGA   66103       C  AAT  C_
                                TTCTGCAC GC   CC  GTGA
                                |||||||| ||   ||  ||||
                                AAGACGTG CG   GG  CACT
                                    A  ___  TC
GAM2876  LOC125268 3'  CTTTCTGCAGCTGCACGC    66104       CC_   ATCC
                                CTTTCTGCA   GCA   CGT
                                |||||||||   |||   |||
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                                GAAAGACGT  CGT  GCG
                                     CGA  ____
GAM2876 LOC221810 3' TTCTGCACTGTCAGTCTTGTG 66105       CG_ A CC
                                TTCTGCAC  CA TC GTG
                                ||||||||  || || |||
                                AAGACGTG  GT AG CAC
                                     ACA C AA
GAM2876 LOC51008 5' CTTTCTGCAATATCGTGA   66106       CCGCA CC
                                CTTTCTGCA   AT CGTGA
                                |||||||||   || |||||
                                GAAAGACGT   TA GCACT
                                     _____ TA
GAM2876 LOC91801 3' TTTCTGCACGTGATTCCATG 66107       C CA C
                                TTTCTGCAC G AT CCGTG
                                ||||||||| |  || |||||
                                AAAGACGTG C  TA GGTAC
                                     _ AC A
GAM2877 APPBP2  3' ATACCTAGGATTGCAAT   66110      CAT
                                ATACCTG  GTTGCAAT
                                |||||||  ||||||||
                                TATGGAT  TAACGTTA
                                     CC_
GAM2877 CUL4B   3' TAAAATACCTGGCCACA   66111        CAT TG
                                TAAAATACCTG  GT CA
                                ||||||||||  || ||
                                ATTTTATGGAC  CG GT
                                     ___ GT
GAM2877 DCN     3' TAAAACATCCACATTGCA   66112      C TG  GT
                                TAAAATA C  CAT  TGCA
                                |||||||  |  |||  ||||
                                ATTTTGT G  GTA  ACGT
                                     A GT  __
GAM2877 DCN     3' TAAAACATCCACATTGCA   66112      C TG  GT
                                TAAAATA C  CAT  TGCA
                                |||||||  |  |||  ||||
                                ATTTTGT G  GTA  ACGT
                                     A GT  __
GAM2877 DCN     3' TAAAACATCCACATTGCA   66112      C TG  GT
                                TAAAATA C  CAT  TGCA
                                |||||||  |  |||  ||||
                                ATTTTGT G  GTA  ACGT
                                     A GT  __
GAM2877 DCN     3' TAAAACATCCACATTGCA   66112      C TG  GT
                                TAAAATA C  CAT  TGCA
                                |||||||  |  |||  ||||
                                ATTTTGT G  GTA  ACGT
                                     A GT  __
GAM2877 DCN     3' TAAAACATCCACATTGCA   66112      C TG  GT
                                TAAAATA C  CAT  TGCA
                                |||||||  |  |||  ||||
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                                ATTTTGT G  GTA  ACGT
                                   A GT   __
GAM2877 DCN     3'  TAAAACATCCACATTGCA    66112       C TG   GT
                                TAAAATA C  CAT  TGCA
                                ||||||| |  |||  ||||
                                ATTTTGT G  GTA  ACGT
                                   A GT   __
GAM2877 GAS41   3'  TAAAATACCTATATAGCA    66113         GC    T
                                TAAAATACCT  ATGT GCA
                                ||||||||||  |||| |||
                                ATTTTATGGA  TATA CGT
                                      __    T
GAM2877 PPARGC1  3'  TAAAATACCTGCATTTAAC   66114            GTT
                                TAAAATACCTGCAT   GC
                                ||||||||||||||   ||
                                ATTTTATGGACGTA   TG
                                      AAT
GAM2877 TEM7    3'  CAAAATACCTGTGTGTGCA    66115          CA   T
                                TAAAATACCTG  TGT GCA
                                ||||||||||  |||  |||
                                GTTTTATGGAC  ACA CGT
                                      AC   _
GAM2877 CTCFL   3'  TAAAATACCTGCAATGTT    66116           _
                                TAAAATACCTGCA TGTT
                                ||||||||||||| ||||
                                ATTTTATGGACGT ACAA
                                      T
GAM2877 DKFZP434B172 3'  AAATACTTGCACGCCATGCAAT 66117       C      __
             C                    AAATAC TGCATGT  TGCAATC
                                ||||||| |||||||  |||||||
                                TTTATG ACGTGCG  ACGTTAG
                                   A      GT
GAM2877 ELF2    3'  TAAAATACCTATATTAGCA    66118          C  GTT
                                TAAAATACCTG AT   GCA
                                ||||||||||| ||   |||
                                ATTTTATGGAT TA   CGT
                                      A  AT_
GAM2877 GL004   5'  TAAAATACTGCTACCCTGCA   66119        C  _  G
                                TAAAATAC TGC AT TTGCA
                                |||||||| ||| || |||||
                                ATTTTATG ACG TG GACGT
                                      _  A  G
GAM2877 HHLA2   3'  TAAAATACCTTGTCAAATCAAT 66120          GCATGTTG
             C                    TAAAATACCT       CAATC
                                ||||||||||       |||||
                                ATTTTATGGA       GTTAG
                                      ACAGTTTA
GAM2877 HSOBRGRP  3'  TAAAATGCCGCATGTGC     66121        A  T     T
                                TAAAAT CC GCATGT GC
                                |||||| || |||||| ||
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                                ATTTTA GG CGTACA CG
                                   C  _     _
GAM2877  LOC115207 3'  TAAAATACTTGGCATGTT    66122        CT_
                                TAAAATAC   GCATGTT
                                ||||||||   |||||||
                                ATTTTATG   CGTACAA
                                     AAC
GAM2877  LOC147219 3'  TAAAATACCTGAGTACACA    66123          CATGT
                                TAAAATACCTG    TGCA
                                ||||||||||     ||||
                                ATTTTATGGAC    GTGT
                                       TCAT_
GAM2877  LOC151057 3'  AATACCTGCAGTGAAATC    66124         T  T C
                                AATACCTGCA GT G AATC
                                |||||||||| || | ||||
                                TTATGGACGT CA C TTAG
                                      _  _ T
GAM2877  LOC151273 3'  TAAAATACCTATATTAGCA    66118          C  GTT
                                TAAAATACCTG AT   GCA
                                |||||||||| ||   |||
                                ATTTTATGGAT TA   CGT
                                       A  AT_
GAM2877  LOC155434 3'  TAAAATACCTGTTCCGTC    66125          CA_
                                TAAAATACCTG   TGTT
                                ||||||||||   ||||
                                ATTTTATGGAC   GCAG
                                       AAG
GAM2878  EIF4E    3'  ATCAGAATCACTAATATTA    66128       TTT
                                ATCAGA   ATCATTAATATTA
                                ||||||   ||||||||||||
                                TAGTCT   TAGTGATTATAAT
                                      ___
GAM2878  IGF1     3'  ATCAGATTTATCTTTTGAAAAT 66129          ATT____
            ATT                   ATCAGATTTATC      AATATT
                                ||||||||||||      ||||||
                                TAGTCTAAATAG      TTATAA
                                      AAAACTT
GAM2878  SPS2     3'  AGATTTATCAACAATATT    66130          T
                                AGATTTATCA TAATATT
                                |||||||||| |||||||
                                TCTAAATAGT GTTATAA
                                      T
GAM2878  BIRC8    5'  ATCAGATTCACCTCGAATATTA 66131          ATT
                                ATCAGATTTATC   AATATTA
                                ||||||||||||   |||||||
                                TAGTCTAAGTGG   TTATAAT
                                      AGC
GAM2878  FLJ10178 3'  ATCAGATTTATCTTGATAC    66132          A  A
                                ATCAGATTTATC TT ATAT
                                |||||||||||| || ||||
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                                TAGTCTAAATAG AA TATG
                                      _  C
GAM2878 KIAA0997 3' CAGATTTACACAAATATTA   66133       T  T
                                CAGATTTA CAT AATATTA
                                |||||||| ||| |||||||
                                GTCTAAAT GTG TTATAAT
                                     _  T
GAM2878 MGC14433 3' AGATTTATCAATAAAATATTA 66134        TT__
                                AGATTTATCA   AATATTA
                                ||||||||||   |||||||
                                TCTAAATAGT   TTATAAT
                                      TATT
GAM2878 SERP1    3' TCAAATTTATCAGAACATT   66135         TT
                                TCAGATTTATCA  AATATT
                                ||||||||||||  ||||||
                                AGTTTAAATAGT  TTGTAA
                                      C_
GAM2879 BIN2     3' TCTATAGATACTTTTGC     66138       ACACT
                                TCTATAGA    TTTTTGC
                                ||||||||    |||||||
                                AGATATCT    GAAAACG
                                     AT___
GAM2879 CDH1     3' AGAATACTTTTCTCAGCT    66139     C      G
                                AGAA ACTTTTTT CAGCT
                                |||| |||||||| |||||
                                TCTT TGAAAAGA GTCGA
                                  A      _
GAM2879 INMT     3' TATAGAACATTCCCCCTGGCT  66140        C    GCA
                                TATAGAACA TTTTTT   GCT
                                ||||||||| ||||||   |||
                                ATATCTTGT AGGGGGG   CGA
                                     A     AC_
GAM2879 ARPP-21  5' TCTATAGACACTGGAAATGGCT 66141       A   TTTTTGCA
                                TCTATAGA CACT       GCT
                                |||||||| ||||       |||
                                AGATATCT GTGA       CGA
                                     _   CCTTTAC_
GAM2879 C20orf82 5' AGAACTCGCTTTTGCAGCT   66142      ACT
                                AGAAC   TTTTTGCAGCT
                                |||||   ||||||||||||
                                TCTTG   GAAAACGTCGA
                                   AGC
GAM2879 CECR2    3' TCTATAGAATACATTTTTC   66143       C _
                                TCTATAGAA AC TTTTTT
                                ||||||||| || ||||||
                                AGATATCTT TG AAAAAG
                                     A  T
GAM2879 DKFZP564P1916 3' TCTATAGAACAGTTTTAC    66144         CTT
                                TCTATAGAACA   TTTTGC
                                ||||||||||   ||||||
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                                AGATATCTTGT   AAAATG
                                      C__
GAM2879  FLJ10856  3'  TATAGAACATCTTTTTAAAG  66145        C      C
                                TATAGAACA TTTTTTG AG
                                ||||||||| ||||||| ||
                                ATATCTTGT GAAAAAT TC
                                     A      T
GAM2879  FLJ10904  3'  TATAGAACACTAACAG     66146          TTTTT
                                TATAGAACACT    GCAG
                                ||||||||||    ||||
                                ATATCTTGTGA    TGTC
                                      T____
GAM2879  FLJ11011  3'  TCTATAGAAAGTTTCATCTAGC 66147        CAC   TTGC
           T                     TCTATAGAA   TTTT   AGCT
                                |||||||||  ||||   ||||
                                AGATATCTT   AAAG   TCGA
                                     TC_   TAGA
GAM2879  FLJ12572  3'  CTGTAGAACACCAAGCAGCT  66148   A       TTTTT
                                CT TAGAACACT    GCAGCT
                                || |||||||||    ||||||
                                GA ATCTTGTGG    CGTCGA
                                 C       TT___
GAM2879  FLJ12604  5'  TCTTTAGAGCACTGCAGC    66149    A   A   TTTTT
                                TCT TAGA CACT    GCAGC
                                ||| |||| ||||    |||||
                                AGA ATCT GTGA    CGTCG
                                  A   C   _____
GAM2879  FLJ22625  3'  TCTATTGAATATTTTTGCA   66150      A  CACT
                                TCTAT GAA   TTTTTGCA
                                ||||| |||   ||||||||
                                AGATA CTT   AAAAACGT
                                   A  AT__
GAM2879  GAPCENA   5'  TCTGCTAGCTCTTTTTGCAGCT 66151    A_   AACAC
                                TCT  TAG    TTTTTTGCAGCT
                                |||  |||    ||||||||||||
                                AGA  ATC    GAAAAACGTCGA
                                  CG   GA___
GAM2879  KIAA0603  3'  TCTAAGGAGCACTTTCTGC   66152     TA  A      T
                                TCTA  GA CACTTTTT GC
                                ||||  || |||||||| ||
                                AGAT  CT GTGAAAGA CG
                                   TC  C      _
GAM2879  KIAA0931  3'  TCTATAGTGCACTGCAGC    66153       AA   TTTTT
                                TCTATAG  CACT    GCAGC
                                |||||||  ||||    |||||
                                AGATATC  GTGA    CGTCG
                                    AC   _____
GAM2879  LOC147639 5'  TAAAATATTTTTGCAGC     66154       CACT
                                TAGAA    TTTTTGCAGC
                                |||||    ||||||||||
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                                ATTTT   AAAAACGTCG
                                  AT__
GAM2879  LOC150095 5'  TCTATGGAACCTTTTCT     66155      A   A
                                TCTAT GAAC CTTTTTT
                                ||||| |||| |||||||
                                AGATA CTTG GAAAAGA
                                  C   _
GAM2879  LOC150577 3'  CCTATAGAACATAAACTGCAGC 66156          CTTTT
           T                     TCTATAGAACA    TTGCAGCT
                                ||||||||||    ||||||||
                                GGATATCTTGT    GACGTCGA
                                      ATTT_
GAM2879  LOC150967 3'  TATAGAATACTTGCAGCT    66157       C   TTTT
                                TATAGAA ACT    TGCAGCT
                                ||||||| |||    |||||||
                                ATATCTT TGA    ACGTCGA
                                   A  ____
GAM2879  LOC151201 3'  TCTATAAACATTTTTTAC    66158       A  C
                                TCTATAGA CA TTTTTTGC
                                |||||||| || ||||||||
                                AGATATTT GT AAAAAATG
                                  _ _
GAM2879  LOC90594  3'  TATGGAACGCTTTTCCACA   66159     A   A     TG
                                TAT GAAC CTTTTT  CA
                                ||| |||| ||||||  ||
                                ATA CTTG GAAAAG  GT
                                  C   C     GT
GAM2880  ANGPT1    5'  GCTGCGTGTACATATTC     66162       ATA  T
                                GCTGCGT   GT ATGTATTC
                                |||||||   || ||||||||
                                CGACGCA   CA TGTATAAG
                                  ___  _
GAM2880  ANGPT1    5'  GCTGCGTGTACATATTC     66162       ATA  T
                                GCTGCGT   GT ATGTATTC
                                |||||||   || ||||||||
                                CGACGCA   CA TGTATAAG
                                  ___  _
GAM2880  CYB561    3'  TGCGTTGTTTATGTATTC    66163      ATAG
                                TGCGT    TTATGTATTC
                                |||||    ||||||||||
                                ACGCA    AATACATAAG
                                  ACA_
GAM2880  F3        3'  TGCGTTTCCATGTATTCT    66164      ATAG
                                TGCGT    TTATGTATTCT
                                |||||    |||||||||||
                                ACGCA    GGTACATAAGA
                                  AA__
GAM2880  SCD       3'  TGCGTTGTTTATGTATTC    66163      ATAG
                                TGCGT    TTATGTATTC
                                |||||    ||||||||||
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                                ACGCA    AATACATAAG
                                   ACA_
GAM2880 UBE2B    3' CACTGAAGTTATGTATT     66165       CGTAT
                                CGCTG    AGTTATGTATT
                                |||||    ||||||||||
                                GTGAC    TCAATACATAA
                                   T____
GAM2880 HCC8     3' GCTGTGTTACAGCTATGTGTTC 66166      C _        A
           T                     GCTG GT ATAGTTATGT TTCT
                                |||| || |||||||||| ||||
                                CGAC CA TGTCGATACA AAGA
                                  A A         C
GAM2880 LOC148525 5' ACGCTGCGTTATGGTTCGC    66167          _ A   A
                                ACGCTGCGT AT GTT TGT
                                ||||||||| || ||| |||
                                TGCGACGCA TA CAA GCG
                                     A  C  _
GAM2880 LOC151248 3' ACGCTGTGTATGTACTGTTTCT 66168       C    A  TA   A
                                ACGCTG GTAT GT  TGT TTCT
                                |||||| |||| ||  ||| ||||
                                TGCGAC CATA CA  ACA AAGA
                                   A    _ TG  _
GAM2881 ASTN     3' TGAGGCAGGTGCATTAGAGAGT 66171       C      G
                                TGAGGC GGTGTAT TAGAGAGT
                                |||||| ||||||| ||||||||
                                ACTCCG CCACGTA ATCTCTCA
                                   T      _
GAM2881 PDE4A    5' GAGGCTGGGCTTGGGGAGTC   66172      C  T  A  TAGA
                                GAGGC GG GT TG    GAGTC
                                ||||| || || ||    |||||
                                CTCCG CC CG AC    CTCAG
                                   A  _  A  CC__
GAM2881 BCMP1    3' AGGCAAATGTATGTGGAGGGT  66173      CG       A   A
                                AGGC  GTGTATGT GAG GT
                                ||||  |||||||| ||| ||
                                TCCG  TACATACA CTC CA
                                   TT       C   C
GAM2881 FLJ20671 3' TGAGTTATCATTGTAGAGAGTC 66174      GCCGG   A
                                TGAG     TGT TGTAGAGAGTC
                                ||||     ||| ||||||||||||
                                ACTC     GTA ACATCTCTCAG
                                   AATA_  _
GAM2881 FLJ21736 5' GAGGTTGAGGCAGTAGAGAGTC 66175      CC  T   T
                                GAGG  GG GTA GTAGAGAGTC
                                ||||  || ||| ||||||||||
                                CTCC  CT CGT CATCTCTCAG
                                   AA  C  _
GAM2881 KIAA1297 3' TGGGGCCAGTGAGGTAGGAGAG 66176    A       TAT   _
           TC                     TG GGCCGGTG   GTAG AGAGTC
                                || ||||||||   |||| ||||||
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                                AC CCGGTCAC   CATC TCTCAG
                                 C       TC_   C
GAM2881 KIAA1938 3' TGGGGCGGTGGAGGGGAGT   66177    A  C   TATGT  A_
                                TG GGC GGTG    AG  GAGT
                                || ||| ||||    ||  ||||
                                AC CCG CCAC    TC  CTCA
                                 C  _   C____  CC
GAM2881 LOC128308 5' TGGGGCTGGTCCAGGAGGGTC  66178    A  C  G  TGTA  A
                                TG GGC GGT TA   GAG GTC
                                || ||| ||| ||   ||| |||
                                AC CCG CCA GT   CTC CAG
                                 C  A  G  C___  C
GAM2881 LOC254213 3' TGAGGCCGTGTGTGTCGT    66179        _   A_
                                TGAGGCCG GTGT  TGT
                                |||||||| ||||  |||
                                ACTCCGGC CACA  GCA
                                     A   CA
GAM2881 LOC93052  5' TGGGGCCGCTGTGTGTGGAG  66180    A   G  A  A
                                TG GGCCG TGT TGT GAG
                                || ||||| ||| ||| |||
                                AC CCGGC ACA ACA CTC
                                 C   G  C  C
GAM2882 AGTR1    3' TACAAAATGTGCAGTACCAGG  66183        TA  C
                                TACAAAGTGT  CAG ACCAGG
                                ||||||||||  ||| ||||||
                                ATGTTTTACA  GTC TGGTCC
                                     C_  A
GAM2882 AGTR1    3' TACAAAATGTGCAGTACCAGG  66183        TA  C
                                TACAAAGTGT  CAG ACCAGG
                                ||||||||||  ||| ||||||
                                ATGTTTTACA  GTC TGGTCC
                                     C_  A
GAM2882 AGTR1    3' TACAAAATGTGCAGTACCAGG  66183        TA  C
                                TACAAAGTGT  CAG ACCAGG
                                ||||||||||  ||| ||||||
                                ATGTTTTACA  GTC TGGTCC
                                     C_  A
GAM2882 AGTR1    3' TACAAAATGTGCAGTACCAGG  66183        TA  C
                                TACAAAGTGT  CAG ACCAGG
                                ||||||||||  ||| ||||||
                                ATGTTTTACA  GTC TGGTCC
                                     C_  A
GAM2882 AGTR1    3' TACAAAATGTGCAGTACCAGG  66183        TA  C
                                TACAAAGTGT  CAG ACCAGG
                                ||||||||||  ||| ||||||
                                ATGTTTTACA  GTC TGGTCC
                                     C_  A
GAM2882 CD28     3' TACAGGTGCCTGCCACCAGGC  66184     AA   ACAG
                                TACA  GTGTT   CACCAGGC
                                ||||  |||||   ||||||||
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                                ATGT  CACGG   GTGGTCCG
                                  C_    ACG_
GAM2882  CDC7L1   3'  AAGAGCACCAGCACCAGG    66185    T  TA
                                AAG GT  CAGCACCAGG
                                ||| ||  ||||||||||
                                TTC CG  GTCGTGGTCC
                                  T  TG
GAM2882  CX3CR1   3'  CACAGCACAGCAGTGCCAGG   66186    A   GTT    ___
                                CA AGT   ACAGCA   CCAGG
                                || |||   ||||||   |||||
                                GT TCG   TGTCGT   GGTCC
                                 G  ___     CAC
GAM2882  DBT      3'  TACAGGCGTGAGCCACCAGGC  66187     AA   TAC  _
                                TACA  GTGT   AGC ACCAGGC
                                ||||  ||||   ||| |||||||
                                ATGT  CGCA   TCG TGGTCCG
                                  C_   C__   G
GAM2882  F2RL3    3'  ACAAAGTGCCACATGCCAGGC  66188          GCA
                                ACAAAGTGTTACA   CCAGGC
                                ||||||||||||   ||||||
                                TGTTTCACGGTGT   GGTCCG
                                       AC_
GAM2882  F2RL3    3'  TACAGGCGTGAGCCACCAGGC  66187     AA   TAC  _
                                TACA  GTGT   AGC ACCAGGC
                                ||||  ||||   ||| |||||||
                                ATGT  CGCA   TCG TGGTCCG
                                  C_   C__   G
GAM2882  FOS      3'  TGAAAATATCCAGCACCAGG   66189   C      A
                                A AAAGTGTT CAGCACCAGG
                                | |||||||| ||||||||||
                                A TTTTATAG GTCGTGGTCC
                                 C      _
GAM2882  GLI2     3'  GTGCACTCAGCACCAGGC    66190     TA_
                                GTGT   CAGCACCAGGC
                                ||||   ||||||||||
                                CACG   GTCGTGGTCCG
                                  TGA
GAM2882  KLF8     5'  TACAGGTGTGAGCCACCAGGC  66191     AA   TAC  _
                                TACA  GTGT   AGC ACCAGGC
                                ||||  ||||   ||| |||||||
                                ATGT  CACA   TCG TGGTCCG
                                  C_   C__   G
GAM2882  NEBL     3'  CACAATTAGCAGCACCAGGC   66192     AAGT   _
                                TACA    GTTA CAGCACCAGGC
                                ||||    |||| ||||||||||
                                GTGT    TAAT GTCGTGGTCCG
                                  _____   C
GAM2882  PITX2    3'  TACGAAATGTTATACACAGG   66193    A      CA   C
                                TAC AAGTGTTA  GCAC AGG
                                ||| ||||||||  |||| |||
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                                ATG TTTACAAT  TGTG TCC
                                  C       A_   _
GAM2882 RARG     3' GCATCACACAGCATTAGGC   66194      __     CC
                                GTGTT  ACAGCA  AGGC
                                |||||  ||||||  ||||
                                CGTAG  TGTCGT  TCCG
                                   TG     AA
GAM2882 SLC7A6   3' TGAAATGACCTAGCACCAGG  66195   A    TTAC
                                C AAGTG   AGCACCAGG
                                | |||||   |||||||||
                                A TTTAC   TCGTGGTCC
                                 C    TGGA
GAM2882 SYNGR1   3' AAAACACCCAGCACTGGGC   66196     TG  A     CA
                                AAAG  TT CAGCAC  GGC
                                ||||  || ||||||  |||
                                TTTT  GG GTCGTG  CCG
                                  GT  _     AC
GAM2882 TCEB1L   3' TACAGTGTTACAGTGTCAGGC 66197      AA       CAC
                                TACA  GTGTTACAG   CAGGC
                                ||||  |||||||||   |||||
                                ATGT  CACAATGTC   GTCCG
                                  __        ACA
GAM2882 TNFRSF5  3' CACAGCAGCAGCAGCACCAGGC 66198    A  _  TA
                                CA AGT GT  CAGCACCAGGC
                                || ||| ||  ||||||||||
                                GT TCG CG  GTCGTGGTCCG
                                 G   T  TC
GAM2882 XKRY     5' TACAAGGTGTGACAGCAC    66199      A    T
                                TACAA GTGT ACAGCAC
                                ||||| |||| |||||||
                                ATGTT CACA TGTCGTG
                                   C    C
GAM2882 XKRY     5' TACAAGGTGTGACAGCAC    66199      A    T
                                TACAA GTGT ACAGCAC
                                ||||| |||| |||||||
                                ATGTT CACA TGTCGTG
                                   C    C
GAM2882 ALDH9    3' ACAAAGTGCTTACTAGG     66200         ACAGC  C
                                ACAAAGTGTT    AC AGG
                                ||||||||||    || |||
                                TGTTTCACGA    TG TCC
                                     A_____  A
GAM2882 APELIN   3' CACAAAGTTGGGCATCAGGC  66201        GTTACA  C
                                TACAAAGT     GCA CAGGC
                                ||||||||     ||| |||||
                                GTGTTTCA     CGT GTCCG
                                    ACC___   A
GAM2882 BRD1     5' TACAGGGCTGGACCCCACCAGG 66202     AA  GTT  AG
            C                    TACA  GT   AC  CACCAGGC
                                ||||  ||   ||  ||||||||
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                                ATGT  CG   TG  GTGGTCCG
                                  CC  ACC  GG
GAM2882 BRD2     5' CAAGGTGTCAGTCACCAGGC  66203     A   TA  _
                                CAA GTGT  CAG CACCAGGC
                                ||| ||||  ||| ||||||||
                                GTT CACA  GTC GTGGTCCG
                                  C   __  A
GAM2882 C20orf10 5' AATGGAGCAACACCAGTGC   66204     TTA      _
                                AGTG  CAGCACCAG GC
                                ||||  ||||||||| ||
                                TTAC  GTTGTGGTC CG
                                  CTC       A
GAM2882 CARD14   5' CAAAGCAGCACCAGG      66205     TGTTA
                                CAAAG    CAGCACCAGG
                                |||||    ||||||||||
                                GTTTC    GTCGTGGTCC
                                  _____
GAM2882 CHST3    3' TACAAATGTTAAGCACAGGC  66206      G   C   C
                                TACAAA TGTTA AGCAC AGGC
                                |||||| ||||| ||||| ||||
                                ATGTTT ACAAT TCGTG TCCG
                                  _   _   _
GAM2882 DKFZP564D0462 5' AAGTGGTTACACAGGC     66207     _   GCAC
                                AAGTG TTACA   CAGGC
                                ||||| |||||   |||||
                                TTCAC AATGT   GTCCG
                                  C   ____
GAM2882 FBXO22   3' CAGATTTCCACAGCACCGGGC 66208   AAGTG       A
                                CA    TTACAGCACC GGC
                                ||    |||||||||| |||
                                GT    GGTGTCGTGG CCG
                                 CTAAA       C
GAM2882 FLJ11126 3' TACAGGCGTGCGCCACCAGGC 66209    AA_   TACAG
                                TACA  GTGT    CACCAGGC
                                ||||  ||||    ||||||||
                                ATGT  CACG    GTGGTCCG
                                  CCG   CG___
GAM2882 FLJ14326 5' CAGGATGTGGCACCAGGC    66210   AA   TACA
                                CA GTGT   GCACCAGGC
                                || ||||   |||||||||
                                GT TACA   CGTGGTCCG
                                 CC   C___
GAM2882 FLJ14457 3' TACAAATGGCCCCACCAGGC  66211     GT  ACAG
                                TACAAA GTT   CACCAGGC
                                |||||| |||   ||||||||
                                ATGTTT CGG   GTGGTCCG
                                   AC  G___
GAM2882 FLJ14564 3' CACAGGTGGGCTGGCACCAGG 66212    AA  TTACA
                                TACA GTG    GCACCAGG
                                |||| |||    ||||||||
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                                GTGT  CAC    CGTGGTCC
                                  C_   CCGAC
GAM2882  FLJ14800  3'  ACAACAGTGGCAGCACCAGG   66213     _    TTA
                                ACAA AGTG   CAGCACCAGG
                                |||| ||||   ||||||||||
                                TGTT TCAC   GTCGTGGTCC
                                  G   C__
GAM2882  FLJ20359  3'  CACAGAGTGGGCTGCACCAGGC 66214     A    TTACA
                                TACA AGTG    GCACCAGGC
                                |||| ||||    |||||||||
                                GTGT TCAC    CGTGGTCCG
                                  C   CCGA_
GAM2882  FLJ21168  3'  TAAAAGTAAAGGCACCAGGC   66215   C     TTACA
                                A AAAGTG    GCACCAGGC
                                | ||||||    |||||||||
                                A TTTCAT    CGTGGTCCG
                                 T     TTC__
GAM2882  FLJ22169  3'  ATATTCTGACAGCACCAGGC   66216     ___
                                GTGTT   ACAGCACCAGGC
                                |||||   ||||||||||||
                                TATAA   TGTCGTGGTCCG
                                   GAC
GAM2882  HTATIP    5'  ACGGAGTGTTACAAGCCTCAGG 66217    AA       _  AC
           C                     AC  AGTGTTACA GC  CAGGC
                                ||  |||||||| ||  |||||
                                TG  TCACAATGT CG  GTCCG
                                 CC        T  GA
GAM2882  KIAA0266  3'  TACAGGTGCCTGCCACCAGGC  66184     AA    ACAG
                                TACA  GTGTT    CACCAGGC
                                ||||  |||||    ||||||||
                                ATGT  CACGG    GTGGTCCG
                                  C_    ACG_
GAM2882  KIAA0766  3'  ACAAAGTGTTTACTTTAGGC   66218         ACA  ACC
                                ACAAAGTGTT   GC   AGGC
                                ||||||||||   ||   ||||
                                TGTTTCACAA   TG   TCCG
                                      A__  AAA
GAM2882  KIAA0939  3'  CAAAGTGTGAGGCCAGG     66219        TAC  CA
                                CAAAGTGT   AG  CCAGG
                                ||||||||   ||  |||||
                                GTTTCACA   TC  GGTCC
                                     C__  C_
GAM2882  KIAA0945  3'  AGGTTCCCAGCACCAGGC    66220    T   A_
                                AG GTT  CAGCACCAGGC
                                || |||  ||||||||||
                                TC CAA  GTCGTGGTCCG
                                 _   GG
GAM2882  KIAA1363  5'  CAAAGTGTGGCAGTCACTACAG 66221        TA   _   __
           G                     CAAAGTGT  CAG CAC  CAGG
                                ||||||||  ||| |||  ||||
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                                GTTTCACA  GTC GTG  GTCC
                                    CC   A   AT
GAM2882  KIAA1712  3'  AAAGTGTTACGCCGGAGGC   66222         A  ACC
                                AAAGTGTTAC GC   AGGC
                                |||||||||| ||   ||||
                                TTTCACAATG CG   TCCG
                                    _  GCC
GAM2882  MGC22014  3'  CACAACACTACAGCACCAGGC  66223    A  TG
                                CA AG  TTACAGCACCAGGC
                                || ||  ||||||||||||||
                                GT TT  GATGTCGTGGTCCG
                                 G  GT
GAM2882  RBAK      3'  TACAAAATATTGGCACTAGGC  66224         ACA    C
                                TACAAAGTGTT   GCAC AGGC
                                ||||||||||   |||| ||||
                                ATGTTTTATAA   CGTG TCCG
                                      C__    A
GAM2882  RCD-8     3'  CACACACATACAGCACCAGG   66225     AAGTGT
                                TACA     TACAGCACCAGG
                                ||||     ||||||||||||
                                GTGT     ATGTCGTGGTCC
                                  GTGT__
GAM2882  RGS7      3'  TACAAAGTGTGTGCAGTGAC   66226         TACA   CCA
                                TACAAAGTGT    GCA   GGC
                                ||||||||||    |||   |||
                                ATGTTTCACA    CGT   CTG
                                      CA__   CA_
GAM2882  SMARCF1   3'  TACAGTATGTTTACAGTATCAG 66227     AA    _   CAC
           G                     TACA  GTGTT ACAG   CAGG
                                ||||  ||||| ||||   ||||
                                ATGT  TACAA TGTC   GTCC
                                  CA    A    ATA
GAM2882  SMARCF1   3'  TACAGTATGTTTACAGTATCAG 66227     AA    _   CAC
           G                     TACA  GTGTT ACAG   CAGG
                                ||||  ||||| ||||   ||||
                                ATGT  TACAA TGTC   GTCC
                                  CA    A    ATA
GAM2882  SMARCF1   3'  TACAGTATGTTTACAGTATCAG 66227     AA    _   CAC
           G                     TACA  GTGTT ACAG   CAGG
                                ||||  ||||| ||||   ||||
                                ATGT  TACAA TGTC   GTCC
                                  CA    A    ATA
GAM2882  TANK      5'  AAAGTGTTTTCCACAGGC    66228        ACAG   C
                                AAAGTGTT    CAC AGGC
                                ||||||||    ||| ||||
                                TTTCACAA    GTG TCCG
                                    AAG_   _
GAM2882  TANK      5'  AAAGTGTTTTCCACAGGC    66228        ACAG   C
                                AAAGTGTT    CAC AGGC
                                ||||||||    ||| ||||
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                                TTTCACAA   GTG TCCG
                                    AAG_  _
GAM2882  TBX21    3'  CAAGACGCAGCACCAGG    66229    AG  TTA
                                CAA  TG   CAGCACCAGG
                                |||  ||   ||||||||||
                                GTT  GC   GTCGTGGTCC
                                  CT  ___
GAM2882  USP3     5'  TACAAAGTATTTTCAGG    66230         ACAGCAC
                                TACAAAGTGTT     CAGG
                                ||||||||||      ||||
                                ATGTTTCATAA     GTCC
                                      AA_____
GAM2882  WBSCR23  5'  TACAGGTGCATACCACCAGGC  66231     AA   _  AG
                                TACA  GTGT TAC  CACCAGGC
                                ||||  |||| |||  ||||||||
                                ATGT  CACG ATG  GTGGTCCG
                                  C_   T  __
GAM2882  ZFP106   3'  TACAGGTGTGAGCCACCAGGC  66191    AA   TAC  _
                                TACA  GTGT   AGC ACCAGGC
                                ||||  ||||   ||| |||||||
                                ATGT  CACA   TCG TGGTCCG
                                  C_   C__   G
GAM2882  LOC113201 3'  TGAAGCCAATACAGCACTGGG  66232   A   GT_     CA
                                C AAGT   TACAGCAC  GG
                                | ||||   ||||||||  ||
                                A TTCG   ATGTCGTG  CC
                                 C   GTT      AC
GAM2882  LOC122728 3'  TACAAAGCGGACACTGGG    66233       TTACA   CA
                                TACAAAGTG    GCAC  GG
                                |||||||||    ||||  ||
                                ATGTTTCGC    TGTG  CC
                                     C____   AC
GAM2882  LOC131000 3'  TACAAAGTGTTGGGCAC     66234         ACA
                                TACAAAGTGTT   GCAC
                                ||||||||||   ||||
                                ATGTTTCACAA   CGTG
                                      CC_
GAM2882  LOC145368 3'  TACAAAGCGGACACTGGG    66233       TTACA   CA
                                TACAAAGTG    GCAC  GG
                                |||||||||    ||||  ||
                                ATGTTTCGC    TGTG  CC
                                     C____   AC
GAM2882  LOC146545 5'  AGTGTGGACGGCACCAGG    66235     T_  A
                                AGTGT  AC GCACCAGG
                                |||||  || ||||||||
                                TCACA  TG CGTGGTCC
                                   CC  C
GAM2882  LOC150423 3'  TACAAAGCGGACACTGGG    66233       TTACA   CA
                                TACAAAGTG    GCAC  GG
                                |||||||||    ||||  ||
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                                ATGTTTCGC    TGTG  CC
                                     C____    AC
GAM2882  LOC151827 5'  TACAAAGTGTGCACCGG     66236         TACA    A
                                TACAAAGTGT    GCACC GG
                                ||||||||||    ||||| ||
                                ATGTTTCACA    CGTGG CC
                                      ____    _
GAM2882  LOC219594 3'  TACAGTGTTACAGTGTCAGGC  66197     AA       CAC
                                TACA  GTGTTACAG   CAGGC
                                ||||  |||||||||   |||||
                                ATGT  CACAATGTC   GTCCG
                                  __       ACA
GAM2882  LOC219988 5'  TACAAAGTGGTCATCACTAGGC 66237        TTA  G   C
                                TACAAAGTG   CA CAC AGGC
                                |||||||||   || ||| ||||
                                ATGTTTCAC   GT GTG TCCG
                                     CA_  A   A
GAM2882  LOC257461 3'  TACAGTGTTACAGTGTCAGGC  66197     AA       CAC
                                TACA  GTGTTACAG   CAGGC
                                ||||  |||||||||   |||||
                                ATGT  CACAATGTC   GTCCG
                                  __       ACA
GAM2882  LOC51195  3'  CAAAGTGCTTGAGTGCCAGG   66238        AC  CA
                                CAAAGTGTT  AG  CCAGG
                                |||||||||  ||  |||||
                                GTTTCACGA  TC  GGTCC
                                     AC  AC
GAM2882  LOC51313  5'  AGCGGAGCACAGCGCCAGG    66239     T__     A
                                AGTG   TACAGC CCAGG
                                ||||   |||||| |||||
                                TCGC   GTGTCG GGTCC
                                  CTC     C
GAM2882  LOC90233  3'  ACAAAAATGGCACCAGGC     66240       _  TTACA
                                ACAAAG TG    GCACCAGGC
                                |||||| ||    |||||||||
                                TGTTTT AC    CGTGGTCCG
                                   T  _____
GAM2882  LOC91409  3'  CAGGGTGCTCTGGGCACCAGG  66241    AA    ACA_
                                CA  GTGTT    GCACCAGG
                                ||  |||||    ||||||||
                                GT  CACGA    CGTGGTCC
                                 CC    GACC
GAM2882  LOC91963  3'  AAAGTATAGCACCAGG      66242        TAC
                                AAAGTGT   AGCACCAGG
                                |||||||   |||||||||
                                TTTCATA   TCGTGGTCC
                                     ___
GAM2883  ENO2      5'  GAGCTGCCGGCGGAGGCGCACG 66245        __  ACTTCTT
                                GAGCTGC  GC      GGCGCACG
                                |||||||  ||      ||||||||
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                                CTCGACG CG     CCGCGTGC
                                   GC CCT____
GAM2883 INPP5B   5' GAGCTGTCACCACAGGGCGCAC 66246      CG   TCTT
           G                    GAGCTG CACT   GGCGCACG
                                |||||| ||||   ||||||||
                                CTCGAC GTGG   CCGCGTGC
                                   A_   TGTC
GAM2883 FLJ11700 3' GAGCTGTGGCTTCTTGGGCA  66247      CGCA      C
                                GAGCTG   CTTCTTGG GCA
                                ||||||   |||||||| |||
                                CTCGAC   GAAGAACC CGT
                                   ACC_     _
GAM2883 KIAA0997  5' GAGCTGCAGTGGCGGCGGCGCG 66248       CACTTCT     A
           CG                    GAGCTGCG     TGGCGC CG
                                 ||||||||     |||||| ||
                                 CTCGACGT     GCCGCG GC
                                    CACCGCC     C
GAM2883 PPAP2B   5' GAGCTGCGCAGCTTGGGGCGC  66249        _  CTT
                                GAGCTGCGCA CTT   GGCGC
                                |||||||||| |||   |||||
                                CTCGACGCGT GAA   CCGCG
                                   C  CC_
GAM2883 STARD7   5' GAGCTGCGCGATCTGCTGCGCG 66250       ACT  TG_   A
           CG                    GAGCTGCGC   TCT   GCGC CG
                                 |||||||||   |||   |||| ||
                                 CTCGACGCG   AGA   CGCG GC
                                    CT_  CGA   C
GAM2883 STARD7   5' GAGCTGCGCGATCTGCTGCGCG 66250       ACT  TG_   A
           CG                    GAGCTGCGC   TCT   GCGC CG
                                 |||||||||   |||   |||| ||
                                 CTCGACGCG   AGA   CGCG GC
                                    CT_  CGA   C
GAM2883 LOC115574 3' GAGCTGCGCCTTTGGGCTGGCG 66251       A  C___
           C                     GAGCTGCGC CTT   TTGGCGC
                                 ||||||||| |||   |||||||
                                 CTCGACGCG GAA   GACCGCG
                                    _  ACCC
GAM2883 LOC124602 3' GGCTGCGCTGGCGCA     66252   A     ACTTCT
                                G GCTGCGC     TGGCGCA
                                | |||||||     |||||||
                                C CGACGCG     ACCGCGT
                                _     _______
GAM2883 LOC133308 5' GAGCCGCGTGCGATGCCTGGTG 66253       CACTT__    C  A
           CGCG                    GAGCTGCG     CTTGG GC CG
                                   ||||||||     ||||| || ||
                                   CTCGGCGC     GGACC CG GC
                                      ACGCTAC    A  C
GAM2883 LOC168359 5' GCTGCACAGCACAGTTGGCGC  66254      ___   TTC
                                GCTGC   GCAC   TTGGCGC
                                |||||   ||||   |||||||
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                                CGACG  CGTG  AACCGCG
                                  TGT   TC_
GAM2883 LOC203397 3' GGCTGCGCTGGCGCA      66252   A     ACTTCT
                                G GCTGCGC     TGGCGCA
                                | |||||||     |||||||
                                C CGACGCG     ACCGCGT
                                _     _______
GAM2883 LOC51207 5' GCTGTGCACTTCTCTGACG   66255     C      _
                                GCTG GCACTTCT TGGCG
                                |||| |||||||| |||||
                                CGAC CGTGAAGA ACTGC
                                  A       G
GAM2883 LOC84528 5' GAGCTGTGCACTTCTGCA    66256      C       TG
                                GAGCTG GCACTTCT  GCG
                                |||||| ||||||||  |||
                                CTCGAC CGTGAAGA  CGT
                                   A       __
GAM2884 ADRBK1   3' TGCCAGGCCTAACACTG     66259       TC   T
                                TGCCAGGC  AAT ACTG
                                ||||||||  ||| ||||
                                ACGGTCCG  TTG TGAC
                                     GA  _
GAM2884 AKAP13   3' TGCCAGGCACGTTACTAGCTGC 66260       TCA__   _
           TAC                    TGCCAGGC    ATTA CTGCTAC
                                |||||||     |||| |||||||
                                ACGGTCCG    TGAT GACGATG
                                     TGCAA   C
GAM2884 BCL2L2   3' CCAGGCTCAACAGCCCTGC   66261         TA__
                                CCAGGCTCAAT   CTGC
                                ||||||||||    ||||
                                GGTCCGAGTTG   GACG
                                      TCGG
GAM2884 BMP1     3' CCAACCCAATTGCTGCT     66262     G     A
                                CCAG CTCAATT CTGCT
                                |||| ||||||| |||||
                                GGTT GGGTTAA GACGA
                                  _     C
GAM2884 CBS      3' TGCCAGGCCAGGCAGTTAC   66263       ___  A
                                TGCCAGGCT   CA TTAC
                                |||||||||   || ||||
                                ACGGTCCGG   GT AATG
                                     TCC  C
GAM2884 DRG2     3' TGCAGGCTCAGCACTAC     66264     C     AT
                                TGC AGGCTCA  TACTGC
                                ||| |||||||  ||||||
                                ACG TCCGAGT  GTGATG
                                  _     C_
GAM2884 ELAVL2   5' TGCCAGGCTCACAGTAACTA  66265         ATTACT
                                TGCCAGGCTCA    GCTA
                                ||||||||||     ||||
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                                ACGGTCCGAGT     TGAT
                                      GTCAT_
GAM2884  FNTA     3'  TGCAGTTATTACTGCTA     66266     C  GCTCA
                                TGC AG     ATTACTGCTA
                                ||| ||     ||||||||||
                                ACG TC     TAATGACGAT
                                  _  AA___
GAM2884  LZTS1    3'  GCCAGGCTATTCACACTGCT   66267        CAAT_
                                GCCAGGCT    TACTGCT
                                ||||||||    |||||||
                                CGGTCCGA    GTGACGA
                                     TAAGT
GAM2884  NKTR     3'  TGCCAGACTCATGAGCTAC    66268          ATTACT
                                TGCCAGGCTCA     GCTAC
                                ||||||||||      |||||
                                ACGGTCTGAGT     CGATG
                                      ACT___
GAM2884  OPCML    3'  TGTGAGGCTCAATTTTTGC    66269    CC        AC
                                TG  AGGCTCAATT  TGC
                                ||  ||||||||||  |||
                                AC  TCCGAGTTAA  ACG
                                 AC         AA
GAM2884  PCDHAC1  5'  TGCCGGCCGTCACTGCT     66270      A    CAA
                                TGCC GGCT   TTACTGCT
                                |||| ||||   ||||||||
                                ACGG CCGG   AGTGACGA
                                  _    C__
GAM2884  PCDHAC1  5'  TGCCGGCCGTCACTGCT     66270      A    CAA
                                TGCC GGCT   TTACTGCT
                                |||| ||||   ||||||||
                                ACGG CCGG   AGTGACGA
                                  _    C__
GAM2884  PTPN7    3'  TGCCAGGCCTGGTCACCTCT   66271        CAA    G
                                TGCCAGGCT   TTACT CT
                                |||||||||   ||||| ||
                                ACGGTCCGG   AGTGG GA
                                      ACC     A
GAM2884  PTPN7    3'  TGCCAGGCCTGGTCACCTCT   66271        CAA    G
                                TGCCAGGCT   TTACT CT
                                |||||||||   ||||| ||
                                ACGGTCCGG   AGTGG GA
                                      ACC     A
GAM2884  PTPN7    3'  TGCCAGGCCTGGTCACCTCT   66271        CAA    G
                                TGCCAGGCT   TTACT CT
                                |||||||||   ||||| ||
                                ACGGTCCGG   AGTGG GA
                                      ACC     A
GAM2884  S100A1   3'  TGCAGGCTTGGACCGCTAC    66272     C    CAATT
                                TGC AGGCT    ACTGCTAC
                                ||| |||||    ||||||||
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                                ACG TCCGA    TGGCGATG
                                  _    ACC__
GAM2884  TNFRSF11A 3'  TGCCACAAATTACTGCT    66273      GGCTC
                                TGCCA    AATTACTGCT
                                |||||    ||||||||||
                                ACGGT    TTAATGACGA
                                   GT___
GAM2884  WFS1    3'  TGACAGGCTCAAGCTGC    66274    C       TTA
                                TG CAGGCTCAA   CTGC
                                || |||||||||   ||||
                                AC GTCCGAGTT   GACG
                                 T       C__
GAM2884  C6orf37  3'  TGCCAGGCTTAATCTGC    66275        C   TA
                                TGCCAGGCT AAT  CTGC
                                ||||||||| |||  ||||
                                ACGGTCCGA TTA  GACG
                                      A  __
GAM2884  CHST3    3'  GCTGGGGGCCCTACTGCTAC  66276    CA__    AAT
                                GC   GGCTC   TACTGCTAC
                                ||   |||||   |||||||||
                                CG   CCGGG   ATGACGATG
                                 ACCC    ___
GAM2884  CSTL1    5'  TGCCAGGCTGCAGTTCAC    66277        _ A_
                                TGCCAGGCT CA  TTAC
                                ||||||||| ||  ||||
                                ACGGTCCGA GT  AGTG
                                      C  CA
GAM2884  DKFZp761O0113 5'  GCAAACTCAGTTGTTGCTAC  66278    C     A  AC
                                GC AGGCTCA TT  TGCTAC
                                || ||||||| ||  ||||||
                                CG TTTGAGT AA  ACGATG
                                 _     C  CA
GAM2884  ELF4     5'  GCCAGGCTCAAGGCTGC    66279         TTA
                                GCCAGGCTCAA   CTGC
                                ||||||||||   ||||
                                CGGTCCGAGTT   GACG
                                      CC_
GAM2884  FLJ10811  3'  TGCCAGGCACAAGCTGC    66280       T   TTA
                                TGCCAGGC CAA   CTGC
                                |||||||| |||   ||||
                                ACGGTCCG GTT   GACG
                                     T   C__
GAM2884  FLJ12355  3'  TGCCAGGCCTAAGGCCACTG  66281       TC  __
                                TGCCAGGC  AA  TTACTG
                                ||||||||  ||  ||||||
                                ACGGTCCG  TT  GGTGAC
                                     GA  CC
GAM2884  FLJ13441  3'  TGCAGGCTCAGCGCACACTGC  66282    C     AT___
                                TGC AGGCTCA    TACTGC
                                ||| |||||||    ||||||
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                                ACG TCCGAGT    GTGACG
                                  _     CGCGT
GAM2884  FLJ14564  3'  TGCCAAGCTTGATCTCTGC   66283        CA   A
                                TGCCAGGCT  ATT CTGC
                                |||||||||  ||| ||||
                                ACGGTTCGA  TAG GACG
                                     AC   A
GAM2884  FLJ20413  3'  TGCCAGGCCCGGCTCTGC    66284         AA  A
                                TGCCAGGCTC  TT CTGC
                                ||||||||||  || ||||
                                ACGGTCCGGG  GA GACG
                                     CC  _
GAM2884  HSPB7     5'  TGCCAGGCTCCGACTGC     66285         AATT
                                TGCCAGGCTC    ACTGC
                                ||||||||||    |||||
                                ACGGTCCGAG    TGACG
                                     GC__
GAM2884  HSPC065   3'  TGCCAGGCATTCACCATGCT   66286        TCA_   C
                                TGCCAGGC    ATTA TGCT
                                ||||||||    |||| ||||
                                ACGGTCCG    TGGT ACGA
                                     TAAG   _
GAM2884  ICB-1     3'  TGCCAGGCTGTAGCGCC     66287         CAAT  C
                                TGCCAGGCT    TA TGCT
                                |||||||||    || ||||
                                ACGGTCCGA    AT GCGG
                                     C___  C
GAM2884  JM5       3'  TGCCAAGGCTCAGCTCTGC   66288      _     A  A
                                TGCCA GGCTCA TT CTGC
                                ||||| |||||| || ||||
                                ACGGT CCGAGT GA GACG
                                   T     C  _
GAM2884  KIAA0125  3'  TGCAGGCTCAAGGTCCTGC   66289     C       TTA_
                                TGC AGGCTCAA    CTGC
                                ||| ||||||||    ||||
                                ACG TCCGAGTT    GACG
                                  _       CCAG
GAM2884  KIAA0321  5'  TGCCAGACTCTGCCCCTGCT  66290          AA TA
                                TGCCAGGCTC  T  CTGCT
                                ||||||||||  |  |||||
                                ACGGTCTGAG  G  GACGA
                                     AC GG
GAM2884  KIAA0748  5'  TGTCAGGCCCACTGCT      66291    C      AATT
                                TG CAGGCTC    ACTGCT
                                || |||||||    ||||||
                                AC GTCCGGG    TGACGA
                                 A      _____
GAM2884  KIAA0763  3'  CCTATTCATTACTGCTAC     66292    AGGC   A
                                CC    TCA TTACTGCTAC
                                ||    ||| ||||||||||
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                                GG    AGT AATGACGATG
                                 ATA_  _
GAM2884  KIAA0788  3'  TGTCAGACTCAAAAGAACTAC  66293    C       TT__
                                TG CAGGCTCAA    ACTGC
                                || |||||||||    |||||
                                AC GTCTGAGTT    TGATG
                                 A        TTCT
GAM2884  KIAA1030  3'  TGCCAGCTCAATGCCTG     66294       G     TA
                                TGCCAG CTCAAT  CTG
                                |||||| ||||||  |||
                                ACGGTC GAGTTA  GAC
                                   _     CG
GAM2884  KIAA1467  3'  TGCTTGGATCTACTGCTAC    66295     CA  C  AAT
                                TGC  GG TC   TACTGCTAC
                                |||  || ||   |||||||||
                                ACG  CC AG   ATGACGATG
                                 AA  T  ____
GAM2884  KIAA1819  5'  TGCCACCATTATTGCTAC     66296      GGC   A   C
                                TGCCA   TCA TTA TGCTAC
                                ||||||   ||| ||| ||||||
                                ACGGT   GGT AAT ACGATG
                                   ____  _  A
GAM2884  KIAA1922  5'  TGCCAGGCCCAGCTCTG     66297          A  A
                                TGCCAGGCTCA TT CTG
                                |||||||||||| || |||
                                ACGGTCCGGGT GA GAC
                                      C  _
GAM2884  MGC26641  3'  TGCCAGGCTAATTTTCTG    66298         C    A_
                                TGCCAGGCT AATT  CTG
                                ||||||||| ||||  |||
                                ACGGTCCGA TTAA  GAC
                                      _   AA
GAM2884  PTPNS1    3'  TGCCAGGCTAAAGCTAAAGCTA 66299          C  _   CT
                                TGCCAGGCT AA TTA  GCTA
                                |||||||| || |||  ||||
                                ACGGTCCGA TT GAT  CGAT
                                      T  C   TT
GAM2884  RASSF2    3'  GCTAGGCTCAAAGACGCCTGCT 66300    C       TTA___
              A                  GC AGGCTCAA      CTGCTA
                                || ||||||||      ||||||
                                CG TCCGAGTT      GACGAT
                                 A       TCTGCG
GAM2884  RSP3      5'  GCCAGGCTCCCAGCTCTGTTAC 66301          AATTA_  C
                                GCCAGGCTC      CTG TAC
                                |||||||||      ||| |||
                                CGGTCCGAG      GAC ATG
                                      GGTCGA   A
GAM2884  RTP801    3'  TGCCAGCTCAACTCTGC     66302       G      A
                                TGCCAG CTCAATT CTGC
                                |||||| ||||||| ||||
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                                ACGGTC GAGTTGA GACG
                                  _     _
GAM2884  STAB2    5'  TGTCAGGCTGACTTAGCTA   66303    C     CAA   CT
                                TG CAGGCT   TTA  GCTA
                                || ||||||   |||  ||||
                                AC GTCCGA   AAT  CGAT
                                 A     CTG  __
GAM2884  TOR2A    3'  GCCAGGCTCAGAACTGC     66304          ATT
                                GCCAGGCTCA   ACTGC
                                ||||||||||   |||||
                                CGGTCCGAGT   TGACG
                                      CT_
GAM2884  UST      3'  CAGGCTCAGAACTTCTGCT   66305         __  A
                                CAGGCTCA  ATT CTGCT
                                ||||||||  ||| |||||
                                GTCCGAGT  TGA GACGA
                                     CT   A
GAM2884  LOC145195 3'  TGCCACCCACATTATTGCT   66306     AG    _   C
                                TGCC  GCTCA ATTA TGCT
                                ||||  ||||| |||| ||||
                                ACGG  TGGGT TAAT ACGA
                                  __    G   A
GAM2884  LOC150862 3'  TGCTTCAGAGAGTTACTGCTAC 66307     __    CTCAA
                                TGC  CAGG    TTACTGCTAC
                                |||  ||||    ||||||||||
                                ACG  GTCT    AATGACGATG
                                 AA   CTC__
GAM2884  LOC151009 5'  TGCCGGCTTCCTCACTGCT   66308     A   CAA
                                TGCC GGCT   TTACTGCT
                                |||| ||||  ||||||||
                                ACGG CCGA   AGTGACGA
                                  _   AGG
GAM2884  LOC152464 3'  TGCCAAGGCTCAGCTCTGC   66288      _     A  A
                                TGCCA GGCTCA TT CTGC
                                ||||| |||||| || ||||
                                ACGGT CCGAGT GA GACG
                                   T     C  _
GAM2884  LOC152633 5'  TGCGGGGCTCAACTCCCTAC   66309     CA       A_
                                TGC  GGCTCAATT  CTGC
                                |||  |||||||||  ||||
                                ACG  CCGAGTTGA  GATG
                                  CC        GG
GAM2884  LOC154092 3'  GCCAGCTTTGCTGCTA      66310      G  CAA  A
                                GCCAG CT   TT CTGCTA
                                ||||| ||   || ||||||
                                CGGTC GA   AA GACGAT
                                   _ ___  C
GAM2884  LOC201294 3'  TGCTGGACTCCACCGCC     66311     CA    AAT
                                TGC  GGCTC   TACTGCT
                                |||  |||||   |||||||
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                                ACG  CTGAG   GTGGCGG
                                  AC    ___
GAM2884  LOC221399 5'  TGCTGGCTCAACACTG      66312     CA       T
                                TGC  GGCTCAAT ACTG
                                |||  |||||||| ||||
                                ACG  CCGAGTTG TGAC
                                  A_      _
GAM2884  LOC221738 3'  GCTGGGAGCTGATTACTGCTAC 66313    CA__    CA
                                GC    GGCT  ATTACTGCTAC
                                ||    ||||  ||||||||||
                                CG    TCGA  TAATGACGATG
                                 ACCC    C_
GAM2884  LOC222166 3'  TGCCAGGCTCACTGACTGC    66314           ATT
                                TGCCAGGCTCA   ACTGC
                                ||||||||||   |||||
                                ACGGTCCGAGT   TGACG
                                       GAC
GAM2884  LOC253027 5'  GCTAGGCTCAGTCCTTCTGC   66315    C      A  A__
                                GC AGGCTCA TT   CTGC
                                || |||||||  ||   ||||
                                CG TCCGAGT AG   GACG
                                 A      C  GAA
GAM2884  LOC90917  3'  TGTCAGGCTCAGCTCTAAGTGC 66316    C       A  AC___
           T                     TG CAGGCTCA TT     TGCT
                                || ||||||||  ||     ||||
                                AC GTCCGAGT GA     ACGA
                                 A       C  GATTC
GAM2885  CYP4F3    3'  TGTATGGATGGACCATATT    66319         AGAAGTA
                                TGTATGGA      ACCATATT
                                ||||||||      ||||||||
                                ACATACCT      TGGTATAA
                                     ACC_____
GAM2885  SORBS1    3'  TGTGGGAAGAGGTAACTCA    66320     AT     A    _
                                TGT  GGAAGA GTAAC CA
                                |||  |||||| ||||| ||
                                ACA  CCTTCT CATTG GT
                                  C_     C     A
GAM2885  C21orf108 3'  TGTAGGAAGAAGTGGCC      66321      T       AA
                                TGTA GGAAGAAGT  CC
                                |||| |||||||||  ||
                                ACAT CCTTCTTCA  GG
                                  _        CC
GAM2885  KIAA1219  3'  TGTATGGAGAAGGTAACC     66322         A   _
                                TGTATGGA GAAG TAACC
                                |||||||| |||| |||||
                                ACATACCT CTTC ATTGG
                                     _   C
GAM2885  KIAA1673  3'  TGTATGGAGAAGTATATATATT 66323         A     ACC
           A                     TGTATGGA GAAGTA   ATATTA
                                |||||||| ||||||   ||||||
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                                ACATACCT CTTCAT   TATAAT
                                    _     ATA
GAM2885 LRP15    3' TGGATGGGAGAAGTAAACCAC 66324    T   A      _
                                TG ATGG AGAAGTAA CCAT
                                || |||| |||||||| ||||
                                AC TACC TCTTCATT GGTG
                                 C   C       T
GAM2885 LOC153432 5' TGTAGGAAATTTGGCCATATTA 66325     T    AAGTAA
                                TGTA GGAAG     CCATATTA
                                |||| |||||     ||||||||
                                ACAT CCTTT     GGTATAAT
                                   _    AAACC_
GAM2885 LOC159121 5' TGTGTGGAAAAAGGAGAAGCCA 66326     A       TAA___
             TATT                   TGT TGGAAGAAG     CCATATT
                                |||| |||||||||     |||||||
                                ACA ACCTTTTTC     GGTATAA
                                  C       CTCTTC
GAM2886 PRM2     5' GGAGATCTGGTGGCTCCTGG   66329        __   AATA
                                GGAGATCT  TGGC   TTCTGG
                                ||||||||  ||||   ||||||
                                CCTCTAGA  ACCG   AGGACC
                                     CC   ____
GAM2886 PVR      3' GGAGTCTTGGGCCACTCTGG   66330     A    CAA
                                GGAG TCTTGG   TATTCTGG
                                |||| ||||||   ||||||||
                                CCTC AGAACC   GTGAGACC
                                   _     CG_
GAM2886 DKFZp434J0226 5' GGCAGATCTTGGCTTCTTCTGG 66331    _       AATA
                                GG AGATCTTGGC    TTCTGG
                                || ||||||||||    ||||||
                                CC TCTAGAACCG    AAGACC
                                 G        AAG_
GAM2886 EPS8R1   5' TAGAAGATAGGGGTGTTCTGG  66332        CTT  CAATA
                                TAGGAGAT   GG    TTCTGG
                                ||||||||   ||    ||||||
                                ATCTTCTA   CC    AAGACC
                                     T__  CCAC_
GAM2886 FLJ11301 3' GGAGATTTGCTTATTCTGG    66333       CTTG  AA
                                GGAGAT    GC  TATTCTGG
                                ||||||    ||  ||||||||
                                CCTCTA    CG  ATAAGACC
                                   AA__  A_
GAM2886 PTPRN2   3' AGAGACATAAGCAATATTTTGG 66334       CTT       C
                                GGAGAT   GGCAATATT TGG
                                ||||||   ||||||||| |||
                                TCTCTG   TCGTTATAA ACC
                                   TAT       A
GAM2886 PTPRN2   3' AGAGACATAAGCAATATTTTGG 66334       CTT       C
                                GGAGAT   GGCAATATT TGG
                                ||||||   ||||||||| |||
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                                TCTCTG   TCGTTATAA ACC
                                   TAT        A
GAM2886  TU12B1-TY 3'  GGAGACCTACCACAAATGTTTT 66335        TG_    TA_  C
                GG                  GGAGATCT   GCAA   TT TGG
                                    ||||||||   ||||   || |||
                                    CCTCTGGA   TGTT   AA ACC
                                       TGG    TAC  A
GAM2886  LOC150372 5'  GGCAGATCTTGGATCTG     66336    _       CAATAT
                                    GG AGATCTTGG     TCTG
                                    || |||||||||     ||||
                                    CC TCTAGAACC     AGAC
                                     G        T_____
GAM2886  LOC150421 3'  GGGCATCTTGGCCCTCTCTGG  66337    AG       AATA
                                    GG  ATCTTGGC    TTCTGG
                                    ||  ||||||||    ||||||
                                    CC  TAGAACCG    GAGACC
                                     CG       GGA_
GAM2886  LOC155060 3'  TAGGGGATCCTGGCGGAGTCTG 66338      A        AATAT
                G                    TAGG GATCTTGGC     TCTGG
                                     |||| |||||||||     |||||
                                     ATCC CTAGGACCG     AGACC
                                       C        CCTC_
GAM2886  LOC170394 5'  TAGGAGATCTTGATGACCG    66339            CAATATT
                                     TAGGAGATCTTGG      CTG
                                     ||||||||||||       |||
                                     ATCCTCTAGAACT      GGC
                                           ACT____
GAM2887  ADRA2B    3'  TGAGAACCAGGAAGCAGG    66342     A        C
                                     TGA AACCGGGAA GCAGG
                                     ||| ||||||||| |||||
                                     ACT TTGGTCCTT CGTCC
                                       C        _
GAM2887  AGTR1     3'  TGAAAACCGGCACGAAAA    66343         GGAAC   G
                                     TGAAAACCG    GCA GAAAA
                                     |||||||||    ||| |||||
                                     ACTTTTGGC    CGT CTTTT
                                          _____   G
GAM2887  AGTR1     3'  TGAAAACCGGCACGAAAA    66343         GGAAC   G
                                     TGAAAACCG    GCA GAAAA
                                     |||||||||    ||| |||||
                                     ACTTTTGGC    CGT CTTTT
                                          _____   G
GAM2887  AGTR1     3'  TGAAAACCGGCACGAAAA    66343         GGAAC   G
                                     TGAAAACCG    GCA GAAAA
                                     |||||||||    ||| |||||
                                     ACTTTTGGC    CGT CTTTT
                                          _____   G
GAM2887  AGTR1     3'  TGAAAACCGGCACGAAAA    66343         GGAAC   G
                                     TGAAAACCG    GCA GAAAA
                                     |||||||||    ||| |||||
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                                ACTTTTGGC    CGT CTTTT
                                     _____  G
GAM2887  AGTR1    3'  TGAAAACCGGCACGAAAA    66343        GGAAC  G
                                TGAAAACCG    GCA GAAAA
                                |||||||||    ||| |||||
                                ACTTTTGGC    CGT CTTTT
                                     _____  G
GAM2887  CAV1     3'  TGAAATTGGCACCAGGAAAA  66344      ACCG  A  G
                                TGAAA   GG AC CAGGAAAA
                                |||||   || || ||||||||
                                ACTTT   CC TG GTCCTTTT
                                   AA__  G  _
GAM2887  CIT      3'  GAAAGCGGGAACAGCAGG    66345      AC     _
                                GAAA  CGGGAAC GCAGG
                                ||||  ||||||| |||||
                                CTTT  GCCCTTG CGTCC
                                  C_     T
GAM2887  CTNS     5'  TGAAAACCCGGAGGGGAGGA  66346       G  ACGC
                                TGAAAACC GGA   AGGA
                                |||||||| |||   ||||
                                ACTTTTGG CCT   TCCT
                                     G  CCCC
GAM2887  DLG5     5'  GAAAACTGGGAGCAGA      66347       C   AC
                                GAAAAC GGGA  GCAGG
                                |||||| ||||  |||||
                                CTTTTG CCCT  CGTCT
                                   A   __
GAM2887  FGFR1    3'  TGAAGGCAGGCCACACAGGAA 66348     AAC   A_
                                TGAA  CGGG  ACGCAGGAA
                                ||||  ||||  |||||||||
                                ACTT  GTCC  TGTGTCCTT
                                  CC_   GG
GAM2887  FGFR1    3'  TGAAGGCAGGCCACACAGGAA 66348     AAC   A_
                                TGAA  CGGG  ACGCAGGAA
                                ||||  ||||  |||||||||
                                ACTT  GTCC  TGTGTCCTT
                                  CC_   GG
GAM2887  FGFR1    3'  TGAAGGCAGGCCACACAGGAA 66348     AAC   A_
                                TGAA  CGGG  ACGCAGGAA
                                ||||  ||||  |||||||||
                                ACTT  GTCC  TGTGTCCTT
                                  CC_   GG
GAM2887  GRM6     3'  GAAAACAGCAAATGCAGGAAAA 66349      C  G  C_
            C                    GAAAAC GG AA  GCAGGAAAAC
                                ||||||  || ||  ||||||||||
                                CTTTTG TC TT  CGTCCTTTTG
                                   _  G  TA
GAM2887  KCNE1L   3'  TGAAAACTGGGGAGGCAAGAAA 66350       C  AAC
            A                    TGAAAAC GGG   GCAGGAAAA
                                |||||||  |||   |||||||||
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                                ACTTTTG CCC   CGTTCTTTT
                                    A   CTC
GAM2887  MYCN     3'  TGGAAACTTGGAACACACAA   66351    A   CG       G
                                TG AAAC  GGAACGCA GA
                                || ||||  |||||||| ||
                                AC TTTG  CCTTGTGT TT
                                 C    AA       G
GAM2887  MYLK2    3'  AACCGGGAGCGGCTTCAAC    66352        AC  A  AA__
                                AACCGGGA  GC GG    AAC
                                ||||||||  || ||    |||
                                TTGGCCCT  CG CC    TTG
                                    __  _  GAAG
GAM2887  NUP98    3'  TGAAAACCAGGGACCAAA     66353          A  G
                                TGAAAACCGGG AC CAGG
                                |||||||||||  || ||||
                                ACTTTTGGTCC TG GTTT
                                      C  _
GAM2887  SLC9A1   5'  TGAAACCGGGAAGCGGCCGGGA 66354       A      _  _ A_
                                TGAAA CCGGGAA CG C  GGA
                                ||||| |||||||  || |  |||
                                ACTTT GGCCCTT GC G  CCT
                                   _      C  C GC
GAM2887  TCEA1    3'  TAAAAATTTGATTTGCAGGAAA 66355       CCG  AAC
            AC                    TGAAAA   GG   GCAGGAAAAC
                                ||||||   ||   ||||||||||
                                ATTTTT   CT   CGTCCTTTTG
                                    AAA  AAA
GAM2887  TMEPAI   3'  TGAAAACCTGGAGAACAAGA   66356        G   AC
                                TGAAAACC GGA  GCAGGA
                                ||||||||  |||  ||||||
                                ACTTTTGG CCT  TGTTCT
                                     A   CT
GAM2887  ATP6V1B2  3'  TGGGAACCGAGAGTGCAAAAGG 66357    AA       AC  ___
            AA                    TG  AACCGGGA  GCA   GGAA
                                ||  ||||||||  |||   ||||
                                AC  TTGGCTCT  CGT   CCTT
                                 CC       CA   TTT
GAM2887  DKFZP586A0522 3'  TGAGAACTGGAATGCAGGAAAA 66358     A   CG    C
            C                     TGA AAC  GGAA GCAGGAAAAC
                                ||| |||  |||| ||||||||||
                                ACT TTG  CCTT CGTCCTTTTG
                                  C   A_    A
GAM2887  FLJ11608  3'  TGAAAACCAGGAGTGCAAA   66359           AC
                                TGAAAACCGGGA  GCAGG
                                ||||||||||||  |||||
                                ACTTTTGGTCCT  CGTTT
                                      CA
GAM2887  FLJ12443  3'  TGGAAACCAGGGCTGACAGGAA 66360    A    _   AAC
                                TG AAACC GGG   GCAGGAA
                                || ||||| |||   |||||||
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                                AC TTTGG CCC   TGTCCTT
                                 C    T  GAC
GAM2887  FLJ13646  3'  AAAGCAGAAAATGCAGGAAAA  66361    C     C_
                                AAA CGGGAA  GCAGGAAAA
                                ||| ||||||  |||||||||
                                TTT GTCTTT  CGTCCTTTT
                                  C     TA
GAM2887  FLJ13855  3'  TGAAAGTGGGAACACTTAAA  66362     ACC      AG
                                TGAAA  GGGAACGC  GAA
                                |||||  ||||||||  |||
                                ACTTT  CCCTTGTG  TTT
                                   CA_      AA
GAM2887  FLJ20400  3'  GAAAAGATACAATGCAGGAAAA 66363     CCGGGAAC
            C                    GAAAA      GCAGGAAAAC
                                |||||      ||||||||||
                                CTTTT      CGTCCTTTTG
                                   CTATGTTA
GAM2887  IL1RAPL1  5'  CCGGGAAAAAAAAAAC     66364       CGC
                                CCGGGAA   AGGAAAAC
                                |||||||   ||||||||
                                GGCCCTT   TTTTTTTG
                                    T__
GAM2887  KIAA0349  3'  AAAACTGGGAAGGAAA     66365      C   ACGC
                                AAAAC GGGA   AGGAAA
                                ||||| ||||   ||||||
                                TTTTG CCCT   TCCTTT
                                   A   _____
GAM2887  KIAA1033  3'  GAATTGGGGGAAAAGGAAAAC  66366    AACC   CGC
                                GAA   GGGAA   AGGAAAAC
                                |||   |||||  ||||||||
                                CTT   CCCTT   TCCTTTTG
                                  AACC   T__
GAM2887  KIAA1157  3'  GAAAACTGGGGGCAAAA     66367      C  AAC
                                GAAAAC GGG   GCAGGA
                                |||||| |||   ||||||
                                CTTTTG CCC   CGTTTT
                                    A  C__
GAM2887  MGC10812  3'  TGGAAACCAGGGGACAGA    66368    A      AAC
                                TG AAACCGGG   GCAGG
                                || ||||||||   |||||
                                AC TTTGGTCC   TGTCT
                                 C       CC_
GAM2887  MGC15429  3'  TGAAAGCCAGGCAGGAAA    66369      A   GAAC
                                TGAAA CCGG   GCAGGAAA
                                ||||| ||||   ||||||||
                                ACTTT GGTC   CGTCCTTT
                                   C   _____
GAM2887  MGC3101   3'  TGGAAACCAGGGAAGGA     66370    A   _   ACGC
                                TG AAACC GGGA   AGGA
                                || ||||| ||||   ||||
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                                AC TTTGG CCCT   TCCT
                                 C    T  ____
GAM2887 MUC17   3' TGAAAAATGAGCAGGAAA   66371      CCGG  AC
                                TGAAAA   GA  GCAGGAAA
                                ||||||   ||  ||||||||
                                ACTTTT   CT  CGTCCTTT
                                   TA__  __
GAM2887 OAZ1    5' CCGAAACCAGGAAAAC     66372     G   G
                                CCGG AAC CAGGAAAAC
                                |||| ||| |||||||||
                                GGCT TTG GTCCTTTTG
                                  _  _
GAM2887 OAZ2    3' GAAAGCCAACAGCAGGGAAAC 66373     A   GAAC    A
                                GAAA CCGG   GCAGG AAAC
                                |||| ||||   ||||| ||||
                                CTTT GGTT   CGTCC TTTG
                                  C   GT__    C
GAM2887 ST7L    5' AAACCGGGAGTCGGGAA    66374       A_  CA
                                AAACCGGGA  CG  GGAA
                                |||||||||  ||  ||||
                                TTTGGCCCT  GC  CCTT
                                     CA  __
GAM2887 ST7L    5' AAACCGGGAGTCGGGAA    66374       A_  CA
                                AAACCGGGA  CG  GGAA
                                |||||||||  ||  ||||
                                TTTGGCCCT  GC  CCTT
                                     CA  __
GAM2887 ST7L    5' AAACCGGGAGTCGGGAA    66374       A_  CA
                                AAACCGGGA  CG  GGAA
                                |||||||||  ||  ||||
                                TTTGGCCCT  GC  CCTT
                                     CA  __
GAM2887 ST7L    5' AAACCGGGAGTCGGGAA    66374       A_  CA
                                AAACCGGGA  CG  GGAA
                                |||||||||  ||  ||||
                                TTTGGCCCT  GC  CCTT
                                     CA  __
GAM2887 ST7L    5' AAACCGGGAGTCGGGAA    66374       A_  CA
                                AAACCGGGA  CG  GGAA
                                |||||||||  ||  ||||
                                TTTGGCCCT  GC  CCTT
                                     CA  __
GAM2887 ST7L    5' AAACCGGGAGTCGGGAA    66374       A_  CA
                                AAACCGGGA  CG  GGAA
                                |||||||||  ||  ||||
                                TTTGGCCCT  GC  CCTT
                                     CA  __
GAM2887 LOC118491 5' TGAAGGCCGGGATGCAGA   66375     AA    AC
                                TGAA  CCGGGA  GCAGG
                                ||||  ||||||  |||||
                                ACTT  GGCCCT  CGTCT
                                  CC    A_
GAM2887 LOC145676 5' TGAGGACCAGGAATGGCTCGG 66376    AA     C_  A_
                                TGA  ACCGGGAA  GC  GG
                                |||  ||||||||  ||  ||
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                                ACT  TGGTCCTT  CG  CC
                                  CC       AC  AG
GAM2887  LOC148195 3'  TGAAACCGGGAGGCAGA     66377      A     AC
                                TGAAA CCGGGA  GCAGG
                                ||||| ||||||  |||||
                                ACTTT GGCCCT  CGTCT
                                   _     C_
GAM2887  LOC157858 5'  TGAAACCGGGAGGCAGA     66377      A     AC
                                TGAAA CCGGGA  GCAGG
                                ||||| ||||||  |||||
                                ACTTT GGCCCT  CGTCT
                                   _     C_
GAM2887  LOC196529 3'  TGAGAACTGGAATGCAGGAAAA 66358     A   CG    C
              C                  TGA AAC  GGAA GCAGGAAAAC
                                ||| |||  |||| ||||||||||
                                ACT TTG  CCTT CGTCCTTTTG
                                  C  A_   A
GAM2887  LOC203084 3'  TAAAAATTTGATTTGCAGGAAA 66355       CCG  AAC
              AC                   TGAAAA   GG   GCAGGAAAAC
                                ||||||   ||   ||||||||||
                                ATTTTT   CT   CGTCCTTTTG
                                   AAA  AAA
GAM2887  LOC221543 3'  AACCGGGAACAACATAGG    66378          _  __
                                AACCGGGAACG CA  GG
                                |||||||||| ||  ||
                                TTGGCCCTTGT GT  CC
                                      T  AT
GAM2887  LOC254566 5'  TGGGAACCGAGAGCCAGGA   66379    AA      ACG
                                TG  AACCGGGA   CAGGA
                                ||  ||||||||   |||||
                                AC  TTGGCTCT   GTCCT
                                 CC       CG_
GAM2887  LOC255045 3'  AAAGCGGAAAATGCAGGAAAA  66380     C     C_
                                AAA CGGGAA  GCAGGAAAA
                                ||| ||||||  |||||||||
                                TTT GCCTTT  CGTCCTTTT
                                  C     TA
GAM2887  LOC257596 3'  AACCGGGAACAACATAGG    66378          _  __
                                AACCGGGAACG CA  GG
                                |||||||||| ||  ||
                                TTGGCCCTTGT GT  CC
                                      T  AT
GAM2887  LOC51125  3'  TGAAATCTGGGAGGTGCAAAA  66381      ACC   AC_
                                TGAAA   GGGA   GCAGGA
                                |||||   ||||   ||||||
                                ACTTT   CCCT   CGTTTT
                                   AGA   CCA
GAM2887  LOC51295  3'  GAGCCCCAAGCAGGAAAAC   66382    AAA   GAAC
                                GA   CCGG   GCAGGAAAAC
                                ||   ||||   ||||||||||
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                                CT  GGTT   CGTCCTTTTG
                                 CGG  ____
GAM2888 ATP8B2   3' TCCATAAAATGATATAATT   66385       TTC
                                TCCATAGA  GATATAATT
                                ||||||||  |||||||||
                                AGGTATTT  CTATATTAA
                                    TA_
GAM2888 MSR1     3' TTACTTCATGATTCAAT     66386      C  A
                                TTACT CAT GATTCGAT
                                ||||| ||| ||||||||
                                AATGA GTA CTAAGTTA
                                  A  _
GAM2888 MSR1     3' TTACTTCATGATTCAAT     66386      C  A
                                TTACT CAT GATTCGAT
                                ||||| ||| ||||||||
                                AATGA GTA CTAAGTTA
                                  A  _
GAM2889 HSD11B1  3' ACCTATGTTTACTAACAAT   66389      C      _
                                ACCTA GTTTATTA TAAT
                                ||||| |||||||| ||||
                                TGGAT CAAATGAT GTTA
                                  A       T
GAM2889 TERF1    3' TATGACCTTGTTTATTAT    66390       AC
                                TATGACCT  GTTTATTAT
                                ||||||||  |||||||||
                                ATACTGGA  CAAATAATA
                                    A_
GAM2889 FKSG14   3' ATGACCTTCCCATTATAAT   66391       ACG
                                ATGACCT   TTTATTATAAT
                                |||||||   ||||||||||
                                TACTGGA   GGGTAATATTA
                                    A__
GAM2889 LOC127294 3' GACCTGCTTTATAATC     66392      AC   AT
                                GACCT  GTTT  TATAATC
                                |||||  ||||  |||||||
                                CTGGA  CGAA  ATATTAG
                                   __   __
GAM2889 LOC158668 3' TATGACCTTGTTTATTAT   66390       AC
                                TATGACCT  GTTTATTAT
                                ||||||||  |||||||||
                                ATACTGGA  CAAATAATA
                                    A_
GAM2889 LOC253782 3' TATGACCTGTGCTTAGCCATA 66393       AC   _
                                TATGACCT  GTTTA TTATA
                                ||||||||  |||||  |||||
                                ATACTGGA  CGAAT GGTAT
                                    CA    C
GAM2889 LOC51189  3' ATGACAATTTATTATAATCT  66394      CTAC
                                ATGAC   GTTTATTATAATCT
                                |||||   ||||||||||||||
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                                TACTG    TAAATAATATTAGA
                                  T___
GAM2890  ATRN     3'  GAATTAAGGGGCCAGTCCAC   66397        AAAA    A
                                GAATTAAG    CAGT TCGC
                                ||||||||    |||| ||||
                                CTTAATTC    GTCA GGTG
                                    CCCG    _
GAM2890  TPP2     3'  AGGCATTAAGAAAACACCAT   66398    A_         G
                                AG  ATTAAGAAAACA TAT
                                ||  ||||||||||| |||
                                TC  TAATTCTTTTGT GTA
                                 CG          G
GAM2890  EMR2     3'  AAAAATTAAGAAATCCAGATCG 66399           A_   T
                                AAGAATTAAGAAA  CAG ATCG
                                ||||||||||||  ||| ||||
                                TTTTTAATTCTTT  GTC TAGC
                                       AG   _
GAM2890  FLJ21977 5'  AAGAGTAAGAAAACAGTCCC   66400      AT         AT
                                AAGA  TAAGAAAACAGT  C
                                ||||  ||||||||||||  |
                                TTCT  ATTCTTTTGTCA  G
                                  C_          GG
GAM2890  RNF8     3'  AAGAATCAAGAAGATAGT    66401           AAC
                                AAGAATTAAGAA   AGT
                                ||||||||||||   |||
                                TTCTTAGTTCTT   TCA
                                       CTA
GAM2890  SGP28    3'  AAGAATTAAGACAGCAT     66402           AAA
                                AAGAATTAAGA   CAGTAT
                                ||||||||||||   ||||||
                                TTCTTAATTCT   GTCGTA
                                          ___
GAM2890  LOC145624 5'  AAGGATGAAGAAAACAGT    66403     A  T
                                AAG AT AAGAAAACAGT
                                ||| || ||||||||||
                                TTC TA TTCTTTTGTCA
                                  C  C
GAM2890  LOC253861 3'  AAGAATTAAGAACAACAAT   66404           _
                                AAGAATTAAGAA AACAGT
                                |||||||||||| ||||||
                                TTCTTAATTCTT TTGTTA
                                       G
GAM2891  FMN2     3'  TAGAAATAACATTTTACCCA   66407       T         AA
                                TAGAA ATAACATTTTA  TA
                                ||||| ||||||||||  ||
                                ATCTT TATTGTAAAAT  GT
                                   _          GG
GAM2891  TLR3     3'  TAGAATATAATCATTTACAAAT 66408          _    _
            A                    TAGAATATAA CATTT TAAATA
                                ||||||||| ||||| ||||||
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                                ATCTTATATT GTAAA GTTTAT
                                      A     T
GAM2891  DKFZP434J1813 3'  AAATGTAACATTCTAAATA    66409      A
                                GAAT TAACATTTTAAATA
                                |||| ||||||||||||||
                                TTTA ATTGTAAGATTTAT
                                  C
GAM2891  FLJ14129  3'  TAGAAAATAACATTTTAAAAAA 66410       T          T
            T                    TAGAA ATAACATTTTAAA AAT
                                |||||| |||||||||||| |||
                                ATCTT TATTGTAAAATTT TTA
                                   T          T
GAM2892  APOBEC1   3'  TACCTTGTGAACATTTCT    66413      A  A
                                TACCT GT AACATTTTT
                                ||||| || |||||||||
                                ATGGA CA TTGTAAAGA
                                   A  C
GAM2892  APOBEC1   3'  TACCTTGTGAACATTTCT    66413      A  A
                                TACCT GT AACATTTTT
                                ||||| || |||||||||
                                ATGGA CA TTGTAAAGA
                                   A  C
GAM2892  CHGB     3'  CTGAGACAAACATTTTTCC   66414    _  _
                                CT AG TAAACATTTTTCC
                                || || ||||||||||||
                                GA TC GTTTGTAAAAAGG
                                 C  T
GAM2892  DUSP5    3'  TACCTAGCAAGTACCCTTC   66415         AC
                                TACCTAGTAA  ATTTTTC
                                ||||||||||  |||||||
                                ATGGATCGTT  TGGGAAG
                                      CA
GAM2892  GRIN2A   3'  TACCCAGTAGGCATGTCC    66416        AA   TTT
                                TACCTAGTA  CAT   TCC
                                |||||||||  |||   |||
                                ATGGGTCAT  GTA   AGG
                                     CC   C__
GAM2892  MEOX1    3'  CCTTAGTCATTTTTCC      66417     _  AAA
                                CCT AGT   CATTTTTCC
                                ||| |||   |||||||||
                                GGA TCA   GTAAAAAGG
                                  A  ___
GAM2892  MEOX1    3'  CCTTAGTCATTTTTCC      66417     _  AAA
                                CCT AGT   CATTTTTCC
                                ||| |||   |||||||||
                                GGA TCA   GTAAAAAGG
                                  A  ___
GAM2892  OPA1     3'  TACCCAGTAAGGTCATCT    66418         A__
                                TACCTAGTAA   CATTT
                                ||||||||||   |||||
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                              ATGGGTCATT  GTAGA
                                   CCA
GAM2892 OPA1    3' TACCCAGTAAGGTCATCT   66418       A__
                              TACCTAGTAA  CATTT
                              ||||||||||  |||||
                              ATGGGTCATT  GTAGA
                                   CCA
GAM2892 OPA1    3' TACCCAGTAAGGTCATCT   66418       A__
                              TACCTAGTAA  CATTT
                              ||||||||||  |||||
                              ATGGGTCATT  GTAGA
                                   CCA
GAM2892 OPA1    3' TACCCAGTAAGGTCATCT   66418       A__
                              TACCTAGTAA  CATTT
                              ||||||||||  |||||
                              ATGGGTCATT  GTAGA
                                   CCA
GAM2892 OPA1    3' TACCCAGTAAGGTCATCT   66418       A__
                              TACCTAGTAA  CATTT
                              ||||||||||  |||||
                              ATGGGTCATT  GTAGA
                                   CCA
GAM2892 PCDH11X 3' ACCTAGTAAAATTATTTTC  66419       CAT_
                              ACCTAGTAAA   TTTTC
                              ||||||||||   |||||
                              TGGATCATTT   AAAAG
                                   TAAT
GAM2892 PCDH11Y 3' ACCTAGTAAAATTATTTTC  66419       CAT_
                              ACCTAGTAAA   TTTTC
                              ||||||||||   |||||
                              TGGATCATTT   AAAAG
                                   TAAT
GAM2892 PCDH11Y 3' ACCTAGTAAAATTATTTTC  66419       CAT_
                              ACCTAGTAAA   TTTTC
                              ||||||||||   |||||
                              TGGATCATTT   AAAAG
                                   TAAT
GAM2892 PPP2R1B 3' CTAGTAAAGGCCTTTTCC   66420      CA_
                              CTAGTAAA  TTTTTCC
                              ||||||||  |||||||
                              GATCATTT  GAAAAGG
                                   CCG
GAM2892 RAB5B   3' TACCTAGGAACACCCTCC   66421      TA
                              TACCTAG  AACATTTTTC
                              |||||||  ||||||||||
                              ATGGATC  TTGTGGGAGG
                                   C_
GAM2892 RPA2    3' CCTGGTAGCATCCTTCC    66422    A  AA
                              CCT GTA  CATTTTTCC
                              ||| |||  |||||||||
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                                GGA CAT  GTAGGAAGG
                                  C  C_
GAM2892  SERPINA5  3'  CCCATTCCAACATTTTTCC   66423     GTA_
                                CCTA   AACATTTTTCC
                                ||||   ||||||||||
                                GGGT   TTGTAAAAAGG
                                  AAGG
GAM2892  TAF5    3'  TACCTAGTTACATACATTCC  66424       AA   TT_
                                TACCTAGT  ACAT   TTCC
                                ||||||||  ||||  ||||
                                ATGGATCA  TGTA   AAGG
                                    A_   TGT
GAM2892  TAF5    3'  TACCTAGTTACATACATTCC  66424       AA   TT_
                                TACCTAGT  ACAT   TTCC
                                ||||||||  ||||  ||||
                                ATGGATCA  TGTA   AAGG
                                    A_   TGT
GAM2892  AD-017   3'  TACCTAGCTGACACATCTTTTT 66425       AA   ____
            CC                   TACCTAGT  ACAT   TTTTCC
                                ||||||||  ||||   ||||||
                                ATGGATCG  TGTG   AAAAGG
                                    AC   TAGA
GAM2892  C1orf26  3'  TACCTATGAAACATTTCT    66426      GT
                                TACCTA  AAACATTTTT
                                ||||||  ||||||||||
                                ATGGAT  TTTGTAAAGA
                                   AC
GAM2892  C20orf13  3'  TACCCAGTAATACGCTTCT   66427        _ A
                                TACCTAGTAA AC TTTTT
                                |||||||||| || |||||
                                ATGGGTCATT TG GAAGA
                                     A  C
GAM2892  DKFZp434A171 3'  TAGTAAACACATTTTTCC    66428        __
                                TAGTAAACAT  TTTTCC
                                ||||||||||  ||||||
                                ATCATTTGTG  AAAAGG
                                     TA
GAM2892  DKFZP434F1735 5'  TACCTAGCAAATCTTTCC    66429        AC
                                TACCTAGTAA  ATTTTTCC
                                ||||||||||  ||||||||
                                ATGGATCGTT  TAGAAAGG
                                    __
GAM2892  DKFZP586B0923 3'  TACCCAGCATTTTTTC     66430       AACA
                                TACCTAGTA   TTTTTC
                                |||||||||   ||||||
                                ATGGGTCGT   AAAAAG
                                    A___
GAM2892  FLJ10898  5'  CCTAGTAAAGTATTTTCC    66431       CAT
                                CCTAGTAAA   TTTTCC
                                |||||||||   ||||||
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                                GGATCATTT  AAAAGG
                                     CAT
GAM2892  FLJ13855  3'  CACCTAAAGCACATTTTT   66432      TAA
                                TACCTAG  ACATTTTT
                                |||||||  ||||||||
                                GTGGATT  TGTAAAAA
                                   TCG
GAM2892  FLJ20344  3'  ACCTCAGCATACATTTTT   66433    _  A
                                ACCT AGTA ACATTTTT
                                |||| |||| ||||||||
                                TGGA TCGT TGTAAAAA
                                  G   A
GAM2892  FLJ22671  3'  TACCCAGCACATTCATTTTT  66434       AA__
                                TACCTAGTA   CATTTTT
                                |||||||||   |||||||
                                ATGGGTCGT   GTAAAAA
                                     GTAA
GAM2892  GAB3     3'  TACCTAGTCACTTCT     66435      AAA
                                TACCTAGT  CATTTTT
                                ||||||||  |||||||
                                ATGGATCA  GTGAAGA
                                    ___
GAM2892  KIAA0332  3'  ACCTAGTAAACAATCC    66436        TTTT
                                ACCTAGTAAACA  TCC
                                ||||||||||||  |||
                                TGGATCATTTGT  AGG
                                    T___
GAM2892  KIAA0408  3'  TACCTAATAGGTTTTTCC   66437       AACA
                                TACCTAGTA  TTTTTCC
                                |||||||||  |||||||
                                ATGGATTAT  AAAAAGG
                                     CC__
GAM2892  KIAA1483  3'  TACCCACACATTTTTC    66438     GTAA
                                TACCTA  ACATTTTTC
                                ||||||  |||||||||
                                ATGGGT  TGTAAAAAG
                                   G___
GAM2892  KIAA1710  3'  ACCTGTGTCTCATTTTTCC  66439    A_ AAA
                                ACCT  GT  CATTTTTCC
                                ||||  ||  |||||||||
                                TGGA  CA  GTAAAAAGG
                                  CA  GA_
GAM2892  MGC14407  5'  ACCACATAAACATTTTTCC  66440    TA
                                ACC  GTAAACATTTTTCC
                                |||  |||||||||||||
                                TGG  TATTTGTAAAAAGG
                                  TG
GAM2892  MGC2817   3'  CACCGTAAAACATTTTTC   66441    TAGT
                                TACC   AAACATTTTTC
                                ||||   ||||||||||
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                                GTGG   TTTGTAAAAAG
                                  CAT_
GAM2892  N4BP1    3'  TACCCAAAACATTTTT     66442      GT
                                TACCTA  AAACATTTTT
                                ||||||  ||||||||||
                                ATGGGT  TTTGTAAAAA
                                  __
GAM2892  NXN      3'  TACCTTAGCTACATTTTTC   66443     _  AA
                                TACCT AGT  ACATTTTTC
                                ||||| |||  |||||||||
                                ATGGA TCG  TGTAAAAAG
                                   A  A_
GAM2892  NY-REN-41 3'  TACAATTTAAACATTTTTCC  66444    CTAG
                                TAC   TAAACATTTTTCC
                                |||   ||||||||||||
                                ATG   ATTTGTAAAAAGG
                                  TTAA
GAM2892  RAB10    3'  TACCTAGCAAGTTACATC    66445        ___
                                TACCTAGTAA   ACATT
                                ||||||||||   |||||
                                ATGGATCGTT   TGTAG
                                     CAA
GAM2892  RGS19    3'  CACCTAGTAAGGACATGTTTCC 66446         __   T
                                TACCTAGTAA  ACAT TTTCC
                                ||||||||||  |||| |||||
                                GTGGATCATT  TGTA AAAGG
                                     CC   C
GAM2892  TUSP     3'  TACCTAGTAACTCTTTCC    66447        A A
                                TACCTAGTAA C TTTTTCC
                                |||||||||| | |||||||
                                ATGGATCATT G AGAAAGG
                                     _ _
GAM2892  LOC115294 3'  CTAAAACAACATTTTTCC    66448     TA_
                                CTAG   AACATTTTTCC
                                ||||   ||||||||||
                                GATT   TTGTAAAAAGG
                                  TTG
GAM2892  LOC142948 3'  TACCCAGTGACCCTTCC     66449       AAAC
                                TACCTAGT   ATTTTTCC
                                ||||||||   ||||||||
                                ATGGGTCA   TGGGAAGG
                                    C___
GAM2892  LOC154386 3'  TACCCAGTAAACAATAACTCC  66450          TTT_
                                TACCTAGTAAACA   TTCC
                                ||||||||||||   ||||
                                ATGGGTCATTTGT   GAGG
                                       TATT
GAM2892  LOC157798 5'  TACCTAGCAATATCCTT     66451         AC
                                TACCTAGTAA  ATTTTT
                                ||||||||||  ||||||
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                                ATGGATCGTT  TAGGAA
                                      A_
GAM2892  LOC200081 3'  CCTAGGGACACCTTTTCC    66452      TAA   _
                                CCTAG   ACAT TTTTCC
                                |||||   |||| ||||||
                                GGATC   TGTG AAAAGG
                                   CC_   G
GAM2892  LOC202181 3'  CACCTGGTATCACTTTTC    66453      A   AA
                                TACCT GTA  CATTTTTC
                                ||||| |||  ||||||||
                                GTGGA CAT  GTGAAAAG
                                   C   A_
GAM2892  LOC221509 3'  CACCCAATAACGTTTTTC    66454         ACA
                                TACCTAGTAA   TTTTTC
                                ||||||||||   ||||||
                                GTGGGTTATT   AAAAAG
                                      GC_
GAM2892  LOC91496  5'  ACCTCTAAGCATTTTTCC    66455     AG   A
                                ACCT  TAA CATTTTTCC
                                ||||  ||| |||||||||
                                TGGA  ATT GTAAAAAGG
                                  G_   C
GAM2893  FLJ20364  5'  CGCTCAGCTAGCTCTCGAGT   66458        ACT
                                CGCTCGGC   TAGCTCTCGAGT
                                ||||||||   ||||||||||||
                                GCGAGTCG   ATCGAGAGCTCA
                                      ____
GAM2893  GMEB2     3'  CGCTCGGCACCTGGCTCT    66459          A
                                CGCTCGGCACTT GCTCT
                                |||||||||||| |||||
                                GCGAGCCGTGGA CGAGA
                                       C
GAM2893  ZER6      3'  GCATGGTGCTTAGCTCTCAGT  66460    TC  CA       G
                                GC  GG  CTTAGCTCTC AGT
                                ||  ||  |||||||||| |||
                                CG  CC  GAATCGAGAG TCA
                                 TA  AC        _
GAM2893  LOC161734 3'  TCTTCACATAGTTCTCGAGT   66461    GG   T   C
                                TC  CAC TAG TCTCGAGT
                                ||  ||| ||| ||||||||
                                AG  GTG ATC AGAGCTCA
                                 AA   T   A
GAM2894  BCL2L2    3'  CCCTATTTGTCCCTTTGGGC   66464          AGACG
                                CCCTGTTTGTCT    GGGC
                                ||||||||||||    ||||
                                GGGATAAACAGG    CCCG
                                       GAAA_
GAM2894  CENPB     3'  GCCCCTCTGCCCAGGATGGGGC 66465       GT       AC_
                                GCCCCT  TTGTCTAG   GGGGC
                                ||||||  ||||||||   |||||
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                                CGGGGA  GACGGGTC   CCCCG
                                   __       CTA
GAM2894  CHRNA4   3'  ACCCCTGGCTGGATGGGG    66466       T   TCTA  C
                                GCCCCTG TTG    GA GGGG
                                ||||||| |||    || ||||
                                TGGGGAC GAC    CT CCCC
                                   C  _____  A
GAM2894  CYLN2    3'  GCCCCCGTTAGGAGATGGGGC  66467        TGTCT   C
                                GCCCCTGTT     AGA GGGGC
                                |||||||||     ||| |||||
                                CGGGGGCAA     TCT CCCCG
                                     TCC__   A
GAM2894  G6PT1    3'  CCTGTTTGTCTGAAGGC     66468          A  CG
                                CCTGTTTGTCT GA  GGGC
                                |||||||||| ||  ||||
                                GGACAAACAGA CT  TCCG
                                          _  __
GAM2894  GAS7     3'  GCCTCTGTTTGTTTCAGAGC   66469     C       CTAGA
                                GCC CTGTTTGT     CGGGGC
                                ||| ||||||||     ||||||
                                CGG GACAAACA     GTCTCG
                                  A       AA___
GAM2894  PBP      3'  GCCTCTGGTTGTCTAGGTGAG  66470     C   T       AC
                                GCC CTG TTGTCTAG  GGG
                                ||| ||| ||||||||  |||
                                CGG GAC AACAGATC  CTC
                                  A   C       CA
GAM2894  POLL     3'  GCTCCTGCTTAAAATGGGGC   66471    C       TCT   C
                                GC CCTGTTTG   AGA GGGGC
                                || ||||||||   ||| |||||
                                CG GGACGAAT   TTT CCCCG
                                 A       ___   A
GAM2894  TFAP2C   3'  GCCCCCGTTTGAACACGGGG   66472          TCTAG
                                GCCCCTGTTTG     ACGGGG
                                ||||||||||     ||||||
                                CGGGGGCAAAC     TGCCCC
                                      TTG__
GAM2894  C20orf108 3'  TATTTGTAGTAGAGACGGGG   66473       CT___
                                TGTTTGT     AGACGGGG
                                |||||||     ||||||||
                                ATAAACA     TCTGCCCC
                                   TCATC
GAM2894  C20orf39  3'  CTGCTTATGACGGGG       66474        CTA
                                CTGTTTGT   GACGGGG
                                ||||||||   |||||||
                                GACGAATA   CTGCCCC
                                           ___
GAM2894  CRTAM    3'  GCTCCTCTTTGTGCCTTGGGGC 66475    C   G    _  AGAC
                                GC CCT TTTGT CT    GGGGC
                                || ||| ||||| ||    |||||
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                                CG GGA AAACA GG    CCCCG
                                 A  G    C  AA__
GAM2894  DKFZP434C131 3'  CCCTCTTTGTCCAGGG      66476      G       GAC
                                CCCT TTTGTCTA   GGG
                                |||| ||||||||   |||
                                GGGA AAACAGGT   CCC
                                  G       ___
GAM2894  DKFZP761I2123 3'  GCCTCTGCTTGAAGCTGGGG   66477     C      TCT  AC
                                GCC CTGTTTG   AG  GGGG
                                ||| |||||||   ||  ||||
                                CGG GACGAAC   TC  CCCC
                                  A      T__  GA
GAM2894  FLJ10933  3'  GCCCTTGTTTTTTAACAAAGC  66478      C     GTCTA
                                GCCC TGTTT    GACGGGGC
                                |||| |||||    ||||||||
                                CGGG ACAAA    TTGTTTCG
                                  A    AAA__
GAM2894  FLJ14594  3'  GCCCCTGTGTAGGTGGGG    66479        TTGTC   AC
                                GCCCCTGT    TAG  GGGG
                                ||||||||    |||  ||||
                                CGGGGACA    ATC  CCCC
                                    C_____   CA
GAM2894  FLJ21916  3'  GCCTCTGTCCAGGTGGGGC   66480     CCTG       AC
                                GCC    TTTGTCTAG  GGGGC
                                |||    |||||||||  |||||
                                CGG    AGACAGGTC  CCCCG
                                 _____        CA
GAM2894  FLJ23403  3'  GTTTCTCTTAGGGACGGGGC   66481      G   A___
                                GTTT TCT    GACGGGGC
                                |||| |||    ||||||||
                                CAAA AGA    CTGCCCCG
                                  G   ATCC
GAM2894  GCN2      3'  GCCTCTGTCTGTTTGAATGAGG 66482     C       CTA  C
                                GCC CTGTTTGT   GA GGGG
                                ||| ||||||||   || ||||
                                CGG GACAGACA   TT CTCC
                                  A       AAC  A
GAM2894  GMPPB     5'  CCCGTTTGAGGAGGCGGGGC   66483        TCT  A
                                CCTGTTTG   AG CGGGGC
                                ||||||||   || ||||||
                                GGGCAAAC   TC GCCCCG
                                    TCC  C
GAM2894  KCNN1     3'  GCCTGGGCAGTCTGGGCGGGGC 66484     CCT  TT    AGA
                                GCC   GT  GTCT   CGGGGC
                                |||   ||  ||||   ||||||
                                CGG   CG  CAGA   GCCCCG
                                  ACC  T_    CCC
GAM2894  KIAA0290  5'  GCCCCTGTCTGACGGGG     66485          GTCTA
                                GCCCCTGTTT    GACGGGG
                                ||||||||||    |||||||
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                                CGGGGACAGA    CTGCCCC
                                      _____
GAM2894 KIAA0356 3' GCCCCTGTCTGTAGAGGGG   66486          CT  C
                                GCCCCTGTTTGT  AGA GGGG
                                |||||||||||  ||| ||||
                                CGGGGACAGACA  TCT CCCC
                                      __  _
GAM2894 KIAA1130 3' GCCCTCTGCCTTAGATGGGGC 66487     _    GTC   C
                                GCCC CTGTTT   TAGA GGGGC
                                |||| ||||||   |||| |||||
                                CGGG GACGGA   ATCT CCCCG
                                  A     ___   A
GAM2894 KIAA1656 3' ACCCCTGTTTGTTATGGG    66488          CTAGACG
                                GCCCCTGTTTGT      GGG
                                ||||||||||||      |||
                                TGGGGACAAACA      CCC
                                      ATA____
GAM2894 LIPG    3' CCTTGTTTGTCTCACGTCTGGG 66489    C       AG ____
             GC                   CC TGTTTGTCT  AC    GGGGC
                                || |||||||||  ||    |||||
                                GG ACAAACAGA  TG    CCCCG
                                 A        G_  CAGA
GAM2894 MGC15873 3' CCCTGTTTCCTCATGGGGC   66490        G   AGAC
                                CCCTGTTT TCT    GGGGC
                                |||||||| |||    |||||
                                GGGACAAA GGA    CCCCG
                                     _  GTA_
GAM2894 NCBP2   3' GCTTTGTAGAGACGGGG    66491    CCCTG    CT
                                GC    TTTGT  AGACGGGG
                                ||    |||||  ||||||||
                                CG    AAACA  TCTGCCCC
                                 ______    TC
GAM2894 PDZD2   5' ACTTCTGACCTCTCTAGATGGG 66492    CC  _  G     C
             G                   GC  CTG TTT TCTAGA GGGG
                                ||  ||| ||| |||||| ||||
                                TG  GAC GGA AGATCT CCCC
                                 AA   T   G     A
GAM2894 SPTLC2  3' CTTTTTAGTAGAGACGGGG   66493    G   _  CT
                                CT TTT GT  AGACGGGG
                                || ||| ||  ||||||||
                                GA AAA CA  TCTGCCCC
                                 A   T  TC
GAM2894 SREC    3' GCTCTGGTTTGTCTGTCCTGGC 66494    CC  _     AGACGG
                                GC  CTG TTTGTCT     GGC
                                ||  ||| |||||||     |||
                                CG  GAC AAACAGA     CCG
                                 A_   C      CAGGA_
GAM2894 UHRF1   3' GCTCCAGTTTGTCTGCAGG   66495    C  T      AGA
                                GC CC GTTTGTCT   CGGG
                                || || ||||||||   ||||
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                                CG GG CAAACAGA   GTCC
                                 A  T       C__
GAM2894  LOC145225 3'  CTGCTCTGGACGGGGC      66496      TTG   A
                                CTGT   TCT GACGGGGC
                                ||||   ||| ||||||||
                                GACG   AGA CTGCCCCG
                                  ___   C
GAM2894  LOC146667 3'  GCCCCTGTGTGGTCCTGGGGC  66497        TT_   AGAC
                                GCCCCTGT   GTCT    GGGGC
                                ||||||||   ||||    |||||
                                CGGGGACA   CAGG    CCCCG
                                     CAC    A___
GAM2894  LOC150445 3'  GCCTCTGGTTGTCTAGGTGAG  66470     C   T       AC
                                GCC CTG TTGTCTAG  GGG
                                ||| ||| ||||||||  |||
                                CGG GAC AACAGATC  CTC
                                  A   C       CA
GAM2894  LOC154089 3'  TGTTTGTTTGAGACAGGG     66498        CT_
                                TGTTTGT   AGACGGGG
                                |||||||   ||||||||
                                ACAAACA   TCTGTCCC
                                    AAC
GAM2894  LOC164668 5'  GCCCCTGCTTGTCTGAGG     66499             AGAC
                                GCCCCTGTTTGTCT    GGGG
                                ||||||||||||||    ||||
                                CGGGGACGAACAGA    CTCC
                                                  _____
GAM2894  LOC199733 3'  CTGTTTTTTAGACAGGG      66500       GTC
                                CTGTTT   TAGACGGGG
                                ||||||   |||||||||
                                GACAAA   ATCTGTCCC
                                   AA_
GAM2894  LOC200058 3'  CCTGTCTGTCTCTCAGG      66501           AGA
                                CCTGTTTGTCT   CGGG
                                ||||||||||   ||||
                                GGACAGACAGA   GTCC
                                      GA_
GAM2894  LOC200282 3'  GCCTCTGTTCCAGCAGTGGGGC 66502     C    TTG    AC__
                                GCC CTGT   TCTAG    GGGGC
                                ||| ||||   |||||    |||||
                                CGG GACA   AGGTC    CCCCG
                                  A    ___     GTCA
GAM2894  LOC203052 3'  GCCCTTGCTTGCCCTGGGG    66503      C        AGAC
                                GCCC TGTTTGTCT    GGGG
                                |||| |||||||||    ||||
                                CGGG ACGAACGGG    CCCC
                                  A        A___
GAM2894  LOC219988 5'  GCCATCTGTTTAGGTGGGG    66504     CCT     C   AC
                                GCC   GTTTGT TAG  GGGG
                                |||   |||||| |||  ||||
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                                CGG   TAGACA ATC  CCCC
                                 ___     A   CA
GAM2894  LOC253792 5'  CCCTGTTTGTCAGGG      66505          TAGAC
                                CCCTGTTTGTC    GGGG
                                ||||||||||    ||||
                                GGGACAAACAG    TCCC
                                      _____
GAM2894  LOC257445 5'  CCCTCTTTGTCCAGGG     66476     G      GAC
                                CCCT TTTGTCTA   GGG
                                |||| ||||||||   |||
                                GGGA AAACAGGT   CCC
                                  G      ___
GAM2894  LOC51279  3'  CCTGTCTGGGATGGGGC    66506        TCTA  C
                                CCTGTTTG   GA GGGGC
                                ||||||||   || |||||
                                GGACAGAC   CT CCCCG
                                    C___  A
GAM2895  CKAP1     5'  GCTTCGTGGGTATTCGCTTCTG 66509       TTT_   CCACCC
              C                  GCTTTGTG   TTC    CTGC
                                 ||||||||   |||    ||||
                                 CGAAGCAC   AAG    GACG
                                    CCAT   CGAA__
GAM2895  LAMA4     3'  GCTTTGTGTTTCTTTCAGTGC  66510          CC  CCCC
                                GCTTTGTGTTTTT  CA   TGC
                                ||||||||||||  ||   |||
                                CGAAACACAAAGA  GT   ACG
                                      AA  C___
GAM2895  PBX2      3'  GCCTTGTGAGAGCCCCCACCCC 66511       TTT_
              TG                  GCTTTGTG   TTCCCACCCCTG
                                  ||||||||   ||||||||||||
                                  CGGAACAC   GGGGGTGGGGAC
                                     TCTC
GAM2895  SH3GL1    3'  GCTGTGTGCTCATCTCTG    66512    T     T  CCACCC
                                GCT TGTGTTT TC     CTG
                                ||| ||||||| ||     |||
                                CGA ACACGAG AG     GAC
                                  C      T  A_____
GAM2895  SLC4A1    3'  GCCTTTGCTTCTACCCCTG   66513      G      CCC
                                GCTTT TGTTTTT   ACCCCTG
                                ||||| |||||||   |||||||
                                CGGAA ACGAAGA   TGGGGAC
                                   _      ___
GAM2895  TEM7R     3'  TTTGTGTTTGTTCTCACTCTTG 66514        _   C   CCC
              C                   TTTGTGTTT TTC CAC   TGC
                                  |||||||||| ||| |||   |||
                                  AAACACAAA AAG GTG   ACG
                                      C   A   AGA
GAM2895  TRO       3'  GCTCTTGTACCCATCCCTG   66515      G   TTTT   C
                                GCTTT TGT    CCCA CCCTG
                                ||||| |||    |||| |||||
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                                CGAGA ACA    GGGT GGGAC
                                  _  T___    A
GAM2895 BRD2     3'  GCTTTGCACACTCCCACCCTTG 66516       TG TT       C
              C                   GCTTTG  T  TTCCCACCC TGC
                                  ||||||  |  |||||||||| |||
                                  CGAAAC  G  GAGGGTGGG ACG
                                     GT T_       A
GAM2895 C6orf26  3'  GCCTTGCACCCATCCTGCCTCT 66517      TG  TT   CA  C
              G                   GCTTTG  TT  TCC  CC CTG
                                  ||||||  ||  |||  || |||
                                  CGGAAC  GG  AGG  GG GAC
                                     GT  GT   AC  A
GAM2895 CDW92    3'  GCTTTATGTTCCATGTTTCTG  66518          TCCCACCC
                                  GCTTTGTGTTTT       CTG
                                  ||||||||||||       |||
                                  CGAAATACAAGG       GAC
                                         TACAAA__
GAM2895 DKFZP434G1411 3'  CTCTTTTTTCCCACTCT     66519     GTG        CC
                                  CTTT   TTTTTCCCAC  CT
                                  ||||   ||||||||||  ||
                                  GAGA   AAAAAGGGTG  GA
                                    ___         A_
GAM2895 FLJ10350  3'  GCTCTTGCCGCTCTTGCTCCTG 66520      G   TT   CCACC
              C                   GCTTT TGT  TTC    CCTGC
                                  ||||| |||  |||    |||||
                                  CGAGA ACG  GAG    GGACG
                                    _  GC   AACGA
GAM2895 FLJ10415  3'  GCTTCCTTTTCATCCCTG    66521      GTG     CCAC
                                  GCTTT   TTTTTC    CCCTG
                                  |||||   ||||||    |||||
                                  CGAAG   GAAAAG    GGGAC
                                    ___     TA__
GAM2895 FLJ10508  3'  ACTTTGTGTTTACTTCTG    66522          TTCCC  CC
                                  GCTTTGTGTTT     AC  CTG
                                  ||||||||||     ||  |||
                                  TGAAACACAAA     TG  GAC
                                        _____  AA
GAM2895 FLJ14596  5'  GCTTAGTGCCTGCTCCCACTTC 66523     T     _      CC
              TGC                   GCTT GTGTTT TTCCCAC  CTGC
                                  |||| |||||| |||||||  ||||
                                  CGAA CACGGA GAGGGTG  GACG
                                    T     C      AA
GAM2895 H-plk    5'  TGTTTTTCTCATCCCTGC    66524         C  C
                                  TGTTTTTC CA CCCTGC
                                  |||||||| || ||||||
                                  ACAAAAAG GT GGGACG
                                       A  A
GAM2895 HSPC144   5'  GCCTTGTGTTACCTTGTTATCC 66525          TTTCCCAC__  C
              TTGC                   GCTTTGTGTT        CC TGC
                                  ||||||||||         || |||
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                                CGGAACACAA        GG ACG
                                     TGGAACAATA  A
GAM2895  KIAA0016  3'  GCTCCCTTTCCCACCCCTG   66526      GTGT
                                GCTTT   TTTTCCCACCCCTG
                                |||||   ||||||||||||||
                                CGAGG   GAAAGGGTGGGGAC
                                  ____
GAM2895  KIAA1025  3'  TTTGTGTTTTTTTTCTTTTTCT 66527          CCCACCC__
           GC                    TTTGTGTTTTT       CTGC
                                 ||||||||||        ||||
                                 AAACACAAAAA       GACG
                                      AAAGAAAAA
GAM2895  KIAA1393  3'  GCCTTGTGTTTTAGGCCATTCT 66528          TC_  CCCC
           TGC                   GCTTTGTGTTTT  CCA   TGC
                                 ||||||||||||  |||   |||
                                 CGGAACACAAAA  GGT   ACG
                                       TCC   AAGA
GAM2895  LAPTM4A   3'  ATATTTTTCTTGCCTCTGC   66529        CCA  C
                                 GTGTTTTTC   CC CTGC
                                 |||||||||   || ||||
                                 TATAAAAAG   GG GACG
                                      AAC  A
GAM2895  PURB      3'  TTTGTTTTTTCCCTCTG     66530      G      ACCC
                                 TTTGT TTTTTCCC    CTG
                                 ||||| ||||||||    |||
                                 AAACA AAAAAGGG    GAC
                                   _       A___
GAM2895  RSHL1     3'  GCCTTCCTTTTCTATCCCTGC  66531      GTG     CCAC
                                 GCTTT   TTTTTC    CCCTGC
                                 |||||   ||||||    ||||||
                                 CGGAA   GAAAAG    GGGACG
                                   G__     ATA_
GAM2895  TSLRP     5'  GCTTTTCACCCTTCACCCCTGC 66532      GTGTTTT  __
                                 GCTTT      TCC  CACCCCTGC
                                 |||||      |||  |||||||||
                                 CGAAA      GGG  GTGGGGACG
                                   AGT_____   AA
GAM2895  LOC113523 3'  CCTTTTGTTTTTCCTATTCTTG 66533      G        CACCCC
           C                      CTTT TGTTTTTCC      TGC
                                  |||| |||||||||      |||
                                  GGAA ACAAAAAGG      ACG
                                    A        ATAAGA
GAM2895  LOC121219 5'  TTCTGCTCCTTCCACTTCTGC  66534    G      C    CC
                                 TT TGTTTTT CCAC  CTGC
                                 || ||||||| ||||  ||||
                                 AA ACGAGGA GGTG  GACG
                                  G      A    AA
GAM2895  LOC133688 3'  GCCATGGTTTTTCTTGCTTCTG 66535     T  T      CCACCC
                                 GCT TG GTTTTTC      CTG
                                 ||| || |||||||      |||
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                                CGG AC CAAAAAG     GAC
                                  T _      AACGAA
GAM2895  LOC145241 5'  CTTTGCACTTCTGCCCCTGC   66536      TG    CCCA
                                CTTTG  TTTTT    CCCCTGC
                                |||||  |||||   |||||||
                                GAAAC  GAAGA    GGGGACG
                                   GT    C___
GAM2895  LOC145693 3'  GCTGTACAAAGTTCCCACCTCT 66537     T GT TTT       C
            GC                    GCT T  G   TTCCCACC CTGC
                                ||| |  |   |||||||| ||||
                                CGA A  T   AAGGGTGG GACG
                                  C TG TTC       A
GAM2895  LOC146237 3'  CTTTGTGTTTCCTGCACGCCCT 66538           CC  _   _
            TGC                   CTTTGTGTTTTT  CAC CCCT GC
                                ||||||||||||  ||| |||| ||
                                GAAACACAAAGG  GTG GGGA CG
                                      AC   C    A
GAM2895  LOC155066 3'  GTGTTGCTTCCCACTCCTG    66539      _      C
                                GTGTT TTTCCCAC CCTG
                                |||||  |||||||| ||||
                                CACAA GAAGGGTG GGAC
                                   C       A
GAM2895  LOC157660 3'  TTTGACAATCTCACCCCTGC   66540     TGTTTT  C
                                TTTG     TC CACCCCTGC
                                ||||     || |||||||||
                                AAAC     AG GTGGGGACG
                                  TGTT__  A
GAM2895  LOC159201 5'  GCTTCTTCTTCCCGTCCTTG   66541      GTG       AC  C
                                GCTTT   TTTTTCCC  CC TG
                                |||||   ||||||||  || ||
                                CGAAG   AAGAAGGG  GG AC
                                   ___       CA  A
GAM2895  LOC220282 5'  TTTGTGCTCCACTTATCTCTGC 66542        TTTC    CC____
                                TTTGTGTT    CCAC     CTGC
                                ||||||||    ||||     ||||
                                AAACACGA    GGTG     GACG
                                     _____    AATAGA
GAM2895  LOC257144 3'  ACTTTGTGTCCCATCCCTG    66543        TTTT    C
                                GCTTTGTG    TCCCA CCCTG
                                ||||||||    ||||| |||||
                                TGAAACAC    AGGGT GGGAC
                                     _____     A
GAM2895  LOC58489  3'  GCTCTCATTCCCATTCCTG    66544      GTGTTT     CC
                                GCTTT     TTCCCA  CCTG
                                |||||     ||||||  ||||
                                CGAGA     AAGGGT  GGAC
                                   GT_____     AA
GAM2895  LOC90625  3'  GCTCTCTTCCTGCCTCTG    66545      TGTGT     CA  C
                                GCTT    TTTTCC  CC CTG
                                ||||    ||||||  || |||
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                                CGAG    AGAAGG  GG GAC
                                  _____     AC  A
GAM2896  APAF1    3'  TAAAACCTGATGTGTGTTGTTA 66548       A  A      A
                                TAAGAT TGA TGTGTGTT TTA
                                |||||| ||| |||||||| |||
                                ATTTTG ACT ACACACAA AAT
                                   G  _       C
GAM2896  APAF1    3'  TAAAACCTGATGTGTGTTGTTA 66548       A  A      A
                                TAAGAT TGA TGTGTGTT TTA
                                |||||| ||| |||||||| |||
                                ATTTTG ACT ACACACAA AAT
                                   G  _       C
GAM2896  DISC1    3'  GATATGAATAGGAGTTAC    66549         TGT
                                GATATGAATG   GTTAT
                                ||||||||||   |||||
                                CTATACTTAT   CAATG
                                      CCT
GAM2896  PLAUR    5'  AAATATGAATGTGGCTGATTA  66550           T  _
                                AGATATGAATGTG GTT ATTA
                                |||||||||||| ||| ||||
                                TTTATACTTACAC CGA TAAT
                                      _  C
GAM2896  EPB41L1  3'  GATATGGAGTTGGTTATTAC   66551       AATG  T
                                GATATG    TG GTTATTAC
                                ||||||    || ||||||||
                                CTATAC    AC CAATAATG
                                   CTCA  _
GAM2896  FLJ11193 3'  TAAGACATGTCTGTTGTT    66552        AA   G
                                TAAGATATG  TGT TGTT
                                |||||||||  ||| ||||
                                ATTCTGTAC  ACA ACAA
                                      AG   _
GAM2896  KIAA1559 3'  TAAGATATAATTATATGTTAT  66553          A
                                TAAGATATGA TGTGTGTTAT
                                |||||||||| ||||||||||
                                ATTCTATATT ATATACAATA
                                      A
GAM2896  YWHAQ    3'  TAAAATATGGGTATGCAATT   66554        AAT     T
                                TAAGATATG   GTGTGT ATT
                                |||||||||   |||||| |||
                                ATTTTATAC   CATACG TAA
                                      C__      T
GAM2896  LOC145376 3'  AGATATGGAATGTACCAGGTTA 66555        _     T___
            C                    AGATATG AATGTG    GTTAT
                                |||||||| ||||||    |||||
                                TCTATAC TTACAT    CAATG
                                   C     GGTC
GAM2896  LOC203536 3'  TAAGCGTGTGTGTGTTATT    66556      ATA  AA
                                TAAG   TG  TGTGTGTTATT
                                ||||   ||  ||||||||||
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                                ATTC   AC  ACACACAATAA
                                  GC_  __
GAM2897  GATA3    3'  TACAATATAAGTTATATGCAAT 66559          _   _
                                TACAATATAAGT ATAT TAAT
                                |||||||||||| |||| ||||
                                ATGTTATATTCA TATA GTTA
                                       A    C
GAM2897  RANBP9   3'  CACAATATAAGTGTGAGCTCTT 66560          ATATTAA
           G                     TACAATATAAGT      TTTTG
                                |||||||||||       |||||
                                GTGTTATATTCA      AGAAC
                                       CACTCG_
GAM2897  SSFA2    3'  TACAGTGTAAGTACATTAA   66561     ATA
                                TACA   TAAGTATATTAA
                                ||||   ||||||||||||
                                ATGT   ATTCATGTAATT
                                  CAC
GAM2898  DKFZp547A023 3'  TTCATATGGCAGTCATATTTCA 66564       AATTTTA
           G                     TTCATAT      ATATTTCAG
                                |||||||      |||||||||
                                AAGTATA      TATAAAGTC
                                    CCGTCAG
GAM2898  DKFZP564O123 3'  TTCATATAATTATAATTCTCA  66565         T   A
                                TTCATATAATT TAAT TTTCA
                                |||||||||| |||| |||||
                                AAGTATATTAA ATTA AGAGT
                                       T   _
GAM2898  KIAA0332  3'  TCATATAATTTTTCA      66566          AATATT
                                TCATATAATTTT     TCA
                                ||||||||||||     |||
                                AGTATATTAAAA     AGT
                                          _______
GAM2898  ZDHHC2   3'  TTCATATAATTCTTAATAC   66567          _
                                TTCATATAATTTT AATAT
                                |||||||||||| |||||
                                AAGTATATTAAGA TTATG
                                       A
GAM2898  LOC129446 3'  TTCATAAAATCTTATTTCAGA  66568      T    TAA
                                TTCATA AATTT   TATTTCAGA
                                |||||| |||||   |||||||||
                                AAGTAT TTAGA   ATAAAGTCT
                                   T    ____
GAM2898  LOC149722 5'  TTCATATAATGTATATTCAGA  66569        TTTA    T
                                TTCATATAAT    ATATT CAGA
                                ||||||||||    ||||| ||||
                                AAGTATATTA    TATAA GTCT
                                      CA__     _
GAM2898  LOC151414 3'  TTCACATAATTTATCTTCAGA  66570          TAATA
                                TTCATATAATTT     TTTCAGA
                                ||||||||||||     |||||||
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                                AAGTGTATTAAA    GAAGTCT
                                      TA___
GAM2899  GOT2    3'  TAAGTCTACATGGTTA     66573        TAATAA
                                TAAGTTTAC    ATGGTTA
                                |||||||||    |||||||
                                ATTCAGATG    TACCAAT
                                      _______
GAM2899  LMAN1   3'  TAAGTTTACTAACAAGTG    66574            A
                                TAAGTTTACTAATAA TG
                                |||||||||||||| ||
                                ATTCAAATGATTGTT AC
                                      C
GAM2899  OSR1    3'  TAAGTTTACTAACGGAACTCTG 66575           AAA____
           G                     TAAGTTTACTAAT      TGG
                                |||||||||||||      |||
                                ATTCAAATGATTG      ACC
                                      CCTTGAG
GAM2899  ARF6    3'  TAAGTTTACTATACTGGTC   66576         ATAAA
                                TAAGTTTACTA    TGGTT
                                ||||||||||    |||||
                                ATTCAAATGAT    ACCAG
                                      ATG__
GAM2899  CGI-01  3'  GTTCTGAATAAATGGTTAA   66577     ACT
                                GTTT   AATAAATGGTTAA
                                ||||   ||||||||||||
                                CAAG   TTATTTACCAATT
                                  AC_
GAM2899  ELF1    3'  CAAGTTTACTAATGGACCGC   66578          AA  G
                                TAAGTTTACTAAT  AT GT
                                ||||||||||||  || ||
                                GTTCAAATGATTA  TG CG
                                      CC  G
GAM2899  ELL2    3'  CAAGTTTACTAATACTGA    66579           AA
                                TAAGTTTACTAATA  TGG
                                ||||||||||||  |||
                                GTTCAAATGATTAT  ACT
                                      G_
GAM2899  FLJ11053 3' AGTTTCTGCTAAATGGTTAAA 66580      A  AA
                                AGTTT CT  TAAATGGTTAAA
                                |||||  ||  ||||||||||||
                                TCAAA GA  ATTTACCAATTT
                                  _  CG
GAM2899  KCNMB2  3'  TTTACCATCTAATGGTTAAA  66581       ATA
                                TTTACTA   AATGGTTAAA
                                |||||||   ||||||||||
                                AAATGGT   TTACCAATTT
                                    AGA
GAM2899  MAN1    3'  TAAGTTTACTGAAACAAAT   66582         __
                                TAAGTTTACT  AATAAAT
                                |||||||||  |||||||
```

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                                ATTCAAATGA  TTGTTTA
                                      CT
GAM2899  LOC90841  3'  AGTTTACTGATAGACAACTAAA 66583        A   A  GG
                                AGTTTACT ATA AT  TTAAA
                                |||||||| ||| ||  |||||
                                TCAAATGA TAT TG  GATTT
                                     C   C  TT
GAM2900  LOC221975 3'  GCTGAAATGTGCATGACGGT   66586    ___    CC  T
                                GT   AATGT  GC ATGACGGT
                                ||   |||||  || ||||||||
                                CG   TTACA  CG TACTGCCA
                                 ACT    __ _
GAM2900  LOC91179  5'  CGCAGTGTCCGCTGCCGCAGT  66587      A       A_  A
                                CGTA TGTCCGCT  TG CGGT
                                |||| ||||||||  || ||||
                                GCGT ACAGGCGA  GC GTCA
                                  C       CG  _
GAM2901  ADAMTS13  3'  CGCGGCACTGCTCGTTGGC    66590     AA    G  CA   C
                                CGC  GCAC GT  CGT GGC
                                |||  |||| ||  ||| |||
                                GCG  CGTG CG  GCA CCG
                                  C_   A  A_   A
GAM2901  ADM      3'  GCGAGCACGGCTGTGGC     66591     A       CAC  C
                                GC AGCACGGT   GT GGC
                                || ||||||||   || |||
                                CG TCGTGCCG   CA CCG
                                 C       A__  _
GAM2901  ITPKB    3'  GCAGGCACGGTCTTCCAGGC   66592     A       ACG  _
                                GCA GCACGGTC   TC GGC
                                ||| ||||||||   || |||
                                CGT CGTGCCAG   GG CCG
                                  C       AA_  T
GAM2901  KCNQ4    5'  CGGGCACGGTCCGGGGC     66593    CAA       A  TC
                                CG   GCACGGTC CG  GGC
                                ||   |||||||| ||  |||
                                GC   CGTGCCAG GC  CCG
                                 C__       _  C_
GAM2901  LAMB1    5'  GCAGCCACGGGGACGCGGC    66594     AG    TC   T
                                GCA  CACGG  ACG CGGC
                                |||  |||||  ||| ||||
                                CGT  GTGCC  TGC GCCG
                                  CG    CC  _
GAM2901  TJP1     5'  CGCAGCCCGGCCACGTCGGC   66595     A  A
                                CGCA GC CGGTCACGTCGGC
                                |||| || ||||||||||||
                                GCGT CG GCCGGTGCAGCCG
                                  _  G
GAM2901  TMEM1    3'  CGCAAGCACAGTGCTGGGC    66596          CAC  C_
                                CGCAAGCACGGT   GT  GGC
                                ||||||||||||   ||  |||
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                                GCGTTCGTGTCA  CG  CCG
                                      ___  AC
GAM2901 BTN3A3   3' CAAGTCACATGTCATGTTGG  66597     _   _   C  C
                                CAAG CACG GTCA GT GG
                                |||| |||| |||| || ||
                                GTTC GTGT CAGT CA CC
                                  A   A   A  A
GAM2901 FLJ20275 3' GCAAGCACGGAGGTGGC     66598         TCAC  C
                                GCAAGCACGG   GT GGC
                                ||||||||||   || |||
                                CGTTCGTGCC   CA CCG
                                     TC__  _
GAM2901 FLJ20979 5' GCACGCGCGGTCACGTGGC   66599    A  A       C
                                GCA GC CGGTCACGT GGC
                                ||| || ||||||||| |||
                                CGT CG GCCAGTGCA CCG
                                  G  C       _
GAM2901 FLJ22938 3' CGTCAACGTCTTCACGTCGGC 66600   CA   ACGG
                                CG  AGC   TCACGTCGGC
                                ||  |||   ||||||||||
                                GC  TTG   AGTGCAGCCG
                                 AG   CAGA
GAM2901 MGC4825  5' CGCAAGCAGGCAGCGG      66601        C  T  C T
                                CGCAAGCA GG CA G CGG
                                |||||||| || || | |||
                                GCGTTCGT CC GT C GCC
                                     _  _  _ _
GAM2901 NCOR1    5' CGCGGCCACGGCGCGCGGC   66602    AAG     CA  T
                                CGC   CACGGT  CG CGGC
                                |||   ||||||  || ||||
                                GCG   GTGCCG  GC GCCG
                                  CCG     C_  _
GAM2901 SEMA5A   5' CACGAGCACGGTCCCCGAGC  66603    A       A_  TC
                                CGC AGCACGGTC  CG  GGC
                                ||| |||||||||  ||  |||
                                GTG TCGTGCCAG  GC  TCG
                                  C       GG  __
GAM2901 SS18L1   3' CACAAACAATTCATGTTGGC  66604       CGG   C  C
                                CGCAAGCA   TCA GT GGC
                                ||||||||   ||| || |||
                                GTGTTTGT   AGT CA CCG
                                     TA_   A  A
GAM2901 WBSCR20A 3' GCAAGCACCGGCTGCGGC    66605        _   CAC T
                                GCAAGCAC GGT   G CGGC
                                |||||||| |||   | ||||
                                CGTTCGTG CCG   C GCCG
                                     G   A__ _
GAM2901 LOC126961 3' CGAAGCACGGGCGTGTGGC  66606    C      TCA   C_
                                CG AAGCACGG   CGT  GGC
                                || ||||||||   |||  |||
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                                GC TTCGTGCC   GCA  CCG
                                 _      C__   CA
GAM2901  LOC128272 5'  GCCAGCACGGTCCAGGGC    66607    A       A  TC
                                GC AGCACGGTC CG  GGC
                                || ||||||||| ||  |||
                                CG TCGTGCCAG GT  CCG
                                 G       _ C_
GAM2901  LOC158061 5'  CGCAAGCACGTACCAGGGC    66608         GTCA  TC
                                CGCAAGCACG    CG  GGC
                                ||||||||||    ||  |||
                                GCGTTCGTGC    GT  CCG
                                      ATG_  C_
GAM2901  LOC200138 5'  GCTACAACGGTCACGTCGG    66609    AA  _
                                GC  GCA CGGTCACGTCGG
                                ||  ||| ||||||||||||
                                CG  TGT GCCAGTGCAGCC
                                 A_  T
GAM2901  LOC200958 3'  CGCAGCTGCAGTCTGTCGG    66610     A  A_    AC
                                CGCA GC  CGGTC  GTCGG
                                |||| ||  |||||  |||||
                                GCGT CG  GTCAG  CAGCC
                                  _ AC    A_
GAM2901  LOC253064 5'  GCAGCACAGCAGTGTCGGC    66611     A      CAC
                                GCA GCACGGT   GTCGGC
                                ||| |||||||   ||||||
                                CGT CGTGTCG   CAGCCG
                                  _      TCA
GAM2901  LOC257395 3'  CGAAGCACGGGCGTGTGGC    66606    C       TCA   C_
                                CG AAGCACGG   CGT  GGC
                                || ||||||||   |||  |||
                                GC TTCGTGCC   GCA  CCG
                                 _      C__   CA
GAM2901  LOC91308  3'  GCCAAGCAACCACACGTTGG   66612    _    _ G T    C
                                GC AAGCA C G CACGT GG
                                || ||||| | | ||||| ||
                                CG TTCGT G T GTGCA CC
                                 G    T G _    A
GAM2901  LOC91355  5'  GCAGCACGATGTCGG       66613     A      CAC
                                GCA GCACGGT   GTCGG
                                ||| |||||||   |||||
                                CGT CGTGCTA   CAGCC
                                  _     ____
GAM2902  CCND2     3'  TAGAAAAAGACCAGGATA    66616     TTC  TA
                                TGGA   GG  ACCAGGATA
                                ||||   ||  |||||||||
                                ATCT   TC  TGGTCCTAT
                                  TTT  __
GAM2902  GUCY1A3   3'  TGGCATTCCACCAGGATA    66617     _    GGTA
                                TGG ATTC    ACCAGGATA
                                ||| ||||    |||||||||
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                                ACC TAAG   TGGTCCTAT
                                  G   G___
GAM2902 HSPA4    3' TGAATAAACAGGCCAGGATA  66618     T__  TAA
                                TGGAT  CGG  CCAGGATA
                                |||||  |||  ||||||||
                                ACTTA  GTC  GGTCCTAT
                                   TTT  C__
GAM2902 SCRT1    3' CGGATTTGGCAGAGGAT    66619     C   ACC
                                TGGATT GGTA  AGGAT
                                |||||| ||||  |||||
                                GCCTAA CCGT  TCCTA
                                   A   C__
GAM2902 SLC17A5  3' TAGATTTAAACCAGGAT    66620     CGGT
                                TGGATT   AACCAGGAT
                                ||||||   |||||||||
                                ATCTAA   TTGGTCCTA
                                   AT__
GAM2902 TEC      3' TAGACTGACCAGGAT      66621     C GTA
                                TGGATT G  ACCAGGAT
                                |||||| |  ||||||||
                                ATCTGA C  TGGTCCTA
                                  _ ___
GAM2902 XRCC3    5' TGGGCTGGCCACCAGGAT   66622    AT C  A
                                TGG  T GGT ACCAGGAT
                                |||  | ||| ||||||||
                                ACC  A CCG TGGTCCTA
                                  CG _  G
GAM2902 BHMT     3' TGGATCCAGTGTTGACTAGGAT 66623        A___  C
                                TGGATTCGGT   AC AGGAT
                                ||||||||||   || |||||
                                ACCTAGGTCA   TG TCCTA
                                     CAAC  A
GAM2902 BLCAP    3' TGGGGCAGCTGACCAGGAT  66624    ATT   A_
                                TGG  CGGT  ACCAGGAT
                                |||  ||||  ||||||||
                                ACC  GTCG  TGGTCCTA
                                  CC_   AC
GAM2902 DKFZP434D146 3' GGATAGAGAAAACCAGGATA  66625    TC  T_
                                GGAT  GG  AACCAGGATA
                                ||||  ||  ||||||||||
                                CCTA  TC  TTGGTCCTAT
                                  TC  TT
GAM2902 DMTF1    5' TGGAAGAACCAGGAT     66626    TTC  T
                                TGGA  GG AACCAGGAT
                                ||||  || |||||||||
                                ACCT  TC TTGGTCCTA
                                  ___ _
GAM2902 FLJ10058 3' TGGACTGAGAACCAGGAT   66627      C  T
                                TGGATT GG AACCAGGAT
                                |||||| || |||||||||
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                                ACCTGA TC TTGGTCCTA
                                   C  _
GAM2902  FLJ13052  3'  GGATTCGGGCCTGGATA     66628        TAA  A
                                GGATTCGG   CC GGATA
                                ||||||||   || |||||
                                CCTAAGCC   GG CCTAT
                                     C__  A
GAM2902  FLJ23132  3'  TGGATTCAGTTAGAGATA    66629         AACCA
                                TGGATTCGGT    GGATA
                                ||||||||||    |||||
                                ACCTAAGTCA    TCTAT
                                      ATC__
GAM2902  HGC6.1.1  3'  TAGAAACTTAACCAGGATA   66630     TTCGG
                                TGGA    TAACCAGGATA
                                ||||    ||||||||||
                                ATCT    ATTGGTCCTAT
                                  TTGA_
GAM2902  LGALS8    5'  TGGACTTTTCAGGACCAGG   66631      ___   TA
                                TGGAT   TCGG  ACCAGG
                                |||||   ||||  ||||||
                                ACCTG   AGTC  TGGTCC
                                   AAA   C_
GAM2902  NUDT12    5'  TAGAGGCAACCAGGAT     66632     TTC
                                TGGA   GGTAACCAGGAT
                                ||||   ||||||||||||
                                ATCT   CCGTTGGTCCTA
                                  ___
GAM2902  NUDT3     3'  TGGCCAGGGCCAGGATA     66633     AT   TAA
                                TGG  TCGG   CCAGGATA
                                |||  ||||   ||||||||
                                ACC  GGTC   GGTCCTAT
                                  __   CC_
GAM2902  SV2       5'  GGAGGCTAAGCCAGGATA    66634     TTC  _ _
                                GGA   GGT AA CCAGGATA
                                |||   ||| || ||||||||
                                CCT   CCG TT GGTCCTAT
                                  ___  A  C
GAM2902  WDR9      3'  TGGTTTTGATAACCAGGAT    66635     A  C
                                TGG TT GGTAACCAGGAT
                                ||| || ||||||||||||
                                ACC AA CTATTGGTCCTA
                                  A  A
GAM2902  LOC131827 3'  AGATTGAGAACCAGGATA    66636      C  T
                                GGATT GG AACCAGGATA
                                ||||| || ||||||||||
                                TCTAA TC TTGGTCCTAT
                                   C  _
GAM2902  LOC146108 5'  TGGTTATCCGCACCAGGATA  66637     AT_  G   A
                                TGG   TC GTA CCAGGATA
                                |||   || ||| ||||||||
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                                ACC   AG CGT GGTCCTAT
                                  AAT  G  _
GAM2902  LOC146745 5'  AGACTGGCCAGGATA      66638      C  TAA
                                GGATT GG   CCAGGATA
                                ||||| ||   ||||||||
                                TCTGA CC   GGTCCTAT
                                  _  ___
GAM2902  LOC147353 3'  TGTGTCCAGTAATCAGGATA   66639    GA      C
                                TG  TTCGGTAA CAGGATA
                                ||  |||||||| |||||||
                                AC  AGGTCATT GTCCTAT
                                 AC       A
GAM2902  LOC149837 3'  TGAACCCAGAGCCGGGAT    66640         TAA  A
                                TGGATTCGG   CC GGAT
                                |||||||||   || ||||
                                ACTTGGGTC   GG CCTA
                                      TC_  C
GAM2902  LOC152059 3'  GAGGCAGAACCAGGATA     66641    TT   T
                                GA  CGG AACCAGGATA
                                ||  ||| ||||||||||
                                CT  GTC TTGGTCCTAT
                                 CC  _
GAM2902  LOC201243 5'  AGACTGGCCAGGATA      66638      C  TAA
                                GGATT GG   CCAGGATA
                                ||||| ||   ||||||||
                                TCTGA CC   GGTCCTAT
                                  _  ___
GAM2902  LOC254297 5'  TGGGGTACACCCAGGATA    66642     ATTC   A__
                                TGG    GGTA   CCAGGATA
                                |||    ||||   ||||||||
                                ACC    CCAT   GGTCCTAT
                                  ____   GTG
GAM2902  LOC255252 5'  GGACCCGCAGTAGCCGGGAT   66643        __   A  A
                                GGATTCG  GTA CC GGAT
                                |||||||  ||| || ||||
                                CCTGGGC  CAT GG CCTA
                                    GT   C  C
GAM2902  LOC90874  3'  TGGGTCAGTCCCAGGATA    66644     AT    AA
                                TGG  TCGGT  CCAGGATA
                                |||  |||||  ||||||||
                                ACC  AGTCA  GGTCCTAT
                                  C_    G_
GAM2903  GABRP     3'  GCCACTGGGAGAGTGTT     66647      C      C
                                GTCAC GGGAGGGT GTT
                                ||||| |||||||| |||
                                CGGTG CCCTCTCA CAA
                                   A       _
GAM2903  KIAA0084  5'  TCCGTCCCGGGAGGAAAGTT   66648       A       TC
                                TCCGTC CCGGGAGGG  GTT
                                |||||| |||||||||  |||
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                                AGGCAG GGCCCTCCT  CAA
                                  _       TT
GAM2903  KIAA0561  3'  TCCATCGCTGGGATTACATTGT 66649      ACC   GGGT
             T                   TCCGTC  GGGA   CGTTGTT
                                 ||||||  ||||   |||||||
                                 AGGTAG  CCCT   GTAACAA
                                    CGA   AAT_
GAM2903  PRMT6    3'  TCCGTTGTTGAGGGGGATCACT 66650     CACC__  A
                                 TCCGT    GGG GGGTCGTT
                                 |||||     ||| ||||||||
                                 AGGCA     CCC CCTAGTGA
                                   ACAACT  _
GAM2903  LOC161734 3'  TCCGTTGCTGGTGAGGCACTGT 66651     CACC  GA   T
                                 TCCGT   GG  GGG CGTTGT
                                 |||||   ||  ||| ||||||
                                 AGGCA   CC  TCC GTGACA
                                   ACGA  AC  _
GAM2903  LOC90342  5'  TCCGTCATGGGGAGGGTCTTGT 66652       CC       G
             T                   TCCGTCA  GGGAGGGTC TTGTT
                                 |||||||  ||||||||| |||||
                                 AGGCAGT  CCCTCCCAG AACAA
                                    AC       _
GAM2904  IFNB1    3'  TAAAATTTAAATAAATAAAAAT 66655        T_
             AA                   TGAAATTT  ATAAATAAAAATAA
                                  ||||||||  ||||||||||||||
                                  ATTTTAAA  TATTTATTTTTATT
                                     TT
GAM2904  ZFP36L2  3'  TGAAACTTCGTAATAAAAATAA 66656       TA   A
                                 TGAAATTT  TAA TAAAAATAA
                                 ||||||||  ||| |||||||||
                                 ACTTTGAA  ATT ATTTTTATT
                                    GC  _
GAM2905  FACL2    3'  TCTTTTGATATGAAAACCAC   66659      A      TTACT
                                 TCTTTT ATATGAA    TCAC
                                 |||||| |||||||    ||||
                                 AGAAAA TATACTT    GGTG
                                    C      TT___
GAM2905  P23      5'  TCTTTTAAATGATCACATTCA  66660       T   A   _
                                 TCTTTTAA ATGA TTAC TTCA
                                 |||||||| |||| |||| ||||
                                 AGAAAATT TACT AGTG AAGT
                                    _   _   T
GAM2905  PIGC     3'  TTTTAATAGAAACCACATCACT 66661       T      T
                                 TTTTAATA GAATTAC TCACT
                                 |||||||| ||||||| |||||
                                 AAAATTAT TTTGGTG AGTGA
                                    C      T
GAM2905  ZNF195   3'  TCTTTTAGTATGAACTCT    66662       A      A
                                 TCTTTTA TATGAATT CT
                                 ||||||| |||||||| ||
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                                AGAAAAT ATACTTGA GA
                                    C       _
GAM2905 BMF      3' TCCTTTGGGCCTTACTTCACT 66663       AATATGAA
                                TCTTTT       TTACTTCACT
                                ||||||       ||||||||||
                                AGGAAA       AATGAAGTGA
                                   CCCGG___
GAM2905 CGI-142  3' TCTCTTAATATGCAGCATTCA 66664          AATTAC
                                TCTTTTAATATG     TTCA
                                ||||||||||||     ||||
                                AGAGAATTATAC     AAGT
                                      GTCGT_
GAM2905 FLJ13659 3' TCTCCAGTATGAATTACTT   66665      TAA
                                TCTTT   TATGAATTACTT
                                |||||   ||||||||||||
                                AGAGG   ATACTTAATGAA
                                   TC_
GAM2905 FLJ14621 3' TCTTTTAATACGGGTATTACT 66666          A__
                                TCTTTTAATATG   ATTACT
                                ||||||||||||   ||||||
                                AGAAAATTATGC   TAATGA
                                      CCA
GAM2905 MAIL     3' TCTTTTAATATAACCCACT    66667          A
                                TCTTTTAATATGA TTACT
                                |||||||||||| |||||
                                AGAAAATTATATT GGTGA
                                       G
GAM2905 RALGPS1A 3' TTTTAACATGAAACCACT    66668          _
                                TTTTAATATGAA TTACT
                                |||||||||||| |||||
                                AAAATTGTACTT GGTGA
                                       T
GAM2905 TTTY6    3' TTTTAACAGAAATATTTCACT  66669       T  T  C
                                TTTTAATA GAA TA TTCACT
                                |||||||| ||| || ||||||
                                AAAATTGT CTT AT AAGTGA
                                     _  T  A
GAM2905 LOC158281 5' TCTTTTAAATGATCACATTCA  66660       T   A   _
                                TCTTTTAA ATGA TTAC TTCA
                                |||||||| |||| |||| ||||
                                AGAAAATT TACT AGTG AAGT
                                     _   _   T
GAM2905 LOC90459 3' TCTTTTATTGACTAACTTCACT 66670       ATA  ATT
                                TCTTTTA  TGA  ACTTCACT
                                |||||||  |||  ||||||||
                                AGAAAAT  ACT  TGAAGTGA
                                   A__   GAT
GAM2906 AGTR1    3' GGAAATAAAAAATAACA     66673          CCGCA
                                GGAAATAAAAGA    TAACA
                                ||||||||||||    |||||
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                                CCTTTATTTTTT    ATTGT
                                      _____
GAM2906 AGTR1    3' GGAAATAAAAAATAACA    66673         CCGCA
                                GGAAATAAAAGA    TAACA
                                ||||||||||||    |||||
                                CCTTTATTTTTT    ATTGT
                                      _____
GAM2906 AGTR1    3' GGAAATAAAAAATAACA    66673         CCGCA
                                GGAAATAAAAGA    TAACA
                                ||||||||||||    |||||
                                CCTTTATTTTTT    ATTGT
                                      _____
GAM2906 AGTR1    3' GGAAATAAAAAATAACA    66673         CCGCA
                                GGAAATAAAAGA    TAACA
                                ||||||||||||    |||||
                                CCTTTATTTTTT    ATTGT
                                      _____
GAM2906 AGTR1    3' GGAAATAAAAAATAACA    66673         CCGCA
                                GGAAATAAAAGA    TAACA
                                ||||||||||||    |||||
                                CCTTTATTTTTT    ATTGT
                                      _____
GAM2906 CLECSF12 3' GGAAATAAAAATAGCACCAG  66674        ACC   AA
                                GGAAATAAAAG  GCAT  CAG
                                ||||||||||   ||||  |||
                                CCTTTATTTTT  CGTG  GTC
                                      AT_   __
GAM2906 JDP1     5' CGGAAACAAGAGGCACA    66675        A  ACC
                                CGGAAATAA AG   GCATA
                                |||||||| ||   |||||
                                GCCTTTGTT TC   CGTGT
                                     C  ___
GAM2906 NPM1     5' CGGAGATAAAAGAACGCTGCTC 66676     A      C   ATAA_
            CAG                   CGGA ATAAAAGA CGC    CAG
                                |||| |||||||| |||    |||
                                GCCT TATTTTCT GCG    GTC
                                  C       T   ACGAG
GAM2906 PCLO     3' GGAAACAAAGGAGAAACA    66677        A  CCGCAT
                                GGAAATAAA GA     AACA
                                |||||||| ||     ||||
                                CCTTTGTTT CT     TTGT
                                     C  CT____
GAM2906 PTGER3   3' GGAAACAGGACATAACA    66678       AAAGACC
                                GGAAATA      GCATAACA
                                |||||||      ||||||||
                                CCTTTGT      TGTATTGT
                                    CC_____
GAM2906 RECQL5   3' GGAAATAAAAACACACA    66679         AC
                                GGAAATAAAAG  CGCATA
                                ||||||||||  ||||||
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                                CCTTTATTTTT  GTGTGT
                                          __
GAM2906  STAU2    3'  CAGAAATAAAAGTAAC      66680          ACCGCA
                                CGGAAATAAAAG     TAAC
                                ||||||||||||    ||||
                                GTCTTTATTTTC     ATTG
                                          _______
GAM2906  THO2     3'  GGAAATAAAAACTGAACCCA   66681          _____   G
                                GGAAATAAAA    GACC CA
                                ||||||||||    |||| ||
                                CCTTTATTTT    TTGG GT
                                      TGAC   _
GAM2906  TPD52L2  3'  GAGATAAAAAATTGCGTAACAG 66682    A       CC  A
                                GA ATAAAAGA  GC TAACAG
                                || ||||||||  || ||||||
                                CT TATTTTTT  CG ATTGTC
                                 C       AA  C
GAM2906  24432    5'  GGAAATAAGAGCACACACACAG 66683        A  AC     A
                                GGAAATAA AG  CGCATA CAG
                                ||||||||  ||  |||||| |||
                                CCTTTATT TC  GTGTGT GTC
                                     C  GT     _
GAM2906  EVI5     3'  GAAATAAAAGATTCCACCAACA 66684          __    A
            G                    GAAATAAAAGA  CCGC TAACAG
                                ||||||||||  |||| ||||||
                                CTTTATTTTCT  GGTG GTTGTC
                                      AA   _
GAM2906  FLJ10996 3'  GGGAACAAAAGGTACCATGGCA 66685    A       __  ____
                                GG AATAAAAG  ACC   GCA
                                || ||||||||  |||   |||
                                CC TTGTTTTC  TGG   CGT
                                 C       CA   TAC
GAM2906  FLJ14454 3'  GGAAATAAAGGAGAGAAACAG  66686        A  CCGCAT
                                GGAAATAAA GA     AACAG
                                |||||||||  ||     |||||
                                CCTTTATTT CT     TTGTC
                                     C  CTCT__
GAM2906  GNG4     3'  GGAGAGGGGAGACCGCACCCAC 66687     AATAAA       A_
            AG                    GGA     AGACCGCAT  ACAG
                                |||     |||||||||  ||||
                                CCT     TCTGGCGTG  TGTC
                                  CTCCCC        GG
GAM2906  KIAA1877 3'  GGAAATAAAAGCCTTTGCCAG  66688          A  GCATAA
                                GGAAATAAAAG CC      CAG
                                ||||||||||| ||     |||
                                CCTTTATTTTC GG     GTC
                                      _  AAACG_
GAM2906  RGS17    3'  GGAGACAAAGACCATAAC    66689     AATA      GC
                                GGA    AAAGACC  ATAAC
                                |||    |||||||  |||||
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                                CCT   TTTCTGG  TATTG
                                  CTG_     __
GAM2906  SNFT     3'  GGAAATGGCTCTGCATAACAG  66690       AAAAGACC
                                GGAAAT      GCATAACAG
                                ||||||      |||||||||
                                CCTTTA      CGTATTGTC
                                   CCGAGA__
GAM2906  LOC147299 3'  GGAAATAAAATGTTGCTTAA  66691         GACC  A
                                GGAAATAAAA   GC TAA
                                ||||||||||   || |||
                                CCTTTATTTT   CG ATT
                                      ACAA  A
GAM2906  LOC149722 5'  GGAAATAAAAGGCATACA    66692         ACC    A
                                GGAAATAAAAG  GCATA CA
                                ||||||||||   ||||| ||
                                CCTTTATTTTC  CGTAT GT
                                      ___    _
GAM2906  LOC152845 5'  GGAAGCAAAAGACTCGCCACAG 66693     A      _  ATA
                                GGAA TAAAAGAC CGC   ACAG
                                |||| |||||||| |||   ||||
                                CCTT GTTTTCTG GCG   TGTC
                                  C       A  G__
GAM2906  LOC154739 5'  GGGGATAAAAGAACCAACAC   66694    AA      _  _
                                GG  ATAAAAGA CCG CAT
                                ||  |||||||| ||| |||
                                CC  TATTTTCT GGT GTG
                                 CC       T  T
GAM2906  LOC158549 3'  GGAAATAAAAACTGAACCCA   66681         ____   G
                                GGAAATAAAA   GACC CA
                                ||||||||||   |||| ||
                                CCTTTATTTT   TTGG GT
                                      TGAC   _
GAM2906  LOC203276 3'  GGGGATAAAAGAACCAACAT   66695    AA      _  _
                                GG  ATAAAAGA CCG CAT
                                ||  |||||||| ||| |||
                                CC  TATTTTCT GGT GTA
                                 CC       T  T
GAM2906  LOC203305 3'  GGGGATAAAAGAACCAACAT   66695    AA      _  _
                                GG  ATAAAAGA CCG CAT
                                ||  |||||||| ||| |||
                                CC  TATTTTCT GGT GTA
                                 CC       T  T
GAM2906  LOC254243 3'  GGGGATAAAAGAACCAACAT   66695    AA      _  _
                                GG  ATAAAAGA CCG CAT
                                ||  |||||||| ||| |||
                                CC  TATTTTCT GGT GTA
                                 CC       T  T
GAM2906  LOC255527 5'  GGAAATAAAAGAGTTTGCA    66696         CC__
                                GGAAATAAAAGA   GCA
                                ||||||||||||   |||
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                                CCTTTATTTTCT   CGT
                                       CAAA
GAM2906 LOC90038 3' GGGGATAAAAGAACCAACAT  66695   AA      _  _
                                GG  ATAAAAGA CCG CAT
                                ||  |||||||| ||| |||
                                CC  TATTTTCT GGT GTA
                                 CC       T   T
GAM2907 BAG2    3' TATTTTATCATTTTTACA    66699    G
                                TAT TTATCATTTTTATA
                                ||| ||||||||||||||
                                ATA AATAGTAAAAATGT
                                  A
GAM2907 NASP    5' TATGCTATCATTATTT      66700          TTTATA
                                TATGTTATCATT     ATTT
                                ||||||||||||     ||||
                                ATACGATAGTAA     TAAA
                                                 _______
GAM2907 PRO0245  5' TGCTCTAATTTTTATAATTTT  66701     ATC
                                TGTT   ATTTTTATAATTTT
                                ||||   ||||||||||||||
                                ACGA   TAAAAATATTAAAA
                                  GAT
GAM2907 LOC126669 3' TGTCATCATTTTCCCTTTTC  66702          ATAA
                                TGTTATCATTTTT    TTTTC
                                ||||||||||||    |||||
                                ACAGTAGTAAAAG    AAAAG
                                       GG__
GAM2908 SLC20A1  5' TATAATAAATAATATATATTAT 66705       T       C
            A                    TATAATA ATAATATAT TTATA
                                ||||||| ||||||||| |||||
                                ATATTAT TATTATATA AATAT
                                    T       T
GAM2908 UBE2H    3' TATAATATATATATATC     66706          A
                                TATAATATATA TATATC
                                |||||||||| ||||||
                                ATATTATATAT ATATAG
                                            _
GAM2908 KIAA0469 3' TATAAATATAGAATACCTTATA 66707      T    AT
                                TATAA ATATA  ATATCTTATA
                                ||||| |||||  ||||||||||
                                ATATT TATAT  TATGGAATAT
                                   _    CT
GAM2908 KIAA1165 3' TAAAATGAAATATATCTTATA  66708    T  AT
                                TAA AT  AATATATCTTATA
                                ||| ||  ||||||||||||
                                ATT TA  TTATATAGAATAT
                                  T  CT
GAM2908 ZYG      3' TATAATATATATATATCTCA   66709          A
                                TATAATATATA TATATCTTA
                                |||||||||| |||||||||
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                                ATATTATATAT ATATAGAGT
                                          _
GAM2908  LOC222008 3'  TATAATATATAAATATCC    66710          T
                                TATAATATATAA ATATCT
                                |||||||||||| ||||||
                                ATATTATATATT TATAGG
                                          _
GAM2908  LOC92370  3'  TAATATATAAAACACCTTATAA 66711          T
                                TAATATATAA ATATCTTATAA
                                |||||||||| ||||||||||
                                ATTATATATT TGTGGAATATT
                                       T
GAM2909  AHR       3'  TACAGGTTTAAAGTTTTGA   66714     T   CATAC
                                TACA GTT    AAAGTTTTGA
                                |||| |||    ||||||||||
                                ATGT CAA    TTTCAAAACT
                                  C  A____
GAM2909  FAT       3'  ACATGTTCATGTATCTGA    66715         ACAAA  _
                                ACATGTTCAT    GT TTTGA
                                ||||||||||    || |||||
                                TGTACAAGTA    CA AGACT
                                      _____ T
GAM2909  PUM2      3'  ATGTTTATACAAAATACTGAC  66716      C       T
                                ATGTT ATACAAAGT TTGAC
                                ||||| ||||||||| |||||
                                TACAA TATGTTTTA GACTG
                                   A       T
GAM2909  ZNFN2A1   5'  ACATCAGCTACAAAGTTTTG   66717     GTTCA
                                ACAT    TACAAAGTTTTG
                                ||||    ||||||||||||
                                TGTA    ATGTTTCAAAAC
                                  GTCG_
GAM2909  FLJ12436  3'  ACATTAGCACAAAGTTTTGA   66718     GTTCA
                                ACAT    TACAAAGTTTTGA
                                ||||    ||||||||||||||
                                TGTA    GTGTTTCAAAACT
                                  ATC__
GAM2909  PPAP2A    3'  TACATGTTTATACATAAGC    66719       C    _
                                TACATGTT ATACA AAGT
                                |||||||| ||||| ||||
                                ATGTACAA TATGT TTCG
                                     A    A
GAM2909  LOC148388 3'  TGCTGTACAAAGGGTTTTGAC  66720     CA    __
                                TGTT  TACAAA  GTTTTGAC
                                ||||  ||||||  ||||||||
                                ACGA  ATGTTT  CAAAACTG
                                  C_    CC
GAM2909  LOC152274 3'  TACATGCTCGTATACATGA    66721        __    AAGTTT
                                TACATGTTC  ATACA     TGA
                                |||||||||  |||||     |||
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                                ATGTACGAG  TATGT     ACT
                                     CA    _______
GAM2909  LOC152941 3'  CGTTCATCATATTTTGAC    66722        A  AA
                                TGTTCAT CA  GTTTTGAC
                                ||||||| ||  ||||||||
                                GCAAGTA GT  TAAAACTG
                                   _ A_
GAM2909  LOC202781 3'  CATGAAACAAAGTTTTGA    66723     TTCAT
                                CATG    ACAAAGTTTTGA
                                ||||    ||||||||||||
                                GTAC    TGTTTCAAAACT
                                  TT___
GAM2909  LOC93166  3'  TACATGTTCTTGCAATCTTGAC 66724         ATACAA
                                TACATGTTC     AGTTTTGAC
                                |||||||||     |||||||||
                                ATGTACAAG     TTAGAACTG
                                     AACG__
GAM2910  ABCD4     3'  AACTGATTAAAAGATTTCCA  66727         AA  GCG
                                AACTGGTTAAA  AGA  CCA
                                ||||||||||  |||  |||
                                TTGACTAATTT  TCT  GGT
                                     __  AAA
GAM2910  ABCD4     3'  AACTGATTAAAAGATTTCCA  66727         AA  GCG
                                AACTGGTTAAA  AGA  CCA
                                ||||||||||  |||  |||
                                TTGACTAATTT  TCT  GGT
                                     __  AAA
GAM2910  ABCD4     3'  AACTGATTAAAAGATTTCCA  66727         AA  GCG
                                AACTGGTTAAA  AGA  CCA
                                ||||||||||  |||  |||
                                TTGACTAATTT  TCT  GGT
                                     __  AAA
GAM2910  ABCD4     3'  AACTGATTAAAAGATTTCCA  66727         AA  GCG
                                AACTGGTTAAA  AGA  CCA
                                ||||||||||  |||  |||
                                TTGACTAATTT  TCT  GGT
                                     __  AAA
GAM2910  AICDA     3'  AACTGATTGAAAGTGAGC    66728        A  AA
                                AACTGGTT AAA  GAGC
                                |||||||| |||  ||||
                                TTGACTAA TTT  CTCG
                                    C   CA
GAM2910  DXF68S1E  3'  AACTGGTTAAGAGGAGCA    66729         AAAA
                                AACTGGTTAA    GAGCG
                                ||||||||||    |||||
                                TTGACCAATT    CTCGT
                                     CTC_
GAM2910  EGF       3'  ACTGCTTAAAAGAGCA      66730      G    AA
                                ACTG TTAAA  AGAGCG
                                |||| |||||  ||||||
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                                TGAC AATTT  TCTCGT
                                  G    __
GAM2910  FOG2     3'  ACTGGTTAGAACAACA      66731        AAAAA     C
                                ACTGGTT     AGAGCG CA
                                |||||||     |||||| ||
                                TGACCAA     TCTTGT GT
                                    _____      T
GAM2910  G22P1    3'  AACTGGCTGAGGACAAGGCCA  66732         AAAAAA   C
                                AACTGGTT     GAG GCCA
                                ||||||||     ||| ||||
                                TTGACCGA     TTC CGGT
                                    CTCCTG   _
GAM2910  HLCS     3'  AACTGGCTTAAAAGCTCCAAA  66733         AAAA     G
                                AACTGGTT    AAGAGC CCAAA
                                ||||||||    |||||| |||||
                                TTGACCGA    TTTTCG GGTTT
                                    A___     A
GAM2910  NEBL     5'  ACTGGTTAAGAAATCCAA     66734         AAAA    CG
                                ACTGGTTA    AGAG  CCAA
                                ||||||||    ||||  ||||
                                TGACCAAT    TCTT  GGTT
                                    _____    TA
GAM2910  PGM1     3'  AACTGGTTAGTGAAAAAGTCA  66735         AA_     _
                                AACTGGTTA   AAAGAG CG
                                |||||||||   |||||| ||
                                TTGACCAAT   TTTTTC GT
                                    CAC     A
GAM2910  PIK3R3   3'  AACTGGTCAGAAAAGATACTGT 66736         A     _ GC_
            CAAA                   AACTGGTTA AAAAGA GC   CAAA
                                |||||||||| |||||| ||   ||||
                                TTGACCAGT TTTTCT TG   GTTT
                                    C     A  ACA
GAM2910  PTGFRN   3'  GCAGAAAAGAGAGAGCGCCAA  66737    TA   ____
                                GT  AAAA   AGAGCGCCAA
                                ||  ||||   ||||||||||
                                CG  TTTT   TCTCGCGGTT
                                  TC    CTC
GAM2910  SIRT2    3'  CTGGTTAAGAGGGGGCCA     66738        AAAA   C__
                                CTGGTTA    AGAG   GCCA
                                |||||||    ||||   ||||
                                GACCAAT    TCTC   CGGT
                                    _____    CCC
GAM2910  SIRT2    3'  CTGGTTAAGAGGGGGCCA     66738        AAAA   C__
                                CTGGTTA    AGAG   GCCA
                                |||||||    ||||   ||||
                                GACCAAT    TCTC   CGGT
                                    _____    CCC
GAM2910  SLC25A13 3'  CTGGTTAAGAAAACACC      66739         AAA
                                CTGGTTAA   AGAGCGCC
                                ||||||||   ||||||||
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                                GACCAATT   TTTTGTGG
                                    C__
GAM2910  UPF3A    3'  TGGTTAAAATCGCAGTGCCAAA 66740        AAG_  C
                                TGGTTAAAA    AG GCCAAA
                                |||||||||    || ||||||
                                ACCAATTTT    TC CGGTTT
                                    AGCG  A
GAM2910  UPF3A    3'  TGGTTAAAATCGCAGTGCCAAA 66740        AAG_  C
                                TGGTTAAAA    AG GCCAAA
                                |||||||||    || ||||||
                                ACCAATTTT    TC CGGTTT
                                    AGCG  A
GAM2910  VSX1     3'  AACTGGTTAAAGTGCCA     66741        AAAAA   C
                                AACTGGTTA    GAG GCCA
                                |||||||||    ||| ||||
                                TTGACCAAT    TTC CGGT
                                    _____  A
GAM2910  ARHGEF15 3'  AACTGGCTTGAGAGGGCACA   66742        AAAAA   C  _
                                AACTGGTT    AGAG GC CA
                                ||||||||    |||| || ||
                                TTGACCGA    TCTC CG GT
                                    AC___   C  T
GAM2910  C11orf23 3'  AACTGGTTATAAAAAGAACACC 66743        _
            AAA                   AACTGGTTA AAAAAGAGCGCCAAA
                                |||||||||  ||||||||||||||||
                                TTGACCAAT TTTTTCTTGTGGTTT
                                    A
GAM2910  EHM2     3'  ACTGGTTAGAGGTGAGCTGCCA 66744        AAAAA   _
            AA                    ACTGGTTA    GAGC GCCAAA
                                ||||||||    |||| ||||||
                                TGACCAAT    CTCG CGGTTT
                                    CTCCA   A
GAM2910  FLJ10525 3'  AACTGGCTAAGAGGC       66745        AAAA   C
                                AACTGGTTA   AGAG GC
                                |||||||||   |||| ||
                                TTGACCGAT   TCTC CG
                                    ____   _
GAM2910  FLJ10702 3'  AGTCAAAAGAGTGCCA      66746        AA   C
                                GGTTAAA  AGAG GCCA
                                |||||||  |||| ||||
                                TCAGTTT  TCTC CGGT
                                    __   A
GAM2910  FLJ11848 3'  AACTGGTTTAAGAACA      66747        AAAA
                                AACTGGTT   AAGAGCG
                                ||||||||   |||||||
                                TTGACCAA   TTCTTGT
                                    A___
GAM2910  FLJ13611 5'  CTGGTTAAAGAGATCTCCA   66748        AA  GCG
                                CTGGTTAAA  AGA  CCA
                                |||||||||  |||  |||
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                                GACCAATTT  TCT   GGT
                                     C_   AGA
GAM2910  FLJ21551  3' ACTGGTTAAAAAGGGCA     66749          A A
                                ACTGGTTAAAAA G GCG
                                |||||||||||| | |||
                                TGACCAATTTTT C CGT
                                       _ C
GAM2910  FLJ22341  3' AACTGGTAAAAAACG       66750        TAAA
                                AACTGGT    AAAGAGCG
                                |||||||    ||||||||
                                TTGACCA    TTTTTTGC
                                      ____
GAM2910  KIAA0349  3' TGGTTAAAAAAATCCAA     66751          GAGCG
                                TGGTTAAAAAA    CCAA
                                ||||||||||     ||||
                                ACCAATTTTTT    GGTT
                                       TA___
GAM2910  KIAA0365  3' CTGGTTAAAAAATCTACACCA 66752           GA_
                                CTGGTTAAAAAA   GCGCCA
                                ||||||||||||   ||||||
                                GACCAATTTTTT   TGTGGT
                                       AGA
GAM2910  KIAA0453  3' ACTAGTTAGGAAAAAGCCAAA 66753        AA    GC
                                ACTGGTTA  AAAGA  GCCAAA
                                ||||||||  |||||  ||||||
                                TGATCAAT  TTTTT  CGGTTT
                                     CC    __
GAM2910  KIAA0663  3' TGGTTAAAGGCCACCAAA    66754       AAA  AG
                                TGGTTAA   AG  CGCCAAA
                                |||||||   ||  |||||||
                                ACCAATT   TC  GTGGTTT
                                     ___  CG
GAM2910  KIAA1204  3' AACTGGTCTAAAAGAACAC   66755        AA
                                AACTGGTT  AAAAGAGCGC
                                ||||||||  ||||||||||
                                TTGACCAG  TTTTCTTGTG
                                     A_
GAM2910  KIAA1735  3' AACTGGTTTAAGAGACA     66756        AAAA    _
                                AACTGGTT    AAGAG CG
                                ||||||||    ||||| ||
                                TTGACCAA    TTCTC GT
                                     A___     T
GAM2910  KIAA1798  3' CTGGTTAAAAGCTCAA      66757        AAAA   GC
                                CTGGTTAA   GAGC  CAA
                                ||||||||   ||||  |||
                                GACCAATT   TTCG  GTT
                                     _____   A_
GAM2910  MGC2488   3' ACTGGTTAATAAAAGAGC    66758         _
                                ACTGGTTAA AAAAGAGC
                                ||||||||| ||||||||
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                                TGACCAATT TTTTCTCG
                                     A
GAM2910  MKNK1    3'  TGGTTAAAAACACCAAA     66759        AAAA
                                TGGTTAA    GAGCGCCAAA
                                |||||||    ||||||||||
                                ACCAATT    TTTGTGGTTT
                                      ____
GAM2910  NMT1     3'  AACTGGCTAAAGAGCCC     66760         AAA    G
                                AACTGGTTAA   AGAGC CC
                                ||||||||||   ||||| ||
                                TTGACCGATT   TCTCG GG
                                     ___   _
GAM2910  PELI2    3'  AACTTGGTTAAAAACCCAA   66761     _    AAAA   G
                                AACT GGTTAA    GAGC CCAA
                                |||| ||||||    |||| ||||
                                TTGA CCAATT    TTTG GGTT
                                  A    ____   _
GAM2910  RNF2     3'  TAATTAAAAGAGCGCCAAA   66762        AA
                                TGGTTAAA  AGAGCGCCAAA
                                ||||||||  ||||||||||
                                ATTAATTT  TCTCGCGGTTT
                                     __
GAM2910  RNF9     3'  CTGGTTCAAGAACCCA      66763       AAAA     G
                                CTGGTT    AAGAGC CCA
                                ||||||    |||||| |||
                                GACCAA    TTCTTG GGT
                                   G___    _
GAM2910  SNRPD1   3'  AACTGATTAAAAAGCA      66764          AAA
                                AACTGGTTAAA   GAGCG
                                ||||||||||   |||||
                                TTGACTAATTT   TTCGT
                                     ___
GAM2910  WIT-1    3'  ACTGGTTAAAAAAAATCG    66765            G
                                ACTGGTTAAAAAAAGA CG
                                |||||||||||||| ||
                                TGACCAATTTTTTTT GC
                                       A
GAM2910  LOC146224 5'  TGGTTAAAAAATGCCAAA    66766          GAGC
                                TGGTTAAAAAA    GCCAAA
                                ||||||||||    ||||||
                                ACCAATTTTTT    CGGTTT
                                      A___
GAM2910  LOC147858 5'  AACTGAAAAGAGCGTCA     66767       TTAAA      C
                                AACTGG    AAAGAGCG CA
                                ||||||    |||||||| ||
                                TTGACT    TTTCTCGC GT
                                     _____      A
GAM2910  LOC148709 3'  AACTGGTTCAGGAGCTCTTGCC 66768        AAAAAA   _____
            A                    AACTGGTT     GAGC    GCCA
                                ||||||||     ||||    ||||
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                                TTGACCAA     CTCG    CGGT
                                     GTC___    AGAA
GAM2910  LOC149706 5'  ACTGGTTAGAAAAACA      66769         AAA
                                ACTGGTTA   AAGAGCG
                                ||||||||   |||||||
                                TGACCAAT   TTTTTGT
                                     C__
GAM2910  LOC149827 3'  AACTGATTGGAAGAGGCC     66770         AAAA     C
                                AACTGGTT    AAGAG GCC
                                ||||||||    ||||| |||
                                TTGACTAA    TTCTC CGG
                                     CC__     _
GAM2910  LOC151643 3'  TGGCTAAAAAAAAAAATCAAA  66771              CGC
                                TGGTTAAAAAAGAG   CAAA
                                ||||||||||||||   ||||
                                ACCGATTTTTTTTT   GTTT
                                          TTA
GAM2910  LOC200563 5'  AACTGTTTAAAAAGAAGCAC   66772       G      AG
                                AACTG TTAAAAA  AGCGC
                                ||||| |||||||  |||||
                                TTGAC AATTTTT  TCGTG
                                   A      CT
GAM2910  LOC201505 5'  AACTGAAAAGAGCGTCA      66767       TTAAA       C
                                AACTGG     AAAGAGCG CA
                                ||||||     |||||||| ||
                                TTGACT     TTTCTCGC GT
                                     _____       A
GAM2910  LOC202316 3'  AACTGGTCAGGGGCACTTCAA  66773          AAAAAGA   __
                                AACTGGTTA      GCGC  CAA
                                |||||||||      ||||  |||
                                TTGACCAGT      CGTG  GTT
                                     CCC_____    AA
GAM2910  LOC219347 5'  ACTGGTTAATGGGAGATCCA   66774         AAAA   CG
                                ACTGGTTAA    GAG  CCA
                                |||||||||    |||  |||
                                TGACCAATT    CTC  GGT
                                     ACC_   TA
GAM2910  LOC57795  3'  CTGGTTAAAAAGAATAC      66775           A   CG
                                CTGGTTAAAAA GAG  C
                                |||||||||| |||  |
                                GACCAATTTTT CTT  G
                                     _   AT
GAM2910  LOC84524  3'  AACTGGTTTAAAAAAATCA    66776         A      G
                                AACTGGTT AAAAAGA CG
                                |||||||| ||||||| ||
                                TTGACCAA TTTTTTT GT
                                     A      A
GAM2911  COL4A3    3'  AACACTAGTTTAATGTTT     66779       ACTTT    A
                                AACACT     GGTT GATGTTT
                                ||||||     |||| |||||||
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                                TTGTGA    TCAA TTACAAA
                                   _____  A
GAM2911  COL4A3   3'  AACACTAGTTTAATGTTT    66779      ACTTT   A
                                AACACT    GGTT GATGTTT
                                ||||||    |||| |||||||
                                TTGTGA    TCAA TTACAAA
                                   _____  A
GAM2911  COL4A3   3'  AACACTAGTTTAATGTTT    66779      ACTTT   A
                                AACACT    GGTT GATGTTT
                                ||||||    |||| |||||||
                                TTGTGA    TCAA TTACAAA
                                   _____  A
GAM2911  DPYSL2   3'  CTACTTTGTGATGTTT     66780       GTTA
                                CTACTTTG   GATGTTT
                                ||||||||   |||||||
                                GATGAAAC   CTACAAA
                                    A___
GAM2911  HK1      5'  AACACAGCAAGATAGATGTTTT 66781     TACTTT  T
                                AACAC     GG TAGATGTTTT
                                |||||     || ||||||||||
                                TTGTG     TC ATCTACAAAA
                                   TCGT__  T
GAM2911  HK1      5'  AACACAGCAAGATAGATGTTTT 66781     TACTTT  T
                                AACAC     GG TAGATGTTTT
                                |||||     || ||||||||||
                                TTGTG     TC ATCTACAAAA
                                   TCGT__  T
GAM2911  HK1      5'  AACACAGCAAGATAGATGTTTT 66781     TACTTT  T
                                AACAC     GG TAGATGTTTT
                                |||||     || ||||||||||
                                TTGTG     TC ATCTACAAAA
                                   TCGT__  T
GAM2911  HOXC13   3'  AACCCTGCTTTGGTTGGA    66782     A  A      A
                                AAC CT CTTTGGTT GA
                                ||| || |||||||| ||
                                TTG GA GAAACCAA CT
                                  G  C       C
GAM2911  TYR      3'  ACATTACTTTGAGTTAGA    66783     C     _
                                ACA TACTTTG GTTAGA
                                ||| ||||||| ||||||
                                TGT ATGAAAC CAATCT
                                  A      T
GAM2911  DKFZp761B1514 3'  AACACCTATTTAGATGTTT   66784       ACTTTGG
                                AACACT      TTAGATGTTT
                                ||||||      ||||||||||
                                TTGTGG      AATCTACAAA
                                   ATA____
GAM2911  EFA6R    3'  CCACTTTGGTTCTTTGTTTT   66785          AGA
                                CTACTTTGGTT   TGTTTT
                                ||||||||||   ||||||
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                                GGTGAAACCAA   ACAAAA
                                      GAA
GAM2911  FLJ30574  3'  AACATCTGTTTAACCAGATGTT 66786     _ AC    TT
             TT                   AACA CT  TTTGG  AGATGTTTT
                                  |||| ||  |||||  |||||||||
                                  TTGT GA  AAATT  TCTACAAAA
                                    A  C_    GG
GAM2911  KIAA0514  3'  CACTACTTGGGTTATTCTATTT 66787        T    GA_
                                  CACTACTT GGTTA   TGTTT
                                  |||||||| |||||   |||||
                                  GTGATGAA CCAAT   ATAAA
                                       C    AAG
GAM2911  KIAA0750  3'  CACTCTTTGGTTGACATT    66788     A      A
                                  CACT CTTTGGTT GATGTT
                                  |||| |||||||| ||||||
                                  GTGA GAAACCAA CTGTAA
                                    _      _
GAM2911  KIAA1560  3'  CATAACTTTGGTTGAGAT    66789    CT      _
                                  CA  ACTTTGGTT AGAT
                                  ||  ||||||||| ||||
                                  GT  TGAAACCAA TCTA
                                   AT        C
GAM2911  KIAA1705  3'  AACATACTTTGGTTAATACATT 66790     C         _
                                  AACA TACTTTGGTTAG ATGTT
                                  |||| |||||||||||| |||||
                                  TTGT ATGAAACCAATT TGTAA
                                    _          A
GAM2911  MAL2     3'  ACATTACTTTTGGAATGTTTT  66791     C     _ TTA
                                  ACA TACTTT GG   GATGTTTT
                                  ||| |||||| ||   ||||||||
                                  TGT ATGAAA CC   TTACAAAA
                                    A     A ____
GAM2911  MAP-1    3'  TACTCAGAACTAGATGTTTT   66792      T_ GT
                                  TACTT  G  TAGATGTTTT
                                  |||||  |  ||||||||||
                                  ATGAG  T  ATCTACAAAA
                                     TC TG
GAM2911  LOC253752 3'  ACATTACTTTGAGTTAGA    66783     C      _
                                  ACA TACTTTG GTTAGA
                                  ||| ||||||| ||||||
                                  TGT ATGAAAC CAATCT
                                    A      T
GAM2911  LOC257048 3'  ACTCTATCTTAGATGTTT    66793       G_
                                  ACTTTG  TTAGATGTTT
                                  ||||||  ||||||||||
                                  TGAGAT  AATCTACAAA
                                     AG
GAM2912  BHLHB3   3'  TGGGAATAGATGCACTTGA   66796        AAATAC    GT
                                  TGGGAATA     TACT  TGA
                                  ||||||||     ||||  |||
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                                ACCCTTAT     GTGA  ACT
                                    CTAC__   __
GAM2912 ITK     3'  TGGGAATAATAATATTACCTCA 66797         _   C   GT_
             TG                   TGGGAATAA AATA TACT   TG
                                  ||||||||| |||| ||||   ||
                                  ACCCTTATT TTAT ATGG   AC
                                      A   A   AGT
GAM2912 MPV17   3'  TGGGAATAAGACTATTATCAAG 66798        AAT   C   TG
                                  TGGGAATAA   ACTA TGT  AG
                                  |||||||||   |||| |||  ||
                                  ACCCTTATT   TGAT ATA  TC
                                      C__   A   GT
GAM2912 MSR1    3'  TGGGAATAAAAATGCTGA    66799          TACTAC
                                  TGGGAATAAAA     TGTTGA
                                  ||||||||||      ||||||
                                  ACCCTTATTTT     ACGACT
                                       T_____
GAM2912 RNMT    3'  TGGGAATAATGGTGCTGA    66800         AATACTAC
                                  TGGGAATAA       TGTTGA
                                  |||||||||       ||||||
                                  ACCCTTATT       ACGACT
                                      ACC_____
GAM2912 SCP2    3'  TGGGAAGAAAATACTGTTTCTG 66801       T       ACTG
                                  TGGGAA AAAATACT    TTG
                                  |||||| ||||||||    |||
                                  ACCCTT TTTTATGA    GAC
                                     C       CAAA
GAM2912 SFRP4   3'  TGGGTATAAAATACTTGA    66802     A        ACTGT
                                  TGGG ATAAAATACT    TGA
                                  |||| ||||||||||    |||
                                  ACCC TATTTTATGA    ACT
                                    A        _____
GAM2912 DKFZP564K0822 3'  TGGGAATACAAAATTGTTGAG  66803         AAATACTAC
                                  TGGGAATA        TGTTGAG
                                  ||||||||        |||||||
                                  ACCCTTAT        ACAACTC
                                      GTTTTA___
GAM2912 KIAA0564  3'  TGGGAATAAGGTACATTTTG   66804         AA   TACTG
                                  TGGGAATAA  TAC    TTG
                                  |||||||||  |||    |||
                                  ACCCTTATT  ATG    AAC
                                      CC   TAA__
GAM2912 KIAA0769  3'  TGGGAATAAAATAATGCCG    66805           CTAC
                                  TGGGAATAAAATA    TGTTG
                                  ||||||||||||    |||||
                                  ACCCTTATTTTAT    ACGGC
                                       T___
GAM2912 KIAA1163  3'  TGGGAATCAAATACTAACCAAG 66806        A       CTG TG
                                  TGGGAAT AAATACTA   T  AG
                                  ||||||| ||||||||   |  ||
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                                ACCCTTA TTTATGAT   G  TC
                                    G       T__ GT
GAM2912  KIAA1332  3'  GGAATAAAATCCTTTGTTG   66807          A  AC
                                GGAATAAAAT CT  TGTTG
                                |||||||||| ||  |||||
                                CCTTATTTTA GG  ACAAC
                                      _  AA
GAM2912  SFRS11    3'  TGGGAATAAATTATTACT    66808          A  C
                                TGGGAATAAA TA TACT
                                |||||||||| || ||||
                                ACCCTTATTT AT ATGA
                                      A  A
GAM2912  ZNF387    3'  TGGGAGTGGAATTACTGTTGAG 66809       ATAAAATAC
                                TGGGA        TACTGTTGAG
                                |||||        ||||||||||
                                ACCCT        ATGACAACTC
                                   CACCTTA__
GAM2912  LOC138639 3'  TGGGAATAAGGCTTGGTGTGTT 66810          AATACTAC_
           GAG                    TGGGAATAA        TGTTGAG
                                |||||||||        |||||||
                                ACCCTTATT        ACAACTC
                                     CCGAACCAC
GAM2912  LOC147299 3'  TGGAAATAAAATGTTG      66811           TACTAC
                                TGGGAATAAAA     TGTTG
                                ||||||||||     |||||
                                ACCTTTATTTT     ACAAC
                                      _______
GAM2912  LOC90019  5'  CGGGAATAAGCAGCTGTTGAG  66812          AATACTA
                                TGGGAATAA      CTGTTGAG
                                |||||||||      ||||||||
                                GCCCTTATT      GACAACTC
                                     CGTC___
GAM2913  DKFZP564A022 3'  TCAAATGTTTGTCTTATA    66815       CTAGCCA
                                TCAAAT      TTGTCTTATA
                                ||||||      ||||||||||
                                AGTTTA      AACAGAATAT
                                   CA_____
GAM2913  DKFZP586D0824 5'  CAGTCCTGTTGTCTTATAG   66816     _  A_
                                TAG CC  TTGTCTTATAG
                                ||| ||  ||||||||||||
                                GTC GG  AACAGAATATC
                                  A  AC
GAM2913  FLJ11240  3'  AAATATAGTTGTCTTATAG   66817      C   CCA
                                AAAT TAG   TTGTCTTATAG
                                |||| |||   ||||||||||||
                                TTTA ATC   AACAGAATATC
                                  T  ___
GAM2913  FLJ20086  3'  TCAATTTAGCAGCCATCTTATA 66818      ATC    CA TG
           G                     TCAA   TAGC  T  TCTTATAG
                                ||||   ||||  |  ||||||||
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                                AGTT  ATCG  G  AGAATATC
                                  AA_   TC GT
GAM2913  LOC203257 5'  TCAAATCTATCCAAGCATATAG 66819        G  TT  CT
                                TCAAATCTA CCA  GT  TATAG
                                ||||||||| |||  ||  |||||
                                AGTTTAGAT GGT  CG  ATATC
                                     A  T_  T_
GAM2914  BHLHB3   3'  TGGGAATAGATGCACTTGA   66796       AAATAC   GT
                                TGGGAATA     TACT  TGA
                                ||||||||     ||||  |||
                                ACCCTTAT     GTGA  ACT
                                   CTAC__   __
GAM2914  ITK      3'  TGGGAATAATAATATTACCTCA 66797        _   C   GT_
            TG                    TGGGAATAA AATA TACT   TG
                                ||||||||| |||| ||||   ||
                                ACCCTTATT TTAT ATGG   AC
                                     A   A   AGT
GAM2914  MPV17    3'  TGGGAATAAGACTATTATCAAG 66798        AAT   C   TG
                                TGGGAATAA   ACTA TGT  AG
                                |||||||||   |||| |||  ||
                                ACCCTTATT   TGAT ATA  TC
                                     C__   A   GT
GAM2914  MSR1     3'  TGGGAATAAAAATGCTGA    66799         TACTAC
                                TGGGAATAAAA     TGTTGA
                                ||||||||||     ||||||
                                ACCCTTATTTT     ACGACT
                                      T_____
GAM2914  RNMT     3'  TGGGAATAATGGTGCTGA    66800        AATACTAC
                                TGGGAATAA       TGTTGA
                                |||||||||       ||||||
                                ACCCTTATT       ACGACT
                                     ACC_____
GAM2914  SCP2     3'  TGGGAAGAAAATACTGTTTCTG 66801       T       ACTG
                                TGGGAA AAAATACT    TTG
                                |||||| ||||||||    |||
                                ACCCTT TTTTATGA    GAC
                                   C       CAAA
GAM2914  SFRP4    3'  TGGGTATAAAATACTTGA    66802      A        ACTGT
                                TGGG ATAAAATACT    TGA
                                |||| ||||||||||    |||
                                ACCC TATTTTATGA    ACT
                                  A        _____
GAM2914  DKFZP564K0822 3'  TGGGAATACAAAATTGTTGAG  66803        AAATACTAC
                                TGGGAATA        TGTTGAG
                                ||||||||        |||||||
                                ACCCTTAT        ACAACTC
                                     GTTTTA___
GAM2914  KIAA0564  3'  TGGGAATAAGGTACATTTTG   66804         AA   TACTG
                                TGGGAATAA  TAC    TTG
                                |||||||||  |||    |||
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                                ACCCTTATT  ATG    AAC
                                     CC   TAA__
GAM2914  KIAA0769  3'  TGGGAATAAAATAATGCCG   66805          CTAC
                                TGGGAATAAAATA   TGTTG
                                ||||||||||||   |||||
                                ACCCTTATTTTAT   ACGGC
                                      T___
GAM2914  KIAA1163  3'  TGGGAATCAAATACTAACCAAG 66806       A      CTG TG
                                TGGGAAT AAATACTA   T  AG
                                ||||||| ||||||||  |  ||
                                ACCCTTA TTTATGAT   G  TC
                                    G       T__ GT
GAM2914  KIAA1332  3'  GGAATAAAATCCTTTGTTG   66807         A  AC
                                GGAATAAAAT CT  TGTTG
                                |||||||||| ||  |||||
                                CCTTATTTTA GG  ACAAC
                                      _  AA
GAM2914  SFRS11   3'  TGGGAATAAATTATTACT    66808         A  C
                                TGGGAATAAA TA TACT
                                |||||||||| || ||||
                                ACCCTTATTT AT ATGA
                                      A  A
GAM2914  ZNF387   3'  TGGGAGTGGAATTACTGTTGAG 66809      ATAAAATAC
                                TGGGA       TACTGTTGAG
                                |||||       ||||||||||
                                ACCCT       ATGACAACTC
                                   CACCTTA__
GAM2914  LOC138639 3'  TGGGAATAAGGCTTGGTGTGTT 66810        AATACTAC_
            GAG                   TGGGAATAA       TGTTGAG
                                |||||||||       |||||||
                                ACCCTTATT       ACAACTC
                                     CCGAACCAC
GAM2914  LOC147299 3'  TGGAAATAAAATGTTG      66811          TACTAC
                                TGGGAATAAAA     TGTTG
                                ||||||||||     |||||
                                ACCTTTATTTT     ACAAC
                                      _______
GAM2914  LOC90019  5'  CGGGAATAAGCAGCTGTTGAG  66812        AATACTA
                                TGGGAATAA      CTGTTGAG
                                |||||||||      ||||||||
                                GCCCTTATT      GACAACTC
                                     CGTC___
GAM2915  CRIM1    3'  TGATTGGCTTGGAAGAAAA   66823    T     ___
                                TG ATTGGCTT   AGAAAA
                                || ||||||||   ||||||
                                AC TAACCGAA   TCTTTT
                                 _       CCT
GAM2915  GHR      3'  TGTTTTGGCTTAAACGTTATT  66824     A       AAAC
                                TGT TTGGCTTAGA    TATT
                                ||| ||||||||||    ||||
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                                ACA AACCGAATTT   ATAA
                                  A        GCA_
GAM2915 C1orf17  3' TGTCTTGGCTTAGGACTAT   66825    A      AAA
                                TGT TTGGCTTAG  ACTAT
                                ||| |||||||||  |||||
                                ACA AACCGAATC  TGATA
                                  G       C__
GAM2915 LHFP     3' TGTATTGGATTAGAACTAC   66826       C    AA
                                TGTATTGG TTAGA  ACTAT
                                |||||||| |||||  |||||
                                ACATAACC AATCT  TGATG
                                     T    __
GAM2915 NET-2    3' TATATTGACTTGGAGACTATT 66827         A  AA
                                TGTATTGGCTT GA  ACTATT
                                |||||||||| ||  ||||||
                                ATATAACTGAA CT  TGATAA
                                      C  C_
GAM2915 LOC253786 5' TGTAATGGATCTAAAACTATT 66828     T  CTTAG
                                TGTA TGG    AAAACTATT
                                |||| |||    |||||||||
                                ACAT ACC    TTTTGATAA
                                  T  TAGA_
GAM2916 AGTR1    5' CTCCCGCCCGCCGCCTCGG   66831         GA  C
                                CTCCCGCCCGC  CC CGG
                                ||||||||||  || |||
                                GAGGGCGGGCG  GG GCC
                                      GC  A
GAM2916 AGTR1    5' CTCCCGCCCGCCGCCTCGG   66831         GA  C
                                CTCCCGCCCGC  CC CGG
                                ||||||||||  || |||
                                GAGGGCGGGCG  GG GCC
                                      GC  A
GAM2916 AGTR1    5' CTCCCGCCCGCCGCCTCGG   66831         GA  C
                                CTCCCGCCCGC  CC CGG
                                ||||||||||  || |||
                                GAGGGCGGGCG  GG GCC
                                      GC  A
GAM2916 AGTR1    5' CTCCCGCCCGCCGCCTCGG   66831         GA  C
                                CTCCCGCCCGC  CC CGG
                                ||||||||||  || |||
                                GAGGGCGGGCG  GG GCC
                                      GC  A
GAM2916 AP2A1    5' CTCCGCCCGCGGTCCGG    66832     C     ACC
                                CTCC GCCCGCG  CCGG
                                |||| |||||||  ||||
                                GAGG CGGGCGC  GGCC
                                  _     CA_
GAM2916 AP2A1    5' CTCCGCCCGCGGTCCGG    66832     C     ACC
                                CTCC GCCCGCG  CCGG
                                |||| |||||||  ||||
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                                GAGG CGGGCGC   GGCC
                                  _      CA_
GAM2916 BAALC    5'  CTCCCGCCCGCGCTGCAGCCGC 66833          ACC___   G
              GCGG                  CTCCCGCCCGCG     CCG CGCGG
                                    ||||||||||||     ||| |||||
                                    GAGGGCGGGCGC     GGC GCGCC
                                          GACGTC  _
GAM2916 BTEB1    5'  CCCGCCCGGCACGGCGCGG   66834        _ ACCC
                                    CCCGCCCG CG    CGGCGCGG
                                    ||||||||  ||    ||||||||
                                    GGGCGGGC GT    GCCGCGCC
                                         C  _____
GAM2916 CD63     5'  CTCCCGCCGCGGCTCCGG    66835        C   ACC
                                    CTCCCGCC GCG   CCGG
                                    ||||||||  |||   ||||
                                    GAGGGCGG CGC   GGCC
                                         _  CGA
GAM2916 COL1A1   5'  CTCCTGCTCCGACCCCGA    66836     C  CCG
                                    CTCC GC   CGACCCCGG
                                    ||||  ||   |||||||||
                                    GAGG CG   GCTGGGGCT
                                      A  AG_
GAM2916 DVL1     3'  CTCCCGTCCTGGCCCCCACG   66837       C  GCGA    G
                                    CTCCCG CC    CCCC GCG
                                    ||||||  ||    ||||  |||
                                    GAGGGC GG    GGGG TGC
                                       A  ACC_    G
GAM2916 EDNRA    5'  TCCCGGGCTCCGGCGCG     66838      CCC  GACC
                                    TCCCG   GC    CCGGCGCG
                                    |||||   ||    ||||||||
                                    AGGGC   CG    GGCCGCGC
                                      C__  A___
GAM2916 EGLN1    5'  CTTCCTCCAGGCCGGCGCGG   66839    C  GC   CGACC
                                    CT CC  CCG    CCGGCGCGG
                                    || ||  |||    |||||||||
                                    GA GG  GGT    GGCCGCGCC
                                     A  A_   CC___
GAM2916 HDAC1    5'  CTCCCGCCCGCGGCTCCG    66840           ACC
                                    CTCCCGCCCGCG   CCG
                                    ||||||||||||   |||
                                    GAGGGCGGGCGC   GGC
                                          CGA
GAM2916 KCNA7    5'  CCCCGACGCCCGGCCCCGGTGC 66841     __     CGA     C
              GG                    CTCC  CGCCCG   CCCCGG GCGG
                                    ||||  ||||||   |||||| ||||
                                    GGGG  GCGGGC   GGGGCC CGCC
                                      CT     C__      A
GAM2916 KIF5C    5'  CCTGCCCGCGACCACGCGG   66842    C        CCG
                                    CC GCCCGCGACC   GCGCGG
                                    || ||||||||||   ||||||
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                                GG CGGGCGCTGG   TGCGCC
                                 A       ___
GAM2916 LNK     5'  CTCCCGCCCGCCGGCTCCTCGC 66843         GAC__  _  G_
              TCGCGG                  TCCCGCCCGC    CC CG  CGCGG
                                |||||||||    || ||  |||||
                                AGGGCGGGCG    GG GC  GCGCC
                                      GCCGA  A  GA
GAM2916 LRP3    5'  CTCCTGCCCCGCGGCTCCG   66844     C   G  ACCC   G_
                                CTCC GCCC CG   CGGC  CG
                                |||| |||| ||   ||||  ||
                                GAGG CGGG GC   GCCG  GC
                                  A   _ _____   AG
GAM2916 MYO1D   5'  CTCCCGCCGCGGCTGCCGG   66845       C   ACC_
                                CTCCCGCC GCG   CCGG
                                |||||||| |||   ||||
                                GAGGGCGG CGC   GGCC
                                     _  CGAC
GAM2916 NCKAP1  5'  CTCCCGCCCGCGACCTCCG   66846            _
                                CTCCCGCCCGCGACC CCG
                                |||||||||||||| |||
                                GAGGGCGGGCGCTGG GGC
                                         A
GAM2916 PIK3R2  3'  TCCTGCCCTGACCCCAG    66847    C   GC
                                TCC GCCC  GACCCCGG
                                ||| ||||  ||||||||
                                AGG CGGG  CTGGGGTC
                                  A   A_
GAM2916 PITPN   5'  CTCCCGCCCGCTGCCCGCCG   66848         GAC   G
                                CTCCCGCCCGC   CCCG CG
                                ||||||||||   |||| ||
                                GAGGGCGGGCG   GGGC GC
                                      AC_   G
GAM2916 PRDM16  3'  TCCCTTCCGCGACCCCACGCGG 66849     GC        G
                                TCCC  CCGCGACCCCG CGCGG
                                ||||  |||||||||| |||||
                                AGGG  GGCGCTGGGGT GCGCC
                                  AA        _
GAM2916 SERPINE1 3'  CTCCCGCCTTGGCCTCCCAA   66850       C__  GAC
                                CTCCCGCC   GC   CCCGG
                                ||||||||   ||   |||||
                                GAGGGCGG   CG   GGGTT
                                     AAC  GA_
GAM2916 SLC20A2  5'  CCCGCCCGGTCCCGGCGCGG   66851       CGAC
                                CCCGCCCG   CCCGGCGCGG
                                ||||||||   ||||||||||
                                GGGCGGGC   GGGCCGCGCC
                                     CA__
GAM2916 SNX9    5'  CTCCGGCTGGGCCCCGGCGCGG 66852     C  CCGCGA
                                CTCC GC     CCCCGGCGCGG
                                |||| ||     ||||||||||
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                                GAGG CG     GGGGCCGCGCC
                                  C  ACCC__
GAM2916  STK6     5'  CTCCCACCTGCGACCCAAG   66853        C      C
                                CTCCCGCC GCGACCC GG
                                |||||||| ||||||| ||
                                GAGGGTGG CGCTGGG TC
                                    A      T
GAM2916  XPR1     5'  CCCACATGGGCCCCGGCGCGG  66854       A___
                                CCCGCG   CCCCGGCGCGG
                                ||||||   ||||||||||
                                GGGTGT   GGGGCCGCGCC
                                   ACCC
GAM2916  CACNA1H  5'  CTCCCGGCCGCGGCTCGACTCC 66855       C    ACCC   G_
            GG                    CTCCCG CCGCG   CGGC  CGG
                                |||||| |||||   ||||  |||
                                GAGGGC GGCGC   GCTG  GCC
                                   C    CGA_   AG
GAM2916  CBCIP2   5'  CTCCCGCTCGGACTGCGG    66856       C  C   CCCG   C
                                CTCCCGC CG GAC   GCG G
                                ||||||| || |||   ||| |
                                GAGGGCG GC CTG   CGC C
                                   A  _   A___   A
GAM2916  CCNG2    5'  CCCGCCCGCGGCCTCGCGG   66857         ACC  GG
                                CCCGCCCGCG   CC  CGCGG
                                ||||||||||   ||  |||||
                                GGGCGGGCGC   GG  GCGCC
                                     C__  A_
GAM2916  DKFZp434E0519 3'  CTCCCGCCCTGGCCTCCCAA   66858         __  GAC
                                CTCCCGCCC  GC   CCCGG
                                |||||||||  ||   |||||
                                GAGGGCGGG  CG   GGGTT
                                     AC  GA_
GAM2916  DKFZP434N1511 3'  CTCCCGCCTCGGCCTCCCAA   66859         _  CGAC
                                CTCCCGCC CG    CCCGG
                                |||||||| ||    |||||
                                GAGGGCGG GC    GGGTT
                                    A  CGGA
GAM2916  DNCI2    5'  CTCCCGCCTGCAACTTCCCGG  66860         C    __
                                CTCCCGCC GCGAC  CCCGG
                                ||||||| |||||  |||||
                                GAGGGCGG CGTTG  GGGCC
                                    A     AA
GAM2916  DOK4     5'  CTCATGCCCGCGTCACGGCGCG 66861     CC      ACCC
            G                    CTC  GCCCGCG   CGGCGCGG
                                |||  |||||||   ||||||||
                                GAG  CGGGCGC   GCCGCGCC
                                  TA      AGT_
GAM2916  DZIP1    5'  CTCCCCTCCGCGATCTCCCTCC 66862       GC     _____ _
            GG                    CTCCC  CCGCGA   CC CCGG
                                |||||  ||||||   || ||||
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                                GAGGG  GGCGCT   GG GGCC
                                  GA    AGAG  A
GAM2916  ENDO180   3'  CTCCCGCCCTGGCCCTGCCGCG 66863        GCGA _____  GCG
             C                   CTCCCGCCC   CC    CCG  C
                                 |||||||||   ||    |||  |
                                 GAGGGCGGG   GG    GGC  G
                                     ACCG  ACIII  GCG
GAM2916  FGF19     5'  CTCCTGCTCTGACGGCGCG   66864     C  CCGC   CCC
                                 CTCC GC   GAC   GGCGCG
                                 |||| ||   |||   ||||||
                                 GAGG CG   CTG   CCGCGC
                                   A  AGA_  ___
GAM2916  FLJ11053  5'  TCCCGCCCATGGTCGCG    66865        CGACCCC  _
                                 TCCCGCCCG     GG CGCG
                                 |||||||||      || ||||
                                 AGGGCGGGT     CC GCGC
                                     A_______  A
GAM2916  FLJ11273  5'  TCCCGGGCTGCTTCGGCGCGG  66866     CCC  GACCC
                                 TCCCG  GC    CGGCGCGG
                                 |||||  ||    ||||||||
                                 AGGGC  CG    GCCGCGCC
                                   C__  ACGAA
GAM2916  FLJ12242  5'  CTCCCGCCCCCGGTCCCG    66867        G  AC
                                 CTCCCGCCC CG  CCCG
                                 ||||||||| ||  ||||
                                 GAGGGCGGG GC  GGGC
                                     G  CA
GAM2916  FLJ21736  3'  TCCCACCCGATCCTGGTGTGG  66868        CGAC  C  CGC
                                 TCCCGCCCG   CC GG   GG
                                 |||||||||   || ||   ||
                                 AGGGTGGGC   GG CC   CC
                                     TA__  A  ACA
GAM2916  FLJ22301  5'  CTCTCGCCCGCGTCGGC    66869    C      ACCC
                                 CTC CGCCCGCG   CGGC
                                 ||| ||||||||   ||||
                                 GAG GCGGGCGC   GCCG
                                   A      A___
GAM2916  FLJ22393  5'  CTCCTCCCCGCGGCCCCGG   66870    CG     A
                                 CTCC  CCCGCG CCCCGG
                                 ||||  |||||| ||||||
                                 GAGG  GGGCGC GGGGCC
                                   AG     C
GAM2916  FLJ22814  3'  CTCCCGCCTTGGCCTCCCAA  66850       C__  GAC
                                 CTCCCGCC   GC   CCCGG
                                 ||||||||   ||   |||||
                                 GAGGGCGG   CG   GGGTT
                                     AAC  GA_
GAM2916  FLJ23375  5'  CCCGCCCGCCGGGGCGCGG   66871        GACCCC
                                 CCCGCCCGC     GGCGCGG
                                 |||||||||     |||||||
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                                GGGCGGGCG    CCGCGCC
                                     GCC___
GAM2916 FLJ23476 3' CTCCCGCCTGGGCCTCCCAG  66872       C__ GAC
                                CTCCCGCC  GC  CCCGG
                                ||||||||  ||  |||||
                                GAGGGCGG  CG  GGGTC
                                    ACC  GA_
GAM2916 GPS2    3' CTCCCGCCCGGTGGCCCCGG  66873       CGA_
                                CTCCCGCCCG  CCCCGG
                                ||||||||||  ||||||
                                GAGGGCGGGC  GGGGCC
                                     CACC
GAM2916 GPS2    5' CTCCCGCCCGGTGGCCCCGG  66873       CGA_
                                CTCCCGCCCG  CCCCGG
                                ||||||||||  ||||||
                                GAGGGCGGGC  GGGGCC
                                     CACC
GAM2916 HSNOV1  3' TCCCGCCCTGGCCTGAGGCCGC 66874     GCGA _________  GCG
           GCCG                 CGCCC  CC     CCG  CG
                                |||||  ||     |||  ||
                                GCGGG  GG     GGC  GC
                                  ACC_ ACTCCIII  GCG
GAM2916 KIAA0211 5' CTCCCGCCCGAGGCGGGCTGCG 66875       ___  ACCCCG
           CGG                  CTCCCGCCC  GCG    GCGCGG
                                |||||||||  |||    ||||||
                                GAGGGCGGG  CGC    CGCGCC
                                     CTC  CCGA__
GAM2916 KIAA0215 5' CTCCCGCCCTCGGCCCTCG  66876       G  A  _
                                CTCCCGCCC CG CCC CG
                                ||||||||| || ||| ||
                                GAGGGCGGG GC GGG GC
                                     A  C  A
GAM2916 KIAA1608 5' CCCGCCCGCGGCCGACCGG  66877       ACC   G
                                CCCGCCCGCG  CCGGC CGG
                                ||||||||||  ||||| |||
                                GGGCGGGCGC  GGCTG GCC
                                     C__   _
GAM2916 KIAA1957 3' CCCGCCAGCACCCGGTGTGG  66878     C  AC   CGC
                                CCCGCC GCG  CCCGG  GG
                                ||||||  |||  |||||  ||
                                GGGCGG CGT  GGGCC  CC
                                   T  __    ACA
GAM2916 LCHN    5' CTCCCGCCTGCGGCTGCG   66879       C  GACCCC  _
                                CTCCCGCC GC    GGC GCG
                                ||||||||  ||    ||| |||
                                GAGGGCGG CG    CCG CGC
                                     A _______  A
GAM2916 MAPK13  5' TCTCGGCGGCCCCGGCGTGG  66880   C  CCC  A     C
                                TC CG  GCG CCCCGGCG GG
                                || ||  ||| ||||||||  ||
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                                AG GC   CGC GGGGCCGC CC
                                 A ___  C       A
GAM2916  MGC21621  5'  CTCCCGCCTCCGGCCGGCG   66881        CG  ACC
                                CTCCCGCC  CG   CCGGCG
                                ||||||||  ||   ||||||
                                GAGGGCGG  GC   GGCCGC
                                    AG  C__
GAM2916  MGC5442   3'  CTCCCGCCGCGGCGC      66882        C  GACCCC
                                CTCCCGCC GC     GGCGC
                                ||||||||  ||     |||||
                                GAGGGCGG CG     CCGCG
                                   _ _______
GAM2916  NFAT5     5'  CCTCGCTTCCTGCCGGCGCGG  66883    _  GA  __
                                CC CGC  CC  CCGGCGCGG
                                ||  |||  ||  |||||||||
                                GG GCG  GG  GGCCGCGCC
                                 A   AA  AC
GAM2916  PCDH17    5'  CTCCCGCCCGGACTTCGG    66884         C   CC
                                CTCCCGCCCG GAC  CGG
                                ||||||||||  |||  |||
                                GAGGGCGGGC CTG  GCC
                                    _   AA
GAM2916  SHC3      5'  GCCGGCCCCGGCGCGG      66885     C  GAC
                                GCC GC   CCCGGCGCGG
                                |||  ||   ||||||||||
                                CGG CG   GGGCCGCGCC
                                  C  ___
GAM2916  SIAT4A    3'  CTCCCGCCTCGGCCTCCCAA   66859         _  CGAC
                                CTCCCGCC CG    CCCGG
                                ||||||||  ||    |||||
                                GAGGGCGG GC    GGGTT
                                    A  CGGA
GAM2916  LOC115861 3'  CTCCCGCCTTGGCCTCCCCAA  66886         C__  GA
                                CTCCCGCC   GC  CCCCGG
                                ||||||||   ||  ||||||
                                GAGGGCGG   CG  GGGGTT
                                    AAC  GA
GAM2916  LOC146223 5'  CTCTCGCCCGCCGCCCGG    66887     C      GAC
                                CTC CGCCCGC   CCCGG
                                |||  |||||||   |||||
                                GAG GCGGGCG   GGGCC
                                  A      GC_
GAM2916  LOC146952 5'  GCTTCGGACCGGCGCGG     66888    C_  C    CC
                                GC  CG GACC  GGCGCGG
                                ||  || ||||  |||||||
                                CG  GC CTGG  CCGCGCC
                                 AA  _   __
GAM2916  LOC149401 5'  CTCCCGCCCACGGTTCTGCCGC 66889          ACC_______  GCG
            GC                   TCCCGCCCGCG       CCG   C
                                ||||||||||        |||   |
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                                AGGGCGGGTGC       GGC  G
                                     CAAGACIII  GCG
GAM2916  LOC149711 3'  CTCCCACCTGTGATCCCAG   66890        CGC  C
                                CTCCCGCC  GA CCCGG
                                ||||||||  || |||||
                                GAGGGTGG  CT GGGTC
                                    ACA  A
GAM2916  LOC153579 3'  CTCCCACCCGCGGTGGTCTGCG 66891          ACCCC  C__
           G                     CTCCCGCCCGCG    GG  GCGG
                                ||||||||||||    ||  ||||
                                GAGGGTGGGCGC    CC  CGCC
                                      CA___  AGA
GAM2916  LOC196047 5'  CTCCCGCCCTGGCCTTCCGG  66892        GCGA  __
                                CTCCCGCCC   CC  CCGG
                                |||||||||   ||  ||||
                                GAGGGCGGG   GG  GGCC
                                     ACC_  AA
GAM2916  LOC219397 3'  CCCCTGCGGCCGGCGCGG    66893    G  C   ACC
                                CC CC GCG   CCGGCGCGG
                                || || |||   |||||||||
                                GG GG CGC   GGCCGCGCC
                                 _ A   C__
GAM2916  LOC254263 5'  CCTCGCCCGCGGCTCCCTCG  66894    _      A__  _
                                CC CGCCCGCG   CCC CG
                                || ||||||||   ||| ||
                                GG GCGGGCGC   GGG GC
                                 A       CGA   A
GAM2916  LOC256306 3'  TCCTGCCTGCAACCCCAG    66895    C   C
                                TCC GCC GCGACCCCGG
                                ||| ||| ||||||||||
                                AGG CGG CGTTGGGGTC
                                  A   A
GAM2916  LOC256586 5'  CTCCCGCCGCGGCCTGCCGG  66896        C   A  __
                                CTCCCGCC GCG CC  CCGG
                                |||||||| ||| ||  ||||
                                GAGGGCGG CGC GG  GGCC
                                     _  C  AC
GAM2916  LOC63928  5'  CTCCCACCCGCGACCCGG    66897             C
                                CTCCCGCCCGCGACCC GG
                                |||||||||||||||| ||
                                GAGGGTGGGCGCTGGG CC
                                                _
GAM2916  LOC64744  5'  CCGCAGCCCCTCGGCGCGG   66898      A_  _
                                CCGCG  CCC CGGCGCGG
                                |||||  ||| ||||||||
                                GGCGT  GGG GCCGCGCC
                                   CG   A
GAM2916  LOC91291  5'  CTCCCGCCTGTAATCCCAG   66899        CGC  C
                                CTCCCGCC   GA CCCGG
                                ||||||||   || |||||
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                                GAGGGCGG  TT GGGTC
                                    ACA  A
GAM2917  ANK1    3'  ACACTCCCGCAGAGCG     66902        CAC
                                GCACTTTTGC  AGAGCG
                                ||||||||||  ||||||
                                TGTGAGGGCG  TCTCGC
                                    ____
GAM2917  ANK1    3'  ACACTCCCGCAGAGCG     66902        CAC
                                GCACTTTTGC  AGAGCG
                                ||||||||||  ||||||
                                TGTGAGGGCG  TCTCGC
                                    ____
GAM2917  ATP7A   3'  AAAAGATATTTTTGCCAACAG  66903     CAC_     _
                                AAAAG   TTTTGCCA CAG
                                |||||   |||||||| |||
                                TTTTC   AAAACGGT GTC
                                   TATA      T
GAM2917  CTNND2  3'  AAAAAGCACTTTGTTGACAAGG 66904          __  C  CA
            AG                    AAAAAGCACTTT  TG CA  GAG
                                ||||||||||||  || ||  |||
                                TTTTTTCGTGAAA  AC GT  CTC
                                      CA  T  TC
GAM2917  HD      3'  AAAGAGCACTTCTGCCACA   66905    A
                                AAA AGCACTTTTGCCACA
                                ||| ||||||||||||||
                                TTT TCGTGAAGACGGTGT
                                  C
GAM2917  MTAP    5'  AAGCGAGCCACAGAGCG    66906     ACTTTT
                                AAGC    GCCACAGAGCG
                                ||||    ||||||||||
                                TTCG    CGGTGTCTCGC
                                  CT____
GAM2917  ODC1    3'  GCACTCTTGAGTAGCG     66907        CCAC  _
                                GCACTTTTG   AG AGCG
                                |||||||||   || ||||
                                CGTGAGAAC   TC TCGC
                                     ____  A
GAM2917  PCDH7   5'  GGAGACTACTCGCGTCACAGAG 66908   A  C  _   __
            CG                    A AG ACT TTTGC  CACAGAGCG
                                | || ||| |||||  |||||||||
                                C TC TGA GAGCG  GTGTCTCGC
                                 C  _  T    CA
GAM2917  PCDH7   5'  GGAGACTACTCGCGTCACAGAG 66908   A  C  _   __
            CG                    A AG ACT TTTGC  CACAGAGCG
                                | || ||| |||||  |||||||||
                                C TC TGA GAGCG  GTGTCTCGC
                                 C  _  T    CA
GAM2917  PCDH7   5'  GGAGACTACTCGCGTCACAGAG 66908   A  C  _   __
            CG                    A AG ACT TTTGC  CACAGAGCG
                                | || ||| |||||  |||||||||
```

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                                C TC TGA GAGCG  GTGTCTCGC
                                 C _  T    CA
GAM2917  WNT7A    5'  AGCACGGGAGCCACGGAGCG   66909      TTTT    A
                                AGCAC   GCCAC GAGCG
                                |||||   ||||| |||||
                                TCGTG   CGGTG CTCGC
                                   CCCT    C
GAM2917  YWHAG    5'  AGGACCGACCCACAGAGCG   66910    C   TTTG
                                AG ACT   CCACAGAGCG
                                || |||   ||||||||||
                                TC TGG   GGTGTCTCGC
                                 C  CTG_
GAM2917  C1orf34  3'  AAGCACCTTCAACAGCAG    66911          GC  _
                                AAGCACTTTT  CA CAG
                                ||||||||||  || |||
                                TTCGTGGAAG  GT GTC
                                      TT  C
GAM2917  DKFZP434B044 3'  AAGCACTTTTATAGAG      66912          CCAC
                                AAGCACTTTTG   AGAG
                                ||||||||||    ||||
                                TTCGTGAAAAT   TCTC
                                      A___
GAM2917  FLJ20546  3'  AAAAAGCACTTCTGCCAAAG   66913              C
                                AAAAAGCACTTTTGCCA AG
                                |||||||||||||||| ||
                                TTTTTCGTGAAGACGGT TC
                                       T
GAM2917  KIAA1691  3'  AGCAGGCGCCAGCACAGAGCG  66914     CTTT   ___
                                AGCA   TGCC   ACAGAGCG
                                ||||   ||||   ||||||||
                                TCGT   GCGG   TGTCTCGC
                                  CC__   TCG
GAM2917  NFAT5    3'  AAAAGGCACTTTTCCATAG   66915     A      G   C
                                AAAA GCACTTTT CCA AG
                                |||| |||||||| ||| ||
                                TTTT CGTGAAAA GGT TC
                                  C       _  A
GAM2917  LOC145474 5'  AAAAATCACTTCCAGGACAGAG 66916      G    TT CC
                                AAAAA CACTT  G  ACAGAG
                                ||||| |||||  |  ||||||
                                TTTTT GTGAA  T  TGTCTC
                                   A    GG CC
GAM2917  LOC148479 3'  AAAAACACTTTGGAG       66917          T CCACA
                                AAAAGCACTTT G    GAG
                                |||||||||||  |    |||
                                TTTTTGTGAAA C    CTC
                                       _ _____
GAM2917  LOC153469 3'  ACTGTTTGACACAGAGCG    66918    _   C
                                ACT TTTG CACAGAGCG
                                ||| |||| |||||||||
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                                TGA AAAC GTGTCTCGC
                                  C    T
GAM2917  LOC158563 3'  AACACTGAGGCACAGAGCG   66919       TTT  C
                                AGCACT   GC ACAGAGCG
                                ||||||   || ||||||||
                                TTGTGA   CG TGTCTCGC
                                   CTC  _
GAM2917  LOC200853 3'  AAAAACACAGGGCCACAG    66920        TTTT
                                AAAAGCAC    GCCACAG
                                ||||||||    |||||||
                                TTTTTGTG    CGGTGTC
                                     TCC_
GAM2917  LOC51611  3'  GCACCTCTTCACAGGGCG    66921        GC    A
                                GCACTTTT  CACAG GCG
                                ||||||||  ||||| |||
                                CGTGGAGA  GTGTC CGC
                                     A_    C
GAM2918  AP2B1     3'  TGTAGGAAAAGAGGGTT     66924           A A
                                TGTAGGAAAAGA G GTT
                                |||||||||||| | |||
                                ACATCCTTTTCT C CAA
                                       _ C
GAM2918  CSN10     3'  TGTAAGGAGAGAAGAGCT    66925      _   AA
                                TGTA GGA  AGAAGAGTT
                                |||| |||  |||||||||
                                ACAT CCT  TCTTCTCGA
                                  T  C_
GAM2918  IL2RG     3'  TGAGGGAGAAGAAAAACATGTT 66926    TA   A       TTC
            CG                    TG  GGA AAGAAGAG   GTTCG
                                ||  ||| ||||||||   |||||
                                AC  CCT TTCTTTTT   CAAGC
                                 TC   C       GTA
GAM2918  MAGEA10   5'  TGTAGAAAAGAGGGGTTCCCT  66927      G     AGA    G
                                TGTAG AAAAGA   GTTC TT
                                ||||| ||||||   |||| ||
                                ACATC TTTTCT   CAAG GA
                                   _     CCC    G
GAM2918  RGS5      3'  GTGGGGAAAGAAGGCCTTCG   66928    A  A      A   CG
                                GT GG AAAGAAG GTT  TTCG
                                || || ||||||| |||  ||||
                                CA CC TTTCTTC CGG  AAGC
                                 C  C      _  ___
GAM2918  TRPC5     3'  TGTGGAAAAGAATTTGTT    66929     A       GA_
                                TGT GGAAAAGAA   GTT
                                |||  |||||||||   |||
                                ACA CCTTTTCTT   CAA
                                  _        AAA
GAM2918  VEGFB     3'  TGAGGGGAGGAAGAGCCAGTT  66930    T   AAAA      TC
                                TG AGG    GAAGAGT  GTT
                                || |||    |||||||  |||
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                                AC TCC    CTTCTCG  CAA
                                 _  CCTC      GT
GAM2918  KIAA0247  3'  TAGGAAAAGGGAGGGTT     66931         AA   TTC
                                TAGGAAAAG  GAG   GTT
                                |||||||||  |||   |||
                                ATCCTTTTC  CTC   CAA
                                     C_   C__
GAM2918  KIAA0435  5'  TGCAGGAAGAGAGGAGTCTCAT 66932         A   A   _
                                TGTAGGAA AGA GAGT TCGT
                                |||||||| ||| |||| ||||
                                ACGTCCTT TCT CTCA AGTA
                                     C   C    G
GAM2918  LOC132617 3'  TGTGGGAAAAGAAGGACT    66933     A         AG
                                TGT GGAAAAGAAG  TT
                                ||| ||||||||||  ||
                                ACA CCTTTTCTTC  GA
                                  C         CT
GAM2918  LOC165741 3'  TGTAGGAATGGAACAAGTTCG  66934         AA   _
                                TGTAGGAA  GAA GAGTTCG
                                ||||||||  ||| |||||||
                                ACATCCTT  CTT TTCAAGC
                                     AC   G
GAM2919  HLA-DQA1  3'  TCTGTGTTACTGGACATGAC   66937         T  CACT
                                TCTGTGTT AC    CGTGAC
                                |||||||| ||    ||||||
                                AGACACAA TG    GTACTG
                                     _ ACCT
GAM2919  KCNJ5     3'  TCTGTGTTCACTGAAGCCAGTG 66938          CA___  C
            AC                    TCTGTGTTTAC     CT GTGAC
                                ||||||||||||     || |||||
                                AGACACAAGTG     GG CACTG
                                      ACTTC  T
GAM2919  MUC12     3'  TCTGTGTTTGCAGCTCTCCTGA 66939         ACCA__   G
                                TCTGTGTTT      CTC TGA
                                |||||||||      ||| |||
                                AGACACAAA      GAG ACT
                                     CGTCGA   G
GAM2919  PDPK1     3'  TCTGCGTTCCCCTTGTGA     66940         A  A  C
                                TCTGTGTTT CC CT GTGA
                                ||||||||| || || ||||
                                AGACGCAAG GG GA CACT
                                     _ _  A
GAM2919  SIGLEC6   3'  TCTGTGTTTATGTCACTCG    66941          C__
                                TCTGTGTTTA   CACTCG
                                ||||||||||   ||||||
                                AGACACAAAT   GTGAGC
                                      ACA
GAM2919  DKFZP586B2420 3'  CGTGTTTACTACCTGA      66942         C   CG
                                TGTGTTTAC ACT  TGA
                                ||||||||| |||  |||
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                                GCACAAATG TGG  ACT
                                      A  __
GAM2919  DKFZP586G1517 3'  TCTGTGTTTCCCTGCCCGA   66943        A  A  C  GA
                                TCTGTGTTT CC CT GT  CGA
                                ||||||||| || || ||  |||
                                AGACACAAA GG GA CG  GCT
                                      _ _ _ G_
GAM2919  FLJ10099  5'  CTGGGCTCACTCGTGGCG    66944    T   TAC      A
                                CTG GTT   CACTCGTG CG
                                ||| |||   |||||||| ||
                                GAC CGA   GTGAGCAC GC
                                  C  ___       C
GAM2919  FLJ10300  5'  TCTGTGTTCACCATTCTG    66945          C  G
                                TCTGTGTTTACCA TC TG
                                |||||||||||| || ||
                                AGACACAAGTGGT AG AC
                                       A  _
GAM2919  FLJ14075  3'  TCTGTGTTTAACACCCTAACGA 66946         C    G
                                TCTGTGTTTA CACTC TGACGA
                                |||||||||| ||||| ||||||
                                AGACACAAAT GTGGG ATTGCT
                                      T    _
GAM2919  KIAA1582  5'  CCTGTGTTTGCTGGCACAGCG  66947        AC___  TC
                                TCTGTGTTT    CAC  GTG
                                |||||||||    |||  |||
                                GGACACAAA    GTG  CGC
                                     CGACC   T_
GAM2919  NXP-2     3'  TGTGTTTAACCGTGA      66948        CC  T
                                TGTGTTTA  AC CGTGA
                                ||||||||  || |||||
                                ACACAAAT  TG GCACT
                                     __  _
GAM2919  SENP8     5'  TCTGTGTTGGCCGGAAAGCGAC 66949        TA  ACTC_
                                TCTGTGTT  CC    GTGAC
                                ||||||||  ||    |||||
                                AGACACAA  GG    CGCTG
                                     CC  CCTTT
GAM2919  TA-PP2C   3'  TCTGTGTTTTATCATAGCATGA 66950        AC_  CT_    C
           TGA                   TCTGTGTTT   CA   CGTGA GA
                                |||||||||   ||   ||||| ||
                                AGACACAAA   GT   GTACT CT
                                     ATA  ATC    A
GAM2919  TCL6      5'  TCTGTGTTTCTCAGA      66951        ACCA   T
                                TCTGTGTTT    CTCG GA
                                |||||||||    |||| ||
                                AGACACAAA    GAGT CT
                                     _____   _
GAM2919  TCL6      5'  TCTGTGTTTCTCAGA      66951        ACCA   T
                                TCTGTGTTT    CTCG GA
                                |||||||||    |||| ||
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                                AGACACAAA   GAGT CT
                                     ____   _
GAM2919 USP20    3' TCTGTGTTTATTCTGAC     66952         CCAC  G
                                TCTGTGTTTA   TC TGAC
                                ||||||||||   || ||||
                                AGACACAAAT   AG ACTG
                                     A___  _
GAM2919 LOC149010 5' CGTGTACCCTTGTGATGA    66953      TT  A  C   C
                                TGTGT  ACC CT GTGA GA
                                |||||  ||| || |||| ||
                                GCACA  TGG GA CACT CT
                                   __  _ A   A
GAM2919 LOC196485 5' TCTGTGTTTCCCAGTGCG    66954        A  CTC  A
                                TCTGTGTTT CCA  GTG CG
                                ||||||||| |||  ||| ||
                                AGACACAAA GGT  CAC GC
                                     G  ___  _
GAM2919 LOC197358 3' TGTGTTTTTCATGACA      66955       ACCAC
                                TGTGTTT    TCGTGACG
                                |||||||    ||||||||
                                ACACAAA    AGTACTGT
                                   A____
GAM2920 AMPH     3' TAGAGGAGCTGTTTTTATAGTG 66958     CA     CTC
           TT                    TGG  GAGCTG   TTATAGTGTT
                                |||  ||||||   ||||||||||
                                ATC  CTCGAC   AATATCACAA
                                  TC     AAA
GAM2920 DJ102H19.4 5' TGGGGAGCTGCTCTATGT    66959     CA       TATA
                                TGG  GAGCTGCTCT   GTGT
                                |||  ||||||||||   ||||
                                ACC  CTCGACGAGA   TACA
                                  C_        _____
GAM2920 GRIN3A   3' TGGTCGAAGCTTATAGTGT    66960     CA   CT   CT
                                TGG  GAG  GCT  TATAGTGT
                                |||  |||  |||  ||||||||
                                ACC  CTT  CGA  ATATCACA
                                  AG  __  __
GAM2920 KIAA0293  3' TGGTCAGTCTTATAGTGT    66961     _  AGCTGC
                                TGG CAG     TCTTATAGTGT
                                |||  |||     ||||||||||
                                ACC GTC     AGAATATCACA
                                  A  _______
GAM2920 KIAA1024  3' TGGCAGAGCTTCTTCTGT    66962         GC   ATA
                                TGGCAGAGCT  TCTT   GT
                                ||||||||||  ||||   ||
                                ACCGTCTCGA  AGAA   CA
                                     __    GA_
GAM2920 MGC32124  3' TGGCAGAGCTCTCTGTGTGTT  66963         G    TATA
                                TGGCAGAGCT CTCT    GTGTT
                                ||||||||||  ||||    |||||
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                                ACCGTCTCGA GAGA   CACAA
                                      _   CA__
GAM2920  LOC151571 5'  TGGCAGAGCTGCGCGTGCCCGT 66964          TCTTATA_
            GTT                   TGGCAGAGCTGC      GTGTT
                                  ||||||||||||      |||||
                                  ACCGTCTCGACG      CACAA
                                        CGCACGGG
GAM2920  LOC153769 3'  TGGCAGAAGTTGTTCTAATGCT 66965       _ C  C   TAT
                                  TGGCAGA G TG TCT   AGTGTT
                                  ||||||| | || |||   ||||||
                                  ACCGTCT C AC AGA   TTACGA
                                      T A  A  ___
GAM2921  PPIF     3'  TTAGTGTTGCAGTTTCAC    66968       C  A
                                  TTAGTG TG AGTTTCAC
                                  |||||| || ||||||||
                                  AATCAC AC TCAAAGTG
                                     A  G
GAM2921  TTC3     5'  GTGCTAAAGTTTCAGACTAAGG 66969            C  __
                                  GTGCTGAAGTTTCA GAC  AGG
                                  |||||||||||||| |||  |||
                                  CACGATTTCAAAGT CTG  TCC
                                        _  AT
GAM2921  KIAA0993  3'  TTAGTTTGAAGTTTCATGTTAC 66970      GC        CG__
            AGG                     TTAGT  TGAAGTTTCA    ACAGG
                                    |||||  ||||||||||    |||||
                                    AATCA  ACTTCAAAGT    TGTCC
                                       A_         ACAA
GAM2921  TIGA1    5'  TCAGTGCTGGCAGCGGCAG   66971         AA  TTCA  A
                                  TTAGTGCTG  GT    CG CAG
                                  |||||||||  ||    || |||
                                  AGTCACGAC  CG    GC GTC
                                       __  TC__  C
GAM2921  LOC91408  5'  TTAGTGCTAGTGGCGGCAG   66972         GA   TTCA  A
                                  TTAGTGCT  AGT    CG CAG
                                  ||||||||  |||    || |||
                                  AATCACGA  TCA    GC GTC
                                       __   CC__  C
GAM2922  GNAZ     3'  TGTTGTATTGGTTTTTGCTGCA 66975    C        CTCAA__
            TA                      TG TGTATTGGT      GCATA
                                    || |||||||||      |||||
                                    AC ACATAACCA      CGTAT
                                     A        AAAACGA
GAM2922  KLHL3    3'  TGCTGTAACTGATCAAGCAT   66976        _   TC
                                  TGCTGTA TTGG  TCAAGCAT
                                  ||||||| ||||  ||||||||
                                  ACGACAT GACT  AGTTCGTA
                                      T   __
GAM2922  MGC1842  3'  TGCTGTGCTGGTCCCCAGCAT  66977        A       A
                                  TGCTGT TTGGTCTC AGCAT
                                  |||||| |||||||| |||||
```

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                                ACGACA GACCAGGG TCGTA
                                   C       G
GAM2922  LOC148137 3'  TGCTGCTGCTGCTCAAGCAT   66978       ATTG T
                                TGCTGT    G CTCAAGCAT
                                ||||||    | |||||||||
                                ACGACG    C GAGTTCGTA
                                   ACGA _
GAM2922  LOC51696  3'  TGCTGTATTGTTTCAAA     66979         GTC
                                TGCTGTATTG   TCAAG
                                ||||||||||   |||||
                                ACGACATAAC   AGTTT
                                      AA_
GAM2923  C11orf8   3'  ACAGTTGTGCAAATCTGTGTTG 66982    CA     TG___     A
                GTTTT                  AC  TTGTGT     TGTGTT GTTTT
                                ||  ||||||     |||||| |||||
                                TG  AACACG     ACACAA CAAAA
                                 TC     TTTAG     C
GAM2923  CALB1     3'  CATTTGTTGAATTTTAGTTTT  66983      G     TGTG
                                CATT TGTTG    TTAGTTTT
                                |||| |||||    ||||||||
                                GTAA ACAAC    AATCAAAA
                                  _     TTAA
GAM2923  CEACAM1   3'  ACTATTGGTTATATATTTGGTT 66984    C    T        A_
                TT                   AC ATTG GTTGTGTGTT  GTTTT
                                || |||| ||||||||||  |||||
                                TG TAAC CAATATATAA  CAAAA
                                 A    _         AC
GAM2923  NRXN1     3'  TTATGTTTTGTGTTGGTTTT   66985       G     A
                                TTGTGTT TGTGTT GTTTT
                                |||||||  ||||||  |||||
                                AATACAA ACACAA CAAAA
                                   A     C
GAM2923  NRXN1     3'  TTATGTTTTGTGTTGGTTTT   66985       G     A
                                TTGTGTT TGTGTT GTTTT
                                |||||||  ||||||  |||||
                                AATACAA ACACAA CAAAA
                                   A     C
GAM2923  TFDP2     3'  ATTGTGTTTCTCTAGTTTT    66986        GTGTG
                                ATTGTGTT     TTAGTTTT
                                ||||||||     ||||||||
                                TAACACAA     GATCAAAA
                                   AGA__
GAM2923  TLL2      5'  ACCGTCGTGAGACAGGTTAGTT 66987     A     TTGTGT
                TT                   ACC TTGTG      GTTAGTTTT
                                ||| |||||      |||||||||
                                TGG AGCAC      CAATCAAAA
                                 C     TCTGTC
GAM2923  DKFZp547M236 3'  ATTGTGGTACTTTAGTTTT    66988       TT   TG
                                ATTGTG  GTG  TTAGTTTT
                                ||||||  |||  ||||||||
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                                TAACAC  CAT  AATCAAAA
                                   __   GA
GAM2923  DKFZP564D172 3'  CATTGCACAAGTGTTGGTTTT  66989      TG TGT    A
                                CATTG  T   GTGTT GTTTT
                                |||||  |   ||||| |||||
                                GTAAC  G   CACAA CAAAA
                                   GT TT_    C
GAM2923  FLJ13187  3'  ACCATTCTGTGCTTTTAGTTTT 66990       G   T  GTG
                                ACCATT TGT GT   TTAGTTTT
                                |||||| ||| ||   ||||||||
                                TGGTAA ACA CG   AATCAAAA
                                   G   _  AA_
GAM2923  GMFB     3'  TTGTGTCAGTTGTTGGTTTT   66991       GTG    A
                                TTGTGTT   TGTT GTTTT
                                |||||||   |||| |||||
                                AACACAG   ACAA CAAAA
                                     TCA    C
GAM2923  KIAA0332  3'  CCTTTTGTTGTGTTAGTTTT   66992    ATTG      GT
                                CC    TGTTGTGT  TAGTTTT
                                ||    ||||||||  |||||||
                                GG    ACAACACA  ATCAAAA
                                 AAA_       __
GAM2923  KIAA0961  3'  TGTGTTACACAATAGTTTT    66993       TG GT
                                TGTGTTG  T  TAGTTTT
                                |||||||  |  |||||||
                                ACACAAT  G  ATCAAAA
                                     GT TT
GAM2923  KIAA1303  3'  CATTGTGGTTGTGTTCTGTTT  66994        _     GTTA
                                CATTGTG TTGTGT    GTTT
                                ||||||| ||||||    ||||
                                GTAACAC AACACA    CAAA
                                     C      AGA_
GAM2923  KIAA1399  3'  TTGAGTTGGTGTTGGTTTT    66995     T    T    A
                                TTG GTTG GTGTT GTTTT
                                ||| |||| ||||| |||||
                                AAC CAAC CACAA CAAAA
                                  T    _    C
GAM2923  KIAA1594  3'  ACCTTTGTTATTTGTTAGTTTT 66996     ATTG     G
                                ACC    TGTTGT TGTTAGTTTT
                                |||    |||||| ||||||||||
                                TGG    ACAATA ACAATCAAAA
                                  AA__      A
GAM2923  LPAAT-gamma1 3'  CTGCACTCTGTGTGTTGGTTTT 66997     TG __       A
                                TTG  T  TGTGTGTT GTTTT
                                |||  |  |||||||| |||||
                                GAC  G  ACACACAA CAAAA
                                  GT AG       C
GAM2923  RTVP1    3'  CCATATGTGAATGAGGTTGGTT 66998      _    TT   T_   A
              TT                   CCAT TGTG  GTG  GTT GTTTT
                                |||| ||||  |||  ||| |||||
```

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                                GGTA ACAC  TAC  CAA CAAAA
                                  T   T_  TC   C
GAM2923  VPS29    3'  ACTGTGTTGTGGACATTTT   66999          TGTTA
                                ATTGTGTTGTG    GTTTT
                                ||||||||||    |||||
                                TGACACAACAC    TAAAA
                                      CTG__
GAM2923  VPS29    3'  ACTGTGTTGTGGACATTTT   66999          TGTTA
                                ATTGTGTTGTG    GTTTT
                                ||||||||||    |||||
                                TGACACAACAC    TAAAA
                                      CTG__
GAM2923  LOC125434 3'  ATTGGTTGTGTGTGTTTT    67000     T       TA
                                ATTG GTTGTGTGT  GTTTT
                                |||| |||||||||  |||||
                                TAAC CAACACACA  CAAAA
                                  _       __
GAM2923  LOC129452 3'  GTACTGTGTGTTGGTTTT    67001          A
                                GTGTTGTGTGTT GTTTT
                                |||||||||||| |||||
                                CATGACACACAA CAAAA
                                       C
GAM2923  LOC145609 5'  TGTTGCTCATTTGTTAGTTTT  67002       G____
                                TGTTGT    TGTTAGTTTT
                                ||||||    ||||||||||
                                ACAACG    ACAATCAAAA
                                   AGTAA
GAM2923  LOC146794 3'  TGTGTTGTGCAGAATTTT    67003         GTT
                                TGTGTTGTGT   AGTTTT
                                ||||||||||   ||||||
                                ACACAACACG   TTAAAA
                                      TC_
GAM2924  NEDD4    3'  TTATATGCTTGTAATTTCTAG  67006       AC       C
                                TTGTGT  CTTGTAAT TCTAG
                                ||||||  |||||||| |||||
                                AATATA  GAACATTA AGATC
                                   C_       A
GAM2924  KIAA1610  3'  TATTGTGTATCTTATTTTCACT 67007         C     AA  T
                                TATTGTGTA CTTGT  TC CT
                                ||||||||| |||||  || ||
                                ATAACACAT GAATA  AG GA
                                      A     AA  T
GAM2924  LOC202460 5'  TATTATGTGCCTACAACTCTAG 67008         A   TGTAAT
                                TATTGTGT CCT      CTCTAG
                                |||||||| |||     ||||||
                                ATAATACA GGA     GAGATC
                                     C   TGTT__
GAM2925  ARPC2    5'  GGTAAGGGAGGCAAGGACGGAG 67011    G    TTT       AA
            G                    GG AAGG   GTAAGGAC  AGG
                                || ||||   ||||||||  |||
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                                CC TTCC   CGTTCCTG  TCC
                                 A   CTC      CC
GAM2925  CEBPA    3'  GGGAAAGCTGAGGGCAAAGGA  67012        TGTA   A
                                GGGAAGGTT    AGG CAAAGGA
                                |||||||||    ||| |||||||
                                CCCTTTCGA    TCC GTTTCCT
                                     C___   C
GAM2925  CYLN2    3'  GGGAAGATGGCAGGGCGAGG   67013        TT   A  ACAA
                                GGGAAGGT  GTA GG    AGG
                                ||||||||  ||| ||    |||
                                CCCTTCTA  CGT CC    TCC
                                    C_   C  GC__
GAM2925  DNLC2A   3'  GGGAAGGTTGGTGCACACAGG  67014         T  AAGG   A
                                GGGAAGGTT GT    ACA AGG
                                ||||||||| ||    ||| |||
                                CCCTTCCAA CA    TGT TCC
                                     C  CG__   G
GAM2925  EFNB1    3'  GGGAAGGTGGCAAGGGGGGCGA 67015         TT     ACAA__
           GG                    GGGAAGGT  GTAAGG     AGG
                                ||||||||  ||||||     |||
                                CCCTTCCA  CGTTCC     TCC
                                    C_     CCCCGC
GAM2925  EGFL4    5'  GGTGAGGGTGAGTGGGGGACAG 67016    _  A   TT  AA_    A
           AGG                    GG GA GGT  GT   GGACA AGG
                                || || |||  ||   ||||| |||
                                CC CT CCA  CA   CCTGT TCC
                                 A  C   CT  CCC    C
GAM2925  ELK1     3'  GGGAGGTTGGCAGACAAAGGA  67017      A    T  AA
                                GGGA GGTT GT  GGACAAAGGA
                                |||| |||| ||  ||||||||||
                                CCCT CCAA CG  TCTGTTTCCT
                                  _    C  __
GAM2925  EZH1     3'  GGGGGACAGCAGGGACAAAGGA 67018     AA  TTT   A
                                GGG  GG   GTA GGACAAAGGA
                                |||  ||   ||| ||||||||||
                                CCC  CC   CGT CCTGTTTCCT
                                  __  TGT   C
GAM2925  HNF3A    3'  GGGTAGAGAGGACAAAGG    67019     A   TTTGTA
                                GGG AGG     AGGACAAAGG
                                ||| |||     ||||||||||
                                CCC TCT     TCCTGTTTCC
                                  A   C_____
GAM2925  IL2RB    3'  GGGAAGTTTGTCACCTAGATGA 67020       G    AA___   CAA
           GG                    GGGAAG TTTGT    GGA   AGG
                                ||||||| |||||    |||   |||
                                CCCTTC AAACA    TCT   TCC
                                   _    GTGGA   AC_
GAM2925  ITGAL    3'  GGAAGGTTCAGGCAGAGG    67021         GTA   A  A
                                GGAAGGTTT   AGG CA AGG
                                |||||||||   ||| || |||
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                                CCTTCCAAG   TCC GT TCC
                                    ___  _ C
GAM2925  JUNB     3'  GGGGTGTCCGTAAAGGGGCAGG 67022     AAG        ACAA
                                GGG  GTTTGTAAGG   AGG
                                |||  ||||||||||   |||
                                CCC  CAGGCATTTC   TCC
                                  CA_        CCCG
GAM2925  MYO1D    3'  GGACAGTAAGGACAGAGGA   67023    TTT        A
                                GG  GTAAGGACA AGGA
                                ||  ||||||||| ||||
                                CC  CATTCCTGT TCCT
                                 TGT        C
GAM2925  PLA2G2D  3'  GGGGGTGAGGAAGGACAAGGG  67024     AA  TTGT       A
                                GGG  GGT   AAGGACAA GG
                                |||  |||   |||||||| ||
                                CCC  CCA   TTCCTGTT CC
                                  __  CTCC       C
GAM2925  PRKACA   3'  GGGAGAGGGGGCAGGAGGGTGA 67025      _  TTT  A  CA___
             AGG                   GGGA AGG  GTA GGA    AAGG
                                |||| |||  ||| |||   ||||
                                CCCT TCC  CGT CCT    TTCC
                                  C  CC_  _  CCCAC
GAM2925  PRKCH    3'  GGGAAGGTCCGATAGAGGA   67026          TA__
                                GGGAAGGTTTG   AGGA
                                ||||||||||   ||||
                                CCCTTCCAGGC   TCCT
                                      TATC
GAM2925  SOX12    3'  GGGGTGTCAGAGGGACAAAGGA 67027     AAG  TGTAA
                                GGG  GTT    GGACAAAGGA
                                |||  |||    ||||||||||
                                CCC  CAG    CCTGTTTCCT
                                  CA_  TCTC_
GAM2925  SYN2     3'  GGGAAAGTTGGAGGTGGGGGA  67028         TGTA  ACAAA
                                GGGAAGGTT   AGG   GGA
                                |||||||||   |||   |||
                                CCCTTTCAA   TCC   CCT
                                     CC__  ACCC_
GAM2925  SYNGR2   3'  GGGAAAGTCCAGGGCAGAGG  67029          GTA  A  A
                                GGGAAGGTTT  AGG CA AGG
                                |||||||||   ||| || |||
                                CCCTTTCAGG  TCC GT TCC
                                     ___  C  C
GAM2925  TBX6     3'  GGGAGGTTTGTGATGGAGGCAG 67030      A     A____  A  A
             AGG                   GGGA GGTTTGT    AGG CA AGG
                                |||| |||||||    ||| || |||
                                CCCT CCAAACA    TCC GT TCC
                                  _     CTACC  _  C
GAM2925  UBTF     3'  GGGGAGGCCAGGGGGGCAAGGG 67031     A    TGTAA  A  A
             A                    GGG AGGTT    GG CAA GGA
                                |||  |||||    || ||| |||
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                                CCC TCCGG    CC GTT CCT
                                  C    TCCCC  _  C
GAM2925 UCP2    3' GGGAAGGTGGTAGGTAAAGGA 67032       TT  A  AC
                                GGGAAGGT  GTA GG  AAAGGA
                                ||||||||  ||| ||  ||||||
                                CCCTTCCA  CAT CC  TTTCCT
                                    C_  _ A_
GAM2925 AP1M2   3' GGGAAAGCTCCAAGGGCGAGG 67033        G    ACAA
                                GGGAAGGTTT TAAGG   AGG
                                ||||||||||| |||||   |||
                                CCCTTTCGAG GTTCC   TCC
                                      _   CGC_
GAM2925 BLCAP   3' AGGAGGAAGGGCAAAGGA    67034     A  TTTGT   A
                                GGGA GG    AAGG CAAAGGA
                                |||| ||    |||| |||||||
                                TCCT CC    TTCC GTTTCCT
                                  _ _____   C
GAM2925 BRPF3   3' GGGAAGGTCTGTGGGTGGG   67035         AA  ACAAA
                                GGGAAGGTTTGT  GG    GG
                                ||||||||||||  ||    ||
                                CCCTTCCAGACA  CC    CC
                                      __ CAC__
GAM2925 C1QR1   3' GGGAAGGTTTTGAGGAACTGGA 67036        GTA   CAAA
                                GGGAAGGTTT   AGGA   GGA
                                |||||||||   ||||   |||
                                CCCTTCCAAA   TCCT   CCT
                                     AC_   TGA_
GAM2925 CAPN6   3' GGGAAGGCTTCATGGAGG    67037        G  A   CAAA
                                GGGAAGGTTT TA GGA   GG
                                |||||||||| || |||   ||
                                CCCTTCCGAA GT CCT   CC
                                      _ A  ____
GAM2925 DKFZp434A1010 3' GAGGGCCCCCAGGATGGAGG  67038    A    G  A   CAA
                                GA GGTTT TA GGA   AGG
                                || ||||| || |||   |||
                                CT CCGGG GT CCT   TCC
                                 C    G  _   ACC
GAM2925 E46L    5' AGGAAGGCGAGGAGGACGAAGG 67039       TTGTA    A
                                GGGAAGGT    AGGAC AAGG
                                ||||||||    ||||| ||||
                                TCCTTCCG    TCCTG TTCC
                                    CTCC_    C
GAM2925 EFS2    3' GGGGGCTTTGGCAGGCAGGGGA 67040    AA    GTA_  A  AA
                                GGG  GGTTT   AGG CA  GGA
                                |||  |||||   ||| ||  |||
                                CCC  CCGAA   TCC GT  CCT
                                  __    ACCG   _  CC
GAM2925 FLJ20128 3' GGGAAGGTGGTTGATGAAGGA  67041       TTGTAAG  CA
                                GGGAAGGT     GA  AAGGA
                                ||||||||     ||  |||||
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                                CCCTTCCA      CT  TTCCT
                                    CCAA___  AC
GAM2925 HSPC065  3' GGGAAGGTTTGGCCAAAGG   67042          TAAGGA
                                GGGAAGGTTTG     CAAAGG
                                ||||||||||      ||||||
                                CCCTTCCAAAC     GTTTCC
                                     CG____
GAM2925 IL18BP   3' GGGAAGGTTTTTAAGGGCCGGG 67043         G    ACAAA
           GA                     GGGAAGGTTT TAAGG    GGA
                                ||||||||||  |||||    |||
                                CCCTTCCAAA ATTCC    CCT
                                     A    CGGCC
GAM2925 KIAA1111 3' GAGAAGGCAATGGGGGTAAAGG 67044        TTGTAA  AC
                                GGGAAGGT     GG  AAAGG
                                ||||||||     ||  |||||
                                CTCTTCCG     CC  TTTCC
                                     TTACC_  CA
GAM2925 KIAA1817 3' AGGAAGGTTGCGGGGGGTGGGGG 67045        T  AA  ACAAA
                                GGGAAGGTT GT  GG    GG
                                |||||||||  ||  ||    ||
                                TCCTTCCAA CG  CC    CC
                                     _  CC  CACCC
GAM2925 KIAA1870 5' GGGAGGTTTGTGGGTGCTGG   67046     A     AA  ACAAA
                                GGGA GGTTTGT  GG    GG
                                ||||  |||||||  ||    ||
                                CCCT CCAAACA  CC    CC
                                  _     __  CACGA
GAM2925 LRG      3' GGAAGGAAGGACAAGGG     67047       TTTGT       A
                                GGAAGG     AAGGACAA GG
                                ||||||     ||||||||  ||
                                CCTTCC     TTCCTGTT CC
                                    ______       C
GAM2925 MGC10818 3' GAGAAGACAAGGATGAAGGA   67048       TTTG     CA
                                GGGAAGG    TAAGGA  AAGGA
                                |||||||    ||||||  |||||
                                CTCTTCT    GTTCCT  TTCCT
                                    _____      AC
GAM2925 MGC11271 3' GGGAGGTTTGTAGGGTCCACTA 67049     A       A  A_  A_
           GGA                     GGGA GGTTTGTA GG  CA  AGGA
                                ||||  ||||||||  ||  ||  ||||
                                CCCT CCAAACAT CC  GT  TCCT
                                  _       C  AG  GA
GAM2925 MGC15854 5' GGGAAGGCGTGGGGGCAGGGGA 67050        T  TAA  A  AA
                                GGGAAGGT TG   GG CA  GGA
                                ||||||||  ||   ||  ||  |||
                                CCCTTCCG AC   CC GT  CCT
                                     C  CC_  _  CC
GAM2925 PXR2b    3' GGGAAGGTTCTAGACGAAGGA  67051          GTAA    A
                                GGGAAGGTTT    GGAC AAGGA
                                ||||||||||    |||| |||||
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                                CCCTTCCAAG    TCTG TTCCT
                                     A___    C
GAM2925  RAB25    3'  GGGCTGAAGTGGGGACAAGGG  67052     AA  TT  TAA     A
                                GGG  GG  TG   GGACAA GG
                                |||  ||  ||   ||||||| ||
                                CCC  CT  AC   CCTGTT CC
                                  GA  TC  C__     C
GAM2925  SCOP     3'  GGGAAGGCTGGGACAGGGG   67053        TGTAA    AA
                                GGGAAGGTT    GGACA  GG
                                |||||||||    |||||  ||
                                CCCTTCCGA    CCTGT  CC
                                     C____    CC
GAM2925  UBP1     3'  GGGAAGGTTTTGGATGAAGGA  67054         GTAA   CA
                                GGGAAGGTTT   GGA  AAGGA
                                ||||||||||   |||  |||||
                                CCCTTCCAAA   CCT  TTCCT
                                     A___   AC
GAM2925  USP24    3'  GAGAAGGTGAGAATAGGGTAGG 67055        TT__   A  ACAA
                                GGGAAGGT    GTA GG    AGG
                                ||||||||    ||| ||    |||
                                CTCTTCCA    TAT CC    TCC
                                     CTCT   C  A___
GAM2925  LOC157858 3'  GGGAAGGTTGGTGAGGCAAGGA 67056         T  A   A   A
                                GGGAAGGTT GT AGG CAA GGA
                                ||||||||| || ||| ||| |||
                                CCCTTCCAA CA TCC GTT CCT
                                     C  C   _   _
GAM2925  LOC158156 3'  GGGAAGGTTTGAAATCAGCAGG 67057          T   GACAA
                                GGGAAGGTTTG AAG     AGG
                                |||||||||||| |||     |||
                                CCCTTCCAAAC TTT     TCC
                                      _   AGTCG
GAM2925  LOC200734 3'  GGGTGGAAAAGGACAAGGG    67058     AA  TTTGT      A
                                GGG  GG     AAGGACAA GG
                                |||  ||     |||||||| ||
                                CCC  CC     TTCCTGTT CC
                                  A_  TT___       C
GAM2925  LOC220045 5'  GGGGGGGCTGAGGGGGCAGAGG 67059     AA   T TAA  A  A
                                GGG  GGTT G   GG CA AGG
                                |||  |||| |   || || |||
                                CCC  CCGA C   CC GT TCC
                                  CC   _ TCC  C  C
GAM2925  LOC221585 3'  AGGAAGGTTTTGCAGAGGA    67060          _   _
                                GGGAAGGTTT GTA AGGA
                                |||||||||| ||| ||||
                                TCCTTCCAAA CGT TCCT
                                     A   C
GAM2925  LOC221655 3'  GGGAAGGTATGTTATGGAAGGA 67061         T   AA_   CAA
                                GGGAAGGT TGT   GGA   AGGA
                                |||||||| |||   |||   ||||
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                                CCCTTCCA ACA   CCT   TCCT
                                     T  ATA  ___
GAM2925  LOC221773 3'  GGGAAGGAGGGCGGGGCAGAGG 67062       TTT  AA  A  A
                                GGGAAGG  GT  GG CA AGG
                                |||||||  ||  || || |||
                                CCCTTCC  CG  CC GT TCC
                                    TCC  CC  _  C
GAM2925  LOC221832 5'  GAAGGTTTCAAAGTGAGG    67063       G    ACAA
                                GAAGGTTT TAAGG   AGG
                                |||||||| |||||   |||
                                CTTCCAAA GTTTC   TCC
                                     _    AC__
GAM2925  LOC55954  3'  GGGGGTCAGTCGGGGGCAAGG  67064    AA   T  AA  ACA
                                GGG  GGTT GT  GG   AAGG
                                |||  |||| ||  ||   ||||
                                CCC  CCAG CA  CC   TTCC
                                  __   T  GC  CCG
GAM2925  LOC57115  3'  GGGAAGGCTCACCAGGCAGAGG 67065       TG A   A  A
                                GGGAAGGTT  T AGG CA AGG
                                |||||||||  | ||| || |||
                                CCCTTCCGA  G TCC GT TCC
                                     GT G  _  C
GAM2925  LOC88584  3'  GGGAAAGTTTAGAGTGAGG   67066        ___  A
                                GGGAAGGTTT   GT AGG
                                ||||||||||   || |||
                                CCCTTTCAAA   CA TCC
                                      TCT  C
GAM2926  COG2     5'  TGCGCAGACCGACTCGGCGGC  67069    C     AC   GC
                                TGC GCAGACC  CTC  GGCGGC
                                ||| |||||||  |||  ||||||
                                ACG CGTCTGG  GAG  CCGCCG
                                  _     CT  __
GAM2926  DVL3     3'  GCCGCAGGCTGCCACACGTGG  67070       ACCA  T   GC
                                GCCGCAG   CC CGCG  GG
                                |||||||   || ||||  ||
                                CGGCGTC   GG GTGC  CC
                                    CGAC  T   A_
GAM2926  GRAF     5'  TGCTGCAACCACCTGCCCGGGC 67071    C   A    C ___
                                TGC GCAG CCACCT GC   GGC
                                ||| |||| |||||| ||   |||
                                ACG CGTT GGTGGA CG   CCG
                                  A   _     _ GGC
GAM2926  ISLR     3'  TGCTTCAGACCACCTCCCAGC  67072    CG        G
                                TGC  CAGACCACCTC CGGC
                                |||  |||||||||| ||||
                                ACG  GTCTGGTGGAG GTCG
                                  AA         G
GAM2926  LASS1    3'  TGCGCAGGGTCCGCGGCGG   67073    C   ACCACC
                                TGC GCAG     TCGCGGCGG
                                ||| ||||     |||||||||
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                                ACG CGTC     GGCGCCGCC
                                  _   CCA___
GAM2926 MATK     5' TGCCACAGGCCAGGCG     67074        A   CCTCGC
                                TGCCGCAG CCA     GGCG
                                |||||||| |||     ||||
                                ACGGTGTC GGT     CCGC
                                    C  _______
GAM2926 POU4F1   5' GCCGCGGCGGTCGCGGCGGC  67075      AGACCACC
                                GCCGC      TCGCGGCGGC
                                |||||      ||||||||||
                                CGGCG      AGCGCCGCCG
                                  CCGCC___
GAM2926 PPP2R5E  5' TGCCCCGGACCCGGCGGCGGC 67076     GCA   ACCTC
                                TGCC  GACC    GCGGCGGC
                                ||||  ||||    ||||||||
                                ACGG  CTGG    CGCCGCCG
                                  GGC   GC___
GAM2926 PTGER3   5' TGCTGGGACCGCGGCCGCGGCG 67077    CGCA   ACC_
            GC                    TGC   GACC   TCGCGGCGGC
                                |||   ||||   ||||||||||
                                ACG   CTGG   GGCGCCGCCG
                                 ACC_   CGCC
GAM2926 SGT      3' GCTGCAGGGCCGCGGCGG    67078    C   ACCACC
                                GC GCAG     TCGCGGCGG
                                || ||||     |||||||||
                                CG CGTC     GGCGCCGCC
                                 A   CC_____
GAM2926 SNRP70   5' TGTCCGGAGGCTCGCGGCGGC  67079    _   C  ACCAC
                                TG CCG AG    CTCGCGGCGGC
                                || ||| ||    ||||||||||
                                AC GGC TC    GAGCGCCGCCG
                                 A  C  C_____
GAM2926 C22orf20 3' GCAGACCACCTGACAGGC    67080          C  _
                                GCAGACCACCT GC GGC
                                |||||||||| || |||
                                CGTCTGGTGGA TG CCG
                                       C  T
GAM2926 CLLD8    5' TGTCGGGGGCCAGCCACGGCGG 67081    C  CAGA   C T
                                TG CG    CCA C CGCGGCGG
                                || ||    ||| | ||||||||
                                AC GC    GGT G GTGCCGCC
                                 A  CCCC   C _
GAM2926 DKFZP566N034 5' GCTGCGGATCCCGGCGGCGGC  67082    C  A  CCA   C
                                GC GC GA   CCT GCGGCGGC
                                || || ||   ||| ||||||||
                                CG CG CT   GGG CGCCGCCG
                                 A  C  A__   C
GAM2926 FLJ13881 5' TGCTGCAGCCGGCGGCGG    67083     C    A  ACCTC
                                TGC GCAG CC    GCGGCGG
                                ||| |||| ||    |||||||
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                                ACG CGTC GG    CGCCGCC
                                  A   _ C____
GAM2926  FLJ20689  5'  TGCCGCAGCCACCTCCAACGGC 67084        A     G
                                TGCCGCAG CCACCTC CGGCGGC
                                |||||||| ||||||| |||||||
                                ACGGCGTC GGTGGAG GTTGCCG
                                          _     _
GAM2926  FLJ23471  5'  TGCCGCGACCGCCCGGC    67085      A   A  TCG
                                TGCCGC GACC CC   CGGC
                                |||||| |||| ||   ||||
                                ACGGCG CTGG GG   GCCG
                                   _   C  ___
GAM2926  FOXD4    5'  GCCGCAGACCTTGGCGG    67086         ACCTCGC
                                GCCGCAGACC     GGCGG
                                ||||||||||     |||||
                                CGGCGTCTGG     CCGCC
                                     AA_____
GAM2926  IL14     3'  TGCCGTGAGCTGCAGCGG    67087      CA  CCAC  C
                                TGCCG  GA    CT GCGGCGG
                                |||||  ||    || |||||||
                                ACGGC  CT    GA CGTCGCC
                                  A_  C___  _
GAM2926  KIAA0445  5'  TGCTGCTGGGCCACCTGCAGGC 67088    C  AGA_    C  _
                                TGC GC    CCACCT GC GGC
                                ||| ||    |||||| || |||
                                ACG CG    GGTGGA CG CCG
                                  A  ACCC     _ T
GAM2926  KIAA0451  3'  TGCCGCAGGCCAGCATGGTGGC 67089        A   CCT  C  C
                                TGCCGCAG CCA   CG GG GGC
                                |||||||| |||   || || |||
                                ACGGCGTC GGT   GT CC CCG
                                     C   C__  A  A
GAM2926  KIAA1301  3'  TGTCACAGACCATCTTATTGC  67090    C       C  CGCG
                                TG CGCAGACCA CT    GC
                                || |||||||| ||    ||
                                AC GTGTCTGGT GA    CG
                                 A        A  ATAA
GAM2926  KIAA1719  5'  TGCCGCAGGGTGGCCAGGGCGG 67091        ACCA_  TC_   C
            TGGC                  TGCCGCAG    CC   GCGG GGC
                                |||||||     ||   |||| |||
                                ACGGCGTC    GG   CGCC CCG
                                     CCACC  TCC    A
GAM2926  NMP200   5'  TGCCGGGACTGCTCCGCGGC   67092      CA   CACC
                                TGCCG  GAC    TCGCGGC
                                |||||  |||    |||||||
                                ACGGC  CTG    GGCGCCG
                                  C_   ACGA
GAM2926  PNMA1    5'  TGCCGAAGTCGCGGCG      67093      C  ACCACC
                                TGCCG AG     TCGCGGCG
                                |||||  ||     ||||||||
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                                ACGGC TC     AGCGCCGC
                                  T _______
GAM2926 ULK2     5' CGCTTCCCCGCCTCGCGGCGGC 67094     AGA_ A
                                CGC   CC CCTCGCGGCGGC
                                |||   || ||||||||||||
                                GCG   GG GGAGCGCCGCCG
                                  AAGG  C
GAM2926 UNC93B1  5' TACTGCGGACTCGCGGCGG   67095    C A  CACC
                                TGC GC GAC   TCGCGGCGG
                                ||| || |||   |||||||||
                                ATG CG CTG   AGCGCCGCC
                                  A  C  _____
GAM2926 LOC124222 5' GCCGCAGGGACAGCTCGCGGCG 67096       AC_ C
              GC                  GCCGCAG  CA CTCGCGGCGGC
                                |||||||  || ||||||||||
                                CGGCGTC  GT GAGCGCCGCCG
                                    CCT  C
GAM2926 LOC144317 5' CCGGCACTTCGCGGCGG    67097    CAGAC  C
                                CCG    CAC TCGCGGCGG
                                |||    ||| |||||||||
                                GGC    GTG AGCGCCGCC
                                  C____  A
GAM2926 LOC145123 5' TGCCGCAGTCCGCGGCGG   67098       A  ACCTC
                                TGCCGCAG CC    GCGGCGG
                                |||||||| ||    |||||||
                                ACGGCGTC GG    CGCCGCC
                                    A _____
GAM2926 LOC147808 3' TGCCGCAGATGCCGCAATGG  67099       CCACC    C
                                TGCCGCAGA    TCGCGG GG
                                |||||||||    |||||| ||
                                ACGGCGTCT    GGCGTT CC
                                     AC___     A
GAM2926 LOC149579 5' TGCTGCTGGGCCACCTGCAGGC 67088    C AGA_    C _
                                TGC GC   CCACCT GC GGC
                                ||| ||   |||||| || |||
                                ACG CG   GGTGGA CG CCG
                                  A ACCC     _ T
GAM2926 LOC253634 5' TGCCCAGACCACCTTGGGC   67100     G       CGC
                                TGCC CAGACCACCT  GGC
                                |||| ||||||||||  |||
                                ACGG GTCTGGTGGA  CCG
                                  _        AC_
GAM2926 LOC256401 5' TGCCAGCAGAGGGGCGCGGCGG 67101     _    CCACCT
              C                   TGCC GCAGA     CGCGGCGGC
                                |||| |||||     |||||||||
                                ACGG CGTCT     GCGCCGCCG
                                  T    CCCC__
GAM2927 APBA1    5' TCCGCGGGCCCGCGGGAG    67104    A       CCC
                                TTC CGGGCCCGCG  GAG
                                ||| ||||||||||  |||
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                                AGG GCCCGGGCGC   CTC
                                  C        C__
GAM2927 HTR1D    3'  TTCACGGACAACTGGGAGAG  67105         CC  GCCC
                                TTCACGGGC  GC    GAGAG
                                |||||||||  ||    |||||
                                AAGTGCCTG  TG    CTCTC
                                     T_  ACC_
GAM2927 MYO1D    5'  GGGCCCGCGATGAGCTCGGGAG 67106         _____  C  A
                                GGGCCCGC    GC CG GAG
                                ||||||||    || || |||
                                CCCGGGCG    CG GC CTC
                                     CTACT  A  C
GAM2927 ACY-3    5'  TTCATGGGCCCACGTGGCCCCA 67107      C       ___    G
            GAG                    TTCA GGGCCCGC   GCCC AGAG
                                |||| ||||||||   |||| ||||
                                AAGT CCCGGGTG   CGGG TCTC
                                  A       CAC    G
GAM2927 LOC123591 5'  CTCACGGATGCCCGGGAGA    67108         CCCGC    A
                                TTCACGGG    GCCCG GAGA
                                ||||||||    ||||| ||||
                                GAGTGCCT    CGGGC CTCT
                                     A____    C
GAM2928 ABCA1    3'  CTAGTGATTGAAGAGATGAAA  67111        CGAATC
                                TTAGTGA     AAGAGATGAAA
                                |||||||     ||||||||||
                                GATCACT     TTCTCTACTTT
                                     AAC___
GAM2928 CGI-127  3'  TTAGTTTAAGAGATGAA     67112       GACGAATC
                                TTAGT       AAGAGATGAA
                                |||||       ||||||||||
                                AATCA       TTCTCTACTT
                                   AA_______
GAM2928 DKFZp547C176 3'  ATGACCAAGAGATGAA      67113       GAAT
                                GTGAC    CAAGAGATGAA
                                |||||    ||||||||||
                                TACTG    GTTCTCTACTT
                                     ____
GAM2928 FLJ10374  3'  GTGGAAGGAAGAGATGA     67114     AC   TC
                                GTG  GAA  AAGAGATGA
                                |||  |||  |||||||||
                                CAC  CTT  TTCTCTACT
                                  __  CC
GAM2928 FLJ23191  5'  TTACTGACGAATCATGAAA    67115     G        A
                                TTA TGACGAATCA GAGA
                                ||| |||||||||| ||||
                                AAT ACTGCTTAGT CTTT
                                  G        A
GAM2928 KIAA1045  3'  TTAGTGACAAGTTAAGACG    67116          ATCAA
                                TTAGTGACGA    GAGATG
                                ||||||||||    ||||||
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                                AATCACTGTT    TTCTGC
                                     CAA__
GAM2928 RAB22A   3' TTAGAGATGGCAGAGATGAAA 67117     T CGAATCA
                                TTAG GA      AGAGATGAAA
                                |||| ||      ||||||||||
                                AATC CT      TCTCTACTTT
                                  T ACCG___
GAM2928 RAB40A   5' TTAGGATAAAGGAGATGAA   67118     T CG TCAA
                                TTAG GA AA   GAGATGAA
                                |||| || ||   ||||||||
                                AATC CT TT   CTCTACTT
                                  _ AT C___
GAM2928 LOC116150 3' TGACTACAATTAAGAGATGAAA 67119     G__  C
                                TGAC  AAT AAGAGATGAAA
                                ||||  ||| ||||||||||
                                ACTG  TTA TTCTCTACTTT
                                  ATG  A
GAM2928 LOC147160 3' TTAATGATGGAGAAAGATGAAA 67120       CGAATCA
                                TTAGTGA      AGAGATGAAA
                                |||||||      ||||||||||
                                AATTACT      TTTCTACTTT
                                    ACCTC__
GAM2928 LOC90670  3' TTAGTGGTTCAGGAGAGATGAA 67121       ACGAA  __
                                TTAGTG   TCA  AGAGATGAA
                                ||||||   |||  |||||||||
                                AATCAC   AGT  TCTCTACTT
                                   CA___  CC
GAM2929 EN1      3' TCAACGTCATTGTCCATT    67124          _ G
                                TCAACGTCATT TC ATT
                                |||||||||| || |||
                                AGTTGCAGTAA AG TAA
                                      C G
GAM2929 MS4A1    3' TCCACGTCACTTTATTT     67125    A       CGAT
                                TC ACGTCATTT   TATTT
                                || |||||||||   |||||
                                AG TGCAGTGAA   ATAAA
                                 G       _____
GAM2929 FLJ13105 3' TCAACGACATTCATATATATTT 67126       T    CGAT_
            C                    TCAACG CATTT    TATTTC
                                |||||| |||||    ||||||
                                AGTTGC GTAAG    ATAAAG
                                   T    TATAT
GAM2929 KIAA1586 5' GTCATTTCTAGATTATTT    67127        __
                                GTCATTTC  GATTATTT
                                ||||||||  ||||||||
                                CAGTAAAG  CTAATAAA
                                     AT
GAM2929 MAP2K6   3' TCAACCTTTCCCATTATTTC  67128      GTCA   G
                                TCAAC   TTTC ATTATTTC
                                |||||   |||| ||||||||
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                                AGTTG   AAGG TAATAAAG
                                  GA__   G
GAM2929 MAP2K6   3' TCAACCTTTCCCATTATTTC  67128     GTCA   G
                                TCAAC   TTTC ATTATTTC
                                |||||   |||| ||||||||
                                AGTTG   AAGG TAATAAAG
                                  GA__   G
GAM2929 MBLL39   5' TCAGTGTCATCTCTGGCTTTC 67129    AC      GATTA
                                TCA GTCATTTC    TTTC
                                |||  ||||||||    ||||
                                AGT CAGTAGAG    AAAG
                                 CA      ACCG_
GAM2929 MBLL39   5' TCAGTGTCATCTCTGGCTTTC 67129    AC      GATTA
                                TCA GTCATTTC    TTTC
                                |||  ||||||||    ||||
                                AGT CAGTAGAG    AAAG
                                 CA      ACCG_
GAM2929 MEF-2    3' TCAACATTTCAATTATTT    67130       CAT
                                TCAACGT   TTCGATTATTT
                                |||||||   ||||||||||
                                AGTTGTA   AAGTTAATAAA
                                   ___
GAM2929 RAB10    3' AACATCATTTCATTATATTT  67131         AT_
                                AACGTCATTTCG   TATTT
                                ||||||||||||  |||||
                                TTGTAGTAAAGT   ATAAA
                                      AAT
GAM2929 LOC152502 3' TCAACATCATTCTCCTTATTT 67132         CGA
                                TCAACGTCATTT   TTATTT
                                ||||||||||||  ||||||
                                AGTTGTAGTAAG   AATAAA
                                      AGG
GAM2930 ITGA4    5' TTAACGGTGGTTGGGGCCTAGA 67135         TGTACGA
            A                    TTAACGGTGGTT      TAGAA
                                ||||||||||||      |||||
                                AATTGCCACCAA      ATCTT
                                      CCCCGG_
GAM2930 MRPL49   3' GGGGTTTGTGTCACAGAA    67136   T     ACG
                                GG GGTTTGT   ATAGAA
                                || |||||||  ||||||
                                CC CCAAACA   TGTCTT
                                 _     CAG
GAM2930 MRPS12   3' TTAATAGTGGTCCTGATGGAA 67137     CG     GTAC   A
                                TTAA  GTGGTTT   GAT GAA
                                ||||  |||||||   ||| |||
                                AATT  CACCAGG   CTA CTT
                                  AT     A___   C
GAM2930 MRPS12   3' TTAATAGTGGTCCTGATGGAA 67137     CG     GTAC   A
                                TTAA  GTGGTTT   GAT GAA
                                ||||  |||||||   ||| |||
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                                AATT  CACCAGG   CTA CTT
                                  AT      A___   C
GAM2930  MRPS12   3'  TTAATAGTGGTCCTGATGGAA  67137     CG      GTAC   A
                                TTAA  GTGGTTT   GAT GAA
                                ||||  |||||||   ||| |||
                                AATT  CACCAGG   CTA CTT
                                  AT      A___   C
GAM2930  PCDHA11   5'  AACGGTGGCATCCGGTATGATG 67138         TT___   C   A
           GA                     AACGGTGGT    GTA GAT GA
                                |||||||||    ||| ||| ||
                                TTGCCACCG    CAT CTA CT
                                     TAGGC   A   C
GAM2930  PCDHA11   5'  AACGGTGGCATCCGGTATGATG 67138         TT___   C   A
           GA                     AACGGTGGT    GTA GAT GA
                                |||||||||    ||| ||| ||
                                TTGCCACCG    CAT CTA CT
                                     TAGGC   A   C
GAM2930  C20orf45  3'  TTAATGGTGGTTTATAGCATAG 67139      C         CG
                                TTAA GGTGGTTTGTA  ATAG
                                |||| ||||||||||  ||||
                                AATT CCACCAAATAT  TATC
                                  A         CG
GAM2931  CTBP1    3'  TCTCTGCAGTGCCAGGGCCAC  67142        ACATCAAT    __
                                TCTCTGCA      CCAGG  CAC
                                ||||||||      |||||  |||
                                AGAGACGT      GGTCC  GTG
                                     CAC_____    CG
GAM2931  JPH3     3'  TCCCTGCAGCGCCTCCCCGGGC 67143        ACA  AA   A
           AC                     TCTCTGCA   TC  TCC GGCAC
                                ||||||||   ||  ||| |||||
                                AGGGACGT   GG  GGG CCGTG
                                     CGC  AG   C
GAM2931  KCNK10   5'  TCTCTGCAGCTCAAAACCTGC  67144        ACA   T_  AG
                                TCTCTGCA   TCAA  CC  GC
                                ||||||||   ||||  ||  ||
                                AGAGACGT   AGTT  GG  CG
                                     CG_    TT  A_
GAM2931  MBP      3'  TCTGCAACGCCCATGTCCAGGC 67145        A_   A_
           AC                     TCTGCAAC  TCA  TCCAGGCAC
                                ||||||||  |||  |||||||||
                                AGACGTTG  GGT  AGGTCCGTG
                                     CG   AC
GAM2931  MEN1     3'  TCTCTGTGTACTCCCAGGCA   67146       CAACA  AAT
                                TCTCTG    TC   CCAGGCA
                                ||||||    ||   |||||||
                                AGAGAC    AG   GGTCCGT
                                   ACATG  ___
GAM2931  PDHB     3'  TCTTGCAGTACAAATCCAGG   67147     C    AC  C
                                TCT TGCA  AT AATCCAGG
                                |||  ||||  ||  ||||||||
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                                AGA ACGT  TG TTAGGTCC
                                  _   CA  T
GAM2931  PIGA    3'  TCTGCAACATTCCTCCAGG   67148        CAA
                                TCTGCAACAT   TCCAGG
                                ||||||||||  ||||||
                                AGACGTTGTA   AGGTCC
                                     AGG
GAM2931  PIGA    3'  TCTGCAACATTCCTCCAGG   67148        CAA
                                TCTGCAACAT   TCCAGG
                                ||||||||||  ||||||
                                AGACGTTGTA   AGGTCC
                                     AGG
GAM2931  PPIA    3'  CTCTGCAATCCAGCTAGGCA  67149       AC   AATCC
                                CTCTGCA  ATC    AGGCA
                                |||||||  |||    |||||
                                GAGACGT  TAG    TCCGT
                                   __   GTCGA
GAM2931  SHANK2  3'  TCTGCAACACACAGTAC    67150        T  ATC  _
                                TCTGCAACA CA   CAG GC
                                |||||||||  ||  ||| ||
                                AGACGTTGT GT   GTC TG
                                     _ ___   A
GAM2931  SLC21A2  3'  TCTCTCAACCCAGGC      67151     TGCAACA
                                TCTC      TCAATCCAGGC
                                ||||      ||||||||||
                                AGAG      AGTTGGGTCCG
                                  ________
GAM2931  TAF6    5'  TCTCTCCAATGCAGGC      67152      GCAACA    C
                                TCTCT     TCAAT CAGGC
                                |||||     ||||| |||||
                                AGAGA     GGTTA GTCCG
                                  _______    C
GAM2931  ARHU    3'  TCTCTGCAATACCAAGC     67153        CATCAAT
                                TCTCTGCAA      CCAGGC
                                |||||||||      ||||||
                                AGAGACGTT      GGTTCG
                                     AT_____
GAM2931  C3IP1   3'  TCTTTGCAACATATGAGGCAC  67154    C      CAATCC
                                TCT TGCAACAT     AGGCAC
                                ||| ||||||||     ||||||
                                AGA ACGTTGTA     TCCGTG
                                  A       TAC___
GAM2931  DKFZp547D155 3'  TCTCTGGCAGCTCCTCCCAGGC 67155       _  ACA  AA
            A                    TCTCTG CA   TC  TCCAGGCA
                                 ||||||  ||   ||  ||||||||
                                 AGAGAC GT   AG  GGGTCCGT
                                    C  CG_  GA
GAM2931  FLJ10829  3'  TCTCTGCAAATGTCACAATAGC 67156        CA_   ATCCA
            A                    TCTCTGCAA   TCA    GGCA
                                 |||||||||   |||    ||||
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                                AGAGACGTT  AGT    TCGT
                                     TAC  GTTA_
GAM2931  FLJ13340  3'  TCTACAACATCAAGCA     67157          ATCCA
                                TCTGCAACATCA    GGCA
                                ||||||||||||    ||||
                                AGATGTTGTAGT    TCGT
                                      _____
GAM2931  FLJ20375  3'  TCTCAGCAATACCAGGCA    67158     T   CATCAAT
                                TCTC GCAA      CCAGGCA
                                |||| ||||      |||||||
                                AGAG CGTT      GGTCCGT
                                  T   AT_____
GAM2931  FLJ22329  3'  CTTTGTGACATGAGTGCCAGGC 67159    C  CA   CAAT_
           AC                     CT TG  ACAT    CCAGGCAC
                                || ||  ||||    ||||||||
                                GA AC  TGTA    GGTCCGTG
                                 A  AC    CTCAC
GAM2931  KIAA0429  5'  TCTCTGTGGACACCCAGGCAC  67160      CAACATCA
                                TCTCTG       ATCCAGGCAC
                                ||||||       ||||||||||
                                AGAGAC       TGGGTCCGTG
                                   ACCTG___
GAM2931  KIAA0848  3'  TCTTGCAGTTTCCAGGCA    67161    C   ACATCAA
                                TCT TGCA      TCCAGGCA
                                ||| ||||      ||||||||
                                AGA ACGT      AGGTCCGT
                                  _   CAA____
GAM2931  KIAA1497  5'  TCTCTCAATTCCAGGC     67162      G   CATCAA
                                TCTCT CAA     TCCAGGC
                                ||||| |||     |||||||
                                AGAGA GTT     AGGTCCG
                                  _  A_____
GAM2931  KIAA1904  3'  TCCCTGCAGCCCTCCAGGCA  67163       ACA  AA
                                TCTCTGCA  TC  TCCAGGCA
                                ||||||||  ||  ||||||||
                                AGGGACGT  GG  AGGTCCGT
                                     CG_  __
GAM2931  MDS006   3'  TCTCTGTAGTTCCAGGCCAGGC 67164      CAACA  AT
           AC                     TCTCTG    TCA  CCAGGCAC
                                ||||||    |||  ||||||||
                                AGAGAC    GGT  GGTCCGTG
                                   ATCAA   CC
GAM2931  MGC32104  3'  TCTCTGCAGCCTCACTAGCA  67165       ACA  ATCCA
                                TCTCTGCA  TCA    GGCA
                                ||||||||  |||    ||||
                                AGAGACGT  AGT    TCGT
                                     CGG  GA___
GAM2931  TBDN100   3'  TCTACAACATCAAGCA     67157          ATCCA
                                TCTGCAACATCA    GGCA
                                ||||||||||||    ||||
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                                AGATGTTGTAGT    TCGT
                                      _____
GAM2931 ZDHHC3   3' TCTCTGCAATGCTCAGCCA   67166       CA_  AT
                                TCTCTGCAA  TCA CCA
                                |||||||||  ||| |||
                                AGAGACGTT  AGT GGT
                                     ACG  C_
GAM2931 LOC112476 3' CTCTGCGACCTGCCAGGCAC  67167      A ATCAAT
                                CTCTGC AC    CCAGGCAC
                                |||||| ||    ||||||||
                                GAGACG TG    GGTCCGTG
                                   C GAC___
GAM2931 LOC134530 3' CTCTGCAATCCAGCTAGGCA  67149      AC  AATCC
                                CTCTGCA ATC   AGGCA
                                |||||||  |||   |||||
                                GAGACGT  TAG   TCCGT
                                    __  GTCGA
GAM2931 LOC148490 5' TCTCTCCAGCTTAGTCCAGGCA 67168     G ACATCAA
             C                   TCTCT CA     TCCAGGCAC
                                |||||  ||     |||||||||
                                AGAGA GT     AGGTCCGTG
                                  G CGAATC_
GAM2931 LOC149535 5' TCCTGCCCACCCAATCCAGG  67169   T   A_ A
                                TC CTGC  AC TCAATCCAGG
                                || ||||  || ||||||||||
                                AG GACG  TG GGTTAGGTCC
                                 _   GG  _
GAM2931 LOC158314 3' TCTCTGCACCCCCAGGCA    67170       ACATCAA
                                TCTCTGCA     TCCAGGCA
                                ||||||||     ||||||||
                                AGAGACGT     GGGTCCGT
                                     GG_____
GAM2931 LOC163115 5' TCTCTGAGCAGGGCCCAGGCA 67171      CAA  TCAA
                                TCTCTG  CA   TCCAGGCA
                                ||||||  ||   ||||||||
                                AGAGAC  GT   GGGTCCGT
                                   TC_  CCC_
GAM2931 LOC196746 5' TCTCTGCAGCCACCCAGG    67172       ACATCA
                                TCTCTGCA     ATCCAGG
                                ||||||||     |||||||
                                AGAGACGT     TGGGTCC
                                     CGG___
GAM2931 LOC199907 3' TCTCTGCACTGTCATCAGG   67173       ACA  ATC
                                TCTCTGCA  TCA  CAGG
                                ||||||||  |||  ||||
                                AGAGACGT  AGT  GTCC
                                     GAC  A__
GAM2931 LOC200492 3' TCTTTCAGGGTAAATCCAGGCA 67174    CTG  ACATC
                                TCT  CA    AATCCAGGCA
                                |||  ||    ||||||||||
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                                AGA  GT    TTAGGTCCGT
                                  AA_  CCCAT
GAM2931  LOC202915 3'  TCTGTGACCCATCCCAGGCAC  67175     CA  A   A
                                TCTG  AC TCA TCCAGGCAC
                                ||||  || ||| |||||||||
                                AGAC  TG GGT GGGTCCGTG
                                  AC  _   A
GAM2931  LOC202934 3'  TCTGCAGCTTTTCCAGGCAC   67176      ACATCAA
                                TCTGCA      TCCAGGCAC
                                ||||||      |||||||||
                                AGACGT      AGGTCCGTG
                                   CGAAA__
GAM2931  LOC204845 5'  TCTGTGCAGTGTCCAGGCAC   67177    C   ACATCAA
                                TCT TGCA      TCCAGGCAC
                                ||| ||||      |||||||||
                                AGA ACGT      AGGTCCGTG
                                  C   CAC_____
GAM2931  LOC221738 5'  TCTCTGCAGTGCTCCAGGCAC  67178       ACATCAA
                                TCTCTGCA      TCCAGGCAC
                                ||||||||      |||||||||
                                AGAGACGT      AGGTCCGTG
                                    CACG___
GAM2931  LOC221960 3'  TCTCTGCAAAATTAAAACA    67179       C  C  TC
                                TCTCTGCAA AT AA  CA
                                ||||||||| || ||  ||
                                AGAGACGTT TA TT  GT
                                     T  A  TT
GAM2931  LOC254312 5'  TCTCTGCAGGCATCCAAGGGGC 67180       A_   AATCCA
                                TCTCTGCA  CATC     GGC
                                ||||||||  ||||     |||
                                AGAGACGT  GTAG     CCG
                                    CC    GTTCC_
GAM2931  LOC255465 3'  TCTGCAGCTTTTCCAGGCAC   67176      ACATCAA
                                TCTGCA      TCCAGGCAC
                                ||||||      |||||||||
                                AGACGT      AGGTCCGTG
                                   CGAAA__
GAM2931  LOC51054  5'  CCTTTGCAACCTTTCCAGGCA  67181     C     ATCAA
                                TCT TGCAAC    TCCAGGCA
                                ||| ||||||    ||||||||
                                GGA ACGTTG    AGGTCCGT
                                  A     GAA__
GAM2931  LOC51622  3'  TCTCTGCAAAATTAAAACA   67179       C  C  TC
                                TCTCTGCAA AT AA  CA
                                ||||||||| || ||  ||
                                AGAGACGTT TA TT  GT
                                     T  A  TT
GAM2931  LOC90321  5'  TCTGCACAGGGTCCAGGCA   67182      A  TCAA
                                TCTGCA CA    TCCAGGCA
                                |||||| ||    ||||||||
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                                AGACGT GT    AGGTCCGT
                                   _ CCC_
GAM2931  LOC91548  5'  TCTGCAACATCTGGCA      67183          AATCCA
                                TCTGCAACATC     GGCA
                                ||||||||||     ||||
                                AGACGTTGTAG     CCGT
                                      A_____
GAM2932  DKFZP434G1411 3'  TATTGCATTTTGTTGACTTAAT 67186      A        TTTG
           CT                    TATT CGTTTTGTTG    AATCT
                                ||||| ||||||||||   |||||
                                ATAA GTAAAACAAC    TTAGA
                                  C         TGAA
GAM2932  KR19     5'  TATTACTTTTTGGAGTGAATCT 67187       G     TT  TT
                                TATTAC TTTTG  GT  GAATCT
                                |||||| |||||  ||  ||||||
                                ATAATG AAAAC  CA  CTTAGA
                                   A    CT  __
GAM2932  LOC202759 5'  TATTACTTTTTGGAGTGAATCT 67187       G     TT  TT
                                TATTAC TTTTG  GT  GAATCT
                                |||||| |||||  ||  ||||||
                                ATAATG AAAAC  CA  CTTAGA
                                   A    CT  __
GAM2933  DLC1     5'  GAGCGAAGCGCCCTC      67190      ATA  TC
                                GAGC   GG  GGTGCCCTC
                                ||||   ||  |||||||||
                                CTCG   CT  TCGCGGGAG
                                    ___  __
GAM2933  CAP350    5'  AGAGTGTCGCCTCCGCCCTCG  67191     CATAG   GG
                                AGAG    GTC  TGCCCTCG
                                ||||    |||  ||||||||
                                TCTC    CGG  GCGGGAGC
                                  ACAG_   AG
GAM2933  CBX1     3'  TAAGAGCATGGGCCCT      67192         AGGTC  T
                                TAAGAGCAT    GG GCCCT
                                |||||||||    || |||||
                                ATTCTCGTA    CC CGGGA
                                      _____  _
GAM2933  FLJ12899  3'  TAAGAGCATGGTGGCCTC    67193         AGGTC    C
                                TAAGAGCAT    GGTG CCTC
                                |||||||||    |||| ||||
                                ATTCTCGTA    CCAC GGAG
                                     _____    C
GAM2933  FLJ21087  5'  GCATGCACGTGCCCTCG     67194      AG  CG
                                GCAT  GT  GTGCCCTCG
                                ||||  ||  |||||||||
                                CGTA  CG  CACGGGAGC
                                  __ TG
GAM2933  LHPP     3'  GAGCCTTCACAGTGCCCTCG   67195      ATAGGT
                                GAGC     CGGTGCCCTCG
                                ||||     ||||||||||
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                                CTCG     GTCACGGGAGC
                                  GAAGT_
GAM2933  LOC115073 5'  GAGCGGGGCGGTGCCCTCG   67196     ATA  T
                                GAGC   GG CGGTGCCCTCG
                                ||||   || ||||||||||
                                CTCG   CC GCCACGGGAGC
                                  CC_  _
GAM2933  LOC149297 5'  GAGGCGGCGGGTGCCCTCG   67197    CATA   C
                                GAG    GGT GGTGCCCTCG
                                |||    ||| ||||||||||
                                CTC    CCG CCACGGGAGC
                                  CG__   C
GAM2933  LOC92017  5'  GAGAGGTGGGCCACCCTC    67198    CAT    C  _
                                GAG   AGGT GGT GCCCTC
                                |||   |||| ||| ||||||
                                CTC   TCCA CCG TGGGAG
                                  ____   C   G
GAM2934  E2F1     3'  TGCAGATTGGAGGGTGG     67201      CT      A
                                TGTAG  ATTGGAGG TGG
                                |||||  |||||||| |||
                                ACGTC  TAACCTCC ACC
                                   __       C
GAM2934  ITGA11   3'  GTTTCTCTGGAGGATGG     67202    AG  A
                                GT  CT TTGGAGGATGG
                                ||  || ||||||||||
                                CA  GA GACCTCCTACC
                                 AA  _
GAM2934  Di-Ras2  3'  TGTGCTTTGGGGGATGGAG   67203    A   A   A
                                TGT GCT TTGG GGATGGAG
                                ||| ||| |||| ||||||||
                                ACA CGA AACC CCTACCTC
                                  _  _    C
GAM2934  PIP5K2B  3'  TGTATTCCAGACAGGATGGAG  67204     GCTA TG  __
                                TGTA    T  GA  GGATGGAG
                                ||||    |  ||  ||||||||
                                ACAT    G  CT  CCTACCTC
                                  AA__ GT  GT
GAM2934  LOC144473 3'  CAATGTAGCTTTTGGGGGTGG  67205          A   A  A
                                TAATGTAGCT TTGG GG TGG
                                |||||||||| |||| || |||
                                GTTACATCGA AACC CC ACC
                                     A    _  C
GAM2935  ARL8     3'  AATTCTCTGGTTGGGAGGGAGT 67208      G      A
                                AGTT TCTGGTT GGAGGGAGT
                                |||| ||||||| |||||||||
                                TTAA AGACCAA CCTCCCTCA
                                  G      C
GAM2935  C1QR1    3'  TGAGCTGTCTGGTTGGG     67209            AGGA
                                TGAGTTGTCTGGTT    GGG
                                ||||||||||||||    |||
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                                ACTCGACAGACCAA   CCC
                                      ____
GAM2935 FLJ12529 3' TGGGTGTCTGGAGGGA     67210    A  T   GGTTA
                                TG GT GTCT    GGAGGGA
                                || || ||||    |||||||
                                AC CA CAGA    CCTCCCT
                                 C  _   _____
GAM2935 KIAA1042 3' TGATTTGTCTAGCTTAGGAGGG 67211     G       _     A
             GGT                   TGA TTGTCTGGTT AGGAGGG GT
                                ||| |||||||||| ||||||| ||
                                ACT AACAGATCGA TCCTCCC CA
                                  A        A     C
GAM2935 KIAA1634 3' TGAGTTGTTGGGTTAAAGAGT  67212        CT    GAG
                                TGAGTTGT  GGTTAG   GGAGT
                                ||||||||  ||||||   |||||
                                ACTCAACA  CCAATT   TCTCA
                                     AC     ___
GAM2935 LOC124602 5' TGAGTTGCTGGTCCTTGGAGT  67213       T    AGGAG
                                TGAGTTG CTGGTT    GGAGT
                                ||||||| ||||||    |||||
                                ACTCAAC GACCAG    CCTCA
                                    _     GAA__
GAM2935 LOC203397 5' TGAGTTGCTGGTCCTTGGAGT  67213       T    AGGAG
                                TGAGTTG CTGGTT    GGAGT
                                ||||||| ||||||    |||||
                                ACTCAAC GACCAG    CCTCA
                                    _     GAA__
GAM2936 NLGN2    5' AGACGGTAGTTGAGCGTGG   67216    _   ATC    GT
                                AGA GGTA   GAGCG  TGG
                                ||| ||||   |||||  |||
                                TCT CCAT   CTCGC  ACC
                                  G   CAA    __
GAM2936 ZIC3     5' AGGGGTGGCGGCGGTTGG    67217    A   AAT  A
                                AG GGT   CG GCGGTTGG
                                || |||   || ||||||||
                                TC CCA   GC CGCCAACC
                                 C   CC_  _
GAM2936 FLJ20511 3' AGAGGTGGTCAGCGGCTGCTA  67218       AA  G      G
                                AGAGGT  TC AGCGGTTG TTA
                                ||||||  || |||||||| |||
                                TCTCCA  AG TCGCCGAC GAT
                                   CC  _      _
GAM2936 FLJ21616 3' AGAGGGAAGTTTGGTTGGTT   67219      TAATC   C__
                                AGAGG    GAG   GGTTGGTT
                                |||||    |||   ||||||||
                                TCTCC    TTC   CCAACCAA
                                   C_____   AAA
GAM2936 H2AV     3' GAGGAAGAGGGTTGGTTA    67220      TAATC   C
                                GAGG    GAG GGTTGGTTA
                                ||||    ||| |||||||||
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                                CTCC    CTC CCAACCAAT
                                  TT___  _
GAM2936 KIAA1634 3' AGGGGCTAATTGAGTTGTTGG 67221   A  _  C  CG
                                AG GGT AAT GAG  GTTGG
                                || ||| ||| |||  |||||
                                TC CCG TTA CTC  CAACC
                                 C  A  A  AA
GAM2936 NXN     3' AGGGGTGATCGAACGTGG    67222   A  A     GT
                                AG GGT ATCGAGCG  TGG
                                || ||| ||||||||  |||
                                TC CCA TAGCTTGC  ACC
                                 C  C     __
GAM2936 TRIM5   3' AGAGGCAATTGGGTGAT     67223        CGAGC  T
                                AGAGGTAAT    GG TGGT
                                |||||||||    || ||||
                                TCTCCGTTA    CC ACTA
                                      A____  C
GAM2936 LOC132617 3' AGAGGTGGTTGGTCA      67224      AATCGAGC
                                AGAGGT      GGTTGGTTA
                                ||||||      |||||||||
                                TCTCCA      CCAACCAGT
                                  _________
GAM2937 AXUD1   3' TAGGACTACAAGGCAAAAGGGG 67227       ____    AATC
                                TAGGACTA   GCAAAA   GGGG
                                ||||||||   ||||||   ||||
                                ATCCTGAT   CGTTTT   CCCC
                                     GTTC    ____
GAM2937 BPGM    3' CTAGCTCTGGAAAATCGGGG  67228     AA___
                                CTAGC    AAAATCGGGG
                                |||||    ||||||||||
                                GATCG    TTTTAGCCCC
                                   AGACC
GAM2937 BTG2    3' TAGGACAGTAGGAATCAGG   67229      T  CAAAA
                                TAGGAC AG    AATCGGG
                                |||||| ||    |||||||
                                ATCCTG TC    TTAGTCC
                                   _ ATCC_
GAM2937 DHCR7   3' AGGACTAGTAAAGGTGACTGGG 67230       C  AA__  C
                                AGGACTAG AAA   AT GGG
                                |||||||| |||   || |||
                                TCCTGATC TTT   TG CCC
                                     A  CCAC  A
GAM2937 EIF2AK3  3' TAGGACTATAAAACTACGG  67231       GC   AAT
                                TAGGACTA  AAAA  CGG
                                ||||||||  ||||  |||
                                ATCCTGAT  TTTT  GCC
                                     A_   GAT
GAM2937 TTC1    3' TAGGACAGCCAGAATCGGGG  67232      T  AAAA
                                TAGGAC AGC   AATCGGGG
                                |||||| |||   ||||||||
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                                ATCCTG TCG    TTAGCCCC
                                   _  GTC_
GAM2937  FLJ12568  3'  TAGGACTATGGAAAAATTGG  67233        GCA     C
                                TAGGACTA   AAAAAT GG
                                ||||||||   |||||| ||
                                ATCCTGAT   TTTTTA CC
                                     ACC     A
GAM2937  FLJ20254  3'  TAGGACTACAAGGGAGGGG   67234        G   AAAATC
                                TAGGACTA CAA     GGGG
                                |||||||| |||     ||||
                                ATCCTGAT GTT     CCCC
                                   _  CCCT__
GAM2937  KIAA0121  5'  GGGCTAGCAAAGAAAACCAG  67235    A       __
                                GG CTAGCAAA  AAATCGG
                                || ||||||||  |||||||
                                CC GATCGTTT  TTTGGTC
                                 C       CT
GAM2937  KIAA1130  3'  TAGGACCAGCAGGGG       67236          AAAAATC
                                TAGGACTAGCA      GGGG
                                ||||||||||       ||||
                                ATCCTGGTCGT      CCCC
                                                 _______
GAM2937  KIAA1948  5'  TAGGAGTTAGCAAAAAAAAAG 67237      C_        TC
           G                     TAGGA  TAGCAAAAAA  GGGG
                                 |||||  ||||||||||  ||||
                                 ATCCT  ATCGTTTTTT  TTCC
                                    CA         TT
GAM2937  LIAS     5'  TAGGACTAGCGCAGTGCAGGG  67238         AAAAAAT
                                TAGGACTAGC       CGGGG
                                ||||||||||       |||||
                                ATCCTGATCG       GTCCC
                                      CGTCAC_
GAM2937  PRKWNK2   3'  GGCACAACAGGAATCGGGG   67239    AC     AAA
                                GG  TAGCA   AATCGGGG
                                ||  |||||   ||||||||
                                CC  GTTGT   TTAGCCCC
                                 GT    CC_
GAM2937  LOC145824 5'  CAGCACTTAAAGAATCGGGG   67240    G   AGC   A
                                TAG ACT   AAA AATCGGGG
                                ||| |||   ||| ||||||||
                                GTC TGA   TTT TTAGCCCC
                                  G   A__   C
GAM2937  LOC149721 5'  GAACTAGCAGAAATCACGGGG  67241         A   AT_
                                GGACTAGCA AAA   CGGGG
                                ||||||||| |||   |||||
                                CTTGATCGT TTT   GCCCC
                                      C   AGT
GAM2937  LOC150135 3'  CAGGCGAGAGAAAATCGGGG   67242      ACT  CAA
                                TAGG   AG   AAAATCGGGG
                                ||||   ||   ||||||||||
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                                GTCC  TC  TTTTAGCCCC
                                  GC_ TC_
GAM2937 LOC150244 5' CAGGATAAGGGAATCGGGG  67243     CT CAAAA
                                TAGGA AG   AATCGGGG
                                ||||| ||   ||||||||
                                GTCCT TC   TTAGCCCC
                                   AT CC___
GAM2937 LOC150381 3' AGGGCAGGAAAGAATCGGGG 67244    AC  C  A
                                AGG TAG AAA AATCGGGG
                                ||| ||| ||| ||||||||
                                TCC GTC TTT TTAGCCCC
                                  C_  C  C
GAM2937 LOC150933 3' TAGGACTACAGGAATGGG   67245       G AAA  C
                                TAGGACTA CA  AAT GGG
                                |||||||| ||  ||| |||
                                ATCCTGAT GT  TTA CCC
                                     _ CC_  _
GAM2937 LOC196549 5' CAGGGAGCAGGAATCGGGG  67246    ACT  AAA
                                TAGG  AGCA  AATCGGGG
                                ||||  ||||  ||||||||
                                GTCC  TCGT  TTAGCCCC
                                  C__   CC_
GAM2937 LOC204820 3' GGGTACAAAAAATTGGGG   67247    ACTA      C
                                GG   GCAAAAAAT GGGG
                                ||   ||||||||| ||||
                                CC   TGTTTTTTA CCCC
                                 CA__       A
GAM2937 LOC221710 5' TAGGGCTAACAAAATATGG  67248     A       A  C
                                TAGG CTAGCAAAA AT GG
                                |||| ||||||||| || ||
                                ATCC GATTGTTTT TA CC
                                  C       A  _
GAM2937 LOC254065 5' AGGGCTGGCAAAATCCAGGG 67249    A  A    AA
                                AGG CT GCAAAA  TCGGGG
                                ||| || ||||||  ||||||
                                TCC GA CGTTTT  GGTCCC
                                  C  C    A_
GAM2937 LOC257153 5' GGACAGGCAAAACCAGGG   67250     TA   AA
                                GGAC  GCAAA  ATCGGGG
                                ||||  |||||  |||||||
                                CCTG  CGTTT  TGGTCCC
                                  TC   __
GAM2937 LOC257313 5' GGACTAGCAAAGAAACAG   67251         A  T
                                GGACTAGCAAA AA CGG
                                |||||||||| || |||
                                CCTGATCGTTT TT GTC
                                       C  T
GAM2937 LOC51075  3' TAGGACTAGCGACAAAGTTAGG 67252         AAA  TCG
                                TAGGACTAGC  AAA  GGG
                                ||||||||||  |||  |||
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                                ATCCTGATCG  TTT  TCC
                                     CTG  CAA
GAM2938 APOL1   3' GGGCAGATCAAGAGGTCAGG  67255   A       C  AC
                                GG CAGATCGAGA GG  CAGG
                                || |||||||||| ||  ||||
                                CC GTCTAGTTCT CC  GTCC
                                 C        _ A_
GAM2938 DFFB    3' CGGGCAGATCACCTGAGGTCAG 67256    A     AGAC  AC
           G                     CGG CAGATCG   GG  CAGG
                                ||| |||||||   ||  ||||
                                GCC GTCTAGT   TC  GTCC
                                  C     GGAC  CA
GAM2938 DVL3    3' ACGGACGGATGGAGAGAG    67257      A  C   C
                                ACGGAC GAT GAGA GG
                                |||||| ||| |||| ||
                                TGCCTG CTA CTCT TC
                                   C  C   C
GAM2938 FUS1    3' CAGGTAGGTCGGAAGAATCAGG 67258    AC  A  A  C  C
                                CGG  AG TCG GA GGA CAGG
                                |||  || ||| || ||| ||||
                                GTC  TC AGC CT CTT GTCC
                                  CA  C  _ T  A
GAM2938 HDAC5   5' ACGGACGGGACGGGAGCCCGG  67259      A_  C_  A_
                                ACGGAC  GAT  GAG  CGG
                                ||||||  |||  |||  |||
                                TGCCTG  CTG  CTC  GCC
                                   CC   CC   GG
GAM2938 HDAC5   5' ACGGACGGGACGGGAGCCCGG  67259      A_  C_  A_
                                ACGGAC  GAT  GAG  CGG
                                ||||||  |||  |||  |||
                                TGCCTG  CTG  CTC  GCC
                                   CC   CC   GG
GAM2938 HDLBP   3' ACTGACATGCCGGGTGGACCAG 67260   G   GA  AGAC
           G                     AC GACA  TCG   GGACCAGG
                                || ||||  |||   ||||||||
                                TG CTGT  GGC   CCTGGTCC
                                 A   AC   CCA_
GAM2938 HLCS    5' ACAGGTGGATCACGAGGTCAGG 67261    ACA   A  C  AC
                                ACGG  GATCG GA GG  CAGG
                                ||||  ||||| || ||  ||||
                                TGTC  CTAGT CT CC  GTCC
                                  CAC   G  _ A_
GAM2938 KIF1B   5' CAGACCGACGGGCGGACCGGG  67262       GA__    A
                                CAGATCGA   CGGACC GG
                                ||||||||   |||||| ||
                                GTCTGGCT   GCCTGG CC
                                     GCCC    C
GAM2938 LIF     3' GGACAGATGGACAACTCCGGG  67263       CGA   A_  A
                                GGACAGAT  GACGG  CC GG
                                ||||||||  |||||  || ||
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                                CCTGTCTA  CTGTT  GG CC
                                    C__    GA  C
GAM2938  LMO1     3'  GGACAGACGGGCCTGGAGGCCA 67264        ____ GA  C  A
              GG                  GGACAGAT   C  GA GG CCAGG
                                  ||||||||   |  || || |||||
                                  CCTGTCTG   G  CT CC GGTCC
                                      CCCG AC  _  _
GAM2938  MDFI     3'  GGGTAGGAGAGGACCAGG   67265    AC  ATC   C
                                  GG  AG   GAGA GGACCAGG
                                  ||  ||   |||| ||||||||
                                  CC  TC   CTCT CCTGGTCC
                                   CA  ___   _
GAM2938  MRPL49   3'  ACAGGCCAAGGTGGACCAG   67266     AT   AC
                                  ACAG  CGAG  GGACCAG
                                  ||||  ||||  |||||||
                                  TGTC  GTTC  CCTGGTC
                                    CG   CA
GAM2938  NCOA6    5'  ACGGGTGGATCACTTGAGGTCA 67267     ACA    AGAC  AC
              GG                  ACGG   GATCG   GG  CAGG
                                  ||||   |||||   ||  ||||
                                  TGCC   CTAGT   TC  GTCC
                                    CAC    GAAC  CA
GAM2938  NR3C2    3'  CAGACAGACAATTTGGACTGGG 67268       T   GAC   CA
                                  CGGACAGA CGA   GGAC  GG
                                  |||||||| |||   ||||  ||
                                  GTCTGTCT GTT   CCTG  CC
                                      _  AAA   AC
GAM2938  PRX      3'  GGACAGATCGAGGGCAG     67269          AC  AC
                                  GGACAGATCGAG  GG  CAG
                                  ||||||||||||  ||  |||
                                  CCTGTCTAGCTC  CC  GTC
                                          __  __
GAM2938  RPH3AL   3'  CGGGCGGATCACTTGAGACCAG 67270     ACA    AGAC
              G                    CGG   GATCG   GGACCAGG
                                  |||   |||||   ||||||||
                                  GCC   CTAGT   TCTGGTCC
                                    CGC    GAAC
GAM2938  SNX15    3'  ACAGACAGACATGGGCCG    67271         CGAGAC  A  A
                                  ACGGACAGAT     GG CC G
                                  ||||||||||     || || |
                                  TGTCTGTCTG     CC GG C
                                       TAC___  _  C
GAM2938  ASB16    3'  GGAGGAGTGAGGTGGACCAGG  67272    CA  TC   AC
                                  GGA  GA  GAG  GGACCAGG
                                  |||  ||  |||  ||||||||
                                  CCT  CT  CTC  CCTGGTCC
                                    C_  CA   CA
GAM2938  C6orf5   5'  ACGGACAGACAGACTGG     67273          CG   _
                                  ACGGACAGAT  AGAC GG
                                  ||||||||||  ||||  ||
```

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                                TGCCTGTCTG  TCTG CC
                                      __    A
GAM2938  DKFZp761N1114 3'  ACGGGCAGATCATGAGGTCAGG 67274      A      A  C  AC
                                ACGG CAGATCG GA GG  CAGG
                                |||| ||||||| || ||  ||||
                                TGCC GTCTAGT CT CC  GTCC
                                  C      A  _  A_
GAM2938  DOCK3     3'  ACAGACAGATTGGGATCACTGC 67275          C__  G_  GGAC
           AGG                    ACGGACAGAT   GA  AC    CAGG
                                |||||||||   ||  ||    ||||
                                TGTCTGTCTA   CT  TG    GTCC
                                     ACC  AG  AC__
GAM2938  FLJ10081  3'  GGACAGATCACACCTCAGG    67276          AG  GGAC
                                GGACAGATCG  AC    CAGG
                                |||||||||  ||    ||||
                                CCTGTCTAGT  TG    GTCC
                                     G_  GA__
GAM2938  FLJ12649  3'  ACGGGTGGATCTCTTGAGGCCA 67277      ACA    GA__  C  A
           GG                     ACGG   GATC    GA GG CCAGG
                                ||||   ||||    || || |||||
                                TGCC   CTAG    CT CC GGTCC
                                  CAC    AGAA  _  _
GAM2938  FLJ22529  3'  GGCAGATCACTTGAGGTCAGG  67278    A      AGAC  AC
                                GG CAGATCG    GG  CAGG
                                || |||||||    ||  ||||
                                CC GTCTAGT    TC  GTCC
                                 _      GAAC  CA
GAM2938  FLJ32926  3'  ACGGACAGACACTGACCAG    67279          CGAG  G
                                ACGGACAGAT    AC GACCAG
                                ||||||||||    || ||||||
                                TGCCTGTCTG    TG CTGGTC
                                     _____  A
GAM2938  HEAB      5'  GGACAGGTCGAGGGACCAGG   67280       A    AC
                                GGACAG TCGAG  GGACCAGG
                                |||||| |||||  ||||||||
                                CCTGTC AGCTC  CCTGGTCC
                                   C     __
GAM2938  HRMT1L3   3'  ACGGCAGATCGAGGTGA     67281      A       ACG
                                ACGG CAGATCGAG   GA
                                |||| |||||||||   ||
                                TGCC GTCTAGCTC   CT
                                  _        CA_
GAM2938  JAM1      3'  GGCGGATCAAGAGGTCAGG   67282    ACA      C  AC
                                GG   GATCGAGA GG  CAGG
                                ||   |||||||| ||  ||||
                                CC   CTAGTTCT CC  GTCC
                                 GC_       _  A_
GAM2938  JAM1      3'  GGCGGATCAAGAGGTCAGG   67282    ACA      C  AC
                                GG   GATCGAGA GG  CAGG
                                ||   |||||||| ||  ||||
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                                CC   CTAGTTCT CC  GTCC
                                 GC_       _ A_
GAM2938 JAM1     3' GGCGGATCAAGAGGTCAGG   67282    ACA      C  AC
                                GG   GATCGAGA GG  CAGG
                                ||   |||||||| ||  ||||
                                CC   CTAGTTCT CC  GTCC
                                 GC_       _ A_
GAM2938 JAM1     3' GGCGGATCAAGAGGTCAGG   67282    ACA      C  AC
                                GG   GATCGAGA GG  CAGG
                                ||   |||||||| ||  ||||
                                CC   CTAGTTCT CC  GTCC
                                 GC_       _ A_
GAM2938 KIAA0544 5' CGGACATGGCCCGGACCAGG   67283       GATCGAGA
                                CGGACA       CGGACCAGG
                                ||||||       |||||||||
                                GCCTGT       GCCTGGTCC
                                    ACCGG___
GAM2938 KIAA0831 5' GGGCAGATCAAGAGGTTAGG   67284    A        C  ACC
                                GG CAGATCGAGA GG   AGG
                                || ||||||||||  ||   |||
                                CC GTCTAGTTCT CC   TCC
                                 C         _ AA_
GAM2938 KIAA1463 5' ACGGACAGATGGCCTCAG     67285         CGAGAC  AC_
                                ACGGACAGAT     GG   CAG
                                ||||||||||     ||   |||
                                TGCCTGTCTA     CC   GTC
                                       _______  GGA
GAM2938 KIAA1712 3' ACAGGCAGATCACCTGAGGTCA 67286      A      AGAC  AC
             GG                   ACGG CAGATCG    GG  CAGG
                                |||| |||||||    ||  ||||
                                TGTC GTCTAGT    TC  GTCC
                                  C      GGAC  CA
GAM2938 KIAA1742 3' CAGACAGATCAAGGCTGG     67287           AC_
                                CGGACAGATCGAG   GG
                                ||||||||||||   ||
                                GTCTGTCTAGTTC   CC
                                       CGA
GAM2938 KLHL6    3' CGGGCAGATCACAAGGTCAGG  67288     A      A  C  AC
                                CGG CAGATCG GA GG  CAGG
                                ||| ||||||| || ||  ||||
                                GCC GTCTAGT TT CC  GTCC
                                  C      G  _ A_
GAM2938 MYO3B    3' GGACAGATTTAGGGTTAGG    67289        CG  AC  ACC
                                GGACAGAT  AG  GG   AGG
                                ||||||||  ||  ||   |||
                                CCTGTCTA  TC  CC   TCC
                                     AA  __  AA_
GAM2938 NDP52    3' GGACAGATCACGTGAGGCCAGG 67290          AGAC_  A
                                GGACAGATCG    GG CCAGG
                                ||||||||||    || |||||
```

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                                CCTGTCTAGT    CC GGTCC
                                     GCACT  _
GAM2938  NINJ2    3'  ACGGGCAGATCACCTGAGGTCA 67291      A      AGAC  AC
              GG                   ACGG CAGATCG    GG  CAGG
                                   |||| |||||||    ||  ||||
                                   TGCC GTCTAGT    TC  GTCC
                                     C      GGAC  CA
GAM2938  PRAX-1   3'  AGACGAGGTGGGTGGACCAGG  67292     T    AC____
                                   AGA CGAG     GGACCAGG
                                   ||| ||||     ||||||||
                                   TCT GCTC     CCTGGTCC
                                     _    CACCCA
GAM2938  SLC6A14  3'  AGACAGATCACTTGAGGTCGG  67293          ____   A_
                                   GGACAGATC    GAG  CGG
                                   |||||||||    |||  |||
                                   TCTGTCTAG    CTC  GCC
                                        TGAA   CA
GAM2938  TRIM6    3'  CGGGTGGATCACTTGCGGTCAG 67294     ACA    AGA_  AC
              G                    CGG   GATCG    CGG  CAGG
                                   |||   |||||    |||  ||||
                                   GCC   CTAGT    GCC  GTCC
                                     CAC    GAAC   A_
GAM2938  LOC145453 5'  CAGACAGATCCTTGAGGTCAGG 67295          GA_  C  AC
                                   CGGACAGATC   GA GG  CAGG
                                   ||||||||||   || ||  ||||
                                   GTCTGTCTAG   CT CC  GTCC
                                        GAA  _  A_
GAM2938  LOC147341 5'  ACGAGATAGCCGACGTGGACCA 67296     _  C  A    GAC
              GG                     ACG GA AG TCGA   GGACCAGG
                                   ||| || || ||||   ||||||||
                                   TGC CT TC GGCT   CCTGGTCC
                                     T  A  _    GCA
GAM2938  LOC148764 5'  GGAACCAGGGACGGATCAGG   67297     CAG    A_     C
                                   GGA   ATCG  GACGGA CAGG
                                   |||   ||||  |||||| ||||
                                   CCT   TGGT  CTGCCT GTCC
                                     ___    CC     A
GAM2938  LOC151201 3'  GGAGGATCGCTTGAAACCAGG  67298     CA    AGAC
                                   GGA  GATCG    GGACCAGG
                                   |||  |||||    ||||||||
                                   CCT  CTAGC    TTTGGTCC
                                     C_     GAAC
GAM2938  LOC158997 5'  CGGCAGCGATGGACCAG     67299     A   AT   GAC
                                   CGG CAG  CGA   GGACCAG
                                   ||| |||  |||   |||||||
                                   GCC GTC  GCT   CCTGGTC
                                     _   __   A__
GAM2938  LOC255271 5'  GGAAAGCCGAGACGGGCCGGG  67300     C  A       A  A
                                   GGA AG TCGAGACGG CC GG
                                   ||| || |||||||| || ||
```

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                                CCT TC GGCTCTGCC GG CC
                                  T _       C  C
GAM2938  LOC255766 5'  ACGGACAGATGGGGGATTCAGG 67301          CGAGAC   C_
                                ACGGACAGAT     GGA  CAGG
                                ||||||||||     |||  ||||
                                TGCCTGTCTA     CCT  GTCC
                                     CCC___   AA
GAM2938  LOC257449 3'  CAGACAGATCAAGGCTGG    67287           AC_
                                CGGACAGATCGAG   GG
                                ||||||||||||   ||
                                GTCTGTCTAGTTC   CC
                                       CGA
GAM2938  LOC51193  5'  CGAACAGATCACCTGAGGTCGG 67302          ____   A_
                                CGGACAGATC    GAG  CGG
                                ||||||||||    |||  |||
                                GCTTGTCTAG    CTC  GCC
                                     TGGA   CA
GAM2938  LOC90918  3'  GGGCAGATCAACTAAGGTCAGG 67303    A      GAC  AC
                                GG CAGATCGA   GG  CAGG
                                || ||||||||   ||  ||||
                                CC GTCTAGTT   TC  GTCC
                                 C       GAT  CA
GAM2939  COG6      3'  CTGAGTGTATACTTAAAAT   67306     A    _
                                TTGA GTGTA ACTTAAAAT
                                |||| ||||| |||||||||
                                GACT CACAT TGAATTTTA
                                  _    A
GAM2939  EGLN1     5'  TTGAAGTTTACTTAAAA     67307       GTA
                                TTGAAGT   ACTTAAAA
                                |||||||   ||||||||
                                AACTTCA   TGAATTTT
                                    AA_
GAM2939  MAK       3'  TCGAAGTGTCTATTTAAAAT  67308        AAC_
                                TTGAAGTGT    TTAAAAT
                                |||||||||    |||||||
                                AGCTTCACA    AATTTTA
                                     GATA
GAM2939  BANK      3'  TGAAGTGCATTGTAAAAT    67309        ACT
                                TGAAGTGTA   TAAAAT
                                |||||||||   ||||||
                                ACTTCACGT   ATTTTA
                                     AAC
GAM2939  DKFZP434C1715 3'  TTGATGGTAACTTAAAAT    67310     AGT
                                TTGA   GTAACTTAAAAT
                                ||||   ||||||||||||
                                AACT   CATTGAATTTTA
                                  AC_
GAM2939  FLJ10829  3'  TTGAAGTGTAATGCCCCA    67311          ___
                                TTGAAGTGTAA   CTTA
                                ||||||||||   ||||
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                                AACTTCACATT  GGGT
                                      ACG
GAM2939 HYPH    3' TGAAGTGGCTCAAAAT     67312       TAA
                                TGAAGTG  CTTAAAAT
                                |||||||  ||||||||
                                ACTTCAC  GAGTTTTA
                                   C__
GAM2939 PGGT1B  3' TGAAGTGTAAACTTGAAAAT  67313         _  _
                                TGAAGTGTAA CTT AAAAT
                                |||||||||| ||| |||||
                                ACTTCACATT GAA TTTTA
                                      T  C
GAM2939 PRSC    3' TCGAAGTGTAATAAAA     67314         CT
                                TTGAAGTGTAA  TAAAA
                                ||||||||||  |||||
                                AGCTTCACATT  ATTTT
                                      __
GAM2939 UMP-CMPK 3' TTGAAGTGTTACTAAAAT   67315        A  T
                                TTGAAGTGT ACT AAAAT
                                ||||||||| ||| |||||
                                AACTTCACA TGA TTTTA
                                     A  _
GAM2939 ZNF272  3' CTGAAGTGTACGTAAAA    67316         ACT
                                TTGAAGTGTA  TAAAA
                                |||||||||  |||||
                                GACTTCACAT  ATTTT
                                      GC_
GAM2939 LOC153682 3' TTAAAGATAACTTAAAAT  67317       T
                                TTGAAG GTAACTTAAAAT
                                |||||| ||||||||||||
                                AATTTC TATTGAATTTTA
                                     _
GAM2939 LOC81537 3' TTGATTATATGTAACTTAA  67318     A___
                                TTGA   GTGTAACTTAA
                                ||||   ||||||||||
                                AACT   TACATTGAATT
                                  AATA
GAM2940 DYRK1A  3' TTACCCAAGGCTTGTTG    67321       _  GA
                                TTACTCA GGC  TTGTTG
                                ||||||| |||  ||||||
                                AATGGGT CCG  AACAAC
                                     T  __
GAM2940 GYG     3' TCACTCAGCAGTGTTG     67322       G  AT
                                TTACTCAG CG  TGTTG
                                |||||||| ||  |||||
                                AGTGAGTC GT  ACAAC
                                     _ C_
GAM2940 FLJ13031 5' TTACCCACTTGCATTGTTG  67323       G__  G
                                TTACTCA  GC ATTGTTG
                                |||||||  || |||||||
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                                AATGGGT   CG TAACAAC
                                    GAA  _
GAM2940  FLJ32762  3'  TTACCCACTTGCATTGTTG   67323       G__  G
                                TTACTCA   GC ATTGTTG
                                |||||||   || |||||||
                                AATGGGT   CG TAACAAC
                                    GAA  _
GAM2940  HCRTR2    3'  TTACTCAGGTATCCTTG     67324        CG   G
                                TTACTCAGG  ATT TTG
                                |||||||||  ||| |||
                                AATGAGTCC  TAG AAC
                                     A_   G
GAM2940  HSH2      3'  TCACTCTGATGATTGTTG    67325       A GC
                                TTACTC G  GATTGTTG
                                ||||||  |  ||||||||
                                AGTGAG C  CTAACAAC
                                   A TA
GAM2940  KIAA0586  5'  TTACCAGGGACTGTTG      67326     T    C
                                TTAC CAGG GATTGTTG
                                ||||  |||| ||||||||
                                AATG GTCC CTGACAAC
                                  _   _
GAM2940  KIAA0841  3'  TTACTCAGCCACCCCTGTTG   67327        G  AT__
                                TTACTCAG CG    TGTTG
                                ||||||||  ||    |||||
                                AATGAGTC GT    ACAAC
                                     G  GGGG
GAM2940  LHFPL2    3'  TCACTCAGGGCAAGGTTG    67328         _   TT
                                TTACTCAGG CGA  GTTG
                                |||||||||  |||  ||||
                                AGTGAGTCC GTT  CAAC
                                     C   C_
GAM2940  PRO0611   3'  TTATTCAGTTAACTGTTG    67329     C    GC
                                TTA TCAG  GATTGTTG
                                |||  ||||  ||||||||
                                AAT AGTC  TTGACAAC
                                  A    AA
GAM2940  LOC123775 5'  CTACTCAGGTCGCTG       67330         CGA
                                TTACTCAGG   TTGTTG
                                |||||||||   ||||||
                                GATGAGTCC   AGCGAC
                                    ___
GAM2940  LOC134121 3'  TTACCCAAGTTTGTTG      67331         CGA
                                TTACTCAGG   TTGTTG
                                |||||||||   ||||||
                                AATGGGTTC   AACAAC
                                     A__
GAM2940  LOC144079 5'  CTACTCAGGAATTGTTG     67332          C
                                TTACTCAGG GATTGTTG
                                |||||||||  ||||||||
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                                GATGAGTCC TTAACAAC
                                        _
GAM2940  LOC148764 5'  TCACTCAGTGACAGGTTG    67333        GC   T_
                                TTACTCAG  GAT  GTTG
                                ||||||||  |||  ||||
                                AGTGAGTC  CTG  CAAC
                                    A_   TC
GAM2940  LOC150094 3'  TCACTCAGGTGCCCGTTG    67334         CGA
                                TTACTCAGG   TTGTTG
                                |||||||||   ||||||
                                AGTGAGTCC   GGCAAC
                                     ACG
GAM2940  LOC253017 3'  TTACTCAGTGTATATACTGTTG 67335        GCG____
                                TTACTCAG      ATTGTTG
                                ||||||||      |||||||
                                AATGAGTC      TGACAAC
                                    ACATATA
GAM2940  LOC253890 3'  TTACCCAGGGAGTTG       67336         C  TT
                                TTACTCAGG GA  GTTG
                                ||||||||| ||  ||||
                                AATGGGTCC CT  CAAC
                                        _ __
GAM2940  LOC254268 3'  TCACCAACGATTGTTG      67337       CA
                                TTACT  GGCGATTGTTG
                                |||||  ||||||||||
                                AGTGG  TTGCTAACAAC
                                       __
GAM2940  LOC256848 5'  TTACCCAGGCTCCCCTG     67338          GA  G
                                TTACTCAGGC  TT TTG
                                ||||||||||  || |||
                                AATGGGTCCG  GG GAC
                                     A_  G
GAM2940  LOC51320  3'  TCACTCAGCCAAGTTG      67339         G   TT
                                TTACTCAG CGA  GTTG
                                |||||||| |||  ||||
                                AGTGAGTC GTT  CAAC
                                    G  __
GAM2940  LOC90906  3'  TTACCCAGGCCGAGATTG    67340          ___
                                TTACTCAGGC   GATTG
                                |||||||||   |||||
                                AATGGGTCCG   CTAAC
                                     GCT
GAM2940  LOC92104  3'  TTACTCTAGCAATTGTTG    67341       A
                                TTACTC GGCGATTGTTG
                                |||||| ||||||||||
                                AATGAG TCGTTAACAAC
                                   A
GAM2941  IDS       3'  AAGAAACATGGATTACAT    67344         TA
                                AAGAAACAT  GATTATAT
                                |||||||||  ||||||||
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                                TTCTTTGTA  CTAATGTA
                                     C_
GAM2941  SNAI2    3'  AAGAAACATTGATTTCAC    67345         A   A
                                AAGAAACATT GATT TAT
                                |||||||||| |||| |||
                                TTCTTTGTAA CTAA GTG
                                      _   A
GAM2941  CGGBP1   3'  AAGAAACATTAATACCAAA   67346          GATT
                                AAGAAACATTA   ATATTAAA
                                ||||||||||    ||||||||
                                TTCTTTGTAAT   TATGGTTT
                                      ____
GAM2941  KIAA1328 3'  GAAGACATTAGATTATATACAA 67347    _          _
            AT                   GAA ACATTAGATTATAT TAAAT
                                ||| |||||||||||||| |||||
                                CTT TGTAATCTAATATA GTTTA
                                  C          T
GAM2941  MGC2488  3'  AAGAAATATTAGATTCCATT   67348      C      A
                                AAGAAA ATTAGATT TATT
                                |||||| |||||||| ||||
                                TTCTTT TAATCTAA GTAA
                                   A       G
GAM2941  NSG-X    5'  AAGAAACATTAGATATA     67349           T
                                AAGAAACATTAGAT ATA
                                |||||||||||||| |||
                                TTCTTTGTAATCTA TAT
                                      _
GAM2941  SYTL2    5'  AAAACATTAGACATTAA     67350          TAT
                                GAAACATTAGAT   ATTAA
                                ||||||||||||   |||||
                                TTTTGTAATCTG   TAATT
                                      ___
GAM2941  LOC121457 3'  AAAAAACATTAAAAATATTAA  67351          TT
                                AAGAAACATTAGA  ATATTAA
                                ||||||||||||  |||||||
                                TTTTTTGTAATTT  TATAATT
                                       T_
GAM2941  LOC254820 3'  GAAACATTAAACATTAAAT   67352          TAT
                                GAAACATTAGAT   ATTAAAT
                                ||||||||||||   |||||||
                                CTTTGTAATTTG   TAATTTA
                                      ____
GAM2942  APP      3'  TATCAAAGACCCAAAGAT    67355         A  TAT
                                TATCAAAGA CCT   GAT
                                ||||||||| |||   |||
                                ATAGTTTCT GGG   CTA
                                      _  TTT
GAM2942  CCND2    3'  TACCAAAGAACGCCAGAT    67356          C  T
                                TATCAAAGAAC TTA GAT
                                |||||||||| ||| |||
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                                ATGGTTTCTTG GGT CTA
                                      C  _
GAM2942 EIF1AY   3' TATCAGAAACCTTATGA    67357      AA
                                TATCA  GAACCTTATGA
                                |||||  ||||||||||
                                ATAGT  TTTGGAATACT
                                   C_
GAM2942 RAD51L1  3' TATCAAATCAGCTTATGAT   67358       GAAC
                                TATCAAA   CTTATGAT
                                |||||||   ||||||||
                                ATAGTTT   GAATACTA
                                    AGTC
GAM2942 RASGRP1  3' TATCAAAAAACTTTACAAT   67359          C  TG
                                TATCAAAGAAC TTA  AT
                                |||||||||| |||  ||
                                ATAGTTTTTTG AAT  TA
                                      A  GT
GAM2942 RDS      3' TCAAAGAATCTCCTTTGAT   67360        ___   A
                                TCAAAGAA  CCTT TGAT
                                ||||||||  |||| ||||
                                AGTTTCTT  GGAA ACTA
                                    AGA   _
GAM2942 ALK7     3' TACCAAAGAACACTTTTG    67361         _  A
                                TATCAAAGAAC CTT TG
                                |||||||||| ||| ||
                                ATGGTTTCTTG GAA AC
                                      T  A
GAM2942 BM-002   3' CATCAAAGACTATGAT     67362        ACC
                                TATCAAAGA  TTATGAT
                                |||||||||  |||||||
                                GTAGTTTCT  GATACTA
                                     ___
GAM2942 CHUK     3' CACCAACTCCTTATGAT     67363       AGAA
                                TATCAA   CCTTATGAT
                                ||||||   |||||||||
                                GTGGTT   GGAATACTA
                                   GA__
GAM2942 FLJ22843 5' TATCAAAGGCTACCCATGAT  67364        A__   T
                                TATCAAAG  ACCT ATGAT
                                |||||||   |||| |||||
                                ATAGTTTC  TGGG TACTA
                                    CGA   _
GAM2942 HIF1AN   3' CATCAGAGAACCCCAGA     67365      A       T
                                TATCA AGAACCTTA GA
                                ||||| ||||||||| ||
                                GTAGT TCTTGGGGT CT
                                   C       _
GAM2942 KIAA1463 3' TATCAAAGCAACCCACAGA   67366        _    TAT
                                TATCAAAG AACCT   GA
                                |||||||| |||||   ||
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                                ATAGTTTC TTGGG  CT
                                     G    TGT
GAM2942 NUDT11   3' ATCAAAGAACCTTCAGTGAT  67367          A__
                                ATCAAAGAACCTT  TGAT
                                |||||||||||||  ||||
                                TAGTTTCTTGGAA  ACTA
                                      GTC
GAM2942 ZIM3     5' TATCAAAAGCCCCACCTGAT  67368       AA  TA_
                                TATCAAAG CCT  TGAT
                                ||||||||  |||  ||||
                                ATAGTTTT GGG  ACTA
                                     CG  TGG
GAM2942 LOC159089 5' CACCATACCTTATGAT     67369      AAGA
                                TATCA   ACCTTATGAT
                                |||||   ||||||||||
                                GTGGT   TGGAATACTA
                                   A___
GAM2943 CDH11    5' GCTGCGAGCGGCCCCCGC    67372    CA_ A
                                GC  GA GCGGCCCTCGC
                                ||  || ||||||||||
                                CG  CT CGCCGGGGGCG
                                 ACG _
GAM2943 CELSR2   3' AGCCAGAGGCTGGCCTCACAAA 67373       A _   C
                                AGCCAGA GC GGCC TCGCAGA
                                ||||||| || |||| |||||||
                                TCGGTCT CG CCGG AGTGTTT
                                    C A   _
GAM2943 CHRNA2   5' AGCCAGAACGGCTTCATGCAG  67374       G   CC __
                                AGCCAGAA CGGC  TC  GCAG
                                |||||||| ||||  ||  ||||
                                TCGGTCTT GCCG  AG  CGTC
                                    _   A_  TA
GAM2943 EXTL3    3' GCCAGGGGCGGCCCACAG    67375      AA     TC
                                GCCAG  GCGGCCC  GCAG
                                |||||  |||||||  ||||
                                CGGTC  CGCCGGG  TGTC
                                   CC      __
GAM2943 FBXO7    5' CCGGAAGCGGCGACGGGGACG  67376    A      CCT  CA
                                CC GAAGCGGC  CG  GACG
                                || ||||||||  ||  ||||
                                GG CTTCGCCG  GC  CTGC
                                 C       CT_  CC
GAM2943 KCNK4    3' GCCAGAGGTGCCCCCAC     67377       A CG
                                GCCAGA G  GCCCTCGC
                                ||||||  |  ||||||||
                                CGGTCT C  CGGGGGTG
                                   _ CA
GAM2943 MAPK8IP1 3' CCAGAAGCCCCGCAGA     67378       AGC    T
                                CCAGA   GGCCC CGCAGA
                                |||||   ||||| ||||||
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                                GGTCT   TCGGG GCGTCT
                                  ___    _
GAM2943  NPAS2    5'  GCCGGAGCGGCCCCGC     67379     A  A      T
                                GCC GA GCGGCCC CGC
                                ||| || ||||||| |||
                                CGG CT CGCCGGG GCG
                                  C  _      _
GAM2943  PIM2     5'  GCCCGGAAGCGCCCGCAGACG  67380     A_     G   TC
                                GCC  GAAGCG CCC  GCAGACG
                                |||  |||||| |||  |||||||
                                CGG  CTTCGC GGG  CGTCTGC
                                  GC     _  __
GAM2943  SLC6A8   5'  AGTCAGAAGCAGTCCACG    67381    C       C  T
                                AG CAGAAGCGG CC CG
                                || |||||||| || ||
                                TC GTCTTCGTC GG GC
                                 A        A  T
GAM2943  SLC7A5   3'  GCCAGAAGGGGCTGCCGGGC   67382        C   __  TC
                                GCCAGAAG GGC  CC  GC
                                |||||||| |||  ||  ||
                                CGGTCTTC CCG  GG  CG
                                     C   AC  CC
GAM2943  STAT4    5'  AGTCAGAAGCGCCCCTCACAG  67383    C       G
                                AG CAGAAGCG CCCTCGCAG
                                || |||||||| |||||||||
                                TC GTCTTCGC GGGAGTGTC
                                 A       G
GAM2943  TLX1     5'  GCCAGAAGCCGAGGACAGA   67384         ___  CCCTC
                                GCCAGAAGC   GG    GCAGA
                                |||||||||   ||    |||||
                                CGGTCTTCG   CC    TGTCT
                                     GCT  _____
GAM2943  ZNF278   5'  AGCGAGAAGCGGGGCGCAGCAG 67385     C       CCCTC_
           ACG                    AGC AGAAGCGG     GCAGACG
                                |||  ||||||||     |||||||
                                TCG TCTTCGCC     CGTCTGC
                                  C       CCGCGT
GAM2943  ZNF278   5'  AGCGAGAAGCGGGGCGCAGCAG 67385     C       CCCTC_
           ACG                    AGC AGAAGCGG     GCAGACG
                                |||  ||||||||     |||||||
                                TCG TCTTCGCC     CGTCTGC
                                  C       CCGCGT
GAM2943  ZNF278   5'  AGCGAGAAGCGGGGCGCAGCAG 67385     C       CCCTC_
           ACG                    AGC AGAAGCGG     GCAGACG
                                |||  ||||||||     |||||||
                                TCG TCTTCGCC     CGTCTGC
                                  C       CCGCGT
GAM2943  ZNF278   5'  AGCGAGAAGCGGGGCGCAGCAG 67385     C       CCCTC_
           ACG                    AGC AGAAGCGG     GCAGACG
                                |||  ||||||||     |||||||
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                                TCG TCTTCGCC     CGTCTGC
                                  C       CCGCGT
GAM2943 BET1     5' AGCTAGGGGCGACCCGGACCGC 67386     C  AA      ___
                                AGC AG  GCGGCCC   TCGC
                                ||| ||  |||||||   ||||
                                TCG TC  CGCTGGG   GGCG
                                  A  CC      CCT
GAM2943 KIAA0450 5' GCCAGAGGGGCCCTCACA    67387       A C
                                GCCAGA G GGCCCTCGCA
                                |||||| | ||||||||||
                                CGGTCT C CCGGGAGTGT
                                    _ C
GAM2943 KIAA1530 5' AGCAGGGGCGGCCCTAAC    67388     C  AA       C
                                AGC AG  GCGGCCCT GC
                                ||| ||  |||||||| ||
                                TCG TC  CGCCGGGA TG
                                  _  CC       T
GAM2943 KIAA1656 3' GCCGCAGGCGGCCCCTCTGCAG 67389     AGAA     _ _   A
              GCG                   GCC    GCGGCCC TC GCAG CG
                                ||||    ||||||| || |||| ||
                                CGG    CGCCGGG AG CGTC GC
                                  CGTC      G  A    C
GAM2943 KIAA1813 5' GCCAGCGGCCTCGCAGC     67390      GAA     C     A
                                GCCA   GCGGCC TCGCAG C
                                ||||   |||||| |||||| |
                                CGGT   CGCCGG AGCGTC G
                                  ____     _     C
GAM2943 LAP3     5' AGGCAGGGCAGCCCTTGC     67391     C   AA       C
                                AG CAG  GCGGCCCT GC
                                || |||  |||||||| ||
                                TC GTC  CGTCGGGA CG
                                 C  C_       A
GAM2943 MGC14425 5' GCCCGCACCCGGCTCTCGCAGA 67392     AGAAG_   C
              CG                    GCC      CGGC CTCGCAGACG
                                |||      |||| ||||||||||
                                CGG      GCCG GAGCGTCTGC
                                  GCGTGG    A
GAM2943 MGC32043 3' GCCAGAAATGGCTCTCATAG   67393        C   C    C
                                GCCAGAAG GGC CTCG AG
                                |||||||| ||| |||| ||
                                CGGTCTTT CCG GAGT TC
                                     A   A    A
GAM2943 NBL1     5' GCGGGGGGCGGCCCCGCGACG  67394    CAGAA      T   A
                                GC     GCGGCCC CGC GACG
                                ||     ||||||| ||| ||||
                                CG     CGCCGGG GCG CTGC
                                 CCCCC      _  _
GAM2943 ODZ2     3' GACGCTGGCCCTCGCGGA     67395     A  _       A
                                GA GC GGCCCTCGC GA
                                || || ||||||||| ||
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                                CT CG CCGGGAGCG CT
                                 G A       C
GAM2943 ZNF37A   5' GCCCGAAGCGGCTCCCGCGACG 67396    A      C    A
                                GCC GAAGCGGC CTCGC GACG
                                ||| |||||||| ||||| ||||
                                CGG CTTCGCCG GGGCG CTGC
                                  G       A    _
GAM2943 LOC149566 5' AACCAGAAGTATCGTAGA    67397        CGGCCC   C
                                AGCCAGAAG     TCG AGA
                                |||||||||     ||| |||
                                TTGGTCTTC     AGC TCT
                                      AT____   A
GAM2943 LOC255147 3' AGCTTGGAGCGGCCCCCGCAA 67398    CAGA
                                AGC    AGCGGCCCTCGCAG
                                |||    ||||||||||||||
                                TCG    TCGCCGGGGGCGTT
                                  AACC
GAM2943 LOC257302 5' ACCAGAAGTGGCTTTCTCAG   67399       C   CC  G
                                GCCAGAAG GGC  TC CAG
                                |||||||| |||  || |||
                                TGGTCTTC CCG  AG GTC
                                     A   AA  A
GAM2944 MAP1B    3' GGGTGGGAGGTATCATTA    67402    A   C  ACC  CG
                                GG GTGG GA   GG  TCATTA
                                || |||| ||   ||  ||||||
                                CC CACC CT   CC  AGTAAT
                                 _   _ ____  AT
GAM2944 MAP1B    3' GGGTGGGAGGTATCATTA    67402    A   C  ACC  CG
                                GG GTGG GA   GG  TCATTA
                                || |||| ||   ||  ||||||
                                CC CACC CT   CC  AGTAAT
                                 _   _ ____  AT
GAM2944 HEAB     5' GGAGGGGCGGCTGTTGTCATTA 67403     T   AACCGGC
              T                  GGAG GGCG      GTCATTAT
                                 |||| ||||      ||||||||
                                 CCTC CCGC      CAGTAATA
                                   C    CGACAA_
GAM2944 KIAA0537  3' GGAGTGGCATCTTGTCATT   67404        AACCGGC
                                GGAGTGGCG      GTCATT
                                |||||||||      ||||||
                                CCTCACCGT      CAGTAA
                                     AGAA___
GAM2944 MGC35558  3' GGAGTGGCGAGTGGCCCAC   67405         ACC   G
                                GGAGTGGCGA   GGC TCAT
                                ||||||||||   ||| ||||
                                CCTCACCGCT   CCG GGTG
                                      CA_   _
GAM2945 FLJ30213  3' TCCCTGACTGCTGCCCACTCCT 67408        GA  ACGA  A
                                TCCCTGAC  CT    AC CCT
                                ||||||||  ||    || |||
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                                AGGGACTG  GA    TG GGA
                                    AC  CGGG  A
GAM2945  MY014    5'  TCCCCGACGTCGGGCATCTAA  67409        ACTA  AA  C
                                TCCCTGACG    CG  CA CTAA
                                |||||||||    ||  || ||||
                                AGGGGCTGC    GC  GT GATT
                                     A___  CC  A
GAM2945  NEUGRIN  5'  CCCGGGGAGCTGAACACCT   67410     AC  _  AC
                                CCTG  GA CT  GAACACCT
                                ||||  || ||  ||||||||
                                GGGC  CT GA  CTTGTGGA
                                  CC  C  __
GAM2945  PTPRT    3'  CCTTTGACCCAAAGAACACCT  67411    GAC    AC__
                                CCT   GACT   GAACACCT
                                |||   ||||   ||||||||
                                GGA   CTGG   CTTGTGGA
                                  AA_   GTTT
GAM2945  TMG3     3'  TCTCTGACAACTGACTTCCTAA 67412    C       AC  ACA
                                TC CTGACGACT  GA   CCTAA
                                || |||||||||  ||   |||||
                                AG GACTGTTGA  CT   GGATT
                                 A        __  GAA
GAM2945  TU12B1-TY 3'  CCCTGATGGCGAAAACACCTA  67413       ___   CTAC
                                CCCTGA   CGA    GAACACCTA
                                ||||||   |||    |||||||||
                                GGGACT   GCT    TTTGTGGAT
                                   ACC   ____
GAM2945  LOC154789 5'  CCTGACAAAACTGGACATCT   67414        CT  GA_   C
                                CCTGACGA  AC   ACA CT
                                ||||||||  ||   ||| ||
                                GGACTGTT  TG   TGT GA
                                     T_  ACC   A
GAM2945  LOC203429 3'  TCCCTGACACTAGCCT      67415        G    CGAACA
                                TCCCTGAC ACTA     CCT
                                |||||||| ||||     |||
                                AGGGACTG TGAT     GGA
                                     _    C_____
GAM2946  ABCA10   5'  CCAGTTACTCTTCAGAGAGT   67418     A__  A  _
                                CCG   GC CT CAGAGAGT
                                |||   || || ||||||||
                                GGT   TG GA GTCTCTCA
                                  CAA  A  A
GAM2946  HSPC065  3'  TACCCCACTGGGCATGGTACTC 67419      CGA  A_________  AGA
            TCTGA                 CCTAC   GC       CTC   GA
                                |||||   ||       |||   ||
                                GGGTG   CG       GAG   CT
                                  ACC  TACCAIIIT   AGA
GAM2946  MGC2827  3'  TACATTTCACATATTCAGAGAG 67420     CGAG   ____
            T                   TAC    CAC    TCAGAGAGT
                                |||    |||    |||||||||
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                                ATG   GTG   AGTCTCTCA
                                  TAAA  TATA
GAM2946 P66     3' CTCCTGGCACTCAGAGGGT   67421    A GA       A
                                CT CC  GCACTCAGAG GT
                                || ||  |||||||||| ||
                                GA GG  CGTGAGTCTC CA
                                 _ AC        C
GAM2946 SRCRB4D  3' CCAGCCGAGCACCATCTGAGT 67422    TA      T GA_
                                CC  CCGAGCAC CA   GAGT
                                ||  |||||||| ||   ||||
                                GG  GGCTCGTG GT   CTCA
                                 TC       _ AGA
GAM2946 TU12B1-TY 3' CCCATAGCACTCAGAGAGT   67423     TACCG
                                CCC    AGCACTCAGAGAGT
                                |||    ||||||||||||||
                                GGG    TCGTGAGTCTCTCA
                                  TA___
GAM2946 LOC144571 3' ACTCTGTCAAACCTCAGAGAGT 67424    C  AC    A
                                AC CT  CGAGC CTCAGAGAGT
                                || ||  ||||| ||||||||||
                                TG GA  GTTTG GAGTCTCTCA
                                 A  CA    _
GAM2946 LOC148089 3' CCCTGCTCTTCAGAGAG     67425      ACCGA  A  _
                                CCCT    GC CT CAGAGAG
                                ||||    || || |||||||
                                GGGA    CG GA GTCTCTC
                                  _____  A  A
GAM2946 LOC256112 3' TACCCTACTGAGACAAGGTACT 67426    C   _ A_________   AGA
            CTCTGAG                TAC GAG C       CTC   GAG
                                ||| ||| |       |||   |||
                                ATG CTC G       GAG   CTC
                                  A   T TTCCAIIIT   AGA
GAM2946 LOC51339  3' TACCTTGCCGGATGCTCAGAAA 67427     CTA   AGCA
            GT                  TACC   CCG    CTCAGAGAGT
                                ||||   |||   ||||||||||
                                ATGG   GGC    GAGTCTTTCA
                                  AAC   CTAC
GAM2946 LOC90784  5' ACCCTGCCGGGTAACTCAGAG  67428      A   AGC_
                                ACCCT CCG    ACTCAGAG
                                ||||| |||    ||||||||
                                TGGGA GGC    TGAGTCTC
                                  C   CCAT
GAM2947 OTP     3'  TCCCTAACATTGTGCTGTCCCT 67431         AT_  GAACA
                                TCCCTAACG   TGC    CCT
                                |||||||||   |||    |||
                                AGGGATTGT   ACG    GGA
                                     AAC   ACAG_
GAM2947 PEX13    3' CTAGCAGCAAAACACCTGA   67432     A  ATT    _
                                CTA CG   GCGAA CACCTGA
                                ||| ||   ||||| |||||||
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                                GAT GT   CGTTT GTGGACT
                                  C ___    T
GAM2947 C21orf25 3' CCTAAGACTGACACCTG    67433      C    CGA
                                CCTAA GATTG   ACACCTG
                                ||||| |||||   |||||||
                                GGATT CTGAC   TGTGGAC
                                   _    ____
GAM2947 ITPK1    3' TCCCCAACGGTGGACCACCTG 67434        AT  C  A
                                TCCCTAACG  TG GA CACCTG
                                |||||||||  || || ||||||
                                AGGGGTTGC  AC CT GTGGAC
                                     C_ _  G
GAM2947 MGC2941  3' CCCCTAACCGCCGGGCATCTG 67435       GAT  _ AA  C
                                TCCCTAAC   TGC G  CA CTG
                                ||||||||   ||| |  || |||
                                GGGGATTG   GCG C  GT GAC
                                     ___  G CC  A
GAM2947 NEUGRIN  5' TCCCGGGGAGCTGAACACCTGA 67436     TAAC  TT  _
                                TCCC   GA  GC GAACACCTGA
                                ||||   ||  || ||||||||||
                                AGGG   CT  CG CTTGTGGACT
                                  CCC_ __  A
GAM2947 PTPRT    3' CCTTTGACCCAAAGAACACCTG 67437    AAC   GC__
          A                      CCT   GATT   GAACACCTGA
                                |||   ||||   ||||||||||
                                GGA   CTGG   CTTGTGGACT
                                  AA_   GTTT
GAM2947 LOC152185 5' TCCCCAACCGGGCGCCTG    67438       GATT   AACA
                                TCCCTAAC   GCG   CCTG
                                ||||||||   |||   ||||
                                AGGGGTTG   CGC   GGAC
                                     GCC_  ____
GAM2948 IRTA2    3' TTCTCTTGCTCCACGTCTAT   67441    A      TTCA
                                TTC CTTGCTCT   CTAT
                                ||| ||||||||   ||||
                                AAG GAACGAGG   GATA
                                  A       TGCA
GAM2948 SPG4     3' TCCACTTGCTTATAATTATCC  67442         CTTTCAC
                                TTCACTTGCT      TATCC
                                ||||||||||      |||||
                                AGGTGAACGA      ATAGG
                                     ATATTA_
GAM2948 SYT4     5' TTCACTTGCCTGGATCTCA   67443         C___
                                TTCACTTGCT   TTTCA
                                ||||||||||   |||||
                                AAGTGAACGG   AGAGT
                                     ACCT
GAM2948 XDH      3' TTCACTTGTCTTCCAAATCCCA 67444        C      CT
                                TTCACTTG TCTTTCA  ATCCCA
                                |||||||| |||||||  ||||||
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                                AAGTGAAC AGAAGGT  TAGGGT
                                    _      T_
GAM2948 XDH      3'  TTCACTTGTCTTCCAAATCCCA 67444        C      CT
                                TTCACTTG TCTTTCA  ATCCCA
                                |||||||| |||||||  ||||||
                                AAGTGAAC AGAAGGT  TAGGGT
                                    _      T_
GAM2948 ZNF9     3'  TTCAGTTGCTCTTTCCATC   67445     C        AC
                                TTCA TTGCTCTTTC  TATC
                                |||| ||||||||||  ||||
                                AAGT AACGAGAAAG  GTAG
                                  C        __
GAM2948 FLJ13984 3'  TTCACTTGTTTTTTCCTA    67446        CTC    A
                                TTCACTTG   TTTC CTA
                                ||||||||   |||| |||
                                AAGTGAAC   AAAG GAT
                                     AAA   _
GAM2948 FLJ20005 5'  TTCACTTGTTTCCTAT      67447        CTC    A
                                TTCACTTG   TTTC CTAT
                                ||||||||   |||| ||||
                                AAGTGAAC   AAAG GATA
                                     ___   _
GAM2948 KDELR2   3'  TTCACTTTTGGAACTATCCCA  67448        GCTCTTTC
                                TTCACTT       ACTATCCCA
                                |||||||       |||||||||
                                AAGTGAA       TGATAGGGT
                                    AACCT___
GAM2948 KIAA1582 5'  TTCACTTGCTGTAGTTCCA   67449         C___
                                TTCACTTGCT    TTTCA
                                ||||||||||    |||||
                                AAGTGAACGA    AAGGT
                                      CATC
GAM2948 KIAA1627 5'  CCGGCTTTTCACTATCCC    67450    T   C
                                CT GCT TTTCACTATCCC
                                || ||| ||||||||||||
                                GG CGA AAAGTGATAGGG
                                 C  _
GAM2948 MAIL     3'  TTCACTTGTTCTTTTCTAT    67451        C    CA
                                TTCACTTG TCTTT  CTAT
                                |||||||| |||||  ||||
                                AAGTGAAC AGAAA  GATA
                                     A    A_
GAM2948 MGC11287 3'  TTCACTTGTCTTCTCTGTCTCA 67452        C    CA  A  C
                                TTCACTTG TCTTT  CT TC CA
                                |||||||| |||||  || || ||
                                AAGTGAAC AGAAG  GA AG GT
                                     _    A_  C  A
GAM2948 MGC14839 3'  ACCTGCTCTTTCTGCACT    67453          ___
                                ACTTGCTCTTTC   ACT
                                ||||||||||||   |||
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                                TGGACGAGAAAG  TGA
                                      ACG
GAM2948 p25      3' TTCCTTGCTCTTTATTTCC  67454    A       CACTA
                                TTC CTTGCTCTTT    TCC
                                ||| ||||||||||    |||
                                AAG GAACGAGAAA    AGG
                                  _       TAA__
GAM2948 SNX16    5' CTTAGGAATTCACTATCTCA  67455    CTCT       C
                                CTTG   TTCACTATC CA
                                ||||   ||||||||| ||
                                GAAT   AAGTGATAG GT
                                  CCTT       A
GAM2948 STAM2    3' TTCACCTGCTATTATTCCA  67456        C___
                                TTCACTTGCT   TTTCA
                                ||||||||||   |||||
                                AAGTGGACGA   AAGGT
                                      TAAT
GAM2948 WWP1     5' TTGTTCTTTCACTCTTTCCA  67457    C       ATC_
                                TTG TCTTTCACT   CCA
                                ||| |||||||||   |||
                                AAC AGAAAGTGA   GGT
                                  A       GAAA
GAM2948 LOC132617 3' CTTGCTTTCACTGTTCC    67458      CT     A_
                                CTTGCT  TTCACT  TCC
                                ||||||  ||||||  |||
                                GAACGA  AAGTGA  AGG
                                   __     CA
GAM2948 LOC145824 5' TTCTCTTGCTCTTTCAACT   67459    A         _
                                TTC CTTGCTCTTTCA CT
                                ||| ||||||||||| ||
                                AAG GAACGAGAAAGT GA
                                  A          T
GAM2948 LOC148443 3' TTGCTCTCTCAATGTCTCA   67460         CTA  C
                                TTGCTCTTTCA   TC CA
                                ||||||||||   || ||
                                AACGAGAGAGT   AG GT
                                      TAC  A
GAM2948 LOC169166 3' TCCCCAAGTTCTTTCACTGTC  67461    A  TGC_      A
                                TTC CT    TCTTTCACT TC
                                ||| ||    |||||||| ||
                                AGG GG    AGAAAGTGA AG
                                  _  TTCA       C
GAM2948 LOC196758 3' TTCACCTGCTCTTTCTCCA   67462           A
                                TTCACTTGCTCTTTC CTA
                                |||||||||||||| |||
                                AAGTGGACGAGAAAG GGT
                                       A
GAM2948 LOC55862  5' CTTCTCTTTTACTATCCCA   67463    G     C
                                CTT CTCTTT ACTATCCCA
                                ||| |||||| |||||||||
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                                GAA GAGAAA TGATAGGGT
                                  _     A
GAM2948 LOC90495 5' TTCACTTGTCTTTAACT     67464        C    C
                                TTCACTTG TCTTT ACT
                                |||||||| ||||| |||
                                AAGTGAAC AGAAA TGA
                                     _    T
GAM2948 LOC91818 5' CTCACTTGTTCTTTCCATAC  67465        C     AC
                                TTCACTTG TCTTTC  TAT
                                |||||||| ||||||  |||
                                GAGTGAAC AGAAAG  ATG
                                     A     GT
GAM2949 CELSR1   3' GCGAACACTGGGGACCCAG   67468        C  AAT  AG
                                GCGAACAC TG   GA  CGG
                                |||||||| ||   ||  |||
                                CGCTTGTG AC   CT  GTC
                                     _ CC_  GG
GAM2949 GNB3     3' GAACACCTGAATGAGATGG   67469           AGC
                                GAACACCTGAATGA   GG
                                ||||||||||||||   ||
                                CTTGTGGACTTACT   CC
                                         CTA
GAM2949 HS2ST1   3' GAATCAACTGAATGGAGTGG  67470    _ C      A  C
                                GAA CA CTGAATG AG GG
                                ||| || ||||||| || ||
                                CTT GT GACTTAC TC CC
                                  A  T      C  A
GAM2949 ID1      5' GCGAAAAAAATGAGGTGGAAG 67471      CACCT     AGC
                                GCGAA    GAATGA   GGAAG
                                |||||    ||||||   |||||
                                CGCTT    TTTACT   CCTTC
                                   TT___     CCA
GAM2949 POLR2E   5' GCGAATGCCTGAATGCAG    67472      CA      GAA
                                GCGAA  CCTGAAT   GCGG
                                |||||  |||||||   ||||
                                CGCTT  GGACTTA   CGTC
                                   AC      ___
GAM2949 USH3A    5' GCTGACACCTGAATGTTGAGAA 67473    GA         AAGC
             G                   GC  ACACCTGAATG    GGAAG
                                 ||  ||||||||||    |||||
                                 CG  TGTGGACTTAC    TCTTC
                                  AC         AAC_
GAM2949 CNNM1    5' GCGAACACACTGAGTAGGG    67474        _   ATGA  C
                                GCGAACAC CTGA    AG GG
                                |||||||| ||||    || ||
                                CGCTTGTG GACT    TC CC
                                     T   CA__  _
GAM2949 DKFZp434E0519 3' GCAATATCTGAATAAAAGGA   67475      ACAC        C
                                GCGA    CTGAATGAAG GGA
                                ||||    |||||||||| |||
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                                CGTT   GACTTATTTT CCT
                                  ATA_       _
GAM2949  DKFZP434F0318 3'  GCTAGCATCTGGGTGAAACAG  67476    GAA  C   AA
                                GC   CA CTG  TGAAGCGG
                                ||   || |||  ||||||||
                                CG   GT GAC  ACTTTGTC
                                 ATC  A   CC
GAM2949  DKFZP434K1772 5'  ACGGACATAGAAGCGGAA    67477     A   CCTGAAT
                                GCG ACA      GAAGCGGAA
                                ||| |||      |||||||||
                                TGC TGT      CTTCGCCTT
                                  C   AT_____
GAM2949  FLJ23132  3'  GAAACAGAGTGAAGCGG     67478     C  CT  A
                                GAA AC  GA TGAAGCGG
                                ||| ||  || ||||||||
                                CTT TG  CT ACTTCGCC
                                  _  T_  C
GAM2949  KIAA0429  5'  GCAACACCTGGTCTGGGA    67479    G      AA_  AAGC
                                GC AACACCTG   TG   GGA
                                || ||||||||   ||   |||
                                CG TTGTGGAC   AC   CCT
                                 _       CAG  _____
GAM2949  KIAA0980  5'  GCAGCACCTGAATATTTAGAAG 67480     AA        AAGC
                                GCG  CACCTGAATG   GGAAG
                                |||  ||||||||||   |||||
                                CGT  GTGGACTTAT   TCTTC
                                  C_        AAA_
GAM2949  SERPING1  3'  GCGGACACCTGAGGCAGGA   67481     A      ATGAA  _
                                GCG ACACCTGA    GC GGA
                                ||| ||||||||    || |||
                                CGC TGTGGACT    CG CCT
                                  C       C_____  T
GAM2949  TReP-132  5'  GCAAACACCTGGGTGAAA    67482          AA
                                GCGAACACCTG  TGAAG
                                ||||||||||  |||||
                                CGTTTGTGGAC  ACTTT
                                       CC
GAM2949  TReP-132  5'  GCAAACACCTGGGTGAAA    67482          AA
                                GCGAACACCTG  TGAAG
                                ||||||||||  |||||
                                CGTTTGTGGAC  ACTTT
                                       CC
GAM2949  TSGA2    5'  GCGACGCGGACGAAGCGG    67483     ACACC  A
                                GCGA    TG ATGAAGCGG
                                ||||    || |||||||||
                                CGCT    GC TGCTTCGCC
                                  GC___  C
GAM2949  LOC148696 5'  GAGTGTCTGAATGAGAGTGGA  67484    ACAC       _  C
                                GA   CTGAATGA AG GGA
                                ||   |||||||| || |||
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                                CT    GACTTACT TC CCT
                                 CACA       C  A
GAM2949  LOC219997 3'  GAACACCTGGATGAGCA     67485          A    A
                                GAACACCTG ATGA GCG
                                ||||||||| |||| |||
                                CTTGTGGAC TACT CGT
                                     C   _
GAM2950  PPEF1     3'  TTAGTAGTTTTCTCTTGTACCA 67488       G_ _________  TTTGAT
           TCAAG                   TAGTTT  TC       CC     G
                                ||||||  ||       ||     |
                                ATCAAA  AG       GG     C
                                   AG  AACAIIIT  TAGTTT
GAM2950  ODZ2      3'  AGTGGTTTGTCCCGCAGCTGGT 67489     A        TTTGA
                                AGT GTTTGTCCC     TGGT
                                ||| |||||||||     ||||
                                TCA CAAACAGGG     ACCA
                                  C        CGTCG
GAM2950  PRO0611   3'  ATAGTTTGTTTTTTTTGTGGT  67490         CCC_    A
                                GTAGTTTGT    TTTG TGGT
                                |||||||||    |||| ||||
                                TATCAAACA    AAAC ACCA
                                     AAAA    _
GAM2950  RASSF2    3'  TTAGTAGTTTGCTTTGTACCAT 67491         C_________  TTTGAT
           CAAG                    GTAGTTTGT        CC     G
                                |||||||||        ||     |
                                CATCAAACG        GG     C
                                     AAACAIIIT  TAGTTT
GAM2950  LOC157292 3'  TTAGTAGTTTGTTGCTTT     67492           CC
                                TTAGTAGTTTGT  CTTT
                                ||||||||||||  ||||
                                AATCATCAAACA  GAAA
                                      AC
GAM2950  LOC158288 5'  TAGTTTGTCTCTAATAGT     67493          CC
                                TAGTTTGTC  TTTGATGGT
                                |||||||||  |||||||||
                                ATCAAACAG  AGATTATCA
                                     __
GAM2950  LOC219940 3'  GTTGGTTTGTCTTTAATG     67494    A_      CC
                                GT  GTTTGTC  TTTGATG
                                ||  |||||||  |||||||
                                CA  CAAACAG  AAATTAC
                                 AC      __
GAM2950  LOC254085 5'  GCAGTTTTTTTTTGGTGGT    67495        GTCCC    A
                                GTAGTTT     TTTG TGGT
                                |||||||     |||| ||||
                                CGTCAAA     AAAC ACCA
                                    AAA__    C
GAM2951  BCL7A     3'  GAGAGGAACCGCATCA      67498          ACAGAA
                                GAGAGGAACC      CATCA
                                ||||||||||      |||||
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                                CTCTCCTTGG     GTAGT
                                      C_____
GAM2951  CTF1    3'  TGAAGGAAAGGAGGACATCAAA 67499     G    CCAC  A
                                TGA AGGAA   AG ACATCAAA
                                ||| |||||   || ||||||||
                                ACT TCCTT   TC TGTAGTTT
                                  _    TCC_  C
GAM2951  DBY     3'  GAGCCAACAGGACATCAA    67500     GAA  _  A
                                GAG   CCA CAG ACATCAA
                                |||   ||| ||| |||||||
                                CTC   GGT GTC TGTAGTT
                                  ___   T   C
GAM2951  DDX3    3'  GAGCCAACAGGACATCAA    67500     GAA  _  A
                                GAG   CCA CAG ACATCAA
                                |||   ||| ||| |||||||
                                CTC   GGT GTC TGTAGTT
                                  ___   T   C
GAM2951  DMD     3'  TGAGAGGAGTTCAAATATACAT 67501        ACCA   ___
            CAAA                   TGAGAGGA   CAGA   ACATCAAA
                                ||||||||   ||||  ||||||||
                                ACTCTCCT   GTTT   TGTAGTTT
                                     CAA_   ATA
GAM2951  MEF2D   3'  TGAGAGGAAGAAGACAT    67502        CCAC   A
                                TGAGAGGAA   AGA CAT
                                |||||||||   ||| |||
                                ACTCTCCTT   TCT GTA
                                     CT__   _
GAM2951  MGAT1   3'  TGAGAGGAGCCTGTGTGTCAAA 67503        A  ACAGAACA
                                TGAGAGGA CC       TCAAA
                                |||||||| ||       |||||
                                ACTCTCCT GG       AGTTT
                                     C  ACACAC__
GAM2951  MTMR2   3'  TGAGGGGAACCACTGGAA    67504      A       A_
                                TGAG GGAACCAC  GAA
                                |||| ||||||||  |||
                                ACTC CCTTGGTG  CTT
                                  C       AC
GAM2951  OXCT    3'  TGAGAGGAGGTACAGTACA   67505        ACC   A
                                TGAGAGGA   ACAG ACA
                                ||||||||   |||| |||
                                ACTCTCCT   TGTC TGT
                                     CCA   A
GAM2951  SET     3'  TGAGAGAAAAGCATCA      67506        CCAC  AA
                                TGAGAGGAA   AG  CATCA
                                |||||||||   ||  |||||
                                ACTCTCTTT   TC  GTAGT
                                           _____ __
GAM2951  TLL2    5'  GAGAGGAACCGCAGGTTCA   67507         A   AACA
                                GAGAGGAACC CAG   TCA
                                |||||||||| |||   |||
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                                CTCTCCTTGG GTC   AGT
                                      C  CA__
GAM2951  ZYX      3'  TGGGAGGGGCTAGACATCAAA  67508    A   AACCAC  A
                                TG GAGG     AGA CATCAAA
                                || ||||     ||| |||||||
                                AC CTCC     TCT GTAGTTT
                                 C   CCGA__  _
GAM2951  BLR1     5'  TGAGAGGAACCCTAGCTCTC  67509         AC  AACA
                                TGAGAGGAACC  AG   TC
                                ||||||||||  ||   ||
                                ACTCTCCTTGG  TC   AG
                                      GA  GAG_
GAM2951  DEFCAP   5'  TGGGAGGAGCCGCAGAGCA   67510    A    A A   A
                                TG GAGGA CC CAGA CA
                                || ||||| || |||| ||
                                AC CTCCT GG GTCT GT
                                 C    C C   C
GAM2951  DEFCAP   5'  TGGGAGGAGCCGCAGAGCA   67510    A    A A   A
                                TG GAGGA CC CAGA CA
                                || ||||| || |||| ||
                                AC CTCCT GG GTCT GT
                                 C    C C   C
GAM2951  DEFCAP   5'  TGGGAGGAGCCGCAGAGCA   67510    A    A A   A
                                TG GAGGA CC CAGA CA
                                || ||||| || |||| ||
                                AC CTCCT GG GTCT GT
                                 C    C C   C
GAM2951  DEFCAP   5'  TGGGAGGAGCCGCAGAGCA   67510    A    A A   A
                                TG GAGGA CC CAGA CA
                                || ||||| || |||| ||
                                AC CTCCT GG GTCT GT
                                 C    C C   C
GAM2951  DKFZp761G2113 3'  TGAGAGGAACTGAAGCCAGTCA 67511         CAC  AACA
           A                    TGAGAGGAAC   AG   TCAA
                                ||||||||||  ||   ||||
                                ACTCTCCTTG   TC   AGTT
                                      ACT  GGTC
GAM2951  DNAJC8   3'  TGCCAAACACCACAGGGCATCA 67512    AG   A     AA
                                TG  AGG ACCACAG  CATCA
                                ||  ||| |||||||  |||||
                                AC  TTT TGGTGTC  GTAGT
                                 GG   G     CC
GAM2951  FLJ10743 3'  GAGAGGAATCATGAAGCA    67513       C  CA  _
                                GAGAGGAA CA  GAA CA
                                |||||||| ||  ||| ||
                                CTCTCCTT GT  CTT GT
                                     A  A_   C
GAM2951  FLJ11175 3'  TGAGAAGAAGTGGCATCAGA   67514        C___  _
                                TGAGAGGAA    CA CAGA
                                |||||||||    || ||||
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                                ACTCTTCTT   GT GTCT
                                     CACC  A
GAM2951  FLJ11235  3'  TGAGAGGAAACTCCATCAA   67515        CC  AGAA
                                TGAGAGGAA  AC   CATCAA
                                |||||||||  ||   ||||||
                                ACTCTCCTT  TG   GTAGTT
                                     __  AG__
GAM2951  FLJ20445  3'  TGAGAGAACTGCAGAACA   67516       G   CA
                                TGAGAG AAC  CAGAACA
                                ||||||  |||  |||||||
                                ACTCTC TTG  GTCTTGT
                                   _  AC
GAM2951  FLJ22671  3'  GAGGGGCCACACACTCAAA   67517     AA    GA  A
                                GAGG  CCACA  AC TCAAA
                                ||||  |||||  || |||||
                                CTCC  GGTGT  TG AGTTT
                                  CC    G_  _
GAM2951  KIAA0057  3'  GAGAGCTTAGAACATCAA    67518      GAACCAC
                                GAGAG      AGAACATCAA
                                |||||      ||||||||||
                                CTCTC      TCTTGTAGTT
                                   GAA____
GAM2951  KIAA0152  3'  TGGAGGAGCCACAAAACA    67519    A    A
                                TG GAGGA CCACAGAACA
                                || ||||| ||||||||||
                                AC CTCCT GGTGTTTTGT
                                 _    C
GAM2951  KIAA0663  3'  TGAAGGAAACCAACATCAA   67520     A      CAGA
                                TGAG GGAACCA    ACATCAA
                                |||| |||||||    |||||||
                                ACTT CTTTGGT    TGTAGTT
                                  C      _____
GAM2951  MGC1203   3'  TGAAAGGATAGGAGGACATC   67521        ACCAC  A
                                TGAGAGGA     AG ACATC
                                ||||||||     || |||||
                                ACTTTCCT     TC TGTAG
                                     ATCC_  C
GAM2951  MGC15429  5'  TGATGAGGGGCCACAGAACA   67522     _   AA
                                TGA GAGG  CCACAGAACA
                                ||| ||||  ||||||||||
                                ACT CTCC  GGTGTCTTGT
                                  A   CC
GAM2951  OS4       3'  TGAGAGGGACACGAACATCA   67523       AAC   A
                                TGAGAGG   CAC GAACATCA
                                |||||||   ||| ||||||||
                                ACTCTCC   GTG CTTGTAGT
                                     CT_  _
GAM2951  PCDH19    3'  TGAGAGGACTCATACATCA   67524        ACCA  GA
                                TGAGAGGA    CA  ACATCA
                                ||||||||    ||  ||||||
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                                ACTCTCCT   GT  TGTAGT
                                    GA__  A_
GAM2951  UBCE7IP5  5'  TGAGAGGATATCTTCCAAGCAT 67525       A_____  C  AA
           CA                    TGAGAGGA    CCA AG  CATCA
                                |||||||||    ||| ||  |||||
                                ACTCTCCT    GGT TC  GTAGT
                                    ATAGAA  _ __
GAM2951  ZNF297B   3'  GAGAAACAGGACATCAA    67526      ACC   A
                                GAGGA  ACAG ACATCAA
                                |||||  |||| |||||||
                                CTCTT  TGTC TGTAGTT
                                   ___   C
GAM2951  LOC126917 3'  GAGGGAAGAACATCAA     67527     A  ACCAC
                                GAG GGA    AGAACATCAA
                                ||| |||    ||||||||||
                                CTC CCT    TCTTGTAGTT
                                 _  _____
GAM2951  LOC152286 3'  TGAGAGAGTCCATATCAA    67528       AA  CAGAAC
                                TGAGAGG  CCA     ATCAA
                                |||||||  |||     |||||
                                ACTCTCT  GGT     TAGTT
                                    CA  A_____
GAM2951  LOC253019 3'  TGAAGGAAACCAACATCAA   67520     A     CAGA
                                TGAG GGAACCA   ACATCAA
                                |||| |||||||   |||||||
                                ACTT CTTTGGT   TGTAGTT
                                  C     ____
GAM2951  LOC253975 3'  TGAAGGAAACCAACATCAA   67520     A     CAGA
                                TGAG GGAACCA   ACATCAA
                                |||| |||||||   |||||||
                                ACTT CTTTGGT   TGTAGTT
                                  C     ____
GAM2951  LOC63923  3'  TGGGAGGAACCAATTATCAA  67529    A      CAGAAC
                                TG GAGGAACCA     ATCAA
                                || |||||||||     |||||
                                AC CTCCTTGGT     TAGTT
                                 C       TAA___
GAM2951  LOC91064  5'  TGAGAGGAACCCACACAGA   67530         ___
                                TGAGAGGAACC   ACAGA
                                ||||||||||   |||||
                                ACTCTCCTTGG   TGTCT
                                      GTG
GAM2952  CAV1     5'  CGCTGGAGGGGGGCGGTGGCTG 67533     C     A_  TCCAC   C
           G                     CGT GGAGGG  GC     GGC GG
                                |||  ||||||  ||     ||| ||
                                GCG CCTCCC  CG     CCG CC
                                  A     CC  CCA__   A
GAM2952  FGFR1    5'  GTCGCAAGAGCTCCGCGGCCGG 67534      GA       A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
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                                CAGC  TTCTCGAGG GCCGGCC
                                  G_       C
GAM2952  FGFR1    5'  GTCGCAAGAGCTCCGCGGCCGG 67534     GA       A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
                                CAGC  TTCTCGAGG GCCGGCC
                                  G_       C
GAM2952  FGFR1    5'  GTCGCAAGAGCTCCGCGGCCGG 67534     GA       A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
                                CAGC  TTCTCGAGG GCCGGCC
                                  G_       C
GAM2952  FGFR1    5'  GTCGCAAGAGCTCCGCGGCCGG 67534     GA       A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
                                CAGC  TTCTCGAGG GCCGGCC
                                  G_       C
GAM2952  FGFR1    5'  GTCGCAAGAGCTCCGCGGCCGG 67534     GA       A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
                                CAGC  TTCTCGAGG GCCGGCC
                                  G_       C
GAM2952  FGFR1    5'  GTCGCAAGAGCTCCGCGGCCGG 67534     GA       A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
                                CAGC  TTCTCGAGG GCCGGCC
                                  G_       C
GAM2952  MYO3A    3'  CGTCGGGGGGAGGTTTCCCGA  67535      A    C__  A
                                CGTCGG GGGAG   TCC CGG
                                |||||| |||||   ||| |||
                                GCAGCC CCCTC   AGG GCT
                                   _    CAA  _
GAM2952  PPP4C    3'  GTTGGAGGGGGGCAGGGGCCGG  67536    C     A  TCCAC
                                GT GGAGGG GC     GGCCGG
                                || |||||| ||     ||||||
                                CA CCTCCC CG     CCGGCC
                                 A     C  TCC__
GAM2952  SLC23A1  5'  CGTTGGGGAGAGCAGCG     67537     C  A     TCCAC   C
                                CGT GG GGGAGC     GGC G
                                ||| || ||||||     ||| |
                                GCA CC CTCTCG     TCG C
                                  A  C     _____   A
GAM2952  SOX12    3'  ATCGGAGGGGGCTGGCTGCTGG 67538         A   CCACG  C
                                GTCGGAGGG GCT     GC GG
                                |||||||||| |||     || ||
                                TAGCCTCCC CGA     CG CC
                                     C   CCGA_  A
GAM2952  ARF6     5'  CGTCGGAGGAGCCGGGGCCGG  67539         G   CCAC
                                CGTCGGAGG AGCT    GGCCGG
                                ||||||||| ||||    ||||||
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                                GCAGCCTCC TCGG   CCGGCC
                                      _   CC__
GAM2952 ASB16   5' GTGGGGGAGCCCGCGGCTGG  67540   C A    T A   C
                                GT GG GGGAGC CC CGGC GG
                                || || |||||| || |||| ||
                                CA CC CCCTCG GG GCCG CC
                                 _ _    _ C   A
GAM2952 DKFZP434H204 5' CGTTGAAGAGCTCGTGGCTGG 67541    CG   G    CAC  C
                                CGT  GAGG AGCTC   GGC GG
                                |||  |||| |||||   ||| ||
                                GCA  CTTC TCGAG   CCG CC
                                  A_   _    CA_  A
GAM2952 EIF3S8   5' CGCGGAGGTGCTACGGCCG   67542   T    GA  CC
                                CG CGGAGG  GCT  ACGGCCG
                                || ||||||  |||  |||||||
                                GC GCCTCC  CGA  TGCCGGC
                                 _    A_  __
GAM2952 FLJ10315 5' GTCGGAGGCGACGGCGGCCGG 67543       GA  TCCA
                                GTCGGAGG  GC   CGGCCGG
                                ||||||||  ||   |||||||
                                CAGCCTCC  TG   GCCGGCC
                                     GC  CC__
GAM2952 FLJ12442 5' GTCGGAGGGGAGCCAGCTGG  67544        _  TCCA   C
                                GTCGGAGGG AGC   CGGC GG
                                ||||||||| |||   |||| ||
                                CAGCCTCCC TCG   GTCG CC
                                     C  _____   A
GAM2952 FLJ12895 3' CGTCTGGGATTCACGGCCG   67545    GGA   GCTC
                                CGTC  GGGA   CACGGCCG
                                ||||  ||||   ||||||||
                                GCAG  CCCT   GTGCCGGC
                                  A__   AA__
GAM2952 FLJ20297 3' GCGGAGGGAGGGAAAGGCCGG 67546   T      CTCCAC
                                G CGGAGGGAG     GGCCGG
                                | |||||||||     ||||||
                                C GCCTCCCTC     CCGGCC
                                _       CCTTT_
GAM2952 FLJ21432 3' CGTCAGAATCTCATTTGTGGCT 67547       GGGAG  CAC___  C
           GG                   CGTCGGA    CTC     GGC GG
                                |||||||    |||     ||| ||
                                GCAGTCT    GAG     CCG CC
                                   TA___   TAAACA   A
GAM2952 KIAA0893 5' CGGCGGAGGAGAACGCGGCTGG 67548   T    _   TCCA   C
                                CG CGGAGG GAGC   CGGC GG
                                || |||||| ||||   |||| ||
                                GC GCCTCC CTTG   GCCG CC
                                 C    T   C___   A
GAM2952 KIAA1500 3' GTAGGAGGGAGTTCTCTGTGG  67549   C      __  CAC
                                GT GGAGGGAG  CTC   GG
                                || ||||||||  |||   ||
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                                CA CCTCCCTC  GAG   CC
                                 T       AA   ACA
GAM2952  KIAA1643  5'  CGCGGAGGCACGGCC      67550    T     GAGCTC
                                CG CGGAGG     CACGGCC
                                || ||||||     |||||||
                                GC GCCTCC     GTGCCGG
                                 _     _______
GAM2952  MGC26744  5'  TCGGAGGGTCGCGGCCG     67551         AGC  CA
                                TCGGAGGG   TC  CGGCCG
                                ||||||||   ||  ||||||
                                AGCCTCCC   AG  GCCGGC
                                     ___  C_
GAM2952  RNF10     5'  CGTTGGGGGAGCTCAGCGG   67552     C  A       CA
                                CGT GG GGGAGCTC  CGG
                                ||| || ||||||||  |||
                                GCA CC CCCTCGAG  GCC
                                  A  _       TC
GAM2952  LOC170127 5'  GTCGGGGGAGCTCATGG     67553       A       CAC
                                GTCGG GGGAGCTC   GG
                                ||||| ||||||||   ||
                                CAGCC CCCTCGAG   CC
                                   _       TA_
GAM2952  LOC253758 5'  CATCCCACGGCTCCACGGCTGG 67554      GGAGGGA         C
                                CGTC      GCTCCACGGC GG
                                ||||      |||||||||| ||
                                GTAG      CGAGGTGCCG CC
                                  GGTGC__         A
GAM2952  LOC254345 5'  GTTGGGGGAGGCGGGGGCCGG  67555    C  A    CTCCAC
                                GT GG GGGAG     GGCCGG
                                || || |||||     ||||||
                                CA CC CCCTC     CCGGCC
                                 A  _    CGCCC_
GAM2952  LOC257327 5'  TCGGCCGCGGCTTCACGGCCGG 67556      AGGGA   C
                                TCGG    GCT CACGGCCGG
                                ||||    ||| |||||||||
                                AGCC    CGA GTGCCGGCC
                                  GGCGC   A
GAM2952  LOC90639  3'  TCGGAGGGGCTCGCGGCCGG   67557         A    CA
                                TCGGAGGG GCTC  CGGCCGG
                                |||||||| ||||  |||||||
                                AGCCTCCC CGAG  GCCGGCC
                                     _    C_
GAM2953  COL2A1    3'  CCTGCGCCCGGCACCTG     67560      A  A  A  A
                                CCTG CG CT CG GCACCTG
                                |||| || || || |||||||
                                GGAC GC GG GC CGTGGAC
                                  _ _ _ _
GAM2953  COL2A1    3'  CCTGCGCCCGGCACCTG     67560      A  A  A  A
                                CCTG CG CT CG GCACCTG
                                |||| || || || |||||||
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                                GGAC GC GG GC CGTGGAC
                                  _ _ _ _
GAM2953  EXTL3    3'  TCCCGTGGTGAGAAGCACCTGA 67561     _ AC  CTAC
                                TCCC TG  GA   GAGCACCTGA
                                |||| ||  ||   ||||||||||
                                AGGG AC  CT   TTCGTGGACT
                                  C  CA  C___
GAM2953  SPTBN2   3'  TCCCTGTCGACTGTCCCTG   67562      A    ACGAGCA
                                TCCCTG CGACT      CCTG
                                |||||| |||||      ||||
                                AGGGAC GCTGA      GGAC
                                   A    CAG____
GAM2953  FLJ30213 3'  TCCCTGACTGCTGCCCACTCCT 67563       GA  ACGA  A
            GA                    TCCCTGAC  CT   GC CCTGA
                                |||||||| ||   || |||||
                                AGGGACTG  GA   TG GGACT
                                     AC  CGGG  A
GAM2953  ICB-1    3'  TGACGACTTTAACCACCTGA   67564       AC  G
                                TGACGACT  GA CACCTGA
                                |||||||| || |||||||
                                ACTGCTGA  TT GTGGACT
                                     AA  G
GAM2953  KIAA1140 3'  TCCCTGAGGCCCCGCACCTGA  67565       CGA  ACGA
                                TCCCTGA   CT   GCACCTGA
                                |||||||  ||   ||||||||
                                AGGGACT   GG   CGTGGACT
                                    CC_  GG__
GAM2953  KIAA1199 3'  TCCCTGACAGTTGGCTCCCACC 67566        ACTACGAG_
            TG                    TCCCTGACG       CACCTG
                                |||||||||       ||||||
                                AGGGACTGT       GTGGAC
                                     CAACCGAGG
GAM2953  KIAA1655 5'  TCCCTGTTTTCTGGAGCACCTG 67567       ACGA  AC
                                TCCCTG   CT  GAGCACCTG
                                ||||||   ||  |||||||||
                                AGGGAC   GA  CTCGTGGAC
                                   AAAA  C_
GAM2953  LOC200197 3'  TCCCTGACAGCCAGGTGAGCAT 67568        A  C__   CC
            TTG                   TCCCTGACG CTA   GAGCA  TG
                                |||||||| |||   |||||  ||
                                AGGGACTGT GGT   CTCGT  AC
                                     C   CCA    AA
GAM2953  LOC203429 3'  TCCCTGACACTAGCCT      67415       G   CGAGCA
                                TCCCTGAC ACTA     CCT
                                |||||||| ||||     |||
                                AGGGACTG TGAT     GGA
                                     _   C_____
GAM2953  LOC222066 3'  TCCCTGATGACTTTAGCACCTG 67569       C   ACG
                                TCCCTGA GACT   AGCACCTG
                                ||||||| ||||  ||||||||
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                                AGGGACT CTGA   TCGTGGAC
                                   A   AA_
GAM2953  LOC254124 3'  CCCGGTCCATGAGCACCTG   67570     ACGA   C
                                CCTG   CTA GAGCACCTG
                                ||||   ||| |||||||||
                                GGGC   GGT CTCGTGGAC
                                  CA__   A
GAM2953  LOC51333  3'  TCCTTGACAACTCACTTG    67571    C      ACGAG   C
                                TCC TGACGACT    CAC TG
                                ||| ||||||||    ||| ||
                                AGG ACTGTTGA    GTG AC
                                  A      _____   A
GAM2954  CUL4B     3'  GAATCTTGTGTAATAGTCT    67574        CAC  T_   A
                                GAATCTTGT   GT  TAG TCT
                                |||||||||   ||  ||| |||
                                CTTAGAACA   CA  ATC AGA
                                     ___  TT   _
GAM2954  PML       5'  TCGATTCTCGGTTTAGATC    67575     A    TCAC
                                TCGA TCTTG   GTTTAGATC
                                |||| |||||   |||||||||
                                AGCT AGAGC   CAAATCTAG
                                  A   _____
GAM2954  PML       5'  TCGATTCTCGGTTTAGATC    67575     A    TCAC
                                TCGA TCTTG   GTTTAGATC
                                |||| |||||   |||||||||
                                AGCT AGAGC   CAAATCTAG
                                  A   _____
GAM2954  PML       5'  TCGATTCTCGGTTTAGATC    67575     A    TCAC
                                TCGA TCTTG   GTTTAGATC
                                |||| |||||   |||||||||
                                AGCT AGAGC   CAAATCTAG
                                  A   _____
GAM2954  PML       5'  TCGATTCTCGGTTTAGATC    67575     A    TCAC
                                TCGA TCTTG   GTTTAGATC
                                |||| |||||   |||||||||
                                AGCT AGAGC   CAAATCTAG
                                  A   _____
GAM2954  PML       5'  TCGATTCTCGGTTTAGATC    67575     A    TCAC
                                TCGA TCTTG   GTTTAGATC
                                |||| |||||   |||||||||
                                AGCT AGAGC   CAAATCTAG
                                  A   _____
GAM2954  PML       5'  TCGATTCTCGGTTTAGATC    67575     A    TCAC
                                TCGA TCTTG   GTTTAGATC
                                |||| |||||   |||||||||
                                AGCT AGAGC   CAAATCTAG
                                  A   _____
GAM2954  PML       5'  TCGATTCTCGGTTTAGATC    67575     A    TCAC
                                TCGA TCTTG   GTTTAGATC
                                |||| |||||   |||||||||
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                                AGCT AGAGC    CAAATCTAG
                                  A    ____
GAM2954  PML      5'  TCGATTCTCGGTTTAGATC    67575      A     TCAC
                                TCGA TCTTG    GTTTAGATC
                                |||| |||||    |||||||||
                                AGCT AGAGC    CAAATCTAG
                                  A    ____
GAM2954  SIP      3'  TCTATTATTGTCATGTTTAGAT 67576    GAATC     C
                                TC    TTGTCA GTTTAGAT
                                ||    |||||| ||||||||
                                AG    AACAGT CAAATCTA
                                 ATAAT     A
GAM2955  MAK      3'  TTCGAAGTGTCTATTTAAA    67579     A       CG
                                TTC AAGTGTCTA  TTAGA
                                ||| |||||||||  |||||
                                AAG TTCACAGAT  AATTT
                                  C       A_
GAM2955  FLJ13352  3'  TTCAAAGTGTTCTGTTAG    67580          _  AC
                                TTCAAAGTGT CT  GTTAG
                                |||||||||| ||  |||||
                                AAGTTTCACA GA  CAATC
                                      A  __
GAM2955  LOC255452 3'  AAGTGTCTATTGCGCTTGA    67581          ___    A
                                AAGTGTCTA   CGTT GA
                                |||||||||   |||| ||
                                TTCACAGAT   GCGA CT
                                      AAC    A
GAM2956  CTNNB1    3'  GTAGCAGTATTCACTATAAC   67584       AC   GG
                                GTAGCA  ATT  TTGTAAC
                                ||||||  |||  |||||||
                                CATCGT  TAA  GATATTG
                                   CA   GT
GAM2956  HMG20A    3'  GTAGCAACATGACAGGTAGT   67585          T___   T
                                GTAGCAACAT    GGT GT
                                ||||||||||    ||| ||
                                CATCGTTGTA    CCA CA
                                      CTGT   T
GAM2956  SALL2     3'  TCTAGCAACATTCCTTA     67586     G        GG
                                TC TAGCAACATT  TTG
                                || ||||||||||  |||
                                AG ATCGTTGTAA  AAT
                                 _        GG
GAM2956  GRP3      3'  TATCATAGCAACTGTGTA     67587          AT  GT
                                TATCGTAGCAAC  TG  TGTA
                                ||||||||||||  ||  ||||
                                ATAGTATCGTTG  AC  ACAT
                                        __  __
GAM2956  LOC222444 3'  CATCGTGGCGACGTGGTGGC   67588       A  A  AT    T
                                TATCGT GC AC  TGGT GT
                                |||||| || ||  |||| ||
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                                GTAGCA CG TG  ACCA CG
                                   C  C  C_   C
GAM2957  AD-020    3'  TAAAGAGCAATGCAATAT    67591       ACT
                                TAAAGA  ATGCAATAT
                                ||||||  |||||||||
                                ATTTCT  TACGTTATA
                                   CGT
GAM2957  AD-020    3'  TAAAGAGCAATGCAATAT    67591       ACT
                                TAAAGA  ATGCAATAT
                                ||||||  |||||||||
                                ATTTCT  TACGTTATA
                                   CGT
GAM2957  COASTER   3'  TAAAGAACTAATGCTATTTGG  67592         _  AATA   A
                                TAAAGAACTA TGC   TATT GG
                                |||||||||| |||   |||| ||
                                ATTTCTTGAT ACG   ATAA CC
                                      T  ____   A
GAM2957  LOC149706 5'  TAAAGGCTGTGCAGACACCAGG 67593      AA  A   AT
                                TAAAG  CT TGCA  ATATTAGG
                                |||||  || ||||  ||||||||
                                ATTTC  GA ACGT  TGTGGTCC
                                   C_  C   C_
GAM2957  LOC200488 5'  GAACTATGTGGCACATTGGG   67594        CAA     A
                                GAACTATG   TATATT GG
                                ||||||||   |||||| ||
                                CTTGATAC   GTGTAA CC
                                     ACC     C
GAM2958  CDC25C    3'  CTCATTCTGTAGTGTTTATTTT 67597      AA__    A
            TC                   CTCGT    TAGT TTTATTTTTC
                                |||||    |||| ||||||||||
                                GAGTA    ATCA AAATAAAAAG
                                   AGAC    C
GAM2958  CDC25C    3'  CTCATTCTGTAGTGTTTATTTT 67597      AA__    A
            TC                   CTCGT    TAGT TTTATTTTTC
                                |||||    |||| ||||||||||
                                GAGTA    ATCA AAATAAAAAG
                                   AGAC    C
GAM2958  ZNF165    3'  CACTTGCCCAATATTTATTTTT 67598     C  AA
                                CACT GT  TAGTATTTATTTTT
                                |||| ||  |||||||||||||
                                GTGA CG  GTTATAAATAAAAA
                                   A  G_
GAM2958  AP4E1     3'  CACTTGTAATAATCCCCATTTT 67599     C       A
            C                    CACT GTAATAGT TTTATTTTT
                                |||| |||||||| |||||||||
                                GTGA CATTATTA GGGTAAAAG
                                   A       G
GAM2958  FLJ13490  3'  ACTCTTAAGCATTATTTTTC   67600     GTAAT     T
                                ACTC    AGTATT ATTTTTC
                                ||||    |||||| |||||||
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                                TGAG    TCGTAA TAAAAAG
                                  AAT__    _
GAM2958 LOC256895 3' CACTCTGCAAATTTATTTTTC 67601     _   TAGT
                                CACTC GTAA   ATTTATTTTTC
                                ||||| ||||   ||||||||||
                                GTGAG CGTT   TAAATAAAAAG
                                  A  ____
GAM2959 B4GALT1  3' TCAGTGGTAGGAGTGTCTT   67604    ATA      G
                                TCA  GTAGGAGTG TTTT
                                |||  ||||||||| ||||
                                AGT  CATCCTCAC AGAA
                                 CAC       _
GAM2959 RPS6KA5  3' TCACATAGTACTTGTTTTCTGT 67605    _    GGAGTG
                                TCA ATAGTA    GTTTTCTGT
                                ||| ||||||    |||||||||
                                AGT TATCAT    CAAAAGACA
                                 G    GAA___
GAM2959 TRPM8    3' CAGTATTGGGCAAGTTTTCTGT 67606     ___ AGT
                                TAGTA  GG  GGTTTTCTGT
                                |||||  ||  ||||||||||
                                GTCAT  CC  TCAAAAGACA
                                  AAC  GT_
GAM2959 ARHU     3' CAGTGGGATGTTTTCTG    67607    A  GTG
                                TAGT GGA  GTTTTCTG
                                |||| |||  ||||||||
                                GTCA CCT  CAAAAGAC
                                 C  A__
GAM2959 KIAA1715 3' TCAATAGTGTGGGTCTTTG   67608       AGGA   T  C
                                TCAATAGT   GTGG TTT TG
                                ||||||||   |||| ||| ||
                                AGTTATCA   CACC AGA AC
                                    _____  C  A
GAM2959 KIAA1893 3' GTAGAAGGGGTTCTTCTGT   67609       T    _
                                GTAGGAG GGTTTT CTGT
                                ||||||| |||||| ||||
                                CATCTTC CCAAGA GACA
                                    C     A
GAM2959 MGC2508  3' TAATATGGATGTTTTCTG    67610     _  GTG
                                TAGTA GGA  GTTTTCTG
                                ||||| |||  ||||||||
                                ATTAT CCT  CAAAAGAC
                                  A  A__
GAM2959 MSTP043  3' CAATAGAAGTTTTTTTCTGT  67611        GG
                                TAGTAGGAGT  TTTTCTGT
                                ||||||||||  ||||||||
                                GTTATCTTCA  AAAAGACA
                                      AA
GAM2959 SEMA4G   5' CAGTGGTGGTGGTGGCCCTGT 67612    A  A_   T_
                                TAGT GG  GTGGT  TTCTGT
                                |||| ||  |||||  ||||||
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                                GTCA CC  CACCA  GGGACA
                                  _ AC    CC
GAM2959  LOC129401 3'  TCAATGCTGAGTTTTCTG    67613      A  AG   GGT
                                TCAAT GT  GAGT   TTTCTG
                                ||||| ||  ||||   ||||||
                                AGTTA CG  CTCA   AAAGAC
                                  _ A_   ___
GAM2959  LOC54516 3'  TAATGGTATGGTTTCTG     67614     A  A     T
                                TAGT GG GTGGTTT CTG
                                |||| || ||||||| |||
                                ATTA CC TACCAAA GAC
                                  _ A      _
GAM2960  ADAMTS5  3'  TGAAATAGCTGCAGACCTACTT 67617       A   A
           T                     TGAAATA CTG TAGACCTACTTT
                                ||||||| ||| ||||||||||||
                                ACTTTAT GAC GTCTGGATGAAA
                                    C  _
GAM2960  SSX3     3'  GAGGTAACTGACAATACTT   67618    AA       ACC
                                GA  TAACTGATAG   TACTT
                                ||  ||||||||||   |||||
                                CT  ATTGACTGTT   ATGAA
                                 CC        ___
GAM2960  LOC144486 3'  TGAAAGGCTGACCGCCTACTTT 67619      TAA    AGA
                                TGAAA   CTGAT   CCTACTTT
                                |||||   |||||   ||||||||
                                ACTTT   GACTG   GGATGAAA
                                   CC_    GC_
GAM2961  ABCA2    3'  GGCGGTGAGCAGTGCCAGG   67623        CACACA   C
                                GGCGGTGAGC     GCC GG
                                ||||||||||     ||| ||
                                CCGCCACTCG     CGG CC
                                      TCA___   T
GAM2961  ABCA2    3'  AGGGTGTACGCAGCCCGG    67622    C   AGCC  A
                                GG GGTG    AC CAGCCCGG
                                || ||||    || ||||||||
                                TC CCAC    TG GTCGGGCC
                                 _    A___  C
GAM2961  ABCA2    3'  AGGGTGTACGCAGCCCGG    67622    C   AGCC  A
                                GG GGTG    AC CAGCCCGG
                                || ||||    || ||||||||
                                TC CCAC    TG GTCGGGCC
                                 _    A___  C
GAM2961  ABCA2    3'  GGCGGTGAGCAGTGCCAGG   67623        CACACA   C
                                GGCGGTGAGC     GCC GG
                                ||||||||||     ||| ||
                                CCGCCACTCG     CGG CC
                                      TCA___   T
GAM2961  ALPI     3'  AGACGGTGGGGCACGCGG    67624        A_  CACACA  C
                                AGGCGGTG  GC     GC CGG
                                ||||||||  ||     || |||
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                                TCTGCCAC  CG     TG GCC
                                    CC _______  C
GAM2961  APOBEC3B  5'  ACGTTCGCCACACAGTCCGGG  67625     GTGA       C
                                GCG    GCCACACAG CCGGG
                                |||    ||||||||| |||||
                                TGC    CGGTGTGTC GGCCC
                                  AAG_       A
GAM2961  CLPS      3'  AGGAGGTGGCCAGCCCGG    67626     C    A    CACA
                                AGG GGTG GCCA    GCCCGG
                                ||| |||| ||||    ||||||
                                TCC CCAC CGGT    CGGGCC
                                  T   _   _____
GAM2961  CRACC     3'  AGGTGTGAGCCACCATGCCGGG 67627     CG        A  GC
                                AGG  GTGAGCCAC CA  CCGGG
                                |||  ||||||||| ||  |||||
                                TCC  CACTCGGTG GT  GGCCC
                                  A_        _ AC
GAM2961  GNA11     5'  AGGCGGGGCGGGCCGGCCCGGG 67628      __    A   ACACA
                                AGGC  GGTG GCC    GCCCGGG
                                ||||  |||| |||    |||||||
                                TCCG  CCGC CGG    CGGGCCC
                                  CC    C   C_____
GAM2961  GRM3      5'  GGCGGTGAGCCTGCACCCGGG  67629          ACACA
                                GGCGGTGAGCC    GCCCGGG
                                ||||||||||    |||||||
                                CCGCCACTCGG    TGGGCCC
                                      ACG__
GAM2961  IFNAR1    3'  AGGTGTGAGCCACCGTGCCCGG 67630     CG        ACA
             G                   AGG  GTGAGCCAC   GCCCGGG
                                |||  |||||||||   |||||||
                                TCC  CACTCGGTG   CGGGCCC
                                  A_        GCA
GAM2961  IL1R1     3'  AGGCGTGAGCCACCACACCGGG 67631      G       A  GC
                                AGGCG TGAGCCAC CA  CCGGG
                                ||||| |||||||| ||  |||||
                                TCCGC ACTCGGTG GT  GGCCC
                                  _       _ GT
GAM2961  KCNC3     3'  AGGCGGTGACAAGAGCCCGGG  67632         GC  CAC
                                AGGCGGTGA  CA   AGCCCGGG
                                |||||||||  ||   ||||||||
                                TCCGCCACT  GT   TCGGGCCC
                                     __  TC_
GAM2961  MSL3L1    5'  AGGCGGTGCGCCGTGGCCGGG  67633         A   ACACA   C
                                AGGCGGTG GCC    GCC GGG
                                |||||||| |||    ||| |||
                                TCCGCCAC CGG    CGG CCC
                                    G   CAC__   _
GAM2961  MSL3L1    5'  AGGCGGTGCGCCGTGGCCGGG  67633         A   ACACA   C
                                AGGCGGTG GCC    GCC GGG
                                |||||||| |||    ||| |||
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                                TCCGCCAC CGG    CGG CCC
                                    G  CAC__  _
GAM2961  MSL3L1   5'  AGGCGGTGCGCCGTGGCCGGG  67633       A  ACACA  C
                                AGGCGGTG GCC    GCC GGG
                                |||||||| |||    ||| |||
                                TCCGCCAC CGG    CGG CCC
                                    G  CAC__  _
GAM2961  MUC4     3'  AGGCGATGAAGTTGGTGGCCTG 67634        CCACACA  C
           GG                    AGGCGGTGAG     GCC GGG
                                ||||||||||     ||| |||
                                TCCGCTACTT     CGG CCC
                                     CAACCAC  A
GAM2961  OVOL1    5'  AGCTGGGCCACCACACAGCCCG 67635    __  GA
           GG                    GGC  GGT  GCCACACAGCCCGGG
                                |||  |||  ||||||||||||||
                                TCG  CCG  TGGTGTGTCGGGCCC
                                 AC  G_
GAM2961  PKD2L1   5'  AGCTGTTTCCACACAGCCTGGG 67636    G  GAG       C
                                GGC GT   CCACACAGCC GGG
                                ||| ||   |||||||||| |||
                                TCG CA   GGTGTGTCGG CCC
                                 A  AA_       A
GAM2961  PRG4     3'  AGGTGTGAGCCATGCAATGGG  67637    CG     CA  CCC
                                AGG  GTGAGCCA  CAG   GGG
                                |||  ||||||||  |||   |||
                                TCC  CACTCGGT  GTT   CCC
                                 A_      AC  A__
GAM2961  PSA      5'  GGCGGTGAGTCAGCCAAG    67638        CCACA    C
                                GGCGGTGAG    CAGCC GG
                                |||||||||    ||||| ||
                                CCGCCACTC    GTCGG TC
                                     A____    T
GAM2961  PSA      5'  GGCGGTGAGTCAGCCAAG    67638        CCACA    C
                                GGCGGTGAG    CAGCC GG
                                |||||||||    ||||| ||
                                CCGCCACTC    GTCGG TC
                                     A____    T
GAM2961  REGL     3'  AGGCAGTATTGGCACAGCTTGG 67639        AGCCA    CC
           G                     AGGCGGTG    CACAGC  GGG
                                ||||||||    ||||||  |||
                                TCCGTCAT    GTGTCG  CCC
                                    AACC_    AA
GAM2961  RNH      5'  GGCGGGACAGCAGCAGCCCGGG 67640      T  G CA  _
                                GGCGG GA C  CA CAGCCCGGG
                                ||||| || |  || |||||||||
                                CCGCC CT G  GT GTCGGGCCC
                                  _  _ TC  C
GAM2961  RNH      5'  GGCGGGACAGCAGCAGCCCGGG 67640      T  G CA  _
                                GGCGG GA C  CA CAGCCCGGG
                                ||||| || |  || |||||||||
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                                CCGCC CT G  GT GTCGGGCCC
                                  _ _ TC  C
GAM2961  SERPINE2  5'  AGACGCCGCGCAGCCCGG    67641      G  A  CACAC
                                AGGCG TG GC    AGCCCGG
                                ||||| || ||    |||||||
                                TCTGC GC CG    TCGGGCC
                                  G  G  _____
GAM2961  SIM2      3'  AGGTGTGAGCCACTGAGCCCGG 67642     CG       AC
                                AGG  GTGAGCCAC  AGCCCGG
                                |||  |||||||||  |||||||
                                TCC  CACTCGGTG  TCGGGCC
                                  A_       AC
GAM2961  SLC21A2   3'  GGCCCACACAGCCCG      67643     GGTGAG
                                GGC     CCACACAGCCCG
                                |||     ||||||||||||
                                CCG     GGTGTGTCGGGC
                                  _______
GAM2961  VMD2      5'  AGGCAGTGGGCTGCAGCAGGTG 67644        A  CACA   CC__
            GG                    AGGCGGTG GC    CAGC    GGG
                                |||||||| ||    ||||    |||
                                TCCGTCAC CG    GTCG    CCC
                                    C  AC__    TCCA
GAM2961  WSX1      3'  AGGCGTGAGCCACTGTGCTGGG 67645      G       ACA  CC
                                AGGCG TGAGCCAC   GC  GGG
                                ||||| ||||||||   ||  |||
                                TCCGC ACTCGGTG   CG  CCC
                                  _       ACA  A_
GAM2961  ZNF137    3'  AGGTGTGAGCCACCGCTCCGGG 67646     CG       ACA  _
                                AGG  GTGAGCCAC   GC CCGGG
                                |||  |||||||||   || |||||
                                TCC  CACTCGGTG   CG GGCCC
                                  A_       G__  A
GAM2961  APBA3     5'  GACGGCCCCGACGTAGCCCGGG 67647       GAG  _  AC
                                GGCGGT   CC AC  AGCCCGGG
                                ||||||   || ||  ||||||||
                                CTGCCG   GG TG  TCGGGCCC
                                    G__  C  CA
GAM2961  DKFZp434D177 5'  GGCTGGTGAGAGCCCG      67648     _     CCACAC
                                GGC GGTGAG     AGCCCG
                                ||| ||||||     ||||||
                                CCG CCACTC     TCGGGC
                                  A     _______
GAM2961  DKFZp434N0650 5'  GGAGGGGGCTGCACAGCCCGGG 67649    C  TGA  CA
                                GG GG   GC  CACAGCCCGGG
                                || ||   ||  ||||||||||
                                CC CC   CG  GTGTCGGGCCC
                                 T  CC_  AC
GAM2961  DKFZp547H236 5'  GGGGGAGGGCGCAGCCCGG    67650    C  T   CCACA
                                GG GG GAG    CAGCCCGG
                                || || |||    ||||||||
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                                CC CC CTC    GTCGGGCC
                                 _ _  CCGC_
GAM2961  DPYSL4   3'  AGGCGGTGGGTGGCATGCACAG 67651       A___  CA_
                                AGGCGGTG   GC   CACAG
                                ||||||||   ||   |||||
                                TCCGCCAC   CG   GTGTC
                                    CCAC  TAC
GAM2961  FADS2    5'  AGCCGGTGTGTGCAGCCCGGG  67652    G    AGCCACA
                                AG CGGTG      CAGCCCGGG
                                || |||||      |||||||||
                                TC GCCAC      GTCGGGCCC
                                 G    ACAC___
GAM2961  FAM10A6  5'  AGGCGGTGGGCGAAGCTGG   67653       A  CACAC   CC
                                AGGCGGTG GC    AGC  GG
                                |||||||| ||    |||  ||
                                TCCGCCAC CG    TCG  CC
                                    C  CT___   A_
GAM2961  FKSG43   3'  GGCCAGCTTTGCACAGCCCGGG 67654     G   CA__
                                GGT AGC    CACAGCCCGGG
                                ||| |||    ||||||||||
                                CCG TCG    GTGTCGGGCCC
                                  G   AAAC
GAM2961  FLJ10891 3'  AGGCGTGAGCCACACGCCTGG  67655      G        A   C
                                AGGCG TGAGCCACAC GCC GG
                                ||||| |||||||||| ||| ||
                                TCCGC ACTCGGTGTG CGG CC
                                  _        _   A
GAM2961  FLJ10932 3'  GGGGTGGGCAGGAAGCCCGGG  67656    C    A  CACAC
                                GG GGTG GC     AGCCCGGG
                                || |||| ||     ||||||||
                                CC CCAC CG     TCGGGCCC
                                 _    C  TCCT_
GAM2961  FLJ13110 3'  AGGTGTGAGCCACAGGTGCTCC 67657     CG        CA_  _  _
            TGGG                   AGG  GTGAGCCACA   GC CC GGG
                                |||  ||||||||||   || || |||
                                TCC  CACTCGGTGT   CG GG CCC
                                  A_         CCA  A  A
GAM2961  FLJ14001 5'  AGGGGTGAGCGCGGTGCCCGGG 67658     C      CACACA
                                AGG GGTGAGC      GCCCGGG
                                ||| |||||||      |||||||
                                TCC CCACTCG      CGGGCCC
                                  _      CGCCA_
GAM2961  FLJ14549 5'  AGCTGGTGAGCCACCTCGG    67659     _        ACAGCC
                                GGC GGTGAGCCAC     CGG
                                ||| ||||||||||     |||
                                TCG CCACTCGGTG     GCC
                                  A        GA_____
GAM2961  FLJ21135 5'  GGCGGTGAGCCGGGCACGTCGG 67660          A__   AGCC
             G                   GGCGGTGAGCC   CAC    CGGG
                                ||||||||||   |||    ||||
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                                CCGCCACTCGG  GTG   GCCC
                                     CCC  CA__
GAM2961  FLJ23519  5'  GGCGGGACAGCAGCAGCCCGGG 67640     T  G CA  _
                                GGCGG GA C  CA CAGCCCGGG
                                ||||| || |  || |||||||||
                                CCGCC CT G  GT GTCGGGCCC
                                  _ _ TC  C
GAM2961  FLJ32356  3'  AGGCGGTGAGTCAGCTG    67661        CCACA   CC
                                AGGCGGTGAG   CAGC  G
                                ||||||||||   ||||  |
                                TCCGCCACTC   GTCG  C
                                     A____   A_
GAM2961  HINT3     5'  GGCGGTGATCCAGGCTTTGGG  67662       G   CACA  CC_
                                GGCGGTGA CCA   GC   GGG
                                |||||||| |||   ||   |||
                                CCGCCACT GGT   CG   CCC
                                    A   C___  AAA
GAM2961  HRIHFB2436 5'  GGCGGTGAGCTGCGGCGAGCCG 67663         CACAC__   C
            GG                    GGCGGTGAGC     AGCC GGG
                                ||||||||||     |||| |||
                                CCGCCACTCG     TCGG CCC
                                     ACGCCGC   _
GAM2961  IGFALS    3'  AGGTGGGGGCCTGAGTCCGGG  67664    C  TGA   ACAC  C
                                AGG GG   GCC   AG CCGGG
                                ||| ||   |||   || |||||
                                TCC CC   CGG   TC GGCCC
                                  A  CC_   AC__  A
GAM2961  JAM1      3'  AGGCGGTGAGCCGACCAGG   67665         ACACA   C
                                AGGCGGTGAGCC    GCC GG
                                ||||||||||||    ||| ||
                                TCCGCCACTCGG    TGG CC
                                     C____   T
GAM2961  JAM1      3'  AGGCGGTGAGCCGACCAGG   67665         ACACA   C
                                AGGCGGTGAGCC    GCC GG
                                ||||||||||||    ||| ||
                                TCCGCCACTCGG    TGG CC
                                     C____   T
GAM2961  JAM1      3'  AGGCGGTGAGCCGACCAGG   67665         ACACA   C
                                AGGCGGTGAGCC    GCC GG
                                ||||||||||||    ||| ||
                                TCCGCCACTCGG    TGG CC
                                     C____   T
GAM2961  JAM1      3'  AGGCGGTGAGCCGACCAGG   67665         ACACA   C
                                AGGCGGTGAGCC    GCC GG
                                ||||||||||||    ||| ||
                                TCCGCCACTCGG    TGG CC
                                     C____   T
GAM2961  JAM1      3'  AGGCGGTGAGCCGACCAGG   67665         ACACA   C
                                AGGCGGTGAGCC    GCC GG
                                ||||||||||||    ||| ||
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                                TCCGCCACTCGG    TGG CC
                                      C____  T
GAM2961 KIAA0210 3' AGGCGGTGAGCTTGCTGG   67666         CACACA  CC
                                AGGCGGTGAGC    GC  GG
                                ||||||||||     ||  ||
                                TCCGCCACTCG    CG  CC
                                      AA____  A_
GAM2961 KIAA0376 5' GGCGGTGAGCTCACCCGG   67667         CACACA
                                GGCGGTGAGC    GCCCGG
                                ||||||||||    ||||||
                                CCGCCACTCG    TGGGCC
                                      AG____
GAM2961 KIAA1157 3' AGGTGGGGACAACCCAGCCTGG 67668    C  T  G C  A    C
             G                   AGG GG GA C AC CAGCC GGG
                                ||| || || | || ||||| |||
                                TCC CC CT G TG GTCGG CCC
                                  A  C  _ T  G    A
GAM2961 KIAA1237 3' AGGCCGTGAGCCACAAAGGG  67669     G       C  CCC
                                AGGC GTGAGCCACA AG   GG
                                |||| |||||||||| ||   ||
                                TCCG CACTCGGTGT TC   CC
                                  G        T  ___
GAM2961 KIAA1829 3' AGGCGTGAGCCACCGCACTGGG 67670     G       ACA  CC
                                AGGCG TGAGCCAC   GC  GGG
                                ||||| ||||||||   ||  |||
                                TCCGC ACTCGGTG   TG  CCC
                                   _       GCG  A_
GAM2961 KIAA1958 3' AGGCGTGAGCCACGCGCCAGG  67671     G       ACA  _
                                AGGCG TGAGCCAC   GC CCGGG
                                ||||| ||||||||   || |||||
                                TCCGC ACTCGGTG   CG GGTCC
                                   _       ___  C
GAM2961 MAP1LC3A 3' AGGCGGTGGGCAGAGCCTCGGG 67672        A  CACAC   _
                                AGGCGGTG GC    AGCC CGGG
                                |||||||| ||    |||| ||||
                                TCCGCCAC CG    TCGG GCCC
                                     C  TC___    A
GAM2961 MGC10772 5' AGGCGGCGGCGGCCCG     67673        A  CACACA
                                AGGCGGTG GC     GCCCG
                                |||||||| ||     |||||
                                TCCGCCGC CG     CGGGC
                                     _  C_____
GAM2961 MGC14376 3' GGCGGTGAAGCCACAGG     67674        _     CAGCCC
                                GGCGGTGA GCCACA     GG
                                |||||||| ||||||     ||
                                CCGCCACT CGGTGT     CC
                                     T    _______
GAM2961 MGC20460 5' AGGCGGTGGAGGGGGAGCCTGG 67675        _  CCACAC   C
             G                   AGGCGGTG AG     AGCC GGG
                                |||||||| ||     |||| |||
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                                TCCGCCAC TC     TCGG CCC
                                    C  CCCC__   A
GAM2961  MGC4663   3'  AGGCGTGAGCCACCGCGCCCGG 67676      G       ACA
             G                   AGGCG TGAGCCAC   GCCCGGG
                                 ||||| ||||||||   |||||||
                                 TCCGC ACTCGGTG   CGGGCCC
                                   _      GCG
GAM2961  MGC5338   5'  AGGCGATGAGTTGCACAG    67677         CCA
                                 AGGCGGTGAG   CACAG
                                 ||||||||||   |||||
                                 TCCGCTACTC   GTGTC
                                      AAC
GAM2961  NR4A3     5'  AGGCGGTGAGCGGCTGGTGGG  67678         CACACA  CC__
                                 AGGCGGTGAGC     GC    GGG
                                 ||||||||||      ||    |||
                                 TCCGCCACTCG     CG    CCC
                                      C_____  ACCA
GAM2961  PFTK1     3'  GGTGGGGCCCCACAGTCCGGG  67679     A_   A    C
                                 GGTG  GCC CACAG CCGGG
                                 ||||  ||| ||||| |||||
                                 CCAC  CGG GTGTC GGCCC
                                   CC   G    A
GAM2961  PIG7      5'  GACGGTGAGCGGCGTCTGGG   67680         CACACA  CC__
                                 GGCGGTGAGC     GC    GGG
                                 |||||||||      ||    |||
                                 CTGCCACTCG     CG    CCC
                                      C_____  CAGA
GAM2961  SEMA4G    5'  AGGCAGTGGCCCAGCCTGG    67681        A   ACA    C
                                 AGGCGGTG GCC   CAGCC GG
                                 |||||||| |||   ||||| ||
                                 TCCGTCAC CGG   GTCGG CC
                                     _  ___     A
GAM2961  LOC129530 5'  AGGTGGTGAGCCCACAG     67682     C       A
                                 AGG GGTGAGCC CACAG
                                 ||| |||||||| |||||
                                 TCC CCACTCGG GTGTC
                                   A       _
GAM2961  LOC138428 5'  AGGCGGTGGCCGAGTCCGG    67683        A   ACAC  C
                                 AGGCGGTG GCC    AG CCGG
                                 |||||||| |||    || ||||
                                 TCCGCCAC CGG    TC GGCC
                                     _   C___   A
GAM2961  LOC144563 3'  AGGTGTGAGCCACCACGCTGGG 67684     CG       ACA  CC
                                 AGG  GTGAGCCAC   GC  GGG
                                 |||  |||||||||   ||  |||
                                 TCC  CACTCGGTG   CG  CCC
                                   A_       GTG  A_
GAM2961  LOC146429 5'  GCGGACACAGCCCGG      67685      TGAGCC
                                 GCGG     ACACAGCCCGG
                                 ||||     ||||||||||
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                                CGCC     TGTGTCGGGCC
                                  _______
GAM2961  LOC146842 5'  GGCGGTGAGTCCTGCCACGTGC 67686        _ A__   AGCC
                GGG                GGCGGTGAG CC   CAC    CGGG
                                   ||||||||| ||   |||    ||||
                                   CCGCCACTC GG   GTG    GCCC
                                      A  ACG   CAC_
GAM2961  LOC147057 5'  GGGGTGGGGCCGCGCAGCCCGG 67687    C    A_   ACA
                G                   GG GGTG  GCC   CAGCCCGGG
                                   || ||||  |||   |||||||||
                                   CC CCAC  CGG   GTCGGGCCC
                                    _   CC   CGC
GAM2961  LOC151632 3'  AGGTGTGAGCCACCACGCTGGG 67684     CG        ACA  CC
                                   AGG  GTGAGCCAC   GC  GGG
                                   |||  |||||||||   ||  |||
                                   TCC  CACTCGGTG   CG  CCC
                                     A_        GTG  A_
GAM2961  LOC152271 3'  AGGTGTGAGCCAACACGCTGGG 67688     CG       _   A  CC
                                   AGG  GTGAGCCA CAC GC  GGG
                                   |||  |||||||| ||| ||  |||
                                   TCC  CACTCGGT GTG CG  CCC
                                     A_       T   _  A_
GAM2961  LOC196746 3'  AGGCGGTGGGCAGTGGCGGTCC 67689         A  CACACAG__   _
                CTGGG                 AGGCGGTG GC        CCC GGG
                                   ||||||||  ||        ||| |||
                                   TCCGCCAC CG        GGG CCC
                                        C  TCACCGCCA   A
GAM2961  LOC197319 3'  AGGTGTGAGCCACCGCCCCCGG 67690     CG       ACAG
                                   AGG  GTGAGCCAC    CCCGG
                                   |||  |||||||||    |||||
                                   TCC  CACTCGGTG    GGGCC
                                     A_        GCGG
GAM2961  LOC199777 5'  ACGGGGCCACACAGCCTGGG   67691      TGA         C
                                   GCGG   GCCACACAGCC GGG
                                   ||||   |||||||||||| |||
                                   TGCC   CGGTGTGTCGG CCC
                                     C__          A
GAM2961  LOC200058 3'  GGCTACACACTGTGCAGCCCGG 67692     GA  _   A___
                G                   GGT  GC CAC    CAGCCCGGG
                                   |||  ||  |||    |||||||||
                                   CCG  TG GTG    GTCGGGCCC
                                     A_  T   ACAC
GAM2961  LOC200904 3'  AGGTGTGAGCCACCATGCTGGG 67693     CG        A  _  CC
                                   AGG  GTGAGCCAC CA GC  GGG
                                   |||  ||||||||| || ||  |||
                                   TCC  CACTCGGTG GT CG  CCC
                                     A_         _  A  A_
GAM2961  LOC202020 3'  AGGCGTGAGCCACCGTGCCGGG 67694       G       ACA   C
                                   AGGCG TGAGCCAC   GCC GGG
                                   |||||  ||||||||   ||| |||
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                                TCCGC ACTCGGTG   CGG CCC
                                  _       GCA   _
GAM2961  LOC202775 5'  GACGGTGAGTCAGATCTCGGG  67695         C  CACAGCC
                                GGCGGTGAG CA      CGGG
                                ||||||||| ||      ||||
                                CTGCCACTC GT      GCCC
                                    A  CTAGA__
GAM2961  LOC203083 3'  AGGTGTGAGCCACCACGCTGGG 67684     CG       ACA  CC
                                AGG  GTGAGCCAC   GC  GGG
                                |||  |||||||||   ||  |||
                                TCC  CACTCGGTG   CG  CCC
                                  A_       GTG  A_
GAM2961  LOC205327 3'  GGTGAACCACACAGCCTGGG   67696              C
                                GGTGAGCCACACAGCC GGG
                                |||||||||||||||| |||
                                CCACTTGGTGTGTCGG CCC
                                          A
GAM2961  LOC207061 5'  AGGCGATGGCTTGGCCCGG    67697        A  CACACA
                                AGGCGGTG GC     GCCCGG
                                |||||||| ||     ||||||
                                TCCGCTAC CG     CGGGCC
                                    _ AAC___
GAM2961  LOC219919 3'  AGGTGTGAGCCACCACGCTGGG 67684     CG       ACA  CC
                                AGG  GTGAGCCAC   GC  GGG
                                |||  |||||||||   ||  |||
                                TCC  CACTCGGTG   CG  CCC
                                  A_       GTG  A_
GAM2961  LOC221683 5'  AGGCAGGGTACAGCCCGG    67698       TGAGCCAC
                                AGGCGG       ACAGCCCGG
                                ||||||       |||||||||
                                TCCGTC       TGTCGGGCC
                                   CCA_____
GAM2961  LOC221795 3'  AGGTGTGAGCCACCACGCTGGG 67684     CG       ACA  CC
                                AGG  GTGAGCCAC   GC  GGG
                                |||  |||||||||   ||  |||
                                TCC  CACTCGGTG   CG  CCC
                                  A_       GTG  A_
GAM2961  LOC254100 3'  AGGCGTGAGCCACAGTATCGGG 67699      G       CAGCC
                                AGGCG TGAGCCACA    CGGG
                                ||||| |||||||||    ||||
                                TCCGC ACTCGGTGT    GCCC
                                  _       CATA_
GAM2961  LOC254176 3'  AGGTGTGAGCCACCACGCTGGG 67684     CG       ACA  CC
                                AGG  GTGAGCCAC   GC  GGG
                                |||  |||||||||   ||  |||
                                TCC  CACTCGGTG   CG  CCC
                                  A_       GTG  A_
GAM2961  LOC254552 5'  GGCGGGGCGCTCAGCCCGGG   67700      TGA  CACA
                                GGCGG   GC   CAGCCCGGG
                                |||||   ||   |||||||||
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                                CCGCC  CG   GTCGGGCCC
                                  CCG A___
GAM2961 LOC256515 3' AGGTGTGAGCCACCACGCTGGG 67684    CG       ACA CC
                                AGG GTGAGCCAC  GC GGG
                                ||| ||||||||| || |||
                                TCC CACTCGGTG  CG CCC
                                  A_       GTG A_
GAM2961 LOC256594 3' AGGTGTGAGCCACCACGCTGGG 67684    CG       ACA CC
                                AGG GTGAGCCAC  GC GGG
                                ||| ||||||||| || |||
                                TCC CACTCGGTG  CG CCC
                                  A_       GTG A_
GAM2961 LOC257115 3' AGGCGTGAGCCACCG      67701      G     CACAGC
                                AGGCG TGAGCCA     CCG
                                ||||| |||||||     |||
                                TCCGC ACTCGGT     GGC
                                  _     _______
GAM2961 LOC257441 5' GGCTGGTGAGAGCCCG     67648    _     CCACAC
                                GGC GGTGAG     AGCCCG
                                ||| ||||||     ||||||
                                CCG CCACTC     TCGGGC
                                  A     _______
GAM2961 LOC56920  3' AGGCGGTGGGCAGTGGCAGGG 67702        A CACACA CC
                                AGGCGGTG GC     GC GGG
                                |||||||| ||     || |||
                                TCCGCCAC CG     CG CCC
                                     C TCAC__ T_
GAM2961 LOC90120  3' GGCGTGGACGCAGCCCGG    67703     G AG CACA
                                GGCG TG C    CAGCCCGG
                                |||| || |   ||||||||
                                CCGC AC G    GTCGGGCC
                                  _ CT C___
GAM2961 LOC90624  3' AGGTGTGAGCCACAGCGCCCGG 67704    CG       CA
           G                     AGG GTGAGCCACA GCCCGGG
                                ||| ||||||||| |||||||
                                TCC CACTCGGTGT CGGGCCC
                                  A_       CG
GAM2961 LOC90719  5' AGGCGGGGAGCCGCCCGCGCTC 67705      T    ACACA_ C
           GGG                    AGGCGG GAGCC     GC CGGG
                                |||||| |||||     || ||||
                                TCCGCC CTCGG     CG GCCC
                                   C    CGGGCG A
GAM2961 LOC92228  3' AGGCGTGAGCCACGCGCCCGG 67706     G      ACA
                                AGGCG TGAGCCAC   GCCCGG
                                ||||| ||||||||   ||||||
                                TCCGC ACTCGGTG   CGGGCC
                                  _      CG_
GAM2962 CYP24     5' GAGGATGGGGTGGGGCGAGGTT 67709      CACAAC A T
           G                     GAGGA     GG G CGAGGTTG
                                |||||     || | ||||||||
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                                CTCCT     CC C GCTCCAAC
                                   ACCCCA  C _
GAM2962  MAD2L2   3'  GAGGCTGAGAAGTCGAGGTTG  67710     ACACAAC
                                GAGG      GGAGTCGAGGTTG
                                ||||      ||||||||||||
                                CTCC      CTTCAGCTCCAAC
                                  GACT___
GAM2962  PUNC     5'  AGGACACAATGGGGCGCGGGTT 67711         C  A  _  A
            G                    AGGACACAA GG GT CG GGTTG
                                |||||||||  ||  ||  ||  |||||
                                TCCTGTGTT CC CG GC CCAAC
                                     A  C  C  _
GAM2962  TCF2     3'  GAGGACACAGAGGGGAAATTG  67712         ACG   TC
                                GAGGACACA   GAG  GAGGTTG
                                |||||||||   |||  |||||||
                                CTCCTGTGT   CTC  CTTTAAC
                                     ___  CC
GAM2962  ABLIM    3'  GAGGACACAGGAGGGT      67713         AC    TCGA
                                GAGGACACA  GGAG   GGT
                                |||||||||  ||||   |||
                                CTCCTGTGT  CCTC   CCA
                                     __   _____
GAM2962  ABLIM    3'  GAGGACACAGGAGGGT      67713         AC    TCGA
                                GAGGACACA  GGAG   GGT
                                |||||||||  ||||   |||
                                CTCCTGTGT  CCTC   CCA
                                     __   _____
GAM2962  C9orf9   3'  GAGGTTGCAGTGAGCCGAGGTT 67714      ACA  ACG
            G                    GAGG   CA   GAGTCGAGGTTG
                                ||||   ||   ||||||||||||
                                CTCC   GT   CTCGGCTCCAAC
                                  AAC  CA_
GAM2962  DKFZp586H0623 3'  GGACATAGTGACAAAGTTG   67715      CAACG  GT
                                GGACA    GA  CGAGGTTG
                                |||||    ||  ||||||||
                                CCTGT    CT  GTTTCAAC
                                   ATCA_  __
GAM2962  FLJ10737  3'  GGGACACAGCGGAGTCA     67716   A      A
                                G GGACACA CGGAGTCG
                                | |||||||  ||||||||
                                C CCTGTGT GCCTCAGT
                                _      C
GAM2962  KIAA1614  3'  GGACAGTGGAGTCAAACCTG  67717      CAAC       G
                                GGACA    GGAGTCGAG TTG
                                |||||    ||||||||| |||
                                CCTGT    CCTCAGTTT GAC
                                   CA__        G
GAM2962  LOC148758 5'  GGACAGTGGAGTCAAACCTG  67717      CAAC       G
                                GGACA    GGAGTCGAG TTG
                                |||||    ||||||||| |||
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                                CCTGT    CCTCAGTTT GAC
                                   CA__       G
GAM2962  LOC201164 3'  GAGGATGCAGTGAGCCGAGGTT 67718      CA  ACG
              G                     GAGGA  CA   GAGTCGAGGTTG
                                    ||||||  ||   ||||||||||||
                                    CTCCT  GT   CTCGGCTCCAAC
                                       AC  CA_
GAM2962  LOC90784  5'  GGACACAGTGGAGATCAAGGTT 67719        AC   _
              G                     GGACACA  GGAG TCGAGGTTG
                                    |||||||  ||||  |||||||||
                                    CCTGTGT  CCTC AGTTCCAAC
                                        CA    T
GAM2963  SOS2     3'  TGACAAAATAATAAACACT    67722          ACTG     _
                                    TGACGAAATA    ATAGAC CT
                                    ||||||||||    ||||||  ||
                                    ACTGTTTTAT    TATTTG GA
                                          ____      T
GAM2963  LOC158696 3'  AAAATTGCATAGACCTAC    67723       AAC  _
                                    GAAAT   TG ATAGACCTAC
                                    ||||||   ||  ||||||||||
                                    TTTTA   AC TATCTGGATG
                                       ___  G
GAM2964  ADM      5'  TCCGAAGTCCAAGCCC      67726        A ATA
                                    TCTGAA G   TCAAGCCC
                                    ||||||  |   ||||||||
                                    AGGCTT C   GGTTCGGG
                                       _ A__
GAM2964  ATP6V0B   3'  CCTGAACACCAAGCC       67727       AAG
                                    TCTGA   ATATCAAGCC
                                    ||||||   ||||||||||
                                    GGACT   TGTGGTTCGG
                                       ___
GAM2964  CENPA    3'  TCTGAAAATTATTTTCAGGCC  67728         A  ___  A
                                    TCTGAAAG TA   TCA GCC
                                    ||||||||  ||   |||  |||
                                    AGACTTTT AT   AGT CGG
                                         A  AAA   C
GAM2964  DPH2L1    3'  TCTGAAAACCACCAGCC     67729         A     A
                                    TCTGAAAG TATCA GCC
                                    ||||||||  |||||  |||
                                    AGACTTTT GTGGT CGG
                                         G    _
GAM2964  EZH1     3'  CCTGGGAGACCAAGCCC     67730      AA    AT
                                    TCTG  AGAT  CAAGCCC
                                    ||||  ||||  |||||||
                                    GGAC  TCTG  GTTCGGG
                                      CC    __
GAM2964  IL1R1    3'  TAAAAGATCTTCCCAAGCCC   67731         A___
                                    TGAAAGAT    TCAAGCCC
                                    ||||||||    ||||||||
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                                ATTTTCTA   GGTTCGGG
                                    GAAG
GAM2964  INPP5D   3'  CCTGAAAACACAAAGCC    67732      A    C
                                TCTGAA GATAT AAGCC
                                ||||||| ||||| |||||
                                GGACTT TTGTG TTCGG
                                   _    T
GAM2964  PARK2    3'  TCTAAAAAGAGAAGCCC    67733      _ TATC
                                TCTGAAA GA   AAGCCC
                                ||||||| ||   ||||||
                                AGATTTT CT   TTCGGG
                                    T  C___
GAM2964  PARK2    3'  TCTAAAAAGAGAAGCCC    67733      _ TATC
                                TCTGAAA GA   AAGCCC
                                ||||||| ||   ||||||
                                AGATTTT CT   TTCGGG
                                    T  C___
GAM2964  PARK2    3'  TCTAAAAAGAGAAGCCC    67733      _ TATC
                                TCTGAAA GA   AAGCCC
                                ||||||| ||   ||||||
                                AGATTTT CT   TTCGGG
                                    T  C___
GAM2964  PIP5K1A  3'  CCTGAGATACCAGGCCC    67734     AA     A
                                TCTGA  GATATCA GCCC
                                |||||  ||||||| ||||
                                GGACT  CTATGGT CGGG
                                   __      C
GAM2964  PVT1     3'  TCTAGAGACACCAGGCC    67735     AA     A
                                TCTG  AGATATCA GCC
                                ||||  |||||||| |||
                                AGAT  TCTGTGGT CGG
                                  C_      C
GAM2964  RNMT     3'  TCTGAAAAGAAAGCCC     67736      _ TATC
                                TCTGAAA GA   AAGCCC
                                ||||||| ||   ||||||
                                AGACTTT CT   TTCGGG
                                    T  _____
GAM2964  SF3A2    5'  CTGGGAGACACCAGAGCCC   67737    AA     _
                                CTG  AGATATCA AGCCC
                                |||  |||||||| |||||
                                GAC  TCTGTGGT TCGGG
                                  CC      C
GAM2964  SH3BP5   3'  TCTGAAAAACCAGCCC     67738       ATCA
                                TCTGAAAGAT   AGCCC
                                ||||||||||   |||||
                                AGACTTTTTG   TCGGG
                                      G___
GAM2964  SLC2A3   5'  CCTGAAAGGGCGACAAGCCC 67739       ATAT_
                                TCTGAAAG    CAAGCCC
                                ||||||||    |||||||
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                                GGACTTTC    GTTCGGG
                                    CCGCT
GAM2964  SLC7A7   3'  TCTAAAACAACCAAGCCC    67740       GAT
                                TCTGAAA   ATCAAGCCC
                                |||||||   |||||||||
                                AGATTTT   TGGTTCGGG
                                    GT_
GAM2964  SYCP1    5'  CCTGAAAAGAAAGCCC      67741       _ TATC
                                TCTGAAA GA    AAGCCC
                                ||||||| ||    ||||||
                                GGACTTT CT    TTCGGG
                                    T ____
GAM2964  TMEPAI   3'  TCTGAAAAGCAGGAGCCC    67742        A  TCA
                                TCTGAAAG TA   AGCCC
                                |||||||| ||   |||||
                                AGACTTTT GT   TCGGG
                                    C  CC_
GAM2964  VANGL2   3'  CCTGAGAACCAAGCCC      67743      AA  T
                                TCTGA  GA ATCAAGCCC
                                |||||  || |||||||||
                                GGACT  CT TGGTTCGGG
                                  __ _
GAM2964  ZNF198   3'  TCCGAAAGACACTGCAAG    67744          __
                                TCTGAAAGATAT  CAAG
                                ||||||||||||  ||||
                                AGGCTTTCTGTG  GTTC
                                    AC
GAM2964  AASDHPPT 3'  TCTGAAAAGATACTCAAG    67745        _   _
                                TCTGAAA GATA TCAAG
                                ||||||| |||| |||||
                                AGACTTT CTAT AGTTC
                                    T   G
GAM2964  C12orf22 3'  TCTGTAAGACACCAGGGCC   67746      A       A_
                                TCTG AAGATATCA  GCC
                                |||| |||||||||  |||
                                AGAC TTCTGTGGT  CGG
                                  A       CC
GAM2964  C20orf85 3'  CCTGAAAAACAGGCCC      67747          TCAA
                                TCTGAAAGATA   GCCC
                                ||||||||||    ||||
                                GGACTTTTTGT   CGGG
                                    C___
GAM2964  CCT4     3'  CTGGAAGACCAAGCCC      67748     A    AT
                                CTG AAGAT  CAAGCCC
                                ||| |||||  |||||||
                                GAC TTCTG  GTTCGGG
                                  C    __
GAM2964  CDW92    3'  TCTGAAAGCATATGCC      67749        _   CAA
                                TCTGAAAG ATAT   GCC
                                |||||||| ||||   |||
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                                AGACTTTC TATA   CGG
                                   G   ___
GAM2964  D4ST-1    3'  CCTGAGAAGCCCCAAGCCC   67750      _  ATA
                                TCTGA AAG   TCAAGCCC
                                ||||| |||   ||||||||
                                GGACT TTC   GGTTCGGG
                                   C  GG_
GAM2964  DKFZp762A227 5'  TCTGGCAAGCCAAGCCC    67751     A_  ATA
                                TCTG  AAG   TCAAGCCC
                                ||||  |||   ||||||||
                                AGAC  TTC   GGTTCGGG
                                  CG  ___
GAM2964  DNM1L     5'  TCTGAAAACACGGGGCCC    67752      A    CAA
                                TCTGAA GATAT   GCCC
                                |||||| |||||   ||||
                                AGACTT TTGTG   CGGG
                                   _    CCC
GAM2964  DNM1L     5'  TCTGAAAACACGGGGCCC    67752      A    CAA
                                TCTGAA GATAT   GCCC
                                |||||| |||||   ||||
                                AGACTT TTGTG   CGGG
                                   _    CCC
GAM2964  FLJ12987  3'  TCTGAAAAATACACC      67753          CAA
                                TCTGAAAGATAT   GCC
                                ||||||||||||   |||
                                AGACTTTTTATG   TGG
                                      ___
GAM2964  FLJ31952  5'  CCTGAAAGACCTCTCAAGC   67754         A__
                                TCTGAAAGAT   TCAAGC
                                ||||||||||   ||||||
                                GGACTTTCTG   AGTTCG
                                     GAG
GAM2964  KIAA0193  3'  TCTGAAAAGATACACAAA    67755       _   _
                                TCTGAAA GATAT CAAG
                                ||||||| ||||| ||||
                                AGACTTT CTATG GTTT
                                   T    T
GAM2964  KIAA0227  3'  TCTGACAAAGCCAAGCCC    67756      AA  TA
                                TCTGA  GA  TCAAGCCC
                                |||||  ||  ||||||||
                                AGACT  TT  GGTTCGGG
                                   G_  TC
GAM2964  KIAA0274  5'  CCTGGACATCAAGTCC      67757     AAA       _
                                TCTG   GATATCAAG CC
                                ||||   |||||||||  ||
                                GGAC   CTGTAGTTC GG
                                  ___        A
GAM2964  KIAA0408  3'  TCTGAAAGTATAGCC       67758        A   CA
                                TCTGAAAG TAT  AGCC
                                ||||||||  |||  ||||
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                                AGACTTTC ATA  TCGG
                                      _  __
GAM2964  KIAA0690  3'  TCTGAGAGCCAAGCCC     67759      A  ATA
                                TCTGA AG   TCAAGCCC
                                ||||| ||   ||||||||
                                AGACT TC   GGTTCGGG
                                   C  ___
GAM2964  KIAA0781  3'  TCTAAACAAATCAAGCCC    67760       AGAT
                                TCTGAA    ATCAAGCCC
                                ||||||    |||||||||
                                AGATTT    TAGTTCGGG
                                   GTT_
GAM2964  KIAA0844  3'  TGAAAGATACCTGAAGCC    67761           __
                                TGAAAGATATC  AAGCC
                                ||||||||||  |||||
                                ACTTTCTATGG  TTCGG
                                      AC
GAM2964  KIAA1465  5'  TCTGGGAGCACCAAGCCC    67762     AA  A
                                TCTG  AG TATCAAGCCC
                                ||||  || ||||||||||
                                AGAC  TC GTGGTTCGGG
                                  CC  _
GAM2964  KRTAP3-3  3'  TCAGAAAGATACCACCC     67763    T        AA
                                TC GAAAGATATC  GCCC
                                || ||||||||||  ||||
                                AG CTTTCTATGG  TGGG
                                 T        __
GAM2964  KRTHB4    3'  CTGGAGACCGTCAAGCCC    67764     AA   A_
                                CTG  AGAT  TCAAGCCC
                                |||  ||||  ||||||||
                                GAC  TCTG  AGTTCGGG
                                  C_   GC
GAM2964  MGC13017  3'  CCTGAAAATATGAGCCC     67765       A    CA
                                TCTGAA GATAT  AGCCC
                                |||||| |||||  |||||
                                GGACTT TTATA  TCGGG
                                   _    C_
GAM2964  MGC2541   3'  CCTGAGATGAGTCAAGCCC    67766      AA   A__
                                TCTGA  GAT   TCAAGCCC
                                |||||  |||   ||||||||
                                GGACT  CTA   AGTTCGGG
                                   __  CTC
GAM2964  MRPS27    3'  TCTGATGCACTTCAAGCCC    67767      AAG  A
                                TCTGA   AT TCAAGCCC
                                |||||   || ||||||||
                                AGACT   TG AGTTCGGG
                                   ACG  A
GAM2964  PDZD2     5'  TCTTGAAATGTCAAGCCC     67768     _   GATA
                                TCT GAAA    TCAAGCCC
                                ||| ||||    ||||||||
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                                AGA CTTT    AGTTCGGG
                                  A    AC__
GAM2964  PLAC3     3'  TCTGAAAGATGGCAATCC     67769          AT   G
                                TCTGAAAGAT  CAA CC
                                ||||||||||  ||| ||
                                AGACTTTCTA  GTT GG
                                      CC   A
GAM2964  PPP1R16B  3'  TCTGAAAAGCAGAGCCC      67770         A  TCA
                                TCTGAAAG TA   AGCCC
                                ||||||||  ||   |||||
                                AGACTTTT GT   TCGGG
                                     C  C__
GAM2964  PRO2900   3'  TCTGAAAGCACCAAGGGTCC   67771         A      ___
                                TCTGAAAG TATCAAG   CC
                                ||||||||  |||||||   ||
                                AGACTTTC GTGGTTC   GG
                                     _      CCA
GAM2964  RHO6      3'  TCTGAAAAACTCATGTCC     67772          A   AG_
                                TCTGAAAGAT TCA   CC
                                ||||||||||  |||   ||
                                AGACTTTTTG AGT   GG
                                      _   ACA
GAM2964  SURB7     3'  TCTGAAAAATACAGCCC      67773           CA
                                TCTGAAAGATAT  AGCCC
                                ||||||||||||  |||||
                                AGACTTTTTATG  TCGGG
                                           __
GAM2964  SYT12     5'  TCTCAAACACACCAAGCCC    67774     G   G
                                TCT AAA ATATCAAGCCC
                                |||  |||  ||||||||||
                                AGA TTT TGTGGTTCGGG
                                  G   G
GAM2964  TCL6      3'  TCTGAAAGTAGCATTGGCC    67775         A  T  A__
                                TCTGAAAG TA CA   GCC
                                ||||||||  ||  ||   |||
                                AGACTTTC AT GT   CGG
                                     _  C  AAC
GAM2964  TCL6      3'  TCTGAAAGTAGCATTGGCC    67775         A  T  A__
                                TCTGAAAG TA CA   GCC
                                ||||||||  ||  ||   |||
                                AGACTTTC AT GT   CGG
                                     _  C  AAC
GAM2964  UBE4B     3'  TCTGAAAATATCTTGCC      67776       A     AA
                                TCTGAA GATATC  GCC
                                ||||||  ||||||  |||
                                AGACTT TTATAG  CGG
                                     _     AA
GAM2964  LOC113246 3'  TCTGGAACATCAAGGCC      67777      AAA       _
                                TCTG   GATATCAAG CC
                                ||||   |||||||||  ||
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                                AGAC   TTGTAGTTC GG
                                  C__       C
GAM2964  LOC123591 3'  TCTGAAAGACAGTGAAGCCC  67778         TC_
                                TCTGAAAGATA   AAGCCC
                                ||||||||||   ||||||
                                AGACTTTCTGT   TTCGGG
                                      CAC
GAM2964  LOC144563 5'  CTGGACATTTCAAGCCC    67779    AAA   __
                                CTG   GATA  TCAAGCCC
                                |||   ||||  ||||||||
                                GAC   CTGT  AGTTCGGG
                                  ___   AA
GAM2964  LOC146272 5'  TCCGGAGAGCCAAGCCC    67780     AA   TA
                                TCTG  AGA  TCAAGCCC
                                ||||  |||  ||||||||
                                AGGC  TCT  GGTTCGGG
                                  C_   C_
GAM2964  LOC151632 5'  CTGGACATTTCAAGCCC    67779    AAA   __
                                CTG   GATA  TCAAGCCC
                                |||   ||||  ||||||||
                                GAC   CTGT  AGTTCGGG
                                  ___   AA
GAM2964  LOC151720 5'  TCTGTGAGAACCAAGCCC    67781     AA   T
                                TCTG  AGA ATCAAGCCC
                                ||||  ||| |||||||||
                                AGAC  TCT TGGTTCGGG
                                  AC  _
GAM2964  LOC152271 3'  CTGGACATTTCAAGCCC    67779    AAA   __
                                CTG   GATA  TCAAGCCC
                                |||   ||||  ||||||||
                                GAC   CTGT  AGTTCGGG
                                  ___   AA
GAM2964  LOC152426 5'  TCTGAAAAACCCTCTTCAGGCC 67782         A____  A
                                TCTGAAAGAT    TCA GCC
                                ||||||||||    ||| |||
                                AGACTTTTTG    AGT CGG
                                      GGAGA   C
GAM2964  LOC154789 5'  CCTGGGATTAGTCAAGCCC   67783     AAA  A__
                                TCTG   GAT   TCAAGCCC
                                ||||   |||   ||||||||
                                GGAC   CTA   AGTTCGGG
                                  C__   ATC
GAM2964  LOC154881 3'  TCTAAATAACCAAGCCC    67784      AGAT
                                TCTGAA    ATCAAGCCC
                                ||||||    |||||||||
                                AGATTT    TGGTTCGGG
                                   AT__
GAM2964  LOC157623 5'  CCTGAAAGTACTGTAGGCCC  67785        A  CAA__
                                TCTGAAAG TAT    GCCC
                                |||||||| |||    ||||
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                                GGACTTTC ATG     CGGG
                                     _  ACATC
GAM2964  LOC166793 3'  CTGAGACAGCATCAAGCC    67786      A__  A
                                CTGA   AG TATCAAGCC
                                ||||   || |||||||||
                                GACT   TC GTAGTTCGG
                                  CTG  _
GAM2964  LOC200904 5'  CTGGACATTTCAAGCCC     67779     AAA   __
                                CTG   GATA  TCAAGCCC
                                |||   ||||  ||||||||
                                GAC   CTGT  AGTTCGGG
                                  ____   AA
GAM2964  LOC206426 3'  CCTGAGATACCAGGCCC     67734      AA      A
                                TCTGA  GATATCA GCCC
                                |||||  ||||||| ||||
                                GGACT  CTATGGT CGGG
                                   __      C
GAM2964  LOC219919 5'  CTGGACATTTCAAGCCC     67779     AAA   __
                                CTG   GATA  TCAAGCCC
                                |||   ||||  ||||||||
                                GAC   CTGT  AGTTCGGG
                                  ____   AA
GAM2964  LOC220549 5'  TCTGAAAGTTGCACCAGCCC   67787        A__    A
                                TCTGAAAG   TATCA GCCC
                                ||||||||   ||||| ||||
                                AGACTTTC   GTGGT CGGG
                                     AAC    _
GAM2964  LOC221632 3'  TCTAAAGAAATCAAGCC     67788       A  T
                                TCTGAA GA ATCAAGCC
                                |||||| || ||||||||
                                AGATTT CT TAGTTCGG
                                   _  T
GAM2964  LOC221795 5'  CTGGACATTTCAAGCCC     67779     AAA   __
                                CTG   GATA  TCAAGCCC
                                |||   ||||  ||||||||
                                GAC   CTGT  AGTTCGGG
                                  ____   AA
GAM2964  LOC256236 3'  TCTGGACCCAAGCCC       67789     AAA   A
                                TCTG   GAT TCAAGCCC
                                ||||   ||| ||||||||
                                AGAC   CTG GGTTCGGG
                                   ____   _
GAM2964  LOC256515 5'  CTGGACATTTCAAGCCC     67779     AAA   __
                                CTG   GATA  TCAAGCCC
                                |||   ||||  ||||||||
                                GAC   CTGT  AGTTCGGG
                                  ____   AA
GAM2964  LOC256594 5'  CTGGACATTTCAAGCCC     67779     AAA   __
                                CTG   GATA  TCAAGCCC
                                |||   ||||  ||||||||
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                                GAC  CTGT  AGTTCGGG
                                 ___   AA
GAM2964  LOC90538  3'  TCTGAAAGAAAGGCAGTAGCCC 67790        TAT_ __
                                TCTGAAAGA   CA  AGCCC
                                |||||||||   ||  |||||
                                AGACTTTCT   GT  TCGGG
                                     TTCC  CA
GAM2965  ASPH      3'  TGTAACAAACTGCAATCT    67793         C   TC
                                TGTAACAAAC GCG  CT
                                |||||||||| |||  ||
                                ACATTGTTTG CGT  GA
                                     A   TA
GAM2965  ASPH      3'  TGTAACAAACTGCAATCT    67793         C   TC
                                TGTAACAAAC GCG  CT
                                |||||||||| |||  ||
                                ACATTGTTTG CGT  GA
                                     A   TA
GAM2965  GPM6B     3'  TGTAACAAAATTGCAGAAACCT 67794        CC_  TCCTC
            A                    TGTAACAAA  GCG    ACCTA
                                |||||||||  |||    |||||
                                ACATTGTTT  CGT    TGGAT
                                     TAA  CTT__
GAM2965  PRDM2     3'  TGTGACAAACCGTGCTCA    67795     A      C TC
                                TGT ACAAACCG G  CTCA
                                ||| |||||||| |  ||||
                                ACA TGTTTGGC C  GAGT
                                  C       A __
GAM2965  STAU2     3'  TGTAACAAGCTGGTCCT     67796        ACC  __
                                TGTAACAA   GC  GTCCT
                                ||||||||   ||  |||||
                                ACATTGTT   CG  CAGGA
                                     ___  AC
GAM2965  DKFZP564C1940 5'  TGTAGCAGCGCTCACC      67797     A  AACC   TC
                                TGTA CA    GCG  CTCACC
                                |||| ||    |||  ||||||
                                ACAT GT    CGC  GAGTGG
                                  C _____  __
GAM2965  FLJ11710  3'  TGTAACAAACCTGCACATCCT  67798          ___
                                TGTAACAAACC   GCGTCCT
                                ||||||||||   |||||||
                                ACATTGTTTGG   TGTAGGA
                                      ACG
GAM2965  FLJ21477  3'  TGTAACAAACCTGCACATTC   67799          _  TCC
                                TGTAACAAACC GCG   TC
                                |||||||||| |||   ||
                                ACATTGTTTGG CGT   AG
                                      A   GTA
GAM2965  FLJ22029  3'  TGAGACAAACCAGCTGCTCA   67800    TA     _ GTC
                                TG  ACAAACC GC   CTCA
                                ||  ||||||| ||   ||||
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                                AC  TGTTTGG CG   GAGT
                                 TC      T  AC_
GAM2965  FLJ23598  3'  TGGCACAGCCCAGGCTCACCTA 67801    TA   AA   CGTC
                                TG  ACA  CCG    CTCACCTA
                                ||  |||  |||    ||||||||
                                AC  TGT  GGT    GAGTGGAT
                                 CG   CG   CC__
GAM2965  MGC11386  3'  TGTAACAAACCTGCACATTC   67799          _   TCC
                                TGTAACAAACC GCG   TC
                                ||||||||||| |||   ||
                                ACATTGTTTGG CGT   AG
                                       A   GTA
GAM2965  MGC4266   3'  TGAACTGCCCTACTCACCTA   67802    T   AAA  GCGTC
                                TG AAC   CC    CTCACCTA
                                || |||   ||    ||||||||
                                AC TTG   GG    GAGTGGAT
                                 _   ACG  AT___
GAM2965  SPINLW1   3'  TGTAACAAACCTGCAGGTCCT  67803          _ __
                                TGTAACAAACC GC  GTCCT
                                |||||||||| ||  |||||
                                ACATTGTTTGG CG  CAGGA
                                       A  TC
GAM2965  SQV7L     5'  TGTAACAAACCTGCACATCCT  67798          ___
                                TGTAACAAACC   GCGTCCT
                                ||||||||||   |||||||
                                ACATTGTTTGG   TGTAGGA
                                       ACG
GAM2965  LOC136263 3'  TGTAAAAGTCTCCTCACCTA   67804      CAAACCGCG
                                TGTAA        TCCTCACCTA
                                |||||        ||||||||||
                                ACATT        AGGAGTGGAT
                                   TTCAG_____
GAM2965  LOC219818 3'  TGTAACAAATCACTCCAGCCTA 67805         C   G   TCA
                                TGTAACAAA CGC TCC   CCTA
                                ||||||||| ||| |||   ||||
                                ACATTGTTT GTG AGG   GGAT
                                      A   _   TC_
GAM2966  ADAM17    3'  GCTGTTATCAATATAAAAGATT 67808    GCAG___
              A                  GC      AGTATAAAAGATTA
                                 ||      ||||||||||||||
                                 CG      TTATATTTTCTAAT
                                  ACAATAG
GAM2966  PDCD2     3'  GCAAGGTATAAAAGATTA    67809      A
                                GCAG GTATAAAAGATTA
                                |||| ||||||||||||
                                CGTT CATATTTTCTAAT
                                   C
GAM2966  FLJ20886  3'  CGCAGAGTTAAAGGATTA    67810         A   A
                                CGCAGAGT TAAA GATTA
                                |||||||| |||| |||||
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                                GCGTCTCA ATTT CTAAT
                                     _   C
GAM2966 INVS    3' CCCAAGGTGTAAAAGATTA   67811   G  C  A  A
                                CC CG AG GT TAAAAGATTA
                                || || || || ||||||||||
                                GG GT TC CA ATTTTCTAAT
                                 _ _ _ C
GAM2966 LOC90918 5' GAGCATTTAAAAAGATTA    67812      ___
                                GAGTAT   AAAAGATTA
                                ||||||   |||||||||
                                CTCGTA   TTTTCTAAT
                                   AAT
GAM2967 CD2AP    3' TGACAAGATAATGAGAAATATT 67815    _    _   TA
           T                    TGA AAGATA TGAG  AAATATTT
                                ||| |||||| ||||  ||||||||
                                ACT TTCTAT ACTC  TTTATAAA
                                  G     T   __
GAM2967 DMXL1    3' AAAATTTAAGTAAAATATTT   67816      A
                                AAGAT TGAGTAAAATATTT
                                ||||| ||||||||||||||
                                TTTTA ATTCATTTTATAAA
                                   A
GAM2967 EIF4G2   3' AAAGATACTCCTAAAATATTT  67817        GAG
                                AAAGATAT   TAAAATATTT
                                ||||||||   ||||||||||
                                TTTCTATG   ATTTTATAAA
                                     AGG
GAM2967 FLRT2    5' AAAGATGAAAGCAAAATGTTTA 67818       AT       A
                                AAAGAT  GAGTAAAAT TTTA
                                ||||||  ||||||||| ||||
                                TTTCTA  TTCGTTTTA AAAT
                                   CT       C
GAM2967 NEDD4L   3' GAAAGGATGTAAAATATTTA   67819      ATAT  _
                                GAAAG    GA GTAAAATATTTA
                                |||||    || ||||||||||||
                                CTTTC    CT CATTTTATAAAT
                                   ____  A
GAM2967 BRP44l   3' GAAAGAAGTAAAATATTTA    67820       TATG
                                GAAAGA    AGTAAAATATTTA
                                ||||||    ||||||||||||||
                                CTTTCT    TCATTTTATAAAT
                                     ____
GAM2967 FLJ12178 3' GAAAGATATGAGTAAAGTTCAT 67821             A__
           TTA                    GAAAGATATGAGTAAA   TATTTA
                                  ||||||||||||||||   ||||||
                                  CTTTCTATACTCATTT   GTAAAT
                                           CAA
GAM2967 KIAA1789 5' TGAAGATATGAAACCTATTTA  67822      A       TAAAA
                                TGAA GATATGAG     TATTTA
                                |||| ||||||||     ||||||
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                                ACTT CTATACTT    ATAAAT
                                  _      TGG__
GAM2967 NMT1    3' TGAAAGATATTTAAAATATTTA 67823         GAG
                                TGAAAGATAT   TAAAATATTTA
                                ||||||||||   ||||||||||
                                ACTTTCTATA   ATTTTATAAAT
                                     A__
GAM2967 SCYB10  3' GAAAGGTGAGGGAAATATTT  67824      ATA   TA
                                GAAAG   TGAG  AAATATTT
                                |||||   ||||  ||||||||
                                CTTTC   ACTC  TTTATAAA
                                   C__   CC
GAM2967 LOC253883 3' AAGATTAAGTAGAATATTTA  67825      A     A
                                AAGAT TGAGTA AATATTTA
                                ||||| |||||| ||||||||
                                TTCTA ATTCAT TTATAAAT
                                  _     C
GAM2968 CSPG2   5' TCGGCGTTGCCCAGGCGGGTCA 67828     ____        A
                                TTGG    GCCCAGGCGG TCA
                                ||||    |||||||||| |||
                                AGCC    CGGGTCCGCC AGT
                                  GCAA         C
GAM2968 NCALD   3' TTAAAGTTGGGCCCTAGTCA  67829      _      A  _
                                TTAAA TTGGGCCC GG CG
                                ||||| |||||||| || ||
                                AATTT AACCCGGG TC GT
                                   C       A  A
GAM2968 STARD4  3' TTTAAATTGGGGCCAGGCA   67830          C
                                TTTAAATTGGG CCAGGCG
                                |||||||||| |||||||
                                AAATTTAACCC GGTCCGT
                                       C
GAM2968 KIAA1987 5' TTCAAATTGGGCCTGTGG    67831           CA_
                                TTTAAATTGGGCC   GG
                                ||||||||||||   ||
                                AAGTTTAACCCGG   CC
                                       ACA
GAM2968 PRC1    3' TTTAAGTTAGGCCCATGGTCA  67832      A       _ _
                                TTTAA TTGGGCCCA GG CG
                                ||||| ||||||||| || ||
                                AAATT AATCCGGGT CC GT
                                   C       A  A
GAM2969 ABCC3   3' CACCAGCACTCGCGT       67835         GT   A
                                CACCGGCAC  TCG CGT
                                |||||||||  ||| |||
                                GTGGTCGTG  AGC GCA
                                        __  _
GAM2969 COL7A1  3' CACTCGCACGCTCACGT     67836     CG       G
                                CAC  GCACGTTC ACGT
                                |||  |||||||| ||||
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                                GTG  CGTGCGAG TGCA
                                  AG       _
GAM2969  LYL1     5'  CACATGGACCCCGACGT     67837     C_  C  G
                                CAC  GG AC TTCGACGT
                                |||  || || ||||||||
                                GTG  CC TG GGGCTGCA
                                  TA  _  _
GAM2969  NOC4     3'  CACCAGCACTCCACGT      67838          GT  G
                                CACCGGCAC  TC ACGT
                                |||||||||  || ||||
                                GTGGTCGTG  AG TGCA
                                     __  G
GAM2969  PFKL     3'  CACCGACAGCGCCACGT     67839          _   CG
                                CACCGGCA CGTT  ACGT
                                |||||||| ||||  ||||
                                GTGGCTGT GCGG  TGCA
                                    C   __
GAM2969  SSPN     3'  CACCGACAGTGCAGCGT     67840         C  T  A
                                CACCGGCA GT CG CGT
                                |||||||| || || |||
                                GTGGCTGT CA GT GCA
                                    _  C  C
GAM2969  C1orf17  3'  CACCAGCACTGCTGATGT    67841          _  C  C
                                CACCGGCAC GTT GA GT
                                |||||||||  ||| || ||
                                GTGGTCGTG CGA CT CA
                                     A  _  A
GAM2969  C20orf28 3'  ACGGGCACATCGTCGATGT   67842    C      __   C
                                AC GGCACGT  TCGA GT
                                || |||||||  |||| ||
                                TG CCGTGTA  AGCT CA
                                  C      GC   A
GAM2969  CNNM4    5'  CACCAGCACGCCGGACGT    67843           TC
                                CACCGGCACGT  GACGT
                                ||||||||||  |||||
                                GTGGTCGTGCG  CTGCA
                                     GC
GAM2969  DKFZp761O132 3'  CACCAGCAGCTCGGACGT    67844         C   _
                                CACCGGCA GTTCG ACGT
                                |||||||| ||||| ||||
                                GTGGTCGT CGAGC TGCA
                                    _    C
GAM2969  FLJ14642 3'  CACCAGCATGCCCGCGT     67845         C    A
                                CACCGGCA GTTCG CGT
                                |||||||| ||||| |||
                                GTGGTCGT CGGGC GCA
                                    A    _
GAM2969  FLJ21415 3'  CCGGCACATCAGAGTTCGATGT 67846         _______     C  III
              A                  CCGGCAC     GTTCGA GT   A
                                 |||||||      |||||| ||   |
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                                GGCCGTG     CAAGCT CA   T
                                    TAGTCT     A  III
GAM2969  FLJ32430  5'  CACTGGCACGCTGCGCGT    67847     C       _  A
                                CAC GGCACGTT CG CGT
                                ||| |||||||| || |||
                                GTG CCGTGCGA GC GCA
                                  A       C  _
GAM2969  KLF12     5'  CACTCGCACACACACGGCGT   67848     _  _    TT  A
                                CAC CG GCACG  CG CGT
                                ||| || |||||  || |||
                                GTG GC TGTGT  GC GCA
                                  A G    GT  C
GAM2969  KLF12     5'  CACTCGCACACACACGGCGT   67848     _  _    TT  A
                                CAC CG GCACG  CG CGT
                                ||| || |||||  || |||
                                GTG GC TGTGT  GC GCA
                                  A G    GT  C
GAM2969  MYH10     3'  CACTGGCATGTCAACAT     67849     C    C  T
                                CAC GGCA GT CGACGT
                                ||| |||| || ||||||
                                GTG CCGT CA GTTGTA
                                  A   A  _
GAM2969  MYO1G     5'  CACCAGCACCTCACCGATGT   67850         G  __   C
                                CACCGGCAC TT  CGA GT
                                |||||||| ||  ||| ||
                                GTGGTCGTG AG  GCT CA
                                     G  TG   A
GAM2969  NYD-SP12  5'  CACCGGCTTCCCAACGT     67851        ACG
                                CACCGGC   TTCGACGT
                                |||||||   ||||||||
                                GTGGCCG   GGGTTGCA
                                   AA_
GAM2969  STX5A     3'  CACCAGCAGCCAATGT      67852        C  T   C
                                CACCGGCA GT CGA GT
                                |||||||| || ||| ||
                                GTGGTCGT CG GTT CA
                                    _  _   A
GAM2969  UQCR      3'  CACCGACAGCCACGT       67853        C   CG
                                CACCGGCA GTT  ACGT
                                |||||||| |||  ||||
                                GTGGCTGT CGG  TGCA
                                    _   __
GAM2969  LOC147165 3'  CACCCGCAGGGCTGACGT    67854      G   C_   C
                                CACC GCA  GTT GACGT
                                |||| |||  ||| |||||
                                GTGG CGT  CGA CTGCA
                                  G   CC   _
GAM2969  LOC255031 5'  CACTGGCACGCCCACGT     67855      C        G
                                CAC GGCACGTTC ACGT
                                ||| |||||||| ||||
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                                GTG CCGTGCGGG TGCA
                                  A       _
GAM2969  LOC255458 5'  CACCAGCATGTGCACGT     67856         C  T G
                                CACCGGCA GT C ACGT
                                |||||||| || | ||||
                                GTGGTCGT CA G TGCA
                                    A  C _
GAM2969  LOC91974  3'  CACAGGCACGTAACAT      67857     C      TC
                                CAC GGCACGT  GACGT
                                ||| |||||||  |||||
                                GTG CCGTGCA  TTGTA
                                  T      __
GAM2969  LOC93512  3'  CACCCGCAGGGCTGACGT    67854      G   C_   C
                                CACC GCA  GTT GACGT
                                |||| |||  ||| |||||
                                GTGG CGT  CGA CTGCA
                                  G   CC   _
GAM2970  IFNW1     3'  TAAATGAGTAAAAATAAATAAC 67860        A    T    T_
              ATC                   TAAATGA TAAAA TAGAT  CATC
                                |||||||| ||||| |||||  ||||
                                ATTTACT ATTTT ATTTA  GTAG
                                    C    T    TT
GAM2970  DKFZp434L0850 3'  AATGAATATTAAATTCATC    67861         AAA
                                AATGAATA   TTAGATTCATC
                                ||||||||   ||||||||||||
                                TTACTTAT   AATTTAAGTAG
                                    ____
GAM2970  FLJ10687  3'  AAATGAATAAATAATTCAT    67862           ATTA
                                AAATGAATAAA    GATTCAT
                                ||||||||||||    |||||||
                                TTTACTTATTT    TTAAGTA
                                      A____
GAM2970  KIAA1726  3'  TGAATAATTAGATTCAT     67863       AA
                                TGAATA  ATTAGATTCAT
                                ||||||  ||||||||||||
                                ACTTAT  TAATCTAAGTA
                                    __
GAM2970  PELI1     5'  AATGAATAAAACAAATCAT    67864           TAGAT
                                AATGAATAAAAT    TCAT
                                ||||||||||||    ||||
                                TTACTTATTTTG    AGTA
                                      TTT__
GAM2970  LOC115297 3'  ATGAGTAAAATTAGATTC     67865      A
                                ATGA TAAAATTAGATTC
                                |||| ||||||||||||
                                TACT ATTTTAATCTAAG
                                  C
GAM2971  AP1B1     3'  GGCACAGCTTCTGTGGCT     67868            A
                                GGCATGGTTTCTGTG CT
                                |||||||||||||| ||
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                                CCGTGTCGAAGACAC GA
                                        C
GAM2971 BBS2    5' CGGCGCCTTCTGTGGCT    67869     AT G      A
                                CGGC  G TTTCTGTG CT
                                ||||  | |||||||| ||
                                GCCG  C GAAGACAC GA
                                  __ G       C
GAM2971 FRK     5' CGGCTTGCTTTCTGTGGCT   67870     A G      A
                                CGGC TG TTTCTGTG CT
                                |||| || |||||||| ||
                                GCCG AC AAAGACAC GA
                                  A G       C
GAM2971 HSPD1   3' GGAATTTCTGTGACTA     67871    CAT
                                GG   GGTTTCTGTGACTA
                                ||   ||||||||||||||
                                CC   TTAAAGACACTGAT
                                 ___
GAM2971 IL20RA  3' GGCATAGTTTAGTTCCTA    67872         CT  GA
                                GGCATGGTTT  GT  CTA
                                ||||||||||  ||  |||
                                CCGTATCAAA  CA  GAT
                                      T_  AG
GAM2971 KRT5    3' GGCTTGGTCTAGACTA     67873     A   TT    T
                                GGC TGG  TCTG GACTA
                                ||| |||  |||| |||||
                                CCG ACC  AGAT CTGAT
                                  A  __   _
GAM2971 LAMC3   3' CGGCAGGGAGTGTGACTA    67874      T  TTTC
                                CGGCA GG    TGTGACTA
                                ||||| ||    ||||||||
                                GCCGT CC    ACACTGAT
                                   C  TC__
GAM2971 MEST    3' CAGCATGGTGACTTGACTA   67875         TT  G
                                CGGCATGGT  CT TGACTA
                                |||||||||  || ||||||
                                GTCGTACCA  GA ACTGAT
                                      CT  _
GAM2971 MKI67   3' GACATCTCCTGTGGCT     67876      GG       A
                                GGCAT  TTTCTGTG CT
                                |||||  |||||||| ||
                                CTGTA  GAGGACAC GA
                                   __       C
GAM2971 MMP19   3' AACGTGGTTTCTGTGGCT   67877     A         A
                                GGC TGGTTTCTGTG CT
                                ||| ||||||||||| ||
                                TTG ACCAAAGACAC GA
                                  C         C
GAM2971 MMP19   3' AACGTGGTTTCTGTGGCT   67877     A         A
                                GGC TGGTTTCTGTG CT
                                ||| ||||||||||| ||
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                                TTG ACCAAAGACAC GA
                                  C         C
GAM2971  MS4A8B   3'  CAGCATGGTTTCCTAGACT   67878          GT
                                CGGCATGGTTTCT  GACT
                                ||||||||||||  ||||
                                GTCGTACCAAAGG  CTGA
                                       AT
GAM2971  PSMD9    3'  CAGCATGTCTGTGGCTA    67879       GTT    A
                                CGGCATG   TCTGTG CTA
                                |||||||   |||||| |||
                                GTCGTAC   AGACAC GAT
                                    ___     C
GAM2971  SH3GL2   3'  CAGCAGTTCTGTGACTA    67880      TGGT
                                CGGCA   TTCTGTGACTA
                                |||||   ||||||||||
                                GTCGT   AAGACACTGAT
                                   C___
GAM2971  SPTAN1   3'  GACATGATGATTGTGACT    67881       TTC
                                GGCATGGT   TGTGACT
                                ||||||||   |||||||
                                CTGTACTA   ACACTGA
                                     CTA
GAM2971  SYNGR1   3'  GGCAGGACAGTCTGTGACT   67882     T  TT__
                                GGCA GG    TCTGTGACT
                                |||| ||    |||||||||
                                CCGT CC    AGACACTGA
                                  _ TGTC
GAM2971  TRIM9    3'  GACCCCCAGTTCTGTGACT   67883     AT__   T
                                GGC    GGTT CTGTGACT
                                |||    |||| ||||||||
                                CTG    TCAA GACACTGA
                                  GGGG   _
GAM2971  TRPM2    5'  CGACATGGTTTCGCAACT    67884          T TG
                                CGGCATGGTTTC G  ACT
                                ||||||||||||  |  |||
                                GCTGTACCAAAG C  TGA
                                       _ GT
GAM2971  ZNFN2A1  3'  GGGTGGTCTCTGACTA     67885    CA      GT
                                GG  TGGTTTCT  GACTA
                                ||  ||||||||  |||||
                                CC  ACCAGAGA  CTGAT
                                 C_       __
GAM2971  ATPAF1   3'  GGCTCATCTCTGTGACT     67886     ATG
                                GGC   GTTTCTGTGACT
                                |||   ||||||||||||
                                CCG   TAGAGACACTGA
                                  AG_
GAM2971  CENTG2   3'  CGGCGCGTGCCGCGTGACTA  67887     A  _   TC
                                CGGC TG GTT  TGTGACTA
                                |||| || |||  ||||||||
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                                GCCG GC CGG  GCACTGAT
                                  C A   C_
GAM2971  COL12A1   3'  GACATCTTCTGTGGCT     67888      GG      A
                                GGCAT  TTTCTGTG CT
                                |||||  |||||||| ||
                                CTGTA  GAAGACAC GA
                                   __       C
GAM2971  COL12A1   3'  GACATCTTCTGTGGCT     67888      GG      A
                                GGCAT  TTTCTGTG CT
                                |||||  |||||||| ||
                                CTGTA  GAAGACAC GA
                                   __       C
GAM2971  DKFZp547I224 3'  GGCATGATTTTGCAGCGGCT   67889         CT__   A
                                GGCATGGTTT    GTG CT
                                ||||||||||    ||| ||
                                CCGTACTAAA    CGC GA
                                      ACGT   C
GAM2971  DKFZp566H0824 3'  GGCATGGTCTCAGCTCACT   67890          T  G_
                                GGCATGGTTTC GT  ACT
                                ||||||||||| ||  |||
                                CCGTACCAGAG CG  TGA
                                      T  AG
GAM2971  FLJ11726  3'  GGCATGGTCTCGGCTCACT   67891          T  G_
                                GGCATGGTTTC GT  ACT
                                ||||||||||| ||  |||
                                CCGTACCAGAG CG  TGA
                                      C  AG
GAM2971  FLJ12668  3'  GGCATGGTGGCAAGTGACTA  67892        TTCT_
                                GGCATGGT    GTGACTA
                                ||||||||    |||||||
                                CCGTACCA    CACTGAT
                                    CCGTT
GAM2971  FLJ13385  3'  GGTATTATCTTTGTGACTA   67893    C  G    C
                                GG AT GTTT TGTGACTA
                                || || |||| ||||||||
                                CC TA TAGA ACACTGAT
                                 A  A   A
GAM2971  FLJ14936  3'  GGCTCCTGTGTCTGTGACTA  67894     ATG_  T
                                GGC    GT TCTGTGACTA
                                |||    || ||||||||||
                                CCG    CA AGACACTGAT
                                  AGGA  C
GAM2971  FLJ14957  3'  GGAAGCCCAGCTGTGACT    67895    CAT    __
                                GG   GGTTT  CTGTGACT
                                ||   |||||  ||||||||
                                CC   TCGGG  GACACTGA
                                 T__     TC
GAM2971  HSU79275  3'  ATGGTAAATCTTGTGACTA   67896      T__   _
                                ATGGT   TCT GTGACTA
                                |||||   ||| |||||||
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                                TACCA   AGA CACTGAT
                                  TTT   A
GAM2971 KALI     3' GGCATGATTTTGGCTCACT   67897         CT  G_
                                GGCATGGTTT  GT  ACT
                                ||||||||||  ||  |||
                                CCGTACTAAA  CG  TGA
                                      AC  AG
GAM2971 KIAA0121 3' CAGCCACTCTGTGACTA    67898     ATGGT
                                CGGC    TTCTGTGACTA
                                ||||    ||||||||||
                                GTCG    GAGACACTGAT
                                  GT___
GAM2971 KIAA0254 3' CAGCACTTCCCTGTGACT   67899       GG TT
                                CGGCAT  T  CTGTGACT
                                ||||||  |  ||||||||
                                GTCGTG  A  GACACTGA
                                   A_ GG
GAM2971 KIAA0820 3' GACATGGTTTGTGCT      67900         TC    A
                                GGCATGGTT  TGTG CT
                                |||||||||  |||| ||
                                CTGTACCAA  ACAC GA
                                     __   _
GAM2971 KIAA0863 3' GGCTGGTCTCCATGACT    67901     A
                                GGC TGGTTTCTGTGACT
                                ||| ||||||||||||||
                                CCG ACCAGAGGTACTGA
                                  _
GAM2971 KIAA1023 3' GACATCTCCTGTGGCT     67876      GG       A
                                GGCAT  TTTCTGTG CT
                                |||||  |||||||| ||
                                CTGTA  GAGGACAC GA
                                   __       C
GAM2971 KIAA1161 5' GGAGATGTTCTGTGACT    67902    CAT  _
                                GG   GGT TTCTGTGACT
                                ||   ||| ||||||||||
                                CC   CTA AAGACACTGA
                                 T__   C
GAM2971 KIAA1254 3' CGGCTTTACTTTCTGTGA   67903     A_  G
                                CGGC  TG TTTCTGTGA
                                ||||  || |||||||||
                                GCCG  AT AAAGACACT
                                  AA  G
GAM2971 KIAA1805 3' GGAATGGTTTCACAAGCTA   67904    C       T TG _
                                GG ATGGTTTC G  A CTA
                                || ||||||||  |  | |||
                                CC TACCAAAG T  T GAT
                                 T       _ GT C
GAM2971 KIAA1813 5' CGACGCCCTGTGACT      67905      ATG   T
                                CGGC   GTT CTGTGACT
                                ||||   ||| ||||||||
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                                GCTG   CGG GACACTGA
                                  ___  _
GAM2971 KIAA1866 3' CAGCATGACGGTCCTGTGA   67906       T__
                                CGGCATGG   TTCTGTGA
                                ||||||||   ||||||||
                                GTCGTACT   AGGACACT
                                    GCC
GAM2971 KIAA1958 3' GGCATGGTCTCGGCTCACT   67891         T G_
                                GGCATGGTTTC GT  ACT
                                |||||||||||  ||  |||
                                CCGTACCAGAG CG  TGA
                                      C  AG
GAM2971 LIMK2    5' GCAAATCCGTCTGTGACT    67907    T   __
                                GCA GGTT  TCTGTGACT
                                ||| ||||  |||||||||
                                CGT TTAG  AGACACTGA
                                  _   GC
GAM2971 MGC12921 5' GGCAGCTGCTGTGACT     67908     TG  T
                                GGCA  GTT CTGTGACT
                                ||||  ||| ||||||||
                                CCGT  CGA GACACTGA
                                  __  C
GAM2971 MGC5149  3' GACATTTCTGTGGCTA     67909     GGT     A
                                GGCAT   TTCTGTG CTA
                                |||||   ||||||| |||
                                CTGTA   AAGACAC GAT
                                  ___     C
GAM2971 MOST2    5' CAGCATGGCCAGGTGGCT    67910        TCT   A
                                CGGCATGGTT   GTG CT
                                ||||||||||   ||| ||
                                GTCGTACCGG   CAC GA
                                      TC_   C
GAM2971 MRPL9    3' GGATGGTTTCGGTCTACT    67911    C      T G_
                                GG ATGGTTTC GT  ACT
                                || ||||||||  ||  |||
                                CC TACCAAAG CA  TGA
                                 _      C  GA
GAM2971 NCBP2    3' GGAACCTTCTGTGACT      67912    C  GG
                                GG AT  TTTCTGTGACT
                                || ||  ||||||||||
                                CC TG  GAAGACACTGA
                                 T  __
GAM2971 PCYT1B   3' GCAGCTCCTGTGACTA      67913     TG
                                GCA  GTTTCTGTGACTA
                                |||  ||||||||||||
                                CGT  CGAGGACACTGAT
                                  __
GAM2971 PIP3-E   3' GACATTGTTTGTGACT      67914      G   TC
                                GGCAT GTT  TGTGACT
                                ||||| |||  |||||||
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                                CTGTA CAA  ACACTGA
                                  A  __
GAM2971  PPP1R15B  5'  CGGCGATGGTTTTCCGACT   67915     _     CTG
                                CGGC ATGGTTT   TGACT
                                |||| |||||||   |||||
                                GCCG TACCAAA   GCTGA
                                  C      AG_
GAM2971  TFIP11    3'  GGGGATTACTGTGACTA     67916    CAT    T
                                GG   GGTT CTGTGACTA
                                ||   |||| |||||||||
                                CC   CTAA GACACTGAT
                                 C__    T
GAM2971  LOC126661 5'  GCGATCCTGTGACTA      67917    AT    T
                                GC  GGTT CTGTGACTA
                                ||  |||| |||||||||
                                CG  CTAG GACACTGAT
                                 __   _
GAM2971  LOC130074 3'  GACAGTTTTGTGACTA     67918     TG    C
                                GGCA  GTTT TGTGACTA
                                ||||  |||| ||||||||
                                CTGT  CAAA ACACTGAT
                                  __   _
GAM2971  LOC132617 3'  GGCATGATTTCAAACT     67919          TGT
                                GGCATGGTTTC   GACT
                                ||||||||||   ||||
                                CCGTACTAAAG   TTGA
                                      T__
GAM2971  LOC147660 3'  GGCGTGATCTGTGACT     67920     A   TT
                                GGC TGG  TCTGTGACT
                                ||| |||  |||||||||
                                CCG ACT  AGACACTGA
                                  C  __
GAM2971  LOC149302 5'  GGCGGCTGCTGTGACT     67921     AT    T
                                GGC  GGTT CTGTGACT
                                |||  |||| ||||||||
                                CCG  CCGA GACACTGA
                                  __   C
GAM2971  LOC151720 5'  CAGCATGGTTTTTGTGACT   67922          C
                                CGGCATGGTTT TGTGACT
                                |||||||||| |||||||
                                GTCGTACCAAA ACACTGA
                                      A
GAM2971  LOC152215 3'  CGTAAGCCCTTTGTGACTA   67923    GCAT    C_
                                CG   GGTTT  TGTGACTA
                                ||   |||||  ||||||||
                                GC   TCGGG  ACACTGAT
                                 AT__    AA
GAM2971  LOC152426 3'  GGCACCTGCCTGTGACT     67924      G_  TT
                                GGCAT  GT  CTGTGACT
                                |||||  ||  ||||||||
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                                CCGTG  CG  GACACTGA
                                  GA  __
GAM2971  LOC155179 3'  GACATCTCCTGTGGCT      67876       GG       A
                                GGCAT  TTTCTGTG CT
                                |||||  |||||||| ||
                                CTGTA  GAGGACAC GA
                                  __       C
GAM2971  LOC157562 5'  GGTGTGGCCATGTGACTA    67925    CA    TC
                                GG  TGGTT  TGTGACTA
                                ||  |||||  ||||||||
                                CC  ACCGG  ACACTGAT
                                 AC    T_
GAM2971  LOC163115 3'  GACATCGGATCTGTGACT    67926      _  TT
                                GGCAT GG  TCTGTGACT
                                |||||  ||  |||||||||
                                CTGTA CC  AGACACTGA
                                  G  T_
GAM2971  LOC169026 3'  GGTAAAATTTTGTGACTA    67927    CAT    C
                                GG   GGTTT TGTGACTA
                                ||   |||||  ||||||||
                                CC   TTAAA ACACTGAT
                                 ATT    _
GAM2971  LOC170106 5'  GGACACTTCCTGTGGCT     67928    C  G       A
                                GG ATG TTTCTGTG CT
                                || ||| |||||||| ||
                                CC TGT AAGGACAC GA
                                 _  G       C
GAM2971  LOC170425 5'  GCATTGGGTTGTGACTA     67929     __  TTC
                                GCAT  GGT   TGTGACTA
                                ||||  |||   ||||||||
                                CGTA  CCA   ACACTGAT
                                  AC  ____
GAM2971  LOC197342 3'  GGCGAGTCCTTCTGTGACT   67930     AT   __
                                GGC  GGTT  TCTGTGACT
                                |||  ||||  |||||||||
                                CCG  TCAG  AGACACTGA
                                  C_   GA
GAM2971  LOC200488 5'  CGGCATGATCATGACT      67931          TCT
                                CGGCATGGTT   GTGACT
                                ||||||||||   ||||||
                                GCCGTACTAG   TACTGA
                                       ____
GAM2971  LOC219667 3'  CAGTTCTGATTTGTGACTA   67932     CA_    TC
                                CGG   TGGTT  TGTGACTA
                                |||   |||||  ||||||||
                                GTC   ACTAA  ACACTGAT
                                  AAG    __
GAM2971  LOC220980 5'  GGCATGGCTCACGTGGCT    67933          C    A
                                GGCATGGTTT TGTG CT
                                |||||||||| |||| ||
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                                CCGTACCGAG GCAC GA
                                      T   C
GAM2971  LOC253461 3'  GGTATATTTTCTGTGGCT    67934    C  G      A
                                GG ATG TTTCTGTG CT
                                || ||| |||||||| ||
                                CC TAT AAAGACAC GA
                                 A  A       C
GAM2971  LOC253502 3'  GGCAGGCCTCTGTGGCT     67935     T       A
                                GGCA GGTTTCTGTG CT
                                |||| |||||||||| ||
                                CCGT CCGGAGACAC GA
                                  _        C
GAM2971  LOC254211 5'  GGCACCTCTCTGTGACT     67936      GG
                                GGCAT  TTTCTGTGACT
                                |||||  ||||||||||
                                CCGTG  AGAGACACTGA
                                   G_
GAM2971  LOC90785  3'  GGTATGGTCTCGGCTCACT   67937    C      T  G_
                                GG ATGGTTTC GT  ACT
                                || |||||||| ||  |||
                                CC TACCAGAG CG  TGA
                                 A       C  AG
GAM2971  LOC91050  3'  AGAATGATTTCTGTGACT    67938    C
                                GG ATGGTTTCTGTGACT
                                || ||||||||||||||
                                TC TACTAAAGACACTGA
                                 T
GAM2971  LOC91380  3'  GGCATGGTCTCGGCTCACT   67891          T  G_
                                GGCATGGTTTC GT  ACT
                                |||||||||| ||  |||
                                CCGTACCAGAG CG  TGA
                                      C  AG
GAM2972  ALDH1A1   3'  CGAATTTGTCTTTTTTTATT  67941    TT   A
                                CG  TTT TCTTTTTTTATT
                                ||  ||| ||||||||||||
                                GC  AAA AGAAAAAAATAA
                                 TT   C
GAM2972  CLIC2     3'  CCACAGTTTTTATTTTCCTT  67942      _      C
                                CCAC GTTTTTAT TTTTTTT
                                |||| |||||||| |||||||
                                GGTG CAAAAATA AAAGGAA
                                  T       _
GAM2972  MGC20576  3'  GCATCATCTTTTTTTAT     67943    TT
                                GT  TTATCTTTTTTTAT
                                ||  ||||||||||||||
                                CG  AGTAGAAAAAAATA
                                 T_
GAM2972  OSBPL3    3'  CCACGTTTCTGTTTTCTT    67944          ATC
                                CCACGTTTTT   TTTTTTT
                                ||||||||||   |||||||
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                                GGTGCAAAGA   AAAAGAA
                                     C__
GAM2972  PLSCR2    5'  GTTTTTATCTTCAGATAT    67945          TTT
                                GTTTTTATCTTT   TAT
                                ||||||||||||  |||
                                CAAAAATAGAAG   ATA
                                      TCT
GAM2972  ROBO2     3'  CCACCTTTCTACTATTTTTTTT 67946     G     C__
           ATT                   CCAC TTTTTAT   TTTTTTTATT
                                ||||| |||||||  ||||||||||
                                GGTG AAAGATG   AAAAAAATAA
                                  G      ATA
GAM2972  LOC126964 3'  ATTTCCATCTTTTTTTAT    67947
                                GTTTTTATCTTTTTTTAT
                                ||||||||||||||||||
                                TAAAGGTAGAAAAAAATA

GAM2972  LOC220776 3'  ACCAGTCAAGCACTTTTTTTAT 67948     C   TTTAT
           T                    ACCA GTT    CTTTTTTTATT
                                ||||| |||    ||||||||||
                                TGGT CAG    GAAAAAAATAA
                                  _  TTCGT
GAM2972  LOC255621 3'  GTCTTTAATCTTTTTTTAT    67949       _
                                GTTTTTA TCTTTTTTTAT
                                |||||||  ||||||||||
                                CAGAAAT AGAAAAAAATA
                                     T
GAM2973  AMELX     5'  TGATGGTTCTTTGAATGTATTC 67952     T   CAATG
                                TGAT GGT    TGAATGTATTC
                                ||||| |||    ||||||||||
                                ACTA CCA    ACTTACATAAG
                                  _  AGAA_
GAM2973  APOBEC2   3'  TGATTGGTTGGTGTCAAATGT  67953       CAA  _
                                TGATTGGT   TGT GAATGT
                                ||||||||   ||| ||||||
                                ACTAACCA   ACA TTTACA
                                     ACC   G
GAM2973  ATP6V1A1  3'  TGATTGGTCAACTGGCTGT    67954         G  AA
                                TGATTGGTCAAT TG  TGT
                                ||||||||||| ||  |||
                                ACTAACCAGTTG AC  ACA
                                       _ CG
GAM2973  RUNX1     3'  TGGTTGGCAATGTCTCTGT    67955    A   T    GAA
                                TG TTGG CAATGT   TGT
                                || |||| ||||||   |||
                                AC AACC GTTACA   ACA
                                 C   _     GAG
GAM2973  LOC221810 3'  TGTTGGTCAATTATGTATT    67956    A      GTGA
                                TG TTGGTCAAT    ATGTATT
                                || |||||||||    |||||||
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                                AC AACCAGTTA    TACATAA
                                 _       A___
GAM2974  PCSK2    3'  TATCACCCATTTGAATGACAG  67959          A____
                                TATCGCCCATTT    ACAG
                                ||||||||||||    ||||
                                ATAGTGGGTAAA    TGTC
                                      CTTAC
GAM2974  RRM2     3'  TATCGCCGCCGTGAGTACAAAA 67960        CATTTAAC
                                TATCGCC       AGTACAAAA
                                |||||||       |||||||||
                                ATAGCGG       TCATGTTTT
                                    CGGCAC__
GAM2974  H-L(3)MBT 3'  TATCTCCATTTTACAGACAA   67961     GC     A    T
                                TATC  CCATTT ACAG ACAA
                                ||||  |||||| |||| ||||
                                ATAG  GGTAAA TGTC TGTT
                                  A_     A   _
GAM2974  OR51E2   3'  TATCTCTCATCACAAGTACAAA 67962     GCC    TA   _
                                TATC   CATT  ACA GTACAAA
                                ||||   ||||  ||| |||||||
                                ATAG   GTAG  TGT CATGTTT
                                  AGA    __   T
GAM2974  LOC202559 3'  TCACGCCAACAGTACA      67963      _   TTTA
                                TCGC CCA    ACAGTACA
                                |||| |||    ||||||||
                                AGTG GGT    TGTCATGT
                                  C   _____
GAM2974  LOC51049  5'  TATGGCCCCCACAGTACAA    67964     C    ATTTA
                                TAT GCCC     ACAGTACAA
                                ||| ||||     |||||||||
                                ATA CGGG     TGTCATGTT
                                  C    GG___
GAM2975  AMELX    5'  TGATGGTTCTTTGAATGTATTC 67952      T   CAATG
                                TGAT GGT     TGAATGTATTC
                                |||| |||     ||||||||||
                                ACTA CCA     ACTTACATAAG
                                  _   AGAA_
GAM2975  APOBEC2  3'  TGATTGGTTGGTGTCAAATGT  67953         CAA   _
                                TGATTGGT   TGT GAATGT
                                ||||||||   ||| ||||||
                                ACTAACCA   ACA TTTACA
                                    ACC   G
GAM2975  ATP6V1A1  3'  TGATTGGTCAACTGGCTGT    67954          G  AA
                                TGATTGGTCAAT TG  TGT
                                |||||||||||| ||  |||
                                ACTAACCAGTTG AC  ACA
                                      _ CG
GAM2975  RUNX1    3'  TGGTTGGCAATGTCTCTGT    67955    A    T     GAA
                                TG TTGG CAATGT   TGT
                                || |||| ||||||   |||
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                                AC AACC GTTACA   ACA
                                 C   _     GAG
GAM2975  LOC221810 3'  TGTTGGTCAATTATGTATT   67956    A       GTGA
                                TG TTGGTCAAT    ATGTATT
                                || |||||||||    |||||||
                                AC AACCAGTTA    TACATAA
                                 _       A___
GAM2976  DDEF2     3'  TATGAATCTTACCCTCGC    67968       TC    C
                                TATGAAT  TACCC CGT
                                |||||||  ||||| |||
                                ATACTTA  ATGGG GCG
                                    GA    A
GAM2976  CDV-1     3'  TGAATTCTACCACATTA     67969          CC
                                TGAATTCTACC  CGTTA
                                ||||||||||  |||||
                                ACTTAAGATGG  GTAAT
                                       T_
GAM2976  FLJ12985  3'  TATGAATTCACCTGTGTT    67970        T  CCC
                                TATGAATTC ACC   GTT
                                ||||||||| |||   |||
                                ATACTTAAG TGG   CAA
                                     _  ACA
GAM2976  FLJ20160  3'  ATGAATTCTATCTCTTCCCAGT 67971         C_____  C
           T                     ATGAATTCTA     CCC GTT
                                ||||||||||     ||| |||
                                TACTTAAGAT     GGG CAA
                                     AGAGAA   T
GAM2976  KIAA1396  3'  TATGAATTCTTCCCTGTAAAGC 67972         A  CC  TA__
           ATT                    TATGAATTCT CCC  GT    CATT
                                |||||||||| |||  ||    ||||
                                ATACTTAAGA GGG  CA    GTAA
                                     A  A_  TTTC
GAM2976  KIAA1871  3'  TATGAATTCTCCGACGTT    67973         A  CC
                                TATGAATTCT CC  CGTT
                                |||||||||| ||  ||||
                                ATACTTAAGA GG  GCAA
                                     _  CT
GAM2976  MGC17337  3'  TATGAATTCTAATTAAGAGACA 67974          CCCCCGTT
           TT                    TATGAATTCTA       ACATT
                                ||||||||||       |||||
                                ATACTTAAGAT       TGTAA
                                     TAATTCTC
GAM2976  STAG2     3'  TATGAATTCTATTATCCCATC  67975         CC__
                                TATGAATTCTA   CCCGTT
                                ||||||||||   ||||||
                                ATACTTAAGAT   GGGTAG
                                     AATA
GAM2976  LOC138639 3'  TGAAACCCTCTGTTACATT   67976     TTCT   CC_
                                TGAA   ACCC   GTTACATT
                                ||||   ||||  ||||||||
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                                ACTT   TGGG  CAATGTAA
                                  ____   AGA
GAM2976 LOC221787 3' GAAAAACCCTTTGTTACATT  67977    TTCT   CC_
                                GAA   ACCC  GTTACATT
                                |||   ||||  ||||||||
                                CTT   TGGG  CAATGTAA
                                  TT__   AAA
GAM2976 LOC255624 3' TATGAATTCACCTGTGTT    67970        T  CCC
                                TATGAATTC ACC  GTT
                                ||||||||| |||  |||
                                ATACTTAAG TGG  CAA
                                      _  ACA
GAM2976 LOC90573  3' TAAATTCTACTCCAGGACATAC 67978         _ CCGT__
             ATT                  TGAATTCTAC CC     TACATT
                                |||||||||| ||     ||||||
                                ATTTAAGATG GG     ATGTAA
                                      A  TCCTGT
GAM2977 BCL2L2   3' CGTTCCCTAAATCCCACTC   67981          A G  GT
                                CGTTCCCTAAA T CT  GCTC
                                |||||||||||| | ||  ||||
                                GCAAGGGATTT A GG  TGAG
                                      _ G  __
GAM2977 MECP2    3' ACGCTTGAAATGCTGTGTTC  67982      CCCTA       C
                                ACGTT    AAATGCTGTG TC
                                |||||    |||||||||| ||
                                TGCGA    TTTACGACAC AG
                                  AC___        A
GAM2977 NCAM2    3' TACGTTCCCTGAAATTCC    67983         A   G
                                TACGTTCCCT AAAT CT
                                |||||||||| |||| ||
                                ATGCAAGGGA TTTA GG
                                      C   A
GAM2977 SYT1     3' GCTTGACAAAATGCTGTGTTC 67984     CCC         C
                                GTT   TAAAATGCTGTG TC
                                |||   |||||||||||| ||
                                CGA   GTTTTACGACAC AG
                                  ACT          A
GAM2977 ELKS     3' GTTGCCCTGGCTGGTGCTC   67985    _   AAAAT   _
                                GTT CCCT    GCTG TGCTC
                                ||| ||||    |||| |||||
                                CAA GGGA    CGAC ACGAG
                                  C   C____   C
GAM2977 GIT2     3' TACATGAAATGCTGTG     67986      TCCCTA
                                TACGT     AAATGCTGTG
                                |||||     ||||||||||
                                ATGTA     TTTACGACAC
                                  C_____
GAM2977 GIT2     3' TACATGAAATGCTGTG     67986      TCCCTA
                                TACGT     AAATGCTGTG
                                |||||     ||||||||||
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                                ATGTA     TTTACGACAC
                                  C_____
GAM2977 GIT2     3' TACATGAAATGCTGTG     67986      TCCCTA
                                TACGT     AAATGCTGTG
                                |||||     ||||||||||
                                ATGTA     TTTACGACAC
                                  C_____
GAM2977 MGC2541  3' TACATTCCCTGAGATGAGT   67987         AAA  CT
                                TACGTTCCCT  ATG  GT
                                ||||||||||  |||  ||
                                ATGTAAGGGA  TAC  CA
                                     CTC  T_
GAM2977 PRO1048  3' TTCTTTAAAATGCAAACTC   67988    CC      TGT
                                TTC  TAAAATGC  GCTC
                                |||  ||||||||  ||||
                                AAG  ATTTTACG  TGAG
                                 AA      TT_
GAM2977 SYNCOILIN 3' TACATTCTTTAAAATACT    67989       CC
                                TACGTTC  TAAAATGCT
                                |||||||  |||||||||
                                ATGTAAG  ATTTTATGA
                                    AA
GAM2977 LOC132617 3' GTGATCCCTAAAGGCTGT    67990    __      AT
                                GT  TCCCTAAA  GCTGT
                                ||  ||||||||  |||||
                                CA  AGGGATTT  CGACA
                                 CT      C_
GAM2977 LOC150378 5' GTTCCCTGGGGTGCCATGCTC 67991       AAAA
                                GTTCCCT   TGCTGTGCTC
                                |||||||   ||||||||||
                                CAAGGGA   ACGGTACGAG
                                    CCCC
GAM2977 LOC219529 3' GTTCCTGTTATCCTGTGCTC  67992      CTAAA  G
                                GTTCC    AT CTGTGCTC
                                |||||    || ||||||||
                                CAAGG    TA GACACGAG
                                  ACAA_  G
GAM2978 BCL2     3' AAGGTTGTCATTAAATATC    67995          CGAAC
                                AAGGTTGTCGTTA    ATATC
                                ||||||||||||    |||||
                                TTCCAACAGTAAT    TATAG
                                       T____
GAM2978 KIAA0924  3' AAGGTTGTGAACATATC     67996       CGTTAC
                                AAGGTTGT     GAACATATC
                                ||||||||     |||||||||
                                TTCCAACA     CTTGTATAG
                                      _______
GAM2978 MAAT1    5' AGCTTGTCGTTGTTGGCATAT  67997    G      ACGAA
                                AG TTGTCGTT    CATAT
                                || ||||||||    |||||
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                                TC AACAGCAA    GTATA
                                 G       CAACC
GAM2978  LOC170425 5'  GGCTGTCGTCTTCATATC    67998          ACGAA
                                GGTTGTCGTT    CATATC
                                ||||||||||    ||||||
                                CCGACAGCAG    GTATAG
                                     AA___
GAM2978  LOC255096 3'  AAAGTTGTCCTTGAACATGTCC 67999          G  AC     A
                                AAGGTTGTC TT  GAACAT TCC
                                ||||||||| ||  |||||| |||
                                TTTCAACAG AA  CTTGTA AGG
                                     G __     C
GAM2979  ADRB3    3'  CCACAGCCAGCCCATCC     68002           TTA
                                CTACAGCCAGTTCA   TCC
                                ||||||||||||||   |||
                                GGTGTCGGTCGGGT   AGG
                                          ___
GAM2979  MTMR8    3'  TACAGTGAGCCTCATTATC    68003      CC  _
                                TACAG  AGT TCATTATC
                                |||||  ||| ||||||||
                                ATGTC  TCG AGTAATAG
                                   AC   G
GAM2979  NR1I2    3'  GACCTACAGGTCAGTGCACTCT 68004        C_   T   A
              C                  GACCTACAG  CAGT CATT TC
                                |||||||||  |||| |||| ||
                                CTGGATGTC  GTCA GTGA AG
                                     CA   C   G
GAM2979  NR1I2    3'  GACCTACAGGTCAGTGCACTCT 68004        C_   T   A
              C                  GACCTACAG  CAGT CATT TC
                                |||||||||  |||| |||| ||
                                CTGGATGTC  GTCA GTGA AG
                                     CA   C   G
GAM2979  RUNX1    3'  GACCTACAGCGAGATC      68005         C  TTCATT
                                GACCTACAGC AG     ATC
                                |||||||||| ||     |||
                                CTGGATGTCG TC     TAG
                                     C _______
GAM2979  DQX1     5'  CACAGCCAGTTCAGACTCCC   68006          TTA
                                TACAGCCAGTTCA   TCCC
                                ||||||||||||   ||||
                                GTGTCGGTCAAGT   AGGG
                                       CTG
GAM2979  FLJ12768 3'  CACTAGCAGTTCATTGTC    68007    _  C      A
                                TAC AGC AGTTCATT TC
                                ||| ||| |||||||| ||
                                GTG TCG TCAAGTAA AG
                                  A  _      C
GAM2979  KIAA1266 3'  CTACAGCATCATTATCC     68008       CAGT
                                CTACAGC   TCATTATCC
                                |||||||   |||||||||
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                                GATGTCG   AGTAATAGG
                                   T___
GAM2979 KIAA1559 3' GCTTTCAGTTCATTATTCC   68009   ___       _
                                GC  CAGTTCATTAT CC
                                ||  |||||||||| ||
                                CG  GTCAAGTAATA GG
                                 AAA        A
GAM2979 KIAA1668 3' ACCTCTGCAACGGTTCATTATC 68010    A__   CA
          CC                     ACCT  CAGC  GTTCATTATCCC
                                ||||  ||||  ||||||||||||
                                TGGA  GTTG  CAAGTAATAGGG
                                  GAC   C_
GAM2979 PSR     3' AACCTACAGCTGGGGCATCC  68011        CAGTTCAT
                                GACCTACAGC      TATCC
                                ||||||||||      |||||
                                TTGGATGTCG      GTAGG
                                     ACCCC___
GAM2979 TLOC1   5' GACCTGAGCCAATTATC    68012     AC      C
                                GACCT  AGCCAGTT ATT
                                |||||  |||||||| |||
                                CTGGA  TCGGTTAA TAG
                                  C_      _
GAM2979 LOC90167 3' CTACAACTTCATTAT     68013      CAG
                                CTACAGC   TTCATTAT
                                |||||||   ||||||||
                                GATGTTG   AAGTAATA
                                   ___
GAM2980 DAB2    3' TATGAAGGGATGTGGTGG   68016     T
                                TATGA GGGATGTGGTGG
                                ||||| ||||||||||||
                                ATACT CCCTACACCACC
                                   T
GAM2980 LNK     3' TGGTGGGATGTGCTGTGCC  68017   A      G  GGT
                                TG TGGGATGTG TG   TGCC
                                || |||||||| ||   ||||
                                AC ACCCTACAC AC   ACGG
                                 C       G  ___
GAM2980 PEA15   3' TGGGTAGATGGTGGGTTGC  68018    AT_
                                TGGG   GTGGTGGGTTGC
                                ||||   ||||||||||||
                                ACCC   TACCACCCAACG
                                  ATC
GAM2980 DKFZp434E1822 3' TGAGGGGATGTGGCAAAGGT  68019    T       __
                                TGA GGGATGTGGT  GGGT
                                ||| ||||||||||  ||||
                                ACT CCCTACACCG  TCCA
                                  C        TT
GAM2980 FLJ12650 3' TGGTGGGATGGGATGGGCC  68021   A     T
                                TG TGGGATG GGTGGGTT
                                || ||||||| ||||||||
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                                AC ACCCTAC CTACCCGG
                                 C      C
GAM2980  FLJ12650  3'  GATGGTGGGGTGGGGTTGC   68020     GA  T    _
                                GATGG  TG GGTGGG TTGC
                                |||||  || |||||| ||||
                                CTACC  AC CCACCC AACG
                                  __ C     C
GAM2980  IKKE      3'  TGATGGGATGGGATCTTGCC  68022        T  TGGG
                                TGATGGGATG GG    TTGCC
                                |||||||||| ||    |||||
                                ACTACCCTAC CC    AACGG
                                      _ TAG_
GAM2980  KIAA1423  3'  TGATGGGGTGGCACTGTGCC  68023      AT     G_  T
                                TGATGGG  GTGGTG  GT GCC
                                |||||||  ||||||  || |||
                                ACTACCC  CACCGT  CA CGG
                                   __     GA  _
GAM2980  KIAA1884  3'  CATGATGGGATGTGTCCTAC  68024          GTGGG
                                TATGATGGGATGTG    TTGC
                                ||||||||||||||    ||||
                                GTACTACCCTACAC    GATG
                                       AG___
GAM2980  LOC148936 5'  TGATGGGAGGGGTTGC     68025       TGTG T
                                TGATGGGA    G GGGTTGC
                                ||||||||    | |||||||
                                ACTACCCT    C CCCAACG
                                      _____ _
GAM2980  LOC148938 5'  TGATGGGAGGGGTTGC     68025       TGTG T
                                TGATGGGA    G GGGTTGC
                                ||||||||    | |||||||
                                ACTACCCT    C CCCAACG
                                      _____ _
GAM2981  NEU1      3'  TGAAGGCAGAATACCCCTGT  68028     T  A      AATG
                                TGA AG CAGAATGC    CTGT
                                ||| || ||||||||    ||||
                                ACT TC GTCTTATG    GACA
                                  _ C       GG__
GAM2981  GOLPH3    3'  TGTAGGCAGAATGCTAGATGTA 68029    A   A      AATGC
                                TG TAG CAGAATGC     TGTA
                                || ||| ||||||||     ||||
                                AC ATC GTCTTACG     ACAT
                                  _  C       ATCT_
GAM2981  INVS      3'  TGATTGACAAAACAATGCTGT  68030     A     AT
                                TGAT GACAGA  GCAATGCTGT
                                |||| ||||||  ||||||||||
                                ACTA CTGTTT  TGTTACGACA
                                   A     __
GAM2981  LOC155006 3'  TGAGGACAGAATGCAATA     68031     TA
                                TGA  GACAGAATGCAATG
                                |||  ||||||||||||||
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                                ACT  CTGTCTTACGTTAT
                                  C_
GAM2981  LOC51082  3'  TGAAGGACAGAGTATGCTGTA  68032     TA     ATGCA
                                TGA  GACAGA    ATGCTGTA
                                |||  ||||||    ||||||||
                                ACT  CTGTCT    TACGACAT
                                  TC     CA___
GAM2982  ABCD4     3'  GGAGATTCAGTGTCCC      68035        C  CAT
                                GGAGATTC AG   TGTTCC
                                |||||||| ||   ||||||
                                CCTCTAAG TC   ACAGGG
                                     _ ___
GAM2982  APBA2     5'  CAGGAGATTCAGCAACGC    68036         C    T
                                CAGGAGATTC AGCA TGT
                                |||||||||| |||| |||
                                GTCCTCTAAG TCGT GCG
                                     _    T
GAM2982  DIAPH2    3'  CAGGAGACTCCATTCC      68037          GCATTG
                                CAGGAGATTCCA     TTCC
                                ||||||||||||     ||||
                                GTCCTCTGAGGT     AAGG
                                     _______
GAM2982  ETV5      5'  TGAGAGGTTTCAGCATTG    68038   A    A  C
                                C GGAG TT CAGCATTG
                                | |||| || ||||||||
                                A TCTC AA GTCGTAAC
                                 C    C  A
GAM2982  FAAH      5'  CAGGAGACTCGCGTGTTCC   68039         CA  AT
                                CAGGAGATTC  GC  TGTTCC
                                ||||||||||  ||  ||||||
                                GTCCTCTGAG  CG  ACAAGG
                                     __  C_
GAM2982  GAD1      3'  CAGGAGATCTAGTTATTATCCA 68040         CCAGC    T
           A                     CAGGAGATT    ATTGT CCAA
                                ||||||||||    ||||| ||||
                                GTCCTCTAG     TAATA GGTT
                                     ATCAA    _
GAM2982  HUNK      3'  CAGGGGTTCCAGCAAGTTCC   68041      AGA      TT
                                CAGG   TTCCAGCA  GTTCC
                                ||||   ||||||||  |||||
                                GTCC   AAGGTCGT  CAAGG
                                  CC_       T_
GAM2982  IRF2      3'  GGAGATCCAGCAGGCTC     68042       T     TT
                                GGAGAT CCAGCA  GTTC
                                ||||||  ||||||  ||||
                                CCTCTA GGTCGT  CGAG
                                   _     C_
GAM2982  RABIF     3'  AGAGATTCCAGTTGAACCAA  68043          CA   TT
                                GGAGATTCCAG  TTG  CCAA
                                ||||||||||  |||  ||||
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                                TCTCTAAGGTC  AAC  GGTT
                                     __   TT
GAM2982 RBP5     5' TGAGAGATTCCAGCCAGCTCC 68044   A        ATT
                                C GGAGATTCCAGC   GTTCC
                                | ||||||||||||   |||||
                                A TCTCTAAGGTCG   CGAGG
                                 C          GT_
GAM2982 RDS      3' GGAGATTCAGACTTTC      68045        C C   G
                                GGAGATTC AG ATT TTC
                                |||||||| || ||| |||
                                CCTCTAAG TC TGA AAG
                                     _ _  _
GAM2982 TACC1    3' AGGAGGCTCCAGCACTGTC   68046      AT
                                AGGAG  TCCAGCATTGTT
                                |||||  ||||||||||||
                                TCCTC  AGGTCGTGACAG
                                   CG
GAM2982 TTN      3' CAGGAGATGTTACTTTTCCAA 68047       TCCA  ATTG
                                CAGGAGAT   GC   TTCCAA
                                ||||||||   ||   ||||||
                                GTCCTCTA   TG   AAGGTT
                                     CAA_  AA__
GAM2982 TTN      3' CAGGAGATGTTACTTTTCCAA 68047       TCCA  ATTG
                                CAGGAGAT   GC   TTCCAA
                                ||||||||   ||   ||||||
                                GTCCTCTA   TG   AAGGTT
                                     CAA_  AA__
GAM2982 TTN      3' CAGGAGATGTTACTTTTCCAA 68047       TCCA  ATTG
                                CAGGAGAT   GC   TTCCAA
                                ||||||||   ||   ||||||
                                GTCCTCTA   TG   AAGGTT
                                     CAA_  AA__
GAM2982 A4GALT   5' CAGGAGCTTCCAGCAGGAACC 68048      A      TTGTT
                                CAGGAG TTCCAGCA    CC
                                |||||| ||||||||    ||
                                GTCCTC AAGGTCGT    GG
                                   G       CCTT_
GAM2982 C1orf34  3' CAGGAGATCTGGCCTCCA    68049        CCA  ATTG
                                CAGGAGATT   GC   TTCCA
                                |||||||||  ||   |||||
                                GTCCTCTAG   CG   GAGGT
                                     AC_  _____
GAM2982 CLONE24945 3' AGGGGATTCCAGCACCACC   68050    A        TG
                                AGG GATTCCAGCAT  TT
                                ||| ||||||||||  ||
                                TCC CTAAGGTCGTG  GG
                                  C         GT
GAM2982 DEPC-1   5' CAGAAGATTTTGTTCC      68051         CCAGCA
                                CAGGAGATT     TTGTTCC
                                |||||||||     |||||||
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                                GTCTTCTAA     AACAAGG
                                          ______
GAM2982  DKFZP434K2235 3'  CAGGAGACTCCAGTCTTA    68052          CA
                                CAGGAGATTCCAG  TTG
                                ||||||||||||  |||
                                GTCCTCTGAGGTC  AAT
                                    AG
GAM2982  DKFZP564F013 3'  GGATCCTGGCATTGTTCCAA  68053    GAT  A_
                                GGA  TCC  GCATTGTTCCAA
                                |||  |||  ||||||||||||
                                CCT  AGG  CGTAACAAGGTT
                                  ___  AC
GAM2982  DKFZP566I1024 3'  CAGGAGATTTTATTGGCCCCA  68054        CCAGCATT
                                CAGGAGATT      GTTCCA
                                |||||||||      ||||||
                                GTCCTCTAA      CGGGGT
                                    AATAAC__
GAM2982  DKFZP761F241 3'  CAGCAGGTTCCAGCACCA    68055    G  A
                                CAG AG TTCCAGCATTG
                                ||| || ||||||||||||
                                GTC TC AAGGTCGTGGT
                                  G  C
GAM2982  FBXO25   5'  CAGGAGATCTCCAGTCCTG   68056       _    CA
                                CAGGAGAT TCCAG  TTG
                                |||||||| |||||  |||
                                GTCCTCTA AGGTC  GAC
                                    G    AG
GAM2982  FLJ11160  3'  CAGGGGACTTCCATTCCA    68057     A   _  GCATTG
                                CAGG GATT CCA     TTCCA
                                |||| |||| |||     |||||
                                GTCC CTGA GGT     AAGGT
                                  C   A  _______
GAM2982  FLJ13840  5'  GGAGATTCCGGAGAGGCGTC   68058        __ CAT
                                GGAGATTCC  AG   TGTT
                                |||||||||  ||   ||||
                                CCTCTAAGG  TC   GCAG
                                    CC  TCC
GAM2982  FLJ22659  5'  GGAGACTCCGGGAACCTCCAA  68059        AGCATTG
                                GGAGATTCC      TTCCAA
                                |||||||||      ||||||
                                CCTCTGAGG      GAGGTT
                                    CCCTTG_
GAM2982  HUMGT198A 3'  TTCCTTTAGCATTGTTCCAA   68060     ___
                                TTCC   AGCATTGTTCCAA
                                ||||   ||||||||||||
                                AAGG   TCGTAACAAGGTT
                                  AAA
GAM2982  HUMGT198A 3'  TTCCTTTAGCATTGTTCCAA   68060     ___
                                TTCC   AGCATTGTTCCAA
                                ||||   ||||||||||||
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                                AAGG   TCGTAACAAGGTT
                                  AAA
GAM2982 IDN3     3' CAGGAGATTCTGCCATTTTACA 68061         CA  ATTG  C
                                CAGGAGATTC  GC    TT CA
                                ||||||||||  ||    || ||
                                GTCCTCTAAG  CG    AA GT
                                     A_  GTAA  T
GAM2982 KDELR3   3' AGGAGGGACATTGTTCCA    68062      ATTCCA
                                AGGAG     GCATTGTTCCA
                                |||||     ||||||||||
                                TCCTC     TGTAACAAGGT
                                  CC_____
GAM2982 KIAA0410 3' CAGGAGATTTTGCTC       68063         CCAGCA    C
                                CAGGAGATT     TTGTT C
                                |||||||||     ||||| |
                                GTCCTCTAA     AACGA G
                                     _______    A
GAM2982 KIAA0429 3' GGAGATTCTACGACTGCCCA   68064        CA _    T
                                GGAGATTC  GC ATTGT CCA
                                ||||||||  || ||||| |||
                                CCTCTAAG  TG TGACG GGT
                                     A_  C    _
GAM2982 KIAA0446 5' CAGGGATTCTGTTCC       68065      A    CAGCAT
                                CAGG GATTC     TGTTCC
                                |||| |||||     ||||||
                                GTCC CTAAG     ACAAGG
                                  _    _______
GAM2982 KIAA0546 3' CAGGAGATTCTAATGTTTGCCA 68066          CAGCAT   __
            A                    CAGGAGATTC     TGTT  CCAA
                                ||||||||||     ||||  ||||
                                GTCCTCTAAG     ACAA  GGTT
                                     ATT___    AC
GAM2982 KIAA1010 3' AGAGATTCTAGTGAGCATCA   68067        C_____
                                GGAGATTC    AGCATTG
                                ||||||||    |||||||
                                TCTCTAAG    TCGTAGT
                                     ATCAC
GAM2982 KIAA1303 3' GAAGATTCTGGTGTTGCCGCC  68068        CAGCA    _
                                GGAGATTC    TTGTT CC
                                ||||||||    ||||| ||
                                CTTCTAAG    AACGG GG
                                     ACCAC    C
GAM2982 KIAA1754 3' GGAGATCCAGGCATGGTT     68069       T   _  T
                                GGAGAT CCAG CAT GTT
                                |||||| |||| ||| |||
                                CCTCTA GGTC GTA CAA
                                  _   C  C
GAM2982 MGC23284 3' GGGAATTCCAGAATTCCA     68070    AG      CATT
                                GG  ATTCCAG    GTTCCA
                                ||  |||||||    ||||||
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                                CC  TAAGGTC    TAAGGT
                                 CT      T___
GAM2982  NFAT5    3'  CAGGAGACTTTAGCACCG    68071         CC
                                CAGGAGATT  AGCATTG
                                |||||||||  |||||||
                                GTCCTCTGA  TCGTGGC
                                     AA
GAM2982  PPP1R14C  3'  GGAGAGTTTCACCCTGTTCCA  68072       TTCCA  A
                                GGAGA    GC TTGTTCCA
                                |||||    || ||||||||
                                CCTCT    TG GACAAGGT
                                   CAAAG  G
GAM2982  SHANK3   3'  CAGGAGACTTTGGGGTCCA   68073         CCAGCA  T__
                                CAGGAGATT     TTG   TCCA
                                |||||||||     |||   ||||
                                GTCCTCTGA     AAC   AGGT
                                     _______  CCC
GAM2982  UBE3B    3'  AGGAGATTCAGTGTTTCA    68074         C  CAT   C
                                AGGAGATTC AG   TGTT CA
                                ||||||||| ||   |||| ||
                                TCCTCTAAG TC   ACAA GT
                                     _ ___    A
GAM2982  UNC5D    3'  CAAGAGATTTTATAACATT   68075         CC__
                                CAGGAGATT   AGCATT
                                |||||||||   ||||||
                                GTTCTCTAA   TTGTAA
                                     AATA
GAM2982  VRP      5'  AGGAGATTTTGTTCC      68076         CCAGCA
                                AGGAGATT     TTGTTCC
                                ||||||||     |||||||
                                TCCTCTAA     AACAAGG
                                     _______
GAM2982  ZNF304   3'  CAGGAGATTTTCGCACCA    68077         CCA
                                CAGGAGATT   GCATTG
                                |||||||||   ||||||
                                GTCCTCTAA   CGTGGT
                                     AAG
GAM2982  LOC115442 3'  CAGGAGGTCCAGCACACCCCC  68078       AT       TG
                                CAGGAG  TCCAGCAT  TTCC
                                ||||||  ||||||||  ||||
                                GTCCTC  AGGTCGTG  GGGG
                                   C_       TG
GAM2982  LOC132720 3'  AGGAAATACATTGTTTCA    68079         TCCA       C
                                AGGAGAT    GCATTGTT CA
                                |||||||    |||||||| ||
                                TCCTTTA    TGTAACAA GT
                                     ____       A
GAM2982  LOC135138 3'  GGAGGTTTCAAGTCCCA     68080      A  C   CATT
                                GGAG TT CAG    GTTCCA
                                |||| || |||    ||||||
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                                CCTC AA GTT    CAGGGT
                                  C  A  ____
GAM2982  LOC144817 3'  CAGGGAATTTTAGCATTAT   68081     AG   CC
                                CAGG  ATT  AGCATTGT
                                ||||  |||  ||||||||
                                GTCC  TAA  TCGTAATA
                                  CT   AA
GAM2982  LOC151438 5'  CAAGCCCAGCATTGTTC     68082     AGAT
                                CAGG    TCCAGCATTGTTC
                                ||||    ||||||||||||||
                                GTTC    GGGTCGTAACAAG
                                  ____
GAM2982  LOC152485 3'  CAGGAGATTCCGGGAGCTCC   68083          AGCATT
                                CAGGAGATTCC     GTTCC
                                ||||||||||      |||||
                                GTCCTCTAAGG     CGAGG
                                      CCCT__
GAM2982  LOC152897 5'  CAGGAGATTGTGGTGCATGCT  68084         CCA__   T
                                CAGGAGATT    GCAT GTT
                                |||||||||    |||| |||
                                GTCCTCTAA    CGTA CGA
                                     CACCA   _
GAM2982  LOC153811 3'  GGAGATTCTGCCTCCA      68085        CA  ATTG
                                GGAGATTC  GC    TTCCA
                                ||||||||  ||    |||||
                                CCTCTAAG  CG    GAGGT
                                    A_  ____
GAM2982  LOC157737 3'  CAGGAGATCCAGGTTCCA    68086        T   CATT
                                CAGGAGAT CCAG    GTTCCA
                                |||||||| ||||    ||||||
                                GTCCTCTA GGTC    CAAGGT
                                   _    ____
GAM2982  LOC158314 3'  CAGGAGTATTCATGTTCCA   68087       _   CAGCAT
                                CAGGAG ATTC     TGTTCCA
                                ||||||  ||||     |||||||
                                GTCCTC TAAG     ACAAGGT
                                   A   T_____
GAM2982  LOC161696 5'  CAGGAGATCCAGCTGCTC    68088        T    AT
                                CAGGAGAT CCAGC  TGTTC
                                |||||||| |||||  |||||
                                GTCCTCTA GGTCG  ACGAG
                                   _    __
GAM2982  LOC164173 3'  CAGGAGATTTTAAGTGCTGCT  68089         CC_  CA
                                CAGGAGATT   AG  TTGTT
                                |||||||||   ||  |||||
                                GTCCTCTAA   TC  GACGA
                                     AAT  AC
GAM2982  LOC199221 3'  CAGGGATTCCAGGTGTC     68090      A      CAT
                                CAGG GATTCCAG   TGTT
                                |||| ||||||||   ||||
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                                GTCC CTAAGGTC   ACAG
                                  _      C__
GAM2982  LOC200163 3'  CAGAAGATTTCAATTCCA    68091        C  GCATT
                                CAGGAGATT CA    GTTCCA
                                ||||||||| ||    ||||||
                                GTCTTCTAA GT    TAAGGT
                                    A _____
GAM2982  LOC201183 5'  AGAGGGTTCCAGCATCATC   68092     A_       TG
                                GGAG  TTCCAGCAT  TT
                                ||||  |||||||||  ||
                                TCTC  AAGGTCGTA  AG
                                  CC        GT
GAM2982  LOC201229 5'  CAGGAGATTTGCAGGCAC    68093        C_  _
                                CAGGAGATT  CAG CAT
                                |||||||||  ||| |||
                                GTCCTCTAA  GTC GTG
                                    AC   C
GAM2982  LOC253649 5'  CAGAAGATTCTGAAGGCTTCCA 68094         CAGCATTG
                                CAGGAGATTC       TTCCA
                                ||||||||||       |||||
                                GTCTTCTAAG       AAGGT
                                    ACTTCCG_
GAM2982  LOC253650 5'  CAGAAGATTCTGAAGGCTTCCA 68094         CAGCATTG
                                CAGGAGATTC       TTCCA
                                ||||||||||       |||||
                                GTCTTCTAAG       AAGGT
                                    ACTTCCG_
GAM2982  LOC255157 5'  CAGGGGGCTCTGGCACTGCCAC 68095     AGA   CA      _
            CA                    CAGG   TTC  GCATTGTT CCA
                                ||||   |||  |||||||| |||
                                GTCC   GAG  CGTGACGG GGT
                                  CCC   AC       T
GAM2982  LOC255242 5'  CAGGAGATTTCGTTGACC    68096        CCAGCA    __
                                CAGGAGATT     TTGTT  CC
                                |||||||||     |||||  ||
                                GTCCTCTAA     AGCAA  GG
                                    _______    CT
GAM2982  LOC90777  3'  CAGGAGATTCTAGCCTACC    68097        C   ATTGTT
                                CAGGAGATTC AGC     CC
                                |||||||||| |||     ||
                                GTCCTCTAAG TCG     GG
                                    A   GAT___
GAM2982  LOC92771  3'  GGAGATTCCAGGCCCC      68098         CATT
                                GGAGATTCCAG    GTTCC
                                ||||||||||    |||||
                                CCTCTAAGGTC    CGGGG
                                     ____
GAM2983  AMD1      3'  TCACTGCATCAATCCAGAA    68101         CGTGC
                                TTACTGCATCAA     TCAGAA
                                ||||||||||    ||||||
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                                AGTGACGTAGTT    GGTCTT
                                      A____
GAM2983  BRCA1    5'  TACATCCGTCTCAGAAA     68102       AA   G
                                TGCATC  CGT CTCAGAAA
                                ||||||  ||| ||||||||
                                ATGTAG  GCA GAGTCTTT
                                  __  _
GAM2983  BRCA1    3'  TACATCCGTCTCAGAAA     68102       AA   G
                                TGCATC  CGT CTCAGAAA
                                ||||||  ||| ||||||||
                                ATGTAG  GCA GAGTCTTT
                                  __  _
GAM2983  CLC      3'  CTACTGCATTGTAAACTTTCAG 68103         C___   GTGC
                                TTACTGCAT   AAC   TCAG
                                |||||||||   |||   ||||
                                GATGACGTA   TTG   AGTC
                                     ACAT   AA__
GAM2983  CSE1L    3'  TTAATGCAGCTGTGCTCAGAA  68104     C   TCAAC
                                TTA TGCA    GTGCTCAGAA
                                ||| ||||    ||||||||||
                                AAT ACGT    CACGAGTCTT
                                  T   CGA__
GAM2983  ENPP2    3'  TACTGCAGATGCTCAGAAA    68105       TCAAC
                                TACTGCA    GTGCTCAGAAA
                                |||||||    ||||||||||
                                ATGACGT    TACGAGTCTTT
                                    C____
GAM2983  ITGA1    3'  TTACTACATTATCAGA      68106         CAACG  C
                                TTACTGCAT    TG TCAGA
                                |||||||||    || |||||
                                AATGATGTA    AT AGTCT
                                     _____  _
GAM2983  NLGN1    3'  TTACTGCAGTTAGTTTGTCAGA 68107        TCAACG_  C
                                TTACTGCA      TG TCAGA
                                ||||||||      || |||||
                                AATGACGT      AC AGTCT
                                    CAATCAA  _
GAM2983  PAX5     3'  TACTGCATCGGTCCCAGA    68108         AAC  G
                                TACTGCATC   GT CTCAGA
                                |||||||||   || ||||||
                                ATGACGTAG   CA GGGTCT
                                     C__  _
GAM2983  TSG      3'  TTACTGCATTTTTTCAGAA   68109         CAACGTGC
                                TTACTGCAT      TCAGAA
                                |||||||||      ||||||
                                AATGACGTA      AGTCTT
                                     AAAA____
GAM2983  FLJ12934 3'  TGCTTCAGGATGCTCAGA    68110     A   AC
                                TGC TCA  GTGCTCAGA
                                ||| |||  |||||||||
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                                ACG AGT  TACGAGTCT
                                  A  CC
GAM2983  FLJ20160  3'  TTACTGCACTGGCAGA     68111        CAACG  CT
                                TTACTGCAT    TG  CAGA
                                |||||||||    ||  ||||
                                AATGACGTG    AC  GTCT
                                      _____  C_
GAM2983  GHITM    3'  TTACTGCATTTATTCTCCAGAA 68112        CAACGTG  _
           A                     TTACTGCAT      CTC AGAAA
                                 |||||||||      ||| |||||
                                 AATGACGTA      GAG TCTTT
                                      AATAA__   G
GAM2983  HTGN29   3'  TTACTGCAATAAAACGGTTCAG 68113        TC__   TGC
                                TTACTGCA   AACG   TCAG
                                ||||||||   ||||   ||||
                                AATGACGT   TTGC   AGTC
                                     TATT   CA_
GAM2983  KIAA0603  3'  CTGCATCAACTTTCAGA     68114        GTGC
                                CTGCATCAAC    TCAGA
                                ||||||||||    |||||
                                GACGTAGTTG    AGTCT
                                      AA__
GAM2983  MGC4268   5'  TCACTGAGCGTGCTCAG     68115      CATCAA
                                TTACTG     CGTGCTCAG
                                ||||||     |||||||||
                                AGTGAC     GCACGAGTC
                                   TC_____
GAM2983  UBCE7IP5  3'  CCTTCCCAAACGTGCTTAGAA  68116    GCA   _     C
                                CT   TCAA CGTGCT AGAA
                                ||   |||| |||||| ||||
                                GG   GGTT GCACGA TCTT
                                 AAG    T     A
GAM2983  USP29    3'  CTGCATCAGTTGGTCTAGA    68117        ACG  C  _
                                CTGCATCA   TG TC AGA
                                ||||||||   || || |||
                                GACGTAGT   AC AG TCT
                                     CA_  C  A
GAM2983  LOC143381 3'  CTGCCCAAGTGCTCAGA     68118      A    C
                                CTGC TCAA GTGCTCAGA
                                |||| |||| |||||||||
                                GACG GGTT CACGAGTCT
                                  _    _
GAM2983  LOC146784 5'  CTGCATCAGCCCAAA       68119        ACGT
                                CTGCATCA    GCTCAGA
                                ||||||||    |||||||
                                GACGTAGT    CGGGTTT
                                      _____
GAM2983  LOC153937 3'  TTACTGCATTTGTGGAGA    68120         CAAC   CTC
                                TTACTGCAT    GTG   AGA
                                |||||||||    |||   |||
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                                AATGACGTA   CAC  TCT
                                     AA__   C__
GAM2984  GPR48    3'  TTAAATGAATAAAATGAAA   68123            T
                                TTAAATGAATAAAAT AGA
                                ||||||||||||||| |||
                                AATTTACTTATTTTA TTT
                                        C
GAM2984  PAFAH1B1 3'  TTAAATCAATATCAGATTCAT  68124      G   AAA
                                TTAAAT AATA   TTAGATTCAT
                                |||||| ||||  ||||||||||
                                AATTTA TTAT   AGTCTAAGTA
                                   G   ___
GAM2984  STAU2    3'  CTAAATGATTAGATTCA     68125        ATAAAA
                                TTAAATGA     TTAGATTCA
                                ||||||||     |||||||||
                                GATTTACT     AATCTAAGT

                                _______
GAM2984  DKFZp434L0850 3'  AATGAATATTAAATTCAT    68126        AAA
                                AATGAATA   TTAGATTCAT
                                ||||||||   ||||||||||
                                TTACTTAT   AATTTAAGTA

                                ___
GAM2984  FLJ30294 3'  TTAAGTGAATAAAACTAG    68127     A
                                TTAA TGAATAAAATTAG
                                |||| ||||||||||||
                                AATT ACTTATTTTGATC
                                  C
GAM2984  KIAA1040 3'  TTAAGTGAATAAAATTAAA   68128     A
                                TTAA TGAATAAAATTAGA
                                |||| ||||||||||||||
                                AATT ACTTATTTTAATTT
                                  C
GAM2984  KIAA1726 3'  TGAATAATTAGATTCA      68129       AA
                                TGAATA  ATTAGATTCA
                                ||||||  ||||||||||
                                ACTTAT  TAATCTAAGT

                                __
GAM2985  LIP8     5'  TGCAGCGCAGAGCGGGTGCGGA 68132        TATTA   ATA
                                TGCAGCGT    CGG   CGGA
                                ||||||||    |||   ||||
                                ACGTCGCG    GCC   GCCT
                                     TCTC_   CAC
GAM2986  ACTR1B   3'  GAGGGGAAGGCTGCAGGG    68135    A   AACTTTA
                                GAG GGAA      TTGCAGGG
                                ||| ||||      ||||||||
                                CTC CCTT      GACGTCCC
                                  C   CC_____
GAM2986  DRD2     3'  TGAGAAGGGATACATTGCAGGG 68136        AAAACTT
                                TGAGAGG      TATTGCAGGG
                                |||||||      ||||||||||
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                                ACTCTTC      GTAACGTCCC
                                   CCTAT__
GAM2986  EYA1     5'  GAGTGGAGCGCCTCTGCAGGG  68137     A   AAA    AT
                                GAG GGA   CTTT  TGCAGGG
                                ||| |||   ||||  |||||||
                                CTC CCT   GGAG  ACGTCCC
                                  A   CGC    __
GAM2986  GPR4     5'  TGAGAAGGAGATGGTTTGCAGG 68138      _   AAACTTTA
              G                  TGAGA GGA       TTGCAGGG
                                ||||| |||       ||||||||
                                ACTCT CCT       AACGTCCC
                                   T   CTACCA__
GAM2986  MEN1     5'  GAGAGGAAAGGCAGTGCAGGG  68139         ACTT  T
                                GAGAGGAAA    TA TGCAGGG
                                |||||||||    || |||||||
                                CTCTCCTTT    GT ACGTCCC
                                      CC__  C
GAM2986  MPV17    3'  AAGAGGGGCATTGCAGG     68140       AAAACTT
                                GAGAGG      TATTGCAGG
                                ||||||      |||||||||
                                TTCTCC      GTAACGTCC
                                   CC_____
GAM2986  NXT1     5'  TGGAAGGAGGGCTCCACCAGGG 68141    AG    AAA     TG
                                TG  AGGA   CTTTAT  CAGGG
                                ||  ||||   ||||||  |||||
                                AC  TCCT   GAGGTG  GTCCC
                                 CT    CCC     __
GAM2986  PARG     3'  TGAGTGGAAGGCTCACAGG   68142     A    AA   TATT
                                TGAG GGAA  CTT    GCAGG
                                |||| ||||  |||    |||||
                                ACTC CCTT  GAG    TGTCC
                                  A    CC  ____
GAM2986  PSD      5'  TGAGAGGAGACTTCCCGG    68143        AA    ATTGCA
                                TGAGAGGA  ACTTT     GG
                                ||||||||  |||||     ||
                                ACTCTCCT  TGAAG     CC
                                     C_     GG____
GAM2986  RAB3B    3'  TGAGAGAAAGCCCCGCAGG   68144         AA  TTAT
                                TGAGAGGAA  CT    TGCAGG
                                |||||||||  ||    ||||||
                                ACTCTCTTT  GG    GCGTCC
                                     CG  ____
GAM2986  C6orf26  3'  TGAGAGGAGGGTTTAGACACGG 68145         AAAC    TT  _
              G                  TGAGAGGA    TTTA  GCA GGG
                                ||||||||    ||||  ||| |||
                                ACTCTCCT    AAAT  TGT CCC
                                     CCC_    C_   G
GAM2986  CBARA1   3'  GAGAGGAAATGGCACTTGCAGG 68146         ACTTTA
              G                  GAGAGGAAA     TTGCAGGG
                                |||||||||     ||||||||
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                                CTCTCCTTT     AACGTCCC
                                      ACCGTG
GAM2986  DKFZp434E0519 3'  TGAGAGAAGAACATTATGCAGG 68147        A   T   T
            G                   TGAGAGGA AAC TTAT GCAGGG
                                |||||||| ||| |||| ||||||
                                ACTCTCTT TTG AATA CGTCCC
                                     C   T   _
GAM2986  DKFZp434E2220 5'  TGAGCTTCTATTTTGTTGCAGG 68148     AGGAAAAC   A
            G                   TGAG       TTT TTGCAGGG
                                ||||       ||| ||||||||
                                ACTC       AAA AACGTCCC
                                  GAAGATA_   C
GAM2986  DKFZP564L2423 3'  TGAAAGGAAGGTAAGGCAGGG  68149         AACTT  TT
                                TGAGAGGAA    TA  GCAGGG
                                |||||||||    ||  ||||||
                                ACTTTCCTT    AT  CGTCCC
                                     CC___  TC
GAM2986  DNAL4    3'  TGGCAGGAAAAGGCCCTGCAGG 68150    AG     CTTTA
            G                   TG  AGGAAAA    TTGCAGGG
                                ||  |||||||    ||||||||
                                AC  TCCTTTT    GACGTCCC
                                 CG     CCGG_
GAM2986  FLJ13162  5'  TGAGAGGAGAGACTGCAGGG   68151        AAACTTT
                                TGAGAGGA     ATTGCAGGG
                                ||||||||     |||||||||
                                ACTCTCCT     TGACGTCCC
                                     CTC____
GAM2986  FLJ21820  3'  GAGAGGAGGAGCCTGCAGGG   68152       AAACTTTA
                                GAGAGGA      TTGCAGGG
                                |||||||      ||||||||
                                CTCTCCT      GACGTCCC
                                    CCTCG___
GAM2986  FLJ31528  3'  TGAGGGCAAGACAGGCAGG    68153     A  _  A  TTTATT
                                TGAG GG AA AC     GCAGG
                                |||| || || ||     |||||
                                ACTC CC TT TG     CGTCC
                                  _  G  C  TC____
GAM2986  HSPC065   3'  GAGAGGAGACCTAGGGGTGTGG 68154        AA   TAT__  CA
            GG                  GAGAGGA  ACTT    TG  GGG
                                |||||||  ||||    ||  |||
                                CTCTCCT  TGGA    AC  CCC
                                    C_   TCCCC  AC
GAM2986  KIAA0552  5'  GAGGGGAGGGGCCGCTGCAGGG 68155     A   AAACT TA
                                GAG GGA    T  TTGCAGGG
                                ||| |||    |  ||||||||
                                CTC CCT    G  GACGTCCC
                                  C   CCCC_ GC
GAM2986  KIAA0976  3'  TGAAAGGAGCACATTGTGGGG  68156        AA  TTT   CA
                                TGAGAGGA  AC   ATTG  GGG
                                ||||||||  ||   ||||  |||
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                                ACTTTCCT  TG   TAAC  CCC
                                    CG  ___    AC
GAM2986  MLL4     3'  TGACAGACTTTATTGTGGGG   68157     G  GAAA       CA
                                TGA AG    ACTTTATTG  GGG
                                ||| ||    |||||||||  |||
                                ACT TC    TGAAATAAC  CCC
                                  G  ____        AC
GAM2986  NFAT5    5'  GAGGGGGAACTCCACGGG    68158     A  AA       TGCA
                                GAG GG  AACTTTAT    GGG
                                ||| ||  ||||||||    |||
                                CTC CC  TTGAGGTG    CCC
                                  _  CC       ____
GAM2986  NFAT5    5'  GAGGGGGAACTCCACGGG    68158     A  AA       TGCA
                                GAG GG  AACTTTAT    GGG
                                ||| ||  ||||||||    |||
                                CTC CC  TTGAGGTG    CCC
                                  _  CC       ____
GAM2986  SEMA4F   3'  TGGAAGGAAAACTGAGATGGGG 68159     AG       TTAT  CA
                                TG  AGGAAAACT    TG  GGG
                                ||  |||||||||    ||  |||
                                AC  TCCTTTTGA    AC  CCC
                                 CT        CTCT  __
GAM2986  SFXN2    5'  TGAGAGGAGGACCTGGGCTGGG 68160         AA    TATT  A
                                TGAGAGGA  ACTT    GC GGG
                                ||||||||  ||||    || |||
                                ACTCTCCT  TGGA    CG CCC
                                     CC    CC__  A
GAM2986  SIMRP7   3'  GAGAGGGGAGAACTCTGCAGGG 68161       AA__     TAT
                                GAGAGG    AACTT   TGCAGGG
                                ||||||    |||||   |||||||
                                CTCTCC    TTGAG   ACGTCCC
                                   CCTC     ___
GAM2986  VPS28    3'  GAGAGCATCTTTATTGTGGGG  68162      GAAAA      CA
                                GAGAG    CTTTATTG  GGG
                                |||||    ||||||||  |||
                                CTCTC    GAAATAAC  CCC
                                   GTA__       AC
GAM2986  LOC127281 3'  TGAAGGAGAGTTTTATTGCAG  68163     G   AAAC
                                TGA AGGA    TTTATTGCAG
                                ||| ||||    ||||||||||
                                ACT TCCT    AAATAACGTC
                                  _    CTCA
GAM2986  LOC145566 5'  TGAGAGAGAACCTGCAGG    68164       AA    TTAT
                                TGAGAGG  AACT    TGCAGG
                                |||||||  ||||    ||||||
                                ACTCTCT  TTGG    ACGTCC
                                    C_   _____
GAM2986  LOC146443 5'  TGGAGGAAGGCTTGCACCACAG 68165     A     AA  _  TG
            GG                    TG GAGGAA  CTT TAT  CAGGG
                                || ||||||  ||| |||  |||||
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                                AC CTCCTT  GAA GTG  GTCCC
                                 _     CC   C   GT
GAM2986  LOC148697 3'  TGAGCAGGAAAAGTTGTGGGG  68166     _     CTTTA   CA
                                TGAG AGGAAAA    TTG  GGG
                                |||| |||||||    |||  |||
                                ACTC TCCTTTT    AAC  CCC
                                  G      C____   AC
GAM2986  LOC149194 5'  TGAGAGGAAGCTGTCCAGG   68167        AA  TTATTG
                                TGAGAGGAA  CT     CAGG
                                |||||||||  ||     ||||
                                ACTCTCCTT  GA     GTCC
                                     C_  CAG___
GAM2986  LOC51195  3'  TGAGTGGGGGACTTGCAAGG   68168     A  AAA   TTAT
                                TGAG GG   ACT    TGCAGGG
                                |||| ||   |||    |||||||
                                ACTC CC   TGA    ACGTTCC
                                  A  CCC   ____
GAM2986  LOC91963  5'  TAAGAGGAAGACAAAAATGCAG 68169         A  TTTAT
            GG                    TGAGAGGAA AC     TGCAGGG
                                |||||||||  ||     |||||||
                                ATTCTCCTT TG     ACGTCCC
                                     C  TTTTT
GAM2987  DDEF2    3'  TAAAAAGTGGGATGTTTGGGAG 68172         TA   AG  A
            TA                    TAAAAAGTG  GTG  TG GAGTA
                                |||||||||  |||  || |||||
                                ATTTTTCAC  TAC  AC CTCAT
                                     CC   AA  C
GAM2987  DMXL1    3'  AGTGTGGTGAATTAAGT     68173      A     GA
                                AGTGT GTGAGT  GAGT
                                |||||  ||||||  ||||
                                TCACA CACTTA  TTCA
                                  C     A_
GAM2987  EGFL5    3'  TAAAAAGTGTAGGACCAAGGT  68174          T  G    A
                                TAAAAAGTGTAG GA TGAG GT
                                |||||||||||| || |||| ||
                                ATTTTTCACATC CT GTTC CA
                                       _  G   _
GAM2987  ITGBL1   3'  GTGAGTTTAAAGTGAGAGTA   68175     T  ___
                                GTG AGT   GAGTGAGAGTA
                                |||  |||   ||||||||||
                                CAC TCA   TTCACTCTCAT
                                  _   AAT
GAM2987  MGAT2    3'  AAGTGTGTCAAGAGAGT     68176       A  G  T
                                AAGTGT GT AG GAGAGT
                                ||||||  ||  ||  ||||||
                                TTCACA CA TT CTCTCA
                                   _  G  _
GAM2987  OAS2     3'  AAAAGTTTAAGTGAGGGT    68177       GTAG       A
                                AAAAGT    TGAGTGAG GT
                                ||||||    ||||||||  ||
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                                TTTTCA    ATTCACTC CA
                                   A___       C
GAM2987  PTPN7    3'  AAGAGTAGTTGGTGGGAGT   68178    T    GA   A
                                AAG GTAGT  GTG GAGT
                                ||| |||||  ||| ||||
                                TTC CATCA  CAC CTCA
                                  T    AC   C
GAM2987  PTPN7    3'  AAGAGTAGTTGGTGGGAGT   68178    T    GA   A
                                AAG GTAGT  GTG GAGT
                                ||| |||||  ||| ||||
                                TTC CATCA  CAC CTCA
                                  T    AC   C
GAM2987  PTPN7    3'  AAGAGTAGTTGGTGGGAGT   68178    T    GA   A
                                AAG GTAGT  GTG GAGT
                                ||| |||||  ||| ||||
                                TTC CATCA  CAC CTCA
                                  T    AC   C
GAM2987  C17orf31 5'  AAAGTGTACTGTGGGAGT    68179       G GA   A
                                AAAGTGTA T  GTG GAGT
                                |||||||| |  ||| ||||
                                TTTCACAT A  CAC CTCA
                                     G __   C
GAM2987  C9orf14  5'  AAGTGGCAGGTGAGAGTA    68180     TA  GA
                                AAGTG  GT  GTGAGAGTA
                                |||||  ||  |||||||||
                                TTCAC  CG  CACTCTCAT
                                   __  TC
GAM2987  CREG     3'  TAAAAAGCTGTGGAGAGT    68181       GTA   AGT
                                TAAAAAGT   GTG   GAGAGT
                                ||||||||   |||   ||||||
                                ATTTTTCG   CAC   CTCTCA
                                     A__   ___
GAM2987  CXYorf1  3'  AAAAGGCTGAGTGAGGGT    68182     T  AG      A
                                AAAAG GT  TGAGTGAG GT
                                |||||  ||  |||||||| ||
                                TTTTC CG  ACTCACTC CA
                                   _ __       C
GAM2987  DJ971N18.2 3'  TGAAGAGTGTGGAGAGC    68183   A  T  A  AGT
                                A AAG GT GTG   GAGAGT
                                | ||| || |||   ||||||
                                A TTC CA CAC   CTCTCG
                                 C  T  _  ___
GAM2987  FLJ10346 5'  TGAATGAGTGTGCGAGGGT   68184   A   T   A   A
                                A AGTG AGTG GTGAG GT
                                | |||| |||| ||||| ||
                                A TTAC TCAC CGCTC CA
                                 C   _   A   C
GAM2987  FLJ10971 3'  TAAAAAGTGTACGTTGTGGGTG 68185          ____  A
                                TAAAAAGTGTA   GTG GTG
                                ||||||||||   ||| |||
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                                ATTTTTCACAT   CAC CAC
                                      GCAA  C
GAM2987  FLJ13611  3'  TAAAAAGTGTGCTGACTCGTG  68186        AG  ___
                                TAAAAAGTGT  TGA  GTG
                                ||||||||||  |||  |||
                                ATTTTTCACA  ACT  CAC
                                      CG  GAG
GAM2987  FLJ23467  3'  AAAAGTGTTAGTGCCAGGTG  68187       _  A___
                                AAAAGTGT AGTG   GTG
                                ||||||||| ||||   |||
                                TTTTCACA TCAC   CAC
                                     A   GGTC
GAM2987  KIAA0494  3'  AAAAAGGTGTGGGGTGAGAGT  68188      T A  A_
                                AAAAAG GT GTG  GTGAGAGT
                                |||||| || |||  ||||||||
                                TTTTTC CA CAC  CACTCTCA
                                   _ _  CC
GAM2987  KIAA1130  3'  GTGACAGTGTGGGTGAGAGT  68189    _   A__
                                GTG TAGTG  GTGAGAGT
                                ||| |||||  ||||||||
                                CAC GTCAC  CACTCTCA
                                  T    ACC
GAM2987  KIAA1754  3'  AAGTGTAGCTGAAAAAGT   68190        GAGT
                                AAGTGTAGT   GAGAGT
                                |||||||||   ||||||
                                TTCACATCG   TTTTCA
                                      ACT_
GAM2987  LEC3    3'  TAAAAAGTGGTAGTGCAGGTG  68191        _   A__
                                TAAAAAGTG TAGTG  GTG
                                ||||||||| |||||  |||
                                ATTTTTCAC ATCAC  CAC
                                      C    GTC
GAM2987  MGC32043  3'  TGAAAGCTGATGACAGTGGGAG 68192   A   GTA  __  A
            T                    A AAAGT  GTGA  GTG GAGT
                                | |||||  ||||  ||| ||||
                                A TTTCG  TACT  CAC CTCA
                                 C    AC_  GT  C
GAM2987  MGC861   3'  GCAAGAGTGAGTGTGGGAGT  68193    T_     A__
                                GTG  AGTGAGTG  GAGT
                                |||  ||||||||  ||||
                                CGT  TCACTCAC  CTCA
                                  TC      ACC
GAM2987  MRG15   3'  AAACATAAGTGAGTGAGAGT  68194    TG  _
                                AAG  TA GTGAGTGAGAGT
                                |||  || ||||||||||||
                                TTT  AT CACTCACTCTCA
                                  GT  T
GAM2987  PRO1048  3'  AAATGTAATAGAGAGT     68195        AGT
                                AAGTGTAGTG  GAGAGT
                                ||||||||||  ||||||
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                                TTTACATTAT  CTCTCA
                                    ___
GAM2987  SEC31B-1  3'  AGTGTAGTATTAGGGAGAGT  68196        __ T
                                AGTGTAGTG  AG GAGAGT
                                |||||||||  || ||||||
                                TCACATCAT  TC CTCTCA
                                     AA  C
GAM2987  LOC130813 3'  TAAAAAGTGTGTAAGAGT    68197         AGTGA
                                TAAAAAGTGT    GTGAGAGT
                                ||||||||||    ||||||||
                                ATTTTTCACA    CATTCTCA
                                    _____
GAM2987  LOC145781 3'  TAAAAAGTGTATGCCTCTGAGT 68198          _ ____
           G                     TAAAAAGTGTA GT    GAGTG
                                ||||||||||| ||    |||||
                                ATTTTTCACAT CG    CTCAC
                                       A  GAGA
GAM2987  LOC147004 3'  AAAGTGTCATGAGAGT      68199       AGTGA
                                AAAGTGT    GTGAGAGT
                                |||||||    ||||||||
                                TTTCACA    TACTCTCA
                                    G____
GAM2987  LOC150170 5'  AGGTAAAAGTGGGAGTA     68200    T   T    A
                                AG GTAG GAGTG GAGTA
                                || |||| ||||| |||||
                                TC CATT TTCAC CTCAT
                                 _   _    C
GAM2987  LOC150175 5'  AGGTAAAAGTGGGAGTA     68200    T   T    A
                                AG GTAG GAGTG GAGTA
                                || |||| ||||| |||||
                                TC CATT TTCAC CTCAT
                                 _   _    C
GAM2987  LOC150215 5'  AGGTAAAAGTGGGAGTA     68200    T   T    A
                                AG GTAG GAGTG GAGTA
                                || |||| ||||| |||||
                                TC CATT TTCAC CTCAT
                                 _   _    C
GAM2987  LOC150218 5'  AGGTAAAAGTGGGAGTA     68200    T   T    A
                                AG GTAG GAGTG GAGTA
                                || |||| ||||| |||||
                                TC CATT TTCAC CTCAT
                                 _   _    C
GAM2987  LOC163231 5'  TAATGAATGAGTGGGTGAGAGT 68201     AA   T   A
                                TAA  AGTG AGTG GTGAGAGT
                                |||  |||| |||| ||||||||
                                ATT  TTAC TCAC CACTCTCA
                                  AC   _   C
GAM2987  LOC200093 3'  AAAAGGCTGAGTGAGGGT    68182      T  AG      A
                                AAAAG GT  TGAGTGAG GT
                                ||||| ||  |||||||| ||
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                                TTTTC CG  ACTCACTC CA
                                  _ __      C
GAM2987 LOC201689 5' AAAGTGTAGTCCAAGGGTA  68202       GAG   A
                                AAAGTGTAGT  TGAG GTA
                                ||||||||||  |||| |||
                                TTTCACATCA  GTTC CAT
                                    G__   C
GAM2987 LOC91040 3' AAAAGGCTGAGTGAGGGT   68182     T AG     A
                                AAAAG GT  TGAGTGAG GT
                                ||||| ||  |||||||| ||
                                TTTTC CG  ACTCACTC CA
                                  _ __      C
GAM2988 SERPINB5 3' GCAGCATATTAAGGTGTTGAT 68205      AG  TA  C
                                GCAGCATA  TAG  TGT GAT
                                ||||||||  |||  ||| |||
                                CGTCGTAT  ATT  ACA CTA
                                    A_  CC  A
GAM2988 LOC256158 5' TCGCAGTACAGGTAGGCTG  68206     C  A  TA
                                TCGCAG ATA GTAG  TG
                                ||||||| ||| ||||  ||
                                AGCGTC TGT CATC  AC
                                   A  C   CG
GAM2989 ABCC1   3' AAGAGGACCATCCAGGGCC   68209     A AGTGG
                                AAGAG AT    CCAGGGCC
                                ||||| ||    ||||||||
                                TTCTC TG    GGTCCCGG
                                  C  GTA__
GAM2989 ABCC1   3' AAGAGGACCATCCAGGGCC   68209     A AGTGG
                                AAGAG AT    CCAGGGCC
                                ||||| ||    ||||||||
                                TTCTC TG    GGTCCCGG
                                  C  GTA__
GAM2989 ABCC1   3' AAGAGGACCATCCAGGGCC   68209     A AGTGG
                                AAGAG AT    CCAGGGCC
                                ||||| ||    ||||||||
                                TTCTC TG    GGTCCCGG
                                  C  GTA__
GAM2989 ADRA2A  3' GAAGGGGAATTAGCCAGGGC  68210     A_   AG
                                GAAG  GAAT  TGGCCAGGGC
                                ||||  ||||  ||||||||||
                                CTTC  CTTA  ATCGGTCCCG
                                  CC    __
GAM2989 BRCA1   3' GAGAGGAGCTCCCAGGGCC   68211     AT   GG
                                GAGA  AGT  CCAGGGCC
                                ||||  |||  ||||||||
                                CTCT  TCG  GGTCCCGG
                                  CC   AG
GAM2989 BRCA1   3' GAGAGGAGCTCCCAGGGCC   68211     AT   GG
                                GAGA  AGT  CCAGGGCC
                                ||||  |||  ||||||||
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                          CTCT TCG GGTCCCGG
                            CC  AG
GAM2989 BRCA1   3' GAGAGGAGCTCCCAGGGCC  68211    AT  GG
                          GAGA AGT CCAGGGCC
                          |||| ||| ||||||||
                          CTCT TCG GGTCCCGG
                            CC  AG
GAM2989 BRCA1   3' GAGAGGAGCTCCCAGGGCC  68211    AT  GG
                          GAGA AGT CCAGGGCC
                          |||| ||| ||||||||
                          CTCT TCG GGTCCCGG
                            CC  AG
GAM2989 BRCA1   3' GAGAGGAGCTCCCAGGGCC  68211    AT  GG
                          GAGA AGT CCAGGGCC
                          |||| ||| ||||||||
                          CTCT TCG GGTCCCGG
                            CC  AG
GAM2989 BRCA1   3' GAGAGGAGCTCCCAGGGCC  68211    AT  GG
                          GAGA AGT CCAGGGCC
                          |||| ||| ||||||||
                          CTCT TCG GGTCCCGG
                            CC  AG
GAM2989 BRCA1   3' GAGAGGAGCTCCCAGGGCC  68211    AT  GG
                          GAGA AGT CCAGGGCC
                          |||| ||| ||||||||
                          CTCT TCG GGTCCCGG
                            CC  AG
GAM2989 BRCA1   3' GAGAGGAGCTCCCAGGGCC  68211    AT  GG
                          GAGA AGT CCAGGGCC
                          |||| ||| ||||||||
                          CTCT TCG GGTCCCGG
                            CC  AG
GAM2989 BRCA1   3' GAGAGGAGCTCCCAGGGCC  68211    AT  GG
                          GAGA AGT CCAGGGCC
                          |||| ||| ||||||||
                          CTCT TCG GGTCCCGG
                            CC  AG
GAM2989 BRCA1   3' GAGAGGAGCTCCCAGGGCC  68211    AT  GG
                          GAGA AGT CCAGGGCC
                          |||| ||| ||||||||
                          CTCT TCG GGTCCCGG
                            CC  AG
GAM2989 BRCA1   3' GAGAGGAGCTCCCAGGGCC  68211    AT  GG
                          GAGA AGT CCAGGGCC
                          |||| ||| ||||||||
                          CTCT TCG GGTCCCGG
                            CC  AG
GAM2989 BRCA1   3' GAGAGGAGCTCCCAGGGCC  68211    AT  GG
                          GAGA AGT CCAGGGCC
                          |||| ||| ||||||||
                          CTCT TCG GGTCCCGG
                            CC  AG
GAM2989 CHGA    3' AAGGGGACAGCAGAGCCAGGGC 68212    AGA  __
          C                 AAG  ATAGT GGCCAGGGCC
                          |||  ||||| ||||||||||
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                                TTC   TGTCG  TCGGTCCCGG
                                  CCC    TC
GAM2989  CHRM1    3'  AAGGAAAGAACATTTGGGGCC  68213    A      GTGGCCA
                                AAG AGAGAATA      GGGCC
                                ||| ||||||||      |||||
                                TTC TTTCTTGT      CCCGG
                                  C       AAAC___
GAM2989  CNTNAP2  3'  GAAGAGAATGTTGGGGGCC   68214        AG   CCA
                                GAAGAGAAT  TGG   GGGCC
                                |||||||||  |||   |||||
                                CTTCTCTTA  ACC   CCCGG
                                      CA   ___
GAM2989  CREBL2   3'  AGAAGAGAGAGTGGTAAG    68215        AT    CC
                                AGAAGAGA  AGTGG  AGG
                                ||||||||  |||||  |||
                                TCTTCTCT  TCACC  TTC
                                     C_    A_
GAM2989  CYP1A2   3'  GAAGAGAAACAAGGGC      68216        TAGTG  C
                                GAAGAGAA    GC AGGGC
                                ||||||||    || |||||
                                CTTCTCTT    TG TCCCG
                                     _____  T
GAM2989  DEDD     3'  AGGAGAGAGTGGAAAGGGCC   68217    A    ATA    CC
                                AG AGAGA   GTGG  AGGGCC
                                || |||||   ||||  ||||||
                                TC TCTCT   CACC  TCCCGG
                                 C     ___    TT
GAM2989  E2F1     3'  AGGGACAGGGGGCTCCAGGGC  68218    A  A   T  ___
                                AG GA TAG GG   CCAGGGC
                                || || ||| ||   |||||||
                                TC CT GTC CC   GGTCCCG
                                 C  _   C  CGA
GAM2989  EN2      5'  GAGAGACGCGAGGCCAGGGCC  68219    A    ATAGT
                                GA GAGA    GGCCAGGGCC
                                || ||||    ||||||||||
                                CT CTCT    CCGGTCCCGG
                                 _    GCGCT
GAM2989  ENC1     3'  AAGAAGAGAATGAGTTCAGGCC 68220          _   GGCCA
                                AAGAAGAGAAT AGT    GGGCC
                                |||||||||| |||    |||||
                                TTCTTCTCTTA TCA    TCCGG
                                      C   AG___
GAM2989  ENO2     3'  AAGAACAGGGAACCTAGGG   68221        T  __  _
                                GAGAATAG GG  CC AGGG
                                |||||||| ||  || ||||
                                TTCTTGTC CC  GG TCCC
                                     _ TT  A
GAM2989  ERH      3'  AAGAGGAGGTAACGGGGG    68222      A   AATA    CA
                                AAGA GAG   GTGGC  GGG
                                |||| |||   |||||  |||
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                                TTCT CTC    CATTG  CCC
                                  C  ____    CC
GAM2989  EXTL3    3'  GAAGAGAATGTGAGTTGGCCCT 68223        A  _________  CAGG
                 G                 AAGAGAAT GTG       GC   G
                                   |||||||| |||       ||   |
                                   TTCTCTTA CAC       CG   C
                                      _  TCAAIIIC  GGAC
GAM2989  FGFR1    3'  AGAAGAGAAGGGAGGGC     68224        AT  T  CC
                                   AGAAGAGA  AG GG  AGGGC
                                   ||||||||  || ||  |||||
                                   TCTTCTCT  TC CC  TCCCG
                                      __  _  __
GAM2989  FGFR1    3'  AGAAGAGAAGGGAGGGC     68224        AT  T  CC
                                   AGAAGAGA  AG GG  AGGGC
                                   ||||||||  || ||  |||||
                                   TCTTCTCT  TC CC  TCCCG
                                      __  _  __
GAM2989  FGR      3'  GAAGAAATAGTGCTTGGGGCC  68225       A    GCCA
                                   GAAGAGA TAGTG   GGGCC
                                   ||||||| |||||   |||||
                                   CTTCTTT ATCAC   CCCGG
                                      _    GAAC
GAM2989  GABRE    5'  GAGCAGGCAGAGGGCCAGGGC  68226     AA__  T_
                                   GAG   TAG  GGCCAGGGC
                                   |||   |||  |||||||||
                                   CTC   GTC  CCGGTCCCG
                                     GTCC   TC
GAM2989  HCN4     3'  AAGAAGAGGGAAGGAAGGGCC  68227        AATAGT  CC
                                   AAGAAGAG     GG  AGGGCC
                                   ||||||||     ||  ||||||
                                   TTCTTCTC     CC  TCCCGG
                                      CCTT__  T_
GAM2989  HS3ST3A1 5'  GAGGCAGCGGCCGGGGC     68228     AA       A
                                   GAG  TAGTGGCC GGGC
                                   |||  |||||||| ||||
                                   CTC  GTCGCCGG CCCG
                                     C_       C
GAM2989  IKBKB    3'  AAGAGGAAGTGAGGATGGGGCC 68229      AAT    CCA__
                                   AAGAG   AGTGG    GGGCC
                                   |||||   |||||    |||||
                                   TTCTC   TCACT    CCCGG
                                      CT_    CCTAC
GAM2989  ITGA9    3'  AAGAAGAGAACAGCATCAGTGG 68230            GC  ___
                GGCC                  AAGAAGAGAATAGTG  CA   GGGCC
                                      ||||||||||||||  ||   |||||
                                      TTCTTCTCTTGTCGT  GT   CCCGG
                                               A_  CAC
GAM2989  JUP      3'  GAAGCTTTAGTGGCCAGGGCC  68231      AGAA
                                   GAAG    TAGTGGCCAGGGCC
                                   ||||    ||||||||||||||
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                                CTTC    ATCACCGGTCCCGG
                                  GAA_
GAM2989  MASP1    3'  AAGAAGGGAAGGAGGCCAGGGC 68232       A   TAGT
              C                   AAGAAG GAA    GGCCAGGGCC
                                  |||||| |||    ||||||||||
                                  TTCTTC CTT    CCGGTCCCGG
                                     C   CCT_
GAM2989  MPP2     3'  AGGAAAGGACCAGGG       68233    A   T  T
                                  AG GAA AG GGCCAGGG
                                  || ||| || ||||||||
                                  TC CTT TC CTGGTCCC
                                   _   _ _
GAM2989  MTAP     3'  AGAAGAGAATGGTGGGG     68234          A    CCA
                                  AGAAGAGAAT GTGG   GG
                                  |||||||||| ||||   ||
                                  TCTTCTCTTA CACC   CC
                                        C   ___
GAM2989  MYO1A    3'  AGGAGAGAACAAGAAGGG    68235    A       T  CC
                                  AG AGAGAATAG GG  AGGG
                                  || |||||||| ||  ||||
                                  TC TCTCTTGTT CT  TCCC
                                   C       _ __
GAM2989  MYO1F    3'  GAGAAGGCAGTATCCCAGGGCC 68236      __    G_
                                  GAGAA  TAGTG  CCAGGGCC
                                  |||||  |||||  ||||||||
                                  CTCTT  GTCAT  GGTCCCGG
                                     CC    AG
GAM2989  NPTX1    3'  AAGGAGAGGGGTGCTGGGGCC  68237     A    AATA   G CA
                                  AAG AGAG    GTG C  GGGCC
                                  ||| ||||    ||| |  |||||
                                  TTC TCTC    CAC G  CCCGG
                                    C    CC__   _ AC
GAM2989  OVOL1    5'  AGAAGAGAGGGTCCAGCGG    68238         ATA T  _    _
                                  AGAAGAGA   G GG CCAG GG
                                  ||||||||   | || |||| ||
                                  TCTTCTCT   C CC GGTC CC
                                       ___ _  A    G
GAM2989  PFKFB2   3'  AAGGGCAGGAGGCCAGGGC    68239     AA   T_
                                  GAG  TAG  GGCCAGGGC
                                  |||  |||  |||||||||
                                  TTC  GTC  CCGGTCCCG
                                    CC   CT
GAM2989  PFKFB4   3'  GAGAGACCACCGGCCAGGGCC  68240    A    A  G
                                  GA GAGA TA TGGCCAGGGCC
                                  || |||| || ||||||||||
                                  CT CTCT GT GCCGGTCCCGG
                                   _    G  G
GAM2989  PLCB2    3'  GAAGAGGGGTGAGCCAGGG    68241       AATA   _
                                  GAAGAG    GTG GCCAGGG
                                  ||||||    ||| |||||||
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                                CTTCTC   CAC CGGTCCC
                                   CC__  T
GAM2989 PPARBP   5' AAGAGGAGGGTGCTCGAGGCC 68242     A  AATA  GCCA
                                AAGA GAG   GTG   GGGCC
                                |||| |||   |||   |||||
                                TTCT CTC   CAC   TCCGG
                                  C  C___  GAGC
GAM2989 PTGFRN   3' AGAGAGGAATAGTGGTGGC   68243    A  _     CCAG
                                AGA GAG AATAGTGG   GGC
                                ||| ||| ||||||||   |||
                                TCT CTC TTATCACC   CCG
                                  _  C      A___
GAM2989 PYCR1    3' AGAAGAGAAGGTGGTGGC    68244       TA   CCAG
                                AGAAGAGAA  GTGG   GGC
                                |||||||||  ||||   |||
                                TCTTCTCTT  CACC   CCG
                                     C_   A___
GAM2989 RDS      3' GAGGGGAGGGGCCCCAGGGCC 68245    AAT  T   __
                                GAG   AG GGCC  AGGGCC
                                |||   || ||||  ||||||
                                CTC   TC CCGG  TCCCGG
                                  CCC  C   GG
GAM2989 REG1A    3' AGAAGAGAGTGTCCAGG     68246       ATA  G
                                AGAAGAGA   GTG CCAGG
                                ||||||||   ||| |||||
                                TCTTCTCT   CAC GGTCC
                                     ___   A
GAM2989 RFX1     3' GAGGGGGGCGGCCAAGGGGCC 68247     AATA     __
                                GAG   GTGGCCA  GGGCC
                                |||   |||||||  |||||
                                CTC   CGCCGGT  CCCGG
                                  CCCC      TC
GAM2989 SIGLECL1 3' AGAAGAGAATGGTGGGTACC  68248       A   CCAGG
                                AGAAGAGAAT GTGG    GCC
                                |||||||||| ||||    |||
                                TCTTCTCTTA CACC    TGG
                                     C   CA___
GAM2989 SIGLECL1 3' AGAAGAGAATGGTGGGTACC  68248       A   CCAGG
                                AGAAGAGAAT GTGG    GCC
                                |||||||||| ||||    |||
                                TCTTCTCTTA CACC    TGG
                                     C   CA___
GAM2989 SLC12A7  3' AGCGGAGCCATGGCCAGGGC  68249    AA  AATA
                                AG  GAG   GTGGCCAGGGC
                                ||  |||   ||||||||||
                                TC  CTC   TACCGGTCCCG
                                 GC  GG__
GAM2989 TRIM8    3' AAGAGGAGAAACAAGCCCGGGG 68250     A    TAGT   A_
            CC                   AAGA GAGAA   GGCC  GGGCC
                                |||| |||||   ||||  |||||
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                                TTCT CTCTT   TCGG  CCCGG
                                  C    TGT_   GC
GAM2989  TRPV4    3'  GAGAGGCAGGGGCTGGGGCC  68251     A_  T  CA
                                GAGA  TAG GGC  GGGCC
                                ||||  ||| |||  |||||
                                CTCT  GTC CCG  CCCGG
                                  CC   C   AC
GAM2989  WBSCR14  3'  GAAGGGCAGAGCCAGGGCC   68252     AGAA  T
                                GAAG   TAG GGCCAGGGCC
                                ||||   ||| ||||||||||
                                CTTC   GTC TCGGTCCCGG
                                  CC__  _
GAM2989  WBSCR14  3'  GAAGGGCAGAGCCAGGGCC   68252     AGAA  T
                                GAAG   TAG GGCCAGGGCC
                                ||||   ||| ||||||||||
                                CTTC   GTC TCGGTCCCGG
                                  CC__  _
GAM2989  XRCC5    3'  AAAAAGAGAATAAGGG      68253          GTGGCC
                                AAGAAGAGAATA     AGGG
                                ||||||||||||     ||||
                                TTTTTTCTCTTAT     TCCC
                                          _______
GAM2989  ZNF261   3'  AAGAAGATAAAAGCCAGGG   68254       GAATAGT
                                AAGAAGA      GGCCAGGG
                                |||||||      ||||||||
                                TTCTTCT      TCGGTCCC
                                    ATTT___
GAM2989  ACAS2L   3'  GAAGGACAAGCCAGGGC     68255     A  ATAGT
                                GAAG GA     GGCCAGGGC
                                |||| ||     |||||||||
                                CTTC CT     TCGGTCCCG
                                  _  GT___
GAM2989  ANLN     5'  GAAGAGAAAAGTGAGTCGGCCC 68256       T  _________  CAGG
            TGGC                  AGAGAA AGTG       GC    GC
                                |||||| ||||       ||    ||
                                TCTCTT TCAC       CG    CG
                                   T   TCAGIIIC  GGAC
GAM2989  ARHGAP9  3'  AAGAAGAGAAGCAGGG      68257        ATAGT  C
                                AAGAAGAGA    GGC AGGG
                                |||||||||    ||| ||||
                                TTCTTCTCT    TCG TCCC
                                          _____  _
GAM2989  BTN3A1   3'  GAAAAGAACCTCAGGGC     68258        AGTGGC
                                GAAGAGAAT     CAGGGC
                                |||||||||     ||||||
                                CTTTTCTTG     GTCCCG
                                    GA_____
GAM2989  C4.4A    3'  AGAAGAGGGGTACCCAGGGCC  68259       AATA  G
                                AGAAGAG    GTG CCAGGGCC
                                |||||||    ||| ||||||||
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                                TCTTCTC   CAT GGTCCCGG
                                   CC__   G
GAM2989  CAT56    3'  GAGAAGAATGGGGAGGGCC   68260      T    CC
                                GAGAA AGTGG  AGGGCC
                                ||||| |||||  ||||||
                                CTCTT TTACC  TCCCGG
                                   C    CC
GAM2989  CBX6     3'  AGGAAAGAGCCAGGG      68261    A   T  T
                                AG GAA AG GGCCAGGG
                                || ||| || ||||||||
                                TC CTT TC TCGGTCCC
                                 _  _ _
GAM2989  CD2BP2   5'  AAGAAGAGATGCTTGCGCCAGG 68262         ATAG  _
              GC                  AAGAAGAGA   TG GCCAGGGC
                                |||||||||   || ||||||||
                                TTCTTCTCT   AC CGGTCCCG
                                     ACGA  G
GAM2989  CHST3    3'  AGAGGAGAAGCCAGGGC    68263    A   ATAGT
                                AGA GAGA    GGCCAGGGC
                                ||| ||||    |||||||||
                                TCT CTCT    TCGGTCCCG
                                  C   _____
GAM2989  CRELD1   5'  AAGGAGAGGAGGCCAGAG    68264    A   AATAGT
                                AAG AGAG    GGCCAGGG
                                ||| ||||    ||||||||
                                TTC TCTC    CCGGTCTC
                                  C   CT____
GAM2989  CRMP5    3'  GAAGGGGAAAGGGCCAGGGCC  68265    A_  T  T
                                GAAG  GAA AG GGCCAGGGCC
                                ||||  ||| || ||||||||||
                                CTTC  CTT TC CCGGTCCCGG
                                  CC  _ _
GAM2989  CRMP5    3'  AGAGGAAGGGCTGGCCAGGGC  68266    _  TA _
                                AGAG AA  G TGGCCAGGGC
                                |||| ||  | ||||||||||
                                TCTC TT  C ACCGGTCCCG
                                  C  CC G
GAM2989  CXorf1   3'  AAGAAGAGGAAATTGAAGGG   68267       AATAG   CC
                                AAGAAGAG    TGG  AGGG
                                ||||||||    |||  ||||
                                TTCTTCTC    ACT  TCCC
                                    CTTTA   __
GAM2989  DDX39    3'  GAGGAGCTGGGCCAGGGCC    68268    A   AATAGT
                                GA GAG     GGCCAGGGCC
                                || |||     ||||||||||
                                CT CTC     CCGGTCCCGG
                                 C  GAC___
GAM2989  DJ167A19.1 5'  GAAGAAAATTTGCAGGG     68269        AGTG  C
                                GAAGAGAAT   GC AGGG
                                |||||||||   || ||||
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                                CTTCTTTTA   CG TCCC
                                     AA__  _
GAM2989  DKFZP564K0322 3'  AACAAGAGAATAAAGAGGG   68270    G       TGGCC
                                AA AAGAGAATAG    AGGG
                                || ||||||||||    ||||
                                TT TTCTCTTATT    TCCC
                                 G        TC___
GAM2989  DRIL2    3'  GAAGAGACTAGTGGCCTGGG   68271       A      A
                                GAAGAGA TAGTGGCC GGG
                                ||||||| |||||||| |||
                                CTTCTCT ATCACCGG CCC
                                    G       A
GAM2989  EFNA5    3'  AGAGAAGCCAAGGGCCAGGGC  68272    AG  AAT  T
                                AGA  AG   AG GGCCAGGGC
                                |||  ||   || |||||||||
                                TCT  TC   TC CCGGTCCCG
                                  CT  GGT  _
GAM2989  FER1L4   3'  AAGAAGATGCGTCAGCTGGGGC 68273       GAATA  _   CA
                                AAGAAGA    GT GGC  GGGC
                                |||||||    || |||  ||||
                                TTCTTCT    CA TCG  CCCG
                                    ACG__  G   AC
GAM2989  FLJ10415 3'  GAAGAAAAAACCTAGGGC    68274       TAGT   _
                                GAAGAGAA   GGCC AGGGC
                                ||||||||   |||| |||||
                                CTTCTTTT   TTGG TCCCG
                                     _____   A
GAM2989  FLJ10716 3'  AAGAAAAGGGGGCTGGGGC   68275       AATAGT   CA
                                AAGAAGAG    GGC  GGGC
                                ||||||||    |||  ||||
                                TTCTTTTC    CCG  CCCG
                                    CC_____  AC
GAM2989  FLJ10842 3'  AAGAAGAGAAATGGAAGGGCC  68276        TA   CC
                                AAGAAGAGAA  GTGG  AGGGCC
                                ||||||||||  ||||  ||||||
                                TTCTTCTCTT  TACC  TCCCGG
                                     __   T_
GAM2989  FLJ22055 3'  AAGAAGAGAACTGGTGGC    68277         A_
                                AAGAAGAGAAT  GTGGC
                                ||||||||||  |||||
                                TTCTTCTCTTG  CACCG
                                      AC
GAM2989  FLJ22215 3'  GAGCAGGGTTGTGGCCAGGGCC 68278    AATA___
                                GAG      GTGGCCAGGGCC
                                |||      ||||||||||||
                                CTC      CACCGGTCCCGG
                                  GTCCCAA
GAM2989  FLJ22969 3'  AAGAAAAGAGCCAGGG      68279        ATAGTG
                                AAGAAGAGA    GCCAGGG
                                |||||||||    |||||||
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                                TTCTTTTTCT     CGGTCCC
                                       ______
GAM2989  FLJ23231  3'  AAGAAGAGGGTGTAGACGGAGG 68280        AA__  _  CC
              GCC                    AAGAAGAG   TAG TGG  AGGGCC
                                |||||||||   ||| |||  ||||||
                                TTCTTCTC   ATC GCC  TCCCGG
                                    CCAC   T  __
GAM2989  FRAT1    3'  GAGAGGAGGAACCCAGGGCC   68281     AT  TG  _
                                GAGA  AG  GCC AGGGCC
                                ||||  ||  ||| ||||||
                                CTCT  TC  TGG TCCCGG
                                  CC  CT   G
GAM2989  GMEB2    3'  GATGAGGGCTTCTCCAGGGCC  68282    A   AATA  GG__
                                GA GAG    GT    CCAGGGCC
                                || |||    ||    ||||||||
                                CT CTC    CG    GGTCCCGG
                                 A   C___  AAGA
GAM2989  GPS2     3'  GAAGAGGGGTACCAGGGCC    68283       AATA   G
                                GAAGAG    GTG CCAGGGCC
                                ||||||    ||| ||||||||
                                CTTCTC    CAT GGTCCCGG
                                   CC__   _
GAM2989  HA-1     3'  GAAAAGGGAGTCCAGGGC     68284       AAT   GG
                                GAAGAG   AGT  CCAGGGC
                                ||||||   |||  |||||||
                                CTTTTC   TCA  GGTCCCG
                                   CC_   __
GAM2989  HLA-DRB3  5'  AGAAGAGGACAGGACCAGGGGC 68285        A    T       _
              C                   AGAAGAG ATAG GGCCAGGG CC
                                ||||||| |||| |||||||| ||
                                TCTTCTC TGTC CTGGTCCC GG
                                   C    _       C
GAM2989  HN1L     3'  AAGAAGAGTAATGTCAGGG    68286        AA    GC
                                AAGAAGAG  TAGTG  CAGGG
                                ||||||||  |||||  |||||
                                TTCTTCTC  ATTAC  GTCCC
                                     __     A_
GAM2989  HRIHFB2122 3'  AGACAGAGGGGGACCAGGG    68287     _   AATAGT
                                AGA AGAG     GGCCAGGG
                                ||| ||||     ||||||||
                                TCT TCTC     CTGGTCCC
                                  G    CCC___
GAM2989  KIAA0266  3'  AGGAAGTGGAATCAGGGC    68288    A  AT    C__
                                AG GA  AGTGG   CAGGGC
                                || ||  |||||   ||||||
                                TC CT  TCACC   GTCCCG
                                 _ __     TTA
GAM2989  KIAA0350  3'  GAAGGGTGGACCAGGGCC    68289     TA   _
                                GAA  GTGG CCAGGGCC
                                |||  |||| ||||||||
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                              CTT  CACC GGTCCCGG
                                CC    T
GAM2989 KIAA0352 3' AGAAGAGGATGTTCAAGGC   68290       AATA   GC
                              AGAAGAG   GTG  CAGGGC
                              |||||||   |||  ||||||
                              TCTTCTC   TAC  GTTCCG
                                 C___   AA
GAM2989 KIAA0427 3' GAAGGGGAGGGCCAGGGCC   68291     AGAAT  T
                              GAAG    AG GGCCAGGGCC
                              ||||    || ||||||||||
                              CTTC    TC CCGGTCCCGG
                                CCC__  _
GAM2989 KIAA0444 3' AGGGGAAATGTCAGCCAGGG  68292    AA   ATAG
                              AG  GAGA   TGGCCAGGG
                              ||  ||||   |||||||||
                              TC  CTTT   GTCGGTCCC
                               CC   ACA_
GAM2989 KIAA0522 3' AAGAAGAGGAGCTGGGGC    68293       AATAGT   CA
                              AAGAAGAG    GGC  GGGC
                              ||||||||    |||  ||||
                              TTCTTCTC    TCG  CCCG
                                   C_____   AC
GAM2989 KIAA0720 5' AGGAACAGGACCAGGG     68294    A    T
                              AG GAATAG GGCCAGGG
                              || |||||| ||||||||
                              TC CTTGTC CTGGTCCC
                               _    _
GAM2989 KIAA0792 3' GATGAGGCCACTGGCCAGGGC 68295   A   AA  G
                              GA GAG  TA TGGCCAGGGC
                              || |||  || ||||||||||
                              CT CTC  GT ACCGGTCCCG
                               A  CG  G
GAM2989 KIAA0980 5' AAGGGAAGGTGGGGCCAGGGC 68296    A  TAGT_
                              AAG GAA    GGCCAGGGC
                              ||| |||    |||||||||
                              TTC CTT    CCGGTCCCG
                                C   CCACC
GAM2989 KIAA0997 3' AAAAGAGAGTAACTCTAGGG  68297       ATA    C__
                              AGAAGAGA   GTGGC   AGGG
                              ||||||||   |||||   ||||
                              TTTTCTCT   CATTG   TCCC
                                   ___     AGA
GAM2989 KIAA1024 3' AAGAGGAGAATAGTGGGGC   68298     A        CCAG
                              AAGA GAGAATAGTGG    GGC
                              |||| ||||||||||    |||
                              TTCT CTCTTATCACC    CCG
                                C         _____
GAM2989 KIAA1034 3' GAAGGATGGGGCCAGGGC    68299     A  ATAGT
                              GAAG GA    GGCCAGGGC
                              |||| ||    |||||||||
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                                CTTC CT    CCGGTCCCG
                                  _ ACC__
GAM2989 KIAA1466 5' AAGCAGGGGGGCCACCCAGGGC 68300    _ AATA G  _
            C                    AAG AG   GT GCC AGGGCC
                                ||| ||   || ||| ||||||
                                TTC TC   CG TGG TCCCGG
                                  G CCCC G  G
GAM2989 KIAA1656 3' AGGCAGAGGGTGAGCCAGGGCC 68301   A_   AATA  _
                                AG AGAG   GTG GCCAGGGCC
                                ||  ||||   ||| |||||||||
                                TC TCTC   CAC CGGTCCCGG
                                 CG  C___  T
GAM2989 KIAA1762 5' GAGAAGGGGGTTGGCCAGGGC 68302     TAG___
                                GAGAA    TGGCCAGGGC
                                |||||    ||||||||||
                                CTCTT    ACCGGTCCCG
                                   CCCCCA
GAM2989 KIAA1762 3' AGAAGAGAGAGTGGCGAAG   68303       AT    C
                                AGAAGAGA AGTGGC AGG
                                |||||||| |||||| |||
                                TCTTCTCT TCACCG TTC
                                     C_    C
GAM2989 KIAA1878 3' AAGAAGAGCAAGCCTGCGCCGG 68304       AAT  __ _  A
            GGC                   AAGAAGAG  AGT G GCC GGGC
                                |||||||  |||  | ||| ||||
                                TTCTTCTC  TCG C CGG CCCG
                                     GT_  GA G  C
GAM2989 LSM4    3' GAAGCGAAGGGCCAGGGCC   68305    A AT  T
                                GAAG GA AG GGCCAGGGCC
                                |||| ||  || ||||||||||
                                CTTC CT  TC CCGGTCCCGG
                                  G  __ _
GAM2989 LY6G5C   3' AAGAGGAAGAGCCAAGGC   68306     AAT  T
                                AAGAG  AG GGCCAGGGC
                                |||||  || |||||||||
                                TTCTC  TC TCGGTTCCG
                                   CT_ _
GAM2989 MAP2K5   5' AAGAAAGAGCCCCAGGGC   68307      AT  GG
                                AAGAGA AGT CCAGGGC
                                ||||||  |||  |||||||
                                TTCTTT TCG GGTCCCG
                                   C_  G_
GAM2989 MAP2K5   3' GAGGGCAGGGAAGCCAGGGCC 68308    AA  T__
                                GAG TAG  GGCCAGGGCC
                                |||  |||  ||||||||||
                                CTC GTC  TCGGTCCCGG
                                  CC  CCT
GAM2989 MBC3205  5' GAGAACAGAGGCGTCGGGGCC 68309       T  CA__
                                GAGAATAG GGC   GGGCC
                                |||||||| |||   |||||
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                                CTCTTGTC CCG   CCCGG
                                     T  CAGC
GAM2989  MGC2562  3'  AAGAGGAAAATAGTGCTGCTGG 68310          _________  CAGG
            CCCTGGC                GAGAATAGTG       GC   GC
                                |||||||||         ||   ||
                                CTTTTATCAC        CG   CG
                                     GACGAIIIC  GGAC
GAM2989  MUF1     3'  AAGATAGAACTGGTGGTTGGGG 68311     AG    A_   CCA
                                AAGA  AGAAT  GTGG   GGG
                                ||||  |||||  ||||   |||
                                TTCT  TCTTG  CACC   CCC
                                  A_    AC    AAC
GAM2989  NDP52    3'  AAGAAAGAAAGCAAGCCAGGGC 68312     A    TAGT
            C                   AAGA GAGAA    GGCCAGGGCC
                                |||| |||||    ||||||||||
                                TTCT TTCTT    TCGGTCCCGG
                                  _    TCGT
GAM2989  NUDT3    3'  AAGAAAACGTCTGGCCAGGGCC 68313       AG_
                                AAGAGAAT   TGGCCAGGGCC
                                ||||||||   ||||||||||
                                TTCTTTTG   ACCGGTCCCGG
                                     CAG
GAM2989  PADI2    3'  GAAGGAGGCAAACGCCAGGGCC 68314     A  A_   TG
                                GAAG GA  TAG  GCCAGGGCC
                                |||| ||  |||  |||||||||
                                CTTC CT  GTT  CGGTCCCGG
                                  _ CC   TG
GAM2989  POLE3    3'  AAGAAGAGGAAGCCTGGG    68315       AATAGT   A
                                AAGAAGAG     GGCC GGG
                                ||||||||     |||| |||
                                TTCTTCTC     TCGG CCC
                                     CT____    A
GAM2989  PPP1R1A  3'  AAGAAAAGAGAACCTGGGGC   68316       ATAGT   A_
                                AAGAAGAGA    GGCC  GGGC
                                |||||||||    ||||  ||||
                                TTCTTTTCT    TTGG  CCCG
                                     C____    AC
GAM2989  PRO0800  5'  AAGAAGAAAATATTTAGGGCC  68317         GTGGCC
                                AAGAAGAGAATA     AGGGCC
                                ||||||||||||     ||||||
                                TTCTTCTTTTAT     TCCCGG
                                       AAA___
GAM2989  PRSS21   3'  AGAAGAGAACCAGGGC      68318       ATAGTG
                                AGAAGAGA     GCCAGGGC
                                ||||||||     ||||||||
                                TCTTCTCT     TGGTCCCG
                                       _______
GAM2989  PRSS21   3'  AGAAGAGAACCAGGGC      68318       ATAGTG
                                AGAAGAGA     GCCAGGGC
                                ||||||||     ||||||||
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                                TCTTCTCT     TGGTCCCG
                                         _______
GAM2989  RAB11B    3'  AAGAAGAGATCGAGAGCTGGGG 68319         AT_  T   CA
                                AAGAAGAGA   AG GGC  GGG
                                |||||||||   || |||  |||
                                TTCTTCTCT   TC TCG  CCC
                                     AGC  _   AC
GAM2989  RAB3-GAP150 3'  AAGGAGTGGAATTTAGCCAGGG 68320     A  A_   AG
                                AAG AG  GAAT  TGGCCAGGG
                                |||  ||  ||||  |||||||||
                                TTC TC  CTTA  ATCGGTCCC
                                  C  AC    A_
GAM2989  SAMP14    3'  AGAAGGGATGAAGCCAGGGCC  68321      A  ATAGT
                                AGAAG GA    GGCCAGGGCC
                                |||||  ||    ||||||||||
                                TCTTC CT    TCGGTCCCGG
                                   C  ACT__
GAM2989  SDCCAG16  3'  GAAGTGAAGTCAGGGC     68322     A  AT   GGC
                                GAAG GA  AGT   CAGGGC
                                ||||  ||  |||   ||||||
                                CTTC CT  TCA   GTCCCG
                                  A  __  ___
GAM2989  SHAPY     3'  GAAAAGGGGGTGACCTGGG    68323       AATA     A
                                GAAGAG    GTGGCC GGG
                                ||||||    |||||| |||
                                CTTTTC    CACTGG CCC
                                    CCC_     A
GAM2989  SLC2A11   3'  GAGGGAGTGAGGACCAGGGCC  68324    A_   AAT  T
                                GA  GAG   AG GGCCAGGGCC
                                ||  |||   || ||||||||||
                                CT  CTC   TC CTGGTCCCGG
                                 CC   AC_  _
GAM2989  SR-A1     3'  GAAGAGCTGGCCAGGGC     68325       AATAG
                                GAAGAG    TGGCCAGGGC
                                ||||||    ||||||||||
                                CTTCTC    ACCGGTCCCG
                                    G____
GAM2989  SRF       3'  GAGGGGCAGAGCCAGGGC    68326     AA_   T
                                GAG   TAG GGCCAGGGC
                                |||   ||| |||||||||
                                CTC   GTC TCGGTCCCG
                                  CCC   _
GAM2989  SRp25     3'  AGAAGAGACTGGGCTGGGCC   68327        ATAGT   CA
                                AGAAGAGA    GGC  GGGCC
                                ||||||||    |||  |||||
                                TCTTCTCT    CCG  CCCGG
                                     GAC__   A_
GAM2989  SRp25     3'  AGAAGAGACTGGGCTGGGCC   68327        ATAGT   CA
                                AGAAGAGA    GGC  GGGCC
                                ||||||||    |||  |||||
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                                TCTTCTCT    CCG  CCCGG
                                    GAC__   A_
GAM2989  STAT2    3'  GAAAAGAAGAAATTCAGGGC   68328        T  TGGC
                                GAAGAGAA AG    CAGGGC
                                |||||||| ||    ||||||
                                CTTTTCTT TT    GTCCCG
                                    C  TAA_
GAM2989  SYT13    3'  AAGAAGAGAATGCTGGTCGGCC 68329        A T_________   CAGG
              CTG                   AAGAGAAT G        GGC    G
                                |||||||| |        |||    |
                                TTCTCTTA C        CCG    C
                                    _ GACCAGIII   GGAC
GAM2989  TP53TG1  3'  GAAGAGAATTGTTACCAGGG   68330        A  G
                                GAAGAGAAT GT GCCAGGG
                                ||||||||| || |||||||
                                CTTCTCTTA CA TGGTCCC
                                     A  A
GAM2989  TRIM35   3'  GAAGAAATAACAGGG       68331       AATA     C
                                GAAGAG    GTGGC AGGG
                                ||||||    ||||| ||||
                                CTTCTT    TATTG TCCC
                                    _____    _
GAM2989  TRIM35   3'  GAAGATGACGTTGGCCAGGGC  68332      _  ATAG
                                GAAGA GA    TGGCCAGGGC
                                ||||| ||    ||||||||||
                                CTTCT CT    ACCGGTCCCG
                                   A  GCA_
GAM2989  USP8     5'  GAGAACAGGTGCTAGGGC    68333        TG  C
                                GAGAATAG  GC AGGGC
                                ||||||||  || |||||
                                CTCTTGTC  CG TCCCG
                                    CA  A
GAM2989  WSB1     5'  AGAAGAGAGTGGCGACC     68334        ATA    CAG
                                AGAAGAGA   GTGGC   GGCC
                                ||||||||   |||||   ||||
                                TCTTCTCT   CACCG   CTGG
                                    ____    ____
GAM2989  WSB1     5'  AGAAGAGAGTGGCGACC     68334        ATA    CAG
                                AGAAGAGA   GTGGC   GGCC
                                ||||||||   |||||   ||||
                                TCTTCTCT   CACCG   CTGG
                                    ____    ____
GAM2989  ZIN      3'  AGGGGAGGGGCAGCCAGGCCGG 68335    AA   AA_   __   A
              GGC                   AG  GAG   TAGT  GGCC GGGC
                                ||  |||   ||||  |||| ||||
                                TC  CTC   GTCG  CCGG CCCG
                                 CC   CCC    GT    C
GAM2989  ZNF282   3'  GAAGAGAGACCAGGAGGGCC   68336        ATAGT    ___
                                GAAGAGA    GGCCA   GGGCC
                                |||||||    |||||   |||||
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                                CTTCTCT    CTGGT   CCCGG
                                   _____    CCT
GAM2989  LOC112868 3'  GAGGAGGTGGCAGCACCAGGGC 68337    A   AA__    G
             C                   GA GAG    TAGTG CCAGGGCC
                                 || |||    ||||| ||||||||
                                 CT CTC    GTCGT GGTCCCGG
                                  C   CACC    _
GAM2989  LOC115399 3'  GAGAAGGGCCAGGGC      68338      AT  T
                                 GAGA  AG GGCCAGGGC
                                 ||||  || |||||||||
                                 CTCT  TC CCGGTCCCG
                                   __ _
GAM2989  LOC123775 5'  AAAAGAGAATATTGGGG     68339          G   CCA
                                 AGAAGAGAATA TGG   GG
                                 |||||||||| |||   ||
                                 TTTTCTCTTAT ACC   CC
                                       A  ___
GAM2989  LOC130644 3'  AGAAGAAAAGCCTCAGGGC    68340        ATAGT   __
                                 AGAAGAGA    GGCC  AGGGC
                                 ||||||||    ||||  |||||
                                 TCTTCTTT    TCGG  TCCCG
                                      _____   AG
GAM2989  LOC136319 5'  AAGAAGAGAAGGAGGG      68341         TAGT  CC
                                 AAGAAGAGAA    GG  AGGG
                                 ||||||||||    ||  ||||
                                 TTCTTCTCTT    CC  TCCC
                                      ____ __
GAM2989  LOC144742 5'  AGAGAGGGGTGACCAGGGC    68342      ATA
                                 AGAGA   GTGGCCAGGGC
                                 |||||   ||||||||||||
                                 TCTCT   CACTGGTCCCG
                                    CCC
GAM2989  LOC144810 5'  GAGGGAGGTAGGCCAGGGCC   68343     AATA  _
                                 GAG    GT GGCCAGGGCC
                                 |||    || ||||||||||
                                 CTC    CA CCGGTCCCGG
                                   CCTC  T
GAM2989  LOC145501 3'  GAGAAAAATGAGTGGCCAGGG  68344    AG    _
                                 GA  AGAAT AGTGGCCAGGG
                                 ||  ||||| ||||||||||||
                                 CT  TTTTA TCACCGGTCCC
                                  CT    C
GAM2989  LOC146667 5'  AGAAGAGAAGGGGGACAGGG   68345         TAGT  C
                                 AGAAGAGAA    GG CAGGG
                                 |||||||||    || |||||
                                 TCTTCTCTT    CC GTCCC
                                       CCC_  T
GAM2989  LOC150273 3'  AGATGGAGAGGGGGCCAGGGCC 68346     A_   ATAGT
                                 AGA  GAGA    GGCCAGGGCC
                                 |||  ||||    ||||||||||
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                                TCT  CTCT    CCGGTCCCGG
                                  AC   CCC__
GAM2989  LOC152316 5'  GAAGAGAATGGATGGAC     68347       ATA   CCA
                                GAAGAGA   GTGG   GGGC
                                |||||||   ||||   ||||
                                CTTCTCT   TACC   CCTG
                                    ___    TA_
GAM2989  LOC152762 3'  AAAAGAGAACGTGCTGGGG    68348         A   G CA
                                AGAAGAGAAT GTG C  GGG
                                |||||||||| ||| |  |||
                                TTTTCTCTTG CAC G  CCC
                                      _   _ AC
GAM2989  LOC154452 3'  AAAGAGAAGTCAGGG       68349       AT   GGC
                                GAAGAGA  AGT   CAGGG
                                |||||||  |||   |||||
                                TTTCTCT  TCA   GTCCC
                                   __   ____
GAM2989  LOC157858 5'  AAGAGCAGGAACCAGGGC    68350      AA   TG
                                AAGAG  TAG  GCCAGGGC
                                |||||  |||  ||||||||
                                TTCTC  GTC  TGGTCCCG
                                   __   CT
GAM2989  LOC158835 3'  AGAAGAAAATGGTGTAGCTGGC 68351       A  __________  CAGG
            CCTGGC                 GAGAAT GTG       GC    GC
                                |||||| |||        ||    ||
                                CTTTTA CAC        CG    CG
                                   C   ATCGAIIIC  GGAC
GAM2989  LOC196337 3'  AAGAAGAGGAGGGAGGG     68352        AAT  T  CC
                                AAGAAGAG   AG GG  AGGG
                                ||||||||   || ||  ||||
                                TTCTTCTC   TC CC  TCCC
                                     C__  _  __
GAM2989  LOC204119 5'  AGAAGGGAATATACCCAGGG   68353      A    G  G
                                AGAAG GAATA TG CCAGGG
                                ||||| ||||| || ||||||
                                TCTTC CTTAT AT GGTCCC
                                   C    _  G
GAM2989  LOC219942 3'  AAGAAGAGGAAGGCTGGGGCC  68354        AATAGT   CA
                                AAGAAGAG     GGC  GGGCC
                                ||||||||     |||  |||||
                                TTCTTCTC     CCG  CCCGG
                                     CTT___   AC
GAM2989  LOC221477 3'  AAGGCAGGGAGGACTAGGGCC  68355     A_  A  ATA T   C
                                AAG  AG GA   G GGC AGGGCC
                                |||  || ||   | ||| ||||||
                                TTC  TC CT   C CTG TCCCGG
                                  CG  C  ___ _   A
GAM2989  LOC221833 3'  GGAAAGGGAAAGCCAGGGC   68356   A    A   TAGT
                                A GAAG GAA    GGCCAGGGC
                                | |||| |||    |||||||||
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                                C TTTC CTT    TCGGTCCCG
                                 C   C  ____
GAM2989  LOC222136 3'  AGAAGAGAATGTTGAACAAG   68357        AG  GC
                                AGAAGAGAAT  TG  CAGG
                                ||||||||||  ||  ||||
                                TCTTCTCTTA  AC  GTTC
                                     CA  TT
GAM2989  LOC222414 3'  GAAGAGGTGGAGGGGGGCC   68358      AATA   CCA_
                                GAAGAG   GTGG   GGGCC
                                ||||||   ||||   |||||
                                CTTCTC   CACC   CCCGG
                                   ____   TCCC
GAM2989  LOC222962 3'  GAAGGCAATGGGAGGGC    68359     AGAA    CC
                                GAAG   TAGTGG  AGGGC
                                ||||   ||||||  |||||
                                CTTC   GTTACC  TCCCG
                                  C___    C_
GAM2989  LOC254302 3'  AGGAGAGAGTAGAGGCCAGAGC 68360    A    A  T
            C                    AG AGAGA TAG GGCCAGGGCC
                                || ||||| ||| ||||||||||
                                TC TCTCT ATC CCGGTCTCGG
                                 C    C  T
GAM2989  LOC254874 3'  AGGAGAGAGTAGAGGCCAGAGC 68360    A    A  T
            C                    AG AGAGA TAG GGCCAGGGCC
                                || ||||| ||| ||||||||||
                                TC TCTCT ATC CCGGTCTCGG
                                 C    C  T
GAM2989  LOC255809 5'  GAAAGGAGAACCAGGGC    68361     AT  T
                                GAGA  AG GGCCAGGGC
                                ||||  || |||||||||
                                CTTT  TC TTGGTCCCG
                                  CC  _
GAM2989  LOC256158 5'  GAAGGGAAGGCCAGGGCC   68362     A  TAGT
                                GAAG GAA   GGCCAGGGCC
                                |||| |||   ||||||||||
                                CTTC CTT   CCGGTCCCGG
                                  C  ____
GAM2989  LOC257492 3'  AAAGAGAAGTCAGGG      68349       AT  GGC
                                GAAGAGA  AGT   CAGGG
                                |||||||  |||   |||||
                                TTTCTCT  TCA   GTCCC
                                   __  ___
GAM2989  LOC257606 3'  AAAGAGAAGTCAGGG      68349       AT  GGC
                                GAAGAGA  AGT   CAGGG
                                |||||||  |||   |||||
                                TTTCTCT  TCA   GTCCC
                                   __  ___
GAM2989  LOC51705  3'  GAGAACAGGAGAGCCCCGGG  68363       T__   A_
                                GAGAATAG   GGCC  GGG
                                ||||||||   ||||  |||
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                                CTCTTGTC  TCGG  CCC
                                    CTC   GG
GAM2989 LOC81558 3' AAAAAGAGGACCCAGGGC   68364       A  AGTGG
                                AAGAAGAG AT    CCAGGGC
                                |||||||| ||    |||||||
                                TTTTTCTC TG    GGTCCCG
                                    C _____
GAM2989 LOC90297 5' GAGGACAGAGCCTACCCAGGGC 68365    A  ____  G
          C                      GAG ATAG   TG CCAGGGCC
                                ||| ||||   || ||||||||
                                CTC TGTC   AT GGTCCCGG
                                  C   TCGG  G
GAM2989 LOC92465 5' GAAGGAGAATGGTGATTGCC  68366     _   A  ___
                                GAAG AGAAT GTG  GCC
                                |||| ||||| |||  |||
                                CTTC TCTTA CAC  CGG
                                  C    C  TAA
GAM2990 DYRK1B   3' TGTGAGAAAGCTCTTTACTGGG 68369     A  T  AA_
                                TGTGA AAA GT  TTACTGGG
                                ||||| ||| ||  ||||||||
                                ACACT TTT CG  AATGACCC
                                  C  _  AGA
GAM2990 HMGA2    3' TATGAAAAATGAGGTATACTGG 68370        TAAT_
          G                     TGTGAAAAATG    TACTGGG
                                ||||||||||    |||||||
                                ATACTTTTTAC    ATGACCC
                                      TCCAT
GAM2990 IL12RB2  3' GTGAAGGATGTAATTTTAAGG  68371     AA      ACT
                                GTGAA  ATGTAATT  GGG
                                |||||  ||||||||  |||
                                CACTT  TACATTAA  TCC
                                  CC      AAT
GAM2990 ITGA2    3' TGTTAAAATGCAGATTGCTGGG 68372    GA     _  A
                                TGT  AAAATGTA ATT CTGGG
                                |||  |||||||| ||| |||||
                                ACA  TTTTACGT TAA GACCC
                                  A_      C  C
GAM2990 PDE4D    3' TGTGAAAAATGATTATTTGGG  68373        TAATTAC
                                TGTGAAAAATG     TGGG
                                ||||||||||      ||||
                                ACACTTTTTAC     ACCC
                                      TAATAA_
GAM2990 PPP3CB   3' TGTGAAAAATTAGCACATGG   68374       GTAAT  _
                                TGTGAAAAAT    TAC TGG
                                ||||||||||    ||| |||
                                ACACTTTTTA    GTG ACC
                                      ATC__   T
GAM2990 SNCA     3' TGAGAAATGTCATGACTGGG   68375    A    A  T
                                TGA AAATGT AT ACTGGG
                                ||| |||||| || ||||||
```

```
                                ACT TTTACA TA TGACCC
                                  C     G  C
GAM2990  SNCA     3'  TGAGAAATGTCATGACTGGG  68375     A     A  T
                                TGA AAATGT AT ACTGGG
                                ||| |||||| || ||||||
                                ACT TTTACA TA TGACCC
                                  C     G  C
GAM2990  BRAG     5'  TGGAAGAATTCTCACTGGG   68376    T   A   GTAA
                                TG GAA AAT    TTACTGGG
                                || ||| |||    ||||||||
                                AC CTT TTA    AGTGACCC
                                 _   C   AG__
GAM2990  DKFZp761G0313 3'  TGTAAAAATTATACTGG     68377         A   AATT
                                TGTGAAAA TGT    ACTGG
                                |||||||| |||    |||||
                                ACATTTTT ATA    TGACC
                                     A   ____
GAM2990  DKFZp762K2015 3'  TATGAGAAATGTAATATGG    68378      A       TAC
                                TGTGA AAATGTAAT   TGG
                                ||||| |||||||||   |||
                                ATACT TTTACATTA   ACC
                                   C       T__
GAM2990  FLJ14351  3'  TGTGAAGATGGCCACTGGG    68379       AA   TAA
                                TGTGAA  ATG   TTACTGGG
                                ||||||  |||   ||||||||
                                ACACTT  TAC   GGTGACCC
                                   C_   C__
GAM2990  FLJ14803  3'  TGGAATTTACTAATTACTGGG  57687    T   AAATG
                                TG GAA    TAATTACTGGG
                                || |||    ||||||||||
                                AC CTT    ATTAATGACCC
                                 _   AAATG
GAM2990  GPS1     3'  TGGGAAATGGTGCCACTGGG   68380    AA    TAA
                                TG  AAATG   TTACTGGG
                                ||  |||||   ||||||||
                                AC  TTTAC   GGTGACCC
                                 CC    CAC
GAM2990  KIAA0469  3'  TATGAGAAAAAAAATTACTGGG 68381      A   TGT
                                TGTGA AAA   AATTACTGGG
                                ||||| |||   ||||||||||
                                ATACT TTT   TTAATGACCC
                                   C   TTT
GAM2990  KIAA0789  3'  TGGAGAGATGTGTCACTGGG   68382    T  AAA   AA
                                TG GA   ATGT  TTACTGGG
                                || ||   ||||  ||||||||
                                AC CT   TACA  AGTGACCC
                                 _ CTC    C_
GAM2990  KIAA0848  3'  CGTGAGGATGGAGTTACTGGG  68383      AAA   TAA
                                TGTGA   ATG   TTACTGGG
                                |||||   |||   ||||||||
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                                GCACT   TAC   AATGACCC
                                   CC_  CTC
GAM2990  KIAA1006  3'  TGTGAATGATGTAAAACATGG  68384      AA     TT  _
                                TGTGAA  ATGTAA  AC TGG
                                ||||||  ||||||  || |||
                                ACACTT  TACATT  TG ACC
                                   AC     T_  T
GAM2990  KIAA1211  3'  TGTGAATGGATGTGCCTTCTGG 68385      AA_   AA  A
            G                    TGTGAA   ATGT  TT CTGGG
                                ||||||   ||||  || |||||
                                ACACTT   TACA  GA GACCC
                                   ACC   CG  A
GAM2990  KIAA1328  3'  TGTGAAAAATGTATTGG     68386          ATTAC
                                TGTGAAAAATGTA    TGG
                                ||||||||||||     |||
                                ACACTTTTTACAT    ACC
                                      A____
GAM2990  KIAA1332  3'  TGTGAAAAATGGGGTCATGG   68387         TAA   C
                                TGTGAAAAATG   TTA TGG
                                ||||||||||   ||| |||
                                ACACTTTTTAC   AGT ACC
                                     CCC  _
GAM2990  KIAA1726  3'  TGGAAAAATGTAACTGG     68388    T       ATT
                                TG GAAAAATGTA   ACTGG
                                || ||||||||||   |||||
                                AC CTTTTTACAT   TGACC
                                _       ___
GAM2990  NCBP1     3'  TGTGAAAAGTTATGCTACTGGG 68389        ___   AAT
                                TGTGAAAA   ATGT   TACTGGG
                                ||||||||   ||||   |||||||
                                ACACTTTT   TACG   ATGACCC
                                    CAA   ___
GAM2990  SCAMP-4   3'  TGTGAAAATGTCTTGCCTGGG  68390       A   AATTA
                                TGTGAAAA TGT    CTGGG
                                |||||||| |||    |||||
                                ACACTTTT ACA    GACCC
                                    _  GAACG
GAM2990  TCL6      3'  TGTAAAAATGCCTGCCTGGG   68391       A   AATTA
                                TGTGAAAA TGT    CTGGG
                                |||||||| |||    |||||
                                ACATTTTT ACG    GACCC
                                    _  GACG_
GAM2990  TCL6      3'  TGTAAAAATGCCTGCCTGGG   68391       A   AATTA
                                TGTGAAAA TGT    CTGGG
                                |||||||| |||    |||||
                                ACATTTTT ACG    GACCC
                                    _  GACG_
GAM2990  ZFP106    3'  TGGGAAATGTAGTCACCAGG   68392    AA     A   TG
                                TG  AAATGTA TTAC  GG
                                ||  ||||||| ||||  ||
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                                AC  TTTACAT AGTG  CC
                                 CC      C    GT
GAM2990  LOC119548 5'  TGGAAAAATGGCCCAGCTGGG  68393    T      TAA  _
                                TG GAAAAATG   TTA CTGGG
                                || ||||||||   ||| |||||
                                AC CTTTTTAC   GGT GACCC
                                 _       CG_  C
GAM2990  LOC137964 5'  TGTGGAGGGGTAATCACTGG   68394     AAAAAT
                                TGTG     GTAATTACTGG
                                ||||     ||||||||||
                                ACAC     CATTAGTGACC
                                  CTCCC_
GAM2990  LOC152627 5'  TGTAAAAAATGTAGTATCTG   68395          ATTA
                                TGTGAAAAATGTA    CTG
                                ||||||||||||    |||
                                ACATTTTTTACAT    GAC
                                        CATA
GAM2990  LOC152845 5'  GTGAAAAATGTGGTCATGG    68396         AA   C
                                GTGAAAAATGT  TTA TGG
                                ||||||||||  ||| |||
                                CACTTTTTACA  AGT ACC
                                      CC  _
GAM2990  LOC153146 5'  TGTGGGAGTGACCACTGGG    68397     AAAAAT  A
                                TGTG     GT ATTACTGGG
                                ||||     || |||||||||
                                ACAC     CA TGGTGACCC
                                  CCT___  C
GAM2990  LOC154739 5'  TGTGAAAAACTCTATTGGG    68398         GTAAT  C
                                TGTGAAAAAT     TA TGGG
                                ||||||||||     || ||||
                                ACACTTTTTG     AT ACCC
                                      AG___  A
GAM2990  LOC164684 3'  TGTCAACCAAATTACTGGG    68399     G  AAATGT
                                TGT AA     AATTACTGGG
                                ||| ||     ||||||||||
                                ACA TT     TTAATGACCC
                                  G  GGT___
GAM2990  LOC201628 3'  TGTAAGATGGAATTACTGGG   68400      AAA   T
                                TGTGA   ATG AATTACTGGG
                                |||||   ||| ||||||||||
                                ACATT   TAC TTAATGACCC
                                   C__   C
GAM2990  LOC57228  3'  TGTGAAAAAAGATGACTGGG   68401        TGTA  T
                                TGTGAAAAA    AT ACTGGG
                                |||||||||    || ||||||
                                ACACTTTTT    TA TGACCC
                                      TC__  C
GAM2991  CAPZA1    5'  CCTACAAGTTTTTCTGGTG    68404        ___     C
                                CCTACAG   TTTCTG TG
                                |||||||   |||||| ||
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                                GGATGTT   AAAGAC AC
                                   CAA     C
GAM2991  CLASP2   3'  TACAGTTTTATTGCCAGTA   68405        C  C  TA
                                TACAGTTT TG TG  CCAGTA
                                |||||||| || ||  ||||||
                                ATGTCAAA AT AC  GGTCAT
                                   _  A  __
GAM2991  CYBB     3'  CAGTTACCCTGCTGTATTAGTA 68406      __       CC
                                CAGTT  TCTGCTGTA  AGTA
                                |||||  |||||||||  ||||
                                GTCAA  GGACGACAT  TCAT
                                  TG        AA
GAM2991  PSEN2    5'  CCTCAGTTTCTTCATCAGT   68407     A      GCTGTAC
                                CCT CAGTTTCT      CAGT
                                ||| ||||||||      ||||
                                GGA GTCAAAGA      GTCA
                                  _       AGTA___
GAM2991  PSEN2    5'  CCTCAGTTTCTTCATCAGT   68407     A      GCTGTAC
                                CCT CAGTTTCT      CAGT
                                ||| ||||||||      ||||
                                GGA GTCAAAGA      GTCA
                                  _       AGTA___
GAM2991  SIRT1    3'  CCACAGTTTTGGAAAATGCCAG 68408        C  CT__  A
            T                    CTACAGTTT TG    GT CCAGT
                                |||||||| ||    || |||||
                                GGTGTCAAA AC    TA GGTCA
                                      _ CTTT  C
GAM2991  SORCS1   3'  CCTAGAGTTTCTAATTCAGTA  68409     C       CTGTAC
                                CCTA AGTTTCTG     CAGTA
                                |||| ||||||||     |||||
                                GGAT TCAAAGAT     GTCAT
                                  C       TAA___
GAM2991  XT3      3'  CCTGCAGCTTTCTGCTGT    68410     A    _
                                CCT CAGTTT CTGCTGT
                                ||| |||||| |||||||
                                GGA GTCGAA GACGACA
                                  C     A
GAM2991  ZNF141   3'  TACAGTTTCTCTCCGGT     68411         G  GTA  A
                                TACAGTTTCT CT   CC GT
                                |||||||||| ||   || ||
                                ATGTCAAAGA GA   GG CA
                                      _ ___  C
GAM2991  ZNF256   5'  TACAGTTTCTGACCA       68412          CTGT
                                TACAGTTTCTG    ACCA
                                ||||||||||    ||||
                                ATGTCAAAGAC    TGGT
                                      ____
GAM2991  ZNF266   3'  TACAGTTTCTCTCCAGT     68413         G  GTA
                                TACAGTTTCT CT   CCAGT
                                |||||||||| ||   |||||
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                                ATGTCAAAGA GA   GGTCA
                                      _ ___
GAM2991  AF9Q34   3'  TACAGTTTTTGCACTAG     68414        CTGC    C
                                TACAGTTT    TGTAC AG
                                ||||||||    ||||| ||
                                ATGTCAAA    ACGTG TC
                                     A___     A
GAM2991  AKAP11   3'  CAGTTTCTGGACACAAACTAGT 68415         CTGT___  C
            A                    CAGTTTCTG      AC AGTA
                                ||||||||||      || ||||
                                GTCAAAGAC      TG TCAT
                                     CTGTGTT  A
GAM2991  COP9     3'  TACATTTCTACGTTTGTCAGTA 68416      G     ___   AC
                                TACA TTTCTGC   TGT  CAGTA
                                |||| |||||||   |||  |||||
                                ATGT AAAGATG   ACA  GTCAT
                                  _      CAA  __
GAM2991  DSCR1L1  3'  CCTCAGTTTCACCAG       68417     A      TGCTGT
                                CCT CAGTTTC     ACCAG
                                ||| |||||||     |||||
                                GGA GTCAAAG     TGGTC
                                  _     _______
GAM2991  FLJ11795 3'  CTACATTTCTGCAGCGAGT    68418      G      T  ACC
                                CTACA TTTCTGC GT   AGT
                                ||||| ||||||| ||   |||
                                GATGT AAAGACG CG   TCA
                                   _      T  C__
GAM2991  FLJ13710 3'  CCTCAGTTTCCCTGTCAGT    68419     A      G    AC
                                CCT CAGTTTCT CTGT  CAGT
                                ||| |||||||| ||||  ||||
                                GGA GTCAAAGG GACA  GTCA
                                  _      _   __
GAM2991  FLJ20211 3'  CTCAGTTTCTGCCCAAGT     68420    A        TGTA  _
                                CT CAGTTTCTGC    CCA GT
                                || ||||||||||    ||| ||
                                GA GTCAAAGACG    GGT CA
                                  _        _____   T
GAM2991  FLJ22490 3'  CCCTTCATTTCTGCTGTATCAG 68421     ACA          C
            TA                    CCT   GTTTCTGCTGTA CAGTA
                                |||   |||||||||||| |||||
                                GGG   TAAAGACGACAT GTCAT
                                  AAG          A
GAM2991  HNRPA3   3'  CCTACATTTCTGCTGCA     68422       G
                                CCTACA TTTCTGCTGTA
                                |||||| ||||||||||
                                GGATGT AAAGACGACGT
                                     _
GAM2991  KIAA0599 3'  CTACAGTCTTTTGACAGT     68423         CTGC  TAC
                                CTACAGTTT    TG   CAGT
                                |||||||||    ||   ||||
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                                GATGTCAGA   AC  GTCA
                                     AA__  T__
GAM2991  KIAA0826  3'  CTACAGTTTCTATATGGAGTA  68424          C  ACC
                                CTACAGTTTCTG TGT  AGTA
                                |||||||||||| |||  ||||
                                GATGTCAAAGAT ATA  TCAT
                                      _  CC_
GAM2991  KIAA0836  3'  CCTGTAGTTTCTGTGTA    68425    AC      C
                                CCT  AGTTTCTG TGTA
                                |||  |||||||| ||||
                                GGA  TCAAAGAC ACAT
                                  CA       _
GAM2991  KIAA1671  3'  CCTGCAGTTGCTGTCCC    68426    A   TTC    A
                                CCT CAGT   TGCTGT CC
                                ||| ||||   |||||| ||
                                GGA GTCA   ACGACA GG
                                  C   ___     G
GAM2991  MGC13053  5'  CAGTGCGCTGTACCGGT    68427     TTC       A
                                CAGT   TGCTGTACC GT
                                ||||   ||||||||| ||
                                GTCA   GCGACATGG CA
                                  C__        C
GAM2991  NFAT5     3'  TACATTTCCACTGCTAGTA   68428     G   TG   ACC
                                TACA TTTC  CTGT   AGTA
                                |||| ||||  ||||   ||||
                                ATGT AAAG  GACG   TCAT
                                  _   GT   A__
GAM2991  NLN       3'  CCTTCAGTTTCCAGGCCAGTA  68429    A      GCTGTA
                                CCT CAGTTTCT     CCAGTA
                                ||| ||||||||     ||||||
                                GGA GTCAAAGG     GGTCAT
                                  A       TCC___
GAM2991  P5-1      3'  CTACAGTTCTGTAATCTCAGTA 68430       T   CT  AC
                                CTACAGTT CTG  GT  CAGTA
                                |||||||| |||  ||  |||||
                                GATGTCAA GAC  TA  GTCAT
                                      _  AT  GA
GAM2991  PDZD2     3'  AGTCCGTGTCTGTACCAGT   68431     TC  _
                                AGTT  TG CTGTACCAGT
                                ||||  || ||||||||||
                                TCAG  AC GACATGGTCA
                                  GC  A
GAM2991  PHF3      3'  CTACAGTTTCTTTAAAAACAGT 68432          GCTGTAC
                                CTACAGTTTCT      CAGT
                                ||||||||||      ||||
                                GATGTCAAAGA      GTCA
                                      AATTTTT
GAM2991  SGP28     3'  CCTACAATTTCTCAGCTA    68433          __
                                CCTACAGTTTCT  GCTG
                                ||||||||||||  ||||
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                                GGATGTTAAAGA  CGAT
                                      GT
GAM2991  SIMRP7   3'  ACAGCTTGTACCAGT      68434       TCTGC
                                ACAGTT    TGTACCAGT
                                ||||||    |||||||||
                                TGTCGA    ACATGGTCA
                                  _____
GAM2991  LOC129676 5'  CACAGGACATGCTGTACTGGT  68435      TTTC       CA
                                TACAG   TGCTGTAC  GT
                                |||||   ||||||||  ||
                                GTGTC   ACGACATG  CA
                                   CTGT       AC
GAM2991  LOC133584 3'  CTCAGTTTCTCATCAGT     68436    A      GCTG  C
                                CT CAGTTTCT    TA CAGT
                                || ||||||||    || ||||
                                GA GTCAAAGA    GT GTCA
                                 _      _____  A
GAM2991  LOC144266 5'  CCAGCAGTTTCTGAATCCACAG 68437    TA       CT  AC_
            T                    CC  CAGTTTCTG  GT   CAGT
                                ||  |||||||||  ||   ||||
                                GG  GTCAAAGAC  TA   GTCA
                                 TC       T_  GGT
GAM2991  LOC149072 5'  AGTTTCTGTCTATAAAGTA   68438        _    CC
                                AGTTTCTG CTGTA  AGTA
                                |||||||| |||||  ||||
                                TCAAAGAC GATAT  TCAT
                                     A    T_
GAM2991  LOC150596 3'  CCTGTAGTTTCTAGATCCTCAG 68439     AC       CTGTAC
            T                    CCT  AGTTTCTG     CAGT
                                |||  ||||||||     ||||
                                GGA  TCAAAGAT     GTCA
                                  CA       CTAGGA
GAM2991  LOC153346 3'  CTACAGTTTCTGTGATGTA   68440          C__
                                CTACAGTTTCTG   TGTA
                                ||||||||||||   ||||
                                GATGTCAAAGAC   ACAT
                                       ACT
GAM2991  LOC200058 3'  CAGTTTCTAGCCCAGT      68441        _  TGTA
                                CAGTTTCT GC    CCAGT
                                |||||||| ||    |||||
                                GTCAAAGA CG    GGTCA
                                     T _____
GAM2991  LOC51134  3'  CTACAGTTTTTGTATATAGTA  68442        C  C    CC
                                CTACAGTTT TG TGTA  AGTA
                                ||||||||| || ||||  ||||
                                GATGTCAAA AC ATAT  TCAT
                                     A  _    A_
GAM2991  LOC51161  5'  CCTGTGGTTCCTGCCACCTGT  68443     ACA       GT   A
                                CCT   GTTTCTGCT  ACC GT
                                |||   |||||||||  ||| ||
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                                GGA   CAAGGACGG  TGG CA
                                  CAC        __   A
GAM2991  LOC92346  5'  TACAGTTTCAATACCAGTA   68444         TGCT
                                TACAGTTTC   GTACCAGTA
                                |||||||||   |||||||||
                                ATGTCAAAG   TATGGTCAT
                                     T___
GAM2992  COL9A2   3'  CTCAAGCTGAGGGGTG     68447          ATCC
                                CTCGAGCTGAGG   GTG
                                ||||||||||||   |||
                                GAGTTCGACTCC   CAC
                                       C___
GAM2992  HOXC5    3'  CGAGCTGAGGGGAGATGG    68448         ATCCGT
                                CGAGCTGAGG     GATGG
                                ||||||||||     |||||
                                GCTCGACTCC     CTACC
                                      CCT___
GAM2992  MYF6     5'  CTCGATCTGAACTGGGTGATGG 68449      G    GATCC
              A                  CTCGA CTGAG    GTGATGGA
                                |||||  |||||    ||||||||
                                GAGCT GACTT    CACTACCT
                                   A    GACC_
GAM2992  RFX2     3'  TCGAGCTGCGGATCTGCCGG   68450       A    C  GA
                                TCGAGCTG GGATC GT  TGG
                                |||||||| |||||  ||  |||
                                AGCTCGAC CCTAG CG  GCC
                                     G    A  __
GAM2992  TLL2     5'  GCTGAGGAGCCAATGG      68451        T  GT
                                GCTGAGGA CC  GATGG
                                |||||||| ||  |||||
                                CGACTCCT GG  TTACC
                                     C  __
GAM2992  ARFGEF2  3'  AGTTGGAGACTGTGATGGA   68452    C  AG   CC
                                AG TG  GAT  GTGATGGA
                                || ||  |||  ||||||||
                                TC AC  CTG  CACTACCT
                                 A  CT   A_
GAM2992  CIDEB    5'  TCAGTTGCAGCCGTGATGGA   68453    G  C  A  AT
                                TC AG TG GG  CCGTGATGGA
                                || || || ||  ||||||||||
                                AG TC AC TC  GGCACTACCT
                                 _  A  G  __
GAM2992  FLJ21916 3'  CTCCAGCTGAGGGCAGTATGGA 68454     G       ATCC   A
                                CTC AGCTGAGG    GTG TGGA
                                ||| ||||||||    ||| ||||
                                GAG TCGACTCC    CAT ACCT
                                  G       CGT_  _
GAM2992  KIAA1706 5'  CTCGGGCGGGGATCCGC     68455      A  T A
                                CTCG GC G GGATCCGT
                                |||| || | ||||||||
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                                GAGC CG C CCTAGGCG
                                  C  _ C
GAM2992  KIAA1728  5'  CTCCAGCTGAGGATTCTGCTTT 68456     G        _ C  GA
              GG                  CTC AGCTGAGGAT C GT  TGG
                                  ||| |||||||||| | ||  |||
                                  GAG TCGACTCCTA G CG  ACC
                                    G         A A  AA
GAM2992  MGC26847  3'  CTCGAGCTGGGCGCATGTGGA  68457         A  ATC    A
                                  CTCGAGCTG GG   CGTG TGGA
                                  ||||||||| ||   |||| ||||
                                  GAGCTCGAC CC   GTAC ACCT
                                        _ GC_   _
GAM2992  MIDORI   3'  CTCGAGCTGTGGGTCCCAGGA  68458         A  A   GTGAT
                                  CTCGAGCTG GG TCC     GGA
                                  ||||||||| || |||     |||
                                  GAGCTCGAC CC AGG     CCT
                                        A  C   GT___
GAM2992  TPD52L1   5'  TCGAGCTGAGGGCGGCGG    68459          ATCC   A
                                  TCGAGCTGAGG    GTG TGG
                                  ||||||||||    ||| |||
                                  AGCTCGACTCC    CGC GCC
                                         ____   C
GAM2992  TRAF4    3'  CTCAGCTGAGGATCTTCCGG   68460     G         CGTGA
                                  CTC AGCTGAGGATC     TGG
                                  ||| ||||||||||     |||
                                  GAG TCGACTCCTAG     GCC
                                    _         AAG__
GAM2992  LOC124045 3'  GAGCTGAGGGTTGCTGGA    68461         ATCCG  A
                                  GAGCTGAGG     TG TGGA
                                  |||||||||     || ||||
                                  CTCGACTCC     AC ACCT
                                        CA___  G
GAM2992  LOC145231 3'  GAGCTGGTCCAGTGATGGA    68462       GA  A   _
                                  GAGCT  GG TCC GTGATGGA
                                  |||||  || ||| ||||||||
                                  CTCGA  CC AGG CACTACCT
                                     __  _   T
GAM2992  LOC150372 5'  GAATTGGGGAGTGTATGGA    68463     C  A   TCC   _
                                  GAG TG GGA   GTG ATGGA
                                  ||| || |||   ||| |||||
                                  CTT AC CCT   CAC TACCT
                                    A  C  ___   A
GAM2992  LOC207043 3'  TCGAGCTGGTGGTAGA      68464         AGGATCC   A
                                  TCGAGCTG      GTG TGGA
                                  ||||||||      ||| ||||
                                  AGCTCGAC      CAC ATCT
                                        ________  C
GAM2992  LOC91960  5'  TCAGGCTGGGGTGATGG     68465     A    A  ATCC
                                  TCG GCTG GG    GTGATGG
                                  ||| |||| ||    |||||||
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                                AGT CGAC CC    CACTACC
                                  C    _ _____
GAM2993  ABCA3    3'  TAAAGGATGAGATAAACTTGGA 68468        AAATAA    CA
                GA                  TAAAGGA     AGACT  GAGA
                                    |||||||     |||||  ||||
                                    ATTTCCT     TTTGA  CTCT
                                        ACTCTA     AC
GAM2993  ALDH3B2  3'  AAGGAAACTGAGGCTCAGAGA  68469        ATAA  A
                                    AAGGAAA    AG CTCAGAGA
                                    |||||||    || ||||||||
                                    TTCCTTT    TC GAGTCTCT
                                        GAC_  C
GAM2993  BDP1     3'  TAAAGAAAAATGAAGATAAAAG 68470          A    CTC_
                AG                  TAAAGGAAAAT AAGA    AGAG
                                    ||||||||||| ||||    ||||
                                    ATTTCTTTTTA TTCT    TCTC
                                          C    ATTT
GAM2993  DOCK1    3'  TGAGGTAAACAGCAGACTCAG  68471    A   A     A_
                                    A AGG AAATA  AGACTCAG
                                    | ||| |||||  ||||||||
                                    A TCC TTTGT  TCTGAGTC
                                     C   A     CG
GAM2993  DUOX1    5'  GAAAATAATAGGGGCTCAGGGA 68472         _ A__     A
                                    GAAAATAA AG   CTCAG GA
                                    |||||||| ||   ||||| ||
                                    CTTTTATT TC   GAGTC CT
                                         A  CCC     C
GAM2993  FBXL7    3'  TGAGGAAAAATAAAGGCCAGA  68473    A      _     A T
                                    A AGGAAAA TAAAG C CAGA
                                    | ||||||| ||||| | ||||
                                    A TCCTTTT ATTTC G GTCT
                                     C       T     C _
GAM2993  GNS      3'  TAAAGGAAGAGACCAGAG     68474         AATAA    T
                                    TAAAGGAA     AGAC CAGAG
                                    ||||||||     |||| |||||
                                    ATTTCCTT     TCTG GTCTC
                                         C____    _
GAM2993  IGSF8    3'  TAAAGGAAGAGTGGACAGAG   68475         AATAAA   TC
                                    TAAAGGAA     GAC  AGAG
                                    ||||||||     |||  ||||
                                    ATTTCCTT     CTG  TCTC
                                         CTCAC_   __
GAM2993  IQGAP1   3'  AAGAAAATGAAGAAACCAGA   68476         A    C_
                                    AGGAAAAT AAGA  TCAGA
                                    |||||||| ||||  |||||
                                    TTCTTTTA TTCT  GGTCT
                                         C    TT
GAM2993  KCNK6    3'  TGAGGAAATCAAGGCTCAGAGA 68477    A     ATA   A
                                    A AGGAAA   AAG CTCAGAGA
                                    | ||||||   ||| ||||||||
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                                A TCCTTT   TTC GAGTCTCT
                                 C     AG_   C
GAM2993  MS4A3    3'  TGAGGAAAAATAGATCAGAGA  68478   A     TAA   C
                                A AGGAAAA   AGA TCAGAGA
                                | |||||||   ||| |||||||
                                A TCCTTTT   TCT AGTCTCT
                                 C      TA_   _
GAM2993  PCDHB9   3'  TAAAGGGAGGTAAAGAACAGA  68479      AAAA     CT
                                TAAAGG   TAAAGA  CAGA
                                ||||||   ||||||  ||||
                                ATTTCC   ATTTCT  GTCT
                                   CTCC     T_
GAM2993  PTK2B    3'  TAAAGGAAGAAAGAGAAAGAG  68480       AAT    CTC
                                TAAAGGAA   AAAGA   AGAG
                                ||||||||   |||||   ||||
                                ATTTCCTT   TTTCT   TCTC
                                     C__    CTT
GAM2993  SORCS1   3'  TGAGGCAAAGACTTTAGAG   68481   A  AAAA      C_
                                A AGG   TAAAGACT  AGAG
                                | |||   ||||||||  ||||
                                A TCC   GTTTCTGA  TCTC
                                 C  _____       AA
GAM2993  STAU2    3'  AAGGAAAATGGAGAAGAGA   68482        AA   CTC
                                AAGGAAAAT  AGA   AGAGA
                                |||||||||  |||   |||||
                                TTCCTTTTA  TCT   TCTCT
                                     CC   ___
GAM2993  VPREB3   3'  GGAAGCAAGGCTCAGAGA    68483     AATA   A
                                GGAA    AAG CTCAGAGA
                                ||||    ||| ||||||||
                                CCTT    TTC GAGTCTCT
                                  CG__   C
GAM2993  C20orf188 3'  AGGAAAATGAGGCAGAG     68484        AAA  CT
                                AGGAAAAT   GA  CAGAG
                                ||||||||   ||  |||||
                                TCCTTTTA   CT  GTCTC
                                     ___  CC
GAM2993  CABP4    5'  GGATAACAGGGCTCAGAGA   68485     A    AAGA
                                GGA AATA    CTCAGAGA
                                ||| ||||    ||||||||
                                CCT TTGT    GAGTCTCT
                                  A   CCC_
GAM2993  CL683    3'  TGAAGAAAATAATACAGAG   68486   A        AGACT
                                A AGGAAAATAA     CAGAG
                                | ||||||||||     |||||
                                A TTCTTTTATT     GTCTC
                                 C         AT___
GAM2993  DKFZP434C212 3'  AGGGAAATAAAGGCACAGA   68487     A       ACT
                                AGG AAATAAAG   CAGA
                                ||| ||||||||   ||||
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                                TCC TTTATTTC   GTCT
                                  C       CGT
GAM2993  DKFZP564B1023 3'  AAAGAAAAGAACTCAGG     68488         TAAA      A
                                AAGGAAAA    GACTCAG G
                                ||||||||    ||||||| |
                                TTTCTTTT    TTGAGTC C
                                    C___      C
GAM2993  EPB41L1   3'  AAGAGAAAATGAAGACCCATGA 68489     _     A      _
           GA                     AAG GAAAAT AAGACTCA GAGA
                                ||| |||||| |||||||| ||||
                                TTC CTTTTA TTCTGGGT CTCT
                                  T     C       A
GAM2993  FLJ12409  3'  AAAGCCCTCAAAGACTTAGAG  68490      AAAA       C
                                AAGG    TAAAGACT AGAG
                                ||||    |||||||| ||||
                                TTTC    GTTTCTGA TCTC
                                   GGGA       A
GAM2993  FLJ22649  3'  AAGAAACATAACTCAGAG    68491       ATAAA
                                AGGAAA    GACTCAGAG
                                ||||||    |||||||||
                                TTCTTT    TTGAGTCTC
                                   GTA__
GAM2993  FLJ23462  3'  TAAAGGAAAGAAAGTGCTTTAG 68492         AT    A_  C_
           AG                     TAAAGGAAA  AAAG  CT  AGAG
                                |||||||||  ||||  ||  ||||
                                ATTTCCTTT  TTTC  GA  TCTC
                                    C_   AC  AA
GAM2993  FLJ30681  3'  GGAAAATAAATCAAAGA     68493          GAC
                                GGAAAATAAA   TCAGAGA
                                ||||||||||   |||||||
                                CCTTTTATTT   AGTTTCT
                                      ___
GAM2993  HAPIP     3'  GGAGAAAAACTTCAGAG     68494     AAAT      _
                                GGA    AAAGACT CAGAG
                                |||    ||||||| |||||
                                CCT    TTTTTGA GTCTC
                                  C___      A
GAM2993  KIAA0211  3'  AGGAAAATAGAGCTCTGAG    68495         A  A   A
                                AGGAAAATA AG CTC GAG
                                ||||||||| || ||| |||
                                TCCTTTTAT TC GAG CTC
                                    C  _   A
GAM2993  KIAA0258  3'  AGGAAACAGGCTCAGAGA    68496       ATAA  A
                                AGGAAA    AG CTCAGAGA
                                ||||||    || ||||||||
                                TCCTTT    TC GAGTCTCT
                                   G___  C
GAM2993  KIAA0332  3'  TAAAGAAAAAATTCAGAG    68497          TAAAGAC
                                TAAAGGAAAA      TCAGAG
                                ||||||||||      ||||||
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                                ATTTCTTTTT      AGTCTC
                                      TA_____
GAM2993  KIAA0795  3'  AAGGAAAGGAATACCCAGAGA  68498       ATAAAG
                                AAGGAAA     ACTCAGAGA
                                |||||||     |||||||||
                                TTCCTTT     TGGGTCTCT
                                    CCTTA_
GAM2993  KIAA1202  3'  TAAAGGAAAGATGAAACAAGAG 68499        ATAA    TC
                                TAAAGGAAA   AGAC  AGAG
                                |||||||||   ||||  ||||
                                ATTTCCTTT   TTTG  TCTC
                                      CTAC   T_
GAM2993  KIAA1238  3'  AAGGAAAATAGCACTGGAGA   68500        AAG   CA
                                AAGGAAAATA   ACT  GAGA
                                ||||||||||   |||  ||||
                                TTCCTTTTAT   TGA  CTCT
                                      CG_   C_
GAM2993  KIAA1257  3'  AGGAAAGTGAGACTCAGAGA   68501      ATAA
                                AGGAAA   AGACTCAGAGA
                                ||||||   ||||||||||||
                                TCCTTT   TCTGAGTCTCT
                                    CAC_
GAM2993  KIAA1462  3'  TAAAAGAAAATAAAATGAAAGA 68502           ACTC
           GA                    TAAAGGAAAATAAAG   AGAGA
                                ||||||||||||||   |||||
                                ATTTTCTTTTATTTT   TCTCT
                                        ACTT
GAM2993  KIAA1674  3'  TAAAGGGAATAAAAACATGAGA 68503      AA       TCA
                                TAAAGG  AATAAAGAC   GAGA
                                ||||||  |||||||||   ||||
                                ATTTCC  TTATTTTTG   CTCT
                                    C_       TA_
GAM2993  KIAA1674  3'  TAAAGGAAATGAAAAGATGGAG 68504       AT_    CTCA
           A                     TAAAGGAAA   AAAGA   GAGA
                                |||||||||   |||||   ||||
                                ATTTCCTTT   TTTCT    CTCT
                                      ACT    AC__
GAM2993  KIAA1786  3'  AAGGAAACTAGGCTCAGAGA   68505      ATAA  A
                                AAGGAAA    AG CTCAGAGA
                                |||||||    || ||||||||
                                TTCCTTT    TC GAGTCTCT
                                    GA__  C
GAM2993  KIAA1804  3'  TAAAGGGGAATAATAACAGAGA 68506      AA    AGACT
                                TAAAGG  AATAA    CAGAGA
                                ||||||  |||||    ||||||
                                ATTTCC  TTATT    GTCTCT
                                    CC    ATT__
GAM2993  KIAA1813  5'  AAGGAAGGAGACAGGCTCAGAG 68507      AATAA_  A
           A                     AAGGAA     AG CTCAGAGA
                                ||||||     || ||||||||
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                                TTCCTT     TC GAGTCTCT
                                   CCTCTG  C
GAM2993 KIAA1813 5' AAGAGACAAAGACTCGGAG   68508     AA        A
                                AGGA  ATAAAGACTC GAG
                                ||||  |||||||||| |||
                                TTCT  TGTTTCTGAG CTC
                                  C_        C
GAM2993 KRTAP4-7 3' AAAGAAAATAAGGAAATCAGA 68509          A  C_
                                AAGGAAAATAA GA  TCAGA
                                |||||||||| ||  |||||
                                TTTCTTTTATT CT  AGTCT
                                       C  TT
GAM2993 MCAM     3' AGGAAACCAGCTCAGAGA    68510       ATAA  A
                                AGGAAA    AG CTCAGAGA
                                ||||||    || ||||||||
                                TCCTTT    TC GAGTCTCT
                                   GG__  _
GAM2993 MGC12435 3' TAAAGGAAAAAAAAAGATGAGA 68511          T_    CTCA
                                TAAAGGAAAA  AAAGA    GAGA
                                ||||||||||  |||||    ||||
                                ATTTCCTTTT  TTTCT    CTCT
                                      TT    A___
GAM2993 MGC15476 3' TGAGGAAAGTGACGCCCAGAGA 68512   A     ATAAAGA
                                A AGGAAA      CTCAGAGA
                                | ||||||      ||||||||
                                A TCCTTT      GGGTCTCT
                                 C     CACTGC_
GAM2993 MGC3248  3' AGGAAAATGAAGACACCAGGGA 68513        A    _   A
                                AGGAAAAT AAGAC TCAG GA
                                |||||||| ||||| |||| ||
                                TCCTTTTA TTCTG GGTC CT
                                     C    T   C
GAM2993 NFAT5    3' TGAGGAAAATACTTTTGGTTCA 68514   A       AAGAC___
           GAGA                   A AGGAAAATA       TCAGAGA
                                | |||||||||       |||||||
                                A TCCTTTTAT       AGTCTCT
                                 C        GAAAACCA
GAM2993 NRN1     3' GGAAAATAAAGGCAGTGA    68515          ACT   A
                                GGAAAATAAAG   CAG GA
                                ||||||||||   ||| ||
                                CCTTTTATTTC   GTC CT
                                      C__   A
GAM2993 PRO0611  3' AAGAAAAATAACTAGAG     68516         AAG   C
                                AAGGAAAATA   ACT AGAG
                                ||||||||||   ||| ||||
                                TTCTTTTTAT   TGA TCTC
                                      ___   _
GAM2993 PRO2521  3' TAAAGGGAAAACCCAGAG    68517       AAAATA
                                TAAAGG     AAGACTCAGAG
                                ||||||     ||||||||||
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                                ATTTCC     TTTTGGGTCTC
                                   C_____
GAM2993  PRO2893   3'  TAAAGGAGCAATGAAAATATAG 68518       A_   A   CTC
            AGA                    TAAAGGA  AAT AAGA   AGAGA
                                |||||||  ||| ||||  |||||
                                ATTTCCT  TTA TTTT   TCTCT
                                    CG   C   ATA
GAM2993  RBM12     3'  TAAAAGAAAATGAGGACTTTAG 68519          AAA   CAG
            A                   TAAAGGAAAAT   GACT   AGA
                                ||||||||||   ||||  |||
                                ATTTTCTTTTA   CTGA   TCT
                                      CTC   AA_
GAM2993  RILP      3'  GGAAACTGAGACTCAGAGA   68520      ATAA
                                GGAAA   AGACTCAGAGA
                                |||||   ||||||||||
                                CCTTT   TCTGAGTCTCT
                                   GAC_
GAM2993  SEC61A1   3'  TAAGGGAAAACAATGGTGTCTT 68521     A       AGA___  C
            AGAGA                   TAA GGAAAATAA     CT AGAGA
                                ||| |||||||||     || |||||
                                ATT CCTTTTGTT     GA TCTCT
                                  C       ACCACA  A
GAM2993  STAF65(gamma) 3'  CAAAGGAAAATGAAGATAAGA  68522          A   CTC
                                TAAAGGAAAAT AAGA   AGA
                                |||||||||| ||||  |||
                                GTTTCCTTTTA TTCT   TCT
                                      C   AT_
GAM2993  STXBP3    3'  AAAGAAAAACTACACTTAGAG  68523         AAAG   C
                                AAAGGAAAAT    ACT AGAG
                                ||||||||||    ||| ||||
                                TTTCTTTTTG    TGA TCTC
                                      ATG_   A
GAM2993  TJP4      5'  AAGGAGGCAGGCTCAGAGA   68524      AAATAA  A
                                AAGGA     AG CTCAGAGA
                                |||||     || ||||||||
                                TTCCT     TC GAGTCTCT
                                   CCG___  C
GAM2993  TOR2A     3'  AGAGACAGAGGCTCAGAG    68525     AA   A  A
                                GGA  ATA AG CTCAGAG
                                |||  ||| || |||||||
                                TCT  TGT TC GAGTCTC
                                  C_   C  C
GAM2993  TP53TG3   3'  AAAGAAAATAAACACAGCCTTA 68526          G  TC____
            GAGA                    AAGGAAAATAAA AC     AGAGA
                                ||||||||||||  ||     |||||
                                TTTCTTTTATTT TG     TCTCT
                                      G  TCGGAA
GAM2993  WIT-1     5'  AAGGAAACTGAGGCTCAGAGA  68469        ATAA  A
                                AAGGAAA    AG CTCAGAGA
                                |||||||    || ||||||||
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                                TTCCTTT   TC GAGTCTCT
                                   GAC_  C
GAM2993  LOC112724 3'  TGAAGAAACCAAGGCTCAGAGA 68527   A     ATA   A
                                A AGGAAA   AAG CTCAGAGA
                                | ||||||   ||| ||||||||
                                A TTCTTT   TTC GAGTCTCT
                                 C     GG_  C
GAM2993  LOC127428 3'  AAGAAAAATAAAGCTAG     68528           A  C
                                AAGGAAAATAAAG CT AG
                                |||||||||||| || ||
                                TTCTTTTTATTTC GA TC
                                      _ _
GAM2993  LOC146237 3'  AGGGGGACAAAGACTCAGGGA  68529     AAA         A
                                AGG   ATAAAGACTCAG GA
                                |||   |||||||||||| ||
                                TCC   TGTTTCTGAGTC CT
                                  CCC          C
GAM2993  LOC147525 3'  AGGGAGACAAAGACTTGGAGA  68530     AAA       CA
                                AGG   ATAAAGACT  GAGA
                                |||   |||||||||  ||||
                                TCC   TGTTTCTGA  CTCT
                                  CTC        AC
GAM2993  LOC148753 3'  AGAAAATGGAGTCTCAGAGA   68531       AA  A
                                GGAAAAT  AG CTCAGAGA
                                |||||||  || ||||||||
                                TCTTTTA  TC GAGTCTCT
                                   CC  A
GAM2993  LOC149302 5'  AGGTAAAGGCTCAGAGA     68532     AAAA    A
                                AGG    TAAAG CTCAGAGA
                                |||    ||||| ||||||||
                                TCC    ATTTC GAGTCTCT
                                  ____     C
GAM2993  LOC150319 5'  AGGAAACTGAGGCTCAGAGA   68533       ATAA  A
                                AGGAAA    AG CTCAGAGA
                                ||||||    || ||||||||
                                TCCTTT    TC GAGTCTCT
                                   GAC_  C
GAM2993  LOC150848 3'  AAAGAAAGTAAAACAGAG     68534       A    ACT
                                AAGGAAA TAAAG   CAGAG
                                ||||||| |||||   |||||
                                TTTCTTT ATTTT   GTCTC
                                   C    ___
GAM2993  LOC150862 3'  TAAAGGAGATTAAAGACCAATC 68535       AAA     ___
            AGA                   TAAAGGA   TAAAGAC   TCAGA
                                |||||||   |||||||  |||||
                                ATTTCCT   ATTTCTG   AGTCT
                                   CTA      GTT
GAM2993  LOC150998 3'  AAGGAACTGAGGCTCAGAGA   68536       AATAA  A
                                AAGGAA     AG CTCAGAGA
                                ||||||     || ||||||||
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                                TTCCTT    TC GAGTCTCT
                                   GAC__  C
GAM2993  LOC151361 3'  AAGAGAAAATAAAAAGTGGAGA 68537     _        CTCA
                                AAG GAAAATAAAGA   GAGA
                                ||| |||||||||||   ||||
                                TTC CTTTTATTTTT   CTCT
                                  T         CAC_
GAM2993  LOC151701 5'  AAGGAAAAGTGGAGGAGACTCG 68538        TAA____    A
                GAG                AAGGAAAA      AGACTC GAG
                                |||||||||     |||||| |||
                                TTCCTTTT      TCTGAG CTC
                                     CACCTCC     C
GAM2993  LOC152220 3'  AAGGAGAGAAAGACTAGCAGA  68539      AAAT     __
                                AAGGA   AAAGACT  CAGA
                                |||||   |||||||  ||||
                                TTCCT   TTTCTGA  GTCT
                                   CTC_     TC
GAM2993  LOC159963 5'  TGAAGAAAATGATTACCAGAG  68540   A      AAAG  T
                                A AGGAAAAT   AC CAGAG
                                | ||||||||   || |||||
                                A TTCTTTTA   TG GTCTC
                                 C       CTAA  _
GAM2993  LOC170395 3'  TAAAGGAAATGAAAAGATGGAG 68504        AT_    CTCA
                A                TAAAGGAAA   AAAGA   GAGA
                                |||||||||   |||||   ||||
                                ATTTCCTTT   TTTCT   CTCT
                                      ACT    AC__
GAM2993  LOC196528 3'  TAAAGGAAAATGAGTCCAGA   68541         AA  A T
                                TAAAGGAAAAT  AG C CAGA
                                ||||||||||  || | ||||
                                ATTTCCTTTTA  TC G GTCT
                                       C_  A _
GAM2993  LOC200563 5'  AAAGGAAAATAAAAATGGAG   68542           CTCA
                                AAAGGAAAATAAAGA   GAG
                                ||||||||||||||   |||
                                TTTCCTTTTATTTTT   CTC
                                          AC__
GAM2993  LOC201626 3'  AGGAAAACAAGGAAAGAGA   68543         A  CTC
                                AGGAAAATAA GA   AGAGA
                                |||||||||| ||   |||||
                                TCCTTTTGTT CT   TCTCT
                                      C  T__
GAM2993  LOC219848 3'  TGAGGAAACCAAGGCTCAGAGA 68544   A     ATA   A
                                A AGGAAA   AAG CTCAGAGA
                                | ||||||   ||| ||||||||
                                A TCCTTT   TTC GAGTCTCT
                                 C     GG_   C
GAM2993  LOC222008 3'  AAGGCAGGGCAAACTCAGAGA  68545     AAAATAA
                                AAGG      AGACTCAGAGA
                                ||||      ||||||||||
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                                TTCC      TTTGAGTCTCT
                                  GTCCCG_
GAM2993  LOC255328 3'  TAAAGCAAACGGACTCAGAGA  68546      G   ATAAA
                                TAAAG AAA    GACTCAGAGA
                                ||||| |||    ||||||||||
                                ATTTC TTT    CTGAGTCTCT
                                   G   GC___
GAM2993  LOC257358 3'  AAGGAAAAGAGGGGCTGCAGAG 68547        TAAAGA  _
            A                    AAGGAAAA     CT CAGAGA
                                ||||||||     || ||||||
                                TTCCTTTT     GA GTCTCT
                                     CTCCCC  C
GAM2994  GNB1     3'  ACAGAGCAGCAACGAGAA    68550      AA  ATA
                                ATAGA  CA   CAACGAGAA
                                |||||  ||   |||||||||
                                TGTCT  GT   GTTGCTCTT
                                   C_  C__
GAM2994  HF1      3'  AAAACAATACATAAAAAAT    68551          AC
                                GAAACAATACA  GAGAAAT
                                ||||||||||  |||||||
                                TTTTGTTATGT  TTTTTTA
                                      A_
GAM2994  MCL1     3'  ATAGAAACAAAACAGTAAG    68552         T   AC
                                ATAGAAACAA ACA  GAG
                                |||||||||| |||  |||
                                TATCTTTGTT TGT  TTC
                                      T   CA
GAM2994  MOX2     3'  TAAGAAACAATACAGAATTAAA 68553    T         ACGAG
            TA                    A AGAAACAATACA     AAATA
                                | ||||||||||||     |||||
                                A TCTTTGTTATGT     TTTAT
                                 T          CTTAA
GAM2994  ORC2L    3'  TAGAAACAATAAGAGA      68554          CAAC
                                TAGAAACAATA    GAGA
                                ||||||||||    ||||
                                ATCTTTGTTAT    CTCT
                                      T___
GAM2994  PCDH15   3'  GAAAGCACAATGAGAAATA    68555      CAA    C
                                GAAA   TACAA GAGAAATA
                                ||||   ||||| ||||||||
                                CTTT   GTGTT CTCTTTAT
                                  C__     A
GAM2994  RNGTT    3'  TAGAAACAATGCAATTCACAAA 68556          A  ____
            AA                    TAGAAACAAT CA    ACGAGAA
                                ||||||||||  ||    |||||||
                                ATCTTTGTTA GT    TGTTTTT
                                      C  TAAG
GAM2994  STMN1    3'  TAGAAAAGATGCAACAAGAAA  68557       CA  A
                                TAGAAA  AT CAACGAGAAA
                                ||||||  ||  ||||||||||
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                                ATCTTT  TA GTTGTTCTTT
                                   TC  C
GAM2994  ZNF74    5'  ACAGAAACAGCATCGAGGAATA 68558         ATA  A    A
                                ATAGAAACA   CA CGAG AATA
                                |||||||||   || |||| ||||
                                TGTCTTTGT   GT GCTC TTAT
                                     C__  A   C
GAM2994  C14orf4  3'  ATAGAAACATACGACGAAAA  68559         A   A
                                ATAGAAACA TAC ACGAGAA
                                ||||||||| ||| |||||||
                                TATCTTTGT ATG TGCTTTT
                                     _  C
GAM2994  C20orf7  3'  ACAGAAACAATATGAAACTGAA 68560          C__  GA
            AT                   ATAGAAACAATA  AAC  GAAAT
                                ||||||||||||  |||  |||||
                                TGTCTTTGTTAT  TTG  CTTTA
                                      ACT  A_
GAM2994  CLIC4    3'  AGAAACAGCCTATGAGAAATA  68561       ATACAAC
                                AGAAACA      GAGAAATA
                                |||||||      ||||||||
                                TCTTTGT      CTCTTTAT
                                   CGGATA_
GAM2994  FLJ10315 3'  AGAAACAGTACGTAACAAAAA  68562       A  __
                                AGAAACA TAC  AACGAGAA
                                ||||||| |||  ||||||||
                                TCTTTGT ATG  TTGTTTTT
                                   C   CA
GAM2994  FLJ11362 3'  GAAACAATACAAATTAAATA  68563          CGAG
                                GAAACAATACAA   AAATA
                                ||||||||||||   |||||
                                CTTTGTTATGTT   TTTAT
                                      TAA_
GAM2994  FLJ20186 3'  TAGACAGTACAACGAGGAAAT  68564     AA  A      _
                                TAGA  CA TACAACGAG AAAT
                                ||||  || ||||||||| ||||
                                ATCT  GT ATGTTGCTC TTTA
                                  __ C       C
GAM2994  FLJ22794 3'  GAAGAAGTAAAACAATGAGAAA 68565   T   AC  T   C
            TA                   A AGAA  AA ACAA GAGAAATA
                                | ||||  || |||| ||||||||
                                C TCTT  TT TGTT CTCTTTAT
                                 T   CA  T   A
GAM2994  FOXP1    3'  ACAGAAAGCTACAAACGAGAAA 68566       CAA   _
            T                    ATAGAAA   TACAA CGAGAAAT
                                |||||||   ||||| ||||||||
                                TGTCTTT   ATGTT GCTCTTTA
                                   CG_    T
GAM2994  FTSJ1    3'  ATATGAACAATACTTCAAGA   68567     GA      AA
                                ATA  AACAATAC  CGAGA
                                |||  ||||||||  |||||
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                                TAT  TTGTTATG  GTTCT
                                  AC       AA
GAM2994  KIAA0089  3'  ATAGAAACATCCACAGAATGAG 68568         A_   AC__   A
              GAATA                  ATAGAAACA  TACA   GAG AATA
                                |||||||||  ||||   ||| ||||
                                TATCTTTGT  GTGT   CTC TTAT
                                    AG   CTTA   C
GAM2994  KIAA0417  3'  AGAAACAGTACACAGGGAGA   68569       A   AC__
                                AGAAACA TACA   GAGA
                                |||||||  ||||   ||||
                                TCTTTGT ATGT   CTCT
                                   C   GTCC
GAM2994  KIAA0997  3'  TAAAAACAATGGATTAAGAAAT 68570          ACAAC
                                TAGAAACAAT    GAGAAAT
                                ||||||||||    |||||||
                                ATTTTTGTTA    TTCTTTA
                                     CCTAA
GAM2994  KIAA1238  3'  ATAAAAACAATATCAGAAATA  68571          CAA G
                                ATAGAAACAATA   C AGAAATA
                                ||||||||||||   | |||||||
                                TATTTTTGTTAT   G TCTTTAT
                                      A__ _
GAM2994  KIAA1243  3'  AAAACAATAAGAGAAATA    68572         CAAC
                                GAAACAATA   GAGAAATA
                                |||||||||   ||||||||
                                TTTTGTTAT   CTCTTTAT
                                     T___
GAM2994  KIAA1456  3'  ATAGAAAGGCAAACGAGAAATA 68573        CAATAC
                                ATAGAAA     AACGAGAAATA
                                |||||||     ||||||||||||
                                TATCTTT     TTGCTCTTTAT
                                   CCGT__
GAM2994  KLF12     3'  ACAGAAACACTATGAGAAAT   68574         ATACAAC
                                ATAGAAACA      GAGAAAT
                                |||||||||      |||||||
                                TGTCTTTGT      CTCTTTA
                                     GATA___
GAM2994  PARVA     3'  AGAGACAGTACAGTAAGAAATA 68575     A   A   AC
                                AGA ACA TACA  GAGAAATA
                                ||| ||| ||||  ||||||||
                                TCT TGT ATGT  TTCTTTAT
                                  C   C   CA
GAM2994  POLR2B    3'  ATAGAAACAAGACACCAAGA   68576         T   A
                                ATAGAAACAA ACA CGAGA
                                |||||||||| ||| |||||
                                TATCTTTGTT TGT GTTCT
                                     C   G
GAM2994  TA-PP2C   3'  GAAAGAACATCGAGAAAT    68577      CAAT   A
                                GAAA    ACA CGAGAAAT
                                ||||    ||| ||||||||
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                                CTTT    TGT GCTCTTTA
                                  CT__   A
GAM2994  VEST1    5'  GAAACAATAACAGAGAA     68578          _  AC
                                GAAACAATA CA  GAGAA
                                ||||||||| ||  |||||
                                CTTTGTTAT GT  CTCTT
                                     T  __
GAM2994  LOC149448 3'  CAGAAAGAACGAGAAATA    68579       CAATAC
                                TAGAAA     AACGAGAAATA
                                ||||||     ||||||||||
                                GTCTTT     TTGCTCTTTAT
                                   C_____
GAM2994  LOC157922 3'  AAACATACAGTGAGAAATA    68580       A    AC
                                AAACA TACA  GAGAAATA
                                ||||| ||||  ||||||||
                                TTTGT ATGT  CTCTTTAT
                                   _    CA
GAM2994  LOC222166 3'  ACAGAAACAATATTCAGAAATA 68581            CAA G
                                ATAGAAACAATA   C AGAAATA
                                ||||||||||||   | |||||||
                                TGTCTTTGTTAT   G TCTTTAT
                                      AA_ _
GAM2995  KCNA7    3'  TAAATGCAAAACAGCCCGATGT 68584    C       __    TT   C
              G                  A AATGCAAA  AGCC  CGA GTG
                                 | ||||||||  ||||  ||| |||
                                 A TTACGTTT  TCGG  GCT CAC
                                  T       TG   __   A
GAM2995  KIF3C    3'  ACAATGCAAAGGCGATGT    68585          A  CTTC  C
                                ACAATGCAAA GC    GA GT
                                |||||||||| ||    || ||
                                TGTTACGTTT CG    CT CA
                                      C  ____  A
GAM2995  PAFAH1B2  3'  TACAATGCAAAGTGCCTT    68586           A_
                                TACAATGCAAA  GCCTT
                                ||||||||||  |||||
                                ATGTTACGTTT  CGGAA
                                      CA
GAM2995  MGC32124  3'  TACAAGCAAAAGCTTTTC    68587       T       C_
                                TACAA GCAAAAGC  TTC
                                ||||| ||||||||  |||
                                ATGTT CGTTTTCG  AAG
                                   _       AA
GAM2995  ZNF33A    3'  TACAATGCTGAAAAGCAGTGGT 68588         __     CTTCGAC
              GTG                   TACAATGC  AAAAGC      GTG
                                    ||||||||  ||||||      |||
                                    ATGTTACG  TTTTCG      CAC
                                       AC     TCACCA_
GAM2995  LOC93109  3'  TACGAAGCAAAAGCTTCTGTG  68589     AAT       C   GAC
                                TAC   GCAAAAGC TTC   GTG
                                |||   |||||||| |||   |||
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                                ATG  CGTTTTCG AAG  CAC
                                  CTT      _  A__
GAM2996 ABCB6   5' AGAGGGGCGCGGACATCC   68592     AAACA  C     _
                                AGAGG    GGC GCGGACA CC
                                |||||    ||| ||||||| ||
                                TCTCC    CCG CGCCTGT GG
                                  _____  _     A
GAM2996 ADAR    3' AGAGGAAATGGACCGCAG   68593       CA
                                AGAGGAAA  GGCCGCGG
                                ||||||||  ||||||||
                                TCTCCTTT  CTGGCGTC
                                     AC
GAM2996 ADAR    3' AGAGGAAATGGACCGCAG   68593       CA
                                AGAGGAAA  GGCCGCGG
                                ||||||||  ||||||||
                                TCTCCTTT  CTGGCGTC
                                     AC
GAM2996 ADAR    3' AGAGGAAATGGACCGCAG   68593       CA
                                AGAGGAAA  GGCCGCGG
                                ||||||||  ||||||||
                                TCTCCTTT  CTGGCGTC
                                     AC
GAM2996 AKAP2   5' AAGGAAACTGATGGGCACC   68594       A  CCGC  A
                                GAGGAAAC GG   GG CACC
                                |||||||| ||   || ||||
                                TTCCTTTG CT   CC GTGG
                                     A  AC__  _
GAM2996 ANGPT4  3' AGAGGGATGGGCCCCGAACACC 68595     AAACA   G
            C                    AGAGG    GGCC CGGACACCC
                                |||||    |||| |||||||||
                                TCTCC    CCGG GCTTGTGGG
                                   CTAC_   G
GAM2996 APBA2   3' AGAGGGGGCAGACACC     68596     AAACA  CC
                                AGAGG    GG  GCGGACACC
                                |||||    ||  |||||||||
                                TCTCC    CC  CGTCTGTGG
                                  _____  __
GAM2996 APM1    3' GAGGTGGGAAACAGACACC   68597     AAACA  CC
                                GAGG    GG  GCGGACACC
                                ||||    ||  |||||||||
                                CTCC    CC  TGTCTGTGG
                                  AC___  TT
GAM2996 ARHGAP6 5' GGAGCAGGCTCTGCGCGGACA 68598    AA   ____
                                GGA  CAGGC   CGCGGACA
                                |||  |||||   ||||||||
                                CCT  GTCCG   GCGCCTGT
                                  C_   AGAC
GAM2996 BAK1    3' GAGGAGACGGCCACAGCC    68599     A  A     ACA
                                GAGGA AC GGCCGCGG   CC
                                ||||| || ||||||||   ||
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                                CTCCT TG CCGGTGTC   GG
                                  C _      ___
GAM2996 BARHL1   3' GAGGGCACAGGCCACAGAC   68600     AA
                                GAGG  ACAGGCCGCGGAC
                                ||||  ||||||||||||
                                CTCC  TGTCCGGTGTCTG
                                  CG
GAM2996 CA7      3' GAGGGAGAAGGCCACGTCACC 68601     AAAC      GA
                                GAGG   AGGCCGCG  CACC
                                ||||   ||||||||  ||||
                                CTCC   TCCGGTGC  GTGG
                                  CTCT      A_
GAM2996 CDH19    5' AGAGGAAACAGGACGTCAC   68602         CC   GA
                                AGAGGAAACAGG  GCG  CAC
                                ||||||||||||  |||  |||
                                TCTCCTTTGTCC  TGC  GTG
                                       __  A_
GAM2996 CGTHBA   3' GAGGGGGCCACAGGGCAC    68603     AAACA      A_
                                GAGG    GGCCGCGG  CAC
                                ||||    ||||||||  |||
                                CTCC    CCGGTGTC  GTG
                                  C____       CC
GAM2996 COG3     3' AGAGGAAAGGATGACACC    68604       AC   CCGCG
                                AGAGGAA  AGG    GACACC
                                |||||||  |||    ||||||
                                TCTCCTT  TCC    CTGTGG
                                   __  TA___
GAM2996 COL4A6   5' AGGGAAACAGGCTCAGCGGTGC 68605    A        _ _   ACA
            CC                    AG GGAAACAGGC C GCGG   CCC
                                || ||||||||| | ||||  |||
                                TC CCTTTGTCCG G CGCC   GGG
                                 _        A T   AC_
GAM2996 COX7A1   5' GAGGAGGCGGTCCAGACCC   68606      AACA  CG__    A
                                GAGGA   GGC   CGGAC CC
                                |||||   |||   ||||| ||
                                CTCCT   CCG   GTCTG GG
                                  _____  CCAG    _
GAM2996 ELK1     3' GAGGAAACAGGCAGGACCC   68607          CGC   A
                                GAGGAAACAGGC   GGAC CC
                                ||||||||||||  |||| ||
                                CTCCTTTGTCCG   CCTG GG
                                       T__   _
GAM2996 FANCG    5' GAGGAAACGAGTCAGCAACCC 68608        AG CCG   AC
                                GAGGAAAC  G   CGG  ACCC
                                ||||||||  |   |||  ||||
                                CTCCTTTG  C   GTC  TGGG
                                     CT A__   GT
GAM2996 GGT1     3' GGAGACAGGCCAGGGAGGCACC 68609     A       C   __
                                GGA ACAGGCCG GGA  CACC
                                ||| |||||||| |||  ||||
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                                CCT TGTCCGGT CCT  GTGG
                                  C       C   CC
GAM2996 GLS      5'  AGAGGAAAGGGCAGCTAC    68610        CA   C  GG
                                AGAGGAAA  GGC GC  AC
                                ||||||||  ||| ||  ||
                                TCTCCTTT  CCG CG  TG
                                    C_   T  A_
GAM2996 INMT     3'  AGATGAAATACAGGACACC    68611     G    CAG  CGC
                                AGA GAAA   GC   GGACACC
                                ||| ||||   ||   |||||||
                                TCT CTTT   TG   CCTGTGG
                                  A   A__  T__
GAM2996 JRK      3'  AGAGGAAATGGGCCCAGGGACA 68612        CA    GC_    __
              TGCC                  AGAGGAAA  GGCC   GGACA  CC
                                ||||||||  ||||   |||||  ||
                                TCTCCTTT  CCGG   CCTGT  GG
                                    AC    GTC    AC
GAM2996 KCNS3    3'  AGAGAAACAGGCACAAACACCC 68613      G       C
                                AGAG AAACAGGC GCGGACACCC
                                |||| |||||||| ||||||||||
                                TCTC TTTGTCCG TGTTTGTGGG
                                  _       _
GAM2996 LTBP3    3'  GAGGAAGGCAGGCAGCGCCC   68614       A_    C   GACA
                                GAGGAA  CAGGC GCG    CCC
                                ||||||  ||||| |||    |||
                                CTCCTT  GTCCG CGC    GGG
                                   CC    T  _____
GAM2996 MAB21L1  5'  AGAAACGGGCCGCAACAC    68615       A      G
                                GGAAAC GGCCGCG ACAC
                                |||||| ||||||| ||||
                                TCTTTG CCGGCGT TGTG
                                   C      _
GAM2996 MECP2    3'  GAGGGGGCAGACACCC      68616      AAACA  CC
                                GAGG    GG  GCGGACACCC
                                ||||    ||  ||||||||||
                                CTCC    CC  CGTCTGTGGG
                                  ______  __
GAM2996 NDST2    3'  GAGGGGCCAGGCCACTCGGGTG 68617      AAA       _______  ACA
              C                  GAGG   CAGGCCGC     GG   C
                                ||||   ||||||||     ||   |
                                CTCC   GTCCGGTG     CC   G
                                  CCG       AGIIIC  ACA
GAM2996 NIPSNAP1 3'  GGAAACAGCCAAGCCAC     68618        G    C  A
                                GGAAACA GCCG GG CAC
                                ||||||| |||| || |||
                                CCTTTGT CGGT TC GTG
                                   _   _  G
GAM2996 NRD1     5'  GGGAACAGGCCTGAACCC    68619    A       GC    A
                                GG AACAGGCC  GGAC CC
                                || ||||||||  |||| ||
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                                CC TTGTCCGG  CTTG GG
                                 C       A_   _
GAM2996  PACSIN1   3'  AGGGGAAACAGGGCTGG     68620    A       CC  _
                                AG GGAAACAGG  GC GG
                                || |||||||||  || ||
                                TC CCTTTGTCC  CG CC
                                 C        __  A
GAM2996  PPP1R11   5'  GAGGAAGGGGGATGAGACACCC 68621       ACA  CCGC
                                GAGGAA   GG    GGACACCC
                                ||||||   ||    ||||||||
                                CTCCTT   CC    TCTGTGGG
                                   CC_  CTAC
GAM2996  PPP1R11   5'  GAGGAAGGGGGATGAGACACCC 68621       ACA  CCGC
                                GAGGAA   GG    GGACACCC
                                ||||||   ||    ||||||||
                                CTCCTT   CC    TCTGTGGG
                                   CC_  CTAC
GAM2996  PPT2      5'  GAGGAAACAGGCGGAGCGATCC 68622          C__   ACA
                                GAGGAAACAGGC   GCGG   CC
                                ||||||||||||   ||||   ||
                                CTCCTTTGTCCG   CGCT   GG
                                      CCT    A__
GAM2996  PPT2      5'  GAGGAAACAGGCGGAGCGATCC 68622          C__   ACA
                                GAGGAAACAGGC   GCGG   CC
                                ||||||||||||   ||||   ||
                                CTCCTTTGTCCG   CGCT   GG
                                      CCT    A__
GAM2996  SFN       3'  AGAGGAAACATGGTCACACCC  68623         _  C GCGG
                                AGAGGAAACA GG C    ACACCC
                                |||||||||| || |    ||||||
                                TCTCCTTTGT CC G    TGTGGG
                                     A  A ____
GAM2996  SH3BP2    3'  AGAGGTGGCCTTGGACACC    68624      AAACA    GC
                                AGAGG    GGCC  GGACACC
                                |||||    ||||  |||||||
                                TCTCC    CCGG  CCTGTGG
                                   A____    AA
GAM2996  SIX3      5'  GAGGAAGGGCGTAAGGGACACC 68625       ACA   CGC__
              C                  GAGGAA   GGC    GGACACCC
                                 ||||||   |||    ||||||||
                                 CTCCTT   CCG    CCTGTGGG
                                    C__   CATTC
GAM2996  SLC1A3    3'  AGGGGAAACAGAGGGCAG    68626    A       CC
                                AG GGAAACAGG  GCGG
                                || |||||||||  ||||
                                TC CCTTTGTCT  CGTC
                                 C        CC
GAM2996  SLC7A5    3'  AGGGAGCAGGCATGGCACC    68627    A   AA    CGC  A
                                AG GGA  CAGGC   GG CACC
                                || |||  |||||   || ||||
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                                TC CCT  GTCCG   CC GTGG
                                 _  C_    TA_ _
GAM2996 SLC7A7   3' AGAGGAGTAGGTAGGCACACCC 68628       AAC   CCGC _
                                AGAGGA  AGG   GG ACACCC
                                ||||||  |||   || ||||||
                                TCTCCT  TCC   CC TGTGGG
                                   CA_  AT__  G
GAM2996 SMARCD2  3' AGAGGGTGACAGCAGACAC   68629      AAACA  C
                                AGAGG   GGC GCGGACAC
                                |||||    ||| ||||||||
                                TCTCC    CTG CGTCTGTG
                                  CA___  T
GAM2996 SORCS2   3' AGAGGAGACACCCTGGGCAC  68630       A  GG  GC  A
                                AGAGGA ACA  CC  GG CAC
                                |||||| |||  ||  || |||
                                TCTCCT TGT  GG  CC GTG
                                   C  G_  A_  C
GAM2996 STUB1    3' AGGGGAAACAGTCCAGAGTCC  68631    A      G   C  ACA
                                AG GGAAACAG CCG GG   CC
                                || |||||||| ||| ||   ||
                                TC CCTTTGTC GGT TC   GG
                                 C       A   C  A__
GAM2996 SURF4    3' AGGAGAAACAGGAACACC    68632    AG      CCGCG
                                AG  GAAACAGG    GACACC
                                ||  ||||||||    ||||||
                                TC  CTTTGTCC    TTGTGG
                                 CT       _____
GAM2996 TTID     3' AGAGAAAACGGGTAAAACAG   68633        A  CC__
                                AGAGGAAAC GG    GCGG
                                ||||||||| ||    ||||
                                TCTCTTTTG CC    TGTC
                                     C  ATTT
GAM2996 UCP1     5' AGAGGAAAAGGCTCCAGCC    68634        C   CG   ACA
                                AGAGGAAA AGGC  CGG   CC
                                |||||||| ||||  |||   ||
                                TCTCCTTT TCCG  GTC   GG
                                    _   AG   ___
GAM2996 WFS1     3' AGAGGGAACAGGGTGCTTGGGT 68635     A     CC _______  ACA
             GTCC                  AGG AACAGG  GC     GG   CC
                                ||| ||||||  ||     ||   ||
                                TCC TTGTCC  CG     CC   GG
                                  C     CA  AAIIIC  ACA
GAM2996 ATP6V1D  5' AGAGGCAGCAGGGACACC    68636      AAA   CCGCG
                                AGAGG   CAGG    GACACC
                                |||||   ||||    ||||||
                                TCTCC   GTCC    CTGTGG
                                   GTC   _____
GAM2996 BRDG1    5' AGAGGAAAAGGCAAC       68637        C   CGCG
                                AGAGGAAA AGGC    GAC
                                |||||||| ||||    |||
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                                TCTCCTTT TCCG    TTG
                                  _   _____
GAM2996 CAS1     3' AAAGGAAACAGGTGAACG    68638          CC_
                                AGAGGAAACAGG   GCG
                                ||||||||||||  |||
                                TTTCCTTTGTCC   TGC
                                     ACT
GAM2996 Di-Ras2  3' GGAATTAAGAACGGACACCC  68639     AC   CC
                                GGAA  AGG  GCGGACACCC
                                ||||  |||  ||||||||||
                                CCTT  TTC  TGCCTGTGGG
                                  AA   T_
GAM2996 DKFZp434P0531 3' GGGAACAGCCCCAGATCC    68640    A    G  G    CA
                                GG AACAG CC CGGA  CC
                                || ||||| || ||||  ||
                                CC TTGTC GG GTCT  GG
                                 C    G  _    A_
GAM2996 DKFZp566H0824 5' AGAGGAAACAGTCTGTGCAA  68641          GCC__
                                AGAGGAAACAG    GCGG
                                ||||||||||     ||||
                                TCTCCTTTGTC    CGTT
                                     AGACA
GAM2996 DKFZP586F1524 3' AGGGAAACAGGCACATGCCC  68642    A        C   GACA
                                AG GGAAACAGGC GCG    CCC
                                || ||||||||| |||    |||
                                TC CCTTTGTCCG TGT    GGG
                                 _        _  AC__
GAM2996 DKFZP586I2223 3' GGAAGTAGCAGACACCC    68643    AAC  GCC
                                GGA   AG   GCGGACACCC
                                |||   ||   ||||||||||
                                CCT   TC   CGTCTGTGGG
                                  ___  AT_
GAM2996 DKFZP586I2223 3' GGAAGTAGCAGACACCC    68643    AAC  GCC
                                GGA   AG   GCGGACACCC
                                |||   ||   ||||||||||
                                CCT   TC   CGTCTGTGGG
                                  ___  AT_
GAM2996 DKFZP586I2223 3' GGAAGTAGCAGACACCC    68643    AAC  GCC
                                GGA   AG   GCGGACACCC
                                |||   ||   ||||||||||
                                CCT   TC   CGTCTGTGGG
                                  ___  AT_
GAM2996 DRIL2    3' GAGGAAGCTGGACACC     68644      AACA  CGC
                                GAGGA   GGC   GGACACC
                                |||||   |||   |||||||
                                CTCCT   TCG   CCTGTGG
                                   _____  A__
GAM2996 EPB41L1  3' GAGGAAACAGTGCCCTAGA   68645         _   GC
                                GAGGAAACAG GCC  GGA
                                |||||||||| |||  |||
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                                CTCCTTTGTC CGG  TCT
                                     A   GA
GAM2996  FLJ00058  5'  AGGGAAACAGGAGCACC     68646    A       CCGC  A
                                AG GGAAACAGG    GG CACC
                                || |||||||||    || ||||
                                TC CCTTTGTCC    TC GTGG
                                 _       _____  _
GAM2996  FLJ10110  3'  AGGGAAACAGGACAG      68647    A       CC
                                AG GGAAACAGG  GCGG
                                || |||||||||  ||||
                                TC CCTTTGTCC  TGTC
                                 _       __
GAM2996  FLJ10687  3'  GGAAACAGGACAGTCATATACC 68648         CC    A _____
                C                GGAAACAGG  GCGG C    ACCC
                                |||||||||  |||| |    ||||
                                CCTTTGTCC  TGTC G    TGGG
                                     __    A TATA
GAM2996  FLJ10852  3'  AAGGGGAACAGGCCACAA    68649     A_
                                GAGG  AACAGGCCGCGG
                                ||||  ||||||||||||
                                TTCC  TTGTCCGGTGTT
                                  CC
GAM2996  FLJ11078  3'  GAGGGAGGAGAAAAAAGACACC 68651      AAAC   CCGC
                C                GAGG    AGG    GGACACCC
                                ||||    |||    ||||||||
                                CTCC    TCT    TCTGTGGG
                                  CTCC   TTTT
GAM2996  FLJ11078  3'  AGGGGAGGCAGACACGTGCCC  68650    A   AA    C   GACA
                                AG GGA  CAGGC GCG    CCC
                                || |||  ||||| |||    |||
                                TC CCT  GTCTG TGC    GGG
                                 C   CC     _   AC__
GAM2996  FLJ13055  3'  AGAGGAAAAGGGGTAC      68652        C   CCGC  AC
                                AGAGGAAA AGG    GG  AC
                                |||||||| |||    ||  ||
                                TCTCCTTT TCC    CC  TG
                                     _   _____  A_
GAM2996  FLJ20257  5'  GAGGAGGTGGCCGCGGCC    68653      AACA       ACA
                                GAGGA    GGCCGCGG   CC
                                |||||    ||||||||   ||
                                CTCCT    CCGGCGCC   GG
                                  CCA_       ____
GAM2996  FLJ21916  3'  AGAGGGCAGGTGACCCACCC   68654      AAA    CC  GGA
                                AGAGG   CAGG  GC   CACCC
                                |||||   ||||  ||   |||||
                                TCTCC   GTCC  TG   GTGGG
                                  C__    AC  G__
GAM2996  FLJ21919  3'  AGGGGAAGCAGGAAGGGACACC 68655    A    A    CCGC
                C                AG GGAA CAGG    GGACACCC
                                || |||| ||||    ||||||||
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                                TC CCTT GTCC    CCTGTGGG
                                 C    C    TTC_
GAM2996  FLJ22378  3'  AGAGGAAATGGGGAAAACAC   68656        CA  CCGC
                                AGAGGAAA  GG    GGACAC
                                ||||||||  ||    ||||||
                                TCTCCTTT  CC    TTTGTG
                                    AC  CT__
GAM2996  GMPPA     5'  AGGAAACAATGGTTTGGGCACC 68657         GCCGC_  A
                                AGGAAACAG     GG CACC
                                |||||||||     || ||||
                                TCCTTTGTT     CC GTGG
                                     ACCAAA  C
GAM2996  KIAA0557  3'  GAGGAAACGGGCAGCTGGCA   68658         A   C   _   A
                                GAGGAAAC GGC GC GG CA
                                |||||||| ||| || || ||
                                CTCCTTTG CCG CG CC GT
                                    C   T  A  _
GAM2996  KIAA0561  3'  AGAGGAATTGTTTACGGACAC  68659        ACAGGCC
                                AGAGGAA      GCGGACAC
                                |||||||      ||||||||
                                TCTCCTT      TGCCTGTG
                                    AACAAA_
GAM2996  KIAA0779  3'  GGAAACAGGCAAAGCATAC    68660         C__   G
                                GGAAACAGGC   GCG AC
                                ||||||||||   ||| ||
                                CCTTTGTCCG   CGT TG
                                     TTT   A
GAM2996  KIAA1205  3'  GAGGGGGCAGCACAGACACACC 68661      AAACA   __        _
                                GAGG    GGC  CGCGGACAC CC
                                ||||    |||  |||||||||| ||
                                CTCC    CCG  GTGTCTGTG GG
                                  C_____   TC        T
GAM2996  KIAA1260  3'  GGAAATAGGCCACACAGAC    68662       C      __
                                GGAAA AGGCCGC  GGAC
                                |||||  |||||||  ||||
                                CCTTT TCCGGTG  TCTG
                                   A      TG
GAM2996  KIAA1271  5'  AGAGGAAACGAGACTCGGGTAC 68663          _    CG   AC
            CC                   AGAGGAAAC AGGC  CGG  ACCC
                                |||||||| ||||  |||  ||||
                                TCTCCTTTG TCTG  GCC  TGGG
                                     C    A_   CA
GAM2996  KIAA1402  5'  AGGGGGAACAGACCCCAGTGCC 68664    A  A      G   ACA
            C                    AG GG AACAGGCC CGG   CCC
                                || || |||||||| |||   |||
                                TC CC TTGTCTGG GTC   GGG
                                 C  C       G   AC_
GAM2996  KIAA1535  3'  AGGGAAACAGAGACA       68665     A       GCCGC
                                AG GGAAACAG     GGACA
                                || ||||||||     |||||
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                                TC CCTTTGTC    TCTGT
                                 _     _____
GAM2996 KIAA1602 3' AGAGGAAACAGGCTGGA    68666          CGC
                                AGAGGAAACAGGC  GGA
                                ||||||||||||  |||
                                TCTCCTTTGTCCG  CCT
                                       A__
GAM2996 KIAA1750 3' GAGGAAACAGCAGGAGGCAC  68667        GCCGC  A
                                GAGGAAACAG    GG CAC
                                ||||||||||    || |||
                                CTCCTTTGTC    CC GTG
                                     GTCCT  _
GAM2996 KIAA1795 3' AGAGGAAACAGGCTCAGTTATC 68668          CG  ACA_
            C                    AGAGGAAACAGGC  CGG   CC
                                ||||||||||||  |||   ||
                                TCTCCTTTGTCCG  GTC   GG
                                       A_  AATA
GAM2996 MACMARCKS 3' AGGGGAAGGCTGGACAC    68669    A  AAC   CGC
                                AG GGA  AGGC  GGACAC
                                || |||  ||||  ||||||
                                TC CCT  TCCG  CCTGTG
                                 C  ___   A__
GAM2996 MAD4    3' AGAGGCGGCACACACGGACGTC 68670      AAA  G  C    AC
            C                    AGAGG  CA GC GCGGAC  CC
                                |||||  || || ||||||  ||
                                TCTCC  GT TG TGCCTG  GG
                                   GCC  G  _    CA
GAM2996 MCRS1   3' AGGGGAAACAGGCCGGAGAGGG 68671    A        C  CA_
            CCC                    AG GGAAACAGGCCG GGA  CCC
                                || ||||||||||| |||  |||
                                TC CCTTTGTCCGGC TCT  GGG
                                 C         C  CCC
GAM2996 MGC13170 3' GAGGTTGGGGGCAGACACCC  68672     AAACA  CC
                                GAGG   GG  GCGGACACCC
                                ||||   ||  ||||||||||
                                CTCC   CC  CGTCTGTGGG
                                  AA___  CC
GAM2996 MGC3035  5' GAGGAAACAGCAACAC     68673        G CGCG
                                GAGGAAACAG C   GACAC
                                |||||||||| |   |||||
                                CTCCTTTGTC G   TTGTG
                                      _ ____
GAM2996 MIG     3' GAGAGATAGGATAAACACCC  68674    _ AAC  CCGC
                                GAG GA  AGG   GGACACCC
                                ||| ||  |||   ||||||||
                                CTC CT  TCC   TTTGTGGG
                                  T  A__  TA__
GAM2996 MUC17   3' AGGGAGGACGGGGACACC   68675    AAAC  C  C
                                AGG   AGG CG GGACACC
                                |||   ||| || |||||||
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                                TCC   TCC GC CCTGTGG
                                  C___   T  C
GAM2996  PDE4DIP   3'  AAGGGGGACAGGCCAACC   68676    AA_     CGGAC
                                GAGG  ACAGGCCG   ACC
                                ||||  ||||||||   |||
                                TTCC  TGTCCGGT   TGG
                                  CCC     _____
GAM2996  PRDX2     3'  GGGCACAGGTGGACACCC   68677   AA   CCGC
                                GG  ACAGG   GGACACCC
                                ||  |||||   ||||||||
                                CC  TGTCC   CCTGTGGG
                                 CG   A___
GAM2996  RHOBTB2   3'  AGGGGAGGCAGCCACAGTCC  68678   A  AACA     ACA
                                AG GGA   GGCCGCGG  CC
                                || |||   ||||||||  ||
                                TC CCT   TCGGTGTC  GG
                                 C  CCG_     A__
GAM2996  SSH2      3'  AGATGAAACAGGTGAACAC   68679    G     CCGC
                                AGA GAAACAGG   GGACAC
                                ||| ||||||||   ||||||
                                TCT CTTTGTCC   CTTGTG
                                  A      A___
GAM2996  LOC118472 3'  GAGGAGACAGGCCGTCCAC   68680     A     CGGA
                                GAGGA ACAGGCCG   CAC
                                ||||| ||||||||   |||
                                CTCCT TGTCCGGC   GTG
                                   C      AG__
GAM2996  LOC127002 5'  AAGGGGAACAGGCCTGGGTCC  68681    A_     GC  ACA
                                GAGG  AACAGGCC  GG  CC
                                ||||  ||||||||  ||  ||
                                TTCC  TTGTCCGG  CC  GG
                                  CC      A_  CA_
GAM2996  LOC145225 3'  AGAGGAAATGGTGCCAGGGAAT 68682       CAG_   C  CA_
           GCCC                  AGAGGAAA   GCCG GGA  CCC
                                ||||||||   |||| |||  |||
                                TCTCCTTT   CGGT CCT  GGG
                                    ACCA   C  TAC
GAM2996  LOC146784 5'  AGGGGAAACAGGCACTCCTACC 68683   A       C  GGAC
           C                    AG GGAAACAGGC GC   ACCC
                                || ||||||||| ||   ||||
                                TC CCTTTGTCCG TG   TGGG
                                 C        _  AGGA
GAM2996  LOC146823 3'  GAGGAGAAGAGGACACC    68684     AAC  CCGC
                                GAGGA  AGG   GGACACC
                                |||||  |||   |||||||
                                CTCCT  TCT   CCTGTGG
                                  CT_  _____
GAM2996  LOC147229 3'  GAGGAAACCCCCTTGGGTGCCC 68685       AGG  GC  ACA
                                GAGGAAAC  CC  GG  CCC
                                ||||||||  ||  ||  |||
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                                CTCCTTTG  GG  CC  GGG
                                    GG_  AA  CAC
GAM2996  LOC149072 5'  AGAGGAAAAGGCTGGGGTTGCC 68686       C   CGC  ACA
                                AGAGGAAA AGGC  GG  CC
                                |||||||| ||||  ||  ||
                                TCTCCTTT TCCG  CC  GG
                                    _   ACC  AAC
GAM2996  LOC149153 5'  GAGGGTGTGGGCAAACACCC  68687     AAACA  CC
                                GAGG   GG  GCGGACACCC
                                ||||    ||  ||||||||||
                                CTCC    CC  CGTTTGTGGG
                                  CACA_  __
GAM2996  LOC149401 5'  AGAGTAAACAGGCTGAAC    68688     G      CGC
                                AGAG AAACAGGC  GGAC
                                |||| ||||||||  ||||
                                TCTC TTTGTCCG  CTTG
                                  A      A__
GAM2996  LOC149401 5'  AGGGGAAACAGGCAGGGCA   68689    A       CGC  A
                                AG GGAAACAGGC  GG CA
                                || ||||||||||  || ||
                                TC CCTTTGTCCG  CC GT
                                 C        TC_  _
GAM2996  LOC150319 5'  AGAGAGGCGGTTAAGACATCC  68690     GAAAC   CGC__   _
                                AGAG    AGGC    GGACA CC
                                ||||    ||||    ||||| ||
                                TCTC    TCCG    TCTGT GG
                                  _____   CCAAT    A
GAM2996  LOC151525 5'  AGAGGGAACAGGCCCCGCC   68691     A      G  GACA
                                AGAGG AACAGGCC CG   CC
                                ||||| |||||||| ||   ||
                                TCTCC TTGTCCGG GC   GG
                                  C      G  ____
GAM2996  LOC152328 3'  GGAAACAGAGCTTATGACTGCC 68692       _  CGCG  A_
            C                    GGAAACAG GC   GAC  CCC
                                |||||||| ||   |||  |||
                                CCTTTGTC CG   CTG  GGG
                                    T  AATA  AC
GAM2996  LOC165257 5'  GGAGAGCCGCGGACGCC    68693    AACA       A
                                GGA   GGCCGCGGAC CC
                                |||   |||||||||| ||
                                CCT   TCGGCGCCTG GG
                                  C___        C
GAM2996  LOC219690 3'  AGAGGAAAGAGCAGACA    68694       AC  CC
                                AGAGGAA  AGG  GCGGACA
                                |||||||  |||  |||||||
                                TCTCCTT  TCT  CGTCTGT
                                   __  __
GAM2996  LOC220558 5'  AGAGGCGGCGGCCGCGGTGCCC 68695      AAACA      ACA
                                AGAGG   GGCCGCGG  CCC
                                |||||   ||||||||  |||
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                                TCTCC    CCGGCGCC  GGG
                                  GCCG_      AC_
GAM2996  LOC254381 5'  AGAGGAAATAGGCCCGGCA   68696       C    G  A
                                AGAGGAAA AGGCC CGG CA
                                |||||||| ||||| ||| ||
                                TCTCCTTT TCCGG GCC GT
                                    A    _  _
GAM2996  LOC255019 3'  AAGGGGATAGAGCAGACAC   68697     AAAC  CC
                                GAGG   AGG  GCGGACAC
                                ||||   |||  ||||||||
                                TTCC   TCT  CGTCTGTG
                                  CCTA  __
GAM2996  LOC255019 3'  AAGGGGATAGAGCAGACAC   68697     AAAC  CC
                                GAGG   AGG  GCGGACAC
                                ||||   |||  ||||||||
                                TTCC   TCT  CGTCTGTG
                                  CCTA  __
GAM2996  LOC256416 3'  GAGGAAGGGGCCGCAGAGCAGC 68698       ACA      _ _
            C                    GAGGAA  GGCCGCGGA CA CC
                                |||||| ||||||||| || ||
                                CTCCTT  CCGGCGTCT GT GG
                                   CC_       C  C
GAM2996  LOC51200  3'  AAGGAAACACAGGATACC    68699        GGC  C   C
                                GAGGAAACA  CG GGA ACC
                                |||||||||  || ||| |||
                                TTCCTTTGT  GT CCT TGG
                                     ___  _  A
GAM2996  LOC51313  5'  AGAGGACACAGGCCGGAGCCC  68700      A      C  ACA
                                AGAGGA ACAGGCCG GG  CCC
                                |||||| |||||||| ||  |||
                                TCTCCT TGTCCGGC TC  GGG
                                   G       C  ____
GAM2996  LOC51667  3'  AGAGGAAGCAGTCGGGACACCC 68701       A  GC  C
                                AGAGGAA CAG  CG GGACACCC
                                ||||||| |||  || ||||||||
                                TCTCCTT GTC  GC CCTGTGGG
                                    C  A_  _
GAM2996  LOC51673  3'  GAGGAAGGGGCCGCAGAGCAGC 68698       ACA      _ _
            C                    GAGGAA  GGCCGCGGA CA CC
                                |||||| ||||||||| || ||
                                CTCCTT  CCGGCGTCT GT GG
                                   CC_       C  C
GAM2996  LOC91351  3'  GAGGGGAGGGCACAAACATCC  68702     AAAC  C     _
                                GAGG   AGG CGCGGACA CC
                                ||||   ||| |||||||| ||
                                CTCC   TCC GTGTTTGT GG
                                  CC__  C      A
GAM2996  LOC91523  3'  AGAGGAAATAAGGCCTAGGTCC 68703       C_   GC  ACA
                                AGAGGAAA  AGGCC  GG  CC
                                ||||||||  |||||  ||  ||
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                                TCTCCTTT  TCCGG  CC   GG
                                    AT    AT  A__
GAM2996  LOC92080  3'  GAGGGAAGAGGCAGACACCC   68704     A  C    CGC
                                GAGG AA AGGC   GGACACCC
                                |||| || ||||   ||||||||
                                CTCC TT TCCG   TCTGTGGG
                                  C  C   ___
GAM2996  LOC92299  5'  GAGGAGGCGAGCCGCAGCGCC  68705      AACA      ACA
                                GAGGA   GGCCGCGG   CC
                                |||||   ||||||||  ||
                                CTCCT   TCGGCGTC   GG
                                   CCGC      GC_
GAM2997  PCDHB9    3'  AAGGATGGCAAACCA      68708       T   TGAATA
                                AAGGATG GCA     AACCA
                                ||||||| |||     |||||
                                TTCCTAC CGT     TTGGT
                                  _  _______
GAM2997  SRR       3'  AGGATGTGCTGTGGTTTAAACC 68709        A_  AA_
              A                  AGGATGTGC  TG   TAAACCA
                                |||||||||  ||   |||||||
                                TCCTACACG  AC   ATTTGGT
                                    AC  CAA
GAM2997  CDH26     3'  AAGGAGGCAATCGAATAAAC   68710      TGT   __
                                AAGGA   GCA  TGAATAAAC
                                |||||   |||  |||||||||
                                TTCCT   CGT  GCTTATTTG
                                   C__   TA
GAM2997  KIAA0557  3'  GGATGTGCACAGACCA     68711          AATAA
                                GGATGTGCATG    ACCA
                                ||||||||||    ||||
                                CCTACACGTGT    TGGT
                                      C____
GAM2997  PIK3R4    3'  AAGAGATGCATAAGTAAAC    68712      T       A
                                AGGA GTGCATGA TAAAC
                                |||| |||||||| |||||
                                TTCT TACGTATT ATTTG
                                  C       C
GAM2997  ZER6      3'  AAGAGTATAGGAATAAACCA   68713     GA    CAT
                                AAG  TGTG   GAATAAACCA
                                |||  ||||   ||||||||||
                                TTC  ATAT   CTTATTTGGT
                                  TC    C__
GAM2997  LOC143888 3'  GGATAGAAATAAACCAA     68714       TGCAT
                                GGATG    GAATAAACCAA
                                |||||    ||||||||||
                                CCTAT    TTTATTTGGTT
                                   C____
GAM2997  LOC154761 3'  AAGGGTGTGCATAATCCCA   68715      A        ATAAA
                                AAGG TGTGCATGA    CCA
                                |||| |||||||||    |||
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                                TTCC ACACGTATT    GGT
                                  C       AG___
GAM2997  LOC164395 3'  GGATAAACGCATGAATAA    68716      __
                                GGATG  TGCATGAATAA
                                |||||  ||||||||||
                                CCTAT  GCGTACTTATT
                                   TT
GAM2997  LOC220097 3'  AGGAGTACAGAATAAACCA   68717     T    T
                                AGGA GTGCA GAATAAACCA
                                |||| ||||| ||||||||||
                                TCCT CATGT CTTATTTGGT
                                  _    _
GAM2997  LOC254428 3'  AAGGATACGAGAGTAAACCAAT 68718         CAT  A
                                AAGGATGTG   GA TAAACCAAT
                                |||||||||   || |||||||||
                                TTCCTATGC   CT ATTTGGTTA
                                     T__  C
GAM2998  FKBP14    3'  CATTTTATTACAAAGAAACTCA 68721       CC  T  C
            CA                    TATTTTA  AT GA AAACTCACA
                                |||||||  || || |||||||||
                                GTAAAAT  TG TT TTTGAGTGT
                                    AA  T  C
GAM2998  H2AFY     3'  CATTTTACTAAATCAACTCACA 68722       CATT  CA
                                TATTTTAC    GA  AACTCACA
                                ||||||||    ||  ||||||||
                                GTAAAATG    TT  TTGAGTGT
                                     AT__  AG
GAM2998  H2AFY     3'  CATTTTACTAAATCAACTCACA 68722       CATT  CA
                                TATTTTAC    GA  AACTCACA
                                ||||||||    ||  ||||||||
                                GTAAAATG    TT  TTGAGTGT
                                     AT__  AG
GAM2998  H2AFY     3'  CATTTTACTAAATCAACTCACA 68722       CATT  CA
                                TATTTTAC    GA  AACTCACA
                                ||||||||    ||  ||||||||
                                GTAAAATG    TT  TTGAGTGT
                                     AT__  AG
GAM2998  KIAA0286  3'  CATTTTACCATGTACATAATTC 68723         TG  _  C
            ACA                   TATTTTACCAT  ACA AA TCACA
                                ||||||||||  ||| || |||||
                                GTAAAATGGTA  TGT TT AGTGT
                                      CA   A  A
GAM2998  KIAA0418  3'  ATTTTAAACAAACTCAC     68724       CCATT
                                ATTTTA    GACAAACTCAC
                                ||||||    ||||||||||
                                TAAAAT    TTGTTTGAGTG
                                          _____
GAM2998  UBP1      3'  TTTCACTGGGACAAACTCAC   68725       CATT
                                TTTTAC    GACAAACTCAC
                                ||||||    ||||||||||
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                                AAAGTG   CTGTTTGAGTG
                                   ACC_
GAM2998  LOC222166 3'  TATTTTACCATGGACACCCA  68726          T   AA
                                TATTTTACCAT GAC  ACTCA
                                |||||||||||  |||  |||||
                                ATAAAATGGTA CTG  TGGGT
                                      C   __
GAM2998  LOC257479 5'  TTTTACCAAATGCAACTC    68727        T_  A   A
                                TTTTACCA  TG CAA CTC
                                ||||||||  || ||| |||
                                AAAATGGT  AC GTT GAG
                                     TT  _  _
GAM2999  CHST1     3'  TCAAAAGCTTGAGAAGTCGCCT 68730         C  ACAA_
              C                  TCAAAAGCT GA    CGCCTC
                                |||||||||  ||    ||||||
                                AGTTTTCGA CT    GCGGAG
                                     A  CTTCA
GAM2999  GRLF1     3'  CCAAGGGCTCGAACCCT     68731      AA       AACG
                                TCAA  GCTCGAAC   CCT
                                ||||  ||||||||   |||
                                GGTT  CGAGCTTG   GGA
                                  CC       _____
GAM2999  HLCS      3'  CTTAAAAGCTCCAAATCCTC   68732    C       G  CAACG
                                CT AAAAGCTC AA    CCTC
                                || ||||||| ||    ||||
                                GA TTTTCGAG TT    GGAG
                                 A       G  TA___
GAM2999  RB1CC1    5'  ACTCAGAAAACCGGCAACGCCT 68733       _    T  AA
              C                  ACTCA AAAGC CG  CAACGCCTC
                                ||||| ||||| ||  |||||||||
                                TGAGT TTTTG GC  GTTGCGGAG
                                  C    _ C_
GAM2999  SCD       3'  CTCAAAAGACAAGGATGCCT   68734        CT   ACAAC
                                CTCAAAAG  CGA    GCCT
                                ||||||||  |||    ||||
                                GAGTTTTC  GTT    CGGA
                                     T_   CCTA_
GAM2999  TAF7      5'  CTCAGCGAGCTCTCTTCGCCTC 68735      AA_    GAACAA
                                CTCA   AGCTC     CGCCTC
                                ||||   |||||     ||||||
                                GAGT   TCGAG     GCGGAG
                                  CGC    AGAA__
GAM2999  TM4SF4    5'  TCAAAAGCTCCTCACTGCCTC  68736         GAA  AC
                                TCAAAAGCTC   CA  GCCTC
                                ||||||||||   ||  |||||
                                AGTTTTCGAG   GT  CGGAG
                                      GA_  GA
GAM2999  WNT2      5'  CCCGAAAGCTCTGCGCGCCTC  68737     A      GAACAA
                                CTC AAAGCTC     CGCCTC
                                ||| |||||||     ||||||
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                                GGG TTTCGAG     GCGGAG
                                  C      ACGC__
GAM2999 BCAA     5'  CTCAAGAGTCTCCCTCCGCTTC 68738      A _  GAACAA  C
                                CTCAA AG CTC     CGC TC
                                ||||| || |||     ||| ||
                                GAGTT TC GAG     GCG AG
                                   C  A  GGAG__  A
GAM2999 C22orf20 3'  TCAACAGGTAACAACGCTTC  68739     A  CTCG       C
                                TCAA AG   AACAACGC TC
                                |||| ||   |||||||| ||
                                AGTT TC   TTGTTGCG AG
                                  G  CA__       A
GAM2999 FLJ22418 3'  ACTTAGAAGCTCAACAAGC   68740     CAA     G    C
                                ACT   AAGCTC AACAA GC
                                |||   |||||| ||||| ||
                                TGA   TTCGAG TTGTT CG
                                  ATC     _    _
GAM2999 KIAA0543 3'  ACTCAGGGGCTGAAACCT    68741      AAA   C   CAAC
                                ACTCA   GCT GAA    GCCT
                                |||||   ||| |||    ||||
                                TGAGT   CGA CTT    TGGA
                                   CCC  _  _____
GAM2999 KIAA0788 3'  ACCCAAAAGTAAATGCCT    68742        CTC   CAAC
                                ACTCAAAAG   GAA    GCCT
                                |||||||||   |||    ||||
                                TGGGTTTTC   TTT    CGGA
                                     A__   A___
GAM2999 KIAA1321 3'  CTTTAAAGCTCAAGGATGCCTC 68743    CA       ACAAC
                                CT  AAAGCTCGA    GCCTC
                                ||  |||||||||    |||||
                                GA  TTTCGAGTT    CGGAG
                                 AA       CCTA_
GAM2999 M96      3'  TCAAAACAAACAACG       68744       GCT
                                TCAAAA   CGAACAACG
                                ||||||   |||||||||
                                AGTTTT   GTTTGTTGC
                                   ___
GAM2999 SEC61A1  3'  CTCGAAACCTCGAGCTCCTC   68745     A  G    ACAACG
                                CTC AAA CTCGA     CCTC
                                ||| ||| |||||     ||||
                                GAG TTT GAGCT     GGAG
                                  C   G    CGA___
GAM2999 LOC115400 5'  TCAAAAGCTGAGCAGGGC    68746        C  A  AC
                                TCAAAAGCT GA CA  GC
                                ||||||||| || ||  ||
                                AGTTTTCGA CT GT  CG
                                     _ C  CC
GAM2999 LOC121838 5'  ACTCAAAACTCCATGCCT    68747        G  GAA  AC
                                ACTCAAAA CTC   CA  GCCT
                                |||||||| |||   ||  ||||
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                                TGAGTTTT GAG   GT  CGGA
                                   _  ___  A_
GAM3000  C18orf1   3'  AGGGATTTGGATGGATTCTTC  68750        A  GACCT
                                AGGGATTT GA    TTCTTC
                                |||||||| ||    ||||||
                                TCCCTAAA CT    AAGAAG
                                    C  ACCT_
GAM3000  CYP4F3    3'  AAAGGGATTTTCTTTTCTT   68751         AGAGACC
                                AGAGGGATTT     TTTCTT
                                ||||||||||     ||||||
                                TTTCCCTAAA     AAAGAA
                                     AGA____
GAM3000  DLG3      3'  AGAGGGACTTGATTTCTT    68752         A  GACC
                                AGAGGGATTT GA   TTTCTT
                                |||||||||| ||   ||||||
                                TCTCCCTGAA CT   AAAGAA
                                   _  ____
GAM3000  IL1R1     3'  AGAGGGCATTTATTGCCCTTT  68753       _    GAGA
                                AGAGGG ATTTA   CCTTT
                                |||||| |||||   |||||
                                TCTCCC TAAAT   GGAAA
                                   G    AACG
GAM3000  MLANA     3'  AGAGGGATTTGGGAACCC    68754         AGA
                                AGAGGGATTT   GACCT
                                |||||||||   |||||
                                TCTCCCTAAA   TTGGG
                                     CCC
GAM3000  MUC4      3'  AGACGGTAGTTGGGCCTTTCTT 68755    G  ATT   AGA__
            C                    AGA GG   TAG    CCTTTCTTC
                                ||| ||   |||    |||||||||
                                TCT CC   ATC    GGAAAGAAG
                                  G  ___   AACCC
GAM3000  RRM2B     3'  AAGGGATTAAATCCTTTCTTC  68756        T   GA
                                GAGGGATT AGA  CCTTTCTTC
                                |||||||| |||  |||||||||
                                TTCCCTAA TTT  GGAAAGAAG
                                    _  A_
GAM3000  FLJ10546  3'  GAGGGATTTAGAATTTCTTC   68757          ACC
                                GAGGGATTTAGAG   TTTCTTC
                                ||||||||||||   |||||||
                                CTCCCTAAATCTT   AAAGAAG
                                     ___
GAM3000  FLJ10713  3'  GAGGGAATTAACAGCCTTTCTT 68758       T   _  A
                                GAGGGA TTAG AG CCTTTCTT
                                |||||| |||| || ||||||||
                                CTCCCT AATT TC GGAAAGAA
                                   T   G  _
GAM3000  KIAA0022  3'  AGAGGGATTACTTTTCTT    68759         TAGAG  C
                                AGAGGGATT    AC TTTCTT
                                |||||||||    || ||||||
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                                TCTCCCTAA    TG AAAGAA
                                      _____ A
GAM3000 KIAA0930 3' AGAGGGATTTAGGGCCT     68760          AGA
                                AGAGGGATTTAG   CCT
                                ||||||||||||  |||
                                TCTCCCTAAATC   GGA
                                      CC_
GAM3000 MGC21621 3' GAGAGGAAACAGATCTTTCTTC 68761    _  TT   GAC
                                GAG GGA  TAGA   CTTTCTTC
                                ||| |||  ||||  ||||||||
                                CTC CCT  GTCT   GAAAGAAG
                                  T  TT   A__
GAM3000 MGC27277 3' AAAGGGATTTAGGACTTTTC  68762          A  C
                                AGAGGGATTTAG GAC TTTC
                                |||||||||||| ||| ||||
                                TTTCCCTAAATC CTG AAAG
                                      _  A
GAM3000 SMA3     3' GGGATCCAGGGATCTTTCTTC  68763        A  C
                                GGGATTTAG GA CTTTCTTC
                                ||||||||| || ||||||||
                                CCCTAGGTC CT GAAAGAAG
                                     C  A
GAM3000 Spir-1   5' GAGGGCTTAATTCCCTTTCTTC 68764      A    AGA
                                GAGGG TTTAG   CCTTTCTTC
                                ||||| |||||   |||||||||
                                CTCCC GAATT   GGAAAGAAG
                                   _    AAG
GAM3000 SYT13    3' AGAGGGATTCGATATTTTTTC  68765        A  GACC_
                                AGAGGGATTT GA    TTTC
                                |||||||||| ||    ||||
                                TCTCCCTAAG CT    AAAG
                                     _ ATAAA
GAM3000 LOC129401 3' AGGGATTTTTAGTTTTCTT   68766       AG  ACC
                                AGGGATTT  AG   TTTCTT
                                ||||||||  ||  ||||||
                                TCCCTAAA  TC   AAAGAA
                                     AA  A__
GAM3000 LOC143888 3' GAGGGATTCCACCTTT      68767        AGAG
                                GAGGGATTT    ACCTTT
                                |||||||||    ||||||
                                CTCCCTAAG    TGGAAA
                                     G___
GAM3000 LOC165552 3' GAGGCATTCCCTTCTTTCTT   68768     G   AGAGAC
                                GAGG ATTT     CTTTCTT
                                |||| ||||     |||||||
                                CTCC TAAG     GAAAGAA
                                  G   GGAA__
GAM3000 LOC196996 3' GAGGGATCTGGAATATTTTC   68769        A   ACC
                                GAGGGATTT GAG   TTTC
                                ||||||||| |||   ||||
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                                CTCCCTAGA CTT   AAAG
                                     C   ATA
GAM3000  LOC200301 3'  AAAGGGGTTCCTTTCT      68770       A  TAGAGA
                                AGAGGG TT      CCTTTCT
                                |||||| ||      |||||||
                                TTTCCC AA      GGAAAGA
                                   C _______
GAM3000  LOC201115 5'  AGGGGGATGTCCTTTCTT     68771     A     TTAGAGA
                                AG GGGAT       CCTTTCTT
                                || |||||       ||||||||
                                TC CCCTA       GGAAAGAA
                                 C     CA_____
GAM3000  LOC221416 3'  GGGATGTCACCTTTCTTC     68772       TTAGAG
                                GGGAT      ACCTTTCTTC
                                |||||      ||||||||||
                                CCCTA      TGGAAAGAAG
                                   CAG___
GAM3000  LOC253891 3'  AGAGGGACTTAGGGACCCC    68773            A
                                AGAGGGATTTAG GACCTT
                                |||||||||||| ||||||
                                TCTCCCTGAATC CTGGGG
                                       C
GAM3000  LOC254945 5'  AGGGAGACCTACAGGCTTTTCT 68774     A       G  ACC
          T                      AG GGGATTTA AG   TTTCTT
                                || |||||||| ||   ||||||
                                TC CTCTGGAT TC   AAAGAA
                                 C       G  CGA
GAM3000  LOC256830 5'  GAGGAGATTCTCTCTTTCTTC  68775      _     AGAGAC
                                GAGG GATTT     CTTTCTTC
                                |||| |||||     ||||||||
                                CTCC CTAAG     GAAAGAAG
                                  T    AGA___
GAM3001  PCDH11X   3'  TACATCTGTAGAATATGATTG  68778          T_
                                TATATCTGT  GATATGATTG
                                |||||||||  ||||||||||
                                ATGTAGACA  TTATACTAAC
                                       TC
GAM3001  RHEB2     3'  ATATAAATTGAAAATATGATTG 68779       TC_  TT
                                ATATA   TG  GATATGATTG
                                |||||   ||  ||||||||||
                                TATAT   AC  TTATACTAAC
                                   TTA  TT
GAM3002  RECQL5    3'  CAGGGCCCAATTCAATCCA    68782     A       C
                                CA GGCCCAAT CAATCCG
                                || |||||||| |||||||
                                GT CCGGGTTA GTTAGGT
                                 C       A
GAM3002  SMARCD1   3'  TGAGGCCCAATCCATTCCA    68783    A          A
                                C AGGCCCAATCCA TCCG
                                | |||||||||||| ||||
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                                A TCCGGGTTAGGT AGGT
                                 C          A
GAM3002  SMARCD1   3'  TGAGGCCCAATCCATTCCA    68783    A          A
                                C AGGCCCAATCCA TCCG
                                | ||||||||||| ||||
                                A TCCGGGTTAGGT AGGT
                                 C          A
GAM3002  FLJ20808  5'  GGCCCTAATCCAATATGACCCG 68784       _       CC_ TT
              C                   GGCCC AATCCAAT   G  CGC
                                  ||||| ||||||||   |  |||
                                  CCGGG TTAGGTTA   T  GCG
                                     A       TAC GG
GAM3002  FLJ32191  5'  AAGCCCAATTTCGGGTTCGC   68785         CCAATCC
                                  AGGCCCAAT      GTTCGC
                                  |||||||||      ||||||
                                  TTCGGGTTA      CAAGCG
                                       AAGCC__
GAM3002  KIAA1196  3'  CAGGGCCCGAACTAGTCCGT   68786    A    _  CCAA
                                  CA GGCCC AAT    TCCGT
                                  || ||||| |||    |||||
                                  GT CCGGG TTG    AGGCA
                                   C    C   ATC_
GAM3002  PDEF      5'  CAAGGCCCAACCTGAGGGGCTT 68787           CAATCC   C
              GC                    CAAGGCCCAATC     GTT GC
                                    ||||||||||||     ||| ||
                                    GTTCCGGGTTGG     CGA CG
                                          ACTCCC   A
GAM3002  PTK6      5'  CAGGGCCCAATGTCAGGAGCTG 68788    A       CCAATCC   C
              C                    CA GGCCCAAT       GTT GC
                                   || ||||||||       ||| ||
                                   GT CCGGGTTA       CGA CG
                                    C       CAGTCCT   _
GAM3002  LOC131880 5'  CAGGGCCCAGGCCGATCCATTC 68789    A     AT  A
              G                    CA GGCCCA  CC ATCCGTTCG
                                   || ||||||  || |||||||||
                                   GT CCGGGT  GG TAGGTAAGC
                                    C     CC  C
GAM3002  LOC150245 3'  CAAGGCCCACATCTGTC     68790         ATC  A  C
                                   CAAGGCCCA   CA TC GTT
                                   |||||||||   || || |||
                                   GTTCCGGGT   GT AG CAG
                                        ___  _  A
GAM3002  LOC151171 5'  TGAGCCTGATCCCGTTCG    68791    A   CA    AATC
                                   A GGCC  ATCC    CGTTCG
                                   | ||||  ||||    ||||||
                                   A TCGG  TAGG    GCAAGC
                                    C   AC    ____
GAM3002  LOC206338 5'  CAAGGCCCAACCAACACGC    68792          T    TC
                                   CAAGGCCCAA CCAA  CGT
                                   |||||||||| ||||  |||
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                                GTTCCGGGTT GGTT  GCG
                                      _   GT
GAM3002 LOC90835 5' CAAGGCCGGGCCCGTTCG    68793       CAATCCAA
                                CAAGGCC       TCCGTTCG
                                |||||||       ||||||||
                                GTTCCGG       GGGCAAGC
                                   CCC_____
GAM3003 FLJ21657 3' TTAGAATAGTATATAAAATA  68796     T       C
                                TTAG AATAGTATA AAGATA
                                |||| ||||||||| ||||||
                                AATC TTATCATAT TTTTAT
                                  _       A
GAM3004 ADAM12   3' TCTCTATCCTGGTGTGGC    68799    _  A       A
                                TC CTG TTCTGGTGT GC
                                || ||| ||||||||| ||
                                AG GAT AGGACCACA CG
                                 A  _       C
GAM3004 AMPD1    5' TCCTTGATTCTAGGATAGC    68800     _      TG
                                TCCT GATTCTGG  TAGC
                                |||| ||||||||  ||||
                                AGGA CTAAGATC  ATCG
                                  A       CT
GAM3004 CHD2     3' TCCCTGATACCTAGTGTGGC   68801       _      A
                                TTCCTGAT TCTGGTGT GC
                                |||||||| |||||||| ||
                                AGGGACTA GGATCACA CG
                                     T       C
GAM3004 DLEC1    3' TTCCTGATGCTGACAAAGC    68802       T   GT T
                                TTCCTGAT CTG  G AGC
                                |||||||| |||  | |||
                                AAGGACTA GAC  T TCG
                                     C   TG T
GAM3004 FAP      3' TTCAGATTCTGATACAG     68803     CT
                                TTC  GATTCTGGTGTAG
                                |||  ||||||||||||
                                AAG  CTAAGACTATGTC
                                  T_
GAM3004 FCN2     3' TCTCTGACACCTTGTAGC    68804    _   T  GG
                                TC CTGAT CT  TGTAGC
                                || ||||| ||  ||||||
                                AG GACTG GG  ACATCG
                                 A    T  A_
GAM3004 FREB     3' TTCCTGATCTAGACAGC     68805       T   TGT
                                TTCCTGAT CTGG   AGC
                                |||||||| ||||   |||
                                AAGGACTA GATC   TCG
                                     _   TG_
GAM3004 GUCY1A3  5' CTCCTGATGAGCTGTAG     68806       TCT  _
                                TTCCTGAT   GG TGTAG
                                ||||||||   || |||||
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                                GAGGACTA   TC ACATC
                                    C__  G
GAM3004  LRP8     3'  TTCCTGACTTCCTGGGGT    68807        __    T
                                TTCCTGAT  TCTGG GT
                                ||||||||  ||||| ||
                                AAGGACTG  GGACC CA
                                    AA    C
GAM3004  LRP8     3'  TTCCTGACTTCCTGGGGT    68807        __    T
                                TTCCTGAT  TCTGG GT
                                ||||||||  ||||| ||
                                AAGGACTG  GGACC CA
                                    AA    C
GAM3004  MNT      3'  TTCCTGATGTCTCAACGATGTG 68808       _  ____    A  III
              GCG                   TCCTGAT TCT   GGTGT GC   G
                                ||||||| |||   ||||| ||   |
                                AGGACTA AGA   CTACA CG   C
                                    C   GTTG    C  III
GAM3004  PLA2G2D  3'  TTCTTGGTTCTGGTGTTGC   68809    C  A      A
                                TTC TG TTCTGGTGT GC
                                ||| || |||||||||| ||
                                AAG AC AAGACCACA CG
                                  A  C       A
GAM3004  PML      3'  CTCCTGGCCCTGGTGTAG    68810      AT
                                TTCCTG  TCTGGTGTAG
                                ||||||  ||||||||||
                                GAGGAC  GGACCACATC
                                    CG
GAM3004  PML      3'  CTCCTGGCCCTGGTGTAG    68810      AT
                                TTCCTG  TCTGGTGTAG
                                ||||||  ||||||||||
                                GAGGAC  GGACCACATC
                                    CG
GAM3004  RELN     3'  TTCCTGATATCAGATGTAG   68811       _  T
                                TTCCTGAT TC GGTGTAG
                                |||||||| || |||||||
                                AAGGACTA AG CTACATC
                                    T  T
GAM3004  YES1     3'  TTCCTGATTAGATTTAG     68812       CT   G
                                TTCCTGATT  GGT TAG
                                |||||||||  ||| |||
                                AAGGACTAA  CTA ATC
                                     T_   A
GAM3004  A2BP1    5'  TTCCTGATTACCCCTTAGC   68813       _  GGTG
                                TTCCTGATT CT    TAGC
                                |||||||||  ||    ||||
                                AAGGACTAA GG    ATCG
                                     T  GGA_
GAM3004  BATF     5'  TTCCTGACTTCTCCTGGGC   68814       ____    T
                                TTCCTGAT    TCTGG GT
                                ||||||||    ||||| ||
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                                AAGGACTG   GGACC CG
                                    AAGA   _
GAM3004  FGD3     5'  TTCCTGATGCCACCAGC     68815        T   GTG
                                TTCCTGAT CTG   TAGC
                                |||||||| |||   ||||
                                AAGGACTA GGT   GTCG
                                    C   G__
GAM3004  FLJ11164 3'  TTCCTGATTCATCCAGC     68816         TG  G
                                TTCCTGATTC  GT TAGC
                                ||||||||||  || ||||
                                AAGGACTAAG  TA GTCG
                                     __  G
GAM3004  FLJ20320 3'  CTCCTGCCTGGTGTGGC     68817       AT       A
                                TTCCTG  TCTGGTGT GC
                                ||||||  |||||||| ||
                                GAGGAC  GGACCACA CG
                                   __       C
GAM3004  FLJ21596 3'  TTCCTGATTTCACTGTAG     68818         CT G
                                TTCCTGATT  G TGTAG
                                |||||||||  | |||||
                                AAGGACTAA  T ACATC
                                    AG G
GAM3004  FLJ22160 3'  TTCCTGACTCCCTTGAGC     68819          GG  T
                                TTCCTGATTCT  TG AGC
                                ||||||||||  || |||
                                AAGGACTGAGG  AC TCG
                                     GA  _
GAM3004  FLJ22160 3'  TCCCTGATTTCCTGCAGC     68820         _  GG
                                TTCCTGATT CT  TGTAGC
                                |||||||||  ||  ||||||
                                AGGGACTAA GG  ACGTCG
                                    A  __
GAM3004  FLJ32389 3'  TTCCAGAGTCTGGTGTGGC    68821      T  T       A
                                TTCC GA TCTGGTGT GC
                                ||||  ||  |||||||| ||
                                AAGG CT AGACCACA CG
                                  T  C       C
GAM3004  GMFB     3'  TTCCTGACTTCTAAATTAG    68822         _   TG
                                TTCCTGATT CTGG  TAG
                                |||||||||  ||||  |||
                                AAGGACTGA GATT  ATC
                                    A    TA
GAM3004  HSPC065  3'  TCTCTGTTCTGGTGTGGC     68823    _  A       A
                                TC CTG TTCTGGTGT GC
                                ||  |||  |||||||||  ||
                                AG GAC AAGACCACA CG
                                 A  _       C
GAM3004  KIAA0171 3'  TTCCTGACTTAAATGATGGC   68824         CT   TA_
                                TTCCTGATT  GGTG   GC
                                |||||||||  ||||   ||
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                                AAGGACTGA  TTAC   CG
                                     AT    TAC
GAM3004  KIAA0286  3'  TTCCTGATTTCATAGC      68825         CTGG
                                TTCCTGATT    TGTAGC
                                |||||||||    ||||||
                                AAGGACTAA    GTATCG
                                     A___
GAM3004  KIAA0918  3'  TTCCTGATACCACGTCAG     68826        T  _  G
                                TTCCTGAT CTG GT TAG
                                |||||||| ||| || |||
                                AAGGACTA GGT CA GTC
                                     T  G  _
GAM3004  KIAA1388  3'  TTCCTAACCTATGTGGC      68827        T  G  A
                                TTCCTGAT CTG TGT GC
                                |||||||| ||| ||| ||
                                AAGGATTG GAT ACA CG
                                     _  _  C
GAM3004  KIAA1831  5'  TTCCGATTCCATCCCAGC     68828     T      GTG
                                TTCC GATTCTG   TAGC
                                |||| |||||||   ||||
                                AAGG CTAAGGT   GTCG
                                  _      AGG
GAM3004  KIAA1915  3'  TTCCTGACTTTTGGTATAG    68829        C_
                                TTCCTGATT  TGGTGTAG
                                |||||||||  ||||||||
                                AAGGACTGA  ACCATATC
                                     AA
GAM3004  KIAA1922  3'  TTCCTAATTCTATCAATGT    68830          ___
                                TTCCTGATTCTG   GTGT
                                ||||||||||||   ||||
                                AAGGATTAAGAT   TACA
                                       AGT
GAM3004  MGC10765  3'  TTCCTTATTTGATGTAA      68831      G   C
                                TTCCT ATT TGGTGTAG
                                ||||| ||| ||||||||
                                AAGGA TAA ACTACATT
                                  A  _
GAM3004  MGC2752   5'  TTCCCGATTCTACTGAGC     68832          G  T
                                TTCCTGATTCTG TG AGC
                                |||||||||||| || |||
                                AAGGGCTAAGAT AC TCG
                                       G  _
GAM3004  moblak    3'  TTCCTGATTTCATGGAGT     68833         _ _  T
                                TTCCTGATT C TGG GT
                                ||||||||| | ||| ||
                                AAGGACTAA G ACC CA
                                     A T   T
GAM3004  SCGF      5'  TTCCCGATTCTCCCAGC      68834          GGTG
                                TTCCTGATTCT    TAGC
                                ||||||||||    ||||
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                                AAGGGCTAAGA   GTCG
                                      GG__
GAM3004  SEMA4G   3'  TTCCTAAAGAAGTGTAGC    68835       TTCT
                                TTCCTGA   GGTGTAGC
                                |||||||   ||||||||
                                AAGGATT   TCACATCG
                                    TCT_
GAM3004  SEMA4G   3'  TTCCTAAAGAAGTGTAGC    68835       TTCT
                                TTCCTGA   GGTGTAGC
                                |||||||   ||||||||
                                AAGGATT   TCACATCG
                                    TCT_
GAM3004  SLC12A8  3'  TTCCTGATGTCACCCTGGGT  68836        _____   T
                                TTCCTGAT    TCTGG GT
                                ||||||||    ||||| ||
                                AAGGACTA    GGACC CA
                                     CAGTG   _
GAM3004  LOC121838 5'  CTCCTCACTGGTGTAG     68837      G TT
                                TTCCT A  CTGGTGTAG
                                ||||| |  |||||||||
                                GAGGA T  GACCACATC
                                   G __
GAM3004  LOC144809 5'  TTCCTATTCAGTGTAG     68838       A  T
                                TTCCTG TTC GGTGTAG
                                |||||| ||| |||||||
                                AAGGAT AAG TCACATC
                                   _  _
GAM3004  LOC146146 5'  CTCCTGATTCTGAGAAGAGC  68839          _ TGT
                                TTCCTGATTCTG G   AGC
                                ||||||||||||| |   |||
                                GAGGACTAAGAC C   TCG
                                       T TTC
GAM3004  LOC147711 5'  TCCTGATTTTTGATAATGGC  68840        C_   TA_
                                TCCTGATT  TGGTG   GC
                                ||||||||  |||||   ||
                                AGGACTAA  ACTAT   CG
                                     AA    TAC
GAM3004  LOC148229 3'  TTCCTGATATGCCAGC     68841        TCTG   _
                                TTCCTGAT    GTGT AGC
                                ||||||||    |||| |||
                                AAGGACTA    TACG TCG
                                     _____   G
GAM3004  LOC148809 3'  TTCTAGATTCTGGTCCAGC   68842     CT       G
                                TTC  GATTCTGGT TAGC
                                |||  ||||||||| ||||
                                AAG  CTAAGACCA GTCG
                                  AT        G
GAM3004  LOC149086 5'  TTCCTGACTTCCTCATTGGC  68843        __  G  GTA
                                TTCCTGAT  TCT GT   GC
                                ||||||||  ||| ||   ||
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                                AAGGACTG  GGA TA   CG
                                    AA   G  AC_
GAM3004  LOC152445 5'  TTCCTGACTACTCATTAGC    68844         _  G  G
                                TTCCTGATT CT GT TAGC
                                ||||||||| || || ||||
                                AAGGACTGA GA TA ATCG
                                    T  G  _
GAM3004  LOC153514 5'  TTCCTGATTTCCATGTGGC    68845         _   G   A
                                TTCCTGATT CTG TGT GC
                                ||||||||| ||| ||| ||
                                AAGGACTAA GGT ACA CG
                                    A   _   C
GAM3004  LOC154442 3'  TTCCTGATTTAAATCTAGC    68846         CT   G
                                TTCCTGATT  GGT TAGC
                                |||||||||  ||| ||||
                                AAGGACTAA  TTA ATCG
                                    AT   G
GAM3004  LOC157867 5'  TTCCTGATGCTTTACAGC     68847         T  GG
                                TTCCTGAT CT  TGTAGC
                                |||||||| ||  ||||||
                                AAGGACTA GA  ATGTCG
                                    C  A_
GAM3004  LOC201522 3'  TTCCCGATGGGGTTGTGGC    68848         TCT   _  A
                                TTCCTGAT   GGT GT GC
                                ||||||||   ||| || ||
                                AAGGGCTA   CCA CA CG
                                    CC_   A  C
GAM3004  LOC220001 5'  TTCCTCCCGGTGTAGC      68849       GAT
                                TTCCT   TCTGGTGTAGC
                                |||||   ||||||||||
                                AAGGA   GGGCCACATCG
                                   ___
GAM3004  LOC220549 5'  TCTCGATGATGGTGTAGC     68850     C    TC
                                TC TGAT  TGGTGTAGC
                                || ||||  |||||||||
                                AG GCTA  ACCACATCG
                                 A    CT
GAM3004  LOC254876 3'  TTCCTGATGTCTGCCATTAGC  68851         _   G   _
                                TTCCTGAT TCTG TGT AGC
                                |||||||| |||| ||| |||
                                AAGGACTA AGAC GTA TCG
                                    C   G   A
GAM3004  LOC257455 3'  TTCCTGATATGCCAGC       68841         TCTG   _
                                TTCCTGAT    GTGT AGC
                                ||||||||    |||| |||
                                AAGGACTA    TACG TCG
                                    ____   G
GAM3004  LOC93082  3'  CTCCTCTCCTGGTGTGGC     68852       GA       A
                                TTCCT  TTCTGGTGT GC
                                |||||  ||||||||| ||
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                                GAGGA  AGGACCACA CG
                                  G_       C
GAM3005  SCML2    3'  TACAACAAATGGCTAATAC   68855        TGCTATAC
                                TACAACAA       CTAATAC
                                ||||||||       |||||||
                                ATGTTGTT       GATTATG
                                    TACC____
GAM3005  ASB13    3'  TACAAGAGTTGGAGACCTAATA 68856      CAATGCTAT
             CT                   TACAA        ACCTAATACT
                                ||||||        ||||||||||
                                ATGTT        TGGATTATGA
                                  CTCAACCTC
GAM3005  FLJ21272 3'  ACAATAATGCTACAGATACT   68857     C       CCTA
                                ACAA AATGCTATA    ATACT
                                |||| |||||||||    |||||
                                TGTT TTACGATGT    TATGA
                                  A       C___
GAM3005  FLJ22055 3'  CAACAATAACATTCTAATACT  68858       C   AC
                                CAACAATG TAT  CTAATACT
                                |||||||| |||  ||||||||
                                GTTGTTAT GTA  GATTATGA
                                    T   A_
GAM3005  MacGAP   3'  CACAACTTGCCATACCT     68859       AA
                                TACAAC  TGCTATACCT
                                ||||||  ||||||||||
                                GTGTTG  ACGGTATGGA
                                  A_
GAM3005  MGC12458 3'  ACAACAATCCATTCTAAT    68860       G    AC
                                ACAACAAT CTAT  CTAAT
                                |||||||| ||||  |||||
                                TGTTGTTA GGTA  GATTA
                                    _    A_
GAM3005  NPD009   3'  TACATTAATGCTATACACAAT  68861     AC        C
                                TACA  AATGCTATAC TAAT
                                ||||  |||||||||| ||||
                                ATGT  TTACGATATG GTTA
                                  AA         T
GAM3005  LOC145945 3'  TACAACAATGTTTGACCCATAC 68862          CTAT    A
             T                    TACAACAATG    ACCTA TACT
                                ||||||||||    ||||| ||||
                                ATGTTGTTAC    TGGGT ATGA
                                    AAAC    _
GAM3006  A1BG     3'  TAGCTGGGTGTGGTGGT     68865     A  CCGTCA
                                TAGT GG     TGTGGTGGT
                                |||| ||     |||||||||
                                ATCG CC     ACACCACCA
                                  A  C_____
GAM3006  DMD      3'  TAGTAGTCATTTGGTGTGGTGG 68866       GC   CA__
             TA                   TAGTAG  CGT    TGTGGTGGTA
                                ||||||  |||   ||||||||||
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                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
                          ATCATC GTA   ACACCACCAT
                            A_  AACC
GAM3006 DMD    3' TAGTAGTCATTTGGTGTGGTGG 68866     GC  CA__
           TA                TAGTAG CGT   TGTGGTGGTA
                          |||||| |||   ||||||||||
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                                ATCATC  GTA   ACACCACCAT
                                   A_  AACC
GAM3006 DMD     3' TAGTAGTCATTTGGTGTGGTGG 68866      GC  CA__
             TA                  TAGTAG  CGT   TGTGGTGGTA
                                 ||||||  |||   ||||||||||
                                ATCATC  GTA   ACACCACCAT
                                   A_  AACC
GAM3006 DMD     3' TAGTAGTCATTTGGTGTGGTGG 68866      GC  CA__
             TA                  TAGTAG  CGT   TGTGGTGGTA
                                 ||||||  |||   ||||||||||
                                ATCATC  GTA   ACACCACCAT
                                   A_  AACC
GAM3006 FCGR2A   3' TAGTAGGCTGCTTGTGATTGG  68867       C  CA    _
                                TAGTAGGC GT  TGTGGT GG
                                ||||||||  ||  ||||||  ||
                                ATCATCCG CG  ACACTA CC
                                     A  A_    A
GAM3006 LLGL1    3' TAGCTGGGCGTGGTGGTGG   68868     A  C   CAT
                                TAGT GG CGT   GTGGTGG
                                ||||  ||  |||   |||||||
                                ATCG CC GCA   CACCACC
                                  A  C   C__
GAM3006 MRPL49   3' TAGCAGGCTGTGGTGGT     68869       CGTCA
                                TAGTAGGC    TGTGGTGGT
                                ||||||||    |||||||||
                                ATCGTCCG    ACACCACCA
                                            _____
GAM3006 MXI1     3' TAGAGGCTGTCATGCATGG    68870     T   C      G
                                TAG AGGC GTCATGTG TGG
                                |||  ||||  ||||||||  |||
                                ATC TCCG CAGTACGT ACC
                                  _   A      _
GAM3006 MXI1     3' TAGAGGCTGTCATGCATGG    68870     T   C      G
                                TAG AGGC GTCATGTG TGG
                                |||  ||||  ||||||||  |||
                                ATC TCCG CAGTACGT ACC
                                  _   A      _
GAM3006 PPP1R12B 3' TAGGGGGCGGTGGTGGTGG   68871     TA  C  CAT
                                TAG  GGC GT   GTGGTGG
                                |||  |||  ||   |||||||
                                ATC  CCG CA   CACCACC
                                  CC   C  C__
GAM3006 RANBP3   3' TAGTGTGCCGTCATCGGTGG  68872      AG      G
                                TAGT  GCCGTCAT TGGTGG
                                ||||  ||||||||  ||||||
                                ATCA  CGGCAGTA GCCACC
                                  CA       _
GAM3006 SHOX     3' TAGCTGGGTGTGGTGGT     68865      A  CCGTCA
                                TAGT GG     TGTGGTGGT
                                ||||  ||    |||||||||
```

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                                ATCG CC     ACACCACCA
                                  A  C_____
GAM3006  STC1     3'  TAGTAGGCCTTATCACACTGTA 68873         __    TG G
                A                  TAGTAGGCC  GTCA  T GTGG
                                   |||||||||  ||||  | ||||
                                   ATCATCCGG  TAGT  G CATT
                                        AA    GT A
GAM3006  BIKE     3'  AGTAGGTGGTGGTGGTGG    68874       CC  CAT
                                   AGTAGG  GT   GTGGTGG
                                   ||||||  ||   |||||||
                                   TCATCC  CA   CACCACC
                                     AC  C__
GAM3006  C20orf139 5'  GTAGGCCGCGTAGCGGTGG   68875         CAT
                                   GTAGGCCGT   GTGGTGG
                                   |||||||||   |||||||
                                   CATCCGGCG   CGCCACC
                                        CAT
GAM3006  FLJ20257  5'  CAGTGGGTGGTGGTGGT     68876     A  CC  CAT
                                   TAGT GG  GT   GTGGTGGT
                                   ||||  ||  ||   ||||||||
                                   GTCA CC  CA   CACCACCA
                                     _  __  C__
GAM3006  KIAA0469  3'  TAGCTGGGCGTGGTGGTGG   68868     A  C   CAT
                                   TAGT GG CGT   GTGGTGG
                                   ||||  ||  |||   |||||||
                                   ATCG CC GCA   CACCACC
                                     A  C   C__
GAM3006  KIAA1582  5'  TAGTGGTGGTGGTGGTGG    68877     A  CC  CAT
                                   TAGT GG  GT   GTGGTGG
                                   ||||  ||  ||   |||||||
                                   ATCA CC  CA   CACCACC
                                     _  AC  C__
GAM3006  MGC10471  5'  GTGGGCCGTGTGGTGG      68878    A     CAT
                                   GT GGCCGT   GTGGTGG
                                   ||  ||||||   |||||||
                                   CA CCGGCA   CACCACC
                                    C     ____
GAM3006  MGC20460  5'  TAGGAGGCGGTGGTGGTGG    68879    T   C  CAT
                                   TAG AGGC GT   GTGGTGG
                                   |||  ||||  ||   |||||||
                                   ATC TCCG CA   CACCACC
                                     C   C  C__
GAM3006  PROL3    3'  TAGTGGTGTCTTTTGTGGTGGT 68880     A  CC   A__
                                   TAGT GG  GTC   TGTGGTGGT
                                   ||||  ||  |||   |||||||||
                                   ATCA CC  CAG   ACACCACCA
                                     _  A_   AAA
GAM3006  PTPNS1   3'  TAGTGGTGGTGGTGGTGG    68877     A  CC  CAT
                                   TAGT GG  GT   GTGGTGG
                                   ||||  ||  ||   |||||||
```

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                                ATCA CC  CA   CACCACC
                                  _ AC  C__
GAM3006  TADA3L    3'  TAGCTGGGCGTGGTGGTGG   68868     A  C   CAT
                                TAGT GG CGT   GTGGTGG
                                |||| || |||   |||||||
                                ATCG CC GCA   CACCACC
                                  A  C   C__
GAM3006  TTTY13    3'  GGTAGCTACGATGGTGGTAA   68881    CC TC  _
                                GG  G  ATG TGGTGGTAA
                                ||  |  ||| |||||||||
                                CC  C  TGC ACCACCATT
                                 AT GA   T
GAM3006  TU12B1-TY 3'  TAGCTGGATGTGGTGGT     68882     A  CCGTC
                                TAGT GG    ATGTGGTGGT
                                |||| ||    ||||||||||
                                ATCG CC    TACACCACCA
                                  A _____
GAM3006  LOC128077 3'  TAGCTGGGCGTGGTGGTGG   68868     A  C   CAT
                                TAGT GG CGT   GTGGTGG
                                |||| || |||   |||||||
                                ATCG CC GCA   CACCACC
                                  A  C   C__
GAM3006  LOC146958 5'  GCTGGCATGGTGTGGTGGT   68883    A   C  CA
                                GT GGC GT  TGTGGTGGT
                                || ||| ||  |||||||||
                                CG CCG TA  ACACCACCA
                                 A  _  CC
GAM3006  LOC149296 5'  TAGGAGGCCTGGGTGGTGGT  68884     T    GTCAT
                                TAG AGGCC    GTGGTGGT
                                ||| |||||    ||||||||
                                ATC TCCGG    CACCACCA
                                  C    ACC__
GAM3006  LOC149506 3'  TAGCTGGGCGTGGTGGTGG   68868     A  C   CAT
                                TAGT GG CGT   GTGGTGG
                                |||| || |||   |||||||
                                ATCG CC GCA   CACCACC
                                  A  C   C__
GAM3006  LOC151719 5'  GGTGGTGATGGTGGTGGTA   68885    CC  C  _
                                GG  GT ATG TGGTGGTA
                                ||  || ||| ||||||||
                                CC  CA TAC ACCACCAT
                                 AC  C   C
GAM3006  LOC152485 3'  TAGTGGGTCTTGAGGTGG    68886     A  CC   A  T
                                TAGT GG  GTC TG GGTGG
                                |||| ||  ||| || |||||
                                ATCA CC  CAG AC CCACC
                                  _ __   A  T
GAM3006  LOC153134 5'  TAGTAGGTCTCATTTGGTAG   68887       CCG   G
                                TAGTAGG   TCAT TGGTGG
                                |||||||   |||| ||||||
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                                ATCATCC   AGTA ACCATC
                                   AG_   A
GAM3006  LOC164397 5'  GTAGGTCTGCCAGTGGTAG   68888      CC_   T
                                GTAGG   GTCA GTGGTGG
                                |||||   |||| |||||||
                                CATCC   CGGT CACCATC
                                  AGA   _
GAM3006  LOC169611 3'  TAGCTGGGTGTGGTGGT     68865     A  CCGTCA
                                TAGT GG     TGTGGTGGT
                                |||| ||     |||||||||
                                ATCG CC     ACACCACCA
                                  A  C_____
GAM3006  LOC200845 5'  TAGCTGGGCGTGGTGGTGG   68868     A  C   CAT
                                TAGT GG CGT   GTGGTGG
                                |||| || |||   |||||||
                                ATCG CC GCA   CACCACC
                                  A  C   C__
GAM3006  LOC219920 5'  CAGTGGGCGGCCGTGGTGGT   68889     A   C   AT
                                TAGT GGC GTC  GTGGTGGT
                                |||| ||| |||  ||||||||
                                GTCA CCG CGG  CACCACCA
                                  C   C   __
GAM3006  LOC255130 5'  GGAGGTTGGACATGGTGGTA   68890    CC  C__
                                GG  GT   ATGTGGTGGTA
                                ||  ||   ||||||||||
                                CC  CA   TGTACCACCAT
                                 TC  ACC
GAM3006  LOC91963  3'  TAGCTGGATGTGGTGGTA    68891     A  CCGTC
                                TAGT GG    ATGTGGTGGTA
                                |||| ||    ||||||||||
                                ATCG CC    TACACCACCAT
                                  A  _____
GAM3006  LOC93297  3'  TAATAGGTCTTGTGGTGGT    68892       CCG  A
                                TAGTAGG   TC TGTGGTGGT
                                |||||||   || |||||||||
                                ATTATCC   AG ACACCACCA
                                    ___  A
GAM3007  LIPA      3'  TGTGATCAATAACGACAGTA   68895          AC  T
                                TGTGATCAATAA  AC GTG
                                ||||||||||||  || |||
                                ACACTAGTTATT  TG CAT
                                       GC  T
GAM3007  MADH3     3'  TGTGATAATAGACACTATA    68896       C   A
                                TGTGAT AATA ACACTGTG
                                |||||| |||| ||||||||
                                ACACTA TTAT TGTGATAT
                                   _   C
GAM3007  ALDH9     3'  TGTGATCAATTAGTTGTAAATA 68897          AAACAC
                                TGTGATCAAT     TGTGAATA
                                ||||||||||     ||||||||
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                                ACACTAGTTA     ACATTTAT
                                      ATCA__
GAM3007  DKFZP434L1717 3'  TGTGACAATAAACATGAAT   68898      T       CTG
                                TGTGA CAATAAACA   TGAAT
                                ||||| |||||||||   |||||
                                ACACT GTTATTTGT   ACTTA
                                  _       ____
GAM3007  DKFZp761D112 3'  TGTGAATAATAAACACTG    68899      TC
                                TGTGA  AATAAACACTG
                                |||||  ||||||||||
                                ACACT  TTATTTGTGAC
                                   TA
GAM3007  FLJ14213  3'  TGGATCAATAAATACTA     68900    T        C
                                TG GATCAATAAA ACTG
                                || |||||||||| ||||
                                AC CTAGTTATTT TGAT
                                 _        A
GAM3007  FLJ22578  3'  TGTGGTCAATAAACATGGGCCT 68901      A        _____  _
            GGTG                   TGTG TCAATAAACA     CTG TG
                                |||| ||||||||||     ||| ||
                                ACAC AGTTATTTGT     GAC AC
                                  C         ACCCG   C
GAM3007  N4BP3    3'  TGTGATCAGTGACACCTGTG   68902        ATAA   _
                                TGTGATCA    ACAC TGTG
                                ||||||||    |||| ||||
                                ACACTAGT    TGTG ACAC
                                     CAC_    G
GAM3007  NSBP1    3'  GTGGACACAACATTGTGAATA  68903     AT  ATA    C
                                GTG  CA   AACA TGTGAATA
                                |||  ||   |||| ||||||||
                                CAC  GT   TTGT ACACTTAT
                                  CT  G__    A
GAM3007  LOC143162 3'  TGTGATTAGTACTGTGAATA   68904       CAATAAAC
                                TGTGAT       ACTGTGAATA
                                ||||||       ||||||||||
                                ACACTA       TGACACTTAT
                                   ATCA____
GAM3007  LOC146325 3'  TGTGATCAATAAATAACTGTG  68905           C_
                                TGTGATCAATAAA  ACTGTG
                                ||||||||||||  ||||||
                                ACACTAGTTATTT  TGACAC
                                       AT
GAM3007  LOC147649 3'  TGTGATCAGAAAACATACTG   68906        AT   __
                                TGTGATCA  AAAC  ACTG
                                ||||||||  ||||  ||||
                                ACACTAGT  TTTG  TGAC
                                     CT    TA
GAM3007  LOC149372 3'  TGTGGTCAACAAACACAGC    68907      A        T
                                TGTG TCAATAAACAC GT
                                |||| |||||||||| ||
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                                ACAC AGTTGTTTGTG CG
                                  C         T
GAM3007  LOC157740 3'  TGTGGCAATTTACTTTGTGAAT 68908     AT    AA  AC
             A                   TGTG  CAAT  AC  TGTGAATA
                                 ||||  ||||  ||  ||||||||
                                 ACAC  GTTA  TG  ACACTTAT
                                   C_   AA  AA
GAM3007  LOC196205 3'  TGTGATCAATAGTAAA      68909          AACACT
                                 TGTGATCAATA     GTGAA
                                 ||||||||||     |||||
                                 ACACTAGTTAT     CATTT
                                                 _____
GAM3007  LOC196738 3'  TGTGATTAGTACTGTGAATA   68904       CAATAAAC
                                 TGTGAT       ACTGTGAATA
                                 ||||||       ||||||||||
                                 ACACTA       TGACACTTAT
                                    ATCA____
GAM3007  LOC200860 3'  TGTGATCACTAAGCATGGA    68910        A   A  C  T
                                 TGTGATCA TAA CA TG GA
                                 ||||||||| ||| || || ||
                                 ACACTAGT ATT GT AC CT
                                     G  C  _  _
GAM3007  LOC90750  3'  GTGATGAATGCTGTGAAT    68911      C   AAACA
                                 GTGAT AAT    CTGTGAAT
                                 ||||| |||    ||||||||
                                 CACTA TTA    GACACTTA
                                   C  C____
GAM3008  FLJ13449  3'  AGTGCTATTTCTCCATCATG   68914        CG   __
                                 AGTGCTAT  CTT  TCGTG
                                 ||||||||  |||  |||||
                                 TCACGATA  GAG  AGTAC
                                     AA   GT
GAM3008  KIAA0984  3'  AAGTGCTACTTCACCTCTGTGT 68915         __     TC
             G                    AAGTGCTA  TCGCTT  GTGTG
                                  ||||||||  ||||||  |||||
                                  TTCACGAT  AGTGGA  CACAC
                                     GA     GA
GAM3008  KIAA1196  3'  TAAAGTGCATCCCATTTTCGTG 68916        TA_   C
             TGA                   TAAAGTGC   TCG TTTCGTGTGA
                                   ||||||||   ||| ||||||||||
                                   ATTTCACG   GGT AAAGCACACT
                                      TAG   A
GAM3008  MGC26766  3'  TAAAGTGCTGTTTGCTCAGTGA 68917         ATC_   TCGT
                                 TAAAGTGCT   GCTT   GTGA
                                 |||||||||   ||||   ||||
                                 ATTTCACGA   CGAG   CACT
                                     CAAA   T___
GAM3008  LOC219899 5'  TAAAATGCTGTTTGTGTG    68918        ATCGC   C
                                 TAAAGTGCT    TTT GTGTG
                                 |||||||||    ||| |||||
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                                ATTTTACGA     AAA CACAC
                                     C____  _
GAM3009  AMOT     3'  TGGAACAAAAACTAGT      68921         TTTTT
                                TGGAATAG     AACTAGT
                                ||||||||     |||||||
                                ACCTTGTT     TTGATCA
                                     T____
GAM3009  ESAM     3'  TGAGATGGTTTTCCCACAGTAA 68922     GA  A     AAC
              AG                   TG  AT GTTTTT   TAGTAAAG
                                ||  || ||||||   ||||||||
                                AC  TA CAAAAG   GTCATTTC
                                 TC  C     GGT
GAM3009  FLJ21615  3'  TGGAATAGTTTTAATACAG    68923           TAAC
                                TGGAATAGTTTT    TAG
                                ||||||||||||    |||
                                ACCTTATCAAAA    GTC
                                       TTAT
GAM3009  KIAA0379  3'  TGAAATAGTTTTCTTAGT     68924           AAC
                                TGGAATAGTTTTT   TAGT
                                ||||||||||||   ||||
                                ACTTTATCAAAAG   ATCA
                                       A__
GAM3009  KIAA1117  3'  TGGGATAGTTCTTATTTAG    68925     A        AC
                                TGG ATAGTTTTTA  TAG
                                ||| ||||||||||  |||
                                ACC TATCAAGAAT  ATC
                                  C         AA
GAM3009  LOC143785 3'  TGGGATAGCTTTTGGAGCCCAG 68926     A        AA___
                                TGG ATAGTTTTT    CTAG
                                ||| |||||||||    ||||
                                ACC TATCGAAAA    GGTC
                                  C        CCTCG
GAM3009  LOC197358 3'  TGGGATGATTTTTAACCAG    68927     A  A
                                TGG AT GTTTTTAACTAG
                                ||| ||  ||||||||||||
                                ACC TA TAAAAATTGGTC
                                  C  C
GAM3010  CDH5     3'  CATTTCCCTGAATGTGGTTCAG 68930       A  A   CGC
                                CATTTC CT GAA   TGGTTCAG
                                ||||||  ||  |||   ||||||||
                                GTAAAG GG CTT   ACCAAGTC
                                   _  A   AC_
GAM3010  GLS      3'  CATTTCACTAAACACAGCTTCA 68931           A   T   _
              G                   CATTTCACTAGA CGC GGTT CAG
                                ||||||||||||  ||| ||||  |||
                                GTAAAGTGATTT GTG TCGA GTC
                                       _   _    A
GAM3010  MNAT1    3'  TTTTGCTAGCTCCCTGGTTCAG 68932     CA    AACG
                                TTT  CTAG    CTGGTTCAG
                                |||  ||||    |||||||||
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                              AAA  GATC   GACCAAGTC
                                AC   GAGG
GAM3010  OSCAR    3'  CATTTTACAGAGCGCTGATT  68933     C  T  A
                              CATTT AC AGA CGCTGGTT
                              ||||| || ||| ||||||||
                              GTAAA TG TCT GCGACTAA
                                 A  _  C
GAM3010  OSCAR    3'  CATTTTACAGAGCGCTGATT  68933     C  T  A
                              CATTT AC AGA CGCTGGTT
                              ||||| || ||| ||||||||
                              GTAAA TG TCT GCGACTAA
                                 A  _  C
GAM3010  OSCAR    3'  CATTTTACAGAGCGCTGATT  68933     C  T  A
                              CATTT AC AGA CGCTGGTT
                              ||||| || ||| ||||||||
                              GTAAA TG TCT GCGACTAA
                                 A  _  C
GAM3010  PMX1     3'  CATTTCACCAGAGCTC     68934         ACGCTG
                              CATTTCACTAGA     GTTC
                              ||||||||||||     ||||
                              GTAAAGTGGTCT     CGAG
                                        _______
GAM3010  PMX1     3'  CATTTCACCAGAGCTC     68934         ACGCTG
                              CATTTCACTAGA     GTTC
                              ||||||||||||     ||||
                              GTAAAGTGGTCT     CGAG
                                        _______
GAM3010  ADMP     3'  CATTTCACTGAATGTGAACAG 68935        A  CGC  TT
                              CATTTCACT GAA  TGG  CAG
                              ||||||||| |||  |||  |||
                              GTAAAGTGA CTT  ACT  GTC
                                    _  AC_  T_
GAM3010  DDX32    5'  ATTTCCTGGCTGGTTCA     68936      A  AGAAC
                              ATTTC CT    GCTGGTTCA
                              ||||| ||    |||||||||
                              TAAAG GA    CGACCAAGT
                                 _  C_____
GAM3010  FACTP140 3'  CATTTCACTAGAAGCGG     68937          C  T
                              CATTTCACTAGAA GC GG
                              |||||||||||| || ||
                              GTAAAGTGATCTT CG CC
                                        _  _
GAM3010  FLJ23153 3'  CATTTCACTAGAATTCA     68938          ACGCTG
                              CATTTCACTAGA     GTTCA
                              ||||||||||||     |||||
                              GTAAAGTGATCT     TAAGT
                                        _______
GAM3010  HAPIP    3'  CATTTTATTAGAACACATTCAA 68939      CAC      TG
                              CATTT  TAGAACGC  GTTCAG
                              |||||  ||||||||  ||||||
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                                GTAAA  ATCTTGTG  TAAGTT
                                  ATA      __
GAM3010  MGC4170   3'  CATTTCACAGGACGCTGTCAAC 68940       T  A    GTT_
            AG                   CATTTCAC AG ACGCTG   CAG
                                ||||||||  || ||||||   |||
                                GTAAAGTG TC TGCGAC   GTC
                                   _  C     AGTT
GAM3010  SLC11A2   3'  CATTTCACGAGAACATCAG   68941       T    CT
                                CATTTCAC AGAACG  GG
                                ||||||||  ||||||  ||
                                GTAAAGTG TCTTGT  TC
                                   C     AG
GAM3010  LOC127003 3'  TTTCACTATAATTAGTTCAG   68942       GAACGC
                                TTTCACTA     TGGTTCAG
                                ||||||||     ||||||||
                                AAAGTGAT     ATCAAGTC
                                   ATTA__
GAM3010  LOC150271 3'  CATTTCACAGAGCATCGG    68943       T  A  C
                                CATTTCAC AGA CG TGG
                                ||||||||  ||| ||  |||
                                GTAAAGTG TCT GT GCC
                                   _  C  A
GAM3010  LOC151826 3'  TTCACTAGAACAGGATT     68944         CT
                                TTCACTAGAACG  GGTT
                                ||||||||||||  ||||
                                AAGTGATCTTGT  CTAA
                                     C_
GAM3010  LOC152220 3'  CATTTCACTAGATGTGG     68945         ACGC
                                CATTTCACTAGA    TGG
                                ||||||||||||    |||
                                GTAAAGTGATCT    ACC
                                     AC__
GAM3010  LOC157660 3'  TTTTACTTTTTCTGGTTCAG   68946    C   AGAACG
                                TTT ACT     CTGGTTCAG
                                |||  |||     |||||||||
                                AAA TGA     GACCAAGTC
                                  A   AAAA__
GAM3010  LOC158450 5'  CATTTCAGTTTCTGGTTCA    68947       CTAGAACG
                                CATTTCA       CTGGTTCA
                                |||||||       ||||||||
                                GTAAAGT       GACCAAGT
                                   CAAA_____
GAM3010  LOC158504 5'  CATTTCAGTTTCTGGTTCA    68947       CTAGAACG
                                CATTTCA       CTGGTTCA
                                |||||||       ||||||||
                                GTAAAGT       GACCAAGT
                                   CAAA_____
GAM3010  LOC221895 3'  ATTTCACTAAATGGGTATC    68948         ACGCT  _
                                ATTTCACTAGA    GGT TC
                                ||||||||||    ||| ||
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                                TAAAGTGATTT    CCA AG
                                      AC___   T
GAM3010 LOC54103 5' CATTTCACAGAATGTTCTGTTT 68949        T   CG__   G
           CAG                   CATTTCAC AGAA   CTG TTCAG
                                 |||||||| ||||   ||| |||||
                                 GTAAAGTG TCTT   GAC AAGTC
                                     _   ACAA   A
GAM3010 LOC90538 3' CATCTCACTGGGACTGGTT   68950        AGAAC
                                 CATTTCACT    GCTGGTT
                                 |||||||||    |||||||
                                 GTAGAGTGA    TGACCAA
                                      CCC__
GAM3010 LOC92078 3' CATTCCACTAGAAGTTCA    68951          ACGCT
                                 CATTTCACTAGA    GGTTCA
                                 ||||||||||||    ||||||
                                 GTAAGGTGATCT    TCAAGT
                                                 _____
GAM3010 LOC93496 3' TTTCACCAGAACATTCGG    68952          C_
                                 TTTCACTAGAACG  TGG
                                 ||||||||||||  |||
                                 AAAGTGGTCTTGT  GCC
                                       AA
GAM3011 KIAA0408 3' AGGTTTTTCCATTTAAAAGTTA 68955     C_        TA
           T                      AGGT  TTCCATTTAAA  TTAT
                                  ||||  ||||||||||  ||||
                                  TCCA  AAGGTAAATTT  AATA
                                    AA         TC
GAM3011 LOC148438 3' AGGCTTTCCATTTGAAAC    68956    TC      _
                                 AGG  TTCCATTT AAAT
                                 |||  |||||||| ||||
                                 TCC  AAGGTAAA TTTG
                                   GA       C
GAM3011 LOC204084 5' AAGTCTTCCATTTGAAAC    68957          _
                                 AGGTCTTCCATTT AAAT
                                 |||||||||||| ||||
                                 TTCAGAAGGTAAA TTTG
                                       C
GAM3012 GPC3    3' TTCGAAAACATAACACA     68960         ATCC
                                 TTCGAAAATA    TAACACA
                                 |||||||||    |||||||
                                 AAGCTTTTGT    ATTGTGT
                                               ____
GAM3012 NYX     3' AAACGCCTCCTAACACAT    68961     AA_
                                 AAAT   TCCTAACACAT
                                 ||||   ||||||||||
                                 TTTG   AGGATTGTGTA
                                   CGG
GAM3012 RAG1    3' CATTCAAAATAGTTCCTACA   68962        ATAA    A
                                 CATTCGAAA    TCCTA CA
                                 |||||||||    ||||| ||
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                                GTAAGTTTT   AGGAT GT
                                     ATCA   _
GAM3012 ALTE    3' TCGAAAATACAACACA     68963        ATCC
                                TCGAAAATA   TAACACA
                                |||||||||   |||||||
                                AGCTTTTAT   GTTGTGT
                                     ____
GAM3012 GHITM   3' CATTCAAAAGTAAAACACACAT 68964        A  TCCTA
                                CATTCGAAA TAA    ACACAT
                                ||||||||| |||    ||||||
                                GTAAGTTTT ATT    TGTGTA
                                     C  TTG__
GAM3012 KIAA1091 3' CACTCGAAGGTCATCTCTAGCA 68965       AATA  _  A
           CAT                   CATTCGAA   ATC CTA CACAT
                                ||||||||   ||| ||| |||||
                                GTGAGCTT   TAG GAT GTGTA
                                     CCAG  A  C
GAM3012 KIAA1309 3' ACCAGAGGGTAATCCTAACA  68966   TC  AAA
                                AT  GA   TAATCCTAACA
                                ||  ||   ||||||||||
                                TG  CT   ATTAGGATTGT
                                 GT  CCC
GAM3012 LOC158219 3' GAAAATAAATACCTAATACAT  68967       T__    C
                                GAAAATAA   CCTAA ACAT
                                ||||||||   ||||| ||||
                                CTTTTATT   GGATT TGTA
                                     TAT    A
GAM3013 BTEB1   3' CATAAAGACAGCTGTGCT    68970        A  ACAA
                                CATAGAGACA GC    GCT
                                |||||||||| ||   |||
                                GTATTTCTGT CG    CGA
                                     _ ACA_
GAM3013 C18orf1  3' CACACAGGTTGTAAGCATGAGC 68971       AGAC_    CA
           T                    CACATAG    AAGCA  AGCT
                                |||||||    |||||  ||||
                                GTGTGTC    TTCGT  TCGA
                                    CAACA    AC
GAM3013 CLC     3' TCACGTAGAGACAGGGATTAGC 68972  A     A__________  ACAA
           TTGTGC                TAGAGAC        AGC   GC
                                |||||||        |||   ||
                                ATCTCTG        TCG   CG
                                C      TCCCTAAIII  AACA
GAM3013 FADD    3' CTCACACAGGGGCCAAGAGCT  68973        AGA_   CACA
                                CTCACATAG   CAAG   AGCT
                                |||||||||   ||||   ||||
                                GAGTGTGTC   GTTC   TCGA
                                     CCCG   ____
GAM3013 GAB2    3' CACAGCCCATGGGCACAAGCT  68974      AGA  A__
                                CATAG   CA   GCACAAGCT
                                |||||   ||   |||||||||
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                                GTGTC  GT  CGTGTTCGA
                                  GG_ ACC
GAM3013 GAB2    3' CACAGCCCATGGGCACAAGCT 68974     AGA A__
                                CATAG  CA  GCACAAGCT
                                |||||  ||  |||||||||
                                GTGTC  GT  CGTGTTCGA
                                  GG_ ACC
GAM3013 GARP    3' TCACATAGGGGCAGACACAAGG 68975       AGA AG   _
           CT                    TCACATAG  CA CACAAG CT
                                ||||||||  ||  |||||| ||
                                AGTGTATC  GT GTGTTC GA
                                    CCC CT    C
GAM3013 IL6     3' CTCCATAGAGAACAACATAAG 68976    A     CA   C
                                CTC CATAGAGA AGCA AAG
                                ||| ||||||||  |||| |||
                                GAG GTATCTCT TTGT TTC
                                 _      TG   A
GAM3013 PTPRA   5' TCATGTAGAGACAGGTCTAGCT 68977  CA    A_________ ACAA
           TGTGC                   TAGAGAC       AGC   GC
                                 |||||||       |||   ||
                                 ATCTCTG       TCG   CG
                                AC     TCCAGAIII  AACA
GAM3013 SFRP1   3' CTGACACAAAGGCAGGCACAGG 68978   C      A A   A
           CT                    CT ACATAGAG CA GCACA GCT
                                || |||||||| || ||||| |||
                                GA TGTGTTTC GT CGTGT CGA
                                 C      C C   C
GAM3013 SH3BP2  3' CTCGTCTAGAGACAAGCACGGC 68979    ACA         AA
           C                     CTC  TAGAGACAAGCAC  GCT
                                |||  ||||||||||||| |||
                                GAG  ATCTCTGTTCGTG  CGG
                                  CAG         C_
GAM3013 VAT1    3' CACACACACACAAGCACA   68980      GAG
                                CACATA  ACAAGCACA
                                ||||||  |||||||||
                                GTGTGT  TGTTCGTGT
                                   GTG
GAM3013 BMF     3' CTCGCTAGAGACAGCCAGGCT 68981    ACA     A A A
                                CTC  TAGAGACA GC CA GCT
                                |||  |||||||| || || |||
                                GAG  ATCTCTGT CG GT CGA
                                  CG_      _ _ C
GAM3013 CALN1   3' CATAGAGACAAGAAAGCT   68982         CAC
                                CATAGAGACAAG  AAGCT
                                ||||||||||||  |||||
                                GTATCTCTGTTC  TTCGA
                                       T__
GAM3013 DVS27   3' CTACATAGAGACTTAAGC   68983   C      __
                                CT ACATAGAGAC  AAGC
                                || ||||||||||  ||||
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                                GA TGTATCTCTG  TTCG
                                 _        AA
GAM3013  FLJ21596  3'  CTCACATAAGACAGGCA     68984        A     A
                                CTCACAT GAGACA GCA
                                ||||||| |||||| |||
                                GAGTGTA TTCTGT CGT
                                   _     C
GAM3013  H2AFJ     3'  ACATAGAAATAAAAACAGCT   68985         C   C   A
                                ACATAGAGA AAG ACA GCT
                                ||||||||| ||| ||| |||
                                TGTATCTTT TTT TGT CGA
                                     A   T   _
GAM3013  KIAA1046  3'  CTACATAAAAAAGCATGAGCT  68986    C       CA    CA
                                CT ACATAGAGA  AGCA  AGCT
                                || |||||||||  ||||  ||||
                                GA TGTATTTTT  TCGT  TCGA
                                 _       __    AC
GAM3013  KIAA1765  3'  TCACATAGAAATGACTCAGGCT 68987          CAA  A  A
                                TCACATAGAGA   GC CA GCT
                                ||||||||||   || || |||
                                AGTGTATCTTT   TG GT CGA
                                      AC_  A  C
GAM3013  KIAA1838  3'  CACAGAATCAGGCACAAGCT   68988        A  A
                                CATAGAG CA GCACAAGCT
                                ||||||| || |||||||||
                                GTGTCTT GT CGTGTTCGA
                                    A  C
GAM3013  MacGAP    3'  TCATTAGAGACATCAAGAGCT  68989     CA       AG  CA
                                TCA  TAGAGACA  CA  AGCT
                                |||  ||||||||  ||  ||||
                                AGT  ATCTCTGT  GT  TCGA
                                  A_       A_  TC
GAM3013  MGC27277  3'  CTAACATTTGGACAAGCATGAG 68990    C    AGA       CA
                                CT ACAT   GACAAGCA  AG
                                || ||||   ||||||||  ||
                                GA TGTA   CTGTTCGT  TC
                                 T    AAC       AC
GAM3013  LOC126302 3'  CTCACTAGATACACAAGC    68991      A    GACAA
                                CTCAC TAGA    GCACAAGC
                                ||||| ||||    ||||||||
                                GAGTG ATCT    TGTGTTCG
                                   _    A____
GAM3013  LOC149566 3'  CTCCACCCACAGGCACAAGCT  68992     A   AGAG   A
                                CTC CAT    ACA GCACAAGCT
                                ||| |||    ||| |||||||||
                                GAG GTG    TGT CGTGTTCGA
                                  _   GG__   C
GAM3013  LOC150622 3'  CTCATATAGCTCACAAGC    68993      C    AGACAAG
                                CTCA ATAG      CACAAGC
                                |||| ||||      |||||||
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                                GAGT TATC      GTGTTCG
                                  A   GA_____
GAM3013  LOC154789 5'  CTCACAGAGAGAATAAGTTAGC 68994    T    CA_________  ACAA
             TTGTGC                 CA AGAGA        AGC   GC
                                || |||||        |||   ||
                                GT TCTCT        TCG   CG
                                 C    TATTCAAIII  AACA
GAM3013  LOC157623 5'  TAGAGACAAGGAAACT      68995         CAC
                                TAGAGACAAG   AAGCT
                                ||||||||||  |||||
                                ATCTCTGTTC   TTTGA
                                      C__
GAM3013  LOC158863 3'  CATAGAGATTATGACAAGCT   68996        CAAGC
                                CATAGAGA    ACAAGCT
                                ||||||||    |||||||
                                GTATCTCT    TGTTCGA
                                     AATAC
GAM3013  LOC197131 3'  CCACATAGAGATTGAGTTAGCT 68997        CA_________  ACAA
             TGTGC                  CATAGAGA        AGC   GC
                                ||||||||        |||   ||
                                GTATCTCT        TCG   CG
                                     AACTCAAIII  AACA
GAM3013  LOC221975 3'  CAGAGAGACAAGTACAAG    68998    T       C
                                CA AGAGACAAG ACAAG
                                || |||||||| |||||
                                GT TCTCTGTTC TGTTC
                                 C        A
GAM3013  LOC253128 3'  CTCACATAGGGAGCAGTTAGCT 68999       A  _ A_______  ACAA
             TGG                    CACATAG GA C      AGC   G
                                ||||||| || |      |||   |
                                GTGTATC CT G      TCG   C
                                    C  C TCAAIII  AACA
GAM3013  LOC91695  5'  CTCACATAGAGGTAGTGAAGCT 69000        ACA________  ACAA
             TGG                    CACATAGAG        AGC   G
                                |||||||||        |||   |
                                GTGTATCTC        TCG   C
                                     CATCACTIII  AACA
GAM3014  OGG1      3'  CTGGTGGCTCCTGAG      69003         GCT
                                CTGGTGGCT   TCTGGG
                                |||||||||  ||||||
                                GACCACCGA   GGACTC
                                      ___
GAM3014  SLC6A8    3'  CTGCCACTGCTGCTTCTGGG   69004     GTG__
                                CTG    GCTGCTTCTGGG
                                |||    ||||||||||||
                                GAC    CGACGAAGACCC
                                  GGTGA
GAM3014  TZFP      3'  CTGGGGCGCTTCTGGGGCG   69005     T   T       A
                                CTGG GGC GCTTCTGGG CG
                                |||| ||| ||||||||| ||
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                                GACC CCG CGAAGACCC GC
                                  _  _       C
GAM3014  ACAS2L   3'  TGGGGGCTGCTTCTGGGACG   69006     T
                                TGG GGCTGCTTCTGGGACG
                                ||| ||||||||||||||||
                                ACC CCGACGAAGACCCTGC
                                  C
GAM3014  LOC146488 3'  CTGCCACTGCTGCTTCTGGG   69004     GTG__
                                CTG    GCTGCTTCTGGG
                                |||    ||||||||||||
                                GAC    CGACGAAGACCC
                                  GGTGA
GAM3014  LOC157624 5'  CTGGGGGGCTCTGGGA      69007      T  CT   T
                                CTGG GG  GCT CTGGGA
                                |||| ||  ||| ||||||
                                GACC CC  CGA GACCCT
                                  _ C_  _
GAM3014  LOC199848 5'  TGGCTGTGCTTCTGGGC     69008       __        A
                                TGGCT  GCTTCTGGG C
                                |||||  ||||||||| |
                                ACCGA  CGAAGACCC G
                                   CA        C
GAM3015  AMOT     3'  TGGAACAAAAACTAGT      68921         TTTTT
                                TGGAATAG    AACTAGT
                                ||||||||    |||||||
                                ACCTTGTT    TTGATCA
                                     T_____
GAM3015  ESAM     3'  TGAGATGGTTTTCCCACAGTAA 68922    GA  A     AAC
            AG                    TG  AT GTTTTT   TAGTAAAG
                                ||  || ||||||   ||||||||
                                AC  TA CAAAAG   GTCATTTC
                                 TC  C     GGT
GAM3015  FLJ21615  3'  TGGAATAGTTTTAATACAG   68923           TAAC
                                TGGAATAGTTTT    TAG
                                ||||||||||||   |||
                                ACCTTATCAAAA    GTC
                                       TTAT
GAM3015  KIAA0379  3'  TGAAATAGTTTTCTTAGT    68924            AAC
                                TGGAATAGTTTTT   TAGT
                                ||||||||||||   ||||
                                ACTTTATCAAAAG   ATCA
                                       A__
GAM3015  KIAA1117  3'  TGGGATAGTTCTTATTTAG    68925     A        AC
                                TGG ATAGTTTTTA  TAG
                                ||| ||||||||||  |||
                                ACC TATCAAGAAT  ATC
                                  C         AA
GAM3015  LOC143785 3'  TGGGATAGCTTTTGGAGCCCAG 68926     A        AA___
                                TGG ATAGTTTTT    CTAG
                                ||| |||||||||    ||||
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                                ACC TATCGAAAA    GGTC
                                  C       CCTCG
GAM3015  LOC197358 3'  TGGGATGATTTTTAACCAG   68927    A  A
                                TGG AT GTTTTTAACTAG
                                ||| || ||||||||||||
                                ACC TA TAAAAATTGGTC
                                  C  C
GAM3016  TPARL    3'  GGATGGTTTTTATATG     69012     C  AATT
                                GGATG GT    TTTTATATG
                                ||||| ||    |||||||||
                                CCTAC CA    AAAATATAC
                                  _ ____
GAM3017  CASP4    5'  TTAGTGCATTCCAACAGGTGAG 69015       C    TAAAAAC
            A                    TTAGTGCA TCTA      GAGA
                                ||||||||| ||||      ||||
                                AATCACGT AGGT      CTCT
                                     A    TGTCCA_
GAM3017  HNRPF    3'  GCATTTTATAAAAACGAGA   69016    CTC
                                GCA   TATAAAAACGAGA
                                |||   ||||||||||||||
                                CGT   ATATTTTTGCTCT
                                  AAA
GAM3017  PRKG2    3'  TTAGTAGTACTCAAACGAG   69017      C_   TATAA
                                TTAGTG  ACTC    AAACGAG
                                ||||||  ||||    |||||||
                                AATCAT  TGAG    TTTGCTC
                                   CA   ______
GAM3017  KIAA0410 3'  TCAGTGCATCTCAAAGATGAG 69018       C   A    AAC
                                TTAGTGCA TCT TAAA   GAG
                                |||||||| ||| ||||   |||
                                AGTCACGT AGA GTTT   CTC
                                     _   _    CTA
GAM3017  KIAA0993 3'  AGTAGCTCTATAAAAATGAGA  69019     CA         C
                                AGTG  CTCTATAAAAA GAGA
                                ||||  |||||||||| ||||
                                TCAT  GAGATATTTTT CTCT
                                  C_         A
GAM3017  SLC25A21 3'  TTAGTGCACTTTAAAAA     69020         CTA
                                TTAGTGCACT   TAAAAA
                                ||||||||||   ||||||
                                AATCACGTGA   ATTTTT
                                     A__
GAM3017  TRPV6    3'  ATGCACCCAGGAAAATGAGA   69021        TATA   C
                                GTGCACTC    AAAA GAGA
                                ||||||||    |||| ||||
                                TACGTGGG    TTTT CTCT
                                     TCC_   A
GAM3017  XLKD1    3'  GTGCACTCCATAGTCCAA    69022          AAAA
                                GTGCACTCTATA    CGA
                                ||||||||||||    |||
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                                CACGTGAGGTAT   GTT
                                      CAG_
GAM3017 ZTL1    3' TTAGTGGTCCACAAAGAGTGAG 69023       CAC      AAC_
                                TTAGTG  TCTATAAA   GAG
                                ||||||  ||||||||   |||
                                AATCAC  AGGTGTTT   CTC
                                   C__      CTCA
GAM3018 JAM2    5' GGGGGTGTGGGGGTAGGGGCT 69026        TCCTTAA    A
                                GGGGGTGT     TAGGG CT
                                ||||||||     ||||| ||
                                CCCCCACA     ATCCC GA
                                     CCCCC__    C
GAM3018 BCKDK   5' AGGGGGTGTGGGTGGGTAGGGG 69027         TCCTTAA    A
             CT                   AGGGGGTGT     TAGGG CT
                                ||||||||||     ||||| ||
                                TCCCCCCACA     ATCCC GA
                                     CCCACCC    C
GAM3018 GTPBP2  3' AGGGGATGGGGGGAGATAGGGAC 69028        TTCCTTA
             T                    AGGGGGTG     ATAGGGACT
                                ||||||||     |||||||||
                                TCCCCTAC     TATCCCTGA
                                     CCCCTC_
GAM3018 KIAA1061 3' AGGGGGTGTTCCTTGGCCCAGG 69029           AA__    A
             GCT                    AGGGGGTGTTCCTT   TAGGG CT
                                ||||||||||||||   ||||| ||
                                TCCCCCCACAAGGAA   GTCCC GA
                                       CCGG    _
GAM3018 KIAA1817 3' GGGACAGTTGGTAGGGACT   69030     GT   CCTTAA
                                GGGG  GTT    TAGGGACT
                                ||||  |||    ||||||||
                                CCCT  CAA    ATCCCTGA
                                  GT   CC____
GAM3018 KIAA1856 3' GGGGGTGTGCTGGGGAC    69031       TC  TAATA
                                GGGGGTGT  CT    GGGAC
                                ||||||||  ||    |||||
                                CCCCCACA  GA    CCCTG
                                     C_  C____
GAM3018 SERPINA10 5' AGGGGGTGCTCCTGGA     69032          TAATAG
                                AGGGGGTGTTCCT     GGA
                                |||||||||||||     |||
                                TCCCCCACGAGGA     CCT
                                          _____
GAM3018 LOC148936 5' AGGTGGTGCCCCAGTAGGGACT 69033     G      TTAA
                                AGG GGTGTTCC    TAGGGACT
                                ||| ||||||||    ||||||||
                                TCC CCACGGGG    ATCCCTGA
                                  A       TC__
GAM3018 LOC148938 5' AGGTGGTGCCCCAGTAGGGACT 69033     G      TTAA
                                AGG GGTGTTCC    TAGGGACT
                                ||| ||||||||    ||||||||
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                                TCC CCACGGGG   ATCCCTGA
                                  A       TC__
GAM3018  LOC152286 3'  AGGGGGTGATGGGAATGGGGGC 69034        TTCCTT  A  A
             T                    AGGGGGTG     AAT GGG CT
                                  ||||||||     ||| ||| ||
                                  TCCCCCAC     TTA CCC GA
                                       TACCC_  C  C
GAM3018  LOC254122 3'  GGGCAGGGTCCTTAATGGGG  69035     __ T  T     A
                                  GGG  GG GT CCTTAAT GGG
                                  |||  || || ||||||| |||
                                  CCC  CC CA GGAATTA CCC
                                    GT  _  _      C
GAM3019  PSMC6    3'  CTTTAACTTTATTTTTACAATA 69038           C   TT
             A                    CTTTAATTTTATT TTAT  TAA
                                  |||||||||||| ||||  |||
                                  GAAATTGAAATAA AATG  ATT
                                           A   TT
GAM3019  TYRO3    3'  CTTCAATTTTATTTCTATTTTA 69039           CT
             AA                     CTTTAATTTTATT  TATTTTAAA
                                  ||||||||||||  |||||||||
                                  GAAGTTAAAATAA  ATAAAATTT
                                           AG
GAM3019  GNG11    3'  TTTAATTTCATTCTTCCTTC  69040            A
                                  TTTAATTTTATTCTT TTTT
                                  |||||||||||||| ||||
                                  AAATTAAAGTAAGAA GAAG
                                            G
GAM3020  ERBB3    3'  GTGAGATAATGTAGGT      69043          AATG
                                  GTGAGATAATGT   AGGT
                                  ||||||||||||   ||||
                                  CACTCTATTACA   TCCA
                                               _____
GAM3020  DKFZP547N043 3'  GTGAGATAATACAGGT      69044          TAATG
                                  GTGAGATAATG    AGGT
                                  ||||||||||     ||||
                                  CACTCTATTAT    TCCA
                                         G_____
GAM3020  PF1      5'  TACGTGAGGTTGTGGTACGTGA 69045        ATAAT_  A_
             GGTG                     TACGTGAG     GTA  TGAGGTG
                                  ||||||||     |||  |||||||
                                  ATGCACTC     CAT  ACTCCAC
                                       CAACAC  GC
GAM3020  WBSCR17  3'  CGTGGGGTGAAATGAGGTG   69046     AGATAA  T
                                  CGTG     TG AATGAGGTG
                                  ||||     || |||||||||
                                  GCAC     AC TTACTCCAC
                                    CCC___  T
GAM3021  COL18A1  3'  TGAGATGGGGGCCCTGGATG  69049     C    T  _____
                                  TGA ATGGG GG   GGATG
                                  ||| ||||| ||   |||||
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                                ACT TACCC CC    CCTAC
                                  C    _ GGGA
GAM3021  COL18A1  3'  TGAGATGGGGGCCCTGGATG  69049    C    T ____
                                TGA ATGGG GG    GGATG
                                ||| ||||| ||    |||||
                                ACT TACCC CC    CCTAC
                                  C    _ GGGA
GAM3021  COL18A1  3'  TGAGATGGGGGCCCTGGATG  69049    C    T ____
                                TGA ATGGG GG    GGATG
                                ||| ||||| ||    |||||
                                ACT TACCC CC    CCTAC
                                  C    _ GGGA
GAM3021  CRY2     3'  TGACATGGCAGTCTGGATG   69050       __ GG
                                TGACATGG  GT  GGATG
                                ||||||||  ||  |||||
                                ACTGTACC  CA  CCTAC
                                     GT  GA
GAM3021  PCDH11Y  5'  TAACATGGGTTTAAAATG    69051        GG_
                                TGACATGGGT   GGATG
                                ||||||||||   |||||
                                ATTGTACCCA   TTTAC
                                      AAT
GAM3021  PCDH11Y  5'  TAACATGGGTTTAAAATG    69051        GG_
                                TGACATGGGT   GGATG
                                ||||||||||   |||||
                                ATTGTACCCA   TTTAC
                                      AAT
GAM3021  PIM2     3'  TGACATGGCCATGGGATG    69052       G _
                                TGACATGG TG GGGATG
                                |||||||| || ||||||
                                ACTGTACC GT CCCTAC
                                     G  A
GAM3021  PTMS     3'  GACATGACGCTGGGGGATG   69053       _ __
                                GACATGG GT  GGGGATG
                                ||||||| ||  |||||||
                                CTGTACT CG  CCCCTAC
                                     G  AC
GAM3021  C1orf34  3'  TGCTATGGGCAGGGGATG    69054    AC    _
                                TG  ATGGGT GGGGATG
                                ||  |||||| |||||||
                                AC  TACCCG CCCCTAC
                                  GA     T
GAM3021  C20orf175 3'  TGAGGCAAGTGGGGGATG    69055    CA       _
                                TGA  TGGGTGGGG ATG
                                |||  ||||||||| |||
                                ACT  GTTCACCCC TAC
                                  CC        C
GAM3021  CIDEB    5'  TGAATGGGGCAGGGGATG    69056    C    T__
                                TGA ATGGG   GGGGATG
                                ||| |||||   |||||||
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                                ACT TACCC   CCCCTAC
                                  _    CGT
GAM3021  DKFZP434H132 5'  TGAATGGGCACGAAGATG    69057     C     __
                                TGA ATGGGT  GGGGATG
                                ||| ||||||  |||||||
                                ACT TACCCG  CTTCTAC
                                  _     TG
GAM3021  DKFZp761O132 5'  TGACAGGTATTAGGGATG    69058      T  G__
                                TGACA GG   TGGGGATG
                                ||||| ||   ||||||||
                                ACTGT CC   ATCCCTAC
                                   _ ATA
GAM3021  FLJ14007  3'  TGATCATGGTAAGAAGATG   69059    _    GT_
                                TGA CATGG   GGGGATG
                                ||| |||||   |||||||
                                ACT GTACC   CTTCTAC
                                  A     ATT
GAM3021  FLJ22362  3'  GATGTGGGGCAGCTGGGGATGC 69060    CA   _____      III
                                GA  TGGG    TGGGGATG   C
                                ||  ||||    ||||||||  |
                                CT  ACCC    ACCCCTAC   G
                                 AC    CGTCG       III
GAM3021  FLJ22596  5'  TGAGATGAGATGGGGATG    69061     C  _
                                TGA ATG GGTGGGGATG
                                ||| ||| ||||||||||
                                ACT TAC CTACCCCTAC
                                  C   T
GAM3021  HN1L     3'  TAAAATGAAGTGGGGATG    69062     C   _
                                TGA ATGG GTGGGGATG
                                ||| |||| |||||||||
                                ATT TACT CACCCCTAC
                                  T    T
GAM3021  JDD1     3'  TGAATGGTGTTTAGGATG    69063     C   _ G_
                                TGA ATGG GT  GGGATG
                                ||| |||| ||  ||||||
                                ACT TACC CA  TCCTAC
                                  _    A  AA
GAM3021  Kv6.3    3'  TGAAAATGGAGTGGGGATG   69064     C_   _
                                TGA  ATGG GTGGGGATG
                                |||  |||| |||||||||
                                ACT  TACC CACCCCTAC
                                  TT    T
GAM3021  LOC144231 5'  TGAGATGGGGTGGGGATGC   69065     C    _      III
                                TGA ATGGG TGGGGATG   C
                                ||| ||||| ||||||||  |
                                ACT TACCC ACCCCTAC   G
                                  C    C       III
GAM3021  LOC144231 5'  TGAGATGGGTGATGGATG    69066     C      _
                                TGA ATGGGTGG GGATG
                                ||| |||||||| |||||
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                                ACT TACCCACT CCTAC
                                  C       A
GAM3021  LOC146540 3'  TGAATGGATAGAGGGATG    69067    C     __
                                TGA ATGGGT  GGGGATG
                                ||| ||||||  |||||||
                                ACT TACCTA  TCCCTAC
                                  _     TC
GAM3021  LOC147976 3'  TGGCATGGGCATCGAGATG   69068    A      G__
                                TG CATGGGT   GGGATG
                                || |||||||   ||||||
                                AC GTACCCG   CTCTAC
                                 C      TAG
GAM3021  LOC150094 3'  GACATGAAGAAGGGGATG    69069        T__
                                GACATGGG   GGGGATG
                                ||||||||   |||||||
                                CTGTACTT   CCCCTAC
                                     CTT
GAM3021  LOC255397 5'  TGGGATGGAGCTGGGGATG   69070    AC   _ _
                                TG  ATGG G TGGGGATG
                                ||  |||| | ||||||||
                                AC  TACC C ACCCCTAC
                                 CC    T G
GAM3021  LOC91208  5'  TGACAGGGAGGCCTGGATG   69071      T   T ___
                                TGACA GGG GG   GGATG
                                ||||| ||| ||   |||||
                                ACTGT CCC CC   CCTAC
                                   _  T  GGA
GAM3022  APPL      3'  AGAATGCATTGTAGAAGTAG   69074        CC      GG
                                AGAATGCA  GTAGGAG  G
                                ||||||||  |||||||  |
                                TCTTACGT  CATCTTC  C
                                     AA      AT
GAM3022  CARPX     3'  GCATCACAGGGGGGCATG    69075    C     A
                                GCA CGTAGG GGGGCATG
                                ||| |||||| ||||||||
                                CGT GTGTCC CCCCGTAC
                                  A     _
GAM3022  CD7       3'  AGAAGCACCGTGGGGC      69076     T      AGGA
                                AGAA GCACCGT    GGGGC
                                |||| |||||||    |||||
                                TCTT CGTGGCA    CCCCG
                                  _      _____
GAM3022  EPB41L2   3'  GAATGCTGCCGAAGGGCATG   69077       ACC  AG
                                GAATGC   GT  GAGGGGCATG
                                ||||||   ||  ||||||||||
                                CTTACG   CG  CTTCCCGTAC
                                   A__  G_
GAM3022  FGFR1     3'  GAGTACTGGTCCAGGGGCATG  69078    A   ACC  AGG
                                GA TGC   GT   AGGGGCATG
                                || |||   ||   |||||||||
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                                CT ATG   CA   TCCCCGTAC
                                 C  AC_  GG_
GAM3022 EDG1     3' AGAACGTTGAGGAGGGGTATG 69079      CACCGT      C
                                AGAATG     AGGAGGGG ATG
                                ||||||     |||||||| |||
                                TCTTGC     TCCTCCCC TAC
                                   AAC___      A
GAM3022 FLJ10769 3' AGAATCCATCTGGGGCAT    69080     GCA   AGGA
                                AGAAT  CCGT   GGGGCAT
                                |||||  ||||   |||||||
                                TCTTA  GGTA   CCCCGTA
                                   ___   GA__
GAM3022 FLJ23604 3' AGAATGCACTGGGAGATGCATG 69081        CGTA   GG
                                AGAATGCAC   GGAG  GCATG
                                |||||||||   ||||  |||||
                                TCTTACGTG   CCTC  CGTAC
                                     AC__   TA
GAM3022 KIAA0298 3' AGAATGGCAAGCCAAGGGGCAT 69082      _  CC  AG
             G                   AGAATG CA  GT  GAGGGGCATG
                                ||||||  ||  ||  ||||||||||
                                TCTTAC GT  CG  TTCCCCGTAC
                                   C  T_  G_
GAM3022 KIAA0522 3' GAATGGCGGGGGGGGCAT    69083     CACC TA  A
                                GAATG   G  GG GGGGCAT
                                |||||   |  || |||||||
                                CTTAC   C  CC CCCCGTA
                                   _____ GC  _
GAM3022 MAPK8IP3 3' AGGGCGCACCGTGGGGGAC   69084   AA      A  A
                                AG  TGCACCGT GG GGGGC
                                ||  |||||||| || |||||
                                TC  GCGTGGCA CC CCCTG
                                 CC       _  _
GAM3022 MGC5139  5' AGTGTGCCCAGGGGCAT     69085   AA   A  GTAGG
                                AG  TGC CC    AGGGGCAT
                                ||  ||| ||    ||||||||
                                TC  ACG GG    TCCCCGTA
                                 AC   _  ______
GAM3022 UBE3B    3' AGAGGCGCTGTGGACGGCATG  69086    A_   ACC  A   G  G
                                AGA  TGC   GT GGA GG CATG
                                |||  |||   || ||| || ||||
                                TCT  GCG   CA CCT CC GTAC
                                  CC   A__  _   G  _
GAM3022 WBSCR23  3' AGAATGTATTGGAGGAG     69087      CACC  A
                                AGAATG    GT GGAGGGG
                                ||||||    || |||||||
                                TCTTAC    TA CCTCCTC
                                   A___  A
GAM3022 LOC158056 5' AGAAGGGCCAAGGAGGGG    69088     TGCA   T
                                AGAA    CCG AGGAGGGG
                                ||||    ||| ||||||||
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                                TCTT   GGT TCCTCCCC
                                  CCC_  _
GAM3022 LOC257127 5' AGGGTGCACCGTGAGGGG   69089   AA      AG
                                AG  TGCACCGT  GAGGGG
                                ||  ||||||||  ||||||
                                TC  ACGTGGCA  CTCCCC
                                 CC       __
GAM3023 CKMT2    5' TCACTTGGCTTGTGACT     69092        CC   A
                                TCGCTTGGT  TGT ACT
                                |||||||||  ||| |||
                                AGTGAACCG  ACA TGA
                                     A_   C
GAM3023 DLG5     3' CCACTCTGCCTGTAACT     69093       G T
                                TCGCTT G CCTGTAACT
                                ||||||| | |||||||||
                                GGTGAG C GGACATTGA
                                   A _
GAM3023 EGLN1    5' TCACTTGAGTATACTGTAACT  69094       _ C__
                                TCGCTTG GT   CTGTAACT
                                ||||||| ||   ||||||||
                                AGTGAAC CA   GACATTGA
                                    T  TAT
GAM3023 HTR2C    5' TCGTTGGCCCCTAACT      69095     C      G
                                TCG TTGGTCCT TAACT
                                ||| |||||||| |||||
                                AGC AACCGGGG ATTGA
                                  _      _
GAM3023 MTMR6    3' TCACTTAAGATGTAACT     69096        TCC
                                TCGCTTGG   TGTAACT
                                ||||||||   |||||||
                                AGTGAATT   ACATTGA
                                    CT_
GAM3023 NCAM1    3' TCACTAAGCTGTAACT      69097      T  TC
                                TCGCT GG  CTGTAACT
                                |||||  ||  ||||||||
                                AGTGA TC  GACATTGA
                                   T  __
GAM3023 SNX5     3' TCACCTGCTGTAACT       69098       GTC
                                TCGCTTG   CTGTAACT
                                |||||||   ||||||||
                                AGTGGAC   GACATTGA
                                     ____
GAM3023 TDGF1    3' TCACTTGGTTTACAACT     69099        CC
                                TCGCTTGGT  TGTAACT
                                |||||||||  |||||||
                                AGTGAACCA  ATGTTGA
                                     A_
GAM3023 ACAA2    5' TCGCTTAGCAGCAACT      69100        CCT
                                TCGCTTGGT   GTAACT
                                |||||||||   ||||||
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                                AGCGAATCG  CGTTGA
                                     T__
GAM3023  D21S2056E 3'  TCCTTGGCCCCTAACT     69101    G       G
                                TC CTTGGTCCT TAACT
                                || ||||||||| |||||
                                AG GAACCGGGG ATTGA
                                 _       _
GAM3023  DJ473B4   3'  TCTTTTAGTCCTGTAACT    69102    GC
                                TC  TTGGTCCTGTAACT
                                ||  ||||||||||||||
                                AG  AATCAGGACATTGA
                                 AA
GAM3023  DKFZP586M0622 3'  TCATTAACCTGTAACT     69103    C   T
                                TCG TTGG CCTGTAACT
                                ||| |||| |||||||||
                                AGT AATT GGACATTGA
                                 _  _
GAM3023  FLJ11806  5'  TCATTTGGTCCTGACT     69104    C       TA
                                TCG TTGGTCCTG  ACT
                                ||| |||||||||  |||
                                AGT AACCAGGAC  TGA
                                 A       __
GAM3023  FLJ12761  3'  TCGCTTGGTGCCGTGGCACT  69105        _ _  TA
                                TCGCTTGGT CC TG  ACT
                                ||||||||| || ||  |||
                                AGCGAACCA GG AC  TGA
                                     C  C  CG
GAM3023  FLJ32332  3'  TCTCTTGGCCCTGACT     69106    G       TA
                                TC CTTGGTCCTG  ACT
                                || ||||||||||  |||
                                AG GAACCGGGAC  TGA
                                 A       __
GAM3023  GMPPB     5'  CCAGAAGCCCTGTAACT     69107    CTT
                                TCG   GGTCCTGTAACT
                                |||   ||||||||||||
                                GGT   TCGGGACATTGA
                                 CT_
GAM3023  KIAA1729  3'  TCGTGTTCCTGTAACT     69108    CT  G
                                TCG  TG TCCTGTAACT
                                |||  || ||||||||||
                                AGC  AC AGGACATTGA
                                 __  A
GAM3023  Kv6.3     3'  TCGGGGTCTCCTGTAACT    69109    CTT __
                                TCG   GG  TCCTGTAACT
                                |||   ||  ||||||||||
                                AGC   CC  AGGACATTGA
                                 C__  AG
GAM3023  MGC5466   5'  TCCCTCTCTCTGTAACT    69110    G   GG _
                                TC CTT  TC CTGTAACT
                                || |||  || ||||||||
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                                AG GAG  AG GACATTGA
                                 G   __  A
GAM3023  YAP      5'  TCACTTGACACCTAACT     69111         TC  G
                                TCGCTTGG  CT TAACT
                                ||||||||  || |||||
                                AGTGAACT  GG ATTGA
                                    GT  _
GAM3023  LOC125704 3'  CCGCCTCCTGTAACT      69112       TGG
                                TCGCT   TCCTGTAACT
                                |||||   ||||||||||
                                GGCGG   AGGACATTGA
                                  ____
GAM3023  LOC149837 5'  TCACTTGACCATAACT      69113         T  T
                                TCGCTTGG CC GTAACT
                                |||||||| || ||||||
                                AGTGAACT GG TATTGA
                                  _  _
GAM3023  LOC219372 5'  TCGCTTAGTACTAAACT     69114         C   T
                                TCGCTTGGT CTG AACT
                                ||||||||| ||| ||||
                                AGCGAATCA GAT TTGA
                                     T  _
GAM3024  TRIM9    3'  AAAGATCTTGCCCATGAGTCT  69117         CG   G    A
                                AAGGATCT  TGC CTAT AGTCT
                                ||||||||  ||| |||| |||||
                                TTTCTAGA  ACG GGTA TCAGA
                                   __   _   C
GAM3024  LOC152464 3'  GGGTCTCTGCCTTCCTGGGTCT 69118    A   G   G  ATAA__
                                GG TCTC TGC CT     GTCT
                                || |||| ||| ||     ||||
                                CC AGAG ACG GA     CAGA
                                 C   _  _ AGGACC
GAM3025  AQP6     5'  CTGGTGCCTTGGCCGTTCCTT  69121         AC    TCACCC
                                CTGGTGCC  GGTT     CCTT
                                ||||||||  ||||     ||||
                                GACCACGG  CCGG     GGAA
                                     AA    CAA___
GAM3025  WNT5A    5'  CTGGTGCCAGGCGCTGCCTCCT 69122         C   TTCA  C
           T                     CTGGTGCCA GGT    CC CCTT
                                |||||||| |||    || ||||
                                GACCACGGT CCG    GG GGAA
                                     _  CGAC  A
GAM3025  CARD14   5'  TGGTGCCAGCTGCCTCCT    69123         CG   TCA  C
                                TGGTGCCA  GTT   CC CCT
                                ||||||||  |||   || |||
                                ACCACGGT  CGA   GG GGA
                                     __  C__  A
GAM3025  DIO2     5'  CTGGTTCCCCTTCACCCTCTT  69124       G  ACGGT      C
                                CTGGT CC     TTCACCC CTT
                                ||||| ||     ||||||| |||
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                                GACCA GG    AAGTGGG GAA
                                  A  GG___     A
GAM3025  PRO0386   5'  CTGGTGCTTCCTGGTACCCCCT 69125       CAC__  TTC
             T                   CTGGTGC    GGT   ACCCCCTT
                                 |||||||    |||  ||||||||
                                 GACCACG    CCA   TGGGGGAA
                                    AAGGA  ___
GAM3025  LOC148397 5'  GGTGCTGGTCCCACCTCCTT   69126      CAC   TT   C
                                 GGTGC   GGT  CACC CCTT
                                 |||||   |||  |||| ||||
                                 CCACG   CCA  GTGG GGAA
                                   A__   GG   A
GAM3025  LOC148872 5'  CTGCTGCGTTTCACCTCCT    69127     G   CACG      C
                                 CTG TGC    GTTTCACC CCT
                                 ||| |||    |||||||| |||
                                 GAC ACG    CAAAGTGG GGA
                                   G  ____      A
GAM3025  LOC163026 5'  TGATGCCATGGCTTTCCT     69128        C    CACCC
                                 TGGTGCCA GGTTT    CCT
                                 |||||||| |||||    |||
                                 ACTACGGT CCGAA    GGA
                                     A    A____
GAM3025  LOC256849 5'  CTGGTGCCTGGTTCAGAGCCTT 69129        AC   T  CCC
                                 CTGGTGCC  GGTT CA   CCTT
                                 ||||||||  |||| ||   ||||
                                 GACCACGG  CCAA GT   GGAA
                                     A_   _  CTC
GAM3026  ALDH3B2   3'  GGGCATGTGTGTGTGAGG    69132    T   AC  ACAT
                                 GG GCAT  TG    TGTGAGG
                                 || ||||  ||    |||||||
                                 CC CGTA  AC    ACACTCC
                                  _   C_  AC__
GAM3026  COL4A6    3'  GGTGACTGTTGTGAG      69133     CAT   ACA
                                 GGTG   ACTG   TTGTGAG
                                 ||||   ||||   |||||||
                                 CCAC   TGAC   AACACTC
                                   ___   ___
GAM3026  COL4A6    3'  GGTGACTGTTGTGAG      69133     CAT   ACA
                                 GGTG   ACTG   TTGTGAG
                                 ||||   ||||   |||||||
                                 CCAC   TGAC   AACACTC
                                   ___   ___
GAM3026  ITSN2     3'  GTGCATGGCTTTGTGAGGG   69134      A_  GACA
                                 GTGCAT  CT    TTGTGAGGG
                                 ||||||  ||    |||||||||
                                 CACGTA  GA    AACACTCCC
                                    CC  ____
GAM3026  NHLH1     5'  GGTACACATTGTGGG       69135      ATACTG      A
                                 GGTGC     ACATTGTG GG
                                 |||||     |||||||| ||
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                                CCATG     TGTAACAC CC
                                  _______      _
GAM3026 PSMB9     3'  AGTGTATGCTGACATCTAGGAG 69136      C  A       GT_
              GG                    GGTG AT CTGACATT   GAGGG
                                |||| || ||||||||  |||||
                                TCAC TA GACTGTAG   CTCCC
                                  A  C       ATC
GAM3026 APR-3     5'  GGTGCATATCTGGCTGGGCAGG 69137         _  ACATT  G
              G                     GGTGCATA CTG    GT AGGG
                                |||||||| |||    || ||||
                                CCACGTAT GAC    CG TCCC
                                    A   CGACC  _
GAM3026 C11orf21  3'  GGTGCGGCCCACATGTGAGGG  69138      ATA  G    T
                                GGTGC   CT ACAT GTGAGGG
                                |||||   || |||| |||||||
                                CCACG   GG TGTA CACTCCC
                                   CC_  G    _
GAM3026 C20orf150 3'  GGTGCATACTGGGTTCCAGGG  69139          ACA  G G
                                GGTGCATACTG   TT T AGGG
                                ||||||||||   || | ||||
                                CCACGTATGAC   AA G TCCC
                                      CC_  G _
GAM3026 C20orf36  3'  GTGCATGTTGCATGAGG     69140       AC  A  TTG
                                GTGCAT  TG CA   TGAGG
                                ||||||  || ||   |||||
                                CACGTA  AC GT   ACTCC
                                   CA  _  ____
GAM3026 FLJ10342  3'  GGTGGTACTGACATCAGG    69141     CA        GTG
                                GGTG  TACTGACATT   AGG
                                ||||  ||||||||||   |||
                                CCAC  ATGACTGTAG   TCC
                                  C_         ____
GAM3026 FLJ14166  3'  GTGCTGGCTGTGAGGG      69142     ATAC  ACA
                                GTGC    TG   TTGTGAGGG
                                ||||    ||   |||||||||
                                CACG    AC   GACACTCCC
                                  _____  C__
GAM3026 KIAA0408  5'  GGTCAATTACATTGTGAGGG   69143     G  TACTG
                                GGT CA    ACATTGTGAGGG
                                ||| ||    ||||||||||||
                                CCA GT    TGTAACACTCCC
                                  _  TAA__
GAM3026 RA-GEF-2  3'  GGTGCTATGAGATGTGGGG   69144      A  C   CAT    A
                                GGTGC TA TGA   TGTG GGG
                                ||||| || |||   |||| |||
                                CCACG AT ACT   ACAC CCC
                                   _  _   CT_    _
GAM3026 RA-GEF-2  3'  AGTGTGTAACCTTTGTGAGGG  69145      CATAC    A_
                                GGTG    TGAC  TTGTGAGGG
                                ||||    ||||  |||||||||
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                                TCAC    ATTG  AACACTCCC
                                  AC___    GA
GAM3026  RNF38    3'  GGTACATGCTGGTATATAGG  69146       A  ACAT  G
                                GGTGCAT CTG   TGT AGG
                                ||||||| |||   ||| |||
                                CCATGTA GAC   ATA TCC
                                    C  CAT_  _
GAM3026  LOC150197 3'  GGTGTCTGCCTGTGTGAGGG  69147     CATA  ACAT
                                GGTG   CTG   TGTGAGGG
                                ||||   |||   ||||||||
                                CCAC   GAC   ACACTCCC
                                  A___  GGAC
GAM3026  LOC201229 3'  GGTGTGTGACAACTGTGAGGG  69148     CATAC   _
                                GGTG    TGACA TTGTGAGGG
                                ||||    ||||| |||||||||
                                CCAC    ACTGT GACACTCCC
                                  AC___    T
GAM3026  LOC202934 3'  GGTCATGCTGATGTAAGAG   69149    G  A   CAT
                                GGT CAT CTGA  TGTGAGGG
                                ||| ||| ||||  ||||||||
                                CCA GTA GACT  ACATTCTC
                                  _  C   ___
GAM3026  LOC90625  5'  GGTGGTAGCTTTTTGTGAGGG  69150     CATA  GACA
                                GGTG   CT   TTGTGAGGG
                                ||||   ||   |||||||||
                                CCAC   GA   AACACTCCC
                                  CATC  AA__
GAM3027  AGL      3'  ATTACTGTCACAACTGTCC   69153        _   A
                                GTTACTGTC TAACT TCC
                                ||||||||| ||||| |||
                                TAATGACAG GTTGA AGG
                                     T    C
GAM3027  AGL      3'  ATTACTGTCACAACTGTCC   69153        _   A
                                GTTACTGTC TAACT TCC
                                ||||||||| ||||| |||
                                TAATGACAG GTTGA AGG
                                     T    C
GAM3027  AGL      3'  ATTACTGTCACAACTGTCC   69153        _   A
                                GTTACTGTC TAACT TCC
                                ||||||||| ||||| |||
                                TAATGACAG GTTGA AGG
                                     T    C
GAM3027  AGL      3'  ATTACTGTCACAACTGTCC   69153        _   A
                                GTTACTGTC TAACT TCC
                                ||||||||| ||||| |||
                                TAATGACAG GTTGA AGG
                                     T    C
GAM3027  AGL      3'  ATTACTGTCACAACTGTCC   69153        _   A
                                GTTACTGTC TAACT TCC
                                ||||||||| ||||| |||
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                                TAATGACAG GTTGA AGG
                                     T    C
GAM3027 AGL      3' ATTACTGTCACAACTGTCC   69153        _    A
                                GTTACTGTC TAACT TCC
                                ||||||||| ||||| |||
                                TAATGACAG GTTGA AGG
                                     T    C
GAM3027 ALDH1B1  3' ATTACTCCTCTATCCCC    69154      G   AA
                                GTTACT TCT  CTATCCCC
                                |||||| |||  ||||||||
                                TAATGA GGA  GATAGGGG
                                  _  __
GAM3027 CD79B    5' GTCACTGCTCTGTCCCC    69155       CTAA  A
                                GTTACTGT   CT TCCCC
                                ||||||||   || |||||
                                CAGTGACG   GA AGGGG
                                     A___  C
GAM3027 CD79B    5' GTCACTGCTCTGTCCCC    69155       CTAA  A
                                GTTACTGT   CT TCCCC
                                ||||||||   || |||||
                                CAGTGACG   GA AGGGG
                                     A___  C
GAM3027 GLB1     3' GTTACTGTGCTGTCAGCCCC  69156       _ AAC  T
                                GTTACTGT CT   TA CCCC
                                |||||||| ||   || ||||
                                CAATGACA GA   GT GGGG
                                     C  CA_  C
GAM3027 HOXB5    3' CTGACCCAGACTATCCCC    69157    _   _
                                CTG TCTA ACTATCCCC
                                ||| |||| |||||||||
                                GAC GGGT TGATAGGGG
                                  T   C
GAM3027 PTPRJ    3' GCTACTGTTTAAATATTCC   69158       C   C   C
                                GTTACTGT TAA TAT CC
                                |||||||| ||| ||| ||
                                CGATGACA ATT ATA GG
                                     A   T   A
GAM3027 S100B    3' GTTACTGTTAACAAGAGTCCC 69159       C   TA___
                                GTTACTGT TAAC    TCCC
                                |||||||| ||||    ||||
                                CAATGACA ATTG    AGGG
                                     _   TTCTC
GAM3027 TMPRSS3  5' TTACAAATTTAACTATCC    69160     T_ C
                                TTAC  GT TAACTATCC
                                ||||  || |||||||||
                                AATG  TA ATTGATAGG
                                  TT  A
GAM3027 ZFP36    3' ATTACTGTCCCCCAAGTCCCC 69161        AA  __
                                GTTACTGTCT  CTA  TCCCC
                                ||||||||||  |||  |||||
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                                TAATGACAGG  GGT  AGGGG
                                     G_   TC
GAM3027  C20orf80  5'  GTTACTGTTCACCAGATTCC   69162        CTA   ___
                                GTTACTGT   ACTA   TCC
                                ||||||||   ||||   |||
                                CAATGACA   TGGT   AGG
                                     AG_    CTA
GAM3027  DCOHM     3'  GTCACTGTGCTCAATCCCC    69163        _  AACT
                                GTTACTGT CT    ATCCCC
                                ||||||||  ||    ||||||
                                CAGTGACA GA    TAGGGG
                                     C  GT__
GAM3027  DKFZp761G0313 3'  GTCACTGTTTAACTGCCC    69164        C    AT
                                GTTACTGT TAACT  CC
                                ||||||||  |||||  ||
                                CAGTGACA ATTGA  GG
                                     A    CG
GAM3027  FLJ10851  3'  GTTACTGCTGAACTCCC     69165        CT   TA
                                GTTACTGT  AAC  TCCC
                                ||||||||  |||  ||||
                                CAATGACG  TTG  AGGG
                                     AC   __
GAM3027  FLJ23510  3'  GTCACTGTCTGAGATCATCC   69166         AAC__
                                GTTACTGTCT     TATCC
                                ||||||||||     |||||
                                CAGTGACAGA     GTAGG
                                      CTCTA
GAM3027  KIAA0258  3'  TTACTGTCTCCACCCC      69167        AA
                                TTACTGTCT  CTATCCC
                                |||||||||  |||||||
                                AATGACAGA  GGTGGGG
                                      __
GAM3027  KIAA0295  3'  TTACTGTCCCCTATTTCC    69168         AA   CC
                                TTACTGTCT  CTAT  CC
                                |||||||||  ||||  ||
                                AATGACAGG  GATA  GG
                                     G_    AA
GAM3027  KIAA0335  3'  GTTCTTGGTAACTATCCC    69169     A  GTC
                                GTT CT   TAACTATCCC
                                |||  ||   ||||||||||
                                CAA GA   ATTGATAGGG
                                  _  ACC
GAM3027  KIAA0960  3'  TACTGTCTTAAATATCTCC    69170         _  C   _
                                TACTGTCT AA TATC CC
                                ||||||||  ||  ||||  ||
                                ATGACAGA TT ATAG GG
                                     A  T    A
GAM3027  KIAA1085  5'  GTTATCTGAATCACTATTCCC  69171      _   TCTA    _
                                GTTA CTG    ACTAT CCC
                                ||||  |||    |||||  |||
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                                CAAT GAC    TGATA GGG
                                  A  TTAG    A
GAM3027 KIAA1789 5' GTTCCCTCAAAACTATCC    69172     A  G  T_
                                GTT CT TC  AACTATCC
                                ||| || ||  ||||||||
                                CAA GG AG  TTGATAGG
                                  _  G  TT
GAM3027 KIAA1821 3' GTTACTGCTAATCCC       69173        T   ACT
                                GTTACTG CTA   ATCCC
                                ||||||| |||   |||||
                                CAATGAC GAT   TAGGG
                                     _  ___
GAM3027 MGC15606 5' GTTACGTCTAACTTTCC     69174       T       A
                                GTTAC GTCTAACT TCC
                                ||||| |||||||| |||
                                CAATG CAGATTGA AGG
                                  _       A
GAM3027 MLZE     3' ATTACTGTCTCTACTCC     69175          AA   TC
                                GTTACTGTCT  CTA  CC
                                ||||||||||  |||  ||
                                TAATGACAGA  GAT  GG
                                     __  GA
GAM3027 PRO0641  3' GTTGATGCTACTATCCCC    69176     AC  T   A
                                GTT  TG CTA CTATCCCC
                                |||  || ||| ||||||||
                                CAA  AC GAT GATAGGGG
                                  CT  _  _
GAM3027 TLE4     3' ATTGCTGTTCTCCATCCCC   69177     A   _  AA
                                GTT CTGT CT  CTATCCCC
                                ||| |||| ||  ||||||||
                                TAA GACA GA  GGTAGGGG
                                  C   A  __
GAM3027 ZNF238   3' TTACTTCCCCTATCCCC     69178       G   AA
                                TTACT TCT  CTATCCCC
                                ||||| |||  ||||||||
                                AATGA AGG  GATAGGGG
                                  _  G_
GAM3027 LOC124460 3' GTCACTGCTGTATCCCC    69179        T  AAC
                                GTTACTG CT   TATCCCC
                                ||||||| ||   |||||||
                                CAGTGAC GA   ATAGGGG
                                     _  C__
GAM3027 LOC138050 5' GTTACTATCAACTGGATCC  69180          T   __
                                GTTACTGTC AACT  ATCC
                                ||||||||| ||||  ||||
                                CAATGATAG TTGA  TAGG
                                     _   CC
GAM3027 LOC145622 3' GCTACTGTTACTGTTCCC   69181         CTA  A_
                                GTTACTGT   ACT  TCCC
                                ||||||||   |||  ||||
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                                CGATGACA  TGA  AGGG
                                    A__   CA
GAM3027  LOC148166 5'  GTTCTGTGGGGTCTATCCCC  69182     A   CTAA_
                                GTT CTGT    CTATCCCC
                                ||| ||||    ||||||||
                                CAA GACA    GATAGGGG
                                  _   CCCCA
GAM3027  LOC150159 3'  GCTACTGTCATCACATCC    69183        TA_  T
                                GTTACTGTC  AC ATCC
                                |||||||||  || ||||
                                CGATGACAG  TG TAGG
                                     TAG  _
GAM3027  LOC162333 5'  GTTTCTGTCTGCTTCTGTCCCC 69184     A     AA__  A
                                GTT CTGTCT   CT TCCCC
                                ||| ||||||   || |||||
                                CAA GACAGA   GA AGGGG
                                  A     CGAA  C
GAM3027  LOC170063 3'  TACAATCTAACTGTCCCC    69185     T      A
                                TAC GTCTAACT TCCCC
                                ||| |||||||| |||||
                                ATG TAGATTGA AGGGG
                                  T       C
GAM3027  LOC197342 3'  GTTGATGTCTAACACCC     69186     AC      T
                                GTT  TGTCTAAC ATCC
                                |||  |||||||| ||||
                                CAA  ACAGATTG TGGG
                                  CT      _
GAM3027  LOC197407 3'  GTTACTGTCTCCAATCCC    69187         AACT
                                GTTACTGTCT   ATCCC
                                ||||||||||   |||||
                                CAATGACAGA   TAGGG
                                     GGT_
GAM3027  LOC197408 5'  GTTACTGTCTCCAATCCC    69187         AACT
                                GTTACTGTCT   ATCCC
                                ||||||||||   |||||
                                CAATGACAGA   TAGGG
                                     GGT_
GAM3027  LOC202400 3'  GTTACCATGCCTAGCTATC   69188      __    A
                                GTTACT  GTCTA CTATC
                                ||||||  ||||| |||||
                                CAATGG  CGGAT GATAG
                                   TA    C
GAM3027  LOC221474 3'  ATTACTATAACCACTATCCCC  69189       CTA_
                                GTTACTGT   ACTATCCCC
                                ||||||||   |||||||||
                                TAATGATA   TGATAGGGG
                                     TTGG
GAM3027  LOC257336 5'  GTTACTGTTCACCAGATTCC  69162       CTA   ___
                                GTTACTGT   ACTA   TCC
                                ||||||||   ||||   |||
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                              CAATGACA  TGGT  AGG
                                 AG_   CTA
GAM3027 LOC51207 3' GTCACCACCCAGCTATCCC  69190     TG   A
                              GTTAC  TCTA CTATCCC
                              ||||||  |||| |||||||
                              CAGTG  GGGT GATAGGG
                                 GT   C
GAM3027 LOC90326 3' GCTACTGTCTCGATCCCC   69191       AACT
                              GTTACTGTCT   ATCCCC
                              ||||||||||   ||||||
                              CGATGACAGA   TAGGGG
                                   GC__
GAM3028 ANGPT1   5' AGATATTTATTGCATAGTAGCT 69194     C    TTC
                              AGATA TTATT  TAGTAGCT
                              ||||| |||||  ||||||||
                              TCTAT AATAA  ATCATCGA
                                 A    CGT
GAM3028 ANGPT1   5' AGATATTTATTGCATAGTAGCT 69194     C    TTC
                              AGATA TTATT  TAGTAGCT
                              ||||| |||||  ||||||||
                              TCTAT AATAA  ATCATCGA
                                 A    CGT
GAM3028 DCN     3' TAAGAATATCTCTAGTAGC   69195     TACTTAT
                              TAAGA     TTTCTAGTAGC
                              |||||     ||||||||||
                              ATTCT     AGAGATCATCG
                                 TAT_____
GAM3028 DCN     3' TAAGAATATCTCTAGTAGC   69195     TACTTAT
                              TAAGA     TTTCTAGTAGC
                              |||||     ||||||||||
                              ATTCT     AGAGATCATCG
                                 TAT_____
GAM3028 DCN     3' TAAGAATATCTCTAGTAGC   69195     TACTTAT
                              TAAGA     TTTCTAGTAGC
                              |||||     ||||||||||
                              ATTCT     AGAGATCATCG
                                 TAT_____
GAM3028 DCN     3' TAAGAATATCTCTAGTAGC   69195     TACTTAT
                              TAAGA     TTTCTAGTAGC
                              |||||     ||||||||||
                              ATTCT     AGAGATCATCG
                                 TAT_____
GAM3028 DCN     3' TAAGAATATCTCTAGTAGC   69195     TACTTAT
                              TAAGA     TTTCTAGTAGC
                              |||||     ||||||||||
                              ATTCT     AGAGATCATCG
                                 TAT_____
GAM3028 DCN     3' TAAGAATATCTCTAGTAGC   69195     TACTTAT
                              TAAGA     TTTCTAGTAGC
                              |||||     ||||||||||
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                                ATTCT      AGAGATCATCG
                                   TAT_____
GAM3028  SACM2L    3'  AAATATTTATTTTCTGCAGACT 69196      C       A   _
                                AGATA TTATTTTCT GTAG CT
                                ||||| ||||||||| |||| ||
                                TTTAT AATAAAAGA CGTC GA
                                   A       _   T
GAM3028  SACM2L    3'  AAATATTTATTTTCTGCAGACT 69196      C       A   _
                                AGATA TTATTTTCT GTAG CT
                                ||||| ||||||||| |||| ||
                                TTTAT AATAAAAGA CGTC GA
                                   A       _   T
GAM3028  DIS3      3'  GAATTAAACCTTTCTAGTAGCT 69197    TACTTA_
                                GA      TTTTCTAGTAGCT
                                ||      ||||||||||||
                                CT      GAAAGATCATCGA
                                 TAATTTG
GAM3028  ETL       3'  TAAAATACTTTTTGTCTAGTAG 69198         A  T
                                TAAGATACTT TT TCTAGTAG
                                |||||||||| || ||||||||
                                ATTTTATGAA AA AGATCATC
                                      A  C
GAM3028  FLJ13188  3'  GATGCTTAAATAGTAGCT    69199     A    TTTTC
                                GAT CTTA    TAGTAGCT
                                ||| ||||    ||||||||
                                CTA GAAT    ATCATCGA
                                  C   TT___
GAM3028  KIAA1271  3'  AGATACTTTTTTCAAAGCT    69200        A    TAGT
                                AGATACTT TTTTC    AGCT
                                |||||||| |||||    ||||
                                TCTATGAA AAAAG    TCGA
                                     _    TT__
GAM3028  KIAA1557  5'  AGGGACTTGGTTATTAGTAGCT 69201    AT    AT  TC
                                AG  ACTT  TT  TAGTAGCT
                                ||  ||||  ||  ||||||||
                                TC  TGAA  AA  ATCATCGA
                                 CC    CC  TA
GAM3028  LOC124989 3'  AAATATTTATTTTCTAGC    69202      C
                                AGATA TTATTTTCTAGT
                                ||||| ||||||||||||
                                TTTAT AATAAAAGATCG
                                   A
GAM3028  LOC203080 5'  ATACTTATTTTTAGC       69203          CTAG
                                ATACTTATTTT    TAGC
                                ||||||||||    ||||
                                TATGAATAAAA    ATCG
                                                ____
GAM3028  LOC254794 5'  TAAGAACTTGTTTTCCAGC    69204      T    A
                                TAAGA ACTT TTTTCTAGT
                                ||||| |||| |||||||||
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                                ATTCT TGAA AAAAGGTCG
                                   _   C
GAM3029  ABCG5    3'  TAAACATATTTTTAAGCT    69207          _
                                TAAACATATTTT AAGCT
                                |||||||||||| |||||
                                ATTTGTATAAAA TTCGA
                                      A
GAM3029  IL26     3'  TATAAACATATTTCTAGC    69208           A
                                TATAAACATATTTT AGC
                                |||||||||||||| |||
                                ATATTTGTATAAAG TCG
                                      A
GAM3029  CTHRC1   3'  TAAACATATTTAGCTTTGCT  69209         TA    A
                                TAAACATATTT  AGCTTT CT
                                ||||||||||  |||||| ||
                                ATTTGTATAAA  TCGAAA GA
                                      __     C
GAM3029  PDE4DIP  3'  ACACAGACTAGGCTTTACT   69210      TT   A
                                ACATA  TTA GCTTTACT
                                |||||  ||| ||||||||
                                TGTGT  GAT CGAAATGA
                                   CT   C
GAM3029  Spir-1   3'  TATAAGTAATTTTAAGCCTTTT 69211      ACAT       __
            ACT                   TATAA   ATTTTAAGCT  TTACT
                                |||||   ||||||||||  |||||
                                ATATT   TAAAATTCGG  AATGA
                                   CAT_        AA
GAM3029  LOC154062 3'  ATAAACATATCACTCTAGGCTT 69212          ___  A
            TA                    ATAAACATATT   TTA GCTTTA
                                ||||||||||   ||| ||||||
                                TATTTGTATAG   GAT CGAAAT
                                      TGA   C
GAM3030  FLJ13614  3'  TTTAAAATGTTAACACTC    69215          _
                                TTTAAAATGTTAA ACTT
                                |||||||||||| ||||
                                AAATTTTACAATT TGAG
                                      G
GAM3030  LOC115749 3'  TTTAAAATTTTAAACTTCT   69216        G
                                TTTAAAAT TTAAACTTTT
                                |||||||| ||||||||||
                                AAATTTTA AATTTGAAGA
                                     A
GAM3030  LOC150215 5'  TTTAAAATGCTAGTTTTGTT  69217          AAC
                                TTTAAAATGTTA   TTTTGTT
                                ||||||||||||   |||||||
                                AAATTTTACGAT   AAAACAA
                                      C__
GAM3031  C20orf28  3'  GACCTGCACGGTCTCTT     69220         ACC
                                GACCTGCACG   CTCTT
                                ||||||||||   |||||
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                                CTGGACGTGC   GAGAA
                                     CA_
GAM3031  CHL1     3'  AACCTGCATGACTCTCTT    69221        C   C
                                GACCTGCA GAC CTCTT
                                |||||||| ||| |||||
                                TTGGACGT CTG GAGAA
                                    A   A
GAM3031  DKFZP434H0820 3'  GACCTGCACGTTCTGGGCCTT  69222         ACCC   TCGA
                                GACCTGCACG   TCT   CTT
                                ||||||||||   |||   |||
                                CTGGACGTGC   AGA   GAA
                                     A___   CCCG
GAM3031  FLJ22794  3'  GACCTGCACATTTTTCTGAGCA 69223         ACCC   TCG_
            CTT                   GACCTGCACG   TCT   ACTT
                                ||||||||||   |||   ||||
                                CTGGACGTGT   AGA   TGAA
                                     AAAA   CTCG
GAM3031  LOC132617 3'  GAACAGGGCTCTCTTCGACTT  69224   T   CGACC
                                C GCA    CTCTTCGACTT
                                | |||    ||||||||||
                                C TGT    GAGAAGCTGAA
                                 T   CCCGA
GAM3031  LOC200448 3'  CTGCACGACCCTGGCAACTT   69225          CTT
                                CTGCACGACCCT   CGACTT
                                ||||||||||||   ||||||
                                GACGTGCTGGGA   GTTGAA
                                      CC_
GAM3032  NRGN     3'  CTTAGGGCGCCCTCCGCA    69228     C  A      T
                                CTTA GG CGCCCTCC CG
                                |||| || |||||||| ||
                                GAAT CC GCGGGAGG GT
                                  C  _       C
GAM3032  DNAJC5   3'  CTTCCAGTCCCCTCCTCGA   69229     A   ACG
                                CTT CGG   CCCTCCTCGA
                                ||| |||   ||||||||||
                                GAA GTC   GGGAGGAGCT
                                  G   AG_
GAM3032  KIAA1094  5'  CTACGGACGCCCTAGAC     69230          CCTC
                                TTACGGACGCCCT   GAC
                                ||||||||||||    |||
                                GATGCCTGCGGGA   CTG
                                      T___
GAM3033  JAG2     3'  CAAATATACAGAGTGCT     69233        T   AAGC
                                CAAATATAT AGAG   GCT
                                ||||||||| ||||   |||
                                GTTTATATG TCTC   CGA
                                     _   A___
GAM3033  PMX1     5'  GCAGATGTATTAGAGAGC    69234     A  A       A
                                GCA AT TATTAGAGA GC
                                ||| || ||||||||| ||
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                                CGT TA ATAATCTCT CG
                                  C  C       _
GAM3033  PMX1     5'  GCAGATGTATTAGAGAGC    69234     A  A       A
                                GCA AT TATTAGAGA GC
                                ||| || ||||||||| ||
                                CGT TA ATAATCTCT CG
                                  C  C       _
GAM3033  C21orf25  3'  AGCAAAATTCTGAAGCGCT   69235       TAT   AGA
                                AGCAAA   ATT   GAAGCGCT
                                ||||||   |||   ||||||||
                                TCGTTT   TAA   CTTCGCGA
                                   ___   GA_
GAM3033  FLJ13725  5'  GCTATAGGTGGAGAAGCGCT   69236    AAA    TTA_
                                GC   TATA    GAGAAGCGCT
                                ||   ||||    ||||||||||
                                CG   ATAT    CTCTTCGCGA
                                 ___    CCAC
GAM3033  IAN4L1    3'  ATACATTAGAAGTGCTC     69237         GA  C
                                ATATATTAGA  AG GCTC
                                ||||||||||  || ||||
                                TATGTAATCT  TC CGAG
                                      __  A
GAM3033  KIAA0546  3'  AGCAAATATTTTAGAATGCCTC 69238         A     AA  G
                                AGCAAATAT TTAGAG  GC CTC
                                ||||||||| ||||||  || |||
                                TCGTTTATA AATCTT  CG GAG
                                     A     A_ _
GAM3033  MUC13     3'  GCATGATTAGAGAAGTGCTC   69239     AATAT        C
                                GCA     ATTAGAGAAG GCTC
                                |||     |||||||||| ||||
                                CGT     TAATCTCTTC CGAG
                                  AC___         A
GAM3033  STK38L    3'  AAATATATTAGTGGAGTGCT   69240          AGA  C
                                AAATATATTAG   AG GCT
                                ||||||||||   || |||
                                TTTATATAATC   TC CGA
                                      ACC  A
GAM3033  LOC133418 3'  AGCAATAAAAAAGAAGTGCT   69241      AAT   TT      C
                                AGCA   ATA  AGAGAAG GCT
                                ||||   |||  ||||||| |||
                                TCGT   TAT  TTTCTTC CGA
                                   ___   TT      A
GAM3033  LOC149657 3'  GCAGATTTATTAGAGAAA    69242     A  A
                                GCA AT TATTAGAGAAG
                                ||| || ||||||||||
                                CGT TA ATAATCTCTTT
                                  C  A
GAM3033  LOC51320  3'  AGCAAATATATAATATCAGTGC 69243          TAGAGA  C
            T                    AGCAAATATAT     AG GCT
                                ||||||||||     || |||
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                                TCGTTTATATA     TC CGA
                                      TTATAG  A
GAM3034  GRINL1A  3'  TGAAAGACATGTAATAAATGCT 69246     CA       TA
                                TGAA  ACATGTAAT  GAATGCT
                                ||||  |||||||||  |||||||
                                ACTT  TGTACATTA  TTTACGA
                                  TC       __
GAM3034  OTP      3'  TGACCAGTATGTAACAAGAATG 69247     A  AC      T
              CT                  TGA CA  ATGTAAT AGAATGCT
                                ||| ||  ||||||| ||||||||
                                ACT GT  TACATTG TCTTACGA
                                  G  CA      T
GAM3034  PIN4     3'  TGACTAACATGTAAAACAAATG 69248     AC       TTA
                                TGA  AACATGTAA   GAATG
                                |||  |||||||||   |||||
                                ACT  TTGTACATT   TTTAC
                                  GA        TTG
GAM3034  STC1     3'  CAACATGTGAGAACTGCT    69249        AATT   _
                                CAACATGT    AGAA TGCT
                                ||||||||    |||| ||||
                                GTTGTACA    TCTT ACGA
                                     C___    G
GAM3034  C2orf6   3'  TGAACCACATAGAATG      69250      A   TGTAAT
                                TGAAC ACA     TAGAATG
                                ||||| |||     |||||||
                                ACTTG TGT     ATCTTAC
                                  G  _______
GAM3034  EIF2C2   3'  TGACAACATCAGAATG      69251     A    TGTAA
                                TGA CAACA     TTAGAATG
                                ||| |||||     ||||||||
                                ACT GTTGT     AGTCTTAC
                                  _    ______
GAM3034  GFR      3'  TGAGCAGCATGCAATATGC    69252     A  A      TAGA
                                TGA CA CATGTAAT    ATGC
                                ||| || ||||||||    ||||
                                ACT GT GTACGTTA    TACG
                                  C  C       _____
GAM3034  HT014    3'  TGGGCAACTTGACAAGAATGCT 69253     AA    A  TAATT
                                TG  CAAC TG    AGAATGCT
                                ||  |||| ||    ||||||||
                                AC  GTTG AC    TCTTACGA
                                  CC    A  TGT__
GAM3034  SIAT8C   5'  TGGACAGTGGCACAAAGAATGC 69254    A   ACAT   ATT
              T                   TG ACA    GTA   AGAATGCT
                                || |||    |||   ||||||||
                                AC TGT    CGT   TCTTACGA
                                  C   CAC_   GTT
GAM3034  TSPEAR   3'  ACATGTGATTAAAATGCT    69255       A
                                ACATGT ATTAGAATGCT
                                ||||||  ||||||||||
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```
                                TGTACA TAATTTTACGA
                                   C
GAM3035 CNP      3' TTCTAGGGGCATAAGTGGTGGT 69258     CG     TGT
                                TTC  GGGGGT   GGTGGTGGT
                                |||  ||||||   |||||||||
                                AAG  TCCCCG   TCACCACCA
                                  A_     TAT
GAM3035 PIK3C2B   5' TTCTGGAGGGTTGTGACATGGT 69259     C         GT G
                                TTC GGGGGGTTGTG  G TGGT
                                ||| ||||||||||  | ||||
                                AAG CCTCCCAACAC  T ACCA
                                  A         TG _
GAM3035 PX19     3' TCTGGGGTGCTGTGGTGGTGGT 69260    C    G
                                TC GGGG GTTGTGGTGGTGGT
                                || |||| ||||||||||||||
                                AG CCCC CGACACCACCACCA
                                 A   A
GAM3035 SLC1A4   3' CTCTGGGGTGGTGGTGG     69261     C    GGTTG
                                TTC GGGG    TGGTGGTGG
                                ||| ||||    |||||||||
                                GAG CCCC    ACCACCACC
                                  A   _____
GAM3035 TOX      3' CGGGGGGCGGGGGGGTGGTGGT  69262        TGT_
                                CGGGGGGT   GGTGGTGGT
                                ||||||||   |||||||||
                                GCCCCCCCG   CCACCACCA
                                     CCCC
GAM3035 KIAA0461  3' TTCAGGGGGGGAGTGGTGGT   69263     C     TT
                                TTC GGGGGG  GTGGTGGT
                                ||| ||||||  ||||||||
                                AAG CCCCCC  CACCACCA
                                  T     T_
GAM3035 KIAA1719  5' TTCCGGAGGGAGGTGGTGGT   69264         TT
                                TTCCGGGGGGG  GTGGTGGT
                                ||||||||||  ||||||||
                                AAGGCCTCCC  CACCACCA
                                      TC
GAM3035 LATS1    3' GGGTAGGGTGGTGGTGGT    69265     _   TT
                                GGG GGG  GTGGTGGTGGT
                                ||| |||  ||||||||||
                                CCC TCC  CACCACCACCA
                                  A  __
GAM3035 MGC32104  3' TTCTGTGGGGTTGGTGGT    69266     CGG    TG
                                TTC   GGGGT  TGGTGGT
                                |||   |||||  |||||||
                                AAG   CCCCA  ACCACCA
                                  ACA    __
GAM3035 LOC253148 5' CCGGGACTGGTGGTGGTGGT   69267       GGTT
                                CCGGGG   GTGGTGGTGGT
                                ||||||   ||||||||||
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                                GGCCCT   CACCACCACCA
                                   GAC_
GAM3035  LOC255446 3'  GGGGGGTCAGGGTGGTGGT   69268         T
                                GGGGGGTTG GGTGGTGGT
                                ||||||||| |||||||||
                                CCCCCCAGT CCACCACCA
                                     C
GAM3035  LOC256078 5'  TCTCGTGTGTTGTGGTGGTGGT 69269    _ GGGG
                                TC CG   GTTGTGGTGGTGGT
                                || ||   ||||||||||||||
                                AG GC   CAACACCACCACCA
                                 A  ACA_
GAM3035  LOC256338 3'  TCTGGGGTGCTGTGGTGGTGGT 69260    C   G
                                TC GGGG GTTGTGGTGGTGGT
                                || |||| ||||||||||||||
                                AG CCCC CGACACCACCACCA
                                 A   A
GAM3035  LOC90393  3'  TTCTGGGGGGTTTTGCCAGAGT 69270    C      G  G   T
                                TTC GGGGGGTT TG TGG GGT
                                ||| |||||||| || ||| |||
                                AAG CCCCCCAA AC GTC TCA
                                  A       A  G  _
GAM3036  KCNQ1    3'  TCCAAATCACCACAAATTAT   69273       T    G   T
                                TCCAAAT CACCA CGA TTAT
                                ||||||| ||||| ||| ||||
                                AGGTTTA GTGGT GTT AATA
                                     _    _  T
GAM3036  AFAP     3'  TCCAAATTCTCCAAGAAATAT  69274        A   C  TT
                                TCCAAATTC CCAG GA  TAT
                                ||||||||| |||| ||  |||
                                AGGTTTAAG GGTT CT  ATA
                                     A   _ TT
GAM3036  CYB5-M   3'  TCTGAATTCACCAGGGTTCGAT 69275  CA      G_______  TTTA
            AAT                   AATTCACCA      CGA   T
                                  |||||||||      |||   |
                                  TTAAGTGGT      GCT   A
                                AC       CCCAAIII  ATTT
GAM3036  CYB5-M   3'  TCTGAATTCACCAGGGTTCGAT 69275  CA      G_______  TTTA
            AAT                   AATTCACCA      CGA   T
                                  |||||||||      |||   |
                                  TTAAGTGGT      GCT   A
                                AC       CCCAAIII  ATTT
GAM3036  MEGF10   3'  CAAATTTACCATGCAGCTC   69276      C   _  A
                                CAAATT ACCA GCG TTT
                                |||||| |||| ||| |||
                                GTTTAA TGGT CGT GAG
                                   A   A   C
GAM3037  GAGED2   3'  TTGGTGAAAGCTGCAAAACTTT 69279        TC__    A
            ATT                   TTGGTGAAA   CAAGG TTTATT
                                  |||||||||   ||||| ||||||
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                              AACCACTTT   GTTTT AAATAA
                                   CGAC    G
GAM3037 GAGED2   3' TTGGTGAAAGCTGCAAAACTTT 69279        TC__    A
           ATT                  TTGGTGAAA   CAAGG TTTATT
                              |||||||||   ||||| ||||||
                              AACCACTTT   GTTTT AAATAA
                                   CGAC    G
GAM3037 GAGED2   3' TTGGTGAAAGCTGCAAAACTTT 69279        TC__    A
           ATT                  TTGGTGAAA   CAAGG TTTATT
                              |||||||||   ||||| ||||||
                              AACCACTTT   GTTTT AAATAA
                                   CGAC    G
GAM3037 SCN1A    3' TGGTGAAATTTAAGAATTT   69280        CC
                              TGGTGAAAT  AAGGATTT
                              |||||||||  ||||||||
                              ACCACTTTA  TTCTTAAA
                                   AA
GAM3037 WHSC1L1  3' TTGGTGAAGTGGCATTTATT  69281       ATCCAA _
                              TTGGTGAA    GG ATTTATT
                              ||||||||    || |||||||
                              AACCACTT    CC TAAATAA
                                   CA____ G
GAM3037 BANP     5' TTAGTGGGATCCATTTCACTAT 69282      AA    AGGAT
           TA                   TTGGTG  ATCCA    TTATTA
                              ||||||  |||||    ||||||
                              AATCAC  TAGGT    GATAAT
                                 CC    AAAGT
GAM3037 C11orf15 3' TTGGTGAAATCAACAAGG    69283         __
                              TTGGTGAAATC  CAAGG
                              ||||||||||  |||||
                              AACCACTTTAG  GTTCC
                                    TT
GAM3037 DKFZp761A132 3' TTGATGGAAAATAGGATTTATT 69284      _  TCCA
                              TTGGTG AAA   AGGATTTATT
                              |||||| |||   ||||||||||
                              AACTAC TTT   TCCTAAATAA
                                 C  TA__
GAM3037 FLJ12428 3' TTGGTGAAATCTAGATTC    69285         CAA
                              TTGGTGAAATC  GGATTT
                              ||||||||||  ||||||
                              AACCACTTTAG  TCTAAG
                                    A__
GAM3037 FLJ20637 3' TGGTGAAGGAGTGGATTTATT 69286       ATCCAA
                              TGGTGAA    GGATTTATT
                              |||||||    |||||||||
                              ACCACTT    CCTAAATAA
                                 CCTCA_
GAM3037 KIAA0220 5' TTAGTGGGATCCATTTCACTAT 69282      AA    AGGAT
           TA                   TTGGTG  ATCCA    TTATTA
                              ||||||  |||||    ||||||
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                                AATCAC  TAGGT    GATAAT
                                   CC    AAAGT
GAM3037  KIAA0397  3'  TTGGTGGAGGCCAAGGACTCA  69287      AAAT
                                TTGGTG   CCAAGGATTTA
                                ||||||   ||||||||||
                                AACCAC   GGTTCCTGAGT
                                   CTCC
GAM3037  NTKL      3'  GTGAAATAGAATTTATT     69288       CCA
                                GTGAAAT   AGGATTTATT
                                |||||||  ||||||||||
                                CACTTTA   TCTTAAATAA
                                    ___
GAM3037  SNX10     3'  TTGGTAAAATTAAATTTATTA  69289        CCAA
                                TTGGTGAAAT   GGATTTATTA
                                ||||||||||   ||||||||||
                                AACCATTTTA   TTTAAATAAT
                                     A___
GAM3037  LOC124302 5'  TTAGTGGGATCCATTTCACTAT 69282      AA    AGGAT
            TA                   TTGGTG  ATCCA    TTATTA
                                ||||||  |||||    ||||||
                                AATCAC  TAGGT    GATAAT
                                   CC    AAAGT
GAM3037  LOC219894 3'  TTAGCACCTATCAGGGATTTAT 69290      AAATC  A
            TA                   TTGGTG    CA GGATTTATTA
                                ||||||    || ||||||||||
                                AATCGT    GT CCTAAATAAT
                                   GGATA  C
GAM3038  CD2AP     3'  TCACCCAAAATATAAACAGCA  69293       C   CTTGA
                                TCACCCAA ATA     AGCA
                                ||||||||  |||    ||||
                                AGTGGGTT TAT     TCGT
                                     T   ATTTG
GAM3038  HMGCR     3'  CACTCAACATATTTTTCAC    69294     C      C  GAAG
                                CAC CAACATA TT    CAC
                                |||  |||||||  ||    |||
                                GTG GTTGTAT AA    GTG
                                  A      A  AA__
GAM3038  HS2ST1    3'  CACCCAATATGTTTGAAG     69295       C  AC
                                CACCCAA AT  TTGAAG
                                |||||||  ||  ||||||
                                GTGGGTT TA  AACTTC
                                     A  CA
GAM3038  LANCL1    3'  CACTTGAACAGAATTTGAAGCA 69296     CC_   TAC_
            CCA                    CAC   AACA   TTGAAGCACCA
                                |||   ||||   ||||||||||
                                GTG   TTGT   AACTTCGTGGT
                                  AAC   CTTA
GAM3038  LHX4      3'  TCACCTTGTGCTACCAAAGCAC 69297      CAACA_   T
                                TCACC     TACT GAAGCAC
                                |||||     |||| |||||||
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                                AGTGG     ATGG TTTCGTG
                                  AACACG   _
GAM3038 MAGEA8   3' CACCCAACATGCTCCCCAC   69298          A   GAA
                                CACCCAACAT CTT   GC
                                |||||||||| |||   ||
                                GTGGGTTGTA GAG   TG
                                     C   GGG
GAM3038 NFYC     3' CACTCAACATATTGAAA     69299     C      C
                                CAC CAACATA TTGAAG
                                ||| ||||||| ||||||
                                GTG GTTGTAT AACTTT
                                  A      _
GAM3038 PLS3     3' CACTTAGCATACTTGGCCTACC 69300     CCAA       AA __
             A                   CAC   CATACTTG  GC  ACCA
                                |||   |||||||| ||  ||||
                                GTG   GTATGAAC  CG  TGGT
                                  AATC       __  GA
GAM3038 SLC38A2  3' TCACCCAATGTAGCAC      69301        CATACT  A
                                TCACCCAA     TG AGCAC
                                ||||||||     || |||||
                                AGTGGGTT     AC TCGTG
                                     _______ A
GAM3038 ST3GALVI 3' CATCCAACATATTTTAAAC   69302    C       C  G
                                CA CCAACATA TT AAGC
                                || |||||||| || ||||
                                GT GGTTGTAT AA TTTG
                                 A       A  A
GAM3038 SURF4    3' ACCCAATAAAACACTTGGCACC 69303       C___       AA
             A                   ACCCAA   ATACTTG  GCACCA
                                ||||||   |||||||  ||||||
                                TGGGTT   TGTGAAC  CGTGGT
                                   ATTT      __
GAM3038 BRAG     3' TCACTTAACATACCTTACAGGA 69304      CC       GA_  C
             C                   TCAC  AACATACTT   AG AC
                                ||||  |||||||||   || ||
                                AGTG  TTGTATGGA   TC TG
                                  AA        ATG  C
GAM3038 CL683    3' TCTCCCTTTGAAGCACC     69305    A   AACATAC
                                TC CCC      TTGAAGCACC
                                || |||      ||||||||||
                                AG GGG      AACTTCGTGG
                                 A  A_______
GAM3038 CLSTN3   3' TCCCCAACACAGTGAGTGC   69306    A       CT   A_
                                TC CCCAACATA  TGA  GC
                                || |||||||||  |||  ||
                                AG GGGTTGTGT  ACT  CG
                                 _       C_   CA
GAM3038 FLJ10432 3' CCACCTTCTCCTTGAAGCGCC 69307      CAACATA      A
                                TCACC      CTTGAAGC CC
                                |||||      |||||||| ||
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                                GGTGG      GAACTTCG GG
                                  AAGAG__       C
GAM3038  FLJ21168  3'  TCACTCACATAAAGCAC     69308      CCA    CTTG
                                TCAC   ACATA    AAGCAC
                                ||||   |||||    ||||||
                                AGTG   TGTAT    TTCGTG
                                  AG_    ____
GAM3038  GREB1     3'  TCAGCCAACATAAAGAGTGC   69309     C       CTT  A_
                                TCA CCAACATA   GA  GC
                                ||| ||||||||   ||  ||
                                AGT GGTTGTAT   CT  CG
                                  C       TT_  CA
GAM3038  KIAA0087  3'  TCACTAAACATACTGCTTAATA 69310      CC       TG__  GC
              CCA                  TCAC  AACATACT    AA  ACCA
                                ||||  ||||||||   ||  ||||
                                AGTG  TTGTATGA    TT  TGGT
                                  AT       CGAA  A_
GAM3038  KIAA0140  3'  TCACCCAACAACTGCCC     69311          T   TGAA  A
                                TCACCCAACA ACT    GC CC
                                |||||||||| |||    || ||
                                AGTGGGTTGT TGA    CG GG
                                     _  ____  _
GAM3038  KIAA0472  3'  TCACCCAAATACTTCGCA     69312         C     GAA
                                TCACCCAA ATACTT   GCA
                                |||||||| ||||||   |||
                                AGTGGGTT TATGAA   CGT
                                     _     G__
GAM3038  KIAA1210  3'  TCACCCAAGGAGAAAGCATCA  69313         CATACTT     C
                                TCACCCAA      GAAGCA CA
                                ||||||||      |||||| ||
                                AGTGGGTT      TTTCGT GT
                                     CCTC___      A
GAM3038  QKI       3'  CACCCAATATAATAAAGTAC   69314        C   CT    C
                                CACCCAA ATA  TGAAG AC
                                ||||||| |||  ||||| ||
                                GTGGGTT TAT  ATTTC TG
                                     A  T_    A
GAM3038  RBBP4     3'  TCACCCAAAATGGAGATGGCAT 69315         C  ACTT  A_   C
              CA                   TCACCCAA AT    GA  GCA CA
                                ||||||| ||    ||  ||| ||
                                AGTGGGTT TA    CT  CGT GT
                                     T  CCT_  AC   A
GAM3038  UST       3'  CCCAACATGTACTCACATCA   69316        __    GAA   C
                                CCCAACA  TACTT   GCA CA
                                |||||||  |||||   ||| ||
                                GGGTTGT  ATGAG   TGT GT
                                     AC     ___   A
GAM3038  LOC119548 3'  CACTCAACATACATTTGCATCA 69317     C       TTGAA   C
                                CAC CAACATAC     GCA CA
                                ||| ||||||||     ||| ||
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                                GTG GTTGTATG    CGT GT
                                  A       TAAA_  A
GAM3038  LOC124044 3'  TCCCCAGCAAAGAGAAGCACCA 69318    A    A  TACTT
                                TC CCCA CA    GAAGCACCA
                                || |||| ||    |||||||||
                                AG GGGT GT    CTTCGTGGT
                                 _    C  TTCT_
GAM3038  LOC148250 5'  TCCCCCAACTTTGAAGCAC   69319    A     ATAC
                                TC CCCAAC    TTGAAGCAC
                                || ||||||    |||||||||
                                AG GGGTTG    AACTTCGTG
                                 G     A___
GAM3038  LOC152274 3'  CCCAACATGTATAGAAGTGCCA 69320         ACTT_    CA
                                CCCAACAT    GAAG  CCA
                                ||||||||    ||||  |||
                                GGGTTGTA    CTTC  GGT
                                     CATAT    AC
GAM3038  LOC152627 5'  TCACCTGAATACTTAGAAGC   69321       CAAC     _
                                TCACC    ATACTT GAAGC
                                |||||    |||||| |||||
                                AGTGG    TATGAA CTTCG
                                   ACT_     T
GAM3038  LOC196264 3'  ACCTTCTCTCTTGAAGCACCA  69322     CAACATA
                                ACC      CTTGAAGCACCA
                                |||      ||||||||||||
                                TGG      GAACTTCGTGGT
                                  AAGAGA_
GAM3038  LOC257486 3'  TCACCCAAGGAGAAAGCATCA  69313         CATACTT     C
                                TCACCCAA      GAAGCA CA
                                ||||||||      |||||| ||
                                AGTGGGTT      TTTCGT GT
                                     CCTC___     A
GAM3038  LOC51696  3'  ACCTAAACATATTTGCAACAC  69323     C_     C   A
                                ACC  AACATA TTG AGCAC
                                |||  |||||| ||| |||||
                                TGG  TTGTAT AAC TTGTG
                                  AT     A   G
GAM3039  BNC       3'  TGTATCAGTGAAAGACCTCTTG 69326     T     ATT   A
                                TGT ATCGG   AAA ACCTCTTG
                                ||| |||||   ||| ||||||||
                                ACA TAGTC   TTT TGGAGAAC
                                  _    AC_   C
GAM3039  MGC2491   3'  TGTATCGGATCAGCTTCTT    69327     T       AAAACC
                                TGT ATCGGATTA     TCTT
                                ||| |||||||||     ||||
                                ACA TAGCCTAGT     AGAA
                                  _       CGA___
GAM3039  LOC154089 3'  TCACCAGAAACCTCTTG     69328         TTAAA
                                TTATCGGA    AACCTCTTG
                                ||||||||    |||||||||
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                                AGTGGTCT    TTGGAGAAC
                                      _____
GAM3040  PIK3R3   3'  TACTTTATTGCAATGTCTTTAT 69331        A    AA
                                TACTTTATT CGATG  TCTTTAT
                                ||||||||| |||||  |||||||
                                ATGAAATAA GTTAC  AGAAATA
                                    C    __
GAM3040  SPOCK    3'  TTATTACGATGTTCTTT     69332          AA
                                TTATTACGATG  TCTTT
                                ||||||||||  |||||
                                AATAATGCTAC  AGAAA
                                     A_
GAM3040  PTPNS1   3'  TTTATTACCCAGAAATCTTTAT 69333       GAT_
                                TTTATTAC    GAATCTTTAT
                                ||||||||    ||||||||||
                                AAATAATG    TTTAGAAATA
                                    GGTC
GAM3041  ARHGEF6  3'  TCTGTGACTGTCTTCTAAAC   69336          G   CG
                                TCTGTGACTGTCT CTG  GAC
                                |||||||||||| |||  |||
                                AGACACTGACAGA GAT  TTG
                                      A   __
GAM3041  CACNG3   5'  TGCCTTTTGCTGCGGGCAC    69337      ___      A
                                TGTCT   GCTGCGG CAC
                                |||||   ||||||| |||
                                ACGGA   CGACGCC GTG
                                   AAA      C
GAM3041  GGCX     3'  TCTGTGACTGGCTGCTTCTAC  69338         T    GCGG
                                TCTGTGACTG CTGCT    AC
                                |||||||||| |||||    ||
                                AGACACTGAC GACGA    TG
                                     C     AGA_
GAM3041  HPS4     5'  CTGTGGCTGTCTGCAGAAC    69339       A       TGC
                                CTGTG CTGTCTGC   GGAC
                                ||||| ||||||||   ||||
                                GACAC GACAGACG   CTTG
                                   C       T__
GAM3041  MS4A1    3'  TGTGACTGTGACTGTGTGG    69340         __  C  C
                                TGTGACTGT  CTG TG GG
                                |||||||||  ||| || ||
                                ACACTGACA  GAC AC CC
                                     CT   _  A
GAM3041  NONO     3'  CCTGTGACCTTTGTGGAC     69341         GTCTGC  C
                                TCTGTGACT     TG GGAC
                                |||||||||     || ||||
                                GGACACTGG     AC CCTG
                                     AA_____  A
GAM3041  ATPAF1   3'  TCTGTGACTGCTTGCGACAAGC 69342          TC   T   GA
              AC                  TCTGTGACTG  TGC GCG  CAC
                                ||||||||||  ||| |||  |||
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                                AGACACTGAC  ACG TGT  GTG
                                      GA   C   TC
GAM3041  CDKL2    5'  TGTGATTTCTTCTGCGGAC   69343      CTG   G
                                TGTGA   TCT CTGCGGAC
                                ||||||   ||| ||||||||
                                ACACT   AGA GACGCCTG
                                   AA_   A
GAM3041  DIM1     3'  CTGTGACTTTTGTGGACA    69344        GTCTGC  C
                                CTGTGACT     TG GGACA
                                ||||||||     || |||||
                                GACACTGA     AC CCTGT
                                     AA____  A
GAM3041  DKFZP434C1715 3'  TCTGAGAATGGCTGCGGACAC  69345     T  C  TCT
                                TCTG GA TG   GCTGCGGACAC
                                |||| || ||   ||||||||||
                                AGAC CT AC   CGACGCCTGTG
                                  T  T  ___
GAM3041  FYCO1    5'  TCGGTGGCTGTCTGCTCAG    69346    T   A       G
                                TC GTG CTGTCTGCT CGG
                                || ||| ||||||||| |||
                                AG CAC GACAGACGA GTC
                                 C   C       _
GAM3041  KIAA0417  3'  TCTGTGACTGTTTGGGAAGGA  69347          C  CTGC
                                TCTGTGACTGT TG    GGA
                                |||||||||| ||    |||
                                AGACACTGACA AC    CCT
                                       A  CCTT
GAM3041  KIAA0992  3'  TCTGTGACTGCTGATGC     69348          T   C
                                TCTGTGACTG CTG TGC
                                ||||||||| ||| |||
                                AGACACTGAC GAC ACG
                                      _   T
GAM3041  KIAA1766  3'  TCTGTGGCTGCTTTTGCGGCAC 69349       A   T  GC    A
                                TCTGTG CTG CT  TGCGG CAC
                                |||||| ||| ||  ||||| |||
                                AGACAC GAC GA  ACGCC GTG
                                   C   _  AA    _
GAM3041  LANCL2    3'  TGTGGCTGCTCTGCAGACAC   69350     A   T  G
                                TGTG CTG CT CTGCGGACAC
                                |||| ||| || ||||||||||
                                ACAC GAC GA GACGTCTGTG
                                  C   _ _
GAM3041  LIMK2     3'  TGTGACTGTTTGTTTCAGAC   69351         C  CTG
                                TGTGACTGT TG   CGGAC
                                |||||||| ||   |||||
                                ACACTGACA AC   GTCTG
                                      A  AAA
GAM3041  LIMK2     3'  TGTGACTGTTTGTTTCAGAC   69351         C  CTG
                                TGTGACTGT TG   CGGAC
                                |||||||| ||   |||||
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                                ACACTGACA AC   GTCTG
                                     A  AAA
GAM3041  PPI5PIV   3'  TCTGTGACTGCCCCCAGGGCAC 69352          G   C  A
                                TCTGTGACTGTCT CTG GG CAC
                                |||||||||||| ||| || |||
                                AGACACTGACGGG GGT CC GTG
                                       _   C  _
GAM3041  RENT2     3'  TCTGTGACATGTTGACGGGCA  69353        _  C  CT    A
                                TCTGTGAC TGT TG  GCGG CA
                                |||||||| ||| ||  |||| ||
                                AGACACTG ACA AC  TGCC GT
                                     T   _  __    C
GAM3041  RENT2     3'  TCTGTGACATGTTGACGGGCA  69353        _  C  CT    A
                                TCTGTGAC TGT TG  GCGG CA
                                |||||||| ||| ||  |||| ||
                                AGACACTG ACA AC  TGCC GT
                                     T   _  __    C
GAM3041  LOC146455 3'  CCTGTGACCTTTGTGGAC    69341         GTCTGC  C
                                TCTGTGACT     TG GGAC
                                |||||||||     || ||||
                                GGACACTGG     AC CCTG
                                     AA_____  A
GAM3041  LOC150208 5'  TGTGTGTTGTCTGCTACA    69354      AC_
                                TGTG   TGTCTGCTGCG
                                ||||   ||||||||||
                                ACAC   ACAGACGATGT
                                  ACA
GAM3041  LOC151414 3'  TCTGTGACTATTTAAGGACA   69355          C  CTGC
                                TCTGTGACTGT TG    GGACA
                                |||||||||| ||    |||||
                                AGACACTGATA AT    CCTGT
                                      A  T____
GAM3041  LOC158125 5'  TGGTTGCCTGCTGTGGGCA    69356    AC       C  A
                                TG  TGTCTGCTG GG CA
                                ||  ||||||||| || ||
                                AC  ACGGACGAC CC GT
                                 CA        A  C
GAM3041  LOC158279 5'  TCTGTGACTGTCTCTGGC     69357           G  _
                                TCTGTGACTGTCT CTG C
                                |||||||||||| ||| |
                                AGACACTGACAGA GAC G
                                       _   C
GAM3041  LOC169021 5'  CTGTGATTGTCTGCTGAC     69358       C       _
                                CTGTGA TGTCTGCTG C
                                |||||| ||||||||| |
                                GACACT ACAGACGAC G
                                   A        T
GAM3041  LOC220864 5'  TCTGTGACTGTCTCTGGC     69357           G  _
                                TCTGTGACTGTCT CTG C
                                |||||||||||| ||| |
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                                AGACACTGACAGA GAC G
                                       _  C
GAM3041  LOC254381 5'  CGTGACTGTCTGCTTGAGA   69359          GC
                                TGTGACTGTCTGCT  GGA
                                ||||||||||||||  |||
                                GCACTGACAGACGA  TCT
                                       AC
GAM3041  LOC91050  3'  TCTGTGACTGCTGGTCTGTGC  69360        ____  C
                                TCTGTGACTGT   CTG TGC
                                ||||||||||    ||| |||
                                AGACACTGACG   GAC ACG
                                      ACCA  _
GAM3042  TBX2      3'  CCGTTGACCACGGCTGGGA   69363    C     AC  GC_
                                TCG TGACCACG  GC   GA
                                ||| ||||||||  ||   ||
                                GGC ACTGGTGC  CG   CT
                                  A       __ ACC
GAM3042  ZNF268    5'  CCGTTGACCACGACGGGCG   69364    C       C
                                TCG TGACCACGACG GCG
                                ||| ||||||||||| |||
                                GGC ACTGGTGCTGC CGC
                                  A         C
GAM3042  FLJ23816  3'  TCGCTGACGCACGGGGCG    69365       _   AC
                                TCGCTGAC CACG  GCG
                                ||||||||  ||||  |||
                                AGCGACTG GTGC  CGC
                                     C    CC
GAM3043  BRCA1     3'  CCTGGAAAGGCCACTTTG    69368        __
                                CTTGGAAAGG  ATTTTG
                                ||||||||||  ||||||
                                GGACCTTTCC  TGAAAC
                                      GG
GAM3043  BRCA1     3'  CCTGGAAAGGCCACTTTG    69368        __
                                CTTGGAAAGG  ATTTTG
                                ||||||||||  ||||||
                                GGACCTTTCC  TGAAAC
                                      GG
GAM3043  BRCA1     3'  CCTGGAAAGGCCACTTTG    69368        __
                                CTTGGAAAGG  ATTTTG
                                ||||||||||  ||||||
                                GGACCTTTCC  TGAAAC
                                      GG
GAM3043  BRCA1     3'  CCTGGAAAGGCCACTTTG    69368        __
                                CTTGGAAAGG  ATTTTG
                                ||||||||||  ||||||
                                GGACCTTTCC  TGAAAC
                                      GG
GAM3043  BRCA1     3'  CCTGGAAAGGCCACTTTG    69368        __
                                CTTGGAAAGG  ATTTTG
                                ||||||||||  ||||||
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                                GGACCTTTCC  TGAAAC
                                      GG
GAM3043  BRCA1    3'  CCTGGAAAGGCCACTTTG    69368          __
                                CTTGGAAAGG  ATTTTG
                                ||||||||||  ||||||
                                GGACCTTTCC  TGAAAC
                                      GG
GAM3043  BRCA1    3'  CCTGGAAAGGCCACTTTG    69368          __
                                CTTGGAAAGG  ATTTTG
                                ||||||||||  ||||||
                                GGACCTTTCC  TGAAAC
                                      GG
GAM3043  BRCA1    3'  CCTGGAAAGGCCACTTTG    69368          __
                                CTTGGAAAGG  ATTTTG
                                ||||||||||  ||||||
                                GGACCTTTCC  TGAAAC
                                      GG
GAM3043  BRCA1    3'  CCTGGAAAGGCCACTTTG    69368          __
                                CTTGGAAAGG  ATTTTG
                                ||||||||||  ||||||
                                GGACCTTTCC  TGAAAC
                                      GG
GAM3043  BRCA1    3'  CCTGGAAAGGCCACTTTG    69368          __
                                CTTGGAAAGG  ATTTTG
                                ||||||||||  ||||||
                                GGACCTTTCC  TGAAAC
                                      GG
GAM3043  BRCA1    3'  CCTGGAAAGGCCACTTTG    69368          __
                                CTTGGAAAGG  ATTTTG
                                ||||||||||  ||||||
                                GGACCTTTCC  TGAAAC
                                      GG
GAM3043  CPNE3    3'  TTGGAAAGATTGCCTAA     69369         ATT    A
                                TTGGAAAGG   TTGCT TAA
                                |||||||||   ||||| |||
                                AACCTTTCT   AACGG ATT
                                    ____    _
GAM3043  EDNRA    3'  TTGGAAAGCATTTCTTCT    69370         G    G_
                                TTGGAAAG ATTTT  CT
                                ||||||| |||||  ||
                                AACCTTTC TAAAG  GA
                                     G    AA
GAM3043  GRB10    3'  CTTGAAAAGGGTTTACC     69371          AT
                                CTTGGAAAGG  TTTGCT
                                ||||||||||  ||||||
                                GAACTTTTCC  AAATGG
                                      C_
GAM3043  OGT      5'  TGGGAAGTCAGTTGCTATAAG 69372     A   GATT
                                TGG AAG    TTGCTATAAG
                                |||  |||    ||||||||||
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                                ACC TTC    AACGATATTC
                                  C   AGTC
GAM3043  TH1L     3'  CTTGGAAAGGAGTTCCCC    69373          T   G
                                CTTGGAAAGGA TTT CT
                                |||||||||| ||| ||
                                GAACCTTTCCT AAG GG
                                      C   G
GAM3043  WHSC1    3'  TTGGAGAGACACCCTGCTGTAA 69374      A  _      A
           G                     TTGGA AGG ATTTTGCT TAAG
                                ||||| ||| |||||||| ||||
                                AACCT TCT TGGGACGA ATTC
                                   C  G       C
GAM3043  C20orf70 3'  CCTGGAGGGAGATGCTATAAG  69375      AA   TTT
                                CTTGGA  GGA   TGCTATAAG
                                ||||||  |||   |||||||||
                                GGACCT  CCT   ACGATATTC
                                   C_   CT_
GAM3043  FLJ10546 5'  TTGGGAACAGTTGCTATA    69376     AAA   T_
                                TTGG   GGAT  TTGCTATA
                                ||||   ||||  ||||||||
                                AACC   CTTG  AACGATAT
                                  ___    TC
GAM3043  FLJ20331 3'  TTGAAAAAACTGCTTGCTATAA 69377         AT_
           G                     TTGGAAAGG   TTTGCTATAAG
                                |||||||||   ||||||||||
                                AACTTTTTT   GAACGATATTC
                                     GAC
GAM3043  FLJ23441 3'  GAGAGTCCCCTTGCTATAAG   69378    A  GA_
                                GA AG   TTTTGCTATAAG
                                || ||   ||||||||||||
                                CT TC   GGAACGATATTC
                                 C  AGG
GAM3043  FLJ25473 5'  CTCGGAAAGGGCTGTAA     69379         ATTTT   A
                                CTTGGAAAGG    GCT TAA
                                ||||||||||    ||| |||
                                GAGCCTTTCC    CGA ATT
                                      _____  C
GAM3043  KIAA0472 3'  CTGGAAAGGGAACTATA     69380         ATTTT
                                TTGGAAAGG    GCTATA
                                |||||||||    ||||||
                                GACCTTTCC    TGATAT
                                     CT___
GAM3043  KIAA1018 3'  CCTGGAGGCCTGCTAT      69381       AA  AT
                                CTTGGA  GG  TTTGCTAT
                                ||||||  ||  ||||||||
                                GGACCT  CC  GGACGATA
                                  __  __
GAM3043  KIAA1634 3'  CTGGAAAAATGCTGCTGTAAG  69382         G  T    A
                                TTGGAAAG AT TTGCT TAAG
                                |||||||| || ||||| ||||
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                                GACCTTTT TA GACGA ATTC
                                    _ C    C
GAM3043 KPNB3    3' CTTGGAAAGGTTTTTCCA    69383        A   G
                                CTTGGAAAGG TTTT CTA
                                |||||||||| |||| |||
                                GAACCTTTCC AAAA GGT
                                     A   _
GAM3043 RAB33B   3' TTGGAAGTGATTTTGCAACA  69384      AG      T
                                TTGGAA  GATTTTGC ATA
                                ||||||  |||||||| |||
                                AACCTT  CTAAAACG TGT
                                   CA       T
GAM3043 LOC150606 3' CTTGGAGGTTGCTATA     69385      AA  ATT
                                CTTGGA  GG   TTGCTATA
                                ||||||  ||   ||||||||
                                GAACCT  CC   AACGATAT
                                  __  ___
GAM3043 LOC158332 3' TTGGAATCTCGGGTTTTGCT  69386      A___  A
                                TTGGAA   GG TTTTGCT
                                ||||||   || |||||||
                                AACCTT   CC AAAACGA
                                   AGAG  C
GAM3043 LOC167147 5' CCTGGGGGATGCTATAA    69387     AAA   TTT
                                CTTGG   GGA   TGCTATAA
                                |||||   |||   ||||||||
                                GGACC   CCT   ACGATATT
                                  C__   ___
GAM3044 A1BG     3' CCATTTCCACAGCGTCCAG   69390        ACC  AA
                                CCATTTCCACA   GC  CCGG
                                ||||||||||   ||  ||||
                                GGTAAAGGTGT   CG  GGTC
                                      ___  CA
GAM3044 CTNNB1   3' AACCATTTTTTATAACCGCA  69391       CCAC_
                                AACCATTT    AACCGCA
                                ||||||||    |||||||
                                TTGGTAAA    TTGGCGT
                                     AAATA
GAM3044 IL1R1    3' AACCAGTTTTAACAACCG    69392      _  CC
                                AACCA TTT  ACAACCG
                                ||||| |||  |||||||
                                TTGGT AAA  TGTTGGC
                                  C   AT
GAM3044 LARS2    3' CCATTTCCACATATTGGCCGGT 69393       A_________  CAAC
           TGCG                   ATTTCCACA       CCG   CG
                                |||||||||       |||   ||
                                TAAAGGTGT       GGC   GC
                                     ATAACCIII  CAAC
GAM3044 MAP3K12  3' CATTTCCACAGCTGCCAG    69394        ACC  AA
                                CATTTCCACA   GC  CCGG
                                ||||||||||   ||  ||||
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                                GTAAAGGTGT   CG  GGTC
                                     ___  AC
GAM3044  SLC7A6   3'  CCATTCTCATACAGCAACCGG  69395      TC  CA  C
                                CCATT  CA  AC GCAACCGG
                                |||||  ||  || ||||||||
                                GGTAA  GT  TG CGTTGGCC
                                   GA  A_  T
GAM3044  FLJ14855 3'  ACCACTTCCACAGGTTGGCCGG 69396        AC_________  CAAC
           TTGCG                  ATTTCCACA        CG   CG
                                |||||||||        ||   ||
                                TGAAGGTGT        GC   GC
                                     CCAACCIIIG  CAAC
GAM3044  FLJ22329 3'  AACCATTCTTCAACCCAACTGG 69397        CCA    G   C
                                AACCATTT   CAACC CAAC GG
                                ||||||||   ||||| |||| ||
                                TTGGTAAG   GTTGG GTTG CC
                                     AA_    _   A
GAM3044  GMPPB    3'  CCACTTCCACAGCTGTGCCGGT 69398        AC_________  CAAC
           TGCG                   ATTTCCACA        CG   CG
                                |||||||||        ||   ||
                                TGAAGGTGT        GC   GC
                                     CGACACIIIG  CAAC
GAM3044  HTATIP2  3'  AACCATTTCTCCAGTGTGGCCG 69399      CA  AC_________  CAAC
           GTTGCG                 ATTTC  CA        CG   CG
                                |||||  ||        ||   ||
                                TAAAG  GT        GC   GC
                                   AG  CACACCIIIG  CAAC
GAM3044  PPFIA2   5'  ACCATTTCCCTGCTGGCAGCCG 69400        ACAACC   A
           G                    ACCATTTCC     GCA CCGG
                                |||||||||     ||| ||||
                                TGGTAAAGG     CGT GGCC
                                     GACGAC   C
GAM3044  SAMSN1   3'  CATTTCCACAATTATTACAATT 69401         CC___   CC
           GG                     CATTTCCACAA    GCAA  GG
                                ||||||||||    ||||  ||
                                GTAAAGGTGTT    TGTT  CC
                                      AATAA    AA
GAM3044  TU3A     5'  CCACTTCCACGATGCGGCCGGT 69402        AA_________  CAAC
           TGCG                   ATTTCCAC        CCG   CG
                                |||||||         |||   ||
                                TGAAGGTG        GGC   GC
                                     CTACGCCIII  CAAC
GAM3044  LOC123792 3'  CCATCTCCTGCGTGCGCAGCCG 69403        ACAAC_   A
           G                    CCATTTCC     CGCA CCGG
                                ||||||||     |||| ||||
                                GGTAGAGG     GCGT GGCC
                                     ACGCAC   C
GAM3044  LOC150819 3'  AACTGTTTCCACAGCCAGC   69404     CA       A  _
                                AAC  TTTCCACA CC GC
                                |||  |||||||| || ||
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                                TTG  AAAGGTGT GG CG
                                  AC       C  T
GAM3044  LOC254100 5'  CCACTTCCAGGTCTTGCGACCG 69405         CAACC_  A
             G                    CCATTTCCA     GC ACCGG
                                  |||||||||     || |||||
                                  GGTGAAGGT     CG TGGCC
                                       CCAGAA  C
GAM3044  LOC90322  3'  ACCATTTCCACATGCCCTTGG  69406          ACC  AACC
                                  ACCATTTCCACA   GC    GG
                                  ||||||||||||   ||    ||
                                  TGGTAAAGGTGT   CG    CC
                                         A__  GGAA
GAM3045  OCLN      5'  TCCCTGACCACCCCGGGGTGCG 69409        GA G_________   GAA
             CTTCGC                   TGACCAC  C        CGC   GC
                                  |||||||  |        |||   ||
                                  ACTGGTG  G        GCG   CG
                                      GG CCCCACIII   AAG
GAM3045  ZNF268    5'  CCGTTGACCACGACGGGCG    69364     C         C
                                  TCG TGACCACGACG GCG
                                  ||| ||||||||||| |||
                                  GGC ACTGGTGCTGC CGC
                                    A         C
GAM3045  FLJ23816  3'  TCGCTGACGCACGGGGCG     69365         _    AC
                                  TCGCTGAC CACG  GCG
                                  |||||||| ||||  |||
                                  AGCGACTG GTGC  CGC
                                       C    CC
GAM3045  LOC115708 3'  TCGCTGACCATATAAGGTGCGC 69410      CGA__________   GCGAA
             TTCGCGC                  GACCA          CGC     GC
                                  |||||          |||     ||
                                  CTGGT          GCG     CG
                                     ATATTCCACIII   AAGCG
GAM3045  LOC222070 5'  TCCCTGACCACATGAGTGAAG  69411    G        ACGCGC
                                  TC CTGACCACG     GAAG
                                  || |||||||||     ||||
                                  AG GACTGGTGT     CTTC
                                   G        ACTCA_
GAM3046  ABCA4     3'  GATGGCCCGGGGTTTC      69414          TAGCTT
                                  GATGGCCCGGG     GTTTC
                                  ||||||||||      |||||
                                  CTACCGGGCCC     CAAAG
                                                  _____
GAM3046  COL4A6    5'  GATGCTTGGAGGCTGTTTCC   69415     G CCG  TA   T
                                  GATG C   GG  GCT GTTTCC
                                  |||| |   ||  ||| ||||||
                                  CTAC G   CC  CGA CAAAGG
                                    _ AA_  TC   _
GAM3046  COX6A1    3'  GCCCGGGTAGTGGTCC      69416          CT  TT
                                  GCCCGGGTAG  TG  TCC
                                  ||||||||||  ||  |||
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                                CGGGCCCATC  AC  AGG
                                      __  C_
GAM3046  GPR81    3'  TGGCCTGGAATGTTTCC     69417      C   TAGCT
                                TGGCC GGG    TGTTTCC
                                ||||| |||    |||||||
                                ACCGG CCT    ACAAAGG
                                   A  T____
GAM3046  LFG      5'  GGCCCGGGTGGCCGCTT     69418        A   T
                                GGCCCGGGT GCT GTTT
                                ||||||||| ||| ||||
                                CCGGGCCCA CGG CGAA
                                      C  _
GAM3046  LILRB4   3'  TGGTCCGGGCAAGGTTT     69419     C      CTT
                                TGG CCGGGTAG   GTTT
                                ||| ||||||||   ||||
                                ACC GGCCCGTT   CAAA
                                  A       C__
GAM3046  MSF      3'  GAGGCCCCTTCCCTTGTTTCC  69420    T    GGGTAG
                                GA GGCCC     CTTGTTTCC
                                || |||||     |||||||||
                                CT CCGGG     GAACAAAGG
                                 _    GAAGG_
GAM3046  C4orf6   5'  GAGGCTGGCAGGGCTTGTTT   69421    T  C__   TA
                                GA GGC   CGGG  GCTTGTTT
                                || |||   ||||  ||||||||
                                CT CCG   GTCC  CGAACAAA
                                 _  ACC   __
GAM3046  FLJ10546 5'  GATGCTTAACTGCTTGTTTTCC 69422      G CCG  TA      _
                                GATG C   GG  GCTTGTTT CC
                                |||| |   ||  |||||||| ||
                                CTAC G   TT  CGAACAAA GG
                                  _ AA_  GA       A
GAM3046  FLJ32734 5'  TGGCTGCACTCTTGTTTC    69423     CCGG   G_
                                TGGC   GTA  CTTGTTTC
                                ||||   |||  ||||||||
                                ACCG   CGT  GAACAAAG
                                  A___   GA
GAM3046  HSPB7    3'  TGGCTCGGGGATGTTTCCC   69424     C   TAGCT
                                TGGC CGGG    TGTTTCCC
                                |||| ||||    ||||||||
                                ACCG GCCC    ACAAAGGG
                                  A   CT___
GAM3046  KIAA0319 3'  TGGCCCGGGTGTGATCC     69425        AGCT  TT
                                TGGCCCGGGT   TG  TCC
                                ||||||||||   ||  |||
                                ACCGGGCCCA   AC  AGG
                                      C___  T_
GAM3046  ORCTL4   3'  GATGGTCTGGGGGCCTGGCCC  69426      CCC   TA    TTT
                                GATGG   GGG  GCTTG   CCC
                                |||||   |||  |||||   |||
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                                CTACC  CCC  CGGAC  GGG
                                  AGA  C_   C__
GAM3046  POPX1    3'  TGACCTGAAGTTTGTTTCCC  69427     CG  T  C
                                TGGCC  GG AG TTGTTTCCC
                                |||||  || || |||||||||
                                ACTGG  CT TC AACAAAGGG
                                  A_  _  A
GAM3046  RNF36    5'  GCAGATGTAGCTTGTTTTCC  69428   CCGG       _
                                GC   GTAGCTTGTTT CC
                                ||   |||||||||| ||
                                CG   CATCGAACAAA GG
                                 TCTA        A
GAM3046  TTTY9    5'  GATGCCCGGGCACGTTTCC   69429    G      GCT
                                GATG CCCGGGTA  TGTTTCC
                                |||| ||||||||  |||||||
                                CTAC GGGCCCGT  GCAAAGG
                                  _     ___
GAM3046  LOC145988 5'  GATGTTCCACTTGTTTC    69430    GC  GGGTA
                                GATG  CC   GCTTGTTTC
                                ||||  ||   |||||||||
                                CTAC  GG   TGAACAAAG
                                  AA  _____
GAM3046  LOC148343 5'  GATGCCTGGGTGACTTGTTTC  69431    G  C   AG
                                GATG CC GGGT  CTTGTTTC
                                |||| || ||||  ||||||||
                                CTAC GG CCCA  GAACAAAG
                                  _ A   CT
GAM3046  LOC149134 5'  TGGCTTCAGGTTTGTTTCC   69432    C_   AGC
                                TGGC  CGGGT   TTGTTTCC
                                ||||  |||||   ||||||||
                                ACCG  GTCCA   AACAAAGG
                                  AA   ___
GAM3046  LOC149319 5'  GACGGTCCGCTTGTTTTCC   69433     C  GGGTA     _
                                GATGG CC    GCTTGTTT CC
                                |||||  ||   |||||||| ||
                                CTGCC GG    CGAACAAA GG
                                  A  _____      A
GAM3046  LOC163833 5'  GATGGAGATGGCTTGTTTC   69434     CCC   A
                                GATGG  GGGT GCTTGTTTC
                                |||||  |||| |||||||||
                                CTACC  TCTA CGAACAAAG
                                  ___   C
GAM3046  LOC254936 5'  GATGTTCCACTTGTTTC    69430    GC  GGGTA
                                GATG  CC   GCTTGTTTC
                                ||||  ||   |||||||||
                                CTAC  GG   TGAACAAAG
                                  AA  _____
GAM3046  LOC257302 5'  GATGTTCCACTTGTTTC    69430    GC  GGGTA
                                GATG  CC   GCTTGTTTC
                                ||||  ||   |||||||||
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                                CTAC  GG    TGAACAAAG
                                  AA  _____
GAM3046 LOC85415 3' GGCCTGAACATGTTTGTTTCC  69435     C GG  GC_
                                GGCC G  TA   TTGTTTCC
                                |||| |  ||   ||||||||
                                CCGG C  GT   AACAAAGG
                                  A TT  ACA
GAM3046 LOC91689 3' GATAGCCTGGGCCTATGTTTC  69436       C   AGCT
                                GATGGCC GGGT   TGTTTC
                                ||||||| ||||   ||||||
                                CTATCGG CCCG   ACAAAG
                                   A   GAT_
GAM3046 LOC92822 3' TGGCCCAGGTGGTGGTTCC   69437        AGCT  T
                                TGGCCCGGGT   TG TTCC
                                ||||||||||   || ||||
                                ACCGGGTCCA   AC AAGG
                                      CC__  C
GAM3047 ADCY7    3' ATCCTTCTAGTTTTGAAG    69440      TAGGG
                                ATCCT    TTTAGTTTTGAAG
                                |||||    ||||||||||||||
                                TAGGA    AGATCAAAACTTC
                                  _____
GAM3047 ASH1     3' CTCTGGGGTAGCTCTTGGAGC  69441     A  TT     GA_
                                CTT GGG  TAGTTTT   AGC
                                ||| |||  |||||||   |||
                                GAG CCC  ATCGAGA   TCG
                                  A  C_     ACC
GAM3047 CENTD1   3' CTTATAGTTCAGTTTTGGAG   69442     G         A
                                CTTA GGTTTAGTTTTG AG
                                |||| |||||||||||| ||
                                GAAT TCAAGTCAAAAC TC
                                  A         C
GAM3047 CENTD1   3' CTTATAGTTCAGTTTTGGAG   69442     G         A
                                CTTA GGTTTAGTTTTG AG
                                |||| |||||||||||| ||
                                GAAT TCAAGTCAAAAC TC
                                  A         C
GAM3047 DGCR6    3' ATCCTAGGGTTTGACAGC    69443      T    ___
                                ATCCT AGGGTT   TAGT
                                ||||| ||||||   ||||
                                TAGGA TCCCAA   GTCG
                                  _     ACT
GAM3047 IRS1     3' TCCTTAAGGTTGAAGATGAAG 69444         TAGTTT
                                TCCTTAGGGTT     TGAAG
                                ||||||||||      |||||
                                AGGAATTCCAA     ACTTC
                                      CTTCT_
GAM3047 PCYT1A   3' TCCTTAGGTTTAGTGTTG    69445       G     T
                                TCCTTAGG TTTAGT TTG
                                |||||||| |||||| |||
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                                AGGAATCC AAATCA AAC
                                   _     C
GAM3047 SDC2     3' CTTTGGGTTTGCTGAG     69446     A     A TT   A
                                CTT GGGTTT GT  TGA G
                                ||| |||||| ||  ||| |
                                GAA CCCAAA CG  ACT C
                                  A     _ __   C
GAM3047 SECTM1   3' CCTTAGGGACGTTTTGGGGC  69447        TTTA     AA
                                CCTTAGGG   GTTTTG  GC
                                ||||||||   ||||||  ||
                                GGAATCCC   CAAAAC  CG
                                     TG__     CC
GAM3047 DGCR6L   3' ATCCTAGGGTTTGACAGC    69443      T     ___
                                ATCCT AGGGTT   TAGT
                                ||||| ||||||   ||||
                                TAGGA TCCCAA   GTCG
                                   _     ACT
GAM3047 FLJ14824 3' CTTAAAAGTTTTGAAG      69448       GTTT
                                CTTAGG   AGTTTTGAAG
                                ||||||   ||||||||||
                                GAATTT   TCAAAACTTC
                                   _____
GAM3047 MGC16063 5' CTTAAGGGTTTGACCTGAAGC 69449     _     AGT
                                CTTA GGGTTT   TTTGAAGC
                                |||| ||||||   ||||||||
                                GAAT CCCAAA   GGACTTCG
                                  T     CT_
GAM3047 MISS     3' TCCTAGGGTTTATCTAGTTTGA 69450     T      GT___
                                TCCT AGGGTTTA     TTTGA
                                |||| ||||||||     |||||
                                AGGA TCCCAAAT     AAACT
                                   _       AGATC
GAM3047 OSBPL3   3' CCTTGGGGTGCTTTGGGGC   69451     A   TTA     AA
                                CCTT GGGT   GTTTTG  GC
                                |||| ||||   ||||||  ||
                                GGAA CCCA   CGAAAC  CG
                                  C    ___      CC
GAM3047 TOMM70A  3' TCTTTAGGGTTCAGTTGAAG  69452    C         TT
                                TC TTAGGGTTTAGT  TGAAG
                                || ||||||||||||  |||||
                                AG AATCCCAAGTCA  ACTTC
                                 A          __
GAM3047 LOC254170 3' ATCCTTAAGGTTTGGTAACAA  69453           A  TT
                                ATCCTTAGGGTTT GT  TGA
                                |||||||||||| ||  |||
                                TAGGAATTCCAAA CA  GTT
                                        C  TT
GAM3047 LOC90620 3' CTCAGGGTTTAGCTCAGA    69454             T
                                CTTAGGGTTTAGTTT GA
                                |||||||||||||| ||
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                                GAGTCCCAAATCGAG CT
                                        T
GAM3048 ERBB2IP  5' TTGGTGGGGGTTGGGGT    69457      T  T
                                TTGGT GGG GGTTGGGGT
                                ||||| ||| |||||||||
                                AACCA CCC CCAACCCCA
                                  _  _
GAM3048 TSPEAR   3' TTGGTTGAGTGAATTGGGGTG 69458          _
                                TTGGTTGGGTGG TTGGGGTG
                                |||||||||||| ||||||||
                                AACCAACTCACT AACCCCAC
                                        T
GAM3048 LOC221479 3' GTTGGTTGGCGAAGGGGGTG  69459        G  TT
                                GTTGGTTGG TGG  GGGGTG
                                ||||||||| |||  ||||||
                                CAACCAACC GCT  CCCCAC
                                     _  TC
GAM3049 ADORA2A  3' TGGTGTGTGGGTGGC      69462          GAGTGAT
                                TGGTGTGTGGGT     GGC
                                ||||||||||||      |||
                                ACCACACACCCA     CCG
                                          _______
GAM3049 BAZ1B    3' TGGTATGTGGGTGGGCTGG   69463          A  GA
                                TGGTGTGTGGGTG GT  TGG
                                |||||||||||| ||  |||
                                ACCATACACCCAC CG  ACC
                                        C  __
GAM3049 CSRP1    3' GGTGTGGTGGGTGATGGTGG  69464      _     G  A
                                GGTGTG TGGGTGA TG TGG
                                |||||| ||||||| || |||
                                CCACAC ACCCACT AC ACC
                                   C      _ C
GAM3049 EFNB1    3' GTGTGTGGAAGGGTGGCA    69465       GT   TGA
                                GTGTGTGG  GAG   TGGCA
                                ||||||||  |||   |||||
                                CACACACC  TTC   ACCGT
                                     __  CC_
GAM3049 HS3ST4   3' GTGTGTGGGTGGGTGTG     69466         A  A
                                GTGTGTGGGTG GTG TG
                                |||||||||||| ||| ||
                                CACACACCCAC CAC AC
                                       C  _
GAM3049 LGMN     5' TGGTGGCAGTGGTGGC      69467      T  GGGTG   A
                                TGGTG GT    AGTG TGGC
                                ||||| ||    |||| ||||
                                ACCAC CG    TCAC ACCG
                                  _ _____   C
GAM3049 MAPK4    3' TGGTGTGAGGGTGAACGCA   69468       T     TGATG
                                TGGTGTG GGGTGAG    GCA
                                |||||||| |||||||    |||
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                                ACCACAC CCCACTT    CGT
                                   T     G____
GAM3049 MNT     3' TGGTGTGTGTGTGTCCAGGTGG 69469        G  AGTGA_
                                TGGTGTGTG GTG     TGG
                                ||||||||| |||     |||
                                ACCACACAC CAC     ACC
                                    A  AGGTCC
GAM3049 POU2AF1  5' GTGTGTGGGTGTGAAGG    69470        GA   T
                                GTGTGTGGGT  GTGA GG
                                ||||||||||  |||| ||
                                CACACACCCA  CACT CC
                                     __   T
GAM3049 RAD18    3' TGATGTGTTTGGGCTGGGTGAT 69471        __   GA_
           GGCAG                  TGGTGTGT  GGGT  GTGATGGCAG
                                |||||||  ||||  ||||||||||
                                ACTACACA  CCCG  CACTACCGTC
                                    AA   ACC
GAM3049 SH3GL1   3' TGGGTGTGGGTGGCTGGTGG  69472    T      AG  A
                                TGG GTGTGGGTG  TG TGG
                                ||| |||||||||  || |||
                                ACC CACACCCAC  AC ACC
                                  _       CG  C
GAM3049 SH3GL1   3' TGGGTGGCTGGTGGTGGCA   69473    TGT   G  A  A
                                TGG   GTGG TG GTG TGGCA
                                |||   |||| || ||| |||||
                                ACC   CACC AC CAC ACCGT
                                  ____   G  _  C
GAM3049 SLC1A4   3' TGGTTTTCTCTGGGGTGGTGGT 69474     GTGT____    A  A
           GG                    TGGT      GGGTG GTG TGG
                                ||||       ||||| ||| |||
                                ACCA       CCCAC CAC ACC
                                  AAAGAGAC    _  C
GAM3049 CAPN6    3' TGGTGGTGAGTGGTGGTGG   69475     T     A  A
                                TGGTG GTGGGTG GTG TGG
                                ||||| ||||||| ||| |||
                                ACCAC CACTCAC CAC ACC
                                  _      _  C
GAM3049 CAPN6    3' TGGTGGTGGTGGTGGTGG    69476     T   G  A  A
                                TGGTG GTGG TG GTG TGG
                                ||||| |||| || ||| |||
                                ACCAC CACC AC CAC ACC
                                  _   _ _  C
GAM3049 CAPN6    3' TGGTGAGTGGTGGTGGTGG   69477     T   G  A  A
                                TGGTG GTGG TG GTG TGG
                                ||||| |||| || ||| |||
                                ACCAC CACC AC CAC ACC
                                  T   _ _  C
GAM3049 DKFZp761O17121 5' TGGTGAGTGGGTGGCAGTAG  69478     T     A  GA
                                TGGTG GTGGGTG GT  TGG
                                ||||| ||||||| ||  |||
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                                ACCAC CACCCAC CG  ATC
                                  T      _ TC
GAM3049  FLJ12595  3'  GTGAGTGGGTGGTGGTGG    69479     T      A   A
                                GTG GTGGGTG GTG TGG
                                ||| ||||||| ||| |||
                                CAC CACCCAC CAC ACC
                                  T      _  C
GAM3049  FLJ20257  5'  GGCAGTGGGTGGTGGTGG    69482     T      A   A
                                GGTG GTGGGTG GTG TGG
                                |||| ||||||| ||| |||
                                CCGT CACCCAC CAC ACC
                                  _      _  C
GAM3049  FLJ20257  5'  TGGGTGGTGGTGGTGGTGG   69481     T   TG    A   A
                                TGG GTG  GGTG GTG TGG
                                ||| |||  |||| ||| |||
                                ACC CAC  CCAC CAC ACC
                                  _  CA   _  C
GAM3049  FLJ20257  5'  TGGTGGTGGTGGTGGCGG    69480      T   G  A   A
                                TGGTG GTGG TG GTG TGG
                                ||||| |||| || ||| |||
                                ACCAC CACC AC CAC GCC
                                  _   _ _  C
GAM3049  FYCO1     3'  TGGTGTGTGGTGGGTTTGG   69483         G  A  GA
                                TGGTGTGTGG TG GT  TGG
                                |||||||||| || ||  |||
                                ACCACACACC AC CA  ACC
                                      _ C  A_
GAM3049  HYPC      5'  TGTGTGAGTGGTGGTGG     69484         A   A
                                TGTGTGGGTG GTG TGG
                                |||||||||| ||| |||
                                ACACACTCAC CAC ACC
                                      _  C
GAM3049  KIAA0987  3'  TGATGTGGGTAGTGGTGG    69485   T      G    A
                                G GTGTGGGT AGTG TGG
                                | |||||||| |||| |||
                                A TACACCCA TCAC ACC
                                 C       _   C
GAM3049  KIAA1001  5'  TGGTGGCAGTGGTGATGGCAG  69486      T TG G  A
                                TGGTG G  G TG GTGATGGCAG
                                ||||| |  | || ||||||||||
                                ACCAC C  C AC CACTACCGTC
                                   _ GT _ _
GAM3049  KIAA1211  3'  TGGTGTGTGGGTGGGTGTG   69487           A   A
                                TGGTGTGTGGGTG GTG TG
                                |||||||||||| ||| ||
                                ACCACACACCCAC CAC AC
                                      C  _
GAM3049  KIAA1405  3'  TGGGTGTGGGCTCTGTGGCAG  69488     T      GAG  A
                                TGG GTGTGGGT   TG TGGCAG
                                ||| ||||||||   || ||||||
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                                ACC CACACCCG   AC ACCGTC
                                  _      AG_  _
GAM3049 KIAA1582 5' TGGTAGTGGTGGTGGTGGTGG 69489     _  TG   A  A
                                TGGT GTG  GGTG GTG TGG
                                |||| |||  |||| ||| |||
                                ACCA CAC  CCAC CAC ACC
                                  T  CA   _  C
GAM3049 KIAA1813 5' TGGTGTGTGGGAGAGACGG   69490          T  GT
                                TGGTGTGTGGG GA  GATGG
                                |||||||||| ||  |||||
                                ACCACACACCC CT  CTGCC
                                       T __
GAM3049 KIAA1906 3' TGGGTGTGGGTTATATGGTGG 69491     T      GA_  A
                                TGG GTGTGGGT   GTG TGG
                                ||| ||||||||   ||| |||
                                ACC CACACCCA   TAC ACC
                                  _      ATA  C
GAM3049 KPNA6    3' GGTGTGTGGTGGCTGATGG   69492        G  AG
                                GGTGTGTGG TG  TGATGG
                                ||||||||| ||  ||||||
                                CCACACACC AC  ACTACC
                                      _ CG
GAM3049 MGC15631 3' TGGTGTGCGGTGACATTGGGTG 69493         G  _____
           ATGGC                  GGTGTGTGG TGA     GTGATGGC
                                |||||||| |||     ||||||||
                                CCACACGCC ACT     CACTACCG
                                      _  GTAACC
GAM3049 PEG10    3' TGGTGGTGGGAGCGATGG    69494      T    TG
                                TGGTG GTGGG  AGTGATGG
                                ||||| |||||  ||||||||
                                ACCAC CACCC  TCGCTACC
                                  _    __
GAM3049 PRKRI    5' TGGTGGGTGGGTGAGCTGG   69495      T       GA
                                TGGTG GTGGGTGAGT  TGG
                                ||||| ||||||||||  |||
                                ACCAC CACCCACTCG  ACC
                                   C        __
GAM3049 SRF      3' TGGGGAGTGAGTGAGTGATGG  69496    TGT
                                TGG   GTGGGTGAGTGATGG
                                |||   ||||||||||||||
                                ACC   CACTCACTCACTACC
                                  CCT
GAM3049 ZDHHC8   3' GGTGCTGGGTGATGGCAG    69497      G      GTGA
                                GGTGT TGGGTGA    TGGCAG
                                ||||| |||||||    ||||||
                                CCACG ACCCACT    ACCGTC
                                  _     _____
GAM3049 LOC120400 5' GTGTGTGGCACTGGTGGTGG  69498        G__  A  A
                                GTGTGTGG   TG GTG TGG
                                ||||||||   || ||| |||
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                                CACACACC   AC CAC ACC
                                    GTG  _   C
GAM3049  LOC149606 3'  TGGTGGTGGGATGGC      69499      T    TGAGTG
                                TGGTG GTGGG     ATGGC
                                ||||| |||||     |||||
                                ACCAC CACCC     TACCG
                                  _    _______
GAM3049  LOC149832 5'  GTGTGCAGGGTGGTGGCA    69500      TG  TGA   A
                                GTGTG  GG   GTG TGGCA
                                |||||  ||   ||| |||||
                                CACAC  CC   CAC ACCGT
                                   GT  ___   C
GAM3049  LOC152426 3'  TGGTGTGAGAAGTGATGG    69501       T GGT
                                TGGTGTG G   GAGTGATGG
                                |||||||  |   |||||||||
                                ACCACAC C   TTCACTACC
                                    T ___
GAM3049  LOC152441 5'  TGGTTGCAGTGGGTGATGGCAG 69502     G  TG G  A
                                TGGT TG  G TG GTGATGGCAG
                                |||| ||  | || ||||||||||
                                ACCA AC  C AC CACTACCGTC
                                  _  GT _  C
GAM3049  LOC199720 3'  GCGTGGCTGGTGGTGGCAG   69503      G  A   A
                                GTGTGG TG GTG TGGCAG
                                |||||| || ||| ||||||
                                CGCACC AC CAC ACCGTC
                                   G  _   C
GAM3049  LOC254181 5'  TGGTGTTGGGTGGGGAGTG   69504       ___    T
                                TGGTGT   GTGGG GAGTG
                                ||||||   ||||| |||||
                                ACCACA   CACCC CTCAC
                                   ACC    _
GAM3049  LOC255126 5'  GGTGCCTGAGTGAGTGGTGGCA 69505      G        A
            G                    GGTGT TGGGTGAGTG TGGCAG
                                |||||  |||||||||| ||||||
                                CCACG ACTCACTCAC ACCGTC
                                  G         C
GAM3049  LOC55565  3'  TGGGTGTGGGTGGGTGGG    69506    T       A   AT
                                TGG GTGTGGGTG GTG  GG
                                ||| |||||||| |||  ||
                                ACC CACACCCAC CAC  CC
                                  _        C  __
GAM3050  F8       5'  TTTGCAGAGCATTTTA      69509         ACA
                                TTTGCGGA   CATTTTA
                                ||||||||   |||||||
                                AAACGTCT   GTAAAAT
                                    C__
GAM3050  PHLDA3    3'  TTTGCAGGGCATTTCATTT   69510        AACA
                                TTTGCGG    CATTTTATTT
                                |||||||    ||||||||||
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                                AAACGTC   GTAAAGTAAA
                                   CC__
GAM3050  SFRS7    3'  AGAAACATTTTATTTAA     69511      C
                                GGAA ACATTTTATTTAA
                                |||| ||||||||||||
                                TCTT TGTAAAATAAATT
                                  _
GAM3050  KIAA0632 3'  TTTGCAGAACATATTATA    69512          C   T
                                TTTGCGGAACA ATT TA
                                |||||||||| ||| ||
                                AAACGTCTTGT TAA AT
                                      A   T
GAM3051  ADAMTS13 3'  GGGACGTGAGCTGGGTGAT   69515    A        CTA
                                GG ACGTGGGCTG   GAT
                                || ||||||||||   |||
                                CC TGCACTCGAC   CTA
                                 C         CCA
GAM3051  CHD2     3'  TAAGGACTGTGGGCTGGTA   69516       AC       C
                                TAAGGA  GTGGGCTG TA
                                ||||||  |||||||| ||
                                ATTCCT  CACCCGAC AT
                                   GA       C
GAM3051  KCND2    5'  AGAAACGTGGTCCAGA      69517         GCTG
                                AGGAACGTGG    CTAGA
                                ||||||||||    |||||
                                TCTTTGCACC    GGTCT
                                      A___
GAM3051  LIFR     3'  GGAACTAACGCTGCTAGATA  69518      GTGG
                                GGAAC    GCTGCTAGATA
                                |||||    ||||||||||
                                CCTTG    CGACGATCTAT
                                   ATTG
GAM3051  MTAP     3'  TAAAGAGAAATTGCTAGAT   69519       ACGT  GC
                                TAAGGA    GG  TGCTAGAT
                                ||||||    ||  ||||||||
                                ATTTCT    TT  ACGATCTA
                                   CT__  A_
GAM3051  NGB      3'  GGAGCCTGGGCTACAACAGATA 69520     ACG       __
            C                    GGA   TGGGCTGC  TAGATAC
                                |||   ||||||||  |||||||
                                CCT   ACCCGATG  GTCTATG
                                  CGG       TT
GAM3051  VDR      3'  TAAGGAACGTGGCTTTCAGAT  69521           G  GC
                                TAAGGAACGTGG CT  TAGAT
                                |||||||||||| ||  |||||
                                ATTCCTTGCACC GA  GTCTA
                                      _ AA
GAM3051  DKFZp547D155 3'  GGATCTGGGCTGCAATAC    69522     ACG       TA
                                GGA   TGGGCTGC  GATAC
                                |||   ||||||||  |||||
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                                CCT  ACCCGACG  TTATG
                                  AG_      __
GAM3051  FLJ20489  3'  AAGAGGTCTCTGCTAGATA   69523     AC  GGG
                                AGGA  GT   CTGCTAGATA
                                ||||  ||   ||||||||||
                                TTCT  CA   GACGATCTAT
                                  C_  GA_
GAM3051  HSPC213   3'  GGAACACATTGCTAGGTAC   69524      TGGGC    A
                                GGAACG    TGCTAG TAC
                                ||||||    |||||| |||
                                CCTTGT    ACGATC ATG
                                   GTA__     C
GAM3051  KIAA1957  3'  CAAGGGACGTCCCTGGGTAC   69525      A   _____  C
                                TAAGG ACGT    GGG TGC
                                ||||| ||||    ||| |||
                                GTTCC TGCA    CCC ATG
                                   C    GGGA  _
GAM3051  MGC13033  3'  AGGCTGCCGGGCTGCTAGATA  69526     AACG
                                AGG    TGGGCTGCTAGATA
                                |||    ||||||||||||||
                                TCC    GCCCGACGATCTAT
                                  GACG
GAM3051  LOC145225 3'  TAAGGGATTGGGGCCCTGATAC 69527      AACGT    G  A
                                TAAGG     GGGCT CT GATAC
                                |||||     ||||| || |||||
                                ATTCC     CCCGG GA CTATG
                                   CTAAC    _  _
GAM3051  LOC150819 5'  AGGGCGTGAGCTGGAT      69528     AA       CTA
                                AGG  CGTGGGCTG   GAT
                                |||  |||||||||   |||
                                TCC  GCACTCGAC   CTA
                                  C_       ___
GAM3051  LOC196812 3'  TAAAGAACTATCTGTTAGGTAC 69529        GTGGG   C   A
                                TAAGGAAC     CTG TAG TAC
                                ||||||||     ||| ||| |||
                                ATTTCTTG     GAC ATC ATG
                                     ATA__   A   C
GAM3051  LOC255975 5'  AGGCATGAGCTGGAT       69530     AA       CTA
                                AGG  CGTGGGCTG   GAT
                                |||  |||||||||   |||
                                TCC  GTACTCGAC   CTA
                                  __       ___
GAM3052  ALDH1B1   3'  GGAATTGCTGGACTGTGACTGG 69533        CA   ___   C
                                GGAATTGC  GGAC   GAC GG
                                ||||||||  ||||   ||| ||
                                CCTTAACG  CCTG   CTG CC
                                     A_    ACA   A
GAM3052  ASC       3'  GGGATTGCCAGGGGCTGACCGG 69534    A       AC__
                                GG ATTGCCAGG    GACCGG
                                || |||||||||    ||||||
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                                CC TAACGGTCC    CTGGCC
                                 C        CCGA
GAM3052  FZD1     5'  GGGGCTGCCAGGGGCACGGCCG 69535    AA       ___   A
                G                 GG  TTGCCAGG   ACG CCGG
                                  ||  ||||||||   ||| ||||
                                  CC  GACGGTCC   TGC GGCC
                                   CC       CCG   C
GAM3052  KIAA1211  5'  CGGGCCCAGGACGATCGG    69536     AATTG        C
                                  CGG    CCAGGACGA CGG
                                  |||    ||||||||| |||
                                  GCC    GGTCCTGCT GCC
                                    CG___        A
GAM3052  LOC116236 3'  CCGCAGTTGCCAGAGCATTCGG 69537     GAA      GA  AC
                                  CCG   TTGCCAG  CG  CGG
                                  |||   |||||||  ||  |||
                                  GGC   AACGGTC  GT  GCC
                                    GTC      TC  AA
GAM3052  LOC160376 5'  CACTGGGGCTGCCAGGAC    69538     C  AA
                                  CAC GG  TTGCCAGGAC
                                  ||| ||  ||||||||||
                                  GTG CC  GACGGTCCTG
                                    A  CC
GAM3052  LOC253071 5'  GAATTGCCAGGAACTTCCTGG  69539           _ GA  _
                                  GAATTGCCAGGA C  CC GG
                                  ||||||||||||  |  || ||
                                  CTTAACGGTCCT G  GG CC
                                         T AA  A
GAM3053  OAT      3'  TAGATGCCATTACATTATTTAG 69542           ATGATA
                                  TAGATGCTATTA     ATTTAG
                                  ||||||||||||     ||||||
                                  ATCTACGGTAAT     TAAATC
                                         GTAA__
GAM3053  CREG     3'  TAGAAGCTATTAAGAGAT    69543      T       T_
                                  TAGA GCTATTAA  GAT
                                  |||| ||||||||  |||
                                  ATCT CGATAATT  CTA
                                    T       CT
GAM3053  LOC146092 5'  AATGCTATCTTTATGATAATTT 69544         A__
                AG                  GATGCTATT   ATGATAATTTAG
                                    |||||||||   ||||||||||||
                                    TTACGATAG   TACTATTAAATC
                                        AAA
GAM3054  ATM      3'  TAAAGTATGTTGGCAGGTTAA  69547          CAAT_
                                  TAAAGTATGTT    GTTAA
                                  ||||||||||     |||||
                                  ATTTCATACAA    CAATT
                                         CCGTC
GAM3054  ATM      3'  TAAAGTATGTTGGCAGGTTAA  69547          CAAT_
                                  TAAAGTATGTT    GTTAA
                                  ||||||||||     |||||
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                                ATTTCATACAA    CAATT
                                     CCGTC
GAM3054  PUM1     3'  TACCTTTCAATGTTAATA    69548    G_
                                TAT  TTCAATGTTAATA
                                |||  |||||||||||||
                                ATG  AAGTTACAATTAT
                                  GA
GAM3054  RAD54B   3'  TGAATATGTTCAGATGTC    69549    A       _
                                A AGTATGTTCA ATGTT
                                | ||||||||| |||||
                                A TTATACAAGT TACAG
                                 C        C
GAM3054  WEE1     3'  AATATGCCAATCAATGTTAATA 69550       ___
                AA                AGTATGT   TCAATGTTAATAAA
                                |||||||   ||||||||||||||
                                TTATACG   AGTTACAATTATTT
                                    GTT
GAM3054  KIAA0660 3'  AGATGTCAATGTTAAT     69551    T   T
                                AG ATGT CAATGTTAAT
                                || |||| ||||||||||
                                TC TACA GTTACAATTA
                                 _   _
GAM3054  KIAA0680 3'  AAAGTATGAGTAGTTAATAAA  69552        TTCAAT
                                AAAGTATG     GTTAATAAA
                                ||||||||     |||||||||
                                TTTCATAC     CAATTATTT
                                     TCAT__
GAM3054  KIAA1641 3'  AAAGCTTATCAGTGTTAATAA  69553      A   T  A
                                AAAGT TGT CA TGTTAATAA
                                ||||| ||| || |||||||||
                                TTTCG ATA GT ACAATTATT
                                   A   _  C
GAM3055  CLN5     5'  AATGTGTATTTGGAGCTGA    69556       ___
                                GATGTGT   TGGAGCTGA
                                |||||||   |||||||||
                                TTACACA   ACCTCGACT
                                    TAA
GAM3055  GBF1     3'  AGGCTGCAGATGACAGCTG    69557    AT      TGTTGG
                                AG  TGCAGATG     AGCTG
                                ||  ||||||||     |||||
                                TC  ACGTCTAC     TCGAC
                                 CG       TG_____
GAM3055  GPR62    3'  AGGGTGCAGATGGGAAAGCTGA 69558    AT      TGTT
                                AG  TGCAGATG   GGAGCTGA
                                ||  ||||||||   ||||||||
                                TC  ACGTCTAC   TTTCGACT
                                 CC       CC__
GAM3055  MUC3B    5'  AGTTGTGGATGTGCTGA     69559    A   CA
                                AG TTG  GATGTGTTGG
                                || |||  ||||||||||
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                                TC AAC  CTACACGACT
                                 _   AC
GAM3055  MYCL1    3'  AGATGGCAGAAAGCTGGAGCTG 69560     T    TGT
              A                  AGAT GCAGA   GTTGGAGCTGA
                                 |||| |||||   ||||||||||
                                 TCTA CGTCT   CGACCTCGACT
                                   C    TT_
GAM3055  PDK4     5'  GACTGCAGGTGCGCTGGCTG   69561        A     GA
                                 GATTGCAG TGTGTTG  GCTG
                                 |||||||| |||||||  ||||
                                 CTGACGTC ACGCGAC  CGAC
                                      C      __
GAM3055  PPP1R12B 3'  AGATTGGGATGGGGCT      69562       CA   TGTT  A
                                 AGATTG  GATG   GG GCT
                                 ||||||  ||||   || |||
                                 TCTAAC  CTAC   CC CGA
                                    C_   _____ _
GAM3055  PRKY     3'  GATTACAGGTGTGAGCC     69563        AT   TG
                                 GATTGCAG  GTGT  GAGCT
                                 ||||||||  ||||  |||||
                                 CTAATGTC  CACA  CTCGG
                                      __   __
GAM3055  S100A1   5'  AGGTTGCAAATGTGGCTGCTG  69564    A        TTGGA
                                 AG TTGCAGATGTG    GCTG
                                 || ||||||||||     ||||
                                 TC AACGTTTACAC    CGAC
                                  C         CGA__
GAM3055  SIM2     3'  GATTACAGGTGTGAGCCACTGA 69565        A   TTGGA
                                 GATTGCAG TGTG    GCTGA
                                 |||||||| ||||    |||||
                                 CTAATGTC ACAC    TGACT
                                      C   TCGG_
GAM3055  ARHGAP9  5'  AGATTCAGGAGCAGGAGTTG   69566      G   ATGT  T   C
                                 AGATT CAG   GT GGAG TG
                                 ||||| |||   || |||| ||
                                 TCTAA GTC   CG CCTC AC
                                    _  CT__  T   A
GAM3055  CYP2S1   3'  CTGCAGATCCAGGGGAGTTG   69567       G  TT   C
                                 TTGCAGAT TG  GGAG TG
                                 |||||||| ||  |||| ||
                                 GACGTCTA GT  CCTC AC
                                      G  CC   A
GAM3055  FLJ10619 3'  ATTGTAAGAGTTGGAGCTGA   69568     C_   TGT
                                 ATTG  AGA   GTTGGAGCTGA
                                 ||||  |||   ||||||||||
                                 TAAC  TCT   CAACCTCGACT
                                   AT   ___
GAM3055  FLJ12650 3'  AGATGCAGACGCGGGGTTGG   69569     T      ___
                                 AGAT GCAGATGT   GTTGG
                                 |||| ||||||||   |||||
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                                TCTA CGTCTGCG   CAACC
                                  _      CCC
GAM3055  FLJ12666  3'  AGGATGCAAAGTTGGAGCTGA  69570    AT     TGT
                                AG  TGCAGA   GTTGGAGCTGA
                                ||  ||||||   ||||||||||
                                TC  ACGTTT   CAACCTCGACT
                                 CT     ___
GAM3055  GPR103    3'  GATTACAGATGGAGTTGG    69571          T_
                                GATTGCAGATG  GTTGG
                                ||||||||||  |||||
                                CTAATGTCTAC  CAACC
                                       CT
GAM3055  KIAA0445  3'  GACTGCAGGTGTTGCTGG    69572        A  _
                                GATTGCAG TGT GTTGG
                                |||||||| ||| |||||
                                CTGACGTC ACA CGACC
                                     C   A
GAM3055  KIAA0892  3'  TGCAGATGTTTGGAAGCTGA   69573         G    _
                                TGCAGATGT TTGGA GCTGA
                                ||||||||| ||||| |||||
                                ACGTCTACA AACCT CGACT
                                      _    T
GAM3055  MGC5139   5'  AGGTTCCAGATGTGTGTTGA   69574    A  G       TG_
                                AG TT CAGATGTGT   GA
                                || || |||||||||   ||
                                TC AA GTCTACACA   CT
                                 C  G        CAA
GAM3055  p25       3'  AGATTCGCTTTGGAGCTG    69575      GCAGA   G
                                AGATT    TGT TTGGAGCTG
                                |||||    ||| |||||||||
                                TCTAA    GCG AACCTCGAC
                                   _____  A
GAM3055  PRKRI     5'  AGGTTACAGGGGGAGGAGCTGA 69576    A     ATGTGTT
                                AG TTGCAG      GGAGCTGA
                                || ||||||      ||||||||
                                TC AATGTC      CCTCGACT
                                 C     CCCCT__
GAM3055  RASD2     3'  TGCAGGTATGCAGAGCTG    69578      A    T
                                TGCAG TGTGT GGAGCTG
                                ||||| ||||| |||||||
                                ACGTC ATACG TCTCGAC
                                   C    _
GAM3055  RASD2     3'  TGCAGAGCTGGGGCTG      69577       TGT    A
                                TGCAGA   GTTGG GCTG
                                ||||||   ||||| ||||
                                ACGTCT   CGACC CGAC
                                    ___    C
GAM3055  TCL6      5'  GATTGCAGGTGTGTAGCTG   69579        A    TGG
                                GATTGCAG TGTGT   AGCTG
                                |||||||| |||||   |||||
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                                CTAACGTC ACACA   TCGAC
                                    C    ___
GAM3055  TCL6     5'  GATTGCAGGTGTGTAGCTG   69579       A    TGG
                                GATTGCAG TGTGT   AGCTG
                                |||||||| |||||   |||||
                                CTAACGTC ACACA   TCGAC
                                    C    ___
GAM3055  TCL6     5'  GATTGCAGGTGTGTAGCTG   69579       A    TGG
                                GATTGCAG TGTGT   AGCTG
                                |||||||| |||||   |||||
                                CTAACGTC ACACA   TCGAC
                                    C    ___
GAM3055  TCL6     5'  GATTGCAGGTGTGTAGCTG   69579       A    TGG
                                GATTGCAG TGTGT   AGCTG
                                |||||||| |||||   |||||
                                CTAACGTC ACACA   TCGAC
                                    C    ___
GAM3055  LOC115294 3'  TTGTGGAATTACTGGAGCTGA  69580     CA  TG
                                TTG  GA  TGTTGGAGCTGA
                                |||  ||  ||||||||||||
                                AAC  CT  ATGACCTCGACT
                                  AC  TA
GAM3055  LOC132617 3'  AGATTGCAGGGAGCCGA     69581         ATGTGTT
                                AGATTGCAG      GGAGCTGA
                                |||||||||      ||||||||
                                TCTAACGTC      CCTCGGCT
                                               ________
GAM3055  LOC146184 5'  AGATTGTGATGTGCTGA     69582       CA
                                AGATTG  GATGTGTTGG
                                ||||||  ||||||||||
                                TCTAAC  CTACACGACT
                                   A_
GAM3055  LOC150370 3'  GAGTGTGGATGAAGCCAGGCTG 69583    T  CA    T_  TG A
                                GA TG  GATG  GT  G GCTG
                                || ||  ||||  ||  | ||||
                                CT AC  CTAC  CG  C CGAC
                                 C  AC    TT  GT _
GAM3055  LOC153579 3'  GATTACAGGTGTGAGCCACTG  69584        A    TTGGA
                                GATTGCAG TGTG     GCTG
                                |||||||| ||||     ||||
                                CTAATGTC ACAC     TGAC
                                    C    TCGG_
GAM3055  LOC221583 3'  GATTGCAGAGGCTGAGGGCTGA 69585         T  GTT  A
                                GATTGCAGA GT   GG GCTGA
                                ||||||||| ||   || |||||
                                CTAACGTCT CG   CC CGACT
                                     C  ACT  _
GAM3055  LOC221747 3'  GATTGTACGGAGTGGGGCTGA  69586      CA__  T   TT  A
                                GATTG   GA GTG  GG GCTGA
                                |||||   || |||  || |||||
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                                CTAAC    CT CAC  CC CGACT
                                   ATGC  _  __  _
GAM3055  LOC254419 5'  AGAATGTAGATATTGGAGTTG  69587     T  C     GT    C
                                AGA TG AGATGT  TGGAG TG
                                ||| || ||||||  ||||| ||
                                TCT AC TCTATA  ACCTC AC
                                  T  A     __     A
GAM3056  DKFZP434F2021 3'  AACGATTATTAAATTGCC    69590     A    G
                                AAC ATTA TTAAATTGCT
                                ||| |||| ||||||||||
                                TTG TAAT AATTTAACGG
                                  C   _
GAM3056  KIAA0087  3'  ATCAGTTAAACCTCTGTGTT   69591          TG  A
                                ATTAGTTAAAT  CT TGTT
                                ||||||||||  || ||||
                                TAGTCAATTTG  GA ACAA
                                       GA  C
GAM3056  PRO1866   5'  TAGTTCCCCTGCTATGTT    69592      AAA
                                TAGTT   TTGCTATGTT
                                |||||   ||||||||||
                                ATCAA   GACGATACAA
                                   GGG
GAM3056  ZNF17     3'  AACAATTACTTACCATGT    69593        G TAAAT
                                AACAATTA T    TGCTATGT
                                |||||||| |    ||||||||
                                TTGTTAAT A    ATGGTACA
                                    G _____
GAM3056  LOC144363 3'  TAGCTAAATTGCTATGTT    69594
                                TAGTTAAATTGCTATGTT
                                ||||||||||||||||||
                                ATCGATTTAACGATACAA

GAM3056  LOC203276 3'  AACAAATAGTTAAATATGT    69595      T      TTGC
                                AACAA TAGTTAAA    TATGT
                                ||||| ||||||||    |||||
                                TTGTT ATCAATTT    ATACA
                                   T      ____
GAM3056  LOC203305 3'  AACAAATAGTTAAATATGT    69595      T      TTGC
                                AACAA TAGTTAAA    TATGT
                                ||||| ||||||||    |||||
                                TTGTT ATCAATTT    ATACA
                                   T      ____
GAM3056  LOC254243 3'  AACAAATAGTTAAATATGT    69595      T      TTGC
                                AACAA TAGTTAAA    TATGT
                                ||||| ||||||||    |||||
                                TTGTT ATCAATTT    ATACA
                                   T      ____
GAM3056  LOC90038  3'  AACAAATAGTTAAATATGT    69595      T      TTGC
                                AACAA TAGTTAAA    TATGT
                                ||||| ||||||||    |||||
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                                TTGTT ATCAATTT    ATACA
                                  T      ____
GAM3057  LOC150208 5'  TAATGATAAACTAGTTAATGGT 69598         TATA  A
                                TGATGATAA    TA TTAATGGT
                                |||||||||    || ||||||||
                                ATTACTATT    AT AATTACCA
                                     TG__  C
GAM3057  LOC254028 3'  TGATGATAATAATGG       69599          TATAATTA
                                TGATGATAATA       ATGG
                                ||||||||||        ||||
                                ACTACTATTAT       TACC

                                          _________
GAM3058  AMELX     3'  CATTCCCCTCTCATCTTCT    69602        A   T
                                CATTTCTT TCT CATCTTCT
                                |||||||| ||| ||||||||
                                GTAAGGGG AGA GTAGAAGA

                                   _  _
GAM3058  APP       3'  CACTTCCATTTTCATCTTCT   69603        T  C
                                CATTTCT AT TTCATCTTCT
                                ||||||| || ||||||||||
                                GTGAAGG TA AAGTAGAAGA
                                   _  A
GAM3058  CA2       3'  ATTTCTTATCCTATATTCT    69604          C  C
                                ATTTCTTATCTT AT TTCT
                                |||||||||||| || ||||
                                TAAAGAATAGGA TA AAGA
                                      _  T
GAM3058  DNMT2     3'  TTTCTTTTCATCTCTCTTCT   69605       A  T  A_
                                TTTCTT TC TC  TCTTCT
                                |||||| || ||  ||||||
                                AAAGAA AG AG  AGAAGA
                                   A  T  AG
GAM3058  DPH2L1    3'  CATTTCTTGATCTTTCACTC   69606         _    _  T
                                CATTTCTT ATCTT CA CTT
                                |||||||| ||||| || |||
                                GTAAAGAA TAGAA GT GAG
                                     C    A  _
GAM3058  EVI2A     5'  CACTTCTTTTCTTGTCTTCT   69607        A    CA
                                CATTTCTT TCTT  TCTTCT
                                |||||||| ||||  ||||||
                                GTGAAGAA AGAA  AGAAGA
                                     A    C_
GAM3058  FGF7      3'  TTCTTAACTGCATCTTCT     69608       T  T
                                TTCTTA CT CATCTTCT
                                |||||| || ||||||||
                                AAGAAT GA GTAGAAGA
                                   T  C
GAM3058  KCNMB3    5'  CATTTCTTCTCTCCTCT      69609        A    A
                                CATTTCTT TCTTC TCT
                                |||||||| ||||| |||
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                                GTAAAGAA AGAGG AGA
                                    G   _
GAM3058 KLF7    3' TTTCCTTCTTCATCTTCT   69610      A
                                TTTCTT TCTTCATCTTCT
                                |||||| ||||||||||||
                                AAAGGA AGAAGTAGAAGA
                                  _
GAM3058 MBTPS1  5' CATTTCTTTCTCCGCTTCT  69611       A   AT
                                CATTTCTT TCTTC  CTTCT
                                |||||||| |||||  |||||
                                GTAAAGAA AGAGG  GAAGA
                                    _   C_
GAM3058 MGAM    3' CACTTTTACTATCATCTTCT 69612     C   CT
                                CATTT TTAT  TCATCTTCT
                                ||||| ||||  |||||||||
                                GTGAA AATG  AGTAGAAGA
                                  _   AT
GAM3058 MSL3L1  5' TTTCATCATTTTCATCTT   69613     _   C
                                TTTC TTAT TTCATCTT
                                |||| |||| ||||||||
                                AAAG AGTA AAGTAGAA
                                  T   A
GAM3058 NCOA6   5' TTATCCAGGTCATCTTCT   69614     ___
                                TTATCT  TCATCTTCT
                                ||||||  |||||||||
                                AATAGG  AGTAGAAGA
                                   TCC
GAM3058 NEBL    3' CATTTTCTTCATCTT      69615     CTTA
                                CATTT   TCTTCATCTT
                                |||||   ||||||||||
                                GTAAA   AGAAGTAGAA
                                  ____
GAM3058 NQO1    3' CATTTCTCATCTCTTC     69616         TTCA
                                CATTTCTTATC   TCTTC
                                ||||||||||   |||||
                                GTAAAGAGTAG   AGAAG
                                   ____
GAM3058 PLOD2   3' ATTCCTCTCATCTTC      69617      ATCT
                                ATTTCTT   TCATCTTC
                                |||||||   ||||||||
                                TAAGGAG   AGTAGAAG
                                  ____
GAM3058 PTPN12  3' ATTTCTTACATCTTC      69618       TCTT
                                ATTTCTTA   CATCTTC
                                ||||||||   |||||||
                                TAAAGAAT   GTAGAAG
                                  ____
GAM3058 SORCS1  3' CATTTCTCACAAGAATCTTCT 69619        CTTC
                                CATTTCTTAT   ATCTTCT
                                |||||||||   |||||||
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                                GTAAAGAGTG   TAGAAGA
                                     TTCT
GAM3058 SYBL1   3' ATTTAAACCTTCATCTTCT   69620     CTT
                                ATTT  ATCTTCATCTTCT
                                ||||  ||||||||||||
                                TAAA  TGGAAGTAGAAGA
                                  TT_
GAM3058 USH2A   3' CTTCTTCATCTTCATCTT    69621      _
                                TTTCT TATCTTCATCTT
                                ||||| ||||||||||||
                                GAAGA GTAGAAGTAGAA
                                   A
GAM3058 ZNF192  5' CTACCTTCTTTATCTTCT    69622        ___
                                TTATCTTC  ATCTTCT
                                ||||||||  |||||||
                                GATGGAAG  TAGAAGA
                                     AAA
GAM3058 ZNF35   5' CAATTCTGCAGTCATCTTCT  69623   T   TATCT
                                CA TTCT    TCATCTTCT
                                || ||||    |||||||||
                                GT AAGA    AGTAGAAGA
                                 T   CGTC_
GAM3058 C1orf34 3' TTTCTGGCTCATCTTCT     69624      TATC
                                TTTCT   TTCATCTTCT
                                |||||   ||||||||||
                                AAAGA   GAGTAGAAGA
                                   CC__
GAM3058 CCR1    3' TTTGCTCATTCATCTTCT    69625    _   CT
                                TTT CTTAT  TCATCTTCT
                                ||| |||||  |||||||||
                                AAA GAGTA  AGTAGAAGA
                                  C   __
GAM3058 EST-YD1 5' CTTCTCAGCATCATCTTCT   69626       TCT
                                TTTCTTA  TCATCTTCT
                                |||||||  |||||||||
                                GAAGAGT  AGTAGAAGA
                                     CGT
GAM3058 FBXO25  5' CATCTCTTCCAGCCATCTTCT 69627        ATCT
                                CATTTCTT   TCATCTTCT
                                ||||||||   |||||||||
                                GTAGAGAA   GGTAGAAGA
                                     GGTC
GAM3058 FBXO5   3' CTATCCTCTTTATCTTCT    69628        ___
                                TTATCTTC  ATCTTCT
                                ||||||||  |||||||
                                GATAGGAG  TAGAAGA
                                     AAA
GAM3058 FLJ10996 5' CATTTTGTTCTTCATCTTCT 69629     CTTA
                                CATTT   TCTTCATCTTCT
                                |||||   ||||||||||||
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                                GTAAA   AGAAGTAGAAGA
                                  ACA_
GAM3058 FLJ11016 3' ATTTCCTATTTCACGTTCT   69630        C    C
                                ATTTCTTAT TTCAT TTCT
                                ||||||||| ||||| ||||
                                TAAAGGATA AAGTG AAGA
                                     _    C
GAM3058 FLJ20707 3' CATCTCTTCTTCATCTTCT   69631       TA
                                CATTTCT  TCTTCATCTTCT
                                |||||||  ||||||||||||
                                GTAGAGA  AGAAGTAGAAGA
                                   __
GAM3058 FLJ22746 3' TTCTTCTTCATCTTCT     69632     TA
                                TTCT  TCTTCATCTTCT
                                ||||  ||||||||||||
                                AAGA  AGAAGTAGAAGA
                                  __
GAM3058 FLJ23790 5' CATATCTTGATGTCATCTTCT 69633    T   ATCT
                                CAT TCTT   TCATCTTCT
                                ||| ||||   |||||||||
                                GTA AGAA   AGTAGAAGA
                                  T   CTAC
GAM3058 G2      3' CATTCCCTCTCATCTTCT    69634       ATC
                                CATTTCTT   TTCATCTTCT
                                ||||||||   ||||||||||
                                GTAAGGGA   GAGTAGAAGA
                                   ___
GAM3058 HRH4    3' CATCTCTTAGCCTTCTTCT   69635       T  CA
                                CATTTCTTA CTT  TCTTCT
                                ||||||||| |||  ||||||
                                GTAGAGAAT GGA  AGAAGA
                                     C  __
GAM3058 HSPC063  5' CATTTCTTGTTTCTCATCCT  69636       A__  T
                                CATTTCTT   TCT CATCTT
                                ||||||||   ||| ||||||
                                GTAAAGAA   AGA GTAGGA
                                    CAA  _
GAM3058 KIAA0042 5' CATTTCTTATGTATCCATTTCT 69637        C__   C
                                CATTTCTTAT   TTCAT TTCT
                                ||||||||||   ||||| ||||
                                GTAAAGAATA   AGGTA AAGA
                                     CAT   _
GAM3058 KIAA0493 5' CATATCTTGATGTCATCTTCT 69633    T   ATCT
                                CAT TCTT   TCATCTTCT
                                ||| ||||   |||||||||
                                GTA AGAA   AGTAGAAGA
                                  T   CTAC
GAM3058 KIAA1430 3' TTTCTTACGCTAAGTCTTCT  69638       _ TCA
                                TTTCTTAT CT   TCTTCT
                                |||||||| ||   ||||||
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                                AAAGAATG GA   AGAAGA
                                    C  TTC
GAM3058  KIAA1464  3'  CAATTCTCTGCCTCATCTTCT  69639    T    AT
                                CA TTCTT  CTTCATCTTCT
                                || |||||  ||||||||||
                                GT AAGAG  GGAGTAGAAGA
                                  T    AC
GAM3058  KIAA1559  3'  CATTTCCTATTTCCCTCT    69640         C   AT
                                CATTTCTTAT TTC  CTTCT
                                |||||||||| |||  |||||
                                GTAAAGGATA AAG  GGAGA
                                     _  __
GAM3058  KIAA1789  5'  TTTCTTATACTCTCCACTCTT  69641        ___     _
                                TTTCTTA   TCTTCA TCTT
                                |||||||   |||||| ||||
                                AAAGAAT   AGAGGT AGAA
                                    ATG     G
GAM3058  KIAA1831  3'  CACTCCTTCTTCATTTTCT    69642       TA      C
                                CATTTCT  TCTTCAT TTCT
                                |||||||  ||||||| ||||
                                GTGAGGA  AGAAGTA AAGA
                                   __      A
GAM3058  LEC3      3'  ATTTCTGTGTCATCTTCT    69643       TATCT
                                ATTTCT    TCATCTTCT
                                ||||||    |||||||||
                                TAAAGA    AGTAGAAGA
                                   CAC__
GAM3058  MGC27277  3'  ATTTCTTATCACATCATCATCT 69644         T__    T
                                ATTTCTTATC   TCATC TCT
                                ||||||||||   ||||| |||
                                TAAAGAATAG   AGTAG AGA
                                      TGT    T
GAM3058  MRF2      3'  CACTCACTTCTTCATCTTCT   69645      _  TA
                                CATTT CT  TCTTCATCTTCT
                                ||||| ||  ||||||||||||
                                GTGAG GA  AGAAGTAGAAGA
                                   T  __
GAM3058  NUDT12    3'  TTCTTATCATTCCTTCT     69646        _   AT
                                TTCTTATC TTC  CTTCT
                                |||||||| |||  |||||
                                AAGAATAG AAG  GAAGA
                                     T  __
GAM3058  NYD-SP18  3'  TTTCCTATTACCACTTCT    69647       CT   T
                                TTTCTTAT  TCA CTTCT
                                ||||||||  ||| |||||
                                AAAGGATA  GGT GAAGA
                                     AT  _
GAM3058  ODZ2      3'  TTTCTTATCTTCGCTTCT    69648          AT
                                TTTCTTATCTTC  CTTCT
                                ||||||||||||  |||||
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                                AAAGAATAGAAG  GAAGA
                                      C_
GAM3058  PPP4R2   5'  TCTTCCTCTTCATCTTCT    69649     A_
                                TCTT  TCTTCATCTTCT
                                ||||  ||||||||||||
                                AGAA  AGAAGTAGAAGA
                                  GG
GAM3058  SFRS6    3'  CATTTCCTTAGAGCCTCATCTT 69650       AT___
                                CATTTCTT    CTTCATCTT
                                ||||||||    |||||||||
                                GTAAAGGA    GGAGTAGAA
                                     ATCTC
GAM3058  TRAD     3'  TTCTTATCTTTGCCCTTCT   69651        CA_
                                TTCTTATCTT   TCTTCT
                                ||||||||||   ||||||
                                AAGAATAGAA   GGAAGA
                                      ACG
GAM3058  VIT1     3'  TTCTTATCTACCTTCT     69652        TC
                                TTCTTATCT  ATCTTCT
                                |||||||||  |||||||
                                AAGAATAGA  TGGAAGA
                                      __
GAM3058  LOC127133 3'  CATTTCTTCACAGATCTTCT   69653       ATCTTC
                                CATTTCTT     ATCTTCT
                                ||||||||     |||||||
                                GTAAAGAA     TAGAAGA
                                     GTGTC_
GAM3058  LOC128008 5'  CATTCCTTGATCCATCTTCT   69654       ATC
                                CATTTCTT   TTCATCTTCT
                                ||||||||   ||||||||||
                                GTAAGGAA   AGGTAGAAGA
                                     CT_
GAM3058  LOC131744 5'  CTTCTTCTTCTTCATCTTCT   69655      A_
                                TTTCTT  TCTTCATCTTCT
                                ||||||  ||||||||||||
                                GAAGAA  AGAAGTAGAAGA
                                   GA
GAM3058  LOC145317 3'  TTCTTATCTGTCCTTCT     69656       TCA
                                TTCTTATCT   TCTTCT
                                |||||||||   ||||||
                                AAGAATAGA   GGAAGA
                                      CA_
GAM3058  LOC145368 5'  ATTCCTCAGCATCTTCT     69657       TCTT
                                ATTTCTTA    CATCTTCT
                                ||||||||    ||||||||
                                TAAGGAGT    GTAGAAGA
                                     C___
GAM3058  LOC147804 5'  CATCTTCTTCATCTT       69658      CTTA
                                CATTT    TCTTCATCTT
                                |||||    ||||||||||
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                              GTAGA   AGAAGTAGAA
                                ____
GAM3058  LOC150291 3'  CATTGTTTTATCTTCACCCCCT 69659     TC_
                              CATT   TTATCTTCATCTTCT
                              ||||   ||||||||||||||
                              GTAA   AATAGAAGTGGGGGA
                                CAA
GAM3058  LOC150423 5'  ATTCCTCAGCATCTTCT     69657       TCTT
                              ATTTCTTA   CATCTTCT
                              ||||||||   ||||||||
                              TAAGGAGT   GTAGAAGA
                                  C___
GAM3058  LOC150538 3'  TTCTCCCCCATCTTCT      69660      AT
                              TTCTT  CTTCATCTTCT
                              |||||  ||||||||||
                              AAGAG  GGGGTAGAAGA
                                ___
GAM3058  LOC151246 3'  CATTAAGCATTTCATCTTCT   69661     TCT   C
                              CATT   TAT TTCATCTTCT
                              ||||   ||| ||||||||||
                              GTAA   GTA AAGTAGAAGA
                                TTC  _
GAM3058  LOC200854 3'  TCTTCATCTTCATCTTCT    69662     _
                              TCT TATCTTCATCTTCT
                              ||| ||||||||||||||
                              AGA GTAGAAGTAGAAGA
                                A
GAM3058  LOC202460 5'  TTTCTTATCAAATCTTCT    69663       TTC
                              TTTCTTATC   ATCTTCT
                              |||||||||   |||||||
                              AAAGAATAG   TAGAAGA
                                   TT_
GAM3058  LOC203112 5'  CATGTCTTCATCATCTTCT   69664     T   ATCT
                              CAT TCTT    TCATCTTCT
                              ||| ||||    |||||||||
                              GTA AGAA    AGTAGAAGA
                                C   GT__
GAM3058  LOC219347 5'  TTCCTATGGCATCTTCT     69665       CTT
                              TTCTTAT   CATCTTCT
                              |||||||   ||||||||
                              AAGGATA   GTAGAAGA
                                  CC_
GAM3058  LOC221271 3'  TTCTTATCATCATCCTTCT   69666       T   _
                              TTCTTATC TCATC TTCT
                              |||||||| ||||| ||||
                              AAGAATAG AGTAG AAGA
                                   T    G
GAM3058  LOC221454 5'  ATCTCAAACTTTCATCTTCT   69667      TT TC
                              ATTTC  A  TTCATCTTCT
                              |||||  |  ||||||||||
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                                TAGAG  T  AAGTAGAAGA
                                   TT GA
GAM3058  LOC221738 5'  ATTTCTTATCTGACATCT    69668          T_
                                ATTTCTTATCT  CATCT
                                ||||||||||  |||||
                                TAAAGAATAGA  GTAGA
                                      CT
GAM3058  LOC253612 5'  CATTTCTTTCTTCTTCTTCT   69669        A    A
                                CATTTCTT TCTTC TCTTCT
                                |||||||| ||||| ||||||
                                GTAAAGAA AGAAG AGAAGA
                                     _    A
GAM3058  LOC254219 3'  CTCTGATCTTCATCTTCT    69670      T
                                TTCT ATCTTCATCTTCT
                                |||| ||||||||||||
                                GAGA TAGAAGTAGAAGA
                                  C
GAM3058  LOC255849 3'  CATTTCTTGCCCCATTTCT    69671        AT     C
                                CATTTCTT  CTTCAT TTCT
                                ||||||||  |||||| ||||
                                GTAAAGAA  GGGGTA AAGA
                                     C_     _
GAM3058  LOC256815 3'  CTTCTTATCTTTCCACCT    69672          __
                                TTTCTTATCT  TCATCT
                                ||||||||||  ||||||
                                GAAGAATAGA  GGTGGA
                                      AA
GAM3058  LOC55954  3'  TTTCTCCCCCATCTTCT     69673       AT
                                TTTCTT  CTTCATCTTCT
                                ||||||  ||||||||||
                                AAAGAG  GGGGTAGAAGA
                                    __
GAM3058  LOC57105  3'  CATCTCCCTACTCATCTTCT   69674        ATC
                                CATTTCTT   TTCATCTTCT
                                ||||||||   ||||||||||
                                GTAGAGGG   GAGTAGAAGA
                                     AT_
GAM3058  LOC57149  3'  ATTTCTGATGCCCATCTTCT   69675       T  C
                                ATTTCT AT TTCATCTTCT
                                |||||| || ||||||||||
                                TAAAGA TA GGGTAGAAGA
                                   C  C
GAM3058  LOC90378  5'  CATCTTCATCATCATCTTCT   69676      C    T
                                CATTT TTATC TCATCTTCT
                                ||||| ||||| |||||||||
                                GTAGA AGTAG AGTAGAAGA
                                   _    T
GAM3058  LOC92303  3'  CACTTCTCTGTCATCTT     69677        ATCT
                                CATTTCTT    TCATCTT
                                ||||||||    |||||||
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                                GTGAAGAG   AGTAGAA
                                    AC__
GAM3059 CALN1    3' GAGCCAACCTGTGTTTGTC   69680     _     ACTTGAC
                                GAGC AACCTGT      TTGTC
                                |||| |||||||      |||||
                                CTCG TTGGACA      AACAG
                                  G      CA_____
GAM3059 CEP3     3' GAGTAACCTGTGCCTTTATGAC 69681   C     A T_______   CTTG
             AAT                  G AACCTGT C       TGA   T
                                | ||||||| |       |||   |
                                C TTGGACA G       ACT   A
                                 A      C GAAATIII  GTTC
GAM3059 DKFZp761N0624 3' GAGCATCTGTACTTGAC     69682      AC
                                GAGCA  CTGTACTTGAC
                                |||||  ||||||||||
                                CTCGT  GACATGAACTG
                                   A_
GAM3059 ECE2     3' GAGGGTCTGTACTCATGTC   69683     CAAC       ACT
                                GAG   CTGTACTTG   TGTC
                                |||   |||||||||   ||||
                                CTC   GACATGAGT   ACAG
                                  CCA_       ___
GAM3059 FLJ13852 3' GAGCCACCTGGCCACTTGTCA 69684     A    TA  TG
                                GAGC ACCTG  CT  ACTTGTCA
                                |||| |||||  ||  ||||||||
                                CTCG TGGAC  GG  TGAACAGT
                                  G    C_  __
GAM3059 KIAA1958 3' GCAACTTGTGCTTCAGTCA   69685      C   A   GACTT
                                GCAAC TGT CTT     GTCA
                                ||||| ||| |||     ||||
                                CGTTG ACA GAA     CAGT
                                   A   C   GT___
GAM3059 MGC4604  3' GAGATTATACTTGGCTTGT   69686     CAACC      A
                                GAG    TGTACTTG CTTGT
                                |||    |||||||| |||||
                                CTC    ATATGAAC GAACA
                                  TA___       C
GAM3059 RPS6KB1  3' GCAATTTGTACTTGCCTA    69687     CC       A
                                GCAA  TGTACTTG CTTG
                                ||||  |||||||| ||||
                                CGTT  ACATGAAC GGAT
                                   AA       _
GAM3059 SYT13    3' GCCAAGTATGACTTGACTTGT  69688    AACC  _
                                GC    TGT ACTTGACTTGT
                                ||    ||| ||||||||||
                                CG    ATA TGAACTGAACA
                                 GTTC   C
GAM3059 LOC127428 3' GAGCAATTTGTTTTCAACTTA 69689       CC   AC TG
                                GAGCAA  TGT  T  ACTTG
                                ||||||  |||  |  |||||
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                                CTCGTT  ACA  A  TGAAT
                                   AA   AA GT
GAM3059  LOC152502 3'  GAGCAGAAGTACTTGACTTGTC 69690      ACCT
                                GAGCA   GTACTTGACTTGTC
                                |||||   ||||||||||||||
                                CTCGT   CATGAACTGAACAG
                                  CTT_
GAM3059  LOC51133  5'  AGCAGTCTGTCACTTGTC    69691     AC   ACTTG
                                AGCA  CTGT    ACTTGTC
                                ||||  ||||    |||||||
                                TCGT  GACA    TGAACAG
                                  CA   G____
GAM3060  KNSL1     3'  AGCCATTAGTCAGATGTCTGGG 69694        __   TA_  C
                                AGCCATTG  CGG   TC GGG
                                ||||||||  |||   || |||
                                TCGGTAAT  GTC   AG CCC
                                     CA   TAC  A
GAM3060  MAN2B1    5'  GCTGTAGCCCTGGGCAAT    69695    G  _  _
                                GC GTA TCC GGGCAAT
                                || ||| ||| |||||||
                                CG CAT GGG CCCGTTA
                                 A   C   A
GAM3060  WARS      5'  GCCACTGGTCACGCTGGGCA   69696       CGG   CC_
                                GCCATTG   TAT   GGGCA
                                |||||||   |||   |||||
                                CGGTGAC   GTG   CCCGT
                                    CA_   CGA
GAM3060  C20orf54  5'  GCCATGGCGGTATCTGC     69697      T      CGG
                                GCCAT GCGGTATC   GC
                                ||||| ||||||||   ||
                                CGGTA CGCCATAG   CG
                                   C       A__
GAM3060  KIAA1143  3'  AGCCATTGTGTCTGGCCTGGG  69698        CG  AT__  _
                                AGCCATTG  GT    CC GGG
                                ||||||||  ||    || |||
                                TCGGTAAC  CA    GG CCC
                                     A_  GACC  A
GAM3060  PPP4R1L   5'  AGCTACTGCTGTGTGGGCAATC 69699     C    G  ATCC
                                AGC ATTGC GT    GGGCAATC
                                ||| ||||| ||    ||||||||
                                TCG TGACG CA    CCCGTTAG
                                  A    A  CA__
GAM3060  ZNF297B   5'  AGCCTTGAACTCTTGGGTAATC 69700     A   CGGTA  C_   C
                                AGCC TTG     TC  GGG AATC
                                |||| |||     ||  ||| ||||
                                TCGG AAC     AG  CCC TTAG
                                   _   TTG__  AA   A
GAM3060  LOC146350 5'  AGCTGTGTGGCTTCAGGGCAAT 69701     CAT  C   A  C
              C                   AGC   TG GGT TC GGGCAATC
                                |||   || ||| || ||||||||
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                                TCG   AC CCG AG CCCGTTAG
                                  AC_  A   A  T
GAM3060  LOC147219 5'  AGCTGTTGTGTATACAAGCAAT 69702     CA   CG    C
                                AGC  TTG  GTAT CGGGCAAT
                                |||  |||  |||| ||||||||
                                TCG  AAC  CATA GTTCGTTA
                                  AC   A_   T
GAM3060  LOC147837 3'  GCCATCACATCCGGGTAAT    69703      TG GGT      C
                                GCCAT  C   ATCCGGG AAT
                                |||||  |   ||||||| |||
                                CGGTA  G   TAGGCCC TTA
                                   GT ___      A
GAM3060  LOC253044 3'  ATTATTGTATCTGGGTGATC   69704     CG    C   CA
                                ATTG  GTATC GGG  ATC
                                ||||  ||||| |||  |||
                                TAAT  CATAG CCC  TAG
                                  AA    A   AC
GAM3061  CALCR     3'  TGATATGTTCGGTTCCTGGG   69707         CA  GAC   C
                                TGATATGTTT  GT   CCT GG
                                ||||||||||  ||   ||| ||
                                ACTATACAAG  CA   GGA CC
                                      C_  A__   C
GAM3061  MGC24447  3'  TGTTAATAGTGACCCTCGGA   69708     TC_
                                TGTT   AGTGACCCTCGGA
                                ||||   ||||||||||||
                                ACAA   TCACTGGGAGCCT
                                  TTA
GAM3061  SFRS10    3'  TGGTATGTTTCATGGACTGGA  69709    A       GT   CCTC
                                TG TATGTTTCA  GAC    GGA
                                || |||||||||  |||    |||
                                AC ATACAAAGT  CTG    CCT
                                 C        AC   A___
GAM3062  CHAC      3'  ATAAATGGACATATGGGCA    69712           AGAT
                                ATAAGTGGACATAT    GCA
                                ||||||||||||||    |||
                                TATTTACCTGTATA    CGT
                                        CC__
GAM3062  GGCX      3'  ACAAGTGGCAGGGTGCAG     69713        A  TATAGA
                                ATAAGTGG CA     TGCAG
                                |||||||| ||     |||||
                                TGTTCACC GT     ACGTC
                                    _ CCC___
GAM3062  ITPKB     3'  GTGGACAGATGCAGA       69714        TATA
                                GTGGACA    GATGCAGA
                                |||||||    ||||||||
                                CACCTGT    CTACGTCT
                                     ____
GAM3062  KCNAB1    3'  TAAGTGGACATAACATTAGA   69715           ____
                                TAAGTGGACATA    TAGA
                                ||||||||||||    ||||
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                                ATTCACCTGTAT   ATCT
                                      TGTA
GAM3062 KLRC4    5' ATAAGTGGTGTATATTTTGACA 69716       ACA   GA_ _
             G                   ATAAGTGG  TATA  TG CAG
                                 ||||||||  ||||  || |||
                                 TATTCACC  ATAT  AC GTC
                                     AC_   AAA  T
GAM3062 MLF2     3' CAAGTCAGTAGATGCAGA    69717      _ ACATA
                                 TAAGT GG    TAGATGCAGA
                                 |||||| ||    ||||||||||
                                 GTTCA TC    ATCTACGTCT
                                    G _____
GAM3062 NR1I2    3' GTGTTCAAATGGATGCAGA   69718    GA  T  A
                                 GTG  CA AT GATGCAGA
                                 |||  || || ||||||||
                                 CAC  GT TA CTACGTCT
                                   AA  T  C
GAM3062 NR1I2    3' GTGTTCAAATGGATGCAGA   69718    GA  T  A
                                 GTG  CA AT GATGCAGA
                                 |||  || || ||||||||
                                 CAC  GT TA CTACGTCT
                                   AA  T  C
GAM3062 SCA1     3' AAGTGGACATAGTACAGA    69719        TA   A
                                 AAGTGGACA  TAG TGCAGA
                                 |||||||||  ||| ||||||
                                 TTCACCTGT  ATC ATGTCT
                                          __  _
GAM3062 C11orf25 5' AGTGGCAGATGCAGA      69720      ACATA
                                 AGTGG    TAGATGCAGA
                                 |||||    ||||||||||
                                 TCACC    GTCTACGTCT
                                   _____
GAM3062 CEP3     3' ATAAGTGACAACATCTGATGTA 69721       __    ATA   C
             GAA                   ATAAGTG  GACAT   GATG AGAA
                                   |||||||  |||||   |||| ||||
                                   TATTCAC  TTGTA   CTAC TCTT
                                      TG    GA_   A
GAM3062 FHX      3' GTGGACATGATCCATGA     69722        ATA  G  _
                                 GTGGACAT   GAT CA GA
                                 ||||||||   ||| || ||
                                 CACCTGTA   CTA GT CT
                                      ___  G  A
GAM3062 FLJ10352 3' TAAATGTTGAGTTGTAGATGCA 69723      GACATA__
             GAA                   TAAGTG      TAGATGCAGAA
                                   ||||||      ||||||||||
                                   ATTTAC      ATCTACGTCTT
                                     AACTCAAC
GAM3062 FLJ22127 3' GTGGACATATGGACTCGA    69724        A  GCA
                                 GTGGACATAT GAT   GA
                                 |||||||||| |||   ||
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                                CACCTGTATA CTG   CT
                                      C   AG_
GAM3062  GDAP1L1   3'  GTGGCATGGATGCAGA      69725      A   ATA
                                GTGG CAT   GATGCAGA
                                |||| |||   ||||||||
                                CACC GTA   CTACGTCT
                                  _   C__
GAM3062  H-L(3)MBT 3'  AGTGGGTAGAGAGCAGA     69726       ACA  T   T
                                AGTGG   TA AGA GCAGA
                                |||||   || ||| |||||
                                TCACC   AT TCT CGTCT
                                  C__  C   _
GAM3062  KIAA1340  3'  ATAAATGGGCATAGCTTAGA   69727         A   ___
                                ATAAGTGG CATA   TAGA
                                |||||||| ||||   ||||
                                TATTTACC GTAT   ATCT
                                     C    CGA
GAM3062  KNSL7     3'  AGGGTGTATATGGATGCAGAA  69728    T  AC_   A
                                AG GG   ATAT GATGCAGAA
                                || ||   |||| |||||||||
                                TC CC   TATA CTACGTCTT
                                 _ ACA    C
GAM3062  P5-1      3'  GTGGGTACATAAATGGAG     69729      AC       C
                                GTGG  ATATAGATG AG
                                ||||  |||||||||  ||
                                CACC  TGTATTTAC TC
                                  CA        C
GAM3062  PP1044    5'  TAAATGGATATAGGTAAAGATG 69730         C   T____
            CAG                    TAAGTGGA ATA     AGATGCAG
                                |||||||| |||     ||||||||
                                ATTTACCT TAT     TCTACGTC
                                     A   CCATT
GAM3062  SIRPB1    3'  TAAGTGGACACATGCA      69731           ATAG
                                TAAGTGGACAT    ATGCA
                                ||||||||||    |||||
                                ATTCACCTGTG    TACGT
                                              ____
GAM3062  LOC148811 3'  TAAGGGGAGAGATGCAG     69732      T   CATAT
                                TAAG GGA     AGATGCAG
                                |||| |||     ||||||||
                                ATTC CCT     TCTACGTC
                                  C   C____
GAM3062  LOC149711 3'  TAAGTGGATAGACATATGGA   69733         ____    A
                                TAAGTGGA    CATAT GA
                                ||||||||    ||||| ||
                                ATTCACCT    GTATA CT
                                     ATCT    C
GAM3062  LOC150630 5'  AGTGGCAGAAGATGCAG     69734       A  TAT
                                AGTGG CA   AGATGCAG
                                ||||| ||   ||||||||
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                                TCACC GT   TCTACGTC
                                  _ CT_
GAM3062  LOC150819 5'  AGTTGGACTAAAATGCAG    69735     _    ATAT
                                AGT GGAC    AGATGCAG
                                ||| ||||    ||||||||
                                TCA CCTG    TTTACGTC
                                  A    AT__
GAM3062  LOC154877 3'  AGTGGAATGGATGCAGA     69736       CAT  A
                                AGTGGA   AT GATGCAGA
                                ||||||   || ||||||||
                                TCACCT   TA CTACGTCT
                                   ___  C
GAM3062  LOC158327 3'  ATAAGTGGTGTCCCTGCAGAA  69737         ACATATAGA
                                ATAAGTGG        TGCAGAA
                                ||||||||        |||||||
                                TATTCACC        ACGTCTT
                                     ACAGGG___
GAM3062  LOC196540 3'  GGAGTACATGGATGCAGA    69738     C_    A
                                GGA  ATAT GATGCAGA
                                |||  |||| ||||||||
                                CCT  TGTA CTACGTCT
                                  CA    C
GAM3062  LOC220394 5'  ATGGACATATTCTGAGA     69739          AGA  C
                                GTGGACATAT   TG AGA
                                ||||||||||   || |||
                                TACCTGTATA   AC TCT
                                      AG_  _
GAM3062  LOC254428 3'  ATAGGTGGACATGGGTCAACAG 69740     A       ATAGAT
                                ATA GTGGACAT      GCAG
                                ||| ||||||||      ||||
                                TAT CACCTGTA      TGTC
                                  C       CCCAGT
GAM3062  LOC92405  3'  TAAGTAGACATGTGTAACAGAA 69741           ATAGAT
                                TAAGTGGACAT     GCAGAA
                                ||||||||||      ||||||
                                ATTCATCTGTA     TGTCTT
                                      CACAT_
GAM3063  BCL10     3'  ACTGAGGTTTAGGCCAA     69744       AAGACT
                                ACTGA     TTTAGGCCAA
                                |||||     ||||||||||
                                TGACT     AAATCCGGTT
                                   CC_____
GAM3063  BNC       3'  TCAGTGAAAGACCTCTTGGGCT 69745     C          A_   C
              AAG                    TCA TGAAAGACTTTT  GGC AAG
                                ||| ||||||||||||  ||| |||
                                AGT ACTTTCTGGAGA  CCG TTC
                                  C          AC   A
GAM3063  CACNG1    3'  TCTCTGGAAGGTTCCAGGCCAA 69746    A   A   AC
              G                     TC CTG AAG  TTTTAGGCCAAG
                                || ||| |||  ||||||||||||
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                                AG GAC TTC  AAGGTCCGGTTC
                                 A   C   C_
GAM3063  CDKN2C   5'  TCCTGGGAAACGTAGGCCAAG  69747    A   AA    TTT
                                TC CTG  AGAC   TAGGCCAAG
                                || |||  ||||   |||||||||
                                AG GAC  TTTG   ATCCGGTTC
                                 _   CC    C__
GAM3063  CXorf6   3'  ACTGAAAGGCTTTAAACCA   69748        A    T
                                ACTGAAAG CTTT AGGCCA
                                |||||||| |||| ||||||
                                TGACTTTC GAAA TTTGGT
                                     C    _
GAM3063  G1P3     3'  ACTGGAAGAGTTAGGCCAAG   69749     A    CTT
                                ACTG AAGA   TTAGGCCAAG
                                |||| ||||   ||||||||||
                                TGAC TTCT   AATCCGGTTC
                                  C    C__
GAM3063  G1P3     3'  ACTGGAAGAGTTAGGCCAAG   69749     A    CTT
                                ACTG AAGA   TTAGGCCAAG
                                |||| ||||   ||||||||||
                                TGAC TTCT   AATCCGGTTC
                                  C    C__
GAM3063  G1P3     3'  ACTGGAAGAGTTAGGCCAAG   69749     A    CTT
                                ACTG AAGA   TTAGGCCAAG
                                |||| ||||   ||||||||||
                                TGAC TTCT   AATCCGGTTC
                                  C    C__
GAM3063  HIP2     3'  TCACTGAAAAACTAAGTTGG   69750          TTTA_
                                TCACTGAAAGACT     GG
                                ||||||||||||     ||
                                AGTGACTTTTTGA     CC
                                       TTCAA
GAM3063  PCDHGC3  5'  TCGCTGAGAAACTTTCAG    69751    A    A
                                TC CTGA AGACTTTTAG
                                || |||| ||||||||||
                                AG GACT TTTGAAAGTC
                                 C    C
GAM3063  PCDHGC3  5'  TCGCTGAGAAACTTTCAG    69751    A    A
                                TC CTGA AGACTTTTAG
                                || |||| ||||||||||
                                AG GACT TTTGAAAGTC
                                 C    C
GAM3063  PCDHGC3  5'  TCGCTGAGAAACTTTCAG    69751    A    A
                                TC CTGA AGACTTTTAG
                                || |||| ||||||||||
                                AG GACT TTTGAAAGTC
                                 C    C
GAM3063  POP4     3'  TCACTGAAAGGTGGACATTTAG 69752          ____   T
              G                  TCACTGAAA    GAC TTTAGG
                                 |||||||||    ||| ||||||
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                                AGTGACTTT   CTG AAATCC
                                     CCAC   T
GAM3063  PRKRA    3'  ACTGAAAGATTTTTTAAG    69753        C_
                                ACTGAAAGA  TTTTAGG
                                |||||||||  |||||||
                                TGACTTTCT  AAAATTC
                                     AA
GAM3063  TBL2     3'  CTGAAAGGCTTCCACC     69754       A    AG
                                CTGAAAG CTTTT  GCC
                                |||||||| |||||  |||
                                GACTTTC GAAGG  TGG
                                    C    __
GAM3063  TBL2     3'  CTGAAAGGCTTCCACC     69754       A    AG
                                CTGAAAG CTTTT  GCC
                                |||||||| |||||  |||
                                GACTTTC GAAGG  TGG
                                    C    __
GAM3063  UNG      3'  TCACTGAAAGTCTAACCA   69755        A  TTTA
                                TCACTGAAAG CT   GGCCA
                                |||||||||| ||   |||||
                                AGTGACTTTC GA   TTGGT
                                     A  _____
GAM3063  UNG      3'  TCACTGAAAGTCTAACCA   69755        A  TTTA
                                TCACTGAAAG CT   GGCCA
                                |||||||||| ||   |||||
                                AGTGACTTTC GA   TTGGT
                                     A  _____
GAM3063  ZNF261   3'  TCACTGAAGGGACAGGCCA  69756       A_  TTTT
                                TCACTGAA  GAC   AGGCCA
                                ||||||||  |||   ||||||
                                AGTGACTT  CTG   TCCGGT
                                     CC  _____
GAM3063  BTN1A1   3'  TCACTGAAGGATGACTTCTAGG 69757       A___
                                TCACTGAA   GACTTTTAGG
                                ||||||||   ||||||||||
                                AGTGACTT   CTGAAGATCC
                                     CCTA
GAM3063  C20orf44 3'  TCATGAAAGGGGAGGCCAA  69758    C    ACTTTT
                                TCA TGAAAG     AGGCCAA
                                ||| ||||||     |||||||
                                AGT ACTTTC     TCCGGTT
                                  _     CCC___
GAM3063  CCNE1    3'  TGGGAGTCCCTTAGGTCAAG  69759    AA  A      C
                                TG  AG CTTTTAGG CAAG
                                ||  || |||||||| ||||
                                AC  TC GGGAATCC GTTC
                                 CC  A       A
GAM3063  CCNE1    3'  TGGGAGTCCCTTAGGTCAAG  69759    AA  A      C
                                TG  AG CTTTTAGG CAAG
                                ||  || |||||||| ||||
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                                AC  TC GGGAATCC GTTC
                                 CC  A       A
GAM3063  DKFZP434B1727 3'  TCACTGAAAGGTTTTTGG    69760          AC    A
                                TCACTGAAAG  TTTT GG
                                ||||||||||  |||| ||
                                AGTGACTTTC  AAAA CC
                                     CA   _
GAM3063  DKFZP564O1863 3'  TCAGCTGAAAGGTTTTAAG   69761    _     AC
                                TCA CTGAAAG  TTTTAGG
                                ||| |||||||  |||||||
                                AGT GACTTTC  AAAATTC
                                  C      C_
GAM3063  FLJ20086  3'  TCACTGAAAGTTTAATTAAG   69762          ACTT_
                                TCACTGAAAG    TTAGG
                                ||||||||||    |||||
                                AGTGACTTTC    AATTC
                                     AAATT
GAM3063  FLJ20371  3'  TCATGAGAGGCTCTTAGG    69763    C   A  A
                                TCA TGA AG CTTTTAGG
                                ||| ||| || ||||||||
                                AGT ACT TC GAGAATCC
                                  _  C  C
GAM3063  H326     5'  TCACTGAAGTAAGGACCAGGC  69764        A____   TTT
                                TCACTGAA    GACT   AGGC
                                ||||||||    ||||   ||||
                                AGTGACTT    CTGG   TCCG
                                     CATTC   ___
GAM3063  HBXAP    3'  TCACAGAAAGACTTCAGG    69765     T        T
                                TCAC GAAAGACTTT AGG
                                |||| |||||||||| |||
                                AGTG CTTTCTGAAG TCC
                                  T        _
GAM3063  MGC21621  3'  GAAAGACTTAGCTACAAG    69766         TTA  __
                                GAAAGACTT   GGC  CAAG
                                |||||||||   |||  ||||
                                CTTTCTGAA   TCG  GTTC
                                     ___   AT
GAM3063  PRO1580   5'  CTGAGGGAGAGTGGAGGCCAAG 69767      A__   CTTTT
                                CTGA   AGA    AGGCCAAG
                                ||||   |||    ||||||||
                                GACT   TCT    TCCGGTTC
                                  CCC   CACC_
GAM3063  PRO2325   5'  TCATTGTAAGACTTTTGG    69768     C  A       A
                                TCA TG AAGACTTTT GG
                                ||| || |||||||| ||
                                AGT AC TTCTGAAAA CC
                                  A  A       _
GAM3063  RRN3     3'  TCACTGAAAGCTCATCAGTCAA 69769          A  _   GC
            G                    TCACTGAAAG CTT TTAG  CAAG
                                ||||||||| ||| ||||  ||||
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                                AGTGACTTTC GAG AGTC  GTTC
                                      _  T   A_
GAM3063  STIP-1    3'  TCACTAAAAGGTTTTAGG    69770         AC
                                TCACTGAAAG  TTTTAGG
                                ||||||||||  |||||||
                                AGTGATTTTC  AAAATCC
                                     C_
GAM3063  VDU1      3'  CACTGAAAGACTTTATGG    69771           TA
                                CACTGAAAGACTTT  GG
                                ||||||||||||||  ||
                                GTGACTTTCTGAAA  CC
                                        TA
GAM3063  LOC146512 3'  CTGGGAGACTCAGGCCAAG   69772     AA     TT
                                CTG  AGACTT  AGGCCAAG
                                |||  ||||||  ||||||||
                                GAC  TCTGAG  TCCGGTTC
                                  CC     __
GAM3063  LOC146669 5'  TCACTGAGGGTCTTCCAGG   69773       AAGA
                                TCACTGA   CTTTTAGG
                                |||||||   ||||||||
                                AGTGACT   GAAGGTCC
                                    CCCA
GAM3063  LOC200312 3'  TCCTGAAAGACGGTCAGG    69774    A       TT
                                TC CTGAAAGAC  TTAGG
                                || |||||||||  |||||
                                AG GACTTTCTG  AGTCC
                                  _       CC
GAM3063  LOC202986 5'  TCACTGAAAGATCTAGG     69775          CT
                                TCACTGAAAGA  TTTAGG
                                ||||||||||  ||||||
                                AGTGACTTTCT  AGATCC
                                        __
GAM3063  LOC203536 3'  TCACTGAAGAATTTAGCACA  69776        A  CT    GC
                                TCACTGAA GA  TTTAG  CA
                                ||||||||  ||  |||||  ||
                                AGTGACTT CT  AAATC  GT
                                     _  T_    GT
GAM3063  LOC221395 3'  TCACTGAAGTATTTCCTAGG  69777        AGAC_
                                TCACTGAA    TTTTAGG
                                ||||||||    |||||||
                                AGTGACTT    AGGATCC
                                    CATAA
GAM3063  LOC221596 3'  TCACTGAAGGCTTTTCCA    69778        A A    AGG
                                TCACTGAA G CTTTT   CCA
                                ||||||||  |  |||||   |||
                                AGTGACTT C GAAAA   GGT
                                     _ C    ___
GAM3063  LOC256940 3'  TCACTGAAGGGCTTTCAA    69779        AGA
                                TCACTGAA   CTTTTAG
                                ||||||||   |||||||
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                                AGTGACTT   GAAAGTT
                                     CCC
GAM3063  LOC89919  5'  TCACTTGATTAGGCCA      69780       _  AAGACTT
                                TCACT GA      TTAGGCCA
                                ||||| ||      ||||||||
                                AGTGA CT      AATCCGGT
                                  A  _______
GAM3063  LOC93496  3'  TCACTGAAGGATATTAGG     69781         A  CTT
                                TCACTGAA GA   TTAGG
                                |||||||| ||   |||||
                                AGTGACTT CT   AATCC
                                     C  AT_
GAM3064  CGTHBA    3'  AGCTAGCTCTTCCTCCAG     69784           ATAACG
                                AGCTAGTTCTTC     TCCAG
                                ||||||||||||     |||||
                                TCGATCGAGAAG     AGGTC
                                       G_____
GAM3064  CIT       3'  AGCTAGTTCTATATAGCAG    69785          TC   ACGTC
                                AGCTAGTTCT  ATA    CAG
                                ||||||||||  |||    |||
                                TCGATCAAGA  TAT    GTC
                                      TA   C____
GAM3064  PIP5K1B   3'  AGCTAGTTTTCTATAAAGT    69786         C  _   C
                                AGCTAGTT TTC ATAA GT
                                |||||||| ||| |||| ||
                                TCGATCAA AAG TATT CA
                                     _  A   T
GAM3064  C6.1A     3'  AGTTAGTTCCTTTTCATTCCAG 69787     C       CATAACG
              A                  AG TAGTTCTT      TCCAGA
                                 || ||||||||      ||||||
                                 TC ATCAAGGA      AGGTCT
                                  A       AAAGTA_
GAM3064  KIAA0555  3'  CTAGTTCTTCCTCCAG      69788          ATAACG
                                CTAGTTCTTC     TCCAG
                                ||||||||||     |||||
                                GATCAAGAAG     AGGTC
                                      G_____
GAM3064  KIAA0638  3'  GCTGGTTCTTCAGGAGGCCAGA 69789     A       TAAC T
                                GCT GTTCTTCA    G CCAGA
                                ||| ||||||||    | |||||
                                CGA CAAGAAGT    C GGTCT
                                  C       CCTC _
GAM3064  KIAA0766  3'  GCTAATTCTTCATTGTGCCAG  69790           AAC  _
                                GCTAGTTCTTCAT   GT CCAG
                                ||||||||||||   || ||||
                                CGATTAAGAAGTA   CA GGTC
                                       A__  C
GAM3064  KIAA1041  3'  CAGTTCTTCATGCTGCTCAG   69791          AAC TC
                                TAGTTCTTCAT   G  CAG
                                ||||||||||   |  |||
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                                GTCAAGAAGTA   C  GTC
                                      CGA GA
GAM3064  KIAA1046  3'  AGTCAGTTCTTTTATTCCAGA  69792    C       CATAACG
                                AG TAGTTCTT       TCCAGA
                                || ||||||||       ||||||
                                TC GTCAAGAA       AGGTCT
                                 A       AATA___
GAM3064  LOC122726 3'  AGCAAGTTCTTCATTATATCTA 69793     T        AAC   C
           G                     AGC AGTTCTTCAT   GTC AG
                                ||| ||||||||||   ||| ||
                                TCG TCAAGAAGTA   TAG TC
                                  T        ATA   A
GAM3064  LOC200235 3'  AGCCAGTTCTGAGTTTGTTCAG 69794          TCATAAC  C
           A                     AGCTAGTTCT      GT CAGA
                                ||||||||||       || ||||
                                TCGGTCAAGA      CA GTCT
                                      CTCAAA_  A
GAM3064  LOC255232 3'  AGCTGTTTCTTCATGGGCAAAA 69795      AG       AA_  TC_
           CAG                     AGCT  TTCTTCAT   CG   CAG
                                ||||  ||||||||   ||   |||
                                TCGA  AAGAAGTA   GT   GTC
                                  CA       CCC  TTT
GAM3065  ACN      3'  GGTGACCCAGTCCTGGCCCC   69798      __    C
                                GGTG  CCAG CCTGGCCCC
                                ||||  |||| |||||||||
                                CCAC  GGTC GGACCGGGG
                                  TG    A
GAM3065  CBS      5'  TGAAACGTGCGTCCTGGCCC   69799     T   G   CAGC
                                TGA ACG TGC    CCTGGCCC
                                ||| ||| |||    ||||||||
                                ACT TGC ACG    GGACCGGG
                                  T   _   CA__
GAM3065  CHRNB4    5'  AGCGCCGGTCCTGGCCCC    69800       AGC
                                GGTGCC   CCTGGCCCC
                                ||||||   |||||||||
                                TCGCGG   GGACCGGGG
                                    CCA
GAM3065  DBN1     5'  GGCGGGGCGCCCTGGCCCC    69801      CCA_
                                GGTG    GCCCTGGCCCC
                                ||||    ||||||||||
                                CCGC    CGGGACCGGGG
                                  CCCG
GAM3065  ENG      5'  TGACAGCAGCAGTCCTGGCCCC 69802    T    GC   C
                                A ACGGT  CAG CCTGGCCCC
                                | |||||  ||| |||||||||
                                A TGTCG  GTC GGACCGGGG
                                 C    TC   A
GAM3065  ESRRA    3'  GATGGCATTGCCCTGGCCC    69803      C  __
                                GGTG CA  GCCCTGGCCC
                                |||| ||  ||||||||||
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                                CTAC GT  CGGGACCGGG
                                  C  AA
GAM3065  GGA1     3'  GGGCCTGAGGTCCTGGCCC   69804    T  __ C_
                                GG GCC  AG  CCTGGCCC
                                || |||  ||  ||||||||
                                CC CGG  TC  GGACCGGG
                                 _  AC  CA
GAM3065  MAP3K11  5'  GGCATCCGGGCCCTGGCCC   69805     _ A_
                                GGTG CC  GCCCTGGCCC
                                |||| ||  ||||||||||
                                CCGT GG  CGGGACCGGG
                                  A  CC
GAM3065  MTM1     3'  TAATGCGGTGCCAGGGTCCC   69806     A       CCCT  _
                                TGAT CGGTGCCAG    GG CCC
                                |||| |||||||||    || |||
                                ATTA GCCACGGTC    CC GGG
                                  C        _____  A
GAM3065  MYO1A    5'  GGGGCATAAGAGTCCTGGCCCC 69807    T  C____  C
                                GG GC     AG CCTGGCCCC
                                || ||     || |||||||||
                                CC CG     TC GGACCGGGG
                                 C  TATTC  A
GAM3065  PACSIN1  3'  CGGTGGGGCAGCCCTGGTTCC  69808      C__       CC
                                CGGTG   CAGCCCTGG  CC
                                |||||   |||||||||  ||
                                GCCAC   GTCGGGACC  GG
                                   CCC        AA
GAM3065  TNXB     5'  CACAGGCTCTGGCCCC      69809      TGCCA  C
                                TACGG     GC CTGGCCCC
                                |||||     || ||||||||
                                GTGTC     CG GACCGGGG
                                   ______  A
GAM3065  VHL      3'  TGATCTGCCTGCCCTGGCC   69810     ACGG   A
                                TGAT    TGCC GCCCTGGCC
                                ||||    |||| |||||||||
                                ACTA    ACGG CGGGACCGG
                                  G___    A
GAM3065  BICD2    3'  TGACAAGTGGCCCTGGCCC   69811      C   CCA
                                TGATA GGTG   GCCCTGGCCC
                                ||||| ||||   ||||||||||
                                ACTGT TCAC   CGGGACCGGG
                                   _   ___
GAM3065  DKFZp564A176 3'  GTGCCGCAGCCCTGGCTCC   69813       __       _
                                GTGCC  AGCCCTGGC CC
                                |||||  ||||||||| ||
                                CACGG  TCGGGACCG GG
                                   CG        A
GAM3065  DKFZp564A176 5'  GGCCTCAGCTCTGGCCCC    69812     GC   C
                                GGT  CAGC CTGGCCCC
                                |||  |||| ||||||||
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                                CCG  GTCG GACCGGGG
                                  GA    A
GAM3065  EPN2     3'  GATCAGGGCCAGCCCTGGTCCC 69814     A   T         _
                                GAT CGG GCCAGCCCTGG CCC
                                ||| ||| |||||||||||| |||
                                CTA GTC CGGTCGGGACC GGG
                                  _   C          A
GAM3065  FLJ31300 3'  GATTCATGAGCCCTGGCCC    69815     A  G  CC
                                GAT CG TG  AGCCCTGGCCC
                                ||| || ||  ||||||||||
                                CTA GT AC  TCGGGACCGGG
                                  A  _  __
GAM3065  KIAA0125 3'  ACTTTGCTGGCCCTGGCCC    69816    GG   CA
                                AC  TGC  GCCCTGGCCC
                                ||  |||  ||||||||||
                                TG  ACG  CGGGACCGGG
                                 AA   AC
GAM3065  KIAA0182 3'  TGACTGGCAGCCCTGGCC    69817     AC  TGC
                                TGAT  GG   CAGCCCTGGCC
                                ||||  ||   ||||||||||
                                ACTG  CC   GTCGGGACCGG
                                  A_  ____
GAM3065  KIAA0514 3'  CGGCTCAGCCGGCCCTGGC    69818      ___   A
                                CGGT   GCC GCCCTGGC
                                ||||   ||| ||||||||
                                GCCG   CGG CGGGACCG
                                  AGT   C
GAM3065  KIAA0547 3'  TGATCTGCCAGCCTTGGCC    69819     ACGG      C
                                TGAT    TGCCAGCC TGGCC
                                ||||    |||||||| |||||
                                ACTA    ACGGTCGG ACCGG
                                  G___       A
GAM3065  KIAA1138 3'  TGAGTGTGGCCCTGGCCC    69820    C    CCA
                                A GGTG   GCCCTGGCCC
                                | ||||   ||||||||||
                                A TCAC   CGGGACCGGG
                                 C    AC_
GAM3065  KIAA1586 5'  TGATCTGCCAGCCTTGGCC    69819     ACGG      C
                                TGAT    TGCCAGCC TGGCC
                                ||||    |||||||| |||||
                                ACTA    ACGGTCGG ACCGG
                                  G___       A
GAM3065  KIAA1879 5'  TGACTGTCCTGAGCCCTGGC   69821     ACG  G  __
                                TGAT   GT CC  AGCCCTGGC
                                ||||   || ||  |||||||||
                                ACTG   CA GG  TCGGGACCG
                                  A__  _  AC
GAM3065  MGC15827 3'  GGGACCGGCCCTGGCCCC    69822    TG  A
                                GG  CC GCCCTGGCCCC
                                ||  || ||||||||||
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                                CC  GG CGGGACCGGGG
                                 CT  C
GAM3065  MGC26988  3'  CGGTTGTAGCCCTGGCTCC   69823     GCC       _
                                CGGT   AGCCCTGGC CC
                                ||||   ||||||||| ||
                                GCCA   TCGGGACCG GG
                                  ACA        A
GAM3065  LOC127281 5'  CGCTGCCAGCCCTGGTTCC   69824    G          CC
                                CG TGCCAGCCCTGG  CC
                                || ||||||||||||  ||
                                GC ACGGTCGGGACC  GG
                                 G          AA
GAM3065  LOC151614 3'  TGATCCACCAGCCTTGGCC   69825     ACGGT      C
                                TGAT    GCCAGCC TGGCC
                                ||||    ||||||| |||||
                                ACTA    TGGTCGG ACCGG
                                  GG___      A
GAM3065  LOC152897 3'  TGATCTGCCAGCCTTGGCC   69819     ACGG       C
                                TGAT    TGCCAGCC TGGCC
                                ||||    |||||||| |||||
                                ACTA    ACGGTCGG ACCGG
                                  G___       A
GAM3065  LOC157848 3'  GGTGCTCAGCTCTGGCCCC   69826      _   C
                                GGTGC CAGC CTGGCCCC
                                ||||| |||| ||||||||
                                CCACG GTCG GACCGGGG
                                  A   A
GAM3065  LOC158292 5'  TGGCACGGTGCTAGGAACATGG 69827    A       C  CCC__
            C                    TG TACGGTGC AG     TGGC
                                || ||||||||  ||     ||||
                                AC GTGCCACG TC     ACCG
                                 C       A  CTTGT
GAM3065  LOC219920 5'  GGTGGGTTCAGCCTGGCCCC   69828     C___    C
                                GGTG    CAGCC TGGCCCC
                                ||||    ||||| |||||||
                                CCAC    GTCGG ACCGGGG
                                  CCAA    _
GAM3065  LOC92661  3'  TAAAACGGTTGGCCCTGGCC   69829    T    GCCA
                                TGA ACGGT    GCCCTGGCC
                                ||| |||||    |||||||||
                                ATT TGCCA    CGGGACCGG
                                  T    AC__
GAM3066  ADAM22    5'  CCGCCGAGTCCGTTTCCCTC   69832       _   __
                                CCGCCGAG CCGT  TCCTC
                                |||||||| ||||  |||||
                                GGCGGCTC GGCA  GGGAG
                                    A   AA
GAM3066  ADAM22    5'  CCGCCGAGTCCGTTTCCCTC   69832       _   __
                                CCGCCGAG CCGT  TCCTC
                                |||||||| ||||  |||||
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                                GGCGGCTC GGCA  GGGAG
                                    A   AA
GAM3066  ADAM22   5'  CCGCCGAGTCCGTTTCCCTC  69832       _   __
                                CCGCCGAG CCGT  TCCTC
                                |||||||| ||||  |||||
                                GGCGGCTC GGCA  GGGAG
                                    A   AA
GAM3066  ADAM22   5'  CCGCCGAGTCCGTTTCCCTC  69832       _   __
                                CCGCCGAG CCGT  TCCTC
                                |||||||| ||||  |||||
                                GGCGGCTC GGCA  GGGAG
                                    A   AA
GAM3066  ADRA1D   3'  GCCCAGTTCCTCAGGGA    69833    G GCC
                                GCC A  GTTCCTCAGGGA
                                ||| |  ||||||||||||
                                CGG T  CAAGGAGTCCCT
                                  G ___
GAM3066  ANK1     5'  CCCCTGAGTCCCCCAGGGAC  69834   G  GAGCC
                                CC CC    GTTCCTCAGGGAC
                                || ||    ||||||||||||
                                GG GG    CAGGGGGTCCCTG
                                 _ ACT__
GAM3066  ANK1     5'  CCCCTGAGTCCCCCAGGGAC  69834   G  GAGCC
                                CC CC    GTTCCTCAGGGAC
                                || ||    ||||||||||||
                                GG GG    CAGGGGGTCCCTG
                                 _ ACT__
GAM3066  ANK1     5'  CCCCTGAGTCCCCCAGGGAC  69834   G  GAGCC
                                CC CC    GTTCCTCAGGGAC
                                || ||    ||||||||||||
                                GG GG    CAGGGGGTCCCTG
                                 _ ACT__
GAM3066  ARHGAP6  3'  CCACCGAGGCCAATTTGGGGAC 69835       _  TTCCTCA
                                CCGCCGAG CCG     GGGAC
                                |||||||| |||     |||||
                                GGTGGCTC GGT     CCCTG
                                    C  TAAAC__
GAM3066  CDC25B   3'  GACCCATCCTCAGGGAC    69836   G   T
                                GA CCGT CCTCAGGGAC
                                || |||| ||||||||||
                                CT GGTA GGAGTCCCTG
                                 G  _
GAM3066  CDC25B   3'  GACCCATCCTCAGGGAC    69836   G   T
                                GA CCGT CCTCAGGGAC
                                || |||| ||||||||||
                                CT GGTA GGAGTCCCTG
                                 G  _
GAM3066  CYP1B1   5'  CGCCGAGCCCCGCTGCCCTTGG 69837       __  _  CA_
            GGAC                  CGCCGAGCC  GTT CCT   GGGAC
                                |||||||||  ||| |||  |||||
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                                GCGGCTCGG  CGA GGG   CCCTG
                                     GG   C   AAC
GAM3066  EN2     5'  CCGCCGAGTCTTCCGAGGG   69838        CCG    TC
                                CCGCCGAG   TTCC  AGGG
                                ||||||||   ||||  ||||
                                GGCGGCTC   AAGG  TCCC
                                    AG_    C_
GAM3066  GNAI2   3'  CCCCCATCTTCCTCAGGG    69839    G   AGCCG
                                CC CCG     TTCCTCAGGG
                                || |||     ||||||||||
                                GG GGT     AAGGAGTCCC
                                 G   AG___
GAM3066  ID3     3'  CCGCCGAGCGTGCCGAGGCGGG 69840          C  T  TCA__
                                CCGCCGAGC GT CC     GGG
                                ||||||||| || ||     |||
                                GGCGGCTCG CA GG     CCC
                                     _  C  CTCCG
GAM3066  IHPK1   3'  GCCAAGCCCACCAGGG      69841         GTT C
                                GCCGAGCC   C TCAGGG
                                ||||||||   | ||||||
                                CGGTTCGG   G GGTCCC
                                    ___ T
GAM3066  IL27    3'  GCTGGCCCTTTCAGGGAC    69842    CGA   G  CC
                                GC   GCC TT  TCAGGGAC
                                ||   ||| ||  ||||||||
                                CG   CGG AA  AGTCCCTG
                                 AC_   G  __
GAM3066  KRT1    3'  GCTGAACTGTTTCTCAGGGA   69843    C    C   C
                                GC GAGC GTT CTCAGGGA
                                || |||| ||| ||||||||
                                CG CTTG CAA GAGTCCCT
                                 A    A   A
GAM3066  LAMA5   5'  CCCCGAGCTCCAGGGA      69844    G     CGT   TC
                                CC CCGAGC   TCC  AGGGA
                                || ||||||   |||  |||||
                                GG GGCTCG   AGG  TCCCT
                                 _     ____   __
GAM3066  LSS     3'  CGCTGTGCCTCCTCAGGG    69845     CGA   GT
                                CGC   GCC  TCCTCAGGG
                                |||   |||  |||||||||
                                GCG   CGG  AGGAGTCCC
                                  ACA   __
GAM3066  MALT1   5'  CCTCCGAGCCGCGGAGGCAGGG 69846    G        TCCT_
                                CC CCGAGCCGT     CAGGG
                                || |||||||||     |||||
                                GG GGCTCGGCG     GTCCC
                                 A         CCTCC
GAM3066  NFKB1   5'  CGCCGGGCCGCTCCGG      69847       A       TCA
                                CGCCG GCCGTTCC   GG
                                ||||| ||||||||   ||
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                                GCGGC CGGCGAGG  CC
                                  C      ___
GAM3066 PPP2R2B  3' CCAGCCTTTCTCAGGGA    69848   G   G  C
                                CC AGCC TTC TCAGGGA
                                || |||| ||| |||||||
                                GG TCGG AAG AGTCCCT
                                 _   A  _
GAM3066 PRKCABP  3' CCGCCGAGGTGTGATGGGGAC 69849       CC  TCCTCA
                                CCGCCGAG  GT    GGGAC
                                ||||||||  ||    |||||
                                GGCGGCTC  CA    CCCTG
                                    CA  CTAC__
GAM3066 RANBP3   3' GCCGACTCAGCCAGGGAC    69850     _  C_
                                GCCG TTC  TCAGGGAC
                                |||| |||  ||||||||
                                CGGC GAG  GGTCCCTG
                                  T  TC
GAM3066 RFC4     5' CCGCCGGCTCGTTCCTCAGG  69851      A  _
                                CCGCCG GC CGTTCCTCAGG
                                |||||| || ||||||||||
                                GGCGGC CG GCAAGGAGTCC
                                   _ A
GAM3066 RXRA     3' CCAGCCGGGCCAAGGCGGGGAC 69852   _   A   TTCCTCA
                                CC GCCG GCCG     GGGAC
                                || |||| ||||     |||||
                                GG CGGC CGGT     CCCTG
                                 T   C   TCCGC__
GAM3066 SRRM2    5' CCTCCTCGCTTCCTCAGGG   69853   G  GA  CG
                                CC CC  GC  TTCCTCAGGG
                                || ||  ||  ||||||||||
                                GG GG  CG  AAGGAGTCCC
                                 A  AG  __
GAM3066 TEM8     5' CGCCACGACCCTCAGGGAC   69854     AGC  TT
                                CGCCG  CG  CCTCAGGGAC
                                |||||  ||  ||||||||||
                                GCGGT  GC  GGAGTCCCTG
                                   ___ TG
GAM3066 TEM8     5' CGCCACGACCCTCAGGGAC   69854     AGC  TT
                                CGCCG  CG  CCTCAGGGAC
                                |||||  ||  ||||||||||
                                GCGGT  GC  GGAGTCCCTG
                                   ___ TG
GAM3066 TEM8     5' CGCCACGACCCTCAGGGAC   69854     AGC  TT
                                CGCCG  CG  CCTCAGGGAC
                                |||||  ||  ||||||||||
                                GCGGT  GC  GGAGTCCCTG
                                   ___ TG
GAM3066 DJ37E16.5 3' GATGGGTCCACCCAGGGAC  69855    GCC  _
                                GA  GTTC CTCAGGGAC
                                ||  |||| |||||||||
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                                CT   CAGG GGGTCCCTG
                                 ACC    T
GAM3066  DNAJC5   3'  GCCGGCCTCCCAGGGA      69856      A   GT   T
                                GCCG GCC  TCC CAGGGA
                                |||| |||  ||| ||||||
                                CGGC CGG  AGG GTCCCT
                                  _   __   _
GAM3066  DNAJC5   3'  GCCGGCCTCCCAGGGA      69856      A   GT   T
                                GCCG GCC  TCC CAGGGA
                                |||| |||  ||| ||||||
                                CGGC CGG  AGG GTCCCT
                                  _   __   _
GAM3066  DOC-1R   5'  CCAGCCGGCCGCTCCTCGGGG  69857    _   A        A
                                CC GCCG GCCGTTCCTC GGG
                                || |||| |||||||||| |||
                                GG CGGC CGGCGAGGAG CCC
                                 T   _         C
GAM3066  EIF5     5'  CCGCCGAGCAGCGGGGAGGG   69858         C  TCCTC
                                CCGCCGAGC GT     AGGG
                                ||||||||| ||     ||||
                                GGCGGCTCG CG     TCCC
                                     T  CCCC_
GAM3066  FAM3A    3'  GCCGGGCTGCTCCCAGAGA    69859      A  C    T
                                GCCG GC GTTCC CAGGGA
                                |||| || ||||| ||||||
                                CGGC CG CGAGG GTCTCT
                                  C  A    _
GAM3066  FLJ10385 5'  CGAAGTTCTCAGGGA       69860      CC    C
                                CGAG  GTTC TCAGGGA
                                ||||  |||| |||||||
                                GCTT  CAAG AGTCCCT
                                  __   _
GAM3066  FLJ11082 5'  CCGCCAAGCCGCGGGGA     69861           TCCTCA
                                CCGCCGAGCCGT     GGGA
                                ||||||||||||     ||||
                                GGCGGTTCGGCG     CCCT
                                       C_____
GAM3066  FLJ12242 3'  GCCTGAGGGCCTTCAGGGAC   69862     _  CCGTT  _
                                GCC GAG    CCT CAGGGAC
                                ||| |||    ||| |||||||
                                CGG CTC    GGA GTCCCTG
                                  A   CC___   A
GAM3066  FLJ20315 3'  GCTGTACCCACCTCAGGGAC   69863    CGA   GTT
                                GC   GCC   CCTCAGGGAC
                                ||   |||   ||||||||||
                                CG   TGG   GGAGTCCCTG
                                 ACA   GT_
GAM3066  FLJ22167 5'  GCCCAGTGCCCTCAGGGA    69864     G  CC  T
                                GCC AG  GT CCTCAGGGA
                                ||| ||  || |||||||||
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                                CGG TC  CG GGAGTCCCT
                                  G  A_  _
GAM3066  GOLGB1   5'  CCGCCGCGCCCCGCCAGGGAC  69865       AGC     _
                                CCGCCG   CGTTCC TCAGGGAC
                                ||||||   |||||| ||||||||
                                GGCGGC   GCGGGG GGTCCCTG
                                   ___     C
GAM3066  HSJ1     3'  CCTGGGCTTCACCAGGGAC   69866    GA_  CG   C
                                CC   GC  TTC TCAGGGAC
                                ||   ||  ||| ||||||||
                                GG   CG  AAG GGTCCCTG
                                 ACC  __   T
GAM3066  HTCD37   5'  CCGCCCGGGACTCAGGGA    69867      GAGC  TTC
                                CCGCC    CG   CTCAGGGA
                                |||||    ||   ||||||||
                                GGCGG    GC   GAGTCCCT
                                   _____  CCT
GAM3066  KBRAS2   3'  CCACTGAGCCCAGCCAGGG   69868     C     GTTCC
                                CCGC GAGCC     TCAGGG
                                |||| |||||     ||||||
                                GGTG CTCGG     GGTCCC
                                  A     GTC__
GAM3066  KIAA0040 3'  GCCAGTGGCAGTTCAGGGAC   69869      A__   C  TCC
                                GCCG   GC GT   TCAGGGAC
                                ||||   || ||   ||||||||
                                CGGT   CG CA   AGTCCCTG
                                  CAC  T  ___
GAM3066  KIAA0152 5'  CCGCCTGAGCCGCCGGGGAC   69870       _       CCTCA
                                CCGCC GAGCCGTT     GGGAC
                                ||||| ||||||||     |||||
                                GGCGG CTCGGCGG     CCCTG
                                   A       C_____
GAM3066  KIAA0258 5'  GCCCGCCCCTCAGGGA      69871     GAGC
                                GCC    CGTTCCTCAGGGA
                                |||    ||||||||||||||
                                CGG    GCGGGGAGTCCCT
                                  _____
GAM3066  KIAA0286 3'  CCACTCTCCTTCCTCAGGGA   69872      CGAG  G
                                CCGC    CC TTCCTCAGGGA
                                ||||    || ||||||||||||
                                GGTG    GG AAGGAGTCCCT
                                  AGA_  _
GAM3066  KIAA0326 3'  GCGGACTCTTCAGGGAC     69873    C  GCCG   C
                                GC GA    TTC TCAGGGAC
                                || ||    ||| ||||||||
                                CG CT    GAG AGTCCCTG
                                 C  _____   A
GAM3066  KIAA0391 3'  GCTGAGCCATTCAGGA      69874    C       CTCA
                                GC GAGCCGTTC    GGGA
                                || |||||||||    ||||
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                                CG CTCGGTAAG   TCCT
                                 A      ____
GAM3066 KIAA0527 5' CCGCCGAACTCCCGGGGG   69875       CGT   CA
                                CCGCCGAGC  TCCT GGG
                                |||||||||  |||| |||
                                GGCGGCTTG  AGGG CCC
                                     ___   CC
GAM3066 KIAA0668 3' CGAAGGCCCTCAGGGAC    69876    CCGT
                                CGAG   TCCTCAGGGAC
                                ||||   ||||||||||
                                GCTT   GGGAGTCCCTG
                                  CC__
GAM3066 KIAA1091 3' CCAGTTTTCCTCAGGGA    69877   G CCG
                                CC AG  TTCCTCAGGGA
                                || ||  ||||||||||
                                GG TC  AAGGAGTCCCT
                                 _ AA_
GAM3066 KIAA1866 3' CGTCGTGCCGTTCCAAGG   69878   C A     TC
                                CG CG GCCGTTCC AGG
                                || || ||||||||  |||
                                GC GC CGGCAAGG TCC
                                 A A      T_
GAM3066 KLK7    5' GCTGAGCCGCTCAGGG     69879   C    TTC
                                GC GAGCCG  CTCAGGG
                                || ||||||  |||||||
                                CG CTCGGC  GAGTCCC
                                 A    ___
GAM3066 KLK7    5' GCTGAGCCGCTCAGGG     69879   C    TTC
                                GC GAGCCG  CTCAGGG
                                || ||||||  |||||||
                                CG CTCGGC  GAGTCCC
                                 A    ___
GAM3066 MMP28   3' CGCCGCTGACCTCCTCAGGGA 69880     A__  GT
                                CGCCG  GCC TCCTCAGGGA
                                |||||  |||  ||||||||||
                                GCGGC  TGG AGGAGTCCCT
                                   GAC  __
GAM3066 NMT1    3' GCCTAGCCACCCCAGGGAC   69881    G   TT
                                GCC AGCCG CCTCAGGGAC
                                ||| |||||  ||||||||||
                                CGG TCGGT  GGGGTCCCTG
                                  A   __
GAM3066 NY-REN-25 5' CGCCGGCCGGCTCAGGGAC   69882     A   TTC
                                CGCCG GCCG  CTCAGGGAC
                                ||||| ||||  |||||||||
                                GCGGC CGGC  GAGTCCCTG
                                   _   C__
GAM3066 NYD-SP29  5' GCCGACTGTTGCCAGGAC    69883     G C  _ TCA
                                GCCGA C GTT CC  GGGAC
                                ||||| | ||| ||  |||||
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                                CGGCT G CAA GG   TCCTG
                                  _ A   C  ___
GAM3066  SEMA4B   5'  CCCCCGAGTCGCCCCGGGGG  69884    G    C     TCA
                                CC CCGAG CGTTCC   GGG
                                || ||||| ||||||   |||
                                GG GGCTC GCGGGG   CCC
                                 G    A     CC_
GAM3066  SYNPO2   3'  GCTAGGCATTCTCAGGGAC   69885    CG  C    C
                                GC  AG CGTTC TCAGGGAC
                                ||  || ||||| ||||||||
                                CG  TC GTAAG AGTCCCTG
                                 A_  C    _
GAM3066  TXNL     5'  CCGCCGAGTCTTCTCCCGGGAC 69887        CCG_    CA
                                CCGCCGAG    TTCCT  GGGAC
                                ||||||||    |||||  |||||
                                GGCGGCTC    GAGGG  CCCTG
                                     AGAA    __
GAM3066  TXNL     5'  GCCGAGTCACGCCAGGGAC   69886       C  TT  TC
                                GCCGAG CG  CC  AGGGAC
                                |||||| ||  ||  ||||||
                                CGGCTC GT  GG  TCCCTG
                                   A  GC  __
GAM3066  LOC128439 3'  GCCAAGCCGTTTCTCAAGG   69888          C
                                GCCGAGCCGTT CTCAGGG
                                |||||||||||| |||||||
                                CGGTTCGGCAA GAGTTCC
                                       A
GAM3066  LOC146988 5'  GCTGACCCGCATCCAGGGAC   69889    C  G    TC T
                                GC GA CCGT  C CAGGGAC
                                || || ||||  | |||||||
                                CG CT GGCG  G GTCCCTG
                                 A  G    TA _
GAM3066  LOC149421 5'  CCGCTGAGCCGCTGAGGG    69890     C       CCTC
                                CCGC GAGCCGTT    AGGG
                                |||| ||||||||    ||||
                                GGCG CTCGGCGA    TCCC
                                  A       C___
GAM3066  LOC151124 5'  CCTGAGCCGTTCTCTTCAG    69891    _       _ _
                                CC GAGCCGTTC CT CAG
                                || |||||||| || |||
                                GG CTCGGCAAG GA GTC
                                 A        A  A
GAM3066  LOC155066 5'  GCCGGGCCGGCGTTCAGGGAC  69892      A    TTCC
                                GCCG GCCG    TCAGGGAC
                                |||| ||||    ||||||||
                                CGGC CGGC    AGTCCCTG
                                  C    CGCA
GAM3066  LOC196932 5'  CCACCGGCTGGTCTCAGGGA   69893       A  CGTTC
                                CCGCCG GC     CTCAGGGA
                                |||||| ||     ||||||||
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                                GGTGGC CG    GAGTCCCT
                                   _ ACCA_
GAM3066  LOC201182 5'  CCACTGAGCCCAGCCAGGG   69868     C    GTTCC
                                CCGC GAGCC    TCAGGG
                                |||| |||||    ||||||
                                GGTG CTCGG    GGTCCC
                                  A    GTC__
GAM3066  LOC203595 5'  CCGCAGTCTCTCCTCAGGG   69894     CG  CCG
                                CCGC  AG   TTCCTCAGGG
                                ||||  ||   ||||||||||
                                GGCG  TC   GAGGAGTCCC
                                  __ AGA
GAM3066  LOC205272 5'  CCACCGGGCTGTGGCGGAAGGG 69895       A  C  TCCTC_
            A                    CCGCCG GC GT     AGGGA
                                ||||||  ||  ||     |||||
                                GGTGGC CG CA     TCCCT
                                   C  A  CCGCCT
GAM3066  LOC207089 3'  CGCCGGGCCGTTCCCGGAC   69896      A       CAG
                                CGCCG GCCGTTCCT   GGAC
                                |||||  |||||||||   ||||
                                GCGGC CGGCAAGGG   CCTG
                                  C       ___
GAM3066  LOC254173 3'  CCGCCGAGGTCGCTGGAATGGG 69897        C_   CCTCA
                                CCGCCGAG  CGTT    GGG
                                ||||||||  ||||    |||
                                GGCGGCTC  GCGA    CCC
                                     CA    CCTTA
GAM3066  LOC254544 5'  CCGAGCCGCGGCTGGGGAC   69898        TC  CA
                                CCGAGCCGT  CT  GGGAC
                                |||||||||  ||  |||||
                                GGCTCGGCG  GA  CCCTG
                                     CC  C_
GAM3066  LOC254848 5'  CCATCGAGCCCAAGTCAGGGAC 69899     C     GTTCC
                                CCG CGAGCC    TCAGGGAC
                                |||  ||||||    ||||||||
                                GGT GCTCGG    AGTCCCTG
                                  A     GTTC_
GAM3066  LOC257464 5'  GCCGGGTGTTCCTCAGGG    69900     AGCC
                                GCCG   GTTCCTCAGGG
                                ||||   ||||||||||
                                CGGC   CAAGGAGTCCC
                                  CCA_
GAM3066  LOC257476 3'  GCCAAGCCCACCAGGG      69841        GTT C
                                GCCGAGCC   C TCAGGG
                                ||||||||   | ||||||
                                CGGTTCGG   G GGTCCC
                                     ___ T
GAM3066  LOC58525  5'  CCGGCCGGGGGCTCAGGGAC  69901     A   TTC_
                                CCG GCCG   CTCAGGGAC
                                ||| ||||   |||||||||
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                                GGC CGGC   GAGTCCCTG
                                  _   CCCC
GAM3067 COL10A1  3' TTCACATACGTTTTTACGTTGC 69904          CTGGCC  C
                                TTCACGTACGTT     CG TGC
                                ||||||||||||     || |||
                                AAGTGTATGCAA     GC ACG
                                       AAAT__  A
GAM3067 FKBP5    3' TTCACGTCTGTGACACTGC   69905      TACGT   GCC
                                TTCACG    TCTG   CGCTGC
                                ||||||    ||||   ||||||
                                AAGTGC    AGAC   GTGACG
                                   _____   ACT
GAM3067 TLK2     3' CGCTATGTTCCAAACCCGCTGC 69906    AC_   TG _
                                CGT   GTTC  G CCCGCTGC
                                |||   ||||  | ||||||||
                                GCG   CAAG  T GGGCGACG
                                  ATA    GT T
GAM3067 TLK2     3' CGCTATGTTCCAAACCCGCTGC 69906    AC_   TG _
                                CGT   GTTC  G CCCGCTGC
                                |||   ||||  | ||||||||
                                GCG   CAAG  T GGGCGACG
                                  ATA    GT T
GAM3067 LOC150527 5'  TTCACGTAGGAACATGCCTGCT 69907        CGTTCTG   C
             GC                   TTCACGTA      GCC GCTGC
                                ||||||||      ||| |||||
                                AAGTGCAT      CGG CGACG
                                    CCTTGTA   A
GAM3068 C9       3' GCATGTTGCTATTTA      69910        TCCG
                                GCATGTT    GTTATTTA
                                |||||||    ||||||||
                                CGTACAA    CGATAAAT
                                   ____
GAM3068 NT5C2    3' TAATGCATGTTCTGTAGT    69911          CC_
                                TAATGCATGTTT   GGT
                                ||||||||||||   |||
                                ATTACGTACAAG   TCA
                                       ACA
GAM3068 FLJ20445 3' ATACATTTTTGGTTATTTA   69912       GTTTCC
                                ATGCAT     GGTTATTTA
                                ||||||     |||||||||
                                TATGTA     CCAATAAAT
                                   AAAA__
GAM3068 GOLPH2   3' TAATGATGTGGCCAGTTATTT  69913      C    TT
                                TAATG ATGT  CCGGTTATTT
                                ||||| ||||  ||||||||||
                                ATTAC TACA  GGTCAATAAA
                                   _   CC
GAM3068 HSC3     3' ATGCATGTTTCGTAAGTT    69914          C__
                                ATGCATGTTTC   GGTT
                                ||||||||||   ||||
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                                TACGTACAAAG  TCAA
                                      CAT
GAM3068 MAP2K6   3' CAATGCTTCCTGGTTATTTA  69915   C      _
                                G ATGTTTCC GGTTATTTA
                                | |||||||| |||||||||
                                G TACGAAGG CCAATAAAT
                                 T       A
GAM3068 MAP2K6   3' CAATGCTTCCTGGTTATTTA  69915   C      _
                                G ATGTTTCC GGTTATTTA
                                | |||||||| |||||||||
                                G TACGAAGG CCAATAAAT
                                 T       A
GAM3068 PRO0097  5' TAATACATGGTTATTT     69916        GTTTCC
                                TAATGCAT     GGTTATTT
                                ||||||||     ||||||||
                                ATTATGTA     CCAATAAA

                                   _______
GAM3068 PRO0365  3' ATGCATGTTTTTATTAT    69917         CCG
                                ATGCATGTTT   GTTAT
                                ||||||||||   |||||
                                TACGTACAAA   TAATA
                                      AA_
GAM3068 PTP4A1   3' AATGCATGTCATTATTTA   69918         TCCG
                                AATGCATGTT   GTTATTTA
                                ||||||||||   ||||||||
                                TTACGTACAG   TAATAAAT

                                   _____
GAM3068 LOC130535 3' GCATGTGGGAGTTATTTA  69919       TTCC
                                GCATGT   GGTTATTTA
                                ||||||   |||||||||
                                CGTACA   TCAATAAAT
                                   CCC_
GAM3068 LOC221362 3' ATGCTCTGTTTTGGTTATTTAC 69920     A_   CC
                                ATGC  TGTTT  GGTTATTTAC
                                ||||  |||||  ||||||||||
                                TACG  ACAAA  CCAATAAATG
                                  AG    A_
GAM3069 CASR     5' TGGTCCTTGAGTCTTTGGAAGC 69923     AAG  TAA  C
                                TGGT   TGA   TC TTGGAAGC
                                ||||   |||   || ||||||||
                                ACCA   ACT   AG AACCTTCG
                                  GGA   C__  A
GAM3069 DPYSL3   3' TGGTAAGTGAAGAAAGAGAGGC 69924         TAATCCTT   A
                                TGGTAAGTGA       GGA GC
                                ||||||||||       ||| ||
                                ACCATTCACT       TCT CG
                                      TCTTTC__   C
GAM3069 PDPK1    3' TGGCAGGTGGTCTGGAAG    69925      A   ATAA  CT
                                TGGTA GTG    TC  TGGAAG
                                ||||| |||    ||  ||||||
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                                ACCGT CAC   AG  ACCTTC
                                  C  C___  __
GAM3069 PLA2G5   3' TGGTGATGATAATCTGATCGC 69926     AA      CT  AA
                                TGGT  GTGATAATC  TGG  GC
                                ||||  |||||||||  |||  ||
                                ACCA  TACTATTAG  ACT  CG
                                  C_      __  AG
GAM3069 C11orf11 3' TGGGTGGTGAGGATCCTTGG  69927    TAA   TA
                                TGG  GTGA  ATCCTTGG
                                |||  ||||  ||||||||
                                ACC  CACT  TAGGAACC
                                 CAC   CC
GAM3069 C2F     5' TGGTGGGTGATATCTGG    69928     AA    A  CT
                                TGGT  GTGATA TC  TGG
                                ||||  ||||||  ||  |||
                                ACCA  CACTAT AG  ACC
                                  CC    _  __
GAM3069 FLJ12934 3' TGGTAAGTGAGATGGCGGAAGC 69929         TAATCCT
                                TGGTAAGTGA     TGGAAGC
                                ||||||||||     |||||||
                                ACCATTCACT     GCCTTCG
                                     CTACC__
GAM3069 FLJ21736 3' TGGTGGGTGCTCTTGGAAGC  69930     AA  ATAATC
                                TGGT  GTG    CTTGGAAGC
                                ||||  |||    |||||||||
                                ACCA  CAC    GAACCTTCG
                                  CC  GA____
GAM3069 KIAA1280 5' TGGTAGATCTCCTTGGAG   69931     AGT  AA     A
                                TGGTA  GAT  TCCTTGGA G
                                |||||  |||  |||||||| |
                                ACCAT  CTA  AGGAACCT C
                                  ___  G_     C
GAM3069 KRTAP4-7 3' TGGTGGTGGGCTCTTTGGAAGC 69932     AA  ATAA  C
                                TGGT  GTG   TC TTGGAAGC
                                ||||  |||   || ||||||||
                                ACCA  CAC   AG AACCTTCG
                                  C_  CCG_  A
GAM3069 PPP1R13B 3' TGGCAAAATTCAGTCCTTGGAG 69933       TGA  A     A
           GC                   TGGTAAG   TA TCCTTGGA GC
                                |||||||   || |||||||| ||
                                ACCGTTT   GT AGGAACCT CG
                                   TAA  C      C
GAM3069 PRO1880  5' GCTAATAATGATCTTTGGAAGC 69934    A    A  C
                                GT AGTGAT ATC TTGGAAGC
                                || |||||| ||| ||||||||
                                CG TTATTA TAG AACCTTCG
                                 A    C  A
GAM3069 SCYB10   3' GTGGTCCATCCTTGGAAGC   69935    ATA_
                                GTG   ATCCTTGGAAGC
                                |||   ||||||||||||
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                                CAC    TAGGAACCTTCG
                                  CAGG
GAM3069  LOC158987 3'  TGGCAAGTGATTAGCTTTGGGA 69936          AATCC    A
              G                    TGGTAAGTGAT    TTGG AG
                                   ||||||||||    |||| ||
                                   ACCGTTCACTA    AACC TC
                                         ATCGA    C
GAM3069  LOC196812 3'  TGGTAAGTGACTGGCCTGGG  69937          AAT   T
                                   TGGTAAGTGAT   CCT GG
                                   ||||||||||   ||| ||
                                   ACCATTCACTG   GGA CC
                                         ACC   C
GAM3069  LOC221398 3'  TGGAGGCCTTAGTCCTTGGA  69938     TAA  GA  A
                                   TGG   GT  TA TCCTTGGA
                                   |||   ||  || ||||||||
                                   ACC   CG  AT AGGAACCT
                                     TC_  GA  C
GAM3069  LOC221468 3'  GTAAGTGATGATCCACATGG  69939         A    T__
                                   GTAAGTGAT ATCC   TGG
                                   ||||||||| ||||   |||
                                   CATTCACTA TAGG   ACC
                                        C    TGT
GAM3070  IGF2R    3'  TCTCAAACCTGAGTAATT    69942     _     TTGCAC
                                   TCT AAACCT     GAGTAATT
                                   ||| ||||||     ||||||||
                                   AGA TTTGGA     CTCATTAA
                                     G     _______
GAM3070  ING1     3'  TAAACCTTTGTTACTGAAT   69943          C_  _
                                   TAAACCTTTG  AC GAGT
                                   ||||||||||  || ||||
                                   ATTTGGAAAC  TG CTTA
                                         AA  A
GAM3070  PRKY     3'  TCTACATTTTGCACAGTGATT  69944      AACC      G   A
                                   TCTA    TTTGCAC AGT ATT
                                   ||||    ||||||| ||| |||
                                   AGAT    AAACGTG TCA TAA
                                     GTA_      _   C
GAM3070  TGFBR2   3'  TCCAAACCTTTGCATGTA    69945            CGA
                                   TCTAAACCTTTGCA   GTA
                                   ||||||||||||||   |||
                                   AGGTTTGGAAACGT   CAT
                                           A__
GAM3070  TMEM2    3'  AACCCTTACAAGTAATT     69946          CG
                                   AACCTTTGCA  AGTAATT
                                   ||||||||||  |||||||
                                   TTGGGAATGT  TCATTAA
                                              __
GAM3070  H2AFY2   3'  TCAAAACCTTTTTAGGAGTA   69947    T       GCAC
                                   TC AAACCTTT    GAGTA
                                   || ||||||||    |||||
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                                AG TTTGGAAA   CTCAT
                                 T      AATC
GAM3070 KIAA1077 3' TCTAAATCCTTCAAGTAATTA 69948      _   TGCA
                                TCTAAA CCTT   CGAGTAATTA
                                |||||| ||||   ||||||||||
                                AGATTT GGAA   GTTCATTAAT
                                   A  ____
GAM3071 APTX    5' TTGACATATCCCTTGTTACAC 69951         G   T
                                TTGACATATCC TTGTT CAC
                                |||||||||| ||||| |||
                                AACTGTATAGG AACAA GTG
                                      G   T
GAM3071 NKX3A   3' TTCACTGTCTCTGTTGTTTCA 69952   G ATA_ C
                                TT AC   TC GTTGTTTCA
                                || ||   || |||||||||
                                AA TG   AG CAACAAAGT
                                 G ACAG  A
GAM3071 PAH     3' TTGACTTATTTGTTGTTTCTCC 69953      A  CC      A
             AT                  TTGAC TAT  GTTGTTTC CCAT
                                ||||| |||  |||||||| ||||
                                AACTG ATA  CAACAAAG GGTA
                                   A  AA      A
GAM3071 PDE4D   3' TTGACATATTTGTTGCTTC   69954        CC
                                TTGACATAT  GTTGTTTC
                                |||||||||  ||||||||
                                AACTGTATA  CAACGAAG
                                     AA
GAM3071 ANXA10  5' TTGCATAAACTTGTTTCAC   69955    A   TCCG
                                TTG CATA   TTGTTTCAC
                                ||| ||||   |||||||||
                                AAC GTAT   AACAAAGTG
                                  _   TTG_
GAM3071 DT1P1A10 3' TTGCATGTTCATCTCACCA   69956    A  ATCCG TG
                                TTG CAT    T  TTTCACCA
                                ||| |||    |  ||||||||
                                AAC GTA    A  AGAGTGGT
                                  _  CA___ GT
GAM3071 FLJ21290 3' TTGACATATCTGTCTC     69957         CGT
                                TTGACATATC   TGTTTC
                                ||||||||||   ||||||
                                AACTGTATAG   ACAGAG
                                             ___
GAM3071 MGC2848  3' TTGACAAATCTATCATTTCA  69958      T  CG TG
                                TTGACA ATC  T  TTTCA
                                |||||| |||  |  |||||
                                AACTGT TAG  A  AAAGT
                                    T  AT GT
GAM3071 RNO2    5' TTGCATGTCATTTCACC    69959    A  ATCC  TG
                                TTG CAT   GT  TTTCACC
                                ||| |||   ||  |||||||
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                                AAC GTA    CA  AAAGTGG
                                  _  _____  GT
GAM3071  LOC127534 3'  TTGACATATACTGTTGCC    69960         CC_
                                TTGACATAT   GTTGTT
                                |||||||||   ||||||
                                AACTGTATA   CAACGG
                                     TGA
GAM3071  LOC151438 5'  TTGGCATTATCTGTTGTCACTC 69961     A  _  C    TT   _
            AT                    TTG CAT ATC GTTG  TCAC CAT
                                |||  |||  |||  ||||  ||||  |||
                                AAC GTA TAG CAAC  AGTG GTA
                                  C   A   A   __    A
GAM3071  LOC154872 3'  CTGACATATTTTCTCAC     69962         CCGTTG
                                TTGACATAT     TTTCAC
                                |||||||||     ||||||
                                GACTGTATA     AGAGTG
                                     AA_____
GAM3072  ADAMTS13  3'  GAGCTGGGCTCTGACA      69965        T    GCTA
                                GAGCTGG GCTT    GACA
                                |||||||  ||||    ||||
                                CTCGACC CGAG    CTGT
                                   _    A___
GAM3072  B4GALT5   3'  AGCTGGTAATGTAGGCAC    69966         CT  C   A
                                AGCTGGTG  TG TAG CAC
                                ||||||||  ||  |||  |||
                                TCGACCAT  AC ATC GTG
                                     T_  _   C
GAM3072  EGR4      3'  CGAGCTGGTGCTGAATAG    69967           TGC
                                CGAGCTGGTGCT   TAG
                                ||||||||||||   |||
                                GCTCGACCACGA   ATC
                                       CTT
GAM3072  FMR2      3'  CGAGCTGGTTGTTAAACA    69968         GCT  C
                                CGAGCTGGT   TG TAGACA
                                |||||||||   ||  ||||||
                                GCTCGACCA   AC ATTTGT
                                     ___  A
GAM3072  KCNK3     3'  CGGCTGGTGCAAGCAGGCAC   69969    A       TT  T  A
                                CG GCTGGTGC  GC AG CAC
                                ||  ||||||||  ||  ||  |||
                                GC CGACCACG  CG TC GTG
                                  _       TT  _  C
GAM3072  S100A10   5'  CGAGCTGGGCGAGCTGGAC    69970         T  TT   A
                                CGAGCTGG GC  GCT GAC
                                ||||||||  ||  |||  |||
                                GCTCGACC CG  CGA CTG
                                     _ CT   C
GAM3072  SHANK2    3'  ACAAGCTGGTGGGATTCCTAGA 69971           C__  G
            CAC                     ACGAGCTGGTG   TT CTAGACAC
                                ||||||||||   ||  ||||||||
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                                TGTTCGACCAC   AA GATCTGTG
                                      CCT  G
GAM3072  SMTN     3'  CGGGCGGGCAGGCTAGACA   69972    A  T  T  TT
                                CG GC GG GC  GCTAGACA
                                || || || ||  ||||||||
                                GC CG CC CG  CGATCTGT
                                 C  _  _  TC
GAM3072  TPK1     3'  AGCCCTTGTTGTTAGACA    69973     GG  C   C
                                AGCT  TG TTG TAGACA
                                ||||  || ||| ||||||
                                TCGG  AC AAC ATCTGT
                                  GA  _   A
GAM3072  ABIN-2   5'  CGAGCTGGTCCTGCAG      69974         G    T
                                CGAGCTGGT CTTGC AG
                                ||||||||| ||||| ||
                                GCTCGACCA GGACG TC

                                      _    _
GAM3072  BG1      5'  GAGCTGGTGGTGTAGA      69975         CT  C
                                GAGCTGGTG  TG TAGA
                                |||||||||  || ||||
                                CTCGACCAC  AC ATCT
                                     C_  _
GAM3072  BPESC1   3'  GAAGAATGTTTGCTAGA     69976     CT   C
                                GAG  GGTG TTGCTAGA
                                |||  |||| ||||||||
                                CTT  TTAC AACGATCT
                                  C_   A
GAM3072  C1orf2   3'  ACCAGCTGGTGCCTGTGGCTGG 69977    G         ___   A
            A                    AC AGCTGGTGCTT   GCT GA
                                || ||||||||||   ||| ||
                                TG TCGACCACGGA   CGA CT
                                 G         CAC   C
GAM3072  C1orf2   3'  ACCAGCTGGTGCCTGTGGCTGG 69977    G         ___   A
            A                    AC AGCTGGTGCTT   GCT GA
                                || ||||||||||   ||| ||
                                TG TCGACCACGGA   CGA CT
                                 G         CAC   C
GAM3072  C1QR1    3'  CGAGCTGGGTGTGTGAGA    69978         _  CT  CT
                                CGAGCTGG TG  TG  AGA
                                |||||||| ||  ||  |||
                                GCTCGACC AC  AC  TCT
                                     C  __  AC
GAM3072  CHRFAM7A 3'  TAGTTCCCATGCTAGACA    69979     G_  _
                                TGGT  CT TGCTAGACA
                                ||||  || |||||||||
                                ATCA  GG ACGATCTGT
                                  AG  T
GAM3072  FGF19    5'  ACGGGTAGGTGCCCAAGACAC  69980     AGCT      CT
                                ACG   GGTGCTTG  AGACAC
                                |||   ||||||||  ||||||
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                                TGC   CCACGGGT  TCTGTG
                                  CCAT      __
GAM3072 FLJ12650 3' GCAAGGGCTTTGCTAGAC    69981    T_ T   _
                                GC  GG GCTT GCTAGAC
                                ||  || |||| |||||||
                                CG  CC CGAA CGATCTG
                                 TT  _   A
GAM3072 FLJ20033 3' ACTGGCTGGTGCTACCAAGACA 69982    GA       T   _
             C                   AC  GCTGGTGCT GCTA GACAC
                                ||  ||||||||| |||| |||||
                                TG  CGACCACGA TGGT CTGTG
                                 AC        _   T
GAM3072 KIAA0429  5' GCTGGTGCTCAAAACA     69983          CT
                                GCTGGTGCTTG  AGACA
                                ||||||||||  |||||
                                CGACCACGAGT  TTTGT

                                    __
GAM3072 KIAA0987  3' CGGGCTGTGCTGCAGCA    69984    A   G   T  T  A
                                CG GCTG TGCT GC AG CA
                                || |||| |||| || || ||
                                GC CGAC ACGA CG TC GT
                                 C   _   _ _ _
GAM3072 MGC21675  5' ACGAGCTGTGCACACGGCTGGG 69985        _ TG TT_   AGA
             CAC                   ACGAGCTG G  C   GCT   CAC
                                |||||||| |  |   |||   |||
                                TGCTCGAC C  G   CGA   GTG
                                     A GT TGC   CCC
GAM3072 MGC3101   3' GAGCTGGGGCTCCCAGACAC   69986       T   G
                                GAGCTGG GCTT CTAGACAC
                                ||||||| |||| ||||||||
                                CTCGACC CGAG GGTCTGTG
                                    C   _
GAM3072 PAK6      5' CAGGCTGGTGCTTGTCTCTAG  69987    A        ___
                                CG GCTGGTGCTTG   CTAG
                                || ||||||||||   ||||
                                GT CGACCACGAAC   GATC
                                 C         AGA
GAM3072 SIAT4A    3' GAGCGGTGCCCAGGCA     69988     T    TTG   A
                                GAGC GGTGC   CTAG CA
                                |||| |||||   |||| ||
                                CTCG CCACG   GGTC GT
                                  _    ___    C
GAM3072 SMARCF1   3' GAGCTGGACTAGACA      69989       TGCTT
                                GAGCTGG    GCTAGACA
                                |||||||    ||||||||
                                CTCGACC    TGATCTGT

                                   _____
GAM3072 STMN3     5' ACGGCTGGTGCTGCAG     69990     A       T  T
                                ACG GCTGGTGCT GC AG
                                ||| ||||||||| || ||
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                                TGC CGACCACGA CG TC
                                  _       _ _
GAM3072  TACTILE   3'  CAAGTTGGTGCTTGTTAG    69991     C       C
                                CGAG TGGTGCTTG TAG
                                |||| ||||||||| |||
                                GTTC ACCACGAAC ATC
                                  A       A
GAM3072  LOC112724 5'  CGGGCTGGGAACTCTAGACAC  69992    A    T_   TG
                                CG GCTGG  GCT  CTAGACAC
                                || |||||  |||  ||||||||
                                GC CGACC  TGA  GATCTGTG
                                 C    CT  __
GAM3072  LOC128954 5'  CGTGCTGGTGCGAGCGGAGACA 69993    A      TT  T_
            C                    CG GCTGGTGC  GC  AGACAC
                                || ||||||||  ||  ||||||
                                GC CGACCACG  CG  TCTGTG
                                 A       CT  CC
GAM3072  LOC130589 3'  CGAGCTGGTCATTAGACA    69994        GCT GC
                                CGAGCTGGT   T  TAGACA
                                |||||||||   |  ||||||
                                GCTCGACCA   G  ATCTGT
                                     ___ TA
GAM3072  LOC143384 3'  AGCTGGTGACAGACA       69995       CTT  T
                                AGCTGGTG   GC AGACA
                                ||||||||   || |||||
                                TCGACCAC   TG TCTGT
                                     ___  _
GAM3072  LOC146819 3'  GAGCTGGTTCTTGGAAC     69996       G    CTA
                                GAGCTGGT CTTG   GAC
                                |||||||| ||||   |||
                                CTCGACCA GAAC   TTG
                                     A   C__
GAM3072  LOC146821 3'  GAGCTGGTTCTTGGAAC     69996       G    CTA
                                GAGCTGGT CTTG   GAC
                                |||||||| ||||   |||
                                CTCGACCA GAAC   TTG
                                     A   C__
GAM3072  LOC150225 3'  CGAACTGGCCAGCCTAGA    69997        __  TTG
                                CGAGCTGGT  GC   CTAGA
                                |||||||||  ||   |||||
                                GCTTGACCG  CG   GATCT
                                     GT  ___
GAM3072  LOC152641 5'  CGAGCTGGTGCGGCGAC     69998         TT  TA
                                CGAGCTGGTGC  GC  GAC
                                ||||||||||  ||  |||
                                GCTCGACCACG  CG  CTG
                                      C_  __
GAM3072  LOC154084 5'  GAACTGGTGCTCCAGA      69999         TG
                                GAGCTGGTGCT  CTAGA
                                ||||||||||  |||||
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                                CTTGACCACGA  GGTCT
                                           __
GAM3072  LOC164295 5'  CGGGCAGGTGGGCAGACAC    70000    A  T    CTT  T
                                CG GC GGTG   GC AGACAC
                                || || ||||   || |||||||
                                GC CG CCAC   CG TCTGTG
                                 C  T   C__  _
GAM3072  LOC201522 3'  GAGCTGGTTGTTCCACAGCAC  70001        GC__ TG T  A
                                GAGCTGGT    T  C AG CAC
                                ||||||||    |  | || |||
                                CTCGACCA    G  G TC GTG
                                     ACAA GT _  _
GAM3073  LOC200734 3'  TAGGATGTGTTTATATTTACAC 70004       C_____
                                TAGGAT     ATATTTACAT
                                ||||||     ||||||||||
                                ATCCTA     TATAAATGTG
                                   CACAAA
GAM3074  COL4A3    3'  ATATTTCATTTGGTTATA    70007        ATC
                                ATATTTCAT   GGTTATA
                                |||||||||   |||||||
                                TATAAAGTA   CCAATAT
                                     AA_
GAM3074  COL4A3    3'  ATATTTCATTTGGTTATA    70007        ATC
                                ATATTTCAT   GGTTATA
                                |||||||||   |||||||
                                TATAAAGTA   CCAATAT
                                     AA_
GAM3074  COL4A3    3'  ATATTTCATTTGGTTATA    70007        ATC
                                ATATTTCAT   GGTTATA
                                |||||||||   |||||||
                                TATAAAGTA   CCAATAT
                                     AA_
GAM3074  MRPL10    3'  ATATTTCATTTTATTATAAAG  70008         ATCG
                                ATATTTCAT    GTTATAAAG
                                |||||||||    |||||||||
                                TATAAAGTA    TAATATTTC
                                     AAA_
GAM3074  PCDH19    3'  AATATTTCATTATCAATATAAA 70009          _     T
              G                  AATATTTCAT ATCGGT ATAAAG
                                ||||||||| |||||| ||||||
                                TTATAAAGTA TAGTTA TATTTC
                                     A     _
GAM3074  SBBI26    3'  AAATATTTCATGTTTTGGCTA  70010          ATC__
                                AAATATTTCAT    GGTTA
                                ||||||||||    |||||
                                TTTATAAAGTA    CCGAT
                                     CAAAA
GAM3075  ALK       5'  TACCAGCTGCTACCACC     70013       A       AACA
                                TACTA CTGCTATT    ACC
                                ||||| ||||||||    |||
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                                ATGGT GACGATGG    TGG
                                   C      ____
GAM3075 CDH1     3' TACTAACTGCATCACTAACCA 70014          T    AC
                                TACTAACTGC ATTA  AACCA
                                |||||||||| ||||  |||||
                                ATGATTGACG TAGT  TTGGT
                                      _   GA
GAM3075 MBL2     3' TACTACTGCTGCTGCTAAC   70015      A__    A
                                TACTA   CTGCT TTAAC
                                |||||   ||||| |||||
                                ATGAT   GACGA GATTG
                                   GAC    C
GAM3075 MLF1     3' TACTAACTGTTAAAACAATCA 70016        C  TT    C
                                TACTAACTG TA  AACAA CA
                                |||||||| ||  ||||| ||
                                ATGATTGAC AT  TTGTT GT
                                      A  T_    A
GAM3075 PKDREJ   3' CCAGCACGCTATTAATAACCA 70017     AC_       C
                                CTA   TGCTATTAA AACCA
                                |||   ||||||||| |||||
                                GGT   GCGATAATT TTGGT
                                  CGT        A
GAM3075 TBL2     3' TACTACTGCCACTGGCC     70018       A       AACAA
                                TACTA CTGCTATT     CC
                                ||||| ||||||||     ||
                                ATGAT GACGGTGA     GG
                                   _       CC___
GAM3075 ARHV     3' TACTACTTGCTATGCAGCCA   70019      AC     TAA  A
                                TACTA  TGCTAT   CA CCA
                                |||||  ||||||   || |||
                                ATGAT  ACGATA   GT GGT
                                   GA     C__  C
GAM3075 DKFZP434P0721 3' TACCAACTGCTGAAACAACCA  70020          ATT
                                TACTAACTGCT   AACAACCA
                                ||||||||||   ||||||||
                                ATGGTTGACGA   TTGTTGGT
                                      CT_
GAM3075 DRCTNNB1A 3' TACCAATACTATTAATAAC    70021       C       C
                                TACTAA TGCTATTAA AAC
                                |||||| ||||||||| |||
                                ATGGTT ATGATAATT TTG
                                   _       A
GAM3075 FLJ13310 5' TACTAACTGCTTCTCTACCA   70022          A  AACA
                                TACTAACTGCT TT    ACCA
                                |||||||||| ||    ||||
                                ATGATTGACGA GA    TGGT
                                      A  GA__
GAM3075 KIAA0570 3' ACTAATTTGCATAACAACCA   70023      C_   TAT
                                ACTAA  TGC   TAACAACCA
                                |||||  |||   |||||||||
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                                TGATT  ACG   ATTGTTGGT
                                  AA  T__
GAM3075  KIAA1034  3'  CTAACTGCAAACAACCA     70024        TATT
                                CTAACTGC   AACAACCA
                                ||||||||   ||||||||
                                GATTGACG   TTGTTGGT
                                    T___
GAM3075  KIAA1300  3'  CTGGCTGCCACTCCAACCA   70025   AA      AA
                                CT  CTGCTATT  CAACCA
                                ||  ||||||||  ||||||
                                GA  GACGGTGA  GTTGGT
                                 CC       G_
GAM3075  NAG73     3'  TAACAGCTTATTAACAACCA  70026    T  _
                                TAAC GCT ATTAACAACCA
                                |||| ||| ||||||||||
                                ATTG CGA TAATTGTTGGT
                                  T  A
GAM3075  LOC115669 3'  AACTACTATAGCAACCA     70027        TAA
                                AACTGCTAT   CAACCA
                                |||||||||   ||||||
                                TTGATGATA   GTTGGT
                                    TC_
GAM3075  LOC118851 5'  CACTAATTGCTTCAAACCA   70028      C   A   CA
                                TACTAA TGCT TTAA  ACCA
                                |||||| |||| ||||  ||||
                                GTGATT ACGA AGTT  TGGT
                                   A   _   __
GAM3075  LOC142820 3'  TACTAACTGCTCTCCAACCA  70029         ATTAA
                                TACTAACTGCT    CAACCA
                                ||||||||||    ||||||
                                ATGATTGACGA    GTTGGT
                                      GAG__
GAM3075  LOC147400 3'  TACTGCTGCTACTGGAACC   70030     AA      AAC
                                TACT  CTGCTATT   AACC
                                ||||  ||||||||   ||||
                                ATGA  GACGATGA   TTGG
                                  C_       CC_
GAM3075  LOC152179 5'  CACTAACTGTTAAAACA     70031        C  TT
                                TACTAACTG TA  AACA
                                ||||||||| ||  ||||
                                GTGATTGAC AT  TTGT
                                    A  T_
GAM3075  LOC158662 3'  TACTGCTGCTACTGGAACCA  70032     AA      AAC
                                TACT  CTGCTATT   AACCA
                                ||||  ||||||||   |||||
                                ATGA  GACGATGA   TTGGT
                                  C_       CC_
GAM3076  DISC1     3'  GCATTGAGTGAAACAGGT    70035        CGTCT
                                GCATTGAG    AGGCAGGT
                                ||||||||    ||||||||
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                                CGTAACTC    TTTGTCCA
                                    AC___
GAM3076 ENTPD6   3' GCATTGAGCAGGGCCCAGGTC 70036        TCTA  __
                                GCATTGAGCG   GGC  AGGTC
                                ||||||||||   |||  |||||
                                CGTAACTCGT   CCG  TCCAG
                                     C___   GG
GAM3076 SCA1     3' GCCTAGAGTTTAGGCAGGT   70037    ATTG  C  C
                                GC   AG GT TAGGCAGGT
                                ||   || || |||||||||
                                CG   TC CA ATCCGTCCA
                                 GA__  T  A
GAM3076 SORCS3   3' GCATTGAGCAGGCCTGGCGGGT 70038         __   A   A
                                GCATTGAGC  GTCT GGC GGT
                                |||||||||  |||| ||| |||
                                CGTAACTCG  CGGA CCG CCA
                                     TC   _  C
GAM3076 C20orf124 3' TAGCATTGGAGGGGGCAGGTC  70039       _ CGTCTA
                                TAGCATTG AG     GGCAGGTC
                                |||||||| ||     ||||||||
                                ATCGTAAC TC     CCGTCCAG
                                    C  CC____
GAM3076 KIAA0872  3' CAGCATTGAGGGCGGG      70040         CGTCTA   A
                                TAGCATTGAG     GGC GG
                                ||||||||||     ||| ||
                                GTCGTAACTC     CCG CC
                                      _______  C
GAM3076 NLI-IF   3' CATTGGTCAGGGGCAGGTC   70041      AGC   TA_
                                CATTG   GTC   GGCAGGTC
                                |||||   |||   ||||||||
                                GTAAC   CAG   CCGTCCAG
                                   ___   TCC
GAM3076 LOC127348 3' TAGCATGACATCCAGGTGGGTC 70042       T  G       CA
                                TAGCAT GA CGTCTAGG  GGTC
                                |||||| || ||||||||  ||||
                                ATCGTA CT GTAGGTCC  CCAG
                                   _ _       AC
GAM3076 LOC148936 5' GCATTGAGTGTCTGCAA     70043        C    AG
                                GCATTGAG GTCT  GCAG
                                |||||||| ||||  ||||
                                CGTAACTC CAGA  CGTT
                                    A   __
GAM3076 LOC148938 5' GCATTGAGTGTCTGCAG     70044        C    AG
                                GCATTGAG GTCT  GCAG
                                |||||||| ||||  ||||
                                CGTAACTC CAGA  CGTC
                                    A   __
GAM3076 LOC149535 3' TAGCATTGACGGTCAGGT    70045         G  TCTAGG
                                TAGCATTGA CG     CAGGT
                                ||||||||| ||     |||||
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                                ATCGTAACT GC     GTCCA
                                    _ CA____
GAM3076  LOC202934 3'  GCATTGAGTGTCTGCAG     70044        C   AG
                                GCATTGAG GTCT  GCAG
                                |||||||| ||||  ||||
                                CGTAACTC CAGA  CGTC
                                   A   __
GAM3076  LOC219348 3'  ATTAAACAGTCTGGGTGGGTC  70046       _   A  CA
                                ATTGAGC GTCT GG  GGTC
                                ||||||| |||| ||  ||||
                                TAATTTG CAGA CC  CCAG
                                   T   C  AC
GAM3076  LOC255465 3'  GCATTGAGTGTCTGCAG     70044        C   AG
                                GCATTGAG GTCT  GCAG
                                |||||||| ||||  ||||
                                CGTAACTC CAGA  CGTC
                                   A   __
GAM3077  HDAC9-PENDING 3'  TTACATATCTTTGAAG      70049       ACC
                                TTACAT   GTTTTTGAAG
                                ||||||   ||||||||||
                                AATGTA   TAGAAACTTC
                                    ___
GAM3077  TRIM6    3'  TTTACATTATTTTTTGAAGT   70050        ACCG
                                TTTACAT    TTTTTGAAGT
                                |||||||    ||||||||||
                                AAATGTA    AAAAACTTCA
                                   ATA_
GAM3078  ACP1     3'  AGTTGTATTTTTATAACTC    70053          G  G
                                AGTTGTATTTTTA AA TC
                                |||||||||||| || ||
                                TCAACATAAAAAT TT AG
                                      A  G
GAM3078  ACP1     3'  AGTTGTATTTTTATAACTC    70053          G  G
                                AGTTGTATTTTTA AA TC
                                |||||||||||| || ||
                                TCAACATAAAAAT TT AG
                                      A  G
GAM3078  GPC1     3'  GTTGTATTTTTGGCAAAGTC   70054          A__
                                GTTGTATTTTT   GAAGTC
                                ||||||||||   ||||||
                                CAACATAAAAA   TTTCAG
                                      CCG
GAM3078  GPR85    3'  AGTTGTATATTTAGAACCCCAA 70055        T     G  G
                                AGTTGTAT TTTAGAA TC AA
                                |||||||| ||||||| || ||
                                TCAACATA AAATCTT GG TT
                                   T      G  G
GAM3078  KAL1     3'  AGTTGATTTTTCATATCGAATC 70056      T     AGAA
                                AGTTG ATTTTT    GTCGAATC
                                ||||| ||||||    ||||||||
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                                TCAAC TAAAAA   TAGCTTAG
                                  _     GTA_
GAM3078  VCAM1    3'  AGTTGCATTTTTAGGCCA    70057          AA
                                AGTTGTATTTTTAG  GTCG
                                ||||||||||||||  ||||
                                TCAACGTAAAAATC  CGGT
                                                 __
GAM3078  VCAM1    3'  AGTTGCATTTTTAGGCCA    70057          AA
                                AGTTGTATTTTTAG  GTCG
                                ||||||||||||||  ||||
                                TCAACGTAAAAATC  CGGT
                                                 __
GAM3078  C7orf14  5'  AGCTGTTCAGGAAGAAGTCGA  70058      ATTTTT
                                AGTTGT     AGAAGTCGA
                                ||||||     |||||||||
                                TCGACA     TCTTCAGCT
                                   AGTCCT
GAM3078  GNB4     3'  TTGTATTTTTAGAAGAGA    70059          TC
                                TTGTATTTTTAGAAG  GA
                                ||||||||||||||  ||
                                AACATAAAAATCTTC  CT
                                          T_
GAM3078  KIAA1828 5'  GCTGGTTTTGGAAGTCGA    70060     TAT   A
                                GTTG   TTTT GAAGTCGA
                                ||||   |||| ||||||||
                                CGAC   AAAA CTTCAGCT
                                  C__    C
GAM3079  AKAP13   3'  CACGCCCCATGGCCTGTGC   70063         _ AC
                                CACGCCCCATG C  GTGC
                                ||||||||||| |  ||||
                                GTGCGGGGTAC G  CACG
                                       C GA
GAM3079  APTX     5'  CCACGCCCAATCACAACTGC  70064       C  G   __
                                CCACGCCC AT CACG  TGC
                                |||||||| || ||||  |||
                                GGTGCGGG TA GTGT  ACG
                                     T  _   TG
GAM3079  ASK      5'  CACGCCACGCGCCGTGCCC   70065      CC   A_
                                CACGCC  ATGC  CGTGCCC
                                ||||||  ||||  |||||||
                                GTGCGG  TGCG  GCACGGG
                                   __    CG
GAM3079  ATP8B2   5'  CACCCCCATGCAAACC     70066    G      CGT
                                CAC CCCCATGCA   GCC
                                ||| |||||||||   |||
                                GTG GGGGTACGT   TGG
                                  _       T__
GAM3079  CD209    5'  CCACTCTCCCCCAGTGTCC   70067     G__   ATG  C  _
                                CCAC   CCCC   CA GTG CC
                                ||||   ||||   || ||| ||
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                                GGTG  GGGG  GT CAC GG
                                  AGA   ___ _  A
GAM3079 CDKN1A  3' CCAGCCCCATATGAGCCC   70068    C      CACGT
                                CCA GCCCCATG    GCCC
                                ||| ||||||||    ||||
                                GGT CGGGGTAT    CGGG
                                  _      ACT__
GAM3079 DSCAM   5' CCGCGCCCCACGCTGCGGCC  70069   A       A_ T
                                CC CGCCCCATGC  CG GCC
                                || ||||||||||  || |||
                                GG GCGGGGTGCG  GC CGG
                                 C        AC  _
GAM3079 EGFL4   3' CCACGCCTATGACAGTGCC   70070       CC  _ C
                                CCACGCC  ATG CA GTGCC
                                |||||||  ||| || |||||
                                GGTGCGG  TAC GT CACGG
                                    A_  T  _
GAM3079 ESPN    5' GGACGCCATGCACGTG     70071   C    CC
                                C ACGCC  ATGCACGTG
                                | |||||  |||||||||
                                C TGCGG  TACGTGCAC
                                 C    __
GAM3079 FUT5    3' CCAGGCCCCATGCCGGCC    70072    C       A  T
                                CCA GCCCCATGC CG GCC
                                ||| |||||||| || |||
                                GGT CGGGGTACG GC CGG
                                  C       _ _
GAM3079 GLTSCR1  3' CAAACACATGCGCGTGTCC   70073   C  CC    A   _
                                CA GC  CATGC CGTG CC
                                || ||  ||||| |||| ||
                                GT TG  GTACG GCAC GG
                                 T  T_    C   A
GAM3079 HOXA3   3' CCAGGCCCCATGCTGGAGCC  70074    C       ACGT
                                CCA GCCCCATGC    GCC
                                ||| |||||||||    |||
                                GGT CGGGGTACG    CGG
                                  C       ACCT
GAM3079 HR      5' CACGCCCCACTGGCCTGTG   70075         __ AC
                                CACGCCCCAT  GC  GTG
                                ||||||||||  ||  |||
                                GTGCGGGGTG  CG  CAC
                                      AC  GA
GAM3079 ID3     3' CCGCGCCCCACGCTGCCC    70076   A       ACG
                                CC CGCCCCATGC   TGCCC
                                || ||||||||||   |||||
                                GG GCGGGGTGCG   ACGGG
                                 C       ___
GAM3079 IHPK1   3' CACGTGCCAACAGGTGCC    70077     CC  T  C
                                CACG  CCA GCA GTGCC
                                ||||  ||| ||| |||||
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                                GTGC  GGT TGT CACGG
                                  AC  _  C
GAM3079 KCNQ1    3' CCACTCAACCACGTGCCC    70078     GCCC  TG
                                CCAC   CA  CACGTGCCC
                                ||||   ||  |||||||||
                                GGTG   GT  GTGCACGGG
                                  A___  TG
GAM3079 LRP4     3' CCAGGCTGAGACACGTGCCC   70079     C  CCCAT
                                CCA GC    GCACGTGCCC
                                ||| ||    ||||||||||
                                GGT CG    TGTGCACGGG
                                  C  ACTC_
GAM3079 LY9      3' CCAGGCCCCATGAGGTCC    70080     C      CAC  G
                                CCA GCCCCATG   GT CC
                                ||| ||||||||   || ||
                                GGT CGGGGTAC   CA GG
                                  C       TC_  _
GAM3079 MAP3K7IP1 3' CCTGCCCCATGCCAGGCCC   70081    AC       A  T
                                CC  GCCCCATGC CG GCCC
                                ||  |||||||||| || ||||
                                GG  CGGGGTACG GT CGGG
                                 A_        _  C
GAM3079 MFGE8    3' CACGCCCTACTTTGCCC     70082       CA   ACG
                                CACGCCC  TGC   TGCCC
                                |||||||  |||   |||||
                                GTGCGGG  ATG   ACGGG
                                    __   AA_
GAM3079 MKPX     5' CCGCGCCCCACTCCGCCC    70083    A      GCACG
                                CC CGCCCCAT    TGCCC
                                || ||||||||    |||||
                                GG GCGGGGTG    GCGGG
                                 C       AG___
GAM3079 MN1      3' CCATCCCCCATGCAGACC    70084     CG       CGT
                                CCA  CCCCATGCA   GCC
                                |||  |||||||||   |||
                                GGT  GGGGTACGT   TGG
                                  AG       C__
GAM3079 MSF      3' CCACGGCCCACACGTGCCC   70085      C   AT
                                CCACG CCC  GCACGTGCCC
                                ||||| |||  ||||||||||
                                GGTGC GGG  TGTGCACGGG
                                   C  __
GAM3079 MYOM2    3' CCACACCCATGTGCC       70086        C  GCAC
                                CCACGCCC AT   GTGCC
                                |||||||| ||   |||||
                                GGTGTGGG TA   CACGG
                                    _ _____
GAM3079 NCAM1    5' CACGCGCCATGGTACCC     70087      C    CAC
                                CACGC CCATG   GTGCCC
                                ||||| |||||   ||||||
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                              GTGCG GGTAC   CATGGG
                                C     ___
GAM3079  NCOR2    3'  CACGCCTGCCGTGCCC      70088       CCA   A
                              CACGCC   TGC CGTGCCC
                              ||||||   ||| |||||||
                              GTGCGG   ACG GCACGGG
                                 ___   _
GAM3079  NPTX1    3'  CCAGGCCCCATGCTGC      70089     C       ACG
                              CCA GCCCCATGC   TGC
                              ||| |||||||||   |||
                              GGT CGGGGTACG   ACG
                                C       ___
GAM3079  PGLS     3'  CCAGCCCCATGGGCCGCGTGCC 70090     C      __  A_
                              CCA GCCCCAT  GC  CGTGCC
                              ||| |||||||  ||  ||||||
                              GGT CGGGGTA  CG  GCACGG
                                _      CC  GC
GAM3079  PKD2     3'  CACCCCACTCCCCACGTGTCC  70091        G___     _
                              CGCCCCAT    CACGTG CC
                              ||||||||    |||||| ||
                              GTGGGGTG    GTGCAC GG
                                   AGGG     A
GAM3079  POLD1    3'  CCCGCCCCATGGGATGC     70092    A       CAC
                              CC CGCCCCATG   GTGC
                              || |||||||||   ||||
                              GG GCGGGGTAC   TACG
                                _       CC_
GAM3079  POLR2A   3'  CCGCACCCCACGTGCCC     70093    A     ATGC
                              CC CGCCCC    ACGTGCCC
                              || ||||||    ||||||||
                              GG GTGGGG    TGCACGGG
                                C     _____
GAM3079  PTPRJ    5'  CGCGCCCTGGAACGTGCCC   70094     _   A  C_
                              CGC CCC TG  ACGTGCCC
                              ||| ||| ||  ||||||||
                              GCG GGG AC  TGCACGGG
                                C   _  CT
GAM3079  RPL10    3'  CCATGCCACACACGTG      70095     C   CC
                              CCA GCC  ATGCACGTG
                              ||| |||  |||||||||
                              GGT CGG  TGTGTGCAC
                                A   __
GAM3079  RPS6KA2  3'  CCCGCCCTGTGTGCACACCC   70096    A    CA__    GT
                              CC CGCCC    TGCAC  GCCC
                              || |||||    |||||  ||||
                              GG GCGGG    ACGTG  TGGG
                                _     ACAC     __
GAM3079  S100B    3'  CCACGCCCTTGCAGGGCC     70097        CA    CGT
                              CCACGCCC  TGCA   GCC
                              ||||||||  ||||   |||
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                                GGTGCGGG  ACGT   CGG
                                    A_    CC_
GAM3079  SCTR     3'  CCTGCCCCACAGTGCC      70098    AC    AT   C
                                CC  GCCCC  GCA GTGCC
                                ||  |||||  ||| |||||
                                GG  CGGGG  TGT CACGG
                                 A_    __  _
GAM3079  TCF2     3'  CGCTTCCCATGACACGCCC    70099     __     C
                                CGC  CCCATG ACGTGCCC
                                |||  |||||| ||||||||
                                GCG  GGGTAC TGTGCGGG
                                  AA     _
GAM3079  TYRO3    3'  CCACTCCTGCCAGCTGCC     70100      G __   T  ACG
                                CCAC CC  CCA GC   TGCC
                                |||| ||  ||| ||   ||||
                                GGTG GG  GGT CG   ACGG
                                  A  AC   _  ___
GAM3079  VASP     5'  CCCGCCCCATAGAGTCC      70101    A       CAC  G
                                CC CGCCCCATG   GT CC
                                || |||||||||   || ||
                                GG GCGGGGTAT   CA GG
                                 _       CT_ _
GAM3079  WFDC1    5'  CGCGTCCAGCACATGCCC     70102     C_   T
                                CGC  CCA GCACGTGCCC
                                |||  ||| ||||||||||
                                GCG  GGT CGTGTACGGG
                                  CA   _
GAM3079  ZNF74    5'  CACGCCCCGGCACACCC      70103        AT    GT
                                CACGCCCC  GCAC  GCCC
                                ||||||||  ||||  ||||
                                GTGCGGGG  CGTG  TGGG
                                    C_    __
GAM3079  AGS3     5'  CCACACCCTGTGTCAGCCC    70104        CA  _  CGT
                                CCACGCCC  TG CA   GCCC
                                ||||||||  || ||   ||||
                                GGTGTGGG  AC GT   CGGG
                                    AC  A  ___
GAM3079  APCL     3'  CCACGCCCACATGTGATG     70105        _    CAC
                                CCACGCCC CATG   GTG
                                |||||||| ||||   |||
                                GGTGCGGG GTAC   TAC
                                    T    AC_
GAM3079  BICD2    3'  ACGCCCCATGGCGCC       70106          CAC
                                ACGCCCCATG   GTGCC
                                ||||||||||   |||||
                                TGCGGGGTAC   CGCGG
                                             ___
GAM3079  C20orf124 3'  CCGCGCCCCCACGGCCACCC   70107     A       CA GT
                                CC CGCCCCATG  C  GCCC
                                || |||||||||  |  ||||
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                                GG GCGGGGTGC  G  TGGG
                                 C        CG __
GAM3079  CALN1    3'  CGTCTCCACGCACTGTGTCC   70108    CC_      _  _
                                CG   CCATGCAC GTG CC
                                ||   |||||||| ||| ||
                                GC   GGTGCGTG CAC GG
                                 AGA       A   A
GAM3079  CARHSP1  3'  CCACACCCCACACCTGCCC   70109         AT   G
                                CCACGCCCC  GCAC TGCCC
                                |||||||||  |||| |||||
                                GGTGTGGGG  TGTG ACGGG
                                      __   G
GAM3079  DKFZp434C0923 3'  CCACGCCCCCTGGCCAGCCC  70110         AT_  A  T
                                CCACGCCCC   GC CG GCCC
                                |||||||||   || || ||||
                                GGTGCGGGG   CG GT CGGG
                                     GAC  _  _
GAM3079  DKFZP564D1378 5'  CCACACTCCGTACGCCGTCC  70111       _ C_   A   G
                                CCACGC CC  ATGC CGT CC
                                ||||||  ||  |||| ||| ||
                                GGTGTG GG  TGCG GCA GG
                                   A  CA   _  _
GAM3079  EDG2     3'  CACACCCCACCTTGCCC     70112          GCACG
                                CACGCCCCAT    TGCCC
                                ||||||||||    |||||
                                GTGTGGGGTG    ACGGG
                                     GA___
GAM3079  EDG2     3'  CACACCCCACCTTGCCC     70112          GCACG
                                CACGCCCCAT    TGCCC
                                ||||||||||    |||||
                                GTGTGGGGTG    ACGGG
                                     GA___
GAM3079  FLJ11700  3'  GCCCCACACATTCGTGCCC   70113          __
                                GCCCCATGCA  CGTGCCC
                                ||||||||||  |||||||
                                CGGGGTGTGT  GCACGGG
                                     AA
GAM3079  FLJ12681  3'  CCACATCCTGGCCGGGCGTGTC 70114       _ CCA_  CA   _
            C                    CCACG CC    TG  CGTG CC
                                |||||  ||    ||  |||| ||
                                GGTGT GG    GC  GCAC GG
                                   A  ACCG  CC   A
GAM3079  FLJ12816  3'  CCAGCCCCATGGCAATGGTGCC 70115     C       _ C__
                                CCA GCCCCATG CA   GTGCC
                                |||  |||||||| ||   |||||
                                GGT CGGGGTAC GT   CACGG
                                  _       C  TAC
GAM3079  FLJ14547  5'  CCACGCGCCCGCAACTGCCC   70116       _  AT   CG
                                CCACGC CCC  GCA  TGCCC
                                ||||||  |||  |||  |||||
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                                GGTGCG GGG  CGT  ACGGG
                                   C   __  TG
GAM3079  FLJ21087  5'  CCAGGGGGCATGCACGTGCCC  70117    CGCCC
                                CCA    CATGCACGTGCCC
                                |||    ||||||||||||
                                GGT    GTACGTGCACGGG
                                  CCCCC
GAM3079  FLJ22393  3'  CACGTGTGCACATGTGCCC   70118    CCCCA   __
                                CACG    TGCAC  GTGCCC
                                ||||    |||||  ||||||
                                GTGC    ACGTG  CACGGG
                                  AC___    TA
GAM3079  FLJ22529  3'  CCACGCCCCATGGCAGGCC   70119         _  CGT
                                CCACGCCCCATG CA   GCC
                                ||||||||||| ||   |||
                                GGTGCGGGGTAC GT   CGG
                                       C  C__
GAM3079  G4        5'  CCACACCCCACGGTGTCC    70120         CAC  _
                                CCACGCCCCATG   GTG CC
                                ||||||||||||   ||| ||
                                GGTGTGGGGTGC   CAC GG
                                       ___  A
GAM3079  GBTS1     3'  CCACGCCCATGGTGCC     70121       C   CAC
                                CCACGCCC ATG   GTGCC
                                ||||||| |||   |||||
                                GGTGCGGG TAC   CACGG
                                   _  ___
GAM3079  HT002     5'  CCACGCTCCCGCTGTCC     70122      _  AT  AC  G
                                CCACGC CCC  GC  GT CC
                                |||||| |||  ||  || ||
                                GGTGCG GGG  CG  CA GG
                                   A   __  A_  _
GAM3079  IL-17RE   3'  CCACGCGCGCCACGTGCC    70123      CCCA  _
                                CCACGC    TGC ACGTGCC
                                ||||||    ||| |||||||
                                GGTGCG    GCG TGCACGG
                                   C___   G
GAM3079  KIAA0082  3'  CCATCAGTCCCACGTGCCC   70124    _  CC  ATG
                                CCA CG  CC   CACGTGCCC
                                ||| ||  ||   |||||||||
                                GGT GT  GG   GTGCACGGG
                                  A  CA  ___
GAM3079  KIAA0296  3'  CCACGCCCCCACGTGC      70125       ATG
                                CCACGCCCC   CACGTGC
                                |||||||||   |||||||
                                GGTGCGGGG   GTGCACG
                                      ___
GAM3079  KIAA0596  3'  CCCGCCCCATGCAGCC      70126    A       CGT
                                CC CGCCCCATGCA   GCC
                                || ||||||||||   |||
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                                GG GCGGGGTACGT   CGG
                                 _       ___
GAM3079  KIAA0939  3'  CCACACCCCAGCCTGCCC    70127         T  ACG
                                CCACGCCCCA GC   TGCCC
                                |||||||||| ||   |||||
                                GGTGTGGGGT CG   ACGGG
                                      _  G__
GAM3079  KIAA0945  5'  CACCCCCACAGACGTGCCC   70128    G      C
                                CAC CCCCATG ACGTGCCC
                                ||| ||||||| ||||||||
                                GTG GGGGTGT TGCACGGG
                                  _      C
GAM3079  KIAA1030  3'  CGTCTCCCATGCAGGTGCCC  70129    C__       C
                                CG   CCCATGCA GTGCCC
                                ||   |||||||| ||||||
                                GC   GGGTACGT CACGGG
                                 AGA       C
GAM3079  KIAA1036  3'  CCACCCCCCATCACAGGCC   70130     G     G   T
                                CCAC CCCCAT CACG GCC
                                |||| |||||| |||| |||
                                GGTG GGGGTA GTGT CGG
                                  G     _   C
GAM3079  KIAA1196  3'  CCACACCCTGCAGGTG      70131        CA   C
                                CCACGCCC  TGCA GTG
                                ||||||||  |||| |||
                                GGTGTGGG  ACGT CAC
                                     __   C
GAM3079  KIAA1237  3'  CACGCCCCGCATGCC       70132        AT   CG
                                CACGCCCC  GCA  TGCC
                                ||||||||  |||  ||||
                                GTGCGGGG  CGT  ACGG
                                     __   __
GAM3079  KIAA1281  5'  CCTGCCCCACGAATGTGTCC  70133    AC       CAC  _
                                CC  GCCCCATG   GTG CC
                                ||  ||||||||   ||| ||
                                GG  CGGGGTGC   CAC GG
                                 A_       TTA   A
GAM3079  KIAA1453  3'  CAGCCCCATGCGGTCC      70134    C       AC  G
                                CA GCCCCATGC  GT CC
                                || |||||||||  || ||
                                GT CGGGGTACG  CA GG
                                 _       C_  _
GAM3079  KIAA1911  5'  CCGGCTCAGCTGACGTGCCC  70135    AC  CC  T  __
                                CC  GC  CA GC  ACGTGCCC
                                ||  ||  || ||  ||||||||
                                GG  CG  GT CG  TGCACGGG
                                 C_  A_  _  AC
GAM3079  KLF5      5'  CCCGCCCCACCGTGC       70136    A      GCA
                                CC CGCCCCAT   CGTGC
                                || ||||||||   |||||
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                              GG GCGGGGTG  GCACG
                                _    ____
GAM3079 LIM     3' CACGCCCCACCATGCCC    70137        GCA
                              CACGCCCCAT  CGTGCCC
                              ||||||||||  |||||||
                              GTGCGGGGTG  GTACGGG
                                    ____
GAM3079 MAP3K6  5' CCAGCCCCATGGTACC     70138    C      CAC
                              CCA GCCCCATG  GTGCC
                              ||| ||||||||  |||||
                              GGT CGGGGTAC  CATGG
                                _    ____
GAM3079 MAPK11  3' CACGCTCATCCACACGTGCCC 70139     CC  __
                              CACGC  CAT  GCACGTGCCC
                              |||||  |||  ||||||||||
                              GTGCG  GTA  TGTGCACGGG
                                 A_  GG
GAM3079 MCC2    3' CCACACCCCATCAGGCCC    70140        G  CGT
                              CCACGCCCCAT CA  GCCC
                              |||||||||||  ||  ||||
                              GGTGTGGGGTA GT  CGGG
                                     _ C__
GAM3079 MGC11349 5' CCACATCCTGCACGTG     70141     CC  A
                              CCACG  CC TGCACGTG
                              |||||  ||  ||||||||
                              GGTGT  GG ACGTGCAC
                                 A_  _
GAM3079 MGC4737  3' CCACGCCCTCAGGCTGTGCCC 70142       _  T  AC
                              CCACGCCC CA GC  GTGCCC
                              ||||||||  ||  ||  ||||||
                              GGTGCGGG GT CG  CACGGG
                                   A  C  A_
GAM3079 MR      5' CCACGCCCCGCTGCAGCC    70143       A_   CGT
                              CCACGCCCC  TGCA  GCC
                              |||||||||  ||||  |||
                              GGTGCGGGG  ACGT  CGG
                                   CG   ____
GAM3079 NPEPL1  5' CCACGCCCCGGCCCTGCCC   70144       AT  ACG
                              CCACGCCCC  GC  TGCCC
                              |||||||||  ||  |||||
                              GGTGCGGGG  CG  ACGGG
                                   C_  GG_
GAM3079 NTT5    3' CCAGGCCCCATGAACACCC   70145    C      C  GT
                              CCA GCCCCATG AC  GCCC
                              ||| ||||||||  ||  ||||
                              GGT CGGGGTAC TG  TGGG
                                C      T  __
GAM3079 NXPH3   3' CCCGCCCCACCCGTGCCC    70146    A      GCA
                              CC CGCCCCAT  CGTGCCC
                              ||  ||||||||  |||||||
```

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                                GG GCGGGGTG   GCACGGG
                                 _      G__
GAM3079  POR1     3'  CCACACCCTGGGGCTGCCC   70147        CAT_  ACG
                                CCACGCCC   GC   TGCCC
                                ||||||||   ||   |||||
                                GGTGTGGG   CG   ACGGG
                                    ACCC  ___
GAM3079  SCLY     5'  CCCGCCCCACTGCTGCC     70148    A     _   ACG
                                CC CGCCCCA TGC   TGCC
                                || ||||||| |||   ||||
                                GG GCGGGGT ACG   ACGG
                                 _      G  ___
GAM3079  SNPH     3'  CCCGCCCCATCTTTGCCC    70149    A      GCACG
                                CC CGCCCCAT    TGCCC
                                || ||||||||    |||||
                                GG GCGGGGTA    ACGGG
                                 _      GAA__
GAM3079  SNPH     3'  CCAGCCCCATGTGTACCC    70150    C      CAC
                                CCA GCCCCATG   GTGCCC
                                ||| ||||||||   ||||||
                                GGT CGGGGTAC   CATGGG
                                  _      A__
GAM3079  STRAIT11499 5'  TGACCGGAATGCACGTGCC   70151   C   CC_
                                A GCC   ATGCACGTGCC
                                | |||   ||||||||||
                                A TGG   TACGTGCACGG
                                 C   CCT
GAM3079  VILL     3'  CCACGCCCTCTGGCAGGTCC   70152        CA  _  C  G
                                CCACGCCC  TG CA GT CC
                                ||||||||  || || || ||
                                GGTGCGGG  AC GT CA GG
                                    AG  C  C  _
GAM3079  ZNF84    5'  CGTGTCCCGCGCACGCGCCC   70153    C__   A
                                CG   CCC TGCACGTGCCC
                                ||   ||| ||||||||||
                                GC   GGG GCGTGCGCGGG
                                 ACA   C
GAM3079  ZSIG11   5'  ACGCCCCAGTGGGTATGCC   70154        _  CAC
                                ACGCCCCA TG   GTGCC
                                |||||||| ||   |||||
                                TGCGGGGT AC   TACGG
                                    C  CCA
GAM3079  LOC118978 5'  CCAGCCCCATGGCTGCAGCCC  70155     C       CAC  _
                                CCA GCCCCATG   GT GCCC
                                ||| ||||||||   || ||||
                                GGT CGGGGTAC   CG CGGG
                                  _      CGA  T
GAM3079  LOC127281 3'  CCACGCCCACCCGCTGC     70156        CAT  A  _
                                CCACGCCC   GC CG TGC
                                ||||||||   || || |||
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                                GGTGCGGG  TG GC ACG
                                    ___  G  G
GAM3079  LOC144266 5'  CCACACCCCATGCTGGTCC   70157          AC  G
                                CCACGCCCCATGC  GT CC
                                ||||||||||||  || ||
                                GGTGTGGGGTACG  CA GG
                                      AC  _
GAM3079  LOC145868 3'  CCATGCCTTTGCACATGC    70158    C   CCA
                                CCA GCC   TGCACGTGC
                                ||| |||   |||||||||
                                GGT CGG   ACGTGTACG
                                  A   AA_
GAM3079  LOC146336 3'  CCACGCCCCTGCTGCGGCC   70159        A   A_  T
                                CCACGCCCC TGC  CG GCC
                                ||||||||| |||  || |||
                                GGTGCGGGG ACG  GC CGG
                                     _   AC  _
GAM3079  LOC147299 3'  CACGCCCTGCAGGCTGCC    70160       CA    C _
                                CACGCCC  TGCA G TGCC
                                |||||||  |||| | ||||
                                GTGCGGG  ACGT C ACGG
                                    __    C G
GAM3079  LOC147515 3'  CACCCTCCATGCACCTGCCC   70161     G  _      G
                                CAC CC CCATGCAC TGCCC
                                ||| || |||||||| |||||
                                GTG GG GGTACGTG ACGGG
                                  _  A       G
GAM3079  LOC149995 3'  CACCCTCCATGCACCTGCCC   70161     G  _      G
                                CAC CC CCATGCAC TGCCC
                                ||| || |||||||| |||||
                                GTG GG GGTACGTG ACGGG
                                  _  A       G
GAM3079  LOC150054 5'  CCAGGCCCCATGGCATCC    70162     C       CA   G
                                CCA GCCCCATG  CGT CC
                                ||| ||||||||  ||| ||
                                GGT CGGGGTAC  GTA GG
                                  C       C_  _
GAM3079  LOC150290 5'  CCACGCCCCTGAGCAGCCC   70163        AT_   CGT
                                CCACGCCCC   GCA   GCCC
                                |||||||||   |||   ||||
                                GGTGCGGGG   CGT   CGGG
                                     ACT   ____
GAM3079  LOC150759 3'  CCACACAGCCAGCATGTGTCC  70164       C_   T   C   _
                                CCACGC  CCA GCA GTG CC
                                ||||||  ||| ||| ||| ||
                                GGTGTG  GGT CGT CAC GG
                                   TC   _   A   A
GAM3079  LOC151323 3'  CCACACAGCCAGCATGTGTCC  70164       C_   T   C   _
                                CCACGC  CCA GCA GTG CC
                                ||||||  ||| ||| ||| ||
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                                GGTGTG  GGT CGT CAC GG
                                   TC   _   A   A
GAM3079  LOC152009 5'  CCACTGCTCCATGGTCC     70165      _ C    CAC  G
                                CCAC GC CCATG   GT CC
                                |||| || |||||   || ||
                                GGTG CG GGTAC   CA GG
                                  A  A    ____  _
GAM3079  LOC154789 5'  CCACGCCCCAGGTGCGCC     70166          TGCAC
                                CCACGCCCCA     GTGCC
                                ||||||||||     |||||
                                GGTGCGGGGT     CGCGG
                                      CCA__
GAM3079  LOC154789 5'  CCACACCCCACCCTGCCC     70167          GCACG
                                CCACGCCCCAT     TGCCC
                                ||||||||||     |||||
                                GGTGTGGGGTG     ACGGG
                                       GG___
GAM3079  LOC163412 5'  CACGCCCCGGCACTTGCC     70168        AT    G
                                CACGCCCC  GCAC TGCC
                                ||||||||  |||| ||||
                                GTGCGGGG  CGTG ACGG
                                     C_    A
GAM3079  LOC199796 5'  CCAGCCCCACGATGCC      70169     C       CAC
                                CCA GCCCCATG   GTGCC
                                ||| ||||||||   |||||
                                GGT CGGGGTGC   TACGG
                                  _      ___
GAM3079  LOC200399 3'  CCACACAGCCAGCATGTGTCC  70164       C_   T   C   _
                                CCACGC  CCA GCA GTG CC
                                ||||||  ||| ||| ||| ||
                                GGTGTG  GGT CGT CAC GG
                                   TC   _   A   A
GAM3079  LOC202500 5'  CCACGCCCTACGGATGCCC    70170        C   CAC
                                CCACGCCC ATG   GTGCCC
                                |||||||| |||   ||||||
                                GGTGCGGG TGC   TACGGG
                                     A   C__
GAM3079  LOC202915 3'  CCAGCCTCACAGGTGCCC     70171     C   C AT   C
                                CCA GCC C  GCA GTGCCC
                                ||| ||| |  ||| ||||||
                                GGT CGG G  TGT CACGGG
                                  _   A __   C
GAM3079  LOC203636 3'  CCATTCCCCATGCAGGGGATGC 70172     CG        C___
            CC                    CCA  CCCCATGCA    GTGCCC
                                ||| |||||||||   ||||||
                                GGT  GGGGTACGT    TACGGG
                                  AA        CCCC
GAM3079  LOC204970 3'  CAGCTCCACACGCGTGCCC    70173    C  C     A
                                CA GC CCATGC CGTGCCC
                                || || |||||| |||||||
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                                GT CG GGTGTG GCACGGG
                                 _ A     C
GAM3079  LOC220003 5'  CCACGCCCTGAGTCTGGCGTGC 70174        CA____  CA
                 CC                CCACGCCC     TG  CGTGCCC
                                   ||||||||     ||  |||||||
                                   GGTGCGGG     AC  GCACGGG
                                       ACTCAG  C_
GAM3079  LOC220279 5'  GCCACAGTTGCACGTGCC    70175     C  __
                                   GCC CA  TGCACGTGCC
                                   ||| ||  ||||||||||
                                   CGG GT  ACGTGCACGG
                                     T  CA
GAM3079  LOC221463 3'  CACGTGCCATGCCGTCC     70176      CC     A   G
                                   CACG  CCATGC CGT CC
                                   ||||  |||||| ||| ||
                                   GTGC  GGTACG GCA GG
                                     AC     _  _
GAM3079  LOC221922 5'  CCACGCCCCCACCTGTCC    70177         ATG   G  _
                                   CCACGCCCC   CAC TG CC
                                   |||||||||   ||| || ||
                                   GGTGCGGGG   GTG AC GG
                                        ___  G  A
GAM3079  LOC221975 5'  CCAGCGCCCCGGACGTGCCC   70178     _     ATGC
                                   CCA CGCCCC    ACGTGCCC
                                   ||| ||||||    ||||||||
                                   GGT GCGGGG    TGCACGGG
                                     C     CC__
GAM3079  LOC253502 3'  CCACGCCCTGGATGCC      70179        CA  CAC
                                   CCACGCCC  TG   GTGCC
                                   ||||||||  ||   |||||
                                   GGTGCGGG  AC   TACGG
                                        __  C__
GAM3079  LOC254381 5'  CCGGCCGCCACCACGTGCCC   70180    AC  _   G
                                   CC  GCC CCAT CACGTGCCC
                                   ||  ||| |||| |||||||||
                                   GG  CGG GGTG GTGCACGGG
                                    C_  C   _
GAM3079  LOC254532 5'  CACCCCTGCAAGTGCCC     70181       A   C
                                   CGCCCC TGCA GTGCCC
                                   |||||| |||| ||||||
                                   GTGGGG ACGT CACGGG
                                      _   T
GAM3079  LOC255042 3'  CCACACCCCATAGTCC      70182           CAC  G
                                   CCACGCCCCATG   GT CC
                                   ||||||||||||   || ||
                                   GGTGTGGGGTAT   CA GG
                                          ___  _
GAM3079  LOC256536 3'  CGCCCCACGCCCGTGTCC    70183          A   _
                                   CGCCCCATGC CGTG CC
                                   |||||||||| |||| ||
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                                GCGGGGTGCG GCAC GG
                                      G   A
GAM3079  LOC257476 3'  CACGTGCCAACAGGTGCC    70077     CC  T  C
                                CACG  CCA GCA GTGCC
                                |||| ||| ||| |||||
                                GTGC  GGT TGT CACGG
                                  AC  _  C
GAM3079  LOC257554 5'  CCACACCCCAAGGTGTCC    70184         TGCAC  _
                                CCACGCCCCA    GTG CC
                                ||||||||||    ||| ||
                                GGTGTGGGGT    CAC GG
                                      TC___   A
GAM3079  LOC51236  3'  CCAGTCCCCACGCCGTGCCC  70185    CG      A
                                CCA  CCCCATGC CGTGCCC
                                |||  |||||||| |||||||
                                GGT  GGGGTGCG GCACGGG
                                  CA      _
GAM3079  LOC90522  3'  CCACGCCCTGGGGCGGTGGCC  70186       CAT_  AC  _
                                CCACGCCC   GC  GTG CC
                                ||||||||   ||  ||| ||
                                GGTGCGGG   CG  CAC GG
                                     ACCC  C_  C
GAM3079  LOC90841  3'  CGCATGTTCCTAACGTGCCC  70187    C____  A  C
                                CGC    CC TG ACGTGCCC
                                |||    || || ||||||||
                                GCG    GG AT TGCACGGG
                                  TACAA  _  _
GAM3079  LOC92170  3'  CCCTGCCCTGAACATGCCC   70188   AC   CA  C
                                CC  GCCC  TG ACGTGCCC
                                ||  ||||  || ||||||||
                                GG  CGGG  AC TGTACGGG
                                 GA   __  T
GAM3080  ESRRG     3'  TTAATAAATGGCTGAAAAGTG  70191          CAT   T
                                TTAATAAATGGCT   GGAA GTG
                                ||||||||||||   |||| |||
                                AATTATTTACCGA   CTTT CAC
                                      ___    T
GAM3080  CRELD1    3'  AATAAGTGGCAATGGGGTGTG  70192     A   TC   AA
                                AATAA TGGC  ATGG  TGTG
                                ||||| ||||  ||||  ||||
                                TTATT ACCG  TACC  ACAC
                                  C   T_   CC
GAM3080  HBXAP     3'  TTAATAACTGGCCCGCTGGTGT 70193       A    A_  AA
           G                    TTAATAA TGGCTC  TGG  TGTG
                                |||||||  ||||||  |||  ||||
                                AATTATT ACCGGG  ACC  ACAC
                                    G    CG  __
GAM3080  NAG73     5'  TTAGTAAATGGCTGATGG    70194    A       C
                                TTA TAAATGGCT ATGG
                                |||  |||||||| ||||
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                                AAT ATTTACCGA TACC
                                  C       C
GAM3080  LOC124411 3'  ATAAATGGCTTCAGATGGAGTG 70195          _ __    A
            TG                    ATAAATGGCT CA  TGGA TGTG
                                  |||||||||| ||  |||| ||||
                                  TATTTACCGA GT  ACCT ACAC
                                       A  CT    C
GAM3080  LOC197416 3'  ATAAATGGCTTCAGATGGAGTG 70195          _ __    A
            TG                    ATAAATGGCT CA  TGGA TGTG
                                  |||||||||| ||  |||| ||||
                                  TATTTACCGA GT  ACCT ACAC
                                       A  CT    C
GAM3080  LOC92606  3'  TTAATAAATGGGCTTCTCTGTG 70196          _ CATGGAA
                                  TTAATAAATGG CT      TGTG
                                  |||||||||| ||      ||||
                                  AATTATTTACC GA      ACAC
                                        C  AGAG___
GAM3081  APPL      3'  TAACTGGTTTCCTATCTACTGA 70199        CTGCATA
                                  TAGCTGG      TATCTACTGA
                                  |||||||      ||||||||||
                                  ATTGACC      ATAGATGACT
                                     AAAGG__
GAM3081  FN1       3'  TGGCTGCATATGCTTTCCTATT 70200          A____   C
            GA                    TGGCTGCATAT    TCTA TGA
                                  ||||||||||    |||| |||
                                  ACCGACGTATA    GGAT ACT
                                        CGAAA   A
GAM3081  MNDA      3'  GCTAGAATATATCTACTGA   70201      CTGC
                                  GCTGG   ATATATCTACTGA
                                  |||||   ||||||||||||
                                  CGATC   TATATAGATGACT
                                    T___
GAM3081  PTPN23    5'  TAGCTGCTGCAGCTGCTG    70202      G    TATAT  A
                                  TAGCTG CTGCA    CT CTG
                                  |||||| |||||    || |||
                                  ATCGAC GACGT    GA GAC
                                     _    C____  C
GAM3081  ANKRD6    3'  AGTGACATATATCTACTG    70203    CT
                                  GG  GCATATATCTACTG
                                  ||  ||||||||||||||
                                  TC  TGTATATAGATGAC
                                   AC
GAM3081  DKFZP434P0721 3'  TAGTGCACTATGTCTACTG   70204    C   _  A
                                  TGG TGCAT AT TCTACTG
                                  ||| ||||| || |||||||
                                  ATC ACGTG TA AGATGAC
                                    _    A  C
GAM3081  LANCL2    3'  GCTGGCTGTGTTGCCTACTG   70205        CATATA
                                  GCTGGCTG     TCTACTG
                                  ||||||||     |||||||
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                                CGACCGAC     GGATGAC
                                     ACAAC_
GAM3081  RGS11    3'  GCTGGCTGATTTACTG      70206        CATAT  C
                                GCTGGCTG    AT TACTG
                                ||||||||    || |||||
                                CGACCGAC    TA ATGAC
                                     _____  A
GAM3081  SDC3     5'  ACTGGCTGCAAAACTTGCTG   70207         TATAT  A_
                                GCTGGCTGCA    CT  CTG
                                ||||||||||    ||  |||
                                TGACCGACGT    GA  GAC
                                     TTT__  AC
GAM3081  TIEG     5'  ACTGGCTGCTAGGCTGCTG    70208         A  TAT  A
                                GCTGGCTGC TA   CT CTG
                                ||||||||| ||   || |||
                                TGACCGACG AT   GA GAC
                                     _ CC_  C
GAM3081  LOC115399 3'  TAGCTGCTGCATGTGGTGCTG  70209       G     ATATCTA
                                TAGCTG CTGCAT      CTG
                                |||||| ||||||      |||
                                ATCGAC GACGTA      GAC
                                   _     CACCAC_
GAM3081  LOC153397 3'  TGGCTGCATTCAAAATTTACTG 70210         AT___  C
           A                     TGGCTGCAT    AT TACTGA
                                 |||||||||    || ||||||
                                 ACCGACGTA    TA ATGACT
                                      AGTTT  A
GAM3081  LOC51063  3'  GCTGGGCTTCCATTGTCTACTG 70211       _ G_   ATA
                                GCTGG CT  CAT   TCTACTG
                                ||||| ||  |||   |||||||
                                CGACC GA  GTA   AGATGAC
                                   C  AG   AC_
GAM3081  LOC91301  5'  GCTGGCTGTACATGGGGCAGCT 70212         C    ATCTA__
           GA                    GCTGGCTG ATAT      CTGA
                                 ||||||| ||||      ||||
                                 CGACCGAC TGTA      GACT
                                      A    CCCCGTC
GAM3082  DPP6     5'  GGGGCTTTTTAATATTTTGCTT 70215         TACC____
           T                     GGGGTTTTTT       GCTTT
                                 ||||||||||       |||||
                                 CCCCGAAAAA       CGAAA
                                      TTATAAAA
GAM3082  IL13     3'  TCCTGGGGTCCACTGCTT    70216     CC     TTTT  C
                                TCC  GGGGTT    TAC GCTT
                                |||  ||||||    ||| ||||
                                AGG  CCCCAG    GTG CGAA
                                  A_     ____   A
GAM3082  JAM3     3'  GGGTTTTTTTGAAGCTTT    70217          ACC
                                GGGTTTTTTT   GCTTT
                                ||||||||||   |||||
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                                CCCAAAAAAA  CGAAA
                                     CTT
GAM3082 RNPEPL1  3' TCCCTGGGGTATTGCTT    70218     C    T  TTTACC
                                TCCC GGGGT TT     GCTT
                                |||| ||||| ||     ||||
                                AGGG CCCCA AA     CGAA
                                  A    T _______
GAM3082 CAP350   3' GGGGTTTTTCTAATATACTTT  70219          CC__
                                GGGGTTTTTTTA   GCTTT
                                ||||||||||||   |||||
                                CCCCAAAAAGAT   TGAAA
                                      TATA
GAM3082 CSEN     3' TCCCCAGGGTTTGTGCTT    70220          TTTTACC
                                TCCCCGGGGTTT      GCTT
                                ||||||||||||      ||||
                                AGGGGTCCCAAA      CGAA
                                      CA_____
GAM3082 FLJ25415 3' CCTTGGTCTTTTTTGTTGCTTT 70221    GG       ACC_
                                CC  GGTTTTTTT   GCTTT
                                ||  |||||||||   |||||
                                GG  CCAGAAAAA   CGAAA
                                 AA       ACAA
GAM3082 OSRF     3' CCAGGGTTTTTAAAGCTTT   70222          TTACC
                                CCGGGGTTTTT    GCTTT
                                ||||||||||    |||||
                                GGTCCCAAAAA    CGAAA
                                      TTT__
GAM3082 LOC116437 3' GGGTTTTCTTCTCGCTTT    70223         AC
                                GGGTTTTTTT  CGCTTT
                                |||||||||  ||||||
                                CCCAAAAGAA  GCGAAA
                                     GA
GAM3082 LOC148759 3' TCCTGGGGTTTTTTGCT     70224     CC        TACC
                                TCC  GGGGTTTTTT   GCT
                                |||  ||||||||||   |||
                                AGG  CCCCAAAAAA   CGA
                                  A_        _____
GAM3082 LOC219790 3' TCACCCATTTTTTTTTATTGCT 70225    _   GGG       CC
           TT                    TC CCCG   TTTTTTTA  GCTTT
                                 || ||||   ||||||||  |||||
                                 AG GGGT   AAAAAAAT  CGAAA
                                  T    AA_       AA
GAM3083 MYOZ1    5' CACGAGCTGGGCAGGCG     70228        AC    A
                                CACGAGC  GGGCG GCG
                                |||||||  ||||| |||
                                GTGCTCG  CCCGT CGC
                                    A_    C
GAM3083 RAB36    3' CACGAGACGGGTGGGATGAGTG 70229      C    C_____   CGA
           GGCATA                  CGAG ACGGG     GAG   GCATA
                                |||| |||||     |||   |||||
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                                GCTC TGCCC     CTC   CGTAT
                                  _    ACCCTA   ACC
GAM3083  SORCS3   5'  CGCGCCGGCGAGCGAGCGAGC  70230    A  A__
                                CG GC   CGGGCGAGCGAGC
                                || ||   ||||||||||||||
                                GC CG   GCTCGCTCGCTCG
                                 G  GCC
GAM3083  UPF3A    3'  CACAGCACGCTTTGCGGGCAT  70231     G     GGCGA   A
                                CAC AGCACG     GCG GCAT
                                ||| ||||||     ||| ||||
                                GTG TCGTGC     CGC CGTA
                                  _     GAAA_   C
GAM3083  UPF3A    3'  CACAGCACGCTTTGCGGGCAT  70231     G     GGCGA   A
                                CAC AGCACG     GCG GCAT
                                ||| ||||||     ||| ||||
                                GTG TCGTGC     CGC CGTA
                                  _     GAAA_   C
GAM3083  FLJ11588 5'  CACGACACGGGCAGCG      70232      G      G
                                CACGA CACGGGC AGCG
                                ||||| ||||||| ||||
                                GTGCT GTGCCCG TCGC
                                    _      _
GAM3083  RAI1     3'  CACGGGAGAAGCGAGCAT     70233       C  _
                                CACGGG GA GCGAGCAT
                                |||||| || ||||||||
                                GTGCCC CT CGCTCGTA
                                   T  T
GAM3083  LOC113763 3'  CACGGGCAGGGTGAGCA     70234      A   C   C
                                CACG GCA GGG GAGCG
                                |||| ||| ||| |||||
                                GTGC CGT CCC CTCGT
                                  C   _   A
GAM3083  LOC200000 3'  GAGCACGGGATCAGTGGGCAT  70235         CG_  CGA
                                GAGCACGGG   AG   GCAT
                                |||||||||   ||   ||||
                                CTCGTGCCC   TC   CGTA
                                     TAG  ACC
GAM3083  LOC200812 5'  GCAGGTGGAGCGAGCAT     70236     C  GC
                                GCA GG  GAGCGAGCAT
                                ||| ||  ||||||||||
                                CGT CC  CTCGCTCGTA
                                  _ AC
GAM3083  LOC90826  5'  CACGAGGAGGTAGTGGGCATA 70237       CAC   CG  CGA
                                CACGAG   GGG  AG   GCATA
                                ||||||   |||  ||   |||||
                                GTGCTC   TCC  TC   CGTAT
                                   C__   A_  ACC
GAM3084  AF5Q31   5'  TGAGGCAGGCGGGGGCGG    70240   C       __
                                A GGGCGGGC  GGGCGG
                                | ||||||||  ||||||
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                                A TCCGTCCG  CCCGCC
                                 C       CC
GAM3084  AP2A1    5'  CGGGCGGGCGGGCGGGC     70241              III
                                CGGGCGGGCGGGCGGG  C
                                ||||||||||||||||  |
                                GCCCGCCCGCCCGCCC  G
                                          III
GAM3084  AP2A1    5'  CGGGCGGGCGGGCGGGC     70241              III
                                CGGGCGGGCGGGCGGG  C
                                ||||||||||||||||  |
                                GCCCGCCCGCCCGCCC  G
                                          III
GAM3084  ARHD     5'  GAGCGGGCGGGCGGGCGG    70242    AA
                                GA  CGGGCGGGCGGGCGG
                                ||  ||||||||||||||
                                CT  GCCCGCCCGCCCGCC
                                 C_
GAM3084  CDC25A   5'  GAGGCCAGCGGGCGGGCGGG   70243    AACG
                                GA   GGCGGGCGGGCGGG
                                ||   ||||||||||||||
                                CT   TCGCCCGCCCGCCC
                                 CCGG
GAM3084  COL5A3   3'  GAGGAGGCAGGCATTGGGGGTG 70244    AAC      _____  C
           GG                     GA  GGGCGGGC    GGG GGG
                                ||  ||||||||    ||| |||
                                CT  TCCGTCCG    CCC CCC
                                 CC_      TAACC  A
GAM3084  FASN     5'  TGAGGGCGCGGGCGGCGGTGCG 70245    AGAAA     G  _
           GG                     TGA    CGGGCGG CGG GCGGG
                                |||    ||||||| ||| |||||
                                ACT    GCCCGCC GCC CGCCC
                                 CCCGC      _  A
GAM3084  KCNQ2    3'  TGAGGAGGGCCGCGGGCGG   70246    A  AAC   GG
                                TGA GA   GGGC  GCGGGCGG
                                ||| ||   ||||  ||||||||
                                ACT CT   CCCG  CGCCCGCC
                                 C  ___   G_
GAM3084  LAMB1    5'  TGAAGGGGCGGGCGGCCG    70247      AAAC       G
                                TGAAG   GGGCGGGCGG CG
                                |||||   |||||||||| ||
                                ACTTC   CCCGCCCGCC GC
                                   ____        G
GAM3084  MGAT2    5'  GAAGGGGCGGGCGGGCGG    70248     AAAC
                                GAAG   GGGCGGGCGGGCGG
                                ||||   ||||||||||||||
                                CTTC   CCCGCCCGCCCGCC
                                  ____
GAM3084  NOX4     5'  GAAGGAGCGGGCGGCGGCCGGG 70249     AAA     G  G
                                GAAG  CGGGCGG CGG CGGG
                                ||||  ||||||| ||| ||||
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                                CTTC   GCCCGCC GCC GCCC
                                  CTC      _  G
GAM3084  SCA2     5'  TGAGGAGCGGGCGGCGCGCTGG 70250     A  AA      G  G  _
              G                    TGA GA  CGGGCGG CG GC GGG
                                   ||| ||  ||||||| || || |||
                                   ACT CT  GCCCGCC GC CG CCC
                                     C  C_      _  G  A
GAM3084  TAZ      5'  GAGGAAACGGGAAGGCGGG   70251    A       C
                                   GA GAAACGGG GGGCGGG
                                   || |||||||| |||||||
                                   CT CTTTGCCC TCCGCCC
                                    C       T
GAM3084  YY1      5'  AGAGGGGGCGGGCGGCGG    70252     AAC         G
                                   AGA   GGGCGGGCGG CGG
                                   |||   |||||||||| |||
                                   TCT   CCCGCCCGCC GCC
                                     CC_         _
GAM3084  C4S-2    3'  GAGCGGGCGGGCGGGCGGG   70253    AA
                                   GA  CGGGCGGGCGGGCGGG
                                   ||  ||||||||||||||||
                                   CT  GCCCGCCCGCCCGCCC
                                    C_
GAM3084  DKFZP564D172 3'  GAGGAGGCGTGCGGGTGGG   70254    AAC    G    C
                                   GA   GGGCG GCGGG GGG
                                   ||   ||||| ||||| |||
                                   CT   TCCGC CGCCC CCC
                                    CC_    A    A
GAM3084  FAF1     3'  GAGACGAGCGTGTGGGTGGG   70255    A      GGC   C
                                   GA ACGGGCG   GGG GGG
                                   || |||||||   ||| |||
                                   CT TGCTCGC   CCC CCC
                                    C      ACA   A
GAM3084  FLJ13262  3'  AGAAAGCAGGCGGGCGGG    70256      ACG
                                   AGAA   GGCGGGCGGGCGGG
                                   ||||   ||||||||||||||
                                   TCTT   TCGTCCGCCCGCCC
                                          ___
GAM3084  FLJ22865  5'  GAAAGGCGGGCGGGCCAG    70257     AC          G
                                   GAA  GGGCGGGCGGGC GG
                                   |||  |||||||||||| ||
                                   CTT  TCCGCCCGCCCG TC
                                     __           G
GAM3084  FXYD3    3'  GAGGAGGCAGAGGGCGG     70258    AAC      C
                                   GA   GGGCGGG GGGCGG
                                   ||   ||||||| ||||||
                                   CT   TCCGTCT CCCGCC
                                    CC_      _
GAM3084  FXYD3    3'  GAGGAGGCAGAGGGCGG     70258    AAC      C
                                   GA   GGGCGGG GGGCGG
                                   ||   ||||||| ||||||
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                                CT   TCCGTCT CCCGCC
                                 CC_      _
GAM3084  GRIN3A    5'  GAGCAGGCAGGCGGGCGG    70259    AA
                                GA  CGGGCGGGCGGGCGG
                                ||  ||||||||||||||
                                CT  GTCCGTCCGCCCGCC
                                 C_
GAM3084  KIAA0247  5'  AGAGGAAGCGGGCGGGAGG   70260    AAC        C
                                AGA   GGGCGGGCGGG GG
                                |||   |||||||||| ||
                                TCT   TTCGCCCGCCC CC
                                  CC_         T
GAM3084  KIAA0552  5'  TGAGGAAACGGGGGTCTGGG   70261    A       C  GC_
                                TGA GAAACGGG GG   GGG
                                ||| ||||||| ||   |||
                                ACT CTTTGCCC CC   CCC
                                  C       _ AGA
GAM3084  KIAA1656  3'  TGAGGAAGCAGGCGGGCAA    70262    A  AACG
                                TGA GA    GGCGGGCGGGCGG
                                ||| ||    ||||||||||||
                                ACT CT    TCGTCCGCCCGTT
                                  C _____
GAM3084  PRDM12    3'  TGAGGAAACGGGCAGGGACCGA 70263    A         C  G
            G                    TGA GAAACGGGCGGG GG CGGG
                                ||| |||||||||| || ||||
                                ACT CTTTGCCCGTCC CT GCTC
                                  C          _  G
GAM3084  UREB1     3'  TGAGGAAACAGGCGGCGGG    70264    A         G
                                TGA GAAACGGGCGG CGGG
                                ||| |||||||||| ||||
                                ACT CTTTGTCCGCC GCCC
                                  C         _
GAM3084  VAMP4     5'  CGGTGCTGGGCGGGCGGG     70265    _ _
                                CGG GC GGGCGGGCGGG
                                ||| || ||||||||||
                                GCC CG CCCGCCCGCCC
                                  A  A
GAM3084  WNT10A    5'  GAAGAGCGGGCGAACCGG     70266    AC         _
                                GAA  GGGCGGGCGGGC GG
                                |||  |||||||||||| ||
                                CTT  CTCGCCCGCTTG CC
                                  __          G
GAM3084  WSB1      5'  AGAGGAGACGGGCGGGG      70267    AAC        C
                                AGA   GGGCGGGCGGG G
                                |||   |||||||||| |
                                TCT   TCTGCCCGCCC C
                                  CC_         _
GAM3084  WSB1      5'  AGAGGAGACGGGCGGGG      70267    AAC        C
                                AGA   GGGCGGGCGGG G
                                |||   |||||||||| |
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                                TCT   TCTGCCCGCCC C
                                  CC_         _
GAM3084  LOC132617 5'  GAAGAACGGGCCTGCGGG    70268       A    GG
                                GAAGAA CGGGC  GCGGG
                                |||||| |||||  |||||
                                CTTCTT GCCCG  CGCCC
                                   _    GA
GAM3084  LOC146280 5'  TGAAGGGGTCGGACGCCGGGCG 70269      AAA_     GG
            GG                    TGAAG   CGGGCG  CGGGCGGG
                                |||||   ||||||  ||||||||
                                ACTTC   GCCTGC  GCCCGCCC
                                   CCCA     G_
GAM3084  LOC149837 3'  AGAAGGGGGCAGGCGGGTGGG  70270      AC         C
                                AGAA  GGGCGGGCGGG GGG
                                ||||  |||||||||| |||
                                TCTT  CCCGTCCGCCC CCC
                                  CC          A
GAM3084  LOC152137 5'  GAGGAGACAGAAAGGCGGGCGG 70271    A  A    C
            G                    GA GA ACGGG GGGCGGGCGGG
                                || || ||||| ||||||||||
                                CT CT TGTCT TCCGCCCGCCC
                                 C  C    T
GAM3084  LOC164118 3'  GAAGCGGAGGCAGGCGGGTGGG 70272      AAAC         C
                                GAAG   GGGCGGGCGGG GGG
                                ||||   |||||||||| |||
                                CTTC   TCCGTCCGCCC CCC
                                  GCC_         A
GAM3084  LOC196500 3'  TGCGGAAACGAGGTGGGTGGG  70273    AA    _ C   C
                                TG  GAAACG GG GGG GGG
                                ||  |||||| || ||| |||
                                AC  CTTTGC CC CCC CCC
                                 GC     T  A   A
GAM3084  LOC203668 5'  TGAGGAAATTAGAGCGGGCGGG 70274    A   C__
            CGGG                   TGA GAAA   GGGCGGGCGGGCGGG
                                ||| ||||   ||||||||||||||
                                ACT CTTT   CTCGCCCGCCCGCCC
                                  C    AAT
GAM3084  LOC254552 5'  GAAGAGGCGGGGCGAGGCGGG  70275      AACG    _ _
                                GAAGA   GGCGGG CG GGCGGG
                                |||||   |||||| || ||||||
                                CTTCT   CCGCCC GC CCGCCC
                                   _____     C  T
GAM3084  LOC257054 5'  GAGGAGGGACACGGCGGGCGGG 70276    A  AAC    _
                                GA GA   GGGCG GGCGGGCGGG
                                || ||   ||||| ||||||||||
                                CT CT   CCTGT CCGCCCGCCC
                                 C  C__    G
GAM3085  CLECSF11  5'  ACTTCCTCTATCAGGTGGGT   70279        AT   ACA
                                ACTTCCTT  TCAG   GGT
                                ||||||||  ||||  |||
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                                TGAAGGAG  AGTC   CCA
                                    AT    CAC
GAM3085  COL4A5   3'  CACTTCCTTATTTCTTTAGTA  70280          CAGACA
                                TACTTCCTTATT     GGTA
                                ||||||||||||     ||||
                                GTGAAGGAATAA     TCAT
                                    AGAAA_
GAM3085  COL4A5   3'  CACTTCCTTATTTCTTTAGTA  70280          CAGACA
                                TACTTCCTTATT     GGTA
                                ||||||||||||     ||||
                                GTGAAGGAATAA     TCAT
                                    AGAAA_
GAM3085  COL4A5   3'  CACTTCCTTATTTCTTTAGTA  70280          CAGACA
                                TACTTCCTTATT     GGTA
                                ||||||||||||     ||||
                                GTGAAGGAATAA     TCAT
                                    AGAAA_
GAM3085  EDG6     3'  TACCTCCTTGTCCAGGGT    70281          A    ACA
                                TACTTCCTT TTCAG   GGT
                                ||||||||| |||||   |||
                                ATGGAGGAA AGGTC   CCA
                                    C    ___
GAM3085  EIF2C1   3'  CACTTCCTTGAAGCTTGGGTA  70282          ATTC  ACA_
                                TACTTCCTT    AG    GGTA
                                |||||||||    ||    ||||
                                GTGAAGGAA    TC    CCAT
                                    CT__  GAAC
GAM3085  FGF18    3'  CTTCCTTATTTTTCATGTA    70283          CAGA  G
                                CTTCCTTATT    CA GTA
                                ||||||||||    || |||
                                GAAGGAATAA    GT CAT
                                    AAA_  A
GAM3085  GOSR1    3'  TTCCTTATTCCAGACCAGG    70284           _   _
                                TTCCTTATTC AGAC AGG
                                |||||||||| |||| |||
                                AAGGAATAAG TCTG TCC
                                    G    G
GAM3085  HCS      3'  TTCCTTATTTCTGAAGGTA    70285          _ A  C
                                TTCCTTATT C GA AGGTA
                                ||||||||| | || |||||
                                AAGGAATAA G CT TCCAT
                                    A A  _
GAM3085  KCND2    5'  TTCCCTCCAAGACAGGTA    70286        ATTC
                                TTCCTT    AGACAGGTA
                                ||||||    |||||||||
                                AAGGGA    TCTGTCCAT
                                   GGT_
GAM3085  PLAG1    3'  TACTTCCTTATTAACA      70287          CA
                                TACTTCCTTATT  GACA
                                ||||||||||||  ||||
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                                ATGAAGGAATAA  TTGT
                                      __
GAM3085  PRKG1    3'  CTTTCTTAGTTAGACAAGTA  70288    C   TTC
                                CTT CTTA   AGACAGGTA
                                ||| ||||   |||||||||
                                GAA GAAT   TCTGTTCAT
                                  A   CAA
GAM3085  SIGLEC6  3'  TACTTCCTCTAGTTCACAGGT  70289        A__  AG
                                TACTTCCTT   TTC  ACAGGT
                                |||||||||   |||  ||||||
                                ATGAAGGAG   AAG  TGTCCA
                                     ATC  __
GAM3085  TLX1     3'  CTTAACAGTTCAGACAGGT   70290     _____
                                CTTA   TTCAGACAGGT
                                ||||   ||||||||||
                                GAAT   AAGTCTGTCCA
                                  TGTC
GAM3085  TMC2     3'  CTTCCCTAAAGGACAGGT    70291       TTCA
                                CTTCCTTA   GACAGGT
                                ||||||||   |||||||
                                GAAGGGAT   CTGTCCA
                                     TTC_
GAM3085  TRIM     3'  TACTTCCCTAAGTATTAGGTA  70292         TTCAGAC
                                TACTTCCTTA     AGGTA
                                ||||||||||     |||||
                                ATGAAGGGAT     TCCAT
                                      TCATAA_
GAM3085  ZNF138   5'  TTCCTTGTTCCAGACAGGTA  70293      A_
                                TTCCTT  TTCAGACAGGTA
                                ||||||  ||||||||||||
                                AAGGAA  AGGTCTGTCCAT
                                   CA
GAM3085  CDCA4    3'  TACTTCCTCACCCAGGGCAGGT 70294            A_
                                TACTTCCTTATTCAG  CAGGT
                                ||||||||||||||  |||||
                                ATGAAGGAGTGGGTC  GTCCA
                                         CC
GAM3085  CLDN4    3'  CACTTCCCAGGCAGGT      70295       TTATT   A
                                TACTTCC    CAG CAGGT
                                |||||||    ||| |||||
                                GTGAAGG    GTC GTCCA
                                     _____  C
GAM3085  FLJ11042 3'  TTCCATTAGACAGGTA      70296     TT   C
                                TTCC  ATT AGACAGGTA
                                ||||  ||| |||||||||
                                AAGG  TAA TCTGTCCAT
                                  __  _
GAM3085  FLJ13942 3'  TACTTTCTCATTCACAG     70297      C      AG
                                TACTT CTTATTC  ACAG
                                ||||| |||||||  ||||
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                                ATGAA GAGTAAG  TGTC
                                  A     __
GAM3085  FLJ14906  3'  CACTCTTCAGACAGGT     70298      CCTTA
                                TACTT    TTCAGACAGGT
                                |||||    ||||||||||
                                GTGAG    AAGTCTGTCCA
                                  _____
GAM3085  FLJ20005  5'  CTTCTCCTAACAGGCAGGT   70299     _   TT   A
                                CTTC CTTA  CAG CAGGT
                                |||| ||||  ||| |||||
                                GAAG GGAT  GTC GTCCA
                                  A   T_  C
GAM3085  FLJ20625  3'  TACTTCCTTTATCGAGGGT   70300        AT  A  CA
                                TACTTCCTT  TC GA  GGT
                                |||||||||  || ||  |||
                                ATGAAGGAA  AG CT  CCA
                                     AT  _  C_
GAM3085  FLJ22530  3'  TTCCCTATATTACAGGTA    70301       TCAG
                                TTCCTTAT   ACAGGTA
                                ||||||||   |||||||
                                AAGGGATA   TGTCCAT
                                    TAA_
GAM3085  FLJ22693  3'  CACTTCCTTGGGCAATGGGT  70302        ATT   ACA
                                TACTTCCTT   CAG   GGT
                                |||||||||  |||  |||
                                GTGAAGGAA   GTT   CCA
                                     CCC   AC_
GAM3085  H-plk     5'  TTCCTTGCTCCAGACAGGTA  70303      A_
                                TTCCTT  TTCAGACAGGTA
                                ||||||  ||||||||||||
                                AAGGAA  AGGTCTGTCCAT
                                   CG
GAM3085  KIAA0441  3'  ACTTTTTTATTCAAAGGGGTA 70304     CC       CA
                                ACTT  TTATTCAGA  GGTA
                                ||||  |||||||||  ||||
                                TGAA  AATAAGTTT  CCAT
                                  AA       CC
GAM3085  KIAA1320  3'  TACTTCCTGTTCAAACA     70305       TA
                                TACTTCCT  TTCAGACA
                                ||||||||  ||||||||
                                ATGAAGGA  AAGTTTGT
                                    C_
GAM3085  KIAA1649  5'  CTTCCTTATCTAGAAGGT    70306        TC   C
                                CTTCCTTAT  AGA AGGT
                                |||||||||  ||| ||||
                                GAAGGAATA  TCT TCCA
                                     GA  _
GAM3085  PRO0767   3'  TACTTCCTTATTCTACAA    70307          AG
                                TACTTCCTTATTC  ACAG
                                ||||||||||||  ||||
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                                ATGAAGGAATAAG  TGTT
                                      A_
GAM3085  PRO1257   5'  TACTTCCTGATTCTCATGTA   70308        T   AGA  G
                                TACTTCCT ATTC   CA GTA
                                |||||||| ||||   || |||
                                ATGAAGGA TAAG   GT CAT
                                     C    A__  A
GAM3085  STX12     3'  CTTTCTATGCAGACAGGT    70309     CC   T
                                CTT  TTAT CAGACAGGT
                                |||  |||| |||||||||
                                GAA  GATA GTCTGTCCA
                                  A_   C
GAM3085  VILL      3'  CACTTCCTTGTGGGACGGGT  70310        ATTCA   A
                                TACTTCCTT    GAC GGT
                                |||||||||    ||| |||
                                GTGAAGGAA    CTG CCA
                                     CACC_  C
GAM3085  VPS4B     3'  TTCCTTATTAGCAAAGGT    70311        C  AC_
                                TTCCTTATT AG   AGGT
                                |||||||||  ||   ||||
                                AAGGAATAA TC   TCCA
                                     _  GTT
GAM3085  ZNF90     5'  TTCCTTGCTCCAGACAGGT   70312       A_
                                TTCCTT  TTCAGACAGGT
                                ||||||  ||||||||||
                                AAGGAA  AGGTCTGTCCA
                                   CG
GAM3085  LOC115265 3'  TTCCCTAGTGACAGGTA     70313       TTCA
                                TTCCTTA    GACAGGTA
                                |||||||    ||||||||
                                AAGGGAT    CTGTCCAT
                                   CA__
GAM3085  LOC123688 5'  TTCCCGCAGACAGGTA      70314      TATT
                                TTCCT    CAGACAGGTA
                                |||||    ||||||||||
                                AAGGG    GTCTGTCCAT
                                  C___
GAM3085  LOC142927 5'  TACTTGCTCTGGACAGGTA    70315      C   ATTCA
                                TACTT CTT    GACAGGTA
                                ||||| |||    ||||||||
                                ATGAA GAG    CTGTCCAT
                                  C   AC___
GAM3085  LOC146332 3'  CACTTCCTGAGACAGGT     70316        TATTC
                                TACTTCCT    AGACAGGT
                                ||||||||    ||||||||
                                GTGAAGGA    TCTGTCCA
                                     C____
GAM3085  LOC153114 5'  TACTTCTTTATTCAAGG     70317       C      GAC
                                TACTTC TTATTCA   AGG
                                ||||||  |||||||   |||
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                                ATGAAG AATAAGT   TCC
                                   A     ___
GAM3085  LOC154007 3'  TACATACTTTTTAGACAGGT   70318     TTC   A  C
                                TAC   CTT TT AGACAGGT
                                |||   ||| || ||||||||
                                ATG   GAA AA TCTGTCCA
                                  TAT   A  _
GAM3085  LOC197125 3'  TACTTCATTTATTCAACAAGTA 70319       C_      A
                                TACTTC  TTATTCAG CAGGTA
                                ||||||  |||||||| ||||||
                                ATGAAG  AATAAGTT GTTCAT
                                   TA       _
GAM3085  LOC203350 3'  CTTCCCCAGACAGGT       70320       TATT
                                CTTCCT    CAGACAGGT
                                ||||||    |||||||||
                                GAAGGG    GTCTGTCCA

                                   _____
GAM3085  LOC220930 5'  TTCCTTATTCGAAGGAGGT    70321         A  C__
                                TTCCTTATTC GA   AGGT
                                |||||||||| ||   ||||
                                AAGGAATAAG CT   TCCA
                                      _  TCC
GAM3086  KIAA1128  3'  CTTGAGGTCTGTCTGCGGTGCG 70324      T  CC  GAGTG
                                CTTG GG  TC    GCGGTGCG
                                |||| ||  ||    ||||||||
                                GAAC CC  AG    CGCCACGC
                                  T  __  ACAGA
GAM3086  KIAA1643  3'  CTTGTGGCCTGTGGGGCAGCAT 70325         CGAGT     __
            GCG                   CTTGTGGCCT    GGCGGT  GCG
                                ||||||||||    ||||||  |||
                                GAACACCGGA    CCGTCG  CGC
                                      CACC_     TA
GAM3086  LOC115399 3'  CTCGTGGCCTTGGGTGC     70326         CGAG   CG
                                CTTGTGGCCT    TGG  GTGC
                                ||||||||||    |||  ||||
                                GAGCACCGGA    ACC  CACG
                                      _____   __
GAM3086  LOC144563 5'  CTTGTGGCCTCTGGAATG    70327          __
                                CTTGTGGCCTC  GAGTG
                                ||||||||||  |||||
                                GAACACCGGAG  CTTAC
                                      AC
GAM3086  LOC151632 5'  CTTGTGGCCTCTGGAATG    70327          __
                                CTTGTGGCCTC  GAGTG
                                ||||||||||  |||||
                                GAACACCGGAG  CTTAC
                                      AC
GAM3086  LOC152271 3'  CTTGTGGCCTCTGGAATG    70327          __
                                CTTGTGGCCTC  GAGTG
                                ||||||||||  |||||
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                                GAACACCGGAG  CTTAC
                                      AC
GAM3086  LOC200904 5'  CTTGTGGCCTCTGGAATG    70327          __
                                CTTGTGGCCTC  GAGTG
                                ||||||||||  |||||
                                GAACACCGGAG  CTTAC
                                      AC
GAM3086  LOC219919 5'  CTTGTGGCCTCTGGAATG    70327          __
                                CTTGTGGCCTC  GAGTG
                                ||||||||||  |||||
                                GAACACCGGAG  CTTAC
                                      AC
GAM3086  LOC221795 5'  CTTGTGGCCTCTGGAATG    70327          __
                                CTTGTGGCCTC  GAGTG
                                ||||||||||  |||||
                                GAACACCGGAG  CTTAC
                                      AC
GAM3086  LOC256515 5'  CTTGTGGCCTCTGGAATG    70327          __
                                CTTGTGGCCTC  GAGTG
                                ||||||||||  |||||
                                GAACACCGGAG  CTTAC
                                      AC
GAM3086  LOC256594 5'  CTTGTGGCCTCTAGAATG    70328          __
                                CTTGTGGCCTC  GAGTG
                                ||||||||||  |||||
                                GAACACCGGAG  CTTAC
                                      AT
GAM3087  GRB10     3'  GTGGTGTAACTGCAATGT    70331         CG    _
                                GTGGTGTAAC  TGTAG GT
                                ||||||||||  ||||| ||
                                CACCACATTG  ACGTT CA
                                      __     A
GAM3087  DKFZP434K028 3'  TCGCGTGGTGTAGGCGGGT    70332     _      ACC   TA
                                TCG GTGGTGTA   GTG  GGT
                                ||| ||||||||   |||  |||
                                AGC CACCACAT   CGC  CCA
                                  G       C__  __
GAM3087  MGC2654   3'  GGTGGTGTGATCGTACAGGT   70333        AAC
                                GGTGGTGT   CGTGTAGGT
                                ||||||||   |||||||||
                                CCACCACA   GCATGTCCA
                                     CTA
GAM3087  NX-17     3'  TCAGTGGTGTTGGTGGGTA   70334         AACC   TA
                                TCGGTGGTGT   GTG  GGTA
                                ||||||||||   |||  ||||
                                AGTCACCACA   CAC  CCAT
                                      AC__  __
GAM3088  PTGIS     3'  AATCATCAAAATCAATGACT   70337          GTTCT
                                AGTCATCAAAAT    TGACT
                                ||||||||||||    |||||
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                                TTAGTAGTTTTA    ACTGA
                                      GTT__
GAM3088 UNC119   3' TAAGTTGTCCGGAAGTCCTGAC 70338     CA  AAAAT  T
           T                   TAAGT  TC    GT CTTGACT
                               |||||  ||    || |||||||
                               ATTCA  AG    CA GGACTGA
                                  AC  GCCTT  _
GAM3088 UNC119   3' TAAGTTGTCCGGAAGTCCTGAC 70338     CA  AAAAT  T
           T                   TAAGT  TC    GT CTTGACT
                               |||||  ||    || |||||||
                               ATTCA  AG    CA GGACTGA
                                  AC  GCCTT  _
GAM3088 KIAA1500 3' AGTCATCAAATTACTTGA    70339        ATGTT
                               AGTCATCAAA    CTTGA
                               ||||||||||    |||||
                               TCAGTAGTTT    GAACT
                                     AAT__
GAM3088 MY014    3' TAAATTTTCATGTTCTTGACT  70340     CA   AAA
                               TAAGT  TCA   TGTTCTTGACT
                               |||||  |||   ||||||||||
                               ATTTA  AGT   ACAAGAACTGA
                                  AA  ___
GAM3088 PLSCR4   3' TAAGTTGCTCAGAGATCTTGAC 70341     CA_  AAATGT
           T                   TAAGT   TCA     TCTTGACT
                               |||||   |||     ||||||||
                               ATTCA   AGT     AGAACTGA
                                  ACG   CTCT__
GAM3088 LOC143570 5' AGTCCTCAAGCATCCTTGGCT  70342     A   AAT     A
                               AGTC TCAA   GTTCTTG CT
                               |||| ||||   ||||||| ||
                               TCAG AGTT   TAGGAAC GA
                                 G   CG_     C
GAM3088 LOC157858 3' TCATCAAAGTGACAGCGACT   70343       A  TTCT
                               TCATCAAA TG    TGACT
                               |||||||| ||    |||||
                               AGTAGTTT AC    GCTGA
                                    C  TGTC
GAM3089 EGR2     5' TATTAATCAATTGCTCCTC    70346        CA  CACT
                               TATTAATCAA  GC    TCTTC
                               ||||||||||  ||    |||||
                               ATAATTAGTT  CG    AGGAG
                                     AA  ____
GAM3089 TAP2     3' AATCTGCAGCCACTTCTT    70347     AA
                               AATC  CAGCCACTTCTT
                               ||||  ||||||||||||
                               TTAG  GTCGGTGAAGAA
                                 AC
GAM3089 HNRPA3   3' CATTAATCAATAGCTGCACTT  70348        C  __
                               TATTAATCAA AGC  CACTT
                               |||||||||| |||  |||||
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                                GTAATTAGTT TCG  GTGAA
                                     A   AC
GAM3089  PDE4DIP   3'  TATCAATCAGAAACTTTCTTCA 70349        AC   CAC
                                TATTAATCA  AGC   TTCTTCA
                                |||||||||  |||   |||||||
                                ATAGTTAGT  TTG   AAGAAGT
                                     CT   A__
GAM3089  LOC145078 3'  CATTAATCAATAGCTGCACTT  70348         C   __
                                TATTAATCAA AGC  CACTT
                                |||||||||| |||  |||||
                                GTAATTAGTT TCG  GTGAA
                                     A   AC
GAM3089  LOC148981 3'  CATTAATCAGTAGCTGCACTT  70350        AC   __
                                TATTAATCA  AGC  CACTT
                                |||||||||  |||  |||||
                                GTAATTAGT  TCG  GTGAA
                                     CA   AC
GAM3089  LOC165666 5'  CATTAATCAAAGTCTTCTT    70351         C  CCA
                                TATTAATCAA AG   CTTCTT
                                |||||||||| ||   ||||||
                                GTAATTAGTT TC   GAAGAA
                                     _  A__
GAM3089  LOC220988 3'  CATTAATCAATAGCTGCACTT  70348         C   __
                                TATTAATCAA AGC  CACTT
                                |||||||||| |||  |||||
                                GTAATTAGTT TCG  GTGAA
                                     A   AC
GAM3089  LOC255190 3'  CATTAATCAATAGCTGCACTT  70348         C   __
                                TATTAATCAA AGC  CACTT
                                |||||||||| |||  |||||
                                GTAATTAGTT TCG  GTGAA
                                     A   AC
GAM3089  LOC257319 3'  TATTAATCAACAGTGTCCCA   70352           ____
                                TATTAATCAACAG    CCA
                                ||||||||||||    |||
                                ATAATTAGTTGTC    GGT
                                       ACAG
GAM3090  ALDH3B2   5'  GCGCAGAAGCTGCTTGTTTTCT 70355      T_   TG      C
           T                     GCGCA  GGT  TGCTTGTT TCTT
                                 |||||  |||  |||||||| ||||
                                 CGCGT  TCG  ACGAACAA AGAA
                                    CT   __       A
GAM3090  CBFA2T1   3'  GCGTTGGTTGTGTTGTC     70356     CA      C
                                 GCG  TGGTTGTG TTGTT
                                 |||  |||||||| |||||
                                 CGC  ACCAACAC AACAG
                                   A_       _
GAM3090  ITPKB     3'  GCTTGGAACATTTTGTTCTCTT 70357     A   TTGTGC
                                 GC TGG     TTGTTCTCTT
                                 || |||     ||||||||||
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                                CG ACC     AACAAGAGAA
                                 A  TTGTAA
GAM3090  MAP3K7IP2 3'  GTTCAAGTTTGCTTGTT    70358   CG  T   G
                                G  CA GGTT TGCTTGTT
                                |  || |||| ||||||||
                                C  GT TCAA ACGAACAA
                                 AA  _   _
GAM3090  TGM4     3'  GCTTATGGTTGTGTTGGCCT   70359    GC       C   TT
                                GC  ATGGTTGTG TTG  CT
                                ||  ||||||||| |||  ||
                                CG  TACCAACAC AAC  GA
                                 AA        _  CG
GAM3090  mPA-PLA1  3'  GCCTGTGGTTGTAGCTTTCT   70360    GCA     _   GT
                                GC   TGGTTGT GCTT  TCT
                                ||   ||||||| ||||  |||
                                CG   ACCAACA CGAA  AGA
                                 GAC      T   __
GAM3090  NMP200   3'  ATGGTTATTGTTTTCT     70361        GCT   C
                                ATGGTTGT   TGTT TCT
                                ||||||||   |||| |||
                                TACCAATA   ACAA AGA
                                     ___   A
GAM3090  OSBPL10   3'  GCTGTGGTTGTGCATGTT    70362    GCA       T
                                GC   TGGTTGTGC TGTT
                                ||   |||||||| ||||
                                CG   ACCAACACG ACAA
                                 AC_       T
GAM3090  RBAK     3'  GGCAGTATGCTTGTTCTCTT   70363    __
                                GGT  TGTGCTTGTTCTCTT
                                |||  ||||||||||||||
                                CCG  ATACGAACAAGAGAA
                                  TC
GAM3090  UBE4B    3'  GCGTGTGGCTGTGTTTGT    70364    CA      C
                                GCG  TGGTTGTG TTGT
                                |||  |||||||| ||||
                                CGC  ACCGACAC AACA
                                  AC       A
GAM3090  USP24    3'  GCTGGGATGCTTGTTTTCT   70365    A   TT      C
                                GC TGG  GTGCTTGTT TCT
                                || |||  ||||||||| |||
                                CG ACC  TACGAACAA AGA
                                 _  C_       A
GAM3091  FGF5     3'  CAGCAATGTCTGCAATACT   70368       _  ATACC
                                CAGCAATG CT    TAATACT
                                |||||||| ||    |||||||
                                GTCGTTAC GA    GTTATGA
                                     A  C____
GAM3091  FGF5     3'  CAGCAATGTCTGCAATACT   70368       _  ATACC
                                CAGCAATG CT    TAATACT
                                |||||||| ||    |||||||
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                                GTCGTTAC GA    GTTATGA
                                    A  C____
GAM3091  MLLT4    3'  AGTGATGCTACACATACT    70369    CA       CTA
                                AG  ATGCTATAC   ATACT
                                ||  |||||||||   |||||
                                TC  TACGATGTG   TATGA
                                 AC       ___
GAM3091  SOX11    3'  TACAGCAATGTCATACACC    70370         C__
                                TACAGCAATG   TATACC
                                ||||||||||   ||||||
                                ATGTCGTTAC   ATGTGG
                                      AGT
GAM3091  MAD4     3'  CAGCAATGACGTTTAATACT   70371        CTATACC
                                CAGCAATG      TAATACT
                                ||||||||      |||||||
                                GTCGTTAC      ATTATGA
                                    TGCAA__
GAM3091  MBLL39   3'  TAAGCATACCATATTTAATACT 70372   C    A      CC
                                A AGCA TGCTATA  TAATACT
                                | |||| |||||||  |||||||
                                A TCGT ATGGTAT  ATTATGA
                                 T   _      AA
GAM3091  MBLL39   3'  TAAGCATACCATATTTAATACT 70372   C    A      CC
                                A AGCA TGCTATA  TAATACT
                                | |||| |||||||  |||||||
                                A TCGT ATGGTAT  ATTATGA
                                 T   _      AA
GAM3091  MGC14433 3'  TACAGCAAAGTTATACAACACA 70373        TGC    CTA
            CT                   TACAGCAA   TATAC   ATACT
                                ||||||||   |||||   |||||
                                ATGTCGTT   ATATG   TGTGA
                                    TCA    TTG
GAM3091  NPD009   3'  TACATTAATGCTATACACAAT  68861     GC       C
                                TACA  AATGCTATAC TAAT
                                ||||  |||||||||| ||||
                                ATGT  TTACGATATG GTTA
                                  AA        T
GAM3091  RBM12    3'  TACAGCAATGTTTATCCT    70374         C_   A
                                TACAGCAATG  TAT CCT
                                ||||||||||  ||| |||
                                ATGTCGTTAC  ATA GGA
                                     AA  _
GAM3091  LOC257444 5'  AGCAATGCTGAACTGATACT   70375        AT  CTA
                                AGCAATGCT  AC   ATACT
                                |||||||||  ||   |||||
                                TCGTTACGA  TG   TATGA
                                    CT  AC_
GAM3092  FOXD1    3'  TACAATAATAATTGCCAGTAAA 70378         T    T  C
            A                    TACAATAAT AATT CT GTAAAA
                                |||||||| |||| || ||||||
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                                ATGTTATTA TTAA GG CATTTT
                                      _   C  T
GAM3092 BLP1     3'  TACAAGGTTTATTTTCTCGTA  70379      TAA   A
                                TACAA   TTA TTTCTCGTA
                                |||||   ||| |||||||||
                                ATGTT   AAT AAAGAGCAT
                                   CCA   A
GAM3092 KIAA0470 3'  AATAGTTAATTTCCGTAAA   70380     A      T
                                AATA TTAATTTC CGTAAA
                                |||| |||||||| ||||||
                                TTAT AATTAAAG GCATTT
                                  C      _
GAM3092 WDR7     3'  TACAATAAATTAATTTCCAT   70381       _      T
                                TACAATAA TTAATTTC CGT
                                |||||||| |||||||| |||
                                ATGTTATT AATTAAAG GTA
                                     T      _
GAM3092 LOC220766 3'  AATAGTTAATTTCCGTAAA   70380     A      T
                                AATA TTAATTTC CGTAAA
                                |||| |||||||| ||||||
                                TTAT AATTAAAG GCATTT
                                  C      _
GAM3093 PMP2     3'  TGGCAGATAGGATTAGTA    70384          GG
                                TGGCAGATAGG  TGGTA
                                ||||||||||  |||||
                                ACCGTCTATCC  ATCAT
                                      TA
GAM3093 FLJ10895 3'  TTACTGCAGATTGGTA      70385       G    AGGGG
                                TTACTG CAGAT    TGGTA
                                |||||| |||||    |||||
                                AATGAC GTCTA    ACCAT
                                   _    _____
GAM3093 H2AV     3'  TTACTGGGGATAGGAATG    70386       CA
                                TTACTGG  GATAGGGGTG
                                |||||||  ||||||||||
                                AATGACC  CTATCCTTAC
                                    C_
GAM3093 KIAA0377 3'  CTGGTGGAAGGGGTGAGT    70387     CA  T     _
                                CTGG  GA AGGGGTG GT
                                ||||  || |||||||  ||
                                GACC  CT TCCCCAC CA
                                  AC  _      T
GAM3093 RGS18    3'  TACTGGCAGATACTGTA     70388          GGG
                                TACTGGCAGATA   GTG
                                ||||||||||||   |||
                                ATGACCGTCTAT   CAT
                                      GA_
GAM3093 LOC147004 3'  TTACTGCAGATAGGATGTG   70389       G      _
                                TTACTG CAGATAGGG GTG
                                |||||| ||||||||| |||
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                                AATGAC GTCTATCCT CAC
                                  _       A
GAM3093  LOC206426 3'  TTATTGGCAGATAAGTTATG   70390     C        G_
                                TTA TGGCAGATAGG  GTG
                                ||| ||||||||||  |||
                                AAT ACCGTCTATTC  TAC
                                  A         AA
GAM3093  LOC253461 3'  TACTGGAGGGGGTGGTAT    70391       C  ATA
                                TACTGG AG   GGGGTGGTAT
                                |||||| ||   ||||||||||
                                ATGACC TC   CCCCACCATA
                                  _ ____
GAM3093  LOC256145 3'  ACTGGCAGGCGGGTGGT     70392        ATAG
                                ACTGGCAG    GGGTGGT
                                ||||||||    |||||||
                                TGACCGTC    CCCACCA
                                     CG__
GAM3094  PCDHB14   3'  TGTCTAGATTTAAGTTAC    70395          _
                                TGTCTGGATTTA GTTAC
                                |||||||||||| |||||
                                ACAGATCTAAAT CAATG
                                       T
GAM3094  PPP3CB    3'  TGCCTGGAGCTCTGAGTT    70396        _  __
                                TGTCTGGA TTT  AGTT
                                |||||||| |||  ||||
                                ACGGACCT GAG  TCAA
                                     C   AC
GAM3094  DKFZp434F2322 3'  TGTCTGGACCAGGAGTTA    70397          T__
                                TGTCTGGATT   AGTTA
                                ||||||||||   |||||
                                ACAGACCTGG   TCAAT
                                      TCC
GAM3094  KIAA1043  3'  TGCCTGGATAAGAGTTAC    70398         TT_
                                TGTCTGGAT   AGTTAC
                                |||||||||   ||||||
                                ACGGACCTA   TCAATG
                                     TTC
GAM3094  USP2      3'  GTCTGAACACTTTAGTTA    70399        ___
                                GTCTGGAT   TTAGTTA
                                ||||||||   |||||||
                                CAGACTTG   AATCAAT
                                     TGA
GAM3094  LOC130576 5'  TATCTGGATAGGCAGTTA    70400         T__
                                TGTCTGGAT   TAGTTA
                                |||||||||   ||||||
                                ATAGACCTA   GTCAAT
                                      TCC
GAM3094  LOC220573 3'  TGTTTGGATAATAGTTAC    70401     C    T_
                                TGT TGGAT  TAGTTAC
                                ||| |||||  |||||||
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                                ACA ACCTA  ATCAATG
                                  A     TT
GAM3095  ASS      3'  ACGCTGCCAGCCGGGGAGAACA 70404          _     ATCT
                                ACGCTGCCA CCGGG    ACA
                                ||||||||| |||||    |||
                                TGCGACGGT GGCCC    TGT
                                     C     CTCT
GAM3095  ASS      3'  ACGCTGCCAGCCGGGGAGAACA 70404          _     ATCT
                                ACGCTGCCA CCGGG    ACA
                                ||||||||| |||||    |||
                                TGCGACGGT GGCCC    TGT
                                     C     CTCT
GAM3095  CDR2     5'  ACGCCGCCGCCGGGCCCAAC   70405         A     ATCTA
                                ACGCTGCC CCGGG     CAAC
                                |||||||| |||||     ||||
                                TGCGGCGG GGCCC     GTTG
                                     C     GG___
GAM3095  CYP2B6   3'  TGACTGTGGTCTACAAC     70406    C    CCACCG  A
                                A GCTG      GG TCTACAAC
                                | ||||      || ||||||||
                                A TGAC      CC AGATGTTG
                                 C    A_____ _
GAM3095  FZD3     3'  GCTTCATTTAGCTACAACA    70407     GC  CCG  AT
                                GCT  CA   GG  CTACAACA
                                |||  ||   ||  ||||||||
                                CGA  GT   TC  GATGTTGT
                                  A_  AAA  __
GAM3095  PPP2R5A  5'  CGCTGCCATCGCGGGTCC     70408         C__    A
                                CGCTGCCA   CGGG TCT
                                ||||||||   |||| |||
                                GCGACGGT   GCCC AGG
                                     AGC    _
GAM3095  ATP6V0A1 3'  GCTCCTTCCATCTACAA      70409     G  A_  GGG
                                GCT CC  CC   ATCTACAA
                                ||| ||  ||   ||||||||
                                CGA GG  GG   TAGATGTT
                                  _  AA  ____
GAM3095  CTRP5    5'  CGCTGGCACCGGGAGCCCGGAC 70410       C       T  ACA
                                CGCTG CACCGGGA CT   AC
                                ||||| |||||||| ||   ||
                                GCGAC GTGGCCCT GG   TG
                                   C       C  GCC
GAM3095  DKFZP434M154 5'  ACGCCGCCGCCGGTCCCTGAC  70411         A    GA  _
                                ACGCTGCC CCGG  TCT AC
                                |||||||| ||||  ||| ||
                                TGCGGCGG GGCC  GGA TG
                                     C    AG   C
GAM3095  FLJ22940 5'  ACGCTGCCACCGCTTCGCCTGC 70412           GGA__   A
              AACA                   ACGCTGCCACCG     TCT CAACA
                                ||||||||||||     ||| |||||
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                                TGCGACGGTGGC    GGA GTTGT
                                      GAAGC   C
GAM3095  FLJ25012  3'  ACTCTGCCACCCAGGCTGCA  70413    G      G  AT  A
                                AC CTGCCACC GG  CT CA
                                || |||||||| ||  || ||
                                TG GACGGTGG TC  GA GT
                                 A       G  C_  C
GAM3095  KIAA0703  5'  GCTGACACGTGCTACAACA   70414     C   C GGAT
                                GCTG CAC G    CTACAACA
                                |||| ||| |    ||||||||
                                CGAC GTG C    GATGTTGT
                                  T   _ AC__
GAM3095  KIAA1136  3'  TGCCACCAAAGTTTACAA    70415          ATC
                                TGCCACCGGG   TACAA
                                ||||||||||   |||||
                                ACGGTGGTTT   ATGTT
                                      CAA
GAM3095  RASGRP4   3'  ACGCTGTTGCTGAGACCTAC  70416       CCACC
                                ACGCTG    GGGATCTAC
                                ||||||    |||||||||
                                TGCGAC    CTCTGGATG
                                   AACGA
GAM3095  LOC152286 3'  GCTGCCACGTGCCCAGCAAC  70417        C GGA   _
                                GCTGCCAC G   TCTA CAAC
                                |||||||| |   |||| ||||
                                CGACGGTG C   GGGT GTTG
                                     _ AC_    C
GAM3095  LOC153505 3'  CGCGGCCACCGGGACCCACA  70418     T
                                CGC GCCACCGGGATCTACA
                                ||| ||||||||||||||||
                                GCG CGGTGGCCCTGGGTGT
                                  C
GAM3095  LOC222933 5'  GCTACCACTGGGATTTCTA   70419        C   __
                                GCTGCCAC GGGA  TCTA
                                |||||||| ||||  ||||
                                CGATGGTG CCCT  AGAT
                                     A   AA
GAM3096  FBP1      3'  TCTACAGCATTTGATGGTG   70422          TCCGTGC
                                TCTACAGTATTT      GGTG
                                ||||||||||||      ||||
                                AGATGTCGTAAA      CCAC
                                      CTA____
GAM3096  GA        3'  TCCATAGTATTTTTGGTG    70423     C      CCGTGC
                                TCTA AGTATTTT     GGTG
                                |||| ||||||||     ||||
                                AGGT TCATAAAA     CCAC
                                  A       A_____
GAM3096  KIAA1172  3'  CAGTATTTTTTGTTATTTTGTG 70424        CC  GCG___
             G                   CAGTATTTT  GT     GTGG
                                 |||||||||  ||     ||||
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                                GTCATAAAA CA     CACC
                                     AA ATAAAA
GAM3096 SLC7A11   3' CACAGTATTTTCTAATACTGG 70425          C_   _
                                TACAGTATTTTC GTGC GG
                                |||||||||||| |||| ||
                                GTGTCATAAAAG TATG CC
                                      AT   A
GAM3096 LOC157697 5' TCTACATATTTTCCTTGG    70426      G      GTGC
                                TCTACA TATTTTCC   GG
                                |||||| ||||||||   ||
                                AGATGT ATAAAAGG   CC
                                   _      AA__
GAM3096 LOC220071 5' TCTACAGTATTGTCTAATAATT 70427          T  CGTGCGG
             GG                   TCTACAGTATT TC      TGG
                                |||||||||| ||      |||
                                AGATGTCATAA AG      ACC
                                      C ATTATTA
GAM3097 BCAS1     3' AAGAATATATACATGGAGCGTG 70430      C__  TC____    III
             TTTGGGGAT               TATACA  GGC    GGGGA  T
                                |||||| |||    |||||  |
                                ATATGT  TCG    CCCCT  A
                                   ACC  CACAAA    III
GAM3097 C8orf1    3' AGCATACATATCCCTTGGGGA 70431         CACGG  C
                                AGCATATATA    CT GGGGA
                                ||||||||||    || |||||
                                TCGTATGTAT    GA CCCCT
                                     AGG__  A
GAM3097 DIAPH2    3' ATATATACAGAGGGG      70432         C  CTC
                                ATATATACA GG   GGGG
                                ||||||||| ||   ||||
                                TATATATGT CT   CCCC
                                     _ ___
GAM3097 DKFZP566E144 3' GCATATATGTACCAAGGGA   70433        ACACG   C
                                GCATATAT    GCT GGGGA
                                ||||||||    ||| |||||
                                CGTATATA    TGG TCCCT
                                     CA___   T
GAM3097 HRLP5     5' GCACTGGGGGCGGCTCGGGGA 70434     ATATACA
                                GCAT      CGGCTCGGGGA
                                ||||      ||||||||||
                                CGTG      GCCGAGCCCCT
                                  ACCCCC_
GAM3097 HSA249128 3' AAGCATATATGCCTGGG     70435         ACACG  TC
                                AAGCATATAT    GC  GGG
                                ||||||||||    ||  |||
                                TTCGTATATA    CG  CCC
                                     _____  GA
GAM3097 MAC30     3' AAGCATATATGCTGTGGGTCAG 70436         ACAC_  C
             G                   AAGCATATAT    GG TCGGG
                                ||||||||||    || |||||
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                                TTCGTATATA    CC AGTCC
                                     CGACA  C
GAM3097  RNPC2    3'  AAGCTATATACATAAGGG    70437     A      CGGCTC
                                AAGC TATATACA     GGGG
                                |||| ||||||||     ||||
                                TTCG ATATATGT     TCCC
                                  _       AT_____
GAM3097  ZFP67    3'  ATATGTATCACTCCTTGGGG   70438     A  _   GG  C
                                ATAT TA CAC  CT GGGG
                                |||| || |||  || |||||
                                TATA AT GTG  GA CCCC
                                  C  A   AG  A
GAM3097  LOC153259 5'  GCATATATCCATGGCTGGG   70439        A  C    C
                                GCATATAT CA GGCT GGG
                                |||||||| || ||||| |||
                                CGTATATA GT CCGA CCC
                                     G  A   _
GAM3097  LOC158263 5'  AAGCATATGTACATTGCAGG   70440        A    CG  TC
                                AAGCATAT TACA  GC  GGG
                                |||||||| ||||  ||  |||
                                TTCGTATA ATGT  CG  TCC
                                     C    AA  __
GAM3098  ASCL1    5'  TCTAAGAAAAAAAAAAGCA    70443      _
                                TCTAA AAAAAAAAAAGCA
                                ||||| ||||||||||||
                                AGATT TTTTTTTTTTCGT
                                  C
GAM3098  CPNE3    3'  TCTTAAAAAAAAAAAAGCACA   70444     A
                                TCT AAAAAAAAAAAGCACA
                                ||| ||||||||||||||||
                                AGA TTTTTTTTTTTCGTGT
                                  A
GAM3098  HNMT     5'  TCCAAAAAAAAAAAAAAATGCT 70445             CACAC
                                TCTAAAAAAAAAAAAG    GCT
                                ||||||||||||||||    |||
                                AGGTTTTTTTTTTTTT    CGA
                                          TTA__
GAM3098  HNRPH2   3'  AAAAAAAAAAAAGTGTACACT  70446          CAC
                                AAAAAAAAAAAAG   ACGCT
                                ||||||||||||   |||||
                                TTTTTTTTTTTTC   TGTGA
                                     ACA
GAM3098  LARS     3'  AAAAAAAAAAAAGCTGCT    70447           ACAC
                                AAAAAAAAAAAAGC    GCT
                                ||||||||||||||   |||
                                TTTTTTTTTTTTCG    CGA
                                     A___
GAM3098  MAK      3'  TCTAAAAAAAAAAAAAAAAGC 70448             CACAC
              T                  TCTAAAAAAAAAAAG    GCT
                                ||||||||||||||||    |||
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                                AGATTTTTTTTTTTTT    CGA
                                      TTTT_
GAM3098  PER2     3'  TCTAAAACAAAAAAAGCAACA  70449       A       C
                                TCTAAAA AAAAAAAGCA ACG
                                ||||||| |||||||||| |||
                                AGATTTT TTTTTTTCGT TGT
                                    G       _
GAM3098  PIAS1    3'  CCTAAAAAAAGGAAAAAAAACA 70450         __     C
           CGCT                   TCTAAAAAAA  AAAAAG ACACGCT
                                ||||||||||  |||||| |||||||
                                GGATTTTTTT  TTTTTT TGTGCGA
                                      CC     T
GAM3098  PPP1R12A 3'  TAAAAAAAAAAAGGCCAC    70451          A  A
                                TAAAAAAAAAAA GC CAC
                                |||||||||||| || |||
                                ATTTTTTTTTTT CG GTG
                                      C  _
GAM3098  RAB30    3'  TAAAAAAACAAAAGCAACATGC 70452        A     _  C
           T                    TAAAAAAA AAAAGCA CA GCT
                                ||||||||| ||||||| || |||
                                ATTTTTTT TTTTCGT GT CGA
                                    G      T  A
GAM3098  SEDL     3'  TCAAAAAAAAAAAAAGCGAGCT 70453    T          ACAC
                                TC AAAAAAAAAAAAGC    GCT
                                || ||||||||||||||    |||
                                AG TTTTTTTTTTTTCG    CGA
                                 T           CT__
GAM3098  SHANK2   3'  TCTAAAAAGAATAAAAGCAC   70454        _  A
                                TCTAAAAA AA AAAAGCAC
                                |||||||| || ||||||||
                                AGATTTTT TT TTTTCGTG
                                    C  A
GAM3098  TBXA2R   3'  TCTAAAAAAAAAAATAGCA    70455          _
                                TCTAAAAAAAAAAA AGCA
                                |||||||||||||| ||||
                                AGATTTTTTTTTTT TCGT
                                      A
GAM3098  ASPN     3'  TAAAAAAAAAAAAGCATATGCT 70456            CAC   III
           A                    TAAAAAAAAAAAAGCA   GCT   A
                                |||||||||||||||   |||   |
                                ATTTTTTTTTTTTCGT   CGA   T
                                      ATA   III
GAM3098  C17orf26 3'  AAAAAAAAAAAAGCCAGACT   70457          A  C
                                AAAAAAAAAAAAGC CA GCT
                                |||||||||||||| || |||
                                TTTTTTTTTTTTCG GT TGA
                                      _  C
GAM3098  COQ7     3'  TAAAAAAAAAAAAACAAAC    70458           C
                                TAAAAAAAAAAAAGCA AC
                                |||||||||||||||| ||
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                                ATTTTTTTTTTTTTGT TG
                                          T
GAM3098  DKFZp762L0311 3'  TCTCAAAAAAAAAAAAGTACA  70459     _          C
                                TCT AAAAAAAAAAAAG ACA
                                ||| |||||||||||||| |||
                                AGA TTTTTTTTTTTTC TGT
                                  G           A
GAM3098  FLJ10826 3'  AAAAAAAAAAAAGCCAACT    70460            A  C
                                AAAAAAAAAAAAGC CA GCT
                                |||||||||||||| || |||
                                TTTTTTTTTTTTCG GT TGA
                                          _ _
GAM3098  FLJ10846 3'  TCTCAAAAAAAAAAAGTCCA   70461     A          CA
                                TCT AAAAAAAAAAAG  CA
                                ||| ||||||||||||  ||
                                AGA TTTTTTTTTTTC  GT
                                  G           AG
GAM3098  FLJ14803 3'  TCTAAAAAAAAAAAAGAC     70462             C
                                TCTAAAAAAAAAAAAG AC
                                |||||||||||||||| ||
                                AGATTTTTTTTTTTC TG
                                          _
GAM3098  FLJ22055 3'  TCTAAAAAAAAAAAAAGTGGAG 70463         A__________   ACAC
                   CGTGTGC                AAAAAAAA         AGC    GC
                                ||||||||         |||    ||
                                TTTTTTTT         TCG    CG
                                     TTTCACCIII   CACA
GAM3098  HSPC039   3'  TCTAAAAAAAGAGAAGCAACA  70464          AAA    C
                                TCTAAAAAAA   AAGCA ACG
                                ||||||||||   ||||| |||
                                AGATTTTTTT   TTCGT TGT
                                     CTC    _
GAM3098  KIAA0090  3'  TCAAAAAAAAAAAAAGCACCTG 70465    T            AC
                   CT                   TC AAAAAAAAAAAAGCAC  GCT
                                || ||||||||||||||  |||
                                AG TTTTTTTTTTTTCGTG  CGA
                                  T            GA
GAM3098  KIAA0420  3'  TCTAAAGGCAAAAAAGCAACAC 70466       AAA        C
                   T                   TCTAAA   AAAAAAGCA ACGCT
                                ||||||   |||||||||| |||||
                                AGATTT   TTTTTTCGT TGTGA
                                   CCG       _
GAM3098  KIAA0515  3'  AAAAAAAAAACAAAAAACGCT   70467          C___
                                AAAAAAAAGCA    ACGCT
                                ||||||||||    |||||
                                TTTTTTTTTGT    TGCGA
                                      TTTT
GAM3098  KIAA0847  3'  TCTAAAAAAAAAAAATCA     70468             G
                                TCTAAAAAAAAAAAA CA
                                |||||||||||||| ||
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                                AGATTTTTTTTTTTT GT
                                        A
GAM3098  KIAA0863  3'  TAAAAAAAAAAAAACAGCT   70469            CAC
                                TAAAAAAAAAAAAGCA   GCT
                                ||||||||||||||||   |||
                                ATTTTTTTTTTTTTGT   CGA
                                        ____
GAM3098  KIAA1193  3'  TCTAAAAAAAAAAAAGCA     70470          A
                                TCTAAAAAAAAAAA GCA
                                |||||||||||||| |||
                                AGATTTTTTTTTTT CGT
                                        _
GAM3098  KIAA1257  3'  TCAAAAAAAAAAAAAAGTGCAAA 70471    T         CA  C
                  CT                  TC AAAAAAAAAAAAG  CA GCT
                                || ||||||||||||  || |||
                                AG TTTTTTTTTTTC  GT TGA
                                 T          AC  T
GAM3098  KIAA1586  3'  TCCAAAAAAAAAAAAAGAC    70472            C
                                TCTAAAAAAAAAAAAG AC
                                |||||||||||||||| ||
                                AGGTTTTTTTTTTTC TG
                                        _
GAM3098  KPNA6     3'  TCTAAAAAAAAAAAAAAGCAGG 70473            CA  C
                  CT                  TCTAAAAAAAAAAAAG  CA GCT
                                ||||||||||||||||  || |||
                                AGATTTTTTTTTTTTT  GT CGA
                                        TC  C
GAM3098  LCHN      3'  TCTAAAAAGAGGAAAGCAAGGC 70474        AAAA     CAC
                  T                   TCTAAAAA    AAAGCA   GCT
                                ||||||||    ||||||   |||
                                AGATTTTT    TTTCGT   CGA
                                     CTCC     TC_
GAM3098  MGC14436  5'  TCCAAAAAAAAAAAAAAAAGCT 70475            CACAC
                                TCTAAAAAAAAAAAAG    GCT
                                ||||||||||||||||    |||
                                AGGTTTTTTTTTTTTT    CGA
                                        TTT__
GAM3098  MIG-6     3'  TCTAAAAAAAAAAAAGCA    70476
                                TCTAAAAAAAAAAAAGCA
                                ||||||||||||||||||
                                AGATTTTTTTTTTTCGT

GAM3098  PELI2     3'  AAAAAAAAAAAAGCCCACA   70477          A
                                AAAAAAAAAAAAGC CACG
                                |||||||||||||| ||||
                                TTTTTTTTTTTTCG GTGT
                                        G
GAM3098  RAB39     3'  TCTCAAAAAAAAAAAGCAACA  70478    A         C
                                TCT AAAAAAAAAAGCA ACG
                                ||| |||||||||||||| |||
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                                AGA TTTTTTTTTTTCGT TGT
                                  G          _
GAM3098  SNX11    3'  TCCAAAAAGAAAGGAGCCCAC  70479        A   AA   A
                                TCTAAAAA AAA  AGC CAC
                                |||||||| |||  ||| |||
                                AGGTTTTT TTT  TCG GTG
                                     C   CC   G
GAM3098  TNKS2    3'  TCTAAAAAACAGGAGCACTTTG 70480         AAAAA    AC_
              CT                  TCTAAAAAA    AGCAC   GCT
                                |||||||||    |||||  |||
                                AGATTTTTT    TCGTG   CGA
                                     GTCC_    AAA
GAM3098  TRIP3    3'  TCCAGGAGTCAAGCACACGCT  70481     AAAAAAAAA
                                TCTA        AAGCACACGCT
                                ||||        ||||||||||
                                AGGT        TTCGTGTGCGA
                                  CCTCAG___
GAM3098  LOC139341 3'  TCTTAAAAAAAAAAAGTCAGCC 70482     A          CA  C
                                TCT AAAAAAAAAAAG  CA GCT
                                ||| ||||||||||||  || |||
                                AGA TTTTTTTTTTTC  GT CGG
                                  A          A_  _
GAM3098  LOC143872 3'  TCTAAGAAAAAAAAAACA    70483       A
                                TCTAA AAAAAAAAAGCA
                                ||||| ||||||||||||
                                AGATT TTTTTTTTTTGT
                                   C
GAM3098  LOC146050 3'  TCCAAAAAAAAAAAAAAGAGCT 70484              CACAC
                                TCTAAAAAAAAAAAAG     GCT
                                ||||||||||||||||     |||
                                AGGTTTTTTTTTTTTT     CGA
                                          TCT__
GAM3098  LOC150282 3'  CTAAAAAAGAAAAAGCCAC    70485        A      A
                                CTAAAAAA AAAAAGC CAC
                                |||||||| ||||||| |||
                                GATTTTTT TTTTTCG GTG
                                     C      _
GAM3098  LOC153592 3'  TCCAAAAAAAAAAAAAAAGC   70486            ___
                                TCTAAAAAAAAAAA   AGC
                                ||||||||||||||   |||
                                AGGTTTTTTTTTTT   TCG
                                       TTT
GAM3098  LOC202934 3'  TCTAAAAAAAAAAAACAC    70487             G
                                TCTAAAAAAAAAAAA CAC
                                ||||||||||||||| |||
                                AGATTTTTTTTTTTT GTG
                                          _
GAM3098  LOC221540 3'  TCTAAAAAAAAAATGGCCA    70488           AA  A
                                TCTAAAAAAAAAA  GC CA
                                ||||||||||||  || ||
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                                AGATTTTTTTTTT  CG GT
                                      AC  _
GAM3098  LOC257354 3'  TCTAAAGGCAAAAAAGCAACAC 70466       AAA       C
           T                    TCTAAA   AAAAAAGCA ACGCT
                                ||||||   ||||||||| |||||
                                AGATTT   TTTTTTCGT TGTGA
                                   CCG       _
GAM3098  LOC257545 3'  TCTAAAAAAAAAATGGCCA   70488          AA  A
                                TCTAAAAAAAAAA  GC CA
                                ||||||||||||  || ||
                                AGATTTTTTTTTT  CG GT
                                      AC  _
GAM3098  LOC257598 3'  TCTAAAAAAAAAATGGCCA   70488          AA  A
                                TCTAAAAAAAAAA  GC CA
                                ||||||||||||  || ||
                                AGATTTTTTTTTT  CG GT
                                      AC  _
GAM3099  CDC25B   3'  TCTGACCCATCCTCAGGG    70491    A  A   C
                                TCT ACC ATCC CAGGG
                                ||| ||| |||| |||||
                                AGA TGG TAGG GTCCC
                                  C  G   A
GAM3099  CDC25B   3'  TCTGACCCATCCTCAGGG    70491    A  A   C
                                TCT ACC ATCC CAGGG
                                ||| ||| |||| |||||
                                AGA TGG TAGG GTCCC
                                  C  G   A
GAM3099  PRLR     3'  TAACCAATCATTCCATTAGTCA 70492        C__  GG  C
           AG                    TAACCAATC   CCA  GG CAAG
                                |||||||||   |||  || ||||
                                ATTGGTTAG   GGT  TC GTTC
                                     TAA   AA  A
GAM3099  SFTPD    3'  TCTGGCCAAACTCCTGGGCCAA 70493    AA   TCC  AG
           G                     TCT  CCAA   CC  GGGCCAAG
                                |||  ||||   ||  ||||||||
                                AGA  GGTT   GG  CCCGGTTC
                                  CC   TGA  A_
GAM3099  TACC3    5'  TCTGCTCCACGCCGGGGGCCAA 70494    AA_  ATCC  A
           G                     TCT   CCA   CC GGGGCCAAG
                                |||   |||   || |||||||||
                                AGA   GGT   GG CCCCGGTTC
                                  CGA   GC__  C
GAM3099  TCP10    3'  TCTAACCAAGTTTCCTAAATAG 70495        ___  CCAG_
           G                     TCTAACCAA  TCC    GGG
                                |||||||||  |||    |||
                                AGATTGGTT  AGG    TCC
                                     CAA   ATTTA
GAM3099  THBD     3'  TCTAACCAGCTCCCATGGG   70496        A_   CA
                                TCTAACCA  TCCC  GGG
                                ||||||||  ||||  |||
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                                AGATTGGT AGGG CCC
                                    CG   TA
GAM3099 C21orf93 5' TCCTGTGTCTCTCCAGGGGCCA 70497    AACCAA C
                                TCT    TC CCAGGGGCCA
                                |||    || ||||||||||
                                AGG    AG GGTCCCCGGT
                                  ACACAG A
GAM3099 C5orf6   3' TCAGCCAATCCCTCAGTGAG  70498   TAA     _ _
                                TC  CCAATCCC CAG GGG
                                ||  |||||||| ||| |||
                                AG  GGTTAGGG GTC CTC
                                 TC_     A  A
GAM3099 CMG2     3' TCAAACCGATCCCCAGGAG   70499   T  A
                                TC AACC ATCCCCAGGGG
                                || |||| ||||||||||
                                AG TTGG TAGGGGTCCTC
                                 T  C
GAM3099 COPB     5' TAACCAATCCTTGACACAAG  70500       CCAGG  _
                                TAACCAATCC   GGC CAAG
                                ||||||||||   ||| ||||
                                ATTGGTTAGG   CTG GTTC
                                     AA___  T
GAM3099 DNAJA3   3' TCTAACCATCTCCCTCTGCC  70501      A_  CAGGG
                                TCTAACCA TCCC   GCC
                                |||||||| ||||   |||
                                AGATTGGT AGGG   CGG
                                    AG  AGA__
GAM3099 FLJ12994 3' TCTAACCATTTCCTACTGAAG 70502      A_  CCA_
                                TCTAACCA TCC  GGGG
                                |||||||| |||  ||||
                                AGATTGGT AGG  CTTC
                                    AA  ATGA
GAM3099 FLJ12994 3' TCTAACCATTTCCTACTGAAG 70502      A_  CCA_
                                TCTAACCA TCC  GGGG
                                |||||||| |||  ||||
                                AGATTGGT AGG  CTTC
                                    AA  ATGA
GAM3099 FLJ14486 3' TCTAACCAGCCCCAGCCCCA  70503      AT   GGG
                                TCTAACCA CCCCAG  CCA
                                |||||||| ||||||  |||
                                AGATTGGT GGGGTC  GGT
                                    C_    GG_
GAM3099 FLJ20079 3' CTAACCAACAGGGGC     70504       TCCC
                                CTAACCAA  CAGGGGC
                                ||||||||  |||||||
                                GATTGGTT  GTCCCCG
                                          ____
GAM3099 KIAA0159 5' TCCGGCCAATCCCCGGC    70505    AA      AGG
                                TCT CCAATCCCC  GGC
                                ||| |||||||||  |||
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                                AGG  GGTTAGGGG   CCG
                                  CC       ___
GAM3099  KIAA0446  5'  TCTGTCAATCCCCACTTGAG   70506     AAC       ___
                                TCT   CAATCCCCA   GGG
                                |||   |||||||||   |||
                                AGA   GTTAGGGGT   CTC
                                  CA_       GAA
GAM3099  KIAA1300  3'  TCCAACCAGTCCTCAAAAG    70507        A   C
                                TCTAACCA TCC CAGGGG
                                |||||||| ||| ||||||
                                AGGTTGGT AGG GTTTTC
                                     C   A
GAM3099  KIAA1349  3'  TCTAACCAGTTCCCTATTAATG 70508        A_    CAG____
              GG                  TCTAACCA  TCCC      GGG
                                |||||||  ||||      |||
                                AGATTGGT  AGGG      CCC
                                     CA    ATAATTA
GAM3099  KIAA1396  3'  TCTAACCAGTCCCAATGAG    70509        A    CAG
                                TCTAACCA TCCC   GGG
                                |||||||| ||||   |||
                                AGATTGGT AGGG   CTC
                                     C    TTA
GAM3099  KIAA1805  3'  TCTAACCAATGTTCCAGAG    70510         CC_
                                TCTAACCAAT   CCAGGG
                                ||||||||||   ||||||
                                AGATTGGTTA   GGTCTC
                                      CAA
GAM3099  KIAA1877  3'  TCTAACCAAGTTCTCATGTCAG 70511        __  CC  GG__
              CCAAG                 CTAACCAA  TC  CA    GGCCAAG
                                |||||||  ||  ||    |||||||
                                GATTGGTT  AG  GT    TCGGTTC
                                     CA  A_  ACAG
GAM3099  KIAA1883  3'  AACCAGAGGCCCCTCCAGGGGC 70512       A____   _
              C                    AACCA    TCC CCAGGGGCC
                                |||||    ||| |||||||||
                                TTGGT    GGG GGTCCCCGG
                                   CTCCG   A
GAM3099  MGC27434  3'  CCTAGCCAATTCAATAAGCCAA 70513      A    CCCCAG
              G                    TCTA CCAAT     GGGCCAAG
                                |||| |||||     ||||||||
                                GGAT GGTTA     TTCGGTTC
                                  C    AGTTA_
GAM3099  NINJ2     3'  CCTAGCCAATCCCTAAATCCAA 70514      A       C   GG
              G                    TCTA CCAATCCC AGG  CCAAG
                                |||| |||||||| |||  |||||
                                GGAT GGTTAGGG TTT  GGTTC
                                  C       A  A_
GAM3099  POLR2D    3'  TCTCACCAGTTTGGGAGGCCAA 70515     A    ATCCCCA
              G                    TCT ACCA      GGGGCCAAG
                                ||| ||||      |||||||||
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                                AGA TGGT      CTCCGGTTC
                                  G   CAAACC_
GAM3099  PTK6     3'  TCTCACTGGTCATAAGGCCAAG 70516     A  CAA  CCCA
                                TCT AC   TC   GGGGCCAAG
                                ||| ||   ||   |||||||||
                                AGA TG   AG   TTCCGGTTC
                                  G  ACC  TA__
GAM3099  SCYA28   3'  CTAACCAATCATGGCCAA    70517         CCCAGG
                                CTAACCAATC     GGCCAA
                                ||||||||||     ||||||
                                GATTGGTTAG     CCGGTT
                                      TA____
GAM3099  VEST1    5'  CCTAACCAATCTTCAGAAG   70518          CC
                                TCTAACCAATC  CAGGGG
                                ||||||||||  ||||||
                                GGATTGGTTAG  GTCTTC
                                      AA
GAM3099  LOC202551 3'  TCTAACCAAGTTTCCTAAATAG 70495        ___   CCAG_
              G                   TCTAACCAA   TCC    GGG
                                |||||||||   |||    |||
                                AGATTGGTT   AGG    TCC
                                     CAA   ATTTA
GAM3099  LOC92539  5'  TCTAACCAATCCCAGTGAG   70519           C  _
                                TCTAACCAATCCC AG GGG
                                |||||||||||| || |||
                                AGATTGGTTAGGG TC CTC
                                      _ A
GAM3100  AKAP13   3'  AGGCAGGTTTTTCTTTTTCATT 70522       T   GA
                                AGGCAG GTT  TTTTTTTTCATT
                                |||||| |||  ||||||||||||
                                TCCGTC CAA  AAGAAAAAGTAA
                                   _   A_
GAM3100  FCAR     3'  AGGTTGTGTTTTCTTTTCATT  70523     CA    GAT
                                AGG  GTGTT   TTTTTTTCATT
                                |||  |||||   ||||||||||
                                TCC  CACAA   AAGAAAAGTAA
                                  AA    ___
GAM3100  GALNT1   3'  TGTTGATTTTTTTTCATT    70524
                                TGTTGATTTTTTTTTCATT
                                ||||||||||||||||||
                                ACAACTAAAAAAAAAGTAA

GAM3100  MYF5     3'  AGGCAGTATTATATTTTT    70525          _
                                AGGCAGTGTTG ATTTTT
                                |||||||||| ||||||
                                TCCGTCATAAT TAAAAA
                                      A
GAM3100  ONECUT2  5'  AGGCGGTGTAGGCAGCCTTCAT 70526      A    TGATTTT
              T                   AGGC GTGT      TTTTCATT
                                |||| ||||      ||||||||
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                                TCCG CACA      GGAAGTAA
                                  C    TCCGTC_
GAM3100  ALLC     5'  AGGCATTGAAGTTTTTTTCATT 70527      GTG    T_
                                AGGCA   TTGA  TTTTTTTCATT
                                |||||   ||||  ||||||||||
                                TCCGT   AACT  AAAAAAAGTAA
                                  ____   TC
GAM3100  CG005    3'  AGGCACTGTAGCCTTTTTTT   70528      G   TGA
                                AGGCA TGT   TTTTTTTT
                                ||||| |||   ||||||||
                                TCCGT ACA   GAAAAAAA
                                  G   TCG
GAM3100  DKFZp547A023 3'  AAGCAGTGTTGGTTTTTAACAT 70529          A    TTT
            T                    AGGCAGTGTTG TTTTT   CATT
                                ||||||||||| |||||   ||||
                                TTCGTCACAAC AAAAA   GTAA
                                      C    TT_
GAM3100  KIAA1006  3'  GCAAAGATTTTTTTTCATT    70530     TT
                                GTG  GATTTTTTTTCATT
                                |||  ||||||||||||||
                                CGT  CTAAAAAAAAGTAA
                                  TT
GAM3100  PB1      3'  GTGTGTGTTTTTTTTCATT    70531      _  A
                                GTGT TG TTTTTTTTCATT
                                |||| || ||||||||||||
                                CACA AC AAAAAAAAGTAA
                                  C  _
GAM3100  LOC151121 3'  AGCAGTGTTTTTTTCA      70532         GATTT
                                GGCAGTGTT    TTTTTCA
                                |||||||||    |||||||
                                TCGTCACAA    AAAAAGT
                                     _____
GAM3100  LOC254719 3'  AGGCACTGAATTTTTTTT    70533      G  TT
                                AGGCA TG  GATTTTTTTT
                                ||||| ||  ||||||||||
                                TCCGT AC  TTAAAAAAAA
                                  G  __
GAM3100  LOC256846 5'  AGGCAAGTGTCATCTTTTTCAT 70534       _     AT
            T                    AGGCA GTGTTG  TTTTTTTCATT
                                ||||| ||||||  ||||||||||||
                                TCCGT CACAGT  AGAAAAAGTAA
                                  T     __
GAM3100  LOC257109 3'  AGGCAGTGATGGTGAAGTTCAT 70535        T  ATTTTTT
            T                    AGGCAGTG TG      TTCATT
                                ||||||||| ||      ||||||
                                TCCGTCAC AC      AAGTAA
                                     T  CACTTC_
GAM3101  RPL27A   3'  TTTTAAAAGTAGTTAGCATTTA 70538           CT  TAA_
            ATG                    TTTTAAAAGTAGT  GT    GATG
                                ||||||||||||| ||   ||||
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                                AAAATTTTCATCA  CG   TTAC
                                      AT  TAAA
GAM3101  CUGBP2   3'  TTTTGGAAGTAGTCTGTTA   70539     AA
                                TTTT  AAGTAGTCTGTTA
                                ||||  ||||||||||||||
                                AAAA  TTCATCAGACAAT
                                  CC
GAM3101  DMTF1    3'  AAAATAGCCTGAGAT      70540          TTA
                                AAAGTAGTCTG   AGAT
                                ||||||||||   ||||
                                TTTTATCGGAC   TCTA
                                      ___
GAM3101  KIAA0057  3'  TTTTAAAAATAGACCTCTAAGA 70541          T  G
              TG                  TTTTAAAAGTAG CT TTAAGATG
                                ||||||||||||| || ||||||||
                                AAAATTTTTATC GG GATTCTAC
                                      T  A
GAM3101  KIAA1546  3'  TTAAAAGTGGTCACAGATG   70542        A   TGTTA
                                TTAAAAGT GTC    AGATG
                                |||||||| |||    |||||
                                AATTTTCA CAG    TCTAC
                                    C   TG___
GAM3102  AMPH     5'  GCGCAGCGGGGCTGGCGGCGGC 70545     G   C_  AC   A
              G                   GCG AGCG  GC  GGC GCGGCG
                                ||| ||||  ||  ||| ||||||
                                CGC TCGC  CG  CCG CGCCGC
                                  G   CC  A_  C
GAM3102  ASS      5'  CGGGCTCGGGCAGCGG     70546    A  G  CAC
                                CGG GC CG   GGCAGCGG
                                ||| || ||   ||||||||
                                GCC CG GC   CCGTCGCC
                                  _  A  ___
GAM3102  BCR      5'  GCGGGGCCCGTCTCAGCGGCG  70547     A  G  CACGG
                                GCGG GC CG    CAGCGGCG
                                ||||  || ||    ||||||||
                                CGCC CG GC    GTCGCCGC
                                  C  G  AGA__
GAM3102  BCR      5'  GCGGGGCCCGTCTCAGCGGCG  70547     A  G  CACGG
                                GCGG GC CG    CAGCGGCG
                                ||||  || ||    ||||||||
                                CGCC CG GC    GTCGCCGC
                                  C  G  AGA__
GAM3102  BIN1     5'  GCGGAGCGTGCGCCGGACGGGC 70548        __   A  CA   _
              G                   GCGGAGC  GCGC CGG  GCGG CG
                                |||||||  |||| |||  |||| ||
                                CGCCTCG  CGCG GCC  TGCC GC
                                    CA   _  __   C
GAM3102  BIN1     5'  GCGGAGCGTGCGCCGGACGGGC 70548        __   A  CA   _
              G                   GCGGAGC  GCGC CGG  GCGG CG
                                |||||||  |||| |||  |||| ||
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                                CGCCTCG  CGCG GCC  TGCC GC
                                   CA   _  __   C
GAM3102  CALCA    5'  GCGGTGGCAGCGGCGGCGGCG  70549     AGCGC  _   A
                                GCGG    GCA CGGC GCGGCG
                                ||||    ||| |||| ||||||
                                CGCC    CGT GCCG CGCCGC
                                  AC___  C   C
GAM3102  CELSR2   5'  CGGGTCAACGGCGGCGGCG   70550    AG  CGC    A
                                CGG  CG   ACGGC GCGGCG
                                |||  ||   ||||| ||||||
                                GCC  GT   TGCCG CGCCGC
                                 CA  ___    C
GAM3102  CHAD     5'  GCGGGGCGCGGGCAGCGGCG   70551     A    CAC
                                GCGG GCGCG   GGCAGCGGCG
                                |||| |||||   ||||||||||
                                CGCC CGCGC   CCGTCGCCGC
                                  C    ___
GAM3102  COL15A1  5'  GCGGCGCTCGGCAGCGGC    70552    GAGC   A
                                GCG   GCGC CGGCAGCGGC
                                |||   |||| ||||||||||
                                CGC   CGCG GCCGTCGCCG
                                 _____   A
GAM3102  COL4A2   5'  GCGGAGCGCGGAGCCCTGG   70553        CAC   AGC
                                GCGGAGCGCG   GGC   GG
                                ||||||||||   |||   ||
                                CGCCTCGCGC   TCG   CC
                                      C__   GGA
GAM3102  CPT1A    5'  GCGGCAGCGGCAGCGGCAGCGG 70554     _   C   _
            CG                    GCGG AGCG GCA CGGCAGCGGCG
                                ||||| |||| ||| ||||||||||
                                CGCC TCGC CGT GCCGTCGCCGC
                                  G   _  C
GAM3102  CTGF     5'  GCGGAGCGGAGGGCGCGGTGGC 70555        C___  A   CA
            GGCG                   GCGGAGCG   GC CGG  GCGGCG
                                ||||||||   || |||  ||||||
                                CGCCTCGC   CG GCC  CGCCGC
                                     CTCC  C   AC
GAM3102  DDEF2    5'  GCGGGCGCGCACAGCCGGCG   70556     A        AG
                                GCGG GCGCGCACGGC  CGGCG
                                |||| ||||||||||  |||||
                                CGCC CGCGCGTGTCG  GCCGC
                                  _        __
GAM3102  DGCR2    3'  GGAGCCACAGTGGCAGCGG    70557      G    C_
                                GGAGC CGCA  GGCAGCGG
                                |||||  ||||  ||||||||
                                CCTCG GTGT  CCGTCGCC
                                  _   CA
GAM3102  EVX1     5'  GGAGCGCGACCGCGGCGG    70558        C  G  A
                                GGAGCGCG AC GC GCGG
                                |||||||| || || ||||
```

```
                                CCTCGCGC TG CG CGCC
                                    _ G  C
GAM3102  FACL4    5'  GCGGAGCGGGGGCGCGCGG   70559       CGCAC  A_
                                GCGGAGCG    GGC  GCGG
                                ||||||||    |||  ||||
                                CGCCTCGC    CCG  CGCC
                                    CC___   CG
GAM3102  FACL4    5'  GCGGAGCGGGGGCGCGCGG   70559       CGCAC  A_
                                GCGGAGCG    GGC  GCGG
                                ||||||||    |||  ||||
                                CGCCTCGC    CCG  CGCC
                                    CC___   CG
GAM3102  FMR2     5'  GGGCGGCAGCGGCGGCGGCG  70560    A  C  _   A
                                GG GCG GCA CGGC GCGGCG
                                || ||| ||| |||| ||||||
                                CC CGC CGT GCCG CGCCGC
                                 _  _  C   C
GAM3102  FMR2     5'  CGGGGCAGAGGCAGCGGCG   70562    A  CGCAC
                                CGG GCG    GGCAGCGGCG
                                ||| |||    ||||||||||
                                GCC CGT    CCGTCGCCGC
                                  C  CT___
GAM3102  FMR2     5'  GCGGGCCGGCGGCGGCAGCGGC 70561     A  __  CA
           G                     GCGG GC  GCG  CGGCAGCGGCG
                                 |||| ||  |||  ||||||||||
                                 CGCC CG  CGC  GCCGTCGCCGC
                                   _ GC   C_
GAM3102  FOXG1B   5'  GCGGCGCGCGGGCGGCG    70563     A   CAC  A
                                GCGG GCGCG   GGC GCG
                                |||| |||||   ||| |||
                                CGCC CGCGC   CCG CGC
                                  G    ___   C
GAM3102  FOXG1B   5'  GGGGCGGCGGGCGGCAGCGGCG 70564    A  _  CA
                                GG GCG CG  CGGCAGCGGCG
                                || ||| ||  ||||||||||
                                CC CGC GC  GCCGTCGCCGC
                                 C  C  CC
GAM3102  GDA      5'  GCGGAGCGCAGCGCGG      70565        GCAC  A
                                GCGGAGCGC    GGC GCGG
                                |||||||||    ||| ||||
                                CGCCTCGCG    TCG CGCC
                                             ____  _
GAM3102  GPI      5'  GCGAGGCGCGTGGGCGCGCGGC 70566    GA   CAC  A_
           G                     GCG  GCGCG   GGC  GCGGCG
                                 |||  |||||   |||  ||||||
                                 CGC  CGCGC   CCG  CGCCGC
                                   TC    AC_   CG
GAM3102  GRM3     5'  GCTGACCGCGGTGGCAGCGGCG 70567    G  G   CAC
                                GC GA CGCG   GGCAGCGGCG
                                || || ||||   ||||||||||
```

```
                                CG CT GCGC  CCGTCGCCGC
                                 A  G   CA_
GAM3102  GTF2E2   5'  GCGGCGGCGGCGGCAGCGGCG  70568     AGC  CA
                                GCGG  GCG  CGGCAGCGGCG
                                ||||  |||  ||||||||||
                                CGCC  CGC  GCCGTCGCCGC
                                  GC_  C_
GAM3102  GUCY1A2  5'  GCGGCCGAGGCGGTGGCGGCG  70569     AG  CGCA  CA
                                GCGG  CG   CGG  GCGGCG
                                ||||  ||   |||  ||||||
                                CGCC  GC   GCC  CGCCGC
                                  G_  TCC_  AC
GAM3102  GUCY1B3  5'  GCAGAGGCGGCAGCGGC    70570       C  GCAC
                                GCGGAG GC   GGCAGCGGC
                                ||||||  ||   |||||||||
                                CGTCTC CG   CCGTCGCCG

                                  _  _____
GAM3102  HDAC5    5'  GCGGCGGCGGCAGCAGCGGCG  70571     A_  C  CG
                                GCGG  GCG GCA  GCAGCGGCG
                                ||||  ||| |||  |||||||||
                                CGCC  CGC CGT  CGTCGCCGC
                                  GC  _  __
GAM3102  HDAC5    5'  GCGGCGGCGGCAGCAGCGGCG  70571     A_  C  CG
                                GCGG  GCG GCA  GCAGCGGCG
                                ||||  ||| |||  |||||||||
                                CGCC  CGC CGT  CGTCGCCGC
                                  GC  _  __
GAM3102  HMGA2    5'  GCGGGAGCAGGCAGCGGC    70572     _   CGCAC
                                GCGG AGCG    GGCAGCGGC
                                |||| ||||    |||||||||
                                CGCC TCGT    CCGTCGCCG
                                  C  _____
GAM3102  IGFBP4   5'  GCGGCGCGCGGGCGAGCGGCG  70573     A   CAC  _
                                GCGG GCGCG   GGC AGCGGCG
                                |||| |||||   ||| |||||||
                                CGCC CGCGC   CCG TCGCCGC
                                  G   ___  C
GAM3102  IGFBP7   5'  GCGGGGTGCGGTGGCAGCGG  70574     AGC  CAC
                                GCGG  GCG  GGCAGCGG
                                ||||  |||  ||||||||
                                CGCC  CGC  CCGTCGCC
                                  CCA  CA_
GAM3102  ISL1     5'  GCGGAGGCGCTGCGGCGGCG  70575       C  ACG  A
                                GCGGAG GCGC  GC GCGGCG
                                ||||||  ||||  || ||||||
                                CGCCTC CGCG  CG CGCCGC
                                   _  A__  C
GAM3102  JAG2     5'  GCGGCAGCGGCAGAGGCGGCGG 70576    _  C  ____  A
            CGGCG                  CGG AGCG GCA   CGGC GCGGCG
                                ||| |||| |||   |||| ||||||
```

```
                                GCC TCGC CGT    GCCG CGCCGC
                                  G    _  CTCC    C
GAM3102  KCNF1    5'  CGGGGCGCGCAGGCAGCGGCG  70577     A      C
                                CGG GCGCGCA GGCAGCGGCG
                                ||| ||||||| ||||||||||
                                GCC CGCGCGT CCGTCGCCGC
                                  C      _
GAM3102  KCNQ2    5'  GCGGAGCGCGGGGGGCGGCG   70578          CAC  CA
                                GCGGAGCGCG   GG  GCGGCG
                                ||||||||||   ||  ||||||
                                CGCCTCGCGC   CC  CGCCGC
                                      ____  CC
GAM3102  LBX1     5'  GCGGGCCAGGCAGCGGCG    70579      A  G  CAC
                                GCGG GC CG   GGCAGCGGCG
                                |||| || ||   ||||||||||
                                CGCC CG GT   CCGTCGCCGC

                                  _ _ ____
GAM3102  MAML1    5'  GCGGAGCGGGCTCGCGCGCGGC 70580         C  A  _  A
              G                   GCGGAGCG GC CG GC GCGGCG
                                ||||||||| || || || ||||||
                                CGCCTCGC CG GC CG CGCCGC
                                    C  A  G  _
GAM3102  MAP3K5   5'  CGGGCAGCAACGGCGGCGGCG  70581     A   C   _    A
                                CGG GCG GCA CGGC GCGGCG
                                ||| ||| ||| |||| ||||||
                                GCC CGT CGT GCCG CGCCGC
                                  _   _   T    C
GAM3102  MAPK8IP1  5'  GCGGAGCGCGGCGCGGAGGAGG 70582          _ A   CA___
              CGGCG                  GCGGAGCGCG C CGG     GCGGCG
                                |||||||||| | |||     ||||||
                                CGCCTCGCGC G GCC     CGCCGC
                                      C C   TCCTC
GAM3102  MAPT     5'  GGGCGGTGGCAGCGGCG     70583    A   CGCAC
                                GG GCG     GGCAGCGGCG
                                || |||     ||||||||||
                                CC CGC     CCGTCGCCGC
                                  _   CA___
GAM3102  MAPT     5'  GGGCGGTGGCAGCGGCG     70583    A   CGCAC
                                GG GCG     GGCAGCGGCG
                                || |||     ||||||||||
                                CC CGC     CCGTCGCCGC
                                  _   CA___
GAM3102  MAPT     5'  GGGCGGTGGCAGCGGCG     70583    A   CGCAC
                                GG GCG     GGCAGCGGCG
                                || |||     ||||||||||
                                CC CGC     CCGTCGCCGC
                                  _   CA___
GAM3102  MAPT     5'  GGGCGGTGGCAGCGGCG     70583    A   CGCAC
                                GG GCG     GGCAGCGGCG
                                || |||     ||||||||||
```

```
                                CC CGC    CCGTCGCCGC
                                 _  CA___
GAM3102  MGAT3    5'  GCGGCAGCAGCGGCGGCGGCG  70584     _   C  AC   A
                                GCGG AGCG GC  GGC GCGGCG
                                |||| |||| ||  ||| ||||||
                                CGCC TCGT CG  CCG CGCCGC
                                  G   _ __   C
GAM3102  MME      5'  ACGGGGCCGGGTGGCAGTGGCG 70585     A  G  CAC    C
                                GCGG GC CG   GGCAG GGCG
                                |||| || ||   ||||| ||||
                                TGCC CG GC   CCGTC CCGC
                                  C  _  CCA    A
GAM3102  MSI1     5'  GCGGGCAGCGGAGCGGCGGCGG 70586     A  _  CA_   A
              CG                  GCGG GC GCG   CGGC GCGGCG
                                |||| || |||   |||| ||||||
                                CGCC CG CGC   GCCG CGCCGC
                                  _  T   CTC    C
GAM3102  MYO1D    5'  GGGGCGCGCACGCCGCTCGGCG 70587    A       G AG__
                                GG GCGCGCACG C    CGGCG
                                || |||||||| |    |||||
                                CC CGCGCGTGC G    GCCGC
                                 C        _ GCGA
GAM3102  NAP1L3   5'  GCGGAGGTGGCAGCGGC     70588       CGCGCAC
                                GCGGAG      GGCAGCGGC
                                ||||||      |||||||||
                                CGCCTC      CCGTCGCCG
                                   CA_____
GAM3102  NEK4     5'  GGGATGCGGCGGCAGCGGCG   70589   C   GC   CA
                                G GGA  GCG  CGGCAGCGGCG
                                | |||  |||  ||||||||||
                                C CCT  CGC  GCCGTCGCCGC
                                 _  A_  C_
GAM3102  NFYC     5'  ACGGAGCGCGCGCGAAGCG    70590          A  C
                                GCGGAGCGCGC CGG AGCG
                                |||||||||| ||| ||||
                                TGCCTCGCGCG GCT TCGC
                                       C  _
GAM3102  NORE1    5'  GCGGCAGCTTTGGCAGCGGCG  70591     _  GCGCAC
                                GCGG AGC     GGCAGCGGCG
                                |||| |||     ||||||||||
                                CGCC TCG     CCGTCGCCGC
                                  G  AAA___
GAM3102  P3       5'  GCAAACGCGCGGCGGCGGCG   70592    G     AC   A
                                GCG AGCGCGC  GGC GCGGCG
                                ||| |||||||  ||| ||||||
                                CGT TTGCGCG  CCG CGCCGC
                                  _      __  C
GAM3102  PK428    5'  GCAGCAGCTGCGGCGGCGGCG  70593     _  GC  AC   A
                                GCGG AGC  GC  GGC GCGGCG
                                |||| |||  ||  ||| ||||||
```

```
                                CGTC TCG  CG  CCG CGCCGC
                                  G  A_ __  C
GAM3102  PNUTL1   5'  GCGGGGCGCGACAACAAGCGGC 70594     A    C    _
             G                    GCGG GCGCG ACGGCA GCGGCG
                                  |||| ||||| |||||| ||||||
                                  CGCC CGCGC TGTTGT CGCCGC
                                    C    _     T
GAM3102  POMZP3   5'  GGAGCGCGGCGCCGGGCG    70595        _ A_  CA
                                  GGAGCGCG C  CGG  GCG
                                  |||||||| |  |||  |||
                                  CCTCGCGC G  GCC  CGC
                                      C CG  __
GAM3102  PPP6C    5'  GCGGCAACAGCGGCGGCGGCG  70596     AGCGC  _   A
                                  GCGG    GCA CGGC GCGGCG
                                  ||||    ||| |||| ||||||
                                  CGCC    TGT GCCG CGCCGC
                                    GT___  C   C
GAM3102  PTMS     5'  GCGGCGGCGACACGGCAGCGGC 70597     A_  C
             G                    GCGG  GCG GCACGGCAGCGGCG
                                  ||||  ||| ||||||||||||||
                                  CGCC  CGC TGTGCCGTCGCCGC
                                    GC  _
GAM3102  PTPRJ    5'  CGGAGACATGGCAGCGGCG   70598      CGC  C
                                  CGGAG   GCA GGCAGCGGCG
                                  |||||   ||| ||||||||||
                                  GCCTC   TGT CCGTCGCCGC
                                     ___  A
GAM3102  RFP      5'  GCGGGGGCGCACGGGCA     70599     AGC      CA
                                  GCGG   GCGCACGG  GCG
                                  ||||   ||||||||  |||
                                  CGCC   CGCGTGCC  CGT
                                    CC_      __
GAM3102  RIMS1    5'  GGAGGAGCAGCGGCGGCGGCG  70600     CGC  _   A
                                  GGAG   GCA CGGC GCGGCG
                                  ||||   ||| |||| ||||||
                                  CCTC   CGT GCCG CGCCGC
                                    CT_  C   C
GAM3102  SLIT3    5'  GCGGGGCGCTCCGGGCGGCGGC 70601     A   GCA___   A
             GGCG                   GCGG GCGC     CGGC GCGGCG
                                    |||| ||||     |||| ||||||
                                    CGCC CGCG     GCCG CGCCGC
                                      C   AGGCCC   C
GAM3102  TFDP1    5'  GCGGAGCGCGGGGCGGC     70603         CAC  CA
                                  GCGGAGCGCG   GG  GCGGC
                                  ||||||||||   ||  |||||
                                  CGCCTCGCGC   CC  CGCCG
                                               ___  __
GAM3102  TFDP1    5'  GCGGGGCGGCGCGGAGAGGCG  70602     A  C  A  C  C
                                  GCGG GCG GC CGG AG GGCG
                                  |||| ||| || ||| || ||||
```

```
                                CGCC CGC CG GCC TC CCGC
                                  C  _ C  _ T
GAM3102 TMEFF2  5' GCGGCAGCAGAGGCGGCGGCG 70604    _  CGCAC  A
                                GCGG AGCG   GGC GCGGCG
                                |||| ||||   ||| ||||||
                                CGCC TCGT   CCG CGCCGC
                                  G  CT___  C
GAM3102 TP53BP2  5' GCGGCGGCGGCGGCAGCGGCG 70568    AGC  CA
                                GCGG  GCG  CGGCAGCGGCG
                                ||||  |||  ||||||||||
                                CGCC  CGC  GCCGTCGCCGC
                                  GC_  C_
GAM3102 TPM1    5' GCGAGCGCGCGGTCGGC    70605    G    AC  CAG
                                GCG AGCGCGC  GG  CGGC
                                ||| |||||||  ||  ||||
                                CGC TCGCGCG  CC  GCCG
                                 _    __ A__
GAM3102 UBTF    5' GCGGAGCGCGGCGCG      70606       GCAC  A
                                GCGGAGCGC   GGC GCG
                                |||||||||   ||| |||
                                CGCCTCGCG   CCG CGC
                                     ____  _
GAM3102 USP13   5' GCGGGGTCTGCCGGCGGCGGCG 70607    AGCGC A  A
                                GCGG   GC CGGC GCGGCG
                                ||||   || |||| ||||||
                                CGCC   CG GCCG CGCCGC
                                  CCAGA _  C
GAM3102 WEE1    5' GCGGACGGTGGCGGCAGCGGCG 70608     G  CGCA
                                GCGGA CG   CGGCAGCGGCG
                                ||||| ||   ||||||||||
                                CGCCT GC   GCCGTCGCCGC
                                  _ CACC
GAM3102 WNT6    5' GCGAGCGCAACGGCGGCG   70609    G    C   A
                                GCG AGCGCG ACGGC GCG
                                ||| |||||| ||||| |||
                                CGC TCGCGT TGCCG CGC
                                 _    _   C
GAM3102 YWHAB   5' GTGGCTGCAGCGGCGGCGGCG 70610   GA  GC  _  A
                                G  GC  GCA CGGC GCGGCG
                                |  ||  ||| |||| ||||||
                                C  CG  CGT GCCG CGCCGC
                                AC  A_  C   C
GAM3102 YWHAB   5' GTGGCTGCAGCGGCGGCGGCG 70610   GA  GC  _  A
                                G  GC  GCA CGGC GCGGCG
                                |  ||  ||| |||| ||||||
                                C  CG  CGT GCCG CGCCGC
                                AC  A_  C   C
GAM3102 ZNF10   5' GCGGAGCGCGAAGAGCGGCG  70611       CAC  C
                                GCGGAGCGCG  GG AGCGGCG
                                ||||||||||  || |||||||
```

```
                                CGCCTCGCGC   TC TCGCCGC
                                      T__  _
GAM3102  ZNF219   5'  GCGGGCGGCGGCGGCGGCG   70613     A   C  AC   A
                                GCGG GCG GC  GGC GCGGCG
                                |||| ||| ||  ||| ||||||
                                CGCC CGC CG  CCG CGCCGC
                                  _  _ __  C
GAM3102  ZNF219   5'  GCGGAGCGGGCGGCGGCGGCG  70612        C  AC   A
                                GCGGAGCG GC  GGC GCGGCG
                                |||||||| ||  ||| ||||||
                                CGCCTCGC CG  CCG CGCCGC
                                     C __  C
GAM3102  ZNF278   5'  GCGGGGCGCGCACGGGGGCGG  70614     A        CA
                                GCGG GCGCGCACGG  GCGG
                                |||| ||||||||||  ||||
                                CGCC CGCGCGTGCC  CGCC
                                  C         CC
GAM3102  ZNF278   5'  GCGGGGCGCGCACGGGGGCGG  70614     A        CA
                                GCGG GCGCGCACGG  GCGG
                                |||| ||||||||||  ||||
                                CGCC CGCGCGTGCC  CGCC
                                  C         CC
GAM3102  ZNF278   5'  GCGGGGCGCGCACGGGGGCGG  70614     A        CA
                                GCGG GCGCGCACGG  GCGG
                                |||| ||||||||||  ||||
                                CGCC CGCGCGTGCC  CGCC
                                  C         CC
GAM3102  ZNF278   5'  GCGGGGCGCGCACGGGGGCGG  70614     A        CA
                                GCGG GCGCGCACGG  GCGG
                                |||| ||||||||||  ||||
                                CGCC CGCGCGTGCC  CGCC
                                  C         CC
GAM3102  ADNP     5'  GGGGCCGGACAGCGGCGGCG   70615    A  G  C    A
                                GG GC CG ACGGC GCGGCG
                                || || || ||||| ||||||
                                CC CG GC TGTCG CGCCGC
                                 C  _  C    C
GAM3102  AKR7A2   5'  GCGAAGCGCGCAGTGGACGGCG 70616           C__   A
            GCG                   GCGGAGCGCGCA   GGC GCGGCG
                                ||||||||||||   ||| ||||||
                                CGCTTCGCGCGT   CTG CGCCGC
                                      CAC   C
GAM3102  APELIN   5'  GGGAGCGGCAGCGGC      70617   C    GCGCAC
                                G GGAGC     GGCAGCGGC
                                | |||||     |||||||||
                                C CCTCG     CCGTCGCCG
                                _    _______
GAM3102  C20orf121 5'  GCGGAGCGCGGGTCAATCGGCG 70618          CAC  _   _
                                GCGGAGCGCG   GG CAG CGGCG
                                ||||||||||   || ||| |||||
```

```
                                CGCCTCGCGC   CC GTT GCCGC
                                      ___  A   A
GAM3102  C20orf39  5'  CGGGCGCGGGGCAGCGGCG   70619     A    CAC
                                CGG GCGCG   GGCAGCGGCG
                                ||| |||||   ||||||||||
                                GCC CGCGC   CCGTCGCCGC
                                  _    C__
GAM3102  C20orf97  5'  GCGGACGCGCGCGGAGC     70620      G    A  C
                                GCGGA CGCGC CGG AGC
                                ||||| ||||| ||| |||
                                CGCCT GCGCG GCC TCG
                                   _    C  _
GAM3102  CAMTA2    3'  GCGTGCGCAGCGAAGGCAGTGG 70621     GA   _ AC_    C
                                GCG  GCGC GC   GGCAG GG
                                |||  |||| ||   ||||| ||
                                CGC  CGCG CG   CCGTC CC
                                  A_   T  CTT    A
GAM3102  CCNE1     5'  GCCGAGCGCGCGGCGGTGGCG  70622    G      AC   AGC
                                GC GAGCGCGC  GGC   GGCG
                                || ||||||||  |||   ||||
                                CG CTCGCGCG  CCG   CCGC
                                 G       __  CCA
GAM3102  CENTG2    5'  GGAGCGCGCCGCGGC       70623         A GGCA
                                GGAGCGCGC C    GCGGC
                                ||||||||| |    |||||
                                CCTCGCGCG G    CGCCG
                                      _ _____
GAM3102  CL25022   5'  GCGGCGGCGACGGCAGCGG   70624     AGC   C
                                GCGG   GCG ACGGCAGCGG
                                ||||   ||| ||||||||||
                                CGCC   CGC TGCCGTCGCC
                                  GC_   _
GAM3102  CPLX1     5'  GCGGGGCGCGCTCGGGC     70625     A     A   CA
                                GCGG GCGCGC CGG  GC
                                |||| |||||| |||  ||
                                CGCC CGCGCG GCC  CG
                                  C     A  __
GAM3102  DC-TM4F2  5'  GCGCGCGGCGGCGGCAGCGGCG 70626     GA   C  A_
                                GCG  GCG GC  CGGCAGCGGCG
                                |||  ||| ||  ||||||||||
                                CGC  CGC CG  GCCGTCGCCGC
                                  G_   _  CC
GAM3102  DKFZP761F241 5'  CGGGGCGCACGGGGCGGCGGCG 70627     A     AC   A
                                CGG GCGCGC  GGC GCGGCG
                                ||| ||||||  ||| ||||||
                                GCC CGCGTG  CCG CGCCGC
                                  C     CC   C
GAM3102  DPYSL4    5'  GCGGGGCCGCACGGCTCCG   70628      A  G       AG
                                GCGG GC CGCACGGC  CG
                                |||| || ||||||||  ||
```

```
                                CGCC CG GCGTGCCG  GC
                                  C _       AG
GAM3102  FBXO26   5' CGGAGGCGGCAGCGGC      70629      C  GCAC
                                CGGAG GC    GGCAGCGGC
                                ||||| ||    |||||||||
                                GCCTC CG    CCGTCGCCG
                                  _ ____
GAM3102  FLJ10350 5' CGGGGTCTCAGCGGCGGCGGCG 70630     AGCGCG _   A
                                CGG     CA CGGC GCGGCG
                                |||     || |||| ||||||
                                GCC     GT GCCG CGCCGC
                                 CCAGA_ C    C
GAM3102  FLJ13262 3' GGTCGCGCGGCAGCGGCG    70631    AG    AC
                                GG  CGCGC  GGCAGCGGCG
                                ||  |||||  ||||||||||
                                CC  GCGCG  CCGTCGCCGC
                                 A_    __
GAM3102  FLJ13262 3' GCGCGGCAGCGGCGGCGGCG   70632      _ _   A
                                GCGCG CA CGGC GCGGCG
                                ||||| || |||| ||||||
                                CGCGC GT GCCG CGCCGC
                                  C  C   C
GAM3102  FLJ14129 5' GCGGGACGCGCGGGCCACGGCG 70633     AG    AC   A
                                GCGG  CGCGC  GGC GCGGCG
                                ||||  |||||  ||| ||||||
                                CGCC  GCGCG  CCG TGCCGC
                                  CT    C_   G
GAM3102  FLJ14840 5' GCAGCCAGCGTACGGCAGCGGC 70634     AGC   C
           G                     GCGG   GCG ACGGCAGCGGCG
                                ||||   ||| ||||||||||||
                                CGTC   CGC TGCCGTCGCCGC
                                  GGT   A
GAM3102  FLJ20330 5' GAGCTGCAGCGCGGCAGCGGCG 70635     _ _ A
                                GAGC GC GC CGGCAGCGGCG
                                |||| || || ||||||||||
                                CTCG CG CG GCCGTCGCCGC
                                  A  T  C
GAM3102  FLJ20557 5' GCGGGGCCGGGAGCGGC     70636     A  G  CAC  C
                                GCGG GC CG   GG AGCGGC
                                |||| || ||   || ||||||
                                CGCC CG GC   CC TCGCCG
                                  C  _ ___  _
GAM3102  FLJ20979 5' GTGGCGCGCGCGGGCACGGGCG 70637   C  A    AC   GC
                                G GG GCGCGC  GGCA  GGCG
                                | || ||||||  ||||  ||||
                                C CC CGCGCG  CCGT  CCGC
                                 A  G     C_   GC
GAM3102  FLJ22362 5' GCGGAGCGGGCGCGGGTCTGCG 70638        C  A   CA__
                                GCGGAGCG GC CGG    GCG
                                |||||||| || |||    |||
```

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                                CGCCTCGC CG GCC    CGC
                                    C  C   CAGA
GAM3102  FLJ22405  5'  GCCGAGGCAGCGGCGGCGGCG  70639    G   C   CA    A
                                GC GAG GCG  CGGC GCGGCG
                                || ||| |||  |||| ||||||
                                CG CTC CGT  GCCG CGCCGC
                                 G   _   C_   C
GAM3102  FLJ23375  5'  GCGGGGCGCGGCAGCGGCG   70640     A   GCAC
                                GCGG GCGC   GGCAGCGGCG
                                |||| ||||   ||||||||||
                                CGCC CGCG   CCGTCGCCGC
                                  C   _____
GAM3102  FLJ25132  5'  GGAGCGCGCGGCCCGG      70641        AC   AG
                                GGAGCGCGC  GGC  CGG
                                |||||||||  |||  |||
                                CCTCGCGCG  CCG  GCC
                                     __   G_
GAM3102  FRAT1    5'  GCGGAGCGGGCGCGGAGC    70642       C  A   C
                                GCGGAGCG GC CGG AGC
                                |||||||| || ||| |||
                                CGCCTCGC CG GCC TCG
                                    C  C   _
GAM3102  GRM5     5'  GCGGGGCCCGCGGCGGTGGCG  70643     A  G   AC   AGC
                                GCGG GC CGC  GGC   GGCG
                                |||| || |||  |||   ||||
                                CGCC CG GCG  CCG   CCGC
                                  C  G   __   CCA
GAM3102  H2AFY    5'  GCGGCGGCTCGGTGGCGGCG   70644    GA   C  A   CA
                                GCG  GCG GC CGG  GCGGCG
                                |||  ||| || |||  ||||||
                                CGC  CGC CG GCC  CGCCGC
                                  __   _  A   AC
GAM3102  H2AFY    5'  GCGGCGGCTCGGTGGCGGCG   70644    GA   C  A   CA
                                GCG  GCG GC CGG  GCGGCG
                                |||  ||| || |||  ||||||
                                CGC  CGC CG GCC  CGCCGC
                                  __   _  A   AC
GAM3102  HIC      5'  GCGGCAACTGCGGCAGCGG   70645     AGC  GCA
                                GCGG   GC   CGGCAGCGG
                                ||||   ||   |||||||||
                                CGCC   TG   GCCGTCGCC
                                  GT_  AC_
GAM3102  HNT      5'  GCGGAGCGAGCGCGGGGACTGA 70646        C  A   C_____
            GCGG                    GCGGAGCG GC CGG     AGCGG
                                ||||||||| || |||     |||||
                                CGCCTCGC CG GCC     TCGCC
                                    T  C   CCTGAC
GAM3102  IL-17RE  3'  GCAGGGCGCGCAGCGGC     70647     A   GCACG
                                GCGG GCGC    GCAGCGGC
                                |||| ||||    ||||||||
```

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                                CGTC CGCG    CGTCGCCG
                                  C  _____
GAM3102 KIAA0133 5' GGAGGACGGCGGCAGCGGCG  70648     C  CA
                                GGAG GCG  CGGCAGCGGCG
                                |||| |||  ||||||||||
                                CCTC TGC  GCCGTCGCCGC
                                  C  C_
GAM3102 KIAA0769 5' GCGAGCGCGCGCGTGTGCGCCG 70649   G     A _________ AGCG
           CG                     G AGCGCGC CG       GC   G
                                | |||||| ||       ||   |
                                C TCGCGCG GC       CG   C
                                 _     C  ACACIIIG  GCGA
GAM3102 KIAA1416 3' GGAGGCCACAGCAGCGGCG   70650     C  G
                                GGAG GC CACGGCAGCGGCG
                                |||| || ||||||||||||
                                CCTC CG GTGTCGTCGCCGC
                                  _ _
GAM3102 KIAA1576 5' GCGGGGCGCACGGGCTGCGG  70651     A    AC  A
                                GCGG GCGCGC  GGC GCGG
                                |||| ||||||  ||| ||||
                                CGCC CGCGTG  CCG CGCC
                                  C    C_  A
GAM3102 KIAA1706 5' CGGAGGCGGCGGCAGCGGCG  70652     C  CA
                                CGGAG GCG  CGGCAGCGGCG
                                ||||| |||  ||||||||||
                                GCCTC CGC  GCCGTCGCCGC
                                  _  C_
GAM3102 KIAA1742 5' GCGGTGGCGGCGGCAGCGGCG 70653    A_  C  AC
                                GCGG  GCG GC  GGCAGCGGCG
                                ||||  ||| ||  ||||||||||
                                CGCC  CGC CG  CCGTCGCCGC
                                  AC  _ ___
GAM3102 LUC7L   5' GCAGGCGGTGGCAGCGGC   70654     A  CGCAC
                                GCGG GCG    GGCAGCGGC
                                |||| |||    |||||||||
                                CGTC CGC    CCGTCGCCG
                                  _  CA___
GAM3102 MAP2K3  5' GCGGAGGAGCAGCGGCGGCGGC 70655      CGC  _   A
           G                    GCGGAG  GCA CGGC GCGGCG
                                ||||||  ||| |||| ||||||
                                CGCCTC  CGT GCCG CGCCGC
                                   CT_  C   C
GAM3102 MGC10772 5' GCGGGGGACAGCAGCGGC   70656    AGCGCGC
                                GCGG     ACGGCAGCGGC
                                ||||     ||||||||||
                                CGCC     TGTCGTCGCCG
                                  CCC_____
GAM3102 MGC10940 5' GCGGCGACAGCGGCGGCGGCG 70657    GA  C  _   A
                                GCG  GCG GCA CGGC GCGGCG
                                |||  ||| ||| |||| ||||||
```

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                                CGC  CGC TGT GCCG CGCCGC
                                  __  _  C   C
GAM3102 MGC14425 3' GGCCGCGGCGCGGTGGCGGCG 70658   A_  C A  CA
                                GG  GCG GC CGG  GCGGCG
                                ||  ||| || |||  ||||||
                                CC  CGC CG GCC  CGCCGC
                                 GG  _ C  AC
GAM3102 MGC15438 3' GCGGAGCGCAGCCCCGAGCGGC 70659        _ A_ GC
          G                      GCGGAGCGC GC  CG  AGCGGCG
                                |||||||||  ||  ||  |||||||
                                CGCCTCGCG CG  GC  TCGCCGC
                                     T  GG  __
GAM3102 MGC16202 5' GCGAGCGCGCGCGCCTCG   70660    G     A  G AG
                                GCG AGCGCGC CG C  CG
                                ||| ||||||| || |  ||
                                CGC TCGCGCG GC G  GC
                                  _     C  _ GA
GAM3102 MGC23427 5' GCGGGCGGGCAGCGG     70661    A  CGCAC
                                GCGG GCG    GGCAGCGG
                                |||| |||    ||||||||
                                CGCC CGC    CCGTCGCC
                                  _  _____
GAM3102 MGC2615  5' GGAGGCCCGGCAGCGGCG   70662    C  GCA
                                GGAG GC  CGGCAGCGGCG
                                |||| ||  ||||||||||
                                CCTC CG  GCCGTCGCCGC
                                  _ G__
GAM3102 MGC2744  5' GCAGGAGACCACGGTGGTGG  70663   _  C G   CAGC
                                GC GGAG GC CACGG   GG
                                || |||| || |||||   ||
                                CG CCTC TG GTGCC   CC
                                 T   _ _    ACCA
GAM3102 MSI2    5' GCGGAGCCGGGGCAGCGGCG  70664      G  CAC
                                GCGGAGC CG  GGCAGCGGCG
                                ||||||| ||  ||||||||||
                                CGCCTCG GC  CCGTCGCCGC
                                    _ C__
GAM3102 PCAF    5' GTGGCGGCGGCGGCAGCGGCG 70665   GA  C  A_
                                G  GCG GC  CGGCAGCGGCG
                                |  ||| ||  ||||||||||
                                C  CGC CG  GCCGTCGCCGC
                                AC  _  CC
GAM3102 PCDH17  5' GCTGAGGCAGCGGCGGCGGCG 70666   G  C  CA  A
                                GC GAG GCG  CGGC GCGGCG
                                || ||| |||  |||| ||||||
                                CG CTC CGT  GCCG CGCCGC
                                 A  _  C_   C
GAM3102 PTP4A1  5' GCGGAGCGGCGGTGGCG    70667      C  AC  CA
                                GCGGAGCG GC  GG  GCG
                                |||||||| ||  ||  |||
```

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                                CGCCTCGC CG  CC  CGC
                                    _ __  AC
GAM3102  RALGPS1A  5'  GGAGCGGCCCAGCGGCAGCGGC 70668       _ G  _
             G                   GGAGCG C CA CGGCAGCGGCG
                                 ||||||  | || ||||||||||
                                 CCTCGC G GT GCCGTCGCCGC
                                    C G  C
GAM3102  RNF10    5'  GCGGAGCGGGCGCGG      70669        CGCAC   A
                                 GCGGAGCG    GGC GCGG
                                 ||||||||    ||| ||||
                                 CGCCTCGC    CCG CGCC
                                      _____  _
GAM3102  SAST     5'  GCGGAGGCGGCGGCGGCG    70670       C  GCAC   A
                                 GCGGAG GC    GGC GCGGCG
                                 ||||||  ||    ||| ||||||
                                 CGCCTC CG    CCG CGCCGC
                                    _  ____   C
GAM3102  SCAP     5'  GCGGAGCGCGGCGTGCGCG    70671         CA  _  A
                                 GCGGAGCGCG  CG GC GCG
                                 ||||||||||  || || |||
                                 CGCCTCGCGC  GC CG CGC
                                       C_  A  _
GAM3102  SDCCAG3   5'  GCGGGGTGGCGCCCGGGTGGCG 70672      AGC_   A   CAGC
                                 GCGG    GCGC CGG    GGCG
                                 ||||    |||| |||    ||||
                                 CGCC    CGCG GCC    CCGC
                                   CCAC    G   CA__
GAM3102  SFRS4     5'  GCGAGAGCACGGCGGCAGCGGC 70673     _      CA
             G                    GCG GAGCGCG  CGGCAGCGGCG
                                  ||| |||||||  ||||||||||
                                  CGC CTCGTGC  GCCGTCGCCGC
                                    T      C_
GAM3102  SHARP     5'  GCGGTGGCGTCGGCAGCGGCG  70674      AGC   CA
                                 GCGG   GCG  CGGCAGCGGCG
                                 ||||   |||  ||||||||||
                                 CGCC   CGC  GCCGTCGCCGC
                                   AC_   A_
GAM3102  SSBP4     5'  GCGGCGGCGGCGGCAGCGGCG  70568      AGC   CA
                                 GCGG   GCG  CGGCAGCGGCG
                                 ||||   |||  ||||||||||
                                 CGCC   CGC  GCCGTCGCCGC
                                   GC_   C_
GAM3102  STK25     5'  GCGAAGCAACGGTGGTGGCG   70675        CGC    CAGC
                                 GCGGAGCG   ACGG    GGCG
                                 ||||||||   ||||    ||||
                                 CGCTTCGT   TGCC    CCGC
                                      ___    ACCA
GAM3102  SV2      5'  GCGGGCGGAGGCGGCAGCGGCG 70676      A   CGCA
                                 GCGG GCG    CGGCAGCGGCG
                                 |||| |||    ||||||||||
```

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                                CGCC CGC   GCCGTCGCCGC
                                  _  CTCC
GAM3102  TEX27    5'  GCGGCGGCAGCGGTGGCGGCG  70677    GA  C  _  CA
                                GCG  GCG GCA CGG  GCGGCG
                                |||  ||| ||| |||  |||||||
                                CGC  CGC CGT GCC  CGCCGC
                                 __  _  C  AC
GAM3102  TSCOT    5'  GGAGCGCGCCGGCCAGTGGCG  70678        A  _ C
                                GGAGCGCGC CGGC AG GGCG
                                ||||||||| |||| || ||||
                                CCTCGCGCG GCCG TC CCGC
                                     _  G  A
GAM3102  XT2      5'  GCGAGCGCGCGCACGGGCG   70679     A_       CA
                                GCGG  GCGCGCACGG  GCG
                                ||||  ||||||||||  |||
                                CGCT  CGCGCGTGCC  CGC
                                  CG        __
GAM3102  LOC115294 5'  GTGGCGCGGGCAGCGGC    70680   GA    CAC
                                G  GCGCG   GGCAGCGGC
                                |  |||||   |||||||||
                                C  CGCGC   CCGTCGCCG
                                 AC   ___
GAM3102  LOC146315 5'  GCGCAGCGCCAGGCAGTGG   70681    G    G  C    C
                                GCG AGCGC CA GGCAG GG
                                ||| ||||| || ||||| ||
                                CGC TCGCG GT CCGTC CC
                                  G   _ _   A
GAM3102  LOC147341 5'  GCGGAGCGCAGCGCGGC    70682        GCAC   A
                                GCGGAGCGC   GGC GCGGC
                                |||||||||   ||| |||||
                                CGCCTCGCG   TCG CGCCG
                                     ____  _
GAM3102  LOC147645 5'  GAGCAGCGAGCGGCGGCGGCG  70683     _  CA   A
                                GAGC GCG  CGGC GCGGCG
                                |||| |||  |||| ||||||
                                CTCG CGC  GCCG CGCCGC
                                  T  TC   C
GAM3102  LOC149297 5'  GGAGGCGGCAGCGGCG     70684     C  GCAC
                                GGAG GC   GGCAGCGGCG
                                |||| ||   ||||||||||
                                CCTC CG   CCGTCGCCGC
                                  _ ____
GAM3102  LOC150155 5'  GCGGCAGCGTGAAGCCCGGCGG 70685     _   C___  A   A
           CG                   GCGG AGCG   GC CGGC GCG
                                |||| ||||   || |||| |||
                                CGCC TCGC   CG GCCG CGC
                                  G   ACTT  G   C
GAM3102  LOC151127 5'  GCGGTGGCGGTAGCAGCGGCG  70686     AGC   CAC
                                GCGG   GCG   GGCAGCGGCG
                                ||||   |||   ||||||||||
```

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                                CGCC  CGC  TCGTCGCCGC
                                  AC_  CA_
GAM3102  LOC151127 5'  GCGGTAGCAGCGGCGGCGG   70687     _   C  AC  A
                                GCGG AGCG GC  GGC GCGG
                                |||| |||| ||  ||| ||||
                                CGCC TCGT CG  CCG CGCC
                                  A   _ __  C
GAM3102  LOC152106 5'  GCGGAGGCAGCGGCGGC    70688      C  GCAC  A
                                GCGGAG GC   GGC GCGGC
                                |||||| ||   ||| |||||
                                CGCCTC CG   TCG CGCCG
                                   _ _____  C
GAM3102  LOC152641 5'  GCGGCGACGCCGGCAGCGGCG  70689     AGC   A
                                GCGG  GCGC CGGCAGCGGCG
                                ||||  |||| ||||||||||
                                CGCC  TGCG GCCGTCGCCGC
                                  GC_  _
GAM3102  LOC153572 3'  GCGGGGGGCTCAGCAGCGGCG  70690     AGCGC  A
                                GCGG   GC CGGCAGCGGCG
                                ||||   || ||||||||||
                                CGCC   CG GTCGTCGCCGC
                                  CCC__  A
GAM3102  LOC157740 5'  CGGAGCCCAACGGCAGCGGCG  70691      G  C
                                CGGAGC CG ACGGCAGCGGCG
                                |||||| || ||||||||||||
                                GCCTCG GT TGCCGTCGCCGC
                                   G  _
GAM3102  LOC200862 5'  GCGGTGCGCAGCAGCGGCGGCG 70692     A   _  _   A
            GCG                  GCGG GCGC GCA CGGC GCGGCG
                                |||| |||| ||| |||| ||||||
                                CGCC CGCG CGT GCCG CGCCGC
                                  A   T  C   C
GAM3102  LOC219513 3'  GCGGAGCGCGCGCAGGTCTCG  70693         A  CAG_
                                GCGGAGCGCGC CGG   CG
                                |||||||||| |||   ||
                                CGCCTCGCGCG GTC   GC
                                      C  CAGA
GAM3102  LOC221312 5'  GCGGAGCGTGGGCCTCGGCG  70694       CGCAC  AG
                                GCGGAGCG   GGC  CGGCG
                                ||||||||   |||  |||||
                                CGCCTCGC   CCG  GCCGC
                                    AC___  GA
GAM3102  LOC221496 5'  GCGGGCCGGGCGCGCAGCGGCG 70695     A  G  CA  _
                                GCGG GC CG  CG GCAGCGGCG
                                |||| || ||  || |||||||||
                                CGCC CG GC  GC CGTCGCCGC
                                  _ _  CC  G
GAM3102  LOC221749 5'  GCGGGGCGGCGCGGCGGCG   70696     A  C  A   A
                                GCGG GCG GC CGGC GCG
                                |||| ||| || |||| |||
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                                CGCC CGC CG GCCG CGC
                                  C  _ C  C
GAM3102  LOC253070 3'  GCGGAGAGCGCAGCGGC    70697      C  GCACG
                                GCGGAG GC   GCAGCGGC
                                |||||| ||   ||||||||
                                CGCCTC CG   CGTCGCCG
                                   T _____
GAM3102  LOC254986 5'  GTGGCGCGGGCAGCGGC    70680   GA   CAC
                                G  GCGCG  GGCAGCGGC
                                |  |||||  |||||||||
                                C  CGCGC  CCGTCGCCG
                                 AC   ___
GAM3102  LOC255925 5'  GGGGGGCGCGCGCAGCGGCG  70698   C  A    ACG
                                G GG GCGCGC  GCAGCGGCG
                                | || ||||||  |||||||||
                                C CC CGCGCG  CGTCGCCGC
                                 C  C    ___
GAM3102  LOC256586 5'  CGGAGCGCGAGCGCGGCGGCGG 70699        __ A   A
            CG                   CGGAGCGC  GC CGGC GCGGCG
                                |||||||| || |||| ||||||
                                GCCTCGCG  CG GCCG CGCCGC
                                    CT  C   C
GAM3102  LOC51063  5'  GCGGTGCAGGGCAGCGGC    70700     AGCGC  C
                                GCGG    GCA GGCAGCGGC
                                ||||    ||| |||||||||
                                CGCC    CGT CCGTCGCCG
                                  A____  C
GAM3102  LOC51092  5'  GCAGGGCGGCAGTGGCAGCGG  70701     A  C  C_
                                GCGG GCG GCA  GGCAGCGG
                                |||| ||| |||  ||||||||
                                CGTC CGC CGT  CCGTCGCC
                                  C  _  CA
GAM3102  LOC64150  5'  GGGACGCTGGCGGCGGCGGCG  70702   AG  GCA   A
                                GG  CGC  CGGC GCGGCG
                                ||  |||  |||| ||||||
                                CC  GCG  GCCG CGCCGC
                                 CT  ACC   C
GAM3103  ARSD     3'  GTGCAGCTGCAGAACGTGA   70705        CGC    C C
                                GTGCAGCTGC  AGAGC G GA
                                ||||||||||  ||||| | ||
                                CACGTCGACG  TCTTG C CT
                                    ___    _ A
GAM3103  HLX1     5'  GCGCGGCTGCCGCAGTCCAGCC 70706     A       ___    C
            GGA                   GTGC GCTGCCGCAG  AGCCG GA
                                |||| ||||||||||  ||||| ||
                                CGCG CGACGGCGTC  TCGGC CT
                                  C        AGG   _
GAM3103  IHPK1    3'  GTGCAGCTTTGCTCGCTGTGAG 70707        __ _  A__
                                GTGCAGCT  GC CGC  GAG
                                ||||||||  || |||  |||
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                                CACGTCGA  CG GCG   CTC
                                    AA  A   ACA
GAM3103  KCNN2    5'  GCGCAGCTGTTGCACCGGA   70708        CC  AGA    C
                                GTGCAGCTG  GC   GCCG GA
                                |||||||||  ||   |||| ||
                                CGCGTCGAC  CG   TGGC CT
                                    AA  ____   _
GAM3103  LEF1     5'  GCAGCTGCCGCGGCGCCCGAA  70709          AGA   G
                                GCAGCTGCCGC   GCC CGAA
                                ||||||||||   ||| ||||
                                CGTCGACGGCG   CGG GCTT
                                      CCG   _
GAM3103  LTK      5'  GTGTGCTGCCGCTGGCGA    70710     CA      AGAGCC
                                GTG  GCTGCCGC     GCGA
                                |||  ||||||||     ||||
                                CAC  CGACGGCG     CGCT
                                  A_       AC_____
GAM3103  MUC4     3'  GTGCAGCTGTCTCTGAGCGTGA 70711         CCGCA    C C
                A                GTGCAGCTG     GAGC G GAA
                                |||||||||     |||| | |||
                                CACGTCGAC     CTCG C CTT
                                    AGAGA    _ A
GAM3103  PYGB     5'  GTGCAGCTGCTCTGGCGCG   70712         CGCAGA  C
                                GTGCAGCTGC      GC GCG
                                ||||||||||      || |||
                                CACGTCGACG      CG CGC
                                     AGAC__  _
GAM3103  RAGE     3'  GCAGCTGCGCGGGCCGCG    70713        C  AGA
                                GCAGCTGC GC   GCCGCG
                                ||||||||  ||   ||||||
                                CGTCGACG CG   CGGCGC
                                    _  CC_
GAM3103  TNFRSF7  3'  GTGCAGCTACCGCAGGTGC   70714             A_
                                GTGCAGCTGCCGCAG  GC
                                ||||||||||||||  ||
                                CACGTCGATGGCGTC  CG
                                      CA
GAM3103  CALCYON  5'  GCAGCTGCTGCAGGACGCG   70715        C    AG C
                                GCAGCTGC GCAG  C GCG
                                ||||||||  ||||  | |||
                                CGTCGACG CGTC  G CGC
                                    A   CT _
GAM3103  CHDH     5'  GCCCCGGAGCCGCGA      70716     G   CA
                                GCT CCG  GAGCCGCGA
                                |||  |||  |||||||||
                                CGG GGC  CTCGGCGCT
                                  _   __
GAM3103  FLJ21865 3'  GTGCAGCTGCAGCGGCC     70717          C  AGA
                                GTGCAGCTGC GC   GCC
                                |||||||||  ||   |||
```

```
                                CACGTCGACG CG   CGG
                                      T  C__
GAM3103  KIAA0125  3'  GTGAGCCACTCAGAGCCGCGA  70718     C   TG CG
                                GTG AGC  C  CAGAGCCGCGA
                                ||| |||  |  ||||||||||
                                CAC TCG  G  GTCTCGGCGCT
                                  _  GT A_
GAM3103  KIAA0676  3'  GTGCAGCTGGTGCGAGGCG   70719         CC  A   CC
                                GTGCAGCTG  GC GAG  GCG
                                |||||||||  || |||  |||
                                CACGTCGAC  CG CTC  CGC
                                      CA  _  __
GAM3103  MGC13090  3'  TGCAGCCGCTCAGGGCCG    70720         CG   A
                                TGCAGCTGC  CAG GCCG
                                |||||||||  ||| ||||
                                ACGTCGGCG  GTC CGGC
                                      A_   C
GAM3103  MGC15730  5'  GCAGCGCGGAGAGCCGCG    70721      T  C C
                                GCAGC GC G AGAGCCGCG
                                ||||| || | |||||||||
                                CGTCG CG C TCTCGGCGC
                                  _ _ C
GAM3103  MGC16824  5'  GCAGCTGCCAAGGCTGCG    70722         C  A  C
                                GCAGCTGCCG AG GC GCG
                                |||||||||| || || |||
                                CGTCGACGGT TC CG CGC
                                      _ _  A
GAM3103  MGC4663   5'  GTGCGGCTTCCACAGAGCTGCG 70723     A   G       C
            A                    GTGC GCT CCGCAGAGC GCGA
                                |||| ||| ||||||||| ||||
                                CACG CGA GGTGTCTCG CGCT
                                  C  A       A
GAM3103  RBMS1    5'  AGCTGCCGTGCAGGGTCGCG   70724       __   AGC
                                AGCTGCC  GCAG   CGCG
                                |||||||  ||||   ||||
                                TCGACGG  CGTC   GCGC
                                    CA   CCA
GAM3103  RBMS1    5'  AGCTGCCGTGCAGGGTCGCG   70724       __   AGC
                                AGCTGCC  GCAG   CGCG
                                |||||||  ||||   ||||
                                TCGACGG  CGTC   GCGC
                                    CA   CCA
GAM3103  RBMS1    5'  AGCTGCCGTGCAGGGTCGCG   70724       __   AGC
                                AGCTGCC  GCAG   CGCG
                                |||||||  ||||   ||||
                                TCGACGG  CGTC   GCGC
                                    CA   CCA
GAM3103  SOX6     3'  ATGCAGCTGCACACGCCG    70725         C   GA
                                GTGCAGCTGC GCA  GCCG
                                |||||||||| |||  ||||
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                                TACGTCGACG TGT  CGGC
                                      _  G_
GAM3103  TRIM38   3'  TGCAGCTGCTGCAGGCTCA   70726        C   A  _
                                TGCAGCTGC GCAG GC CG
                                ||||||||| |||| || ||
                                ACGTCGACG CGTC CG GT
                                     A   _  A
GAM3103  LOC120227 5'  GTGCAGCTTCCACAGAGCTGCG 70727        G       C
           A                    GTGCAGCT CCGCAGAGC GCGA
                                |||||||| ||||||||| ||||
                                CACGTCGA GGTGTCTCG CGCT
                                     A       A
GAM3103  LOC144893 5'  GTGCAGCTGTCTCCCGCGA   70728        CCGCAGAG
                                GTGCAGCTG       CCGCGA
                                |||||||||       ||||||
                                CACGTCGAC       GGCGCT
                                     AGAG____
GAM3103  LOC150157 5'  GTGCAGCTCTGGAGCTGTTGCG 70729        GCCGCA   C___
                                GTGCAGCT     GAGC   GCG
                                ||||||||     ||||   |||
                                CACGTCGA     CTCG   CGC
                                     GAC___   ACAA
GAM3103  LOC196890 5'  GTGCAGCTCTGGAGCTGTTGCG 70729        GCCGCA   C___
                                GTGCAGCT     GAGC   GCG
                                ||||||||     ||||   |||
                                CACGTCGA     CTCG   CGC
                                     GAC___   ACAA
GAM3103  LOC257476 3'  GTGCAGCTTTGCTCGCTGTGAG 70707        __ _  A__
                                GTGCAGCT  GC CGC   GAG
                                ||||||||  || |||   |||
                                CACGTCGA  CG GCG   CTC
                                     AA  A   ACA
GAM3103  LOC257478 3'  GTGCAGCTGCGCCGGCG     70730        CGCAGA   _
                                GTGCAGCTGC     GCCG CG
                                ||||||||||     |||| ||
                                CACGTCGACG     CGGC GC
                                     _______   C
GAM3103  LOC91812  5'  GTGCAGCTCGCTGTGGCCAGAA 70731        GC   AGA_   C
                                GTGCAGCT  CGC   GCCG GAA
                                ||||||||  |||   |||| |||
                                CACGTCGA  GCG   CGGT CTT
                                     __  ACAC   _
GAM3103  LOC91813  5'  GTGCAGCTCGCTGTGGCCAGAA 70731        GC   AGA_   C
                                GTGCAGCT  CGC   GCCG GAA
                                ||||||||  |||   |||| |||
                                CACGTCGA  GCG   CGGT CTT
                                     __  ACAC   _
GAM3103  LOC92078  3'  GTGTGCTGGAGGAGCCGCG   70732     CA   CCGCA
                                GTG  GCTG    GAGCCGCG
                                |||  ||||    ||||||||
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                                CAC  CGAC    CTCGGCGC
                                  A_   CTC__
GAM3104  CA7      3'  GGTGGGGCTGCTGCCACTGC  70735     T A       TG G
                                GGT G GGCTGCTGC  C GC
                                ||| | |||||||||  | ||
                                CCA C CCGACGACG  G CG
                                  _ C       GT A
GAM3104  DTNA     3'  GGTGAGGCTGCTGCCAGGCTGC 70736     T          C
                                GGT GAGGCTGCTGCTG GGCTGC
                                ||| |||||||||||| ||||||
                                CCA CTCCGACGACGGT CCGACG
                                  _          _
GAM3104  DTNA     3'  GGTGAGGCTGCTGCCAGGCTGC 70736     T          C
                                GGT GAGGCTGCTGCTG GGCTGC
                                ||| |||||||||||| ||||||
                                CCA CTCCGACGACGGT CCGACG
                                  _          _
GAM3104  HIVEP3   5'  GGTTGAGGCTGCTGGG      70737            CTGC
                                GGTTGAGGCTGCTG   GG
                                ||||||||||||   ||
                                CCAACTCCGACGAC   CC
                                       ____
GAM3104  HUNK     3'  GGTTGAGGCTGCAGTGAACTG  70738          TGC  C
                                GGTTGAGGCTGC   TG GGCTG
                                ||||||||||   || |||||
                                CCAACTCCGACG   AC TTGAC
                                      TC_  _
GAM3104  RAI3     3'  GGTCGAGGCTGCACTGGGCTG  70739          T    C
                                GGTTGAGGCTGC GCTG GGCTG
                                |||||||||| |||| |||||
                                CCAGCTCCGACG TGAC CCGAC
                                       _   _
GAM3104  AMOT     5'  GGCTGCTGCTGTGGCTGC    70740          C
                                GGCTGCTGCTG GGCTGC
                                |||||||||| ||||||
                                CCGACGACGAC CCGACG
                                      A
GAM3104  CCNE2    5'  GGCTGGGGCTGCTGCTTAGCT  70741       A        GC
                                GGTTG GGCTGCTGCT  GGCT
                                ||||| |||||||||  ||||
                                CCGAC CCGACGACGA  TCGA
                                   C        A_
GAM3104  CGI-203  5'  GGCTGAGGTTGCTGATCTGC   70742        C    __
                                GGTTGAGG TGCTG  CTGC
                                |||||||| |||||  ||||
                                CCGACTCC ACGAC  GACG
                                     A    TA
GAM3104  DDX25    5'  GGCTGAGGTTTGAAAAGTGGCT 70743        C_  CTGCTGC
            G                    GGTTGAGG  TG      GGCTG
                                ||||||||  ||      |||||
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                                CCGACTCC  AC      CCGAC
                                    AA  TTTTCA_
GAM3104  EDR2     5'  GGCGGCTGCTGCTGTTGTGGCT 70744     TGA         C___
              G                   GGT   GGCTGCTGCTG    GGCTG
                                  |||   ||||||||||    |||||
                                  CCG   CCGACGACGAC    CCGAC
                                    ___         AACA
GAM3104  ERp44    3'  GGTTGATGCTGCTGTTGAAAGG 70745       G      C  C__
              C                   GGTTGA GCTGCTG TG   GGC
                                  ||||||| ||||||| ||   |||
                                  CCAACT CGACGAC AC   CCG
                                     A      A  TTT
GAM3104  FLJ10716 5'  GGTTGAGGCTGCAGTGAGCCG  70746           TGC  C
                                  GGTTGAGGCTGC   TG GGCTG
                                  ||||||||||||   || |||||
                                  CCAACTCCGACG   AC TCGGC
                                         TC_  _
GAM3104  FLJ11618 3'  GGCTGGGGTTGCTGCCGTGAGG 70747      A  C       C__
              CTGC                  GGTTG GG TGCTGCTG   GGCTGC
                                  ||||| || ||||||||   ||||||
                                  CCGAC CC ACGACGGC   CCGACG
                                     C  A       ACT
GAM3104  FLJ11618 3'  GGTTGAGGCTTCTGTTCCCAGG 70748          G   __  GC
                                  GGTTGAGGCT CTG  CT  GG
                                  |||||||||| |||  ||  ||
                                  CCAACTCCGA GAC  GG  CC
                                        A   AA  GT
GAM3104  FLJ12505 5'  GGCTGGGGCTGCTGGGGCTTGC 70749      A       CTGC   _
                                  GGTTG GGCTGCTG    GGCT GC
                                  ||||| ||||||||    |||| ||
                                  CCGAC CCGACGAC    CCGA CG
                                     C       C___    A
GAM3104  FLJ20127 5'  GGTTGAGGATGGTGGCTG    70750         C  CTGCTGC
                                  GGTTGAGG TG      GGCTG
                                  |||||||| ||      |||||
                                  CCAACTCC AC      CCGAC
                                       T  CA_____
GAM3104  HNRPU    5'  GGCGGCTGCTGCGGCTGC    70751     T
                                  GGC GCTGCTGCGGCTGC
                                  ||| ||||||||||||||
                                  CCG CGACGACGCCGACG
                                    C
GAM3104  HNRPU    5'  GGCGGCTGCTGCGGCTGC    70751     T
                                  GGC GCTGCTGCGGCTGC
                                  ||| ||||||||||||||
                                  CCG CGACGACGCCGACG
                                    C
GAM3104  HSPC228  3'  GGTTGAGGCTGCTGATGAATGC 70752           C  CG_
                                  GGTTGAGGCTGCTG TG   GC
                                  |||||||||||||| ||   ||
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                                CCAACTCCGACGAC AC   CG
                                       T  TTA
GAM3104  KIAA1115  5'  GGTTGAGGCTGCCGGTGCTCTG 70753           C   GG
              C                  GGTTGAGGCTGCTG TGC  CTGC
                                 |||||||||||||| |||  ||||
                                 CCAACTCCGACGGC ACG  GACG
                                       C   A_
GAM3104  KIAA1321  5'  GGCTGAGGCTGCGGGCTGC   70754          T_
                                 GGTTGAGGCTGC  GCTGC
                                 ||||||||||||  |||||
                                 CCGACTCCGACG  CGACG
                                       CC
GAM3104  KIAA1819  5'  GGTGGGGCTGCTGTTGCTGCTG 70755    T A      C   G
              C                  GGT G GGCTGCTG TGC GCTGC
                                 ||| | |||||||| ||| |||||
                                 CCA C CCGACGAC ACG CGACG
                                   _ C       A   A
GAM3104  KIAA1910  5'  GGTGGAGTTCTTGCTGTGGTTG 70756    T   GCTG  _   C  C
              C                  GGT GAG    CT GCTG GG TGC
                                 ||| |||    || |||| || |||
                                 CCA CTC    GA CGAC CC ACG
                                   C   AA__  A    A  A
GAM3104  MGC10200  3'  GGTTGAGGCTGCAGTGAGCCA  70757          TGC  C
                                 GGTTGAGGCTGC   TG GGCTG
                                 ||||||||||||   || |||||
                                 CCAACTCCGACG   AC TCGGT
                                       TC_  _
GAM3104  MGC13138  3'  GGTTGAGGCTGCAGTTAGCCCT 70758          TGCT_  GG
              G                  GGTTGAGGCTGC    GC  CTG
                                 ||||||||||||    ||  |||
                                 CCAACTCCGACG    CG  GAC
                                       TCAAT  G_
GAM3104  RASD2    3'  GGTTGGAGCTGCTGCTTTGAGC 70759      AG       GC_
                                 GGTTG  GCTGCTGCT   GGC
                                 |||||  |||||||||   |||
                                 CCAAC  CGACGACGA   TCG
                                    CT        AAC
GAM3104  SELB     3'  GGTGGGGGCTGCTGCTGC    70760     TGA
                                 GGT   GGCTGCTGCTGC
                                 |||   ||||||||||||
                                 CCA   CCGACGACGACG
                                   CCC
GAM3104  UBE2E1   5'  GGCGGCTGCTGCTGCGGCTGC  70761     TGA
                                 GGT   GGCTGCTGCTGCGGCTGC
                                 |||   ||||||||||||||||||
                                 CCG   CCGACGACGACGCCGACG
                                       ____
GAM3104  VILL     3'  GGTTGATGCTGCTGCCGGGCTG 70762       G        C
              C                  GGTTGA GCTGCTGCTG GGCTGC
                                 |||||| |||||||||| ||||||
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                                CCAACT CGACGACGGC CCGACG
                                   A        _
GAM3104  LOC120400 5'  GGTTGAGGATGGTGGCTG    70750        C  CTGCTGC
                                GGTTGAGG TG      GGCTG
                                |||||||| ||      |||||
                                CCAACTCC AC      CCGAC
                                     T  CA_____
GAM3104  LOC129676 5'  GAGCCATCTGCTGCTGTGGCTG 70763     G___       C
              C                  GAG    CTGCTGCTG GGCTGC
                                |||    ||||||||| ||||||
                                CTC    GACGACGAC CCGACG
                                  GGTA        A
GAM3104  LOC149132 5'  GGTTGAGGCTGCAGTCAGCTGC 70764          TGCTG
                                GGTTGAGGCTGC     CGGCTGC
                                ||||||||||||     |||||||
                                CCAACTCCGACG     GTCGACG
                                       TCA__
GAM3104  LOC152282 3'  GGCTGGGGCTGCTGCTGC     70765      A
                                GGTTG GGCTGCTGCTGC
                                ||||| ||||||||||||
                                CCGAC CCGACGACGACG
                                   C
GAM3104  LOC157653 5'  GGTTGAGGCTGCAGTTGGA    70766          TGC  C
                                GGTTGAGGCTGC   TG GG
                                ||||||||||||   || ||
                                CCAACTCCGACG   AC CT
                                       TCA  _
GAM3104  LOC202908 5'  GGTTGAGGCTGCAGTCAGCTG  70767          TGCTG
                                GGTTGAGGCTGC     CGGCTG
                                ||||||||||||     ||||||
                                CCAACTCCGACG     GTCGAC
                                       TCA__
GAM3104  LOC221960 3'  GGTTGAGGCTGCAGTGAGCCA  70757          TGC  C
                                GGTTGAGGCTGC   TG GGCTG
                                ||||||||||||   || |||||
                                CCAACTCCGACG   AC TCGGT
                                       TC_  _
GAM3104  LOC222057 5'  GGTTGAGGCTGCAGTCAGCTGC 70764          TGCTG
                                GGTTGAGGCTGC     CGGCTGC
                                ||||||||||||     |||||||
                                CCAACTCCGACG     GTCGACG
                                       TCA__
GAM3104  LOC253391 5'  GGTTGAGGCTCCTCCTGC     70768         G  G
                                GGTTGAGGCT CT CTGC
                                |||||||||| || ||||
                                CCAACTCCGA GA GACG
                                      G  G
GAM3104  LOC255975 5'  GGTTGAGGCTGCAGTCAGCTG  70767          TGCTG
                                GGTTGAGGCTGC     CGGCTG
                                ||||||||||||     ||||||
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                                CCAACTCCGACG    GTCGAC
                                      TCA__
GAM3104  LOC256878 5'  GGTTGAGGCTGCAGTCAGCTG  70767          TGCTG
                                GGTTGAGGCTGC    CGGCTG
                                ||||||||||||    ||||||
                                CCAACTCCGACG    GTCGAC
                                      TCA__
GAM3104  LOC51622  3'  GGTTGAGGCTGCAGTGAGCCA  70757          TGC  C
                                GGTTGAGGCTGC   TG GGCTG
                                ||||||||||||  || |||||
                                CCAACTCCGACG   AC TCGGT
                                      TC_ _
GAM3105  EBAF      3'  TGCATTGCTCAGCTGTA     70771      CG  AAATA
                                TGCAT  GT    TAGCTGTA
                                |||||  ||    ||||||||
                                ACGTA  CG    GTCGACAT
                                   A_  A____
GAM3105  F7        3'  TGCATCGGTGTGTTTGCGTAT  70772        AAATATA  T
                                TGCATCGGT      GC GTAT
                                |||||||||      || ||||
                                ACGTAGCCA      CG CATA
                                     CACAAA_ _
GAM3105  F7        3'  TGCATCGGTGTGTTTGCGTAT  70772        AAATATA  T
                                TGCATCGGT      GC GTAT
                                |||||||||      || ||||
                                ACGTAGCCA      CG CATA
                                     CACAAA_ _
GAM3105  MGC3771   3'  GCATCGGTAAATGTTCTA    70773          ATAG
                                GCATCGGTAAAT   CTG
                                ||||||||||||   |||
                                CGTAGCCATTTA   GAT
                                      CAA_
GAM3105  LOC146438 3'  GCATCGGTAAATGTTCTA    70773          ATAG
                                GCATCGGTAAAT   CTG
                                ||||||||||||   |||
                                CGTAGCCATTTA   GAT
                                      CAA_
GAM3106  BTC       3'  TGCTTGATAAATGGTAGC    70776    A       A  T
                                TG TTGATAAATG TA GC
                                || ||||||||| || ||
                                AC AACTATTTAC AT CG
                                  G        C  _
GAM3106  GRM1      3'  TGATTGATAAAGATTTTACAAA 70777          T   A_
                                TGATTGATAAA GAT  TGCAAA
                                |||||||||| |||  ||||||
                                ACTAACTATTT CTA  ATGTTT
                                      _  AA
GAM3106  HAP1      3'  TGCAAATGATATGCAAA     70778    A
                                TG TAAATGATATGCAAA
                                || ||||||||||||||
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                                AC GTTTACTATACGTTT
                                  _
GAM3106 IL1A     3' TGATTGGTACTATGCAAAAT  70779       ATAAATGA
                                TGATTG       TATGCAAAAT
                                ||||||       ||||||||||
                                ACTAAC       ATACGTTTTA
                                   CATG____
GAM3106 PMX1     3' TGATTGATTGATTGCA      70780        AAA   A
                                TGATTGAT   TGAT TGCA
                                ||||||||   |||| ||||
                                ACTAACTA   ACTA ACGT
                                   ___   _
GAM3106 PMX1     3' TGATTGATTGATTGCA      70780        AAA   A
                                TGATTGAT   TGAT TGCA
                                ||||||||   |||| ||||
                                ACTAACTA   ACTA ACGT
                                   ___   _
GAM3106 C20orf21 3' TGATTGATAAGCTGACAAAAAA 70781         A_    TGC
             AAT                  TGATTGATAA  TGATA   AAAAT
                                ||||||||||  |||||   |||||
                                ACTAACTATT  ACTGT   TTTTA
                                     CG     TTT
GAM3106 DKFZp434D177 3' TGATTAATAAATGATAAAAC  70782            T_
                                TGATTGATAAATGATA  GC
                                ||||||||||||||||  ||
                                ACTAATTATTTACTAT  TG
                                       TT
GAM3106 FLJ23516 3' TGGTTGACAAATCACATG    70783    A       G
                                TG TTGATAAAT ATATG
                                || |||||||| |||||
                                AC AACTGTTTA TGTAC
                                 C        G
GAM3106 GP       3' TGATTGGTAAATGATGCACAAA 70784       A       AT
             A                   TGATTG TAAATGAT  GCAAAA
                                ||||||| ||||||||  ||||||
                                ACTAAC ATTTACTA  TGTTTT
                                   C       CG
GAM3106 KIAA0798 3' ATTGATAATATGATGCAA    70785        _   TA
                                ATTGATAA ATGA  TGCAA
                                ||||||||| ||||  |||||
                                TAACTATT TACT  ACGTT
                                    A   __
GAM3106 KIAA1265 3' TGATTGATTGATATATACCAAA 70786        AAA     ___
             AT                   TGATTGAT   TGATATG   CAAAAT
                                ||||||||   |||||||   ||||||
                                ACTAACTA   ACTATAT   GTTTTA
                                     ___      ATG
GAM3106 KIAA1911 5' TGATTGATGAATGATGC     70787        A    TA
                                TGATTGAT AATGA  TGC
                                |||||||| |||||  |||
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                                ACTAACTA TTACT  ACG
                                    C    __
GAM3106 USP25    3' TGATAGATACAATATGCAAAAT 70788     T   AA TG
                                TGAT GAT  A  ATATGCAAAAT
                                |||| |||  |  ||||||||||
                                ACTA CTA  T  TATACGTTTTA
                                  T  __ GT
GAM3107 ATP11B   3' TGACTTGGTGCTTGCCAC    70791          __
                                TGACTTGGTGC  GCCGC
                                ||||||||||  |||||
                                ACTGAACCACG  CGGTG
                                      AA
GAM3107 CLDN3    3' TGGCCTGGTGCGCGCTCCAGCT 70792    A       C  CG
                                TG CTTGGTGCGC GC  TCAGCT
                                || ||||||||| ||  ||||||
                                AC GGACCACGCG CG  GGTCGA
                                 C        _ A_
GAM3107 LIPA     3' TGACTTGGTGGTACACAGC   70793         CGCCGC  T
                                TGACTTGGTG     CG CAGC
                                |||||||||      || ||||
                                ACTGAACCAC     GT GTCG
                                      CAT___  _
GAM3107 TRIM9    3' TGACTTGGTGGGCTGTC     70794         CGCC  C
                                TGACTTGGTG    GC GTC
                                |||||||||    || |||
                                ACTGAACCAC    CG CAG
                                      C___  A
GAM3107 LOC151283 3' TGATTTGGTGCAGCGGGGTAG  70795     C      C  CC  C
                                TGA TTGGTGCG CG  GT AG
                                ||| ||||||| ||  || ||
                                ACT AACCACGT GC  CA TC
                                  A       C  CC  _
GAM3108 DSC1     3' ATGCATCTGTGGATATTACACT 70798         AA   A__
            AT                    ATGCATCTGT  ATAT   GCTGT
                                |||||||||  ||||  |||||
                                TACGTAGACA  TATA   TGATA
                                      CC    ATG
GAM3108 DSC1     3' ATGCATCTGTGGATATTACACT 70798         AA   A__
            AT                    ATGCATCTGT  ATAT   GCTGT
                                |||||||||  ||||  |||||
                                TACGTAGACA  TATA   TGATA
                                      CC    ATG
GAM3108 GGA3     3' TGCATCTGTCAGGTGT      70799         AAATA  C
                                TGCATCTGT    TAG TGT
                                |||||||||    ||| |||
                                ACGTAGACA    GTC ACA
                                      _____  C
GAM3108 GGA3     3' TGCATCTGTCAGGTGT      70799         AAATA  C
                                TGCATCTGT    TAG TGT
                                |||||||||    ||| |||
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                                ACGTAGACA    GTC ACA
                                      _____  C
GAM3108 KRT10    3' ATGCATCTGTAAATAATGGTCT 70800           TAG__
             GT                   ATGCATCTGTAAATA    CTGT
                                  ||||||||||||||    ||||
                                  TACGTAGACATTTAT    GACA
                                         TACCA
GAM3108 CSRP2BP  3' ATGCGTTTCTCTGTGAGCTGTA 70801    A____    AAATAT
             T                    TGC    TCTGT    AGCTGTAT
                                  |||    |||||    ||||||||
                                  ACG    AGACA    TCGACATA
                                    CAAAG    C_____
GAM3108 FLJ14356 3' GCATCTGTGGATTTAGGTAT  70802       AA  A   CT
                                  GCATCTGT  AT TAG  GTAT
                                  ||||||||  || |||  ||||
                                  CGTAGACA  TA ATC  CATA
                                       CC  A   __
GAM3108 FLJ23516 3' TGCATTTTTAAATAGCTCTAT  70803     CTG   AT     G
                                  TGCAT   TAA  ATAGCT TAT
                                  |||||   |||  |||||| |||
                                  ACGTA   ATT  TATCGA ATA
                                     AAA   __     G
GAM3108 NCOA2    3' TGTGTCTGTAAATACAGCGC   70804    CA          T
                                  TG  TCTGTAAATATAGC GT
                                  ||  ||||||||||||| ||
                                  AC  AGACATTTATGTCG CG
                                   AC           _
GAM3108 RTP801   3' ATGCGTCTGTAAGATAGCTGC  70805     A      AT
                                  ATGC TCTGTAA  ATAGCTGT
                                  |||| |||||||  ||||||||
                                  TACG AGACATT  TATCGACG
                                    C      C_
GAM3108 ZNF387   3' ATGCATCTATGAAGTACTGTAT 70806         AAATATA
                                  ATGCATCTGT      GCTGTAT
                                  ||||||||||      |||||||
                                  TACGTAGATA      TGACATA
                                        CTTCA__
GAM3108 LOC144699 3' ATGCATCTGTGGAATGTAGAGT 70807         A_   A   CT
                                  ATGCATCTGT  AAT TAG  GT
                                  ||||||||||  ||| |||  ||
                                  TACGTAGACA  TTA ATC  CA
                                        CC   C   T_
GAM3108 LOC145781 3' CATCTGTAAAAAGTGTAT    70808         TAT  C
                                  CATCTGTAAA   AG TGTAT
                                  ||||||||||   || |||||
                                  GTAGACATTT   TC ACATA
                                        T__  _
GAM3108 LOC148443 3' TGCATTTATAAATAATTTTTGT 70809      C       TAGC_
             AT                   TGCAT TGTAAATA    TGTAT
                                  ||||| ||||||||    |||||
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                                ACGTA ATATTTAT    ACATA
                                  A       TAAAA
GAM3108  LOC200310 3'  ATGTACTGTAAATAAACAGTAT 70810     CAT       T  T
                                ATG   CTGTAAATA AGC GTAT
                                |||   ||||||||| ||| ||||
                                TAC   GACATTTAT TTG CATA
                                  AT_       _   T
GAM3108  LOC221751 5'  ACGCATCTGTTAGCTGT     70811          AAATA
                                ATGCATCTGT    TAGCTGT
                                ||||||||||    |||||||
                                TGCGTAGACA    ATCGACA
                                      ______
GAM3108  LOC93622  3'  ATGCATCTGTGGCAGAGACTGT 70812          AAATATA
            AT                    ATGCATCTGT      GCTGTAT
                                ||||||||||      |||||||
                                TACGTAGACA      TGACATA
                                     CCGTCTC
GAM3109  C18orf1   3'  TAGGTTTTGAGCACT      70815      GTA
                                TAGGT   TTTGAGCACT
                                |||||   ||||||||||
                                ATCCA   AAACTCGTGA
                                  ___
GAM3109  DUSP14    3'  TAATAAGGGTGTATTTAA    70816      TA
                                TAATA  GGTGTATTTGA
                                |||||  ||||||||||
                                ATTAT  CCACATAAATT
                                  TC
GAM3109  INPP4B    5'  TAATGTAGATGTATCTTCACAC 70817     A         GA
            TA                    TAAT TAGGTGTATTT  GCACTA
                                |||| ||||||||||  ||||||
                                ATTA ATCTACATAGA  TGTGAT
                                  C         AG
GAM3110  EBAF      3'  TGCATTGCTCAGCTGTA     70771      CG  AAATA
                                TGCAT  GT    TAGCTGTA
                                |||||  ||    ||||||||
                                ACGTA  CG    GTCGACAT
                                  A_  A____
GAM3110  F7        3'  TGCATCGGTGTGTTTGCGTAT  70772        AAATATA  T
                                TGCATCGGT     GC GTAT
                                |||||||||     || ||||
                                ACGTAGCCA     CG CATA
                                     CACAAA_  _
GAM3110  F7        3'  TGCATCGGTGTGTTTGCGTAT  70772        AAATATA  T
                                TGCATCGGT     GC GTAT
                                |||||||||     || ||||
                                ACGTAGCCA     CG CATA
                                     CACAAA_  _
GAM3110  MGC3771   3'  GCATCGGTAAATGTTCTA    70773          ATAG
                                GCATCGGTAAAT   CTG
                                ||||||||||||   |||
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                                CGTAGCCATTTA   GAT
                                      CAA_
GAM3110 LOC146438 3' GCATCGGTAAATGTTCTA    70773          ATAG
                                GCATCGGTAAAT   CTG
                                ||||||||||||  |||
                                CGTAGCCATTTA   GAT
                                      CAA_
GAM3111 ABCA1    3' TTCACAGTTGTTAATAAGT   70821         C  CAAC
                                TTCACAGTTG TGA   GGT
                                |||||||||| |||   |||
                                AAGTGTCAAC ATT   TCA
                                     A  AT__
GAM3111 BTG2     3' TTCACAGTTGCTAACCTTGCT 70822           AACGG
                                TTCACAGTTGCTGAC    TGCT
                                ||||||||||||||    ||||
                                AAGTGTCAACGATTG    ACGA
                                       GA___
GAM3111 LRRC2    3' TTCCTAGGCACTGATAACGGTG 70823    AC  TT    C
             CT                   TTC  AG  GCTGA AACGGTGCT
                                ||| ||  ||||| |||||||||
                                AAG  TC  TGACT TTGCCACGA
                                  GA  CG    A
GAM3111 BP75     3' CTCATGGTTGCTGAAATTGCT 70824     CA      CAACGG
                                TTCA  GTTGCTGA     TGCT
                                ||||  ||||||||     ||||
                                GAGT  CAACGACT     ACGA
                                  AC       TTA___
GAM3111 C20orf130 3' CACAGTTGCTGAGGCTGGTGCT 70825          CAAC
                                CACAGTTGCTGA   GGTGCT
                                ||||||||||||  ||||||
                                GTGTCAACGACT   CCACGA
                                      CCGA
GAM3111 KIAA1724  3' TTCCAGTTGCTCAAGCGGTG  70826    A      GA  _
                                TTC CAGTTGCT  CAA CGGTG
                                ||| ||||||||  ||| |||||
                                AAG GTCAACGA  GTT GCCAC
                                  _      __  C
GAM3111 KIAA1819  5' TTCACAGCTCAGGTGGTG    70827        GCTGA  AC_
                                TTCACAGTT    CA   GGTG
                                |||||||||    ||  ||||
                                AAGTGTCGA    GT   CCAC
                                     _____  CCA
GAM3111 LOC219505 5' TTCGAGTTGCTGATATGC    70828    AC       CAACG
                                TTC  AGTTGCTGA    GTGC
                                |||  |||||||||    ||||
                                AAG  TCAACGACT    TACG
                                  C_       A____
GAM3111 LOC91694  3' TTCACAGTTTTGAGTG      70829        GC   CAACG
                                TTCACAGTT  TGA    GTG
                                |||||||||  |||    |||
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                                AAGTGTCAA  ACT    CAC
                                     A_  _____
GAM3112  FSTL1    3'  GCTATGTATCTAGAGG     70832     AGA
                                GTTA  GTATCTAGAGG
                                ||||  ||||||||||
                                CGAT  CATAGATCTCC
                                  A__
GAM3112  GABPB1   3'  TATACAGTATAGATAACCTAGA 70833       TA  GT
           GG                   TATACAGT  AGA  ATCTAGAGG
                                ||||||||  |||  |||||||||
                                ATATGTCA  TCT  TGGATCTCC
                                     TA  AT
GAM3112  MPP1     3'  TATACAGTTGAAGGCAAAGGAG 70834        _  A  TCTA
           G                    TATACAGTT AAG GTA   GAGG
                                |||||||||| ||| |||   ||||
                                ATATGTCAA TTC CGT   CTCC
                                     C  _  TTC_
GAM3112  ABLIM    3'  TATGCACTTAAGAGTCCCAAGG 70835    A  G     A   G
                                TAT CA TTAAGAGT TCTA AGG
                                ||| || |||||||| |||| |||
                                ATA GT AATTCTCA GGGT TCC
                                  C  G      _   _
GAM3112  ABLIM    3'  TATGCACTTAAGAGTCCCAAGG 70835    A  G     A   G
                                TAT CA TTAAGAGT TCTA AGG
                                ||| || |||||||| |||| |||
                                ATA GT AATTCTCA GGGT TCC
                                  C  G      _   _
GAM3112  DKFZP434G1411 3'  AGTTGAGATCCAGAGG     70836     AA  T
                                AGTT  GAG ATCTAGAGG
                                ||||  ||| |||||||||
                                TCAA  CTC TAGGTCTCC
                                   __  _
GAM3112  DKFZp547A023 3'  TACACAGTTGGAAAGTTTGGAG 70837        A_   ATCTA
           G                    TATACAGTT  AGAGT    GAGG
                                |||||||||  |||||    ||||
                                ATGTGTCAA  TTTCA    CTCC
                                     CC    AAC__
GAM3112  KIAA0630  5'  GTTAAGAGTTTTTAGAGG    70838        ATC
                                GTTAAGAGT   TAGAGG
                                |||||||||   ||||||
                                CAATTCTCA   ATCTCC
                                     AAA
GAM3112  KIAA0831  3'  TATACTTAAGAGTATTTACAGG 70839      AG       C  G
                                TATAC  TTAAGAGTAT TA AGG
                                |||||  |||||||||| || |||
                                ATATG  AATTCTCATA AT TCC
                                   __       A  G
GAM3112  KIAA1209  3'  TACAGTTAAGAAAAAGAGG   70840          TATCT
                                TACAGTTAAGAG    AGAGG
                                ||||||||||||    |||||
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                                ATGTCAATTCTT    TCTCC
                                      TT___
GAM3112 MGC14816 5' CAGTTAAGAGTAGATTGCAGG 70841          TCTAG_
                                CAGTTAAGAGTA     AGG
                                ||||||||||||    |||
                                GTCAATTCTCAT     TCC
                                      CTAACG
GAM3112 ZFD25    3' TACAGTTAAGGGTTAAG    70842         A ATCTA
                                TACAGTTAAG GT    GAG
                                ||||||||||| ||    |||
                                ATGTCAATTC CA    TTC
                                      C  A____
GAM3113 KCNJ8    5' TGGGGGCTGCGTGTCCTAAGGA 70845    A          CTA
           G                     TG GGGCTGCGTGTTCTA   GAG
                                || ||||||||||||||   |||
                                AC CCCGACGCACAGGAT   CTC
                                 C           TC_
GAM3113 NDRG2    3' TGAGGGCTGGGTCCCACTCTAG 70846       CGT      AG
                                TGAGGGCTG   GTTCTACT  AG
                                |||||||||   ||||||||  ||
                                ACTCCCGAC   CAGGGTGA  TC
                                      C__       GA
GAM3113 DKFZP564L0862 3' GGGCCCTTCTACTAGA     70847     GCGTG
                                GGGCT    TTCTACTAGA
                                |||||    ||||||||||
                                CCCGG    AAGATGATCT
                                   G____
GAM3113 SARM     3' TGAGGGCTTCGTGCTTTAGAG  70848       G     CTAC
                                TGAGGGCT CGTGTT    TAGAG
                                |||||||| ||||||    |||||
                                ACTCCCGA GCACGA    ATCTC
                                      A     A___
GAM3113 ZSIG11   3' GAGGGCTGGAGAGTCTGCTGGA 70849       CGTGT   A  A
           G                     GAGGGCTG    TCT CT GAG
                                |||||||     ||| || |||
                                CTCCCGAC    AGA GA CTC
                                      CTCTC   C  C
GAM3113 LOC145757 3' TGAGGGCTGCTGTCCCAGGAG  70850         G      CTA
                                TGAGGGCTGC TGTTCTA   GAG
                                |||||||||| |||||||   |||
                                ACTCCCGACG ACAGGGT   CTC
                                      _      C__
GAM3113 LOC200059 3' TGAGGTTGCAGACTACTAGAG  70851      GC    TGTT
                                TGAGG  TGCG    CTACTAGAG
                                |||||  ||||    |||||||||
                                ACTCC  ACGT    GATGATCTC
                                   A_    CT__
GAM3113 LOC220758 5' GGCGGCTGCGTCCAGCCTGGAG 70852     T  _     TA_  A
                                GGC GC GTGTTC   CT GAG
                                ||| || ||||||   || |||
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                                CCG CG CGCAGG   GA CTC
                                  C A     TCG  C
GAM3114 SIAT7D   3' TAAATGTTTTTGTGGAGTGT  70855        AGACT
                                TAAATGTTT    TGGAGTGT
                                |||||||||    ||||||||
                                ATTTACAAA    ACCTCACA
                                     AAC__
GAM3114 HIC      3' TGTAAATATTTAGATTG     70856           C
                                TGTAAATGTTTAGA TTG
                                |||||||||||||| |||
                                ACATTTATAAATCT AAC
                                          _
GAM3114 SB52     3' TGTTATCTGAAAGGTTTGGAGT 70857    AAA_ TTT  AC
             GT                   TGT   TG  AG  TTGGAGTGT
                                |||   ||  ||  |||||||||
                                ACA   AC  TC  AACCTCACA
                                  ATAG  TT_  CA
GAM3114 SIRPB1   3' TGTTTAGATTTGGAGTGT    70858       C
                                TGTTTAGA TTGGAGTGT
                                |||||||| |||||||||
                                ACAAATCT AACCTCACA
                                     A
GAM3114 LOC142955 5' TGTTGACTTGGAGTGT     70859     TA
                                TGTT  GACTTGGAGTGT
                                ||||  ||||||||||||
                                ACAA  CTGAACCTCACA
                                    __
GAM3114 LOC221312 3' TGTAAATGTTGAGATTTGGA  70860        T  C
                                TGTAAATGTT AGA TTGGA
                                |||||||||| ||| |||||
                                ACATTTACAA TCT AACCT
                                      C  A
GAM3115 FLJ22313  3' TGTTACGCTATGTTCTGTTA  70863     AGA  GTA
                                TGTTA   TA   GTTCTGTTA
                                |||||   ||   |||||||||
                                ACAAT   AT   CAAGACAAT
                                   GCG  A__
GAM3115 KIAA1582  5' TGCTAGCCCAGTTCTGTT    70864     A ATAG
                                TGTTA G    TAGTTCTGTT
                                |||||  |    ||||||||||
                                ACGAT C    GTCAAGACAA
                                  _ GG__
GAM3115 KRTAP9-3  3' TGTGAGGATGGTAGTTCTCTT  70865    TAA  A     G
                                TGT   GAT GTAGTTCT TT
                                |||   ||| |||||||| ||
                                ACA   CTA CATCAAGA AA
                                  CTC   C      G
GAM3115 Rpo1-2    3' TGTTAAGAGGGTAGGTCT    70866       TA   T
                                TGTTAAGA  GTAG TCT
                                ||||||||  |||| |||
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                                ACAATTCT  CATC AGA
                                    CC    C
GAM3115  Rpo1-2    3'  TGTTAAGAGGGTAGGTCT    70866        TA    T
                                TGTTAAGA  GTAG TCT
                                ||||||||  |||| |||
                                ACAATTCT  CATC AGA
                                    CC    C
GAM3115  LOC147895 5'  TGCTGAGATAGTAGTTCC    70867      A
                                TGTT AGATAGTAGTTCT
                                |||| ||||||||||||
                                ACGA TCTATCATCAAGG
                                  C
GAM3116  ACTR1B    3'  TGACACACCAGTGGGAGCTG   70870        _   TCT   AA
                                TGACACAC AGT   GGA  CTG
                                |||||||| |||   |||  |||
                                ACTGTGTG TCA   CCT  GAC
                                    G  C__   C_
GAM3116  BCL2A1    5'  TATGACACATGATGATACATGG 70871        CA  TC____   AA
           AGGCTG                 ATGACACA  GT     TGGA  CTG
                                |||||||  ||     ||||  |||
                                TACTGTGT  TA     ACCT  GAC
                                    AC  CTATGT    CC
GAM3116  FOXI1     3'  CATGACATGCACACAGGAAACT 70872        __   GTTCT
           G                    TATGACA  CACA    GGAAACTG
                                |||||||  ||||    ||||||||
                                GTACTGT  GTGT    CCTTTGAC
                                    AC    GT___
GAM3116  PCSK1     3'  TATGATCAATTCTGGAA     70873      CACA
                                TATGA    CAGTTCTGGAA
                                |||||    ||||||||||
                                ATACT    GTTAAGACCTT
                                  A___
GAM3116  RALB      5'  TGACACACAGATGACCCACTG  70874        TTC   AA_
                                TGACACACAG   TGG   ACTG
                                ||||||||||   |||   ||||
                                ACTGTGTGTC   ACT   TGAC
                                     T__   GGG
GAM3116  RASA1     3'  ATGACAAACTCTGGAAACTG   70875      C  AGT
                                ATGACA AC   TCTGGAAACTG
                                |||||| ||   ||||||||||
                                TACTGT TG   AGACCTTTGAC
                                   T  ___
GAM3116  TARBP2    3'  CATGACACACAGTGGCCGG    70876          T_
                                TATGACACACAGT  CTGG
                                ||||||||||||  ||||
                                GTACTGTGTGTCA  GGCC
                                       CC
GAM3116  TRIM14    3'  CATGACATTCTGGAGGCT    70877       CACAG      AA
                                TATGACA    TTCTGGA  CT
                                |||||||    |||||||  ||
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                                GTACTGT    AAGACCT  GA
                                   _____      CC
GAM3116 CYorf14   3'  TGCCCACAGTTCTGGAGACTG  70878    ACA         A
                                TG   CACAGTTCTGGA ACTG
                                ||   |||||||||||| ||||
                                AC   GTGTCAAGACCT TGAC
                                 GG_          C
GAM3116 DKFZp547M236 3'  TGTCATACTTCAGGAAACTG   70879    A  C  AG   T
                                TG CA AC  TTC GGAAACTG
                                || || ||  ||| ||||||||
                                AC GT TG  AAG CCTTTGAC
                                 A  A  __   T
GAM3116 FLJ13912  3'  CGACTGTTTTTGGAAACTG    70880      ACACAG  C
                                TGAC      TT TGGAAACTG
                                ||||      || |||||||||
                                GCTG      AA ACCTTTGAC
                                   ACA___  A
GAM3116 KIAA1364  3'  TGATTACAGCTCTGGAACTG   70881     CAC         A
                                TGA   ACAGTTCTGGAA CTG
                                |||   ||||||||||||| |||
                                ACT   TGTCGAGACCTT GAC
                                  AA_          _
GAM3116 KIAA1553  3'  TATGACACACTGTTTGCATTCG 70882          A   CTGGAA__
             ACTG                    TATGACACAC GTT       ACTG
                                |||||||||| |||       ||||
                                ATACTGTGTG CAA       TGAC
                                      A   ACGTAAGC
GAM3116 KR18     3'  TGGCACACAAGAAACT      70883    A     GTTCT
                                TG CACACA    GGAAACT
                                || ||||||    |||||||
                                AC GTGTGT    TCTTTGA
                                 C    ______
GAM3116 MGC4342   3'  TATGACACACACTGAAA     70884          GTT
                                TATGACACACA   CTGGAA
                                ||||||||||   ||||||
                                ATACTGTGTGT   GACTTT
                                              ___
GAM3116 MRPS35    3'  TGAACACAGCCCGGAACTG    70885     C      T     A
                                TGA ACACAGT CTGGAA CTG
                                ||| ||||||| |||||| |||
                                ACT TGTGTCG GGCCTT GAC
                                  _      _     _
GAM3116 RAB3IL1   3'  TGCAGGCAGTTCTGGGGACTG  70886    A  CA       AA
                                TG CA  CAGTTCTGG  ACTG
                                || ||  |||||||||  ||||
                                AC GT  GTCAAGACC  TGAC
                                 _ CC        CC
GAM3116 RoXaN     3'  GATGCACAGTTTCTGGAA     70887     CA      _
                                GA  CACAGTT CTGGAA
                                ||  ||||||| ||||||
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                                CT  GTGTCAA GACCTT
                                 AC      A
GAM3116  LOC132671 3'  TATAACACACAGTAACTG    70888           T_
                                TATGACACACAGT  CTG
                                |||||||||||||  |||
                                ATATTGTGTGTCA  GAC
                                       TT
GAM3116  LOC154442 3'  CATAACTATTCTGGAA     70889       ACACA
                                TATGAC    GTTCTGGAA
                                ||||||    |||||||||
                                GTATTG    TAAGACCTT
                                   A____
GAM3116  LOC196047 5'  AACATCTCACAGTTCTGGAGGC 70890     ___         AA
            TG                    GACA   CACAGTTCTGGA  CTG
                                ||||   ||||||||||||  |||
                                TTGT   GTGTCAAGACCT  GAC
                                  AGA          CC
GAM3116  LOC199858 5'  TATGACACATAGCCGGA     70891        C  TT
                                TATGACACA AG  CTGGA
                                |||||||||  ||  |||||
                                ATACTGTGT TC  GGCCT
                                     A  __
GAM3116  LOC201696 3'  GACACACAGTTGCAACT     70892          CTGGA
                                GACACACAGTT     AACT
                                ||||||||||     ||||
                                CTGTGTGTCAA     TTGA
                                      CG___
GAM3116  LOC91548  5'  TATGGGAACAGTTCTGGAGGCT 70893     ACAC        AA
            G                     TATG    ACAGTTCTGGA  CTG
                                ||||   ||||||||||  |||
                                ATAC    TGTCAAGACCT  GAC
                                  CCT_         CC
GAM3117  CDC42    3'  CGTCCTAGAAAAGAGGAGGG   70896       C  TC    A
                                CGTCCTA AA  AGAG AGGG
                                |||||||  ||  |||| ||||
                                GCAGGAT TT  TCTC TCCC
                                    C  T_   C
GAM3117  ITGAM    3'  TTCGTGCCTCATGGGAGAAGGG 70897       _  A  ATCA
            A                      TTCGT CCT CA    GAGAAGGGA
                                ||||| ||| ||   |||||||||
                                AAGCA GGA GT    CTCTTCCCT
                                  C   _  ACC_
GAM3117  MGP      5'  TTCGTCCTGCAGGTCAGTCTCA 70898        A  A_   AGA_
            GGG                      TTCGTCCT CA  TCAG    AGGG
                                ||||||||  ||  ||||   ||||
                                AAGCAGGA GT  AGTC    TCCC
                                    C  CC    AGAG
GAM3117  PKIA     3'  TTCATAAGCAATCAGAGAGGGG 70899       CCTA        A
                                TTCGT    CAATCAGAGA GGG
                                |||||    |||||||||| |||
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                                AAGTA    GTTAGTCTCT CCC
                                   TTC_         C
GAM3117  AP3M2    3'  GTCTTAGAATGAAAAGGGA   70900     C  C   CA
                                GTC TA AAT  GAGAAGGGA
                                ||| || |||  |||||||||
                                CAG AT TTA  CTTTTCCCT
                                  A  C   __
GAM3117  LOC124216 3'  TTCATCCTGCCCAAGGAGGGA  70901         ACAA    A  A
                                TTCGTCCT    TCAG GA GGGA
                                ||||||||    |||| || ||||
                                AAGTAGGA    GGTT CT CCCT
                                     CG__    C  _
GAM3117  LOC144501 3'  TTCATCCTGTGGCAGCAAGAAG 70902         ACAATCA_
              GG                   TTCGTCCT       GAGAAGGG
                                ||||||||       ||||||||
                                AAGTAGGA       TTCTTCCC
                                     CACCGTCG
GAM3117  LOC201158 3'  TTCGTCCTCGCCTAGGAGGGA  70903         ACAATCAG  A
                                TTCGTCCT       AG AGGGA
                                ||||||||       || |||||
                                AAGCAGGA       TC TCCCT
                                     GCGGA___  C
GAM3118  C1QTNF7   5'  CTGGACATTGCTGATATC    70906    T    ATTTC
                                CT GATAT    GCTGATATC
                                || |||||    |||||||||
                                GA CTGTA    CGACTATAG
                                 C    A____
GAM3118  FBP17    5'  ACTTGATATATTTCTCAAGAAT 70907           GCT__
              ATC                   ACTTGATATATTTC    GATATC
                                ||||||||||||||    ||||||
                                TGAACTATATAAAG    TTATAG
                                       AGTTC
GAM3118  FLJ23322  3'  TACTTGACATCCCACAGCTG   70908         ATTT _
                                TACTTGATAT    C GCTG
                                ||||||||||    | ||||
                                ATGAACTGTA    G CGAC
                                      GGGT T
GAM3118  FLJ25415  3'  TACTTGCATCTCTGCTGATAT  70909       ATA     _
                                TACTTG   TATTTC GCTGATAT
                                ||||||   |||||| ||||||||
                                ATGAAC   GTAGAG CGACTATA
                                   ___     A
GAM3118  LOC149149 3'  TACTTGATATGATTCATAAT   70910         AT    C
                                TACTTGATAT  TTCG TGAT
                                ||||||||||  |||| ||||
                                ATGAACTATA  AAGT ATTA
                                      CT    _
GAM3119  DTR      3'  TAGATTGTTAAAAACTAAA    70913          T__
                                TAGATTGTTA   ACTAAA
                                ||||||||||   ||||||
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                                ATCTAACAAT   TGATTT
                                     TTT
GAM3119 KCNK2    3' TACATTGTTACCAGAAACA   70914    G      ACTAA
                                TA ATTGTTAT    AGAAACA
                                || ||||||||    |||||||
                                AT TAACAATG    TCTTTGT
                                 G       G____
GAM3119 RAF1     3' GATGTGACTAGAGAAACA    70915    T  TAT    A
                                GAT GT   ACTA AGAAACA
                                ||| ||   |||| |||||||
                                CTA CA   TGAT TCTTTGT
                                  _ C__    C
GAM3119 RRM2B    3' TAGATTGTTATGGAAAGAA   70916          ACT
                                TAGATTGTTAT   AAAGAA
                                ||||||||||   ||||||
                                ATCTAACAATA   TTTCTT
                                      CC_
GAM3119 SH3BP4   3' ATTGATTATACTAAGGAA    70917     _       A
                                ATTG TTATACTAA GAA
                                |||| |||||||| |||
                                TAAC AATATGATT CTT
                                  T        C
GAM3119 TRHDE    3' TAGATTTTATACTAAAA     70918       G
                                TAGATT TTATACTAAAG
                                |||||| ||||||||||
                                ATCTAA AATATGATTTT
                                  _
GAM3119 EDG1     3' GAAAACCATACTAAAGAGACA 70919    TT TT        A
                                GA  G  ATACTAAAGA ACA
                                ||  |  |||||||||| |||
                                CT  T  TATGATTTCT TGT
                                 TT GG         C
GAM3119 FLJ12668 3' GATTGTTAACGGAGGAAACA  70920        T  TAAA
                                GATTGTTA AC    GAAACA
                                |||||||| ||    ||||||
                                CTAACAAT TG    CTTTGT
                                     _ CCTC
GAM3119 HGC6.1.1 3' AGATTTGACTAAAGAAAC    70921      GTTAT
                                AGATT    ACTAAAGAAAC
                                |||||    ||||||||||
                                TCTAA    TGATTTCTTTG
                                   AC___
GAM3119 IBTK     3' TAGATTATTCAGAAGAAACAA 70922         ATACTA
                                TAGATTGTT     AAGAAACAA
                                |||||||||     |||||||||
                                ATCTAATAA     TTCTTTGTT
                                      GTC___
GAM3119 KIAA1128 3' AGATTGTTTTTAAGAAACAA  70923        ATACTA
                                AGATTGTT     AAGAAACAA
                                ||||||||     |||||||||
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                                TCTAACAA     TTCTTTGTT
                                    AAA___
GAM3119  LOC127255 5'  AGACCGTTGCTAGAGAAACAA  70924        ATA   A
                                AGATTGTT   CTA AGAAACAA
                                ||||||||   ||| ||||||||
                                TCTGGCAA   GAT TCTTTGTT
                                    C__   C
GAM3119  LOC131000 3'  AGATTGTTACATTAGAA     70925          CTAA
                                AGATTGTTATA    AGAA
                                ||||||||||    ||||
                                TCTAACAATGT    TCTT
                                      AA__
GAM3119  LOC151162 5'  TGCATTCACTAAAGAAACA    70926     TA_
                                TGT   TACTAAAGAAACA
                                |||   ||||||||||||
                                ACG   GTGATTTCTTTGT
                                  TAA
GAM3119  LOC152018 3'  CAGATGTAAATACTAAAGAAA  70927      T  T_
                                TAGAT GT  ATACTAAAGAAA
                                ||||| ||  ||||||||||||
                                GTCTA CA  TATGATTTCTTT
                                   _  TT
GAM3119  LOC157317 3'  TAGATTGTTATAGTTAAG    70928          CTA
                                TAGATTGTTATA   AAG
                                ||||||||||||   |||
                                ATCTAACAATAT   TTC
                                      CAA
GAM3119  LOC203377 5'  TGCATTCACTAAAGAAACA    70926     TA_
                                TGT   TACTAAAGAAACA
                                |||   ||||||||||||
                                ACG   GTGATTTCTTTGT
                                  TAA
GAM3120  ATRN     3'  TGACACGGGGGTGGGGGCAGG  70931        AGC  CTA
                                TGGCACGG   GT   GGCAGG
                                ||||||||   ||   ||||||
                                ACTGTGCC   CA   CCGTCC
                                    CC_  CCC
GAM3120  BCAR1    3'  TGGCACGAGGTCCTGCAGG    70932       G  C    AG
                                TGGCACG AG GTCT  GCAGG
                                ||||||| || ||||  |||||
                                ACCGTGC TC CAGG  CGTCC
                                   _  _    A_
GAM3120  DAAM2    3'  GATGGTAGAGGTTAGGCAG    70933      CAC    C  C
                                GATGG   GGAG GT TAGGCAG
                                |||||   |||| || |||||||
                                CTACC   TCTC CA ATCCGTC
                                  A__    _  _
GAM3120  FOXE1    5'  GGCGCGGGCCCAGGCG      70934     A   AGC       A
                                GGC CGG   GTCTAGGC G
                                ||| |||   |||||||| |
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                                CCG GCC   CGGGTCCG C
                                  C  ___       C
GAM3120  NRXN3    5'  TGGCACGGGGTGGAGGGAGG  70935        AGC  CT   C
                                TGGCACGG   GT  AGG AGG
                                ||||||||   ||  ||| |||
                                ACCGTGCC   CA  TCC TCC
                                     C__  CC   C
GAM3120  OCRL     3'  GAGGTGGATGTCTAGGCAGG  70936    T  CAC   GC
                                GA GG   GGA  GTCTAGGCAGG
                                || ||   |||  ||||||||||
                                CT CC   CCT  CAGATCCGTCC
                                 _ A__   A_
GAM3120  OCRL     3'  GAGGTGGATGTCTAGGCAGG  70936    T  CAC   GC
                                GA GG   GGA  GTCTAGGCAGG
                                || ||   |||  ||||||||||
                                CT CC   CCT  CAGATCCGTCC
                                 _ A__   A_
GAM3120  PACE     3'  GAGGCACGGAGCACAGG     70937    T       GTCTAG
                                GA GGCACGGAGC     GCAGG
                                || ||||||||||     |||||
                                CT CCGTGCCTCG     TGTCC
                                 _        _______
GAM3120  SMTN     3'  TGGGCGGACGCACAGGCAGG  70938     CA   G   C
                                TGG  CGGA CGT TAGGCAGG
                                |||  |||| ||| ||||||||
                                ACC  GCCT GCG GTCCGTCC
                                  C_   _   T
GAM3120  SMTN     3'  TGGGCGGACGCACAGGCAGG  70938     CA   G   C
                                TGG  CGGA CGT TAGGCAGG
                                |||  |||| ||| ||||||||
                                ACC  GCCT GCG GTCCGTCC
                                  C_   _   T
GAM3120  SMTN     3'  TGGGCGGACGCACAGGCAGG  70938     CA   G   C
                                TGG  CGGA CGT TAGGCAGG
                                |||  |||| ||| ||||||||
                                ACC  GCCT GCG GTCCGTCC
                                  C_   _   T
GAM3120  TLE2     3'  GATGTACGGTTCCTAGGCAGG  70939     GC   AGCG
                                GATG  ACGG   TCTAGGCAGG
                                ||||  ||||   ||||||||||
                                CTAC  TGCC   GGATCCGTCC
                                  A_   AA__
GAM3120  AMOT     5'  TGGCAGCGGACAGGCAG     70940      _   GCGTC
                                TGGCA CGGA    TAGGCAG
                                |||||  ||||    |||||||
                                ACCGT GCCT    GTCCGTC
                                  C  _____
GAM3120  CARD11   3'  TGGGGCGGAGCGTCTGCTGG  70941     CA       AG  A
                                TGG  CGGAGCGTCT  GC GG
                                |||  ||||||||||  || ||
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                                ACC  GCCTCGCAGA  CG CC
                                  CC         __  A
GAM3120 CIDEB    5' CGGCACGGGGCGCGGGTGGG  70942        A   CTA  CA
                                TGGCACGG GCGT   GG  GG
                                |||||||| ||||   ||  ||
                                GCCGTGCC CGCG   CC  CC
                                     C    C__  AC
GAM3120 DEFCAP   5' TGGTGAGGGTATCAGGCAGG  70943    CAC  AGC   T
                                TGG   GG   GTC AGGCAGG
                                |||   ||   ||| ||||||||
                                ACC   CC   TAG TCCGTCC
                                  ACT  CA_  _
GAM3120 KIAA0939 3' GATGGTGCTCCTCTAGGCAGG  70944     CACGGA  G__
                                GATGG     GC   TCTAGGCAGG
                                |||||     ||   ||||||||||
                                CTACC     CG   AGATCCGTCC
                                   A_____  AGG
GAM3120 KIAA1602 3' GATGGCACGGCTGGTGGGCAGG 70945         AGC  CTA
                                GATGGCACGG   GT   GGCAGG
                                ||||||||||   ||   ||||||
                                CTACCGTGCC   CA   CCGTCC
                                      GAC  C__
GAM3120 WDR7     3' GATGGCACTGGGGTGGGCAGG  70946        _ AGC  CTA
                                GATGGCAC GG   GT   GGCAGG
                                |||||||| ||   ||   ||||||
                                CTACCGTG CC   CA   CCGTCC
                                     A  C__  C__
GAM3120 LOC144317 5' GGGACAAGCGTCTGGGCGGG   70947    C   G      A   A
                                GG ACG AGCGTCT GGC GG
                                || ||| ||||||| ||| ||
                                CC TGT TCGCAGA CCG CC
                                 C   _      C   C
GAM3120 LOC150383 3' GATGGCAGGGGGGCAAGCAG   70948        C  A   TCTA
                                GATGGCA GG GCG    GGCAG
                                ||||||| || |||    |||||
                                CTACCGT CC CGT    TCGTC
                                     C  C  _____
GAM3120 LOC58512  3' TGGGGCGGGCTCCTAGGCAGG  70949     CA   A  GT
                                TGG  CGG GC  CTAGGCAGG
                                |||  ||| ||  |||||||||
                                ACC  GCC CG  GATCCGTCC
                                  CC   _  AG
GAM3121 NEBL     3' GTGGAAAGTGGAAAAGTTG    70952        _____
                                GTGGAAA    AGAAGTTG
                                |||||||    ||||||||
                                CACCTTT    TTTTCAAC
                                     CACC
GAM3121 KIAA1155 3' TGTAAAAAAAGAAGTTGC     70953          _
                                TGTGGAAAA GAAGTTGC
                                ||||||||| ||||||||
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                                ACATTTTTT CTTCAACG
                                     T
GAM3121  KIAA1260  3'  TGTAGGAAAGAAATGTTGC   70954      A    __
                                TGTGG AAAGAA  GTTGC
                                ||||| ||||||  |||||
                                ACATC TTTCTT  CAACG
                                   C     TA
GAM3121  KLHL4     3'  TGTAGAAATTCTAAAGTTG   70955       A___
                                TGTGGAAA   GAAGTTG
                                ||||||||   |||||||
                                ACATCTTT   TTTCAAC
                                     AAGA
GAM3121  TRF4-2    3'  TGGGAAAAAACGCAGTTGC   70956   T     ___
                                TG GGAAAAGA   AGTTGC
                                || ||||||||   ||||||
                                AC CCTTTTTT   TCAACG
                                 _       GCG
GAM3121  LOC145608 3'  TGTAGAAAAAAGAGGTTG    70957       __  A
                                TGTGGAAA  AGA GTTG
                                ||||||||  ||| ||||
                                ACATCTTT  TCT CAAC
                                     TT   C
GAM3121  LOC147299 3'  TGTGGAAATAAAATGTTGC   70958       _   _
                                TGTGGAAA AGAA GTTGC
                                |||||||| |||| |||||
                                ACACCTTT TTTT CAACG
                                     A    A
GAM3121  LOC157278 3'  TATGGAAATAAGCAGTTGC   70959       __ A
                                TGTGGAAA  AG AGTTGC
                                ||||||||  || ||||||
                                ATACCTTT  TC TCAACG
                                     AT  G
GAM3122  FZD10     3'  TGTGGAAATCATTTGTT     70962        T  AAA
                                TGTGGAAAT CA   TTGTT
                                ||||||||| ||   |||||
                                ACACCTTTA GT   AACAA
                                     _ A__
GAM3122  SRRM1     3'  TGTGGTAGTTCAAAACAGTGGT 70963      AAA      T  T
              C                  TGTGG   TTCAAAAT GT GTC
                                |||||   |||||||| || |||
                                ACACC   AAGTTTTG CA CAG
                                   ATC       T  C
GAM3122  TGFB3     5'  TGTAGCGCTGGGATTGTTGTCC 70964      AAATTCAAA
                                TGTGG        ATTGTTGTCC
                                |||||        ||||||||||
                                ACATC        TAACAACAGG
                                   GCGACCC__
GAM3122  CCT6B     3'  TGTAGAAATTCAGAATGGCT   70965          A   T
                                TGTGGAAATTCA AAT GTT
                                |||||||||||| ||| |||
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                                ACATCTTTAAGT TTA CGA
                                      C   C
GAM3122  KIAA0202  3'  ATGGAAATTTAAATTGTT    70966        CA
                                GTGGAAATT  AAATTGTT
                                |||||||||  ||||||||
                                TACCTTTAA  TTTAACAA
                                   A_
GAM3122  MRPL10    3'  TGTAGAAATTCAGGACGCGGTC 70967          AAAT   T
                                TGTGGAAATTCA    TGT GTC
                                ||||||||||||    ||| |||
                                ACATCTTTAAGT    GCG CAG
                                      CCT_   C
GAM3122  PRO1600   3'  TGTGGAAGGTTAAATTGTT    70968       ATTCA
                                TGTGGAA    AAATTGTT
                                |||||||    ||||||||
                                ACACCTT    TTTAACAA
                                    CCAA_
GAM3122  TP53INP1  3'  TGTGGAAATATAAAGCCTATC  70969        TC   A_
                                TGTGGAAAT  AAA  TTGTT
                                |||||||||  |||  |||||
                                ACACCTTTA  TTT  GATAG
                                      TA   CG
GAM3122  TP53INP1  3'  TGTGGAAATATAAAGCCTATC  70969        TC   A_
                                TGTGGAAAT  AAA  TTGTT
                                |||||||||  |||  |||||
                                ACACCTTTA  TTT  GATAG
                                      TA   CG
GAM3122  LOC115509 3'  TGTGGAAATTGAAACCCTGTC  70970         C   ATTG
                                TGTGGAAATT AAA    TTGTC
                                |||||||||| |||    |||||
                                ACACCTTTAA TTT    GACAG
                                      C   GG__
GAM3122  LOC137964 5'  TGTGGAAATTAAATAACTGTT  70971         C  _
                                TGTGGAAATT AA AATTGTT
                                |||||||||| || |||||||
                                ACACCTTTAA TT TTGACAA
                                      T  A
GAM3122  LOC151195 3'  TGTGGAGTATAATCCTTGTTGT 70972       AATTCAAAA
            CC                    TGTGGA        TTGTTGTCC
                                |||||||        |||||||||
                                ACACCT        AACAACAGG
                                   CATATTAGG
GAM3122  LOC202781 3'  TGGGAAATTCATTTGTT     70973    T       AAA
                                TG GGAAATTCA   TTGTT
                                || |||||||||   |||||
                                AC CCTTTAAGT   AACAA
                                 _       A__
GAM3122  LOC203413 5'  TGGGAAGTTCTGTGTTGTC    70974    T   A   AAAAT
                                TG GGAA TTC    TGTTGTC
                                || |||| |||    |||||||
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                                AC CCTT AAG    ACAACAG
                                 _   C  AC___
GAM3122  LOC253985 5'  TGCGGAAGTTCATTGT     70975       A   AAATTG
                                TGTGGAA TTCA    TTGT
                                ||||||| ||||    ||||
                                ACGCCTT AAGT    AACA
                                   C  _______
GAM3122  LOC255082 5'  TGGGGAAGTTTCTTGTTGTCC  70976    T   A_  AAAA
                                TG GGAA  TTC   TTGTTGTCC
                                || ||||  |||   |||||||||
                                AC CCTT  AAG   AACAACAGG
                                 C   CA  ____
GAM3123  PLS3     3'  TAAGGTACATTTTTCTTCTA   70979       _     CA
                                TAAGGTAC TTTTTCT  TA
                                |||||||| |||||||  ||
                                ATTCCATG AAAAAGA  AT
                                     T      AG
GAM3123  PELI1    3'  TAAGGTATTTTCTATAATAAA  70980       CT    C
                                TAAGGTA  TTTTCT ATAATAAA
                                |||||||  ||||||| ||||||||
                                ATTCCAT  AAAAGA TATTATTT
                                   __    _
GAM3123  LOC121227 3'  TAAGATACTTTTTTGCATAA   70981          CT
                                TAAGGTACTTTTT  CATAA
                                ||||||||||||  |||||
                                ATTCTATGAAAAA  GTATT
                                      AC
GAM3123  LOC145786 3'  GGCCTTTCTCATAAT      70982     ACT
                                GGT   TTTTCTCATAAT
                                |||   ||||||||||||
                                CCG   GAAAGAGTATTA
                                  ___
GAM3123  LOC149650 3'  GGTACTTTTTTCTCTTAA    70983         _  A
                                GGTACTTTTT CTC TAA
                                |||||||||| ||| |||
                                CCATGAAAAA GAG ATT
                                     A  A
GAM3123  LOC222223 3'  CAAGGTACTTGACCATGTGATA 70984         TT  TCATA
           A                     TAAGGTACTT  TC    ATAA
                                ||||||||||  ||    ||||
                                GTTCCATGAA  GG    TATT
                                     CT  TACAC
GAM3124  FLJ13373  3'  TTTAAACATGGAAATGAT    70987          TTTT
                                TTTAAACATGGA   TGAT
                                ||||||||||||   ||||
                                AAATTTGTACCT   ACTA
                                      TT__
GAM3124  FLJ13456  3'  TTTAAACATAAAACTTGAT   70988          TT
                                TTTAAACATGGA  TTTGAT
                                ||||||||||||  ||||||
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                                AAATTTGTATTT  GAACTA
                                      T_
GAM3124  LOC163087 3'  TAACTATTAGACATGATTTTTG 70989      _  A    G
                                TAACT TTA ACATG ATTTTTG
                                ||||| ||| ||||| |||||||
                                ATTGA AAT TGTAC TAAAAAC
                                   T  C    _
GAM3125  ADCY9    3'  GCGGGTGGGCAATGGGGGGTG  70992     T   T___
                                GTG GTGG   TGGGGGGTG
                                ||| ||||   |||||||||
                                CGC CACC   ACCCCCCAC
                                  C   CGTT
GAM3125  ADORA2A  3'  GAGAGTGGTGTGTGGGTGGC  70993    A   T  GT   G
                                GA AGTG GTG  TGGG GGT
                                || |||| |||  |||| |||
                                CT TCAC CAC  ACCC CCG
                                 C   _  AC   A
GAM3125  HHLA1    5'  GAAAATTTTTGGGGGGTG    70994       GTGTGG
                                GAAAGT     TTGGGGGGTG
                                ||||||     ||||||||||
                                CTTTTA     AACCCCCCAC
                                   AA____
GAM3125  LENG4    5'  GAAGGTGGGTGGGCTGGGTGGT 70995     A  T   _    G
                                GAA GTG GTGG TTGGG GGT
                                ||| ||| |||| ||||| |||
                                CTT CAC CACC GACCC CCA
                                  C  C   C    A
GAM3125  RGS19IP1  3'  GAAAGTGGTGGAGGCGGGGGTG 70996       T   TTG_
                                GAAAGTG GTGG   GGGGGTG
                                ||||||| ||||   |||||||
                                CTTTCAC CACC   CCCCCAC
                                    _   TCCG
GAM3125  SORCS1   3'  GAAAGTGTTGCTTGGGTGGT  70997       G  G   G
                                GAAAGTGT TG TTGGG GGT
                                |||||||| || ||||| |||
                                CTTTCACA AC AACCC CCA
                                     _ G    A
GAM3125  BAT8     3'  GGAATGTGTGAAAGGGTGGT  70998   A      TT  G
                                A AGTGTGTGG  GGG GGT
                                | |||||||||  ||| |||
                                C TTACACACT  CCC CCA
                                 C       TT  A
GAM3125  CXorf1   3'  GAGAGTGAGTAGTAGGGGGTG  70999    A   T   T
                                GA AGTG GTGGT GGGGGGTG
                                || |||| ||||| ||||||||
                                CT TCAC CATCA TCCCCCAC
                                 C   T   _
GAM3125  CYP2S1   3'  GTGTGTGGACATCGGTGGT   71000       ___   GG
                                GTGTGTGG   TTGG  GGT
                                ||||||||   ||||  |||
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                                CACACACC  AGCC  CCA
                                    TGT   A_
GAM3125 EFNA5    5' GCGGTGGGATGGGGGGTGA   71001    T   T_
                                GTG GTGG  TGGGGGGTGA
                                ||| ||||  ||||||||||
                                CGC CACC  ACCCCCCACT
                                  _   CT
GAM3125 FLJ10213 3' AGTGTGATGGTTGATCCTGGT 71002      _     GG__
                                AGTGTG TGGTTGG   GGT
                                |||||| |||||||   |||
                                TCACAC ACCAACT   CCA
                                   T     AGGA
GAM3125 FLJ11320 3' GGAGGGTGTGGTGAAGGGTG  71003   A  T     T
                                A AG GTGTGGT GGGGGGTG
                                | || ||||||| ||||||||
                                C TC CACACCA CTTCCCAC
                                 C  C     _
GAM3125 FLJ22477 3' AAAGTGCTGGGGGGTG     71004       GTGGT
                                AAAGTGT   TGGGGGGTG
                                |||||||   |||||||||
                                TTTCACG   ACCCCCCAC
                                    _____
GAM3125 KIAA0339 3' GTGGTGGGCAGGGGTGAC   71005    T   TTG
                                GTG GTGG  GGGGGTGAC
                                ||| ||||  |||||||||
                                CAC CACC  TCCCCACTG
                                  _   CG_
GAM3125 KIAA0555 3' GAAGGTGTGTGTTGGAG    71006    A     G
                                GAA GTGTGTG TTGGGG
                                ||| ||||||| ||||||
                                CTT CACACAC AACCTC
                                  C     _
GAM3125 KIAA0773 3' GAAGGTGTGTGGTGGGGG   71007    A       T
                                GAA GTGTGTGGT GGGGG
                                ||| ||||||||| |||||
                                CTT CACACACCA CCCCC
                                  C       _
GAM3125 KIAA1096 3' GGAGGGTGCAGGGGGTG    71008   A  T   GGTT
                                A AG GTGT   GGGGGGTG
                                | || ||||   ||||||||
                                C TC CACG   TCCCCCAC
                                 C  C   ____
GAM3125 KIAA1813 5' GAGAGTGGTGGGAGCCTGGGTG 71009   A   T   ____    G
           GC                    GA AGTG GTGG   TTGGG GGT
                                || |||| ||||   ||||| |||
                                CT TCAC CACC   GACCC CCG
                                 C   _   CTCG    A
GAM3125 PGLYRP   3' AGTGTGAGGCTTGGGGGTG   71010      T   G
                                AGTGTG GGTT GGGGGTG
                                |||||| |||| |||||||
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                                TCACAC CCGA CCCCCAC
                                   T   A
GAM3125 SIRPB1   3' GAGAGTCTGTGGTTTATGGC  71011    A  G     GGGG
                                GA AGT TGTGGTT   GGT
                                || ||| |||||||   |||
                                CT TCA ACACCAA   CCG
                                 C  G     ATA_
GAM3125 Spir-1   3' GAAGTGTGGAGGGGGGTG   71012    AGT    TT
                                GAA  GTGTGG  GGGGGGTG
                                |||  ||||||  ||||||||
                                CTT  CACACC  CCCCCCAC
                                  ____    T_
GAM3125 TACTILE  5' AGGGTGTGGGTGGGTGGGTG  71013   T    T   _
                                AG GTGTGG TGGG GGGTG
                                || |||||| |||| |||||
                                TC CACACC ACCC CCCAC
                                 C    C   A
GAM3125 TUB      3' AGTGTGTGTTGATCTCGTG   71014       G   GGG_
                                AGTGTGTG TTGG   GTG
                                |||||||| ||||   |||
                                TCACACAC AACT   CAC
                                     _   AGAG
GAM3125 LOC150135 3' GAGAGTGTGGGCCAGGTGA   71015    A    T   GGG
                                GA AGTGTG GGTT   GGGTGA
                                || |||||| ||||   ||||||
                                CT TCACAC CCGG   TCCACT
                                 C    _   ___
GAM3125 LOC150372 5' AGTGTATGGATAGGTGA    71016        TTGGG
                                AGTGTGTGG    GGGTGA
                                |||||||||    ||||||
                                TCACATACC    TCCACT
                                     TA___
GAM3125 LOC197257 5' AGGGTGTGAGCACTGGGTGGC  71017    T   _ TG_  _
                                AG GTGTG GT   GGG GGT
                                || ||||| ||   ||| |||
                                TC CACAC CG   CCC CCG
                                 C    T  TGA   A
GAM3125 LOC205095 3' GTGGGTGCCTTGGGGGTG    71018    T  G  G
                                GTG GTG TT GGGGGTG
                                ||| ||| || |||||||
                                CAC CAC GA CCCCCAC
                                  C   G  A
GAM3125 LOC222031 3' GAAAGTTGGGGTGGGGGTGAC  71019       G  T   TG
                                GAAAGT TG GGT  GGGGGGTGAC
                                |||||| || |||  |||||||||
                                CTTTCA AC CCA  CCCCCACTG
                                    _ C  __
GAM3125 LOC253196 3' GAAAATCGACTTGGGGGGTGA  71020       G  TGG
                                GAAAGT TG   TTGGGGGGTGA
                                |||||| ||   ||||||||||
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                                CTTTTA GC   AACCCCCCACT
                                   _ TG_
GAM3125 LOC90249 3' GTGTGTGGTTGGGGGGTG    71021
                                GTGTGTGGTTGGGGGGTG
                                ||||||||||||||||||
                                CACACACCAACCCCCCAC

GAM3125 LOC90917 5' ATGTGTGGGGGGGGTG      71022       TTG
                                GTGTGTGG   GGGGGTG
                                ||||||||   |||||||
                                TACACACC   CCCCCAC
                                    ___
GAM3126 AGTR1    3' TCATCGAGTTTCTGACATTGTT 71025     C      CAAAAG
                                TCA TGAGTTTC     ATTGTT
                                ||| ||||||||     ||||||
                                AGT GCTCAAAG     TAACAA
                                  A       ACTG__
GAM3126 AGTR1    3' TCATCGAGTTTCTGACATTGTT 71025     C      CAAAAG
                                TCA TGAGTTTC     ATTGTT
                                ||| ||||||||     ||||||
                                AGT GCTCAAAG     TAACAA
                                  A       ACTG__
GAM3126 AGTR1    3' TCATCGAGTTTCTGACATTGTT 71025     C      CAAAAG
                                TCA TGAGTTTC     ATTGTT
                                ||| ||||||||     ||||||
                                AGT GCTCAAAG     TAACAA
                                  A       ACTG__
GAM3126 AGTR1    3' TCATCGAGTTTCTGACATTGTT 71025     C      CAAAAG
                                TCA TGAGTTTC     ATTGTT
                                ||| ||||||||     ||||||
                                AGT GCTCAAAG     TAACAA
                                  A       ACTG__
GAM3126 AGTR1    3' TCATCGAGTTTCTGACATTGTT 71025     C      CAAAAG
                                TCA TGAGTTTC     ATTGTT
                                ||| ||||||||     ||||||
                                AGT GCTCAAAG     TAACAA
                                  A       ACTG__
GAM3126 COCH     3' TCCTGAGTTTCTAAGA      71026    A       CAA
                                TC CTGAGTTTC   AAGA
                                || |||||||||   ||||
                                AG GACTCAAAG   TTCT
                                  _       A__
GAM3126 CSF2     3' TCCTGAGTTTCTAGCTCTTGTT 71027    A       CAAAAGA
                                TC CTGAGTTTC      TTGTT
                                || |||||||||      |||||
                                AG GACTCAAAG      AACAA
                                  _       ATCGAG_
GAM3126 HAS2     3' TCCTTGAGTTTCCAAAATCCT  71028    AC          GA
                                TC  TGAGTTTCCAAAA  TT
                                ||  ||||||||||||  ||
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                                AG  ACTCAAAGGTTTT  GA
                                 GA          AG
GAM3126  PDE7A    3'  TAAATTCCAAGAGATTGTT   71029       T   A
                                TGAGTT CCAA AGATTGTT
                                ||||||| |||| ||||||||
                                ATTTAA GGTT TCTAACAA
                                   _   C
GAM3126  PTX3     3'  CACTGAGTTTTCAGACC     71030         CCAAA
                                CACTGAGTTT    AGATT
                                ||||||||||    |||||
                                GTGACTCAAA    TCTGG
                                     AG___
GAM3126  RERE     3'  TCACTAAGTTTCTGGGGGACT  71031          CAAAA
                                TCACTGAGTTTC    GATT
                                ||||||||||||    ||||
                                AGTGATTCAAAG    CTGA
                                      ACCCC
GAM3126  ARGBP2   5'  TCCTGAGTTTCCATTCACTGTT 71032    A        AAAG
                                TC CTGAGTTTCCA   ATTGTT
                                || ||||||||||   ||||||
                                AG GACTCAAAGGT   TGACAA
                                 _        AAG_
GAM3126  ATP10D   3'  TGGTCTCTGGAAGATTGT    71033    A    CAA
                                TG GTTTC   AAGATTGT
                                || |||||   ||||||||
                                AC CAGAG   TTCTAACA
                                 _    ACC
GAM3126  FBP17    3'  TCACTGCGTTTCTAAGA     71034       A    CAA
                                TCACTG GTTTC   AAGA
                                |||||| |||||   ||||
                                AGTGAC CAAAG   TTCT
                                   G    A__
GAM3126  KIAA0993 3'  TCACTAAGTTTCTGAAAATGTT 71035          CA   AT
                                TCACTGAGTTTC  AAAG  TGTT
                                ||||||||||||  ||||  ||||
                                AGTGATTCAAAG  TTTT  ACAA
                                      AC   __
GAM3126  KIAA1918 3'  ACTGAGAAAAGATTGT      71036       TTTCC
                                ACTGAG    AAAAGATTGT
                                ||||||    ||||||||||
                                TGACTC    TTTTCTAACA
                                     _____
GAM3126  KRTAP1-1 3'  ACTGGAGTTCAGAAGATTGTT  71037     _   TC  A
                                ACTG AGTT  CA AAGATTGTT
                                |||| ||||  || |||||||||
                                TGAC TCAA  GT TTCTAACAA
                                  C   __ C
GAM3126  OSBPL11  3'  TCACTGAGTTCTCATTGT    71038         TC  AAAGA
                                TCACTGAGTT  CA    TTGT
                                ||||||||||  ||    ||||
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                                AGTGACTCAA  GT    AACA
                                      GA  _____
GAM3126  LOC126302 3'  TCACTGAGTTGCTGGAAAGAT  71039         TCCA_
                                TCACTGAGTT    AAAGAT
                                ||||||||||    ||||||
                                AGTGACTCAA    TTTCTA
                                      CGACC
GAM3126  LOC148171 5'  CACTGAGTCCAAAGAGGTTGTT 71040       TT    _ A
                                CACTGAG  TCCAAA AG TTGTT
                                |||||||  |||||| || |||||
                                GTGACTC  AGGTTT TC AACAA
                                   __     C  C
GAM3126  LOC149124 5'  CACTGAGTCCAAAGAGGTTGTT 71040       TT    _ A
                                CACTGAG  TCCAAA AG TTGTT
                                |||||||  |||||| || |||||
                                GTGACTC  AGGTTT TC AACAA
                                   __     C  C
GAM3126  LOC155006 3'  GCCTCTTCAAGAGATTGTT    71041      __  A
                                GTTTC  CAA AGATTGTT
                                |||||  ||| ||||||||
                                CGGAG  GTT TCTAACAA
                                  AA   C
GAM3126  LOC253805 3'  CACATCTTCAAAAGATTGTT   71042     TGA   C
                                CAC   GTTT CAAAAGATTGTT
                                |||   |||| ||||||||||||
                                GTG   TAGA GTTTTCTAACAA
                                  ___   A
GAM3126  LOC256683 5'  CACTGGGAAGACAAGAAGATTG 71043      AGTTTC  _
            TT                   CACTG     CAA AAGATTGTT
                                |||||     ||| |||||||||
                                GTGAC     GTT TTCTAACAA
                                  CCTTCT   C
GAM3126  LOC51696  3'  TCATTGATTTTCCAAAACAT   71044     C   G       G
                                TCA TGA TTTCCAAAA AT
                                ||| ||| ||||||||| ||
                                AGT ACT AAAGGTTTT TA
                                  A   A       G
GAM3127  ARF3      3'  TGAAGATGGTGGGGAAGGAT   71047        A  AA  C_
                                TGAAGATG TG  GA  GAT
                                |||||||| ||  ||  |||
                                ACTTCTAC AC  CT  CTA
                                     C  CC  TC
GAM3127  ATP8B2    5'  TGAGGATGATGATGTAGGACCA 71048     A       AGACGAT
                                TGA GATGATGA      GACCA
                                ||| ||||||||      |||||
                                ACT CTACTACT      CTGGT
                                  C       ACATC__
GAM3127  BCL2L2    3'  GATGATGAAGGAACAAGGCCA  71049          __   TGA
                                GATGATGAAG  ACGA   CCA
                                ||||||||||  ||||   |||
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                                CTACTACTTC  TGTT   GGT
                                      CT    CC_
GAM3127  DDT      3'  TGAGGATGAAGAAGAGGAT   71050     A    T    C
                                TGA GATGA GAAGA GAT
                                ||| ||||| ||||| |||
                                ACT CTACT CTTCT CTA
                                  C    T    C
GAM3127  KCNS2    3'  TAAAGATGATGGAGAAGA    71051          A   C
                                TGAAGATGATG AGA GA
                                |||||||||||| ||| ||
                                ATTTCTACTAC TCT CT
                                       C   T
GAM3127  POU2F2   3'  TGAAGAGGATGAGGAGGAGAGG 71052       T    A  C  T  __
              CCA                    TGAAGA GATGA GA GA GA  CCA
                                |||||| ||||| || || ||  |||
                                ACTTCT CTACT CT CT CT  GGT
                                    C    C  C  _  CC
GAM3127  PPP1R3D  3'  TGGAGGGTGGTGAAGAACAACC 71053    A  A_  A     CG TG
              A                     TG AG  TG TGAAGA  A  ACCA
                                || ||  || ||||||  |  ||||
                                AC TC  AC ACTTCT  T  TGGT
                                 C  CC  C     __ GT
GAM3127  XRCC5    3'  TGAGGGTGCTGAAGACAGAGGT 71054     AGA  A     _  __
              GAC                    TGA   TG TGAAGAC GA  TGAC
                                |||   || |||||||  ||  ||||
                                ACT   AC ACTTCTG CT  ACTG
                                  CCC  G      T  CC
GAM3127  C1orf16  3'  TGAGGATGATAAGGCGA     71055     A      A A
                                TGA GATGATGA G CGA
                                ||| ||||||||  | |||
                                ACT CTACTATT C GCT
                                  C       _ C
GAM3127  DKFZP434B044 3'  TGGGGATGATAAAGACAGCCA  71056    AA          ATGA
                                TG  GATGATGAAGACG    CCA
                                ||  ||||||||||||    |||
                                AC  CTACTATTTCTGT    GGT
                                 CC           C___
GAM3127  ECG2     3'  TGAAGATGATGATGATGA    71057          AGAC
                                TGAAGATGATGA    GATGA
                                ||||||||||||    |||||
                                ACTTCTACTACT    CTACT
                                       A___
GAM3127  FLJ10097 3'  GAAGATGATGGAATACAGAC   71058         _  G   AT
                                GAAGATGATG AA ACG  GAC
                                |||||||||| || |||  |||
                                CTTCTACTAC TT TGT  CTG
                                       C  A  __
GAM3127  FLJ10514 3'  TGAGGATGATGAAGCAAATG   71059     A        AC
                                TGA GATGATGAAG  GATG
                                ||| ||||||||||  ||||
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                                ACT CTACTACTTC  TTAC
                                  C         GT
GAM3127  FLJ10898  5'  TGAAGATGTGGAGAAGTTCGGC 71060        AT__    A_  A_
              TG                   TGAAGATG    GAAG  CG  TG
                                ||||||||    ||||  ||  ||
                                ACTTCTAC    CTTC  GC  AC
                                    ACCT    AA  CG
GAM3127  FLJ10948  3'  TGAAATGATGAAGGCAATCTGG 71061     A        A  __  A
              CCA                   TGA GATGATGAAG CGA  TG CCA
                                ||| ||||||||||| |||  || |||
                                ACT TTACTACTTC GTT  AC GGT
                                  _        C   AG  C
GAM3127  FLJ14600  5'  TAAAGATGATGGATG       71062           AAGAC
                                TGAAGATGATG     GATG
                                ||||||||||     ||||
                                ATTTCTACTAC     CTAC
                                                _____
GAM3127  FLJ20195  5'  TGAGATGGTGACCTGATGACCA 71063     A    A   AGAC
                                TGA GATG TGA    GATGACCA
                                ||| |||| |||    ||||||||
                                ACT CTAC ACT    CTACTGGT
                                  _    C   GGA_
GAM3127  FLJ20449  3'  TGAAGATGAGTGACAGTGTGTG 71064         _   AGACGA_  A
              GCCA                   TGAAGATGA TGA      TG CCA
                                ||||||||| |||      || |||
                                ACTTCTACT ACT      AC GGT
                                    C   GTCACAC  C
GAM3127  FLJ20452  3'  TAAAGATGATGGCAGTGGCTG  71065          A_  ACGA
                                TGAAGATGATG  AG    TG
                                ||||||||||  ||    ||
                                ATTTCTACTAC  TC    AC
                                      CG  ACCG
GAM3127  KIAA0125  3'  TGAGGGTGGGGAAGACAATTCC 71066     AGA  AT       GA
              A                   TGA   TG  GAAGACGAT  CCA
                                |||   ||  |||||||||  |||
                                ACT   AC  CTTCTGTTA  GGT
                                  CCC  CC        A_
GAM3127  KIAA0298  3'  TGAGGATGATGAAGGGTATGGC 71067     A        ACG   A
              CA                    TGA GATGATGAAG   ATG CCA
                                ||| ||||||||||   ||| |||
                                ACT CTACTACTTC   TAC GGT
                                  C         CCA   C
GAM3127  KIAA0436  3'  TGAAGAGATGAAGACACTG    71068       T        A
                                TGAAGA GATGAAGACG TG
                                ||||||| |||||||||| ||
                                ACTTCT CTACTTCTGT AC
                                    _         G
GAM3127  KIAA0545  3'  TGAAGATGGGAGGAGACAAC   71069         AT  A  C  TG
                                TGAAGATG  GA GA GA  AC
                                ||||||||  || || ||  ||
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                                ACTTCTAC  CT CT CT  TG
                                    C_  C  _  GT
GAM3127  KIAA1058  3'  TGAAGATGTGAAGGGAAT    71070        A    AC
                                TGAAGATG TGAAG  GAT
                                |||||||| |||||  |||
                                ACTTCTAC ACTTC  TTA
                                    _    CC
GAM3127  KIAA1191  5'  TGAAATGATGTGATGAC     71071     A      AAGAC
                                TGA GATGATG    GATGAC
                                ||| |||||||    ||||||
                                ACT TTACTAC    CTACTG
                                  _     A____
GAM3127  LGALS9    3'  TGGGGATGATGAGAGGACC    71072    AA      AGAC  T
                                TG  GATGATGA    GA GACC
                                ||  ||||||||    || ||||
                                AC  CTACTACT    CT CTGG
                                 CC       _____  C
GAM3127  LGALS9    3'  TGGGGATGATGAGAGGACC    71072    AA      AGAC  T
                                TG  GATGATGA    GA GACC
                                ||  ||||||||    || ||||
                                AC  CTACTACT    CT CTGG
                                 CC       _____  C
GAM3127  MMP28     3'  GAAGATGATGGAGCCATCG    71073         A  A  A
                                GAAGATGATG AG CG TG
                                |||||||||| || || ||
                                CTTCTACTAC TC GT GC
                                      C  G  A
GAM3127  SDOS      3'  TGGAGATGATGACAGGATGCCC 71074    A       AGAC    A
              A                  TG AGATGATGA    GATG CCA
                                 || |||||||||    |||| |||
                                 AC TCTACTACT    CTAC GGT
                                  C       GTC_    G
GAM3127  SPEC1     3'  AAGATGATGAGGGTAGCGTGCC 71075         _____  A  A  A
              A                   AAGATGATGA    AG CG TG CCA
                                  ||||||||||    || || || |||
                                  TTCTACTACT    TC GC AC GGT
                                       CCCA  _  _  _
GAM3127  THG-1     3'  TGGGGATGATGAGGAGATG    71076    AA      A  C
                                TG  GATGATGA GA GATG
                                ||  |||||||| || ||||
                                AC  CTACTACT CT CTAC
                                 CC       C  _
GAM3127  LOC120227 5'  TGAAGATACACAAGCGGTG    71077        ATG   A  A
                                TGAAGATG   AAG CG TG
                                ||||||||   ||| || ||
                                ACTTCTAT   TTC GC AC
                                     GTG   _  C
GAM3127  LOC147124 3'  TGGGGATGATGAGAGGACCCCG 71078    AA      A__   GA
              AC                   TG  GATGATGA   GAC  TGAC
                                   ||  ||||||||   |||  ||||
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                                AC  CTACTACT   CTG  GCTG
                                 CC       CTC   GG
GAM3127  LOC148641 5'  TGCAGGTGATGAAGAGGATG   71079    A  A       C
                                TG AG TGATGAAGA GATG
                                || || ||||||||| ||||
                                AC TC ACTACTTCT CTAC
                                 G  C        C
GAM3127  LOC148809 5'  TGAAGATGATGGATTTGAGTGA 71080          AAGAC  _   C
           TCA                    TGAAGATGATG    GA TGA CA
                                ||||||||||     || ||| ||
                                ACTTCTACTAC    CT ACT GT
                                      CTAAA  C   A
GAM3127  LOC149464 3'  TGAGGATGATGATGATGATGATG   71081     A       A  C
                                TGA GATGATGA GA GATG
                                ||| |||||||| || ||||
                                ACT CTACTACT CT CTAC
                                  C       A  A
GAM3127  LOC152313 5'  AGATGATGAGGCAACC      71082         A A GAT
                                AGATGATGA G C   GACC
                                ||||||||| | |   ||||
                                TCTACTACT C G   TTGG
                                     _ C ___
GAM3127  LOC205952 5'  TGAAGATGGGAGGACACTG    71083        AT  A    A
                                TGAAGATG  GA GACG TG
                                ||||||||  || |||| ||
                                ACTTCTAC  CT CTGT AC
                                     C_  C    G
GAM3127  LOC222159 5'  GATGATGATGGAGATAAACA   71084        A_  C    C
                                GATGATGA  GA GATGA CA
                                ||||||||  || ||||| ||
                                CTACTACT  CT CTATT GT
                                     AC  _    T
GAM3127  LOC255313 5'  GACCACGGTGAAGACGGTGACC 71085    AG   A       A
           A                     GA  ATG TGAAGACG TGACCA
                                ||  ||| |||||||| ||||||
                                CT  TGC ACTTCTGC ACTGGT
                                 GG  C       C
GAM3127  LOC257357 5'  GAGAGGTGGACGACGACCA    71086    T  TGAA
                                GA GA    GACGATGACCA
                                || ||    ||||||||||
                                CT CT    CTGCTGCTGGT
                                 _  CCAC
GAM3128  COVA1     3'  AGAGATGCATCAGTGAGCA    71089          AA   TC
                                GGAGATGCATCA  TGA  GCA
                                ||||||||||||  |||  |||
                                TCTCTACGTAGT  ACT  CGT
                                      C_   __
GAM3128  FLJ23058  5'  TAGGAGATGCACTGAAAGC    71090          CAAA   TC
                                TAGGAGATGCAT    TGA  GC
                                ||||||||||||    |||  ||
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                                ATCCTCTACGTG   ACT  CG
                                      ____  TT
GAM3128 KIAA1909 5' TAGGAGATGTGTTGTTCTGCA 71091        CATCAAA  A  _
                                TAGGAGATG      TG TC GCA
                                |||||||||      || || |||
                                ATCCTCTAC      AC AG CGT
                                     ACA____  A  A
GAM3128 LOC154877 3' GGAGATGCATCTGTGCCTGCA 71092         AAA  ATC
                                GGAGATGCATC   TG   GCA
                                ||||||||||  ||  |||
                                CCTCTACGTAG   AC   CGT
                                      AC_  GGA
GAM3128 LOC203257 5' CAGGAGATGCATCAGCTG    71093           AA
                                TAGGAGATGCATCA  TG
                                ||||||||||||| ||
                                GTCCTCTACGTAGT  AC
                                       CG
GAM3128 LOC92710  3' TAGGAGATGGTCAAGGGAGGGC 71094        CA   AT  TC
            A                    TAGGAGATG  TCAA  GA  GCA
                                |||||||||  ||||  ||  |||
                                ATCCTCTAC  AGTT  CT  CGT
                                     C_   CC  CC
GAM3129 ATP11A   3' ACGTTTGTAGTGAATG     71097    T    ATCTAT
                                AC TTTGT     GGTGAATG
                                || |||||     ||||||||
                                TG AAACA     TCACTTAC
                                 C    _______
GAM3129 CLCA3    3' CTTTTGTATCGTCCATGT    71098         TATG  GA
                                CTTTTGTATC    GT  ATGT
                                ||||||||||   ||  ||||
                                GAAAACATAG    CA  TACA
                                      _____ GG
GAM3129 C3orf4   3' GTATTTAGTGGTGAATGT    71099      C  _
                                GTAT TA TGGTGAATGT
                                |||| || ||||||||||
                                CATA AT ACCACTTACA
                                  A  C
GAM3129 D123     3' TTTTTTCCCCAGGTGAATGTA  71100      GTA    T
                                TTTT   TCTA GGTGAATGTA
                                ||||   |||| ||||||||||
                                AAAA   GGGT CCACTTACAT
                                  AAG    _
GAM3129 KIAA0831  5' CTTTTGTAACTATGGAACAT   71101         T     TGA
                                CTTTTGTA CTATGG   AT
                                |||||||| ||||||   ||
                                GAAAACAT GATACC   TA
                                     T     TTG
GAM3129 KIAA1058 3' TCTTGTATTCAACCTGAATGT  71102         C  TGG
                                TTTTGTAT TA   TGAATGT
                                |||||||| ||   |||||||
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                                AGAACATA GT   ACTTACA
                                    A  TGG
GAM3129  LOC154789 5'  ACTTTTGTTCTGTGGTG     71103         A   A
                                ACTTTTGT TCT TGGTG
                                |||||||| ||| |||||
                                TGAAAACA AGA ACCAC
                                    _   C
GAM3129  LOC163231 5'  TTCGCACTGTGGTGAATGT    71104        T  A
                                TTTGTA CT TGGTGAATGT
                                |||||| || ||||||||||
                                AAGCGT GA ACCACTTACA
                                   _ C
GAM3129  LOC196283 3'  ACTTTTTGTTGATGAATGT    71105        _  ATCTA
                                ACTTTT GT     TGGTGAATGT
                                |||||| ||     ||||||||||
                                TGAAAA CA     ACTACTTACA
                                   A ______
GAM3129  LOC91907  3'  TTTTGTACTTTGATGAAGAATG 71106        T  A     ___
             T                   TTTTGTA CT TGGTGA   ATGT
                                |||||||| || |||||||   ||||
                                AAAACAT GA ACTACT   TACA
                                    _ A     TCT
GAM3130  KCNJ16    3'  TATACCTATATATTTTACTTGT 71109        AT__  A
            ATTT                  TATACT    TG TTTACTTGTATTT
                                |||||||   || ||||||||||||
                                ATATGG    AT AAATGAACATAAA
                                   ATAT  A
GAM3130  NEK4      3'  TACTATTCAAGACTTGTATTT  71110        GATTT
                                TACTATT     ACTTGTATTT
                                |||||||     ||||||||||
                                ATGATAA     TGAACATAAA
                                    GTTC_
GAM3130  AK000009  3'  TATACTATTGAATTTGTA     71111          TTTAC
                                TATACTATTGA     TTGTA
                                ||||||||||     |||||
                                ATATGATAACT     AACAT
                                      TA___
GAM3130  CLCA4     3'  CTCTCCTTTACTTGTATTT    71112     ATTGA
                                CT     TTTACTTGTATTT
                                ||     ||||||||||||
                                GA     AAATGAACATAAA
                                 GAGG_
GAM3130  DKFZP564D166 3'  CATACTATGACTTGTATT     71113         T  TTTA
                                TATACTAT GA    CTTGTATT
                                |||||||| ||    ||||||||
                                GTATGATA CT    GAACATAA
                                   _ _____
GAM3130  SEMA3E    3'  ATTGATTTATTTGTATTT     71114          C
                                ATTGATTTA TTGTATTT
                                ||||||||| ||||||||
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                                TAACTAAAT AACATAAA
                                     A
GAM3131  TRHDE    3'  TGTGCAGTGTACAACATACT   71117     ATTTTCA
                                TGTG      TACAACATACT
                                ||||      ||||||||||
                                ACAC      ATGTTGTATGA
                                  GTCAC__
GAM3131  E2F6     3'  TTGTGATATATGACATACT    71118       TTTC   CA
                                TTGTGAT    ATA  ACATACT
                                |||||||    |||  |||||||
                                AACACTA    TAT  TGTATGA
                                    ____   AC
GAM3131  HSPC019  3'  TTGTGATGTACAACATA     71119       TTTCA
                                TTGTGAT     TACAACATA
                                |||||||     |||||||||
                                AACACTA     ATGTTGTAT
                                    C____
GAM3131  LOC143497 5'  TTGTGATTTTTGCACGAC    71120         CA   A
                                TTGTGATTTT  TAC AC
                                ||||||||||  ||| ||
                                AACACTAAAA  GTG TG
                                     AC   C
GAM3131  LOC168667 3'  CTGGTGTATTTATACAACAT   71121    T   _    TC
                                CT GTG ATTT  ATACAACAT
                                || ||| ||||  |||||||||
                                GA CAC TAAA  TATGTTGTA
                                 C   A   __
GAM3132  DMD      5'  TTTTGCTGATTTCCCTGT     71124         C_   A
                                TTTTGCTGG  TCC TTGT
                                |||||||||  ||| ||||
                                AAAACGACT  AGG GACA
                                     AA   _
GAM3132  DMD      5'  TTTTGCTGATTTCCCTGT     71124         C_   A
                                TTTTGCTGG  TCC TTGT
                                |||||||||  ||| ||||
                                AAAACGACT  AGG GACA
                                     AA   _
GAM3132  FABP2    3'  TTTTCTGGCTGAGCATATATTA 71125      G     CCATT
                                TTTT CTGGCT    GTATATTA
                                |||| ||||||    ||||||||
                                AAAA GACCGA    TATATAAT
                                  _     CTCG_
GAM3132  IFRD1    3'  TTTTGCTGTCTTCATAAATAAA 71126        G  C   T_   T
            TTA                   TTTTGCTG CT CAT  GTA ATTA
                                ||||||||  || |||  ||| ||||
                                AAAACGAC GA GTA  TAT TAAT
                                     A  A   TT   T
GAM3132  LOC121512 5'  TTTTGCTGGCCTGTTCCCATT  71127           _____
                                TTTTGCTGGCT    CCATT
                                ||||||||||    |||||
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                                AAAACGACCGG    GGTAA
                                     ACAAG
GAM3132  LOC162333 5'  TTGCTGGCTCCATTGCAT    71128
                                TTGCTGGCTCCATTGTAT
                                ||||||||||||||||||
                                AACGACCGAGGTAACGTA

GAM3132  LOC200163 3'  TTTTGCTGATTCCTTTGT    71129        GC   A
                                TTTTGCTG  TCC TTGT
                                ||||||||  ||| ||||
                                AAAACGAC  AGG AACA
                                     TA   A
GAM3133  GFRA1     3'  AATGTAGGCTGAAATTTATATC 71132       ATATAAT
           AT                    AATGTA      ATTTATATCAT
                                ||||||      ||||||||||
                                TTACAT      TAAATATAGTA
                                   CCGACTT
GAM3133  EAT2      3'  AATGTAATAAAACATAAGATAT 71133         T    TT_
           CAT                    AATGTAATA AATAT   ATATCAT
                                |||||||| |||||   |||||||
                                TTACATTAT TTGTA   TATAGTA
                                     T    TTC
GAM3133  KIAA1280  5'  GCAAAATATTTATATCA     71134      TAT
                                GTAA   AATATTTATATCA
                                ||||   ||||||||||||
                                CGTT   TTATAAATATAGT
                                   ___
GAM3133  PRO1770   5'  TGTAATATAAATATTTACACC  71135         _
                                TGTAATATAA TATTTATATC
                                |||||||||| ||||||||||
                                ACATTATATT ATAAATGTGG
                                     T
GAM3133  SLC5A7    3'  AATGCAATGTAATATTCAC    71136        A
                                AATGTAAT TAATATTTAT
                                |||||||| ||||||||||
                                TTACGTTA ATTATAAGTG
                                     C
GAM3134  DKFZP434B168 3'  TCAATGAATAAATGAACTA    71139           A
                                TTAATGAATAAAT AATTA
                                |||||||||||| |||||
                                AGTTACTTATTTA TTGAT
                                       C
GAM3134  FLJ10724  3'  TTAATGAATGAATAAACCTATT 71140         A      TA
                                TTAATGAAT AATAAAT  ATT
                                ||||||||| |||||||  |||
                                AATTACTTA TTATTTG  TAA
                                     C      GA
GAM3134  RBT1      3'  GAATAGATAAATTAATTCA    71141       A
                                GAATA ATAAATTAATTCA
                                ||||| ||||||||||||
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                                CTTAT TATTTAATTAAGT
                                   C
GAM3135  AXUD1    5'  CGTCCCGGCCGGGGACGCCCC  71144    AGGA
                                CG   GGCCGGGGACGCCCC
                                ||   ||||||||||||||
                                GC   CCGGCCCCTGCGGGG
                                 AGGG
GAM3135  COL6A2   5'  CCGAGGAGGCTCCGCTCC    71145        CGGGGA  _
                                CCGAGGAGGC     CGC CC
                                ||||||||||     ||| ||
                                GGCTCCTCCG     GCG GG
                                      AG____   A
GAM3135  COL6A2   5'  CCGAGGAGGCTCCGCTCC    71145        CGGGGA  _
                                CCGAGGAGGC     CGC CC
                                ||||||||||     ||| ||
                                GGCTCCTCCG     GCG GG
                                      AG____   A
GAM3135  COL9A3   3'  CCGAGGGGCAGCCAGGGGCGCT 71146      A__      A  _
            CC                    CCGAGG   GGCCGGGG CGC CC
                                ||||||   |||||||| ||| ||
                                GGCTCC   TCGGTCCC GCG GG
                                   CCG      C   A
GAM3135  DMD      5'  CGAGGAGGTCTAGGAGGCGCC  71147       CC__   A
                                CGAGGAGG   GGGG CGCC
                                ||||||||   |||| ||||
                                GCTCCTCC   CCTC GCGG
                                     AGAT   C
GAM3135  DMD      5'  CGAGGAGGTCTAGGAGGCGCC  71147       CC__   A
                                CGAGGAGG   GGGG CGCC
                                ||||||||   |||| ||||
                                GCTCCTCC   CCTC GCGG
                                     AGAT   C
GAM3135  DUSP3    3'  GGAGCAAGGACGCCCC     71148     GC
                                GGAG  CGGGGACGCCCC
                                ||||  ||||||||||||
                                CCTC  GTTCCTGCGGGG
                                  __
GAM3135  EMX2     5'  CCGAGGAGCGGGCGCCC     71149       GC   GA
                                CCGAGGAG  CGGG  CGCCC
                                ||||||||  ||||  |||||
                                GGCTCCTC  GCCC  GCGGG
                                   __   __
GAM3135  ENG      3'  CCGAGGAGGCCGGGGCAGCC  71150           AC
                                CCGAGGAGGCCGGGG  GCC
                                ||||||||||||||  |||
                                GGCTCCTCCGGCCCC  CGG
                                      GT
GAM3135  EP300    5'  CACCGAGGAGGCCCCGCTCC  71151          GGGGA  _
                                TACCGAGGAGGCC    CGC CC
                                ||||||||||||     ||| ||
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                                GTGGCTCCTCCGG    GCG GG
                                      G____  A
GAM3135  FCN2    3'  CCGGGGGGGCCAGGCCGACGTT 71152    A  A     __   CC
              CC                  CCG GG GGCCGGG  GACG  CC
                                  ||| || |||||||  ||||  ||
                                  GGC CC CCGGTCC  CTGC  GG
                                    C  C      GG    AA
GAM3135  FCN2    3'  CCGGGGGGGCCAGGCCGACGTT 71152    A  A     __   CC
              CC                  CCG GG GGCCGGG  GACG  CC
                                  ||| || |||||||  ||||  ||
                                  GGC CC CCGGTCC  CTGC  GG
                                    C  C      GG    AA
GAM3135  LCN1    3'  GAGGAGCCAAGGTGTCCC    71153       G     ACG
                                  GAGGAG CCGGGG   CCC
                                  ||||||  ||||||   |||
                                  CTCCTC GGTTCC   GGG
                                     _     ACA
GAM3135  LCN1    3'  GAGGAGCCAAGGTGTCCC    71153       G     ACG
                                  GAGGAG CCGGGG   CCC
                                  ||||||  ||||||   |||
                                  CTCCTC GGTTCC   GGG
                                     _     ACA
GAM3135  LIMK1   5'  CCGGGCCGGGCCGGGGGCGCC  71154    A  A__      A
                                  CCG GG   GGCCGGGG CGCC
                                  |||  ||   |||||||| ||||
                                  GGC CC   CCGGCCCC GCGG
                                    _ GGC       C
GAM3135  LIMK1   5'  CCGGGCCGGGCCGGGGGCGCC  71154    A  A__      A
                                  CCG GG   GGCCGGGG CGCC
                                  |||  ||   |||||||| ||||
                                  GGC CC   CCGGCCCC GCGG
                                    _ GGC       C
GAM3135  PTGS2   5'  GAGGAGTTCCTGGACGTGCTCC 71155      G_  GG   __  _
                                  GAGGAG  CC  GGAC  GC CC
                                  ||||||  ||  ||||  || ||
                                  CTCCTC  GG  CCTG  CG GG
                                     AA  A_   CA  A
GAM3135  SEPN1   3'  CCGGGGAAGCCACTGCCCC   71156    A      GGGAC
                                  CCG GGAGGCCG    GCCCC
                                  |||  ||||||||    |||||
                                  GGC CCTTCGGT    CGGGG
                                    C       GA___
GAM3135  TJP1    5'  CGAGGACGGGCTGGGGGTGTCC 71157       __  C   ACG_
                                  CGAGGA  GGC GGGG   CC
                                  ||||||  ||| ||||   ||
                                  GCTCCT  CCG CCCC   GG
                                     GC   A   CACA
GAM3135  C5orf6  3'  GAGGAGGCTGACTCAACCCC  71158       CGGG  ___
                                  GAGGAGGC   GAC   GCCCC
                                  ||||||||   |||   |||||
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                                CTCCTCCG   CTG  TGGGG
                                    A___   AGT
GAM3135 CART     3' GAGGAGAATGGACGCCCC    71159       CCGG
                                GAGGAGG   GGACGCCCC
                                |||||||   |||||||||
                                CTCCTCT   CCTGCGGGG
                                   TA__
GAM3135 DKFZP564I1171 3' CCGGGAAGGCCAGGCCC    71160    A       GGAC
                                CCG GGAGGCCGG   GCCC
                                ||| |||||||||   ||||
                                GGC CTTCCGGTC   CGGG
                                  C       _____
GAM3135 DKFZP564K0322 5' AGACATCGGGGACGCTCC    71161     __       _
                                AGGC  CGGGGACGC CC
                                ||||  ||||||||| ||
                                TCTG  GCCCCTGCG GG
                                   TA        A
GAM3135 FLJ20446  3' TACTGAGGAGCCAGGAGTGTCC 71162    C     G     ACG_
                                TAC GAGGAG CCGGGG   CC
                                ||| |||||| ||||||   ||
                                ATG CTCCTC GGTCCT   GG
                                  A     _     CACA
GAM3135 FLJ20552  3' CGGGGAGGCTGGGGACGCCCC  71163    A     C
                                CG GGAGGC GGGGACGCCCC
                                || |||||| ||||||||||
                                GC CCTCCG CCCCTGCGGGG
                                 C     A
GAM3135 FLJ20640  5' CGAGGAGGCCGTATCGCC    71164          GGGA
                                CGAGGAGGCCG   CGCC
                                ||||||||||   ||||
                                GCTCCTCCGGC   GCGG
                                      ATA_
GAM3135 FLJ21324  5' TACTGGGGAGGCCGCCTCGGGG 71165   CGA      ________  ACGC
            CGC                   C  GGAGGCCG     GGG   C
                                |  ||||||||     |||   |
                                G  CCTCCGGC     CCC   G
                                 ACC      GGAGIII  CGCA
GAM3135 HAPIP    5' CGAGGAGGCCGGAATCAC    71166           A
                                CGAGGAGGCCGGGG CGC
                                |||||||||||||| |||
                                GCTCCTCCGGCCTT GTG
                                        A
GAM3135 HS6ST    3' CCGGGAAGCCAAGGTGCCCC  71167    A        AC
                                CCG GGAGGCCGGGG  GCCCC
                                ||| ||||||||||  |||||
                                GGC CCTTCGGTTCC  CGGGG
                                  _        A_
GAM3135 KCNH4    5' GAGGGGCCGGGGCGCCCC    71168     A      A
                                GAGG GGCCGGGG CGCCCC
                                |||| |||||||| ||||||
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                                CTCC CCGGCCCC GCGGGG
                                  _     _
GAM3135 KIAA0939 3' CCAAGGAACACGGGGTGCCC  71169       GC    AC
                                CCGAGGAG  CGGGG  GCCC
                                ||||||||  |||||  ||||
                                GGTTCCTT  GCCCC  CGGG
                                    GT    A_
GAM3135 KIAA1655 5' AGGAGGCCACAGGAGCGCC   71170       _   _
                                AGGAGGCCG GGGA CGCC
                                ||||||||| |||| ||||
                                TCCTCCGGT TCCT GCGG
                                     G   C
GAM3135 KIAA1691 3' CCTGGGGAGCTCAGACGCCCC 71171   GA  AG  CGG
                                CC  GG  GC   GGACGCCCC
                                ||  ||  ||   |||||||||
                                GG  CC  CG   TCTGCGGGG
                                 AC  CT  AG_
GAM3135 LENG1    5'  TACCAAGGGGGTTGAGTCTGTG 71172       A  CC   GAC__
             CC                   TACCGAGG GG  GGG    GCC
                                ||||||||  ||  |||    |||
                                ATGGTTCC CC  CTC    CGG
                                    C  AA   AGACA
GAM3135 MARK2    5'  CGGGGAGGCCGGGCAGCC    71173    A       GAC
                                CG GGAGGCCGGG   GCC
                                || ||||||||||   |||
                                GC CCTCCGGCCC   CGG
                                 C        GT_
GAM3135 MGC15937 5'  CACCGAGGCTCCGGGGGTGCC  71174       AGG     AC
                                TACCGAGG   CCGGGG  GCC
                                ||||||||   ||||||  |||
                                GTGGCTCC   GGCCCC  CGG
                                    GA_     CA
GAM3135 MGC4549  3'  GAGGAGGCTGGAGAGGTCC   71175       C    CG_
                                GAGGAGGC GGGGA   CC
                                ||||||||  |||||   ||
                                CTCCTCCG CCTCT   GG
                                    A     CCA
GAM3135 MKP-7    3'  GAGGACTGAGGACGCCCC    71176     _ C
                                GAGG C GGGGACGCCCC
                                |||| | ||||||||||
                                CTCC G CTCCTGCGGGG
                                  T A
GAM3135 PP1201   3'  CCAGGAGGCCGGGGACA    71177    G
                                CC AGGAGGCCGGGGACG
                                || ||||||||||||||
                                GG TCCTCCGGCCCCTGT
                                 _
GAM3135 Rab11-FIP3 5'  CCGAGGAGGCCGGGGGAC    71178           _
                                CCGAGGAGGCCGGGG AC
                                |||||||||||||| ||
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                                GGCTCCTCCGGCCCC TG
                                       C
GAM3135  SLC12A5   3' CCGGGGAGGGGGCGCCC    71179    A   CCG  A
                                CCG GGAGG  GGG CGCCC
                                ||| |||||  ||| |||||
                                GGC CCTCC  CCC GCGGG
                                  C   ___  _
GAM3135  LOC115051 3' CCGGGAAGCCAAGGTGCCCC  71167    A       AC
                                CCG GGAGGCCGGGG  GCCCC
                                ||| ||||||||||  |||||
                                GGC CCTTCGGTTCC  CGGGG
                                  _        A_
GAM3135  LOC150225 3' CCGGGGGCGGTGGGGTGTCCC  71180    A  A  C__   ACG
                                CCG GG GGC  GGGG  CCC
                                ||| || |||  ||||  |||
                                GGC CC CCG  CCCC  GGG
                                  _ _  CCA   ACA
GAM3135  LOC153474 3' CCGGGAAGGCCAGGCCC    71160    A      GGAC
                                CCG GGAGGCCGG   GCCC
                                ||| |||||||||   ||||
                                GGC CTTCCGGTC   CGGG
                                  C      ____
GAM3135  LOC165140 5' CGAGGAGGTTGAAGGTCCC   71181       CC   ACG
                                CGAGGAGG  GGGG  CCC
                                ||||||||  ||||  |||
                                GCTCCTCC  CTTC  GGG
                                     AA   CA_
GAM3135  LOC170221 3' CCGAGGGGTCCGGACGCCCC  71182      A  _  GG
                                CCGAGG GG CC  GGACGCCCC
                                |||||| || ||  |||||||||
                                GGCTCC CC GG  CCTGCGGGG
                                   _  A  __
GAM3135  LOC221975 5' CCCGGCCACCCGGGGACGC   71183   GA  AG  _
                                CC  GG  GCC GGGGACGC
                                ||  ||  ||| ||||||||
                                GG  CC  TGG CCCCTGCG
                                 G_  GG  G
GAM3135  LOC253239 5' CCGAGGAGCCTGTGCCAGTCCC 71184       _____   GGACG
                                CCGAGGAG   GCCGG   CCC
                                ||||||||   |||||   |||
                                GGCTCCTC   CGGTC   GGG
                                     GGACA   A____
GAM3135  LOC253296 3' GAGGAGCTTGACACCCC    71185      G CGGG
                                GAGGAG C   GACGCCCC
                                |||||| |   ||||||||
                                CTCCTC G   CTGTGGGG
                                   _ AA__
GAM3135  LOC253298 5' GAGGAGCTTGACACCCC    71185      G CGGG
                                GAGGAG C   GACGCCCC
                                |||||| |   ||||||||
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                                CTCCTC G   CTGTGGGG
                                   _ AA__
GAM3135  LOC255397 5'  CCGAGGAGGCCGGGTGGCCCC  71186          GAC
                                CCGAGGAGGCCGGG  GCCCC
                                |||||||||||||  |||||
                                GGCTCCTCCGGCCC  CGGGG
                                      AC_
GAM3135  LOC255397 5'  CCGAGGAGGCCGGGTGGCC   71187          GAC
                                CCGAGGAGGCCGGG  GCC
                                |||||||||||||  |||
                                GGCTCCTCCGGCCC  CGG
                                      AC_
GAM3135  LOC257570 3'  GAGGAGCTTGACACCCC    71185      G CGGG
                                GAGGAG C   GACGCCCC
                                ||||||  |  ||||||||
                                CTCCTC G   CTGTGGGG
                                   _ AA__
GAM3135  LOC257571 5'  GAGGAGCTTGACACCCC    71185      G CGGG
                                GAGGAG C   GACGCCCC
                                ||||||  |  ||||||||
                                CTCCTC G   CTGTGGGG
                                   _ AA__
GAM3136  ABCB6    5'  TCACGTAGCCGCTGGGCG    71190         CGC
                                TCACGTAGTCGC  GCG
                                ||||||||||||  |||
                                AGTGCATCGGCG  CGC
                                      ACC
GAM3136  SCO2     5'  CGCGGCGGGGCCGCGCGTCAG  71191    TA  C__     C
                                CG  GT   GCCGCGCG CAG
                                ||  ||   |||||||| |||
                                GC  CG   CGGCGCGC GTC
                                 GC  CCC       A
GAM3136  MGC10772  5'  CAAGTCGTGCGCGCGCCGGC  71192    T    C_      A
                                CG AGTCG  CGCGCGCC GC
                                || |||||  |||||||| ||
                                GT TCAGC  GCGCGCGG CG
                                 _    AC       C
GAM3136  OSBPL2   3'  CATGCAACCGCGTGTCAGC   71193     A  C     CGC
                                CGT GT GCCGCG   CAGC
                                ||| || ||||||   ||||
                                GTA CG TGGCGC   GTCG
                                  _  T     ACA
GAM3136  OSBPL2   3'  CATGCAACCGCGTGTCAGC   71193     A  C     CGC
                                CGT GT GCCGCG   CAGC
                                ||| || ||||||   ||||
                                GTA CG TGGCGC   GTCG
                                  _  T     ACA
GAM3136  RLUCL    5'  CGCGCGCCCGCGCGCTGGC   71194     A T   _     CA
                                CGT G CGCC GCGCGC  GC
                                ||| | |||| ||||||  ||
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                                GCG C GCGG CGCGCG  CG
                                  _ _   G     AC
GAM3136 ZNF37A   5' GTGCTGCAGTGCGCCAGCA   71195    C  C ___
                                GT GC GC   GCGCCAGCA
                                || || ||   |||||||||
                                CA CG CG   CGCGGTCGT
                                 _ A  TCA
GAM3136 LOC222183 5' GTAGTCGCTGCTCAAGCA    71196        C  G  CC
                                GTAGTCGC GC CG  AGCA
                                |||||||| || ||  ||||
                                CATCAGCG CG GT  TCGT
                                     A  A  __
GAM3136 LOC254122 3' TCTCGTAGTCGGCCAG      71197    A      CCGCGC
                                TC CGTAGTCG     GCCAG
                                || |||||||      |||||
                                AG GCATCAGC     CGGTC
                                 A      _______
GAM3137 CAPN1    3' TGGCAATGGGTGGGGCCCAG   71200         ACAA_  A
                                TGGCAATGG    GC TCAG
                                |||||||||    || ||||
                                ACCGTTACC    CG GGTC
                                     CACCC  _
GAM3137 EPHA8    3' TGGAGGGAAGGCATCAGAG   71201     CAAT   CAA
                                TGG   GGA   GCATCAGAG
                                |||   |||   |||||||||
                                ACC   CCT   CGTAGTCTC
                                  TC__   TC_
GAM3137 TNFAIP2  3' GGCAGAAGTAGCATCAGAG   71202     AT  ACA
                                GGCA  GG   AGCATCAGAG
                                ||||  ||   ||||||||||
                                CCGT  TC   TCGTAGTCTC
                                  CT  A__
GAM3137 CPR2     3' TGGGTGAGTGGCCAAGCATCAG 71203     CAA__   A
            AG                    TGG     TGG CAAGCATCAGAG
                                |||     ||| ||||||||||||
                                ACC     ACC GTTCGTAGTCTC
                                  CACTC   G
GAM3137 FLJ10508 3' CATGGCAGCTGGCTTTCATCAG 71204        A_   ACAAG
            AG                    CATGGCA  TGG    CATCAGAG
                                |||||||  |||    ||||||||
                                GTACCGT  ACC    GTAGTCTC
                                    CG   GAAA_
GAM3137 HT002    3' TGGCAAAGGCATCAGA      71205       T  ACAA
                                TGGCAA GG    GCATCAGA
                                ||||||  ||   ||||||||
                                ACCGTT TC    CGTAGTCT
                                   _ _____
GAM3137 KIAA1904 3' TGGGAAAGCAGGGCATCAGAG  71206     CAAT  A  A_
                                TGG    GG CA  GCATCAGAG
                                |||    || ||  |||||||||
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                                ACC    TC GT  CGTAGTCTC
                                  CTT_  _  CC
GAM3137 KIAA1957 3' TGGGAGGGGTGAGCATCAGAG 71207     CAAT  ACA
                                TGG    GG   AGCATCAGAG
                                |||    ||   ||||||||||
                                ACC    CC   TCGTAGTCTC
                                  CTCC  AC_
GAM3137 LDHL     3' CATGGCAAGTGCTGCTACATCA 71208        _  GACAA
           GAG                    CATGGCAA TG     GCATCAGAG
                                |||||||| ||     |||||||||
                                GTACCGTT AC     TGTAGTCTC
                                     C  GACGA
GAM3137 MGC24009 5' ATGGCAATGGAAAGGTTTC   71209          C   CA_
                                ATGGCAATGGA AAG   TC
                                |||||||||| |||   ||
                                TACCGTTACCT TTC   AG
                                      _   CAA
GAM3137 OBSCN    3' CATGGCAGCAGCATCAG     71210       ATGGACA
                                CATGGCA      AGCATCAG
                                |||||||      ||||||||
                                GTACCGT      TCGTAGTC
                                    CG_____
GAM3137 PRO2900  3' TGGCAATGGACAGCAGGAG   71211          A   TCA
                                TGGCAATGGACA GCA   GAG
                                |||||||||||| |||   |||
                                ACCGTTACCTGT CGT   CTC
                                      _   C__
GAM3137 TRIP-Br2 3' ATGGCAACGGTGTCAGA     71212         ACAAGCA
                                ATGGCAATGG      TCAGA
                                ||||||||||      |||||
                                TACCGTTGCC      AGTCT
                                     AC_____
GAM3137 LOC196485 5' CATGGCAATGGGACCCAG    71213         ACAA  A
                                CATGGCAATGG    GC TCAG
                                ||||||||||    || ||||
                                GTACCGTTACC    TG GGTC
                                      C___  _
GAM3137 LOC220763 5' GGCATCAGAAGCATTAGAG   71214     A   CA    C
                                GGCA TGGA  AGCAT AGAG
                                |||| ||||  ||||| ||||
                                CCGT GTCT  TCGTA TCTC
                                  A   __    A
GAM3137 LOC221683 5' TGGTGGGCAGGCATCAGAG   71215     CAA   A  A
                                TGG   TGG CA GCATCAGAG
                                |||   ||| || |||||||||
                                ACC   ACC GT CGTAGTCTC
                                  ___   C  C
GAM3138 DPYSL3   3' TTCTGGTGGAATGGTTCACT   71218     A  AT    C
                                TTC TG  TGGG ATGGTTCACT
                                ||| ||  |||| ||||||||||
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                                AAG AC  ACCT TACCAAGTGA
                                  _ C_   _
GAM3138 MGAM     3' TTCACGAAGCTTGATGGTTCAT 71219       TTG  ___      C
              TC                   TTCATGA   GGC   ATGGTTCA TC
                                |||||||   |||   |||||||| ||
                                AAGTGCT   TCG   TACCAAGT AG
                                   ___   AAC       A
GAM3138 NELL2    3' TTCATAATTGAAAGTTCACTC 71220          CAT
                                TTCATGATTGGG   GGTTCACTC
                                ||||||||||||   |||||||||
                                AAGTATTAACTT   TCAAGTGAG
                                       ___
GAM3138 SEDL     3' TTCATGGTTGGGCACGGTGGCT 71221       A         TCA
              C                    TTCATG TTGGGCATGGT   CTC
                                ||||||| ||||||||||   |||
                                AAGTAC AACCCGTGCCA   GAG
                                   C         CC_
GAM3138 DSCAML1  3' TTCATGATTGGGGGTT     71222          CAT
                                TTCATGATTGGG   GGTT
                                ||||||||||||   ||||
                                AAGTACTAACCC   CCAA
                                       ___
GAM3138 FLJ11259 3' ATGATTTGGGTATATGATC    71223       _  C__
                                ATGATT GGG   ATGGTT
                                |||||| |||   ||||||
                                TACTAA CCC   TACTAG
                                   A   ATA
GAM3138 RAB25    3' TGATAGGGCATGAAGACC    71224     T      TTC
                                TGAT GGGCATGG   ACT
                                |||| ||||||||   |||
                                ACTA CCCGTACT   TGG
                                  T       TC_
GAM3138 LOC157697 5' TTCATGGCTTGACAGTTCA   71225       ATTG   TG
                                TTCATG   GGCA  GTTCA
                                ||||||   ||||  |||||
                                AAGTAC   CTGT  CAAGT
                                   CGAA   __
GAM3138 LOC158038 5' CTCATGATTTATCCTGGTTTAC 71226         GGGCA    C
              TC                   TTCATGATT    TGGTT ACTC
                                |||||||||    ||||| ||||
                                GAGTACTAA    ACCAA TGAG
                                     ATAGG    A
GAM3138 LOC170372 5' TTCATAGTAATGGTTCACT   71227      GATT  GC
                                TTCAT   GG  ATGGTTCACT
                                |||||   ||  ||||||||||
                                AAGTA   TC  TACCAAGTGA
                                   _____ AT
GAM3138 LOC91145  3' CTCAGCATGGTGTGGTTCATTC 71228     TGAT   GCA      C
                                TTCA   TGG   TGGTTCA TC
                                ||||   |||   ||||||| ||
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                                GAGT   ACC  ACCAAGT AG
                                  CGT_  AC_     A
GAM3138 LOC93333 3' TTCATGATTTGGCTCTCT   71229       GGGCA    A
                                TTCATGATT    TGGTTC CT
                                |||||||||    |||||| ||
                                AAGTACTAA    ACCGAG GA
                                     _____     A
GAM3139 C20orf64 3' CACTCAGTTTACCTGTGCCT  71232      CATC   C
                                CATTCGG   TACC GTGCCT
                                |||||||   |||| ||||||
                                GTGAGTC   ATGG CACGGA
                                    AA__   A
GAM3139 FLJ23022 3' CATCCGGCCTCCAGCTTGTG  71233       A   CCC_
                                CATTCGGC TCTA   GTG
                                |||||||| ||||   |||
                                GTAGGCCG AGGT   CAC
                                     G   CGAA
GAM3139 KIAA1281 5' CACTCGGCAAACAAGCCTGTGC 71234        TCTA__ C
            CTC                   CATTCGGCA    CC GTGCCTC
                                |||||||||     || |||||||
                                GTGAGCCGT     GG CACGGAG
                                     TTGTTC  A
GAM3139 SV2B    3' GGCATCCACTACACTC     71235        CCG  _
                                GGCATCTAC   TGC CTC
                                |||||||||   ||| |||
                                CCGTAGGTG   ATG GAG
                                     ___   T
GAM3139 LOC150605 5' CATTGGTCCCCGTGCCT    71236     C  CATCTA
                                CATT GG     CCCGTGCCT
                                ||||  ||     |||||||||
                                GTAA CC     GGGCACGGA
                                  _  AG____
GAM3140 LHX2    5' CTAATGATACATGCTACA    31652         CA
                                TTAATGATACA  CTACA
                                ||||||||||  |||||
                                GATTACTATGT  GATGT
                                      AC
GAM3140 MS4A1   3' TTAATGATACAATACTGC    31653         CACTAC
                                TTAATGATACA     ACTGT
                                ||||||||||     |||||
                                AATTACTATGT     TGACG
                                      TA____
GAM3140 CST9L   3' TTAATGATCTACACTACA    31654       AC
                                TTAATGAT  ACACTACA
                                ||||||||  ||||||||
                                AATTACTA  TGTGATGT
                                     GA
GAM3140 EHM2    3' TTAATGATATCACTGCACCG  31655        CA   A
                                TTAATGATA  CACT CACTG
                                |||||||||  |||| |||||
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                                AATTACTAT  GTGA GTGGC
                                     A_    C
GAM3140  VDAC3    3'  TAACATGACGCTACACTGTCG  31656       C_  A
                                TGATA  AC CTACACTGTCG
                                |||||  || ||||||||||
                                ATTGT  TG GATGTGACAGC
                                   AC  C
GAM3140  ZNF333   3'  TAATAGTGCACACTGCCA    31657       CACAC
                                TGATA    TACACTGTCG
                                |||||    ||||||||||
                                ATTAT    GTGTGACGGT
                                   CAC__
GAM3141  AQP7     3'  GGACAAGCCTTGCTTTATT   71240         G   A_
                                GGACAAGC TTG  TTATT
                                |||||||| |||  |||||
                                CCTGTTCG AAC  AATAA
                                     G   GA
GAM3141  FGF23    3'  GGAGAGTTGGAATTTATTTCCA 71241    A  C    A___
              TT                  C AG GTTG    TTATTTCCATT
                                | || ||||    ||||||||||
                                C TC CAAC    AATAAAGGTAA
                                 C  T    CTTA
GAM3141  PDK4     3'  GGCCAATGTAGATTATTTC    71242     A   GC  T
                                GG CAA  GT GATTATTTC
                                || |||  || |||||||||
                                CC GTT  CA CTAATAAAG
                                 G   A_  T
GAM3141  KIAA1026 3'  GGCAGGTAGGACATTTCCATT  71243     A  A C  T_   T
                                GG CA G GT  GAT ATTTCCATT
                                || || | ||  ||| |||||||||
                                CC GT C CA  CTG TAAAGGTAA
                                 _ _ _  TC   _
GAM3141  KIAA1145 3'  GGACGGAGTGTGCTGCTTTCCA 71244      A_  C  T ATTA
              TT                  GGAC  AG GT G    TTTCCATT
                                ||||  || || |    ||||||||
                                CCTG  TC CA C    AAAGGTAA
                                   CC  A  _ GACG
GAM3141  MAPK6    5'  GGTAAGCACTATTTCC      71245     AC   GTTG
                                GG  AAGC    ATTATTTCC
                                ||  ||||    |||||||||
                                CC  TTCG    TGATAAAGG
                                 A_   _____
GAM3141  LOC145694 5'  GGACGGGCGCTGATTGGCCC   71246      AA       ATT
                                GGAC  GCGTTGATT   TCC
                                ||||  |||||||||   |||
                                CCTG  CGCGACTAA   GGG
                                   CC        CC_
GAM3141  LOC150480 3'  GGACAAGCTTTGCTTTATT    71247         G   A_
                                GGACAAGC TTG  TTATT
                                |||||||| |||  |||||
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                                CCTGTTCG AAC  AATAA
                                    A   GA
GAM3141  LOC150481 3'  GGACAAGCTTTGCTTTATT   71247       G   A_
                                GGACAAGC TTG  TTATT
                                |||||||| |||  |||||
                                CCTGTTCG AAC  AATAA
                                    A   GA
GAM3141  LOC158191 3'  GGACAAGCCTTGCTTTATT   71240       G   A_
                                GGACAAGC TTG  TTATT
                                |||||||| |||  |||||
                                CCTGTTCG AAC  AATAA
                                    G   GA
GAM3141  LOC202781 3'  GGCAAGTGTGGAATTTTCCATT 71248    A   C  T  TTA
                                GG CAAG GT GA   TTTCCATT
                                || |||| || ||   ||||||||
                                CC GTTC CA CT   AAAGGTAA
                                 _   A  C  TA_
GAM3142  POU4F1    3'  TACCCTATACTCCAATCC    71251        G G_
                                TACCTTATA C  TAATCC
                                ||||||||| |  ||||||
                                ATGGGATAT G  GTTAGG
                                     _ AG
GAM3142  RNF6      3'  TACCTTATTTAATAATCC    71252       AGC
                                TACCTTAT   GTAATCC
                                ||||||||   |||||||
                                ATGGAATA   TATTAGG
                                    AAT
GAM3142  DKFZP586A011 3'  TACCTTACAGGTGTGATCC   71253         C_  A
                                TACCTTATAG  GT ATCC
                                ||||||||||  || ||||
                                ATGGAATGTC  CA TAGG
                                     CA  C
GAM3142  FLJ12572  3'  CCTTATAAAGCACTAATCC   71254       __   _
                                CCTTAT  AGCG TAATCC
                                ||||||  |||| ||||||
                                GGAATA  TCGT ATTAGG
                                   TT   G
GAM3142  KIAA0446  5'  TACCTCATGTAATCC       71255       AGC
                                TACCTTAT   GTAATCC
                                ||||||||   |||||||
                                ATGGAGTA   CATTAGG
                                     ___
GAM3142  KIAA0447  3'  TACCCTATTTGCTAATCC    71256       A_  G
                                TACCTTAT  GC TAATCC
                                ||||||||  || ||||||
                                ATGGGATA  CG ATTAGG
                                    AA  _
GAM3142  KIAA1319  3'  CACCTTATAACCATATCC    71257         GTA
                                TACCTTATAGC   ATCC
                                ||||||||||   ||||
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                                GTGGAATATTG   TAGG
                                      GTA
GAM3142  KIAA1509  3'  CACCTGGAAGCGTAATCC    71258      TAT
                                TACCT   AGCGTAATCC
                                |||||   ||||||||||
                                GTGGA   TCGCATTAGG
                                   CCT
GAM3142  KLF5      3'  TACCTTACCACAAATCC     71259        A   T
                                TACCTTAT GCG AATCC
                                ||||||||| ||| |||||
                                ATGGAATG TGT TTAGG
                                     G   _
GAM3142  LOC151457 5'  CACCTTATAGTGCTATCC    71260          C  A
                                TACCTTATAG GT ATCC
                                |||||||||| || ||||
                                GTGGAATATC CG TAGG
                                      A  A
GAM3142  LOC151458 5'  CACCTTATAGTGCTATCC    71260          C  A
                                TACCTTATAG GT ATCC
                                |||||||||| || ||||
                                GTGGAATATC CG TAGG
                                      A  A
GAM3142  LOC162333 5'  CACCTTATGCTGCATGTCC    71261        A  _   A_
                                TACCTTAT GC GTA  TCC
                                |||||||| || |||  |||
                                GTGGAATA CG CGT  AGG
                                     _ A   AC
GAM3142  LOC56270  3'  TACTTTACAGCAACATCC     71262     C       TA
                                TAC TTATAGCG  ATCC
                                ||| ||||||||  ||||
                                ATG AATGTCGT  TAGG
                                  A       TG
GAM3143  AIRE      3'  TTTTGTTTTTGAGACGGAG    71265        C_  _
                                TTTTGTTT  GA ACGGAG
                                ||||||||  || ||||||
                                AAAACAAA  CT TGCCTC
                                     AA  C
GAM3143  ALDH3A2   3'  TTTGTTTCGGAGACAG      71266        GAAC   _
                                TTTGTTTC   GGAG CAG
                                ||||||||   |||| |||
                                AAACAAAG   CCTC GTC
                                     ____   T
GAM3143  BCL7A     3'  TTTTGCTTCACAGCAGA     71267        GAAC G
                                TTTTGTTTC   G AGCAGA
                                |||||||||   | ||||||
                                AAAACGAAG   T TCGTCT
                                     ____ G
GAM3143  CNTNAP2   3'  TATTTTGTTTTGATACAGAA   71268         C  _
                                TATTTTGTTT GA ACGGAG
                                |||||||||| || ||||||
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                                ATAAAACAAA CT TGTCTT
                                     A  A
GAM3143  NR5A2    3'  TTTTGTTTTGAAAGCAGA    71269       C  ACG
                                TTTTGTTT GA   GAGCAGA
                                |||||||| ||   |||||||
                                AAAACAAA CT   TTCGTCT
                                     A  ___
GAM3143  RAD51L1  3'  TATTTTGTTTCTGTGGCAGAA  71270          GAACGGA
                                TATTTTGTTTC      GCAGAA
                                ||||||||||       ||||||
                                ATAAAACAAAG      CGTCTT
                                      ACAC___
GAM3143  ALTE     3'  TTTTGTTTTGAGACGGAG    71271       C  _
                                TTTTGTTT GA ACGGAG
                                |||||||| || ||||||
                                AAAACAAA CT TGCCTC
                                     A  C
GAM3143  BIRC1    3'  TTTTGTTTTGAGACAGACAG  71272       C  _    G
                                TTTTGTTT GA ACGGA CAG
                                |||||||| || ||||| |||
                                AAAACAAA CT TGTCT GTC
                                     A  C    _
GAM3143  C21orf25 3'  TATTGTGTTTCGAATGCAA   71273     T       CGGA
                                TATT TGTTTCGAA    GCAG
                                |||| |||||||||    ||||
                                ATAA ACAAAGCTT    CGTT
                                  C       A___
GAM3143  C21orf41 5'  TTTTGTTTCTCCCAGGCAG   71274       GAA   A
                                TTTTGTTTC   CGG GCAG
                                |||||||||   ||| ||||
                                AAAACAAAG   GTC CGTC
                                     AGG  _
GAM3143  C6orf29  3'  TTTTGTTTTGGAGACAGA    71275       CGAAC   _
                                TTTTGTTT    GGAG CAGA
                                ||||||||    |||| ||||
                                AAAACAAA    CCTC GTCT
                                     A____   T
GAM3143  EPHA7    3'  TTTTGTTTTGAACTGCAA    71276       C   GGA
                                TTTTGTTT GAAC   GCAG
                                |||||||| ||||   ||||
                                AAAACAAA CTTG   CGTT
                                     A   A__
GAM3143  FLJ20399 5'  TATTTTGTTCTGATACTTCAG  71277       TC  _  GGAG
                                TATTTTGTT  GA AC   CAG
                                |||||||||  || ||   |||
                                ATAAAACAA  CT TG   GTC
                                     GA  A  AA__
GAM3143  KIAA0532 3'  TTTTGTTTATGGAACTAGA   71278       CGAAC   _
                                TTTTGTTT    GGAGC AGA
                                ||||||||    ||||| |||
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                                AAAACAAA    CCTTG TCT
                                    TA___    A
GAM3143  KIAA0776  3'  TACTTTGTCTAGAATGGAGTAG 71279        C  C   C
            A                    TATTTTGTTT GAA GGAG AGA
                                 |||||||||| ||| |||| |||
                                 ATGAAACAGA CTT CCTC TCT
                                      T  A   A
GAM3143  KIAA1014  3'  ATTTTGTTTTGGAACAG    71280        CGAAC
                                 ATTTTGTTT    GGAGCAG
                                 |||||||||    |||||||
                                 TAAAACAAA    CCTTGTC
                                    A____
GAM3143  SEC15B   3'  TATCTTGTTATGGGAGCAG   71281        TCGAAC
                                 TATTTTGTT    GGAGCAG
                                 |||||||||    |||||||
                                 ATAGAACAA    CCTCGTC
                                    TAC___
GAM3143  THEA     3'  TTTTGTTTTGAGACAGAG    71282        C _
                                 TTTTGTTT GA ACGGAG
                                 |||||||| || ||||||
                                 AAAACAAA CT TGTCTC
                                    A  C
GAM3143  LOC130535 3'  TTTTGTTTTGAGACGGAG    71271        C _
                                 TTTTGTTT GA ACGGAG
                                 |||||||| || ||||||
                                 AAAACAAA CT TGCCTC
                                    A  C
GAM3143  LOC146540 3'  TTTTGTTTTGAGACAGAG    71282        C _
                                 TTTTGTTT GA ACGGAG
                                 |||||||| || ||||||
                                 AAAACAAA CT TGTCTC
                                    A  C
GAM3143  LOC148166 3'  TTTTGTTTTGAGACAGAG    71282        C _
                                 TTTTGTTT GA ACGGAG
                                 |||||||| || ||||||
                                 AAAACAAA CT TGTCTC
                                    A  C
GAM3143  LOC149448 3'  TATTTTGTTACAGGAGCAG   71283         T  AAC
                                 TATTTTGTT CG   GGAGCAG
                                 |||||||||  ||   |||||||
                                 ATAAAACAA GT   CCTCGTC
                                    T  ____
GAM3143  LOC150174 3'  TTTTGTTTTGAGACAGAG    71282        C _
                                 TTTTGTTT GA ACGGAG
                                 |||||||| || ||||||
                                 AAAACAAA CT TGTCTC
                                    A  C
GAM3143  LOC150213 3'  TTTTGTTTTGAGACAGAG    71282        C _
                                 TTTTGTTT GA ACGGAG
                                 |||||||| || ||||||
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                                AAAACAAA CT TGTCTC
                                    A  C
GAM3143  LOC150406 3'  TATTCTGTTTCTGGCAG     71284          GAACGGA
                                TATTTTGTTTC      GCAG
                                ||||||||||       ||||
                                ATAAGACAAAG      CGTC
                                     AC_____
GAM3143  LOC159053 3'  TTTTGTTTTGAGGCAGA     71285        C  ACG A
                                TTTTGTTT GA   G GCAGA
                                |||||||| ||   | |||||
                                AAAACAAA CT   C CGTCT
                                    A  ___ _
GAM3144  GRM6      3'  TACTATACAGAAGCTCT     71288         C   TACC
                                TACTATACG GAA    CTCT
                                ||||||||| |||    ||||
                                ATGATATGT CTT    GAGA
                                     _  C___
GAM3144  FLJ22944  3'  TACTACACAGCCCTCT      71289         CGAATA
                                TACTATACG     CCCTCT
                                |||||||||     ||||||
                                ATGATGTGT     GGGAGA
                                     C_____
GAM3144  KIAA0040  3'  TACTATACAGCTTGGACCCT   71290        _  GAAT
                                TACTATAC GC    ACCCT
                                |||||||| ||    |||||
                                ATGATATG CG    TGGGA
                                     T  AACC
GAM3144  TOMM70A   3'  TACAGTGCCACTGTACCCTCTA 71291     TATA_   GAA
              T                  TAC    CGC   TACCCTCTAT
                                 |||    |||   ||||||||||
                                 ATG    GTG   ATGGGAGATA
                                   TCACG   AC_
GAM3145  ACTN2     3'  AGCAAAAAGAAAGAATGAACA  71294            __
                                GGCAAAAAGAAAGAA  AACA
                                ||||||||||||||  ||||
                                TCGTTTTTCTTTCTT  TTGT
                                       AC
GAM3145  ADAM28    3'  AGATGAAAAGAAAAAGACACCC 71295     CA        AA
              A                   AGG  AAAAGAAAGA  ACACCCA
                                  |||  ||||||||||  |||||||
                                  TCT  TTTTCTTTTT  TGTGGGT
                                    AC         C_
GAM3145  ANGPT1    3'  AGGCAAAAAGGGGTAGAATACA 71296          AA__    A
                                AGGCAAAAAG    AGAA ACA
                                ||||||||||    |||| |||
                                TCCGTTTTTC    TCTT TGT
                                      CCCA    A
GAM3145  CHD2      3'  AGGCAAAAGGAAAGTGACA    71297         A     AAA
                                AGGCAAAA GAAAG   ACA
                                |||||||| |||||   |||
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                                TCCGTTTT CTTTC   TGT
                                    C    AC_
GAM3145 CNGA3    3' AGGAAGAAGAAAGAAAA    71298    C  A
                                AGG AA AAGAAAGAAAA
                                ||| || ||||||||||
                                TCC TT TTCTTTCTTTT
                                  _ C
GAM3145 COL19A1  3' AGGCAAAAAGATAAACAACC  71299         AAGA    C
                                AGGCAAAAAGA   AAACA CC
                                ||||||||||   ||||| ||
                                TCCGTTTTTCT   TTTGT GG
                                      A___    T
GAM3145 CTBP2    3' AGCAAAAAGAGGTCACCC    71300         AAGAAAA
                                GGCAAAAAGA     CACCC
                                |||||||||      |||||
                                TCGTTTTTCT     GTGGG
                                      CCA____
GAM3145 CYP1B1   3' AGGCAAAAGGATAAATCCACCC 71301        A  A   AAA
             A                   AGGCAAAA GA AGA   CACCCA
                                ||||||| || |||   ||||||
                                TCCGTTTT CT TTT   GTGGGT
                                    C  A   AG_
GAM3145 DDEF2    3' AGGCAAATTCCAAAACACC   71302       AAGAAAG
                                AGGCAAA      AAAACACC
                                |||||||      ||||||||
                                TCCGTTT      TTTTGTGG
                                    AAGG___
GAM3145 DVL3     3' AGGAAAAAAGAAAGAAAA    71304    C
                                AGG AAAAAGAAAGAAAA
                                ||| ||||||||||||||
                                TCC TTTTTCTTTCTTTT
                                  T
GAM3145 DVL3     3' AGGCAGGTGCCAAAACACCCA  71303      AAAAGAAAG
                                AGGCA        AAAACACCCA
                                |||||        ||||||||||
                                TCCGT        TTTTGTGGGT
                                   CCACGG___
GAM3145 DXS1283E 3' AGCTAAGTCACGGAAACACCCA 71305    AAA   AAAGA_
                                GGC   AAG     AAACACCCA
                                |||   |||     |||||||||
                                TCG   TTC     TTTGTGGGT
                                  A__   AGTGCC
GAM3145 EGFL5    5' AGGAAAGAAAGAAACA      71306    CAA        A
                                AGG   AAAGAAAGAAA CA
                                |||   |||||||||| ||
                                TCC   TTTCTTTCTTT GT
                                  ___        _
GAM3145 FOXD2    5' AGGGAGAAAGAACTCACCC    71307    CAAAA       AA
                                AGG    AGAAAGAA  CACCC
                                |||    ||||||||  |||||
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                                TCC    TCTTTCTT  GTGGG
                                  C____      GA
GAM3145  FUT8    3'  GGCAAAGTAGAAAACAACC   71308       AAGAA      C
                                GGCAAA    AGAAAACA CC
                                ||||||    |||||||| ||
                                CCGTTT    TCTTTTGT GG
                                   CA___      T
GAM3145  GNAI3   3'  AGGCAAAAGGAAACAGAAGACA 71309        A  __   A
                                AGGCAAAA GAA  AGAA ACA
                                |||||||| |||  |||| |||
                                TCCGTTTT CTT  TCTT TGT
                                     C  TG   C
GAM3145  HMG20A  5'  GGCCAAAAGAAAGTCCC    71310    A       AAAACA
                                GGC AAAAGAAAG     CCC
                                ||| |||||||||     |||
                                CCG TTTTCTTTC     GGG
                                  G       A_____
GAM3145  ITPR1   5'  AGGATGGAAGCGGAACACCCA 71311    CAAA   AAA  AA
                                AGG   AAG   GA  ACACCCA
                                |||   |||   ||  |||||||
                                TCC   TTC   CT  TGTGGGT
                                  TACC  GC_ __
GAM3145  LUZP1   3'  GGCAAAAGAAAGTGTCAC    71312       A    AAAA
                                GGCAAAA GAAAG    CAC
                                ||||||| |||||    |||
                                CCGTTTT CTTTC    GTG
                                   _    ACA_
GAM3145  LZTS1   3'  GGCAGGAAAGAACACCC     71313     AAAA     AA
                                GGCA   GAAAGA  ACACCC
                                ||||   ||||||  ||||||
                                CCGT   CTTTCT  TGTGGG
                                  C____     __
GAM3145  MPP2    3'  AGGAAAAAGAAAGAAAAC    71314    C
                                AGG AAAAAGAAAGAAAAC
                                ||| ||||||||||||||
                                TCC TTTTTCTTTCTTTTG
                                  _
GAM3145  NOTCH2  3'  GGAGTCAAAGAAAGAAAGCA  71315    CAA_       A
                                GG   AAAGAAAGAAA CA
                                ||   |||||||||| ||
                                CC   TTTCTTTCTTT GT
                                 TCAG         C
GAM3145  NSD1    3'  AGGGGGAAAGAAAGAAAA    71316    CAA
                                AGG   AAAGAAAGAAAA
                                |||   ||||||||||||
                                TCC   TTTCTTTCTTTT
                                  CCC
GAM3145  NSEP1   3'  GGCAAAAAGCAAGCAC      71317         A   AAAA
                                GGCAAAAAG AAG    CAC
                                ||||||||| |||   |||
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                                CCGTTTTTC TTC    GTG
                                     G  ____
GAM3145  P2RY1    3'  AGGCAAAAGAGAAAGTAAA   71318        _     A
                                AGGCAAAA AGAAAG AAA
                                |||||||| |||||| |||
                                TCCGTTTT TCTTTC TTT
                                    C     A
GAM3145  PARG     3'  GGCAGGAAGAAAGAGACCC   71319      AA       AAAC
                                GGCA  AAGAAAGA   ACCC
                                ||||  ||||||||   ||||
                                CCGT  TTCTTTCT   TGGG
                                  CC       C___
GAM3145  PPP2R5C  3'  GGCAAAAAAGAGAGTCTTCCCA  71320          A  AAAACA
                                GGCAAAAAGA AG     CCCA
                                |||||||||| ||     ||||
                                CCGTTTTTCT TC     GGGT
                                      C  AGAA__
GAM3145  PROX1    3'  AGGCAGAAAGAAAACAACC   71321       AAAA         C
                                AGGCA   GAAAGAAAACA CC
                                |||||   |||||||||| ||
                                TCCGT   CTTTCTTTTGT GG
                                  _____         T
GAM3145  RALB     3'  AGGGGAGAAGAAAGAAATTCCA 71322     CAAA         ACAC
                                AGG   AAGAAAGAAA   CCA
                                |||   ||||||||||   |||
                                TCC   TTCTTTCTTT   GGT
                                  CCTC        AA__
GAM3145  RHEB2    5'  AGGCAAAAAAAAGGGGACGCC  71323           AGAAA  A
                                AGGCAAAAAGAA    AC CC
                                ||||||||||||    || ||
                                TCCGTTTTTTTT    TG GG
                                      CCCC_  C
GAM3145  RP42     3'  GGCAAAAAGGAAACTGTACC   71324         AAA   AC__
                                GGCAAAAAG   GAAA   ACC
                                |||||||||   ||||   |||
                                CCGTTTTTC   CTTT   TGG
                                     ___   GACA
GAM3145  RPL36A   5'  GGCGCGGAAAGAAAGAAACC   71325     AA__        AAC
                                GGC   AAAGAAAGAA   ACC
                                |||   ||||||||||   |||
                                CCG   TTTCTTTCTT   TGG
                                  CGCC        ___
GAM3145  S100A4   3'  GGAAAAAAAAAAGTGCCCA   71326    C        AAAACA
                                GG AAAAAGAAAG     CCCA
                                || ||||||||||     ||||
                                CC TTTTTTTTTC     GGGT
                                  T        AC_____
GAM3145  S100A4   3'  GGAAAAAAAAAAGTGCCCA   71326    C        AAAACA
                                GG AAAAAGAAAG     CCCA
                                || ||||||||||     ||||
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                                CC TTTTTTTTTC     GGGT
                                 T        AC____
GAM3145  SELE     3'  GGCAAAAGAAAGAAAGCC    71327        A       ACAC
                                GGCAAAA GAAAGAAA    CC
                                ||||||| ||||||||    ||
                                CCGTTTT CTTTCTTT    GG
                                   _       C___
GAM3145  SFPQ     5'  AGGCAAAAGCGAAGAAGAC    71328        A_   A   A
                                AGGCAAAA  GAA GAA AC
                                ||||||||  ||| ||| ||
                                TCCGTTTT  CTT CTT TG
                                     CG   _   C
GAM3145  SFRS2IP  5'  AAGCAAAAGGAGAGAGAAAA   71329         __   A
                                AGGCAAAA  AGA AGAAAA
                                ||||||||  ||| ||||||
                                TTCGTTTT  TCT TCTTTT
                                     CC   C
GAM3145  SMCY     3'  GGCAAAAATAAAGGTACGCAC  71330        G    AAAA_
                                GGCAAAAA AAAG     CAC
                                |||||||| ||||     |||
                                CCGTTTTT TTTC     GTG
                                     A    CATGC
GAM3145  STIM1    3'  AGGGAAGGAGAGACAGAACACC 71331     C  AA   AAGAA
              CA                   AGG AA  AGA     AACACCCA
                                ||| ||  |||     ||||||||
                                TCC TT  TCT     TTGTGGGT
                                  C  CC   CTGTC
GAM3145  SURF4    3'  AGGAGAAACAGGAACACCC    71332     CAAAA    GAA_
                                AGG     AGAAA    AACACCC
                                |||     |||||    |||||||
                                TCC     TCTTT    TTGTGGG
                                  ______    GTCC
GAM3145  TEC      3'  AGGCAAAAAGGAAGGCCC     71333          A   AAAACA
                                AGGCAAAAAG AAG      CCC
                                |||||||||| |||      |||
                                TCCGTTTTTC TTC      GGG
                                     C   C_____
GAM3145  TLL2     3'  GGCAGAGAGAAAGAAAATGATT 71334      AAA        CAC__
              CCA                   GGCA   AGAAAGAAAA    CCA
                                ||||   ||||||||||     |||
                                CCGT   TCTTTCTTTT    GGT
                                  CTC         ACTAA
GAM3145  TLR4     3'  AGGAAAAAGTGAACACCC    71335     CAAAA     AA
                                AGG     AGAAAG  AACACCC
                                |||     ||||||  |||||||
                                TCC     TTTTTC  TTGTGGG
                                  ______     AC
GAM3145  TLR4     3'  AGGAAAAAGTGAACACCC    71335     CAAAA     AA
                                AGG     AGAAAG  AACACCC
                                |||     ||||||  |||||||
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                                TCC    TTTTTC  TTGTGGG
                                  _____     AC
GAM3145  TLR4     3'  AGGAAAAAGTGAACACCC    71335     CAAAA     AA
                                TCC    TTTTTC  TTGTGGG
                                  _____     AC
GAM3145  TRPC5    3'  AAGCAAAAAGGTTAAGCACCCA 71336          AAAGAAAA
                                AGGCAAAAAG       CACCCA
                                ||||||||||       ||||||
                                TTCGTTTTTC       GTGGGT
                                     CAATTC__
GAM3145  WNT11    3'  AAGCAAAAAACAAAAGAAAACA 71337          __
                                AGGCAAAAA  GAAAGAAAACA
                                |||||||||  ||||||||||
                                TTCGTTTTT  TTTTCTTTTGT
                                     TG
GAM3145  ARF6     3'  AGGAAAAAGAAAGGGAAACA   71338     C        A_
                                AGG AAAAAGAAAG  AAACA
                                ||| ||||||||||  |||||
                                TCC TTTTTCTTTC  TTTGT
                                  _        CC
GAM3145  ATP10B   3'  AGGCAAAAAGCAGAACCAAC   71339          AA    AAC
                                AGGCAAAAAG  AGAA   AC
                                ||||||||||  ||||   ||
                                TCCGTTTTTC  TCTT   TG
                                     G_    GGT
GAM3145  BRD4     3'  GACAAAGAGAGAAAACA     71340       AA   A
                                GGCAA  AGA AGAAAACA
                                |||||  ||| ||||||||
                                CTGTT  TCT TCTTTTGT
                                   __   C
GAM3145  BRE      3'  AGGCAAGAAAGAGGGAGTAACC 71341       AAA      AAAC___
              C                  AGGCA   AGAAAGA      ACCC
                                 |||||   |||||||      ||||
                                 TCCGT   TCTTTCT      TGGG
                                   ___       CCCTCAT
GAM3145  CRK7     3'  AGGAAAAAAACCCAAAACACC  71342     C      AAG
                                AGG AAAAAGA   AAAACACC
                                ||| |||||||   ||||||||
                                TCC TTTTTTT   TTTTGTGG
                                  _      GGG
GAM3145  DCOHM    3'  AGCAAAAAGGCTATGGGCACCC 71343          AAAGAAAA
              A                   GGCAAAAAG       CACCCA
                                  |||||||||       ||||||
                                  TCGTTTTTC       GTGGGT
                                       CGATACCC
GAM3145  DKFZp434L0850 3'  AGGCTGGAAAGAAAGGAACA   71344      AA_       AA
                                AGGC   AAAGAAAG  AACA
                                ||||   ||||||||  ||||
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                                TCCG  TTTCTTTC  TTGT
                                  ACC      C_
GAM3145  DKFZP586A011 3'  AGGATGGAGGGAAACACCCA  71345    CAAAAA  AA   A
                                AGG    GA  GAAA CACCCA
                                |||    ||  |||| ||||||
                                TCC    CT  CTTT GTGGGT
                                  TAC___  CC   _
GAM3145  DKFZP761L0424 3'  AGGAAAAAAGAAAGAAAA   71304    C
                                AGG AAAAAGAAAGAAAA
                                ||| ||||||||||||||
                                TCC TTTTTCTTTCTTTT
                                  T
GAM3145  EAT2    3'  GGCAAAAAAGATGACCC    71346     AAA    AAAC
                                GGCAA  GAAAGA   ACCC
                                |||||  ||||||   ||||
                                CCGTT  TTTTCT   TGGG
                                   ___    AC__
GAM3145  EFNA5   3'  AGGCTGAAAGAAAGAAAACA  71347    AA
                                AGGC  AAAGAAAGAAAACA
                                ||||  ||||||||||||||
                                TCCG  TTTCTTTCTTTTGT
                                  AC
GAM3145  EFS2    5'  AGGAGAAAGAAAACC     71348    CAAAA      AC
                                AGG   AGAAAGAAA  ACC
                                |||   |||||||||  |||
                                TCC   TCTTTCTTT  TGG
                                  _____      __
GAM3145  ENDOFIN  3'  AAGCAAAAAGTCCTGAAGCACC 71349        AAA_  AA
            C                    AGGCAAAAAG   GAA  CACCC
                                ||||||||||   |||  |||||
                                TTCGTTTTTC   CTT  GTGGG
                                     AGGA  C_
GAM3145  FLJ10210  5'  GGGAAGAAAGAAAACCAGCCCA 71350   CAAA        A__
                                GG   AAGAAAGAAAAC  CCCA
                                ||   ||||||||||||  ||||
                                CC   TTCTTTCTTTTG  GGGT
                                 C___         GTC
GAM3145  FLJ10661  3'  AGGCTGAAAAGAACACCC   71351    AAAAA    AA
                                AGGC   GAAAGA  ACACCC
                                ||||   ||||||  ||||||
                                TCCG   TTTTCT  TGTGGG
                                  AC___    __
GAM3145  FLJ10713  3'  GGCAAAAAAAAAAGATCCCC   71352          AAACA
                                GGCAAAAAGAAAGA   CCC
                                ||||||||||||||   |||
                                CCGTTTTTTTTTCT   GGG
                                       AG___
GAM3145  FLJ12298  5'  AGGTGAAGAAAGAGCAAACCCA 71353    CAAA      AAAC
                                AGG   AAGAAAGA   ACCCA
                                |||   ||||||||   |||||
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                                TCC   TTCTTTCT   TGGGT
                                  AC__      CGTT
GAM3145  FLJ12303  3'  AGGCAGAAAAAAACTCAC   71354      AAAA      A_
                                AGGCA   GAAAGAAA  CAC
                                |||||   ||||||||  |||
                                TCCGT   CTTTTTTT  GTG
                                  _____      GA
GAM3145  FLJ13310  3'  GGCAGAAAGAACACC      71355     AAAA     AA   C
                                GGCA   GAAAGA  ACAC C
                                ||||   ||||||  ||||  |
                                CCGT   CTTTCT  TGTG G
                                  _____    __   A
GAM3145  FLJ20040  3'  AGGCAAAAAAGGATTCACACCC 71356         AAA  AA_
            A                    AGGCAAAAAG   GA   ACACCCA
                                ||||||||||   ||   |||||||
                                TCCGTTTTTT   CT   TGTGGGT
                                     C__  AAG
GAM3145  FLJ21324  5'  GGGAAAACTAAAAACACC    71357    C    AGAAA
                                GG AAAA    GAAAACACC
                                || ||||    |||||||||
                                CC TTTT    TTTTTGTGG
                                 C   GA___
GAM3145  GLUC      3'  AGGCAAAAGGGAGATGTACC   71358        A AA   AAAC
                                AGGCAAAA G  AGA   ACC
                                |||||||| |  |||   |||
                                TCCGTTTT C  TCT   TGG
                                    _ CC   ACA_
GAM3145  GPT2      3'  AGGCACAAAGAAAGACGTCTCC 71359      A       AAACAC
            A                    AGGCA AAAGAAAGA     CCA
                                |||||  |||||||||     |||
                                TCCGT TTTCTTTCT     GGT
                                  G       GCAGA_
GAM3145  GT650     3'  GCAAAAAAACCTGAAAACACTC 71360        AA_      C
            A                    GCAAAAAGA   GAAAACAC CA
                                |||||||||   ||||||||  ||
                                CGTTTTTTT   CTTTTGTG GT
                                     GGA       A
GAM3145  KCNK13    3'  GGCAAAAAGAAAGCC      71361          AAAACA
                                GGCAAAAAGAAAG     CC
                                ||||||||||||      ||
                                CCGTTTTTCTTTC     GG
                                          _______
GAM3145  KIAA0090  3'  GGCAAAGAAAGGAAACA     71362      AA     A
                                GGCAA  AGAAAG AAACA
                                |||||  ||||||  |||||
                                CCGTT  TCTTTC TTTGT
                                   __      C
GAM3145  KIAA0426  3'  AGGCATGAAGAAAAAATACC   71363      AA       AAC
                                AGGCA  AAGAAAGAA   ACC
                                |||||  |||||||||   |||
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                                TCCGT  TTCTTTTTT   TGG
                                  AC       A__
GAM3145  KIAA0599  3'  AGCAGAAAGAAAAAGCCC    71364     AAAA       CA
                                GGCA   GAAAGAAAA  CCC
                                ||||   |||||||||  |||
                                TCGT   CTTTCTTTT  GGG
                                  ____       TC
GAM3145  KIAA0628  3'  AAGCTTGAGGGAAACACCC   71365     AAAAA  AA   A
                                AGGC    GA  GAAA CACCC
                                ||||    ||  |||| |||||
                                TTCG    CT  CTTT GTGGG
                                  AA___  CC   _
GAM3145  KIAA0703  5'  AAGCAAAAAGGAGGAAACAACC 71366         AA  A    _
            CA                    AGGCAAAAAG  AG AAACA CCCA
                                ||||||||||  || ||||| ||||
                                TTCGTTTTTC  TC TTTGT GGGT
                                      C_  C    T
GAM3145  KIAA0939  3'  AGGCAAAAAAAACTGACCC   71367          AGAAAAC
                                AGGCAAAAAGAA      ACCC
                                ||||||||||||      ||||
                                TCCGTTTTTTTT      TGGG
                                      GAC____
GAM3145  KIAA0993  3'  AGGCAAAAAGAAAAGAAACCC  71368          _  AAC
                                AGGCAAAAAGAAA GAA   ACCC
                                ||||||||||||| |||   ||||
                                TCCGTTTTTCTTT CTT   TGGG
                                      T   ___
GAM3145  KIAA1254  3'  GGCAAAAAAGGGAAACACTCA  71369        AAA   A   C
                                GGCAAAAAG   GAAA CAC CA
                                |||||||||   |||| ||| ||
                                CCGTTTTTT   CTTT GTG GT
                                      CC_   _   A
GAM3145  KIAA1571  3'  GGAAAAAAGACACCAATACCCA 71370    C      AAGAA  C
                                GG AAAAAGA     AA ACCCA
                                || |||||||     || |||||
                                CC TTTTTCT     TT TGGGT
                                  T      GTGG_  A
GAM3145  KIAA1718  3'  AGGAAAAAAGAAAACC      71371     C       GAAAAC
                                AGG AAAAAGAAA      ACC
                                ||| |||||||||      |||
                                TCC TTTTTCTTT      TGG
                                  T       _______
GAM3145  KLHL8     3'  AGGCAAAAGAAAAGGCAAAAC  71372        AG   __
                                AGGCAAAA  AAAG  AAAAC
                                ||||||||  ||||  |||||
                                TCCGTTTT  TTTC  TTTTG
                                      CT    CG
GAM3145  LGALS8    3'  GGCAAGGACTGAGAACACCCA  71373      AAA  AA  A
                                GGCAA   GA  GA AACACCCA
                                |||||   ||  || ||||||||
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                                CCGTT  CT  CT TTGTGGGT
                                  C__  GA  C
GAM3145 MGC16279 3' AGGCTGAAAAGAACACCC   71351     AAAAA     AA
                                AGGC    GAAAGA  ACACCC
                                ||||    ||||||  ||||||
                                TCCG    TTTTCT  TGTGGG
                                  AC___     __
GAM3145 MGC2641  3' AGGCAGGAAAAAAAAACCC  71374      AAAA       C
                                AGGCA   GAAAGAAAA ACCC
                                |||||   ||||||||| ||||
                                TCCGT   CTTTTTTTT TGGG
                                  C___       _
GAM3145 MGC3130  3' GGCTCTCAGGGAAAACACCCA 71375    AAAA  AAA
                                GGC   AG  GAAAACACCCA
                                |||   ||  ||||||||||
                                CCG   TC  CTTTTGTGGGT
                                  AGAG  C__
GAM3145 MGC32043 3' GGCAGAAAGAGAAAACA    71376     A    AA
                                GGCA AAAGA  GAAAACA
                                |||| |||||  |||||||
                                CCGT TTTCT  CTTTTGT
                                  C    __
GAM3145 MGC4701  5' AGGAAAAAAAAGAGGCACC  71377    CA       AAA
                                AGG  AAAAGAAAGA  CACC
                                |||  ||||||||||  ||||
                                TCC  TTTTTTTTCT  GTGG
                                  __       CC_
GAM3145 MGC5528  5' GGCAAGAAAGAAGTTCCC   71378    AAA      AACA
                                GGCA  AGAAAGAA   CCC
                                ||||  ||||||||   |||
                                CCGT  TCTTTCTT   GGG
                                  ___      CAA_
GAM3145 NUCKS    3' AGACAAAAAGGTAACTTAAACA 71379         AAAGA__
            C                    AGGCAAAAAG     AAACAC
                                ||||||||||     ||||||
                                TCTGTTTTTC     TTTGTG
                                     CATTGAA
GAM3145 NUP133   3' AGTAAAAAGAAAGGGCACC   71380   C       AAAA
                                GG AAAAAGAAAG   CACC
                                || ||||||||||   ||||
                                TC TTTTTCTTTC   GTGG
                                 A       CC__
GAM3145 PCDH19   3' AGGCAAAAATAAGTAAAACA  71381        GA  _
                                AGGCAAAAA  AAG AAAACA
                                |||||||||  ||| ||||||
                                TCCGTTTTT  TTC TTTTGT
                                     A_  A
GAM3145 PRO0767  5' GGCAGGAAGAAAAGAAAGTACC 71382     AA    _   AC
            CA                   GGCA  AAGAAA GAAA  ACCCA
                                ||||  |||||| ||||  |||||
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                                CCGT  TTCTTT CTTT  TGGGT
                                  CC     T   CA
GAM3145  PRO1483   5'  AAGCAAAAAGGATAGAAAATGC 71383          AA_     CA
              CCA                   AGGCAAAAAG   AGAAAA  CCCA
                                |||||||||   ||||||  ||||
                                TTCGTTTTTC   TCTTTT  GGGT
                                     CTA     AC
GAM3145  SART3     3'  AGGCAAAGAAAACAGTCC     71384       AAAGAA       C_
                                AGGCAA     AGAAAACA  CC
                                ||||||     ||||||||  ||
                                TCCGTT     TCTTTTGT  GG
                                   _______      CA
GAM3145  SEMA5A    3'  AGGCAAGATGAAAACACTCA   71385      AAA   AA       C
                                AGGCA   AGA  GAAAACAC CA
                                |||||   |||  |||||||| ||
                                TCCGT   TCT  CTTTTGTG GT
                                   ___   A_       A
GAM3145  ShrmL     5'  AGCTTAAAAAGAAAGAAAGCAC 71386      __           A
                                GGC  AAAAAGAAAGAAA CAC
                                |||  |||||||||||| |||
                                TCG  TTTTTCTTTCTTT GTG
                                  AA           C
GAM3145  SMCR7     3'  AGCTGCCTGAAGAAAACACTCA 71387     AAAAA   A       C
                                GGC     GAA GAAAACAC CA
                                |||     ||| |||||||| ||
                                TCG     CTT CTTTTGTG GT
                                  ACGGA  _       A
GAM3145  TPD52     3'  AGGTAAAGAAAATACACCC    71388     CAA       AAA
                                AGG   AAAGAAAG   ACACCC
                                |||   ||||||||   ||||||
                                TCC   TTTCTTTT   TGTGGG
                                  A__       A__
GAM3145  TU12B1-TY 3'  AGGCAAAAAAGAAAGAAA     71389          _
                                AGGCAAAAA GAAAGAAA
                                ||||||||| ||||||||
                                TCCGTTTTT CTTTCTTT
                                     T
GAM3145  TUSP      5'  AGGCTAGAAAGAAGGCCCC    71390      AAAA       AACA
                                AGGC    AGAAAGAA    CCC
                                ||||    ||||||||    |||
                                TCCG    TCTTTCTT    GGG
                                  A___       CCG_
GAM3145  UST       3'  AGGCAGAAAGAAGGCCC     71391       AAAA      AACA
                                AGGCA    GAAAGAA    CCC
                                |||||    |||||||    |||
                                TCCGT    CTTTCTT    GGG
                                   _____      CC__
GAM3145  ZAK       3'  AGGGGGAAAGAAAGAAAA    71316     CAA
                                AGG   AAAGAAAGAAAA
                                |||   ||||||||||||
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                                TCC   TTTCTTTCTTTT
                                  CCC
GAM3145  ZFP100    3'  GGCAGGGAACAAACACCCA   71392      AAAA   AGA
                                GGCA   GAA   AAACACCCA
                                ||||   |||   |||||||||
                                CCGT   CTT   TTTGTGGGT
                                  CC__   G__
GAM3145  LOC113523 3'  AGGAAAAAAAAAAGGCACC   71393     C        AAAA
                                AGG AAAAAGAAAG   CACC
                                ||| ||||||||||   ||||
                                TCC TTTTTTTTTC   GTGG
                                  T        C___
GAM3145  LOC122792 3'  GCAAAAAGGAAAGTCAC     71394         _   AAAA
                                GCAAAAAG AAAG   CAC
                                |||||||| ||||   |||
                                CGTTTTTC TTTC   GTG
                                     C   A___
GAM3145  LOC133686 3'  AGGAAAGGGAAGGAAAACAC   71395     C   AA   A
                                AGG AAA  GAA GAAAACAC
                                ||| |||  ||| ||||||||
                                TCC TTT  CTT CTTTTGTG
                                  _  CC   C
GAM3145  LOC145828 5'  AAGCAAAAAGAGAGGAGATATC 71396          A  AAAACAC
           CA                     AGGCAAAAAGA AG      CCA
                                ||||||||||| ||      |||
                                TTCGTTTTTCT TC      GGT
                                      C  CTCTATA
GAM3145  LOC145844 3'  AGGGAGAAAGAAAACA      71397     CAAAA
                                AGG    AGAAAGAAAACA
                                |||    ||||||||||||
                                TCC    TCTTTCTTTTGT
                                  C____
GAM3145  LOC146050 3'  GACAGAAAGAAAACCAACC   71398      AAAA        AC_
                                GGCA   GAAAGAAAAC   CC
                                ||||   ||||||||||   ||
                                CTGT   CTTTCTTTTG   GG
                                  ____         GTT
GAM3145  LOC149506 5'  AGGCAAAAGGGAAAGGGACAC  71399         A_    AAA
                                AGGCAAAA  GAAAG   ACAC
                                ||||||||  |||||   ||||
                                TCCGTTTT  CTTTC   TGTG
                                     CC    CC_
GAM3145  LOC149684 3'  AGGCAAAAGGGAGAATGAGCAC 71400         ___   A  AA
                                AGGCAAAA   AGAA GA  AC
                                ||||||||   |||| ||  ||
                                TCCGTTTT   TCTT CT  TG
                                     CCC    A  CG
GAM3145  LOC150035 5'  AGGCAAAAGGAAAGCTCTCCA  71401         A    AAAACAC
                                AGGCAAAA GAAAG      CCA
                                |||||||| |||||      |||
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                                TCCGTTTT CTTTC      GGT
                                     C    GAGA___
GAM3145  LOC150481 3'  AGGAAGAAGAAAGAGGAGCCCA 71402    C  A      AAACA
                                AGG AA AAGAAAGA    CCCA
                                ||| || ||||||||    ||||
                                TCC TT TTCTTTCT    GGGT
                                  _ C       CCTC_
GAM3145  LOC150606 3'  AGGCAAAAGTGAAGACCTCCC  71403        AGA   AAACA
                                AGGCAAAA   AAGA    CCC
                                ||||||||   ||||    |||
                                TCCGTTTT   TTCT    GGG
                                     CAC    GGA__
GAM3145  LOC151121 5'  AGGCAAAAGAGGAGAGTCCCA  71404        A  A_   AAACA
                                AGGCAAAA GA  AGA    CCCA
                                |||||||| ||  |||    ||||
                                TCCGTTTT CT  TCT    GGGT
                                     _  CC   CA___
GAM3145  LOC153606 3'  AGGCTGAAAAGAAAACACC   71405     AAAAA
                                AGGC    GAAAGAAAACACC
                                ||||    ||||||||||||
                                TCCG    TTTTCTTTTGTGG
                                  AC___
GAM3145  LOC154792 3'  AAAAGAGAGAAAACATCCA   71406       A       C
                                AAAAGA AGAAAACA CCA
                                |||||| |||||||| |||
                                TTTTCT TCTTTTGT GGT
                                    C       A
GAM3145  LOC157226 3'  GGCAAAAAGCAAGCAC      71317         A   AAAA
                                GGCAAAAAG AAG    CAC
                                ||||||||| |||    |||
                                CCGTTTTTC TTC    GTG
                                     G   ____
GAM3145  LOC157621 3'  ACAGGAAAGAAAGAGGGTACC  71407     A_       AAAC
                                GCA  AAAGAAAGA    ACC
                                |||  |||||||||    |||
                                TGT  TTTCTTTCT    TGG
                                  CC        CCCA
GAM3145  LOC158191 3'  AGGAAGAAGAAAGAGGAGCCCA 71402    C  A      AAACA
                                AGG AA AAGAAAGA    CCCA
                                ||| || ||||||||    ||||
                                TCC TT TTCTTTCT    GGGT
                                  _ C       CCTC_
GAM3145  LOC158373 3'  GGCAAAAAGCAAGCAC      71317         A   AAAA
                                GGCAAAAAG AAG    CAC
                                ||||||||| |||    |||
                                CCGTTTTTC TTC    GTG
                                     G   ____
GAM3145  LOC164382 3'  AGGCAAGAAAAAAACA      71408       AAA       A
                                AGGCA   AGAAAGAAA CA
                                |||||   ||||||||| ||
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                                TCCGT   TCTTTTTTT GT
                                  ____      _
GAM3145  LOC197131 3'  AGCAAAAAGAAGGTAGGAAAAC 71409          A_____
              A                   GGCAAAAAGAA    GAAAACA
                                  ||||||||||    |||||||
                                  TCGTTTTTCTT    CTTTTGT
                                        CCATC
GAM3145  LOC199870 3'  AGGTAACAAGAAAGAAAA    71410    C  A
                                  AGG AA AAGAAAGAAAA
                                  ||| || ||||||||||
                                  TCC TT TTCTTTCTTTT
                                    A  G
GAM3145  LOC200091 3'  AGGCAAAAGCGAAGAAGAC   71328        A_  A  A
                                  AGGCAAAA  GAA GAA AC
                                  ||||||||  ||| ||| ||
                                  TCCGTTTT  CTT CTT TG
                                       CG  _  C
GAM3145  LOC202934 3'  AGACAAAAAGAAAGAAAA    71411
                                  AGGCAAAAAGAAAGAAAA
                                  ||||||||||||||||||
                                  TCTGTTTTTCTTTCTTTT

GAM3145  LOC203197 3'  AGGCAAAGAAAGCAAC     71412       AA     AA
                                  AGGCAA  AGAAAG  AAC
                                  ||||||  ||||||  |||
                                  TCCGTT  TCTTTC  TTG
                                     __     G_
GAM3145  LOC205327 3'  GGCAGAAGGAAACTTCACCCA  71413     AAAA  A   A__
                                  GGCA   GAA GAAA   CACCCA
                                  ||||   ||| ||||   ||||||
                                  CCGT   CTT CTTT   GTGGGT
                                    _____  C   GAA
GAM3145  LOC220073 5'  AGGCTGAAAAGAACACCC    71351     AAAAA     AA
                                  AGGC    GAAAGA  ACACCC
                                  ||||    ||||||  ||||||
                                  TCCG    TTTTCT  TGTGGG
                                    AC___     __
GAM3145  LOC221354 3'  AGCTTCCAGGAGAACACCCA  71414    AAAA  AAA  A
                                  GGC   AG   GA AACACCCA
                                  |||   ||   || ||||||||
                                  TCG   TC   CT TTGTGGGT
                                    AAGG  ___  C
GAM3145  LOC221687 3'  GACTTAAGAGAGAAAACACC  71415    AAA   A
                                  GGC   AAGA AGAAAACACC
                                  |||   |||| ||||||||||
                                  CTG   TTCT TCTTTTGTGG
                                    AA_   C
GAM3145  LOC221964 3'  AGGATAAGAAAGACACC    71416    CAAA      AAA
                                  AGG   AAGAAAGA   CACC
                                  |||   ||||||||   ||||
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                                TCC    TTCTTTCT   GTGG
                                  TA__      ___
GAM3145  LOC253143 5'  GACAAGAAGAAAGAAAAGGTCC 71417       A         CAC
              A                    GGCAA AAGAAAGAAAA   CCA
                                   ||||| ||||||||||   |||
                                   CTGTT TTCTTTCTTTT   GGT
                                      C          CCA
GAM3145  LOC255147 5'  AGGCAGAAAGAAACAC      71418       AAAA       A
                                   AGGCA    GAAAGAAA CAC
                                   ||||||    |||||||| |||
                                   TCCGT    CTTTCTTT GTG
                                     _____      _
GAM3145  LOC255272 3'  GGAAAAAAAAAAGTGCCCA    71326    C         AAAACA
                                   GG AAAAAGAAAG      CCCA
                                   || ||||||||||      ||||
                                   CC TTTTTTTTTC      GGGT
                                    T         AC_____
GAM3145  LOC255465 3'  AGACAAAAAGAAAGAAAA     71411
                                   AGGCAAAAAGAAAGAAAA
                                   ||||||||||||||||||
                                   TCTGTTTTTCTTTCTTTT

GAM3145  LOC255518 3'  AGGAAGAGGAAAGAAATTTCCC 71419     CAAAAA       ACA
              A                    AGG     GAAAGAAA   CCCA
                                   |||     ||||||||   ||||
                                   TCC     CTTTCTTT   GGGT
                                     TTCTC_       AAA
GAM3145  LOC256733 5'  AGGAAAAAAGAAAGAAAA     71304     C
                                   AGG AAAAAGAAAGAAAA
                                   ||| ||||||||||||||
                                   TCC TTTTTCTTTCTTTT
                                     T
GAM3145  LOC51644  3'  AGGCAAAGGGAGGAAAACACTC 71420        AA  AA       C
              A                    AGGCAAA  GA  GAAAACAC CA
                                   |||||||  ||  |||||||| ||
                                   TCCGTTT  CT  CTTTTGTG GT
                                       CC  C_       A
GAM3145  LOC89919  5'  GACAAAGGCTGTGAAAACACTC 71421       AAGAAA       C
              A                    GGCAAA     GAAAACAC CA
                                   ||||||     |||||||| ||
                                   CTGTTT     CTTTTGTG GT
                                      CCGACA       A
GAM3145  LOC90777  3'  GGCAAAGAAAAGAAACA     71422       AA     GA
                                   GGCAA  AGAAA  AAACA
                                   |||||  |||||  |||||
                                   CCGTT  TCTTT  TTTGT
                                      __     TC
GAM3145  LOC91012  3'  GGCAAAAAAGAAGGAGAA     71423         _   __
                                   GGCAAAAA GAA  AGAA
                                   |||||||| |||  ||||
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                                CCGTTTTT CTT  TCTT
                                     T   CC
GAM3145 LOC91069 3' AGGCTGAAAAGAACACCC    71351     AAAAA     AA
                                AGGC    GAAAGA  ACACCC
                                ||||    ||||||  ||||||
                                TCCG    TTTTCT  TGTGGG
                                  AC___     __
GAM3145 LOC91660 5' AGCCAAAAAGAAGATAAACA  71424    G       A _
                                AG CAAAAAGAA GA AAACA
                                || |||||||| || |||||
                                TC GTTTTTCTT CT TTTGT
                                 G       _ A
GAM3146 AGA     3' TGTAGAGTTGTCATACAGAGAG 71427      ATG       CC
             TT                  TGTAGA   GTCATATGG  AGTT
                                ||||||   |||||||||  ||||
                                ACATCT   CAGTATGTC  TCAA
                                   CAA       TC
GAM3146 CUTL1   3' TAGGGTGGTCCACAGCCAGTT  71428    AA    A
                                TAG  TGGTC TATGGCCAGTT
                                |||  ||||| ||||||||||
                                ATC  ACCAG GTGTCGGTCAA
                                  CC    _
GAM3146 VHL     3' TGTAGAATGTCAATCCTAGTT  71429       G   TATGG _
                                TGTAGAATG TCA    CC AGTT
                                ||||||||| |||    || ||||
                                ACATCTTAC AGT    GG TCAA
                                      _  TA___  A
GAM3146 ERp44   3' TGTAGAATGTCATCTAAAAGTT 71430       G   ATGGCC
                                TGTAGAATG TCAT     AGTT
                                ||||||||| ||||     ||||
                                ACATCTTAC AGTA     TCAA
                                      _   GATTT_
GAM3146 KIAA1034 3' TGTGGGACTGTTTAATGGCCAG 71431    A_  ATG  CAT
             TT                  TGT  GA   GT   ATGGCCAGTT
                                ||| ||  ||  ||||||||||
                                ACA  CT   CA   TACCGGTCAA
                                  CC  GA_  AAT
GAM3147 APPBP2  3' ATGTGCACAAAACCAAAAAATA 71434      G   ATGTGT
                                ATGTGCA AAAA     AAATA
                                ||||||| ||||     |||||
                                TACACGT TTTT     TTTAT
                                   G   GGTTT_
GAM3147 ARG2    3' TGTGAGAATGTGTAAAT    71435     C   AAA
                                TGTG AGA   ATGTGTAAAT
                                |||| |||   ||||||||||
                                ACAC TCT   TACACATTTA
                                  _  ____
GAM3147 ATRX    5' CATGTGCACAAGGAATCAAATA 71436       G  AAATGTG
                                CATGTGCA AA      TAAATA
                                |||||||| ||      ||||||
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                                GTACACGT TT      GTTTAT
                                     G  CCTTA__
GAM3147  BID      3'  ATGTGCAGATTCATGTGT    71437         AAA
                                ATGTGCAGA   ATGTGT
                                |||||||||   ||||||
                                TACACGTCT   TACACA
                                     AAG
GAM3147  CAPZA1   3'  CATGTGCAGGGAATGTG     71438         AAA
                                CATGTGCAG   AATGTG
                                |||||||||   ||||||
                                GTACACGTC   TTACAC
                                     CC_
GAM3147  CD5L     3'  GTGTAAATGTGTAAAT      71439     CAGAA
                                GTG    AAATGTGTAAAT
                                |||    ||||||||||||
                                CAC    TTTACACATTTA
                                  A____
GAM3147  CHST1    3'  TGTGCGTGTGTGGATGTGTAAA 71440      AGAAAA__
              T                  TGTGC       ATGTGTAAAT
                                 |||||       ||||||||||
                                 ACACG       TACACATTTA
                                    CACACACC
GAM3147  CYP3A4   3'  ATGTGCAGGAAAGCATCTG    71441        _  A_  G
                                ATGTGCAG AAA  AT TG
                                |||||||| |||  || ||
                                TACACGTC TTT  TA AC
                                     C   CG  G
GAM3147  EGFL3    3'  CATGTGCAGTGGCCCATAAATA 71442         AAAAATGT
                                CATGTGCAG       GTAAATA
                                |||||||||       |||||||
                                GTACACGTC       TATTTAT
                                     ACCGGG__
GAM3147  EIF1A    3'  ATGTACAGAAGCCTAAAT    71443         AAAT  G
                                ATGTGCAGAA    GT TAAAT
                                ||||||||||    || |||||
                                TACATGTCTT    CG ATTTA
                                     _____  G
GAM3147  FCAR     3'  ATGTGCAGAAAGGTGGGT    71444          AA  T
                                ATGTGCAGAAA  TG GT
                                ||||||||||  || ||
                                TACACGTCTTT  AC CA
                                      CC  C
GAM3147  FCAR     3'  ATGTGCAGAAAGGTGGGT    71444          AA  T
                                ATGTGCAGAAA  TG GT
                                ||||||||||  || ||
                                TACACGTCTTT  AC CA
                                      CC  C
GAM3147  FCAR     3'  ATGTGCAGAAAGGTGGGT    71444          AA  T
                                ATGTGCAGAAA  TG GT
                                ||||||||||  || ||
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                                TACACGTCTTT  AC CA
                                      CC  C
GAM3147  FCAR     3'  ATGTGCAGAAAGGTGGGT    71444          AA  T
                                ATGTGCAGAAA  TG GT
                                ||||||||||  || ||
                                TACACGTCTTT  AC CA
                                      CC  C
GAM3147  FCAR     3'  ATGTGCAGAAAGGTGGGT    71444          AA  T
                                ATGTGCAGAAA  TG GT
                                ||||||||||  || ||
                                TACACGTCTTT  AC CA
                                      CC  C
GAM3147  GPR48    3'  TATCAGATGTGTAAATA     71445     G    AAAA
                                TGT CAGA    TGTGTAAATA
                                ||| ||||    ||||||||||
                                ATA GTCT    ACACATTTAT
                                  _   ____
GAM3147  MANBA    3'  CATGTACAGAAAAATACCCA  71446             TG
                                CATGTGCAGAAAAATG  TA
                                ||||||||||||||||  ||
                                GTACATGTCTTTTTAT  GT
                                      GG
GAM3147  PREP     3'  TGCAGAAAGGTGAAAT      71447        AAT   T
                                TGCAGAAA   GTG AAAT
                                ||||||||   ||| ||||
                                ACGTCTTT   CAC TTTA
                                     C__   _
GAM3147  WASF3    3'  CATGTGCAGAGGTAATGAAAT  71448          AAAAT   T
                                CATGTGCAGA     GTG AAAT
                                ||||||||||     ||| ||||
                                GTACACGTCT     TAC TTTA
                                      CCAT_   _
GAM3147  ZNF141   3'  CATGTGCAAAAAGATGAGCA   71449           A   T
                                CATGTGCAGAAA ATG GTA
                                |||||||||||| ||| |||
                                GTACACGTTTTT TAC CGT
                                       C   T
GAM3147  DKFZp434K2435 3'  TGCAGAAAGATATACGAATA   71450         A    TA
                                TGCAGAAA ATGTG  AATA
                                |||||||| |||||  ||||
                                ACGTCTTT TATAT  TTAT
                                     C    GC
GAM3147  FLJ10824 3'  GTGCAGAAAAATACCAAGTA   71451           T___
                                GTGCAGAAAAATG    GTA
                                ||||||||||||    |||
                                CACGTCTTTTTAT    CAT
                                       GGTT
GAM3147  FLJ10829 3'  ATGTGGAATATATGTAAATA   71452       CA   AA
                                ATGTG  GAA  ATGTGTAAATA
                                |||||  |||  ||||||||||
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                                TACAC  CTT  TATACATTTAT
                                  __  A_
GAM3147  FLJ11259  3'  TGTGCAGAGAGATGTGAAAAT  71453        AAA    T
                                TGTGCAGA   ATGTG AAAT
                                ||||||||   ||||| ||||
                                ACACGTCT   TACAC TTTA
                                    CTC    T
GAM3147  FLJ20069  3'  CATGTGCAGGGATAAGAGCCAA 71454        AAAAATGT  _
           ATA                   CATGTGCAG      GT AAATA
                                |||||||||       || |||||
                                GTACACGTC       CG TTTAT
                                    CCTATTCT  G
GAM3147  FLJ20275  3'  CATGTGCACAAAAAGAGTA   71455        G    TGT
                                CATGTGCA AAAAA   GTA
                                |||||||| |||||   |||
                                GTACACGT TTTTT   CAT
                                    G    CT_
GAM3147  FLJ20373  3'  CATGTGCATGAGAAAAGAGTA  71456        ___    AT
                                CATGTGCA   GAAAA  GTG
                                ||||||||   |||||  |||
                                GTACACGT   CTTTT  CAT
                                    ACT    CT
GAM3147  FLJ20986  3'  TAATACATTAAAAATGTGTAAA 71457   T    G_
           T                    A GTGCA  AAAAATGTGTAAAT
                                | |||||  ||||||||||||||
                                A TATGT  TTTTTACACATTTA
                                 T    AA
GAM3147  FLJ22195  5'  CATGTGCACAGAAAATAGGTG  71458        __    AT_
                                CATGTGCA  GAAAA   GTG
                                ||||||||  |||||   |||
                                GTACACGT  CTTTT   CAC
                                    GT    ATC
GAM3147  GIT2      3'  CATGTGCAAAAGGTGGC     71459         AAA  T
                                CATGTGCAGAA   TG GT
                                ||||||||||   || ||
                                GTACACGTTTT   AC CG
                                    CC_  _
GAM3147  GIT2      3'  CATGTGCAAAAGGTGGC     71459         AAA  T
                                CATGTGCAGAA   TG GT
                                ||||||||||   || ||
                                GTACACGTTTT   AC CG
                                    CC_  _
GAM3147  GIT2      3'  CATGTGCAAAAGGTGGC     71459         AAA  T
                                CATGTGCAGAA   TG GT
                                ||||||||||   || ||
                                GTACACGTTTT   AC CG
                                    CC_  _
GAM3147  GTPBP1    3'  ATGTACAAAAAATGTGT     71460          A
                                ATGTGCAGAAAA TGTGT
                                |||||||||||| |||||
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                                TACATGTTTTTT ACACA
                                          _
GAM3147  HIC      3'  ATGTGTGTATGTATGTGTAAAT 71461      CAGAAAA
              A                  ATGTG      ATGTGTAAATA
                                 |||||      ||||||||||
                                 TACAC      TACACATTTAT
                                    ACATACA
GAM3147  KIAA0063 3'  CATGTGCAGAAAAAGTGC    71462           T
                                 CATGTGCAGAAAAA GTGT
                                 |||||||||||||| ||||
                                 GTACACGTCTTTTT CACG
                                          _
GAM3147  KIAA0433 3'  ATGTGCACAAAGGTGTA     71463       G   AAT
                                 ATGTGCA AAA   GTGTA
                                 ||||||| |||   |||||
                                 TACACGT TTT   CACAT
                                     G   C__
GAM3147  KIAA0441 3'  ATGTGCAGAAAGTGTAAA    71464         AAT
                                 ATGTGCAGAAA   GTGTAAA
                                 ||||||||||   |||||||
                                 TACACGTCTTT   CACATTT
                                          ___
GAM3147  KIAA0871 5'  TGTGCAGAAAAAAAAATA    71465          TGT
                                 TGTGCAGAAAAA   GTA
                                 ||||||||||||   |||
                                 ACACGTCTTTTT   TAT
                                        TTT
GAM3147  KIAA0884 3'  ATGTGCTGTGTGTAAATA    71466       AGAAAAA
                                 ATGTGC      TGTGTAAATA
                                 ||||||      ||||||||||
                                 TACACG      ACACATTTAT
                                    AC_____
GAM3147  KIAA0894 3'  ATGTCAGAAGAATACGTA    71467      G    A
                                 ATGT CAGAA AATGTGTA
                                 |||| ||||| ||||||||
                                 TACA GTCTT TTATGCAT
                                    _    C
GAM3147  KIAA1265 3'  ACGTGCAGGGAAAACAGTA   71468        A_     T
                                 ATGTGCAG  AAAATG GTA
                                 ||||||||  |||||| |||
                                 TGCACGTC  TTTTGT CAT
                                      CC     _
GAM3147  KIAA1297 5'  CATGTACAGATGTAA       71469          AAAATG
                                 CATGTGCAGA     TGTAA
                                 ||||||||||     |||||
                                 GTACATGTCT     ACATT
                                          _____
GAM3147  KIAA1550 3'  CATGTGCAAGTGTGAGTGTGTA 71470          AAAAA__
              A                  CATGTGCAG      TGTGTAA
                                 |||||||||      |||||||
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                                GTACACGTT      ACACATT
                                     CACACTC
GAM3147 KIAA1613 3' ATGTGGGAAAAATGGC      71471      CA       T
                                ATGTG  GAAAAATG GT
                                |||||  |||||||| ||
                                TACAC  CTTTTTAC CG
                                  C_       _
GAM3147 KIAA1715 3' ATATGCTAGTGTGTAAAT    71472       _ AAAAA
                                ATGTGC AG    TGTGTAAAT
                                |||||| ||    |||||||||
                                TATACG TC    ACACATTTA
                                   A ______
GAM3147 KRTHB2   3' ATGTACAGAAGGGGATGGGT   71473         AA__   T
                                ATGTGCAGAA    ATG GT
                                ||||||||||    ||| ||
                                TACATGTCTT    TAC CA
                                      CCCC   C
GAM3147 MGC13090 5' TGTGTCAGAAAAACTGAGGTG  71474     _       _____
                                TGTG CAGAAAAAT    GTG
                                |||| |||||||||    |||
                                ACAC GTCTTTTTG    CAC
                                  A        ACTC
GAM3147 MGC4655  3' TGTACAGATTTTTGTAAATA   71475        AAAATG
                                TGTGCAGA     TGTAAATA
                                ||||||||     ||||||||
                                ACATGTCT     ACATTTAT
                                     AAAA__
GAM3147 NCOA2    5' GTGCAGAAGATCTATAA     71476        AA  G
                                GTGCAGAA  AT TGTAA
                                ||||||||  || |||||
                                CACGTCTT  TA ATATT
                                     C_  G
GAM3147 PEGASUS  3' ATGGGCAGAAAATGGATA    71477     T       A  TG
                                ATG GCAGAAAA TG  TA
                                ||| |||||||| ||  ||
                                TAC CGTCTTTT AC  AT
                                  C       _ CT
GAM3147 RBT1     3' GTGGAAGAAATGTGTAA     71478     CA  _
                                GTG  GAA AAATGTGTAA
                                |||  ||| ||||||||||
                                CAC  CTT TTTACACATT
                                  __  C
GAM3147 SEMA5A   3' CAGGTGCAGAAAGGTGTA    71479    T       AAT
                                CA GTGCAGAAA   GTGTA
                                || |||||||||   |||||
                                GT CACGTCTTT   CACAT
                                 C        C__
GAM3147 SSH3BP1  3' CATAAAGTTAAAAATGTGTAA  71480      TGCAG
                                CATG    AAAAATGTGTAA
                                ||||    ||||||||||||
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                                GTAT    TTTTTACACATT
                                  TTCAA
GAM3147  SSX5     3'  CATGTGTGTGTGTTTGTGTAAA 71481       CAGAAAAA
             T                   CATGTG       TGTGTAAAT
                                 ||||||       |||||||||
                                 GTACAC       ACACATTTA
                                    ACACACAA
GAM3147  LOC113115 3'  ATGTACAGAAGAACAGAGTA   71482         A   GT_
                                 ATGTGCAGAA AAT   GTA
                                 |||||||||| |||   |||
                                 TACATGTCTT TTG   CAT
                                       C   TCT
GAM3147  LOC149448 3'  GTGCAGAAAGAACGAGAAATA  71483         _    TGT
                                 GTGCAGAAA AATG   AAATA
                                 ||||||||| ||||   |||||
                                 CACGTCTTT TTGC   TTTAT
                                       C    TC_
GAM3147  LOC222008 3'  TGTTCTTATAATGTGTAAATA  71484     GCAGAAA
                                 TGT      AATGTGTAAATA
                                 |||      ||||||||||||
                                 ACA      TTACACATTTAT
                                   AGAATA_
GAM3147  LOC253725 3'  GTGCAGAAAAATACTAAGTA   71485           T___
                                 GTGCAGAAAAATG    GTA
                                 ||||||||||||    |||
                                 CACGTCTTTTTAT    CAT
                                        GATT
GAM3147  LOC254314 3'  CATGTGCACAGAAATGGAGC   71486        GAA    T_
                                 CATGTGCA   AAATG  GT
                                 ||||||||   |||||  ||
                                 GTACACGT   TTTAC  CG
                                      GTC    CT
GAM3147  LOC255978 5'  CATGTGCGGGAAATGTA     71487        A_   AAAT
                                 CATGTGC  GAA    GTGTA
                                 |||||||  |||    |||||
                                 GTACACG  CTT    TACAT
                                     CC  ____
GAM3147  LOC92017  5'  CATGTGCAGAATGTCCAA     71488          AAA    G
                                 CATGTGCAGA   ATGT TAA
                                 ||||||||||   |||| |||
                                 GTACACGTCT   TACA GTT
                                        ___    G
GAM3148  BCRP2     3'  TCTCTGGAGATGAGGGTGG    71491    C     T    ACTA  _
                                 TC CTGGAG ATGAG    GG GG
                                 || |||||| |||||    || ||
                                 AG GACCTC TACTC    CC CC
                                  A     _    ____  A
GAM3148  FVT1      3'  CTGGACTTAATCTCTAGGGGG  71492      GTA   GA_
                                 CTGGA   TGA   CTAGGGGG
                                 |||||   |||   ||||||||
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                                GACCT   ATT   GATCCCCC
                                  GA_   AGA
GAM3148  G6PT1    3'  TCCCTGGAGTCTGAGGTATTGG 71493         A    ACTAG
                                TCCCTGGAGT TGAG    GG
                                |||||||||| ||||    ||
                                AGGGACCTCA ACTC    CC
                                     G   CATAA
GAM3148  APCL     3'  CCCTGGAGCATTGGGGG    71494          GAGACTA
                                CCCTGGAGTAT     GGGG
                                ||||||||||      ||||
                                GGGACCTCGTA     CCCC
                                     AC_____
GAM3148  BRPF3    3'  TCCCTGGAGTTGGGAAGTGGG  71495         A  A  CT  _
                                TCCCTGGAGT TG GA  AG GGG
                                |||||||||| || ||  || |||
                                AGGGACCTCA AC CT  TC CCC
                                     _  C  __  A
GAM3148  FLJ13479 3'  CCCGGAGTGTGGTGCTGGGGGG 71496        A  AGA  A
                                CCTGGAGT TG   CT GGGGG
                                |||||||| ||   || |||||
                                GGGCCTCA AC   GA CCCCC
                                     C  CAC  C
GAM3148  FLJ20297 3'  CCTGGAGTGGAGACTTAAG   71497        AT     AG
                                CCTGGAGT  GAGACT  GG
                                ||||||||  ||||||  ||
                                GGACCTCA  CTCTGA  TC
                                     C_     AT
GAM3148  FLJ20297 3'  CCTGGAGTGGAGACTTAAG   71497        AT     AG
                                CCTGGAGT  GAGACT  GG
                                ||||||||  ||||||  ||
                                GGACCTCA  CTCTGA  TC
                                     C_     AT
GAM3148  KIAA0290 3'  TCCGTGGAGTATGGGCCTCAGG 71498     C       AGA  A
            G                    TCC TGGAGTATG   CT GGGG
                                ||| |||||||||   || ||||
                                AGG ACCTCATAC   GA TCCC
                                  C       CCG  G
GAM3148  KIAA0429 5'  CCTGGAGTGTGATTTTGGGG   71499        A   GACTA
                                CCTGGAGT TGA    GGGG
                                |||||||| |||    ||||
                                GGACCTCA ACT    CCCC
                                     C   AAAA_
GAM3148  KIAA0821 5'  CCCGGAGCCGGGGCTGGGGGG  71500        ATGAGA  A
                                CCTGGAGT     CT GGGGG
                                ||||||||     || |||||
                                GGGCCTCG     GA CCCCC
                                     GCCCC_  C
GAM3148  NBL1     3'  TCCCTGGAGATGGGAAGTGGGG 71501         T   A  CTA
                                TCCCTGGAG ATG GA   GGGG
                                ||||||||| ||| ||   ||||
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                                AGGGACCTC TAC CT   CCCC
                                      _  C  TCA
GAM3148  PTPRT    3'  TCCCTGGAGTTGAGCGGG    71502         A    ACTA
                                TCCCTGGAGT TGAG    GGG
                                |||||||||| ||||    |||
                                AGGGACCTCA ACTC    CCC
                                      _   G___
GAM3148  TCL6     3'  TCCTTGGGGATGAGACAG    71503     C   AGT      T
                                TCC TGG   ATGAGAC AG
                                ||| |||   ||||||| ||
                                AGG ACC   TACTCTG TC
                                  A  CC_     _
GAM3148  TCL6     3'  TCCTTGGGGATGAGACAG    71503     C   AGT      T
                                TCC TGG   ATGAGAC AG
                                ||| |||   ||||||| ||
                                AGG ACC   TACTCTG TC
                                  A  CC_     _
GAM3148  LOC150358 3'  CTGAGCACCGCTAGGGGG    71504     G    GAGA
                                CTG AGTAT    CTAGGGGG
                                ||| |||||    ||||||||
                                GAC TCGTG    GATCCCCC
                                  _    GC__
GAM3148  LOC150776 3'  CCTGGAGTGGAGACTTAAG    71497        AT     AG
                                CCTGGAGT  GAGACT  GG
                                ||||||||  ||||||  ||
                                GGACCTCA  CTCTGA  TC
                                     C_     AT
GAM3148  LOC196746 3'  TCCCTGGGGCATGAGATGGG   71505        A       CTA
                                TCCCTGG GTATGAGA   GGG
                                ||||||| ||||||||   |||
                                AGGGACC CGTACTCT   CCC
                                    C       A__
GAM3148  LOC203378 5'  TCCCTGGAGTGTGAGGGAAAGG 71506          A    ACT
                                TCCCTGGAGT TGAG   AGGG
                                |||||||||| ||||   ||||
                                AGGGACCTCA ACTC   TTCC
                                      C    CCT
GAM3149  CHN1     3'  TATAAAACATTCCTTCATCT   71509          AGCA
                                TATAAAGCATTT    CATCT
                                ||||||||||||    |||||
                                ATATTTTGTAAG    GTAGA
                                       GAA_
GAM3149  MAP3K7IP2 3'  TAAAGCATTTAAACTTCT    71510          C  A
                                TAAAGCATTTAG AC TCT
                                |||||||||||| || |||
                                ATTTCGTAAATT TG AGA
                                      _ A
GAM3149  RTDR1    3'  TAAAGAGACTTAGCACAT    71511       C_
                                TAAAG  ATTTAGCACAT
                                |||||  ||||||||||
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                                ATTTC  TGAATCGTGTA
                                   TC
GAM3149  STAU2    3'  TATAAAGCATTTCATTATTCT  71512          AGCACA
                                TATAAAGCATTT     TCT
                                ||||||||||||     |||
                                ATATTTCGTAAA     AGA
                                      GTAATA
GAM3149  ALDH9    3'  TACAAGGCACTTAATGCACAT  71513      A     __
                                TATAA GCATTTA  GCACAT
                                ||||| |||||||  ||||||
                                ATGTT CGTGAAT  CGTGTA
                                   C      TA
GAM3149  CHUK     3'  TAAAAGCATTTCACAT     71514   T       AG
                                A AAAGCATTT  CACAT
                                | |||||||||  |||||
                                A TTTCGTAAA  GTGTA
                                 T      __
GAM3149  DKFZp547G183 3'  TATAAAGCACTTAGTACA    71515           C
                                TATAAAGCATTTAG ACA
                                |||||||||||||| |||
                                ATATTTCGTGAATC TGT
                                         A
GAM3149  DKFZp564K142 3'  TAAGGCACTACACATCT     71516     A     TA
                                TAA GCATT  GCACATCT
                                ||| |||||  ||||||||
                                ATT CGTGA  TGTGTAGA
                                  C    __
GAM3149  FLJ10813  5'  TAAAGCATTAGCTCATCT    71517         T   A
                                TAAAGCATT AGC CATCT
                                ||||||||| ||| |||||
                                ATTTCGTAA TCG GTAGA
                                      _  A
GAM3149  FLJ13855  3'  TACAGGGCACCTAAAGCACAT  71518      AA     __
                                TATA  GCATTT  AGCACAT
                                ||||  ||||||  |||||||
                                ATGT  CGTGGA  TCGTGTA
                                   CC     TT
GAM3149  FLJ20015  3'  TATAAAGCACTCTTCAAACATC 71519           AG __
            T                    TATAAAGCATTT  C  ACATCT
                                ||||||||||||  |  ||||||
                                ATATTTCGTGAG  G  TGTAGA
                                      AA TT
GAM3149  KIAA0408  3'  TATAAAACATTTATGAACAT   71520           GC_
                                TATAAAGCATTTA   ACAT
                                ||||||||||||   ||||
                                ATATTTTGTAAAT   TGTA
                                         ACT
GAM3149  KIAA0555  3'  TAGAGCACTCACACCATCT   71521    A      G   _
                                TA AGCATTTA CAC ATCT
                                || |||||||| ||| ||||
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                                AT TCGTGAGT GTG TAGA
                                 C       _  G
GAM3149 KIAA1211 3' TACAAAGTTGACACATCT    71522       CAT  AG
                                TATAAAG   TT  CACATCT
                                |||||||   ||  |||||||
                                ATGTTTC   AA  GTGTAGA
                                    ___  CT
GAM3149 KIAA1240 5' ATAAAGCATTTTCATCT     71523         AGCA
                                ATAAAGCATTT   CATCT
                                ||||||||||    |||||
                                TATTTCGTAAA   GTAGA
                                      A___
GAM3149 MGC12466 3' ATAAAGTGTTCTAACACAT   71524      CA_
                                ATAAAG   TTTAGCACAT
                                ||||||   ||||||||||
                                TATTTC   AGATTGTGTA
                                   ACA
GAM3149 MGC12466 3' ATAAAGTGTTCTAACACAT   71524      CA_
                                ATAAAG   TTTAGCACAT
                                ||||||   ||||||||||
                                TATTTC   AGATTGTGTA
                                   ACA
GAM3149 NAT5     3' CATAAAGCATCTAGAGTATCT 71525           CAC
                                TATAAAGCATTTAG   ATCT
                                ||||||||||||||   ||||
                                GTATTTCGTAGATC   TAGA
                                      TCA
GAM3149 NMA      3' TAAAAGCAAATAACACAT    71526   T     TT
                                A AAAGCA  TAGCACAT
                                | ||||||  ||||||||
                                A TTTCGT  ATTGTGTA
                                 T     TT
GAM3149 ORF1-FL49 3' AAAGTCATTTAGCACATCT   71527     _
                                AAAG CATTTAGCACATCT
                                |||| ||||||||||||||
                                TTTC GTAAATCGTGTAGA
                                  A
GAM3149 POLE3    3' TACAAAGCATTACAATCT    71528         TA   C
                                TATAAAGCATT  GCA ATCT
                                ||||||||||  ||| ||||
                                ATGTTTCGTAA  TGT TAGA
                                      __  _
GAM3149 RI58     3' TATAAAGTATTTAGCACA    71529       C
                                TATAAAG ATTTAGCACA
                                ||||||| ||||||||||
                                ATATTTC TAAATCGTGT
                                   A
GAM3149 RNF8     3' TAAAGCATTTTTTCCACAT   71530         AG__
                                TAAAGCATTT   CACAT
                                |||||||||    |||||
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                                ATTTCGTAAA   GTGTA
                                     AAAG
GAM3149  STRN3    3'  CATAAATTAAGCACATCT    71531      GCATTT
                                TATAAA     AGCACATCT
                                ||||||     |||||||||
                                GTATTT     TCGTGTAGA
                                   AAT___
GAM3149  LOC121536 3'  TATAAAGCTAGCTCAT      71532       ATT   A
                                TATAAAGC   TAGC CAT
                                ||||||||   |||| |||
                                ATATTTCG   ATCG GTA
                                     ___   A
GAM3149  LOC144962 5'  TGAAAGCATTTCTTCATCT    71533   T       AGCA
                                A AAAGCATTT    CATCT
                                | |||||||||    |||||
                                A TTTCGTAAA    GTAGA
                                 C       GAA_
GAM3149  LOC145945 3'  TATAAAGCATTTACAACA    71534          GC
                                TATAAAGCATTTA  ACA
                                ||||||||||||  |||
                                ATATTTCGTAAAT  TGT
                                      GT
GAM3149  LOC149373 3'  TATAAAACAAAGGCACGTCT   71535        TTTA   A
                                TATAAAGCA    GCAC TCT
                                |||||||||    |||| |||
                                ATATTTTGT    CGTG AGA
                                     TTC_    C
GAM3149  LOC150933 3'  TATAAAACACTTCTGCACAT   71536         A_
                                TATAAAGCATTT  GCACAT
                                ||||||||||||  ||||||
                                ATATTTTGTGAA  CGTGTA
                                      GA
GAM3149  LOC154866 3'  TACAAAAATAACAGCACAT    71537       CATT
                                TATAAAG    TAGCACAT
                                |||||||    ||||||||
                                ATGTTTT    GTCGTGTA
                                    TATT
GAM3149  LOC81034  3'  TATAAAGCATTCATC       71538         TAGCA
                                TATAAAGCATT    CATC
                                ||||||||||     ||||
                                ATATTTCGTAA    GTAG
                                     _____
GAM3150  PCDHB13   3'  CTGGGTTAAAGAATGAATTGT  71541       CATTTA
                                CTGGGT     GATGAATTGT
                                ||||||     ||||||||||
                                GACCCA     TTACTTAACA
                                   ATTTC_
GAM3150  TGFA     3'  CACGGGTCATAGAATT      71542     T     TTAGAT
                                CAC GGGTCAT     GAATT
                                ||| |||||||     |||||
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                                GTG CCCAGTA     CTTAA
                                  _     T_____
GAM3150 BHMT     3' CTGGGTCATTATATAAATTGT 71543         TAG
                                CTGGGTCATT  ATGAATTGT
                                ||||||||||  |||||||||
                                GACCCAGTAA  TATTTAACA
                                     TA_
GAM3150 KIAA0563 5' CACTAGGTTATTTCACCATTGT 71544        C   AGATGA
                                CACTGGGT ATTT     ATTGT
                                |||||||| ||||     |||||
                                GTGATCCA TAAA     TAACA
                                    A   GTGG__
GAM3150 ZTL1     3' ACTGAGTCATTTAATCTTCATT 71545           ATGA_
             GT                   ACTGGGTCATTTAG    ATTGT
                                |||||||||||||     |||||
                                TGACTCAGTAAATT    TAACA
                                      AGAAG
GAM3150 LOC144747 5' CACTGGGTTATTTGAATGATTG 71546        C   AG   A
             T                    CACTGGGT ATTT  ATGA TTGT
                                |||||||| ||||  |||| ||||
                                GTGACCCA TAAA  TACT AACA
                                    A   CT   _
GAM3150 LOC147343 5' CACTGAGTCATTTACTTG    71547           GA
                                CACTGGGTCATTTA  TG
                                ||||||||||||||  ||
                                GTGACTCAGTAAAT  AC
                                      GA
GAM3150 LOC158130 3' CATTGGGTGATCTTTGAATTGT 71548    C    C   AGA
                                CA TGGGT ATTT   TGAATTGT
                                || ||||| ||||   ||||||||
                                GT ACCCA TAGA   ACTTAACA
                                 A    C   A__
GAM3151 LOC197287 3' CCTCCTCCCTCGAGACGGTG   71551    GTACA
                                CC    CCTCGAGACGGTG
                                ||    ||||||||||||||
                                GG    GGAGCTCTGCCAC
                                 AGGAG
GAM3152 ATP8A2   3' TCCCTATAGTGAGACGAACC   71554          A  T
                                TCCCTATAGTGA AC GATT
                                |||||||||||| || ||||
                                AGGGATATCACT TG TTGG
                                      C  C
GAM3152 CRIM1    3' TCCAGGAGCTGATTAGT     71555     CTAT  T  AA
                                TCC   AG GA  CTGATTAGT
                                |||   || ||  |||||||||
                                AGG   TC CT  GACTAATCA
                                  _____  _  C_
GAM3152 FOP      3' TCCCTGTAATGAAACTGA    71556       A
                                TCCCT TAGTGAAACTGA
                                ||||| ||||||||||||
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                                AGGGA ATTACTTTGACT
                                  C
GAM3152 CIB1     3' CCTTTATTACTGATTAGT    71557     A  GTGAA
                                CCT TA    ACTGATTAGT
                                ||| ||    ||||||||||
                                GGA AT    TGACTAATCA
                                  A  AA___
GAM3152 CTDP1    3' CCTGTAGTAAAACTTCTTA   71558     A        GA
                                CCT TAGTGAAACT  TTA
                                ||| ||||||||||  |||
                                GGA ATCATTTTGA  AAT
                                  C         AG
GAM3152 DCOHM    3' TCTCTATAGTAAAGTCTG    71559    C        A_
                                TC CTATAGTGAA  CTG
                                || ||||||||||  |||
                                AG GATATCATTT  GAC
                                  A         CA
GAM3152 EVI5     3' TCCCAAATAACTGGCTGATTAG 71560      TAT    AA__
              TA                  TCCC   AGTGA   CTGATTAGTA
                                ||||   |||||   ||||||||||
                                AGGG   TTATT   GACTAATCAT
                                  T__    GACC
GAM3152 FLJ10081 3' CTAGTGGTGAAACCAAGAGTA  71561     TA_      TG TT
                                CTA   GTGAAAC  A  AGTA
                                |||   |||||||  |  ||||
                                GAT   CACTTTG  T  TCAT
                                  CAC      GT C_
GAM3152 KIAA1817 3' TCCCTACAGTGGGACAGT    71562          AAACT   T
                                TCCCTATAGTG    GAT AGT
                                ||||||||||    ||| |||
                                AGGGATGTCAC    CTG TCA
                                      C____   _
GAM3152 PGRMC2   3' TCTTCATAGTGAGATTAAT   71563    CC       AACT
                                TC  TATAGTGA   GATTAGT
                                ||  ||||||||   |||||||
                                AG  GTATCACT   CTAATTA
                                  AA       ____
GAM3152 LOC200862 5' TCTCTATAGTAGAAACTA   71564    C      _
                                TC CTATAGT GAAACTG
                                || ||||||| |||||||
                                AG GATATCA CTTTGAT
                                  A      T
GAM3152 LOC56267 3' CCCTTGTGGTCTGTGATTAGTA 71565      ATA   AAAC_
                                CCCT   GTG    TGATTAGTA
                                ||||   |||    |||||||||
                                GGGA   CAC    ACTAATCAT
                                  A__   CAGAC
GAM3153 AMFR     3' AGTTCTTTTTTATTTCTTTAAT 71568        ___
              A                   GGTTCTT   TATTTCTTTAATA
                                |||||||   ||||||||||||
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                                TCAAGAA  ATAAAGAAATTAT
                                   AAA
GAM3153  AMFR     3'  AGTTCTTTTTTATTTCTTTAAT 71568       ___
                A                GGTTCTT  TATTTCTTTAATA
                                 |||||||  ||||||||||||
                                TCAAGAA  ATAAAGAAATTAT
                                   AAA
GAM3153  CD8A     3'  AGTGGTTCTTATTTCCTTA  71569   C     T
                                AG GGTTCTT ATTTCTTTA
                                || ||||||| |||||||||
                                TC CCAAGAA TAAAGGAAT
                                 A     _
GAM3153  NXF5     5'  ACGGCATTATTTCTTTAAT  71570     TCT
                                GCGGT  TTATTTCTTTAAT
                                |||||  ||||||||||||
                                TGCCG  AATAAAGAAATTA
                                   T__
GAM3153  NXF5     5'  ACGGCATTATTTCTTTAAT  71570     TCT
                                GCGGT  TTATTTCTTTAAT
                                |||||  ||||||||||||
                                TGCCG  AATAAAGAAATTA
                                   T__
GAM3153  NXF5     5'  ACGGCATTATTTCTTTAAT  71570     TCT
                                GCGGT  TTATTTCTTTAAT
                                |||||  ||||||||||||
                                TGCCG  AATAAAGAAATTA
                                   T__
GAM3153  NXF5     5'  ACGGCATTATTTCTTTAAT  71570     TCT
                                GCGGT  TTATTTCTTTAAT
                                |||||  ||||||||||||
                                TGCCG  AATAAAGAAATTA
                                   T__
GAM3153  NXF5     5'  ACGGCATTATTTCTTTAAT  71570     TCT
                                GCGGT  TTATTTCTTTAAT
                                |||||  ||||||||||||
                                TGCCG  AATAAAGAAATTA
                                   T__
GAM3153  BNIP-S   3'  AGCGGTTCTTCAAGATTTAAT  71571          TTTC
                                AGCGGTTCTTTA  TTTAAT
                                ||||||||||||  ||||||
                                TCGCCAAGAAGT  AAATTA
                                      TCT_
GAM3153  FLJ12078 3'  AAGCTTTCAATTATTTCTTTAA 71572     GG  T_
                T                AAGC  TTC  TTATTTCTTTAAT
                                 ||||  |||  ||||||||||||
                                TTCG  AAG  AATAAAGAAATTA
                                  A_  TT
GAM3153  FLJ23594 3'  AAGTGGTCTTTATTCAATAAT  71573    C  T     T TT
                                AAG GGT CTTTATT C  TAAT
                                ||| ||| ||||||| |  ||||
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                                TTC CCA GAAATAA G  ATTA
                                  A  _      _ TT
GAM3153  MGC4415   3'  AGTGGTTCTTCTCTTT     71574    C       ATT
                                AG GGTTCTTT   TCTTT
                                || ||||||||   |||||
                                TC CCAAGAAG   AGAAA
                                 A      ___
GAM3153  LOC158927 3'  GGTCCACTTTCTTTAATA    71575      TTTA
                                GGTTC    TTTCTTTAATA
                                |||||    ||||||||||
                                CCAGG    AAAGAAATTAT
                                   TG__
GAM3154  ACN       5'  CCTGGTATAACCATAATCGGAG 71578    GC  CTT__      A
            ATG                    CC  GG    CTATAATC GAGATG
                                ||  ||    |||||||| ||||||
                                GG  CC    GGTATTAG CTCTAC
                                 A_  ATATT       C
GAM3154  BMPR1B    3'  GGCTTTCTGCAGAGATG     71579      _  ATAAT
                                GGCTT CT    CAGAGATG
                                ||||| ||    ||||||||
                                CCGAA GA    GTCTCTAC
                                   A  C____
GAM3154  CERD4     3'  GGCTTCTTAGCAGAGATG    71580       ATAAT
                                GGCTTCT    CAGAGATG
                                |||||||    ||||||||
                                CCGAAGA    GTCTCTAC
                                    ATC__
GAM3154  EGLN1     5'  CCTCGGCTTCTGCCTCGGAG   71581    G       ATAA  A
                                CC CGGCTTCT    TC GAG
                                || ||||||||    || |||
                                GG GCCGAAGA    AG CTC
                                 A       CGG_  C
GAM3154  FREB      3'  CCTGGCTTCTATTTACTGGATG 71582    GC        AATCAGA
                                CC  GGCTTCTAT      GATG
                                ||  |||||||||      ||||
                                GG  CCGAAGATA      CTAC
                                 A_        AATGAC_
GAM3154  KIAA1143  3'  CCTGGCTTCTATAACAAG    71583    GC          C
                                CC  GGCTTCTATAAT AG
                                ||  ||||||||||| ||
                                GG  CCGAAGATATTG TC
                                 A_          T
GAM3154  MGC2452   5'  GGCTTCACCAGAGAT      71584       TATA
                                GGCTTC    ATCAGAGAT
                                ||||||    |||||||||
                                CCGAAG    TGGTCTCTA
                                          ____
GAM3154  LOC123792 3'  CCGCGGCCTCACCAGGGAT    71585          TATA    A
                                CCGCGGCTTC    ATCAG GAT
                                ||||||||||    ||||| |||
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                                GGCGCCGGAG   TGGTC CTA
                                     ____    C
GAM3155 IL1RAP   3' TAAGTAATTAATGAATGAT   71588          AG  A
                                TAAGTAATTAAT  AT GAT
                                |||||||||||  || |||
                                ATTCATTAATTA  TA CTA
                                      CT  _
GAM3155 KIAA1467 3' GTAATTAACAGAGATCCC    71589          TA
                                GTAATTAATAGA  GATTTT
                                |||||||||||  ||||||
                                CATTAATTGTCT  CTAGGG
                                     __
GAM3156 BACH1    3' TAAGCTATAGCAAACTGTTAAA 71592     AA   T
             AA                   TAG  TATA CAAACTGTTAAAAA
                                |||  |||| ||||||||||||||
                                ATT  ATAT GTTTGACAATTTTT
                                  CG   C
GAM3156 CDH6     3' TAGGATATAACAAACTAT    71593     A    T
                                TAG ATATA CAAACTGT
                                ||| ||||| ||||||||
                                ATC TATAT GTTTGATA
                                  C    T
GAM3156 HHIP     3' TAGAATATTCAAACAGTC    71594         A     T
                                TAGAATAT TCAAAC GTT
                                |||||||| |||||| |||
                                ATCTTATA AGTTTG CAG
                                     _     T
GAM3156 MAN1A2   5' TAGAATACATTGAACTGTC   71595          CA
                                TAGAATATAT  AACTGTT
                                ||||||||||  |||||||
                                ATCTTATGTA  TTGACAG
                                      AC
GAM3156 MSX2     3' TAAAATATATCAAATTGT    71596            C
                                TAGAATATATCAAA TGT
                                |||||||||||||| |||
                                ATTTTATATAGTTT ACA
                                       A
GAM3156 SUDD     3' TAAAATATGTCAAACATGGTTA 71597         A     T__
             AA                   TAGAATAT TCAAAC   GTTAAA
                                |||||||| ||||||   ||||||
                                ATTTTATA AGTTTG   CAATTT
                                    C     TAC
GAM3156 DKFZp434B0417 3' GAATATATCACAAGTAAAA   71598          AACT  T
                                GAATATATCA    GT AAAA
                                ||||||||||    || ||||
                                CTTATATAGT    CA TTTT
                                      GTT_  _
GAM3156 FLJ21551 3' AAATATATCTTCTCTGTTAA  71599          AAA_
                                GAATATATC    CTGTTAA
                                |||||||||    |||||||
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                                TTTATATAG   GACAATT
                                    AAGA
GAM3156 KIAA0022 3' TAGAAAGTATCAAAATGTACAA 71600      TA     C  _
            AA                   TAGAA  TATCAAA TGT TAAAA
                                 ||||| ||||||| ||| |||||
                                 ATCTT  ATAGTTT ACA GTTTT
                                    TC      T  T
GAM3156 KIAA0630 3' AGACTATACAAGCTGTTAAAAA 71601    A   T  A
                                 AGA TATA CAA CTGTTAAAAA
                                 ||| |||| ||| ||||||||||
                                 TCT ATAT GTT GACAATTTTT
                                   G   _  C
GAM3156 KIAA1877 3' AGAATTCCCAAAGCTGTTAAAA 71602      ATA    _
            A                     AGAAT   TCAAA CTGTTAAAAA
                                 |||||   ||||| ||||||||||
                                 TCTTA   GGTTT GACAATTTTT
                                    AG_    C
GAM3156 UNC5D    3' TAAAATGTATCAAACATCTAAA 71603       A      TG
            AA                    TAGAAT TATCAAAC  TTAAAAA
                                 ||||||| ||||||||  |||||||
                                 ATTTTA ATAGTTTG  GATTTTT
                                    C       TA
GAM3156 LOC200563 5' GAACGCATTCAAACTGTTA   71604    TA  _
                                 GAA  TAT CAAACTGTTA
                                 |||  ||| ||||||||||
                                 CTT  GTA GTTTGACAAT
                                   GC   A
GAM3156 LOC221035 3' GAATATATCATGTTA      71605         AAC
                                 GAATATATCA   TGTTA
                                 ||||||||||   |||||
                                 CTTATATAGT   ACAAT
                                        ___
GAM3157 IGF1     3' TAAATGATGCCATTGCA     71608         GCGTT
                                 TGAATGATGC    TATTGCA
                                 ||||||||||    |||||||
                                 ATTTACTACG    GTAACGT
                                       _____
GAM3157 NFIC     3' TGAGTGTGTGCGTCTAT     71609     A  A  C
                                 TGA TG TG GCGTTTAT
                                 ||| || || ||||||||
                                 ACT AC AC CGCAGATA
                                   C  _  A
GAM3157 TFRC     3' TGAAGATGTCATTGCA      71610     T   CGCGT
                                 TGAA GATG    TTATTGCA
                                 |||| ||||    ||||||||
                                 ACTT CTAC    AGTAACGT
                                    _   _____
GAM3157 FLJ20094 3' TGAATGGTACCTTTTATTGCA 71611       A   GCG
                                 TGAATG TGC   TTTATTGCA
                                 |||||| |||  |||||||||
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                                ACTTAC ATG   AAATAACGT
                                   C  GA_
GAM3157 KIAA1026 5' TGCATGATGCGCGGGGGGCGC 71612    A       TTTAT
                                TG ATGATGCGCG    TGC
                                || ||||||||||    |||
                                AC TACTACGCGC    GCG
                                 G        CCCCC
GAM3157 KIAA1623 3' TGAATGACTGATATTGCA    71613       GCGCGTT
                                TGAATGAT     TATTGCA
                                ||||||||     |||||||
                                ACTTACTG     ATAACGT
                                     ACT____
GAM3157 MAWBP    3' TGAATTATTGATTTATTGCACA 71614      G  GCGC
                                TGAAT AT    GTTTATTGCACA
                                ||||| ||    ||||||||||||
                                ACTTA TA    TAAATAACGTGT
                                   A  AC__
GAM3157 PTPN3    3' TAAATGATGCCATAATTGCA   71615        G   TT
                                TGAATGATGC CGT  ATTGCA
                                |||||||||| |||  ||||||
                                ATTTACTACG GTA  TAACGT
                                      _  T_
GAM3157 SSH1     3' TGGATGTGTGCGCCTAT     71616    A   A  C
                                TG ATG TG GCGTTTAT
                                || ||| || ||||||||
                                AC TAC AC CGCGGATA
                                 C  _  A
GAM3157 LOC150378 3' TGAATGATGTCGGCTCGGCA   71617        _  C    ATT
                                TGAATGATG CG GTTT   GCA
                                ||||||||| || ||||   |||
                                ACTTACTAC GC CGAG   CGT
                                     A  _   C__
GAM3157 LOC152641 3' TGAATGATGTTGTTAGTACA   71618        CGC   TAT
                                TGAATGATG   GTT   TGCA
                                |||||||||   |||   ||||
                                ACTTACTAC   CAA   ATGT
                                     AA_  TC_
GAM3158 ARHGAP6  3' TCCAGGAGAACTTTCCCTTGA  71621      CA  TTGAA
                                TCCAGG  AG    TTCCCTTGA
                                ||||||  ||    |||||||||
                                AGGTCC  TC    AAGGGAACT
                                   __  TTGA_
GAM3158 KCNJ15   5' TCCAGACAGGTTGCCTTG    71622        A   AATTC
                                TCCAGGCA GTTG    CCTTG
                                |||||||| ||||    |||||
                                AGGTCTGT CAAC    GGAAC
                                     C   _____
GAM3158 LMO2     3' TCCATGCAGTTTTCCCTTG   71623     G   A  GAA
                                TCCA GCA GTT   TTCCCTTG
                                |||| ||| |||   ||||||||
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                                AGGT CGT CAA   AAGGGAAC
                                  A  _  ___
GAM3158  MMP3     3'  CACGCTCAAGTTCCCTTGA   71624    G  AAG TG A
                                CA GC   T  A TTCCCTTGA
                                || ||   |  | |||||||||
                                GT CG   A  T AAGGGAACT
                                 G  ___ GT C
GAM3158  TRIM14   3'  AGGCAAGTTTATAACCTT    71625        GA  TC
                                AGGCAAGTT  AT  CCTT
                                |||||||||  ||  ||||
                                TCCGTTCAA  TA  GGAA
                                     A_  TT
GAM3158  ZNF35    3'  TCTAGGCAAGCTTTATTCTTTG 71626    C       GA    CC
              A                  TC AGGCAAGTT  ATTC  TTGA
                                || |||||||||  ||||  ||||
                                AG TCCGTTCGA  TAAG  AACT
                                 A        AA    A_
GAM3158  ATP9A    3'  AGCAAGTTCCCCTTG      71627        TGAA
                                GGCAAGT    TTCCCTTG
                                |||||||    ||||||||
                                TCGTTCA    AGGGGAAC
                                     ____
GAM3158  C1orf24  3'  TCCAGATTAAATTCCCTTG   71628      GCAA
                                TCCAG    GTTGAATTCCCTTG
                                |||||    ||||||||||||||
                                AGGTC    TAATTTAAGGGAAC
                                     ____
GAM3158  FLJ10057 3'  CAGAATCTGAATTCCCTTG   71629     CAAG
                                CAGG    TTGAATTCCCTTG
                                ||||    ||||||||||||||
                                GTCT    GACTTAAGGGAAC
                                  TA__
GAM3158  IRLB     5'  AGATCAAAATTCCCTTGA    71630     _  AGTT
                                AGG CA    GAATTCCCTTGA
                                ||| ||    ||||||||||||
                                TCT GT    TTTAAGGGAACT
                                  A  ____
GAM3158  KIAA0789 3'  CCTGGGCAATCTCTTCCCTTGA 71631    A_    GTTGAA
                                CC  GGCAA     TTCCCTTGA
                                ||  |||||     |||||||||
                                GG  CCGTT     AAGGGAACT
                                 AC     AGAG__
GAM3158  KIAA0978 3'  CAGGTAGGTTAACTCCCTTG   71632      CAA    A
                                CAGG   GTTGA TTCCCTTG
                                ||||   ||||| ||||||||
                                GTCC   CAATT GAGGGAAC
                                  ATC    _
GAM3158  MSP      3'  GGCAGTCTTTCCCTTGA     71633      A   GAA
                                GGCA GTT   TTCCCTTGA
                                |||| |||   |||||||||
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                                CCGT CAG   AAGGGAACT
                                  _  A__
GAM3158  NIBAN    3'  TCCAGATTAAATTCCCTTG   71628      GCAA
                                TCCAG   GTTGAATTCCCTTG
                                |||||   ||||||||||||||
                                AGGTC   TAATTTAAGGGAAC
                                  ____
GAM3158  NMT1     3'  AGCAGTTACATTCCCTTGA   71634     A   A
                                GGCA GTTG ATTCCCTTGA
                                |||| |||| ||||||||||
                                TCGT CAAT TAAGGGAACT
                                  _   G
GAM3158  SAD1     3'  CCCAGGCAAGTGGGCTCTTG  71635          TGAATTCC
                                TCCAGGCAAGT      CTTG
                                ||||||||||       ||||
                                GGGTCCGTTCA      GAAC
                                      CCCGA___
GAM3158  LOC133482 5'  TCGAGGACTTCGGGGTTCCCTT 71636    C   CAAG   AA_
             G                   TC AGG   TTG   TTCCCTTG
                                || |||   |||   ||||||||
                                AG TCC   AGC   AAGGGAACC
                                 C   TGA_   CCC
GAM3158  LOC153688 3'  TCCAGCAGCTCTTCCCTTG   71637      G  A  TGAA
                                TCCAG CA GT   TTCCCTTG
                                ||||| || ||   ||||||||
                                AGGTC GT CG   AAGGGAAC
                                  _ _  AG__
GAM3158  LOC157621 3'  GACCATGGATTCCCTTGA    71638     AAGT  A
                                GGC   TG ATTCCCTTGA
                                |||   || ||||||||||
                                CTG   AC TAAGGGAACT
                                  GT__  C
GAM3158  LOC168082 5'  GGGGTAGTGACCTTTCCCTTG  71639    CA_   T  A__
                                GG   AGT GA   TTCCCTTG
                                ||   ||| ||   ||||||||
                                CC   TCA CT   AAGGGAAC
                                 CCA   _  GGA
GAM3159  AMPH     3'  ACAAACACAGATACTGTTGA   71642          C   TAT
                                ACAAACACAGA ATT   TTGA
                                |||||||||| |||   ||||
                                TGTTTGTGTCT TGA   AACT
                                      A   C__
GAM3159  ASB2     5'  TGACAGACACAGGGCTCTG   71643      A     ACATTTA
                                TGACA ACACAG      TTTG
                                ||||| ||||||      ||||
                                ACTGT TGTGTC      AGAC
                                   C     CCG____
GAM3159  RET      3'  TGATGGACACAGACCAACACT  71644     CAA       ATT
                                TGA   ACACAGAC   TATT
                                |||   ||||||||   ||||
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                                ACT   TGTGTCTG   GTGA
                                  ACC       GTT
GAM3159 RET      3' TGATGGACACAGACCAACACT 71644     CAA       ATT
                                TGA   ACACAGAC   TATT
                                |||   ||||||||   ||||
                                ACT   TGTGTCTG   GTGA
                                  ACC       GTT
GAM3159 TEM7     3' TGACAACCGCAGACATCT    71645       ACA
                                TGACAA   CAGACATTT
                                ||||||   |||||||||
                                ACTGTT   GTCTGTAGA
                                   GGC
GAM3159 YWHAG    3' TGACAAACACCAGACATT    71646          _
                                TGACAAACAC AGACATT
                                |||||||||| |||||||
                                ACTGTTTGTG TCTGTAA
                                      G
GAM3159 bA430M15.1 3' TGGCAAAACAGACATACCTTG 71647    A   C       TTA
                                TG CAAA ACAGACAT   TTTG
                                || |||| ||||||||   ||||
                                AC GTTT TGTCTGTA   GAAC
                                 C   _       TG_
GAM3159 C1orf9   3' GACAAGTGTTCAGATTTATTTG 71648      ACA__    CA
                                GACAA    CAGA  TTTATTTG
                                |||||    ||||  ||||||||
                                CTGTT    GTCT  AAATAAAC
                                   CACAA   __
GAM3159 DEFA3    3' AACAAGGCATTTATTTG     71649      C  A
                                AACA AG CATTTATTTG
                                |||| || ||||||||||
                                TTGT TC GTAAATAAAC
                                   _ C
GAM3159 DEPP     3' TGACAGATACAAACATTT    71650       AAC
                                TGACA   ACAGACATTT
                                |||||   ||||||||||
                                ACTGT   TGTTTGTAAA
                                   CTA
GAM3159 DJ167A19.1 3' TGCAGACACAGACATCATGTGA 71651    A  A         T  T
                                TG CA ACACAGACATT AT TGA
                                || || |||||||||| || |||
                                AC GT TGTGTCTGTAG TA ACT
                                 _ C         _ C
GAM3159 KIAA0084 3' TGATAAACACAGCATACAT    71652     C       A   T
                                TGA AAACACAG CAT TAT
                                ||| |||||||| ||| |||
                                ACT TTTGTGTC GTA GTA
                                  A       _  T
GAM3159 KIAA1796 3' GACAGATACACAACTATTTGA  71653      A__      ACAT
                                GACA   ACACAG    TTATTTGA
                                ||||   ||||||    ||||||||
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                                CTGT   TGTGTT    GATAAACT
                                  CTA     ____
GAM3159  TNFAIP3   3'  TGAAAACACTGAAGTTTATTTG 71654     C     A  CA
                                TGA AAACAC GA  TTTATTTG
                                ||| |||||| ||  ||||||||
                                ACT TTTGTG CT  AAATAAAC
                                  _     A  TC
GAM3159  TRIM2     3'  CAAACATGACATCCTATTTG   71655       CA     _
                                CAAACA  GACATT TATTTG
                                ||||||  |||||| ||||||
                                GTTTGT  CTGTAG ATAAAC
                                   A_     G
GAM3159  LOC151521 3'  CAGACACAGACATTTCACTGA  71656    A          AT
                                CA ACACAGACATTT  TTGA
                                || ||||||||||||  ||||
                                GT TGTGTCTGTAAA  GACT
                                 C          GT
GAM3159  LOC158584 5'  TGACAGACCCAGGCACCATTTG 71657       A  A   A    T
              A                  TGACA AC CAG CATT ATTTGA
                                 |||||| || ||| |||| ||||||
                                 ACTGT TG GTC GTGG TAAACT
                                   C  G   C   _
GAM3159  LOC201242 5'  AACAAAGACATCTTCCTTG    71658      C       A_
                                AACA AGACATTT  TTTG
                                |||| ||||||||  ||||
                                TTGT TCTGTAGA  GAAC
                                  T       AG
GAM3159  LOC54516  3'  TGACAAACACAAACATCTACTG 71659                  T
              A                  TGACAAACACAGACATTTATT GA
                                 |||||||||||||||||||| ||
                                 ACTGTTTGTGTTTGTAGATGA CT
                                                  _
GAM3160  AOC3      3'  CAGCCTCCCAAACAGGCT     71662      ACAATG
                                CAGC     CTAAACAGGCT
                                ||||     ||||||||||
                                GTCG     GGTTTGTCCGA
                                  GAG___
GAM3160  CNTN2     3'  GCACAGTGTCAGGCCACC     71663      A  CTAAA
                                GCACA TG    CAGGCTATT
                                ||||| ||    |||||||||
                                CGTGT AC    GTCCGGTGG
                                  C  A____
GAM3160  EIF5A2    3'  CAGCACAATCTGAAAACAA    71664         G  __
                                CAGCACAAT CT  AAACAG
                                ||||||||| ||  ||||||
                                GTCGTGTTA GA  TTTGTT
                                      _ CT
GAM3160  ITK       3'  CAACACAATGCTGCC       71665           AAACAG
                                CAGCACAATGCT     GCT
                                ||||||||||||     |||
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                                GTTGTGTTACGA     CGG
                                           _______
GAM3160  MSL3L1    3'  AGCATAGGCTAAACAACCA   71666      CAAT       G
                                AGCA    GCTAAACAG CTA
                                ||||    ||||||||| |||
                                TCGT    CGATTTGTT GGT
                                  ATC_       _
GAM3160  MYH11     3'  AGACAATGCTAAGTACAG    71667    C        __
                                AG ACAATGCTAA  ACAG
                                || ||||||||||  ||||
                                TC TGTTACGATT  TGTC
                                 _        CA
GAM3160  MYH11     3'  AGACAATGCTAAGTACAG    71667    C        __
                                AG ACAATGCTAA  ACAG
                                || ||||||||||  ||||
                                TC TGTTACGATT  TGTC
                                 _        CA
GAM3160  ZNF236    3'  CAGCTACCTGGTAGGCTAT   71668      ACAA    AAAC
                                CAGC    TGCT    AGGCTAT
                                ||||    ||||    |||||||
                                GTCG    ATGG    TCCGATA
                                  _____   ACCA
GAM3160  DDM36     3'  AATGCTAAGAGCCTACT     71669        AC  G
                                AATGCTAA  AG CTATT
                                ||||||||  || |||||
                                TTACGATT  TC GATGA
                                     C_  G
GAM3160  DKFZp434E2220 5'  AGCACAATACTGGATGGCT    71670          AAACA
                                AGCACAATGCT     GGCT
                                ||||||||||     ||||
                                TCGTGTTATGA     CCGA
                                      CCTA_
GAM3160  FLJ10852  3'  GCACAATGACTGGACAAA    71671        _  AA
                                GCACAATG CT  ACAGG
                                |||||||| ||  |||||
                                CGTGTTAC GA  TGTTT
                                     T  CC
GAM3160  KIAA1084  3'  CAGCATACAGTCCACAGGCTAT 71672      CAA   TAA__
            T                    CAGCA   TGC    ACAGGCTATT
                                |||||   |||    ||||||||||
                                GTCGT   ATG    TGTCCGATAA
                                  ____  TCAGG
GAM3160  NUDT11    3'  CAGCACAATACTGAACATCT   71673          A    GG
                                CAGCACAATGCT AACA  CT
                                |||||||||||| ||||  ||
                                GTCGTGTTATGA TTGT  GA
                                      C    A_
GAM3160  SIAT8A    5'  CAGCACAAAGCTAGGC      71674        T   AAAC
                                CAGCACAA GCT    AGGC
                                |||||||| |||    ||||
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                                GTCGTGTT CGA    TCCG
                                    T  ____
GAM3160  ZNF33A    3'  CAGTACAATGCTGAAAAGC    71675     C       A  C
                                CAG ACAATGCT AA AGGC
                                ||| |||||||| || ||||
                                GTC TGTTACGA TT TTCG
                                  A       C  _
GAM3160  LOC144363 3'  CAGTCACCAGCAGGCTAT     71676     _  AAT  TAAAC
                                CAG CAC   GC    AGGCTAT
                                ||| |||   ||    |||||||
                                GTC GTG   CG    TCCGATA
                                  A  GT_  ______
GAM3160  LOC152316 5'  CAGCACAATGCCAGGC      71677          TAAA
                                CAGCACAATGC    CAGGC
                                ||||||||||    |||||
                                GTCGTGTTACG    GTCCG

                                     ____
GAM3160  LOC169026 3'  CAGCAGAATGCTAAGTAGTTAT 71678      C       AC  GC
             T                   CAGCA AATGCTAA  AG  TATT
                                ||||| ||||||||  ||  ||||
                                GTCGT TTACGATT  TC  ATAA
                                   C       CA  A_
GAM3161  BSN       3'  GGGCCTTTTACTGCCTGCCCTG 71681     ACCC   GCAC
                                GGGC    TGC    CCTGCCCTG
                                ||||    |||    |||||||||
                                CCCG    ATG    GGACGGGAC
                                  GAAA   AC__
GAM3161  DUSP7     5'  GGGCCGGGCAGCCCTGCCCTG  71682     ACCC  C  _
                                GGGC    TG GCA CCCTGCCCTG
                                ||||    || ||| ||||||||||
                                CCCG    GC CGT GGGACGGGAC
                                  ____  C  C
GAM3161  GALNT2    3'  GGGCTACGCACACCCTGCTCTG 71683      ACCC          C
                                GGGC    TGCGCACCCTGC CTG
                                ||||    |||||||||||| |||
                                CCCG    GCGTGTGGGACG GAC
                                  AT__          A
GAM3161  HCK       3'  GGGCACCCCCTGGCCCTGCCCT 71684         GCGCA
             G                   GGGCACCCT     CCCTGCCCTG
                                |||||||||     ||||||||||
                                CCCGTGGGG     GGGACGGGAC
                                    GACC_
GAM3161  HM13      3'  GGTATCCTGCTGCCCCCTGCCC 71685    GCAC    _ A
             TG                   GG    CCTGC GC CCCTGCCCTG
                                ||    ||||| || ||||||||||
                                CC    GGACG CG GGGACGGGAC
                                 ATA_     A  G
GAM3161  KCNA7     5'  GGACGCCCGCCCTGCCCT    71686      A   TGCGCA
                                GGGC CCC      CCCTGCCCT
                                |||| |||      |||||||||
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                                CCTG GGG     GGGACGGGA
                                  C   C_____
GAM3161  MRPS12   3'  GGGCACCCTTTGCACCCC    71687        GC
                                GGGCACCCT  GCACCCT
                                |||||||||  |||||||
                                CCCGTGGGA  CGTGGGG
                                     AA
GAM3161  MRPS12   3'  GGGCACCCTTTGCACCCC    71687        GC
                                GGGCACCCT  GCACCCT
                                |||||||||  |||||||
                                CCCGTGGGA  CGTGGGG
                                     AA
GAM3161  MRPS12   3'  GGGCACCCTTTGCACCCC    71687        GC
                                GGGCACCCT  GCACCCT
                                |||||||||  |||||||
                                CCCGTGGGA  CGTGGGG
                                     AA
GAM3161  NRL      3'  GAGCACCCTGTGCAGGTCTG   71688        C   CC_
                                GGGCACCCTG GCA   CTG
                                |||||||||| |||   |||
                                CTCGTGGGAC CGT   GAC
                                     A   CCA
GAM3161  OVOL1    3'  GGGACCTGCAGCCCCTGCCCTG 71689     CAC    _  A
                                GGG   CCTGC GC CCCTGCCCTG
                                |||   ||||| || ||||||||||
                                CCC   GGACG CG GGGACGGGAC
                                  T__     T  _
GAM3161  PACE     3'  AGGCACCTGCCTTGCC      71690        C   GCAC C
                                GGGCACC TGC    C TGCC
                                ||||||| |||    | ||||
                                TCCGTGG ACG    G ACGG
                                   _  _____ A
GAM3161  PROK1    3'  GGGCTCCCTACACCTGCC    71691      A      CAC
                                GGGC CCCTGCG   CCTGCC
                                |||| |||||||   ||||||
                                CCCG GGGATGT   GGACGG
                                  A      ___
GAM3161  RARA     3'  GGGCCCTTGCTCTGCCCT    71692      A  C   GCACC
                                GGGC CC TGC    CTGCCCT
                                |||| || |||    |||||||
                                CCCG GG ACG    GACGGGA
                                  _  A   A_____
GAM3161  SREBF2   3'  GGGCTGCCCAGTTTCTGCCCTG 71693      ACCC   G  CC__
                                GGGC    TGC CA    CTGCCCTG
                                ||||    ||| ||    ||||||||
                                CCCG    ACG GT    GACGGGAC
                                  _____   G  CAAA
GAM3161  TCIRG1   5'  GGGCTGCTCCAACCTCCTGCCC 71694     ACC  G  _ AC
            TG                    GGGC   CT CG C  CCTGCCCTG
                                ||||   || || |  |||||||||
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                                CCCG  GA GT G  GGACGGGAC
                                  AC_  G  T GA
GAM3161 VEGF    3' GGGCACGTGGATCCTGCCCTG 71695      CC  CGCAC
                                GGGCAC  TG    CCTGCCCTG
                                ||||||  ||    |||||||||
                                CCCGTG  AC    GGACGGGAC
                                   C_  CTA__
GAM3161 WBSCR5  3' GGGACCTACTCTGCCCT    71696    CAC    GCACC
                                GGG   CCTGC    CTGCCCT
                                |||   |||||    |||||||
                                CCC   GGATG    GACGGGA
                                  T__    A____
GAM3161 WBSCR5  3' GGGACCTACTCTGCCCT    71696    CAC    GCACC
                                GGG   CCTGC    CTGCCCT
                                |||   |||||    |||||||
                                CCC   GGATG    GACGGGA
                                  T__    A____
GAM3161 WBSCR5  3' GGGACCTACTCTGCCCT    71696    CAC    GCACC
                                GGG   CCTGC    CTGCCCT
                                |||   |||||    |||||||
                                CCC   GGATG    GACGGGA
                                  T__    A____
GAM3161 ZNF147  3' GGGAGTAGGTCACCCTGCCCTG 71697    CACCCTGCG
                                GGG       CACCCTGCCCTG
                                |||       ||||||||||||
                                CCC       GTGGGACGGGAC
                                  TCATCCA__
GAM3161 AP3S2   3' GGGCACCCTCTCAGACCTGCCC 71698        GCG  C_
           TG                     GGGCACCCT   CA  CCTGCCCTG
                                |||||||||   ||  |||||||||
                                CCCGTGGGA   GT  GGACGGGAC
                                     GA_  CT
GAM3161 C1QR1   3' GGGTGTCTGAGGCCTGCCCTG  71699    CACC   CGCAC
                                GGG   CTG    CCTGCCCTG
                                |||   |||    |||||||||
                                CCC   GAC    GGACGGGAC
                                  ACA_   TCC__
GAM3161 C8orf17  3' GGGCCTTGGGACCCTGCCCTG  71700     ACCC  CGC
                                GGGC   TG   ACCCTGCCCTG
                                ||||   ||   ||||||||||||
                                CCCG   AC   TGGGACGGGAC
                                  GA__  CC_
GAM3161 CDC14B  3' GGGCACCCTGGGCACCACGTTT 71701          C    C  CC_
           CTG                    GGGCACCCTG GCACC TG   CTG
                                |||||||||| ||||| ||   |||
                                CCCGTGGGAC CGTGG GC   GAC
                                     C    T  AAA
GAM3161 CENTB5  3' GGCCACCCTTTCTGCCCT    71702    G    GCGCACC
                                GG CACCCT      CTGCCCT
                                || ||||||      |||||||
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                                CC GTGGGA      GACGGGA
                                 G     AA_____
GAM3161  DKFZP566J091 3'  GCACCCTCGTCCTCCTGCCCTG 71703        G  CAC_
                                GCACCCT CG    CCTGCCCTG
                                ||||||| ||    |||||||||
                                CGTGGGA GC    GGACGGGAC
                                   _  AGGA
GAM3161  FEM-2    3'  GGGCACCCTGTCCACTGCC    71704          CGCA  _
                                GGGCACCCTG    CC CTGCC
                                ||||||||||    || |||||
                                CCCGTGGGAC    GG GACGG
                                      A___  T
GAM3161  FLJ10120 3'  GGGCACCCTGTTCCCTCCT    71705          CGCA    GC
                                GGGCACCCTG    CCCT  CCT
                                ||||||||||    ||||  |||
                                CCCGTGGGAC    GGGA  GGA
                                      AA__    __
GAM3161  HSJ1     3'  AGGTGCTGCGCGGCTCTGCCCT 71706     CACC     ACC_
              G                    GGG    CTGCGC    CTGCCCTG
                                |||    ||||||    ||||||||
                                TCC    GACGCG    GACGGGAC
                                  AC__     CCGA
GAM3161  HSPC052  5'  GGCACCCTGCGCTGCCCT    71707           ACCC
                                GGCACCCTGCGC    TGCCCT
                                ||||||||||||    ||||||
                                CCGTGGGACGCG    ACGGGA
                                                _____
GAM3161  KIAA0445 3'  GGGCCTCTGACCCCTGCCCTG  71708     ACC   C  A
                                GGGC   CTG GC CCCTGCCCTG
                                ||||   ||| || ||||||||||
                                CCCG   GAC TG GGGACGGGAC
                                  GA_   _ _
GAM3161  KIAA0514 3'  GGGCTTCATACCAGCCCTGCCC 71709      ACCC   G  _
              TG                   GGGC    TGC CA CCCTGCCCTG
                                ||||    ||| || ||||||||||
                                CCCG    ATG GT GGGACGGGAC
                                  AAGT   _  C
GAM3161  KIAA0544 3'  GGGCCTCCTGCCCTTGCCCTG  71710     AC    GCA  C
                                GGGC  CCTGC   CC TGCCCTG
                                ||||  |||||   || |||||||
                                CCCG  GGACG   GG ACGGGAC
                                  GA    ___  A
GAM3161  KIAA0700 3'  GGGCGGCGTCCTGCCCT     71711      ACCCT   CAC
                                GGGC    GCG   CCTGCCCT
                                ||||    |||   ||||||||
                                CCCG    CGC   GGACGGGA
                                  C_____   A__
GAM3161  KIAA1089 3'  GGGCCTGCTCCCTGCCCT    71712      ACC    GCA
                                GGGC   CTGC   CCCTGCCCT
                                ||||   ||||   |||||||||
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                                CCCG  GACG  GGGACGGGA
                                  ___   A__
GAM3161 KIAA1922 3' AGGCACCTTGTGCAGACCTG  71713      C  C  C_
                                GGGCACC TG GCA  CCTG
                                ||||||| || |||  ||||
                                TCCGTGG AC CGT  GGAC
                                   A  A  CT
GAM3161 KIAA1949 5' GTCCACCCCCACCCTGTCCTG 71714   GG    GCG    C
                                G  CACCCT  CACCCTG CCTG
                                |  ||||||  ||||||| ||||
                                C  GTGGGG  GTGGGAC GGAC
                                 AG    ___     A
GAM3161 KIAA1949 5' GTCCACCCCCACCCTGTCCTG 71714   GG    GCG    C
                                G  CACCCT  CACCCTG CCTG
                                |  ||||||  ||||||| ||||
                                C  GTGGGG  GTGGGAC GGAC
                                 AG    ___     A
GAM3161 KIAA1949 5' GTCCACCCCCACCCTGTCCTG 71714   GG    GCG    C
                                G  CACCCT  CACCCTG CCTG
                                |  ||||||  ||||||| ||||
                                C  GTGGGG  GTGGGAC GGAC
                                 AG    ___     A
GAM3161 MGC16332 5' GGGCACCCAGCGTGCCC    71715       T  CACCC
                                GGGCACCC GCG    TGCCC
                                |||||||| |||    |||||
                                CCCGTGGG CGC    ACGGG
                                    T  _____
GAM3161 MGC20781 3' GGCCACCCTGGCCTCTGCTCTG 71716   G    C  ACC   C
                                GG CACCCTG GC   CTGC CTG
                                || ||||||| ||   |||| |||
                                CC GTGGGAC CG   GACG GAC
                                 G     _  GA_   A
GAM3161 MGC26684 3' GGGCTACCCACCCCCACCCTGC 71717    _   TGCG_
           CCTG                 GGGC ACCC    CACCCTGCCCTG
                                |||| ||||    ||||||||||||
                                CCCG TGGG    GTGGGACGGGAC
                                  A   TGGGG
GAM3161 MGC4796  3' GGGCTGTCCCTGTCCCTGCCCT 71718    A__    CGCA
           G                    GGGC  CCCTG   CCCTGCCCTG
                                ||||  |||||   ||||||||||
                                CCCG  GGGAC   GGGACGGGAC
                                  ACA   A___
GAM3161 MLN64   3' GACAGGCTGCCCTGCCCTG   71719    CC   GCAC
                                GGCA  CTGC   CCTGCCCTG
                                ||||  ||||   |||||||||
                                CTGT  GACG   GGACGGGAC
                                  CC   ____
GAM3161 P24B    3' GGGCACCCAGTCACCATTCTGT 71720       TGCG   ___   C
           CCTG                 GGGCACCC   CACC   CTG CCTG
                                ||||||||   ||||   ||| ||||
```

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                                CCCGTGGG   GTGG  GAC GGAC
                                    TCA_   TAA  A
GAM3161 p25     3' GGGCAGCCCTCTGCCC     71721      _   GCGCACC
                                GGGCA CCCT     CTGCCC
                                ||||| ||||     ||||||
                                CCCGT GGGA     GACGGG
                                  C  _______
GAM3161 PPAP2A  3' GGGCACCCTGCTGCC      71722          GCACCC
                                GGGCACCCTGC    TGCC
                                ||||||||||    ||||
                                CCCGTGGGACG    ACGG
                                          ______
GAM3161 SDOS    3' GCCCGGACCACCCTGCTCTG  71723   A  CT  G      C
                                GC CC  GC CACCCTGC CTG
                                || ||  || |||||||| |||
                                CG GG  TG GTGGGACG GAC
                                 _ CC  _      A
GAM3161 SLC38A5  5' GGCTGCCTAGGCTCCTGCTCTG 71724    AC   C  AC    C
                                GGC  CCTG GC  CCTGC CTG
                                |||  |||| ||  ||||| |||
                                CCG  GGAT CG  GGACG GAC
                                  AC   C  A_    A
GAM3161 STC2    3' GGGCCCTGCCTTGCCCT    71725     AC    GCAC C
                                GGGC  CCTGC   C TGCCCT
                                ||||  |||||   | ||||||
                                CCCG  GGACG   G ACGGGA
                                  __    ____ A
GAM3161 WBSCR17  3' GGGTCCCTGTGCTGCCCT   71726    CA    C  ACCC
                                GGG  CCCTG GC   TGCCCT
                                |||  ||||| ||   ||||||
                                CCC  GGGAC CG   ACGGGA
                                  A_    A  ____
GAM3161 LOC112868 5' GGGCAGCTGAGACCCCTGCCCT 71727      CC   C_  A
           G                     GGGCA  CTG  GC CCCTGCCCTG
                                |||||  |||  || ||||||||||
                                CCCGT  GAC  TG GGGACGGGAC
                                   C_   TC  _
GAM3161 LOC115073 5' GGGCACCCTGGGCACCACG   71728         C    C
                                GGGCACCCTG GCACC TG
                                |||||||||| ||||| ||
                                CCCGTGGGAC CGTGG GC
                                     C    T
GAM3161 LOC127703 5' GGGCTCTGTGCGTCCTGCCCT  71729     ACC   C  AC
                                GGGC   CTG GC  CCTGCCCT
                                ||||   ||| ||  ||||||||
                                CCCG   GAC CG  GGACGGGA
                                  A__   A  CA
GAM3161 LOC138835 3' GGGCACCCTGCCCGTGC     71730          GCA  C
                                GGGCACCCTGC   CC TGC
                                ||||||||||   || |||
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                                CCCGTGGGACG  GG ACG
                                     ___  C
GAM3161  LOC146854 5'  GGGCCACCCGCATCTCTGCCCT 71731     AC     CACC
                G                 GGGC  CCTGCG   CTGCCCTG
                                  ||||  ||||||   ||||||||
                                  CCCG  GGGCGT   GACGGGAC
                                    GT     AGA_
GAM3161  LOC148014 3'  GGGCTCTGCTATTCTGCCCTG  71732     ACC   GCACC
                                  GGGC  CTGC   CTGCCCTG
                                  ||||  ||||   ||||||||
                                  CCCG  GACG   GACGGGAC
                                    A__   ATAA_
GAM3161  LOC148545 3'  GGCATTGCTCATACTCTGCCCT 71733     CCC   GC__  C
                G                 GGCA  TGC   AC CTGCCCTG
                                  ||||  |||   || ||||||||
                                  CCGT  ACG   TG GACGGGAC
                                    A__   AGTA  A
GAM3161  LOC150005 3'  AGGCCTGCATTCTGCCCT    71734     ACC    CACC
                                  GGGC  CTGCG   CTGCCCT
                                  ||||  |||||   |||||||
                                  TCCG  GACGT   GACGGGA
                                    ___    AA__
GAM3161  LOC151429 3'  GGTGCCTCTGCCCTGCCCTG   71735    CA  _   GCAC
                                  GG  CC CTGC   CCTGCCCTG
                                  ||  || ||||   |||||||||
                                  CC  GG GACG   GGACGGGAC
                                   AC  A   _____
GAM3161  LOC151701 5'  GGGCCTCTTCTGGCCTCTGCCC 71736     ACC__   C  ACC
                TG                  GGGC    CTG GC   CTGCCCTG
                                    ||||    ||| ||   ||||||||
                                    CCCG    GAC CG   GACGGGAC
                                      GAGAA   _  GA_
GAM3161  LOC151720 5'  AGGCTGAGTTGTGCTCTGCCCT 71737     ACCC_  C  ACC
                G                   GGGC    TG GC   CTGCCCTG
                                    ||||    || ||   ||||||||
                                    TCCG    AC CG   GACGGGAC
                                      ACTCA  A  A__
GAM3161  LOC151963 5'  GCGTCCCTGCCCTGCCCTG   71738    A_    GCAC
                                  GC  CCCTGC   CCTGCCCTG
                                  ||  ||||||   |||||||||
                                  CG  GGGACG   GGACGGGAC
                                   CA     _____
GAM3161  LOC169693 3'  GGGCCCCTGGCCTGCCCTGCCC 71739      A    C  A__
                TG                  GGGC CCCTG GC   CCCTGCCCTG
                                    |||| ||||| ||   ||||||||||
                                    CCCG GGGAC CG   GGGACGGGAC
                                      _    _  GAC
GAM3161  LOC197342 3'  GGCCAGCGCGTGCACCCTGCC  71740     ACCC  __
                                  GGC   TGC  GCACCCTGCC
                                  |||   |||  ||||||||||
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                                CCG   GCG  CGTGGGACGG
                                  GTC_   CA
GAM3161  LOC200197 3'  GGGCATTGCCTTCTGCCCT   71741      CCC   GCACC
                                GGGCA   TGC    CTGCCCT
                                |||||   |||    |||||||
                                CCCGT   ACG    GACGGGA
                                  A__   GAA__
GAM3161  LOC203636 3'  GGGCACCCAGTGCCGGGGCCTC 71742        TGC  ACCCT  _
           TG                     GGGCACCC   GC    GCC CTG
                                |||||||   ||    ||| |||
                                CCCGTGGG   CG    CGG GAC
                                    TCA  GCCC_   A
GAM3161  LOC204845 5'  GGGTGCTTTCCGCACCCTGCTC 71743     CACCCTG        C
           TG                     GGG      CGCACCCTGC CTG
                                |||      |||||||||| |||
                                CCC      GCGTGGGACG GAC
                                  ACGAAAG        A
GAM3161  LOC206887 5'  GGACACCCTCTTTGCCCT    71744         GCGCACCC
                                GGGCACCCT       TGCCCT
                                |||||||||       ||||||
                                CCTGTGGGA       ACGGGA
                                    GAA_____
GAM3161  LOC219537 3'  GGGCACCCTGCCCATCTCTG   71745          G  CC_
                                GGGCACCCTGC CA   CTG
                                |||||||||| ||   |||
                                CCCGTGGGACG GT   GAC
                                     G  AGA
GAM3161  LOC255057 3'  GGGCTGCCCCAGGAACCCTGCT 71746     A_    CGC      C
           CTG                    GGGC  CCCTG   ACCCTGC CTG
                                ||||  |||||   ||||||| |||
                                CCCG  GGGGT   TGGGACG GAC
                                  AC    CCT      A
GAM3161  LOC256789 5'  GGACGTCCTGCGCATCCT    71747      AC       C
                                GGGC  CCTGCGCA CCT
                                ||||  |||||||| |||
                                CCTG  GGACGCGT GGA
                                  CA       A
GAM3161  LOC51042  3'  GGGCAATTCCTCTGCCCT    71748      C__  GCGCACC
                                GGGCA   CCT     CTGCCCT
                                |||||   |||     |||||||
                                CCCGT   GGA     GACGGGA
                                  TAA  ________
GAM3161  LOC51725  3'  GGGCTGCCCTGTGCATTCTG   71749     A_    C   CC
                                GGGC  CCCTG GCA  CTG
                                ||||  ||||| |||  |||
                                CCCG  GGGAC CGT  GAC
                                  AC    A   AA
GAM3162  DGS-A    3'  GGTTTGGTTTCTCTTGGTC    71752      A_      TCCC
                                GGTT  GTTTCTCT    TGGTT
                                ||||  ||||||||    |||||
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                                CCAA  CAAAGAGA    ACCAG
                                  AC       ____
GAM3162  DKFZP434F1735 5'  ATCCTTTTTCTTTTCCCTGGTT 71753     AG_    C
                                GTT   TTTCT TTCCCTGGTT
                                |||   ||||| ||||||||||
                                TAG   AAAGA AAGGGACCAA
                                  GAA     A
GAM3162  FLJ12190  3'  GAGGTCACTTCCCTGG      71754        GTTTCT
                                GAGGTTA     CTTCCCTGG
                                |||||||     |||||||||
                                CTCCAGT     GAAGGGACC
                                          _______
GAM3162  KIAA1867  5'  GGTTAGTTTCTCTTCCTTGGC  71755              C
                                GGTTAGTTTCTCTTCC TGGT
                                |||||||||||||||| ||||
                                CCAATCAAAGAGAAGG ACCG
                                           A
GAM3162  KIAA1908  5'  GGCGTTCTTTTCTCTGGT    71756     TAGT    C   C
                                GGT    TTCT TTC CTGGT
                                |||    |||| ||| |||||
                                CCG    AAGA AAG GACCA
                                  C___    A   A
GAM3162  LOC149535 3'  GAGGATGGCTTTCCCTGGT    71757      TTA    CTCT
                                GAGG   GTTT    TCCCTGGT
                                ||||   ||||    ||||||||
                                CTCC   CGAA    AGGGACCA
                                  TAC    _____
GAM3162  LOC257482 3'  GGTTGTTTTCTCTTCAGCT    71758     AG       CCT
                                GGTT  TTTCTCTTC   GGTT
                                ||||  |||||||||   ||||
                                CCAA  AAAGAGAAG   TCGA
                                  CA        ___
GAM3162  LOC93333  5'  GGTTTGTTTGCTCTTGGTT    71759      A    _    TCCC
                                GGTT GTTT CTCT    TGGTT
                                |||| |||| ||||    |||||
                                CCAA CAAA GAGA    ACCAA
                                  A    C    ____
GAM3163  EXTL3     3'  TAAGTACGGAGGCAAGCCT    71762       GA  ATA T
                                TAAGTA  GA   G GTAAGCCT
                                ||||||  ||   | ||||||||
                                ATTCAT  CT   C CGTTCGGA
                                   GC  ___ _
GAM3163  TCTA      3'  AGTGGGGAGGAGCTGAGCCTG  71763     A__   AAT   GTA
                                AGT   GAG   AGT   AGCCTG
                                |||   |||   |||   ||||||
                                TCA   CTC   TCG   TCGGAC
                                  CCC   C__   AC_
GAM3163  FLJ20051  3'  AATAGAGAGATGAGAGTCTG   71764         ATA   TA  C
                                AGTAGAGA   GTG  AG CTG
                                ||||||||   |||  || |||
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                                TTATCTCT  TAC  TC GAC
                                    C__   TC  A
GAM3163  FLJ20308  3'  AAGTGGAGAACAGCAGAGCCTG 71765     A       GTA
                                AAGT GAGAATAGT   AGCCTG
                                |||| |||||||||   ||||||
                                TTCA CTCTTGTCG   TCGGAC
                                  C       TC_
GAM3163  KIAA0931  3'  ATAGAGAAGGTGAGCCTG    71766       TA  TA
                                GTAGAGAA  GTG  AGCCTG
                                ||||||||  |||  ||||||
                                TATCTCTT  CAC  TCGGAC
                                    C_  __
GAM3163  KLK14    3'  AGTAGAGAGAGGAGGGCCTG   71767       AT  TGTAA
                                AGTAGAGA  AG    GCCTG
                                ||||||||  ||    |||||
                                TCATCTCT  TC    CGGAC
                                    C_  CTCC_
GAM3163  LOC144248 3'  TAAGAGAGAACTGACAGGCCTG 71768     T     AG  _  A
                                TAAG AGAGAAT  TG TA GCCTG
                                |||| |||||||  || || |||||
                                ATTC TCTCTTG  AC GT CGGAC
                                  _     __ T  C
GAM3163  LOC56906  3'  AAGTAGAGAATAGGGATGT   71769          ___
                                AAGTAGAGAATAG   TGT
                                ||||||||||||   |||
                                TTCATCTCTTATC   ACA
                                       CCT
GAM3164  CASP8    3'  AAGCTCTTCAAAGGTCGT    71772          _
                                AAGCTCTTCAAAG TCGT
                                |||||||||||| ||||
                                TTCGAGAAGTTTC AGCA
                                       C
GAM3164  COG6     3'  AAAAAATTCTTCAAACCTTTCA 71773       C       GTCG
            TA                    AAAAAG TCTTCAAA    TCATA
                                |||||| ||||||||    |||||
                                TTTTTT AGAAGTTT    AGTAT
                                   A       GGAA
GAM3164  EPB41    3'  AAAAAGCTCTTCAAAAGGATCA 71774            TC
                                AAAAAGCTCTTCAAAG  GTCA
                                ||||||||||||||||  ||||
                                TTTTTCGAGAAGTTTT  TAGT
                                       CC
GAM3164  F3       3'  AAAAAGCTTTTCAAAAGTC   71775        C     _
                                AAAAAGCT TTCAAA GTC
                                |||||||| |||||| |||
                                TTTTTCGA AAGTTT CAG
                                    A     T
GAM3164  GALE     3'  GGAAAGCTCTTTCAGAGC    71776   A       _  A
                                A AAAGCTCTT CA AGT
                                | |||||||||  || |||
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                                C TTTCGAGAA GT TCG
                                 C        A  C
GAM3164  LAMB2    3'  AGCTCTTCAGTGCAT       71777          AA  C T
                                AGCTCTTCA  GT G CAT
                                |||||||||  || | |||
                                TCGAGAAGT  CA C GTA
                                     __  _ _
GAM3164  MTIF2    5'  AAAAAGCTTCTCCAATGTCAT  71778          _     A
                                AAAAAGCT CTTCAA GTCGT
                                |||||||| |||||| |||||
                                TTTTTCGA GAGGTT CAGTA
                                     A     A
GAM3164  NFATC3   3'  GCCCTTCAAATGACCATA    71779          GTCG
                                GCTCTTCAAA    TCATA
                                ||||||||||    |||||
                                CGGGAAGTTT    GGTAT
                                      ACT_
GAM3164  OAS3     3'  GCTCTTCAATAGCCCACATA   71780          _   GT
                                GCTCTTCAA AGTC  CATA
                                ||||||||| ||||  ||||
                                CGAGAAGTT TCGG  GTAT
                                     A    GT
GAM3164  P53AIP1  3'  AAAAGGCTCCTCAAGGTCA    71781      A        A
                                AAAA GCTCTTCAA GTCG
                                |||| ||||||||| ||||
                                TTTT CGAGGAGTT CAGT
                                  C        C
GAM3164  PPP1R2   3'  AAAAAGCTCTATAATATC     71782          TC  A
                                AAAAAGCTCT  AA GTC
                                ||||||||||  || |||
                                TTTTTCGAGA  TT TAG
                                      TA  A
GAM3164  RAG1     3'  AAAAAGCTCTTTTGAATC     71783          CAA
                                AAAAAGCTCTT   AGTC
                                ||||||||||   ||||
                                TTTTTCGAGAA   TTAG
                                      AAC
GAM3164  S100A12  3'  AAAAAGCCTTCAGAGAGC     71784        T    A  TC
                                AAAAAGC CTTCA AG  GT
                                ||||||| ||||| ||  ||
                                TTTTTCG GAAGT TC  CG
                                   _    C  T_
GAM3164  APMCF1   3'  AGCTCTTCAAGCAGCACAT    71785          A  C  _
                                AGCTCTTCAA GT GT CAT
                                |||||||||| || || |||
                                TCGAGAAGTT CG CG GTA
                                      _  T  T
GAM3164  BTN2A2   3'  AAAAGCTCTTTAAAGTCCTCA  71786          C     G
                                AAAAGCTCTT AAAGTC TCA
                                |||||||||| |||||| |||
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                                TTTTCGAGAA TTTCAG AGT
                                      A     G
GAM3164  DKFZP762N2316 3'  AAGTCTTCTACCGTCAT     71787     C     AAAG
                                AAG TCTTC    TCGTCAT
                                ||| |||||    |||||||
                                TTC AGAAG    GGCAGTA
                                  _    AT__
GAM3164  FLJ11850  3'  GGAAAGCTCTTCAGCACACATA 71788    A         AAGT  T
                                A AAAGCTCTTCA    CG CATA
                                | ||||||||||    || ||||
                                C TTTCGAGAAGT    GT GTAT
                                 C          CGT_ _
GAM3164  FLJ12586  3'  GCTCTTCATTCCAATCAT     71789         AAG   _
                                GCTCTTCA   TCG TCAT
                                ||||||||   ||| ||||
                                CGAGAAGT   GGT AGTA
                                     AA_   T
GAM3164  IRF7      3'  AAGCACTCGATGTCGTCATA   71790      T   CAAA
                                AAGC CTT    GTCGTCATA
                                |||| |||    |||||||||
                                TTCG GAG    CAGCAGTAT
                                  T   CTA_
GAM3164  KIAA0335  3'  AAAAACTCTTCAAGCAT     71791            A T
                                AAAAGCTCTTCAA G CGT
                                |||||||||||| | |||
                                TTTTTGAGAAGTT C GTA
                                          _ _
GAM3164  KIAA1323  3'  AAAAAGCTTATCAACAGC     71792         CT    _
                                AAAAAGCT  TCAA AGT
                                ||||||||  |||| |||
                                TTTTTCGA  AGTT TCG
                                     AT    G
GAM3164  KIAA1466  3'  AAAAAGCTCTTGATGTTTCATA 71793           CAAAGTCG
                                AAAAAGCTCTT       TCATA
                                ||||||||||       |||||
                                TTTTTCGAGAA       AGTAT
                                      CTACAA__
GAM3164  KIAA1870  3'  AAAAGTTTCTTCAAAGTC     71794       C_
                                AAAAG  TCTTCAAAGTC
                                |||||  ||||||||||
                                TTTTC  AGAAGTTTCAG
                                   AA
GAM3164  PIK3R4    5'  GGAAAGCTCTCGGGGTCTCA   71795    A       CAAA   G
                                A AAAGCTCTT    GTC TCA
                                | |||||||||    ||| |||
                                C TTTCGAGAG    CAG AGT
                                 C        CCC_  _
GAM3164  SLC12A8   3'  AGCTCTTCAAACTGGGTGTCGT 71796          _______
                                AGCTCTTCAAA     GTCGT
                                ||||||||||      |||||
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                                TCGAGAAGTTT     CAGCA
                                      GACCCA
GAM3164  SMCR5    3'  AAAGCTCTCCAAAGAGGT    71797           TC
                                AAAGCTCTTCAAAG  GT
                                |||||||||||||  ||
                                TTTCGAGAGGTTTC  CA
                                      TC
GAM3164  T2BP     3'  AGCTCTTCATCCATCATA    71798         AAG
                                AGCTCTTCA   TCGTCATA
                                |||||||||   ||||||||
                                TCGAGAAGT   GGTAGTAT
                                     A__
GAM3164  LOC146176 3'  AAAAGCTCTTGGTCAT      71799          CAAA
                                AAAAGCTCTT    GTCGT
                                ||||||||||    |||||
                                TTTTCGAGAA    CAGTA
                                     C___
GAM3164  LOC146489 5'  AAAAAGCCCTTCACGTTGT    71800           AA  C
                                AAAAAGCTCTTCA  GT GT
                                ||||||||||||  || ||
                                TTTTTCGGGAAGT  CA CA
                                      G_  A
GAM3164  LOC153205 5'  AAAAAGTTCTTCAGGATC     71801       C     AA
                                AAAAAG TCTTCA  GTC
                                ||||||| ||||||  |||
                                TTTTTC AGAAGT  TAG
                                   A     CC
GAM3164  LOC153338 5'  AAAAAGCCCTTTGGCCCTGCAT 71802          CAAA   GT_
           A                     AAAAAGCTCTT    GTC   CATA
                                ||||||||||    |||   ||||
                                TTTTTCGGGAA    CGG   GTAT
                                      AC__   GAC
GAM3164  LOC153743 3'  AAAAAGCTCTATAATATC     71782          TC  A
                                AAAAAGCTCT  AA GTC
                                ||||||||||  || |||
                                TTTTTCGAGA  TT TAG
                                      TA  A
GAM3164  LOC157773 5'  AGTTCTTCAAAGTCTCA      71803    C         G
                                AG TCTTCAAAGTC TCA
                                || ||||||||||| |||
                                TC AGAAGTTTCAG AGT
                                 A          _
GAM3164  LOC158078 3'  AAGCTCTCAACACACAT      71804        T   AGT  T
                                AAGCTCT CAA   CG CAT
                                ||||||| |||   || |||
                                TTCGAGA GTT   GT GTA
                                    _  GT_  _
GAM3164  LOC201229 3'  AGCCCTTCAGGCACTGTCAT   71805         AA_ TC
                                AGCTCTTCA   G  GTCAT
                                |||||||||   |  |||||
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                                TCGGGAAGT   T  CAGTA
                                     CCG GA
GAM3164  LOC221738 3'  AAAAAACTTTTCAGAAGATCCA 71806        C   _  TCG
              TA                    AAAAAGCT TTCA AAG   TCATA
                                    |||||||| |||| |||   |||||
                                    TTTTTTGA AAGT TTC   GGTAT
                                         A   C   TA_
GAM3164  LOC257467 3'  AGCTCTTCATCCATCATA    71798         AAG
                                    AGCTCTTCA   TCGTCATA
                                    |||||||||   ||||||||
                                    TCGAGAAGT   GGTAGTAT
                                         A__
GAM3165  NRAP     3'  GCAGTGCATATAGCTGTT    71809      A  __
                                    GTAGT GCA  TAGCTGTT
                                    ||||| |||  ||||||||
                                    CGTCA CGT  ATCGACAA
                                       _  AT
GAM3165  VNN1     3'  TGCACAGTGCATGGCTGTT    71810        A   A
                                    TGCGTAGT GCAT GCTGTT
                                    |||||||| |||| ||||||
                                    ACGTGTCA CGTA CGACAA
                                         _   C
GAM3165  CABP5    3'  TGCGTAGTGGTGAAGTCTGGGC 71811      _____ CATA_    III
              TGTTA                  GTAGT    AG    GCTGTT  A
                                    |||||    ||    ||||||  |
                                    CATCA    TC    CGACAA  T
                                       CCACT  AGACC     III
GAM3165  DKFZp434O0515 3'  TGGTAGTAGCAAGGTGTT    71812    C       T  C
                                    TG GTAGTAGCA AG TGTT
                                    || |||||||| || ||||
                                    AC CATCATCGT TC ACAA
                                     _       _  C
GAM3165  FLJ13110  3'  TGCGTAGTAATGGAACAGTT   71813         CAT   T
                                    TGCGTAGTAG   AGC GTT
                                    ||||||||||   ||| |||
                                    ACGCATCATT   TTG CAA
                                         ACC   T
GAM3165  FLJ20297  3'  TGTCACAGAGCGTAGCTGTT   71814    _    T   A
                                    TG CGTAG AGC TAGCTGTT
                                    || ||||| ||| ||||||||
                                    AC GTGTC TCG ATCGACAA
                                     A    _  C
GAM3165  FLJ20297  3'  TGTCACAGAGCGTAGCTGTT   71814    _    T   A
                                    TG CGTAG AGC TAGCTGTT
                                    || ||||| ||| ||||||||
                                    AC GTGTC TCG ATCGACAA
                                     A    _  C
GAM3165  KIAA0157  3'  TGCGTAGTAGGTAGCTG     71815         CA
                                    TGCGTAGTAG  TAGCTG
                                    ||||||||||  ||||||
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                                ACGCATCATC  ATCGAC
                                      C_
GAM3165 KIAA1155 3' TGTGTAGTAGCACAAAAGTT  71816   C        CT
                                TG GTAGTAGCATAG  GTT
                                || ||||||||||||  |||
                                AC CATCATCGTGTT  CAA
                                 A         TT
GAM3165 KIAA1796 3' TGGTAGTATTAGCTGTT    71817   C    GCA
                                TG GTAGTA   TAGCTGTT
                                || ||||||   ||||||||
                                AC CATCAT   ATCGACAA
                                 _    A__
GAM3165 MAP3K2   3' TGCTTTGTAAATAGCTGTT   71818    GTA   C
                                TGC   GTAG ATAGCTGTT
                                |||   |||| |||||||||
                                ACG   CATT TATCGACAA
                                  AAA   _
GAM3165 MGC4170  3' TGTGTAGTAGCCACCTG    71819   C      A  G
                                TG GTAGTAGC TA CTG
                                || ||||||||| || |||
                                AC CATCATCG GT GAC
                                 A       _ G
GAM3165 MSE55    3' TGGTAGGAACCAGCTGTT    71820   C   T  A
                                TG GTAG AGC TAGCTGTT
                                || |||| ||| ||||||||
                                AC CATC TTG GTCGACAA
                                 _   C  _
GAM3165 PRO0943  5' TGCCGTCTTAAATAGCTGTT  71821    _ AG  C
                                TGC GT  TAG ATAGCTGTT
                                ||| ||  ||| |||||||||
                                ACG CA  ATT TATCGACAA
                                  G  GA  _
GAM3165 TNRC6    3' TGTGCAGAGAATAGCTGTT   71822   C   T  C
                                TG GTAG AG ATAGCTGTT
                                || |||| || |||||||||
                                AC CGTC TC TATCGACAA
                                 A   _ T
GAM3165 LOC152018 3' GCGTAGAATAGCTGTT    71823      TAGC
                                GCGTAG   ATAGCTGTT
                                ||||||   |||||||||
                                CGCATC   TATCGACAA
                                   T___
GAM3165 LOC166602 5' TGCATGTGTTAGCTGTT    71824      A  AGCA
                                TGCGT GT   TAGCTGTT
                                ||||| ||   ||||||||
                                ACGTA CA   ATCGACAA
                                   _ CA__
GAM3165 LOC221662 3' TGCTTCACAATAGCATGGCTGT 71825    G___      A
            T                    TGC   TAGTAGCAT GCTGTT
                                 |||   ||||||||| ||||||
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                                ACG    GTTATCGTA CGACAA
                                  AAGT        C
GAM3165  LOC253389 5'  GTGAGCAACATGGCTGTT    71826    _       A
                                GT AGTAGCAT GCTGTT
                                || |||||||| ||||||
                                CA TCGTTGTA CGACAA
                                 C       C
GAM3166  FLJ14840  3'  GGCTGGGCCCAGAAATGGGT   71829     C    GT  C__    A
                                GGC GGGC  CC   GATG GT
                                ||| ||||  ||   |||| ||
                                CCG CCCG  GG   TTAC CA
                                  A   __ TCT    C
GAM3167  PART1     3'  AGCCAGTTAGACTTGTTATG   71832         TTT  G
                                AGCCGGTTA   AC TTGTTATG
                                |||||||||   || ||||||||
                                TCGGTCAAT   TG AACAATAC
                                      C__  _
GAM3167  KIAA1548  3'  GCTTGTTATGAAGTTGTTATG  71833    CG     TTAC
                                GC  GTTAT    GTTGTTATG
                                ||  |||||    |||||||||
                                CG  CAATA    CAACAATAC
                                 AA     CTT_
GAM3168  BMP6      3'  GGTTTTTGGGGGAGGAGGGT   71836      G         _  C
                                GGTT TTTGGGGGAG AG GGT
                                |||| |||||||||| || |||
                                CCAA AAACCCCCTC TC CCA
                                  _         C  _
GAM3168  EPB42     3'  AGGGTTGGCAGGAGAGTGGT   71837     TTGT   _      C
                                AGG    TTGG GGGAGAG GGT
                                |||    |||| ||||||| |||
                                TCC    AACC TCCTCTC CCA
                                  C___    G      A
GAM3168  KCNK3     3'  GGGTGCTGGGGGAGAGTGGT   71838    T    T        C
                                GG TGTT GGGGGAGAG GGT
                                || |||| ||||||||| |||
                                CC ACGA CCCCCTCTC CCA
                                 C    _        A
GAM3168  AK5       3'  GGTTGGTGGGGGGCGG      71839       TT     AGA
                                GGTTG  TGGGGG   GCGG
                                |||||  ||||||   ||||
                                CCAAC  ACCCCC   CGCC
                                   C_     ____
GAM3168  BRDG1     3'  TAGGTTTTTTGGGAATTGGT   71840       G       AGAGC
                                TAGGTT TTTGGGGG     GGT
                                ||||||| ||||||||     |||
                                ATCCAA AAACCCTT     CCA
                                   A       AA___
GAM3168  CCIN      5'  GGTTGTTTGCAGAGCGG      71841          GGGG
                                GGTTGTTTG    AGAGCGG
                                |||||||||    |||||||
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                                CCAACAAAC   TCTCGCC
                                     G___
GAM3168  FLJ20297  5'  GGCTGGAGGAGAGTGG     71842    TGTT       C
                                GGT   TGGGGGAGAG GG
                                |||   |||||||||| ||
                                CCG   ACCTCCTCTC CC
                                 ____        A
GAM3168  PPP1R10   5'  GGTGGTTTGGGAAGGGAGGGT  71843    T     __ A   C
                                GGT GTTTGGG  GG GAG GGT
                                ||| |||||||  || ||| |||
                                CCA CAAACCC  CC CTC CCA
                                  C      TT  _   _
GAM3168  THEA      3'  TAGGTTTTTGAGGGTGG     71844       G      AGAGC
                                TAGGTT TTTGGGGG    GG
                                ||||||| ||||||||    ||
                                ATCCAA AAACTCCC    CC
                                   _       A____
GAM3168  LOC127703 3'  GGTTTGTTTGGGAACTGGT   71845     _       AGAGC
                                GGTT GTTTGGGGG    GGT
                                |||| |||||||||    |||
                                CCAA CAAACCCTT    CCA
                                  A       GA___
GAM3168  LOC144473 3'  GATTGGTTGGGGAGTGGT    71846      T    GAG  C
                                GGTTG TTGGGG   AG GGT
                                ||||| ||||||   || |||
                                CTAAC AACCCC   TC CCA
                                   C     ___  A
GAM3168  LOC151904 3'  GGTTGTTTGGGGGGTGGT    71847           AGAGC
                                GGTTGTTTGGGGG    GGT
                                ||||||||||||    |||
                                CCAACAAACCCCC    CCA
                                       CA___
GAM3168  LOC157653 5'  GGTTGTTGGGGGAGAGC     71848       T
                                GGTTGTT GGGGGAGAGC
                                ||||||| ||||||||||
                                CCAACAA CCCCCTCTCG
                                   _
GAM3169  IGF1      3'  TGCTGAATATCTGTTTTAGA   71851        CTAAATA
                                TGCTGGAT      TTTTAGA
                                ||||||||      |||||||
                                ACGACTTA      AAAATCT
                                     TAGAC__
GAM3169  TGFA      3'  TGCTGGACCTAGGAACTAGAAC 71852          AATATT
                                TGCTGGATCTA     TTAGAAC
                                ||||||||||     |||||||
                                ACGACCTGGAT     GATCTTG
                                       CCTT__
GAM3169  WASF3     3'  CTGGATTTAAATTTCAGAA   71853      C    AT
                                CTGGAT TAAAT  TTTAGAA
                                |||||| |||||  |||||||
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                                GACCTA ATTTA  AAGTCTT
                                   A    __
GAM3169  AD034    3'  ACTGGATCTAGACTCTAGA   71854         AAT
                                GCTGGATCTA   ATTTTAGA
                                ||||||||||  ||||||||
                                TGACCTAGAT   TGAGATCT
                                     C__
GAM3169  FLJ20618 3'  TGCTGAATCTGGGTAGAA    71855         AAATATTT
                                TGCTGGATCT      TAGAA
                                ||||||||||      |||||
                                ACGACTTAGA      ATCTT
                                     CCC_____
GAM3169  NX-17    3'  TGTCAGAAAAATATTTTAGAA  71856    CT   TCT
                                TG  GGA   AAATATTTTAGAA
                                ||  |||   ||||||||||||
                                AC  TCT   TTTATAAAATCTT
                                 AG   T__
GAM3169  PRDM10   3'  TGCTGGATTCAAGCTCCAG    71857        C   ATA
                                TGCTGGAT TAA   TTTTAG
                                |||||||| |||   ||||||
                                ACGACCTA GTT   GAGGTC
                                     A   C__
GAM3169  RBAK     3'  GCTGGGGATATTTTAGA     71858      ATCTAA
                                GCTGG     ATATTTTAGA
                                |||||     ||||||||||
                                CGACC     TATAAAATCT
                                   CC_____
GAM3169  TIGD5    3'  TGCTGGATTTGGATTCCTGGAA 71859        CTAAATA    A
              C                  TGCTGGAT      TTTT GAAC
                                ||||||||      |||| ||||
                                ACGACCTA      AGGA CTTG
                                     AACCTA_    C
GAM3169  LOC130535 3'  TGGATCCAATTTTAG       71860         AAT
                                TGGATCTA   ATTTTAG
                                ||||||||   |||||||
                                ACCTAGGT   TAAAATC
                                     ___
GAM3169  LOC154790 5'  TGCTGGTCTAAGGCCTCTGGA  71861       A    ATA    A
                                TGCTGG TCTAA   TTTT GA
                                |||||| |||||   |||| ||
                                ACGACC AGATT   GAGA CT
                                   _    CCG    C
GAM3169  LOC158863 3'  TGCTGGATCTAAATTTTAAGA  71862            A   T
                                TGCTGGATCTAAAT TTT AGA
                                |||||||||||||| ||| |||
                                ACGACCTAGATTTA AAA TCT
                                        _   T
GAM3169  LOC161742 3'  TGTTGGATTAAATACTTT    71863    C    C
                                TG TGGAT TAAATATTTT
                                || ||||| ||||||||||
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                                AC ACCTA ATTTATGAAA
                                 A    _
GAM3169  LOC219744 5'  TGCTGGGTCTGAATTTTTCAG  71864       A   A   A
                                TGCTGG TCT AAT TTTTAG
                                |||||| ||| ||| ||||||
                                ACGACC AGA TTA AAAGTC
                                   C   C   A
GAM3169  LOC257319 3'  TGCTGGTTTAATTTTAGAA   71865       ATCTAAAT
                                TGCTGG       ATTTTAGAA
                                ||||||       |||||||||
                                ACGACC       TAAAATCTT
                                   AAAT____
GAM3170  ANKH      3'  GCGGAAGGGAAATTTAAGA   71868    A   T   A
                                GC GAAG GAAA TTTGGGA
                                || |||| |||| |||||||
                                CG CTTC CTTT AAATTCT
                                 C   C   _
GAM3170  CA12      3'  TAGCAGAAGGAAATCAGAGGGA 71869        T   ATTT_
                                TAGCAGAAG GAAA    GGGA
                                ||||||||| ||||    ||||
                                ATCGTCTTC CTTT    CCCT
                                     _   AGTCT
GAM3170  CACNA1C   3'  GCAAAAGTGAAAACAGG    71870           TT
                                GCAGAAGTGAAAAT  GGG
                                |||||||||||||  |||
                                CGTTTTCACTTTTG  TCC
                                              __
GAM3170  CLECSF12  3'  GCAGAATGAAAATTCAAG    71871       G       TG
                                GCAGAA TGAAAATT  GG
                                |||||| ||||||||  ||
                                CGTCTT ACTTTTAA  TC
                                   _       GT
GAM3170  COX11     3'  TAGAGGAGTGAAAATCTCTAGG 71872     C  A       __
                                TAG AG AGTGAAAATT  TGGG
                                ||| || ||||||||||  ||||
                                ATC TC TCACTTTTAG  ATCC
                                  _ C         AG
GAM3170  DDX26     5'  ACAGGAGTGGGGACCTGGGA  71873     A   AAA
                                GCAG AGTG   ATTTGGGA
                                |||| ||||  ||||||||
                                TGTC TCAC   TGGACCCT
                                  C   CCC
GAM3170  GAB2      3'  GCAGAAGTGGAGCTGGAA    71874        AAAAT
                                GCAGAAGTG    TTGGGA
                                |||||||||    ||||||
                                CGTCTTCAC    GACCTT
                                     CTC__
GAM3170  GAB2      3'  GCAGAAGTGGAGCTGGAA    71874        AAAAT
                                GCAGAAGTG    TTGGGA
                                |||||||||    ||||||
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                                CGTCTTCAC    GACCTT
                                     CTC__
GAM3170 GALNT2   3' GCAGAAGTGAAAGCTGGAA   71875          AT
                                GCAGAAGTGAAA  TTGGGA
                                |||||||||||  ||||||
                                CGTCTTCACTTT  GACCTT
                                       C_
GAM3170 GPR84    3' AGAGACTTGATTTGGGA    71876    C   AG   AAA
                                AG AGA  TGA   TTTGGGA
                                || |||  |||   |||||||
                                TC TCT  ACT   AAACCCT
                                 _  GA  ___
GAM3170 KIF3C    3' GCAGAAAGCAGAGTTTGGGAAG 71877       _ _  AAA
                                GCAGAA GT GA   TTTGGGAAG
                                |||||| || ||   |||||||||
                                CGTCTT CG CT   AAACCCTTC
                                    T  T  C__
GAM3170 MLF2     3' GCAGAATGAAAAATCAAG    71878       G     T TG
                                GCAGAA TGAAAA T  GG
                                |||||| |||||| |  ||
                                CGTCTT ACTTTT A  TC
                                   _     T GT
GAM3170 PIK3C2B  3' ACAGAAATGGAGTTTGGGA   71879         AAAA
                                GCAGAAGTG    TTTGGGA
                                |||||||||    |||||||
                                TGTCTTTAC    AAACCCT
                                     CTC_
GAM3170 PRKACA   3' GCAGAAGTGGGCTGGGA     71880         AAAAT
                                GCAGAAGTG    TTGGGA
                                |||||||||    ||||||
                                CGTCTTCAC    GACCCT
                                     CC___
GAM3170 PSMD9    3' TAGCGAAGTGAAAGGA      71881      A       AATTT
                                TAGC GAAGTGAA    GGGA
                                |||| ||||||||    ||||
                                ATCG CTTCACTT    TCCT
                                  _      _____
GAM3170 PXF      3' TAGCAGAAGTGAGAATCTGTAA 71882           A     _
            AAG                   TAGCAGAAGTGA AATTTG GGAAG
                                |||||||||||| |||||| |||||
                                ATCGTCTTCACT TTAGAC TTTTC
                                       C     A
GAM3170 SLC22A2  5' CAGGGGTGAAGCCCAGGAAG  71883     AA    AA  TG
                                CAG  GTGAA  TT  GGAAG
                                |||  |||||  ||  |||||
                                GTC  CACTT  GG  CCTTC
                                  CC    C_  GT
GAM3170 SLC7A8   3' CAGCAGGAGTGGCTGGGAA   71884       A   AAAAT
                                TAGCAG AGTG    TTGGGAA
                                |||||| ||||    |||||||
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                                GTCGTC TCAC    GACCCTT
                                   C   C____
GAM3170 SOX13    3' GCAGAGATGAAAACAGCAAG  71885      AG     TT  G
                                GCAGA  TGAAAAT  GG AAG
                                ||||||  |||||||  || |||
                                CGTCT  ACTTTTG  TC TTC
                                   CT      __  G
GAM3170 TXNRD1   3' TAGCAGGAATGAAAAAGAA   71886      A      TTTG
                                TAGCAG AGTGAAAA   GGAA
                                |||||| ||||||||   ||||
                                ATCGTC TTACTTTT   TCTT
                                   C      ____
GAM3170 CORO1B   3' GCAGAAGCTGAGTGGGAAG   71887       GAAAATT
                                GCAGAAGT      TGGGAAG
                                ||||||||      |||||||
                                CGTCTTCG      ACCCTTC
                                     ACTC___
GAM3170 DICER1   3' AGCAGAAGTGAGGAAAG     71888          AAATTT
                                AGCAGAAGTGA     GGGAAG
                                ||||||||||      ||||||
                                TCGTCTTCACT     CCTTTC
                                                _______
GAM3170 DKFZP434O047 5' GCAGAGGTGACTGGGAA     71889      A   AAAT
                                GCAGA GTGA    TTGGGAA
                                ||||| ||||    |||||||
                                CGTCT CACT    GACCCTT
                                   C   ____
GAM3170 DKFZP566G1424 5' GCAGAAAAGCTGGTTTGGGAAG 71890       TGAAAA
                                GCAGAAG     TTTGGGAAG
                                |||||||     |||||||||
                                CGTCTTT     AAACCCTTC
                                    TCGACC
GAM3170 FHX      3' GCAGAAGTAAGGATTGAA    71891          AAAT
                                GCAGAAGTGA    TTGGG
                                ||||||||||    |||||
                                CGTCTTCATT    AACTT
                                      CCT_
GAM3170 FLJ11078 3' TAGAGAAGTGAGATGGA     71892     C      AAATT
                                TAG AGAAGTGA     TGGG
                                ||| ||||||||     ||||
                                ATC TCTTCACT     ACCT
                                  _       CT___
GAM3170 FLJ13544 3' AGAAGTGAGGCTTGGAA     71893        AAA
                                AGAAGTGA   TTTGGGA
                                ||||||||   |||||||
                                TCTTCACT   GAACCTT
                                     CC_
GAM3170 FLJ14126 3' CAGTAGAGGTGGCCCCGGGAAG 71894     C   A   AAAA
                                TAG AGA GTG    TTTGGGAAG
                                ||| ||| |||    |||||||||
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                                GTC TCT CAC    GGGCCCTTC
                                  A   C   CG__
GAM3170  FLJ20105  5'  TAGAAGAGGTGAAGGCTGAG   71895     C   A    AAT
                                TAG AGA GTGAA   TTGGG
                                ||| ||| |||||   |||||
                                ATC TCT CACTT   GACTC
                                  T   C    CC_
GAM3170  FLJ21126  3'  CAGAAGTGGAACTGAGG     71896       AA   T
                                CAGAAGTG  AATT GGG
                                ||||||||  |||| |||
                                GTCTTCAC  TTGA TCC
                                     C_   C
GAM3170  FLJ21156  3'  AGAAGTGAGGAATATGGG    71897       A_   T
                                AGAAGTGA  AAT TGGG
                                ||||||||  ||| ||||
                                TCTTCACT  TTA ACCC
                                     CC   T
GAM3170  FLJ23537  3'  GAAGGAGGGGTTTGGGAAG   71898     T  AAA_
                                GAAG GA    TTTGGGAAG
                                |||| ||    |||||||||
                                CTTC CT    AAACCCTTC
                                  _  CCCC
GAM3170  FLJ30294  3'  TAGCAGAAGTGAATGCCAAGGA 71899           AATTT
                                TAGCAGAAGTGAA    GGGA
                                ||||||||||||    ||||
                                ATCGTCTTCACTT    TCCT
                                       ACGGT
GAM3170  GCHFR     3'  GCGGTGATGATTTGGGAAG   71900    AGAA   AA
                                GC    GTGA  ATTTGGGAAG
                                ||    ||||  ||||||||||
                                CG    CACT  TAAACCCTTC
                                 C___    AC
GAM3170  GMPPB     5'  ACAGGACTTGGGGTTTGGGAAG 71901     _ AG  AAAA
                                GCAG A  TG    TTTGGGAAG
                                |||| |  ||    |||||||||
                                TGTC T  AC    AAACCCTTC
                                  C GA  CCC_
GAM3170  H-L(3)MBT 3'  TAGCAGAAGTGACGCTGGG   71902          AAAT
                                TAGCAGAAGTGA    TTGGG
                                ||||||||||||    |||||
                                ATCGTCTTCACT    GACCC
                                       GC__
GAM3170  KIAA0254  3'  AGCAGAAGTGGGAGAGAA    71903         AAAATTT
                                AGCAGAAGTG      GGGAA
                                ||||||||||      |||||
                                TCGTCTTCAC      CTCTT
                                      CCT____
GAM3170  KIAA0461  3'  TAGCAGAAGTGAATGACCAATG 71904           AATT___
              GG                  TAGCAGAAGTGAA      TGGG
                                ||||||||||||      ||||
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                                ATCGTCTTCACTT      ACCC
                                      ACTGGTT
GAM3170 KIAA0841 3' CAGCAGGTGAAGATTTGGGA  71905       AA    A
                                TAGCAG  GTGAA ATTTGGGA
                                ||||||  ||||| ||||||||
                                GTCGTC  CACTT TAAACCCT
                                   __    C
GAM3170 KIAA1054 3' GCAGAAGTGAGAGAA       71906          AAATTT
                                GCAGAAGTGA     GGGAA
                                ||||||||||     |||||
                                CGTCTTCACT     CTCTT
                                       _______
GAM3170 KIAA1543 5' GCGGAAGGTGAAGACAGGA   71907    A   _    AATT
                                GC GAAG TGAA    TGGGA
                                || |||| ||||    |||||
                                CG CTTC ACTT    GTCCT
                                 C    C    CT__
GAM3170 KIAA1776 3' ACAGAAGTGAAAGCCTGAG   71908           A
                                GCAGAAGTGAAA TTTGGG
                                |||||||||||| ||||||
                                TGTCTTCACTTT GGACTC
                                      C
GAM3170 KIAA1941 3' TAGCAGAAGTAGAAGTGAG   71909          _  AATT
                                TAGCAGAAGT GAA    TGGG
                                |||||||||| |||    ||||
                                ATCGTCTTCA CTT    ACTC
                                      T   C___
GAM3170 MGC15873 3' GCAACATGAGAATTTGGG    71910     AA    A
                                GCAG  GTGA AATTTGGG
                                ||||  |||| ||||||||
                                CGTT  TACT TTAAACCC
                                  G_    C
GAM3170 MGC3113  3' GCAGAAGTGAGAAGGACGGG  71911          A  TT_
                                GCAGAAGTGA AA   TGGG
                                |||||||||| ||   ||||
                                CGTCTTCACT TT   GCCC
                                      C  CCT
GAM3170 PP1201   3' TAGCAGAAGGAAAGAACCCAGA 71912         T   __   TG
            A                    TAGCAGAAG GAAA  ATT  GGA
                                |||||||| ||||  |||  |||
                                ATCGTCTTC CTTT  TGG  CTT
                                      _   CT   GT
GAM3170 PRO0245  5' GCAGAGTGAAAATGCGAG    71913      A       T
                                GCAGA GTGAAAAT TGGG
                                ||||| |||||||| ||||
                                CGTCT CACTTTTA GCTC
                                   _      C
GAM3170 PRO1580  5' AGCAGAAGTGAAGAGAA     71914           AATTT
                                AGCAGAAGTGAA    GGGAA
                                ||||||||||||    |||||
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                                TCGTCTTCACTT    CTCTT
                                        _____
GAM3170 Rabip4R  3' GAAGTGAAAATGAAATGAAG  71915        TTGG_
                                GAAGTGAAAAT    GAAG
                                ||||||||||    ||||
                                CTTCACTTTTA    CTTC
                                    CTTTA
GAM3170 TCEA3    3' TAGCAGAGAGTTTGGGAA    71916      _  GAAAAT
                                TAGCAGA AGT    TTGGGAA
                                ||||||| |||    |||||||
                                ATCGTCT TCA    AACCCTT
                                   C  ______
GAM3170 LOC144747 5' GCAGAAGTGAGAAGAACGAG  71917        A  TT_
                                GCAGAAGTGA AA  TGGG
                                |||||||||| ||  ||||
                                CGTCTTCACT TT  GCTC
                                    C  CTT
GAM3170 LOC146237 3' TAGCAGAAGGAGAAAGGGG   71918        T  A  TTT
                                TAGCAGAAG GA AA  GGG
                                ||||||||| || ||  |||
                                ATCGTCTTC CT TT  CCC
                                     _ C  TC_
GAM3170 LOC148293 3' GCAGAAGCGAAGGGAA     71919        AATTT
                                GCAGAAGTGAA    GGGAA
                                ||||||||||    |||||
                                CGTCTTCGCTT    CCCTT
                                        _____
GAM3170 LOC148760 3' GCAGATGTAATTTGGGAAG   71920     A   AAA
                                GCAGA GTGA  TTTGGGAAG
                                ||||| ||||  |||||||||
                                CGTCT CATT  AAACCCTTC
                                   A  ___
GAM3170 LOC149837 5' AAGTGAGATTTGGGAAG     71921      AA
                                AAGTGA  ATTTGGGAAG
                                ||||||  ||||||||||
                                TTCACT  TAAACCCTTC
                                   C_
GAM3170 LOC155072 3' GCAGAAGTGAAAGATCGGA   71922        AT
                                GCAGAAGTGAAA  TTGGG
                                ||||||||||||  |||||
                                CGTCTTCACTTT  AGCCT
                                    CT
GAM3170 LOC200035 5' TAGCGGAGGCGCCTGGGAA   71923     A  A  AAAA
                                TAGC GA GTG    TTTGGGAA
                                |||| || |||    ||||||||
                                ATCG CT CGC    GGACCCTT
                                  C  C  ____
GAM3170 LOC201685 5' TAGCAGAATTGGAAAGGGA   71924       GT_   ATTT
                                TAGCAGAA  GAAA   GGGA
                                ||||||||  ||||   ||||
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                                ATCGTCTT  CTTT   CCCT
                                    AAC   ____
GAM3170  LOC202868 3'  GCAGAAGTGAAAGATCGGA   71922          AT
                                GCAGAAGTGAAA  TTGGG
                                |||||||||||  |||||
                                CGTCTTCACTTT  AGCCT
                                     CT
GAM3170  LOC219848 3'  GCAGAAGTGGAAATACACTGG  71925        A   ___
                                GCAGAAGTG AAAT   TTGG
                                |||||||||  ||||  ||||
                                CGTCTTCAC TTTA   GACC
                                    C   TGT
GAM3170  LOC222057 3'  GCAGAAGCCTTTGGGA     71926        GAAAA
                                GCAGAAGT    TTTGGGA
                                ||||||||    |||||||
                                CGTCTTCG    AAACCCT
                                    G____
GAM3170  LOC255975 5'  GCAGAAGCCTTTGGGA     71926        GAAAA
                                GCAGAAGT    TTTGGGA
                                ||||||||    |||||||
                                CGTCTTCG    AAACCCT
                                    G____
GAM3170  LOC51093  5'  ACGGAAGTGAAGCCGGA    71927    A      AAT
                                GC GAAGTGAA   TTGGG
                                || ||||||||  |||||
                                TG CTTCACTT   GGCCT
                                 C      C__
GAM3170  LOC90309  5'  GCAGAAGTGAGAGAAATTGGG  71928          AAAT__
                                GCAGAAGTGA    TTGGG
                                ||||||||||    |||||
                                CGTCTTCACT    AACCC
                                     CTCTTT
GAM3170  LOC90459  3'  GCGAAAGTGAAAACAGG    71929    AG       TT
                                GC  AAGTGAAAAT  GGG
                                ||  ||||||||||  |||
                                CG  TTCACTTTTG  TCC
                                 CT        __
GAM3171  BAT2      3'  TACTCTTTTTTAACAAACAGC  71932          CCT  C
                                TACTCTTTTT   CA ACAGC
                                |||||||||   || |||||
                                ATGAGAAAAA   GT TGTCG
                                     ATT  T
GAM3171  BAT2      3'  TACTCTTTTTTAACAAACAGC  71932          CCT  C
                                TACTCTTTTT   CA ACAGC
                                |||||||||   || |||||
                                ATGAGAAAAA   GT TGTCG
                                     ATT  T
GAM3171  COL19A1   3'  TGATACTCCCTTTTCATGCAG  71933    A       CC   CA
                                C GTACTCTTTTT  TCA  CAG
                                | ||||||||||  |||  |||
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                                A TATGAGGGAAA  AGT  GTC
                                 C          __   AC
GAM3171  GALNT3   3'  ATGCTCTTTTTCGTACAG    71934    A       CTCAC
                                GT CTCTTTTTC    ACAG
                                || |||||||||    ||||
                                TA GAGAAAAAG    TGTC
                                 C       CA___
GAM3171  HSPA1L   5'  CAGTAATCTTTTTCCAAAC    71935      C       TC
                                CAGTA TCTTTTTCC  AC
                                ||||| |||||||||  ||
                                GTCAT AGAAAAAGG  TG
                                   T       TT
GAM3171  HSPA1L   5'  CAGTAATCTTTTTCCAAAC    71935      C       TC
                                CAGTA TCTTTTTCC  AC
                                ||||| |||||||||  ||
                                GTCAT AGAAAAAGG  TG
                                   T       TT
GAM3171  NEU3     3'  CAGTGCTCTTTCCACTGCA    71936     A      TC _
                                CAGT CTCTTTT  CT CA
                                |||| |||||||  || ||
                                GTCA GAGAAAG  GA GT
                                  C      GT  C
GAM3171  SH2D1A   3'  AGTGCTTGTTTTAGCACACAG  71937     A  CT   CCT
                                AGT CT  TTTT   CACACAG
                                ||| ||  ||||   |||||||
                                TCA GA  AAAA   GTGTGTC
                                  C  AC   TC_
GAM3171  AP4S1    5'  CAGTATTTTTCCAAATACAG   71938      CTC      TCAC
                                CAGTA   TTTTTCC    ACAG
                                |||||   |||||||    ||||
                                GTCAT   AAAAAGG    TGTC
                                   ____      TTTA
GAM3171  CGI-127  3'  CAGATTTTTTTCCTTACATAGC 71939     TACTC       C   C
                                CAG     TTTTTCCT ACA AGC
                                |||     |||||||| ||| |||
                                GTC     AAAAAGGA TGT TCG
                                  TAA__       A   A
GAM3171  DKK2     5'  CAGTGCTCCTTTTCAAAGTTAG 71940      A       CTCACAC
            C                    CAGT CTCTTTTTC      AGC
                                ||||| |||||||||      |||
                                GTCA GAGGAAAAG      TCG
                                  C       TTTCAA_
GAM3171  EIF4G3   3'  CAGTACCTTTTTCCTCCA    71941       T        A
                                CAGTAC CTTTTTCCTC CA
                                |||||| |||||||||| ||
                                GTCATG GAAAAAGGAG GT
                                   _       _
GAM3171  FLJ12704 3'  CAGTCTCTTCCCTTCTCACACA 71942      A       C_
            G                    CAGT CTCTTTTT  CTCACACAG
                                |||| ||||||||  |||||||||
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                                GTCA GAGAAGGG  GAGTGTGTC
                                  _      AA
GAM3171  FLJ13910  3'  CAGTACTCTTTCTCCTCAC   71943
                                CAGTACTCTTTTTCCTCAC
                                ||||||||||||||||||
                                GTCATGAGAAAGAGGAGTG

GAM3171  FLJ14054  3'  TACCAACTTCCTCATGTAGC  71944    T TT      CAC
                                TAC C  TTTCCTCA   AGC
                                ||| |  ||||||||   |||
                                ATG G  GAAGGAGT   TCG
                                  _ TT       ACA
GAM3171  FLJ20123  5'  GCTCCTCTCTCCTCATATAGC  71945    A T        CAC
                                GT C CTTTTTCCTCA   AGC
                                || | ||||||||||   |||
                                CG G GAGAGAGGAGT   TCG
                                 A _         ATA
GAM3171  FLJ20273  3'  AGTACTTTTTTCACACAG    71946      C   TCC
                                AGTACT TTTT   TCACACAG
                                |||||| ||||   ||||||||
                                TCATGA AAAA   AGTGTGTC
                                   _   ____
GAM3171  FLJ20420  5'  TCTTTTCCCGCACAGC      71947        TCA
                                TCTTTTTCC   CACAGC
                                |||||||||   ||||||
                                AGAAAAGGG   GTGTCG
                                     C__
GAM3171  HSPC228   3'  GTATTTATTTTTCACACAGC  71948    CTCT   CC
                                GTA    TTTT  TCACACAGC
                                |||    ||||  |||||||||
                                CAT    AAAA  AGTGTGTCG
                                  AAAT    __
GAM3171  KIAA0257  3'  CAGCACAAAGTCCTCATACAG  71949       TCTTTT     C
                                CAGTAC     TCCTCA ACAG
                                ||||||     |||||| ||||
                                GTCGTG     AGGAGT TGTC
                                   TTTC__     A
GAM3171  KIAA1340  3'  GTCTCTTTTTTCCACCAG    71950    A       C T   A
                                GT CTCTTTTT C CAC CAG
                                || ||||||||| | ||| |||
                                CA GAGAAAAA G GTG GTC
                                  _       A _   _
GAM3171  KIAA1911  5'  ATGCTCTTAACACATCACACAG 71951    A    TTTCC_
            C                    GT CTCTT     TCACACAGC
                                || |||||     |||||||||
                                TA GAGAA     AGTGTGTCG
                                 C    TTGTGT
GAM3171  MAP       3'  CAGGGCCGTTTTCTCACACAGC 71952     TA  C    TC
                                CAG  CT TTTT  CTCACACAGC
                                |||  || ||||  ||||||||||
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                                GTC  GG AAAA  GAGTGTGTCG
                                  CC  C   __
GAM3171  MBD2     3'  CAGGGTTCTTTTCCACAG    71953     TAC      CCTCA
                                CAG   TCTTTTT    CACAG
                                |||   |||||||    |||||
                                GTC   AGAAAAG    GTGTC
                                  CCA     ______
GAM3171  RNF9     3'  CAGTGCTCTTTCTATGCAG   71954      A       CCTCACA
                                CAGT CTCTTTTT      CAG
                                ||||  ||||||||      |||
                                GTCA GAGAAAGA      GTC
                                  C       TAC____
GAM3171  TSGA14   3'  ATACTTTTTTCCTATACAG   71955       C       CAC
                                GTACT TTTTTCCT   ACAG
                                |||||  ||||||||   ||||
                                TATGA AAAAAGGA   TGTC
                                  _       TA_
GAM3171  LOC120856 3'  CACTATTTTTCCTCTACCTTAC 71956      C       _______
              ACAGC                    TACT TTTTTCCTC      ACACAGC
                                ||||  |||||||||      |||||||
                                GTGA AAAAAGGAG      TGTGTCG
                                  T        ATGGAA
GAM3171  LOC126669 3'  AGTACTCTTCTCACA       71957          TTTC
                                AGTACTCTT    CTCACA
                                |||||||||    ||||||
                                TCATGAGAA    GAGTGT
                                           _____
GAM3171  LOC148193 3'  CAGTAGTTTTTTTCCCCCA    71958       CTC        A
                                CAGTA   TTTTTCCTC CA
                                |||||   |||||||||  ||
                                GTCAT   AAAAAGGGG GT
                                   CAA       _
GAM3171  LOC148760 3'  CAGTGTCCTTTTTCCTCA     71959      AC
                                CAGT  TCTTTTTCCTCA
                                ||||  ||||||||||||
                                GTCA  GGAAAAAGGAGT
                                  CA
GAM3171  LOC157958 3'  GTGCCTTCTTCACTCACATGGC 71960     A T      _      CA
                                GT C CTTTTTC CTCACA  GC
                                ||  |  |||||||  ||||||  ||
                                CA G GAAGAAG GAGTGT  CG
                                 C _       T      AC
GAM3171  LOC167040 5'  CAGTCTCTTTTTCCTCAC     71961      A
                                CAGT CTCTTTTTCCTCAC
                                ||||  ||||||||||||||
                                GTCA GAGAAAAAGGAGTG
                                  _
GAM3171  LOC202934 5'  GTATTAGTCCATTTTCACACAG 71962     CTC  TT   ____
              C                   GTA   TT  TCC    TCACACAGC
                                |||   ||  |||   |||||||||
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                                CAT   AA  AGG    AGTGTGTCG
                                  ___  TC   TAAA
GAM3171  LOC221421 3'  CAGTACCCTTGGCCTGCACAG  71963          TTT   CA
                                CAGTACTCTT   CCT  CACAG
                                ||||||||||   |||  |||||
                                GTCATGGGAA   GGA  GTGTC
                                     CC_   C_
GAM3171  LOC221662 3'  AGTACTCTCTTATACAG     71964          TCCTCAC
                                AGTACTCTTTT      ACAG
                                ||||||||||       ||||
                                TCATGAGAGAA      TGTC
                                      TA_____
GAM3171  LOC255465 5'  GTATTAGTCCATTTTCACACAG 71962     CTC  TT  ____
             C                   GTA   TT  TCC    TCACACAGC
                                |||   ||  |||    |||||||||
                                CAT   AA  AGG    AGTGTGTCG
                                  ___  TC   TAAA
GAM3171  LOC257618 5'  CAGTAATCTTTTTCCAAAC    71935      C        TC
                                CAGTA TCTTTTTCC  AC
                                ||||| |||||||||  ||
                                GTCAT AGAAAAAGG  TG
                                   T        TT
GAM3171  LOC51701  3'  AGTTCTCTTTCTATACAG     71965     A       CCTCAC
                                AGT CTCTTTTT     ACAG
                                ||| ||||||||     ||||
                                TCA GAGAAAGA     TGTC
                                  A       TA____
GAM3172  BCL11B    3'  CACACCAACAGGATAGTATC   71968      GT_   T    AC
                                CACAC   CGG GATA  ATC
                                |||||   ||| ||||  |||
                                GTGTG   GTC CTAT  TAG
                                   GTT   _    CA
GAM3172  SHOC2     5'  CAGCATGGAGTAACATCCA    71969    _   C  TGA
                                CA CGT GG   TAACATCCA
                                || ||| ||   |||||||||
                                GT GTA CC   ATTGTAGGT
                                 C   _  TC_
GAM3172  AFAP      3'  CATGTCTTGGTGACAAAAGCAT 71970    C   __       ___
             C                   CA GTC  GGTGATAA   CATC
                                || |||  ||||||||   ||||
                                GT CAG  CCACTGTT   GTAG
                                 A   AA       TTC
GAM3172  FLJ12644  5'  CCCAGAAATGATGACATCCAC  71971    A  CGTC     A
                                CC CA    GGTGAT ACATCCAC
                                || ||    |||||| ||||||||
                                GG GT    TTACTA TGTAGGTG
                                 _  CT__      C
GAM3172  FLJ21901  3'  CACACGATAACATTCA      71972       GTCGGT       C
                                CACAC     GATAACAT CA
                                |||||     |||||||| ||
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                                GTGTG     CTATTGTA GT
                                  _______       A
GAM3172  KIAA0321  3'  CCACATGTCTGCATATCCA   71973      C   G   ATAAC
                                CCACA GTC GTG     ATCCA
                                ||||| ||| |||     |||||
                                GGTGT CAG CGT     TAGGT
                                   A   A   A____
GAM3172  KIAA0931  3'  CCACTGTCTGGATGACATCCAC 71974      AC   GGT   A
                                CCAC  GTC   GAT ACATCCAC
                                ||||  |||   ||| ||||||||
                                GGTG  CAG   CTA TGTAGGTG
                                  A_   AC_   C
GAM3172  KIAA1679  3'  CCATGTGTAGTGATAACAT   71975     CAC  C
                                CCA   GT GGTGATAACAT
                                |||   || ||||||||||
                                GGT   CA TCACTATTGTA
                                  ACA  _
GAM3172  PRMT3     5'  CCACTCAGATATGATAACATCT 71976      A  TCG         C
              AC                  CCAC CG   GTGATAACATC AC
                                ||||  ||   |||||||||| ||
                                GGTG GT   TACTATTGTAG TG
                                  A  CTA         A
GAM3172  LOC146177 3'  CCACAGGGCAGTGATAGCGTCC 71977       CGT       ACA
                                CCACA   CGGTGATA   TCC
                                |||||   ||||||||   |||
                                GGTGT   GTCACTAT   AGG
                                   CCC       CGC
GAM3172  LOC147669 3'  ACATGGGTGACATCCA      71978      C     TAA
                                ACGT GGTGA   CATCCA
                                |||| |||||   ||||||
                                TGTA CCACT   GTAGGT
                                  C    ___
GAM3172  LOC199675 3'  CCACACTCAGAGTGACATC    71979       G    TGATA
                                CCACAC TCGG     ACATC
                                |||||| ||||     |||||
                                GGTGTG AGTC     TGTAG
                                   _    TCAC_
GAM3172  LOC221683 5'  ACAAAAGTGATAATGTCCA    71980     TC       CA
                                ACG  GGTGATAA  TCCA
                                |||  ||||||||  ||||
                                TGT  TCACTATT  AGGT
                                  TT       AC
GAM3172  LOC256158 5'  CCACACATCGGCTCTGTCCAC  71981            GATAACA
                                CCACACGTCGGT      TCCAC
                                ||||||||||||      |||||
                                GGTGTGTAGCCG      AGGTG
                                       AGAC___
GAM3172  LOC256254 5'  CCACACATTAACATCC      71982         CGGTGA
                                CCACACGT     TAACATCC
                                ||||||||     ||||||||
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                                GGTGTGTA     ATTGTAGG
                                         _______
GAM3172 LOC56270 5' CCACACGCAAAGCATCC     71983       T   TGATAA
                                CCACACG CGG     CATCC
                                ||||||| |||     |||||
                                GGTGTGC GTT     GTAGG
                                    _   TC____
GAM3172 LOC56270 5' CCACACGCAAAGCATCC     71983       T   TGATAA
                                CCACACG CGG     CATCC
                                ||||||| |||     |||||
                                GGTGTGC GTT     GTAGG
                                    _   TC____
GAM3173 COL6A2   3' GAATGGTCCTGGGGAAGGTGG  71986       T      CGTTT
                                GAATGGT CCTGGGG     TGG
                                ||||||| |||||||     |||
                                CTTACCA GGACCCC     ACC
                                    _      TTCC_
GAM3173 MSI1     3' ATGGTTCCAGGGGCTCGG     71987       T     GTT
                                ATGGTTCC GGGGC   TTGG
                                |||||||| |||||   ||||
                                TACCAAGG CCCCG   AGCC
                                     T    ___
GAM3173 SLC8A2   3' AGGATGGTTACTGGGGGT     71988    A     C     C
                                AG ATGGTT CTGGGG GT
                                || |||||| |||||| ||
                                TC TACCAA GACCCC CA
                                 C     T     _
GAM3173 FLJ12876 5' AGAATGTTCCTGGGGTCA     71989       G       _
                                AGAATG TTCCTGGGG CG
                                |||||| ||||||||| ||
                                TCTTAC AAGGACCCC GT
                                    _       A
GAM3173 HA-1     3' AGAATGGTTTCTGGAGTCCCTG 71990         C     CG
                                AGAATGGTT CTGGGG  TTTTG
                                ||||||||| ||||||  |||||
                                TCTTACCAA GACCTC  GGGAC
                                      A     A_
GAM3173 KIAA0599 3' AGGATGTTTCCTGGGGAC     71991    A   G       _
                                AG ATG TTCCTGGGG C
                                || ||| ||||||||| |
                                TC TAC AAGGACCCC G
                                 C   A        T
GAM3173 KIAA1161 5' GGTTCCTGGGAGTACATGG    71992          C  TT_
                                GGTTCCTGGGG GT   TGG
                                |||||||||| ||   |||
                                CCAAGGACCCT CA   ACC
                                       _ TGT
GAM3173 LOC133121 3' AGGATGGCTCCTGGGTGT    71993    A          GC
                                AG ATGGTTCCTGGG  GT
                                || ||||||||||  ||
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                                TC TACCGAGGACCC  CA
                                 C         A_
GAM3173  LOC158382 3'  AGAATGGTTTTTGGAGGACA   71994        CC  _ _
                                AGAATGGTT  TGG GG CG
                                |||||||||  ||| || ||
                                TCTTACCAA  ACC CC GT
                                     AA   T  T
GAM3173  LOC257319 3'  AAAATGGTTTTTGGTTTTG   71995        CC   GGCG
                                AGAATGGTT  TGG   TTTTG
                                |||||||||  |||   |||||
                                TTTTACCAA  ACC   AAAAC
                                     AA  ____
GAM3174  ANXA11   5'  CACTCGGGGCACTGGGGAGCCG 71998    _    TG CGCCA   AA
                                CAC CGGGG  T    GGA  CCG
                                ||| |||||  |    |||  |||
                                GTG GCCCC  G    CCT  GGC
                                  A    GT ACC__   C_
GAM3174  CLTC     5'  CCGGGGACGCAGGAAAC     71999       TGT   C
                                CCGGGG   CGC AGGAAAC
                                ||||||   ||| |||||||
                                GGCCCC   GCG TCCTTTG
                                   T__   _
GAM3174  DGCR2    5'  CCGGGGCGGCTGGGAGGCCG   72000        TC  CA   AA
                                CCGGGGTG  GC  GGA  CCG
                                ||||||||  ||  |||  |||
                                GGCCCCGC  CG  CCT  GGC
                                     __ AC   CC
GAM3174  DKK1     5'  CCTGGGTCCCCAGGAAACC   72001    GG  T   G
                                CC  GG GTC CCAGGAAACC
                                ||  || ||| ||||||||||
                                GG  CC CAG GGTCCTTTGG
                                 A_  _   G
GAM3174  DNMT3B   5'  CCGACCGCCAGGGAGCCG    72002     GGTG      AAA
                                CCGG   TCGCCAGG   CCG
                                ||||   ||||||||   |||
                                GGCT   GGCGGTCC   GGC
                                  ____       CTC
GAM3174  DRD2     3'  CCGGGGTGAAGAGGAGGCCG   72003        TCGCC   AA
                                CCGGGGTG    AGGA  CCG
                                ||||||||    ||||  |||
                                GGCCCCAC    TCCT  GGC
                                     TTC__    CC
GAM3174  ESRRA    5'  CCGGAGTGAGCCGGGGGCCG   72004        TC   A  AAA
                                CCGGGGTG  GCC GG   CCG
                                ||||||||  ||| ||   |||
                                GGCCTCAC  CGG CC   GGC
                                     T_   C  CC_
GAM3174  FGFR1    3'  CACCGGGGTATGGGGAGCC   72005         CGCCA   AA
                                CACCGGGGTGT    GGA  CC
                                ||||||||||    |||  ||
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                                GTGGCCCCATA    CCT  GG
                                      CC___   C_
GAM3174  GALC     5'  GGCGTTGCCAGGAAGCCG    72006      C      A
                                GGTGT GCCAGGAA CCG
                                ||||| |||||||| |||
                                CCGCA CGGTCCTT GGC
                                   A       C
GAM3174  HDAC7A   3'  CACCAGGGCATCGCCAGGA   72007
                                CACCGGGGTGTCGCCAGGA
                                ||||||||||||||||||
                                GTGGTCCCGTAGCGGTCCT

GAM3174  HDAC7A   3'  CACCAGGGCATCGCCAGGA   72007
                                CACCGGGGTGTCGCCAGGA
                                ||||||||||||||||||
                                GTGGTCCCGTAGCGGTCCT

GAM3174  TPTE     5'  CCGGGGGTCCCTAGAGCCG   72008       T   G  A   AA
                                CCGGGG GTC CC GGA  CCG
                                |||||| ||| || |||  |||
                                GGCCCC CAG GG TCT  GGC
                                   _   _ A   C_
GAM3174  ASE-1    3'  CCTGGGTGACACCAGGAGAC   72009    G    T      A
                                CC GGGTG CGCCAGGA AC
                                || ||||| |||||||| ||
                                GG CCCAC GTGGTCCT TG
                                 A    T       C
GAM3174  C6orf26  3'  CACCGGAGTCTCAGGAGG    72010         G   CC
                                CACCGGGGT TCG  AGG
                                ||||||||| |||  |||
                                GTGGCCTCA AGT  TCC
                                      G   CC
GAM3174  CHK      3'  GGTAAGGGCCGGGAAACCG   72011      TC_   A
                                GGTG   GCC GGAAACCG
                                ||||   ||| ||||||||
                                CCAT   CGG CCTTTGGC
                                   TCC   C
GAM3174  CORO1B   5'  CACCGGGGGCGCAGG       72012        T T   C
                                CACCGGGG G CGC AGG
                                |||||||| | ||| |||
                                GTGGCCCC C GCG TCC
                                      _ _   _
GAM3174  DKFZp762E1312 5'  CACCGGGGTGTCCTCGAAGG   72013           GCC__
                                CACCGGGGTGTC    AGG
                                ||||||||||||    |||
                                GTGGCCCCACAG    TCC
                                      GAGCT
GAM3174  DNAL4    3'  CACTGGGCGTGGCTCAGGAAAC 72014     CG     C  _
                                CAC  GGGTGT GC CAGGAAAC
                                |||  |||||| || ||||||||
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                                GTG  CCCGCA CG GTCCTTTG
                                  A_     C  A
GAM3174  FKBP4    5'  CGGGGCGTGCGGGAGGCCG   72015        C  CA   AA
                                CGGGGTGT GC  GGA  CCG
                                |||||||| ||  |||  |||
                                GCCCCGCA CG  CCT  GGC
                                     _ C_   CC
GAM3174  FLJ20330 5'  CGCGGCCGCCAGGAGGCC    72016    G   GT      AA
                                CG GGT  CGCCAGGA  CC
                                || |||  ||||||||  ||
                                GC CCG  GCGGTCCT  GG
                                 G  __       CC
GAM3174  HNK-1ST   3'  CCTACCTTGTTGCCAGGAAGCC 72017    GGGG_  C      A
           G                     CC     TGT GCCAGGAA CCG
                                ||     ||| |||||||| |||
                                GG     ACA CGGTCCTT GGC
                                 ATGGA   A       C
GAM3174  KIAA1218  3'  CACTGGGGTGTCGTGAGG    72018     C       CC
                                CAC GGGGTGTCG  AGG
                                ||| |||||||||  |||
                                GTG CCCCACAGC  TCC
                                  A        AC
GAM3174  MGC24976  5'  GGGGCGTCCCCGCCGGGGGGCC 72019         ___   A  AAA
           G                     GGGGTGTC   GCC GG   CCG
                                |||||||   ||| ||   |||
                                CCCCGCAG   CGG CC   GGC
                                     GGG   C  CCC
GAM3174  MGC2647   3'  CACTGGGGTGCCGTCCCCTCCC 72020     C       _  AGGAAA
           G                     CAC GGGGTGTCG CC      CCG
                                ||| |||||||| ||      |||
                                GTG CCCCACGGC GG      GGC
                                  A        A  GGAG__
GAM3174  MGC4701   5'  CACCTGGGTGCAGACGGGGA   72021      G     C_  CA
                                CACC GGGTGT  GC  GGA
                                |||| ||||||  ||  |||
                                GTGG CCCACG  TG  CCT
                                  A     TC  CC
GAM3174  MSH5     3'  CACCGGAGTCTCAGGAGG    72010         G   CC
                                CACCGGGGT TCG  AGG
                                ||||||||| |||  |||
                                GTGGCCTCA AGT  TCC
                                     G   CC
GAM3174  PP1628   5'  CCGGGGTGTCTCCCGAGG    72022          G_  _
                                CCGGGGTGTC  CC AGG
                                ||||||||||  || |||
                                GGCCCCACAG  GG TCC
                                      AG  C
GAM3174  SEC24B   5'  CACTGAGGGTGTCACCCGGGAC 72023     C _         A  AA
           CG                     CAC G GGGTGTCGCC GG  ACCG
                                ||| | ||||||||| ||  ||||
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                                GTG C CCCACAGTGG CC  TGGC
                                  A T        G  C_
GAM3174  SLI     5'  CGGGGTGTAGCCAGCC      72024        C    GAAA
                                CGGGGTGT GCCAG    CC
                                |||||||| |||||    ||
                                GCCCCACA CGGTC    GG
                                     T    _____
GAM3174  T2BP    5'  CCGGGGTGCGGGGAACC     72025        T  CCA    A
                                CCGGGGTG CG   GGAA CC
                                |||||||| ||   |||| ||
                                GGCCCCAC GC   CCTT GG
                                     _ C__    _
GAM3174  TIGD5   5'  CGGGGCTGTAGCGGTAGGAGGC 72026      _   C  C__    AA
            CG                    CGGGG TGT GC   AGGA  CCG
                                |||||  ||| ||   ||||  |||
                                GCCCC ACA CG   TCCT  GGC
                                   G   T  CCA    CC
GAM3174  TOB2    5'  CGCCGGGCCAGGGGACCG    72027   A   GGTGTC     AA
                                C CCGG     GCCAGG  ACCG
                                | ||||     ||||||  ||||
                                G GGCC     CGGTCC  TGGC
                                 C    _______     CC
GAM3174  TTTY2   5'  CACCAGGGTGTCAGG       72028          GCC
                                CACCGGGGTGTC   AGG
                                ||||||||||||   |||
                                GTGGTCCCACAG   TCC
                                          ___
GAM3174  LOC148753 3'  GGCTCATCGCCAGGAAAC    72029    GG
                                GG  TGTCGCCAGGAAAC
                                ||  ||||||||||||||
                                CC  GTAGCGGTCCTTTG
                                 GA
GAM3174  LOC150933 3'  CCAGGGTGCCAGACAGGAAAC  72030          C_
                                CCGGGGTGTCG  CAGGAAAC
                                ||||||||||  ||||||||
                                GGTCCCACGGT  GTCCTTTG
                                      CT
GAM3174  LOC159148 5'  CACCAGGGTGTCAGG       72028          GCC
                                CACCGGGGTGTC   AGG
                                ||||||||||||   |||
                                GTGGTCCCACAG   TCC
                                          ___
GAM3174  LOC162992 5'  ACCGGGGTGTCCTGGGCAGGGG 72031          GC___    AA
            AC                    ACCGGGGTGTC    CAGG  AC
                                ||||||||||     ||||  ||
                                TGGCCCCACAG    GTCC  TG
                                      GACCC    CC
GAM3174  LOC196738 3'  ACCGAGCTCAGGAGACC     72032      GGTGTC  _    A
                                ACCGG     GC CAGGA ACC
                                |||||     || ||||| |||
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                                TGGCT     CG GTCCT TGG
                                  _______ A    C
GAM3174 LOC200734 3' ACCAGGGAGCTGGGAGGCCG  72033       TGTC  CA   AA
                                ACCGGGG   GC  GGA  CCG
                                |||||||   ||  |||  |||
                                TGGTCCC   CG  CCT  GGC
                                   T___  AC   CC
GAM3174 LOC90288 5' ACCGGGGTATCAAATAAACCG  72034          CCAGG
                                ACCGGGGTGTCG    AAACCG
                                ||||||||||||    ||||||
                                TGGCCCCATAGT    TTTGGC
                                      TTA__
GAM3175 H4F2     3' TGGGAGCTGACAGAATTT    72037     A      GT
                                TGG AGCTGGC  GGAATTT
                                ||| |||||||  |||||||
                                ACC TCGACTG  TCTTAAA
                                  C      __
GAM3175 PAX9     3' CTGCTGGAGACGGAAT      72038        AGCT   GT
                                CTGCTGGA   GGC  GGAAT
                                ||||||||   |||  |||||
                                GACGACCT   CTG  CCTTA
                                     _____  __
GAM3175 H11      5' CTGCTGGAGGCTGGAGGCGG  72039        A    C_
                                CTGCTGGA GCTGG  GTGG
                                |||||||| |||||  ||||
                                GACGACCT CGACC  CGCC
                                     C    TC
GAM3175 KIAA0365 3' CTGCTGGAGGTTATGATCGGG  72040        AGC__   _  T
                                CTGCTGGA    TGG CG GG
                                ||||||||    ||| || ||
                                GACGACCT    ACT GC CC
                                     CCAAT   A  _
GAM3175 LY6G5C   3' GCTGGAAACTGGTGGAATTT   72041          CG
                                GCTGGAAGCTGG  TGGAATTT
                                ||||||||||||  ||||||||
                                CGACCTTTGACC  ACCTTAAA
                                      __
GAM3175 P15-2    3' CTGCTGAAGCTGTGG       72042       G    GGC
                                CTGCTG AAGCT   GTGG
                                ||||||| |||||   ||||
                                GACGAC TTCGA   CACC
                                   _    ___
GAM3175 SLC2A13  3' TGTAGGAGGCACTTTGGAATTT 72043    CT   A  TGGCG
                                TG  GGA GC    TGGAATTT
                                ||  ||| ||    ||||||||
                                AC  CCT CG    ACCTTAAA
                                  AT   C  TGAA_
GAM3175 TRIM22   3' CTGCTGGAATCTAGATTTGGGA 72044        G   CG_   A
             TTT                  CTGCTGGAA CTGG   TGG ATTT
                                ||||||||| ||||   ||| ||||
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                                GACGACCTT GATC   ACC TAAA
                                      A    TAA   C
GAM3175  LOC144501 3'  CTGCTGGGAGCTGGCTGG    72046        A      G
                                CTGCTGG AGCTGGC TGG
                                ||||||| ||||||| |||
                                GACGACC TCGACCG ACC
                                    C      _
GAM3175  LOC144501 3'  CTGGTGGGATGTGGAATT    72045      AAGC   C__
                                CTGG    TGG   GTGGAATT
                                ||||    |||   ||||||||
                                GACC    ACC   CACCTTAA
                                  ____   CTA
GAM3175  LOC147057 5'  CTGCTGGAGCTGGCGTG     72047        A
                                CTGCTGGA GCTGGCGTG
                                |||||||| |||||||||
                                GACGACCT CGACCGCAC

                                   _
GAM3175  LOC153516 3'  CTGTGCCTGGCGTGGAATTT   72048     GAAG
                                CTG    CTGGCGTGGAATTT
                                |||    ||||||||||||||
                                GAC    GACCGCACCTTAAA
                                  ACG_
GAM3175  LOC221496 3'  CTGGAGGCAGCTGTGGAATTT  72049       A  T   _
                                CTGGA GC GGC GTGGAATTT
                                ||||| || ||| |||||||||
                                GACCT CG TCG CACCTTAAA
                                   C  _   A
GAM3175  LOC255147 5'  CTGCTAGAACTGCGTG       72050         G   G
                                CTGCTGGAA CTG CGTG
                                ||||||||| ||| ||||
                                GACGATCTT GAC GCAC

                                      _   _
GAM3175  LOC256942 3'  CTGCTGGAGTGATGGGATT    72051         A C  GC    A
                                CTGCTGGA G TG  GTGG ATT
                                |||||||| | ||  |||| |||
                                GACGACCT C AC  TACC TAA
                                     _ _ __    C
GAM3176  ASCL1    3'  TGATGGGAGTTACTATAAC    72054    T      AAA  A
                                A ATGGGAGT   GC TATAAC
                                | ||||||||   || ||||||
                                A TACCCTCA   TG ATATTG
                                 C       A__  _
GAM3176  LOC150538 3'  TATATGGGCAAACACAT      72055         AGTA
                                TATATGGG    AAGCATAT
                                ||||||||    ||||||||
                                ATATACCC    TTTGTGTA
                                     G___
GAM3177  F2R      3'  TGACATTCATTTATTACTGTA  72058    T         ___
                                A ACATTCATTTAT   TGTA
                                | ||||||||||||   ||||
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                                A TGTAAGTAAATA   ACAT
                                 C          ATG
GAM3177 ITGA1    3'  TATACATTCATTCATTGC    72059
                                TATACATTCATTTATTGT
                                ||||||||||||||||||
                                ATATGTAAGTAAGTAACG

GAM3177 TNF      3'  ATACATTCATCTGTAAATAA  72060          TAT
                                ATACATTCATT   TGTAAATAA
                                ||||||||||   |||||||||
                                TATGTAAGTAG   ACATTTATT
                                              ___
GAM3177 C1orf28  3'  TACATTCATTTAAATGTAA   72061          T_
                                TACATTCATTTA  TGTAA
                                ||||||||||||  |||||
                                ATGTAAGTAAAT  ACATT
                                       TT
GAM3177 FLJ10933 3'  ATTCATTTACTATAAATAA   72062
                                ATTCATTTATTGTAAATAA
                                ||||||||||||||||||
                                TAAGTAAATGATATTTATT

GAM3177 KIAA1712 3'  TATACATACATACCATAAATA  72063       T  TT   TG
                                TATACAT CA  TAT  TAAATA
                                ||||||| ||  |||  ||||||
                                ATATGTA GT  ATG  ATTTAT
                                     T __   GT
GAM3177 PDE3A    3'  TATACATTCATTAGGCAA    72064          TATT
                                TATACATTCATT    GTAA
                                ||||||||||||    ||||
                                ATATGTAAGTAA    CGTT
                                       TC__
GAM3177 TFEC     3'  TATACATTTATTTATCCTA   72065        C      G
                                TATACATT ATTTATT TA
                                |||||||| ||||||| ||
                                ATATGTAA TAAATAG AT
                                     A      G
GAM3177 LOC154184 3'  TATACATTCATTAATTCTATAT 72066          T   G  A
             AA                   TATACATTCATT ATT TA ATAA
                                ||||||||||||| ||| || ||||
                                ATATGTAAGTAA TAA AT TATT
                                       T   G  A
GAM3177 LOC202451 5'  TATACATTCATTGTCTTCTA   72067          TA_  G
                                TATACATTCATT   TT TA
                                ||||||||||||   || ||
                                ATATGTAAGTAA   AA AT
                                       CAG  G
GAM3177 LOC203411 3'  TATACATTCTTTACAGATTGTA 72068         A    ____
                                TATACATTC TTTAT    TGTA
                                |||||||| |||||    ||||
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                                ATATGTAAG AAATG   ACAT
                                      _    TCTA
GAM3177 LOC257551 3' ATACATTCATCTGTAAATAA  72060        TAT
                                ATACATTCATT  TGTAAATAA
                                ||||||||||  |||||||||
                                TATGTAAGTAG  ACATTTATT
                                      ___
GAM3177 LOC257601 3' ATACATTCATCTGTAAATAA  72060        TAT
                                ATACATTCATT  TGTAAATAA
                                ||||||||||  |||||||||
                                TATGTAAGTAG  ACATTTATT
                                      ___
GAM3178 ABL1    3' GCCCTTGCAGACCTGCC    72071       TC  GC
                                GTCCTTGCA GGC GCC
                                |||||||||  |||  |||
                                CGGGAACGT CTG CGG
                                      __  GA
GAM3178 ABL1    3' GCCCTTGCAGACCTGCC    72071       TC  GC
                                GTCCTTGCA GGC GCC
                                |||||||||  |||  |||
                                CGGGAACGT CTG CGG
                                      __  GA
GAM3178 CDC20   5' GTCCTTGCAGTTGGTGCCTACG 72072       TC_ C GCC
                                GTCCTTGCA  GG GC  CG
                                |||||||||  || ||  ||
                                CAGGAACGT  CC CG  GC
                                     CAA  A  GAT
GAM3178 CNTN2   3' GTCCTTGCTGCTGCTCGA   72073       ATCG GC C
                                GTCCTTGC   GC GC CGA
                                ||||||||   ||  || |||
                                CAGGAACG   CG  CG GCT
                                    A___  A_  A
GAM3178 HIRA    5' GTCCCTCAGCGCGCCCG    72074     TGCA
                                GTCCT   TCGGCGCGCCCG
                                |||||   ||||||||||||
                                CAGGG   AGTCGCGCGGGC
                                     _____
GAM3178 NFATC2  5' GTCCTGGACGCGCCCG     72075     T CATC
                                GTCCT G   GGCGCGCCCG
                                ||||| |   ||||||||||
                                CAGGA C   CTGCGCGGGC
                                     _ _____
GAM3178 PIWIL1  5' GTCCTTGCACCTCAGCCCGAG 72076        GG C
                                GTCCTTGCATC CG GCCCGAG
                                ||||||||||| || |||||||
                                CAGGAACGTGG GT CGGGCTC
                                      A_ _
GAM3178 CCRL2   3' AGCCTTGCACGGTGCCTGA  72077   T    T  CGC  C
                                AG CCTTGCA CGG  GCC GA
                                || ||||||| |||  ||| ||
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                                TC GGAACGT GCC   CGG CT
                                 _     _  A__   A
GAM3178 FLJ10342 5' AGCTTTGCGCCGCGCCTGA   72078    CC   ATC G    C
                                AGT  TTGC   G CGCGCC GA
                                |||  ||||   | |||||| ||
                                TCG  AACG   C GCGCGG CT
                                  A_   ___ G     A
GAM3178 FLJ23323 3' AGCCCTTGTATCCATTATGCTC 72079       C   GGCGC_  C
           GAG                    AGTCCTTG ATC     GC CGAG
                                |||||||| |||     || ||||
                                TCGGGAAC TAG     CG GCTC
                                    A   GTAATA  A
GAM3178 MRPS7    5' CTGCCCTCGGCGCGCCTGAG   72080     A_       C
                                TTGC  TCGGCGCGCC GAG
                                ||||  |||||||||| |||
                                GACG  AGCCGCGCGG CTC
                                  GG        A
GAM3178 UBE2D1   5' GTCCCTGCTCCGTGTGCGCCCG 72081       AT  GC_
           AG                     GTCCTTGC  CG   GCGCCCGAG
                                |||||||  ||   |||||||||
                                CAGGGACG  GC   CGCGGGCTC
                                    AG  ACA
GAM3178 LOC149086 3'  AGTCCTTTCATCCCCG     72082       G    GGCGCG
                                AGTCCTT CATC     CCCG
                                ||||||| ||||     ||||
                                TCAGGAA GTAG     GGGC
                                    A   _______
GAM3178 LOC200953 5'  AGTCCTTGTGGCCCTCG     72083       CATC   GCG  _
                                AGTCCTTG    GGC   CC CG
                                ||||||||    |||   || ||
                                TCAGGAAC    CCG   GG GC
                                    A___    ___   A
GAM3179 FXR2     3'  GGGGGTGTTCAGAGAGAGATTG 72086     ATA_      TCA____
           GGGC                    GGG    TTCAGAGA      GGGC
                                |||    ||||||||      ||||
                                CCC    AAGTCTCT      CCCG
                                  CCAC       CTCTAAC
GAM3179 HTRA3    3'  AGATGGGTGTTCACAGGGG    72087     _   ATA    G  ATCA
                                AGA GGG   TTCA AG    GGG
                                ||| |||   |||| ||    |||
                                TCT CCC   AAGT TC    CCC
                                  A  AC_   G  ____
GAM3179 NRAP     3'  GGGATGGTCGGGGATCAGGG   72088      AT  AGA
                                GGGAT  TC   GATCAGGG
                                |||||  ||   ||||||||
                                CCCTA  AG   CTAGTCCC
                                   CC  CCC
GAM3179 PYGM     5'  AGAGGGATGCTCAGGTTACTGG 72089        A    AGATCAG
           C                     AGAGGGAT TTCAG      GGC
                                |||||||| |||||      |||
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                                TCTCCCTA GAGTC      CCG
                                    C    CAATGA_
GAM3179 RAP1GA1  3' AGAGGGATGCTCAGGG      72090        A    AGATCA
                                AGAGGGAT TTCAG     GG
                                |||||||| |||||     ||
                                TCTCCCTA GAGTC     CC
                                    C    _______
GAM3179 RENT1    3' GAGGTGTTCGGATCAGGG    72091     GATA   AGA
                                GAGG   TTC   GATCAGGG
                                ||||   |||   ||||||||
                                CTCC   AAG   CTAGTCCC
                                  AC__   C__
GAM3179 SCG3     5' AAGGGATAAGCAGGGTTGGGGC 72092        TT   AGATCA
                                GAGGGATA  CAG     GGGC
                                ||||||||  |||     ||||
                                TTCCCTAT  GTC     CCCG
                                    TC   CCAAC_
GAM3179 WWOX     3' GAGGGACATTTGGAAGGGGC   72093        CA   ATCA
                                GAGGGATATT  GAG   GGGC
                                ||||||||||  |||   ||||
                                CTCCCTGTAA  CTT   CCCG
                                     AC   C___
GAM3179 APM2     3' GGCTGCCCGGAGATCAGGGC   72094    ATA   A
                                GG   TTC GAGATCAGGGC
                                ||   ||| ||||||||||
                                CC   GGG CTCTAGTCCCG
                                 GAC   C
GAM3179 ELF4     3' AGGGGATATTCACATATAGGG  72095    A       GAG  C
                                AG GGGATATTCA   AT AGGG
                                || ||||||||||   || ||||
                                TC CCCTATAAGT   TA TCCC
                                 _       GTA  _
GAM3179 KDELR3   3' GAGGGACATTGTTCCAGATTGG 72096        ____     GATCA
              GG                  GAGGGATA    TTCAGA    GGG
                                ||||||||    ||||||    |||
                                CTCCCTGT    AGGTCT    CCC
                                    AACA     AAC__
GAM3179 KIAA0450 3' AGAGGAGTCGGATCAGGG    72097      ATAT  AGA
                                AGAGGG   TC   GATCAGGG
                                ||||||   ||   ||||||||
                                TCTCCT   AG   CTAGTCCC
                                   C___  C__
GAM3179 PTK6     5' AGAGGGAGTGGAATCAGGG   72098       TATTCAGA
                                AGAGGGA      GATCAGGG
                                |||||||      ||||||||
                                TCTCCCT      TTAGTCCC
                                    CACC____
GAM3179 TUBB5    3' AGAGGGGATTCAGAGAT     72099       AT
                                AGAGGG  ATTCAGAGAT
                                ||||||  ||||||||||
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                                TCTCCC  TAAGTCTCTA
                                   C_
GAM3179  WNT10A    3'  GAGGGGACCTCGATCAGGGC  72100      ATA   AGA
                                GAGGG   TTC   GATCAGGGC
                                |||||   |||   |||||||||
                                CTCCC   GAG   CTAGTCCCG
                                   CTG   ___
GAM3179  LOC148089 3'  AGAGGGATGTGTCAAAGGG   72101       AT_   AGATC
                                AGAGGGAT   TCAG    AGGG
                                ||||||||   ||||    ||||
                                TCTCCCTA   AGTT    TCCC
                                     CAC   _____
GAM3179  LOC199692 3'  GATGGATATTCAATGCAGGGC  72102    G       AGAT
                                GA GGATATTCAG    CAGGGC
                                || ||||||||||    ||||||
                                CT CCTATAAGTT    GTCCCG
                                 A         AC__
GAM3179  LOC205669 5'  AGAGGGATTTCGAGG       72103        A   A  GATCA
                                AGAGGGAT TTC GA     GG
                                |||||||| ||| ||     ||
                                TCTCCCTA AAG CT     CC
                                      _   _ _____
GAM3179  LOC221683 3'  AGAAGCTAGAGATCAGGG    72104      GATATTC
                                AGAGG      AGAGATCAGGG
                                |||||      ||||||||||
                                TCTTC      TCTCTAGTCCC
                                   GA_____
GAM3180  C20orf151 3'  GCGTCCAAGATTGTGCT     72107        TA    CCAC
                                GCGTTCAA  GTTG    GCT
                                ||||||||  ||||    |||
                                CGCAGGTT  TAAC    CGA
                                     C_    A___
GAM3180  FLJ20378  5'  AAGCCTTCAATGCTACCACAC  72108     G     A
                                AAGC TTCAAT GTTGCCACGC
                                |||| |||||| ||||||||||
                                TTCG AAGTTA CGATGGTGTG
                                   G     _
GAM3180  LOC147727 5'  AAGCATTCAAGAACACCACGCT 72109          TAGT
            T                    AAGCGTTCAA    TGCCACGCTT
                                ||||||||||    ||||||||||
                                TTCGTAAGTT    GTGGTGCGAA
                                     CTT_
GAM3180  LOC253512 5'  GCGTTCAATGAATAGTCGC    72110       ____
                                GCGTTCA    ATAGTTGC
                                |||||||    ||||||||
                                CGCAAGT    TATCAGCG
                                     TACT
GAM3181  DMD       3'  TTTGTGTGTGTGTGTGTAT    72113       _
                                TTTGT TGTGTGTGTGTAT
                                ||||| ||||||||||||
```

AAACA ACACACACACATA
C
GAM3181 DMD 3' TTTGTGTGTGTGTGTGTAT 72113 _
TTTGT TGTGTGTGTGTAT
||||| ||||||||||||
AAACA ACACACACACATA
C
GAM3181 DMD 3' TTTGTGTGTGTGTGTGTAT 72113 _
TTTGT TGTGTGTGTGTAT
||||| ||||||||||||
AAACA ACACACACACATA
C
GAM3181 DMD 3' TTTGTGTGTGTGTGTGTAT 72113 _
TTTGT TGTGTGTGTGTAT
||||| ||||||||||||
AAACA ACACACACACATA
C
GAM3181 DMD 3' TTTGTGTGTGTGTGTGTAT 72113 _
TTTGT TGTGTGTGTGTAT
||||| ||||||||||||
AAACA ACACACACACATA
C
GAM3181 DMD 3' TTTGTGTGTGTGTGTGTAT 72113 _
TTTGT TGTGTGTGTGTAT
||||| ||||||||||||
AAACA ACACACACACATA
C
GAM3181 DMD 3' TTTGTGTGTGTGTGTGTAT 72113 _
TTTGT TGTGTGTGTGTAT
||||| ||||||||||||
AAACA ACACACACACATA
C
GAM3181 DMD 3' TTTGTGTGTGTGTGTGTAT 72113 _
TTTGT TGTGTGTGTGTAT
||||| ||||||||||||
AAACA ACACACACACATA
C
GAM3181 DMD 3' TTTGTGTGTGTGTGTGTAT 72113 _
TTTGT TGTGTGTGTGTAT
||||| ||||||||||||
AAACA ACACACACACATA
C
GAM3181 DMD 3' TTTGTGTGTGTGTGTGTAT 72113 _
TTTGT TGTGTGTGTGTAT
||||| ||||||||||||
AAACA ACACACACACATA
C
GAM3181 DMD 3' TTTGTGTGTGTGTGTGTAT 72113 _
TTTGT TGTGTGTGTGTAT
||||| ||||||||||||
AAACA ACACACACACATA
C
GAM3181 DMD 3' TTTGTGTGTGTGTGTGTAT 72113 _
TTTGT TGTGTGTGTGTAT
||||| ||||||||||||

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                                AAACA ACACACACACATA
                                   C
GAM3181  DMD      3'  TTTGTGTGTGTGTGTGTAT   72113      _
                                TTTGT TGTGTGTGTGTAT
                                ||||| ||||||||||||
                                AAACA ACACACACACATA
                                   C
GAM3181  DMD      3'  TTTGTGTGTGTGTGTGTAT   72113      _
                                TTTGT TGTGTGTGTGTAT
                                ||||| ||||||||||||
                                AAACA ACACACACACATA
                                   C
GAM3181  PCDH11X  3'  TTTGTTCTGTGTGTGTTATTG 72114      G       ATA
                                TTTGTT TGTGTGTGT   TATTG
                                |||||| |||||||||  |||||
                                AAACAA ACACACACA   ATAAC
                                   G      ___
GAM3181  PCDH11X  3'  TTTGTTCTGTGTGTGTTATTG 72114      G       ATA
                                TTTGTT TGTGTGTGT   TATTG
                                |||||| |||||||||  |||||
                                AAACAA ACACACACA   ATAAC
                                   G      ___
GAM3181  PCDH11Y  3'  TTTGTTCTGTGTGTGTTATTG 72114      G       ATA
                                TTTGTT TGTGTGTGT   TATTG
                                |||||| |||||||||  |||||
                                AAACAA ACACACACA   ATAAC
                                   G      ___
GAM3181  CDW92    3'  TTTATGTGTGTGTGTATATATT 72115      T
            G                    TTTGT GTGTGTGTGTATATATTG
                                ||||| ||||||||||||||||||
                                AAATA CACACACACATATATAAC

                                   _
GAM3181  FLJ11598 3'  TTTGTGTGTGTGTGTAT    72116      T
                                TTTGT GTGTGTGTGTAT
                                ||||| ||||||||||||
                                AAACA CACACACACATA

                                   _
GAM3181  KIAA1061 3'  TCTGCAGTGTGTGTGTAT    72117      T
                                TTTGT GTGTGTGTGTAT
                                ||||| ||||||||||||
                                AGACG CACACACACATA
                                   T
GAM3181  KIAA1374 3'  TTTGTGTGTGTGTGTATA    72118      T
                                TTTGT GTGTGTGTGTATA
                                ||||| ||||||||||||
                                AAACA CACACACACATAT

                                   _
GAM3181  LOC153222 3'  TTTGTGTGTGTGTGTGTA    72119      _
                                TTTGT TGTGTGTGTGTA
                                ||||| ||||||||||||
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                                AAACA ACACACACACAT
                                   C
GAM3182  PPP4R1   3'  AAGGAAAATGCTCTGCCAAT  72122       _  AAG
                                AAGGAAA TGT  TCTGCCAAT
                                ||||||| |||  |||||||||
                                TTCCTTT ACG  AGACGGTTA
                                    T  ___
GAM3182  PRKY     3'  AAGAAAATACTGCCAA     72123        TAAGT
                                AAGGAAATG    CTGCCAA
                                |||||||||    |||||||
                                TTCTTTTAT    GACGGTT
                                     _____
GAM3182  SLC5A2   3'  TCATGGGAAGTGACTGCCAAT  72124    A_   A  TAAGT
                                TCA  GGAA TG    CTGCCAAT
                                |||  |||| ||    ||||||||
                                AGT  CCTT AC    GACGGTTA
                                  AC   C  T____
GAM3182  TTC3     5'  AGGGTAAGTCTGCCAA     72125    AAAT
                                AGG   GTAAGTCTGCCAA
                                |||   ||||||||||||
                                TCC   CATTCAGACGGTT
                                    ____
GAM3182  YWHAG    3'  TCAGGTTCTAAGTCTGTCA   72126    A  AAATG      C
                                TCA GG    TAAGTCTG CA
                                ||| ||    |||||||| ||
                                AGT CC    ATTCAGAC GT
                                  _ AAG__      A
GAM3182  A2BP1    5'  TCAAGGAAGCTGTAAGTTCCAC 72127       A_     _ TG
                                TCAAGGAA  TGTAAGT C  C
                                ||||||||  ||||||| |  |
                                AGTTCCTT  ACATTCA G  G
                                     CG      A GT
GAM3182  FLJ22693 3'  AGGAAATGTGGGTTTGCGCAAT 72128        AA  C  _
                                AGGAAATGT  GT TGC CAAT
                                |||||||||  || ||| ||||
                                TCCTTTACA  CA ACG GTTA
                                     CC  A   C
GAM3182  KIAA0461 3'  CAGGGAAGTGTAAGTCAAC   72129    A   A      T
                                CA GGAA TGTAAGTC GC
                                || |||| |||||||| ||
                                GT CCTT ACATTCAG TG
                                 C   C       T
GAM3182  KIAA0924 3'  TCAAGGAAAGTATCCT      72130         T   AG
                                TCAAGGAAA GTA  TCT
                                ||||||||| |||  |||
                                AGTTCCTTT CAT  GGA
                                     _  A_
GAM3182  KIAA0931 3'  AGGAAGCTGTCTGCCAA     72131      AT  AA
                                AGGAA  GT  GTCTGCCAA
                                |||||  ||  |||||||||
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                                TCCTT  CG  CAGACGGTT
                                  __  A_
GAM3182  KIAA1878  3'  CAGGGAAATGTACAGAGGCCA  72132    A       AGTCT
                                CA GGAAATGTA    GCCA
                                || |||||||||    ||||
                                GT CCTTTACAT    CGGT
                                 C       GTCTC
GAM3182  MGC26778  3'  TCATGGAAATGTGATGTGAGC  72133    A      AA_  CT
                                TCA GGAAATGT   GT  GC
                                ||| ||||||||   ||  ||
                                AGT CCTTTACA   CA  CG
                                  A       CTA  CT
GAM3182  NIP30     3'  CAGGGAAGTCGCCATCTGCCAA 72134    A   A_   AA
           T                     CA GGAA  TGT  GTCTGCCAAT
                                || ||||  |||  ||||||||||
                                GT CCTT  GCG  TAGACGGTTA
                                 C   CA   G_
GAM3182  PEAS      3'  TCAAGGAAGGGTGGGATTTATC 72135        AT  AA_____
           TGC                    TCAAGGAA  GT      GTCTGC
                                |||||||  ||      ||||||
                                AGTTCCTT  CA      TAGACG
                                    CC  CCCTAAA
GAM3182  POLR3K    3'  AAGGGAATGTCAACTGCCAAT  72136     A    AAGT
                                AAGG AATGT    CTGCCAAT
                                |||| |||||    ||||||||
                                TTCC TTACA    GACGGTTA
                                  C    GTT_
GAM3182  PSR       3'  TCAGGAAATGACAGTCTG    72137     A     TA
                                TCA GGAAATG  AGTCTG
                                ||| |||||||  ||||||
                                AGT CCTTTAC  TCAGAC
                                  _      TG
GAM3182  STARD7    3'  TCAAGGAAGTGTTTAAGT    72138        A  __
                                TCAAGGAA TGT  AAGT
                                |||||||| |||  ||||
                                AGTTCCTT ACA  TTCA
                                    C   AA
GAM3182  STARD7    3'  TCAAGGAAGTGTTTAAGT    72138        A  __
                                TCAAGGAA TGT  AAGT
                                |||||||| |||  ||||
                                AGTTCCTT ACA  TTCA
                                    C   AA
GAM3182  LOC148946 5'  TCCAGGAAGTGGCCTGCCAAT  72139    A    A  TAA
                                TC AGGAA TG   GTCTGCCAAT
                                || ||||| ||   ||||||||||
                                AG TCCTT AC   CGGACGGTTA
                                 G    C  ___
GAM3182  LOC151199 3'  AAGAAAATGTAGCCATGC    72140          A  _
                                AAGGAAATGTA GTC TGC
                                |||||||||| ||| |||
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                                TTCTTTTACAT CGG ACG
                                      _  T
GAM3182 LOC51267 3' TCTGGGAAGTGACTGCCAA  72141   AA   A TAAGT
                                TC  GGAA TG    CTGCCAA
                                ||  |||| ||    |||||||
                                AG  CCTT AC    GACGGTT
                                 AC   C  T____
GAM3183 ALX3    3' TGAGCCAAGTAAGCTG     72144       AATGA
                                TGAGCCA    GGTGAGTTG
                                |||||||    |||||||||
                                ACTCGGT    TCATTCGAC
                                      _____
GAM3183 B4GALT1  3' TGAGCCAAGGGGAGCTG    72145       AATG  T
                                TGAGCCA    AGG GAGTTG
                                |||||||    ||| ||||||
                                ACTCGGT    TCC CTCGAC
                                    ____  C
GAM3183 CASP7    3' TGATTGAATGGATAAATTGT  72146    GCCA   A
                                TGA    AATG GGTGAGTTGT
                                |||    |||| ||||||||||
                                ACT    TTAC CTATTTAACA
                                  AAC_   _
GAM3183 CASP7    3' TGATTGAATGGATAAATTGT  72146    GCCA   A
                                TGA    AATG GGTGAGTTGT
                                |||    |||| ||||||||||
                                ACT    TTAC CTATTTAACA
                                  AAC_   _
GAM3183 CASP7    3' TGATTGAATGGATAAATTGT  72146    GCCA   A
                                TGA    AATG GGTGAGTTGT
                                |||    |||| ||||||||||
                                ACT    TTAC CTATTTAACA
                                  AAC_   _
GAM3183 CASP7    3' TGATTGAATGGATAAATTGT  72146    GCCA   A
                                TGA    AATG GGTGAGTTGT
                                |||    |||| ||||||||||
                                ACT    TTAC CTATTTAACA
                                  AAC_   _
GAM3183 CERD4    3' TGGGCCAAATGGAGATATTGT 72147    A      _   GA
                                TG GCCAAATG AGGT  GTTGT
                                || |||||||| ||||  |||||
                                AC CGGTTTAC TCTA  TAACA
                                 C       C   __
GAM3183 CKTSF1B1 3' TGAGCCGGGGTGAGGTGGGTT 72148       AAA_     A
                                TGAGCC   TGAGGTG GTT
                                ||||||   ||||||| |||
                                ACTCGG   ACTCCAC CAA
                                   CCCC      C
GAM3183 CNGB3    3' TGAGCCAGATGAGTTA     72149       AATGA
                                TGAGCCA    GGTGAGTTG
                                |||||||    |||||||||
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                                ACTCGGT    CTACTCAAT
                                       _____
GAM3183 COL4A2   3' GAGTTGAACAATGTGAGTTGT 72150    CCA  TG G
                                GAG   AA  A GTGAGTTGT
                                |||   ||  | |||||||||
                                CTC   TT  T CACTCAACA
                                  AAC  GT A
GAM3183 EIF2C1   3' TGAGTCACATGAGACACCTGT 72151     C  A    GT AG
                                TGAG CA ATGAG  G  TTGT
                                |||| || |||||  |  ||||
                                ACTC GT TACTC  T  GACA
                                  A  G    TG G_
GAM3183 GORASP1  3' TGAGCCAAGTGTAGCATTGT  72152        A  A   GA
                                TGAGCCAA TG GGT  GTTGT
                                |||||||| || |||  |||||
                                ACTCGGTT AC TCG  TAACA
                                     C  A  __
GAM3183 HUS1     3' TGAGCCAAGGAGGTCAAT    72153        AT    G
                                TGAGCCAA  GAGGT AGT
                                ||||||||  ||||| |||
                                ACTCGGTT  CTCCA TTA
                                     C_    G
GAM3183 PACE4    5' TGGACCAAATGGGGTCG     72154    AG      A  TGA
                                TG  CCAAATG GG   GTTG
                                ||  ||||||| ||   ||||
                                AC  GGTTTAC CC   CAGC
                                 CT      _ ___
GAM3183 RFXAP    3' TGAGCTAGATGAGTCA      72155      CAAATG
                                TGAGC     AGGTGAGTTG
                                |||||     ||||||||||
                                ACTCG     TCTACTCAGT
                                  A_____
GAM3183 RPL10    3' TGAGCAGGGCTGAGTTG     72156      CAAATG  __
                                TGAGC     AGG  TGAGTTG
                                |||||     |||  |||||||
                                ACTCG     TCC  ACTCAAC
                                  _______  CG
GAM3183 SCA1     3' TGAGTCCACATGAGTTG     72157     _  AATGAG
                                TGAG CCA     GTGAGTTG
                                |||| |||     ||||||||
                                ACTC GGT     TACTCAAC
                                  A  G_____
GAM3183 SERPINB3 3' TGAGCCAAGAGAATCTGTTGT 72158        AT   TGA_
                                TGAGCCAA  GAGG   GTTGT
                                ||||||||  ||||   |||||
                                ACTCGGTT  CTCT   CAACA
                                     __   TAGA
GAM3183 SERPINB4 3' TGAGCCAAGAGAATCTGTTGT 72158        AT   TGA_
                                TGAGCCAA  GAGG   GTTGT
                                ||||||||  ||||   |||||
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                                ACTCGGTT  CTCT   CAACA
                                    __   TAGA
GAM3183  WFDC1    3'  TGAGCTGAATGTGAACTGT   72159      CAAA   _   GT
                                TGAGC   TGAG GTGA  TGT
                                |||||   |||| ||||  |||
                                ACTCG   ACTT CACT  ACA
                                   ____   A   TG
GAM3183  AQP10    3'  TGAGTGAAGTGAGGGTTGT   72160     CCAAA      __
                                TGAG   TGAGGTGA  GTTGT
                                ||||   ||||||||  |||||
                                ACTC   ACTTCACT  CAACA
                                  _____      CC
GAM3183  C22orf20 3'  TAAGCCAGGTTCAAGTTGT   72161       AATGA   __
                                TGAGCCA   GGT  GAGTTGT
                                |||||||   |||  |||||||
                                ATTCGGT   CCA  TTCAACA
                                   _____  AG
GAM3183  DKFZP564D0462 5'  GAGCCAAGTTCCGAGTTGT   72162       ATGAGG
                                GAGCCAA    TGAGTTGT
                                |||||||    ||||||||
                                CTCGGTT    GCTCAACA
                                    CAAG__
GAM3183  DKFZP586M1523 3'  TGAGTAAAGTGAGGCTG    72163     CCAAA       _
                                TGAG   TGAGGTGAG TTG
                                ||||   ||||||||| |||
                                ACTC   ATTTCACTC GAC
                                  _____      C
GAM3183  FLJ13096 5'  TGACCTGGAATGAGTTG    72164    G  AAA  AG
                                TGA CC  TG  GTGAGTTG
                                ||| ||  ||  ||||||||
                                ACT GG  AC  TACTCAAC
                                  _ ___ CT
GAM3183  FLJ21272 5'  TGAGTTGAGAGAGTTG     72165     CCAAA    T
                                TGAG   TGAGG GAGTTG
                                ||||   ||||| ||||||
                                ACTC   ACTCT CTCAAC
                                  A____   _
GAM3183  FLJ23047 3'  TGATCAAATGAATTTAGTTGT  72166    GC      GTG
                                TGA  CAAATGAG  AGTTGT
                                |||  ||||||||  ||||||
                                ACT  GTTTACTT  TCAACA
                                  A_      AAA
GAM3183  FLJ23420 3'  AGCCAAATGAGAACCATTGT  72167          TGA
                                AGCCAAATGAGG  GTTGT
                                ||||||||||||  |||||
                                TCGGTTTACTCT  TAACA
                                       TGG
GAM3183  FLJ32861 3'  AGCCAGAATGAGTTG      72168      AAT  G
                                AGCCA  GAG TGAGTTG
                                |||||  ||| |||||||
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                                TCGGT   CTT ACTCAAC
                                  ___   _
GAM3183 IGFALS    3'  TGAGCCAGGTGGGGGCCTGAGT 72169       AA  A ___
                                TGAGCCA  TG GG   TGAGT
                                |||||||  || ||   |||||
                                ACTCGGT  AC CC   ACTCA
                                    CC  C  CGG
GAM3183 KIAA0227  3'  TGAATGCTAGGTGAGTTGT    72170    A   __
                                C AATG  AGGTGAGTTGT
                                | ||||  ||||||||||
                                A TTAC  TCCACTCAACA
                                 C    GA
GAM3183 KIAA1155  3'  TGAGTCACATGGGGAAATGT   72171     C  A   A  T   T
                                TGAG CA ATG GG GAG TGT
                                |||| || ||| || ||| |||
                                ACTC GT TAC CC CTT ACA
                                  A  G   _  _   T
GAM3183 KIAA1437  5'  TGAGCCACAGTGGGGTGGCT   72172       AA_  A    A
                                TGAGCCA   TG GGTG GTT
                                |||||||   || |||| |||
                                ACTCGGT   AC CCAC CGA
                                    GTC  C    _
GAM3183 KIAA1715  3'  TGAGCCAAATAAATTTTTGT   72173          GTGAG
                                TGAGCCAAATGAG    TTGT
                                ||||||||||||     ||||
                                ACTCGGTTTATTT    AACA
                                      AAA__
GAM3183 KIAA1981  3'  TGGGCCGACGGACTGAGTTGT  72174    A   AA   A  _
                                TG GCC  ATG GG TGAGTTGT
                                || |||  ||| || ||||||||
                                AC CGG  TGC CT ACTCAACA
                                 C   C_   _  G
GAM3183 LASP1     3'  TGAATCAAGTGAGGCCAGGGTT 72175    GC   A     G __
          GT                      TGA  CAA TGAGGT A  GTTGT
                                |||  ||| ||||||  |  |||||
                                ACT  GTT ACTCCG T  CAACA
                                  TA   C     G CC
GAM3183 STARD7    3'  TGAGTCAATGGGTGATATTGT  72176     CCA    A    _
                                TGAG   AATG GGTGA GTTGT
                                ||||   |||| ||||| |||||
                                ACTC   TTAC CCACT TAACA
                                  AG_    _    A
GAM3183 STARD7    3'  TGAGTCAATGGGTGATATTGT  72176     CCA    A    _
                                TGAG   AATG GGTGA GTTGT
                                ||||   |||| ||||| |||||
                                ACTC   TTAC CCACT TAACA
                                  AG_    _    A
GAM3183 LOC127534 3'  TGAGCTGATGAGGTCAGCT   72177      CAA      G
                                TGAGC   ATGAGGT AGTT
                                |||||   ||||||| ||||
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                                ACTCG   TACTCCA TCGA
                                  AC_      G
GAM3183  LOC129676 5'  TGAGCCAGAGGGGATCTGT   72178       AAT   T  G
                                TGAGCCA   GAGG GA TTGT
                                |||||||   |||| || ||||
                                ACTCGGT   CTCC CT GACA
                                    ___    C  A
GAM3183  LOC144583 3'  TGAGCCAGGTGGGCTG      72179       AATGA   A
                                TGAGCCA    GGTG GTTG
                                |||||||    |||| ||||
                                ACTCGGT    CCAC CGAC
                                    _____   C
GAM3183  LOC155006 5'  TGAGCCGGTCCTGCGGAGTTGT 72180       AAATGAG  _
                                TGAGCC      GTG AGTTGT
                                ||||||      ||| ||||||
                                ACTCGG      CGC TCAACA
                                   CCAGGA_  C
GAM3183  LOC157381 3'  TGGGCTCAATGAGGCAGT    72181    A  CA      G
                                TG GC  AATGAGGT AGT
                                || ||  |||||||| |||
                                AC CG  TTACTCCG TCA
                                 C  AG       _
GAM3183  LOC165693 3'  TGGCTGAATGAGCTG       72182    A  CAAA   G
                                TG GC    TGAG TGAGTTG
                                || ||    |||| |||||||
                                AC CG    ACTT ACTCGAC
                                 _ ____   _
GAM3183  LOC169369 5'  TGAGCGAGTTGAGTTG      72183      CAAAT   G
                                TGAGC    GAG TGAGTTG
                                |||||    ||| |||||||
                                ACTCG    CTC ACTCAAC
                                  _____  A
GAM3183  LOC200093 3'  TGAGCTGGGTGAGCT       72184      CAAA  A
                                TGAGC    TG GGTGAGTT
                                |||||    || ||||||||
                                ACTCG    AC CCACTCGA
                                  ____ _
GAM3183  LOC200230 3'  TGAGCTGGGTGAAGTG      72185      CAAA  A     T
                                TGAGC    TG GGTGAG TG
                                |||||    || |||||| ||
                                ACTCG    AC CCACTT AC
                                  ____ _     C
GAM3183  LOC253128 5'  TGAGCCGGGCGAGGGAGAGT   72186       AAA    T   TT
                                TGAGCC   TGAGG GAG  GT
                                ||||||   ||||| |||  ||
                                ACTCGG   GCTCC CTC  CA
                                   CCC    _   T_
GAM3183  LOC90133  3'  AGCTGAGGTCACGAGTTGT   72187     CAAA     ___
                                AGC    TGAGGT   GAGTTGT
                                |||    ||||||   |||||||
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                                TCG   ACTCCA  CTCAACA
                                 _____    GTG
GAM3183 LOC91040 3' TGAGCTGGGTGAGCT     72184     CAAA  A
                                TGAGC   TG GGTGAGTT
                                |||||   || ||||||||
                                ACTCG   AC CCACTCGA
                                  _____ _
GAM3184 MSN     3' CAGTTGACATCCTGGA     72190       CT    T
                                CAGTTGAC  GTTTTG GA
                                ||||||||  |||||| ||
                                GTCAACTG  TAGGAC CT
                                    __    _
GAM3184 TCFL4   3' AACCAGCTGACCAGTGTGA  72191         TGTTT
                                AACCAGTTGACC    TGTGA
                                ||||||||||||    |||||
                                TTGGTCGACTGG    ACACT
                                      TC___
GAM3184 C1orf22  3' CACTTAGAGTGTTTTGTGAAG 72192   G  ACC
                                CA TTG   TGTTTTGTGAAG
                                || |||   ||||||||||||
                                GT AAT   ACAAAACACTTC
                                 G  CTC
GAM3184 FLJ20974 3' AGCTGGTTTACTGCTGTGAAG 72193     AC___   TT
                                AGTTG    CTGT  TGTGAAG
                                |||||    ||||  |||||||
                                TCGAC    GACG  ACACTTC
                                   CAAAT   __
GAM3184 KIAA0014 3' AACCAGTGCTTTTGTGAA    72194      TGACCTG
                                AACCAGT     TTTTGTGAA
                                |||||||     |||||||||
                                TTGGTCA     AAAACACTT
                                    CG_____
GAM3184 KIAA1898 3' ACCAGGTGGCCTGTCCCCTGA 72195     T  A     G
                                ACCAG TG CCTGTTTT TGA
                                ||||| || |||||||| |||
                                TGGTC AC GGACAGGG ACT
                                   C  C      G
GAM3184 PDE10A   3' CCAGCTGATTTCTGAACGTG  72196      C__  TTT
                                CCAGTTGA  CTG  TGTG
                                ||||||||  |||  ||||
                                GGTCGACT  GAC  GCAC
                                     AAA  TT_
GAM3184 PRO2389  3' CCAGTTGAATCCTCAACGTGAA 72197       __  GTTT
            G                    CCAGTTGA  CCT   TGTGAAG
                                ||||||||  |||   |||||||
                                GGTCAACT  GGA   GCACTTC
                                     TA  GTT_
GAM3184 PRO2964  5' AACCATTTGATCTGTTTTA   72198     G   C
                                AACCA TTGA CTGTTTTG
                                ||||| |||| ||||||||
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                                TTGGT AACT GACAAAAT
                                  A    A
GAM3184  SERHL     3'  CCAGCTGAGTTGTGAA      72199        CCTGTT
                                CCAGTTGA     TTGTGAA
                                ||||||||     |||||||
                                GGTCGACT     AACACTT
                                    C_____
GAM3184  LOC146512 3'  CCAGTTGATTTTTTCTAA    72200        CCTG   G
                                CCAGTTGA    TTTT TGA
                                ||||||||    |||| |||
                                GGTCAACT    AAAA ATT
                                    AA__    G
GAM3184  LOC148293 5'  CCACTTGAACCATTGTGAAG   72201     G   _  TGTT
                                CCA TTGA CC    TTGTGAAG
                                ||| |||| ||    ||||||||
                                GGT AACT GG    AACACTTC
                                  G    T  T___
GAM3184  LOC170217 5'  AACCAGTTGTTCTGGA      72202        TGACC      T
                                AACCAGT     TGTTTTG GA
                                |||||||     ||||||| ||
                                TTGGTCA     ACAAGAC CT
                                    _____      _
GAM3184  LOC170218 5'  AACCAGTTGTTCTGGA      72202        TGACC      T
                                AACCAGT     TGTTTTG GA
                                |||||||     ||||||| ||
                                TTGGTCA     ACAAGAC CT
                                    _____      _
GAM3184  LOC90049  3'  CCACTTGAACCATTGTGAAG   72201     G   _  TGTT
                                CCA TTGA CC    TTGTGAAG
                                ||| |||| ||    ||||||||
                                GGT AACT GG    AACACTTC
                                  G    T  T___
GAM3185  C18orf1   3'  GGTGGAAATCTTTTTC      72205        CCTC
                                GGTGGA   GTCTTTTTC
                                ||||||   |||||||||
                                CCACCT   TAGAAAAAG
                                   T___
GAM3185  MUCDHL    3'  ACGGTGGAGTTCACTTTC    72206        CC   T
                                ACGGTGGA  TCG CTTTT
                                ||||||||  ||| |||||
                                TGCCACCT  AGT GAAAG
                                    CA  _
GAM3185  MUCDHL    3'  ACGGTGGAGTTCACTTTC    72206        CC   T
                                ACGGTGGA  TCG CTTTT
                                ||||||||  ||| |||||
                                TGCCACCT  AGT GAAAG
                                    CA  _
GAM3185  ICK       3'  TGGACCTTTTGTCTTTTTC   72207        C__
                                TGGACCT   GTCTTTTTC
                                |||||||   |||||||||
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                                ACCTGGA  CAGAAAAAG
                                    AAA
GAM3185 KLF12    3' AACAGTGGATGTTTTTTT    72208        CCTC  C
                                AACGGTGGA   GT TTTTT
                                |||||||||   || |||||
                                TTGTCACCT   CA AAAAA
                                    A___  A
GAM3185 MGC15429 3' CGGTGGCCCTCCCTTTCT    72209      A   G
                                CGGTGG CCTC TCTTTTT
                                |||||| |||| |||||||
                                GCCACC GGAG GGAAAGA
                                   G   _
GAM3185 MGC4663  3' CGGTGGTCGCCTTTTCC     72210      ACC       T
                                CGGTGG   TCGTCTTTT CC
                                ||||||   ||||||||| ||
                                GCCACC   AGCGGAAAA GG
                                   ___       _
GAM3185 LOC120227 5' CGGTGGTCGCCTTTTCC    72210      ACC       T
                                CGGTGG   TCGTCTTTT CC
                                ||||||   ||||||||| ||
                                GCCACC   AGCGGAAAA GG
                                   ___       _
GAM3185 LOC130543 5' GGTAGCCTTGTCTTTTTC    72211      A   C
                                GGTGG CCT GTCTTTTTC
                                ||||| ||| |||||||||
                                CCATC GGA CAGAAAAAG
                                   _  A
GAM3185 LOC145622 3' AACAGTGGGTTTTTTCCA    72212        ACCTC  C
                                AACGGTGG    GT TTTTTCCG
                                ||||||||    || ||||||||
                                TTGTCACC    CA AAAAAGGT
                                    _____ _
GAM3185 LOC159193 5' ACGGTGAATTTCCGTTTCCG  72213        CCTCG   T
                                ACGGTGGA    TCT TTTCCG
                                ||||||||    ||| ||||||
                                TGCCACTT    AGG AAAGGC
                                     AA___   C
GAM3185 LOC219649 5' ACGCTGGAGGGTATCTTTTT  72214     G   CCTC
                                ACG TGGA   GTCTTTTT
                                ||| ||||   ||||||||
                                TGC ACCT   TAGAAAAA
                                  G   CCCA
GAM3185 LOC51604  3' GATGGAAATCTTTTTC      72215       CCTC
                                GGTGGA   GTCTTTTTC
                                ||||||   |||||||||
                                CTACCT   TAGAAAAAG
                                   T___
GAM3185 LOC89894  5' GGTAGGCCTTGTCATCTTC   72216      A   C   T
                                GGTGG CCT GTC TTTTC
                                ||||| ||| ||| |||||
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                                CCATC GGA CAG AGAAG
                                   C   A   T
GAM3186 COG7     3'  TCAGATAGTCGATGTCAGT   72219     A      GCC  C
                                TCA ATAGTCGA   TC GT
                                ||| ||||||||   || ||
                                AGT TATCAGCT   AG CA
                                  C       AC_  T
GAM3186 ZF       5'  TAGTCGAGCCAAGGCGCG    72220          TCC T
                                TAGTCGAGCC   G CGCG
                                ||||||||||   | ||||
                                ATCAGCTCGG   C GCGC
                                      TTC _
GAM3186 LOC90750 3'  TCAAACAGTTGAATGTCG    72221         C   CCTCC
                                TCAAATAGT GAG    GTCG
                                ||||||||| |||    ||||
                                AGTTTGTCA CTT    CAGC
                                     A   A____
GAM3187 ABR      3'  GGCAGCCGGCTTTGTACAAGG  72224        A  CC  _
                                GGCGGCCG CT  GT CGAGG
                                |||||||| ||  || |||||
                                CCGTCGGC GA  CA GTTCC
                                     C  AA  T
GAM3187 ABR      3'  GGCAGCCGGCTTTGTACAAGG  72224        A  CC  _
                                GGCGGCCG CT  GT CGAGG
                                |||||||| ||  || |||||
                                CCGTCGGC GA  CA GTTCC
                                     C  AA  T
GAM3187 ACHE     5'  AGGCGGCCGATGTTCCCCGGCG 72225          ____    T
                                AGGCGGCCGA   CTCCG CG
                                ||||||||||   ||||| ||
                                TCCGCCGGCT   GGGGC GC
                                      ACAA    C
GAM3187 ACHE     5'  AGGCGGCCGATGTTCCCCGGCG 72225          ____    T
                                AGGCGGCCGA   CTCCG CG
                                ||||||||||   ||||| ||
                                TCCGCCGGCT   GGGGC GC
                                      ACAA    C
GAM3187 ADAM17   3'  AGGCGGCCTGGAGTCTGGGGCG 72226       GACTCC  GA_
                                AGGCGGCC     GTC  GGCG
                                ||||||||     |||  ||||
                                TCCGCCGG     CAG  CCGC
                                     ACCT__  ACC
GAM3187 ADARB1   3'  AGGGGCTGACTCCATTAGCG  72227    C  C      CGA
                                AGG GGC GACTCCGT   GGCG
                                ||| ||| ||||||||   ||||
                                TCC CCG CTGAGGTA   TCGC
                                  _  A       A__
GAM3187 BTAF1    5'  AGCGGCCGGTGCGGCGTGGGGC 72228       ACTC  T  A__
            G                    GGCGGCCG   CG CG   GGCG
                                ||||||||   || ||   ||||
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                                TCGCCGGC   GC GC  CCGC
                                    CAC_ C  ACC
GAM3187 CYP26A1  5' AGGTGTGCTGAGCTCCGAGGCG 72229    CG_ C _   GTC
                                AGG  GC GA CTCC  GAGGCG
                                |||  || || ||||  ||||||
                                TCC  CG CT GAGG  CTCCGC
                                  ACA  A  C  ___
GAM3187 EMP3    3' GGCAGCCGAGCGAGGC     72230        CTCC T
                                GGCGGCCGA   G CGAGGC
                                |||||||||   | ||||||
                                CCGTCGGCT   C GCTCCG
                                     _____ _
GAM3187 EP300   5' GGCGGCCGGCGGAGGC     72231        ACTCC  C
                                GGCGGCCG    GT GAGGC
                                ||||||||    || |||||
                                CCGCCGGC    CG CTCCG
                                    ______ C
GAM3187 GLS     5' GGCGGCCGGTTTCCTCGGG   72232        AC_  G  A
                                GGCGGCCG  TCC TCG GG
                                ||||||||  ||| ||| ||
                                CCGCCGGC  AGG AGC CC
                                    CAA  _  _
GAM3187 GMDS    3' GGCGGGCCGGGCTCCGAGGCG 72233      _  A_   GTC
                                GGCGG CCG  CTCC  GAGGCG
                                ||||| |||  ||||  ||||||
                                CCGCC GGC  GAGG  CTCCGC
                                  C  CC  ___
GAM3187 GNA11   5' GGCGGCCGAGGCGGGGCG   72234        CTCC T  A
                                GGCGGCCGA   G CG GGCG
                                |||||||||   | || ||||
                                CCGCCGGCT   C GC CCGC
                                     C___ _ C
GAM3187 LMO1    5' GGCGCCGACTCGGGGC     72235     G     CGTC A
                                GGCG CCGACTC   G GGC
                                |||| |||||||   | |||
                                CCGC GGCTGAG   C CCG
                                  _     ____ C
GAM3187 RBM3    5' AGGCGGCCAGGCTCTGTC   72236        A_  C
                                AGGCGGCCG  CTC GTC
                                |||||||||  ||| |||
                                TCCGCCGGT  GAG CAG
                                     CC  A
GAM3187 RFNG    3' AGGCAGCCCTGGGTCGGGG  72237       GA  CC   A
                                AGGCGGCC  CT  GTCG GG
                                ||||||||  ||  |||| ||
                                TCCGTCGG  GA  CAGC CC
                                    __ CC   C
GAM3187 RNF6    5' GGCGGCCGTTCTCTCGGG   72238        A_  CG  A
                                GGCGGCCG  CTC  TCG GG
                                ||||||||  |||  ||| ||
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                                CCGCCGGC  GAG  AGC CC
                                    AA  __  _
GAM3187 TSG     5' GGTCGGCCGAGCCCGGGGCG  72239   _     CT  TCGA
                                GG CGGCCGA  CCG   GGCG
                                || |||||||  |||   ||||
                                CC GCCGGCT  GGC   CCGC
                                 A      CG  C___
GAM3187 C9orf7   3' GGCAGCCGAGGGGCCTTGAGG 72240        CT__ GTC
                                GGCGGCCGA   CC  GAGG
                                |||||||||   ||  ||||
                                CCGTCGGCT   GG  CTCC
                                     CCCC  AA_
GAM3187 CENTG2   5' GGCCGCCGAGCCCGGGGCG   72241    G   CT  TCGA
                                GGC GCCGA  CCG   GGCG
                                ||| |||||  |||   ||||
                                CCG CGGCT  GGC   CCGC
                                  G    CG  C___
GAM3187 DKFZp434N074 5'  GGCGGCCAGTGTGAGCTCGAGG 72242        ACTCCG__
            CG                   GGCGGCCG      TCGAGGCG
                                |||||||       ||||||||
                                CCGCCGGT      AGCTCCGC
                                    CACACTCG
GAM3187 DLGAP1   3' GGCGGCCGGGCTGCGGGGCG  72243       A_  CC T  A
                                GGCGGCCG  CT  G CG GGCG
                                ||||||||  ||  | || ||||
                                CCGCCGGC  GA  C GC CCGC
                                    CC  __ _  C
GAM3187 DLGAP1   3' GGCGGCCGGGCTGCGGGGCG  72243       A_  CC T  A
                                GGCGGCCG  CT  G CG GGCG
                                ||||||||  ||  | || ||||
                                CCGCCGGC  GA  C GC CCGC
                                    CC  __ _  C
GAM3187 FLJ10904 5' GGCGGCCGACGGCGGGGGCG  72244        TC  TCGA
                                GGCGGCCGAC  CG   GGCG
                                ||||||||||  ||   ||||
                                CCGCCGGCTG  GC   CCGC
                                     CC  CC__
GAM3187 FLJ21870 5' AGCGGCCGGCTCCCGACGGCG 72245       A   GT  _
                                GGCGGCCG CTCC  CGA GGCG
                                |||||||| ||||  ||| ||||
                                TCGCCGGC GAGG  GCT CCGC
                                    C   __  G
GAM3187 KIAA0010 5' GGCGGGCGGGGCACGGGGCG  72246     C  ACTC  T  A
                                GGCGG CG   CG CG GGCG
                                ||||| ||   || || ||||
                                CCGCC GC   GT GC CCGC
                                  C  CCC_  _  C
GAM3187 KIAA0668 5' AGCGGCCGGGCCCGGGGC   72247       AC   TCGA
                                GGCGGCCG  TCCG   GGC
                                ||||||||  ||||   |||
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                                TCGCCGGC  GGGC   CCG
                                    CC   C___
GAM3187  KIAA0893  5'  AAGCGGCCGGCTCCGGGC    72248        A    TCGA
                                AGGCGGCCG CTCCG   GGC
                                ||||||||| |||||   |||
                                TTCGCCGGC GAGGC   CCG
                                    C   ____
GAM3187  KIAA1118  5'  AAGCGGCCGGACGGCCGGGG   72249        _ TCC   A
                                AGGCGGCCG AC   GTCG GG
                                ||||||||| ||   |||| ||
                                TTCGCCGGC TG   CGGC CC
                                    C  C__   C
GAM3187  KIAA1161  5'  AGGCGGCCACTTCCAGCCAGCG 72250         AC  _  GA
                                AGGCGGCCG  TCC GTC  GGCG
                                |||||||||  ||| |||  ||||
                                TCCGCCGGT  AGG CGG  TCGC
                                    GA   T  __
GAM3187  KIAA1402  5'  AGGCGCCGGCTCCGCCG     72251      G   A
                                AGGCG CCG CTCCGTCG
                                ||||| ||| ||||||||
                                TCCGC GGC GAGGCGGC
                                  _  C
GAM3187  MSI2     5'  GGCGGCCGGCTCCGAGC     72252        A    TCGA
                                GGCGGCCG CTCCG   GGC
                                |||||||| |||||   |||
                                CCGCCGGC GAGGC   TCG
                                    C   ____
GAM3187  PARD6A   5'  AGGCGGCCCGCCGAGGC     72253        GACTC
                                AGGCGGCC    CGTCGAGGC
                                ||||||||    |||||||||
                                TCCGCCGG    GCGGCTCCG
                                    _____
GAM3187  RAB14    5'  GGCGGTCGACCGAGGC      72254      C   TCCGT
                                GGCGG CGAC    CGAGGC
                                ||||| ||||    ||||||
                                CCGCC GCTG    GCTCCG
                                  A   _____
GAM3187  RAB5EP   5'  AGGCGGCCGGCCTCGGGGAGCG 72255         A TC  TC   G
                                AGGCGGCCG C  CG  GAG CG
                                ||||||||| |  ||  ||| ||
                                TCCGCCGGC G  GC  CTC GC
                                    C GA  CC  _
GAM3187  LOC124842 3'  AGGCGGCCCGCTCCGCACG   72256        GA    _
                                AGGCGGCC  CTCCGT CG
                                ||||||||  |||||| ||
                                TCCGCCGG  GAGGCG GC
                                    GC     T
GAM3187  LOC157651 3'  GGCGGCCGGGCAGAGGC     72257        ACTCC  C
                                GGCGGCCG    GT GAGGC
                                ||||||||    || |||||
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                                CCGCCGGC    CG CTCCG
                                    C____  T
GAM3187  LOC157651 3'  GGCGGCCGGGCAGAGGC    72257       ACTCC  C
                                GGCGGCCG    GT GAGGC
                                ||||||||    || |||||
                                CCGCCGGC    CG CTCCG
                                    C____  T
GAM3187  LOC158293 5'  GGCGGCCGACCGGCCTGAGGCG 72258         T C  _
                                GGCGGCCGAC C GTC GAGGCG
                                |||||||||| | ||| ||||||
                                CCGCCGGCTG G CGG CTCCGC
                                     _ C   A
GAM3187  LOC199745 5'  AGCCGGCCAACCGTTGGGGCG  72259    G     CT    CGA
                                AG CGGCCGA  CCGT   GGCG
                                || |||||||  ||||   ||||
                                TC GCCGGTT  GGCA   CCGC
                                 G      __    ACC
GAM3187  LOC201522 3'  GGTGGCCGACTCGTAGCGCCTC 72260    C       ________  CGAG
             A                   GG GGCCGACTC      CGT    G
                                || |||||||||      |||    |
                                CC CCGGCTGAG      GCG    T
                                 A       CATCIII   GAGC
GAM3187  LOC90233  5'  GGCGGCCGACCGGGGC      72261         TCCGT  A
                                GGCGGCCGAC    CG GGC
                                ||||||||||    || |||
                                CCGCCGGCTG    GC CCG
                                      _____  C
GAM3187  LOC92228  5'  AGGCGGCCGACCTTCGGC    72262          CCGTCGA
                                AGGCGGCCGACT      GGC
                                ||||||||||||      |||
                                TCCGCCGGCTGG      CCG
                                      AAG____
GAM3188  CALD1    3'  TTAGTGTGTTTGTATATG    72265       AAAATAAA
                                TTAGTGT       TGTATATG
                                |||||||       ||||||||
                                AATCACA       ACATATAC
                                    CAA_____
GAM3188  CALD1    3'  TTAGTGTGTTTGTATATG    72265       AAAATAAA
                                TTAGTGT       TGTATATG
                                |||||||       ||||||||
                                AATCACA       ACATATAC
                                    CAA_____
GAM3188  EGR3     3'  GTGTATGTTATGTATATGT   72266      AAATAA
                                GTGTA     ATGTATATGT
                                |||||     ||||||||||
                                CACAT     TACATATACA
                                   ACAA__
GAM3188  ERBB3    3'  GTGTAAAATGAGATAATATGT  72267         AAATGT
                                GTGTAAAAT     ATATGT
                                |||||||||     ||||||
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                                CACATTTTA     TATACA
                                     CTCTAT
GAM3188 CLIC4    3' TTAGTGTAAGAATAAATGT   72268         _
                                TTAGTGTAA AATAAATGT
                                ||||||||| |||||||||
                                AATCACATT TTATTTACA
                                     C
GAM3188 EIF5     3' TTAGTGTAAAGTGTAGCATGAT 72269          ATAAAT   _
             GT                   TTAGTGTAAA     GTAT ATGT
                                ||||||||||     |||| ||||
                                AATCACATTT     CGTA TACA
                                     CACAT_    C
GAM3188 OR2C3    5' ATGATCAAATAAATGTGTATGT 72270     TA_        A
                                GTG   AAATAAATGT TATGT
                                |||   |||||||||| |||||
                                TAC   TTTATTTACA ATACA
                                  TAG         C
GAM3188 PRO2955  3' TTAGTGTAATGTGGGCATATAT 72271         AATAA__
             ATAT                  TTAGTGTAA      ATGTATATGT
                                |||||||||      ||||||||||
                                AATCACATT      TATATATATA
                                     ACACCCG
GAM3188 LOC196411 3' TTACTGTAGAATATATATATAT 72272     G    A    A
             GT                    TTA TGTA AATA ATGTATATGT
                                ||| |||| |||| ||||||||||
                                AAT ACAT TTAT TATATATACA
                                  G    C    A
GAM3188 LOC199957 3' TTAATGTATGTTATGTATATGT 72273        AAATAA
                                TTAGTGTA     ATGTATATGT
                                ||||||||     ||||||||||
                                AATTACAT     TACATATACA
                                     ACAA__
GAM3189 TCEA1    3' ACTCAAGTTGCTTTAAAAATTT 72276    GG   C    C
                                GC  GGG TGCT TAAAAATTT
                                ||  ||| |||| |||||||||
                                TG  TTC ACGA ATTTTTAAA
                                 AG   A    A
GAM3189 DKFZP727G051 3' GCAGGCTCTTTAAAAATTT   72277    GG    G  C
                                GC  GGGCT CT TAAAAATTT
                                ||  ||||| || |||||||||
                                CG  TCCGA GA ATTTTTAAA
                                 __     _ A
GAM3189 EIF4G3   3' GCCTTAAAGTTGCTCTAAAGAT 72278    G__   C       A
             TT                    GC   GGGG TGCTCTAAA ATTT
                                ||   |||| ||||||||| ||||
                                CG   TTTC ACGAGATTT TAAA
                                 GAA    A       C
GAM3189 GNB4     3' AAGAACTGCTTTAGGAATT   72279          C  AA
                                GGGGGCTGCT TA  AATT
                                |||||||||| ||  ||||
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                                TTCTTGACGA AT  TTAA
                                      A  CC
GAM3189  LOC203084 3'  ACCCAAGTTGCTTTAAAAATTT 72280    G   GGC   C
                                AC CGGG   TGCT TAAAAATTT
                                || ||||   |||| |||||||||
                                TG GTTC   ACGA ATTTTTAAA
                                 G   A__   A
GAM3190  GFRA2    3'  AGGGCCCACGGTGCTGCAGAC  72283       T    CCA_
                                AGGGCCC ACGGT   CAGAC
                                ||||||| |||||   |||||
                                TCCCGGG TGCCA   GTCTG
                                    _   CGAC
GAM3190  HMMR     3'  TTAAAGGCCAATCCACAGA   72284        CTAC
                                TTAAGGGCC   GGTCCACAGA
                                |||||||||   ||||||||||
                                AATTTCCGG   TTAGGTGTCT
                                     ____
GAM3190  HMMR     3'  TTAAAGGCCAATCCACAGA   72284        CTAC
                                TTAAGGGCC   GGTCCACAGA
                                |||||||||   ||||||||||
                                AATTTCCGG   TTAGGTGTCT
                                     ____
GAM3190  LPIN2    3'  TTAAGGGCTCGTGGAGTTGTCA 72285       CCTAC_  C__
            CAGA                TTAAGGGC    GGT  CACAGA
                                ||||||||    |||  ||||||
                                AATTCCCG    TCA  GTGTCT
                                    AGCACC  ACA
GAM3190  ZNF289   3'  AAGGGCTCAGTCCACAG    72286      CCTA
                                AAGGGC   CGGTCCACAG
                                ||||||   ||||||||||
                                TTCCCG   GTCAGGTGTC
                                   A___
GAM3190  KIAA0495 5'  AAGGGTCTCCACCACAGAC   72287     CC  ACGGT
                                AAGGG  CT   CCACAGAC
                                |||||  ||   ||||||||
                                TTCCC  GA   GGTGTCTG
                                   A_  GGT__
GAM3190  KIAA1750 3'  GGGCCTCGGTCCACAG     72288     CTA
                                GGGCC   CGGTCCACAG
                                |||||   ||||||||||
                                CCCGG   GCCAGGTGTC
                                   A__
GAM3190  KIAA1821 3'  AGGGCCCCATCTCATGGAC   72289       ACG  _  CA
                                AGGGCCCT   GTC CA  GAC
                                ||||||||   ||| ||  |||
                                TCCCGGGG   TAG GT  CTG
                                    ___   A  AC
GAM3190  NR6A1    3'  TTAAAGACGGTCCACAG     72290     GCCCT
                                TTAAGG    ACGGTCCACAG
                                ||||||    ||||||||||
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                                AATTTC    TGCCAGGTGTC
                                      _____
GAM3190 NR6A1    3' TTAAAGACGGTCCACAG     72290       GCCCT
                                TTAAGG    ACGGTCCACAG
                                ||||||    ||||||||||
                                AATTTC    TGCCAGGTGTC
                                      _____
GAM3190 NR6A1    3' TTAAAGACGGTCCACAG     72290       GCCCT
                                TTAAGG    ACGGTCCACAG
                                ||||||    ||||||||||
                                AATTTC    TGCCAGGTGTC
                                      _____
GAM3190 LOC145693 5' GGGGACTTCGGTCCACAG    72291     CC  A
                                GGG  CT CGGTCCACAG
                                |||  || ||||||||||
                                CCC  GA GCCAGGTGTC
                                  CT  A
GAM3190 LOC160379 5' TTAAAGGCTTTAAATCCATGGA 72292         CCTAC     CA
                                TTAAGGGC    GGTCCA  GA
                                ||||||||    ||||||  ||
                                AATTTCCG    TTAGGT  CT
                                     AAAT_     AC
GAM3190 LOC201283 3' TTAAAGGCTTCCTTCCAC    72293         __  ACGG
                                TTAAGGGC  CCT    TCCAC
                                ||||||||  |||   |||||
                                AATTTCCG  GGA   AGGTG
                                     AA  _____
GAM3191 AVP      5' GCGAGACGCGGCCGCCACC   72296    GA  CGAT  A
                                GCG  AC   CG CCGCCACC
                                |||  ||   || ||||||||
                                CGC  TG   GC GGCGGTGG
                                  TC  C___  C
GAM3191 CORO1C   5' GCGAAGCCTCCAACCGCTGCC  72297      A  GA      CA
                                GCGGA CC  TCGACCGC  CC
                                |||||  ||  ||||||||  ||
                                CGCTT GG  GGTTGGCG  GG
                                   C  A_       AC
GAM3191 HLCS     5' AAGCAGAACCGCGCTGTCAC   72298          ATCGAC  ___
                                AAGCGGAACCG     CGC   CAC
                                ||||||||||     |||   |||
                                TTCGTCTTGGC     GCG   GTG
                                      _______  ACA
GAM3191 HRB      5' AGCCGGGACAACCGCCGCC    72299     _  AAC     A
                                AGC GG   CGATCG CCGCC
                                |||  ||   ||||||  |||||
                                TCG CC   GTTGGC GGCGG
                                  G  CT_     _
GAM3191 PRKRA    5' GGAGCTCCAGCGCCGCCACC   72300     A__   AT  A
                                GGA   CCG  CG CCGCCACC
                                |||   |||  || ||||||||
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                                CCT  GGT  GC GGCGGTGG
                                  CGA  C_  _
GAM3191 ZNF184   5' AAGCGCATTGACCGCCAC   72301     GAAC  ATC
                                AAGCG   CG   GACCGCCAC
                                |||||   ||   |||||||||
                                TTCGC   GT   CTGGCGGTG
                                  _____  AA_
GAM3191 CDCA4    5' GCGGGGCGAGCGACCGCCAC  72302     AAC   T
                                GCGG   CGA CGACCGCCAC
                                ||||   ||| ||||||||||
                                CGCC   GCT GCTGGCGGTG
                                  CC_   C
GAM3191 FLJ10563 5' AAGGGGAGCCTCCGCCAC   72303    C   A  GATCGA
                                AAG GGA CC     CCGCCAC
                                ||| ||| ||     |||||||
                                TTC CCT GG     GGCGGTG
                                  C   C  A_____
GAM3191 FLJ10996 5' AAGCGGAAACTCCCTCTGCCGC 72304        ___  GA  GA
              C                  AAGCGGAA   CC  TC  CCGCC
                                 ||||||||   ||  ||  |||||
                                 TTCGCCTT   GG  AG  GGCGG
                                     TGA  G_  AC
GAM3191 FLJ10997 3' AAGCGAAACTGAACATGC    72305        C  T  ACC
                                AAGCGGAAC GA CG   GC
                                ||||||||| || ||   ||
                                TTCGCTTTG CT GT   CG
                                     A  T  A__
GAM3191 FLJ22637 5' GCGAGGGCCACCACCGCCACC  72306    _ AA  G   G
                                GCG G  CC ATC ACCGCCACC
                                ||| |  || ||| |||||||||
                                CGC C  GG TGG TGGCGGTGG
                                  T CC  _   _
GAM3191 KCNT1    5' AAGCGAGTGGGAGCCGCCACC  72307      AACC  TCGA
                                AAGCGG   GA   CCGCCACC
                                ||||||   ||   ||||||||
                                TTCGCT   CT   GGCGGTGG
                                   CACC  C___
GAM3191 KIAA0252 5' AGTGGGACCGCCACTGCCGCC  72308   C  A   A   A__
                                AG GG ACCG TCG   CCGCC
                                || || |||| |||   |||||
                                TC CC TGGC GGT   GGCGG
                                 A  C    _   GAC
GAM3191 KIAA0415 3' AACGGAACTGATCGCGCAC   72309       C    AC   C
                                AGCGGAAC GATCG  CGC AC
                                |||||||| |||||  ||| ||
                                TTGCCTTG CTAGC  GCG TG
                                     A    __   _
GAM3191 MGC19570 3' AAGTAGAACCAATGCTGCCACC 72310    CG      CGACC
                                AAG  GAACCGAT    GCCACC
                                |||  ||||||||    ||||||
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                                TTC  CTTGGTTA    CGGTGG
                                  AT       CGA__
GAM3191  LOC116412 5'  GCGGAGCCGTCCTCCCGCCACC 72311      A   A  GA
                                GCGGA CCG TC  CCGCCACC
                                ||||| ||| ||  ||||||||
                                CGCCT GGC GG  GGCGGTGG
                                   C   A  AG
GAM3191  LOC132740 3'  GGAGACCGCGGCCGCCACC    72312     _   AT  A
                                GGA ACCG  CG CCGCCACC
                                ||| ||||  || ||||||||
                                CCT TGGC  GC GGCGGTGG
                                  C    __  C
GAM3191  LOC148872 3'  GCGGCAGGAGGGACCGCCAC   72313      AACC  TC
                                GCGG    GA  GACCGCCAC
                                ||||    ||  |||||||||
                                CGCC    CT  CTGGCGGTG
                                   GTC_  CC
GAM3191  LOC150984 5'  AGCGGGGCCGCCGCCAC     72314      AA   ATCGA
                                AGCGG  CCG    CCGCCAC
                                |||||  |||    |||||||
                                TCGCC  GGC    GGCGGTG
                                   CC   ______
GAM3191  LOC163412 5'  AGTGGCTGCCTCGGCCGCCACC 72315    C  AA_  GA   A
                                AG GG   CC  TCG CCGCCACC
                                || ||   ||  ||| ||||||||
                                TC CC   GG  AGC GGCGGTGG
                                 A  GAC  __   C
GAM3191  LOC201305 3'  AAGAGGAACCGAGGCACTGC   72316     C       TCG  C
                                AAG GGAACCGA   AC GC
                                ||| ||||||||   || ||
                                TTC CCTTGGCT   TG CG
                                  T       CCG  A
GAM3191  LOC255397 5'  GCTGGGCACGATGCCGCCACC  72317    _ AAC    CGA
                                GC GG   CGAT   CCGCCACC
                                || ||   ||||   ||||||||
                                CG CC   GCTA   GGCGGTGG
                                 A  CGT    C__
GAM3191  LOC256598 5'  GGAGACCGCGGCCGCCACC    72312     _   AT  A
                                GGA ACCG  CG CCGCCACC
                                ||| ||||  || ||||||||
                                CCT TGGC  GC GGCGGTGG
                                  C    __  C
GAM3191  LOC96597  5'  AGCAGAACCAGACATCGC     72318         ATC  __
                                AGCGGAACCG   GAC  CGC
                                ||||||||||   |||  |||
                                TCGTCTTGGT   CTG  GCG
                                       ___   TA
GAM3192  CDK2      3'  GCAGCAGGAGGCTTGGG     72321     A    TTG
                                GCA TAGGA   GGCTTGGG
                                ||| |||||   ||||||||
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                                CGT GTCCT   CCGAACCC
                                  C    ___
GAM3192 CEACAM7  3' TCACGATGAGGCTTGG     72322     AATAG   T
                                TCGC    GAT GGGCTTGG
                                ||||    ||| ||||||||
                                AGTG    CTA TCCGAACC
                                  _____  C
GAM3192 MRPS18A  3' CATCGTGGTGGGGTGGG    72323     CAATA  AT   CT
                                CATCG    GG  TGGG  TGGG
                                |||||    ||  ||||  ||||
                                GTAGC    CC  ACCC  ACCC
                                  A____ __   C_
GAM3193 DDX11    3' CTCAAGTGGTTGAGA      72326         ATATGT
                                TTCAAGTGGT     TGAGA
                                ||||||||||     |||||
                                GAGTTCACCA     ACTCT
                                       _______
GAM3193 DDX11    3' CTCAAGTGGTTGAGA      72326         ATATGT
                                TTCAAGTGGT     TGAGA
                                ||||||||||     |||||
                                GAGTTCACCA     ACTCT
                                       _______
GAM3193 FCMD     3' TTCAAGTGATATAAGAGAGA  72327           TGTT
                                TTCAAGTGGTATA    GAGA
                                ||||||||||||    ||||
                                AAGTTCACTATAT    CTCT
                                       TCT_
GAM3193 LY9      3' TTCAGCAGTGTTGAGAA     72328     A TG  ATAT
                                TTCA G  GT    GTTGAGAA
                                |||| |  ||    ||||||||
                                AAGT C  CA    CAACTCTT
                                  _ GT  _____
GAM3193 MASP1    3' ATGAGCCGGTTGAGAAAG    72329     _  ATAT
                                GTG GT    GTTGAGAAAG
                                ||| ||    ||||||||||
                                TAC CG    CAACTCTTTC
                                  T  GC__
GAM3193 PRKAG1   3' TTCAAGTGTATGTGTGAG    72330       GTA    _
                                TTCAAGTG   TATGT TGAG
                                ||||||||   ||||| ||||
                                AAGTTCAC   ATACA ACTC
                                     ___     C
GAM3193 SYBL1    3' TTCAGGTGTGTATAAGAAA   72331     A  _    TGTTG
                                TTCA GTG GTATA    AGAAA
                                |||| ||| |||||    |||||
                                AAGT CAC CATAT    TCTTT
                                  C   A    ______
GAM3193 DDX12    3' CTCAAGTGGTTGAGA      72326         ATATGT
                                TTCAAGTGGT     TGAGA
                                ||||||||||     |||||
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                                GAGTTCACCA     ACTCT
                                          _______
GAM3193  FLJ10142  3'  TTCAGGTGGTACAGGGAG    72332      A       TGTT
                                TTCA GTGGTATA    GAG
                                |||| ||||||||    |||
                                AAGT CACCATGT    CTC
                                  C       CC__
GAM3193  FLJ11088  3'  AAGTGATATATCAGATCAAA   72333          ___  TG
                                AAGTGGTATAT   GT  AG
                                ||||||||||   ||  ||
                                TTCACTATATA   TA  TT
                                      GTC  GT
GAM3193  FLJ21791  3'  TTCATAGTTATGTTGAG     72334      AG    A
                                TTCA  TGGT TATGTTGAG
                                ||||  |||| |||||||||
                                AAGT  ATCA ATACAACTC
                                  __   _
GAM3193  KIAA1045  3'  CTCAAGTGTTCTGTTGGGGAA  72335        GTATA    A_
                                TTCAAGTG    TGTTG  GAA
                                ||||||||    |||||  |||
                                GAGTTCAC    ACAAC  CTT
                                     AAG__    CC
GAM3193  MGC20496  3'  TTCAAGTGGTAGTGTTG     72336          TA
                                TTCAAGTGGTA  TGTTG
                                ||||||||||  |||||
                                AAGTTCACCAT  ACAAC
                                      C_
GAM3193  LOC144373 3'  CTCAAGTGGTTGAGA       72326         ATATGT
                                TTCAAGTGGT     TGAGA
                                ||||||||||     |||||
                                GAGTTCACCA     ACTCT
                                          _______
GAM3193  LOC201229 5'  TTCAAGTGGTGCATGAGTAG   72337          A    TTG
                                TTCAAGTGGT TATG   AG
                                |||||||||| ||||   ||
                                AAGTTCACCA GTAC   TC
                                      C    TCA
GAM3193  LOC257464 5'  TTCAAGTGTATTGCAGGGAGA  72338        G   A   T__
                                TTCAAGTG TAT TGT   GAGA
                                |||||||| ||| |||   ||||
                                AAGTTCAC ATA ACG   CTCT
                                     _   _   TCC
GAM3194  AP2B1     3'  GACACACTTTTCCTTCT     72341     A       CTCAA
                                GA CACACTTTT    CCTTCT
                                || |||||||||    ||||||
                                CT GTGTGAAAA    GGAAGA
                                  _      ______
GAM3194  CRIM1     3'  GAACACCTTTTTCTTTTTCT   72342       AC     CAACC
                                GAACAC  TTTTCT    TTCT
                                ||||||  ||||||    ||||
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                                CTTGTG  AAAAGA    AAGA
                                   GA     AA___
GAM3194  SNK     3'  GAATGCACTTTTCCAGCC    72343    CA      T  A
                                GAA  CACTTTTC CA CC
                                |||  |||||||| || ||
                                CTT  GTGAAAAG GT GG
                                  AC       _  C
GAM3194  TNFSF4   3'  AAACACACACACAATCTTCTG  72344        TTTTCT   C
                                GAACACAC     CAA CTTCTG
                                ||||||||     ||| |||||||
                                TTTGTGTG     GTT GAAGAC
                                     TGT___   A
GAM3194  USP11    5'  ACACTTCGACCTTCTG      72345        TCTCA
                                ACACTTT     ACCTTCTG
                                |||||||     ||||||||
                                TGTGAAG     TGGAAGAC
                                    C_____
GAM3194  CEP3     3'  GAATACACTTTTCCAAAC    72346    C        C
                                GAA ACACTTTTCT AAC
                                ||| ||||||||||| |||
                                CTT TGTGAAAAGG TTG
                                  A         T
GAM3194  CLDN8    3'  CACACTTTTATCTTTCTTCTG  72347          C  AAC
                                CACACTTTT TC   CTTCTG
                                |||||||||  ||   ||||||
                                GTGTGAAAA AG   GAAGAC
                                      T  AAA
GAM3194  FLJ13593 3'  ACCACTTTTCTTAGCAAC    72348    A        ___
                                AC CACTTTTCT   CAAC
                                || |||||||||   ||||
                                TG GTGAAAAGA   GTTG
                                  _        ATC
GAM3194  H-plk    5'  GAACTTGTTTTTCTCATCCCT  72349      ACAC       A
                                GAAC    TTTTCTCA CCTT
                                ||||    |||||||| ||||
                                CTTG    AAAAGAGT GGGA
                                   AACA       A
GAM3194  KIAA0237  3'  GAAACACTGCTGGACAACCTTC 72350     C    TTTCT_
            TG                    GAA ACACT     CAACCTTCTG
                                ||| |||||     ||||||||||
                                CTT TGTGA     GTTGGAAGAC
                                  _     CGACCT
GAM3194  KIAA0319  3'  GACACACTTTTTAGTTCT    72351    A       CTCAACC
                                GA CACACTTTT      TTCT
                                || |||||||||      ||||
                                CT GTGTGAAAA      AAGA
                                  _        ATC_____
GAM3194  KIAA1254  3'  ACTTTTCTCAAGCTCTG     72352          C  T
                                ACTTTTCTCAA CT CTG
                                |||||||||| || |||
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                                TGAAAAGAGTT GA GAC
                                      C  _
GAM3194  KIAA1879  5'  CACATGCTCTCTGACCTTCTG  72353     CTT    A_
                                CACA   TTCTC  ACCTTCTG
                                ||||   |||||  ||||||||
                                GTGT   GAGAG  TGGAAGAC
                                  AC_    AC
GAM3194  LASP1     3'  GAACGCACTTTCCTCACCACTG 72354     A        A  TT
                                GAAC CACTTTTCTCA CC  CTG
                                |||| ||||||||||| ||  |||
                                CTTG GTGAAAGGAGT GG  GAC
                                  C          _  T_
GAM3194  MGC3048   3'  GAACACACTTCTCCTGGTTCTG 72355           CAACC
                                GAACACACTTTTCT    TTCTG
                                ||||||||||||||    |||||
                                CTTGTGTGAAGAGG    AAGAC
                                         ACC__
GAM3194  LOC115131 5'  GGACACCTTTGCCGTCTTCTG  72356   C      C  AAC
                                A ACACTTTT TC   CTTCTG
                                | ||||||||  ||   ||||||
                                C TGTGGAAA GG   GAAGAC
                                 C       C  CA_
GAM3194  LOC138130 5'  GAATGCACTTCCCGTCTTCTG  72357    CA    TT TCAAC
                                GAA  CACTT  C    CTTCTG
                                |||  |||||  |    ||||||
                                CTT  GTGAA  G    GAAGAC
                                  AC    GG CA___
GAM3194  LOC144473 5'  CATTTTTCCAACCTTTCTG   72358   C    T     _
                                CA TTTTC CAACCTT CTG
                                || ||||| ||||||| |||
                                GT AAAAG GTTGGAA GAC
                                 A    _      A
GAM3194  LOC253650 3'  GAGCACACTTCTCTCTCT    72359    A        AACCT
                                GA CACACTTTTCTC    TCT
                                || ||||||||||||    |||
                                CT GTGTGAAGAGAG    AGA
                                 C          _____
GAM3194  LOC57107  3'  AAACATATTTTTCTCAATCC   72360      CAC       _
                                GAACA   TTTTCTCAA CC
                                |||||   |||||||||| ||
                                TTTGT   AAAAGAGTT GG
                                   ATA        A
GAM3195  GPR30     3'  GAGCGCTGCTGCTCCTCGTGGG 72363    A        ATAC
                                GA CGTTGCTGCTT    CGTGGG
                                || ||||||||||    ||||||
                                CT GCGACGACGAG    GCACCC
                                 C         GA__
GAM3195  DKFZp547J036 3'  ACGTCGCTGGCCGTGG      72364         CTTATA
                                ACGTTGCTG     CCGTGG
                                |||||||||     ||||||
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                                TGCAGCGAC     GGCACC
                                     C_____
GAM3195  STRN3    5'  CGTTGCTGTGTGCCTGCCGTGG 72365        ____    ATA
             G                    CGTTGCT    GCTT   CCGTGGG
                                  |||||||    ||||   |||||||
                                  GCAACGA    CGGA   GGCACCC
                                      CACA    C__
GAM3195  LOC133671 5'  GAGCGCTGCTGCTCAGCTGTGG 72366     A          TACC
             G                    GA CGTTGCTGCTTA    GTGGG
                                  || ||||||||||||    |||||
                                  CT GCGACGACGAGT    CACCC
                                   C          CGA_
GAM3196  CUGBP2   3'  AGTGGTTTTACTGCAAG     72369       CG    CG  A
                                  AGTGG  TTTGC  TG CAAG
                                  |||||  |||||  || ||||
                                  TCACC  AAATG  AC GTTC
                                     A_    __  _
GAM3196  TIGD5    5'  GTAGCGTTTGACGCCTGGGACA 72370          C   GACAA
                                  GTGGCGTTTG CGT    GACA
                                  ||||||||| |||    ||||
                                  CATCGCAAAC GCG    CTGT
                                        T   GACC_
GAM3197  AMFR     3'  GAGGACTGAGGTCCAGTGG   72373     C  G   ACA AC
                                  GAG AC TGA   G  CCAGTGG
                                  ||| || |||   |  |||||||
                                  CTC TG ACT   C  GGTCACC
                                    C  _  ___ CA
GAM3197  BZRP     3'  ACAGACTAGCAGGCCCAGTGG  72374     CG GAA   A
                                  GCA  T   CAG CCCAGTGG
                                  |||  |   ||| ||||||||
                                  TGT  G   GTC GGGTCACC
                                    CT ATC   C
GAM3197  GNL1     5'  GGCACGTGAGAGCCAGTGGC   72375    A      ACA  C
                                  G GCACGTGA   GA CCAGTGGC
                                  | ||||||||   || ||||||||
                                  C CGTGCACT   CT GGTCACCG
                                  _       ___  C
GAM3197  GNL1     5'  GGCACGTGAGAGCCAGTGGC   72375    A      ACA  C
                                  G GCACGTGA   GA CCAGTGGC
                                  | ||||||||   || ||||||||
                                  C CGTGCACT   CT GGTCACCG
                                  _       ___  C
GAM3197  HDAC4    3'  ACGCCAAGAGGCCCAGTGGC   72376      G  C  A
                                  ACGT AA AG CCCAGTGGC
                                  |||| || || |||||||||
                                  TGCG TT TC GGGTCACCG
                                    G  C  C
GAM3197  PIR51    3'  GAACACGTGGATGAGTGG    72377         AACA  CCC
                                  GAGCACGTG   GA   AGTGG
                                  |||||||||   ||   |||||
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                                CTTGTGCAC   CT   TCACC
                                     ____  AC_
GAM3197  PTPRK    3'  GAGCATGTGAACAAGACC    72378      C     _
                                GAGCA GTGAACA GACC
                                ||||| ||||||| ||||
                                CTCGT CACTTGT CTGG
                                   A      T
GAM3197  WHSC1    3'  CGTGGTCAGCCCCAGTGGC   72379     AA   A
                                CGTG  CAG CCCAGTGGC
                                ||||  ||| |||||||||
                                GCAC  GTC GGGTCACCG
                                  CA   G
GAM3197  WHSC1    3'  CGTGGTCAGCCCCAGTGGC   72379     AA   A
                                CGTG  CAG CCCAGTGGC
                                ||||  ||| |||||||||
                                GCAC  GTC GGGTCACCG
                                  CA   G
GAM3197  WHSC1    3'  CGTGGTCAGCCCCAGTGGC   72379     AA   A
                                CGTG  CAG CCCAGTGGC
                                ||||  ||| |||||||||
                                GCAC  GTC GGGTCACCG
                                  CA   G
GAM3197  ZNF174   5'  GAGGCGCGCAGGCCCAGTGGC  72380     CA    AA   A
                                GAG  CGTG  CAG CCCAGTGGC
                                |||  ||||  ||| |||||||||
                                CTC  GCGC  GTC GGGTCACCG
                                 C_   __   C
GAM3197  BTBD2    3'  GCACGTGACAGGTGG       72381         A   ACCCA
                                GCACGTGA CAG     GTGG
                                |||||||| |||     ||||
                                CGTGCACT GTC     CACC
                                     _  ______
GAM3197  C1QR1    3'  AAGCACGTGTTTGAGCCCAGTG 72382          AAC_  A
            G                    GAGCACGTG    AG CCCAGTGG
                                |||||||||    || ||||||||
                                TTCGTGCAC    TC GGGTCACC
                                     AAAC  _
GAM3197  C20orf55 3'  GCGAATTCCAGGCCCAGTGGC  72383       ___   A
                                GTGAA   CAG CCCAGTGGC
                                |||||   ||| |||||||||
                                CGCTT   GTC GGGTCACCG
                                   AAG   C
GAM3197  C20orf72 3'  AGCACTCAGATCCAGTGGC    72384      GTGAA    C
                                AGCAC     CAGA CCAGTGGC
                                |||||     |||| ||||||||
                                TCGTG     GTCT GGTCACCG
                                   A_____    A
GAM3197  DKFZP564G202 3'  GAGGTAAGGGGCCCAGTGG    72385     CAC    ACAGA
                                GAG   GTGA     CCCAGTGG
                                |||   ||||     ||||||||
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                                CTC   CATT    GGGTCACC
                                  ____   CCCC_
GAM3197  FLJ13639  3'  GAGACGTGAACAGATCACTG   72386    C        CC  G
                                GAG ACGTGAACAGA  CA TG
                                ||| ||||||||||  || ||
                                CTC TGCACTTGTCT  GT AC
                                  _        A_  G
GAM3197  FLJ13855  5'  GAGCGTGGGGTCCCAGTGG   72387     AC   AACAGA
                                GAGC  GTG     CCCAGTGG
                                ||||  |||     ||||||||
                                CTCG  CAC     GGGTCACC
                                  __  CCCA__
GAM3197  MGC1842   3'  AGCATGTGAACAGGCTGGGC   72388     C       ACCCAGT
                                AGCA GTGAACAG      GGC
                                |||| ||||||||      |||
                                TCGT CACTTGTC      CCG
                                  A       CGAC___
GAM3197  OSBPL3    5'  GAGTATGGAAGTCCCCAGTGGC 72389     CAC   AACAGA
                                GAG   GTG     CCCAGTGGC
                                |||   |||     |||||||||
                                CTC   TAC     GGGTCACCG
                                  A__   CTTCAG
GAM3197  P114-RHO-GEF 3'  GAGCGTGTGAACAGCAACGG   72390      AC       ACC
                                GAGC  GTGAACAG   CAGTGG
                                ||||  ||||||||   ||||||
                                CTCG  CACTTGTC   GTTGCC
                                  CA       ___
GAM3197  PIP5K1C   3'  ACGTGAACAGCGGGTGGC    72391          ACCCA
                                ACGTGAACAG    GTGGC
                                ||||||||||    |||||
                                TGCACTTGTC    CACCG
                                     GCC__
GAM3197  LOC115704 3'  ACATGTGAACAGGCAGT     72392     C       ACC
                                GCA GTGAACAG   CAGT
                                ||| ||||||||   ||||
                                TGT CACTTGTC   GTCA
                                  A       C__
GAM3197  LOC147299 3'  GGCATGTGTTTTGACCCAGTGG 72393    A   C   AACA
                                G GCA GTG    GACCCAGTGG
                                | ||| |||    ||||||||||
                                C CGT CAC    CTGGGTCACC
                                 _   A   AAAA
GAM3197  LOC196955 3'  GAGTGCGTGAACAGGACTCGC  72394     CA       _  CCA
                                GAG  CGTGAACAG AC   GT
                                |||  ||||||||| ||   ||
                                CTC  GCACTTGTC TG   CG
                                  AC        C  AG_
GAM3197  LOC257541 5'  GGCACGTGAGAGCCAGTGGC   72375    A       ACA  C
                                G GCACGTGA   GA CCAGTGGC
                                | ||||||||   || ||||||||
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                                C CGTGCACT   CT GGTCACCG
                                _       ___  C
GAM3197  LOC58509  5'  AGCACGTGCGCGTCCAGTGGC  72395        AACAGAC
                                AGCACGTG      CCAGTGGC
                                ||||||||      ||||||||
                                TCGTGCAC      GGTCACCG
                                    GCGCA__
GAM3197  LOC63928  5'  GAGGCGTGGCCGCCCCAGTGGC 72396     CA    AACAGA
                                GAG  CGTG     CCCAGTGGC
                                |||  ||||     |||||||||
                                CTC  GCAC     GGGTCACCG
                                  C_   CGGCG_
GAM3197  LOC90785  3'  GCCGGGAGGCCCAGTGGC    72397    A  T  ACA A
                                GC CG GA   G CCCAGTGGC
                                || || ||   | |||||||||
                                CG GC CT   C GGGTCACCG
                                 _ C  ___ C
GAM3197  LOC91351  3'  GAGCACATATGCATTTAGTGGC 72398         AA  GACCC
                                GAGCACGTG  CA    AGTGGC
                                |||||||||  ||    ||||||
                                CTCGTGTAT  GT    TCACCG
                                     AC  AAA__
GAM3198  YES1      3'  TACAAAGTTGTTTTTCTTGGC  72401          ACAC   _
                                TACAAAGTTGTT   CTTG C
                                ||||||||||||   |||| |
                                ATGTTTCAACAA   GAAC G
                                     AAA_   C
GAM3198  ZNF264    3'  AAAAATTACATCTTGTGGC   72402    TT     C    C
                                AG  GTTACA CTTG GGC
                                ||  |||||| |||| |||
                                TT  TAATGT GAAC CCG
                                 TT     A    A
GAM3198  ABHD3     3'  TACAAAGTTGTTTTGTTTGCCG 72403         ACA________  TTGC
            CAG                   CAAAGTTGTT        CC    G
                                ||||||||||        ||    |
                                GTTTCAACAA        GG    C
                                     AACAAAIIIC  CGTT
GAM3198  CBX3      3'  TACAAAGTTGTTCTTCCTGGC  72404          ACA   T
                                TACAAAGTTGTT   CCT GC
                                ||||||||||||   ||| ||
                                ATGTTTCAACAA   GGA CG
                                     GAA   C
GAM3198  CBX3      3'  TACAAAGTTGTTCTTCCTGGC  72404          ACA   T
                                TACAAAGTTGTT   CCT GC
                                ||||||||||||   ||| ||
                                ATGTTTCAACAA   GGA CG
                                     GAA   C
GAM3198  DHRS2     5'  AAGTTGCAGACCCTTGCGG   72405        T_  A
                                AAGTTGT  AC CCTTGCGG
                                |||||||  || ||||||||
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                                TTCAACG  TG GGAACGCC
                                    TC  _
GAM3198  HH114    3'  TAAAAGTTGTTATGTCAGCATG 72406    C        CACCTT  __
              GC                    A AAAGTTGTTA     GC  GGC
                                | ||||||||||     ||  |||
                                A TTTCAACAAT     CG  CCG
                                 T        ACAGT_  TA
GAM3198  HSA9761   3'  AAAGTTGTGCGTCTCTGCGGC  72407         TACACC
                                AAAGTTGT     TTGCGGC
                                ||||||||     |||||||
                                TTTCAACA     GACGCCG
                                     CGCAGA
GAM3198  IL22R    3'  CAAAGTTGTGACATCAGTGCCG 72408       T  A__________  TTGC
              CAAGG                 AGTTGT AC        CC    GG
                                |||||| ||         ||    ||
                                TCAACA TG         GG    CC
                                   C  TAGTCAIIIC  CGTT
GAM3198  SEP15    3'  TACAAAGTTTTTATGCAG    72409         G   CACCT
                                TACAAAGTT TTA     TGCGG
                                |||||||||  |||     |||||
                                ATGTTTCAA AAT     ACGTC
                                     A  ______
GAM3198  LOC154739 5'  AAAGTTGTCACATCTTGTGGC  72410           C    C
                                AAAGTTGTTACA CTTG GGC
                                |||||||||||| |||| |||
                                TTTCAACAGTGT GAAC CCG
                                      A    A
GAM3198  LOC170372 5'  CAAAGTTGTTATGTATAGGC   72411           CACCT  C
                                CAAAGTTGTTA     TG GGC
                                ||||||||||     || |||
                                GTTTCAACAAT     AT CCG
                                      ACAT_  _
GAM3198  LOC257485 3'  AAAGTTGTTCCATTGTGGC    72412         ACA  _   C
                                AAAGTTGTT   CC TTG GGC
                                |||||||||   || ||| |||
                                TTTCAACAA   GG AAC CCG
                                     ___  T   A
GAM3199  PDE7A    3'  ACAGGCACATATTAAAATGAGT 72415         _
              AT                    ACAGGTAT TATTAAAATGAGTAT
                                |||||||| ||||||||||||||
                                TGTCCGTG ATAATTTTACTCATA
                                     T
GAM3199  PPEF1    5'  CACAGGTCTTATTGAAGAG    72416        A    AAAAT
                                CACAGGT TTATT     GAG
                                ||||||| |||||     |||
                                GTGTCCA AATAA     CTC
                                    G    CTT__
GAM3199  RAP1GA1   3'  CACAGGGGCTTCCAAAATGGGT 72417       TA  A       A
              AT                    CACAGG  TT TTAAAATG GTAT
                                ||||||  || |||||||| ||||
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                                GTGTCC  GA GGTTTTAC CATA
                                   CC  A       C
GAM3199  TNFSF6   3'  CAGGCACTAAGATGAGT     72418          TTAAA
                                CAGGTATTA    ATGAGT
                                |||||||||    ||||||
                                GTCCGTGAT    TACTCA
                                     TC___
GAM3199  COVA1    3'  AGATATTATTAAAATTAGGTAT 72419              GA_
                                AGGTATTATTAAAAT   GTAT
                                ||||||||||||||   ||||
                                TCTATAATAATTTTA   CATA
                                         ATC
GAM3199  DKFZP564G092 3'  ACAGGTATAAATACATGGGTAT 72420         TATTAAA   A
                                ACAGGTAT      ATG GTAT
                                ||||||||      ||| ||||
                                TGTCCATA      TAC CATA
                                     TTTATG_   C
GAM3199  FLJ21313  3'  CAGGGTGTTTCAACCAATGAGT 72421      TATTA   __
            AT                   CAGG    TTAA  AATGAGTAT
                                ||||    ||||  |||||||||
                                GTCC    AGTT  TTACTCATA
                                  CACAA    GG
GAM3199  NEDD5    3'  CACAGGTACTGTTAAAATG    72422          A
                                CACAGGTATT TTAAAATG
                                |||||||||| ||||||||
                                GTGTCCATGA AATTTTAC
                                      C
GAM3199  PRO2086  5'  TAAAGTAGCGTTAAAATGAGT  72423   C    TTA
                                A AGGTA   TTAAAATGAGT
                                | |||||   ||||||||||
                                A TTCAT   AATTTTACTCA
                                 T    CGC
GAM3199  USP15    3'  AGTATTATTAGAGCA       72424          AAAT
                                GGTATTATTA    GAGTA
                                ||||||||||    |||||
                                TCATAATAAT    CTCGT
                                      _____
GAM3199  VIT1     5'  AGGTGATTCTCAATGAGTAT   72425      _   ATTAA
                                AGGT ATT     AATGAGTAT
                                |||| |||     |||||||||
                                TCCA TAA     TTACTCATA
                                  C   GAG__
GAM3199  LOC126969 3'  ACAGATACCTAAATGGGTAT   72426         ATTA    A
                                ACAGGTATT    AAATG GTAT
                                |||||||||    ||||| ||||
                                TGTCTATGG    TTTAC CATA
                                     A___     C
GAM3200  CD2AP    3'  AATGATACTGTGTGTCTCAAAG 72429      ___    ATT__      III
            AATACG                ATAC   GTGT    AGAATAC   G
                                ||||   ||||    |||||||  |
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                                TATG  CACA    TCTTATG  C
                                  ACA   GAGTT     III
GAM3200 GLDC    3' TCAAGATGCTTTTATTAGAATA 72430     T  ACGTG
            C                    TCAA GAT    TATTAGAATAC
                                 |||| |||    ||||||||||
                                 AGTT CTA    ATAATCTTATG
                                   _  CGAAA
GAM3200 HLCS    5' TCACTGATACGTCGTCCAG   72431    A     _ A
                                 TCA TGATACGT GT TTAG
                                 ||| |||||||| || ||||
                                 AGT ACTATGCA CA GGTC
                                   G      G _
GAM3200 PPP2R5E  3' TCAATGATATATGCAACTAATA 72432       CG   TTAG
            C                    TCAATGATA  TGTA   AATAC
                                 |||||||||  ||||   |||||
                                 AGTTACTAT  ACGT   TTATG
                                       AT   TGA_
GAM3200 DKFZp434G179 3' AATGATTGTTTTATTAGAATA  72433      ACGTG
                                 AATGAT    TATTAGAATA
                                 ||||||    ||||||||||
                                 TTACTA    ATAATCTTAT
                                    ACAAA
GAM3200 DKFZP434P0721 3' TCAATGATAGTGTAAAAAAT  72434       C    TT
                                 TCAATGATA GTGTA  AGAAT
                                 ||||||||| |||||  |||||
                                 AGTTACTAT CACAT  TTTTA
                                       _    T_
GAM3200 KIAA0443  5' TCAATAATACAGATAGA    72435         TGTAT
                                 TCAATGATACG    TAGA
                                 ||||||||||    ||||
                                 AGTTATTATGT    ATCT
                                       CT___
GAM3200 KLF12    3' TCAATGATGTTTTATACTAGAA 72436       ACG_
            TAC                    TCAATGAT    TGTATTAGAATAC
                                 ||||||||    ||||||||||||
                                 AGTTACTA    ATATGATCTTATG
                                      CAAA
GAM3200 LRMP    3' TCAAGATCCATATATTAG    72437     T  A
                                 TCAA GAT CGTGTATTAG
                                 |||| ||| ||||||||||
                                 AGTT CTA GTATATAATC
                                   _  G
GAM3200 MGC23937 3' TCAGTAATTTGCATTAGAATA  72438    A   ACG
                                 TCA TGAT   TGTATTAGAATA
                                 ||| ||||   ||||||||||||
                                 AGT ATTA   ACGTAATCTTAT
                                   C   A__
GAM3200 ZNF297B  3' TCAGTATACGTGTGTCAG    72439    ATG      A
                                 TCA   ATACGTGT TTAG
                                 |||   |||||||| ||||
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                                AGT   TATGCACA AGTC
                                  CA_       C
GAM3200  LOC221400 3'  TCAAATCTTGTATTAGAATAC  72440      TGATACG
                                TCAA      TGTATTAGAATAC
                                ||||      ||||||||||||
                                AGTT      ACATAATCTTATG
                                  TAGA___
GAM3201  BCL11A    3'  TTAATTGTCCTATCTGAGC    72443          A  G   AT
                                TTAATTGTCCTA TC TGA  GC
                                |||||||||||| || |||  ||
                                AATTAACAGGAT AG ACT  CG
                                          _ _  __
GAM3201  F2RL3     3'  ATTGCACAGTATCGTGAATG   72444       CCTA_
                                ATTGT    ATCGTGAATG
                                |||||    ||||||||||
                                TAACG    TAGCACTTAC
                                   TGTCA
GAM3201  PACE      3'  ATTGTCCTAATGGGAGGGGTGC 72445          CGT  A___
             A                   ATTGTCCTAAT   GA   TGCA
                                ||||||||||   ||   ||||
                                TAACAGGATTA   CT   ACGT
                                      CC_  CCCC
GAM3201  SRGAP2    3'  TTAATTGTCCTTGTTTGC    72446          AATCG  AA
                                TTAATTGTCCT    TG  TGC
                                ||||||||||    ||  |||
                                AATTAACAGGA    AC  ACG
                                      _____  AA
GAM3201  TDG       3'  TTAATTGCTCCTAATCCCTGAT 72447        _     _ G   A
             GCA                   TTAATTG TCCTAAT C TGA TGCA
                                ||||||| ||||||| | ||| ||||
                                AATTAAC AGGATTA G ACT ACGT
                                    G      G G   _
GAM3201  KIAA1040  3'  TTAATTATCCTAATTG      72448           CGTGAA
                                TTAATTGTCCTAAT     TG
                                ||||||||||||||     ||
                                AATTAATAGGATTA     AC
                                          ______
GAM3201  LOC158038 3'  TAATTGTCCGTGAGTG      72449         TAATC   A
                                TAATTGTCC    GTGA TG
                                |||||||||    |||| ||
                                ATTAACAGG    CACT AC
                                      _____   C
GAM3202  BHLHB3    3'  TAGTGTGTGGAGGGTGGGGTGG 72452     C       CGATCCT
             TG                    TAG GTGTGGAG      TGGTG
                                ||| ||||||||      |||||
                                ATC CACACCTC      ACCAC
                                  A       CCACCCC
GAM3202  MGC10715  5'  GTGTGGAGCACAGCTGGTG   72453          ATCC
                                GTGTGGAGCG    TTGGTG
                                ||||||||||   ||||||
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                                CACACCTCGT   GACCAC
                                     GTC_
GAM3202 LOC148932 3' GTGTGGAGTGATTCCAGTG   72454       C  _  TT
                                GTGTGGAG GAT CC  GGTG
                                |||||||| ||| ||  ||||
                                CACACCTC CTA GG  TCAC
                                    A  A  __
GAM3203 AKAP13   3' GGACACAGCCAGTGGGGGGT  72457   A    AA_  ACT
                                A ACGCA  AG  TGGGGGGT
                                | |||||  ||  ||||||||
                                C TGTGT  TC  ACCCCCCA
                                 C    CGG  ___
GAM3203 AQP8     3' GCAGTGGAAGCAGGGGGTCG  72458    AAA  CT
                                GCA  GA  TGGGGGGTCG
                                |||  ||  ||||||||||
                                CGT  CT  GTCCCCCAGC
                                  CAC  TC
GAM3203 CD14     3' GCAAAGGGTTGAATTGGTCG  72459     A AC   GG_
                                GCAAA G  TTGG  GGTCG
                                ||||| |  ||||  |||||
                                CGTTT C  AACT  CCAGC
                                   _ CC   TAA
GAM3203 DSP      5' GCGGAAGGCTCGCGAGGTCG  72460    AA  A   G
                                GC  AAG CTTG GGGGTCG
                                ||  ||| |||| |||||||
                                CG  TTC GAGC CTCCAGC
                                 CC  C   G
GAM3203 EPB49    3' GCAAAAGGCTTGGAAGCTCG  72461       A      G
                                GCAAAAG CTTGGGGG TCG
                                ||||||| |||||||| |||
                                CGTTTTC GAACCTTC AGC
                                    C       G
GAM3203 PFKFB4   3' GGACACAAAGGACTTGGG    72462   A     A
                                A ACGCAAA GACTTGGG
                                | ||||||| ||||||||
                                C TGTGTTT CTGAACCC
                                 C      C
GAM3203 TESK1    3' AACGCGAGCCGGGGGGTCG   72463      AAAA  C
                                AACGC   GA TTGGGGGGTCG
                                |||||   || ||||||||||
                                TTGCG   CT GGCCCCCCAGC
                                   _____  C
GAM3203 TRAF5    5' GGACGCGCAGGAAGGGGTC   72464   A   AAA  ACTT
                                A ACGC  AG   GGGGGGTC
                                | ||||  ||   ||||||||
                                C TGCG  TC   TTCCCCAG
                                 C   CG_  C___
GAM3203 ZFP103   5' ACGGGAGAGAGAAGGGTCG   72465    CAAA  CTT
                                ACG   AGA  GGGGGGTCG
                                |||   |||  |||||||||
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                                TGC   TCT  CTTCCCAGC
                                  CC__  CT_
GAM3203 AP3S2    3' GCAAATGACTTGGGCATGT   72466     A      GG_
                                GCAAA GACTTGGG  GT
                                ||||| ||||||||  ||
                                CGTTT CTGAACCC  CA
                                   A      GTA
GAM3203 DKFZP434N014 5' CGCGAAGACGGCGGGGGTCG  72467    AA    TTG
                                CGC  AAGAC  GGGGGTCG
                                |||  |||||  ||||||||
                                GCG  TTCTG  CCCCCAGC
                                  C_   CCG
GAM3203 DNAJC5   3' AAACACAGGAGGAGGGGTC   72468       AA  ACTT
                                AAACGCA  AG   GGGGGGTC
                                |||||||  ||   ||||||||
                                TTTGTGT  TC   CTCCCCAG
                                    CC  _____
GAM3203 FLJ10298 3' AACCCAGGAGACGGAGGT    72469    G  AA   TTG
                                AAC CA  AGAC  GGGGGT
                                |||  ||  ||||  ||||||
                                TTG GT  TCTG  CCTCCA
                                  G  CC   ___
GAM3203 FLJ14768 3' GCGGGGAAGATCGTTAGGGTCG 72470    AA__   C  G_
                                GC   AAGA TTG  GGGGTCG
                                ||   |||| |||  |||||||
                                CG   TTCT AGC  TCCCAGC
                                 CCCC   _  AA
GAM3203 FLJ20700 3' AAACCCAGGAGACAGAGGT   72471     G  AA   TTG
                                AAAC CA  AGAC  GGGGGT
                                ||||  ||  ||||  ||||||
                                TTTG GT  TCTG  TCTCCA
                                  G  CC   ___
GAM3203 ISL2     5' GCAGAAGGACGAGGGTCG    72472     A  _  TTG
                                GCA AAG AC  GGGGGTCG
                                ||| ||| ||  ||||||||
                                CGT TTC TG  CTCCCAGC
                                  C  C  ___
GAM3203 KIAA0356 3' GGACACAGAGGAACCGGGGTCG 72473   A    AAA_   TGG
                                A ACGCA   GACT  GGGGTCG
                                | |||||   ||||  |||||||
                                C TGTGT   TTGG  CCCCAGC
                                 C    CTCC   ___
GAM3203 KIAA1084 3' AAACGCAGGAGACATGGATC  72474       AA   TTGGG
                                AAACGCA  AGAC    GGGTC
                                |||||||  ||||    |||||
                                TTTGCGT  TCTG    CCTAG
                                    CC   TA___
GAM3203 KIAA1200 3' ACTAAAGGGTTCCTGAAGGGT  72475    A   A___
                                GC AAAG   CTTGGGGGGT
                                || ||||   ||||||||||
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                                TG TTTC   GGACTTCCCA
                                 A   CCAA
GAM3203 KIAA1254 3' AACCCAGGAGACAGAGGT   72476    G  AA   TTG
                                AAC CA  AGAC   GGGGGT
                                ||| ||  ||||   ||||||
                                TTG GT  TCTG   TCTCCA
                                  G  CC   ___
GAM3203 MGC10966 5' ACGCTGGAGCAGGAGGGGGTCG 72477     AAA  ACTT
                                ACGC   AG   GGGGGGTCG
                                ||||   ||   |||||||||
                                TGCG   TC   TCCCCCAGC
                                  ACC  GTCC
GAM3203 MGC15523 5' GCGAGAGGCCTCGGGGGTCG   72478   AAA  A   G
                                GC   AG CTT GGGGGTCG
                                ||   || ||| ||||||||
                                CG   TC GGA CCCCCAGC
                                 CTC  C   G
GAM3203 MGC4638  3' AACCCAGGAGACGGAGGT   72469    G  AA   TTG
                                AAC CA  AGAC   GGGGGT
                                ||| ||  ||||   ||||||
                                TTG GT  TCTG   CCTCCA
                                  G  CC   ___
GAM3203 phospho1  3' GCTAGAAGGGAGTGCGGGGGTC 72479    AA_  ACT_ _
           G                     GC   AAG    TG GGGGGTCG
                                ||   |||    || ||||||||
                                CG   TTC    AC CCCCCAGC
                                 ATC   CCTC  G
GAM3203 RALGPS1A 3' ACGCAGAGGACGCTTCGGGGT  72480      AAA  _  GG
                                ACGCA   GAC TT  GGGGT
                                |||||   ||| ||  |||||
                                TGCGT   CTG GA  CCCCA
                                   CTC   C  AG
GAM3203 RLUCL    3' CAAGAGACTGCAGCAGGT    72481     A    _  G
                                CAA AGACT TGG GGGT
                                ||| ||||| ||| ||||
                                GTT TCTGA GTC TCCA
                                  C    C   G
GAM3203 RMP      5' GCCGAAGGGGGCGAGGGGTCG  72482    AA   ACT_
                                GC  AAG    TGGGGGGTCG
                                ||  |||    ||||||||||
                                CG  TTC    GCTCCCCAGC
                                 GC   CCCC
GAM3203 SKRP1    5' ACCAAGAGACTGAGTC      72483    G   A    TGGG
                                AC CAA AGACT    GGGTC
                                || ||| |||||    |||||
                                TG GTT TCTGA    CTCAG
                                 _   C    _____
GAM3203 LOC120973 5' GCAAAAGGCTTGAAAGAT    72484        A   GG
                                GCAAAAG CTTG  GGGT
                                ||||||| ||||  ||||
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                                CGTTTTC GAAC  TCTA
                                    C    TT
GAM3203  LOC124446 5'  GCGAAGAGATAAACAGGGGTCG 72485    _ A   CTTG_
                                GC AA AGA    GGGGGTCG
                                || || |||    ||||||||
                                CG TT TCT    TCCCCAGC
                                 C  C   ATTTG
GAM3203  LOC124753 5'  GCAAAAGACAGAAGGT      72486         TT
                                GCAAAAGAC  GGGGGGT
                                |||||||||  |||||||
                                CGTTTTCTG  TCTTCCA
                                           __
GAM3203  LOC146988 3'  GGACACAGGAGATTTGGAA   72487   A    AA   C
                                A ACGCA  AGA TTGGGG
                                | |||||  ||| ||||||
                                C TGTGT  TCT AACCTT
                                 C    CC   A
GAM3203  LOC148229 5'  CGCAAAGGACTGGTGGTCG   72488      A   T  GG
                                CGCAAA GACT GG  GGTCG
                                |||||| |||| ||  |||||
                                GCGTTT CTGA CC  CCAGC
                                    C    _  A_
GAM3203  LOC51042  3'  AAACCCAGAGGCAAAAGGGGT  72489     G  AA  ACTT
                                AAAC CA  AG   GGGGGGT
                                |||| ||  ||   |||||||
                                TTTG GT  TC   TTCCCCA
                                  G  C_  CGTT
GAM3203  LOC89932  3'  AACCCAGGAGACGGAGGT    72469    G  AA   TTG
                                AAC CA  AGAC   GGGGGT
                                ||| ||  ||||   ||||||
                                TTG GT  TCTG   CCTCCA
                                  G  CC   ___
GAM3204  IL8       3'  TAGCAGACTAGGGTTGCCAGAT 72492         _______
              T                  TAGCAGACTA      TAGATT
                                 ||||||||||      ||||||
                                 ATCGTCTGAT      GTCTAA
                                       CCCAACG
GAM3204  NUDT12    3'  ACAGACTGTTGTAATTAGTT   72493       ATAGAT
                                 GCAGACT     TAATTAGTT
                                 |||||||     |||||||||
                                 TGTCTGA     ATTAATCAA
                                     CAAC__
GAM3205  COL4A5    3'  CCCGGGATACAGCAGGATTAG  72496     AA      TACT
                                 TCC  GATACAGT   ATTAG
                                 |||  ||||||||   |||||
                                 GGG  CTATGTCG   TAATC
                                   CC       TCC_
GAM3205  COL4A5    3'  CCCGGGATACAGCAGGATTAG  72496     AA      TACT
                                 TCC  GATACAGT   ATTAG
                                 |||  ||||||||   |||||
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                                GGG  CTATGTCG   TAATC
                                  CC      TCC_
GAM3205  COL4A5   3'  CCCGGGATACAGCAGGATTAG  72496    AA     TACT
                                TCC  GATACAGT   ATTAG
                                |||  ||||||||   |||||
                                GGG  CTATGTCG   TAATC
                                  CC      TCC_
GAM3205  FLRT2    5'  ACTTCAGGCTACAGTTACTAT  72497    C  AGA
                                ACT CA   TACAGTTACTAT
                                |||  ||   ||||||||||||
                                TGA GT   ATGTCAATGATA
                                  A  CCG
GAM3205  KIAA1673 3'  TCCAAGATGGTACTGTTAG   72498       ACA  T   A
                                TCCAAGAT   GT ACT TTAG
                                ||||||||   || ||| ||||
                                AGGTTCTA   CA TGA AATC
                                     C__  _   C
GAM3205  PMVK     3'  CTCCAAGAGGTTTATTA     72499       TACA   AC
                                CTCCAAGA    GTT  TATTA
                                ||||||||    |||  |||||
                                GAGGTTCT    CAA  ATAAT
                                     C___   __
GAM3205  PMVK     3'  CTCCAAGAGGTTTATTA     72499       TACA   AC
                                CTCCAAGA    GTT  TATTA
                                ||||||||    |||  |||||
                                GAGGTTCT    CAA  ATAAT
                                     C___   __
GAM3206  EXTL1    3'  CTGAGACCTTTGATGGGGTCTC 72502     TC  A___
                                TTGG  CC    ATGGGGTCTC
                                ||||  ||    ||||||||||
                                GACT  GG    TACCCCAGAG
                                  CT  AAAC
GAM3206  CENTG1   3'  GCGTGTTGAGCTGGGGTCT   72503     A  _  CCCAA
                                GCGT TTG GT    TGGGGTCT
                                |||| ||| ||    ||||||||
                                CGCA AAC CG    ACCCCAGA
                                  C   T  _____
GAM3206  DKFZP586B2420 3'  TTGGTCCCAGAGGGGTCTC   72504        AT
                                TTGGTCCCA  GGGGTCTC
                                |||||||||  ||||||||
                                AACCAGGGT  CCCCAGAG
                                     CT
GAM3206  FYCO1    3'  GTGTGGTGGGTTTGGGGTCTC  72505    AT   CCCAA
                                GT  TGGT    TGGGGTCTC
                                ||  ||||    |||||||||
                                CA  ACCA    ACCCCAGAG
                                 C_   CCCAA
GAM3206  KIAA0711 5'  GTGCTGGTCTCAGGAGCTC   72506    A    C  AT   T
                                GT TTGGTC CA  GGGG CTC
                                || |||||| ||  |||| |||
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                                CA GACCAG GT  CCTC GAG
                                 C     A __   _
GAM3206  PP3501   3'  GTTTGGTTTGGGGTCT     72507    A    CCCAA
                                GT TTGGT    TGGGGTCT
                                || |||||    ||||||||
                                CA AACCA    ACCCCAGA
                                 _    A____
GAM3206  LOC145439 5'  CTGGTGCTGATGGGGTCTC    72508      CCCA
                                TTGGT    ATGGGGTCTC
                                |||||    ||||||||||
                                GACCA    TACCCCAGAG
                                   CGAC
GAM3206  LOC54505  5'  GTATTGGTCATGGCATCT    72509        CCA    G
                                GTATTGGTC   ATGG GTCT
                                |||||||||   |||| ||||
                                CATAACCAG   TACC TAGA
                                     ___    G
GAM3207  DGKA     5'  CTTCCGTTGCTTGGACCTCTTC 72512        ACCCA   GATA
              A                  CTTCCGTTG    ACT    TCA
                                 |||||||||    |||    |||
                                 GAAGGCAAC    TGG    AGT
                                      GAACC   AGA_
GAM3207  PIGR     5'  CTCCCGTTGATCTGACTTC    72513         CCCAA    A
                                CTTCCGTTGA    CTGAT TC
                                ||||||||||    ||||| ||
                                GAGGGCAACT    GACTG AG
                                      A____    A
GAM3207  AQP9     3'  TTCTGCTGTTCTGATATC    72514    C    ACCCAA
                                TTC GTTG     CTGATATC
                                ||| ||||     ||||||||
                                AAG CGAC     GACTATAG
                                  A   AA____
GAM3207  FLJ10388  3'  TTCCGTTGCATTGGATGTATCA 72515        ACCCAAC  A
                                TTCCGTTG      TG TATCA
                                ||||||||      || |||||
                                AAGGCAAC      AC ATAGT
                                     GTAACCT  _
GAM3207  KIAA0783  3'  CTGCCGTTGACTTAAAACTGGA 72516    T      CC__    AT
              TCA                  CT CCGTTGAC    AACTG  ATCA
                                   || ||||||||    |||||  ||||
                                   GA GGCAACTG    TTGAC  TAGT
                                    C       AATT    C_
GAM3207  MDS018   3'  CTTCCATTGATTTGACAT    72517         CCCAAC
                                CTTCCGTTGA     TGATAT
                                ||||||||||     ||||||
                                GAAGGTAACT     ACTGTA
                                      AA____
GAM3207  LOC158147 3'  CATCTGTCCAACTGATGTC    72518      GAC        A
                                CGTT   CCAACTGAT TC
                                ||||   |||||||| ||
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                                GTAG   GGTTGACTA AG
                                  ACA        C
GAM3207  LOC165693 5'  CTCCCGTTGACTGAT       72519          CCAAC
                                CTTCCGTTGAC    TGAT
                                ||||||||||    ||||
                                GAGGGCAACTG    ACTA
                                              _____
GAM3207  LOC90631  3'  TTCCCCCCCAACTGATGTCA  72520     GTTGA        A
                                TTCC    CCCAACTGAT TCA
                                ||||    |||||||||| |||
                                AAGG    GGGTTGACTA AGT
                                  GG___         C
GAM3207  LOC91966  5'  CTTCCGTCTGTCACTGATGTC  72521       GACCCA     A
                                CTTCCGTT     ACTGAT TC
                                ||||||||     |||||| ||
                                GAAGGCAG     TGACTA AG
                                     ACAG__     C
GAM3208  AGL       3'  ATATTATAATAAATGAGAT   72524          _
                                ATATTATAATAAATG GAT
                                |||||||||||||| |||
                                TATAATATTATTTAC CTA
                                        T
GAM3208  AGL       3'  ATATTATAATAAATGAGAT   72524          _
                                ATATTATAATAAATG GAT
                                |||||||||||||| |||
                                TATAATATTATTTAC CTA
                                        T
GAM3208  AGL       3'  ATATTATAATAAATGAGAT   72524          _
                                ATATTATAATAAATG GAT
                                |||||||||||||| |||
                                TATAATATTATTTAC CTA
                                        T
GAM3208  AGL       3'  ATATTATAATAAATGAGAT   72524          _
                                ATATTATAATAAATG GAT
                                |||||||||||||| |||
                                TATAATATTATTTAC CTA
                                        T
GAM3208  AGL       3'  ATATTATAATAAATGAGAT   72524          _
                                ATATTATAATAAATG GAT
                                |||||||||||||| |||
                                TATAATATTATTTAC CTA
                                        T
GAM3208  AGL       3'  ATATTATAATAAATGAGAT   72524          _
                                ATATTATAATAAATG GAT
                                |||||||||||||| |||
                                TATAATATTATTTAC CTA
                                        T
GAM3208  DNAJC6    3'  TATATTACAATAAATATGAT  72525            _
                                TATATTATAATAAATG GAT
                                |||||||||||||| |||
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                                ATATAATGTTATTTAT CTA
                                          A
GAM3208  FLJ11577  3'  TCAGAATAAATGGATAAA    72526     T
                                TTA AATAAATGGATAAA
                                ||| |||||||||||||
                                AGT TTATTTACCTATTT
                                  C
GAM3208  KIAA1925  3'  TATATTTTAATAAATACGACAA 72527       A       _
            A                    TATATT TAATAAATG GATAAA
                                ||||||| ||||||||| ||||||
                                ATATAA ATTATTTAT CTGTTT
                                    A       G
GAM3209  PCOLN3    3'  TGACACAGGCAGCATCGT    72530        _ AAT   AC
                                TGACACAG CA   GTA  CGT
                                |||||||| ||   |||  |||
                                ACTGTGTC GT   CGT  GCA
                                     C ____  A_
GAM3209  PIP5K1A   3'  TGGCACAGCAATGACC      72531    A      A  TA
                                TG CACAGCAA TG  ACC
                                || |||||||| ||  |||
                                AC GTGTCGTT AC  TGG
                                 C      _ __
GAM3209  FLJ12891  3'  TGACACAACAAGACCCCGT   72532          ATGTAA
                                TGACACAGCAA     CCGT
                                ||||||||||     ||||
                                ACTGTGTTGTT     GGCA
                                      CTGG__
GAM3209  FLJ20320  3'  TGACAAGCAAATATAGCCAT   72533      C        A
                                TGACA AGCAAATGTA CCGT
                                ||||| |||||||||| ||||
                                ACTGT TCGTTTATAT GGTA
                                   _        C
GAM3209  FLJ23420  3'  TAACACAGCAAACAACTGT    72534          GT   C
                                TGACACAGCAAAT  AAC GT
                                ||||||||||||  ||| ||
                                ATTGTGTCGTTTG  TTG CA
                                      __  A
GAM3209  KIAA0111  3'  ACACAGCAGGTGAACAGT     72535        AA  T   C
                                ACACAGCA  TG AAC GT
                                ||||||||  || ||| ||
                                TGTGTCGT  AC TTG CA
                                     CC  _   T
GAM3209  KIAA0557  3'  GACACAGCAAGGCCCCGT     72536         AT  AA
                                GACACAGCAA  GT  CCGT
                                ||||||||||  ||  ||||
                                CTGTGTCGTT  CG  GGCA
                                      C_  G_
GAM3209  KIAA1949  3'  GACACAGCAAGTAAGCGT     72537         AT   C
                                GACACAGCAA  GTAA CGT
                                ||||||||||  |||| |||
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                                CTGTGTCGTT  CATT GCA
                                     __    C
GAM3209  KIAA1949  3'  GACACAGCAAGTAAGCGT    72537         AT   C
                                GACACAGCAA  GTAA CGT
                                ||||||||||  |||| |||
                                CTGTGTCGTT  CATT GCA
                                     __    C
GAM3209  KIAA1949  3'  GACACAGCAAGTAAGCGT    72537         AT   C
                                GACACAGCAA  GTAA CGT
                                ||||||||||  |||| |||
                                CTGTGTCGTT  CATT GCA
                                     __    C
GAM3209  MIC2L1    3'  TGACACAGCAAACTGAC     72538          GTA
                                TGACACAGCAAAT   AC
                                |||||||||||||   ||
                                ACTGTGTCGTTTG   TG
                                       AC_
GAM3209  LOC146381 5'  TGACACAGAAGTGTGTTTCGT  72539        C  A   AAC_
                                TGACACAG AA TGT    CGT
                                |||||||| || |||    |||
                                ACTGTGTC TT ACA    GCA
                                     _  C   CAAA
GAM3209  LOC148137 3'  TAACACAGTGAAACACCGT    72540        CA  TGTA
                                TGACACAG  AA    ACCGT
                                ||||||||  ||    |||||
                                ATTGTGTC  TT    TGGCA
                                     AC  TG__
GAM3209  LOC157798 5'  TGACACAGCAAGACTCCGT    72541          ATGTAA
                                TGACACAGCAA     CCGT
                                ||||||||||      ||||
                                ACTGTGTCGTT     GGCA
                                       CTGA__
GAM3209  LOC164397 5'  GACACAGCAAACTCCATCGT   72542           GTAAC
                                GACACAGCAAAT    CGT
                                ||||||||||||    |||
                                CTGTGTCGTTTG    GCA
                                       AGGTA
GAM3209  LOC197439 5'  TGACACAGAAGTGTGTTTCGT  72539        C  A   AAC_
                                TGACACAG AA TGT    CGT
                                |||||||| || |||    |||
                                ACTGTGTC TT ACA    GCA
                                     _  C   CAAA
GAM3209  LOC221042 3'  TAACACAGCAAACCCCGT     72543          GTAA
                                TGACACAGCAAAT    CCGT
                                ||||||||||||    ||||
                                ATTGTGTCGTTTG    GGCA
                                       G___
GAM3209  LOC92609  3'  GACACAGCAGGTGTGGCGT    72544         AA   AAC
                                GACACAGCA  TGT   CGT
                                |||||||||  |||   |||
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                                CTGTGTCGT  ACA   GCA
                                     CC   CC_
GAM3210 C21orf55 5'  TAAACGCTAAAACGGAGC    72547          TC   TATC
                                TAAACGCTAAA  ATG    AGC
                                ||||||||||  |||    |||
                                ATTTGCGATTT  TGC    TCG
                                      __   C___
GAM3210 FLJ10687 3'  TAAATGCTGAACATCAGCACAG 72548     C   AA__    T   T
             CT                   TAAA GCT    ATCA GTA CAGCT
                                |||| |||    |||| ||| |||||
                                ATTT CGA    TAGT CGT GTCGA
                                  A  CTTG   _  _
GAM3210 MGC16169 3'  GCTAAATCTGTCTTGTCAGCT  72549        A   A___
                                GCTAAATC TGT    TCAGCT
                                ||||||||| |||    ||||||
                                CGATTTAG ACA    AGTCGA
                                     _  GAAC
GAM3210 PRO2133  3'  TAAACGCTAATATTACAAGTCA 72550          _ C   TA
             G                    TAAACGCTAA AT ATG  TCAG
                                ||||||||||  || |||  ||||
                                ATTTGCGATT TA TGT  AGTC
                                      A  A   TC
GAM3210 SLC2A10  3'  GCTATACACCATGTATTGGCT  72551     A__       CA
                                GCTA   ATCATGTAT  GCT
                                ||||   |||||||||  |||
                                CGAT   TGGTACATA  CGA
                                  ATG        AC
GAM3210 LOC92223  5'  GCCTAAAATTGTGTATCAGCT  72552     __    CA
                                GCT  AAAT  TGTATCAGCT
                                |||  ||||  ||||||||||
                                CGG  TTTA  ACATAGTCGA
                                  AT    AC
GAM3211 KIAA0229  3'  TTTGGTACCTCAAAGTG     72555      C    TCTTTC
                                TTTGG ACCTC     AAAGTG
                                ||||| |||||     ||||||
                                AAACC TGGAG     TTTCAC
                                  A    _______
GAM3211 LOC153914 5'  TTTAGCACTTTTCCCCCAGTGT 72556        CTC   TT  AA
                                TTTGGCAC   TCT  CA  GTGT
                                ||||||||   |||  ||  ||||
                                AAATCGTG   AGG  GT  CACA
                                     AAA   GG  __
GAM3211 LOC200470 3'  TTTGGCTACAAATTTTCAAAGT 72557       _ CTCTC
             GT                   TTTGGC AC    TTTCAAAGTGT
                                ||||||  ||    ||||||||||
                                AAACCG TG    AAAGTTTCACA
                                  A  TTTA_
GAM3211 LOC201229 3'  TTTGGCGTCTCTCCTTGGTTCA 72558       AC       CAAA_
             TGT                  TTTGGC  CTCTCTTT    GTGT
                                ||||||  ||||||||    ||||
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                                AAACCG  GAGAGGAA    TACA
                                   CA       CCAAG
GAM3211  LOC222159 5'  TTTGGCTTCTCTCAATACAAAG 72559       AC    TTT_
             TGT                   TTTGGC  CTCTC   CAAAGTGT
                                |||||| |||||   ||||||||
                                AAACCG  GAGAG   GTTTCACA
                                   AA    TTAT
GAM3212  CADPS    3'  TGGTATGTAGCCATCCTT    72562         __   G
                                TGGTGTGTA  TATC CTT
                                ||||||||| |||| |||
                                ACCATACAT  GTAG GAA
                                     CG   _
GAM3212  DDX10    3'  TGGAGATACGATCGCTTC    72563    TGT   _
                                TGG   GTAT ATCGCTTC
                                |||   |||| ||||||||
                                ACC   TATG TAGCGAAG
                                  TC_   C
GAM3212  IL5RA    3'  TGGTGTGTCTGGGTGTATTGCT 72564       A_______  C    III
             TCG                   GGTGTGT      TAT GCTTC   G
                                |||||||      ||| |||||  |
                                CCACACA      ATA CGAAG   C
                                   GACCCAC   A    III
GAM3212  CAMK1G   3'  TGGTGGGCACCGCTTC     72565      T    AT
                                TGGTG GTAT  CGCTTC
                                ||||| ||||  ||||||
                                ACCAC CGTG  GCGAAG
                                   C   __
GAM3212  KIAA0020  5'  TGCTGATTCATCGCTTC    72566    G  T  A
                                TG TG GT TATCGCTTC
                                || || || |||||||||
                                AC AC TA GTAGCGAAG
                                 G  _  A
GAM3212  KIAA1776  3'  TGGTCAGCCATCGCTTC    72567     GT  A
                                TGGT  GT TATCGCTTC
                                ||||  || |||||||||
                                ACCA  CG GTAGCGAAG
                                   GT  _
GAM3212  MGC4827   3'  TGGTGTATATAGGGGAGCTT   72568         TC___
                                TGGTGTGTATA    GCTT
                                ||||||||||    ||||
                                ACCACATATAT    CGAA
                                     CCCCT
GAM3212  NESHBP   5'  TGGTGTGTGTCACTTC     72569        ATA
                                TGGTGTGT   TCGCTTC
                                ||||||||   |||||||
                                ACCACACA   AGTGAAG
                                     C__
GAM3212  VEST1    5'  TGGTGTGTCATCCTTC     72570        A   G
                                TGGTGTGT TATC CTTC
                                |||||||| |||| ||||
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                                ACCACACA GTAG GAAG
                                      _   _
GAM3212  LOC120241 5'  TGGCTCGCAATCGCTTC     72571      G   T
                                TGGT TGTA ATCGCTTC
                                |||| |||| ||||||||
                                ACCG GCGT TAGCGAAG
                                  A   _
GAM3212  LOC124615 5'  TGGATGTGACCGCTTC      72572     _   TAT
                                TGG TGTG   ATCGCTTC
                                ||| ||||   ||||||||
                                ACC ACAC   TGGCGAAG
                                  T   ____
GAM3212  LOC143720 3'  TGGTGTGTATAGGGGAGCTT   72573          TC____
                                TGGTGTGTATA    GCTT
                                ||||||||||     ||||
                                ACCACACATAT    CGAA
                                       CCCCT
GAM3212  LOC144698 3'  TGGTGTGTGTAACGTTC     72574        A  T  C
                                TGGTGTGT TA CG TTC
                                |||||||| || || |||
                                ACCACACA AT GC AAG
                                     C  T  _
GAM3212  LOC147157 3'  TGGTGTGACGGCACTTC     72575        T  AT
                                TGGTGTG AT  CGCTTC
                                ||||||| ||  ||||||
                                ACCACAC TG  GTGAAG
                                    _  CC
GAM3212  LOC149734 3'  TGGTCTATACCGCTTC      72576      GTG
                                TGGT   TATATCGCTTC
                                ||||   ||||||||||
                                ACCA   ATATGGCGAAG
                                  G__
GAM3212  LOC86651  5'  TGGTGTGTAACGACTTC     72577        T  C
                                TGGTGTGTA AT GCTTC
                                ||||||||| || |||||
                                ACCACACAT TG TGAAG
                                      _  C
GAM3213  AANAT     3'  AGAGGAGCCCAGGGCAGAGACG 72580      CA     CCAT
            GG                    AGAGG  CCCAG    GAGACGGG
                                |||||  |||||   ||||||||
                                TCTCC  GGGTC    CTCTGCCC
                                   TC    CCGT
GAM3213  CD37      3'  AGGGGCACGCAGCCACGTGGG  72581    A    C       AGAC
                                AG GGCAC CAGCCATG    GGG
                                || ||||| ||||||||    |||
                                TC CCGTG GTCGGTGC    CCC
                                 C    C       A___
GAM3213  CNP       3'  AGAGGCACCATGGAGGCAAGAT 72582          CAGCCAT_   C
            GGG                    AGAGGCACC       GAGA GGG
                                |||||||||       |||| |||
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                                TCTCCGTGG      TTCT CCC
                                     TACCTCCG   A
GAM3213  CPE     5'  GGCCACCCAGAGGAGACGGG  72583    _    CCAT
                                GGC ACCCAG   GAGACGGG
                                ||| ||||||   ||||||||
                                CCG TGGGTC   CTCTGCCC
                                  G     TC__
GAM3213  EHD2    3'  GGCCCCTCCCAGCCATGGGGTG 72584    A___       AGAC
             GG                  GGC   CCCAGCCATG   GGG
                                |||   ||||||||||   |||
                                CCG   GGGTCGGTAC   CCC
                                  GGGA       CCCA
GAM3213  HOXD4   5'  GGTTCCCAGCCAAAGCTGGG  72585   CA      T   AC
                                GG  CCCAGCCA GAG  GGG
                                ||  |||||||| |||  |||
                                CC  GGGTCGGT TTC  CCC
                                 AA       _   GA
GAM3213  KCNS2   3'  AGAGGCAGCTCAGCAATGTGGG 72586       CC_   C   AGAC
                                AGAGGCA   CAGC ATG   GGG
                                |||||||   |||| |||   |||
                                TCTCCGT   GTCG TAC   CCC
                                    CGA   T   A___
GAM3213  MAP2K2  3'  AGAGGCACCCCGGCCAGGACGG 72587         A_   TGA
             G                   AGAGGCACCC  GCCA   GACGGG
                                ||||||||||  ||||   ||||||
                                TCTCCGTGGG  CGGT   CTGCCC
                                      GC   C__
GAM3213  NFATC1  3'  AGGGTACCCAGCCGCAGGTGGG 72588   A  C      ATG  AC
                                AG GG ACCCAGCC   AG  GGG
                                || || ||||||||   ||  |||
                                TC CC TGGGTCGG   TC  CCC
                                 _  A      CG_  CA
GAM3213  OAS2    3'  GAGGCACCGTGGCCGCTTTCAG 72589        CA_   ATGAGA
             G                   GAGGCACC   GCC     CGGG
                                ||||||||   |||     ||||
                                CTCCGTGG   CGG     GTCC
                                     CAC   CGAAA_
GAM3213  OTP     3'  AGGGGCGGCCGGGAGACGG   72590    A   ACCCA   AT
                                AG GGC    GCC  GAGACGG
                                || |||    |||  |||||||
                                TC CCG    CGG  CTCTGCC
                                 C   C____   CC
GAM3213  PDAP1   3'  GGCTCCTGGCCATGAGGG    72591     A  CA      AC
                                GGC CC  GCCATGAG  GG
                                ||| ||  ||||||||  ||
                                CCG GG  CGGTACTC  CC
                                  A  AC       __
GAM3213  SDC4    3'  AGAGGACCCAGCCAGCTGG   72592      C       TGA AC
                                AGAGG ACCCAGCCA   G  GG
                                ||||| |||||||||   |  ||
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                                TCTCC TGGGTCGGT   C  CC
                                  _       ___ GA
GAM3213  SNX9     3'  AAGGCACCTGTGGGAGACGGG  72593        CAGCCAT
                                GAGGCACC      GAGACGGG
                                ||||||||      ||||||||
                                TTCCGTGG      CTCTGCCC
                                    ACACC__
GAM3213  SPHK2    3'  GAGGCACCGGAGTGGATGGG   72594        CAGCCA  A  C
                                GAGGCACC     TG GA GGG
                                ||||||||     || || |||
                                CTCCGTGG     AC CT CCC
                                    CCTC__  _  A
GAM3213  WHSC1    3'  AGGGGACCCAGCCAGCCATGGA 72595    A  C       ____  A
            CGGG                    G GG ACCCAGCCA    TG GACGGG
                                | || |||||||||    || ||||||
                                C CC TGGGTCGGT    AC CTGCCC
                                 _  C        CGGT  _
GAM3213  WHSC1    3'  AGGGGACCCAGCCAGCCATGGA 72595    A  C       ____  A
            CGGG                    G GG ACCCAGCCA    TG GACGGG
                                | || |||||||||    || ||||||
                                C CC TGGGTCGGT    AC CTGCCC
                                 _  C        CGGT  _
GAM3213  WHSC1    3'  AGGGGACCCAGCCAGCCATGGA 72595    A  C       ____  A
            CGGG                    G GG ACCCAGCCA    TG GACGGG
                                | || |||||||||    || ||||||
                                C CC TGGGTCGGT    AC CTGCCC
                                 _  C        CGGT  _
GAM3213  ARHGEF16 3'  AGAGGGGCCCAGCCAGCCAACG 72596      CA       TGA
            GG                    AGAGG  CCCAGCCA   GACGGG
                                |||||  ||||||||   ||||||
                                TCTCC  GGGTCGGT   TTGCCC
                                   CC       CGG
GAM3213  BOP      5'  AGAGACACCTGCACAGATGGG  72597        CA  C  G   C
                                AGAGGCACC  GC AT AGA GGG
                                |||||||||  || || ||| |||
                                TCTCTGTGG  CG TG TCT CCC
                                    A_  _  _   A
GAM3213  CBX6     3'  GGCACCCAGACAGGGATGGG   72598        C  TGA  C
                                GGCACCCAG CA   GA GGG
                                |||||||||  ||   || |||
                                CCGTGGGTC GT   CT CCC
                                    T  CC_  A
GAM3213  COX4I2   3'  AGAGGCTCCCAGCCAG      72599       A       TGAGAC
                                AGAGGC CCCAGCCA      G
                                ||||||  ||||||||     |
                                TCTCCG GGGTCGGT      C
                                   A       _______
GAM3213  DJ37E16.5 3'  AGAGTGCCCAGCCACTGCTGGG 72600      GCA       GAGAC
                                AGAG   CCCAGCCAT    GGG
                                ||||   |||||||||    |||
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                                TCTC  GGGTCGGTG   CCC
                                  AC_       ACGA_
GAM3213 FLJ10842 3' AGGGGTACTTGCCATGAAA  72601   A  C  CCA
                                AG GG AC   GCCATGAGA
                                || || ||   |||||||||
                                TC CC TG   CGGTACTTT
                                 C  A  AA_
GAM3213 FLJ14490 3' AGAGGACCTTGGAGACGG   72602      C   CAGCCAT
                                AGAGG ACC      GAGACGG
                                ||||| |||      |||||||
                                TCTCC TGG      CTCTGCC
                                   _  AAC____
GAM3213 GBTS1    3' GGCACCCACATGCGG      72603        GC   AGA
                                GGCACCCA  CATG   CGG
                                ||||||||  ||||   |||
                                CCGTGGGT  GTAC   GCC

                                    __   ____
GAM3213 GGA2     3' AGAGGCACCACAGTTATCCCTG 72604         _  CCATGAGAC
             GG                   AGAGGCACC CAG        GGG
                                |||||||||  |||        |||
                                TCTCCGTGG GTC        CCC
                                     T   AATAGGGA_
GAM3213 HUMZD58C02 3'  AGAGGCACCAGGCCCTAGCGGG 72605         CA   ATG  A
                                AGAGGCACC  GCC   AG CGGG
                                |||||||||  |||   || ||||
                                TCTCCGTGG  CGG   TC GCCC
                                     TC   GA_  _
GAM3213 KIAA0284  3' GAGGCACCCGCCCACAG     72606         A   ATGAG
                                GAGGCACCC GCC    ACGG
                                |||||||||  |||    ||||
                                CTCCGTGGG CGG    TGTC
                                     _  G____
GAM3213 KIAA0557  3' AGCAGGCAGCGACCATGAGATG 72607    _    CCCA       C
             GG                   AG AGGCA   GCCATGAGA GGG
                                || |||||   ||||||||| |||
                                TC TCCGT   TGGTACTCT CCC
                                 G    CGC_       A
GAM3213 KIAA0596  3' AGGGGCTTTCAAAACAAGGCGG 72608    A   ACC   CC TG  A
             G                    AG GGC   CAG  A  AG CGGG
                                || |||   |||  |  || ||||
                                TC CCG   GTT  T  TC GCCC
                                 C   AAA   T_ GT  C
GAM3213 KIAA0607  3' GAGGCACCACAGCCGAGG    72609        _    ATGA  C
                                GAGGCACC CAGCC    GA GG
                                |||||||| |||||    || ||
                                CTCCGTGG GTCGG    CT CC
                                     T    _____  _
GAM3213 KIAA0669  5' AGAGGCACGCCGGCTCCTCTGG 72610         _  A  CATGAGAC
             G                    AGAGGCAC CC GC       GGG
                                ||||||||  || ||       |||
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                                TCTCCGTG GG CG       CCC
                                    C  C  AGGAGA__
GAM3213  KIAA1257  3'  AGAGGGGCTCAGTCAAAAAGGG 72611      CACC   C  T    C
                                AGAGG    CAG CA GAGA GGG
                                |||||    ||| || |||| |||
                                TCTCC    GTC GT TTTT CCC
                                   CCGA   A  _    _
GAM3213  LGI4      3'  AGGGGCCCCAGCCATGCCCAG  72612    A   A        AGA
                                AG GGC CCCAGCCATG   CGG
                                || ||| ||||||||||   |||
                                TC CCG GGGTCGGTAC   GTC
                                 C   _         GG_
GAM3213  MGC4701   5'  AGAGGCACCTGGGTGCAGACGG 72613         CAGCCA  _
              G                   AGAGGCACC     TG AGACGGG
                                |||||||||      || |||||||
                                TCTCCGTGG      AC TCTGCCC
                                     ACCC__  G
GAM3213  MGC4701   5'  AGGGTCACCCAGCTGTGAC    72614    A  _       CA  A
                                AG GG CACCCAGC  TG GAC
                                || || ||||||||  || |||
                                TC CC GTGGGTCG  AC CTG
                                 _  A       __  A
GAM3213  N4BP3     3'  AGAGCCACCCAGCCGGCTGGG  72615      G        ATGAGAC
                                AGAG CACCCAGCC      GGG
                                |||| |||||||||       |||
                                TCTC GTGGGTCGG      CCC
                                   G        CCGA___
GAM3213  NKIR      3'  AGAGGCACCAGTCCCCGG     72616         C  _  ATGAGA
                                AGAGGCACC AG CC     CGG
                                ||||||||| || ||     |||
                                TCTCCGTGG TC GG     GCC
                                     _  A  G_____
GAM3213  NY-REN-41 3'  GAGGCACTTGCCATAAG      72617        CCA
                                GAGGCAC   GCCATGAG
                                |||||||   ||||||||
                                CTCCGTG   CGGTATTC
                                    AA_
GAM3213  SAMHD1    3'  AGAGGCACCTTGGCTAAAATGG 72618         CA_  CA    C
              G                   AGAGGCACC   GC  TGAGA GGG
                                |||||||||   ||  ||||| |||
                                TCTCCGTGG   CG  ATTTT CCC
                                     AAC  __    A
GAM3213  SLC2A4RG  3'  AGAGGCACTTTGAGTGGTGGG  72619        CCAGCCA   AC__
                                AGAGGCAC      TGAG    GGG
                                ||||||||      ||||    |||
                                TCTCCGTG      ACTC    CCC
                                    AA_____    ACCA
GAM3213  TU12B1-TY 3'  AGAGGCACTGGGCTGTAATGTG 72620         CCA  CA   GAC
              G                   AGAGGCAC   GC  TGA   GG
                                ||||||||   ||  |||   ||
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                                TCTCCGTG  CG  ATT  CC
                                    ACC  AC  ACA
GAM3213  LOC123099 3'  AGAGCACCCAGGTCATGGTGGG 72621     G     C_   AGAC
                                AGAG CACCCAG  CATG   GGG
                                |||| |||||||  ||||   |||
                                TCTC GTGGGTC  GTAC   CCC
                                  _     CA   CA__
GAM3213  LOC145988 5'  AGGGGCACCCAGTCCCCGCTGC 72622    A      _ A  AGA
           GGG                    AG GGCACCCAG CC TG  CGGG
                                || |||||||| || ||  ||||
                                TC CCGTGGGTC GG GC  GCCC
                                 C       A  G  GAC
GAM3213  LOC146429 3'  GGTACTCAGCCATGCCCCAGG  72623    C  C      AGA
                                GG AC CAGCCATG  CGGG
                                || || ||||||||  ||||
                                CC TG GTCGGTAC  GTCC
                                 A  A      GGG
GAM3213  LOC147229 5'  AGAGGCTCCAGCCACTGG    72624      AC      GAGAC
                                AGAGGC  CCAGCCAT    GG
                                ||||||  ||||||||    ||
                                TCTCCG  GGTCGGTG    CC
                                   A_      A____
GAM3213  LOC148029 5'  GGCACCATAAACCCAGGTGGG  72625      C__   ATG  AC
                                GGCACC  AGCC  AG  GGG
                                ||||||  ||||  ||  |||
                                CCGTGG  TTGG  TC  CCC
                                   TAT   G__  CA
GAM3213  LOC148077 5'  AGAGGCACCTGGGCGAGGCGGG 72626        CA_  CAT  A
                                AGAGGCACC  GC  GAG CGGG
                                |||||||||  ||  ||| ||||
                                TCTCCGTGG  CG  CTC GCCC
                                     ACC  ___  C
GAM3213  LOC152674 5'  AGCACCCAGCTATGGTCATGGG 72627         C  AGAC_
                                GGCACCCAGC ATG    GGG
                                |||||||||| |||    |||
                                TCGTGGGTCG TAC    CCC
                                     A  CAGTA
GAM3213  LOC153603 5'  AGAGGGACCCAGTGAGACGGG  72628     C    CCA
                                AGAGG ACCCAG  TGAGACGGG
                                ||||| ||||||  |||||||||
                                TCTCC TGGGTC  ACTCTGCCC
                                  C    ___
GAM3213  LOC199680 5'  GAAGCGTCTGGCCATGAGTGG  72629     ACCCA      AC
                                GAGGC   GCCATGAG  GG
                                |||||   ||||||||  ||
                                CTTCG   CGGTACTC  CC
                                  CAGAC      A_
GAM3213  LOC200316 3'  AGGGGCACCCAGGCTGGG   72630   A      CCA  AGAC
                                AG GGCACCCAG  TG   GG
                                || |||||||||  ||   ||
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                                TC CCGTGGGTC   AC    CC
                                 C       CG_  ____
GAM3213  LOC203339 5'  GAGGCACCCCCCGCGAGGCGGG 72631         AG  A    A
                                GAGGCACCC  CC TGAG CGGG
                                |||||||||  || |||| ||||
                                CTCCGTGGG  GG GCTC GCCC
                                     G_  C    C
GAM3213  LOC203339 5'  GAGGCACCCCCCGCGAGGCGGG 72631         AG  A    A
                                GAGGCACCC  CC TGAG CGGG
                                |||||||||  || |||| ||||
                                CTCCGTGGG  GG GCTC GCCC
                                     G_  C    C
GAM3213  LOC220739 3'  GGCACCCATGCTGAGGG     72632         _  CA    AC
                                GGCACCCA GC  TGAG  GG
                                ||||||||  ||  ||||  ||
                                CCGTGGGT CG  ACTC  CC
                                     A  __   __
GAM3213  LOC221254 3'  AGAGGCACTGCAGCCCCTGGG  72633         C_    ATGAGAC
                                AGAGGCAC  CAGCC      GGG
                                ||||||||  |||||      |||
                                TCTCCGTG  GTCGG      CCC
                                     AC    GGA____
GAM3213  LOC254428 3'  GAGGCACCCACCATGAAAC    72634          G
                                GAGGCACCCA CCATGAGAC
                                |||||||||| |||||||||
                                CTCCGTGGGT GGTACTTTG
                                          _
GAM3213  LOC256867 5'  GGTCCCCAGGAGACGGG     72635    CA    CCAT
                                GG  CCCAG    GAGACGGG
                                ||  |||||    ||||||||
                                CC  GGGTC    CTCTGCCC
                                 AG    ____
GAM3213  LOC90520  5'  GAGGCACCCCCCGCGAGGCGGG 72631         AG  A    A
                                GAGGCACCC  CC TGAG CGGG
                                |||||||||  || |||| ||||
                                CTCCGTGGG  GG GCTC GCCC
                                     G_  C    C
GAM3213  LOC90520  3'  GAGGCACCCCCCGCGAGGCGGG 72631         AG  A    A
                                GAGGCACCC  CC TGAG CGGG
                                |||||||||  || |||| ||||
                                CTCCGTGGG  GG GCTC GCCC
                                     G_  C    C
GAM3213  LOC91179  3'  AGAGGCACCAGGCCCTAGCGGG 72605         CA   ATG  A
                                AGAGGCACC  GCC   AG CGGG
                                |||||||||  |||   || ||||
                                TCTCCGTGG  CGG   TC GCCC
                                     TC   GA_  _
GAM3214  SIL      3'  TATGATATAGGATAATG     72638          T  CG
                                TATGATATAG GA  ATG
                                ||||||||||  ||  |||
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                                ATACTATATC CT  TAC
                                      _ AT
GAM3214  ELF2     3'  TATGATATATATATATGTATG  72639        GTGACG
                                TATGATATA     ATGTATG
                                |||||||||     |||||||
                                ATACTATAT     TACATAC
                                    ATATA_
GAM3214  FLJ11565  3'  TGTATAATGTGATGTATG    72640    A      AC
                                TG TATAGTG  GATGTATG
                                || |||||||  ||||||||
                                AC ATATTAC  CTACATAC
                                 _      A_
GAM3214  MGC26954  3'  CCTATGGTATTTGGATGTATG  72641       A   AG  AC
                                TCTATG TAT  TG  GATGTATG
                                |||||| |||  ||  ||||||||
                                GGATAC ATA  AC  CTACATAC
                                   C   A_ __
GAM3214  LOC112448 5'  TCTATGATGTATTGTGAGGTAT 72642        A  G  AC  T
           G                     TCTATGAT TA TG  GA GTATG
                                |||||||| || ||  || |||||
                                AGATACTA AT AC  CT CATAC
                                     C A  A_  C
GAM3214  LOC145725 5'  TCTATGGTGAGGTGTGACATAT 72643       ATATA   AC
           G                     TCTATG    GTG  GATGTATG
                                ||||||    |||  ||||||||
                                AGATAC    CAC  CTGTATAC
                                   CACTC   A_
GAM3214  LOC145732 5'  TCTATGGTGAGGTGTGACATAT 72643       ATATA   AC
           G                     TCTATG    GTG  GATGTATG
                                ||||||    |||  ||||||||
                                AGATAC    CAC  CTGTATAC
                                   CACTC   A_
GAM3214  LOC196957 5'  TCTATGGTGAGGTGTGACATAT 72643       ATATA   AC
           G                     TCTATG    GTG  GATGTATG
                                ||||||    |||  ||||||||
                                AGATAC    CAC  CTGTATAC
                                   CACTC   A_
GAM3214  LOC196961 5'  TCTATGGTGAGGTGTGACATAT 72643       ATATA   AC
           G                     TCTATG    GTG  GATGTATG
                                ||||||    |||  ||||||||
                                AGATAC    CAC  CTGTATAC
                                   CACTC   A_
GAM3214  LOC197138 5'  TCTATGGTGAGGTGTGACATAT 72643       ATATA   AC
           G                     TCTATG    GTG  GATGTATG
                                ||||||    |||  ||||||||
                                AGATAC    CAC  CTGTATAC
                                   CACTC   A_
GAM3214  LOC254826 3'  TGATTCTTGCGATGTATG    72644      ATAG  A
                                TGAT    TG CGATGTATG
                                ||||    || |||||||||
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                                ACTA    AC GCTACATAC
                                  AGA_  _
GAM3215  CACNA1D   3'  CCAGTCTGCCCCTCGC      72647         GCCGT  _
                                TCAGTCTGT     CCC CGC
                                |||||||||     ||| |||
                                GGTCAGACG     GGG GCG
                                     _____  A
GAM3215  CDR2      5'  TCAGCCCCGTTCCCGCCG     72648       TGTG   C
                                TCAGTC    CCGT CCCGCCG
                                ||||||    |||| |||||||
                                AGTCGG    GGCA GGGCGGC
                                    ____   A
GAM3215  CNTN2     3'  TCATGTCTGGTGTTCCTGCCG  72649     _    TGCCG   CC
                                TCA GTCTG     TCC  GCCG
                                ||| |||||     |||  ||||
                                AGT CAGAC     AGG  CGGC
                                  A    CACA_   A_
GAM3215  EVC       5'  TCAGGCTGCCGCCCCGCCG    72650      T  GT    T
                                TCAG CT  GCCG CCCCGCCG
                                |||| ||  |||| ||||||||
                                AGTC GA  CGGC GGGGCGGC
                                  C  __   _
GAM3215  FADD      3'  TCAGCCTGGCTTCCTGC      72651         T  CG   CC
                                TCAGTCTG GC  TCC  GC
                                |||||||| ||  |||  ||
                                AGTCGGAC CG  AGG  CG
                                     _ A_   A_
GAM3215  GADD45G   3'  TCAGACCAAGGTCCCCGCCG   72652      T   TGCC
                                TCAG CTG    GTCCCCGCCG
                                |||| |||    ||||||||||
                                AGTC GGT    CAGGGGCGGC
                                  T   TC__
GAM3215  GCGR      5'  TCGGCTTGGCTCCCCGCCG    72653    A TC  T  CG
                                TC G  TG GC  TCCCCGCCG
                                || |  || ||  |||||||||
                                AG C  AC CG  AGGGGCGGC
                                 C GA  _  __
GAM3215  HYAL1     5'  CCAGTCTGCCCGCTCGTCCCTG 72654          __ _     C
              C                  TCAGTCTGT  GC CGTCCC GC
                                 |||||||||  || |||||| ||
                                 GGTCAGACG  CG GCAGGG CG
                                      GG  A     A
GAM3215  JUN       5'  GCTGGCTGTCGTCCCCGC    72655    T   T  ___
                                G CTG GC   CGTCCCCGC
                                | ||| ||   |||||||||
                                C GAC CG   GCAGGGGCG
                                 _   _  ACA
GAM3215  LPIN2     3'  CCAGAAGCACCCGTCCCCGC   72656      TCT TG  _
                                TCAG   G  CC GTCCCCGC
                                ||||   |  || ||||||||
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                                GGTC   C  GG CAGGGGCG
                                  TT_ GT  G
GAM3215  MMP19    5'  TCAGTCCAGAACTCGTCTTCGT 72657       GT_ _   CC  C
              CG                  TCAGTCT   GC CGTC  CG CG
                                  |||||||   || ||||  || ||
                                  AGTCAGG   TG GCAG  GC GC
                                     TCT  A    AA  A
GAM3215  MMP19    5'  TCAGTCCAGAACTCGTCTTCGT 72657       GT_ _   CC  C
              CG                  TCAGTCT   GC CGTC  CG CG
                                  |||||||   || ||||  || ||
                                  AGTCAGG   TG GCAG  GC GC
                                     TCT  A    AA  A
GAM3215  NEU1     5'  CCGGTCTGGAGGCCCCGCCG   72658    A    TGCC T
                                  TC GTCTG    G CCCCGCCG
                                  || |||||    | ||||||||
                                  GG CAGAC    C GGGGCGGC
                                   C    CTC_ _
GAM3215  SLC5A5   5'  TCGGCCTCCCTGTCCCCGC    72659    A   GTG  _
                                  TC GTCT   CC GTCCCCGC
                                  || ||||   || ||||||||
                                  AG CGGA   GG CAGGGGCG
                                   C   G__  A
GAM3215  TFF1     3'  TCAATCTGTGTTGTGAGCCG   72660         CC  CCCC
                                  TCAGTCTGTG  GT   GCCG
                                  ||||||||||  ||   ||||
                                  AGTTAGACAC  CA   CGGC
                                        AA  CT__
GAM3215  TXNRD1   5'  CAATGCTGTCGTCCCCGCCG   72661     _   GC
                                  CAGT CTGT  CGTCCCCGCCG
                                  |||| ||||  ||||||||||
                                  GTTA GACA  GCAGGGGCGGC
                                    C   __
GAM3215  WW45     5'  GCCGGCCGTCTCCGCCG     72662   T  T     C
                                  G CTG GCCGTC CCGCCG
                                  | ||| |||||| ||||||
                                  C GGC CGGCAG GGCGGC
                                   _  _     A
GAM3215  DJ726C3.2 3'  CAGTCTGCTCCCCGC       72663         GCCG
                                  CAGTCTGT    TCCCCGC
                                  ||||||||    |||||||
                                  GTCAGACG    AGGGGCG
                                              _____
GAM3215  DKFZP434C171 5'  TCAGTCTGTCTATGGTCTCCTG 72664          GCC__  _  C
              C                    TCAGTCTGT     GTC CC GC
                                   |||||||||     ||| || ||
                                   AGTCAGACA     CAG GG CG
                                         GATAC   A  A
GAM3215  DKFZP434L1123 5'  CAGTCTGTGCATCAGTCGC   72665          C   CC_
                                  CAGTCTGTGC GTC   CGC
                                  |||||||||| |||   |||
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                                GTCAGACACG TAG   GCG
                                      _  TCA
GAM3215  DKFZP761I2123 3'  TCTGTGAGCGTGTCCCCGCCG  72666       CC___
                                TCTGTG    GTCCCCGCCG
                                ||||||    ||||||||||
                                AGACAC    CAGGGGCGGC
                                   TCGCA
GAM3215  FLJ00001  3'  CAGCAGGAGGCCGTCCCCGC   72667     CTGT_
                                CAGT    GCCGTCCCCGC
                                ||||    ||||||||||
                                GTCG    CGGCAGGGGCG
                                  TCCTC
GAM3215  FLJ12076  3'  CAGTCTGTGTCCCCTGC     72668        GCC     _
                                CAGTCTGT   GTCCCC GC
                                ||||||||   |||||| ||
                                GTCAGACA   CAGGGG CG
                                     ___     A
GAM3215  FLJ12389  3'  CCAGCCCCACCGTTCCCGC    72669       G     C
                                TCAGTCT TGCCGT CCCGC
                                ||||||| |||||| |||||
                                GGTCGGG GTGGCA GGGCG
                                   _     A
GAM3215  FLJ22378  3'  TCAACCCTGGCTGTCCCCGC   72670     GT  GT  C
                                TCA  CT  GC GTCCCCGC
                                |||  ||  || ||||||||
                                AGT  GG  CG CAGGGGCG
                                  TG  AC  A
GAM3215  FLJ23360  3'  CAGGAGGTGGCTGTCCCCGC   72671     TCT  _ C
                                CAG   GTG C GTCCCCGC
                                |||   ||| | ||||||||
                                GTC   CAC G CAGGGGCG
                                  CTC   C A
GAM3215  FOXO3A    5'  TCAAGTCTGTGCTGTCTTCG   72672     _       C   CC
                                TCA GTCTGTGC GTC  CG
                                ||| |||||||| |||  ||
                                AGT CAGACACG CAG  GC
                                  T       A   AA
GAM3215  KIAA0476  5'  GTCCCCGCGTCCCCGCCG    72673     G   C
                                GTCT TGC GTCCCCGCCG
                                |||| ||| ||||||||||
                                CAGG GCG CAGGGGCGGC
                                  G  _
GAM3215  KIAA0861  3'  CCAGTCTGCGGCCCCCGCCG   72674          CC
                                TCAGTCTGTG  GTCCCCGCCG
                                ||||||||||  ||||||||||
                                GGTCAGACGC  CGGGGGCGGC
                                      __
GAM3215  KIAA1200  5'  TCGCGGCCGTCCCCGCCG    72675    _  T
                                TC TG GCCGTCCCCGCCG
                                || || ||||||||||||
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                                AG GC CGGCAGGGGCGGC
                                 C  _
GAM3215  KIAA1754  5'  CGGTCCCGGTCCCCGCCG    72676   T  G  _
                                C GT CCG TCCCCGCCG
                                | || ||| |||||||||
                                G CA GGC AGGGGCGGC
                                 C  G   C
GAM3215  SLC38A5   3'  CCAGTCTGCAGCCTCTGC    72677         _  G  CCC
                                TCAGTCTGT GCC TC   GC
                                ||||||||| ||| ||   ||
                                GGTCAGACG CGG AG   CG
                                      T   _  A__
GAM3215  STK39     5'  GCCGCCGCCGTCCCCGCCG   72678     TG
                                GTC  TGCCGTCCCCGCCG
                                |||  ||||||||||||||
                                CGG  GCGGCAGGGGCGGC
                                  CG
GAM3215  LOC113251 5'  TCAGCCCAATCGTTCCCGCCG  72679        TGC   C
                                TCAGTCTG   CGT CCCGCCG
                                ||||||||   ||| |||||||
                                AGTCGGGT   GCA GGGCGGC
                                     TA_   A
GAM3215  LOC154428 5'  TCAGCTGTGCCGTCCCCAGC   72680      T          _
                                TCAG CTGTGCCGTCCCC GC
                                |||| |||||||||||| ||
                                AGTC GACACGGCAGGGG CG
                                  _           T
GAM3215  LOC163126 5'  TCAGGCTGTGCCGGGGCCG    72681      T       TCCCC
                                TCAG CTGTGCCG     GCCG
                                |||| ||||||||     ||||
                                AGTC GACACGGC     CGGC
                                  C       CC___
GAM3215  LOC170395 3'  TCAGTCTGTGGCCGAAGGCCCG 72682          _   TC__
                                TCAGTCTGTG CCG    CCCG
                                |||||||||| |||    ||||
                                AGTCAGACAC GGC    GGGC
                                      C   TTCC
GAM3215  LOC204084 5'  TCAGTCTGTACAAAGGTGCCG  72683          CGTCCCC
                                TCAGTCTGTGC       GCCG
                                ||||||||||       ||||
                                AGTCAGACATG       CGGC
                                       TTTCCA_
GAM3215  LOC220758 5'  GCGGCGCTGTCCCCGCCG    72684    CT    C
                                GT  GTGC GTCCCCGCCG
                                ||  |||| ||||||||||
                                CG  CGCG CAGGGGCGGC
                                 C_    A
GAM3216  LOC200933 3'  GGACATTCGGGAATTT      72687       CC    A
                                GGACA  TTTG GGAATTT
                                |||||  |||| |||||||
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                                CCTGT  AAGC CCTTAAA

                                  __  _
GAM3217 BAAT     3' TATCAGGTTTTTACCCT     72690        G
                                TATCAGGT TTTTATTTT
                                |||||||| |||||||||
                                ATAGTCCA AAAATGGGA

                                  _
GAM3217 FLJ11088 3' TATCGGTGTTTTATTTCC    72691      A
                                TATC GGTGTTTTATTTTT
                                |||| ||||||||||||||
                                ATAG CCACAAAATAAAGG

                                 _
GAM3217 FLJ20644 3' TATCAAGTGTTTTATTTAGACC 72692              TTT
             AT                   TATCAGGTGTTTTATTT   CTAT
                                |||||||||||||||||   ||||
                                ATAGTTCACAAAATAAA   GGTA
                                           TCT
GAM3217 KIAA0981 3' AGTTTTTATTTTTTCTAT    72693     G
                                GGT TTTTATTTTTTCTAT
                                ||| |||||||||||||||
                                TCA AAAATAAAAAAGATA

                                 _
GAM3217 KIAA1505 5' GCGTGTTATTTTTTCTAT    72694      T
                                GTGT TTATTTTTTCTAT
                                |||| ||||||||||||
                                CGCA AATAAAAAAGATA
                                  C
GAM3217 KIAA1805 3' TATCAGGTTCATTTTTT     72695        GTT
                                TATCAGGT   TTATTTTTT
                                ||||||||   |||||||||
                                ATAGTCCA   AGTAAAAAA

                                   ___
GAM3217 LOC151194 3' TATCAGGTTTTTTAAATTT   72696        G    TT
                                TATCAGGT TTTTA  TTT
                                |||||||| |||||  |||
                                ATAGTCCA AAAAT  AAA
                                     A    TT
GAM3218 ANKH     3' AGGGAACAAAATACGATG    72699    T        AGCG
                                AG GGAACAAAATAT    GATG
                                || ||||||||||||    ||||
                                TC CCTTGTTTTATG    CTAC

                                 _       ____
GAM3218 ANKH     3' AGGGAACAAAATACGATG    72699    T        AGCG
                                AG GGAACAAAATAT    GATG
                                || ||||||||||||    ||||
                                TC CCTTGTTTTATG    CTAC

                                 _       ____
GAM3218 CHD2     3' AGAGGAACAAAGATAAGGATGA 72700    T      AT   C
                                AG GGAACAAA  ATAG GGATGA
                                || ||||||||  |||| ||||||
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                                TC CCTTGTTT  TATT CCTACT
                                 T       C_   _
GAM3218  D12S2489E 3'  AGTGGGACAAACATAGGATG  72701      A    A   GC
                                AGTGG ACAAA TATA  GGATG
                                ||||| ||||| ||||  |||||
                                TCACC TGTTT GTAT  CCTAC
                                   C    _   __
GAM3218  DDX24     3'  GTGGAGTGAAACACAAGGGTG  72702      ACA      C  A
                                GTGGA   AAATATAG GG TG
                                |||||   |||||||| || ||
                                CACCT   TTTGTGTT CC AC
                                   CAC       C  _
GAM3218  KRT6B     3'  AGTGGAACAGGTATTGATG   72703        AAATA  GCG
                                AGTGGAACA    TA   GATG
                                |||||||||    ||   ||||
                                TCACCTTGT    AT   CTAC
                                      CC___  AA_
GAM3218  MAP4K2    3'  GTGGAACAAAATGGAATGGATG 72704          AT  C
                                GTGGAACAAAAT  AG GGATG
                                ||||||||||||  || |||||
                                CACCTTGTTTTA  TT CCTAC
                                      CC  A
GAM3218  MDM1      3'  AGTGGAACAGAATGGA      72705         A   ATAGC
                                AGTGGAACA AAT     GGA
                                ||||||||| |||     |||
                                TCACCTTGT TTA     CCT
                                      C  ______
GAM3218  PUM1      3'  AGTGAACAAAATATGTGG    72706      G        AGC
                                AGTG AACAAAATAT   GG
                                |||| ||||||||||   ||
                                TCAC TTGTTTTATA   CC
                                  _        CA_
GAM3218  RAD54B    3'  AGTTGAACAAAAGGCAGGGGTG 72707     G       TA   C  A
              A                  AGT GAACAAAA  TAG GG TGA
                                ||| ||||||||  ||| || |||
                                TCA CTTGTTTT  GTC CC ACT
                                  A       CC   _  C
GAM3218  ROR2      3'  AGTGGGCAAAATACACATGG   72708      AA       GC_
                                AGTGG  CAAAATATA   GG
                                |||||  |||||||||   ||
                                TCACC  GTTTTATGT   CC
                                   C_        GTA
GAM3218  SLC19A2   3'  GTGGAACAAAGAGGCTATGA   72709         ATATA  GG
                                GTGGAACAAA    GC  ATGA
                                ||||||||||    ||  ||||
                                CACCTTGTTT    CG  TACT
                                      CTC__   A_
GAM3218  SYN3      3'  GTGGAACAGAATGGGTACAG   72710        A   ATA_
                                GTGGAACA AAT    GCGG
                                |||||||| |||    ||||
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                                CACCTTGT TTA    TGTC
                                    C   CCCA
GAM3218  SYN3     3'  GTGGAACAGAATGGGTACAG   72710        A   ATA_
                                GTGGAACA AAT    GCGG
                                |||||||| |||    ||||
                                CACCTTGT TTA    TGTC
                                    C   CCCA
GAM3218  SYN3     3'  GTGGAACAGAATGGGTACAG   72710        A   ATA_
                                GTGGAACA AAT    GCGG
                                |||||||| |||    ||||
                                CACCTTGT TTA    TGTC
                                    C   CCCA
GAM3218  TGFBR3   3'  GTGGGGTGAATACAACGGGTGA 72711      AACAA        A
                                GTGG    AATATAGCGG TGA
                                ||||    |||||||||| |||
                                CACC    TTATGTTGCC ACT
                                  CCAC_        C
GAM3218  C17orf26 3'  ATGGAGCAGGAGGGGCGGATGA 72712      A  AAATATA
                                GTGGA CA      GCGGATGA
                                ||||| ||      ||||||||
                                TACCT GT      CGCCTACT
                                  C  CCTCCC_
GAM3218  C9orf9   3'  GTGGGGCAAGGAGCAGATG   72713      AA   AATAT
                                GTGG  CAA    AGCGGATG
                                ||||  |||    ||||||||
                                CACC  GTT    TCGTCTAC
                                  CC   CC___
GAM3218  CXYorf1  3'  AGTAGAACAAGATATTTGAAAT 72714         A    AGC
            G                    AGTGGAACAA ATAT   GGATG
                                ||||||||||| ||||   |||||
                                TCATCTTGTT TATA   TTTAC
                                     C    AAC
GAM3218  DDX34    3'  ATGGAACAGAATGAAT      72715        A   ATAGC
                                GTGGAACA AAT    GGAT
                                |||||||| |||    ||||
                                TACCTTGT TTA    CTTA
                                    C   _____
GAM3218  FLJ10159 3'  AGTGAAACAGAATCATGGGTGA 72716         A   A  GC  A
                                AGTGGAACA AAT TA  GG TGA
                                ||||||||| ||| ||  || |||
                                TCACTTTGT TTA GT  CC ACT
                                     C   _  A_  C
GAM3218  FLJ10330 3'  ATGGAACAAAGTAATCAAATGA 72717         A  TAG
                                GTGGAACAAA TA   CGGATGA
                                |||||||||| ||   |||||||
                                TACCTTGTTT AT   GTTTACT
                                     C  TA_
GAM3218  KDELR2   3'  AGTGGAATGCAAGTTTGAGGGA 72718        __   AATAT  C
            TG                   AGTGGAA  CAA    AG GGATG
                                |||||||  |||    || |||||
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                                TCACCTT  GTT    TC CCTAC
                                   AC   CAAAC  _
GAM3218  LOC115265 3'  GTGGGGCAAACTACAAATGA  72719     AA   ATATA
                                GTGG  CAAA    GCGGATGA
                                ||||  ||||    ||||||||
                                CACC  GTTT    TGTTTACT
                                  CC   GA___
GAM3218  LOC130644 3'  AGTGGAAAAAGAGAAACGGGTG 72720       C   ATAT    A
            A                    AGTGGAA AAA   AGCGG TGA
                                ||||||| |||   ||||| |||
                                TCACCTT TTT   TTGCC ACT
                                   _  CTCT    C
GAM3218  LOC170396 3'  AGTGGGACAAAACATGAGGGGT 72721      A       _  C  A
            G                    AGTGG ACAAAATAT AG GG TG
                                ||||| |||||||| || || ||
                                TCACC TGTTTTGTA TC CC AC
                                   C       C  _  C
GAM3218  LOC200093 3'  AGTAGAACAAGATATTTGAAAT 72714        A   AGC
            G                    AGTGGAACAA ATAT   GGATG
                                ||||||||| ||||   |||||
                                TCATCTTGTT TATA   TTTAC
                                     C   AAC
GAM3218  LOC201484 5'  AGTGGAACGTAATAAAAGTGA  72722       AAAAT   C  A
                                AGTGGAAC    ATAG GG TGA
                                ||||||||    |||| || |||
                                TCACCTTG    TATT TC ACT
                                     CAT__   T  _
GAM3218  LOC255102 3'  GTGAATGATATAGCGGGTGA  72723     ACAAA       A
                                GTGGA    ATATAGCGG TGA
                                |||||    ||||||||| |||
                                CACTT    TATATCGCC ACT
                                   AC___       C
GAM3218  LOC255105 3'  GTGAATGATATAGCGGGTGA  72723     ACAAA       A
                                GTGGA    ATATAGCGG TGA
                                |||||    ||||||||| |||
                                CACTT    TATATCGCC ACT
                                   AC___       C
GAM3218  LOC90120  5'  AGTAGAGTAGGAAGCGGATGA  72724      ACAAAATAT
                                AGTGGA       AGCGGATGA
                                ||||||       |||||||||
                                TCATCT       TCGCCTACT
                                   CATCCT___
GAM3218  LOC91040  3'  AGTAGAACAAGATATTTGAAAT 72714        A   AGC
            G                    AGTGGAACAA ATAT   GGATG
                                ||||||||| ||||   |||||
                                TCATCTTGTT TATA   TTTAC
                                     C   AAC
GAM3219  FLJ10706  3'  AAGTATTTTCAGTTGACAAAGC 72727       AC      CT_
                                AAGTATT  CAGTTGAC   GT
                                |||||||  ||||||||   ||
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                                TTCATAA  GTCAACTG   CG
                                   AA       TTT
GAM3219  LOC91149  3'  TATTGCCAGTTGACATATT   72728      A       C
                                TATT CCAGTTGAC TGTT
                                |||| ||||||||| ||||
                                ATAA GGTCAACTG ATAA
                                  C        T
GAM3220  EDAR      3'  TGACACTGGCTGGCCTTAC   72731          ATTA  A  C
                                TGATACTGGC   GG CC TAC
                                ||||||||||   || || |||
                                ACTGTGACCG   CC GG ATG
                                     A___  _  A
GAM3220  SLC1A4    3'  TGTACTGGCAAGAAAGGGCTCT 72732    A       TT__   ACC
            A                    TG TACTGGCA   AGG   CTA
                                || ||||||||   |||   |||
                                AC ATGACCGT   TCC   GAT
                                 _       TCTT   CGA
GAM3220  HARS2     3'  TGATACTGCACTCCT       72733        G   AGGAC
                                TGATACTG CATT    CCT
                                |||||||| ||||    |||
                                ACTATGAC GTGA    GGA
                                     _   _____
GAM3220  OSBPL8    3'  TGATACTGTAAAACAGTTTTAC 72734        GCAT_  GACCC
            A                    TGATACTG    TAG    TACA
                                ||||||||    |||    ||||
                                ACTATGAC    GTC    ATGT
                                    ATTTT   AAA__
GAM3220  LOC158308 3'  TGGCACTGGCATTGCCT     72735    A        AGGAC
                                TG TACTGGCATT    CCT
                                || ||||||||||    |||
                                AC GTGACCGTAA    GGA
                                 C        C____
GAM3220  LOC196872 3'  TGATGTGGCACCACCCCCT   72736     AC      GGA
                                TGAT  TGGCATTA   CCCT
                                ||||  ||||||||   ||||
                                ACTA  ACCGTGGT   GGGA
                                  C_       GG_
GAM3220  LOC202347 3'  TGAACTTCCAGGACCTTAC   72737    T   GGCAT     C
                                TGA ACT    TAGGACC TAC
                                ||| |||    ||||||| |||
                                ACT TGA    GTCCTGG ATG
                                  _  AG___      A
GAM3220  LOC255524 5'  TGGCATTCAGGGCCCTC     72738       _   A   A
                                TGGCAT TAGG CCCT C
                                |||||| |||| |||| |
                                ACCGTA GTCC GGGA G
                                   A   C   C
GAM3220  LOC92539  5'  GATACTGAGGACTCTC      72739       GCATT    C  A
                                GATACTG    AGGAC CT C
                                |||||||    ||||| || |
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                                CTATGAC    TCCTG GA G
                                   _____    A  C
GAM3221 ASGR2    5' GGTGGTGGCCTGGGTAGGATCT 72742       AG  TAC   C
            G                   GGTGGTGG  TG   AGGA CTG
                                |||||||| ||   |||| |||
                                CCACCACC  AC   TCCT GAC
                                    GG  CCA    A
GAM3221 DHCR24   3' TGGTGGCTGGGGTGGGCCT   72743      _  A   TACA  A
                                TGGTGG TGG GTG   GG CCT
                                |||||| ||| |||   || |||
                                ACCACC ACC CAC   CC GGA
                                   G   C  ____ _
GAM3221 DIA1     3' TGGGGTGGGCCCTGGGACCTG  72744    T    A  GTACA
                                TGG GGTGG GT    GGACCTG
                                ||| ||||| ||    |||||||
                                ACC CCACC CG    CCTGGAC
                                 _    _ GGAC_
GAM3221 DISC1    3' TGATGGTGGGGTGAATAGG   72745        A   TAC
                                TGGTGGTGG GTG   AGG
                                ||||||||| |||   |||
                                ACTACCACC CAC   TCC
                                     C   TTA
GAM3221 DNAJB1   3' GGAGGAGTGTACAGGGTCTG   72746    T         AC
                                GG GGAGTGTACAGG  CTG
                                || ||||||||||||  |||
                                CC CCTCACATGTCC  GAC
                                 T          CA
GAM3221 HDAC7A   5' TGGTGTGTCTGCACAGGGCCTG 72747      G  GAG      A
                                TGGTG TG   TGTACAGG CCTG
                                ||||| ||   |||||||| ||||
                                ACCAC AC   ACGTGTCC GGAC
                                   _ AG_       C
GAM3221 HDAC7A   5' TGGTGTGTCTGCACAGGGCCTG 72747      G  GAG      A
                                TGGTG TG   TGTACAGG CCTG
                                ||||| ||   |||||||| ||||
                                ACCAC AC   ACGTGTCC GGAC
                                   _ AG_       C
GAM3221 SLC4A1   3' TGGTGGGGGAGGGTCTAGGGCC 72748      T   T  AC   A
            TG                   TGGTGG GGAG GT  AGG CCTG
                                ||||||| |||| ||  ||| ||||
                                ACCACC CCTC CA  TCC GGAC
                                   C   C  GA   C
GAM3221 SORCS2   3' TGGGGCGGCCGTGTGTGGGGTC 72749    T    A_   ACA  AC
            TG                   TGG GGTGG  GTGT   GG  CTG
                                ||| |||||  ||||   ||  |||
                                ACC CCGCC  CACA   CC  GAC
                                  _    GG   CAC  CA
GAM3221 FLJ14524 3' TGGGGTGGAGCCCGGGGTCTG  72750    T      GTACA  AC
                                TGG GGTGGAGT    GG  CTG
                                ||| ||||||||    ||  |||
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                                ACC CCACCTCG    CC  GAC
                                  _      GGC__  CA
GAM3221  FOXJ1    3'  GGTGGTGGGGTGTCTGTGGACC 72751       A   ACA_
            TG                   GGTGGTGG GTGT   GGACCTG
                                |||||||| ||||   |||||||
                                CCACCACC CACA   CCTGGAC
                                    C   GACA
GAM3221  KIAA0450  3'  TGGTGGCGGGGGGACCAGGGCCT 72752        AGTGTA   A
            G                    TGGTGGTGG     CAGG CCTG
                                |||||||||     |||| ||||
                                ACCACCGCC     GTCC GGAC
                                     CCCTG_   C
GAM3221  KIAA1115  3'  TGGTTGAAAGTGCAGGGTCTG  72753     GGT     TA   AC
                                TGGT  GGAGTG  CAGG  CTG
                                ||||  ||||||  ||||  |||
                                ACCA  TTTCAC  GTCC  GAC
                                  AC_     __   CA
GAM3221  OSBPL5   3'  TGGGGTGGTTCCAGGACCT   72754    T   AGTGTA
                                TGG GGTGG     CAGGACCT
                                ||| |||||     ||||||||
                                ACC CCACC     GTCCTGGA
                                  _    AAG___
GAM3221  PRO0529   3'  TGGTGGTGGGGTTGTCCT    72755        A  _  ACAGGA
                                TGGTGGTGG GT GT     CCT
                                ||||||||| || ||     |||
                                ACCACCACC CA CA     GGA
                                     C  A  _______
GAM3221  PURB     3'  TGGTGGTTGGGTGGAGGCCTG  72756       _  A   TAC   A
                                TGGTGGT GG GTG   AGG CCTG
                                ||||||| || |||   ||| ||||
                                ACCACCA CC CAC   TCC GGAC
                                    A  _   C__   _
GAM3221  LOC116071 3'  TGGTGGTGACAGGGCC      72757        GAGTGT    A
                                TGGTGGTG     ACAGG CC
                                ||||||||     ||||| ||
                                ACCACCAC     TGTCC GG
                                     _______     C
GAM3221  LOC144017 5'  GGGGAGGTGTGTAGGACCTG   72758    T  T  A   AC
                                GG GG GG GTGT  AGGACCTG
                                || || || ||||  ||||||||
                                CC CC CC CACA  TCCTGGAC
                                 _  T  A   __
GAM3221  LOC145693 5'  TGGTGGTGGGGTGCCTGCCTG  72759        A   ACAGGA
                                TGGTGGTGG GTGT     CCTG
                                ||||||||| ||||     ||||
                                ACCACCACC CACG     GGAC
                                     C   GAC___
GAM3221  LOC222031 3'  TGGGGTGGAGTGGATGGATCTG 72760     T       TACA   C
                                TGG GGTGGAGTG    GGA CTG
                                ||| |||||||||    ||| |||
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                                ACC CCACCTCAC    CCT GAC
                                  _       CTA_   A
GAM3221 LOC91069 3' GGTGGTAACATGTGGGGTCTG 72761        A    ACA  AC
                                GGTGGTGG GTGT   GG  CTG
                                |||||||| ||||   ||  |||
                                CCACCATT TACA   CC  GAC
                                     G    C__  CA
GAM3222 CDH5     3' GGGCTGCAGGGGGTTTG     72764      ATTGA  __
                                GGGCT    GTA  GGGTTTG
                                |||||    |||  |||||||
                                CCCGA    CGT  CCCAAAC
                                   ______  CC
GAM3222 DTR      3' TGAGGGGAAGTGGGGTTTG   72765   T   CTATT   A
                                C AGGG    GAGT GGGTTTG
                                | ||||    |||| |||||||
                                A TCCC    TTCA CCCAAAC
                                 C   C____   C
GAM3222 EPM2A    3' CAGGGTTGTTGGGTAGAGAAGG 72766      CTA  A    TTT
                                TAGGG   TTG GTAGGG   GG
                                |||||   ||| ||||||   ||
                                GTCCC   AAC CATCTC   CC
                                   AAC   C     TT_
GAM3222 GATA2    3' GGGCTGCTAAGGGTTTG     72767      A   AGT
                                GGGCT TTG   AGGGTTTG
                                ||||| |||   ||||||||
                                CCCGA GAT   TCCCAAAC
                                   C  ___
GAM3222 NDUFV3   5' CTGGGGCTATTGGCTATCCCCG 72768    A       A  AGGG
            G                    CT GGGCTATTG GT    TTTGG
                                || |||||||| ||    |||||
                                GA CCCGATAAC CG    GGGCC
                                 C       _ ATAG
GAM3222 PIGR     3' CAGGGGTTGTGAGGGTTTG   72769      CTA   AGT
                                TAGGG   TTG   AGGGTTTG
                                |||||   |||   ||||||||
                                GTCCC   AAC   TCCCAAAC
                                   C__   AC_
GAM3222 APELIN   3' GGGCTATTGTGGGACTTGG   72770        AGTA  _
                                GGGCTATTG    GGG TTTGG
                                |||||||||    ||| |||||
                                CCCGATAAC    CCC GAACC
                                     A___   T
GAM3222 CABP5    3' CTGGGGCTTTTGGGCTTTG   72771    A    A  AGTA  G
                                CT GGGCT TTG    GG TTTG
                                || ||||| |||    || ||||
                                GA CCCGA AAC    CC AAAC
                                 C    A  _____ G
GAM3222 CLIPR-59 3' CTGGGGCTCTTGGAATTTG   72772    A    A  AGTA
                                CT GGGCT TTG    GGGTTTG
                                || ||||| |||    |||||||
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                                GA CCCGA AAC    CTTAAAC
                                 C    G  ____
GAM3222  FLJ13397  3'  CAGGGCTGTTGGGACAAATTTG 72773       A   AGTA
              G                   TAGGGCT TTG    GGGTTTGG
                                  ||||||| |||    ||||||||
                                  GTCCCGA AAC    TTTAAACC
                                      C   CCTG
GAM3222  MGC2306   3'  GGGCTGCTAAGGGTTTG     72767      A   AGT
                                  GGGCT TTG   AGGGTTTG
                                  ||||| |||   ||||||||
                                  CCCGA GAT   TCCCAAAC
                                     C  ___
GAM3222  LOC116173 3'  TAGGGCTGGGGTGGGGTTTGG  72774       ATTGA  A
                                  TAGGGCT     GT GGGTTTGG
                                  |||||||     || ||||||||
                                  ATCCCGA     CA CCCAAACC
                                      CCC__  C
GAM3222  LOC199953 3'  CTGGGGCTGTAGGGTGGGG    72775    A    ATTGA     TT
                                  CT GGGCT    GTAGGGT  GG
                                  || |||||    |||||||  ||
                                  GA CCCGA    CATCCCA  CC
                                   C    ______      CC
GAM3222  LOC220549 5'  GGGTCTGGGAAGGGTTTGG    72776     _ ATT  GT
                                  GGG CT   GA  AGGGTTTGG
                                  ||| ||   ||  |||||||||
                                  CCC GA   CT  TCCCAAACC
                                    A  CC_  __
GAM3223  PTPN7    5'  TTGGAGCTGGTTGGGCAGC    72779          A_   AGTTC
                                  TTGGAGCTGGT  GGCG    GC
                                  ||||||||||  ||||    ||
                                  AACCTCGACCA  CCGT    CG
                                        AC   ______
GAM3223  SOLH     3'  TTGGGGCTGGCAGGTGAGCGGG 72780      A       C    TC_
              GC                    TTGG GCTGGTAGG GAGT   GC
                                  |||| |||||||| ||||   ||
                                  AACC CGACCGTCC CTCG   CG
                                    C       A    CCC
GAM3223  TIMM17B   5'  TTGGAGCTGGAGGAAGTGC    72781          T   C    TC
                                  TTGGAGCTGG AGG GAGT  GC
                                  |||||||||| ||| ||||  ||
                                  AACCTCGACC TCC TTCA  CG
                                             _  _   __
GAM3223  DUSP10   5'  TTGGAGCTGGAGGGAGTT    72782          T   C
                                  TTGGAGCTGG AGG GAGTT
                                  |||||||||| ||| |||||
                                  AACCTCGACC TCC CTCAA
                                             _  _
GAM3223  PIG11    3'  TTGGAGCTGGAGGATGCTGGCG 72783       TA__________    AGTT
              AACTCG                 AGCTGG        GGCG   CG
                                  ||||||         ||||   ||
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                                TCGACC         CCGC   GC
                                   TCCTACGAIII   TTGA
GAM3223 PRDM12   3' TTGGGGCTGGAGGGCGAGTCGC 72784     A    TA      _
            GC                   TTGG GCTGG  GGCGAGTT CGC
                                |||| |||||  |||||||| |||
                                AACC CGACC  CCGCTCAG GCG
                                  C    TC       C
GAM3224 DNCI1    3' GGAACCATAGACTTTTGT    72787    C    AA
                                GGA CTGTA  ACTTTTGT
                                ||| |||||  ||||||||
                                CCT GGTAT  TGAAAACA
                                  T    C_
GAM3224 RAD17    5' CTTAAACTGTAAAATTTTTGT  72788       C      C
                                CTTGGAC TGTAAAA TTTTGT
                                ||||||| ||||||| ||||||
                                GAATTTG ACATTTT AAAACA
                                   _     A
GAM3224 APMCF1   3' CTTGGCTCTGCTATTTTGT   72789      AC   AAAAC
                                CTTGG  CTGT    TTTTGT
                                |||||  ||||    ||||||
                                GAACC  GACG    AAAACA
                                   GA   AT___
GAM3224 DKFZP564I122 3' TACTTGGACACCTATTTTTGT  72790        __    AAAAC
                                TACTTGGA  CCTGT    TTTTGT
                                ||||||||  |||||    ||||||
                                ATGAACCT  GGATA    AAAACA
                                    GT    _____
GAM3224 FLJ10724  3' TACTTGGAAGAGCTCAAAACTT 72791        CCTG__
            TTGT                  TACTTGGA     TAAAACTTTTGT
                                ||||||||     ||||||||||||
                                ATGAACCT     GTTTTGAAAACA
                                    TCTCGA
GAM3224 KIAA1634  3' TACTTGGACTGTGAAACT    72792         C   A
                                TACTTGGAC TGT AAACT
                                ||||||||| ||| |||||
                                ATGAACCTG ACA TTTGA
                                    _  C
GAM3224 RRN3     3' TACCTGGACCTCCATTTTTGT  72793          G  AAAC
                                TACTTGGACCT TA   TTTTGT
                                |||||||||| ||   ||||||
                                ATGGACCTGGA GT   AAAACA
                                     G  A___
GAM3224 LOC200132 3' TTGGCAGTAAAACTTTTGT   72794     ACCT
                                TTGG   GTAAAACTTTTGT
                                ||||   ||||||||||||
                                AACC   CATTTTGAAAACA
                                  GT__
GAM3225 ADH5     5' GGGGGCGGGGCGTGGGGGG   72797         GGTA
                                GGGGGCGGGG   GTGGGGGG
                                |||||||||   ||||||||
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                              CCCCCGCCCC   CACCCCCC
                                   G___
GAM3225 ARHGAP6  3' GGAGGGCGGGGGGCTCGGGG  72798   _       AG
                              GG GGGCGGGGGGT  TGGGG
                              || ||||||||||  |||||
                              CC CCCGCCCCCCG  GCCCC
                               T        A_
GAM3225 ARHGAP6  3' GGAGGGCGGGGGGCTCGGGG  72798   _       AG
                              GG GGGCGGGGGGT  TGGGG
                              || ||||||||||  |||||
                              CC CCCGCCCCCCG  GCCCC
                               T        A_
GAM3225 ARIX     5' GGGGGCGGGGGCGGGGG    72799        GTAG
                              GGGGGCGGGGG   TGGGGG
                              ||||||||||   ||||||
                              CCCCCGCCCCC   GCCCCC
                                   _____
GAM3225 ATP2B3   3' GGGGACGGGGGCGGGGG    72800        GTAG
                              GGGGGCGGGGG   TGGGGG
                              ||||||||||   ||||||
                              CCCCTGCCCCC   GCCCCC
                                   _____
GAM3225 BAZ2A    3' GGGGGGTGGGAGGTGGG    72801     CG    TA
                              GGGGG  GGGGG  GTGGG
                              |||||  |||||  |||||
                              CCCCC  CCCTC  CACCC
                                 CA    __
GAM3225 C1orf6   3' TAGGGGTTGGGGGGTAGGG   72802     GC      T
                              TAGGGG  GGGGGGTAG GG
                              ||||||  |||||||| ||
                              ATCCCC  CCCCCCATC CC
                                 AA       _
GAM3225 C5R1     3' GGGGGTGGGGGGGTGGG     72803     C     AGT
                              GGGGG GGGGGGT   GGG
                              ||||| |||||||   |||
                              CCCCC CCCCCCA   CCC
                                 A      ____
GAM3225 CACNA1S  5' CAGGGGGCGGGGCAGGAGTGGG 72804          __ T
           GGG                  TAGGGGGCGGGG  GG AGTGGGGGGG
                              ||||||||||||  || |||||||||
                              GTCCCCCGCCCC  CC TCACCCCCC
                                     GT _
GAM3225 CALM3    3' GGGGTGGGGAGGTGGTGGGGGG 72806     C   _  A      III
           CC                   GGGG GGGG GGT GTGGGGGG   CC
                              |||| |||| ||| ||||||||   ||
                              CCCC CCCC CCA CACCCCCC   GG
                                A   T  C       III
GAM3225 CALM3    3' CAGGGGGTGGGGGGGTGGGG   72805       C     AGT
                              TAGGGGG GGGGGGT   GGGG
                              ||||||| |||||||   ||||
```

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                                GTCCCCC CCCCCCA  CCCC
                                   A     ___
GAM3225  CRABP1   3'  GGGGGGTGGGGGTGGGGG   72807      CG     AGT
                                GGGGG  GGGGGT  GGGGG
                                |||||  ||||||  |||||
                                CCCCC  CCCCCA  CCCCC
                                  CA    ___
GAM3225  DNM1     3'  TAGGGGGTGGGAGGGATGGCGG 72808       C  _  TA_
            GGG                   TAGGGGG GGG GGG  GTGGGGG
                                |||||||  ||| |||  |||||||
                                ATCCCCC CCC CCC  CGCCCCC
                                   A  T  TAC
GAM3225  DRIL1    5'  CAGGGGGCGGGGGCGGGGG   72809          GTAG
                                TAGGGGGCGGGGG   TGGGGG
                                ||||||||||||   ||||||
                                GTCCCCCGCCCCC   GCCCCC
                                      _____
GAM3225  EMX2     5'  GGGGGTGGGGGTGGGGG    72810      C    GTAG
                                GGGGG GGGGG   TGGGGG
                                |||||  |||||   ||||||
                                CCCCC CCCCC   ACCCCC
                                  A    _____
GAM3225  GCGR     3'  GGGGGTGGGGGGGTAGGTGGGGG 72811      C       _
                                GGGGG GGGGGGTAG TGGGGG
                                |||||  |||||||||  ||||||
                                CCCCC CCCCCCATC ACCCCC
                                  A       C
GAM3225  GNB1     3'  GGGGGCGGGGCGGGGG     72812         GGTAG
                                GGGGGCGGGG    TGGGGG
                                ||||||||||    ||||||
                                CCCCCGCCCC    GCCCCC
                                     ______
GAM3225  HOXB5    5'  GGGGGGGGGGTTGGGGG    72813     C      AG
                                GGGG GGGGGGT  TGGGGG
                                ||||  |||||||  ||||||
                                CCCC CCCCCCA  ACCCCC
                                  _     __
GAM3225  HOXC6    3'  GGGGGCGGGGGTGGGGG    72814         GTAG
                                GGGGGCGGGGG   TGGGGG
                                ||||||||||   ||||||
                                CCCCCGCCCCC   ACCCCC
                                     _____
GAM3225  IGSF8    5'  GGGGGCCGGAAGGGTGGGGGG  72815      _    TA
                                GGGGGC GGGGGG  GTGGGGGG
                                ||||||  ||||||  ||||||||
                                CCCCCG CCTTCC  CACCCCCC
                                   G    __
GAM3225  KCNC3    3'  GGGGGGGGGGGTGGGG      72816     C     AGT
                                GGGG GGGGGGT   GGGG
                                ||||  |||||||   ||||
```

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                                CCCC CCCCCCA  CCCC
                                  _    ___
GAM3225 LAG3    5' AGGGGGCAGTGGTGGGGG   72817       GG  AGT
                                AGGGGGCGG GGT  GGGGG
                                ||||||||| |||  |||||
                                TCCCCCGTC CCA  CCCCC
                                   A_  ___
GAM3225 LAG3    5' GGGGGTGGGGGGGTAAAGG   72818     C      T
                                GGGGG GGGGGGTAG GG
                                ||||| ||||||||| ||
                                CCCCC CCCCCCATT CC
                                  A       T
GAM3225 LDB1    5' GGGGGCGGGGGGGCCGCGGGG  72819         A
                                GGGGGCGGGGGGGT GTGGGG
                                |||||||||||| ||||||
                                CCCCCGCCCCCCG CGCCCC
                                      G
GAM3225 MSN     3' GGGGGGTGGTGGCCAGGGGG  72820     CG  G  AGT
                                GGGGG  GG GGT  GGGGG
                                |||||  || |||  |||||
                                CCCCC  CC CCG  CCCCC
                                  CA  A  GT_
GAM3225 MSX2    3' GGGGCGGTGGGGGGGCGGGGG  72821      _   TA
                                GGGGCGG GGGG  GTGGGGG
                                ||||||| ||||  |||||||
                                CCCCGCC CCCC  CGCCCCC
                                   A   C_
GAM3225 NEUROD2 3' GGGGGCTGGGGACAGGGGGG  72822     G   GT  T
                                GGGGGC GGGG  AG GGGGG
                                |||||| ||||  || |||||
                                CCCCCG CCCC  TC CCCCC
                                  A   TG  _
GAM3225 NTSR1   3' TAGGGGGTGGGAGGGGGG   72823      C    TAGT
                                TAGGGGG GGGGGG   GGGG
                                ||||||| ||||||   ||||
                                ATCCCCC CCCTCC   CCCC
                                   A    _____
GAM3225 PDGFB   5' GGGGGCTGGGGAGGGGGG   72824     GG   T  T
                                GGGGGC  GGGG AG GGGGG
                                ||||||  |||| || |||||
                                CCCCCG  CCCC TC CCCCC
                                  A_   _ _
GAM3225 PMM2    3' TAGGGGGCTGGGGGGTGGG   72825      G    AGT
                                TAGGGGGC GGGGGT  GGG
                                |||||||| ||||||  |||
                                ATCCCCCG CCCCCA  CCC
                                   A    ____
GAM3225 RAB3A   3' GGTGGGCGGGGGGGGGGG    72826   _      TAGT
                                GG GGGCGGGGGG   GGGG
                                || ||||||||||   ||||
```

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                                CC CCCGCCCCCC   CCCC
                                 A       ____
GAM3225 RAD21   5' AGGGGGTGGGGAAAGGGGGG  72827      C    T T
                                AGGGGG GGGGGG AG GGGGG
                                |||||| |||||| || |||||
                                TCCCCC CCCCTT TC CCCCC
                                   A    _ _
GAM3225 RCE1    3' GGGGGGTGGGGGGGTGGGG   72828     CG   TA
                                GGGGG GGGGG GTGGGG
                                ||||| ||||| ||||||
                                CCCCC CCCCC CACCCC
                                  CA   __
GAM3225 SGT     3' GGGGGCGGGGGCTGTAAAAGG 72829         GTA
                                GGGGGCGGGGG GTGGGGGG
                                |||||||||| ||||||||
                                CCCCCGCCCCC CATTTTCC
                                      GA_
GAM3225 SHB     3' GGGGGCTGGTTGGTGGGGGG  72830      GG GGTA
                                GGGGGC GG  GTGGGGGG
                                |||||| ||  ||||||||
                                CCCCCG CC  CACCCCCC
                                   A_ AAC_
GAM3225 SLC21A3 3' GGGGTGGGGGAAGGGGGG   72831     C    T T
                                GGGG GGGGGG AG GGGGG
                                |||| |||||| || |||||
                                CCCC CCCCCT TC CCCCC
                                  A    _ _
GAM3225 SOD3    3' GGTGGGTGGGGAGGGGTGGGGG 72832   _  C    TA
          G                      GG GGG GGGGGG GTGGGGGG
                                || ||| |||||| ||||||||
                                CC CCC CCCCTC CACCCCCC
                                 A  A    CC
GAM3225 TCF3    3' GGTGGGGTGGGGTGGGGG   72833   C  _ TA
                                GG GGGG GG GTGGGGG
                                || |||| ||  |||||||
                                CC CCCC CC  CACCCCC
                                 A   A C_
GAM3225 TCF8    3' GGGGGGTGGGGAGGGGG    72834     CG   TAGT
                                GGGGG GGGGG  GGGGG
                                ||||| |||||  |||||
                                CCCCC CCCCT  CCCCC
                                  CA   _____
GAM3225 TFAP4   3' GGGGGCTGGGGGGGTGGG    72835     G    TA
                                GGGGGC GGGGG GTGGG
                                |||||| ||||| |||||
                                CCCCCG CCCCC CACCC
                                   A   __
GAM3225 TOX     3' GGGGGCGGGGGGGTGGTGG   72836          A
                                GGGGGCGGGGGGGT GTGG
                                |||||||||||| ||||
```

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                                CCCCCGCCCCCCA CACC
                                      C
GAM3225 A2BP1    5' GGGGGCTGGGGCGAAGGGGG  72837      GG    AGT
                                GGGGGC GGGGT  GGGGG
                                |||||| |||||  |||||
                                CCCCCG CCCCG  CCCCC
                                   A_    CTT
GAM3225 AK5      3' TAGGAGGTGGTGGTTGGTGGGG 72838      C  GG  A_
             GG                   TAGGGGG GG  GGT  GTGGGGGG
                                |||||||  ||  |||  ||||||||
                                ATCCTCC CC  CCA  CACCCCCC
                                   A  A_  AC
GAM3225 BCL2L1   3' GGGGTGGGGGGTTGGGGG    72839     CG    AG
                                GGGG  GGGGGT  TGGGGG
                                ||||  ||||||  ||||||
                                CCCC  CCCCCA  ACCCCC
                                  A_    __
GAM3225 C20orf149 3' GGGGGGTGGGAGGTGGGG    72840     CG    TA
                                GGGGG  GGGGG  GTGGGG
                                |||||  |||||  ||||||
                                CCCCC  CCCTC  CACCCC
                                   CA    __
GAM3225 C20orf149 3' GGGAGGTGGGGAGGGGG    72841     CG    TAGT
                                GGGGG  GGGGG   GGGGG
                                |||||  |||||   |||||
                                CCCTC  CCCCT   CCCCC
                                   CA    _____
GAM3225 C8orf2   3' GGGGGGTGGGGGGGTGGGGG   72843     CG    TA
                                GGGGG  GGGGG  GTGGGGG
                                |||||  |||||  |||||||
                                CCCCC  CCCCC  CACCCCC
                                   CA    __
GAM3225 C8orf2   3' GGGGGTGGGGGGGTGGGGGG   72842     C     AGT
                                GGGGG GGGGGGT  GGGGGG
                                ||||| |||||||  ||||||
                                CCCCC CCCCCCA  CCCCCC
                                   A     ____
GAM3225 CDK5RAP3 5' GGGGTGCGGGGGGTGGGGG    72844     _     GTAG
                                GGGG GCGGGGG   TGGGGG
                                |||| |||||||   ||||||
                                CCCC CGCCCCC   ACCCCC
                                   A     _____
GAM3225 CLSTN3   3' GGGGGCCGGGGGGAGGGG     72845     G    TAGT
                                GGGGGC GGGGG   GGGGG
                                |||||| |||||   |||||
                                CCCCCG CCCCC   TCCCC
                                   G    _____
GAM3225 DKFZP434G156 5' GGGGGTGGGGGGCTGGCTGCGG 72846      C     AG__  G
             G                   GGGGG GGGGGGT   TG GGG
                                ||||| |||||||   || |||
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                                CCCCC CCCCCCG   AC CCC
                                  A      ACCG  G
GAM3225  DREV1    3'  GGGGGTGGGGGGGAGGGG    72847      C     TAGT
                                GGGGG GGGGGG   GGGGG
                                ||||| ||||||   |||||
                                CCCCC CCCCCC   TCCCC
                                  A    ____
GAM3225  EPB41L1  3'  GGGGTGGGGGGAAGGGG     72848     C     TAGT
                                GGGG GGGGGG   GGGGG
                                |||| ||||||   |||||
                                CCCC CCCCCT   TCCCC
                                  A    ____
GAM3225  FLJ10314 5'  TAGGGGGTGGGGGGTAGACCAG  72849       CG      _ G
                                TAGGGGG  GGGGGTAG T GG
                                |||||||  |||||||| | ||
                                ATCCCCC  CCCCCATC G TC
                                   A_       T G
GAM3225  FLJ12921 3'  GGGGGGTGGGGGGTGGCTTAG   72850      CG     A  GG
                                GGGGG  GGGGGT GT  GG
                                |||||  |||||| ||  ||
                                CCCCC  CCCCCA CG  TC
                                  CA     C  AA
GAM3225  FLJ20079 3'  AGGGGGCGGGGAGGGGGGG    72851          TAGT
                                AGGGGGCGGGGGGG   GGGGG
                                |||||||||||||   |||||
                                TCCCCCGCCCCTC   CCCCC
                                                ____
GAM3225  FLJ21369 3'  GGGGGTGGGGGGGGGGG     72852      C     TAGT
                                GGGGG GGGGGG   GGGG
                                ||||| ||||||   ||||
                                CCCCC CCCCCC   CCCC
                                  A    ____
GAM3225  FLJ22195 5'  GGGGGTGGGGAGGTGAAGAGGG 72853      C   _   AGT
                                GGGGG GGGG GGT   GGGGG
                                ||||| |||| |||   |||||
                                CCCCC CCCC CCA   CTCCC
                                  A   T   CTT
GAM3225  HCNP     3'  AGGGGGTGGGGAGGGGGG    72854      C     TAGT
                                AGGGGG GGGGGG   GGGGG
                                |||||| ||||||   |||||
                                TCCCCC CCCCTC   CCCCC
                                  A    ____
GAM3225  HOMER-2B 3'  GGGGGCGGGGGGGCAGGGGG   72855           T
                                GGGGGCGGGGGGGTAG GGGG
                                |||||||||||||| ||||
                                CCCCCGCCCCCCGTC CCCC
                                               _
GAM3225  HSJ1     3'  GGGGTGTGGGGGGCCTGGGG  72856     GC_     AG
                                GGGG   GGGGGGT  TGGGG
                                ||||   |||||||  |||||
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                                CCCC  CCCCCCG  ACCCC
                                  ACA     G_
GAM3225 HSRNAFEV 5' GGGCGGTGGGAGATGGGGGG  72857      G  TA
                                GGGCGG GGG  GTGGGGGG
                                |||||| |||  ||||||||
                                CCCGCC CCC  TACCCCCC
                                   A  TC
GAM3225 IMP-2    3' GGGGGCGGGAGGCGGGG    72858          AGT
                                GGGGGCGGGGGGT  GGGG
                                ||||||||||||  ||||
                                CCCCCGCCCTCCG  CCCC
                                        ___
GAM3225 KIAA0227 3' GGGGGTGGGGGTGGGG     72859     C    GTAG
                                GGGGG GGGGG   TGGGG
                                ||||| |||||   |||||
                                CCCCC CCCCC   ACCCC
                                   A   ____
GAM3225 KIAA0427 5' GGGGGTGGGGGAAGGGG    72860     C    TAGT
                                GGGGG GGGGGG   GGGGG
                                ||||| ||||||   |||||
                                CCCCC CCCCCT   TCCCC
                                   A    ____
GAM3225 KIAA0450 5' TAGAGGGGTGGGGGGTAGTAGA 72861    _   C
          GGG                   TAG GGGG GGGGGGTAGTGGGGGG
                                ||| |||| ||||||||||||||||
                                ATC CCCC CCCCCCATCATCTCCC
                                  T   A
GAM3225 KIAA0545 3' TAAGGGGTGGGGGTGGGGG  72862      C    GTAG
                                TAGGGGG GGGGG   TGGGGG
                                ||||||| |||||   ||||||
                                ATTCCCC CCCCC   ACCCCC
                                   A   ____
GAM3225 KIAA0964 3' GGGGCGGGGGGAGGGGGG   72863        T  T
                                GGGGCGGGGGG AG GGGGG
                                |||||||||| || |||||
                                CCCCGCCCCCC TC CCCCC
                                      _ _
GAM3225 KIAA1100 5' CAGGGGGCGGGGGAGGGGG  72864          TAGT
                                TAGGGGGCGGGGGG   GGGGG
                                ||||||||||||   |||||
                                GTCCCCCGCCCCCT   CCCCC
                                      ____
GAM3225 KIAA1328 3' GGGGGTGGGGGGGGTGGGG  72865     C    TA
                                GGGGG GGGGGG  GTGGGG
                                ||||| ||||||  ||||||
                                CCCCC CCCCCC  CACCCC
                                   A    __
GAM3225 KIAA1580 5' GGGGGCGGGGGCGGGGG    72799         GTAG
                                GGGGGCGGGGG   TGGGGG
                                ||||||||||   ||||||
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                              CCCCCGCCCCC   GCCCCC
                                    ____
GAM3225 KIAA1644 3' AGAAACTGGGGTGGTGGGGGG 72866   GG GG   A
                              GG GC GGGGT GTGGGGGG
                              || || ||||| ||||||||
                              TC TG CCCCA CACCCCCC
                               TT A_   C
GAM3225 KIAA1706 3' GGGGGCGGGGGAAGGGGG   72867        TAGT
                              GGGGGCGGGGGG  GGGGGG
                              ||||||||||||  ||||||
                              CCCCCGCCCCCT  TCCCCC
                                    _____
GAM3225 KIAA1817 3' GGGGGTGGGGGGCGTGGGGGG 72868    C    A
                              GGGGG GGGGGGT GTGGGGGG
                              ||||| ||||||| ||||||||
                              CCCCC CCCCCCG CACCCCCC
                                 A    _
GAM3225 KIAA1878 3' GGGGGCGGGGGGTGGGG    72869        AGT
                              GGGGGCGGGGGGT  GGGG
                              ||||||||||||  ||||
                              CCCCCGCCCCCCA  CCCC
                                    ___
GAM3225 KIAA1883 3' GGGGGCGGGGGCCCGGGG   72870        G AG
                              GGGGGCGGGGG T TGGGG
                              |||||||||| | |||||
                              CCCCCGCCCCC G GCCCC
                                    _ G_
GAM3225 MGC10902 3' ACGGGGTGTGCTGGTGGGGGG 72871     G A___
                              GCGGGG GT  GTGGGGGG
                              |||||| ||  ||||||||
                              TGCCCC CA  CACCCCCC
                                 A CGAC
GAM3225 MGC10924 3' AGGGGGGTGGGGGTGGGGG  72872     CG   AGT
                              AGGGGG GGGGGT  GGGGG
                              ||||||  ||||||  |||||
                              TCCCCC  CCCCCA  CCCCC
                                 CA   ___
GAM3225 MICAL   5' GAGGGCGGGGGCGGGGG    72873        GTAG
                              GGGGGCGGGGG  TGGGGG
                              ||||||||||  ||||||
                              CTCCCGCCCCC  GCCCCC
                                    _____
GAM3225 NKD2    3' GGGGGGTGGGGGCTGGG    72874     CG   AG
                              GGGGG GGGGGT TGGG
                              |||||  ||||||  ||||
                              CCCCC  CCCCCG  ACCC
                                 CA   __
GAM3225 OAZ     3' AGGGGGTGGGGGGGGTGGGGGG 72875     C   TA
                              AGGGGG GGGGGG  GTGGGGGG
                              |||||| ||||||  ||||||||
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                                TCCCCC CCCCCC  CACCCCCC
                                   A    __
GAM3225  P8      3'  AGGGGTGGGGGGGTGTGG    72876      C     A
                                GGGGG GGGGGGT GTGG
                                ||||| ||||||| ||||
                                TCCCC CCCCCCA CACC
                                   A    _
GAM3225  PF1     5'  GGGGGGAGGGTGATGGGGGG  72877     C     A
                                GGGG GGGGGGT GTGGGGGG
                                |||| ||||||| ||||||||
                                CCCC CCTCCCA TACCCCCC
                                  _     C
GAM3225  PPY2    3'  TAGGGGGCGGGAGGTAGTG   72878
                                TAGGGGGCGGGGGGGTAGTG
                                ||||||||||||||||||
                                ATCCCCCGCCCTCCATCAC

GAM3225  SCAMP5  3'  GGAGGGTGGGGGTGGGGG   72879     CG    AGT
                                GGGGG  GGGGGT  GGGGG
                                |||||  ||||||  |||||
                                CCTCC  CCCCCA  CCCCC
                                   CA    ___
GAM3225  SEMA4B  5'  GGGGGCGGGAGGTGGG     72880          AGT
                                GGGGGCGGGGGGT  GGG
                                ||||||||||||  |||
                                CCCCCGCCCTCCA  CCC
                                          ___
GAM3225  SEMA6A  5'  GGGGGCTGGGGGAGGGGGG  72881      G   T  T
                                GGGGGC GGGGG AG GGGGG
                                ||||||| ||||| || |||||
                                CCCCCG CCCCC TC CCCCC
                                   A    _ _
GAM3225  STMN3   3'  GGGGGCGGGGGTGGGG     72882         GTAG
                                GGGGGCGGGGG   TGGGG
                                ||||||||||   |||||
                                CCCCCGCCCCC   ACCCC
                                          ____
GAM3225  TEX27   3'  AGGGGGCGGGGGGCCCTGGGG 72883          AG
                                AGGGGGCGGGGGGT TGGGG
                                ||||||||||||| |||||
                                TCCCCCGCCCCCCG ACCCC
                                      GG
GAM3225  TUBB5   3'  GGGGGGTGGGGGGTGAAAGG  72884     CG   TA  GG
                                GGGGG GGGGG GTG GGG
                                ||||| ||||| ||| |||
                                CCCCC CCCCC CAC TCC
                                   CA    __  TT
GAM3225  UBP1    3'  GGGGGTGGGGGGTTAGGG   72885      C     AG
                                GGGGG GGGGGGT TGGGG
                                ||||| ||||||| |||||
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                                CCCCC CCCCCCA  ATCCC
                                  A     __
GAM3225  WIRE     3'  GGGGTGGTGGGGTGGGGG    72886     C  _    AGT
                                GGGG GG GGGGT   GGGGG
                                |||| || |||||   |||||
                                CCCC CC CCCCA   CCCCC
                                  A  A   ____
GAM3225  ZNF238   3'  GGGGGTGGAGGGTGGTGGTGGG 72887      C      A___
              GGG                 GGGGG GGGGGGT   GTGGGGGG
                                |||||| |||||||   ||||||||
                                CCCCC CCTCCCA   CACCCCCC
                                  A      CCAC
GAM3225  LOC113230 3'  GGGGGTGGGGGGGAGTGGGG   72888      C     T
                                GGGGG GGGGGG AGTGGGG
                                ||||| |||||| |||||||
                                CCCCC CCCCCC TCACCCC
                                  A     _
GAM3225  LOC144473 3'  GGGGGTGGGGGGGTGGAAATAAG 72889      C      ___
              G                  GGGGG GGGGGGT   AGTGGGG
                                |||||| |||||||   |||||||
                                CCCCC CCCCCCA   TTATTCC
                                  A      CCT
GAM3225  LOC147160 5'  GGTGGGCGGGGAAGGGGG    72890    _       TAGT
                                GG GGGCGGGGGG   GGGGG
                                || ||||||||||   |||||
                                CC CCCGCCCCTT   CCCCC
                                 A       _____
GAM3225  LOC147791 5'  TAGGGGGTGCGGCCTGGGGGG  72891       CGGGG   AG
                                TAGGGGG    GGT  TGGGGGG
                                |||||||    |||  |||||||
                                ATCCCCC    CCG  ACCCCCC
                                    ACG__   G_
GAM3225  LOC148046 3'  GGGGCGGCTGTAGTGGGGGG   72892       GGG
                                GGGGCGG   GTAGTGGGGGG
                                |||||||   ||||||||||
                                CCCCGCC   CATCACCCCCC
                                    GA_
GAM3225  LOC153525 5'  AGGGGGGTGGGGGTGGGGG   72872      CG     AGT
                                AGGGGG  GGGGGT   GGGGG
                                ||||||  ||||||   |||||
                                TCCCCC  CCCCCA   CCCCC
                                   CA     ___
GAM3225  LOC158067 3'  GGGGGCTGGGGGGCAGGGG    72893       G      T
                                GGGGGC GGGGGGTAG GGG
                                |||||| |||||||| |||
                                CCCCCG CCCCCGTC CCC
                                  A      _
GAM3225  LOC197138 3'  AGGGGGGTGGGGGGGTGGG    72894       CG     TA
                                AGGGGG  GGGGG  GTGGG
                                ||||||  |||||  |||||
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                                TCCCCC  CCCCC  CACCC
                                   CA    __
GAM3225  LOC202347 3'  GGGGGCGGGGGGGGGG     72895          TAGT
                                GGGGGCGGGGGG   GGGG
                                ||||||||||||   ||||
                                CCCCCGCCCCCC   CCCC
                                       ____
GAM3225  LOC203636 3'  GGGGGCTGGGGGGGGG     72896       G    TAGT
                                GGGGGC GGGGG   GGGG
                                ||||||| |||||   ||||
                                CCCCCG CCCCC   CCCC
                                   A    ____
GAM3225  LOC221463 3'  GGGGGCGGGGGGGTGGTTCATAG 72897           A  GGG_
                                GGGGGCGGGGGGGT GT   GG
                                |||||||||||| ||   ||
                                CCCCCGCCCCCCA CA   TC
                                       C  AGTA
GAM3225  LOC254219 5'  GGGGGGTGGGGGCGTGGG   72898      CG     A
                                GGGGG  GGGGGT GTGGG
                                |||||  |||||| |||||
                                CCCCC  CCCCCG CACCC
                                   CA    _
GAM3225  LOC257200 3'  GGGAGGTGGGGGGTTGGG   72900     _ C      AG
                                GGG GG GGGGGGT  TGGG
                                ||| || |||||||  ||||
                                CCC CC CCCCCCA  ACCC
                                  T  A     __
GAM3225  LOC257200 3'  GGGGGGTGGGAGGTGGGGGG  72899      CG    TA
                                GGGGG  GGGGG  GTGGGGGG
                                |||||  |||||  ||||||||
                                CCCCC  CCCTC  CACCCCCC
                                   CA    __
GAM3225  LOC89944  3'  GGGGGGTGGGGGGGCGGGGG  72901      CG    TA
                                GGGGG  GGGGG  GTGGGGG
                                |||||  |||||  |||||||
                                CCCCC  CCCCC  CGCCCCC
                                   CA    __
GAM3225  LOC90631  3'  GGGGGCAGGGGGGCAGGGG   72902           T
                                GGGGGCGGGGGGGTAG GGG
                                |||||||||||||| |||
                                CCCCCGTCCCCCGTC CCC
                                       _
GAM3225  LOC91813  5'  GGGGGGTGGGGGGTGGGGG   72807      CG     AGT
                                GGGGG  GGGGGT   GGGGG
                                |||||  ||||||   |||||
                                CCCCC  CCCCCA   CCCCC
                                   CA     ____
GAM3226  IL18RAP   3'  TCACTCGCCGTCTGTCCAG   72905         T    __
                                TCACTCGCC GTCTG  CGG
                                ||||||||| |||||  |||
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                                AGTGAGCGG CAGAC  GTC
                                     _    AG
GAM3226 ZNF266   3' ACTCACCTGTTTGAAAACCC  72906        C  CG
                                ACTCGCCTGT TG  GACCT
                                |||||||||| ||  |||||
                                TGAGTGGACA AC  TTGGG
                                     A  TT
GAM3226 C20orf80 5' TCACCCGCCTGTCTATCCT   72907           CGGA
                                TCACTCGCCTGTCTG   CCT
                                ||||||||||||||   |||
                                AGTGGGCGGACAGAT   GGA
                                      A___
GAM3226 CLONE24945 3' TCATTCGTCTGCCTGCTGAGCT 72908    C  C     G ___
           CCTAT                 TCA TCG CTGTCTGC GA  CCTAT
                                ||| ||| |||||||| ||  |||||
                                AGT AGC GACGGACG CT  GGATA
                                  A  A      A  CGA
GAM3226 KIAA1363 3' GCTGTCTGCAATTACTAT   72909   C      AC_
                                GC TGTCTGCGG  CTAT
                                || |||||||||  ||||
                                CG ACAGACGTT  GATA
                                 _       AAT
GAM3226 LOC152890 5' CGCCGTCTGCGGGCCTA    72910    T      A
                                CGCC GTCTGCGG CCTA
                                |||| |||||||| ||||
                                GCGG CAGACGCC GGAT
                                   _      C
GAM3227 ATP2B2   3' AAGTTCTTCGGTTCCAT    72913        AAC  A
                                AGGTTCTTC  TT CCGT
                                |||||||||  || ||||
                                TTCAAGAAG  AA GGTA
                                     CC_ _
GAM3227 B3GALT3  5' AAGGTTCTTTACACTCGGGGTG 72914        CA_  ACC
                                AAGGTTCTT  ACTT  GTG
                                |||||||||  ||||  |||
                                TTCCAAGAA  TGAG  CAC
                                     ATG   CCC
GAM3227 B3GALT3  5' AAGGTTCTTTACACTCGGGGTG 72914        CA_  ACC
                                AAGGTTCTT  ACTT  GTG
                                |||||||||  ||||  |||
                                TTCCAAGAA  TGAG  CAC
                                     ATG   CCC
GAM3227 B3GALT3  5' AAGGTTCTTTACACTCGGGGTG 72914        CA_  ACC
                                AAGGTTCTT  ACTT  GTG
                                |||||||||  ||||  |||
                                TTCCAAGAA  TGAG  CAC
                                     ATG   CCC
GAM3227 COL16A1  5' GGTTCTCTATCTCTCCGTGACG 72915       CAA  A
                                GGTTCTT  CTT CCGTGACG
                                |||||||  ||| ||||||||
```

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                                CCAAGAG   GAG GGCACTGC
                                    ATA   A
GAM3227  HMGB3    3'  AGGTTCTTGAACTTTCATTGA  72916        C    ACCG
                                AGGTTCTT AACTT    TGA
                                |||||||| |||||    |||
                                TCCAAGAA TTGAA    ACT
                                    C     AGTA
GAM3227  DKFZP434A1315 3'  GGTCCTTCAGTTTAAATGGTG  72917         AC   CC__
                                GGTTCTTCA  TTA    GTG
                                |||||||||  |||    |||
                                CCAGGAAGT  AAT    CAC
                                     CA   TTAC
GAM3227  SLC38A4   5'  AAGGTTCTTCCACTTTGTG   72918         A    ACC
                                AAGGTTCTTC ACTT   GTG
                                |||||||||| ||||   |||
                                TTCCAAGAAG TGAA   CAC
                                     G    A__
GAM3227  LOC149117 3'  GGTTCATCAGTTTACCACACG  72919      T   AC      G
                                GGTTC TCA  TTACCGT ACG
                                ||||| |||  ||||||| |||
                                CCAAG AGT  AATGGTG TGC
                                   T   CA     _
GAM3227  LOC149117 3'  GGTTCATCAGTTTACCACACG  72919      T   AC      G
                                GGTTC TCA  TTACCGT ACG
                                ||||| |||  ||||||| |||
                                CCAAG AGT  AATGGTG TGC
                                   T   CA     _
GAM3227  LOC149117 3'  GGTTCATCAGTTTACCACACG  72919      T   AC      G
                                GGTTC TCA  TTACCGT ACG
                                ||||| |||  ||||||| |||
                                CCAAG AGT  AATGGTG TGC
                                   T   CA     _
GAM3227  LOC149117 3'  GGTTCATCAGTTTACCACACG  72919      T   AC      G
                                GGTTC TCA  TTACCGT ACG
                                ||||| |||  ||||||| |||
                                CCAAG AGT  AATGGTG TGC
                                   T   CA     _
GAM3228  MLLT2    3'  AAAATACCTTACATCCGTT   72922         _  TC
                                AAAATACCT AT  CCGTT
                                ||||||||| ||  |||||
                                TTTTATGGA TG  GGCAA
                                     A  TA
GAM3228  FLJ20700  3'  AAAATACTTCCCGCT      72923        CTA
                                AAAATAC   TTCCCGTT
                                |||||||   ||||||||
                                TTTTATG   AAGGGCGA
                                     ___
GAM3228  FLJ21106  3'  TAAAATACCTGGCCATT     72924          ATTC
                                TAAAATACCT    CCGTT
                                ||||||||||    |||||
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                                ATTTTATGGA   GGTAA
                                     CC__
GAM3228 PP1044   5' CAAAATGCCGAGCCCCGTT   72925      A  TAT
                                TAAAAT CC   TCCCGTT
                                |||||| ||   |||||||
                                GTTTTA GG   GGGGCAA
                                   C  CTC
GAM3228 LOC257407 3' AAAATACCAGTCTCCCTGTT   72926       TA_   _
                                AAAATACC   TTCCC GTT
                                ||||||||   ||||| |||
                                TTTTATGG   GAGGG CAA
                                     TCA    A
GAM3229 EBNA1BP2  3' TAAATCATTATTTATCATAAAA 72929          __
             T                   TAAATTATTATT  TTATAAAAT
                                ||||||||||||  |||||||||
                                ATTTAGTAATAA  AGTATTTTA
                                       AT
GAM3229 TAF9L    3' TATTACCTTATAAAATAAA   72930
                                TATTATTTTATAAAATAAA
                                ||||||||||||||||||
                                ATAATGGAATATTTTATTT

GAM3230 GIPR     3' CTCTGACTTAATTCTA      72933        AAGTA   C
                                CTCTGACT    TAA TCTA
                                ||||||||    ||| ||||
                                GAGACTGA    ATT AGAT
                                     _____  A
GAM3230 FLJ11151 3' TACGTTGACTAAACTCT    72934    TC     GTATA
                                TAC  TGACTAA    ACTCT
                                |||  |||||||    |||||
                                ATG  ACTGATT    TGAGA
                                  CA     _____
GAM3230 GAB1     3' CTTTGACTTCAACTCTA     72935    C    AAGTA
                                CT TGACT    TAACTCTA
                                || |||||    ||||||||
                                GA ACTGA    GTTGAGAT
                                 A    A____
GAM3230 KIAA0229 3' CTCTGACTGCAGCTCT     72936       AA   TAA
                                CTCTGACT  GTA   CTCT
                                ||||||||  |||   ||||
                                GAGACTGA  CGT   GAGA
                                     __   C__
GAM3230 KIAA1615 3' TCTGACTAGGAGTGCTAACTCT 72937        __   A_
                                TCTGACTA  AGT  TAACTCT
                                ||||||||  |||  |||||||
                                AGACTGAT  TCA  ATTGAGA
                                     CC   CG
GAM3230 MGC14433 3' TACTCTGATAATACAGCT    72938       CTA     A
                                TACTCTGA   AGTATA CT
                                ||||||||   |||||| ||
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                                ATGAGACT  TTATGT GA
                                    A__    C
GAM3230 MGC2488  3' TGACCAAGGTGTAACTCT   72939       TA_
                                TGACTAAG  TAACTCT
                                ||||||||  |||||||
                                ACTGGTTC  ATTGAGA
                                    CAC
GAM3230 TNKS2    3' TACTCTGATTAACTCT     72940       CTAAGTA
                                TACTCTGA    TAACTCT
                                ||||||||    |||||||
                                ATGAGACT    ATTGAGA
                                    A______
GAM3231 TIMP3    3' CCATCTTGGGGTAGTCCAGAT 72943       A__ __
                                TCATCTTGG  AG CAGAT
                                |||||||||  ||  |||||
                                GGTAGAACC  TC GTCTA
                                     CCA  AG
GAM3231 UBE2E3   5' TATCTCTTGGAAAACTCG   72944    A      CAGA
                                TATC TCTTGGAAG   TCG
                                |||| |||||||||   |||
                                ATAG AGAACCTTT   AGC
                                  _      TG__
GAM3231 AKL3L    3' TCATCTTGAAAGATC      72945        AGC
                                TCATCTTGGA  AGATC
                                ||||||||||  |||||
                                AGTAGAACTT  TCTAG
                                     ___
GAM3231 APOL3    3' CATCGAACCGGGGGCAGGTCG 72946    ___   AA   A
                                CATC  TTGG GCAG TCG
                                ||||  ||||  |||| |||
                                GTAG  GGCC CGTC AGC
                                  CTT   CC   C
GAM3231 MGC20460 5' TCATCTTAGGGCATCAGGTCG 72947       AAG__  A
                                TCATCTTGG   CAG TCG
                                |||||||||   ||| |||
                                AGTAGAATC   GTC AGC
                                     CCGTA  C
GAM3231 LOC168283 5' ATCCGTTCTGGGAGCAGATCG 72948   ATC_   A
                                ATC   TTGG AGCAGATCG
                                |||   |||| |||||||||
                                TAG   GACC TCGTCTAGC
                                  GCAA   C
GAM3232 ABCE1    3' AAGACTGAAAACAAACAA   72951      AAA
                                AGGATT  AAAACAAACAA
                                ||||||  ||||||||||
                                TTCTGA  TTTTGTTTGTT
                                   C__
GAM3232 CD9      3' AACAAGCAAAAACAAACAA  72952      ATTAA
                                AACAGG   AAAAACAAACAA
                                ||||||   ||||||||||
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                                TTGTTC    TTTTTGTTTGTT
                                   G____
GAM3232  CD9     3'  GGCAAAAAAACAAACAAC    72953    AT
                                GG  TAAAAAAACAAACAAC
                                ||  ||||||||||||||||
                                CC  GTTTTTTTGTTTGTTG
                                 __
GAM3232  DAPK1   3'  AAAAAGAAAAAAACAAACAAC  72954     TT
                                AGGA  AAAAAAACAAACAAC
                                ||||  ||||||||||||||
                                TTTT  TTTTTTTGTTTGTTG
                                  TC
GAM3232  EPHB2   3'  ACAAGAAAAGAACAAACAAC   72955      TTA   A
                                ACAGGA   AAA AACAAACAAC
                                ||||||   ||| ||||||||||
                                TGTTCT   TTT TTGTTTGTTG
                                   ___   C
GAM3232  FOXI1   3'  AGAAAATAAGAAAACAAACAAC 72956     T_   A
                                AGGA  TAA AAAACAAACAAC
                                ||||  ||| ||||||||||||
                                TCTT  ATT TTTTGTTTGTTG
                                  TT   C
GAM3232  FRDA    3'  CAGGAATAAAAAAAATAAACAA 72957      T      C_
            C                    CAGGA TAAAAAAA  AAACAAC
                                ||||| ||||||||  |||||||
                                GTCCT ATTTTTTT  TTTGTTG
                                   T       TA
GAM3232  IL22RA2  3'  ACAGGATTAAAAACTAAAC   72958          AAC
                                ACAGGATTAAAAA   AAAC
                                ||||||||||||   ||||
                                TGTCCTAATTTTT   TTTG
                                       GA_
GAM3232  ILF1    3'  CAACACAAAGAAACAAACAAC  72959    G  T   A
                                CAG AT AAA AAACAAACAAC
                                ||| || ||| ||||||||||
                                GTT TG TTT TTTGTTTGTTG
                                  G  _   C
GAM3232  LIFR    3'  AGATGATAAAAAAACAAACAAC  72960     TA_
                                GGAT   AAAAAACAAACAAC
                                ||||   ||||||||||||||
                                TCTA   TTTTTTGTTTGTTG
                                  CTA
GAM3232  NEK2    3'  ACAGGATTAAAAGCCCAA    72961          AAA
                                ACAGGATTAAAA   CAA
                                ||||||||||||   |||
                                TGTCCTAATTTT   GTT
                                       CGG
GAM3232  NEK4    3'  AACAGTAATCAAACAAACAAC  72962      GATTAAAA
                                AACAG       AAACAAACAAC
                                |||||       ||||||||||
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                                TTGTC      TTTGTTTGTTG
                                  ATTAG___
GAM3232  NUP153   3'  ACAAGACTAAACAAACAA    72963         AAAA
                                ACAGGATTAA   ACAAACAA
                                ||||||||||   ||||||||
                                TGTTCTGATT   TGTTTGTT
                                          ____
GAM3232  PPP1CB   3'  GGATCTAAAAACAAACAAC   72964      AA
                                GGATT AAAAACAAACAAC
                                |||||  ||||||||||||
                                CCTAG  TTTTTGTTTGTTG
                                  A_
GAM3232  PTMA     3'  AACAGGCCAAAAAAAATAAACA 72965       ATT      C
                                AACAGG   AAAAAAA AAACA
                                ||||||   ||||||| |||||
                                TTGTCC   TTTTTTT TTTGT
                                   GGT      A
GAM3232  RNPEP    3'  AACAGGAATTTGGGAACAAACA 72966        TTAAAAA
            A                    AACAGGA      AACAAACAA
                                |||||||      |||||||||
                                TTGTCCT      TTGTTTGTT
                                   TAAACCC
GAM3232  SMCY     3'  AGGATTTAAGAAACAAAC    72967       A  A
                                AGGATT AA AAACAAAC
                                |||||| || ||||||||
                                TCCTAA TT TTTGTTTG
                                   A  C
GAM3232  SORBS1   3'  AACAGGATTTGAAAGAACAA   72968        AA  _
                                AACAGGATT  AAA AACAA
                                |||||||||  ||| |||||
                                TTGTCCTAA  TTT TTGTT
                                     AC   C
GAM3232  SRGAP2   3'  ACAGGATTAAAAAAAAAAA    72969            C
                                ACAGGATTAAAAAAA AAA
                                ||||||||||||||| |||
                                TGTCCTAATTTTTTT TTT
                                          T
GAM3232  AGMAT    3'  AACAGCCAAAAACAAACA     72970      GATTAA
                                AACAG     AAAAACAAACA
                                |||||     ||||||||||
                                TTGTC     TTTTTGTTTGT
                                  GG____
GAM3232  CGI-142  3'  AACAGGATTGATAAAACCCAAA 72971        A__    AA
            C                    AACAGGATT   AAAA  CAAAC
                                |||||||||   ||||  |||||
                                TTGTCCTAA   TTTT  GTTTG
                                     CTA    GG
GAM3232  CITED2   3'  AGGAGTAAAAACAAACAAC   72972      TTAA
                                AGGA   AAAAACAAACAAC
                                ||||   ||||||||||||
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                                TCCT    TTTTTGTTTGTTG
                                  CA__
GAM3232  FLJ10199  3' AGAAGCAAAACAAACAAC    72973     TTAAA
                                GGA     AAAACAAACAAC
                                |||     ||||||||||||
                                TCT     TTTTGTTTGTTG
                                  TCG__
GAM3232  FLJ10244  3' AACAATGAAAAACAAACAAC   72974      GATTAA
                                AACAG     AAAAACAAACAAC
                                |||||     ||||||||||||
                                TTGTT     TTTTTGTTTGTTG
                                  AC____
GAM3232  FLJ11011  3' ACAGGATTAAAGGACAA     72975          AAA
                                ACAGGATTAAA   ACAA
                                ||||||||||   ||||
                                TGTCCTAATTT   TGTT
                                      CC_
GAM3232  FLJ13782  3' CAGGACTGGCAAACAAACA    72976        AAAA
                                CAGGATT    AAACAAACA
                                |||||||    |||||||||
                                GTCCTGA    TTTGTTTGT
                                   CCG_
GAM3232  FLJ20281  3' ACAGGTTAGGGAACAAACAAC  72977       A   AAAA
                                ACAGG TTA    AACAAACAAC
                                ||||| |||    ||||||||||
                                TGTCC AAT    TTGTTTGTTG
                                  _  CCC_
GAM3232  FLJ21079  3' CAAAATAAAAAAACAAACAAC  72978       T
                                CAGGAT AAAAAAACAAACAAC
                                |||||| ||||||||||||||||
                                GTTTTA TTTTTTTGTTTGTTG
                                  _
GAM3232  FLJ21106  3' AAAATCCAGAAAACAAACAAC  72979        AAA
                                AGGATT   AAAACAAACAAC
                                ||||||   ||||||||||||
                                TTTTAG   TTTTGTTTGTTG
                                   GTC
GAM3232  FLJ22195  5' AGGATGAGGAGGAACAAACAAC 72980       TAAAAA_
                                AGGAT      AACAAACAAC
                                |||||      ||||||||||
                                TCCTA      TTGTTTGTTG
                                  CTCCTCC
GAM3232  KIAA0317  3' CAGGATTAGAAAAAAAAAAC   72981         _     C
                                CAGGATTA AAAAAA AAAC
                                |||||||| |||||| ||||
                                GTCCTAAT TTTTTT TTTG
                                     C     T
GAM3232  KIAA0354  3' ACAGCACATAGGGAAACAAACA 72982      G  TAAAA_
           A                     ACAG AT     AAACAAACAA
                                ||||  ||     ||||||||||
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                                TGTC TG     TTTGTTTGTT
                                  G  TATCCC
GAM3232  KIAA0923  3'  ACAGGGAAGTCCAAACAAACAA 72983      ATTAAAA
                C                  ACAGG      AAACAAACAAC
                                   |||||      ||||||||||
                                   TGTCC      TTTGTTTGTTG
                                     CTTCAGG
GAM3232  KIAA1046  3'  AGGATTTTAAACAAACAA    72984       AAAA
                                   AGGATT    AAACAAACAA
                                   ||||||    ||||||||||
                                   TCCTAA    TTTGTTTGTT
                                     AA__
GAM3232  KIAA1238  3'  AACAAAAGGAAAAAAACAAACA 72985       TT
                AC                   AACAGGA  AAAAAAACAAACAAC
                                   |||||||  ||||||||||||||
                                   TTGTTTT  TTTTTTTGTTTGTTG
                                      CC
GAM3232  KIAA1553  3'  AAAATCCAAAAAACAAACAAC  72986       A
                                   AGGATT AAAAAACAAACAAC
                                   |||||| ||||||||||||||
                                   TTTTAG TTTTTTGTTTGTTG
                                      G
GAM3232  MGC10471  3'  CAGGACCAAATAAATAAC    72987         A   CA
                                   CAGGATTAAA AAA  AAC
                                   |||||||||| |||  |||
                                   GTCCTGGTTT TTT  TTG
                                        A   A_
GAM3232  MGC3038   3'  AACAGGATTTAGGAAACAGAC  72988        AAAA    A
                                   AACAGGATT    AAACA AC
                                   |||||||||    ||||| ||
                                   TTGTCCTAA    TTTGT TG
                                        ATCC    C
GAM3232  NR6A1     3'  AGGTTAAAAAAACAGACAA    72989     A        A
                                   AGG TTAAAAAAACA ACAA
                                   ||| |||||||||| ||||
                                   TCC AATTTTTTTGT TGTT
                                     _         C
GAM3232  NR6A1     3'  AGGTTAAAAAAACAGACAA    72989     A        A
                                   AGG TTAAAAAAACA ACAA
                                   ||| |||||||||| ||||
                                   TCC AATTTTTTTGT TGTT
                                     _         C
GAM3232  NR6A1     3'  AGGTTAAAAAAACAGACAA    72989     A        A
                                   AGG TTAAAAAAACA ACAA
                                   ||| |||||||||| ||||
                                   TCC AATTTTTTTGT TGTT
                                     _         C
GAM3232  PDGFC     3'  AACAAGATTAGAAAAGCCAACA 72990         A   ACA
                                   AACAGGATTA AAAA   AACA
                                   |||||||||| ||||   ||||
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                                TTGTTCTAAT TTTT   TTGT
                                      C    CGG
GAM3232  RNF38    3'  AACAGGGGGACAAACAAACA   72991       ATTAAAA
                                AACAGG      AAACAAACA
                                ||||||      |||||||||
                                TTGTCC      TTTGTTTGT
                                   CCCTG__
GAM3232  RTP801   3'  AACAAGATACAAAACAAACAAC 72992        TAAA
                                AACAGGAT    AAAACAAACAAC
                                ||||||||    ||||||||||||
                                TTGTTCTA    TTTTGTTTGTTG
                                     TG__
GAM3232  sdolf    5'  AACAGGATCAGAGCAAACA    72993         AAAAAA
                                AACAGGATTA     CAAACA
                                ||||||||||     ||||||
                                TTGTCCTAGT     GTTTGT
                                      CTC___
GAM3232  TNRC6    3'  ACAGGAATAGAAAAACAA     72994       T  A
                                ACAGGA TA AAAAACAA
                                |||||| || ||||||||
                                TGTCCT AT TTTTTGTT
                                   T  C
GAM3232  USP25    3'  AACAGGACTGGAAAACCAA    72995        AA   A
                                AACAGGATT  AAAA CAA
                                |||||||||  |||| |||
                                TTGTCCTGA  TTTT GTT
                                      CC    G
GAM3232  ZAK      3'  CAGGGTTAAAACAAAAAACAAC 72996      A     A  C
                                CAGG TTAAAA AA AAACAAC
                                |||| |||||| || |||||||
                                GTCC AATTTT TT TTTGTTG
                                  C     G  T
GAM3232  ZNF297B  3'  AACAGGATTTGGGAAAGCAAAC 72997         AAA_   A
                                AACAGGATT    AAA CAAAC
                                |||||||||    ||| |||||
                                TTGTCCTAA    TTT GTTTG
                                      ACCC   C
GAM3232  ZNF297B  3'  AACAGGATTTGGGAAAGCAAAC 72997         AAA_   A
                                AACAGGATT    AAA CAAAC
                                |||||||||    ||| |||||
                                TTGTCCTAA    TTT GTTTG
                                      ACCC   C
GAM3232  LOC122609 3'  AACAGGATTGGGTGGCTTAAAC 72998         AAAAAAAC_
            AAC                   AACAGGATT        AAACAAC
                                |||||||||        |||||||
                                TTGTCCTAA        TTTGTTG
                                      CCCACCGAA
GAM3232  LOC145123 3'  AACAGGCCAAAAAAAATAAACA 72965       ATT      C
                                AACAGG   AAAAAAA AAACA
                                ||||||   ||||||| |||||
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                                TTGTCC   TTTTTTT TTTGT
                                   GGT      A
GAM3232  LOC146050 3'  CAGGAAAAACAAGGAACAAACA 72999      TT  AAA__
                                CAGGA  AA     AACAAACA
                                |||||  ||    ||||||||
                                GTCCT  TT    TTGTTTGT
                                   TT  GTTCC
GAM3232  LOC149670 3'  CAGGAGCAGGGAAACAAACAA  73000      T  AAA
                                CAGGA TA   AAACAAACAA
                                |||||  ||   ||||||||||
                                GTCCT GT   TTTGTTTGTT
                                   C  CCC
GAM3232  LOC158332 3'  AACTGAACAAAGGGAACAAACA 73001     A   TAAAAA
            AC                    AAC GGAT     AACAAACAAC
                                |||  ||||     ||||||||||
                                TTG CTTG     TTGTTTGTTG
                                  A   TTTCCC
GAM3232  LOC196411 3'  GGCAATAAAAAAACAAGCA   73002    AT_        A
                                GG   TAAAAAAACAA CA
                                ||   ||||||||||| ||
                                CC   ATTTTTTTGTT GT
                                 GTT         C
GAM3232  LOC253228 3'  ACAGGAATAATAAAAACAAACA 73003       T  _
            AC                    ACAGGA TAA AAAAACAAACAAC
                                ||||||  ||| ||||||||||||
                                TGTCCT ATT TTTTTGTTTGTTG
                                   T  A
GAM3232  LOC255855 5'  ACAAGAAAAAAACAAACAAC   73004       TTA
                                ACAGGA   AAAAAACAAACAAC
                                ||||||   ||||||||||||||
                                TGTTCT   TTTTTTGTTTGTTG
                                   ___
GAM3232  LOC91565  3'  AACTCAACAAAAAAAGACAAAC 73005     AG   T     _
            AAC                    AAC  GAT AAAAAA ACAAACAAC
                                |||  ||| |||||| |||||||||
                                TTG  TTG TTTTTT TGTTTGTTG
                                  AG   T     C
GAM3232  LOC92876  5'  ACAAGAAAAAAACAAACAAC   73004       TTA
                                ACAGGA   AAAAAACAAACAAC
                                ||||||   ||||||||||||||
                                TGTTCT   TTTTTTGTTTGTTG
                                   ___
GAM3233  CALD1     3'  TCAACATAAATACAAAAGAGCG 73008          G    AAAA
            A                     TTAACATAAATA AAAA    CGA
                                ||||||||||| ||||    |||
                                AGTTGTATTTAT TTTT    GCT
                                       G    CTC_
GAM3234  BAIAP3    3'  CCAGGGCCGGGGCTGGCA    73011      A  CCCAT      AA
                                TCAG GT     CGGGGCT  CA
                                ||||  ||     |||||||  ||
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                                GGTC CG    GCCCCGA  GT
                                  C _____      CC
GAM3234  GEMIN5   5'  TCACAGTCCCATCGTCGGAGCT 73012     G     ___
                                TCA AGTCCCA   TCGGGGCT
                                ||| |||||||   ||||||||
                                AGT TCAGGGT   AGCCTCGA
                                  G      AGC
GAM3234  GNL1     5'  AGAGGAGGCGGGGCTAGCAG   73013     TCCCAT      A
                                AGAG     CGGGGCTA CAG
                                ||||     |||||||| |||
                                TCTC     GCCCCGAT GTC
                                  CTCC__       C
GAM3234  GNL1     5'  AGAGGAGGCGGGGCTAGCAG   73013     TCCCAT      A
                                AGAG     CGGGGCTA CAG
                                ||||     |||||||| |||
                                TCTC     GCCCCGAT GTC
                                  CTCC__       C
GAM3234  HMGB2    5'  TCAGAGTCCCGCAGAGC     73014         AT
                                TCAGAGTCCC  CGGGGC
                                ||||||||||  ||||||
                                AGTCTCAGGG  GTCTCG
                                      C_
GAM3234  HNF4A    3'  TCAAAGTCTTGTTATCAGAGC  73015        CC___
                                TCAGAGTC    ATCGGGGC
                                ||||||||    ||||||||
                                AGTTTCAG    TAGTCTCG
                                     AACAA
GAM3234  NEK4     3'  AGAGTCCCTCGAATACA      73016        A    GCTA
                                AGAGTCCC TCGGG    ACA
                                |||||||| |||||    |||
                                TCTCAGGG AGCTT    TGT
                                     _    A___
GAM3234  SNCAIP   5'  TCAGAGCTCTTACCTGGTGG   73017       _  CC   _ _
                                TCAGAG TC  ATC GG GG
                                |||||| ||  ||| || ||
                                AGTCTC AG  TGG CC CC
                                   G  AA   A  A
GAM3234  SYNGR1   3'  AGGGGTCTCCCAGGGCTAACAG 73018    A_   _ AT
                                AG  GTC CC  CGGGGCTAACAG
                                ||  ||| ||  ||||||||||||
                                TC  CAG GG  GTCCCGATTGTC
                                 CC   A  __
GAM3234  C3IP1    5'  GAGTGCGGCGCGGGGCTAGCAG 73019      CCCAT_      A
                                GAGT     CGGGGCTA CAG
                                ||||     |||||||| |||
                                CTCA     GCCCCGAT GTC
                                  CGCCGC       C
GAM3234  CDT6     3'  TCAGAGTCTGATCGCCA     73020        CC   GGG
                                TCAGAGTC  ATC   GCTA
                                ||||||||  |||   ||||
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                                AGTCTCAG  TAG   CGGT
                                    AC  ___
GAM3234  FLJ20232  3'  TCAGAGTCTTGCTACAAACAG  73021       CCATCGGG  T
                                TCAGAGTC       GC AACAG
                                ||||||||       || |||||
                                AGTCTCAG       TG TTGTC
                                    AACGA___  T
GAM3234  FLJ23468  5'  TCAGAGTCATCACTAA      73022        CC   GGG
                                TCAGAGTC  ATC   GCTAA
                                ||||||||  |||   |||||
                                AGTCTCAG  TAG   TGATT
                                    __  ___
GAM3234  KLF12     3'  TCAGAGTCCACACACAATTGAC 73023         _  _  GGCTA
           AG                     TCAGAGTCC CAT CGG    ACAG
                                ||||||||| ||| |||    ||||
                                AGTCTCAGG GTG GTT    TGTC
                                    T   T   AAC__
GAM3234  LIN-7-C   3'  TCACAGTCCCACACTAA     73024     G      CGGG
                                TCA AGTCCCAT    GCTAA
                                ||| ||||||||    |||||
                                AGT TCAGGGTG    TGATT
                                  G      _____
GAM3234  MDN1      3'  TCAGAGTCCCATGCTCCTGGC  73025          ___  GG
                                TCAGAGTCCCA   TC  GGC
                                ||||||||||   ||  |||
                                AGTCTCAGGGT   AG  CCG
                                      ACG  GA
GAM3234  TREX2     5'  TCAGGGCCTGGGCGCTGGCAG  73026     A   CCATC  _  AA
                                TCAG GTC    GGG GCT  CAG
                                |||| |||    ||| |||  |||
                                AGTC CGG    CCC CGA  GTC
                                  C   A_____   G   CC
GAM3234  TREX2     5'  TCAGGGCCTGGGCGCTGGCAG  73026     A   CCATC  _  AA
                                TCAG GTC    GGG GCT  CAG
                                |||| |||    ||| |||  |||
                                AGTC CGG    CCC CGA  GTC
                                  C   A_____   G   CC
GAM3234  LOC133923 5'  TCAGAGCTTCATTGCAGGAC   73027       CC   __
                                TCAGAGT  CAT  CGGGGC
                                |||||||  |||  ||||||
                                AGTCTCG  GTA  GTCCTG
                                    AA   AC
GAM3234  LOC145748 5'  TCGGAGTCCCACACACAACAG  73028    A       CGGG  _
                                TC GAGTCCCAT    GC TAACAG
                                || |||||||||    || ||||||
                                AG CTCAGGGTG    TG GTTGTC
                                  C        _____  T
GAM3234  LOC146957 3'  GAGTCCCACTGGCTGTCAG    73029        CGG    AA
                                GAGTCCCAT   GGCT  CAG
                                |||||||||   ||||  |||
```

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                                CTCAGGGTG   CCGA  GTC
                                    A__    CA
GAM3234  LOC147136 3'  TCAGGGCCGAGGCTGACA    73030      A  CCCAT      A
                                TCAG GT     CGGGGCT ACA
                                |||| ||     ||||||| |||
                                AGTC CG     GCTCCGA TGT
                                  C _____       C
GAM3234  LOC155376 5'  TCAGAGTCCAGTCTGGTGG    73031         CA  _  _
                                TCAGAGTCC  TC GG GG
                                |||||||||  || || ||
                                AGTCTCAGG  AG CC CC
                                    TC  A  A
GAM3234  LOC158402 5'  AGAGTCTCCAAGGCTGACAG   73032       _   TCG     A
                                AGAGTC CCA   GGGCT ACAG
                                |||||| |||   ||||| ||||
                                TCTCAG GGT   TCCGA TGTC
                                   A   ___    C
GAM3234  LOC253532 5'  TCAGAGTCCAGTCTGGTGG    73031         CA  _  _
                                TCAGAGTCC  TC GG GG
                                |||||||||  || || ||
                                AGTCTCAGG  AG CC CC
                                    TC  A  A
GAM3234  LOC254875 5'  TCAGAGTCCAGTCTGGTGG    73031         CA  _  _
                                TCAGAGTCC  TC GG GG
                                |||||||||  || || ||
                                AGTCTCAGG  AG CC CC
                                    TC  A  A
GAM3234  LOC255480 3'  TCAGAGTCTCTTGACAACA    73033        CCA  GG   T
                                TCAGAGTC   TC  GGC AACA
                                ||||||||   ||  ||| ||||
                                AGTCTCAG   AG  CTG TTGT
                                    ___  AA   _
GAM3234  LOC257327 5'  TCGGAGTCCATCTTTGGACAG  73034    A     C   GG_  CTA
                                TC GAGTCC ATC   GG   ACAG
                                || |||||| |||   ||   ||||
                                AG CTCAGG TAG   CC   TGTC
                                 C     _   AAA  ___
GAM3234  LOC257541 5'  AGAGGAGGCGGGGCTAGCAG   73013     TCCCAT      A
                                AGAG     CGGGGCTA CAG
                                ||||     |||||||| |||
                                TCTC     GCCCCGAT GTC
                                  CTCC__       C
GAM3234  LOC51267  3'  TCAGAGTCTTAATGGACACAG  73035       CCATCG   TA
                                TCAGAGTC     GGGC  ACAG
                                ||||||||     ||||  ||||
                                AGTCTCAG     CCTG  TGTC
                                    AATTA_   __
GAM3234  LOC86651  5'  TCAGAGTCCATCAATCCA    73036        C    GG
                                TCAGAGTCC ATCGG  CTA
                                ||||||||| |||||  |||
```

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                                AGTCTCAGG TAGTT  GGT
                                      _    A_
GAM3235  ADD1    3'  GCTCTGAGCCCTTTTCCAGCC  73039    AAGC      C
                                GC   AGCCCTTT CCAGCC
                                ||   |||||||| ||||||
                                CG   TCGGGAAA GGTCGG
                                 AGAC       A
GAM3235  ADD1    3'  GCTCTGAGCCCTTTTCCAGCC  73039    AAGC      C
                                GC   AGCCCTTT CCAGCC
                                ||   |||||||| ||||||
                                CG   TCGGGAAA GGTCGG
                                 AGAC       A
GAM3235  ARVCF   3'  TCCAAGTTCTTTCCCAGCCC  73040    G   CAGCC
                                TC CAAG    CTTTCCCAGCCC
                                || ||||    ||||||||||||
                                AG GTTC    GAAAGGGTCGGG
                                 _   AA___
GAM3235  B3GAT1  3'  GCCCCCTCTTTCCCAGCCC   73041    AG  _
                                GC  CC CTTTCCCAGCCC
                                ||  || ||||||||||||
                                CG  GG GAAAGGGTCGGG
                                 GG  A
GAM3235  B3GAT1  3'  GCCCCCTCTTTCCCAGCCC   73041    AG  _
                                GC  CC CTTTCCCAGCCC
                                ||  || ||||||||||||
                                CG  GG GAAAGGGTCGGG
                                 GG  A
GAM3235  CENTD2  5'  TCGCAAACAGCCTGGCCC    73042          CTTT
                                TCGCAAGCAGCC   CCC
                                ||||||||||||   |||
                                AGCGTTTGTCGG   GGG
                                       ACC_
GAM3235  EFEMP2  3'  TCGTGGTGCAGAGCTCCCAGC  73043    CAA_   CCCT
                                TCG   GCAG   TTCCCAGC
                                |||   ||||   ||||||||
                                AGC   CGTC   GAGGGTCG
                                  ACCA   TC__
GAM3235  EFNB2   3'  GCAGCCAGCCCTTTCCCCAGCC 73044    AG         _
            C                    GCA  CAGCCCTTTCCC AGCCC
                                ||| ||||||||||| |||||
                                CGT  GTCGGGAAAGGG TCGGG
                                  CG          G
GAM3235  ERBB2IP 5'  GCAGGAGTTTCCCAGCCC    73045     CCC
                                GCAG   TTTCCCAGCCC
                                ||||   ||||||||||
                                CGTC   AAAGGGTCGGG
                                  CTC
GAM3235  EXTL1   3'  TCGCAAGCCAGTCCTGGGGCC  73046        _ C   TTCCCA
                                TCGCAAGC AG CCT     GCC
                                |||||||| || |||     |||
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                                AGCGTTCG TC GGA     CGG
                                    G  A   CCC___
GAM3235  GBF1     3'  GCAGTCCCCCACCCAGCCC    73047      _    TT
                                GCAG CCCT  CCCAGCCC
                                |||| ||||  ||||||||
                                CGTC GGGG  GGGTCGGG
                                  A    GT
GAM3235  GNAT1    5'  TCCCAGGCACCCTTCTGGCCC  73048    G  A   G     CCCA
                                TC CA GCA CCCTTT    GCCC
                                || || ||| ||||||    ||||
                                AG GT CGT GGGAAG    CGGG
                                 G  C   _     AC__
GAM3235  KCND2    5'  TCCAAGTAGCCCTTCCC     73049    G    C
                                TC CAAG AGCCCTTTCC
                                || |||| ||||||||||
                                AG GTTC TCGGGAAGGG
                                 _    A
GAM3235  MGA      3'  GCAAACAGCTCTTTCGC     73050          C     CCA
                                GCAAGCAGC CTTTC   GC
                                ||||||||| |||||   ||
                                CGTTTGTCG GAAAG   CG
                                     A    ___
GAM3235  MSH2     3'  GCAAACAGTCCTCAGTTACAGC 73051         C    TCC__
                                GCAAGCAG CCTT     CAGC
                                |||||||| ||||     ||||
                                CGTTTGTC GGAG     GTCG
                                     A    TCAAT
GAM3235  MSR1     3'  AGCAGCCCTCCAGTCC      73052          TTC   _
                                AGCAGCCCT   CCAG CC
                                |||||||||   |||| ||
                                TCGTCGGGA   GGTC GG
                                     ___    A
GAM3235  RANBP3   3'  TCTGAGCAGCCCCCGGCC    73053    GCA       TTTC  A
                                TC   AGCAGCCC    CC GCC
                                ||   ||||||||    || |||
                                AG   TCGTCGGG    GG CGG
                                 AC_       _____  C
GAM3235  RGS16    3'  TCGAAGCAGCCTCTCCCCCCAG 73054     C       _  TT   _
              C                  TCG AAGCAGCC CT  CCC AGC
                                 ||| |||||||| ||  ||| |||
                                 AGC TTCGTCGG GA  GGG TCG
                                   _       A  GG   G
GAM3235  RLBP1    3'  TCTCAAGCAGCCCTTTCCTAGC 73055    G            C
              C                  TC CAAGCAGCCCTTTCC AGCC
                                 || |||||||||||||| ||||
                                 AG GTTCGTCGGGAAAGG TCGG
                                  A             A
GAM3235  RPP20    5'  GCAAGCAGCCAGCCAGC     73056          CTTTC
                                GCAAGCAGCC    CCAGC
                                ||||||||||    |||||
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                                CGTTCGTCGG    GGTCG
                                      TC___
GAM3235 RPS6KA5  3' ACAAGCAGCTCAAATCTAGCCC 73057        CCTT_ CC
                                GCAAGCAGC    TC AGCCC
                                |||||||||    || |||||
                                TGTTCGTCG    AG TCGGG
                                     AGTTT A_
GAM3235 SCNN1G   3' TCACAAGCGGCTCCAGC     73058        A CCTTTC
                                TCGCAAGC GC     CCAGC
                                |||||||| ||     |||||
                                AGTGTTCG CG     GGTCG
                                     C A_____
GAM3235 SLC7A6   3' AAGCAGCTTTCCTCCCAG    73059       CC_
                                AAGCAGC   TTTCCCAG
                                |||||||   ||||||||
                                TTCGTCG   GGAGGGTC
                                     AAA
GAM3235 STAT6    5' AAGCAGTGGCTGCCCCAGCCC 73060       CC_ T
                                AAGCAG   CT TCCCAGCCC
                                ||||||   || |||||||||
                                TTCGTC   GA GGGGTCGGG
                                    ACC C
GAM3235 STK18    5' TCCAAGCAGCCAGCCGGCC   73061    G       CTTTC A
                                TC CAAGCAGCC    CC GCC
                                || |||||||||    || |||
                                AG GTTCGTCGG    GG CGG
                                 _       TC___ C
GAM3235 SYNJ1    5' TCGGAGGCAGCCCTCTTCCTCC 73062    CAA       C AG
                                TCG   GCAGCCCTTT CC  CC
                                |||   |||||||||| ||  ||
                                AGC   CGTCGGGAGA GG  GG
                                  CTC        A  A_
GAM3235 TAL1     5' TCGCAAACAGCTTTCCGCC   73063         CC    CA
                                TCGCAAGCAGC  TTTCC  GCC
                                ||||||||||  |||||  |||
                                AGCGTTTGTCG  AAAGG  CGG
                                      __    __
GAM3235 ZNF205   3' CCGCTCCCCCTTTCCTGGCC   73064     AAGCAG      CA
                                TCGC     CCCTTTCC  GCC
                                ||||     ||||||||  |||
                                GGCG     GGGAAAGG  CGG
                                  AGG___       AC
GAM3235 BPESC1   3' ACACTCAGCCCTTTCCCAGCCC 73065     AG
                                GCA  CAGCCCTTTCCCAGCCC
                                |||  |||||||||||||||||
                                TGT  GTCGGGAAAGGGTCGGG
                                  GA
GAM3235 C14orf3  5' CCGCAAGCACCTCCTGGC    73066        G  CTT   CA
                                TCGCAAGCA CC   TCC  GC
                                |||||||| ||   |||  ||
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                                GGCGTTCGT GG   AGG  CG
                                      _ ___   AC
GAM3235  DEPC-1    5'  GCAGCCCTCGCAGCCC      73067         TCC
                                GCAGCCCTT   CAGCCC
                                |||||||||   ||||||
                                CGTCGGGAG   GTCGGG
                                     C__
GAM3235  FLJ14326  3'  TCTAAGCAGCCCTTGGGGACAG 73068    GC         TCC__
                                TC  AAGCAGCCCTT    CAG
                                ||  ||||||||||     |||
                                AG  TTCGTCGGGAA    GTC
                                 A_         CCCCT
GAM3235  FLJ21438  5'  TCCAAGCAGCACCAGC      73069    G      CCTTTC
                                TC CAAGCAGC     CCAGC
                                || ||||||||     |||||
                                AG GTTCGTCG     GGTCG
                                 _       T_____
GAM3235  FLJ22341  3'  TCGCAGGCAGACCCTGTTC    73070      A   _   _
                                TCGCA GCAG CCCT TTC
                                ||||| |||| |||| |||
                                AGCGT CGTC GGGA AAG
                                   C    T    C
GAM3235  FLJ23360  3'  CGCAGGCGGGGCTCCCAGCC   73071     A  A__  CCTT
                                CGCA GC   GC    TCCCAGCC
                                |||| ||   ||    ||||||||
                                GCGT CG   CG    AGGGTCGG
                                  C  CCC  _____
GAM3235  GPR105    3'  GCAAACAGCTCTCTAGCCC    73072         C    CCC
                                GCAAGCAGC CTTT   AGCCC
                                ||||||||| ||||   |||||
                                CGTTTGTCG GAGA   TCGGG
                                     A    ___
GAM3235  KIAA0596  3'  TCCAAGCAGCCCCGCAG     73073    G         TTCC
                                TC CAAGCAGCCCT    CAG
                                || ||||||||||    |||
                                AG GTTCGTCGGGG    GTC
                                 _         C___
GAM3235  KIAA0821  3'  GCCCTGCGGCCTTTTCCCAG   73074    AA_  A   C
                                GC   GC GCC TTTCCCAG
                                ||   || ||| ||||||||
                                CG   CG CGG AAAGGGTC
                                 GGA  C   A
GAM3235  KIAA0865  3'  CCACACTTTTCCCAGCC     73075      AGCAGCCC
                                TCGCA       TTTCCCAGCC
                                |||||       ||||||||||
                                GGTGT       AAAGGGTCGG
                                   GA_______
GAM3235  KIAA1032  3'  TCTCAAGCAGCTCTTTAAGCC  73076    G       C    CCC
                                TC CAAGCAGC CTTT   AGCC
                                || |||||||| ||||   ||||
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                                AG GTTCGTCG GAAA   TCGG
                                 A      A   T__
GAM3235 KIAA1277 3' TCCCAGGCGGCTCCCAGGTCC 73077    G  A  A  CCTT    __
                                TC CA GC GC   TCCCAG  CC
                                || || || ||   ||||||  ||
                                AG GT CG CG   AGGGTC  GG
                                 G  C  C ____     CA
GAM3235 KIAA1649 3' GCAAGCAGTGAGCCCCCGGC  73078       CCCT    A
                                GCAAGCAG   TTCCC GC
                                ||||||||   ||||| ||
                                CGTTCGTC   GGGGG CG
                                     ACTC    C
GAM3235 KIAA1649 3' GCAAGCAGTGAGCCCCCGGC  73078       CCCT    A
                                GCAAGCAG   TTCCC GC
                                ||||||||   ||||| ||
                                CGTTCGTC   GGGGG CG
                                     ACTC    C
GAM3235 MGC13090 3' CGCGGGCAGCCCTTGTCC    73079     AA       _
                                CGC  GCAGCCCTT TCC
                                |||  ||||||||| |||
                                GCG  CGTCGGGAA AGG
                                  CC       C
GAM3235 MGC23427 3' GCAAGCAGCTCTAGTACTCGGT 73080        C ____  CCAG
           CC                     GCAAGCAGC CT   TTC   CC
                                |||||||| ||   |||   ||
                                CGTTCGTCG GA   GAG   GG
                                     A  TCAT   CCA_
GAM3235 MGC3329  3' TCTAGGCAGTGCTGCCCAGCCC 73081   GCAA   CC  TT
                                TC   GCAG  CT  CCCAGCCC
                                ||   ||||  ||  ||||||||
                                AG   CGTC  GA  GGGTCGGG
                                 ATC_   AC  C_
GAM3235 MGC5149  5' TCACAAGCAGCGGCTATTTCAG 73082         C_  TTCC
           CC                     TCGCAAGCAGC  CT   CAGCC
                                ||||||||||  ||   |||||
                                AGTGTTCGTCG  GA   GTCGG
                                      CC  TAAA
GAM3235 MKP-7   3' TCCAAGCAGCTCCAGAGCC   73083   G     CCTT  C_
                                TC CAAGCAGC   TCC  AGCC
                                || ||||||||   |||  ||||
                                AG GTTCGTCG   AGG  TCGG
                                 _      ____  TC
GAM3235 NAG73   5' TCTTGGGCAGCACCCCAGCCC  73084   GCAA   CCTT
                                TC   GCAGC   TCCCAGCCC
                                ||   |||||   |||||||||
                                AG   CGTCG   GGGGTCGGG
                                 AACC    T___
GAM3235 p25     3' TCCAGGCACTGAACTTCCCAGC 73085   G  A  GCCC_
           CC                     TC CA GCA    TTTCCCAGCCC
                                || || |||    ||||||||||
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                                AG GT CGT    GAAGGGTCGGG
                                 _ C  GACTT
GAM3235 PTGES2   3' GCAAACATGTCCCAGTCC   73086       GCCCTT    _
                                GCAAGCA    TCCCAG CC
                                |||||||    |||||| ||
                                CGTTTGT    AGGGTC GG
                                    AC____     A
GAM3235 SEMA4C   3' TCACACAGCCTTTCCCAGCCC 73087     AA    C
                                TCGC  GCAGCC TTTCCCAGCCC
                                ||||  |||||| ||||||||||
                                AGTG  TGTCGG AAAGGGTCGGG
                                  __    _
GAM3235 SENP2    3' GCAAGCAGCCCTCTGCACCC  73088           CCCA
                                GCAAGCAGCCCTTT   GCCC
                                ||||||||||||||   ||||
                                CGTTCGTCGGGAGA   TGGG
                                        CG__
GAM3235 SIAT4B   5' GCCACTCTTTTCCCAGCCC   73089    _  ___
                                GCC CTT   TCCCAGCCC
                                ||| |||   |||||||||
                                CGG GAG   AGGGTCGGG
                                  T  AAA
GAM3235 TSPAN-5  3' TCAGTGAGCAGCATTTCCCAG 73090    CA_    CC
                                TCG   AGCAGC  TTTCCCAG
                                |||   ||||||  ||||||||
                                AGT   TCGTCG  AAAGGGTC
                                  CAC     T_
GAM3235 USP24    3' TCACAGCAGCTTTCCCAGTCC  73091      A    CC      _
                                TCGCA GCAGC  TTTCCCAG CC
                                |||||| |||||  |||||||| ||
                                AGTGT CGTCG  AAAGGGTC GG
                                   _    __       A
GAM3235 VTI2     5' GCCCTGGGCCCTTTCCTAGCCC 73092    AAGCA       C
                                GC    GCCCTTTCC AGCCC
                                ||    ||||||||| |||||
                                CG    CGGGAAAGG TCGGG
                                 GGACC        A
GAM3235 LOC126123 5' GCAGGCAGCCCCAGCC     73093    A     TTTCC
                                GCA GCAGCCC    CAGCC
                                ||| |||||||    |||||
                                CGT CGTCGGG    GTCGG
                                  C     _____
GAM3235 LOC127703 5' CCGGGCAGCGCGCCCAGCCC  73094    CAA    CCTTT
                                TCG   GCAGC    CCCAGCCC
                                |||   |||||    ||||||||
                                GGC   CGTCG    GGGTCGGG
                                  C__    CGC__
GAM3235 LOC143308 5' TCCAAGCCCCTTTTCAGCC   73095    G    AG     CC
                                TC CAAGC  CCCTTT  CAGCC
                                || |||||  ||||||  |||||
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                                AG GTTCG  GGGAAA  GTCGG
                                 _    __     A_
GAM3235  LOC145748 3'  TCCCAGGCAGCCCCAGCC    73096    G  A     TTTCC
                                TC CA GCAGCCC    CAGCC
                                || || |||||||    |||||
                                AG GT CGTCGGG    GTCGG
                                 G  C     _____
GAM3235  LOC147895 5'  TCGCAGGCAGCCCCTTCC    73097      A
                                TCGCA GCAGCCCTTTCC
                                ||||| ||||||||||||
                                AGCGT CGTCGGGGAAGG
                                   C
GAM3235  LOC148530 5'  TCTCAAGCAGCTTTCCACACC  73098    G      CC    CA
                                TC CAAGCAGC  TTTCC  GCC
                                || ||||||||  |||||  |||
                                AG GTTCGTCG  AAAGG  TGG
                                 A       __    TG
GAM3235  LOC152426 5'  TCCAGGCAGCCCTCCCAGC    73099    G  A     TT
                                TC CA GCAGCCC  TCCCAGC
                                || || |||||||  |||||||
                                AG GT CGTCGGG  AGGGTCG
                                 _ C     __
GAM3235  LOC153572 3'  CCGCGGGCAGCCCCGGTGGCCC 73100      AA      TTCCCA
                                TCGC  GCAGCCCT     GCCC
                                ||||  ||||||||     ||||
                                GGCG  CGTCGGGG     CGGG
                                  CC       CCAC__
GAM3235  LOC196337 5'  TCGCAAGCAGGCCTTCCAGC   73101          C    TC
                                TCGCAAGCAG CCTT  CCAGC
                                |||||||||| ||||  |||||
                                AGCGTTCGTC GGAA  GGTCG
                                      C   __
GAM3235  LOC199733 3'  GCAGCCCCACCAGCCC      73102         TTC
                                GCAGCCCT   CCAGCCC
                                ||||||||   |||||||
                                CGTCGGGG   GGTCGGG
                                     T__
GAM3235  LOC200473 3'  GCAGGACTCTTCCCAGTCC    73103      CC   _    _
                                GCAG  CTTT CCCAG CC
                                ||||  |||| ||||| ||
                                CGTC  GAGA GGGTC GG
                                  CT    A    A
GAM3235  LOC204820 3'  GCCCATGTGGCCCTTTCCTGGC 73104    AAGCA__       CA
            CC                   GC      GCCCTTTCC  GCCC
                                ||      |||||||||  ||||
                                CG      CGGGAAAGG  CGGG
                                 GGTACAC        AC
GAM3235  LOC206324 5'  TCCCAGGGGACCTTTTCCCAG  73105    G  AGCA   C
                                TC CA    GCC TTTCCCAG
                                || ||    ||| ||||||||
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                                AG GT    TGG AAAGGGTC
                                 G  CCCC   A
GAM3235  LOC221421 3'  GCGGCAGCAAGAGCCCAGCCC  73106    AA    CCTTT
                                GC  GCAGC    CCCAGCCC
                                ||  |||||    ||||||||
                                CG  CGTCG    GGGTCGGG
                                 C_    TTCTC
GAM3235  LOC222112 5'  TCGCGGTCAGCCTTCCCCGGCC 73107     AAG    C     A
              C                  TCGC   CAGCC TTTCCC GCCC
                                ||||   ||||| |||||| ||||
                                AGCG   GTCGG AAGGGG CGGG
                                  CCA    _     C
GAM3235  LOC253223 5'  TCGGGAGCAGCCCTGGTGCCC  73108    CA       TTCCCA
                                TCG  AGCAGCCCT     GCCC
                                |||  |||||||||     ||||
                                AGC  TCGTCGGGA     CGGG
                                  CC        CCA___
GAM3235  LOC254531 5'  CCGAAGCACTTTTCCCAG    73109    C    G CC
                                TCG AAGCA C  TTTCCCAG
                                ||| ||||| |  ||||||||
                                GGC TTCGT G  AAAGGGTC
                                  _    _ A_
GAM3235  LOC255620 5'  TCACAAGCAGCACCGCCAGC   73110          _  TTTC
                                TCGCAAGCAGC CC    CCAGC
                                ||||||||||| ||    |||||
                                AGTGTTCGTCG GG    GGTCG
                                       T  C___
GAM3235  LOC257513 5'  TCGGGAGCAGCCCTGGTGCCC  73108    CA       TTCCCA
                                TCG  AGCAGCCCT     GCCC
                                |||  |||||||||     ||||
                                AGC  TCGTCGGGA     CGGG
                                  CC        CCA___
GAM3235  LOC257567 5'  TCGGGAGCAGCCCTGGTGCCC  73108    CA       TTCCCA
                                TCG  AGCAGCCCT     GCCC
                                |||  |||||||||     ||||
                                AGC  TCGTCGGGA     CGGG
                                  CC        CCA___
GAM3235  LOC90381  3'  TCTGAGCAGTGCCCCCAGC   73111    GCA    CCCT
                                TC   AGCAG    TTCCCAGC
                                ||   |||||    ||||||||
                                AG   TCGTC    GGGGGTCG
                                 AC_     AC__
GAM3235  LOC91960  5'  CCGGGCAGCCCTCGCCC     73112     CAA       T
                                TCG   GCAGCCCTT CCC
                                |||   ||||||||| |||
                                GGC   CGTCGGGAG GGG
                                  C__        C
GAM3235  LOC91966  5'  TCGCAAGCGCCCCGGGCC    73113         A    TTCCCA
                                TCGCAAGC GCCCT     GCC
                                |||||||| |||||     |||
```

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                                AGCGTTCG CGGGG     CGG
                                     _    CC____
GAM3235 LOC96597 5' TCCAGGCAGCCCTCTAGAGC  73114    G  A       CCC
                                TC CA GCAGCCCTTT   AGC
                                || || ||||||||||   |||
                                AG GT CGTCGGGAGA   TCG
                                 _ C        TC_
GAM3236 DPYD     3' ACTACTTATAGATTCATA    73117    A  C_
                                AC GC  GTAGATTCATA
                                || ||  ||||||||||
                                TG TG  TATCTAAGTAT
                                 A  AA
GAM3236 DSCAM    3' TACAACCGCTGTCCAGTCATGC 73118       A  C  AGAT    A
           TG                     TACAAC GC GT    TCAT CTG
                                ||||||| || ||    |||| |||
                                ATGTTG CG CA    AGTA GAC
                                    G  A  GGTC    C
GAM3236 FLJ10697 3' CAACAGCCTAGACAGTACTG  73119        G    TCA
                                CAACAGCC TAGAT   TACTG
                                |||||||| |||||   |||||
                                GTTGTCGG ATCTG   ATGAC
                                     _    TC_
GAM3236 FLJ11125 5' ACAGCAGGGATTCATACT    73120      CGTA
                                ACAGC    GATTCATACT
                                |||||    ||||||||||
                                TGTCG    CTAAGTATGA
                                   TCC_
GAM3236 FLJ12389 3' TACAACAGCTGTAGGTTTC   73121         C    A_
                                TACAACAGC GTAG  TTC
                                ||||||||| ||||  |||
                                ATGTTGTCG CATC  AAG
                                     A    CA
GAM3236 FLJ22833 3' TACAACAGTAGTTAAGATGTAC 73122        CC  __    TCA
           TG                     TACAACAG  GT  AGAT   TACTG
                                ||||||||  ||  ||||   |||||
                                ATGTTGTC  CA  TCTA   ATGAC
                                    AT  AT    C__
GAM3236 KIAA0161 3' TACATCAAGCAGGGTTCATACT 73123     A   CC    A_
           G                     TACA CAG  GTAG  TTCATACTG
                                |||| |||  ||||  |||||||||
                                ATGT GTT  CGTC  AAGTATGAC
                                  A   __    CC
GAM3236 KIAA0854 3' CAACCAGAGTTCATACT     73124       T  A
                                CAGCCG AG TTCATACT
                                |||||| || ||||||||
                                GTTGGT TC AAGTATGA
                                   C  _
GAM3236 KIAA1434 3' CAGCAGCCTCAAGGTTCATACT 73125    A    GT_  A
           G                     CA CAGCC   AG TTCATACTG
                                || |||||   || |||||||||
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                                GT GTCGG  TC AAGTATGAC
                                 C    AGT  C
GAM3236  PP1665   5'  ACGGCAGCCGTAGATGCCCG  73126   AA       TCATA
                                AC  CAGCCGTAGAT    CTG
                                ||  ||||||||||    |||
                                TG  GTCGGCATCTA    GGC
                                 CC        CG___
GAM3236  SENP7    3'  TACACAGTATTCATAC     73127     A   CCGTAG
                                TACA CAG     ATTCATAC
                                |||| |||     ||||||||
                                ATGT GTC     TAAGTATG
                                  _  A_____
GAM3236  TNRC6    3'  ACAGCTGCCCCCCATACTG   73128      C  AGA
                                ACAGC GT   TTCATACTG
                                ||||| ||   |||||||||
                                TGTCG CG   GGGTATGAC
                                   A  GG_
GAM3236  XT2      3'  CAGCAGTAGTTCATACT     73129     C   A
                                CAGC GTAG TTCATACT
                                |||| |||| ||||||||
                                GTCG CATC AAGTATGA
                                  T   _
GAM3236  LOC149706 5'  CAGCCCCACCTCATACTG    73130      G  GA
                                CAGCC TA  TTCATACTG
                                ||||| ||  |||||||||
                                GTCGG GT  GAGTATGAC
                                   G  G_
GAM3237  C20orf1  3'  CACTGGTGCAGTTGGTGA    73133     G      TCA
                                CAC TGGTGCG   GGTGA
                                ||| |||||||   |||||
                                GTG ACCACGT   CCACT
                                  _     CAA
GAM3237  COL5A1   3'  CGTAGATGAAGTCAGGTG    73134      _  C_
                                CGTGG TG  GTCAGGTG
                                ||||| ||  ||||||||
                                GCATC AC  CAGTCCAC
                                   T  TT
GAM3237  DFFB     3'  CACGTGGTTCAACGTGA     73135        GCG   _
                                CACGTGGT   TCAG GTGA
                                ||||||||   |||| ||||
                                GTGCACCA   AGTT CACT
                                     ___   G
GAM3237  EPB72    3'  CAGCGGTGTCAGGTG       73136    C    GC
                                CA GTGGT  GTCAGGTG
                                || |||||  ||||||||
                                GT CGCCA  CAGTCCAC
                                 _   __
GAM3237  FLT1     3'  ACGTGATGCATTGGGTGA    73137          CA
                                ACGTGGTGCGT  GGTGA
                                ||||||||||  |||||
```

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                                TGCACTACGTA CCACT
                                      AC
GAM3237 FUT6    5' CACCTGTCATCAGGTGA    73138    G GTG
                                CAC TG  CGTCAGGTGA
                                ||| ||  ||||||||||
                                GTG AC  GTAGTCCACT
                                  G A__
GAM3237 GCG     3' CACGTGGCTAGCAGGTGA   73139       GCGT
                                CACGTGGT   CAGGTGA
                                ||||||||   |||||||
                                GTGCACCG   GTCCACT
                                     ATC_
GAM3237 GFI1    3' ACTTGGTAGCCGGTGA     73140   G   C  A
                                AC TGGTG GTC GGTGA
                                || ||||| ||| |||||
                                TG ACCAT CGG CCACT
                                 A   _  _
GAM3237 GRM6    3' CACAGTGGACCACAGGTGA  73141    _   T GT
                                CAC GTGG GC  CAGGTGA
                                ||| |||| ||  |||||||
                                GTG CACC TG  GTCCACT
                                  T   _ GT
GAM3237 HPSE    3' ACATCACTCAGGTGA      73142    GG  G
                                ACGT  TGC TCAGGTGA
                                ||||  ||| ||||||||
                                TGTA  GTG AGTCCACT
                                   __  _
GAM3237 HS3ST3B1 5' CACGCTGGACGCCCGGGTG  73143    _  T   A_
                                CACG TGG GCGTC  GGTG
                                |||| ||| |||||  ||||
                                GTGC ACC TGCGG  CCAC
                                  G  _   GC
GAM3237 HSF2BP  3' CACATGGTACATGGTGA    73144         CA
                                CACGTGGTGCGT  GGTGA
                                ||||||||||||  |||||
                                GTGTACCATGTA  CCACT
                                      __
GAM3237 JAM3    3' CACATGGTGCTGTCGTG    73145         _  AG
                                CACGTGGTGC GTC  GTG
                                |||||||||| |||  |||
                                GTGTACCACG CAG  CAC
                                     A  __
GAM3237 LIF     3' CACGTGGGCGGGACTGA    73146       T  TCA __
                                CACGTGG GCG   GG  TGA
                                ||||||| |||   ||  |||
                                GTGCACC CGC   CC  ACT
                                   _  ____ TG
GAM3237 LOXL2   3' CACATGGTGCTCAGTGA    73147         G  G
                                CACGTGGTGC TCAG TGA
                                |||||||||| |||| |||
```

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                                GTGTACCACG AGTC ACT
                                      _  _
GAM3237 NARS    3' CACTTGATGTTCAGGTGA   73148    G   CG
                                CAC TGGTG  TCAGGTGA
                                ||| |||||  ||||||||
                                GTG ACTAC  AGTCCACT
                                  A    A_
GAM3237 POLR2J  3' CACGTCGGTGTCAGGGTGA  73149     _  GC    _
                                CACGT GGT  GTCAGG TGA
                                ||||| |||  |||||| |||
                                GTGCA CCA  CAGTCC ACT
                                   G  __    C
GAM3237 PTGFR   3' CACATGGCCAGGGTGA     73150       GCGT   _
                                CACGTGGT   CAGG TGA
                                ||||||||   |||| |||
                                GTGTACCG   GTCC ACT
                                     ____  C
GAM3237 PTPN2   3' CAATGTTGGTCAGGTGA    73151   C  G  C
                                A GTG TG GTCAGGTGA
                                | ||| || |||||||||
                                G TAC AC CAGTCCACT
                                 T  A  _
GAM3237 SLC2A2  3' CGCTATATGATCAGGTGA   73152    G__  C
                                CGT  GTG GTCAGGTGA
                                |||  ||| |||||||||
                                GCG  TAC TAGTCCACT
                                  ATA  _
GAM3237 STK10   3' ACATTAGGTTCAGGTGA    73153    __  GCG
                                ACGT  GGT  TCAGGTGA
                                ||||  |||  ||||||||
                                TGTA  CCA  AGTCCACT
                                  AT  ___
GAM3237 TNFRSF8 3' CACGTGGCTGCCCGATGA   73154       GC  A
                                CACGTGGT  GTC GGTGA
                                ||||||||  ||| |||||
                                GTGCACCG  CGG CTACT
                                     A_  G
GAM3237 UBE2L6  3' CACCTGTGGCCAGGTGA    73155    G  G  C
                                CAC TG TG GTCAGGTGA
                                ||| || || |||||||||
                                GTG AC AC CGGTCCACT
                                  G  _  _
GAM3237 ZNF157  3' CACTGTGGTGCCCTGGTGA  73156    _    G  A
                                CAC GTGGTGC TC GGTGA
                                ||| ||||||| || |||||
                                GTG CACCACG GG CCACT
                                  A     _ A
GAM3237 ACY-3   3' CATGGTGCATGGTAGGTG   73157        C__
                                CGTGGTGCGT  AGGTG
                                ||||||||||  |||||
```

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                                GTACCACGTA   TCCAC
                                     CCA
GAM3237 BANP     5' CACAGTGCAACCAGGTGA    73158    TG    _
                                CG  GTGCG TCAGGTGA
                                ||  ||||| ||||||||
                                GT  CACGT GGTCCACT
                                 GT    T
GAM3237 CAMTA1   3' CACTGATCGTTTAGGTG     73159     G   G  C_
                                CAC TGGT CGT  AGGTG
                                ||| |||| |||  |||||
                                GTG ACTA GCA  TCCAC
                                  _   _  AA
GAM3237 CRSP3    3' ACATCATCTGTCAGGTGA    73160     G  GC
                                ACGT GT  GTCAGGTGA
                                |||| ||  |||||||||
                                TGTA TA  CAGTCCACT
                                  G  GA
GAM3237 DGKD     3' CACATGTGCCCCAGGTGA    73161      G  G
                                CACGTG TGC TCAGGTGA
                                |||||| ||| ||||||||
                                GTGTAC ACG GGTCCACT
                                   _  G
GAM3237 DKFZP586I2223 3' ACGTGGACAAGGTGA      73162      T  TC
                                ACGTGG GCG  AGGTGA
                                |||||| |||  ||||||
                                TGCACC TGT  TCCACT
                                   _  __
GAM3237 DKFZP586I2223 3' ACGTGGACAAGGTGA      73162      T  TC
                                ACGTGG GCG  AGGTGA
                                |||||| |||  ||||||
                                TGCACC TGT  TCCACT
                                   _  __
GAM3237 DKFZP586I2223 3' ACGTGGACAAGGTGA      73162      T  TC
                                ACGTGG GCG  AGGTGA
                                |||||| |||  ||||||
                                TGCACC TGT  TCCACT
                                   _  __
GAM3237 DKFZP727M111 5' GTGGTGCAGACCCAGGTG    73163       ___
                                GTGGTGCG   TCAGGTG
                                ||||||||   |||||||
                                CACCACGT   GGTCCAC
                                     CTG
GAM3237 EIF4B    3' ACCTGGTGCAAAATGA     73164    G     TC
                                AC TGGTGCG  AGGTGA
                                || |||||||  ||||||
                                TG ACCACGT  TTTACT
                                 G     __
GAM3237 FLJ10607 3' ACGTGGTGTGAGTCAATG    73165       C__    G
                                ACGTGGTG   GTCAG TG
                                ||||||||   ||||| ||
```

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                                TGCACCAC   CAGTT AC
                                    ACT    _
GAM3237  FLJ12443  3'  CACTGAAAAATCAGGTGA    73166    G   TGC
                                CAC TGG   GTCAGGTGA
                                ||| |||   |||||||||
                                GTG ACT   TAGTCCACT
                                  _  TTT
GAM3237  FLJ13204  3'  ACATTCTGATCAGGTGA     73167     GG  C
                                ACGT  TG GTCAGGTGA
                                ||||  || |||||||||
                                TGTA  AC TAGTCCACT
                                  AG  _
GAM3237  FLJ14326  3'  CACGTGTGTGAATCTAGG    73168       _   C   _
                                CACGTG GTG GTC AGG
                                |||||| ||| ||| |||
                                GTGCAC CAC TAG TCC
                                    A   T   A
GAM3237  FLJ20085  5'  CACAATCACGTCAGGTGA    73169     TGG
                                CACG   TGCGTCAGGTGA
                                ||||   ||||||||||||
                                GTGT   GTGCAGTCCACT
                                  TA_
GAM3237  FLJ21272  3'  CACATGGTAAATCAGGTG    73170         C
                                CACGTGGTG GTCAGGTG
                                ||||||||| ||||||||
                                GTGTACCAT TAGTCCAC
                                     T
GAM3237  FLJ23191  5'  CGTGGTGCGCCCCAGTGA    73171           A_
                                CGTGGTGCGTC  GGTGA
                                ||||||||||  |||||
                                GCACCACGCGG  TCACT
                                      GG
GAM3237  FLJ31762  3'  CACAGTATAAATCGTTAGGTGA 73172     _   GTG__   C
                                CAC GTG    CGT AGGTGA
                                ||| |||    ||| ||||||
                                GTG CAT    GCA TCCACT
                                  T   ATTTA   A
GAM3237  FOXN4     3'  CACTGTGGTGGCGTGA      73173     _     C  CAG
                                CAC GTGGTG GT   GTGA
                                ||| |||||| ||   ||||
                                GTG CACCAC CG   CACT
                                  A     _ ____
GAM3237  HM74      3'  CACGGAAGCCAGGTGA      73174      T  TGC
                                CACG GG   GTCAGGTGA
                                |||| ||   |||||||||
                                GTGC CT   CGGTCCACT
                                  _ T__
GAM3237  KIAA0284  3'  CACGTAAACATCAGGTG     73175        T
                                CACGTGG GCGTCAGGTG
                                ||||||| ||||||||||
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                                GTGCATT TGTAGTCCAC
                                      _
GAM3237 KIAA1145 3' CGCTGGGCTGGTCAGGTG    73176    _  T __
                                CG TGG GC  GTCAGGTG
                                || ||| ||  ||||||||
                                GC ACC CG  CAGTCCAC
                                 G  _  AC
GAM3237 KIAA1247 3' GCCTGTGCAGTCAGGTGA    73177    G_   _
                                GT  GTGC GTCAGGTGA
                                ||  |||| |||||||||
                                CG  CACG CAGTCCACT
                                 GA   T
GAM3237 KIAA1297 3' CACGTGGTGGCCGTG       73178        C   AG
                                CACGTGGTG GTC  GTG
                                ||||||||| |||  |||
                                GTGCACCAC CGG  CAC
                                      _  __
GAM3237 LGP1     3' ATGGGCAAATGTCAGGTGA   73179     T ____
                                GTGG GC    GTCAGGTGA
                                |||| ||    |||||||||
                                TACC CG    CAGTCCACT
                                  _ TTTA
GAM3237 MGC3047  3' CACATGGTGGTACAGGTG    73180        C _
                                CACGTGGTG GT CAGGTG
                                |||||||| || ||||||
                                GTGTACCAC CA GTCCAC
                                      _ T
GAM3237 MRPS34   3' CACGTCGCGGAAGGTGA     73181      GG   TC
                                CACGT  TGCG  AGGTGA
                                |||||  ||||  ||||||
                                GTGCA  GCGC  TCCACT
                                   __   CT
GAM3237 NPEPL1   5' CACGCGGTGCAGGTG       73182        GTC
                                CACGTGGTGC   AGGTG
                                ||||||||||   |||||
                                GTGCGCCACG   TCCAC
                                      ____
GAM3237 OATL1    5' CACGTCGAGCGAGGTGA     73183      _ T  TC
                                CACGT GG GCG  AGGTGA
                                ||||| || |||  ||||||
                                GTGCA CT CGC  TCCACT
                                   G  _  __
GAM3237 PEF      3' CACTGGCATCAGGGTG      73184     G   GC    _
                                CAC TGGT  GTCAGG TG
                                ||| ||||  |||||| ||
                                GTG ACCG  TAGTCC AC
                                  _   __     C
GAM3237 SDCCAG33 3' CACATAGATCAGGTG       73185       TGC
                                CACGTGG   GTCAGGTG
                                |||||||   ||||||||
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                                GTGTATC   TAGTCCAC
                                   ___
GAM3237  SEMA3C   5'  CACGTCGCAAAGGTGA     73186      GG   TC
                                CACGT  TGCG  AGGTGA
                                |||||  ||||  ||||||
                                GTGCA  GCGT  TCCACT
                                   __   T_
GAM3237  SIMRP7   3'  CACCTGTGCAGCAGGTG     73187     G  G   T
                                CAC TG TGCG CAGGTG
                                ||| || |||| ||||||
                                GTG AC ACGT GTCCAC
                                  G  _   C
GAM3237  TUBA1    5'  CACGTTGAGTCGGGGTGA    73188      GG  C   A_
                                CACGT  TG GTC  GGTGA
                                |||||  || |||  |||||
                                GTGCA  AC CAG  CCACT
                                   __ T   CC
GAM3237  LOC127602 5'  CATGGTGGGTGAAGGTGA    73189       C  C_
                                CGTGGTG GT  AGGTGA
                                |||||||  ||  ||||||
                                GTACCAC CA  TCCACT
                                    C  CT
GAM3237  LOC139673 3'  ACCTGGTGCAAAATGA      73164    G      TC
                                AC TGGTGCG  AGGTGA
                                ||  |||||||  ||||||
                                TG ACCACGT  TTTACT
                                 G      __
GAM3237  LOC149460 3'  CATTGTGCCCCCAGGTGA    73190     G   G  _
                                CGT GTGC TC AGGTGA
                                |||  |||| ||  ||||||
                                GTA CACG GG TCCACT
                                  A   G  G
GAM3237  LOC149566 5'  CACCTATGTTTCAGGTGA    73191     G  G  CG
                                CAC TG TG  TCAGGTGA
                                |||  ||  ||  ||||||||
                                GTG AT AC  AGTCCACT
                                  G  _  AA
GAM3237  LOC150159 5'  CACGCGCCACCCAGGTG     73192       G   G
                                CACGTG TGC TCAGGTG
                                ||||||  |||  |||||||
                                GTGCGC GTG GGTCCAC
                                   G   _
GAM3237  LOC151525 5'  CACGTGCCGCGCAGGTGA    73193       G   T
                                CACGTG TGCG CAGGTGA
                                ||||||  ||||  |||||||
                                GTGCAC GCGC GTCCACT
                                   G   _
GAM3237  LOC154084 5'  CACTAAGTATCAGGTGA     73194     GT   GC
                                CAC  GGT  GTCAGGTGA
                                |||  |||  |||||||||
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                                GTG  TCA  TAGTCCACT
                                  AT   __
GAM3237  LOC158293 3'  CACGATGGGTATCAGGGTG   73195     _  TGC    _
                                CACG TGG   GTCAGG TG
                                |||| |||   |||||| ||
                                GTGC ACC   TAGTCC AC
                                  T  CA_    C
GAM3237  LOC200170 3'  CACGTGGCTCCGGTGA     73196       GCG  A
                                CACGTGGT   TC GGTGA
                                ||||||||   || |||||
                                GTGCACCG   AG CCACT
                                     ___  G
GAM3237  LOC200473 5'  CACGTGCTGGATAGTGA    73197      G  C  CA
                                CACGTG TG GT  GGTGA
                                |||||| || ||  |||||
                                GTGCAC AC TA  TCACT
                                   G  C  __
GAM3237  LOC200819 3'  CACTGGAGGTCAGGTGA    73198    G   TGC
                                CAC TGG   GTCAGGTGA
                                ||| |||   |||||||||
                                GTG ACC   CAGTCCACT
                                  _   TC_
GAM3237  LOC201931 3'  GTGGCAGCTTGTCAGGTG    73199     _ __
                                GTGGT GC  GTCAGGTG
                                ||||| ||  ||||||||
                                CACCG CG  CAGTCCAC
                                   T  AA
GAM3237  LOC220002 3'  CATGGTGGGGCCAGGTGA    73200       C_
                                CGTGGTG  GTCAGGTGA
                                |||||||  |||||||||
                                GTACCAC  CGGTCCACT
                                    CC
GAM3237  LOC254018 3'  CAATAGGCTGTCAGGTGA    73201   C   T  _
                                A GTGG GC GTCAGGTGA
                                | |||| || |||||||||
                                G TATC CG CAGTCCACT
                                 T   _  A
GAM3237  LOC254594 5'  CATGGTGGGGCCAGGTGA    73200       C_
                                CGTGGTG  GTCAGGTGA
                                |||||||  |||||||||
                                GTACCAC  CGGTCCACT
                                    CC
GAM3237  LOC255925 5'  CACATGATCCGCTCAGGTG   73202       G  _
                                CACGTGGT CG TCAGGTG
                                |||||||| || |||||||
                                GTGTACTA GC AGTCCAC
                                     G  G
GAM3237  LOC256867 3'  CACGGGCCGCAAGGTG      73203     T   G   C
                                CACG GGT CGT AGGTG
                                |||| ||| ||| |||||
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                                GTGC CCG GCG TCCAC
                                  _  _  T
GAM3237 LOC51055 5' CACGCTGGTGTCAGATG    73204     _   GC
                                CACG TGGT  GTCAGGTG
                                |||| ||||  ||||||||
                                GTGC ACCA  CAGTCTAC
                                  G   __
GAM3237 LOC90786 5' CACTGTGGCCCAGGTG     73205    _    GCG
                                CAC GTGGT   TCAGGTG
                                ||| |||||   |||||||
                                GTG CACCG   GGTCCAC
                                  A   ___
GAM3237 LOC91056 3' CACCTGGCCTCAGGTGA    73206    G   GCG
                                CAC TGGT   TCAGGTGA
                                ||| ||||   ||||||||
                                GTG ACCG   AGTCCACT
                                  G   G__
GAM3237 LOC91308 3' CACGTGGTCAGGAGTGA    73207       G  TCA
                                CACGTGGT CG   GGTGA
                                |||||||| ||   |||||
                                GTGCACCA GT   TCACT
                                    _ CC_
GAM3237 LOC91923 5' CACATGGTACACCATGGGTGA 73208         GT __
                                CACGTGGTGC  CA  GGTGA
                                |||||||||  ||  |||||
                                GTGTACCATG  GT  CCACT
                                     TG  AC
GAM3238 UBE2I   3' TGGCGCAGAACCGAGATGCTGC 73211     A  T_  GTT
                                TGGC CA  GC   AGATGCTGC
                                ||||  ||  ||   |||||||||
                                ACCG GT  TG   TCTACGACG
                                  C  CT  GC_
GAM3238 C1orf16  3' GGCACATGTCCGTGCTG    73212       GC   AGA
                                GGCACAT  GTT   TGCTG
                                |||||||  |||   |||||
                                CCGTGTA  CAG   ACGAC
                                   __  GC_
GAM3238 FLJ11186 3' TGGCACATGTTTAATTCTG   73213        CG    ATG
                                TGGCACATG  TTAG   CTG
                                |||||||||  ||||   |||
                                ACCGTGTAC  AATT   GAC
                                     A_   AA_
GAM3238 FLJ20618 3' TGGGGTGTGGTCCAATGCTGC 73214    CACA  C   A
                                TGG   TG GTT GATGCTGC
                                |||   || ||| ||||||||
                                ACC   AC CAG TTACGACG
                                  CCAC  _  G
GAM3238 KIAA0552 3' TATGGCACTGCACGTCTGCTGC 73215        A   TTAGA
                                TATGGCAC TGCG    TGCTGC
                                |||||||| ||||    ||||||
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                                ATACCGTG ACGT    ACGACG
                                    _   GCAG_
GAM3238  MAPKAPK2  3'  TATGGCACTGCTGCT      73216        A   GTTAGA
                                TATGGCAC TGC     TGCT
                                |||||||| |||     ||||
                                ATACCGTG ACG     ACGA
                                    _  _______
GAM3238  NTN4      3'  TATGGCACTGTGTTCATG    73217        A  C   AG
                                TATGGCAC TG GTT  ATG
                                |||||||| || |||  |||
                                ATACCGTG AC CAA  TAC
                                    _ A   G_
GAM3238  ZIM2      3'  TGGCAGCATAAGCTGATGCTGC 73218      _   C   A
                                TGGCA CATG GTT GATGCTGC
                                ||||| |||| ||| ||||||||
                                ACCGT GTAT CGA CTACGACG
                                   C    T  _
GAM3238  ZNF282    3'  TGTGCAGTGACAAGATGCTGC  73219    _  CAT   TT
                                TG GCA   GCG  AGATGCTGC
                                || |||   |||  |||||||||
                                AC CGT   TGT  TCTACGACG
                                 A   CAC   __
GAM3238  LOC128308 5'  GCTAGATGCGTTGGGTGCTGC  73220    AC_     AGA
                                GC   ATGCGTT   TGCTGC
                                ||   |||||||   ||||||
                                CG   TACGCAA   ACGACG
                                 ATC      CCC
GAM3238  LOC145826 5'  GGCACTCCCCTAGATGCTGC   73221      ATGCG
                                GGCAC    TTAGATGCTGC
                                |||||    ||||||||||
                                CCGTG    GATCTACGACG
                                   AGGG_
GAM3238  LOC147183 3'  TGGCATACGTTCTCTGTTGC   73222      CA     AGA  C
                                TGGCA  TGCGTT   TG TGC
                                |||||  ||||||   || |||
                                ACCGT  ATGCAA   AC ACG
                                   __     GAG  A
GAM3238  LOC152992 3'  TATGATATGAAGATGCTG    73223      CAC   CGTT
                                TATGG   ATG    AGATGCTG
                                |||||   |||    ||||||||
                                ATACT   TAC    TCTACGAC
                                   A__   T___
GAM3238  LOC200583 3'  TGGATGTGCTTTAAGATGCTGC 73224     CACA   GTT_
                                TGG    TGC    AGATGCTGC
                                |||    |||    |||||||||
                                ACC    ACG    TCTACGACG
                                  TAC_   AAAT
GAM3238  LOC221814 3'  TGGAGCAGGTAGATGCTGC   73225     CACAT   T_
                                TGG    GCG  TAGATGCTGC
                                |||    |||  ||||||||||
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                                ACC    CGT  ATCTACGACG
                                 T____   CC
GAM3238  LOC90155  3'  TGGTATGTGAATCAAGATGCTG 73226    CACA  C   _
             C                   TGG   TG GTTA GATGCTGC
                                 |||   || |||| ||||||||
                                 ACC   AC TAGT CTACGACG
                                   ATAC  T   T
GAM3239  ABCD4     3'  AGACTGAACACTGGGAGA    73229       A  G  A_
                                 AGACTGAG CG TG  AGA
                                 |||||||| || ||  |||
                                 TCTGACTT GT AC  TCT
                                      _  G  CC
GAM3239  ABCD4     3'  AGACTGAACACTGGGAGA    73229       A  G  A_
                                 AGACTGAG CG TG  AGA
                                 |||||||| || ||  |||
                                 TCTGACTT GT AC  TCT
                                      _  G  CC
GAM3239  ABCD4     3'  AGACTGAACACTGGGAGA    73229       A  G  A_
                                 AGACTGAG CG TG  AGA
                                 |||||||| || ||  |||
                                 TCTGACTT GT AC  TCT
                                      _  G  CC
GAM3239  ABCD4     3'  AGACTGAACACTGGGAGA    73229       A  G  A_
                                 AGACTGAG CG TG  AGA
                                 |||||||| || ||  |||
                                 TCTGACTT GT AC  TCT
                                      _  G  CC
GAM3239  CCNDBP1   5'  GGAAGCTGAGAGAAGAC    73230   T   A    CGGT
                                 G GAAG CTGAGA   GAAGAC
                                 | |||| ||||||   ||||||
                                 C CTTC GACTCT   CTTCTG
                                 _   _    ____
GAM3239  GA        3'  GTGAAGAGCTGGGATGGT    73231       _  A  C
                                 GTGAAGA CTG GA GGT
                                 ||||||| ||| || |||
                                 CACTTCT GAC CT CCA
                                     C   C  A
GAM3239  LPIN2     3'  GTGAGGACTAAGAAATTAAG  73232     A      C   G
                                 GTGA GACTGAGA GGT AAG
                                 |||| |||||||| ||| |||
                                 CACT CTGATTCT TTA TTC
                                   C       _  A
GAM3239  MYO1E     5'  GTGAGGGCGAGACGGCGGCGAC 73233     A AC        AA
             T                   GTGA G  TGAGACGGTG  GACT
                                 |||| |  ||||||||||  ||||
                                 CACT C  GCTCTGCCGC  CTGA
                                   _ CC         CG
GAM3239  NDUFV3    3'  GTGAAGACGGTGGAAG      73234     AGACTG      _
                                 GTGA     AGACGGTG AAG
                                 ||||     |||||||| |||
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                                CACT     TCTGCCAC TTC
                                  _______       C
GAM3239  NRAS     3'  GTGAAGACTAGGATAGAC    73235         AGAC  TGA
                                GTGAAGACTG   GG   AGAC
                                ||||||||||   ||   ||||
                                CACTTCTGAT   CC   TCTG
                                     _____  TA_
GAM3239  PTHR2    3'  GTGAAGACCTGAGGTCTGGC   73236        _   AC__
                                GTGAAGAC TGAG   GGT
                                |||||||| ||||   |||
                                CACTTCTG ACTC   CCG
                                     G   CAGA
GAM3239  TEM5     3'  GTGAAGACTGGGAGGGAACCCT 73237         A  C  T   GA
                                GTGAAGACTG GA GG GAA  CT
                                |||||||||| || || |||  ||
                                CACTTCTGAC CT CC CTT  GA
                                      C  _  _   GG
GAM3239  TNR      3'  ATGGAGACTGAGGGTCAGGCT  73238     A       AC   GA  A
                                GTG AGACTGAG  GGT  AG CT
                                ||| ||||||||  |||  || ||
                                TAC TCTGACTC  CCA  TC GA
                                  C       __   G_  C
GAM3239  TYRO3    3'  GAATCAGAAAGATGGTGAAGA  73239     GACT_   C
                                GAA    GAGA GGTGAAGA
                                |||    |||| ||||||||
                                CTT    TTCT CCACTTCT
                                  AGTCT   A
GAM3239  ZNF255   3'  ATGAAGACTGAGTGAAGAC   73240          GACG
                                GTGAAGACTGA   GTGAAGAC
                                ||||||||||   ||||||||
                                TACTTCTGACT   CACTTCTG
                                     _____
GAM3239  C20orf98 3'  GTGGAGACTGAAGGTAA     73241     A       AC
                                GTG AGACTGAG  GGTGA
                                ||| ||||||||  |||||
                                CAC TCTGACTT  CCATT
                                  C       __
GAM3239  C8orf14  5'  GTGAAGATTTGGAAAGTAA   73242        C_  A  C
                                GTGAAGA  TG GA GGTGA
                                |||||||  || || |||||
                                CACTTCT  AC CT TCATT
                                    AA  _  T
GAM3239  CLIC4    3'  GTGAATGGACACAATGGTGA  73243       __  TGA  C
                                GTGAA  GAC   GA GGTGA
                                |||||  |||   || |||||
                                CACTT  CTG   TT CCACT
                                   AC   TG_  A
GAM3239  DKFZP586N0721 3'  GTGAAGGTGAGTGAAGC     73244       AC   GACG     A
                                GTGAAG  TGA   GTGAAG C
                                ||||||  |||   |||||| |
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                                CACTTC  ACT    CACTTC G
                                   C_  _____     C
GAM3239  FLJ20628  3'  GTGAAGAATGAGATGGCCCAAC 73245        C    C   GAA
              T                    GTGAAGA TGAGA GGT   GACT
                                   ||||||| ||||| |||   ||||
                                   CACTTCT ACTCT CCG   TTGA
                                      T    A   GG_
GAM3239  KIAA0161  3'  GTGAAGAGTGAGGTGA      73246        C   GAC
                                   GTGAAGA TGA   GGTGA
                                   ||||||| |||   |||||
                                   CACTTCT ACT   CCACT
                                      C  ___
GAM3239  MCM10    3'  AGACTGAGGTGGGAGGACT    73247         AC  T  A
                                   AGACTGAG  GG GA GACT
                                   ||||||||  || || ||||
                                   TCTGACTC  CC CT CTGA
                                        CA  _  C
GAM3239  moblak   3'  AGACTGAGGCTCGAGACT    73248         ACGG   A
                                   AGACTGAG    TGA GACT
                                   ||||||||    ||| ||||
                                   TCTGACTC    GCT CTGA
                                        CGA_  _
GAM3239  NEIL2    3'  TGGAGGCTGAGATGAAGACT   73249    A  A     CGG
                                   TG AG CTGAGA   TGAAGACT
                                   || || ||||||   ||||||||
                                   AC TC GACTCT   ACTTCTGA
                                    C  C     ___
GAM3239  PTPNS1   3'  GTGAAGACTGAATAAATAGGGC 73250           AC_____
                                   GTGAAGACTGAG      GGT
                                   ||||||||||||      |||
                                   CACTTCTGACTT      CCG
                                          ATTTATC
GAM3239  TIAF1    3'  GTGAAGATGGAGATGA      73251        C  A  C
                                   GTGAAGA TG GA GGTGA
                                   ||||||| || || |||||
                                   CACTTCT AC CT CTACT
                                      _  _  _
GAM3239  TRIM6    3'  GTGAAGATTGTAGTGAAGACT  73252        C  AGAC
                                   GTGAAGA TG    GGTGAAGACT
                                   ||||||| ||    ||||||||||
                                   CACTTCT AC    TCACTTCTGA
                                      A  A___
GAM3239  UQCRH    3'  ATGAAGACTGGGGTGAA     73253          AGAC
                                   GTGAAGACTG    GGTGAA
                                   ||||||||||    ||||||
                                   TACTTCTGAC    CCACTT
                                         C___
GAM3239  ZFP95    3'  GTGAAGACTGAATGTCAAC    73254          GACG   AA
                                   GTGAAGACTGA    GTG  GAC
                                   ||||||||||    |||  |||
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                                CACTTCTGACT   TAC  TTG
                                      ____  AG
GAM3239  ZFP95    3'  GTGAAGACTGAATGTCAAC   73254         GACG   AA
                                GTGAAGACTGA   GTG  GAC
                                ||||||||||   |||  |||
                                CACTTCTGACT   TAC  TTG
                                      ____  AG
GAM3239  ZNF224   3'  ATGAAGACTGAGTGAAGAC   73240         GACG
                                GTGAAGACTGA   GTGAAGAC
                                ||||||||||   ||||||||
                                TACTTCTGACT   CACTTCTG
                                      ____
GAM3239  LOC132235 5'  GTGAAGGCTGAGGGTG     73255       A    AC
                                GTGAAG CTGAG  GGTG
                                ||||||  |||||  ||||
                                CACTTC GACTC  CCAC
                                   C    __
GAM3239  LOC147077 5'  GTGGAACTGAGAGTGAGA    73256     AA      CG   A
                                GTG  GACTGAGA  GTGA GA
                                |||  ||||||||  ||||  ||
                                CAC  TTGACTCT  CACT CT
                                  C_      __   _
GAM3239  LOC149013 3'  GAAGACCAGGTGGAGAC     73257        AGAC   A
                                GAAGACTG    GGTG AGAC
                                ||||||||    ||||  ||||
                                CTTCTGGT    CCAC TCTG
                                      ____  C
GAM3239  LOC149103 3'  TGAAGACTGAGATGGTGATCAA 73258          C    A_
            CT                    TGAAGACTGAGA GGTGA  GACT
                                ||||||||||||  |||||  ||||
                                ACTTCTGACTCT CCACT  TTGA
                                      A    AG
GAM3239  LOC150299 3'  GTGAAAACTGGGTGAGA     73259         AGAC    A
                                GTGAAGACTG    GGTGA GA
                                ||||||||||    |||||  ||
                                CACTTTTGAC    CCACT CT
                                      ____    _
GAM3239  LOC152359 5'  GTGAAGACTGGGACGACA    73260         A   GT
                                GTGAAGACTG GACG  G
                                ||||||||||  ||||  |
                                CACTTCTGAC CTGC  T
                                     C   TG
GAM3239  LOC219673 3'  AGGCTGAGACAGGAGGA     73261    A       T  A
                                AG CTGAGACGG GA GA
                                ||  |||||||||  ||  ||
                                TC GACTCTGTC CT CT
                                 C       _  C
GAM3239  LOC93380  3'  GTGAAGATGGAAAACTTGAAGA 73262       CT_    GG
            CT                    GTGAAGA   GAGAC  TGAAGACT
                                |||||||   |||||  ||||||||
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                                CACTTCT   TTTTG  ACTTCTGA
                                    ACC    A_
GAM3240  CNGA1    5'  TGGGAGGTGAAGACTGCAG   73265    A  C        AGA
                                TG GA GGTGAAGACTG   CGG
                                || || ||||||||||   |||
                                AC CT CCACTTCTGAC   GTC
                                 C  _        ____
GAM3240  HDAC4    5'  CGGGACGGTGAGGGCTGGG   73266    A      AGA   AGAC
                                TG GACGGTGA   CTG    GG
                                || ||||||||   |||    ||
                                GC CTGCCACT   GAC    CC
                                 C       CCC  _____
GAM3240  PKD1     3'  TGAGACGGTGCAGGGAGTACGG 73267          A  ACT   _
              T                  TGAGACGGTG AG   GAG ACGGT
                                ||||||||||  ||   ||| |||||
                                ACTCTGCCAC TC   CTC TGCCA
                                      G  C__   A
GAM3240  MIC2L1   3'  TGGGATGGGGAAGACTGAA   73268    A  C  T
                                TG GA GG GAAGACTGAG
                                || || || ||||||||||
                                AC CT CC CTTCTGACTT
                                 C  A  C
GAM3240  LOC197414 3'  TGGATGGTGAGACAGACGG   73269    A  C    A   TG
                                TG GA GGTGA GAC  AGACGG
                                || || ||||| |||  ||||||
                                AC CT CCACT CTG  TCTGCC
                                 _ A    _  __
GAM3240  LOC256158 5'  TGGACGGTGAGGGTGAAGG   73270    A      A AC    AC
                                TG GACGGTGA G  TGAG  GG
                                || |||||||| |  ||||  ||
                                AC CTGCCACT C  ACTT  CC
                                 _       _ CC   __
GAM3241  MTAP     3'  TCTTTGTATGCATCTCTGATA  73273     G     __    A
                                TCT TTGTAT  ATCT CTGATA
                                ||| ||||||  |||| ||||||
                                AGA AACATA  TAGA GACTAT
                                  _     CG   _
GAM3241  NUMB     3'  CTCTGCTGGGCAGTTGCTGATA 73274         TA  TCTA
                                CTCTGTTG  TA    CTGATA
                                ||||||||  ||    ||||||
                                GAGACGAC  GT    GACTAT
                                     CC  CAAC
GAM3241  C6orf33  3'  TCTGTTTCTTACTGAT      73275       GTATA  _
                                TCTGTT    TCT ACTGAT
                                ||||||    ||| ||||||
                                AGACAA    AGA TGACTA
                                   ______  A
GAM3241  FLJ11795 3'  CTCAGTTTTCCTACTGATA   73276     T   GTATA
                                CTC GTT    TCTACTGATA
                                ||| |||    ||||||||||
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                                GAG CAA    GGATGACTAT
                                  T  AA___
GAM3241  FLJ31952  5'  TCTGTTGTATTTACAGA    73277        ATC  T
                                TCTGTTGTAT  TAC GA
                                ||||||||||  ||| ||
                                AGACAACATA  ATG CT
                                     A__  T
GAM3241  KIAA1492  3'  TATTGTATCTACTGAT     73278       TA
                                TGTTGTA  TCTACTGAT
                                |||||||  |||||||||
                                ATAACAT  AGATGACTA
                                   __
GAM3241  SAMHD1    3'  AACCCTTATTATCTACTGAT  73279      GTTGTA
                                AACTCT     TATCTACTGAT
                                ||||||     ||||||||||
                                TTGGGA     ATAGATGACTA
                                   ATA___
GAM3241  LOC113523 3'  TCTGTGGTAGTACTGATA    73280     T  TATC
                                TCTGT GTA    TACTGATA
                                ||||| |||    ||||||||
                                AGACA CAT    ATGACTAT
                                  C  C___
GAM3241  LOC169505 3'  TCTGTTTGGACCACTGATA   73281      GTATAT
                                TCTGTT     CTACTGATA
                                ||||||     |||||||||
                                AGACAA     GGTGACTAT
                                   ACCT__
GAM3241  LOC90936  3'  TCTTGGACGTGTCTACTGATA  73282    GT__  ATA
                                TCT   TGT   TCTACTGATA
                                |||   |||   ||||||||||
                                AGA   GCA   AGATGACTAT
                                  ACCT  C__
GAM3242  MADH6     5'  AAAGACCCCACATGGGCC    73285     T  G    ACGA
                                AAAGA CC CTACG    GCC
                                ||||| || |||||    |||
                                TTTCT GG GGTGT    CGG
                                  _ _    ACC_
GAM3242  METTL1    3'  AAAGATCCCCTATGGTCCAA  73286       G  CGACGAG
                                AAAGATCC CTA      CCAA
                                |||||||| |||      ||||
                                TTTCTAGG GAT      GGTT
                                     G  ACCA___
GAM3242  METTL1    3'  AAAGATCCCCTATGGTCCAA  73286       G  CGACGAG
                                AAAGATCC CTA      CCAA
                                |||||||| |||      ||||
                                TTTCTAGG GAT      GGTT
                                     G  ACCA___
GAM3242  METTL1    3'  AAAGATCCCCTATGGTCCAA  73286       G  CGACGAG
                                AAAGATCC CTA      CCAA
                                |||||||| |||      ||||
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                                TTTCTAGG GAT      GGTT
                                    G   ACCA___
GAM3242  RECQL    5'  GATCCGCTACAGACCGGC    73287          _  GA
                                GATCCGCTAC GAC  GC
                                |||||||||| |||  ||
                                CTAGGCGATG CTG  CG
                                     T   GC
GAM3242  SART2    5'  AAAGATCCGCTCCCAGC     73288          ACGA G
                                AAAGATCCGCT   C AGC
                                ||||||||||    | |||
                                TTTCTAGGCGA   G TCG
                                      GG__ _
GAM3242  CCT5     5'  GGAGACCGCTACGGAAGC    73289   A  T      AC
                                A AGA CCGCTACG  GAGC
                                | ||| ||||||||  ||||
                                C TCT GGCGATGC  TTCG
                                 C  _       C_
GAM3242  DKFZP434J1813 5'  GGAGACCCGCTGCGGGCC    73290   A       ACGA  A
                                A AGATCCGCT   CG GCC
                                | |||||||||   || |||
                                C TCTGGGCGA   GC CGG
                                 C       C___  C
GAM3242  FLJ11175  3'  AAAGATCCCTAAAGGTTTGAGC 73291        G   CGAC___
                                AAAGATCC CTA      GAGC
                                |||||||| |||      ||||
                                TTTCTAGG GAT      CTCG
                                    _  TTCCAAA
GAM3242  FLJ13204  5'  CGAGGTCCCGGCGAGCCAAC   73292   A  A   GCTA  A
                                A AG TCC   CG CGAGCCAAC
                                | || |||   || ||||||||||
                                G TC AGG   GC GCTCGGTTG
                                 C  C   _____  C
GAM3242  FLJ13769  3'  AAAGGCCTTGCTGTGAGCCAAC 73293      AT C_   ACGAC
                                AAAG  C  GCT    GAGCCAAC
                                ||||  |  |||    ||||||||
                                TTTC  G  CGA    CTCGGTTG
                                  CG AA   CA___
GAM3242  FLJ14054  3'  AAAGGTCTGCAACGAACAAAC  73294      A  C  T   _
                                AAAG TC GC ACGA CGAGC
                                |||| || || |||| |||||
                                TTTC AG CG TGCT GTTTG
                                  C  A  T   T
GAM3242  KIAA1706  5'  GATCCGCCAGAGCCA       73295          CGAC
                                GATCCGCTA   GAGCCA
                                |||||||||   ||||||
                                CTAGGCGGT   CTCGGT
                                     _____
GAM3242  KIAA1755  3'  AAAGATCCAGCTACAGTTGCCA 73296          _     ACGA
            AC                    AAAGATCC GCTACG   GCCAAC
                                ||||||| ||||||   ||||||
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                                TTTCTAGG CGATGT    CGGTTG
                                     T     CAA_
GAM3242  KIAA1987  3'  GGAGATCCGCACTCCAGC    73297    A      T  GA G
                                A AGATCCGC AC  C AGC
                                | |||||||| ||  | |||
                                C TCTAGGCG TG  G TCG
                                 C       _  AG _
GAM3242  ZWINT     3'  AAAGATCCAAATACGTGAG    73298        C_   AC
                                AAAGATCCG  TACG  GAG
                                |||||||||  ||||  |||
                                TTTCTAGGT  ATGC  CTC
                                     TT    A_
GAM3242  ZWINT     3'  AAAGATCCAAATACGTGAG    73298        C_   AC
                                AAAGATCCG  TACG  GAG
                                |||||||||  ||||  |||
                                TTTCTAGGT  ATGC  CTC
                                     TT    A_
GAM3242  LOC219722 5'  AAAGATCCGCCTACCTCGGC   73299         _   GA  A
                                AAAGATCCGC TAC  CG GC
                                |||||||||| |||  || ||
                                TTTCTAGGCG ATG  GC CG
                                     G   GA  _
GAM3242  LOC220895 3'  AAAGATCCCCTATGGTCCGAA  73300        G   CGA__
                                AAAGATCC CTA     CGAG
                                |||||||| |||    ||||
                                TTTCTAGG GAT     GCTT
                                     G   ACCAG
GAM3242  LOC257169 5'  GATCCGCCCCGCCGAGTCA    73301        TA  A    C
                                GATCCGC  CG CGAG CA
                                |||||||  || |||| ||
                                CTAGGCG  GC GCTC GT
                                    GG  G    A
GAM3243  FLJ20136  3'  TTTATCTCTGATCAAGGAT    73304        G    AT  T
                                TTTATCTC TGAT  AG GAT
                                |||||||| ||||  || |||
                                AAATAGAG ACTA  TC CTA
                                     _    GT  _
GAM3243  INA       3'  TTTATCTCTGGCAGTGAT     73305        G  ATA
                                TTTATCTC TG   TAGTGAT
                                |||||||| ||   |||||||
                                AAATAGAG AC   GTCACTA
                                     _  C__
GAM3244  GNB1      3'  TATTTTCAAAACATTGATTTG  73308       AA       C
                                TATTTT  CAAAGCAT GATTTG
                                ||||||  |||||||| ||||||
                                ATAAAA  GTTTTGTA CTAAAC
                                    __       A
GAM3244  MSL3L1    3'  TTTTAAAAAAGCACCTGATTT  73309       C       _
                                TTTTAA AAAGCATC GATTT
                                |||||| |||||||| |||||
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                                  AAAATT TTTCGTGG CTAAA
                                     T       A
GAM3244  SET      3'  TATTGTAACAAAGCAACTTG   73310      T        TCG
                                  TATT TAACAAAGCA   ATTTG
                                  |||| ||||||||||   |||||
                                  ATAA ATTGTTTCGT   TGAAC
                                    C         ___
GAM3244  FLJ14564  3'  CTTTAACAAAGCAGGATT     73311            TC
                                  TTTTAACAAAGCA  GATT
                                  ||||||||||||  ||||
                                  GAAATTGTTTCGT  CTAA
                                           C_
GAM3244  LOC113763 3'  TTTTAACAGAGCATCACATG   73312         A      ATT
                                  TTTTAACA AGCATCG   TG
                                  |||||||| |||||||   ||
                                  AAAATTGT TCGTAGT   AC
                                       C      GT_
GAM3244  LOC116411 3'  TTTAACAAAGCACATCTTGC   73313           T  A
                                  TTTAACAAAGCA CG TTTGC
                                  |||||||||||| || |||||
                                  AAATTGTTTCGT GT GAACG
                                           _  A
GAM3244  LOC163115 3'  TATTCTAACAAATGAGATTTG  73314            GCATC
                                  TATTTTAACAAA    GATTTG
                                  ||||||||||||    ||||||
                                  ATAAGATTGTTT    CTAAAC
                                           ACT__
GAM3245  EPS15    3'  TCTCTAAATCCAGATAAA    73317          __
                                  TCTCTAAGTT  GATAAA
                                  ||||||||||  ||||||
                                  AGAGATTTAG  CTATTT
                                        GT
GAM3245  CAMP-GEFII 3'  TCCCTAAATTACATAAAC    73318           _
                                  TCTCTAAGTTG ATAAAC
                                  |||||||||||| ||||||
                                  AGGGATTTAAT TATTTG
                                         G
GAM3245  DKFZp566D133 5'  TCTCTAAATCTTTTAAAC    73319          GA_
                                  TCTCTAAGTT   TAAAC
                                  ||||||||||   |||||
                                  AGAGATTTAG   ATTTG
                                        AAA
GAM3245  LOC253959 5'  TCTCTAAATCTTTTAAAC    73319          GA_
                                  TCTCTAAGTT   TAAAC
                                  ||||||||||   |||||
                                  AGAGATTTAG   ATTTG
                                        AAA
GAM3245  LOC256730 3'  TCACTAAGTTGTCCAAAC    73320    T       A_
                                  TC CTAAGTTG  TAAAC
                                  || ||||||||  |||||
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                                AG GATTCAAC  GTTTG
                                 T       AG
GAM3246  CRI1     3'  GTTGATAGAATAACTGTTCATA 73323      C  TTT
                                GTTGA AG   TAACTGTTCATA
                                |||||| ||   ||||||||||||
                                CAACT TC   ATTGACAAGTAT
                                   A  TT_
GAM3246  CSNK1A1  3'  GCTGAAGACTGTTCAT      73324      C  TTTTA
                                GTTGA AG    ACTGTTCAT
                                |||||| ||    |||||||||
                                CGACT TC    TGACAAGTA
                                  _ _____
GAM3246  DXF68S1E 3'  TGTTACAGTTGTGTTCAT    73325      A    TTAAC
                                TGTTG CAGTT    TGTTCAT
                                ||||| |||||    |||||||
                                ACAAT GTCAA    ACAAGTA
                                   _    C____
GAM3246  FBXL5    5'  TTGCATAATTTAACTGTTCATA 73326     A  GT_
                                TTG CA   TTTAACTGTTCATA
                                ||| ||   ||||||||||||||
                                AAC GT   AAATTGACAAGTAT
                                  _ ATT
GAM3246  GALC     3'  TGTAGACAGTTTTAATTGT    73327     T        C
                                TGT GACAGTTTTAA TGT
                                ||| |||||||||| |||
                                ACA CTGTCAAAATT ACA
                                  T         A
GAM3246  IL22RA2  3'  TGTTGATAGTTTTAATTCA    73328       C      ACT
                                TGTTGA AGTTTTA   GTTCA
                                |||||| |||||||   |||||
                                ACAACT TCAAAAT   TAAGT
                                   A      ___
GAM3246  MADH3    3'  TTGGCAGACACAGCTGTTCATA 73329     A   TTT  A
                                TTG CAG   TA CTGTTCATA
                                ||| |||   || ||||||||||
                                AAC GTC   GT GACAAGTAT
                                  C   TGT  C
GAM3246  RORB     5'  TGTTAACAGTTTTGATGTT    73330           AAC
                                TGTTGACAGTTTT   TGTT
                                ||||||||||||   ||||
                                ACAATTGTCAAAA   ACAA
                                       CT_
GAM3246  TCTE1L   3'  TGTTGATAGCTTTAAAGC    73331       C       CT
                                TGTTGA AGTTTTAA  GT
                                |||||| ||||||||  ||
                                ACAACT TCGAAATT  CG
                                   A       T_
GAM3246  FLJ10846 3'  TGTTGACATTTTCCATCAT    73332        G   AACTGT
                                TGTTGACA TTTT     TCAT
                                |||||||| ||||     ||||
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                                ACAACTGT AAAG     AGTA
                                    A   GT____
GAM3246 FLJ10933 3' TATTGATGCAAATGCTGTTCAT 73333       CA  TTTAA
                                TGTTGA  GT    CTGTTCAT
                                ||||||  ||    ||||||||
                                ATAACT  CG    GACAAGTA
                                   A_  TTTAC
GAM3246 KIAA1582 5' TGTTTACAGTTTTATTGTT   73334     G       AC
                                TGTT ACAGTTTTA  TGTT
                                |||| |||||||||  ||||
                                ACAA TGTCAAAAT  ACAA
                                  A       A_
GAM3246 MAP      3' TTGACAGTTTTTAATTGT    73335          _ C
                                TTGACAGTTTT AA TGT
                                |||||||||| || |||
                                AACTGTCAAAA TT ACA
                                       A  A
GAM3246 LOC220164 3' TGTTTATTTAAATAACTGTTCA 73336     GACAGTTT
             TA                   TGTT       TAACTGTTCATA
                                ||||       ||||||||||||
                                ACAA       ATTGACAAGTAT
                                  ATAAATTT
GAM3247 ARHGEF12 3' TCCTTGTTTATTAACAGAATTT 73339        _ C   TT  C
             AC                   TCCTTGTT AT AACA  GT TTAC
                                |||||||| || ||||  || ||||
                                AGGAACAA TA TTGT  TA AATG
                                    A  A   CT  _
GAM3247 PCSK2    3' CTTGTTATGTAACAGCCCC   73340        C_   TT
                                CTTGTTAT  AACA  GTCTT
                                ||||||||  ||||  |||||
                                GAACAATA  TTGT  CGGGG
                                    CA   __
GAM3247 PDE7A    3' TTGTAAACATTGTCTT     73341      TATC
                                TTGT   AACATTGTCTT
                                ||||   ||||||||||
                                AACA   TTGTAACAGAA
                                  T___
GAM3247 SGK      3' GTTATTAACCGTATCTTAC   73342      C   AT
                                GTTAT AAC  TGTCTTAC
                                ||||| |||  ||||||||
                                CAATA TTG  ATAGAATG
                                   A   GC
GAM3247 CLSTN2   3' TCCTTGTTGTGACTGTCCT   73343        ATCAAC
                                TCCTTGTT     ATTGTCTT
                                ||||||||     ||||||||
                                AGGAACAA     TGACAGGA
                                    CAC___
GAM3247 DKFZP586D0824 5' TCCCTGTTCAGTCCTGTTGTCT 73344         ATCAACA_
             TA                   TCCTTGTT       TTGTCTTA
                                ||||||||       ||||||||
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                                AGGGACAA       AACAGAAT
                                    GTCAGGAC
GAM3247  FLJ10035  3'  TTGTTTCAGAATTGTCTTA   73345      A   AC
                                TTGTT TCA  ATTGTCTTA
                                ||||| |||  |||||||||
                                AACAA AGT  TAACAGAAT
                                  _  CT
GAM3247  FLJ21272  3'  TCCTTGTTATTCATATTGT   73346         _ AC
                                TCCTTGTTAT CA  ATTGT
                                |||||||||| ||  |||||
                                AGGAACAATA GT  TAACA
                                     A  A_
GAM3247  GK001     3'  TTGTTATCAGCATCTCCCAC  73347         A   G
                                TTGTTATCA CATT TCTTAC
                                ||||||||| |||| ||||||
                                AACAATAGT GTAG AGGGTG
                                     C   _
GAM3247  KIAA1979  3'  TCACTGTCAACATTGTCTT   73348   TG  A
                                T  TT TCAACATTGTCTT
                                |  || ||||||||||||
                                A  GA AGTTGTAACAGAA
                                 GT  C
GAM3247  N4BP2     5'  CTTGTTATCCAACATGTCTT  73349         _    T
                                CTTGTTATC AACAT GTCTT
                                ||||||||| ||||| |||||
                                GAACAATAG TTGTA CAGAA
                                     G   _
GAM3247  P66       3'  TCCTTGTTATAACATCTC    73350         C    G
                                TCCTTGTTAT AACATT TC
                                |||||||||| |||||| ||
                                AGGAACAATA TTGTAG AG
                                       _    _
GAM3247  RNAH      3'  TCTTTGTTATCATCATTA    73351    C       A
                                TC TTGTTATCA CATTG
                                || ||||||||| |||||
                                AG AACAATAGT GTAAT
                                  A       A
GAM3247  ROBO2     5'  TCCTTGTCATCAATTCGAACTT 73352           CA  T_
                                TCCTTGTTATCAA  TTG  CTT
                                ||||||||||||  |||  |||
                                AGGAACAGTAGTT  AGC  GAA
                                       A_  TT
GAM3247  SNRK      5'  TCCTTATTATCACAGTGT    73353          A  T
                                TCCTTGTTATCA CA TGT
                                |||||||||||| || |||
                                AGGAATAATAGT GT ACA
                                       _ C
GAM3247  USP25     3'  TCCTTGTCATTAACACCTTAC  73354         C    TGT
                                TCCTTGTTAT AACAT   CTTAC
                                |||||||||| |||||  |||||
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                                AGGAACAGTA TTGTG   GAATG
                                     A    ___
GAM3247  LOC118851 5'  TCCTTATTATTATACAGTCTTA 73355         CA_   TT
              C                   TCCTTGTTAT   ACA  GTCTTAC
                                  ||||||||||   |||  |||||||
                                  AGGAATAATA   TGT  CAGAATG
                                     ATA  __
GAM3247  LOC151826 3'  GTTATCAAAATGCTTAC     73356        CAT  T
                                  GTTATCAA   TG CTTAC
                                  ||||||||   || |||||
                                  CAATAGTT   AC GAATG
                                     TT_ _
GAM3247  LOC201848 3'  TCCTTGTTATAGAACTTGT    73357         C_   A
                                  TCCTTGTTAT  AAC TTGT
                                  ||||||||||  ||| ||||
                                  AGGAACAATA  TTG AACA
                                     TC  _
GAM3248  HK1       3'  TCCAGCCAATAAATAAC     73360      A       CA
                                  TCCA CCGATAAAT  AGC
                                  |||| |||||||||  |||
                                  AGGT GGTTATTTA  TTG
                                    C       __
GAM3248  HK1       3'  TCCAGCCAATAAATAAC     73360      A       CA
                                  TCCA CCGATAAAT  AGC
                                  |||| |||||||||  |||
                                  AGGT GGTTATTTA  TTG
                                    C       __
GAM3248  HK1       3'  TCCAGCCAATAAATAAC     73360      A       CA
                                  TCCA CCGATAAAT  AGC
                                  |||| |||||||||  |||
                                  AGGT GGTTATTTA  TTG
                                    C       __
GAM3248  HK1       3'  TCCAGCCAATAAATAAC     73360      A       CA
                                  TCCA CCGATAAAT  AGC
                                  |||| |||||||||  |||
                                  AGGT GGTTATTTA  TTG
                                    C       __
GAM3248  HK1       3'  TCCAGCCAATAAATAAC     73360      A       CA
                                  TCCA CCGATAAAT  AGC
                                  |||| |||||||||  |||
                                  AGGT GGTTATTTA  TTG
                                    C       __
GAM3248  P1P373C6  3'  TCCAACCAGATGTCCTAAAGTG 73361        _   AAATC_   C
              C                   TCCAACC GAT     AAG GC
                                  |||||||  |||     ||| ||
                                  AGGTTGG CTA     TTC CG
                                     T   CAGGAT   A
GAM3249  RI58      3'  TTGAGGGTGTGGAACTGTGGTA 73364     TA    T__    ACA
                                  TTG  GGTGT   GCTGT   GTA
                                  |||  |||||   |||||   |||
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                                AAC  CCACA   TGACA   CAT
                                  TC    CCT    C__
GAM3249  ZNF221    5'  TTGTAGGCTGTTTGAAGCAGT  73365       _   GCTGTA
                                TTGTAGG TGTT     CAGT
                                ||||||| ||||     ||||
                                AACATCC ACAA     GTCA
                                    G    ACTTC_
GAM3250  ANGPT2    3'  CTTGGTTGTGACAGCAGCGT   73368    G   A       A
                                CT TGG TGTGACAGCA CGT
                                || ||| |||||||||| |||
                                GA ACC ACACTGTCGT GCA
                                 _  A        C
GAM3250  CHAC      3'  TTGCTGTGTGTCTTCAGGCA   73369       GA   GA_  _
                                TTGCTGTG  TGT   CAG CA
                                ||||||||  |||   ||| ||
                                AACGACAC  ACA   GTC GT
                                    __  GAA   C
GAM3250  HYAL1     3'  TTGCTGTGCAACCTTGGGCAAC 73370        _   G_  ACA
           GT                     TTGCTGTG GAT  TG   GCAACGT
                                ||||||||  |||  ||   |||||||
                                AACGACAC TTG  AC   CGTTGCA
                                    G   GA  C__
GAM3250  HYAL1     3'  TTGCTGTGCAACCTTGGGCAAC 73370        _   G_  ACA
           GT                     TTGCTGTG GAT  TG   GCAACGT
                                ||||||||  |||  ||   |||||||
                                AACGACAC TTG  AC   CGTTGCA
                                    G   GA  C__
GAM3250  FLJ20651  3'  TTGCTGTGAATGTCAG      73371           GA
                                TTGCTGTGGATGT  CAG
                                ||||||||||||  |||
                                AACGACACTTACA  GTC
                                          __
GAM3250  GBTS1     3'  TGCTGTGGATGTGGC       73372           ACA
                                TGCTGTGGATGTG   GC
                                ||||||||||||   ||
                                ACGACACCTACAC   CG
                                          ___
GAM3251  YWHAZ     3'  TTAATGCTACCCAATGTCA    73375      A       AA
                                TTAGT CTACCCAAT  TCA
                                ||||| |||||||||  |||
                                AATTA GATGGGTTA  AGT
                                   C        C_
GAM3251  MGC10200  3'  ATACGAAAGCCCAATAATCAGA 73376      TA___        A
           TG                     GTAC    CCCAATAATCA ATG
                                ||||    |||||||||||| |||
                                TATG    GGGTTATTAGT TAC
                                  CTTTC         C
GAM3251  NBR2      5'  TTAATACTATTCAGATCAAATG 73377         CC  ATA
                                TTAGTACTA  CA   ATCAAATG
                                |||||||||  ||   ||||||||
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                                AATTATGAT  GT   TAGTTTAC
                                     AA  C__
GAM3251  LOC153139 5'  TTAGTATTAACCAATAAT    73378       C  C
                                TTAGTA TA CCAATAAT
                                |||||| || ||||||||
                                AATCAT AT GGTTATTA
                                   A  T
GAM3251  LOC154184 5'  TTAGTATTAACCAATAAT    73378       C  C
                                TTAGTA TA CCAATAAT
                                |||||| || ||||||||
                                AATCAT AT GGTTATTA
                                   A  T
GAM3251  LOC221601 5'  TTAGTATTAACCAATAAT    73378       C  C
                                TTAGTA TA CCAATAAT
                                |||||| || ||||||||
                                AATCAT AT GGTTATTA
                                   A  T
GAM3252  CD244    5'  TGGGGAGCAGAACTGCCTTG   73381     A   A  CTCA
                                TGG GAG CG    AACTGCCTTG
                                ||| ||| ||    ||||||||||
                                ACC CTC GT    TTGACGGAAC
                                  C   _  C___
GAM3252  CELSR3   3'  TGGGGAGCAGGAGGCTGCCTTG 73382     A   A  CTCAAA
                                TGG GAG CG     CTGCCTTG
                                ||| ||| ||     ||||||||
                                ACC CTC GT     GACGGAAC
                                  C   _  CCTCC_
GAM3252  GPC6     5'  TGGGAAGGCTGCTGCCTT    73383     AG  AC   CAAA
                                TGG  AG  GCT    CTGCCTT
                                |||  ||  |||    |||||||
                                ACC  TC  CGA    GACGGAA
                                  CT  __   C___
GAM3252  C1orf17  3'  TGGGGAGATGAGGCTGCCTTG  73384     A    CGCTCAAA
                                TGG GAGA       CTGCCTTG
                                ||| ||||       ||||||||
                                ACC CTCT       GACGGAAC
                                  C    ACTCC___
GAM3252  FLJ20254  3'  TGGAGAGAAGCTGAGCCTT    73385        C   CAAACT
                                TGGAGAGA GCT     GCCTT
                                |||||||| |||     |||||
                                ACCTCTCT CGA     CGGAA
                                     T   CT____
GAM3252  FLJ20871  3'  TGGATGGGCTAAGCTGCCTTG  73386      GAGAC   C  A
                                TGGA    GCT AA CTGCCTTG
                                ||||    ||| || ||||||||
                                ACCT    CGA TT GACGGAAC
                                  ACC__   _  C
GAM3252  NXPH3    3'  GAGGGCATTTCAGACTGCCTTG 73387     AC  ___   A
                                GAG  GC   TCA ACTGCCTTG
                                |||  ||   ||| |||||||||
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                                CTC  CG   AGT TGACGGAAC
                                  C_  TAA   C
GAM3252  SDC3     3'  GAACTCTCTTGGACTGCCTTG  73388     ACG   AA__
                                GAG   CTC    ACTGCCTTG
                                |||   |||    |||||||||
                                CTT   GAG    TGACGGAAC
                                  GA_   AACC
GAM3252  LOC130813 3'  TGCAGACCCAAGCTGCCTT    73389    G  AGAC     A
                                TG AG    GCTCAA CTGCCTT
                                || ||    |||||| |||||||
                                AC TC    TGGGTT GACGGAA
                                 G  _____     C
GAM3252  LOC255328 3'  TGGAGAGAGTTCCTGACCTT   73390         CGCTCAAA  _
                                TGGAGAGA       CTG CCTT
                                ||||||||       ||| ||||
                                ACCTCTCT       GAC GGAA
                                     CAAG_____   T
GAM3252  LOC90835  5'  GGAGAGATGTTCAAGCTCC    73391        CGC    A  G
                                GGAGAGA   TCAA CT CC
                                |||||||   |||| || ||
                                CCTCTCT   AGTT GA GG
                                    ACA    C  _
GAM3252  LOC90841  3'  GGAGAGAGACTGCCTT      73392        CGCTCAA
                                GGAGAGA      ACTGCCTT
                                |||||||      ||||||||
                                CCTCTCT      TGACGGAA
                                    C_______
GAM3253  SDC2     3'  GCGCATAAAAGTTTAAA     73395     AGT
                                GTG   TAAAAGTTTAAA
                                |||   ||||||||||||
                                CGC   ATTTTCAAATTT
                                  GT_
GAM3253  FLJ21820  3'  TTTTACTGAGCAGTTTAA    73396       G    TAAA
                                TTTTAC TGAGT    AGTTTAA
                                |||||| |||||    |||||||
                                AAAATG ACTCG    TCAAATT
                                   _    _____
GAM3253  PSR      3'  TTTCACCCAAGTGAAAGTTTAA 73397       G    TA
            A                    TTTTAC TGAGT  AAAGTTTAAA
                                |||||| |||||  ||||||||||
                                AAAGTG GTTCA  TTTCAAATTT
                                   G    C_
GAM3254  ENPP2    3'  ACTAACATTTTTAATGTC    73400           TA
                                ACTAACATTTTTA  GTT
                                ||||||||||||  |||
                                TGATTGTAAAAAT  CAG
                                        TA
GAM3254  FGF2     3'  ACATTTTTACATAAAATCATT  73401          GTT_
                                ACATTTTTATA    ATCATT
                                ||||||||||    ||||||
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                                TGTAAAAATGT   TAGTAA
                                      ATTT
GAM3254  GPR48    3'  TAACACTTTTATATATC     73402          GT
                                TAACATTTTTATA  TATC
                                |||||||||||||  ||||
                                ATTGTGAAAATAT  ATAG
                                       __
GAM3254  PCDHA9   3'  ACTGGCATTTTCATAGTTAT   73403     AA
                                ACT  CATTTTTATAGTTAT
                                |||  ||||||||||||||
                                TGA  GTAAAAGTATCAATA
                                  CC
GAM3254  XRCC2    3'  CTGACATTTTTATAATAGCCAT 73404    A          TA
            T                    CT ACATTTTTATAGT  TCATT
                                || ||||||||||||  |||||
                                GA TGTAAAAATATTA  GGTAA
                                 C          TC
GAM3254  BAL      3'  CTAACATTTTTATACTATCATC 73405           __
            ATT                    CTAACATTTTTATA  GTTATCATT
                                |||||||||||||  |||||||||
                                GATTGTAAAAATAT  TAGTAGTAA
                                       GA
GAM3254  DC8      3'  ACAAATAATAGTTATCATT   73406     TTTTT
                                ACA    ATAGTTATCATT
                                |||    ||||||||||||
                                TGT    TATCAATAGTAA
                                  TTAT_
GAM3254  DKFZp761H079 3'  CCAACATTTTTATTCTCATT   73407          AGTTA
                                CTAACATTTTTAT    TCATT
                                ||||||||||||    |||||
                                GGTTGTAAAAATA    AGTAA
                                       AG___
GAM3254  FLJ11275  3'  CTAATATTTTTATAAATCCCAT 73408      C        TTA
            T                    CTAA ATTTTTATAG   TCATT
                                |||| ||||||||||   |||||
                                GATT TAAAAATATT   GGTAA
                                   A        TAG
GAM3254  FLJ23120  3'  ACTACATTTTTATAGCT     73409      A
                                ACTA CATTTTTATAGTT
                                |||| ||||||||||||
                                TGAT GTAAAAATATCGA
                                   _
GAM3254  KIAA0493  3'  ACTAACATATAAAATTATCATT 73410        TTTTAT
                                ACTAACAT     AGTTATCATT
                                ||||||||     ||||||||||
                                TGATTGTA     TTAATAGTAA
                                     TATT__
GAM3254  KIAA0855  3'  CTAACATTTTTTATCAT     73411          ATAGT
                                CTAACATTTTT    TATCAT
                                ||||||||||    ||||||
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                                GATTGTAAAAA    ATAGTA
                                      _____
GAM3254  LOC139420 3'  ACTAACATTTTTTATAGTT   73412          _
                                ACTAACATTTTT ATAGTT
                                |||||||||||| ||||||
                                TGATTGTAAAAA TATCAA
                                      A
GAM3254  LOC145868 5'  TAACATTTTTATATATCAT   73413          GT
                                TAACATTTTTATA  TATCAT
                                ||||||||||||  ||||||
                                ATTGTAAAAATAT  ATAGTA
                                      __
GAM3254  LOC256861 3'  CCAACATTTTTATTTATTAT  73414          A_
                                CTAACATTTTTAT  GTTAT
                                ||||||||||||  |||||
                                GGTTGTAAAAATA  TAATA
                                      AA
GAM3255  TEM7     3'  CCTCAGACAGTAGATAAAAAT  73417      T  A  A
                                CCTCAG TAG TA ATAAAAAT
                                |||||| ||| || ||||||||
                                GGAGTC GTC AT TATTTTTA
                                   T  _  C
GAM3255  HSPC043  3'  TCAGTTAGAACAAAAA     73418        TAA
                                TCAGTTAGA  ATAAAAA
                                |||||||||  |||||||
                                AGTCAATCT  TGTTTTT
                                      ___
GAM3255  XLKD1    3'  CTCAGCAAAAATAAAAAT    73419      TAGAT
                                CTCAGT    AAATAAAAAT
                                ||||||    ||||||||||
                                GAGTCG    TTTATTTTTA
                                   TT___
GAM3255  LOC145978 3'  CCTTAGTCAGAGATAAAAAT  73420    C     TAA
                                CCT AGTTAGA  ATAAAAAT
                                ||| |||||||  ||||||||
                                GGA TCAGTCT  TATTTTTA
                                  A     C__
GAM3255  LOC201627 3'  TCAGTTAAATACAGTAAAAAT  73421          AA_
                                TCAGTTAGATA  TAAAAAT
                                ||||||||||  |||||||
                                AGTCAATTTAT  ATTTTTA
                                      GTC
GAM3255  LOC51031  5'  CTCAAAAATAAATAAAAAT   73422     TT
                                CTCAG  AGATAAATAAAAAT
                                |||||  ||||||||||||||
                                GAGTT  TTTATTTATTTTTA
                                      __
GAM3255  LOC51200  3'  TACCCCAGCACAAAT      73423        TAG
                                TACCTCAGT  ATAAAT
                                |||||||||  ||||||
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                                ATGGGGTCG   TGTTTA
                                        ___
GAM3255  LOC90620  3'  TACCTCAGCTATGCTCAAAT   73424          GA__
                                TACCTCAGTTA    TAAAT
                                ||||||||||    |||||
                                ATGGAGTCGAT    GTTTA
                                      ACGA
GAM3256  LOC203078 3'  TATCACATGTGATAAATG    73427         C   TGTGC
                                TATCGCATG GAT    GAATG
                                |||||||| |||    |||||
                                ATAGTGTAC CTA    TTTAC
                                     A  _____
GAM3257  DKFZp761N0624 3'  CTTTACACGTCAGAA       73430          ACCAAC
                                CTTTGCACGT     CAGAA
                                ||||||||||     |||||
                                GAAATGTGCA     GTCTT
                                        _______
GAM3257  LOC153146 5'  TCTGCACAACCAGAAG      73431         TACCA      C
                                TTTGCACG     ACCAGAA G
                                ||||||||     ||||||| |
                                AGACGTGT     TGGTCTT C
                                     _____       A
GAM3258  AMHR2     3'  TATGTTGGCATGTACATTGATG 73434       CGA  G  _
           A                     TATGT   GG ATG ACATTGATGA
                                |||||   || ||| ||||||||||
                                ATACA   CC TAC TGTAACTACT
                                   A__  G   A
GAM3258  FLJ13102  3'  TGTTGAAGGATGTGCTGGTG   73435     C       ACA   A
                                TGT GAGGGATG   TTG TG
                                ||| ||||||||   ||| ||
                                ACA CTTCCTAC   GAC AC
                                  A       AC_   C
GAM3258  LOC147976 5'  TGTCACAGGTGGCATTGATG   73436       A   A  A
                                TGTCG GGG TG CATTGATG
                                ||||| ||| || ||||||||
                                ACAGT TCC AC GTAACTAC
                                   G   _  C
GAM3259  CUL5      3'  CAGCACAAACTTTACAAC     73439        TAACT
                                CAGCAC     CTTTACAAC
                                ||||||     |||||||||
                                GTCGTG     GAAATGTTG
                                    TTT__
GAM3259  MAP4      3'  GCAGCACTGACCCCCAAC     73440         A     TT
                                GCAGCACT ACTCT  AC
                                |||||||| |||||  ||
                                CGTCGTGA TGGGG  TG
                                     C     GT
GAM3259  MAP4      3'  GCAGCACTGACCCCCAAC     73440         A     TT
                                GCAGCACT ACTCT  AC
                                |||||||| |||||  ||
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                                CGTCGTGA TGGGG  TG
                                    C     GT
GAM3259  MAPRE3    3'  TGCAGCACTGACACAAAGCACC 73441          A  TCTTTACA
             C                   TGCAGCACT AC       ACCC
                                 ||||||||| ||       ||||
                                 ACGTCGTGA TG       TGGG
                                     C  TGTTTCG_
GAM3259  MEN1      5'  TGCAGCACTCGTTTCCCAC    73442          AAC_    T
                                 TGCAGCACT    TCTT AC
                                 |||||||||    |||| ||
                                 ACGTCGTGA    AGGG TG
                                     GCAA    _
GAM3259  MEN1      5'  TGCAGCACTCGTTTCCCAC    73442          AAC_    T
                                 TGCAGCACT    TCTT AC
                                 |||||||||    |||| ||
                                 ACGTCGTGA    AGGG TG
                                     GCAA    _
GAM3259  MYBPH     3'  TGCAGCACCTGGCTCTCATCAC 73443          AA_     __    A
             AGCC                    TGCAGCACT   CTCTT  TACA CC
                                 |||||||||   |||||  |||| ||
                                 ACGTCGTGG   GAGAG  GTGT GG
                                     ACC     TA    C
GAM3259  COTL1     3'  TGCAGAGATGTTCTTTACAATC 73444       CACTAAC        _
             C                   TGCAG       TCTTTACAA CC
                                 |||||       ||||||||| ||
                                 ACGTC       AGAAATGTT GG
                                    TCTACA_        A
GAM3259  DKFZP564A2416 3'  TGTAACATTAACTCTCTA     73445     C    C
                                 TG AGCA TAACTCTTTA
                                 || |||| ||||||||||
                                 AC TTGT ATTGAGAGAT
                                  A    A
GAM3259  KCNK13    5'  TGTGGCGCCAGCTCCCCACGTC 73446     CA  A   A       AA
             C                   TG  GC CTA CTCTTTAC  CC
                                 ||  || ||| ||||||||  ||
                                 AC  CG GGT GAGGGGTG  GG
                                  AC  C   C       CA
GAM3259  KIAA1157  3'  TACAGCACATTTACAGCC     73447         TAACTC      A
                                 TGCAGCAC     TTTACA CC
                                 ||||||||     |||||| ||
                                 ATGTCGTG     AAATGT GG
                                     T_____     C
GAM3259  KIAA1384  5'  GCAGTCACTCTTTACAA     73448       CACTA
                                 GCAG    ACTCTTTACAA
                                 ||||    ||||||||||||
                                 CGTC    TGAGAAATGTT
                                   AG___
GAM3259  MGC14376  3'  GCACTATTTTTACAACC     73449        ACTC
                                 GCACTA    TTTACAACC
                                 ||||||    |||||||||
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                                CGTGAT    AAATGTTGG
                                   AA__
GAM3259  MMD      3'  GCACTGACTTTTACAACC    73450      A   C
                                GCACT ACT TTTACAACC
                                ||||| ||| |||||||||
                                CGTGA TGA AAATGTTGG
                                   C   _
GAM3259  SARCOSIN  3'  AGCCTTCTTTACAATCC     73451     A  AAC       _
                                AGC CT   TCTTTACAA CC
                                ||| ||   ||||||||| ||
                                TCG GA   AGAAATGTT GG
                                  _ ___       A
GAM3259  TBDN100   3'  CAGCAGCTTCTTTACA      73452      _  AAC
                                CAGCA CT   TCTTTACA
                                ||||| ||   ||||||||
                                GTCGT GA   AGAAATGT
                                   C  ___
GAM3259  UXS1      5'  TGCACCACTAGTCCACAAC    73453     G    ACTC
                                TGCA CACTA    TTTACAAC
                                |||| |||||    ||||||||
                                ACGT GTGAT    AGGTGTTG
                                  G    C___
GAM3259  ZDHHC2    5'  GCGCTAACTCCCCATCC     73454    A         CAA
                                GC CTAACTCTTTA   CC
                                || ||||||||||   ||
                                CG GATTGAGGGGT   GG
                                 C         A__
GAM3259  ZNF387    3'  TACAGCACTGAACACAA     73455         _  TCTTT
                                TGCAGCACT AAC     ACAA
                                ||||||||| |||     ||||
                                ATGTCGTGA TTG     TGTT
                                     C  _____
GAM3259  LOC124801 3'  TGCACACTGGCTCTACAA     73456      G   AACT
                                TGCA CACT    CTTTACAA
                                |||| ||||    ||||||||
                                ACGT GTGA    GAGATGTT
                                  _   CC__
GAM3259  LOC144305 3'  CAGCATACTTTACAACC     73457      CTAACT
                                CAGCA     CTTTACAACC
                                |||||     ||||||||||
                                GTCGT     GAAATGTTGG
                                   AT____
GAM3259  LOC147180 5'  TGCAGTATCAACTCTTGTAC   73458      CAC      _
                                TGCAG   TAACTCTT TAC
                                |||||   |||||||| |||
                                ACGTC   GTTGAGAA ATG
                                   ATA       C
GAM3259  LOC148946 3'  TACAGTACTCTTTATAAC     73459      CACTA      C
                                TGCAG    ACTCTTTA AAC
                                |||||    |||||||| |||
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                                ATGTC    TGAGAAAT TTG
                                  A____      A
GAM3259  LOC150630 3'  TGCAGCACTGAGTCGCCAGCC  73460        AAC  TTTA  A
                                TGCAGCACT   TC    CA CC
                                |||||||||   ||    || ||
                                ACGTCGTGA   AG    GT GG
                                     CTC  CG__  C
GAM3259  LOC199858 5'  GCAGCACTAATCTCTGCAATCC 73461         C    A  _
                                GCAGCACTAA TCTTT CAA CC
                                |||||||||| ||||| ||| ||
                                CGTCGTGATT AGAGA GTT GG
                                      _    C  A
GAM3259  LOC201910 3'  TGAGCACTAATTTCTTGAC   73462    C      C_   T
                                TG AGCACTAA  TCTT AC
                                || ||||||||  |||| ||
                                AC TCGTGATT  AGAA TG
                                 _      AA   C
GAM3259  LOC220143 3'  CAGCACTAAGTCATACA     73463        C  TT
                                CAGCACTAA TC  TACA
                                |||||||||  ||  ||||
                                GTCGTGATT AG  ATGT
                                     C  T_
GAM3259  LOC92597  3'  GCACTAATCTTTTTTACAACC  73464       _  C_
                                GCACTAA CT  TTTACAACC
                                ||||||| ||  |||||||||
                                CGTGATT GA  AAATGTTGG
                                    A  AA
GAM3260  ADRBK1    3'  TCAGGGAAGTGGGAGTG     73467    T  CT   A
                                TC GG  AAG TGGGAGTG
                                || ||  ||| ||||||||
                                AG CC  TTC ACCCTCAC
                                 T  C_  _
GAM3260  ATP2B4    5'  TCTGGCTAAGGCCGGGGAGTG  73468         AT__
                                TCTGGCTAAG    GGGAGTG
                                ||||||||||    |||||||
                                AGACCGATTC    CCCTCAC
                                      CGGC
GAM3260  CACNA1S   3'  TCCTGCAGGTGGGAGTG     73469     G  TA  A
                                TCT GC  AG TGGGAGTG
                                ||| ||  || ||||||||
                                AGG CG  TC ACCCTCAC
                                  A  __  C
GAM3260  CELL      3'  TCGGGGGAGATGGGAGTG    73470    T  CTA
                                TC GG   AGATGGGAGTG
                                || ||   ||||||||||
                                AG CC   TCTACCCTCAC
                                 C  CC_
GAM3260  HPS4      3'  TACCTGCGGCGTGGGAGTG   73471       __  TAAGA
                                TATCT  GGC    TGGGAGTG
                                |||||  |||    ||||||||
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                                ATGGA  CCG    ACCCTCAC
                                  CG   C____
GAM3260  ICAM1    3'  TATCTGACTGAGGACAATG   73472        AA  T  G
                                TATCTGGCT  GA GG AGTG
                                |||||||||  || || ||||
                                ATAGACTGA  CT CT TTAC
                                     __  C  G
GAM3260  ITPR3    3'  TCTGGCAGAGTGGGAGTG    73473       TA  A
                                TCTGGC  AG TGGGAGTG
                                ||||||  || ||||||||
                                AGACCG  TC ACCCTCAC
                                   TC  _
GAM3260  KCNK3    3'  CATCTGTAAAATGGGAGTG   73474       GC
                                TATCTG  TAAGATGGGAGTG
                                ||||||  ||||||||||||
                                GTAGAC  ATTTTACCCTCAC

                                 __
GAM3260  MAML1    3'  CATCTGACATGGGAGTG     73475        TAAG
                                TATCTGGC   ATGGGAGTG
                                ||||||||   |||||||||
                                GTAGACTG   TACCCTCAC

                                 _____
GAM3260  MCL1     3'  TCTGGCTAGGTTGCTAGGGTG 73476         AGA___   A
                                TCTGGCTA     TGGG GTG
                                ||||||||     |||| |||
                                AGACCGAT     ATCC CAC
                                     CCAACG   _
GAM3260  NR1I2    3'  TCTTGGCCCGGGAGTG      73477    _   AAGA
                                TCT GGCT   TGGGAGTG
                                ||| ||||   ||||||||
                                AGA CCGG   GCCCTCAC
                                  A  _____
GAM3260  NR1I2    3'  TCTTGGCCCGGGAGTG      73477    _   AAGA
                                TCT GGCT   TGGGAGTG
                                ||| ||||   ||||||||
                                AGA CCGG   GCCCTCAC
                                  A  _____
GAM3260  AKAP8    3'  TCTGGCCTTTGGGAGTG     73478       AAGA
                                TCTGGCT   TGGGAGTG
                                |||||||   ||||||||
                                AGACCGG   ACCCTCAC
                                    AA__
GAM3260  FLJ20546 3'  TCTGGTTAAGAACAGGTG    73479     C    TG  A
                                TCTGG TAAGA  GG GTG
                                ||||| |||||  || |||
                                AGACC ATTCT  TC CAC
                                   A    TG  _
GAM3260  FLJ21438 5'  TCCTGCAGATGGGAGTG     73480    G  TA
                                TCT GC  AGATGGGAGTG
                                ||| ||  ||||||||||
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                              AGG CG  TCTACCCTCAC
                                A  __
GAM3260  KIAA0296  3'  ATCTGGCTGCTGAGGGTG    73481        AAGA    A
                              ATCTGGCT    TGGG GTG
                              ||||||||    |||| |||
                              TAGACCGA    ACTC CAC
                                  CG__    C
GAM3260  KIAA0453  3'  TCTTTGTAAAATGGGGGTG   73482     GGC       A
                              TCT   TAAGATGGG GTG
                              |||   ||||||||| |||
                              AGA   ATTTTACCC CAC
                                AAC       C
GAM3260  KIAA0773  3'  TGGCCCTCAGGTGGGAGTG   73483      A__  A
                              TGGCT   AG TGGGAGTG
                              |||||   || ||||||||
                              ACCGG   TC ACCCTCAC
                                 GAG  C
GAM3260  KIAA1046  3'  TCTTGTCCAGTATGGGAGTG  73484     GG_  AG
                              TCT   CTA  ATGGGAGTG
                              |||   |||  |||||||||
                              AGA   GGT  TACCCTCAC
                                ACA   CA
GAM3260  KIAA1196  3'  TATCTGTGGGCTTTGGGAGTG 73485      ___   AAGA
                              TATCT   GGCT    TGGGAGTG
                              |||||   ||||    ||||||||
                              ATAGA   CCGA    ACCCTCAC
                                 CAC    A___
GAM3260  KIAA1463  3'  TATTTGGCCAAGATATAG    73486     C        GG
                              TAT TGGCTAAGATG  AG
                              ||| ||||||||||  ||
                              ATA ACCGGTTCTAT  TC
                                A         A_
GAM3260  KIAA1615  3'  TATCTGACTAGGAGT       73487         AAGAT
                              TATCTGGCT    GGGAGT
                              |||||||||    ||||||
                              ATAGACTGA    TCCTCA
                                           _____
GAM3260  KIAA1678  3'  TATCCTAGGATGGGAGTG    73488     TGG   A
                              TATC   CTA GATGGGAGTG
                              ||||   ||| ||||||||||
                              ATAG   GAT CTACCCTCAC
                                ___   C
GAM3260  MGC2603   3'  CATCTGGCTGGGCGCG      73489        AAGAT   A
                              TATCTGGCT    GGG GTG
                              |||||||||    ||| |||
                              GTAGACCGA    CCC CGC
                                   _____   G
GAM3260  MYO3B     3'  TCTGGGGGAGGTGGGAGTG   73490      CTA  A
                              TCTGG   AG TGGGAGTG
                              |||||   || ||||||||
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                                AGACC   TC ACCCTCAC
                                   CCC  C
GAM3260  PGGT1B   5'  TCTGCAGGGATGGGAGTG    73491     G TAA
                                TCTG C   GATGGGAGTG
                                |||| |   ||||||||||
                                AGAC G   CTACCCTCAC
                                  _ TCC
GAM3260  PRO2900  3'  CATCTGGAGTGGGAGT      73492       CTA  A
                                TATCTGG   AG TGGGAGT
                                |||||||   || |||||||
                                GTAGACC   TC ACCCTCA
                                    ___ _
GAM3260  SCAND2   3'  CATCTGGCTGGGGAACTG    73493        AAGAT    _
                                TATCTGGCT    GGGAG TG
                                |||||||||    ||||| ||
                                GTAGACCGA    CCCTT AC
                                     C____    G
GAM3260  SMAP1    3'  CTGGCTAATTTTGGGGTG    73494       GA_   A
                                CTGGCTAA   TGGG GTG
                                ||||||||   |||| |||
                                GACCGATT   ACCC CAC
                                    AAA   _
GAM3260  LOC147990 3'  TCTGGCTGGACGCAGTG     73495       AA   GG
                                TCTGGCT  GATG  AGTG
                                |||||||  ||||  ||||
                                AGACCGA  CTGC  TCAC
                                   C_   G_
GAM3260  LOC148490 5'  ATCTGGCTTGAGGAGTG     73496       AAGA  _
                                ATCTGGCT    TG GGAGTG
                                ||||||||    || ||||||
                                TAGACCGA    AC CCTCAC
                                    _____  T
GAM3260  LOC157349 5'  TCTGGCTAATGGGGAGTG    73497        GAT
                                TCTGGCTAA   GGGAGTG
                                |||||||||   |||||||
                                AGACCGATT   CCCTCAC
                                    AC_
GAM3260  LOC157421 5'  CTGGTAGATGGGAGTG      73498     CTA
                                CTGG   AGATGGGAGTG
                                ||||   ||||||||||||
                                GACC   TCTACCCTCAC
                                  A__
GAM3260  LOC161829 5'  ATCTGGCTGAGGAAATG     73499       AA  T
                                ATCTGGCT  GA GGGAGTG
                                ||||||||  || |||||||
                                TAGACCGA  CT CCTTTAC
                                    __ _
GAM3260  LOC222182 3'  TATGCTGAGAGTGGGATGGGAG 73500     _   CTAA__
            TG                    TAT CTGG     GATGGGAGTG
                                ||| ||||     ||||||||||
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                                ATA GACT     CTACCCTCAC
                                  C    CTCACC
GAM3260  LOC254170 3'  TATCTGGCTGGCCAGAGTG   73501         AAGATG
                                TATCTGGCT     GGAGTG
                                |||||||||     ||||||
                                ATAGACCGA     TCTCAC
                                     CCGG__
GAM3260  LOC255397 5'  TCTGGTCTCGGGAGTG      73502      _  AAGA
                                TCTGG CT    TGGGAGTG
                                ||||| ||    ||||||||
                                AGACC GA    GCCCTCAC
                                  A ____
GAM3260  LOC257130 3'  TCTGGCCATGGGAGTG      73503        AAG
                                TCTGGCT   ATGGGAGTG
                                |||||||   |||||||||
                                AGACCGG   TACCCTCAC
                                   ___
GAM3260  LOC90906  5'  TATTTGGCCGGGAGCA      73504     C     AAGAT
                                TAT TGGCT    GGGAGTG
                                ||| |||||    |||||||
                                ATA ACCGG    CCCTCGT
                                  A   _____
GAM3260  LOC92078  3'  TATCTGGCTGGCGATGGG    73505         AA_
                                TATCTGGCT   GATGGG
                                |||||||||   ||||||
                                ATAGACCGA   CTACCC
                                     CCG
GAM3261  CDYL      3'  GGGTAAGAACTGGACGTATTT  73508     C       AC  _
                                GGG AAGAATTG  CG ATTT
                                ||| ||||||||  || ||||
                                CCC TTCTTGAC  GC TAAA
                                  A       CT  A
GAM3261  EXTL2     5'  GGGCCAGCCGATTTAT      73509      A  AATTGA
                                GGGC AG     CCGATTTAT
                                |||| ||     |||||||||
                                CCCG TC     GGCTAAATA
                                  G _______
GAM3261  IGFBP5    5'  GGGAGAGAAAAATGGATTTATC 73510     CA    TTGACC
            T                    GGG  AGAA     GATTTATCT
                                |||  ||||     |||||||||
                                CCC  TCTT     CTAAATAGA
                                  TC    TTTAC_
GAM3262  ADH5      3'  GTCTTAGGTAACACGCAG    73513     GT_   T
                                GTC   GGT GACACGCAG
                                |||   ||| |||||||||
                                CAG   CCA TTGTGCGTC
                                  AAT   _
GAM3262  CRAT      5'  GTCCGCGGACACGCAG      73514     _    TTG
                                GTC GTGG   ACACGCAG
                                ||| ||||   ||||||||
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                                CAG CGCC   TGTGCGTC
                                  G   ___
GAM3262 DCLRE1C  3' GTCATGGCTCACTGCAG    73515        G  AC
                                GTCGTGGTT AC  GCAG
                                ||||||||| ||  ||||
                                CAGTACCGA TG  CGTC
                                    G  A_
GAM3262 KCNK6    3' GTCATGGTTAAGGGCAG    73516         CAC
                                GTCGTGGTTGA   GCAG
                                ||||||||||   ||||
                                CAGTACCAATT   CGTC
                                     CC_
GAM3262 MAN2A2   3' GCCTTCAGTGACACGCAG   73517    GT_   T
                                GTC   GGT GACACGCAG
                                |||   ||| |||||||||
                                CGG   TCA CTGTGCGTC
                                  AAG   _
GAM3262 MYD88    3' GTCGTGGTCACAGCAG     73518        G   C
                                GTCGTGGTT ACA GCAG
                                ||||||||| ||| ||||
                                CAGCACCAG TGT CGTC
                                      _   _
GAM3262 P4HB     3' GTCATGGCGACACTGCAG   73519        T    _
                                GTCGTGGT GACAC GCAG
                                |||||||| ||||| ||||
                                CAGTACCG CTGTG CGTC
                                    _    A
GAM3262 PMM2     3' ATCAAGGTGACATGCAG    73520     T  T   C
                                GTCG GGT GACA GCAG
                                |||| ||| |||| ||||
                                TAGT CCA CTGT CGTC
                                  T   _   A
GAM3262 PRY      3' ATCGTGGTTCCACTCAG    73521        GA   G
                                GTCGTGGTT  CAC CAG
                                |||||||||  ||| |||
                                TAGCACCAA  GTG GTC
                                     G_   A
GAM3262 SYNGR1   3' GTCTGTGGGACACGCAG    73522     _   TT
                                GTC GTGG  GACACGCAG
                                ||| ||||  |||||||||
                                CAG CACC  CTGTGCGTC
                                  A   __
GAM3262 ARAP3    3' GTCCTGGGACACGCAG     73523     G   TT
                                GTC TGG  GACACGCAG
                                ||| |||  |||||||||
                                CAG ACC  CTGTGCGTC
                                  G   __
GAM3262 FLJ22169 5' GTCATAGTCCACGCAG     73524        GA
                                GTCGTGGTT  CACGCAG
                                |||||||||  |||||||
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                                CAGTATCAG  GTGCGTC
                                           __
GAM3262  FLJ22814  3'  GTCGAGGTGACAGCAG      73525      T  T   C
                                GTCG GGT GACA GCAG
                                |||| ||| |||| ||||
                                CAGC CCA CTGT CGTC
                                  T  _   _
GAM3262  KIAA0057  3'  GTCATGGTTTCATGCAG     73526         GA  C
                                GTCGTGGTT  CA GCAG
                                |||||||||  || ||||
                                CAGTACCAA  GT CGTC
                                     A_  A
GAM3262  KIAA0544  3'  GCCACAGTGACACGCAG     73527      TG  T
                                GTCG  GT GACACGCAG
                                ||||  || |||||||||
                                CGGT  CA CTGTGCGTC
                                  GT  _
GAM3262  KIAA0763  3'  GCCAGATGACATGCAG      73528      T  T   C
                                GTCG GGT GACA GCAG
                                |||| ||| |||| ||||
                                CGGT CTA CTGT CGTC
                                  _  _   A
GAM3262  KIAA1136  3'  GTCATAACTTGCATGCAG    73529        _  A  C
                                GTCGTGG TTG CA GCAG
                                ||||||| ||| || ||||
                                CAGTATT AAC GT CGTC
                                    G  _ A
GAM3262  KIAA1218  5'  GTCGTGGTCCCACAGCAG    73530         GA  _
                                GTCGTGGTT  CAC GCAG
                                |||||||||  ||| ||||
                                CAGCACCAG  GTG CGTC
                                     G_  T
GAM3262  RIN3      3'  GTCGCGGTCGGGAGTGCGCAG  73531          ACA___
                                GTCGTGGTTG     CGCAG
                                ||||||||||     |||||
                                CAGCGCCAGC     GCGTC
                                      CCTCAC
GAM3262  SEPT3     3'  GTCAGAGACACGCAG       73532      T  TT
                                GTCG GG  GACACGCAG
                                |||| ||  |||||||||
                                CAGT CT  CTGTGCGTC
                                  _ __
GAM3262  STK29     3'  GCCTGAGACACGCAG       73533     G   TT
                                GTC TGG  GACACGCAG
                                ||| |||  |||||||||
                                CGG ACT  CTGTGCGTC
                                  _  __
GAM3262  ZER6      5'  GTCGGGGCTCGGGACGCGCAG  73534      T   ___  A
                                GTCG GGTT   GAC CGCAG
                                |||| ||||   ||| |||||
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                                CAGC CCGA   CTG GCGTC
                                  C    GCC   C
GAM3262  LOC129676 5'  GTTTCAGCTGACATGCAG    73535    CG       C
                                GT  TGGTTGACA GCAG
                                ||  ||||||||| ||||
                                CA  GTCGACTGT CGTC
                                 AA        A
GAM3262  LOC144017 5'  GCCGTGGCGGGAGGCACGC   73536        T_ __
                                GTCGTGGT  GA  CACGC
                                ||||||||  ||  |||||
                                CGGCACCG  CT  GTGCG
                                     CC  CC
GAM3262  LOC146057 5'  GCCGTGGCGGACGCAG     73537        T   AC
                                GTCGTGGT GAC  GCAG
                                |||||||| |||  ||||
                                CGGCACCG CTG  CGTC
                                     C  __
GAM3262  LOC159160 3'  ATCGTGGTTCCACTCAG     73521        GA   G
                                GTCGTGGTT  CAC CAG
                                |||||||||  ||| |||
                                TAGCACCAA  GTG GTC
                                     G_  A
GAM3262  LOC163782 3'  GTCGTGGCTGACTCCCAG    73538          ACG
                                GTCGTGGTTGAC   CAG
                                ||||||||||||   |||
                                CAGCACCGACTG   GTC
                                       AGG
GAM3262  LOC221042 5'  GTCGTGATGACGCAG       73539        T   AC
                                GTCGTGGT GAC  GCAG
                                |||||||| |||  ||||
                                CAGCACTA CTG  CGTC
                                     _  __
GAM3262  LOC256855 3'  GTCGTAGCCACGCAG       73540        TGA
                                GTCGTGGT   CACGCAG
                                ||||||||   |||||||
                                CAGCATCG   GTGCGTC
                                     ___
GAM3262  LOC91250  5'  GTCATGGCTCACTGCAG     73515        G  AC
                                GTCGTGGTT AC  GCAG
                                |||||||||  ||  ||||
                                CAGTACCGA TG  CGTC
                                     G  A_
GAM3263  GUCY1A3   5'  TCAGGCAGCTCAGGCGACAGGG 73543     A      AG   GA
            TG                   TTAG CAGCTCAG  GAT  GGTG
                                ||||  ||||||||  |||  ||||
                                AGTC GTCGAGTC  CTG  CCAC
                                  C       CG   TC
GAM3263  UNRIP     3'  TTAGATGTTCAGAGGCAGT    73544      CAGC      ATGA
                                TTAGA    TCAGAGG    GGT
                                |||||    |||||||    |||
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                                AATCT   AGTCTCC   TCA
                                  ACA_     G___
GAM3263 KIAA1602 5' TTAGACAGCTGTGGGGGCG   73545        CAGA  ATGA
                                TTAGACAGCT   GG   GGTG
                                ||||||||||   ||   ||||
                                AATCTGTCGA   CC   CCGC
                                     CA__  C___
GAM3263 TIAF1    3' AGACAAAGAGGGTGGGGTG   73546      CTC    A  A
                                AGACAG   AGAGG TG GGTG
                                ||||||   ||||| || ||||
                                TCTGTT   TCTCC AC CCAC
                                   ___    C  C
GAM3263 ZNF-U69274 3' GATAGCTTGAGGAGGTG    73547    C   CA    TGA
                                GA AGCT  GAGGA   GGTG
                                || ||||  |||||   ||||
                                CT TCGA  CTCCT   CCAC
                                 A   A_    ___
GAM3263 LOC146895 5' TTAGACAGCCAGGATGCGG   73548        CAG     A
                                TTAGACAGCT   AGGATG GG
                                ||||||||||   |||||| ||
                                AATCTGTCGG   TCCTAC CC
                                     ___     G
GAM3263 LOC150208 5' TTAGAAGCTCAGAGGCATG   73549      C        _
                                TTAGA AGCTCAGAGG ATG
                                ||||| |||||||||| |||
                                AATCT TCGAGTCTCC TAC
                                  _        G
GAM3264 COL1A1   3' CTGAGGGTGGGGGCCACTTGGG 73552    A      T  TG___
           T                     CT AGGGTGGG GT     GGGT
                                || |||||||| ||     ||||
                                GA TCCCACCC CG     CCCA
                                 C       C  GTGAA
GAM3264 DES      3' CTGAGGCTGGGTGTGGTGT   73553    A   G      T  G
                                CT AGG TGGGTGT GG GT
                                || ||| ||||||| || ||
                                GA TCC ACCCACA CC CA
                                 C   G      _ A
GAM3264 EEF1A1   3' TAAGAGTGGGGTGGCAGGTAT  73554         T  T  __
                                TAAGGGTGGG GT GG  GGTAT
                                |||||||||| || ||  |||||
                                ATTCTCACCC CA CC  CCATA
                                     _ _ GT
GAM3264 JAM2     5' GGGTGGGGGGGATTGGGTGT   73555       T__     _
                                GGGTGGG   GTTGGG GT
                                |||||||   |||||| ||
                                CCCACCC   TAACCC CA
                                    CCC     A
GAM3264 KIF2     3' CTAGGAGTGGGCAAGGTAT    73556     A       GTT
                                CTA GGGTGGGT   GGGGTAT
                                ||| ||||||||   |||||||
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                                GAT CTCACCCG   TTCCATA
                                  C      ___
GAM3264  LASS1    3'  CTGAGGGCGGGGCCGGTGT   73557    A      T    G
                                CT AGGGTGGG GTTGG GT
                                || |||||||| ||||| ||
                                GA TCCCGCCC CGGCC CA
                                 C       _    A
GAM3264  SLC7A8   3'  GGGTGGGTGCAGGTAT     73558         TG
                                GGGTGGGTGT  GGGTAT
                                ||||||||||  ||||||
                                CCCACCCACG  TCCATA
                                          __
GAM3264  DKFZP566G1424 5'  CTAAGGGTGAGTCTCAGGTGT  73559          G TG  _
                                CTAAGGGTGGGT T  GG GT
                                |||||||||||| |  || ||
                                GATTCCCACTCA A  CC CA
                                       G GT  A
GAM3264  FLJ12484  3'  CTGAGGGTGGGGTAGTGT    73560    A      T  T  G
                                CT AGGGTGGG GT GG GT
                                || |||||||| || || ||
                                GA TCCCACCC CA TC CA
                                 C       _ _  A
GAM3264  FLJ31762  3'  CCAAGGGTGGGAGGT      73561          TGTTG
                                CTAAGGGTGGG    GGGT
                                ||||||||||     ||||
                                GGTTCCCACCC    TCCA
                                          _____
GAM3264  KIAA0930  3'  GGGCGTGGGTGAGGTAT     73562      _  T  T
                                GGGTG GG GT GGGGTAT
                                ||||| || || |||||||
                                CCCGC CC CA CTCCATA
                                   A  _  _
GAM3264  RAI17    3'  GAGTGTGTTTATGGGGTAT   73563      G  GT_
                                GGGTG GT   TGGGGTAT
                                ||||| ||   ||||||||
                                CTCAC CA   ACCCCATA
                                   A  AAT
GAM3264  LOC121133 5'  AGGGCGTGTGTGTTGGGGT   73564       G__
                                AGGGTG   GTGTTGGGGT
                                ||||||   ||||||||||
                                TCCCGC   CACAACCCCA
                                    ACA
GAM3264  LOC133121 3'  CTGAGGATGGCTCCTGGGTGT  73565    A      GTG    _
                                CT AGGGTGG   TTGGG GT
                                || |||||||   ||||| ||
                                GA TCCTACC   GACCC CA
                                 C      GAG    A
GAM3264  LOC145919 3'  CTAAGGGTGGGGAGAGGC    73566          TGTT
                                CTAAGGGTGGG    GGGGT
                                ||||||||||    |||||
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                                GATTCCCACCC   CTCCG
                                      CT__
GAM3264  LOC145980 3'  TAAGGTTGGGTGTCTCAAT   73567      G      GG
                                TAAGG TGGGTGTT  GGT
                                ||||| ||||||||  |||
                                ATTCC ACCCACAG  TTA
                                   A       AG
GAM3264  LOC147160 5'  GGGTGGGTGGGGTAT      73568       GTT
                                GGGTGGGT   GGGGTAT
                                ||||||||   |||||||
                                CCCACCCA   CCCCATA
                                    ____
GAM3264  LOC148371 3'  TAAGAGTGGGGTGGCAGGTAT  73554         T  T  __
                                TAAGGGTGGG GT GG  GGTAT
                                |||||||||| || ||  |||||
                                ATTCTCACCC CA CC  CCATA
                                      _ _  GT
GAM3264  LOC150372 5'  AGGGTGAAATGATGGGGT    73569        _  T
                                AGGGTGGG TG TGGGGT
                                |||||||| || ||||||
                                TCCCACTT AC ACCCCA
                                     T  T
GAM3264  LOC221838 3'  TAAGAGTGGGGTGGCAGGTAT  73554         T  T  __
                                TAAGGGTGGG GT GG  GGTAT
                                |||||||||| || ||  |||||
                                ATTCTCACCC CA CC  CCATA
                                      _ _  GT
GAM3264  LOC221839 3'  TAAGAGTGGGGTGGCAGGTAT  73554         T  T  __
                                TAAGGGTGGG GT GG  GGTAT
                                |||||||||| || ||  |||||
                                ATTCTCACCC CA CC  CCATA
                                      _ _  GT
GAM3264  LOC256273 5'  CTGAGGGTTGGTGGGTGGT   73570    A    G   TT  _
                                CT AGGGT GGTG  GG GGT
                                || ||||| ||||  || |||
                                GA TCCCA CCAC  CC CCA
                                 C    A   __ A
GAM3264  LOC257484 5'  CTGAGGGTGGGTGTGAG     73571    A        T
                                CT AGGGTGGGTGT GGG
                                || ||||||||||| |||
                                GA TCCCACCCACA CTC
                                 C         _
GAM3264  LOC51696  3'  AGGGCAAGCTTGGGGTAT    73572     TG   G
                                AGGG  GGT TTGGGGTAT
                                ||||  ||| |||||||||
                                TCCC  TCG AACCCCATA
                                  GT  _
GAM3265  MBP       3'  TAAAGCTTTGATTCATAGAC   73575        CAA     CT
                                TAAAGCTT   ATTCAT  GAC
                                ||||||||   ||||||  |||
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                                ATTTCGAA  TAAGTA  CTG
                                    AC_    T_
GAM3265 MS4A4A   5' TAAAGCTCCAAGTATATTTGAC 73576         ATTC  C
                                TAAAGCTTCAA   AT TGAC
                                ||||||||||   || ||||
                                ATTTCGAGGTT   TA ACTG
                                     CATA  A
GAM3265 NKX3A    3' AAACTTCAAGTCACAGAC    73577        AT   CT
                                AAGCTTCAA  TCAT  GAC
                                |||||||||  ||||  |||
                                TTTGAAGTT  AGTG  CTG
                                    C_   T_
GAM3265 TIMELESS 3' TAAAGCTCCCCATCTG     73578        AAAT
                                TAAAGCTTC   TCATCTG
                                |||||||||   |||||||
                                ATTTCGAGG   GGTAGAC
                                     ____
GAM3265 APCL     3' AAGCTTTCACCTCATCTG    73579       _ AA
                                AAGCTT CA  TTCATCTG
                                |||||| ||  ||||||||
                                TTCGAA GT  GAGTAGAC
                                   A  G_
GAM3265 FPGT     3' TAAAGTCAGTTCATCTG     73580      CT  AA
                                TAAAG  TCA  TTCATCTG
                                |||||  |||  ||||||||
                                ATTTC  AGT  AAGTAGAC
                                   __  C_
GAM3265 HEY1     3' TAAAGCTGATCATCTGA     73581       TCAAAT
                                TAAAGCT    TCATCTGA
                                |||||||    ||||||||
                                ATTTCGA    AGTAGACT
                                    CT____
GAM3265 KIAA0377 3' AAAGCTTCATAATCATATCTG 73582         AAT  __
                                AAAGCTTCA  TCA  TCTG
                                |||||||||  |||  ||||
                                TTTCGAAGT  AGT  AGAC
                                     ATT  AT
GAM3265 KIAA0410 3' AAGCTTCAAACCTGA      73583        ATTC
                                AAGCTTCAA   ATCTGA
                                |||||||||   ||||||
                                TTCGAAGTT   TGGACT
                                     ____
GAM3265 KIAA1493 3' AGAATCACTTCATCTGAC   73584    CT  AA
                                AG  TCA  TTCATCTGAC
                                ||  |||  ||||||||||
                                TC  AGT  AAGTAGACTG
                                 TT  G_
GAM3265 PRO0246  5' AAGCTTCAGTTTCAGGTCTGAC 73585        AA  __
                                AAGCTTCA  TTCA  TCTGAC
                                ||||||||  ||||  ||||||
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                                TTCGAAGT  AAGT  AGACTG
                                    CA   CC
GAM3265  SDS3     3'  AAACTTGGAAATTCATCTG   73586      C_
                                AAGCTT  AAATTCATCTG
                                ||||||  ||||||||||
                                TTTGAA  TTTAAGTAGAC
                                   CC
GAM3265  STIM2    3'  TAAAGCTTGTAAGTCCATCGTG 73587       CAAA_    _
                                TAAAGCTT    TTCATC TG
                                ||||||||    |||||| ||
                                ATTTCGAA    AGGTAG AC
                                    CATTC    C
GAM3265  LOC123036 3'  AAACTTCAACCTTCTG     73588       AT  A
                                AAGCTTCAA  TC TCTG
                                |||||||||  || ||||
                                TTTGAAGTT  GG AGAC
                                    __  A
GAM3265  LOC167837 5'  TAAAACTGTTTTCATCTG    73589      TCAAA
                                TAAAGCT    TTCATCTG
                                |||||||    ||||||||
                                ATTTTGA    AAGTAGAC
                                    CAA__
GAM3265  LOC199704 3'  AAGCTTCAAGTCAGTGA     73590       AT   TC
                                AAGCTTCAA  TCA  TGA
                                |||||||||  |||  |||
                                TTCGAAGTT  AGT  ACT
                                    C_   C_
GAM3265  LOC199923 3'  AAGCCTCAAACTCCTG      73591          AT
                                AAGCTTCAAATTC  CTG
                                ||||||||||||  |||
                                TTCGGAGTTTGAG  GAC
                                       __
GAM3265  LOC220020 3'  AAGTCTTCAAATTCCTCTG   73593    _       A
                                AAG CTTCAAATTC TCTG
                                ||| |||||||||| ||||
                                TTC GAAGTTTAAG AGAC
                                  A        G
GAM3265  LOC220020 3'  TGAGCTTCAACTCCTGA     73592   A      A   AT
                                A AGCTTCAA TTC  CTGA
                                | ||||||| |||  ||||
                                A TCGAAGTT GAG  GACT
                                 C      _  __
GAM3265  LOC255565 3'  AAGCCTCAGGCCCCCTCTG   73594       AA  A_
                                AAGCTTCA  TTC  TCTG
                                ||||||||  |||  ||||
                                TTCGGAGT  GGG  AGAC
                                    CC   GG
GAM3265  LOC90010  3'  AAGCCTCAGGCCCCCTCTG   73594       AA  A_
                                AAGCTTCA  TTC  TCTG
                                ||||||||  |||  ||||
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                                TTCGGAGT  GGG  AGAC
                                    CC   GG
GAM3265  LOC93333  5'  TAAAGCTTACAAAGATATAATC 73595        _   TTC___
             TGA                  TAAAGCTT CAAA     ATCTGA
                                  |||||||| ||||     ||||||
                                  ATTTCGAA GTTT     TAGACT
                                     T   CTATAT
GAM3266  APTX     5'  TTCGCTGGTGCCGGCTGTCCTG 73598     A   ATATATTG
             T                    TTC CTGG       TGTCCTGT
                                  ||| ||||       ||||||||
                                  AAG GACC       ACAGGACA
                                    C   ACGGCCG_
GAM3266  GPLD1    3'  TCCACTGGATGTGCCACT    73599         TATAT    _
                                  TTCACTGGA    TGTGTC CT
                                  |||||||||    |||||| ||
                                  AGGTGACCT    ACACGG GA
                                       _____     T
GAM3266  NCOA6IP  3'  TTCACTGATATTTAAGTCCTGT 73600       G   A  T
                                  TTCACTG ATAT TTG GTCCTGT
                                  ||||||| |||| ||| |||||||
                                  AAGTGAC TATA AAT CAGGACA
                                     _   _  T
GAM3266  BANP     5'  TGGATATACAGTTCTGT     73601         T  GTC
                                  TGGATATAT GT   CTGT
                                  |||||||||  ||   ||||
                                  ACCTATATG CA   GACA
                                       T  A__
GAM3266  FLJ12547 3'  CTCACTGGATGTGCCT      73602         TATAT   T
                                  TTCACTGGA    TGTG CCT
                                  |||||||||    |||| |||
                                  GAGTGACCT    ACAC GGA
                                       _____   _
GAM3266  KIAA0220  5'  TGGATATACAGTTCTGT     73601         T  GTC
                                  TGGATATAT GT   CTGT
                                  |||||||||  ||   ||||
                                  ACCTATATG CA   GACA
                                       T  A__
GAM3266  NEDD5    3'  TTCACTGGAATCTCATTTTGT  73603         TA__   G
                                  TTCACTGGA    TATT TGT
                                  |||||||||    |||| |||
                                  AAGTGACCT    GTAA ACA
                                       TAGA    A
GAM3266  LOC124302 5'  TGGATATACAGTTCTGT     73601         T  GTC
                                  TGGATATAT GT   CTGT
                                  |||||||||  ||   ||||
                                  ACCTATATG CA   GACA
                                       T  A__
GAM3266  LOC169166 3'  TTCACTGGAATTATTTTGT    73604         TA   G
                                  TTCACTGGA  TATT TGT
                                  |||||||||  |||| |||
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                                AAGTGACCT  ATAA ACA
                                     TA    A
GAM3266  LOC203335 3'  TTCACTGAATATAATGGTCTTG 73605            T  T   C
              T                   TTCACTGGATATA TG GTC TGT
                                  ||||||||||||| || ||| |||
                                  AAGTGACTTATAT AC CAG ACA
                                        T  _   A
GAM3267  STMN2     3'  GCAGGGGGATTTACTATT     73608       TGTTA
                                  GCAGG     GATTTACTATT
                                  |||||     ||||||||||
                                  CGTCC     CTAAATGATAA
                                    CC___
GAM3267  DDX35     3'  AGGTATAAAGGTTTACTATTA  73609       T_  A
                                  AGGTGT  AG TTTACTATTA
                                  ||||||  || ||||||||||
                                  TCCATA  TC AAATGATAAT
                                     TT  C
GAM3267  LOC220766 3'  ACAGACAGGATTTACTATT    73610      GT TTA
                                  GCAG  G   GATTTACTATT
                                  ||||  |   ||||||||||
                                  TGTC  T   CTAAATGATAA
                                    TG C__
GAM3267  LOC255446 3'  ACCGGCATCAGATTTATTATTA 73611     A          C
                                  GC GGTGTTAGATTTA TATTA
                                  || ||||||||||||| |||||
                                  TG CCGTAGTCTAAAT ATAAT
                                   G           A
GAM3268  SOX12     3'  GGATCGCTCTACACTCGCCCCC 73614     CCACA      A
                                  GGA     CTACACTC TTTTT
                                  |||     |||||||| |||||
                                  CCT     GATGTGAG GGGGG
                                    AGCGA       C
GAM3268  VIPR2     3'  GGAACAAGACATTCATTTTTAA 73615     CC   CT   C
                                  GGA  ACA  ACA TCATTTTTAA
                                  |||  |||  ||| ||||||||||
                                  CCT  TGT  TGT AGTAAAAATT
                                    __   TC   A
GAM3268  CHL1      3'  GGACCACACTGCCTTCCCCCT  73616          ACA  CA
                                  GGACCACACT   CT  TTTTT
                                  ||||||||||   ||  |||||
                                  CCTGGTGTGA   GA  GGGGA
                                       CG_  AG
GAM3268  FLJ25422  5'  AGATTACACTTTTGTCATTTTT 73617     CC     ACAC
              AA                    GGA  ACACT    TCATTTTTAA
                                  |||  |||||    ||||||||||
                                  TCT  TGTGA    AGTAAAAATT
                                    AA    AAAC
GAM3268  MSTP028   3'  GGCCACACTGAATTTCTA    73618    A      ACACTC
                                  GG CCACACT     ATTTTTA
                                  || |||||||     |||||||
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                                CC GGTGTGA     TAAAGAT
                                 _      CT_____
GAM3268 NFAT5    5' GAACTACAGGTCATTTTTA   73619   C     C_
                                A ACTACA  TCATTTTTA
                                | ||||||  |||||||||
                                C TGATGT  AGTAAAAAT
                                 T     CC
GAM3268 PANK     3' GGCCACGCTGCACCATTTTT  73620    A   A A   T
                                GG CCAC CT CAC CATTTTT
                                || |||| || ||| |||||||
                                CC GGTG GA GTG GTAAAAA
                                 _   C  C   _
GAM3268 PCDH16   5' GGCCACGCTTCATCCTT     73621    A   A  ACAC
                                GG CCAC CT    TCATTTTT
                                || |||| ||    ||||||||
                                CC GGTG GA    AGTAGGAA
                                 _   C  _____
GAM3268 RI58     3' GGACTGCTCTCATTTTTA    73622     CACA  ACA
                                GGAC    CT   CTCATTTTTA
                                ||||    ||   ||||||||||
                                CCTG    GA   GAGTAAAAAT
                                  AC__  ____
GAM3268 TP53INP1 3' AAACAATGCTACACTCATTTTT 73623     CACA
                                GGAC    CTACACTCATTTTT
                                ||||    |||||||||||||
                                TTTG    GATGTGAGTAAAAA
                                  TTAC
GAM3268 TP53INP1 3' AAACAATGCTACACTCATTTTT 73623     CACA
                                GGAC    CTACACTCATTTTT
                                ||||    |||||||||||||
                                TTTG    GATGTGAGTAAAAA
                                  TTAC
GAM3268 VMP      3' GGACCACATTAGCCATT     73624        C  CAC
                                GGACCACA TA   TCATT
                                |||||||| ||   |||||
                                CCTGGTGT AT   GGTAA
                                     A  C__
GAM3268 LOC121301 5' GACCACTTTCTCATTTTT    73625       ACTACA
                                GACCAC     CTCATTTTT
                                ||||||     |||||||||
                                CTGGTG     GAGTAAAAA
                                   AAA___
GAM3268 LOC147276 3' GAACCCCACGACATTTATTTTT 73626      A   T   CTC
           AA                     GGACC CAC ACA   ATTTTTAA
                                |||||| ||| |||   ||||||||
                                CTTGG GTG TGT   TAAAAATT
                                  G   C   AAA
GAM3269 ALDH2    3' TTTCTTGGTTTTGTTGC     73629          CTTAT
                                TTTCTTGGTTT    TTGT
                                ||||||||||    ||||
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                                AAAGAACCAAA    AACG
                                      AC___
GAM3269 DNASE1   5' TTTCTTGGTTCTTTTGT    73630        T  AT
                                TTTCTTGGTT CTT  TTGT
                                |||||||||| |||  ||||
                                AAAGAACCAA GAA  AACA
                                     _  __
GAM3269 KRT10    3' TTTCTTGGTTTCTGATTCA   73631          T
                                TTTCTTGGTTTCT ATTTG
                                |||||||||||| |||||
                                AAAGAACCAAAGA TAAGT
                                       C
GAM3269 TNC      3' TTTCTGGTTTCTGTTGTAT   73632     T     TAT
                                TTTCT GGTTTCT   TTGTAT
                                ||||| |||||||   ||||||
                                AAAGA CCAAAGA   AACATA
                                   _     C__
GAM3269 AP1S3    3' TTCTTGAGGGTATTTGTAT   73633      TTTCT
                                TTCTTGG    TATTTGTAT
                                |||||||    |||||||||
                                AAGAACT    ATAAACATA
                                    CCC__
GAM3269 EBNA1BP2 3' TTTCTTGGTTCTTTGTA    73634         CTTA
                                TTTCTTGGTTT    TTTGTA
                                ||||||||||    ||||||
                                AAAGAACCAAG    AAACAT
                                      ____
GAM3269 FLJ10482 3' TTTCTTGGTATCTTAAGGGT  73635        T    TTT
                                TTTCTTGGT TCTTA   GT
                                ||||||||| |||||   ||
                                AAAGAACCA AGAAT   CA
                                     T    TCC
GAM3269 FLJ22794 5' TCTTGGTTTCTCCTGT     73636         AT
                                TCTTGGTTTCTT  TTGT
                                |||||||||||  ||||
                                AGAACCAAAGAG  GACA
                                      __
GAM3269 GPR64    3' TCTTGGTTTCTTCTTGTA    73637         A
                                TCTTGGTTTCTT TTTGTA
                                |||||||||||| ||||||
                                AGAACCAAAGAA GAACAT
                                      _
GAM3269 KIAA1229 3' TTTCTTGTTTTTCTCAGGTAT 73638      G_     TTT
                                TTTCTTG  TTTCTTA   GTAT
                                |||||||  |||||||   ||||
                                AAAGAAC  AAAGAGT   CATA
                                    AA      C__
GAM3269 KIAA1804 3' TTTCTTGGCTTTTTGT     73639         CTTA
                                TTTCTTGGTTT    TTTGT
                                ||||||||||    |||||
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                                AAAGAACCGAA    AAACA
                                      ____
GAM3269  KIAA1979  3'  TTTTATGGTTTCTCTCCAGTAT 73640     CT        A TT
                                TTT  TGGTTTCTT T  GTAT
                                |||  |||||||||| |  ||||
                                AAA  ACCAAAGAG G  CATA
                                  AT        A GT
GAM3269  MSTP043   3'  TTTCTGGTGGTTTATTTGT    73641      T   TTC
                                TTTCT GGT   TTATTTGT
                                ||||| |||   ||||||||
                                AAAGA CCA   AATAAACA
                                   _  CCA
GAM3269  LOC129526 3'  TTTCTTAGTTTCTTTTCTAT   73642            A
                                TTTCTTGGTTTCTT TTTGT
                                |||||||||||||| |||||
                                AAAGAATCAAAGAA AGATA
                                         A
GAM3269  LOC144486 3'  TTTCTTGGCTTTTTGTA     73643          CTTA
                                TTTCTTGGTTT    TTTGTA
                                ||||||||||    ||||||
                                AAAGAACCGAA    AAACAT
                                      ____
GAM3269  LOC158696 3'  TTTCTTGGTTTATATATG    73644          CT   T
                                TTTCTTGGTTT  TAT TG
                                ||||||||||  ||| ||
                                AAAGAACCAAA  ATA AC
                                      T_   T
GAM3269  LOC200854 3'  TTTCTTGGTTTTTTCTTTCTG  73645          ___    A
                                TTTCTTGGTT   TCTT TTTG
                                ||||||||||   |||| ||||
                                AAAGAACCAA   AGAA AGAC
                                      AAA   _
GAM3269  LOC200916 3'  TTTCTTGGTATTTCTCATGTAT 73646          __     TT
            A                    TTTCTTGGT  TTCTTA  TGTATA
                                ||||||||  ||||||  ||||||
                                AAAGAACCA  AAGAGT  ACATAT
                                      TA     __
GAM3269  LOC255177 3'  TTTCTGGTTTTACTTGT     73647      T    CT
                                TTTCT GGTTT  TATTTGT
                                ||||| |||||  |||||||
                                AAAGA CCAAA  ATGAACA
                                   _    __
GAM3270  APAF1     3'  TATAATACAAAAAAATACA    73650          CAAGC
                                TATAATGCAAAA    AATACA
                                ||||||||||||    ||||||
                                ATATTATGTTTT    TTATGT
                                      T_____
GAM3270  APAF1     3'  TATAATACAAAAAAATACA    73650          CAAGC
                                TATAATGCAAAA    AATACA
                                ||||||||||||    ||||||
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                                ATATTATGTTTT    TTATGT
                                      T____
GAM3270 CSF2RB   3' ATAATGCAGAACCTACAA    73651        A  AA
                                ATAATGCA AAC  GCAA
                                |||||||| |||  ||||
                                TATTACGT TTG  TGTT
                                     C   GA
GAM3270 E2F3     3' TAATGCAAACAAAATACA    73652         A  GC
                                TAATGCAAA CAA  AATACA
                                ||||||||| |||  ||||||
                                ATTACGTTT GTT  TTATGT
                                      _  __
GAM3270 KLHL1    3' TATAATACAAAACAAATTAC  73653             CAA
                                TATAATGCAAAACAAG   TAC
                                ||||||||||||||||   |||
                                ATATTATGTTTTGTTT   ATG
                                      A__
GAM3270 LIG4     5' ACGCAGGTAAAGCAGGCAATAC 73654      ___  _ A
             A                   ATGCA   AAA CA GCAATACA
                                 |||||   ||| || ||||||||
                                 TGCGT   TTT GT CGTTATGT
                                    CCA   C  C
GAM3270 PSAP     3' TAGTGCAAAACAAAAATCAC  73655    A        CAA
                                TA TGCAAAACAAG   TAC
                                || ||||||||||   |||
                                AT ACGTTTTGTTT   GTG
                                 C         TTA
GAM3270 PUM2     3' TATAAGCAAAACAAAATACAA  73656      T       GC
                                TATAA GCAAAACAA  AATACAA
                                ||||| |||||||||  |||||||
                                ATATT CGTTTTGTT  TTATGTT
                                      _       __
GAM3270 ARF6     3' TGAATGCAAAATAAGCCATCTA 73657    T       C    AA__
             CA                   A AATGCAAAA AAGC    TACA
                                  | |||||||| ||||    ||||
                                  A TTACGTTTT TTCG    ATGT
                                   C        A    GTAG
GAM3270 BCAA     3' CATAATAAAATAAGCAATACAA 73658        CA   C
                                TATAATG  AAA AAGCAATACAA
                                |||||||  ||| ||||||||||
                                GTATTAT  TTT TTCGTTATGTT
                                     __   A
GAM3270 DKFZP434L0117 3'  TATAATCAAAATACGCAATACA 73659       G    CAA
             A                   TATAAT CAAAA   GCAATACAA
                                 ||||||| |||||   |||||||||
                                 ATATTA GTTTT   CGTTATGTT
                                     _    ATG
GAM3270 HDAC9-PENDING 3'  TAATGCAAAACAACTGACAA   73660           ___
                                TAATGCAAAACAA   GCAA
                                ||||||||||||   ||||
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                                ATTACGTTTTGTT  TGTT
                                       GAC
GAM3270  HNOEL-iso 3'  TAATGCAAAATGTTGCAATACA 73661         CAA_
             A                  TAATGCAAAA   GCAATACAA
                                ||||||||||   |||||||||
                                ATTACGTTTT   CGTTATGTT
                                     ACAA
GAM3270  KIAA0040  3'  TAATACAGTCACAATACAA   73662       AAACAA
                                TAATGCA     GCAATACAA
                                |||||||     |||||||||
                                ATTATGT     TGTTATGTT
                                   CAG___
GAM3270  MMD       3'  GCACCAAACAGGCAATACAA  73663     __    A
                                GCA  AAACA GCAATACAA
                                |||  ||||| |||||||||
                                CGT  TTTGT CGTTATGTT
                                  GG    C
GAM3270  MST4      3'  TATAATGAATAAGCAATACAA 73664       CAA  C
                                TATAATG   AA AAGCAATACAA
                                |||||||   || ||||||||||
                                ATATTAC   TT TTCGTTATGTT
                                   ___ A
GAM3270  RNF11     3'  TGCAAAACATAAAATACAA   73665        AGC
                                TGCAAAACA   AATACAA
                                |||||||||   |||||||
                                ACGTTTTGT   TTATGTT
                                     ATT
GAM3270  SHARP     3'  ATACAAATGAGTGGGCAATACA 73666       ACAA___
             A                   ATGCAAA      GCAATACAA
                                 |||||||      |||||||||
                                 TATGTTT      CGTTATGTT
                                    ACTCACC
GAM3270  STRN3     3'  TATAATGCAGAAAAACTTCAAT 73667        ___   AAG
             ACAA                   TATAATGCA   AAAC   CAATACAA
                                    |||||||||   ||||   ||||||||
                                    ATATTACGT   TTTG   GTTATGTT
                                         CTT    AA_
GAM3270  LOC144747 5'  TACAATGCAAAACAACA     73668            G
                                TATAATGCAAAACAA CA
                                |||||||||||||| ||
                                ATGTTACGTTTTGTT GT
                                                _
GAM3270  LOC153642 3'  TAATACAAAACAAAGACCAACA 73669           ___
                                TAATGCAAAACAAG   CAATA
                                ||||||||||||||   |||||
                                ATTATGTTTTGTTT   GTTGT
                                         CTG
GAM3270  LOC154792 3'  TATAAGCAAATGCAATACA   73670      T    ACAA
                                TATAA GCAAA    GCAATACA
                                ||||| |||||    ||||||||
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                                ATATT CGTTT    CGTTATGT
                                  _     A___
GAM3270  LOC219686 3'  TATAAGCAAGACAAAGCAA   73671      T   A   _
                                TATAA GCAA ACAA GCAA
                                ||||| |||| |||| ||||
                                ATATT CGTT TGTT CGTT
                                  _   C   T
GAM3270  LOC221037 3'  TATAATACAAAACAGCTATA  73672           A  A
                                TATAATGCAAAACA GC ATA
                                |||||||||||||| || |||
                                ATATTATGTTTTGT CG TAT
                                        _ A
GAM3271  BAALC    3'  TCAGGCAGCAGTTTGCTGCGCA 73675      _____  T_____  CAGAT
           TCTG                   GGCAGC   TGC    CGC    G
                                |||||||   |||    |||    |
                                CCGTCG   ACG    GCG    C
                                   TCAA   ACIII   TAGAC
GAM3271  ECM1     5'  TCAGGCAAGTCTGGATG     73676       _ _  CTCGCCA
                                TCAGGCA G CTG      GATG
                                ||||||| | |||      ||||
                                AGTCCGT C GAC      CTAC
                                   T A  ________
GAM3271  KIF3C    3'  TCAGGGGCTGCTCGCCA     73677      CA
                                TCAGG  GCTGCTCGCCA
                                |||||  ||||||||||
                                AGTCC  CGACGAGCGGT
                                  C_
GAM3271  MIC2     3'  TCAGGCAGCTGTTCTAACC   73678          C  __
                                TCAGGCAGCTG TC  GCC
                                |||||||||| ||  |||
                                AGTCCGTCGAC AG  TGG
                                      A  AT
GAM3271  MYOZ1    5'  TCAGCCGGCTGCTCGGGCAG  73679      G A_      C_
                                TCAG C  GCTGCTCG  CAG
                                |||| |  ||||||||  |||
                                AGTC G  CGACGAGC  GTC
                                  _ GC       CC
GAM3271  SCNN1G   3'  TCAGGTGGCCAGATG      73680      CAGC  CTC
                                TCAGG   TG   GCCAGATG
                                |||||   ||   ||||||||
                                AGTCC   AC   CGGTCTAC
                                   _____ ____
GAM3271  VENTX2   3'  CCAGGTAGGAGCCAGGTGCG  73681      C  CTGCTC    A
                                TCAGG AG     GCCAG TGCG
                                ||||| ||     ||||| ||||
                                GGTCC TC     CGGTC ACGC
                                  A  CT_____    C
GAM3271  ARHF     3'  TCAGGCTGTGGCCAGATG    73682       AGC  CTC
                                TCAGGC   TG   GCCAGATG
                                ||||||   ||   ||||||||
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                                AGTCCG  AC  CGGTCTAC
                                   ___ AC_
GAM3271 BTBD3   3' TCAGGCAAGTTGGAACCAGATG 73683       CTGCTC
                                TCAGGCAG    GCCAGATG
                                ||||||||    ||||||||
                                AGTCCGTT    TGGTCTAC
                                    CAACCT
GAM3271 FLJ20309 3' TCAGCAGCTGGGCAGGATG   73684    G    CTC  CA
                                TCAG CAGCTG  GC  GATG
                                |||| ||||||  ||  ||||
                                AGTC GTCGAC  CG  CTAC
                                  _    C__ TC
GAM3271 FLJ22246 3' CAGGCAGGCCAGATG     73685      CTGCTC
                                CAGGCAG    GCCAGATG
                                |||||||    ||||||||
                                GTCCGTC    CGGTCTAC

                                _______
GAM3271 FTSJ3   3' TCAGACAGCTGTGATGTGCGCA 73686       CT_________  CAGAT
           TCTG                 GGCAGCTG       CGC   G
                                ||||||||       |||   |
                                CTGTCGAC       GCG   C
                                   ACTACACIII  TAGAC
GAM3271 HSPC251  3' TCAGGCAGCTGCTTTTGCGCAT 73687        T________  CAGAT
           CTG                  AGGCAGCTGC     CGC   G
                                ||||||||||     |||   |
                                TCCGTCGACG     GCG   C
                                   AAAACIII  TAGAC
GAM3271 MYH7B   3' CAGGTGGCCTCAGCCAGATG  73688    CA  TG  _
                                CAGG  GC  CTC GCCAGATG
                                ||||  ||  ||| ||||||||
                                GTCC  CG  GAG CGGTCTAC
                                  AC  __  T
GAM3271 SEMA6B  3' AGACAGCTGCTGCCGATG   73689        C   A
                                AGGCAGCTGCT GCC GATG
                                |||||||||||| ||| ||||
                                TCTGTCGACGA CGG CTAC
                                   _  _
GAM3271 SEMA6B  3' AGACAGCTGCTGCCGATG   73689        C   A
                                AGGCAGCTGCT GCC GATG
                                |||||||||||| ||| ||||
                                TCTGTCGACGA CGG CTAC
                                   _  _
GAM3271 SEMA6B  3' AGACAGCTGCTGCCGATG   73689        C   A
                                AGGCAGCTGCT GCC GATG
                                |||||||||||| ||| ||||
                                TCTGTCGACGA CGG CTAC
                                   _  _
GAM3271 LOC119587 5' TCGGGCAGCTGGCTCTCATGTG 73690    A     _  GC  GA
                                TC GGCAGCTG CTC  CA  TG
                                || |||||||| |||  ||  ||
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                                AG CCGTCGAC GAG  GT  AC
                                 C       C   A_  AC
GAM3271  LOC132332 3'  AGACAGCCCTAGATG       73691        G  CGCC
                                AGGCAGCT CT    AGATG
                                |||||||| ||    |||||
                                TCTGTCGG GA    TCTAC
                                   _  ____
GAM3271  LOC161003 5'  CAGGCAGCAACTCAGATG    73692        T   GCC
                                CAGGCAGC GCTC   AGATG
                                |||||||| ||||   |||||
                                GTCCGTCG TGAG   TCTAC
                                     T   ___
GAM3272  AASS     3'  AACAAAATATAATTCCC     73695        GTATC
                                AACAAAA    TATAATTCCC
                                |||||||    ||||||||||
                                TTGTTTT    ATATTAAGGG
                                   _____
GAM3272  ATRX     3'  ACAAAAGTATTTCATAACT    73696         C_
                                ACAAAAGTAT  TATAATT
                                ||||||||||  |||||||
                                TGTTTTCATA  GTATTGA
                                      AA
GAM3272  ATRX     3'  ACAAAAGTATTTCATAACT    73696         C_
                                ACAAAAGTAT  TATAATT
                                ||||||||||  |||||||
                                TGTTTTCATA  GTATTGA
                                      AA
GAM3272  CELSR1   3'  AAAAGTATCTCCACCTTTCCCA 73697          ATAA__
                                AAAAGTATCT     TTCCCA
                                ||||||||||     ||||||
                                TTTTCATAGA     AAGGGT
                                      GGTGGA
GAM3272  CMAR     3'  AAAGTATCTCAACAATTCTCA  73698         __     C
                                AAAGTATCT  ATAATTC CA
                                |||||||||  ||||||| ||
                                TTTCATAGA  TGTTAAG GT
                                     GT      A
GAM3272  GCH1     3'  CAAAAGTATCTACACTC      73699            A
                                CAAAAGTATCTATA TTC
                                |||||||||||||| |||
                                GTTTTCATAGATGT GAG
                                      _
GAM3272  HCS      3'  CAAAAGCACCATTCCC       73700          TATA
                                CAAAAGTATC    ATTCCC
                                ||||||||||    ||||||
                                GTTTTCGTGG    TAAGGG
                                      ____
GAM3272  HIVEP2   3'  TAACAAAAGTATATATAAT    73701           C
                                TAACAAAAGTAT TATAAT
                                |||||||||||| ||||||
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                                ATTGTTTTCATA ATATTA
                                       T
GAM3272  PXMP3    3'  ACAAAAGCTGTCCATTATTC   73702        A_    A
                                ACAAAAGT  TCTAT ATTC
                                ||||||||  ||||| ||||
                                TGTTTTCG  AGGTA TAAG
                                    AC    A
GAM3272  PYCS     5'  TAACCAAAGTATCTTCCC    73703     A       ATAAT  _
                                TAAC AAAGTATCT    TCC C
                                |||| |||||||||    ||| |
                                ATTG TTTCATAGA    AGG G
                                  G       _____  A
GAM3272  SPG7     3'  AAAGTATCTCAACAATTCTCA  73698         __      C
                                AAAGTATCT  ATAATTC CA
                                |||||||||  ||||||| ||
                                TTTCATAGA  TGTTAAG GT
                                     GT      A
GAM3272  AFAP     3'  ACAAAAGCATCTGTCC      73704          ATAAT
                                ACAAAAGTATCT    TCC
                                ||||||||||||    |||
                                TGTTTTCGTAGA    AGG
                                       C____
GAM3272  DKFZP564G092 5'  ACAGGTATTCTATAATTCC   73705     AAA   _
                                ACA   GTAT CTATAATTCC
                                |||   |||| ||||||||||
                                TGT   CATA GATATTAAGG
                                  C__   A
GAM3272  FLJ11838 3'  AAGGAATATATAATTCCC    73706     T_  C
                                AAG  AT TATAATTCCC
                                |||  || ||||||||||
                                TTC  TA ATATTAAGGG
                                  CT  T
GAM3272  FLJ22944 5'  AAATATTACATAATTCCCA   73707       C_
                                AAGTAT  TATAATTCCCA
                                ||||||  ||||||||||
                                TTTATA  GTATTAAGGGT
                                    AT
GAM3272  KIAA0171 3'  CAAAAGTATATACATTCC    73708         C    A
                                CAAAAGTAT TATA TTCC
                                |||||||| |||| ||||
                                GTTTTCATA ATGT AAGG
                                      T   _
GAM3272  KLF12    3'  TAACCGAAGAGTTAATTCCC  73709     AA   TATCTA
                                TAAC  AAG     TAATTCCC
                                ||||  |||     ||||||||
                                ATTG  TTC     ATTAAGGG
                                  GC   TCA___
GAM3272  PCDH19   3'  ACAAAAGCAATATGATTCC   73710         TC   A
                                ACAAAAGTA  TAT ATTCC
                                |||||||||  ||| |||||
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                                TGTTTTCGT  ATA TAAGG
                                     T_   C
GAM3272  TSPAN-2   3'  TAACAAGAATCAGGAATTCCCA 73711       AAGT   TAT
                                TAACAA    ATC   AATTCCCA
                                ||||||    |||   ||||||||
                                ATTGTT    TAG   TTAAGGGT
                                   CT__   TCC
GAM3272  LOC157317 3'  CAAAAGCACCATTCCC      73700         TATA
                                CAAAAGTATC    ATTCCC
                                ||||||||||    ||||||
                                GTTTTCGTGG    TAAGGG
                                      _____
GAM3272  LOC91531  5'  ACAACTGGCTATAATTCCCA   73712      AAGTAT
                                ACAA     CTATAATTCCCA
                                ||||     ||||||||||||
                                TGTT     GATATTAAGGGT
                                  GACC__
GAM3273  KIAA0561  5'  CTGCGGCAGCCACGTCCTCGGC 73715    A      CA     ATA__
              GT                  CT CGGCAGT  CACGTC    CGT
                                || |||||||  ||||||    |||
                                GA GCCGTCG  GTGCAG    GCA
                                 C       __      GAGCC
GAM3273  LOC150862 3'  CTACAGCAGTTACATTGTACGT 73716        C  A_________  TCATA
              ATGC                  CGGCAGT AC        CG     C
                                ||||||| ||        ||    |
                                GTCGTCA TG        GC     G
                                    A  TAACAIIIT  ATACT
GAM3273  LOC221543 5'  TGACGGCAGTTGTGCCAATCGT 73717   T      CACAC    TA
                                C ACGGCAGT    GTCA  CGT
                                | ||||||||    ||||  |||
                                A TGCCGTCA    CGGT  GCA
                                 C       ACA__    TA
GAM3273  LOC257596 5'  TGACGGCAGTTGTGCCAATCGT 73717   T      CACAC    TA
                                C ACGGCAGT    GTCA  CGT
                                | ||||||||    ||||  |||
                                A TGCCGTCA    CGGT  GCA
                                 C       ACA__    TA
GAM3274  FLJ13081  3'  CATCATTACTAATTTATATAAT 73720         CTAAAA
                                TATCATTACT     TATATAAT
                                ||||||||||     ||||||||
                                GTAGTAATGA     ATATATTA
                                      TTAA__
GAM3275  CLECSF12  3'  CATCATCAGATTTTATGT    73723        __
                                CATCATT  ATTTTATGT
                                |||||||  |||||||||
                                GTAGTAG  TAAAATACA
                                    TC
GAM3275  HTR2C     3'  TATTACATCTCATTATCCT    73724        CCA
                                TATTACA   TCATTATTTT
                                |||||||   ||||||||||
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                                ATAATGT   AGTAATAGGA
                                   AG_
GAM3275  FLJ31737  3'  CCATCATTAACATTATGT    73725        TT_
                                CCATCATTA   TTATGT
                                |||||||||   ||||||
                                GGTAGTAAT   AATACA
                                   TGT
GAM3275  KIAA0419  3'  TACACTGTCTCAATTTTATGT  73726      CA  ATT
                                TACAC  TC   ATTTTATGT
                                |||||  ||   |||||||||
                                ATGTG  AG   TAAAATACA
                                   AC  AGT
GAM3275  KIAA0565  5'  TTACCCCATCCTTTTTATGT   73727     A    ATTA
                                TTAC CCATC    TTTTATGT
                                |||| |||||    ||||||||
                                AATG GGTAG    AAAATACA
                                  G    GA__
GAM3275  ROBO2     3'  TTACAGCCATCATTATCC     73728      _
                                TTACA CCATCATTATTT
                                ||||| ||||||||||||
                                AATGT GGTAGTAATAGG
                                   C
GAM3275  LOC150967 5'  TACACCAAACATTTTATGT    73729       TCAT
                                TACACCA    TATTTTATGT
                                |||||||    ||||||||||
                                ATGTGGT    GTAAAATACA
                                   TT__
GAM3275  LOC201287 5'  TTACCCCATCCTTTTTATGT   73727     A    ATTA
                                TTAC CCATC    TTTTATGT
                                |||| |||||    ||||||||
                                AATG GGTAG    AAAATACA
                                  G    GA__
GAM3275  LOC222160 5'  TATTATCACCATCATTTACTAT 73730      _       _  T
            ATGT                   TATTA CACCATCATT ATT TATGT
                                |||||  |||||||||| ||| |||||
                                ATAAT GTGGTAGTAA TGA ATACA
                                   A        A   T
GAM3275  LOC256207 5'  TTACCCCATCCTTTTTATGT   73727     A    ATTA
                                TTAC CCATC    TTTTATGT
                                |||| |||||    ||||||||
                                AATG GGTAG    AAAATACA
                                  G    GA__
GAM3276  APP       3'  TCGATTCTTAAAGCATATGT   73733      CAT   TT   C
                                TCGAT   TCTT  AGCA ATGT
                                |||||   ||||  |||| ||||
                                AGCTA   AGAA  TCGT TACA
                                   ____   TT   A
GAM3276  APPBP2    3'  TCAATCATGTTTTGGCATGTGT 73734        TC   A   CA
                                TCGATCAT  TTTT GCA  TGT
                                ||||||||  |||| |||  |||
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                                AGTTAGTA  AAAA CGT  ACA
                                    C_    C   AC
GAM3276  CCR2     3'  GATTATTCCCTGAGCACATGT  73735     C      T
                                GAT ATTCTTT AGCACATGT
                                ||| ||||||| |||||||||
                                CTA TAAGGGA TCGTGTACA
                                  A      C
GAM3276  ABLIM    3'  GACATTTCATCTGCACATGT   73736     CA   T   A
                                GAT  TTC TTT GCACATGT
                                |||  ||| ||| ||||||||
                                CTG  AAG AGA CGTGTACA
                                  TA   T   _
GAM3276  ABLIM    3'  GACATTTCATCTGCACATGT   73736     CA   T   A
                                GAT  TTC TTT GCACATGT
                                |||  ||| ||| ||||||||
                                CTG  AAG AGA CGTGTACA
                                  TA   T   _
GAM3276  DNAJC6   3'  GAACATTCTTCCACATGT    73737    T      TAG
                                GA CATTCTTT   CACATGT
                                || ||||||||   |||||||
                                CT GTAAGAAG   GTGTACA
                                 T      ___
GAM3276  LOC158629 5'  TCAGTCATTCTTTATCCATGT  73738     A        TAGCA
                                TCG TCATTCTTT     CATGT
                                ||| |||||||||     |||||
                                AGT AGTAAGAAA     GTACA
                                  C        TAG__
GAM3276  LOC219540 5'  GATTACTTTCAGCCTGCATGT  73739     CATT      A__
                                GAT    CTTTTAGC   CATGT
                                |||    ||||||||   |||||
                                CTA    GAAAGTCG   GTACA
                                  AT__       GAC
GAM3277  AQP6     5'  CTTCTTGATTCTTCCT      73742    C       AGCA
                                CT CTTGATTTT    TCCT
                                || |||||||||    ||||
                                GA GAACTAAGA    AGGA
                                 A       ____
GAM3277  BIN1     3'  TCCTCTTGATTTCCCT      73743       C      AGCAT
                                TCCTC TTGATTTT     CCT
                                ||||| ||||||||     |||
                                AGGAG AACTAAAG     GGA
                                   _      _____
GAM3277  BIN1     3'  TCCTCTTGATTTCCCT      73743       C      AGCAT
                                TCCTC TTGATTTT     CCT
                                ||||| ||||||||     |||
                                AGGAG AACTAAAG     GGA
                                   _      _____
GAM3277  BRCA1    3'  TCCTTGATTTTCTTCCT     73744          AGCA
                                TCCTTGATTTT    TCCT
                                ||||||||||    ||||
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                                AGGAACTAAAA   AGGA
                                      GA__
GAM3277 FGF1    3' TCCTTCTGAAATCATCCTC   73745    CC   TTTTAG
                                TCCT  TTGA    CATCCTC
                                ||||  ||||    |||||||
                                AGGA  GACT    GTAGGAG
                                  A_   TTA___
GAM3277 FGF1    3' TCCTTCTGAAATCATCCTC   73745    CC   TTTTAG
                                TCCT  TTGA    CATCCTC
                                ||||  ||||    |||||||
                                AGGA  GACT    GTAGGAG
                                  A_   TTA___
GAM3277 FGF1    3' TCCTTCTGAAATCATCCTC   73745    CC   TTTTAG
                                TCCT  TTGA    CATCCTC
                                ||||  ||||    |||||||
                                AGGA  GACT    GTAGGAG
                                  A_   TTA___
GAM3277 HDAC7A   3' TCCTCCATGTCTGTATCTTCT  73746     T  A   TAGC   C
                                TCCTCC TG TTT   ATC TCT
                                |||||| || |||   ||| |||
                                AGGAGG AC AGA   TAG AGA
                                   T  _   CA__   A
GAM3277 HDAC7A   3' TCCTCCATGTCTGTATCTTCT  73746     T  A   TAGC   C
                                TCCTCC TG TTT   ATC TCT
                                |||||| || |||   ||| |||
                                AGGAGG AC AGA   TAG AGA
                                   T  _   CA__   A
GAM3277 LIMK1   3' CCTCCTTGAGGAACGTCCTCT  73747       TTTT   A
                                CCTCCTTGA   AGC TCCTCT
                                |||||||||   ||| ||||||
                                GGAGGAACT   TTG AGGAGA
                                     CC__   C
GAM3277 MAPK14   3' TTGATTTTCAGCATTTCT   73748      _    CC
                                TTGATTT TAGCAT  TCT
                                ||||||| ||||||  |||
                                AACTAAA GTCGTA  AGA
                                   A     A_
GAM3277 MAPK14   3' TTGATTTTCAGCATTTCT   73748      _    CC
                                TTGATTT TAGCAT  TCT
                                ||||||| ||||||  |||
                                AACTAAA GTCGTA  AGA
                                   A     A_
GAM3277 MAPK14   3' TTGATTTTCAGCATTTCT   73748      _    CC
                                TTGATTT TAGCAT  TCT
                                ||||||| ||||||  |||
                                AACTAAA GTCGTA  AGA
                                   A     A_
GAM3277 PAX3    3' TTGATTCCTAGTGTCCTCT   73749      _  CA
                                TTGATTT TAG  TCCTCT
                                ||||||| |||  ||||||
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                                AACTAAG ATC  AGGAGA
                                    G   AC
GAM3277  VIPR2    3'  TCCTCCTTGGCTCCCCT     73750         ATTTTA  A
                                TCCTCCTTG     GC TCCTCT
                                |||||||||     || ||||||
                                AGGAGGAAC     CG AGGGGA
                                          _______ _
GAM3277  AFAP     3'  TCGCCTGATAGCATCCT     73751    _    TTT
                                TC CTTGA   TAGCATCCT
                                || |||||   |||||||||
                                AG GGACT   ATCGTAGGA
                                 C    ___
GAM3277  C6orf9   5'  TCCTCCTTGGTTTATGGGCATT 73752         A   TA__    CC
              TCT                  TCCTCCTTG TTT    GCAT  TCT
                                |||||||||| |||    ||||  |||
                                AGGAGGAAC AAA    CGTA  AGA
                                     C   TACC    A_
GAM3277  CENTG3   3'  TCCTTGGCTTCGTCCTCT    73753       AT   AGCA
                                TCCTTG  TTT    TCCTCT
                                ||||||  |||    ||||||
                                AGGAAC  AAG    AGGAGA
                                   CG   C___
GAM3277  COLEC10  3'  CCTCAGTTTAGCATTTTCT   73754      GAT      CC
                                CCTT   TTTAGCAT  TCT
                                ||||   ||||||||  |||
                                GGAG   AAATCGTA  AGA
                                  TC_       AA
GAM3277  FLJ12595 5'  CTTCTTTATTTCAGCCTC    73755    C   G      ATC
                                CT CTT ATTTTAGC   CTC
                                || ||| ||||||||   |||
                                GA GAA TAAAGTCG   GAG
                                 A   A      ____
GAM3277  FLJ20045 5'  CCTCCTTGAGGCTGTAGTGTCT 73756         TTT__   CA  C
              TCT                  CCTCCTTGA     TAG  TC TCT
                                |||||||||     |||  || |||
                                GGAGGAACT     ATC  AG AGA
                                     CCGAC   AC  A
GAM3277  FLJ23468 5'  CTTCTTGATTTCTTCCT     73757    C       AGCA
                                CT CTTGATTTT    TCCT
                                || |||||||||    ||||
                                GA GAACTAAAG    AGGA
                                 A        A____
GAM3277  KCNH8    3'  TCCTTTGGAAACTACATCCTCT 73758       __  TT   G
                                TCCTT  GA  TTA CATCCTCT
                                |||||  ||  ||| ||||||||
                                AGGAA  CT  GAT GTAGGAGA
                                   AC  TT  _
GAM3277  KIAA0254 3'  TCCTCCTGATTTATCCT     73759        T    TAGC
                                TCCTCCT GATTT    ATCCT
                                ||||||| |||||    |||||
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                                AGGAGGA CTAAA    TAGGA
                                  _   _____
GAM3277 KIAA0443 5' TCCTCCTTTATTTCAAGCCTCT 73760        G      CAT
                                TCCTCCTT ATTTTAG   CCTCT
                                |||||||| |||||||   |||||
                                AGGAGGAA TAAAGTT   GGAGA
                                    A      C__
GAM3277 KIAA0769 3' TCCTCCTTGTTTTTTGCTC    73761         A    A  A
                                TCCTCCTTG TTTT GC TC
                                ||||||||| |||| || ||
                                AGGAGGAAC AAAA CG AG
                                    A    A  _
GAM3277 KIAA1280 5' CCTTCTTCAGCATCTTC     73762      GA        C
                                CCTT  TTTTAGCATC TC
                                ||||  |||||||||| ||
                                GGAA  GAAGTCGTAG AG
                                  __        A
GAM3277 KIAA1328 3' CTTGATCCTCTGGCATCCTCT  73763         A__
                                CTTGATTTT   GCATCCTCT
                                |||||||||   |||||||||
                                GAACTAGGA   CGTAGGAGA
                                    GAC
GAM3277 KIAA1775 3' CCCTCCTTGAGAACTCATTTTC 73764          TTTTAG   CC
             T                   TCCTCCTTGA     CAT  TCT
                                ||||||||||     |||  |||
                                GGGAGGAACT     GTA  AGA
                                     CTTGA_   AA
GAM3277 KIAA1822 3' TCCTTTGTTCAGGTGTCCTCT  73765      GAT    CA_
                                TCCTT   TTTAG   TCCTCT
                                |||||   |||||   ||||||
                                AGGAA   AAGTC   AGGAGA
                                   AC_    CAC
GAM3277 MGC16386 3' TCTTCCCTGGCATTCTCT    73766    C     ATTTTA   C
                                TC TCCTTG     GCAT CTCT
                                || ||||||     |||| ||||
                                AG AGGGAC     CGTA GAGA
                                 A     _______   A
GAM3277 MGC27277 3' CTCCTTGACTTCCCT       73767           AGCAT
                                CTCCTTGATTTT    CCT
                                ||||||||||||    |||
                                GAGGAACTGAAG    GGA
                                      _____
GAM3277 PIP3-E   3' CTTGTCCATAGCATTCTCT   73768      A TT     C
                                CTTG T  TAGCAT CTCT
                                |||| |  |||||| ||||
                                GAAC G  ATCGTA GAGA
                                  A GT     A
GAM3277 PMFBP1   5' CTCCTTTAACCTTTAGTATTTT 73769       GA__     C  CC
             CT                   CTCCTT    TTTTAG AT  TCT
                                ||||||   |||||| ||  |||
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                                GAGGAA   GAAATC TA  AGA
                                   ATTG     A  AA
GAM3277  PNMA5    3'  TCCTCCTTATTCTCCT      73770         A   TAGCA
                                TCCTCCTTG TTT    TCCT
                                ||||||||| |||    ||||
                                AGGAGGAAT AAG    AGGA
                                      _  _____
GAM3277  PRO0245  5'  CTTGATTTTTTTCCCTCT    73771         AGCA
                                CTTGATTTT   TCCTCT
                                |||||||||   ||||||
                                GAACTAAAA   GGGAGA
                                     AAA_
GAM3277  RHOBTB2  3'  TCCTCCGTGGGACTCCATC   73772       TT__    TAG
                                TCCTCC   GATTT   CATC
                                ||||||   |||||   ||||
                                AGGAGG   CTGAG   GTAG
                                   CACC    ___
GAM3277  LOC130951 3'  CTTTTTTTACACCATCCTCT   73773     GA  _  G
                                CTT  TTT TA CATCCTCT
                                |||  ||| || ||||||||
                                GAA  AAA GT GTAGGAGA
                                  AA   T  G
GAM3277  LOC144583 3'  TCTTCCCTGACACATTCT    73774    C       TTTA    C
                                TC TCCTTGAT    GCAT CT
                                || ||||||||    |||| ||
                                AG AGGGACTG    TGTA GA
                                 A       _____    A
GAM3277  LOC145676 5'  TCCTTCTCTGATTTTAGATC   73775     _ C         C
                                TCCT C TTGATTTTAG ATC
                                |||| | |||||||||| |||
                                AGGA G GACTAAAATC TAG
                                  A A        _
GAM3277  LOC149603 5'  TCCGCCTTGATTTTGGCA    73776     T         A
                                TCC CCTTGATTTT GCA
                                ||| |||||||||| |||
                                AGG GGAACTAAAA CGT
                                  C         C
GAM3277  LOC152024 5'  TCCCCCTTGGATCCGTCT    73777          ATTTTAGC   _
                                TCCTCCTTG       ATCC TCT
                                |||||||||       |||| |||
                                AGGGGGAAC       TAGG AGA
                                     C_________    C
GAM3277  LOC152245 3'  TCCTGCAGTTTTAGCATC    73778     _ GA
                                TCCT T  TTTTAGCATC
                                |||| |  ||||||||||
                                AGGA G  AAAATCGTAG
                                  C TC
GAM3277  LOC153910 5'  CTTGATTTTCCAATCTCT    73779         AG  TC
                                CTTGATTTT  CA  CTCT
                                |||||||||  ||  ||||
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                                GAACTAAAA  GT  GAGA
                                     G_  TA
GAM3277  LOC159036 3'  TCCTCCTTCATTCTTCCT    73780        G    AGCA
                                TCCTCCTT ATTTT    TCCT
                                |||||||| |||||    ||||
                                AGGAGGAA TAAGA    AGGA
                                     G    _____
GAM3277  LOC162333 5'  CTCTCTTGATTTGGCCTC    73781     _      TAGCAT
                                CTC CTTGATTT     CCTC
                                ||| ||||||||     ||||
                                GAG GAACTAAA     GGAG
                                  A       CC____
GAM3277  LOC196476 3'  TCCTTCTGATTTTATTTGTCTT 73782     CC        GCA_  C
              CT                  TCCT  TTGATTTTA    TC TCT
                                ||||  |||||||||    || |||
                                AGGA  GACTAAAAT    AG AGA
                                  A_        AAAC  A
GAM3277  LOC203257 5'  CTCCTTGAAGTCATCTTCT    73783        TTTTAG    C
                                CTCCTTGA     CATC TCT
                                ||||||||     |||| |||
                                GAGGAACT     GTAG AGA
                                     TCA___    A
GAM3277  LOC219731 5'  TCCTCCTTGTTTCTCCTC    73784         A    AGCA
                                TCCTCCTTG TTTT    TCCTC
                                ||||||||| ||||    |||||
                                AGGAGGAAC AAAG    AGGAG
                                          _   _____
GAM3277  LOC221876 3'  TCCTCCTTATTCCTTTCCT    73785         A    AGCA
                                TCCTCCTTG TTTT    TCCT
                                ||||||||| ||||    ||||
                                AGGAGGAAT AGGA    AGGA
                                     A    A___
GAM3277  LOC51644  3'  CTCCTGACTCCATGCATC    73786       T      _
                                CTCCT GATTTTA GCATC
                                ||||| ||||||| |||||
                                GAGGA CTGAGGT CGTAG
                                   _       A
GAM3277  LOC90371  5'  CTCTTTAATTTCCCTC      73787     C       AGCAT
                                CTC TTGATTTT     CCTC
                                ||| ||||||||     ||||
                                GAG AATTAAAG     GGAG
                                  A       ______
GAM3277  LOC91351  3'  CCTTTGCCTTGGCATCCTCT   73788     ___     ATTTTA
                                CCT   CCTTG     GCATCCTCT
                                |||   |||||     |||||||||
                                GGA   GGAAC     CGTAGGAGA
                                  AAC    _______
GAM3278  DBT       3'  TATCCATAATTACTATTAGAC  73791       T    AATTT
                                TATCC ATAA     TTATTAGAC
                                ||||| ||||     |||||||||
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                                ATAGG TATT    GATAATCTG
                                   _   AAT__
GAM3278 RP42    3' TATCCTAAAAAATTTTCAT   73792       T
                                TATCCTA AAAATTTTTAT
                                ||||||| ||||||||||
                                ATAGGAT TTTTAAAAGTA
                                    T
GAM3278 SIP     3' TCCTATAAACATTTTTAT    73793        _
                                TCCTATAAA ATTTTTAT
                                ||||||||| |||||||
                                AGGATATTT TAAAAATA
                                     G
GAM3278 ZNF214  3' TCCTATCTTTTATTAG     73794       AAAA
                                TCCTAT   TTTTTATTAG
                                ||||||   ||||||||||
                                AGGATA   GAAAATAATC
                                  ____
GAM3278 FLJ20136 3' TCCAGATTTTTTTATTAGAC  73795    TATAAAA
                                TCC      TTTTTATTAGAC
                                |||      ||||||||||||
                                AGG      AAAAATAATCTG
                                  TCTAA__
GAM3278 KIAA0376 3' TCCTAAGGATCCTATTAGAC  73796      TAAAAT
                                TCCTA     TTTTATTAGAC
                                |||||     ||||||||||
                                AGGAT     AGGATAATCTG
                                   TCCT__
GAM3278 POPX1   3' TATCCTATAAACACATGATTAG 73797          ATTTTT
                                TATCCTATAAA     ATTAG
                                ||||||||||     |||||
                                ATAGGATATTT     TAATC
                                      GTGTAC
GAM3278 TFEC    3' TATCCTATAAAGTTTGAACTTT 73798          A   TTA__
            AGAC                 TATCCTATAAA TTT    TTAGAC
                                ||||||||||| |||    ||||||
                                ATAGGATATTT AAA    AATCTG
                                      C   CTTGA
GAM3279 DSC2    3' AATGTGCATTTGACCAAAGA  73801      A    AGA
                                AATGT CATTT   GATTAGAGA
                                ||||| |||||   |||||||||
                                TTACA GTAAA   CTGGTTTCT
                                   C    ___
GAM3279 DSC2    3' AATGTGCATTTGACCAAAGA  73801      A    AGA
                                AATGT CATTT   GATTAGAGA
                                ||||| |||||   |||||||||
                                TTACA GTAAA   CTGGTTTCT
                                   C    ___
GAM3279 MBL2    3' ATGAACATTGATTAGAG     73802     T    TAGA
                                ATG ACATT    GATTAGAG
                                ||| |||||    ||||||||
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                                TAC TGTAA    CTAATCTC
                                  T    _____
GAM3279  PSG4     3'  CAATGTGCATTTAAAGGAG   73803       A       ATTA
                                TAATGT CATTTAGAG    GAG
                                |||||| |||||||||    |||
                                GTTACA GTAAATTTC    CTC
                                   C       _____
GAM3279  SLC9A6   3'  TGTACACAGATTAGAG      73804       TTAG
                                TGTACAT    AGATTAGAG
                                |||||||    |||||||||
                                ACATGTG    TCTAATCTC
                                           _____
GAM3279  DKFZP586B0923 3'  TACATTTAGAAACTGAG     73805            A
                                TACATTTAGAGATT GAG
                                |||||||||||||| |||
                                ATGTAAATCTTTGA CTC
                                           _
GAM3279  HARS2    3'  TGTACATTAGATCTTGAGA   73806        T   GA  A
                                TGTACATT AGA  TT GAGA
                                |||||||| |||  || ||||
                                ACATGTAA TCT  AA CTCT
                                     _   AG  _
GAM3279  KIAA0295  3'  TAATGTACACTTTACAGA    73807          _ G
                                TAATGTACATTT A AGA
                                |||||||||||| | |||
                                ATTACATGTGAA T TCT
                                      A G
GAM3279  KIAA1972  3'  TGTACAACTGATTAGAGA    73808       TTTAGA
                                TGTACA     GATTAGAGA
                                ||||||     |||||||||
                                ACATGT     CTAATCTCT
                                   TGA___
GAM3279  SDCBP    3'  TGTACATTTCAGGTTAATAGAG 73809        _   AGAT_
            A                    TGTACATT TAG     TAGAGA
                                |||||||| |||     ||||||
                                ACATGTAA GTC     ATCTCT
                                     A   CAATT
GAM3279  ZNF387   3'  TGTACATTTACACAGAG     73810         GAGAT
                                TGTACATTTA     TAGAG
                                ||||||||||     |||||
                                ACATGTAAAT     GTCTC
                                      GT___
GAM3279  LOC145622 3'  TGTATATTGGAAATTAGAGA   73811      C   TA
                                TGTA ATT  GAGATTAGAGA
                                |||| |||  ||||||||||
                                ACAT TAA  CTTTAATCTCT
                                  A   C_
GAM3279  LOC147658 3'  ATGTACATTTAAGAAGA     73812          A    TT
                                ATGTACATTT GAGA  AGA
                                |||||||||| ||||  |||
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                                TACATGTAAA TTCT  TCT
                                      _   __
GAM3279  LOC151196 3'  TGTACATTTTTTAGAG      73813         AGAGA
                                TGTACATTT    TTAGAG
                                |||||||||    ||||||
                                ACATGTAAA    AATCTC
                                     A____
GAM3279  LOC157506 3'  TATACATTTAGATACAGAG    73814           GAT
                                TGTACATTTAGA   TAGAG
                                ||||||||||||  |||||
                                ATATGTAAATCT   GTCTC
                                      AT_
GAM3280  GAD1      3'  AGTTGTTGGACAAGCTGGTT   73817     CA       G  CA
                                GGT  TTGGACGGG TG  GTT
                                |||  ||||||||| ||  |||
                                TCA  AACCTGTTC AC  CAA
                                  AC        G  __
GAM3280  ITGA5     3'  GGTGATTGGTGGTGCAGTT    73818     C    ACGG
                                GGT ATTGG    GGTGCAGTT
                                ||| |||||    |||||||||
                                CCA TAACC    CCACGTCAA
                                  C    A___
GAM3280  NFASC     3'  GGTCATTGGGAGGGGGC      73819         AC    T
                                GGTCATTGG  GGGG GC
                                |||||||||  |||| ||
                                CCAGTAACC  CCCC CG
                                     CT   _
GAM3280  LOC113763 3'  GGGGAGGCGGGGTGTAGTT    73820    TCATT  A      C
                                GG     GG CGGGGTG AGTT
                                ||     || ||||||| ||||
                                CC     CC GCCCCAC TCAA
                                 CCT__  _      A
GAM3280  LOC153020 3'  GGCCATTGGGAAGGCGGTT    73821         AC     CA
                                GGTCATTGG  GGGGTG  GTT
                                |||||||||  ||||||  |||
                                CCGGTAACC  TTCCGC  CAA
                                     C_     __
GAM3280  LOC159121 5'  GGTGTGGCTGGGGTGCAGTT   73822     CAT   AC
                                GGT   TGG  GGGGTGCAGTT
                                |||   |||  ||||||||||
                                CCA   ACC  CCCCACGTCAA
                                  C__   GA
GAM3281  GRM8      3'  TAGTTTTCCTTTTGTGA      73825       CCGTG  G
                                TAGTT    TT CTTTTGTGA
                                |||||    || |||||||||
                                ATCAA    AA GAAAACACT
                                   ______ G
GAM3281  NELL2     3'  GTAATTTTCCTTTTGTGA     73826       CCGTG  G
                                GTAGTT    TT CTTTTGTGA
                                ||||||    || |||||||||
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                                CATTAA    AA GAAAACACT
                                   _____  G
GAM3281  LOC123283 3'  GTAGCTGCTGCTTTTGTG    73827      TCCG
                                GTAGT   TGTTGCTTTTGTG
                                |||||   ||||||||||||||
                                CATCG   ACGACGAAAACAC
                                  ____
GAM3282  ANXA3    3'  TTCATTTATGAGCTGCTAC    73830       ACGT   T
                                TTCGTTTAT   GCT GCTAC
                                |||||||||   ||| |||||
                                AAGTAAATA   CGA CGATG
                                     CT__   _
GAM3282  COL4A6   3'  TTCATTTATTTTATTTGCTA   73831       ACG  C
                                TTCGTTTAT   TG TTGCTA
                                |||||||||   || ||||||
                                AAGTAAATA   AT AACGAT
                                     AA_  A
GAM3282  COL4A6   3'  TTCATTTATTTTATTTGCTA   73831       ACG  C
                                TTCGTTTAT   TG TTGCTA
                                |||||||||   || ||||||
                                AAGTAAATA   AT AACGAT
                                     AA_  A
GAM3282  CPA3     3'  ACTTCGTTATGGTGCTAC    73832       TATAC    T
                                ACTTCGTT    GTGCT GC
                                ||||||||    ||||| ||
                                TGAAGCAA    CACGA TG
                                    TAC__    _
GAM3282  OSBP     5'  TTCAGTTTATGCGCCTG     73833     _     AC
                                TTC GTTTAT  GTGCTTG
                                ||| ||||||  |||||||
                                AAG CAAATA  CGCGGAC
                                  T     __
GAM3282  OXTR     3'  ACTTCGTTTTCATATTGTTTGT 73834       __    C_  GC_
            TGC                   ACTTCGT  TTATA  GT   TTGC
                                |||||||  |||||  ||   ||||
                                TGAAGCA  AGTAT  CA   AACG
                                    AA    AA  AAC
GAM3282  KIAA0547 3'  ACTTAGGTTTGTGTTTGCTAC  73835     C_   ATAC   C
                                ACTT  GTTT    GTG TTGCTAC
                                ||||  ||||    ||| |||||||
                                TGAA  CAAA    CAC AACGATG
                                  TC    ____   A
GAM3282  LOC151318 3'  TTCCTTTTGATGCTTGCT    73836     G   ATAC
                                TTC TTT    GTGCTTGCT
                                ||| |||    |||||||||
                                AAG AAA    TACGAACGA
                                  G   AC__
GAM3282  LOC152405 3'  ACTTTGTTCTATACACTTTGCT 73837      CG_       GC
                                ACTT   TTTATACGT  TTGCT
                                ||||   |||||||||  |||||
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                                TGAA  AGATATGTG  AACGA
                                  ACA       A_
GAM3282  LOC255704 3'  TTCATTCCCATGCTTGCT    73838       ATA
                                TTCGTTT  CGTGCTTGCT
                                |||||||  ||||||||||
                                AAGTAAG  GTACGAACGA
                                   G__
GAM3283  KIAA0685  5'  TTGTGGTTTTTTTCTTGGAG  73841        CGCGC  CA
                                TTGTGGTTTT    CT  GAG
                                ||||||||||    ||  |||
                                AACACCAAAA    GA  CTC
                                      AAA__  AC
GAM3283  ST6GalNAcI 3'  CACTGTATCCTGTGCCTTGGAG 73842       GTT  GC_   CA
                                CATTGTG  TTC  GCCT  GAG
                                |||||||  |||  ||||  |||
                                GTGACAT  AGG  CGGA  CTC
                                   ___  ACA   AC
GAM3283  LOC147057 3'  TAATCCTTTGCGCCTCAG    73843       C_
                                TGGTTTT  GCGCCTCAG
                                |||||||  |||||||||
                                ATTAGGA  CGCGGAGTC
                                   AA
GAM3284  ABCD2    3'  ACTATGATTCTCAGAATCC    73846     CAT       _
                                ACTA  TTCTCAGAA CC
                                ||||  ||||||||| ||
                                TGAT  AAGAGTCTT GG
                                  ACT       A
GAM3284  CYP1B1   3'  CACATTTCTCAATCTAAAAAA  73847          AACC
                                TACATTTCTCAG   AAAAA
                                ||||||||||||   |||||
                                GTGTAAAGAGTT   TTTTT
                                      AGAT
GAM3284  GRAF     3'  CTGCATTTCTCAGTGGCAAA  73848    A       AAC
                                CT CATTTCTCAG  CAAA
                                || ||||||||||  ||||
                                GA GTAAAGAGTC  GTTT
                                 C        ACC
GAM3284  RAD23B   3'  CTGCATTTCTCCATTGGCCCCA 73849    A      AGAA____
            AAA                   CT CATTTCTC       CCAAAA
                                || ||||||||       ||||||
                                GA GTAAAGAG       GGTTTT
                                 C       GTAACCGG
GAM3284  RSN      3'  TACATTTATAACCAAAAAT   73850       CTCAG
                                TACATTT    AACCAAAAAT
                                |||||||    ||||||||||
                                ATGTAAA    TTGGTTTTTA
                                   TA___
GAM3284  WHSC1L1  3'  ACTACACTTCTTGAAATTCCTA 73851         CA  __ _
            AAAAT                 ACTACATTTCT  GAA  CC AAAAAT
                                ||||||||||  |||  || ||||||
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                                TGATGTGAAGA  TTT  GG TTTTTA
                                      AC   AA  A
GAM3284  ZNF144    3'  ACTTGCTCCTCAGAACCA    73852     ACA
                                ACT   TTTCTCAGAACCA
                                |||   ||||||||||||||
                                TGA   GAGGAGTCTTGGT
                                  AC_
GAM3284  AKAP5     5'  ACAACAAGAACCAAAA      73853     T   TTTCTC
                                AC ACA      AGAACCAAAA
                                || |||      ||||||||||
                                TG TGT      TCTTGGTTTT
                                 T  _______
GAM3284  COQ3      3'  ACTATAGTTCTCAGAAACAA  73854      CAT       C
                                ACTA   TTCTCAGAA CAA
                                ||||   ||||||||| |||
                                TGAT   AAGAGTCTT GTT
                                   ATC        T
GAM3284  D13S106E  3'  CTTCATGGGCAGAACCAAA   73855     A   TTCT
                                CT CAT    CAGAACCAAA
                                || |||    ||||||||||
                                GA GTA    GTCTTGGTTT
                                 A   CCC_
GAM3284  DKFZP434A0225 3'  TACAAACTCAGAACTGAAA   73856      TTT       CA
                                TACA   CTCAGAAC  AAA
                                ||||   ||||||||  |||
                                ATGT   GAGTCTTG  TTT
                                   TT_       AC
GAM3284  DKFZP434C131 3'  CTTCTCGGAGCCAAAAAT    73857       A  A
                                TTTCTC GA CCAAAAAT
                                |||||| || ||||||||
                                GAAGAG CT GGTTTTTA
                                    C  C
GAM3284  FLJ11117  3'  CTACATTTACTCAGCTGGATAA 73858         _    AACC__
            AAAT                   CTACATTT CTCAG     AAAAAT
                                |||||||| |||||     ||||||
                                GATGTAAA GAGTC     TTTTTA
                                     T     GACCTA
GAM3284  FLJ22031  3'  ACCATATTTTCTAGACCAAAAA 73859      CA_    C   A
            T                   ACTA   TTTCT AGA CCAAAAAT
                                ||||   ||||| ||| ||||||||
                                TGGT   AAAGA TCT GGTTTTTA
                                  ATA    _  _
GAM3284  KCNH7     3'  ACATTTGGAACCAAAA      73860       CTCA
                                ACATTT    GAACCAAAA
                                ||||||    |||||||||
                                TGTAAA    CTTGGTTTT
                                   C___
GAM3284  KIAA0157  3'  ACTACTTTTTCAGAACC     73861       A   C
                                ACTAC TTT TCAGAACC
                                ||||| ||| ||||||||
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                                TGATG AAA AGTCTTGG
                                  _  A
GAM3284  KIAA0493  5'  CACATTTCTCAGGCCAA     73862          AA
                                TACATTTCTCAG  CCAA
                                ||||||||||||  ||||
                                GTGTAAAGAGTC  GGTT
                                      C_
GAM3284  KIAA1243  3'  TTTCTGAATAGAACCAAAA    73863      C___
                                TTTCT    AGAACCAAAA
                                |||||    ||||||||||
                                AAAGA    TCTTGGTTTT
                                   CTTA
GAM3284  KIAA1497  5'  CACATTTCTCAGAACACA     73864           _
                                TACATTTCTCAGAAC CA
                                |||||||||||||| ||
                                GTGTAAAGAGTCTTG GT
                                       T
GAM3284  RNF2      3'  CTTCCCAGGACCAGAAAT     73865       A   A
                                TTTCTCAG ACCA AAAT
                                |||||||| |||| ||||
                                GAAGGGTC TGGT TTTA
                                     C   C
GAM3284  TRABID    5'  ACTACATTCCACCTCCAAAAAT 73866         TCAGAA
                                ACTACATTTC     CCAAAAAT
                                |||||||||      ||||||||
                                TGATGTAAGG     GGTTTTTA
                                      TGGA__
GAM3284  LOC129852 5'  ACTACCAGAGCCAAAA      73867      ATTTCT   A
                                ACTAC     CAGA CCAAAA
                                |||||     |||| ||||||
                                TGATG     GTCT GGTTTT
                                  _______   C
GAM3284  LOC146226 5'  CACATTTCCCCAAAAA      73868        CAGAA
                                TACATTTCT    CCAAAAA
                                |||||||||    |||||||
                                GTGTAAAGG    GGTTTTT
                                             _____
GAM3284  LOC147929 5'  ACTACATTTCCCAGGGTCC   73869           AA_
                                ACTACATTTCTCAG   CC
                                ||||||||||||||   ||
                                TGATGTAAAGGGTC   GG
                                       CCA
GAM3284  LOC148446 3'  CATCTGGAACCAAAAA      73870      CTCA
                                CATTT    GAACCAAAAA
                                |||||    ||||||||||
                                GTAGA    CTTGGTTTTT
                                   C___
GAM3284  LOC152445 3'  ACTTCATTTCTCCAAAAA    73871     A     CAGAA
                                ACT CATTTCT    CCAAAAA
                                ||| |||||||    |||||||
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                                TGA GTAAAGA    GGTTTTT
                                  A     _____
GAM3284  LOC152715 3'  TACATTTCACATCCCAAAA   73872        T  GAA
                                TACATTTC CA   CCAAAA
                                |||||||| ||   ||||||
                                ATGTAAAG GT   GGTTTT
                                     T  AG_
GAM3284  LOC199848 5'  ACTGGGTTTCTCCCCTCCAAAA 73873     ACA     AGAA
              AT                  ACT   TTTCTC    CCAAAAAT
                                |||   ||||||   ||||||||
                                TGA   AAAGAG    GGTTTTTA
                                  CCC     GGGA
GAM3284  LOC51028  3'  ACAGCATTTGGAAAAACCAAAA 73874    TA    CTC
              AT                  AC  CATTT   AGAACCAAAAAT
                                ||  |||||   ||||||||||||
                                TG  GTAAA   TTTTGGTTTTTA
                                 TC    CCT
GAM3285  COL16A1   3'  AAAGGGCAGATAGTTTTG    73877        _  _
                                AAAGGGCA ATA TTTTG
                                |||||||| ||| |||||
                                TTTCCCGT TAT AAAAC
                                     C   C
GAM3285  FZD8     3'  AGGGCAATGGTTAAATCATTT  73878        ATT   C
                                AGGGCAAT   TTG GTCATTT
                                ||||||||   ||| |||||||
                                TCCCGTTA   AAT TAGTAAA
                                     CC_   T
GAM3285  RAD1     3'  GGAGTGCAATGGCGTCATT   73879   A  G    ATTTT
                                A AG GCAAT    GCGTCATT
                                | || |||||    ||||||||
                                C TC CGTTA    CGCAGTAA
                                 C  A    C____
GAM3285  RAD1     3'  GGAGTGCAATGGCGTCATT   73879   A  G    ATTTT
                                A AG GCAAT    GCGTCATT
                                | || |||||    ||||||||
                                C TC CGTTA    CGCAGTAA
                                 C  A    C____
GAM3285  RAD1     3'  GGAGTGCAATGGCGTCATT   73879   A  G    ATTTT
                                A AG GCAAT    GCGTCATT
                                | || |||||    ||||||||
                                C TC CGTTA    CGCAGTAA
                                 C  A    C____
GAM3285  ALTE     3'  GGGCAATATTTTAAAATTCATT 73880          CG__
              T                   GGGCAATATTTTG   TCATTT
                                ||||||||||||   ||||||
                                CCCGTTATAAAAT   AGTAAA
                                       TTTA
GAM3285  KIAA0435  3'  AAGGGTGATACTTTGTACATTT 73881      CA      CGT
                                AAGGG  ATATTTTG   CATTT
                                |||||  ||||||||   |||||
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                                TTCCC  TATGAAAC   GTAAA
                                  AC       AT_
GAM3285  SYNPO2    5'  AAGGGCAATGCTTTTGCAT   73882         A_
                                AAGGGCAAT  TTTTGCGT
                                |||||||||  ||||||||
                                TTCCCGTTA  AAAACGTA
                                    CG
GAM3285  UBA2      3'  AAAAGGCAACATGCAT      73883          TTT
                                AAAGGGCAATA   TGCGT
                                ||||||||||   |||||
                                TTTTCCGTTGT   ACGTA
                                     ___
GAM3285  LOC153606 5'  GGAGGGCAATTTTTTGGCCATT 73884    A       A     C
                                A AGGGCAAT TTTTG GTCATT
                                | |||||||| ||||| ||||||
                                C TCCCGTTA AAAAC CGGTAA
                                 C       A    _
GAM3285  LOC221174 3'  AAAGGCAACAAAGTGTCATTT  73885          TTTTGC
                                AAGGGCAATA     GTCATTT
                                ||||||||||     |||||||
                                TTTCCGTTGT     CAGTAAA
                                     TTCA__
GAM3286  C14orf1   3'  TAAGTTTCATAGTTCAC     73888          A
                                TAAGTTTCATA GTTTAT
                                ||||||||||| ||||||
                                ATTCAAAGTAT CAAGTG
                                     _
GAM3286  HSPA4     3'  CAAGTTTAAGACAGGTTTATTT 73889        C__   A
           TATT                   TAAGTTT   ATA GTTTATTTTATT
                                |||||||   ||| ||||||||||||
                                GTTCAAA   TGT CAAATAAAATAA
                                    TTC   C
GAM3286  DKFZP586B0923 3'  TAAGTCAGTTTATTTTAT    73890       TCATA
                                TAAGTT    AGTTTATTTTAT
                                ||||||    ||||||||||||
                                ATTCAG    TCAAATAAAATA
                                     ______
GAM3286  P2RX1     3'  GTTTCATTCTATTTTATT    73891        AAG
                                GTTTCAT   TTTATTTTATT
                                |||||||   ||||||||||
                                CAAAGTA   AGATAAAATAA
                                     ___
GAM3286  SMBP      3'  CAAGTTTCCCTCTATTTATTTT 73892         ATAA_
           ATT                    TAAGTTTC    GTTTATTTTATT
                                ||||||||    ||||||||||||
                                GTTCAAAG    TAAATAAAATAA
                                    GGAGA
GAM3287  C11orf9   3'  TATTACATGGAGTGGGGCTCG  73895          C  ACA
                                TATTATATGGAG GG   TCG
                                |||||||||||| ||   |||
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                                ATAATGTACCTC CC   AGC
                                      A  CCG
GAM3287  LOC122614 3'  ATATAAAGGTGGATGTCGA   73896        C_  CA
                                ATATGGAG  GGA  TCGA
                                ||||||||  |||  ||||
                                TATATTTC  CCT  AGCT
                                    CA   AC
GAM3288  MAPK10   5'  TAAGTAAAGATATGAGTGACT  73899         C   AAC_
                                TAAGTAAAG ATAT   GACT
                                ||||||||| ||||   ||||
                                ATTCATTTC TATA   CTGA
                                     _   CTCA
GAM3288  TP63     3'  AATAAAGCATATAAAAC     73900           C
                                AGTAAAGCATATAA GAC
                                |||||||||||||| |||
                                TTATTTCGTATATT TTG
                                      _
GAM3288  KLF5     3'  AGTAAAGCCATATACATTAC   73901         _    ACG_
                                AGTAAAGC ATATA   AC
                                |||||||| |||||   ||
                                TCATTTCG TATAT   TG
                                    G    GTAA
GAM3289  BCL2A1   3'  TACATGGGGACAAAATTTCCA  73904         AA    GC
                                TACATGGG  ACAAA  ATTTCCA
                                ||||||||  |||||  |||||||
                                ATGTACCC  TGTTT  TAAAGGT
                                    C_    __
GAM3289  CACNA1D  3'  TACATGGGAGAAGCAGACTCCA 73905          AACA   T_
                                TACATGGGA   AAGCA  TTCCA
                                |||||||||   |||||  |||||
                                ATGTACCCT   TTCGT  GAGGT
                                     C___    CT
GAM3289  CDK3     5'  TGGGAAACAGAAGGCACT    73906         _  _
                                TGGGAAACA AAG CATT
                                ||||||||| ||| ||||
                                ACCCTTTGT TTC GTGA
                                     C  C
GAM3289  DAAM2    3'  ACATGGGAAACAGACACT    73907           AA
                                ACATGGGAAACA  GCATT
                                ||||||||||||  |||||
                                TGTACCCTTTGT  TGTGA
                                      C_
GAM3289  EDN3     3'  TACATGGTGGGATAACATCTCC 73908        GAAACAA
           A                    TACATGG      AGCATTTCCA
                                |||||||      ||||||||||
                                ATGTACC      TTGTAGAGGT
                                   ACCCTA_
GAM3289  EIF2C1   3'  CATGGGAAGGATTTCC      73909        AACAA  C
                                CATGGGA    AG ATTTCC
                                |||||||    || ||||||
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                                GTACCCT    TC TAAAGG
                                      _____ C
GAM3289  ERBB3    3'  TGATGGGAAACAAAGGCA    73910   C         _
                                A ATGGGAAACAAAG CA
                                | ||||||||||||| ||
                                A TACCCTTTGTTTC GT
                                 C           C
GAM3289  GYG2     3'  CATGAGAAATAAACCTTCCA   73911         CA   A
                                CATGGGAAA  AAGC TTTCCA
                                |||||||||  |||| ||||||
                                GTACTCTTT  TTTG GAAGGT
                                      A_   _
GAM3289  IL2RG    3'  TACATGGGGGCACAAAATTCCA 73912        AA_    CAT
                                TACATGGG   ACAAAG   TTCCA
                                ||||||||   ||||||   |||||
                                ATGTACCC   TGTTTT   AAGGT
                                     CCG     ___
GAM3289  OGN      3'  CATGGGAAACATTTAGCTTTTC 73913         A__   A
                                CATGGGAAACA   AGC TTTC
                                ||||||||||   ||| ||||
                                GTACCCTTTGT   TCG AAAG
                                      AAA   A
GAM3289  OGN      3'  CATGGGAAACATTTAGCTTTTC 73913         A__   A
                                CATGGGAAACA   AGC TTTC
                                ||||||||||   ||| ||||
                                GTACCCTTTGT   TCG AAAG
                                      AAA   A
GAM3289  OGN      3'  CATGGGAAACATTTAGCTTTTC 73913         A__   A
                                CATGGGAAACA   AGC TTTC
                                ||||||||||   ||| ||||
                                GTACCCTTTGT   TCG AAAG
                                      AAA   A
GAM3289  ORC1L    3'  TACATGAGAGCCATTTCC    73914        AACAAA  _
                                TACATGGGA     GC ATTTCC
                                |||||||||     || |||||||
                                ATGTACTCT     CG TAAAGG
                                      _______ G
GAM3289  RRM2B    3'  TGGGAAACAAAGAGATTTC   73915          C_
                                TGGGAAACAAAG  ATTTC
                                ||||||||||||  |||||
                                ACCCTTTGTTTC  TAAAG
                                      TC
GAM3289  TMEFF2   3'  TACATGGGAAAGAAAAAAC   73916          C__
                                TACATGGGAAA   AAAGC
                                ||||||||||   |||||
                                ATGTACCCTTT   TTTTG
                                      CTT
GAM3289  AFAP     3'  TACATGGGAGACCGCTTTCC   73917         A  AAA  A
                                TACATGGGA AC   GC TTTCC
                                |||||||||  ||   || |||||
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                                ATGTACCCT TG   CG AAAGG
                                     C  G__  _
GAM3289  C11orf23  3'  TACATGGGTGGCAAGATCT   73918       AAACA   C
                                TACATGGG    AAG ATTT
                                ||||||||    ||| ||||
                                ATGTACCC    TTC TAGA
                                    ACCG_  _
GAM3289  C17orf31  5'  CATAGGAAACTTCTGCATTTCC 73919        AAA_
           A                     CATGGGAAAC   GCATTTCCA
                                ||||||||||   |||||||||
                                GTATCCTTTG   CGTAAAGGT
                                     AAGA
GAM3289  DVS27     3'  CACATGGGAAATAAGGATT   73920        CA   C
                                TACATGGGAAA  AAG ATT
                                ||||||||||  ||| |||
                                GTGTACCCTTT  TTC TAA
                                      A_  C
GAM3289  FLJ10607  3'  TGGGAAACAATACACCCC    73921        A    TT
                                TGGGAAACAA GCAT  C
                                |||||||||| ||||  |
                                ACCCTTTGTT TGTG  G
                                     A   GG
GAM3289  FLJ11210  3'  TAATGGGAAATAAACAAATTC  73922   C      CA    T_
                                A ATGGGAAA  AAGCA  TTC
                                | ||||||||  |||||  |||
                                A TACCCTTT  TTTGT  AAG
                                 T      A_    TT
GAM3289  FLJ12577  3'  TACAGATGGGCAAAGCATTT   73923     __   AAA
                                TACA  TGGG   CAAAGCATTT
                                ||||  ||||   ||||||||||
                                ATGT  ACCC   GTTTCGTAAA
                                  CT   ___
GAM3289  FLJ13848  3'  TACATGAGGAACGAGAAGTCCT 73924      _   ACA_  CA
           TC                    TACATG GGAA   AAG  TTTC
                                ||||||  ||||   |||  ||||
                                ATGTAC CCTT   TTC  GAAG
                                   T   GCTC   AG
GAM3289  GOLPH3    3'  TACATGGGAAGCAAAATCC   73925       AACAA   TT_
                                TACATGGGA    AGCA   TCC
                                |||||||||    ||||   |||
                                ATGTACCCT    TCGT   AGG
                                     _____    TTT
GAM3289  KIAA0268  3'  TACATGTTCTTAAAGCATTTCC 73926      GGAAAC
           A                     TACATG     AAAGCATTTCCA
                                ||||||     ||||||||||||
                                ATGTAC     TTTCGTAAAGGT
                                   AAGAA_
GAM3289  KIAA0608  3'  TACATAGGAAACAAAAAACCT  73927            C
                                TACATGGGAAACAAAG ATTT
                                ||||||||||||||| ||||
```

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                                ATGTATCCTTTGTTTT TGGA
                                         T
GAM3289 KIAA0843 3' ATGGGAAACAAAAATATCCA  73928          C  T
                                ATGGGAAACAAAG AT TCCA
                                |||||||||||| || ||||
                                TACCCTTTGTTTT TA AGGT
                                       _  T
GAM3289 KIAA0931 3' TACATGGGAAGAAGAGCATC  73929         ACAA
                                TACATGGGAA   AGCATT
                                ||||||||||   ||||||
                                ATGTACCCTT   TCGTAG
                                     CTTC
GAM3289 KIAA1203 3' TACATTGGAAACAATCACTTC 73930      G       AG
                                TACAT GGAAACAA  CATTTC
                                ||||| ||||||||  ||||||
                                ATGTA CCTTTGTT  GTGAAG
                                   A       A_
GAM3289 KIAA1727 3' TACATGGAAGCATCT       73931        AAACAA
                                TACATGGG     AGCATTT
                                ||||||||     |||||||
                                ATGTACCT     TCGTAGA
                                          _______
GAM3289 KIAA1843 3' CATGGGAAGCAGCACACCA   73932        ACAA    TT
                                CATGGGAA   AGCAT  CCA
                                ||||||||   |||||  |||
                                GTACCCTT   TCGTG  GGT
                                     CG__    T_
GAM3289 KLF12    3' ATGGGAAGCATTCTCTTTCCA 73933       A  AAGCA
                                ATGGGAA CA     TTTCCA
                                ||||||| ||     ||||||
                                TACCCTT GT     AAAGGT
                                    C  AAGAG
GAM3289 LRBA     3' TGAGCTCAAGAGCATTTCCA  73934      AAA  _
                                TGGG   CAA AGCATTTCCA
                                ||||   ||| ||||||||||
                                ACTC   GTT TCGTAAAGGT
                                  GA_   C
GAM3289 MGC5466  3' CAATGAAAAAATAAAGCATTTT 73935   C   GG   C_       C
           CA                     A ATG  AAA  AAAGCATTT CA
                                | |||  |||  |||||||| ||
                                G TAC  TTT  TTTCGTAAA GT
                                 T   TT   TA       A
GAM3289 NRBF-2   3' CACCAGATGAAGCATTTCC   73936     G   AACA
                                CAT GGA   AAGCATTTCC
                                ||| |||   ||||||||||
                                GTG TCT   TTCGTAAAGG
                                  G   AC__
GAM3289 SFXN2    3' TACATGGGTAAAAGTTTCC   73937        AAAC   CA
                                TACATGGG   AAAG  TTTCC
                                ||||||||   ||||  |||||
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                                ATGTACCC   TTTC  AAAGG
                                    AT__   __
GAM3289  STX3A    3'  ATGGGAAGATCACATTTCCA  73938       ACAAA
                                ATGGGAA    GCATTTCCA
                                |||||||    |||||||||
                                TACCCTT    TGTAAAGGT
                                   CTAG_
GAM3289  SULT1C2  3'  TGAGGACTGAAGCATTTCCA  73939    _  AACA
                                TG GGA   AAGCATTTCCA
                                || |||   ||||||||||
                                AC CCT   TTCGTAAAGGT
                                 T  GAC_
GAM3289  TA-KRP   3'  TACATGGGAAATGGAAACA   73940         CA_
                                TACATGGGAAA  AAGCA
                                ||||||||||  |||||
                                ATGTACCCTTT  TTTGT
                                      ACC
GAM3289  TREX1    5'  ACATGGGAAACAGAGGGAGCA  73941          A____
                                ACATGGGAAACA    AGCA
                                ||||||||||||    ||||
                                TGTACCCTTTGT    TCGT
                                      CTCCC
GAM3289  TREX1    5'  ACATGGGAAACAGAGGGAGCA  73941          A____
                                ACATGGGAAACA    AGCA
                                ||||||||||||    ||||
                                TGTACCCTTTGT    TCGT
                                      CTCCC
GAM3289  TSPAN-3  3'  TACATGGGTACATTATTTCCA  73942       AA  AAGC
                                TACATGGG  ACA   ATTTCCA
                                ||||||||  |||   |||||||
                                ATGTACCC  TGT   TAAAGGT
                                   A_  AA__
GAM3289  TTTY2    5'  CACATGGGAGGCAGAGCCGTTT 73943        AA  A  A_
            C                    TACATGGGA  CA AGC  TTTC
                                |||||||||  || |||  ||||
                                GTGTACCCT  GT TCG  AAAG
                                     CC  C   GC
GAM3289  TUCAN    3'  TACAGGGAAACAACAATTT   73944     T       AGC
                                TACA GGGAAACAA   ATTT
                                |||| |||||||||   ||||
                                ATGT CCCTTTGTT   TAAA
                                  _       GT_
GAM3289  VAV3     3'  ATGGAAAACATTTACTTC    73945         AAGC
                                ATGGGAAACA    ATTTC
                                ||||||||||   |||||
                                TACCTTTTGT    TGAAG
                                      AAA_
GAM3289  LOC115297 3'  GGGAAACAAATTATTTTCA   73946         GC   C
                                GGGAAACAAA  ATTT CA
                                ||||||||||  |||| ||
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                                CCCTTTGTTT  TAAA GT
                                     AA    A
GAM3289  LOC130814 3'  CATAGGAAACAATAATCTC    73947          AGC
                                CATGGGAAACAA   ATTTC
                                ||||||||||||  |||||
                                GTATCCTTTGTT   TAGAG
                                      AT_
GAM3289  LOC144809 3'  TACATGGGCAAACTTCC     73948        AAA   AGC
                                TACATGGG   CAA   ATTTCC
                                ||||||||   |||   ||||||
                                ATGTACCC   GTT   TGAAGG
                                    ___   ___
GAM3289  LOC149711 3'  TACATGGGGAAGTAAACACCT  73949        AAACA
                                TACATGGG    AAGCATTT
                                ||||||||    ||||||||
                                ATGTACCC    TTTGTGGA
                                     CTTCA
GAM3289  LOC159148 5'  CACATGGGAGGCAGAGCCGTTT 73943         AA  A   A_
              C                  TACATGGGA  CA AGC  TTTC
                                ||||||||||  || |||  ||||
                                GTGTACCCT  GT TCG  AAAG
                                     CC  C   GC
GAM3289  LOC201287 3'  TAATGGGAAACAAAATATC    73950    C          C
                                A ATGGGAAACAAAG ATT
                                | ||||||||||||| |||
                                A TACCCTTTGTTTT TAG
                                 T           A
GAM3289  LOC203286 3'  TGGGAAACAATGCCCTCCA    73951          A  A
                                TGGGAAACAA GC TTTCCA
                                |||||||||| || ||||||
                                ACCCTTTGTT CG GGAGGT
                                      A  _
GAM3289  LOC222224 3'  TACATGGAGAAATGGAGCA    73952        _    CAA
                                TACATGG GAAA   AGCA
                                ||||||| ||||   ||||
                                ATGTACC CTTT   TCGT
                                     T    ACC
GAM3289  LOC253639 3'  CATGGGAGATAAAGATTTC    73953        AAC    C
                                CATGGGA   AAAG ATTTC
                                |||||||   |||| |||||
                                GTACCCT   TTTC TAAAG
                                     CTA    _
GAM3289  LOC254268 3'  CATGGGAAATAATTATTTC    73954         CA  GC
                                CATGGGAAA  AA  ATTTC
                                |||||||||  ||  |||||
                                GTACCCTTT  TT  TAAAG
                                      A_  AA
GAM3289  LOC90049  3'  TACATGGGGAAAAAAACATT   73955         A  C
                                TACATGGG AA AAAGCATT
                                |||||||| || ||||||||
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                                ATGTACCC TT TTTTGTAA
                                     C  T
GAM3290  CASP7    5'  GCATCGAGGGTACAGCAGGCCT 73958     GAA   C__
                                GCA   CGAG   ACAGCAGGCCT
                                |||   ||||   ||||||||||||
                                CGT   GCTC   TGTCGTCCGGA
                                  A__    CCA
GAM3290  DLST     3'  TGGAGAGCGTGAGGGCAGGCCT 73959     C   A  AGCACA
                                TGG AGA CG     GCAGGCCT
                                ||| ||| ||     ||||||||
                                ACC TCT GC     CGTCCGGA
                                  _  C  ACTCC_
GAM3290  F2RL3    3'  TGGCAGAAGGGAGTTCCAGGTC 73960        C_   CACAG   C
             T                   TGGCAGAA  GAG    CAGG CT
                                ||||||||  |||    |||| ||
                                ACCGTCTT  CTC    GTCC GA
                                     CC   AAG__    A
GAM3290  GPC1     3'  TGGAGGAAGGACACAGCAGGC  73961     CA   C  G
                                TGG  GAA GA CACAGCAGGC
                                |||  ||| || ||||||||||
                                ACC  CTT CT GTGTCGTCCG
                                  TC   C  _
GAM3290  HIC1     5'  TGGGGACGGGTAGCAGGCC    73962     CA  A  AGCAC
                                TGG  GA CG    AGCAGGCC
                                |||  || ||    ||||||||
                                ACC  CT GC    TCGTCCGG
                                  C_  _  CCA__
GAM3290  ID3      3'  GGCAGAACGGGCGCCAGCACCT 73963         A  A_   AG
                                GGCAGAACG GC  CAGC  GCCT
                                |||||||| ||  ||||  ||||
                                CCGTCTTGC CG  GTCG  TGGA
                                     C  CG   __
GAM3290  LARS2    3'  TGTCAGAACCACAGCAGGCCT  73964    G     GAG
                                TG CAGAAC   CACAGCAGGCCT
                                || ||||||   ||||||||||||
                                AC GTCTTG   GTGTCGTCCGGA
                                 A     ____
GAM3290  PDGFRB   5'  GGCAGGGCGAGCACAGGC    73965      AA    ACA
                                GGCAG  CGAGC   GCAGGC
                                |||||  |||||   ||||||
                                CCGTC  GCTCG   TGTCCG
                                   CC    ____
GAM3290  SCD      3'  TGGCAGGGGAGCACAGGGG   73966       AAC       CA
                                TGGCAG   GAGCACAG  GG
                                ||||||   ||||||||  ||
                                ACCGTC   CTCGTGTC  CC
                                   CC_       C_
GAM3290  SH3GL1   3'  TGCCAGAGTGACACAGGCC   73967    G   AC  G ACA
                                TG CAGA  GA C   GCAGGCC
                                || ||||  || |   |||||||
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                                AC GTCT  CT G   TGTCCGG
                                 G   CA  _ ___
GAM3290  SLC9A6   3'  GCTGATGTAAGCACAGCAGGC  73968    A  AC_
                                GC GA   GAGCACAGCAGGC
                                || ||   ||||||||||||
                                CG CT   TTCGTGTCGTCCG
                                 A  ACA
GAM3290  STX1A    3'  GGCAGGATGAGACTGCAGGCCT 73969      AAC   C  A
                                GGCAG   GAG AC GCAGGCCT
                                |||||   ||| || ||||||||
                                CCGTC   CTC TG CGTCCGGA
                                   CTA   _  A
GAM3290  SUDD     5'  TGGCAGGACGGGCAGCAGGC   73970      A   A   CA
                                TGGCAG ACG GCA  GCAGGC
                                |||||| ||| |||  ||||||
                                ACCGTC TGC CGT  CGTCCG
                                   C   C   __
GAM3290  ARFGAP1  3'  TGGGACGAGCACAGGGGC    73971     CAGA       CA
                                TGG    ACGAGCACAG  GGC
                                |||    ||||||||||  |||
                                ACC    TGCTCGTGTC  CCG
                                  C___        C_
GAM3290  DKFZP434H132 3'  GGCAGGTGGCTCACAGCAGGCC 73972       AACGAG
            T                    GGCAG     CACAGCAGGCCT
                                |||||     ||||||||||||
                                CCGTC     GTGTCGTCCGGA
                                   CACCGA
GAM3290  FLJ12876 3'  TGGCAGAATGAGCTGCAGAGG  73973        C    A_   C
                                TGGCAGAA GAGC  CAG AGG
                                |||||||| ||||  ||| |||
                                ACCGTCTT CTCG  GTC TCC
                                     A   AC   _
GAM3290  FLJ20035 3'  TGACAGAACATGGCAGG     73974          AGCACA
                                TGGCAGAACG     GCAGG
                                ||||||||||     |||||
                                ACTGTCTTGT     CGTCC
                                      AC____
GAM3290  FLJ20400 3'  TGGGACGAAAGCACAGCAGGC  73975     CA_  AC
                                TGG   GA  GAGCACAGCAGGC
                                |||   ||  ||||||||||||||
                                ACC   CT  TTCGTGTCGTCCG
                                  CTG  __
GAM3290  HCA4     3'  TGGTGAGTGAGTACAGCAAG   73976     CA  AC   C
                                TGG  GA  GAG ACAGCAGG
                                |||  ||  ||| ||||||||
                                ACC  CT  CTC TGTCGTTC
                                  A_  CA   A
GAM3290  KIAA0239  5'  TGGGGAATGAGGTGGACAGGCC 73977     CA   C   CACA
            T                    TGG  GAA GAG    GCAGGCCT
                                |||  ||| |||    ||||||||
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                                ACC  CTT CTC    TGTCCGGA
                                  C_   A   CACC
GAM3290 KIAA1404 3' GCAGATGCAGGCAGCAGGCCT 73978      ACGA  __
                                GCAGA   GCA  CAGCAGGCCT
                                |||||   |||  ||||||||||
                                CGTCT   CGT  GTCGTCCGGA
                                   A___   CC
GAM3290 KIAA1464 3' TGGCAGGCAGGCAGGC     73979      AACGA   CA
                                TGGCAG    GCA  GCAGGC
                                ||||||    |||  ||||||
                                ACCGTC    CGT  CGTCCG
                                   _____  C_
GAM3290 MGC13183 3' TAGCAGAATGAGCGCCT    73980       C    ACAGCAG
                                TGGCAGAA GAGC      GCCT
                                |||||||| ||||      ||||
                                ATCGTCTT CTCG      CGGA
                                    A   ________
GAM3290 P5326    3' TGGCAGGGATGGGCAAGCC   73981      AAC  GCACA
                                TGGCAG   GA    GCAGGCC
                                ||||||   ||    |||||||
                                ACCGTC   CT    CGTTCGG
                                   C__   ACC__
GAM3290 PDEF     5' GCAGGGAGCTGGCAGCAGGC  73982     AAC    A__
                                GCAG   GAGC   CAGCAGGC
                                ||||   ||||   ||||||||
                                CGTC   CTCG   GTCGTCCG
                                  C__    ACC
GAM3290 PRO1777  3' GCAGAGTAAAAGCAGGCCT   73983     AC   CAC
                                GCAGA  GAG   AGCAGGCCT
                                |||||  |||   |||||||||
                                CGTCT  TTT   TCGTCCGGA
                                   CA   ___
GAM3290 RAB1B    3' GGCAACTGCACAGCAGGCCT   73984     GA  GA
                                GGCA  AC  GCACAGCAGGCCT
                                ||||  ||  ||||||||||||
                                CCGT  TG  CGTGTCGTCCGGA
                                   __  A_
GAM3290 SLC12A5  3' GCTGGAACGAGCATGCAGTGCC 73985    A_       CA   _
             T                   GC  GAACGAGCA  GCAG GCCT
                                 ||  |||||||||  ||||  ||||
                                 CG  CTTGCTCGT  CGTC CGGA
                                  AC       A_    A
GAM3290 SPEC1    3' TGGCAGAATGGATACCAGTTCC 73986       C_  GCA   CAGG
             T                   TGGCAGAA  GA   CAG    CCT
                                 ||||||||  ||   |||    |||
                                 ACCGTCTT  CT   GTC    GGA
                                     AC  ATG   AA__
GAM3290 LOC124976 3' TGCCAGGGCCACTCAGCAGGCC 73987    G   AACGA  A
             T                   TG CAG    GC CAGCAGGCCT
                                 || |||    || ||||||||||
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                                AC GTC     TG GTCGTCCGGA
                                 G   CCGG_  A
GAM3290  LOC145725 3'  TGGCAGAGCAGGCACAGCA   73988        A  A
                                TGGCAGA CG GCACAGCA
                                ||||||| || ||||||||
                                ACCGTCT GT CGTGTCGT
                                    C  C
GAM3290  LOC145732 3'  TGGCAGAGCAGGCACAGCA   73988        A  A
                                TGGCAGA CG GCACAGCA
                                ||||||| || ||||||||
                                ACCGTCT GT CGTGTCGT
                                    C  C
GAM3290  LOC151176 3'  ACAGGAGCACAGCAGGC     73989      AAC
                                GCAG   GAGCACAGCAGGC
                                ||||   ||||||||||||||
                                TGTC   CTCGTGTCGTCCG
                                  ____
GAM3290  LOC151512 5'  TGGCAGAAGGGGCAAGCAGGGC 73990         CGA   C     _
              CT                  TGGCAGAA   GCA AGCAGG CCT
                                ||||||||   ||| |||||| |||
                                ACCGTCTT   CGT TCGTCC GGA
                                    CCC   _     C
GAM3290  LOC159199 5'  TGGCAGGGGGGCTGCAGGCC   73991       AACGA  ACA
                                TGGCAG    GC   GCAGGCC
                                ||||||    ||   |||||||
                                ACCGTC    CG   CGTCCGG
                                   CCC__  A__
GAM3290  LOC168576 5'  TGGGGTGCGCACAGCAGCAGGC 73992     CAGAA  A   _
                                TGG    CG GCA CAGCAGGC
                                |||    || ||| ||||||||
                                ACC    GC TGT GTCGTCCG
                                  CCAC_  G   C
GAM3290  LOC196513 5'  GCAGAACGAGCGAGCTGCCT   73993          AC   AG
                                GCAGAACGAGC  AGC  GCCT
                                ||||||||||  |||  ||||
                                CGTCTTGCTCG  TCG  CGGA
                                      C_   A_
GAM3290  LOC196957 3'  TGGCAGAGCAGGCACAGCA   73988        A  A
                                TGGCAGA CG GCACAGCA
                                ||||||| || ||||||||
                                ACCGTCT GT CGTGTCGT
                                    C  C
GAM3290  LOC196961 3'  TGGCAGAGCAGGCACAGCA   73988        A  A
                                TGGCAGA CG GCACAGCA
                                ||||||| || ||||||||
                                ACCGTCT GT CGTGTCGT
                                    C  C
GAM3290  LOC197138 3'  TGGCAGAGCAGGCACAGCA   73988        A  A
                                TGGCAGA CG GCACAGCA
                                ||||||| || ||||||||
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                                ACCGTCT GT CGTGTCGT
                                    C  C
GAM3290  LOC200081 3'  TGGAGAATCAGCTCAGCAGGCC 73994     C    CG   A
             T                   TGG AGAA  AGC CAGCAGGCCT
                                 ||| ||||  ||| ||||||||||
                                 ACC TCTT  TCG GTCGTCCGGA
                                   _   AG   A
GAM3290  LOC222493 5'  TGACAGAAAACAGCACAGTGGG 73995        CG_     CA  C
             TCT                   TGGCAGAA   AGCACAG  GG CT
                                 ||||||||   |||||||  || ||
                                 ACTGTCTT   TCGTGTC  CC GA
                                     TTG      AC  A
GAM3290  LOC245727 3'  TGGCAGAGCAGGCACAGCA    73988        A  A
                                 TGGCAGA CG GCACAGCA
                                 ||||||| || ||||||||
                                 ACCGTCT GT CGTGTCGT
                                    C  C
GAM3290  LOC256080 5'  TGGCAGAATGAGGCATGG     73996        C   CACA  _
                                 TGGCAGAA GAG    GCA GG
                                 |||||||| |||    ||| ||
                                 ACCGTCTT CTC    CGT CC
                                    A   ____   A
GAM3290  LOC51075  3'  TGGCCACAAGCATGGCAGGCCT 73997      AGA      CA
                                 TGGC   ACGAGCA  GCAGGCCT
                                 ||||   |||||||  ||||||||
                                 ACCG   TGTTCGT  CGTCCGGA
                                   G__      AC
GAM3291  IL4R     3'  CCATACAGCTGGGCATGGGT   74000     GC      CC   A
                                 CCA  ACAGCTGG  TAT GGGT
                                 |||  ||||||||  ||| ||||
                                 GGT  TGTCGACC  GTA CCCA
                                   A_       C_  _
GAM3291  KAI1     5'  ACCAGTGCAGCTGGTCACACCC 74001    CA     _________  TATAG
             TATG                   AG  CAGCTG       GCC    G
                                 ||  ||||||       |||    |
                                 TC  GTCGAC       TGG    C
                                  AC     CAGTGIII   GATAT
GAM3291  LPIN1    5'  CAGGCATGGCTGGCCCCGG   74002     _ CA      ATA
                                 CAG CA  GCTGGCCT   GG
                                 ||| ||  ||||||||   ||
                                 GTC GT  CGACCGGG   CC
                                   C  AC       G__
GAM3291  PLAUR    3'  GCACACTGGCCTGAGGT     74003      G      ATA
                                 GCACA CTGGCCT   GGGT
                                 ||||| |||||||   ||||
                                 CGTGT GACCGGA   TCCA
                                    _      C__
GAM3291  TNFRSF6B  3'  CCAGTGCAGCTGGTGCACAGGG 74004      CA      CC
             T                   CCAG  CAGCTGG  TATAGGGT
                                 ||||  |||||||  ||||||||
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                                GGTC  GTCGACC  GTGTCCCA
                                  AC      AC
GAM3291  ANGPTL4   3'  CCAGTCTGGCTGGCCCCAAG   74005     CACA      A
                                CCAG   GCTGGCCT TAGG
                                ||||   |||||||| ||||
                                GGTC   CGACCGGG GTTC
                                  AGAC      _
GAM3291  DKFZP434K046 3'  CCAGCATGGCTCGGCGGG    74006      CA  _  CTATA
                                CCAGCA  GCT GGC    GGG
                                ||||||  ||| |||    |||
                                GGTCGT  CGA CCG    CCC
                                   AC   G  _____
GAM3291  DKFZp547I014 5'  ACTAGCATACTGGCCTA    74007    C   CA
                                AC AGCA  GCTGGCCTA
                                || ||||  |||||||||
                                TG TCGT  TGACCGGAT
                                 A   A_
GAM3291  EPB41L1   5'  ACCAGCACGCCTGGGCCCGGGG 74008       A  __    ATA
           T                     ACCAGCAC GCT  GGCCT   GGGT
                                |||||||| |||  |||||   ||||
                                TGGTCGTG CGG  CCGGG   CCCA
                                    _  AC    C__
GAM3291  FLJ10751  3'  ACCAGGACAGCTGGTCACCC   74009      C      ___
                                ACCAG ACAGCTGG   CCT
                                ||||| ||||||||   |||
                                TGGTC TGTCGACC   GGG
                                   C       AGT
GAM3291  FLJ10751  3'  ACCAGGACAGCTGGTCACCC   74009      C      ___
                                ACCAG ACAGCTGG   CCT
                                ||||| ||||||||   |||
                                TGGTC TGTCGACC   GGG
                                   C       AGT
GAM3291  FLJ11715  3'  CAGCACAGTCTGGGGTACCCTA 74010       _  ________   TATAG
           TG                     AGCACAG CTG      GCC    G
                                ||||||| |||      |||    |
                                TCGTGTC GAC      TGG    C
                                    A   CCCAIII   GATAT
GAM3291  HSPB7    3'  CCAGCTGGCTGGGGGCACGGGG 74011      ACA    CC_  TA
           T                     CCAGC   GCTGG   TA  GGGT
                                |||||   |||||   ||  ||||
                                GGTCG   CGACC   GT  CCCA
                                   AC_    CCC  GC
GAM3291  KRTAP4-7  3'  CAGCACAGTAGAAGGG     74012        C   CCTAT
                                CAGCACAG TGG    AGGG
                                |||||||| |||    ||||
                                GTCGTGTC ATC    TCCC
                                    _  T_____
GAM3291  TIGD5    5'  ACCAGCCGTGGCTGGCCTTGAA 74013       ACA_      AT
           GGT                     ACCAGC   GCTGGCCT  AGGGT
                                ||||||   ||||||||  |||||
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                                TGGTCG   CGACCGGA  TTCCA
                                   GCAC       AC
GAM3291  TLE4     3'  CAATACAGCTGGCTCCATCTGT 74014     C       _   AGG
                                CAG ACAGCTGGC CTAT   GT
                                ||| ||||||||| ||||   ||
                                GTT TGTCGACCG GGTA   CA
                                  A       A   GA_
GAM3291  WBSCR17  3'  CCAGCAGAGCGTGGGGTACCCT 74015     C  _ ________  TATAG
            ATG                   AGCA AGC TG      GCC    G
                                |||| ||| ||      |||    |
                                TCGT TCG AC      TGG    C
                                  C   C  CCCAIII   GATAT
GAM3291  ZNF212   3'  ACCAGCCACCAGTCCCTGTGGG 74016      A  G TG _   ATA_
            GT                    ACCAGC CA C  G CCT    GGGT
                                |||||| || |  | |||    ||||
                                TGGTCG GT G  C GGG    CCCA
                                  _  _ GT A   ACAC
GAM3291  LOC113523 3'  ACACAGCTGGCAAATGGGT   74017          CT  A
                                GCACAGCTGGC  AT GGGT
                                ||||||||||  || ||||
                                TGTGTCGACCG  TA CCCA
                                     TT  _
GAM3291  LOC145268 3'  CAGGTACAGCTGGCTCCAGGGT 74018     C_       CTA
                                CAG  ACAGCTGGC   TAGGGT
                                |||  |||||||||   ||||||
                                GTC  TGTCGACCG   GTCCCA
                                  CA       AG_
GAM3291  LOC146733 3'  CAGCACAGCAGGAGGGAGGGT  74019        T  CCTAT
                                CAGCACAGC GG     AGGGT
                                |||||||| ||     |||||
                                GTCGTGTCG CC     TCCCA
                                     T  TCCC_
GAM3291  LOC149322 3'  AGACGCAGGCATATAGGGT   74020    C  A  T   C
                                AG AC GC GGC TATAGGGT
                                || || || ||| ||||||||
                                TC TG CG CCG ATATCCCA
                                 _  _  T   T
GAM3291  LOC150407 3'  GCTAGCCTGCCTTTATGGG   74021    AC   G   A  _
                                GC  AGCT GCCT TA GGG
                                ||  |||| |||| || |||
                                CG  TCGG CGGA AT CCC
                                 A_   A   A  A
GAM3291  LOC155435 3'  CAGCACAGCTGCAGGG      74022          GCCTA
                                CAGCACAGCTG    TAGGG
                                ||||||||||    |||||
                                GTCGTGTCGAC    GTCCC
                                               _____
GAM3291  LOC157621 3'  CCAGCACAGCTGCTTTACCCTA 74023          ________  TATAG
            TG                    CAGCACAGCTG      GCC    G
                                ||||||||||      |||    |
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                                GTCGTGTCGAC      TGG    C
                                      GAAAIII  GATAT
GAM3291  LOC158055 3'  CCGGCCCAGCTGGGGACAAGGG 74024    A  A     CCTAT
              T                    CC GC CAGCTGG    AGGGT
                                   || || |||||||    |||||
                                   GG CG GTCGACC    TCCCA
                                    C  G     CCTGT
GAM3291  LOC158117 3'  ACACAACTACCCTATGGGGT  74025        G    A
                                   GCACAGCTG CCTAT GGGT
                                   ||||||||| ||||| ||||
                                   TGTGTTGAT GGATA CCCA
                                         G    C
GAM3291  LOC158476 5'  AGCATAGCTGGCCTGGC    74026     C       ATAG
                                   AGCA AGCTGGCCT   GGT
                                   |||| |||||||||   |||
                                   TCGT TCGACCGGA   CCG
                                     A       ____
GAM3291  LOC200138 5'  CCGGCGCAGCCGGCATTGGGT  74027    A  A      CT  A
                                   CC GC CAGCTGGC  AT GGGT
                                   || || ||||||||  || ||||
                                   GG CG GTCGGCCG  TA CCCA
                                    C  C       __  A
GAM3291  LOC203275 3'  ACACAACTACCCTATGGGGT  74025        G    A
                                   GCACAGCTG CCTAT GGGT
                                   ||||||||| ||||| ||||
                                   TGTGTTGAT GGATA CCCA
                                         G    C
GAM3291  LOC220635 3'  AGACGCAGGCATATAGGGT   74020    C  A  T   C
                                   AG AC GC GGC TATAGGGT
                                   || || || ||| ||||||||
                                   TC TG CG CCG ATATCCCA
                                    _ _  T   T
GAM3291  LOC253891 3'  CAGCACAGCGCAGGG       74028        TG  CTAT
                                   CAGCACAGC  GC    AGGG
                                   |||||||||  ||    ||||
                                   GTCGTGTCG  CG    TCCC
                                              __  ____
GAM3291  LOC255452 3'  CCAGACAGCTGGGTGGG     74029     C      CCTATA
                                   CCAG ACAGCTGG     GGG
                                   |||| ||||||||     |||
                                   GGTC TGTCGACC     CCC
                                     _       CA____
GAM3292  ATP1A2   3'  GAGTGTAATGGCACGATC    74032        AGAAT   C
                                   GAGTGTAAT    CAC GTC
                                   |||||||||    ||| |||
                                   CTCACATTA    GTG TAG
                                         CC___   C
GAM3292  CRHR1    3'  GAGTGTAAGCAGCACGTTGTC  74033        _   AAT   C__
                                   GAGTGTAA TAG   CAC   GTC
                                   |||||||| |||   |||   |||
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                                CTCACATT GTC   GTG   CAG
                                     C   ___   CAA
GAM3292 DNMT2    3'  TAGGGGCAAGAATCACCGTC  74034    AGT   AT
                                TAG   GTA  AGAATCACCGTC
                                |||   |||  ||||||||||||
                                ATC   CGT  TCTTAGTGGCAG
                                  CC_   __
GAM3292 HSPA9B   3'  TGTTAGAATCACTGTC     74035    AA       C
                                TGT  TAGAATCAC GTC
                                |||  ||||||||| |||
                                ACA  ATCTTAGTG CAG
                                  __       A
GAM3292 LTB      3'  TAGAGGTAATAGAGGCCGTC  74036     T      ATCA
                                TAGAG GTAATAGA   CCGTC
                                ||||| ||||||||   |||||
                                ATCTC CATTATCT   GGCAG
                                   _      CC__
GAM3292 ANGPTL4  3'  CAGAGCCAAGAGTCACCGTC  74037      GTAAT   A
                                TAGAGT    AGA TCACCGTC
                                ||||||    ||| ||||||||
                                GTCTCG    TCT AGTGGCAG
                                   GT___   C
GAM3292 FLJ10314 3'  GAGTGCAATGGCACTGTC    74038        AGAAT   C
                                GAGTGTAAT    CAC GTC
                                |||||||||    ||| |||
                                CTCACGTTA    GTG CAG
                                     CC___   A
GAM3292 FLJ10613 3'  TAGAGTGCAATGGTGCCGTC  74039         AGAATCA
                                TAGAGTGTAAT      CCGTC
                                ||||||||||       |||||
                                ATCTCACGTTA      GGCAG
                                      CCAC___
GAM3292 FLJ20139 3'  TAGAGTGTAAGTATAGCTTGTC 74040        ___   AA__
                                TAGAGTGTA   ATAG   TC
                                |||||||||   ||||   ||
                                ATCTCACAT   TATC   AG
                                     TCA    GAAC
GAM3292 KIAA0494 5'  GTGTGATGATCACCGT     74041     A  A  A
                                GTGT AT GA TCACCGT
                                |||| || || |||||||
                                CACA TA CT AGTGGCA
                                  C  _  _
GAM3292 RANBP6   5'  CAGAGCTGGAATCACTGT    74042      GTAATA     C
                                TAGAGT     GAATCAC GT
                                ||||||     ||||||| ||
                                GTCTCG     CTTAGTG CA
                                   AC____      A
GAM3292 LOC146540 3' GAGTGCAATGGAGCCATC    74043        A  ATCA
                                GAGTGTAAT GA    CCGTC
                                ||||||||| ||    |||||
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                                CTCACGTTA CT    GGTAG
                                     C  C___
GAM3292  LOC147727 5'  GAGTGCAATGGAGCAATC    74044         __ _
                                GAGTGTAAT  AG AATC
                                |||||||||  || ||||
                                CTCACGTTA  TC TTAG
                                     CC  G
GAM3293  BN51T    3'  TAGGAGGCTCAGAAAGG     74047          CGTTAC
                                TAGGAGGCTCG     AAGG
                                ||||||||||      ||||
                                ATCCTCCGAGT     TTCC
                                      CT_____
GAM3293  CD4      3'  CAGGAGGTTCTGCACAGGGT   74048       C  GC  T   A
                                TAGGAGG TC  GT ACA GGT
                                ||||||| ||  || ||| |||
                                GTCCTCC AG  CG TGT CCA
                                    A  A_  _   C
GAM3293  EGLN1    5'  GAGGCTCGCTCCAGTCAAGGT  74049         GTTA__
                                GAGGCTCGC     CAAGGT
                                |||||||||     ||||||
                                CTCCGAGCG     GTTCCA
                                      AGGTCA
GAM3293  RSN      3'  TAGGGGTTTTTCTACAAGGT   74050      A  CTCGCG
                                TAGG GG     TTACAAGGT
                                |||| ||     |||||||||
                                ATCC CC     GATGTTCCA
                                  _  AAAAA_
GAM3293  C1orf24  3'  TAGGAAGCTCCGGTGTGAGGT  74051          G  TTACA
                                TAGGAGGCTC CG     AGGT
                                |||||||||| ||     ||||
                                ATCCTTCGAG GC     TCCA
                                      _  CACAC
GAM3293  DMWD     3'  TAGGAGGCTGGGGGCATGGGGT 74052          C___    TACAA
                                TAGGAGGCT    GCGT    GGT
                                |||||||||    ||||    |||
                                ATCCTCCGA    CGTA    CCA
                                     CCCC    CC___
GAM3293  FLJ13153 3'  CAGGAGGCTTTGCAAGG     74053          CGCG  A
                                TAGGAGGCT    TT CAAGG
                                |||||||||    || |||||
                                GTCCTCCGA    AA GTTCC
                                     _____  C
GAM3293  KIAA0513 3'  GGGGGCTACCAACAAGGT    74054     A    C  GTT
                                GG GGCT GC   ACAAGGT
                                || |||| ||   |||||||
                                CC CCGA TG   TGTTCCA
                                 C    _  GT_
GAM3293  KIAA1257 3'  GGAGGCTCTGACTTACGGGGT  74055         GCG_   AA
                                GGAGGCTC    TTAC  GGT
                                ||||||||    ||||  |||
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                                CCTCCGAG   AATG  CCA
                                    ACTG   CC
GAM3293 KIAA1908 5' GGAGGCCGCAGGAGAACAGGGT 74056      T   TT___  A
                                GGAGGC CGCG    ACA GGT
                                |||||| ||||    ||| |||
                                CCTCCG GCGT    TGT CCA
                                   _   CCTCT   C
GAM3293 MAPKAPK3 3' AGGAGGCTTAGGGTCAGGGT  74057      CGC_   CAA
                                AGGAGGCT   GTTA  GGT
                                ||||||||   ||||  |||
                                TCCTCCGA   CAGT  CCA
                                    ATCC   C__
GAM3293 OSBPL10  5' TAGGAGGCCGATCTGCAGG   74058      T  C   ACA
                                TAGGAGGC CG GTT   AGG
                                |||||||| || |||   |||
                                ATCCTCCG GC TAG   TCC
                                   _ _   ACG
GAM3293 RAB39    3' CAGGAGGCTGAGGTAAGGT   74059      CGC  TAC
                                TAGGAGGCT   GT   AAGGT
                                |||||||||   ||   |||||
                                GTCCTCCGA   CA   TTCCA
                                    CTC  ___
GAM3293 SEC15B   3' CAGGAGGCTGAACAGACAAGGT 74060      C_   TT
                                TAGGAGGCT  GCG  ACAAGGT
                                |||||||||  |||  |||||||
                                GTCCTCCGA  TGT  TGTTCCA
                                    CT   C_
GAM3293 LOC126302 3' CAGGAAGCCGTGTTATGGGGT  74061      T  C    CAA
                                TAGGAGGC CG GTTA   GGT
                                |||||||| || ||||   |||
                                GTCCTTCG GC CAAT   CCA
                                   _ A    ACC
GAM3293 LOC145815 5' AGGAGGCTCGTTCCAAAGGT   74062      CG   C
                                AGGAGGCTCG  TTA AAGGT
                                ||||||||||  ||| |||||
                                TCCTCCGAGC  GGT TTCCA
                                    AA   _
GAM3293 LOC146894 3' CAGGAGGCTCATTTGAGGT    74063      CGTTACA
                                TAGGAGGCTCG      AGGT
                                ||||||||||       ||||
                                GTCCTCCGAGT      TCCA
                                    AAAC___
GAM3293 LOC165229 5' TAAGAGGCTCGTGAAGAAGG   74064       CGTTAC
                                TAGGAGGCTCG     AAGG
                                ||||||||||      ||||
                                ATTCTCCGAGC     TTCC
                                    ACTTC_
GAM3293 LOC221491 5' GGAGGCTCAGGCCGGAGGT    74065      C   ACA
                                GGAGGCTCG GTT   AGGT
                                ||||||||| |||   ||||
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                                CCTCCGAGT CGG   TCCA
                                     C   CC_
GAM3293  LOC255299 5'  TAGGAGGCCTGGTACGGGGT   74066        CGC  T  AA
                                TAGGAGGCT   GT AC  GGT
                                |||||||||   || ||  |||
                                ATCCTCCGG   CA TG  CCA
                                     AC_  _  CC
GAM3293  LOC255518 3'  CAGGAGGTTAGTACAAGGT    74067       CTCGCGT
                                TAGGAGG      TACAAGGT
                                |||||||      ||||||||
                                GTCCTCC      ATGTTCCA
                                    AATC___
GAM3293  LOC256867 3'  GGATTGCAAGCGTTACAAGGT  74068     G_  TC
                                GGA  GC  GCGTTACAAGGT
                                |||  ||  ||||||||||||
                                CCT  CG  CGCAATGTTCCA
                                  AA  TT
GAM3294  S100A5    5'  TCTGAAATCTGATGGAACAA   74071    G    TA
                                TC GAAGT  CTGATGGAACAA
                                || |||||  ||||||||||||
                                AG CTTTA  GACTACCTTGTT
                                 A    __
GAM3294  TMEM2     3'  TCGGGGGTTTAGAACAAC    74072     AA   ACTGA
                                TCGG  GTT    TGGAACAAC
                                ||||  |||    |||||||||
                                AGCC  CAA    ATCTTGTTG
                                  CC  _____
GAM3294  ARFGEF2   3'  GGAGACTGTGATGGAACA    74073     AG  AC
                                GGA  TT  TGATGGAACA
                                |||  ||  ||||||||||
                                CCT  GA  ACTACCTTGT
                                  CT  C_
GAM3294  CGI-94    3'  GAAGTTACTAGAAAACGACA  74074         AT    A
                                GAAGTTACTG  GGAAC ACA
                                ||||||||||  ||||| |||
                                CTTCAATGAT  TTTTG TGT
                                      C_    C
GAM3294  FLJ12577  3'  GGAAGCTAATATGGAGCA    74075        CTG    A
                                GGAAGTTA   ATGGA CA
                                ||||||||   ||||| ||
                                CCTTCGAT   TACCT GT
                                     TA_    C
GAM3294  KIAA1676  3'  GGAAGATGTTGGAACAA     74076      TTAC  A
                                GGAAG    TG TGGAACAA
                                |||||    || ||||||||
                                CCTTC    AC ACCTTGTT
                                   T___  A
GAM3294  LOC115294 3'  TCTGAGGTTGCTGATGGA    74077    G  A   A
                                TC GA GTT CTGATGGA
                                || || ||| ||||||||
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                                AG CT CAA GACTACCT
                                 A  C   C
GAM3294  LOC152804 3'  TCGGAAATTATTCACAAC    74078          CTGATGGA
                                TCGGAAGTTA       ACAAC
                                ||||||||||       |||||
                                AGCCTTTAAT       TGTTG
                                     AAG_____
GAM3294  LOC255270 5'  TCTGAAATCTGATGGAACAA   74071    G     TA
                                TC GAAGT  CTGATGGAACAA
                                || |||||  ||||||||||||
                                AG CTTTA  GACTACCTTGTT
                                 A    __
GAM3295  COX7C     3'  TAGTATGGCATATGAGTTCTAG 74081          TTTTCTC    C
              T                  TAGTATGGC      GTTC AGT
                                |||||||||       |||| |||
                                ATCATACCG      CAAG TCA
                                     TATACT_    A
GAM3295  KIAA1078  3'  TGGTTTACATTCCAGT      74082     C   TCT
                                TGG TTT   CGTTCCAGT
                                ||| |||   |||||||||
                                ACC AAA   GTAAGGTCA
                                  _   T__
GAM3295  KIAA1458  3'  GTATGGTTTTGTTCCAG     74083       C    CTC
                                GTATGG TTTT   GTTCCAG
                                |||||| ||||   |||||||
                                CATACC AAAA   CAAGGTC
                                   _    ____
GAM3295  OSBPL8    3'  TAGGATAGCTCTTGTTTCAGT  74084     T       CTC   C
                                TAG ATGGCTTTT   GTT CAGT
                                ||| |||||||||   ||| ||||
                                ATC TATCGAGAA   CAA GTCA
                                  C         ___   A
GAM3295  ZFD25     3'  GTATGGCTTTTCTCCAG     74085           TCGT
                                GTATGGCTTTTC    TCCAG
                                ||||||||||||    |||||
                                CATACCGAAAAG    AGGTC
                                      _____
GAM3295  LOC169693 3'  GTGTGGCTTTTCCTCCCACAGT 74086     A        CG TC
                                GT TGGCTTTTCT  T  CAGT
                                || ||||||||||  |  ||||
                                CA ACCGAAAAGG  G  GTCA
                                 C         AG GT
GAM3295  LOC257443 3'  GTATGGTTTTGTTCCAG     74083       C    CTC
                                GTATGG TTTT   GTTCCAG
                                |||||| ||||   |||||||
                                CATACC AAAA   CAAGGTC
                                   _    ____
GAM3295  LOC92379  3'  GTATGGCTTCTTTCCAG     74087          CTCG
                                GTATGGCTTTT    TTCCAG
                                ||||||||||    ||||||
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                                CATACCGAAGA   AAGGTC
                                      ____
GAM3296 COPA     3' GGAGATGATTAAGAGTTGG   74090       CGT_
                                GGAGGTGAT   AGTTGG
                                |||||||||   ||||||
                                CCTCTACTA   TCAACC
                                     ATTC
GAM3296 ARFGAP1  3' GGAGGTGAGGGTTGGCATG   74091       TCGTA
                                GGAGGTGA    GTTGGCATG
                                ||||||||    |||||||||
                                CCTCCACT    CAACCGTAC
                                    CC___
GAM3297 MLC1     3' TAAGAAAATAAGAAAGTGCA   74094         ___
                                TAAGAAAATAAGAA   GCA
                                ||||||||||||||   |||
                                ATTCTTTTATTCTT   CGT
                                         TCA
GAM3297 MLC1     3' TAAGAAAATAAGAAAGTGCA   74094         ___
                                TAAGAAAATAAGAA   GCA
                                ||||||||||||||   |||
                                ATTCTTTTATTCTT   CGT
                                         TCA
GAM3297 PTPRK    3' AAGAAAATAAGCCAGTTA    74095       AGA   A
                                AAGAAAATA   AGC CAGTTA
                                |||||||||   ||| ||||||
                                TTCTTTTAT   TCG GTCAAT
                                      ___  _
GAM3297 RRM2B    3' GAAAAAATGAAAACACAGTT   74096     TAA_
                                GAAAA    GAAGCACAGTT
                                |||||    ||||||||||||
                                CTTTT    TTTTGTGTCAA
                                   TTAC
GAM3297 CKAP2    3' AAAAAACAAGGGCATAGTTAT  74097       AA   C
                                AGAAAATAAG  GCA AGTTAT
                                ||||||||||  ||| ||||||
                                TTTTTTGTTC  CGT TCAATA
                                      C_   A
GAM3297 GZMK     3' GAAAAAAGAAGCAAGT      74098      T      C
                                GAAAA AAGAAGCA AGT
                                ||||| |||||||| |||
                                CTTTT TTCTTCGT TCA
                                     _      _
GAM3297 KIAA0141 3' TAAGAAGGAAGAAGGTAAGTTA 74099      AAT     CAC
           T                     TAAGAA   AAGAAG   AGTTAT
                                 ||||||   ||||||   ||||||
                                 ATTCTT   TTCTTC   TCAATA
                                    CC_     CAT
GAM3297 OATPRP4  3' AAGAAAAGAAGGCACAGTT   74100      ATA    _
                                AAGAAA   AGAAG CACAGTT
                                ||||||   ||||| |||||||
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                                TTCTTT   TCTTC GTGTCAA
                                   ___     C
GAM3297  OSBPL6    3'  TAAGAAACATAATTGTGCATAG 74101        _    GAA_   C
              TTAT                  TAAGAAA ATAA    GCA AGTTAT
                                    ||||||| ||||    ||| ||||||
                                    ATTCTTT TATT    CGT TCAATA
                                       G    AACA   A
GAM3297  PPFIBP1   3'  TAAGACAATAAGAGGCAAGT   74102       A      A   C
                                    TAAGA AATAAGA GCA AGT
                                    ||||| ||||||| ||| |||
                                    ATTCT TTATTCT CGT TCA
                                       G      C  _
GAM3297  YME1L1    3'  GAAACCAAGCACAGTTA     74103      ATAAG
                                    GAAA    AAGCACAGTTA
                                    ||||    ||||||||||
                                    CTTT    TTCGTGTCAAT
                                      GG___
GAM3297  YME1L1    3'  GAAACCAAGCACAGTTA     74103      ATAAG
                                    GAAA    AAGCACAGTTA
                                    ||||    ||||||||||
                                    CTTT    TTCGTGTCAAT
                                      GG___
GAM3297  LOC129526 3'  GAAAATATTAATACAGTTAT   74104        AG  GC
                                    GAAAATA  AA  ACAGTTAT
                                    |||||||  ||  ||||||||
                                    CTTTTAT  TT  TGTCAATA
                                       AA  A_
GAM3297  LOC150630 5'  TAAGAAAATGGAAGCAC     74105         AA
                                    TAAGAAAAT  GAAGCAC
                                    |||||||||  |||||||
                                    ATTCTTTTA  CTTCGTG
                                         C_
GAM3297  LOC151188 3'  TAAAAAAATAATGTTTACAGTT 74106           GAAGC
                                    TAAGAAAATAA    ACAGTT
                                    ||||||||||    ||||||
                                    ATTTTTTTATT    TGTCAA
                                          ACAAA
GAM3298  CLECSF2   3'  TATGTGTAGCCTGACACGT    74109      CAGA
                                    TATG    TGTGGTCTGACACGT
                                    ||||    ||||||||||||||
                                    ATAC    ACATCGGACTGTGCA
                                       ____
GAM3298  JAM3      3'  GCAACTATGGTCTGATGTGTA  74110      A        CAC
                                    GCAG TGTGGTCTGA   GTA
                                    |||| ||||||||||   |||
                                    CGTT ATACCAGACT   CAT
                                      G         ACA
GAM3298  GRIN3A    3'  GCAGGGCGATCTGGCATGT    74111      AT       A  C
                                    GCAG  GTGGTCTG CA GT
                                    ||||  |||||||| || ||
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                                CGTC  CGCTAGAC GT CA
                                  C_       C  A
GAM3298  TSPEAR    3'  GCAGGTGTGGTCTGGGCTGCGT 74112      A        ACA__
                                GCAG TGTGGTCTG     CGT
                                |||| |||||||||     |||
                                CGTC ACACCAGAC     GCA
                                  C        CCGAC
GAM3298  LOC165693 5'  GATGTGGCCTTTGGCACGT    74113          GA__
                                GATGTGGTCT    CACGT
                                ||||||||||    |||||
                                CTACACCGGA    GTGCA
                                      AACC
GAM3298  LOC92305  3'  ATGCGGTCCAGGTCTGGCACGT 74114      AGATGT     A
           A                     ATGC     GGTCTG CACGTA
                                ||||     |||||| ||||||
                                TACG     CCAGAC GTGCAT
                                  CCAGGT     C
GAM3299  ADK       3'  GGAAATAAACATCATTTTT    74117      C    T
                                GGAAA AAAT ATCATTTTT
                                ||||| |||| |||||||||
                                CCTTT TTTG TAGTAAAAA
                                  A   _
GAM3299  ADK       3'  GGAAATAAACATCATTTTT    74117      C    T
                                GGAAA AAAT ATCATTTTT
                                ||||| |||| |||||||||
                                CCTTT TTTG TAGTAAAAA
                                  A   _
GAM3299  COL4A3    3'  GGAAACAAATTGAAACTTT    74118          ATC
                                GGAAACAAATT   ATTTT
                                ||||||||||   |||||
                                CCTTTGTTTAA   TGAAA
                                      CTT
GAM3299  COL4A3    3'  GGAAACAAATTGAAACTTT    74118          ATC
                                GGAAACAAATT   ATTTT
                                ||||||||||   |||||
                                CCTTTGTTTAA   TGAAA
                                      CTT
GAM3299  COL4A3    3'  GGAAACAAATTGAAACTTT    74118          ATC
                                GGAAACAAATT   ATTTT
                                ||||||||||   |||||
                                CCTTTGTTTAA   TGAAA
                                      CTT
GAM3299  ATP5F1    3'  GAAACAAACTTTTCATTTTTA  74119          A_
                                GAAACAAATT  TCATTTTTA
                                |||||||||  |||||||||
                                CTTTGTTTGA  AGTAAAAAT
                                      AA
GAM3299  CED-6     3'  GGAAACAAATATTTTT      74120          TATC
                                GGAAACAAAT    ATTTTT
                                |||||||||    ||||||
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                                CCTTTGTTTA    TAAAAA
                                      ____
GAM3299  FLJ20073  3'  AGAGACAAATTTCATTTTT    74121     A      A
                                GGA ACAAATT TCATTTTT
                                ||| ||||||| ||||||||
                                TCT TGTTTAA AGTAAAAA
                                  C      _
GAM3299  FLJ20147  3'  TACAGAAACTACTATTGTTTTT 74122          AA     CA
              A                   TACGGAAAC  ATTAT  TTTTTA
                                ||||||||| |||||  ||||||
                                ATGTCTTTG  TGATA  AAAAAT
                                      A_    AC
GAM3299  NET-6     3'  TACAAGTAAATTATCATTTTTA 74123       AAAC
                                TACGG    AAATTATCATTTTTA
                                |||||    ||||||||||||||
                                ATGTT    TTTAATAGTAAAAAT
                                   CA__
GAM3300  CORO1C    3'  TCGCTGGTTGACAAATCT    74126    ACA      T   T
                                TC   TGGTTGG CAG TCT
                                ||   ||||||| ||| |||
                                AG   ACCAACT GTT AGA
                                 CG_      _   T
GAM3300  DIO1      3'  TCCCATAATTGGTTCTAAA    74127    A        CAGT
                                TC CATGGTTGGT    TCTAAA
                                || ||||||||||    ||||||
                                AG GTATTAACCA    AGATTT
                                 G         ____
GAM3300  DUSP11    3'  TCAATGCTTCAGTTCTAAA    74128     C   G TGG
                                TCA ATG T   TCAGTTCTAAA
                                ||| ||| |   ||||||||||
                                AGT TAC A   AGTCAAGATTT
                                  _   G ___
GAM3300  GPR62     3'  CCACATGCCAGTTCT       74129       GGTTG
                                TCACAT    GTCAGTTCT
                                ||||||    |||||||||
                                GGTGTA    CGGTCAAGA
                                      _____
GAM3300  GRM1      3'  TCACATGGTTTGTTCT      74130          GGTCA
                                TCACATGGTT    GTTCT
                                ||||||||||    |||||
                                AGTGTACCAA    CAAGA
                                      A____
GAM3300  ZNF2      3'  TCATATGGTTGGTGACAG    74131     C       __
                                TCA ATGGTTGGT  CAG
                                ||| |||||||||  |||
                                AGT TACCAACCA  GTC
                                  A        CT
GAM3300  ZNFN2A1   3'  TGGATGGTACACAGTTCTA    74132     T    ___
                                TGG TGGT   CAGTTCTA
                                ||| ||||   ||||||||
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                                ACC ACCA   GTCAAGAT
                                  T    TGT
GAM3300 ATP10D   3' CAGGCTACTGTCAGTTTTAAAA 74133    T    __      C
                                CA GGTTG  GTCAGTT TAAAA
                                || |||||  ||||||| |||||
                                GT CCGAT  CAGTCAA ATTTT
                                 _    GA      A
GAM3300 CGI-127  5' ATGGCTGAAGTTCTAAAA    74134        TC
                                ATGGTTGG  AGTTCTAAAA
                                ||||||||  ||||||||||
                                TACCGACT  TCAAGATTTT
                                     __
GAM3300 DKFZP434I092 3' CCATATGGTTGGAGGCCTA   74135    C      TC  TT
                                TCA ATGGTTGG  AG  CTA
                                ||| ||||||||  ||  |||
                                GGT TACCAACC  TC  GAT
                                  A       __ CG
GAM3300 FLJ13158 3' TCCATGGTGTTCTAA      74136    A    TGGTCA
                                TC CATGGT     GTTCTAA
                                || ||||||     |||||||
                                AG GTACCA     CAAGATT
                                 _    _______
GAM3300 GTF2E1   3' ACCAGTCTGGTCAGTTCTAAA  74137    ATGG
                                AC    TTGGTCAGTTCTAAA
                                ||    ||||||||||||||
                                TG    GACCAGTCAAGATTT
                                 GTCA
GAM3300 HSU24186  5' CAGTGGTTGCTACATTCTAAAA 74138    _     GTCA
                                CA TGGTTG    GTTCTAAAA
                                || ||||||    |||||||||
                                GT ACCAAC    TAAGATTTT
                                 C     GATG
GAM3300 KIAA0562  3' TCACACGGTTGGCAATT     74139          T
                                TCACATGGTTGG CAGTT
                                |||||||||||| |||||
                                AGTGTGCCAACC GTTAA
                                      _
GAM3300 KIAA1918  5' TCACACTGTAAACAGTTCTAA  74140       G  TGGT
                                TCACAT GT    CAGTTCTAA
                                |||||| ||    |||||||||
                                AGTGTG CA    GTCAAGATT
                                   A  TTT_
GAM3300 MEGF10   3' CACGGGTATAGTTCTAAA    74141      TTG  C
                                CATGG   GT AGTTCTAAA
                                |||||   || |||||||||
                                GTGCC   TA TCAAGATTT
                                  CA_  _
GAM3300 MGC5139  5' ACAGTGGACGCCAGTTCT    74142     _   TTG
                                ACA TGG   GTCAGTTCT
                                ||| |||   |||||||||
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                                TGT ACC   CGGTCAAGA
                                  C   TG_
GAM3300 SEF      5' TCACAGGCTCGGGTTCTAAA  74143      T   _ TCA
                                TCACA GGTT GG   GTTCTAAA
                                ||||| |||| ||   ||||||||
                                AGTGT CCGA CC   CAAGATTT
                                   _    G ___
GAM3300 STK39    3' TCACAGTCAGTTTTAAA     74144      TGGTTG      C
                                TCACA     GTCAGTT TAAA
                                |||||     ||||||| ||||
                                AGTGT     CAGTCAA ATTT
                                   _______      A
GAM3300 SYNPO2   3' TCCATGGTTGGTCAGACTC   74145    A          _
                                TC CATGGTTGGTCAG TTC
                                || |||||||||||| |||
                                AG GTACCAACCAGTC GAG
                                 _           T
GAM3300 TOB2     3' TCACATGGCTTGGAATCCT    74146          _ TC
                                TCACATGGTT GG  AGTTCT
                                |||||||||| ||  ||||||
                                AGTGTACCGA CC  TTAGGA
                                      A __
GAM3300 TOLLIP   3' CGTCTGGGAAGTTCTAAA    74147    G    TC
                                TG TTGG  AGTTCTAAA
                                || ||||  |||||||||
                                GC GACC  TCAAGATTT
                                 A    CT
GAM3300 LOC115110 3' CACTTCGGTTGGTTCTA     74148     A_       CAGT
                                CAC  TGGTTGGT    TCTA
                                |||  ||||||||    ||||
                                GTG  GCCAACCA    AGAT
                                  AA       _____
GAM3300 LOC154084 3' TCACAGCAGTTCTAA       74149       TGGTTG T
                                TCACA     G CAGTTCTAA
                                |||||     | |||||||||
                                AGTGT     C GTCAAGATT
                                   _______ _
GAM3300 LOC200059 3' CCACAGGTCAGTTCT       74150       TGGTT
                                TCACA     GGTCAGTTCT
                                |||||     ||||||||||
                                GGTGT     CCAGTCAAGA
                                   ______
GAM3300 LOC92181  3' ACATAGTTGTTGAGTGTTCTAA 74151          GTCA__
             AA                   ACATGGTTG      GTTCTAAAA
                                |||||||||      |||||||||
                                TGTATCAAC      CAAGATTTT
                                      AACTCA
GAM3300 LOC93017  3' TGGATGTTAGTTCTAAAA    74152     TTG  C
                                TGG   GT AGTTCTAAAA
                                |||   || ||||||||||
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                                ACC   CA TCAAGATTTT
                                  TA_  A
GAM3301  CARM1    3'  CAACACGTTTCCTCATTTATTT 74155       ____    ATT
             T                   CGACACG   CTCGT   TTATTTT
                                 |||||||   |||||  |||||||
                                 GTTGTGC   GAGTA  AATAAAA
                                    AAAG   ___
GAM3301  HGRG8    3'  CACGACACGTTTTACAGTATTT 74156        CTCG   TT
             T                   TACGACACG   TAT  TATTTT
                                 |||||||||   |||  ||||||
                                 GTGCTGTGC   ATG  ATAAAA
                                      AAA_  TC
GAM3301  TRPM3    3'  ACGCTGGCTATTTTATTTT   74157      C  _
                                 ACGCT GT ATTTTATTTT
                                 ||||| || ||||||||||
                                 TGCGA CG TAAAATAAAA
                                    C  A
GAM3301  LOC115294 3'  CACACTTTTTGTATTTTATTTT 74158      C___
                                 CACGCT   GTATTTTATTTT
                                 ||||||   ||||||||||||
                                 GTGTGA   CATAAAATAAAA
                                    AAAA
GAM3301  LOC145623 3'  TACTGCATGCTCGGTCATTTT  74159    GA  C    TATT
                                 TAC  CA GCTCG   TTATTTT
                                 |||  || |||||   |||||||
                                 ATG  GT CGAGC   AGTAAAA
                                   AC  A    C___
GAM3302  BACE     3'  TATTTTTCAGTATCCCCTGCA  74162         C    ATC
                                 TATTTTTTAG ATCCT   GCA
                                 |||||||||| |||||   |||
                                 ATAAAAAGTC TAGGG   CGT
                                      A    GA_
GAM3302  BACE     3'  TATTTTTCAGTATCCCCTGCA  74162         C    ATC
                                 TATTTTTTAG ATCCT   GCA
                                 |||||||||| |||||   |||
                                 ATAAAAAGTC TAGGG   CGT
                                      A    GA_
GAM3302  CHAC     3'  TTTTTTAGCATCCAGAATACA  74163          TATC_
                                 TTTTTTAGCATCC    GCA
                                 ||||||||||||    |||
                                 AAAAAATCGTAGG    TGT
                                       TCTTA
GAM3302  HAGH     5'  TTTTTTGGCACCGCAC     74164       A   CCTAT
                                 TTTTTT GCAT    CGCAC
                                 |||||| ||||    |||||
                                 AAAAAA CGTG    GCGTG
                                    C   _____
GAM3302  SF3B1    3'  TTTTTTAGCATTTTGTACACA  74165         CCTATC
                                 TTTTTTAGCAT    GCACA
                                 ||||||||||     |||||
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                                AAAAAATCGTA     TGTGT
                                     AAACA_
GAM3302 XK      3' TATTTATTAGCATCAACGAC  74166      T      CTAT  C
                                TATTT TTAGCATC    CG AC
                                ||||| ||||||||    || ||
                                ATAAA AATCGTAG    GC TG
                                   T       TT__  _
GAM3302 YWHAB   3' TTTTTTTTTTTTTTATCGCACA 74167       AGCATCC
                                TTTTTT      TATCGCACA
                                ||||||      |||||||||
                                AAAAAA      ATAGCGTGT
                                   AAAAAAA
GAM3302 YWHAB   3' TTTTTTTTTTTTTTATCGCACA 74167       AGCATCC
                                TTTTTT      TATCGCACA
                                ||||||      |||||||||
                                AAAAAA      ATAGCGTGT
                                   AAAAAAA
GAM3302 GDF10   3' TATTTTTTAGTATTCCCAC   74168         CA_
                                TATTTTTTAG   TCCTAT
                                ||||||||||   ||||||
                                ATAAAAAATC   AGGGTG
                                     ATA
GAM3302 LOC149372 5' TTCTTTAGCATTCACA     74169          CCTA
                                TTTTTTAGCAT    TCGCA
                                ||||||||||    |||||
                                AAGAAATCGTA    AGTGT
                                     ____
GAM3303 ACE2    3' TGCTCAGCACTGCTCAAACA  74172     AG   _  A T
                                TGC  TCAG AC G CTCAAACA
                                |||  |||| || | ||||||||
                                ACG  AGTC TG C GAGTTTGT
                                  __   G  A _
GAM3303 COG3    3' TCTGCAGTCAGCACTGAGC   74173          _ __
                                TCTGCAGTCAG AC  AGT
                                |||||||||| ||  |||
                                AGACGTCAGTC TG  TCG
                                     G  AC
GAM3303 DDIT3   5' TCTGCAGTTGGATCAGTCT   74174        CA  _
                                TCTGCAGT  GA CAGTCT
                                ||||||||  || ||||||
                                AGACGTCA  CT GTCAGA
                                    AC  A
GAM3303 LYPLA1  3' TCTACAGTAGTTGGTTTCAAAC 74175        C  ACA  C
                                TCTGCAGT AG   GT TCAAAC
                                |||||||| ||   || ||||||
                                AGATGTCA TC   CA AGTTTG
                                   _ AAC  A
GAM3303 NESH    3' TCTGCAGCAGGCCTC       74176        T   ACA
                                TCTGCAG CAG   GTCTC
                                ||||||| |||   |||||
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                                AGACGTC GTC   CGGAG
                                      _  ___
GAM3303 RGL      3' TCTGCATTTTAGTCTCAAA   74177       GTCAGAC
                                TCTGCA      AGTCTCAAA
                                ||||||      |||||||||
                                AGACGT      TCAGAGTTT
                                   AAAA___
GAM3303 SLC4A4   3' TCAGCAGTCAATACATTTCAA 74178    T      _  GTC
                                TC GCAGTCAG ACA   TCAA
                                || ||||||| |||   ||||
                                AG CGTCAGTT TGT   AGTT
                                 T       A  AA_
GAM3303 SS18     3' ACAGGACAGTCTCAAA     74179     TCA
                                GCAG   GACAGTCTCAAA
                                ||||   ||||||||||||
                                TGTC   CTGTCAGAGTTT
                                  ___
GAM3303 ATP9A    3' TCTGAGGTCCTTCTCAAAC   74180     CA   AGACAG
                                TCTG  GTC     TCTCAAAC
                                ||||  |||     ||||||||
                                AGAC  CAG     AGAGTTTG
                                  TC   GA____
GAM3303 DKFZP434I0714 5' TGAGTCAGACCTGAAAC     74181    C       AGT  C
                                TG AGTCAGAC   CT AAAC
                                || ||||||||   || ||||
                                AC TCAGTCTG   GA TTTG
                                 _       ___  C
GAM3303 DKFZp564I1922 3' TGCAGTCAGAGCACAGACA   74182          CA  CT  A
                                TGCAGTCAGA  GT  CA ACA
                                ||||||||||  ||  || |||
                                ACGTCAGTCT  CG  GT TGT
                                      __  T_  C
GAM3303 DKFZp566D234 3'  TCTACAGTGTCTCAA       74183         CAGACA
                                TCTGCAGT     GTCTCAA
                                ||||||||     |||||||
                                AGATGTCA     CAGAGTT
                                  _______
GAM3303 FEZ2     3' TCTGCAGTGTACACTTTCTCAA 74184         CAG   G__
                                TCTGCAGT   ACA   TCTCAA
                                ||||||||   |||   ||||||
                                AGACGTCA   TGT   AGAGTT
                                    CA_   GAA
GAM3303 FLJ12542 3'  TCTGGACAGTCTCAAA     74185     CAGTCA
                                TCTG     GACAGTCTCAAA
                                ||||     ||||||||||||
                                AGAC     CTGTCAGAGTTT
                                  _______
GAM3303 FLJ12949 3'  TCTGCAGCAGATAGTACT    74186        T   C  _
                                TCTGCAG CAGA AGT CT
                                ||||||| |||| ||| ||
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                                AGACGTC GTCT TCA GA
                                   _   A   T
GAM3303  FLJ13984  3'  TCTGCAATCAGATGACAAT   74187          ___
                                TCTGCAGTCA   GACAGT
                                ||||||||||   ||||||
                                AGACGTTAGT   CTGTTA
                                     CTA
GAM3303  FLJ14117  3'  TCTGCAGTCAGAGGGAGAAGAA 74188          C__  TCTC
           AACA                    TCTGCAGTCAGA   AG    AAACA
                                ||||||||||||   ||   |||||
                                AGACGTCAGTCT   TC    TTTGT
                                      CCC  TTCT
GAM3303  FLJ20081  3'  TCTCAAACTCCAGTCTCAA   74189     G   TCAGA
                                TCT CAG    CAGTCTCAA
                                ||| |||    |||||||||
                                AGA GTT    GTCAGAGTT
                                  _  TGAG_
GAM3303  KIAA0514  5'  TCTCATCATCAGTCTCAA    74190     G  G   GA
                                TCT CA TCA  CAGTCTCAA
                                ||| || |||  |||||||||
                                AGA GT AGT  GTCAGAGTT
                                  _ _  A_
GAM3303  KIAA1910  3'  TCTGCAGTGTGGGCAGCACCAA 74191        CAGA_   CT
                                TCTGCAGT    CAGT  CAA
                                ||||||||    ||||  |||
                                AGACGTCA    GTCG  GTT
                                     CACCC    TG
GAM3303  KRTHB5    3'  TCTGCATTGGACAGTCCC    74192       GTCA
                                TCTGCA    GACAGTCTC
                                ||||||    |||||||||
                                AGACGT    CTGTCAGGG
                                   AAC_
GAM3303  MGC2487   5'  CTGCAGTCATCGGCTCGGACA  74193         GACA T   AA
                                CTGCAGTCA    G CTC  ACA
                                |||||||||    | |||  |||
                                GACGTCAGT    C GAG  TGT
                                      AGC_ _   CC
GAM3303  MLL3      5'  TCTGCAGTAGACACCCCA    74194         C    G
                                TCTGCAGT AGACA TCTCA
                                |||||||| ||||| |||||
                                AGACGTCA TCTGT GGGGT
                                      _    _
GAM3303  PRDM15    3'  GCCATAACAGTCTTGAACA   74195      _      CA
                                GTCA GACAGTCT  AACA
                                |||| ||||||||  ||||
                                CGGT TTGTCAGA  TTGT
                                  A       AC
GAM3303  RNF40     3'  CCTGCAGCCCAGTCTCAAACA  74196         AGA
                                TCTGCAGTC   CAGTCTCAAACA
                                |||||||||   ||||||||||||
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                                GGACGTCGG  GTCAGAGTTTGT
                                    ___
GAM3303  LOC144747 5'  TCTGCAGTCAGCAGAAGACA  74197          A  TCT_
                                TCTGCAGTCAG CAG   CA
                                |||||||||| |||   ||
                                AGACGTCAGTC GTC   GT
                                      _  TTCT
GAM3303  LOC150135 5'  TCTGCAGTGGACAGTCT    74198        CA
                                TCTGCAGT  GACAGTCT
                                ||||||||  ||||||||
                                AGACGTCA  CTGTCAGA
                                     C_
GAM3303  LOC152315 5'  TCTGCAGTCGGAAGTCT    74199         A  C
                                TCTGCAGTC GA AGTCT
                                ||||||||| || |||||
                                AGACGTCAG CT TCAGA
                                      C  _
GAM3303  LOC152441 3'  TCTGGAGTCAGACAGAACT   74200      C        T_
                                TCTG AGTCAGACAG  CT
                                |||| ||||||||||  ||
                                AGAC TCAGTCTGTC  GA
                                  C         TT
GAM3303  LOC157922 3'  TCTGCAGTTTGAGATAGATTCA 74201        C__   C  TC
           A                     TCTGCAGT   AGA AG  TCAA
                                |||||||   ||| ||  ||||
                                AGACGTCA   TCT TC  AGTT
                                     AAC   A  TA
GAM3303  LOC197408 5'  TCTGCAGCTCAGAAGGTAAACA 74202        _    CA  CTC
                                TCTGCAG TCAGA  GT   AAACA
                                ||||||| |||||  ||   |||||
                                AGACGTC AGTCT  CA   TTTGT
                                    G    TC  ___
GAM3303  LOC220635 5'  TCTGCAGTAGACACCCCA    74194        C    G
                                TCTGCAGT AGACA TCTCA
                                |||||||| ||||| |||||
                                AGACGTCA TCTGT GGGGT
                                      _    _
GAM3303  LOC255177 5'  CAGTCCCAATCTCAAA     74203       AGA
                                CAGTC   CAGTCTCAAA
                                |||||   ||||||||||
                                GTCAG   GTTAGAGTTT
                                  G__
GAM3303  LOC57826  3'  TCTACAGTCAATTTCAAA    74204          GACA  C
                                TCTGCAGTCA   GT TCAAA
                                ||||||||||   || |||||
                                AGATGTCAGT   TA AGTTT
                                      _____  A
GAM3304  BCL10     3'  GAATTTTGGCAAACCGAGATC  74207       CA   _  GT
                                GAATTT  GCAA CTG  AGATC
                                ||||||  |||| |||  |||||
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                                CTTAAA  CGTT GGC  TCTAG
                                   AC    T  __
GAM3304  CDR2     3'  AGGAATTTCTGCAACAAGT    74208          A     T
                                AGGAATTTC GCAAC GGT
                                ||||||||| ||||| |||
                                TCCTTAAAG CGTTG TCA
                                     A     T
GAM3304  DPYD     3'  AGCAATTTCAGCGAAGGGGAT  74209    G        AACT  TA
                                AG AATTTCAGC    GG  GAT
                                || |||||||||    ||  |||
                                TC TTAAAGTCG    TC  CTA
                                 G        CT__  CC
GAM3304  FUT6     5'  AGGAGTCTCAGCAGGCTGG    74210      A       A_
                                AGGA TTTCAGCA  CTGG
                                |||| ||||||||  ||||
                                TCCT AGAGTCGT  GACC
                                  C       CC
GAM3304  HSPD1    3'  AGGAATTTCTGTGACTACAACT 74211          A_______
                                AGGAATTTC       GCAACT
                                |||||||||       ||||||
                                TCCTTAAAG       TGTTGA
                                     ACACTGA
GAM3304  IGF1     3'  AGGAATTTAGTGCAACTGG    74212         CA_
                                AGGAATTT   GCAACTGG
                                ||||||||   ||||||||
                                TCCTTAAA   CGTTGACC
                                     TCA
GAM3304  SURF4    3'  AGAATCAATTGGTAGA       74213       TTCAG   C
                                GGAAT     CAA TGGTAGA
                                |||||     ||| |||||||
                                TCTTA     GTT ACCATCT
                                  _____   A
GAM3304  TSSC4    3'  AGGAGCTTCAGCAAGGT      74214       A       CT
                                AGGA TTTCAGCAA  GGT
                                |||| |||||||||  |||
                                TCCT GAAGTCGTT  CCA
                                  C       __
GAM3304  DKFZP564D172 3'  AGGATTTTCAGCAGTAATGCGG 74215       A       ACTG_ TA
            AT                    AGGA TTTCAGCA     G  GAT
                                |||| ||||||||     |  |||
                                TCCT AAAGTCGT     C  CTA
                                  A       CATTA GC
GAM3304  DKFZP586J0619 3'  AGGGATTTCAGCATCACCAGGT 74216      A       __  _
                                AGG ATTTCAGCA  ACT GGT
                                ||| |||||||||  ||| |||
                                TCC TAAAGTCGT  TGG CCA
                                  C       AG   T
GAM3304  FLJ20086 3'  AGGAGTTTCAACAATGGGT    74217       A       CT
                                AGGA TTTCAGCAA  GGT
                                |||| |||||||||  |||
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                                TCCT AAAGTTGTT  CCA
                                  C       AC
GAM3304  FLJ22390  5'  AGGATTTCACAGGGTAGAT   74218     A    G  ACT
                                AGGA TTTCA CA   GGTAGAT
                                |||| ||||| ||   |||||||
                                TCCT AAAGT GT   CCATCTA
                                  _    _ C__
GAM3304  FLJ23436  3'  AGAGTTTCAGCAGCTACCAA  74219    A      A  G
                                GGA TTTCAGCA CTG TAG
                                ||| |||||||| ||| |||
                                TCT AAAGTCGT GAT GTT
                                  C       C  G
GAM3304  KIAA0159  5'  GGAATCTTAGCGACGAGT    74220       C  A  T
                                GGAATTT AGC AC GGT
                                ||||||| ||| || |||
                                CCTTAGA TCG TG TCA
                                    A  C  C
GAM3304  KIAA1497  5'  AGGAACTTCAGTGACTAGT   74221         CA
                                AGGAATTTCAG  ACTGGT
                                ||||||||||  ||||||
                                TCCTTGAAGTC  TGATCA
                                      AC
GAM3304  KIAA1853  3'  GGAATGTTCAGCAGATGGT   74222      _     AC
                                GGAAT TTCAGCA  TGGT
                                ||||| |||||||  ||||
                                CCTTA AAGTCGT  ACCA
                                   C      CT
GAM3304  KIAA1962  3'  AGGGTTTCAGTAACTGACAA  74223    AA    C    GT
                                AGG  TTTCAG AACTG  AG
                                |||  |||||| |||||  ||
                                TCC  AAAGTC TTGAC  TT
                                  C_     A    TG
GAM3304  KRT6IRS   3'  AGGAATTTCACCAAGCTTGGT  74224        G  _ _
                                AGGAATTTCA CAA CT GGT
                                |||||||||| ||| || |||
                                TCCTTAAAGT GTT GA CCA
                                      G  C  A
GAM3304  POFUT1    3'  AGGAATTTTAGAACCACAAGGT 74225       C  C  ____
                                AGGAATTT AG AACT   GGT
                                |||||||| || ||||   |||
                                TCCTTAAA TC TTGG   CCA
                                    A  _   TGTT
GAM3304  PPP1R16B  3'  AGGGATTTCAGCGTCAGT    74226    A      AAC
                                AGG ATTTCAGC   TGGT
                                ||| ||||||||   ||||
                                TCC TAAAGTCG   GTCA
                                  C       CA_
GAM3304  RAB35     3'  AGGAATTTCACATCAGGT    74227         G  ACT
                                AGGAATTTCA CA   GGT
                                ||||||||||  ||   |||
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                                TCCTTAAAGT GT   CCA
                                      _  AGT
GAM3304  LOC129607 3'  AGGAATTTTAGGTAATCACCTG 74228        C _____  A
                 GT                    AGGAATTT AG     CA CTGGT
                                       |||||||| ||     || |||||
                                       TCCTTAAA TC     GT GACCA
                                           A  CATTA  G
GAM3304  LOC147991 5'  AGAGATTTCAGCAATCCAAT   74229    GA        _ TG
                                       AG  ATTTCAGCAA C  GT
                                       ||  ||||||||||| |  ||
                                       TC  TAAAGTCGTT G  TA
                                        TC         A GT
GAM3304  LOC150519 3'  AGGAATTCAGCAAGTGAT    74230        T     C
                                       AGGAATT CAGCAA TGGT
                                       ||||||| |||||| ||||
                                       TCCTTAA GTCGTT ACTA
                                          _     C
GAM3304  LOC152217 3'  AGGAATTTGGCAGCTGTAG   74231         CA   A   G
                                       AGGAATTT  GCA CTG TAG
                                       ||||||||  ||| ||| |||
                                       TCCTTAAA  CGT GAC ATC
                                           C_   C   _
GAM3304  LOC154442 3'  AGGAATTTTGGAGATTGGTATA 74232         CAGCAAC    G
                 TC                    AGGAATTT       TGGTA ATC
                                       ||||||||       ||||| |||
                                       TCCTTAAA       ACCAT TAG
                                           ACCTCTA     A
GAM3304  LOC157567 3'  AGGAATTTTACAACAGC     74233         CA    T
                                       AGGAATTT  GCAAC GGT
                                       ||||||||  ||||| |||
                                       TCCTTAAA  TGTTG TCG
                                           A_     _
GAM3304  LOC170393 3'  AGGAATTTTGACAGGAGAT    74234         CA   ACT  T
                                       AGGAATTT  GCA   GG AGAT
                                       ||||||||  |||   || ||||
                                       TCCTTAAA  TGT   CC TCTA
                                           AC  ___  _
GAM3304  LOC203257 5'  AGGAATTTCAACATCTCTAGGT 74235            A ___
                                       AGGAATTTCAGCA CT   GGT
                                       |||||||||||| ||   |||
                                       TCCTTAAAGTTGT GA   CCA
                                              A  GAT
GAM3304  LOC254822 5'  AGGAATTTTACAGCTGG     74236         CA   A
                                       AGGAATTT  GCA CTGG
                                       ||||||||  ||| ||||
                                       TCCTTAAA  TGT GACC
                                           A_   C
GAM3304  LOC90750  3'  GGATTTTCAGCAGCTGGC    74237     A       A
                                       GGA TTTCAGCA CTGGT
                                       ||| |||||||| |||||
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                                CCT AAAGTCGT GACCG
                                  A       C
GAM3305  APAF1    5'  GAGCTGTCAACCATGAGCCA  74240    A   AC      T_
                                GA CTG  CAACCATG  TCA
                                || |||  ||||||||  |||
                                CT GAC  GTTGGTAC  GGT
                                 C   A_      TC
GAM3305  APAF1    5'  GAGCTGTCAACCATGAGCCA  74240    A   AC      T_
                                GA CTG  CAACCATG  TCA
                                || |||  ||||||||  |||
                                CT GAC  GTTGGTAC  GGT
                                 C   A_      TC
GAM3305  APXL     3'  ACTGACCAGCATTCACGCA   74241       ACCA
                                ACTGACCA   TGTTCACGCA
                                ||||||||   ||||||||||
                                TGACTGGT   GTAAGTGCGT
                                    C___
GAM3305  ARNT2    3'  GAACTGACCTACCCATGT    74242       AA_
                                GAACTGACC  CCATGT
                                |||||||||  ||||||
                                CTTGACTGG  GGTACA
                                     ATG
GAM3305  HIF1A    3'  GAACTAACCAAGTTTGTGC   74243        CCA  TCAC
                                GAACTGACCAA  TGT   GC
                                ||||||||||  |||   ||
                                CTTGATTGGTT  ACA   CG
                                      CAA  _____
GAM3305  KIF5C    3'  GAACTGACTGGCTGATCAGCA 74244       CAACCA  T   C
                                GAACTGAC     TG TCA GCA
                                ||||||||     || ||| |||
                                CTTGACTG     AC AGT CGT
                                     ACCG__  T   _
GAM3305  RNF7     3'  AACTGATCAACCATAAGCATGC 74245      C      TT  C
            A                    AACTGA CAACCATG  CA GCA
                                ||||||  ||||||||  || |||
                                TTGACT GTTGGTAT  GT CGT
                                   A       TC  A
GAM3305  C20orf21 3'  GAGCTGACCAAGCACACG    74246    A      CCAT  T
                                GA CTGACCAA    GT CACG
                                || ||||||||    || ||||
                                CT GACTGGTT    CG GTGC
                                 C       _____  T
GAM3305  FLJ21817 3'  GACTGACCAATCACAACACG   74247    A      C    TT
                                GA CTGACCAA CATG  CACG
                                || |||||||| ||||  ||||
                                CT GACTGGTT GTGT  GTGC
                                 _       A   T_
GAM3305  FLJ22671 5'  GAGCTGGCCACCATGCC     74248    A   A   A
                                GA CTG CCA CCATGTT
                                || ||| ||| |||||||
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                                CT GAC GGT GGTACGG
                                 C  C  _
GAM3305 GPS2    5' GAACTGACAATTGACACAC   74249       CAACCA TT
                                GAACTGAC    TG CACGC
                                ||||||||    || |||||
                                CTTGACTG    AC GTGTG
                                    TTA___  T_
GAM3305 HIC2    3' GAACTGACGGCCATCCCCGC  74250       CAA  G  A
                                GAACTGAC  CCAT TTC CGC
                                ||||||||  |||| ||| |||
                                CTTGACTG  GGTA GGG GCG
                                    CC_   _  _
GAM3305 PRO0097 5' GAACTAACTAACATATGC    74251       C  C   TCAC
                                GAACTGAC AAC ATGT   GC
                                |||||||| ||| ||||   ||
                                CTTGATTG TTG TATA   CG
                                    A  _  _____
GAM3305 LOC145815 5' GAACTGACAACTGACGAGTGC 74252       C  C_  TTCAC
                                GAACTGAC AAC  ATG    GC
                                |||||||| |||  |||    ||
                                CTTGACTG TTG  TGC    CG
                                    _  AC  TCA__
GAM3305 LOC149108 3' CTGACCACACCATCAGCA    74253       _  TGT  C
                                CTGACCA ACCA  TCA GCA
                                ||||||| ||||  ||| |||
                                GACTGGT TGGT  AGT CGT
                                    G  ____  _
GAM3305 LOC253461 3' GAACTGCCATCATGTTCACG  74254      A  AC
                                GAACTG CCA  CATGTTCACG
                                |||||| |||  ||||||||||
                                CTTGAC GGT  GTACAAGTGC
                                   _  A_
GAM3305 LOC91263  5' GAACTGACTGCTTGCTTGGCAC 74255       CAACCA  ___
          G                      GAACTGAC    TGTT  CACG
                                 ||||||||    ||||  ||||
                                 CTTGACTG    ACGA  GTGC
                                     ACGA__   ACC
GAM3306 ACCN1   3' GGAGCGAGGTCTAGGCAGCTA 74258       A_  AC A
                                GGAGCGAG  CTA  CA CTA
                                ||||||||  |||  || |||
                                CCTCGCTC  GAT  GT GAT
                                    CA  CC  C
GAM3306 ADA     3' CAGGAGCATCAGTAACTGACTA 74259       AGAC   CA
                                CAGGAGCG   TAAC  ACTA
                                ||||||||   ||||  ||||
                                GTCCTCGT   ATTG  TGAT
                                    AGTC   AC
GAM3306 BECN1   5' GGAGCGAGGCCTCCAGAACTA  74260       A  AA  __
                                GGAGCGAG CT  CCA  ACTA
                                |||||||| ||  |||  ||||
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                                CCTCGCTC GG  GGT  TGAT
                                     C  A_   CT
GAM3306  FUT1     3'  AGAGCAAGACGCTGGCCAACTA 74261          TAA__
                                GGAGCGAGAC     CCAACTA
                                ||||||||||     |||||||
                                TCTCGTTCTG     GGTTGAT
                                     CGACC
GAM3306  GLRX     3'  CAGTAGCAGATAACCAACT    74262     G   G   C
                                CAG AGC AGA TAACCAACT
                                ||| ||| ||| |||||||||
                                GTC TCG TCT ATTGGTTGA
                                  A  _  _
GAM3306  ICMT     3'  GGGCAAGCCCAACTA       74263     A     A TAA
                                GG GCGAG C   CCAACTA
                                || ||||| |   |||||||
                                CC CGTTC G   GGTTGAT
                                 _    _ ____
GAM3306  IL1RAPL2  5'  CAGGAGCGAAACACCAGCT    74264           TA    A
                                CAGGAGCGAGAC  ACCA CT
                                ||||||||||||  |||| ||
                                GTCCTCGCTTTG  TGGT GA
                                      __    C
GAM3306  DKFZP434P1750 3'  CAGGAGCGACAGAGACCCCAGC 74265        ____      AA   A
            T                    CAGGAGC    GAGACT  CCA CT
                                 |||||||    ||||||  ||| ||
                                 GTCCTCG    CTCTGG  GGT GA
                                      CTGT      __   C
GAM3306  DKFZP667C165 3'  GGTACAAAAACCAACTA     74266     A      CTA
                                GG GCGAGA   ACCAACTA
                                || ||||||   ||||||||
                                CC TGTTTT   TGGTTGAT
                                 A     ____
GAM3306  FLJ12875  3'  CAGGAGGCCTGCCTGACCAACT 74267        _ GAGA  A
                                CAGGAG C    CT ACCAACT
                                |||||| |    || |||||||
                                GTCCTC G    GA TGGTTGA
                                    C GACG  C
GAM3306  FLJ12910  3'  AAGAACAAGGTTAACTAACTA  74268          AC    C
                                AGGAGCGAG  TAAC AACTA
                                |||||||||  |||| |||||
                                TTCTTGTTC  ATTG TTGAT
                                     CA    A
GAM3306  FLJ21687  3'  CAGAAGCGCAGGCTAGCC     74269         _  A   A
                                CAGGAGCG AG CTA CC
                                |||||||| || ||| ||
                                GTCTTCGC TC GAT GG
                                     G  C   C
GAM3306  KIAA0352  3'  AAGAGTGGAGCTAACCAGCT   74270       C_   A      A
                                AGGAG  GAG CTAACCA CT
                                |||||  ||| ||||||| ||
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                                TTCTC  CTC GATTGGT GA
                                  AC  _     C
GAM3306 KIAA0475 3' GGAATTAAGACTGACCAACTA 74271     C_    A
                                GGAG  GAGACT ACCAACTA
                                |||| ||||||| ||||||||
                                CCTT  TTCTGA TGGTTGAT
                                  AA    C
GAM3306 KIAA1393 3' CAGGAGCATATGAAATTAAC  74272       ____   C
                                CAGGAGC   GAGA TAAC
                                |||||||   |||| ||||
                                GTCCTCG   CTTT ATTG
                                    TATA   A
GAM3306 KLF12    3' CAGGACGAGACTTCAACT    74273     G     AAC
                                CAGGA CGAGACT   CAACT
                                ||||| |||||||   |||||
                                GTCCT GCTCTGA   GTTGA
                                  _     A__
GAM3306 L3MBTL   3' CAGGCCTAAGACTAACCAGCT 74274     AGC       A
                                CAGG   GAGACTAACCA CT
                                ||||   |||||||||||| ||
                                GTCC   TTCTGATTGGT GA
                                  GGA         C
GAM3306 PTD012   3' AGGAATTATGGCTAGCCAACTA 74275     CGAGA_   A
                                AGGAG     CTA CCAACTA
                                |||||     ||| |||||||
                                TCCTT     GAT GGTTGAT
                                  AATACC   C
GAM3306 RNF40    3' CAGGGTCCCCAAACCAACTA   74276     AGCGAGA   _
                                CAGG      CTAA CCAACTA
                                ||||      |||| |||||||
                                GTCC      GGTT GGTTGAT
                                  CAGG___    T
GAM3306 SCAMP5   3' CAGGAGCAGATAAAACT     74277      G   C   CC
                                CAGGAGC AGA TAA  AACT
                                ||||||| ||| |||  ||||
                                GTCCTCG TCT ATT  TTGA
                                   _  _  __
GAM3306 SERP1    3' CAAGTACAGAGACTGATTAACT 74278     A  _     AACC
                                CAGG GC GAGACT    AACT
                                |||| || ||||||    ||||
                                GTTC TG CTCTGA    TTGA
                                  A  T     CTAA
GAM3306 ZIC4     3' AGGAGCGAGAAAACCCTAACTA 74279        CT   __
                                AGGAGCGAGA  AACC  AACTA
                                ||||||||||  ||||  |||||
                                TCCTCGCTCT  TTGG  TTGAT
                                     T_   GA
GAM3306 LOC146229 3' AGAGCGAGACTCCATCT    74280        AA   A
                                GGAGCGAGACT  CCA CT
                                ||||||||||  ||| ||
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                                TCTCGCTCTGA  GGT GA
                                     __  A
GAM3306  LOC147160 5'  CAGGAGCAGAGCGTAAACCAGC 74281        _  ACT_    A
                T                    CAGGAGC GAG    AACCA CT
                                     ||||||| |||    ||||| ||
                                     GTCCTCG CTC    TTGGT GA
                                        T  GCAT    C
GAM3306  LOC149692 3'  AGAGCGAGACTCCATCT     74280          AA  A
                                     GGAGCGAGACT  CCA CT
                                     |||||||||||  ||| ||
                                     TCTCGCTCTGA  GGT GA
                                     __  A
GAM3306  LOC220003 3'  CAGGAGCGGGCTATATACTA  74282        AGA  ACCA
                                     CAGGAGCG   CTA   ACTA
                                     ||||||||   |||   ||||
                                     GTCCTCGC   GAT   TGAT
                                        CC_   ATA_
GAM3306  LOC254057 3'  CAGGGGCGAGACTATTTCAGAC 74283     A       AC_ _
                T                    CAGG GCGAGACTA   CA ACT
                                     |||| |||||||||   || |||
                                     GTCC CGCTCTGAT   GT TGA
                                       C       AAA  C
GAM3306  LOC255919 3'  AGAGCGAGACTCCGTCTA    74284          AA  AA
                                     GGAGCGAGACT  CC  CTA
                                     ||||||||||  ||  |||
                                     TCTCGCTCTGA  GG  GAT
                                     __  CA
GAM3306  LOC89894  5'  GGAGCGGGTCCCAACCAACT  74285       AGA_
                                     GGAGCG   CTAACCAACT
                                     ||||||   ||||||||||
                                     CCTCGC   GGTTGGTTGA
                                        CCAG
GAM3307  ANKRA2    5'  GTCCCTCTCTCCTTTTTT    74288     G  _
                                     GTC TCT TCTCCTTTTTT
                                     ||| ||| ||||||||||
                                     CAG GGA AGAGGAAAAAA
                                       _  G
GAM3307  DTR       3'  TCTCCTTCTTCTTCTTCTTTTT 74289    C  AG  G     C
                T                    TC CC  TC TCTTCT CTTTTTT
                                     || ||  || |||||| |||||||
                                     AG GG  AG AGAAGA GAAAAAA
                                      A  A_  A     A
GAM3307  F2RL3     3'  GTGTCCTCTCCTCTTCT     74290    C
                                     GT GTCTTCTCCTTTTTT
                                     || ||||||||||||||
                                     CA CAGGAGAGGAGAAGA
                                      _
GAM3307  HOXC6     3'  TCCCTCTTTTTTTTCCTTTTTT 74291      CAG  GTCTTC_
                                     TCCC   TC      TCCTTTTTT
                                     ||||   ||      |||||||||
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                                AGGG  AG     AGGAAAAAA
                                  ___ AAAAAAA
GAM3307 IGF1    3' GTGTCCTCTCTTTTTTT    74292   C     C
                                GT GTCTTCTC TTTTTT
                                || |||||||| ||||||
                                CA CAGGAGAG AAAAAA
                                 _      A
GAM3307 NFIB    3' CCAGTCTTCCTCTTTTCCTTTT 74293      G   ___
           TT                    CCAGTC TCTTC  TCCTTTTTT
                                |||||| |||||  |||||||||
                                GGTCAG AGGAG  AGGAAAAAA
                                   A    AAA
GAM3307 OGT     3' TCCCTCGGCCGCCCTTTTTT  74294    CA_   CTTCT
                                TCCC  GTCGT   CCTTTTTT
                                ||||  |||||   ||||||||
                                AGGG  CGGCG   GGAAAAAA
                                  AGC   _____
GAM3307 PCYT1A  3' TCCCCAGTTGTCTTTCCTTT  74295      C   C
                                TCCCCAGT GTCTT TCCTTT
                                |||||||| ||||| ||||||
                                AGGGGTCA CAGAA AGGAAA
                                    A   _
GAM3307 PLXNA2  3' TCCTCTTTCTCTCTTTTTT   74296   G  _  _
                                TC TCTT CTC CTTTTTT
                                || |||| ||| |||||||
                                AG AGAA GAG GAAAAAA
                                 G   A  A
GAM3307 RBBP2   3' GTCATCTTCTTCTCTTTT    74297        C
                                GTCGTCTTCT CTTTTTT
                                |||||||||| |||||||
                                CAGTAGAAGA GAGAAAA
                                     A
GAM3307 ZNF83   5' TCTCCTGTATTACTCTCCTTTT 74298   C  A  CGTC
           TT                    TC CC GT   TTCTCCTTTTTT
                                || || ||   ||||||||||||
                                AG GG CA   GAGAGGAAAAAA
                                 A  A  TAAT
GAM3307 ABCC13  3' TCCCCGCCCTCTCTTTTTTT  74299     AGTC      C
                                TCCCC   GTCTTCTC TTTTTT
                                |||||   |||||||| ||||||
                                AGGGG   CGGGAGAG AAAAAA
                                  ____      A
GAM3307 ARHGEF16 5' TCCCCAGCGTCTTCTTGTTTTT 74300       T      CC
                                TCCCCAG CGTCTTCT  TTTTT
                                ||||||| ||||||||  |||||
                                AGGGGTC GCAGAAGA  AAAAA
                                   _      AC
GAM3307 ARSDR1  3' CCAGTATTCTCCTTCTCT    74301      CGTC
                                CCAGT   TTCTCCTTTTTT
                                |||||   ||||||||||||
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                                GGTCA    AAGAGGAAGAGA
                                  T___
GAM3307  CAMKK2    5'  CCCCGACTCCCTTTTT      74302      A TCGTCTT
                                CCCC G      CTCCTTTTTT
                                |||| |      ||||||||||
                                GGGG T      GAGGGAAAAA
                                  C ________
GAM3307  CORO1A    3'  TCCCCCCCCCCTTTTTT     74303       AGTCGTC
                                TCCCC      TTCTCCTTTTTT
                                ||||||      ||||||||||||
                                AGGGG      GGGGGGAAAAAA
                                  ________
GAM3307  DGKD      3'  GTTGTTTTTCTCCTTTTT    74304     C  C_
                                GT GT  TTCTCCTTTTT
                                || ||  ||||||||||
                                CA CA  AAGAGGAAAAA
                                 A  AA
GAM3307  DKFZp434A171 3'  TCCTTTCTAATTCTTCTCTTTT 74305     CCAGTCG_      C
           TTT                    TCC       TCTTCTC TTTTTT
                                |||       ||||||| ||||||
                                AGG       AGAAGAG AAAAAA
                                  AAAGATTA      A
GAM3307  DKFZP434P211 3'  TCCCTGCTCCCCTTTTTT    74306      CA  CGTCT
                                TCCC  GT    TCTCCTTTTTT
                                ||||  ||    ||||||||||
                                AGGG  CG    AGGGGAAAAAA
                                  A_ ______
GAM3307  FLJ20211  3'  TCCCCAAGTCGTTTTTCTTTTT 74307       _    C  CTC
           T                    TCCCCA GTCGT TT   CTTTTTT
                                ||||||| ||||| ||   |||||||
                                AGGGGT CAGCA AA   GAAAAAA
                                   T    A  A__
GAM3307  FLJ20277  3'  CCCAGAGGGCTTCTCCTTTTTT 74308       TCGT
                                CCCAG    CTTCTCCTTTTTT
                                |||||    ||||||||||||||
                                GGGTC    GAAGAGGAAAAAA
                                   TCCC
GAM3307  FLJ21551  3'  CCCCCAACCTCTTTTTTTTTTT 74309       GT G    CTCC
           T                    TCCCCA  C TCTT    TTTTTT
                                ||||||  | ||||    ||||||
                                GGGGGT  G AGAA    AAAAAA
                                   TG _    AAAA
GAM3307  FLJ25012  5'  TCCACAGAGTTCCTTTTTC    74310     C   TC  CTTC
                                TCC CAG  GT    TCCTTTTTT
                                ||| |||  ||    |||||||||
                                AGG GTC  CA    AGGAAAAAG
                                  T   T_ _____
GAM3307  GT650     3'  TCGTTTTTTCTCCTTTTT     74311      C__
                                TCGT   TTCTCCTTTTT
                                ||||   ||||||||||
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                              AGCA   AAGAGGAAAAA
                                AAA
GAM3307  KIAA0090  3'  CCCCTACCCTCTTTCTCCTTTT 74312      AG  G   _
              TT                  CCCC  TC TCTT CTCCTTTTTT
                                  ||||  || |||| ||||||||||
                                  GGGG  GG AGAA GAGGAAAAAA
                                    AT  G    A
GAM3307  KIAA0408  3'  TCCTGGTGTTTTCTCCCCT    74313     CCA  C  C
                                  TCC   GT GT TTCTCCTTT
                                  |||   || || |||||||||
                                  AGG   CA CA AAGAGGGGA
                                    AC_  _  A
GAM3307  KIAA1580  5'  CCAATCATCCTTTTT       74314        TCTTC
                                  CCAGTCG    TCCTTTTT
                                  |||||||    ||||||||
                                  GGTTAGT    AGGAAAAA
                                               _____
GAM3307  KIAA1726  3'  CCAGTCTGAATCCTTTTTT    74315       GTCTTC
                                  CCAGTC     TCCTTTTTT
                                  ||||||     |||||||||
                                  GGTCAG     AGGAAAAAA
                                     ACTT__
GAM3307  KIAA1870  3'  CCAGGGGATCCTTCTTTTTTTT 74317      TCG__     CC
              T                    CCAG    TCTTCT  TTTTTT
                                   ||||    ||||||  ||||||
                                   GGTC    GGAAGA  AAAAAA
                                     CCCTA     AA
GAM3307  KIAA1870  3'  GTCTTTCCTTTTCTCCTTTTTT 74316     G_  ___
                                  GTC  TCT   TCTCCTTTTTT
                                  |||  |||   ||||||||||
                                  CAG  AGG   AGAGGAAAAAA
                                    AA   AAA
GAM3307  RAB10    3'  CCTTCCTGCTTTTCCTTTTTT  74318    AG  GT   C
                                  CC  TC  CTT TCCTTTTTT
                                  ||  ||  ||| |||||||||
                                  GG  GG  GAA AGGAAAAAA
                                   AA  AC   A
GAM3307  SCN12A   3'  TCCTGGTGTCTTCTTCCTT    74319     CCA  C      _
                                  TCC   GT GTCTTCT CCTT
                                  |||   || ||||||| ||||
                                  AGG   CA CAGAAGA GGAA
                                    AC_  _      A
GAM3307  LOC147990 3'  CCCCCTCAACTTTTTTCTTTTT 74320      AG   T   CTC_
              T                    CCCC  TCG CTT    CTTTTTT
                                   ||||  ||| |||    |||||||
                                   GGGG  AGT GAA    GAAAAAA
                                     G_   T   AAAA
GAM3307  LOC148562 3'  CCAGCTTTTCCTTTTTT     74321      TCGT   C
                                  CCAG    CTT TCCTTTTTT
                                  ||||    ||| |||||||||
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                                GGTC    GAA AGGAAAAAA
                                  ____  A
GAM3307  LOC150142 5'  TCCCCAGCCGTTTTTAGCC    74322          C  CT_
                                TCCCCAGTCGT TT   CC
                                |||||||||| ||   ||
                                AGGGGTCGGCA AA   GG
                                      A  ATC
GAM3307  LOC150213 3'  TCCCTGTTCCCCCCCTTTTTT  74323      CAGTCG
                                TCCC     TCTTCTCCTTTTTT
                                ||||     ||||||||||||||
                                AGGG     AGGGGGGGAAAAAA
                                  ACA___
GAM3307  LOC150236 3'  TCCCCCCCCCCTTTTTT     74303       AGTCGTC
                                TCCCC      TTCTCCTTTTTT
                                |||||      ||||||||||||
                                AGGGG      GGGGGGAAAAAA
                                  ________
GAM3307  LOC151512 3'  GTCTTCCTTCTTTTCCTTTTTT 74324     G_    ___
                                GTC  TCTTC   TCCTTTTTT
                                |||  |||||   |||||||||
                                CAG  GGAAG   AGGAAAAAA
                                  AA    AAA
GAM3307  LOC153561 3'  CCCAGCTCCTTTTTT       74325       TCGTCTT
                                CCCAG      CTCCTTTTTT
                                |||||      ||||||||||
                                GGGTC      GAGGAAAAAA
                                  ________
GAM3307  LOC154789 5'  TCCTAAGTCTTTCCTTTTTT   74326     CC    GTCTTC
                                TCC  AGTC     TCCTTTTTT
                                |||  ||||     |||||||||
                                AGG  TCAG     AGGAAAAAA
                                  AT    AA____
GAM3307  LOC159036 3'  CCTACTTCCTTCTTCTTTTTT  74327     AG CG     C
                                CC  T  TCTTCT CTTTTTT
                                ||  |  |||||| |||||||
                                GG  G  GGAAGA GAAAAAA
                                 AT AA     A
GAM3307  LOC204965 5'  GTCTCTCCACCTTTTTT     74328     G     T
                                GTC TCTTC CCTTTTTT
                                ||| ||||| ||||||||
                                CAG AGAGG GGAAAAAA
                                  _     T
GAM3307  LOC254059 5'  CCAGTCTCTTCTCCTCTTT    74329       G
                                CCAGTC TCTTCTCCTTTTT
                                |||||| ||||||||||||
                                GGTCAG AGAAGAGGAGAAA
                                   _
GAM3308  ACADVL    3'  GCTTCGGCTTTGGCTTGA    74332       TAC
                                GCTTC   TTTTGGCTTGA
                                |||||   ||||||||||
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                                CGAAG   GAAACCGAACT
                                  CC_
GAM3308  PTGIS    3'  TAGCTTCTATTTTTTTTAAA   74333        C    GGC
                                TAGCTTCTA TTTT   TTGAA
                                ||||||||| ||||   |||||
                                ATCGAAGAT AAAA   AATTT
                                     _    AA_
GAM3308  RAG1     3'  CAGTTTCTATTCCTGACTTGA  74334     C    C
                                TAG TTCTA TTTTGGCTTGA
                                ||| ||||| ||||||||||
                                GTC AAGAT AGGACTGAACT
                                  A    A
GAM3308  RNTRE    3'  TACTTTTGTACCTTGAAA    74335        G__
                                TACTTTTG   CTTGAAA
                                ||||||||   |||||||
                                ATGAAAAC   GAACTTT
                                     ATG
GAM3308  SNX5     3'  GCTTCTACTTGTTTCCAGAA   74336         TTGG  T
                                GCTTCTACTT    CT GAA
                                ||||||||||    || |||
                                CGAAGATGAA    GG CTT
                                      CAAA  T
GAM3308  Di-Ras2  3'  TAGCTGTAATTTGGCTTGAAAG 74337      TCTACT
                                TAGCT     TTTGGCTTGAAAG
                                |||||     |||||||||||||
                                ATCGA     AAACCGAACTTTC
                                  CATT__
GAM3308  HAGE     3'  ACTTCTATTTTTATTAAAGAAA 74338       C    GCTT_
              G                  GCTTCTA TTTTG    GAAAG
                                |||||||  |||||    |||||
                                TGAAGAT AAAAT    CTTTC
                                   A    AATTT
GAM3308  KIAA0063 3'  GCTTCTCTTTTGTCCCAGA   74339      A    G_  T
                                GCTTCT CTTTTG  CT GA
                                ||||||  ||||||  || ||
                                CGAAGA GAAAAC  GG CT
                                   _     AG  T
GAM3308  KIAA1853 3'  AGCTTTTGCTTTTGGCTTG   74340      CTA
                                AGCTT   CTTTTGGCTTG
                                |||||   ||||||||||||
                                TCGAA   GAAAACCGAAC
                                  AAC
GAM3308  MGC11034 3'  GCTTCTACTTTTGCTACTGAA  74341          G  __
                                GCTTCTACTTTTG CT  TGAA
                                |||||||||||||  ||  ||||
                                CGAAGATGAAAAC GA  ACTT
                                       _ TG
GAM3308  MKRN1    3'  GCTTTTACTTTTGAACCTG   74342     C       _
                                GCTT TACTTTTGG CTTG
                                ||||  |||||||| ||||
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                                CGAA ATGAAAACT GGAC
                                  A       T
GAM3308  MKRN4    3'  GCTTTTACTTTTGAACCTG   74342     C       _
                                GCTT TACTTTTGG CTTG
                                |||| ||||||||| ||||
                                CGAA ATGAAAACT GGAC
                                  A       T
GAM3308  SLC26A7  3'  ACTTCTGCTTTTCCTTGGAAG  74343       A    GG   A
                                GCTTCT CTTTT  CTTG AAG
                                |||||| |||||  |||| |||
                                TGAAGA GAAAA  GAAC TTC
                                   C    G_   C
GAM3308  SURB7    3'  CTTCTCCTTTGGCTTGA     74344       A
                                CTTCT CTTTTGGCTTGA
                                ||||| ||||||||||||
                                GAAGA GGAAACCGAACT

                                  _
GAM3308  LOC143884 3'  TAGTTTTTACTTTTGGTGAA   74345     C  C       CT
                                TAG TT TACTTTTGG  TGAA
                                ||| || |||||||||  ||||
                                ATC AA ATGAAAACC  ACTT
                                  A  A       __
GAM3308  LOC148562 3'  TAACTTTTGGGCTTGAAA    74346    T      _
                                C ACTTTTGG CTTGAAA
                                | ||||||||| |||||||
                                A TGAAAACC GAACTTT
                                 T       C
GAM3308  LOC149506 5'  CTTCTACTTTCTCACAGAGA   74347          G_  TT_
                                CTTCTACTTTT  GC   GA
                                ||||||||||  ||   ||
                                GAAGATGAAAG  TG   CT
                                       AG  TCT
GAM3308  LOC201696 3'  TAGTTCCTACTTTGGATG    74348     C       T  CT
                                TAG TTCTACTTT GG  TG
                                ||| |||||||| ||  ||
                                ATC AGGATGAAA CC  AC
                                  A       _  T_
GAM3309  BACH1    3'  GTAGAGACTGAAGCGGGG    74351     T   GAA
                                GTA AGGC   AAGCGGGG
                                ||| ||||   ||||||||
                                CAT TCTG   TTCGCCCC
                                  C   AC_
GAM3309  SRC      3'  AACATGTTTGGGGGACGGAGCG 74352        ATA  C  AA_
            GGG                   AACATGT   GG GA   AGCGGGG
                                |||||||   || ||   |||||||
                                TTGTACA   CC CT   TCGCCCC
                                    AAC  C  GCC
GAM3309  CECR7    5'  GCAGTGGGAGTGGAAAGCGGGG 74353     TA  C  ____
                                GTA  GG GA    AAAGCGGGG
                                |||  || ||    |||||||||
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                                CGT  CC CT    TTTCGCCCC
                                  CA  _  CACC
GAM3309  DKFZP434N1511 5'  AACACGTAAGGGAGTGGG    74354         T   C  AAA C
                                AACATGTA AGG GA   G GGG
                                |||||||| ||| ||   | |||
                                TTGTGCAT TCC CT   C CCC
                                     _   _  ___ A
GAM3309  DNAJA4    3'  CATGCACAGGGAGTGGG     74355          C  AAA C
                                CATGTATAGG GA   G GGG
                                |||||||||| ||   | |||
                                GTACGTGTCC CT   C CCC
                                     _  ___ A
GAM3309  FLJ10242  5'  AACAGTGTAACTCAAAGCGGGG 74356     _    TAG  GA
                                AACA TGTA   GC  AAAGCGGGG
                                |||| ||||   ||  |||||||||
                                TTGT ACAT   TG  TTTCGCCCC
                                  C   ___  AG
GAM3309  KIAA0773  3'  ATGTATAGGTGAGGTCGTGG   74357         C  AAAG  _
                                ATGTATAGG GA    CG GG
                                |||||||| ||    || ||
                                TACATATCC CT    GC CC
                                     A  CCA_  A
GAM3309  KIAA1546  3'  ATGTGTAGAGTTGTAAGCGGGG 74358      A    CGAA_
                                ATGT TAGG     AAGCGGGG
                                |||| ||||     ||||||||
                                TACA ATCT     TTCGCCCC
                                  C    CAACA
GAM3309  TU3A      3'  TGTACGGAGAAGCGGGG     74359       A  C  AA
                                TGTAT GG GA  AGCGGGG
                                ||||| || ||  |||||||
                                ACATG CC CT  TCGCCCC
                                   _  T  __
GAM3310  ACK1      5'  TCCCCGCACTCTTCTGCGCCCG 74362        _   C    TA  A
            ACT                    TCCCCG ACTC TCTG  CT GACT
                                |||||| |||| ||||  || ||||
                                AGGGGC TGAG AGAC  GG CTGA
                                   G    A    GC  G
GAM3310  HKE4      3'  TCCCCGACTCCTCCTGTTACC  74363            _  _
                                TCCCCGACTCCTC TGT ACT
                                |||||||||||| ||| |||
                                AGGGGCTGAGGAG ACA TGG
                                     G   A
GAM3310  RBM8A     3'  CCCCCGCTCCTTTGAC      74364        A    C  T
                                TCCCCG CTCCT TG AC
                                |||||| ||||| || ||
                                GGGGGC GAGGA AC TG
                                   _    A  _
GAM3310  SUFU      3'  TCCCTGGCCCCAGCTAAACTAG 74365      CGA   T_  T    A
            GCT                    TCCC   CTCC  CTG ACTAG CT
                                ||||   ||||  ||| ||||| ||
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                                AGGG  GGGG  GAT TGATC GA
                                  ACC   TC  T    C
GAM3310 C1orf34  3' CCCCGACTCCTCAGGAGGACT 74366          TGTACTA
                                CCCCGACTCCTC      GACT
                                ||||||||||||      ||||
                                GGGGCTGAGGAG      CTGA
                                      TCCTC__
GAM3310 CCR5     3' GACTCCTCTCTGACC       74367         GTA  A
                                GACTCCTCT   CT GACT
                                |||||||||   || ||||
                                CTGAGGAGA   GA CTGG
                                     ___ _
GAM3310 CRTAC1   3' CCCACTCCCCTGCTGGACT   74368     G        ACTA
                                CCC ACTCCTCTGT    GACT
                                ||| ||||||||||    ||||
                                GGG TGAGGGGACG    CTGA
                                  _        AC__
GAM3310 CSEN     3' TCCCAGACTCCTCTGAGCT   74369     C        TA
                                TCCC GACTCCTCTG  CT
                                |||| ||||||||||  ||
                                AGGG CTGAGGAGAC  GA
                                  T         TC
GAM3310 DKFZP566K1924 3' CCCCCATTTCTACTAGC     74370       AC  CTCTG     A
                                TCCCCG  TC    TACTAG C
                                ||||||  ||    |||||| |
                                GGGGGT  AG    ATGATC G
                                   AA  _____     C
GAM3310 FLJ12899  3' CCCATTTTTCAGTGACTAGACT 74371      ACTCC  T  _
                                CCCG    TC GT ACTAGACT
                                ||||    || || ||||||||
                                GGGT    AG CA TGATCTGA
                                  AAAA_  T  C
GAM3310 FLJ13158  3' CCCTGTTCTACCTAACTAGACT 74372     GAC  CT  GT
                                CCC   TC  CT  ACTAGACT
                                |||   ||  ||  ||||||||
                                GGG   AG  GG  TGATCTGA
                                  ACA  AT  AT
GAM3310 HT002    3' TCTCCGACTCCTTCACAC    74373    C       CT
                                TC CCGACTCCT  GTAC
                                || |||||||||  ||||
                                AG GGCTGAGGA  TGTG
                                 A        AG
GAM3310 KIAA0323  3' CAACTCCTTGTAAGA       74374         C    CT
                                CGACTCCT TGTA  AGA
                                |||||||| ||||  |||
                                GTTGAGGA ACAT  TCT
                                     _   ___
GAM3310 KIAA0914  3' TCCCCGATCCTCTGTATGCAGG 74375        C       C_   A
             CT                   TCCCCGA TCCTCTGTA  TAG CT
                                |||||||| |||||||||  ||| ||
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                                AGGGGCT AGGAGACAT  GTC GA
                                    _       AC   C
GAM3310  KIAA1396  3'  TCCCCGACTCCTTGCACT    74376          C
                                TCCCCGACTCCT TGTACT
                                |||||||||||| ||||||
                                AGGGGCTGAGGA ACGTGA
                                       _
GAM3310  LW-1      5'  CCTCCGACTCCCCACTGGACT  74377    _       TGT   A
                                CC CCGACTCCTC   ACT GACT
                                || ||||||||||   ||| ||||
                                GG GGCTGAGGGG   TGA CTGA
                                 A         ___   C
GAM3310  PKNOX2    3'  CCCCTGGCTTCCCACTGGACT  74378     GA_ _  _   T
                                CCCC   CT CCT CTG ACT
                                ||||   || ||| ||| |||
                                GGGG   GA GGG GAC TGA
                                   ACC  A   T   C
GAM3310  LOC127281 5'  TCCCCGACTCCCTGTTCC    74379          T    A
                                TCCCCGACTCC CTGT CT
                                |||||||||||| |||| ||
                                AGGGGCTGAGG GACA GG
                                       _    A
GAM3310  LOC138150 5'  TCTCCGGCCCCCCCGCTAGACT  74380    C   A     TGTA
                                TC CCG CTCCTC    CTAGACT
                                || ||| ||||||    |||||||
                                AG GGC GGGGGG    GATCTGA
                                 A   C     C___
GAM3310  LOC149606 3'  CCCCGACTAATCTGTGCTGGAC 74381         CC     A  A
              T                  CCCCGACT  TCTGT CT GACT
                                 ||||||||  ||||| || ||||
                                 GGGGCTGA  AGACA GA CTGA
                                      TT    C  C
GAM3310  LOC155064 5'  TCCCCGACTCTCTGGGCT    74382          C    TA
                                TCCCCGACTC TCTG  CT
                                |||||||||| ||||  ||
                                AGGGGCTGAG AGAC  GA
                                       _    CC
GAM3310  LOC157313 5'  CCCCGGCTCCTCTGTCCGGA   74383       A        A TA
                                CCCCG CTCCTCTGT C  GA
                                ||||| |||||||| |  ||
                                GGGGC GAGGAGACA G  CT
                                   C        _ GC
GAM3310  LOC254057 3'  GACTCCTCCACTGGACT     74384          GT   A
                                GACTCCTCT  ACT GACT
                                |||||||||  ||| ||||
                                CTGAGGAGG  TGA CTGA
                                       __   C
GAM3310  LOC90120  5'  TCTCCGGCCCCCCCGCTAGACT  74380    C   A     TGTA
                                TC CCG CTCCTC    CTAGACT
                                || ||| ||||||    |||||||
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                                AG GGC GGGGGG   GATCTGA
                                 A  C    C___
GAM3311  ABCA2   3'  GAGAGCGATGGCAGCTGGG   74387       GCGA  G  _
                                GAGAGCGA   GC AGC GGG
                                ||||||||   || ||| |||
                                CTCTCGCT   CG TCG CCC
                                     AC__  _  A
GAM3311  ABCA2   3'  GAGAGCGATGGCAGCTGGG   74387       GCGA  G  _
                                GAGAGCGA   GC AGC GGG
                                ||||||||   || ||| |||
                                CTCTCGCT   CG TCG CCC
                                     AC__  _  A
GAM3311  ALOX5   5'  GAGCAGCGAGCGCCGG     74388     G      AG
                                GAGC AGCGAGCG  CGG
                                |||| ||||||||  |||
                                CTCG TCGCTCGC  GCC
                                  _      G_
GAM3311  ANKH    5'  CGACGGGGGCGACGGGCGAGCG 74389    GAGA_   G  A
           GG                     CGA    GCGA CG GCGAGCGGG
                                |||    |||| || |||||||||
                                GCT    CGCT GC CGCTCGCCC
                                 GCCCC   _  C
GAM3311  ANKH    5'  CGACGGGGGCGACGGGCGAGCG 74389    GAGA_   G  A
           GG                     CGA    GCGA CG GCGAGCGGG
                                |||    |||| || |||||||||
                                GCT    CGCT GC CGCTCGCCC
                                 GCCCC   _  C
GAM3311  AREG    5'  AAGAGCGAGTGGAGACCGGG  74390       CGAGC  G
                                GAGAGCGAG    GA CGGG
                                |||||||||    || ||||
                                TTCTCGCTC    CT GCCC
                                     ACCT_  G
GAM3311  ASIC4   5'  GAGCGAGCGAGTGAGCGAG   74391        C
                                GAGCGAGCGAG GAGCGGG
                                |||||||||| |||||||
                                CTCGCTCGCTC CTCGCTC
                                      A
GAM3311  BDNF    5'  GAGCGGGCGGGTGCGCCCGGG  74392     A  A__  AG
                                GAGCG GCG  GCG  CGGG
                                ||||| |||  |||  ||||
                                CTCGC CGC  CGC  GCCC
                                   C  CCA  GG
GAM3311  CA14    5'  GAGAGAGCGAGCGAGCTCCTGG 74393           GAGC
                                GAGAGAGCGAGCGAGC   GG
                                ||||||||||||||||   ||
                                CTCTCTCGCTCGCTCG   CC
                                          AGGA
GAM3311  CTBP1   5'  CGAGAGGCGCGAGCGGCCGCGG 74394      A_     A  GA
           G                     CGAGAG  GCGAGCG GC  GCGGG
                                ||||||  ||||||| ||  |||||
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                                GCTCTC  CGCTCGC CG  CGCCC
                                   CG      _ G_
GAM3311  DVL3     3'  GAGGGAGTGAGCGTGCCACCAA 74395     A   C     A  GA  __
                GG                  GAG GAG GAGCG GC  GC  GGG
                                    ||| ||| ||||| ||  ||  |||
                                    CTC CTC CTCGC CG  TG  TCC
                                      C   A    A  G_  GT
GAM3311  ELOVL4   5'  CGACGGGGCGAGCGGCGGCCGG 74396     GAGA      A   AG
                G                   CGA   GCGAGCG GCG  CGGG
                                    |||   ||||||| |||  ||||
                                    GCT   CGCTCGC CGC  GCCC
                                      GCCC      _  CG
GAM3311  GPX1     5'  GAGAGTGCGCCCGAGCGGG   74397      CGA   AG
                                    GAGAG   GCG  CGAGCGGG
                                    |||||   |||  ||||||||
                                    CTCTC   CGC  GCTCGCCC
                                       A__   GG
GAM3311  IGFBP2   5'  GAGCGAGCGAGCGGGCGGG   74399           A
                                    GAGCGAGCGAGCG GCGGG
                                    |||||||||||| |||||
                                    CTCGCTCGCTCGC CGCCC
                                            C
GAM3311  IGFBP2   5'  GAGCGGGCGGGCGGGCAG    74400      A   A   A
                                    GAGCG GCG GCG GCGG
                                    ||||| ||| ||| ||||
                                    CTCGC CGC CGC CGTC
                                       C   C   C
GAM3311  IGFBP2   5'  CGAGCGAGCGAGCGGGCGGGCG 74398     A       A   A
                GG                  CGAG GAGCGAGCG GCG GCGGG
                                    |||| ||||||||| ||| |||||
                                    GCTC CTCGCTCGC CGC CGCCC
                                      G       C   C
GAM3311  INHBB    3'  AGAGGGCGAGCGAGTTCGG   74401      A       CGAG
                                    AGAG GCGAGCGAG    CGG
                                    |||| |||||||||    |||
                                    TCTC CGCTCGCTC    GCC
                                      C       AA__
GAM3311  MADH1    5'  CGAGTGGCCGGGCGAGCGG   74402      AGA  GAG  A
                                    CGAG   GC   CG GCGAGCGG
                                    ||||   ||   || ||||||||
                                    GCTC   CG   GC CGCTCGCC
                                      AC_  ___  C
GAM3311  NPAS2    5'  GAGACGAGGCGGCGAGCGGG  74404      G   _  A
                                    GAGA CGAG CG GCGAGCGGG
                                    |||| |||| || |||||||||
                                    CTCT GCTC GC CGCTCGCCC
                                      _   C  _
GAM3311  NPAS2    5'  GAGGCGGCGAGCGGGCGCGG  74403     A  A     A  _
                                    GAG GCG GCGAGCG GCG GG
                                    ||| ||| ||||||| ||| ||
```

```
                                CTC CGC CGCTCGC CGC CC
                                  _ _     C  G
GAM3311 PCBP1    5' CGCGGGAGCGAGCGGGAGCGGG 74405    AGA      __    A
           CGGG                   CG  GAGCGAGC  GAGCG GCGGG
                                ||  |||||||| ||||| |||||
                                GC  CTCGCTCG  CTCGC CGCCC
                                 GCC      CC    C
GAM3311 POU3F4   3' CGAGAGAGCGAGCGAACG    74406
                                CGAGAGAGCGAGCGAGCG
                                ||||||||||||||||||
                                GCTCTCTCGCTCGCTTGC

GAM3311 PTEN     5' CGGGAGGCGAGCGAGG      74407    A  AGCGA       C
                                CG GAG    GCGAGCGAG G
                                || |||    ||||||||| |
                                GC CTC    CGCTCGCTC C
                                 C  _____       T
GAM3311 YY1      5' GAGGAAGGCGGCGAGCGGGCGG 74408    AG  _  A     A
           G                     GAG  AG CG GCGAGCG GCGGG
                                |||  || || ||||||| |||||
                                CTC  TC GC CGCTCGC CGCCC
                                 CT  C  _     C
GAM3311 BDG-29   5' CGAGGAAGCGAAGCTCGAGCGG 74409     AG   _  GAG
           G                     CGAG  AGCGA GC   CGAGCGGG
                                ||||  ||||| ||   ||||||||
                                GCTC  TCGCT CG   GCTCGCCC
                                  CT    T  A__
GAM3311 C20orf39 5' GAGCGAGCGAGCGTGCGG    74410           A
                                GAGCGAGCGAGCG GCGG
                                |||||||||||| ||||
                                CTCGCTCGCTCGC CGCC
                                       A
GAM3311 C4S-2    3' GAGCGGGCGGGCGGGCGGG   70253      A  A  A
                                GAGCG GCG GCG GCGGG
                                ||||| ||| ||| |||||
                                CTCGC CGC CGC CGCCC
                                   C  C  C
GAM3311 C4S-2    3' GAGCGGGCGGGCGGGCGGG   70253      A  A  A
                                GAGCG GCG GCG GCGGG
                                ||||| ||| ||| |||||
                                CTCGC CGC CGC CGCCC
                                   C  C  C
GAM3311 C4S-2    3' CGAGCGGGCGGGCGGGCGAGCG 74411     AGA  A  A
           GG                    CGAG  GCG GCG GCGAGCGGG
                                ||||  ||| ||| |||||||||
                                GCTC  CGC CGC CGCTCGCCC
                                  GCC  C  C
GAM3311 C4S-2    3' AGGAGCGGGCGAGCGGGCGGG 74412    A    A     A
                                AG GAGCG GCGAGCG GCGGG
                                || ||||| ||||||| |||||
```

```
                                TC CTCGC CGCTCGC CGCCC
                                 _    C      C
GAM3311 CENTG2   5' GCGGCCGGCGAGCGAGCGGG  74413     A___
                                GCG   GCGAGCGAGCGGG
                                |||   ||||||||||||
                                CGC   CGCTCGCTCGCCC
                                  CGGC
GAM3311 CKAP4    5' GAGGCGAGCGAGCGCGG    74414     A        GA
                                GAG GCGAGCGAGC  GCGG
                                ||| ||||||||||  ||||
                                CTC CGCTCGCTCG  CGCC
                                  _        __
GAM3311 CRF      3' GAGGGCCGGGCAGCGAGCGGG 74415     A  _ A  G
                                GAG GC G GC AGCGAGCGGG
                                ||| || | || ||||||||||
                                CTC CG C CG TCGCTCGCCC
                                  C  G C  _
GAM3311 Di-Ras2  3' GAGAGAGCAAGTGTGCTTTGGG 74416          CGA  GAGC
                                GAGAGAGCGAG   GC    GGG
                                ||||||||||   ||    |||
                                CTCTCTCGTTC   CG    CCC
                                      ACA  AAA_
GAM3311 DOC-1R   5' CGGAAGGGCGAGCGGGCACG   74417    AG  A      A  GA
                                CG  AG GCGAGCG GC  GCG
                                ||  || |||||| ||  |||
                                GC  TC CGCTCGC CG  TGC
                                 CT  C      C  __
GAM3311 ECRG4    5' CGGGAGAGGGGTGCGAGCGGG  74418    A    CGAGCGA
                                CG GAGAG      GCGAGCGGG
                                || |||||      |||||||||
                                GC CTCTC      CGCTCGCCC
                                 C    CCCA___
GAM3311 FAF1     5' CGGGGAAACCGAGCGAGCGAGC 74420    A_   G
           GGG                    CG  GAGA CGAGCGAGCGAGCGGG
                                ||  |||| ||||||||||||||||
                                GC  CTTT GCTCGCTCGCTCGCCC
                                 CC   G
GAM3311 FAF1     5' CGGGGAAACCGAGCGAGCGAGC 74419  _   G           III
           GGGCC                   GAGA CGAGCGAGCGAGCGGG  CC
                                 |||| ||||||||||||||||  ||
                                 CTTT GCTCGCTCGCTCGCCC  GG
                                C   G            III
GAM3311 FLJ10346 5' CGAGGGAGTGAGTGAATGAGTG 74421     A  C  C  C  C
           GG                    CGAG GAG GAG GAG GAG GGG
                                |||| ||| ||| ||| ||| |||
                                GCTC CTC CTC CTT CTC CCC
                                  C  A  A  A  A
GAM3311 FXYD5    5' CCAGGGGAGCGCGAGCGGGCGG 74422   G A_   GA     A
           G                     C AG  GAGC  GCGAGCG GCGGG
                                | ||  ||||  ||||||| |||||
```

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                                G TC  CTCG  CGCTCGC CGCCC
                                 G  CC   __     C
GAM3311  HSPC048   5'  CGGGAGCGCGAGCGAGTCCCAG 74423    A   A       CGAG
                                CG GAG GCGAGCGAG   CGG
                                || ||| |||||||||   |||
                                GC CTC CGCTCGCTC   GTC
                                 C  G       AGG_
GAM3311  ILF3      5'  GAGCGGGCGGGCGGGCAG    74400      A   A   A
                                GAGCG GCG GCG GCGG
                                ||||| ||| ||| ||||
                                CTCGC CGC CGC CGTC
                                   C   C   C
GAM3311  KLF3      3'  GAGAGAGCCAAGTGAGTGGG   74424        GAG   C   C
                                GAGAGAGC   CGAG GAG GGG
                                ||||||||   |||| ||| |||
                                CTCTCTCG   GTTC CTC CCC
                                     ___   A   A
GAM3311  OSMR      5'  GAGCAGAGCGGGGACGGGCGGG 74425     _    A__   A
                                GAGC GAGCG   GCG GCGGG
                                |||| |||||   ||| |||||
                                CTCG CTCGC   TGC CGCCC
                                  T    CCC   C
GAM3311  PIGPC1    5'  GAGCGGAGCGGAGCGGAGCGGG 74426      _   _   _
                                GAGCG AGCG AGCG AGCGGG
                                ||||| |||| |||| ||||||
                                CTCGC TCGC TCGC TCGCCC
                                   C   C   C
GAM3311  PP2447    3'  AGGGGCCCGAGCGGGCGGG   74427    A_ GAG     A
                                AG  GC   CGAGCG GCGGG
                                ||  ||   |||||| |||||
                                TC  CG   GCTCGC CGCCC
                                 CC  G__     C
GAM3311  PPAP2B    5'  GAGCGAGCGAGTGGGCAGCGCG 74428          _____   A_
            GG                    GAGCGAGCGA   GCG  GCGGG
                                ||||||||||   |||  |||||
                                CTCGCTCGCT   CGT  CGCCC
                                      CACC   CG
GAM3311  PPAP2B    5'  GAGTGCGCGAGCGAGCGAGTGG 74429     AGA          C
            G                    GAG   GCGAGCGAGCGAG GGG
                                |||   |||||||||||||| |||
                                CTC   CGCTCGCTCGCTC CCC
                                  ACG           A
GAM3311  RIG-I     5'  AGGAGGGCGTGGCGAGCGGG   74430    A   CGA   A_
                                AG GAG   GCG  GCGAGCGGG
                                || |||   |||  |||||||||
                                TC CTC   CGC  CGCTCGCCC
                                 _  C__   AC
GAM3311  TGFB1I1   3'  GAGAGGGCGAGCCGAGCGGG   74431      A     GAG
                                GAGAG GCGAGC   CGAGCGGG
                                ||||| ||||||   ||||||||
```

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                                CTCTC CGCTCG   GCTCGCCC
                                  C     ___
GAM3311  TLK1     5'  CGAGAGAGCGAGGGCTGG    74432          CGA  GAGC
                                CGAGAGAGCGAG   GC    GG
                                ||||||||||||  ||    ||
                                GCTCTCTCGCTC   CG    CC
                                       C__  A___
GAM3311  ZNF342   5'  GAGCGAGCGGGCGGGCAG    74433         A   A
                                GAGCGAGCG GCG GCGG
                                ||||||||| ||| ||||
                                CTCGCTCGC CGC CGTC
                                      C   C
GAM3311  LOC112868 3'  CGAGAGAGAGAGCGAGCACGG  74434         C       GA
                                CGAGAGAG GAGCGAGC  GCGG
                                |||||||| ||||||||  ||||
                                GCTCTCTC CTCGCTCG  TGCC
                                     T      __
GAM3311  LOC201911 3'  AGGGCGGGTGGGCGGGCGAGCG 74435    A   A____   A
              GG                   AG GCG    GCG GCGAGCGGG
                                || |||    ||| |||||||||
                                TC CGC    CGC CGCTCGCCC
                                 C   CCACC   C
GAM3311  LOC221424 5'  CCAGAGAGCGAGCGGGCG    74436   G         A
                                C AGAGAGCGAGCG GCG
                                | ||||||||||| |||
                                G TCTCTCGCTCGC CGC
                                 G          C
GAM3311  LOC253489 5'  CGAGGGACCGAGCGAGACGG   74437     A  G      CGA
                                CGAG GA CGAGCGAG   GCGG
                                |||| || ||||||||   ||||
                                GCTC CT GCTCGCTC   TGCC
                                  C  G      ___
GAM3311  LOC256167 3'  GAAGAGCACCAGCGAGCGGG   74438    G    GA  G
                                GA AGAGC  GC AGCGAGCGGG
                                || |||||  || ||||||||||
                                CT TCTCG  TG TCGCTCGCCC
                                 _    __  G
GAM3311  LOC95633  5'  CGAGAGAGCCAGGCGGGCGGG  74439         G  CGA   A
                                CGAGAGAGC AG   GCG GCGGG
                                ||||||||| ||   ||| |||||
                                GCTCTCTCG TC   CGC CGCCC
                                      G  ___   C
GAM3312  GBAS     3'  TGCTATTCAAGGTGTTCATTT  74442     A     TTTTA
                                TGC TATTTA    TGTTCATTT
                                ||| ||||||    |||||||||
                                ACG ATAAGT    ACAAGTAAA
                                  _     TCC__
GAM3312  NT5C3    3'  TGCATATTATTTCACCATT    74443         T      GTT
                                TGCATATT ATTTTAT   CATT
                                |||||||| |||||||   ||||
```

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                                ACGTATAA TAAAGTG   GTAA
                                  _     ___
GAM3312  PACSIN1   3'  TGCATACTTTGTTTTGTTC   74444        AT   A
                                TGCATATTT  TTT TGTTC
                                |||||||||  ||| |||||
                                ACGTATGAA  AAA ACAAG
                                    AC  _
GAM3312  FLJ21603  3'  TGCATACTTTATTGGATGTCAT 74445        _  TT   T
              TT                  TGCATATTT ATT  ATGT CATTT
                                |||||||||  |||  |||| |||||
                                ACGTATGAA TAA  TACA GTAAA
                                    A  CC   _
GAM3312  FLJ21657  3'  TATTTATTTTATGTTTATTT   74446            C
                                TATTTATTTTATGTT ATTT
                                |||||||||||||| ||||
                                ATAAATAAAATACAA TAAA
                                          A
GAM3312  KIAA0884  3'  TGCATATTTGTCTGATGTT   74447        A   T
                                TGCATATTT TTT ATGTT
                                |||||||||  ||| |||||
                                ACGTATAAA AGA TACAA
                                    C   C
GAM3312  PEGASUS   3'  TGCATTTTATATTCAT     74448      ATTTAT
                                TGCAT     TTTATGTTCAT
                                |||||     ||||||||||
                                ACGTA     AAATATAAGTA
                                  _______
GAM3312  LOC158292 5'  TGCACATTTATTTTAATCATTT 74449             TGT
                                TGCATATTTATTTTA   TCATTT
                                ||||||||||||||   ||||||
                                ACGTGTAAATAAAAT   AGTAAA
                                          T__
GAM3312  LOC158819 3'  TGCATGTTTACTTTATGTT   74450      A
                                TGCAT TTTATTTTATGTT
                                ||||| ||||||||||||
                                ACGTA AAATGAAATACAA
                                   C
GAM3312  LOC220980 3'  TGCATACTTATTTTGTGTT   74451            A
                                TGCATATTTATTTT TGTT
                                |||||||||||||| ||||
                                ACGTATGAATAAAA ACAA
                                          C
GAM3313  ALS2CR3   3'  GGATACATAATTTAACCA    74454     CA
                                GGA  ACATAATTTAGCTA
                                |||  ||||||||||||||
                                CCT  TGTATTAAATTGGT
                                  A_
GAM3313  LOC113523 3'  GGAGACATAATTTTATAGA   74455     CA       AGC
                                GGA  ACATAATTT   TATAGA
                                |||  |||||||||   ||||||
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                                CCT  TGTATTAAA   ATATCT
                                  C_       ___
GAM3313  LOC219920 5'  GACAACACATTTAGTTATAGAT 74456         A    C
                                GACAACATA TTTAG TATAGAT
                                ||||||||| ||||| |||||||
                                CTGTTGTGT AAATC ATATCTA
                                      _    A
GAM3314  XK      3'  TCCCTGTGTAGGGCTCATTATT 74459         C   T  GACTC__
           TGT                    TCCCTGTG AGG GC      TTGT
                                ||||||||| ||| ||      ||||
                                AGGGACAC TCC CG      AACA
                                     A  _ AGTAATA
GAM3314  ZNF75    3'  CCTTATGTATCAACTCTTGT   74460     GTGCAG  _
                                CCT     GTG CGACTCTTGT
                                |||     ||| ||||||||||
                                GGA     CAT GTTGAGAACA
                                  ATA___   A
GAM3314  DKFZp586H0623 3'  TCCCTGTGGGGCCTCTTG    74461        CA  T  GA
                                TCCCTGTG  GG GC  CTCTTG
                                ||||||||  || ||  ||||||
                                AGGGACAC  CC CG  GAGAAC
                                     __  _  __
GAM3314  FLJ22269  3'  TGCAGGTGCGCGCTTGT     74462          ACT
                                TGCAGGTGCG   CTTGT
                                ||||||||||   |||||
                                ACGTCCACGC   GAACA
                                      GC_
GAM3314  FLJ23120  3'  TGTGAAGGTACATTTTTGT    74463     C      ACTC
                                TGTG AGGTGCG    TTGT
                                |||| |||||||    ||||
                                ACAC TCCATGT    AACA
                                  T      AAA_
GAM3314  KDELR3   3'  TCTTTGTGCAGGTGGCCGA   74464    CC        __
                                TC  TGTGCAGGTG  CGA
                                ||  ||||||||||  |||
                                AG  ACACGTCCAC  GCT
                                 AA         CG
GAM3314  SMARCF1   3'  TGTGCAGGTCACCAACTTGT   74465         G  ACT_
                                TGTGCAGGT CG    CTTGT
                                |||||||| ||    |||||
                                ACACGTCCA GT    GAACA
                                     _ GGTT
GAM3314  SMARCF1   3'  TGTGCAGGTCACCAACTTGT   74465         G  ACT_
                                TGTGCAGGT CG    CTTGT
                                |||||||| ||    |||||
                                ACACGTCCA GT    GAACA
                                     _ GGTT
GAM3314  SMARCF1   3'  TGTGCAGGTCACCAACTTGT   74465         G  ACT_
                                TGTGCAGGT CG    CTTGT
                                |||||||| ||    |||||
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                                ACACGTCCA GT    GAACA
                                     _ GGTT
GAM3314  LOC151902 3'  CTGGGCAGAACCATTCTTGT  74466     T    T  GAC
                                CTG GCAGG GC   TCTTGT
                                ||| ||||| ||   ||||||
                                GAC CGTCT TG   AGAACA
                                  C    _ GTA
GAM3314  LOC152485 3'  TGTGCAGGTTGAGATTGT    74467         GC  CTC
                                TGTGCAGGT  GA   TTGT
                                |||||||||  ||   ||||
                                ACACGTCCA  CT   AACA
                                     A_  CT_
GAM3314  LOC153688 3'  TCTTTGTGCAAGTCCTTG    74468    CC       GCGAC
                                TC  TGTGCAGGT    TCTTG
                                ||  |||||||||    |||||
                                AG  ACACGTTCA    GGAAC
                                 AA       _____
GAM3314  LOC220739 3'  TCCCTGGACACCGGCTTTTGT  74469      TG  GGTG  A  C
                                TCCCTG  CA    CG CT TTGT
                                ||||||  ||    || || ||||
                                AGGGAC  GT    GC GA AACA
                                   CT  G___  C  A
GAM3314  LOC92305  5'  TCCCCGTGCGGGTGCGGCC   74470        A     A
                                TCCCTGTGC GGTGCG CT
                                ||||||||| |||||| ||
                                AGGGGCACG CCACGC GG
                                     C     C
GAM3314  LOC92379  3'  CCCCTGTGTGGATCCTCTTGT  74471       CA  TGCGA
                                TCCCTGTG  GG    CTCTTGT
                                ||||||||  ||    |||||||
                                GGGGACAC  CC    GAGAACA
                                    A_  TAG__
GAM3315  AGM1     3'  TTTATAAAGAATTATTC     74474          CA
                                TTTATAAAGAAT  TATTC
                                ||||||||||||  |||||
                                AAATATTTCTTA  ATAAG
                                              __
GAM3315  BCL10    3'  TTTATAAAAAGTCATATTC    74475         A
                                TTTATAAAGA TCATATTC
                                |||||||||| ||||||||
                                AAATATTTTT AGTATAAG
                                     C
GAM3315  EIF5     3'  TTTATAATAGAACCTCATTAG  74476       _     ATAT
                                TTTATAA AGAATC    TCATTAG
                                ||||||| ||||||    |||||||
                                AAATATT TCTTGG    AGTAATC
                                    A     _____
GAM3315  LOC221718 3'  TAAAGCTAAATCATGTTCATTA 74477      ___     A
            G                    TAAAG   AATCAT TTCATTAG
                                 |||||   |||||| ||||||||
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                                ATTTC  TTAGTA AAGTAATC
                                  GAT    C
GAM3316  DDX20    3'  TTGCTTTTATTGTTTTTA    74480       A
                                TTGCTTT ATTGTTTTTG
                                ||||||| ||||||||||
                                AACGAAA TAACAAAAAT
                                    A
GAM3316  DHFR     3'  TTGCTTTAAGTGTTTGGCA   74481        T    TT
                                TTGCTTTAA TGTTT  GTA
                                ||||||||| |||||  |||
                                AACGAAATT ACAAA  CGT
                                    C    C_
GAM3316  DSG1     3'  TTGCTTCAATTCGAGAAGTAAA 74482         GTTTTT
           CT                     TTGCTTTAATT    GTAAACT
                                ||||||||||     |||||||
                                AACGAAGTTAA    CATTTGA
                                     GCTCTT
GAM3316  EBI2     3'  TTGCTTTATGTTGTTCTC    74483       A_
                                TTGCTTTA  TTGTTTTT
                                ||||||||  ||||||||
                                AACGAAAT  AACAAGAG
                                    AC
GAM3316  GYPA     3'  TTGCTTTTATTAAAAATGTAAA 74484       A   TTTT
                                TTGCTTT ATTG   TGTAAA
                                ||||||| ||||   ||||||
                                AACGAAA TAAT   ACATTT
                                    A   TTTT
GAM3316  HTR2A    3'  TTGTTTTAATTATTTTTATA  74485    C
                                TTG TTTAATTGTTTTTGTA
                                ||| ||||||||||||||||
                                AAC AAATTAATAAAAATAT
                                  A
GAM3316  MGA      3'  CTGCTTTAATTGTTTTAAC   74486          TGTA
                                TTGCTTTAATTGTTTT   AAC
                                ||||||||||||||||   |||
                                GACGAAATTAACAAAA   TTG
                                                   ____
GAM3316  OPA1     3'  TTACTTTAATTGTTGAAATAA  74487          TTT
                                TTGCTTTAATTGTT  GTAA
                                ||||||||||||||  ||||
                                AATGAAATTAACAA  TATT
                                     CTT
GAM3316  OPA1     3'  TTACTTTAATTGTTGAAATAA  74487          TTT
                                TTGCTTTAATTGTT  GTAA
                                ||||||||||||||  ||||
                                AATGAAATTAACAA  TATT
                                     CTT
GAM3316  OPA1     3'  TTACTTTAATTGTTGAAATAA  74487          TTT
                                TTGCTTTAATTGTT  GTAA
                                ||||||||||||||  ||||
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                                AATGAAATTAACAA  TATT
                                       CTT
GAM3316 OPA1    3' TTACTTTAATTGTTGAAATAA 74487          TTT
                                TTGCTTTAATTGTT  GTAA
                                |||||||||||||  ||||
                                AATGAAATTAACAA  TATT
                                       CTT
GAM3316 OPA1    3' TTACTTTAATTGTTGAAATAA 74487          TTT
                                TTGCTTTAATTGTT  GTAA
                                |||||||||||||  ||||
                                AATGAAATTAACAA  TATT
                                       CTT
GAM3316 XYLB    3' TTGCTTTGTTTGTTTTGC    74488       AA     T
                                TTGCTTT  TTGTTTT GT
                                |||||||  ||||||| ||
                                AACGAAA  AACAAAA CG
                                    CA     _
GAM3316 LOC220164 3' TTCCTTTAATTGTCACTG    74489    G       T
                                TT CTTTAATTGTT TTG
                                || ||||||||||| |||
                                AA GAAATTAACAG GAC
                                 G         T
GAM3317 ARCN1   3' GGTAGCAACAGCAGCAGACATG 74492    C  T     T__
                                GG AGC ACAGCAGC  TATG
                                || ||| ||||||||  ||||
                                CC TCG TGTCGTCG  GTAC
                                 A  T      TCT
GAM3317 CDK3    3' AGGCAGCTGGGGCAGCAGCT  74493       A___
                                AGGCAGCT   CAGCAGCT
                                ||||||||   ||||||||
                                TCCGTCGA   GTCGTCGA
                                    CCCC
GAM3317 CELSR1  3' AGGCAGCTGTAGGGCTTCTAG 74494       AC CA   A
                                AGGCAGCT  AG  GCTT TGG
                                ||||||||  ||  |||| |||
                                TCCGTCGA  TC  CGAA ATC
                                    CA  C_   G
GAM3317 EGFL4   3' AGGCAGCTGGAGCAGCAGT   74495       AC    TTAT
                                AGGCAGCT  AGCAGC   GGT
                                ||||||||  ||||||   |||
                                TCCGTCGA  TCGTCG   TCA
                                    CC    ____
GAM3317 HRMT1L1 3' GGTGGCCACGGCAGCTCCTG  74496   CA   A    A
                                GG  GCTAC GCAGCTT TG
                                ||  ||||| ||||||| ||
                                CC  CGGTG CGTCGAG AC
                                 AC    C     G
GAM3317 HTR4    3' AGACGGCTATAGCAGCATAC  74497    A   C    T
                                AGGC GCTA AGCAGC TAT
                                |||| |||| |||||| |||
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                                TCTG CGAT TCGTCG ATG
                                  C   A     T
GAM3317 KCNK3    3' GGTAATTATCAGCAATTATGGT 74498    C  C  _     C
              G                    GG AG TA CAGCAG TTATGGTG
                                || || || |||||| ||||||||
                                CC TT AT GTCGTT AATACCAC
                                 A  A  A     _
GAM3317 LAMA5    3' AGGCAGCTGCAGGGGCCT    74499         A   CA
                                AGGCAGCT CAG  GCTT
                                |||||||| |||  ||||
                                TCCGTCGA GTC  CGGA
                                     C   CC
GAM3317 MTMR3    3' AGGCAGCTCGGCAGTTACAGTG 74500         ACA    C
                                AGGCAGCT   GCAG TTATGGTG
                                ||||||||   |||| ||||||||
                                TCCGTCGA   CGTC AATGTCAC
                                     GC_   _
GAM3317 NOV      3' GGCGCAGCAGCTACAGGTG   74501     A  TAC      TAT
                                GGC GC   AGCAGCT   GGTG
                                ||| ||   |||||||   ||||
                                CCG CG   TCGTCGA   CCAC
                                  _ ___      TGT
GAM3317 RAGE     3' AGGCAGCTGCGCGGGCCGCGGG 74502         ACA  A_   TAT
              TG                   AGGCAGCT   GC  GCT   GGTG
                                |||||||   ||  |||   ||||
                                TCCGTCGA   CG  CGG   CCAC
                                     CG_  CC   CGC
GAM3317 RRAS     3' AGGCAGCTAGTCCCGAGAGCTT 74503        C_____  C    A
              GTGGTG                 GCAGCTA     AG AGCTT TGGTG
                                |||||||     || ||||| |||||
                                CGTCGAT     TC TCGAA ACCAC
                                    CAGGGC  _     C
GAM3317 THBS1    3' AGGTACTACAGTAGCTT     74504     CA      C
                                AGG  GCTACAG AGCTT
                                |||  ||||||| |||||
                                TCC  TGATGTC TCGAA
                                  A_      A
GAM3317 YWHAG    3' AGGGAGCTGCAGCAGCTT    74505     C    A
                                AGG AGCT CAGCAGCTT
                                ||| |||| |||||||||
                                TCC TCGA GTCGTCGAA
                                  C   C
GAM3317 AKAP10   3' AGGTAACTGCATTATGGT    74506     C    ACA   GC
                                AGG AGCT   GCA  TTATGGT
                                ||| ||||   |||  |||||||
                                TCC TTGA   CGT  AATACCA
                                  A   ___  __
GAM3317 ALDH5A1  3' AGGCAGCTGGGCTGTGGT    74507         ACAGCA   TA
                                AGGCAGCT     GCT  TGGT
                                ||||||||     |||  ||||
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                                TCCGTCGA     CGA  ACCA
                                    CC_____   C_
GAM3317 Cab45    3'  AGGCAGCTGCGGGACCTGGGTG 74508        ACA  A__    AT
                                AGGCAGCT   GC   GCTT  GGTG
                                ||||||||   ||   ||||  ||||
                                TCCGTCGA   CG   TGGA  CCAC
                                    ____  CCC    C_
GAM3317 KIAA0082 3'  AGCGGCTATGGCAGACAGCGGT 74509     A    CA    _ TTA
              G                   GGC GCTA  GCAG C   TGGTG
                                ||| ||||  |||| |   |||||
                                TCG CGAT  CGTC G   GCCAC
                                  C    AC    T TC_
GAM3317 KIAA0450 5'  AGGCGGCCACAGCAGTGGCG   74510     A        CTTA
                                AGGC GCTACAGCAG    TGGTG
                                ||||  ||||||||||    |||||
                                TCCG CGGTGTCGTC    ACCGC
                                  C         _____
GAM3317 KIAA0542 3'  AGGCAGCAGCAGCAGCTC     74511        TA
                                AGGCAGC  CAGCAGCTT
                                |||||||  |||||||||
                                TCCGTCG  GTCGTCGAG
                                    TC
GAM3317 MAP2K7   3'  AGGCAGCTGGGTGGCCAAGTG  74512        ACAGCA   TAT
                                AGGCAGCT     GCT   GGTG
                                ||||||||     |||   ||||
                                TCCGTCGA     CGG   TCAC
                                    CCCAC_   T__
GAM3317 MGC4707  3'  GGCAGCACAGCAAGG       74513       T     CTTAT
                                GGCAGC ACAGCAG     GG
                                ||||||| |||||||     ||
                                CCGTCG TGTCGTT     CC
                                  _      ______
GAM3317 PPP1R1A  3'  AGGCAGCTTGGCAGGAGGGTG  74514        ACA    CTTAT
                                AGGCAGCT   GCAG    GGTG
                                ||||||||   ||||    ||||
                                TCCGTCGA   CGTC    CCAC
                                    AC_    CTC__
GAM3317 UPLC1    3'  AGGCAGCTGTGTTGGCCATTGG 74515       ACAGCA   TA
              TG                   AGGCAGCT     GCT  TGGTG
                                ||||||||     |||  |||||
                                TCCGTCGA     CGG  ACCAC
                                    CACAAC   TA
GAM3317 VPS28    3'  AGGCAGCTGCAGACAGTGAGTT 74516        A   _   CTTATG
              GTG                   AGGCAGCT CAG CAG     GTG
                                ||||||||  ||| |||     |||
                                TCCGTCGA GTC GTC     CAC
                                    C   T   ACTCAA
GAM3317 LOC136288 5'  AGGAGCTGCAGCAGCTC     74517     C    A
                                AGG AGCT CAGCAGCTT
                                |||  |||| |||||||||
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                                TCC TCGA GTCGTCGAG
                                  _   C
GAM3317  LOC138050 5'  AGGCAGCTGCAGCACTAG    74518       ACA    TTA
                                AGGCAGCT   GCAGC   TGG
                                ||||||||   |||||   |||
                                TCCGTCGA   CGTCG   ATC
                                    ___    TG_
GAM3317  LOC145719 3'  AGGCAGCTGAGGCGGGACAGTG 74519       ACA  AGCTT
                                AGGCAGCT   GC    ATGGTG
                                ||||||||   ||    ||||||
                                TCCGTCGA   CG    TGTCAC
                                    CTC  CCC__
GAM3317  LOC145720 3'  AGGCAGCTGAGGCGGGACAGTG 74519       ACA  AGCTT
                                AGGCAGCT   GC    ATGGTG
                                ||||||||   ||    ||||||
                                TCCGTCGA   CG    TGTCAC
                                    CTC  CCC__
GAM3317  LOC146287 5'  AGGCAGCTGCAATGGCCTCTG  74520       A   CA   A
                                AGGCAGCT CAG  GCTT TG
                                |||||||| |||  |||| ||
                                TCCGTCGA GTT  CGGA AC
                                    C   AC    G
GAM3317  LOC150282 5'  AGGCAACTGCAGAAGATGGTG  74521       ACA   CTT
                                AGGCAGCT   GCAG   ATGGTG
                                ||||||||   ||||   ||||||
                                TCCGTTGA   CGTC   TACCAC
                                    ___    TTC
GAM3317  LOC161247 5'  AGGCAGCTGCGGCGGT     74522       ACA  A  TTAT
                                AGGCAGCT   GC GC    GGT
                                ||||||||   || ||    |||
                                TCCGTCGA   CG CG    CCA
                                    ___  C  ____
GAM3317  LOC196955 5'  GGTGGCCATAGCACAAGGGGTG 74523    CA    C    G TTAT
                                GG  GCTA AGCA C    GGTG
                                ||  |||| |||| |    ||||
                                CC  CGGT TCGT G    CCAC
                                 AC    A    _ TTCC
GAM3317  LOC197114 3'  AGGCAGCTGAGGCGGGACAGTG 74519       ACA  AGCTT
                                AGGCAGCT   GC    ATGGTG
                                ||||||||   ||    ||||||
                                TCCGTCGA   CG    TGTCAC
                                    CTC  CCC__
GAM3317  LOC197117 3'  AGGCAGCTGAGGCGGGACAGTG 74519       ACA  AGCTT
                                AGGCAGCT   GC    ATGGTG
                                ||||||||   ||    ||||||
                                TCCGTCGA   CG    TGTCAC
                                    CTC  CCC__
GAM3317  LOC221474 5'  GGCTGCCAGCCCACCATGGTG  74524     A  TA   A_   T
                                GGC GC  CAGC  GCT ATGGTG
                                ||| ||  ||||  ||| ||||||
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                                CCG CG  GTCG  TGG TACCAC
                                  A __   GG  _
GAM3317 LOC90141 3' GGCAGCTGAGCAGCTCA    74525       AC
                                GGCAGCT  AGCAGCTTA
                                |||||||  |||||||||
                                CCGTCGA  TCGTCGAGT
                                   C_
GAM3318 ACTR3    3' TCCTGTATAATCATGT     74528       TTT
                                TTTTGT   ATAATCATGT
                                ||||||   ||||||||||
                                AGGACA   TATTAGTACA
                                   ___
GAM3318 SAMHD1   3' TTTTGTTTTTAGCCATGT   74529        A  AT
                                TTTTGTTTT TA  CATGT
                                ||||||||| ||  |||||
                                AAAACAAAA AT  GTACA
                                     _ CG
GAM3318 LOC219731 5' TCTTTGGTTTTATAATCAAAAC 74530      T         TGT
             TG                   TCTTT GTTTTATAATCA   CTG
                                |||||| ||||||||||||   |||
                                AGAAA CAAAATATTAGT   GAC
                                  C          TTT
GAM3318 LOC256880 5' CTTTTGTTTGTTATGTCT    74531        TATAATC
                                CTTTTGTTT      ATGTCT
                                |||||||||      ||||||
                                GAAAACAAA      TACAGA
                                     CAA____
GAM3319 ATP6V1G2  5' TGCTGTTTTGAATGCTG     74534    C   CTCT   C
                                TGC TGT    TTT AATGCTG
                                ||| |||    ||| |||||||
                                ACG ACA    AAA TTACGAC
                                  _  _____  C
GAM3319 DNMT3B   3' TGTCTGTCCCTGACTGCTGT   74535    C      TTTCAA
                                TG CTGTCTCT     TGCTGT
                                || ||||||||     ||||||
                                AC GACAGGGA     ACGACA
                                 A       CTG___
GAM3319 EMX2     3' CCTGTCTCTTTTGCT       74536          TCAA
                                CCTGTCTCTTT    TGCT
                                ||||||||||    ||||
                                GGACAGAGAAA    ACGA
                                     _____
GAM3319 GCNT2    5' CTGTTTTCCAACGTGCTGT    74537     CTC     __
                                CTGT   TTTTCAA  TGCTGT
                                ||||   |||||||  ||||||
                                GACA   AAAGGTT  ACGACA
                                  ___      GC
GAM3319 MAPT     3' TGCCTTCTCTTTTTAACCCGCT 74538      G      CAA__
             GT                   TGCCT TCTCTTTT    TGCTGT
                                ||||| ||||||||    ||||||
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                                ACGGA AGAGAAAA    GCGACA
                                  _      ATTGG
GAM3319  MAPT    3'  TGCCTTCTCTTTTTAACCCGCT 74538      G      CAA__
            GT                   TGCCT TCTCTTTT    TGCTGT
                                |||||  ||||||||    ||||||
                                ACGGA AGAGAAAA    GCGACA
                                  _      ATTGG
GAM3319  MAPT    3'  TGCCTTCTCTTTTTAACCCGCT 74538      G      CAA__
            GT                   TGCCT TCTCTTTT    TGCTGT
                                |||||  ||||||||    ||||||
                                ACGGA AGAGAAAA    GCGACA
                                  _      ATTGG
GAM3319  MAPT    3'  TGCCTTCTCTTTTTAACCCGCT 74538      G      CAA__
            GT                   TGCCT TCTCTTTT    TGCTGT
                                |||||  ||||||||    ||||||
                                ACGGA AGAGAAAA    GCGACA
                                  _      ATTGG
GAM3319  NR4A2   3'  TGCTTGTCCCTTTTTTATG   74539    C       CA
                                TGC TGTCTCTTTT  ATG
                                |||  ||||||||||  |||
                                ACG ACAGGGAAAA  TAC
                                  A        AA
GAM3319  PDE4D   3'  TACCTGTTTCTTTTCACCG   74540      C     AAT
                                TGCCTGT TCTTTTC   GCTG
                                |||||||  |||||||   ||||
                                ATGGACA AGAAAAG   TGGC
                                    A     ___
GAM3319  PLEK    3'  TATCTGTTTCAATGGGTGCTGT 74541     CT    ____
                                TGTCT  TTTCAA    TGCTGT
                                |||||  ||||||    ||||||
                                ATAGA  AAAGTT    ACGACA
                                  C_     ACCC
GAM3319  RAB5C   3'  TGGCTGTCACAATAATGCTGT  74542    C    TCTTTTC
                                TG CTGTC      AATGCTGT
                                ||  |||||     ||||||||
                                AC GACAG      TTACGACA
                                 C    TGTTA__
GAM3319  RALBP1  3'  GCCTGTCTCGCGGTGCTGT   74543       TTTTCAA
                                GCCTGTCTC      TGCTGT
                                |||||||||      ||||||
                                CGGACAGAG      ACGACA
                                    CGCC___
GAM3319  SLBP    3'  TGTCTGACTTCAGAATGCTGT  74544     CT   __
                                TGTCT  TTTCA  ATGCTGT
                                |||||  |||||  |||||||
                                ACAGA  GAAGT  TACGACA
                                  CT    CT
GAM3319  APOL3   3'  CTGTCTCTTTGCCTGCTGT   74545        TCAA
                                CTGTCTCTTT   TGCTGT
                                ||||||||||   ||||||
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                                GACAGAGAAA   ACGACA
                                     CGG_
GAM3319 DNAH8    5' TGCCTGTCTCTCTTTTAATG  74546          C_
                                TGCCTGTCTCTTTT  AATG
                                ||||||||||||||  ||||
                                ACGGACAGAGAGAA  TTAC
                                      AA
GAM3319 FLJ11151 3' TGCTGTTTCATAATGCTG    74547    C  C  TTTTC
                                TGC TGT TC    AATGCTG
                                ||| ||| ||    |||||||
                                ACG ACA AG    TTACGAC
                                  _  A  TA___
GAM3319 FLJ11726 3' TGTCTTTGTCAGTGCTG     74548     C  T  A
                                TGTCT TT TCA TGCTG
                                ||||| || ||| |||||
                                ACAGA AA AGT ACGAC
                                   _ C  C
GAM3319 FLJ14146 3' TCTCTTCCAAATATGCTGT   74549       CA__
                                TCTCTTTT   ATGCTGT
                                ||||||||   |||||||
                                AGAGAAGG   TACGACA
                                     TTTA
GAM3319 KIAA1309 3' TGTCTTTTTTCCAATATCTGT 74550     C_      _
                                TGTCT  TTTTCAATG CTGT
                                |||||  |||||||| ||||
                                ACAGA  AAAGGTTAT GACA
                                   AA       A
GAM3319 KIAA1598 5' TGCTTGCCTCTTTAGATCTGT 74551    C       TCAATG
                                TGC TGTCTCTTT     CTGT
                                ||| |||||||||     ||||
                                ACG ACGGAGAAA     GACA
                                  A       TCTA__
GAM3319 LGI4     5' TGCCTGTTTCTTTTTTTCTGT 74552      C     CAATG
                                TGCCTGT TCTTTT    CTGT
                                ||||||| ||||||    ||||
                                ACGGACA AGAAAA    GACA
                                    A     AAA__
GAM3319 MGC2817  3' TGCCTGTTTGTTTTCAAT    74553      CTC
                                TGCCTGT   TTTTCAAT
                                |||||||   ||||||||
                                ACGGACA   AAAAGTTA
                                    AAC
GAM3319 MGC3251  3' TGCCTGCCTCTTTTTGCC    74554          CAA
                                TGCCTGTCTCTTTT   TGCT
                                ||||||||||||||   ||||
                                ACGGACGGAGAAAA   ACGG
                                         ___
GAM3319 PPP1R10  3' TGCTTTCTCTTTCCACTG    74555    CTG      AAT
                                TGC   TCTCTTTTC   GCTG
                                |||   |||||||||   ||||
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                                ACG   AGAGAAAGG   TGAC
                                  AA_       ___
GAM3319  RoXaN    3'  TGTCTGTCTCTTTTGCT     74556    C        TCAA
                                TG CTGTCTCTTT    TGCT
                                || ||||||||||    ||||
                                AC GACAGAGAAA    ACGA
                                 A        _____
GAM3319  LOC120534 3'  TGCTTGTGCTTTCAATGTTGT  74557     C   CTC       C
                                TGC TGT   TTTTCAATG TGT
                                ||| |||   ||||||||| |||
                                ACG ACA   GAAAGTTAC ACA
                                  A  C__        A
GAM3319  LOC126435 5'  TGCCTCTCTCTTTGGGTCTGT  74558      G      TCAATG
                                TGCCT TCTCTTT     CTGT
                                ||||| |||||||     ||||
                                ACGGA AGAGAAA     GACA
                                   G      CCCA__
GAM3319  LOC138389 5'  CCTGTCCTCTTGGTGCTGT    74559       T    CAA
                                CCTGTC CTTTT   TGCTGT
                                |||||| |||||   ||||||
                                GGACAG GAGAA   ACGACA
                                    _    CC_
GAM3319  LOC144308 3'  TGCCTGCCCGGATCAGTGCTGT 74560         CTTT   A
                                TGCCTGTCT    TCA TGCTGT
                                |||||||||    ||| ||||||
                                ACGGACGGG    AGT ACGACA
                                      CCT_   C
GAM3319  LOC145317 3'  CCTGTCTCTTCCCTCGCTGT   74561          TT AA
                                CCTGTCTCTT  C  TGCTGT
                                ||||||||||  |  ||||||
                                GGACAGAGAA  G  GCGACA
                                      GG A_
GAM3319  LOC147514 5'  TGTCTCTTTTAGCTACTGT    74562          CAA
                                TGTCTCTTTT   TGCTGT
                                ||||||||||   ||||||
                                ACAGAGAAAA   ATGACA
                                      TCG
GAM3319  LOC151701 5'  GCCTGACCATTTGGTGCTGT   74563      T  C   TCAA
                                GCCTG CT TTT    TGCTGT
                                ||||| || |||    ||||||
                                CGGAC GG AAA    ACGACA
                                   T  T   CC__
GAM3319  LOC152620 3'  TGCCTGTCTTTTTCTAGCT    74564         C     AAT
                                TGCCTGTCT TTTTC   GCT
                                ||||||||| |||||   |||
                                ACGGACAGA AAAAG   CGA
                                      _    AT_
GAM3319  LOC153792 3'  TGTCTTTTCCAATGCTG     74565       C
                                TGTCT TTTTCAATGCTG
                                ||||| ||||||||||||
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                                ACAGA AAAGGTTACGAC
                                  _
GAM3319 LOC162048 5' TGCCTCTCAGCAGTGCTG   74566      TT  A
                                TGTCTCTT  CA TGCTG
                                ||||||||  || |||||
                                ACGGAGAG  GT ACGAC
                                    TC  C
GAM3319 LOC200273 5' TGTCTCTTTTAGCTACTGT  74562       CAA
                                TGTCTCTTTT  TGCTGT
                                ||||||||||  ||||||
                                ACAGAGAAAA  ATGACA
                                     TCG
GAM3319 LOC203274 5' CCTGTCCTCTTGGTGCTGT  74559     T   CAA
                                CCTGTC CTTTT  TGCTGT
                                |||||| |||||  ||||||
                                GGACAG GAGAA  ACGACA
                                  _   CC_
GAM3319 LOC57826  3' TGCCGCAATTCAATGCTG   74567    T  CTCTT
                                TGCC GT   TTCAATGCTG
                                |||| ||   ||||||||||
                                ACGG CG   AAGTTACGAC
                                  _ TT___
GAM3319 LOC91097  5' TGTCCTGTCTACAAATGCTGT  74568  _    CTTTTC
                                TG CCTGTCT    AATGCTGT
                                || |||||||    ||||||||
                                AC GGACAGA    TTACGACA
                                 A     TGT___
GAM3320 ALDH3B1   3' CCACCAGCCGCAGGCGA    74571       A  AGTC  G
                                TCACCAGCC CA   GG GA
                                ||||||||| ||   || ||
                                GGTGGTCGG GT   CC CT
                                     C ____  G
GAM3320 AP1B1     3' TCACAGCCACAGGAGCAGGGG  74572    C    __  C
                                TCAC AGCCACA  AGT GGGG
                                |||| |||||||  ||| ||||
                                AGTG TCGGTGT  TCG CCCC
                                  _     CC   T
GAM3320 APBA2     3' TCCCAGCCAAGGGGG      74573   A    CA  TC
                                TC CCAGCCA  AG  GGGG
                                || |||||||  ||  ||||
                                AG GGTCGGT  TC  CCCC
                                  _     __ __
GAM3320 BAI2      5' CCATCCCTAAGTCGGGGAC   74574    G  AC
                                CCA CC  AAGTCGGGGAC
                                ||| ||  ||||||||||
                                GGT GG  TTCAGCCCCTG
                                 A  GA
GAM3320 BAZ2A     5' TCACCAGCAACAGAAGG    74575       C   A TC
                                TCACCAGC ACA G  GGG
                                |||||||| ||| |  |||
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                                AGTGGTCG TGT C  TCC
                                     T   _ T_
GAM3320  BTAF1    3'  CCAGCCACAAACCTTGGGGA  74576          GT __
                                CCAGCCACAA  C  GGGGA
                                ||||||||||  |  |||||
                                GGTCGGTGTT  G  CCCCT
                                      TG AA
GAM3320  CDC25A   5'  CCACCAGCCACAGGCACGGG  74577            A  _
                                TCACCAGCCACA GT CGGG
                                ||||||||||||| || ||||
                                GGTGGTCGGTGT CG GCCC
                                      C  T
GAM3320  CDH5     3'  TCACCAGCCTTACCAGGG    74578          ACAAG
                                TCACCAGCC    TCGGGG
                                |||||||||    ||||||
                                AGTGGTCGG    GGTCCC
                                      AAT__
GAM3320  CHRM1    3'  CCACCGGCCTTTCCCGGGGAC  74579       A   ACAAG
                                TCACC GCC    TCGGGGAC
                                ||||| |||    ||||||||
                                GGTGG CGG    GGCCCCTG
                                   C   AAAG_
GAM3320  CHST1    5'  CACCAGCTACCTGGTCGGGGAC 74580        C  AA_
                                CACCAGC AC   GTCGGGGAC
                                ||||||| ||   |||||||||
                                GTGGTCG TG   CAGCCCCTG
                                     A  GAC
GAM3320  CLN6     3'  TCAACAGCCACAGTAGG     74581     C      A  C
                                TCA CAGCCACA GT GGG
                                ||| |||||||| || |||
                                AGT GTCGGTGT CA TCC
                                  T       _  _
GAM3320  CREBBP   3'  TCACCAGCAATGACGA      74582         CACA   C  G
                                TCACCAGC    AGT GG GA
                                ||||||||    ||| || ||
                                AGTGGTCG    TTA CT CT
                                     _____   _  G
GAM3320  DFNA5    3'  TCACCAGCACAGGAGGG     74583         C   A TC
                                TCACCAGC ACA G  GGG
                                ||||||||| ||| |  |||
                                AGTGGTCG TGT C  CCC
                                     _   _ CT
GAM3320  EHD2     3'  CCAGCCACAGACACGTGGG   74584          AG _  _
                                CCAGCCACA  T CG GGG
                                |||||||||  | || |||
                                GGTCGGTGT  G GC CCC
                                      CT T  A
GAM3320  EN2      3'  TCCCAGCCACAGATGGA     74585     A       A TCGG
                                TC CCAGCCACA G    GGA
                                || |||||||| |    |||
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                                AG GGTCGGTGT C    CCT
                                 _       _ TA__
GAM3320  EP300    5'  TCATCGCCACAAGGAGGCGGGG 74586     CCA      T___
                                TCA   GCCACAAG    CGGGG
                                |||   ||||||||    |||||
                                AGT   CGGTGTTC    GCCCC
                                  AG_       CTCC
GAM3320  FGFR2    3'  TCACCAGTCAGCAGCCAAAGAC 74587        C  CA
                                TCACCAG CA  AGTCGGGGAC
                                |||||||  ||  ||||||||||
                                AGTGGTC GT  TCGGTTTCTG
                                    A  CG
GAM3320  FNTB     3'  CCACCAGCTACAGAGG      74588        C   AGTC
                                TCACCAGC ACA    GGGG
                                ||||||||  |||    ||||
                                GGTGGTCG TGT    CTCC
                                    A   _____
GAM3320  FRAT2    3'  TCACCAGCCACCGAATCGG    74589          A_
                                TCACCAGCCAC  AGTCGG
                                ||||||||||  ||||||
                                AGTGGTCGGTG  TTAGCC
                                      GC
GAM3320  GAS7     3'  TCACCAGCTAGGCAAGG     74590        CACA  T
                                TCACCAGC    AG CGGGG
                                ||||||||    ||  |||||
                                AGTGGTCG    TC GTTCC
                                    A___  C
GAM3320  GCN5L2   3'  CCACCAGCTACTCTAGAGGGG  74591         C  A__  TC
                                TCACCAGC AC   AG  GGGG
                                ||||||||  ||   ||  ||||
                                GGTGGTCG TG   TC  CCCC
                                    A  AGA  T_
GAM3320  GRIK5    3'  TCACCAGCACATAGTGGG     74592         C   _   C
                                TCACCAGC ACA AGT GGG
                                |||||||  ||| ||| |||
                                AGTGGTCG TGT TCA CCC
                                    _   A   _
GAM3320  IMMP2L   5'  TCACGGCCAGAGCCGGGG    74593      CA    CA
                                TCAC  GCCA  AGTCGGGG
                                ||||  ||||  ||||||||
                                AGTG  CGGT  TCGGCCCC
                                  C_    C_
GAM3320  KCNH3    5'  TCGCCGCCCACAAATCCCGGG  74594     A  AG       G_
                                TC CC  CCACAAGTC  GGG
                                ||  ||  |||||||||  |||
                                AG GG  GGTGTTTAG  CCC
                                 C  CG        GG
GAM3320  KRT6B    3'  TCACTTGCCATTCAGGGAC    74595      CA    CAAG
                                TCAC  GCCA    TCGGGGAC
                                ||||  ||||    ||||||||
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                                AGTG  CGGT   AGTCCCTG
                                  AA   A___
GAM3320  LASS1    3'  TCACCAGCAGCAGCGAGG    74596       CACA  T
                                TCACCAGC   AG CGGGG
                                ||||||||   || |||||
                                AGTGGTCG   TC GCTCC
                                    TCG_ _
GAM3320  LENG4    5'  TCCTCAGCCACAAGAGAG    74597    AC       TC
                                TC  CAGCCACAAG  GGGG
                                ||  ||||||||||  ||||
                                AG  GTCGGTGTTC  TCTC
                                 GA        __
GAM3320  MARS     5'  TCTCCAGCCACAGGCAA     74598    A       AGTC  G
                                TC CCAGCCACA   GG GA
                                || |||||||||   || ||
                                AG GGTCGGTGT   CC TT
                                 A       ____  G
GAM3320  MATK     5'  CCGCCGGCCTGCTCCGGGGAC  74599    A  A   ACAAG
                                TC CC GCC    TCGGGGAC
                                || || |||    ||||||||
                                GG GG CGG    GGCCCCTG
                                 C  C   ACGA_
GAM3320  MBD3     3'  CCACCAGCCGCATGGCAGGG   74600        A  AGT
                                TCACCAGCC CA   CGGGG
                                |||||||| ||   |||||
                                GGTGGTCGG GT   GTCCC
                                     C  ACC
GAM3320  MUC1     3'  TCACCAGCCCAAACAGGG    74601        A    T
                                TCACCAGCC CAAG CGGGG
                                ||||||||| |||| |||||
                                AGTGGTCGG GTTT GTCCC
                                     _   _
GAM3320  PKIA     5'  CCAGCCACGGGGGGAGCGGGG  74602        A_____  T
                                CCAGCCAC     AG CGGGG
                                ||||||||     || |||||
                                GGTCGGTG     TC GCCCC
                                    CCCCCC  _
GAM3320  PML      3'  TGACCACAAGGTTGGGGAC   74603   A      TC_
                                C GCCACAAG   GGGGAC
                                | ||||||||   ||||||
                                A TGGTGTTC   CCCCTG
                                 C       CAA
GAM3320  POU2AF1  5'  CACCGGCCCCGCGGGGAC    74604     A   ACAA T
                                CACC GCC    G CGGGGAC
                                |||| |||    | |||||||
                                GTGG CGG    C GCCCCTG
                                  C   GG__ _
GAM3320  SPINT2   5'  CCACCAGCCGTTGGGG      74605        ACAA  C
                                TCACCAGCC    GT GGGG
                                |||||||||    || ||||
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                                GGTGGTCGG   CA CCCC
                                    ____ A
GAM3320 ST3GALVI 3' TCACCAGCAGCAACAGA    74606       CA  GT
                                TCACCAGC  CAA  CGGG
                                ||||||||  |||  ||||
                                AGTGGTCG  GTT  GTCT
                                    TC  __
GAM3320 TLL1    3' ACCAGCCATAGGGAGAC    74607       CA  TC
                                ACCAGCCA  AG  GGGGAC
                                ||||||||  ||  ||||||
                                TGGTCGGT  TC  CCTCTG
                                    A_ __
GAM3320 UFD1L   3' CAGCCACAGTAGTGGGAC   74608       A  CG_
                                CAGCCACA GT   GGGAC
                                |||||||| ||   |||||
                                GTCGGTGT CA   CCCTG
                                    _ TCA
GAM3320 VAMP8   3' TCCCAGCCACATGCTGGG   74609   A       A  C
                                TC CCAGCCACA GT GGG
                                || |||||||| || |||
                                AG GGTCGGTGT CG CCC
                                 _       A  A
GAM3320 WASF3   3' TCACTGCCCACAAGCCCAA  74610    CAG       G
                                TCAC   CCACAAGTC GG
                                ||||   |||||||| ||
                                AGTG   GGTGTTCGG TT
                                  ACG       G
GAM3320 XPNPEP1  3' TCACTGGCCAAAGAAGTCGGGG 74611    CA   C__
                                TCAC  GCCA   AAGTCGGGG
                                ||||  ||||   |||||||||
                                AGTG  CGGT   TTCAGCCCC
                                  AC   TTC
GAM3320 AP3D1   3' TCACCAGCCCACGAGA     74612       A  AGT   G
                                TCACCAGCC CA   CGGG A
                                ||||||||| ||   |||| |
                                AGTGGTCGG GT   GCTC T
                                    _ ___   G
GAM3320 BDG-29  3' TCACCAGCCACAGAGA     74613         AGTCG
                                TCACCAGCCACA    GGGA
                                ||||||||||||    ||||
                                AGTGGTCGGTGT    CTCT
                                    _____
GAM3320 BPESC1  3' TCACCAGTCAAGGCCTCGGG  74614       CCA   ___
                                TCACCAG   CAAG   TCGGG
                                |||||||   ||||   |||||
                                AGTGGTC   GTTC   AGCCC
                                    A__   CGG
GAM3320 BTN2A1  3' CAGCCACACTCAGGGAC    74615       AG
                                CAGCCACA  TCGGGGAC
                                ||||||||  ||||||||
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                                GTCGGTGT  AGTCCCTG
                                    G_
GAM3320  C20orf116 3'  TCACCAGCTTCCAAGGGAC   74616       CA_  AGTC
                                TCACCAGC  CA   GGGGAC
                                ||||||||  ||   ||||||
                                AGTGGTCG  GT   TCCCTG
                                    AAG  ____
GAM3320  CBX6    3'  TCCCCAGCCACCCCCAGGG   74617    A      AAG
                                TC CCAGCCAC  TCGGGG
                                || ||||||||  ||||||
                                AG GGTCGGTG  GGTCCC
                                 G      GG_
GAM3320  CDC14B  3'  TCACCAGCATGCCGTTGGGAC  74618       CACAA   __
                                TCACCAGC   GTCG  GGGAC
                                ||||||||   ||||  |||||
                                AGTGGTCG   CGGC  CCCTG
                                    TA___   AA
GAM3320  CML2    3'  TCATTGCAGTCAGAGGTTGGGG 74619    C__  C  CAA  C
            A                    TCA  CAG CA  GT GGGGA
                                |||  ||| ||  || |||||
                                AGT  GTC GT  CA CCCCT
                                  AAC  A  CTC  A
GAM3320  CNNM4   3'  CCAGCCACAGAGGAGAGGAC  74620        _  TC
                                CCAGCCACA AG  GGGGAC
                                |||||||| ||  ||||||
                                GGTCGGTGT TC  CTCCTG
                                     C  CT
GAM3320  CSMD1   5'  TCACCAACCGTAAGGG     74621        ACAA  C
                                TCACCAGCC   GT GGGG
                                |||||||||   || ||||
                                AGTGGTTGG   CA TCCC
                                    ____  T
GAM3320  CXYorf1  3'  TCCCAGCCACCTCGGGG    74622    A      AAG
                                TC CCAGCCAC  TCGGGG
                                || ||||||||  ||||||
                                AG GGTCGGTG  AGCCCC
                                 _      G__
GAM3320  D21S2056E 3'  TCACAGCCACAGGCGGAG   74623     C      A T
                                TCAC AGCCACA G CGGGG
                                |||| ||||||| | |||||
                                AGTG TCGGTGT C GCCTC
                                  _      C _
GAM3320  DKFZp547I014 5'  ACTAGCACAAGCCAGGG    74624    C   C
                                AC AGC ACAAGTCGGGG
                                || ||| ||||||||||
                                TG TCG TGTTCGGTCCC
                                 A  _
GAM3320  DKFZp547J036 3'  TCACCAGCTAAATAGGA    74625       CAC   CG
                                TCACCAGC  AAGT  GGGA
                                ||||||||  ||||  ||||
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                                AGTGGTCG   TTTA  TCCT
                                    A__    __
GAM3320  DKFZp566H0824 5'  TCCCCAGCCCCGGGGA      74626    A     ACAAG
                                TC CCAGCC     TCGGGGA
                                || ||||||     |||||||
                                AG GGTCGG     GGCCCCT
                                 G     _____
GAM3320  DKFZP727M111 5'  TCACCAGCTGCACTGCTGGGG  74627         __   AA  C
                                TCACCAGC  CAC  GT GGGG
                                ||||||||  |||  || ||||
                                AGTGGTCG  GTG  CG CCCC
                                    AC   A_  A
GAM3320  DNAJA4   3'  TCACCGCCCACTTCCCGGGG   74628       A   A  AG__
                                TCACC GCC CA    TCGGGG
                                ||||| ||| ||    ||||||
                                AGTGG CGG GT    GGCCCC
                                  _   _  GAAG
GAM3320  ECE2     5'  TCACCAGCCATCACGG      74629          CAAG   G
                                TCACCAGCCA    TCG GG
                                ||||||||||    ||| ||
                                AGTGGTCGGT    AGT CC
                                     _____   G
GAM3320  FKBP4    3'  TCATCAGCCACACCGTCGGGG  74630     C       A_
                                TCA CAGCCACA  GTCGGGG
                                ||| ||||||||  |||||||
                                AGT GTCGGTGT  CAGCCCC
                                  A       GG
GAM3320  FLJ11184  5'  TCACCAACCGCAGGAG      74631          A  AGTC
                                TCACCAGCC CA    GGGG
                                |||||||||  ||    ||||
                                AGTGGTTGG GT    CCTC
                                     C  _____
GAM3320  FLJ11827  3'  TCATCGCCACAGTCAAGG    74632     CCA     A
                                TCA   GCCACA GTCGGGG
                                |||   |||||| |||||||
                                AGT   CGGTGT CAGTTCC
                                  AG_     _
GAM3320  FLJ12572  3'  TCATGGCCACAGTCTGTGGGAC 74633     CCA     A   G__
                                TCA   GCCACA GTC   GGGAC
                                |||   |||||| |||   |||||
                                AGT   CGGTGT CAG   CCCTG
                                  AC_     _   ACA
GAM3320  FLJ12666  5'  TCGCCAGCCAAGCCGG      74634    A      CA
                                TC CCAGCCA  AGTCGG
                                || |||||||  ||||||
                                AG GGTCGGT  TCGGCC
                                 C      __
GAM3320  FLJ12750  3'  CCACCAGCCACCCAGGG      74635           AAG
                                TCACCAGCCAC   TCGGGG
                                ||||||||||   ||||||
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                                GGTGGTCGGTG  GGTCCC
                                     ___
GAM3320 FLJ13052 3' CCAGCCACTGGCAAGAC    74636       AA  CG
                                CCAGCCAC  GT  GGGAC
                                ||||||||  ||  |||||
                                GGTCGGTG  CG  TTCTG
                                   AC  __
GAM3320 FLJ20511 5' TCATCAGCCCCAAGCCGGA   74637    C    A
                                TCA CAGCC CAAGTCGGG
                                ||| ||||| |||||||||
                                AGT GTCGG GTTCGGCCT
                                  A    G
GAM3320 FLJ21324 5' TCACCAGCTCACAGGA     74638       _   AGTCGG
                                TCACCAGC CACA     GGA
                                |||||||| ||||     |||
                                AGTGGTCG GTGT     CCT
                                   A   _______
GAM3320 FLJ22405 3' TCACCAGTCAAGAGGCTGGGG 74639      C  CAA_  C
                                TCACCAG CA    GT GGGG
                                ||||||| ||    || ||||
                                AGTGGTC GT    CG CCCC
                                   A  TCTC  A
GAM3320 FLJ23309 3' TCACCAGCTCAGCACAGGG   74640       CACA  _
                                TCACCAGC    AGT CGGGG
                                ||||||||    ||| |||||
                                AGTGGTCG    TCG GTCCC
                                   AG__   T
GAM3320 FREQ    3' TCACCAGCCACAGGAA     74641         AGTC  GG
                                TCACCAGCCACA    GG  A
                                ||||||||||||    ||  |
                                AGTGGTCGGTGT    CC  T
                                      _____  TT
GAM3320 GIT1    3' CCACCAGCTGAGTCGGGGAC  74642       CACA
                                TCACCAGC    AGTCGGGGAC
                                ||||||||    ||||||||||
                                GGTGGTCG    TCAGCCCCTG
                                   AC__
GAM3320 GPR     5' TCAGCAGCCACAAGAAGG    74643    C       TC
                                TCA CAGCCACAAG  GGG
                                ||| ||||||||||  |||
                                AGT GTCGGTGTTC  TCC
                                  C        T_
GAM3320 GTF3C1  3' TCACCAGCCAGGCTGAGGGAC  74644        CAAGTC
                                TCACCAGCCA     GGGGAC
                                ||||||||||     ||||||
                                AGTGGTCGGT     TCCCTG
                                     CCGAC_
GAM3320 KIAA0391 5' TCGCAAGCCGCAAACCAGGGGA 74645    ACC   A  GT _
            C                    TC   AGCC CAA  C GGGGAC
                                ||   |||| |||  | ||||||
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                                AG   TCGG GTT  G CCCCTG
                                 CGT    C   TG T
GAM3320 KIAA0557 3' TCACCAGCAAAAACTGGGGAC 74646        CAC   TC
                                TCACCAGC   AAG  GGGGAC
                                ||||||||   |||  ||||||
                                AGTGGTCG   TTT  CCCCTG
                                     TT_   GA
GAM3320 KIAA1340 5' CACCAGCCGCAGGCCCGG    74647        A  A   G
                                CACCAGCC CA GTC GG
                                |||||||| || ||| ||
                                GTGGTCGG GT CGG CC
                                     C  C   G
GAM3320 KIAA1350 3' ACTGGCCACAAAATAGGGGGAC 74648    CA       TC__
                                AC  GCCACAAG    GGGGAC
                                ||  ||||||||    ||||||
                                TG  CGGTGTTT    CCCCTG
                                 AC       TATC
GAM3320 KIAA1808 3' CCGCCAGCCACAGCACAAGGAC 74649    A        A  _
                                TC CCAGCCACA GT CGGGGAC
                                || |||||||| || |||||||
                                GG GGTCGGTGT CG GTTCCTG
                                 C        _  T
GAM3320 KIAA1862 3' TCCCTGGCCACGCAGGA     74650    A  A_    AA T
                                TC CC  GCCAC  G CGGGG
                                || ||  |||||  | |||||
                                AG GG  CGGTG  C GTCCT
                                 _  AC    __ _
GAM3320 KIF13B   3' TCCCAGCCACAAGCTGA     74651    A          C
                                TC CCAGCCACAAGT GG
                                || ||||||||||| ||
                                AG GGTCGGTGTTCG CT
                                 _          A
GAM3320 KIF13B   3' TCCCAGCCACAAGCTGA     74651    A          C
                                TC CCAGCCACAAGT GG
                                || ||||||||||| ||
                                AG GGTCGGTGTTCG CT
                                 _          A
GAM3320 KOC1     3' TCACCAGCCAGAAGTAAAAA   74652          C   C
                                TCACCAGCCA AAGT GGGGA
                                |||||||||| |||| |||||
                                AGTGGTCGGT TTCA TTTTT
                                      C   _
GAM3320 MGC10981 3' TCATCAGCCACATAGAAGGAC  74653     C       _  TC
                                TCA CAGCCACA AG  GGGGAC
                                ||| |||||||| ||  ||||||
                                AGT GTCGGTGT TC  TTCCTG
                                  A       A  __
GAM3320 MGC14433 3' TCATCAGCTTAATCAGGGA    74654     C    CACA
                                TCA CAGC    AGTCGGGGA
                                ||| ||||    |||||||||
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                                AGT GTCG    TTAGTCCCT
                                  A    AA__
GAM3320  MGC861    3'  TCCCAGCCACGGCGGG      74655     A       AA T
                                TC CCAGCCAC  G CGGG
                                || ||||||||  | ||||
                                AG GGTCGGTG  C GCCC
                                  _       C_ _
GAM3320  MRPS18B   3'  TCACTGGCCACAAAAGA     74656      CA       TCGG
                                TCAC  GCCACAAG   GGA
                                ||||  ||||||||   |||
                                AGTG  CGGTGTTT   TCT
                                  AC       _____
GAM3320  NY-REN-25 5'  TCGCCGGCCGGCTCAGGGAC  74657     A  A   ACAAG
                                TC CC GCC    TCGGGGAC
                                || || |||    ||||||||
                                AG GG CGG    AGTCCCTG
                                 C  C   CCG__
GAM3320  PALM      3'  TCCCAGCCACCCAGGG      74658     A       AAG
                                TC CCAGCCAC   TCGGGG
                                || ||||||||   ||||||
                                AG GGTCGGTG   GGTCCC
                                  _      ____
GAM3320  PINK1     3'  TCACCAGCTCCATGCAGGGAC  74659         CA  A T
                                TCACCAGC  CA G CGGGGAC
                                ||||||||  || | |||||||
                                AGTGGTCG  GT C GTCCCTG
                                     AG  A _
GAM3320  RAB40B    3'  CCACCAGCTGCCGGGG      74660         CACAA
                                TCACCAGC    GTCGGGG
                                ||||||||    |||||||
                                GGTGGTCG    CGGCCCC
                                     A_____
GAM3320  RNF20     3'  TCACCAGCTCAGTCCTGAC   74661         CACA    GGG
                                TCACCAGC   AGTC   GAC
                                ||||||||   ||||   |||
                                AGTGGTCG   TCAG   CTG
                                     AG__    GA_
GAM3320  SDS3      3'  TCATAGCAGTCGGGGA      74662     CC   CACA
                                TCA  AGC   AGTCGGGGA
                                |||  |||   |||||||||
                                AGT  TCG   TCAGCCCCT
                                  A_  _____
GAM3320  SEMA4G    5'  TCCCAGCCACAGTAGGGG    74663     A       A  C
                                TC CCAGCCACA GT GGGG
                                || |||||||| || ||||
                                AG GGTCGGTGT CA CCCC
                                  _       _ T
GAM3320  TRAP95    3'  TCGCCAACCACGGGGGA     74664     A       AAGTC
                                TC CCAGCCAC    GGGGA
                                || ||||||||    |||||
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                                AG GGTTGGTG    CCCCT
                                 C      C____
GAM3320  UBP1     5'  TCACCAGCGGCGCCCGGGAC  74665       CACAA  G
                                TCACCAGC    GTC GGGAC
                                ||||||||    ||| |||||
                                AGTGGTCG    CGG CCCTG
                                    CCG__   G
GAM3320  ZNF297B  3'  ACCAGCCACAGAGAAGAC    74666        A TC
                                ACCAGCCACA G  GGGGAC
                                |||||||||| |  ||||||
                                TGGTCGGTGT C  CTTCTG
                                      _ T_
GAM3320  ZNF297B  3'  ACCAGCCACAGAGAAGAC    74666        A TC
                                ACCAGCCACA G  GGGGAC
                                |||||||||| |  ||||||
                                TGGTCGGTGT C  CTTCTG
                                      _ T_
GAM3320  LOC113444 3'  TCACCACCCACAGTAGGAC   74667      G    A  CG
                                TCACCA CCACA GT  GGGAC
                                |||||| ||||| ||  |||||
                                AGTGGT GGTGT CA  TCCTG
                                   G    _ __
GAM3320  LOC113523 3'  ACCAGCCACAAAAGAGG     74668          TC
                                ACCAGCCACAAG  GGGG
                                ||||||||||||  ||||
                                TGGTCGGTGTTT  CTCC
                                      T_
GAM3320  LOC118611 5'  CCATTGGCCAGAGCCGGGG   74669    ___   CA
                                CCA   GCCA  AGTCGGGG
                                |||   ||||  ||||||||
                                GGT   CGGT  TCGGCCCC
                                  AAC   C_
GAM3320  LOC118851 5'  TCACCAGGCACAAATCTGG   74670      C      G
                                TCACCAG CACAAGTC GG
                                ||||||| |||||||| ||
                                AGTGGTC GTGTTTAG CC
                                    C       A
GAM3320  LOC123876 5'  TCACCAGCCACCACTCAGG   74671         AAG
                                TCACCAGCCAC   TCGGG
                                ||||||||||   |||||
                                AGTGGTCGGTG   AGTCC
                                      GTG
GAM3320  LOC137075 5'  TCACCAGCCGCCAGCCGGG   74672       ACA
                                TCACCAGCC   AGTCGGG
                                |||||||||   |||||||
                                AGTGGTCGG   TCGGCCC
                                     CGG
GAM3320  LOC144058 5'  TCAGTGGCTCCATCGGGGAC  74673    CCA  CA  AG
                                TCA   GC  CA  TCGGGGAC
                                |||   ||  ||  ||||||||
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                                AGT  CG  GT  AGCCCCTG
                                  CAC  AG  __
GAM3320  LOC144603 3'  TCACCAGTCAAGAGGCTGGGG  74639       C  CAA_  C
                                TCACCAG CA   GT GGGG
                                ||||||| ||   || ||||
                                AGTGGTC GT   CG CCCC
                                    A  TCTC  A
GAM3320  LOC144742 5'  TCACCAGGTTGCAATCAAGG  74674       CCACA
                                TCACCAG   AGTCGGGG
                                |||||||   ||||||||
                                AGTGGTC   TTAGTTCC
                                    CAACG
GAM3320  LOC145717 5'  CACCGGCTACAAGCCGCCCGGG 74675     A  C    ____
            G                    CACC GC ACAAGT   CGGGG
                                |||| || ||||||   |||||
                                GTGG CG TGTTCG   GCCCC
                                  C  A    GCGG
GAM3320  LOC146669 5'  TCACCAGCAGCAGGTTGGG   74676       CA  A  C
                                TCACCAGC  CA GT GGG
                                ||||||||  || || |||
                                AGTGGTCG  GT CA CCC
                                     TC  C  A
GAM3320  LOC148166 5'  CCACCAGCCACGCACGAGG   74677         AAGT
                                TCACCAGCCAC   CGGGG
                                ||||||||||   |||||
                                GGTGGTCGGTG   GCTCC
                                      CGT_
GAM3320  LOC149566 3'  TCACCTGGCTGTCAGGGA   74678      A_  CACAA
                                TCACC  GC   GTCGGGGA
                                |||||  ||   ||||||||
                                AGTGG  CG   CAGTCCCT
                                  AC  A____
GAM3320  LOC149685 5'  TCACCAGCGGCATCAAAGGG  74679       CACAA  __
                                TCACCAGC   GTC  GGGG
                                |||||||   |||  ||||
                                AGTGGTCG   TAG  TCCC
                                    CCG__  TT
GAM3320  LOC150622 3'  TCACCAGCCCAGCCTTGAC   74680       A  A  GGG
                                TCACCAGCC CA GTC  GAC
                                ||||||||| || |||  |||
                                AGTGGTCGG GT CGG  CTG
                                     _ _  AA_
GAM3320  LOC151877 3'  TCATTAGCCATCAGGGA    74681    CC   CAAG
                                TCA  AGCCA   TCGGGGA
                                |||  |||||   |||||||
                                AGT  TCGGT   AGTCCCT
                                  AA   ____
GAM3320  LOC153277 3'  TCACCAGCTACCAAGTTGGA  74682       CA_   C
                                TCACCAGC  CAAGT GGG
                                ||||||||  ||||| |||
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                                AGTGGTCG   GTTCA CCT
                                    ATG    A
GAM3320  LOC155006 3'  CCATTAGCCACAAATTGG    74683     CC        C
                                TCA  AGCCACAAGT GG
                                |||  |||||||||| ||
                                GGT  TCGGTGTTTA CC
                                  AA         A
GAM3320  LOC157860 3'  TCACAGCCACAAGGAAAAGG   74684      C        TC_
                                TCAC AGCCACAAG   GGGG
                                |||| |||||||||   ||||
                                AGTG TCGGTGTTC   TTCC
                                  _        CTT
GAM3320  LOC158055 3'  TCACCAGCCGCCGGCCCAGCTG 74685       ACA_____   C     III
            GGGACG                  CAGCC       AGT GGGGAC   G
                                |||||       ||| ||||||   |
                                GTCGG       TCG CCCCTG   C
                                   CGGCCGGG   A     III
GAM3320  LOC164397 5'  TCATCAGCCACACGGG      74686     C       AGT
                                TCA CAGCCACA   CGGG
                                ||| ||||||||   ||||
                                AGT GTCGGTGT   GCCC
                                  A       ___
GAM3320  LOC196812 3'  TCACCAGCAGCAGGCCAAA    74687         CA  A
                                TCACCAGC  CA GTCGGG
                                ||||||||  || ||||||
                                AGTGGTCG  GT CGGTTT
                                     TC  C
GAM3320  LOC197350 5'  TCAGCAGCTGCACCAGGGAC   74688     C    CA  AG
                                TCA CAGC  CA  TCGGGGAC
                                ||| ||||  ||  ||||||||
                                AGT GTCG  GT  GGTCCCTG
                                  C    AC  __
GAM3320  LOC200093 3'  TCCCAGCCACCTCGGGG     74622     A       AAG
                                TC CCAGCCAC   TCGGGG
                                || ||||||||   ||||||
                                AG GGTCGGTG   AGCCCC
                                 _       G__
GAM3320  LOC203052 3'  CCAGCCACGTCCATAGGGG    74689         AA  _____
                                CCAGCCAC  GTC    GGGG
                                ||||||||  |||    ||||
                                GGTCGGTG  CAG    CCCC
                                     __   GTAT
GAM3320  LOC203221 5'  TCACCAGCAGTGGGCGA     74690         CACA   C  _
                                TCACCAGC    AGT GGG GA
                                ||||||||    ||| ||| ||
                                AGTGGTCG    TCA CCC CT
                                     _____   _   G
GAM3320  LOC219722 3'  TCACCAGCTGTAATGAGCGGA  74691         CACA   C  _
                                TCACCAGC    AGT GG GGA
                                ||||||||    ||| || |||
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                                AGTGGTCG    TTA TC CCT
                                     ACA_   C  G
GAM3320  LOC220522 3'  CCACCAGCCGTGCGGA      74692          ACAA  _
                                TCACCAGCC    GT CGGG
                                |||||||||    || ||||
                                GGTGGTCGG    CA GCCT
                                     _____  C
GAM3320  LOC245727 5'  CACCGGCTACAAGCCGCCCGGG 74675      A  C     _____
              G                    CACC GC ACAAGT    CGGGG
                                |||| || ||||||    |||||
                                GTGG CG TGTTCG    GCCCC
                                  C  A     GCGG
GAM3320  LOC254532 3'  TCACCAGCCACAGACACTGGG  74693           AG CG_
                                TCACCAGCCACA  T   GGG
                                ||||||||||||  |   |||
                                AGTGGTCGGTGT  G   CCC
                                       CT TGA
GAM3320  LOC257426 3'  TCATAGCCACAAGCACAGAC   74695     CC        T  G
                                TCA  AGCCACAAG CG GGAC
                                |||  ||||||||| || ||||
                                AGT  TCGGTGTTC GT TCTG
                                  A_         _  G
GAM3320  LOC257426 3'  TCATCAGCCAGGGCAGTGGGG  74694     C     CA__   C
                                TCA CAGCCA    AGT GGGG
                                ||| ||||||    ||| ||||
                                AGT GTCGGT    TCA CCCC
                                  A     CCCG  _
GAM3320  LOC90249  3'  CACCAGCCAGCCCTGGGGAC   74696         CAA   __
                                CACCAGCCA   GTC  GGGGAC
                                |||||||||   |||  ||||||
                                GTGGTCGGT   CGG  CCCCTG
                                     ___   GA
GAM3320  LOC90637  5'  TCACCTGGCTCTCGTCGGGGAC 74697      A_  CACAA
                                TCACC  GC    GTCGGGGAC
                                |||||  ||    |||||||||
                                AGTGG  CG    CAGCCCCTG
                                   AC  AGAG_
GAM3320  LOC90841  5'  CCAGCCACAGCCATCTGGAC   74698         A   GG__
                                CCAGCCACA GTC    GGAC
                                ||||||||| |||    ||||
                                GGTCGGTGT CGG    CCTG
                                     _   TAGA
GAM3320  LOC91040  3'  TCCCAGCCACCTCGGGGAC    74699    A       AAG
                                TC CCAGCCAC   TCGGGGAC
                                || ||||||||   ||||||||
                                AG GGTCGGTG   AGCCCCTG
                                  _       G__
GAM3320  LOC91097  3'  TCACCAGCTCACAGGA       74638          _   AGTCGG
                                TCACCAGC CACA     GGA
                                |||||||| ||||     |||
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                                AGTGGTCG GTGT     CCT
                                   A   _______
GAM3320  LOC91156  5'  TCACCAGCTACAAAGG      74700        C    GTC
                                TCACCAGC ACAA   GGG
                                |||||||| ||||   |||
                                AGTGGTCG TGTT   TCC
                                   A   ___
GAM3321  ATM       5'  TATATTACCTTATTTCCAAA   74703         CACAGAA
                                TATATTACC      TTCCAAA
                                |||||||||      |||||||
                                ATATAATGG      AAGGTTT
                                   AATA___
GAM3321  ATM       5'  TATATTACCTTATTTCCAAA   74703         CACAGAA
                                TATATTACC      TTCCAAA
                                |||||||||      |||||||
                                ATATAATGG      AAGGTTT
                                   AATA___
GAM3321  GNAT2     3'  ATTACCCAGATTCCAA      74704         CA  A
                                ATTACCCA  GA TTCCAA
                                ||||||||  || ||||||
                                TAATGGGT  CT AAGGTT
                                   __  _
GAM3321  UBQLN1    3'  TTATAACAGCACAGAATTCCAA 74705       TTACC
                                TTATA     CACAGAATTCCAA
                                |||||     ||||||||||||||
                                AATAT     GTGTCTTAAGGTT
                                   TGTC_
GAM3321  YWHAH     3'  TTATTTACCCATTGAATTCCAA 74706      A      CA
            A                    TTAT TTACCCA  GAATTCCAAA
                                |||| |||||||  ||||||||||
                                AATA AATGGGT  CTTAAGGTTT
                                  _      AA
GAM3321  ZNF8      3'  TTATATTACCTGTGAACTC    74707          CACA
                                TTATATTACC    GAATTC
                                ||||||||||    ||||||
                                AATATAATGG    CTTGAG
                                   ACA_
GAM3321  ARHGAP5   5'  CATTACAATCACAGAATTCCA  74708       C__
                                TATTAC   CACAGAATTCCA
                                ||||||   ||||||||||||
                                GTAATG   GTGTCTTAAGGT
                                   TTA
GAM3321  FLJ20303  3'  TTATTTTACCCTTTATTCCAAA 74709      A     ACAGA
                                TTAT TTACCC     ATTCCAAA
                                |||| ||||||    ||||||||
                                AATA AATGGG     TAAGGTTT
                                  A     AAA__
GAM3321  FLJ23091  3'  TTATATTATGCCACAAAAC    74710         C_
                                TTATATTA  CCACAGAAT
                                ||||||||  |||||||||
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                                AATATAAT  GGTGTTTTG
                                    AC
GAM3321  KIAA0626  3'  TTATATTACAAAATTCCAA   74711       ACCC
                                TTATATT   ACAGAATTCCAA
                                |||||||   ||||||||||||
                                AATATAA   TGTTTTAAGGTT
                                    ____
GAM3321  KIAA1946  3'  TATATTACTTACAAAACT    74712       CC
                                TATATTAC  ACAGAATT
                                ||||||||  ||||||||
                                ATATAATG  TGTTTTGA
                                    AA
GAM3321  MEGF10    3'  TCATATTATCCCTACAATTC  74713        _  _  GA
                                TTATATTA CCC ACA  ATTC
                                |||||||| ||| |||  ||||
                                AGTATAAT GGG TGT  TAAG
                                    A  A  __
GAM3321  MGC4473   3'  TATTATCCCACAGAGTTC    74714      _      A
                                TATTA CCCACAGA TTC
                                ||||| |||||||| |||
                                ATAAT GGGTGTCT AAG
                                   A       C
GAM3321  LOC140219 5'  TTATATCATCCACAATTTCC  74715        C     AA
                                TTATATTA CCACAG  TTCC
                                |||||||| ||||||  ||||
                                AATATAGT GGTGTT  AAGG
                                    A     A_
GAM3322  KIAA1671  3'  AATAACATAGGCCAACGA    74718        TAATTCTA
                                AATAACAT       CCAACGA
                                ||||||||       |||||||
                                TTATTGTA       GGTTGCT
                                    TCC_____
GAM3323  GABPA     3'  GAAGATTCAAATTCAGTAATA  74721      CTC       A
                                GAAGA   CAGATTCA TAATA
                                |||||   |||||||| |||||
                                CTTCT   GTTTAAGT ATTAT
                                   AA_       C
GAM3323  KIF3B     3'  ATGAAGCTCTGAATCTCAATAA 74722       A  CA  _
            TA                   ATGAAG CTC  GAT TCAATAATA
                                ||||||  |||  |||  |||||||||
                                TACTTC GAG  TTA AGTTATTAT
                                   _  AC  G
GAM3323  PCTP      3'  TGAAGACTTCCCCTCCTAATA  74723        _  AGA  _
                                TGAAGACT CC   TTC AATA
                                |||||||| ||   ||| ||||
                                ACTTCTGA GG   AGG TTAT
                                    A  GG_  A
GAM3323  TNS       3'  ATAAGGACTCCAGGTTTC    74724      A       A_
                                ATGA GACTCCAG  TTC
                                |||| ||||||||  |||
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                                TATT CTGAGGTC  AAG
                                  C       CA
GAM3323  DKFZp434G118 3'  ATGAAGACTTAGGACAAT    74725         CC  ATT
                                ATGAAGACT  AG   CAAT
                                |||||||||  ||   ||||
                                TACTTCTGA  TC   GTTA
                                     A_  CT_
GAM3323  DKFZP434I092 3'  TGAAGTAACTGGATTCAATAAT 74726       __   CCA
                                TGAAG  ACT   GATTCAATAAT
                                |||||  |||   ||||||||||||
                                ACTTC  TGA   CTAAGTTATTA
                                   AT   C__
GAM3323  DKFZp564I1922 3'  GAAGACTCTAGATTCAAT    74727         C
                                GAAGACTC AGATTCAAT
                                |||||||| |||||||||
                                CTTCTGAG TCTAAGTTA
                                     A
GAM3323  DMTF1    3'  TGAAGATCTAATTACAATAATA 74728       C  CA   _
                                TGAAGA TC  GATT CAATAATA
                                |||||| ||  |||| ||||||||
                                ACTTCT AG  TTAA GTTATTAT
                                   _ A_   T
GAM3323  KIAA0441  3'  ATGAAAACCATTCAATAAT   74729         CCAG
                                ATGAAGACT   ATTCAATAAT
                                |||||||||   ||||||||||
                                TACTTTTGG   TAAGTTATTA
                                     ____
GAM3323  KIAA1163  3'  ATGGGGACTACAGATTCA    74730     AA   C
                                ATG  GACT CAGATTCA
                                |||  |||| ||||||||
                                TAC  CTGA GTCTAAGT
                                  CC   T
GAM3323  MGC4309   3'  TGAAGACTCTGAGGTTCA    74731         C_  A
                                TGAAGACTC  AG TTCA
                                |||||||||  || ||||
                                ACTTCTGAG  TC AAGT
                                     AC  C
GAM3323  TUBGCP3   3'  ATGAAGACTTTTAGAGACAA  74732         CC_   TT
                                ATGAAGACT   AGA  CAA
                                |||||||||   |||  |||
                                TACTTCTGA   TCT  GTT
                                     AAA   CT
GAM3324  CDCA4    3'  ATCACTGATATTTAAGAA    74735       CC
                                GTTATT  GATATTTAAGAA
                                ||||||  ||||||||||||
                                TAGTGA  CTATAAATTCTT
                                     __
GAM3324  COL12A1   3'  GTTATTCCGGCATAGA      74736         A   TTA
                                GTTATTCCG TAT   AGA
                                ||||||||| |||   |||
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                                CAATAAGGC GTA   TCT
                                     C  ___
GAM3324 COL12A1  3' GTTATTCCGGCATAGA     74736        A   TTA
                                GTTATTCCG TAT   AGA
                                ||||||||| |||   |||
                                CAATAAGGC GTA   TCT
                                     C  ___
GAM3324 LAMP3    3' TGAATTATTCCTTGACTAAGAA 74737   A       GATAT
                                A AGTTATTCC    TTAAGAA
                                | |||||||||    |||||||
                                A TTAATAAGG    GATTCTT
                                 C       AACT_
GAM3324 MADHIP   3' TAAAGTTATGACATTTGAGAA  74738        TCC      A
                                TAAAGTTAT   GATATTT AGAA
                                |||||||||   ||||||| ||||
                                ATTTCAATA   CTGTAAA TCTT
                                     ___      C
GAM3324 PDP      3' AGTTATTCCACTTAAGAA    74739        GAT
                                AGTTATTCC   ATTTAAGAA
                                |||||||||   |||||||||
                                TCAATAAGG   TGAATTCTT
                                     ___
GAM3324 LOC157663 3' AGTTATTCCACTTAAGAA    74739        GAT
                                AGTTATTCC   ATTTAAGAA
                                |||||||||   |||||||||
                                TCAATAAGG   TGAATTCTT
                                     ___
GAM3325 ARHG     3' ACAAGGCACCAAGGCACAACTG 74742      T   A   A_
                                ACAAG GTA CAA  CACAACTG
                                ||||| ||| |||  ||||||||
                                TGTTC CGT GTT  GTGTTGAC
                                   _  G   CC
GAM3325 CRMP1    3' AGCATGAACACAACTG      74743      AACA
                                AGTGT    AACACAACTG
                                |||||    ||||||||||
                                TCGTA    TTGTGTTGAC
                                   C___
GAM3325 NUP62    3' TAACAAATGTGACAGGGACCGG 74744         A   A__  ACAA
             GCTG                  TAACAAGTGT ACA   AC    CTG
                                |||||||||| |||   ||    |||
                                ATTGTTTACA TGT   TG    GAC
                                     C   CCC  GCCC
GAM3325 TSN      3' CAACAAGCCAGCAACAAACACA 74745        __
             ACTG                  TAACAAGT  GTAACAAACACAACTG
                                ||||||||  ||||||||||||||||
                                GTTGTTCG  CGTTGTTTGTGTTGAC
                                     GT
GAM3325 ASAH     3' AGTGTCAGGAACACAACTG   74746      AACA
                                AGTGT    AACACAACTG
                                |||||    ||||||||||
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                                TCACA    TTGTGTTGAC
                                   GTCC
GAM3325  FLJ12700  3'  TAACAAGTGAGGGGTGCAACTG 74747          TAACAAACA
                                TAACAAGTG        CAACTG
                                |||||||||        ||||||
                                ATTGTTCAC        GTTGAC
                                     TCCCCAC__
GAM3325  FLJ12903  3'  AATGACATTAAACACAACTG   74748      TAAC_
                                AGTG    AAACACAACTG
                                ||||    ||||||||||
                                TTAC    TTTGTGTTGAC
                                  TGTAA
GAM3325  FLJ13490  3'  TAACAAGTGTAGTAAAAACGAA 74749          AC__    AC_
            AACTG                  TAACAAGTGTA    AAAC   AACTG
                                |||||||||||    ||||   |||||
                                ATTGTTCACAT    TTTG   TTGAC
                                       CATT    CTT
GAM3325  FLJ20147  3'  AAGTGTAATAAATACAAC    74750        C   C
                                AAGTGTAA AAA ACAAC
                                |||||||| ||| |||||
                                TTCACATT TTT TGTTG
                                     A   A
GAM3325  FLJ20487  3'  AATGAGCAAGCACAACTG    74751      TAA   A
                                AGTG   CAA CACAACTG
                                ||||   ||| ||||||||
                                TTAC   GTT GTGTTGAC
                                  TC_   C
GAM3325  FLJ23506  3'  TAAAAAGTGCAACACAGCT   74752     C      ACAA     A
                                TAA AAGTGTA    ACACA CT
                                ||| |||||||    ||||| ||
                                ATT TTCACGT    TGTGT GA
                                  T      _____     C
GAM3325  GOLPH3    3'  TAACAAGTGTAATAATACAA   74753          CAAAC
                                TAACAAGTGTAA     ACAA
                                ||||||||||||     ||||
                                ATTGTTCACATT     TGTT
                                       ATTA_
GAM3325  KIAA0495  3'  TAACAAGTGAAACAGGCAACTG 74754          T    AACA
                                TAACAAGTG AACA    CAACTG
                                ||||||||| ||||    ||||||
                                ATTGTTCAC TTGT    GTTGAC
                                     T    CC__
GAM3325  KIAA1957  3'  CATTTATAAACAAACACAGCTG 74755    AG    _      A
                                CA  TGTAA CAAACACA CTG
                                ||  ||||| |||||||| |||
                                GT  ATATT GTTTGTGT GAC
                                 AA    T       C
GAM3325  MRPL35    3'  ACAAGTGTTATGAACACAA    74756        AACA
                                ACAAGTGT    AACACAA
                                ||||||||    |||||||
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                                TGTTCACA    TTGTGTT
                                    ATAC
GAM3325  LOC143524 3'  AGTGCCAATAACACAACTG    74757      AACA
                                AGTGT    AACACAACTG
                                |||||    ||||||||||
                                TCACG    TTGTGTTGAC
                                   GTTA
GAM3325  LOC144559 5'  AGTGCCAATAACACAACTG    74757      AACA
                                AGTGT    AACACAACTG
                                |||||    ||||||||||
                                TCACG    TTGTGTTGAC
                                   GTTA
GAM3325  LOC149506 3'  ACAGGCCCAAAACACAACTG   74758     A  G   CA
                                ACA GT TAA  AACACAACTG
                                ||| || |||  ||||||||||
                                TGT CG GTT  TTGTGTTGAC
                                  C  G  __
GAM3325  LOC151031 3'  TAAGGAGTGTAACAACTCAGCT 74759     CA        ACA  A
             G                   TAA  AGTGTAACAA   CA CTG
                                |||  ||||||||||   || |||
                                ATT  TCACATTGTT   GT GAC
                                  CC        GA_  C
GAM3325  LOC152742 3'  GTGAAGCCAAAAACACAACTG  74760     TAA_  __
                                GTG    CAA  ACACAACTG
                                |||    |||  |||||||||
                                CAC    GTT  TGTGTTGAC
                                  TTCG   TT
GAM3325  LOC219918 5'  AGTGCCAATAACACAACTG    74757      AACA
                                AGTGT    AACACAACTG
                                |||||    ||||||||||
                                TCACG    TTGTGTTGAC
                                   GTTA
GAM3325  LOC220071 5'  AGTGCCAACAACACAACTG    74761      _    A
                                AGTGT AACAA CACAACTG
                                ||||| ||||| ||||||||
                                TCACG TTGTT GTGTTGAC
                                   G    _
GAM3325  LOC221463 3'  AATGCTTCGATAAACACAACTG 74762      AAC___
                                AGTGT     AAACACAACTG
                                |||||     ||||||||||
                                TTACG     TTTGTGTTGAC
                                   AAGCTA
GAM3325  LOC254532 5'  CAGGTGTAACAAAAGCAGCT   74763    A        CA  A
                                CA GTGTAACAAA  CA CT
                                || ||||||||||  || ||
                                GT CACATTGTTT  GT GA
                                 C         TC  C
GAM3325  LOC255515 3'  AGTGCCAATAACACAACTG    74757      AACA
                                AGTGT    AACACAACTG
                                |||||    ||||||||||
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                                TCACG   TTGTGTTGAC
                                  GTTA
GAM3325 LOC90906 3' AGTGCCAATAACACAACTG   74757      AACA
                                AGTGT   AACACAACTG
                                |||||   ||||||||||
                                TCACG   TTGTGTTGAC
                                  GTTA
GAM3326 GABPB1   3' TGGCTGTACCTTTGTTGT    74766     TGTTA       A
                                TGGT    TGTGCCTTT TTGT
                                ||||    ||||||||| ||||
                                ACCG    ACATGGAAA AACA
                                  _____       C
GAM3326 PTD002   3' TGGTTGTTATTTGTCTAAGAAG 74767         G  C  TTATT
           T                     TGGTTGTTAT TG CT    GT
                                ||||||||||  || ||    ||
                                ACCAACAATA AC GA    CA
                                      A  A  TTCTT
GAM3327 ATP11A   3' TGGTATGTGTACACGTGCATG  74770    A     C  _
                                TG TATGTG AC CGTGTGTG
                                || ||||||  || ||||||||
                                AC ATACAC TG GCACGTAC
                                 C     A  T
GAM3327 ATP8B2   3' TGATATGTGTGTGTGT      74771         CACC
                                TGATATGTG   GTGTGT
                                |||||||||   ||||||
                                ACTATACAC   CACACA
                                     A___
GAM3327 KCNJ1    5' TGATAGTGGAGTCGTGTGATTT 74772      T   CACCG
                                TGATA GTG    TGTGTGATTT
                                ||||| |||    ||||||||||
                                ACTAT CAC    GCACACTAAA
                                  _  CTCA_
GAM3327 NAPB     3' TGATATGTGTGTGTGTG     74773        CACC
                                TGATATGTG   GTGTGTG
                                |||||||||   |||||||
                                ACTATACAC   CACACAC
                                     A___
GAM3327 PATE     3' TGTGTGTGTGTGTGATTT    74774      CACC
                                TGTG   GTGTGTGATTT
                                ||||   ||||||||||
                                ACAC   CACACACTAAA
                                  ACA_
GAM3327 SVIL     3' TGACATGTGTACTGTTTGT   74775        C  C  G
                                TGATATGTG AC GT TGT
                                ||||||||| || || |||
                                ACTGTACAC TG CA ACA
                                     A  A  A
GAM3327 SVIL     3' TGACATGTGTACTGTTTGT   74775        C  C  G
                                TGATATGTG AC GT TGT
                                ||||||||| || || |||
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                                ACTGTACAC TG CA ACA
                                     A  A  A
GAM3327  C11orf25  3'  TGTATGTGTGCATATGTGTGAT 74776    _ A     CC
              TT                  TG AT TGTGCA  GTGTGTGATTT
                                  || || ||||||  ||||||||||
                                  AC TA ACACGT  TACACACTAAA
                                   A  C     A_
GAM3327  FLJ13373  5'  TGATATGTTTATCATAATTGAT 74777        GCAC    TG
              TT                  TGATATGT    CGTG  TGATTT
                                  ||||||||    ||||  ||||||
                                  ACTATACA    GTAT  ACTAAA
                                      AATA    TA
GAM3327  SR-BP1    3'  TGATATGTGTGTGTGTG     74773         CACC
                                  TGATATGTG    GTGTGTG
                                  |||||||||    |||||||
                                  ACTATACAC    CACACAC
                                       A___
GAM3327  LOC197287 5'  TGGTATGTGTACACGTGCATG  74770    A     C  _
                                  TG TATGTG AC CGTGTGTG
                                  || |||||| || ||||||||
                                  AC ATACAC TG GCACGTAC
                                   C     A  T
GAM3327  LOC222159 5'  TGATATGTGCATTGAGATT    74778          CCGTG  T
                                  TGATATGTGCA     TG GATT
                                  ||||||||||     || ||||
                                  ACTATACACGT     AC CTAA
                                        A_____  T
GAM3328  COMT      5'  TGCAGGATGAACTCGTTC     74781    A  A  CC
                                  TG CA GA  GGATTCGTTC
                                  || || ||  ||||||||||
                                  AC GT CT  CTTGAGCAAG
                                   _  C  A_
GAM3328  PTGFR     3'  TGACAAGAATGGGCCCATTC   74782        CC  AT
                                  TGACAAGA  GG  TCGTTC
                                  ||||||||  ||  ||||||
                                  ACTGTTCT  CC  GGTAAG
                                       TA  CG
GAM3328  WHSC1     3'  TGACAGACCCAGCACTTGTTC  74783      A   _ _   C
                                  TGACA GACC GG ATT GTTC
                                  ||||| |||| || ||| ||||
                                  ACTGT CTGG TC TGA CAAG
                                     _   G  G   A
GAM3328  CHUK      3'  TGACAAGACATGAAAGATTGTT 74784         C_____    C
                                  TGACAAGAC     GGATT GTT
                                  |||||||||     ||||| |||
                                  ACTGTTCTG     TCTAA CAA
                                        TACTT    _
GAM3328  DDX31     3'  TGACAAGAACTGGACATC     74785         _ C   _
                                  TGACAAGA C GGAT TC
                                  |||||||| | |||| ||
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                                ACTGTTCT G CCTG AG
                                    T A   T
GAM3328 FLJ10813 3' TGACAAAATTGGAGACATT   74786       CC   TT
                                TGACAAGA  GGA  CGTT
                                ||||||||  |||  ||||
                                ACTGTTTT  CCT  GTAA
                                    AA   CT
GAM3328 FLJ12761 3' TGACAAGAACTAATAGTTC   74787       CCG   TC
                                TGACAAGA   GAT  GTTC
                                ||||||||   |||  ||||
                                ACTGTTCT   TTA  CAAG
                                    TGA   T_
GAM3328 KIAA1596 5' TGAGAGACCAGAGGCGTT    74788     CA      TT
                                TGA  AGACCGGA  CGTT
                                |||  ||||||||  ||||
                                ACT  TCTGGTCT  GCAA
                                  C_      CC
GAM3328 NIR3     3' TGACAAGCCGGACCCGTC    74789       A
                                TGACAAG CCGGATTCGTT
                                |||||||  ||||||||||
                                ACTGTTC GGCCTGGGCAG
                                   _
GAM3328 SDCCAG3   5' GACAAGACCGGCGCTC     74790         ATT
                                GACAAGACCGG   CGTTC
                                ||||||||||   |||||
                                CTGTTCTGGCC   GCGAG
                                     ___
GAM3328 SS18L1    3' TGACAAAATCAGAGGTTC    74791        C   TTC
                                TGACAAGA CGGA   GTTC
                                ||||||||  ||||   ||||
                                ACTGTTTT GTCT   CAAG
                                    A   C__
GAM3328 LOC132617 3' TGATAGACCAAATGTTC     74792     CA       TC
                                TGA  AGACCGGAT  GTTC
                                |||  |||||||||  ||||
                                ACT  TCTGGTTTA  CAAG
                                  A_       __
GAM3328 LOC139375 5' TAATGAGACCAAATACTGTTC  74793     CA       TC_
                                TGA  AGACCGGAT   GTTC
                                |||  |||||||||   ||||
                                ATT  TCTGGTTTA   CAAG
                                  AC        TGA
GAM3328 LOC148932 3' GACAAGACTCCAAAGTTC    74794        __    _
                                GACAAGA  CCGGA TTC
                                |||||||  ||||| |||
                                CTGTTCT  GGTTT AAG
                                    GA    C
GAM3328 LOC150282 5' TGGTCAGACTCAGAACGTTC  74795    ACA   _   TT
                                TG   AGAC CGGA  CGTTC
                                ||   |||| ||||  |||||
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                                AC   TCTG GTCT  GCAAG
                                 CAG    A    T_
GAM3328  LOC157226 5'  TGATGAAACCATATCCGTTC   74796     CA     G
                                TGA  AGACCG ATTCGTTC
                                |||  |||||| ||||||||
                                ACT  TTTGGT TAGGCAAG
                                  AC     A
GAM3328  LOC158373 5'  TGATGAAACCATATCCGTTC   74796     CA     G
                                TGA  AGACCG ATTCGTTC
                                |||  |||||| ||||||||
                                ACT  TTTGGT TAGGCAAG
                                  AC     A
GAM3328  LOC165614 5'  GACAAGATCGGGTGCGTTC    74797        C   ATT
                                GACAAGA CGG   CGTTC
                                |||||||  |||   |||||
                                CTGTTCT GCC   GCAAG
                                     A   CAC
GAM3328  LOC199858 5'  TGATAAGACCAGTGAATTC    74798     C       ___
                                TGA AAGACCGG   ATTC
                                |||  ||||||||   ||||
                                ACT TTCTGGTC   TAAG
                                  A       ACT
GAM3329  GNRHR     5'  TTTTAGATATATCTGTATTA   74801       AT        T
                                TTTTA  TATATCTGT TTA
                                |||||  |||||||| |||
                                AAAAT  ATATAGACA AAT
                                   CT        T
GAM3329  BLZF1     3'  TATTTTAAATATATCTAT     74802         T
                                TATTTTAA TATATCTGT
                                ||||||||  |||||||||
                                ATAAAATT ATATAGATA
                                     T
GAM3329  KIAA0141  3'  TAATCCAATATCTGTTTTA    74803       __
                                TAATT  ATATCTGTTTTA
                                |||||  ||||||||||||
                                ATTAG  TATAGACAAAAT
                                   GT
GAM3329  LOC256940 5'  TTTAATTAGCTCTGTTTTA    74804         TA
                                TTTAATTA  TCTGTTTTA
                                ||||||||  |||||||||
                                AAATTAAT  AGACAAAAT
                                     CG
GAM3330  EPB41     5'  TCTGTTTTGAGTTCCGGTTCA  74807         ATAT   GAG
                                TCTGTTTT    AGT   GGTTCA
                                ||||||||    |||   ||||||
                                AGACAAAA    TCA   CCAAGT
                                     C___   AGG
GAM3330  GPR30     5'  TCTGTTTTAAATGGTGAATCCA 74808         T  A    GG
                                TCTGTTTTA AT GTGA  GTTCA
                                |||||||||  ||  ||||  |||||
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                                AGACAAAAT TA CACT  TAGGT
                                     T  C   __
GAM3330  PMCHL1   3'  TGTCTTATATGCTTTAGGTT  74809        A  GA_
                                TGTTTTATAT GT   GGGTT
                                |||||||||| ||   |||||
                                ACAGAATATA CG   TCCAA
                                      _  AAA
GAM3330  TRIM14   3'  TCAGTTTTATATGGTT     74810    T      AGTGAG
                                TC GTTTTATAT     GGTT
                                || |||||||||     ||||
                                AG CAAAATATA     CCAA
                                 T       _______
GAM3330  CARD14   3'  CCTGCACGTGGTGAGGGTTCA  74811      TTTATATA
                                TCTGT       GTGAGGGTTCA
                                |||||       ||||||||||
                                GGACG       CACTCCCAAGT
                                   TGCAC___
GAM3330  CHST3    3'  TCTGTTCTGTGGGGTT     74812        ATATA  A
                                TCTGTTTT    GTG GGGTT
                                ||||||||    ||| |||||
                                AGACAAGA    CAC CCCAA
                                      _____  _
GAM3330  KIAA0972 3'  TCTGATTCACAGTGAGGGTT  74813     TTTTA
                                TCTG    TATAGTGAGGGTT
                                ||||    ||||||||||||
                                AGAC    GTGTCACTCCCAA
                                  TAA__
GAM3330  PBEF     3'  TCTGTTTTATGTGATCATC   74814        ATA   GG
                                TCTGTTTTAT   GTGA  GTT
                                ||||||||||   ||||  |||
                                AGACAAAATA   CACT  TAG
                                      ___   AG
GAM3330  LOC148293 5'  TCTGTTTTATAAAGAAGCAAGT 74815          T  TGA_
            T                   TCTGTTTTATA AG    GGGTT
                                |||||||||| ||    |||||
                                AGACAAAATAT TC    TTCAA
                                      T  TTCG
GAM3330  LOC254672 3'  TGTCTTATATGTTTTAGGTT   74816        A  GA_
                                TGTTTTATAT GT   GGGTT
                                |||||||||| ||   |||||
                                ACAGAATATA CA   TCCAA
                                      _  AAA
GAM3330  LOC90049  3'  TCTGTTTTATAAAGAAGCAAGT 74815          T  TGA_
            T                   TCTGTTTTATA AG    GGGTT
                                |||||||||| ||    |||||
                                AGACAAAATAT TC    TTCAA
                                      T  TTCG
GAM3331  A1BG     3'  TCCTGGGAGGAATGAGGGA   74819     G    A  CG
                                TCC TGGGA GA  ATGGGGGA
                                ||| ||||| ||  ||||||||
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                                AGG ACCCT CT  TACTCCCT
                                  _    C  __
GAM3331  ABCC1    3'  TCCGTGGGAAGCACCAGGAAA  74820          A G  G
                                TCCGTGGGAAG C AT GGGGAA
                                |||||||||||  | ||  ||||||
                                AGGCACCCTTC G TG TCCTTT
                                      _ _  G
GAM3331  ABCC1    3'  TCCGTGGGAAGCACCAGGAAA  74820          A G  G
                                TCCGTGGGAAG C AT GGGGAA
                                |||||||||||  | ||  ||||||
                                AGGCACCCTTC G TG TCCTTT
                                      _ _  G
GAM3331  ABCC1    3'  TCCGTGGGAAGCACCAGGAAA  74820          A G  G
                                TCCGTGGGAAG C AT GGGGAA
                                |||||||||||  | ||  ||||||
                                AGGCACCCTTC G TG TCCTTT
                                      _ _  G
GAM3331  ATP1B2   3'  TGGGAAGGCGAATGGGGGAA  74821        A  _
                                TGGGAAG CGA TGGGGGAA
                                |||||||  |||  ||||||||
                                ACCCTTC GCT ACCCCCTT
                                    C   T
GAM3331  C18orf2  3'  TCCATGGGAAGGTGAAGGGAG  74822           AC  T
                                TCCGTGGGAAG  GA GGGGG
                                ||||||||||  ||  |||||
                                AGGTACCCTTC  CT CCCTC
                                      CA  T
GAM3331  CALCR    3'  TCCTGGGAGGATGGAGA     74823     G    AGAC
                                TCC TGGGA   GATGGGGG
                                |||  |||||   ||||||||
                                AGG ACCCT   CTACCTCT
                                  _    C___
GAM3331  CELSR2   3'  TCTTTGGGAAGGGAAAGGGGA  74824    CG      AC  T
                                TC  TGGGAAG  GA GGGGGA
                                ||  |||||||  ||  ||||||
                                AG  ACCCTTC  CT TCCCCT
                                 AA      C_  T
GAM3331  CLN5     3'  GTGGGAAGAGGGAGA       74825         CGAT
                                GTGGGAAGA   GGGGGA
                                |||||||||   ||||||
                                CACCCTTCT   CCCTCT
                                     _____
GAM3331  CUL4B    3'  GTGGGAAAAATGAGGGA     74826         CG
                                GTGGGAAGA  ATGGGGGA
                                |||||||||  ||||||||
                                CACCCTTTT  TACTCCCT
                                     __
GAM3331  DLG4     3'  GTGGGAGAGGATGGGGGA    74827       A  C
                                GTGGGA GA GATGGGGGA
                                ||||||  ||  |||||||||
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                                CACCCT CT CTACCCCCT
                                   _ C
GAM3331  DPP6    3'  TCCGAGGGAAGAGGGAG    74828     T     CGAT
                                TCCG GGGAAGA   GGGGG
                                |||| |||||||   |||||
                                AGGC CCCTTCT   CCCTC
                                  T     _____
GAM3331  EFNA3   3'  TCTCTGGGGGGACAAAGGGAGA 74829    CG   AA    T
                                TC  TGGG  GACGA GGGGGA
                                ||  ||||  ||||| ||||||
                                AG  ACCC  CTGTT CCCTCT
                                 AG   CC    T
GAM3331  FBXL11  3'  TCGGTGGGGAGTCAGGGGAA  74830    C    A  ACGA
                                TC GTGGG AG   TGGGGGAA
                                || ||||| ||   ||||||||
                                AG CACCC TC   GTCCCCTT
                                 C    C  A___
GAM3331  GATA3   5'  TCGGTGGGGGGATGGGAA    74831    C    AAGAC
                                TC GTGGG    GATGGGGG
                                || |||||    ||||||||
                                AG CACCC    CTACCCTT
                                 C    CC___
GAM3331  HAS3    3'  CGTGGGAGATGAAGGAA     74832       AGAC
                                CGTGGGA   GATGGGGGAA
                                |||||||   ||||||||||
                                GCACCCT   CTACTTCCTT
                                   _____
GAM3331  HOXB9   3'  GTTGGAAGGAGAGGGAAA    74833    G    AC  T
                                GT GGAAG  GA GGGGGAAA
                                || |||||  || ||||||||
                                CA CCTTC  CT CTCCCTTT
                                 A    __ _
GAM3331  JPH3    3'  TCCCTGGGGTCTGGTGGGGGAA 74834     G   AAGACGA
           A                     TCC TGGG      TGGGGGAAA
                                ||| ||||      |||||||||
                                AGG ACCC      ACCCCCTTT
                                  G   CAGACC_
GAM3331  LCP1    3'  TCCTGGGAGGCGGAGGGGGGAA 74835     G    AGAC  T
                                TCC TGGGA   GA GGGGGAA
                                ||| |||||   || |||||||
                                AGG ACCCT   CT CCCCCTT
                                  _    CCGC  C
GAM3331  MAPK4   3'  TCTTTGGGAGTGTTGGGGGAA  74836   CG    AGACGA
                                TC  TGGGA    TGGGGGAA
                                ||  |||||    ||||||||
                                AG  ACCCT    ACCCCCTT
                                 AA    CACA__
GAM3331  NPHP1   3'  TCCGTGGGAAGCTGAGGG    74837         ACGA
                                TCCGTGGGAAG   TGGGGG
                                ||||||||||   ||||||
```

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                                AGGCACCCTTC   ACTCCC
                                      G___
GAM3331  PAK1    5'  TCCGCGGGGGGGCAAGGGGGGA 74838        AAGA  T
                                TCCGTGGG   CGA GGGGGA
                                ||||||||   ||| ||||||
                                AGGCGCCC   GTT CCCCCT
                                     CCCC  C
GAM3331  PBX2    3'  GTGGGAAGAAGGGGGA     74839         CGAT
                                GTGGGAAGA   GGGGGA
                                |||||||||   ||||||
                                CACCCTTCT   CCCCCT
                                      T___
GAM3331  PEA15   3'  TCCTGGAGGATGGGGGAA   74840    G   AAGAC
                                TCC TGGG    GATGGGGGAA
                                ||| ||||    ||||||||||
                                AGG ACCT    CTACCCCCTT
                                  _   C____
GAM3331  PTGFRN  3'  GTGGGGGAGCAGGGGGAAA  74841     A_  ACGAT
                                GTGGG  AG    GGGGGAAA
                                |||||  ||    ||||||||
                                CACCC  TC    CCCCCTTT
                                   CC  GT___
GAM3331  STC1    3'  CGTGGGGAGAAAAGGGGGG   74842      A  C  T
                                CGTGGG AGA GA GGGGG
                                |||||| ||| || |||||
                                GCACCC TCT TT CCCCC
                                    C   T  C
GAM3331  TEM8    3'  GTGGGAGCCTGGGGGAA     74843      A ACGA
                                GTGGGA G    TGGGGGAA
                                |||||| |    ||||||||
                                CACCCT C    ACCCCCTT
                                   _ GG__
GAM3331  TFG     5'  CGTGGCAGGTGGGGGAA     74844      GA  ACGA
                                CGTGG  AG    TGGGGGAA
                                |||||  ||    ||||||||
                                GCACC  TC    ACCCCCTT
                                   G_  C___
GAM3331  TM6SF2  3'  TCCATGGGGGGATGATGGG   74845       AA  C
                                TCCGTGGG  GA GATGGG
                                ||||||||  || ||||||
                                AGGTACCC  CT CTACCC
                                     CC  A
GAM3331  YWHAB   5'  CCGTGGGAGGGCTGCAGGGAA  74847       AGACGA  _
                                CCGTGGGA     TG GGGGAA
                                ||||||||     || ||||||
                                GGCACCCT     AC TCCCTT
                                     CCCG__  G
GAM3331  YWHAB   5'  CCCGTGGGAGGGCTGCAGGGAA 74846        AGACGA  _
                                TCCGTGGGA     TG GGGGAA
                                |||||||||     || ||||||
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                                GGGCACCCT     AC TCCCTT
                                     CCCG__  G
GAM3331  CGB1     5'  TCCGTGGGGGAGTGAGACAGGG 74848        A_  AC_
              A                   TCCGTGGG  AG   GATGGGGG
                                  ||||||||  ||   ||||||||
                                  AGGCACCC  TC   CTGTCCCT
                                       CC  ACT
GAM3331  CGB2     5'  TCCGTGGGGGAGTGAGACAGGG 74848        A_  AC_
              A                   TCCGTGGG  AG   GATGGGGG
                                  ||||||||  ||   ||||||||
                                  AGGCACCC  TC   CTGTCCCT
                                       CC  ACT
GAM3331  CNNM1    3'  CCTGTGGGAGGCCTTGGGGGAA 74849    _     AGACGA
                                  CC GTGGGA     TGGGGGAA
                                  || ||||||     ||||||||
                                  GG CACCCT     ACCCCCTT
                                    A     CCGGA_
GAM3331  CYP2S1   3'  TCAGTGGGAAGATACTCTGGGG 74850    C        __ GA
              A                   TC GTGGGAAGA  C  TGGGGG
                                  || |||||||||  |  ||||||
                                  AG CACCCTTCT  G  ACCCCT
                                    T        AT AG
GAM3331  DPYSL4   3'  CCTGTGGGGAGGGGGA      74851    _    AAGAC  T
                                  CC GTGGG    GA GGGGGA
                                  || |||||    || ||||||
                                  GG CACCC    CT CCCCCT
                                    A   ______  _
GAM3331  DRF1     3'  TCCATGGGAGGGACTGCAGGGA 74852        A_   GAT_
              G                   TCCGTGGGA  GAC    GGGGG
                                  |||||||||  |||    |||||
                                  AGGTACCCT  CTG    CCCTC
                                       CC   ACGT
GAM3331  FKSG43   3'  TCCGGGGAAAGGGGGGGA    74853     T     ACGAT
                                  TCCG GGGAAG    GGGGGA
                                  |||| ||||||    ||||||
                                  AGGC CCCTTT    CCCCCT
                                    _     CC___
GAM3331  FLJ10110 3'  TCCTGGGAAAACAGGGGGAA   74854     G        AT
                                  TCC TGGGAAGACG  GGGGGAA
                                  ||| ||||||||||  |||||||
                                  AGG ACCCTTTTGT  CCCCCTT
                                    _        __
GAM3331  FLJ11539 5'  GTGGGAGGGAGTTGGGGGA   74855       A_  CGA
                                  GTGGGA  GA   TGGGGGA
                                  ||||||  ||   |||||||
                                  CACCCT  CT   ACCCCCT
                                     CC  CA_
GAM3331  FLJ12221 3'  TCCCTGGGTCAAGGTGGGGGAA 74856     G   AA  CGA
              A                   TCC TGGG  GA   TGGGGGAAA
                                  ||| ||||  ||   |||||||||
```

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                                AGG ACCC  TT   ACCCCCTTT
                                  G   AG  CC_
GAM3331  FLJ12547  3'  CGTGGGAAGATGAGG      74857         CGA
                                CGTGGGAAGA   TGGGG
                                ||||||||||  |||||
                                GCACCCTTCT   ACTCC
                                     ___
GAM3331  FLJ12650  3'  GTGGAGGGAGGTGGGGAAA   74858      AA  CGA
                                GTGGG  GA   TGGGGGAA
                                |||||  ||  ||||||||
                                CACCT  CT   ACCCCTTT
                                   CC  CC_
GAM3331  FLJ13046  5'  CGTGGGAACACGGTTATCAGG  74859        G  ___  G
                                CGTGGGAA ACG   AT GGG
                                |||||||| |||   || |||
                                GCACCCTT TGC   TA TCC
                                     G   CAA  G
GAM3331  FLJ13855  3'  CCTGTGGGAAATAATGGGGGAA 74860    _       AC
                                CC GTGGGAAG  GATGGGGGAA
                                || ||||||||  ||||||||||
                                GG CACCCTTT  TTACCCCCTT
                                 A       A_
GAM3331  FLJ20452  3'  GTGGGAGGAATAGGGAAA    74861       A  CG
                                GTGGGA GA  ATGGGGGAA
                                ||||||  ||  |||||||||
                                CACCCT CT  TATCCCTTT
                                   C  __
GAM3331  FLJ32658  5'  CATGGGGAGGGATGGGAAA   74862       A  AC     GG
                                CGTGGG AG  GATGGG  A
                                ||||||  ||  ||||||  |
                                GTACCC TC  CTACCC  T
                                   C  C_     TT
GAM3331  FLJ32919  5'  TCCGTGAGGGAGGCGGCAGG   74863       _  A  A  AT
                                TCCGTG GG AG CG  GGG
                                ||||||  ||  ||  ||  |||
                                AGGCAC CC TC GC  TCC
                                   T  C  C  CG
GAM3331  GBA2      5'  CCCGTGGGAAGGTGACCCTGGG 74864          AC   GG_
                                TCCGTGGGAAG  GAT   GGG
                                ||||||||||  |||   |||
                                GGGCACCCTTC  CTG   CCC
                                      CA   GGA
GAM3331  H11       3'  CCTGGGTGATGGGGGA     74865    G    AAGAC
                                CC TGGG    GATGGGGGA
                                || ||||    |||||||||
                                GG ACCC    CTACCCCCT
                                 _   A____
GAM3331  KIAA0212  3'  GTGGGGAGAAGGGGAAA     74866      A   CGAT
                                GTGGG AGA    GGGGGAAA
                                |||||  |||   ||||||||
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                                CACCC TCT    TCCCCTTT
                                  C  _____
GAM3331  KIAA1196  3'  TCCCTGGGGAATGGGGGA    74867     G    AAGAC
                                TCC TGGG    GATGGGGGA
                                ||| ||||    |||||||||
                                AGG ACCC    TTACCCCCT
                                  G   C_____
GAM3331  KIAA1300  3'  TCCTGGGAGGGAAAGGGAGA   74868     G    A_  CGAT
                                TCC TGGGA  GA   GGGGGA
                                ||| |||||  ||   ||||||
                                AGG ACCCT  CT   CCCTCT
                                  _    CC  TT__
GAM3331  KIAA1718  3'  GTGGGAAGGTAGGGGAA    74869        ACGA
                                GTGGGAAG   TGGGGGAA
                                ||||||||   ||||||||
                                CACCCTTC   ATCCCCTT
                                     C___
GAM3331  KIAA1754  3'  TCCTGGGGATGGGGGA     74870     G    AAGAC
                                TCC TGGG    GATGGGGGA
                                ||| ||||    |||||||||
                                AGG ACCC    CTACCCCCT
                                  _   _____
GAM3331  MGC10960  3'  TCCTGGGGAGATGGAGG     74871     G    AA  C
                                TCC TGGG  GA GATGGGGG
                                ||| ||||  || ||||||||
                                AGG ACCC  CT CTACCTCC
                                  _   __ _
GAM3331  ROBO4     3'  GTGATCCAAATGGTGGGGGAA  74872      GA_   CGA
                                GTGG   AGA   TGGGGGAA
                                ||||   |||   ||||||||
                                CACT   TTT   ACCCCCTT
                                  AGG   ACC
GAM3331  SHANK3    5'  TCCGTGGGGAGAAAGCCGGGGA 74873         A   CGA_
            A                    TCCGTGGG AGA    TGGGGGA
                                |||||||| |||    |||||||
                                AGGCACCC TCT    GCCCCTT
                                     C   TTCG
GAM3331  SMCR5     3'  TGGGAAGGGATGAAGGGAA    74874        AC    _
                                TGGGAAG  GATGG GGGAA
                                |||||||  ||||| |||||
                                ACCCTTC  CTACT CCCTT
                                     C_    T
GAM3331  SSTK      3'  CCCGTGGGAAGAAAGGGAG    74875           CGAT
                                TCCGTGGGAAGA   GGGGG
                                ||||||||||||   |||||
                                GGGCACCCTTCT   CCCTC
                                       TT__
GAM3331  TERA      3'  GTGGGAGTGGGGGAA       74876        A ACGA
                                GTGGGA G   TGGGGGAA
                                |||||| |   ||||||||
```

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                                CACCCT C    ACCCCCTT
                                  _ _____
GAM3331  ZYG      3'  TCCGTGGGAGGCTCCCTCGGAA 74877          AGACGA__
                 G                 TCCGTGGGA       TGGGGG
                                   |||||||||       ||||||
                                   AGGCACCCT       GCCTTC
                                       CCGAGGGA
GAM3331  LOC124750 5'  TCCGTGGGAGTGCGGGCGA   74878          AGACGA   G
                                   TCCGTGGGA     TGGG GA
                                   |||||||||     |||| ||
                                   AGGCACCCT     GCCC CT
                                       CAC___    G
GAM3331  LOC124961 3'  TCAGTGGGAGGACAGAGGAGG  74879    C     A    AT
                                   TC GTGGGA GACG  GGGGG
                                   || |||||| ||||  |||||
                                   AG CACCCT CTGT  CCTCC
                                    T     C    CT
GAM3331  LOC126526 3'  TCAGTGGGGAGTGGGGGAA   74880    C     A  ACGA
                                   TC GTGGG AG    TGGGGGAA
                                   || ||||| ||    ||||||||
                                   AG CACCC TC    ACCCCCTT
                                    T    C  _____
GAM3331  LOC126661 5'  TGGGGAACTGGGGGAA      47779      AA   GA
                                   TGGG  GAC  TGGGGGAA
                                   ||||  |||  ||||||||
                                   ACCC  TTG  ACCCCCTT
                                     C_   __
GAM3331  LOC139483 5'  TGGGGACATCTTGGGGGAA   74881      AA    A__
                                   TGGG  GACG   TGGGGGAA
                                   ||||  ||||   ||||||||
                                   ACCC  CTGT   ACCCCCTT
                                     __    AGA
GAM3331  LOC143384 3'  GTGAACTGATGGGGGAAA    74882      AAGAC
                                   GTGGG    GATGGGGGAAA
                                   |||||    ||||||||||
                                   CACTT    CTACCCCCTTT
                                      GA___
GAM3331  LOC147180 5'  TCTGTGGGGGGACAAGGGAG  74883    C    AA    T
                                   TC GTGGG  GACGA GGGGG
                                   || |||||  ||||| |||||
                                   AG CACCC  CTGTT CCCTC
                                    A    CC    _
GAM3331  LOC150935 3'  TCAGTGGGGAGGTGGTGA    74884    C    AAGAC  T  _  _
                                   TC GTGGG    GA GG GG GA
                                   || |||||    || || || ||
                                   AG CACCC    CT CC CC CT
                                    T    ______ _  A  A
GAM3331  LOC154881 3'  TCCATGGGAGAAGGGGGAA   74885          AGAC  T
                                   TCCGTGGGA   GA GGGGGAA
                                   |||||||||   || |||||||
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                                AGGTACCCT   CT CCCCCTT
                                     ____ T
GAM3331  LOC155179 3'  GTGGGGATGGGGGAA      74886      AAGAC
                                GTGGG    GATGGGGGAA
                                |||||    ||||||||||
                                CACCC    CTACCCCCTT
                                  _____
GAM3331  LOC157254 3'  TCCGTGGGGAGATGAAGGGGGA 74887        A  C  T
                                TCCGTGGG AGA GA GGGGGA
                                |||||||| ||| || ||||||
                                AGGCACCC TCT CT CCCCCT
                                     C  A  T
GAM3331  LOC157627 3'  CGTGGGAAGGCATCTGGAGG  74888        A  A_
                                CGTGGGAAG CG  TGGGGG
                                ||||||||| ||  ||||||
                                GCACCCTTC GT  ACCTCC
                                      C  AG
GAM3331  LOC164695 5'  CCTGTGGGAAGGCTATGGAAA  74889   _      ACG   GG
                                CC GTGGGAAG   ATGG  G
                                || ||||||||   ||||  |
                                GG CACCCTTC   TACC  T
                                 A       CGA   TT
GAM3331  LOC197285 3'  TCCTGGGAAGACGCCATGAAA  74890    G       __  GG
                                TCC TGGGAAGACG  ATG  G
                                ||| ||||||||||  |||  |
                                AGG ACCCTTCTGC  TAC  T
                                  _       GG   TT
GAM3331  LOC199927 3'  CATAAAAGTGATGGGGG    74891      G  AC
                                CGTGG AAG  GATGGGGG
                                ||||| |||  ||||||||
                                GTATT TTC  CTACCCCC
                                   _  A_
GAM3331  LOC200205 3'  TCAGTGGGAAGGGGGA     74892    C     GACGAT
                                TC GTGGGAA     GGGGGA
                                || |||||||     ||||||
                                AG CACCCTT     CCCCCT
                                 T     _______
GAM3331  LOC203636 3'  TCCATGGGAGGACCACGGGAG  74893        A  G
                                TCCGTGGGA GAC ATGGGGG
                                ||||||||| ||| |||||||
                                AGGTACCCT CTG TGCCCTC
                                      C  G
GAM3331  LOC221632 5'  TCCGGGGGGAGAGGGGA     74894     T  A  CGATG
                                TCCG GGG AGA    GGGGA
                                |||| ||| |||    |||||
                                AGGC CCC TCT    CCCCT
                                  _  C  _____
GAM3331  LOC253129 3'  TCGGTGGGGGGATGGGAA    74831    C    AAGAC
                                TC GTGGG    GATGGGGGG
                                || |||||    |||||||||
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                                AG CACCC    CTACCCTT
                                 C    CC___
GAM3331 LOC51112 5' TCCGTGAGGAAGGTGACAGAAG 74895       _    AC
                                TCCGTG GGAAG  GATGGGGG
                                |||||| |||||  ||||||||
                                AGGCAC CCTTC  CTGTCTTC
                                   T    CA
GAM3331 LOC51195 3' TCTATGGGGAGGACAAAGGGAG 74896    CG   AA_    T
             A                   TC  TGGG   GACGA GGGGGA
                                ||  ||||   ||||| ||||||
                                AG  ACCC   CTGTT CCCTCT
                                 AT   CTC    T
GAM3331 LOC90917 5' TCCTGGGAGGAGTGGGAAA   74897     G    A  CGA   GG
                                TCC TGGGA GA   TGGG  A
                                ||| ||||| ||   ||||  |
                                AGG ACCCT CT   ACCC  T
                                  _    C  C__    TT
GAM3331 LOC91974 5' TCCTGGGAAGACACTGGGGA   74898     G        A
                                TCC TGGGAAGACG TGGGGG
                                ||| |||||||||| ||||||
                                AGG ACCCTTCTGT ACCCCT
                                  _        G
GAM3331 LOC92659 5' TCCGTGGGGAGCTGGCCAGGAG 74899         A  ACGA_
                                TCCGTGGG AG    TGGGGG
                                |||||||| ||    ||||||
                                AGGCACCC TC    GTCCTC
                                     C  GACCG
GAM3332 BMP4    3' TGGTGTGTGTGTGTGGTGT   74902    C   C     TC
                                TGG GTG GTGTGTG  TGT
                                ||| ||| |||||||  |||
                                ACC CAC CACACAC  ACA
                                  A   A      C_
GAM3332 BMP4    3' TGGTGTGTGTGTGTGGTGT   74902    C   C     TC
                                TGG GTG GTGTGTG  TGT
                                ||| ||| |||||||  |||
                                ACC CAC CACACAC  ACA
                                  A   A      C_
GAM3332 BMP4    3' TGGTGTGTGTGTGTGGTGT   74902    C   C     TC
                                TGG GTG GTGTGTG  TGT
                                ||| ||| |||||||  |||
                                ACC CAC CACACAC  ACA
                                  A   A      C_
GAM3332 CACNG2   3' GTGTGTGTGTTTTTTTGTTTTT 74903    C     GTC__
                                GTG GTGTGT    TGTTTTT
                                ||| ||||||    |||||||
                                CAC CACACA    ACAAAAA
                                  A     AAAAA
GAM3332 CDH12    3' GTGTGTGTGTGTGTGTTT    74904    C      C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
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                                CAC CACACACA ACAAA
                                  A       C
GAM3332  CSPG3    3'  GTGTGTGTGTGTGTGTTT    74904     C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD      3'  GTGTGTGTGTGTGTGTTT    74904     C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD      3'  GTGTGTGTGTGTTTGTTTT   74905     C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD      3'  GTGTGTGTGTGTTTGTTTT   74905     C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD      3'  GTGTGTGTGTGTTTGTTTT   74905     C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD      3'  GTGTGTGTGTGTGTGTTT    74904     C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD      3'  GTGTGTGTGTGTTTGTTTT   74905     C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD      3'  GTGTGTGTGTGTTTGTTTT   74905     C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD      3'  GTGTGTGTGTGTTTGTTTT   74905     C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD      3'  GTGTGTGTGTGTTTGTTTT   74905     C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
```

```
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD     3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD     3'  GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD     3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD     3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD     3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD     3'  GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD     3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD     3'  GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD     3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
```

```
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD    3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD    3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD    3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD    3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD    3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD    3'  GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD    3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD    3'  GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD    3'  GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD    3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
```

```
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD     3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD     3'  GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD     3'  GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD     3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD     3'  GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD     3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD     3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332  DMD     3'  GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD     3'  GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DMD     3'  GTGTGTGTGTGTTTGTTTT   74905    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
```

```
                                CAC CACACACA ACAAAA
                                  A       A
GAM3332 EN2     3' GTGTGTGTGTGTGTTC     74906    C      CT
                                GTG GTGTGTGT  GTTT
                                ||| ||||||||  ||||
                                CAC CACACACA  CAAG
                                  A       __
GAM3332 FMR2    3' TGAGTGTGTGTGTGTGTGT   74907    C  C      C
                                TGG GTG GTGTGTGT TGT
                                ||| ||| |||||||| |||
                                ACT CAC CACACACA ACA
                                  _  A       C
GAM3332 KIF1B   3' GTGTGTGTGTGTGTGTTT    74904    C      C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332 MAPK10  3' GCGTGTGTGTGTGTTCCAT   74908      C      _
                                GCGTG GTGTGTGT CTGT
                                ||||| |||||||| ||||
                                CGCAC CACACACA GGTA
                                   A       A
GAM3332 MAPK10  3' GCGTGTGTGTGTGTTCCAT   74908      C      _
                                GCGTG GTGTGTGT CTGT
                                ||||| |||||||| ||||
                                CGCAC CACACACA GGTA
                                   A       A
GAM3332 MNT     3' GTGTGTGTGTGTGTGTCCC   74909    C      C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAGGG
                                  A       C
GAM3332 NR2E1   3' GTGTGTGTGTGTGTTC      74906    C      CT
                                GTG GTGTGTGT  GTTT
                                ||| ||||||||  ||||
                                CAC CACACACA  CAAG
                                  A       __
GAM3332 SCN8A   3' TGAGTGTGTGTGTGTGTTTTC 74910    C  C      CT
                                TGG GTG GTGTGTGT  GTTTTT
                                ||| ||| ||||||||  ||||||
                                ACT CAC CACACACA  CAAAAG
                                  _  A       __
GAM3332 SHANK2  3' GTGGTGTGTGTTTTGTTTT   74911    C      C_
                                GTG GTGTGTGT  TGTTTT
                                ||| ||||||||  ||||||
                                CAC CACACACA  ACAAAA
                                  _       AA
GAM3332 TFAP4   5' GTGTGTGTGTGTGTGTTT    74904    C      C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
```

```
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  DKFZp762A227 3'  GTGTGTGTGTGTGTGTTTT   74912    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       C
GAM3332  FLJ10718 3'  GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  FLJ14686 3'  GTGTGTGTGTGTGTGTTTT   74912    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       C
GAM3332  FLJ20043 3'  GCGTGTGTGTGTGTGTTT   74913      C       C
                                GCGTG GTGTGTGT TGTTT
                                ||||| |||||||| |||||
                                CGCAC CACACACA ACAAA
                                   A       C
GAM3332  FLJ21290 3'  GTGTGTGTGTGTGTGTTTT   74912    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
                                CAC CACACACA ACAAAA
                                  A       C
GAM3332  KIAA0416 3'  GTGTGTGTGTGTGTGCTTTT   74914    C       C
                                GTG GTGTGTGT TGTTTTT
                                ||| |||||||| |||||||
                                CAC CACACACA ACGAAAA
                                  A       C
GAM3332  KIAA0544 3'  GTGTGTGTGTGTGTATTTTT   74915    C       C
                                GTG GTGTGTGT TGTTTTT
                                ||| |||||||| |||||||
                                CAC CACACACA ATAAAAA
                                  A       C
GAM3332  KIAA0869 3'  GTGTGTGTGTGTTTTGTTTTT  74916    C       C_
                                GTG GTGTGTGT  TGTTTTT
                                ||| |||||||  |||||||
                                CAC CACACACA  ACAAAAA
                                  A       AA
GAM3332  KIAA1577 3'  TGGTGTGTGTGTGTGTCT    74917    C  C
                                TGG GTG GTGTGTGTCT
                                ||| ||| ||||||||||
                                ACC CAC CACACACAGA
                                  A  A
GAM3332  KIAA1623 3'  GTGTGTGTGTGTGTGTTTT   74912    C       C
                                GTG GTGTGTGT TGTTTT
                                ||| |||||||| ||||||
```

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                                CAC CACACACA ACAAAA
                                  A       C
GAM3332 MAP3K2   3' GTGTGTGTGTGTGTGTTTTT  74918    C       C
                                GTG GTGTGTGT TGTTTTT
                                ||| |||||||| |||||||
                                CAC CACACACA ACAAAAA
                                  A       C
GAM3332 MGC15882 3' CGTGTGTGTGTGTGTAGCTT  74919     C       CT_
                                CGTG GTGTGTGT   GTTT
                                |||| ||||||||   ||||
                                GCAC CACACACA   CGAA
                                  A       CAT
GAM3332 PRO1386  5' GTGTGTGTGTGTGTGTTT    74904    C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332 SEMA3E   3' GGTGTGTGTGTGTGTGTGTT  74920   C  C      C
                                GG GTG GTGTGTGT TGTT
                                || ||| |||||||| ||||
                                CC CAC CACACACA ACAA
                                 A  A       C
GAM3332 SEMA5B   3' GTGTGTGTGTGTGTTCC     74922    C       CT
                                GTG GTGTGTGT  GTTTT
                                ||| ||||||||  |||||
                                CAC CACACACA  CAAGG
                                  A       __
GAM3332 SEMA5B   3' AGTGTGTGTGTGTGTGTGTT  74921   C  C      C
                                GG GTG GTGTGTGT TGTT
                                || ||| |||||||| ||||
                                TC CAC CACACACA ACAA
                                 A  A       C
GAM3332 SEPT3    3' GTGTGTGTGTTTAGTTTTT   74923    C     GTCT
                                GTG GTGTGT    GTTTTT
                                ||| ||||||    ||||||
                                CAC CACACA    CAAAAA
                                  A     AAT_
GAM3332 SLC6A14  3' TAGGTGTGTGTGTGTGTGTT  74924    C  C      C
                                TGG GTG GTGTGTGT TGTT
                                ||| ||| |||||||| ||||
                                ATC CAC CACACACA ACAA
                                  _  A       C
GAM3332 TRAF3    3' GTGTGTGTGTGTGTGTTTTT  74918    C       C
                                GTG GTGTGTGT TGTTTTT
                                ||| |||||||| |||||||
                                CAC CACACACA ACAAAAA
                                  A       C
GAM3332 TRAF3    5' GTGTGTGTGTGTGTGTTTTT  74918    C       C
                                GTG GTGTGTGT TGTTTTT
                                ||| |||||||| |||||||
```

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                                CAC CACACACA ACAAAAA
                                  A       C
GAM3332  LOC132235 5'  GCGTGTGTGTGTGTGTGTT   74925      C       C
                                GCGTG GTGTGTGT TGTT
                                ||||| |||||||| ||||
                                CGCAC CACACACA ACAA
                                   A       C
GAM3332  LOC146856 3'  GTGTGTGTGTGTGTTTT     74926     C       CT
                                GTG GTGTGTGT  GTTTT
                                ||| ||||||||  |||||
                                CAC CACACACA  CAAAA
                                  A       __
GAM3332  LOC148188 5'  GTGTGTGTTGGCCTTGTTTTT  74927     C    GT   _
                                GTG GTGT  GTCT GTTTTT
                                ||| ||||  |||| ||||||
                                CAC CACA  CGGA CAAAAA
                                  A   AC   A
GAM3332  LOC150112 3'  AGTGTGCGTGTGTGTGTGTT   74928    C         C
                                GG GTGCGTGTGTGT TGTT
                                || ||||||||||| ||||
                                TC CACGCACACACA ACAA
                                 A          C
GAM3332  LOC151196 3'  GTGTTTATGTGTCTGTTTTT   74929     CG
                                GTG  TGTGTGTCTGTTTTT
                                |||  |||||||||||||||
                                CAC  ATACACAGACAAAAA
                                  AA
GAM3332  LOC158263 3'  GTGTGTGTGTGCACATTT    74930     C       CT
                                GTG GTGTGTGT  GTTT
                                ||| ||||||||  ||||
                                CAC CACACACG  TAAA
                                  A       TG
GAM3332  LOC219649 3'  GTGTGTGTGTGTGTGTTTTTA  74931     C       C      III
                                GTG GTGTGTGT TGTTTTT   A
                                ||| ||||||| |||||||   |
                                CAC CACACACA ACAAAAA   T
                                  A       C      III
GAM3332  LOC219972 3'  GTGTGTGTGTGTGTTC      74906     C       CT
                                GTG GTGTGTGT  GTTT
                                ||| ||||||||  ||||
                                CAC CACACACA  CAAG
                                  A       __
GAM3332  LOC221042 5'  GTGTGTGTGTGTGTGTTT    74904     C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
                                CAC CACACACA ACAAA
                                  A       C
GAM3332  LOC253982 3'  GTGTGTGTGTGTGTATTT    74932     C       C
                                GTG GTGTGTGT TGTTT
                                ||| |||||||| |||||
```

```
                                CAC CACACACA ATAAA
                                  A       C
GAM3333 GUCY2F   5' TGCGGATGCTGAAGAGTGA   74935    C  _ CCTT
                                TGC GGA GC    TGAAGAGTGA
                                ||| ||| ||    ||||||||||
                                ACG CCT CG    ACTTCTCACT
                                  _   A  ____
GAM3333 HOXC13   5' TGCTGGAGCTTTTTAAAAA   74936    C    CC
                                TGC GGAGC  TTTGAAGA
                                ||| |||||  ||||||||
                                ACG CCTCG  AAATTTTT
                                  A    AA
GAM3333 MYO10    3' TGTCAGGGTCCTTTGAAGA   74937    C   AGC
                                TG CGG   CCTTTGAAGA
                                || |||   ||||||||||
                                AC GTC   GGAAACTTCT
                                 A   CCA
GAM3333 MGC4266  3' TGCTGGGGGTCTTTGAAGGC   74938    C  AGCC      A
                                TGC GG    CTTTGAAG GT
                                ||| ||    |||||||| ||
                                ACG CC    GAAACTTC CG
                                  A  CCCA      _
GAM3333 LOC145757 3' TGCTGGTGTCCAAGAGTGA   74939    C  AG_  CTTTG
                                TGC GG   CC    AAGAGTGA
                                ||| ||   ||    ||||||||
                                ACG CC   GG    TTCTCACT
                                  A  ACA  _____
GAM3333 LOC149576 5' GCCGGAGTGTGAGAGTG    74940       CCCTT   A
                                GCCGGAG    TGA GAGTG
                                |||||||    ||| |||||
                                CGGCCTC    ACT CTCAC
                                    AC___   _
GAM3333 LOC90462  3' TGCTGGGCCTCTTTGGCAG   74941    C  A  _    A_
                                TGC GG GCC CTTTG  AG
                                ||| || ||| |||||  ||
                                ACG CC CGG GAAAC  TC
                                  A  _   A    CG
GAM3334 ADCY7    3' TGCATGCCTTTGGGATTGGCG  74944     AGA  G   A
                                TGTAT   CT TTTG GATTGGCG
                                |||||   || |||| ||||||||
                                ACGTA   GG AAAC CTAACCGC
                                   C__  _   C
GAM3334 CACNA2D2 3' TGTAAGGGCCAGATTGGC    74945     T  ACT   TG
                                TGTA AG   GTT  AGATTGGC
                                ||||  ||   |||  ||||||||
                                ACAT TC   CGG  TCTAACCG
                                  _  C__   __
GAM3334 ZNF221   5' TAGGCTGTTTGAAGCA      74946     A      GATT
                                TAG CTGTTTGA    GGCG
                                ||| ||||||||    ||||
```

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                                ATC GACAAACT    TCGT
                                  C      _____
GAM3335  LDOC1    3'  TCAATGTCTGAAAAGGC     74949       A
                                TCAATG TCTGAAAAGGC
                                |||||| ||||||||||
                                AGTTAC AGACTTTTCCG
                                   _
GAM3335  CTCFL    3'  TCAATGATCTTGAAATACAGG  74950          _   ___
                                TCAATGATCT GAAA   AGG
                                |||||||||| ||||   |||
                                AGTTACTAGA CTTT   TCC
                                     A    ATG
GAM3335  DKK2     5'  GATCTGAAGAGAATCGAG    74951        A   CC
                                GATCTGAA AGG  TCGAG
                                |||||||| |||  |||||
                                CTAGACTT TCT  AGCTC
                                     C   T_
GAM3335  HA-1     5'  CCAACAGGAAAAGGCTTCG   74952       ATCT      C
                                TCAATG    GAAAAGGC TCG
                                ||||||    |||||||| |||
                                GGTTGT    CTTTTCCG AGC
                                   C___       A
GAM3335  MGC11386 3'  TCAATGATTTGAAATCTCTGAG 74953         C     AGGC  _
                                TCAATGAT TGAAA    CTC GAG
                                |||||||| |||||    ||| |||
                                AGTTACTA ACTTT    GAG CTC
                                     A     A___   A
GAM3335  RNPS1    3'  TGAGGTCAGAAGAGGCCTCGAG 74954     __  T   A
                                TGA  TC GAA AGGCCTCGAG
                                |||  || ||| ||||||||||
                                ACT  AG CTT TCCGGAGCTC
                                  CC  T   C
GAM3335  RNPS1    3'  TGAGGTCAGAAGAGGCCTCGAG 74954     __  T   A
                                TGA  TC GAA AGGCCTCGAG
                                |||  || ||| ||||||||||
                                ACT  AG CTT TCCGGAGCTC
                                  CC  T   C
GAM3335  SPEC1    3'  TCAATGATCAGAAGTCCACCTT 74955         T   AAG_   C
            GAG                   TCAATGATC GAA    GCCT GAG
                                |||||||| |||    |||| |||
                                AGTTACTAG CTT    TGGA CTC
                                     T   CAGG    A
GAM3335  LOC129138 3'  TCAATGACTGGGAGGAAAAGG  74956        CT____
                                TCAATGAT     GAAAAGG
                                ||||||||     |||||||
                                AGTTACTG     CTTTTCC
                                     ACCCTC
GAM3335  LOC149722 5'  AATGATCTAAAGGTAACACG   74957          AA_   CT
                                AATGATCTGAA   GGC  CG
                                ||||||||||   |||  ||
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                                TTACTAGATTT  TTG  GC
                                      CCA  T_
GAM3335  LOC153027 3'  TGAAGTCAGAAGAGGCCTCGAG 74958    __ T  A
                                TGA  TC GAA AGGCCTCGAG
                                |||  || ||| ||||||||||
                                ACT  AG CTT TCCGGAGCTC
                                  TC  T  C
GAM3335  LOC92935  3'  TCAGTAGTCTGAAAAAGAACGA 74959    A  A       CCT
           G                     TCA TG TCTGAAAAGG  CGAG
                                ||| || ||||||||||  ||||
                                AGT AT AGACTTTTTC  GCTC
                                  C  C       TT_
GAM3336  TAPBP    3'  TAAGTTCTAGTACCATAAATAT 74962        ATT  A
           T                     TAGGTTCTA  CTA AAATATT
                                |||||||||  ||| |||||||
                                ATTCAAGAT  GGT TTTATAA
                                      CAT  A
GAM3337  ARG1     3'  TAGCTTTGTCTCCTGAT    74965    ATTC  T
                                TAGC   TT TCTCCTGAT
                                ||||   || |||||||||
                                ATCG   AA AGAGGACTA
                                  A___  C
GAM3337  B3GALT5  5'  GCATTCTTCTCTGATC    74966         CCT
                                GCATTCTTTTCT  GATC
                                ||||||||||||  ||||
                                CGTAAGAAGAGA  CTAG
                                      ___
GAM3337  DMD      5'  CAGCATCTTTCTCCTGAT    74967      CT
                                TAGCATT  TTTCTCCTGAT
                                |||||||  ||||||||||||
                                GTCGTAG  AAAGAGGACTA
                                     __
GAM3337  DUSP5    3'  TAACTGCCTTTTCTCCTG    74968     AT
                                TAGC  TCTTTTCTCCTG
                                ||||  ||||||||||||
                                ATTG  GGAAAAGAGGAC
                                  AC
GAM3337  KMO      3'  TAGTATTTTTTTCCCCAACTGA 74969    C  C     ___
           T                     TAG ATT TTTTCTCC  TGAT
                                ||| ||| ||||||||  ||||
                                ATC TAA AAAAGGGG  ACTA
                                  A  A       TTG
GAM3337  MBNL     5'  TAGAGCTTTTCTCTTGAT    74970    CATT      C
                                TAG   CTTTTCTC TGAT
                                |||   |||||||| ||||
                                ATC   GAAAAGAG ACTA
                                  TC__       A
GAM3337  MTM1     3'  CAGCTCCTTTCTTCTGAT    74971     AT      C
                                TAGC  TCTTTTCT CTGAT
                                ||||  |||||||| |||||
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                                GTCG  AGGAAAGA GACTA
                                  __      A
GAM3337  NCALD    3'  AGTCACATTTTTCTCCTG    74972    _  TC
                                AG CAT  TTTTCTCCTG
                                || |||  ||||||||||
                                TC GTG  AAAAGAGGAC
                                 A   TA
GAM3337  PTPRJ    3'  TAGATCCCTTTTCCTG     74973    C      C
                                TAG ATTCTTTT TCCTG
                                ||| |||||||| |||||
                                ATC TAGGGAAA AGGAC
                                  _      _
GAM3337  RAB18    3'  TAGTGTTCTTTCTCCAAAT   74974    CA     T   T
                                TAG  TTCTTT CTCC GAT
                                |||  |||||| |||| |||
                                ATC  AAGAAA GAGG TTA
                                  AC     _   T
GAM3337  RNF7     3'  TAACATTCTTTTTTAACTGATC 74975          CTC_
                                TAGCATTCTTTT   CTGATC
                                ||||||||||||   ||||||
                                ATTGTAAGAAAA   GACTAG
                                       AATT
GAM3337  TRIM39   5'  CAGCATACTTCTCCTGATC   74976      TCT
                                TAGCAT   TTTCTCCTGATC
                                ||||||   ||||||||||||
                                GTCGTA   GAAGAGGACTAG
                                   T__
GAM3337  APOL6    3'  GCATTCTTTTGAGTTTCTGAT  74977         CTC___
                                GCATTCTTTT     CTGAT
                                ||||||||||     |||||
                                CGTAAGAAAA     GACTA
                                      CTCAAA
GAM3337  DKFZP586A011 3'  GCAGACCTCTCCTGATC     74978     TT  TT
                                GCA  CT  TCTCCTGATC
                                |||  ||  ||||||||||
                                CGT  GG  AGAGGACTAG
                                  CT  __
GAM3337  DKFZp761P1010 3'  ACATTCTTTTCTAGCCCT    74979          ___
                                GCATTCTTTTCT   CCT
                                ||||||||||||   |||
                                TGTAAGAAAAGA   GGA
                                       TCG
GAM3337  DKFZp762M136 3'  GCAGAACCCTTCTCCTGAT   74980     TT_
                                GCA   CTTTTCTCCTGAT
                                |||   ||||||||||||
                                CGT   GGGAAGAGGACTA
                                  CTT
GAM3337  FLJ20896  3'  ACATTCCCCTCCTGATC     74981        TT
                                GCATTCT  TCTCCTGATC
                                |||||||  ||||||||||
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                                TGTAAGG  GGAGGACTAG
                                   __
GAM3337  FLJ22746  3'  TAGCATTCATGTTCAACCTGAT 74982        TT_  T_
                                TAGCATTC  TTC  CCTGAT
                                ||||||||  |||  ||||||
                                ATCGTAAG  AAG  GGACTA
                                    TAC  TT
GAM3337  KIAA0895  3'  CAGCATTCTTTCTGAT     74983          TCTC
                                TAGCATTCTTT   CTGAT
                                ||||||||||   |||||
                                GTCGTAAGAAA   GACTA
                                   ____
GAM3337  KIAA0914  3'  GCATTCTTTTTCCCCATC    74984         C   G
                                GCATTCTTTT TCCT ATC
                                |||||||||| |||| |||
                                CGTAAGAAAA AGGG TAG
                                    _   G
GAM3337  KIAA1046  3'  TAGCACTCAAACTTCCTGATC  74985        TTTTC
                                TAGCATTC    TCCTGATC
                                ||||||||    ||||||||
                                ATCGTGAG    AGGACTAG
                                    TTTGA
GAM3337  MAWBP    3'  ATTCCTCCTTCTCTTGAT    74986        __   C
                                ATTCTTT  TCTC TGAT
                                |||||||  |||| ||||
                                TAAGGAG  AGAG ACTA
                                    GA   A
GAM3337  P8       3'  TAGCTTTCTTTTCTGGGGGATC 74987     A       CCT_
                                TAGC TTCTTTTCT   GATC
                                |||| |||||||||   ||||
                                ATCG AAGAAAAGA   CTAG
                                  A       CCCC
GAM3337  PLPL     3'  TAACATTTTATTCCTGATC   74988       CT  TC
                                TAGCATT  TT  TCCTGATC
                                |||||||  ||  ||||||||
                                ATTGTAA  AA  AGGACTAG
                                    __ TA
GAM3337  PSMD12   3'  GCTTCTTCTCCTGAT      74989    A   TT
                                GC TTCT  TCTCCTGAT
                                || ||||  |||||||||
                                CG AAGA  AGAGGACTA
                                  _   __
GAM3337  SLC26A7  3'  TAACAGTCTTTTCCTG      74990      T    TC
                                TAGCA TCTTT  TCCTG
                                ||||| |||||  |||||
                                ATTGT AGAAA  AGGAC
                                  C    __
GAM3337  SPATA1   5'  TAGCATTCCACTCATTCCTG  74991         T  __
                                TAGCATTCT TTC  TCCTG
                                ||||||||| |||  |||||
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                                ATCGTAAGG GAG  AGGAC
                                     T   TA
GAM3337  LOC121274 5'  TAACCTCGTTTCTCCTG     74992      A   T
                                TAGC TTC TTTCTCCTG
                                |||| ||| |||||||||
                                ATTG GAG AAAGAGGAC
                                  _   C
GAM3337  LOC144558 5'  CATTCCCCACCCTGATC     74993        TT T
                                CATTCTT  C CCTGATC
                                |||||||  | |||||||
                                GTAAGGG  G GGACTAG
                                    GT _
GAM3337  LOC148014 3'  GCTATTCTGCCCTGATC     74994    _    TTTC
                                GC ATTCT    TCCTGATC
                                || |||||    ||||||||
                                CG TAAGA    GGGACTAG
                                 A    C___
GAM3337  LOC149832 5'  GCATTCTCTGCTTGAT      74995         T  CC
                                GCATTCTTT CT  TGAT
                                ||||||||| ||  ||||
                                CGTAAGAGA GA  ACTA
                                     C  __
GAM3337  LOC149837 3'  GCCTCAATTTTCTCCTGAT    74996    A  __
                                GC TTC  TTTTCTCCTGAT
                                || |||  ||||||||||||
                                CG GAG  AAAAGAGGACTA
                                 _   TT
GAM3337  LOC151623 5'  CATTCCCCACCCTGATC     74993        TT T
                                CATTCTT  C CCTGATC
                                |||||||  | |||||||
                                GTAAGGG  G GGACTAG
                                    GT _
GAM3337  LOC201628 5'  CAGCATTCTTTTCAGGCCT    74997            T__
                                TAGCATTCTTTTC   CCT
                                ||||||||||||   |||
                                GTCGTAAGAAAAG   GGA
                                        TCC
GAM3337  LOC219401 3'  TAGTATTTTTTCCCCATGAT   74998     C   C      _
                                TAG ATT TTTTCTCC TGAT
                                ||| ||| |||||||| ||||
                                ATC TAA AAAAGGGG ACTA
                                  A   _       T
GAM3337  LOC221692 3'  TAGCCTCAGACTTCTGATC    74999      A   TTTT  C
                                TAGC TTC    CT CTGATC
                                |||| |||    || ||||||
                                ATCG GAG    GA GACTAG
                                   _   TCT_  A
GAM3337  LOC221760 3'  TAGCAATCCTCTTCCTGATC   75000       T     C
                                TAGCA TCTTTT TCCTGATC
                                ||||| |||||| ||||||||
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                                ATCGT AGGAGA AGGACTAG
                                  T     _
GAM3337  LOC255461 5'  CATTCCCCACCCTGATC     74993        TT T
                                CATTCTT  C CCTGATC
                                |||||||  | |||||||
                                GTAAGGG  G GGACTAG
                                   GT _
GAM3337  LOC255516 5'  CATTCCCCACCCTGATC     74993        TT T
                                CATTCTT  C CCTGATC
                                |||||||  | |||||||
                                GTAAGGG  G GGACTAG
                                   GT _
GAM3337  LOC90593  3'  ACATTCATGGTTTCTCTTGAT  75001       T___     C
                                GCATTC    TTTCTC TGAT
                                ||||||    |||||| ||||
                                TGTAAG    AAAGAG ACTA
                                   TACC     A
GAM3338  C4BPB     5'  CACCCAGCTCAGACACC     75004        CCGAA   A
                                CACCCGGT    TCA ACACC
                                ||||||||    ||| |||||
                                GTGGGTCG    AGT TGTGG
                                    _____  C
GAM3338  JAG2      5'  CCCGGCCCGGCTCCCACCCG   75005         AA  AAA
                                CCCGGTCCG  TC   CACCCG
                                |||||||||  ||   ||||||
                                GGGCCGGGC  AG   GTGGGC
                                     CG  G__
GAM3338  ARHU      5'  CACCCGGTCCGGGAAGCGACGC 75006          AATCAA_  A
            CCG                    CACCCGGTCCG      AC CCCG
                                ||||||||||       || ||||
                                GTGGGCCAGGC      TG GGGC
                                      CCTTCGC  C
GAM3338  BDH       5'  CACCCGGCGCCGCGCAGGTGCC 75007         _   AAT  AACA
            CG                     CACCCGGT CCG   CA    CCCG
                                |||||||| |||   ||    ||||
                                GTGGGCCG GGC   GT    GGGC
                                    C   GC_  CCAC
GAM3338  BRD2      5'  CCCGGTCCAGCATAACCCG   75008         AAT  AAC
                                CCCGGTCCG   CA   ACCCG
                                |||||||||   ||   |||||
                                GGGCCAGGT   GT   TGGGC
                                     C__  AT_
GAM3338  FLJ12707  5'  CGTTCTGAACCAAATGTCCG   75009    G  C       CAC
                                CG TC GAATCAAA   CCG
                                || || ||||||||   |||
                                GC AG CTTGGTTT   GGC
                                 A  A       ACA
GAM3338  FLJ21839  5'  CACCCGGGCCCCCAAAAACACC 75010         _   GAATC
            CG                     CACCCGG TCC     AAACACCCG
                                |||||||  |||     |||||||||
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                                GTGGGCC GGG    TTTGTGGGC
                                    C  GGTT_
GAM3338 FOXO3A   5' CACCCGGTCGAATGGCCC   75011       C   CAAACA
                                CACCCGGTC GAAT    CCC
                                ||||||||| ||||    |||
                                GTGGGCCAG CTTA    GGG
                                    _   CC____
GAM3338 SLC37A1  5' CCCGGTCCGGGAACGCCC   75012       AATCA  A
                                CCCGGTCCG   AAC CCC
                                |||||||||   ||| |||
                                GGGCCAGGC   TTG GGG
                                    CC___  C
GAM3338 LOC257169 5' CCCAGTCCGAATTGACTCC  75013         CAA  A
                                CCCGGTCCGAAT  AC CC
                                ||||||||||||  || ||
                                GGGTCAGGCTTA  TG GG
                                      AC_  A
GAM3339 BNIP3L   3' TAAAATGCCTCAACAGAGT   75016     CA  G    _
                                TAAAA  CC TCAACGG GT
                                |||||  || ||||||| ||
                                ATTTT  GG AGTTGTC CA
                                   AC  _     T
GAM3339 MASP1    3' ACACAGTGTGGGTCTTTT    75017     C  CAAC
                                ACAC GT   GGGTCTTTT
                                |||| ||   |||||||||
                                TGTG CA   CCCAGAAAA
                                  T  CA__
GAM3339 KIAA1463 3' TAAAACACTGGTCAAAATGT  75018       C_   CGG
                                TAAAACAC  GTCAA  GT
                                ||||||||  |||||  ||
                                ATTTTGTG  CAGTT  CA
                                     AC    TTA
GAM3339 NTT73    3' TAAAACACTGTTTTTATTTGTC 75019       C  CAACGG__
            TTTT                  TAAAACAC GT      GTCTTTT
                                |||||||| ||      |||||||
                                ATTTTGTG CA      CAGAAAA
                                     A  AAAATAAA
GAM3339 RALGPS1A 3' CAAAATACAGTGGTGGGTCTTT 75020     C  C  CAAC
            T                  TAAAA AC GT   GGGTCTTTT
                                ||||| || ||   |||||||||
                                GTTTT TG CA   CCCAGAAAA
                                   A  T  CCA_
GAM3339 SPRY4    3' TAAAACACCGTTAGCATCCGG  75021         ___  A_
                                TAAAACACCGT   CA  CGG
                                ||||||||||   ||  |||
                                ATTTTGTGGCA   GT  GCC
                                      ATC  AG
GAM3339 LOC135293 3' TAAAACACCATCAGACAGGT  75022          _
                                TAAAACACCGTCA ACGGGT
                                |||||||||||| ||||||
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                                ATTTTGTGGTAGT TGTCCA
                                      C
GAM3339  LOC219667 3'  AAACACTGTCAGTCTTT     75023       C    ACGG
                                AAACAC GTCA    GTCTTT
                                |||||| ||||    ||||||
                                TTTGTG CAGT    CAGAAA
                                   A   _____
GAM3340  ASCL1     3'  TTTTCTTCTTCTCTTT      75026         AT
                                TTTTCTTT  TTCTCTTT
                                ||||||||  ||||||||
                                AAAAGAAG  AAGAGAAA
                                    __
GAM3340  BRCA1     3'  TCTCATTTCCCATTTCTCTTT  75027       C     TT
                                TCTTA TTTTCT  ATTTCTCTTT
                                ||||| ||||||  ||||||||||
                                AGAGT AAAGGG  TAAAGAGAAA
                                  _    __
GAM3340  CCND1     3'  TTTTCTCTCTCTCTCTTT    75028         A
                                TTTTCTTT TTTCTCTTT
                                |||||||| |||||||||
                                AAAAGAGA AGAGAGAAA
                                     G
GAM3340  CYP2J2    3'  TCTTACTTTCCTTGCCCCTTT  75029           TATT
                                TCTTACTTTTCTT    TCTCTTT
                                ||||||||||||    |||||||
                                AGAATGAAAGGAA    GGGGAAA
                                      C___
GAM3340  FMR2      3'  TCTCAGACATTTCTCTTT    75030      TT_
                                TTTC   TATTTCTCTTT
                                ||||   ||||||||||
                                AGAG   GTAAAGAGAAA
                                  TCT
GAM3340  GATA3     3'  TCTTTTTTTTTCTTTTCTCTTT 75031      AC_       ATT
                                TCTT   TTTTCTTT   TCTCTTT
                                ||||   ||||||||   |||||||
                                AGAA   AAAAGAAA   AGAGAAA
                                  AAA       ___
GAM3340  IRTA1     3'  TCTATTTTTCTTTTTCTCTTT  75032     TAC       AT
                                TCT   TTTTCTTT  TTCTCTTT
                                |||   ||||||||  ||||||||
                                AGA   AAAAGAAA  AAGAGAAA
                                  TA_       __
GAM3340  KCNK6     3'  TCTTACTTTTCTTTCTTTTTCT 75033           A   C
            TT                   TCTTACTTTTCTTT TTT TCTTT
                                ||||||||||||| ||| |||||
                                AGAATGAAAAGAAA AAA AGAAA
                                      G   A
GAM3340  KCNK6     3'  TCTTACTTTTCTTTCTTTTTCT 75033           A   C
            TT                   TCTTACTTTTCTTT TTT TCTTT
                                ||||||||||||| ||| |||||
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                                AGAATGAAAAGAAA AAA AGAAA
                                       G   A
GAM3340  MAGEB4   3'  TTACTTTTCTTCCCTT      75034          TTATT
                                TTACTTTTCT    TCTCTT
                                ||||||||||    ||||||
                                AATGAAAAGA    AGGGAA
                                      _____
GAM3340  MMP16    3'  TCTTCTTTTTCTCCTCTTCT  75035      AC      TA
                                TCTT  TTTTCTT  TTTCT
                                ||||  |||||||  |||||
                                AGAA  AAAAGAG  GAAGA
                                  GA      GA
GAM3340  PHF1     3'  TTTTGTTTATTTCTCTTT    75036      C
                                TTTT TTTATTTCTCTTT
                                |||| ||||||||||||
                                AAAA AAATAAAGAGAAA
                                  C
GAM3340  SOX4     3'  TCTTTTTTCCCTTTTCTCTTT  75037      AC       A
                                TCTT  TTTTCTTT TTTCTCTTT
                                ||||  |||||||| |||||||||
                                AGAA  AAAAGGGA AAAGAGAAA
                                   __       _
GAM3340  TRPS1    3'  TCTTGCTTTCTCTTTTCTCTTT 75038      A   T   A
                                TCTT CTTT CTTT TTTCTCTTT
                                |||| |||| |||| |||||||||
                                AGAA GAAA GAGA AAAGAGAAA
                                  C   _   _
GAM3340  AGPAT1   3'  TTTTCTCTCTCTCTTT      75039        TA
                                TTTTCTT  TTTCTCTTT
                                |||||||  |||||||||
                                AAAAGAG  AGAGAGAAA
                                     __
GAM3340  AGPAT1   3'  TTTTCTCTCTCTCTCTTT    75028         A
                                TTTTCTTT TTTCTCTTT
                                |||||||| |||||||||
                                AAAAGAGA AGAGAGAAA
                                     G
GAM3340  ALK7     3'  TCTTCCTTTTCTGTCTTTTCT  75040      A      _ A
                                TCTT CTTTTCT TT TTTCT
                                |||| ||||||| || |||||
                                AGAA GAAAAGA AG AAAGA
                                  G      C  A
GAM3340  ARHU     3'  TCTCACTTTTTTTCTC      75041          CTTTA
                                TCTTACTTTT    TTTCTC
                                ||||||||||    ||||||
                                AGAGTGAAAA    AAAGAG
                                      _____
GAM3340  CNNM1    3'  CTTTTCTTTTCTCTT       75042          ATT
                                CTTTTCTTT   TCTCTT
                                |||||||||   ||||||
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                                GAAAAGAAA   AGAGAA
                                        ___
GAM3340  DCOHM     3'  TTTTCTTTTTCCTCTTC     75043         A
                                TTTTCTTT TTTCTCTTT
                                |||||||| |||||||||
                                AAAAGAAA AAGGAGAAG
                                       _
GAM3340  FLJ14327  3'  TCTTTTCTTTTCTTAATTTTTC 75044    A_      T   C    III
            TTTA                   TT  CTTTTCTT ATTT TCTTT   A
                                ||  |||||||| |||| |||||   |
                                AA  GAAAAGAA TAAA AGAAA   T
                                 AA       T   A    III
GAM3340  FLJ21159  3'  TCTTGTTTTTTTCTTCAAGCCT 75045     AC__       TT
            CTTT                   TCTT   TTTTCTTTA  TCTCTTT
                                ||||   |||||||||  |||||||
                                AGAA   AAAAGAAGT  GGAGAAA
                                  CAAA       TC
GAM3340  FLJ25438  3'  CTTCTTTTACTTCTCTT     75046      C
                                CTTTT TTTATTTCTCTT
                                ||||| ||||||||||||
                                GAAGA AAATGAAGAGAA
                                  _
GAM3340  FLJ25438  3'  TCTTGATTTTCTTTCTCTTC   75047     AC      TATT
                                TCTT  TTTTCTT   TCTCTTT
                                ||||  |||||||   |||||||
                                AGAA  AAAAGAA   AGAGAAG
                                  CT     _____
GAM3340  KIAA0087  3'  TCTCTACTTTTCTTTTTCT   75048     _       AT
                                TCTT ACTTTTCTTT  TTCT
                                |||| ||||||||||  ||||
                                AGAG TGAAAAGAAA  AAGA
                                  A       __
GAM3340  KIAA0182  3'  TTACTTTTCTTCTTCT      75049          AT
                                TTACTTTTCTTT  TTCT
                                ||||||||||||  ||||
                                AATGAAAAGAAG  AAGA
                                       __
GAM3340  KIAA0316  3'  TTTTCTTTTCTCTCTCTT    75050        A_
                                TTTTCTTT  TTTCTCTT
                                ||||||||  ||||||||
                                AAAAGAAA  AGAGAGAA
                                     AG
GAM3340  KIAA0335  3'  TTACTTTTCTTTTCCT      75051          AT
                                TTACTTTTCTTT  TTCT
                                ||||||||||||  ||||
                                AATGAAAAGAAA  AGGA
                                       __
GAM3340  KIAA0595  3'  TCACTTTTTTCCATTTCT    75052        C
                                TTACTTTT TTTATTTCT
                                |||||||| |||||||||
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                                AGTGAAAA AGGTAAAGA
                                    A
GAM3340 KIAA1486 3' TCTTACTGTTTCTACTTCT  75053      _   TT
                                TCTTACT TTTCT  ATTTCT
                                ||||||| |||||  ||||||
                                AGAATGA AAAGA  TGAAGA
                                   C   __
GAM3340 LGI4    5' TCTAATTTTCTGTTTCTCTTT 75054    TAC    TTA
                                TCT  TTTTCT  TTTCTCTTT
                                |||  ||||||  |||||||||
                                AGA  AAAAGA  AAAGAGAAA
                                  TT_    C__
GAM3340 MGC22014 3' TCCTGTTTTTCTCCCCTCTTT 75055     AC    TTA TT
                                TCTT  TTTTCT  T  CTCTTT
                                ||||  ||||||  |  ||||||
                                AGGA  AAAAGA  G  GAGAAA
                                  CA    ___ GG
GAM3340 PCDH17  3' CTTTTTTTCTTTTCTCTT   75056     C  A
                                CTTTT TTT TTTCTCTT
                                ||||| ||| ||||||||
                                GAAAA AAG AAAGAGAA
                                   A  A
GAM3340 SAMHD1  3' TCTTTCTTTTCTTTCTCTCTTT 75057    A      TA
                                TCTT CTTTTCTT  TTTCTCTTT
                                |||| ||||||||  |||||||||
                                AGAA GAAAAGAA  AGAGAGAAA
                                  A      __
GAM3340 SEMA3C  3' TCTTCCTTTTCTATTTCT   75058    A     TT
                                TCTT CTTTTCT  ATTTCT
                                |||| |||||||  ||||||
                                AGAA GAAAAGA  TAAAGA
                                  G     __
GAM3340 VEZATIN  3' TCTTACTTTTCTTCTATCTC  75059          ATT
                                TCTTACTTTTCTTT  TCTC
                                ||||||||||||||  ||||
                                AGAATGAAAAGAAG  AGAG
                                        AT_
GAM3340 LOC123876 3' TCTTTCCCTACTTTATTTCT  75061    A   T
                                TCTT CTTT CTTTATTTCT
                                |||| |||| ||||||||||
                                AGAA GGGA GAAATAAAGA
                                  A   T
GAM3340 LOC123876 3' CTTTCTTCTTTCTCTTT    75060       A
                                TTTTCTTT TTTCTCTTT
                                |||||||| |||||||||
                                GAAAGAAG AAAGAGAAA
                                    _
GAM3340 LOC138389 3' TCTTTCTTTTCTTTTTCT   75062    A      AT
                                TCTT CTTTTCTTT  TTCT
                                |||| |||||||||  ||||
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                                AGAA GAAAAGAAA  AAGA
                                  A       __
GAM3340  LOC146485 5'  TCTTGTCTTTCTCGCTCTCTTT 75063      AC      TAT
                                TCTT  TTTTCTT   TTCTCTTT
                                ||||  |||||||   ||||||||
                                AGAA  GAAAGAG   GAGAGAAA
                                  CA      C__
GAM3340  LOC146723 3'  TTTTCTTTTCTTTCTCTT    75064        A_
                                TTTTCTTT  TTTCTCTT
                                ||||||||  ||||||||
                                AAAAGAAA  AAAGAGAA
                                     AG
GAM3340  LOC147341 3'  CTTTTCTTTTTTCTCTTT    75065         A
                                CTTTTCTTT TTTCTCTTT
                                ||||||||| |||||||||
                                GAAAAGAAA AAAGAGAAA

                                     _
GAM3340  LOC152445 3'  TCTTACTTCTTGACCATCTCTT 75066          CTTTATT
           T                     TCTTACTTTT      TCTCTTT
                                ||||||||||      |||||||
                                AGAATGAAGA      AGAGAAA
                                      ACTGGT_
GAM3340  LOC153222 3'  TTTTCTTTTTTTTCTCCTT   75067        A_
                                TTTTCTTT  TTTCTCTTT
                                ||||||||  |||||||||
                                AAAAGAAA  AAAGAGGAA
                                     AA
GAM3340  LOC163255 5'  TTACTTTTTTCTATTATACTCT 75068        C     ____
           CTTT                    TTACTTTT TTTATT    TCTCTTT
                                ||||||||| ||||||    |||||||
                                AATGAAAA AGATAA    AGAGAAA
                                     A     TATG
GAM3340  LOC201685 3'  TCTTTCTTTTCTTTTTCTTCTT 75069      A        A  TC
           T                     TCTT CTTTTCTTT TT  TCTTT
                                |||| |||||||| ||  |||||
                                AGAA GAAAAGAAA AA  AGAAA
                                  A        _  GA
GAM3340  LOC219843 5'  TCTTCTTTTTCTTCATCC    75070      AC
                                TCTT  TTTTCTTTATTT
                                ||||  ||||||||||||
                                AGAA  AAAAGAAGTAGG
                                  GA
GAM3340  LOC221712 5'  TCTTGCTTTTCACTGTCTCTTT 75071      A     TTTATT
                                TCTT CTTTTC      TCTCTTT
                                |||| ||||||      |||||||
                                AGAA GAAAAG      AGAGAAA
                                  C     TGAC__
GAM3340  LOC253018 3'  TTACTGTTCCTGCTTCTCTTT  75072       T    TA
                                TTACT TTCTT  TTTCTCTTT
                                ||||| |||||  |||||||||
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                                AATGA AAGGA  GAAGAGAAA
                                  C    C_
GAM3340  LOC257548 3'  TTACTGTTCCTGCTTCTCTTT  75072      T    TA
                                TTACT TTCTT  TTTCTCTTT
                                ||||| |||||  |||||||||
                                AATGA AAGGA  GAAGAGAAA
                                  C    C_
GAM3340  LOC257610 3'  TTACTGTTCCTGCTTCTCTTT  75072      T    TA
                                TTACT TTCTT  TTTCTCTTT
                                ||||| |||||  |||||||||
                                AATGA AAGGA  GAAGAGAAA
                                  C    C_
GAM3340  LOC90110  5'  CTTTTCTTTTCTCTT       75042          ATT
                                CTTTTCTTT   TCTCTT
                                |||||||||   ||||||
                                GAAAAGAAA   AGAGAA

                                    ___
GAM3340  LOC91963  3'  TCTTTTCTTTTCTTTGTTTCT  75073      A_       A
                                TCTT  CTTTTCTTT TTTCT
                                ||||  ||||||||| |||||
                                AGAA  GAAAAGAAA AAAGA
                                  AA        C
GAM3341  AK1       3'  AGGGGCTGGGGACTTGCG    75076      A_       _
                                AGGG  TGGGGACT GCG
                                ||||  |||||||| |||
                                TCCC  ACCCCTGA CGC
                                  CG        A
GAM3341  AP3B2     5'  AGGAGGAGGTTGCGGCGCG    75077      T    AC
                                GGGA GGGG  TGCGGCGCG
                                |||| ||||  |||||||||
                                TCCT CCTC  ACGCCGCGC
                                  _    CA
GAM3341  ATP1B1    5'  AGGGTGGGTGGCTGCGGCGCG  75078      A    GA_
                                AGGG TGGG   CTGCGGCGCG
                                |||| ||||   ||||||||||
                                TCCC ACCC   GACGCCGCGC
                                  _    ACC
GAM3341  BARX1     3'  GGGGTGGGGGTGCAGGCG     75079      A    AC    C
                                GGG TGGGG  TGCGG GCG
                                ||| |||||  ||||| |||
                                CCC ACCCC  ACGTC CGC
                                  C    C_    _
GAM3341  BAZ1B     5'  AGGGGTGAGAGGGCGGCGCG   75080      A    ACT
                                AGGG TGGGG   GCGGCGCG
                                |||| |||||   ||||||||
                                TCCC ACTCT   CGCCGCGC
                                  C    CC_
GAM3341  CAPNS1    3'  GGAATGGGGAGACCCG       75081          CTGC   G
                                GGGATGGGGA    GGC CG
                                ||||||||||    ||| ||
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                                CCTTACCCCT  CTG GC
                                     ____  G
GAM3341  CHIC2   5'  GGGATGGGGTCTGGACCG   75082       A  C  G
                                GGGATGGGG CTG GGC CG
                                ||||||||| ||| ||| ||
                                CCCTACCCC GAC CTG GC
                                    A  _  _
GAM3341  COL4A1  5'  AGGGACGGCTGCCCGGCG   75083      GGA  __
                                AGGGATGG  CTGC  GGCG
                                ||||||||  ||||  ||||
                                TCCCTGCC  GACG  CCGC
                                    ___   GG
GAM3341  CUL3    5'  GGGGGCGGCGGCGGCGCG   75084    AT  _  ACT
                                GGG  GG GG  GCGGCGCG
                                |||  || ||  ||||||||
                                CCC  CC CC  CGCCGCGC
                                  __  G  GC_
GAM3341  CYP2F1  3'  AGGGATGAGGGCAGAC     75085       ACT  C
                                AGGGATGGGG  GCGG GC
                                ||||||||||  |||| ||
                                TCCCTACTCC  CGTC TG
                                    ___   _
GAM3341  DDB1    3'  AGAGACAAAAGGGCTGTGGCG  75086      ___  A  C
                                AGGGAT  GGGG CTG GGCG
                                ||||||  |||| ||| ||||
                                TCTCTG  TCCC GAC CCGC
                                   TTT   _  A
GAM3341  DIA1    3'  AGGGCGTGGGGTGCGCG    75087    A_   AC  G
                                AGGG  TGGGG  TGCG CG
                                ||||  |||||  |||| ||
                                TCCC  ACCCC  ACGC GC
                                  GC   __   _
GAM3341  DIA1    3'  AGGGATGGGGCTGGGCG    75088       A  C
                                AGGGATGGGG CTG GGCG
                                |||||||||| ||| ||||
                                TCCCTACCCC GAC CCGC
                                    _  _
GAM3341  EXTL1   3'  GGGTGAAGAGTGCGGCGCG  75089    A    C
                                GGG TGGGGA TGCGGCGCG
                                ||| |||||| |||||||||
                                CCC ACTTCT ACGCCGCGC
                                  _    C
GAM3341  FGFR4   3'  GGGATGGGGACTAAGCG    75090         C
                                GGGATGGGGACTG GGCG
                                |||||||||||| ||||
                                CCCTACCCCTGAT TCGC
                                    _
GAM3341  FGFR4   3'  GGGATGGGGACTAAGCG    75090         C
                                GGGATGGGGACTG GGCG
                                |||||||||||| ||||
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                                CCCTACCCCTGAT TCGC
                                          _
GAM3341  GATA6    5'  AGAGATGGGGGAAGGCGGCGCG 75091          ACT_
                                AGGGATGGGG   GCGGCGCG
                                ||||||||||   ||||||||
                                TCTCTACCCC   CGCCGCGC
                                     CTTC
GAM3341  GRB10    5'  GGGTCGGGAACGCAGCGCG   75092    A     T
                                GGG TGGGGAC GCGGCGCG
                                ||| ||||||| ||||||||
                                CCC GCCCTTG CGTCGCGC
                                  A     _
GAM3341  HDAC5    3'  AGGGATGGGGGCCGGGGCG   75093        A  C
                                AGGGATGGGG CTG GGCG
                                |||||||||| ||| ||||
                                TCCCTACCCC GGC CCGC
                                     C  C
GAM3341  HDAC5    3'  AGGGATGGGGGCCGGGGCG   75093        A  C
                                AGGGATGGGG CTG GGCG
                                |||||||||| ||| ||||
                                TCCCTACCCC GGC CCGC
                                     C  C
GAM3341  HK2      5'  AGGGGAGGCGGGCGGCGCG   75094     AT   ACT
                                AGGG  GGGG  GCGGCGCG
                                ||||  ||||  ||||||||
                                TCCC  CTCC  CGCCGCGC
                                  __   GCC
GAM3341  HMGA2    5'  AGGGCTGGGGACGCCGGCG   75095     A     TG
                                AGGG TGGGGAC  CGGCG
                                |||| |||||||  |||||
                                TCCC ACCCCTG  GCCGC
                                  G     CG
GAM3341  HMGN2    5'  GGGATGCAGCGGCGCG      75096      G GACT
                                GGGATG G   GCGGCGCG
                                |||||| |   ||||||||
                                CCCTAC T   CGCCGCGC
                                   G ____
GAM3341  IGFBP1   5'  GGAGGGTGGCGGCGGCGCG   75097    T _ ACT
                                GGA GG GG  GCGGCGCG
                                ||| || ||  ||||||||
                                CCT CC CC  CGCCGCGC
                                  C  A  GC_
GAM3341  INSM1    3'  GGGAGGGGGCAGCGC      75098     T   ACT
                                GGGA GGGG  GCGGCGC
                                |||| ||||  |||||||
                                CCCT CCCC  CGTCGCG
                                  _  ___
GAM3341  LASS1    3'  GAGATGGGCGACAGGCGCG   75099       _  TGC
                                GGGATGGG GAC  GGCGCG
                                ||||||||  |||  ||||||
```

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                                CTCTACCC CTG   CCGCGC
                                    G   T__
GAM3341  LMO2     5'  GGGAGGGGACCGTGCG      75100      T       CG
                                GGGA GGGGACTG  GCG
                                |||| ||||||||  |||
                                CCCT CCCCTGGC  CGC
                                  _       A_
GAM3341  MUS81    3'  GGGCTGGGGGCTGTTTCACG   75101     A     A   CGG
                                GGG TGGGG CTG   CGCG
                                ||| ||||| |||   ||||
                                CCC ACCCC GAC   GTGC
                                  G    C   AAA
GAM3341  NTSR1    3'  AGGGATAGGGGCTGCACCG    75102          A     G
                                AGGGATGGGG CTGCG CG
                                |||||||||| ||||| ||
                                TCCCTATCCC GACGT GC
                                      C    G
GAM3341  OAS3     3'  AGGGATGGAGGCTGTCAA     75103          A   _
                                AGGGATGGGG CTG CGG
                                |||||||||| ||| |||
                                TCCCTACCTC GAC GTT
                                      C   A
GAM3341  PCTK3    3'  AAGGATGGGGAGGCTGTGCG   75104           __   CG
                                AGGGATGGGGA  CTG  GCG
                                ||||||||||  |||  |||
                                TTCCTACCCCT  GAC  CGC
                                     CC   A_
GAM3341  PLIN     3'  AGGGTTGGGGATGAAC      75105      A     C  C
                                AGGG TGGGGA TG GGC
                                |||| |||||| || |||
                                TCCC ACCCCT AC TTG
                                  A     _ _
GAM3341  POU3F2   3'  GGGAGGGGGAGCCCCGCG    75106      T    CT  GG
                                GGGA GGGGA  GC  CGCG
                                |||| |||||  ||  ||||
                                CCCT CCCCT  CG  GCGC
                                  C     __ GG
GAM3341  PPP1R12B 3'  AGGGGTGGGGGCAGCA      75107      A    ACT
                                AGGG TGGGG   GCGGCG
                                |||| |||||   ||||||
                                TCCC ACCCC   CGTCGT
                                  C    ____
GAM3341  PPP1R12B 3'  AGGGGTGGGGGCAGCA      75107      A    ACT
                                AGGG TGGGG   GCGGCG
                                |||| |||||   ||||||
                                TCCC ACCCC   CGTCGT
                                  C    ____
GAM3341  PPP1R12B 3'  AGGGGTGGGGGCAGCA      75107      A    ACT
                                AGGG TGGGG   GCGGCG
                                |||| |||||   ||||||
```

```
                                TCCC ACCCC   CGTCGT
                                  C    ___
GAM3341  PRCP     3'  AGGGATGGGGACTTACAA    75108          _
                                AGGGATGGGGACT GCGG
                                |||||||||||| |||| 
                                TCCCTACCCCTGA TGTT
                                       A
GAM3341  PRKCL1   5'  GGGGCGGGCGCGGCGCG     75109     A   GAC
                                GGG TGGG   TGCGGCGCG
                                ||| ||||   |||||||||
                                CCC GCCC   GCGCCGCGC
                                  C    ___
GAM3341  PTPRG    5'  GGGCTGAGCGCGGCGCG     75110     A   GAC
                                GGG TGGG   TGCGGCGCG
                                ||| ||||   |||||||||
                                CCC ACTC   GCGCCGCGC
                                  G    ___
GAM3341  RTN4R    3'  GGGGTGGCGGGCGGCAGGCG   75111     A  _  ACT    __
                                GGG TGG GG   GCGGC  GCG
                                ||| ||| ||   |||||  |||
                                CCC ACC CC   CGCCG  CGC
                                  C   G ___     TC
GAM3341  RYR1     5'  AGGGAGGGGGCTGCGGGC    75112      T   A     C
                                AGGGA GGGG CTGCGG GC
                                ||||| |||| |||||| ||
                                TCCCT CCCC GACGCC CG
                                   C   _     _
GAM3341  SLC9A3R2 3'  AGGATGGGGGCTCACCG     75113         A  G  G
                                GGGATGGGG CT CG CG
                                ||||||||| || || ||
                                TCCTACCCC GA GT GC
                                      C  _  G
GAM3341  SORCS2   3'  GGAATGGGGGCTGTGGCA    75114         A   C
                                GGGATGGGG CTG GGCG
                                ||||||||| ||| ||||
                                CCTTACCCC GAC CCGT
                                      C   A
GAM3341  SP4      5'  GGGGTGGGGGCGAGGCG     75115     A    ACT   C
                                GGG TGGGG   GCGG GCG
                                ||| |||||   |||| |||
                                CCC ACCCC   CGCT CGC
                                  C    ___    C
GAM3341  SRR      3'  AGGGATGGGAGGCACA      75116          ACTGC
                                AGGGATGGGG    GGCGCG
                                ||||||||||    ||||||
                                TCCCTACCCT    CCGTGT
                                       _____
GAM3341  SUFU     5'  GGCGATGGGGGCTGCAGCG   75117    _     A
                                GG GATGGGG CTGCGGCG
                                || ||||||| ||||||||
```

```
                                CC CTACCCC GACGTCGC
                                 G      C
GAM3341  SYNGR1   3'  AGGGGCGGGGGCAGGC     75118     A    ACT   C
                                AGGG TGGGG   GCGG GC
                                |||| |||||   |||| ||
                                TCCC GCCCC   CGTC CG
                                  C    ___   _
GAM3341  TEGT     3'  AGGGATTGGGGCTCTCAC    75119      _   A  GCGG
                                AGGGAT GGGG CT   CGC
                                |||||| |||| ||   |||
                                TCCCTA CCCC GA   GTG
                                   A   _ GA__
GAM3341  TGFB1    5'  GGGATGAAGGCGGCG      75120        ACT
                                GGGATGGGG   GCGGCG
                                |||||||||   ||||||
                                CCCTACTTC   CGCCGC

                                    ___
GAM3341  UGCG     5'  AGGGTGGGCGCCCGGTGCG   75121     A   GA  G   C
                                AGGG TGGG  CT CGG GCG
                                |||| ||||  || ||| |||
                                TCCC ACCC  GG GCC CGC
                                  _   GC  _   A
GAM3341  WHSC1L1  5'  AGGGACGGGGGGTCGCCGCG   75122        ACTG  G
                                AGGGATGGGG    CG CGCG
                                ||||||||||    || ||||
                                TCCCTGCCCC    GC GCGC
                                      CA__  G
GAM3341  WHSC1L1  5'  AGGGACGGGGGGTCGCCGCG   75122        ACTG  G
                                AGGGATGGGG    CG CGCG
                                ||||||||||    || ||||
                                TCCCTGCCCC    GC GCGC
                                      CA__  G
GAM3341  WNT5A    5'  AGGATGGGGGCAGGACGCG   75123        ACT  _  _
                                GGGATGGGG   GC GG CGCG
                                |||||||||   || || ||||
                                TCCTACCCC   CG CC GCGC
                                     ___  T  T
GAM3341  XPNPEP2  5'  AGGGTGGGGGCTGGCG     75124     A    ACT  _
                                AGGG TGGGG   GC GGCG
                                |||| |||||   || ||||
                                TCCC ACCCC   CG CCGC
                                  _    ___  A
GAM3341  AD-003   5'  AGGGAGGGCGGCGGCGCG    75125      TG   ACT
                                AGGGA  GGG   GCGGCGCG
                                |||||  |||   ||||||||
                                TCCCT  CCC   CGCCGCGC
                                   __  GC_
GAM3341  C20orf177 5'  GGGACGCCCGGCTGCGGCGCG  75126       G__  A
                                GGGATG   GG CTGCGGCGCG
                                ||||||   || ||||||||||
```

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                                CCCTGC   CC GACGCCGCGC
                                   GGG  _
GAM3341  C3IP1    5'  GGGATGGAGTGCGGCGCG    75127         AC
                                GGGATGGGG  TGCGGCGCG
                                |||||||||  |||||||||
                                CCCTACCTC  ACGCCGCGC
                                          __
GAM3341  C5orf5   5'  AAGCTACGGCTGTGGCGCG   75128     A  G  A   C
                                GGG TG GG CTG GGCGCG
                                ||| || || ||| ||||||
                                TTC AT CC GAC CCGCGC
                                  G  G  _  A
GAM3341  CAMTA2   3'  AGGGGTGTGGGAGCAAGGCG   75129      A  _   CT  __
                                AGGG TG GGGA  GC  GGCG
                                |||| || ||||  ||  ||||
                                TCCC AC CCCT  CG  CCGC
                                  C  A   __  TT
GAM3341  CAPN6    3'  AGGGTTGGGGACTTAAAGCCG  75130      A       GC_  G
                                AGGG TGGGGACT   GGC CG
                                |||| ||||||||   ||| ||
                                TCCC ACCCCTGA   TCG GC
                                  A       ATT  _
GAM3341  CARD11   5'  GGGCTGCGGGCGGCGCG     75131     A  G  ACT
                                GGG TG GG   GCGGCGCG
                                ||| || ||   ||||||||
                                CCC AC CC   CGCCGCGC
                                  G  G  ___
GAM3341  CASKIN1  3'  GGGAGGGCCCGGGCGGCGCG   75132      T   GA  __
                                GGGA GGG  CT  GCGGCGCG
                                |||| |||  ||  ||||||||
                                CCCT CCC  GG  CGCCGCGC
                                  _  G_  CC
GAM3341  CHST3    5'  AGGGATGGAGGCGCTGCG    75133         _  A_
                                AGGGATGG GG  CTGCG
                                ||||||||  ||  |||||
                                TCCCTACC CC  GACGC
                                     T  GC
GAM3341  CLSTN1   5'  GGGATGGGGAGCGACGCG    75134          CT
                                GGGATGGGGA  GCGGCGCG
                                ||||||||||  ||||||||
                                CCCTACCCCT  CGCTGCGC
                                          __
GAM3341  CNNM3    3'  GGGATGGGGGCAGGC       75135         ACT   C
                                GGGATGGGG   GCGG GC
                                |||||||||   |||| ||
                                CCCTACCCC   CGTC CG
                                          ___   _
GAM3341  CORO1B   3'  GGGGTGGGAACTGACCCCTGCG 75136     A       CG____
                                GGG TGGGGACTG     GCG
                                ||| |||||||||     |||
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                                CCC ACCCTTGAC     CGC
                                  C        TGGGGA
GAM3341  DDM36    3'  AGGGCTGGGGACTGACCAC   75137     A       _ G
                                AGGG TGGGGACTG C GC
                                |||| ||||||||| | ||
                                TCCC ACCCCTGAC G TG
                                  G        T G
GAM3341  DKFZP761E1824 5'  GGGAGGGGACCAGCCGGCG   75138     T     _ _
                                GGGA GGGGACT GC GGCG
                                |||| ||||||| || ||||
                                CCCT CCCCTGG CG CCGC
                                  _      T  G
GAM3341  DSCAML1   3'  GGCGTGTGGGGCTGCGGCGCG  75139    GA__    A
                                GG    TGGGG CTGCGGCGCG
                                ||    ||||| ||||||||||
                                CC    ACCCC GACGCCGCGC
                                 GCAC    _
GAM3341  FBP17    3'  GATGGGGAGGACAGGCG     75140        CT    C
                                GATGGGGA  GCGG GCG
                                ||||||||  |||| |||
                                CTACCCCT  TGTC CGC
                                     CC    _
GAM3341  FLJ11939  3'  AGGGAGGGGCTGGGGCG     75141      T    A   C
                                AGGGA GGGG CTG GGCG
                                ||||| |||| ||| ||||
                                TCCCT CCCC GAC CCGC
                                  _    _   C
GAM3341  FLJ12089  5'  GGGCTGGGGACGGCGCG     75142     A      TGC
                                GGG TGGGGAC   GGCGCG
                                ||| |||||||   ||||||
                                CCC ACCCCTG   CCGCGC
                                  G      ___
GAM3341  FLJ12765  5'  GGGGGCGACGCGGCGC      75143     AT  G   T
                                GGG  GG GAC GCGGCGC
                                |||  || ||| |||||||
                                CCC  CC CTG CGCCGCG
                                  __  G   _
GAM3341  FLJ13265  3'  AGGAAGACTGCGGCGCG     75144     TGG
                                GGGA   GGACTGCGGCGCG
                                ||||   ||||||||||||||
                                TCCT   TCTGACGCCGCGC
                                  ___
GAM3341  FLJ14126  3'  GGGCTGGGGACTTAGCCG    75145     A      GC   G
                                GGG TGGGGACT  GGC CG
                                ||| ||||||||  ||| ||
                                CCC ACCCCTGA  TCG GC
                                  G       A_   _
GAM3341  FLJ20048  3'  GGGATGGGGGTGGGGGCG    75146         AC  C  C
                                GGGATGGGG  TG GG GCG
                                |||||||||  || || |||
```

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                                CCCTACCCC  AC CC CGC
                                     C_ _  C
GAM3341  FLJ21916  5'  AGGGCGTGGGGGCGGCG    75147     A_    ACT
                                AGGG  TGGGG   GCGGCG
                                ||||  |||||   ||||||
                                TCCC  ACCCC   CGCCGC
                                  GC    ___
GAM3341  GS3955    5'  GGGCACAGAGTTGCGGCGCG   75148    _     AC
                                GGG ATGGGG  TGCGGCGCG
                                ||| ||||||  |||||||||
                                CCC TGTCTC  ACGCCGCGC
                                  G     A_
GAM3341  GTPBP1    3'  GGGGTGGGGGCAATGCG     75149     A    ACT    C
                                GGG TGGGG   GCGG GCG
                                ||| |||||   |||| |||
                                CCC ACCCC   CGTT CGC
                                  C    ___    A
GAM3341  HRIHFB2436 5'  GGGACGGGGAGACGC       75150          CTGC
                                GGGATGGGGA    GGCGC
                                ||||||||||    |||||
                                CCCTGCCCCT    CTGCG
                                      _____
GAM3341  HSA243666 3'  GGGATGGGGTGGGATGTGCG   75151          AC  C  C___
                                GGGATGGGG  TG GG    GCG
                                |||||||||  || ||    |||
                                CCCTACCCC  AC CC    CGC
                                     __ _  TACA
GAM3341  KCNK13    5'  GGGAGGGGGCGTGGCGCG    75152      T    AC  C
                                GGGA GGGG  TG GGCGCG
                                ||||  ||||  ||  ||||||
                                CCCT  CCCC  GC CCGCGC
                                  C    __  A
GAM3341  KIAA0379  5'  AAGGTAAGCTGCGGCG      75153      A    GA
                                AGGG TGGG  CTGCGGCG
                                ||||  ||||  ||||||||
                                TTCC  ATTC  GACGCCGC
                                   _    __
GAM3341  KIAA0515  3'  AGGGATGGGCGGCTGGGCCG   75154          GA_   C   G
                                AGGGATGGG   CTG GGC CG
                                |||||||||   ||| ||| ||
                                TCCCTACCC   GAC CCG GC
                                     GCC   _   _
GAM3341  KIAA1138  3'  AGGGTGGGGACCGGCG      75155      A      TG
                                AGGG TGGGGAC  CGGCG
                                ||||  |||||||  |||||
                                TCCC  ACCCCTG  GCCGC
                                   _      __
GAM3341  KIAA1533  5'  AGCGATGGGGAGCTGCTTGGCG 75156     G       _    __
                                AG GATGGGGA CTGC  GGCG
                                ||  |||||||| ||||  ||||
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                                TC CTACCCCT GACG  CCGC
                                 G       C   AA
GAM3341  KIAA1553  3'  AGGAATGGGGGCAGCG      75157          ACT
                                AGGGATGGGG   GCGGCG
                                ||||||||||   ||||||
                                TCCTTACCCC   CGTCGC
                                      ___
GAM3341  KIAA1602  3'  AGGGACTGGGGGGCTGCG    75158       __   A
                                AGGGAT  GGGG CTGCG
                                ||||||  |||| |||||
                                TCCCTG  CCCC GACGC
                                   AC   C
GAM3341  KIAA1607  3'  GGGATGGGCACACGGCG     75159        G  T
                                GGGATGGG AC GCGGCG
                                |||||||| || ||||||
                                CCCTACCC TG TGCCGC
                                     G  _
GAM3341  KIAA1978  3'  GGGAGGGGGCTGCGGCA     75160      T   A
                                GGGA GGGG CTGCGGCG
                                |||| |||| ||||||||
                                CCCT CCCC GACGCCGT
                                  C   _
GAM3341  LGI3      5'  GGATGCGGACTGCGGCGCG   75161       G
                                GGATG GGACTGCGGCGCG
                                ||||| ||||||||||||
                                CCTAC CCTGACGCCGCGC
                                   G
GAM3341  MANBAL    3'  AGGGATGGGGGATGTACAG   75162          AC__
                                AGGGATGGGG    TGCGG
                                ||||||||||    |||||
                                TCCCTACCCC    ATGTC
                                      CTAC
GAM3341  MAPKAPK5  5'  GGGATGAGGACCCCGGCG    75163           G
                                GGGATGGGGACT CGGCG
                                |||||||||||| |||||
                                CCCTACTCCTGG GCCGC
                                       G
GAM3341  MAPKAPK5  5'  GGGATGAGGACCCCGGCG    75163           G
                                GGGATGGGGACT CGGCG
                                |||||||||||| |||||
                                CCCTACTCCTGG GCCGC
                                       G
GAM3341  MGC10818  5'  AGGAGGTGAGGGTGGCGCG   75164      __    ACTGC
                                GGGA  TGGGG    GGCGCG
                                ||||  |||||    ||||||
                                TCCT  ACTCC    CCGCGC
                                  CC    CA___
GAM3341  MGC13053  5'  GGGATGGAGGCTGCCCCG    75165          A   GG
                                GGGATGGGG CTGC  CG
                                ||||||||| ||||  ||
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                                CCCTACCTC GACG  GC
                                     C   GG
GAM3341  MGC4175  5'  GGGTGGGGGCTCACACGCG   75166    A   A _  G
                                GGG TGGGG CT GCG CGCG
                                ||| ||||| || ||| ||||
                                CCC ACCCC GA TGT GCGC
                                  _    C  G  _
GAM3341  MGC4796  3'  GGGCATGGGGAGAAAGGGGCG  75167    _     CTGC  C
                                GGG ATGGGGA   GG GCG
                                ||| |||||||   || |||
                                CCC TACCCCT   CC CGC
                                  G      CTTT  C
GAM3341  MMP28    5'  GGGATGGGACTGCTCTGCG   75168       G    GGC
                                GGGATGGG ACTGC   GCG
                                |||||||| |||||   |||
                                CCCTACCC TGACG   CGC
                                     _    AGA
GAM3341  MMP28    5'  GGGATGGGACTGCTCTGCG   75168       G    GGC
                                GGGATGGG ACTGC   GCG
                                |||||||| |||||   |||
                                CCCTACCC TGACG   CGC
                                     _    AGA
GAM3341  NKX2C    5'  GGGGCGGGGAGGCAGCGCG   75169    A     CT
                                GGG TGGGGA  GCGGCGCG
                                ||| ||||||  ||||||||
                                CCC GCCCCT  CGTCGCGC
                                  C     C_
GAM3341  NMP200   5'  GGAATGGGGACAGCCGCG    75170         T  G
                                GGGATGGGGAC GC GCG
                                |||||||||||  || |||
                                CCTTACCCCTG CG CGC
                                       T  G
GAM3341  NXPH3    3'  AGGGATGAGGCGGCA      75171        GACT
                                AGGGATGGG   GCGGCG
                                |||||||||   ||||||
                                TCCCTACTC   CGCCGT
                                            ____
GAM3341  NYD-SP11 5'  AGGGACGGGTACGGCG     75172        GAC
                                AGGGATGGG   TGCGGCG
                                |||||||||   |||||||
                                TCCCTGCCC   ATGCCGC
                                            ___
GAM3341  PSIP1    5'  AGGAGATGCGGCGGCGCG    75173    _   G GACT
                                AGG GATG G   GCGGCGCG
                                ||| |||| |   ||||||||
                                TCC CTAC C   CGCCGCGC
                                  T   G ____
GAM3341  PSIP2    5'  AGGAGATGCGGCGGCGCG    75173    _   G GACT
                                AGG GATG G   GCGGCGCG
                                ||| |||| |   ||||||||
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                                TCC CTAC C    CGCCGCGC
                                  T   G ____
GAM3341  SDCCAG43  3'  GGTGTGGAGACGGCGCG     75174    GA      TGC
                                GG  TGGGGAC   GGCGCG
                                ||  |||||||   ||||||
                                CC  ACCTCTG   CCGCGC
                                 AC      ___
GAM3341  SLC26A1   3'  AGGGCTGGGGGCTGCTCG    75175     A    A   GG
                                AGGG TGGGG CTGC  CG
                                |||| ||||| ||||  ||
                                TCCC ACCCC GACG  GC
                                  G    C   A_
GAM3341  SMPD2     5'  GGGACGGGGGCGGCCGGCG   75176         ACT    __
                                GGGATGGGG   GCGGC  GCG
                                |||||||||   |||||  |||
                                CCCTGCCCC   CGCCG  CGC
                                     ___    GC
GAM3341  TIAF1     3'  GGGGTGGGGGCTGGAGGTGCG  75177     A    A   C_  C
                                GGG TGGGG CTG  GG GCG
                                |||  ||||| |||  ||  |||
                                CCC ACCCC GAC  CC CGC
                                  C    C   CT  A
GAM3341  UBAP      3'  AGGGATGGTGGTTCTGCG     75178         _  A_
                                AGGGATGG GG  CTGCG
                                |||||||| ||  |||||
                                TCCCTACC CC  GACGC
                                    A  AA
GAM3341  UBN1      3'  GGGATGGGGCGGCAC       75179         GACT
                                GGGATGGG    GCGGCGC
                                ||||||||    |||||||
                                CCCTACCC    CGCCGTG
                                     ____
GAM3341  LOC115574 3'  AGGGATGGGGGCTCCCCAC    75180          A  GCGG
                                AGGGATGGGG CT    CGC
                                |||||||||| ||    |||
                                TCCCTACCCC GA    GTG
                                     C  GGG_
GAM3341  LOC115757 3'  AGGATGGGGTACAGTGGCG    75181          _  TGC
                                GGGATGGGG AC   GGCG
                                |||||||| ||   ||||
                                TCCTACCCC TG   CCGC
                                    A  TCA
GAM3341  LOC126123 5'  GGGATGAGGGCGGAGCG     75182         ACT    C
                                GGGATGGGG   GCGG GCG
                                |||||||||   |||| |||
                                CCCTACTCC   CGCC CGC
                                     ___    T
GAM3341  LOC126528 3'  AGGGATGGTGGTTGGCAGGGCG 75183         _  ACT    C
                                AGGGATGG GG   GCGG GCG
                                ||||||| ||   |||| |||
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                                TCCCTACC CC   CGTC CGC
                                    A  AAC    C
GAM3341  LOC128977 5'  AGGGCGGCTGCGGCGCG     75184      A   GGA
                                AGGG TGG   CTGCGGCGCG
                                |||| |||   ||||||||||
                                TCCC GCC   GACGCCGCGC
                                  _   ___
GAM3341  LOC129642 5'  AGGATGGGGATGCAGCGGCGCG 75185          CT__
                                GGGATGGGGA    GCGGCGCG
                                ||||||||||    ||||||||
                                TCCTACCCCT    CGCCGCGC
                                     ACGT
GAM3341  LOC143384 5'  GGAGAGGGCTGCGGTGCG    75186     T    A     C
                                GGA GGGG CTGCGG GCG
                                ||| |||| |||||| |||
                                CCT TCCC GACGCC CGC
                                  C    _     A
GAM3341  LOC145719 5'  AGGGATGGCGGGCTGGAG    75187         _  A   C
                                AGGGATGG GG CTG GG
                                |||||||| || ||| ||
                                TCCCTACC CC GAC TC
                                    G  C   C
GAM3341  LOC147057 3'  AGGCATGGGAGTGGCGGCGCG  75188     G      ACT
                                AGG ATGGGG   GCGGCGCG
                                ||| ||||||   ||||||||
                                TCC TACCCT   CGCCGCGC
                                  G     CAC
GAM3341  LOC147136 3'  GGTGATGGGGATTGTCAG     75189    _       C  _
                                GG GATGGGGA TG CGG
                                || |||||||| || |||
                                CC CTACCCCT AC GTC
                                 A       A  A
GAM3341  LOC147299 3'  AGGGATGGGGCCTGGATGCG   75190          A   C GC
                                AGGGATGGGG CTG G  GCG
                                |||||||||| ||| |  |||
                                TCCCTACCCC GAC C  CGC
                                     G   _ TA
GAM3341  LOC147791 3'  GGGAGGGACTGCGGTGCG     75191      TG         C
                                GGGA  GGGACTGCGG GCG
                                ||||  |||||||||| |||
                                CCCT  CCCTGACGCC CGC
                                  __         A
GAM3341  LOC147958 3'  GGGCGGGAATTGCGGCGCG    75192     A      C
                                GGG TGGGGA TGCGGCGCG
                                ||| |||||| |||||||||
                                CCC GCCCTT ACGCCGCGC
                                  _     A
GAM3341  LOC150197 3'  AAGGATGGGGACATCGCG     75193           TGCGG
                                AGGGATGGGGAC     CGCG
                                ||||||||||||     ||||
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                                TTCCTACCCCTG    GCGC
                                    TA___
GAM3341  LOC150203 5'  GGGATGGAGTGGGGTGCG    75194        AC  C  C
                                GGGATGGGG  TG GG GCG
                                |||||||||  || || |||
                                CCCTACCTC  AC CC CGC
                                    __  C  A
GAM3341  LOC152586 5'  AGGGACGGGGTTGAGCGCG    75195         AC  C
                                AGGGATGGGG  TG GGCGCG
                                ||||||||||  || ||||||
                                TCCCTGCCCC  AC TCGCGC
                                    A_  _
GAM3341  LOC158436 3'  GGGATGGGGAGTGGACG     75196         C  C
                                GGGATGGGGA TG GGCG
                                |||||||||| || ||||
                                CCCTACCCCT AC CTGC
                                    C  _
GAM3341  LOC159090 5'  GGGGCGGGGGCTGGGGGCG   75197     A    A   C  C
                                GGG TGGGG CTG GG GCG
                                ||| ||||| ||| || |||
                                CCC GCCCC GAC CC CGC
                                  C    C   _  C
GAM3341  LOC166206 5'  GGAATGGGGGCCGGGGCGCG   75198         A   C
                                GGGATGGGG CTG GGCGCG
                                ||||||||| ||| ||||||
                                CCTTACCCC GGC CCGCGC
                                    C   C
GAM3341  LOC170394 5'  GGGATGGAGGCCGAGGGCGCG  75199         A   C_
                                GGGATGGGG CTG  GGCGCG
                                ||||||||| |||  ||||||
                                CCCTACCTC GGC  CCGCGC
                                    C   TC
GAM3341  LOC200091 3'  GGATGACACAGGCGGCGCG    75200       G G  T_
                                GGATG G AC  GCGGCGCG
                                ||||| | ||  ||||||||
                                CCTAC T TG  CGCCGCGC
                                   _ G  TC
GAM3341  LOC202126 3'  AGGGACTGGAAACGTGGTGCG  75201       _  GG  T C  C
                                AGGGA TGG  AC G GG GCG
                                ||||| |||  || | || |||
                                TCCCT ACC  TG C CC CGC
                                   G   TT  _ A  A
GAM3341  LOC219731 5'  GGATGGCAACACGTGGCGCG   75202       G  _  C
                                GGATGG GAC TG GGCGCG
                                |||||| ||| || ||||||
                                CCTACC TTG GC CCGCGC
                                   G   T  A
GAM3341  LOC221882 3'  AGGGAGGGGACCAGCG      75203       T     TG
                                AGGGA GGGGAC  CGGCG
                                ||||| ||||||  |||||
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                                TCCCT CCCCTG  GTCGC
                                  _    __
GAM3341  LOC255941 5'  GGGATGGGGGCGGCG      75204        ACT
                                GGGATGGGG   GCGGCG
                                |||||||||   ||||||
                                CCCTACCCC   CGCCGC
                                   ___
GAM3341  LOC256867 5'  GGGTATGGGGAGCATCG     75205    _     CT   G
                                GGG ATGGGGA  GCG CG
                                ||| |||||||  ||| ||
                                CCC TACCCCT  CGT GC
                                  A      __  A
GAM3341  LOC90515  5'  GGGATGGGGAGGGAGGGCGCG 75206        CTGC_
                                GGGATGGGGA    GGCGCG
                                ||||||||||    ||||||
                                CCCTACCCCT    CCGCGC
                                     CCCTC
GAM3341  LOC91748  3'  AGGATGGGGGGCGGCG     75207        ACT
                                GGGATGGGG   GCGGCG
                                |||||||||   ||||||
                                TCCTACCCC   CGCCGC
                                   C__
GAM3341  LOC92223  5'  AGGGAGGGGGCAGCG      75208      T   ACT
                                AGGGA GGGG   GCGGCG
                                |||||  ||||  ||||||
                                TCCCT CCCC   CGTCGC
                                  _   ____
GAM3341  LOC92340  3'  AGGGGTGGGGGGCCCAGCG   75209     A    A_  G
                                AGGG TGGGG  CT CGGCG
                                ||||  |||||  ||  |||||
                                TCCC ACCCC  GG GTCGC
                                  C    CC  _
GAM3342  ADAT1     3'  CTTGTCCTGCGTGGAGGAAGGC 75212          CTCC_  A
            A                   TTTGTCCTGCGTG    AG CA
                                ||||||||||||    || ||
                                GAACAGGACGCAC    TC GT
                                      CTCCT  C
GAM3342  GLS       3'  TTTGTCCTGTGTGCACAA    75213        C   TC
                                TTTGTCCTG GTGC  CAG
                                |||||||| ||||  |||
                                AAACAGGAC CACG  GTT
                                     A   T_
GAM3342  SFRS7     3'  TTTGTCCCAATTTCAGACAA  75214        C  GCTC
                                TTTGTCCTG GT    CAGACAA
                                |||||||| ||    |||||||
                                AAACAGGGT TA    GTCTGTT
                                     _  AA__
GAM3342  WWP2      3'  TTTGTCCCGTGGATACCCAGGC 75215        C__   T   A
            A                   TTTGTCCTG   GTGC CCAG CA
                                |||||||||   |||| |||| ||
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                                AAACAGGGC   TATG GGTC GT
                                     ACC   _   C
GAM3342  FBXO2    3'  TTTGCCCCTCCAGGCA     75216       TGCGTG     A
                                TTTGTCC     CTCCAG CA
                                |||||||     |||||| ||
                                AAACGGG     GAGGTC GT
                                   _______     C
GAM3342  FLJ14621 3'  TTTGTCCCTCCCTTTCCAGACA 75217        GCGTGC
                                TTTGTCCT     TCCAGACA
                                ||||||||     ||||||||
                                AAACAGGG     AGGTCTGT
                                     AGGGAA
GAM3342  HSP105B  3'  TTTGTTCTGCATGCTGCTAAC  75218      C       CCA
                                TTTGT CTGCGTGCT   GAC
                                ||||| |||||||||   |||
                                AAACA GACGTACGA   TTG
                                   A        CGA
GAM3342  HT014    3'  TTTGTCCTTCCCAACA      75219       GCGTGC   A
                                TTTGTCCT     TCC GACA
                                ||||||||     ||| ||||
                                AAACAGGA     AGG TTGT
                                     _______  G
GAM3342  KIAA0255 3'  TTTATTTTGCGTGCCTGCAG   75220      CC      C_
                                TTTGT  TGCGTGCT  CAG
                                |||||  ||||||||  |||
                                AAATA  ACGCACGG  GTC
                                   AA       AC
GAM3342  KIAA1317 3'  TGTTTCTGACTTCAGACAAC   75221     C_  CGT   C
                                TGT  CTG   GCT CAGACAAC
                                |||  |||   ||| ||||||||
                                ACA  GAC   TGA GTCTGTTG
                                  AA  ___   A
GAM3342  LHFPL2   3'  TTTGTCCTCTGTGCTTTCC   75222       GC   __
                                TTTGTCCT  GTGC  TCC
                                ||||||||  ||||  |||
                                AAACAGGA  CACG  AGG
                                     GA    AA
GAM3342  MGC21675 3'  TTTGTCCTGGTGTCCAG     75223        C   C
                                TTTGTCCTG GTG TCCAG
                                ||||||||| ||| |||||
                                AAACAGGAC CAC AGGTC
                                     _   _
GAM3342  SLC12A5  3'  TTTGCTCTTGCCAACCAGACAA 75224     TC  GCG   __
                                TTTG  CT   TGCT  CCAGACAA
                                ||||  ||   ||||  ||||||||
                                AAAC  GA   ACGG  GGTCTGTT
                                  GA  ___    TT
GAM3342  STRN3    3'  TTTGTGCCTGCCCCAGA     75225      CCT  G
                                TTTGT   GC TGCTCCAGA
                                |||||   || |||||||||
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                                AAACA  CG ACGGGGTCT
                                   ___ G
GAM3342  ZFP67    3'  TCTGTCCTGCGTGCTCCCAC  75226              AG
                                TTTGTCCTGCGTGCTCC  AC
                                ||||||||||||||||  ||
                                AGACAGGACGCACGAGG  TG
                                      G_
GAM3342  ZNF297B  3'  TCTTTCCTCTTTCCAGACAA  75227    G   GCGTGC
                                TTT TCCT     TCCAGACAA
                                ||| ||||     |||||||||
                                AGA AGGA     AGGTCTGTT
                                  A   GAA___
GAM3342  LOC144266 5'  TTTGTCCTGTGTGCCTTTGAC  75228        C    CCA
                                TTTGTCCTG GTGCT  GAC
                                ||||||||| |||||  |||
                                AAACAGGAC CACGG  CTG
                                      A    AAA
GAM3342  LOC152502 3'  TTTGTCCTCGTGCTTCAGGCCA 75229        G    C  A_
                                TTTGTCCT CGTGCT CAG  CA
                                |||||||| |||||| |||  ||
                                AAACAGGA GCACGA GTC  GT
                                     _     A  CG
GAM3342  LOC158969 5'  CTTGTCCTGCCAGTATCTAGAC 75230         __  C  C
           A                     TTTGTCCTGC  GTG TC AGACA
                                ||||||||||  ||| || |||||
                                GAACAGGACG  CAT AG TCTGT
                                      GT  _  A
GAM3342  LOC256906 3'  TTGTCCCCTCCAGACA     75231       GCGTG
                                TTGTCCT    CTCCAGACA
                                |||||||    |||||||||
                                AACAGGG    GAGGTCTGT

                                  _____
GAM3342  LOC257146 5'  TTTGTCCTGTCGTGCTCTTTTG 75232        _     CA___
           GAC                    TTTGTCCTG CGTGCTC    GAC
                                ||||||||| |||||||    |||
                                AAACAGGAC GCACGAG    CTG
                                     A      AAAAC
GAM3343  GRAP2    5'  ACTTTGTGCTGTCTTCCAT   75235      G     CCC
                                ACTTTG TGCTGTC  TTCTAT
                                |||||| |||||||  ||||||
                                TGAAAC ACGACAG  AAGGTA

                                  _    ___
GAM3343  RHAG     3'  CTTTGGTTACTCCCTT     75236       _  GTC
                                CTTTGGT GCT  CCCTT
                                ||||||| |||  |||||
                                GAAACCA TGA  GGGAA
                                   A  ___
GAM3343  RNMT     3'  TTTGGTACAACTTCTAT     75237        TGTCCC
                                TTTGGTGC     CTTCTAT
                                ||||||||     |||||||
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                                AAACCATG     GAAGATA
                                    TT____
GAM3343 BM-002   3' ACTTTGCTACCCCCTTCT    75238     TGG   GT
                                ACTT  TGCT  CCCCTTCT
                                ||||  ||||  ||||||||
                                TGAA  ACGA  GGGGAAGA
                                  ___   TG
GAM3343 FLJ20330 3' ACTTTGTGCTGTCTTCT     75239      G     CCC
                                ACTTTG TGCTGTC  TTCT
                                |||||| |||||||  ||||
                                TGAAAC ACGACAG  AAGA
                                  _     ___
GAM3343 KIAA0895 3' ACCTTGGCACCGTTTCT     75240       TG   CCCC
                                ACTTTGG  CTGT   TTCT
                                |||||||  ||||   ||||
                                TGGAACC  GGCA   AAGA
                                   GT   _____
GAM3343 LGI4     5' CTTTGGTGTCTAATTTTCT   75241       _  TCCCC
                                CTTTGGTG CTG    TTCT
                                |||||||| |||    ||||
                                GAAACCAC GAT    AAGA
                                    A  TAA__
GAM3343 PPP4R2   5' TTCGGTGCTGATACTTCTATT 75242        TCCC
                                TTTGGTGCTG   CTTCTATT
                                ||||||||||   ||||||||
                                AAGCCACGAC   GAAGATAA
                                     TAT_
GAM3343 PRO2000  5' CTTGGTGCTGTTCTCT     75243        CCCC
                                TTTGGTGCTGT   TTCT
                                ||||||||||   ||||
                                GAACCACGACA   GAGA
                                    A___
GAM3343 LOC200854 5' TTCGGTGCTGATACTTCTATT 75242        TCCC
                                TTTGGTGCTG   CTTCTATT
                                ||||||||||   ||||||||
                                AAGCCACGAC   GAAGATAA
                                     TAT_
GAM3343 LOC202404 5' ACCTTTTTCTGGTTTCCTTCTA 75244     GGTG  TCC_
           TT                   ACTTT   CTG   CCTTCTATT
                                |||||   |||   |||||||||
                                TGGAA   GAC   GGAAGATAA
                                  AAA_  CAAA
GAM3343 LOC221662 3' CTTTGGTGCCTGTCCACC    75245       _   _
                                CTTTGGTGC TGTCC CC
                                ||||||||| ||||| ||
                                GAAACCACG ACAGG GG
                                     G    T
GAM3343 LOC90918 5' TTTGGTACTGTCAGTTCT    75246         CCC
                                TTTGGTGCTGTC  TTCT
                                ||||||||||||  ||||
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                                AAACCATGACAG  AAGA
                                      TC_
GAM3343 LOC92181 3' CTTGGTGCTGTCCTTC     75247          CC
                                TTTGGTGCTGTCC TTC
                                |||||||||||| |||
                                GAACCACGACAGG AAG
                                      __
GAM3344 HELZ     3' TGTAACAATACACAAATTTAAA 75250      A   T
                                TGTAA CAAT ATATAAATTTAAA
                                ||||| |||| ||||||||||||
                                ACATT GTTA TGTGTTTAAATTT
                                  _  _
GAM3344 PDE7A    3' TGTAAACAATTAATAAA     75251          T
                                TGTAAACAATTA ATAAA
                                |||||||||||| |||||
                                ACATTTGTTAAT TATTT
                                      _
GAM3344 SHOC2    3' TGTAAACAATACATAAAATTTA 75252         T    _
             AA                   TGTAAACAAT ATATAAA TTTAAA
                                |||||||||| ||||||| ||||||
                                ACATTTGTTA TGTATTT AAATTT
                                      _     T
GAM3344 SOX9     3' TGTAAACAATAATATACAAA  75253         __
                                TGTAAACAAT  TATATAAA
                                |||||||||  ||||||||
                                ACATTTGTTA  ATATGTTT
                                      TT
GAM3344 C1orf22  3' TGTAAACATTATATAAA    75254        A
                                TGTAAACA TTATATAAA
                                |||||||| |||||||||
                                ACATTTGT AATATATTT
                                     _
GAM3344 LAPTM4A  3' TGCAAACGATTATATAAA   75255        A
                                TGTAAAC ATTATATAAA
                                ||||||| ||||||||||
                                ACGTTTG TAATATATTT
                                    C
GAM3344 MGC21675 3' TGTAAACAATATATACAA   75256         _
                                TGTAAACAAT TATATAA
                                |||||||||| |||||||
                                ACATTTGTTA ATATGTT
                                      T
GAM3344 LOC93297 3' TAAACAATTATATACACTAA  75257           AAT
                                TAAACAATTATATA  TTAA
                                ||||||||||||||  ||||
                                ATTTGTTAATATAT  GATT
                                        GT_
GAM3345 CFTR     3' TGTAATATATGTTTGAAACATT 75260     C    CA
             A                   TGTA ATATA  TTTGGAACATTA
                                |||| |||||  ||||||||||||
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                                ACAT TATAT  AAACTTTGTAAT
                                  _    AC
GAM3345  DISC1    3'  TACATATACAAGAAGGCATT   75261        TTT_  AA
                                TACATATACA   GG  CATT
                                ||||||||||   ||  ||||
                                ATGTATATGT   CC  GTAA
                                     TCTT  __
GAM3345  MADH6    3'  TGTCCATATACACACATT    75262    A       TTGGA
                                TGT CATATACAT    ACATT
                                ||| |||||||||    |||||
                                ACA GTATATGTG    TGTAA
                                  G      _____
GAM3345  RECK     3'  TGTGCATACACACAAGAA    75263    A       TT
                                TGT CATATACAT  GGA
                                ||| |||||||||  |||
                                ACA GTATGTGTG  CTT
                                  C       TT
GAM3345  SOS2     3'  TGTACATACATGGCATATT   75264        CATT   AAC
                                TGTACATATA   TGG   ATT
                                ||||||||||   |||   |||
                                ACATGTATGT   ACC   TAA
                                     ____  GTA
GAM3345  BIRC1    3'  TGTACATATACTTTCTGA    75265         A   G
                                TGTACATATAC TTT GA
                                |||||||||| ||| ||
                                ACATGTATATG AAG CT
                                     A   A
GAM3345  FLJ10970 3'  TGTAATATACATTTAATAGCAC 75266     C        GA___
            ATTA                   TGTA ATATACATTTG    ACATTA
                                |||| ||||||||||    ||||||
                                ACAT TATATGTAAAT    TGTAAT
                                  _        TATCG
GAM3345  KIAA1580 5'  TGCACATATACACATTTG    75267          __
                                TGTACATATACAT  TTG
                                ||||||||||||  |||
                                ACGTGTATATGTG  AAC
                                      TA
GAM3345  SDF1     3'  GTGCATATACATTTTTTCATT  75268    A       GGAA
                                GT CATATACATTT    CATT
                                || ||||||||||    ||||
                                CA GTATATGTAAA    GTAA
                                 C         AAA_
GAM3345  LOC135154 3'  TGTACATATTCAGAAAACA   75269        A  TTT
                                TGTACATAT CA   GGAACA
                                |||||||| ||   ||||||
                                ACATGTATA GT   TTTTGT
                                     A  C__
GAM3345  LOC151877 3'  TGTATCTATAGAATGGAACATT 75270     CA   CATT
            A                   TGTA  TATA    TGGAACATTA
                                ||||  ||||    ||||||||||
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                                ACAT  ATAT   ACCTTGTAAT
                                  AG   CTT_
GAM3345  LOC158230 3'  TGTCACATAGATTTGGAA    75271     A     C
                                TGT CATATA ATTTGGAA
                                ||| |||||| ||||||||
                                ACA GTGTAT TAAACCTT
                                  _     C
GAM3345  LOC51136  3'  CATATACATTAGGTTGAACATT 75272          TG___
              A                  CATATACATT    GAACATTA
                                 ||||||||||    ||||||||
                                 GTATATGTAA    CTTGTAAT
                                      TCCAA
GAM3346  DMD      3'  AGTATTTATATACTTATAGACA 75275        GATGG__
              T                  AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                 TCATAAAT     TATCTGTA
                                     ATATGAA
GAM3346  DMD      3'  AGTATTTATATACTTATAGACA 75275        GATGG__
              T                  AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                 TCATAAAT     TATCTGTA
                                     ATATGAA
GAM3346  DMD      3'  AGTATTTATATACTTATAGACA 75275        GATGG__
              T                  AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                 TCATAAAT     TATCTGTA
                                     ATATGAA
GAM3346  DMD      3'  AGTATTTATATACTTATAGACA 75275        GATGG__
              T                  AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                 TCATAAAT     TATCTGTA
                                     ATATGAA
GAM3346  DMD      3'  AGTATTTATATACTTATAGACA 75275        GATGG__
              T                  AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                 TCATAAAT     TATCTGTA
                                     ATATGAA
GAM3346  DMD      3'  AGTATTTATATACTTATAGACA 75275        GATGG__
              T                  AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                 TCATAAAT     TATCTGTA
                                     ATATGAA
GAM3346  DMD      3'  AGTATTTATATACTTATAGACA 75275        GATGG__
              T                  AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                 TCATAAAT     TATCTGTA
                                     ATATGAA
GAM3346  DMD      3'  AGTATTTATATACTTATAGACA 75275        GATGG__
              T                  AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                 TCATAAAT     TATCTGTA
                                     ATATGAA
GAM3346  DMD      3'  AGTATTTATATACTTATAGACA 75275        GATGG__
              T                  AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                 TCATAAAT     TATCTGTA
                                     ATATGAA
GAM3346  DMD      3'  AGTATTTATATACTTATAGACA 75275        GATGG__
              T                  AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
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                                TCATAAAT     TATCTGTA
                                   ATATGAA
GAM3346  DMD     3'  AGTATTTATATACTTATAGACA 75275       GATGG__
             T                   AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                TCATAAAT     TATCTGTA
                                   ATATGAA
GAM3346  DMD     3'  AGTATTTATATACTTATAGACA 75275       GATGG__
             T                   AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                TCATAAAT     TATCTGTA
                                   ATATGAA
GAM3346  DMD     3'  AGTATTTATATACTTATAGACA 75275       GATGG__
             T                   AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                TCATAAAT     TATCTGTA
                                   ATATGAA
GAM3346  DMD     3'  AGTATTTATATACTTATAGACA 75275       GATGG__
             T                   AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                TCATAAAT     TATCTGTA
                                   ATATGAA
GAM3346  DMD     3'  AGTATTTATATACTTATAGACA 75275       GATGG__
             T                   AGTATTTA     GTAGACAT
                                 ||||||||     ||||||||
                                TCATAAAT     TATCTGTA
                                   ATATGAA
GAM3346  HPSE    3'  CAGTATTTGGAACAAGGTA   75276       A  T__
                                CAGTATTT GA   GGGTA
                                ||||||||  ||   |||||
                                GTCATAAA CT   TCCAT
                                   C  TGT
GAM3346  RAG2    3'  TGAGTATTTGGGTAAA     75277   C     TAGA
                                A AGTATT    TGGGTAGA
                                |  ||||||    ||||||||
                                A TCATAA    ACCCATTT
                                 C     ____
GAM3346  RET     3'  TACAGTATTTGAATGAGAC   75278        AG   GGT
                                TACAGTATTT  ATG   AGAC
                                ||||||||||  |||   ||||
                                ATGTCATAAA  TAC   TCTG
                                   CT   ___
GAM3346  RET     3'  TACAGTATTTGAATGAGAC   75278        AG   GGT
                                TACAGTATTT  ATG   AGAC
                                ||||||||||  |||   ||||
                                ATGTCATAAA  TAC   TCTG
                                   CT   ___
GAM3346  RET     3'  TACAGTATTTGAATGAGAC   75278        AG   GGT
                                TACAGTATTT  ATG   AGAC
                                ||||||||||  |||   ||||
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                                ATGTCATAAA TAC  TCTG
                                     CT  ___
GAM3346 RET     3' TACAGTATTTGAATGAGAC  75278       AG  GGT
                                TACAGTATTT ATG  AGAC
                                |||||||||| |||  ||||
                                ATGTCATAAA TAC  TCTG
                                     CT  ___
GAM3346 FLJ13340 3' TACAGTGTTTCAGGGGTGA  75279      A_   AT  A
                                TACAGT TTTAG GGGT GA
                                |||||| ||||| |||| ||
                                ATGTCA AAGTC CCCA CT
                                   CA   __  _
GAM3346 FLJ32783 3' GCAACTGGGAGATGGGTAGACA 75280    TTT___
             T                   GTA     AGATGGGTAGACAT
                                |||     ||||||||||||||
                                CGT     TCTACCCATCTGTA
                                  TGACCC
GAM3346 KIAA1041 3' CAGATTTAGAAAAGCAGACAT  75281    T     TG
                                CAG ATTTAGA  GGTAGACAT
                                ||| |||||||  |||||||||
                                GTC TAAATCT  TCGTCTGTA
                                  _     TT
GAM3346 KIAA1243 3' ACAGTATTTTGTAGGTA    75282       AGA
                                ACAGTATTT   TGGGTA
                                |||||||||   ||||||
                                TGTCATAAA   ATCCAT
                                     AC_
GAM3346 M96     3' TACAGTCTTTCAGTAGGCA  75283      A_   A
                                TACAGT  TTTAG TGGGTA
                                ||||||  ||||| ||||||
                                ATGTCA  AAGTC ATCCGT
                                   GA   _
GAM3346 TBDN100  3' TACAGTGTTTCAGGGGTGA  75279      A_   AT  A
                                TACAGT  TTTAG  GGGT GA
                                ||||||  |||||  |||| ||
                                ATGTCA  AAGTC  CCCA CT
                                   CA   __  _
GAM3346 LOC158204 3' CAGTATTTAATGGCAAA    75284       GATG
                                CAGTATTTA   GGTAGA
                                |||||||||   ||||||
                                GTCATAAAT   CCGTTT
                                     TA__
GAM3346 LOC51074 3' CAGTATTTAGTGGCAAA    75285       ATG
                                CAGTATTTAG  GGTAGA
                                ||||||||||  ||||||
                                GTCATAAATC  CCGTTT
                                     A__
GAM3347 BCL7C   5' CCCGTCCGGCGGGCTC     75288      AAA
                                CCCGT  CGGCGGGCTC
                                |||||  ||||||||||
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                                GGGCA  GCCGCCCGAG
                                  G__
GAM3347 DPH2L1   3' CCCCTGCAGACGGCGGGCTC  75289     _  A
                                CCCC GTA ACGGCGGGCTC
                                |||| ||| ||||||||||
                                GGGG CGT TGCCGCCCGAG
                                  A  C
GAM3347 EDR1     5' CCTCCGCGGCGGGCTC     75290    _  TAAA
                                CC CCG   CGGCGGGCTC
                                || |||   ||||||||||
                                GG GGC   GCCGCCCGAG
                                 A  ____
GAM3347 FLJ14840 5' CCTCCGCAGGCGGGCTC    75291    _   AAC
                                CC CCGTA  GGCGGGCTC
                                || |||||  |||||||||
                                GG GGCGT  CCGCCCGAG
                                 A   ___
GAM3347 FLJ22548 5' CACTCCACGGCGGCGGGCTC  75292    _ _ TAAA
                                TAC CC CG   CGGCGGGCTC
                                ||| || ||   ||||||||||
                                GTG GG GC   GCCGCCCGAG
                                  A  T  C___
GAM3347 KIAA1040 3' TACTCCGTGACAGCAAGTTC  75293    C   AA     C
                                TAC CCGT  ACGGCGGG TC
                                ||| ||||  |||||||| ||
                                ATG GGCA  TGTCGTTC AG
                                  A   C_     A
GAM3347 KIAA1383 3' CCCATAAATATATCAGGCTC  75294       CGG__
                                CCCGTAAA    CGGGCTC
                                ||||||||    |||||||
                                GGGTATTT    GTCCGAG
                                     ATATA
GAM3347 KIAA1554 3' TACCCCGCAAGTGGACTC    75295       AAC  C
                                TACCCCGTA   GG GGGCTC
                                |||||||||   || ||||||
                                ATGGGGCGT   TC CCTGAG
                                     ___  A
GAM3347 KIAA1940 5' CCAGCAGGGCGGCGGGCTC   75296   C   AA_
                                CC GTA   CGGCGGGCTC
                                || |||   ||||||||||
                                GG CGT   GCCGCCCGAG
                                 T   CCC
GAM3347 MGC16075 5' CACCCCGTGGGCATCAGGGCT 75297       AAAC  ____
                                TACCCCGT   GGC   GGGCT
                                ||||||||   |||   |||||
                                GTGGGGCA   CCG   CCCGA
                                     C___   TAGT
GAM3347 NCOA5    5' TACCAGCGCGGCGGGCTC    75298     CC  AAA
                                TACC  GT   CGGCGGGCTC
                                ||||  ||   ||||||||||
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                                ATGG  CG   GCCGCCCGAG
                                  T_  C__
GAM3347  NETO1     5'  CCTCCGCCCCGGGCGGGCTC   75299    _    AAAC
                                CC CCGT    GGCGGGCTC
                                || ||||    |||||||||
                                GG GGCG    CCGCCCGAG
                                 A    GGGC
GAM3347  NICE-3    3'  TACCCTTTAGACACAAGCTC   75300      CG  A   G
                                TACCC  TA ACG CGGGCTC
                                |||||  || ||| |||||||
                                ATGGG  AT TGT GTTCGAG
                                   AA  C   _
GAM3347  LOC115098 3'  CACCCCGTGGGTGAACTGGCTC 75301        AAAC_   G
                                TACCCCGT     GGC GGCTC
                                ||||||||     ||| |||||
                                GTGGGGCA     TTG CCGAG
                                     CCCAC   A
GAM3347  LOC130617 5'  ACCCCGCACTCTGGCGGGCTC  75302        AAC_
                                ACCCCGTA    GGCGGGCTC
                                ||||||||    |||||||||
                                TGGGGCGT    CCGCCCGAG
                                     GAGA
GAM3347  LOC138835 5'  CCCAACAGGCGGCGGGCTC    75303     CG  AA
                                CCC  TA  CGGCGGGCTC
                                |||  ||  ||||||||||
                                GGG  GT  GCCGCCCGAG
                                  TT  CC
GAM3347  LOC150372 3'  TACCCCGTAGGCACT       75304        AAC   GG
                                TACCCCGTA   GGC  GCT
                                |||||||||   |||  |||
                                ATGGGGCAT   CCG  TGA
                                      ___   __
GAM3347  LOC154386 3'  TACCCAGTAAACAATAACTC   75305      C       CG
                                TACCC GTAAACGG  GGCTC
                                |||||  ||||||||  |||||
                                ATGGG CATTTGTT  TTGAG
                                   T       A_
GAM3347  LOC169611 3'  TACGCCCGTGGCAGGCT     75306     _    AAAC
                                TAC CCCGT    GGCGGGCT
                                |||  |||||    ||||||||
                                ATG GGGCA    CCGTCCGA
                                  C    _____
GAM3347  LOC201522 3'  CACCCCAGCGGCGGGCTC    75307       TAAA
                                TACCCCG    CGGCGGGCTC
                                |||||||    ||||||||||
                                GTGGGGT    GCCGCCCGAG
                                    C___
GAM3347  LOC96234  3'  TACCCCGCTAGGCACGCC    75308        AAAC    G
                                TACCCCGT    GGCG GCT
                                ||||||||    |||| |||
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                                ATGGGGCG   CCGT CGG
                                    AT__   G
GAM3348 CISH    3' CAGTACCAGGACATCCA    75311       C
                                CAGTACCA GGACATCCA
                                |||||||| |||||||||
                                GTCATGGT CCTGTAGGT
                                    _
GAM3348 CISH    3' CAGTACCAGGACATCCA    75311       C
                                CAGTACCA GGACATCCA
                                |||||||| |||||||||
                                GTCATGGT CCTGTAGGT
                                    _
GAM3348 F2R     3' CAGTGGATGGGCATCCAGAAGT 75312     ACCAC  A
                                CAGT    GG CATCCAGAAGT
                                ||||    || ||||||||||
                                GTCA    CC GTAGGTCTTCA
                                  CCTAC  _
GAM3348 F2RL3   3' CAGTTCTGCAGGCCAGAAGT  75313     ACCA   ACAT
                                CAGT   CGG   CCAGAAGT
                                ||||   |||   ||||||||
                                GTCA   GTC   GGTCTTCA
                                  AGAC  C___
GAM3348 MAT1A   3' AGACCACTTACCCCAGAAGT  75314    T    GG  A
                                AG ACCAC  AC TCCAGAAGT
                                || |||||  || |||||||||
                                TC TGGTG  TG GGGTCTTCA
                                 _    AA  _
GAM3348 MGP     3' AGTATCACACCAGAAG      75315      C   GACAT
                                AGTA CACG    CCAGAAG
                                |||| ||||    |||||||
                                TCAT GTGT    GGTCTTC
                                  A   ______
GAM3348 PON2    3' AGTAGTCACAGTGCCAGAAGT  75316     C_    ACAT
                                AGTA  CACGG   CCAGAAGT
                                ||||  |||||   ||||||||
                                TCAT  GTGTC   GGTCTTCA
                                  CA    AC__
GAM3348 SLC22A2  5' AGGTCCAACATCCAGGAGT   75317    TA   CGG      A
                                AG  CCA   ACATCCAG AGT
                                ||  |||   |||||||| |||
                                TC  GGT   TGTAGGTC TCA
                                 CA  ___       C
GAM3348 AP3M2   3' CAGTCCATTTCCAGAAG     75318     A   CGGACA
                                CAGT CCA     TCCAGAAG
                                |||| |||     ||||||||
                                GTCA GGT     AGGTCTTC
                                  _  AA_____
GAM3348 DLGAP1   5' CAGGGTCATGGACACCCGGAAG 75319     TAC  C      A
            T                    CAG   CA GGACATCC GAAGT
                                |||   || |||||||| |||||
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                                GTC   GT CCTGTGGG CTTCA
                                  CCA  A       C
GAM3348  FLJ11259  3'  CAGTACCCTGAACCCAGAAGT  75320        ACG  C
                                CAGTACC   GA ATCCAGAAGT
                                |||||||   || ||||||||||
                                GTCATGG   CT TGGGTCTTCA
                                    GA_  _
GAM3348  FLJ31300  3'  GTGCCAGGGTCCAGAAGT    75321    A   C  ACA
                                GT CCA GG   TCCAGAAGT
                                || ||| ||   |||||||||
                                CA GGT CC   AGGTCTTCA
                                 C   C  ___
GAM3348  KIAA1678  3'  AGTATAGTTATCCAGAAGT   75322     CCAC  AC
                                AGTA   GG  ATCCAGAAGT
                                ||||   ||  ||||||||||
                                TCAT   TC  TAGGTCTTCA
                                  A___  AA
GAM3348  PSTPIP2   3'  GCTCCAAATCCAGAAGT     75323    A   CGGAC
                                GT CCA    ATCCAGAAGT
                                || |||    ||||||||||
                                CG GGT    TAGGTCTTCA
                                 A  T____
GAM3348  VDAC3     3'  CAGTTTGACCTCCAGAAG    75324     ACCACG   A
                                CAGT     GAC TCCAGAAG
                                ||||     ||| ||||||||
                                GTCA     CTG AGGTCTTC
                                  AA____   G
GAM3348  LOC92578  5'  CAGTACCATGGGTCAGCCC   75325        C  A_  _
                                CAGTACCA GG  CA TCC
                                |||||||| ||  || |||
                                GTCATGGT CC  GT GGG
                                    A  CA  C
GAM3349  ATP11A    3'  TCATCCTTTTCTTTTTTA    75328          C
                                TCATTCTTTTCT TTTTTA
                                |||||||||||| ||||||
                                AGTAGGAAAAGA AAAAAT
                                                _
GAM3349  C14orf1   3'  TCGTTCATTTCTCTTTCC    75329    A   T
                                TC TTC TTTCTCTTTTT
                                || ||| ||||||||||
                                AG AAG AAAGAGAAAGG
                                 C   T
GAM3349  CASP10    3'  TCATTCCTTGACATTTTTTTAT 75330        TCTC__
           GA                    TCATTCTTT     TTTTTATGA
                                 |||||||||     |||||||||
                                 AGTAAGGAA     AAAAATACT
                                     CTGTAA
GAM3349  CASP10    3'  TCATTCCTTGACATTTTTTTAT 75330        TCTC__
           GA                    TCATTCTTT     TTTTTATGA
                                 |||||||||     |||||||||
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                                AGTAAGGAA     AAAAATACT
                                     CTGTAA
GAM3349  CD3E     3'  ATTTTTTTCTCTCTCAGCTGA  75331     C         TA_
                                ATT TTTTCTCTTTT   TGA
                                ||| ||||||||||   |||
                                TAA AAAAGAGAGAG   ACT
                                  A          TCG
GAM3349  EGFL5    3'  TCATTTTTTTCTCTATAACTG  75332      C       TTTTA
                                TCATT TTTTCTCT     TG
                                ||||| ||||||||     ||
                                AGTAA AAAAGAGA     AC
                                   A       TATTG
GAM3349  GPR17    3'  TCAGTTCTTCCTTTTTATG    75333     _     TCT
                                TCA TTCTTT   CTTTTTATG
                                ||| ||||||   |||||||||
                                AGT AAGAAG   GAAAAATAC
                                  C     ___
GAM3349  IL11     3'  TCATTCTTTCTTTTTTG     75334         TTC      A
                                TCATTCTT   TCTTTTT TG
                                ||||||||   ||||||| ||
                                AGTAAGAA   AGAAAAA AC
                                     ___      _
GAM3349  KRT4     3'  TCATTTTCTTCTCTGCCCATG  75335      C       T
                                TCATT TTTTCTCT TTTATG
                                ||||| |||||||| ||||||
                                AGTAA AGAAGAGA GGGTAC
                                   A       C
GAM3349  KRT6B    3'  TCATTTTTCTTCTCAGAATTAT 75336      C_      TTT_
             G                   TCATT  TTTTCTC    TTATG
                                |||||  |||||||    |||||
                                AGTAA  AGAAGAG    AATAC
                                   AA      TCTT
GAM3349  MN1      3'  TCATTCTATTCTCTTTCTCTG  75337        T        A
                                TCATTCT TTCTCTTTTT TG
                                ||||||| |||||||||| ||
                                AGTAAGA AAGAGAAAGA AC
                                     T         G
GAM3349  PPP1R2   3'  ATCCTTTTCTTCACTCTATGA  75338          _ T
                                ATTCTTTTCT C TTTTATGA
                                |||||||||| | ||||||||
                                TAGGAAAAGA G GAGATACT
                                      A T
GAM3349  RAD9     3'  TTCTTTTCTTTTTTTAATGA   75339         C     _
                                TTCTTTTCT TTTTTA TGA
                                ||||||||| |||||| |||
                                AAGAAAAGA AAAAAT ACT
                                     A     T
GAM3349  SON      3'  TCATTTTTTACTCCCTTCTTAT 75340       CTT__
             GA                   TCATT     TTCTCTTTTTATGA
                                |||||     ||||||||||||||
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                              AGTAA    GAGGGAAGAATACT
                                 AAAAT
GAM3349 SON     3' TCATTTTTTACTCCCTTCTTAT 75340      CTT__
           GA                  TCATT    TTCTCTTTTTATGA
                               |||||    ||||||||||||||
                               AGTAA    GAGGGAAGAATACT
                                 AAAAT
GAM3349 SON     3' TCATTTTTTACTCCCTTCTTAT 75340      CTT__
           GA                  TCATT    TTCTCTTTTTATGA
                               |||||    ||||||||||||||
                               AGTAA    GAGGGAAGAATACT
                                 AAAAT
GAM3349 SYT4    3' TTCTTTTCTCTTTTCTGA    75341            A
                               TTCTTTTCTCTTTTT TGA
                               |||||||||||||| |||
                               AAGAAAAGAGAAAAG ACT

GAM3349 TTC3    3' CACAGCTTCTCTTTTTGTG   75342    TCT       A
                               CAT   TTTCTCTTTTT TG
                               |||   |||||||||| ||
                               GTG   GAAGAGAAAAA AC
                                 TC_        C
GAM3349 XRCC2   3' TCAGTCTTGTTCCTTTTTATG  75343    T   _   T
                               TCA TCTT TTC CTTTTTATG
                               ||| |||| ||| |||||||||
                               AGT AGAA AAG GAAAAATAC
                                 C   C  _
GAM3349 C19orf7  3' TCATTTTTCTCTTTTT     75344      CT
                               TCATT  TTTCTCTTTTT
                               |||||  ||||||||||
                               AGTAA  AAAGAGAAAAA

GAM3349 C5orf5   5' CATTCTTTTGTCATTTATG   75345        C  TT
                               CATTCTTTT TC  TTTATG
                               |||||||| ||  ||||||
                               GTAAGAAAA AG  AAATAC
                                     C  T_
GAM3349 DKFZp761F2014 3' TCTTCTTTTCTCTTTTCA    75346    A
                               TC TTCTTTTCTCTTTTTA
                               || ||||||||||||||||
                               AG AAGAAAAGAGAAAAGT

GAM3349 FLJ11016 3' ATTCCAACTCTTTTTATG    75347      TTT
                               ATTCT   CTCTTTTTATG
                               |||||   ||||||||||
                               TAAGG   GAGAAAAATAC
                                 TT_
GAM3349 FLJ13081 3' TCCTTTCCTTTTATGA      75348        CT
                               TCTTTTCT  TTTTATGA
                               ||||||||  ||||||||
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                                AGGAAAGG  AAAATACT
                                    __
GAM3349  FLJ13433  3'  TCATTCTTCTTTTAATG     75349        TTTC     T
                                TCATTCT    TCTTTT ATG
                                |||||||    |||||| |||
                                AGTAAGA    AGAAAA TAC
                                    ____     T
GAM3349  FLJ30927  3'  TCATTCTTTTCATTACCATTTA 75350          T___  T
              TG                   TCATTCTTTTC    CT TTTATG
                                |||||||||||    || ||||||
                                AGTAAGAAAAG    GG AAATAC
                                     TAAT  T
GAM3349  KIAA0677  3'  TCATTCCTTTTCTTTTTA     75351          C
                                TCATTCTTTT TCTTTTTA
                                |||||||||| ||||||||
                                AGTAAGGAAA AGAAAAAT
                                    _
GAM3349  KIAA1466  5'  TCATTCCTTTTCTTTCATG    75352          C     T
                                TCATTCTTTT TCTTTT ATG
                                |||||||||| |||||| |||
                                AGTAAGGAAA AGAAAG TAC
                                    _     _
GAM3349  KIAA1856  3'  TCTTTTCTTTTTTTTTATGA   75353        C__
                                TCTTTTCT   TTTTTATGA
                                ||||||||   |||||||||
                                AGAAAAGA   AAAAATACT
                                     AAA
GAM3349  KIAA1985  3'  TCATTCTTCTTCTTGTG     75354        TTTC      A
                                TCATTCT    TCTTTTT TG
                                |||||||    ||||||| ||
                                AGTAAGA    AGAAGAA AC
                                    ____     C
GAM3349  MAIL      3'  TTCTTTTCTATTTTATG     75355          CT
                                TTCTTTTCT  TTTTATG
                                |||||||||  |||||||
                                AAGAAAAGA  AAAATAC
                                     T_
GAM3349  N4BP3     3'  TCATTCTTTTTCTTTTCTGA   75356          C      A
                                TCATTCTTTT TCTTTTT TGA
                                |||||||||| ||||||| |||
                                AGTAAGAAAA AGAAAAG ACT
                                    _     _
GAM3349  PRO0641   3'  TCATTCCTTTTTTTACCACTTA 75357          CT___  T
              TGA                   TCATTCTTTT     CT TTTATGA
                                |||||||||     || |||||||
                                AGTAAGGAAA     GG GAATACT
                                     AAAAT  T
GAM3349  SEMA5A    3'  TTCTTTTCTTCTCAAATATGA  75359          _   TT_
                                TTCTTTTCT CTT   TATGA
                                ||||||||| |||   |||||
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                                AAGAAAAGA GAG   ATACT
                                     A   TTT
GAM3349  SEMA5A    3'  CATTCTTTTTCTTCATTTTATG 75358         _  _ T
              A                   CATTCTTTT CT C TTTTATGA
                                  ||||||||| || | ||||||||
                                  GTAAGAAAA GA G AAAATACT
                                       A  A T
GAM3349  SPRY4     3'  TCATTCCTTTTCTTCTT     75360          C
                                  TCATTCTTTT TCTTTTT
                                  |||||||||| |||||||
                                  AGTAAGGAAA AGAAGAA
                                           _
GAM3349  TBX21     3'  TCTTCTTTTCTCCAGCTG    75361    A        TTTTA
                                  TC TTCTTTTCTCT    TG
                                  || ||||||||||     ||
                                  AG AAGAAAAGAGG    AC
                                   _         TCG__
GAM3349  UBF-fl    3'  TCATTCTTTTTTCTTTTT    75362          C
                                  TCATTCTTTT TCTTTTT
                                  |||||||||| |||||||
                                  AGTAAGAAAA AGAAAAA
                                       A
GAM3349  LOC131873 3'  TTCTTTCCAAATTTTATGA   75363        TCT
                                  TTCTTTTC   TTTTATGA
                                  ||||||||   ||||||||
                                  AAGAAAGG   AAAATACT
                                      TTT
GAM3349  LOC148195 3'  TTCTTTTCTCTTTAAGCTGA  75364           TTA_
                                  TTCTTTTCTCTTT    TGA
                                  ||||||||||||    |||
                                  AAGAAAAGAGAAA    ACT
                                        TTCG
GAM3349  LOC158332 3'  TTCTCTTCCCCCCATGA     75365          TT
                                  TTCTTTTCTCTT  TATGA
                                  ||||||||||||  |||||
                                  AAGAGAAGGGGG  GTACT
                                          __
GAM3349  LOC162605 3'  ATTCTTTTCTCTAAAATGA   75366          TTTT
                                  ATTCTTTTCTCT    ATGA
                                  ||||||||||||    ||||
                                  TAAGAAAAGAGA    TACT
                                       TTT_
GAM3349  LOC201895 3'  TCATTTTTTCTCTCTTC     75367      C
                                  TCATT TTTTCTCTTTTT
                                  ||||| ||||||||||||
                                  AGTAA AAAAGAGAGAAG
                                      _
GAM3349  LOC205927 5'  CTCTCCCTCTCTTTTTGTG   75368       _       A
                                  TTCTTT TCTCTTTTT TG
                                  |||||| ||||||||| ||
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                                GAGAGG AGAGAAAAA AC
                                   G       C
GAM3349  LOC253926 3'  TCCGTTTTCACCTTTTTATGA  75369    _    _
                                TTC TTTTC TCTTTTTATGA
                                ||| ||||| ||||||||||
                                AGG AAAAG GGAAAAATACT
                                  C    T
GAM3349  LOC255446 3'  TCGATCTTTTCTCAGAACATG  75370    AT       TTTT
                                TC  TCTTTTCTC    TATG
                                ||  |||||||||   ||||
                                AG  AGAAAAGAG   GTAC
                                 CT       TCTT
GAM3350  KIAA1841  3'  TTAAAATAATAATAACAT    75373
                                TTAAAATAATAATAATAT
                                ||||||||||||||||||
                                AATTTTATTATTATTGTA

GAM3351  ANXA8    3'  CTTTGCTCTTGTTCTTCTG   75376        CA__
                                CTTTGTTCT   TTTCTG
                                |||||||||   ||||||
                                GAAACGAGA   GAAGAC
                                     ACAA
GAM3351  ANXA8    3'  CTTTGCTCTTGTTCTTCTG   75376        CA__
                                CTTTGTTCT   TTTCTG
                                |||||||||   ||||||
                                GAAACGAGA   GAAGAC
                                     ACAA
GAM3351  CTBP1    3'  GCCTTTGTTTTGTTTTTCTAA  75377        CTCA_
                                GCCTTTGTT    TTTCTGA
                                |||||||||    |||||||
                                CGGAAACAA    AAAGATT
                                     AACAA
GAM3351  FGF1     3'  CTTTGTCCCTGTTTCTGGTCAT 75378        CA    AC
                                CTTTGTTCT  TTTCTG  CAT
                                |||||||||  ||||||  |||
                                GAAACAGGG  AAAGAC  GTA
                                     AC     CA
GAM3351  FGF1     3'  CTTTGTCCCTGTTTCTGGTCAT 75378        CA    AC
                                CTTTGTTCT  TTTCTG  CAT
                                |||||||||  ||||||  |||
                                GAAACAGGG  AAAGAC  GTA
                                     AC     CA
GAM3351  FGF1     3'  CTTTGTCCCTGTTTCTGGTCAT 75378        CA    AC
                                CTTTGTTCT  TTTCTG  CAT
                                |||||||||  ||||||  |||
                                GAAACAGGG  AAAGAC  GTA
                                     AC     CA
GAM3351  GAB2     3'  CCTTGTCCTTTTTCTGA    75379        CA
                                CTTTGTTCT  TTTCTGA
                                |||||||||  |||||||
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                                GGAACAGGA  AAAGACT
                                     A_
GAM3351  GAB2     3'  CCTTGTCCTTTTTCTGA     75379         CA
                                CTTTGTTCT  TTTCTGA
                                |||||||||  |||||||
                                GGAACAGGA  AAAGACT
                                     A_
GAM3351  MAK      5'  GCTTTTGTCCTCACACTG    75380    C         TT
                                GC TTTGTTCTCAT  CTG
                                || ||||||||||  |||
                                CG AAACAGGAGTG  GAC
                                 A         T_
GAM3351  NFIA     3'  GCCTTTGCTGTTTGACCA    75381         CTCATTTC
                                GCCTTTGTT       TGACCA
                                |||||||||       ||||||
                                CGGAAACGA       ACTGGT
                                     CAA_____
GAM3351  PKHD1    3'  GCCTTTGTTCTGATCTCCA   75382          C
                                GCCTTTGTTCT ATTTCTG
                                |||||||||| |||||||
                                CGGAAACAAGA TAGAGGT
                                      C
GAM3351  ADG-90   3'  GCCTTTGTTCATACAGACCAT  75383          TCATTTCT
                                GCCTTTGTTC       GACCAT
                                |||||||||        ||||||
                                CGGAAACAAG       CTGGTA
                                      TATGT___
GAM3351  ATP1B4   3'  GCTTTTGTTCTCATCTTTCC   75384    C         TT   GA
                                GC TTTGTTCTCA  TCT  CC
                                || ||||||||||  |||  ||
                                CG AAACAAGAGT  AGA  GG
                                 A         __   AA
GAM3351  DKFZp547G183 3'  GCCTTTGTTCTTGCTTCT    75385          CA
                                GCCTTTGTTCT  TTTCT
                                ||||||||||  |||||
                                CGGAAACAAGA  GAAGA
                                      AC
GAM3351  FLJ10922 3'  CTTTGTTTCACCGACCA     75386        C   TTT
                                CTTTGTT TCA   CTGACCA
                                ||||||| |||   |||||||
                                GAAACAA AGT   GGCTGGT
                                     _  ___
GAM3351  FLJ12526 3'  GCCTTTGTTTCCATAGGTCCCA 75387         CT   TTCTGA
           T                    GCCTTTGTT  CAT     CCAT
                                |||||||||  |||     ||||
                                CGGAAACAA  GTA     GGTA
                                     AG   TCCAG_
GAM3351  FLJ23537 3'  GCCTTTGTTTTCCTA       75388         CTCA
                                GCCTTTGTT    TTTCTG
                                |||||||||    ||||||
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                                CGGAAACAA   AAGGAT
                                      ____
GAM3351  GLIO703   3'  CTTTGTCCCTGTTTCTGGTCAT 75378        CA    AC
                                CTTTGTTCT  TTTCTG  CAT
                                |||||||||  ||||||  |||
                                GAAACAGGG  AAAGAC  GTA
                                     AC     CA
GAM3351  MGC15619  5'  GCCTTTGTTCTTAGTGAGCTCC 75389         CATTTCTGA_
           CAT                   GCCTTTGTTCT        CCAT
                                ||||||||||         ||||
                                CGGAAACAAGA        GGTA
                                     ATCACTCGAG
GAM3351  MGC32104  3'  CCTTTGTCATTTCTGA     75390       TTC
                                CCTTTG   TCATTTCTGA
                                ||||||   ||||||||||
                                GGAAAC   AGTAAAGACT
                                   ___
GAM3351  PRO1853   5'  CTTTGTTCCATCATGACCAT   75391       T   TC
                                CTTTGTTC CATT  TGACCAT
                                |||||||| ||||  |||||||
                                GAAACAAG GTAG  ACTGGTA
                                    _   T_
GAM3351  SCDGF-B   3'  GCCTGAGCTATTTCTGA     75392     TT  CTC
                                GCCT  GTT   ATTTCTGA
                                ||||  |||   ||||||||
                                CGGA  CGA   TAAAGACT
                                  CT  ___
GAM3351  SCDGF-B   3'  GCCTGAGCTATTTCTGA     75392     TT  CTC
                                GCCT  GTT   ATTTCTGA
                                ||||  |||   ||||||||
                                CGGA  CGA   TAAAGACT
                                  CT  ___
GAM3351  LOC142972 3'  CTTTGCTCTTGTTCTTCTG   75376        CA__
                                CTTTGTTCT   TTTCTG
                                |||||||||   ||||||
                                GAAACGAGA   GAAGAC
                                     ACAA
GAM3351  LOC143888 3'  GCCTTTGTTCTTGGCC      75393         CATTTC  A
                                GCCTTTGTTCT     TG CC
                                ||||||||||     || ||
                                CGGAAACAAGA     AC GG
                                     _____ C
GAM3351  LOC147080 3'  GCCTTTGCTCTCCTGATCA   75394          ATTT   C
                                GCCTTTGTTCTC   CTGA CA
                                ||||||||||||   |||| ||
                                CGGAAACGAGAG   GACT GT
                                     ____   A
GAM3351  LOC148809 3'  GCCTTTGCTCTCATTCTG    75395           T
                                GCCTTTGTTCTCATT CTG
                                ||||||||||||||| |||
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                                CGGAAACGAGAGTAA GAC
                                                _
GAM3351  LOC149773 5'  GCCTTTGTTTTCCTTTTGCC  75396        C  A  C  A
                                GCCTTTGTT TC TTT TG CC
                                ||||||||| || ||| || ||
                                CGGAAACAA AG GAA AC GG
                                     A  _  A  _
GAM3351  LOC150113 5'  CTTTTGGTTTTCTGACCAT   75397     GTTCTCA
                                CTTT      TTTCTGACCAT
                                ||||      ||||||||||
                                GAAA      AAAGACTGGTA
                                  ACCA___
GAM3351  LOC150335 5'  CTTTTCCCTTCTGAC      75398     GT   AT
                                CTTT  TCTC  TTCTGAC
                                ||||  ||||  |||||||
                                GAAA  AGGG  AAGACTG
                                  __   __
GAM3351  LOC200091 3'  GCCTTTGTCCTCGTCT     75399          ATT
                                GCCTTTGTTCTC   TCT
                                ||||||||||||   |||
                                CGGAAACAGGAG   AGA
                                      C__
GAM3351  LOC219722 3'  ACCTTTGTTCTTGCAGCACTG  75400          __  TTT
                                GCCTTTGTTCT  CA   CTG
                                ||||||||||  ||   |||
                                TGGAAACAAGA  GT   GAC
                                      AC  CGT
GAM3351  LOC220549 5'  GCCTTTGTTCCCGAATCCTG   75401          AT_
                                GCCTTTGTTCTC   TTCTG
                                ||||||||||||   |||||
                                CGGAAACAAGGG   AGGAC
                                      CTT
GAM3351  LOC257095 5'  GCTTTTGCTCTCTCTGACCAT  75402    C       ATT
                                GC TTTGTTCTC   TCTGACCAT
                                || |||||||||   |||||||||
                                CG AAACGAGAG   AGACTGGTA
                                 A       ___
GAM3352  AGM1      3'  TTAGTGTTTAAGAAAAACA    63661          T
                                TTAGTGTTTAA AAAAATA
                                |||||||||| |||||||
                                AATCACAAATT TTTTTGT
                                      C
GAM3352  CD80      3'  TTAGTGTTTAATAGATAATGA  75405          AAAAT
                                TTAGTGTTTAATA    ATGG
                                ||||||||||||    ||||
                                AATCACAAATTAT    TACT
                                       CTAT_
GAM3352  CLECSF5   3'  TTAGTGTTGTAATAAAAAATAT 75406        _       _
              GA                  TTAGTGTT TAATAAAAA TATGG
                                ||||||||| ||||||||| |||||
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                                AATCACAA ATTATTTTT ATACT
                                    C        T
GAM3352  IL21R    3'  GTGTTTAATAAATATCTCTTGG 63663          A  A___
              G                  GTGTTTAATAAA AT    TGGG
                                 |||||||||||| ||    ||||
                                 CACAAATTATTT TA    ACCC
                                       A  GAGA
GAM3352  KERA     3'  TTAGTGTTAATAAGCTATGGA  75407        T    AAA
                                 TTAGTGTT AATAA   TATGGG
                                 |||||||| |||||   ||||||
                                 AATCACAA TTATT   ATACCT
                                     _    CG_
GAM3352  YES1     3'  TTAGAGTTTAATACTTGGG    63664      T       AAAATA
                                 TTAG GTTTAATA     TGGG
                                 |||| ||||||||      ||||
                                 AATC CAAATTAT     ACCC
                                   T       GA____
GAM3352  LOC200059 3'  TTAGTGTTTAAAAAAAT     63666          T
                                 TTAGTGTTTAA AAAAAT
                                 |||||||||||| ||||||
                                 AATCACAAATT TTTTTA
                                           _
GAM3353  IKBKB    3'  AAGCTGTAAAGTGAGAGA     75410          AC  _
                                 AAGCTGTAAA  GA AGG
                                 ||||||||||  || |||
                                 TTCGACATTT  CT TCT
                                       CA  C
GAM3353  LIG4     5'  AGCTGTAAAATGAGATCT     75411          C  A  _
                                 AGCTGTAAAA GA GG CT
                                 |||||||||| || || ||
                                 TCGACATTTT CT CT GA
                                       A  _  A
GAM3353  MAPK1    3'  AAGCTGTAGAAGGAAAAAGAAT 75412          A  C     CT
              TG                   AAGCTGTA AA GAAGG  AATTG
                                 |||||||| || |||||  |||||
                                 TTCGACAT TT CTTTT  TTAAC
                                      C  C     TC
GAM3353  ROR2     3'  GCTGTAAAATGAATGGACC    75413          C   _  _
                                 GCTGTAAAA GAA GG CT
                                 ||||||||| ||| || ||
                                 CGACATTTT CTT CC GG
                                       A   A  T
GAM3353  RXRB     3'  AGCTGTAAAGGGAAGGCC     75414          AC
                                 AGCTGTAAA  GAAGGCT
                                 |||||||||  |||||||
                                 TCGACATTT  CTTCCGG
                                       CC
GAM3353  AMOT     3'  AACTGTGAAAAGGTGGCTAATT 75415        A   CGAA
              G                    AGCTGT AAA    GGCTAATTG
                                 ||||||  |||    |||||||||
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                                TTGACA TTT   CCGATTAAC
                                   C  TCCA
GAM3353  FLJ20400  3'  AAGCTGTGGGACGAAAGC   75416       AAA
                                AAGCTGT  ACGAAGGC
                                |||||||  ||||||||
                                TTCGACA  TGCTTTCG
                                   CCC
GAM3353  KIAA1503  3'  AAGCTGTAGAAGAAGGC    75417       A  C
                                AAGCTGTA AA GAAGGC
                                |||||||| || ||||||
                                TTCGACAT TT CTTCCG
                                    C  _
GAM3353  MLCB      3'  AAGCTGTAAAGCTAAGGGC  75418        ACG  _
                                AAGCTGTAAA  AAGG C
                                ||||||||||  |||| |
                                TTCGACATTT  TTCC G
                                     CGA   C
GAM3353  RNF38     3'  AACTGTGAAGACTAAT     75419      AAAAC
                                AGCTGT   GAAGGCTAAT
                                ||||||   ||||||||||
                                TTGACA   CTTCTGATTA
                                   _____
GAM3354  ARHA      3'  GGGCTGTGCTTGCAGCAAG  75422     GTA      ATT
                                GGGC  TGCTTGTA  TAAG
                                ||||  ||||||||  ||||
                                CCCG  ACGAACGT  GTTC
                                  AC_      C__
GAM3354  STRIN     3'  AGGCGTATGTTCATTAAGA  75423       C TG AATT
                                GGGCGTATG T  T   TAAGA
                                ||||||||| |  |   |||||
                                TCCGCATAC A  A   ATTCT
                                     A GT ____
GAM3354  LOC92497  3'  GGGCTGTGTTACCCTTTAAGAT 75424     GTA  C   AA
                                GGGC  TG TTGT  TTTAAGAT
                                ||||  || ||||  ||||||||
                                CCCG  AC AATG  AAATTCTA
                                  AC_  _   GG
GAM3355  GAB2      3'  CTTCCACTAGCCCATTTT   75427       T
                                CTTCTACT GCCCATTTT
                                |||||||| |||||||||
                                GAAGGTGA CGGGTAAAA
                                     T
GAM3355  GAB2      3'  CTTCCACTAGCCCATTTT   75427       T
                                CTTCTACT GCCCATTTT
                                |||||||| |||||||||
                                GAAGGTGA CGGGTAAAA
                                     T
GAM3355  CYYR1     3'  TCTGAACTTCATTTCCCACTTT 75428   CA    TACTTG
                                TC  AACTTC    CCCATTTT
                                ||  ||||||    ||||||||
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                                AG  TTGAAG     GGGTGAAA
                                 AC     TAAA__
GAM3355  DKFZP564O123 3'  TCCAAACTGTTCCCATTT    75429        TCTACTTG
                                TCCAAACT       CCCATTT
                                ||||||||       |||||||
                                AGGTTTGA       GGGTAAA
                                    CAA_____
GAM3355  GOLPH2    3'  AACTTCTAGGCCCCATTTT    75430        CTTG
                                AACTTCTA    CCCATTTT
                                ||||||||    ||||||||
                                TTGAAGAT    GGGTAAAA
                                    CCG_
GAM3355  GPT2      3'  TCCAGCTTCTCCAATCCCATTT 75431      AA     A  TG_
              T                  TCCA  CTTCT CT   CCCATTTT
                                ||||  ||||| ||   ||||||||
                                AGGT  GAAGA GG   GGGTAAAA
                                  C_     _ TTA
GAM3355  TBPL1     3'  TCCAAACTTTTATTTGTGCAC  75432        C  C   CC
                                TCCAAACTT TA TTG  CAT
                                |||||||||| || |||  |||
                                AGGTTTGAA AT AAC  GTG
                                     A  A   AC
GAM3355  USP10     3'  CTTCATTATTTGCCCATTTT   75433      TAC__
                                CTTC     TTGCCCATTTT
                                ||||     ||||||||||||
                                GAAG     AACGGGTAAAA
                                  TAATA
GAM3355  LOC149420 3'  CCAAACTTCTATCAATAATCAT 75434          CT__  CC
              TTT                  CCAAACTTCTA    TG  CATTTT
                                ||||||||||||    ||  ||||||
                                GGTTTGAAGAT    AT  GTAAAA
                                      AGTT  TA
GAM3355  LOC150407 3'  TCCGGCACTCTGCCCATTT    75435     AA_   CTACT
                                TCC   ACTT    TGCCCATTT
                                |||   ||||    |||||||||
                                AGG   TGAG    ACGGGTAAA
                                  CCG   _____
GAM3355  LOC220072 5'  TTCCACTTGCAGACACTTT    75436         C__
                                TTCTACTTGC   CATTTT
                                ||||||||||   ||||||
                                AAGGTGAACG   GTGAAA
                                     TCT
GAM3355  LOC220739 3'  CAAGCTTCTACTTGGACC     75437     A        C_
                                CAA CTTCTACTTG  CC
                                ||| ||||||||||  ||
                                GTT GAAGATGAAC  GG
                                  C        CT
GAM3356  DUSP1     3'  TCCTTATGTAACAAAATG     75440     CA       T
                                TCC  ATGTAACA AATG
                                |||  |||||||| ||||
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                                AGG  TACATTGT TTAC
                                  AA       T
GAM3356  GALNT7   3'  CCTAATGTAACAGAAAGTA   75441    C       T  T
                                CC AATGTAACA AA GTA
                                || ||||||||| || |||
                                GG TTACATTGT TT CAT
                                 A       C  T
GAM3356  GGCX     3'  CCTAATGTAATAATGCA     75442    C     AC
                                CC AATGTA  ATAATGTA
                                || ||||||  ||||||||
                                GG TTACAT  TATTACGT
                                 A     __
GAM3356  HRH2     5'  TCCCAATGTGACAACTAT    75443         A   TAA
                                TCCCAATGT ACA   TGT
                                ||||||||| |||   |||
                                AGGGTTACA TGT   ATA
                                      C   TG_
GAM3356  KPNA1    3'  TCCCATAACTCTAATGTAA   75444      ATG   A_
                                TCCCA   TAAC  TAATGTAA
                                |||||   ||||  ||||||||
                                AGGGT   ATTG  ATTACATT
                                   ____   AG
GAM3356  FLJ10260 5'  TGTGCACACAATGTAAAT    75445     A_
                                TGT  ACATAATGTAAAT
                                |||  ||||||||||||
                                ACA  TGTGTTACATTTA
                                  CG
GAM3356  FLJ11336 3'  CCAATGCAACATTAGAGTA   75446          AAT_
                                CCAATGTAACAT    GTA
                                ||||||||||||   |||
                                GGTTACGTTGTA    CAT
                                       ATCT
GAM3356  KIAA1297 3'  CCACTGAGCATAATGTAA    75447     A  TAA
                                CCA TG   CATAATGTAA
                                ||| ||   ||||||||||
                                GGT AC   GTATTACATT
                                  G  TC_
GAM3356  STK3     3'  TCCCAATGCAATCATATAAAT  75448         CATA
                                TCCCAATGTAA    ATGTAAAT
                                ||||||||||    ||||||||
                                AGGGTTACGTT    TATATTTA
                                       AG__
GAM3357  UBE2A    3'  CAGCAATAACTCAGGATTTGAG 75451      CTT
           T                    TAGTA   ACTCAGGATTTGAGT
                                |||||   ||||||||||||||
                                GTCGT   TGAGTCCTAAACTCA
                                   TAT
GAM3357  FLJ10829 3'  ATAGTACTGCATACATTTGAGT 75452        TACT  GG_
                                ATAGTACT    CA   ATTTGAGT
                                ||||||||    ||   ||||||||
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                                TATCATGA   GT   TAAACTCA
                                    C___  ATG
GAM3357 KIAA1775 3' TAGTAGTGCCAAGGATTTGAGT 75453      CTTA  C
                                TAGTA   CT AGGATTTGAGT
                                ||||||   || ||||||||||
                                ATCAT   GG TCCTAAACTCA
                                   CAC_  T
GAM3357 MacGAP   3' TAGACTTATTCAGGACT     75454     T    C
                                TAG ACTTA TCAGGATT
                                ||| ||||| ||||||||
                                ATC TGAAT AGTCCTGA
                                  _    A
GAM3357 LOC91585 3' ACAGTAATTTCAGGATTTGAGT 75455       C  AC
                                ATAGTA TT  TCAGGATTTGAGT
                                |||||| ||  ||||||||||||
                                TGTCAT AA  AGTCCTAAACTCA
                                   T  __
GAM3358 ATP5J    5' GTTGTGCTTCCTTGTACCTCGT 75458    G   AGG__
                                GT GTG    TTGTACCTCGT
                                || |||    ||||||||||
                                CA CAC    AACATGGAGCA
                                 A  GAAGG
GAM3359 ADH1A    3' TTAGTTCTCATTTGGATTTTA  75461          ACTAAA
                                TTAGTTCTTAT     GATTTTA
                                ||||||||||     |||||||
                                AATCAAGAGTA     CTAAAAT
                                      AAC___
GAM3359 ADH1C    3' TTAGTTCTCATTTGGATTTTA  75461          ACTAAA
                                TTAGTTCTTAT     GATTTTA
                                ||||||||||     |||||||
                                AATCAAGAGTA     CTAAAAT
                                      AAC___
GAM3359 C1orf1   3' TTAGTTCTTGTAACTAAA    75462         AT_
                                TTAGTTCTT   ACTAAA
                                |||||||||   ||||||
                                AATCAAGAA   TGATTT
                                     CAT
GAM3359 MTL5     3' TAGTTCTCTAGAGATTTT    75463        TATA   A
                                TAGTTCT    CTA AGATTTT
                                |||||||    ||| |||||||
                                ATCAAGA    GAT TCTAAAA
                                    _____   C
GAM3359 FLJ22649 3' TTAGTTCTTATACCAAAA    75464
                                TTAGTTCTTATACTAAAG
                                ||||||||||||||||||
                                AATCAAGAATATGGTTTT

GAM3359 NFAT5    3' TTAGTTCTTATACAAAG     75465           T
                                TTAGTTCTTATAC AAAG
                                |||||||||||| ||||
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                                AATCAAGAATATG TTTC
                                          _
GAM3359  SFRS10   3'  TTAGTTCTAATACTAGCAG   75466       T     A_
                                TTAGTTCT ATACTA  AG
                                |||||||| ||||||  ||
                                AATCAAGA TATGAT  TC
                                     T     CG
GAM3360  COPS4    3'  TATCACAAATCTCAAACTTTTT 75469         C    ATC
           AG                     TATCACAAATC TAAA   TTTAG
                                |||||||||||| ||||   |||||
                                ATAGTGTTTAG GTTT   AAATC
                                      A   GAA
GAM3360  SQV7L    5'  TCACGAATCCGAAACCTCT   75470     A    TA
                                TCAC AATCC  AAATCTTT
                                |||| |||||  ||||||||
                                AGTG TTAGG  TTTGGAGA
                                  C    C_
GAM3360  STRN3    3'  CACAAACAAAATCTTTAG    75471       CCT
                                CACAAAT   AAAATCTTTAG
                                |||||||   ||||||||||
                                GTGTTTG   TTTTAGAAATC
                                          ___
GAM3360  UNC5D    3'  TATCACAAATTCAACTCATCTT 75472         _ CTAAA
           TAG                    TATCACAAAT C    ATCTTTAG
                                |||||||||| |    ||||||||
                                ATAGTGTTTA G    TAGAAATC
                                      A TTGAG
GAM3360  LOC92935 3'  TCCGAATCCTCAATCTTTAG  75473    ACA     AA
                                TC   AATCCT  AATCTTTAG
                                ||   ||||||  |||||||||
                                AG   TTAGGA  TTAGAAATC
                                 GC_     G_
GAM3361  ARCN1    3'  GAAAGGAGGGGACTGATGA   75476     CTAT    A_
                                GAAA    GAGG  ACTGATGA
                                ||||    ||||  ||||||||
                                CTTT    CTCC  TGACTACT
                                  C___    CC
GAM3361  CALU     3'  TGTGAGGTATGAGGATCCCTG  75477      AAC       A  GA
                                TGTGA   TATGAGGA CT  TG
                                |||||   |||||||| ||  ||
                                ACACT   ATACTCCT GG  AC
                                   CC_       A  G_
GAM3361  CD3E     3'  TGTGAGGGTGTGACTACTGATG 75478      AACTA   GGA
           A                     TGTGA    TGA   ACTGATGA
                                |||||     |||   ||||||||
                                ACACT     ACT   TGACTACT
                                   CCCAC   GA_
GAM3361  CTSB     3'  TGGAGGTACTGGGGGAACTGAT 75479    T  AACTA  A_
           G                     TG GA    TG  GGAACTGATG
                                || ||    ||  ||||||||||
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                                AC CT    AC  CCTTGACTAC
                                 _  CCATG  CC
GAM3361  INPP5B   3'  GTGGGTTGCAGAGGAACTGGTG 75480     AAACTAT       A
              A                  GTG      GAGGAACTG TGA
                                 |||      ||||||||| |||
                                 CAC      CTCCTTGAC ACT
                                   CCAACGT       C
GAM3361  TRRAP    3'  GTGAAACTATGGGGCTTCTGTG 75481          A  AA_  A
              A                  GTGAAACTATG GG   CTG TGA
                                 |||||||||| ||   ||| |||
                                 CACTTTGATAC CC   GAC ACT
                                       C  GAA  _
GAM3361  BNIP-S   3'  TGTGAATTTGGAACTGATG   75482       ACTATGA
                                 TGTGAA      GGAACTGATG
                                 ||||||      ||||||||||
                                 ACACTT      CCTTGACTAC
                                    AAA____
GAM3361  CDW92    3'  TGTGCGGCTATGAAACAGATG  75483     AAA       AACT
                                 TGTG   CTATGAGG    GATG
                                 ||||   ||||||||    ||||
                                 ACAC   GATACTTT    CTAC
                                   GCC       GT__
GAM3361  DKFZP434O125 3'  TGTGCTTAGAGGAACTGGTG   75484      AAACTAT       A
                                 TGTG      GAGGAACTG TG
                                 ||||      ||||||||| ||
                                 ACAC      CTCCTTGAC AC
                                   GAAT___        C
GAM3361  KIAA0040  3'  TGTGAGACTGCACTGATG    75485      A   ATGAGGA
                                 TGTGA ACT      ACTGATG
                                 ||||| |||      |||||||
                                 ACACT TGA      TGACTAC
                                   C   CG_____
GAM3361  KIAA0222  3'  TATGGGACTATGGACGATG    75486      AA     A  AAC
                                 TGTG  ACTATG GG   TGATG
                                 ||||  |||||| ||   |||||
                                 ATAC  TGATAC CT   GCTAC
                                   CC     _  ___
GAM3361  KIAA0894  3'  TGAAAAGGAACTGAT       75487      ACTAT
                                 TGAA    GAGGAACTGAT
                                 ||||    ||||||||||
                                 ACTT    TTCCTTGACTA
                                          _____
GAM3361  KIAA1493  3'  TGTGGGGTGGGACTGATG    75488      AAACTA  A   A
                                 TGTG     TG GGA CTGATG
                                 ||||     || ||| ||||||
                                 ACAC     AC CCT GACTAC
                                   CCC___  _   _
GAM3361  MRPL32    3'  TGTTAAACTATACTGATG    75489     G      GAGGA
                                 TGT AAACTAT    ACTGATG
                                 ||| |||||||    |||||||
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                                ACA TTTGATA    TGACTAC
                                  A     _____
GAM3361  LOC137492 3'  TGTGAATTTAGCCACTGATGA  75490       ACTATG  GA
                                TGTGAA     AG  ACTGATGA
                                ||||||     ||  ||||||||
                                ACACTT     TC  TGACTACT
                                   AAA___  GG
GAM3361  LOC148343 5'  TGGACTCTTGAGGAGCTGGTG  75491    T  AA  A     A   A
                                TG GA  CT TGAGGA CTG TG
                                || ||  || |||||| ||| ||
                                AC CT  GA ACTCCT GAC AC
                                 _ GA _     C   C
GAM3361  LOC158292 5'  TGTAAAACTGTCCAGCCGGCTG 75492         ATGA  AA__
            ATG                   TGTGAAACT   GG   CTGATG
                                |||||||||   ||   ||||||
                                ACATTTTGA   TC   GACTAC
                                     CAGG  GGCC
GAM3361  LOC161742 3'  GTGAAACGCCAAGAACTGATGA 75493        TATG
                                GTGAAAC   AGGAACTGATGA
                                |||||||   ||||||||||||
                                CACTTTG   TTCTTGACTACT
                                   CGG_
GAM3361  LOC57105  3'  TGGAGACTATGAGTGAATGA   75494    T  A      _   C
                                TG GA ACTATGAG GAA TGA
                                || || |||||||| ||| |||
                                AC CT TGATACTC CTT ACT
                                 _ C       A   _
GAM3362  ADARB1    3'  CAGCGTGGGGATGATAAAAA   75497       AA   TA
                                TAGCGTG  GGA  TGATAAAAA
                                |||||||  |||  |||||||||
                                GTCGCAC  CCT  ACTATTTTT
                                   C_   __
GAM3362  ANKRD3    3'  GCGTGTGGAGATAAAAA     75498      AA   TAT
                                GCGTG  GGA   GATAAAAA
                                |||||  |||   ||||||||
                                CGCAC  CCT   CTATTTTT
                                   A_   ____
GAM3362  C6orf5    3'  TAGCCTGAAGTGATTGATA    75499     G    _   A
                                TAGC TGAAG GAT TGATA
                                |||| ||||| ||| |||||
                                ATCG ACTTC CTA ACTAT
                                  G    A   _
GAM3362  CNNM2     3'  AGTGTGAATAATGATAAAA    75500    C    GGAT
                                AG GTGAA    ATGATAAAA
                                || |||||    |||||||||
                                TC CACTT    TACTATTTT
                                 A    AT__
GAM3362  FLJ14054  3'  TAGCGTAAGGGTTCTGATGAAA 75501         A  ATA   A
            A                    TAGCGTGA GG   TGAT AAAA
                                |||||||| ||   |||| ||||
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                                ATCGCATT CC   ACTA TTTT
                                    C  AAG    C
GAM3362  KIAA1323  3'  TAGGGTGAGGGATACAGA    75502     C    A     _
                                TAG GTGA GGATAT GA
                                ||| |||| |||||| ||
                                ATC CACT CCTATG CT
                                  C   C     T
GAM3362  KIAA1843  3'  TAGTGTGAAGGAGATTATG    75503     C       ___
                                TAG GTGAAGGA   TATG
                                ||| ||||||||   ||||
                                ATC CACTTCCT   ATAC
                                  A       CTA
GAM3362  MGC29667  3'  TAGCATGAGGGTAAGATA    75504         A  A  T
                                TAGCGTGA GG TA GATA
                                |||||||| || || ||||
                                ATCGTACT CC AT CTAT
                                    C  _  T
GAM3362  LOC160897 3'  TAGCGAGACATGATAAAA    75505      TGAA
                                TAGCG    GGATATGATAAAA
                                |||||    ||||||||||||||
                                ATCGC    TCTGTACTATTTT
                                   _____
GAM3363  TREM1     3'  ACATTCTCGTGGGTTCGT    75508         __
                                ACATTCTC  GGGTTCGT
                                ||||||||  ||||||||
                                TGTAAGAG  CCCAAGCA
                                    CA
GAM3363  KIAA0426  3'  TACATTCTTTATACGAGTTTGT 75509         ______     C  III
             A                   TACATTCT    CGGGTT GT   A
                                ||||||||    |||||| ||   |
                                ATGTAAGA    GCTCAA CA   T
                                    AATAT     A  III
GAM3363  KIAA1710  3'  TACATTCCTACCGAGGTTCGT  75510         ___ _
                                TACATTCT   CG GGTTCGT
                                ||||||||   || |||||||
                                ATGTAAGG   GC CCAAGCA
                                    ATG  T
GAM3363  KIAA1979  5'  CACATTCTTCACATTCGT    75511         _  G
                                TACATTCT CG GTTCGT
                                |||||||| || ||||||
                                GTGTAAGA GT TAAGCA
                                    A  G
GAM3363  LOC121344 3'  TACATCCTCACTGGTTTGT    75512         __   C
                                TACATTCTCG  GGTT GT
                                ||||||||||  |||| ||
                                ATGTAGGAGT  CCAA CA
                                     GA    A
GAM3364  A1BG      3'  CAACACAGTGAGACCCTGTC   75515      AA_      CA
                                TAATA   TGAGACCC  TC
                                |||||   ||||||||  ||
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                                GTTGT  ACTCTGGG AG
                                  GTC      AC
GAM3364 ACLY    3' ACAATGAGGAAGACCCCATCC 75516     AAAT
                                ATAAT  GAGACCCCATCC
                                |||||  ||||||||||||
                                TGTTA  TTCTGGGGTAGG
                                  CTCC
GAM3364 APAF1   3' CAACATAGTGAGACCCTGTC  75517     AA_     CA
                                TAATA  TGAGACCC TC
                                |||||  |||||||| ||
                                GTTGT  ACTCTGGG AG
                                  ATC      AC
GAM3364 APAF1   3' CAACATAGTGAGACCCTGTC  75517     AA_     CA
                                TAATA  TGAGACCC TC
                                |||||  |||||||| ||
                                GTTGT  ACTCTGGG AG
                                  ATC      AC
GAM3364 CASP2   3' TAACATGGTGAAACCCTGTC  75518     AA_     CA
                                TAATA  TGAGACCC TC
                                |||||  |||||||| ||
                                ATTGT  ACTTTGGG AG
                                  ACC      AC
GAM3364 CASP2   3' TAACATGGTGAAACCCTGTC  75518     AA_     CA
                                TAATA  TGAGACCC TC
                                |||||  |||||||| ||
                                ATTGT  ACTTTGGG AG
                                  ACC      AC
GAM3364 CASP2   3' TAACATGGTGAAACCCTGTC  75518     AA_     CA
                                TAATA  TGAGACCC TC
                                |||||  |||||||| ||
                                ATTGT  ACTTTGGG AG
                                  ACC      AC
GAM3364 CASP2   3' TAACATGGTGAAACCCTGTC  75518     AA_     CA
                                TAATA  TGAGACCC TC
                                |||||  |||||||| ||
                                ATTGT  ACTTTGGG AG
                                  ACC      AC
GAM3364 CLECSF12 3' TAACAAAGTGAGACCCTATC  75519       _     C
                                TAATAAA TGAGACCC ATC
                                ||||||| |||||||| |||
                                ATTGTTT ACTCTGGG TAG
                                   C       A
GAM3364 CR1     3' TAACATGGTGAAACCCCGTC  75520     AA_      A
                                TAATA  TGAGACCCC TC
                                |||||  ||||||||| ||
                                ATTGT  ACTTTGGGG AG
                                  ACC       C
GAM3364 G6PC    3' CAACATAGTGAGACCCTGTC  75517     AA_     CA
                                TAATA  TGAGACCC TC
                                |||||  |||||||| ||
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                                GTTGT  ACTCTGGG AG
                                  ATC      AC
GAM3364 GPR4    3' CAACACAGTGAGACCCTGTC  75515     AA_     CA
                                TAATA  TGAGACCC TC
                                |||||  |||||||| ||
                                GTTGT  ACTCTGGG AG
                                  GTC      AC
GAM3364 HUS1    3' CAACACAGTGAGACCCTGTC  75515     AA_     CA
                                TAATA  TGAGACCC TC
                                |||||  |||||||| ||
                                GTTGT  ACTCTGGG AG
                                  GTC      AC
GAM3364 JRK     3' CAACACAGTGAGACCCTGTC  75515     AA_     CA
                                TAATA  TGAGACCC TC
                                |||||  |||||||| ||
                                GTTGT  ACTCTGGG AG
                                  GTC      AC
GAM3364 LIF     3' TAAATAATAAATAAGGGCC   75521          AC
                                TAAATAATAAATGAG CC
                                |||||||||||||| ||
                                ATTTATTATTTATTC GG
                                         CC
GAM3364 LLGL1   3' TAACATGGTGAAACCCCATC  75522     AA_
                                TAATA  TGAGACCCCATC
                                |||||  ||||||||||||
                                ATTGT  ACTTTGGGGTAG
                                  ACC
GAM3364 NPR2L   3' TAACAGAGTGAGACCCCGTC  75523     AA_      A
                                TAATA  TGAGACCCC TC
                                |||||  ||||||||| ||
                                ATTGT  ACTCTGGGG AG
                                  CTC      C
GAM3364 PKDREJ  3' AAGAATAAATGAGAAGCACC  75524   T       CCC
                                AA AATAAATGAGA  CATC
                                || ||||||||||  ||||
                                TT TTATTTACTCT  GTGG
                                 C        TC_
GAM3364 RGR     3' AAACCACAATGAGACCTTATC  75525    AATA      CC
                                AAAT   AATGAGACC ATC
                                ||||   ||||||||| |||
                                TTTG   TTACTCTGG TAG
                                  GTG_      AA
GAM3364 SAS     3' TAACATGGTGAAACCCTGTC  75518     AA_     CA
                                TAATA  TGAGACCC TC
                                |||||  |||||||| ||
                                ATTGT  ACTTTGGG AG
                                  ACC      AC
GAM3364 SLC15A1 3' TAACATGGTGAAACCCCATC  75522     AA_
                                TAATA  TGAGACCCCATC
                                |||||  ||||||||||||
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                                ATTGT  ACTTTGGGGTAG
                                  ACC
GAM3364 TAF7L    3' AATAACAACCAGCTCCATCC  75526       A G  ACC
                                AATAATAA T AG  CCATCC
                                |||||||| | ||  ||||||
                                TTATTGTT G TC  GGTAGG
                                    _ G  GA_
GAM3364 TAT      3' TAACATGGTGAAACCCTGTC  75518      AA_     CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                ATTGT  ACTTTGGG  AG
                                  ACC      AC
GAM3364 TPMT     3' CAACAAAGTGAGACCCTGTC  75527       _      CA
                                TAATAAA TGAGACCC  TC
                                ||||||| ||||||||  ||
                                GTTGTTT ACTCTGGG  AG
                                   C      AC
GAM3364 VENTX2   3' TAACATGGTGAAACCCCAT   75528      AA_
                                TAATA  TGAGACCCCAT
                                |||||  ||||||||||
                                ATTGT  ACTTTGGGGTA
                                  ACC
GAM3364 VIPR2    3' TAACATGGTGAAACCCTGTC  75518      AA_     CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                ATTGT  ACTTTGGG  AG
                                  ACC      AC
GAM3364 ANKT     3' CAACACAGTGAGACCCTGTC  75515      AA_     CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                GTTGT  ACTCTGGG  AG
                                  GTC      AC
GAM3364 C(27)-3BETA-HSD 3' CAATATAGTGAGACCCTGTC  75529      AA_     CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                GTTAT  ACTCTGGG  AG
                                  ATC      AC
GAM3364 CKAP2    3' CAAATAATAAAAACCCCAT   75530       AAT
                                TAAATAATA  GAGACCCCAT
                                |||||||||  ||||||||||
                                GTTTATTAT  TTTTGGGGTA
                                    ___
GAM3364 COLEC12  3' CAACAGAGTGAGACCCTGTC  75531      AA_     CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                GTTGT  ACTCTGGG  AG
                                  CTC      AC
GAM3364 DKFZP564K0322 3' CAACAGAGTGAGACCCTGTC  75531      AA_     CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
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                                GTTGT  ACTCTGGG  AG
                                   CTC      AC
GAM3364  DKFZP564O0423 3'  CAACATAGTGAGACCCCATC  75532     AA_
                                TAATA  TGAGACCCCATC
                                |||||  ||||||||||||
                                GTTGT  ACTCTGGGGTAG
                                   ATC
GAM3364  DKFZP586A0522 3'  CAACACAGTGAGACCCTGTC  75515     AA_     CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                GTTGT  ACTCTGGG  AG
                                   GTC      AC
GAM3364  FLJ10038  3'  ATAATAAATGAGAGTGGATC  75533          CCCC
                                ATAATAAATGAGA   ATC
                                ||||||||||||   |||
                                TATTATTTACTCT   TAG
                                      CACC
GAM3364  FLJ10292  3'  TAAATGACAAATAACCCCTCCC 75534     A     GA  __
            ATCC                  TAAAT ATAAATGA  CC  CCATCC
                                |||||  ||||||||  ||  ||||||
                                ATTTA TGTTTATT  GG  GGTAGG
                                   C      GG  AG
GAM3364  FLJ10846  3'  TAACATGGTGAGACCCTGTC  75535     AA_     CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                ATTGT  ACTCTGGG  AG
                                   ACC      AC
GAM3364  FLJ11193  3'  TAACATGGTGAGACCCCATC  75536     AA_
                                TAATA  TGAGACCCCATC
                                |||||  ||||||||||||
                                ATTGT  ACTCTGGGGTAG
                                   ACC
GAM3364  FLJ14054  3'  TAAATAATGAAGAGGCCACCC  75537       AAAT   CC
                                TAAATAAT   GAGA  CCATCC
                                ||||||||   ||||  ||||||
                                ATTTATTA   TTCT  GGTGGG
                                     C___   CC
GAM3364  FLJ20508  3'  CAATATAGTGAGACCCTATC  75538     AA_     C
                                TAATA  TGAGACCC ATC
                                |||||  |||||||| |||
                                GTTAT  ACTCTGGG TAG
                                   ATC      A
GAM3364  FLJ22167  5'  TAACACAGTGAGACCCCATC  75539     AA_
                                TAATA  TGAGACCCCATC
                                |||||  ||||||||||||
                                ATTGT  ACTCTGGGGTAG
                                   GTC
GAM3364  GREB1     3'  TAACATGGTGAAACCCCGTC  75520     AA_      A
                                TAATA  TGAGACCCC TC
                                |||||  ||||||||| ||
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                                ATTGT  ACTTTGGGG AG
                                   ACC       C
GAM3364 HARS2    3' TAACATGGTAAAACCCCGTC  75540     AA_      A
                                TAATA  TGAGACCCC TC
                                |||||  ||||||||| ||
                                ATTGT  ATTTTGGGG AG
                                   ACC       C
GAM3364 HSA277841 3' TGATAATAAACAACAGGACCCC 75541   A     TG ___
             ATC                  A ATAATAAA  A   GACCCCATC
                                | ||||||||  |  |||||||||
                                A TATTATTT  T   CTGGGGTAG
                                 C       GT GTC
GAM3364 KIAA0459 3' TAACATGGTGAAACCCCGTC  75520     AA_      A
                                TAATA  TGAGACCCC TC
                                |||||  ||||||||| ||
                                ATTGT  ACTTTGGGG AG
                                   ACC       C
GAM3364 KIAA0737 3' CAACATAGTGAGACCCCATC  75532     AA_
                                TAATA  TGAGACCCCATC
                                |||||  ||||||||||||
                                GTTGT  ACTCTGGGGTAG
                                   ATC
GAM3364 KIAA1821 3' CAACACAGTGAGACCCTGTC  75515     AA_     CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                GTTGT  ACTCTGGG  AG
                                   GTC       AC
GAM3364 KIAA1829 3' GGATAACAGAGTGAGACCCTGT 75542   A    AA_     CA
             C                   A ATAATA  TGAGACCC  TC
                                | ||||||  ||||||||  ||
                                C TATTGT  ACTCTGGG  AG
                                 C     CTC       AC
GAM3364 KIAA1940 3' AACGAGGGGACCCCATCC    75543     ___
                                AATGA  GACCCCATCC
                                |||||  ||||||||||
                                TTGCT  CTGGGGTAGG
                                   CCC
GAM3364 KIAA1975 5' TAACATGGTGAAACCCCATC  75522     AA_
                                TAATA  TGAGACCCCATC
                                |||||  ||||||||||||
                                ATTGT  ACTTTGGGGTAG
                                   ACC
GAM3364 LIM      3' AATAATAAATGCCAAACC    75544        __
                                AATAATAAATG  AGACC
                                ||||||||||  |||||
                                TTATTATTTAC  TTTGG
                                       GG
GAM3364 MESDC2   3' CAACAGAGTGAGACCCTGTC  75531     AA_      CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
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                                GTTGT  ACTCTGGG  AG
                                   CTC       AC
GAM3364  MYT1     3'  AATAATAAATACAGAATTCCAT 75545          _  CC_
                                AATAATAAATG AGA   CCAT
                                |||||||||||  |||   ||||
                                TTATTATTTAT TCT   GGTA
                                      G   TAA
GAM3364  NEDD5    3'  TAAAAATAAATGAGACAGCC   75546     T         C_
                                TAAA AATAAATGAGAC  CC
                                ||||  ||||||||||||  ||
                                ATTT TTATTTACTCTG  GG
                                   _         TC
GAM3364  PRDM10   3'  TAAATAAGAAATGCCACCTTCC 75547       T    AG  __  A_
              TGTCC                  TAAATAA AAATG  ACC  CC  TCC
                                |||||||  |||||  |||  ||  |||
                                ATTTATT TTTAC  TGG  GG  AGG
                                    C    GG   AA  AC
GAM3364  SREC     3'  TAACATGGTGAAACCCTGTC   75518      AA_      CA
                                TAATA   TGAGACCC  TC
                                |||||   ||||||||  ||
                                ATTGT   ACTTTGGG  AG
                                   ACC       AC
GAM3364  STK38L   3'  AATAAATGAAACCCTATC    75548           C
                                AATAAATGAGACCC ATC
                                ||||||||||||||  |||
                                TTATTTACTTTGGG TAG
                                      A
GAM3364  LOC113523 5'  TAACATGGTGAAACCCTGTC   75518      AA_      CA
                                TAATA   TGAGACCC  TC
                                |||||   ||||||||  ||
                                ATTGT   ACTTTGGG  AG
                                   ACC       AC
GAM3364  LOC116411 5'  AATGAACGAGACTCCGTC    75549     A       C  A
                                AAT AATGAGAC CC TC
                                |||  ||||||||  ||  ||
                                TTA TTGCTCTG GG AG
                                  C       A  C
GAM3364  LOC128077 3'  TAACATGGTGAAACCCCGTC   75520      AA_       A
                                TAATA   TGAGACCCC TC
                                |||||   |||||||||  ||
                                ATTGT   ACTTTGGGG AG
                                   ACC        C
GAM3364  LOC130813 3'  CAACATAGTGAGACCCTATC   75550      AA_      C
                                TAATA   TGAGACCC ATC
                                |||||   ||||||||  |||
                                GTTGT   ACTCTGGG TAG
                                   ATC       A
GAM3364  LOC147429 3'  TAACATGGTGAAACCCCATC   75522      AA_
                                TAATA   TGAGACCCCATC
                                |||||   ||||||||||||
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                                ATTGT  ACTTTGGGGTAG
                                   ACC
GAM3364  LOC147990 3'  CAACAAAGTGAGACCCTGTC  75527       _      CA
                                TAATAAA TGAGACCC  TC
                                ||||||| ||||||||  ||
                                GTTGTTT ACTCTGGG  AG
                                    C       AC
GAM3364  LOC149194 3'  CAACAAAATGAGATCCCATC  75551       _    C
                                TAATAAA TGAGA CCCATC
                                ||||||| ||||| ||||||
                                GTTGTTT ACTCT GGGTAG
                                    T    A
GAM3364  LOC150960 3'  CAACAGGGTGAGACCCCATC  75552      AA_
                                TAATA  TGAGACCCCATC
                                |||||  ||||||||||||
                                GTTGT  ACTCTGGGGTAG
                                   CCC
GAM3364  LOC151979 5'  TAACATGGTGAAACCCCGTC  75520      AA_       A
                                TAATA  TGAGACCCC TC
                                |||||  ||||||||| ||
                                ATTGT  ACTTTGGGG AG
                                   ACC       C
GAM3364  LOC152445 3'  TAACATGGTGAAACCCTGTC  75518      AA_      CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                ATTGT  ACTTTGGG  AG
                                   ACC       AC
GAM3364  LOC153811 3'  CAACAGAGTGAGACCCTGTC  75531      AA_      CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                GTTGT  ACTCTGGG  AG
                                   CTC       AC
GAM3364  LOC153883 3'  AATAATCTTGGCCCCATCC   75553      AAA  AGA
                                AATAAT  TG  CCCCATCC
                                ||||||  ||  ||||||||
                                TTATTA  AC  GGGGTAGG
                                   GA_  C__
GAM3364  LOC154877 3'  CAACATGGTGAGACCCTGTC  75554      AA_      CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                GTTGT  ACTCTGGG  AG
                                   ACC       AC
GAM3364  LOC170082 5'  TAACATGGTGAAACCCCATC  75522      AA_
                                TAATA  TGAGACCCCATC
                                |||||  ||||||||||||
                                ATTGT  ACTTTGGGGTAG
                                   ACC
GAM3364  LOC196529 3'  CAACACAGTGAGACCCTGTC  75515      AA_      CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
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                                GTTGT  ACTCTGGG  AG
                                  GTC      AC
GAM3364  LOC205251 5'  TAACATGGTGAAACCCTGTCC  75555     AA_     CA
                                TAATA  TGAGACCC  TCC
                                |||||  ||||||||  |||
                                ATTGT  ACTTTGGG  AGG
                                  ACC      AC
GAM3364  LOC219673 3'  CAACATAGTGAGACCCTGTC  75517     AA_     CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                GTTGT  ACTCTGGG  AG
                                  ATC      AC
GAM3364  LOC220074 3'  TAACATGGTGAAACCCCGTC  75520     AA_     A
                                TAATA  TGAGACCCC TC
                                |||||  |||||||||  ||
                                ATTGT  ACTTTGGGG AG
                                  ACC      C
GAM3364  LOC51336  3'  TAACAGAGTGAGACCCTGTC  75556     AA_     CA
                                TAATA  TGAGACCC  TC
                                |||||  ||||||||  ||
                                ATTGT  ACTCTGGG  AG
                                  CTC      AC
GAM3364  LOC81034  3'  TAACATGGTGAAACCCCAT   75528     AA_
                                TAATA  TGAGACCCCAT
                                |||||  ||||||||||
                                ATTGT  ACTTTGGGGTA
                                  ACC
GAM3364  LOC89231  3'  CAACATAGTGAGACCCCATC  75532     AA_
                                TAATA  TGAGACCCCATC
                                |||||  ||||||||||||
                                GTTGT  ACTCTGGGGTAG
                                  ATC
GAM3364  LOC89919  3'  TAACATGGTGAAACCCCGTC  75520     AA_     A
                                TAATA  TGAGACCCC TC
                                |||||  |||||||||  ||
                                ATTGT  ACTTTGGGG AG
                                  ACC      C
GAM3364  LOC90352  3'  TAAATGACAAATAACCCCTCCC 75534     A     GA  __
          ATCC                   TAAAT ATAAATGA  CC  CCATCC
                                |||||  ||||||||  ||  ||||||
                                ATTTA TGTTTATT  GG  GGTAGG
                                  C       GG  AG
GAM3364  LOC92841  3'  TAACATGGTGAAACCCCGTC  75520     AA_     A
                                TAATA  TGAGACCCC TC
                                |||||  |||||||||  ||
                                ATTGT  ACTTTGGGG AG
                                  ACC      C
GAM3365  KIAA1831  5'  GCGGGTGGTGGTGGGG     75559      GGCC    C
                                GCGGGT   GGTGG GGGG
                                ||||||   |||||  ||||
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                                CGCCCA   CCACC CCCC
                                   ____    A
GAM3365 KIAA1872 3' TTGGTGGGAGGTATTGACGGGG 75560     C  T  CCGG
             T                   TTGG GGG GG   TGGCGGGGT
                                 |||| ||| ||   |||||||||
                                 AACC CCC CC   ACTGCCCCA
                                   A  T  ATA_
GAM3365 LOC148014 3' TGGCGGGTGAAGGGCGGGGT  75561         CC  T
                                 TGGCGGGTGG  GG GGCGGGGT
                                 ||||||||||  || ||||||||
                                 ACCGCCCACT  TC CCGCCCCA
                                    __  _
GAM3366 ARHI    3' TACATGTAACATAGTG     75564      T  TC
                                 TACAT GTG  ACATAGTG
                                 ||||| |||  ||||||||
                                 ATGTA CAT  TGTATCAC
                                    _  __
GAM3366 BAI3    3' TACATTGTGCTTCATGGTG   75565         CA  A
                                 TACATTGTGT  CAT GTG
                                 ||||||||||  ||| |||
                                 ATGTAACACG  GTA CAC
                                       AA  C
GAM3366 CSNK1G3  3' CACAGTACTTCACATAGTG   75566     T  TG
                                 TACA TG  TCACATAGTG
                                 |||| ||  ||||||||||
                                 GTGT AT  AGTGTATCAC
                                   C  GA
GAM3366 KCNA7    3' CTGTAGGACTCACATAGTG   75567      ____
                                 TTGTG   TCACATAGTG
                                 |||||   ||||||||||
                                 GACAT   AGTGTATCAC
                                    CCTG
GAM3366 ZNF124   3' ACATCTCATTCACATAGTG   75568      GTG_
                                 ACATT   TCACATAGTG
                                 |||||   ||||||||||
                                 TGTAG   AGTGTATCAC
                                    AGTA
GAM3366 DKFZP434P211 3' TACATCGTGCGCCAGTG    75569         CACA
                                 TACATTGTGT   TAGTG
                                 ||||||||||   |||||
                                 ATGTAGCACG   GTCAC
                                       CG__
GAM3366 FLJ23604  3' TACATCTCTGCCATATAGTG  75570       G_   C
                                 TACATT  TGTCA ATAGTG
                                 ||||||  ||||| ||||||
                                 ATGTAG  ACGGT TATCAC
                                    AG    A
GAM3366 HDAC9-PENDING 3' TACATTATGTACAGTG     75571         CAC
                                 TACATTGTGT   ATAGTG
                                 ||||||||||   ||||||
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                                ATGTAATACA  TGTCAC
                                    ___
GAM3366 KIAA0961 3' TACATTATCGTCATTATAGTG 75572       _  C_
                                TACATTGT GTCA ATAGTG
                                |||||||| |||| ||||||
                                ATGTAATA CAGT TATCAC
                                    G   AA
GAM3366 KIAA1205 3' TACATTATGTACAAGGTG   75573       C  TA
                                TACATTGTGT ACA GTG
                                |||||||||| ||| |||
                                ATGTAATACA TGT CAC
                                     _  TC
GAM3366 OSBPL3   3' CACATTGTGTTCATCTTG   75574       CA  AG
                                TACATTGTGT CAT TG
                                |||||||||| ||| ||
                                GTGTAACACA GTA AC
                                     A_  GA
GAM3366 STRN3    3' TACAAAATATCACATAGTG   75575    TT
                                TACA GTGTCACATAGTG
                                |||| ||||||||||||
                                ATGT TATAGTGTATCAC
                                  TT
GAM3366 UBA2     3' TACATTAATATACATAGTG   75576      _ C
                                TACATTG TGT ACATAGTG
                                ||||||| ||| ||||||||
                                ATGTAAT ATA TGTATCAC
                                    T  _
GAM3366 LOC144253 3' TACAAGTCACATAGTG    75577    TTGT
                                TACA   GTCACATAGTG
                                ||||   ||||||||||
                                ATGT   CAGTGTATCAC
                                  T___
GAM3366 LOC147276 3' ACATTGTGTACAGAGTAGTG  75578       C  ___
                                ACATTGTGT ACA  TAGTG
                                ||||||||| |||  |||||
                                TGTAACACA TGT  ATCAC
                                    _  CTC
GAM3366 LOC150174 3' TACATCGTGCGCCAGTG    75569       CACA
                                TACATTGTGT   TAGTG
                                ||||||||||   |||||
                                ATGTAGCACG   GTCAC
                                     CG__
GAM3366 LOC150213 3' TACATCGTGCGTCAGTG    75579       CACA
                                TACATTGTGT   TAGTG
                                ||||||||||   |||||
                                ATGTAGCACG   GTCAC
                                     CA__
GAM3366 LOC153810 3' CACATCTTCACATAGTG    75580      GTG
                                TACATT  TCACATAGTG
                                ||||||  ||||||||||
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                                GTGTAG  AGTGTATCAC
                                   A__
GAM3366 LOC154881 3' TACATTGTGATCAATGGTG   75581        _  C A
                                TACATTGTG TCA AT GTG
                                ||||||||| ||| || |||
                                ATGTAACAC AGT TA CAC
                                      T  _ C
GAM3366 LOC221477 3' ACAATGCACATAGTG      75582    TT  T
                                ACA  GTG CACATAGTG
                                |||  ||| |||||||||
                                TGT  TAC GTGTATCAC
                                  __  _
GAM3366 LOC222128 3' CACATTGTGCCATAGTG    75583        CA
                                TACATTGTGT  CATAGTG
                                ||||||||||  |||||||
                                GTGTAACACG  GTATCAC
                                      __
GAM3366 LOC255452 5' CATGTGACCCACATAGTG   75584    T  __
                                CAT GTG  TCACATAGTG
                                ||| |||  ||||||||||
                                GTA CAC  GGTGTATCAC
                                  _  TG
GAM3366 LOC92578  5' TACCTTGGCCACACATAGTG  75585    A  T    __
                                TAC TTG GTCACAT  AGTG
                                ||| ||| |||||||  ||||
                                ATG AAC CGGTGTG  TCAC
                                  G  _     TA
GAM3367 ATP6V0D1  5' TGCGGGAGCGGCGGGACCGG  75588        A_  GA
                                TGCGGGGGCGGC  GAC  GG
                                ||||||||||||  |||  ||
                                ACGCCCTCGCCG  CTG  CC
                                       CC  G_
GAM3367 CGB     5' TGTGGGGGCGGCAAGGCCA   75589   C       GACG
                                TG GGGGGCGGCA   AGGTCG
                                || ||||||||||   ||||||
                                AC CCCCCGCCGT   TCCGGT
                                 A       _____
GAM3367 CNTFR    3' TGGGGGGCGGCAGGCCCGG   75590   C       ACGA
                                TG GGGGGCGGCAG   GG
                                || ||||||||||   ||
                                AC CCCCCGCCGTC   CC
                                 _        CGGG
GAM3367 EGFL4    3' TGCAGGGGGTGGTGGAGGTGG 75591    _   C CAGAC   C
                                TGC GGGGG GG    GAGGT GG
                                ||| ||||| ||    ||||| ||
                                ACG CCCCC CC    CTCCA CC
                                  T    A AC___   _
GAM3367 FMNL     5' GGGGGCGGCAGGTCTCCGG   75592         ACGAGG
                                GGGGGCGGCAG     TCGG
                                ||||||||||     ||||
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                                CCCCCGCCGTC     GGCC
                                      CAGA__
GAM3367  FOXE1    5'  GCGGGGGCAGCGAGGTCG    75593          AGAC
                                GCGGGGGCGGC   GAGGTCG
                                ||||||||||    |||||||
                                CGCCCCCGTCG   CTCCAGC
                                      ____
GAM3367  ILF1     3'  TGTGAGGGCGGCGGGGAG    75594    C       AGAC A  TC
                                TG GGGGGCGGC   G GG  G
                                || |||||||||   | ||  |
                                AC CTCCCGCCG   C CC  C
                                 A       ____ C  TA
GAM3367  ISL1     5'  TGCGGCGGCGGCAGACTCGG  75595      G        GA
                                TGCGG GGCGGCAGAC  GG
                                ||||| ||||||||||  ||
                                ACGCC CCGCCGTCTG  CC
                                   G         AG
GAM3367  MLLT2    3'  GGGGGCGGCAGGAGCG     75596          AC   GT
                                GGGGGCGGCAG  GAG  CG
                                ||||||||||  |||  ||
                                CCCCCGCCGTC  CTC  GC
                                      __  __
GAM3367  MOCS2    3'  TGGGGGGCGGTGAGGTGGG   75597    C       CAGAC    C
                                TG GGGGGCGG    GAGGT GG
                                || ||||||||    ||||| ||
                                AC CCCCCGCC    CTCCA CC
                                 _       A____    C
GAM3367  PAX2     3'  TGCGGGGGTCGTGGGATGGCCG 75598     _  GCA A________  AGGT
            ACCTCG                GGGG CG   G       CG    CG
                                ||||  ||   |       ||    ||
                                CCCC GC   C       GC    GC
                                  A  ACC TACCIIIG  TGGA
GAM3367  PAX2     3'  TGCGGGGGTCGTGGGATGGCCG 75598     _  GCA A________  AGGT
            ACCTCG                GGGG CG   G       CG    CG
                                ||||  ||   |       ||    ||
                                CCCC GC   C       GC    GC
                                  A  ACC TACCIIIG  TGGA
GAM3367  RCN1     3'  TGCGGGGGGGGCAGGTCTGCGG 75599       C    A____  A
            GTCGG                  GCGGGGG GGCAG    CG GGTCGG
                                ||||||| |||||    || ||||||
                                CGCCCCC CCGTC    GC CCAGCC
                                    C    CAGAC  _
GAM3367  SPON2    5'  TGCGGGGGCGGCGGGGGC    75600          AGACGA
                                TGCGGGGGCGGC     GGT
                                ||||||||||||     |||
                                ACGCCCCCGCCG     CCG
                                      CCC___
GAM3367  TNNT2    3'  TGTGGGGGCAGGCAGGAG    75601    C     _    AC
                                TG GGGGGC GGCAG  GAG
                                || |||||| |||||  |||
```

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                                AC CCCCCG CCGTC  CTC
                                 A     T    __
GAM3367  CARM1    3'  GCGGGGGCGGCGGGCG      75602          AGAC A   C
                                GCGGGGGCGGC    G GGT G
                                ||||||||||    | ||| |
                                CGCCCCCGCCG    C CCG C
                                      ____ _   T
GAM3367  CDC14B   5'  TGCGGGGACGGCGGGCGCCGG  75603          AGACGAG
                                TGCGGGGGCGGC      GTCGG
                                ||||||||||||      |||||
                                ACGCCCCTGCCG      CGGCC
                                      CCCG___
GAM3367  CDC14B   5'  TGCGGGGACGGCGGGCGCCGG  75603          AGACGAG
                                TGCGGGGGCGGC      GTCGG
                                ||||||||||||      |||||
                                ACGCCCCTGCCG      CGGCC
                                      CCCG___
GAM3367  CDC14B   5'  TGCGGGGACGGCGGGCGCCGG  75603          AGACGAG
                                TGCGGGGGCGGC      GTCGG
                                ||||||||||||      |||||
                                ACGCCCCTGCCG      CGGCC
                                      CCCG___
GAM3367  CGB5     5'  TGTGGGGGCGGCAAGGCCA    75589    C       GACG
                                TG GGGGGCGGCA    AGGTCG
                                || ||||||||||    ||||||
                                AC CCCCCGCCGT    TCCGGT
                                 A        _____
GAM3367  CGB8     5'  TGTGGGGGCGGCAAGGCCA    75589    C       GACG
                                TG GGGGGCGGCA    AGGTCG
                                || ||||||||||    ||||||
                                AC CCCCCGCCGT    TCCGGT
                                 A        _____
GAM3367  CYP2S1   3'  TGTGGGGGCGGCGTGTCTCAGT 75604    C       AGACGA_  C
            GG                    TG GGGGGCGGC      GGT GG
                                || |||||||||      ||| ||
                                AC CCCCCGCCG      TCA CC
                                 A        CACAGAG  _
GAM3367  DKFZP434M154 5'  TGCGGGGGCGGCAGCTGG    75605           ACGA
                                TGCGGGGGCGGCAG    GG
                                ||||||||||||||    ||
                                ACGCCCCCGCCGTC    CC
                                      GA__
GAM3367  DKFZP564I0422 5'  TGTGGGGGCGGAGGCGAAG    75606    C      C  A
                                TG GGGGGCGG AG CGAGG
                                || |||||||| || |||||
                                AC CCCCCGCC TC GCTTC
                                 A        _ C
GAM3367  DOK4     5'  GCGGGGGCGGCAGGGCG     75607           ACGA  T
                                GCGGGGGCGGCAG    GG CG
                                ||||||||||||||    || ||
```

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                                CGCCCCCGCCGTC   CC GC
                                      ____ _
GAM3367 MGC22793 5' TGCGGGGGTCGCAGACGCTCCA 75608       CG     AGGT__
           ACGG                 TGCGGGGG GCAGACG    CGG
                                |||||||| |||||||     |||
                                ACGCCCCC CGTCTGC    GCC
                                    AG     GAGGTT
GAM3367 NBL1    5' TGCGGGGGTCGCGGGCCG   75609       _ GCAGA A   _
                                TGCGGGGG CG    CG GGTC G
                                |||||||| ||    || |||| |
                                ACGCCCCC GC    GC CCGG C
                                    A _____ _   G
GAM3367 NIFU    5' CGGGGGCGGGCGGGGTCG   75610       CAGA A
                                CGGGGGCGG   CG GGTCG
                                |||||||||   || |||||
                                GCCCCCGCC   GC CCAGC
                                     C___ C
GAM3367 ODC-p   3' GCGGGGGTGGCAGGGTG    75611      C   ACGA C
                                GCGGGGG GGCAG   GGT G
                                ||||||| |||||   ||| |
                                CGCCCCC CCGTC   CCA C
                                    A   ____  _
GAM3367 PRKWNK2  5' TGCGGGGGCTGCGGGCCG   75612       G AGAC A   _
                                TGCGGGGGC GC   G GGTC G
                                ||||||||| ||   | |||| |
                                ACGCCCCCG CG   C CCGG C
                                     A _____ _   G
GAM3367 RAB35   5' GCGCGGGCGGGCGGGGTCGG  75613    G    CAGA A
                                GCG GGGCGG   CG GGTCGG
                                ||| ||||||   || ||||||
                                CGC CCCGCC   GC CCAGCC
                                  G    C___ C
GAM3367 SLC21A11 5' CGGTTGCGGCAGATGAGGTCGG 75614    GG      C
                                CGG  GCGGCAGA GAGGTCGG
                                |||  |||||||| ||||||||
                                GCC  CGCCGTCT CTCCAGCC
                                  AA       A
GAM3367 SMURF2   5' GCGGGGGCGGCGGGGGCG   75615        AGAC A  T
                                GCGGGGGCGGC   G GG CG
                                ||||||||||   | || ||
                                CGCCCCCGCCG   C CC GC
                                      ____ C  C
GAM3367 SMURF2   5' GCGGGGGCGGCGGGC      75616        AGAC A  T
                                GCGGGGGCGGC   G GG C
                                ||||||||||   | || |
                                CGCCCCCGCCG   C CC G
                                      ____ _  _
GAM3367 TIAF1   3' TGTGGGGGCAGGGAGGTG   75617   C     CAGAC   C
                                TG GGGGGCGG   GAGGT G
                                || ||||||||   ||||| |
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                                AC CCCCCGTC    CTCCA C
                                 A      C____    A
GAM3367  LOC147160 5'  TGCGGCGGGAATACGAGGTCGG 75618      G  C  CAG
                                TGCGG GG GG   ACGAGGTCGG
                                ||||| || ||   ||||||||||
                                ACGCC CC CT   TGCTCCAGCC
                                   G  _  TA_
GAM3367  LOC147958 3'  TGCGGGGGCGGGGATGCCG   75619          CAGAC  G
                                TGCGGGGGCGG    GA GTCG
                                ||||||||||    || ||||
                                ACGCCCCCGCC    CT CGGC
                                      C____  A
GAM3367  LOC148114 5'  GGAGCCGGGCGAGGTCGG    75620     G   CAGA
                                GGGG CGG    CGAGGTCGG
                                |||| |||    |||||||||
                                CCTC GCC    GCTCCAGCC
                                  G   C___
GAM3367  LOC149657 3'  TGTGGGGGCGCAGGCTGGCCGA 75621       G   A_________  AGGT
            CCC                   GGGGGCG CAG       CG    C
                                |||||||  |||       ||    |
                                CCCCCGC GTC       GC    G
                                   _   CGACCIIIG  TGGA
GAM3367  LOC149657 3'  TGTGGGGGCGCAGGCTGGCCGA 75621       G   A_________  AGGT
            CCC                   GGGGGCG CAG       CG    C
                                |||||||  |||       ||    |
                                CCCCCGC GTC       GC    G
                                   _   CGACCIIIG  TGGA
GAM3367  LOC149657 3'  TGTGGGGGCGCAGGCTGGCCGA 75621       G   A_________  AGGT
            CCC                   GGGGGCG CAG       CG    C
                                |||||||  |||       ||    |
                                CCCCCGC GTC       GC    G
                                   _   CGACCIIIG  TGGA
GAM3367  LOC149657 3'  TGTGGGGGCGCAGGCTGGCCGA 75621       G   A_________  AGGT
            CCC                   GGGGGCG CAG       CG    C
                                |||||||  |||       ||    |
                                CCCCCGC GTC       GC    G
                                   _   CGACCIIIG  TGGA
GAM3367  LOC157226 5'  GCGGGGGCGGCGGGT      75622          AGAC A
                                GCGGGGGCGGC   G GGT
                                ||||||||||   | |||
                                CGCCCCCGCCG   C CCA
                                      ____ _
GAM3367  LOC158125 3'  TGAGGGGAGCGGGTGAGGTCGG 75623    C   _   CAGAC
                                TG GGGG GCGG    GAGGTCGG
                                || |||| ||||    ||||||||
                                AC CCCC CGCC    CTCCAGCC
                                 T   T   CA___
GAM3367  LOC201780 5'  CGGGGGCGGCGGGCC      75624          AGAC A
                                CGGGGGCGGC   G GGTC
                                |||||||||   | ||||
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                                GCCCCCGCCG   C CCGG
                                     _____ _
GAM3367  LOC201965 5'  TGTGGGGGCGGCACAGTC    75625    C        GACGA
                                TG GGGGGCGGCA    GGTC
                                || ||||||||||    ||||
                                AC CCCCCGCCGT    TCAG
                                 A        G____
GAM3367  LOC221692 3'  TGCGGGGGCGTCGGGC      75626         GCAGA  A  T
                                TGCGGGGGCG    CG GG C
                                ||||||||||    || || |
                                ACGCCCCCGC    GC CC G
                                      A____  _  _
GAM3367  LOC256160 5'  CGGGGGCGGCGGGCC       75624         AGAC A
                                CGGGGGCGGC    G GGTC
                                ||||||||||   | ||||
                                GCCCCCGCCG    C CCGG
                                     _____ _
GAM3367  LOC256310 3'  TGCGTGGGGCTGAGGTCG    75627     _    GGCAGAC
                                TGCG GGGGC      GAGGTCG
                                |||| |||||      |||||||
                                ACGC CCCCG      CTCCAGC
                                  A    A_______
GAM3368  ATP11B    3'  TTGTATATATGATATACC    75630         AAC
                                TTGTATATAT   GTACC
                                ||||||||||   |||||
                                AACATATATA   TATGG
                                      CTA
GAM3368  GALNT7    3'  TTGTAATGATACCATGAT    75631      TATATAAC
                                TTGTA       GTACCATGAT
                                |||||       ||||||||||
                                AACAT       TATGGTACTA
                                   TAC_____
GAM3368  MYO1E     3'  TTATATATACAGTATATGATC  75632         AC   CC
                                TTGTATATATA  GTA  ATGATC
                                ||||||||||  |||  ||||||
                                AATATATATGT  CAT  TACTAG
                                      __  A_
GAM3368  KIAA0196  3'  TTGCATGTAATACCATGAT    75633      A  TAAC
                                TTGTAT TA    GTACCATGAT
                                |||||| ||    ||||||||||
                                AACGTA AT    TATGGTACTA
                                   C  ____
GAM3368  PCDH10    3'  CTGAAACAATAATGTACCATGA 75634     TATAT    C
                 T                TTG     ATAA GTACCATGAT
                                  |||     |||| ||||||||||
                                  GAC     TATT CATGGTACTA
                                    TTTGT    A
GAM3369  ATP1A2    3'  TTAGATAGGGAGTAAGGGA    75637          C
                                TTGGATAGGGGG AAGGGA
                                |||||||||||| ||||||
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                                AATCTATCCCTC TTCCCT
                                      A
GAM3369 B3GALT5  3' CATTGATCAAAAACAAGGGA  75638      ATA
                                CATTGG  GGGGGCAAGGGA
                                ||||||  ||||||||||||
                                GTAACT  TTTTTGTTCCCT
                                   AG_
GAM3369 B3GALT5  3' CATTGATCAAAAACAAGGGA  75638      ATA
                                CATTGG  GGGGGCAAGGGA
                                ||||||  ||||||||||||
                                GTAACT  TTTTTGTTCCCT
                                   AG_
GAM3369 B3GALT5  3' CATTGATCAAAAACAAGGGA  75638      ATA
                                CATTGG  GGGGGCAAGGGA
                                ||||||  ||||||||||||
                                GTAACT  TTTTTGTTCCCT
                                   AG_
GAM3369 B3GALT5  3' CATTGATCAAAAACAAGGGA  75638      ATA
                                CATTGG  GGGGGCAAGGGA
                                ||||||  ||||||||||||
                                GTAACT  TTTTTGTTCCCT
                                   AG_
GAM3369 B3GALT5  3' CATTGATCAAAAACAAGGGA  75638      ATA
                                CATTGG  GGGGGCAAGGGA
                                ||||||  ||||||||||||
                                GTAACT  TTTTTGTTCCCT
                                   AG_
GAM3369 C1QB     3'  CATTGGCTGGGCAAGGG    75639      ATAGG
                                CATTGG   GGGCAAGGG
                                ||||||   |||||||||
                                GTAACC   CCCGTTCCC
                                   GA___
GAM3369 CSF3     3'  CATGGGATGGGGAGGG     75640    T   A   GCA
                                CAT GGAT GGGG  AGGG
                                ||| |||| ||||  ||||
                                GTA CCTA CCCC  TCCC
                                  C   _  ___
GAM3369 CXCL16   3'  CACTGGGGTAGGCAAGGGA  75641      ATA  _
                                CATTGG  GG GGGCAAGGGA
                                ||||||  || ||||||||||
                                GTGACC  CC TCCGTTCCCT
                                   ___  A
GAM3369 CYFIP1   3'  TGGTAACTGGCAAGGGA    75642    A  GG
                                TGG TAG  GGCAAGGGA
                                ||| |||  |||||||||
                                ACC ATT  CCGTTCCCT
                                  _  GA
GAM3369 GRB7     3'  CACTGGATGGGTGGAGGG    75643       A  _  CA
                                CATTGGAT GGG GG  AGGG
                                |||||||| ||| ||  ||||
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                                GTGACCTA CCC CC  TCCC
                                   _  A  __
GAM3369  ISLR     3'  CATTGGTAGGGGCAAGGG    75644       ATA
                                CATTGG  GGGGGCAAGGG
                                ||||||  ||||||||||
                                GTAACC  TCCCCGTTCCC
                                  A__
GAM3369  KRT4     3'  CATTGGACTGGGAAGGGA    75645        A   GCA
                                CATTGGAT GGGG  AGGGA
                                |||||||| ||||  |||||
                                GTAACCTG CCCT  TCCCT
                                   A  ____
GAM3369  MASP1    3'  TGGATAGGCCGAAGGAGGG   75646        _____  CA
                                TGGATAGG   GGG  AGGG
                                ||||||||   |||  ||||
                                ACCTATCC   TCC  TCCC
                                   GGCT  __
GAM3369  MEN1     3'  ATTGGATAGGAGATTCAGA   75647          CAA
                                ATTGGATAGGGGGG  GGG
                                ||||||||||||  |||
                                TAACCTATCCTCT  TCT
                                     AAG
GAM3369  PDE4A    3'  ATTGGGTAGGGGGCAGG     75648      A       A
                                ATTGG TAGGGGGCA GG
                                ||||| |||||||| ||
                                TAACC ATCCCCCGT CC
                                  C       _
GAM3369  PPP1R14B 3'  ACTGAGGGGGCAGGGGA    75649     GAT      A
                                ATTG  AGGGGGCA GGGA
                                ||||  |||||||| ||||
                                TGAC  TCCCCCGT CCCT
                                  ___       C
GAM3369  PYGB     3'  CATTGGATGGCTACAAAGG   75650       A  GG
                                CATTGGAT GG  GCAAGGG
                                |||||||| ||  |||||||
                                GTAACCTA CC  TGTTTCC
                                   _  GA
GAM3369  RARG     3'  CATTGGAAGGGGTGGGGA    75651       T    GCAA
                                CATTGGA AGGGG   GGGA
                                ||||||| |||||   ||||
                                GTAACCT TCCCC   CCCT
                                   _    AC__
GAM3369  RDX      3'  TGGAAAGGGCAAGGGA      75652     TA
                                TGGA  GGGGGCAAGGGA
                                ||||  ||||||||||||
                                ACCT  TTCCCGTTCCCT
                                  __
GAM3369  RFX1     3'  TTGAGCTTGGGGGCAAGGGA  75653    _ ATA
                                TTG G  GGGGGCAAGGGA
                                ||| |  ||||||||||||
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                                AAC C   CCCCCGTTCCCT
                                  T GAA
GAM3369  SLC38A3   3'  CACTGGATGGGAGCAGGGG   75654        A      A
                                CATTGGAT GGGGGCA GGG
                                |||||||| ||||||| |||
                                GTGACCTA CCCTCGT CCC
                                     _      C
GAM3369  SLC7A5    3'  CACTGGATGGTGAGGGG     75655        A  _   CAA
                                CATTGGAT GG GGG   GGG
                                |||||||| || |||   |||
                                GTGACCTA CC CTC   CCC
                                     _ A  ___
GAM3369  SOX10     3'  CACTGGGAGGCAAGGG      75656       ATAG
                                CATTGG   GGGGCAAGGG
                                ||||||   ||||||||||
                                GTGACC   CTCCGTTCCC
                                     _____
GAM3369  TNS       3'  CACTGGCCCTGGGCAAGGG   75657       ATAGG
                                CATTGG    GGGCAAGGG
                                ||||||    |||||||||
                                GTGACC    CCCGTTCCC
                                   GGGA_
GAM3369  TTC3      5'  TTCAATGGGGGGCAAGGG    75658    G   A
                                TT GAT GGGGGCAAGGG
                                || ||| ||||||||||
                                AA TTA CCCCCGTTCCC
                                 G   C
GAM3369  VTN       3'  ATTGGGCTGGGGGAAGGA    75659      ATA    C
                                ATTGG   GGGGG AAGGG
                                |||||   ||||| |||||
                                TAACC   CCCCC TTCCT
                                   CGA    _
GAM3369  7h3       3'  TCGGGGGGGGGGGCAAGGG    75660     ATA
                                TTGG   GGGGGCAAGGG
                                ||||   ||||||||||
                                AGCC   CCCCCGTTCCC
                                  CCC
GAM3369  ABHD2     3'  CTGAAACAGGGGGGTGAGGG   75661      _      CA
                                TTGGA TAGGGGG  AGGG
                                ||||| |||||||  ||||
                                GACTT GTCCCCC  TCCC
                                   T      AC
GAM3369  C12orf22  3'  TTAGATAAAATAAGGGA     75662          GGC
                                TTGGATAGGG   AAGGGA
                                ||||||||||   ||||||
                                AATCTATTTT   TTCCCT
                                     A__
GAM3369  C20orf124 3'  CATTGGAGGGGGCAGG      75663        TA      A
                                CATTGGA  GGGGGCA GG
                                |||||||  ||||||| ||
```

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                                GTAACCT  CCCCCGT CC
                                   __    _
GAM3369 C21orf42 3' CATTAGATGGAATAGGGA   75664       A   GCA
                                CATTGGAT GGGG  AGGGA
                                |||||||| ||||  |||||
                                GTAATCTA CCTT  TCCCT
                                   _   A__
GAM3369 CIDEB    3' CATTGGTAGGGGATTAGA   75665      A     CA
                                CATTGG TAGGGGG  AGG
                                |||||| |||||||  |||
                                GTAACC ATCCCCT  TCT
                                   _     AA
GAM3369 CKAP4    3' CAAGAAATTGGGGGGGTAGGG  75666   TT   A    CA
                                CA  GGAT GGGGG  AGGG
                                ||  |||| |||||  ||||
                                GT  TTTA CCCCC  TCCC
                                 TC   A    CA
GAM3369 CLIPR-59 5' TGGGGGAGGCAAGGGA     75667    ATA
                                TGG  GGGGGCAAGGGA
                                |||  ||||||||||||
                                ACC  CCTCCGTTCCCT
                                 C__
GAM3369 DKFZP434M154 3' CTGGGTGGAAGAAGGGA    75668     ATA    C
                                TTGG  GGGGG AAGGGA
                                ||||  ||||| ||||||
                                GACC  CCTTC TTCCCT
                                  CA_   _
GAM3369 DMWD     3' CAGTGGGTGGGGGACAAGG   75669    T  ATA
                                CA TGG  GGGGGCAAGG
                                || |||  ||||||||||
                                GT ACC  CCCCTGTTCC
                                 C  CAC
GAM3369 FLJ12221 3' ATTGGAGAGCAAGGG      75670      TAGG
                                ATTGGA   GGGCAAGGG
                                ||||||   |||||||||
                                TAACCT   CTCGTTCCC
                                   ____
GAM3369 FLJ12229 3' TTGGAGGAGCGAGGGA     75671     TAG    A
                                TTGGA  GGGGC AGGGA
                                |||||  ||||| |||||
                                AACCT  CCTCG TCCCT
                                   ___    C
GAM3369 FLJ12484 5' CACTGCTTGGGGCAAGGGA  75672     GATAG
                                CATTG    GGGGCAAGGGA
                                |||||    ||||||||||||
                                GTGAC    CCCCGTTCCCT
                                  GAA__
GAM3369 FLJ12484 5' CACTGCTTGGGGCAAGGGA  75672     GATAG
                                CATTG    GGGGCAAGGGA
                                |||||    ||||||||||||
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                                GTGAC    CCCCGTTCCCT
                                  GAA__
GAM3369 FLJ14213 3' CATTGGATACGTCATTGGGA  75673       GGGGG A_
                                CATTGGATA    CA GGGA
                                |||||||||    || ||||
                                GTAACCTAT    GT CCCT
                                     GCA__ AA
GAM3369 GIT2     3' CTGGCTTACAGGGGTGAGGGA 75674     ___     GCA
                                TTGG  ATAGGGG  AGGGA
                                ||||  |||||||  |||||
                                GACC  TGTCCCC  TCCCT
                                  GAA     AC_
GAM3369 GIT2     3' CTGGCTTACAGGGGTGAGGGA 75674     ___     GCA
                                TTGG  ATAGGGG  AGGGA
                                ||||  |||||||  |||||
                                GACC  TGTCCCC  TCCCT
                                  GAA     AC_
GAM3369 GIT2     3' CTGGCTTACAGGGGTGAGGGA 75674     ___     GCA
                                TTGG  ATAGGGG  AGGGA
                                ||||  |||||||  |||||
                                GACC  TGTCCCC  TCCCT
                                  GAA     AC_
GAM3369 HRLP5    3' CATTGAGAGAAGGCAAGGGA  75675      AT
                                CATTGG AGGGGGCAAGGGA
                                ||||||  |||||||||||||
                                GTAACT  TCTTCCGTTCCCT
                                   C_
GAM3369 KIAA0193 3' TTGGTTATGGGGCAAGGGA   75676     A  G
                                TTGG TA GGGGCAAGGGA
                                |||| || ||||||||||
                                AACC AT CCCCGTTCCCT
                                  A  A
GAM3369 KIAA0326 3' CATTGTGGAACAGTGAGGGA  75677      GATAG     ___
                                CATTG    GGGGCA  AGGGA
                                |||||    ||||||  |||||
                                GTAAC    CCTTGT  TCCCT
                                   A____     CAC
GAM3369 KIAA0564 3' TTGGATAGGAGCATTTTGG   75678         G  AG__
                                TTGGATAGGGG CA   GG
                                |||||||||| ||   ||
                                AACCTATCCTC GT   CC
                                      _ AAAA
GAM3369 KIAA1036 3' TTGGGGAGGCAAGGG      75679     ATA
                                TTGG  GGGGGCAAGGG
                                ||||  ||||||||||
                                AACC  CCTCCGTTCCC
                                   ___
GAM3369 KIAA1100 5' TGGGCAGGGGGCGGGGGA   75680     A      AA
                                TGG TAGGGGGC  GGGA
                                ||| ||||||||  ||||
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                                ACC GTCCCCCG  CCCT
                                  C       CC
GAM3369 KIAA1949 5' TTGGGGAGGCAAGGA      75681     ATA
                                TTGG   GGGGGGCAAGGG
                                ||||   ||||||||||||
                                AACC   CCTCCGTTCCT
                                  ___
GAM3369 KIAA1949 5' TTGGGGAGGCAAGGA      75681     ATA
                                TTGG   GGGGGGCAAGGG
                                ||||   ||||||||||||
                                AACC   CCTCCGTTCCT
                                  ___
GAM3369 KIAA1949 5' TTGGGGAGGCAAGGA      75681     ATA
                                TTGG   GGGGGGCAAGGG
                                ||||   ||||||||||||
                                AACC   CCTCCGTTCCT
                                  ___
GAM3369 LIMR     3' CTGGGCCAGAGGCAAGGGA   75682     ATA
                                TTGG   GGGGGGCAAGGGA
                                ||||   |||||||||||||
                                GACC   TCTCCGTTCCCT
                                  CGG
GAM3369 NPTXR    3' TTGCATGGGGGGACAAGGG    75683     G  A
                                TTG AT GGGGGGCAAGGG
                                ||| || ||||||||||||
                                AAC TA CCCCTGTTCCC
                                  G  C
GAM3369 NPTXR    3' TTGCATGGGGGGACAAGGG    75683     G  A
                                TTG AT GGGGGGCAAGGG
                                ||| || ||||||||||||
                                AAC TA CCCCTGTTCCC
                                  G  C
GAM3369 PHYHIP   3' CAATGCCAAGGGGCGAGGG   75684     T  GA       A
                                CA TG  TAGGGGGC AGGG
                                || ||  |||||||| ||||
                                GT AC  GTTCCCCG TCCC
                                 T  G_       C
GAM3369 PPFIA4   3' ATTGACTATGAGGCAAGGGA  75685      ATAG
                                ATTGG    GGGGCAAGGGA
                                |||||    ||||||||||||
                                TAACT    CTCCGTTCCCT
                                   GATA
GAM3369 RAB10    3' CAATGGATAGACAGGAAGGGA 75686    T       G  C
                                CA TGGATAGG GG AAGGGA
                                || |||||||| || ||||||
                                GT ACCTATCT TC TTCCCT
                                 T       G  C
GAM3369 SEC14L1  3' CTGGGAGGGGGCAGGGGA    75687     AT       A
                                TTGG  AGGGGGCA GGGA
                                ||||  |||||||| ||||
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                                GACC  TCCCCCGT CCCT
                                  C_      C
GAM3369  SLC2A10   3'  CACTGGATACAAGGG      75688        AGGGG
                                CATTGGAT    GCAAGGG
                                ||||||||    |||||||
                                GTGACCTA    TGTTCCC
                                      _____
GAM3369  TBX21     5'  GGAGCAGGGGGCGGGGGA    75689    _      AA
                                GGA TAGGGGGC  GGGA
                                ||| ||||||||  ||||
                                CCT GTCCCCCG  CCCT
                                  C       CC
GAM3369  LOC135932 3'  ATTGGATATGGGGTAGG     75690        G    CA
                                ATTGGATA GGGG  AGG
                                |||||||| ||||  |||
                                TAACCTAT CCCC  TCC
                                     A    A_
GAM3369  LOC146562 3'  TGGAGGGGGCAGGGGA      75691      TA      A
                                TGGA  GGGGGCA GGGA
                                ||||  ||||||| ||||
                                ACCT  CCCCCGT CCCT
                                  __      C
GAM3369  LOC148114 5'  CTGGGTGGCAAGCAAGGG    75692      ATA  _
                                TTGG   GG GGGCAAGGG
                                ||||   || |||||||||
                                GACC   CC TTCGTTCCC
                                  CA_  G
GAM3369  LOC149108 3'  CATTGGATGTGGGTCCCAGGA  75693         AG   GCAA
                                CATTGGAT  GGG    GGGA
                                ||||||||  |||    ||||
                                GTAACCTA  CCC    TCCT
                                     CA   AGGG
GAM3369  LOC149465 3'  CATTGGGAGGTTGAAGGGA    75694       ATA    GC_
                                CATTGG   GGGG   AAGGGA
                                ||||||   ||||   ||||||
                                GTAACC   CTCC   TTCCCT
                                   ___    AAC
GAM3369  LOC150311 5'  TTGGTAACAAAGGGCAGGGG   75695      __        A
                                TTGG  ATAGGGGGCA GGG
                                ||||  |||||||||| |||
                                AACC  TGTTTCCCGT CCC
                                  AT         C
GAM3369  LOC150848 5'  ATTGTATAGAGACAAAAGGGA  75696      G      GC_
                                ATTG ATAGGGG   AAGGGA
                                |||| |||||||   ||||||
                                TAAC TATCTCT   TTCCCT
                                  A      GTT
GAM3369  LOC151904 5'  CATCGGAGTCAGGGCAAGGG   75697        TAG
                                CATTGGA   GGGGCAAGGG
                                |||||||   ||||||||||
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                                GTAGCCT   TCCCGTTCCC
                                    CAG
GAM3369  LOC152328 3'  CATTTGATAGGGGAGGG     75698      G       GCA
                                CATT GATAGGGG   AGGG
                                |||| ||||||||   ||||
                                GTAA CTATCCCC   TCCC
                                  A      ___
GAM3369  LOC152667 3'  TTGGATAGAGAGGGGG       75699           CAA
                                TTGGATAGGGGGG   GGG
                                ||||||||||||   |||
                                AACCTATCTCTC   CCC
                                          ___
GAM3369  LOC153232 5'  ATTGCATACAAGACAAGGG    75700      G   G
                                ATTG ATA GGGGCAAGGG
                                |||| ||| ||||||||||
                                TAAC TAT TTCTGTTCCC
                                  G   G
GAM3369  LOC157627 3'  CATTGGATACGGTTATGCGGGA 75701          G  GGCAA_
                                CATTGGATA GG     GGGA
                                ||||||||| ||     ||||
                                GTAACCTAT CC     CCCT
                                     G  AATACG
GAM3369  LOC157697 5'  TTGGATAAATGTCAAGGG     75702          GGG
                                TTGGATAGG   CAAGGG
                                |||||||||   ||||||
                                AACCTATTT   GTTCCC
                                     ACA
GAM3369  LOC158490 3'  TTGGGTAGGGGACCTGGG     75703      A       AA
                                TTGG TAGGGGGC  GGG
                                |||| ||||||||  |||
                                AACC ATCCCCTG  CCC
                                  C       GA
GAM3369  LOC219914 5'  CTGGATAGGGGCGAAGAAGGG  75704           GC___
                                TTGGATAGGGG    AAGGG
                                ||||||||||    |||||
                                GACCTATCCCC    TTCCC
                                      GCTTC
GAM3369  LOC254439 3'  CACTGGATGGGGTGGGG      75705         A   GCAA
                                CATTGGAT GGGG   GGG
                                |||||||| ||||   |||
                                GTGACCTA CCCC   CCC
                                     _   AC__
GAM3369  LOC58512  3'  TCGGACCAGGTGGGCAGGGGA  75706       _  _    A
                                TTGGAT AGG GGGCA GGGA
                                |||||| ||| ||||| ||||
                                AGCCTG TCC CCCGT CCCT
                                   G  A    C
GAM3369  LOC92148  5'  TGGTTGTGGGGGCAAGGGA   75707     ATA_
                                TGG   GGGGGCAAGGGA
                                |||   ||||||||||||
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                              ACC   CCCCCGTTCCCT
                                AACA
GAM3370 ATP8B2   3' ACCAACCACAACATAAAA   75710    A    CCA
                              ACC AGCCAT  AACATAAAA
                              ||| ||||||  |||||||||
                              TGG TTGGTG  TTGTATTTT
                                _    ___
GAM3370 COX7A2L  3' AAGCCATCCAAGTAAAAA   75711         ACA
                              AAGCCATCCAA  TAAAAA
                              ||||||||||  ||||||
                              TTCGGTAGGTT  ATTTTT
                                    C__
GAM3370 CYP19    3' GCCCCAGACATAAAAA     75712    AT  A
                              GCC  CCA ACATAAAAA
                              |||  ||| |||||||||
                              CGG  GGT TGTATTTTT
                                __  C
GAM3370 CYP19    3' GCCCCAGACATAAAAA     75712    AT  A
                              GCC  CCA ACATAAAAA
                              |||  ||| |||||||||
                              CGG  GGT TGTATTTTT
                                __  C
GAM3370 EIF5A2   3' CAAAGTCCTCACATAAAAAC  75713     CCA  AA
                              CAAG  TCC  ACATAAAAAC
                              ||||  |||  ||||||||||
                              GTTT  AGG  TGTATTTTTG
                                C__  AG
GAM3370 FBXL11   3' CCAAAAAACAAACATAAAAAC 75714     CCATC
                              CCAAG    CAAACATAAAAAC
                              |||||    ||||||||||||
                              GGTTT    GTTTGTATTTTTG
                                 TTT__
GAM3370 FOXO1A   3' ACCAAGCCATTTAAACATAA  75715        CC
                              ACCAAGCCAT  AAACATAA
                              ||||||||||  ||||||||
                              TGGTTCGGTA  TTTGTATT
                                    AA
GAM3370 KCNA5    3' AGCCACTTACCAGGCATAAAAA 75716      ___  AA
                              AGCCAT  CCA  CATAAAAA
                              ||||||  |||  ||||||||
                              TCGGTG  GGT  GTATTTTT
                                 AAT  CC
GAM3370 SLC6A3   3' GCCATTCGCAAACATAAAAAC  75717     _ _
                              GCCAT C CAAACATAAAAAC
                              ||||| | ||||||||||||
                              CGGTA G GTTTGTATTTTTG
                                 A C
GAM3370 TAL1     3' ACCGTGCCGTCTTCACAAAAA  75718    AA  A  CAAA
                              ACC  GCC TC   CATAAAAA
                              |||  ||| ||   ||||||||
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                                TGG  CGG AG    GTGTTTTT
                                  CA   C  AA__
GAM3370  TP63     3'  CAAGCCATCCAAAACAA     75719            C
                                CAAGCCATCCAAA ATAA
                                |||||||||||| ||||
                                GTTCGGTAGGTTT TGTT
                                          _
GAM3370  UBE4A    3'  CCATAGCCATTCATAAAAA    75720     _     CCAAA
                                CCA AGCCAT     CATAAAAA
                                ||| ||||||     ||||||||
                                GGT TCGGTA     GTATTTTT
                                  A     A____
GAM3370  WNT1     3'  ACCAAGTCATCGATAAAAA    75721       C    CAAAC
                                ACCAAG CATC     ATAAAAA
                                |||||| ||||     |||||||
                                TGGTTC GTAG     TATTTTT
                                   A    C____
GAM3370  B3GALT6  3'  ACCAAGTTCTGACATAAAA    75722       CCA  CAA
                                ACCAAG   TC   ACATAAAA
                                ||||||   ||   ||||||||
                                TGGTTC   AG   TGTATTTT
                                   A__  AC_
GAM3370  DKFZP434D0127 3'  CCGAGCCAATTAAGACATAAAA 75723     A     TCCAA_
            A                    CC AGCCA      ACATAAAAA
                                || |||||      |||||||||
                                GG TCGGT      TGTATTTTT
                                 C     TAATTC
GAM3370  DKFZP434J037 3'  ACAAAGCCAAGAACATAAAAA  75724     C      TCCA
                                AC AAGCCA     AACATAAAAA
                                || ||||||    ||||||||||
                                TG TTCGGT    TTGTATTTTT
                                 T     TC__
GAM3370  FLJ10498  3'  AGCCGTCTCCAAAATAAAAAC  75725       A__      C
                                AGCC   TCCAAA ATAAAAAC
                                ||||   |||||| ||||||||
                                TCGG   AGGTTT TATTTTTG
                                  CAG     _
GAM3370  FLJ10936  5'  ACCGACCAAACAAGCATAAAAA 75726      AA    TC   A
                                ACC  GCCA  CAA CATAAAAA
                                |||  ||||  ||| ||||||||
                                TGG  TGGT  GTT GTATTTTT
                                  C_    TT   C
GAM3370  FLJ11127  3'  CAAGCCACCAACTCCCAAA    75727        T    ACA_
                                CAAGCCA CCAA    TAAA
                                ||||||| ||||    ||||
                                GTTCGGT GGTT    GTTT
                                    _    GAGG
GAM3370  FLJ21106  3'  ACCGCGCCCAGCCAGCATAAAA 75728      AA   AT_   AA
                                ACC  GCC   CCA  CATAAAA
                                |||  |||   |||  |||||||
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                                TGG  CGG   GGT  GTATTTT
                                  CG   GTC   C_
GAM3370  FLJ22679  3'  ACCAATGATCACAAATATAAAA 75729      GCC   _    C
              AC                    ACCAA   ATC CAAA ATAAAAAC
                                |||||   ||| |||| ||||||||
                                TGGTT   TAG GTTT TATTTTTG
                                  AC_   T    A
GAM3370  FLJ22679  3'  ACCAATGATCACAAATATAAAA 75729      GCC   _    C
              AC                    ACCAA   ATC CAAA ATAAAAAC
                                |||||   ||| |||| ||||||||
                                TGGTT   TAG GTTT TATTTTTG
                                  AC_   T    A
GAM3370  FRAT1    3'  CAAGCCATTGACTATAAAAAC  75730        CCAA  _
                                CAAGCCAT    AC ATAAAAAC
                                ||||||||    || ||||||||
                                GTTCGGTA    TG TATTTTTG
                                     AC__   A
GAM3370  HEY2     3'  AGCCATCCAAAAAAAAAA    75731          CAT
                                AGCCATCCAAA   AAAAA
                                ||||||||||   |||||
                                TCGGTAGGTTT   TTTTT
                                      TT_
GAM3370  KALI     3'  CCAGACCATCCAGGGCCATGGA 75732     AG      AA__   AA
              AAC                   CCA  CCATCCA    CAT  AAAC
                                |||  |||||||    |||  ||||
                                GGT  GGTAGGT    GTA  TTTG
                                  CT      CCCG   CC
GAM3370  KIAA0628  3'  CAGGCAAACCAAACATGAAAA  75733    A  CAT      A
                                CA GC   CCAAACAT AAAA
                                || ||   |||||||| ||||
                                GT CG   GGTTTGTA TTTT
                                 C  TTT       C
GAM3370  KIAA1724  3'  ACCACTGTCAAACATAAAAAC  75734      C__
                                GCCAT   CAAACATAAAAAC
                                |||||   ||||||||||||
                                TGGTG   GTTTGTATTTTTG
                                   ACA
GAM3370  LAMP3    3'  AAGCAATCCCATAAAAA     75735      C    AAA
                                AAGC ATCC   CATAAAAA
                                |||| ||||   ||||||||
                                TTCG TAGG   GTATTTTT
                                  T   ____
GAM3370  MFN2     3'  CCAGCAAATGAACATAAAAAC  75736     A  CATCCA
                                CCA GC     AACATAAAAAC
                                ||| ||     ||||||||||
                                GGT CG     TTGTATTTTTG
                                  _  TTTAC_
GAM3370  MGC2306  3'  CAAGCCAAATAAAACATAAAAA 75737        TCC_
              C                   CAAGCCA    AAACATAAAAAC
                                |||||||    ||||||||||||
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                                GTTCGGT    TTTGTATTTTTG
                                    TTAT
GAM3370  RALGPS1A  3'  ACCAAGCCATTCAAATTTCTAA 75738          C    CA__
              A                  ACCAAGCCAT CAAA    TAAA
                                 |||||||||| ||||    ||||
                                 TGGTTCGGTA GTTT    ATTT
                                      A    AAAG
GAM3370  SAC2      3'  AAGCCATCAAAACTAAAA     75739        C    A
                                 AAGCCATC AAAC TAAAA
                                 |||||||| |||| |||||
                                 TTCGGTAG TTTG ATTTT
                                      T    _
GAM3370  SEMA7A    3'  AAGCCTAACATAAAAA      75740       ATCCA
                                 AAGCC     AACATAAAAA
                                 |||||     ||||||||||
                                 TTCGG     TTGTATTTTT
                                    A____
GAM3370  TUB       3'  ACCAAGCCCTTTGCTACATAAA 75741         ATCCAA_
                                 ACCAAGCC      ACATAAA
                                 ||||||||      |||||||
                                 TGGTTCGG      TGTATTT
                                      GAAACGA
GAM3370  LOC145773 3'  CAAGCCATTGACAGCAAAA    75742         CCAA   _
                                 CAAGCCAT    ACA TAAAA
                                 ||||||||    ||| |||||
                                 GTTCGGTA    TGT GTTTT
                                      AC__   C
GAM3370  LOC154739 5'  ACGAAGCCATCCAAGCATA    75743    C          A
                                 AC AAGCCATCCAA CATA
                                 || ||||||||||| ||||
                                 TG TTCGGTAGGTT GTAT
                                   C          C
GAM3370  LOC162427 3'  CCAGGCCACCCAGCATA      75744     A        AA
                                 CCA GCCATCCA  CATA
                                 ||| ||||||||  ||||
                                 GGT CGGTGGGT  GTAT
                                   C       C_
GAM3370  LOC196264 3'  CCTAAGTTATCCAAACACAA   75745    _   CC
                                 CC AAG  ATCCAAACATAA
                                 || |||  ||||||||||||
                                 GG TTC  TAGGTTTGTGTT
                                   A   AA
GAM3370  LOC203276 3'  ACAAAGCCATCCAAGCATA    75746    C          A
                                 AC AAGCCATCCAA CATA
                                 || ||||||||||| ||||
                                 TG TTCGGTAGGTT GTAT
                                   T          C
GAM3370  LOC203305 3'  ACAAAGCCATCCAAGCATA    75746    C          A
                                 AC AAGCCATCCAA CATA
                                 || ||||||||||| ||||
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                                TG TTCGGTAGGTT GTAT
                                 T         C
GAM3370  LOC254243 3'  ACAAAGCCATCCAAGCATA   75746    C         A
                                AC AAGCCATCCAA CATA
                                || |||||||||| ||||
                                TG TTCGGTAGGTT GTAT
                                 T         C
GAM3370  LOC90038  3'  ACAAAGCCATCCAAGCATA   75746    C         A
                                AC AAGCCATCCAA CATA
                                || |||||||||| ||||
                                TG TTCGGTAGGTT GTAT
                                 T         C
GAM3370  LOC93070  5'  ACCGACCAAACAAGCATAAAAA 75726     AA    TC   A
                                ACC  GCCA  CAA CATAAAAA
                                |||  ||||  ||| ||||||||
                                TGG  TGGT  GTT GTATTTTT
                                  C_   TT   C
GAM3371  ABCG1    3'  GATCAGAAGAGTCTCTGTGTC  75749       AAA    CATAA_
                                GATCAGG   AGAG     TGTC
                                |||||||   ||||     ||||
                                CTAGTCT   TCTC     ACAG
                                    ___    AGAGAC
GAM3371  ALS2     3'  GATGAGGAAGAGCACCTATGT  75750     C    AA      A_
                                GAT AGGA  AGAGCAT  ATGT
                                ||| ||||  |||||||  ||||
                                CTA TCCT  TCTCGTG  TACA
                                  C   __      GA
GAM3371  DLG1     5'  AATCAGGAAGAGGGCACA     75751         A  A
                                GATCAGGAA AG GCATA
                                ||||||||| || |||||
                                TTAGTCCTT TC CGTGT
                                     C  C
GAM3371  FGF5     3'  AGGATTCCACATAATGTCA    75752      AAAGA
                                AGGA    GCATAATGTCA
                                ||||    ||||||||||
                                TCCT    TGTATTACAGT
                                  AAGG_
GAM3371  FGF5     3'  AGGATTCCACATAATGTCA    75752      AAAGA
                                AGGA    GCATAATGTCA
                                ||||    ||||||||||
                                TCCT    TGTATTACAGT
                                  AAGG_
GAM3371  LAMC2    3'  GATCAGGAATGGGGTCAGGTCA 75753         AAGAG_  TAAT
                                GATCAGGAA     CA    GTCA
                                |||||||||     ||    ||||
                                CTAGTCCTT     GT    CAGT
                                     ACCCCA  C___
GAM3371  NCOA6    3'  GACTAGGAAAAGGGCCACAT   75754     C       A  ATA
                                GAT AGGAAAAG GC   AT
                                ||| |||||||| ||   ||
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                                CTG TCCTTTTC CG   TA
                                  A       C  GTG
GAM3371  PTPRE    3'  AATTAGGGAAGATATTAATGTC 75755     C   AA    GCA
              A                    GAT AGG  AAGA   TAATGTCA
                                   ||| |||  ||||   ||||||||
                                   TTA TCC  TTCT   ATTACAGT
                                     A  C_    ATA
GAM3371  PTPRE    3'  AATTAGGGAAGATATTAATGTC 75755     C   AA    GCA
              A                    GAT AGG  AAGA   TAATGTCA
                                   ||| |||  ||||   ||||||||
                                   TTA TCC  TTCT   ATTACAGT
                                     A  C_    ATA
GAM3371  SULT2A1  3'  GACAGGAGAATCAATGTC    75756    T    AAA   CA
                                   GA CAGGA   GAG  TAATGTC
                                   || |||||   |||  |||||||
                                   CT GTCCT   CTT  GTTACAG
                                    _    ___   A_
GAM3371  CNNM1    3'  GATCAGAAAGGGAGATA     75757         AA   C
                                   GATCAGGAA  GAG ATA
                                   |||||||||  ||| |||
                                   CTAGTCTTT  CTC TAT
                                        CC   _
GAM3371  FLJ10546 3'  GATCAGAAATGGTATGATGTCA 75758         AAGAGCATA
                                   GATCAGGAA        ATGTCA
                                   |||||||||        ||||||
                                   CTAGTCTTT        TACAGT
                                        ACCATAC__
GAM3371  FLJ14525 3'  GATTAAGAAAAGAGTGTC    75759     C        CATAA
                                   GAT AGGAAAAGAG     TGTC
                                   ||| ||||||||||     ||||
                                   CTA TTCTTTTCTC     ACAG
                                     A        ______
GAM3371  FLJ20450 3'  GACAGGAAGAACACAGATGTCA 75760    T     AA      _
                                   GA CAGGA  AGAGCATA ATGTCA
                                   || |||||  |||||||| ||||||
                                   CT GTCCT  TCTTGTGT TACAGT
                                    _    __        C
GAM3371  HSPC216  3'  GAACAGGAAAAACTTAGTGTCA 75761    T     AA    A  A
                                   GA CAGGAA  GAGC TA TGTCA
                                   || ||||||  |||| || |||||
                                   CT GTCCTT  TTTG AT ACAGT
                                    T     __    A  C
GAM3371  KIAA0721 3'  AATTGGGAGAAGAGCATGGTCA 75762     CA   A      AAT
                                   GAT  GGA AAGAGCAT   GTCA
                                   |||  ||| ||||||||   ||||
                                   TTA  CCT TTCTCGTA   CAGT
                                     AC   C       C__
GAM3371  KIAA0721 3'  AATTGGGAGAAGAGCATGGTCA 75762     CA   A      AAT
                                   GAT  GGA AAGAGCAT   GTCA
                                   |||  ||| ||||||||   ||||
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                                TTA  CCT TTCTCGTA   CAGT
                                  AC   C       C__
GAM3371  KIAA0830  3'  GATGCAGTAAGCATAATGT    75763     _  GAAAA
                                GAT CAG    GAGCATAATGT
                                ||| |||    ||||||||||
                                CTA GTC    TTCGTATTACA
                                  C   A____
GAM3371  KIAA1210  3'  ATCAGGAAAAATAGATGT     75764          _ CATA
                                ATCAGGAAAAG AG    ATGT
                                |||||||||| ||    ||||
                                TAGTCCTTTTT TC    TACA
                                      A ____
GAM3371  KIAA1900  3'  GAGCAGGGCTGCATAATGT    75765    T    AAAAGA
                                GA CAGG     GCATAATGT
                                || ||||     |||||||||
                                CT GTCC     CGTATTACA
                                 C   CGA___
GAM3371  MGC17299  5'  TCAGGGTAGGAGGTCAATGTCA 75766      AAAA   CA
                                TCAGG   GAG  TAATGTCA
                                |||||   |||  ||||||||
                                AGTCC   CTC  GTTACAGT
                                   CATC   CA
GAM3371  RP4-622L5 3'  GATCAGGAAACAGTATGT    75767        AAGA   TA
                                GATCAGGAA   GCA  ATGT
                                |||||||||   |||  ||||
                                CTAGTCCTT   TGT  TACA
                                     ____  CA
GAM3371  SE57-1    3'  GATCAGGAGATGAACTTATGTC 75768       AAA    ATA
            A                    GATCAGGA   GAGC   ATGTCA
                                ||||||||   ||||   ||||||
                                CTAGTCCT   CTTG   TACAGT
                                    CTA    AA_
GAM3371  LOC149460 5'  GATCAGGAGAGGAGGAATG    75769       AAA   CAT
                                GATCAGGA   GAG   AATG
                                ||||||||   |||   ||||
                                CTAGTCCT   CTC   TTAC
                                    CTC   C__
GAM3371  LOC155179 3'  CAGGAAGAGGGGGCATGGTGTC 75770       A  A__   AA
                                CAGGAA AG   GCAT  TGTC
                                |||||| ||   ||||  ||||
                                GTCCTT TC   CGTA  ACAG
                                   C  CCC    CC
GAM3371  LOC200399 5'  GATAGGAAGAATTAATGTCA   75771     C    AA    CA
                                GAT AGGA  AGAG  TAATGTCA
                                ||| ||||  ||||  ||||||||
                                CTA TCCT  TCTT  ATTACAGT
                                  _   __    A_
GAM3371  LOC221692 3'  CCAGGAAAGGCCTACGATGTC  75772        A A  ATA__
                                TCAGGAAA G GC     ATGTC
                                |||||||| | ||    |||||
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                                GGTCCTTT C CG     TACAG
                                    _ _  GATGC
GAM3371  LOC257095 5'  GGAAAAGAAATATGTCA     75773          C   A
                                GGAAAAGAG ATA TGTCA
                                ||||||||| ||| |||||
                                CCTTTTCTT TAT ACAGT
                                      _   _
GAM3371  LOC257486 3'  ATCAGGAAAAATAGATGT     75764           _  CATA
                                ATCAGGAAAAG AG    ATGT
                                |||||||||| ||    ||||
                                TAGTCCTTTTT TC    TACA
                                     A  ____
GAM3371  LOC90829  5'  AATTAGGAAAAGAGGAAGTCA  75774     C         CATAAT
                                GAT AGGAAAAGAG      GTCA
                                ||| ||||||||||      ||||
                                TTA TCCTTTTCTC      CAGT
                                  A         CTT___
GAM3372  FKBP1A    3'  CCATATGGACTCATGTGC     75777         _     C
                                TCATATGG TTTATG GC
                                |||||||| |||||| ||
                                GGTATACC GAGTAC CG
                                     T     A
GAM3372  HBZ       3'  TCATTGGTTTATTGGCGC     75778      A       __
                                TCAT TGGTTTAT  GCGC
                                |||| ||||||||  ||||
                                AGTA ACCAAATA  CGCG
                                  _       AC
GAM3372  MEF2B     5'  TCATATGGTCCCGGATGC     75779           ___
                                TCATATGGTTT   ATGC
                                ||||||||||   ||||
                                AGTATACCAGG   TACG
                                     GCC
GAM3372  DDX31     3'  TCATGCCAATGTATGCGC     75780      A_   T
                                TCAT  TGGT TATGCGC
                                ||||  |||| |||||||
                                AGTA  GTTA ATACGCG
                                  CG    C
GAM3372  GOLPH4    3'  TCATATAAATGTATGCGC     75781         TT_
                                TCATATGG   TATGCGC
                                ||||||||   |||||||
                                AGTATATT   ATACGCG
                                     TAC
GAM3372  MBD2      3'  TCATACTGCAAATATATGCGC  75782       G  T____
                                TCATAT GT     TATGCGC
                                |||||| ||     |||||||
                                AGTATG CG     ATACGCG
                                   A  TTTAT
GAM3372  LOC135521 3'  CCATATGGATTTATGTGC     75783         _     C
                                TCATATGG TTTATG GC
                                |||||||| |||||| ||
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                                GGTATACC AAATAC CG
                                    T     A
GAM3373 ABCB10   3' CCTTTTTAAAGTTGTCATTTGA 75786      C   A       AT
           CA                    TCTTT TAAA TTGTCATTT  CA
                                 ||||| |||| |||||||||  ||
                                 GGAAA ATTT AACAGTAAA  GT
                                   A   C       CT
GAM3373 LECT2    3' TCTTTCTTGCATTTAT      75787        AAAAT  T
                                 TCTTTCT    TG CATTTAT
                                 |||||||    || |||||||
                                 AGAAAGA    AC GTAAATA
                                      _____ _
GAM3373 PARK2    3' TCTTTCTAAAGTTGCAAATCA  75788         A   CATTT
                                 TCTTTCTAAA TTGT    ATCA
                                 |||||||||| ||||    ||||
                                 AGAAAGATTT AACG    TAGT
                                      C   TT___
GAM3373 PARK2    3' TCTTTCTAAAGTTGCAAATCA  75788         A   CATTT
                                 TCTTTCTAAA TTGT    ATCA
                                 |||||||||| ||||    ||||
                                 AGAAAGATTT AACG    TAGT
                                      C   TT___
GAM3373 PARK2    3' TCTTTCTAAAGTTGCAAATCA  75788         A   CATTT
                                 TCTTTCTAAA TTGT    ATCA
                                 |||||||||| ||||    ||||
                                 AGAAAGATTT AACG    TAGT
                                      C   TT___
GAM3373 PIK3C2B  3' TTTCTCAAATGTCATTTAT   75789      AAAAT
                                 TTTCT    TGTCATTTAT
                                 |||||    ||||||||||
                                 AAAGA    ACAGTAAATA
                                   GTTT_
GAM3373 CYP2C18  3' CTCTGAATTGTCATTTAT    75790      AA
                                 TTCT  AATTGTCATTTAT
                                 ||||  ||||||||||||
                                 GAGA  TTAACAGTAAATA
                                   C_
GAM3373 DKFZP586M1120 3'  TCTCTCTAAAGTTGTTGTTCTC 75791          A   CA  A
           CA                    TCTTTCTAAA TTGT  TTT TCA
                                 |||||||||| ||||  ||| |||
                                 AGAGAGATTT AACA  AAG GGT
                                      C   AC  A
GAM3373 DKFZp761K1423 3'  TCTTTCTAAAGTTTGTACATTT 75792          A_  _
           A                     TCTTTCTAAA  TTGT CATTTA
                                 ||||||||||  |||| ||||||
                                 AGAAAGATTT  AACA GTAAAT
                                      CA   T
GAM3373 FLJ10774 3'  TCTTTCTAGAATGTTATTTAT  75793        AAAT  C
                                 TCTTTCTA    TGT ATTTAT
                                 ||||||||    ||| ||||||
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                                AGAAAGAT   ACA TAAATA
                                    CTT_  A
GAM3373 FLJ13544 3' TCCTTCTAAAATGGTTGTCA  75794         ___
                                TCTTTCTAAAAT  TGTCA
                                ||||||||||||  |||||
                                AGGAAGATTTTA  ACAGT
                                      CCA
GAM3373 KIAA0152 3' TCTTTCTAAAGCTTGAACATT 75795       A_  T_
                                TCTTTCTAAA TTG CATT
                                |||||||||| ||| ||||
                                AGAAAGATTT AAC GTAA
                                     CG  TT
GAM3373 MAP4K3   3' TCTTTCTAGAGTTAACTGTCA 75796      A____
                                TCTTTCTA   AATTGTCA
                                ||||||||   ||||||||
                                AGAAAGAT   TTGACAGT
                                    CTCAA
GAM3373 MGC16063 3' CCTTTCTAAATATTCTGTTTAT 75797       ATTG A_
            CA                   TCTTTCTAAA  TC TTTATCA
                                ||||||||||  || |||||||
                                GGAAAGATTT  AG AAATAGT
                                     ATA_ AC
GAM3373 LOC146050 3' CTTTCTAAACAATACATTTAT 75798       ATTGT
                                CTTTCTAAA   CATTTAT
                                |||||||||   |||||||
                                GAAAGATTT   GTAAATA
                                    GTTAT
GAM3373 LOC254735 5' TCTTTCCAAACTCACATTT  75799        ATTGT
                                TCTTTCTAAA   CATTT
                                ||||||||||   |||||
                                AGAAAGGTTT   GTAAA
                                     GAGT_
GAM3374 BMP1    3' TTTGTGGGGAAGTGGCT    75802     T   CTTCTT
                                TTTGT GGGAA    TGGCT
                                ||||| |||||    |||||
                                AAACA CCCTT    ACCGA
                                  C   C_____
GAM3374 EHD2    3' TTGGGAAGAAGCCTTGGCTT  75803      CTT_
                                TTGGGAA   CTTTGGCTT
                                |||||||   |||||||||
                                AACCCTT   GGAACCGAA
                                    CTTC
GAM3374 FACL4   5' CTTGTTATTCTTTGGCTT    75804      GGAAC
                                TTTGTTG   TTCTTTGGCTT
                                |||||||   ||||||||||
                                GAACAAT   AAGAAACCGAA
                                     _____
GAM3374 FLJ13855 3' TGTTGGGAACTTTTCAA    75805        C TG
                                TGTTGGGAACTT TT  G
                                |||||||||||| ||  |
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                                ACAACCCTTGAA AA  T
                                      _ GT
GAM3374  FLJ22471  3'  TTTGTTGGGATCTTAAAC    75806        ACT   TG
                                TTTGTTGGGA  TCTT  GC
                                ||||||||||  ||||  ||
                                AAACAACCCT  AGAA  TG
                                     ____   TT
GAM3374  TRPC3     3'  TTTGTTGGCAGTTCAGTTGG  75807       GAAC  T_
                                TTTGTTGG   TTC  TTGG
                                ||||||||   |||  ||||
                                AAACAACC   AAG  AACC
                                    GTC_   TC
GAM3374  LOC147514 3'  TTTGCTGGGATTGGGTTTGGCT 75808        ACTTC
           T                     TTTGTTGGGA    TTTGGCTT
                                 ||||||||||    ||||||||
                                 AAACGACCCT    AAACCGAA
                                       AACCC
GAM3374  LOC200273 3'  TTTGCTGGGATTGGGTTTGGCT 75808        ACTTC
           T                     TTTGTTGGGA    TTTGGCTT
                                 ||||||||||    ||||||||
                                 AAACGACCCT    AAACCGAA
                                       AACCC
GAM3374  LOC254419 5'  TCTGTTGGCTTTTGGCT    75809       GAA   CT
                                TTTGTTGG  CTT  TTGGCT
                                ||||||||  |||  ||||||
                                AGACAACC  GAA  AACCGA
                                          ___  __
GAM3374  LOC92799  3'  TTTATTGGGGAGGCTGACTTTG 75810        AA__  T_
           GCTT                    TTTGTTGGG   CT  CTTTGGCTT
                                   |||||||||   ||  |||||||||
                                   AAATAACCC   GA  GAAACCGAA
                                         CTCC  CT
GAM3375  FMO4      3'  TAATAGCAGTTATGATGGAG  75813        CAC   CA_
                                TAATAGCAG  ATG  GAG
                                |||||||||  |||  |||
                                ATTATCGTC  TAC  CTC
                                      AA_  TAC
GAM3375  FMR2      3'  TAGACATGTTGCACATGCAG  75814      ATAGCA
                                TAGATA    GCACATGCAG
                                ||||||    ||||||||||
                                ATCTGT    CGTGTACGTC
                                   ACAA__
GAM3375  FPGS      3'  GATGGCAGCAGCCTCACGGAG  75815    AA     A_   C
                                GAT  TAGCAGC  CATG AG
                                |||  |||||||  |||| ||
                                CTA  GTCGTCG  GTGC TC
                                  CC     GA   C
GAM3375  GHRHR     3'  GATGAGAGCAGACACAGAG   75816    AAT    C  AT
                                GAT  AGCAG AC  GCAGAG
                                |||  ||||| ||  ||||||
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                                CTA   TCGTC TG  TGTCTC
                                  CTC    _ __
GAM3375 GRM1     3' GATAATAGTAGGCATTCAGAG 75817        C CA  G
                                GATAATAG AG  CAT CAGAG
                                ||||||| ||  ||| |||||
                                CTATTATC TC  GTA GTCTC
                                     A C_  A
GAM3375 HUNK     5' TAGACAATAGCGGCTGCCCAG 75818          A ACA  AG
                                TAGATAATAGC GC   TGC  AG
                                |||||||||| ||   |||  ||
                                ATCTGTTATCG CG   ACG  TC
                                       C ___  GG
GAM3375 KCNH3    3' TAGAGGCAGGGGCACATGCAG 75819     TAA  CA
                                TAGA   TAG  GCACATGCAG
                                ||||   |||  ||||||||||
                                ATCT   GTC  CGTGTACGTC
                                  CC_  CC
GAM3375 MAP1A    3' CAGATGACCACATGCAGA    75820      A AGCAG
                                TAGAT AT    CACATGCAGA
                                ||||| ||    ||||||||||
                                GTCTA TG    GTGTACGTCT
                                   C _____
GAM3375 KIAA0247 3' TAGAAATAGCAGCACATG    75821      T
                                TAGA AATAGCAGCACATG
                                |||| ||||||||||||||
                                ATCT TTATCGTCGTGTAC
                                _
GAM3375 LOC159053 3' TAGATAATGTTGGCAATTGTAG 75822        AGCA  CA  C
           AG                     TAGATAAT   GCA  TG AGAG
                                ||||||||   |||  || ||||
                                ATCTATTA   CGT  AC TCTC
                                     CAAC  TA  A
GAM3375 LOC255521 3' TAGGTAGCAGCAGCACTATCAG 75823     A  A       ATG
                                TAG TA TAGCAGCAC   CAG
                                ||| || |||||||||   |||
                                ATC AT GTCGTCGTG   GTC
                                  C  C       ATA
GAM3376 CAPN10   3' CTGTTGGTAGAGTTTCAG    75826     G       G_
                                CTG TGGTAGAGT  CAG
                                ||| |||||||||  |||
                                GAC ACCATCTCA  GTC
                                  A        AA
GAM3376 CAPN10   3' CTGTTGGTAGAGTTTCAG    75826     G       G_
                                CTG TGGTAGAGT  CAG
                                ||| |||||||||  |||
                                GAC ACCATCTCA  GTC
                                  A        AA
GAM3376 EGFL4    5' GTGGAAGCTGCAGCCAC     75827      T  AG
                                GTGG AG  TGCAGCCAC
                                |||| ||  |||||||||
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                                CACC TC  ACGTCGGTG
                                  T  G_
GAM3376  HADH2    3'  CGACTGGTAGGCAGTTAC    75828        _    AG
                                CGACTGGT GGTAG  TGC
                                |||||||| |||||  |||
                                GCTGACCA CCGTC  ATG
                                     T    A_
GAM3376  HD       3'  GACTGGTGGGTGGAGAACGACA 75829         T___    _
            G                    GACTGGTGG   AGAGTG CAG
                                |||||||||   |||||| |||
                                CTGACCACC   TCTTGC GTC
                                     CACC     T
GAM3376  MCCC2    3'  GAATGGTGGTAATGGCTGC   75830    C       AGT  A
                                GA TGGTGGTAG   GC GC
                                || |||||||||   || ||
                                CT ACCACCATT   CG CG
                                 T        AC_  A
GAM3376  MS4A1    3'  GACTGGTGGTAAAATATTTGC  75831             CA_
                                GACTGGTGGTAGAGTG   GC
                                ||||||||||||||||   ||
                                CTGACCACCATTTTAT   CG
                                          AAA
GAM3376  OBP2A    3'  CTGGTGGTAGGGTGGGC     75832          A   CA
                                CTGGTGGTAG GTG  GC
                                |||||||||| |||  ||
                                GACCACCATC CAC  CG
                                     C   C_
GAM3376  OBP2B    3'  CTGGTGGTAGGGTGGGC     75832          A   CA
                                CTGGTGGTAG GTG  GC
                                |||||||||| |||  ||
                                GACCACCATC CAC  CG
                                     C   C_
GAM3376  ORM1     5'  CTGGTGGCTGCAGGGTGCAGTC 75833         ___  A     C
            AC                    CTGGTGGT   AG GTGCAG CAC
                                |||||||||   || |||||| |||
                                GACCACCG   TC CACGTC GTG
                                     ACG  C     A
GAM3376  PLA2G4C  3'  ACTGGCTAGAAGTGCAGTCA   75834       GGTA      C
                                ACTGGT    GAGTGCAG CA
                                ||||||    |||||||| ||
                                TGACCG    TTCACGTC GT
                                    ATC_       A
GAM3376  SLC2A6   3'  CTGGTGGCAGGGATGACTGC   75835          A_   _ A
                                CTGGTGGTAG  GTG C GC
                                ||||||||||  ||| | ||
                                GACCACCGTC  TAC G CG
                                     CC   T A
GAM3376  DHODH    3'  CGATTGGCGTTTACAGTGCAGC 75836     C     G_  G
            CA                    CGA TGGTG  TA AGTGCAGCCA
                                ||| |||||  || ||||||||||
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                                GCT ACCGC  AT TCACGTCGGT
                                  A    AA  G
GAM3376  DKFZP434J1813 5'  GATTGGTGAGGTGCAGCCAC   75837    C    GT  A
                                GA TGGTG  AG GTGCAGCCAC
                                || |||||  || ||||||||||
                                CT ACCAC  TC CACGTCGGTG
                                 A    __ _
GAM3376  DKFZP564I122 3'  GGCTAGAGTGCAGCCA      75838     GG
                                GGT  TAGAGTGCAGCCA
                                |||  ||||||||||||
                                CCG  ATCTCACGTCGGT
                                  __
GAM3376  DKFZP586G1122 3'  GACTGGTGGGAGGGGACAGCCA 75839         T  AGT
                                GACTGGTGG AG   GCAGCCA
                                ||||||||| ||   |||||||
                                CTGACCACC TC   TGTCGGT
                                      C  CCC
GAM3376  DKFZP667O116 3'  TGGTGGCAGCAGCCAC      75840         GAGT
                                TGGTGGTA    GCAGCCAC
                                ||||||||    ||||||||
                                ACCACCGT    CGTCGGTG
                                     _____
GAM3376  FLJ10211  5'  TGGTGGTGGCGGCAGCCA    75841        AGA  _
                                TGGTGGT   GTG CAGCCA
                                |||||||   ||| ||||||
                                ACCACCA   CGC GTCGGT
                                    C__   C
GAM3376  FLJ11301  3'  GACTGTTGGGTGCAGCC     75842      G   TAGA
                                GACTG TGG    GTGCAGCC
                                ||||| |||    ||||||||
                                CTGAC ACC    CACGTCGG
                                   A  _____
GAM3376  KIAA0494  3'  ACTGGTGGTGGGAGCCAGCTAC 75843         A_   G   C
                                ACTGGTGGT  GAGT CAGC AC
                                |||||||||  |||| |||| ||
                                TGACCACCA  CTCG GTCG TG
                                      CC   _   A
GAM3376  KIAA0677  3'  GACTGGGGCCAGTGCAGCCAC  75844       T   AG
                                GACTGG GGT  AGTGCAGCCAC
                                ||||||| |||  ||||||||||||
                                CTGACC CCG  TCACGTCGGTG
                                   _  G_
GAM3376  KIAA1879  5'  CGATTGGTGGCAGAAATAACTA 75845     C         TGC   C
             C                   CGA TGGTGGTAGAG   AGC AC
                                ||| ||||||||||   ||| ||
                                GCT ACCACCGTCTT   TTG TG
                                  A         TA_   A
GAM3376  POMT1    5'  CGGTTGGGGGTGAGGCCGC    75846    AC   T   A   T  A
                                CG  TGG GGT GAG GC GC
                                ||  ||| ||| ||| || ||
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                                GC  ACC CCA CTC CG CG
                                 CA   C   _   _  G
GAM3376  SBBI26   5'  CGATCGGCAGTGCAGC      75847     C    GGTAG
                                CGA TGGT     AGTGCAGC
                                ||| ||||     ||||||||
                                GCT GCCG     TCACGTCG
                                  A   ______
GAM3376  TREX2    5'  CAACTGGTCCATGAAGTGTAGC 75848         G_  AG   C
                                CGACTGGT  GT  AGTG AGC
                                ||||||||  ||  |||| |||
                                GTTGACCA  TA  TCAC TCG
                                     GG  CT    A
GAM3376  TREX2    5'  CAACTGGTCCATGAAGTGTAGC 75848         G_  AG   C
                                CGACTGGT  GT  AGTG AGC
                                ||||||||  ||  |||| |||
                                GTTGACCA  TA  TCAC TCG
                                     GG  CT    A
GAM3376  TRY6     5'  CTGGTGGTGGAAGGCCC     75849         A   T  AG
                                CTGGTGGT GAG GC  CC
                                |||||||| ||| ||  ||
                                GACCACCA CTT CG  GG
                                     C   C  __
GAM3376  LOC127281 3'  CGCCTGGCCTAGGGTGCAGCCA 75850    A    GG   A
           C                     CG CTGGT  TAG GTGCAGCCAC
                                 || |||||  ||| ||||||||||
                                 GC GACCG  ATC CACGTCGGTG
                                  G    G_   C
GAM3376  LOC132332 3'  GACTGGTGGTGGAGTCA     75851          A   G
                                GACTGGTGGT GAGT CA
                                |||||||||| |||| ||
                                CTGACCACCA CTCA GT
                                      C   _
GAM3376  LOC201102 3'  GACTGGTGGTGGAGTCTCA   75852          A   G_
                                GACTGGTGGT GAGT  CA
                                |||||||||| ||||  ||
                                CTGACCACCA CTCA  GT
                                      C   GA
GAM3376  LOC204084 5'  CTGGTGATAGGGCCAAC     75853          A  G
                                CTGGTGGTAG GT CAGC
                                |||||||||| || ||||
                                GACCACTATC CG GTTG
                                      C  _
GAM3376  LOC51200  3'  TGATGCTGAGTGCAGCC     75854       GTA
                                TGGTG   GAGTGCAGCC
                                |||||   ||||||||||
                                ACTAC   CTCACGTCGG
                                   GA_
GAM3376  LOC90784  5'  CGATAGGTGGTGACGGTGGC   75855     CT     A  __   CA
                                CGA  GGTGGT GA  GTG  GC
                                |||  |||||| ||  |||  ||
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                                GCT  CCACCA CT  CAC  CG
                                  AT     _ GC   __
GAM3376  LOC91050  3'  GACTTGATGGGGTGCAGCCA   75856     _    TAGA
                                GACT GGTGG   GTGCAGCCA
                                |||| |||||   |||||||||
                                CTGA CTACC   CACGTCGGT
                                  A    C___
GAM3377  HIS1      3'  GTTAACCAAAATGACAGG    75859      A     TC
                                GTTAA CCAAAAT  GCAGG
                                ||||| |||||||  |||||
                                CAATT GGTTTTA  TGTCC
                                   _     C_
GAM3377  WNT5A     5'  CAAGTTAAACCAGGGGAGCATC 75860          AAATTC  __
            GGG                   TAAGTTAAACCA     GCA  GGG
                                ||||||||||||     |||  |||
                                GTTCAATTTGGT     CGT  CCC
                                      CCCCT_  AG
GAM3377  SSR3      3'  TAAGTCAAACCAACATGGCAGG 75861          AATTC
            G                    TAAGTTAAACCAA    GCAGGG
                                ||||||||||||     ||||||
                                ATTCAGTTTGGTT    CGTCCC
                                      GTAC_
GAM3377  LOC120227 3'  TGATTAAACCAAGTTCAGG   75862   A       AATTCG
                                A GTTAAACCAA     CAGG
                                | ||||||||||     ||||
                                A TAATTTGGTT     GTCC
                                 C        CAA___
GAM3377  LOC154881 3'  TAAGTAAACCAAAATATACAGG 75863      T       TC
                                TAAGT AAACCAAAAT  GCAGG
                                ||||| ||||||||||  |||||
                                ATTCA TTTGGTTTTA  TGTCC
                                   _        TA
GAM3378  DUT       3'  TATTGCTACTTCACTGAG    75866        A_  C
                                TGTTGCTAT  CAC GAG
                                |||||||||  ||| |||
                                ATAACGATG  GTG CTC
                                     AA   A
GAM3378  LRP4      3'  TGTTACTAACACACTTGAG   75867        _   C_
                                TGTTGCTA TACAC  GAG
                                |||||||| |||||  |||
                                ACAATGAT GTGTG  CTC
                                     T    AA
GAM3378  CYorf15B  3'  TGTTACCACACAGTTGAG    75868          CC_
                                TGTTGCTATACA   GAG
                                ||||||||||||   |||
                                ACAATGGTGTGT   CTC
                                      CAA
GAM3378  LOC124944 5'  TGTTGCTACAACACCCGAG   75869         _   _
                                TGTTGCTATA CACC GAG
                                |||||||||| |||| |||
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                                ACAACGATGT GTGG CTC
                                      T   G
GAM3378 LOC151571 5' TGTTGCTATATGAACACATCG 75870        ____   __
                                TGTTGCTAT   ACAC  CG
                                |||||||||   ||||  ||
                                ACAACGATA   TGTG  GC
                                     TACT   TA
GAM3379 BDKRB2   3' TGGGCAGGGCAGGAAT     75873    T      TGCGG
                                TG GCAGGGCA    GGAAT
                                || ||||||||    |||||
                                AC CGTCCCGT    CCTTA
                                 C      _____
GAM3379 BIRC7    3' GGGCGGTGGTCGGGGAATCAG 75874     ATG___
                                GGGC    CGGGGAATCAG
                                ||||    ||||||||||
                                CCCG    GCCCCTTAGTC
                                  CCACCA
GAM3379 BIRC7    3' GGGCGGTGGTCGGGGAATCAG 75874     ATG___
                                GGGC    CGGGGAATCAG
                                ||||    ||||||||||
                                CCCG    GCCCCTTAGTC
                                  CCACCA
GAM3379 CACNA1D  5' TGTGCAGGGCACTGTGCTGG  75875         ___  G
                                TGTGCAGGGCA  TGC GG
                                ||||||||||   ||| ||
                                ACACGTCCCGT  ACG CC
                                      GAC  A
GAM3379 DVL1     3' TGTGCAGGAGGTGGGGGTCAG 75876        CA  C   AA
                                TGTGCAGGG  TG GGGG  TCAG
                                |||||||||  || ||||  ||||
                                ACACGTCCT  AC CCCC  AGTC
                                     CC  _   __
GAM3379 FBXL7    3' TGTGCAAGGCGAGGGATCA   75877        ATGC    A
                                TGTGCAGGGC   GGGGA TCA
                                ||||||||||   ||||| |||
                                ACACGTTCCG   TCCCT AGT
                                     C___    _
GAM3379 G6PD     3' TGGCAGGGCATTGAGG     75878    T      GC
                                TG GCAGGGCAT  GGGG
                                || |||||||||  ||||
                                AC CGTCCCGTA  CTCC
                                 _       A_
GAM3379 HDAC7A   3' TATGTGGGGTGGGAATCA   75879     CA  CATGCG
                                TGTG  GGG    GGGAATCA
                                ||||  |||    ||||||||
                                ATAC  CCC    CCCTTAGT
                                  A_  CA____
GAM3379 HDAC7A   3' TATGTGGGGTGGGAATCA   75879     CA  CATGCG
                                TGTG  GGG    GGGAATCA
                                ||||  |||    ||||||||
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                                ATAC  CCC     CCCTTAGT
                                  A_  CA____
GAM3379  PIK3R2   3'  TGGGCAGGGCAGAGGGTCA   75880    T      TGC    AA
                                TG GCAGGGCA   GGGG  TCA
                                || ||||||||   ||||  |||
                                AC CGTCCCGT   TCCC  AGT
                                 C       C__   __
GAM3379  C1orf16  3'  TGTCTAGGGCGCAAGAATCAG  75881    GC    AT    G
                                TGT  AGGGC  GCGGG AATCAG
                                |||  |||||  ||||| ||||||
                                ACA  TCCCG  CGTTC TTAGTC
                                  GA    __    _
GAM3379  C20orf151 3'  TGTGCAGGGCTGCCTGCTGG   75882         A___   G
                                TGTGCAGGGC    TGC GG
                                ||||||||||    ||| ||
                                ACACGTCCCG    ACG CC
                                      ACGG   A
GAM3379  FGD3     3'  TGTGCAGGGCAGTGGGA     75883          TGCG
                                TGTGCAGGGCA    GGGA
                                ||||||||||    ||||
                                ACACGTCCCGT    CCCT
                                      CA__
GAM3379  FLJ11588  5'  TGTGTAGGACAACGAGAATCAG 75884     C     T    G
                                TGTG AGGGCA GCGGG AATCAG
                                |||| |||||| ||||| ||||||
                                ACAC TCCTGT TGCTC TTAGTC
                                  A     _    _
GAM3379  KIAA0445  5'  TGTGCAGGGCGGAGTGGATCAG 75885          ATGC    A__
                                TGTGCAGGGC    GGGG   ATCAG
                                ||||||||||    ||||   |||||
                                ACACGTCCCG    CCTC   TAGTC
                                      _____   ACC
GAM3379  KIAA0446  5'  TGCAGGGCAGAGGGTCA     75886         TGC    AA
                                TGCAGGGCA   GGGG  TCA
                                |||||||||   ||||  |||
                                ACGTCCCGT   TCCC  AGT
                                     C__    __
GAM3379  KIAA0769  3'  TGTGCAGGGTGCGCAATCCTTC 75887         CA    GGAA
            AG                    TGTGCAGGG  TGCGG    TCAG
                                |||||||||  |||||    ||||
                                ACACGTCCC  GCGTT    AGTC
                                     AC     AGGA
GAM3379  MATR3    3'  TGTGCAGGTACATGAATTAG   75888         _    CGG_
                                TGTGCAGG GCATG    GG
                                ||||||||| |||||    ||
                                ACACGTCC TGTAC    TC
                                     A     TTAA
GAM3379  MGC12760  5'  GTGCAGGGCGGAGAGAATCAG  75889         ATGC
                                GTGCAGGGC    GGGGAATCAG
                                |||||||||    ||||||||||
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                                CACGTCCCG   TCTCTTAGTC
                                     CC__
GAM3379  LOC149579 5'  TGTGCAGGGCGGAGTGGATCAG 75885         ATGC   A__
                                TGTGCAGGGC   GGGG  ATCAG
                                ||||||||||   ||||  |||||
                                ACACGTCCCG   CCTC  TAGTC
                                     _____   ACC
GAM3379  LOC153339 3'  TGTGCAGGTGTGTGCTTTAACA 75890        GCA_   GG__ G
           ATCAG                    TGTGCAGG   TGC   G AATCAG
                                ||||||||   |||   | ||||||
                                ACACGTCC   ACG   T TTAGTC
                                     ACAC  AAAT G
GAM3379  LOC153514 3'  TGTCAGGGCATGTGGGG     75891     G       C
                                TGT CAGGGCATG GGGG
                                ||| ||||||||| ||||
                                ACA GTCCCGTAC CCCC
                                  _       A
GAM3379  LOC155438 3'  TGTGGAGGGTATGCGGAAACAG 75892      C   C     GG AT
                                TGTG AGGG ATGCGG  A  CAG
                                |||| |||| ||||||  |  |||
                                ACAC TCCC TACGCC  T  GTC
                                  C   A     TT __
GAM3379  LOC51011  3'  TGTGCAGGGCCTGTGCAG    75893         A__
                                TGTGCAGGGC  TGCGG
                                ||||||||||  |||||
                                ACACGTCCCG  ACGTC
                                     GAC
GAM3379  LOC63928  5'  TGTGCAGGGTGGCGGGTCA   75894        CAT    GAA
                                TGTGCAGGG  GCGGG  TCA
                                |||||||||  |||||  |||
                                ACACGTCCC  CGCCC  AGT
                                     AC_    ___
GAM3379  LOC95803  3'  TGTGCAGGGCCTGTGCAG    75893         A__
                                TGTGCAGGGC  TGCGG
                                ||||||||||  |||||
                                ACACGTCCCG  ACGTC
                                     GAC
GAM3380  ACTN1    3'  CTTTGTGCTTGGTTATT     75897    GTG   TT
                                CT  GTGT  TTGGTTATT
                                ||  ||||  |||||||||
                                GA  CACG  AACCAATAA
                                 AA_   __
GAM3380  DNLC2A   3'  TAGCATTTTGGTTATTT     75898         T
                                TGGTGTTTT GGTTATTT
                                ||||||||| ||||||||
                                ATCGTAAAA CCAATAAA
                                          _
GAM3380  FKBP1A   3'  CCTTGTGGTGTTTTTTGTT   75899    C         G
                                CC TGTGGTGTTTTT GTT
                                || ||||||||||| |||
```

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                                GG ACACCACAAAAA CAA
                                 A          A
GAM3380  GNAI3    3'  TGGATTATTGGTTATTT     75900     T   T
                                TGG GTT TTGGTTATTT
                                ||| ||| ||||||||||
                                ACC TAA AACCAATAAA
                                  _  T
GAM3380  ZFH4     5'  TGGGGTGTTTTTCGGGTT    75901    T       __
                                TG GGTGTTTTT  GGTT
                                || |||||||||  ||||
                                AC CCACAAAAA  CCAA
                                 C        GC
GAM3380  AKR1D1   3'  CCACTGTGGTGTTTAGCTCTAT 75902    _         TTGG
              TT                 CC CTGTGGTGTTT    TTATTT
                                || ||||||||||    ||||||
                                GG GACACCACAAA    GATAAA
                                 T          TCGA
GAM3380  FLJ14768 3'  CCTTTGTGGGTTTTTGGT    75903    CC    T
                                CC  TGTGG GTTTTTGGT
                                ||  ||||| |||||||||
                                GG  ACACC CAAAAACCA
                                 AA    _
GAM3380  FLJ20073 3'  CCTCTGTGATGTTAATATT    75904    _       TTTG
                                CC CTGTGGTGTT    GTT
                                || ||||||||||    |||
                                GG GACACTACAA    TAA
                                 A         TTA_
GAM3380  FLJ20086 3'  CCTCTGTTGTGCTAGGGTTATT 75905    _   G    TTT
              T                  CC CTGT GTGTT   GGTTATTT
                                || |||| |||||   ||||||||
                                GG GACA CACGA   CCAATAAA
                                 A   A    TC_
GAM3380  ICK      3'  CCCTTTGGAAGCCATGGTTATT 75906      G   T_   TT
              T                  CCCT TGG  GTT  TGGTTATTT
                                |||| |||  |||  |||||||||
                                GGGA ACC  CGG  ACCAATAAA
                                  A  TT   T_
GAM3380  IMP-2    3'  CTGTGTGTTTTTCTCGTT    75907      _ G    G
                                CTGTG GT TTTTT GTT
                                ||||| || ||||| |||
                                GACAC CA AAAGA CAA
                                   A A    G
GAM3380  KIAA0161 3'  CCTTTTGGTGTTTTTGGT    75908    G_
                                CCT  TGGTGTTTTTGGT
                                |||  ||||||||||||
                                GGA  ACCACAAAAACCA
                                  AA
GAM3380  KIAA0705 3'  CTGTGATGTTCTTCACGTTATT 75909          G__
              T                  CTGTGGTGTTTTT   GTTATTT
                                ||||||||||||   |||||||
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                                GACACTACAAGAA   CAATAAA
                                      GTG
GAM3380  KIAA1635  5'  CTGTGGTGCTCTTCTTATTT   75910          GG
                                CTGTGGTGTTTTT  TTATTT
                                |||||||||||||  ||||||
                                GACACCACGAGAA  AATAAA
                                      G_
GAM3380  KIAA1981  3'  CCCCTGTGGGTTTTGTT     75911        T    TG
                                CCCCTGTGG GTTTT  GTT
                                |||||||||  |||||  |||
                                GGGGACACC CAAAA  CAA
                                         _    __
GAM3380  PRO1853   5'  CCCTGTGGTGTTTTCTGAAATT 75912            GGTT
           T                     CCCTGTGGTGTTTTT    ATTT
                                |||||||||||||||    ||||
                                GGGACACCACAAAAG    TAAA
                                      ACTT
GAM3380  TRPV6     3'  CCTCTGGGTGTTTGGTT     75913    _  T     TT
                                CC CTG GGTGTT  TGGTT
                                || ||| ||||||  |||||
                                GG GAC CCACAA  ACCAA
                                 A  _     __
GAM3380  LOC116437 3'  CCTACTGTTTAATTTGGTTATT 75914      TG  GTT_
           T                     CCTG  GT    TTTGGTTATTT
                                ||||  ||    ||||||||||
                                GGAT  CA    AAACCAATAAA
                                  GA  AATT
GAM3380  LOC149420 3'  TGTGATGTTTTACATTCTATTT 75915          TGG__
                                TGTGGTGTTTT    TTATTT
                                ||||||||||    ||||||
                                ACACTACAAAA    GATAAA
                                      TGTAA
GAM3380  LOC163882 3'  TGTGATGTTGGGTATTT     75916        TTT   T
                                TGTGGTGT   TGG TATTT
                                ||||||||   ||| |||||
                                ACACTACA   ACC ATAAA
                                     ___   C
GAM3380  LOC221362 3'  TGCTCTGTTTTGGTTATT    75917     GG     T
                                TGT  TGTTTT GGTTATT
                                |||  |||||| |||||||
                                ACG  ACAAAA CCAATAA
                                  AG     _
GAM3381  EHD3      3'  TGAAGCAAGCCAGGGGAG    75920    T       ACCTTT
                                TG AGCAAGCCA     GGAG
                                || |||||||||     ||||
                                AC TCGTTCGGT     CCTC
                                 T       CC_____
GAM3381  FRK       5'  TGCAGCAAGTCCTACCTGGAGA 75921          _  A    TT
           G                     TGTAGCAAG CC ACCT  GGAGAG
                                |||||||||  ||  ||||  ||||||
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                                ACGTCGTTC GG TGGA  CCTCTC
                                     A  A   __
GAM3381  LRP1     5'  GTAGGGGAGCCTTTGGAG    75922      CA_   AACC
                                GTAG   AGCC   TTTGGAG
                                ||||   ||||   |||||||
                                CATC   TCGG   AAACCTC
                                  CCC   ____
GAM3381  PDE4B    3'  TGTAGCAACTCCTGTGG     75923        G CAA   T
                                TGTAGCAA C   CCT TGG
                                |||||||| |   ||| |||
                                ACATCGTT G   GGA ACC
                                     _ A__   C
GAM3381  PYGM     5'  TGAAGTGACCTTTTGGAGA   75924   C   CCA    _
                                G AAG   ACCTTT GGAGA
                                | |||   |||||| |||||
                                A TTC   TGGAAA CCTCT
                                 C   AC_     A
GAM3381  TNFRSF7  5'  GTGGCAAGCCAACCTTTG    75925    A
                                GT GCAAGCCAACCTTTG
                                || ||||||||||||||
                                CA CGTTCGGTTGGAAAC
                                 C
GAM3381  BANP     5'  TGTAGCAAGCAGCCTCCCCAG  75926         CAA    GG
                                TGTAGCAAGC   CCTTT  AG
                                ||||||||||   |||||  ||
                                ACATCGTTCG   GGAGG  TC
                                      TC_    GG
GAM3381  C3orf1   3'  TGTCAGCAGGCTGACCAAAGAG 75927     _   A  CA   TTT
                                TGT AGCA GC  ACC   GGAG
                                ||| |||| ||  |||   ||||
                                ACA TCGT CG  TGG   TCTC
                                  G   C  AC   TT_
GAM3381  FLJ21709 3'  TGTCGGCAAGCTCCTGGAGAG  75928    A_    CAA   TT
                                TGT  GCAAGC   CCT  GGAGAG
                                |||  ||||||   |||  ||||||
                                ACA  CGTTCG   GGA  CCTCTC
                                  GC     A__   __
GAM3381  HTATIP   3'  TGTGGCCAGCTGACCTTGGAG  75929    A  A   CA    T
                                TGT GC AGC  ACCTT GGAG
                                ||| || |||  ||||| ||||
                                ACA CG TCG  TGGAA CCTC
                                  C  G   AC    _
GAM3381  KIAA0173 3'  GCAGAGGCTTTTGGAGAG    75930     CAA  CAACC
                                GTAG   GC    TTTGGAGAG
                                ||||   ||    |||||||||
                                CGTC   CG    AAACCTCTC
                                  TC_  A____
GAM3381  PTPRN2   3'  GTAGGGCCTTTGGAGAG     75931     CAA   AACC
                                GTAG   GCC   TTTGGAGAG
                                ||||   |||   |||||||||
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                                CATC  CGG   AAACCTCTC
                                  C__  ____
GAM3381 PTPRN2   3' GTAGGGCCTTTGGAGAG    75931     CAA  AACC
                                GTAG  GCC   TTTGGAGAG
                                ||||  |||   |||||||||
                                CATC  CGG   AAACCTCTC
                                  C__  ____
GAM3381 RELB     3' TGTAACAAGCTAGTGCACGGGA 75932         CAACCTT  A
           G                     TGTAGCAAGC     TGG GAG
                                ||||||||||     ||| |||
                                ACATTGTTCG     GCC CTC
                                     ATCACGT  _
GAM3381 ZIM2     3' TGTGGCAACCAATCAATCTGG  75933    A   G   CC__
                                TGT GCAA CCAA   TTTGG
                                ||| |||| ||||   |||||
                                ACA CGTT GGTT   AGACC
                                  C   _   AGTT
GAM3381 LOC127435 3' TGTGGCATAGGCTTTGGAG   75934    A  _ CCAAC
                                TGT GCA AG    CTTTGGAG
                                ||| ||| ||    ||||||||
                                ACA CGT TC    GAAACCTC
                                  C  A  C____
GAM3381 LOC146332 3' TGTAGGAAGCTGGCCAGAG   75935     C   CAA  TTT
                                TGTAG AAGC  CC  GGAG
                                ||||| ||||  ||  ||||
                                ACATC TTCG  GG  TCTC
                                   C   ACC  ___
GAM3381 LOC148418 3' TGTAGCAAGCCCACTTTTTCCA 75936         A  C__  G
           AG                    TGTAGCAAGCC AC  TTT GAG
                                ||||||||||| ||  ||| |||
                                ACATCGTTCGG TG  AAG TTC
                                      G  AAA  G
GAM3381 LOC158263 3' GCTCATGCCTTTGGAGAG    75937   _ A_
                                GC CA  CCTTTGGAGAG
                                || ||  ||||||||||
                                CG GT  GGAAACCTCTC
                                 A  AC
GAM3381 LOC170425 3' TGTAGCAAGTTTATCTGCAA   75938        CCAACC   G
                                TGTAGCAAG     TTTG AG
                                |||||||||     |||| ||
                                ACATCGTTC     AGAC TT
                                     AAAT__   G
GAM3381 LOC196955 5' TGAGCAGGCCAAAGAG     75939   T   A   CCTTT
                                TG AGCA GCCAA    GGAG
                                || |||| |||||    ||||
                                AC TCGT CGGTT    TCTC
                                 _   C    _____
GAM3382 ADK      5' TCACACACCCCGCGCGGCCGG  75942      G   GT
                                TCACA CGCTC  CGCGCGGCCGG
                                ||||| |||||  ||||||||||
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                                AGTGT GTGGG  GCGCGCCGGCC
                                  _    __
GAM3382  ADK      5'  TCACACACCCCGCGCGGCCGG  75942       G    GT
                                TCACA CGCTC  CGCGCGGCCGG
                                ||||| |||||  ||||||||||
                                AGTGT GTGGG  GCGCGCCGGCC
                                  _    __
GAM3382  CDH4     3'  GCGCGGTGCTGGGCAGCGGCCG 75943      TC_  C__  _
             G                   GCGC   GT   GC GCGGCCGG
                                ||||   ||   || ||||||||
                                CGCG   CG   CG CGCCGGCC
                                  CCA  ACC  T
GAM3382  DUSP7    5'  TCGAAGAGCTCGTGCGGCCGG  75944    AC  C     CGC
                                TC  AG GCTCGT   GCGGCCGG
                                ||  || ||||||   ||||||||
                                AG  TC CGAGCA   CGCCGGCC
                                 CT  T     ___
GAM3382  FXYD6    3'  TCACAGCGCACGGTTTGG    75945         TCGTCGC    CC_
                                TCACAGCGC      GCGG   GG
                                |||||||||      ||||   ||
                                AGTGTCGCG      TGCC   CC
                                     ________   AAA
GAM3382  GAS1     5'  GCAGATCCGTTGTGCGGCCGG  75946     C__    CGC
                                GCG   TCGT   GCGGCCGG
                                |||   ||||   ||||||||
                                CGT   GGCA   CGCCGGCC
                                  CTA    ACA
GAM3382  KIF5B    5'  TCGCAGCCGGGGCCGCGGCCGG 75947    A    GCT  TC  _
                                TC CAGC   CG  GC GCGGCCGG
                                || ||||   ||  || ||||||||
                                AG GTCG   GC  CG CGCCGGCC
                                 C    ___  CC  G
GAM3382  LASS1    3'  GCGTCGCGCCGCGGCCGG    75948     C   T   _
                                GCG TCG CGC GCGGCCGG
                                ||| ||| ||| ||||||||
                                CGC AGC GCG CGCCGGCC
                                  _   _   G
GAM3382  RAD17    5'  GCGGTCAGGGCGCGCGGCCGG  75949     C   T__
                                GCG TCG   CGCGCGGCCGG
                                ||| |||   ||||||||||
                                CGC AGT   GCGCGCCGGCC
                                  C   CCC
GAM3382  VGF      3'  TCACAGCGACTTGGAGAGGCTG 75950         _ CGTCGCGC   C
             G                   TCACAGCG CT       GGC GG
                                ||||||||  ||       ||| ||
                                AGTGTCGC GA       CCG CC
                                     T  ACCTCT__   A
GAM3382  C20orf39 5'  GCGCTCGCCTGGCCGG      75951         GCGC
                                GCGCTCGTC    GGCCGG
                                |||||||||    ||||||
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                                CGCGAGCGG   CCGGCC
                                     A___
GAM3382 C5orf7   5' CAGCGCCCCCCGTGGCCGG   75952       G  CGC
                                CAGCGCTC TCG  GGCCGG
                                |||||||| |||  ||||||
                                GTCGCGGG GGC  CCGGCC
                                     G  A__
GAM3382 CENTB5   3' TCACACGCAGGGCCGCGGCCGG 75953     G  TC_ CG
                                TCACA CGC  GT  CGCGGCCGG
                                ||||| |||  ||  |||||||||
                                AGTGT GCG  CG  GCGCCGGCC
                                   _  TCC  __
GAM3382 CENTG2   5' CATGGCCGGGACGCGCGGCCGG 75954   GC  CGT_
                                CA  GCT   CGCGCGGCCGG
                                ||  |||   ||||||||||
                                GT  CGG   GCGCGCCGGCC
                                 AC  CCCT
GAM3382 FLJ10782 3' TCACACGCATCTGTGCGGCTGG 75955     G  TC  GC_   C
                                TCACA CGC  GTC  GCGGC GG
                                ||||| |||  |||  ||||| ||
                                AGTGT GCG  TAG  CGCCG CC
                                   _  __  ACA   A
GAM3382 KIAA0783 5' CCACAGCGCTCCCTGGCCG   75956        G  GCGC
                                TCACAGCGCTC TC   GGCCG
                                |||||||||| ||   |||||
                                GGTGTCGCGAG GG   CCGGC
                                      _ A___
GAM3382 SLC25A21 5' TCGCAGCGCTCTCGCAGAG   75957   A     G   C
                                TC CAGCGCTC TCGCG GG
                                || |||||||| ||||| ||
                                AG GTCGCGAG AGCGT TC
                                 C      _   C
GAM3382 LOC257478 5' TCGCAGTGCCCGTCGCTGAAGT 75958   A  C      GC_  CC
           GG                    TC CAG GCTCGTCGC  GG  GG
                                || ||| |||||||||  ||  ||
                                AG GTC CGGGCAGCG  TC  CC
                                 C  A       ACT  A_
GAM3383 LRRC2    3' TATATAGCTCCAGAGAATAGTG 75961      AC  CCAC
           AG                    TATATAG  CCA   ATAGTGAG
                                |||||||  |||  ||||||||
                                ATATATC  GGT   TATCACTC
                                   GA  CTCT
GAM3383 NEU3     5' TACATAGATTTGTCACATAG  75962       CCCAC
                                TATATAGA   CACATAG
                                ||||||||   |||||||
                                ATGTATCT   GTGTATC
                                     AAACA
GAM3383 UBE2E3   3' TATAAAGATTTGCAGCACAGTG 75963    T  CCCAC  _
           AG                    TATA AGA   CA CATAGTGAG
                                |||| |||   || |||||||||
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                                ATAT TCT    GT GTGTCACTC
                                  T  AAAC_  C
GAM3383 KIAA0323 3' TATAGGGCACGTTATAGTGAG 75964      ACC  CAC
                                TATAG  CAC  ATAGTGAG
                                |||||  |||  ||||||||
                                ATATC  GTG  TATCACTC
                                   CC_  CAA
GAM3383 KIAA0451 5' TATAGACACATAGTG      75965       CCACC
                                TATAGAC    ACATAGTG
                                |||||||    ||||||||
                                ATATCTG    TGTATCAC
                                     _____
GAM3383 KIAA1795 3' TATATAGACTACCACATAG   75966        CC
                                TATATAGAC  ACCACATAG
                                |||||||||  |||||||||
                                ATATATCTG  TGGTGTATC
                                     A_
GAM3383 ODZ2     3' TAGACCCAGAACAAGTG     75967       CC  T
                                TAGACCCA  ACA AGTG
                                ||||||||  ||| ||||
                                ATCTGGGT  TGT TCAC
                                     CT  _
GAM3383 LOC200081 3' GACCCACCCAGGTGAG     75968        A  TA
                                GACCCACC CA  GTGAG
                                |||||||| ||  |||||
                                CTGGGTGG GT  CACTC
                                     _  C_
GAM3384 RAI17    3' GTGCTTTTCTGTGGTGGGTGGT 75971        _  TCTCG  C
                                GTGCTTTTC GTG    GGG GGT
                                ||||||||| |||    ||| |||
                                CACGAAAAG CAC    CCC CCA
                                     A  CA___  A
GAM3384 LOC158107 5' GTGCTTTTGTGGTGGTGG   75972        C  TCTCGG  C
                                GTGCTTTT GTG     GG GG
                                |||||||| |||     || ||
                                CACGAAAA CAC     CC CC
                                     _  CA____  A
GAM3385 CBFA2T3  3' AGACGTTGTCAGGAGGTCTCC 75975          AAAA__
                                AGACGTTGTCAG     TCC
                                ||||||||||||     |||
                                TCTGCAACAGTC     AGG
                                     CTCCAG
GAM3385 CELSR3   3' GCCACGGAGGATCCTGTAA   75976     __ AA
                                GTCA  GA  ATCCTGTAA
                                ||||  ||  |||||||||
                                CGGT  CT  TAGGACATT
                                  GC  CC
GAM3385 CLC      3' AAACTTTCAGGAAATCCTGT  75977     GTTG  A
                                AGAC   TCAG AAATCCTGT
                                ||||   |||| |||||||||
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                                TTTG    AGTC TTTAGGACA
                                  AA__    C
GAM3385  KIF5C    3'  GTTGTCAGTCCCTTGTA     75978         AAAA   _
                                GTTGTCAG    TCCT GTA
                                ||||||||    |||| |||
                                CAACAGTC    GGGA CAT
                                    A___    A
GAM3385  SPG4     3'  AGACTCTAAAAAGTCCTGTAA  75979      GTTG  _    A
                                AGAC    TC AGAAA TCCTGTAA
                                ||||    || ||||| ||||||||
                                TCTG    AG TTTTT AGGACATT
                                  ____  A    C
GAM3385  C14orf3  3'  GACGATGCAATCCTGT      75980      T   CAGAA
                                GACG TGT     AATCCTGT
                                |||| |||     ||||||||
                                CTGC ACG     TTAGGACA
                                  T  _____
GAM3385  FLJ10724 3'  AGATGTTGTAAATTCTCCTGTA 75981     C    C   AAA
            A                    AGA GTTGT AGA   TCCTGTAA
                                ||| ||||| |||   ||||||||
                                TCT CAACA TTT   AGGACATT
                                  A    _   AAG
GAM3385  FLJ12688 3'  AGAGCGTGATAAAATCCTGT   75982     _   T TCAG
                                AGA CGT G    AAAATCCTGT
                                ||| ||| |    ||||||||||
                                TCT GCA C    TTTTAGGACA
                                  C   _ TA__
GAM3385  FLJ14494 3'  AGAAGTTAGCAGAGTCCTGTAA 75983     C    T    AAA
                                AGA GTTG CAGA   TCCTGTAA
                                ||| |||| ||||   ||||||||
                                TCT CAAT GTCT   AGGACATT
                                  T    C    C__
GAM3385  FLJ22160 5'  GTCTCAGAATCCTGTA      75984     G    AA
                                GTT TCAGA  ATCCTGTA
                                ||| |||||  ||||||||
                                CAG AGTCT  TAGGACAT
                                  _    __
GAM3385  ZWINT    3'  GATGTAGTCAGAAATCAAGC   75985    C  T      A  CT
                                GA GT GTCAGAAA TC  GT
                                || || |||||||| ||  ||
                                CT CA CAGTCTTT AG  CG
                                 A  T       _  TT
GAM3385  ZWINT    3'  GATGTAGTCAGAAATCAAGC   75985    C  T      A  CT
                                GA GT GTCAGAAA TC  GT
                                || || |||||||| ||  ||
                                CT CA CAGTCTTT AG  CG
                                 A  T       _  TT
GAM3385  LOC162427 3'  AGACGTTGCAGAAAGCC     75986         T     AT
                                AGACGTTG CAGAAA  C
                                |||||||| ||||||  |
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                                TCTGCAAC GTCTTT  G
                                    _     CG
GAM3385  LOC221766 3'  AGGCGTTGCCAGCTGT      75987    A       AAAATC
                                AG CGTTGTCAG     CTGT
                                || |||||||||     ||||
                                TC GCAACGGTC     GACA
                                 C       _______
GAM3385  LOC91069  3'  GAAGTTGTCAGGATCAGGTA   75988    C       AAA   CT
                                GA GTTGTCAG   ATC  GTA
                                || ||||||||   |||  |||
                                CT CAACAGTC   TAG  CAT
                                 T       C__   TC
GAM3385  LOC91097  5'  GACTTGTCAGAGCTGGTGCTGT 75989     G       AAATC__
                                GAC TTGTCAGA      CTGT
                                ||| ||||||||      ||||
                                CTG AACAGTCT      GACA
                                  _       CGACCAC
GAM3386  WEE1      5'  TCTGCGCGGCGGCGGCCT    75992        T       G
                                TCTGCGC GCGGCGGC CT
                                ||||||| |||||||| ||
                                AGACGCG CGCCGCCG GA
                                    C       _
GAM3386  KIAA1172  5'  CGCGCTGCGGCGGCGGCT    75993              _
                                TGCGCTGCGGCGGCG CT
                                |||||||||||||| ||
                                GCGCGACGCCGCCGC GA
                                       C
GAM3386  KIAA1229  3'  GCTGTGCAGAAGCTCTTTA   75994     CG    C_
                                GCTG  GCGG  GCTCTTTA
                                ||||  ||||  ||||||||
                                CGAC  CGTC  CGAGAAAT
                                  A_    TT
GAM3386  LOC132617 3'  TCTGCGGTGTGGACCATCTTT  75995       C  C  CG  GC
                                TCTGCG TG GG  GC  TCTTT
                                |||||| || ||  ||  |||||
                                AGACGC AC CC  TG  AGAAA
                                    C  A  __  GT
GAM3386  LOC150112 5'  TCTGTGCCTGCGGCGCT     75996     C   GCG
                                TCTG GCT   GCGGCGCT
                                |||| |||   ||||||||
                                AGAC CGG   CGCCGCGA
                                  A   A__
GAM3387  CNN2      3'  GAGGCCAGAGTGAGTTGGGG   75999     T    A   CTA_  A
                                GAG GCCA AGT    TG GGG
                                ||| |||| |||    || |||
                                CTC CGGT TCA    AC CCC
                                  _    C   CTCA  _
GAM3387  DAG1      3'  GAGTGCCAGAGAAAAGGGA    76000         A  TCTAT
                                GAGTGCCA AG     GAGGGA
                                |||||||| ||     ||||||
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                                CTCACGGT TC    TTCCCT
                                    C  TT___
GAM3387  HSF2BP   3'  GAGTATCAAATGAGGG     76001     C   AGTCT
                                GAGTG CAA    ATGAGGG
                                ||||| |||    |||||||
                                CTCAT GTT    TACTCCC
                                   A  _____
GAM3387  LPIN1    3'  ATGCCAACTGCATGAGGGA   76002       AGTC
                                GTGCCAA   TATGAGGGA
                                |||||||   |||||||||
                                TACGGTT   GTACTCCCT
                                    GAC_
GAM3387  PFKL     3'  GCGCCAAAGCCAGGG      76003         TATG
                                GTGCCAAAGTC   AGGG
                                ||||||||||   ||||
                                CGCGGTTTCGG   TCCC
                                              ____
GAM3387  PODXL    3'  GAGTGCCAGGGGCAATGGG   76004       AA_ CT  A
                                GAGTGCCA  GT  ATG GG
                                ||||||||  ||  ||| ||
                                CTCACGGT  CG  TAC CC
                                    CCC  T_  _
GAM3387  PPP2R4   3'  GAGTGCCAAAGCCTGGG    76005          ATGA
                                GAGTGCCAAAGTCT   GGG
                                ||||||||||||||   |||
                                CTCACGGTTTCGGA   CCC
                                             ____
GAM3387  SLC10A2  3'  GATTGCTGCAGAATGAGGGA  76006   G   CAA  TCT
                                GA TGC   AG   ATGAGGGA
                                || |||   ||   ||||||||
                                CT ACG   TC   TACTCCCT
                                 A  ACG  T__
GAM3387  SLC29A2  3'  TGCCAAAGAGCCTGGAGGG   76007      __    AT
                                TGCCAA  AGTCT  GAGGG
                                ||||||  |||||  |||||
                                ACGGTT  TCGGA  CTCCC
                                   TC    C_
GAM3387  TEM8     3'  GTCCAAAGTCCAGGG      76008    G      ATG
                                GT CCAAAGTCT   AGGG
                                || |||||||||   ||||
                                CA GGTTTCAGG   TCCC
                                _      ___
GAM3387  AFAP     3'  GTGGCAAAGTCTGTGGG    76009    C      A  A
                                GTG CAAAGTCT TG GG
                                ||| |||||||| || ||
                                CAC GTTTCAGA AC CC
                                  C      C  _
GAM3387  BLu      5'  GGTGCCAAAGTCTGGG     76010   A        ATGA
                                G GTGCCAAAGTCT   GGG
                                | ||||||||||||   |||
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                                C CACGGTTTCAGA   CCC
                                _       ____
GAM3387  C20orf165 5'  AAGCCCCGGTTTGTGAGGGA  76011     G  AAA  CTA
                                GAGT CC   GT   TGAGGGA
                                |||| ||   ||   |||||||
                                TTCG GG   CA   ACTCCCT
                                  G  C__  AAC
GAM3387  CPSF2    3'  AAGTGCCAAGCAAAGGG    76012        A  CTAT
                                GAGTGCCAA GT   GAGGG
                                |||||||||| ||   |||||
                                TTCACGGTT CG   TTCCC
                                      _ T___
GAM3387  DAPK2    3'  GACTGCCAAAGCGCAGGGA   76013    G       CTATG
                                GA TGCCAAAGT    AGGGA
                                || |||||||||    |||||
                                CT ACGGTTTCG    TCCCT
                                 G       CG___
GAM3387  DDX34    3'  GAGGCCAGGAAGATGGGGG   76014    T   __   TCT   A
                                GAG GCCA  AAG   ATG GGG
                                ||| ||||  |||   ||| |||
                                CTC CGGT  TTC   TAC CCC
                                  _   CC   ___   C
GAM3387  DKFZp586H0623 3'  GAGTGCCAGACCCTGGGGG   76015        AA T  A  A
                                GAGTGCCA  G CT TG GGG
                                ||||||||  | || || |||
                                CTCACGGT  C GG AC CCC
                                     __ T  G  C
GAM3387  FLJ10103  3'  GAGTGGCAAAGTCTTGGA    76016     C      ATGA
                                GAGTG CAAAGTCT   GGG
                                ||||| ||||||||   |||
                                CTCAC GTTTCAGA   CCT
                                   C       A___
GAM3387  FLJ10375  3'  GAGTGACACTGCTATGAGGG   76017      C  AA T
                                GAGTG CA  G CTATGAGGG
                                ||||| ||  | |||||||||
                                CTCAC GT  C GATACTCCC
                                   T  GA _
GAM3387  FLJ10874  3'  ATGCCAAAGTCATAGGG     76018         TATG
                                GTGCCAAAGTC   AGGG
                                ||||||||||   ||||
                                TACGGTTTCAG   TCCC
                                      TA__
GAM3387  FLJ13102  3'  GAGTGCCAGGTGTGGATGGGG  76019       AA_  CT   A
                                GAGTGCCA   GT  ATG GGG
                                ||||||||   ||  ||| |||
                                CTCACGGT   CA  TAC CCC
                                    CCA  CC   _
GAM3387  FLJ21438  3'  GAGTGCCAGGGACTCCGGGG   76020       AAGT  A  A
                                GAGTGCCA    CT TG GGG
                                ||||||||    || || |||
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                                CTCACGGT   GA GC CCC
                                    CCCT  G  _
GAM3387  FLJ32780  3'  GAGTGCCAGTGTGGGG     76021       AA  CTA  A
                                GAGTGCCA  GT   TG GGG
                                ||||||||  ||   || |||
                                CTCACGGT  CA   AC CCC
                                    __  C__  _
GAM3387  FOXD4    5'  GGTGCCAAACTCTGAGGG    76022   A      G   AT
                                G GTGCCAAA TCT  GAGGG
                                | ||||||||  |||  |||||
                                C CACGGTTT AGA  CTCCC
                                 _      G  __
GAM3387  FREQ     3'  TGCCGAAGGACGAGGGA     76023     A   TCT
                                TGCC AAG   ATGAGGGA
                                ||||  |||   ||||||||
                                ACGG TTC   TGCTCCCT
                                  C   C__
GAM3387  GPR      5'  GAGTGGCCGGAGCCACGAGGG  76024      _  AA  T
                                GAGTG CC  AG CTATGAGGG
                                |||||  ||  ||  |||||||||
                                CTCAC GG  TC GGTGCTCCC
                                   C  CC  _
GAM3387  HEYL     3'  AAGTGCCAGGCGGTGGGGG   76025       AA  CTA  A
                                GAGTGCCA  GT   TG GGG
                                ||||||||  ||   || |||
                                TTCACGGT  CG   AC CCC
                                    C_  CC_  C
GAM3387  KIAA1157  3'  GAGTGCCAGGGCAGAACAGGGA 76026       AA  CTATG
                                GAGTGCCA  GT    AGGGA
                                ||||||||  ||    |||||
                                CTCACGGT  CG    TCCCT
                                    CC  TCTTG
GAM3387  KIAA1169  5'  GAGGCCAGCCCACATGAGGG   76027    T   AA   __
                                GAG GCCA  GTCT  ATGAGGG
                                |||  ||||  ||||  |||||||
                                CTC CGGT  CGGG  TACTCCC
                                  _   __   TG
GAM3387  KIAA1184  3'  GAGGCCAGATCATGAGGG    76028    T   AA   T
                                GAG GCCA  GTC ATGAGGG
                                |||  ||||  |||  |||||||
                                CTC CGGT  TAG TACTCCC
                                  _   C_  _
GAM3387  KIAA1805  3'  GGTGTCAAAGTCTCAGGA    76029   A  C      ATG
                                G GTG CAAAGTCT   AGGG
                                | |||  ||||||||  ||||
                                C CAC GTTTCAGA   TCCT
                                 _  A      G__
GAM3387  MGC5521   3'  GAATGTTAAACATGAGGGA   76030      CC   GTC
                                GAGTG  AAA   TATGAGGGA
                                |||||  |||   |||||||||
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                                CTTAC  TTT   GTACTCCCT
                                  AA  ___
GAM3387  POLM     3'  GAGGCCAGAGTGTGCCTGGGGA 76031     T   A  CTA__  A
                                GAG GCCA AGT    TG GGGA
                                ||| |||| |||    || ||||
                                CTC CGGT TCA    AC CCCT
                                  _   C  CACGG  _
GAM3387  SLI      5'  GTGTTAAAGTCCAGGGA    76032    CC     ATG
                                GTG  AAAGTCT  AGGGA
                                |||  |||||||  |||||
                                CAC  TTTCAGG  TCCCT
                                  AA     ___
GAM3387  STK17A   3'  GAGTGTGGTGTGATGAGGGA  76033     CCAAA  CT
                                GAGTG    GT  ATGAGGGA
                                |||||    ||  ||||||||
                                CTCAC    CA  TACTCCCT
                                   ACCA_  C_
GAM3387  TPRA40   3'  GAGGCCAAAGCACCATGGGGA  76034    T      _    A
                                GAG GCCAAAGT CTATG GGGA
                                ||| |||||||| ||||| ||||
                                CTC CGGTTTCG GGTAC CCCT
                                  _      T    _
GAM3387  UPLC1    3'  GAGTCTCGATCTGATGAGGGA  76035     GCCAAA   _
                                GAGT     GTCT ATGAGGGA
                                ||||     |||| ||||||||
                                CTCA     TAGA TACTCCCT
                                  GAGC__   C
GAM3387  WBSCR16  3'  GAGTGCCAGTGGTTCCCGGGA  76036       AAG__  ATGA
                                GAGTGCCA    TCT   GGGA
                                ||||||||    |||   ||||
                                CTCACGGT    AGG   CCCT
                                    CACCA  G___
GAM3387  LOC126661 3'  GAGGCCAAAGTTGGTGG    76037    T      CTA  AG
                                GAG GCCAAAGT   TG  GG
                                ||| ||||||||   ||  ||
                                CTC CGGTTTCA   AC  CC
                                  _      ___  CA
GAM3387  LOC143879 3'  AAGTGTCAGAGTCTATGA    76038     C  A
                                GAGTG CA AGTCTATGA
                                ||||| || |||||||||
                                TTCAC GT TCAGATACT
                                  A  C
GAM3387  LOC146332 3'  AAGTGCCAAAGGTAAGGG    76039         TCTA
                                GAGTGCCAAAG   TGAGGG
                                ||||||||||   ||||||
                                TTCACGGTTTC   ATTCCC
                                      C___
GAM3387  LOC196500 3'  GAGTGCACAAGGGTGGGGA   76040      CA  TCTA  A
                                GAGTGC  AAG   TG GGGA
                                ||||||  |||   || ||||
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                                CTCACG  TTC    AC CCCT
                                   TG   CC__  _
GAM3387  LOC199796 5'  GAGGCCAAAGTCGAGGA     76041     T       TAT
                                GAG GCCAAAGTC   GAGGG
                                ||| |||||||||   |||||
                                CTC CGGTTTCAG   CTCCT
                                  _       ___
GAM3387  LOC205095 3'  GAGTCCTGGGCTGTGAGGG    76042      G  AAA T  A
                                GAGT CC   G CT TGAGGG
                                |||| ||   | || ||||||
                                CTCA GG   C GA ACTCCC
                                  _  ACC _  C
GAM3387  LOC221496 3'  GAGTATTGCTCAAATGAGGGA  76043      ___  _   AGTCT
                                GAGT   GC CAA     ATGAGGGA
                                ||||   || |||     ||||||||
                                CTCA   CG GTT     TACTCCCT
                                  TAA  A  _____
GAM3387  LOC253891 3'  GAATGCCAAAGCCAGGG     76044           TATG
                                GAGTGCCAAAGTC    AGGG
                                ||||||||||||    ||||
                                CTTACGGTTTCGG    TCCC
                                                 ____
GAM3387  LOC254065 5'  AGTGCTGAAGTCCACAGGA    76045      CA       G
                                AGTGC  AAGTCTAT AGGG
                                |||||  |||||||| ||||
                                TCACG  TTCAGGTG TCCT
                                   AC       _
GAM3387  LOC90630  5'  GTTCCAAAGTCATGGG      76046    G      T   A
                                GT CCAAAGTC ATG GG
                                || |||||||| ||| ||
                                CA GGTTTCAG TAC CC
                                 A      _  _
GAM3387  LOC91208  5'  GTCCCAAAGTCATGGG      76047    G      T   A
                                GT CCAAAGTC ATG GG
                                || |||||||| ||| ||
                                CA GGTTTCAG TAC CC
                                 G      _  _
GAM3387  LOC91750  3'  GAGTGCCAGGAGCAGGG     76048        A_   CTATG
                                GAGTGCCA  AGT    AGGG
                                ||||||||  |||    ||||
                                CTCACGGT  TCG    TCCC
                                     CC  _____
GAM3388  BSN       3'  GTGTGCCCAAACTCTGTGTAT  76051        CCG__   C
                                GTGTGCCC    CTG GTAT
                                ||||||||    ||| ||||
                                CACACGGG    GAC CATA
                                     TTTGA   A
GAM3388  MUCDHL    3'  TACTGTGCCCCCACTGGGT    76052    G          C
                                TA TGTGCCCCCGCTG GT
                                || ||||||||||||| ||
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                                AT ACACGGGGGTGAC CA
                                 G          C
GAM3388 PTPRK    3' TAATGTGCTTTCTCCATAT   76053       CCCCG  G
                                TAGTGTGC    CT CGTAT
                                ||||||||    || |||||
                                ATTACACG    GA GTATA
                                    AAA__  G
GAM3388 EAT2     3' AGTGTGCCCCTCCTCTGTAT  76054        CG  GC
                                AGTGTGCCCC  CT  GTAT
                                ||||||||||  ||  ||||
                                TCACACGGGG  GA  CATA
                                     AG  GA
GAM3388 EPHA7    5' TAGTGTGCTCCTTGCAT     76055       CC  GC
                                TAGTGTGC  CC  TGCGT
                                ||||||||  ||  |||||
                                ATCACACG  GG  ACGTA
                                    A_  A_
GAM3388 KIAA0680 3' TAGTGTGCCTGTGACTCCAT  76056       CCC_  G
                                TAGTGTGCC   GCT CGT
                                |||||||||   ||| |||
                                ATCACACGG   TGA GTA
                                     ACAC  G
GAM3388 KIAA1243 3' TAGTGCGCCCCTGAGCCA    76057        C__
                                TAGTGTGCCCC  GCTG
                                ||||||||||  ||||
                                ATCACGCGGGG  CGGT
                                      ACT
GAM3388 PRO2405  5' TAATGTGCTCCTGCTCAT    76058       C  C  G
                                TAGTGTGC CC GCT CGT
                                |||||||| || ||| |||
                                ATTACACG GG CGA GTA
                                    A  A  _
GAM3388 ROBO2    3' TAGTGTGCACTGTACAT     76059       CCCC   CG
                                TAGTGTGC   GCTG  TAT
                                ||||||||   ||||  |||
                                ATCACACG   TGAC  GTA
                                    ____   AT
GAM3388 LOC115219 3' TAGTGTGCCCTGCGT      76060        CCGC
                                TAGTGTGCCC   TGCGT
                                |||||||||   |||||
                                ATCACACGGG   ACGCA
                                     ____
GAM3388 LOC135932 3' CAGTGTGCCCTCGTGCACAT  76061        C  C
                                TAGTGTGCCC CG TGCGTAT
                                |||||||||| || |||||||
                                GTCACACGGG GC ACGTGTA
                                      A  _
GAM3388 LOC149072 5' TACTGTGCCCCAGCTATGT   76062    G      C   C
                                TA TGTGCCCC GCTG GT
                                || |||||||| |||| ||
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                                AT ACACGGGG CGAT CA
                                 G       T   A
GAM3388  LOC153387 5'  TAGTGTGCCTCCTTGACAT   76063        C  GCT
                                TAGTGTGCC CC   GCGT
                                ||||||||| ||   ||||
                                ATCACACGG GG   TGTA
                                     A  AAC
GAM3388  LOC153914 5'  TAATGTGCTCCCACTTGTAT   76064       C     GC
                                TAGTGTGC CCCGCT  GTAT
                                |||||||| ||||||  ||||
                                ATTACACG GGGTGA  CATA
                                     A     A_
GAM3388  LOC164584 3'  TAGCGTGCCTTGTCGGTAT   76065        CCCGC  C
                                TAGTGTGCC    TG GTAT
                                |||||||||    || ||||
                                ATCGCACGG    GC CATA
                                     AACA_  _
GAM3388  LOC93587  3'  ATGTGCCCTCACAGATAT    76066       C   TGC
                                GTGTGCCC CGC   GTAT
                                |||||||| |||   ||||
                                TACACGGG GTG   TATA
                                     A   TC_
GAM3389  AKAP13    3'  CAAGGGCCAGACAGCTGCT   76069       ACT   A
                                TAAGGGC   GGA CAGCTGCT
                                |||||||   ||| ||||||||
                                GTTCCCG   TCT GTCGACGA
                                     G__   _
GAM3389  CDY1      5'  AGACACGGGATTGGAACAGTTG 76070      _____      C
           CT                     GGGCAC    TGGAACAG TGCT
                                |||||||    |||||||| ||||
                                TCTGTG    ACCTTGTC ACGA
                                   CCCTA       A
GAM3389  CDY1      5'  AGACACGGGATTGGAACAGTTG 76070      _____      C
           CT                     GGGCAC    TGGAACAG TGCT
                                |||||||    |||||||| ||||
                                TCTGTG    ACCTTGTC ACGA
                                   CCCTA       A
GAM3389  CDY2      5'  AGACACGGGATTGGAACAGTTG 76070      _____      C
           CT                     GGGCAC    TGGAACAG TGCT
                                |||||||    |||||||| ||||
                                TCTGTG    ACCTTGTC ACGA
                                   CCCTA       A
GAM3389  DNMT3B    5'  GAGCCGGGAGCAGCTGCT    76071     ACT   A
                                GGGC   GGA CAGCTGCT
                                ||||   ||| ||||||||
                                CTCG   CCT GTCGACGA
                                  GC_   C
GAM3389  DYRK1A    5'  CAAGGGCACTGGGGCCGCTGC  76072          AACA
                                TAAGGGCACTGG    GCTGC
                                ||||||||||||    |||||
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                                GTTCCCGTGACC   CGACG
                                     CCGG
GAM3389  EDN3    5'  AAGGGCACTGGGGCCG     76073         AACA
                                AAGGGCACTGG   GCTG
                                ||||||||||   ||||
                                TTCCCGTGACC   CGGC
                                     C___
GAM3389  GRLF1   3'  AGGGCACTGGAGCCATTGC   76074         A_  GC
                                AGGGCACTGGA  CA  TGC
                                ||||||||||  ||  |||
                                TCCCGTGACCT  GT  ACG
                                     CG  A_
GAM3389  MLLT7   3'  AAGGGCACTGGGGGAAGGGCTG 76075         AACA___
           C                     AAGGGCACTGG     GCTGC
                                ||||||||||      |||||
                                TTCCCGTGACC     CGACG
                                     CCCTTCC
GAM3389  NR3C2   3'  AGGGCTCAGAGGCAGCTGCT   76076     ACT   A_
                                AGGGC   GGA  CAGCTGCT
                                |||||   |||  ||||||||
                                TCCCG   TCT  GTCGACGA
                                  AG_   CC
GAM3389  PTGFRN  3'  AAGGGCACTGGCTGTTA    76077        GAACA   C
                                AAGGGCACTG    GCTG TA
                                |||||||||    |||| ||
                                TTCCCGTGAC    CGAC AT
                                     _____   A
GAM3389  CLSTN1  5'  GGGCCTGGGGCCAGCTGC    76078     A   AA_
                                GGGC CTGG   CAGCTGC
                                |||| ||||   |||||||
                                CCCG GACC   GTCGACG
                                  _   CCG
GAM3389  FEM-2   3'  GGGCAGGGGGGTGGCTGCTAC  76079     CT  AACA
                                GGGCA  GG   GCTGCTAC
                                |||||  ||   ||||||||
                                CCCGT  CC   CGACGATG
                                   CC  CCAC
GAM3389  FLJ20972 3'  GGGCACTGCAAACTAC     76080       G  CA
                                GGGCACTG AA  GCTGC
                                ||||||| ||  |||||
                                CCCGTGAC TT  TGATG
                                     G  __
GAM3389  GOLGA1  3'  AGGCTGGGGGACAGCTGCT   76081     ACT  A
                                GGGC   GG ACAGCTGCT
                                ||||   || |||||||||
                                TCCG   CC TGTCGACGA
                                  ACC  C
GAM3389  HEMK    3'  GGGCACTGGGAGCTGC     76082       AAC
                                GGGCACTGG   AGCTGC
                                |||||||||   ||||||
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                                CCCGTGACC  TCGACG
                                     C__
GAM3389 KIAA0255 3' CAAGGGTTAGCAGCTGCTA  76083      CAC  AA
                                TAAGGG  TGG  CAGCTGCTA
                                ||||||  |||  |||||||||
                                GTTCCC  ATC  GTCGACGAT
                                   A__  __
GAM3389 KIAA0601 3' TGAGGTACTGCACTGCTA   76084   A  C   GAACA
                                A GGG ACTG    GCTGCTA
                                | ||| ||||    |||||||
                                A TCC TGAC    TGACGAT
                                 C  A   G____
GAM3389 KIAA1546 3' CAAGGGCACTGGAGTACA   76085          __
                                TAAGGGCACTGGA  ACA
                                ||||||||||||  |||
                                GTTCCCGTGACCT  TGT
                                        CA
GAM3389 KIAA1940 5' GGGCGTGCTGCCACAGCTGCT 76086    A__  GA
                                GGGC  CTG  ACAGCTGCT
                                ||||  |||  |||||||||
                                CCCG  GAC  TGTCGACGA
                                  CAC  GG
GAM3389 MOST2    5' AGGGGATTGGACATGCTGTTAC 76087    CAC   A _   C
                                AGGG  TGGA CA GCTG TAC
                                ||||  |||| || |||| |||
                                TCCC  ACCT GT CGAC ATG
                                  CTA   _ A   A
GAM3389 NR4A3    5' GGGGGGGAGTCACAGCTGCT  76088    CACT  ___
                                GGG   GGA  ACAGCTGCT
                                |||   |||  |||||||||
                                CCC   CCT  TGTCGACGA
                                 CC__  CAG
GAM3389 PP5395   3' GGGGGTGTGGAACAGGCTGC  76089    CAC_     _
                                GGG   TGGAACAG CTGC
                                |||   |||||||| ||||
                                CCC   ACCTTGTC GACG
                                 CCAC      C
GAM3389 RPH3A    3' GGGCACTGTGAGCTTGCTGC  76090       _ ACA_
                                GGGCACTG GA   GCTGC
                                |||||||| ||   |||||
                                CCCGTGAC CT   CGACG
                                    A  CGAA
GAM3389 S164     5' GGGCCACTGGAAATCTGC    76091    _    CAG
                                GGGC ACTGGAA  CTGC
                                |||| |||||||  ||||
                                CCCG TGACCTT  GACG
                                  G     TA_
GAM3389 SDC3     5' GGGCACACAGTTGCTA     76092      TGGA  C
                                GGGCAC   ACAG TGCTA
                                ||||||   |||| |||||
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                                CCCGTG   TGTC ACGAT
                                   ____   A
GAM3389  SEMA3E   3'  TAAGGACAACAGCTGCT    76093       CTGGA
                                TAAGGGCA    ACAGCTGCT
                                ||||||||    |||||||||
                                ATTCCTGT    TGTCGACGA
                                   _____
GAM3389  LOC122727 5'  GGGCTCCGGGCAGCTGCT    76094     A   AA
                                GGGC CTGG  CAGCTGCT
                                |||| ||||  ||||||||
                                CCCG GGCC  GTCGACGA
                                  A   C_
GAM3389  LOC143153 3'  GAGCAGGACAGCTGCTAC    76095     CT   A
                                GGGCA  GGA CAGCTGCTAC
                                |||||  ||| ||||||||||
                                CTCGT  CCT GTCGACGATG
                                   __  _
GAM3389  LOC144453 3'  GGGCACTGGTGCTTCGGCTGCT 76096        AACA___
                                GGGCACTGG      GCTGCT
                                |||||||||      ||||||
                                CCCGTGACC      CGACGA
                                     ACGAAGC
GAM3389  LOC146517 3'  TAAAGGCACATGGGCTGCT   76097        _  AACA
                                TAAGGGCAC TGG   GCTGCT
                                ||||||||| |||   ||||||
                                ATTTCCGTG ACC   CGACGA
                                     T  _____
GAM3389  LOC147174 5'  AGCAGCTGGAATAGCTGCTAC  76098     _    C
                                GGCA CTGGAA AGCTGCTAC
                                |||| |||||| |||||||||
                                TCGT GACCTT TCGACGATG
                                  C     A
GAM3389  LOC148918 5'  GGGCACTGTGGCCACAGCTG   76099       GA___
                                GGGCACTG    ACAGCTG
                                ||||||||    |||||||
                                CCCGTGAC    TGTCGAC
                                     ACCGG
GAM3389  LOC152282 3'  GGGCTGCTGGAGCTGCTAC   76100     A_    ACA
                                GGGC  CTGGA   GCTGCTAC
                                ||||  |||||   ||||||||
                                CCCG  GACCT   CGACGATG
                                  AC    ___
GAM3389  LOC152282 3'  GGGCTGCTGCCGCTGCTAC   76101     A_  GAACA
                                GGGC  CTG    GCTGCTAC
                                ||||  |||    ||||||||
                                CCCG  GAC    CGACGATG
                                  AC  GG___
GAM3389  LOC152282 3'  GGGCTGCTGGAGCTGCTAC   76100     A_    ACA
                                GGGC  CTGGA   GCTGCTAC
                                ||||  |||||   ||||||||
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                                CCCG  GACCT   CGACGATG
                                  AC    ___
GAM3389  LOC157503 3'  AGGGCACTGGGGGTCACTGC   76102         AACA_
                                AGGGCACTGG    GCTGC
                                ||||||||||    |||||
                                TCCCGTGACC    TGACG
                                     CCCAG
GAM3389  LOC157638 3'  AAGGGAGCAGCGGCTGCTAC   76103      CAC   AACA
                                AAGGG   TGG   GCTGCTAC
                                |||||   |||   ||||||||
                                TTCCC   GTC   CGACGATG
                                  TC_   GC__
GAM3389  LOC159121 5'  AGGGCACTGGAGCTGC      76104          ACA
                                AGGGCACTGGA   GCTGC
                                ||||||||||   |||||
                                TCCCGTGACCT   CGACG

                                     ___
GAM3389  LOC163682 5'  GGACAGGGGCAGCTGCT     76105      CT  AA
                                GGGCA  GG  CAGCTGCT
                                |||||  ||  ||||||||
                                CCTGT  CC  GTCGACGA
                                  __  CC
GAM3389  LOC196463 3'  AAGGGTGCTGGAACAGGC    76106      CA       CT
                                AAGGG  CTGGAACAG  GC
                                |||||  |||||||||  ||
                                TTCCC  GACCTTGTC  CG
                                  AC        __
GAM3389  LOC203611 5'  AGACACGGGATTGGAACAGTTG 76070        ______      C
           CT                    GGGCAC    TGGAACAG TGCT
                                ||||||    |||||||| ||||
                                TCTGTG    ACCTTGTC ACGA
                                   CCCTA       A
GAM3389  LOC219295 5'  GGGCGAGCAGGACAGCTGCTAC 76107      ACT__   A
                                GGGC    GGA CAGCTGCTAC
                                ||||    ||| ||||||||||
                                CCCG    CCT GTCGACGATG
                                  CTCGT  _
GAM3389  LOC221178 3'  AGGGGTGGCTTCAGCTGCT   76108     CAC   AA_
                                AGGG   TGG   CAGCTGCT
                                ||||   |||   ||||||||
                                TCCC   ACC   GTCGACGA
                                  C__   GAA
GAM3389  LOC257475 5'  AGGGGTGAGGGCACAGCTGCT  76109     CACT  A_
                                AGGG   GG  ACAGCTGCT
                                ||||   ||  |||||||||
                                TCCC   CC  TGTCGACGA
                                  CACT  CG
GAM3389  LOC56965  3'  AGGGCAGCCTCAGCTGCT    76110       _  GGAA
                                AGGGCA CT    CAGCTGCT
                                ||||||  ||   ||||||||
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                                TCCCGT GG   GTCGACGA
                                   C  A___
GAM3389 LOC56965 3' AGGGCAGCCTCAGCTGCT   76110      _ GGAA
                                AGGGCA CT   CAGCTGCT
                                |||||| ||   ||||||||
                                TCCCGT GG   GTCGACGA
                                   C  A___
GAM3389 LOC64182 3' AAGGGAACAGGACAGCTGCT  76111     C T  A
                                AAGGG AC GGA CAGCTGCT
                                ||||| || ||| ||||||||
                                TTCCC TG CCT GTCGACGA
                                  T  T  _
GAM3389 LOC90639 3' AGGACACTGGGGTTGCTA    76112        AACAGC
                                AGGGCACTGG     TGCTA
                                ||||||||||     |||||
                                TCCTGTGACC     ACGAT
                                      CCA___
GAM3390 C6      3' CTACATATTTTACCTGTT    76115          G
                                CTACATATTTTACT TGTT
                                |||||||||||||| |||||
                                GATGTATAAAATGG ACAA
                                                _
GAM3390 CD2AP   3' TACATATTTTATATGTGCT   76116         C_
                                TACATATTTTA  TGTGTT
                                ||||||||||  ||||||
                                ATGTATAAAAT  ACACGA
                                      AT
GAM3390 CDK7    3' TACATATTTTACATGTGT    76117          _
                                TACATATTTTAC TGTGT
                                |||||||||||| |||||
                                ATGTATAAAATG ACACA
                                       T
GAM3390 ERBB2IP 3' TACATATTTTATTGCATT    76118         C
                                TACATATTTTA TGTGTT
                                |||||||||| ||||||
                                ATGTATAAAAT ACGTAA
                                      A
GAM3390 F8      3' TACATTTTTGTTGTGTTATTT  76119      A   AC
                                TACAT TTTT  TGTGTTATTT
                                ||||| ||||  ||||||||||
                                ATGTA AAAA  ACACAATAAA
                                   _   CA
GAM3390 HD      3' TACATTCACAGTGTTATTT   76120      ATT   T
                                TACAT   TTAC GTGTTATTT
                                |||||   |||| |||||||||
                                ATGTA   AGTG CACAATAAA
                                   ____   T
GAM3390 KCNJ16  3' CCTATATATTTTACTTGTATT  76121     C       _
                                TCTA ATATTTTACT GTGTT
                                |||| |||||||||| |||||
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                                GGAT TATAAAATGA CATAA
                                  A        A
GAM3390  MAGEB4    3'  TCTACCTATTTTACTGTGGAGT 76122       A        ___
             TATTT                  TCTAC TATTTTACTGT   GTTATTT
                                |||||| ||||||||||   |||||||
                                AGATG ATAAAATGACA   CAATAAA
                                   G          CCT
GAM3390  PDX1      3'  TACATATTTTAGCTATAGTT   76123          _   _
                                TACATATTTTA CTGT GTT
                                |||||||||| |||| |||
                                ATGTATAAAAT GATA CAA
                                       C   T
GAM3390  KIAA0215  3'  TCTGTGCATTTTACTATATT   76124     ACA
                                TCT   TATTTTACTGTGTT
                                |||   ||||||||||||||
                                AGA   GTAAAATGATATAA
                                  CAC
GAM3390  KIAA1229  3'  TCTATTTATTTTACTAGCT    76125     CA        T
                                TCTA  TATTTTACTG GTT
                                ||||  |||||||||| |||
                                AGAT  ATAAAATGAT CGA
                                  AA        _
GAM3390  SEMA3E    3'  TACAAATTTTACAAATGTT    76126     T      T_
                                TACA ATTTTAC  GTGTT
                                |||| |||||||  |||||
                                ATGT TAAAATG  TACAA
                                  T      TT
GAM3390  LOC130507 3'  TCTACTTATTTTACAGCTATTT 76127       A       TGT
                                TCTAC TATTTTAC   GTTATTT
                                ||||| ||||||||   |||||||
                                AGATG ATAAAATG   CGATAAA
                                   A       T__
GAM3390  LOC132720 3'  TCTACATGTTTTACTTGTT    76128        A      G
                                TCTACAT TTTTACT TGTT
                                ||||||| ||||||| ||||
                                AGATGTA AAAATGA ACAA
                                    C      _
GAM3390  LOC150886 3'  TACATATTCTCCTGGTTATTT  76129          A   T
                                TACATATTTT CTG GTTATTT
                                |||||||||| ||| |||||||
                                ATGTATAAGA GAC CAATAAA
                                      G  _
GAM3390  LOC163882 3'  TACATATTTTACATACAATTT  76130           T   TT
                                TACATATTTTAC GTG  ATTT
                                |||||||||||| |||  ||||
                                ATGTATAAAATG TAT  TAAA
                                       _  GT
GAM3390  LOC196411 3'  TCTACAGTTTTACTGTA     76131        TA
                                TCTACA  TTTTACTGTG
                                ||||||  ||||||||||
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                                AGATGT  AAAATGACAT
                                  C_
GAM3391  MBP      3'  CCCAGTGTTGAACCCCAGCGTG 76134      ACACCG    G
                                TCCA     GAGCT CCAGCGTG
                                ||||     ||||| ||||||||
                                GGGT     CTTGG GGTCGCAC
                                  CACAA_    _
GAM3391  CENTB5   3'  CCCAGCACTGGGGCTGCCAG   76135      A   C  A
                                TCCA CAC GG GCTGCCAG
                                |||| ||| || ||||||||
                                GGGT GTG CC CGACGGTC
                                  C   A  C
GAM3391  POMT1    3'  TCCAACACTGAGCTGTCC    76136        CG     _
                                TCCAACAC  GAGCTG CC
                                ||||||||  ||||||  ||
                                AGGTTGTG  CTCGAC GG
                                    A_     A
GAM3391  LOC154222 3'  TCCAGCGTAGGGGCTGACCAAG 76137      ACACC  A   _    C
           TG                     TCCA     GG GCTG CCAG GTG
                                ||||     || |||| |||| |||
                                AGGT     CC CGAC GGTT CAC
                                  CGCAT  C    T   _
GAM3391  LOC255397 5'  TCCACCCTTGGGGCTGCCAGCG 76138      A A  __  A
           TG                     TCCA C CC  GG GCTGCCAGCGTG
                                |||| | ||  || ||||||||||||
                                AGGT G GG  CC CGACGGTCGCAC
                                  _ _  AA  C
GAM3392  PPP2R2B  3'  TTAGCTGGCAGCTTTCAATTC  76141      ATA   C
                                TTAG   GTA GCTTTCAATTC
                                ||||   ||| ||||||||||||
                                AATC   CGT CGAAAGTTAAG
                                  GAC   _
GAM3392  PTP4A1   3'  TATTAGATGTGCTCAATT    76142        A  AC  TT
                                TATTAGAT GT  GC  TCAATT
                                |||||||| ||  ||  ||||||
                                ATAATCTA CA  CG  AGTTAA
                                    _  __  __
GAM3392  LOC133418 3'  TATTAGAATACTTTTTTCAATT 76143        TA    GC_
           C                      TATTAGA  GTAC   TTTCAATTC
                                |||||||  ||||   |||||||||
                                ATAATCT  TATG   AAAGTTAAG
                                   __    AAA
GAM3393  BIRC2    3'  CTAGAACATGAATGTTACTAAT 76146      TTTT_   C
           TG                     CTAGA     AATG TACTAATTG
                                |||||     |||| |||||||||
                                GATCT     TTAC ATGATTAAC
                                  TGTAC    A
GAM3393  KIAA0419  3'  TAGATTTTAGTGGGCCACAATT 76147        AT__    T
           G                      TAGATTTTA    GCTAC AATTG
                                |||||||||    ||||| |||||
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                                ATCTAAAAT   CGGTG TTAAC
                                     CACC   _
GAM3393 KIAA1228 3' ACTAGATTTAATGTTGTTACC 76148        T   C___
                                ACTAGATTT AATG   TACT
                                ||||||||| ||||   ||||
                                TGATCTAAA TTAC   ATGG
                                     _   AACA
GAM3393 METAP1   3' TAGATTTTAATAGCCCACT   76149         _  _
                                TAGATTTTAAT GCT ACT
                                |||||||||||| ||| |||
                                ATCTAAAATTA CGG TGA
                                      T  G
GAM3394 CARD14   3' CGTCACAGCATATGTGGGCT  76152        C   A__
                                CGTCACAGC ATAT  GGTT
                                ||||||||| ||||  ||||
                                GCAGTGTCG TATA  CCGA
                                     _   CAC
GAM3394 KIAA1737 3' TCATAGCCAATTACGT     76153    C    TATAG
                                TCA AGCCA    GTTACGT
                                ||| |||||    |||||||
                                AGT TCGGT    TAATGCA
                                  A   _____
GAM3394 MGC4368  3' CGTCACAGCCAGGTAGGCC   76154         TA
                                CGTCACAGCCA  TAGGTT
                                ||||||||||  ||||||
                                GCAGTGTCGGT  ATCCGG
                                      CC
GAM3394 ZMPSTE24 5' GTCACAGCAATATCCGTT    76155       C   AG
                                GTCACAGC ATAT  GTT
                                |||||||| ||||  |||
                                CAGTGTCG TATA  CAA
                                     T   GG
GAM3394 ZNF271   5' CGTCACAGTTATGAGGT     76156       CCA  _
                                CGTCACAG   TAT AGGT
                                ||||||||   ||| ||||
                                GCAGTGTC   ATA TCCA
                                     A__   C
GAM3394 LOC56891 5' GTCACAACCATAGATGTT    76157         TAG
                                GTCACAGCCATA   GTT
                                ||||||||||||   |||
                                CAGTGTTGGTAT   CAA
                                      CTA
GAM3394 LOC89932 3' CGTCACAGCCAGATTTGCATGT 76158         T  AG  TAC
           T                    CGTCACAGCCA AT  GT   GTT
                                ||||||||||| ||  ||   |||
                                GCAGTGTCGGT TA  CG   CAA
                                      C  AA  TA_
GAM3395 CHGA     3' TTCACCAAAAGGTCAGAAG   76161        TATCG
                                TTCACCAAA    CAGAAG
                                |||||||||    ||||||
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                                AAGTGGTTT    GTCTTC
                                     TCCA_
GAM3395 CRTL1    5' CTCACCAAGAGCAGAAG    76162       ATATC
                                TTCACCAA    GCAGAAG
                                ||||||||    |||||||
                                GAGTGGTT    CGTCTTC
                                     CT___
GAM3395 EIF4E    3' TCCTTCACCAATGTTACATGA 76163         ATATC  _
                                TCCTTCACCAA    GCA GA
                                ||||||||||    ||| ||
                                AGGAAGTGGTT    TGT CT
                                      ACAA_  A
GAM3395 FMR2     3' TCCTTCACCAAAAATATCAG  76164         TATCG
                                TCCTTCACCAAA    CAG
                                ||||||||||    |||
                                AGGAAGTGGTTT    GTC
                                      TTATA
GAM3395 MAPK1    3' TCTCTCACCAAATGTCGAG   76165   C       A  C
                                TC TTCACCAAAT TCG AG
                                || ||||||||| ||| ||
                                AG GAGTGGTTTA AGC TC
                                 A        C  _
GAM3395 MUCDHL   3' CCCTTCACCAGCAGA      76166        AATATC
                                TCCTTCACCA    GCAGA
                                |||||||||    |||||
                                GGGAAGTGGT    CGTCT
                                      _______
GAM3395 MUCDHL   3' CCCTTCACCAGCAGA      76166        AATATC
                                TCCTTCACCA    GCAGA
                                |||||||||    |||||
                                GGGAAGTGGT    CGTCT
                                      _______
GAM3395 BMF      3' TCCTCCACCCTCATTGCAG   76167        AAA  C
                                TCCTTCACC  TAT GCAG
                                |||||||||  ||| ||||
                                AGGAGGTGG  GTA CGTC
                                     GA_  A
GAM3395 C6orf33  3' TCCTTCACTGGATTAGTGCAGA 76168       CAAATATC_
           AG                    TCCTTCAC       GCAGAAG
                                 ||||||||       |||||||
                                 AGGAAGTG       CGTCTTC
                                      ACCTAATCA
GAM3395 CCR7     3' TCCTCACCAAGCCAAGAAG   76169    T    ATA  C
                                TCCT CACCAA  TCG AGAAG
                                |||| ||||||  ||| |||||
                                AGGA GTGGTT  GGT TCTTC
                                  _     C__  _
GAM3395 CECR7    5' TCCTCCACCAACAAACGGAAG 76170         ATATC  A
                                TCCTTCACCAA    GC GAAG
                                ||||||||||    || ||||
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                                AGGAGGTGGTT    TG CTTC
                                      GTT__  C
GAM3395  DKFZP434B044 3'  TCCTCCACCAACAGA      76171         AATATC
                                TCCTTCACCA     GCAGA
                                ||||||||||     |||||
                                AGGAGGTGGT     TGTCT
                                       _______
GAM3395  DKK2     5'  CTCCACCAGGACAGGAAG    76172        AATATC   _
                                CTTCACCA     GCAG AAG
                                ||||||||     |||| |||
                                GAGGTGGT     TGTC TTC
                                     CC____    C
GAM3395  KIAA0753  3'  TCATCACCAAACTGAGCCAGA  76173    CT       ATC  _
                                TC  TCACCAAAT   GC AGA
                                ||  |||||||||   || |||
                                AG  AGTGGTTTG   CG TCT
                                 T_       ACT  G
GAM3395  KIAA1043  3'  TCCTGTACCAGCCCCACAGAAG 76174     TC    AATA
                                TCCT  ACCA    TCGCAGAAG
                                ||||  ||||    |||||||||
                                AGGA  TGGT    GGTGTCTTC
                                  CA    CGG_
GAM3395  LHFPL2    3'  CTTCACCAAAATCACAG     76175         T
                                CTTCACCAAA ATCGCAG
                                |||||||||| |||||||
                                GAAGTGGTTT TAGTGTC
                                       _
GAM3395  MGC17998  3'  CCTTCACCAGCACCTGCAG   76176         AA   _
                                CCTTCACCA  TATC GCAG
                                |||||||||  |||| ||||
                                GGAAGTGGT  GTGG CGTC
                                     C_    A
GAM3395  MGC4342   3'  CCCTTCACCAGAACAGAA    76177         AATATC
                                TCCTTCACCA     GCAGAA
                                ||||||||||     ||||||
                                GGGAAGTGGT     TGTCTT
                                      CT____
GAM3395  PRKRIR    3'  CTTCACCAAAAATAACAG    76178         T  C
                                CTTCACCAAA AT GCAG
                                |||||||||| || ||||
                                GAAGTGGTTT TA TGTC
                                      T  T
GAM3395  PRO2176   5'  TCCTTCACTAATATTCAA    76179        CA    CG
                                TCCTTCAC  AATAT  CAG
                                ||||||||  |||||  |||
                                AGGAAGTG  TTATA  GTT
                                     A_    A_
GAM3395  RASSF2    3'  CTTCACCAATACGTACAG    76180         A   C_
                                CTTCACCAA TAT  GCAG
                                ||||||||| |||  ||||
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                                GAAGTGGTT ATG  TGTC
                                      _  CA
GAM3395  SPRY1    3'  TCCTTCACAAATACGAAG    76181        C    T  C
                                TCCTTCAC AAATA CG AG
                                |||||||| ||||| || ||
                                AGGAAGTG TTTAT GC TC
                                      _    _ T
GAM3395  STK29    5'  CTTCACCAGGTAGTCGAAG    76182        AA _  C
                                CTTCACCA  TA TCG AG
                                ||||||||  || ||| ||
                                GAAGTGGT  AT AGC TC
                                     CC  C   T
GAM3395  TCL6     3'  TCCTTTGCAAACACCAGAG    76183      CAC       C
                                TCCTT   CAAATATCG AG
                                |||||   ||||||||| ||
                                AGGAA   GTTTGTGGT TC
                                   AC_       C
GAM3395  TCL6     3'  TCCTTTGCAAACACCAGAG    76183      CAC       C
                                TCCTT   CAAATATCG AG
                                |||||   ||||||||| ||
                                AGGAA   GTTTGTGGT TC
                                   AC_       C
GAM3395  LOC115110 5'  TCCTTCACCAGATCGTGACCAG 76184          AAT   ____
                                TCCTTCACCA   ATCG    CAG
                                ||||||||||   ||||    |||
                                AGGAAGTGGT   TAGC    GTC
                                      C__    ACTG
GAM3395  LOC120939 5'  TCCTTCACCAGAGTACTCCAG  76185          AATA__  G
                                TCCTTCACCA     TC CAG
                                ||||||||||     || |||
                                AGGAAGTGGT     AG GTC
                                      CTCATG  _
GAM3395  LOC143098 5'  TTCACCAAACATATCCCAGA   76186         __    G
                                TTCACCAA  ATATC CAGA
                                ||||||||  ||||| ||||
                                AAGTGGTT  TATAG GTCT
                                     TG    G
GAM3395  LOC159982 5'  CTTCACCAAATGCAGA      76187          ATC
                                CTTCACCAAAT   GCAGA
                                ||||||||||   |||||
                                GAAGTGGTTTA   CGTCT
                                      ___
GAM3395  LOC197379 3'  TCCTTCACTGAAAGTCATCG   76188        CA ___
                                TCCTTCAC  AA   TATCG
                                ||||||||  ||   |||||
                                AGGAAGTG  TT   GTAGC
                                     AC  TCA
GAM3395  LOC219699 5'  TCCTCCACCAAGTATCCGC    76189          A   _
                                TCCTTCACCAA TATC GC
                                |||||||||| |||| ||
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                                AGGAGGTGGTT ATAG CG
                                      C   G
GAM3395  LOC256112 5'  TCCTTCACCAGGCTGTACCGGA 76190          AA___    C
             G                  TCCTTCACCA    TATCG AG
                                ||||||||||    ||||| ||
                                AGGAAGTGGT    ATGGC TC
                                     CCGAC    C
GAM3395  LOC91263  3'  TCTCTCACCAAATGTGATTGAG 76191    C       ATCGC__
             AAG                  TC TTCACCAAAT      AGAAG
                                || ||||||||||      |||||
                                AG GAGTGGTTTA      TCTTC
                                 A        CACTAAC
GAM3396  ARHI     3'  TTTGTTCTTTTCAAAACATTTT 76194          ATGTT
                                TTTGTTCTTTT    TATTTT
                                ||||||||||    ||||||
                                AAACAAGAAAA    GTAAAA
                                      GTTTT
GAM3396  FMN2     3'  TCTTTATTCTTTTATTATTCAT 76195           _
             TTT                  TCTTTGTTCTTTTAT GTTTATTTT
                                ||||||||||||||| |||||||||
                                AGAAATAAGAAAATA TAAGTAAAA
                                       A
GAM3396  MME      3'  TCTTGGTTCACAACTGTTTATT 76196     T   TTTTA
             TT                   TCTT GTTC    TGTTTATTTT
                                |||| ||||    ||||||||||
                                AGAA CAAG    ACAAATAAAA
                                  C   TGTTG
GAM3396  MME      3'  TCTTGGTTCACAACTGTTTATT 76196     T   TTTTA
             TT                   TCTT GTTC    TGTTTATTTT
                                |||| ||||    ||||||||||
                                AGAA CAAG    ACAAATAAAA
                                  C   TGTTG
GAM3396  MME      3'  TCTTGGTTCACAACTGTTTATT 76196     T   TTTTA
             TT                   TCTT GTTC    TGTTTATTTT
                                |||| ||||    ||||||||||
                                AGAA CAAG    ACAAATAAAA
                                  C   TGTTG
GAM3396  MME      3'  TCTTGGTTCACAACTGTTTATT 76196     T   TTTTA
             TT                   TCTT GTTC    TGTTTATTTT
                                |||| ||||    ||||||||||
                                AGAA CAAG    ACAAATAAAA
                                  C   TGTTG
GAM3396  TYROBP   3'  TTTGTGCTTCATGTTTATTTT  76197      T   T
                                TTTGT CTTT ATGTTTATTTT
                                ||||| |||| ||||||||||
                                AAACA GAAG TACAAATAAAA
                                  C   _
GAM3396  COLEC12  3'  TCTTTGTTCTTCTGTGTTT   76198          A
                                TCTTTGTTCTTTT TGTTT
                                |||||||||||| |||||
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                                AGAAACAAGAAGA ACAAA
                                        C
GAM3396 DGKD     3' TCTTTGTTCTTGTTGTTT    76199          TTA
                                TCTTTGTTCTT   TGTTT
                                ||||||||||   |||||
                                AGAAACAAGAA   ACAAA
                                      CA_
GAM3396 FLJ10486 3' TCCTTGTGGCTTATGTTTATTT 76200        TCT
              T                  TCTTTGT   TTTATGTTTATTTT
                                 |||||||   ||||||||||||||
                                 AGGAACA   GAATACAAATAAAA
                                    CC_
GAM3396 GADD45A  3' TTTGTTCCTTTTGACTTATTTT 76201          A _
                                TTTGTTCTTTT TG TTTATTTT
                                |||||||||||  || ||||||||
                                AAACAAGGAAA AC GAATAAAA
                                      _ T
GAM3396 KIAA1389 3' TTTGTTCTCATGTTTATTTT   76202         TT
                                TTTGTTCTT  ATGTTTATTTT
                                |||||||||  ||||||||||
                                AAACAAGAG  TACAAATAAAA
                                      __
GAM3396 RRN3     3' TTTGTCTTTTAAATCCATTTT  76203       T     T
                                TTTGT CTTTTA GTTTATTTT
                                |||||  ||||||  ||||||||
                                AAACA GAAAAT TAGGTAAAA
                                   _     T
GAM3396 TLOC1    3' TCTTTGTTCCTTTTAAAGTTAT 76204           ATGT_
              TTT                  TCTTTGTTCTTTT    TTATTTT
                                   ||||||||||||     |||||||
                                   AGAAACAAGGAAA    AATAAAA
                                         ATTTC
GAM3396 USP10    3' CTTATTTTTTATGTTTATTTT  76205       C
                                TTTGTT TTTTATGTTTATTTT
                                ||||||  ||||||||||||||
                                GAATAA AAAATACAAATAAAA
                                   _
GAM3396 ZFP91    3' TTTCTTCTTTACATATTTATTT 76206     G     _
              T                   TTT TTCTTT TATGTTTATTTT
                                  |||  ||||||  ||||||||||||
                                  AAA AAGAAA GTATAAATAAAA
                                    G     T
GAM3396 LOC143872 3' CTTGTACCTTTGTGTTTATTTT 76207      T    A
                                TTTGT CTTTT TGTTTATTTT
                                |||||  |||||  ||||||||||
                                GAACA GGAAA ACAAATAAAA
                                   T    C
GAM3396 LOC145368 3' CTTATTTTTTATGTTTATTTT  76205       C
                                TTTGTT TTTTATGTTTATTTT
                                ||||||  ||||||||||||||
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                                GAATAA AAAATACAAATAAAA
                                   _
GAM3396  LOC146956 3'  TCTTTGTTCCTTTGTGTTT   76208          A
                                TCTTTGTTCTTTT TGTTT
                                ||||||||||||| |||||
                                AGAAACAAGGAAA ACAAA
                                      C
GAM3396  LOC150157 5'  TCTTTGTTCAGTTTGTTT    76209        TT  A
                                TCTTTGTTC  TT TGTTT
                                |||||||||  || |||||
                                AGAAACAAG  AA ACAAA
                                     TC  _
GAM3396  LOC150423 3'  CTTATTTTTTATGTTTATTTT  76205      C
                                TTTGTT TTTTATGTTTATTTT
                                |||||| ||||||||||||||
                                GAATAA AAAATACAAATAAAA
                                   _
GAM3396  LOC152822 5'  TCTTTGGTTCTTTTGGTTCATT 76210      _     AT
           TT                    TCTTTG TTCTTTT  GTTTATTTT
                                ||||||| |||||||  |||||||||
                                AGAAAC AAGAAAA  CAAGTAAAA
                                   C     C_
GAM3396  LOC196890 5'  TCTTTGTTCAGTTTGTTT    76209        TT  A
                                TCTTTGTTC  TT TGTTT
                                |||||||||  || |||||
                                AGAAACAAG  AA ACAAA
                                     TC  _
GAM3396  LOC202309 5'  TCTTTTGTTCTTTTGGTTATGT 76211      _     ____
           TT                    TCTTT GTTCTTT   TATGTTT
                                ||||| |||||||   |||||||
                                AGAAA CAAGAAA   ATACAAA
                                   A      ACCA
GAM3397  ABCG5    3'  TTTCAGACGTTCAGA      76214      T      GC
                                TTTC AGACGTT  CAGA
                                |||| |||||||  ||||
                                AAAG TCTGCAA  GTCT
                                   _     __
GAM3397  ANXA2    3'  TTTCTAGACCTGTTAGCTGGA  76215        __  _  CA
                                TTTCTAGAC  GTT GC  GA
                                |||||||||  ||| ||  ||
                                AAAGATCTG  CAA CG  CT
                                     GA   T  AC
GAM3397  CUL3     3'  TCTCTAGAAATAACTCAGA   76216        C  T  _
                                TTTCTAGA GT GC CAGA
                                |||||||| || || ||||
                                AGAGATCT TA TG GTCT
                                     T  T  A
GAM3397  DAAM2    3'  TCTCTGGAACCTACCAGA    76217      A  CG
                                TTTCT GA  TTGCCAGA
                                ||||| ||  ||||||||
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                                AGAGA CT  GATGGTCT
                                  C  TG
GAM3397  ESR1     3'  TTTCCAAAGTTGCTGGA     76218        C    CA
                                TTTCTAGA GTTGC  GA
                                |||||||| |||||  ||
                                AAAGGTTT CAACG  CT
                                     _    AC
GAM3397  FOXO1A   3'  TTTCCAGACAGACCAGA     76219         TT
                                TTTCTAGACG  GCCAGA
                                ||||||||||  ||||||
                                AAAGGTCTGT  TGGTCT
                                      C_
GAM3397  FUT1     3'  CTTCTAGAGTAGACCAGA    76220        C  T_
                                TTTCTAGA GT  GCCAGA
                                |||||||| ||  ||||||
                                GAAGATCT CA  TGGTCT
                                     _  TC
GAM3397  GPR85    3'  TTTCTAAAATACCAGA      76221        CGT
                                TTTCTAGA   TGCCAGA
                                ||||||||   |||||||
                                AAAGATTT   ATGGTCT
                                     T__
GAM3397  HHEX     3'  TTTCCAGAATACCAGA      76222        CGT
                                TTTCTAGA   TGCCAGA
                                ||||||||   |||||||
                                AAAGGTCT   ATGGTCT
                                     T__
GAM3397  ITGA7    5'  TTTCAGACGTCTCCCAGA    76223     T     G_
                                TTTC AGACGTT  CCAGA
                                |||| |||||||  |||||
                                AAAG TCTGCAG  GGTCT
                                  _      AG
GAM3397  ITK      3'  TTTCTAGACTGAATGTTCCAGA 76224         _____  G
                                TTTCTAGAC    GTT CCAGA
                                |||||||||    ||| |||||
                                AAAGATCTG    CAA GGTCT
                                     ACTTA  _
GAM3397  PUM2     3'  TTTCTGTACATTGCCAGA    76225      AG
                                TTTCT  ACGTTGCCAGA
                                |||||  ||||||||||
                                AAAGA  TGTAACGGTCT
                                   CA
GAM3397  RBL2     3'  TTTCTAAAAGCTTTGCCAGA  76226        C  __
                                TTTCTAGA GT  TGCCAGA
                                |||||||| ||  |||||||
                                AAAGATTT CG  ACGGTCT
                                     T  AA
GAM3397  SEL1L    3'  TTCTAATGACTTGCCAGA    76227      __  G
                                TTCTA  GAC TTGCCAGA
                                |||||  ||| ||||||||
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                                AAGAT  CTG AACGGTCT
                                   TA  _
GAM3397  SHANK2   3'  TTCCTAGACACCCAGA     76228         TTG
                                TTTCTAGACG   CCAGA
                                ||||||||||   |||||
                                AAGGATCTGT   GGTCT
                                     G__
GAM3397  SMARCD2  3'  TTTCCAAACCTGCCAGA     76229         G
                                TTTCTAGAC TTGCCAGA
                                ||||||||| ||||||||
                                AAAGGTTTG GACGGTCT
                                      _
GAM3397  TNFRSF6  3'  TCTCTAGAATTATCAGA     76230         C   C
                                TTTCTAGA GTTG CAGA
                                |||||||| |||| ||||
                                AGAGATCT TAAT GTCT
                                     _   A
GAM3397  C8orf14  5'  TTTCAGTAACTTGCCAGA    76231      TA_  G
                                TTTC   GAC TTGCCAGA
                                ||||   ||| ||||||||
                                AAAG   TTG AACGGTCT
                                   TCA  _
GAM3397  CNOT8    5'  TCTCTAGAGTCACTCCAGA   76232         C  G__
                                TTTCTAGA GTT   CCAGA
                                |||||||| |||   |||||
                                AGAGATCT CAG   GGTCT
                                     _  TGA
GAM3397  CSTF2    3'  TTTCCAGATTTCTTGCCAG   76233         CG__
                                TTTCTAGA   TTGCCAG
                                ||||||||   |||||||
                                AAAGGTCT   AACGGTC
                                     AAAG
GAM3397  DCNP1    3'  TTTCCAGACAATGTCTCAGA  76234          T  C__
                                TTTCTAGACG TG  CAGA
                                |||||||||| ||  ||||
                                AAAGGTCTGT AC  GTCT
                                      T  AGA
GAM3397  DIO2     5'  TTTCTTGAATTGCCAGA     76235       A  C
                                TTTCT GA GTTGCCAGA
                                ||||| || |||||||||
                                AAAGA CT TAACGGTCT
                                   A  _
GAM3397  DIO2     5'  TTTCTTGAATTGCCAGA     76235       A  C
                                TTTCT GA GTTGCCAGA
                                ||||| || |||||||||
                                AAAGA CT TAACGGTCT
                                   A  _
GAM3397  FLJ11175 3'  TTTCTAGATACCTAGA      76236         CGT   _
                                TTTCTAGA  TGCC AGA
                                ||||||||  |||| |||
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                                AAAGATCT  ATGG TCT
                                   ___   A
GAM3397  FLJ12439  3'  TTTCACAGAGTTGCCAGA   76237    _  C
                                TTTC TAGA GTTGCCAGA
                                |||| |||| |||||||||
                                AAAG GTCT CAACGGTCT
                                  T  _
GAM3397  FLJ12892  5'  TTTCTGGACTACCAAA    76238     A  GT
                                TTTCT GAC  TGCCAGA
                                ||||| |||  |||||||
                                AAAGA CTG  ATGGTTT
                                  C  __
GAM3397  FLJ13593  3'  TTTCTAAACCTTTGCCAG   76239       G_
                                TTTCTAGAC  TTGCCAG
                                |||||||||  |||||||
                                AAAGATTTG  AACGGTC
                                     GA
GAM3397  FLJ14642  3'  TTTCTAGAGTTCCAGA    76240       C  G
                                TTTCTAGA GTT CCAGA
                                |||||||| ||| |||||
                                AAAGATCT CAA GGTCT
                                   _  _
GAM3397  FLJ20033  3'  TTTCAGAAATTGCCAGA   76241    T  C
                                TTTC AGA GTTGCCAGA
                                |||| ||| |||||||||
                                AAAG TCT TAACGGTCT
                                  _  T
GAM3397  FLJ21415  3'  TTCTAGACCTTGAGCCGGA  76242       G  __  A
                                TTCTAGAC TT  GCC GA
                                |||||||| ||  ||| ||
                                AAGATCTG AA  CGG CT
                                     G  CT  C
GAM3397  GAPCENA  3'  TTTCTAGAGTGTCCAGA    76243       C  TG
                                TTTCTAGA GT  CCAGA
                                |||||||| ||  |||||
                                AAAGATCT CA  GGTCT
                                   _  CA
GAM3397  GEMIN7   3'  TTCCTAGAGTTGCAGA     76244       C   C
                                TTTCTAGA GTTGC AGA
                                |||||||| ||||| |||
                                AAGGATCT CAACG TCT
                                   _   _
GAM3397  GPS2     5'  TCTCTGACTGCCAGA      76245     A  GT
                                TTTCT GAC  TGCCAGA
                                ||||| |||  |||||||
                                AGAGA CTG  ACGGTCT
                                  _  __
GAM3397  KIAA0063  3'  TTTCCTGATTTTGCCAGA   76246     A  CG
                                TTTCT GA  TTGCCAGA
                                ||||| ||  ||||||||
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                              AAAGG CT  AACGGTCT
                                 A  AA
GAM3397  KIAA0152  3'  TCTAGACATAACTTCAGA    76247        T  __
                              TCTAGACGT GC  CAGA
                              |||||||||  ||  ||||
                              AGATCTGTA TG  GTCT
                                    T  AA
GAM3397  KIAA0265  3'  TTTCAAAACTGCCAGA     76248     T   GT
                              TTTC AGAC  TGCCAGA
                              ||||  ||||  |||||||
                              AAAG TTTG  ACGGTCT
                                T   __
GAM3397  KIAA0296  3'  TTTCCAGACACAGCAGCCAG  76249        ___  T
                              TTTCTAGAC   GT GCCAG
                              |||||||||   ||  |||||
                              AAAGGTCTG   CG CGGTC
                                    TGT  T
GAM3397  KIAA0377  3'  TTTCCAGACATTTCAGA     76250          GC
                              TTTCTAGACGTT  CAGA
                              ||||||||||||  ||||
                              AAAGGTCTGTAA  GTCT
                                     A_
GAM3397  KIAA0446  3'  TCTCTAGAGGTCTTGCTAG   76251        C  __  C
                              TTTCTAGA GT  TGC AG
                              ||||||||  ||  |||  ||
                              AGAGATCT CA  ACG TC
                                   C  GA   A
GAM3397  KIAA0483  3'  TTTCAGACATTCCAGA     76252     T     G
                              TTTC AGACGTT CCAGA
                              ||||  |||||||  |||||
                              AAAG TCTGTAA GGTCT
                                _      _
GAM3397  KIAA0514  3'  TTCCTAGCCTGCCTGCCAGA  76253       AC_  _
                              TTTCTAG   GT TGCCAGA
                              |||||||   ||  |||||||
                              AAGGATC   CG ACGGTCT
                                   GGA  G
GAM3397  KIAA1138  3'  TTTCTAGAGACGCCAGA     76254       CGT
                              TTTCTAGA   TGCCAGA
                              ||||||||   |||||||
                              AAAGATCT   GCGGTCT
                                   CT_
GAM3397  KIAA1143  3'  TTTCTTAACTTGCCAGA     76255      A  G
                              TTTCT GAC TTGCCAGA
                              |||||  |||  ||||||||
                              AAAGA TTG AACGGTCT
                                 A  _
GAM3397  KIAA1587  3'  TTTCCAGACACCACACCAGA  76256        T__
                              TTTCTAGACG   TGCCAGA
                              ||||||||||   |||||||
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                                AAAGGTCTGT   GTGGTCT
                                     GGT
GAM3397  MGC34923  3'  CTTCTAGACTTGTAGA      76257         G   CC
                                TTTCTAGAC TTG  AGA
                                ||||||||| |||  |||
                                GAAGATCTG AAC  TCT
                                     _  A_
GAM3397  MGC3771   5'  TTTCCGACGCTGCCGGA     76258      A       A
                                TTTCT GACGTTGCC GA
                                ||||| ||||||||| ||
                                AAAGG CTGCGACGG CT
                                   _       C
GAM3397  SCYA25    3'  TTTCCAGTTGCCAGA       76259       GAC
                                TTTCTA   GTTGCCAGA
                                ||||||   |||||||||
                                AAAGGT   CAACGGTCT
                                    ___
GAM3397  SCYD1     3'  TCTCTGAGCTGCCAGA      76260      A  C
                                TTTCT GA GTTGCCAGA
                                ||||| || |||||||||
                                AGAGA CT CGACGGTCT
                                   _ _
GAM3397  SLC7A11   3'  TCTCTAGACTTTCAGA      76261         G  GC
                                TTTCTAGAC TT  CAGA
                                ||||||||| ||  ||||
                                AGAGATCTG AA  GTCT
                                     _ A_
GAM3397  WSB1      3'  TTTCCAGAAACTACCAGA    76262         CG
                                TTTCTAGA  TTGCCAGA
                                ||||||||  ||||||||
                                AAAGGTCT  GATGGTCT
                                     TT
GAM3397  LOC139082 3'  TTTCTAGAGGTTAACCTAGA  76263         C   _ _
                                TTTCTAGA GTTG CC AGA
                                |||||||| |||| || |||
                                AAAGATCT CAAT GG TCT
                                     C    T  A
GAM3397  LOC144583 3'  TCTCTAGAGGCCCAGA      76264         C  TG
                                TTTCTAGA GT  CCAGA
                                |||||||| ||  |||||
                                AGAGATCT CG  GGTCT
                                     C  __
GAM3397  LOC145609 5'  TCTCCTGACTGCCAGA      76265       A  GT
                                TTTCT GAC  TGCCAGA
                                ||||| |||  |||||||
                                AGAGG CTG  ACGGTCT
                                   A  __
GAM3397  LOC146136 5'  TTTCCAGATACTGCAGA     76266         CG   C
                                TTTCTAGA  TTGC AGA
                                ||||||||  |||| |||
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                                AAAGGTCT  GACG TCT
                                    AT   _
GAM3397  LOC148823 3'  TTTCTAAACTTTAGCCAGA   76267        GTT_
                                TTTCTAGAC   GCCAGA
                                |||||||||   ||||||
                                AAAGATTTG   CGGTCT
                                    AAAT
GAM3397  LOC148887 5'  TCTCTAAGGTTGCCAGA    76268       AC
                                TTTCTAG  GTTGCCAGA
                                |||||||  |||||||||
                                AGAGATT  CAACGGTCT
                                   C_
GAM3397  LOC149483 3'  CTTCTAGACCCAATGTCAGA  76269        GT__  C
                                TTTCTAGAC   TG CAGA
                                |||||||||   || ||||
                                GAAGATCTG   AC GTCT
                                    GGTT  A
GAM3397  LOC149878 5'  CTTCTAGAGTCCAGA      76270       C  TG
                                TTTCTAGA GT  CCAGA
                                ||||||||  ||  |||||
                                GAAGATCT CA  GGTCT
                                    _  __
GAM3397  LOC151007 3'  TTTCTAGAAGTTCTTCAGA   76271       C   GC_
                                TTTCTAGA GTT   CAGA
                                ||||||||  |||   ||||
                                AAAGATCT CAA   GTCT
                                    T   GAA
GAM3397  LOC151057 5'  TTTCTAAAGCAGCCGGA    76272       C  T   A
                                TTTCTAGA GT GCC GA
                                ||||||||  ||  |||  ||
                                AAAGATTT CG CGG CT
                                    _  T   C
GAM3397  LOC161357 3'  TTTCCAGAGTTCAACCAGA   76273       C   __
                                TTTCTAGA GTT  GCCAGA
                                ||||||||  |||  ||||||
                                AAAGGTCT CAA  TGGTCT
                                    _   GT
GAM3397  LOC196477 3'  TTTCAGCATTGCCAGA     76274     T  A
                                TTTC AG CGTTGCCAGA
                                ||||  ||  ||||||||||
                                AAAG TC GTAACGGTCT
                                  _  _
GAM3397  LOC200225 3'  TTCCTAGAGCCACCAGA    76275       C  TG
                                TTTCTAGA GT  CCAGA
                                ||||||||  ||  |||||
                                AAGGATCT CG  GGTCT
                                    _  GT
GAM3397  LOC200734 3'  TTTCTAGATGTTCTCCAG   76276       C   G_
                                TTTCTAGA GTT  CCAG
                                ||||||||  |||  ||||
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                                AAAGATCT CAA  GGTC
                                     A   GA
GAM3397  LOC203068 3'  TTCTAGACCCCCCCCAGA    76277        G  G  _
                                TTCTAGAC TT CC AGA
                                |||||||| || || |||
                                AAGATCTG GG GG TCT
                                     G  G  G
GAM3397  LOC203523 3'  CTTCTAGACTTGATTCAG    76278        G   C__
                                TTTCTAGAC TTG   CAG
                                ||||||||| |||   |||
                                GAAGATCTG AAC   GTC
                                      _  TAA
GAM3397  LOC219513 5'  CTTCTCACTCTGCCAGA     76279      AG  G
                                TTTCT  AC TTGCCAGA
                                |||||  || ||||||||
                                GAAGA  TG GACGGTCT
                                   G_  A
GAM3397  LOC221025 3'  TTTCTAGACCTGTTAGCTGGA  76215         __  _  CA
                                TTTCTAGAC  GTT GC  GA
                                |||||||||  ||| ||  ||
                                AAAGATCTG  CAA CG  CT
                                      GA   T  AC
GAM3397  LOC253367 5'  TTTCTAGACGCTTCCAGA    76280           G
                                TTTCTAGACGTT CCAGA
                                |||||||||||| |||||
                                AAAGATCTGCGA GGTCT
                                        A
GAM3397  LOC256880 5'  TCTCTAGAGCCCTGCTAG    76281        C  __  C
                                TTTCTAGA GT  TGC AG
                                |||||||| ||  ||| ||
                                AGAGATCT CG  ACG TC
                                     _ GG   A
GAM3397  LOC51637  3'  TTTCCAAACATGCCAGA     76282          T
                                TTTCTAGACGT GCCAGA
                                |||||||||| ||||||
                                AAAGGTTTGTA CGGTCT
                                        _
GAM3397  LOC51659  3'  TTTCTAGAGCTCCAGA      76283        C   G
                                TTTCTAGA GTT CCAGA
                                |||||||| ||| |||||
                                AAAGATCT CGA GGTCT
                                     _  _
GAM3397  LOC51659  3'  TTTCTAGAGCTCCAGA      76283        C   G
                                TTTCTAGA GTT CCAGA
                                |||||||| ||| |||||
                                AAAGATCT CGA GGTCT
                                     _  _
GAM3397  LOC56920  3'  TTTCTAGAGTAACTTCCCAGA  76284        C  ____ G
                                TTTCTAGA GT    T CCAGA
                                |||||||| ||    | |||||
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                                AAAGATCT CA    A GGTCT
                                    _ TTGA G
GAM3397 LOC89890 3' TTTCTAAACCAAACCAGA    76285        GTT
                                TTTCTAGAC   GCCAGA
                                |||||||||   ||||||
                                AAAGATTTG   TGGTCT
                                     GTT
GAM3397 LOC90317 3' CTTCTAAACAGCCAGA      76286        TT
                                TTTCTAGACG  GCCAGA
                                ||||||||||  ||||||
                                GAAGATTTGT  CGGTCT
                                      __
GAM3397 LOC92755 3' TTCTAGACCCTCCCCAGA    76287        G_ G
                                TTCTAGAC  TT CCAGA
                                ||||||||  || |||||
                                AAGATCTG  AG GGTCT
                                     GG  G
GAM3398 ADRA2B   3' CTGCATGTCGCAATAAG     76290       C   CG
                                CTGCATG CGT  GATGGG
                                ||||||| |||  ||||||
                                GACGTAC GCG  TTATTC
                                    A  __
GAM3398 BARX2    3' CTGCATGCTAGGATATAGGG   76291        CGTC   ___
                                CTGCATGC   GGAT   GGG
                                ||||||||   ||||   |||
                                GACGTACG   CCTA   CCC
                                     AT__   TAT
GAM3398 BRIP1    3' CTGCATTCCAGCCTGGG     76292      G _  GGA
                                CTGCAT CC GTC   TGGG
                                ||||||| || |||   ||||
                                GACGTA GG CGG   ACCC
                                   A  T  ___
GAM3398 CNTN2    3' CTGTGTCCGTCGGAGG      76293     CA _      T
                                CTG  TG CCGTCGGA GG
                                |||  || |||||||| ||
                                GAC  AC GGCAGCCT CC
                                  __  A      _
GAM3398 CTNS     3' CTGGATGTGCTCAGATGGG   76294     C   CCG
                                CTG ATG   TCGGATGGG
                                ||| |||   |||||||||
                                GAC TAC   AGTCTACCC
                                  C   ACG
GAM3398 EGLN1    5' CTGCATGCGTAAATGG      76295        C  C
                                CTGCATGC GT GGATGG
                                |||||||| || ||||||
                                GACGTACG CA TTTACC
                                      _ _
GAM3398 F2RL2    3' CTGCACGCCAGTCTGGG     76296         _  GGA
                                CTGCATGCC GTC   TGGG
                                ||||||||| |||   ||||
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                                GACGTGCGG CAG   ACCC
                                     T  ____
GAM3398  FGFR1    3'  TGCATGCCTGTTCATTGG    76297        _ _  GA
                                TGCATGCC GT CG  TGG
                                |||||||| || ||  |||
                                ACGTACGG CA GT  ACC
                                     A  A  A_
GAM3398  FGFR1    3'  TGCATGCCTGTTCATTGG    76297        _ _  GA
                                TGCATGCC GT CG  TGG
                                |||||||| || ||  |||
                                ACGTACGG CA GT  ACC
                                     A  A  A_
GAM3398  FGFR1    3'  TGCATGCCTGTTCATTGG    76297        _ _  GA
                                TGCATGCC GT CG  TGG
                                |||||||| || ||  |||
                                ACGTACGG CA GT  ACC
                                     A  A  A_
GAM3398  HS3ST4   3'  CTGCTGCCCAGATGGG     76298     A    GT
                                CTGC TGCC  CGGATGGG
                                |||| ||||  ||||||||
                                GACG ACGG  GTCTACCC
                                  _   __
GAM3398  LDOC1    3'  CTGCAGCAATCTGGTGGG    76299      T  C   _  A
                                CTGCA GC GTC GG TGGG
                                ||||| || ||| || ||||
                                GACGT CG TAG CC ACCC
                                  _  T   A  _
GAM3398  MAML1    3'  CTGATGCCAGCAGATGGG    76300     C     T
                                CTG ATGCCG CGGATGGG
                                ||| |||||| ||||||||
                                GAC TACGGT GTCTACCC
                                  _     C
GAM3398  MHC2TA   3'  CTGCACGCCAGCCTGGG     76301         _  GGA
                                CTGCATGCC GTC   TGGG
                                ||||||||| |||   ||||
                                GACGTGCGG CGG   ACCC
                                     T  ____
GAM3398  MS4A1    5'  CTGCATGCTCTGAATAGG    76302        CG  _
                                CTGCATGC  TC GGATGGG
                                ||||||||  || |||||||
                                GACGTACG  AG CTTATCC
                                     __  A
GAM3398  MYO15A   5'  CTGCATGCCGCCTCATGGG   76303           GG
                                CTGCATGCCGTC  ATGGG
                                ||||||||||||  |||||
                                GACGTACGGCGG  TACCC
                                      AG
GAM3398  NDST1    5'  CTGCATGCCGCTCACTCCGTGG 76304          _  GA___
              G                  CTGCATGCCG TCG    TGGG
                                ||||||||||| |||    ||||
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                                GACGTACGGC AGT    ACCC
                                     G  GAGGC
GAM3398  NOX5    5'  CTGCATACCAGCCTGGG    76305       _  GGA
                                CTGCATGCC GTC  TGGG
                                ||||||||| |||  ||||
                                GACGTATGG CGG  ACCC
                                     T  ___
GAM3398  NPY     3'  CTGCATGCATTGGTAGGATGGG 76306       C___  C
                                CTGCATGC   GT GGATGGG
                                ||||||||   || |||||||
                                GACGTACG   CA CCTACCC
                                     TAAC  T
GAM3398  SLC12A6  3'  CTGCAGATCAGATGGG     76307     TGCC
                                CTGCA   GTCGGATGGG
                                |||||   ||||||||||
                                GACGT   TAGTCTACCC
                                   C___
GAM3398  SLC6A3   3'  CTGCATGCGTCCTGGG     76308       C  GGA
                                CTGCATGC GTC  TGGG
                                |||||||| |||  ||||
                                GACGTACG CAG  ACCC
                                     _  G__
GAM3398  SLC6A3   3'  CTGCATGCATCCTGGG     76309       C  GGA
                                CTGCATGC GTC  TGGG
                                |||||||| |||  ||||
                                GACGTACG TAG  ACCC
                                     _  G__
GAM3398  SLC6A3   3'  CTGCATGCGTCCTGGG     76308       C  GGA
                                CTGCATGC GTC  TGGG
                                |||||||| |||  ||||
                                GACGTACG CAG  ACCC
                                     _  G__
GAM3398  SLC6A3   3'  CTGCATGCGTCCTGGG     76308       C  GGA
                                CTGCATGC GTC  TGGG
                                |||||||| |||  ||||
                                GACGTACG CAG  ACCC
                                     _  G__
GAM3398  SLC6A3   3'  CTGCATGCGTCCTGGG     76308       C  GGA
                                CTGCATGC GTC  TGGG
                                |||||||| |||  ||||
                                GACGTACG CAG  ACCC
                                     _  G__
GAM3398  SOX11    3'  CTGCATACCAAGGGGGGGTGGG 76310         TC___  A
                                CTGCATGCCG    GG TGGG
                                ||||||||||    || ||||
                                GACGTATGGT    CC ACCC
                                     TCCCC  C
GAM3398  STK11    3'  CTGCATGCATGGCGGG     76311       C  C  A
                                CTGCATGC GT GG TGGG
                                |||||||| || || ||||
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                                GACGTACG TA CC GCCC
                                    _ _ _
GAM3398 TBXA2R   3' CTGCATGCCCTTCCTGGG    76312        G_ GGA
                                CTGCATGCC  TC   TGGG
                                |||||||||  ||   ||||
                                GACGTACGG  AG   ACCC
                                     GA  G__
GAM3398 TEM6     3' CTGAATGCCGTCGAGG      76313     C        AT
                                CTG ATGCCGTCGG  GG
                                ||| ||||||||||  ||
                                GAC TACGGCAGCT  CC
                                  T        __
GAM3398 C20orf124 3' CCGCGCGGCCCGGATGGG    76314      AT_  GT
                                CTGC   GCC  CGGATGGG
                                ||||   |||  ||||||||
                                GGCG   CGG  GCCTACCC
                                  CGC   __
GAM3398 C20orf60  3' TGCATGCCAGTTAGAGGG    76315        _ CG  T
                                TGCATGCC GT  GA GGG
                                |||||||| ||  || |||
                                ACGTACGG CA  CT CCC
                                     T  AT  _
GAM3398 C5orf4    3' CTGCATGCTCTATAGGGTGGG  76316        C__  C  A
                                CTGCATGC   GT GG TGGG
                                ||||||||   || || ||||
                                GACGTACG   TA CC ACCC
                                     AGA  T  C
GAM3398 C8orf17   3' CTGTGTCTGCCCAAATGGG   76317     CA__   GT
                                CTG    TGCC  CGGATGGG
                                |||    ||||  ||||||||
                                GAC    ACGG  GTTTACCC
                                  ACAG   __
GAM3398 DKFZp434K1210 3' CTGCTGCCCGGGTGGG      76318      A   GT   A
                                CTGC TGCC  CGG TGGG
                                |||| ||||  ||| ||||
                                GACG ACGG  GCC ACCC
                                  _   __  C
GAM3398 DKFZP564O0523 3' CTGCATTCCAGCCTGGG     76292       G  _  GGA
                                CTGCAT CC GTC   TGGG
                                |||||| || |||   ||||
                                GACGTA GG CGG   ACCC
                                   A  T  ____
GAM3398 FLJ10560  3' CTGCACGCCAGCCTGGG     76301         _  GGA
                                CTGCATGCC GTC   TGGG
                                ||||||||| |||   ||||
                                GACGTGCGG CGG   ACCC
                                     T  ____
GAM3398 FLJ13114  3' CTGCATTCCAGCCTGGG     76292       G  _  GGA
                                CTGCAT CC GTC   TGGG
                                |||||| || |||   ||||
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                                GACGTA GG CGG   ACCC
                                   A  T  ___
GAM3398  FLJ13241  3'  CTGGTGCGCAGATGGG     76319    CA   C T
                                CTG  TGC G CGGATGGG
                                |||  ||| | ||||||||
                                GAC  ACG C GTCTACCC
                                  C_  _ _
GAM3398  FLJ14427  3'  TGCATGCCCTCCTGATGGG   76320       G  G_
                                TGCATGCC TC  GATGGG
                                ||||||||  ||  ||||||
                                ACGTACGG AG  CTACCC
                                     G  GA
GAM3398  FLJ21324  5'  CTGCACGCCAGCCTGGG     76301        _  GGA
                                CTGCATGCC GTC   TGGG
                                |||||||||  |||   ||||
                                GACGTGCGG CGG   ACCC
                                     T  ___
GAM3398  FLJ21865  3'  CTGCATGGCGGTGGG       76321       CC T   A
                                CTGCATG  G CGG TGGG
                                |||||||  |  ||| ||||
                                GACGTAC  C GCC ACCC
                                   __ _  _
GAM3398  FLJ23191  5'  CTGATATAAACCGGATGGG   76322    C   CCG_
                                CTG ATG    TCGGATGGG
                                |||  |||    |||||||||
                                GAC TAT    GGCCTACCC
                                  _  ATTT
GAM3398  FLJ23323  3'  CTGCACCAAATGGATGGG    76323     AT    TC_
                                CTGC  GCCG   GGATGGG
                                ||||  ||||   |||||||
                                GACG  TGGT   CCTACCC
                                   __    TTA
GAM3398  FLJ31101  3'  CTGCATTCCAGCCTGGG     76292       G  _  GGA
                                CTGCAT CC GTC   TGGG
                                ||||||  ||  |||   ||||
                                GACGTA GG CGG   ACCC
                                   A  T  ___
GAM3398  GP5       3'  CTGCACGCCAGCCTGGG     76301        _  GGA
                                CTGCATGCC GTC   TGGG
                                |||||||||  |||   ||||
                                GACGTGCGG CGG   ACCC
                                     T  ___
GAM3398  GR6       5'  CTGCATTCCAGCCTGGG     76292       G  _  GGA
                                CTGCAT CC GTC   TGGG
                                ||||||  ||  |||   ||||
                                GACGTA GG CGG   ACCC
                                   A  T  ___
GAM3398  KIAA0555  5'  CTGCTGCCGTCGCGG       76324      A       GA
                                CTGC TGCCGTCG  TGG
                                ||||  ||||||||  |||
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                                GACG ACGGCAGC  GCC
                                  _     __
GAM3398  KIAA0961  3'  CTGCACGCCAGCCTGGG    76301        _  GGA
                                CTGCATGCC GTC   TGGG
                                ||||||||| |||   ||||
                                GACGTGCGG CGG   ACCC
                                    T  ___
GAM3398  KIAA0977  3'  CTGTAAGCCGACAAATGGG   76325    CAT   T
                                CTG   GCCG CGGATGGG
                                |||   |||| ||||||||
                                GAC   CGGC GTTTACCC
                                  ATT   T
GAM3398  KIAA1277  3'  CTGAGCGGCCGGATGGG    76326    CAT  C
                                CTG   GC GTCGGATGGG
                                |||   || ||||||||||
                                GAC   CG CGGCCTACCC
                                  T__  C
GAM3398  KIAA1364  3'  CTGCATGCGGCCCCTGGG   76327       C   GGA
                                CTGCATGC GTC   TGGG
                                |||||||| |||   ||||
                                GACGTACG CGG   ACCC
                                    C   GG_
GAM3398  LNIR      3'  CTGCATGCATGGTGGG     76328       C  C  A
                                CTGCATGC GT GG TGGG
                                |||||||| || || ||||
                                GACGTACG TA CC ACCC
                                    _  _  _
GAM3398  MGC2474   3'  CTGCATTCCAGCCTGGG    76292      G  _  GGA
                                CTGCAT CC GTC   TGGG
                                |||||| || |||   ||||
                                GACGTA GG CGG   ACCC
                                   A  T  ___
GAM3398  MIR       3'  CGCATGGCAGATGGG      76329      CC T
                                TGCATG  G CGGATGGG
                                ||||||  | ||||||||
                                GCGTAC  C GTCTACCC
                                   __ _
GAM3398  NDP52     3'  TGCACGCCAGCCTGGG     76330       _  GGA
                                TGCATGCC GTC   TGGG
                                |||||||| |||   ||||
                                ACGTGCGG CGG   ACCC
                                    T  ___
GAM3398  PCBP3     3'  CTGCATGCCGGTGCATGGG   76331        TCGG
                                CTGCATGCCG    ATGGG
                                ||||||||||    |||||
                                GACGTACGGC    TACCC
                                     CACG
GAM3398  PRDM15    3'  TGGATGCCACAAATGGG     76332    C     T
                                TG ATGCCG CGGATGGG
                                || |||||| ||||||||
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                                AC TACGGT GTTTACCC
                                 C     _
GAM3398  RNP24    3'  TACATGCCAAGAGTGGG     76333         TC  A
                                TGCATGCCG  GG TGGG
                                |||||||||  || ||||
                                ATGTACGGT  TC ACCC
                                     TC  _
GAM3398  SKIP     3'  CTCCATGCCGTGAGTAGG    76334    G       C GA
                                CT CATGCCGT G  TGGG
                                || ||||||||  |  ||||
                                GA GTACGGCA C  ATCC
                                 G       _ TC
GAM3398  SKIP     3'  CTCCATGCCGTGAGTAGG    76334    G       C GA
                                CT CATGCCGT G  TGGG
                                || ||||||||  |  ||||
                                GA GTACGGCA C  ATCC
                                 G       _ TC
GAM3398  TTTY2    5'  TACATGTCGAACGGG       76335      GCC
                                TGCAT   GTCGGATGGG
                                |||||   ||||||||||
                                ATGTA   CAGCTTGCCC
                                  ___
GAM3398  LOC145757 3'  CTGCAGTGTGCGGGGGTGGG   76336      ___   C TC  A
                                CTGCA   TGC G  GG TGGG
                                |||||   ||| |  || ||||
                                GACGT   ACG C  CC ACCC
                                   CAC   _ CC  _
GAM3398  LOC147174 3'  CTGCATGCAGTAGCGG      76337        C  C  A
                                CTGCATGC GT GG TGG
                                |||||||| || || |||
                                GACGTACG CA TC GCC
                                     T  _  _
GAM3398  LOC147299 3'  CTACATGCTGTTTAATTATGGG 76339        C  CGG___
                                CTGCATGC GT     ATGGG
                                |||||||| ||     |||||
                                GATGTACG CA     TACCC
                                     A  AATTAA
GAM3398  LOC147299 3'  CTGATGCCGTCATCGAGGG    76338     C       GAT_
                                CTG ATGCCGTCG    GGG
                                ||| |||||||||    |||
                                GAC TACGGCAGT    CCC
                                  _        AGCT
GAM3398  LOC149478 5'  CTGCGAGCCGGCAAATGGG    76340      AT    T
                                CTGC  GCCG CGGATGGG
                                ||||  |||| ||||||||
                                GACG  CGGC GTTTACCC
                                  CT    C
GAM3398  LOC150113 5'  CTGCAGGCCGTCATAG       76341       T     GG
                                CTGCA GCCGTC  ATGG
                                ||||| ||||||  ||||
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                                GACGT CGGCAG  TATC
                                  C     __
GAM3398  LOC152719 5'  CTGCATTCCAGCCTGGG     76292       G _  GGA
                                CTGCAT CC GTC   TGGG
                                |||||| || |||   ||||
                                GACGTA GG CGG   ACCC
                                   A  T  ___
GAM3398  LOC152765 5'  CTGCATGCCTCAATGGG     76342        G  G
                                CTGCATGCC TCG ATGGG
                                ||||||||| ||| |||||
                                GACGTACGG AGT TACCC
                                    _  _
GAM3398  LOC159148 5'  TACATGTCGAACGGG       76335      GCC
                                TGCAT   GTCGGATGGG
                                |||||   ||||||||||
                                ATGTA   CAGCTTGCCC
                                   ___
GAM3398  LOC164633 3'  CCGCATGCGGTGGATGGG    76343        C  C
                                CTGCATGC GT GGATGGG
                                |||||||| || |||||||
                                GGCGTACG CA CCTACCC
                                   C  _
GAM3398  LOC164684 3'  CTGCATACGTAGTATGGG    76344        C  C  _
                                CTGCATGC GT GG ATGGG
                                |||||||| || || |||||
                                GACGTATG CA TC TACCC
                                   _  _  A
GAM3398  LOC197342 3'  CTGCATGCTGTCAGCGG     76345        C    A
                                CTGCATGC GTCGG TGG
                                |||||||| ||||| |||
                                GACGTACG CAGTC GCC
                                   A    _
GAM3398  LOC199990 3'  TGCATGCCAGGCTGGG      76346         TC  A
                                TGCATGCCG  GG TGGG
                                |||||||||  || ||||
                                ACGTACGGT  CC ACCC
                                   __  G
GAM3398  LOC221272 3'  CTGCATGCAGAGTGGTGGG   76347        C__  C  A
                                CTGCATGC   GT GG TGGG
                                ||||||||   || || ||||
                                GACGTACG   CA CC ACCC
                                   TCT  _  _
GAM3398  LOC256218 3'  CTGCATGCAGTAGCGG      76337        C  C  A
                                CTGCATGC GT GG TGG
                                |||||||| || || |||
                                GACGTACG CA TC GCC
                                   T  _  _
GAM3398  LOC256790 5'  CGCATGTCCAGATGGG      76348       CCG
                                TGCATG   TCGGATGGG
                                ||||||   |||||||||
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                                GCGTAC  GGTCTACCC
                                   A__
GAM3398 LOC56270 5' CTGCATGCCTCTCGCTGGG  76349       G_  GA
                                CTGCATGCC  TCG  TGGG
                                |||||||||  |||  ||||
                                GACGTACGG  AGC  ACCC
                                     AG  G_
GAM3398 LOC91516 5' CCGCATGCCCAGGGTGGG   76350       GTC  A
                                CTGCATGCC  GG TGGG
                                |||||||||  || ||||
                                GGCGTACGG  CC ACCC
                                     GT_  C
GAM3399 ADCY1   5' GCATGGTCAGTCTTGGGC   76353      A_  GG
                                GCATGG  AGT  TTGGGC
                                ||||||  |||  ||||||
                                CGTACC  TCA  AACCCG
                                   AG  G_
GAM3399 ADORA2A  3' TGCAGTGGAGGGCTGGGCC  76354     _   A T
                                TGCA TGGA G GGTTGGGCC
                                |||| |||| | |||||||||
                                ACGT ACCT C CCGACCCGG
                                  C  _ _
GAM3399 AKAP13  3' TGCATAGAAATGTGTGGGC  76355         GT
                                TGCATGGAAGTG  TGGGC
                                ||||||||||||  |||||
                                ACGTATCTTTAC  ACCCG
                                      AC
GAM3399 ANK1    3' TGCCTGGAGGCCGGGCC    76356    A   AGT
                                TGC TGGA  GGTTGGGCC
                                ||| ||||  |||||||||
                                ACG ACCT  CCGGCCCGG
                                  G  ___
GAM3399 ANK1    3' TGCCTGGAGGCCGGGCC    76356    A   AGT
                                TGC TGGA  GGTTGGGCC
                                ||| ||||  |||||||||
                                ACG ACCT  CCGGCCCGG
                                  G  ___
GAM3399 AXIN1   3' TGCACGGAGGTCCGGAGC   76357       AGT  _ _
                                TGCATGGA  GGTT GG GC
                                ||||||||  |||| || ||
                                ACGTGCCT  CCAG CC CG
                                    ___  G  T
GAM3399 BCL2L10  5' TGCTGGGGGGGCCGGGCC    59743    A  AAGT
                                TGC TGG   GGTTGGGCC
                                ||| |||   |||||||||
                                ACG ACC   CCGGCCCGG
                                  _  CC__
GAM3399 BCL9    3' GCATGGAAGGCGAGGC     76358       GT  T
                                GCATGGAA  GGT GGGC
                                ||||||||  ||| ||||
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                                CGTACCTT  CCG TCCG
                                    __  C
GAM3399 BGN     3' TGATGGGGGCCGGGCC     76359   C   AAGT
                                TG ATGG   GGTTGGGCC
                                || ||||   |||||||||
                                AC TACC   CCGGCCCGG
                                 _   C___
GAM3399 C18orf1  3' TGCATGGGGGGCCGGGC    76360       AAGT
                                TGCATGG   GGTTGGGC
                                |||||||   ||||||||
                                ACGTACC   CCGGCCCG
                                    CC__
GAM3399 CASP10   3' TGCAGGGAAGTGGGTGCC   76361     T      TTGG
                                TGCA GGAAGTGG   GCC
                                |||| ||||||||   |||
                                ACGT CCTTCACC   CGG
                                  C      CA__
GAM3399 CBFA2T3  3' TGCGGTGGGGCGATGGGGCC 76362    A_  AA   T
                                TGC  TGG  GTGGT GGGCC
                                |||  |||  ||||| |||||
                                ACG  ACC  CGCTA CCCGG
                                 CC  C_   C
GAM3399 CCR9     3' GCATGGAAGTAAATAGCC    76363         TTG
                                GCATGGAAGTGG  GGCC
                                ||||||||||||  ||||
                                CGTACCTTCATT  TCGG
                                      TA_
GAM3399 CCR9     3' GCATGGAAGTAAATAGCC    76363         TTG
                                GCATGGAAGTGG  GGCC
                                ||||||||||||  ||||
                                CGTACCTTCATT  TCGG
                                      TA_
GAM3399 CDC23    3' TACATGGAGGTAAGGC     76364       AGT  T
                                TGCATGGA  GGT GGGC
                                ||||||||  ||| ||||
                                ATGTACCT  CCA TCCG
                                    ___  T
GAM3399 CDC25A   3' GCATGGAAGTCCCAGGCC   76365        GG TG
                                GCATGGAAGT  T  GGCC
                                ||||||||||  |  ||||
                                CGTACCTTCA  G  CCGG
                                     G_ GT
GAM3399 CLCN7    3' GCATGGGGCTCAGGGCC    76366      AAGT  __
                                GCATGG   GGTT  GGGCC
                                ||||||   ||||  |||||
                                CGTACC   CCGA  CCCGG
                                   ____   GT
GAM3399 CMKLR1   5' TGCTGGAGAGATGGGC     76367    A   A T  T
                                TGC TGGA G GGT GGGC
                                ||| |||| | ||| ||||
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                                ACG ACCT C CTA CCCG
                                  _   _ T  _
GAM3399 CSPG4   3' GCATGGAAGCAATGGGGCC  76368       TG  T
                                GCATGGAAG  GT GGGCC
                                |||||||||  || |||||
                                CGTACCTTC  TA CCCGG
                                     GT  C
GAM3399 CYP3A4  5' TGCATGGAGCTTTCCTGCC  76369       A  GG  GG
                                TGCATGGA GT  TT  GCC
                                |||||||| ||  ||  |||
                                ACGTACCT CG  AG  CGG
                                     _ AA  GA
GAM3399 DIO3    3' TGCGGGAAGCACCGGGCC   76370    AT    GGT
                                TGC  GGAAGT   TGGGCC
                                |||  ||||||   ||||||
                                ACG  CCTTCG   GCCCGG
                                  C_    TG_
GAM3399 DVL3    3' TGCATGGGTGAAGTTGGGCC  76371      AAGT
                                TGCATGG   GGTTGGGCC
                                |||||||   |||||||||
                                ACGTACC   TCAACCCGG
                                    CACT
GAM3399 EN2     3' TGCACACGGTTGGGCC     76372      GAAG
                                TGCATG   TGGTTGGGCC
                                ||||||   ||||||||||
                                ACGTGT   GCCAACCCGG
                                   ____
GAM3399 FGFR2   3' TGATGGAAGTGAAGGGCC   76373   C       TT
                                TG ATGGAAGTGG  GGGCC
                                || ||||||||||  |||||
                                AC TACCTTCACT  CCCGG
                                 _       T_
GAM3399 FXYD7   3' TGCTGGGGGTGCTGGGCC   76374    A  AA  G
                                TGC TGG  GTG TTGGGCC
                                ||| |||  ||| |||||||
                                ACG ACC  CAC GACCCGG
                                  _  CC  _
GAM3399 GBF1    3' TGCAGAGTGGTTGGGC     76375     TG  A
                                TGCA  GA GTGGTTGGGC
                                ||||  || ||||||||||
                                ACGT  CT CACCAACCCG
                                   __ _
GAM3399 GPR62   3' TGCTATGCAGTGTTGGGCC  76376    _  GA   G
                                TGC ATG  AGTG TTGGGCC
                                ||| |||  |||| |||||||
                                ACG TAC  TCAC AACCCGG
                                  A  G_   _
GAM3399 GUCY1B2 3' TGGATGGAAGTTCCAGC    76377   C      GG  G
                                TG ATGGAAGT  TT GGC
                                || ||||||||  || |||
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                                AC TACCTTCA  AG TCG
                                 C       __ G
GAM3399 HBZ     5' TGCACTGGAGTTGGGCC     76378      _   AGTG
                                TGCA TGGA    GTTGGGCC
                                |||| ||||    ||||||||
                                ACGT ACCT    CAACCCGG
                                  G   _____
GAM3399 HMG20A   3' TGATGGGAGAAGACTGGGCC   76379    C    A  T_ GT
                                TG ATGG AG  G  TGGGCC
                                || |||| ||  |  ||||||
                                AC TACC TC  C  ACCCGG
                                 _   C  TT TG
GAM3399 HRMT1L1  3' TGTCTGGAAGTGACAGCC    76380    CA       TTG
                                TG  TGGAAGTGG   GGCC
                                ||  |||||||||   ||||
                                AC  ACCTTCACT   TCGG
                                 AG       G__
GAM3399 HTR6    5' TGCGGGGAAGTGGGAAC     76381     AT      TT
                                TGC  GGAAGTGG  GGGC
                                |||  ||||||||  ||||
                                ACG  CCTTCACC  CTTG
                                  CC       __
GAM3399 INPP5A   3' GCATGGGAGTAACGGCC     76382       A    TTG
                                GCATGG AGTGG   GGCC
                                |||||| |||||   ||||
                                CGTACC TCATT   CCGG
                                   C    G__
GAM3399 KCNK4    3' TGGATGGAAGTGAGGGAAGGGC 76383    C       TT___
            C                    TG ATGGAAGTGG    GGGCC
                                || ||||||||||    |||||
                                AC TACCTTCACT    CCCGG
                                 C        CCCTT
GAM3399 KCNK4    3' TGGATGGAAGTGAGGGAAGGGC 76383    C       TT___
            C                    TG ATGGAAGTGG    GGGCC
                                || ||||||||||    |||||
                                AC TACCTTCACT    CCCGG
                                 C        CCCTT
GAM3399 KCNK4    3' TGGATGGAAGTGAGGGAAGGGC 76383    C       TT___
            C                    TG ATGGAAGTGG    GGGCC
                                || ||||||||||    |||||
                                AC TACCTTCACT    CCCGG
                                 C        CCCTT
GAM3399 LDLR    3' TGCATAGAAGTGGAAGC     76384          TT
                                TGCATGGAAGTGG  GGGC
                                ||||||||||||  ||||
                                ACGTATCTTCACC  TTCG
                                              __
GAM3399 LILRB4   3' TGTATGGAAATGGATGCC    76385    C       TTGG
                                TG ATGGAAGTGG    GCC
                                || ||||||||||    |||
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                                AC TACCTTTACC   CGG
                                 A        TA__
GAM3399  LPIN2    3'  TGCAATGGAAGGAGGCC    76386     _     T GTT
                                TGCA TGGAAG G   GGGCC
                                |||| |||||| |   |||||
                                ACGT ACCTTC C   TCCGG
                                  T     _ ___
GAM3399  MEA      3'  TGCTAAGGTGGTTGGGC    76387     AT  AA
                                TGC  GG  GTGGTTGGGC
                                |||  ||  ||||||||||
                                ACG  TC  CACCAACCCG
                                  AT  __
GAM3399  MTRR     3'  TGCATGGAAGGACAGAG    76388         T  TT
                                TGCATGGAAG GG  GGG
                                |||||||||| ||  |||
                                ACGTACCTTC CT  CTC
                                      _  GT
GAM3399  MTRR     3'  TGCATGGAAGGACAGAG    76388         T  TT
                                TGCATGGAAG GG  GGG
                                |||||||||| ||  |||
                                ACGTACCTTC CT  CTC
                                      _  GT
GAM3399  NAGA     3'  TGCACGGAGGGGCAGGCC   76389         A T  TT
                                TGCATGGA G GG  GGGCC
                                |||||||| | ||  |||||
                                ACGTGCCT C CC  TCCGG
                                     _ _  CG
GAM3399  NESH     3'  TGCATGGAGTAGGGG      76390         A    TT
                                TGCATGGA GTGG  GGG
                                |||||||| ||||  |||
                                ACGTACCT CATC  CCC
                                     _   __
GAM3399  OAS3     3'  TGTGTGGCAGCAGCCAGGGCC  76391    CA   A  TG  _
                                TG  TGG AG  GTT GGGCC
                                ||  ||| ||  ||| |||||
                                AC  ACC TC  CGG CCCGG
                                 AC   G  GT   T
GAM3399  P2RY6    3'  TGCATGGAGCATACCTGGG   76392         A_   G
                                TGCATGGA  GTG TTGGG
                                ||||||||  ||| |||||
                                ACGTACCT  TAT GACCC
                                     CG   G
GAM3399  PAX5     3'  TGCTTGGAAGTGGAGGGCC   76393     A        TT
                                TGC TGGAAGTGG  GGGCC
                                ||| |||||||||  |||||
                                ACG ACCTTCACC  CCCGG
                                  A        T_
GAM3399  PFKFB4   3'  TGCTGGGCAGCTGGGCC    76394     A   AA TG
                                TGC TGG  G  GTTGGGCC
                                ||| |||  |  ||||||||
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                                ACG ACC  C  CGACCCGG
                                  _  __ GT
GAM3399  PRDM2    3'  GCATGCGCGTTGGGCC     76395      GAA   G
                                GCATG   GTG TTGGGCC
                                |||||   ||| |||||||
                                CGTAC   CGC AACCCGG
                                   G__   _
GAM3399  RP2      3'  TGCTGGTGATTGGGC      76396     A   AAG
                                TGC TGG   TGGTTGGGC
                                ||| |||   |||||||||
                                ACG ACC   ACTAACCCG
                                  _  ___
GAM3399  SLC14A1  3'  TGCAGGAAGTGGGGAC     76397      T      TT
                                TGCA GGAAGTGG  GGGC
                                |||| ||||||||  ||||
                                ACGT CCTTCACC  CCTG
                                  _      __
GAM3399  SLC2A3   3'  TGTATGGAAGTGAGGAAGG   76398    C       _ TT
                                TG ATGGAAGTG G  GGG
                                || |||||||| |  |||
                                AC TACCTTCAC C  TCC
                                 A        T CT
GAM3399  TBX2     3'  TGCAGGGACCGCTGGGCC    76399     T   AGTG
                                TGCA GGA    GTTGGGCC
                                |||| |||    ||||||||
                                ACGT CCT    CGACCCGG
                                  C   GG__
GAM3399  TCF2     3'  TGCATAGAAGGGAAACTGGGC  76400          T ___
                                TGCATGGAAG GG   TTGGGC
                                |||||||||| ||   ||||||
                                ACGTATCTTC CC   GACCCG
                                      _ TTT
GAM3399  TNFAIP1  3'  TGCAGGGAAGTGGGGA      76401      T      TT
                                TGCA GGAAGTGG  GGG
                                |||| ||||||||  |||
                                ACGT CCTTCACC  CCT
                                  C       __
GAM3399  TPM4     3'  ATGGAAATGAAGTTGGGCC   76402          __
                                ATGGAAGTG  GTTGGGCC
                                |||||||||  ||||||||
                                TACCTTTAC  CAACCCGG
                                     TT
GAM3399  ZNF42    5'  TGCAGGGAAGTGGGTGGG    76403      T      T
                                TGCA GGAAGTGG TGGG
                                |||| |||||||| ||||
                                ACGT CCTTCACC ACCC
                                  C       C
GAM3399  BRD4     3'  TGCAGGAGGGCCAGGCC     76404      T   A T   TG
                                TGCA GGA G GGT  GGCC
                                |||| ||| | |||  ||||
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                                ACGT CCT C CCG  CCGG
                                  _  _ _  GT
GAM3399 C11orf11 5' TGCATGGAGTCACGGGGC   76405       A  G TT
                                TGCATGGA GT G  GGGC
                                |||||||| || |  ||||
                                ACGTACCT CA T  CCCG
                                    _  G GC
GAM3399 C11orf9  3' TACATGGAGTGGGGC      76406       A   TTG
                                TGCATGGA GTGG   GGC
                                |||||||| ||||   |||
                                ATGTACCT CACC   CCG
                                  _   ____
GAM3399 CECR6    3' TGCATGGAGTGTAAAC      76407       A   GT
                                TGCATGGA GTG  TGGGC
                                |||||||| |||  |||||
                                ACGTACCT CAC  ATTTG
                                  _   __
GAM3399 CIDEB    5' TGCATGGAAGCTGAGAC     76408         GGTT
                                TGCATGGAAGT   GGGC
                                ||||||||||    ||||
                                ACGTACCTTCG   TCTG
                                    AC__
GAM3399 CST7     5' GCATGGAACAGTGGGC      76409       G   T
                                GCATGGAA TGGT GGGC
                                |||||||| |||| ||||
                                CGTACCTT GTCA CCCG
                                  _   _
GAM3399 DC-TM4F2 3' TGCATGGAGGGAGGC      76410       A T  TT
                                TGCATGGA G GG  GGGC
                                |||||||| | ||  ||||
                                ACGTACCT C CC  TCCG
                                  _ _  __
GAM3399 DDX34    3' TGCACGGAGGTGGGCAGGGC  76411       A   TT_
                                TGCATGGA GTGG   GGGC
                                |||||||| ||||   ||||
                                ACGTGCCT CACC   CCCG
                                    C   CGT
GAM3399 DDX35    3' TGCTGGAAGTGGCATGC     76412     A       TGG
                                TGC TGGAAGTGGT   GC
                                ||| ||||||||||   ||
                                ACG ACCTTCACCG   CG
                                  _        TA_
GAM3399 DKFZP564I052 3' TGCTGGAAAGTAGTTTGGG  76413     A   _    _
                                TGC TGGAA GTGGTT GGG
                                ||| ||||| |||||| |||
                                ACG ACCTT CATCAA CCC
                                  _    T     A
GAM3399 DKFZp586G0123 5' TGCCTGGAAACTGGGCC    76414     A    TGG
                                TGC TGGAAG   TTGGGCC
                                ||| ||||||   |||||||
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                                ACG ACCTTT   GACCCGG
                                  G     ___
GAM3399  DKFZP586J0619 3'  TGCATGGAGCGCAGGGCC    76415        A   GTT
                                TGCATGGA GTG   GGGCC
                                |||||||| |||   |||||
                                ACGTACCT CGC   CCCGG
                                     _   GT_
GAM3399  DKFZP586J1624 3'  TGCTGGGCTGCTGGGCC     76416     A   AA  G
                                TGC TGG  GT GTTGGGCC
                                ||| |||  || ||||||||
                                ACG ACC  CG CGACCCGG
                                  _   __ A
GAM3399  DKFZp761G2113 3'  TGCATGGAAGGAAAAGCC    76417          T  TT
                                TGCATGGAAG GG  GGGCC
                                |||||||||| ||  |||||
                                ACGTACCTTC CT  TTCGG
                                     _  T_
GAM3399  DPCR1    3'  GCATGGAAGAGCCAGGGC    76418         T   _
                                GCATGGAAG GGTT GGGC
                                ||||||||| |||| ||||
                                CGTACCTTC TCGG CCCG
                                     _   T
GAM3399  EPSIN    5'  TGCATGCAAAGACTGGGC    76419       G   T GT
                                TGCATG AAG G  TGGGC
                                |||||| ||| |  |||||
                                ACGTAC TTT C  ACCCG
                                   G   _ TG
GAM3399  FBXO24   3'  TGCATGAAGATTCGGCC     76420        AGT   G
                                TGCATGGA   GGTT GGCC
                                ||||||||   |||| ||||
                                ACGTACTT   CTAA CCGG
                                     ___   G
GAM3399  FLJ10504  3'  TGCATGAAGACACTGGGC    76421       G   TGG
                                TGCATG AAG   TTGGGC
                                |||||| |||   ||||||
                                ACGTAC TTC   GACCCG
                                   _   TGT
GAM3399  FLJ10521  3'  GCATGGAGAGCAGCGGGCC   76422        _  TG  T
                                GCATGGA AG  GT GGGCC
                                ||||||| ||  || |||||
                                CGTACCT TC  CG CCCGG
                                   C  GT  _
GAM3399  FLJ10743  3'  TGCCTGGGGACTTGGGCC    76423     A   AAGT  __
                                TGC TGG   GG  TTGGGCC
                                ||| |||   ||  |||||||
                                ACG ACC   CC  AACCCGG
                                  G   ____  TG
GAM3399  FLJ12056  3'  TGCCTGGAAGTAGGGC      76424     A       GTT
                                TGC TGGAAGTG   GGGC
                                ||| ||||||||   ||||
```

```
                                ACG ACCTTCAT   CCCG
                                  G      ___
GAM3399  FLJ12057  3'  GCTGTCAGTGGTTGGGC     76425    A  GA
                                GC TG  AGTGGTTGGGC
                                || ||  ||||||||||
                                CG AC  TCACCAACCCG
                                 _  AG
GAM3399  FLJ14525  3'  TGCTGGGTGCTGGGC       76426    A   AA   G
                                TGC TGG  GTG TTGGGC
                                ||| |||  ||| ||||||
                                ACG ACC  CAC GACCCG
                                  _  __  _
GAM3399  FLJ14950  3'  TGCAGGACAGCTGGG       76427     T   AG
                                TGCA GGA  TGGTTGGG
                                |||| |||  ||||||||
                                ACGT CCT  GTCGACCC
                                  _  __
GAM3399  FLJ20005  3'  TGCATGGGCGGCTAAGGC    76428       AA     _
                                TGCATGG  GTGGTTG GGC
                                |||||||  ||||||| |||
                                ACGTACC  CGCCGAT CCG
                                    __      T
GAM3399  FLJ22056  3'  TGCTGGAACGGGGGC       76429    A    G   TT
                                TGC TGGAA TGG  GGGC
                                ||| ||||| |||  ||||
                                ACG ACCTT GCC  CCCG
                                  _    _  __
GAM3399  FLJ23519  3'  TGCCTGGAGGTGCTGGGCC   76430    A   A   G
                                TGC TGGA GTG TTGGGCC
                                ||| |||| ||| |||||||
                                ACG ACCT CAC GACCCGG
                                  G   C  _
GAM3399  FLJ31300  3'  TGCATGGAGGCTGGCAGGTGGC 76431        A _   TG__
            C                    TGCATGGA G TGGT   GGCC
                                |||||||| | ||||   ||||
                                ACGTACCT C ACCG   CCGG
                                     C G   TCCA
GAM3399  I-4     5'  TGCGAGAGAGTTGGGCC     76432    AT GA  T
                                TGC  G  AG GGTTGGGCC
                                |||  |  || |||||||||
                                ACG  C  TC TCAACCCGG
                                  __ TC  _
GAM3399  IMAGE3451454 3'  TGGATGGAAACGGGGCC    76433    C       TTG
                                TG ATGGAAGTGG   GGCC
                                || ||||||||||   ||||
                                AC TACCTTTGCC   CCGG
                                 C        ___
GAM3399  JDD1    3'  TGAATGTCTTCAGTTGGGCC  76434    C   GAAG
                                TG ATG    TGGTTGGGCC
                                || |||    ||||||||||
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                                AC TAC    GTCAACCCGG
                                 T  AGAA
GAM3399 KCND1    5' TGCCTGGAAGTGGGGG     76435     A       TT
                                TGC TGGAAGTGG  GGG
                                ||| |||||||||  |||
                                ACG ACCTTCACC  CCC
                                  G       __
GAM3399 KIAA0064 3' TGATGGGGAACTGGGCC     76436    C    AAGT __
                                TG ATGG    GG  TTGGGCC
                                || ||||    ||  |||||||
                                AC TACC    CC  GACCCGG
                                 _   _____ TT
GAM3399 KIAA0125 3' TGCAGGAAGCAAGAGGCC    76437     T     TG TT
                                TGCA GGAAG  G  GGGCC
                                |||| |||||  |  |||||
                                ACGT CCTTC  T  TCCGG
                                  _    GT C_
GAM3399 KIAA0446 3' TGCTTGGAGTCTGGGC      76438     A    A  GG
                                TGC TGGA GT  TTGGGC
                                ||| |||| ||  ||||||
                                ACG ACCT CA  GACCCG
                                  A   _ __
GAM3399 KIAA0478 3' GCATGGAAATGAGGGC      76439           TT
                                GCATGGAAGTGG  GGGC
                                ||||||||||||  ||||
                                CGTACCTTTACT  CCCG
                                             __
GAM3399 KIAA0493 3' TGCAGGAAGTGGAACACC    76440     T       TTGG
                                TGCA GGAAGTGG    GCC
                                |||| ||||||||    |||
                                ACGT CCTTCACC    TGG
                                  _       TTG_
GAM3399 KIAA0700 3' TGCAGGAACACGACTGGGCC  76441     T   AG  GT
                                TGCA GGA  TG  TGGGCC
                                |||| |||  ||  ||||||
                                ACGT CTT  GC  ACCCGG
                                  C   GT  TG
GAM3399 KIAA1010 3' GCATGGAACATGGGGCC     76442         _   TTG
                                GCATGGAA GTGG   GGCC
                                |||||||| ||||   ||||
                                CGTACCTT TACC   CCGG
                                     G   ___
GAM3399 KIAA1016 3' TGTATAGATCAAGTTGGGCC  76443    C    AGT
                                TG ATGGA   GGTTGGGCC
                                || |||||   |||||||||
                                AC TATCT   TCAACCCGG
                                 A    AGT
GAM3399 KIAA1018 3' TGCTATGGGGAGCTGGGCC   76444     _   AAGT
                                TGC ATGG    GGTTGGGCC
                                ||| ||||    |||||||||
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                              ACG TACC   TCGACCCGG
                                A   CC__
GAM3399 KIAA1052 3' TGATGGAAGCGGGGC      76445    C       TTG
                              TG ATGGAAGTGG   GGC
                              || ||||||||||   |||
                              AC TACCTTCGCC   CCG
                               _       ____
GAM3399 KIAA1068 3' TGCGTGGTGGCCGGGC     76446    A   AAG
                              TGC TGG   TGGTTGGGC
                              ||| |||   |||||||||
                              ACG ACC   ACCGGCCCG
                                C  ____
GAM3399 KIAA1161 5' TGCATGAAGACTGGGGGC    76447       AG_   TT
                              TGCATGGA   TGG  GGGC
                              ||||||||   |||  ||||
                              ACGTACTT   ACC  CCCG
                                   CTG   __
GAM3399 KIAA1169 5' TGCATAGAAGAGACGGC     76448        T  TTG
                              TGCATGGAAG GG   GGC
                              ||||||||||  ||   |||
                              ACGTATCTTC CT   CCG
                                    T  G__
GAM3399 KIAA1184 3' TGCGGGGAGTGGGCTGGGC   76449     AT   A   _
                              TGC  GGA GTGG TTGGGC
                              |||  ||| |||| ||||||
                              ACG  CCT CACC GACCCG
                                CC   _    C
GAM3399 KIAA1243 3' TGCATGGAGGGTAAGAGC    76450        A T   T_
                              TGCATGGA G GGT  GGGC
                              |||||||| | |||  ||||
                              ACGTACCT C CCA  CTCG
                                   _ _   TT
GAM3399 KIAA1511 3' TGCATAGACTAGACTTGGG   76451        AGT  _
                              TGCATGGA   GG TTGGG
                              ||||||||   || |||||
                              ACGTATCT   CT AACCC
                                   GAT  G
GAM3399 KIAA1877 3' TGCAGGGAAACAAAGGGCC   76452     T    TG TT
                              TGCA GGAAG  G  GGGCC
                              |||| |||||  |  |||||
                              ACGT CCTTT  T  CCCGG
                                C    GT T_
GAM3399 KIAA1954 3' TACAATGAAGTGGTTGGGC   76453     TG
                              TGCA  GAAGTGGTTGGGC
                              ||||  ||||||||||||
                              ATGT  CTTCACCAACCCG
                                TA
GAM3399 KIAA1970 3' TGCATGGAGGGAAGACC     76454        AGT  TT
                              TGCATGGA   GG  GGGCC
                              ||||||||   ||  |||||
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                                ACGTACCT  CC  TCTGG
                                    ___  CT
GAM3399 KIAA1972 3' CATGGAAGTACCACAGGCC  76455       GT_
                                CATGGAAGTG  TGGGCC
                                ||||||||||  ||||||
                                GTACCTTCAT  GTCCGG
                                     GGT
GAM3399 LIN-28   3' TGCAGGAAATGAGGGCC    76456    T     TT
                                TGCA GGAAGTGG  GGGCC
                                |||| ||||||||  |||||
                                ACGT CCTTTACT  CCCGG
                                  _     __
GAM3399 MBLR     3' TGCATGGAGGTGAGC      76457      AGT  T
                                TGCATGGA  GGT GGGC
                                ||||||||  ||| ||||
                                ACGTACCT  CCA CTCG
                                    ___  _
GAM3399 MGC11352 5' TGCATGGAGGGAGGC      76410      A T  TT
                                TGCATGGA G GG  GGGC
                                |||||||| | ||  ||||
                                ACGTACCT C CC  TCCG
                                    _ _ __
GAM3399 MGC20253 3' TACATGGAAACCGGGC     76458       TGG
                                TGCATGGAAG  TTGGGC
                                ||||||||||  ||||||
                                ATGTACCTTT  GGCCCG
                                    ___
GAM3399 MGC2452  5' TGCGGGGAAGTGGTGGC    76459    AT      TG
                                TGC  GGAAGTGGT  GGC
                                |||  |||||||||  |||
                                ACG  CCTTCACCA  CCG
                                  CC       __
GAM3399 MMP28    3' TGATGGAGCCATCGGGCC   76460   C   A  G
                                TG ATGGA GT GTTGGGCC
                                || ||||| || ||||||||
                                AC TACCT CG TAGCCCGG
                                 _    _ G
GAM3399 PI4KII   3' TGCATGGAGCTCCAGCC    76461      A  GG  G
                                TGCATGGA GT  TT GGCC
                                |||||||| ||  || ||||
                                ACGTACCT CG  AG TCGG
                                    _ __ G
GAM3399 PP3501   3' TGCATAGAGCTGGGGGC    76462      AG  TT
                                TGCATGGA  TGG  GGGC
                                ||||||||  |||  ||||
                                ACGTATCT  ACC  CCCG
                                    CG  __
GAM3399 PPP1R10  5' ACACAAGTGGTTGGGC     76463    GG
                                GCAT  AAGTGGTTGGGC
                                ||||  ||||||||||||
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                                TGTG  TTCACCAACCCG
                                  __
GAM3399  PRKWNK2   5'  TGCGATGGGGTCCGGGCC    76464    _   AAGT   _
                                TGC ATGG   GGTT GGGCC
                                ||| ||||   |||| |||||
                                ACG TACC   CCAG CCCGG
                                  C   ____   G
GAM3399  PRO2015   5'  TGAATGGAAATGCTGGGC    76465    C       G
                                TG ATGGAAGTG TTGGGC
                                || |||||||| ||||||
                                AC TACCTTTAC GACCCG
                                 T       _
GAM3399  PRRDH     3'  TGCATGGAGGTGGGGGGTGGGC 76466        A   T___
                                TGCATGGA GTGG   TGGGC
                                |||||||| ||||   |||||
                                ACGTACCT CACC   ACCCG
                                     C   CCCC
GAM3399  PTP4A1    5'  TGCATAGAGGTCGTGC     76467        AGT   G
                                TGCATGGA   GGTTG GC
                                ||||||||   ||||| ||
                                ACGTATCT   CCAGC CG
                                     ___    A
GAM3399  RASGRP4   3'  TGCAGGAAGGCCAGGCC    76468     T   GT   TG
                                TGCA GGAA  GGT  GGCC
                                |||| ||||  |||  ||||
                                ACGT CCTT  CCG  CCGG
                                  _   __  GT
GAM3399  RoXaN     3'  TGCAGGGCCCAGTTGGGC    76469     T  AAG
                                TGCA GG   TGGTTGGGC
                                |||| ||   |||||||||
                                ACGT CC   GTCAACCCG
                                  C  GG_
GAM3399  RPP14     3'  TGCATGAAGCATAAGGCC    76470      G    GTT
                                TGCATG AAGTG   GGGCC
                                |||||| |||||   |||||
                                ACGTAC TTCGT   TCCGG
                                   _    AT_
GAM3399  SEMA4G    5'  TGCATAGAAGTGTGTACGGC   76471          _ TG
                                TGCATGGAAGTG GT  GGC
                                |||||||||||| ||  |||
                                ACGTATCTTCAC CA  CCG
                                       A  TG
GAM3399  SIAT4A    3'  TGTGTGGAGGTTGAACC     76472    CA   AGT
                                TG  TGGA   GGTTGGGCC
                                ||  ||||   |||||||||
                                AC  ACCT   CCAACTTGG
                                 AC   ___
GAM3399  SLC25A21  5'  TGCTGGAAAGCGAGGG      76473     A   _   TT
                                TGC TGGAA GTGG  GGG
                                ||| ||||| ||||  |||
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                                ACG ACCTT CGCT  CCC
                                  _    T   __
GAM3399  SLC26A10  5'  TGCATGGATGGAGGC      76474        AG   TT
                                TGCATGGA  TGG  GGGC
                                ||||||||  |||  ||||
                                ACGTACCT  ACC  TCCG
                                      __  __
GAM3399  STMN3     5'  TGCTGGCGGCGGTTGGGCC   76475     A   AA
                                TGC TGG  GTGGTTGGGCC
                                ||| |||  ||||||||||
                                ACG ACC  CGCCAACCCGG
                                  _  GC
GAM3399  TRAF4     3'  TGTGTAGAAGGCTGGGC     76476     CA    GT
                                TG  TGGAA  GGTTGGGC
                                ||  |||||  ||||||||
                                AC  ATCTT  CCGACCCG
                                  AC    __
GAM3399  ZNF31     3'  TGCATGGAGATTCTGGCC     76477        AGT   G_
                                TGCATGGA   GGTT  GGCC
                                ||||||||   ||||  ||||
                                ACGTACCT   CTAA  CCGG
                                     ____   GA
GAM3399  LOC115129 3'  TGCTGGGAGTACAGGC      76478     A  A   GT
                                TGC TGG AGTG  TGGGC
                                ||| ||| ||||  |||||
                                ACG ACC TCAT  GTCCG
                                  _  C   __
GAM3399  LOC128954 5'  TGATGGGAGCAGCTGGGC    76479    C   A  TG
                                TG ATGG AG  GTTGGGC
                                || |||| ||  |||||||
                                AC TACC TC  CGACCCG
                                  _   C  GT
GAM3399  LOC129303 3'  TGCTGTGGAGGCCGGGCC    76480     A_   AGT
                                TGC  TGGA   GGTTGGGCC
                                |||  ||||   |||||||||
                                ACG  ACCT   CCGGCCCGG
                                  AC   ____
GAM3399  LOC144195 3'  TGTATGGAAGTGAGGAAGG   76398    C       _ TT
                                TG ATGGAAGTG G  GGG
                                || |||||||| |  |||
                                AC TACCTTCAC C  TCC
                                  A        T CT
GAM3399  LOC144594 3'  TGGATGAAGTTGGTTGGG    76481    C    AG
                                TG ATGGA  TGGTTGGG
                                || |||||  ||||||||
                                AC TACTT  ACCAACCC
                                  C    CA
GAM3399  LOC145481 3'  TGCTGGAAGCCGGGC       76482     A      GGT
                                TGC TGGAAGT   TGGGC
                                ||| |||||||   |||||
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                                ACG ACCTTCG   GCCCG
                                  _     ___
GAM3399  LOC146287 5'  TGCGTGAAAGTTAGGC      76483     A      GGT
                                TGC TGGAAGT   TGGGC
                                ||| |||||||   |||||
                                ACG ACTTTCA   ATCCG
                                  C     ___
GAM3399  LOC146429 5'  TGCGTGGTGGTGGGTGCC    76484     A   AAG    T _
                                TGC TGG   TGGT GG GCC
                                ||| |||   |||| || |||
                                ACG ACC   ACCA CC CGG
                                  C  ___   C A
GAM3399  LOC148398 5'  TGTGTGGAAGTAGGGGC     76485    CA       TT
                                TG  TGGAAGTGG  GGGC
                                ||  |||||||||  ||||
                                AC  ACCTTCATC  CCCG
                                  AC       __
GAM3399  LOC149577 5'  TGTATGTAAGTTACTGGGCC   76486    C   G    GG
                                TG ATG AAGT  TTGGGCC
                                || ||| ||||  |||||||
                                AC TAC TTCA  GACCCGG
                                  A   A    AT
GAM3399  LOC149650 3'  TGCATGGGGTTGTGGGCC    76487       AAGT   __
                                TGCATGG    GGT  TGGGCC
                                |||||||    |||  ||||||
                                ACGTACC    CCA  ACCCGG
                                     _____   AC
GAM3399  LOC150378 5'  TGCATGAAAAGGGGGGCC    76488         T  TT
                                TGCATGGAAG GG  GGGCC
                                ||||||||||  ||  |||||
                                ACGTACTTTT CC  CCCGG
                                      _  C_
GAM3399  LOC150819 5'  TGGAAGTGGGATGAGGCC    76489         T_  _
                                TGGAAGTGG  TG GGCC
                                |||||||||  ||  ||||
                                ACCTTCACC  AC CCGG
                                     CT  T
GAM3399  LOC154084 3'  CATGGAAAGAGGGGCC      76490        T  TT
                                CATGGAAG GG  GGGCC
                                ||||||||  ||  |||||
                                GTACCTTT TC  CCCGG
                                     C  __
GAM3399  LOC157280 3'  TGTGTGGCGGCTGGTGGGCC   76491    CA   AA _   T
                                TG  TGG  G TGGT GGGCC
                                ||  |||  | |||| |||||
                                AC  ACC  C ACCA CCCGG
                                  AC   GC G   _
GAM3399  LOC157421 5'  TGCAGGAAGCGAGGC       76492      T      GTT
                                TGCA GGAAGTG   GGGC
                                ||||  |||||||   ||||
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                                ACGT CCTTCGC   TCCG
                                  _     ___
GAM3399  LOC163412 5'  TGCAGGAAGTGGGAGATGC    76493      T       TT  _
                                TGCA GGAAGTGG  GG GC
                                |||| ||||||||  || ||
                                ACGT CCTTCACC  CT CG
                                  _       CT  A
GAM3399  LOC164537 5'  TGCAGGAAACCTGGGCC     76494      T    TGG
                                TGCA GGAAG   TTGGGCC
                                |||| |||||   |||||||
                                ACGT CCTTT   GACCCGG
                                  _    G__
GAM3399  LOC170063 3'  TGCATGAAAGTCTTGGG     76495          GG
                                TGCATGGAAGT  TTGGG
                                ||||||||||  |||||
                                ACGTACTTTCA  AACCC
                                       G_
GAM3399  LOC199718 3'  TGCATGGAGGTTGAA       76496        AGT
                                TGCATGGA   GGTTGGG
                                ||||||||   |||||||
                                ACGTACCT   CCAACTT
                                    ___
GAM3399  LOC203378 5'  TGTATGGAAGTTAGCAGC    76497    C       _  TG
                                TG ATGGAAGT GGT  GGC
                                || |||||||| |||  |||
                                AC TACCTTCA TCG  TCG
                                 A       A  __
GAM3399  LOC219690 3'  TGCGTGGAAGTGAGGGAGC   76498     A       TT
                                TGC TGGAAGTGG  GGGC
                                ||| |||||||||  ||||
                                ACG ACCTTCACT  CTCG
                                  C        CC
GAM3399  LOC221466 3'  TGCATGGAGACCTAGAGGGCC  76499         AG__   TT
                                TGCATGGA    TGG  GGGCC
                                ||||||||    |||  |||||
                                ACGTACCT    ATC  CCCGG
                                     CTGG   T_
GAM3399  LOC221486 3'  GCATGGAAGGGAGGC       76500         T  TT
                                GCATGGAAG GG  GGGC
                                ||||||||| ||  ||||
                                CGTACCTTC CC  TCCG
                                    _ __
GAM3399  LOC221584 3'  TGTGTAGTAGAGGTTGGGC   76501    CA   A  T
                                TG  TGG AG GGTTGGGC
                                ||  ||| || ||||||||
                                AC  ATC TC CCAACCCG
                                 AC   A  T
GAM3399  LOC222159 5'  TGCATTGAGATTGGGCC     76502       G  AGT
                                TGCAT GA   GGTTGGGCC
                                ||||| ||   |||||||||
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                                ACGTA CT   CTAACCCGG
                                  A ___
GAM3399  LOC222999 5'  TGCATGAGGCTGGGC       76503        AAGT
                                TGCATGG    GGTTGGGC
                                |||||||    ||||||||
                                ACGTACT    CCGACCCG
                                    ____
GAM3399  LOC254159 5'  GCATGGGGGGCTGGGCC     76504        AAGT
                                GCATGG    GGTTGGGCC
                                ||||||    |||||||||
                                CGTACC    CCGACCCGG
                                   CC__
GAM3399  LOC254617 5'  TGCTGGGCTGCTGGGCC     76416     A   AA  G
                                TGC TGG  GT GTTGGGCC
                                ||| |||  || ||||||||
                                ACG ACC  CG CGACCCGG
                                  _  __  A
GAM3399  LOC255448 3'  TGTGTGGCGGCTGGTGGGCC   76491    CA   AA _    T
                                TG  TGG  G TGGT GGGCC
                                ||  |||  | |||| |||||
                                AC  ACC  C ACCA CCCGG
                                 AC   GC G   _
GAM3399  LOC256073 3'  TGCAGGAAGTGATGC       76505      T        TGG
                                TGCA GGAAGTGGT   GC
                                |||| |||||||||   ||
                                ACGT CCTTCACTA   CG
                                  _       ___
GAM3399  LOC256942 3'  TGGATGGAGGTGGGGGC     76506    C     A    TT
                                TG ATGGA GTGG  GGGC
                                || ||||| ||||  ||||
                                AC TACCT CACC  CCCG
                                 C    C   __
GAM3399  LOC257464 3'  GCATGGAAAGAGGGC       76507          T  TT
                                GCATGGAAG GG  GGGC
                                ||||||||| ||  ||||
                                CGTACCTTT CT  CCCG
                                    _ __
GAM3399  LOC50999  3'  ATGGAAATCGGTTGGGCC    76508          _
                                ATGGAAGT GGTTGGGCC
                                |||||||| |||||||||
                                TACCTTTA CCAACCCGG
                                    G
GAM3399  LOC90538  3'  TGCATGGAGAAATTAGG     76509         A TG
                                TGCATGGA G  GTTGGG
                                |||||||| |  ||||||
                                ACGTACCT C  TAATCC
                                    _ TT
GAM3399  LOC90785  3'  TGCAGGAAGGCTGGGC      76510      T   GT
                                TGCA GGAA  GGTTGGGC
                                |||| ||||  ||||||||
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                                ACGT CCTT  CCGACCCG
                                  _   __
GAM3399 LOC91748 5' TGCTGGAAGCCGGGC      76482     A      GGT
                                TGC TGGAAGT   TGGGC
                                ||| |||||||   |||||
                                ACG ACCTTCG   GCCCG
                                  _     ____
GAM3400 IL12RB2  3' TTTACATTGGTGTTTACCAGTG 76513          C__     TA_
           TCTTT                 TTTACATTGG   TTACTA   TCTTT
                                ||||||||||   ||||||  |||||
                                AAATGTAACC   AATGGT   AGAAA
                                     ACA     CAC
GAM3400 MGC32104 3' TTTACGTTGATTCCACATCTTT 76514      A   C  A
                                TTTAC TTGG TT CTATATCTTT
                                ||||| |||| || ||||||||||
                                AAATG AACT AA GGTGTAGAAA
                                   C   _ _
GAM3401 ADM      3' TCCGGGGGTCTCAGCATTCATT 76517     TAA    TTTA
           T                    TCCG   GTCTT   GTTCATTT
                                ||||   |||||   ||||||||
                                AGGC   CAGAG   TAAGTAAA
                                  CCC    TCG_
GAM3401 GATM     3' TAAGTCTTTCTCTCATTT    76518          AG
                                TAAGTCTTTTT  TTCATTT
                                ||||||||||  |||||||
                                ATTCAGAAAGA  GAGTAAA
                                          __
GAM3401 VTN      5' AGTCTTAGTTCATTT      76519      TTT
                                AGTCT   TAGTTCATTT
                                |||||   ||||||||||
                                TCAGA   ATCAAGTAAA
                                  ____
GAM3401 SMAP1    3' GTAAGTCTTCAAGTCATTT    76520         TT   T
                                GTAAGTCTTT  AGT CATTT
                                ||||||||||  ||| |||||
                                CATTCAGAAG  TCA GTAAA
                                     T_   _
GAM3402 SIGLEC6  3' TGGGCTATATAATATTG     76523        GCCGG
                                TGGGCTATG    AATATTG
                                |||||||||    |||||||
                                ACCCGATAT    TTATAAC
                                     A_____
GAM3402 FLJ22969 3' TGTGGGCTGTGGTGACCTGG  76524        A___    _
                                TGTGGGCT    TGGCC GG
                                ||||||||    ||||| ||
                                ACACCCGA    ACTGG CC
                                    CACC    A
GAM3402 HPCAL4   3' TGGGCTGTCTGAGAATATTGG 76525       ATGGCC
                                TGGGCT     GGAATATTGG
                                ||||||     ||||||||||
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                                ACCCGA     TCTTATAACC
                                   CAGAC_
GAM3402  LOC149302 5'  GTGGGCTATTCAGAGATATTGG 76526        GGC   _
                                GTGGGCTAT   CGGA ATATTGG
                                |||||||||   |||| |||||||
                                CACCCGATA   GTCT TATAACC
                                     A__   C
GAM3402  LOC154739 5'  TATGGGCTATGGTTGATGTGG  76527         CCG  ATAT
                                TGTGGGCTATGG   GA   TGG
                                ||||||||||||  ||   |||
                                ATACCCGATACC   CT   ACC
                                      AA_  AC__
GAM3402  LOC203276 3'  TATGGGCTATGGCTGATGTGG  76528          CG  ATAT
                                TGTGGGCTATGGC  GA   TGG
                                ||||||||||||| ||   |||
                                ATACCCGATACCG  CT   ACC
                                      A_  AC__
GAM3402  LOC203305 3'  TATGGGCTATGGCTGATGTGG  76528          CG  ATAT
                                TGTGGGCTATGGC  GA   TGG
                                ||||||||||||| ||   |||
                                ATACCCGATACCG  CT   ACC
                                      A_  AC__
GAM3402  LOC254243 3'  TATGGGCTATGGCTGATGTGG  76528          CG  ATAT
                                TGTGGGCTATGGC  GA   TGG
                                ||||||||||||| ||   |||
                                ATACCCGATACCG  CT   ACC
                                      A_  AC__
GAM3402  LOC90038  3'  TATGGGCTATGGCTGATGTGG  76528          CG  ATAT
                                TGTGGGCTATGGC  GA   TGG
                                ||||||||||||| ||   |||
                                ATACCCGATACCG  CT   ACC
                                      A_  AC__
GAM3403  ANGPT1    3'  GACACATAAATATAAAAAA   76531      TG
                                GATAT  ATAAATATAAAAAA
                                |||||  ||||||||||||||
                                CTGTG  TATTTATATTTTTT
                                   __
GAM3403  ITGA9     3'  ATAATATCGATACAAATATAAA 76532          __
              A                  ATGATATTGATA  AATATAAAA
                                 ||||||||||||  |||||||||
                                 TATTATAGCTAT  TTATATTTT
                                       GT
GAM3403  MAN1A1    3'  ATGATATTGAAAAACAGAAA   76533         T    T
                                ATGATATTGA AAATA AAA
                                |||||||||| ||||| |||
                                TACTATAACT TTTGT TTT
                                      T    C
GAM3403  ROBO1     3'  ATGATATTCATAAAATGACAAA 76534        G    T__
              AAA                  ATGATATT ATAAA   ATAAAAAA
                                   |||||||| |||||   ||||||||
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                                TACTATAA TATTT   TGTTTTTT
                                    G    TAC
GAM3403  ROBO1    3'  ATGATATTCATAAAATGACAAA 76534        G    T__
             AAA                  ATGATATT ATAAA   ATAAAAAA
                                ||||||||| |||||   ||||||||
                                TACTATAA TATTT   TGTTTTTT
                                    G    TAC
GAM3403  BCMP1    3'  ATGATATTGACAGCCAAAA   76535          AATA
                                ATGATATTGATA   TAAAA
                                ||||||||||||   |||||
                                TACTATAACTGT   GTTTT
                                      CG__
GAM3403  KIAA1164 3'  TGATATTGATAGGTTATAA   76536          AA_
                                TGATATTGATA   TATAA
                                ||||||||||   |||||
                                ACTATAACTAT   ATATT
                                      CCA
GAM3403  PFDN4    3'  TGATATTGATAGATATGTAAAA 76537          A   __
             AA                   TGATATTGATA ATA  TAAAAAA
                                |||||||||| |||  |||||||
                                ACTATAACTAT TAT  ATTTTTT
                                      C   AC
GAM3403  SLC26A7  3'  ATGCATTGAAAAATATAAAAAA 76538     A     T
             A                    ATG TATTGA AAATATAAAAAAA
                                ||| |||||| ||||||||||||
                                TAC GTAACT TTTATATTTTTTT
                                  _     T
GAM3404  CTNNB1   3'  TAAAAATTAGAAATTGCTGTA  76541       T       AATC
                                TGAAA GTTGGAGA    GCTGTA
                                ||||| ||||||||    ||||||
                                ATTTT TAATCTTT    CGACAT
                                  _       AA__
GAM3404  HIVEP3   5'  TGAAGGTTGGAGACATCTGT   76542      AT       AATCG
                                TGAA  GTTGGAGA    CTGT
                                ||||  ||||||||    ||||
                                ACTT  CAACCTCT    GACA
                                  C_       GTA__
GAM3404  MOCS1    5'  TGCAATGTTGGGGAAGCTG    76543    A       A   ATC
                                TG AATGTTGG GAA   GCTG
                                || |||||||| |||   ||||
                                AC TTACAACC CTT   CGAC
                                 G       C   ___
GAM3404  RGS6     3'  TGTTGGAATACAACTGTA     76544         AA  C
                                TGTTGGAG  AT GCTGTA
                                ||||||||  || ||||||
                                ACAACCTT  TG TGACAT
                                    A_  T
GAM3404  GOLGB1   3'  TGAAGAGTTGGAGAGAAGACCT 76545      AT       AATCG_
             GTA                    TGAA  GTTGGAGA     CTGTA
                                ||||  ||||||||     |||||
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                                ACTT  CAACCTCT     GACAT
                                  CT       CTTCTG
GAM3404  HRD1     3'  TGAAGAGTTGGAGAGGAAGGCT 76546      AT       AATC_
             G                   TGAA  GTTGGAGA     GCTG
                                 ||||  ||||||||     ||||
                                ACTT  CAACCTCT     CGAC
                                  CT       CCTTC
GAM3404  KIAA0087 3'  GAAAAAAGAAATTGCTGT     76547      TGTT       C
                                GAAA    GGAGAAAT GCTGT
                                ||||    |||||||| |||||
                                CTTT    TTTCTTTA CGACA
                                  ____       A
GAM3404  KIAA1077 3'  TGGAATGTTGGTGGCTGT     76548     A       AGAAATC
                                TG AATGTTGG      GCTGT
                                || ||||||||      |||||
                                AC TTACAACC      CGACA
                                 C       AC_____
GAM3404  KIAA1535 5'  TAAAACCGGAAGTCGCTGT     76549       GT     AAA
                                TGAAAT  TGGAG   TCGCTGT
                                ||||||  |||||   |||||||
                                ATTTTG  GCCTT   AGCGACA
                                   __     C__
GAM3404  LOC133923 5'  TGGAATGTTGGAAAGTCCT     76550     A         AA  G
                                TG AATGTTGGAGA  TC CT
                                || ||||||||||  || ||
                                AC TTACAACCTTT  AG GA
                                 C          C_  _
GAM3405  MLLT4    3'  ATATCATTTAAGTACAATTT   76553
                                ATATCATTTAAGTATAGTTT
                                ||||||||||||||||||||
                                TATAGTAAATTCATGTTAAA

GAM3405  TPD52    3'  TACAGTATCATTTTACAGTTT  76554      A       AAG
                                TATA TATCATTT   TATAGTTT
                                ||||  ||||||||   ||||||||
                                ATGT ATAGTAAA   ATGTCAAA
                                  C       ___
GAM3406  CXCL16   5'  GACCGTGCGCTCAGTACTCGGC 76557         A  ____    CC
             C                   GACCGTGC CT    ACTC  GCC
                                 |||||||| ||    ||||  |||
                                CTGGCACG GA    TGAG  CGG
                                    C  GTCA    C_
GAM3406  LAMC1    5'  GACCGCGCTGCTCGCCGAC    76558        ACTA   CC
                                GACCGTGC    CTC  GCCGAC
                                ||||||||    |||  ||||||
                                CTGGCGCG    GAG  CGGCTG
                                    AC__    __
GAM3406  MYCL1    5'  GACCGGCTCCCCGCCG      76559       T  ACTAC
                                GACCG GC     TCCCGCCG
                                ||||| ||     ||||||||
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                                CTGGC CG    GGGGCGGC
                                  _ A____
GAM3406 SLC7A5   3' CGTGCGTGGGCCCCGCCGGCC 76560      ACTAC      A
                                CGTGC    TCCCGCCG CC
                                |||||    |||||||| ||
                                GCACG    GGGGCGGC GG
                                   CACCC       C
GAM3406 C22orf3  5' CCGCGTGACCCCTGCCGACC  76561      CACT    C
                                CCGTG   ACTCC GCCGACC
                                |||||   ||||| |||||||
                                GGCGC   TGGGG CGGCTGG
                                   AC__    A
GAM3406 FLJ10043 3' CGTGCACTACCATGCCCG    76562          ___
                                CGTGCACTACT   CCCG
                                ||||||||||   ||||
                                GCACGTGATGG   GGGC
                                      TAC
GAM3406 KIAA0562 3' GACCGTGCCTGTGCTGAC    76563        A  ACTCCC  C
                                GACCGTGC CT     GC GAC
                                |||||||| ||     || |||
                                CTGGCACG GA     CG CTG
                                     _ CA____  A
GAM3406 LOC116238 5' CCGGCCGCCTCTCCCGCCGGCC 76564     T  A_  A       A
                                CCG GC  CT CTCCCGCCG CC
                                ||| ||  || |||||||| ||
                                GGC CG  GG GAGGGCGGC GG
                                  _ GC  A       C
GAM3406 LOC123316 5' GTGCGCCTCCCGCCGAC     76565      ACTA
                                GTGC    CTCCCGCCGAC
                                ||||    ||||||||||
                                CACG    GAGGGCGGCTG
                                  CG__
GAM3406 LOC202915 3' CCTGTGTGGACCCCGCCGGCC  76566    _   CACT  T      A
                                CC GTG    AC CCCGCCG CC
                                || |||    || ||||||| ||
                                GG CAC    TG GGGCGGC GG
                                 A   ACC_ _      C
GAM3406 LOC255138 5' GACCGTGCCGCCGCTGAC    76567        ACTACTC    C
                                GACCGTGC      CCGC GAC
                                ||||||||      |||| |||
                                CTGGCACG      GGCG CTG
                                     GC_____    A
GAM3406 LOC91960  3' GACCGTGCACTCTCTTGGAGCC 76568          A   CC___
                                GACCGTGCACT CTC     GCC
                                |||||||||| |||     |||
                                CTGGCACGTGA GAG     CGG
                                      _  AACCT
GAM3407 C20orf110 3' GTTGCACCTAAGACATTATA   76571     _  AG_
                                GTT CG   AAGACATTATA
                                ||| ||   ||||||||||
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                                CAA GT   TTCTGTAATAT
                                  C  GGA
GAM3407  DKFZP564D1378 3'  CATGGTCTATAAGATATTATAA 76572        CGAG    C
             G                    TATGGTT    AAGA ATTATAAG
                                  |||||||    |||| ||||||||
                                  GTACCAG    TTCT TAATATTC
                                     ATA_    A
GAM3407  IL18BP    3'  GGAGGAGGAGGCATTATAAG   76573    TTC   A  A
                                  GG   GAG AG CATTATAAG
                                  ||   ||| || |||||||||
                                  CC   CTC TC GTAATATTC
                                   TC_   C  C
GAM3408  LDHA      3'  GTAATGTACACTACTGATATAG 76576        A__   CA
             T                    GTAATGTA   TAT  ATATAGT
                                  ||||||||   |||  |||||||
                                  CATTACAT   ATG  TATATCA
                                     GTG   AC
GAM3408  OXR1      3'  GTAAACGAATCAATATAGT    76577     TGTAAT
                                  GTAA     ATCAATATAGT
                                  ||||     ||||||||||
                                  CATT     TAGTTATATCA
                                    TGCT__
GAM3408  TYK2      5'  TGTAATGTTTCAATATAG     76578        AATA
                                  TGTAATGT    TCAATATAG
                                  ||||||||    |||||||||
                                  ACATTACA    AGTTATATC
                                     A___
GAM3408  KIAA1622  3'  ATATCTTCTAATATCAATATAG 76579      AATG
             T                    ATGT    TAATATCAATATAGT
                                  ||||    ||||||||||||||
                                  TATA    ATTATAGTTATATCA
                                    GAAG
GAM3408  LOC83690  3'  GTAATGTAATACATTAG      76580          T  ATA
                                  GTAATGTAATA CA   TAG
                                  |||||||||| ||   |||
                                  CATTACATTAT GT   ATC
                                        _  A__
GAM3409  ABCC11    3'  TCCAGGAGAAGTTCTCA      76583          CCTG
                                  TCCAGGAGAGG    TTCA
                                  ||||||||||    ||||
                                  AGGTCCTCTTC    GAGT
                                        AA__
GAM3409  ALEX3     5'  CCCGGGAGAGGCTTGGACCC   76584     A       C  TTC
                                  TCC GGAGAGGC TG   ACCC
                                  ||| ||||||| ||   ||||
                                  GGG CCTCTCCG AC   TGGG
                                    C       A  C__
GAM3409  AP1B1     3'  CCCAGGAGGGGGTGGTGCCC   76585        A  CC__
                                  TCCAGGAG GG    TGTTC
                                  ||||||| ||    |||||
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                                GGGTCCTC CC    ACGGG
                                     C  CACC
GAM3409  APRT     3'  CCCAGGAGAGGCGCTGAACCC  76586          _   TTC
                                TCCAGGAGAGGC CTG   ACCC
                                |||||||||||| |||   ||||
                                GGGTCCTCTCCG GAC   TGGG
                                      C   T__
GAM3409  ASIC4    3'  CCCAGGAGGGGTCCCAGACTC  76587        A  _   __
                                TCCAGGAG GG CCTG  TTC
                                |||||||| || ||||  |||
                                GGGTCCTC CC GGGT  GAG
                                     C  A    CT
GAM3409  BTG2     3'  CAGGAGAGGCCTTTTCAC    76588           G
                                CAGGAGAGGCCT TTCAC
                                |||||||||||| |||||
                                GTCCTCTCCGGA AAGTG
                                      A
GAM3409  C21orf2  3'  GAACAGGCCTGTTCATCC    76589     G        _
                                GGA AGGCCTGTTCA CC
                                ||| |||||||||| ||
                                CTT TCCGGACAAGT GG
                                  G          A
GAM3409  C4B      5'  TCCAAGAGAGGTTAGATCC    76590          CCT_
                                TCCAGGAGAGG    GTTC
                                ||||||||||    ||||
                                AGGTTCTCTCC    TAGG
                                      AATC
GAM3409  CARD15   3'  TCCAGGAAGACATTTGCT     76591       G   C__
                                TCCAGGA AGGC   TGTT
                                ||||||| ||||   ||||
                                AGGTCCT TCTG   ACGA
                                     _    TAA
GAM3409  CD97     3'  TCCAGGATGGGACAAGCGCCC  76592       GA  _ CT  TCA
                                TCCAGGA  GG C  GT   CCC
                                |||||||  || |  ||   |||
                                AGGTCCT  CC G  CG   GGG
                                     AC  T TT  C__
GAM3409  CD97     3'  TCCAGGATGGGACAAGCGCCC  76592       GA  _ CT  TCA
                                TCCAGGA  GG C  GT   CCC
                                |||||||  || |  ||   |||
                                AGGTCCT  CC G  CG   GGG
                                     AC  T TT  C__
GAM3409  CLCA3    3'  TCCAGGAAATGTTTAC      76593         GGCC    C
                                TCCAGGAGA    TGTT AC
                                |||||||||    |||| ||
                                AGGTCCTTT    ACAA TG
                                      _____   A
GAM3409  COL10A1  3'  CAAGAGAGGCTTCAC       76594          CTG
                                CAGGAGAGGC   TTCAC
                                |||||||||   |||||
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                                GTTCTCTCCG  AAGTG
                                     ____
GAM3409 COL17A1  3' TCCAGGAAGGCGCCC      76595       G   CT
                                TCCAGGA AGGC  GTTC
                                ||||||| ||||  ||||
                                AGGTCCT TCCG  CGGG
                                     _   __
GAM3409 CPT2     5' TCCGGGCAGGGGCCGCTC    76596    A _ A   T
                                TCC GG AG GGCC GTTC
                                ||| || || |||| ||||
                                AGG CC TC CCGG CGAG
                                  C  G  C   _
GAM3409 CYP46    3' TCCAGGAAGGGCCATGGAGTCC 76597       A   T____
                                TCCAGGAG GGCC    GTTC
                                |||||||| ||||    ||||
                                AGGTCCTT CCGG    CAGG
                                     C   TACCT
GAM3409 DDX11    3' TCCAGGAGGGGAGCTGCCC   76598       A  C_
                                TCCAGGAG GG  CTGTTC
                                |||||||| ||  ||||||
                                AGGTCCTC CC  GACGGG
                                     C  TC
GAM3409 DDX11    3' TCCAGGAGGGGAGCTGCCC   76598       A  C_
                                TCCAGGAG GG  CTGTTC
                                |||||||| ||  ||||||
                                AGGTCCTC CC  GACGGG
                                     C  TC
GAM3409 DXYS155E 3' CAGGAGAGGACGCCGCCC    76599        _ _
                                CAGGAGAGG C CTGTTC
                                ||||||||| | ||||||
                                GTCCTCTCC G GGCGGG
                                      T C
GAM3409 FKRP     5' TCCAGGAGGGCAGTTC      76600       A  CT
                                TCCAGGAG GGC  GTTC
                                |||||||| |||  ||||
                                AGGTCCTC CCG  CAAG
                                     _   T_
GAM3409 GABRP    3' GGAGAGGGCAGCTCACCC    76601       CCT
                                GGAGAGG   GTTCACCC
                                |||||||   ||||||||
                                CCTCTCC   CGAGTGGG
                                    CGT
GAM3409 GPR56    3' CAGGAGAGGCTGAGGGCCC   76602        C  TTCA
                                CAGGAGAGGC TG    CCC
                                |||||||||| ||    |||
                                GTCCTCTCCG AC    GGG
                                      _ TCCC
GAM3409 GRLF1    3' TCCGAGGGAGGGAGCCCACCC 76603    _  A   CCT
                                TCC AGG GAGG   GTTCACCC
                                ||| ||| ||||   ||||||||
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                                AGG TCC CTCC   CGGGTGGG
                                  C   _    CT_
GAM3409  GUSB     3'  TCCAGGAGGCACTTGTTC     76604         AG  C
                                TCCAGGAG  GC TGTTC
                                ||||||||  || |||||
                                AGGTCCTC  TG ACAAG
                                     CG  A
GAM3409  HAS3     3'  CCAGGAGAGCCTGTCATCC    76605         G    T  _
                                CCAGGAGAG CCTGT CA CC
                                ||||||||| ||||| || ||
                                GGTCCTCTC GGACA GT GG
                                     _    _ A
GAM3409  HBQ1     3'  CCTGGGAGAGGCTTTACTC    76606    A_      C_
                                CC  GGAGAGGC  TGTTC
                                ||  ||||||||  |||||
                                GG  CCTCTCCG  ATGAG
                                 AC       AA
GAM3409  HDAC4    5'  TCCAGAAGGGGCCGGGCGGCCC 76607         A    T_  TCA
                                TCCAGGAG GGCC  GT   CCC
                                |||||||| ||||  ||   |||
                                AGGTCTTC CCGG  CG   GGG
                                     C    CC  CC_
GAM3409  HOXB6    3'  TCCAGGAGAGCGCTGGGCCC   76608          _  C  TTCA
                                TCCAGGAGAG GC TG    CCC
                                |||||||||| || ||    |||
                                AGGTCCTCTC CG AC    GGG
                                      G  _  CC__
GAM3409  HRH1     3'  TCCAGGAGGGCTCAAGAGTCC  76609         A   CT____
                                TCCAGGAG GGC      GTTC
                                |||||||| |||      ||||
                                AGGTCCTC CCG      CAGG
                                     _   AGTTCT
GAM3409  ID3      3'  TCCAAGAGAGGAGATACTC    76610           CC_
                                TCCAGGAGAGG   TGTTC
                                ||||||||||   |||||
                                AGGTTCTCTCC   ATGAG
                                      TCT
GAM3409  IREB2    3'  TCCAGGAAGGTTATTC      76611         G   CC
                                TCCAGGA AGG  TGTTC
                                |||||||  |||  |||||
                                AGGTCCT TCC  ATAAG
                                     _   A_
GAM3409  LDB1     5'  CCAGGAGAGGCAGGACCC     76612           CTGTTC
                                CCAGGAGAGGC      ACCC
                                ||||||||||      ||||
                                GGTCCTCTCCG      TGGG
                                      TCC___
GAM3409  MAPRE2   3'  TCCAGGAAGGGATACCATC    76613         A  C__
                                TCCAGGAG GG   CTGTT
                                ||||||||  ||   |||||
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                                AGGTCCTT CC   GGTAG
                                     C  TAT
GAM3409  MPHOSPH9  3'  TCCAGGAGAAGGCATCC     76614          _   CT
                                TCCAGGAGA GGC  GTTC
                                ||||||||| |||  ||||
                                AGGTCCTCT CCG  TAGG
                                      T  __
GAM3409  MUC4      3'  TCCAGGGAGGAGTTGCCC     76615        A    CC_
                                TCCAGG GAGG   TGTTC
                                |||||| ||||   |||||
                                AGGTCC CTCC   ACGGG
                                   _   TCA
GAM3409  NEK6      3'  TCCAGGAAAGGCCTGGTC     76616             T
                                TCCAGGAGAGGCCTG TC
                                |||||||||||||| ||
                                AGGTCCTTTCCGGAC AG
                                          C
GAM3409  NLGN3     3'  TCCTGGGGAGGAAGAGCTATCC 76617     A  A    C____
                                TCC GG GAGG     CTGTTC
                                ||| || ||||     ||||||
                                AGG CC CTCC     GATAGG
                                  A  C    TTCTC
GAM3409  NOTCH2    3'  TCTAGGAAAGGAAAATGTTC   76618    C       CC__
                                TC AGGAGAGG    TGTTC
                                || ||||||||    |||||
                                AG TCCTTTCC    ACAAG
                                 A       TTTT
GAM3409  PABPN1    5'  TCCAGGAGGGAGCTTAC      76619         A  CCT   C
                                TCCAGGAG GG   GTT AC
                                |||||||| ||   ||| ||
                                AGGTCCTC CC   CGA TG
                                     _  T__   A
GAM3409  PACSIN3   3'  TCCTGGGGAGGCCCAGGCACCC 76620     A  A       TT
                                TCC GG GAGGCCTG  CACCC
                                ||| || ||||||||  |||||
                                AGG CC CTCCGGGT  GTGGG
                                  A  C       CC
GAM3409  PACSIN3   3'  TCCAGGAGAAGCTGGGCTC    76621           CT_
                                TCCAGGAGAGGC   GTTC
                                ||||||||||||   ||||
                                AGGTCCTCTTCG   CGAG
                                       ACC
GAM3409  PAWR      5'  TCCAGGAGAGGACGGCCGCCGC 76622           _ _____
              TC                  TCCAGGAGAGG C     CTGTTC
                                ||||||||||| |     ||||||
                                AGGTCCTCTCC G     GGCGAG
                                       T CCGGC
GAM3409  PC        5'  TCCAGAGAGGCCACACTGTTC  76623       G      ____
                                TCCAG AGAGGCC    TGTTC
                                ||||| |||||||    |||||
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                                AGGTC TCTCCGG   ACAAG
                                  _     TGTG
GAM3409  PDE7A    3'  TCCAGGAGGCAGTTTGTCC   76624       A_  CC
                                TCCAGGAG  GG  TGTTC
                                ||||||||  ||  |||||
                                AGGTCCTC  TC  ACAGG
                                    CG  AA
GAM3409  PIK4CB   5'  TCCACGCAGGCCTGTTCATCC  76625     GGAG       _
                                TCCA   AGGCCTGTTCA CC
                                ||||   |||||||||||| ||
                                AGGT   TCCGGACAAGT GG
                                  GCG_        A
GAM3409  PLA2G2D  3'  TCCAGGAGAGGCCTGGCC    76626           TT
                                TCCAGGAGAGGCCTG  C
                                ||||||||||||||  |
                                AGGTCCTCTCCGGAC  G
                                      CG
GAM3409  PLAT     3'  TCCTGGAGAGGCTAGTGTGCA  76627    A      C__   T
                                TCC GGAGAGGC   TGT CA
                                ||| ||||||||   ||| ||
                                AGG CCTCTCCG   ACA GT
                                  A       ATC   C
GAM3409  PLAT     3'  TCCTGGAGAGGCTAGTGTGCA  76627    A      C__   T
                                TCC GGAGAGGC   TGT CA
                                ||| ||||||||   ||| ||
                                AGG CCTCTCCG   ACA GT
                                  A       ATC   C
GAM3409  PLXNA2   3'  TCTGGGAGAGGCCCACC     76628    CA       TGTT
                                TC  GGAGAGGCC    CACC
                                ||  |||||||||    ||||
                                AG  CCTCTCCGG    GTGG
                                 AC       _____
GAM3409  PRX2     3'  TCCAGGAGAAGGTCAC      76629          CCTGT
                                TCCAGGAGAGG    TCAC
                                ||||||||||     ||||
                                AGGTCCTCTTC    AGTG
                                      C_____
GAM3409  PTGS1    3'  TCCAGGAAACTGCAGTGTTTGT 76630         G_  C_____
           TC                     TCCAGGAGA  GC     TGTTC
                                ||||||||  ||     |||||
                                AGGTCCTTT  CG     ACAAG
                                    GA  TCACAA
GAM3409  PTGS1    3'  TCCAGGAAACTGCAGTGTTTGT 76630         G_  C_____
           TC                     TCCAGGAGA  GC     TGTTC
                                ||||||||  ||     |||||
                                AGGTCCTTT  CG     ACAAG
                                    GA  TCACAA
GAM3409  PTPRJ    3'  AAGAGGTGCCACGTACCC    76631      AG  _  TC
                                AGGAG  GCC TGT  ACCC
                                |||||  ||| |||  ||||
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                                TTCTC  CGG GCA  TGGG
                                  CA   T  __
GAM3409  PXF     3'  CAGGGGCTGGGTTCACCC    76632     AGA   CT_
                                CAGG   GGC   GTTCACCC
                                ||||   |||   ||||||||
                                GTCC   CCG   CAAGTGGG
                                  ___   ACC
GAM3409  REGL    3'  TCCTGGAATGTTCACC      76633     A    AGGCC
                                TCC GGAG    TGTTCACC
                                ||| ||||    ||||||||
                                AGG CCTT    ACAAGTGG
                                 A   _____
GAM3409  RET     3'  CCCAGGAGGGGTCTGGGGGAAC 76634        A  C   TTC__
            C                    TCCAGGAG GG CTG    ACC
                                ||||||||  || |||    |||
                                GGGTCCTC CC GAC    TGG
                                    C  A   CCCCT
GAM3409  RLBP1   3'  AGGAGAGGCCCAGAGATTC    76635          _____
                                AGGAGAGGCCT   GTTC
                                ||||||||||    ||||
                                TCCTCTCCGGG    TAAG
                                      TCTC
GAM3409  RXRB    3'  TCCAGAGAGGCCCCCATC     76636      G      GT_
                                TCCAG AGAGGCCT   TC
                                ||||| ||||||||   ||
                                AGGTC TCTCCGGG   AG
                                  _       GGT
GAM3409  SLC25A13  3'  TCCAGGAGAGGGGCTACA    76637          CCT   _
                                TCCAGGAGAGG   GTT CA
                                ||||||||||   ||| ||
                                AGGTCCTCTCC   CGA GT
                                      C__   T
GAM3409  SLC9A1   3'  TCCGGGAGAAGCCTGGATC    76638     A         T_
                                TCC GGAGAGGCCTG  TC
                                ||| ||||||||||  ||
                                AGG CCTCTTCGGAC  AG
                                  C          CT
GAM3409  SORBS1   3'  TCTAAGAGAGGCCGATAAACAT 76639    C         __  TT  _
            CC                    TC AGGAGAGGCC  TG  CA CC
                                || ||||||||||  ||  || ||
                                AG TTCTCTCCGG  AT  GT GG
                                 A         CT  TT  A
GAM3409  TCF1    3'  TCCAGGAAGGGCCACGGTTGCT 76640         A   _____
            C                    TCCAGGAG GGCC    TGTTC
                                ||||||||  ||||    |||||
                                AGGTCCTT CCGG    ACGAG
                                    C    TGCCA
GAM3409  TIMP3   3'  TCTCAGGAGGTGGCATTCACCC 76641    _     A_   CT
                                TC CAGGAG  GGC  GTTCACCC
                                || ||||||  |||  ||||||||
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                                AG GTCCTC  CCG  TAAGTGGG
                                 A     CA  __
GAM3409  TIMP3    3'  CCCAGGAGAGGTGTCC      76642          CC
                                TCCAGGAGAGG  TGTTC
                                ||||||||||  |||||
                                GGGTCCTCTCC  ACAGG
                                          __
GAM3409  TMEPAI   3'  TCCACGGGGGCTCACC      76643      _  AGA  CCT
                                TCCA GG   GG   GTTCACC
                                |||| ||   ||   |||||||
                                AGGT CC   CC   CGAGTGG
                                  G  ___  ___
GAM3409  TREM2    3'  TCCAGGAGAAGCAGTGTTC   76644           C_
                                TCCAGGAGAGGC  TGTTC
                                ||||||||||||  |||||
                                AGGTCCTCTTCG  ACAAG
                                       TC
GAM3409  TXNRD2   3'  TCCAGGAGAGGGTTGAGGCCC 76645          CC  TTCA
                                TCCAGGAGAGG  TG   CCC
                                ||||||||||  ||   |||
                                AGGTCCTCTCC  AC   GGG
                                      CA  TCC_
GAM3409  VIPR1    3'  TCCAGGAGAGGAGCTCCC    76646          CCT   A
                                TCCAGGAGAGG   GTTC CC
                                ||||||||||   |||| ||
                                AGGTCCTCTCC   CGAG GG
                                      T__   _
GAM3409  WNT3A    3'  TCCAGGAAGAAGCCTCATCC  76647        _     _
                                TCCAGGA GAGGCCT GTTC
                                ||||||| ||||||| ||||
                                AGGTCCT CTTCGGA TAGG
                                    T      G
GAM3409  AP3M2    3'  TCCAGGAGGGGACTGACC    76648        A  C   TTC
                                TCCAGGAG GG CTG   ACC
                                |||||||| || |||   |||
                                AGGTCCTC CC GAC   TGG
                                     C  T  ___
GAM3409  Apg4B    3'  CCTGGGAGAGGCACGCCGTCC  76649    A_      ___
                                CC  GGAGAGGC   CTGTTC
                                ||  ||||||||   ||||||
                                GG  CCTCTCCG   GGCAGG
                                 AC       TGC
GAM3409  ATIC     3'  CAGGCGTGACTGTTCACC    76650      AGA   C
                                CAGG   GGC TGTTCACC
                                ||||   ||| ||||||||
                                GTCC   CTG ACAAGTGG
                                  GCA  _
GAM3409  BRD4     3'  TCCAGGAGATGCCACC      76651          G   TGTTC
                                TCCAGGAGA GCC    ACC
                                |||||||| |||    |||
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                                AGGTCCTCT CGG    TGG
                                    A  _____
GAM3409  BTBD2    3'  TCCGGCAGGGGCCGTCC    76652    A _ A   T
                                TCC GG AG GGCC GTTC
                                ||| || || |||| ||||
                                AGG CC TC CCGG CAGG
                                  _ G  C   _
GAM3409  C11orf23 3'  AGAGAGGGGCTCACCC     76653      CCT
                                GGAGAGG   GTTCACCC
                                |||||||   ||||||||
                                TCTCTCC   CGAGTGGG
                                    C__
GAM3409  C20orf13 5'  CAGGAGAGGAATTACCC    76654       CCT   C
                                CAGGAGAGG   GTT ACCC
                                |||||||||   ||| ||||
                                GTCCTCTCC   TAA TGGG
                                    T__   _
GAM3409  C20orf51 5'  CCAGGAGAGGCTGGATCC    76655         CT_
                                CCAGGAGAGGC   GTTC
                                ||||||||||   ||||
                                GGTCCTCTCCG   TAGG
                                     ACC
GAM3409  C20orf64 3'  TCTGGGAGAAGCCTGTCC    76656    CA
                                TC  GGAGAGGCCTGTTC
                                ||  ||||||||||||||
                                AG  CCTCTTCGGACAGG
                                 AC
GAM3409  C6orf32  5'  TCCAGGAGAGAGCAGCCC    76657         _ CT
                                TCCAGGAGAG GC  GTTC
                                |||||||||| ||  ||||
                                AGGTCCTCTC CG  CGGG
                                     T  T_
GAM3409  C9orf12  3'  CCAGGAGCTGTTCACC      76658       AGGC
                                CCAGGAG    CTGTTCACC
                                |||||||    |||||||||
                                GGTCCTC    GACAAGTGG
                                    _____
GAM3409  CABP4    3'  CCTGGGGGAGGCCTGCAGCC   76659    A_ A       TCA
                                CC  GG GAGGCCTGT   CC
                                ||  || |||||||||   ||
                                GG  CC CTCCGGACG   GG
                                 AC  C        TC_
GAM3409  CENTG2   3'  TCCAGGAGGGCCTGAGAC    76660        A     TTC
                                TCCAGGAG GGCCTG   AC
                                |||||||| ||||||   ||
                                AGGTCCTC CCGGAC   TG
                                    _     TC_
GAM3409  CHK      3'  CCCAGGGGAGGCCCAGCC    76661       A      _
                                TCCAGG GAGGCCT GTT
                                |||||| ||||||| |||
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                                GGGTCC CTCCGGG CGG
                                   C      T
GAM3409  CHRAC1    3'  TCGAGGAGGGGCTGCTGTC   76662    C    A  __
                                TC AGGAG GGC  CTGTT
                                || ||||| |||  |||||
                                AG TCCTC CCG  GACAG
                                 C    C  AC
GAM3409  CHST3     3'  TCCAGGAGACGGCAGATTGTC  76663        _  C___
                                TCCAGGAGA GGC   TGTT
                                ||||||||| |||   ||||
                                AGGTCCTCT CCG   ACAG
                                     G  TCTA
GAM3409  DDX12     3'  TCCAGGAGGGGAGCTGCCC   76598       A  C_
                                TCCAGGAG GG  CTGTTC
                                |||||||| ||  ||||||
                                AGGTCCTC CC  GACGGG
                                     C  TC
GAM3409  DKFZP434I216 3'  TCCAGAGAGGCAATGTTC    76664     G    C_
                                TCCAG AGAGGC  TGTTC
                                ||||| ||||||  |||||
                                AGGTC TCTCCG  ACAAG
                                   _     TT
GAM3409  DKFZP434L0117 3'  TCCAGGAAGGGGACTACC    76665       A_  C  GTTC
                                TCCAGGAG  GG CT   ACC
                                ||||||||  || ||   |||
                                AGGTCCTT  CC GA   TGG
                                     CC  T _____
GAM3409  DKFZp434N0650 5'  TCCAGCAGGGTCTTGTCC    76666     G  A  C  _
                                TCCAG AG GG CT GTTC
                                ||||| || || || ||||
                                AGGTC TC CC GA CAGG
                                   G  _  A  A
GAM3409  DKFZP586M1120 3'  TCTGGGAAAGGCATTTCACC  76667    CA      CTG
                                TC  GGAGAGGC   TTCACC
                                ||  ||||||||   ||||||
                                AG  CCTTTCCG   AAGTGG
                                 AC       TA_
GAM3409  ERp44     5'  TCCAGAGAGGCCTCTCACACCC 76668      G      G  _
                                TCCAG AGAGGCCT TT CACCC
                                ||||| |||||||| || |||||
                                AGGTC TCTCCGGA AG GTGGG
                                   _      G  T
GAM3409  FBP17     3'  TCCAGGAAGGCTCACC      76669       G   CTGT
                                TCCAGGA AGGC   TCACC
                                ||||||| ||||   |||||
                                AGGTCCT TCCG   AGTGG
                                     _  _____
GAM3409  FLJ00024  5'  CCAGGGGTAGTTCACCC     76670      AGA  CCT
                                CCAGG  GG  GTTCACCC
                                |||||  ||  ||||||||
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                              GGTCC  CC  CAAGTGGG
                                ___ AT_
GAM3409 FLJ10157 5' TCCGGGGAGAGGCATTC    76671    A_     CT
                              TCC GGAGAGGC GTTC
                              ||| |||||||| ||||
                              AGG CCTCTCCG TAAG
                                CC      __
GAM3409 FLJ10748 5' TCCAGGAGGCGTGACC     76672      GA  C TTC
                              TCCAGGA GGC TG  ACC
                              ||||||| ||| ||  |||
                              AGGTCCT CCG AC  TGG
                                 __  C ___
GAM3409 FLJ10769 3' TCCAAGGTGCCTGTTTAC   76673     AGAG    C
                              TCCAGG   GCCTGTT AC
                              ||||||   ||||||| ||
                              AGGTTC   CGGACAA TG
                                 CA__     A
GAM3409 FLJ11136 5' TCCAGAAGAGCCGTTTCGCCC 76674       G TG  A
                              TCCAGGAGAG CC  TTC CCC
                              |||||||||| ||  ||| |||
                              AGGTCTTCTC GG  AAG GGG
                                    _ CA  C
GAM3409 FLJ11457 3' TCCAGGAGGCGGGGCCATCC  76675      A___  T
                              TCCAGGAG   GGCC GTTC
                              ||||||||   |||| ||||
                              AGGTCCTC   CCGG TAGG
                                   CGCC  _
GAM3409 FLJ11539 5' TCCAAGAGAGATGGGTTGTTTG 76676       CC___  CA
          CC                  TCCAGGAGAGG   TGTT CC
                              ||||||||||    ||||  ||
                              AGGTTCTCTCT   ACAA GG
                                    ACCCA   AC
GAM3409 FLJ11618 5' TCTGGGAGAGCCCGCTC    76677   CA    G
                              TC GGAGAG CCTGTTC
                              ||  |||||| |||||||
                              AG  CCTCTC GGGCGAG
                                AC    _
GAM3409 FLJ11726 3' TCCAGAAGATGTTCACC    76678      GGCC
                              TCCAGGAGA   TGTTCACC
                              |||||||||   ||||||||
                              AGGTCTTCT   ACAAGTGG
                                    ____
GAM3409 FLJ12190 3' TCCAGGAAGGAGACTGTCC   76679      __   C
                              TCCAGGA GAGGC TGTTC
                              |||||||  ||||| |||||
                              AGGTCCT  CTCTG ACAGG
                                   TC   _
GAM3409 FLJ12891 3' TCCAGGGGAGACATTC     76680      A   CT
                              TCCAGG GAGGC  GTTC
                              |||||| |||||  ||||
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                                AGGTCC CTCTG  TAAG
                                   C    __
GAM3409  FLJ13197  3'  TCCAGAAGAAATTCACC     76681          GCCT
                                TCCAGGAGAG    GTTCACC
                                ||||||||||    |||||||
                                AGGTCTTCTT    TAAGTGG
                                      _____
GAM3409  FLJ13693  3'  TCTGGGAGAAGCTCCCCACCC  76682    CA       C G
                                TC  GGAGAGGC T TTCACCC
                                ||  |||||||| | |||||||
                                AG  CCTCTTCG A GGGTGGG
                                 AC       _ G
GAM3409  FLJ14834  5'  CCCAGGAGGGGCCGGGCGCCC  76683        A    ___
                                TCCAGGAG GGCC   TGTTC
                                |||||||| ||||   |||||
                                GGGTCCTC CCGG   GCGGG
                                     C    CCC
GAM3409  FLJ20274  3'  CCTGGGAGAGGCCAACATCC   76684    A_       TGTT  _
                                CC  GGAGAGGCC    CA CC
                                ||  |||||||||    || ||
                                GG  CCTCTCCGG    GT GG
                                 AC       TT__  A
GAM3409  FLJ20356  3'  CCAGGAGAGGCAGGAGACCC   76685          CTGTTC
                                CCAGGAGAGGC     ACCC
                                ||||||||||     ||||
                                GGTCCTCTCCG     TGGG
                                       TCCTC_
GAM3409  FLJ20417  3'  CCAGGAGAGGTCAGCGTCC    76686          CC__
                                CCAGGAGAGG    TGTTC
                                ||||||||||    |||||
                                GGTCCTCTCC    GCAGG
                                       AGTC
GAM3409  FLJ20619  3'  TCCAGAAGAGGCTGGGGGCTC  76687           CT___
                                TCCAGGAGAGGC    GTTC
                                ||||||||||||    ||||
                                AGGTCTTCTCCG    CGAG
                                       ACCCC
GAM3409  FLJ21140  3'  TCTAGAAGAGGTCAACATTC   76688    C       CC__
                                TC AGGAGAGG    TGTTC
                                || ||||||||    |||||
                                AG TCTTCTCC    GTAAG
                                 A       AGTT
GAM3409  FLJ21324  5'  TCCAGGAGGGGCCCGTCC     76689         A
                                TCCAGGAG GGCCTGTTC
                                |||||||| |||||||||
                                AGGTCCTC CCGGGCAGG
                                     C
GAM3409  FLJ21820  3'  CAGGAGACCCAGGTTCAC     76690        GG  T_
                                CAGGAGA  CC  GTTCAC
                                |||||||  ||  ||||||
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                                GTCCTCT  GG  CAAGTG
                                   G_  TC
GAM3409  FLJ22055  3'  CCCAGGAGAGGTGTGAGGTTC  76691          CCT___
                                TCCAGGAGAGG     GTTC
                                ||||||||||      ||||
                                GGGTCCTCTCC     CAAG
                                      ACACTC
GAM3409  FLJ22494  5'  CCCAGGAGGGGCCCCGCTC   76692        A    _
                                TCCAGGAG GGCCT GTTC
                                |||||||| ||||| ||||
                                GGGTCCTC CCGGG CGAG
                                   C    G
GAM3409  FLJ32783  3'  TCCAGGAAGAGGTGATCC    76693        _   CCT
                                TCCAGGA GAGG   GTTC
                                ||||||| ||||   ||||
                                AGGTCCT CTCC   TAGG
                                   T   AC_
GAM3409  FLJ32934  5'  TCCAGGAGATGCCCGCTGAC   76694        G     C
                                TCCAGGAGA GCCTGTT AC
                                ||||||||| ||||||| ||
                                AGGTCCTCT CGGGCGA TG
                                     A      C
GAM3409  FN5       5'  TCCAGGAAGGGCCACACTC   76695        A   _ GT
                                TCCAGGAG GGCC T  TC
                                |||||||| |||| |  ||
                                AGGTCCTT CCGG G  AG
                                   C    T TG
GAM3409  FYCO1     3'  CCCAGGAGAGGCTGATGGTC  76696          C__  T
                                TCCAGGAGAGGC   TG TC
                                ||||||||||||   || ||
                                GGGTCCTCTCCG   AC AG
                                      ACT  C
GAM3409  GALNT12   5'  TCCAGGAAGGTCAGAACATCGC 76697        G   CCTGT___  A
            CC                    TCCAGGA AGG       TC CCC
                                  ||||||| |||       || |||
                                  AGGTCCT TCC       AG GGG
                                     _   AGTCTTGT  C
GAM3409  GDAP1L1   3'  TCCAGGAGAAGCGTGAAGCCC  76698          C  TTCA
                                TCCAGGAGAGGC TG    CCC
                                ||||||||||| ||    |||
                                AGGTCCTCTTCG AC    GGG
                                      C  TTC_
GAM3409  GPS1      3'  TCCTGGAGGCCAAGGTTCACCC 76699     AGGA     T__
                                TCC    GAGGCC   GTTCACCC
                                |||    ||||||   ||||||||
                                AGG    CTCCGG   CAAGTGGG
                                  AC__      TTC
GAM3409  GT650     3'  TCCAGGAAGGCTAAGAAAGTTC 76700        G    CT_____
                                TCCAGGA AGGC      GTTC
                                ||||||| ||||      ||||
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                                AGGTCCT TCCG      CAAG
                                   _   ATTCTTT
GAM3409 HSU79274 5' TCCGGAGAGGCGGCTC     76701    A      CT
                                TCC GGAGAGGC  GTTC
                                ||| ||||||||  ||||
                                AGG CCTCTCCG  CGAG
                                  _      C_
GAM3409 HUMZD58C02 3' TCCAGGAGCGGCTGCAGGACC 76702        A   C   TC_
                                TCCAGGAG GGC TGT   ACC
                                |||||||| ||| |||   |||
                                AGGTCCTC CCG ACG   TGG
                                     G   _   TCC
GAM3409 KCNS1    3' TCTGGGAGAGGCATCGCTC   76703    CA      C_
                                TC  GGAGAGGC  TGTTC
                                ||  ||||||||  |||||
                                AG  CCTCTCCG  GCGAG
                                 AC       TA
GAM3409 KIAA0063 3' CAGGGTCAGGCCTGTTCAC   76704     AG_
                                CAGG   AGGCCTGTTCAC
                                ||||   ||||||||||||
                                GTCC   TCCGGACAAGTG
                                  CAG
GAM3409 KIAA0125 3' CCCAGGAGAGGCCCAGGCCC  76705           __
                                TCCAGGAGAGGCCT  GTTC
                                ||||||||||||||  ||||
                                GGGTCCTCTCCGGG  CGGG
                                        TC
GAM3409 KIAA0435 5' GGAGAGGCTATGCCAGCC    76706        C   _   _
                                GGAGAGGC TGT TCA CC
                                |||||||| ||| ||| ||
                                CCTCTCCG ATA GGT GG
                                     _   C   C
GAM3409 KIAA0555 3' TCCAAGGGAAGCATTCA     76707       A     CT
                                TCCAGG GAGGC  GTTCA
                                |||||| |||||  |||||
                                AGGTTC CTTCG  TAAGT
                                   C     __
GAM3409 KIAA0561 3' TCCAGGTGAGGCCTGTACC   76708       A       TC
                                TCCAGG GAGGCCTGT  ACC
                                |||||| |||||||||  |||
                                AGGTCC CTCCGGACA  TGG
                                   A        __
GAM3409 KIAA0601 3' TCCAGAAGAGGAAGAGCTCACC 76709          CCT_
           C                     TCCAGGAGAGG   GTTCACCC
                                ||||||||||    ||||||||
                                AGGTCTTCTCC    CGAGTGGG
                                       TTCT
GAM3409 KIAA0790 3' TCCAGAGAGGCCCATTC     76710      G
                                TCCAG AGAGGCCTGTTC
                                ||||| ||||||||||||
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                                AGGTC TCTCCGGGTAAG
                                  _
GAM3409 KIAA0876 3' CCCAGGAGAGAGTTTATTC   76711          CC_
                                TCCAGGAGAGG  TGTTC
                                ||||||||||  |||||
                                GGGTCCTCTCT  ATAAG
                                    CAA
GAM3409 KIAA1026 3' CCCAGGAGGGGTCTGAACTC  76712        A  C  __
                                TCCAGGAG GG CTG  TTC
                                |||||||| || |||  |||
                                GGGTCCTC CC GAC  GAG
                                    C  A   TT
GAM3409 KIAA1171 3' TCTGGAAGAGGCTTGCAGCA  76713    CA      C  T_
                                TC  GGAGAGGC TGT  CA
                                ||  |||||||| |||  ||
                                AG  CTTCTCCG ACG  GT
                                 AC       A   TC
GAM3409 KIAA1211 5' CAGGAGAGGCTCCGTGTCC   76714         _   TCA
                                CAGGAGAGGC CTGT   CC
                                |||||||||| ||||   ||
                                GTCCTCTCCG GGCA   GG
                                    A   CA_
GAM3409 KIAA1668 3' TCCAGGAGGGGGGCAGTCC   76715        A_  CT
                                TCCAGGAG  GGC  GTTC
                                ||||||||  |||  ||||
                                AGGTCCTC  CCG  CAGG
                                    CC   T_
GAM3409 KIAA1719 3' TCCAGAGAGGCTGAGCCACC  76717     G    C  T_
                                TCCAG AGAGGC TG  TCACC
                                ||||| |||||| ||  |||||
                                AGGTC TCTCCG AC  GGTGG
                                  _     _ TC
GAM3409 KIAA1719 3' CCAGGGGAGGCCCACACCC   76716     A      GTT
                                CCAGG GAGGCCT   CACCC
                                ||||| |||||||   |||||
                                GGTCC CTCCGGG   GTGGG
                                   C      T__
GAM3409 KIAA1755 5' TCCAGGAGACGGAACACC    76718        _ CCTGTT
                                TCCAGGAGA GG     CACC
                                |||||||| ||     ||||
                                AGGTCCTCT CC     GTGG
                                    G  TT_____
GAM3409 KIAA1862 3' TCCAGGAAGGCAAGAGCCC   76719       G   CT__
                                TCCAGGA AGGC   GTTC
                                ||||||| ||||   ||||
                                AGGTCCT TCCG   CGGG
                                   _   TTCT
GAM3409 KIAA1867 3' CCCAGGAGGGGCACACC     76720        A  CTGTT
                                TCCAGGAG GGC    CACC
                                |||||||| |||    ||||
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                                GGGTCCTC CCG    GTGG
                                    C  T____
GAM3409 KIAA1879 5' TCCAGGAGGGGCTCAGCC   76721       A  CCT   _
                                TCCAGGAG GG  GTTCA CC
                                |||||||| ||  ||||| ||
                                AGGTCCTC CC  CGAGT GG
                                    _ ___    C
GAM3409 KIAA1937 5' TCTGGGAAAGGCCTGGGACC  76722   CA       TTC
                                TC  GGAGAGGCCTG  ACC
                                ||  ||||||||||  |||
                                AG  CCTTTCCGGAC  TGG
                                 AC        CC_
GAM3409 LASP1    3' CCAGGAGAAAGATTCAC    76723        CCT
                                CCAGGAGAGG  GTTCAC
                                ||||||||||  ||||||
                                GGTCCTCTTT  TAAGTG
                                    C__
GAM3409 MAPKAPK5 5' CCGGGAGAGGCGGAGGCTGCTC 76724   A     _____
                                CC GGAGAGGC    CTGTTC
                                || ||||||||    ||||||
                                GG CCTCTCCG    GACGAG
                                 C      CCTCC
GAM3409 MAPKAPK5 5' CCGGGAGAGGCGGAGGCTGCTC 76724   A     _____
                                CC GGAGAGGC    CTGTTC
                                || ||||||||    ||||||
                                GG CCTCTCCG    GACGAG
                                 C      CCTCC
GAM3409 MDS033   5' CCCAGGAGAGCTCAC      76725       GGCCT
                                TCCAGGAGA    GTTCAC
                                |||||||||    ||||||
                                GGGTCCTCT    CGAGTG
                                    _____
GAM3409 MGC11352 3' TCCAGGAAGGTTGTGCATCC  76726      G  CC  T  _
                                TCCAGGA AGG  TGT CA CC
                                ||||||| |||  ||| || ||
                                AGGTCCT TCC  ACA GT GG
                                    _  A_  C  A
GAM3409 MGC12966 3' TCCAGGAGGGTGCATC     76727       A  CC  _
                                TCCAGGAG GG  TGT TC
                                |||||||| ||  ||| ||
                                AGGTCCTC CC  ACG AG
                                    _ ___  T
GAM3409 MGC13053 5' TCCAGGAAGGCTGCATGACC  76728      G   C  TC_
                                TCCAGGA AGGC TGT   ACC
                                ||||||| |||| |||   |||
                                AGGTCCT TCCG ACG   TGG
                                    _   _  TAC
GAM3409 MGC13114 3' TCCAGGAGGGCTGTGTCC    76730       A  C_
                                TCCAGGAG GGC  TGTTC
                                |||||||| |||  |||||
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                                AGGTCCTC CCG  ACAGG
                                     _  AC
GAM3409  MGC13114  3'  TCCAGGAGCAGGCCACTGGCC  76729       _    TGTTCA
                                TCCAGGAG AGGCC     CC
                                |||||||| |||||     ||
                                AGGTCCTC TCCGG     GG
                                     G    TGACC_
GAM3409  MGC13272  3'  TCCAGGAAGGCTGAGCC     76731       G   C  TTCA
                                TCCAGGA AGGC TG    CC
                                ||||||| |||| ||    ||
                                AGGTCCT TCCG AC    GG
                                     _   _ TC__
GAM3409  MGC15619  3'  CCCAGGAGGGGCAGCTGTTC  76732       A  __
                                TCCAGGAG GGC  CTGTTC
                                |||||||| |||  ||||||
                                GGGTCCTC CCG  GACAAG
                                     C   TC
GAM3409  MGC26744  5'  TCACAGATAACTCTGTTCAC  76733    _   AGA  _
                                TC CAGG   GGC CTGTTCAC
                                || ||||   ||| ||||||||
                                AG GTCT   TTG GACAAGTG
                                 T   A__   A
GAM3409  MGC2749   3'  AGAGAGGCCTGCTGGCCC    76734          CA
                                GGAGAGGCCTGTT  CCC
                                ||||||||||||  |||
                                TCTCTCCGGACGA  GGG
                                      CC
GAM3409  MGC33547  3'  TCTAGGAGAGGAACCGTCC   76735    C      C_
                                TC AGGAGAGG  CTGTTC
                                || ||||||||  ||||||
                                AG TCCTCTCC  GGCAGG
                                 A       TT
GAM3409  MIDORI    3'  TCCAGGAGGGATGCTC      76736        A  CC
                                TCCAGGAG GG  TGTTC
                                |||||||| ||  |||||
                                AGGTCCTC CC  ACGAG
                                     _  T_
GAM3409  MIL1      3'  TCCTGGAGGGGGTGCTTTACCC 76737     A   A  CC   C_
                                TCC GGAG GG  TGTT  ACCC
                                ||| |||| ||  ||||  ||||
                                AGG CCTC CC  ACGA  TGGG
                                  A   _  CC   AA
GAM3409  moblak    3'  TCTGGGAAAGGCCAATTC    76738    CA       T
                                TC  GGAGAGGCC GTTC
                                ||  |||||||| ||||
                                AG  CCTTTCCGG TAAG
                                 AC        T
GAM3409  NGEF      3'  CAGGAGAGGCTTGGGCACCC   76739         C  TT
                                CAGGAGAGGC TG  CACCC
                                |||||||||| ||  |||||
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                                GTCCTCTCCG AC  GTGGG
                                     A  CC
GAM3409  NM23-H6   3'  TCTAGGAGAAGTCTGGGCAC   76740    C       C   TT
                                TC AGGAGAGG CTG  CAC
                                || |||||||| |||  |||
                                AG TCCTCTTC GAC  GTG
                                 A       A   CC
GAM3409  NPC1L1    3'  TCCAGGAGGGGCTAATCC    76741         A   CT
                                TCCAGGAG GGC  GTTC
                                |||||||| |||  ||||
                                AGGTCCTC CCG  TAGG
                                     C   AT
GAM3409  NRF       3'  TCCAGCGGAGGCCTGTCATCC  76742       GA       T  _
                                TCCAG  GAGGCCTGT CA CC
                                |||||  ||||||||| || ||
                                AGGTC  CTCCGGACA GT GG
                                   GC        _  A
GAM3409  PCBP4     5'  CCCGGGAGAGGCGGCCGCTC   76743     A       __
                                TCC GGAGAGGC  CTGTTC
                                ||| ||||||||  ||||||
                                GGG CCTCTCCG  GGCGAG
                                  C       CC
GAM3409  PDZD2     5'  CAGTGAGAGGATCTCATCC    76744     _     CCTG    _
                                CAG GAGAGG    TTCA CC
                                ||| ||||||    |||| ||
                                GTC CTCTCC    GAGT GG
                                  A     TA__    A
GAM3409  PIP5K2B   5'  TCCCGGGGAGGCAGCGGCCGCC 76745     A  A    C_  TT A
            C                    TCC GG GAGGC  TG  C CCC
                                ||| || |||||  ||  | |||
                                AGG CC CTCCG  GC  G GGG
                                  G  C    TC  CG C
GAM3409  PIP5K2B   5'  TCCCGGGGAGGCAGCGGCCGCC 76745     A  A    C_  TT A
            C                    TCC GG GAGGC  TG  C CCC
                                ||| || |||||  ||  | |||
                                AGG CC CTCCG  GC  G GGG
                                  G  C    TC  CG C
GAM3409  POLA2     3'  TCCAGGAGAGGCACCACTC    76746          _ TG
                                TCCAGGAGAGGC C  TTC
                                ||||||||||| |  |||
                                AGGTCCTCTCCG G  GAG
                                       T GT
GAM3409  R32184_3  3'  TCCAGGAGGGAGGCGCTC     76747        __    CT
                                TCCAGGA  GAGGC  GTTC
                                |||||||  |||||  ||||
                                AGGTCCT  CTCCG  CGAG
                                    CC    __
GAM3409  RASSF2    3'  TCTAGGAGAGAGTACTGTTC   76748    C       C__
                                TC AGGAGAGG   CTGTTC
                                || ||||||||   ||||||
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                                AG TCCTCTCT   GACAAG
                                 A       CAT
GAM3409  RGS12    3'  CCAGGCCATCCTGTTCACC   76749      AGAGG
                                CCAGG    CCTGTTCACC
                                |||||    ||||||||||
                                GGTCC    GGACAAGTGG
                                   GGTA_
GAM3409  RPIA     3'  TCCTGGAGAGGTACGTCC    76750    A      CC
                                TCC GGAGAGG  TGTTC
                                ||| |||||||  |||||
                                AGG CCTCTCC  GCAGG
                                  A      AT
GAM3409  SE70-2   5'  TCCAGGAGGAGGTGGTCC    76751        _  CCT
                                TCCAGGAG AGG   GTTC
                                |||||||| |||   ||||
                                AGGTCCTC TCC   CAGG
                                     C   AC_
GAM3409  SEC14L2  3'  GGCAGAGGCCCGTGCAGCC   76752   _       T _
                                GG AGAGGCCTGT CA CC
                                || ||||||||||  || ||
                                CC TCTCCGGGCA GT GG
                                 G        C  C
GAM3409  SPINT1   3'  TCCAAGAGGGGCTGGAGCCC   76753       A   C  TTCA
                                TCCAGGAG GGC TG    CCC
                                |||||||| ||| ||    |||
                                AGGTTCTC CCG AC    GGG
                                     C   _  CTC_
GAM3409  SRPK1    3'  TCTAGGAGAGGCTCATCC    76754    C       CT
                                TC AGGAGAGGC  GTTC
                                || |||||||||  ||||
                                AG TCCTCTCCG  TAGG
                                 A        AG
GAM3409  SSB-3    3'  AGGAGAGGCCCCAGCTGTCC   76755          _____
                                AGGAGAGGCCT    GTTC
                                ||||||||||     ||||
                                TCCTCTCCGGG    CAGG
                                       GTCGA
GAM3409  SSB-4    3'  TCCAGGAAGGCCCCCCAACCC  76756       G     G TC
                                TCCAGGA AGGCCT T  ACCC
                                |||||||  ||||||  |  ||||
                                AGGTCCT TCCGGG G  TGGG
                                     _     G GT
GAM3409  STK17A   5'  TCCTGGCCGCCTGTTCAC    76757     A  AGAG
                                TCC GG    GCCTGTTCAC
                                ||| ||    ||||||||||
                                AGG CC    CGGACAAGTG
                                  A  GG__
GAM3409  STMN3    3'  TCCAGGAAGGCCCAGGGTGTCC 76758        G     _____
                                TCCAGGA AGGCCT     GTTC
                                |||||||  ||||||     ||||
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                                AGGTCCT TCCGGG    CAGG
                                    _     TCCCA
GAM3409  TA-NFKBH  3'  GGGGCCTGTTCACCC      76759    AGA
                                GG   GGCCTGTTCACCC
                                ||   ||||||||||||
                                CC   CCGGACAAGTGGG
                                 ___
GAM3409  TIX1      3'  CAGGAGAGACTAACCTCACCC  76760         CTG_
                                CAGGAGAGGC   TTCACCC
                                ||||||||||   |||||||
                                GTCCTCTCTG   GAGTGGG
                                     ATTG
GAM3409  TP53TG3   3'  TCCGTGAGAGGCCCGACC    76761     AG        TTC
                                TCC  GAGAGGCCTG   ACC
                                |||  ||||||||||   |||
                                AGG  CTCTCCGGGC   TGG
                                  CA        ___
GAM3409  USP3      5'  TCTAGGAGAGGAATCTGTC    76762    C       C__
                                TC AGGAGAGG   CTGTT
                                || ||||||||   |||||
                                AG TCCTCTCC   GACAG
                                 A       TTA
GAM3409  VI        3'  TCCAGGAGGTGGGGAGGTCACC 76763         A_  CCTGT
              C                  TCCAGGAG  GG    TCACCC
                                 ||||||||  ||    ||||||
                                 AGGTCCTC  CC    AGTGGG
                                     CA  CCTCC
GAM3409  WNT10A    3'  TCCAGGAGGGGACCTCGATC   76764         A  _   _ T
                                TCCAGGAG GG CCT G TC
                                |||||||| || ||| | ||
                                AGGTCCTC CC GGA C AG
                                     C  T   G T
GAM3409  YKT6      3'  CCCAGGAGAGGCTTTC      76765           CTG
                                TCCAGGAGAGGC   TTC
                                ||||||||||||   |||
                                GGGTCCTCTCCG   AAG
                                      A__
GAM3409  ZAK       3'  CAGGAGAGGCATGAACTC    76766          C  __
                                CAGGAGAGGC TG  TTC
                                |||||||||| ||  |||
                                GTCCTCTCCG AC  GAG
                                     T  TT
GAM3409  LOC113179 3'  TCCAGGAGGGGCGCCC      76767         A   CT
                                TCCAGGAG GGC  GTTC
                                |||||||| |||  ||||
                                AGGTCCTC CCG  CGGG
                                     C   __
GAM3409  LOC124221 5'  TCCAGGAGGGGCACAGCCACC  76768         A   CT_  T
                                TCCAGGAG GGC   GT CACC
                                |||||||| |||   || ||||
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                                AGGTCCTC CCG   CG GTGG
                                     C   TGT  _
GAM3409  LOC124916 5'  TCCAGGAGGGGGCCAGCCC   76769        A_   T
                                TCCAGGAG  GGCC GTTC
                                |||||||| ||||  ||||
                                AGGTCCTC  CCGG CGGG
                                     CC    T
GAM3409  LOC126248 3'  CAGAAGAGGTGTCAC       76770         CC   T
                                CAGGAGAGG  TGT CAC
                                |||||||||  ||| |||
                                GTCTTCTCC  ACA GTG
                                     __   _
GAM3409  LOC126917 3'  CCCAGGAGAGGTCCTGCC    76771          _
                                TCCAGGAGAGG CCTGTT
                                |||||||||||  ||||||
                                GGGTCCTCTCC GGACGG
                                      A
GAM3409  LOC127281 3'  CAGGAGAGGTTCGGCATCC   76772        CC  TT  _
                                CAGGAGAGG  TG  CA CC
                                |||||||||  ||  || ||
                                GTCCTCTCC  GC  GT GG
                                     AA  C_  A
GAM3409  LOC138311 3'  TCCAGGAAGGGTGGCCAGGCCC 76773        A___   T_
                                TCCAGGAG   GGCC  GTTC
                                ||||||||   ||||  ||||
                                AGGTCCTT   CCGG  CGGG
                                     CCCA   TC
GAM3409  LOC143153 3'  TCCAGGAGATGTTCTACATGCT 76774        G_____  C
           C                     TCCAGGAGA     GC TGTTC
                                |||||||||     || |||||
                                AGGTCCTCT     TG ACGAG
                                     ACAAGA  T
GAM3409  LOC143154 3'  TCCAGGAGATGTTCTACATGCT 76774        G_____  C
           C                     TCCAGGAGA     GC TGTTC
                                |||||||||     || |||||
                                AGGTCCTCT     TG ACGAG
                                     ACAAGA  T
GAM3409  LOC143282 5'  TCTGGGAGAGGCGCCAAAGCC  76775    CA      _   TTCA
                                TC  GGAGAGGC CTG   CC
                                ||  |||||||| |||   ||
                                AG  CCTCTCCG GGT   GG
                                 AC       C   TTC_
GAM3409  LOC143392 3'  CCAGGAGAGGCTGTTGTCC   76776         C__
                                CCAGGAGAGGC   TGTTC
                                ||||||||||   |||||
                                GGTCCTCTCCG   ACAGG
                                      ACA
GAM3409  LOC144266 5'  TCACAGGAGAGGCCCAGACTC  76777   _         __
                                TC CAGGAGAGGCCTG  TTC
                                || ||||||||||||  |||
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                                AG GTCCTCTCCGGGT  GAG
                                 T           CT
GAM3409  LOC144373 3'  TCCAGGAGGGGAGCTGCCC    76598         A  C_
                                TCCAGGAG GG  CTGTTC
                                |||||||| ||  ||||||
                                AGGTCCTC CC  GACGGG
                                     C  TC
GAM3409  LOC145098 5'  CAGGAGAGAGCACCGGGACC   76778         _ _   TTC
                                CAGGAGAG GC CTG   ACC
                                |||||||| || |||   |||
                                GTCCTCTC CG GGC   TGG
                                     T  T   CC_
GAM3409  LOC145547 5'  TCCAGGAAGAGGCCTTGGGCCC 76779         _      GTTCA
                                TCCAGGA GAGGCCT     CCC
                                ||||||| |||||||     |||
                                AGGTCCT CTCCGGA     GGG
                                     T      ACCC_
GAM3409  LOC145836 5'  CAGGGAGAGGCCGGTGAGCCC  76780      _      T  TCA
                                CAGG AGAGGCC GT   CCC
                                |||| ||||||| ||   |||
                                GTCC TCTCCGG CA   GGG
                                  C      C  CTC
GAM3409  LOC146229 5'  TCCGGCAGAGGCCCCGCC    76781     A  _      _
                                TCC GG AGAGGCCT GTT
                                ||| || |||||||| |||
                                AGG CC TCTCCGGG CGG
                                  _ G       G
GAM3409  LOC146429 5'  TCCAGGAGCAGGGCAGTGCT   76782         A__   C_
                                TCCAGGAG   GGC  TGTT
                                ||||||||   |||  ||||
                                AGGTCCTC   CCG  ACGA
                                     GTC   TC
GAM3409  LOC146733 5'  CCAGGAGAGGGCACTTGCC    76783         _ _ _
                                CCAGGAGAGG C CT GTT
                                |||||||||| | || |||
                                GGTCCTCTCC G GA CGG
                                      C T  A
GAM3409  LOC146909 3'  TCCAAGAGGGGTATCC      76784         A  CC
                                TCCAGGAG GG  TGTTC
                                |||||||| ||  |||||
                                AGGTTCTC CC  ATAGG
                                     C  __
GAM3409  LOC148426 3'  CAGGCTCCTGTTCACCC     76785      AGAGG
                                CAGG    CCTGTTCACCC
                                ||||    ||||||||||
                                GTCC    GGACAAGTGGG
                                  GA___
GAM3409  LOC150271 3'  TCCATGGGAGGCTCCATCC    76786      _  A    _
                                TCCA GG GAGGC CTGTTC
                                |||| || ||||| ||||||
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                                AGGT CC CTCCG GGTAGG
                                  A _    A
GAM3409  LOC150279 3'  CCTAGGAGAGGCCTGTTCA   76787   _
                                CC AGGAGAGGCCTGTTCA
                                || ||||||||||||||||
                                GG TCCTCTCCGGACAAGT
                                 A
GAM3409  LOC150295 3'  TCCAGGAAAGGATACTC    76788         CC
                                TCCAGGAGAGG  TGTTC
                                ||||||||||  |||||
                                AGGTCCTTTCC  ATGAG
                                       T_
GAM3409  LOC151361 3'  TCTAGGGGAGGCCAGCCC   76789   C  A    T
                                TC AGG GAGGCC GTTC
                                || ||| |||||| ||||
                                AG TCC CTCCGG CGGG
                                 A  C    T
GAM3409  LOC151720 5'  CCCAGGAGAGGGCCACC    76790         CCT  T
                                TCCAGGAGAGG   GT CACC
                                ||||||||||   || ||||
                                GGGTCCTCTCC   CG GTGG
                                      ___  _
GAM3409  LOC152024 5'  TCCAGGAGGGAGGGCTCACC  76791        A  CCT
                                TCCAGGAG GG   GTTCACC
                                |||||||| ||   |||||||
                                AGGTCCTC CC   CGAGTGG
                                     _  TCC
GAM3409  LOC152122 5'  TCCAGGGAGCTCCTGTTCA   76792      A  G_
                                TCCAGG GAG  CCTGTTCA
                                |||||| |||  ||||||||
                                AGGTCC CTC  GGACAAGT
                                   _  GA
GAM3409  LOC152698 5'  TCCAGGAGGCGCTTGGAAACC  76793        AG  C  TTC
                                TCCAGGAG  GC TG   ACC
                                ||||||||  || ||   |||
                                AGGTCCTC  CG AC   TGG
                                     CG  A  CTT
GAM3409  LOC153505 3'  CAGGGGGAGCTGGGCCACCC   76794     A_  GC   T_
                                CAGG  GAG  CTG  TCACCC
                                ||||  |||  |||  ||||||
                                GTCC  CTC  GAC  GGTGGG
                                  CC   __   CC
GAM3409  LOC154789 5'  TCCAGGAGATGAATGCCGCT   76795        G____   T
                                TCCAGGAGA    GCC GTT
                                |||||||||    ||| |||
                                AGGTCCTCT    CGG CGA
                                     ACTTA  _
GAM3409  LOC154881 3'  CAGGGAGAAGCTTTCATCC   76796     _    CTG   _
                                CAGG AGAGGC   TTCA CC
                                |||| ||||||   |||| ||
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                                GTCC TCTTCG   AAGT GG
                                  C     A__    A
GAM3409  LOC155060 3'  CCCAGGAGAGGTTGCTC     76797          CC
                                TCCAGGAGAGG  TGTTC
                                ||||||||||  |||||
                                GGGTCCTCTCC  ACGAG
                                      A_
GAM3409  LOC155072 5'  TCCAGAAGTCTCTGTTCA     76798        AGGC
                                TCCAGGAG    CTGTTCA
                                ||||||||    |||||||
                                AGGTCTTC    GACAAGT
                                     AGA_
GAM3409  LOC157280 5'  TCCAGGAGGCGCTTGGAAACC  76793        AG  C  TTC
                                TCCAGGAG  GC TG   ACC
                                ||||||||  || ||   |||
                                AGGTCCTC  CG AC   TGG
                                     CG  A  CTT
GAM3409  LOC157695 5'  TCCAGGAGATGCTGCTC     76799        G  C
                                TCCAGGAGA GC TGTTC
                                |||||||||  || |||||
                                AGGTCCTCT CG ACGAG
                                      A  _
GAM3409  LOC157860 3'  CCCAGGAGGGGGTGCCC     76800        A  CC
                                TCCAGGAG GG  TGTTC
                                ||||||||  ||  |||||
                                GGGTCCTC CC  ACGGG
                                     _  CC
GAM3409  LOC158230 3'  TCCAGGAGAGGGTGTCAGCC   76801          CC    CA
                                TCCAGGAGAGG  TGTT  CC
                                ||||||||||  ||||  ||
                                AGGTCCTCTCC  ACAG  GG
                                      C_    TC
GAM3409  LOC164397 5'  TCCAGAAGAGGATGTCC     76802          CC
                                TCCAGGAGAGG  TGTTC
                                ||||||||||  |||||
                                AGGTCTTCTCC  ACAGG
                                      T_
GAM3409  LOC170221 3'  TCCAGGAGGGCGCCGATCC    76803        A  _  _
                                TCCAGGAG GGC CTG TTC
                                |||||||| ||| ||| |||
                                AGGTCCTC CCG GGC AGG
                                     _  C   T
GAM3409  LOC170396 3'  CAGGAAAGATGTTTAC      76804         CC    C
                                CAGGAGAGG  TGTT AC
                                |||||||||  |||| ||
                                GTCCTTTCT  ACAA TG
                                      __    A
GAM3409  LOC197201 3'  TCCAGGAAGGCTCAGGCGGCTC 76805         _____    CT
                                TCCAGGAG    AGGC  GTTC
                                ||||||||    ||||  ||||
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                                AGGTCCTT    TCCG  CGAG
                                    CCGAG   C_
GAM3409  LOC199678 3'  TCCAGGAGAAGGTGGCGGAACC 76806          CCT  TC_
             C                   TCCAGGAGAGG   GT   ACCC
                                 ||||||||||   ||   ||||
                                 AGGTCCTCTTC   CG   TGGG
                                     CAC  CCT
GAM3409  LOC200226 3'  CCCAGGAGGGGGTTGCTC    76807        A  CC
                                 TCCAGGAG GG  TGTTC
                                 ||||||||  ||  |||||
                                 GGGTCCTC CC  ACGAG
                                     C  CA
GAM3409  LOC200311 3'  TCCATGGGAGGCTCCATCC    76786      _  A    _
                                 TCCA GG GAGGC CTGTTC
                                 ||||  ||  |||||  ||||||
                                 AGGT CC CTCCG GGTAGG
                                   A  _    A
GAM3409  LOC200491 5'  TCCAGAAGAGGCACGTCC    76808           C
                                 TCCAGGAGAGGC TGTTC
                                 ||||||||||||  |||||
                                 AGGTCTTCTCCG GCAGG
                                       T
GAM3409  LOC202868 5'  TCCAGAAGTCTCTGTTCA    76798         AGGC
                                 TCCAGGAG   CTGTTCA
                                 ||||||||   |||||||
                                 AGGTCTTC   GACAAGT
                                     AGA_
GAM3409  LOC202915 3'  CAGGAGAGGCCCCACC      76810           GTT
                                 CAGGAGAGGCCT   CACC
                                 ||||||||||||   ||||
                                 GTCCTCTCCGGG   GTGG
                                        ___
GAM3409  LOC202915 5'  TCCAGGGAGGCCTGGCC     76809       A       TT
                                 TCCAGG GAGGCCTG  C
                                 ||||||  ||||||||  |
                                 AGGTCC CTCCGGAC  G
                                    _       CG
GAM3409  LOC202934 5'  TCAAGGAGAGGCAAATCAC    76811    C       CTGT
                                 TC AGGAGAGGC   TCAC
                                 ||  |||||||||   ||||
                                 AG TCCTCTCCG   AGTG
                                   T       TTT_
GAM3409  LOC203297 5'  CCAGGGGTAGTTCACCC     76670      AGA  CCT
                                 CCAGG   GG   GTTCACCC
                                 |||||   ||   ||||||||
                                 GGTCC   CC   CAAGTGGG
                                    ___  AT_
GAM3409  LOC219294 3'  TCCAGGAGATGTTCTACATGCT 76774          G_____  C
             C                   TCCAGGAGA     GC TGTTC
                                 |||||||||     || |||||
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                                AGGTCCTCT     TG ACGAG
                                     ACAAGA  T
GAM3409  LOC219295 3'  TCCAGGAGATGTTCTACATGCT 76774         G_____  C
              C                   TCCAGGAGA     GC TGTTC
                                  |||||||||     || |||||
                                  AGGTCCTCT     TG ACGAG
                                       ACAAGA  T
GAM3409  LOC220021 5'  TCCAGAGGGGGATCCTATTC   76812      G  A  ___
                                  TCCAG AG GG   CCTGTTC
                                  ||||| || ||   |||||||
                                  AGGTC TC CC   GGATAAG
                                     _  C  CTA
GAM3409  LOC221312 3'  TCCTAGGAGAGCCTTTATTC   76813     _     G   __
                                  TCC AGGAGAG CCT  GTTC
                                  ||| ||||||| |||  ||||
                                  AGG TCCTCTC GGA  TAAG
                                    A      _  AA
GAM3409  LOC222031 3'  CCCAGGAGGGGCAGCTC     76814        A   CT
                                  TCCAGGAG GGC  GTTC
                                  |||||||| |||  ||||
                                  GGGTCCTC CCG  CGAG
                                       C   T_
GAM3409  LOC222166 3'  CCCAGGAGGGGCAGTGACCC   76815        A   CT  TC
                                  TCCAGGAG GGC  GT  ACCC
                                  |||||||| |||  ||  ||||
                                  GGGTCCTC CCG  CA  TGGG
                                       C   T_  C_
GAM3409  LOC253100 5'  TCCAGGAAGGGGTCCCGTAGCC 76816         A_  _    TCA
                                  TCCAGGAG  GG CCTGT   CC
                                  ||||||||  || |||||   ||
                                  AGGTCCTT  CC GGGCA   GG
                                       CC  A    TC_
GAM3409  LOC255096 3'  TCCAGGAAGGCCTCCCAC     76817        G     G
                                  TCCAGGA AGGCCT TTCAC
                                  ||||||| |||||| |||||
                                  AGGTCCT TCCGGA GGGTG
                                       _     _
GAM3409  LOC255448 5'  TCCAGGAGGCGCTTGGAAACC  76793        AG  C  TTC
                                  TCCAGGAG  GC TG   ACC
                                  ||||||||  || ||   |||
                                  AGGTCCTC  CG AC   TGG
                                       CG  A  CTT
GAM3409  LOC255452 3'  CCCAGGCCCCTGTTCACCC    76818       AGAGG
                                  TCCAGG    CCTGTTCACCC
                                  ||||||    ||||||||||||
                                  GGGTCC    GGACAAGTGGG
                                     GG___
GAM3409  LOC255465 5'  TCAAGGAGAGGCAAGTCAC    76819    C        CT  T
                                  TC AGGAGAGGC  GT CAC
                                  || |||||||||  || |||
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                                AG TCCTCTCCG  CA GTG
                                 T       TT  _
GAM3409  LOC256158 5'  TCCAGGAGGCGGTGGCCGCCC  76820        A____   T
                                TCCAGGAG    GGCC GTTC
                                ||||||||    |||| ||||
                                AGGTCCTC    CCGG CGGG
                                    CGCCA   _
GAM3409  LOC256537 3'  TCCAGGAGCGGCGCAATTTTGT 76821        A  C_____
                 TC                TCCAGGAG GGC      TGTTC
                                ||||||||  |||      |||||
                                AGGTCCTC CCG      ACAAG
                                    G   CGTTAAA
GAM3409  LOC256848 5'  TCCAGGAGGGACCACC      76822        A   TGTTC
                                TCCAGGAG GGCC    ACC
                                ||||||||  ||||    |||
                                AGGTCCTC CTGG    TGG
                                    C   _____
GAM3409  LOC256903 5'  CCTGGGAGAGGCCACAAAATGC 76823    A_       _____
                 CC                CC  GGAGAGGCC     TGTTC
                                ||  |||||||||     |||||
                                GG  CCTCTCCGG     ACGGG
                                 AC        TGTTTT
GAM3409  LOC257358 3'  CAGGAGAAGCCTTGTGCCA   76824          _  _
                                CAGGAGAGGCCT GT TCA
                                ||||||||||||  ||  |||
                                GTCCTCTTCGGA CA GGT
                                      A  C
GAM3409  LOC257472 3'  TCCAGAGAGGCAATGTTC    76664      G     C_
                                TCCAG AGAGGC  TGTTC
                                |||||  ||||||  |||||
                                AGGTC TCTCCG  ACAAG
                                   _     TT
GAM3409  LOC51003  3'  TCCAGGAGATGGTCTTGCCC   76825        _  C  _
                                TCCAGGAGA GG CT GTTC
                                |||||||||  ||  ||  ||||
                                AGGTCCTCT CC GA CGGG
                                     A  A  A
GAM3409  LOC90133  3'  TCCAGGAGTGGCTGCTGTCC   76826        A   __
                                TCCAGGAG GGC  CTGTTC
                                ||||||||  |||  ||||||
                                AGGTCCTC CCG  GACAGG
                                    A   AC
GAM3409  LOC90249  3'  CCGGGAGGGGGCCTGTCC    76827    A   A_
                                CC GGAG  GGCCTGTTC
                                ||  ||||  |||||||||
                                GG CCTC  CCGGACAGG
                                 C    CC
GAM3409  LOC91097  5'  TCCAGGAGGGGCCCGTCC    76689        A
                                TCCAGGAG GGCCTGTTC
                                ||||||||  |||||||||
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                                AGGTCCTC CCGGGCAGG
                                     C
GAM3409 LOC91156 3' TCCAGGAGGTGGAGGCTGCCC 76828       ____    C
                                TCCAGGA   GAGGC TGTTC
                                |||||||   ||||| |||||
                                AGGTCCT   CTCCG ACGGG
                                    CCAC   _
GAM3409 LOC91179 3' TCCAGGAGCGGCTGCAGGACC 76702       A  C  TC_
                                TCCAGGAG GGC TGT  ACC
                                |||||||| ||| |||  |||
                                AGGTCCTC CCG ACG  TGG
                                     G  _  TCC
GAM3409 LOC91748 5' TCCAGAGAGGCTCTGGGGCTC 76829     G    _ ___
                                TCCAG AGAGGC CT  GTTC
                                ||||| |||||| ||  ||||
                                AGGTC TCTCCG GA  CGAG
                                   _    A CCC
GAM3409 LOC92162 5' TCCGGGGAGGGGCTCACCC   76830    A A   CCT
                                TCC GG GAGG  GTTCACCC
                                ||| || ||||  ||||||||
                                AGG CC CTCC  CGAGTGGG
                                  C _   C__
GAM3409 LOC92710 3' CAGGTGAGGCCTGAGACAC   76831    A      TT_
                                CAGG GAGGCCTG  CAC
                                |||| ||||||||  |||
                                GTCC CTCCGGAC  GTG
                                  A      TCT
GAM3409 LOC93259 5' TCCAGGAGATGTTTGACACCC 76832       GGCC  TT
                                TCCAGGAGA   TG  CACCC
                                |||||||||   ||  |||||
                                AGGTCCTCT   AC  GTGGG
                                     ACAA  T_
GAM3410 ALEX2   5' TGAAAAGACGGGGGGTGAACGG 76835     T  GAGT  A
            C                    TGAAA GA   GG GTGAACGGC
                                 |||||  ||   || |||||||||
                                 ACTTT CT   CC CACTTGCCG
                                    T  GCCC  _
GAM3410 APLP2   3' TGGAAGGGGAAGTGAACGG   76836   AG  T  _
                                 TG  AG GGA GTGAACGG
                                 ||  || ||| ||||||||
                                 AC  TC CCT CACTTGCC
                                  CT  C  T
GAM3410 ATP6V0C  3' TGGAATGAGGAGGGGTG    76837   A    _  T  A
                                 TG AATGAG AG GG GTG
                                 || |||||| || || |||
                                 AC TTACTC TC CC CAC
                                  C    C  _  _
GAM3410 B3GALT5  3' TGAAATGAGAGAGCAGCAGATG 76838        T  _   AAC
            GC                    TGAAATGAGAG GG AGTG  GGC
                                  |||||||||| || ||||  |||
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                                ACTTTACTCTC TC TCGT   CCG
                                      _ G    CTA
GAM3410 B3GALT5  3'  TGAAATGAGAGAGCAGCAGATG 76838          T _   AAC
           GC                   TGAAATGAGAG GG AGTG   GGC
                                |||||||||| || ||||   |||
                                ACTTTACTCTC TC TCGT   CCG
                                      _ G    CTA
GAM3410 B3GALT5  3'  TGAAATGAGAGAGCAGCAGATG 76838          T _   AAC
           GC                   TGAAATGAGAG GG AGTG   GGC
                                |||||||||| || ||||   |||
                                ACTTTACTCTC TC TCGT   CCG
                                      _ G    CTA
GAM3410 B3GALT5  3'  TGAAATGAGAGAGCAGCAGATG 76838          T _   AAC
           GC                   TGAAATGAGAG GG AGTG   GGC
                                |||||||||| || ||||   |||
                                ACTTTACTCTC TC TCGT   CCG
                                      _ G    CTA
GAM3410 B3GALT5  3'  TGAAATGAGAGAGCAGCAGATG 76838          T _   AAC
           GC                   TGAAATGAGAG GG AGTG   GGC
                                |||||||||| || ||||   |||
                                ACTTTACTCTC TC TCGT   CCG
                                      _ G    CTA
GAM3410 BCRP2    3'  GAGATGAGGGTGGAGCAG    76839    A    A     GAAC
                                GA ATGAG GTGGAGT    GG
                                || ||||| |||||||    ||
                                CT TACTC CACCTCG    TC
                                 C    C      ____
GAM3410 CRLF1    3'  TGAAGTGAGGGTACAGAGGTGG 76840     A   A   G  TGAAC
           C                     TGAA TGAG GTG AG     GGC
                                |||| |||| ||| ||     |||
                                ACTT ACTC CAT TC     CCG
                                  C   C   G  TCCA_
GAM3410 IGFBP5   3'  AAATGAGATGAAATGAGTGGC  76841        G       AC
                                AAATGAGA TGGAGTGA  GGC
                                |||||||| ||||||||  |||
                                TTTACTCT ACTTTACT  CCG
                                      _       CA
GAM3410 IL1RN    3'  TGGAATGAGGGAGGAAGAGGC  76842    A     AGT   T  C_
                                TG AATGAG   GGAG GAA  GGC
                                || ||||||   |||| |||  |||
                                AC TTACTC   CCTC CTT  CCG
                                 C     ___    _   CT
GAM3410 MMP19    3'  GAAATGAAAGGGTGGGTG    76843          __    A
                                GAAATGAGA  GTGG GTG
                                |||||||||  |||| |||
                                CTTTACTTT  CACC CAC
                                      CC   _
GAM3410 MMP19    3'  GAAATGAAAGGGTGGGTG    76843          __    A
                                GAAATGAGA  GTGG GTG
                                |||||||||  |||| |||
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                                CTTTACTTT  CACC CAC
                                     CC   _
GAM3410  MMP19    3'  GAAATGAAAGGGTGGGTG    76843         __    A
                                GAAATGAGA  GTGG GTG
                                |||||||||  |||| |||
                                CTTTACTTT  CACC CAC
                                     CC   _
GAM3410  MMP19    3'  GAAATGAAAGGGTGGGTG    76843         __    A
                                GAAATGAGA  GTGG GTG
                                |||||||||  |||| |||
                                CTTTACTTT  CACC CAC
                                     CC   _
GAM3410  NT5M     3'  TGAGGTCAGGCTGAACGG    76844      A __ AG
                                TGAG GT  GG  TGAACGG
                                |||| ||  ||  |||||||
                                ACTC CA  CC  ACTTGCC
                                  _ GT  G_
GAM3410  PLA2G4B  3'  TGAATGAGAGTTAGGGGTG   76845      A     __ A
                                TGAA TGAGAGT  GG GTG
                                |||| |||||||  || |||
                                ACTT ACTCTCA  CC CAC
                                  _      AT  C
GAM3410  STX1A    3'  TGGAGTGGAGTGGCAG      76846    A        AA
                                TG GAGTGGAGTG  CGG
                                || ||||||||||  |||
                                AC CTCACCTCAC  GTC
                                 _         C_
GAM3410  WDR1     5'  CGGGAGTGGAGTGGGCGG    76847    A        AA
                                TG GAGTGGAGTG  CGG
                                || ||||||||||  |||
                                GC CTCACCTCAC  GCC
                                  C         CC
GAM3410  WDR1     5'  CGGGAGTGGAGTGGGCGG    76847    A        AA
                                TG GAGTGGAGTG  CGG
                                || ||||||||||  |||
                                GC CTCACCTCAC  GCC
                                  C         CC
GAM3410  DKFZp761J139 5'  TGAAGTGGGAGAGCCAAGCGGC 76848      AT__     G   TGAA
                                TGAA    GAGAGT GAG    CGGC
                                ||||    |||||| |||    ||||
                                ACTT    CTCTCG TTC    GCCG
                                   CACC     G  ____
GAM3410  F23149_1 5'  TGAGATGAGGTGGGCGGG    76849     A    A    A   AAC
                                TGA ATGAG GTGG GTG   GG
                                ||| ||||| |||| |||   ||
                                ACT TACTC CACC CGC   CC
                                  C    _   _  ___
GAM3410  FLJ10759 3'  TGAAGTGGGAGAGGGGCAGGC  76850      A  A   T  A   AAC
                                TGAA TG GAG GG GTG   GGC
                                |||| || ||| || |||   |||
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                                ACTT AC CTC CC CGT   CCG
                                  C  C   T  C  ___
GAM3410  FLJ12910  5'  TGAGAATGGGGGTGGTGTGGC  76851        A_   AAC_
                                TGAGAGTGG  GTG    GGC
                                |||||||||  |||    |||
                                ACTCTTACC  CAC    CCG
                                     CC   CACA
GAM3410  FLJ23548  5'  TGAAATGAGAGTGGGGTACCAG 76852            A   AA
                                TGAAATGAGAGTGG GTG  CGG
                                |||||||||||||| |||  |||
                                ACTTTACTCTCACC CAT  GTC
                                         C   G_
GAM3410  IRF5      3'  TGAAGTGAGAGCGGGTA     76853      A        A
                                TGAA TGAGAGTGG GTG
                                |||| ||||||||| |||
                                ACTT ACTCTCGCC CAT
                                  C        _
GAM3410  KIAA0429  5'  ATGGGAGTGGGGAAGGGC    76854     A     AGT   C
                                ATG GAGTGG   GAA GGC
                                ||| ||||||   ||| |||
                                TAC CTCACC   CTT CCG
                                  C     C__   C
GAM3410  KIAA0451  3'  TGAAAGTGAGAGGAGGTGAGTG 76855      _     TG A    AC
            GC                    TGAAA TGAGAG  G GTGA  GGC
                                |||||  ||||||  | ||||  |||
                                ACTTT ACTCTC  C CACT  CCG
                                   C     CT _    CA
GAM3410  KIAA0494  3'  TGAGAGTGGATGGAAGGC    76856          GT   C
                                TGAGAGTGGA  GAA GGC
                                ||||||||||  ||| |||
                                ACTCTCACCT  CTT CCG
                                      AC  _
GAM3410  KIAA0825  3'  TGAAAGGAGAATGGACGG    76857       T       GTGAA
                                TGAAA GAGAGTGGA     CGG
                                |||||  |||||||||     |||
                                ACTTT CTCTTACCT     GCC
                                   C        _____
GAM3410  MGC5139   3'  TGGAATGTGAGTAACACAA   76858    A    _     _
                                TG GAGTG GAGTGA ACGG
                                || |||||  ||||||  |||||
                                AC CTTAC CTCATT TGTT
                                 _    A     G
GAM3410  PELI2     3'  TGAAATGAAAGTAACAGGAATG 76859             _ T   C
            G                    TGAAATGAGAGTGG AG GAA GG
                                |||||||||||||| || ||| ||
                                ACTTTACTTTCATT TC CTT CC
                                         G _   A
GAM3410  PI4KII    3'  TGAGGGAGAGTGGAGAAAGGC  76860     AAT        T   C
                                TGA   GAGAGTGGAG GAA GGC
                                |||   |||||||||| ||| |||
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                                ACT   CTCTCACCTC TTT CCG
                                  CC_       _  _
GAM3410  RNF38    5'  TGAAGTGAGCATCCTCTTGAAC 76861      A    AGTGGAG_
              GG                  TGAA TGAG       TGAACGG
                                  |||| ||||       |||||||
                                  ACTT ACTC       ACTTGCC
                                    C    GTAGGAGA
GAM3410  SV2B     3'  TGAAGTGAAAAAGAAGTGGATG 76862      A     T     AAC
              GC                  TGAA TGAGAG GGAGTG   GGC
                                  |||| |||||| ||||||   |||
                                  ACTT ACTTTT CTTCAC   CCG
                                    C     T     CTA
GAM3410  TIX1     3'  TGAAATGAGTGTGGAGAAAGGG 76863          A     T   C
              C                    TGAAATGAG GTGGAG GAA GGC
                                  |||||||||| |||||| ||| |||
                                  ACTTTACTC CACCTC TTT CCG
                                       A     _  C
GAM3410  TOMM70A  3'  TGGAATGACAGTATAGAATGGC 76864    A    G    GAGT   C
                                  TG AATGA AGTG    GAA GGC
                                  || ||||| ||||    ||| |||
                                  AC TTACT TCAT    CTT CCG
                                   C    G    AT__   A
GAM3410  LOC124750 5'  TGAAGTGGGCGGTGGAGGGGC  76865      A  AGA_     TGAAC
                                  TGAA TG    GTGGAG     GGC
                                  |||| ||    ||||||     |||
                                  ACTT AC    CACCTC     CCG
                                    C  CCGC     C_____
GAM3410  LOC143173 5'  TGGGATGAGGTGAAGTG     76866    AA    A
                                  TG  ATGAG GTGGAGTG
                                  ||  ||||| ||||||||
                                  AC  TACTC CACTTCAC
                                   CC    _
GAM3410  LOC144262 5'  TGGAATGAGTGTGGACAAACGG 76867    A     A    G
                                  TG AATGAG GTGGA TGAACGG
                                  || |||||| ||||| |||||||
                                  AC TTACTC CACCT GTTTGCC
                                   C     A    _
GAM3410  LOC153196 5'  TGAGGGAGAGTGGGTGGGG    76868     AAT      A   AAC
                                  TGA   GAGAGTGG GTG   GG
                                  |||   |||||||| |||   ||
                                  ACT   CTCTCACC CAC   CC
                                    CC_       _   C__
GAM3410  LOC200298 3'  TGAATGAGAGTGGCTCGTCATG 76869      A       AG  AAC_
              GC                  TGAA TGAGAGTGG  TG    GGC
                                  |||| |||||||||  ||    |||
                                  ACTT ACTCTCACC  GC    CCG
                                    _       GA  AGTA
GAM3410  LOC202052 3'  TGAGATGGAGTGGAGTGCAGTG 76870     A   A        AAC_
              GC                  TGA ATG GAGTGGAGTG    GGC
                                  ||| ||| ||||||||||    |||
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                                ACT TAC CTCACCTCAC    CCG
                                  C  _        GTCA
GAM3410  LOC253918 5'  TGAAGTAAGTGTGGGTG     76871     A   A   A
                                TGAA TGAG GTGG GTG
                                |||| |||| |||| |||
                                ACTT ATTC CACC CAC
                                  C   A   _
GAM3410  LOC255718 5'  TGGGATGGGGTGAACGG     76872    A  G   A
                                TG GA TGG GTGAACGG
                                || || ||| ||||||||
                                AC CT ACC CACTTGCC
                                 C  _  C
GAM3410  LOC55885  3'  TGGAGTGGAGGTGCACGG    76873    A      _  A
                                TG GAGTGGAG TG ACGG
                                || |||||||| || ||||
                                AC CTCACCTC AC TGCC
                                 _      C  G
GAM3411  CASP2     3'  GCAGTCCGTGACTCGGTG    76876     G   CA_
                                GCAGT CCGT   TTGGTG
                                ||||| ||||   ||||||
                                CGTCA GGCA   AGCCAC
                                   _   CTG
GAM3411  CASP2     3'  GCAGTCCGTGACTCGGTG    76876     G   CA_
                                GCAGT CCGT   TTGGTG
                                ||||| ||||   ||||||
                                CGTCA GGCA   AGCCAC
                                   _   CTG
GAM3411  CYP7B1    3'  ACAGTGCCCAATCTATTGGTG  76877        __  _
                                GCAGTGCC  GTC ATTGGTG
                                ||||||||  ||| |||||||
                                TGTCACGG  TAG TAACCAC
                                     GT   A
GAM3411  DAG1      3'  GCAGTGCCCAATGGTG      76878        GT  T
                                GCAGTGCC  CA TGGTG
                                ||||||||  ||  |||||
                                CGTCACGG  GT ACCAC
                                     __  T
GAM3411  HEM1      5'  GCAGGCATCAATGGTG      76879     T  C   T
                                GCAG GC GTCA TGGTG
                                |||| ||  |||| |||||
                                CGTC CG TAGT ACCAC
                                  _ _   T
GAM3411  KLF4      5'  GCGGTGCCGCCAGGTG      76880    A       TT
                                GC GTGCCGTCA  GGTG
                                ||  |||||||||  ||||
                                CG CACGGCGGT  CCAC
                                 C       __
GAM3411  RCE1      3'  GCAGTACCCCTTGGTG      76881        G  A
                                GCAGTGCC TC TTGGTG
                                |||||||| ||  ||||||
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                                CGTCATGG GG AACCAC
                                     _ _
GAM3411 UQCRC1   5' GCAGTACCGTACAGTTGGTG  76882        _ _
                                GCAGTGCCGT CA TTGGTG
                                |||||||||| || ||||||
                                CGTCATGGCA GT AACCAC
                                      T  C
GAM3411 C20orf39 3' GCAGTGCCCGTCTGTCTGGTG 76883       _  A__
                                GCAGTGCC GTC  TTGGTG
                                |||||||| |||  ||||||
                                CGTCACGG CAG  GACCAC
                                     G  ACA
GAM3411 CHERP    3' GCAGCGCCTCCTGGTG     76884       G  A
                                GCAGTGCC TC TTGGTG
                                |||||||| || ||||||
                                CGTCGCGG AG GACCAC
                                     _ _
GAM3411 DKFZP434H204 5' ACACCGGTGTCATTGGTG   76885    G  CC
                                GCA TG  GTCATTGGTG
                                ||| ||  ||||||||||
                                TGT GC  CAGTAACCAC
                                  G  CA
GAM3411 ETL      5' GCGGTGGCCGCAGTGGTG   76886   A  _  T  T
                                GC GTG CCG CA TGGTG
                                || ||| ||| || |||||
                                CG CAC GGC GT ACCAC
                                 C  C  _  C
GAM3411 KIAA0418 3' GCATGTAATCCATTGGTG   76887    _  CCG
                                GCA GTG  TCATTGGTG
                                ||| |||  |||||||||
                                CGT CAT  GGTAACCAC
                                  A  TA_
GAM3411 KIAA1649 3' ACAGTGCCCCTTGGTG     76888       G  A
                                GCAGTGCC TC TTGGTG
                                |||||||| || ||||||
                                TGTCACGG GG AACCAC
                                     _ _
GAM3411 PELI1    3' GCTGCAGTCATTGGTG     76889   AG  C
                                GC  TGC GTCATTGGTG
                                ||  ||| ||||||||||
                                CG  ACG CAGTAACCAC
                                 __  T
GAM3411 PEPP3    3' GCATGTGCTCCACTGGTG   76890   _  CG
                                GCA GTGC  TCATTGGTG
                                ||| ||||  |||||||||
                                CGT CACG  GGTGACCAC
                                  A  A_
GAM3411 RNPS1    3' GCGGTGTGTGCATCGGTG   76891   A  CC _
                                GC GTG  GT CATTGGTG
                                || |||  || ||||||||
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                                CG CAC  CA GTAGCCAC
                                 C   A_  C
GAM3411  RNPS1    3'  GCGGTGTGTGCATCGGTG    76891    A   CC  _
                                GC GTG  GT CATTGGTG
                                || |||  || ||||||||
                                CG CAC  CA GTAGCCAC
                                 C   A_  C
GAM3411  SAE1     3'  GCTGTGCTTCCACTGGTG    76892    A    CG
                                GC GTGC  TCATTGGTG
                                || ||||  |||||||||
                                CG CACG  GGTGACCAC
                                 A    AA
GAM3411  SLC31A2  3'  GCAGTGCCTTCTGGTG     76893        G  AT
                                GCAGTGCC TC  TGGTG
                                |||||||| ||  |||||
                                CGTCACGG AG  ACCAC
                                     A  __
GAM3411  TRIM11   3'  GCAGTGACCCATCGGTG     76894       _  GT
                                GCAGTG CC  CATTGGTG
                                |||||| ||  ||||||||
                                CGTCAC GG  GTAGCCAC
                                   T  __
GAM3411  LOC146315 5'  GCAGCGCCAGGCAGTGGTG    76895         T_  T
                                GCAGTGCCG  CA TGGTG
                                |||||||||  || |||||
                                CGTCGCGGT  GT ACCAC
                                     CC  C
GAM3411  LOC150113 3'  AGTGCCGTGGAGATTGGTG    76896        C___
                                AGTGCCGT    ATTGGTG
                                ||||||||    |||||||
                                TCACGGCA    TAACCAC
                                     CCTC
GAM3411  LOC150287 3'  GCAGTACCTCCACGGTG     76897         GT   T
                                GCAGTGCC  CAT GGTG
                                ||||||||  ||| ||||
                                CGTCATGG  GTG CCAC
                                     AG  _
GAM3411  LOC152790 5'  GCAGTTTGCCATTGGTG     76898      GCC
                                GCAGT   GTCATTGGTG
                                |||||   ||||||||||
                                CGTCA   CGGTAACCAC
                                  AA_
GAM3411  LOC202134 5'  GCAGTGCCGGGCCCATGGTG   76899         ___   T
                                GCAGTGCCG   TCAT GGTG
                                |||||||||   |||| ||||
                                CGTCACGGC   GGTA CCAC
                                     CCG   _
GAM3411  LOC221288 3'  ACAGTGCCCCTTGGTG      76888         G  A
                                GCAGTGCC TC TTGGTG
                                |||||||| || ||||||
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                                TGTCACGG GG AACCAC
                                    _ _
GAM3411  LOC222112 3'  GCAATGCCAACCCTGGTG    76900        TCA
                                GCAGTGCCG   TTGGTG
                                |||||||||   ||||||
                                CGTTACGGT   GACCAC
                                     TGG
GAM3411  LOC256158 5'  GCAGTGCCCGCCTCATTGGTG  76901       G___
                                GCAGTGCC    TCATTGGTG
                                ||||||||    |||||||||
                                CGTCACGG    AGTAACCAC
                                     GCGG
GAM3411  LOC90249  5'  GCAGGTGCCCATTGGTG     76902     _   GT
                                GCAG TGCC  CATTGGTG
                                |||| ||||  ||||||||
                                CGTC ACGG  GTAACCAC
                                  C   __
GAM3412  BID       3'  TGGATGATATGAAGGCCA     76905    _    A  A
                                TGG TGATAT AAG CCA
                                ||| |||||| ||| |||
                                ACC ACTATA TTC GGT
                                  T     C  C
GAM3412  BTEB1     3'  CTCCTGAAACTATAAAGA     76906     A   TGA
                                CTCC TGG   TATAAAGA
                                |||| |||   ||||||||
                                GAGG ACT   ATATTTCT
                                  _   TTG
GAM3412  DOCK1     3'  CTCCATGACGCTAAAGGCCAC  76907       GT ATA    A
                                CTCCATG  G   TAAAG CCAC
                                |||||||  |   ||||| ||||
                                GAGGTAC  C   ATTTC GGTG
                                    TG G__     C
GAM3412  GALNT2    3'  CCTCCAGGGGACACAAAGGCCA 76908       T  T       A
              C                  CCTCCA GG GATATAAAG CCAC
                                ||||||  ||  |||||||||  ||||
                                GGAGGT CC CTGTGTTTC GGTG
                                   C  _        C
GAM3412  NELL2     3'  CTACATGGTGATGTGAGAC    76909    C       ATAA
                                CT CATGGTGAT    AGAC
                                ||  |||||||||    ||||
                                GA GTACCACTA    TCTG
                                  T        CAC_
GAM3412  SDF2      3'  CTCAATGGTGACATGGCCAC   76910     C        AAAGA
                                CTC ATGGTGATAT    CCAC
                                |||  ||||||||||    ||||
                                GAG TACCACTGTA    GGTG
                                  T        CC___
GAM3412  SPS2      3'  CCTCGGAATGCATATAAAGAC  76911      CAT   _
                                CCTC   GGTG ATATAAAGAC
                                ||||   |||| ||||||||||
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                                GGAG   TTAC TATATTTCTG
                                  CC_   G
GAM3412  C20orf16  5'  CCTCCATGGATGTCACAAGAC  76912        _ A    A
                                CCTCCATGG TG TATAA GAC
                                ||||||||| || ||||| |||
                                GGAGGTACC AC GTGTT CTG
                                     T  A    _
GAM3412  C21orf18  3'  CCCCGTGGTGACAGACCA    76913     A     ATAA
                                CTCC TGGTGAT    AGACCA
                                |||| |||||||    ||||||
                                GGGG ACCACTG    TCTGGT
                                  C      _____
GAM3412  FLJ22692  3'  CCTCCATAGTAGCTGGGACTAC 76914          ATATAAA   C
                                CCTCCATGGTG      GAC AC
                                ||||||||||       ||| ||
                                GGAGGTATCAT      CTG TG
                                      CGACC__   A
GAM3412  KIAA0318  3'  CCACTGTGTCAGGATGAAGACC 76915     G   AT___  A
              AC                  CCAT GTG     AT AAGACCAC
                                ||||| |||     || ||||||||
                                GGTG CAC     TA TTCTGGTG
                                  A   AGTCC  C
GAM3412  KIAA0721  3'  TCCACACATATAAAGGTCAC   76916       GTG       AC
                                TCCATG   ATATAAAG  CAC
                                ||||||   ||||||||  |||
                                AGGTGT   TATATTTC  GTG
                                   G__       CA
GAM3412  KIAA0721  3'  TCCACACATATAAAGGTCAC   76916       GTG       AC
                                TCCATG   ATATAAAG  CAC
                                ||||||   ||||||||  |||
                                AGGTGT   TATATTTC  GTG
                                   G__       CA
GAM3412  KIAA1712  3'  TCTCATGGTGAACCTTGAGACC 76917    _       TATAA_
              A                   TC CATGGTGA     AGACCA
                                || ||||||||      ||||||
                                AG GTACCACT      TCTGGT
                                 A       TGGAAC
GAM3412  LYPLA3    3'  CTCCATAGGTTCCCAGAAGGCC 76918       _   GATATA   A
              A                   CTCCAT GGT     AAG CCA
                                ||||||  |||     ||| |||
                                GAGGTA CCA     TTC GGT
                                   T   AGGGTC   C
GAM3412  MRPL19    3'  TCCATGCTCATTAAAGACCA   76919       GTGATA
                                TCCATG     TAAAGACCA
                                ||||||     |||||||||
                                AGGTAC     ATTTCTGGT
                                   GAGTA_
GAM3412  MRPS18B   3'  CTTCAGGGTGATATCCCATCAC 76920    C  T       AAAGAC
                                CT CA GGTGATAT     CAC
                                || || ||||||||     |||
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                                GA GT CCACTATA     GTG
                                 A  C       GGGTA_
GAM3412  OSBPL8    3'  TAATGCACACATAAAGGCCAC  76921       ___       A
                                TGGTG   ATATAAAG CCAC
                                |||||   |||||||| ||||
                                ATTAC   TGTATTTC GGTG
                                   GTG       C
GAM3412  RHOBTB1   3'  CCACCATGGTTAAAGGCCA   76922    T      GATA    A
                                CC CCATGGT    TAAAG CCA
                                || |||||||    ||||| |||
                                GG GGTACCA    ATTTC GGT
                                 T       _____     C
GAM3412  RHOBTB1   3'  CCTTCTAATGATTATAAAGA   76923     CCA      _
                                CCT   TGGTGAT ATAAAGA
                                |||   ||||||| |||||||
                                GGA   ATTACTA TATTTCT
                                  AG_      A
GAM3412  TU3A      3'  CCTCCATGGAGCACCTCTGGGG 76924         TGA   AAA____
              ACCAC                  CTCCATGG   TAT      GACCAC
                                |||||||   |||      ||||||
                                GAGGTACC   GTG      CTGGTG
                                     TC_   GAGACCC
GAM3412  LOC126669 3'  TCTGAGGGAGAAAGACCAC   76925    CAT  T  TAT
                                TC   GG GA   AAAGACCAC
                                ||   || ||   |||||||||
                                AG   CC CT   TTTCTGGTG
                                 ACT  _  C__
GAM3412  LOC151196 5'  CCTTCTGGCTACAAAGAC    76926     CCA    GA
                                CCT   TGGT  TATAAAGAC
                                |||   ||||  |||||||||
                                GGA   ACCG  ATGTTTCTG
                                  AG_   __
GAM3412  LOC152580 5'  CCTCCATGGTGTTGCTGACCAC 76927           ATATAAA
                                CCTCCATGGTG      GACCAC
                                ||||||||||      ||||||
                                GGAGGTACCAC      CTGGTG
                                       AACGA__
GAM3412  LOC158434 5'  CTTCATGGTGATATAGGAGAC  76928    C         A_
                                CT CATGGTGATATA  AGAC
                                || ||||||||||||  ||||
                                GA GTACCACTATAT  TCTG
                                 A          CC
GAM3412  LOC163782 3'  CCATGGTGACAGGCCA      76929          ATAA  A
                                CCATGGTGAT    AG CCA
                                ||||||||||    || |||
                                GGTACCACTG    TC GGT
                                       _____  C
GAM3412  LOC204285 5'  CATGGTGACGAGGGAGACCAC  76930         ATAA_
                                CATGGTGAT     AGACCAC
                                |||||||||     |||||||
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                                GTACCACTG    TCTGGTG
                                     CTCCC
GAM3412  LOC204823 5'  CCTCCTCGGTGAAGACCA    76931      A    TATAA
                                CCTCC TGGTGA    AGACCA
                                ||||| ||||||    ||||||
                                GGAGG GCCACT    TCTGGT
                                   A    _____
GAM3412  LOC220001 5'  CCTCCATGGTTGCAGGTAAGGT 76932        GATATA_  AC
           CAC                    CCTCCATGGT     AAG  CAC
                                ||||||||||     |||  |||
                                GGAGGTACCA     TTC  GTG
                                     ACGTCCA   CA
GAM3412  LOC220758 3'  CCTCCATGTTGATGGATGAGGT 76933       G   ATAA_  AC
           CAC                    CCTCCATG TGAT    AG  CAC
                                |||||||| ||||    ||  |||
                                GGAGGTAC ACTA    TC  GTG
                                   A   CCTAC  CA
GAM3412  LOC253392 5'  CATGGCATGTAAAGACCA    76934      G  A
                                CATGGT AT TAAAGACCA
                                |||||| || |||||||||
                                GTACCG TA ATTTCTGGT
                                   _ C
GAM3413  LOC56912  3'  CAAGTAGCTGACAACGATCT   76937    T   ATTTA
                                TAA TGG    ACAACGATCT
                                ||| |||    ||||||||||
                                GTT ATC    TGTTGCTAGA
                                  C  GAC__
GAM3413  LOC58489  3'  TCCAGTTGTACAACGATC    76938     A   GATTTA
                                TCTA TTG     ACAACGATC
                                |||| |||     |||||||||
                                AGGT AAC     TGTTGCTAG
                                  C  A_____
GAM3413  LOC91923  5'  ATTGGATTTGGCAATGAT    76939       AA   C
                                ATTGGATTT  CAA GAT
                                |||||||||  ||| |||
                                TAACCTAAA  GTT CTA
                                     CC   A
GAM3414  SCN3A     3'  TTAATAGAAGTTGTTTATCAGG 76942      TTATA
                                TTAATA    TTGTTTATCAGG
                                ||||||    ||||||||||||
                                AATTAT    AACAAATAGTCC
                                   CTTC_
GAM3414  VCL       3'  TTAATATTGCATTTATATCAGG 76943       A   GTT
                                TTAATATT TATT   TATCAGG
                                |||||||| ||||   |||||||
                                AATTATAA GTAA   ATAGTCC
                                     C   AT_
GAM3414  VCL       3'  TTAATATTGCATTTATATCAGG 76943       A   GTT
                                TTAATATT TATT   TATCAGG
                                |||||||| ||||   |||||||
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                                AATTATAA GTAA   ATAGTCC
                                    C    AT_
GAM3414 ALS2CR3  3' TATTATAGAGATTATCAGG   76944       TTGT
                                TATTATA    TTATCAGG
                                |||||||    ||||||||
                                ATAATAT    AATAGTCC
                                    CTCT
GAM3414 DKFZP434I0714 3' ATATTATATTGTTCCAG    76945           AT
                                ATATTATATTGTTT  CAG
                                ||||||||||||||  |||
                                TATAATATAACAAG  GTC
                                          __
GAM3415 PFKFB1   3' CACTGGAAGTGGGGTGCCT   76948    C      AAC
                                CAC GGAAGTGG   GCCT
                                ||| ||||||||   ||||
                                GTG CCTTCACC   CGGA
                                  A       CCA
GAM3415 ARHF     3' GGGCACCGGAATCCCCTGGGAT 76949    A      GT_____   AC
             GC                   GG CACCGGAA      GGA  GC
                                || |||||||||      |||  ||
                                CC GTGGCCTT      CCT  CG
                                 C       AGGGGAC   A_
GAM3415 FLJ12547 3' AGGGCATCGGAAGTGGGGTGAC 76950     A  C       AAC_
             CC                   AGG CA CGGAAGTGG    GCCT
                                ||| || |||||||||    ||||
                                TCC GT GCCTTCACC    TGGG
                                  C  A        CCAC
GAM3415 FLJ20294 3' TAGGAGAAAGTGGGGTGCCT   76951      CACC      AAC
                                TAGGA    GGAAGTGG   GCCT
                                |||||    ||||||||   ||||
                                ATCCT    CTTTCACC   CGGA
                                   _____       CCA
GAM3415 FREQ     3' TAGGGGGCTGCCAATGAACGCC 76952     ACACCGGA    G
             T                    TAGG       AGTG AACGCCT
                                ||||       |||| |||||||
                                ATCC       TTAC TTGCGGA
                                  CCCGACGG   _
GAM3415 GR6      5' TAGGGCAATGGGAAACGCC    76953     A  CC  AAGT
                                TAGG CA  GG    GGAACGCC
                                |||| ||  ||    ||||||||
                                ATCC GT  CC    CTTTGCGG
                                  C  TA  _____
GAM3415 HSPC043  5' AGGACACCGGGACCGCC     76954         AAGTG  A
                                AGGACACCGG     GA CGCC
                                ||||||||||     || ||||
                                TCCTGTGGCC     CT GCGG
                                      ______ G
GAM3415 HXCP2    3' GAACAAATGAAGTGGGACG    76955      CCG      A
                                GGACA   GAAGTGG ACG
                                |||||   ||||||| |||
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                                CTTGT   CTTCACC TGC
                                   TTA      C
GAM3415 KRTAP1-3 3' GGATACAGGAAGTGAGTGTCCT 76956     C  C       AACG
                                GGA AC GGAAGTGG    CCT
                                ||| || ||||||||    |||
                                CCT TG CCTTCACT    GGA
                                  A  T       CACA
GAM3415 SMC4L1   3' GGCAAGCTAAGTGGAATGCCT  76957    A  CCGG       C
                                GG CA    AAGTGGAA GCCT
                                || ||    |||||||| ||||
                                CC GT    TTCACCTT CGGA
                                 _ TCGA       A
GAM3416 COX11    3' TAGCTAGGCATATGAGTTTC   76960          CACT  C
                                TAGCTGGGCA    TG GGTTTC
                                ||||||||||    || ||||||
                                ATCGATCCGT    AC TCAAAG
                                      AT__  _
GAM3416 GPR44    3' TAGCTGGGCACCTCACTGTTCC 76961           A  TG G
                                TAGCTGGGCAC CT  C GTTTC
                                |||||||||||  ||  | |||||
                                ATCGACCCGTG GA  G CAAGG
                                      _ GT A
GAM3416 HLA-DQA1 3' TAGCTGGGTGGCTTACTC    76962        CACA    GGTT
                                TAGCTGGG    CTTGC    TC
                                ||||||||    |||||    ||
                                ATCGACCC    GAATG    AG
                                     ACC_    _____
GAM3416 PIGB     5' GGCCTCCTTGCGGTTTCC    76963     ACA
                                GGC   CTTGCGGTTTCC
                                |||   ||||||||||||
                                CCG   GAACGCCAAAGG
                                  GAG
GAM3416 PPL      3' GCTGGACACTTGTGGTTTC   76964       GC      C
                                GCTGG  ACACTTG GGTTTC
                                |||||  ||||||| ||||||
                                CGACC  TGTGAAC CCAAAG
                                   __       A
GAM3416 TRIM14   3' CAGCTGGGCACTCTGGGTTTCC 76965           A  T C
                                TAGCTGGGCAC CT G GGTTTCC
                                |||||||||||  || |  |||||||
                                GTCGACCCGTG GA C CCAAAGG
                                      A  _ _
GAM3416 CENTG2   3' TAGCTGAATTTGTGGTTTC   76966        CACAC   C
                                TAGCTGGG     TTG GGTTTC
                                ||||||||     ||| ||||||
                                ATCGACTT     AAC CCAAAG
                                     A_____   A
GAM3416 DKFZp434A2417 3' TAGCTGGGCATGCCTTATTCC  76967          CACT   GGT_
                                TAGCTGGGCA    TGC    TTCC
                                ||||||||||    |||    ||||
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                                ATCGACCCGT  ACG  AAGG
                                     ____  GAAT
GAM3416 FLJ12442 5' CAGCTGGGCGCGCGTT    76968       ACACTT  _
                                TAGCTGGGC    GCG GTT
                                |||||||||    ||| |||
                                GTCGACCCG    CGC CAA
                                     _______  G
GAM3416 FLJ20277 3' TGGGCACAGCAGTTTCC    76969       CTT
                                TGGGCACA  GCGGTTTCC
                                ||||||||  |||||||||
                                ACCCGTGT  CGTCAAAGG
                                     ___
GAM3416 FLJ23040 3' TAGCTGGGTGTGTTGGTATGTC 76970       CACAC  CG  T
          C                      TAGCTGGG   TTG  GT TCC
                                ||||||||   |||  || |||
                                ATCGACCC   AAC  TA AGG
                                     ACAC_  CA  C
GAM3416 GGA2    3' TAGCTGGGCGTGCTGGCT   76971       ACACT  _
                                TAGCTGGGC   TGC GGTT
                                |||||||||   ||| ||||
                                ATCGACCCG   ACG CCGA
                                     C____  A
GAM3416 GGA2    3' TAGCTGGGCGTGCTGGCT   76971       ACACT  _
                                TAGCTGGGC   TGC GGTT
                                |||||||||   ||| ||||
                                ATCGACCCG   ACG CCGA
                                     C____  A
GAM3416 HSD17B12 3' TAGCTGGACATTGGTTT    76972        CACTTGC
                                TAGCTGGGCA     GGTTT
                                ||||||||||     |||||
                                ATCGACCTGT     CCAAA
                                     AA_____
GAM3416 KIAA0298 3' GCTGGGCAAACCGTTTC    76973       C  TGCG
                                GCTGGGCA ACT   GTTTC
                                |||||||| |||   |||||
                                CGACCCGT TGG   CAAAG
                                     T  ____
GAM3416 KIAA1196 3' TAGCTGGGGGTGCTGGAGTTCC 76974       CACACT  _  T_
                                TAGCTGGG    TGC GG  TTCC
                                ||||||||    ||| ||  ||||
                                ATCGACCC    ACG CC  AAGG
                                     CC____  A  TC
GAM3416 KIAA1881 3' GCTGGGCACGCTGCTTTTT   76975       A  T  GG
                                GCTGGGCAC CT GC  TTT
                                ||||||||| || ||  |||
                                CGACCCGTG GA CG  AAA
                                     C  _  AA
GAM3416 LOC115648 3' TAGCTGGGCGTGCTGGT    76976       ACACT  _
                                TAGCTGGGC   TGC GGT
                                |||||||||   ||| |||
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                                ATCGACCCG    ACG CCA
                                     C____   A
GAM3416  LOC129676 5'  GCTGGGCCACTTCGAGCTC   76977       A    G  _
                                GCTGGGC CACTT CG GTTT
                                ||||||| ||||| || ||||
                                CGACCCG GTGAA GC CGAG
                                   _    _ T
GAM3416  LOC129880 3'  GCTGGGCGAATTTGCAGCC   76978       ACAC
                                GCTGGGC   TTGCGGTT
                                |||||||   ||||||||
                                CGACCCG   AACGTCGG
                                    CTTA
GAM3416  LOC147229 3'  TAGCTGGGCCTGTTTGGGTCC  76979        ACAC   C
                                TAGCTGGGC   TTG GGTTT
                                |||||||||   ||| |||||
                                ATCGACCCG   AAC CCAGG
                                     GACA  _
GAM3416  LOC150519 3'  TAGCTGAGTATACTAAGGCTT  76980       CAC   TGC
                                TAGCTGGG  ACT  GGTTT
                                ||||||||  |||  |||||
                                ATCGACTC  TGA  CCGAA
                                     ATA  TT_
GAM3416  LOC158668 3'  TAGCTGGGTATACTGTTT    76981       CACACT  G
                                TAGCTGGG    TGC GTTT
                                ||||||||    ||| ||||
                                ATCGACCC    ATG CAAA
                                     AT____  A
GAM3416  LOC167153 5'  AGCTGGGCGTACTTGGTC    76982       AC   GC
                                AGCTGGGC  ACTT  GGTT
                                ||||||||  ||||  ||||
                                TCGACCCG  TGAA  CCAG
                                     CA  __
GAM3416  LOC255465 3'  TAGCTGGGCATGGTTGCA    76983        CAC
                                TAGCTGGGCA  TTGCG
                                ||||||||||  |||||
                                ATCGACCCGT  AACGT
                                     ACC
GAM3416  LOC257429 3'  TAGCTGGGTGGCTTACTC    76962       CACA   GGTT
                                TAGCTGGG   CTTGC   TC
                                ||||||||   |||||   ||
                                ATCGACCC   GAATG   AG
                                     ACC_   _____
GAM3417  EPS8     3'  TACATAACATCTGTTTTA    76986        __
                                TACGTAGCG  TGTTTTA
                                |||||||||  |||||||
                                ATGTATTGT  ACAAAAT
                                     AG
GAM3418  FSTL1    3'  GAAGAATAAAGTCAACTTGCC  76989      ACGC
                                GAAGAG   AGTCAACTTGCC
                                ||||||   ||||||||||||
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                                CTTCTT   TCAGTTGAACGG
                                   ATT_
GAM3418 IL1F5   5' TAGGGAGGGGCCCTGAAACTTG 76990    AA  AC  AGTC_
            CC                   TAG  GAG  GC    AACTTGCC
                                ||| ||| ||   ||||||||
                                ATC  CTC  CG    TTGAACGG
                                  C_  CC  GGACT
GAM3418 LFG     3' TAGAAGAGATGTGGACTGTGCC 76991        CGCA  CA  _
                                TAGAAGAGA   GT  ACT TGCC
                                |||||||||   ||  ||| ||||
                                ATCTTCTCT   CA  TGA ACGG
                                     A___  CC  C
GAM3418 NEBL    3' TAGAATAGGCAGCAACTTGC  76992     G  AC   T
                                TAGAA AG  GCAG CAACTTGC
                                ||||| ||  |||| ||||||||
                                ATCTT TC  CGTC GTTGAACG
                                   A __   _
GAM3418 P2RY6   5' GAGAGGAAGTAACTTGCC   76993    CGC  C
                                GAGA  AGT AACTTGCC
                                ||||  ||| ||||||||
                                CTCT  TCA TTGAACGG
                                  CCT  _
GAM3418 RANBP2  3' AAAGGAAATAGTCAACTTG   76994    A  CGC
                                GAAG GA  AGTCAACTTG
                                |||| ||  ||||||||||
                                TTTC CT  TCAGTTGAAC
                                  _ TTA
GAM3418 UBE2V1  3' AAAGACGCAGCAATTTGCC   76995       T  C
                                AGAGACGCAG CAA TTGCC
                                |||||||||| ||| |||||
                                TTTCTGCGTC GTT AACGG
                                      _  A
GAM3418 UBE2V1  3' AAAGACGCAGCAATTTGCC   76995       T  C
                                AGAGACGCAG CAA TTGCC
                                |||||||||| ||| |||||
                                TTTCTGCGTC GTT AACGG
                                      _  A
GAM3418 UBE2V1  3' AAAGACGCAGCAATTTGCC   76995       T  C
                                AGAGACGCAG CAA TTGCC
                                |||||||||| ||| |||||
                                TTTCTGCGTC GTT AACGG
                                      _  A
GAM3418 ARHGAP11A 3' GAGGAAATAGGCACAACTTGC  76996   A   C__  GT
                                GA GAGA  GCA  CAACTTGC
                                || ||||  |||  ||||||||
                                CT CTTT  CGT  GTTGAACG
                                 C   ATC  __
GAM3418 CLDN1   3' TAGAAAGATTAAGTGACTTGC  76997    A   CGC  CA
                                TAGA GAGA  AGT  ACTTGC
                                |||| ||||  |||  ||||||
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                                ATCT TTCT   TCA  TGAACG
                                  _   AAT   C_
GAM3418  DKFZP566B183 3'  TAGTGGGAGAACAACTTGC   76998     AA_   CGCAGT
                                TAG   GAGA     CAACTTGC
                                |||   ||||     ||||||||
                                ATC   CTCT     GTTGAACG
                                  ACC    T_____
GAM3418  FLJ20511  3'  AAAGAGGAGCAGTAACTTGCC  76999       AC    C
                                GAAGAG  GCAGT AACTTGCC
                                ||||||  ||||| ||||||||
                                TTTCTC  CGTCA TTGAACGG
                                   CT    _
GAM3418  FLJ20972  3'  GAAGAGACACCAGAGCTTGC   77000          _ TCAA
                                GAAGAGACGC AG    CTTGC
                                ||||||||||  ||    |||||
                                CTTCTCTGTG TC    GAACG
                                      G  TC__
GAM3418  MCLC      5'  CAGAAGAGGTCGCACAGCTTGC 77001         A_   GT  A
              C                  TAGAAGAG  CGCA  CA CTTGCC
                                ||||||||  ||||  || ||||||
                                GTCTTCTC  GCGT  GT GAACGG
                                     CA    __  C
GAM3418  LOC124801 3'  AAGAATCACAGTCAGCTTG   77002       A       A
                                AAGAG CGCAGTCA CTTG
                                ||||| ||||||||  ||||
                                TTCTT GTGTCAGT GAAC
                                   A       C
GAM3418  LOC129011 3'  TAGAAGGAGCAGCGAACTTGCC 77003       A  C    C
                                TAGAAG GA GCAGT AACTTGCC
                                ||||||  ||  ||||| ||||||||
                                ATCTTC CT CGTCG TTGAACGG
                                   _  _    C
GAM3418  LOC145693 3'  AGAAGAGAGACAACTTGC    77004        CGCA T
                                AGAAGAGA    G CAACTTGC
                                ||||||||    | ||||||||
                                TCTTCTCT    C GTTGAACG
                                     _____ T
GAM3418  LOC150967 5'  GAAGAGACCCAGCATGC     77005        G   T  ACT
                                GAAGAGAC CAG CA   TGC
                                ||||||||  ||| ||   |||
                                CTTCTCTG GTC GT   ACG
                                     G   _  ____
GAM3418  LOC221060 3'  TAGAGGAGGTTAATAAACTTGC 77006      A   ACGC   C
              C                  TAGA GAG    AGT AACTTGCC
                                ||||  |||    ||| ||||||||
                                ATCT CTC    TTA TTGAACGG
                                  C   CAA_   T
GAM3418  LOC221254 5'  CAGAAGAGGTGCTACAGCTTG  77007        AC  AGT  A
                                TAGAAGAG  GC   CA CTTG
                                ||||||||  ||   || ||||
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                                GTCTTCTC  CG   GT GAAC
                                    CA  AT_  C
GAM3418  LOC221550 3'  TAGAAGAGATGGGTTTTTGCC  77008        CGCA  CAAC
                                TAGAAGAGA   GT   TTGCC
                                |||||||||   ||   |||||
                                ATCTTCTCT   CA   AACGG
                                    ACC_  AA__
GAM3418  LOC253011 3'  AGAAGAGTATTTCAACTTG   77009       ACGCAG
                                AGAAGAG     TCAACTTG
                                |||||||     ||||||||
                                TCTTCTC     AGTTGAAC
                                   ATAA__
GAM3418  LOC257495 3'  TAGAAGAGATGGGTTTTTGCC  77008        CGCA  CAAC
                                TAGAAGAGA   GT   TTGCC
                                |||||||||   ||   |||||
                                ATCTTCTCT   CA   AACGG
                                    ACC_  AA__
GAM3418  LOC257576 3'  TAGAAGAGATGGGTTTTTGCC  77008        CGCA  CAAC
                                TAGAAGAGA   GT   TTGCC
                                |||||||||   ||   |||||
                                ATCTTCTCT   CA   AACGG
                                    ACC_  AA__
GAM3419  BUB3     3'  TACGTTACAATTATTTTTC   77012      TT   T
                                TACGT  TACA GTTATTTTTC
                                |||||  |||| ||||||||||
                                ATGCA  ATGT TAATAAAAAG
                                  __   _
GAM3419  FGF2     3'  TACATTTTACAACTTTTGTTAT 77013       _____        III
           TTTTCG                TTTTACA    TGTTATTTTTC  G
                                |||||||    ||||||||||  |
                                AAAATGT    ACAATAAAAAG  C
                                   TGAAA        III
GAM3419  GRIA1    3'  GCAGTACAGTGTTATTTTT   77014    TT   _
                                GT  TACA TGTTATTTTT
                                ||  |||| ||||||||||
                                CG  ATGT ACAATAAAAA
                                 TC   C
GAM3419  TTC3     5'  GTTTTACATGCATTATTTC   77015         TATT
                                GTTTTACATGT   TTTC
                                ||||||||||   ||||
                                CAAAATGTACG   AAAG
                                    TAAT
GAM3419  APOF     3'  TACGTTTTACTGTACAGCCTTC 77016         A  _  T
                                TACGTTTTAC TGT TA TTTTC
                                |||||||||| ||| || |||||
                                ATGCAAAATG ACA GT GGAAG
                                    _  T  C
GAM3419  HGRG8    3'  CACGTTTTACAGTATTTTTC  77017          T  T
                                TACGTTTTACA GT ATTTTTC
                                |||||||||| || |||||||
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                                GTGCAAAATGT CA TAAAAAG
                                      _ _
GAM3419 MAP      3' CACCCCTCAGCATGTTATTTTT 77018     G    _
                                TAC TTTTA CATGTTATTTTT
                                ||| ||||| ||||||||||||
                                GTG GGAGT GTACAATAAAAA
                                  G    C
GAM3419 WBSCR20A 3' TACGTTCTGCATTTTATTTTT 77019        A  G
                                TACGTTTT CAT TTATTTTT
                                |||||||| ||| ||||||||
                                ATGCAAGA GTA AATAAAAA
                                     C  A
GAM3419 LOC130074 3' GTTTTACATAGGACTTTTC   77020         TT
                                GTTTTACATG  ATTTTTC
                                ||||||||||  |||||||
                                CAAAATGTAT  TGAAAAG
                                      CC
GAM3419 LOC51194  3' TACTTTTACATGTACTTTT   77021     G       T
                                TAC TTTTACATGT ATTTTT
                                ||| |||||||||| ||||||
                                ATG AAAATGTACA TGAAAA
                                  _       _
GAM3420 FZD6     3' CAGTGTAACACAAATTTGCTT 77024          T   A
                                TAGTGTAATATA ATTT CTT
                                |||||||||||| |||| |||
                                GTCACATTGTGT TAAA GAA
                                      T   C
GAM3420 NRCAM    3' ATAGAATATATATTTACTT   77025    T
                                GTG AATATATATTTACTT
                                ||| ||||||||||||||
                                TAT TTATATATAAATGAA
                                  C
GAM3420 SHANK2   3' TAGTGCAATAGTATATTTA   77026         _
                                TAGTGTAATA TATATTTA
                                |||||||||| ||||||||
                                ATCACGTTAT ATATAAAT
                                      C
GAM3420 BUP      3' GTGTAATACTGTCTACTT    77027        ATA
                                GTGTAATAT   TTTACTT
                                |||||||||   |||||||
                                CACATTATG   AGATGAA
                                     AC_
GAM3420 EPB41L1  3' ATGTAATATACATAACTT    77028          TT
                                GTGTAATATATAT  ACTT
                                ||||||||||||  ||||
                                TACATTATATGTA  TGAA
                                      T_
GAM3420 EREG     3' TAGGACCATATATATTTACTT  77029     TG A
                                TAG  T ATATATATTTACTT
                                |||  | ||||||||||||||
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                                ATC  G TATATATAAATGAA
                                  CT G
GAM3420  STIM2    3'  TAGTGCAATTACGTTTTACTT  77030        A  A_
                                TAGTGTAAT TAT  TTTACTT
                                ||||||||| |||  |||||||
                                ATCACGTTA ATG  AAATGAA
                                     _  CA
GAM3420  LOC145978 3'  CAGTGCATATATTTACTT    77031      AAT
                                TAGTGT   ATATATTTACTT
                                ||||||   ||||||||||||
                                GTCACG   TATATAAATGAA
                                   ___
GAM3420  LOC162239 3'  TAGTGTAAAAATTTACTT    77032       TATAT
                                TAGTGTAA    ATTTACTT
                                ||||||||    ||||||||
                                ATCACATT    TAAATGAA
                                     TT___
GAM3420  LOC51110  3'  TAGTGTAATTTACATATTT   77033       __
                                TAGTGTAA  TATATATTT
                                ||||||||  |||||||||
                                ATCACATT  ATGTATAAA
                                     AA
GAM3420  LOC91947  3'  TAGGTATACATATATTTACTT  77034    T  _
                                TAG GTA ATATATATTTACTT
                                ||| ||| ||||||||||||||
                                ATC CAT TGTATATAAATGAA
                                  _  A
GAM3420  LOC93538  3'  TAGTGTATACATATATTT    77035      _
                                TAGTGTA ATATATATTT
                                ||||||| ||||||||||
                                ATCACAT TGTATATAAA
                                     A
GAM3421  GYG      3'  TCTGAAGGGAGTGACTGA    77038     C       G_
                                TCTG AAGGGAGTGA  GA
                                |||| ||||||||||  ||
                                AGAC TTCCCTCACT  CT
                                  _       GA
GAM3421  SCD      3'  TCTGCAGAGGGAGTGAGGGC   77039      _       AC
                                TCTGCA AGGGAGTGAGG  GC
                                |||||| ||||||||||  ||
                                AGACGT TCCCTCACTCC  CG
                                   C        __
GAM3421  Di-Ras2   3'  TCTTAAGGACAATAGGACGCAT 77040    GC    AGTG
           C                     TCT  AAGGG   AGGACGCATC
                                |||  |||||   ||||||||||
                                AGA  TTCCT   TCCTGCGTAG
                                  A_    GTTA
GAM3421  FLJ14327  3'  TCTGCAAGGTGGTGGGGGC   77041       GA  A  AC
                                TCTGCAAGG  GTG GG  GC
                                |||||||||  ||| ||  ||
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                                AGACGTTCC  CAC CC  CG
                                     AC   _  C_
GAM3421  FLJ14950  3'  TCTGCAAGGGGGTGCAGGAC   77042          A  _
                                TCTGCAAGGG GTG AGGAC
                                |||||||||| ||| |||||
                                AGACGTTCCC CAC TCCTG
                                      C   G
GAM3421  KIAA1877  3'  TGCAAGGGAGAACGCAT     77043          TGAG
                                TGCAAGGGAG   GACGCAT
                                ||||||||||   |||||||
                                ACGTTCCCTC   TTGCGTA
                                      _____
GAM3421  NSE1      3'  CCTGCGATCTGGGGACGCATC  77044       AAGG  G_  A
                                TCTGC   GA  TG GGACGCATC
                                |||||   ||  || |||||||||
                                GGACG   CT  AC CCTGCGTAG
                                   _____  AG  C
GAM3421  LOC153480 5'  TGCGAGGGAGTGGGAGGACG   77045     A      __
                                TGC AGGGAGT  GAGGACG
                                ||| |||||||  |||||||
                                ACG TCCCTCA  CTCCTGC
                                  C      CC
GAM3422  NPHP1     3'  TTATTAGCTGTGACCTTA     77048     C    C
                                TTA TAGC GTGACCTTG
                                ||| |||| |||||||||
                                AAT ATCG CACTGGAAT
                                  A   A
GAM3422  LOC256821 3'  TTATTAGCGTTTTGTTGACGGT 77049     C    C  GACC
            G                    TTA TAGC GT   TTGACGGTG
                                ||| |||| ||   |||||||||
                                AAT ATCG CA   AACTGCCAC
                                  A   _  AAAC
GAM3423  C4orf1    3'  TCCAGTAAATAAACATTATG   77052           ACTT
                                TCCAGTAAATAAA   TTATG
                                ||||||||||||   |||||
                                AGGTCATTTATTT   AATAC
                                       GT__
GAM3423  C8orf1    3'  CCAGTGTCTCAAATTTTTATGA 77053       AAATA  C
                                CCAGT    AAA TTTTATGA
                                |||||    ||| ||||||||
                                GGTCA    TTT AAAATACT
                                   CAGAG   A
GAM3423  CASP10    3'  TCCAGTAAATGAGGACTGTGA  77054         AAA_  TTTA
                                TCCAGTAAAT   ACT   TGA
                                ||||||||||   |||   |||
                                AGGTCATTTA   TGA   ACT
                                      CTCC  C___
GAM3423  CASP10    3'  TCCAGTAAATGAGGACTGTGA  77054         AAA_  TTTA
                                TCCAGTAAAT   ACT   TGA
                                ||||||||||   |||   |||
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                                AGGTCATTTA   TGA   ACT
                                     CTCC  C___
GAM3423 PPARGC1  3' TCCAGTGTATAAAACTTC   77055      AA
                                TCCAGT  ATAAAACTTT
                                ||||||  ||||||||||
                                AGGTCA  TATTTTGAAG
                                   CA
GAM3423 ACTR1A   3' CAATAAATAAAACGGTTTGAA 77056          TTTTA
                                CAGTAAATAAAAC    TGAA
                                ||||||||||||    ||||
                                GTTATTTATTTTG    ACTT
                                       CCAA_
GAM3423 ARHGEF10 3' TCCAGTAAGTGAAACACTGAA 77057       ATA   TTTTA
                                TCCAGTAA  AAAC    TGAA
                                ||||||||  ||||    ||||
                                AGGTCATT  TTTG    ACTT
                                     CAC   TG___
GAM3423 C22orf5  3' TCCAATAAATAAAGGCGGCGTG 77058          ACTTTTA
             A                   TCCAGTAAATAAA      TGA
                                 ||||||||||||      |||
                                 AGGTTATTTATTT      ACT
                                       CCGCCGC
GAM3423 FLJ10251 3' TCCAGTGGATAAAACCTC   77059      AA
                                TCCAGT  ATAAAACTTT
                                ||||||  ||||||||||
                                AGGTCA  TATTTTGGAG
                                   CC
GAM3423 GNG10    3' TCCAGTAAATGAAACATACATG 77060        A   TTT
             A                   TCCAGTAAAT AAAC  TATGA
                                 ||||||||||| ||||  |||||
                                 AGGTCATTTA TTTG  GTACT
                                       C   TAT
GAM3423 IL18BP   3' TCCATTGAATAATCCTTTATGA 77061     GTA    AA
                                TCCA  AATAA  CTTTTATGA
                                ||||  |||||  |||||||||
                                AGGT  TTATT  GGAAATACT
                                  AAC    A_
GAM3423 KIAA1677 3' CAGTAAATAAAACAAAAACTGA 77062          TTTTA_
                                CAGTAAATAAAAC     TGA
                                ||||||||||||     |||
                                GTCATTTATTTTG     ACT
                                      TTTTTG
GAM3423 KIAA1979 3' TCCAGTATGAATTGTTTTATGA 77063      AATAAAAC
             A                   TCCAGTA      TTTTATGAA
                                 |||||||      |||||||||
                                 AGGTCAT      AAAATACTT
                                    ACTTAAC_
GAM3423 NYD-SP15 3' TCCACTAACTTTATTTTTATGA 77064     G  ATAAAAC
                                TCCA TAA      TTTTATGA
                                |||| |||      ||||||||
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                                AGGT ATT      AAAATACT
                                  G  GAAATA_
GAM3423  PRO2859   5'  CAATAAATGAAACTTCCA    77065        A
                                CAGTAAAT AAACTTTTA
                                |||||||| |||||||||
                                GTTATTTA TTTGAAGGT
                                     C
GAM3423  RIPK2     3'  ATAAATATCCTTTTATGAA   77066       AAA
                                GTAAATA  CTTTTATGAA
                                |||||||  ||||||||||
                                TATTTAT  GAAAATACTT
                                    AG_
GAM3423  SEC24D    3'  GTAAACTTTGCCTTTTATGAA 77067       AAAA_
                                GTAAAT    CTTTTATGAA
                                ||||||    ||||||||||
                                CATTTG    GAAAATACTT
                                   AAACG
GAM3423  UXS1      3'  CCAGTAAATAAAACTGTCA   77068            T
                                CCAGTAAATAAAACT TTA
                                ||||||||||||||| |||
                                GGTCATTTATTTTGA AGT
                                          C
GAM3423  LOC146780 5'  TCCAGTAAGCAGAAACTGATGA 77069        A _    TTT
                                TCCAGTAA TA AAACT  ATGA
                                |||||||| || |||||  ||||
                                AGGTCATT GT TTTGA  TACT
                                     C  C    C__
GAM3423  LOC148254 3'  TCCAGCAAATGAAGTTCCTA  77070         A  AC
                                TCCAGTAAAT AA  TTTTA
                                |||||||||| ||  |||||
                                AGGTCGTTTA TT  AGGAT
                                      C  CA
GAM3423  LOC152559 3'  TCCAATAAACAATGTAAGTTTT 77071          AAC_____
            TATGAA                 CCAGTAAATAA      TTTTATGAA
                                |||||||||||      |||||||||
                                GGTTATTTGTT      AAAATACTT
                                       ACATTCA
GAM3423  LOC157653 5'  CCAGTAAATAATCAATATTGTG 77072          AACTT_  A
            A                   CCAGTAAATAA     TT TGA
                                ||||||||||      || |||
                                GGTCATTTATT     AA ACT
                                       AGTTAT  C
GAM3423  LOC204084 3'  TCCAGTAAATGGATTCTCCTGA 77073         AAAAC   A
                                TCCAGTAAAT    TTTT TGA
                                ||||||||||    |||| |||
                                AGGTCATTTA    AGAG ACT
                                      CCTA_   G
GAM3424  GPR77     3'  TTGGTCACTGCTATATCTCTA  77076        AA  _   C
                                TTGGTCGCT  GTT TATC CTA
                                |||||||||  ||| |||| |||
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                                AACCAGTGA  CGA ATAG GAT
                                     __  T   A
GAM3424 KIAA1678 3' TTGACCACTGAGTTTGTTTCTA 77077    GT   A   ATCC
                                TTG  CGCT AGTTT   CTA
                                |||  |||| |||||   |||
                                AAC  GTGA TCAAA   GAT
                                  TG   C    CAAA
GAM3424 LOC152263 5' TTGGTGTTAAGAATTTCCCTAA 77078     CGC   TTTA
          T                      TTGGT   TAAG   TCCCTAAT
                                 |||||   ||||   ||||||||
                                 AACCA   ATTC   AGGGATTA
                                    CA_   TTAA
GAM3424 LOC200860 3' GGTCGACTTTTATCCCT    77079      _ AAG
                                 GGTCG CT   TTTATCCCT
                                 |||||  ||   |||||||||
                                 CCAGC GA   AAATAGGGA
                                    T ___
GAM3425 FKRP    3' TCTAGTGGCGGAAGCAACCCCT 77082     A       TG  A_
          G                      TCTA TGGTGGAAGCG  GC  CTG
                                 ||||  ||||||||||  ||  |||
                                 AGAT ACCGCCTTCGT  TG  GAC
                                   C         __ GG
GAM3425 PRKRA   3' TGATGTGCATGGCACT     77083      GAA
                                 TGGTG   GCGTGGCACT
                                 |||||   ||||||||||
                                 ACTAC   CGTACCGTGA
                                    A__
GAM3425 FLJ20689 3' TCTGGTGGTGAAAGGAC    77084    AA       CGT
                                 TCT  TGGTGGAAG   GGC
                                 |||  |||||||||   |||
                                 AGA  ACCACTTTC   CTG
                                   CC       ___
GAM3425 FLJ20689 3' TCTGGTGGTGAAAGGAC    77084    AA       CGT
                                 TCT  TGGTGGAAG   GGC
                                 |||  |||||||||   |||
                                 AGA  ACCACTTTC   CTG
                                   CC       ___
GAM3425 FLJ22031 3' TCTAATGGTGTGAAATAT    77085         _   CG
                                 TCTAATGGTG GAAG  T
                                 ||||||||||  ||||  |
                                 AGATTACCAC CTTT  A
                                      A   AT
GAM3425 IMPACT   3' TCTGGGGTGGAAGGAGACTACT 77086    AAT      CGT  _
          G                      TCT   GGTGGAAG   GGC ACTG
                                 |||   ||||||||   ||| ||||
                                 AGA   CCACCTTC   CTG TGAC
                                   CC_      CT_   A
GAM3425 MCJ     3' TAATGGTGGAAGATAAGACTG  77087          C   C
                                 TAATGGTGGAAG GTGG ACTG
                                 ||||||||||| |||| ||||
```

```
                                ATTACCACCTTC TATT TGAC
                                      _   C
GAM3425  SDCCAG33  5'  TGGTGATGGCTGGCACT     77088       AA  G
                                TGGTGG  GC TGGCACT
                                ||||||  || |||||||
                                ACCACT  CG ACCGTGA
                                   AC  _
GAM3425  LOC154792 3'  TCTAATGGGGAAAGGC      77089        T    CGT
                                TCTAATGG GGAAG   GGC
                                |||||||| |||||   |||
                                AGATTACC CCTTT   CCG
                                      _    ___
GAM3425  LOC219793 5'  CTGGTGGTGGAAGTGTAAAC   77090    AA       C   C
                                CT  TGGTGGAAG GTGG AC
                                ||  |||||||||| |||| ||
                                GA  ACCACCTTC CATT TG
                                 CC        A   _
GAM3426  KIAA1819  5'  TTTGACAGCTCTGGAGAAGTT  77093        AC    ATT
                                TTTGACAG  CTGGA   GTT
                                ||||||||  |||||   |||
                                AAACTGTC  GACCT   CAA
                                    GA    CTT
GAM3427  HSD17B12  3'  TGTCCAAGCAAGCCACTTTT   77096    G  T   AA
                                TGT CA GCGA  CCACTTTT
                                ||| || ||||  ||||||||
                                ACA GT CGTT  GGTGAAAA
                                  G  T   C_
GAM3427  KIAA0430  3'  TGTGATGAAGCCACTTT     77097     C  GC   A
                                TGTG AT  GAA CCACTTT
                                |||| ||  ||| |||||||
                                ACAC TA  CTT GGTGAAA
                                  _ __   C
GAM3427  KIAA1464  3'  CAATGGTAGCGGGACCACTTTT 77098      TGCAT   AA
                                TAATG    GCG  ACCACTTTT
                                |||||    |||  |||||||||
                                GTTAC    CGC  TGGTGAAAA
                                   CAT__   CC
GAM3427  LIPI     3'  ATGTGCATGTGGAACACT    77099         C_   AC
                                ATGTGCATG  GAA  CACT
                                |||||||||  |||  ||||
                                TACACGTAC  CTT  GTGA
                                    AC   __
GAM3427  RNF11    3'  ATGTTAGGTTGAGACCACTTTT 77100     GCATGC  A
                                ATGT     GA ACCACTTTT
                                ||||     || |||||||||
                                TACA     CT TGGTGAAAA
                                  ATCCAA  C
GAM3428  AOX1     3'  TAGAAGCCAAGTAGGAGC    77103         ATTA    A  C
                                TGGAAGCCA    AGTAG AG C
                                |||||||||    ||||| || |
```

```
                                ATCTTCGGT   TCATC TC G
                                     ____    C  A
GAM3428  CAPN10   3'  TGGAAGCCGATGGGGTGGAA  77104       A  TAA  A
                                TGGAAGCC AT   GT GAA
                                |||||||| ||   || |||
                                ACCTTCGG TA   CA CTT
                                    C  CCC  C
GAM3428  CAPN10   3'  TGGAAGCCGATGGGGTGGAA  77104       A  TAA  A
                                TGGAAGCC AT   GT GAA
                                |||||||| ||   || |||
                                ACCTTCGG TA   CA CTT
                                    C  CCC  C
GAM3428  CAPN9    3'  GAAGGTCAAGGTCCAGAAGCCA 77105     CCAA   ___
                                GAAG   TTAAG   TAGAAGCCA
                                ||||   |||||   |||||||||
                                CTTC   AGTTC   GTCTTCGGT
                                  C___    CAG
GAM3428  DVL1     3'  TGGGGGCCAGAGAAGCC    77106    AA   ATTAA T
                                TGG  GCCA    G AGAAGCC
                                |||  ||||    | |||||||
                                ACC  CGGT    C TCTTCGG
                                  CC   _____ _
GAM3428  EDN1     3'  TGGAAGCCAGTGAAG      77107        ATTAA  A
                                TGGAAGCCA    GT GAAG
                                |||||||||    || ||||
                                ACCTTCGGT    CA CTTC
                                     _____  _
GAM3428  GOT1     3'  TGGGGCCGGTTTAAACAGAGGC 77108    AA   AA_      A
                                TGG  GCC   TTAAGTAGA GC
                                |||  |||   ||||||||| ||
                                ACC  CGG   AATTTGTCT CG
                                  C_   CCA       C
GAM3428  KRT9     3'  TGGAAGCCAATGGAAAGCC   77109         TAAGTA
                                TGGAAGCCAAT     GAAGCC
                                ||||||||||     ||||||
                                ACCTTCGGTTA     TTTCGG
                                       CC____
GAM3428  KRTHA8   3'  TGGAAGCCATATGTAAGAGGC  77110        AT  A  _  A
                                TGGAAGCCA  TA GTA GA GC
                                |||||||||  || ||| || ||
                                ACCTTCGGT  AT CAT CT CG
                                     __  A   T  C
GAM3428  MBL2     3'  TGGAAGCCACTTAAGTGCC   77111        A     AGAA
                                TGGAAGCCA TTAAGT    GCC
                                |||||||||  ||||||    |||
                                ACCTTCGGT AATTCA    CGG
                                     G     ____
GAM3428  SEPP1    3'  TGGAAGCCAATTCAGTAG    77112          A
                                TGGAAGCCAATT AGTAG
                                ||||||||||| |||||
```

```
                                ACCTTCGGTTAA TCATC
                                      G
GAM3428 SEPP1    3' TGGAAGCCAATTCAGTAG    77112          A
                                TGGAAGCCAATT AGTAG
                                |||||||||||| |||||
                                ACCTTCGGTTAA TCATC
                                      G
GAM3428 SPTBN2   3' TGGAAGCCATTGAGAGCAGC  77113        A A T A
                                TGGAAGCCA TT AG AG AGC
                                ||||||||| || || || |||
                                ACCTTCGGT AA TC TC TCG
                                     _ C _ G
GAM3428 TCF2     3' TGGAAGCCGAGTGAGCC     77114       AATTA  A A
                                TGGAAGCC    AGT GA GCC
                                ||||||||    ||| || |||
                                ACCTTCGG    TCA CT CGG
                                     C____  _ _
GAM3428 TCL1A    3' TAGAAGCTGATTGCGCACGAAG 77115       CA  AA  _
                                TGGAAGC  ATT  GTA GAAG
                                |||||||  |||  ||| ||||
                                ATCTTCG  TAA  CGT CTTC
                                    AC  CG  G
GAM3428 UBE2I    5' TGGGGTTGGGATCAAAGAAGCC 77116    AAGCCA_   GT
           A                     TGG     ATTAA  AGAAGCCA
                                |||      |||||  ||||||||
                                ACC      TAGTT  TCTTCGGT
                                  CCAACCC   __
GAM3428 BLR1     3' TGGCAAGGGCAGAAGTAGAAG  77117    _  CCAATT
                                TGG AAG     AAGTAGAAG
                                ||| |||     |||||||||
                                ACC TTC     TTCATCTTC
                                  G  CCGTC_
GAM3428 BLR1     3' TGGCAAGGGCAGAAGTAGAAG  77117    _  CCAATT
                                TGG AAG     AAGTAGAAG
                                ||| |||     |||||||||
                                ACC TTC     TTCATCTTC
                                  G  CCGTC_
GAM3428 DGKD     3' TGGGAGCCAAAGAGAAGCCA  77118    A    TTA  T
                                TGG AGCCAA   AG AGAAGCCA
                                ||| ||||||  || ||||||||
                                ACC TCGGTT   TC TCTTCGGT
                                  C    ___  _
GAM3428 DGKD     3' TGGGAGCCAAAGAGAAGCCA  77118    A    TTA  T
                                TGG AGCCAA   AG AGAAGCCA
                                ||| ||||||  || ||||||||
                                ACC TCGGTT   TC TCTTCGGT
                                  C    ___  _
GAM3428 DKFZP566K0524 3' TGGAAGCCAATTTGTGTCCAAA 77119          AA_  A_
           G                     TGGAAGCCAATT  GT  GAAG
                                ||||||||||||  ||  ||||
```

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                                ACCTTCGGTTAA  CA  TTTC
                                      ACA  GG
GAM3428  FLJ13693  3'  TGGAGCCCAGGTGTAGAAGC  77120     A  AATTAA
                                TGGA GCC     GTAGAAGC
                                |||| |||     ||||||||
                                ACCT CGG     CATCTTCG
                                  _  GTCCA_
GAM3428  FLJ22173  3'  TGGGGGCCGGAGTAGAAGCC  77121    AA  AATTA
                                TGG  GCC    AGTAGAAGCC
                                |||  |||    ||||||||||
                                ACC  CGG    TCATCTTCGG
                                  CC   CC___
GAM3428  GALNT8   3'  TGGGAGTGTTAGGAGTAGAAGC 77122    A  CCAATTA
            CA                    TGG AG      AGTAGAAGCCA
                                |||  ||      ||||||||||
                                ACC TC      TCATCTTCGGT
                                  C  ACAATCC
GAM3428  GPT2     3'  TGGAAATCAAGCATAGAGGC  77123      GC   TTAA    A
                                TGGAA  CAA    GTAGA GC
                                |||||  |||    ||||| ||
                                ACCTT  GTT    TATCT CG
                                   TA   CG__    C
GAM3428  KRTHB4   3'  TGGGGGCAGAAGCAGGAGCC  77124     AA  CAATT     A
                                TGG  GC    AAGTAG AGCC
                                |||  ||    |||||| ||||
                                ACC  CG    TTCGTC TCGG
                                  CC  TC___     C
GAM3428  KRTHB5   3'  TGGAGCTAAGTAGGAG     77125     A  CAAT     A
                                TGGA GC    TAAGTAG AG
                                ||||  ||    ||||||| ||
                                ACCT CG    ATTCATC TC
                                  _  _____      C
GAM3428  MGC20481  3'  GGAAGTTGGAGGAGAAGCCA  77126      CCAATTA  T
                                GGAAG      AG AGAAGCCA
                                |||||      || ||||||||
                                CCTTC      TC TCTTCGGT
                                   AACC___  C
GAM3428  MGC26651  3'  TGGAAGCCATTTTTAATTTAGG 77127        A__    G_   AA
            GGC                    TGGAAGCCA   TTAA  TAG  GC
                                |||||||||   ||||  |||  ||
                                ACCTTCGGT   AATT  ATC  CG
                                     AAA    AA   CC
GAM3428  MGC5309   3'  TGAAAGCCAGTTGACGCC    77128        ATTAA  A  A
                                TGGAAGCCA     GT GA GCC
                                |||||||||     || || |||
                                ACTTTCGGT     CA CT CGG
                                     _____  A  G
GAM3428  OSBPL8   3'  TAGAAGCCTACTTGTAGAAG   77129        A   AA
                                TGGAAGCC ATT  GTAGAAG
                                ||||||||  |||  |||||||
```

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                                ATCTTCGG TGA  CATCTTC
                                    A  A_
GAM3428  PPP1R3B  3'  TAGAAGGCAAAAGTAGAAGC  77130      C  TT
                                TGGAAG CAA  AAGTAGAAGC
                                ||||||| |||  ||||||||||
                                ATCTTC GTT  TTCATCTTCG
                                   C  __
GAM3428  RAI16    5'  TGAAAGCCGGAATCCAGGAAGC 77131        __   A  TA
                                TGGAAGCC  AATT AG  GAAGC
                                ||||||||  |||| ||  |||||
                                ACTTTCGG  TTAG TC  CTTCG
                                    CC   G __
GAM3428  SH3GLB1  3'  GAGGCTCAAAAGTAGAAGC   77132    A _  TT
                                GA GC CAA  AAGTAGAAGC
                                || || |||  ||||||||||
                                CT CG GTT  TTCATCTTCG
                                 C  A  __
GAM3428  LOC125129 3'  GGAAGCCAATTGGATTTCAAGT 77133        _______
                                GGAAGCCAA      TTAAGT
                                |||||||||      ||||||
                                CCTTCGGTT      AGTTCA
                                    AACCTAA
GAM3428  LOC127281 3'  TGAAAGCCAGAGGAGGGGC   77134        ATTA  T  AA
                                TGGAAGCCA   AG AG  GC
                                |||||||||   || ||  ||
                                ACTTTCGGT   TC TC  CG
                                    C___  C  CC
GAM3428  LOC137593 3'  TGGAAGCCATTAGAGC     77135        ATTAAG   A
                                TGGAAGCCA     TAGA GC
                                |||||||||     |||| ||
                                ACCTTCGGT     ATCT CG
                                    A_____   _
GAM3428  LOC146287 5'  TGGAGAGCAAGGAAGTAGAAGT 77136     _  C  TT       C
           CA                     TGGA AGC AA  AAGTAGAAG CA
                                |||| ||| ||  ||||||||| ||
                                ACCT TCG TT  TTCATCTTC GT
                                  C  _ CC       A
GAM3428  LOC146332 3'  GAGACAGGTAGGTAGAAGCCA  77137    AG CAAT  A
                                GA  C   TA GTAGAAGCCA
                                ||  |   || ||||||||||
                                CT  G   AT CATCTTCGGT
                                 CT TCC_  C
GAM3428  LOC158055 3'  GGAGCCAACAGAAGCC      77138     A     TAAGT
                                GGA GCCAAT    AGAAGCC
                                ||| ||||||    |||||||
                                CCT CGGTTG    TCTTCGG
                                  _    _____
GAM3428  LOC91181  3'  TGGAAACTTAATGTAGAAG   77139       CAA   _
                                TGGAAGC   TTAA GTAGAAG
                                |||||||   |||| |||||||
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                                ACCTTTG  AATT CATCTTC
                                   ___   A
GAM3429 ATP6V1A1 3' AACTTGTTTAATTGGCT    77142      CTAC
                                GGCTT   TTAATTGGCT
                                |||||   ||||||||||
                                TTGAA   AATTAACCGA
                                  CA__
GAM3429 ARHGEF3  3' TGGCTTCTAAAAGTGGCT    77143        CTT  T
                                TGGCTTCTA  AA TGGCT
                                |||||||||  || |||||
                                ACCGAAGAT  TT ACCGA
                                     T__  C
GAM3429 DKFZp547M072 3' TTGGCTTCTGTGACCTGTTGGC 77144         ___   AA
           T                     TTGGCTTCT  ACTT  TTGGCT
                                |||||||||  ||||  ||||||
                                AACCGAAGA  TGGA  AACCGA
                                     CAC   C_
GAM3429 FLJ12529 3' TAATTGGCTCTGCCAGGC    77145        T  A  TAATT
                                TAATTGGCT CT CT    GGC
                                ||||||||| || ||    |||
                                ATTAACCGA GA GG    CCG
                                     _ C  T____
GAM3429 KIAA1384  3' TAATTGGCTCCTGTGG     77146          ACTTAAT
                                TAATTGGCTTCT     TGG
                                ||||||||||||     |||
                                ATTAACCGAGGA     ACC
                                     C_______
GAM3429 MGC10940  3' TAATTGGCTTTTATTAGC    77147         CTAC  A
                                TAATTGGCTT   TTA TTGGC
                                ||||||||||   ||| |||||
                                ATTAACCGAA   AAT AATCG
                                     _____  _
GAM3429 NTT73    3' TAATTGGCTTCAATTACT    77148          ___
                                TAATTGGCTTC  TACT
                                ||||||||||  ||||
                                ATTAACCGAAG  ATGA
                                      TTA
GAM3429 LOC123879 3' TTGGCTTCTGTTAAGAGGCT  77149        AC   TT
                                TTGGCTTCT  TTAA  GGCT
                                |||||||||  ||||  ||||
                                AACCGAAGA  AATT  CCGA
                                     C_   CT
GAM3429 LOC219988 3' TTGATTTCTACTTAATTGGCT  77150    GC
                                TTG  TTCTACTTAATTGGCT
                                |||  ||||||||||||||||
                                AAC  AAGATGAATTAACCGA
                                  TA
GAM3430 FLJ11186  3' TATGTTAGTGACGTCTATC   77153      C       TTGT
                                TATGTT GTGACGTCT   ATC
                                ||||||  |||||||||   |||
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                                ATACAA CACTGCAGA    TAG
                                   T       ____
GAM3430  TRIM5    3'  TATGTGTCGTTTCTTTGT    77154      _   GACG
                                TATGT TCGT    TCTTTGT
                                ||||| ||||    |||||||
                                ATACA AGCA    AGAAACA
                                   C    A___
GAM3431  NEU3     3'  GCATTGAGATTCTCATTG    77157         __   C
                                GCATTGGGA  CTCG TG
                                |||||||||  |||| ||
                                CGTAACTCT  GAGT AC
                                      AA    A
GAM3431  SLC24A1  3'  TACCATTGGGATTCACAGTT   77158    G       C    T
                                TA CATTGGGA TCGC GTT
                                || ||||||||  |||| |||
                                AT GTAACCCT AGTG CAA
                                 G       A    T
GAM3431  FLJ20294 3'  TAGTATTGGCAATGTTACT    77159     C    GACT  C
                                TAG ATTGG    CG TGTTACT
                                ||| |||||    || |||||||
                                ATC TAACC    GT ACAATGA
                                  A    _____  T
GAM3431  FLJ22555 3'  TAGCATTGGAAATGTTA     77160          CTCGC
                                TAGCATTGGGA    TGTTA
                                ||||||||||    |||||
                                ATCGTAACCTT    ACAAT
                                      T_____
GAM3431  KLHL4    3'  TAGCACCTCGTTGTTACTG    77161       TGGGA   C
                                TAGCAT    CTCG TGTTACTG
                                ||||||    |||| ||||||||
                                ATCGTG    GAGC ACAATGAC
                                   ______   A
GAM3431  MYOZ2    3'  CAGCATTGGGATTTGTGAAACT 77162          CTCGC  TT
                                TAGCATTGGGA    TG  ACT
                                ||||||||||    ||  |||
                                GTCGTAACCCT    AC  TGA
                                      AAAC_  TT
GAM3431  RHOBTB1  3'  CAGCATTGGGGTTTGGACTCAA 77163          _______    _
            CTG                   TAGCATTGGG     ACTCG CTG
                                |||||||||     ||||| |||
                                GTCGTAACCC     TGAGT GAC
                                      CAAACC    T
GAM3431  LOC130412 5'  GCATTGGGCTATCGTGCT    77164        AC_   C
                                GCATTGGG   TCG TGTT
                                ||||||||   ||| ||||
                                CGTAACCC   AGC ACGA
                                     GAT   _
GAM3431  LOC153338 3'  TAGCATTGGAACTCATTGCT   77165             C
                                TAGCATTGGGACTCG TGTT
                                |||||||||||||| ||||
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                                ATCGTAACCTTGAGT ACGA
                                       A
GAM3431 LOC90092 3' GCATTGGGGCTGGATGACGCTG 77166        A _______
                                GCATTGGG CT     CGCTG
                                |||||||| ||     |||||
                                CGTAACCC GA     GCGAC
                                    C  CCTACT
GAM3432 CHAC     3' TTGATTTCTTACCCA      77169        GAAA
                                TTGATTTC   TTACCCA
                                ||||||||   |||||||
                                AACTAAAG   AATGGGT
                                    _____
GAM3432 OSBPL1A  3' TAACTTGATTTGGGATTAC   77170         CGAA
                                TAACTTGATTT   ATTAC
                                ||||||||||   |||||
                                ATTGAACTAAA   TAATG
                                      CCC_
GAM3432 OSBPL1A  3' TAACTTGATTTGGGATTAC   77170         CGAA
                                TAACTTGATTT   ATTAC
                                ||||||||||   |||||
                                ATTGAACTAAA   TAATG
                                      CCC_
GAM3432 OSBPL1A  3' TAACTTGATTTGGGATTAC   77170         CGAA
                                TAACTTGATTT   ATTAC
                                ||||||||||   |||||
                                ATTGAACTAAA   TAATG
                                      CCC_
GAM3432 RNPS1    5' TAACTTGATTCTGAGAAAC   77171         C__
                                TAACTTGATTT   GAAAT
                                ||||||||||   |||||
                                ATTGAACTAAG   CTTTG
                                      ACT
GAM3432 RNPS1    5' TAACTTGATTCTGAGAAAC   77171         C__
                                TAACTTGATTT   GAAAT
                                ||||||||||   |||||
                                ATTGAACTAAG   CTTTG
                                      ACT
GAM3432 LOC153027 5' TAACTTGATTCTGAGAAAC   77171         C__
                                TAACTTGATTT   GAAAT
                                ||||||||||   |||||
                                ATTGAACTAAG   CTTTG
                                      ACT
GAM3432 LOC154790 5' CTTGATTTCTTTCACCCAT   77172        GAAA
                                CTTGATTTC   TTACCCAT
                                |||||||||   ||||||||
                                GAACTAAAG   AGTGGGTA
                                    AA__
GAM3433 FZD10    3' CCTCTTAGTTCTTTTGTTA   77175        GGGTA
                                CCTCTTAGT    TTGTTA
                                |||||||||    ||||||
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                                GGAGAATCA    AACAAT
                                     AGAA_
GAM3433  FLJ13117  3'  GCCTCTCTTGGTCAAATAGTTG 77176    _    A _    _
              TTA                   GCC CTCTT GT GGGTA TTGTTA
                                    ||| ||||| || ||||| ||||||
                                    CGG GAGAA CA TTTAT AACAAT
                                      A    C G    C
GAM3434  FLJ14327  3'  GCAGGACTGTCCTGTGGAATCA 77179        TATAA   A
                                    GCGGGACT    GTG AATCA
                                    ||||||||    ||| |||||
                                    CGTCCTGA    CAC TTAGT
                                         CAGGA   C
GAM3434  KIAA0977  3'  GCTGGTAAGTGAAATC     77180    G  ACTTA
                                    GC GG    TAAGTGAAATC
                                    || ||    ||||||||||
                                    CG CC    ATTCACTTTAG
                                     A _____
GAM3434  KIAA1465  3'  TAGCAGGGACTGGTGAAATC   77181     _     TATAA
                                    TAGC GGGACT    GTGAAATC
                                    |||| ||||||    ||||||||
                                    ATCG CCCTGA    CACTTTAG
                                      T     C____
GAM3434  TRIM22    3'  AAGATTGTTATGAGTGAAATC  77182     C__   A
                                    GGGA   TTAT AGTGAAATC
                                    ||||   |||| |||||||||
                                    TTCT   AATA TCACTTTAG
                                      AAC    C
GAM3435  HSD3B2    3'  TTGTCTTCTGGTGTATGA    77185        _ CA
                                    TTGTCTTC GG  TATGG
                                    |||||||| ||  |||||
                                    AACAGAAG CC  ATACT
                                         A  AC
GAM3435  IFI27     3'  CTTATTTTCCTCTGGAGATGC  77186      C   GGCATA
                                    CTTGT TTC     TGGAGATGC
                                    ||||| |||     |||||||||
                                    GAATA AAG     ACCTCTACG
                                      A   GAG___
GAM3435  MAN2A2    3'  CTTGTCTTTGGACGTACGGGTG 77187        C  _ A    AGA
              C                      CTTGTCTT GG C TATGG   TGC
                                    |||||||| || | |||||   |||
                                    GAACAGAA CC G ATGCC   ACG
                                         A  T C    C__
GAM3435  DKFZP547E1010 5'  TTGTTTTCGACATATATG    77188      C        GGAG
                                    TTGT TTCGGCATAT    ATG
                                    |||| ||||||||||    |||
                                    AACA AAGCTGTATA    TAC
                                      A        _____
GAM3435  DKFZP547E1010 5'  TTGTTTTCGACATATATG    77188      C        GGAG
                                    TTGT TTCGGCATAT    ATG
                                    |||| ||||||||||    |||
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                                AACA AAGCTGTATA    TAC
                                  A       _____
GAM3435  FLJ20359  3'  CTTGTCTTCAGGGGCTGGGGTG 77189          CATA   AGA
              C                    CTTGTCTTCGG    TGG   TGC
                                   ||||||||||    |||   |||
                                   GAACAGAAGTC    ACC   ACG
                                         CCCG   CC_
GAM3435  KIAA0553  3'  CTTTTCTGGGATATGGAGATGC 77190     G   TC  C
                                   CTT TCT  GG ATATGGAGATGC
                                   ||| |||  || ||||||||||||
                                   GAA AGA  CC TATACCTCTACG
                                     A  C_ _
GAM3435  KIAA1856  5'  CTTGTCTTCGGGTGAGAGTGC  77191          CATAT    A
                                   CTTGTCTTCGG    GGAG TGC
                                   ||||||||||     |||| |||
                                   GAACAGAAGCC    TCTC ACG
                                         CAC__    _
GAM3435  LOC118851 3'  CTTGTCTTTGGCAATGCAGTGC 77192        C    T   G  A
                                   CTTGTCTT GGCA ATG AG TGC
                                   |||||||| |||| ||| || |||
                                   GAACAGAA CCGT TAC TC ACG
                                       A    _   G  _
GAM3435  LOC163026 5'  TTGTTTCCGGCATACCTTATG  77193      C         GGAG
                                   TTGT TTCGGCATAT    ATG
                                   |||| ||||||||||    |||
                                   AACA AGGCCGTATG    TAC
                                     A         GAA_
GAM3435  LOC256981 5'  CTTGTCTTTGACACGATG    77194         C    ATGGA
                                   CTTGTCTT GGCAT    GATG
                                   |||||||| |||||    ||||
                                   GAACAGAA CTGTG    CTAC
                                       A    ______
GAM3436  FLJ20125  3'  ATCCACTTTCTGTAATATAGT  77197      ____  C
                                   GTCC    TC GTAATATAGT
                                   ||||    || ||||||||||
                                   TAGG    AG CATTATATCA
                                     TGAA  A
GAM3436  KIAA1130  3'  AGCCTTCTGTAATATAGT    77198      C  C
                                   AGTC TC GTAATATAGT
                                   |||| || ||||||||||
                                   TCGG AG CATTATATCA
                                     A  A
GAM3437  LPIN1     3'  GATCCAAACATAAAATTGCA   77201        TTT  C
                                   GATCCG   TA AAAATTGCA
                                   ||||||   || |||||||||
                                   CTAGGT   GT TTTTAACGT
                                      TT_  A
GAM3437  NQO1      3'  AGAAATTTACACAAAATTGCA  77202        CCGTTT
                                   AGAGAT     TACAAAATTGCA
                                   ||||||     ||||||||||||
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                                TCTTTA     GTGTTTTAACGT
                                   AAT___
GAM3437  PPP1R12B  5'  GAGCCCATTTTATGAGATTG   77203     A       CAAA
                                GAG TCCGTTTTA    ATTG
                                ||| |||||||||    ||||
                                CTC GGGTAAAAT    TAAC
                                  _       ACTC
GAM3437  PPP1R12B  5'  GAGCCCATTTTATGAGATTG   77203     A       CAAA
                                GAG TCCGTTTTA    ATTG
                                ||| |||||||||    ||||
                                CTC GGGTAAAAT    TAAC
                                  _       ACTC
GAM3437  AGTRL2    5'  GAAATCCGCAAAGTTGC     77204        TTTTA    A
                                GAGATCCG     CAAA TTGC
                                ||||||||     |||| ||||
                                CTTTAGGC     GTTT AACG
                                     _____   C
GAM3437  DKFZp761N0624  3'  AGGTATCCCTCAAAATTGC    77205    AG    G TTTA
                                AG  ATCC T    CAAAATTGC
                                ||  |||| |    |||||||||
                                TC  TAGG A    GTTTTAACG
                                 CA    G ____
GAM3437  HSD17B12  3'  AGAGATCTTTGTAAATTGC    77206       CGT   ACA
                                AGAGATC   TTT   AAATTGC
                                |||||||   |||   |||||||
                                TCTCTAG   AAA   TTTAACG
                                   ___   CA_
GAM3437  KIAA0014  3'  GAGGCAGACAAAATTGC     77207     ATCC  TTT
                                GAG    GT   ACAAAATTGC
                                |||    ||   ||||||||||
                                CTC    CG   TGTTTTAACG
                                  ____  TC_
GAM3437  KIAA1340  3'  AGAAACCCTTACAAAGTTG    77208        GTT      A
                                AGAGATCC   TTACAAA TTG
                                ||||||||   ||||||| |||
                                TCTTTGGG   AATGTTT AAC
                                   ___       C
GAM3437  KIAA1434  3'  AAGATCTGACCAAAATTGC    77209       CGTTTTA
                                GAGATC      CAAAATTGC
                                ||||||      |||||||||
                                TTCTAG      GTTTTAACG
                                   ACTG___
GAM3437  MGC14161  5'  AGAGATCCCTTTTGATCTGCA  77210        G    ACAAAA
                                AGAGATCC TTTT     TTGCA
                                |||||||| ||||     |||||
                                TCTCTAGG AAAA     GACGT
                                    G    CTA___
GAM3437  LOC257482 3'  AGAGATCCTGTTTTGGTGC    77211        _     ACAAAAT
                                AGAGATCC GTTTT      TGC
                                |||||||| |||||      |||
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                                TCTCTAGG CAAAA      ACG
                                    A    CC_____
GAM3438 CDH13    3' TTTCTCTGCTCTCCCTCTCTG 77214        G  GG  GC
                                TTTCTCTGCT TCC  TC  CTG
                                |||||||||| |||  ||  |||
                                AAAGAGACGA AGG  AG  GAC
                                    G  G_  A_
GAM3438 HRC      5' TTTCTCTGTGTCTCTCCT    77215       C   CGG  G
                                TTTCTCTG TGTC   TC CCT
                                |||||||| ||||   || |||
                                AAAGAGAC ACAG   AG GGA
                                    _   ___  A
GAM3438 PML      3' TTTCTCTGCTGTTCCACACTGC 77216         CCGG   _
                                TTTCTCTGCTGT    TCGC CTGC
                                ||||||||||||    |||| ||||
                                AAAGAGACGACA    GGTG GACG
                                    A___    T
GAM3438 SKIV2L   5' TTTCTCTGTTCTTCCTCTTTGC 77217       CTG_  GG  GCC
                                TTTCTCTG    TCC  TC   TGC
                                ||||||||    |||  ||   |||
                                AAAGAGAC    AGG  AG   ACG
                                    AAGA   __  AA_
GAM3438 FLJ14260 5' TTTCTCTGCAGTGTAAGTGCTT 77218        T  CC_   C  C
          G                      TTTCTCTGC GT   GGT GC TG
                                |||||||| ||   ||| || ||
                                AAAGAGACG CA   TCA CG AC
                                    T  CAT   _  A
GAM3438 FLJ14906 3' CTTCTCTGTTCTAGTTGCTTGC 77219       CTG  CG  C  C
                                TTTCTCTG   TC  GT GC TGC
                                ||||||||   ||  || || |||
                                GAAGAGAC   AG  CA CG ACG
                                    A__  AT  A  A
GAM3438 KIAA0418 3' TTTCTCTGCTTCACCATGTCTG 77220        GT_  _  _
          C                      TTTCTCTGCT   CCG GTC GC
                                ||||||||||   ||| ||| ||
                                AAAGAGACGA   GGT CAG CG
                                    AGT   A   A
GAM3438 KIAA1272 3' TTTCCTGCTGTCATCTGC    77221     T      CG  _
                                TTTC CTGCTGTC  GTC GC
                                |||| ||||||||  ||| ||
                                AAAG GACGACAG  TAG CG
                                  _       __  A
GAM3438 KIAA1649 3' TCTGCCGTCTCACTG       77222        CGG   C
                                TCTGCTGTC   TCGC TG
                                |||||||||   |||| ||
                                AGACGGCAG   AGTG AC
                                    ____   _
GAM3438 KRT6IRS  3' TTTCTCTGCTTCTGGGTGC   77223        G  C  TC
                                TTTCTCTGCT TC GG  GC
                                |||||||||| || ||  ||
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                                AAAGAGACGA AG CC  CG
                                      _ A  CA
GAM3438  MGC13007  5'  TTTCTGCTGCTGTTCCCAGCAC 77224      _     __   T   C
                TGC                    TTTCT CTGCTGT  CCGG CGC TGC
                                       ||||| |||||||  |||| ||| |||
                                       AAAGA GACGACA  GGTC GTG ACG
                                         C      AG   _  _
GAM3438  ZF5128    3'  TTTCTCTGCTGTGGATCTG    77225          CC  TCGC
                                       TTTCTCTGCTGT  GG    CTG
                                       ||||||||||||  ||    |||
                                       AAAGAGACGACA  CC    GAC
                                             __ TA__
GAM3438  ZNF384    3'  TTTCTCTGTTATCTGGGAGGGC 77226        C    C  TC__
                                       TTTCTCTG TGTC GG    GC
                                       |||||||| |||| ||    ||
                                       AAAGAGAC ATAG CC    CG
                                            A    A  CTCC
GAM3438  LOC151199 5'  TTTCTCTGCTTCTGGAGGC    77227          G  C  TC
                                       TTTCTCTGCT TC GG  GC
                                       |||||||||| || ||  ||
                                       AAAGAGACGA AG CC  CG
                                             _ A  TC
GAM3438  LOC158427 3'  TTTCTCTGTTTCTGCAGTCTTG 77228         ___   CC    GCC
                C                       TTTCTCTG   CTGT  GGTC   TGC
                                        ||||||||   ||||  ||||   |||
                                        AAAGAGAC   GACG  TCAG   ACG
                                            AAA    __    A__
GAM3438  LOC158527 3'  TTTCTCTGCTGCATC       77229           CCG
                                       TTTCTCTGCTGT   GTC
                                       ||||||||||||   |||
                                       AAAGAGACGACG   TAG
                                              ___
GAM3438  LOC158584 3'  TTTCTCTGCTTGTCTGCTGGTG 77230          _  C___   C
                C                       TTTCTCTGCT GTC    GGT GC
                                        |||||||||| |||    ||| ||
                                        AAAGAGACGA CAG    CCA CG
                                             A   ACGA  _
GAM3438  LOC197320 3'  TTTCTCTGTGTCTGCTGC    77231         C    CG  C
                                       TTTCTCTG TGTC  GT GC
                                       |||||||| ||||  || ||
                                       AAAGAGAC ACAG  CG CG
                                             _    A_  A
GAM3438  LOC200471 5'  TTTCCCTGCTGTTCTTGCGCAG 77232         _ _________   TCGC
                GCGACC                  TCTGCTGT C       CGG    CT
                                        |||||||| |       |||    ||
                                        GGACGACA G       GTC    GG
                                             A AACGIIIC   CGCT
GAM3438  LOC254848 5'  CTTCTCTGTTGTTTGGAGAACC 77233         C   CC  TC_
                TG                      TTTCTCTG TGT  GG   GCCTG
                                        |||||||| |||  ||   |||||
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                                GAAGAGAC ACA  CC   TGGAC
                                     A   AA  TCT
GAM3439  ATP2B2    3'  GACATAAATAAGTTAAAATAGA 77236         C____
                                GACATAAAT     AAAATAGA
                                |||||||||     ||||||||
                                CTGTATTTA     TTTTATCT
                                     TTCAA
GAM3439  GGA1      3'  TGGACAGACGTAAGACACCCAT 77237         A   AT  AA_
              AG                   TGGATAGAC TAA  CA   ATAG
                                |||||||||| |||  ||   ||||
                                ACCTGTCTG ATT  GT   TATC
                                     C   CT  GGG
GAM3439  GORASP1   3'  TGGATAGACCTAGTCAGGTAGA 77238         ATAAA   AAA
                                TGGATAGAC     TCA   TAGA
                                |||||||||     |||   ||||
                                ACCTATCTG     AGT   ATCT
                                     GATC_   CC_
GAM3439  KIAA1024  3'  TAGATAGACATATAGATAG    77239          AATCAAA
                                TGGATAGACATA      ATAG
                                ||||||||||||      ||||
                                ATCTATCTGTAT      TATC
                                      ATC____
GAM3439  STK33     5'  TGTATAGACATGAAAAGGACAA 77240     G      _   T___
              AATAG                    TG ATAGACAT AAA    CAAAATAG
                                || ||||||||  |||    ||||||||
                                AC TATCTGTA TTT    GTTTTATC
                                 A       C   TCCT
GAM3439  LOC139221 3'  GGATAGACACTCCCAAAA     77241          AAA
                                GGATAGACAT   TCAAAA
                                ||||||||||   ||||||
                                CCTATCTGTG   GGTTTT
                                     AG_
GAM3439  LOC159090 3'  TGTATAGACTCAAAATAG     77242     G     ATAAA
                                TG ATAGAC     TCAAAATAG
                                || ||||||     |||||||||
                                AC TATCTG     AGTTTTATC
                                 A     ______
GAM3440  IL18R1    3'  TCTATTTTGATTATATATGT   77245           ___
                                TCTATTTTGATT   TATGT
                                ||||||||||||   |||||
                                AGATAAAACTAA   ATACA
                                      TAT
GAM3440  MMP20     3'  TCTAATTTGATTTGAAGGCCT  77246      T      AT__
                                TCTA TTTGATTT    GTCT
                                ||||| ||||||||   ||||
                                AGAT AAACTAAA    CGGA
                                  T       CTTC
GAM3440  SLC26A2   3'  TCTTTTTGACTCTGTCCA     77247     A       A
                                TCT TTTTGATTT TGTCTA
                                ||| ||||||||| ||||||
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                                AGA AAAACTGAG ACAGGT
                                  _       _
GAM3440  C1orf22   3'  TTTGTTTCTTGTCTATCC    77248      A   A
                                TTTG TTT TGTCTATCC
                                |||| ||| |||||||||
                                AAAC AAG ACAGATAGG
                                  A   A
GAM3440  CREB-H    3'  TCTGTTTCAATCTGTGTCTGTC 77249     A   TG    A     A
                                TCT TTT  ATTT TGTCT TC
                                ||| |||  |||| ||||| ||
                                AGA AAA  TAGA ACAGA AG
                                  C   GT    C     C
GAM3440  DKFZP564I052 3'  TCTATTTTATTCTATC      77250          ATTTATG
                                TCTATTTTG      TCTATC
                                |||||||||      ||||||
                                AGATAAAAT      AGATAG
                                      A_______
GAM3440  DKFZP566K0524 3'  TATTTTGATATTGTCTA     77251          TTA
                                TATTTTGAT   TGTCTA
                                |||||||||   ||||||
                                ATAAAACTA   ACAGAT
                                      TA_
GAM3440  KIAA1456  3'  TATTTTGATTCCATCC      77252          TTATG
                                TATTTTGAT    TCTATCC
                                |||||||||    |||||||
                                ATAAAACTA    AGGTAGG
                                      _____
GAM3440  MGC29667  3'  TTTTTTTTTATGTCTATC    77253      GA
                                TTTT  TTTATGTCTATC
                                ||||  ||||||||||||
                                AAAA  AAATACAGATAG
                                  AA
GAM3440  MGC29898  3'  TTTGATTCAGTGTCTATC    77254          _      C
                                TTTGATTTA TGTCTAT C
                                ||||||||| ||||||| |
                                AAACTAAGT ACAGATA G
                                      C      A
GAM3440  MIL1      3'  CTATTTTGGTTTATTACCC    77255        A    GTC
                                CTATTTTG TTTAT   TATCC
                                ||||||| |||||   |||||
                                GATAAAAC AAATA   ATGGG
                                      C    ___
GAM3440  PRO0902   3'  TCCATTTTGATTTATCTCT    77256             G
                                TCTATTTTGATTTAT TCT
                                |||||||||||||| |||
                                AGGTAAAACTAAATA AGA
                                        G
GAM3440  PRO1575   5'  TCTACTTGTTATATGTCTATTC 77257        TGATT        C
              A                  TCTATTT     TATGTCTAT CA
                                |||||||     ||||||||| ||
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                                AGATGAA    ATACAGATA GT
                                   CAAT_       A
GAM3440  LOC119392 3'  TTTTGACAAATCTATCCA    77258       TTAT
                                TTTTGAT   GTCTATCCA
                                |||||||   |||||||||
                                AAAACTG   TAGATAGGT
                                   TT__
GAM3440  LOC122553 3'  TCTATTTTGATCTACTTCT   77259            G
                                TCTATTTTGATTTAT TCT
                                |||||||||||||| |||
                                AGATAAAACTAGATG AGA
                                          A
GAM3440  LOC145623 5'  TCTTTTTGATATGTATCTATC  77260    A      TTA
                                TCT TTTTGAT   TGTCTATC
                                ||| |||||||   ||||||||
                                AGA AAAACTA   ATAGATAG
                                  _      TAC
GAM3440  LOC158292 5'  TCTATTTTCATTAATGTCTA   77261       G   T
                                TCTATTTT ATT ATGTCTA
                                |||||||| ||| |||||||
                                AGATAAAA TAA TACAGAT
                                     G   T
GAM3440  LOC201799 3'  TTCTGATTGCCCTATCCA    77262       TTA   _
                                TTTTGAT   TGTC TATCCA
                                |||||||   |||| ||||||
                                AAGACTA   ACGG ATAGGT
                                   ___    G
GAM3440  LOC221300 3'  TTTTGAGAAATGTCTATTCA   77263      TTT      C
                                TTTTGA   ATGTCTAT CA
                                ||||||   |||||||| ||
                                AAAACT   TACAGATA GT
                                   CTT       A
GAM3440  LOC255130 3'  TCTATTTTGGCTTTATCTTCCA 77264        AT  A    A
                                TCTATTTTG  TT TGTCT TCCA
                                |||||||||  || ||||| ||||
                                AGATAAAAC  AA ATAGA AGGT
                                     CG  _    _
GAM3441  ADAM19    3'  TACTCTGGTCACACTCCT    77267         C  GA
                                TACTCTGGTC CG  CCT
                                |||||||||| ||  |||
                                ATGAGACCAG GT  GGA
                                      T  GA
GAM3441  GCNT1     3'  CTCTGGCCTCAAGGCTACC   77268       C   AC
                                CTCTGGTC CGG  CTACC
                                |||||||| |||  |||||
                                GAGACCGG GTT  GATGG
                                     A   CC
GAM3441  GM2A      3'  CACTCTGGTTCCCATTCCT   77269        _   GA
                                TACTCTGGT CCCG  CCT
                                ||||||||| ||||  |||
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                                GTGAGACCA GGGT  GGA
                                    A   AA
GAM3441  NUMB     3'  TACTCTGGGCCTGGACTTGTTC 77270       T  C   CTACC
                CT                  TACTCTGG CC GGAC    CCT
                                    |||||||| || ||||    |||
                                    ATGAGACC GG CCTG    GGA
                                        C  A   AACAA
GAM3441  RAG1     3'  CTCTGGTCCCCTGCAGTTACTC 77271        GGACC__  C
                CT                  CTCTGGTCCC     TAC CCT
                                    ||||||||||     ||| |||
                                    GAGACCAGGG     ATG GGA
                                        GACGTCA   A
GAM3441  SRGAP2   3'  TCTGGTCCTGATACTCC    77272       CG  CC   C
                                    TCTGGTCC  GA  TAC CC
                                    ||||||||  ||  ||| ||
                                    AGACCAGG  CT  ATG GG
                                        A_  __   A
GAM3441  TUFT1    3'  TACTCTGATGCCTATCTACTTC 77273       C  GGAC   CC
                T                   TACTCTGGT CC   CTAC  CT
                                    ||||||||| ||   ||||  ||
                                    ATGAGACTA GG   GATG  GA
                                        C  ATA_   AA
GAM3441  WNT5B    5'  CTCTGGTCCTGCAGTTCCT   77274        __  A_
                                    CTCTGGTCC  CGG  CCT
                                    |||||||||  |||  |||
                                    GAGACCAGG  GTC  GGA
                                        AC   AA
GAM3441  C17orf31 5'  CCTGGTCCTGGGCTTGCCT   77275       C  AC  ACC
                                    TCTGGTCC GG  CT   CCT
                                    |||||||| ||  ||   |||
                                    GGACCAGG CC  GA   GGA
                                        A  C_  AC_
GAM3441  CECR6    3'  ACTCTGGTCAAGCCTTCTGCCC 77276       CC  A   A___
                CT                    ACTCTGGTC  GG CCT    CCCCT
                                    |||||||||  || |||   |||||
                                    TGAGACCAG  TC GGA    GGGGA
                                        T_  _   AGAC
GAM3441  DKFZp564I1922 3'  CACTCTGGTTCTAAATCCT   77277        CCC  _
                                    TACTCTGGT   GGA CCT
                                    |||||||||   ||| |||
                                    GTGAGACCA   TTT GGA
                                        AGA   A
GAM3441  FLJ14442 3'  CACTCTGGTCTTGGCCT    77278        CC  A
                                    TACTCTGGTC  GG CCT
                                    ||||||||||  || |||
                                    GTGAGACCAG  CC GGA
                                        AA  _
GAM3441  GIT1     3'  CTCTGGTCCCCTCACCCCT   77279        GGACC
                                    CTCTGGTCCC    TACCCCT
                                    ||||||||||    |||||||
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                                GAGACCAGGG    GTGGGGA
                                      GA___
GAM3441  KIAA0416  3'  TACATTGGAGGATCTACCCCT  77280    TC   TCCC   C
                                TAC  TGG    GGA CTACCCCT
                                |||  |||    ||| ||||||||
                                ATG  ACC    CCT GATGGGGA
                                  TA   T___   A
GAM3441  LOC146481 5'  ACTCTGGTTCCCTTTTCTTACC 77281        _   GGACC_
           C                     ACTCTGGT CCC      TACCC
                                |||||||| |||      |||||
                                TGAGACCA GGG      ATGGG
                                     A   AAAAGA
GAM3441  LOC148809 3'  TACTCTGGACTTCACATTCCT  77282        ___  C  GA
                                TACTCTGG   TC CG  CCT
                                ||||||||   || ||  |||
                                ATGAGACC   AG GT  GGA
                                     TGA  T  AA
GAM3441  LOC149302 5'  TCTGGTCCACTAATTCTACTCC 77283        CG_  C_    C
           T                     TCTGGTCC   GA  CTAC CCT
                                |||||||   ||  |||| |||
                                AGACCAGG   TT  GATG GGA
                                     TGA  AA    A
GAM3441  LOC150378 3'  CCTGCCCAGGACTTACTCCT   77284     G   C    C   C
                                TCTG TCC GGAC TAC CCT
                                |||| ||| |||| ||| |||
                                GGAC GGG CCTG ATG GGA
                                  _   T    A   A
GAM3441  LOC153592 3'  CTCTGATCCCGTGAATTCCT   77285         _ ___
                                CTCTGGTCCCG GA   CCT
                                |||||||||| ||   |||
                                GAGACTAGGGC CT   GGA
                                      A  TAA
GAM3441  LOC153810 5'  TACTCTGGTTCCCAATAAGTTC 77286        _    ACCTACC
           CT                    TACTCTGGT CCCGG      CCT
                                |||||||| |||||      |||
                                ATGAGACCA GGGTT      GGA
                                     A    ATTCAA_
GAM3441  LOC158177 5'  ACTCTGATCTGGACCTA     77287        CC
                                ACTCTGGTC  GGACCTA
                                |||||||||  |||||||
                                TGAGACTAG  CCTGGAT
                                     A_
GAM3441  LOC201799 3'  CTCTGGTCTGGAACTCTGCCT  77288        CC   C  ACC
                                CTCTGGTC  GGA CT   CCT
                                ||||||||  ||| ||   |||
                                GAGACCAG  CCT GA   GGA
                                     A_   T  GAC
GAM3441  LOC253649 5'  ACTCTGATCTGGACCTA     77287        CC
                                ACTCTGGTC  GGACCTA
                                |||||||||  |||||||
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                                TGAGACTAG  CCTGGAT
                                     A_
GAM3441  LOC253650 5'  ACTCTGATCTGGACCTA     77287         CC
                                ACTCTGGTC  GGACCTA
                                |||||||||  |||||||
                                TGAGACTAG  CCTGGAT
                                     A_
GAM3441  LOC255481 3'  CCCTGGTCCTGTCACCCCT    77289         CGGACC
                                CTCTGGTCC     TACCCCT
                                |||||||||     |||||||
                                GGGACCAGG     GTGGGGA
                                     ACA___
GAM3441  LOC90668  3'  CCTGGTCCTGCCGTCTTGCCCC 77290         ___  GACCTA
           T                     TCTGGTCC   CG     CCCCT
                                |||||||||  ||     |||||
                                GGACCAGG   GC     GGGGA
                                     ACG  AGAAC_
GAM3442  FNTB     3'  CCCTTACAAATGACCAGGGTG  77293     G   TATTA
                                CCC TAC    GACCAGGGTG
                                ||| |||    ||||||||||
                                GGG ATG    CTGGTCCCAC
                                  A   TTTA_
GAM3442  GOSR1    3'  CCTTATTCCAGACCAGGGTG   77294    GTACTA
                                CC     TTAGACCAGGGTG
                                ||     ||||||||||||
                                GG     GGTCTGGTCCCAC
                                  AATAA_
GAM3442  MEIS2    3'  CCCTTATACTATTGGGC     77295     CC      AGACCA
                                CCC  GTACTATT     GGGT
                                |||  ||||||||     ||||
                                GGG  TATGATAA     CCCG
                                  AA      _______
GAM3442  ZNF41    3'  CCTCCCTGCTATTAGATACC   77296    _   GTA      __
                                CC CCC   CTATTAGA  CC
                                || |||   ||||||||  ||
                                GG GGG   GATAATCT  GG
                                  A   AC_       AT
GAM3442  BCKDK    5'  CCGACTTCAGGGACCAGGGTG  77297     T   ATTA_
                                CCG ACT    GACCAGGGTG
                                ||| |||    ||||||||||
                                GGC TGA    CTGGTCCCAC
                                  _   AGTCC
GAM3442  C11orf21  3'  CCTCTGACTATTAGATCCGATG 77298    GT__       _  A__
             GGTG                    CC    ACTATTAGA CC   GGGTG
                                ||   ||||||||| ||   |||||
                                GG   TGATAATCT GG   CCCAC
                                  AGAC       A  CTA
GAM3442  DKFZP547L112 3'  CCAGTGCCTTAGACCAGGGTG  77299    C  A  A
                                CC GT CT TTAGACCAGGGTG
                                || || || ||||||||||||
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                                GG CA GG AATCTGGTCCCAC
                                 T  C  _
GAM3442  FLJ14225  3'  CCGTGTTAGCCAGGGTG     77300      ACTA    A
                                CCGT    TTAG CCAGGGTG
                                ||||    |||| ||||||||
                                GGCA    AATC GGTCCCAC
                                  C___    _
GAM3442  FLJ23153  3'  CCCACCGTACACCAGGGT     77301     _     TATTAG
                                CCC CCGTAC     ACCAGGGT
                                ||| ||||||     ||||||||
                                GGG GGCATG     TGGTCCCA
                                  T     _______
GAM3442  KIAA1266  3'  CCTCGTGCTTCCCAGGGTG   77302    C   A  ATTAGA
                                CC CGT CT     CCAGGGTG
                                || ||| ||     ||||||||
                                GG GCA GA     GGTCCCAC
                                 A   C  AG____
GAM3442  KIAA1978  3'  CCCTTCTACTGTCCCCAGGGTG 77303     GTA    AGA_
                                CCC   CTATT    CCAGGGTG
                                |||   |||||    ||||||||
                                GGG   GATGA    GGTCCCAC
                                  AA_    CAGG
GAM3442  NPTXR     3'  CCCCGCACTTCCTGGGGT    77304         ATTAGA  A_
                                CCCCGTACT     CC  GGGT
                                |||||||||     ||  ||||
                                GGGGCGTGA     GG  CCCA
                                     A______  AC
GAM3442  NPTXR     3'  CCCCGCACTTCCTGGGGT    77304         ATTAGA  A_
                                CCCCGTACT     CC  GGGT
                                |||||||||     ||  ||||
                                GGGGCGTGA     GG  CCCA
                                     A______  AC
GAM3442  LOC115219 3'  CCCTCCTGCCTTCAGACCAGGG 77305     _  GTA  A
              TG                  CCC CC   CT TTAGACCAGGGTG
                                ||| ||   || ||||||||||||||
                                GGG GG   GA AGTCTGGTCCCAC
                                  A  ACG  _
GAM3442  LOC130250 5'  CCATATTAGGGTCCAGGGTG   77306      CTA    A__
                                CCGTA   TTAG   CCAGGGTG
                                |||||   ||||   ||||||||
                                GGTAT   AATC   GGTCCCAC
                                   ___    CCA
GAM3442  LOC160646 3'  CCCTCGGACTTCCCCAGGGTG  77307     _  T   ATTAGA
                                CCC CG ACT     CCAGGGTG
                                ||| || |||     ||||||||
                                GGG GC TGA     GGTCCCAC
                                  A  C   AGG___
GAM3442  LOC222865 3'  CCGTGTTAGCCAGGGTG     77300      ACTA    A
                                CCGT    TTAG CCAGGGTG
                                ||||    |||| ||||||||
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                                GGCA    AATC GGTCCCAC
                                  C___   _
GAM3443 ADCY7    3' GGTAAGAAAAGTAAGATACA   77310    A  A       C
                                GG AA AAAGGTGGG ATACA
                                || || ||||||||| |||||
                                CC TT TTTTCATTC TATGT
                                 A  C       _
GAM3443 APPL     3' GGGGAAAAAAAGATCAATGCA  77311     A       GG__
                                GGG AAAAAAGGT    GCA
                                ||| |||||||||    |||
                                CCC TTTTTTCTA    CGT
                                  C       GTTA
GAM3443 AQP6     3' GGGAAGAAGGTGGAACACA    77312      AAA       C
                                GGGAA   AAGGTGGG ATACA
                                |||||   |||||||| |||||
                                CCCTT   TTCCACCT TGTGT
                                   C__      _
GAM3443 ATP6V1G2 3' TGGGAAAGTAAGGTGTCA    77313       AA     GG
                                TGGGAAA  AAGGTG  CA
                                |||||||  ||||||  ||
                                ACCCTTT  TTCCAC  GT
                                    CA     A_
GAM3443 ATP6V1G2 3' TGGGAAAGTAAGGTGTCA    77313       AA     GG
                                TGGGAAA  AAGGTG  CA
                                |||||||  ||||||  ||
                                ACCCTTT  TTCCAC  GT
                                    CA     A_
GAM3443 BRCA1    3' TGGGAAAAAGTGGTGGTATAC  77314        AA     GC
                                TGGGAAAAA  GGTGG  ATAC
                                |||||||||  |||||  ||||
                                ACCCTTTTT  CCACC  TATG
                                     CA     A_
GAM3443 CLASP2   3' TGGGAAGACAAAGTACAAACAT 77315       AA_   _ TG
                                TGGGAA   AAAG G  GGCAT
                                ||||||   |||| |  |||||
                                ACCCTT   TTTC T  TTGTA
                                   CTG    A GT
GAM3443 COL15A1  3' TGGAAAAAAAATCCAATTATAC 77316         GG   GC
            AA                    TGGGAAAAAAA  TGG  ATACAA
                                |||||||||||  |||  ||||||
                                ACCTTTTTTTT  GTT  TATGTT
                                      AG   AA
GAM3443 DHCR24   3' TGGGAAAGATGAGGCCTGCA  77317      AAAA    _   ATA
                                TGGGAA    AGGTG GGC   CA
                                ||||||    ||||| |||   ||
                                ACCCTT    TCTAC CCG   GT
                                   ____     T   GAC
GAM3443 EFNB1    3' GGGAAAAAGGGGGAT       77318       AA   T   C
                                GGGAAAA  AGG GGG AT
                                |||||||  ||| ||| ||
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                                CCCTTTT  TCC CCC TA
                                   __  _  _
GAM3443  EGFL5    3'  GGAAGAGAGGACACACA     77319      AAAA  T
                                GGAA   AGG GGGCATACA
                                ||||   ||| |||||||||
                                CCTT   TCT CCTGTGTGT
                                  C___  _
GAM3443  EGLN1    5'  GGAGGAGCGCAGGGCATAC   77320     AAAAA  _  _
                                GGA    AG GT GGGCATAC
                                |||    || || ||||||||
                                CCT    TC CG CCCGTATG
                                 CC___  G  T
GAM3443  ENTPD1   5'  TAGGAGAAAAGGCATACA    77321      A  AAGGT
                                TGGGA AAA    GGGCATACA
                                ||||| |||    |||||||||
                                ATCCT TTT    TCCGTATGT
                                   C  _____
GAM3443  FGFR1    3'  TGGGACAAAGAGGTAAACA   77322      A  A
                                TGGGA AAA AGGTGGGCA
                                ||||| ||| |||||||||
                                ACCCT TTT TCCATTTGT
                                   G  C
GAM3443  FGFR1    3'  TGGGACAAAGAGGTAAACA   77322      A  A
                                TGGGA AAA AGGTGGGCA
                                ||||| ||| |||||||||
                                ACCCT TTT TCCATTTGT
                                   G  C
GAM3443  FUT1     3'  TGGGAAGAGCAGGTGGGCAC  77323       AAAA
                                TGGGAA   AGGTGGGCAT
                                ||||||   ||||||||||
                                ACCCTT   TCCACCCGTG
                                   CTCG
GAM3443  FUT5     3'  TGGGAAAGTGAGGTCCCTGGCA 77324       AAA   G___
                                TGGGAAA  AGGT   GGCA
                                |||||||  ||||   ||||
                                ACCCTTT  TCCA   CCGT
                                    CAC   GGGA
GAM3443  FY       5'  AGGAGGAAAAGGAAGAGATA  77325     AA    T_  C
                                GGGA  AAAAGG  GGG ATA
                                ||||  ||||||  ||| |||
                                TCCT  TTTTCC  CTC TAT
                                  CC    TT  _
GAM3443  FZD3     3'  TGGGAAAAGATGGCTACA    77326       AAA    G A
                                TGGGAAA  AGGTGG C TACA
                                |||||||  |||||| | ||||
                                ACCCTTT  TCTACC G ATGT
                                   ___    _ _
GAM3443  GAS7     3'  TGGGAAAAGGTGGTGGC     77327       AAA    __
                                TGGGAAA  AGGTGG  GC
                                |||||||  ||||||  ||
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                                ACCCTTT  TCCACC  CG
                                   ___     AC
GAM3443  GPC4     3'  TGAGAAAAAAACATAC      77328          AGGTGG
                                TGGGAAAAAA     GCATAC
                                ||||||||||     ||||||
                                ACTCTTTTTT     TGTATG
                                       _______
GAM3443  ITGAM    3'  TGGTGAAAAAAAGCAAGATACA 77329     GA       TG  C
                                TGG  AAAAAAGG  GG ATACA
                                |||  ||||||||  || |||||
                                ACC  TTTTTTTC  TC TATGT
                                  AC       GT  _
GAM3443  JTB      3'  TGGGGAAAAGGGGATTCCACCA 77330     AAA     T  ___  _
              CAA                   GGG   AAAAGG GGG   CAT ACAA
                                |||   |||||| |||   ||| ||||
                                CCC   TTTTCC CCT   GTG TGTT
                                  C__     _  AAG   G
GAM3443  KCNK5    3'  TGGGAGGGGAAGGCGGGCA    77331       AAAA
                                TGGGA    AAGGTGGGCA
                                |||||    ||||||||||
                                ACCCT    TTCCGCCCGT
                                   CCCC
GAM3443  KIF3B    3'  TGGGAAAAGATGGTGACA     77332         AAA    G
                                TGGGAAAA   GGTGG CA
                                ||||||||   ||||| ||
                                ACCCTTTT   CCACT GT
                                     CTA    _
GAM3443  MASP1    3'  TGGCAAAAAAGCATAC      77333     G    AAGGTG
                                TGG AAAAA     GGCATAC
                                ||| |||||     |||||||
                                ACC TTTTT     TCGTATG
                                  G    _______
GAM3443  MGP      3'  GGGAAAAAGGGGTGCA      77334         AA   T  _
                                GGGAAAA  AGG GG GCA
                                |||||||  ||| || |||
                                CCCTTTT  TCC CC CGT
                                   __  _ A
GAM3443  MLLT2    3'  GGGGAAAAAAGGTACTGC    77335     A        G_
                                GGG AAAAAAGGTG  GC
                                ||| ||||||||||  ||
                                CCC TTTTTTCCAT  CG
                                  C         GA
GAM3443  MSX2     3'  TGGGAAGGTGAGATA       77336       AAAAA      C
                                TGGGA    AGGTGGG ATA
                                |||||    ||||||| |||
                                ACCCT    TCCACTC TAT
                                       _____     _
GAM3443  MYBBP1A  3'  TGGGGGCAAAGAGGTGGCA   77337      AA_  A     G
                                TGGG   AAA AGGTGG CA
                                ||||   ||| ||||||  ||
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                                ACCC   TTT TCCACC GT
                                  CCG   C     _
GAM3443  NPR1     3'  TGGTAGAAGCAAGGCATACA   77338     GAAAAA   GT
                                TGG      AAG  GGGCATACA
                                |||      |||  |||||||||
                                ACC      TTC  TCCGTATGT
                                  ATC___   GT
GAM3443  PCSK2    3'  TGGGAAAGGCGGATGTGCA    77339       AAAA     ____
                                TGGGAA    AGGTGG    GCA
                                ||||||    ||||||    |||
                                ACCCTT    TCCGCC    CGT
                                   ____      TACA
GAM3443  PDE6H    3'  TAGGAAAAGGTGGTCA      77340        AAA      G
                                TGGGAAA   AGGTGG CA
                                |||||||   |||||| ||
                                ATCCTTT   TCCACC GT
                                   ___      A
GAM3443  PKD2     3'  TGGGAAAAAGAATATGCA     77341         AA    G
                                TGGGAAAAA  GGTG GCA
                                |||||||||  |||| |||
                                ACCCTTTTT  TTAT CGT
                                     C_    A
GAM3443  POU1F1   3'  GGGAGAAAAAGGCTATTATACA 77342      A       GGGC
           A                     GGGA AAAAAGGT    ATACAA
                                 |||| ||||||||    ||||||
                                 CCCT TTTTTCCG    TATGTT
                                   C       ATAA
GAM3443  PTK2B    3'  TGAGAAAAGAAGGGTGCA     77343        A    TGG
                                TGGGAAAA AAGG   GCA
                                ||||||||| ||||   |||
                                ACTCTTTT TTCC   CGT
                                     C    CA_
GAM3443  PYGB     3'  TGGGGAAAAAAGGAGGTGCA   77344      A       T _
                                TGGG AAAAAAGG GG GCA
                                |||| |||||||| || |||
                                ACCC TTTTTTCC CC CGT
                                   C       T  A
GAM3443  RHEB2    5'  GGGAGAGAGCGGCATACA     77345      AAAAAA    G
                                GGGA     GGTGG CATACA
                                ||||     ||||| ||||||
                                CCCT     TCGCC GTATGT
                                   CTC___    _
GAM3443  ZNFN1A3  3'  TGGGAAAACAAAGGTTTCACA  77346         _     GGG
                                TGGGAAAA AAAGGT   CATA
                                |||||||| ||||||   ||||
                                ACCCTTTT TTTCCA   GTGT
                                     G     AA_
GAM3443  ABCA5    3'  TGGTGAAAAAGATGACATACAA 77347     GAA        G
                                TGG   AAAAAGGTGG CATACAA
                                |||   |||||||||| |||||||
```

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                                ACC   TTTTTCTACT GTATGTT
                                  AC_        _
GAM3443  ATP6V1G1  3'  TAGGAAAAAAAGACAACATA   77348           TG G
                                TGGGAAAAAAAGG  G CATA
                                |||||||||||||  | ||||
                                ATCCTTTTTTTCT  T GTAT
                                       GT _
GAM3443  BTEB5     3'  TGGGAAAGAAGGATGGGCA    77349        A  A
                                TGGGAAA AA GGTGGGCA
                                ||||||| || ||||||||
                                ACCCTTT TT CTACCCGT
                                    C  C
GAM3443  CHST3     3'  TGGCAAAAAGACAGTGTGCA   77350     G    AA_   G
                                TGG AAAAA   GGTG GCA
                                ||| |||||   |||| |||
                                ACC TTTTT   TCAC CGT
                                  G    CTG   A
GAM3443  CIC       3'  TGGGGAAAAAAGGGGTGCAT   77351      A       T _
                                TGGG AAAAAAGG GG GCAT
                                |||| |||||||| || ||||
                                ACCC TTTTTTCC CC CGTA
                                  C       _ A
GAM3443  DKFZP434L0117 3'  TGGAGAAGAAAGGTGGACA    77352     GA  A
                                TGG  AA AAAGGTGGGCA
                                |||  || ||||||||||
                                ACC  TT TTTCCACCTGT
                                  TC  C
GAM3443  ERMAP     3'  TGGGAGAAAAGTGGTACA     77353       AAA       _
                                TGGGA   AAAGGTGG GCA
                                |||||   |||||||| |||
                                ACCCT   TTTTCACC TGT
                                  C__       A
GAM3443  FKBP9     3'  TGGGATAGAAAGGTGGGAAT   77354       AAA        C
                                TGGGA   AAAGGTGGG AT
                                |||||   ||||||||| ||
                                ACCCT   TTTCCACCC TA
                                  ATC        T
GAM3443  FLJ10996  3'  TGGGAACAAAAGGTACCAT    77355       A       GG
                                TGGGAA AAAAGGTG  CAT
                                |||||| ||||||||  |||
                                ACCCTT TTTTCCAT  GTA
                                   G       G_
GAM3443  FLJ11783  3'  TGGGAAAAGGAGGTGGAGATA  77356         AA      C
                                TGGGAAAA  AGGTGGG ATA
                                ||||||||  ||||||| |||
                                ACCCTTTT  TCCACCT TAT
                                     CC      C
GAM3443  FLJ13117  5'  TGGGAAACGGAAGTGTGCA    77357        AAA     G
                                TGGGAAA   AGGTG GCA
                                |||||||   ||||| |||
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                                ACCCTTT   TTCAC CGT
                                    GCC    A
GAM3443  FLJ14442  3'  TGGGAGAGCAAAGCAAGTACAA 77358      AAAA   TG  CA
                                TGGGA   AAGG  GG  TACAA
                                |||||   ||||  ||  |||||
                                ACCCT   TTTC  TC  ATGTT
                                   CTCG   GT  __
GAM3443  FLJ22318  3'  TGGGAGGAAGAGGTGGGC    77359      AA  A
                                TGGGA  AA AGGTGGGC
                                |||||  || ||||||||
                                ACCCT  TT TCCACCCG
                                   CC  C
GAM3443  FLJ23045  3'  GGGAAAAAAAGAAAAAAATACA 77360          TG  C
            A                    GGGAAAAAAAGG  GG ATACAA
                                ||||||||||||  || ||||||
                                CCCTTTTTTTCT  TT TATGTT
                                       TT  T
GAM3443  HIRIP5   5'  TGGGAAAAGTGGTCTTTGTACA 77361       AAAA    GCA___
            A                    TGGGAAA   GGTGG     TACAA
                                |||||||   |||||     |||||
                                ACCCTTT   TCACC     ATGTT
                                    ____    AGAAAC
GAM3443  IL18BP   3'  GGGAAAAAAAAAAACATACA   77362          TGG
                                GGGAAAAAAAGG   GCATACA
                                ||||||||||||   |||||||
                                CCCTTTTTTTTT   TGTATGT
                                       ___
GAM3443  KIAA0090  3'  TGGGCAAAGAAAGGAAACA   77363     _  A    T
                                TGGG AAA AAAGG GGGCA
                                |||| ||| ||||| |||||
                                ACCC TTT TTTCC TTTGT
                                  G  C   _
GAM3443  KIAA0352  3'  TGGGGAAAAAAGTTTACA    77364     AA      GG
                                TGGG  AAAAAGGT  GCA
                                ||||  ||||||||  |||
                                ACCC  TTTTTTCA  TGT
                                  C_      AA
GAM3443  KIAA0514  3'  TGGGAAAAAGGGGTGTGTGC   77365        AA   G__
                                TGGGAAAAA  GGTG   GC
                                |||||||||  ||||   ||
                                ACCCTTTTT  CCAC   CG
                                     CC    ACA
GAM3443  KIAA1053  3'  GGGGAAAAAAGGCTGCA     77366     A       GG
                                GGG AAAAAAGGT  GCA
                                ||| |||||||||  |||
                                CCC TTTTTTCCG  CGT
                                  C       A_
GAM3443  KIAA1054  3'  GGAAGAAGAAAAACATACA   77368     AAA   TG
                                GGAA   AAGG  GGCATACA
                                ||||   ||||  ||||||||
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                                CCTT   TTCT  TTGTATGT
                                  C__    TT
GAM3443  KIAA1054  3'  TGGGAAAATGGGTACA      77367        AAAAG     CA
                                TGGGAAA    GTGGG  TACA
                                |||||||    |||||  ||||
                                ACCCTTT    TACCC  ATGT
                                     _____    __
GAM3443  KIAA1091  3'  TGGGAAAAAAGGTCAGAGC    77369          A  __
                                TGGGAAAAAA GGT  GGGC
                                |||||||||| |||  ||||
                                ACCCTTTTTT CCA  CTCG
                                      _  GT
GAM3443  KIAA1096  3'  GGGGGAAAAAGGTAAAAAACAA 77370     AA         CAT
                                GGG  AAAAAGGTGGG   ACAA
                                |||  ||||||||||   ||||
                                CCC  TTTTTCCATTT   TGTT
                                  CC         TT_
GAM3443  KIAA1374  3'  TGGGCAAAAAACTGACATA    77371      _     AGGTG
                                TGGG AAAAAA    GGCATA
                                |||| ||||||    ||||||
                                ACCC TTTTTT    CTGTAT
                                  G     GA___
GAM3443  KIAA1831  5'  TGGGGGAAGATGAGAATA    77372      AAAAA       C
                                TGGG    AAGGTGGG ATA
                                ||||    |||||||| |||
                                ACCC    TTCTACTC TAT
                                  CC___       T
GAM3443  KIAA1957  3'  TGGGGGAGGAAGACACAC    77373      AAAAAA   T
                                TGGG     AGG GGGCATAC
                                ||||     ||| ||||||||
                                ACCC     TCC TCTGTGTG
                                  CC____   T
GAM3443  LIN-28    3'  TGGGAAAGGAAGTACCCAGTAC 77374        AAA    GG  _
           A                     TGGGAAA   AGGTG  CA TACA
                                |||||||   |||||  || ||||
                                ACCCTTT   TTCAT  GT ATGT
                                    CC_    GG  C
GAM3443  LPAAT-delta 3'  GGGAAAAAAAGATTACA     77375           GG
                                GGGAAAAAAAGGT  GCA
                                ||||||||||||  |||
                                CCCTTTTTTTCTA  TGT
                                       A_
GAM3443  MGC11386  3'  TGGGCAAAAAAAGGACATGCA  77376      _       TGG_
                                TGGG AAAAAAAGG    GCA
                                |||| |||||||||    |||
                                ACCC TTTTTTTCC    CGT
                                  G        TGTA
GAM3443  MGC16279  3'  TGGGAAAGTGAGACATAC    77377       AAAAA   _
                                TGGGAA    GGTG GGCATAC
                                ||||||    |||| |||||||
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                                ACCCTT    TCAC CTGTATG
                                   _____   T
GAM3443  MGC19570  3'  GGAGAAAAAGGTCATA     77378     A      GGG
                                GGA AAAAAGGT   CATA
                                ||| ||||||||  ||||
                                CCT TTTTTCCA   GTAT
                                  C      ___
GAM3443  MGC3038   3'  TGGGAAGACAGGATGTCTGTAC 77379      AAAA  _  GGCA
           AA                    TGGGAA   AGG TG   TACAA
                                ||||||   ||| ||   |||||
                                ACCCTT   TCC AC   ATGTT
                                   CTG_  T  AGAC
GAM3443  NET-2     3'  TGGGAGAAAAACAGCATACAA  77380      A    GGTG
                                TGGGA AAAAA   GGCATACAA
                                ||||| |||||   |||||||||
                                ACCCT TTTTT   TCGTATGTT
                                   C    G___
GAM3443  NMT1      3'  TGGGAAAAGGGAGGGCCCTGCA 77381       AAA  T   ATA_
                                TGGGAAAA  GG GGGC   CA
                                ||||||||  || ||||   ||
                                ACCCTTTT  CC CCCG   GT
                                     C__  T   GGAC
GAM3443  NR1I3     3'  GGGAAGGAAGTGAGCAT     77382      AAAA
                                GGGAA   AGGTGGGCAT
                                |||||   ||||||||||
                                CCCTT   TTCACTCGTA
                                   CC__
GAM3443  PRO2730   3'  TGGGAAAGCAGAACTATACA   77383      AAAAA  _   _
                                TGGGAA    GGT GGGC ATACA
                                ||||||    ||| |||| |||||
                                ACCCTT    TCG CTTG TATGT
                                   _____  T   A
GAM3443  RNF11     3'  GGAAAAAAAGAACTGTGCA   77384         __  G
                                GGAAAAAAAGG  TG GCA
                                ||||||||||  || |||
                                CCTTTTTTTCT  AC CGT
                                      TG  A
GAM3443  RNF38     3'  GGGAAAAAAACCAGTGTACA   77385         __   GG
                                GGGAAAAAAA  GGTG  CA
                                |||||||||  ||||  ||
                                CCCTTTTTTT  TCAC  GT
                                     GG   AT
GAM3443  SDS3      3'  GGGAAAAGGGGGTAGGCA    77386       AAA
                                GGGAAAA   GGTGGGCA
                                |||||||   ||||||||
                                CCCTTTT   CCATCCGT
                                    CCC
GAM3443  SERPINH1  3'  TGAGAAAAAAAAACGTACA   77387         GG  GG
                                TGGGAAAAAAA  TG  CA
                                ||||||||||  ||  ||
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                                ACTCTTTTTTT  GC  GT
                                      TT  AT
GAM3443  SPRY1    3'  GGGAAGAGAAGGTGGGAAACA  77388      AAA      CAT
                                GGGAA   AAGGTGGG   ACA
                                |||||   ||||||||   |||
                                CCCTT   TTCCACCC   TGT
                                   CTC       TT_
GAM3443  TP53INP1  3'  GGAAAAAAAGGCCATTGCA   77389          GG__
                                GGAAAAAAAGGT   GCA
                                ||||||||||||   |||
                                CCTTTTTTTCCG   CGT
                                       GTAA
GAM3443  VEZATIN   3'  GGAAAAAAATGCAACATACAA  77390        G TG G
                                GGAAAAAAA G  G CATACAA
                                |||||||| |  | |||||||
                                CCTTTTTTT C  T GTATGTT
                                      A GT _
GAM3443  LOC116228 3'  TGGGAAAAAAATGACTACA   77391          GGTG   A
                                TGGGAAAAAAA   GGC TACA
                                ||||||||||   ||| ||||
                                ACCCTTTTTTT   CTG ATGT
                                      A___  _
GAM3443  LOC121441 3'  TGGGGCAGAAGAGCTATACAA  77392     AAAAAA   T   _
                                TGGG     AGG GGGC ATACAA
                                ||||     ||| |||| ||||||
                                ACCC     TCT CTCG TATGTT
                                  CG_____  T   A
GAM3443  LOC132617 3'  TGGGAAAAGAAGGACTGTGG   77393        A   _____
                                TGGGAAAA AAGG   TGG
                                |||||||| ||||   |||
                                ACCCTTTT TTCC   ACC
                                     C   TGAC
GAM3443  LOC136015 3'  TAGGAAAAAGAGGTACAC    77394        A    G
                                TGGGAAAAA AGGTG GC
                                ||||||||| ||||| ||
                                ATCCTTTTT TCCAT TG
                                      C    G
GAM3443  LOC144524 5'  TGGGAAAAAGAAGATACA    77395        A   TGG
                                TGGGAAAAA AGG   GCA
                                ||||||||| |||   |||
                                ACCCTTTTT TTC   TGT
                                      C   TA_
GAM3443  LOC144524 3'  GGGAAAAAAAGGTAACAATATA 77396           GC__
           CAA                   GGGAAAAAAAGGTGG   ATACAA
                                ||||||||||||||   ||||||
                                CCCTTTTTTTCCATT   TATGTT
                                         GTTA
GAM3443  LOC146957 3'  TGGGAAGTGGAGGTGGGCA   77397       AAAA
                                TGGGAA   AGGTGGGCA
                                ||||||   |||||||||
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                                ACCCTT    TCCACCCGT
                                   CACC
GAM3443  LOC148760 3'  TGGGAAGGTGAGGTCAT     77398       AAAAA    _ _
                                TGGGA     AGGTG GG CAT
                                |||||     ||||| || |||
                                ACCCT     TCCAC CC GTA
                                  _____     T  A
GAM3443  LOC151146 5'  TGGGAAGATGGGGGTGCATCA  77399       AAAAA  T _   A
                                TGGGAA     GG GG GCAT CA
                                ||||||     || || |||| ||
                                ACCCTT     CC CC CGTA GT
                                   CTAC_  _  A   _
GAM3443  LOC152300 3'  TGGGAAGATAAAGGTACCAGGC 77400       AA_     ___
            A                    TGGGAA   AAAGGT   GGGCA
                                ||||||   ||||||   |||||
                                ACCCTT   TTTCCA   TCCGT
                                   CTA     TGG
GAM3443  LOC154788 3'  TAGGAAAAAGAGGTACAC     77394         A     G
                                TGGGAAAAA AGGTG GC
                                ||||||||| ||||| ||
                                ATCCTTTTT TCCAT TG
                                     C     G
GAM3443  LOC158219 3'  TAGGAAAAAAAATTATGTAG   77401           ____
                                TGGGAAAAAAAG    GTGG
                                ||||||||||||    ||||
                                ATCCTTTTTTTT    CATC
                                      AATA
GAM3443  LOC158490 3'  TGGGAAAGTGGGACATAC     77402       AAAAA     _
                                TGGGAA     GGTGGG CATAC
                                ||||||     |||||| |||||
                                ACCCTT     TCACCC GTATG
                                  _____      T
GAM3443  LOC196484 5'  TGGGAAAGTGGGACATAC     77402       AAAAA     _
                                TGGGAA     GGTGGG CATAC
                                ||||||     |||||| |||||
                                ACCCTT     TCACCC GTATG
                                  _____      T
GAM3443  LOC196510 3'  GGGAAAAAAGGGTTTGCA     77403         A   GG
                                GGGAAAAAA GGT  GCA
                                ||||||||| |||  |||
                                CCCTTTTTT CCA  CGT
                                     C   AA
GAM3443  LOC197114 3'  TGGCAAAAAAAGATGTGG     77404     G         _
                                TGG AAAAAAAGGTG GG
                                ||| ||||||||||| ||
                                ACC TTTTTTTCTAC CC
                                  G          A
GAM3443  LOC200220 3'  GGGAAAAAAGGGTTTGCA     77403         A   GG
                                GGGAAAAAA GGT  GCA
                                ||||||||| |||  |||
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                                CCCTTTTTT CCA  CGT
                                     C   AA
GAM3443  LOC220980 5'  TGGGAAAAGGCAGCACCACATA 77405       AAA   TG ____
              CA                   TGGGAAA   AGG  G    GCATACA
                                   |||||||   |||  |   |||||||
                                   ACCCTTT   TCC  C    TGTATGT
                                      ___   GT GTGG
GAM3443  LOC221486 3'  TGGGGAAAAGGTGTGCA     77406     AAA      G
                                   TGGG   AAAAGGTG GCA
                                   ||||   |||||||| |||
                                   ACCC   TTTTCCAC CGT
                                     C__       A
GAM3443  LOC221683 5'  TGGGAGAAGCAGGCAGGGTACA 77407      A  AA   TG  CA
                                   TGGGA AA  AGG  GG  TACA
                                   ||||| ||  |||  ||  ||||
                                   ACCCT TT  TCC  CC  ATGT
                                      C  CG   GT  C_
GAM3443  LOC253129 3'  TGGGAAGCAAAGGTGAGCA   77408       AA
                                   TGGGAA  AAAGGTGGGCA
                                   ||||||  ||||||||||||
                                   ACCCTT  TTTCCACTCGT
                                      CG
GAM3443  LOC254249 5'  TGAGAAAAACTGAGGCATAC   77409        AAGGT
                                   TGGGAAAAA    GGGCATAC
                                   |||||||||    ||||||||
                                   ACTCTTTTT    TCCGTATG
                                        GAC__
GAM3443  LOC257465 3'  TGGGAAAAAGGGTATCTGG   77410        AA   ___
                                   TGGGAAAAA  GGTG   GG
                                   |||||||||  ||||   ||
                                   ACCCTTTTT  CCAT   CC
                                        C_   AGA
GAM3443  LOC90019  5'  TGGGAAGGAAGGTGGGGC    77411       AAA      _
                                   TGGGAA   AAGGTGGG C
                                   ||||||   |||||||| |
                                   ACCCTT   TTCCACCC G
                                      CC_       C
GAM3444  MLANA    3'  GAGCTAAATTGCCATAGGTACA 77414         TA   A___
              TT                    GAGCTAAATT  CTA    TACATT
                                    ||||||||||  |||    ||||||
                                    CTCGATTTAA  GGT    ATGTAA
                                         C_   ATCC
GAM3444  BCAA     3'  TGAACCATACTAATACAT    77415       AATT
                                   TGAGCTA    TACTAATACAT
                                   |||||||    ||||||||||||
                                   ACTTGGT    ATGATTATGTA
                                              _____
GAM3444  LRBA     3'  TGAGCAAATTTAAGTTACATT  77416      T      CTAA
                                   TGAGC AAATTTA    TACATT
                                   ||||| |||||||    ||||||
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                                ACTCG TTTAAAT   ATGTAA
                                  _     TCA_
GAM3444 VDU1    3' TGAGCTAATTTTAACAACA  77417       A   C
                                TGAGCTAA TTTA TAATA
                                |||||||| |||| |||||
                                ACTCGATT AAAT GTTGT
                                    A   T
GAM3444 ZNF33A  3' TGAGCCAACAGTGATACATT  77418       ATTTACTA
                                TGAGCTAA      ATACATT
                                ||||||||      |||||||
                                ACTCGGTT      TATGTAA
                                    GTCAC___
GAM3444 LOC256405 3' TGAGCTATTAATACAT     77419       AATTTAC
                                TGAGCTA     TAATACAT
                                |||||||     ||||||||
                                ACTCGAT     ATTATGTA
                                    A_______
GAM3445 MRPL34  3' TATTACACGTTTAATAATAT  77422       CAGAA
                                TATTGCAC    TTAATAATAT
                                ||||||||    ||||||||||
                                ATAATGTG    AATTATTATA
                                    CA___
GAM3445 LOC152559 3' TTGCACCAAAATCTTCTATC  77423          AATAA
                                TTGCACCAGAATT    TATC
                                ||||||||||||    ||||
                                AACGTGGTTTTAG    ATAG
                                      AAG__
GAM3445 LOC200107 3' TGCCCAAAATTAGTAAT    77424    A       A
                                TGC CCAGAATTA TAAT
                                ||| ||||||||| ||||
                                ACG GGTTTTAAT ATTA
                                  _       C
GAM3445 LOC90777  3' TATTGCACCAGGGATTAA   77425         A_
                                TATTGCACCAG  ATTAA
                                ||||||||||  |||||
                                ATAACGTGGTC  TAATT
                                      CC
GAM3446 ARNT2   3' TCTGGAGAACATGTAGTCACAT 77428    AAT      AT  TC
                                TCT  GAACATGT  AGT  CAT
                                |||  ||||||||  |||  |||
                                AGA  CTTGTACA  TCA  GTA
                                  CCT       __  GT
GAM3446 CIS4    3' TAATAATAATTCTAGTTCCAT  77429      ACATGTA
                                TAATGA      TAGTTCCAT
                                ||||||      |||||||||
                                ATTATT      ATCAAGGTA
                                   ATTAAG_
GAM3446 GNRH1   5' TCTAATGAAATGTGTCTCCA  77430       C   ATAG
                                TCTAATGAA ATGT   TTCCA
                                ||||||||| ||||   |||||
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                                AGATTACTT TACA   GAGGT
                                      _   CA__
GAM3446 HSPA1B   3' TCTAATGAACATATCGGTT   77431          ATA
                                TCTAATGAACATGT   GTT
                                ||||||||||||||  |||
                                AGATTACTTGTATA   CAA
                                      GC_
GAM3446 AFAP     3' TCTAATGACATCAGTTCC    77432       A   GTA
                                TCTAATGA CAT   TAGTTCC
                                |||||||| |||  |||||||
                                AGATTACT GTA   GTCAAGG
                                     _  ___
GAM3446 AFAP     3' TCTAAGGTGTTATAGTTCCAT 77433     TGAACATG
                                TCTAA      TATAGTTCCAT
                                |||||      ||||||||||
                                AGATT      ATATCAAGGTA
                                   CCACA___
GAM3446 DJ79P11.1 3' TAATGAGCATCCTTCCA    77434      ACAT   AG
                                TAATGA   GTAT  TTCCA
                                ||||||   ||||  |||||
                                ATTACT   CGTA  AAGGT
                                    ____   GG
GAM3446 FLJ12747 3' TCTGAGAACATATTTCCA    77435    AAT      ATAG
                                TCT   GAACATGT   TTCCA
                                |||   ||||||||   |||||
                                AGA   CTTGTATA   AAGGT
                                  CT_      _____
GAM3446 HTCD37   3' ATGAATGTTCAGTTCCAT    77436    AC   A
                                ATGA  ATGT TAGTTCCAT
                                ||||  |||| |||||||||
                                TACT  TACA GTCAAGGTA
                                   __   A
GAM3446 KIAA1077 3' TCTGATGAACTGAAATTCCAT 77437    A    A  TAT
                                TCT ATGAAC TG   AGTTCCAT
                                ||| |||||| ||   ||||||||
                                AGA TACTTG AC   TTAAGGTA
                                  C     _  T__
GAM3446 KIAA1161 3' TAATGAACTCACAGTTCCAT  77438       ATG
                                TAATGAAC   TATAGTTCCAT
                                ||||||||   ||||||||||
                                ATTACTTG   GTGTCAAGGTA
                                     A__
GAM3446 KIAA1765 3' TCTAATGGGTGTATAGT     77439       AACA
                                TCTAATG    TGTATAGT
                                |||||||    ||||||||
                                AGATTAC    ACATATCA
                                    CC__
GAM3446 LATS1    3' CTAATGTTATATAGTTCCAT   77440       AACA
                                CTAATG    TGTATAGTTCCAT
                                ||||||    ||||||||||||
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                                GATTAC   ATATATCAAGGTA
                                   A___
GAM3446 NFAT5    3' TCTGGTGAAAATGTATAACCAT 77441    AA   C      TT
                                TCT  TGAA ATGTATAG  CCAT
                                |||  |||| ||||||||  ||||
                                AGA  ACTT TACATATT  GGTA
                                  CC   T      __
GAM3446 PB1      3' TCTAATGGTTTCAGTTCCA   77442       AACATGTA
                                TCTAATG      TAGTTCCA
                                |||||||      ||||||||
                                AGATTAC      GTCAAGGT
                                    CAAA____
GAM3446 LOC197003 3' TCTAATGAACCGTGTGCAT   77443         A___
                                TCTAATGAAC   TGTAT
                                ||||||||||   |||||
                                AGATTACTTG   ACGTA
                                      GCAC
GAM3447 ABCG2    3' TTAGATTAATAAATTAGA    77446        AT
                                TTAGATTAG  TAGATTAGA
                                |||||||||  |||||||||
                                AATCTAATT  ATTTAATCT
                                           __
GAM3447 MAP2K1   3' ATTAGAATAAGAGATTAGA   77447      T   ATT
                                ATTAGA TAG   AGATTAGA
                                ||||||| |||   ||||||||
                                TAATCT ATT   TCTAATCT
                                   T   C__
GAM3447 ZNF175   3' TAAAAACAATTAGATTAGA   77448     TTA
                                TAGA   GATTAGATTAGA
                                ||||   ||||||||||||
                                ATTT   TTAATCTAATCT
                                  TTG
GAM3447 DKFZP434J037 3' TCCATTAGGTAGAGACCATTAG 77449        ATT_    AG
                                TCCATTAG   AGATT  ATTAG
                                ||||||||   |||||  |||||
                                AGGTAATC   TCTGG  TAATC
                                     CATC    __
GAM3447 FLJ10579  3' CCCAATTCTAGATTAGGTTAGA 77450      TTAGA       A
                                TCCA    TTAGATTAG TTAGA
                                ||||    ||||||||| |||||
                                GGGT    GATCTAATC AATCT
                                  TAA__       C
GAM3447 LOC147524 5' TCCATTAGATAGGATTAGA   77451         TA
                                TCCATTAGAT  GATTAGA
                                ||||||||||  |||||||
                                AGGTAATCTA  CTAATCT
                                      TC
GAM3447 LOC149332 5' ATTAGATTAGTTCAAATTAG  77452         A
                                ATTAGATTAG TTAGATTAG
                                |||||||||| |||||||||
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                                TAATCTAATC AGTTTAATC
                                      A
GAM3447  LOC154222 3'  TCCATTAAGTGAGGATTAGA   77453        ATTA_
                                TCCATTAG    GATTAGA
                                ||||||||    |||||||
                                AGGTAATT    CTAATCT
                                     CACTC
GAM3447  LOC91947  3'  CCCATTAGAGGTAGGTTAGA   77454        T_  A
                                TCCATTAGA  TAG TTAGA
                                |||||||||  ||| |||||
                                GGGTAATCT  ATC AATCT
                                     CC   C
GAM3448  ARHGDIB   3'  TGACTAGGGACTCAT       77457        CACTAA
                                TGACTAGG     GGCTCAT
                                ||||||||     |||||||
                                ACTGATCC     CTGAGTA
                                             _______
GAM3448  CNTNAP2   3'  GATTAGGCACTGAGAGCT    77458    C       A  _
                                GA TAGGCACT AG GCT
                                || |||||||| || |||
                                CT ATCCGTGA TC CGA
                                 A       C  T
GAM3448  WISP1     3'  AGGGTAACTAAGGCTCAT    77459     C__
                                AGG   ACTAAGGCTCAT
                                |||   ||||||||||||
                                TCC   TGATTCCGAGTA
                                  CAT
GAM3448  WISP1     3'  AGGGTAACTAAGGCTCAT    77459     C__
                                AGG   ACTAAGGCTCAT
                                |||   ||||||||||||
                                TCC   TGATTCCGAGTA
                                  CAT
GAM3448  CECR2     3'  TGGCTGGCCACTAAGGAAACAC 77460    A  A  _      CT_  T
            AG                    TG CT GGC ACTAAGG   CA CAG
                                || || ||| |||||||   || |||
                                AC GA CCG TGATTCC   GT GTC
                                 C  _   G      TTT  _
GAM3448  KIAA1036  3'  TGACAGGCACTCTCATCA    77461      T      AAGG
                                TGAC AGGCACT    CTCATCA
                                |||| |||||||    |||||||
                                ACTG TCCGTGA    GAGTAGT
                                  _      ____
GAM3448  MGC26610  5'  TGGCCAGGCACTGCAGTC    77462    A       AA  C
                                TG CTAGGCACT  GG TC
                                || |||||||||  || ||
                                AC GGTCCGTGA  TC AG
                                 C        CG  _
GAM3448  MGC5466   3'  TGATGAGGTGCTAAGGCCATC  77463     CT   CA      T
                                TGA  AGG  CTAAGGC CATC
                                |||  |||  ||||||| ||||
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                                ACT  TCC  GATTCCG GTAG
                                  AC   AC      _
GAM3448  LOC151959 5'  TGACTAGACGCTGGGAGCCC   77464         A  AA_
                                TGACTAGGC CT   GGCTC
                                |||||||||  ||   |||||
                                ACTGATCTG GA   TCGGG
                                     C  CCC
GAM3448  LOC222234 5'  TGACTAGGCGTTCTAAACATCA 77465         A__    GCT
           G                     TGACTAGGC   CTAAG   CATCAG
                                |||||||||   |||||   ||||||
                                ACTGATCCG   GATTT   GTAGTC
                                     CAA    ___
GAM3449  CRIM1    3'  ATAGTTACATAAATACTCC    77468           A  CT
                                ATAGTTACATAAA AC  C
                                |||||||||||||  ||  |
                                TATCAATGTATTT TG  G
                                       A  AG
GAM3449  PCDHB11   3'  GTTACATAAAACTAAAAAAGTA 77469          ACCTC_
                                GTTACATAAAA     AAGTA
                                ||||||||||      |||||
                                CAATGTATTTT     TTCAT
                                      GATTTT
GAM3449  PPP3R1    3'  TAGTTACATGATCACTTCAGGT 77470         AAAA  C   A
           A                     TAGTTACAT    AC TCA GTA
                                |||||||||    || ||| |||
                                ATCAATGTA    TG AGT CAT
                                     CTAG  A   C
GAM3449  PTGS2     3'  TAGTGACATAAAAGTCTTCACA 77471      T      AC  ___
           AGTA                    TAGT ACATAAAA  CT   CAAGTA
                                |||| ||||||||  ||   ||||||
                                ATCA TGTATTTT  GA   GTTCAT
                                  C       CA  AGT
GAM3449  C3orf4    3'  CAGTTACAAAGTTAAAATTTCA 77472         TA___   CC
           AGTA                    TAGTTACA    AAAA  TCAAGTA
                                |||||||||    ||||  |||||||
                                GTCAATGT    TTTT  AGTTCAT
                                     TTCAA    AA
GAM3449  DLL1      3'  ATAGTCACATAGACCCGAAGT  77473          AAA   C
                                ATAGTTACATA   ACCT AAGT
                                ||||||||||   |||| ||||
                                TATCAGTGTAT   TGGG TTCA
                                      C__    C
GAM3449  FLJ20033  3'  ATAGTTACACTGAACTGAAGTA 77474         AAA   CTC
                                ATAGTTACAT   AAC   AAGTA
                                |||||||||   |||   |||||
                                TATCAATGTG   TTG   TTCAT
                                      AC_   AC_
GAM3449  FLJ20371  5'  GCTGCGTAAAAGCCTCAAGT   77475     ACA    A
                                GTT   TAAAA CCTCAAGT
                                |||   ||||| ||||||||
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                                CGA   ATTTT GGAGTTCA
                                  CGC    C
GAM3449  FLJ20729  3'  AGTTACATAAAAACTCCA    77476           CT
                                AGTTACATAAAAAC  CA
                                ||||||||||||||  ||
                                TCAATGTATTTTTG  GT
                                      AG
GAM3449  G4        5'  ATAGTCATGCAGCCTCAAGT   77477       CATAAAAA
                                ATAGTTA      CCTCAAGT
                                |||||||      ||||||||
                                TATCAGT      GGAGTTCA
                                   ACGTC___
GAM3449  GPNMB     3'  ACAGTTACATGGAAAGCTGAAA 77478         AA   C  C_
              GTA                  ATAGTTACAT  AAA CT  AAGTA
                                ||||||||||  ||| ||  |||||
                                TGTCAATGTA  TTT GA  TTCAT
                                     CC   C  CT
GAM3449  KIAA0257  3'  GTTACATACCTCAAGT     77479       AAAA
                                GTTACAT    ACCTCAAGT
                                |||||||    |||||||||
                                CAATGTA    TGGAGTTCA
                                     ____
GAM3449  KIAA0261  3'  TAGTTAAGTCAGCCTCAAGTA  77480      CATAAAAA
                                TAGTTA       CCTCAAGTA
                                ||||||       |||||||||
                                ATCAAT       GGAGTTCAT
                                   TCAGTC__
GAM3449  KIAA1586  5'  ATAGATGCAAATAACCTCAAGT 77481     TTA  TAAA
                                ATAG   CA    AACCTCAAGT
                                ||||   ||    ||||||||||
                                TATC   GT    TTGGAGTTCA
                                  TAC  TTA_
GAM3449  MGC16384  3'  GTTACACAACCTGAGT     77482        AAA    CA
                                GTTACATA   ACCT  AGT
                                ||||||||   ||||  |||
                                CAATGTGT   TGGA  TCA
                                     ___    C_
GAM3449  MGC20533  3'  TAGTATATAAAGTGCTCAAGTA 77483     TAC    AAC
                                TAGT   ATAAA   CTCAAGTA
                                ||||   |||||   ||||||||
                                ATCA   TATTT   GAGTTCAT
                                  TA_    CAC
GAM3449  MGC29956  3'  ATAATTACAGCGTGGTTTCAAG 77484         TAAAAACC
              TA                   ATAGTTACA       TCAAGTA
                                |||||||||       |||||||
                                TATTAATGT       AGTTCAT
                                     CGCACCAA
GAM3449  SDFR1     3'  ATAGTTACACAAAACACACAAG 77485           ACCT
              TA                   ATAGTTACATAAAA    CAAGTA
                                ||||||||||||||    ||||||
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                                TATCAATGTGTTTT   GTTCAT
                                      GTGT
GAM3449  SDFR1    3'  ATAGTTACACAAAACACACAAG 77485          ACCT
             TA                   ATAGTTACATAAAA   CAAGTA
                                  ||||||||||||||   ||||||
                                  TATCAATGTGTTTT   GTTCAT
                                        GTGT
GAM3449  LOC145098 3'  GTGAACAGAAACCTCAAGT   77486   T_  TAA
                                  GT  ACA   AAACCTCAAGT
                                  ||  |||   ||||||||||
                                  CA  TGT   TTTGGAGTTCA
                                   CT   C__
GAM3449  LOC158382 3'  ACAGCTCAAAGAACCTCAGGT  77487      A  TAAA     A
                                  ATAGTT CA   AACCTCA GT
                                  |||||| ||   ||||||| ||
                                  TGTCGA GT   TTGGAGT CA
                                     _  TTC_     C
GAM3449  LOC257554 5'  ATAGTCATGCAGCCTCAAGT   77477       CATAAAAA
                                  ATAGTTA       CCTCAAGT
                                  |||||||       ||||||||
                                  TATCAGT       GGAGTTCA
                                      ACGTC___
GAM3449  LOC90246  5'  ATAGTCACATGAATGCCTCAAG 77488         A  AA
             T                    ATAGTTACAT AA  CCTCAAGT
                                  ||||||||||| ||  ||||||||
                                  TATCAGTGTA TT  GGAGTTCA
                                        C  AC
GAM3450  MGC5601   5'  TGGTAGGACCTTGTTAACG   77491      TGTA  TA
                                  TGGTA   AT  TGTTAACG
                                  |||||   ||  ||||||||
                                  ACCAT   TG  ACAATTGC
                                     CC__  GA
GAM3450  LOC152925 3'  TGGTATGTGATATGTCCCTGA  77492       AAT     AAC
                                  TGGTATGT   TATGTT   GA
                                  ||||||||   ||||||   ||
                                  ACCATACA   ATACAG   CT
                                       CT_     GGA
GAM3451  ABCA1    3'  AGTACAGATAATGAAATACAG  77495        C   GTA
                                  AGTACAGAT ATGA   GATACAG
                                  |||||||| ||||   |||||||
                                  TCATGTCTA TACT   TTATGTC
                                        T   ____
GAM3451  CYP19    3'  AGACAGATCATATGTAG     77496    T       A
                                  AG ACAGATCATG GTAG
                                  || ||||||||| ||||
                                  TC TGTCTAGTAT CATC
                                   _        A
GAM3451  CYP19    3'  AGACAGATCATATGTAG     77496    T       A
                                  AG ACAGATCATG GTAG
                                  || ||||||||| ||||
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                                TC TGTCTAGTAT CATC
                                 _        A
GAM3451  HAS2     3'  AGTACAATTATATCAAATACAG 77497        ATCATGAG
                                AGTACAG       TAGATACAG
                                |||||||       |||||||||
                                TCATGTT       GTTTATGTC
                                    AATATA__
GAM3451  PIK3R3   3'  GTCCAGATCATGGGACA     77498    A       AGTA
                                GT CAGATCATG    GATA
                                || |||||||||    ||||
                                CA GTCTAGTAC    CTGT
                                 G       C___
GAM3451  SLC25A15 3'  AGTACAGATATGAAATAG    77499         C    _
                                AGTACAGAT ATGAG TAG
                                ||||||||| ||||| |||
                                TCATGTCTA TACTT ATC
                                     _    T
GAM3451  UBE4A    3'  AGTCTAGATCATGAGGAC     77500     AC        TA
                                AGT  AGATCATGAG  GAT
                                |||  ||||||||||  |||
                                TCA  TCTAGTACTC  CTG
                                 GA        __
GAM3451  BTN2A2   3'  AGATATAGATGTAGATACA    77501      CAT  _
                                AGAT   GA GTAGATACA
                                ||||   || |||||||||
                                TCTA   CT CATCTATGT
                                  TAT  A
GAM3451  C20orf178 3'  GTGCAGACCATGCTATGCAG   77502    A       A___
                                GT CAGATCATG    GTAG
                                || |||||||||    ||||
                                CA GTCTGGTAC    CGTC
                                 C        GATA
GAM3451  DKFZp434K114 3'  AGTACAGATGCAGGATGCAG   77503         _  T  _
                                AGTACAGAT CA GA GTAG
                                ||||||||| || || ||||
                                TCATGTCTA GT CT CGTC
                                     C  C  A
GAM3451  HHLA2    3'  CAGGTCATGAGTTGTCACAG   77504     A       AGA
                                CAG TCATGAGT   TACAG
                                ||| ||||||||   |||||
                                GTC AGTACTCA   GTGTC
                                  C       ACA
GAM3451  HSPC063  3'  AGTACAGATTAGAAAAGTAG   77505         CAT__
                                AGTACAGAT    GAGTAG
                                |||||||||    ||||||
                                TCATGTCTA    TTCATC
                                     ATCTT
GAM3451  KIAA1209 3'  AGACGGATCATGAGATCAG    77506    T  A       __
                                AG AC GATCATGAG  TAG
                                || || |||||||||  |||
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                                TC TG CTAGTACTC  GTC
                                 _ C       TA
GAM3451  KIAA1750  3'  AGAACAGGTGTAGATACA    77507    T   ATCATGA
                                AG ACAG      GTAGATACA
                                || ||||      |||||||||
                                TC TGTC      CATCTATGT
                                 T   CA_____
GAM3451  MGC26954  3'  AGTATAGATACATGACAGATA  77508     C   _    G
                                AGTA AGAT CATGA TAGATA
                                |||| |||| ||||| ||||||
                                TCAT TCTA GTACT GTCTAT
                                  A   T    _
GAM3451  SPIN      3'  ATATAGATATAGGTAGATACAG 77509     C   C   A
                                GTA AGAT ATG GTAGATACAG
                                ||| |||| ||| ||||||||||
                                TAT TCTA TAT CATCTATGTC
                                  A   _  C
GAM3451  ZDHHC5    5'  AGACAGATCAAGATAC      77510    T      TGAGT
                                AG ACAGATCA    AGATAC
                                || ||||||||    ||||||
                                TC TGTCTAGT    TCTATG
                                 _      _____
GAM3451  LOC146839 5'  AGTAAGATTATGAGTAG     77511      C   C
                                AGTA AGAT ATGAGTAG
                                |||| |||| ||||||||
                                TCAT TCTA TACTCATC
                                  _   A
GAM3451  LOC146880 3'  AGTCAGTCTCAGAGTAGATA   77512     A  A_   T
                                AGT CAG  TCA GAGTAGATA
                                ||| |||  ||| |||||||||
                                TCA GTC  AGT CTCATCTAT
                                  _  AG  _
GAM3451  LOC150311 5'  AGTCCAGGTCATGAACTATAG  77513     A  A    ___
                                AGT CAG TCATGA  GTAG
                                ||| ||| ||||||  ||||
                                TCA GTC AGTACT  TATC
                                  G  C     TGA
GAM3451  LOC157695 3'  AGGACAGGTGAATAGATAC    77514    T   ATCA
                                AG ACAG    TGAGTAGATAC
                                || ||||    ||||||||||
                                TC TGTC    ACTTATCTATG
                                 C   C___
GAM3451  LOC206280 5'  AGTGACAGGGTAGATACA     77515    _   ATCATGA
                                AGT ACAG      GTAGATACA
                                ||| ||||      |||||||||
                                TCA TGTC      CATCTATGT
                                  C   C_______
GAM3451  LOC257444 3'  GTAAGATCATGATATAC      77516    C       GTAG
                                GTA AGATCATGA    ATAC
                                ||| |||||||||    ||||
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                                CAT TCTAGTACT    TATG
                                  _       A___
GAM3452  CRR9     3'  TCATTGACAATTCAAGTTGC   77519      A       A
                                TTATT ACAATTCAA TTGC
                                ||||| ||||||||| ||||
                                AGTAA TGTTAAGTT AACG
                                   C       C
GAM3453  NRAS     3'  TGGCAGAGGTGTGTTGAGGTGT 77522    T    ATTCAA_
              GT                  TG CAGAG      GAGGTGTGT
                                || |||||      |||||||||
                                AC GTCTC      CTCCACACA
                                 C    CACACAA
GAM3453  RAD52    3'  TGTCAGAGGTCTGGGCTGGGTC 77523       AT  AAGA   GT_
                                TGTCAGAG  TC    GGT   GTC
                                ||||||||  ||    |||   |||
                                ACAGTCTC  AG    CCG   CAG
                                     C_  AC__   ACC
GAM3453  RAD52    3'  TGTCAGAGGTCTGGGCTGGGTC 77523       AT  AAGA   GT_
                                TGTCAGAG  TC    GGT   GTC
                                ||||||||  ||    |||   |||
                                ACAGTCTC  AG    CCG   CAG
                                     C_  AC__   ACC
GAM3453  RAD52    3'  TGTCAGAGGTCTGGGCTGGGTC 77523       AT  AAGA   GT_
                                TGTCAGAG  TC    GGT   GTC
                                ||||||||  ||    |||   |||
                                ACAGTCTC  AG    CCG   CAG
                                     C_  AC__   ACC
GAM3453  TBXA2R   3'  TGTTGGAGGTTCAAAAGGAAGC 77524     CA   A       T_
                                TGT  GAG TTCAAGAGG  GT
                                |||  ||| |||||||||  ||
                                ACA  CTC AAGTTTTCC  CG
                                  AC   C        TT
GAM3453  TMOD2    3'  TGTTAAAGATTCAATTTATGT  77525     C        GAG
                                TGT AGAGATTCAA   GTGT
                                ||| ||||||||||   ||||
                                ACA TTTCTAAGTT   TACA
                                  A         AAA
GAM3453  ZNF2     3'  TCAGACAAGAGGTGTGT     77526       GATT
                                TCAGA    CAAGAGGTGTGT
                                |||||    ||||||||||||
                                AGTCT    GTTCTCCACACA
                                   _____
GAM3453  KIAA0871 3'  TGTCAGAGTTTGGCTG      77527        A  CAAGA   G
                                TGTCAGAG TT    GGT TG
                                |||||||| ||    ||| ||
                                ACAGTCTC AA    CCG AC
                                     A  ______   _
GAM3453  R3HDM    3'  AGAGATTCAGGGGAAGAGT    77528         A__    T
                                AGAGATTCA   GAGG GT
                                |||||||||   |||| ||
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                                TCTCTAAGT   CTTC CA
                                     CCC    T
GAM3453  LOC130327 3'  GTCAGGGAATAGGTGTGT    77529      A  TTCAAG
                                GTCAG GA     AGGTGTGT
                                ||||| ||     ||||||||
                                CAGTC CT     TCCACACA
                                   C  TA____
GAM3453  LOC202052 5'  GACTCTCAGGAGGTGTGT    77530    GA    A
                                GA  TTCA GAGGTGTGT
                                ||  |||| |||||||||
                                CT  GAGT CTCCACACA
                                 GA    C
GAM3453  LOC202908 5'  TGTCTGGGGCTCAGGTGTGT   77531     AGAGA    AGA
                                TGTC    TTCA   GGTGTGT
                                ||||    ||||   |||||||
                                ACAG    GAGT   CCACACA
                                  ACCCC   ___
GAM3453  LOC222057 5'  TGTCTGGGGCTCAGGTGTGT   77531     AGAGA    AGA
                                TGTC    TTCA   GGTGTGT
                                ||||    ||||   |||||||
                                ACAG    GAGT   CCACACA
                                  ACCCC   ___
GAM3453  LOC255975 5'  TGTCTGGGGCTCAGGTGTGT   77531     AGAGA    AGA
                                TGTC    TTCA   GGTGTGT
                                ||||    ||||   |||||||
                                ACAG    GAGT   CCACACA
                                  ACCCC   ___
GAM3453  LOC256878 5'  TGTCTGGGGCTCAGGTGTGT   77531     AGAGA    AGA
                                TGTC    TTCA   GGTGTGT
                                ||||    ||||   |||||||
                                ACAG    GAGT   CCACACA
                                  ACCCC   ___
GAM3453  LOC257302 5'  TCAGAGATTTGATGGTGT    77532       CAA  _
                                TCAGAGATT   GA GGTGT
                                |||||||||   || |||||
                                AGTCTCTAA   CT CCACA
                                     A__  A
GAM3453  LOC90410  5'  GTCAGGAGGAGGTGTGTC    77533      A  TTCAA
                                GTCAG GA    GAGGTGTGTC
                                ||||| ||    ||||||||||
                                CAGTC CT    CTCCACACAG
                                   _ C_____
GAM3454  ABCC8     3'  ATTTACAAGTGATTTACAG    77536       AAA   _
                                ATTTACA   AGTG TTTACAG
                                |||||||   |||| |||||||
                                TAAATGT   TCAC AAATGTC
                                    ___    T
GAM3454  AFP       3'  TAATTCACAAAAAGTGTTAAAT 77537              TA__
            CAG                   TAATTTACAAAAAGTGTT    CAG
                                  ||||||||||||||||||   |||
```

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                                ATTAAGTGTTTTTCACAA   GTC
                                      TTTA
GAM3454  CALCRL   3'  TTACAAAAAGGACTACGGC   77538        TGT   A
                                TTACAAAAAG   TTAC GC
                                ||||||||||  |||| ||
                                AATGTTTTTC   GATG CG
                                     CT_   C
GAM3454  CHD1     3'  ATTTACAATAATTTACAG    77539       AAAGT
                                ATTTACAA    GTTTACAG
                                ||||||||    ||||||||
                                TAAATGTT    TAAATGTC
                                    AT___
GAM3454  ELMO2    3'  TTTACAAGTGCTGCAG      77540       AAA     TA
                                TTTACA   AGTGTT  CAG
                                ||||||   ||||||  |||
                                AAATGT   TCACGA  GTC
                                   ___     C_
GAM3454  FGFR1    3'  TAATTTAAAAAAATAAAACAGC 77541       C       TTT
                                TAATTTA AAAAAGTG   ACAGC
                                ||||||| ||||||||   |||||
                                ATTAAAT TTTTTTAT   TGTCG
                                   _       TT_
GAM3454  FGFR1    3'  TAATTTAAAAAAATAAAACAGC 77541       C       TTT
                                TAATTTA AAAAAGTG   ACAGC
                                ||||||| ||||||||   |||||
                                ATTAAAT TTTTTTAT   TGTCG
                                   _       TT_
GAM3454  FGFR1    3'  TAATTTAAAAAAATAAAACAGC 77541       C       TTT
                                TAATTTA AAAAAGTG   ACAGC
                                ||||||| ||||||||   |||||
                                ATTAAAT TTTTTTAT   TGTCG
                                   _       TT_
GAM3454  MASP2    3'  TTTACAGAAATGCCAACAGC   77542       AA     TT
                                TTTACA  AAGTGT  ACAGC
                                ||||||  ||||||  |||||
                                AAATGT  TTTACG  TGTCG
                                   C_     GT
GAM3454  MTM1     3'  TAATTTATGAAATATTTACAGC 77543       CAAA
                                TAATTTA    AAGTGTTTACAGC
                                |||||||    |||||||||||||
                                ATTAAAT    TTTATAAATGTCG
                                    AC__
GAM3454  PDE4A    3'  TAATTTACAAACCAACCTTACA 77544         AAGTG
           G                     TAATTTACAAA    TTTACAG
                                 ||||||||||    |||||||
                                 ATTAAATGTTT    GAATGTC
                                       GGTTG
GAM3454  PDE4D    3'  TAATTTACAATTAACATTACAG 77545         AA  TG  T
                                TAATTTACAA  AG  TT ACAG
                                ||||||||||  ||  || ||||
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                                ATTAAATGTT  TT  AA TGTC
                                      AA  GT  _
GAM3454  PEX3     3'  ATTCACTTCTGTTTACAGC   77546       AAAAAG
                                ATTTAC     TGTTTACAGC
                                ||||||     ||||||||||
                                TAAGTG     ACAAATGTCG
                                   AAG___
GAM3454  SLC19A2  3'  ATTTACAAAACTGCATACAG  77547          AG   T
                                ATTTACAAAA  TGT TACAG
                                ||||||||||  ||| |||||
                                TAAATGTTTT  ACG ATGTC
                                      G_  T
GAM3454  ZNF26    3'  TTTACAAAAACACAG       77548          GTGTT
                                TTTACAAAAA     TACAG
                                ||||||||||     |||||
                                AAATGTTTTT     GTGTC

                                      _____
GAM3454  DKFZP564I0422 3'  TTATAAAAAGGTCTACAG    77549     C     T
                                TTA AAAAAG GTTTACAG
                                ||| |||||| ||||||||
                                AAT TTTTTC CAGATGTC
                                  A     _
GAM3454  FLJ22671  3'  TACAAAAAGTGGACAG      77550           TTT
                                TACAAAAAGTG   ACAG
                                ||||||||||   ||||
                                ATGTTTTTCAC   TGTC
                                      C__
GAM3454  KIAA0061  3'  TAATTTAAAAGTATTACAG   77551        CAA       T
                                TAATTTA   AAAGTGTT ACAG
                                |||||||   |||||||| ||||
                                ATTAAAT   TTTCATAA TGTC

                                   ___      _
GAM3454  KIAA0888  3'  TAAATTACAAAAAATAACAG  77552     T          TTT
                                TAA TTACAAAAAGTG   ACAG
                                ||| ||||||||||||   ||||
                                ATT AATGTTTTTTAT   TGTC
                                  T         ___
GAM3454  KIAA1321  3'  TAATTTACAGAAAGGTCTA    77553          A    T
                                TAATTTACA AAAG GTTTA
                                ||||||||| |||| |||||
                                ATTAAATGT TTTC CAGAT
                                      C   _
GAM3454  KIAA1423  3'  TTTACAAATATTTACAG     77554        AAA
                                TTTACAA   GTGTTTACAG
                                |||||||   ||||||||||
                                AAATGTT   TATAAATGTC

                                   ___
GAM3454  KIAA1560  3'  TTTAAAAAACAGGTTTACAGC  77555      C    _  T
                                TTTA AAAA AG GTTTACAGC
                                |||| |||| || |||||||||
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                                AAAT TTTT TC CAAATGTCG
                                  T   G _
GAM3454  PPP1R1B  3'  ATTTACAAAGATTTATTACAGC 77556        AAGTGT
                                ATTTACAAA     TTACAGC
                                |||||||||     |||||||
                                TAAATGTTT     AATGTCG
                                    CTAAAT
GAM3454  PTPNS1   3'  TAATTTACAGGCGTCCACAGC  77557        AAAA
                                TAATTTACA   GTGTTTACAGC
                                |||||||||   ||||||||||
                                ATTAAATGT   CGCAGGTGTCG
                                    C___
GAM3454  ZNF387   3'  TTTACAAAAGACCCAATTTACA 77558        AG ___
             G                   TTTACAAAA  T  GTTTACAG
                                |||||||||  |  ||||||||
                                AAATGTTTT  G  TAAATGTC
                                    CT GGT
GAM3454  LOC129285 3'  TAATTTTAAAAAGTGCACAG   77559      AC       TT
                                TAATTT  AAAAAGTGT  ACAG
                                ||||||  |||||||||  ||||
                                ATTAAA  TTTTTCACG  TGTC
                                   A_       __
GAM3454  LOC145790 3'  TTACAAAGTACTGTTTTACAGC 77560       AAG_    _
                                TTACAAA    TGTTT ACAGC
                                |||||||    ||||| |||||
                                AATGTTT    ACAAA TGTCG
                                    CATG    A
GAM3454  LOC162655 3'  TAATTTACGGAAGTGCTAG   77561       AAA      TAC
                                TAATTTAC   AAGTGTT   AG
                                ||||||||   |||||||   ||
                                ATTAAATG   TTCACGA   TC
                                    CC_     ___
GAM3454  LOC92196  3'  TAATTTACCAAGCAAGTGCAGC 77562       AAA__    TTTA
                                TAATTTAC    AAGTG   CAGC
                                ||||||||    |||||   ||||
                                ATTAAATG    TTCAC   GTCG
                                    GTTCG   _____
GAM3455  CA14     5'  GTGTATTTATCTCTGCTTT   77565     C       AACA
                                GTG ATTTATCTC   GTTTT
                                ||| |||||||||   |||||
                                CAC TAAATAGAG   CGAAA
                                  A       A___
GAM3455  D1S155E  3'  GTGCATTCATTTTTTTTGTTTT 77566        CTCAACA
                                GTGCATTTAT      GTTTT
                                ||||||||||      |||||
                                CACGTAAGTA      CAAAA
                                    AAAAAAA
GAM3455  GAD1     3'  GCGTTTTGAAAAACAGTTTTCC 77567    A   ATCTC
                                GC TTT     AACAGTTTTCC
                                || |||     ||||||||||
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                                CG AAA    TTGTCAAAAGG
                                 C  ACTTT
GAM3455 MADH1    3' ATGCAAGGCTCAATAGTTTTCC 77568      TTTAT    C
                                GTGCA    CTCAA AGTTTTCC
                                |||||    ||||| ||||||||
                                TACGT    GAGTT TCAAAAGG
                                   TCC__    A
GAM3455 NOX4     3' GTGCATCTAACAGTTTTC    77569        TCTCA
                                GTGCATTTA    ACAGTTTTC
                                |||||||||    |||||||||
                                CACGTAGAT    TGTCAAAAG
                                             _____
GAM3455 PAK1     3' GTGCATTTATCTCACAG     77570           A
                                GTGCATTTATCTCA CAG
                                |||||||||||||| |||
                                CACGTAAATAGAGT GTC
                                             _
GAM3455 SHOC2    3' GTGCATTTAGTTCAGCAGC   77571        TC  A
                                GTGCATTTA  TCA CAGT
                                |||||||||  ||| ||||
                                CACGTAAAT  AGT GTCG
                                     CA  C
GAM3455 C11orf23 5' TTATCCTGGTAACAGTTTTCC  77572      C___
                                TTATCT    AACAGTTTTCC
                                ||||||   ||||||||||
                                AATAGG   TTGTCAAAAGG
                                   ACCA
GAM3455 FLJ12934 3' GTGCATTTAACTCAGACAACTT 77573        T   _  GT
           T                    GTGCATTTA CTCA ACA  TTT
                                |||||||| |||| |||  |||
                                CACGTAAAT GAGT TGT  AAA
                                     T   C  TG
GAM3455 FLJ13195 3' GTGCACTTATTTCAGTCAGCT  77574        C  A_
                                GTGCATTTAT TCA  CAGTT
                                |||||||||| |||  |||||
                                CACGTGAATA AGT  GTCGA
                                     A  CA
GAM3455 FLJ23132 3' GTGCATTTTTTGCTTAAACAGT 77575       AT__  C_
           TTTCC                 GTGCATTT   CT  AACAGTTTTCC
                                |||||||   ||  ||||||||||||
                                CACGTAAA   GA  TTGTCAAAAGG
                                   AAAC  AT
GAM3455 FPGT     3' GTGTATTATCTCAGTTTTTCC 77576    CAT      ACAG
                                GTG   TTATCTCA   TTTTCC
                                |||   ||||||||   ||||||
                                CAC   AATAGAGT   AAAAGG
                                  AT_      CA__
GAM3455 KIAA1042 5' GTGCCTTCCTCAGCAGTTTTC  77577     A  A    A
                                GTGC TTT TCTCA CAGTTTTC
                                |||| ||| ||||| ||||||||
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                                CACG GAA GGAGT GTCAAAAG
                                  _  _    C
GAM3455 KIAA1485 3' GTGCATTTATCTTAAAAGT   77578          C  C
                                GTGCATTTATCT AA AGT
                                |||||||||||| || |||
                                CACGTAAATAGA TT TCA
                                       A  T
GAM3455 MIG-6    3' GTGCATTTTTCTTAAGCATGTT 77579        A   C  _  _
          TT                     GTGCATTT TCT AA CA GTTTT
                                |||||||| ||| || || |||||
                                CACGTAAA AGA TT GT CAAAA
                                     A   A  C  A
GAM3455 LOC115219 3' TGCACTTTTTTGGTAGTTTTCC 77580        ATCTCAAC
                                TGCATTT       AGTTTTCC
                                |||||||       ||||||||
                                ACGTGAA       TCAAAAGG
                                    AAAACCA_
GAM3455 LOC135818 3' GTACATTTATCTCTCATTTC   77581           AACA
                                GTGCATTTATCTC    GTTTT
                                ||||||||||||    |||||
                                CATGTAAATAGAG    TAAAG
                                       AG__
GAM3455 LOC139755 5' GTGCTTCCAGCAATAGTTTTCC 77582      A    TCT   C
                                GTGC TTTA   CAA AGTTTTCC
                                |||| ||||   ||| ||||||||
                                CACG AGGT   GTT TCAAAAGG
                                  A   C__   A
GAM3455 LOC145384 3' GCTGTATATCAACAGTTTTC   77583    ATT   C
                                GC   TAT TCAACAGTTTTC
                                ||   ||| ||||||||||||
                                CG   ATA AGTTGTCAAAAG
                                 AC_   T
GAM3456 CENPA    5'  TCCTGCTCGGGCTGCCGGGTCC 77586     C          C
          G                      TCC GCTCGGGCTGTCGG GTCCG
                                ||| |||||||||||||| |||||
                                AGG CGAGCCCGACGGCC CAGGC
                                  A          _
GAM3456 DLEC1    3'  GCTCAGGCTGTTTTGCGGACGC 77587         T________  CGT
          C                      GCTCGGGCTG       CGG   CC
                                ||||||||||       |||   ||
                                CGAGTCCGAC       GCC   GG
                                      AAAACIII   TGC
GAM3456 DLEC1    3'  GCTCAGGCTGTTTTGCGGACGC 77587         T________  CGT
          C                      GCTCGGGCTG       CGG   CC
                                ||||||||||       |||   ||
                                CGAGTCCGAC       GCC   GG
                                      AAAACIII   TGC
GAM3456 SIAH2    5'  TCCTGCTCGGGCTGCGGGCCG  77588     C        T   C T
                                TCC GCTCGGGCTG CGG G CCG
                                ||| |||||||||| ||| | |||
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                                AGG CGAGCCCGAC GCC C GGC
                                  A       _  _ _
GAM3456 TEM6     5' TCCTGCTGGGGCTGTCGG    77589     C  C
                                TCC GCT GGGCTGTCGG
                                ||| ||| ||||||||||
                                AGG CGA CCCGACAGCC
                                  A  C
GAM3456 ANAPC11  5' CCGTTGGCAGCGCCGGCGTCCG 77590     CTCG  __
                                CCG   GGC  TGTCGGCGTCCG
                                |||   |||  ||||||||||||
                                GGC   CCG  GCGGCCGCAGGC
                                  AA__  TC
GAM3456 CLDN15   5' CTCGGGCTCAGGTCCG     77591       TG   C
                                CTCGGGC  TCGG GTCCG
                                |||||||  |||| |||||
                                GAGCCCG  AGTC CAGGC
                                   __   _
GAM3456 CLDN15   5' CTCGGGCTCAGGTCCG     77591       TG   C
                                CTCGGGC  TCGG GTCCG
                                |||||||  |||| |||||
                                GAGCCCG  AGTC CAGGC
                                   __   _
GAM3456 KIAA1545 3' CCGCTCGGAGAGGCGTC    77592        CTGTC
                                CCGCTCGGG    GGCGTC
                                |||||||||    ||||||
                                GGCGAGCCT    CCGCAG
                                     CT___
GAM3456 RAB35    5' TCCCTTCGGGCTGCTC     77593     GC      CGGCG
                                TCCC  TCGGGCTGT    TC
                                ||||  |||||||||    ||
                                AGGG  AGCCCGACG    AG
                                  A_       ______
GAM3456 LOC222936 5' TCCCTTTGGGCTGCTCTGCGGA 77594   GCTC     T________  CGT
           CGCC                   C   GGGCTG      CGG   CC
                                |   ||||||       |||   ||
                                G   CCCGAC       GCC   GG
                                 AAA_     GAGACIII   TGC
GAM3456 LOC254245 3' TCCTGCCCGGGCTGGCTC    77595     C       GTC   G
                                TCC GCTCGGGCT   GGC TC
                                ||| |||||||||   ||| ||
                                AGG CGGGCCCGA   CCG AG
                                  A       ___  _
GAM3457 APAF1    5' GACACAAAGGGAGGAGGTCTT  77598     _         A
                                GGC CGGAGGGAGGAG TCTT
                                ||| ||||||||||| ||||
                                CTG GTTTCCCTCCTC AGAA
                                  T          C
GAM3457 APAF1    5' GACACAAAGGGAGGAGGTCTT  77598     _         A
                                GGC CGGAGGGAGGAG TCTT
                                ||| ||||||||||| ||||
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                                CTG GTTTCCCTCCTC AGAA
                                  T          C
GAM3457 B3GAT1   3' AGGGGCCGGAGGGGGGGAC   77599    A        A  A
                                AG GGCCGGAGGG GG GAT
                                || |||||||||| || |||
                                TC CCGGCCTCCC CC CTG
                                 C         _  C
GAM3457 B3GAT1   3' AGGGGCCGGAGGGGGGGAC   77599    A        A  A
                                AG GGCCGGAGGG GG GAT
                                || |||||||||| || |||
                                TC CCGGCCTCCC CC CTG
                                 C         _  C
GAM3457 B4GALT1  3' AAGGGGCCAGAGGGTGA     77600    A        AG
                                AAG GGCCGGAGGG  GA
                                ||| ||||||||||  ||
                                TTC CCGGTCTCCC  CT
                                  C         A_
GAM3457 B4GALT6  5' AAGAGGTGGAGGGGGGAG    77601       CC     A
                                AAGAGG  GGAGGG GGAG
                                ||||||  |||||| ||||
                                TTCTCC  CCTCCC CCTC
                                   A_     C
GAM3457 E2F3     3' AAGGCTGTGGAGGTTTTAAGAT 77602    C__    ________  GAGAT
           CTCCT                  GC   GGAGG      GAG    CT
                                ||   |||||      |||    ||
                                CG   CCTCC      TTC    GA
                                 ACA    AAAAIII   TAGAG
GAM3457 FKBP1A   3' AAGGGGCTGAGGGAGGAA    77603    A   CG
                                AAG GGC  GAGGGAGGAG
                                ||| |||  ||||||||||
                                TTC CCG  CTCCCTCCTT
                                  C   A_
GAM3457 GAB2     3' AAGGGGCCAGAGGGAGGA    77604    A
                                AAG GGCCGGAGGGAGGA
                                ||| ||||||||||||||
                                TTC CCGGTCTCCCTCCT
                                  C
GAM3457 GAB2     3' AAGGGGCCAGAGGGAGGA    77604    A
                                AAG GGCCGGAGGGAGGA
                                ||| ||||||||||||||
                                TTC CCGGTCTCCCTCCT
                                  C
GAM3457 HOXB9    3' GAGGACTGGGGGTAATCTT   77605     CCGGA  A  A
                                GAGG    GGG GG GATCTT
                                ||||    ||| || ||||||
                                CTCC    CCC CC TTAGAA
                                   TGA__   _  A
GAM3457 MN1      3' AAGGGCCTGGTAGAGGAGGGGA 77606    A   _ _ _    A
           TCTT                    AAG GGCC GG AG GGAGG GATCTT
                                ||| |||| || || ||||| ||||||
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                                TTC CCGG CC TC CCTCC CTAGAA
                                  _   A A T   C
GAM3457 NDRG1    3' AAGGGGCCGGGGAGGAG    77607    A    AG
                                AAG GGCCGG  GGAGGAG
                                ||| ||||||  |||||||
                                TTC CCGGCC  CCTCCTC
                                  C    __
GAM3457 PRG2     3' GAGGTGGAGGGAGGGAT    77608    CC       A
                                GAGG  GGAGGGAGG GAT
                                ||||  ||||||||| |||
                                CTCC  CCTCCCTCC CTA
                                  A_       _
GAM3457 PRKRA    3' AAGGGGCCAGAGGGGAA    77609    A        A
                                AAG GGCCGGAGGG GGA
                                ||| ||||||||| |||
                                TTC CCGGTCTCCC CTT
                                  C        _
GAM3457 TCF7L2   5' GAGGGGAAGGGGGGGGGAGATCT 77610     CC     A__
              T                  GAGG  GGAGGG  GGAGATCTT
                                ||||  ||||||  |||||||||
                                CTCC  CTTCCC  CCTCTAGAA
                                  C_    CCC
GAM3457 TIMP3    3' GAGGCTGGAGGAGTCTC    77611      CGGAG     A
                                GAGGC    GGAGGAG TCTT
                                |||||    ||||||| ||||
                                CTCCG    CCTCCTC AGAG
                                  A_____     _
GAM3457 DCAMKL1  5' AGACGCCGCCGGGGGTCT   77612    G   GA  A AGA
                                AGA GCCG  GGG GG  TCT
                                ||| ||||  ||| ||  |||
                                TCT CGGC  CCC CC  AGA
                                  G   GG  _ ___
GAM3457 DKFZp434I1930 3' AGAGGCCGAAGGGAGGAG   77613
                                AGAGGCCGGAGGGAGGAG
                                ||||||||||||||||||
                                TCTCCGGCTTCCCTCCTC

GAM3457 DKFZp547M072 3' AGGGCTCGGAGGGGGGAA    77614    A  _     A
                                AG GGC CGGAGGG GGAG
                                || ||| ||||||| ||||
                                TC CCG GCCTCCC CCTT
                                  _  A     C
GAM3457 DKFZp547O146 5' AGAGGTTGGGGGGAGGCAG   77615      CC  A    _
                                AGAGG  GG GGGAGG AG
                                |||||  || |||||| ||
                                TCTCC  CC CCCTCC TC
                                  AA  C     G
GAM3457 DKFZp762E1511 5' AAAAAACGGGGGGGGAGAT   77616       C  A  A
                                AAGAGGC GG GGG GGAGAT
                                ||||||| || ||| ||||||
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                                TTTTTTG CC CCC CCTCTA
                                   C  _  _
GAM3457  EMR2     3'  AGAGGCTGTGAAAGAGGTCTT  77617       CG_      AGA
                                AGAGGC  GAGGGAGG  TCTT
                                ||||||  ||||||||  ||||
                                TCTCCG  CTTTCTCC  AGAA
                                   ACA      ____
GAM3457  FLJ11362 3'  AGGGGCTGAGGGAGGAG     77618    A  CG
                                AG GGC  GAGGGAGGAG
                                || |||  ||||||||||
                                TC CCG  CTCCCTCCTC
                                 C  A_
GAM3457  FLJ12488 3'  AGGGGGTTGGGGAGTTGAAATC 77619     CC  A__    __
            TT                   AGG  GG   GGGAG  GAGATCTT
                                ||| ||   |||||  ||||||||
                                TCC  CC   CCCTC  CTTTAGAA
                                  C_  AAC    AA
GAM3457  FOXH1    5'  AAGAGGCTGTGGGGGAGG    77620        C__  A
                                AAGAGGC   GG GGGAGG
                                |||||||   || ||||||
                                TTCTCCG   CC CCCTCC
                                   ACA  _
GAM3457  HRD1     3'  AAGGGGCCTGGGGGGAGG    77621     A   _  A
                                AAG GGCC GG GGGAGG
                                ||| |||| || ||||||
                                TTC CCGG CC CCCTCC
                                  C   A  C
GAM3457  HSPB7    3'  AGAGGCATGGAGGGAGGAG   77622       C_
                                AGAGGC  GGAGGGAGGAG
                                ||||||  ||||||||||
                                TCTCCG  CCTCCCTCCTC
                                   TA
GAM3457  JDD1     3'  GAGGGTGGAGGGAGGCAG    77623      CC       _
                                GAGG  GGAGGGAGG AG
                                ||||  |||||||| ||
                                CTCC  CCTCCCTCC TC
                                  CA       G
GAM3457  KIAA0652 3'  AGAGGTTGGAGGAGGAG     77624      CC    G
                                AGAGG  GGAGG AGGAG
                                |||||  ||||| |||||
                                TCTCC  CCTCC TCCTC
                                  AA    _
GAM3457  KIAA0872 3'  AAGAGGCTGTGGGGGAGG    77620        C__  A
                                AAGAGGC   GG GGGAGG
                                |||||||   || ||||||
                                TTCTCCG   CC CCCTCC
                                   ACA  _
GAM3457  KIAA1271 3'  GAGGCTGGAGAGGAGCTCC   77625      C  GG     A
                                GAGGC GGA  GAGGAG TCT
                                ||||| |||  |||||| |||
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                                CTCCG CCT  CTCCTC AGG
                                  A  __     G
GAM3457  KIAA1505  5'  AGGGGGTGGAGGGAGGAG    77626    A  CC
                                AG GG  GGAGGGAGGAG
                                || ||  ||||||||||
                                TC CC  CCTCCCTCCTC
                                 C  CA
GAM3457  KIAA1937  5'  AAGAGACCGGAGGTGGA     77627           GA
                                AAGAGGCCGGAGG  GGA
                                ||||||||||||  |||
                                TTCTCTGGCCTCC  CCT
                                       A_
GAM3457  MGC26655  5'  AGGAGCCTGGAGGGAGGAA   77628    AG  _
                                AG  GCC GGAGGGAGGAG
                                ||  ||| ||||||||||
                                TC  CGG CCTCCCTCCTT
                                 CT   A
GAM3457  MGC2705   3'  AAGGGGCTGAGGGGGGCGGAT  77629     A   CG    A  A_
                                AAG GGC  GAGGG GG  GAT
                                ||| |||  ||||| ||  |||
                                TTC CCG  CTCCC CC  CTA
                                  C   A_    C  GC
GAM3457  MGC5566   3'  AGGGGCTGGAGAGAGATGCCTT 77630    A   C       AGA
                                AG GGC GGAGGGAGG   TCTT
                                || ||| |||||||||   ||||
                                TC CCG CCTCTCTCT   GGAA
                                 C   A       AC_
GAM3457  NLI-IF    5'  GAGGGGTGGGAGGGAGGGAT   77631      CC__       A
                                GAGG    GGAGGGAGG GAT
                                ||||    ||||||||| |||
                                CTCC    CCTCCCTCC CTA
                                  CCAC       _
GAM3457  PDZ-      3'  AGAGTCTGGATCCTTGAGATCT 77632      GCC   GGGAG
            T                    AGAG   GGA    GAGATCTT
                                ||||   |||    ||||||||
                                TCTC   CCT    CTCTAGAA
                                  AGA   AGGAA
GAM3457  SAMHD1    3'  AAGAGGCCAGAGCTCTCAGATC 77633           GGAGG
            TT                    AAGAGGCCGGAG    AGATCTT
                                ||||||||||||    |||||||
                                TTCTCCGGTCTC    TCTAGAA
                                      GAGAG
GAM3457  SLC26A9   3'  AGAGGCCAGAAGATTTTAAGAT 77634          G_______   AGAT
            CC                    GAGGCCGGAGG       AGG   C
                                ||||||||||||       |||   |
                                CTCCGGTCTTC       TTC   G
                                      TAAAAIII   TAGA
GAM3457  SLC26A9   3'  AGAGGCCAGAAGATTTTAAGAT 77634          G_______   AGAT
            CC                    GAGGCCGGAGG       AGG   C
                                ||||||||||||       |||   |
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                                CTCCGGTCTTC      TTC   G
                                      TAAAAIII  TAGA
GAM3457  ZFP36L2   5'  GAGGTCGGGAGGAGCCCTT   77635     CCGGA      AT
                                GAGG    GGGAGGAG  CTT
                                ||||    |||||||| |||
                                CTCC    CCCTCCTC  GAA
                                  AG___      GG
GAM3457  LOC121036 5'  AGGGGCCGGAGGGCAGGA    77636    A       _
                                AG GGCCGGAGGG AGGA
                                || |||||||||| ||||
                                TC CCGGCCTCCC TCCT
                                 C        G
GAM3457  LOC126755 3'  AAGAGGCAGGAGGGAGGAG    77637       C
                                AAGAGGC GGAGGGAGGAG
                                ||||||| ||||||||||
                                TTCTCCG CCTCCCTCCTC
                                    T
GAM3457  LOC128387 3'  GAGGCTGAGGGAGGAGAC    77638      CG
                                GAGGC  GAGGGAGGAGAT
                                |||||  ||||||||||||
                                CTCCG  CTCCCTCCTCTG
                                  A_
GAM3457  LOC129305 5'  AGGCCGGAGAGAAGGTCTT    77639           AGA
                                AGGCCGGAGGGAGG   TCTT
                                ||||||||||||||   ||||
                                TCCGGCCTCTCTTC   AGAA
                                       C__
GAM3457  LOC145547 3'  AACAGGTTGGAGGGAGGAG    77640    G   CC
                                AA AGG  GGAGGGAGGAG
                                || |||  ||||||||||||
                                TT TCC  CCTCCCTCCTC
                                 G   AA
GAM3457  LOC146227 3'  AAGAGGTGGGAGGGAGGCAGA  77641       CC       _
                                AAGAGG  GGAGGGAGG AGA
                                ||||||  ||||||||| |||
                                TTCTCC  CCTCCCTCC TCT
                                   AC        G
GAM3457  LOC150319 5'  AAGGGGCCGGAGGGGAG     77642     A        AG
                                AAG GGCCGGAGGG  GAG
                                ||| ||||||||||  |||
                                TTC CCGGCCTCCC  CTC
                                  C         __
GAM3457  LOC161244 3'  GATGCTGACGGGGAGATCTT   77643    G  CG  G  A
                                GA GC  GA GG GGAGATCTT
                                || ||  || || |||||||||
                                CT CG  CT CC CCTCTAGAA
                                 A  A_  G  _
GAM3457  LOC254268 3'  GAGGCTGAGGGAGGAGA     77644       CG
                                GAGGC  GAGGGAGGAGA
                                |||||  ||||||||||
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                                CTCCG  CTCCCTCCTCT
                                  A_
GAM3457  LOC255975 5'  AGAGGTCAACTTGAGGAGAT   77645      C   AGG
                                AGAGG CGG   GAGGAGAT
                                ||||| |||   ||||||||
                                TCTCC GTT   CTCCTCTA
                                  A   GAA
GAM3457  LOC90288  3'  GAGGTCGGGGGAAAGTCTCTT  77646     C   A     AGA
                                GAGG CGG GGGAGG   TCTT
                                |||| ||| ||||||   ||||
                                CTCC GCC CCCTTT   AGAA
                                  A   _     CAG
GAM3457  LOC92303  3'  GAGGCTGAGGGAGGAGA     77644      CG
                                GAGGC  GAGGGAGGAGA
                                |||||  ||||||||||
                                CTCCG  CTCCCTCCTCT
                                  A_
GAM3458  AGA       3'  TATGATGATTCCTTTTGGGT   77649          AAGA   A
                                TATGATGATTT    TTG GT
                                ||||||||||    ||| ||
                                ATACTACTAAG    AAC CA
                                      GAA_   C
GAM3458  EGFL5     5'  ATGATGATGTTAAATTGGGTCC 77650        TTA     A
           A                     ATGATGAT   AGATTG GTCCA
                                ||||||||   |||||| |||||
                                TACTACTA   TTTAAC CAGGT
                                    CAA     C
GAM3458  PCDH11X   3'  TATGAGGATTTAAGAACCTCCC 77651      T       TTGAG
                                TATGA GATTTAAGA     TCC
                                ||||| |||||||||     |||
                                ATACT CTAAATTCT     GGG
                                  C        TGGA_
GAM3458  PCDH11X   3'  TATGAGGATTTAAGAACCTCCC 77651      T       TTGAG
                                TATGA GATTTAAGA     TCC
                                ||||| |||||||||     |||
                                ATACT CTAAATTCT     GGG
                                  C        TGGA_
GAM3458  PCDH11Y   3'  TATGAGGATTTAAGAACCTCCC 77651      T       TTGAG
                                TATGA GATTTAAGA     TCC
                                ||||| |||||||||     |||
                                ATACT CTAAATTCT     GGG
                                  C        TGGA_
GAM3458  SURF4     3'  TGAGGTAACTGGGTTGAGTCC  77652     __     TAAGA
                                TGA  TGATT     TTGAGTCC
                                |||  |||||    ||||||||
                                ACT  ATTGA     AACTCAGG
                                  CC    CCC__
GAM3458  TGFB1     3'  TATGGTGACTGAATGAGTTCA  77653      A    TAA  T    C
                                TATG TGATT   GA TGAGT CA
                                |||| |||||   || ||||| ||
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                                ATAC ACTGA   CT ACTCA GT
                                  C     ___  T    A
GAM3458 C2orf6    3'  TATGATGATTTAAACTG     77654          A
                                TATGATGATTTA GATTG
                                |||||||||||| |||||
                                ATACTACTAAAT TTGAC
                                                _
GAM3458 FLJ22794  3'  TATGATGTTTAAGATATCC    77655       A       TGA
                                TATGATG TTTAAGAT   GTCC
                                ||||||| ||||||||   ||||
                                ATACTAC AAATTCTA   TAGG
                                  _      ____
GAM3458 KIAA0252  3'  ATGATTTTAACGAGTCCA     77656       AAGAT
                                ATGATTT    TGAGTCCA
                                |||||||    ||||||||
                                TACTAAA    GCTCAGGT
                                    ATT__
GAM3458 NR6A1     5'  TGACGGGAAGATTGAGTTCA   77657      ATTT        C
                                TGATG    AAGATTGAGT CA
                                |||||    |||||||||| ||
                                ACTGC    TTCTAACTCA GT
                                   CC__         A
GAM3458 ZAK       3'  ATGGTGATTTAAGATAAAGCCA 77658     A         T   T
                                ATG TGATTTAAGAT GAG CCA
                                ||| |||||||||| ||| |||
                                TAC ACTAAATTCTA TTC GGT
                                  C          T  _
GAM3458 LOC158476 3'  TGATTACAGTGAGTCCA     77659      TA  AT
                                TGATT  AG  TGAGTCCA
                                |||||  ||  ||||||||
                                ACTAA  TC  ACTCAGGT
                                   TG  __
GAM3458 LOC254100 3'  TGAGGATCACTTGAGTCCA    77660     T    TAAGA
                                TGA GATT    TTGAGTCCA
                                ||| ||||    |||||||||
                                ACT CTAG    AACTCAGGT
                                  C   TG___
GAM3459 ABR       3'  TAAGTCGAGCCCCTGGA     77663       __   GTGA
                                TAAGT  GGCT   CCTGGA
                                |||||  ||||   ||||||
                                ATTCA  TCGG   GGACCT
                                   GC   _____
GAM3459 ABR       3'  TAAGTCGAGCCCCTGGA     77663       __   GTGA
                                TAAGT  GGCT   CCTGGA
                                |||||  ||||   ||||||
                                ATTCA  TCGG   GGACCT
                                   GC   _____
GAM3459 ADCY2     3'  CAAGTGGCAGAACGATCTGG  77664        TG__  C
                                TAAGTGGC   TGA CTGG
                                ||||||||   ||| ||||
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                                GTTCACCG   GCT GACC
                                    TCTT   A
GAM3459  ALK     5'  TAAATGAAACAGACCTGGA   77665       CTGT
                                TAAGTGG   GACCTGGA
                                |||||||   ||||||||
                                ATTTACT   CTGGACCT
                                    TTGT
GAM3459  ALPI    3'  TGGATCTGGTGACCTGGA    77666    __  _
                                TGG  CTG TGACCTGGA
                                |||  ||| |||||||||
                                ACC  GAC ACTGGACCT
                                  TA   C
GAM3459  CARKL   3'  TAAGTGACTGACCGG      77667       GT   T
                                TAAGTGGCT  GACC GG
                                |||||||||  |||| ||
                                ATTCACTGA  CTGG CC
                                    __   _
GAM3459  COL4A2  3'  TAAGTGCTGCTGCTGGA    77668      G   GAC
                                TAAGTG CTGT   CTGGA
                                ||||||| ||||   |||||
                                ATTCAC GACG   GACCT
                                   _   AC_
GAM3459  DPH2L2  3'  AGTGGCTACTGTACTGGA    77669       _ AC
                                AGTGGCTG TG  CTGGA
                                |||||||| ||  |||||
                                TCACCGAT AC  GACCT
                                    G  AT
GAM3459  DUOX1   3'  TAAATGGCTTGCCATGG     77670       G  A  _
                                TAAGTGGCT TG CC TGG
                                ||||||||| || || |||
                                ATTTACCGA AC GG ACC
                                    _ _  T
GAM3459  GAS7    3'  CAAGTGGCTCTTCCTGGA    77671       GTGA
                                TAAGTGGCT   CCTGGA
                                |||||||||   ||||||
                                GTTCACCGA   GGACCT
                                    GAA_
GAM3459  GNAL    5'  TAAATGGCTGTAAGGA      77672         CCT
                                TAAGTGGCTGTGA  GGA
                                ||||||||||||  |||
                                ATTTACCGACATT  CCT
                                    ___
GAM3459  HCS     3'  AGTGGCTACCACACTGGA    77673       TG  _
                                AGTGGCTG  AC CTGGA
                                ||||||||  || |||||
                                TCACCGAT  TG GACCT
                                    GG  T
GAM3459  HGF     3'  TAAGTGGCCTTAAGTTTGGA  77674       G   CC_
                                TAAGTGGCT TGA   TGGA
                                ||||||||| |||   ||||
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                                ATTCACCGG ATT   ACCT
                                      A   CAA
GAM3459  HSPA4    3'  TAAGAACGTGACCTGGA     77675      T   T
                                TAAG GGC GTGACCTGGA
                                |||| ||| ||||||||||
                                ATTC TTG CACTGGACCT
                                  _  _
GAM3459  MEN1     3'  AGCCACAGTGTGACCTGG     77676     G  __
                                AGT GC  TGTGACCTGG
                                ||| ||  ||||||||||
                                TCG TG  ACACTGGACC
                                  G  TC
GAM3459  MPP2     3'  TAAATGGCGCCTCTGGA      77677        T  GAC
                                TAAGTGGC GT   CTGGA
                                |||||||| ||   |||||
                                ATTTACCG CG   GACCT
                                     _  GA_
GAM3459  NCOA6    5'  TAAGTAGCTCCTTGGA       77678        GTGA  _
                                TAAGTGGCT    CCT GGA
                                |||||||||    ||| |||
                                ATTCATCGA    GGA CCT
                                     _____  A
GAM3459  NT5M     3'  TGATGGCTGCAGACTCTGG    77679    A       _  _
                                A GTGGCTGT GAC CTGG
                                | ||||||||| ||| |||||
                                A TACCGACG CTG GACC
                                 C       T   A
GAM3459  PCDH11X  3'  TAAGTGACTCGTGCTTTGGA   77680         _  ACC
                                TAAGTGGCT GTG   TGGA
                                ||||||||| |||   ||||
                                ATTCACTGA CAC   ACCT
                                     G   GAA
GAM3459  PCDH11X  3'  TAAGTGACTCGTGCTTTGGA   77680         _  ACC
                                TAAGTGGCT GTG   TGGA
                                ||||||||| |||   ||||
                                ATTCACTGA CAC   ACCT
                                     G   GAA
GAM3459  PCDH11Y  3'  TAAGTGACTCGTGCTTTGGA   77680         _  ACC
                                TAAGTGGCT GTG   TGGA
                                ||||||||| |||   ||||
                                ATTCACTGA CAC   ACCT
                                     G   GAA
GAM3459  PODXL    3'  CAAGTGGCTCTGACCTTGG    77681         G    _
                                TAAGTGGCT TGACCT GG
                                ||||||||| |||||| ||
                                GTTCACCGA ACTGGA CC
                                     G     A
GAM3459  PPP3R1   3'  TAAGTGGCATAAATTTGGA    77682        T   CC_
                                TAAGTGGC GTGA   TGGA
                                |||||||| ||||   ||||
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                                ATTCACCG TATT   ACCT
                                     _   TAA
GAM3459  PTGER4   5'  AGTGGCTGTCGATTTTTGGA  77683        _ CC__
                                AGTGGCTGT GA    TGGA
                                ||||||||| ||    ||||
                                TCACCGACA CT    ACCT
                                     G  AAAA
GAM3459  RAB27A   3'  TAAGTGGCTTTAATGG     77684        G   CC
                                TAAGTGGCT TGA  TGG
                                ||||||||| |||  |||
                                ATTCACCGA ATT  ACC
                                     A  __
GAM3459  RFX2     3'  GTGGCTGCGCAGGGACCTGG  77685        _____
                                GTGGCTGT    GACCTGG
                                ||||||||    |||||||
                                CACCGACG    CTGGACC
                                     CGTCC
GAM3459  RRM2     3'  TAACTGGCTGTGCTGG     77686     G      AC
                                TAA TGGCTGTG  CTGG
                                ||| ||||||||  ||||
                                ATT ACCGACAC  GACC
                                  G      __
GAM3459  RRM2B    3'  TAAATGTGCAACCTGGA     77687       GC  TG
                                TAAGTG  TG  ACCTGGA
                                ||||||  ||  |||||||
                                ATTTAC  AC  TGGACCT
                                    __  GT
GAM3459  STMN1    3'  AAGTAACAGCTGACCTGG    77688        T _
                                AAGTGGC G TGACCTGG
                                ||||||| | ||||||||
                                TTCATTG C ACTGGACC
                                    T G
GAM3459  TBX3     3'  AGCAATTCTGTGACCTGGA   77689     TG __
                                AG  G  CTGTGACCTGGA
                                ||  |  ||||||||||||
                                TC  T  GACACTGGACCT
                                 GT AA
GAM3459  TFRC     3'  TAAGTAGAGGACCTGGA     77690       CTGT
                                TAAGTGG    GACCTGGA
                                |||||||    ||||||||
                                ATTCATC    CTGGACCT
                                    TC__
GAM3459  TNFRSF8  3'  AGGGCTGCAGACATCTGG    77691    T    _  __
                                AG GGCTGT GAC  CTGG
                                || |||||| |||  ||||
                                TC CCGACG CTG  GACC
                                 _     T   TA
GAM3459  TRPV1    5'  TAAGTGACTGACCGG       77667        GT   T
                                TAAGTGGCT  GACC GG
                                |||||||||  |||| ||
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                                ATTCACTGA  CTGG CC
                                   __   _
GAM3459  BACH     3'  TAAGTGACTGGACACTGG    77692          T  _
                                TAAGTGGCTG GAC CTGG
                                |||||||||| ||| ||||
                                ATTCACTGAC CTG GACC
                                      _  T
GAM3459  C17orf1A  5'  TAAATGGCTGCCATGGA    77693          TGA  _
                                TAAGTGGCTG   CC TGGA
                                ||||||||||   || ||||
                                ATTTACCGAC   GG ACCT
                                      ___  T
GAM3459  C21orf55  5'  AAGTGGCTTAATTGGA     77694         G   CC
                                AAGTGGCT TGA  TGGA
                                |||||||| |||  ||||
                                TTCACCGA ATT  ACCT
                                     _  A_
GAM3459  C8orf13   3'  CAAGTGGCTTCCGCATTTGGA  77695         G_  ACC_
                                TAAGTGGCT  TG    TGGA
                                |||||||||  ||    ||||
                                GTTCACCGA  GC    ACCT
                                     AG  GTAA
GAM3459  CAC-1     3'  AGTGGCCATCGGGCCTGG    77696          _ A_
                                AGTGGCTGT G  CCTGG
                                |||||||||  |  |||||
                                TCACCGGTA C  GGACC
                                     G CC
GAM3459  DDX33     3'  TAAGCGCCAACCTGGA      77697        G  GT
                                TAAGTG CT  GACCTGGA
                                ||||||  ||  ||||||||
                                ATTCGC GG  TTGGACCT
                                   _  __
GAM3459  DKFZP547E2110 3'  TAAGAGGCTTCACGGTGGCTTG 77698     T  _____  ACC   III
           GAT                    AAG GGCT    GTG   TGGA   T
                                ||| ||||    |||   ||||  |
                                TTC CCGA    CAC   ACCT   A
                                  T   AGTGC   CGA   III
GAM3459  FLJ10210  5'  CAAGTGACGCGTCTGG      77699         T  AC
                                TAAGTGGC GTG  CTGG
                                |||||||| |||  ||||
                                GTTCACTG CGC  GACC
                                     _  A_
GAM3459  FLJ10900  3'  TAAGTGGCTGCTCCATGA    77700          GA  _
                                TAAGTGGCTGT  CC TGG
                                ||||||||||  || |||
                                ATTCACCGACG  GG ACT
                                      A_  T
GAM3459  FLJ10900  3'  TAAGTGGCTGCTCCATGA    77700          GA  _
                                TAAGTGGCTGT  CC TGG
                                ||||||||||  || |||
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                                ATTCACCGACG  GG ACT
                                      A_  T
GAM3459  FLJ12294  3'  AGTGGCTGGTGGGCCTGG    77701        _  A_
                                AGTGGCTG TG  CCTGG
                                ||||||||  ||  |||||
                                TCACCGAC AC  GGACC
                                    C  CC
GAM3459  FLJ12700  3'  AAGTGACTGTCTGGA      77702         GAC
                                AAGTGGCTGT   CTGGA
                                ||||||||||   |||||
                                TTCACTGACA   GACCT
                                     ___
GAM3459  FLJ12899  3'  AGTGGCTACTGCACTGGA    77703        _  AC
                                AGTGGCTG TG  CTGGA
                                ||||||||  ||  |||||
                                TCACCGAT AC  GACCT
                                    G  GT
GAM3459  FLJ13590  5'  AAGTGGCTCACACCTGGA    77704        GTG
                                AAGTGGCT   ACCTGGA
                                ||||||||   |||||||
                                TTCACCGA   TGGACCT
                                    GTG
GAM3459  FLJ20195  3'  TAAGCGGCTGGCGACTTGG    77705         _   C
                                TAAGTGGCTG TGAC TGG
                                ||||||||||  ||||  |||
                                ATTCGCCGAC GCTG ACC
                                     C    A
GAM3459  FLJ20519  3'  AAGTGGCTGAGATGGA      77706        T  CC
                                AAGTGGCTG GA  TGGA
                                |||||||||  ||  ||||
                                TTCACCGAC CT  ACCT
                                     T  __
GAM3459  FYCO1     3'  CAAGTGGCTGGATGGA      77707         T  CC
                                TAAGTGGCTG GA  TGGA
                                ||||||||||  ||  ||||
                                GTTCACCGAC CT  ACCT
                                    _  __
GAM3459  HSPC065   3'  AAGTGGCTGGCTAGCCTGG   77708        _ GA_
                                AAGTGGCTG T   CCTGG
                                |||||||||  |   |||||
                                TTCACCGAC G   GGACC
                                     C ATC
GAM3459  KIAA0143  3'  TAAGCGGCTGTGTAGA      77709          ACC
                                TAAGTGGCTGTG   TGGA
                                ||||||||||||   ||||
                                ATTCGCCGACAC   ATCT
                                     ___
GAM3459  KIAA0227  3'  CAAGCAGATGACCTGGA     77710      TG CT
                                TAAG  G  GTGACCTGGA
                                ||||  |  ||||||||||
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                                GTTC  C  TACTGGACCT
                                  GT __
GAM3459  KIAA0376  3'  TAAATGACACTGCCTGG     77711        TG  A
                                TAAGTGGC  TG CCTGG
                                ||||||||  || |||||
                                ATTTACTG  AC GGACC
                                     TG  _
GAM3459  KIAA0445  5'  TAACTGTGTGACCTGG      77712     G  GC
                                TAA TG  TGTGACCTGG
                                |||  ||  ||||||||||
                                ATT AC  ACACTGGACC
                                  G  __
GAM3459  KIAA0779  3'  TAAGTGGCCAACTTGG      77713        GT   C
                                TAAGTGGCT  GAC TGG
                                |||||||||  ||| |||
                                ATTCACCGG  TTG ACC
                                     __   A
GAM3459  KIAA1450  3'  AAGCAAACTGTGACCTGGA   77714     TG _
                                AAG  G CTGTGACCTGGA
                                |||  | ||||||||||||
                                TTC  T GACACTGGACCT
                                  GT T
GAM3459  KIAA1638  3'  AAGTGCCGACCTGGA       77715      G  GT
                                AAGTG CT  GACCTGGA
                                |||||  ||  ||||||||
                                TTCAC GG  CTGGACCT
                                   _  __
GAM3459  KIAA1679  3'  TAAATGGCAGTCTCCTGG    77716        T  GA
                                TAAGTGGC GT  CCTGG
                                |||||||| ||  |||||
                                ATTTACCG CA  GGACC
                                     T  GA
GAM3459  KIAA1822  3'  TAAGTGACAAATGCCCTGGA  77717        T_  A
                                TAAGTGGC  GTG CCTGGA
                                ||||||||  ||| ||||||
                                ATTCACTG  TAC GGACCT
                                     TT   G
GAM3459  KIAA1944  5'  TGGCTGTGCTGCACCTGGA   77718        ____
                                TGGCTGTG    ACCTGGA
                                ||||||||    |||||||
                                ACCGACAC    TGGACCT
                                     GACG
GAM3459  MGC16279  5'  TGATGGCTGTGCTCTTGGA   77720   A       AC  _
                                A GTGGCTGTG  CT GGA
                                | |||||||||  || |||
                                A TACCGACAC  GA CCT
                                 C        GA  A
GAM3459  MGC16279  5'  TGATGGCTGTGCTCTTGGA   77720   A       AC  _
                                A GTGGCTGTG  CT GGA
                                | |||||||||  || |||
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                                A TACCGACAC  GA CCT
                                 C       GA  A
GAM3459  MGC16279  3'  CAAGTGGTGACCTGG      77719       CTG
                                TAAGTGG   TGACCTGG
                                |||||||   ||||||||
                                GTTCACC   ACTGGACC
                                    ___
GAM3459  MGC3101   3'  AGTGGCTGTCACAGGCCTGG   77721        G ____
                                AGTGGCTGT A    CCTGG
                                |||||||||| |    |||||
                                TCACCGACA T    GGACC
                                     G GTCC
GAM3459  MGC4368   5'  AAGCCACAGGTGACCTGG    77722     G  T_
                                AAGT GC  GTGACCTGG
                                |||| ||  |||||||||
                                TTCG TG  CACTGGACC
                                  G  TC
GAM3459  OSBPL6    5'  CAAGTGGCAGAACCTGGA    77723       TGT
                                TAAGTGGC   GACCTGGA
                                ||||||||   ||||||||
                                GTTCACCG   TTGGACCT
                                     TC_
GAM3459  SEZ6      3'  CAAGTGGCTGGAATTGGA    77724        T  CC
                                TAAGTGGCTG GA  TGGA
                                |||||||||| ||  ||||
                                GTTCACCGAC CT  ACCT
                                      _  TA
GAM3459  SHANK3    3'  GCTGCTGTGTGACCTGGA    77725    G    __
                                GT GCTGT  GACCTGGA
                                || |||||  ||||||||
                                CG CGACA  CTGGACCT
                                 A    CA
GAM3459  SHAPY     3'  TAAATGACCCAGCCTGGA    77726        GTGA
                                TAAGTGGCT    CCTGGA
                                |||||||||    ||||||
                                ATTTACTGG    GGACCT
                                     GTC_
GAM3459  SLC2A13   3'  TAAGTGACTAACCAATTTGGA  77727        GT   ____
                                TAAGTGGCT  GACC    TGGA
                                |||||||||  ||||    ||||
                                ATTCACTGA  TTGG    ACCT
                                     __    TTAA
GAM3459  SYNE-1    3'  GCACACATGTGATCTGGA    77728    _ _    C
                                GTG GC TGTGA CTGGA
                                ||| || ||||| |||||
                                CGT TG ACACT GACCT
                                  G  T    A
GAM3459  TRIM29    3'  AAGTGGCTGTGGTGGA      77729          ACC
                                AAGTGGCTGTG   TGGA
                                ||||||||||   ||||
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                                TTCACCGACAC   ACCT
                                      C__
GAM3459  TU12B1-TY 3'  TGATGGCTGCTGCCCTGGA   77730   A      GA_
                                A GTGGCTGT   CCTGGA
                                | ||||||||   ||||||
                                A TACCGACG   GGACCT
                                 C       ACG
GAM3459  USP25    3'  TAAATGGCTGTAGTCATGGA   77731          ACC_
                                TAAGTGGCTGTG   TGGA
                                ||||||||||||   ||||
                                ATTTACCGACAT   ACCT
                                       CAGT
GAM3459  LOC124411 3'  TAAATGGCTTCAGATGGA    77732        GT_  CC
                                TAAGTGGCT   GA  TGGA
                                |||||||||   ||  ||||
                                ATTTACCGA   CT  ACCT
                                      AGT  __
GAM3459  LOC124895 5'  TGATGGCCATGCTGGA      77733   A       AC
                                A GTGGCTGTG  CTGGA
                                | |||||||||  |||||
                                A TACCGGTAC  GACCT
                                 C       __
GAM3459  LOC146229 3'  TGACTGCACACACTTGGA    77734        _ _ _
                                TGGCTGTG AC CT GGA
                                |||||||| || || |||
                                ACTGACGT TG GA CCT
                                     G  T  A
GAM3459  LOC146713 3'  CAAGTGACTCACCTGG      77735        GTG
                                TAAGTGGCT   ACCTGG
                                |||||||||   ||||||
                                GTTCACTGA   TGGACC
                                      G__
GAM3459  LOC148918 5'  CAAGTGGCTTTCCCTGGA    77736        GTGA
                                TAAGTGGCT    CCTGGA
                                |||||||||    ||||||
                                GTTCACCGA    GGACCT
                                      AAG_
GAM3459  LOC149579 5'  TAACTGTGTGACCTGG      77712     G  GC
                                TAA TG  TGTGACCTGG
                                ||| ||  ||||||||||
                                ATT AC  ACACTGGACC
                                  G  __
GAM3459  LOC149839 5'  AAGTGGCTGTGCTCCTTCTGGA 77737          AC____
                                AAGTGGCTGTG     CTGGA
                                ||||||||||     |||||
                                TTCACCGACAC     GACCT
                                      GAGGAA
GAM3459  LOC153346 5'  TAAGTGGCTGCTTCTGGA    77738          GAC
                                TAAGTGGCTGT   CTGGA
                                ||||||||||   |||||
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                                ATTCACCGACG   GACCT
                                      AA_
GAM3459  LOC158310 5'  TAAGCACCATGACCTGG     77739       G
                                TAAGTG CTGTGACCTGG
                                |||||| ||||||||||
                                ATTCGT GGTACTGGACC
                                  _
GAM3459  LOC165721 5'  AAGTGGCCGGTGGTCTGG    77740         _ AC
                                AAGTGGCTG TG  CTGG
                                ||||||||| ||  ||||
                                TTCACCGGC AC  GACC
                                     C  CA
GAM3459  LOC169026 3'  TAACTTCCAGTGACCTGGA   77741      _____
                                TGGCT   GTGACCTGGA
                                |||||   ||||||||||
                                ATTGA   CACTGGACCT
                                   AGGT
GAM3459  LOC196214 5'  TAAGTGACTCGAGTTTGG    77742        G   CC_
                                TAAGTGGCT TGA   TGG
                                ||||||||| |||   |||
                                ATTCACTGA GCT   ACC
                                     _  CAA
GAM3459  LOC196743 5'  AGTAGCCGGGAGGTCTGGA   77743        T  C__
                                AGTGGCTG GA   CTGGA
                                |||||||| ||   |||||
                                TCATCGGC CT   GACCT
                                     C  CCA
GAM3459  LOC196812 3'  TAAGTGACTGGCCTGG      77744         TGA
                                TAAGTGGCTG   CCTGG
                                ||||||||||   |||||
                                ATTCACTGAC   GGACC
                                      C__
GAM3459  LOC197416 3'  TAAATGGCTTCAGATGGA    77732        GT_  CC
                                TAAGTGGCT   GA  TGGA
                                |||||||||   ||  ||||
                                ATTTACCGA   CT  ACCT
                                     AGT  __
GAM3459  LOC205143 5'  AAGTGGCCAGCCTTGGA     77745        TGA  _
                                AAGTGGCTG   CCT GGA
                                |||||||||   ||| |||
                                TTCACCGGT   GGA CCT
                                     C__   A
GAM3459  LOC221088 5'  AGTGGCCAGCACCTTGGA    77746        TG   _
                                AGTGGCTG  ACCT GGA
                                ||||||||  |||| |||
                                TCACCGGT  TGGA CCT
                                     CG    A
GAM3459  LOC221415 5'  AAGTGGCCCTAGGGGCCTGG  77747        G  A___
                                AAGTGGCT TG    CCTGG
                                |||||||| ||    |||||
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                                TTCACCGG AT   GGACC
                                    G  CCCC
GAM3459  LOC222057 3'  CAAGTGGTGGGCCTGGA    77748       C  TGA
                                TAAGTGG TG   CCTGGA
                                ||||||| ||   ||||||
                                GTTCACC AC   GGACCT
                                   _  CC_
GAM3459  LOC222936 5'  TAGCTGTGTAGACCTGGA    77749       ___
                                TGGCTGT   GACCTGGA
                                |||||||   ||||||||
                                ATCGACA   CTGGACCT
                                    CAT
GAM3459  LOC253675 3'  TGACTGCAGAAGCCTGGA    77750       _ __
                                TGGCTGT GA  CCTGGA
                                ||||||| ||  ||||||
                                ACTGACG CT  GGACCT
                                    T  TC
GAM3459  LOC253998 5'  TAAGTGGCAGCACGTGG     77751       T  G  C
                                TAAGTGGC GT AC TGG
                                |||||||| || || |||
                                ATTCACCG CG TG ACC
                                    T  _  C
GAM3459  LOC255518 3'  AAGTGGCTGCAGCTGGA     77752         GAC
                                AAGTGGCTGT   CTGGA
                                ||||||||||   |||||
                                TTCACCGACG   GACCT
                                     TC_
GAM3459  LOC255838 5'  CAAGTGGCTGCAGGTGGA    77753           ACC
                                TAAGTGGCTGTG   TGGA
                                ||||||||||||   ||||
                                GTTCACCGACGT   ACCT
                                     CC_
GAM3459  LOC255975 5'  CAAGTGGTGGGCCTGGA     77748       C  TGA
                                TAAGTGG TG   CCTGGA
                                ||||||| ||   ||||||
                                GTTCACC AC   GGACCT
                                   _  CC_
GAM3459  LOC90133  5'  GTGGCTGCTGAAAGCCTGG   77754       _  ____
                                GTGGCTG TGA   CCTGG
                                ||||||| |||   |||||
                                CACCGAC ACT   GGACC
                                    G   TTC
GAM3459  LOC92935  3'  CAAATAACTGTGGTTTGGA   77755           ACC
                                TAAGTGGCTGTG   TGGA
                                ||||||||||||   ||||
                                GTTTATTGACAC   ACCT
                                     CAA
GAM3460  BIN2      3'  TCCATCCCTCCCGTAAGGC   77758       CG   __
                                TCCGTCCC  TTCC  AAGGC
                                ||||||||  ||||  |||||
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                                AGGTAGGG  AGGG  TTCCG
                                    __    CA
GAM3460  CDR2    5'  CCCGTTCCCGCCGGCGGCCG  77759      C     CCAA
                                TCCGT CCCGTT   GGCCG
                                ||||| ||||||   |||||
                                GGGCA GGGCGG   CCGGC
                                   A     CCG_
GAM3460  DUSP6   5'  TCCCTCCCTCCAAGGC     77760     G   CGT
                                TCC TCCC   TCCAAGGC
                                ||| ||||   ||||||||
                                AGG AGGG   AGGTTCCG
                                  G   ___
GAM3460  ESRRA   3'  TCCGCCCCAGCCCTTGGGGC  77761        C   CAA_
                                TCCGTCCC GTTC   GGC
                                |||||||| ||||   |||
                                AGGCGGGG CGGG   CCG
                                     T   AACC
GAM3460  EXTL3   3'  CCCGTTAGATTCCAAGGC   77762      CCCC
                                TCCGT   GTTCCAAGGC
                                |||||   ||||||||||
                                GGGCA   TAAGGTTCCG
                                   ATC_
GAM3460  INPPL1  5'  TCCGCCCCGAGACGCTCAGGGC 77763        ____    CAA
                                TCCGTCCC   CGTTC  GGC
                                ||||||||   |||||  |||
                                AGGCGGGG   GCGAG  CCG
                                     CTCT    TC_
GAM3460  LPIN2   3'  CCCGTCCCCGCTGGGGAAGGC  77764          CC__
                                TCCGTCCCCGTT   AAGGC
                                ||||||||||||   |||||
                                GGGCAGGGGCGA   TTCCG
                                       CCCC
GAM3460  POMZP3  5'  TCAGTCCCCACCAGGCCG   77765   C     TT  A
                                TC GTCCCCG  CCA GGCCG
                                || |||||||  ||| |||||
                                AG CAGGGGT  GGT CCGGC
                                 T      __  _
GAM3460  SIX2    5'  CGTCCCCGCGCCGGCCG    77766        T  AA
                                CGTCCCCGT CC  GGCCG
                                |||||||| ||  |||||
                                GCAGGGGCG GG  CCGGC
                                     C  __
GAM3460  TXNRD1  5'  CGTCCCCGCCGGCAGGCCG  77767        CCA
                                CGTCCCCGTT  AGGCCG
                                ||||||||||  ||||||
                                GCAGGGGCGG  TCCGGC
                                      CCG
GAM3460  3-PAP   5'  TCCGCCCATCCCCAAGGCCG  77768      CCG
                                TCCGTCC  TTCCAAGGCCG
                                |||||||  ||||||||||
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                                AGGCGGG  GGGGTTCCGGC
                                   TA_
GAM3460 CBX6     3' CCCGTCCCAAAGAGGCCG   77769        ___
                                CCCGTTCCA  AGGCCG
                                |||||||||  ||||||
                                GGGCAGGGT  TCCGGC
                                     TTC
GAM3460 CEACAM3  3' TCCTTCCCCATCCCCAGGGC  77770    G       AA_
                                TCC TCCCCGTTCC  GGC
                                ||| ||||||||||  |||
                                AGG AGGGGTAGGG  CCG
                                  A        GTC
GAM3460 CEACAM4  3' TCCTTCCCCGTCCCCAGGGC  77771    G       AA_
                                TCC TCCCCGTTCC  GGC
                                ||| ||||||||||  |||
                                AGG AGGGGCAGGG  CCG
                                  A        GTC
GAM3460 CSEN     3' GCCCCAAGGCCAAGGCCG   77772   T    TT_
                                G CCCCG  CCAAGGCCG
                                | |||||  |||||||||
                                C GGGGT  GGTTCCGGC
                                _    TCC
GAM3460 CXorf9   5' TCCGTCCCTGCTCTCCTAG   77773       C __  A
                                TCCGTCCC GT  TCC AG
                                |||||||| ||  ||| ||
                                AGGCAGGG CG  AGG TC
                                     A  AG   A
GAM3460 FLJ10297 5' CCGTCCCCGCTCAGGC     77774         CA
                                CCGTCCCCGTTC  AGGC
                                ||||||||||||  ||||
                                GGCAGGGGCGAG  TCCG
                                          __
GAM3460 FLJ10769 3' TCCGGTCTGCCCTGCTGGGGCC 77775     _ __  _  CCAA
           G                     TCCG TC  CCC GTT   GGCCG
                                |||| ||  ||| |||   |||||
                                AGGC AG  GGG CGA   CCGGC
                                  C  AC   A  CC__
GAM3460 FLJ21839 5' TCCCTCTCCCGCTAGCGAGGCC 77776    G  _    CCA_
           G                     TCC TC CCCGTT   AGGCCG
                                ||| || ||||||   ||||||
                                AGG AG GGGCGA   TCCGGC
                                  G  A    TCGC
GAM3460 KIAA0513 3' TCCCTCCCCGTCCCTGAGGC  77777    G       A_
                                TCC TCCCCGTTCC  AGGC
                                ||| ||||||||||  ||||
                                AGG AGGGGCAGGG  TCCG
                                  G        AC
GAM3460 KIAA0528 5' TCCGTCCCGGCCCCACAAGGC  77778       C    __
                                TCCGTCCC GTTCCA  AGGC
                                |||||||| ||||||  ||||
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                                AGGCAGGG CGGGGT  TCCG
                                    C     GT
GAM3460 KIAA0767 3' GTCCCCATTCGGGAAAGGCCG 77779        C___
                                GTCCCCGTTC   AAGGCCG
                                ||||||||||   |||||||
                                CAGGGGTAAG   TTCCGGC
                                     CCCT
GAM3460 KIAA0774 5' TCCCTTCCCTCCAAGGC    77780    G_   CGT
                                TCC  TCCC   TCCAAGGC
                                |||  ||||   ||||||||
                                AGG  AGGG   AGGTTCCG
                                  GA   ___
GAM3460 KIAA1196 3' TCCGTCCCTACTCCACGAGGC 77781       CG   __
                                TCCGTCCC  TTCCA  AGGC
                                ||||||||  |||||  ||||
                                AGGCAGGG  GAGGT  TCCG
                                     AT    GC
GAM3460 KIAA1458 5' TCCGCCCCCCGCGGGCCG   77782       _ TCCAA
                                TCCGTCCCC GT    GGCCG
                                ||||||||| ||    |||||
                                AGGCGGGGG CG    CCGGC
                                     G  C____
GAM3460 LASP1    3' TCCCTCCCCATCCCCGAGGC  77783    G       A_
                                TCC TCCCCGTTCC  AGGC
                                ||| ||||||||||  ||||
                                AGG AGGGGTAGGG  TCCG
                                  G        GC
GAM3460 MAPKAPK5 5' CCTGTCCCCGCGCGGCCG   77784   _      TCCAA
                                CC GTCCCCGT    GGCCG
                                || ||||||||    |||||
                                GG CAGGGGCG    CCGGC
                                 A       CG___
GAM3460 MAPKAPK5 5' CCTGTCCCCGCGCGGCCG   77784   _      TCCAA
                                CC GTCCCCGT    GGCCG
                                || ||||||||    |||||
                                GG CAGGGGCG    CCGGC
                                 A       CG___
GAM3460 MGC15396 5' TCCGCTCCCTCCCGCGGGCCG 77785    TC  G   AA_
                                TCCG  CCC TTCC   GGCCG
                                ||||  ||| ||||   |||||
                                AGGC  GGG AGGG   CCGGC
                                  GA   _   CGC
GAM3460 MGC19825 5' GCCCCGTTCCAGGGCCG    77786   T       A
                                G CCCCGTTCCA GGCCG
                                | ||||||||| |||||
                                C GGGGCAAGGT CCGGC
                                 _        C
GAM3460 MGC4701  5' TCCGCGGCCCCAAGGCCG   77787     CCCC
                                TCCGT   GTTCCAAGGCCG
                                |||||   ||||||||||||
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                                AGGCG   CGGGGTTCCGGC
                                  C___
GAM3460 MGC9564  3' TCCCTCCTTCCCAAGGC    77788    G  CCG
                                TCC TCC  TTCCAAGGC
                                ||| |||  |||||||||
                                AGG AGG  AGGGTTCCG
                                  G  A__
GAM3460 MO25     5' GTCCCCGTCCTCGGCCG    77789        CAA
                                GTCCCCGTTC  GGCCG
                                ||||||||||  |||||
                                CAGGGGCAGG  CCGGC
                                     AG_
GAM3460 ZNF364   5' CCCGTCCCTCGCCAGGCCG   77790       _   CCA
                                TCCGTCCC CGTT  AGGCCG
                                |||||||| ||||  ||||||
                                GGGCAGGG GCGG  TCCGGC
                                   A   ___
GAM3460 LOC144347 3' CCGTCCCCACCGGCTGAGGC  77791        TT  A____
                                CCGTCCCCG  CC    AGGC
                                |||||||||  ||    ||||
                                GGCAGGGGT  GG    TCCG
                                     __ CCGAC
GAM3460 LOC162048 5' CCTGTCCCCGTTCCCTCTCC  77792   _        AAGG
                                CC GTCCCCGTTCC   CC
                                || ||||||||||   ||
                                GG CAGGGGCAAGG   GG
                                 A         GAGA
GAM3460 LOC196214 5' TCCGTCCCCCCAGGAGGC    77793        GTT  __
                                TCCGTCCCC  CCA  AGGC
                                |||||||||  |||  ||||
                                AGGCAGGGG  GGT  TCCG
                                     ___  CC
GAM3460 LOC199800 5' CCCGTTCCCGCACCGGGC    77794      C    T  AA
                                TCCGT CCCGT CC  GGC
                                ||||| ||||| ||  |||
                                GGGCA GGGCG GG  CCG
                                   A    T  C_
GAM3460 LOC219513 5' TCCCTCCCCGCTCCGGGCCG  77795    G        AA
                                TCC TCCCCGTTCC  GGCCG
                                ||| ||||||||||  |||||
                                AGG AGGGGCGAGG  CCGGC
                                  G        C_
GAM3460 LOC221424 5' TCCTTCCCCGTTCCTAAG    77796    G        _
                                TCC TCCCCGTTCC AAG
                                ||| |||||||||| |||
                                AGG AGGGGCAAGG TTC
                                  A        A
GAM3460 LOC51177  5' TCCGGTTTCACTCAAGGCCG  77797     TCCC    C
                                TCCG   CGTTC AAGGCCG
                                ||||   ||||| |||||||
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                                AGGC    GTGAG TTCCGGC
                                  CAAA    _
GAM3460  LOC90520  3'  TCAGTCCTGATCCCAAGGC   77798    C   CC
                                TC GTCC  GTTCCAAGGC
                                || ||||  ||||||||||
                                AG CAGG  TAGGGTTCCG
                                 T   AC
GAM3461  BACE      3'  ATACTAGGAAAACCCAGCTC  77801      TTA      A
                                ATATT   AAAACCCA CTC
                                |||||   |||||||| |||
                                TATGA   TTTTGGGT GAG
                                   TCC      C
GAM3461  BACE      3'  ATACTAGGAAAACCCAGCTC  77801      TTA      A
                                ATATT   AAAACCCA CTC
                                |||||   |||||||| |||
                                TATGA   TTTTGGGT GAG
                                   TCC      C
GAM3461  DISC1     3'  TTCACATTTTACCAGCTC    77802         AAAAC   A
                                TTCATATTTTA    CCA CTC
                                ||||||||||    ||| |||
                                AAGTGTAAAAT    GGT GAG
                                      _____  C
GAM3461  FGF13     3'  TATGCCAAGAACCCAACT    77803     T   A
                                TAT TTAA AACCCAACT
                                ||| |||| |||||||||
                                ATA GGTT TTGGGTTGA
                                  C   C
GAM3461  HTR2C     3'  TTCACATTCTAAGGGCCCAATT 77804          AAA    C
            C                    TTCATATTTTAA   CCCAA TC
                                ||||||||||||   ||||| ||
                                AAGTGTAAGATT   GGGTT AG
                                      CCC    A
GAM3461  SART2     3'  ATATTAATAAAACCCAATTC  77805      TTA      C
                                ATATT   AAAACCCAA TC
                                |||||   ||||||||| ||
                                TATAA   TTTTGGGTT AG
                                   TTA       A
GAM3461  SGNE1     3'  TTCACATTTTAAAAACCC    77806
                                TTCATATTTTAAAAACCC
                                ||||||||||||||||||
                                AAGTGTAAAATTTTTGGG

GAM3461  DKFZP564D1378 3'  ATAATTTAAAAACCACCATTCA 77807     T       _____
            ACT                   ATA TTTAAAAACC     CAACT
                                ||| ||||||||||     |||||
                                TAT AAATTTTTGG     GTTGA
                                  T        TGGTAA
GAM3461  FLJ20972  3'  TTCATATTGTTGAAACCCTAAT 77808        TTAA    _ C
            TCC                   TTCATATT    AAACCC AA TCC
                                ||||||||    |||||| || |||
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                                AAGTATAA    TTTGGG TT AGG
                                     CAAC     A  A
GAM3461  KIAA0459  3'  TTCACATCCACCTAACTC    77809         TAAAA   C
                                TTCATATTT    ACC AACTC
                                |||||||||    ||| |||||
                                AAGTGTAGG    TGG TTGAG
                                     _____   A
GAM3461  KIAA1348  3'  TATTTTTGCCCCAACTCC    77810       AAAAA
                                TATTTT    CCCAACTCC
                                ||||||    |||||||||
                                ATAAAA    GGGTTGAGG
                                   ACG__
GAM3461  TCFL5     3'  CTCATTGAAAAACCCAATTCC  77811       ATTTT        C
                                TTCAT    AAAAACCCAA TCC
                                |||||    |||||||||| |||
                                GAGTA    TTTTTGGGTT AGG
                                   AC___        A
GAM3461  LOC127281 3'  CTCTGCCCTGAAAACCCAACTC 77812     ATA    A
                                TTC   TTTT AAAACCCAACTC
                                |||   |||| ||||||||||||
                                GAG   GGGA TTTTGGGTTGAG
                                  AC_   C
GAM3461  LOC170384 3'  TATAAAAAAATCCAACTC    77813     TTT    C
                                TAT   AAAAA CCAACTC
                                |||   ||||| |||||||
                                ATA   TTTTT GGTTGAG
                                  TT_    A
GAM3461  LOC201562 3'  TTCACATTTTCATCCAACTC   77814         AAAAAC
                                TTCATATTTT     CCAACTC
                                ||||||||||     |||||||
                                AAGTGTAAAA     GGTTGAG
                                     GTA___
GAM3461  LOC255082 3'  TATTTTAAAAACCGACACC    77815           CA_
                                TATTTTAAAAACC   ACT
                                ||||||||||||   |||
                                ATAAAATTTTTGG   TGG
                                       CTG
GAM3461  LOC256730 3'  TTCATTTTTAAAAACCCACTC  77816      A          A
                                TTCAT TTTTAAAAACCCA CTC
                                ||||| ||||||||||||| |||
                                AAGTA AAAATTTTTGGGT GAG
                                   _          _
GAM3461  LOC91351  3'  TTCATATTTTCTAGCATCCAAC 77817         AAAAAC_
            T                   TTCATATTTT      CCAACT
                                ||||||||||      ||||||
                                AAGTATAAAA      GGTTGA
                                     GATCGTA
GAM3462  ALS2      3'  ACACAGCCTGCATGCAAAACTT 77820        _____   C   CCG
            CC                    ACACAGCC    GCA AAC   CC
                                ||||||||    ||| |||   ||
```

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                                TGTGTCGG    CGT TTG   GG
                                    ACGTA   T   AA_
GAM3462  ATF4     5'  CACAGCTGGACGACCCGCCCC  77821       CGC  A
                                CACAGC   AC ACCCGCCCC
                                ||||||   || |||||||||
                                GTGTCG   TG TGGGCGGGG
                                   ACC  C
GAM3462  BRCA1    3'  ACACAGCTGTACCATCCATTCC 77822        C__  A  A  CG_
                                ACACAGC   GC CA CC   CC
                                |||||||   || || ||   ||
                                TGTGTCG   TG GT GG   GG
                                   ACA  _  A  TAA
GAM3462  BRCA1    3'  ACACAGCTGTACCATCCATTCC 77822        C__  A  A  CG_
                                ACACAGC   GC CA CC   CC
                                |||||||   || || ||   ||
                                TGTGTCG   TG GT GG   GG
                                   ACA  _  A  TAA
GAM3462  CALM2    5'  ACACAACCACTCAGCTCGC    77823         A  ACC
                                ACACAGCCGC CA   CGC
                                |||||||||| ||   |||
                                TGTGTTGGTG GT   GCG
                                    A  CGA
GAM3462  CCNT2    3'  ACAGTAGCACAACCACC     77824      CC       C
                                ACAG  GCACAACC GCC
                                ||||  |||||||| |||
                                TGTC  CGTGTTGG TGG
                                  AT       _
GAM3462  CSNK1G2  3'  CAGCGCCCACCCGCCCC     77825      C  ACA
                                CAGC GC   ACCCGCCCC
                                |||| ||   |||||||||
                                GTCG CG   TGGGCGGGG
                                  _  GG_
GAM3462  DAAM2    3'  ACACACACACCGCCCGCCCCC  77826      GC    AA
                                ACACA  CGCAC  CCCGCCCCC
                                |||||  |||||  |||||||||
                                TGTGT  GTGTG  GGGCGGGGG
                                   __    GC
GAM3462  DHFR     5'  CAGGCGAGGCCCCGCCCCCC   77827     C  CACAA
                                CAG CG    CCCGCCCCCC
                                ||| ||    ||||||||||
                                GTC GC    GGGCGGGGGG
                                  C  TCCG_
GAM3462  DXYS155E 3'  ACACAGCCGGACGACACG    77828         C  A  C
                                ACACAGCCG AC AC CG
                                ||||||||| || || ||
                                TGTGTCGGC TG TG GC
                                    C  C  T
GAM3462  EPHB6    5'  ACGCAGCCCGGCCCGCCCCC   77829    A    GCACAA
                                AC CAGCC     CCCGCCCCC
                                || |||||     |||||||||
```

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                                TG GTCGG     GGGCGGGGG
                                 C    GCC___
GAM3462  EXTL1    3'  ACACGACACGACCCGCCCCCC  77830      AGCC    A
                                ACAC   GCAC ACCCGCCCCCC
                                ||||   |||| ||||||||||
                                TGTG   TGTG TGGGCGGGGGG
                                  C___   C
GAM3462  FANCE    5'  CACGGGTGCCGCGCCGCCCCC  77831     A___    ACAAC
                                CAC   GCCGC    CCGCCCCC
                                |||   |||||    ||||||||
                                GTG   CGGCG    GGCGGGGG
                                  CCCA    C____
GAM3462  FKBP2    5'  ACAGCAGCCAGGGACCCGCCCC 77832     _     CACA
                                ACA CAGCCG    ACCCGCCCC
                                ||| ||||||    |||||||||
                                TGT GTCGGT    TGGGCGGGG
                                  C     CCC_
GAM3462  GSTM4    5'  ACCTAGCGCCAGACCCGCCCCC 77833    AC   C  A  _
                                AC  AGC GC CA ACCCGCCCCC
                                ||  ||| || || ||||||||||
                                TG  TCG CG GT TGGGCGGGGG
                                 GA   _  _  C
GAM3462  HHIP     5'  ACACAGCCTCTCATGTTTCGTT 77834        GCA  ACC__  CC
            CCC                   ACACAGCC   CA    CG  CCC
                                |||||||||   ||    ||  |||
                                TGTGTCGG   GT    GC  GGG
                                     AGA  ACAAA  AA
GAM3462  HNF3G    3'  ACACAGCCAGTACCCCGCTTCC 77835         CACAA    CC
            C                    ACACAGCCG    CCCGC  CCC
                                |||||||||    |||||  |||
                                TGTGTCGGT    GGGCG  GGG
                                     CATG_    AA
GAM3462  JUND     3'  ACACAACCAACGTTTGTTCCCC 77836         C  AACCCG_
                                ACACAGCCG AC      CCCC
                                |||||||||  ||      ||||
                                TGTGTTGGT TG      GGGG
                                     _  CAAACAA
GAM3462  KDR      3'  ACACAGCTTCACATTGAACCTC 77837        CG    ACCC   _
            CC                    ACACAGC  CACA    GCC CCC
                                |||||||  ||||    ||| |||
                                TGTGTCG  GTGT    TGG GGG
                                    AA    AACT   A
GAM3462  MADH6    3'  GCCGCGGCCTCCCACCCGCCC  77838      ACAA_     _
                                GCCGC    CCCGCCC CCC
                                |||||    ||||||| |||
                                CGGCG    GGGTGGG GGG
                                   CCGGA      C
GAM3462  MADH7    3'  ACACAGCCGCACACTCAC    77839           A C
                                ACACAGCCGCACA C CGC
                                |||||||||||| | |||
```

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                                TGTGTCGGCGTGT G GTG
                                      _ A
GAM3462  MAT2A    3'  CAGCCGCACCAGCTCTGCCCTC 77840        AACCC__   _
              C                  CAGCCGCAC      GCCC CC
                                 |||||||||      |||| ||
                                 GTCGGCGTG      CGGG GG
                                     GTCGAGA    A
GAM3462  MSL3L1   3'  CACAGCTGCAGCCTCCC     77841       C   CAACCC  _
                                 CACAGC GCA     GCC CCC
                                 |||||| |||     ||| |||
                                 GTGTCG CGT     CGG GGG
                                    A  ______   A
GAM3462  MXI1     5'  CAGCGCCGGGGCCCGCCCCC   77842     C  ACAA_
                                 CAGC GC    CCCGCCCCC
                                 |||| ||    |||||||||
                                 GTCG CG    GGGCGGGGG
                                   _ GCCCC
GAM3462  MYCL2    5'  CACCGAGCGCGCGACCCGCCC  77843    __  _  ACA
                                 CAC  AGC CGC   ACCCGCCC
                                 |||  ||| |||   ||||||||
                                 GTG  TCG GCG   TGGGCGGG
                                   GC   C   C__
GAM3462  NRAS     5'  CAGCCGCACCCAGACCCGCCCC 77844        A___
                                 CAGCCGCAC    ACCCGCCCC
                                 |||||||||    |||||||||
                                 GTCGGCGTG    TGGGCGGGG
                                     GGTC
GAM3462  PTPN23   5'  ACGAGCCCAGCCCCGCCCC   77845   _   G  CAA
                                 AC AGCC CA   CCCGCCCC
                                 || |||| ||   ||||||||
                                 TG TCGG GT   GGGCGGGG
                                  C   _ CG_
GAM3462  PTPRK    5'  GGACAGCCGCCCGCCCGCCC  77846   C       ACAA
                                 A ACAGCCGC    CCCGCCC
                                 | ||||||||    |||||||
                                 C TGTCGGCG    GGGCGGG
                                  C       GGC_
GAM3462  RAP1GA1  3'  CACAGCCGGCTCCCTGCCCC  77847        CACAA  _
                                 CACAGCCG    CCC GCCCC
                                 ||||||||    ||| |||||
                                 GTGTCGGC    GGG CGGGG
                                     CGA__   A
GAM3462  RPP30    5'  CAGCCGCTGAGCCCGCCCC   77848       ACAA
                                 CAGCCGC    CCCGCCCC
                                 |||||||    ||||||||
                                 GTCGGCG    GGGCGGGG
                                     ACTC
GAM3462  SLC16A2  3'  ACACAGCCTGGCAGTGCCC   77849        __  CAACCC
                                 ACACAGCC  GCA     GCCC
                                 ||||||||  |||     ||||
```

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                                TGTGTCGG CGT     CGGG
                                    AC   CA____
GAM3462 SMARCD1   5' CAGCAGCCGCGCCCGCCCC   77850   _     ACAA
                                CA CAGCCGC   CCCGCCCC
                                || |||||||   ||||||||
                                GT GTCGGCG   GGGCGGGG
                                 C      C___
GAM3462 SMARCD1   5' CAGCAGCCGCGCCCGCCCC   77850   _     ACAA
                                CA CAGCCGC   CCCGCCCC
                                || |||||||   ||||||||
                                GT GTCGGCG   GGGCGGGG
                                 C      C___
GAM3462 SOX12    3' ACCCGGCCGCATCGCCCCC   77851    ACA     CAACC
                                AC   GCCGCA    CGCCCCC
                                ||   ||||||    |||||||
                                TG   CGGCGT    GCGGGGG
                                 GGC     A____
GAM3462 SPG4     5' GCCGCCATAACCCGCCTCCC   77852      AC_      _
                                GCCGC   AACCCGCC CCC
                                |||||   |||||||| |||
                                CGGCG   TTGGGCGG GGG
                                   GTA       A
GAM3462 TBL1X    5' CAGCCGCGCGCCGCCCCC    77853       ACAAC
                                CAGCCGC    CCGCCCCC
                                |||||||    ||||||||
                                GTCGGCG    GGCGGGGG
                                    CGC__
GAM3462 TPD52L2  3' CAACACCCGCACAACCTGCC   77854   C   G       C
                                A ACA CCGCACAACC GCC
                                | ||| |||||||||| |||
                                G TGT GGCGTGTTGG CGG
                                 T   G        A
GAM3462 TSG101   5' ACACAATCGCACACCCC     77855      GC     AACCC
                                ACACA  CGCAC    GCCCC
                                |||||  |||||    |||||
                                TGTGT  GCGTG    TGGGG
                                   TA    _____
GAM3462 VENTX2   3' ACGCAGCCGCAGGACCACGC   77856    A      CA   _
                                AC CAGCCGCA  ACC CGC
                                || ||||||||  ||| |||
                                TG GTCGGCGT  TGG GCG
                                 C       CC   T
GAM3462 ZAP70    3' CACAGCCGCACCCTCCC     77857        ACA    G
                                CACAGCCGC   ACCC CCC
                                |||||||||   |||| |||
                                GTGTCGGCG   TGGG GGG
                                     ___    A
GAM3462 ALY      3' CACAGCCCCAGCCACCGCCCCC 77858       G  CAAC
             C                   CACAGCC CA    CCGCCCCCC
                                |||||||  ||    |||||||||
```

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                                GTGTCGG GT    GGCGGGGGG
                                    G  CGGT
GAM3462  AP1M2    3'  ACACAGCCCGCACCTGCCCTCC 77859         _    AACCC    _
                                ACACAGCC GCAC     GCCC CC
                                |||||||| ||||     |||| ||
                                TGTGTCGG CGTG     CGGG GG
                                    G    GA___    A
GAM3462  Apg4B    3'  ACACAGCGGTGGGCGCGCCCCC 77860        CGCACAACC
              C                  ACACAGC        CGCCCCCC
                                |||||||        ||||||||
                                TGTGTCG        GCGGGGGG
                                    CCACCCGC_
GAM3462  ARHGEF15  3'  CAGCCACACCCGCTCTCC    77861        ACA     CC_
                                CAGCCGC   ACCCGC   CC
                                |||||||   ||||||   ||
                                GTCGGTG   TGGGCG   GG
                                    ___      AGA
GAM3462  BDG-29    3'  ACAGAGCCGCGCTGTCGCCGTC 77862     C     ACAAC__   _
              CCCC                  ACA AGCCGC      CCG CCCCC
                                ||| ||||||      ||| |||||
                                TGT TCGGCG      GGC GGGGG
                                  C     CGACAGC   A
GAM3462  C8orf13   5'  AGCCGCACAGGGCGCCCTCC   77863         ACC    _
                                AGCCGCACA   CGCCC CC
                                |||||||||   ||||| ||
                                TCGGCGTGT   GCGGG GG
                                     CCC    A
GAM3462  caspr5    5'  ACAGCCGCTAGCTGGACTCGCC 77864         ACA____  C    CC
              TTCC                  ACAGCCGC      AC CGCC  CC
                                ||||||||      || ||||  ||
                                TGTCGGCG      TG GCGG  GG
                                     ATCGACC  A    AA
GAM3462  caspr5    5'  ACAGCCGCTAGCTGGACTCGCC 77864         ACA____  C    CC
              TTCC                  ACAGCCGC      AC CGCC  CC
                                ||||||||      || ||||  ||
                                TGTCGGCG      TG GCGG  GG
                                     ATCGACC  A    AA
GAM3462  CBLN1     5'  GCCGGCCCACCCCGCCCCC    77865      _ A  A
                                GCCG C CA CCCGCCCCC
                                |||| | || |||||||||
                                CGGC G GT GGGCGGGGG
                                  C G  G
GAM3462  CTDP1     3'  AACACACCAACCCGCCCC     77866     _   A
                                AGC CGC CAACCCGCCCC
                                ||| ||| ||||||||||
                                TTG GTG GTTGGGCGGGG
                                  T   _
GAM3462  DCTD      3'  CACAGCCACACGCTCCCC     77867          AACCC  _
                                CACAGCCGCAC     GC CCCC
                                ||||||||||     || ||||
```

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                                GTGTCGGTGTG    CG GGGG
                                      _____ A
GAM3462 DHRS2    3' ACGCAGCCGCCCCCACTCC   77868    A     ACAA    C
                                AC CAGCCGC   CCCGC CC
                                || |||||||   ||||| ||
                                TG GTCGGCG   GGGTG GG
                                 C      G___    A
GAM3462 DKFZp547A023 5' ACAGCGGCTGAGGCTCCGCCCC 77869      C  ACAAC__
          C                      ACAGC GC      CCGCCCCC
                                 ||||| ||      ||||||||
                                 TGTCG CG      GGCGGGGG
                                   C  ACTCCGA
GAM3462 DKFZp762K222 5' CAGCCGCACGGCCCGCAGTCCC 77870         AA    ___
          C                      CAGCCGCAC  CCCGC   CCCC
                                 |||||||||  |||||   ||||
                                 GTCGGCGTG  GGGCG   GGGG
                                      CC    TCA
GAM3462 FLJ10035  3' ACATGCTTCGCCCTCCGCCCCC 77871    _ __   ACAAC
                                 ACA GC  CGC    CCGCCCCC
                                 ||| ||  |||    ||||||||
                                 TGT CG  GCG    GGCGGGGG
                                   A  AA   GGA__
GAM3462 FLJ10477  5' CACAGCCATCGCCCGTCTCCC  77872        CACAA   CC_
                                 CACAGCCG    CCCG   CCC
                                 ||||||||    ||||   |||
                                 GTGTCGGT    GGGC   GGG
                                      AGC__    AGA
GAM3462 FLJ10493  5' CACAGCCGCGGCCGCCCGCTCC 77873         ACAA_    C
                                 CACAGCCGC    CCCGC CC
                                 |||||||||    ||||| ||
                                 GTGTCGGCG    GGGCG GG
                                      CCGGC    A
GAM3462 FLJ11181  3' CAGCCGCACTCCAGCCCC    77874         AA  C
                                 CAGCCGCAC  CC GCCCC
                                 |||||||||  || |||||
                                 GTCGGCGTG  GG CGGGG
                                      A_  T
GAM3462 FLJ13265  3' CAGCCGCACGACGACCC     77875         A  CC
                                 CAGCCGCAC AC  GCCC
                                 |||||||||  ||  ||||
                                 GTCGGCGTG TG  TGGG
                                      C  C_
GAM3462 FLJ14356  5' ACAGCCGCACAATCATTTCCC  77876          CCCG__
                                 ACAGCCGCACAA     CCC
                                 ||||||||||||     |||
                                 TGTCGGCGTGTT     GGG
                                       AGTAAA
GAM3462 FLJ14566  5' ACGCAGCCGCACATGCTTCC   77877    A        ACCC  CC
                                 AC CAGCCGCACA    GC  CC
                                 || ||||||||||    ||  ||
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                                TG GTCGGCGTGT   CG  GG
                                 C        A___  AA
GAM3462  FLJ20457  5'  GCCGCCACCCCCGCCCTCC   77878      A  A_     _
                                GCCGC CA  CCCGCCC CC
                                ||||| ||  ||||||| ||
                                CGGCG GT  GGGCGGG GG
                                   _ GG      A
GAM3462  FLJ23093  5'  ACAGCCGCGCAGGCGCTCTCC  77879        A  ACC   CC_
                                ACAGCCGC CA   CGC   CC
                                |||||||| ||   |||   ||
                                TGTCGGCG GT   GCG   GG
                                     C  CC_   AGA
GAM3462  FLJ23323  3'  CACAGCCGTGGTGCCAGCCTCC 77880        CACAA  C   C
                                CACAGCCG    CC GCC CC
                                ||||||||    || ||| ||
                                GTGTCGGC    GG CGG GG
                                     ACCAC  T   A
GAM3462  FOXH1     3'  ACAGCCGCCTCCCTTGCTCCC  77881        ACAA  __  C
                                ACAGCCGC    CCC  GC CCC
                                ||||||||    |||  || |||
                                TGTCGGCG    GGG  CG GGG
                                     GA__   AA  A
GAM3462  FOXO3A    5'  GCAGCAGACACCGCCCCCC   77882    C   CA  _
                                GC GCA  AC CCGCCCCCC
                                || |||  || |||||||||
                                CG CGT  TG GGCGGGGGG
                                 T   C_  T
GAM3462  FREQ      5'  GCCGCGGCCCCCGCCCCCC   77883      ACAA
                                GCCGC    CCCGCCCCCC
                                |||||    ||||||||||
                                CGGCG    GGGCGGGGGG
                                   CCGG
GAM3462  HNT       5'  CAGCCGCACGGCACACGCCCCC 77884        A__  C
              C                  CAGCCGCAC   AC CGCCCCCC
                                 |||||||||   || ||||||||
                                 GTCGGCGTG   TG GCGGGGGG
                                      CCG  T
GAM3462  KIAA0255  3'  ACAGGCCCTCCCGCCCCC    77885     CC  ACAA
                                ACAG  GC    CCCGCCCCC
                                ||||  ||    |||||||||
                                TGTC  CG    GGGCGGGGG
                                   __  GGA_
GAM3462  KIAA0537  5'  CACGGTCCGCGCACCGCCCCCC 77886     AG_   A  AC
                                CAC   CCGC CA  CCGCCCCCC
                                |||   ||||  ||  |||||||||
                                GTG   GGCG GT  GGCGGGGGG
                                  CCA    C  __
GAM3462  KIAA0964  3'  ACACCGCCGCCCGCCCC     77887      A     ACAAC
                                ACAC GCCGC    CCGCCCC
                                |||| |||||    |||||||
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                                TGTG CGGCG    GGCGGGG
                                  G   _____
GAM3462 KIAA1878 3' CACAGCCAGCGGCAACGCTTCC 77888       _ A_   CC  CC
                                CACAGCC GC  CAAC  GC  CC
                                ||||||| ||  ||||  ||  ||
                                GTGTCGG CG  GTTG  CG  GG
                                    T  CC   __  AA
GAM3462 KIAA1938 5' CACAGCCGGGCAACCTCC    77889        CA    CG
                                CACAGCCG  CAACC  CC
                                ||||||||  |||||  ||
                                GTGTCGGC  GTTGG  GG
                                    CC    A_
GAM3462 LSR68    5' CACAGCCGTCATTACTGTCCTC 77890        _ CA  CCG  C
            C                    CACAGCCG CA  AC   CC CC
                                ||||||||  ||  ||   || ||
                                GTGTCGGC GT  TG   GG GG
                                    A  AA  ACA  A
GAM3462 MCM10    3' ACACAGCCAATCCTTTGCTTTC 77891        CACAA  C__  CC_
            C                    ACACAGCCG    CC   GC   CC
                                |||||||||    ||   ||   ||
                                TGTGTCGGT    GG   CG   GG
                                    TA___  AAA  AAA
GAM3462 MGC10814 5' CACAGCCACCTCTGCCTCCC   77892        ACAACCC   _
                                CACAGCCGC      GCC CCC
                                |||||||||      ||| |||
                                GTGTCGGTG      CGG GGG
                                    GAGA___   A
GAM3462 MGC16037 5' CAGCCCCGCCCCCGCCCCCC   77893      GCACAA
                                CAGCC     CCCGCCCCCC
                                |||||     ||||||||||
                                GTCGG     GGGCGGGGGG
                                  GGCGG_
GAM3462 MGC22793 5' ACACAGCCTGGCTGCCGCCTCC 77894        GCACAAC    C
                                ACACAGCC      CCGCC CC
                                ||||||||      ||||| ||
                                TGTGTCGG      GGCGG GG
                                    ACCGAC_    A
GAM3462 MR       5' ACACCGCCAGCACCCCGCCCC  77895     A  _   AA
                                ACAC GCC GCAC  CCCGCCCC
                                |||| ||| ||||  ||||||||
                                TGTG CGG CGTG  GGGCGGGG
                                  G   T   __
GAM3462 MY014    5' AGCCGTACCCCCGCCCCC    77896      C  AA
                                AGCCG AC  CCCGCCCCC
                                ||||| ||  |||||||||
                                TCGGC TG  GGGCGGGGG
                                  A  G_
GAM3462 NIN      5' CACAGCCGGCAGCCCGCCTCC  77897        CA  A     C
                                CACAGCCG  CA CCCGCC CC
                                ||||||||  || |||||| ||
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                                GTGTCGGC  GT GGGCGG GG
                                    C_ C     A
GAM3462  NYD-TSPG  5'  CAGCAGCTGCAGCGCCCCCC  77898   _   C   CAACC
                                CA CAGC GCA    CGCCCCCC
                                || |||| |||    ||||||||
                                GT GTCG CGT    GCGGGGGG
                                 C   A  C____
GAM3462  OSBPL1A   5'  GCCGCAGACCCGCCCTCC    77899      CA      _
                                GCCGCA  ACCCGCCC CC
                                ||||||  |||||||| ||
                                CGGCGT  TGGGCGGG GG
                                   C_      A
GAM3462  PTPN3     3'  ACACAGCCCCACGGCCAACCCT 77900       G   AA  C   _
             CC                   ACACAGCC CAC  CC GCCC CC
                                ||||||||| |||  || |||| ||
                                TGTGTCGG GTG  GG TGGG GG
                                     G   CC  T   A
GAM3462  SEMA5A    5'  CAGCAGCTGCAGCCGCCCCC  77901   _   C   CAAC
                                CA CAGC GCA   CCGCCCCC
                                || |||| |||   ||||||||
                                GT GTCG CGT   GGCGGGGG
                                 C   A  C___
GAM3462  VPS45A    5'  ACAGCCCTTCCCGCCCCC    77902      GCACAA
                                ACAGCC    CCCGCCCCC
                                ||||||    |||||||||
                                TGTCGG    GGGCGGGGG
                                   GAA___
GAM3462  LOC113201 5'  CAGGTCCCTCCCCGCCCCCC  77903    ___  GCACAA
                                CAG   CC    CCCGCCCCCC
                                |||   ||    ||||||||||
                                GTC   GG    GGGCGGGGGG
                                  CAG  AG____
GAM3462  LOC124369 3'  ACACAGCCTGCAGCTCCCC   77904       _   CAACCC  _
                                ACACAGCC GCA    GC CCCC
                                |||||||| |||    || ||||
                                TGTGTCGG CGT    CG GGGG
                                     A  ______  A
GAM3462  LOC127428 3'  CACAAATAACACAGCCTGCTTT 77905     CC_    A  C  CC_
             CC                   CACAG   GCACA CC GC   CC
                                |||||   ||||| || ||   ||
                                GTGTT   TGTGT GG CG   GG
                                   TAT    C  A  AAA
GAM3462  LOC130595 5'  GAACAGCCGCCGCCCC     77906   C      ACAACC
                                A ACAGCCGC     CGCCCC
                                | ||||||||     ||||||
                                C TGTCGGCG     GCGGGG
                                 T      _______
GAM3462  LOC130888 3'  ACACAGCCATGCCTGAGCTCCC 77907        CACAA  C__  C
                                ACACAGCCG    CC   GC CCC
                                |||||||||    ||   || |||
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                                TGTGTCGGT    GG   CG GGG
                                     AC___  ACT  A
GAM3462  LOC132422 5'  ACAGCGGTCAGGGACCCGCCCC 77908      CG_  CA_
              CC                   ACAGC   CA   ACCCGCCCCCC
                                   |||||   ||   ||||||||||
                                   TGTCG   GT   TGGGCGGGGGG
                                     CCA  CCC
GAM3462  LOC138128 5'  CAGCCGCCACCCCCCGCCTTCC 77909       _  AA     CC
                                   CAGCCGC AC  CCCGCC  CC
                                   |||||||  ||  ||||||  ||
                                   GTCGGCG TG  GGGCGG  GG
                                       G  GG     AA
GAM3462  LOC146227 3'  CACAGCGCACAACGGAACC   77910       C      CC_
                                   CACAGC GCACAAC   GCC
                                   ||||||  |||||||   |||
                                   GTGTCG CGTGTTG   TGG
                                      _      CCT
GAM3462  LOC147965 5'  CAGCCGCACGCACAGCCCCC   77911         A_  CC
                                   CAGCCGCAC  AC  GCCCCC
                                   |||||||||  ||  ||||||
                                   GTCGGCGTG  TG  CGGGGG
                                        CG  T_
GAM3462  LOC148089 3'  ACACAGCCTCATCCAATTCTCC 77912         G  __   CCCG
                                   ACACAGCC CA  CAA    CC
                                   ||||||||  ||  |||    ||
                                   TGTGTCGG GT  GTT    GG
                                        A  AG   AAGA
GAM3462  LOC150421 3'  ACACAGCCCGTGCAGCCCC   77913         ___   CAACCC
                                   ACACAGCC   GCA     GCCCC
                                   ||||||||   |||     |||||
                                   TGTGTCGG   CGT     CGGGG
                                        GCA  _______
GAM3462  LOC151963 5'  GCGGCACCCACCCCCGCCCCCC 77914    C    AA___
                                   GC GCAC    CCCGCCCCCC
                                   || ||||    ||||||||||
                                   CG CGTG    GGGCGGGGGG
                                    C   GGTGG
GAM3462  LOC154790 5'  GCTCGGCCCTGCCCGCCCCCC  77915    _  _ ACAA
                                   GC CG C    CCCGCCCCCC
                                   || || |    ||||||||||
                                   CG GC G    GGGCGGGGGG
                                    A  C GGAC
GAM3462  LOC162333 5'  ACACAGCCGCAAGGCTCC     77916          CAACCC  C
                                   ACACAGCCGCA      GC CC
                                   ||||||||||      || ||
                                   TGTGTCGGCGT      CG GG
                                          TC_____  A
GAM3462  LOC200531 5'  CAGCCGCAACGGACTCTGCCCT 77917         _ A_  CC_   _
              CC                   CAGCCGCA C  AC   GCCC CC
                                   ||||||||  |  ||   |||| ||
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                                GTCGGCGT G  TG   CGGG GG
                                     T CC  AGA    A
GAM3462  LOC201707 5'  CACGCCCCGCCTCCGCCCCC  77918     AG_   ACAAC
                                CAC   CCGC    CCGCCCCC
                                |||   ||||    ||||||||
                                GTG   GGCG    GGCGGGGG
                                  CGG   GA___
GAM3462  LOC203392 5'  CAGCCCTGCGCACCCCCC    77920      __  ACAACC
                                CAGCC  GC     CGCCCCCC
                                |||||  ||     ||||||||
                                GTCGG  CG     GTGGGGGG
                                   GA  C_____
GAM3462  LOC203392 5'  ACACACCGCACACCGAGGTTCG 77919      G      A _______
              CC                   ACACA CCGCACA CC     CGCC
                                |||||| ||||||| ||     ||||
                                TGTGT GGCGTGT GG     GCGG
                                  _      _  CTCCAA
GAM3462  LOC219397 3'  CAGCGCCGACCCGCCCC     77921      C  ACA
                                CAGC GC   ACCCGCCCC
                                |||| ||   |||||||||
                                GTCG CG   TGGGCGGGG
                                  _  GC_
GAM3462  LOC219855 5'  ACGGCAGCGCCCGCCCCC    77922    A  C  ACAA
                                AC GC GC    CCCGCCCCC
                                || || ||    |||||||||
                                TG CG CG    GGGCGGGGG
                                 C  T  C___
GAM3462  LOC220073 5'  ACACAACCCCACCTGCCC    77923        G   AACCC
                                ACACAGCC CAC     GCCC
                                |||||||| |||     ||||
                                TGTGTTGG GTG     CGGG
                                     G   GA___
GAM3462  LOC253489 5'  ACAGCGGCCGCCTCGCCCCCC  77924      C  ACAA  _
                                ACAGC GC    CC CGCCCCCC
                                ||||| ||    || ||||||||
                                TGTCG CG    GG GCGGGGGG
                                   C  GC__  A
GAM3462  LOC254423 5'  ACACAGCCACTGTGTCCCCC   77925          ACAACCCG
                                ACACAGCCGC       CCCCC
                                ||||||||||       |||||
                                TGTGTCGGTG       GGGGG
                                      ACACA___
GAM3462  LOC255971 3'  ACCAGCCCCCCGCCCC      77926    A    GCACAA
                                AC CAGCC     CCCGCCCC
                                || |||||     ||||||||
                                TG GTCGG     GGGCGGGG
                                 _    G_____
GAM3462  LOC256158 5'  CAGCCGCACCTCCTGCCC     77927         AA  C
                                CAGCCGCAC  CC GCCC
                                |||||||||  || ||||
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                                GTCGGCGTG  GG CGGG
                                     GA  A
GAM3462  LOC256529 5'  CAGCCGCACAAGAACCCC    77928          CCC
                                CAGCCGCACAA   GCCCC
                                ||||||||||   |||||
                                GTCGGCGTGTT   TGGGG
                                     CT_
GAM3462  LOC257442 5'  ACGCAGGCTTCCCCGCCCCC   77929    A   CC  ACAA
                                AC CAG  GC    CCCGCCCCC
                                || |||  ||    |||||||||
                                TG GTC  CG    GGGCGGGGG
                                 C   __  AAG_
GAM3462  LOC51177  5'  CACGCCCGCTCCCCGCCCC    77930     AG    ACAA
                                CAC  CCGC    CCCGCCCC
                                |||  ||||    ||||||||
                                GTG  GGCG    GGGCGGGG
                                  CG    AG__
GAM3462  LOC90538  3'  ACACAGCCACAGGCCCCC    77931          CAACCC
                                ACACAGCCGCA     GCCCCC
                                ||||||||||      ||||||
                                TGTGTCGGTGT     CGGGGG
                                     C_____
GAM3462  LOC90906  3'  CACAGCCAGTACAACTGCAGCT 77932        C_    CC__  C
           CC                     CACAGCCG  ACAAC    GC CC
                                ||||||||  |||||    || ||
                                GTGTCGGT  TGTTG    CG GG
                                     CA     ACGT  A
GAM3462  LOC90987  5'  ACGCAGGCTTCCCCGCCCCC   77929    A   CC  ACAA
                                AC CAG  GC    CCCGCCCCC
                                || |||  ||    |||||||||
                                TG GTC  CG    GGGCGGGGG
                                 C   __  AAG_
GAM3462  LOC91156  5'  CACAGCCGCGTGTAGCCATCCC 77933         ACAAC_  _
           CC                     CACAGCCGC     CCG CCCCC
                                |||||||||      ||| |||||
                                GTGTCGGCG     GGT GGGGG
                                     CACATC   A
GAM3462  LOC91526  3'  CACAGCCAACACCCTTGCC    77934        C   A   __
                                CACAGCCG ACA CCC  GCC
                                |||||||| ||| |||  |||
                                GTGTCGGT TGT GGG  CGG
                                     _   _   AA
GAM3462  LOC91960  3'  ACACAGCTCCCCGCCCC     77935        CGCACAA
                                ACACAGC      CCCGCCCC
                                |||||||      ||||||||
                                TGTGTCG      GGGCGGGG
                                   AG_____
GAM3462  LOC93129  3'  ACACAGCCTGCAGCTCCCC    77904         _   CAACCC  _
                                ACACAGCC GCA     GC CCCC
                                |||||||| |||     || ||||
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                                TGTGTCGG CGT     CG GGGG
                                    A  ______  A
GAM3463  ADCY6    3'  GAGAGGCAACCTGGGGT     77938     C    T
                                GAG AGGTG ATCTGGGGT
                                ||| ||||| |||||||||
                                CTC TCCGT TGGACCCCA
                                 _    _
GAM3463  ADCY6    3'  GAGAGGCAACCTGGGGT     77938     C    T
                                GAG AGGTG ATCTGGGGT
                                ||| ||||| |||||||||
                                CTC TCCGT TGGACCCCA
                                 _    _
GAM3463  ARHGAP6  3'  GAGTAGGCGTTCAGCAGGT   77939     C     A  TG_
                                GAG AGGTGT TC   GGGT
                                ||| |||||| ||   ||||
                                CTC TCCGCA AG   TCCA
                                  A     _  TCG
GAM3463  ARHGAP6  3'  GAGTAGGCGTTCAGCAGGT   77939     C     A  TG_
                                GAG AGGTGT TC   GGGT
                                ||| |||||| ||   ||||
                                CTC TCCGCA AG   TCCA
                                  A     _  TCG
GAM3463  B3GNT3   5'  AGCCAGGGTCTGGGGT      77940     _   T TA
                                AGC AGG G  TCTGGGGT
                                ||| ||| |  ||||||||
                                TCG TCC C  AGACCCCA
                                  G  _ __
GAM3463  CDH3     3'  GAATGGGAGGCATTGGGGT    77941     CA  T_   C
                                GAG  GG  GTAT TGGGGT
                                |||  ||  |||| ||||||
                                CTT  CC  CGTA ACCCCA
                                  AC  TC   _
GAM3463  CYP11B1  3'  GAGGGGTGGCCTGGGGT     77942     CA    TA
                                GAG  GGTG  TCTGGGGT
                                |||  ||||  ||||||||
                                CTC  CCAC  GGACCCCA
                                  C_   C_
GAM3463  CYP24    5'  GGCCGGTGTCTGGGGT      77943    A  A    TA
                                G GC GGTG  TCTGGGGT
                                | || ||||  ||||||||
                                C CG CCAC  AGACCCCA
                                 _ G   __
GAM3463  CYP26A1  5'  GAGCGCGCCTCCTGGGGT    77944     AG    A_
                                GAGC  GTGT  TCTGGGGT
                                ||||  ||||  ||||||||
                                CTCG  CGCG  GGACCCCA
                                   __   GA
GAM3463  DRG2     3'  GAGCCAGGGTCCTGGGGT    77945      _   T  A
                                GAGC AGG GT TCTGGGGT
                                |||| ||| || ||||||||
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                                CTCG TCC CA GGACCCCA
                                  G  _ _
GAM3463  EN2     3'  GAGCAGGCCTGGGGT      77946       GTAT
                                GAGCAGGT   CTGGGGT
                                ||||||||   |||||||
                                CTCGTCCG   GACCCCA
                                    ____
GAM3463  EPHB4   3'  GAGGCGGTGTCCCTGGGGT  77947    CA   AT
                                GAG  GGTGT  CTGGGGT
                                |||  |||||  |||||||
                                CTC  CCACA  GACCCCA
                                  CG    GG
GAM3463  FEN1    3'  GGCAAATATTCTGGGGT    77948   A     A
                                G GCAGGTGT TCTGGGGT
                                | ||||||||  ||||||||
                                C CGTTTATA AGACCCCA
                                _      _
GAM3463  HRY     5'  GAGCAAGTGCTGAGGGT    77949       TAT  _
                                GAGCAGGTG   CTG GGGT
                                |||||||||   ||| ||||
                                CTCGTTCAC   GAC CCCA
                                     ___  T
GAM3463  ID3     3'  GAGAGGTTCCCGGGGT     77950    C   GTA
                                GAG AGGT   TCTGGGGT
                                ||| ||||   ||||||||
                                CTC TCCA   GGGCCCCA
                                  _   A__
GAM3463  IGFBP5  3'  GAGTGGCGTCCTGGGGT    77951    CA   A
                                GAG  GGTGT TCTGGGGT
                                |||  ||||| ||||||||
                                CTC  CCGCA GGACCCCA
                                  A_   _
GAM3463  IL1RN   3'  GGGCAGGTGGTCGGGGT    77952   A     TA  T
                                G GCAGGTG  TC GGGGT
                                | |||||||  || |||||
                                C CGTCCAC  AG CCCCA
                                 C      C_  _
GAM3463  ISLR    3'  GAGCAGGTCTAGAAGT      77953       G  TCT
                                GAGCAGGT TA   GGGGT
                                ||||||||  ||   |||||
                                CTCGTCCA AT   CTTCA
                                     G  ___
GAM3463  LAIR1   3'  AGCAAAGTCTCTGGGGT    77954       T  A
                                AGCAGG GT TCTGGGGT
                                ||||||  ||  ||||||||
                                TCGTTT CA AGACCCCA
                                    _  G
GAM3463  LAIR1   3'  AGCAAAGTCTCTGGGGT    77954       T  A
                                AGCAGG GT TCTGGGGT
                                ||||||  ||  ||||||||
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                                TCGTTT CA AGACCCCA
                                   _ G
GAM3463 LGALS3BP 3' GAGGGCGTCCTGGGGT     77955     CA    A
                                GAG  GGTGT TCTGGGGT
                                |||  ||||| ||||||||
                                CTC  CCGCA GGACCCCA
                                  __    _
GAM3463 MAB21L1  5' GAGTGTGTGTCCGGGGT     77956     CAG   A
                                GAG   GTGT TCTGGGGT
                                |||   |||| ||||||||
                                CTC   CACA AGGCCCCA
                                  A__    C
GAM3463 MPZ      3' GGCAGGGCCTGGGGT      77957   A    T  AT
                                G GCAGG GT  CTGGGGT
                                | ||||| ||  |||||||
                                C CGTCC CG  GACCCCA
                                _    _ __
GAM3463 MTA1L1   3' GAGCGTGGCCTGGGGT     77958     AG   TA
                                GAGC  GTG  TCTGGGGT
                                ||||  |||  ||||||||
                                CTCG  CAC  GGACCCCA
                                   __  C_
GAM3463 MTMR2    3' GAACATTTTCATCTGGGGT   77959      GGTG
                                GAGCA   TATCTGGGGT
                                |||||   ||||||||||
                                CTTGT   GTAGACCCCA
                                   AAAA
GAM3463 NESH     3' GAGGGGTGTCTGGGGT     77960     CA   TA
                                GAG  GGTG  TCTGGGGT
                                |||  ||||  ||||||||
                                CTC  CCAC  AGACCCCA
                                  C_   __
GAM3463 NF2      3' GGCAGGTCCTGGGGT      77961   A    GTA
                                G GCAGGT   TCTGGGGT
                                | ||||||   ||||||||
                                C CGTCCA   GGACCCCA
                                _    ____
GAM3463 NR1I2    5' GAACAGTGTGCTCTGGGGT   77962      _   A
                                GAGCAG GTGT TCTGGGGT
                                |||||| |||| ||||||||
                                CTTGTC CACG AGACCCCA
                                   A   _
GAM3463 PATE     3' GAGAGGCATCTGGGGT     77963     C   GT
                                GAG AGGT  ATCTGGGGT
                                ||| ||||  |||||||||
                                CTC TCCG  TAGACCCCA
                                  _   __
GAM3463 PGAM1    3' GAGCCAGATCCTCTGGGGT   77964     _   GTA
                                GAGC AGGT   TCTGGGGT
                                |||| ||||   ||||||||
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                                CTCG TCTA   AGACCCCA
                                  G   GG_
GAM3463  PKM2    3'  GAGGAGGGGCTCTGGGGT    77965    C  T  A
                                GAG AGG GT TCTGGGGT
                                ||| ||| || ||||||||
                                CTC TCC CG AGACCCCA
                                  C  C  _
GAM3463  PODXL   5'  GAGCAGGTGGCTGCGGT     77966        TAT  G
                                GAGCAGGTG  CTG GGT
                                |||||||||  ||| |||
                                CTCGTCCAC  GAC CCA
                                     C__  G
GAM3463  PX19    3'  AAGCCTAGCTGTCTGGGGT   77967     A_  GTA
                                GAGC  GGT  TCTGGGGT
                                ||||  |||  ||||||||
                                TTCG  TCG  AGACCCCA
                                  GA  AC_
GAM3463  SCD     5'  GAGCGGAGTTCGGGGT      77968     A  T  A  T
                                GAGC GG GT TC GGGGT
                                |||| || || || |||||
                                CTCG CC CA AG CCCCA
                                  _ T  _ _
GAM3463  SCN4A   3'  GGCAGTGCCCTGGGGT      77969   A   G   A
                                G GCAG TGT TCTGGGGT
                                | |||| ||| ||||||||
                                C CGTC ACG GGACCCCA
                                _   _  _
GAM3463  SCNN1G  3'  AAGTCAGATTGTCTGGGGT   77970    _    GTA
                                GAG CAGGT  TCTGGGGT
                                ||| |||||  ||||||||
                                TTC GTCTA  AGACCCCA
                                  A    AC_
GAM3463  SH3GL1  3'  GAGCAGAGCCTGGGGT      77971       T  AT
                                GAGCAGG GT  CTGGGGT
                                ||||||| ||  |||||||
                                CTCGTCT CG  GACCCCA
                                    _ __
GAM3463  TAPBP   3'  GAGCAGATGATAGGGT      77972        TATC
                                GAGCAGGTG   TGGGGT
                                |||||||||   ||||||
                                CTCGTCTAC   ATCCCA
                                     T___
GAM3463  TCF19   3'  GCAGGTGTGTCCGATGGT    77973        A   _
                                GCAGGTGT TCTGG GGT
                                |||||||| ||||| |||
                                CGTCCACA AGGCT CCA
                                     C    A
GAM3463  TCF19   3'  GCAGGTGTGTCCGATGGT    77973        A   _
                                GCAGGTGT TCTGG GGT
                                |||||||| ||||| |||
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                                CGTCCACA AGGCT CCA
                                    C    A
GAM3463  TCP10    3'  GAGCCGTGCCTGGGGT     77974     AG   AT
                                GAGC  GTGT  CTGGGGT
                                ||||  ||||  |||||||
                                CTCG  CACG  GACCCCA
                                  G_   __
GAM3463  TEM6     3'  GAGCCGGTGTCCACGGT     77975     A   TA   G
                                GAGC GGTG  TCTG GGT
                                |||| ||||  |||| |||
                                CTCG CCAC  AGGT CCA
                                  G   __   G
GAM3463  TM4SF5   3'  GAGCAGGTGTAACCCGGCGGT  77976          _    _
                                GAGCAGGTGTA TCTGG GGT
                                |||||||||||| ||||| |||
                                CTCGTCCACAT GGGCC CCA
                                      T    G
GAM3463  BANP     5'  GCAGATGCCAGGGCTGGGGT   77977        AT___
                                GCAGGTGT    CTGGGGT
                                ||||||||    |||||||
                                CGTCTACG    GACCCCA
                                    GTCCC
GAM3463  BIRC1    5'  GGCATTGTTGTCTGGGGT    77978   A   GG   A_
                                G GCA  TGT  TCTGGGGT
                                | |||  |||  ||||||||
                                C CGT  ACA  AGACCCCA
                                 _  A_   AC
GAM3463  BRAG     3'  GGCAGAGTCCTGGGGT     77979   A    T  A
                                G GCAGG GT TCTGGGGT
                                | ||||| || ||||||||
                                C CGTCT CA GGACCCCA
                                 _    _ _
GAM3463  C1orf2   3'  GAGCAGGCAATTGGGGT     77980        TATC
                                GAGCAGGTG   TGGGGT
                                |||||||||   ||||||
                                CTCGTCCGT   ACCCCA
                                    TA__
GAM3463  C1orf2   3'  GAGCAGGCAATTGGGGT     77980        TATC
                                GAGCAGGTG   TGGGGT
                                |||||||||   ||||||
                                CTCGTCCGT   ACCCCA
                                    TA__
GAM3463  C20orf100 3'  GAGCAGTGCTCCGGGGT     77981      G   A
                                GAGCAG TGT TCTGGGGT
                                |||||| ||| ||||||||
                                CTCGTC ACG AGGCCCCA
                                   _  _
GAM3463  C5orf4   3'  GGGCAAGTCCTCTGGGGT    77982   A    GTA
                                G GCAGGT   TCTGGGGT
                                | ||||||   ||||||||
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                                C CGTTCA   AGACCCCA
                                 C     GG_
GAM3463  C5orf4    3'  GGGCAAGTCCTCTGGGGT    77982    A     GTA
                                G GCAGGT   TCTGGGGT
                                | ||||||   ||||||||
                                C CGTTCA   AGACCCCA
                                 C     GG_
GAM3463  CBARA1    3'  GGCAGGTGTGTGGATGGT    77983    A      ATC  __
                                G GCAGGTGT   TGG  GGT
                                | ||||||||   |||  |||
                                C CGTCCACA   ACC  CCA
                                 _       C__   TA
GAM3463  CENTB5    3'  GAGGAGGCTCTGGGGT     77984     C    GTA
                                GAG AGGT   TCTGGGGT
                                ||| ||||   ||||||||
                                CTC TCCG   AGACCCCA
                                  C   ___
GAM3463  CGI-203   5'  GAGGGGTTTATCTGGGGT    77985     CA   G
                                GAG  GGT TATCTGGGGT
                                |||  ||| ||||||||||
                                CTC  CCA ATAGACCCCA
                                  C_   A
GAM3463  CL24751   5'  GAGGGGATGTTTCTGGGGT    77986     CA    A
                                GAG  GGTGT TCTGGGGT
                                |||  ||||| ||||||||
                                CTC  CTACA AGACCCCA
                                  CC    A
GAM3463  CLDN4     3'  GCAGGGCCCTCCTGGGGT    77987      T  A__
                                GCAGG GT   TCTGGGGT
                                ||||| ||   ||||||||
                                CGTCC CG   GGACCCCA
                                   _ GGA
GAM3463  CNNM4     3'  GAGCAGGGCACTTGGGGT    77988       T   TC
                                GAGCAGG GTA  TGGGGT
                                ||||||| |||  ||||||
                                CTCGTCC CGT  ACCCCA
                                     _  GA
GAM3463  CRA       3'  GCTGGAGTATCCTGGGGT    77989    A  T    _
                                GC GG GTATC TGGGGT
                                || || ||||| ||||||
                                CG CC CATAG ACCCCA
                                 A  T    G
GAM3463  CRA       3'  GAGCCTGATCTGGGGT     77990      AGG  T
                                GAGC   TG ATCTGGGGT
                                ||||   || |||||||||
                                CTCG   AC TAGACCCCA
                                  G__  _
GAM3463  CUGBP2    3'  AGCAGGGAGCCTCTGGGGT   77991       T_  A
                                AGCAGG  GT TCTGGGGT
                                ||||||  || ||||||||
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                                TCGTCC  CG AGACCCCA
                                   CT  G
GAM3463  DKFZP434J214 3'  AAGCAGGTGTAGGAGT     77992          TCT
                                GAGCAGGTGTA   GGGGT
                                ||||||||||   |||||
                                TTCGTCCACAT   CCTCA
                                      ___
GAM3463  DKFZp434P2235 3'  GGCTTTGTGATCTGGGGT    77993    A  AG_   T
                                G GC   GTG ATCTGGGGT
                                | ||   ||| |||||||||
                                C CG   CAC TAGACCCCA
                                 _ AAA  _
GAM3463  DKFZp547D155 3'  GAGCAGGTGGACAGCAGGGGT  77994         T  CT__
                                GAGCAGGTG AT    GGGGT
                                |||||||||  ||    |||||
                                CTCGTCCAC TG    CCCCA
                                      C  TCGT
GAM3463  DKFZp547O146 5'  GAGGGGTGCCTGGGGT     77995     CA    AT
                                GAG  GGTGT  CTGGGGT
                                |||  |||||  |||||||
                                CTC  CCACG  GACCCCA
                                  C_    __
GAM3463  DKFZP564O0523 3'  GCAGGTGTATCACAAGGT    77996          _
                                GCAGGTGTATC TGGGGT
                                |||||||||||  ||||||
                                CGTCCACATAG GTTCCA
                                       T
GAM3463  FLJ10422  3'  GAGAGGGCGGATCTGGGGT   77997     CA   T
                                GAG  GGTG ATCTGGGGT
                                |||  ||||  |||||||||
                                CTC  CCGC TAGACCCCA
                                  TC   C
GAM3463  FLJ13158  3'  AAGCAACACCAGTTTGGGGT   77998       GTG   _____
                                GAGCAG   TATC    TGGGGT
                                ||||||   ||||    ||||||
                                TTCGTT   GTGG    ACCCCA
                                   ___    TCAA
GAM3463  FLJ14001  5'  GAGCGCGGTGCCCGGGGT    77999     A_    AT
                                GAGC  GGTGT  CTGGGGT
                                ||||  |||||  |||||||
                                CTCG  CCACG  GGCCCCA
                                  CG    __
GAM3463  FLJ14397  3'  GGCAGGTGCCAACGGGGT    78000   A      ATC
                                G GCAGGTGT   TGGGGT
                                | ||||||||   ||||||
                                C CGTCCACG   GCCCCA
                                 _      GTT
GAM3463  FLJ20487  3'  GACCAGTGGTCTGGGGT     78001    G   G  TA
                                GA CAG TG  TCTGGGGT
                                || ||| ||  ||||||||
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                                CT GTC AC  AGACCCCA
                                 G   _  C_
GAM3463  FLJ20979  5'  GAACAGGCCCCTGGGGT     78002        GTA
                                GAGCAGGT   TCTGGGGT
                                ||||||||   ||||||||
                                CTTGTCCG   GGACCCCA
                                    G__
GAM3463  FLJ21135  5'  GGGCAGCGGGTCTGGGGT    78003    A    G  TA
                                G GCAG TG  TCTGGGGT
                                | |||| ||  ||||||||
                                C CGTC GC  AGACCCCA
                                 C    _  CC
GAM3463  FLJ21742  3'  GAGCCCCTGCATCTGGGGT    78004      AGG
                                GAGC   TGTATCTGGGGT
                                ||||   ||||||||||||
                                CTCG   ACGTAGACCCCA
                                  GGG
GAM3463  FLJ22341  3'  GAGCAGGCCCTGGGGT      78005        GTA
                                GAGCAGGT   TCTGGGGT
                                ||||||||   ||||||||
                                CTCGTCCG   GGACCCCA
                                    ___
GAM3463  FLJ22393  3'  GGCAGGTGCTGGGGT       78006    A      TAT
                                G GCAGGTG   CTGGGGT
                                | |||||||   |||||||
                                C CGTCCAC   GACCCCA
                                _      ____
GAM3463  FLJ22582  3'  GCAGGTGCACTGTGGGGT    78007          C_
                                GCAGGTGTAT  TGGGGT
                                ||||||||||  ||||||
                                CGTCCACGTG  ACCCCA
                                     AC
GAM3463  FLJ32865  3'  GAGCAGGGGCCTGGGGT     78008        T  AT
                                GAGCAGG GT  CTGGGGT
                                |||||||  ||  |||||||
                                CTCGTCC CG  GACCCCA
                                    C  __
GAM3463  GPR108    3'  GAGGGGTGGTCCCGGGGT    78009     CA    TA
                                GAG  GGTG  TCTGGGGT
                                |||  ||||  ||||||||
                                CTC  CCAC  GGGCCCCA
                                  C_   CA
GAM3463  HMT-1     3'  AGCAGGGGTCCTGGGGT     78010       T  A
                                AGCAGG GT TCTGGGGT
                                ||||||  ||  ||||||||
                                TCGTCC CA GGACCCCA
                                   C  _
GAM3463  HSA9947   3'  GAGTTCCAGTGTCTGGGGT   78011     CA__    TA
                                GAG   GGTG  TCTGGGGT
                                |||   ||||  ||||||||
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                                CTC   TCAC  AGACCCCA
                                  AAGG   __
GAM3463 INADL    5' GAGCAGGTGGGAGCCCGGG   78012        TA__
                                GAGCAGGTG   TCTGGG
                                |||||||||   ||||||
                                CTCGTCCAC   GGGCCC
                                     CCTC
GAM3463 IRF7     3' AGCAGGCAGGCTGGGGT    78013        TAT
                                AGCAGGTG  CTGGGGT
                                ||||||||  |||||||
                                TCGTCCGT  GACCCCA
                                     CC_
GAM3463 KCND1    3' GAAAAATGTCTGGGGT     78014    C    TA
                                GAG AGGTG  TCTGGGGT
                                ||| |||||  ||||||||
                                CTT TTTAC  AGACCCCA
                                  _    __
GAM3463 KCNH4    3' GGCAGCGGTCTGGGGT     78015   A   G  TA
                                G GCAG TG  TCTGGGGT
                                | |||| ||  ||||||||
                                C CGTC GC  AGACCCCA
                                 _   _ C_
GAM3463 KIAA0514 5' GGCATGTCTCTGGGGT     78016   A  GG  A
                                G GCA  TGT TCTGGGGT
                                | |||  ||| ||||||||
                                C CGT  ACA AGACCCCA
                                 _  __  G
GAM3463 KIAA0544 3' GAGAGGTGCTTGGGGT     78017    C    ATC
                                GAG AGGTGT  TGGGGT
                                ||| ||||||  ||||||
                                CTC TCCACG  ACCCCA
                                  _    A__
GAM3463 KIAA0792 5' GACCAGCGAGTCCTGGGGT  78018   G  GT_ A
                                GA CAG  GT TCTGGGGT
                                || |||  || ||||||||
                                CT GTC  CA GGACCCCA
                                 G  GCT  _
GAM3463 KIAA0981 3' GAGGAAATATTCTGGGGT   78019    C    A
                                GAG AGGTGT TCTGGGGT
                                ||| |||||| ||||||||
                                CTC TTTATA AGACCCCA
                                  C    _
GAM3463 KIAA1024 3' GAGTAGGTGTTGGGGT     78020    C    ATC
                                GAG AGGTGT  TGGGGT
                                ||| ||||||  ||||||
                                CTC TCCACA  ACCCCA
                                  A    ___
GAM3463 KIAA1028 3' GAGCAGGCCTCGCTGGGGT  78021       GTAT
                                GAGCAGGT   CTGGGGT
                                ||||||||   |||||||
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                                CTCGTCCG   GACCCCA
                                    GAGC
GAM3463 KIAA1032 3' GGCAATTGGTCTGGGGT    78022   A   G  TA
                                G GCAG TG  TCTGGGGT
                                | |||| ||  ||||||||
                                C CGTT AC  AGACCCCA
                                 _   A  C_
GAM3463 KIAA1363 3' AAGCAGGTGTAGGAGGT    78023        TCT
                                GAGCAGGTGTA  GGGGT
                                ||||||||||  |||||
                                TTCGTCCACAT  CTCCA
                                      C__
GAM3463 KIAA1862 3' GAGAGGGTGGCCTGGGGT   78024    CA   TA
                                GAG  GGTG  TCTGGGGT
                                |||  ||||  ||||||||
                                CTC  CCAC  GGACCCCA
                                  TC   C_
GAM3463 KIAA1881 3' GAGCAGGGCGTGGGGT     78025      T  ATC
                                GAGCAGG GT   TGGGGT
                                |||||||  ||  ||||||
                                CTCGTCC CG   ACCCCA
                                    _  C__
GAM3463 KIAA1940 3' GAGCCAGCTGCTCTGGGGT  78026     _  G   A
                                GAGC AG TGT TCTGGGGT
                                |||| || ||| ||||||||
                                CTCG TC ACG AGACCCCA
                                  G  G  _
GAM3463 KRTHA3B  3' GAGAGGGACCTGGGGT     78027    C  TGT
                                GAG AGG   ATCTGGGGT
                                ||| |||   |||||||||
                                CTC TCC   TGGACCCCA
                                  _  C__
GAM3463 KRTHB4   5' GAGCAAGTGTAGAATGGGT  78028        TCTG
                                GAGCAGGTGTA   GGGT
                                ||||||||||   ||||
                                CTCGTTCACAT   CCCA
                                      CTTA
GAM3463 LRP1B    5' GAGCAGGATGTGGAAGGT   78029      _  ATCT
                                GAGCAGG TGT   GGGGT
                                |||||||  |||   |||||
                                CTCGTCC ACA   TTCCA
                                    T  CC__
GAM3463 LY117    3' GAGGAAGGTGTCTGGGGT   78030    C_   TA
                                GAG  AGGTG  TCTGGGGT
                                |||  |||||  ||||||||
                                CTC  TCCAC  AGACCCCA
                                  CT    __
GAM3463 LY117    3' GAGGAAGGTGTCTGGGGT   78030    C_   TA
                                GAG  AGGTG  TCTGGGGT
                                |||  |||||  ||||||||
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                                CTC  TCCAC  AGACCCCA
                                  CT    __
GAM3463 LY117    3' GAGGAAGGTGTCTGGGGT    78030    C_    TA
                                GAG  AGGTG  TCTGGGGT
                                |||  |||||  ||||||||
                                CTC  TCCAC  AGACCCCA
                                  CT    __
GAM3463 MGC1127  3' AAGCAGGGGCCTGGGGT     78031       T  AT
                                GAGCAGG GT  CTGGGGT
                                |||||||  ||  |||||||
                                TTCGTCC CG  GACCCCA
                                    C  __
GAM3463 MGC1842  3' AGCAGGTGCTTGGGGT      78032        ATC
                                AGCAGGTGT   TGGGGT
                                |||||||||   ||||||
                                TCGTCCACG   ACCCCA
                                     A__
GAM3463 MKRN4    3' ACAGCTGCTATCTGGGGT    78033     G  _
                                GCAG TGT ATCTGGGGT
                                ||||  |||  |||||||||
                                TGTC ACG TAGACCCCA
                                  G   A
GAM3463 NAPA     3' GAGCAGGTGTGGGGCTGGGGT  78034         AT__
                                GAGCAGGTGT   CTGGGGT
                                ||||||||||   |||||||
                                CTCGTCCACA   GACCCCA
                                     CCCC
GAM3463 NK4      5' GAGACAGAGGTCTGGGGT    78035    _   T TA
                                GAG CAGG G  TCTGGGGT
                                |||  ||||  |  ||||||||
                                CTC GTCT C  AGACCCCA
                                  T   C __
GAM3463 PACSIN2  3' GAACAGGTGTATAAAAAAGT  78036          CT_
                                GAGCAGGTGTAT  GGGGT
                                ||||||||||||  |||||
                                CTTGTCCACATA  TTTCA
                                      TTT
GAM3463 PAK6     3' GGCAGGCATACTTGGGGT    78037   A      TC
                                G GCAGGTGTA  TGGGGT
                                |  |||||||||  ||||||
                                C CGTCCGTAT  ACCCCA
                                _       GA
GAM3463 PGLYRP   3' GGCAGGTGTCAGGGT      78038   A      ATC
                                G GCAGGTGT   TGGGGT
                                |  ||||||||  ||||||
                                C CGTCCACA   GTCCCA
                                _     ____
GAM3463 PTPRT    3' GAGCAAGTTCATCGTGGGGT  78039        G   _
                                GAGCAGGT TATC TGGGGT
                                ||||||||  ||||  ||||||
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                                CTCGTTCA GTAG ACCCCA
                                    A   C
GAM3463  RAI15    3'  AAGCAGGTGTGAGAAAGGGT  78040         ATCT_
                                GAGCAGGTGT    GGGGT
                                ||||||||||    |||||
                                TTCGTCCACA    TCCCA
                                     CTCTT
GAM3463  SC65     3'  GCAGGATGGGTCTGGGGT    78041      _  TA
                                GCAGG TG  TCTGGGGT
                                ||||| ||  ||||||||
                                CGTCC AC  AGACCCCA
                                   T  CC
GAM3463  SCYA3    5'  GAGCAGGTGACGGAAT      78042        TATC
                                GAGCAGGTG   TGGGGT
                                |||||||||   ||||||
                                CTCGTCCAC   GCCTTA
                                     T___
GAM3463  SIAT8D   3'  GAGTTGCGTTCCTGGGGT   78043    CAG   A
                                GAG   GTGT TCTGGGGT
                                |||   |||| ||||||||
                                CTC   CGCA GGACCCCA
                                  AA_   A
GAM3463  SLC38A5  5'  GAACAGGTGCAGGGGT     78044         TCT
                                GAGCAGGTGTA   GGGGT
                                ||||||||||   |||||
                                CTTGTCCACGT   CCCCA
                                      ___
GAM3463  TESK2    3'  GAGACAGACCTGGGGT     78045    _  GTGT
                                GAG CAG   ATCTGGGGT
                                ||| |||   |||||||||
                                CTC GTC   TGGACCCCA
                                  T  _____
GAM3463  TP53TG3  3'  AAGCGGCGCTCCTGGGGT   78046    A   A
                                GAGC GGTGT TCTGGGGT
                                |||| ||||| ||||||||
                                TTCG CCGCG GGACCCCA
                                  _    A
GAM3463  TRAF4    3'  GAGACAGGCCCTGGGGT    78047    _   GTA
                                GAG CAGGT   TCTGGGGT
                                ||| |||||   ||||||||
                                CTC GTCCG   GGACCCCA
                                  T   ___
GAM3463  TU3A     3'  GAGCCAGGCCCTCTGGGGT  78048    _   GTA
                                GAGC AGGT   TCTGGGGT
                                |||| ||||   ||||||||
                                CTCG TCCG   AGACCCCA
                                  G   GG_
GAM3463  TUSP     3'  GAGCAGGCTTGACCCTGGGGT 78049       GTA__
                                GAGCAGGT    TCTGGGGT
                                ||||||||    ||||||||
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                                CTCGTCCG    GGACCCCA
                                     AACTG
GAM3463  ZDHHC8   3'  GGCGGTGATCTGGGGT     78050   A  A   T
                                G GC GGTG ATCTGGGGT
                                | || |||| |||||||||
                                C CG CCAC TAGACCCCA
                                 _ _   _
GAM3463  ZER6     3'  GAGCACGTTTCTGGGGT     78051      G  GTA
                                GAGCA GT   TCTGGGGT
                                ||||| ||   ||||||||
                                CTCGT CA   AGACCCCA
                                   G  A__
GAM3463  ZNF211   3'  GAGCAGGTTCAGGAGGT     78052        GTA  T  _
                                GAGCAGGT   TC GG GGT
                                ||||||||   || || |||
                                CTCGTCCA   AG CC CCA
                                     ___  T  T
GAM3463  ZNF282   3'  GAGCAGGTGCACCAACGT    78053          T TG G
                                GAGCAGGTGTA C  G GT
                                |||||||||||  |  | ||
                                CTCGTCCACGT G  T CA
                                      _ GT G
GAM3463  LOC115574 3'  AGCAGGCATTTCTGGGGT    78054         A
                                AGCAGGTGT TCTGGGGT
                                ||||||||| ||||||||
                                TCGTCCGTA AGACCCCA
                                     A
GAM3463  LOC121344 3'  GAACAGGTGTGGCCTTGGT   78055         AT  GG
                                GAGCAGGTGT  CT  GGT
                                ||||||||||  ||  |||
                                CTTGTCCACA  GG  CCA
                                      CC  AA
GAM3463  LOC124222 3'  GAGCAGGTGCACACCCAGGT  78056           _  G
                                GAGCAGGTGTAT CT GGGT
                                |||||||||||| || ||||
                                CTCGTCCACGTG GG TCCA
                                       T  G
GAM3463  LOC124602 3'  GAGCAGGTGTCGGGAGGT    78057         ATCT
                                GAGCAGGTGT    GGGGT
                                ||||||||||    |||||
                                CTCGTCCACA    CTCCA
                                      GCC_
GAM3463  LOC127829 3'  GAACAGGACTCTGGGGT     78058       TGTA
                                GAGCAGG    TCTGGGGT
                                |||||||    ||||||||
                                CTTGTCC    AGACCCCA
                                    TG__
GAM3463  LOC132228 3'  GAACCTGCCATCTGGGGT    78059      AG  G
                                GAGC  GT TATCTGGGGT
                                ||||  || ||||||||||
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                                CTTG  CG GTAGACCCCA
                                  GA  _
GAM3463  LOC144079 5'  GAGCAAGTGAAGCTCTGGGGT  78060         TA__
                                GAGCAGGTG    TCTGGGGT
                                |||||||||    ||||||||
                                CTCGTTCAC    AGACCCCA
                                    TTCG
GAM3463  LOC144483 3'  GAGCCAGATCCTCTGGGGT    77964      _    GTA
                                GAGC AGGT   TCTGGGGT
                                |||| ||||   ||||||||
                                CTCG TCTA   AGACCCCA
                                  G    GG_
GAM3463  LOC144501 5'  GAGCGAGTGAGCCTGGGGT    78061      AG   TA
                                GAGC  GTG  TCTGGGGT
                                ||||  |||  ||||||||
                                CTCG  CAC  GGACCCCA
                                  CT   TC
GAM3463  LOC145809 5'  AGCAGGTGTGTTGGGGT     78062         ATC
                                AGCAGGTGT   TGGGGT
                                |||||||||   ||||||
                                TCGTCCACA   ACCCCA
                                    CA_
GAM3463  LOC146782 3'  GGCTTTGTGATCTGGGGT    77993    A  AG_   T
                                G GC   GTG ATCTGGGGT
                                | ||   ||| |||||||||
                                C CG   CAC TAGACCCCA
                                 _  AAA   _
GAM3463  LOC147004 5'  GAGCTGAGCTCTGGGGT     78063      A  T  A
                                GAGC GG GT TCTGGGGT
                                |||| || || ||||||||
                                CTCG CT CG AGACCCCA
                                  A  _  _
GAM3463  LOC148223 3'  GAGCAGGGTTCCCGGGGT    78064        T  A
                                GAGCAGG GT TCTGGGGT
                                ||||||| || ||||||||
                                CTCGTCC CA GGGCCCCA
                                    _  A
GAM3463  LOC148710 3'  GAGCAGGTGTGAAGGT      78065         ATCT
                                GAGCAGGTGT    GGGGT
                                ||||||||||    |||||
                                CTCGTCCACA    TTCCA
                                    C____
GAM3463  LOC150166 3'  GAGCGGATGTAAAATAAGGT   78066      A     TC_
                                GAGC GGTGTA   TGGGGT
                                |||| ||||||   ||||||
                                CTCG CTACAT   ATTCCA
                                  C     TTT
GAM3463  LOC151171 5'  GAGAGGCCACCTGGGGT     78067     C    G
                                GAG AGGT TATCTGGGGT
                                ||| |||| ||||||||||
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                                CTC TCCG GTGGACCCCA
                                  _   _
GAM3463  LOC151178 5'  GAGCAGATGCCGGGGGT    78068        ATCT
                                GAGCAGGTGT   GGGGT
                                ||||||||||   |||||
                                CTCGTCTACG   CCCCA
                                     GC__
GAM3463  LOC151361 3'  GAGTGGATGGGTCCGGGGT   78069    CA   TA
                                GAG  GGTG  TCTGGGGT
                                |||  ||||  ||||||||
                                CTC  CTAC  AGGCCCCA
                                  AC   CC
GAM3463  LOC151475 3'  AGCAGGCACTGCCTGGGGT   78070      TG A_
                                AGCAGG  T  TCTGGGGT
                                ||||||  |  ||||||||
                                TCGTCC  G  GGACCCCA
                                   GT AC
GAM3463  LOC157349 5'  GGCAGGTGCAGGGGT      78071   A      TCT
                                G GCAGGTGTA   GGGGT
                                | |||||||||   |||||
                                C CGTCCACGT   CCCCA
                                _       ____
GAM3463  LOC157349 5'  GGCAGGTGCAGGGGT      78071   A      TCT
                                G GCAGGTGTA   GGGGT
                                | |||||||||   |||||
                                C CGTCCACGT   CCCCA
                                _       ____
GAM3463  LOC157349 5'  GGCAGGTGCAGGGGT      78071   A      TCT
                                G GCAGGTGTA   GGGGT
                                | |||||||||   |||||
                                C CGTCCACGT   CCCCA
                                _       ____
GAM3463  LOC157931 3'  GAGCTGAGCTCTGGGGT    78063    A  T  A
                                GAGC GG GT TCTGGGGT
                                |||| || || ||||||||
                                CTCG CT CG AGACCCCA
                                  A  _  _
GAM3463  LOC157931 5'  GAGCTATGGATTTGGGGT   78072    AG   T  C
                                GAGC  GTG AT TGGGGT
                                ||||  ||| || ||||||
                                CTCG  TAC TA ACCCCA
                                  A_   C  A
GAM3463  LOC162333 5'  GAGAGGGTTCGCTGGGGT   78073    C   T  AT_
                                GAG AGG GT   CTGGGGT
                                ||| ||| ||   |||||||
                                CTC TCC CA   GACCCCA
                                  _   _  AGC
GAM3463  LOC167040 5'  AAGCAGGTGTGGCCATGGT   78074        AT  GG
                                GAGCAGGTGT  CT  GGT
                                ||||||||||  ||  |||
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                                TTCGTCCACA  GG  CCA
                                      CC  TA
GAM3463  LOC200261 3'  GGCAGGTGTGCCTGGCGG    78075   A      AT   _
                                G GCAGGTGT  CTGG GG
                                | ||||||||  |||| ||
                                C CGTCCACA  GACC CC
                                _      CG   G
GAM3463  LOC200488 5'  GAGAAGGTCTCTGGGGT     78076    C   GTA
                                GAG AGGT   TCTGGGGT
                                ||| ||||   ||||||||
                                CTC TCCA   AGACCCCA
                                  T   G__
GAM3463  LOC200781 3'  GAGCAGGTGCAGGAGAAGGT   78077          TCT_
                                GAGCAGGTGTA    GGGGT
                                ||||||||||    |||||
                                CTCGTCCACGT    TTCCA
                                      CCTC
GAM3463  LOC203397 3'  GAGCAGGTGTCGGGAGGT    78057         ATCT
                                GAGCAGGTGT    GGGGT
                                |||||||||    |||||
                                CTCGTCCACA    CTCCA
                                      GCC_
GAM3463  LOC204820 3'  GCAGGCTGGGTCTGGGGT    78078      _  TA
                                GCAGG TG  TCTGGGGT
                                ||||| ||  ||||||||
                                CGTCC AC  AGACCCCA
                                   G  CC
GAM3463  LOC219562 3'  GGCTTTGTGATCTGGGGT    77993    A  AG_  T
                                G GC   GTG ATCTGGGGT
                                | ||   ||| |||||||||
                                C CG   CAC TAGACCCCA
                                 _ AAA  _
GAM3463  LOC220514 3'  GAACAGGTGTATAAAAAAGT   78036          CT_
                                GAGCAGGTGTAT   GGGGT
                                ||||||||||   |||||
                                CTTGTCCACATA   TTTCA
                                      TTT
GAM3463  LOC221536 3'  GCAGGTGTGTCCGATGGT    77973        A    _
                                GCAGGTGT TCTGG GGT
                                |||||||| ||||| |||
                                CGTCCACA AGGCT CCA
                                     C    A
GAM3463  LOC221641 5'  AGCAGGGCTCTGGGGT      78079       T  A
                                AGCAGG GT TCTGGGGT
                                |||||| || ||||||||
                                TCGTCC CG AGACCCCA
                                   _ _
GAM3463  LOC253716 5'  GATCAAAAATCTGGGGT     78080    G    TGT
                                GA CAGG   ATCTGGGGT
                                || ||||   |||||||||
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                                CT GTTT   TAGACCCCA
                                 A    T__
GAM3463  LOC254181 5'  GAGCCAGTTCTGGGGT      78081      A   GTA
                                GAGC GGT   TCTGGGGT
                                |||| |||   ||||||||
                                CTCG TCA   AGACCCCA
                                  G   ___
GAM3463  LOC255413 3'  GAACAGGTGTTCTCTGGG    78082          A_
                                GAGCAGGTGT  TCTGGG
                                ||||||||||  ||||||
                                CTTGTCCACA  AGACCC
                                      AG
GAM3463  LOC255480 3'  GAGCAAGGTGTCTGGGGT    78083        T  A
                                GAGCAGG GT TCTGGGGT
                                ||||||| || ||||||||
                                CTCGTTC CA AGACCCCA
                                    _  C
GAM3463  LOC256329 3'  GGCAGGTGTCCGCGGT      78084    A      TA    G
                                G GCAGGTG  TCTG GGT
                                | |||||||  |||| |||
                                C CGTCCAC  AGGC CCA
                                _      __    G
GAM3463  LOC256338 3'  AAGCCTAGCTGTCTGGGGT    77967      A_   GTA
                                GAGC  GGT   TCTGGGGT
                                ||||  |||   ||||||||
                                TTCG  TCG   AGACCCCA
                                  GA   AC_
GAM3463  LOC257181 3'  GGCTTTGTGATCTGGGGT    77993    A  AG_   T
                                G GC   GTG ATCTGGGGT
                                | ||   ||| |||||||||
                                C CG   CAC TAGACCCCA
                                 _  AAA   _
GAM3463  LOC51063  3'  GAGCAAGCAGTGGGGT      78085         TATC
                                GAGCAGGTG    TGGGGT
                                |||||||||    ||||||
                                CTCGTTCGT    ACCCCA
                                     C___
GAM3463  LOC56996  3'  GAGTTAGTGTGCTGGGGT    78086     CA    AT
                                GAG  GGTGT  CTGGGGT
                                |||  |||||  |||||||
                                CTC  TCACA  GACCCCA
                                  AA    C_
GAM3463  LOC91373  3'  AGCAGGCAGCTGGGGT      78087         TAT
                                AGCAGGTG   CTGGGGT
                                ||||||||   |||||||
                                TCGTCCGT   GACCCCA
                                     C__
GAM3463  LOC93190  3'  GAGCTGCTCCTGGGGT      78088      AGG   A
                                GAGC   TGT TCTGGGGT
                                ||||   ||| ||||||||
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                                CTCG   ACG GGACCCCA
                                  ___  A
GAM3463 LOC93259 5' AGTGGGTGTGACCTGAGG    78089    CA    _
                                AG  GGTGT ATCTGGGG
                                ||  ||||| ||||||||
                                TC  CCACA TGGACTCC
                                 AC    C
GAM3464 ABCC1    3' GGAAGCACCAGGAAACCACT   78092         ACCGT
                                GGAAGTACCA    GACCACT
                                ||||||||||    |||||||
                                CCTTCGTGGT    TTGGTGA
                                      CCT__
GAM3464 ABCC1    3' GGAAGCACCAGGAAACCACT   78092         ACCGT
                                GGAAGTACCA    GACCACT
                                ||||||||||    |||||||
                                CCTTCGTGGT    TTGGTGA
                                      CCT__
GAM3464 ABCC1    3' GGAAGCACCAGGAAACCACT   78092         ACCGT
                                GGAAGTACCA    GACCACT
                                ||||||||||    |||||||
                                CCTTCGTGGT    TTGGTGA
                                      CCT__
GAM3464 ARHGEF12 3' AGGAAATACTGACCAAAGCTC  78093         CAACCG    ___
                                AGGAAGTAC     TGACCA  CTC
                                |||||||||     ||||||  |||
                                TCCTTTATG     ACTGGT  GAG
                                      _______     TTC
GAM3464 CBFB     3' AGGAGGTGCCAAATGAC     78094     A  A   CC
                                AGGA GT CCAA  GTGAC
                                |||| || ||||  |||||
                                TCCT CA GGTT  TACTG
                                  C  C   __
GAM3464 CBFB     3' AGGAGGTGCCAAATGAC     78094     A  A   CC
                                AGGA GT CCAA  GTGAC
                                |||| || ||||  |||||
                                TCCT CA GGTT  TACTG
                                  C  C   __
GAM3464 DHCR24   3' GGAAGATGCCTGACCACT    78095     TACCAA  G
                                GGAAG     CC TGACCACT
                                |||||     || ||||||||
                                CCTTC     GG ACTGGTGA
                                   TAC___  _
GAM3464 FEZ1     3' AGCAAGTACCAGGGCACTGCTC 78096    G      ACC  G  CA
                                AG AAGTACCA   GT AC  CTC
                                || ||||||||   || ||  |||
                                TC TTCATGGT   CG TG  GAG
                                 G       CC_  _  AC
GAM3464 KLRG1    3' AGGAAGTACCACCTTGCCCTC  78097         A  G  A  A
                                AGGAAGTACCA CC TG CC CTC
                                |||||||||| || || || |||
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                                TCCTTCATGGT GG AC GG GAG
                                      _ A _ _
GAM3464  NAGA     3'  AGGAAGTACAATCTTCTGGTCA 78098        CAACCG_ AC
                CT                  AGGAAGTAC      TG  CACT
                                    |||||||||      ||  ||||
                                    TCCTTCATG      AC  GTGA
                                        TTAGAAG  CA
GAM3464  NKTR     3'  GGATGTATGATGACCACT    78099     A   CCAACC
                                    GGA GTA     GTGACCACT
                                    ||| |||     |||||||||
                                    CCT CAT     TACTGGTGA
                                      A   AC____
GAM3464  NOTCH2   3'  AGGAAGTAACCATAGTACCACT 78100        CCA     __
                                    AGGAAGTA   ACCGTG  ACCACT
                                    ||||||||   ||||||  ||||||
                                    TCCTTCAT   TGGTAT  TGGTGA
                                        ___     CA
GAM3464  PTPN7    3'  AGGGGTACCCCCAGATCACTC  78101     AA    AA   T  C
                                    AGG  GTACC  CCG GA CACTC
                                    |||  |||||  ||| || |||||
                                    TCC  CATGG  GGT CT GTGAG
                                      C_    G_  _ A
GAM3464  PTPN7    3'  AGGGGTACCCCCAGATCACTC  78101     AA    AA   T  C
                                    AGG  GTACC  CCG GA CACTC
                                    |||  |||||  ||| || |||||
                                    TCC  CATGG  GGT CT GTGAG
                                      C_    G_  _ A
GAM3464  TEX13B   5'  AGGAAGTACAGGCCAACCCCG  78102        _____    G
                                    AGGAAGTA    CCAACC TG
                                    ||||||||    |||||| ||
                                    TCCTTCAT    GGTTGG GC
                                        GTCC     G
GAM3464  TEX13B   5'  AGGAAGTACAGGCCAACCCCG  78102        _____    G
                                    AGGAAGTA    CCAACC TG
                                    ||||||||    |||||| ||
                                    TCCTTCAT    GGTTGG GC
                                        GTCC     G
GAM3464  TH1L     3'  AGGAAGTACATAACCTCGAC   78103        C_   G
                                    AGGAAGTAC  AACC TGAC
                                    |||||||||  |||| ||||
                                    TCCTTCATG  TTGG GCTG
                                        TA    A
GAM3464  CMG2     3'  AGGAAGCATCCACAGTTGGCCA 78104        _  ACCG  A
                CT                  AGGAAGTA CCA    TG CCACT
                                    |||||||| |||    || |||||
                                    TCCTTCGT GGT    AC GGTGA
                                        A   GTCA  C
GAM3464  DKFZp547E052 3'  AGGAAGTACTACTAGTGGACTC 78105        CAACC   ACC
                                    AGGAAGTAC    GTG   ACTC
                                    |||||||||    |||   ||||
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                                TCCTTCATG    CAC   TGAG
                                     ATGAT   C__
GAM3464  INPP5E    3'  GGAAGCACCGACCGCCCT    78106        A   TGA  A
                                GGAAGTACC ACCG   CC CT
                                ||||||||| ||||   || ||
                                CCTTCGTGG TGGC   GG GA
                                     C   ___  _
GAM3464  KIAA0082  3'  AGGAAATGGGAGTGACCACT   78107       ACCAACC
                                AGGAAGT      GTGACCACT
                                |||||||      |||||||||
                                TCCTTTA      CACTGGTGA
                                   CCCT___
GAM3464  KLHL8     3'  AGGAAGTATCAAATTTAAC    78108        C   CCG
                                AGGAAGTA CAA   TGAC
                                |||||||| |||   ||||
                                TCCTTCAT GTT   ATTG
                                     A   TAA
GAM3464  NPGPR     5'  AGGAAGCATCAGTATCACCA   78109        C  ACC  G
                                AGGAAGTA CA   GT ACCA
                                |||||||| ||   || ||||
                                TCCTTCGT GT   TA TGGT
                                     A  CA_  G
GAM3464  LOC126297 5'  GGACAGTGCTGGCTGACCACTC 78110     _   ACCAACCG
                                GGA AGT       TGACCACTC
                                ||| |||       |||||||||
                                CCT TCA       ACTGGTGAG
                                  G   CGACCG__
GAM3464  LOC133383 5'  AGGAGGTCCCCTTGACCACT   78111     A  A  AA  G
                                AGGA GT CC  CC TGACCACT
                                |||| || ||  || ||||||||
                                TCCT CA GG  GG ACTGGTGA
                                  C  _  __  A
GAM3464  LOC146184 3'  AGCAGCCAACCGTGGTCATTC  78112      _       AC  C
                                AGTA CCAACCGTG  CA TC
                                |||| |||||||||  || ||
                                TCGT GGTTGGCAC  GT AG
                                  C        CA  A
GAM3464  LOC150848 5'  AGGAAGTATTGGCCAGCT    78113        CCAACCG  A  _
                                AGGAAGTA      TG CCA CT
                                ||||||||      || ||| ||
                                TCCTTCAT      AC GGT GA
                                     A_______  C   C
GAM3464  LOC153561 5'  GGAATGCCCCACAATGACCACT 78114      _ TA   ACC
            C                    GGAA G  CCA   GTGACCACTC
                                ||||  |  |||   ||||||||||
                                CCTT C  GGT   TACTGGTGAG
                                  A GG   GT_
GAM3464  LOC197285 3'  GGAAGCACCGTGCCGCTGCTC  78115         AA_   GACCA
                                GGAAGTACC   CCGT    CTC
                                |||||||||   ||||    |||
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                                CCTTCGTGG  GGCG    GAG
                                     CAC   AC___
GAM3464  LOC220840 3'  AGGATGTACCAACAATCAC   78116     A      C  G
                                AGGA GTACCAAC GT AC
                                |||| |||||||| || ||
                                TCCT CATGGTTG TA TG
                                  A       T  G
GAM3464  LOC254122 3'  GGAAGGGCACTAGTGACCACTC 78117      TAC  ACC
                                GGAAG   CA   GTGACCACTC
                                |||||   ||   ||||||||||
                                CCTTC   GT   CACTGGTGAG
                                   CC_  GAT
GAM3464  LOC254978 5'  GGAATGCCCCACAATGACCACT 78118     _ TA   ACC
                                GGAA G  CCA   GTGACCACT
                                |||| |  |||   |||||||||
                                CCTT C  GGT   TACTGGTGA
                                  A GG   GT_
GAM3465  DMRT2    3'  GCTTGTTGTGGTTGTTAT    78121          G  GG
                                GTTTGTTGTGG TG  AT
                                |||||||||| ||  ||
                                CGAACAACACC AC  TA
                                      A  AA
GAM3465  DTR      3'  TCGTTTTGGTGAGGTGGGTGGG 78122      ____  TT
            ATTATA                 CGTT    TG  GTGGGTGGGATTATA
                                ||||   ||  ||||||||||||||
                                GCAA    AC  CACCCACCCTAATAT
                                  AACC  TC
GAM3465  KIAA1348  3'  TTGTTGGTTTTGTGGGATTATA 78123       TGG__
                                TTGTTG    GTGGGATTATA
                                ||||||    ||||||||||
                                AACAAC    CACCCTAATAT
                                   CAAAA
GAM3465  OSBPL9    3'  GTTTGTTGCTGAATTAT     78124         GGGTG
                                GTTTGTTGT    GGATTAT
                                |||||||||    |||||||
                                CAAACAACG    CTTAATA
                                     A____
GAM3466  DKFZP564C103 3'  TGTTTTATACTGAGGCATGTTT 78127        G  G
                                TGTTTTG TAT TGAGGCATGTTT
                                ||||||| ||| ||||||||||||
                                ACAAAAT ATG ACTCCGTACAAA
                                     _  _
GAM3466  PEG10    3'  GGCATATGTGGGGTATGTTT   78128        A  C__
                                GGTATGTG GG   ATGTTT
                                |||||||| ||   ||||||
                                CCGTATAC CC   TACAAA
                                     A  CCA
GAM3466  LOC201651 3'  TGTTTTGTTATCTAACATGTTT 78129        G  G  AG
                                TGTTTTG TAT TG  GCATGTTT
                                ||||||| ||| ||  ||||||||
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                                ACAAAAC ATA AT  TGTACAAA
                                   A  G  __
GAM3467  EGFL5    3'  CTTGGAGAGATGAGTTCACCT  78132      C  TTACA
                                CTTGG AG    AGTTCACCT
                                ||||| ||    |||||||||
                                GAACC TC    TCAAGTGGA
                                  _  TCTAC
GAM3467  IFNAR1   3'  TACTTGACACAGTTCA      78133        AGTT   A
                                TACTTGGC    ACA GTTCA
                                ||||||||    ||| |||||
                                ATGAACTG    TGT CAAGT
                                     _____  _
GAM3467  PKHD1    3'  TTGAAGGGCAAGTTCACCT    78134      C  TTA
                                TTGG AG   CAAGTTCACCT
                                |||| ||   ||||||||||
                                AACT TC   GTTCAAGTGGA
                                  _  CC_
GAM3467  UNG      3'  TACTTGGCAGTCTGTGCTGCCT 78135           ACAA   CA
                                TACTTGGCAGTT    GTT  CCT
                                ||||||||||||    |||  |||
                                ATGAACCGTCAG    CGA  GGA
                                      ACA_   C_
GAM3467  UNG      3'  TACTTGGCAGTCTGTGCTGCCT 78135           ACAA   CA
                                TACTTGGCAGTT    GTT  CCT
                                ||||||||||||    |||  |||
                                ATGAACCGTCAG    CGA  GGA
                                      ACA_   C_
GAM3467  ZNF189   3'  TACTTGGCAGTCATAATATGTA 78136           C  ___  T
            CAC                    TACTTGGCAGTTA AA   GT CAC
                                ||||||||||||| ||   || |||
                                ATGAACCGTCAGT TT   CA GTG
                                       A  ATA  T
GAM3467  CMG1     5'  ACTTCAGTTGTAAGTTCAC    78137      GG    AC
                                ACTT  CAGTT  AAGTTCAC
                                ||||  |||||  ||||||||
                                TGAA  GTCAA  TTCAAGTG
                                  __    CA
GAM3467  FLJ20793 3'  TACTTGGCATTTAAATGTT    78138        G   CAA
                                TACTTGGCA TTA   GTT
                                ||||||||| |||   |||
                                ATGAACCGT AAT   CAA
                                     A   TTA
GAM3467  KIAA1198 3'  TTGGGAGTTGAGTTCACCT    78139      C    ACA
                                TTGG AGTT   AGTTCACCT
                                |||| ||||   |||||||||
                                AACC TCAA   TCAAGTGGA
                                  C   C__
GAM3467  KIAA1328 3'  TTGGATAAACACAAGTTTGCCT 78140      CAGT_      CA
                                TTGG    TACAAGTT  CCT
                                ||||    ||||||||  |||
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                                AACC    GTGTTCAA  GGA
                                  TATTT       AC
GAM3467  KNSL6    3'  TACTTGGCATTTACCAGAACCT 78141        G   A  TTC
                                TACTTGGCA TTAC AG   ACCT
                                ||||||||| |||| ||   ||||
                                ATGAACCGT AATG TC   TGGA
                                     A   G  T__
GAM3467  QKI      5'  CACTTGGCGGCGGAGTTCGCCT 78142        A  TACA    A
                                TACTTGGC GT    AGTTC CCT
                                |||||||| ||    ||||| |||
                                GTGAACCG CG    TCAAG GGA
                                     C  CC__    C
GAM3467  LOC151391 3'  TACTAGCAATGAGTTCAC    78143     T     TACA     C
                                TACT GGCAGT    AGTTCA C
                                |||| ||||||    |||||| |
                                ATGA TCGTTA    TCAAGT G
                                  _     C___     A
GAM3467  LOC153339 5'  CACTTGACATGAGTTTACC    78144        GTTACA    C
                                TACTTGGCA     AGTT ACC
                                |||||||||     |||| |||
                                GTGAACTGT     TCAA TGG
                                     AC____    A
GAM3467  LOC157506 3'  TTGGCAACAACCTAAGTTCAC  78145       TT  __
                                TTGGCAG  AC  AAGTTCAC
                                |||||||  ||  ||||||||
                                AACCGTT  TG  TTCAAGTG
                                    GT  GA
GAM3467  LOC196746 5'  TTGGACAGCAAGTTCACCT    78146     _  TTA
                                TTGG CAG   CAAGTTCACCT
                                |||| |||   ||||||||||
                                AACC GTC   GTTCAAGTGGA
                                  T  ___
GAM3467  LOC200282 5'  TACTTGACACAGTTCA      78133        AGTT   A
                                TACTTGGC    ACA GTTCA
                                ||||||||    ||| |||||
                                ATGAACTG    TGT CAAGT
                                     ____  _
GAM3467  LOC254987 3'  TACTAGGGTTTACAAGTT    78147     T  CAG
                                TACT GG   TTACAAGTT
                                |||| ||   |||||||||
                                ATGA CC   AATGTTCAA
                                  T  CA_
GAM3467  LOC51291  3'  CTTGGCAGTGACCTGTGTC    78148        T  AA  _
                                CTTGGCAGT AC  GT TC
                                ||||||||| ||  || ||
                                GAACCGTCA TG  CA AG
                                     C  GA  C
GAM3468  PLAG1    3'  CCCCCCATTTACATTAT     78151    A    C
                                CC TCTCA TTACATTAT
                                || ||||| |||||||||
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                                GG GGGGT AATGTAATA
                                 _    A
GAM3469  ABCC1    5'  CGGGCGGCGGGTGATCGGGC   78154    T_ T   C    A
                                CG  CG CGGG GATCG GC
                                ||  || |||| ||||| ||
                                GC  GC GCCC CTAGC CG
                                 CC  C    A    C
GAM3469  ABCC1    5'  CGGGCGGCGGGTGATCGGGC   78154    T_ T   C    A
                                CG  CG CGGG GATCG GC
                                ||  || |||| ||||| ||
                                GC  GC GCCC CTAGC CG
                                 CC  C    A    C
GAM3469  ABCC1    5'  CGGGCGGCGGGTGATCGGGC   78154    T_ T   C    A
                                CG  CG CGGG GATCG GC
                                ||  || |||| ||||| ||
                                GC  GC GCCC CTAGC CG
                                 CC  C    A    C
GAM3469  ABCC1    5'  CGGGCGGCGGGTGATCGGGC   78154    T_ T   C    A
                                CG  CG CGGG GATCG GC
                                ||  || |||| ||||| ||
                                GC  GC GCCC CTAGC CG
                                 CC  C    A    C
GAM3469  ABCC1    5'  CGGGCGGCGGGTGATCGGGC   78154    T_ T   C    A
                                CG  CG CGGG GATCG GC
                                ||  || |||| ||||| ||
                                GC  GC GCCC CTAGC CG
                                 CC  C    A    C
GAM3469  ABCC1    5'  CGGGCGGCGGGTGATCGGGC   78154    T_ T   C    A
                                CG  CG CGGG GATCG GC
                                ||  || |||| ||||| ||
                                GC  GC GCCC CTAGC CG
                                 CC  C    A    C
GAM3469  CYP1B1   5'  CGTCGTCAGTGCCAGGAGC   78155        _ GATC
                                CGTCGTCGG GC   GAGC
                                ||||||||| ||   ||||
                                GCAGCAGTC CG   CTCG
                                      A  GTC_
GAM3469  EFNB1    5'  GCTCCCGGGCGATCGAGC    78156    CG
                                GT  TCGGGCGATCGAGC
                                ||  ||||||||||||||
                                CG  GGCCCGCTAGCTCG
                                 AG
GAM3469  EGFL5    5'  CGTCGTCAGGGTCAGC      78157         CGA  G
                                CGTCGTCGGG   TC AGC
                                ||||||||||   || |||
                                GCAGCAGTCC   AG TCG
                                      C__  _
GAM3469  INPP5A   5'  GTCGTCGAAGAGCGAGC     78158         C  T
                                GTCGTCGGG GA CGAGC
                                ||||||||| || |||||
```

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                                CAGCAGCTT CT GCTCG
                                     _ C
GAM3469 KCNH3    5' CGCCGTCGGGGCCCGGAGC   78159        CGA  _
                                CGTCGTCGGG   TCG AGC
                                |||||||||   ||| |||
                                GCGGCAGCCC   GGC TCG
                                      CG_  C
GAM3469 USP7     5' CGTCGTCGGCGACGGC     78160        G  T  A
                                CGTCGTCGG CGA CG GC
                                ||||||||| ||| || ||
                                GCAGCAGCC GCT GC CG
                                     _  _ _
GAM3469 caspr5   5' CCTCGTCGGGCGCGAGAGC   78161   G       ATC
                                C TCGTCGGGCG   GAGC
                                | ||||||||||   ||||
                                G AGCAGCCCGC   CTCG
                                 G        GCT
GAM3469 caspr5   5' CCTCGTCGGGCGCGAGAGC   78161   G       ATC
                                C TCGTCGGGCG   GAGC
                                | ||||||||||   ||||
                                G AGCAGCCCGC   CTCG
                                 G        GCT
GAM3469 CBX6     3' CCTCGTCCAAAATCGAGC    78162   G    G  C
                                C TCGTC GG GATCGAGC
                                | ||||| || ||||||||
                                G AGCAG TT TTAGCTCG
                                 G    G  _
GAM3469 CDC42BPB 5' CGTCGTCGCGCCCCGGC     78163       G  GA  A
                                CGTCGTCG GC  TCG GC
                                |||||||| ||  ||| ||
                                GCAGCAGC CG  GGC CG
                                     G  G_  _
GAM3469 DGKD     3' CGTCGCCGGGCTCTGC      78164         GA  GA
                                CGTCGTCGGGC  TC  GC
                                ||||||||||  ||  ||
                                GCAGCGGCCCG  AG  CG
                                      __  A_
GAM3469 DKFZP434B205 3' GTTGTCGGGCGACAGGC     78165    C       T  A
                                GT GTCGGGCGA CG GC
                                || |||||||| || ||
                                CA CAGCCCGCT GT CG
                                 A        _ C
GAM3469 FLJ11078 5' CGCCGTCGCGCGTTCGAG    78166        G  A
                                CGTCGTCG GCG TCGAG
                                |||||||| ||| |||||
                                GCGGCAGC CGC AGCTC
                                     G  A
GAM3469 FLJ20400 5' CGTCGCCGCCGCCGCGAGC   78167        GG  AT_
                                CGTCGTCG  CG   CGAGC
                                |||||||| ||   |||||
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                                GCAGCGGC  GC   GCTCG
                                    G_  GGC
GAM3469  FLJ21939  5'  CGCCGTCGGGACCAGC      78168          CG   G
                                CGTCGTCGGG  ATC AGC
                                ||||||||||  ||| |||
                                GCGGCAGCCC  TGG TCG
                                      __   _
GAM3469  KIAA1229  5'  CGTCGTCGTGACGACAGC    78169          _     CG
                                CGTCGTCG GGCGAT  AGC
                                ||||||||| ||||||  |||
                                GCAGCAGC CTGCTG  TCG
                                    A     __
GAM3469  KIAA1466  5'  GTCGCCGGGTGACAGGAG    78170          C   C_
                                GTCGTCGGG GAT  GAG
                                ||||||||| |||  |||
                                CAGCGGCCC CTG  CTC
                                     A   TC
GAM3469  KRTAP3-2  3'  CGTTGTCGGGCACTGAGC    78171     C       ATC
                                CGT GTCGGGCG   GAGC
                                ||| ||||||||   ||||
                                GCA CAGCCCGT   CTCG
                                  A       GA_
GAM3469  MGC4415   3'  GCCGTCGGGCGGGAGC      78172           ATC
                                GTCGTCGGGCG   GAGC
                                ||||||||||   ||||
                                CGGCAGCCCGC   CTCG
                                     C__
GAM3469  MGC4701   5'  CGCCGTCGACACCGAGC     78173          G G
                                CGTCGTCGG C ATCGAGC
                                ||||||||| | |||||||
                                GCGGCAGCT G TGGCTCG
                                     _ _
GAM3469  PNMA1     5'  CGTCGTCGTGCAGCGGGC    78174          G   AT  A
                                CGTCGTCG GCG  CG GC
                                |||||||| |||  || ||
                                GCAGCAGC CGT  GC CG
                                    A   C_  C
GAM3469  RAB24     5'  CGCGTCGGGCTCGAGC      78175     T      GA
                                CG CGTCGGGC  TCGAGC
                                || ||||||||  ||||||
                                GC GCAGCCCG  AGCTCG
                                  _      ___
GAM3469  LOC123096 5'  CGCCGTCGGGGTCCCCGAGC  78176           CGA_
                                CGTCGTCGGG    TCGAGC
                                ||||||||||    ||||||
                                GCGGCAGCCC    GGCTCG
                                     CAGG
GAM3469  LOC150946 3'  CGTTCTCGGGCAAAGAAGC   78177     CG      TC
                                CGT  TCGGGCGA  GAGC
                                |||  ||||||||  ||||
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                                GCA  AGCCCGTT  TTCG
                                  AG       TC
GAM3469  LOC219397 3'  CGTCGTCGAAGACCTGGGC   78178          C   GA_
                                CGTCGTCGGG GATC   GC
                                |||||||||| ||||   ||
                                GCAGCAGCTT CTGG   CG
                                      _   ACC
GAM3469  LOC219920 3'  GTCGTGATAAATCGAGC     78179      C  GC
                                GTCGT GG  GATCGAGC
                                ||||| ||  ||||||||
                                CAGCA CT  TTAGCTCG
                                   _ AT
GAM3469  LOC256542 3'  GCCGTCGGCACGAGC       78180        G  AT
                                GTCGTCGG CG  CGAGC
                                |||||||| ||  |||||
                                CGGCAGCC GT  GCTCG
                                     _ __
GAM3469  LOC256812 5'  CGCTCGGAGATCGAGC      78181     CG    C
                                CGT  TCGGG GATCGAGC
                                |||  ||||| ||||||||
                                GCG  AGCCT CTAGCTCG
                                   __    _
GAM3470  ABCG5    5'  ACCCCGGAGTCCCTTGGGACA  78184      GCA       CA
                                ATCC   GGAGTCCCT  GGACA
                                ||||   |||||||||  |||||
                                TGGG   CCTCAGGGA  CCTGT
                                  G__        AC
GAM3470  ATRN     3'  TCCTGGCTGTGTCCTCAGGA   78185    __ AGGA   C
                                TCC  GC    GTCC TCAGGA
                                |||  ||    |||| ||||||
                                AGG  CG    CAGG AGTCCT
                                  AC  ACA_   _
GAM3470  KCNS3    5'  CACCTGCAGGAGTCCGGAC    78186     C        CTCA
                                CATC GCAGGAGTCC    GGAC
                                |||| ||||||||||    ||||
                                GTGG CGTCCTCAGG    CCTG
                                  A        ____
GAM3470  KIF3C    3'  CATCCCAGGAGTCTATTGGA   78187      G       CCTCA
                                CATCC CAGGAGTC     GGA
                                ||||| ||||||||     |||
                                GTAGG GTCCTCAG     CCT
                                   _       ATAA_
GAM3470  PPP2R5D  3'  GCAGGAGCCATGCTTGGGGCA  78188         C__  CA  A
                                GCAGGAGTC   CT  GG CA
                                |||||||||   ||  || ||
                                CGTCCTCGG   GA  CC GT
                                      TAC  AC  C
GAM3470  PRKCH    5'  CAGGCCAGCCCTCGGGACA   78189      __ T    A
                                CAGG  AG CCCTC GGACA
                                ||||  || ||||| |||||
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                                GTCC  TC GGGAG CCTGT
                                  GG  _    C
GAM3470  ROCK2    5'  CCCGCAGGAGTCCTCGGG    78190           C  A
                                TCCGCAGGAGTCC TC GG
                                |||||||||||| || ||
                                GGGCGTCCTCAGG AG CC
                                       _  C
GAM3470  SLC1A4   3'  GCAGGGCCAGGCCAGGACA   78191      A   CC_
                                GCAGG GTC   TCAGGACA
                                ||||| |||   ||||||||
                                CGTCC CGG   GGTCCTGT
                                   _   TCC
GAM3470  C6orf33  5'  TCCGTGCCGCGCCCTCAGGACA 78192      CAGGA  _
                                TCCG    GT CCCTCAGGACA
                                ||||    || ||||||||||
                                AGGC    CG GGGAGTCCTGT
                                  ACGG_  C
GAM3470  C8orf13  5'  CGCAGGAATCTCGGGGCA    78193         CC  A  A
                                CGCAGGAGTC  TC GG CA
                                ||||||||||  || || ||
                                GCGTCCTTAG  AG CC GT
                                      __  C  C
GAM3470  CCRK     3'  CACAGGAGTCCCTCAGGGCA   78194              A
                                CGCAGGAGTCCCTCAGG CA
                                |||||||||||||||| ||
                                GTGTCCTCAGGGAGTCC GT
                                       C
GAM3470  CINP     3'  TCCGCAGCCGTCTCAGGAC    78195       GA   CC
                                TCCGCAG  GTC  TCAGGAC
                                |||||||  |||  |||||||
                                AGGCGTC  CAG  AGTCCTG
                                   GG  __
GAM3470  CL24751  3'  TCCACAGGGCACAGGC      78196        A  CCCT   A
                                TCCGCAGG GT   CAGG C
                                |||||||| ||   |||| |
                                AGGTGTCC CG   GTCC G
                                     _  T___   C
GAM3470  DKFZp434C0923 3'  CACGAGTCCTTCAGGACA    78197    G     C
                                CA GAGTCC TCAGGACA
                                || |||||| ||||||||
                                GT CTCAGG AGTCCTGT
                                 G     A
GAM3470  DKFZP564D172 3'  CCCGCGCGGTCTCCTTCAGGGC 78198      A_  AG   C    A
            A                    TCCGC  GG  TCC TCAGG CA
                                 |||||  ||  ||| ||||| ||
                                 GGGCG  CC  AGG AGTCC GT
                                    CG  AG   A    C
GAM3470  DKFZp762P2111 3'  TCTGCACTGCCCCTCAGG    78199    C   GGA
                                TC GCA   GTCCCTCAGG
                                || |||   ||||||||||
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                                AG CGT   CGGGGAGTCC
                                 A  GA_
GAM3470  FEM-2    3'  CACTTGTGAGCCCCCTCTCAGG 78200     AG__      ___
                                CGC   GAGTCCC   TCAGG
                                |||   |||||||   |||||
                                GTG   CTCGGGG   AGTCC
                                  AACA      GAG
GAM3470  FLJ13693 3'  TCTGCGGGGTCCCAGGAC    78201    C  A  A    TC
                                TC GC GG GTCCC  AGGAC
                                || || || |||||  |||||
                                AG CG CC CAGGG  TCCTG
                                 A  C  _    __
GAM3470  FLJ14451 3'  CATCCCAACCCCTCCTCAGGAC 78202       G   GAG  _
              A                  CATCC CAG   TC CCTCAGGACA
                                |||||| |||   || ||||||||||
                                GTAGG GTT   GG GGAGTCCTGT
                                  _  GG_  A
GAM3470  FLJ20202 3'  ATCTCGCAATTCCTCAGGA   78203     _    GAGTC
                                ATC CGCAG    CCTCAGGA
                                ||| |||||    ||||||||
                                TAG GCGTT    GGAGTCCT
                                  A    AA___
GAM3470  FLJ20277 3'  CAAGGCCCTCAGGACA      78204      A T
                                CAGG G CCCTCAGGACA
                                |||| | ||||||||||
                                GTTC C GGGAGTCCTGT
                                  _ _
GAM3470  FLJ22246 3'  CATCAGCAGGAGTCAGGA    78205      C       CCTC
                                CATC GCAGGAGTC    AGGA
                                |||| |||||||||    ||||
                                GTAG CGTCCTCAG    TCCT
                                  T       _____
GAM3470  FLJ22494 3'  CGTCAGCGTGCCCTCAGG    78206    _  GA  _
                                CG CAG  GT CCCTCAGG
                                || |||  || ||||||||
                                GC GTC  CA GGGAGTCC
                                 A  G_  C
GAM3470  FLJ23604 3'  TCTGCAGTGTCCTTAGGGCA   78207    C   GA   CTC   A
                                TC GCAG  GTCC   AGG CA
                                || ||||  ||||   ||| ||
                                AG CGTC  CAGG   TCC GT
                                 A   A_   AA_   C
GAM3470  KCNE4    3'  CACCCGCAGGGGTCCCGGGG   78208         A    TCA
                                CATCCGCAGG GTCCC   GG
                                |||||||||| |||||   ||
                                GTGGGCGTCC CAGGG   CC
                                      C    CC_
GAM3470  KIAA0793 3'  CATCTGTTGAGAAGCCTCAGGA 78209     CGCAG   TC_
              CA                  CATC    GAG   CCTCAGGACA
                                ||||    |||   ||||||||||
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                                GTAG    CTC   GGAGTCCTGT
                                  ACAA_  TTC
GAM3470 KIAA0930 3' CATCCCAGGAGTCTAACA    78210      G      CCT
                                CATCC CAGGAGTC   CA
                                ||||| ||||||||   ||
                                GTAGG GTCCTCAG   GT
                                  _       ATT
GAM3470 KPTN     3' CATCCTGTCCTTCAGGAC    78211      GCAGGA   C
                                CATCC     GTCC TCAGGAC
                                |||||     |||| |||||||
                                GTAGG     CAGG AGTCCTG
                                  A_____    A
GAM3470 MGC21675 5' CACCCGCAGGAGTTGGGAC   78212           CCCTCA
                                CATCCGCAGGAGT     GGAC
                                ||||||||||||      ||||
                                GTGGGCGTCCTCA     CCTG
                                       AC____
GAM3470 MGC3222  3' TCCAGCTTTTCTCCTCAGGACA 78213    _ AGGAG _
                                TCC GC    TC CCTCAGGACA
                                ||| ||    || ||||||||||
                                AGG CG    AG GGAGTCCTGT
                                  T  AAA__  A
GAM3470 MGC4054  5' CCCGCAGCGCTCTCAGGACA  78214       GA  CC
                                TCCGCAG  GT  CTCAGGACA
                                |||||||  ||  |||||||||
                                GGGCGTC  CG  GAGTCCTGT
                                    G_  A_
GAM3470 RAB21    3' CATCCACAGAAACTCAGGA   78215          TCC
                                CATCCGCAGGAG   CTCAGGA
                                ||||||||||||   |||||||
                                GTAGGTGTCTTT   GAGTCCT
                                       ___
GAM3470 TRAF3    5' CACCTGCCTCCCTCAGG     78216     C  AGGAG
                                CATC GC    TCCCTCAGG
                                |||| ||    |||||||||
                                GTGG CG    AGGGAGTCC
                                  A  G____
GAM3470 WBSCR21  5' CCTGCAGGGCCCTCAGG     78217    _    A T
                                CC GCAGG G CCCTCAGG
                                || ||||| | ||||||||
                                GG CGTCC C GGGAGTCC
                                 A    _ _
GAM3470 LOC148021 3' TCCACAGGGCACAGGC      78196        A  CCCT   A
                                TCCGCAGG GT    CAGG C
                                |||||||| ||    |||| |
                                AGGTGTCC CG    GTCC G
                                     _ T___    C
GAM3470 LOC149069 3' TCCCCAGGAGTCCCTACA    78218     G         _
                                TCC CAGGAGTCCCT CA
                                ||| ||||||||||| ||
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                                AGG GTCCTCAGGGA GT
                                  G         T
GAM3470  LOC149684 5'  CATCCGCAGGAGTCCAGGC    78219             CTC   A
                                CATCCGCAGGAGTCC   AGG C
                                |||||||||||||||   ||| |
                                GTAGGCGTCCTCAGG   TCC G
                                                  ____  _
GAM3470  LOC150147 3'  CGCACCAGTTTTCAGGACA    78220      GG   CCC
                                CGCA  AGT   TCAGGACA
                                ||||  |||   ||||||||
                                GCGT  TCA   AGTCCTGT
                                  GG   AA_
GAM3470  LOC151602 3'  GCATTTGCCTCCTCAGGAC    78221     GGA  _
                                GCA   GTC CCTCAGGAC
                                |||   ||| |||||||||
                                CGT   CGG GGAGTCCTG
                                  AAA   A
GAM3470  LOC153684 5'  TCCTGCAGGAGAGGTACCGGGA 78222      _      TCCC_  A
            CA                    TCC GCAGGAG     TC GGACA
                                ||| |||||||     || |||||
                                AGG CGTCCTC     GG CCTGT
                                  A      TCCAT  C
GAM3470  LOC170394 5'  TCCGCTCTCCCCTCAGGGCA   78223       AGGAG        A
                                TCCGC     TCCCTCAGG CA
                                |||||     ||||||||| ||
                                AGGCG     GGGGAGTCC GT
                                   AGA__        C
GAM3470  LOC196549 5'  CATCTGAGGAAGAGGCCAGGAC 78224      CGC     TCCC
            A                     CATC   AGGAG    TCAGGACA
                                ||||   |||||    ||||||||
                                GTAG   TCCTT    GGTCCTGT
                                  AC_    CTCC
GAM3470  LOC199899 3'  ATCTCATTAATCCTCAGGACA  78225     CG  GG    C
                                ATC  CA  AGTCC TCAGGACA
                                |||  ||  ||||| ||||||||
                                TAG  GT  TTAGG AGTCCTGT
                                  A_  AA    _
GAM3470  LOC253769 5'  ATCCGCAGTGCGGTTCCTCAGG 78226         GA__  C      A
            GCA                     ATCCGCAG    GT CCTCAGG CA
                                ||||||||    || ||||||| ||
                                TAGGCGTC    CA GGAGTCC GT
                                     ACGC  A      C
GAM3470  LOC256158 5'  TCTCGCAGCTCAGGAC      78227     _    GAGTCC
                                TC CGCAG      CTCAGGAC
                                || |||||      ||||||||
                                AG GCGTC      GAGTCCTG
                                 A    _______
GAM3470  LOC86651  5'  CAACTGTTCCTCAGGACA    78228     GA  C
                                CAG  GT CCTCAGGACA
                                |||  || ||||||||||
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                                GTT  CA GGAGTCCTGT
                                  GA  A
GAM3470  LOC93349  3'  CAACTGTTCCTCAGGACA    78228     GA  C
                                CAG  GT CCTCAGGACA
                                |||  || ||||||||||
                                GTT  CA GGAGTCCTGT
                                  GA  A
GAM3471  ABCB9     3'  AGGGGCGGGTGTGGGGAGG   78231      AC    G    A
                                AGGG  GCGGG GTGGG GAGG
                                ||||  ||||| ||||| ||||
                                TCCC  CGCCC CACCC CTCC
                                  __    A    _
GAM3471  ADAM19    3'  GGGGAGAGGTGGGAGGG     78232     ACGC        A
                                GGG   GGGGGTGGGAG GG
                                |||   |||||||||||| ||
                                CCC   TCTCCACCCTC CC
                                  C___         _
GAM3471  ADAM19    3'  AGGGATGCAGGGGTTTGGGGAG 78233       C      ___
              AGG                  AGGGA GCGGGGGT   GGGAGAGG
                                |||||| ||||||||   ||||||||
                                TCCCT CGTCCCCA   CCCTCTCC
                                  A       AAC
GAM3471  ADAMTS8   3'  GGGTTGCGGCAATGGGAG    78234     AC   G
                                GGG  GCGG GGTGGGAG
                                |||  |||| ||||||||
                                CCC  CGCC TTACCCTC
                                  AA   G
GAM3471  ADH5      5'  AGGGGGGCGGGGCGTGGG    78235      AC    _
                                AGGG  GCGGGG GTGGG
                                ||||  |||||| |||||
                                TCCC  CGCCCC CACCC
                                  CC     G
GAM3471  ADRA1A    5'  AGGGGCGCGCGGGGCTGCCGGG 78236      A   _    ____
                                AGGG CGCG GGGGT    GGG
                                |||| |||| |||||    |||
                                TCCC GCGC CCCCG    CCC
                                  C    G     ACGG
GAM3471  ADRA1A    5'  AGGGGCGCGCGGGGCTGCCGGG 78236      A   _    ____
                                AGGG CGCG GGGGT    GGG
                                |||| |||| |||||    |||
                                TCCC GCGC CCCCG    CCC
                                  C    G     ACGG
GAM3471  ADRA1A    5'  AGGGGCGCGCGGGGCTGCCGGG 78236      A   _    ____
                                AGGG CGCG GGGGT    GGG
                                |||| |||| |||||    |||
                                TCCC GCGC CCCCG    CCC
                                  C    G     ACGG
GAM3471  AF3P21    3'  GGGTGTGGGGTGAAGAGG    78237     ACGCG      G
                                GGG    GGGGTGG AGAGG
                                |||    ||||||| |||||
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                                CCC    CCCCACT TCTCC
                                  ACA__     _
GAM3471 AKAP13   3' GAGGCGGGGTGGGGGAGG    78238   C    G   A
                                GA GCGGGG TGGG GAGG
                                || |||||| |||| ||||
                                CT CGCCCC ACCC CTCC
                                 C     _   C
GAM3471 ALDH3A2  5' GGGCGCTGGGGAGTGGGAG   78239    A  _   _
                                GGG CGC GGGG GTGGGAG
                                ||| ||| |||| |||||||
                                CCC GCG CCCC CACCCTC
                                  _  A   T
GAM3471 AP2A1    3' AGGGTGGGGTGGGAGGG     78240     ACGCG       A
                                AGGG    GGGGTGGGAG GG
                                ||||    |||||||||| ||
                                TCCC    CCCCACCCTC CC
                                  A____       _
GAM3471 AP2A1    3' AGGGTGGGGTGGGAGGG     78240     ACGCG       A
                                AGGG    GGGGTGGGAG GG
                                ||||    |||||||||| ||
                                TCCC    CCCCACCCTC CC
                                  A____       _
GAM3471 AR       5' GGGAGGCGGGGTGGAGAGG   78241     C     GTG
                                GGGA GCGGGG   GGAGAGG
                                |||| ||||||   |||||||
                                CCCT CGCCCC   CCTCTCC
                                  C     A__
GAM3471 ARHC     5' GGGATGCGGAGCTGGGGAGAGG 78242     C     G   _
                                GGGA GCGGGG TGGG AGAGG
                                |||| |||||| |||| |||||
                                CCCT CGCCTC ACCC TCTCC
                                  A     G   C
GAM3471 ARHGDIA  3' GGGATGGGGCGGGGGAGG    78244     CGCG      A
                                GGGA    GGGGTGGG GAGG
                                ||||    |||||||| ||||
                                CCCT    CCCCGCCC CTCC
                                  A___       C
GAM3471 ARHGDIA  3' AGGGAGGCGGACCAGGGTGGGA 78243      C   ____      A
           GGG                    AGGGA GCGG    GGGTGGGAG GG
                                |||||| ||||    |||||||| ||
                                TCCCT CGCC    CCCACCCTC CC
                                  C    TGGT       _
GAM3471 ARHGEF1  3' GGGGTGGGGGGTGGAGGG    78245    ACGC      G  A
                                GGG    GGGGGGTGG AG GG
                                |||    |||||||| || ||
                                CCC    CCCCCACC TC CC
                                  CA__       _ _
GAM3471 ASH1     5' AGGGAAGTGGGGAAGAGG    78246     CGC  G  T
                                AGGGA   GG GG GGGAGAGG
                                ||||||   || || ||||||||
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                                TCCCT  TC CC CCTTCTCC
                                  ___  A  _
GAM3471 ASNS    5' GGGATGGCGGGGTGAGAG   78247     C_    G
                                GGGA  GCGGGG TGGGAG
                                ||||  |||||| ||||||
                                CCCT  CGCCCC ACTCTC
                                  AC     _
GAM3471 ATBF1   5' GGGCCCGGAGACAGGGGAGG  78248    ACG    TG  A
                                GGG   CGGGGG  GG GAGG
                                |||   ||||||  || ||||
                                CCC   GCCTCT  CC CTCC
                                  GG_     GT  C
GAM3471 ATP2A3  3' AGGGGTGAGGCGTAGGGGAGG 78249     ACGC   G    A
                                AGGG    GGG GTGGG GAGG
                                ||||    ||| ||||| ||||
                                TCCC    TCC CATCC CTCC
                                  CAC_  G    C
GAM3471 ATP2B2  5' GGGGGTGGGGGTGGCCGAGG  78250    ACGC      GA
                                GGG   GGGGGTGG  GAGG
                                |||   ||||||||  ||||
                                CCC   CCCCCACC  CTCC
                                  CCA_      GG
GAM3471 ATP2B3  3' GGGGCGGGGGGGCCCGGAGG  78251    AC     T  GA__
                                GGG  GCGGGGG GG   GAGG
                                |||  ||||||| ||   ||||
                                CCC  CGCCCCC CC   CTCC
                                  __     _ GGGC
GAM3471 B3GALT5 5' AGGAGGCTGAGGTGGGAGAGG 78252     C  G
                                GGGA GC GGGGTGGGAGAGG
                                |||| || ||||||||||||
                                TCCT CG CTCCACCCTCTCC
                                  C  A
GAM3471 BACH2   5' AGGGGCGAGGGGAGGCCGG   78253     AC     TG  AGA
                                AGGG  GCGGGGG  GG   GG
                                ||||  |||||||  ||   ||
                                TCCC  CGCTCCC  CC   CC
                                  __     CT  GG_
GAM3471 BAZ2A   3' AGGGATGTAGGAATAAGAG   78254      CGC
                                AGGGA   GGGGGTGGGAG
                                |||||   ||||||||||
                                TCCCT   TCCTTATTCTC
                                   ACA
GAM3471 BCL7A   3' AGGGGTGCAGGGTGGGTGGG  78255     AC    ___
                                AGGG  GCGGGG   GTGGG
                                ||||  ||||||   |||||
                                TCCC  CGTCCC   CACCC
                                  CA     ACC
GAM3471 BSN     3' AGGGGTGGGGTGGGGAG     78256     ACGCG      A
                                AGGG    GGGGTGGG GAG
                                ||||    |||||||| |||
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                                TCCC    CCCCACCC CTC
                                  CA___      _
GAM3471  C1QA    3'  AGAGAGGTGGGTGGGGGAGG  78257      CGC  _     A
                                AGGGA  GG GGGTGGG GAGG
                                |||||  || ||||||| ||||
                                TCTCT  CC CCCACCC CTCC
                                  ___ A      C
GAM3471  CACNB1  3'  AGGGATGCCCCAGGGGAGAGG  78258      C  GGG  T
                                AGGGA GC   GG GGGAGAGG
                                ||||| ||   || ||||||||
                                TCCCT CG   TC CCCTCTCC
                                  A  GGG  _
GAM3471  CALM3   3'  GGGGGTGGGGTGGGGAGG   78259     ACGCG      A
                                GGG    GGGGTGGG GAGG
                                |||    |||||||| ||||
                                CCC    CCCCACCC CTCC
                                  CCA__      _
GAM3471  CASQ1   5'  AGGGGCTCAAGTGGGAGGG   78260     AC  GG      A
                                AGGG  GC  GGGTGGGAG GG
                                ||||  ||  |||||||||| ||
                                TCCC  CG  TTCACCCTC CC
                                  __ AG       _
GAM3471  CAV1    5'  GGGGCGGTGGCTGGGAG    78261     AC   _  G
                                GGG  GCGG GG TGGGAG
                                |||  |||| || ||||||
                                CCC  CGCC CC ACCCTC
                                  __   A  G
GAM3471  CD3E    3'  AGGGAGCGGGGGATCAGG   78262      C      T__
                                AGGGA GCGGGGG   GGG
                                |||||| |||||||   |||
                                TCCCT CGCCCCC   TCC
                                  _      TAG
GAM3471  CDK4    3'  AAGGAGAGGTGGGAGG     78264      CGCG       A
                                AGGGA   GGGGTGGGAG G
                                |||||   |||||||||| |
                                TTCCT   CTCCACCCTC C
                                  _____      _
GAM3471  CDK4    3'  AAGGAGAGGTGGGAGG     78264      CGCG       A
                                AGGGA   GGGGTGGGAG G
                                |||||   |||||||||| |
                                TTCCT   CTCCACCCTC C
                                  _____      _
GAM3471  CDK4    5'  AGGCGCGCGGAAACTGGGAG  78263     GA    GG _
                                AGG  CGCGG  G TGGGAG
                                |||  |||||  | ||||||
                                TCC  GCGCC  T ACCCTC
                                  GC    TT G
GAM3471  CDK4    5'  AGGCGCGCGGAAACTGGGAG  78263     GA    GG _
                                AGG  CGCGG  G TGGGAG
                                |||  |||||  | ||||||
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                                TCC  GCGCC  T ACCCTC
                                  GC     TT G
GAM3471  CDX2     5'  AGGGGCGAGGGGACTCGAGG   78265      AC      T  GA_
                                AGGG  GCGGGGG GG   GAGG
                                ||||  ||||||| ||   ||||
                                TCCC  CGCTCCC CT   CTCC
                                  __      _ GAG
GAM3471  CEBPA    3'  GGAGGGAGGTGGGAGAG     78266     CGC
                                GGA   GGGGGTGGGAGAG
                                |||   ||||||||||||
                                CCT   CCTCCACCCTCTC
                                  C__
GAM3471  CEP2     3'  AGGGACGTGAAAAGGGGGG    78267        C ___    T
                                AGGGACG G   GGGG GGG
                                ||||||| |   |||| |||
                                TCCCTGC C   TCCC CCC
                                    A TTT   _
GAM3471  CETN1    3'  GGGGTGAGGGGGTGAAGAAGG  78268     ACGC       AG
                                GGG   GGGGGTGGG  AGG
                                |||   |||||||||  |||
                                CCC   CCCCCACTT  TCC
                                  CACT       CT
GAM3471  CHST1    3'  AGGGAGTGGGGTGAGCTGGG   78269      CGCG      AGA
                                AGGGA   GGGGTGGG   GG
                                |||||   ||||||||   ||
                                TCCCT   CCCCACTC   CC
                                   CA__       GAC
GAM3471  CIT      3'  GGGACGGGAGGGGAG       78270      GC    T
                                GGGAC  GGGGG GGGAG
                                |||||  ||||| |||||
                                CCCTG  CCCTC CCCTC
                                  __    _
GAM3471  COX7A1   5'  GGGACGCGGCGGGGCTGGG   78271         _  __
                                GGGACGCGG GGG  TGGG
                                |||||||||| |||  ||||
                                CCCTGCGCC CCC  ACCC
                                     G   CG
GAM3471  CSK      5'  AGGGGCGCAGGGGTCCCCAGGG 78272      A       _____
                                AGGG CGCGGGGGT    GGG
                                |||| |||||||||    |||
                                TCCC GCGTCCCCA    CCC
                                  C       GGGGT
GAM3471  CSNK2A2  5'  GGGCGGCGCGGGGCGCAGAGG  78273     AC  _     GG
                                GGG  GCG GGGGTG  AGAGG
                                |||  ||| ||||||  |||||
                                CCC  CGC CCCCGC  TCTCC
                                  GC   G     G_
GAM3471  CSNK2A2  5'  GGGACGCGGGGCGTCGGG    78274          _ _
                                GGGACGCGGGG GT GGG
                                |||||||||| || |||
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                                CCCTGCGCCCC CA CCC
                                      G  G
GAM3471  CXCL16   3'  AGGGCTGAGGTGGGGGAGG   78275     ACGCG      A
                                AGGG    GGGGTGGG GAGG
                                ||||    |||||||| ||||
                                TCCC    CTCCACCC CTCC
                                  GA___      C
GAM3471  CYP27A1  5'  AGGGACGCGGTGACTCGGG   78276         _  G_
                                AGGGACGCGG GG  TGGG
                                |||||||||| ||  ||||
                                TCCCTGCGCC CT  GCCC
                                      A  GA
GAM3471  DAG1     3'  GGGACTTGGGCAGGGGAGAGG  78277      GC  _  T
                                GGGAC  GGG GG GGGAGAGG
                                |||||  ||| || ||||||||
                                CCCTG  CCC TC CCCTCTCC
                                   AA   G  _
GAM3471  DDX19    5'  AGGGATCGTGGGCTCCGGGGG  78278      _  C  _____  T
                                AGGGA CG GGG    GG GGG
                                |||||  || |||    || |||
                                TCCCT GC CCC    CC CCC
                                   A  A   GAGG  _
GAM3471  DLK1     5'  GGGCGCGGGCGCGCAGCGAGG  78279     A     G  _  A
                                GGG CGCGGG GTG GG GAGG
                                |||  ||||||  ||| ||  ||||
                                CCC GCGCCC CGC TC CTCC
                                  _     G   G  G
GAM3471  DLX2     3'  AGGGATGGGGGCTCCGAGG   78280      CGC     GGGA
                                AGGGA   GGGGGT    GAGG
                                |||||   ||||||    ||||
                                TCCCT   CCCCCG    CTCC
                                   A__      AGG_
GAM3471  DNMT3L   5'  GGGAGTGGGGTTCAGGGGAGG  78281      CGCG     ___   A
                                GGGA    GGGGT   GGG GAGG
                                ||||    |||||   ||| ||||
                                CCCT    CCCCA   CCC CTCC
                                  CA__     AGT   _
GAM3471  DRD2     3'  GGGACTGGAGGTGGGAGGG    78282      GC         A
                                GGGAC  GGGGGTGGGAG GG
                                |||||  |||||||||| ||
                                CCCTG  CCTCCACCCTC CC
                                   A_         _
GAM3471  DRIL1    5'  GGGCCGCGGGGGGAGCCGGG    78283     A       ___
                                GGG CGCGGGGG   TGGG
                                ||| ||||||||   ||||
                                CCC GCGCCCCC   GCCC
                                  G       TCG
GAM3471  DRPLA    3'  AGGGGTTGGGCATGGGGGAGG  78284      ACGC   G    A
                                AGGG    GGG GTGGG GAGG
                                ||||    ||| ||||| ||||
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                                TCCC    CCC TACCC CTCC
                                  CAA_  G    C
GAM3471  DTR      3'  GGGAAGTGGGGTTTGGTGGAGG 78285      CGC   G_  GA
                                GGGA  GGGG  TGG  GAGG
                                ||||  ||||  |||  ||||
                                CCCT  CCCC  ACC  CTCC
                                  TCA   AA  AC
GAM3471  EFNB1    3'  GGGGTGTGGGGGCGAAAGGAGA 78286     ACGC     ___
            GG                    GGG   GGGGGTG  GGAGAGG
                                |||   |||||||  |||||||
                                CCC   CCCCCGC  CCTCTCC
                                 CACA     TTT
GAM3471  EGFL4    5'  GGGGCGGGTGTGGGAGGG    78287    AC    G     A
                                GGG  GCGGG GTGGGAG GG
                                |||  ||||| ||||||| ||
                                CCC  CGCCC CACCCTC CC
                                 __    A     _
GAM3471  EGR3     5'  AGGGATGGGCCAGGAGAGG   78288      CGCG  G
                                AGGGA   GGG TGGGAGAGG
                                |||||   ||| |||||||||
                                TCCCT   CCC GTCCTCTCC
                                  A___  G
GAM3471  EHD3     3'  GGGAGTGGCCGAGGAGAGG   78289     CGCGG  G  _
                                GGGA    GG TG GGAGAGG
                                ||||    || || |||||||
                                CCCT    CC GC CCTCTCC
                                  CA___ G  T
GAM3471  EIF5A    3'  AGGGATGAGTGGGGAG     78290      CGCGG     A
                                AGGGA    GGGTGGG GAG
                                |||||    ||||||| |||
                                TCCCT    CTCACCC CTC
                                  A____     _
GAM3471  EN1      3'  GGGCAGCGAGGCGGTGGGGGAG 78291    AC  _ _    A
            G                    GGG  GCG GG GGTGGG GAGG
                                |||  ||| || |||||| ||||
                                CCC  CGC CC CCACCC CTCC
                                 GT   T  G    C
GAM3471  ENIGMA   3'  AGGGAGTGGGGTGGGAG    78292      CGCG
                                AGGGA   GGGGTGGGAG
                                |||||   ||||||||||
                                TCCCT   CCCCACCCTC
                                  CA__
GAM3471  ERBB3    5'  AGGGATGGCAGGGGAGGG    78293      C_     T
                                AGGGA  GCGGGGG GGG
                                |||||  ||||||| |||
                                TCCCT  CGTCCCC CCC
                                  AC     T
GAM3471  EXTL1    3'  GGGGCGGAGGGGGAG      78294    AC     T
                                GGG  GCGGGGG GGGAG
                                |||  ||||||| |||||
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                                CCC  CGCCTCC CCCTC
                                  __     _
GAM3471  EYA2     3'  GGGAGGTGGGGAAGGCGAGG   78295      CGCG    T   A
                                GGGA    GGGG GGG GAGG
                                ||||    |||| ||| ||||
                                CCCT    CCCC TCC CTCC
                                  CCA_    T   G
GAM3471  FAT2     3'  AGGGACTGGGTGGGAG      78296       GCGG
                                AGGGAC    GGGTGGGAG
                                ||||||    |||||||||
                                TCCCTG    CCCACCCTC
                                   A___
GAM3471  FGF8     5'  AGGGCGCGAGCGGAGAG     78297      A     GGTG
                                AGGG CGCGGG    GGAGAG
                                |||| ||||||    ||||||
                                TCCC GCGCTC    CCTCTC
                                  _     G___
GAM3471  FGF8     5'  AGGGCGCGAGCGGAGAG     78297      A     GGTG
                                AGGG CGCGGG    GGAGAG
                                |||| ||||||    ||||||
                                TCCC GCGCTC    CCTCTC
                                  _     G___
GAM3471  FGF8     5'  AGGGCGCGAGCGGAGAG     78297      A     GGTG
                                AGGG CGCGGG    GGAGAG
                                |||| ||||||    ||||||
                                TCCC GCGCTC    CCTCTC
                                  _     G___
GAM3471  FGF8     5'  AGGGCGCGAGCGGAGAG     78297      A     GGTG
                                AGGG CGCGGG    GGAGAG
                                |||| ||||||    ||||||
                                TCCC GCGCTC    CCTCTC
                                  _     G___
GAM3471  FHIT     5'  AGGGACCCGGGAACAGAGG    78298       G    GG GGG
                                AGGGAC CGGG  T   AGAGG
                                |||||| ||||  |   |||||
                                TCCCTG GCCC  G   TCTCC
                                   G    TT ____
GAM3471  FMOD     3'  AGGGGTGAGGTTAGGGAGG    78299      ACGC    G    A
                                AGGG    GGGG TGGG GAGG
                                ||||    |||| |||| ||||
                                TCCC    CTCC ATCC CTCC
                                  CA__    A    _
GAM3471  FXYD7    3'  GGGATGCTGGGGGGTGCTGG    78300      C  _      __
                                GGGA GC GGGGGGTG  GG
                                |||| || |||||||  ||
                                CCCT CG CCCCCAC  CC
                                  A  A      GA
GAM3471  FY       5'  AGGGGCAGGTGGGAGGG      78301      AC  GG       A
                                AGGG  GC  GGGTGGGAG GG
                                ||||  ||  |||||||| ||
```

```
                                TCCC  CG  TCCACCCTC CC
                                  __  __      _
GAM3471  FZD8    3'  AGGGGCTGGGTCTGGGAG    78302     AC  _  GG
                                AGGG  GC GGG  TGGGAG
                                ||||  || |||  ||||||
                                TCCC  CG CCC  ACCCTC
                                  __  A   AG
GAM3471  G6PT1   5'  GGGGTGCAGGAGCTGGAGAGG  78303    AC      G
                                GGG  GCGGGGGT GGAGAGG
                                |||  |||||||| |||||||
                                CCC  CGTCCTCG CCTCTCC
                                  CA       A
GAM3471  GALNT2  3'  AGGGATGCCGGGGCCGAGG   78304     C  G    GGGA
                                AGGGA GC GGGGT   GAGG
                                ||||| || |||||   ||||
                                TCCCT CG CCCCG   CTCC
                                   A  G    G___
GAM3471  GALR1   5'  GGGCGCGCGGGGAGGGAG    78305    A   _   T
                                GGG CGCG GGGG GGGAG
                                ||| |||| |||| |||||
                                CCC GCGC CCCC CCCTC
                                  _   G   T
GAM3471  GGT1    5'  GGGACAGTGGGGGCCCAGG   78306      C_    __
                                GGGACG  GGGGGT  GGG
                                ||||||  ||||||  |||
                                CCCTGT  CCCCCG  TCC
                                   CA     GG
GAM3471  GGT1    5'  GGGACAGTGGGGGCCCAGG   78306      C_    __
                                GGGACG  GGGGGT  GGG
                                ||||||  ||||||  |||
                                CCCTGT  CCCCCG  TCC
                                   CA     GG
GAM3471  GLRA1   5'  AGGGAGGCGGGGAACAGGG   78307      C     T__
                                AGGGA GCGGGGG   GGG
                                |||||  |||||||  |||
                                TCCCT CGCCCCT   CCC
                                   C      TGT
GAM3471  GLTSCR1 3'  GGGGCGGCGGGGAGAG     78308    AC   G  TG
                                GGG  GCGG GG  GGAGAG
                                |||  ||||  ||  ||||||
                                CCC  CGCC CC  CCTCTC
                                  __   G  __
GAM3471  GLTSCR1 3'  GGGACGGGGAAGGGGAGG   78309      C    T  A
                                GGGACG GGGGG GGG GAGG
                                ||||||  |||||  |||  ||||
                                CCCTGC CCCTT CCC CTCC
                                  _    _  _
GAM3471  GNB5    5'  GGGACGCAGCGGAGAG      78310        GGGTG
                                GGGACGCGG    GGAGAG
                                |||||||||    ||||||
```

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                                CCCTGCGTC    CCTCTC
                                     G____
GAM3471  GPR4    3'  AGGGACTGTGGGATGAGAG   78311      GCG
                                AGGGAC   GGGGTGGGAG
                                ||||||   ||||||||||
                                TCCCTG   CCCTACTCTC
                                   ACA
GAM3471  GPT     5'  GGGCAGGGTGGGAGGG     78312    A GCG       A
                                GGG C   GGGGTGGGAG GG
                                ||| |   |||||||||| ||
                                CCC G   TCCCACCCTC CC
                                  _ ___       _
GAM3471  GTF2IRD1  5'  AGGGAGGCGCGGGGAGGGG   78313      __      T
                                AGGGA  CGCGGGGG GGG
                                |||||  |||||||| |||
                                TCCCT  GCGCCCCT CCC
                                   CC       C
GAM3471  GYPC    3'  AGGGGTGCTGGGCGATGGG   78314     AC _  _
                                AGGG  GC GGG GGTGGG
                                ||||  || ||| ||||||
                                TCCC  CG CCC CTACCC
                                  CA  A   G
GAM3471  GYPC    3'  AGGGGTGCTGGGCGATGGG   78314     AC _  _
                                AGGG  GC GGG GGTGGG
                                ||||  || ||| ||||||
                                TCCC  CG CCC CTACCC
                                  CA  A   G
GAM3471  HCFC1   3'  GGGACGGGGTGGGAGGG    78315      GCG       A
                                GGGAC   GGGGTGGGAG GG
                                |||||   |||||||||| ||
                                CCCTG   CCCCACCCTC CC
                                  ____       _
GAM3471  HCN2    3'  GGGCGCGGGGGCGATGAGG   78317    A     G   GA
                                GGG CGCGGGG TGG  GAGG
                                ||| |||||| |||  ||||
                                CCC GCGCCCC GCT  CTCC
                                  _     _  A_
GAM3471  HCN2    3'  AGGGGCGATGGGGGTGGG    78316     A  C_
                                AGGG CG  GGGGGTGGG
                                |||| ||  |||||||||
                                TCCC GC  CCCCCACCC
                                  C  TA
GAM3471  HDAC5   5'  GGGGCTGGGACGGGAGGG    78318    AC  G   GT    A
                                GGG  GC GGG  GGGAG GG
                                |||  || |||  ||||| ||
                                CCC  CG CCC  CCCTC CC
                                  __  A   TG    _
GAM3471  HDAC5   5'  GGGGCTGGGACGGGAGGG    78318    AC  G   GT    A
                                GGG  GC GGG  GGGAG GG
                                |||  || |||  ||||| ||
```

```
                                CCC  CG CCC  CCCTC CC
                                  __ A  TG    _
GAM3471  HDGF     3'  AGGAAGAGGGTGGGAGAGG   78319      CGC
                                AGGGA  GGGGGGTGGGAGAGG
                                |||||  ||||||||||||||
                                TCCTT  CTCCCACCCTCTCC
                                  ____
GAM3471  HHIP     5'  AGGGGCTGGGCGCGGGAG    78320     AC _  G
                                AGGG  GC GGG GTGGGAG
                                ||||  || ||| |||||||
                                TCCC  CG CCC CGCCCTC
                                  __ A  G
GAM3471  HIP2     3'  GGGGTGGGGGGGGGTGAAG    78321     ACGC    T  A
                                GGG    GGGGG GGG GAGG
                                |||    ||||| ||| ||||
                                CCC    CCCCC CCC CTTC
                                  CA__    _  A
GAM3471  HK2      5'  GAGACGCGAGAGGGGAG     78322          T
                                GGGACGCGGGGG GGGAG
                                |||||||||||| |||||
                                CTCTGCGCTCTC CCCTC
                                          _
GAM3471  HOXB2    3'  AGGAGCGCGGGGGGTCGAAAGG  78323     GA       G G
                                AGG  CGCGGGGGT G AGAGG
                                |||  ||||||||| | |||||
                                TCC  GCGCCCCCA C TTTCC
                                  TC        G _
GAM3471  IGFBP4   3'  AGGGAGGTGTGGGGAG      78324      CGC  GG    A
                                AGGGA   GG  GTGGG GAG
                                |||||   ||  ||||| |||
                                TCCCT   CC  CACCC CTC
                                  ____  A_    _
GAM3471  IGFBP5   3'  GGGGCTGGGGGGTGGGAGGG   78325     AC _         A
                                GGG  GC GGGGGGTGGGAG GG
                                |||  || ||||||||||| ||
                                CCC  CG CCCCCACCCTC CC
                                  __ A          _
GAM3471  IL12RB2  3'  AGGGGCTGGGGGGAATTGGG   78326     AC _    ____
                                AGGG  GC GGGGG   TGGG
                                ||||  || |||||   ||||
                                TCCC  CG CCCCC   ACCC
                                  __ A    TTA
GAM3471  IMPDH1   5'  GGGATGAGGGGGGAGAG      78327     CGCG    T
                                GGGA    GGGG GGGAGAG
                                ||||    |||| |||||||
                                CCCT    CTCC CCCTCTC
                                  A____   _
GAM3471  ITGA7    3'  AGGGTGAATGGGAGAG       78328     ACGCGG
                                AGGG     GGGTGGGAGAG
                                ||||     ||||||||||
```

```
                                TCCC     CTTACCCTCTC
                                  A_____
GAM3471  ITGBL1   5'  AGGGAGGCGGCAGGAGGGAGAG 78329      C   _   T
                G                  AGGGA GCGG GGG GGGAGAGG
                                   ||||| |||| ||| ||||||||
                                   TCCCT CGCC TCC CCCTCTCC
                                     C   G   T
GAM3471  JUP      3'  GGGAGCGGGGACAGACAGG   78330     C     TG  AG
                                   GGGA GCGGGGG  GG  AGG
                                   |||| |||||||  ||  |||
                                   CCCT CGCCCCT  CT  TCC
                                     _     GT  G_
GAM3471  KCNC3    5'  GGGGGCGGGGCGGGAGGG    78332    AC    G    A
                                   GGG  GCGGGG TGGGAG GG
                                   |||  |||||| |||||| ||
                                   CCC  CGCCCC GCCCTC CC
                                     C_    _    _
GAM3471  KCNC3    5'  GGGGGCGTGGCTTAGGGGAGAG 78331    AC   GG   ____
                G                  GGG  GCG  GGT   GGGAGAGG
                                   |||  |||  |||   ||||||||
                                   CCC  CGC  CCG   CCCTCTCC
                                     C_   A_   AATC
GAM3471  KCNF1    5'  GGGCGCGCCGCGGGGGAGG   78333    A   GGG   A
                                   GGG CGCG   GTGGG GAGG
                                   ||| ||||   ||||| ||||
                                   CCC GCGC   CGCCC CTCC
                                     _   GG_    C
GAM3471  KCNJ3    5'  GGGGCGGGGGGAGGAAAGG   78334    AC     TG
                                   GGG  GCGGGGG  GGAGAGG
                                   |||  |||||||  |||||||
                                   CCC  CGCCCCC  CCTTTCC
                                     __      CT
GAM3471  KCNK4    3'  AGAGACGCGGGCCTGAGAG   78335         GG
                                   AGGGACGCGGG  TGGGAG
                                   ||||||||||  ||||||
                                   TCTCTGCGCCC  ACTCTC
                                          GG
GAM3471  KCNK5    3'  AGGGGGCTGGTGGGAGGG    78336    ACGC  G_     A
                                   AGGG   GG  GGTGGGAG GG
                                   ||||   ||  |||||||| ||
                                   TCCC   CC  CCACCCTC CC
                                     ____  GA      _
GAM3471  KRT3     3'  GGGCGTGGGGAGCGGAGGG   78338    A  C   _   G  A
                                   GGG CG GGGG GTGG AG GG
                                   ||| || |||| |||| || ||
                                   CCC GC CCCC CGCC TC CC
                                     _ A   T   _ _
GAM3471  KRT3     3'  GGGAGCGGAGGGGAG      78337     C     TG
                                   GGGA GCGGGGG  GGAG
                                   |||| |||||||  ||||
```

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                                CCCT CGCCTCC  CCTC
                                  _     __
GAM3471  KRT8     3'  AGGGGTAGGCTGGGAGGG    78339      ACGCG  G     A
                                AGGG    GGG TGGGAG GG
                                ||||    ||| |||||| ||
                                TCCC    TCC ACCCTC CC
                                  CA___   G     _
GAM3471  LAD1     3'  AGGGGCCTGGCATGAGGGAGG  78340      AC  G_  G    A
                                AGGG  GC  GG GTGGG GAGG
                                ||||  ||  || ||||| ||||
                                TCCC  CG  CC TACTC CTCC
                                  __ GA  G    C
GAM3471  LAD1     3'  GGGGTGGGGGTTGGAGGG    78341     ACGC     G    A
                                GGG    GGGGGT GGAG GG
                                |||    |||||| |||| ||
                                CCC    CCCCCA CCTC CC
                                  CA__      A    _
GAM3471  LASS1    3'  AGGGGGCGGGGTCCCAGGGGAG 78342      AC     GT___   A
             G                   AGGG  GCGGGG    GGG GAGG
                                ||||  ||||||    ||| ||||
                                TCCC  CGCCCC    CCC CTCC
                                  C_     AGGGT   _
GAM3471  LFG      3'  AGGGAGGGCTTGGGAGGG    78343      CGC   GG     A
                                AGGGA   GGG  TGGGAG GG
                                |||||   |||  |||||| ||
                                TCCCT   CCC  ACCCTC CC
                                  ____   GA     _
GAM3471  LOXL2    3'  AGGGGTGGGGGTTGTGGAGAGG 78344      ACGC     _ _
                                AGGG    GGGGGT G GGAGAGG
                                ||||    |||||| | |||||||
                                TCCC    CCCCCA C CCTCTCC
                                  CA__      A A
GAM3471  LRP1     5'  AGGGGCGTGGGTGAAGAGG    78346      AC   G     G
                                AGGG  GCG GGGTGG AGAGG
                                ||||  ||| |||||| |||||
                                TCCC  CGC CCCACT TCTCC
                                  __   A     _
GAM3471  LRP1     3'  AGGGATGGGGCGAGAG      78345       CGCG
                                AGGGA    GGGGTGGGAG
                                |||||    ||||||||||
                                TCCCT    CCCCGCTCTC
                                  A____
GAM3471  LRP6     5'  AGGGGTGGCCAGAAGTGGGGGA 78347      AC_  _       A
             GG                   AGGG   GC GGGGGGTGGG GAGG
                                ||||   || |||||||| ||||
                                TCCC   CG TCTTCACCC CTCC
                                  CAC  G        C
GAM3471  MAP2K2   5'  AGGGGCGCTGGGGCTGAG    78348      A   G     GG
                                AGGG CGC GGGGT  GAG
                                |||| ||| |||||  |||
```

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                                TCCC GCG CCCCG  CTC
                                  C  A    A_
GAM3471  MAP4    5'  AGGGGCGGGGCGCAGGGAGG  78349     AC    _ TG  A
                                AGGG  GCGGGG G  GG GAGG
                                ||||  |||||| |  || ||||
                                TCCC  CGCCCC C  CC CTCC
                                  __     G GT  _
GAM3471  MAP4    5'  AGGGGCGGGGCGCAGGGAGG  78349     AC    _ TG  A
                                AGGG  GCGGGG G  GG GAGG
                                ||||  |||||| |  || ||||
                                TCCC  CGCCCC C  CC CTCC
                                  __     G GT  _
GAM3471  MECP2   3'  GGGAGGTGGGGGGGAGCTGG   78350     CGC  _  T    A_
                                GGGA  GG GGG GGGAG  GG
                                ||||  || ||| |||||  ||
                                CCCT  CC CCC CCCTC  CC
                                  ___  A  _    GA
GAM3471  MEF2D   3'  AGGGAGGGCTGGGAGG     78351      CGCG  G     A
                                AGGGA   GGG TGGGAG G
                                |||||   ||| ||||||  |
                                TCCCT   CCC ACCCTC C
                                  _____  G    _
GAM3471  MGAT5   5'  AGGGGTGGGGAGGAGAGAGG  78352     ACGC    T
                                AGGG   GGGGG GGGAGAGG
                                ||||   ||||| ||||||||
                                TCCC   CCCCT CTCTCTCC
                                  CA__    C
GAM3471  MIC2    3'  GGGACGGGGGGGGTGCCTCGG  78353      C     GGAGA
                                GGGACG GGGGGTG    GG
                                |||||| |||||||    ||
                                CCCTGC CCCCCAC    CC
                                   C     GGAG_
GAM3471  MN1     3'  GGGGATGGAATGGGAGAGG   78354    ACGCG
                                GGG    GGGGTGGGAGAGG
                                |||    ||||||||||||
                                CCC    CCTTACCCTCTCC
                                 CTA__
GAM3471  MSF     3'  GGGGCGGGGGTGGCGTGAGAGG 78355    AC       ___
                                GGG  GCGGGGGTGG   GAGAGG
                                |||  ||||||||||  ||||||
                                CCC  CGCCCCCACC   CTCTCC
                                  __       GCA
GAM3471  MYO1D   3'  AGGGGCGGGGCTCCTCTGGGAG 78356     AC    G_____    A
           GG                   AGGG  GCGGGG     TGGGAG GG
                                ||||  ||||||     |||||| ||
                                TCCC  CGCCCC     ACCCTC CC
                                  __     GAGGAG    _
GAM3471  MYOG    3'  AGGGACTTGGGAACAGAGG   78357      GC   GG GGG
                                AGGGAC  GGG  T   AGAGG
                                ||||||  |||  |   |||||
```

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                                TCCCTG  CCC  G   TCTCC
                                   AA   TT ___
GAM3471  NDRG1    3'  AGGGGCCGGGGAGGAGGG    78358     AC  G    T    A
                                AGGG  GC GGGG GGGAG GG
                                ||||  || |||| ||||| ||
                                TCCC  CG CCCC TCCTC CC
                                  __  G   _    _
GAM3471  NINJ1    3'  AGGGACGCTGGTGCTTTGGGAG 78359         G  GG___
             AGG                   AGGGACGC GG    TGGGAGAGG
                                ||||||||| ||    |||||||||
                                TCCCTGCG CC    ACCCTCTCC
                                    A  ACGAA
GAM3471  NOTCH3   3'  AGGGAGGTGGGGTGGGGAGG   78360      CGCG       A
                                AGGGA    GGGGTGGG GAGG
                                |||||    |||||||| ||||
                                TCCCT    CCCCACCC CTCC
                                   CCA_       _
GAM3471  NPEPPS   5'  AGGGGGCGGAGGGGAG      78361      AC      TG
                                AGGG  GCGGGGG  GGAG
                                ||||  |||||||  ||||
                                TCCC  CGCCTCC  CCTC
                                  C_      __
GAM3471  NPR1     5'  AGGGGCGCGACCGAGGGG    78362      A    __   T
                                AGGG CGCGG  GGG GGG
                                |||| |||||  ||| |||
                                TCCC GCGCT  CTC CCC
                                  C    GG  _
GAM3471  Nrap     3'  AGGGATGGGCTTAAGGAGG   78363      CGC   GG   A
                                AGGGA   GGG  TGGG GAGG
                                |||||   |||  |||| ||||
                                TCCCT   CCC  ATTC CTCC
                                  A__   GA   _
GAM3471  NTSR1    3'  GGGTTAGGGGGTGGGAGGG   78364     ACGC         A
                                GGG    GGGGGTGGGAG GG
                                |||    |||||||||||| ||
                                CCC    CCCCCACCCTC CC
                                 AAT_          _
GAM3471  OTP      3'  AGGGTAGCGTGGTGGGAGAGG  78366     AC   GG
                                AGGG  GCG  GGTGGGAGAGG
                                ||||  |||  ||||||||||
                                TCCC  CGC  CCACCCTCTCC
                                  AT   A_
GAM3471  OTP      3'  GGGACCGGAGGGGAG       78365       G     TG
                                GGGAC CGGGGG  GGAG
                                ||||| ||||||  ||||
                                CCCTG GCCTCC  CCTC
                                   _     __
GAM3471  PACE     3'  GGGACTCCCAGATGGGAGGG  78367       GCGG       A
                                GGGAC    GGGTGGGAG GG
                                |||||    ||||||||| ||
```

```
                                CCCTG   TCTACCCTC CC
                                  AGGG       _
GAM3471  PACSIN1  3'  AGGGGCGGCAGTGGGGAGG   78369     AC   G    A
                                AGGG  GCGG GGTGGG GAGG
                                ||||  |||| |||||| ||||
                                TCCC  CGCC TCACCC CTCC
                                  __   G    _
GAM3471  PACSIN1  3'  AGGAGACGAGAGTGGGAGGG  78368     C         A
                                GGGA GCGGGGGTGGGAG GG
                                |||| |||||||||||| ||
                                TCCT TGCTCTCACCCTC CC
                                  C          _
GAM3471  PAK1     5'  AGGGATGATGGGGGGGCGGGAG 78370      CGC___
                                AGGGA     GGGGGGTGGGAG
                                |||||     ||||||||||
                                TCCCT     CCCCCGCCCTC
                                  ACTACC
GAM3471  PATE     3'  GGAGGTAAGGGTGGGAGAGG   78371     CGC
                                GGA   GGGGGTGGGAGAGG
                                |||   ||||||||||||||
                                CCT   TTCCCACCCTCTCC
                                 CCA
GAM3471  PAX2     3'  AGGGTTGCGGGGGTCGTGGG   78372     AC      ___
                                AGGG  GCGGGGGT   GGG
                                ||||  ||||||||   |||
                                TCCC  CGCCCCCA   CCC
                                  AA       GCA
GAM3471  PAX2     3'  AGGGTTGCGGGGGTCGTGGG   78372     AC      ___
                                AGGG  GCGGGGGT   GGG
                                ||||  ||||||||   |||
                                TCCC  CGCCCCCA   CCC
                                  AA       GCA
GAM3471  PAX2     5'  AGGGAGGGACGGTGGGGGAGG  78373      CGC  __     A
                                AGGGA   GGG  GGTGGG GAGG
                                |||||   |||  |||||| ||||
                                TCCCT   CCC  CCACCC CTCC
                                  ___  TG     C
GAM3471  PAX2     5'  AGGGAGGGACGGTGGGGGAGG  78373      CGC  __     A
                                AGGGA   GGG  GGTGGG GAGG
                                |||||   |||  |||||| ||||
                                TCCCT   CCC  CCACCC CTCC
                                  ___  TG     C
GAM3471  PCBD     3'  AGGGGAGTGGTGGGAG      78374      ACGC  _
                                AGGG    GGG GGTGGGAG
                                ||||    ||| ||||||||
                                TCCC    CTC CCACCCTC
                                  ____  A
GAM3471  PCSK1    5'  AGGAGGCGCGAGAGGAGAGG   78375     C   G   T
                                GGGA GCG GGG GGGAGAGG
                                |||| ||| ||| ||||||||
```

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                                TCCT CGC CTC TCCTCTCC
                                  C  G  _
GAM3471  PDE4A   3'  GGGCAGTGGGGGAAGGTGAGG  78377    ACGC   T  A
                                GGG   GGGGG GGG GAGG
                                |||   ||||| ||| ||||
                                CCC   CCCCC TCC CTCC
                                  GTCA   T  A
GAM3471  PDE4A   3'  GGGGCGGGGGGGGTGAG     78376    AC     T  _
                                GGG  GCGGGGG GG GAG
                                |||  ||||||| || |||
                                CCC  CGCCCCC CC CTC
                                  __     _ A
GAM3471  PDGFRB  5'  GGGCTGCTGTAGGGGAGAGG  78378    AC  GGG  T
                                GGG  GC   GG GGGAGAGG
                                |||  ||   || ||||||||
                                CCC  CG   TC CCCTCTCC
                                  GA  ACA  _
GAM3471  PER2    3'  AGGGTGCAGTGGGAGAG    78379    AC  GGG
                                AGGG  GC   GGTGGGAGAG
                                ||||  ||   ||||||||||
                                TCCC  CG   TCACCCTCTC
                                  A_  ____
GAM3471  PFN1    3'  AGGGATATGGGTAGGGGGAGG  78380     CGCGG     A_
                                AGGGA    GGGTGGG  GAGG
                                |||||    |||||||  ||||
                                TCCCT    CCCATCC  CTCC
                                   ATA__     CC
GAM3471  PIK3CD  3'  AGGCGTGTGGCCAGGGAGG   78381    A  CGG  G   A
                                GGG CG   GG TGGG GAGG
                                ||| ||   || |||| ||||
                                TCC GC   CC GTCC CTCC
                                  _  ACA  G   _
GAM3471  PITX1   3'  GGGCGCGGGATACGAG     78382    A     G  G
                                GGG CGCGGGG TG GAG
                                ||| ||||||| || |||
                                CCC GCGCCCT AT CTC
                                  _     _  G
GAM3471  PLCD1   5'  GGGCGGCGCGGCGGGAGGG   78383    AC   G  G    A
                                GGG  GCG GG TGGGAG GG
                                |||  ||| || ||||||  ||
                                CCC  CGC CC GCCCTC CC
                                  GC   G  _    _
GAM3471  POU3F1  3'  AGGGGCGGGGGTCGTCGAGG  78384     AC     _ GGA
                                AGGG  GCGGGGGT G   GAGG
                                ||||  |||||||| |   ||||
                                TCCC  CGCCCCCA C   CTCC
                                  __      G AG_
GAM3471  PPFIA3  3'  GGGACACGAGACACGGGGGAGG 78385          GT_  A
                                GGGACGCGGGG   GGG GAGG
                                ||||||||||   ||| ||||
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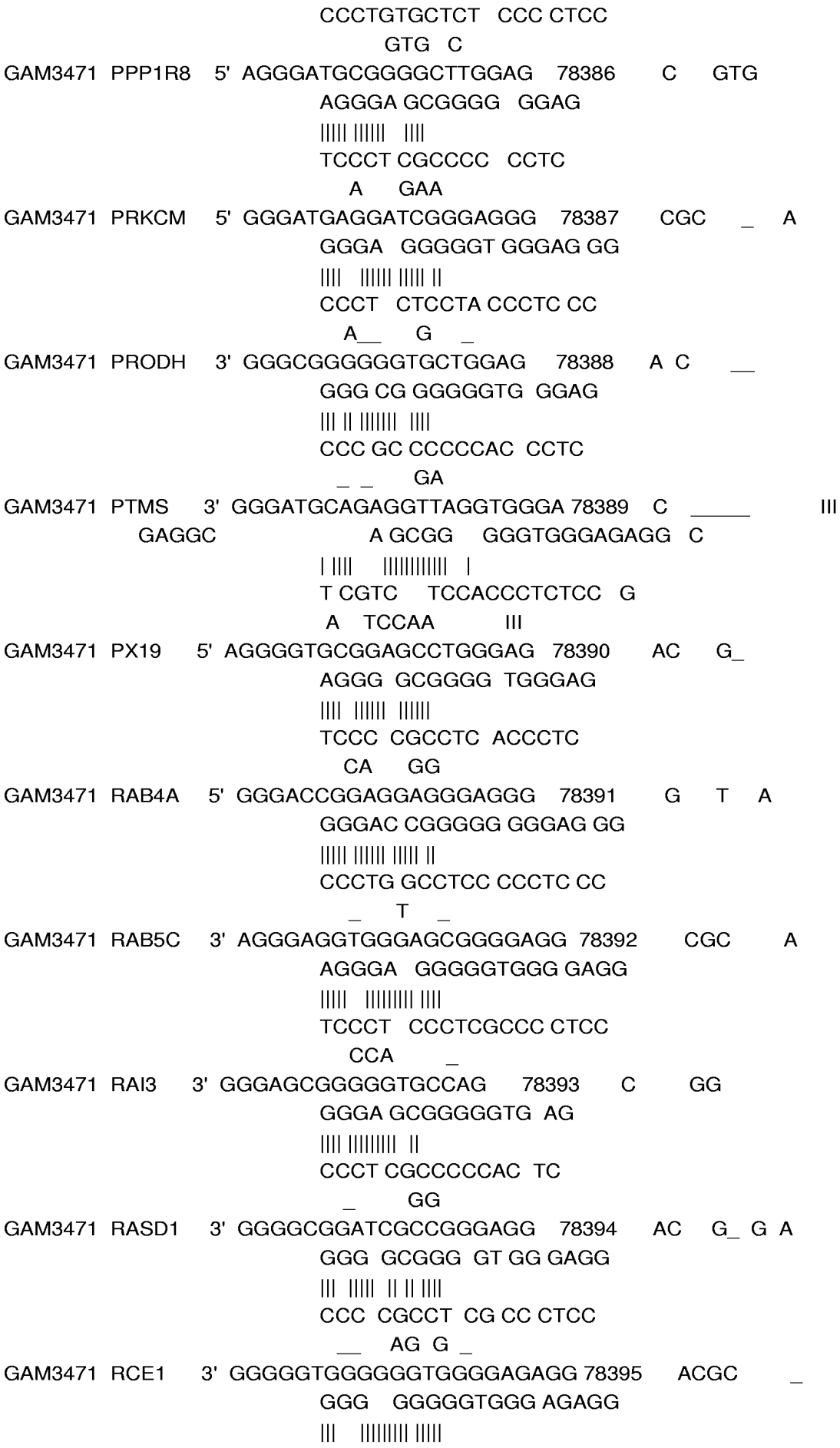
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GTG C
GAM3471 PPP1R8 5' AGGGATGCGGGGCTTGGAG 78386 C GTG
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TCCCT CGCCCC CCTC
A GAA
GAM3471 PRKCM 5' GGGATGAGGATCGGGAGGG 78387 CGC _ A
GGGA GGGGGT GGGAG GG
CCCT CTCCTA CCCTC CC
A__ G _
GAM3471 PRODH 3' GGGCGGGGGGTGCTGGAG 78388 A C __
GGG CG GGGGGTG GGAG
CCC GC CCCCCAC CCTC
_ _ GA
GAM3471 PTMS 3' GGGATGCAGAGGTTAGGTGGGA 78389 C _____ III
GAGGC A GCGG GGGTGGGAGAGG C
T CGTC TCCACCCTCTCC G
A TCCAA III
GAM3471 PX19 5' AGGGGTGCGGAGCCTGGGAG 78390 AC G_
AGGG GCGGGG TGGGAG
TCCC CGCCTC ACCCTC
CA GG
GAM3471 RAB4A 5' GGGACCGGAGGAGGGAGGG 78391 G T A
GGGAC CGGGGG GGGAG GG
CCCTG GCCTCC CCCTC CC
_ T _
GAM3471 RAB5C 3' AGGGAGGTGGGAGCGGGGAGG 78392 CGC A
AGGGA GGGGGTGGG GAGG
TCCCT CCCTCGCCC CTCC
CCA _
GAM3471 RAI3 3' GGGAGCGGGGGTGCCAG 78393 C GG
GGGA GCGGGGGTG AG
CCCT CGCCCCCAC TC
_ GG
GAM3471 RASD1 3' GGGGCGGATCGCCGGGAGG 78394 AC G_ G A
GGG GCGGG GT GG GAGG
CCC CGCCT CG CC CTCC
__ AG G _
GAM3471 RCE1 3' GGGGGTGGGGGGTGGGGAGAGG 78395 ACGC _
GGG GGGGGGTGGG AGAGG

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                                CCC   CCCCCACCC TCTCC
                                  CCAC       C
GAM3471  RCN2     5'  AGGGACGCGAGGAGGGAG    78396           T
                                AGGGACGCGGGGG GGGAG
                                ||||||||||||| |||||
                                TCCCTGCGCTCCT CCCTC
                                                _
GAM3471  RERE     5'  AGGGGCGGCCCGCGGGGAGG   78397     AC   GG_    A
                                AGGG  GCGG   GTGGG GAGG
                                ||||  ||||   ||||| ||||
                                TCCC  CGCC   CGCCC CTCC
                                  __   GGG    _
GAM3471  REST     5'  GGGGGAGAGGTGGGGGAGG    78398     ACGC       A
                                GGG   GGGGGGTGGG GAGG
                                |||   ||||||||| ||||
                                CCC   TCTCCACCC CTCC
                                  CC__       C
GAM3471  RFX1     3'  AGGGGTGGCGGGGGCGGG    78399     AC_
                                AGGG  GCGGGGGTGGG
                                ||||  ||||||||||
                                TCCC  CGCCCCCGCCC
                                  CAC
GAM3471  RFX1     3'  AGGGGTGGCGGGGGCGGG    78399     AC_
                                AGGG  GCGGGGGTGGG
                                ||||  ||||||||||
                                TCCC  CGCCCCCGCCC
                                  CAC
GAM3471  RGR      3'  AGGGTGACAAGGTGGGAGGG   78400     AC     G     A
                                AGGG  GCGGGG TGGGAG GG
                                ||||  |||||| |||||| ||
                                TCCC  TGTTCC ACCCTC CC
                                  AC    _     _
GAM3471  RNMT     3'  AGGGGCTTGGGGCCGGGGGGAG 78401      AC  __    G    A_
           G                     AGGG  GC  GGGG TGGG  GAGG
                                ||||  ||  |||| ||||  ||||
                                TCCC  CG  CCCC GCCC  CTCC
                                  __ AA    G    CC
GAM3471  RPL10    3'  GGGGCATGGGGCCCAGGAG    78402     AC  _    __
                                GGG  GCG GGGGT  GGGAG
                                |||  ||| |||||  |||||
                                CCC  CGT CCCCG  TCCTC
                                  __   A     GG
GAM3471  RTN2     3'  AGGGCTGCGGGGGCTGGG     78403     AC      _
                                AGGG  GCGGGGG TGGG
                                ||||  ||||||| ||||
                                TCCC  CGCCCCC ACCC
                                  GA      G
GAM3471  SCG3     5'  GGGTGTGGGGCGGGAGAGG    78404     ACGCG
                                GGG    GGGGTGGGAGAGG
                                |||    ||||||||||||
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                                CCC    CCCCGCCCTCTCC
                                  ACA__
GAM3471  SCRT1    3'  AGGGGCGCAGAGGCGGGAGAGG 78405      A
                                AGGG CGCGGGGGTGGGAGAGG
                                |||| ||||||||||||||||
                                TCCC GCGTCTCCGCCCTCTCC
                                  C
GAM3471  SERPINE1 3'  GGGCGCGGGGGGGCGCGAG    78406     A      _ G
                                GGG CGCGGGGG TG GAG
                                ||| |||||||| || |||
                                CCC GCGCCCCC GC CTC
                                  _      C  G
GAM3471  SERPINE1 3'  AGGGGCGCGGGGGGGCGCGGG   78407     A      ___
                                AGGG CGCGGGGG   TGGG
                                |||| ||||||||   ||||
                                TCCC GCGCCCCC   GCCC
                                  C       CGC
GAM3471  SERPINE1 3'  GGGCGCGAGGGTCTCAGG    78408     A      ___
                                GGG CGCGGGGGT   GGG
                                ||| |||||||||   |||
                                CCC GCGCTCCCA   TCC
                                  _       GAG
GAM3471  SF3A1    3'  AGGGGGTGGGAGACAGGAGAGG 78409      ACGC    TG
                                AGGG   GGGGG  GGAGAGG
                                ||||   |||||  |||||||
                                TCCC   CCTCT  CCTCTCC
                                  CCAC    GT
GAM3471  SFRP1    5'  AGGCGGCGCGGGCGGGGAGG   78410     AC   G     A
                                GGG  GCG GGGTGGG GAGG
                                |||  ||| ||||||| ||||
                                TCC  CGC CCCGCCC CTCC
                                  GC   G     _
GAM3471  SHANK2   3'  AGGGCAGGGTGGGGGAGG    78411      A GCG      A
                                AGGG C   GGGGTGGG GAGG
                                |||| |   |||||||| ||||
                                TCCC G   TCCCACCC CTCC
                                  _ ___       C
GAM3471  SHC1     3'  GGGGGGCGGGTGTTGAGAGG   78412     AC    G  GG
                                GGG  GCGGG GT  GAGAGG
                                |||  ||||| ||  ||||||
                                CCC  CGCCC CA  CTCTCC
                                  CC    A  A_
GAM3471  SIAT7D   3'  AGGGGCGGCTGGGGAG      78413      AC    GGG   A
                                AGGG  GCGG   TGGG GAG
                                ||||  ||||   |||| |||
                                TCCC  CGCC   ACCC CTC
                                  __   G__   _
GAM3471  SIT      3'  AGGGAGCGGGGGTGGGGAGG   78414      C         A
                                AGGGA GCGGGGGGTGGG GAGG
                                ||||| |||||||||| ||||
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                                TCCCT CGCCCCCACCC CTCC
                                  _       _
GAM3471  SIX1     5'  GGGGCGGCGGCCGCAGGGAGGG 78415     AC   G  ____    A
                                GGG  GCGG GGT   GGGAG GG
                                |||  |||| |||   ||||| ||
                                CCC  CGCC CCG   CCCTC CC
                                  __   G  GCGT   _
GAM3471  SIX3     3'  GGGAAGGAGTGGGGGAGG    78416     CGC       A
                                GGGA  GGGGGTGGG GAGG
                                ||||  ||||||||| ||||
                                CCCT  TCCTCACCC CTCC
                                  ___       C
GAM3471  SLC18A1  3'  AGGGACAGTGTCCATGGGAGGG 78417       CGGGG_     A
                                AGGGACG     GTGGGAG GG
                                |||||||     ||||||| ||
                                TCCCTGT     TACCCTC CC
                                    CACAGG      _
GAM3471  SLC1A1   5'  GGGTGCACAGGGGAGAGG    78418     AC  G  TG
                                GGG  GCG GGG  GGAGAGG
                                |||  ||| |||  |||||||
                                CCC  CGT TCC  CCTCTCC
                                  A_  G  __
GAM3471  SLC4A1   3'  GGGATGTGGAATGGTGGGGGAG 78419     CGC  __     A
           G                     GGGA  GGG  GGTGGG GAGG
                                ||||  |||  |||||| ||||
                                CCCT  CCT  CCACCC CTCC
                                  ACA  TA     C
GAM3471  SLC4A2   3'  AGGGGCAGTGGGGGAG     78420     AC   G  T
                                AGGG  GCGG GG GGGAG
                                ||||  |||| || |||||
                                TCCC  CGTC CC CCCTC
                                  __   A  _
GAM3471  SLC8A2   3'  AGGGGGCGGAGAAGGGAG    78421     AC      T
                                AGGG  GCGGGGG GGGAG
                                ||||  ||||||| |||||
                                TCCC  CGCCTCT CCCTC
                                  C_      T
GAM3471  SLC9A3R2 5'  AGGGGCGCGGGGGAGCTCGGG  78422     A      ____
                                AGGG CGCGGGGG   TGGG
                                |||| ||||||||   ||||
                                TCCC GCGCCCCC   GCCC
                                  C       TCGA
GAM3471  SMG1     5'  GCGGCGCGGTGAGAGAGG    78423     G__
                                GCGG   GGTGGGAGAGG
                                ||||   ||||||||||
                                CGCC   CCACTCTCTCC
                                  GCG
GAM3471  SMT3H1   3'  AGGGAGTGGGGTGGGAGGG   78424      CGCG       A
                                AGGGA   GGGGTGGGAG GG
                                |||||   |||||||||| ||
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                                TCCCT   CCCCACCCTC CC
                                  CA__       _
GAM3471  SNL     3'  AGGAGGTGGCTGGGAGAGG   78425     CGC  _  G
                                GGGA  GG GG TGGGAGAGG
                                ||||  || || |||||||||
                                TCCT  CC CC ACCCTCTCC
                                  ___  A  G
GAM3471  SOX11   3'  AGGGGTGGGGGCTGGGGAGG  78426     ACGC   _   A
                                AGGG   GGGGG TGGG GAGG
                                ||||   ||||| |||| ||||
                                TCCC   CCCCC ACCC CTCC
                                  CA__    G   _
GAM3471  SOX12   3'  GGGCGTGTGCAAAAGGGGGGAG 78427     AC___     T   A
           G                     GGG    GCGGGGG GGG GAGG
                                |||    ||||||| ||| ||||
                                CCC    CGTTTTC CCC CTCC
                                  GCACA     _  C
GAM3471  SOX12   5'  GGCTGGGGGTGGGGGAGG   78428    ACGC       A
                                GG   GGGGGTGGG GAGG
                                ||   ||||||||| ||||
                                CC   CCCCCACCC CTCC
                                 GA__       C
GAM3471  SOX12   3'  AGGGGGCGACGTGGGGAGG   78430     AC   G G    A
                                AGGG  GCG G GTGGG GAGG
                                ||||  ||| | ||||| ||||
                                TCCC  CGC T CACCC CTCC
                                  C_  _ G    _
GAM3471  SOX12   3'  AGGGGGGTGTGGGGAG     78431     ACGC   G    A
                                AGGG   GGG GTGGG GAG
                                ||||   ||| ||||| |||
                                TCCC   CCC CACCC CTC
                                  _____  A    _
GAM3471  SOX12   3'  AGGGGCGTGTGCAAAAGG    78429     AC   GGG   G
                                AGGG  GCG   GTG GAGAGG
                                ||||  |||   ||| ||||||
                                TCCC  CGC   CAC TTTTCC
                                  __   A__   G
GAM3471  SOX13   3'  AGGGGCAGGGCTGGGTGGGAGA 78432     AC    _____
           GG                     AGGG  GCGGGG   GTGGGAGAGG
                                ||||  ||||||   ||||||||||
                                TCCC  CGTCCC   CACCCTCTCC
                                  __     GACC
GAM3471  SOX9    5'  GGGAGGCGAATTGGAGAGG   78433     C    GGTG
                                GGGA GCGGG   GGAGAGG
                                |||| |||||   |||||||
                                CCCT CGCTT   CCTCTCC
                                  C    AA__
GAM3471  SP4     5'  GGGGCGAGGCGGGAG      78434     AC     G
                                GGG  GCGGGG TGGGAG
                                |||  |||||| ||||||
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                                CCC  CGCTCC GCCCTC
                                  __    _
GAM3471  SPI1    3'  GGGGCCTGGAGTGGGGGGAGG  78435    AC  G_      A_
                                GGG  GC  GGGGTGGG  GAGG
                                |||  ||  ||||||||  ||||
                                CCC  CG  CCTCACCC  CTCC
                                  __  GA       CC
GAM3471  SPN     3'  GGGCAGTGGGATGGTGAGAGG  78436    A  CG     _
                                GGG CG  GGGGTGG GAGAGG
                                |||  ||  |||||||  ||||||
                                CCC GT  CCCTACC CTCTCC
                                  _  CA      A
GAM3471  SPON2   5'  AGGACGTGGGAGAAAGGAG   78437      C    T_
                                GGGACG GGGGG  GGGAG
                                ||||||  |||||  |||||
                                TCCTGC CCCTC  TCCTC
                                    A    TT
GAM3471  SPTB    3'  AGGGATGTGGGGAGGATGGAGG 78438      CGCG   T   __
                                AGGGA   GGGG GGGA  GAGG
                                |||||   ||||  ||||  ||||
                                TCCCT   CCCC TCCT  CTCC
                                   ACA_   _   AC
GAM3471  SPTBN2  3'  AAGTCGGCGGGGGTGGGAGAGG 78439    GAC
                                AGG   GCGGGGGTGGGAGAGG
                                |||   ||||||||||||||||
                                TTC   CGCCCCCACCCTCTCC
                                  AGC
GAM3471  SPTBN4  3'  GGATGCGGGGCGGGGGAGG   78440    C    G   A
                                GGA GCGGGG TGGG GAGG
                                |||  ||||||  ||||  ||||
                                CCT CGCCCC GCCC CTCC
                                  A     _   C
GAM3471  SRD5A1  5'  AGGGGCGGCTACCGGAGGG   78441     AC   GG  G   A
                                AGGG  GCGG  GT GGAG GG
                                ||||  ||||  ||  ||||  ||
                                TCCC  CGCC  TG CCTC CC
                                  __   GA  G   _
GAM3471  ST7     3'  GGGATGTGGGGAGTGAGAGAGG 78442     CGC_
                                GGGA   GGGGGTGGGAGAGG
                                ||||   ||||||||||||||
                                CCCT   CCCTCACTCTCTCC
                                  ACAC
GAM3471  STK24   3'  AGGGGCGTAGGGCAAACGGG  78443     AC  _   _____
                                AGGG  GCG GGGGT   GGG
                                ||||  |||  |||||   |||
                                TCCC  CGC TCCCG   CCC
                                  __  A    TTTG
GAM3471  SUOX    5'  AGGGAGACCCTGGGAGGGG   78444     C  ____   T
                                AGGGA GC   GGGGG GGG
                                |||||  ||   |||||  |||
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                                TCCCT TG   CCCTC CCC
                                  C  GGA    _
GAM3471  SUV39H1  3'  GGAGGGCAGCAGTGGGGGAGG  78445     AC   G     A
                                GGG  GCGG GGTGGG GAGG
                                |||  |||| |||||| ||||
                                CCT  CGTC TCACCC CTCC
                                  CC   G     C
GAM3471  TAF4     3'  GAGAGCGGGGTGGGAGGG    78446     C     G     A
                                GGGA GCGGGG TGGGAG GG
                                |||| |||||| |||||| ||
                                CTCT CGCCCC ACCCTC CC
                                  _    _    _
GAM3471  TBL1X    3'  GGGAGGAGAGGGTGGGAGAGG  78447     CGC
                                GGGA   GGGGGTGGGAGAGG
                                ||||   ||||||||||||||
                                CCCT   CTCCCACCCTCTCC
                                  CCT
GAM3471  TBP      3'  AAGAAGGGGGTGGGGGAGG   78448      CGC       A
                                AGGGA   GGGGGTGGG GAGG
                                |||||   ||||||||| ||||
                                TTCTT   CCCCCACCC CTCC
                                  ____       C
GAM3471  TBX1     3'  AGGGGCTGGGGGTGGCGAGG   78449     AC _      GA
                                AGGG  GC GGGGGTGG  GAGG
                                ||||  || ||||||||  ||||
                                TCCC  CG CCCCCACC  CTCC
                                  __ A       G_
GAM3471  TBX5     5'  GGGGCAGCGGCGGGAG      78450     AC   G
                                GGG  GCGG GGTGGGAG
                                |||  |||| ||||||||
                                CCC  CGTC CCGCCCTC
                                  __   G
GAM3471  TBX5     5'  GGGGCAGCGGCGGGAG      78450     AC   G
                                GGG  GCGG GGTGGGAG
                                |||  |||| ||||||||
                                CCC  CGTC CCGCCCTC
                                  __   G
GAM3471  TCF19    5'  GGGGCGCGGGGAAGGAG     78451     A      T
                                GGG CGCGGGGG GGGAG
                                ||| |||||||| |||||
                                CCC GCGCCCCT TCCTC
                                  C      _
GAM3471  TCF19    5'  GGGGCGCGGGGAAGGAG     78451     A      T
                                GGG CGCGGGGG GGGAG
                                ||| |||||||| |||||
                                CCC GCGCCCCT TCCTC
                                  C      _
GAM3471  TCF3     3'  GGGACGGGGGGGCTCAGG    78452      C     __
                                GGGACG GGGGGT  GGG
                                |||||| ||||||  |||
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                                CCCTGC CCCCCG  TCC
                                   C     AG
GAM3471  TFAP2A   3'  GGGCTGGTGAGGCGTGGGAGGG 78454     ACGC_   _     A
                                GGG    GGGG GTGGGAG GG
                                |||    |||| ||||||| ||
                                CCC    CTCC CACCCTC CC
                                  GACCA   G     _
GAM3471  TFAP2A   3'  AGGGGCGGGGCGGGAG     78453     AC     G
                                AGGG  GCGGGG TGGGAG
                                ||||  |||||| ||||||
                                TCCC  CGCCCC GCCCTC
                                   __    _
GAM3471  TFAP2C   3'  GGGACTTGGGGGTGACAAG   78455      GC      GA
                                GGGAC  GGGGGTGG  GAG
                                |||||  ||||||||  |||
                                CCCTG  CCCCCACT  TTC
                                   AA       G_
GAM3471  TFAP4    5'  AGGGAGGCGGGCATGGGAGGG  78456      C    G     A
                                AGGGA GCGGG GTGGGAG GG
                                ||||| ||||| ||||||| ||
                                TCCCT CGCCC TACCCTC CC
                                   C    G     _
GAM3471  THRA     5'  AGGGGGGCGGGCGGTGGGAGGG 78457     AC    _     A
                                AGGG  GCGGG GGTGGGAG GG
                                ||||  ||||| |||||||| ||
                                TCCC  CGCCC CCACCCTC CC
                                   CC    G     _
GAM3471  TLE2     5'  AGGCGGCAAGAGTGGGGGAGG  78458    AC        A
                                GGG  GCGGGGGTGGG GAGG
                                |||  |||||||||| ||||
                                TCC  CGTTCTCACCC CTCC
                                  GC         C
GAM3471  TMEPAI   5'  GGGGCGCGGGGGGCTCGGG   78459    A      ___
                                GGG CGCGGGGG   TGGG
                                ||| ||||||||   ||||
                                CCC GCGCCCCC   GCCC
                                  C       CGA
GAM3471  TNF      3'  AGGGATTGGGGCAGGGGAGG   78460     CGCG   TG  A
                                AGGGA   GGGG  GG GAGG
                                |||||   ||||  || ||||
                                TCCCT   CCCC  CC CTCC
                                   AA__   GT  C
GAM3471  TNFSF4   3'  AGGGGTGGGGGCGGGAG     78461     ACGC
                                AGGG   GGGGGTGGGAG
                                ||||   ||||||||||
                                TCCC   CCCCCGCCCTC
                                  CA__
GAM3471  TULP1    3'  GGGGCGCGGGGAGGAGGG    78462    A     GT    A
                                GGG CGCGGGG  GGGAG GG
                                ||| |||||||  ||||| ||
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                                CCC GCGCCCC  TCCTC CC
                                  C      __    _
GAM3471  UBL5     3'  GGGATGAGGATGGGAGAGG   78463      CGC
                                GGGA  GGGGGTGGGAGAGG
                                ||||  ||||||||||||||
                                CCCT  CTCCTACCCTCTCC
                                  A__
GAM3471  UBQLN2   3'  AGGGAGTGGGGAGACAAGAGG  78464       CGCG   T _
                                AGGGA   GGGG GG GAGAGG
                                |||||   |||| || ||||||
                                TCCCT   CCCC CT TTCTCC
                                   CA__   T  G
GAM3471  UGCG     5'  GGGCGCGGGAGGCGAGAG    78465     A     _
                                GGG CGCGGG GGTGGGAG
                                ||| |||||| ||||||||
                                CCC GCGCCC CCGCTCTC
                                  _     T
GAM3471  VAMP8    3'  AGGGCAGGTGGGAGAG      78466      A GCGG
                                AGGG C    GGGTGGGAGAG
                                |||| |    ||||||||||
                                TCCC G    TCCACCCTCTC
                                  _ _____
GAM3471  VGF      3'  GGGAGCGGGCAACACGGAGGG  78467      C    GGTG__   A
                                GGGA GCGGG     GGAG GG
                                |||| |||||     |||| ||
                                CCCT CGCCC     CCTC CC
                                  _    GTTGTG   _
GAM3471  WFS1     3'  AGGGTGCTTGAAGGTGGGGGAG 78468      AC __       A
            G                    AGGG  GC  GGGGGTGGG GAGG
                                ||||  ||  |||||||| ||||
                                TCCC  CG  CTTCCACCC CTCC
                                  A_  AA       C
GAM3471  ZNF36    5'  GGGCGCTGGGCGAGAAAGG   78469     A   GG
                                GGG CGC  GGGTGGGAGAGG
                                ||| |||  ||||||||||||
                                CCC GCG  CCCGCTCTTTCC
                                  _  A_
GAM3471  ZYX      3'  AGGGGTTGGAAATGGGAGGG   78470      ACGC  GG      A
                                AGGG   GG  GTGGGAG GG
                                ||||   ||  ||||||| ||
                                TCCC   CC  TACCCTC CC
                                  CAA_  TT     _
GAM3471  A2BP1    5'  GGGGCGAAGGGGGAG       78471     AC      T
                                GGG  GCGGGGG GGGAG
                                |||  ||||||| |||||
                                CCC  CGCTTCC CCCTC
                                  __     _
GAM3471  AAK1     5'  GGGGTGGGGGCTGAGGGAGG   78472     ACGC    _   A
                                GGG    GGGGG TGGG GAGG
                                |||    ||||| |||| ||||
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                                CCC   CCCCC ACTC CTCC
                                  CA__    G   C
GAM3471  AEBP1    5'  AGGGCGCGGGGGGTCAGGG   78473     A      T___
                                AGGG CGCGGGGG   GGG
                                |||| ||||||||   |||
                                TCCC GCGCCCCC   CCC
                                  _      CAGT
GAM3471  AFAP     3'  GGGACGGGCACGTGGAGAGG  78474     GC   G  _
                                GGGAC  GGG GTG GGAGAGG
                                |||||  ||| ||| |||||||
                                CCCTG  CCC TGC CCTCTCC
                                   __  G   A
GAM3471  AGPAT1   5'  GGGAGGTGGGAGTGGGAG    78475     CGC
                                GGGA   GGGGGTGGGAG
                                ||||   ||||||||||
                                CCCT   CCCTCACCCTC
                                  CCA
GAM3471  AIF1     3'  GGGATGTGAGGGTGGAAGGG  78476     CGC        A
                                GGGA   GGGGGTGGGAG GG
                                ||||   |||||||||| ||
                                CCCT   CTCCCACCTTC CC
                                  ACA        _
GAM3471  AKAP11   3'  AGAGAGTGGGGGGTGGGGGAGG 78477      CGC       A
                                AGGGA   GGGGGTGGG GAGG
                                |||||   ||||||||| ||||
                                TCTCT   CCCCCACCC CTCC
                                   CAC       C
GAM3471  ALDH9    5'  AGGGGCGGGACCCTCGGGAG   78478     AC     G___
                                AGGG  GCGGGG   TGGGAG
                                ||||  ||||||   ||||||
                                TCCC  CGCCCT   GCCCTC
                                  __     GGGA
GAM3471  ALOXE3   3'  AGGGAGTGGGATGAAAGGG   78479      CGCG     GG  A
                                AGGGA   GGGGTG  AG GG
                                |||||   ||||||  || ||
                                TCCCT   CCCTAC  TC CC
                                  CA__     TT  _
GAM3471  APCL     3'  AGGGGCCGCGGTGGGAG     78480      A_   GGG
                                AGGG  CGC   GGTGGGAG
                                ||||  |||   ||||||||
                                TCCC  GCG   CCACCCTC
                                  CG  ___
GAM3471  Apg4B    3'  GGGAAGGCTCCTGGGAGAGG   78481     C_  GGGGG
                                GGGA  GC    TGGGAGAGG
                                ||||  ||    |||||||||
                                CCCT  CG    ACCCTCTCC
                                  TC  AGG__
GAM3471  ASB16    3'  GGAGGCGGGGACAGGTGGGAGG 78482     C     _____      A
             G                   GGA GCGGGG    GTGGGAG GG
                                ||| ||||||    ||||||| ||
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                                CCT CGCCCC   CACCCTC CC
                                  C     TGTC     _
GAM3471 ATP9A    3' GGCGGGGGGGTGGGGGAGG    78483    A C       A
                                GG CG GGGGGTGGG GAGG
                                || || ||||||||| ||||
                                CC GC CCCCCACCC CTCC
                                 _ _       C
GAM3471 BAG3     5' GGGTGACGTGGCCAGAGAGG   78484     AC   GG   G
                                GGG  GCG  GGT GGAGAGG
                                |||  |||  ||| |||||||
                                CCC  TGC  CCG TCTCTCC
                                  AC   A_   G
GAM3471 BCL2L12  5' AGGGAGGCGGGCAGTCGGAGGG 78485      C    _  G   A
                                AGGGA GCGGG GGT GGAG GG
                                ||||| ||||| ||| |||| ||
                                TCCCT CGCCC TCA CCTC CC
                                   C    G  G   _
GAM3471 BPESC1   3' AGGATGTGGGGACAGCAGAGG  78486     CGC    TG G
                                GGGA   GGGGG  G AGAGG
                                ||||   |||||  | |||||
                                TCCT   CCCCT  C TCTCC
                                  ACA    GT G
GAM3471 C1orf2   5' AGGGACGGGTGGGGAG      78488       GCGG      A
                                AGGGAC    GGGTGGG GAG
                                ||||||    ||||||| |||
                                TCCCTG    CCCACCC CTC
                                          ____      _
GAM3471 C1orf2   5' AGGGACGCCAGCTGTGGGGGGG 78487         _______    T
            G                    AGGGACGC      GGGGG GGG
                                ||||||||      ||||| |||
                                TCCCTGCG      CCCCC CCC
                                    GTCGACA    _
GAM3471 C1orf2   5' AGGGACGCCAGCTGTGGGGGGG 78487         _______    T
            G                    AGGGACGC      GGGGG GGG
                                ||||||||      ||||| |||
                                TCCCTGCG      CCCCC CCC
                                    GTCGACA    _
GAM3471 C20orf149 3' GGGGGTGGGAGGTGGGGAGG   78490     ACGC       A
                                GGG    GGGGGTGGG GAGG
                                |||    ||||||||| ||||
                                CCC    CCTCCACCC CTCC
                                  CCAC       _
GAM3471 C20orf149 3' AGGGATGCGGAGTGGGGAGAGG 78489       C     GT
                                AGGGA GCGGGG  GGGAGAGG
                                ||||| ||||||  ||||||||
                                TCCCT CGCCTC  CCCTCTCC
                                   A     AC
GAM3471 C20orf39  5' GGGCGCGGGCCCCGGGGGAGG  78491     A     GG_   A
                                GGG CGCGGG   TGGG GAGG
                                ||| ||||||   |||| ||||
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                                CCC GCGCCC   GCCC CTCC
                                  _     GGG    C
GAM3471  C20orf98  3'  AGGGGTGCAGGATGAGGAGG   78492      AC     G    A
                                AGGG  GCGGGG TGGG GAGG
                                |||| |||||| |||| ||||
                                TCCC  CGTCCT ACTC CTCC
                                  CA     _   _
GAM3471  C21orf57  5'  AGGGGCTGGAATGGGGGAGG   78493      AC  G       A
                                AGGG  GC GGGGTGGG GAGG
                                |||| || |||||||| ||||
                                TCCC  CG CCTTACCC CTCC
                                  __ A       C
GAM3471  C21orf57  5'  GGGTGCGCGCGGAGAGAGG    78494     A_    G  GTG
                                GGG  CGCG GG   GGAGAGG
                                |||  |||| ||   |||||||
                                CCC  GCGC CC   TCTCTCC
                                  AC    G  ___
GAM3471  C22orf5   3'  AGAGGTGTGGAGGGGGAGAGG  78495      ACGC     T
                                AGGG    GGGGG GGGAGAGG
                                ||||    ||||| ||||||||
                                TCTC    CCTCC CCCTCTCC
                                  CACA    _
GAM3471  C6orf31   3'  GGGAGCGGGGACTTGGGAG    78496      C      __
                                GGGA GCGGGGG  TGGGAG
                                |||| |||||||  ||||||
                                CCCT CGCCCCT  ACCCTC
                                  _      GA
GAM3471  C6orf9    3'  AGGGATCGGGGGGTGCTGG    78497      CG       __
                                AGGGA  CGGGGGTG  GG
                                |||||  ||||||||  ||
                                TCCCT  GCCCCCAC  CC
                                   A_       GA
GAM3471  C9orf7    3'  AGGGGCGGGGGGGTGATGGG    78498      AC      ____
                                AGGG  GCGGGGG    TGGG
                                ||||  |||||||    ||||
                                TCCC  CGCCCCC    ACCC
                                  __       CACT
GAM3471  CACNG4    3'  AGGGGGCGGGTCGGGAG     78499      AC    GG
                                AGGG  GCGGG  TGGGAG
                                ||||  |||||  ||||||
                                TCCC  CGCCC  GCCCTC
                                  C_    A_
GAM3471  CALCYON   5'  AGGACGCGGTCGGGGAG     78500         GGGT   A
                                GGGACGCGG    GGG GAG
                                |||||||||    ||| |||
                                TCCTGCGCC    CCC CTC
                                     AG__   _
GAM3471  CART      3'  AGGGATGGGGATGTATGGAGG  78501      CGC      GGA_
                                AGGGA   GGGGGTG   GAGG
                                |||||   |||||||   ||||
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                                TCCCT   CCCCTAC    CTCC
                                  A__       ATAC
GAM3471  CAT56    3'  AGGGATGTAGGGGAAGAGG    78502       CGCGG   T
                                AGGGA    GGG GGGAGAGG
                                |||||    ||| ||||||||
                                TCCCT    TCC CCTTCTCC
                                  ACA__  _
GAM3471  CBX5     3'  AGGGGTGGGTAGAAAGGAGAGG 78503      ACGC  _ T_
                                AGGG   GGG GG  GGGAGAGG
                                ||||   ||| ||  ||||||||
                                TCCC   CCC TC  TCCTCTCC
                                  CA__   A  TT
GAM3471  CCR7     3'  GGCGACGCGGCAAGTGAG    78504    _      _
                                GG GACGCGG GGGTGGG
                                || ||||||| |||||||
                                CC CTGCGCC TTCACTC
                                 G      G
GAM3471  CDH24    3'  AGGGAGGCGGCCACACGGGAG  78505       C    GGG__
                                AGGGA GCGG    TGGGAG
                                ||||| ||||    ||||||
                                TCCCT CGCC    GCCCTC
                                  C    GGTGT
GAM3471  CDK5RAP3 5'  GGGGTGCGGGGGGTGGGGGTGG  78506     AC         AGA
                                GGG  GCGGGGGTGGG   GG
                                |||  ||||||||||   ||
                                CCC  CGCCCCCACCC   CC
                                  CA          CCA
GAM3471  CDT1     3'  AGGGGCGCTGGGGAAAGG    78507      A  _    T
                                AGGG CGC GGGGG GGG
                                |||| ||| ||||| |||
                                TCCC GCG CCCCT TCC
                                  C   A    T
GAM3471  CENTG3   3'  AGGGATCTGGAGGAGGGAGAGG 78508       CGC    T
                                AGGGA   GGGGG GGGAGAGG
                                |||||   ||||| ||||||||
                                TCCCT   CCTCC CCCTCTCC
                                  AGA    T
GAM3471  CHK      3'  GGGAGCGGGAGACAGGGAGG   78509      C      _   A
                                GGGA GCGGGGG TGGG GAGG
                                |||| ||||||| |||| ||||
                                CCCT CGCCCTC GTCC CTCC
                                  _      T   _
GAM3471  CLSTN3   3'  AGGGATGGGGGGCCGGGGGAGG 78510       CGC     _  A
                                AGGGA   GGGGGT GGG GAGG
                                |||||   |||||| ||| ||||
                                TCCCT   CCCCCG CCC CTCC
                                  AC_     G  C
GAM3471  CPLX1    3'  AGGGGCGCGAGGGGGCCAGG   78511      A       TG  AG
                                AGGG CGCGGGGG  GG  AGG
                                |||| ||||||||  ||  |||
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                                TCCC GCGCTCCC  CC  TCC
                                  C       __  GG
GAM3471  CRMP5    3'  GGGCCTAAGGGGTGGGGGAGG  78512     ACGC       A
                                GGG    GGGGGGTGGG GAGG
                                |||    |||||||||| ||||
                                CCC    TCCCCACCC CTCC
                                  GGAT        C
GAM3471  DDR2     3'  AGGGAGTGGGGGGTGACCAGG   78513      CGC       GAG
                                AGGGA   GGGGGGTGG   AGG
                                |||||   ||||||||   |||
                                TCCCT   CCCCCACT   TCC
                                   CA_       GG_
GAM3471  DIO2     5'  GGTGATAAAGGGGGGTGGGGGAG 78514   _ CGC_       A    III
            GCC                    G GA    GGGGGGTGGG GAGG   CC
                                | ||    |||||||||| ||||   ||
                                C CT    CCCCCACCC CTCC   GG
                                 A  ATTT        C    III
GAM3471  DJ159A19.3 3'  AGGAGATGGGTGGGAGGG    78515      CGCGG       A
                                GGGA     GGGTGGGAG GG
                                ||||     |||||||||| ||
                                TCCT     CCCACCCTC CC
                                   CTA__         _
GAM3471  dJ309H15.1 3'  AGGAGCGCGGGTTGGAG     78516      C   G    G
                                GGGA GCG GGGT GGAG
                                |||| ||| |||| ||||
                                TCCT CGC CCCA CCTC
                                  _   G    A
GAM3471  DKFZP434E2135 5'  GGGATGAGGGAAGAGAGG    78517      CGC     T
                                GGGA   GGGGG GGGAGAGG
                                ||||   ||||| ||||||||
                                CCCT   CTCCC TTCTCTCC
                                  A__     _
GAM3471  DKFZp434F2322 5'  GCGGGGTGCGGGCAGAAG    78518        _    _
                                GCGGGG GTGGG AGAGG
                                |||||| ||||| |||||
                                CGCCCC CGCCC TCTTC
                                    A    G
GAM3471  DKFZp434G118 3'  GGGCGCAGGAATTGGAG     78519     A        G
                                GGG CGCGGGGGT GGAG
                                ||| |||||||| ||||
                                CCC GCGTCCTTA CCTC
                                  _        A
GAM3471  DKFZP434I2117 3'  GGGGTGGGGGTGGGGAGG    78520     ACGC       A
                                GGG    GGGGGGTGGG GAGG
                                |||    |||||||| ||||
                                CCC    CCCCCACCC CTCC
                                  CA__         _
GAM3471  DKFZp434P0531 3'  AGGGGCTGGGGAGGAAGGG   78521      AC  G    T    A
                                AGGG  GC GGGG GGGAG GG
                                ||||  || |||| ||||| ||
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                                TCCC  CG CCCC CCTTC CC
                                  __ A   T    _
GAM3471  DKFZp566H0824 5'  GGGATTGCACCGGAGAGG    78522      C_   GGGG G
                                GGGA  GCG    T GGAGAGG
                                ||||  |||    | |||||||
                                CCCT  CGT    G CCTCTCC
                                  AA  _____ G
GAM3471  DKFZP586G1122 3'  GGGAGTTGAATGGGAGGG    78524      CGCGG        A
                                GGGA    GGGTGGGAG GG
                                ||||    ||||||||| ||
                                CCCT    CTTACCCTC CC
                                  CAA__        _
GAM3471  DKFZP586G1122 3'  AGGTGACTGGTGGGAGGG    78523     _   GCGGG       A
                                AGG GAC    GGTGGGAG GG
                                ||| |||    |||||||| ||
                                TCC CTG    CCACCCTC CC
                                  A  A____       _
GAM3471  DKFZP586J1624 3'  AGGGATGGGGGGTGGCAAGAGG 78525       CGC       _
                                AGGGA   GGGGGTGG GAGAGG
                                |||||   |||||||| ||||||
                                TCCCT   CCCCCACC TTCTCC
                                   AC_       G
GAM3471  DKFZp762M136 5'  GGGACGGGGAGACGGAG     78526       C     TG
                                GGGACG GGGGG  GGAG
                                |||||| |||||  ||||
                                CCCTGC CCCTC  CCTC
                                   _    TG
GAM3471  DLAT     5'  GGGACGAGGGGCACTACGGG   78527       C     _____
                                GGGACG GGGGGT    GGG
                                |||||| ||||||    |||
                                CCCTGC TCCCCG    CCC
                                   _     TGATG
GAM3471  EDR1     5'  AGGGGCGGGGGCGCCGAGG    78528      AC       GGA
                                AGGG  GCGGGGGTG   GAGG
                                ||||  |||||||||   ||||
                                TCCC  CGCCCCCGC   CTCC
                                  __        GG_
GAM3471  EEA1     5'  AGGGACTGGGCCGGGAGGG    78529       GCG   G     A
                                AGGGAC   GGG TGGGAG GG
                                ||||||   ||| |||||| ||
                                TCCCTG   CCC GCCCTC CC
                                   A__   G     _
GAM3471  ELL2     3'  GGGGTGGGGTGGTGGGGAGG   78530     ACGC  _     A
                                GGG    GGG GGTGGG GAGG
                                |||    ||| |||||| ||||
                                CCC    CCC CCACCC CTCC
                                  CAC_   A     _
GAM3471  ENDO180   5'  GGACGCGGGGACCGAGG     78531           TGGGA
                                GGACGCGGGGGG    GAGG
                                ||||||||||     ||||
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                                CCTGCGCCCCT    CTCC
                                      GG___
GAM3471 EPS15R   3' AGGGAGTGGGGTGGCCCGGAGG 78532     CGCG     GA__
                                AGGGA   GGGGTGG   GAGG
                                |||||   |||||||   ||||
                                TCCCT   CCCCACC   CTCC
                                  CA__     GGGC
GAM3471 FBP17    3' AGGGATGGGGCTGCGGAGGG  78533     CGC   G _   A
                                AGGGA  GGGG TG GGAG GG
                                |||||  |||| || |||| ||
                                TCCCT  CCCC AC CCTC CC
                                  A__   G G   _
GAM3471 FLJ00024 3' AGGGACCTGGGGGGGAAG    78534      GCG   T
                                AGGGAC  GGGG GGGAG
                                ||||||  |||| |||||
                                TCCCTG  CCCC CCTTC
                                   GA_   _
GAM3471 FLJ00058 5' GGGGAGGGTGGGAGAG     78535    ACGC
                                GGG   GGGGGTGGGAGAG
                                |||   ||||||||||||
                                CCC   CTCCCACCCTCTC
                                  _____
GAM3471 FLJ10314 5' AGGGGGTGGGGGTAGACCAGAG 78536     ACGC       __
          G                      AGGG   GGGGGTGGG  AGAGG
                                ||||   |||||||||  |||||
                                TCCC   CCCCCATCT  TCTCC
                                  CCA_       GG
GAM3471 FLJ10483 3' AGGGGCGAGGGGACCTGTAGAG 78537     A  C    __ GG
          G                      AGGG CG GGGGG  TG  AGAGG
                                |||| || |||||  ||  |||||
                                TCCC GC CCCCT  AC  TCTCC
                                  C  T    GG  A_
GAM3471 FLJ10604 3' GGGAGCGGGCTGGGGAGG    78538     C   G G   A
                                GGGA GCGG G TGGG GAGG
                                |||| |||| | |||| ||||
                                CCCT CGCC C ACCC CTCC
                                  _   _ G   _
GAM3471 FLJ11588 5' GGGCGCGCGGGGGGCTCTCGG  78539    A   G   T  AGA__
                                GGG CGCG GGG GGG    GG
                                ||| |||| ||| |||    ||
                                CCC GCGC CCC CCC    CC
                                  _   G   _  GAGAG
GAM3471 FLJ11939 3' GGGCGTGGGAGGTGGGGAGG  78540    A  C  _    A
                                GGG CG GGG GGTGGG GAGG
                                ||| || ||| |||||| ||||
                                CCC GC CCC CCACCC CTCC
                                  _ A  T    _
GAM3471 FLJ12221 3' GAGCAGTAGGGGGTGGGGGAGG 78541    ACGC_      A
                                GGG    GGGGGGTGGG GAGG
                                |||    ||||||||| ||||
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                                CTC     CCCCCACCC CTCC
                                  GTCAT         C
GAM3471  FLJ12387  3'  GGGCGGGGCCGGGTGGGAGGG  78542     A  C  __        A
                                GGG CG GG  GGGTGGGAG GG
                                ||| || ||  ||||||||| ||
                                CCC GC CC  CCCACCCTC CC
                                  _  C  GG        _
GAM3471  FLJ12650  3'  GGGCGCGGGGCAGAGG      78544     A      GTGGG
                                GGG CGCGGGG     AGAGG
                                ||| |||||||     |||||
                                CCC GCGCCCC     TCTCC
                                  _      G____
GAM3471  FLJ12650  3'  GGAGGGTAGTGGGAGAG     78543     CGC  _
                                GGA   GGG GGTGGGAGAG
                                |||   ||| ||||||||||
                                CCT   CCC TCACCCTCTC
                                  ___   A
GAM3471  FLJ12783  3'  AGGGAGCGGGGAAGGAG     78545      C      T
                                AGGGA GCGGGGG GGGAG
                                ||||| ||||||| |||||
                                TCCCT CGCCCCT TCCTC
                                  _      _
GAM3471  FLJ13544  3'  GGGAAGCGGGAAGGAGAGG   78546      C     GT
                                GGGA GCGGGG  GGGAGAGG
                                |||| ||||||  ||||||||
                                CCCT CGCCCT  TCCTCTCC
                                  T     __
GAM3471  FLJ14360  5'  AGGGAGGCGGGAGGCGGGAG   78547      C    _
                                AGGGA GCGGG GGTGGGAG
                                ||||| ||||| ||||||||
                                TCCCT CGCCC CCGCCCTC
                                   C    T
GAM3471  FLJ14442  3'  AGGGAAGAGAAAGTGGGAGAGG 78548      CGC GG
                                AGGGA   G  GGTGGGAGAGG
                                |||||   |  ||||||||||
                                TCCCT   C  TCACCCTCTCC
                                   TCT TT
GAM3471  FLJ14708  5'  AGGGGCGTGGGGCTGCCCGGG  78549     AC  _   _____
                                AGGG  GCG GGGGT    GGG
                                ||||  ||| |||||    |||
                                TCCC  CGC CCCCG    CCC
                                  __   A    ACGGG
GAM3471  FLJ14824  3'  AGGGAAAGGTGGGAGGG     78550      CGCG       A
                                AGGGA    GGGGTGGGAG GG
                                |||||    |||||||||| ||
                                TCCCT    TTCCACCCTC CC
                                  _____        _
GAM3471  FLJ20113  3'  GGGCCTGGGGCGGATGGGGAGG 78551     ACGC_ _     A
                                GGG     GG GGGTGGG GAGG
                                |||     || ||||||| ||||
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                                CCC    CC CCTACCC CTCC
                                  GGACC  G     _
GAM3471  FLJ20113  3' AGGGGGCGGGGAAGAAAAGAGG 78552     AC      T_
                                AGGG  GCGGGGG  GGGAGAGG
                                ||||  |||||||  ||||||||
                                TCCC  CGCCCCT  TTTTCTCC
                                  C_      TC
GAM3471  FLJ20424  5' AGGGGCTGGGGGAAGCGAGG   78553     AC  G    TG  A
                                AGGG  GC GGGG  GG GAGG
                                ||||  || ||||  || ||||
                                TCCC  CG CCCC  TC CTCC
                                  __ A    CT  G
GAM3471  FLJ20568  3' GGGAAGAAGGAAGGTGGGAGGG 78554     CGC__         A
                                GGGA    GGGGGGTGGGAG GG
                                ||||    |||||||||||| ||
                                CCCT    CTTCCACCCTC CC
                                  TCTTC         _
GAM3471  FLJ20802  3' AGGGGAGGGTGGGAGAGG    78555     ACGC
                                AGGG    GGGGGGTGGGAGAGG
                                ||||    ||||||||||||||
                                TCCC    CTCCCACCCTCTCC
                                  _____
GAM3471  FLJ21034  3' AGGAGTGTGGTGGGAGAGG    78556     CGCGGG
                                GGGA     GGTGGGAGAGG
                                ||||     ||||||||||
                                TCCT     CCACCCTCTCC
                                  CACA__
GAM3471  FLJ22127  3' AGGAGCGTGGGTTGGAG     78557     C   G    G
                                GGGA GCG GGGT GGAG
                                |||| ||| |||| ||||
                                TCCT CGC CCCA CCTC
                                  _   A    A
GAM3471  FLJ22160  5' AGGGACGGGCGGGAG       78558       GCGG
                                AGGGAC    GGGTGGGAG
                                ||||||    |||||||||
                                TCCCTG    CCCGCCCTC
                                  _____
GAM3471  FLJ22386  3' GGGACAGCGAAGGGGAGAGG   78559       _      TG
                                GGGAC GCGGGGG  GGAGAGG
                                ||||| |||||||  |||||||
                                CCCTG CGCTTCC  CCTCTCC
                                  T      __
GAM3471  FLJ22479  3' AGGTGATGGAAAGTGGGGGAGG 78560     _  CGC GG      A
                                AGG GA   G  GGTGGG GAGG
                                ||| ||   |  |||||| ||||
                                TCC CT   C  TCACCC CTCC
                                  A  AC_ TT     C
GAM3471  FLJ23058  3' AGGGGTTGGGGCAGGCAGAGG  78561      ACGCG    TG  _
                                AGGG    GGGG  GG AGAGG
                                ||||    ||||  || |||||
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                                TCCC    CCCC  CC TCTCC
                                  CAA__   GT  G
GAM3471  FLJ23071  3'  AGGGGTTGGGGTGGGGAGG   78562     ACGCG       A
                                AGGG    GGGGTGGG GAGG
                                ||||    |||||||| ||||
                                TCCC    CCCCACCC CTCC
                                  CAA__       _
GAM3471  FLJ23191  5'  GGGGCTGGGCGGCGGGAG    78563     AC  _   _
                                GGG  GC GGG GGTGGGAG
                                |||  || ||| ||||||||
                                CCC  CG CCC CCGCCCTC
                                  __ A   G
GAM3471  FLJ23506  3'  AGGGACTGGGGAGAGAAGAGA  78564       GC    GT
                                AGGGAC  GGGG  GGGAGAGG
                                ||||||  ||||  ||||||||
                                TCCCTG  CCCC  TCTTCTCT
                                   A_   TC
GAM3471  FLJ30213  5'  GGGATGGGGGTGGGTGGGGGGA 78565     CGC       A_____
            GG                    GGGA   GGGGGTGGG     GAGG
                                ||||   |||||||||     ||||
                                CCCT   CCCCCACCC     CTCC
                                  A__        ACCCCC
GAM3471  FLJ31168  3'  AGGCATGTGGAGGTGGGGGAGG 78566     ACGC_       A
                                GGG     GGGGGTGGG GAGG
                                |||     ||||||||| ||||
                                TCC     CCTCCACCC CTCC
                                  GTACA        C
GAM3471  FLJ31978  3'  AGGGGTGCGAGGGGTGGG    78567     AC  _
                                AGGG  GCG GGGGTGGG
                                ||||  ||| ||||||||
                                TCCC  CGC CCCCACCC
                                  CA   T
GAM3471  FLJ32452  3'  AGGGAAGTGGGGTAGAAGGG   78568      CGCG        A
                                AGGGA    GGGGTGGGAG GG
                                |||||    |||||||||| ||
                                TCCCT    CCCCATCTTC CC
                                   TCA_         _
GAM3471  FLJ32884  3'  AGAGGCAAGCAGGTGGGAGGG  78569     C    __       A
                                GGA GCGGG  GGTGGGAG GG
                                ||| |||||  |||||||| ||
                                TCT CGTTC  CCACCCTC CC
                                  C    GT       _
GAM3471  FXYD5    3'  GGGCGGGCAGGGTTGGGGGAGG 78570     AC_     G    A
                                GGG   GCGGGG TGGG GAGG
                                |||   |||||| |||| ||||
                                CCC   CGTCCC ACCC CTCC
                                  GCC     A   C
GAM3471  GABARAPL3 5'  AGGGCAGAAGGTGGGGTGGGAG 78571      ACGCG___        A
            GG                    AGGG       GGGGTGGGAG GG
                                ||||       |||||||||| ||
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                                TCCC       CCCCACCCTC CC
                                  GTCTTCCA        _
GAM3471  GBTS1    3'  AGGGCCTGAGGTGGGAGAGG   78572      ACGCG
                                AGGG    GGGGTGGGAGAGG
                                ||||    ||||||||||||
                                TCCC    CTCCACCCTCTCC
                                  GGA__
GAM3471  GIT1     3'  AGGGTGTGGGGAGAGAGG    78574      ACGCGG   T
                                AGGG     GGG GGGAGAGG
                                ||||     ||| ||||||||
                                TCCC     CCC CTCTCTCC
                                  ACA___   _
GAM3471  GIT1     3'  AGGGGCGAGAGTGGGGAGG   78573      AC         A
                                AGGG  GCGGGGGTGGG GAGG
                                ||||  |||||||||| ||||
                                TCCC  CGCTCTCACCC CTCC
                                  __         _
GAM3471  GPA33    3'  AGGGAGTGGGAGCTGGAG    78575      CGC      G
                                AGGGA   GGGGGT GGAG
                                |||||   |||||| ||||
                                TCCCT   CCCTCG CCTC
                                  CA_     A
GAM3471  GPS2     5'  GGGACGCGGGCTCCGGAGAGG  78576          GGTG
                                GGGACGCGGG    GGAGAGG
                                ||||||||||    |||||||
                                CCCTGCGCCC    CCTCTCC
                                     GAGG
GAM3471  GPS2     5'  AGGGGCGCGCGAGAGAGAGG   78577      A   G   TG
                                AGGG CGCG GGG  GGAGAGG
                                |||| |||| |||  |||||||
                                TCCC GCGC CTC  TCTCTCC
                                  C   G   __
GAM3471  GREAT    3'  AGGCATGTGGGGTGAGGAGAGG 78578      ACGCG     _
                                GGG     GGGGTG GGAGAGG
                                |||     ||||||| |||||||
                                TCC     CCCCAC CCTCTCC
                                  GTACA     T
GAM3471  GS3955   5'  GGGGGGGTGCGGGAGAG     78579      ACGC    _
                                GGG    GGGG GTGGGAGAG
                                |||    |||| |||||||||
                                CCC    CCCC CGCCCTCTC
                                  _____    A
GAM3471  GS3955   5'  AGGGAGCGAGAGGGGAG     78580       C      T
                                AGGGA GCGGGGG GGGAG
                                ||||| ||||||| |||||
                                TCCCT CGCTCTC CCCTC
                                  _      _
GAM3471  HCNP     3'  AGGGGGGATGGGGGAG      78581      ACGC       A
                                GGG    GGGGGGTGGG GAG
                                |||    ||||||||| |||
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                                TCC    CCCCTACCC CTC
                                 _____       C
GAM3471  HGC6.1.1  5'  AGGGACAGCGGGGGGGACAACAG 78582       _     T  G  _
              G                   AGGGAC GCGGGGG GG AG AGG
                                  |||||| ||||||| || || |||
                                  TCCCTG CGCCCCC CT TT TCC
                                     T      _  G  G
GAM3471  HRD1      3'  AGGGGTGGGGGGAAGAAGAGG   78583     ACGC    T
                                  AGGG    GGGGG GGGAGAGG
                                  ||||    ||||| ||||||||
                                  TCCC    CCCCC TCTTCTCC
                                    CA__     T
GAM3471  HRH3      3'  AGAGGCGTGGCTGAGGGAGG   78584     C   G  G   A
                                  GGA GCG GG TGGG GAGG
                                  ||| ||| || |||| ||||
                                  TCT CGC CC ACTC CTCC
                                    C   A  G    C
GAM3471  HRMT1L3   5'  AGGGACGACGGGCTGGGGG    78585       _   __  T
                                  AGGGACG CGGG  GG GGG
                                  ||||||| ||||  || |||
                                  TCCCTGC GCCC  CC CCC
                                      T   GA  _
GAM3471  HS6ST1    5'  GGGGGCGGGGCCTGGGAGGG   78586     AC     G_     A
                                  GGG  GCGGGG  TGGGAG GG
                                  |||  ||||||  |||||| ||
                                  CCC  CGCCCC  ACCCTC CC
                                    C_     GG     _
GAM3471  HSA011916 3'  AGGGCAGAGAGGGGTGGGAGGG 78587      ACGC_        A
                                  AGGG    GGGGGGTGGGAG GG
                                  ||||    |||||||||||| ||
                                  TCCC    TCCCCACCCTC CC
                                    GTCTC         _
GAM3471  HSA011916 3'  AGGGCAGAGAGGGGTGGGAGGG 78587      ACGC_        A
                                  AGGG    GGGGGGTGGGAG GG
                                  ||||    |||||||||||| ||
                                  TCCC    TCCCCACCCTC CC
                                    GTCTC         _
GAM3471  HSPC072   3'  GGGATGCTCCATGGGAGAGG   78588     C  GGGG
                                  GGGA GC    GTGGGAGAGG
                                  |||| ||    ||||||||||
                                  CCCT CG    TACCCTCTCC
                                    A  AGG_
GAM3471  HSPC157   5'  GGGAGCGGGGGGACGAGG     78589     C      TGGGA
                                  GGGA GCGGGGGG     GAGG
                                  |||| |||||||     ||||
                                  CCCT CGCCCCC     CTCC
                                    _      TG___
GAM3471  HSU79303  3'  AGGGGCGCGGCGGGGAGAGG   78590      A    G  TG
                                  AGGG CGCGG GG  GGAGAGG
                                  |||| ||||| ||  |||||||
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                                TCCC GCGCC CC  CCTCTCC
                                  C    G __
GAM3471 HTF9C    5' AGGGAAGTGCTCAGAGGGGAG 78591      C__ G_   T
                                AGGGA  GC  GGGG GGGAG
                                |||||  ||  |||| |||||
                                TCCCT  CG  TCTC CCCTC
                                  TCA  AG   _
GAM3471 IGF2AS   5' AGGGACGCGGAGGAGAGG    78592         GGGT
                                AGGGACGCGG   GGGAGAGG
                                ||||||||||   ||||||||
                                TCCCTGCGCC   TCCTCTCC
                                      _____
GAM3471 IL18BP   5' GGTGAAAGGTGGGGGAG     78593    _ CGCG      A
                                GG GA   GGGGTGGG GAG
                                || ||   |||||||| |||
                                CC CT   TTCCACCC CTC
                                 A _____      C
GAM3471 ILF3     3' GGGGCGGGGGCCTGGAG     78594    AC      G_
                                GGG  GCGGGGGT  GGAG
                                |||  ||||||||  ||||
                                CCC  CGCCCCCG  CCTC
                                  __       GA
GAM3471 ISYNA1   3' AGGGTCGTGGGGGGCAGCGGG 78595     A  C    _____
                                AGGG CG GGGGG   TGGG
                                |||| || |||||   ||||
                                TCCC GC CCCCC   GCCC
                                  A  A    CGTC
GAM3471 KIAA0125 3' AGGACGGATGTGGGGGAGG   78596      C  GG    A
                                GGGACG GG  GTGGG GAGG
                                ||||||  ||  ||||| ||||
                                TCCTGC CT  CACCC CTCC
                                   _  A_    C
GAM3471 KIAA0173 3' AGGACAGCGGTGGGAGAGG   78597      GC  G
                                GGGAC  GG GGTGGGAGAGG
                                |||||  ||  ||||||||||
                                TCCTG  TC CCACCCTCTCC
                                  __  G
GAM3471 KIAA0184 3' GAGATGCGGGGATTGTTGAGAG 78598     C       GG__
           G                     GGGA GCGGGGGT   GAGAGG
                                ||||  ||||||||   ||||||
                                CTCT CGCCCCTA   CTCTCC
                                  A       ACAA
GAM3471 KIAA0237 5' AGGCACGCGGGGCGGGGAGG  78599    G      G   A
                                AGG ACGCGGGG TGGG GAGG
                                |||  |||||||| |||| ||||
                                TCC TGCGCCCC GCCC CTCC
                                 G      _   _
GAM3471 KIAA0256 3' AGGGATGAGGGAGGAG     78600      CGC    T
                                AGGGA  GGGGG GGGAG
                                |||||  ||||| |||||
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                                TCCCT  CTCCC TCCTC
                                  A__   _
GAM3471 KIAA0280 3' GGGACAGTTGGGGAGAGG   78601     GCG  GGT
                                GGGAC  GG  GGGAGAGG
                                |||||  ||  ||||||||
                                CCCTG  TC  CCCTCTCC
                                  ___  AAC
GAM3471 KIAA0285 3' AGGGATGAGGAGCAGGAGGG  78602     CGC   TG   A
                                AGGGA  GGGGG  GGAG GG
                                |||||  |||||  |||| ||
                                TCCCT  TCCTC  CCTC CC
                                  AC_   GT   _
GAM3471 KIAA0296 3' GGGTCGTGGGGGTGGGTGGAGG 78603    A  C      A_
                                GGG CG GGGGGGTGGG  GAGG
                                ||| || |||||||||  ||||
                                CCC GC CCCCCACCC  CTCC
                                  A  A       AC
GAM3471 KIAA0350 3' AGGGACTTGGGGGGCGGG   78604      GC_
                                AGGGAC  GGGGGTGGG
                                ||||||  |||||||||
                                TCCCTG  CCCCCGCCC
                                   AAC
GAM3471 KIAA0367 3' GGAGGTGGGCTGTGGGAGGG  78605    CGC  G_     A
                                GGA  GGG  GTGGGAG GG
                                |||  |||  ||||||| ||
                                CCT  CCC  CACCCTC CC
                                  CCA  GA     _
GAM3471 KIAA0427 5' AGGGGCGGGTAGGGGGGAGG  78607     AC   __ T  A
                                AGGG  GCGGG  GG GGG GAGG
                                ||||  |||||  || ||| ||||
                                TCCC  CGCCC  CC CCC CTCC
                                  __    AT  _  _
GAM3471 KIAA0427 3' GGGATGGGTCTGATGGGGAGG  78606     CGC  ___     A
                                GGGA  GGG  GGTGGG GAGG
                                ||||  |||  |||||| ||||
                                CCCT  CCC  CTACCC CTCC
                                  A__  AGA    _
GAM3471 KIAA0450 5' AGGGGTGGGGGGGTAGTAGAGG  78608     ACGC      G
                                AGGG   GGGGGTGG AGAGG
                                ||||   |||||||| |||||
                                TCCC   CCCCCATC TCTCC
                                  CAC_      A
GAM3471 KIAA0527 5' AGGAGCGCGGAGAGCCGGGGGA 78609     GA     _ _  A
           GG                     AGG  CGCGGGG GT GGG GAGG
                                ||| |||||| || ||| ||||
                                TCC  GCGCCTC CG CCC CTCC
                                  TC     T  G  C
GAM3471 KIAA0551 3' AGGGGCGGAGGGAGAG     78610     AC    GGT
                                AGGG  GCGGG  GGGAGAG
                                ||||  |||||  |||||||
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                              TCCC  CGCCT   CCCTCTC
                                __   ___
GAM3471  KIAA0557  3'  AGGGGCCTGGGGGCTCAGG   78611     AC __    __
                              AGGG  GC  GGGGGT  GGG
                              ||||  ||  ||||||  |||
                              TCCC  CG  CCCCCG  TCC
                                __ GA     AG
GAM3471  KIAA0562  3'  GGGCACCAGGTGGGAGGG   78612    A  G  G    A
                              GGG CGC GGG TGGGAG GG
                              ||| ||| ||| |||||| ||
                              CCC GTG TCC ACCCTC CC
                                _  G  _    _
GAM3471  KIAA0620  3'  GGGACAGGTGGGAGGG     78613     GCGG      A
                              GGGAC   GGGTGGGAG GG
                              |||||   ||||||||| ||
                              CCCTG   TCCACCCTC CC
                                ____      _
GAM3471  KIAA0720  5'  GGGGCGCGCGGGGAGAG    78614    A   G   T
                              GGG CGCG GGG GGGAG
                              ||| |||| ||| |||||
                              CCC GCGC CCC CTCTC
                                C   G  _
GAM3471  KIAA0721  3'  AGGGATGGGAGGGAGAG    78615     CGCG   T
                              AGGGA   GGGG GGGAGAG
                              |||||   |||| |||||||
                              TCCCT   CCCT CCCTCTC
                                A___   _
GAM3471  KIAA0721  3'  AGGGATGGGAGGGAGAG    78615     CGCG   T
                              AGGGA   GGGG GGGAGAG
                              |||||   |||| |||||||
                              TCCCT   CCCT CCCTCTC
                                A___   _
GAM3471  KIAA0821  5'  GGGAAGCGGGTAGGAG     78617     C  GG
                              GGGA GC  GGGTGGGAG
                              ||||  ||  |||||||||
                              CCCT CG  CCCATCCTC
                                T  __
GAM3471  KIAA0821  3'  AGGGTAGAAGGGTGGGAGAGG  78616     ACGC
                              AGGG   GGGGGTGGGAGAGG
                              ||||   ||||||||||||||
                              TCCC   TTCCCACCCTCTCC
                                ATC_
GAM3471  KIAA0854  3'  GGGGGCAGTGTGGGAGGG   78618    AC   GG    A
                              GGG  GCGG  GTGGGAG GG
                              |||  ||||  ||||||| ||
                              CCC  CGTC  CACCCTC CC
                                C_   A_     _
GAM3471  KIAA0871  5'  AGGAAAAGGGTGGGGGAGG   78619     CGC      A
                              AGGGA   GGGGGTGGG GAGG
                              |||||   ||||||||| ||||
```

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                                TCCTT  TTCCCACCC CTCC
                                  ___      C
GAM3471 KIAA0892 3' AGGGAGTGGGGGGACCAAGAGG 78620     CGC   TGG
                                AGGGA  GGGGG  GAGAGG
                                |||||  |||||  ||||||
                                TCCCT  CCCCC  TTCTCC
                                  CAC    TGG
GAM3471 KIAA0918 3' AGGGGCGGGGGAGGGGGAGG  78621     AC     T  A
                                AGGG  GCGGGGG GGG GAGG
                                ||||  ||||||| ||| ||||
                                TCCC  CGCCCCC CCC CTCC
                                  __     T  C
GAM3471 KIAA0953 5' AGGGGCCCGGGCGGGGAGG   78623     AC  GG     A
                                AGGG  GC  GGGTGGG GAGG
                                ||||  ||  ||||||| ||||
                                TCCC  CG  CCCGCCC CTCC
                                  __ GG     _
GAM3471 KIAA0953 3' GGGATATGGATAGGAGGG    78622     CGCGG      A
                                GGGA    GGGTGGGAG GG
                                ||||    ||||||||| ||
                                CCCT    CCTATCCTC CC
                                  ATA__       _
GAM3471 KIAA0964 3' AGGAGTGCGGGGCGGGGGGAGG 78624     AC    G   A_
                                AGGG  GCGGGG TGGG  GAGG
                                ||||  |||||| ||||  ||||
                                TCCT  CGCCCC GCCC  CTCC
                                  CA     _   CC
GAM3471 KIAA1016 5' GGGGGCGGGCGGGGAG     78625     ACGC  _     A
                                GGG   GG GGGTGGG GAG
                                |||   || ||||||| |||
                                CCC   CC CCCGCCC CTC
                                  _____ G     _
GAM3471 KIAA1042 3' AGGGAGGTGGGAGCAAGAGAGG 78626     CGC    TG
                                AGGGA  GGGGG  GGAGAGG
                                |||||  |||||  |||||||
                                TCCCT  CCCTC  TCTCTCC
                                  CCA    GT
GAM3471 KIAA1045 3' AGGGGCGGTCCAGGAGAGG   78627     AC   GGG
                                AGGG  GCGG   TGGGAGAGG
                                ||||  ||||   |||||||||
                                TCCC  CGCC   GTCCTCTCC
                                  __   AG_
GAM3471 KIAA1061 3' GGGATGGGGTACCAGAGAGG  78628     CGCG    __
                                GGGA   GGGGTG  GGAGAGG
                                ||||   ||||||  |||||||
                                CCCT   CCCCAT  TCTCTCC
                                  A___     GG
GAM3471 KIAA1075 5' GGGAGGATGTGGGGGAGG    78629     CGC  GG    A
                                GGGA   GG  GTGGG GAGG
                                ||||   ||  ||||| ||||
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                              CCCT  CC  CACCC CTCC
                                ___ TA    C
GAM3471 KIAA1205 3' GGGGCGAGAACGGGGAGG   78631    AC    GG   A
                              GGG  GCGGG  TGGG GAGG
                              |||  |||||  |||| ||||
                              CCC  CGCTC  GCCC CTCC
                                __    TT   _
GAM3471 KIAA1205 3' GGGGCTGTGGCTGTGGAGGG  78632    AC  GG_ G _   A
                              GGG  GC   GG TG GGAG GG
                              |||  ||   || || |||| ||
                              CCC  CG   CC AC CCTC CC
                                __ ACA  G  A   _
GAM3471 KIAA1205 3' GGGGTCGGGGCAAGGGGAGAGG 78630    ACG    GT__
                              GGG   CGGGG    GGGAGAGG
                              |||   |||||    ||||||||
                              CCC   GCCCC    CCCTCTCC
                                CA_    GTTC
GAM3471 KIAA1443 5' GGGAAGTGGGGGAGAG     78633     CGC  G  T
                              GGGA   GG GG GGGAGAG
                              ||||   || || |||||||
                              CCCT   TC CC CCCTCTC
                                ___  A  _
GAM3471 KIAA1553 3' AGGGGGAGGTGGTGGGAGAGG  78634     ACGC  _
                              AGGG    GGG GGTGGGAGAGG
                              ||||    ||| ||||||||||
                              TCCC    TCC CCACCCTCTCC
                                CC__   A
GAM3471 KIAA1649 3' GGGAGCGCGGGGGTCGCCGGG  78635     _      _____
                              GGGA CGCGGGGGT    GGG
                              |||| |||||||||    |||
                              CCCT GCGCCCCCA    CCC
                                C       GCGG
GAM3471 KIAA1754 3' AGGGATTGGGGGTAGCTCCAGG 78636      CGC      GAG_
                              AGGGA   GGGGGTGG    AGG
                              |||||   ||||||||    |||
                              TCCCT   CCCCCATC    TCC
                                 AA_      GAGG
GAM3471 KIAA1817 3' GGGGTGGGGGGCGTGGGGGGAG 78637     ACGC   _    A_
          G                    GGG    GGGG GTGGG  GAGG
                              |||    |||| |||||  ||||
                              CCC    CCCC CACCC  CTCC
                                CACC    G    CC
GAM3471 KIAA1887 5' AGAGGGTGAGTGGGAGGG    78638     ACGC _       A
                              AGGG    GG GGGTGGGAG GG
                              ||||    || |||||||| ||
                              TCTC    CC CTCACCCTC CC
                                ____  A       _
GAM3471 KIAA1904 3' AGGGGCGTGGGGAGAGCCGG   78639     AC   G   T    A_
                              AGGG  GCG GGG GGGAG  GG
                              ||||  ||| ||| |||||  ||
```

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                                TCCC  CGC CCC CTCTC  CC
                                  __  A  _    GG
GAM3471  KIAA1910  3'  GGGGCGAGGGAAGAG      78640    AC     TGG
                                GGG  GCGGGGG   GAGAG
                                |||  |||||||   |||||
                                CCC  CGCTCCC   TTCTC
                                  __     ____
GAM3471  KIAA1913  5'  AGGGACCGGGAACGGGAGGG  78641      G   GG    A
                                AGGGAC CGGG  TGGGAG GG
                                ||||||| ||||  |||||| ||
                                TCCCTG GCCC  GCCCTC CC
                                   _   TT    _
GAM3471  KIAA1938  3'  AGGGGCGGGGGGGGGAGGG   78642     AC     T    A
                                AGGG  GCGGGGG GGGAG GG
                                ||||  ||||||| ||||| ||
                                TCCC  CGCCCCC CCCTC CC
                                  __     _   _
GAM3471  KIAA1940  5'  GGGACGCGGGCGAAGCGGA   78643        ___
                                GGGACGCGGG   GGTGGG
                                ||||||||||   ||||||
                                CCCTGCGCCC   TCGCCT
                                     GCT
GAM3471  KIAA1949  5'  GGGTGGTGGGGGGTGATGTGAGA 78644    ACGC     ___
          GG                    GGG   GGGGGGTGG   GAGAGG
                                |||   ||||||||   ||||||
                                CCC   CCCCCACT   CTCTCC
                                  ACCA      ACA
GAM3471  KIAA1949  5'  GGGTGGTGGGGGGTGATGTGAGA 78644    ACGC     ___
          GG                    GGG   GGGGGGTGG   GAGAGG
                                |||   ||||||||   ||||||
                                CCC   CCCCCACT   CTCTCC
                                  ACCA      ACA
GAM3471  KIAA1949  5'  GGGTGGTGGGGGGTGATGTGAGA 78644    ACGC     ___
          GG                    GGG   GGGGGGTGG   GAGAGG
                                |||   ||||||||   ||||||
                                CCC   CCCCCACT   CTCTCC
                                  ACCA      ACA
GAM3471  KIAA1981  5'  GGGGCGCGGGGGGGCGCACGGG  78645    A     _____
                                GGG CGCGGGGG    TGGG
                                ||| ||||||||    ||||
                                CCC GCGCCCCC    GCCC
                                  C       CGCGT
GAM3471  KRTHA3B   3'  AGGGACCTGGGGTGAGGAGG   78646      GCG     A
                                AGGGAC   GGGGTGGG GAGG
                                ||||||   |||||||| ||||
                                TCCCTG   CCCCACTC CTCC
                                   GA_      _
GAM3471  LASP1     3'  AGGAACGCGCGGGGAGGG    78647        _   T
                                AGGGACGCG GGGG GGG
                                ||||||||| |||| |||
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                                TCCTTGCGC CCCC CCC
                                     G   T
GAM3471 LGP1     3' GGGAGTGGGGAAGAGAGG    78648     CGCG   T
                                GGGA   GGGG GGGAGAGG
                                ||||   |||| ||||||||
                                CCCT   CCCC TTCTCTCC
                                  CA__   _
GAM3471 LOH12CR1 5' AGGGACCGGGACGGGGAGG   78649      G  G GT  A
                                AGGGAC CGG G  GGG GAGG
                                |||||| ||| |  ||| ||||
                                TCCCTG GCC C  CCC CTCC
                                   _  _ TG  _
GAM3471 MACMARCKS 3' AGGGAACGTGGCTGGGAG    78650      C  G  G
                                AGGGA GCG GG TGGGAG
                                ||||| ||| || ||||||
                                TCCCT TGC CC ACCCTC
                                   _  A  G
GAM3471 MAN1C1   5' GGGCGCGGTGAGGGGAG    78651    A   _  T
                                GGG CGCGG GGG GGGAG
                                ||| ||||| ||| |||||
                                CCC GCGCC CTC CCCTC
                                  _    A  _
GAM3471 MAP1LC3A 3' AGGGGCGGGGAGCCAGGG    78652     AC    _ __
                                AGGG  GCGGGG GT  GGG
                                ||||  |||||| ||  |||
                                TCCC  CGCCCC CG  CCC
                                  __     T  GT
GAM3471 MAPKAPK2 5' GGGACGCCGGGGCACAGG    78653      G   __
                                GGGACGC GGGGT  GGG
                                ||||||| |||||  |||
                                CCCTGCG CCCCG  TCC
                                    G    TG
GAM3471 MAPKAPK2 5' GGGACGCCGGGGCACAGG    78653      G   __
                                GGGACGC GGGGT  GGG
                                ||||||| |||||  |||
                                CCCTGCG CCCCG  TCC
                                    G    TG
GAM3471 MARCKS   5' AGGGGGGTGGGGGTGGTGGAGA 78654     ACGC      __
           GG                     AGGG   GGGGGTGG  GAGAGG
                                ||||   ||||||||  ||||||
                                TCCC   CCCCCACC  CTCTCC
                                  CCCA       AC
GAM3471 MEIS3    3' AGGGAGGTGGGGGGGGACAGG  78655     CGCG   T   G
                                AGGGA   GGGG GGGA AGG
                                |||||   |||| |||| |||
                                TCCCT   CCCC CCCT TCC
                                  CCA_   _   G
GAM3471 MGC10485 5' AGGGGCACGGCCGGGGGAGG  78656     AC  G G   A
                                AGGG  GCG GG TGGG GAGG
                                ||||  ||| || |||| ||||
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                                TCCC  CGT CC GCCC CTCC
                                  __  G G   C
GAM3471  MGC10870  5'  GGGACGCGGCGGGTGTGG    78657          _   _
                                GGGACGCGG GGGTG GG
                                ||||||||| ||||| ||
                                CCCTGCGCC CCCAC CC
                                    G    A
GAM3471  MGC10924  3'  AGGGGGGTGGGGGTGGGGGTGG 78658     ACGC       AGA
                                AGGG   GGGGGTGGG  GG
                                ||||   |||||||||  ||
                                TCCC   CCCCCACCC  CC
                                  CCCA       CCA
GAM3471  MGC13114  3'  AGGTGTGCGGGGGTGAAGGAGG 78659    GAC        GA
                                AGG  GCGGGGGTGG  GAGG
                                |||  ||||||||||  ||||
                                TCC  CGCCCCCACT  CTCC
                                  ACA        TC
GAM3471  MGC15482  5'  GGGACTGGGCGCCGGAGGG   78660     GC  G G   A
                                GGGAC  GGG GT GGAG GG
                                |||||  ||| || |||| ||
                                CCCTG  CCC CG CCTC CC
                                  A_  G  G   _
GAM3471  MGC15523  5'  AGGGGCCCGGGGCGAGAG    78661     AC  G_
                                AGGG  GC  GGGGTGGGAG
                                ||||  ||  ||||||||||
                                TCCC  CG  CCCCGCTCTC
                                  __  GG
GAM3471  MGC22014  3'  GGGAAGTGGGGGTAAGGGAGG  78662     CGC       A
                                GGGA   GGGGGTGGG GAGG
                                ||||   ||||||||| ||||
                                CCCT   CCCCCATTC CTCC
                                  TCA       C
GAM3471  MGC2376   5'  GGGACTGGGGCAGAGG     78663     GCG    GGG
                                GGGAC   GGGGT   AGAGG
                                |||||   |||||   |||||
                                CCCTG   CCCCG   TCTCC
                                  A__    ____
GAM3471  MGC2452   5'  GGGGCGGTGCGGGGAGG    78664    AC   GG    A
                                GGG  GCGG  GTGGG GAGG
                                |||  ||||  ||||| ||||
                                CCC  CGCC  CGCCC CTCC
                                  __    A_    _
GAM3471  MGC2541   3'  AGGGCTGCTGATGGGAGAGG  78665     AC  GGG
                                AGGG  GC   GGTGGGAGAGG
                                ||||  ||   ||||||||||
                                TCCC  CG   CTACCCTCTCC
                                  GA  A__
GAM3471  MGC2668   3'  AGGGGTGGGGGGAGCAGGAGGG 78666     ACGC_    TG   A
                                AGGG    GGGGG  GGAG GG
                                ||||    |||||  |||| ||
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                                TCCC    CCCTC  CCTC CC
                                  CACCC    GT   _
GAM3471  MGC2749  3'  GGGTGCGGGGGTGGGCTGGG  78667    AC        AGA
                                GGG  GCGGGGGTGGG  GG
                                |||  ||||||||||  ||
                                CCC  CGCCCCCACCC  CC
                                  A_        GAC
GAM3471  MGC4293  5'  GGGACGCGGGGATGTAAG   78668           GG
                                GGGACGCGGGGGTG  AG
                                ||||||||||||  ||
                                CCCTGCGCCCCTAC  TC
                                        AT
GAM3471  MGC4368  3'  AGGGAGGCGGGTCCTCGGGGAG 78669      C    GG__   A
           G                     AGGGA GCGGG   TGGG GAGG
                                |||||  |||||   ||||  ||||
                                TCCCT CGCCC   GCCC CTCC
                                  C    AGGA   _
GAM3471  MGC4796  3'  AGGGACTGGCAGGAGGGG   78670       __      T
                                AGGGAC  GCGGGGG GGG
                                ||||||  |||||||  |||
                                TCCCTG  CGTCCTC CCC
                                   AC     _
GAM3471  MGC5139  3'  GGGAAGCGGGAAGGAG     78671     C     GT
                                GGGA GCGGGG  GGGAG
                                ||||  ||||||  |||||
                                CCCT CGCCCT  TCCTC
                                  T    __
GAM3471  MLN64    3'  GGGACAGCCTGGGAGAGG    78672      _ GGGGG
                                GGGAC GC    TGGGAGAGG
                                |||||  ||    |||||||||
                                CCCTG CG    ACCCTCTCC
                                  T  G____
GAM3471  MSTP028  3'  AGGGAGTGGGGGCGGTGAGAGG 78673      CGC      _
                                AGGGA   GGGGGTGG GAGAGG
                                |||||   ||||||||  ||||||
                                TCCCT   CCCCCGCC CTCTCC
                                  CA_       A
GAM3471  MYL9     3'  GGGGCTGGGGTGTCAGGG    78674    AC  G     GG  A
                                GGG  GC GGGGTG  AG GG
                                |||  ||  ||||||  ||  ||
                                CCC  CG CCCCAC  TC CC
                                  __  A     AG  _
GAM3471  MYT1     5'  GGGGTGCAGGGTGGACTGGGGG 78675    AC     G____    A
             AGG                  GGG  GCGGGG    TGGG GAGG
                                |||  ||||||    ||||  ||||
                                CCC  CGTCCC    ACCC CTCC
                                  CA     ACCTG   C
GAM3471  NALP2    3'  AGGGGCCGGGGAGGAGAGG   78676     AC  G   T
                                AGGG  GC GGGG GGGAGAGG
                                ||||  ||  ||||  ||||||||
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                                TCCC  CG CCCC TCCTCTCC
                                  __ G   _
GAM3471  NECL1    5'  GGGGCTGGGGATGGGGAGG   78677     AC _       A
                                GGG  GC GGGGGTGGG GAGG
                                |||  || |||||||| ||||
                                CCC  CG CCCCTACCC CTCC
                                  __ A       _
GAM3471  NFASC    3'  AGGGGCTGGGGGGCCAGGGGAGG 78678      AC _     __  A
                                AGGG  GC GGGGGT  GGG GAGG
                                ||||  || ||||||  ||| ||||
                                TCCC  CG CCCCCG  CCC CTCC
                                  __ A     GT  _
GAM3471  NK4      3'  GGTGCGCGGTGACGGGGAGG  78679    GA    G GT   A
                                GG  CGCGG G  GGG GAGG
                                ||  ||||| |  ||| ||||
                                CC  GCGCC C  CCC CTCC
                                 AC    A TG  _
GAM3471  NLI-IF   5'  GGGGCGCGGGGGGGAG      78680     A       TG
                                GGG CGCGGGGG  GGAG
                                ||| ||||||||  ||||
                                CCC GCGCCCCC  CCTC
                                  C       __
GAM3471  NLI-IF   3'  AGGGGTGTGAGGGACAGAGG   78681      ACGCG    T  G
                                AGGG    GGGG GG AGAGG
                                ||||    |||| || |||||
                                TCCC    CTCC CT TCTCC
                                  CACA_   _ G
GAM3471  NOL4     5'  AGGGATGGGAAGAGGGGAGG   78682      CGC    T   A
                                AGGGA   GGGGG GGG GAGG
                                |||||   ||||| ||| ||||
                                TCCCT   CCTTC CCC CTCC
                                   AC_    T   _
GAM3471  NR4A3    5'  AGGGGTGGGGGGGCGGGAG    78683     ACGC
                                AGGG   GGGGGTGGGAG
                                ||||   ||||||||||
                                TCCC   CCCCCGCCCTC
                                  CAC_
GAM3471  NXPH3    3'  AGGGGTTGGGGTGGAAGAGG   78684     ACGCG
                                AGGG    GGGGTGGGAGAGG
                                ||||    ||||||||||||
                                TCCC    CCCCACCTTCTCC
                                  CAA__
GAM3471  p25      3'  GGGATTGGCCAGGAGAGG    78685     CGCGG  G
                                GGGA    GG TGGGAGAGG
                                ||||    || |||||||||
                                CCCT    CC GTCCTCTCC
                                  AA___  G
GAM3471  p25      3'  GGGGCTGGGGTAGGAG      78686     AC  G
                                GGG  GC GGGGTGGGAG
                                |||  || ||||||||||
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                                CCC  CG CCCCATCCTC
                                  __  A
GAM3471  PAK7     5'  AGGGGGGCGGGGGCCAGCGGGA 78687      AC       _____     A
                GGG                  AGGG  GCGGGGGT    GGGAG GG
                                |||||  ||||||||   |||||  ||
                                TCCC  CGCCCCCG    CCCTC CC
                                  CC       GTCG    _
GAM3471  PEPP3    3'  AGGGATGAGGTGGGAG      78688       CGCG
                                AGGGA    GGGGTGGGAG
                                |||||    ||||||||||
                                TCCCT    CTCCACCCTC
                                  A___
GAM3471  PF1      5'  GGGAGGTGAGGGGAGGG     78689      CGC  _  T    A
                                GGGA   GG GGG GGGAG GG
                                ||||   ||  ||| |||||  ||
                                CCCT   CC CTC CCCTC CC
                                  ___  A   _    _
GAM3471  phospho1  3'  GGGAGTGCGGGGGGTCGGGAGG  78690      C_       G  A
                                GGGA  GCGGGGGT GG GAGG
                                ||||  |||||||| ||  ||||
                                CCCT  CGCCCCCA CC CTCC
                                  CA       G  _
GAM3471  PLCL2    5'  AGGGACGGGCCCGGGGAGG    78691       GC   GG    A
                                AGGGAC  GGG  TGGG GAGG
                                ||||||  |||  ||||  ||||
                                TCCCTG  CCC  GCCC CTCC
                                   __   GG    _
GAM3471  PLEKHA3   5'  AGGGACGTGGCGGCCTTTAGAG 78692        C  G   GGG_
                G                    AGGGACG GG GGT    AGAGG
                                |||||||  ||  |||    |||||
                                TCCCTGC CC CCG    TCTCC
                                    A  G   GAAA
GAM3471  PLSCR3   3'  AGGGCCCTAGTGGGAGAGG    78693      ACGCGGG
                                AGGG      GGTGGGAGAGG
                                ||||      ||||||||||
                                TCCC      TCACCCTCTCC
                                  GGGA___
GAM3471  PLSCR3   3'  AGGGCCCTAGTGGGAGAGG    78693      ACGCGGG
                                AGGG      GGTGGGAGAGG
                                ||||      ||||||||||
                                TCCC      TCACCCTCTCC
                                  GGGA___
GAM3471  PPP1R14A  5'  GGGCTCGGGCTCGCCGGGAGG  78694     ACG    G__  G  A
                                GGG   CGGG   GT GG GAGG
                                |||   ||||   ||  ||  ||||
                                CCC   GCCC   CG CC CTCC
                                  GA_   GAG  G  _
GAM3471  PPP1R1B   5'  AGGGCGCGGGAGCGGGAG    78695      A
                                AGGG CGCGGGGGTGGGAG
                                |||| ||||||||||||||
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                                TCCC GCGCCCTCGCCCTC
                                  _
GAM3471 PPP2R2A  5' GGGATGGGGGGGGTAGAGAGG  78696     CGC      G
                                GGGA  GGGGGTGG AGAGG
                                ||||  |||||||| |||||
                                CCCT  CCCCCATC TCTCC
                                  ACC      _
GAM3471 PSR      3' GGGCGTGGGGGGTAAGGAGG   78697    A  C       A
                                GGG CG GGGGGGTGGG GAGG
                                ||| || ||||||||| ||||
                                CCC GC CCCCCATTC CTCC
                                  _ A       _
GAM3471 QKI      3' AGGGGTGGGGGGAGGCAGAGG  78698     ACGC    T  G
                                AGGG   GGGGG GG AGAGG
                                ||||   ||||| || |||||
                                TCCC   CCCCC CC TCTCC
                                  CA__    T  G
GAM3471 QSCN6    3' AAGGAGCAAGGGGTGGGAGGG  78699      C  _       A
                                AGGGA GCG GGGGTGGGAG GG
                                ||||| ||| ||||||||||| ||
                                TTCCT CGT CCCCACCCTC CC
                                  _  T       _
GAM3471 RAB11B   3' AGGGACAGCAGGGAGGGG    78700       _     T
                                AGGGAC GCGGGGG GGG
                                |||||| ||||||| |||
                                TCCCTG CGTCCCT CCC
                                   T      C
GAM3471 RAB6B    5' GGTGCGGGAGCCGGAGGG    78701    AC      G   A
                                GG  GCGGGGGT GGAG GG
                                ||  |||||||| |||| ||
                                CC  CGCCCTCG CCTC CC
                                 A_      G   _
GAM3471 RAGD     5' GGGACGGCGGGGGTCCCGGG  78702       _     ____
                                GGGACG CGGGGGT   GGG
                                |||||| |||||||   |||
                                CCCTGC GCCCCCA   CCC
                                   C      GGG
GAM3471 RAI16    3' GGGAGGAATGTGGGAGAGG   78703     CGC   _
                                GGGA  GGGG GTGGGAGAGG
                                ||||  |||| ||||||||||
                                CCCT  CCTT CACCCTCTCC
                                  ____   A
GAM3471 RAP2B    3' GGGACGCCGGCCGCGGAG    78704       GG  G  _
                                GGGACGC  GG TG GGAG
                                |||||||  || || ||||
                                CCCTGCG  CC GC CCTC
                                   G_  G  G
GAM3471 RASGRP4  3' AGGGGTGTTGGGGTTTGTGAAG 78705     ACGCG   __ _   A
            GG                    AGGG    GGGGT  G GGAG GG
                                ||||    |||||  | |||| ||
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                                TCCC    CCCCA  C CTTC CC
                                  CACAA    AA A   _
GAM3471  RBPMS    5'  GGGACGGGGGTGCCTAGAGAGG 78706      C   _ G_
                                GGGACG GGGG GT  GGAGAGG
                                |||||| |||| ||  |||||||
                                CCCTGC CCCC CG  TCTCTCC
                                   _   A  GA
GAM3471  RINZF    5'  AGGGGGCGGGCGGCGGAGAGG  78707     AC    _    G
                                AGGG  GCGGG GGTGG AGAGG
                                ||||  ||||| ||||| |||||
                                TCCC  CGCCC CCGCC TCTCC
                                  C_    G    _
GAM3471  RIP60    3'  AGGGGGCAGGTGGGAGGG    78708     AC  GG       A
                                AGGG  GC  GGGTGGGAG GG
                                ||||  ||  |||||||| ||
                                TCCC  CG  TCCACCCTC CC
                                  C_ __       _
GAM3471  RMP      5'  AGGGGCCGGGGCCGAAGGG   78709     AC  G    G   A
                                AGGG  GC GGGGT GGAG GG
                                ||||  || ||||| |||| ||
                                TCCC  CG CCCCG CTTC CC
                                  __ G    G   _
GAM3471  RNPC1    3'  GGTGCGGGGGTAGAGG     78710    AC      GGG
                                GG  GCGGGGGT   AGAGG
                                ||  ||||||||   |||||
                                CC  CGCCCCCA   TCTCC
                                 A_      ____
GAM3471  SCAM-1   3'  GGGAGTGGGGTGGGGAGG    78711     CGCG      A
                                GGGA    GGGGTGGG GAGG
                                ||||    |||||||| ||||
                                CCCT    CCCCACCC CTCC
                                  CA__       _
GAM3471  SCYB10   3'  AGGGAAGTGATGGGAGAGG   78712      CGC  G
                                AGGGA   GG GGTGGGAGAGG
                                |||||   || ||||||||||
                                TCCCT   TC CTACCCTCTCC
                                   ____ A
GAM3471  SDC3     3'  AGGGAAGGCCTGGGGGAGG   78713     CGC   GG   A
                                AGGGA   GGG  TGGG GAGG
                                |||||   |||  |||| ||||
                                TCCCT   TCC  ACCC CTCC
                                   ____  GG   C
GAM3471  SDCCAG43 3'  AGGGAAGTGGGCAGGAGAGA  78714      CGC  _  TG
                                AGGGA   GG GGG  GGAGAGG
                                |||||   || |||  |||||||
                                TCCCT   TC CCC  CCTCTCT
                                   ____ A   GT
GAM3471  SEMA4G   5'  GGGCGGTGGGGGTGGTGGG   78716    A  C_      GAGA
                                GGG CG  GGGGGTGG    GG
                                ||| ||  ||||||||    ||
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                                CCC GC  CCCCCACC   CC
                                  _ CA      AC__
GAM3471  SEMA4G   3'  GGGGTGGAGGTGGGAGAGG   78715    ACGC
                                GGG   GGGGGGTGGGAGAGG
                                |||   |||||||||||||||
                                CCC   CCTCCACCCTCTCC
                                  CA__
GAM3471  SEMA4G   3'  GGGGTGGAGGTGGGAGAGG   78715    ACGC
                                GGG   GGGGGGTGGGAGAGG
                                |||   |||||||||||||||
                                CCC   CCTCCACCCTCTCC
                                  CA__
GAM3471  SIAT8C   5'  GGGGTGCAGGAGAGGGAG   78717    AC     T
                                GGG  GCGGGGG GGGAG
                                |||  ||||||| |||||
                                CCC  CGTCCTC CCCTC
                                  CA     T
GAM3471  SIMRP7   3'  AGGGGAGATTGGGAGAG    78718    ACGC   GG
                                AGGG   GGG  TGGGAGAG
                                ||||   |||  ||||||||
                                TCCC   CTC  ACCCTCTC
                                  _____  TA
GAM3471  SKD3     3'  AGGACGTGGGGTGAGGAGG   78719      CG      A
                                GGGACG  GGGGTGGG GAGG
                                ||||||  |||||||| ||||
                                TCCTGC  CCCCACTC CTCC
                                   A_      _
GAM3471  SLC26A10 5'  AGGGAGTGTTGGGTGGGAGAGG 78720      CGCGG
                                AGGGA    GGGTGGGAGAGG
                                |||||    ||||||||||||
                                TCCCT    CCCACCCTCTCC
                                   CACAA
GAM3471  SP2      3'  AGGGGTGAGGTGAAGGGAGAGG 78721     ACGCG   ___
                                AGGG    GGGGT   GGGAGAGG
                                ||||    |||||   ||||||||
                                TCCC    CTCCA   CCCTCTCC
                                  CA___    CTT
GAM3471  SQV7L    5'  AGGGGGGTGCGGGAGAG    78722     ACGC   G
                                AGGG   GGG GTGGGAGAG
                                ||||   ||| |||||||||
                                TCCC   CCC CGCCCTCTC
                                  _____  A
GAM3471  SSB-4    3'  GGGCAGTGGGGTGGGGAGG   78723    A  CG      A
                                GGG CG  GGGGTGGG GAGG
                                ||| ||  |||||||| ||||
                                CCC GT  CCCCACCC CTCC
                                  _ CA      _
GAM3471  SSBP3    3'  GGATGGGGTGGGAGGG     78724    CGCG       A
                                GGA   GGGGTGGGAG GG
                                |||   |||||||||| ||
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                                CCT   CCCCACCCTC CC
                                  A___       _
GAM3471  SSH-3   3'  AGGAATGAACTGGGAGAGG   78725     CGCG  G
                                GGGA   GGG TGGGAGAGG
                                ||||   ||| |||||||||
                                TCCT   CTT ACCCTCTCC
                                  TA__   G
GAM3471  SSH-3   3'  AGGGGGCGGGGGTGGGAG    78726     AC
                                AGGG  GCGGGGGTGGGAG
                                ||||  |||||||||||||
                                TCCC  CGCCCCCACCCTC
                                  C_
GAM3471  SSH-3   3'  AGGAATGAACTGGGAGAGG   78725     CGCG  G
                                GGGA   GGG TGGGAGAGG
                                ||||   ||| |||||||||
                                TCCT   CTT ACCCTCTCC
                                  TA__   G
GAM3471  STAG3   3'  AGGGAGTGGAGCTGGGGAGG  78727      CGC   G   A
                                AGGGA  GGGG TGGG GAGG
                                |||||  |||| |||| ||||
                                TCCCT  CCTC ACCC CTCC
                                   CA_   G   _
GAM3471  STI2    3'  AGGGGTGGGGTAGAAAAGA   78728     ACGCG
                                AGGG   GGGGTGGGAGAGG
                                ||||   ||||||||||||
                                TCCC   CCCCATCTTTTCT
                                  CA___
GAM3471  STK29   3'  AGGCGGCGCGGCCAGGGAGG  78729    AC  G G   A
                                GGG  GCG GG TGGG GAGG
                                |||  ||| || |||| ||||
                                TCC  CGC CC GTCC CTCC
                                  GC   G G   _
GAM3471  STK29   3'  GGGAGGCGCGGGTGAGACGAGA 78730     C   G     ___
            GG                    GGGA GCG GGGTGGGA   GAGG
                                ||||  ||| ||||||||   ||||
                                CCCT CGC CCCACTCT   CTCC
                                  C   G       GCT
GAM3471  STMN3   3'  GGGGGCGGGGGTGGGGGAGG  78731    AC        A
                                GGG  GCGGGGGTGGG GAGG
                                |||  |||||||||| ||||
                                CCC  CGCCCCCACCC CTCC
                                  C_         C
GAM3471  STMN3   3'  AGGGGCGCCGGCTCAGAGG   78732     A  GGG  GGG
                                AGGG CGC   GGT   AGAGG
                                |||| |||   |||   |||||
                                TCCC GCG   CCG   TCTCC
                                  C   G__   AG_
GAM3471  STRAIT11499 5'  AGGGACGCAGGGGCACGGG   78733           __
                                AGGGACGCGGGGGT  GGG
                                ||||||||||||||  |||
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                                TCCCTGCGTCCCCG  CCC
                                       TG
GAM3471  SV2     3'  AGGGGTGCGAGGAAGAG     78734     AC     GTGG
                                AGGG  GCGGGG   GAGAG
                                ||||  ||||||   |||||
                                TCCC  CGCTCC   TTCTC
                                  CA    ____
GAM3471  TBX21    5'  AGGGGGCGGGGGACCCGAGG  78735     AC     TGGGA
                                AGGG  GCGGGGG   GAGG
                                ||||  |||||||   ||||
                                TCCC  CGCCCCC   CTCC
                                  C_     TGGG_
GAM3471  TEX27    3'  AGGGGGCGGGGGGCCCTGGGGA 78736     AC     ____   A
            GG                    AGGG  GCGGGGG   TGGG GAGG
                                ||||  |||||||   |||| ||||
                                TCCC  CGCCCCC   ACCC CTCC
                                  C_     CGGG   _
GAM3471  TGIF2    5'  GGGAGCGGGGGGCGCCGGG   78737     C     ____
                                GGGA GCGGGGG   TGGG
                                ||||  |||||||   ||||
                                CCCT CGCCCCC   GCCC
                                  _     CGCG
GAM3471  THG-1    5'  GGGAGGTGGCGGGAGGG     78738     CGC  G      A
                                GGGA   GG GGTGGGAG GG
                                ||||   || ||||||||  ||
                                CCCT   CC CCGCCCTC CC
                                  ___  A      _
GAM3471  TNRC4    3'  AGAGAGGCAGGGGGGTGGGAGG 78739      C  __        A
            G                    AGGGA GC  GGGGGTGGGAG GG
                                |||||  ||  ||||||||||  ||
                                TCTCT CG  CCCCCACCCTC CC
                                  C  TC         _
GAM3471  TOR2A    3'  AGGGTGTGGGGTGGAGGG    78740     ACGCG     G  A
                                AGGG    GGGGTGG AG GG
                                ||||    |||||||  ||  ||
                                TCCC    CCCCACC TC CC
                                  ACA__     _  _
GAM3471  TRAF4    3'  GGGTGGTGGCTGGGGGAGG   78741     ACGC  _  G   A
                                GGG   GG GG TGGG GAGG
                                |||   ||  ||  ||||  ||||
                                CCC   CC CC ACCC CTCC
                                  A___  A  G   C
GAM3471  TRIAD3   3'  AGGGGTCGGCTCCGAGGAGAGG 78742     ACG   GGGT_
                                AGGG   CGG    GGGAGAGG
                                ||||   |||    ||||||||
                                TCCC   GCC    TCCTCTCC
                                  CA_   GAGGC
GAM3471  TRIM29   3'  AGGGCGTGGGCGGGAGAGG   78743     A  CGG
                                AGGG CG   GGGTGGGAGAGG
                                ||||  ||   ||||||||||||
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                                TCCC GC   CCCGCCCTCTCC
                                  _ A__
GAM3471  TUBB5    3'  AGGGAAGCGGGGAGGGAG    78744      C      T
                                AGGGA GCGGGGG GGGAG
                                ||||| ||||||| |||||
                                TCCCT CGCCCCT CCCTC
                                  T     _
GAM3471  TXNL     5'  AGGGACGCGGAGCGGCCGAGG  78745          G   GA
                                AGGGACGCGGGG TGG  GAGG
                                |||||||||||| |||  ||||
                                TCCCTGCGCCTC GCC  CTCC
                                       _  GG
GAM3471  Ubc6p    3'  GGGCACGGGATGTGAGGGAGG  78746     A     _    A
                                GGG CGCGGGG GTGGG GAGG
                                ||| ||||||| ||||| ||||
                                CCC GTGCCCT CACTC CTCC
                                  _     A    C
GAM3471  UBE3B    3'  AGGAGCATGAGGTGGGAGAGG  78747     C  _
                                GGGA GCG GGGGTGGGAGAGG
                                |||| ||| ||||||||||||
                                TCCT CGT CTCCACCCTCTCC
                                  _  A
GAM3471  USP22    5'  GGGGCGGCGGCGAGGGAGG   78748     AC   G     A
                                GGG  GCGG GGTGGG GAGG
                                |||  |||| |||||| ||||
                                CCC  CGCC CCGCTC CTCC
                                  __   G     C
GAM3471  VAV3     3'  GGGAGGTGGATGGGAG      78749      CGC  _
                                GGGA   GG GGGTGGGAG
                                ||||   || |||||||||
                                CCCT   CC CCTACCCTC
                                  ____ A
GAM3471  VELI1    5'  GGGGCGGGGGTGGAGAGG    78750     AC        G
                                GGG  GCGGGGGTGG AGAGG
                                |||  ||||||||| |||||
                                CCC  CGCCCCCACC TCTCC
                                  __        _
GAM3471  VI       3'  AGGGATAGTGGCTGGGAG    78751       CGC  _  G
                                AGGGA   GG GG TGGGAG
                                |||||   || || ||||||
                                TCCCT   TC CC ACCCTC
                                  A__  A  G
GAM3471  ZIC4     5'  AAGGACGGCTGGGGGAGG    78752        _ _    T
                                AGGGACG C GGGGG GG
                                ||||||| | ||||| ||
                                TTCCTGC G CCCCC CC
                                    C A    T
GAM3471  ZNF31    5'  AGGGACTCGGGGAGTGAG    78753       G    _
                                AGGGAC CGGGG GTGGG
                                |||||| ||||| |||||
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                                TCCCTG GCCCC CACTC
                                   A    T
GAM3471  LOC112476 3'  AGGGGGCGGGACGTGGAGAGG  78754     AC    _   G
                                AGGG  GCGGGG GTGG AGAGG
                                ||||  |||||| |||| |||||
                                TCCC  CGCCCT CACC TCTCC
                                  C_    G   _
GAM3471  LOC112868 3'  GGGAGGTGGAGTCTGGAGAGG  78755     CGCG    G_
                                GGGA   GGGGT  GGAGAGG
                                ||||   |||||  |||||||
                                CCCT   CCTCA  CCTCTCC
                                  CCA_   GA
GAM3471  LOC115861 3'  AGGCGTGCGGGGGTGGGGTGGG 78756     AC_        AGA
                                GGG   GCGGGGGTGGG   GG
                                |||   ||||||||||   ||
                                TCC   CGCCCCCACCC   CC
                                  GCA         CAC
GAM3471  LOC118738 3'  GGTGATGCGGCTGAGAGAGG   78757    _ C    GGG
                                GG GA GCGG   TGGGAGAGG
                                || || ||||   |||||||||
                                CC CT CGCC   ACTCTCTCC
                                 A  A   G__
GAM3471  LOC123591 5'  GGGGCGGGGTGGGGAG     78758     AC     G    A
                                GGG  GCGGGG TGGG GAG
                                |||  |||||| |||| |||
                                CCC  CGCCCC ACCC CTC
                                  __     _   _
GAM3471  LOC126526 3'  GGGAGTGGGGGAAGGGAGG   78759      CGC    T   A
                                GGGA   GGGGG GGG GAGG
                                ||||   ||||| ||| ||||
                                CCCT   CCCCC TCC CTCC
                                  CA_    T   _
GAM3471  LOC128344 3'  AGGGAGGTGTACAGGAGAGG   78760      CGC  GG_ TG
                                AGGGA   GG   G  GGAGAGG
                                |||||   ||   |  |||||||
                                TCCCT   CC   T  CCTCTCC
                                   ____  ACA GT
GAM3471  LOC129433 3'  AGGACGCGGGTCCAGAGG    78761          GGTGGG
                                GGGACGCGGG     AGAGG
                                ||||||||||     |||||
                                TCCTGCGCCC     TCTCC
                                     AGG____
GAM3471  LOC129642 3'  GGGACATGGCATGGGAG     78762       CG  G
                                GGGACG  GG GTGGGAG
                                ||||||  || |||||||
                                CCCTGT  CC TACCCTC
                                   A_  G
GAM3471  LOC130574 5'  AGGGAGCGCAGCGGGGAGAGG  78763      _    G  TG
                                AGGGA CGCGG GG  GGAGAGG
                                ||||| ||||| ||  |||||||
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                                TCCCT GCGTC CC  CCTCTCC
                                  C    G  __
GAM3471  LOC132166 5'  AGGGGCGCGAGGGCCCAGG   78764     A       __
                                AGGG CGCGGGGGT  GGG
                                |||| |||||||||  |||
                                TCCC GCGCTCCCG  TCC
                                  C       GG
GAM3471  LOC136345 3'  AGGGACCTGGTTGCATGGGGGA 78765      GC  GG__    A
           GG                    AGGGAC  GG   GTGGG GAGG
                                |||||| ||   ||||| ||||
                                TCCCTG  CC   TACCC CTCC
                                  GA  AACG    C
GAM3471  LOC139770 5'  AGGGGCGGGGAGAGAGAGG   78766     AC      T
                                AGGG  GCGGGGG GGGAGAGG
                                ||||  ||||||| ||||||||
                                TCCC  CGCCCCT CTCTCTCC
                                  __     _
GAM3471  LOC145255 3'  AGGGGTTGGGAGAGTGGGAG   78767     ACGC_
                                AGGG    GGGGGGTGGGAG
                                ||||    ||||||||||
                                TCCC    CTCTCACCCTC
                                  CAACC
GAM3471  LOC145333 5'  AGGGATGACCCACAGGGAGGGG 78768      _____      T
                                AGGGA    CGCGGGGG GGG
                                |||||    |||||||| |||
                                TCCCT    GTGTCCCT CCC
                                  ACTGG      C
GAM3471  LOC145371 3'  AGGGACAGTGGGGGTGGGGGAA 78769       C_      A
           G                     AGGGACG  GGGGGTGGG GAGG
                                |||||||  ||||||||| ||||
                                TCCCTGT  CCCCCACCC CTTC
                                   CA       C
GAM3471  LOC145678 5'  GGGATGGGCTGAGAGAGG    78770     CGCG   G
                                GGGA   GGG TGGGAGAGG
                                ||||   ||| |||||||||
                                CCCT   CCC ACTCTCTCC
                                  A___   G
GAM3471  LOC145801 5'  GGGGCGGATGGGGGAGAGG   78771    AC    _  T
                                GGG  GCGGG GG GGGAGAGG
                                |||  ||||| || ||||||||
                                CCC  CGCCT CC CCCTCTCC
                                  __    A  _
GAM3471  LOC145989 3'  AGGAGGTGGCTGGGAGGG    78772     CGC  _  G    A
                                GGGA   GG GG TGGGAG GG
                                ||||   || || |||||| ||
                                TCCT   CC CC ACCCTC CC
                                  ___  A  G     _
GAM3471  LOC146229 5'  GGGCTCGACTGGTGGGAGGG   78773    ACG   G_      A
                                GGG   CGG  GGTGGGAG GG
                                |||   |||  |||||||| ||
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                                CCC   GCT  CCACCCTC CC
                                  GA_   GA       _
GAM3471  LOC146268 3'  GGGTGTGGAAGAAGGGAGGG   78774     ACGC    T_    A
                                GGG    GGGGG  GGGAG GG
                                |||    |||||  ||||| ||
                                CCC    CCTTC  CCCTC CC
                                  ACA_     TT    _
GAM3471  LOC146315 5'  AGGAAGAAGGTGGGGGAGG    78775       CGC       A
                                AGGGA   GGGGGTGGG GAGG
                                |||||   ||||||||| ||||
                                TCCTT   CTTCCACCC CTCC
                                   ___        C
GAM3471  LOC146513 5'  AGGTGCACGTGGGAGAG     78776     GA   GGGG
                                AGG  CGC    GTGGGAGAG
                                |||  |||    |||||||||
                                TCC  GTG    CACCCTCTC
                                  AC  _____
GAM3471  LOC146733 3'  GGGAGGTGGGGGAGTGGGGGAG 78777      CGC__       A
                  G                 GGGA     GGGGGTGGG GAGG
                                |||||     ||||||||| ||||
                                CCCT     CCCTCACCC CTCC
                                  CCACC        C
GAM3471  LOC146895 5'  AGGATGCGGGGGGTGGGGCGG   78778      C         AGA
                                GGGA GCGGGGGGTGGG   GG
                                |||| ||||||||||   ||
                                TCCT CGCCCCCACCC   CC
                                  A          CG_
GAM3471  LOC146940 3'  GGGAGCGGGGAGGAG       78779      C     GT
                                GGGA GCGGGG  GGGAG
                                |||| ||||||  |||||
                                CCCT CGCCCC  TCCTC
                                  _     ___
GAM3471  LOC147136 5'  GGGCGCTGAGTGGAGGG     78780     A   GG     G  A
                                GGG CGC  GGGTGG AG GG
                                ||| |||  |||||| || ||
                                CCC GCG  CTCACC TC CC
                                  _   A_     _ _
GAM3471  LOC147160 5'  AGGGACGTGGTGGGCGGG     78781        C  _
                                AGGGACG GG GGGTGGG
                                |||||||  || |||||||
                                TCCCTGC CC CCCGCCC
                                    A  A
GAM3471  LOC147165 3'  GGGAGCGGACCCCGAGAGG    78782      C     GGTGG
                                GGGA GCGGG     GAGAGG
                                |||| |||||     ||||||
                                CCCT CGCCT     CTCTCC
                                  _     GGGG_
GAM3471  LOC147180 5'  GGGGCAGTGGGCCATGGGGAGG 78783      AC    _    ___   A
                                GGG  GCGG GGGT   GGG GAGG
                                |||  |||| ||||   ||| ||||
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                                CCC  CGTC CCCG   CCC CTCC
                                  __    A    GTA  _
GAM3471  LOC148397 3'  AGGGGTGCGGGGGCTGCCGTCA 78784      AC       GGGAG__
                GG                  AGGG  GCGGGGGT      AGG
                                ||||  ||||||||      |||
                                TCCC  CGCCCCCG      TCC
                                  CA       ACGGCAG
GAM3471  LOC149501 3'  AGGGGCAGGCTGGGAGGG    78785      AC    G G     A
                                AGGG  GCGG G TGGGAG GG
                                ||||  |||| | |||||| ||
                                TCCC  CGTC C ACCCTC CC
                                  __    _ G     _
GAM3471  LOC149606 3'  GGGTGGCGTGGGTGAGAG    78786     AC   G
                                GGG  GCG GGGTGGGAG
                                |||  ||| |||||||||
                                CCC  CGC CCCACTCTC
                                  AC   A
GAM3471  LOC149668 5'  GGGACGTGGAGGCGATGAGG   78787       C       GA
                                GGGACG GGGGGTGG  GAGG
                                ||||||| ||||||||  ||||
                                CCCTGC CCTCCGCT  CTCC
                                   A       A_
GAM3471  LOC149773 3'  AGGGATGGGGCTGTTGGAGG   78788      CGC    G  GGA
                                AGGGA   GGGG TG   GAGG
                                |||||   |||| ||   ||||
                                TCCCT   CCCC AC   CTCC
                                   A__    G  AAC
GAM3471  LOC150498 3'  AGGGGTGGGATGGGGAG     78789      ACGCG       A
                                AGGG     GGGGTGGG GAG
                                ||||     |||||||| |||
                                TCCC     CCCTACCC CTC
                                  CA___       _
GAM3471  LOC150538 3'  GGGCCGTGGGGGTGGTGGGGG  78790     A  C       GAGA
                                GGG CG GGGGGTGG    GG
                                ||| || ||||||||    ||
                                CCC GC CCCCCACC    CC
                                  G  A       ACCC
GAM3471  LOC151171 5'  AGGAGATGCGGGGCAGAGG    78791     _  C     GTGGG
                                AGG GA GCGGGG     AGAGG
                                ||| || ||||||     |||||
                                TCC CT CGCCCC     TCTCC
                                  T  A     G____
GAM3471  LOC151512 5'  AGGGGCGCGGCTGGGAGAGG   78792      AC   G  G
                                AGGG  GCG GG TGGGAGAGG
                                ||||  ||| || |||||||||
                                TCCC  CGC CC ACCCTCTCC
                                   __   G  G
GAM3471  LOC152402 3'  AGGGAGGTGGGGCGCAGTGGAG 78793       CGC    _ TG GA
                G                   AGGGA   GGGG G  G  GAGG
                                |||||   |||| |  |  ||||
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                                TCCCT   CCCC C  C  CTCC
                                   CCA    G GT AC
GAM3471  LOC152579 3'  AGGGACGCTGGTTGTGGA    78794        _  GG
                                AGGGACGC GG  GTGGG
                                |||||||| ||  |||||
                                TCCCTGCG CC  CACCT
                                     A  AA
GAM3471  LOC153205 3'  GAGAAGGGTGGGGGAGG     78795      CGCG       A
                                GGGA    GGGGTGGG GAGG
                                ||||    |||||||| ||||
                                CTCT    TCCCACCC CTCC
                                  ____       C
GAM3471  LOC153243 3'  AGGGGTAGGCTGGGAGGG    78339      ACGCG   G     A
                                AGGG    GGG TGGGAG GG
                                ||||    ||| |||||| ||
                                TCCC    TCC ACCCTC CC
                                  CA___   G     _
GAM3471  LOC153525 5'  AGGGGGGTGGGGGTGGGGGTGG 78658      ACGC       AGA
                                AGGG   GGGGGTGGG   GG
                                ||||   |||||||||   ||
                                TCCC   CCCCCACCC   CC
                                  CCCA       CCA
GAM3471  LOC153688 3'  AGGGGCCGGGAGGGAG      78796      AC  G    T
                                AGGG  GC GGGG GGGAG
                                ||||  || |||| |||||
                                TCCC  CG CCCT CCCTC
                                  __  G   _
GAM3471  LOC154877 3'  AGGGAAGTGAGCTGTGGGAGAG 78797       CGC   G_
            G                    AGGGA   GGG  GTGGGAGAGG
                                |||||   |||  ||||||||||
                                TCCCT   CTC  CACCCTCTCC
                                   TCA   GA
GAM3471  LOC155032 5'  AGGGACCTGGTTGCATGGGGGA 78765       GC  GG__    A
            GG                   AGGGAC  GG    GTGGG GAGG
                                ||||||  ||    ||||| ||||
                                TCCCTG  CC    TACCC CTCC
                                   GA  AACG    C
GAM3471  LOC157226 5'  GGGGCGGTGGGGGGGAAAGG    78799     AC    _   T
                                GGG  GCGG GGG GGGAGAGG
                                |||  |||| ||| ||||||||
                                CCC  CGCC CCC CCCTTTCC
                                  __    A   _
GAM3471  LOC157226 5'  GGGCGGCGGGGGGGACGGGAGGG 78798     AC      __     A
                                GGG  GCGGGGG  TGGGAG GG
                                |||  |||||||  |||||| ||
                                CCC  CGCCCCC  GCCCTC CC
                                  GC      CT     _
GAM3471  LOC157349 3'  AGGGGCGCAGGGGGCAGAGG    78800      A       GGG
                                AGGG CGCGGGGGT   AGAGG
                                |||| |||||||||   |||||
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                                TCCC GCGTCCCCG   TCTCC
                                  C       ___
GAM3471  LOC157531 5'  AGGGGCGGGGGGGCTGGAG    78801      A  C     G
                                AGGG CG GGGGGT GGAG
                                |||| || |||||| ||||
                                TCCC GC CCCCCG CCTC
                                  C _     A
GAM3471  LOC157848 3'  AGGAGCGTGGGGAAGGGGAGG  78802     GA  C    T   A
                                AGG  CG GGGGG GGG GAGG
                                |||  || ||||| ||| ||||
                                TCC  GC CCCCT CCC CTCC
                                  TC  A    T  _
GAM3471  LOC157931 3'  GGGATGGTGGCAAGTGGGGGAG 78803      CGC_ _      A
            G                    GGGA    GG GGGTGGG GAGG
                                ||||    || ||||||| ||||
                                CCCT    CC TTCACCC CTCC
                                  ACCA  G      C
GAM3471  LOC158056 5'  AGGGGCTGGGGGGCTGGG    78804      AC  __    _
                                AGGG  GC  GGGGG TGGG
                                ||||  ||  ||||| ||||
                                TCCC  CG  CCCCC ACCC
                                  __ AC    G
GAM3471  LOC159090 5'  AGGGGGCGGAGGAGGGAGGG   78805      AC      T    A
                                AGGG  GCGGGGG GGGAG GG
                                ||||  ||||||| ||||| ||
                                TCCC  CGCCTCC CCCTC CC
                                  C_      T    _
GAM3471  LOC159090 5'  GGGGCGGGGGCTAAGGG     78806     AC       GG   A
                                GGG  GCGGGGGT  GAG GG
                                |||  |||||||  ||| ||
                                CCC  CGCCCCCG  TTC CC
                                  __       A_  _
GAM3471  LOC160675 5'  AGGGACTGGGGTTTATTGGAGG 78807       GC    GTG___    A
            G                    AGGGAC  GGGG     GGAG GG
                                ||||||  ||||     |||| ||
                                TCCCTG  CCCC     CCTC CC
                                   A_   AAATAA   _
GAM3471  LOC163412 3'  AGGGGCGTGGGGGCTGAACCAG 78808      A  C     G   GA
                                AGGG CG GGGGGT GGA  GG
                                |||| || |||||| |||  ||
                                TCCC GC CCCCCG CTT  TC
                                  C  A     A   GG
GAM3471  LOC164386 5'  GGGAGGCGGGGGGTACCTGGGGA 78809      C       ____   A
            GG                   GGGA GCGGGGGT    GGG GAGG
                                |||| ||||||||    ||| ||||
                                CCCT CGCCCCCA    CCC CTCC
                                  C       TGGA  _
GAM3471  LOC164386 5'  GGGAGGTGGGGGGTACCCGGGGA 78810      CGC     ____   A
            GG                   GGGA   GGGGGT    GGG GAGG
                                ||||   ||||||    ||| ||||
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                                CCCT   CCCCCA    CCC CTCC
                                  CCA     TGGG  _
GAM3471  LOC164397 5'  AGGAGCGTGGGGGGAACCAGG  78811     GA  C    T   AG
                                AGG  CG GGGGG GGG  AGG
                                |||  || ||||| |||  |||
                                TCC  GC CCCCC CTT  TCC
                                  TC  A    _  GG
GAM3471  LOC168576 5'  AGGGCTGCGGGGGCTCCCAGG  78812      AC       GGGAG
                                AGGG  GCGGGGGT    AGG
                                ||||  ||||||||    |||
                                TCCC  CGCCCCCG    TCC
                                  GA       AGGG_
GAM3471  LOC169831 3'  GGGGTGAAAGGTGGGGGAGG   78813     ACGC       A
                                GGG    GGGGGGTGGG GAGG
                                |||    |||||||||| ||||
                                CCC    TTTCCACCC CTCC
                                  CAC_        C
GAM3471  LOC170393 3'  GGGGCAAGGGTGGGAGGG    78815     AC         A
                                GGG  GCGGGGGGTGGGAG GG
                                |||  |||||||||||||| ||
                                CCC  CGTTCCCACCCTC CC
                                  __          _
GAM3471  LOC170393 3'  GGGGCAAGGGTGGGAGGG    78815     AC         A
                                GGG  GCGGGGGGTGGGAG GG
                                |||  |||||||||||||| ||
                                CCC  CGTTCCCACCCTC CC
                                  __          _
GAM3471  LOC170393 3'  GGGGCAAGGGTGGGAGGG    78815     AC         A
                                GGG  GCGGGGGGTGGGAG GG
                                |||  |||||||||||||| ||
                                CCC  CGTTCCCACCCTC CC
                                  __          _
GAM3471  LOC170393 3'  GGGGCAAGGGTGGGAGGG    78815     AC         A
                                GGG  GCGGGGGGTGGGAG GG
                                |||  |||||||||||||| ||
                                CCC  CGTTCCCACCCTC CC
                                  __          _
GAM3471  LOC170393 3'  GGGGCAAGGGTGGGAGGG    78815     AC         A
                                GGG  GCGGGGGGTGGGAG GG
                                |||  |||||||||||||| ||
                                CCC  CGTTCCCACCCTC CC
                                  __          _
GAM3471  LOC170393 3'  GGGGCAAGGGTGGGAGGG    78815     AC         A
                                GGG  GCGGGGGGTGGGAG GG
                                |||  |||||||||||||| ||
                                CCC  CGTTCCCACCCTC CC
                                  __          _
GAM3471  LOC170393 3'  GGGCTGGGCAAGGGTGGGAGGG 78814     AC__           A
                                GGG    GCGGGGGGTGGGAG GG
                                |||    |||||||||||||| ||
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                                CCC    CGTTCCCACCCTC CC
                                  GACC          _
GAM3471  LOC170393 3'  GGGACGAGTGGGAGG       78816       CGGG       A
                                GGGACG    GGTGGGAG G
                                ||||||    |||||||| |
                                CCCTGC    TCACCCTC C
                                   ____       _
GAM3471  LOC196326 5'  GGGCGCGGGAAATCGGAGAGG  78817     A       _ G
                                GGG CGCGGGGG T GGAGAGG
                                ||| |||||||| | |||||||
                                CCC GCGCCCTT A CCTCTCC
                                  _       T G
GAM3471  LOC196738 3'  GGGATGGGGGGGCTTGCCAGAG 78818      CGC      GGG__
             G                   GGGA   GGGGGT     AGAGG
                                ||||   ||||||     |||||
                                CCCT   CCCCCG     TCTCC
                                  ACC      AACGG
GAM3471  LOC196955 5'  AGGGCTGAGTGGGAGAG     78819      ACGCGG
                                AGGG     GGGTGGGAGAG
                                ||||     ||||||||||
                                TCCC     CTCACCCTCTC
                                  GA____
GAM3471  LOC197350 3'  GGGATGGGGGGGTGGATGGAGG  78820      CGC        A_
                                GGGA   GGGGGTGGG  GAGG
                                ||||   |||||||||  ||||
                                CCCT   CCCCCACCT  CTCC
                                  AC_        AC
GAM3471  LOC199678 3'  GGGGAAGATGGGAGG       78821     ACGC         A
                                GGG    GGGGGTGGGAG G
                                |||    |||||||||||| |
                                CCC    CTTCTACCCTC C
                                  _____         _
GAM3471  LOC199782 3'  GGGGGGCGGGAACTGGGAG    78822      AC      _
                                GGG  GCGGGGG TGGGAG
                                |||  ||||||| ||||||
                                CCC  CGCCCTT ACCCTC
                                  CC       G
GAM3471  LOC200325 5'  GGTGATGGACGTGGGAGAGG   78823    _ CGC   G
                                GG GA   GGG GTGGGAGAGG
                                || ||   ||| ||||||||||
                                CC CT   CCT CACCCTCTCC
                                 A  A__   G
GAM3471  LOC200531 5'  GGGATGCGCGGGCGTCGGG    78824      __     G  _
                                GGGA  CGCGGG GT GGG
                                ||||  |||||| || |||
                                CCCT  GCGCCC CA CCC
                                  AC     G  G
GAM3471  LOC200597 5'  GGGGCTGGAGGAGGAGAGG    78825     AC  _    T
                                GGG  GC GGGGG GGGAGAGG
                                |||  || ||||| ||||||||
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                                CCC  CG CCTCC TCCTCTCC
                                  __  A    _
GAM3471  LOC201158 3'  GGGGTGGGGGGGGCACAAGAGG  78826     ACGC      G
                                GGG    GGGGGTG GAGAGG
                                |||    ||||||| ||||||
                                CCC    CCCCCGT TTCTCC
                                  CACC      G
GAM3471  LOC201175 5'  AGGGGCGAGGCCGGAGAGG    78827      AC     G G
                                AGGG  GCGGGG T GGAGAGG
                                ||||  |||||| | |||||||
                                TCCC  CGCTCC G CCTCTCC
                                  __     _ G
GAM3471  LOC201702 5'  AGGGACCCGGGAACAGAGG    78298       G    GG GGG
                                AGGGAC CGGG  T   AGAGG
                                ||||||| ||||  |   |||||
                                TCCCTG GCCC  G   TCTCC
                                   G    TT ___
GAM3471  LOC201911 3'  GGGAGGCGGCGGGGGAG     78828      C    G  T
                                GGGA GCGG GG GGGAG
                                |||| |||| || |||||
                                CCCT CGCC CC CCCTC
                                  C    G  _
GAM3471  LOC202460 5'  GGGATCGAAAAGAGGGAGGG   78829      _ CG    T    A
                                GGGA CG  GGGG GGGAG GG
                                |||| ||  |||| ||||| ||
                                CCCT GC  TTCT CCCTC CC
                                  A  TT   _    _
GAM3471  LOC202500 5'  AGGGATCTGGGGTGTAGAGG   78830      CGCG     GG
                                AGGGA    GGGGTG  AGAGG
                                |||||    ||||||  |||||
                                TCCCT    CCCCAC  TCTCC
                                   AGA_     A_
GAM3471  LOC203652 5'  GGGTCGCGGGGGGACCGCGGG   78832     A      _____
                                GGG CGCGGGGGG    TGGG
                                ||| ||||||||    ||||
                                CCC GCGCCCCC    GCCC
                                  A       TGGC
GAM3471  LOC203652 5'  GGGACGAGGGTGTGGAGGG    78831       CG     _    A
                                GGGACG  GGGGTG GGAG GG
                                ||||||  |||||| |||| ||
                                CCCTGC  TCCCAC CCTC CC
                                   __      A    _
GAM3471  LOC219818 3'  GGGAGGCCCGCTGGGAGAGG   78833      C  GGGGG
                                GGGA GC     TGGGAGAGG
                                |||| ||     |||||||||
                                CCCT CG     ACCCTCTCC
                                  C  GGCG_
GAM3471  LOC220776 3'  AGGGGCGGGGGGGAAGAG     78834      AC      TG
                                AGGG  GCGGGGG  GGAGAG
                                ||||  |||||||  ||||||
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                                TCCC  CGCCCCC  CTTCTC
                                  __     __
GAM3471  LOC221656 3'  GGGGGCGGGCGGTGGGGGAGG  78835     AC    _     A
                                GGG  GCGGG GGTGGG GAGG
                                |||  ||||| |||||| ||||
                                CCC  CGCCC CCACCC CTCC
                                  C_    G     C
GAM3471  LOC221893 5'  AGGAGCGCGGAGCCGAGAG   78836     GA      G
                                AGG  CGCGGGG TGGGAG
                                |||  ||||||| ||||||
                                TCC  GCGCCTC GCTCTC
                                  TC      G
GAM3471  LOC222166 5'  GGGACGCGGGGCGGCGGGAG   78837           __
                                GGGACGCGGGG  GTGGGAG
                                ||||||||||  |||||||
                                CCCTGCGCCCC  CGCCCTC
                                       GC
GAM3471  LOC253219 5'  AGGGGGCGGTCCCGGGGAGG   78838      AC   GGG   A
                                AGGG  GCGG   TGGG GAGG
                                ||||  ||||   |||| ||||
                                TCCC  CGCC   GCCC CTCC
                                  C_   AGG   _
GAM3471  LOC253367 3'  AGGGGTGGGAGGGAGAG     18507      ACGCG   T
                                AGGG    GGGG GGGAGAG
                                ||||    |||| |||||||
                                TCCC    CCCT CCCTCTC
                                  CA___   _
GAM3471  LOC253737 5'  AGGGACAGTGGGTGAAGAGG   78839        CGG     G
                                AGGGACG   GGGTGG AGAGG
                                |||||||   |||||| |||||
                                TCCCTGT   CCCACT TCTCC
                                    CA_     _
GAM3471  LOC253866 5'  AGGGGCGGGGGAGGGGAGG   78840      AC      T   A
                                AGGG  GCGGGGG GGG GAGG
                                ||||  ||||||| ||| ||||
                                TCCC  CGCCCCC CCC CTCC
                                  __      T   _
GAM3471  LOC253891 3'  AGGGATCGGGGAAGAG      78841       CG    GTGG
                                AGGGA  CGGGG   GAGAG
                                |||||  |||||   |||||
                                TCCCT  GCCCC   TTCTC
                                  A_    _____
GAM3471  LOC253962 5'  AGGCGCAGCTGTGGGGGAGG   78842     A    GG    A
                                GGG CGCGG  GTGGG GAGG
                                ||| |||||  ||||| ||||
                                TCC GCGTC  CACCC CTCC
                                  _    GA    C
GAM3471  LOC254057 5'  GGGACGCGGTGTCTTTCAGAGG 78843         GG  GGG__
                                GGGACGCGG  GT    AGAGG
                                |||||||||  ||    |||||
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                                CCCTGCGCC  CA    TCTCC
                                     A_  GAAAG
GAM3471  LOC254532 5'  AGGGGCCGGGAGGGAGGG    78844     AC  G   T    A
                                AGGG  GC GGGG GGGAG GG
                                ||||  || |||| ||||| ||
                                TCCC  CG CCCT CCCTC CC
                                  __ G   _    _
GAM3471  LOC255057 3'  GGGCGGGGCGGGGGTGGGAGAG 78845     AC__
           G                     GGG   GCGGGGGTGGGAGAGG
                                |||   ||||||||||||||||
                                CCC   CGCCCCCACCCTCTCC
                                  GCCC
GAM3471  LOC255102 3'  GGGGTGTGGAGGTGGGAGTCAG 78846     ACGC        __
           G                     GGG   GGGGGTGGGAG  AGG
                                |||   ||||||||||  |||
                                CCC   CCTCCACCCTC  TCC
                                  CACA         AG
GAM3471  LOC255452 3'  GGGACGCGGGGGCGCTGG    78847            __
                                GGGACGCGGGGGTG  GG
                                ||||||||||||  ||
                                CCCTGCGCCCCCGC  CC
                                       GA
GAM3471  LOC256050 5'  GGGATGCGGGGGGCAGCGGG   78848     C     _____
                                GGGA GCGGGGG   TGGG
                                |||| |||||||   ||||
                                CCCT CGCCCCC   GCCC
                                  A      CGTC
GAM3471  LOC256306 5'  AGGGATGTCGGGGGTACTCAGG 78849      CG_      GGAG
                                AGGGA  CGGGGGTG   AGG
                                |||||  ||||||||   |||
                                TCCCT  GCCCCCAT   TCC
                                   ACA      GAG_
GAM3471  LOC256338 5'  GGGGTGCGGAGCCTGGGAG   78850     AC     G_
                                GGG  GCGGGG  TGGGAG
                                |||  ||||||  ||||||
                                CCC  CGCCTC  ACCCTC
                                  CA     GG
GAM3471  LOC256664 5'  GGGGCGCGGGGACCGAGGAGG  78851     A       G GA
                                GGG CGCGGGGGT G  GAGG
                                ||| ||||||||| |  ||||
                                CCC GCGCCCCTG C  CTCC
                                  C        G TC
GAM3471  LOC256855 5'  AGGGCTGCGGGAGTTACTGGGG 78852      AC       _____  A
           GAGG                   AGGG  GCGGGGGT   GGG GAGG
                                ||||  ||||||||   ||| ||||
                                TCCC  CGCCCTCA   CCC CTCC
                                  GA       ATGA  C
GAM3471  LOC256905 3'  GGGGCGTGGGGGAAAGGGGAGG 78853     A  C    T__  A
                                GGG CG GGGGG   GGG GAGG
                                ||| || |||||   ||| ||||
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                                CCC GC CCCCC   CCC CTCC
                                  C A    TTT  _
GAM3471  LOC256980 3'  GGGGCGGGAGCGAGAG     78854     AC
                                GGG  GCGGGGGTGGGAG
                                |||  |||||||||||||
                                CCC  CGCCCTCGCTCTC
                                  __
GAM3471  LOC257200 3'  AGGGGTGGGGGGTGGGAG    78855     ACGC
                                AGGG   GGGGGTGGGAG
                                ||||   ||||||||||
                                TCCC   CCCCCACCCTC
                                  CAC_
GAM3471  LOC257484 3'  GGGAAGTGGGGGTAAGGGAGG  78662     CGC       A
                                GGGA  GGGGGTGGG GAGG
                                ||||  ||||||||| ||||
                                CCCT  CCCCCATTC CTCC
                                  TCA       C
GAM3471  LOC257551 3'  AGGGATTGGGGCAGGGGAGG   78460     CGCG   TG  A
                                AGGGA   GGGG  GG GAGG
                                |||||   ||||  || ||||
                                TCCCT   CCCC  CC CTCC
                                  AA__   GT  C
GAM3471  LOC257601 3'  AGGGATTGGGGCAGGGGAGG   78460     CGCG   TG  A
                                AGGGA   GGGG  GG GAGG
                                |||||   ||||  || ||||
                                TCCCT   CCCC  CC CTCC
                                  AA__   GT  C
GAM3471  LOC51157  3'  GGGGGCGTGGGCGGAAGGGG   78856    AC  G      A
                                GGG  GCG GGGTGGGAG GG
                                |||  ||| |||||||||| ||
                                CCC  CGC CCCGCCTTC CC
                                  C_  A       C
GAM3471  LOC51279  3'  AAGGATGTGGGGGCTGGGAG   78857     CGC   _
                                AGGGA  GGGGG TGGGAG
                                |||||  ||||| ||||||
                                TTCCT  CCCCC ACCCTC
                                  ACA    G
GAM3471  LOC51608  3'  GGGACGCGGCGGCCAGCAGG   78858       G  G  AG
                                GGGACGCGG GGT GG  AGG
                                |||||||| ||| ||  |||
                                CCCTGCGCC CCG TC  TCC
                                    G  G  G_
GAM3471  LOC51720  5'  GGGAGCGCGGGGGGAGGGGGAG 78859     _     T_  A
            G                    GGGA CGCGGGGG  GGG GAGG
                                ||||  ||||||||  ||| ||||
                                CCCT GCGCCCCC  CCC CTCC
                                  C       CT  C
GAM3471  LOC58512  3'  AGGGGCGCAGGGCGGAGAGG   78860     A     GTG
                                AGGG CGCGGGG   GGAGAGG
                                ||||  |||||||  |||||||
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                                TCCC GCGTCCC   CCTCTCC
                                  C      G__
GAM3471  LOC58525  3'  AGGGAGCAGGAGTGGGGGAGG  78861      C         A
                                AGGGA GCGGGGGTGGG GAGG
                                ||||| |||||||||||| ||||
                                TCCCT CGTCCTCACCC CTCC
                                  _         C
GAM3471  LOC89932  5'  AGGGATGGGGAGGGAG      78862      CGC    T
                                AGGGA   GGGGG GGGAG
                                |||||   ||||| |||||
                                TCCCT   CCCCT CCCTC
                                  A__    _
GAM3471  LOC90139  3'  AGGGGGTGGCATGTGGGAGAGG 78863      ACGC  GG_
                                AGGG    GG   GTGGGAGAGG
                                ||||    ||   ||||||||||
                                TCCC    CC   CACCCTCTCC
                                  CCA_  GTA
GAM3471  LOC90249  3'  AGGGACGGGAGGAGAG      78864        C  GGGT
                                AGGGACG GG    GGGAGAG
                                ||||||| ||    |||||||
                                TCCCTGC CC    TCCTCTC
                                   _ ____
GAM3471  LOC90515  5'  AGGGGGGTGGGATGGGGAGG   78865      ACGCG       A
                                AGGG     GGGGTGGG GAGG
                                ||||     |||||||| ||||
                                TCCC     CCCTACCC CTCC
                                  CCCA_       _
GAM3471  LOC90668  3'  GGGACTGGGGGTGGATAGGG   78866      GC        _  A
                                GGGAC  GGGGGTGGG AG GG
                                |||||  ||||||||| || ||
                                CCCTG  CCCCCACCT TC CC
                                  A_        A  _
GAM3471  LOC90768  5'  AGGTGATGCGGGGCGGAG    78867     _  C     GTG
                                AGG GA GCGGGG   GGAG
                                ||| || ||||||   ||||
                                TCC CT CGCCCC   CCTC
                                  A  A     G__
GAM3471  LOC90835  5'  AGAGGCGCGGGCGAGGGAGG   78868     C   G      A
                                GGA GCG GGGTGGG GAGG
                                ||| ||| ||||||| ||||
                                TCT CGC CCCGCTC CTCC
                                  C   G      C
GAM3471  LOC91050  3'  GGGGTGGGCCTGGTGGGGAGG  78869     ACGC  ___     A
                                GGG    GGG   GGTGGG GAGG
                                |||    |||   |||||| ||||
                                CCC    CCC   CCACCC CTCC
                                  CA__   GGA     _
GAM3471  LOC91445  3'  GGGACTGTGAAGAGGGGAGG   78870      GCG    T   A
                                GGGAC   GGGG GGG GAGG
                                |||||   |||| ||| ||||
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                                CCCTG  CTTC CCC CTCC
                                  ACA   T  _
GAM3471 LOC91695 5' GGGAGCGCGGGGGTCGCCGGG 78635     _      ____
                                GGGA CGCGGGGGT   GGG
                                |||| |||||||||   |||
                                CCCT GCGCCCCCA   CCC
                                  C       GCGG
GAM3471 LOC92154 3' AGGGGGCGGGGAGGAGAGG   78871     AC     GT
                                AGGG  GCGGGG  GGGAGAGG
                                ||||  ||||||  ||||||||
                                TCCC  CGCCCC  TCCTCTCC
                                  C_     __
GAM3471 LOC92312 5' GGGGCGGTGGGGGGCTGGG   78872     AC   _  T  AGA
                                GGG  GCGG GGG GGG  GG
                                |||  |||| ||| |||  ||
                                CCC  CGCC CCC CCC  CC
                                  __   A  _  GAC
GAM3471 LOC92340 3' AGGGGTGAGGGAGAGAG     78873     ACGCG   T
                                AGGG    GGGG GGGAGAG
                                ||||    |||| |||||||
                                TCCC    CTCC CTCTCTC
                                  CA___   _
GAM3471 LOC92661 3' GGGAAGCGGGGGTCTGAG    78874      C       GG
                                GGGA GCGGGGGT  GAG
                                |||| ||||||||  |||
                                CCCT CGCCCCCA  CTC
                                  T       GA
GAM3471 LOC93512 3' GGGAGCGGACCCCGAGAGG   78782     C    GGTGG
                                GGGA GCGGG    GAGAGG
                                |||| |||||    ||||||
                                CCCT CGCCT    CTCTCC
                                  _    GGGG_
GAM3472 HPS1     3' AGGTGCCATCGCTTTAAA    78877     A     G
                                AGGT CCATCG TTTAAA
                                |||| |||||| ||||||
                                TCCA GGTAGC AAATTT
                                  C     G
GAM3472 FLJ20716 3' AGGTACCAATAACAAAAGCT  78878       TCGGTT    _
                                AGGTACCA     TAAAA CT
                                ||||||||     ||||| ||
                                TCCATGGT     GTTTT GA
                                    TATT__    C
GAM3472 HSBP1    3' AGATACCATGTTCAAGAAACT  78879       CG     __
                                AGGTACCAT  GTTTAA  AACT
                                |||||||||  ||||||  ||||
                                TCTATGGTA  CAAGTT  TTGA
                                     __     CT
GAM3472 LOC220883 3' AGGTCCTGTCTCTTTAAAACTA 78880     A  A_  GG
                                AGGT CC  TC  TTTAAAACTA
                                |||| ||  ||  ||||||||||
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                                TCCA GG  AG  AAATTTTGAT
                                  _ AC  AG
GAM3472  LOC221760 3'  GTAGCAGGTTTAAAACTA    78881     C  TC
                                GTA CA  GGTTTAAAACTA
                                ||| ||  ||||||||||||
                                CAT GT  CCAAATTTTGAT
                                  C __
GAM3472  LOC254394 3'  AGGATTGTTCAAAACTAA    78882     TACCATCG
                                AGG       GTTTAAAACTAA
                                |||       ||||||||||||
                                TCC       CAAGTTTTGATT
                                  TAA_____
GAM3473  ADAMTS5   3'  CACCACTGTCACGTGAA     78885     TG C
                                CAT  C TGTCACGTGAA
                                |||  | ||||||||||
                                GTG  G ACAGTGCACTT
                                  GT _
GAM3473  CTSK      3'  TACACTGCACCATCGTG     78886         _    AC
                                TACATTGC CTGTC  GTG
                                |||||||| |||||  |||
                                ATGTGACG GGTAG  CAC
                                     T    __
GAM3473  DHFR      3'  TACACTGCTTTCACTGAA    78887         CTG   G
                                TACATTGC   TCAC TGAA
                                ||||||||   |||| ||||
                                ATGTGACG   AGTG ACTT
                                     AA_   _
GAM3473  FCMD      3'  CACATTGCCTTCCCTGA     78888          G  ACG
                                TACATTGCCT TC   TGA
                                |||||||||| ||   |||
                                GTGTAACGGA AG   ACT
                                      _ GG_
GAM3473  MADH2     3'  TACATTACCTGTACACATAA  78889           _
                                TACATTGCCTGT CACGTGA
                                |||||||||||| |||||||
                                ATGTAATGGACA GTGTATT
                                       T
GAM3473  PEPD      5'  CACCGGCGTCACGTGAA     78890       CC
                                CATTG  TGTCACGTGAA
                                |||||  ||||||||||
                                GTGGC  GCAGTGCACTT
                                   C_
GAM3473  SLC4A7    3'  TACTTGTCTGTCACAATG    78891     A  C      _
                                TAC TTG CTGTCACG TG
                                ||| ||| |||||||| ||
                                ATG AAC GACAGTGT AC
                                  _  A       T
GAM3473  ZNF255    5'  TACACTGCTGGTGTGAA     78892         C  TCAC
                                TACATTGC TG    GTGAA
                                |||||||| ||    |||||
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                                ATGTGACG AC    CACTT
                                     _ CA__
GAM3473 C9orf5   3' TACAGTGCCTGGCACAGAA   78893     T     T   T
                                TACA TGCCTG CACG GAA
                                |||| |||||| |||| |||
                                ATGT ACGGAC GTGT CTT
                                  C     C   _
GAM3473 CYLC1    5' TACGTTGCCTGGACTTGA    78894     A      TC  G
                                TAC TTGCCTG  AC TGA
                                ||| |||||||  || |||
                                ATG AACGGAC  TG ACT
                                  C      C_  A
GAM3473 DKFZp547A023 3' TACATCGCTTGTGTGA      78895         C   CAC
                                TACATTGC TGT   GTGA
                                |||||||| |||   ||||
                                ATGTAGCG ACA   CACT
                                     A  ___
GAM3473 DKFZp761G0313 3' TACATTACCTGTCAATGAA   78896             C
                                TACATTGCCTGTCA GTGAA
                                |||||||||||||| |||||
                                ATGTAATGGACAGT TACTT
                                                _
GAM3473 FLJ10283 5' TACATTGCCTTCACTG      78897          G   G
                                TACATTGCCT TCAC TG
                                |||||||||| |||| ||
                                ATGTAACGGA AGTG AC
                                     _   _
GAM3473 FLJ10432 3' CACGTTGACCTGTGTGA     78898     A  _    CAC
                                TAC TTG CCTGT   GTGA
                                ||| ||| |||||   ||||
                                GTG AAC GGACA   CACT
                                  C   T    ___
GAM3473 FLJ14082 3' TGCACTTTATCACGTGAA    78899     _ __
                                TGC CT  GTCACGTGAA
                                ||| ||  ||||||||||
                                ACG GA  TAGTGCACTT
                                  T  AA
GAM3473 FLJ20856 5' TACATTGCCCTGCCTAATGA  78900          _   AC
                                TACATTGCC TGTC  GTGA
                                |||||||| ||||  ||||
                                ATGTAACGG ACGG  TACT
                                     G    AT
GAM3473 KIAA0222 3' TACATTGCATCGTTTGAA    78901        CT   ACG
                                TACATTGC  GTC   TGAA
                                ||||||||  |||   ||||
                                ATGTAACG  TAG   ACTT
                                     __  CAA
GAM3473 KIAA1228 3' TACATGCACTGTCACGTGAA  78902      T  _
                                TACAT GC CTGTCACGTGAA
                                ||||| || ||||||||||||
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                                ATGTA CG GACAGTGCACTT
                                   _ T
GAM3473  KIAA1854  3'  CACATTGCTGGGCAGTGAA   78903        C  T_  C
                                TACATTGC TG  CA GTGAA
                                |||||||| ||  || |||||
                                GTGTAACG AC  GT CACTT
                                   _ CC  _
GAM3473  UST       3'  TACACTGCTCTTGGTGAA    78904        _ GTCAC
                                TACATTGC CT    GTGAA
                                |||||||| ||    |||||
                                ATGTGACG GA    CACTT
                                   A  AC___
GAM3473  LOC127703 3'  TACATTGCTTTTCATCAGAA  78905        CTG  _  T
                                TACATTGC   TCA CG GAA
                                ||||||||   ||| || |||
                                ATGTAACG   AGT GT CTT
                                   AAA   A  _
GAM3473  LOC134218 3'  TACATTTCTGTCCACATGA   78906       GC    _
                                TACATT  CTGTC ACGTGA
                                ||||||  ||||| ||||||
                                ATGTAA  GACAG TGTACT
                                   A_    G
GAM3473  LOC144348 5'  ACATTGACTTCCACGTGAA   78907       C  GT
                                ACATTG CT  CACGTGAA
                                ||||||  ||  ||||||||
                                TGTAAC GA  GTGCACTT
                                   T  AG
GAM3473  LOC148529 5'  TACATTGCCTGATACATA    78908         TC
                                TACATTGCCTG  ACGTG
                                ||||||||||  |||||
                                ATGTAACGGAC  TGTAT
                                      TA
GAM3473  LOC149041 3'  CACATTGCCTCTGGTGAA    78909         GTCAC
                                TACATTGCCT    GTGAA
                                ||||||||||    |||||
                                GTGTAACGGA    CACTT
                                   GAC__
GAM3473  LOC151877 3'  TACACTGCTGGTGTGAA     78892        C  TCAC
                                TACATTGC TG    GTGAA
                                |||||||| ||    |||||
                                ATGTGACG AC    CACTT
                                   _ CA__
GAM3473  LOC196418 5'  ACATTGACTTCCACGTGAA   78907       C  GT
                                ACATTG CT  CACGTGAA
                                ||||||  ||  ||||||||
                                TGTAAC GA  GTGCACTT
                                   T  AG
GAM3473  LOC219649 3'  TACATTGCCTGTTGA       78910         CACG
                                TACATTGCCTGT    TGA
                                ||||||||||||    |||
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                                ATGTAACGGACA    ACT
                                      ____
GAM3473  LOC219818 3'  TACACTGCCACAGTGA      78911         TGT  C
                                TACATTGCC   CA GTGA
                                |||||||||   || ||||
                                ATGTGACGG   GT CACT
                                     T__  _
GAM3473  LOC221410 3'  CATTGCCTTTAGTCCATG    78912         ___  A
                                CATTGCCT   GTC CGTG
                                ||||||||   ||| ||||
                                GTAACGGA   CAG GTAC
                                     AAT  _
GAM3473  LOC221474 5'  ACATTGCCTGCCATGA      78913           CG
                                ACATTGCCTGTCA  TGA
                                ||||||||||||  |||
                                TGTAACGGACGGT  ACT
                                      __
GAM3473  LOC90075  5'  CACATTGCTTACATTTGA     78914         C  T  CG
                                TACATTGC TG CA  TGA
                                |||||||| || ||  |||
                                GTGTAACG AT GT  ACT
                                     A  _  AA
GAM3474  POLH      3'  TAAAAATTTCATAATTCC     78917           A
                                TAAAAATTTCATAA TTC
                                |||||||||||||| |||
                                ATTTTTAAAGTATT AGG
                                       A
GAM3474  AKR1D1    3'  TAAAATTCTCAAAATTCATATA 78918       A     T
            A                    TAAAA TTTCA AAATTCATATAA
                                |||||  |||||  ||||||||||||
                                ATTTT AGAGT TTTAAGTATATT
                                   A    _
GAM3474  FLJ10081  3'  TAAAAGCTTCATATAGCTCATA 78919       A      AA_
            TA                    TAAAA TTTCATA   TTCATATA
                                |||||  |||||||   ||||||||
                                ATTTT GAAGTAT   GAGTATAT
                                   C      ATC
GAM3475  ACADL     3'  TGTTTGAAGAAAGAGTTCCAT  78922           ATG
                                TGTTTGAAGAAAGA   CCAT
                                ||||||||||||||   ||||
                                ACAAACTTCTTTCT   GGTA
                                       CAA
GAM3475  CRIM1     3'  TGTTTGAAAAGTTACCAC     78923         AAGAA
                                TGTTTGAAGA    TGCCAT
                                ||||||||||    ||||||
                                ACAAACTTTT    ATGGTG
                                      CA___
GAM3475  EVA1      3'  TGTTTGAAGAAATATCCA     78924          GAATG
                                TGTTTGAAGAAA    CCA
                                ||||||||||||    |||
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                                ACAAACTTCTTT    GGT
                                      ATA__
GAM3475 GSTM5    3' TGTTAGAAGAAAGGAAGCCA  78925     T      AAT
                                TGTT GAAGAAAG   GCCA
                                |||| ||||||||   ||||
                                ACAA CTTCTTTC   CGGT
                                  T       CTT
GAM3475 IL10RA   3' TGTTTGAAGGCAGAGTCCA   78926        AA   ATG
                                TGTTTGAAG  AGA   CCA
                                |||||||||  |||   |||
                                ACAAACTTC  TCT   GGT
                                     CG   CA_
GAM3475 NEFH     3' TGTTTGAAGAAGGAGGCC    78927          A  AT
                                TGTTTGAAGAA GA  GCC
                                |||||||||| ||  |||
                                ACAAACTTCTT CT  CGG
                                      C  C_
GAM3475 DKFZP564I0422 3' TGTTTGAAGCAAAGGGTTCC   78928         _   AATG
                                TGTTTGAAG AAAG    CC
                                ||||||||| ||||    ||
                                ACAAACTTC TTTC    GG
                                     G    CCAA
GAM3475 KIAA1912  3' TGTTTGAAAAAGAGTGC     78929          A  A
                                TGTTTGAAGAA GA TGC
                                |||||||||| || |||
                                ACAAACTTTTT CT ACG
                                      _  C
GAM3475 LOC121838 5' TGCTTGAAGAAGCAGCCATA   78930          A AAT
                                TGTTTGAAGAA G   GCCATA
                                |||||||||| |   ||||||
                                ACGAACTTCTT C   CGGTAT
                                      _ GT_
GAM3475 LOC151584 3' TATTTGAAGGAAGGGTAGCACA 78931         A   AAT_ _
              T                  TGTTTGAAG AAG    GC CAT
                                |||||||| |||    || |||
                                ATAAACTTC TTC    CG GTA
                                     C   CCAT  T
GAM3475 LOC253254 5' TGTTTGAAAATCACACTGCCAT 78932          AAGAA_
                                TGTTTGAAGA     TGCCAT
                                |||||||||      ||||||
                                ACAAACTTTT     ACGGTA
                                      AGTGTG
GAM3475 LOC91650  5' TTTGAAGAATCTCCATAAT   78933         AGAATG
                                TTTGAAGAA     CCATAAT
                                |||||||||     |||||||
                                AAACTTCTT     GGTATTA
                                      AGA___
GAM3476 TNFAIP1   3' TAGTGCTGTTTATACATTCAAG 78936   A      A__________  TATA
             CCTATAGG                GTTTATAC        CC    GG
                                |||||||         ||    ||
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                                CAAATATG        GG   CC
                               A       TAAGTTCIII  ATAT
GAM3476 KIAA0040  3'  TAGGCAGTTTATGGCCATATAG 78937     C       ACA  _
             G                   TAG GCAGTTTAT   CC TATAGG
                               ||| |||||||||   || ||||||
                               ATC CGTCAAATA   GG ATATCC
                                 _       CC_  T
GAM3476 MGC10960  5'  AGCGCAGCGGCCATTTATAGG  78938        TTATA  CC
                               AGCGCAGT    CA  TATAGG
                               ||||||||    ||  ||||||
                               TCGCGTCG    GT  ATATCC
                                    CCG__  AA
GAM3476 LOC90459  3'  AGCGCAGTGGCTCACGTCTGTA 78939        TTA_   AC  A
             GG                    AGCGCAGT    TAC  CT TAGG
                               ||||||||    |||  || ||||
                               TCGCGTCA    GTG  GA ATCC
                                    CCGA   CA  C
GAM3477 BCL10    3'  AGTAGTATAATTAGTAAGGTT  78942    C    CATTC
                               AG AGTA     AGTGAGGTT
                               || ||||     |||||||||
                               TC TCAT     TCATTCCAA
                                A    ATTAA
GAM3477 CBR1     3'  AGTAGTACATTAGTGAG     78943    C       C
                               AG AGTACATT AGTGAG
                               || |||||||| ||||||
                               TC TCATGTAA TCACTC
                                A       _
GAM3477 KRT8     3'  GCAGAGCTAGCTGAGGTTTTA  78944      TACATTC  _
                               GCAG      AG TGAGGTTTTA
                               ||||      || ||||||||||
                               CGTC      TC ACTCCAAAAT
                                 TCGA___  G
GAM3477 RAD51L1  3'  AGCAGTACGGTCCTGTTTT    78945        AT  AGTGAG
                               AGCAGTAC  TC     GTTTT
                               ||||||||  ||     |||||
                               TCGTCATG  AG     CAAAA
                                    CC  GA____
GAM3477 STC1     3'  AGCAGCACGTTACTGGTTTTA  78946        ATTCA  GA__
                               AGCAGTAC    GT    GGTTTTA
                               ||||||||    ||    |||||||
                               TCGTCGTG    CA    CCAAAAT
                                    _____  ATGA
GAM3477 UQCRB    3'  AGTAGTTATTCAGTATAAGGTT 78947    C   AC      __
             T                    AG AGT  ATTCAGT  GAGGTTT
                               || |||  |||||||  |||||||
                               TC TCA  TAAGTCA  TTCCAAA
                                A  A_      TA
GAM3477 ANKT     3'  AGAAGTACATTTGGTGGAGTTT 78948    C       CA   AG
                               AG AGTACATT  GTG  GTTT
                               || ||||||||  |||  ||||
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                                TC TCATGTAA  CAC  CAAA
                                 T       AC   CT
GAM3477 ARHE     3'  GCGTCTGTTCAGTGAGGTTTTA 78949    A  ACA
                                GC GT   TTCAGTGAGGTTTTA
                                || ||   ||||||||||||||
                                CG CA   AAGTCACTCCAAAAT
                                 _  GAC
GAM3477 FLJ23142 3'  AACAGTATATCCTAAGGTTTT  78950        C    AG
                                AGCAGTA ATTC  TGAGGTTTT
                                ||||||| ||||  |||||||||
                                TTGTCAT TAGG  ATTCCAAAA
                                    A   __
GAM3477 HERPUD1  3'  AGTAGTACACTTAGTGTAATTT 78951    C       C    AG
                                AG AGTACATT AGTG  GTTT
                                || |||||||| ||||  ||||
                                TC TCATGTGA TCAC  TAAA
                                 A       A    AT
GAM3477 HSPC155  3'  AGCAGTACTGTTTGGTGTGTGT 78952        ATTCA_  AG_
             TT                  AGCAGTAC     GTG   GTTT
                                ||||||||     |||   ||||
                                TCGTCATG     CAC   CAAA
                                    ACAAAC   ACA
GAM3477 KIAA1421 3'  AGCAGTCATGTCATAGGTTTTA 78953       A  _  GTG
                                AGCAGT CAT TCA   AGGTTTTA
                                |||||| ||| |||   ||||||||
                                TCGTCA GTA AGT   TCCAAAAT
                                   _  C   A__
GAM3477 OR51E2   3'  GTACATTCAAAATTTT      78954          TGA
                                GTACATTCAG   GGTTTT
                                ||||||||||   ||||||
                                CATGTAAGTT   TTAAAA
                                     ___
GAM3477 RNF8     3'  AGTACATTCAGGCTTT      78955          GTGA
                                AGTACATTCA    GGTTTT
                                ||||||||||    ||||||
                                TCATGTAAGT    CCGAAA
                                     _____
GAM3477 ZDHHC3   3'  GCATCCATCTTCGGTGAGGTTT 78956     GTA  __  A
             TA                   GCA   CAT  TC GTGAGGTTTTA
                                |||   |||  ||  ||||||||||||
                                CGT   GTA  AG CACTCCAAAAT
                                  AG_   GA  C
GAM3477 LOC255367 5'  AGAAGTGCATTCAGTGGG    78957    C   A       A
                                AG AGT CATTCAGTG GG
                                || ||| ||||||||| ||
                                TC TCA GTAAGTCAC CC
                                 T  C       _
GAM3478 FLJ20340 3'  CCATGTGTATAGTTCTTGTG   78960      TCGG  T
                                CCAT    GT ATAGTTCTTGTG
                                ||||    || ||||||||||||
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                                GGTA    CA TATCAAGAACAC
                                  CA__  _
GAM3478  LOC148930 3'  TCCCTGTCTGTGGTTCTTGTG  78961     AT_  GG  TATA
                                TCC   TC  GT    GTTCTTGTG
                                |||   ||  ||    |||||||||
                                AGG   AG  CA    CAAGAACAC
                                  GAC  A_  C___
GAM3478  LOC255106 3'  CATTCTGGTTATACCCTTGTG  78962       G      G
                                CATTC GGTTATA TTCTTGTG
                                ||||| ||||||| ||||||||
                                GTAAG CCAATAT GGGAACAC
                                   A      _
GAM3479  PSG1      3'  TGGTTCATTCTATCTAT     78965          GT  G
                                TGGTTCATTC  TC TAT
                                ||||||||||  || |||
                                ACCAAGTAAG  AG ATA
                                     AT  _
GAM3479  C20orf108 3'  TAATGGTTTATTCAGTTC     78966         C    _
                                TAATGGTT ATTC GTTC
                                |||||||| |||| ||||
                                ATTACCAA TAAG CAAG
                                    A    T
GAM3479  HSPC129   3'  CAATGGTTTAAATCTTTTGTAT 78967         CAT_  GTTC
              ATT                 TAATGGTT    TC    GTATATT
                                |||||||    ||    |||||||
                                GTTACCAA    AG    CATATAA
                                    ATTT  AAAA
GAM3480  APPL      3'  CATCAAGTGCAGTACATTAGA  78970     A       TGAA
                                CA CAAGTGCA    ATTAGA
                                || ||||||||    ||||||
                                GT GTTCACGT    TAATCT
                                 A       CATG
GAM3480  OPHN1     3'  GACACTATAATTGAAATTAGA  78971      ACAA   CA
                                GACA    GTG  TGAAATTAGA
                                ||||    |||  ||||||||||
                                CTGT    TAT  ACTTTAATCT
                                  GA__   TA
GAM3480  QDPR      3'  GACAACAAGTGCATTTATTAG  78972            GAA
                                GACAACAAGTGCAT   ATTAG
                                ||||||||||||||   |||||
                                CTGTTGTTCACGTA   TAATC
                                       AA_
GAM3480  RARRES1   3'  ACAACTCTTGATATGAAATTAG 78973       AAG  C_
              A                  ACAAC   TG  ATGAAATTAGA
                                |||||   ||  ||||||||||
                                TGTTG   AC  TACTTTAATCT
                                   AGA  TA
GAM3480  ALLC      5'  CACAGCAGCCTGAAATTAG    78974     _   _  A
                                CA AGT GC TGAAATTAG
                                || ||| || |||||||||
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                                GT TCG CG ACTTTAATC
                                 G   T  G
GAM3480  B3GNT1    3'  ACAACAAGATAAATTAG     78975         TGCATG
                                ACAACAAG     AAATTAG
                                ||||||||     |||||||
                                TGTTGTTC     TTTAATC
                                    TA____
GAM3480  B3GNT1    3'  ACAACAAGATAAATTAG     78975         TGCATG
                                ACAACAAG     AAATTAG
                                ||||||||     |||||||
                                TGTTGTTC     TTTAATC
                                    TA____
GAM3480  DKFZP434F0318 3'  CGAGGGCAAGTGCATCAAAGCA 78976     CAA       G   T
            G                    CGA   CAAGTGCAT AAA TAG
                                |||   ||||||||| ||| |||
                                GCT   GTTCACGTA TTT GTC
                                  CCC        G   C
GAM3480  FLJ11184  3'  ACAAAACGTGAAATTAG     78977      T  A
                                ACAAG GC TGAAATTAG
                                ||||| || |||||||||
                                TGTTT TG ACTTTAATC
                                   _  C
GAM3480  FLJ20793  3'  GACAAAATTTACCATGGAATTA 78978       CAAG   _   A
            GA                    GACAA    TGC ATG AATTAGA
                                |||||    ||| ||| |||||||
                                CTGTT    ATG TAC TTAATCT
                                   TTAA   G   C
GAM3480  MacGAP    3'  GACAGGAATACTGTGAAATTAG 78979      ACA     A_
                                GACA   AGTGC  TGAAATTAG
                                ||||   |||||  |||||||||
                                CTGT   TTATG  ACTTTAATC
                                  CC_    AC
GAM3480  LOC130535 3'  GACAATAGGTGCATGACACCAG 78980       CAA       A
                                GACAA   GTGCATGA ATTAG
                                |||||   |||||||| |||||
                                CTGTT   CACGTACT TGGTC
                                   ATC       G
GAM3480  LOC154222 3'  ACAGCAAGGGAGAAATTAG    78981     A    TGCAT
                                ACA CAAG     GAAATTAG
                                ||| ||||     ||||||||
                                TGT GTTC     CTTTAATC
                                  C    CCT__
GAM3480  LOC157983 5'  TGAAGTGGCTGAAATTAG     78982    C     CA
                                A AAGTG  TGAAATTAG
                                | |||||  |||||||||
                                A TTCAC  ACTTTAATC
                                 C     CG
GAM3480  LOC167026 5'  AACAGCATGAAATTGGA      78983      AGT        A
                                AACA   GCATGAAATT GA
                                ||||   |||||||||| ||
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                                TTGT   CGTACTTTAA CT
                                  ___        C
GAM3480  LOC199926 5'  ACAATGCTTGAAATTAG     78984      G   A
                                ACAA TGC TGAAATTAG
                                |||| ||| |||||||||
                                TGTT ACG ACTTTAATC
                                  _   A
GAM3480  LOC202316 5'  ACAATGCTTGAAATTAG     78984      G   A
                                ACAA TGC TGAAATTAG
                                |||| ||| |||||||||
                                TGTT ACG ACTTTAATC
                                  _   A
GAM3480  LOC203289 5'  TGAAGTGGCTGAAATTAG    78982    C     CA
                                A AAGTG  TGAAATTAG
                                | |||||  |||||||||
                                A TTCAC  ACTTTAATC
                                 C    CG
GAM3480  LOC256544 5'  TGAAGTGGCTGAAATTAG    78982    C     CA
                                A AAGTG  TGAAATTAG
                                | |||||  |||||||||
                                A TTCAC  ACTTTAATC
                                 C    CG
GAM3480  LOC93496  3'  GACACGAAAGTGGAAGTTAGA  78985      AC_     CAT   A
                                GACA   AAGTG   GAA TTAGA
                                ||||   |||||   ||| |||||
                                CTGT   TTCAC   CTT AATCT
                                  GCT     ___   C
GAM3481  AKAP4    5'  CACCCAGAAGGGAGATGTGCC  78988          A    ACCGCG
                                CACCCGGAA GGAGA     GCC
                                ||||||||| |||||     |||
                                GTGGGTCTT CCTCT     CGG
                                     C    ACA___
GAM3481  CARD15   3'  CCGGAAAGGAGGGCAGGC    78989           AACC  _
                                CCGGAAAGGAG    GC GGC
                                ||||||||||    || |||
                                GGCCTTTCCTC    CG CCG
                                      C___  T
GAM3481  CENPC1   5'  CCGGAATACCAGGCCGCGGCC  78990        _____   AGAA
                                CCGGAA    AGG    CCGCGGCC
                                ||||||    |||    ||||||||
                                GGCCTT    TCC    GGCGCCGG
                                   ATGG   _____
GAM3481  DLX2     3'  CACCCGGAGGGGAGGGAAGGC  78991         AA    AACCGC
                                CACCCGGA  GGAG     GGC
                                ||||||||  ||||     |||
                                GTGGGCCT  CCTC     CCG
                                    CC    CCTT__
GAM3481  GDF2     5'  CACCCAGAGAGGAGACTGCAGG 78992         A     ACC___
            CGGCC                   CACCCGGA AGGAGA     GCGGCC
                                ||||||||  ||||||     ||||||
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                                GTGGGTCT TCCTCT     CGCCGG
                                    C     GACGTC
GAM3481  HBQ1     3'  CGCCTGGGGATCCCGCGGCC   78993    A  C  AAA   GAA
                                C CC GG   GGA   CCGCGGCC
                                | || ||   |||   ||||||||
                                G GG CC   CCT   GGCGCCGG
                                 C  A  ___   AG_
GAM3481  IFNGR2   5'  CCCGCTCCGGGAACCGCGGCC  78994      GAAA  A
                                CCCG   GG GAACCGCGGCC
                                ||||   || ||||||||||
                                GGGC   CC CTTGGCGCCGG
                                  GAGG  _
GAM3481  IKBKB    3'  CACCATGTGAGAGCCGCGGCC  78995      CGGAAAG   A
                                CACC      GAGA CCGCGGCC
                                ||||      |||| ||||||||
                                GTGG      CTCT GGCGCCGG
                                  TACA___   C
GAM3481  JUND     5'  CCCGGGGGGGGAGTGGCCGCGGC 78996       AAA   AA_
              C                  CCCGG   GGAG   CCGCGGCC
                                |||||   ||||   ||||||||
                                GGGCC   CCTC   GGCGCCGG
                                  CCC    ACC
GAM3481  MAP2K2   5'  CCCGGGGCTGCGGCCGCGGCC  78997       AAA  AGAA__
                                CCCGG   GG     CCGCGGCC
                                |||||   ||     ||||||||
                                GGGCC   CC     GGCGCCGG
                                  ___  GACGCC
GAM3481  MGAT2    5'  CCCGGAAAAAGCTCAGCCGCGG 78998         G  AA___
                                CCCGGAAAG AG    CCGCGG
                                ||||||||| ||    ||||||
                                GGGCCTTTT TC    GGCGCC
                                     _  GAGTC
GAM3481  MSF      3'  CCTCGGGGAGGCCGCGGC    78999    _   AAA    AA
                                CC CGG   GGAG  CCGCGGC
                                || |||   ||||  |||||||
                                GG GCC   CCTC  GGCGCCG
                                 A   ___    C_
GAM3481  PAX2     3'  CACCCGGAAGGCGAGGGCAG   79000         A  A  ACC
                                CACCCGGAA GG GA   GCGG
                                |||||||| || ||   ||||
                                GTGGGCCTT CC CT   CGTC
                                     _  G  CC_
GAM3481  PAX2     3'  CACCCGGAAGGCGAGGGCAG   79000         A  A  ACC
                                CACCCGGAA GG GA   GCGG
                                |||||||| || ||   ||||
                                GTGGGCCTT CC CT   CGTC
                                     _  G  CC_
GAM3481  PTGER2   5'  CCTGGAAAAGAGATGCGCC   79001    C        ACC   G
                                CC GGAAAGGAGA   GCG CC
                                || ||||||||||   ||| ||
```

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                                GG CCTTTTCTCT   CGC GG
                                 A        A__  _
GAM3481  PTGER3   5'  ACTCCGCTGCTGGGACCGCGGC 79002    _  GAAA_  A  A
                C                 AC CCG    GG GA CCGCGGCC
                                  || |||    || || ||||||||
                                  TG GGC    CC CT GGCGCCGG
                                   A  GACGA  _  _
GAM3481  PXMP3    3'  CCTGGAAAGGAGAAGACAGTGG 79003    C        CCGC__
                C                 CC GGAAAGGAGAA     GGC
                                  || ||||||||||     |||
                                  GG CCTTTCCTCTT     CCG
                                   A         CTGTCA
GAM3481  SHANK2   3'  CCCGGAAAGCAGAGGACGG   79004        G   ACC
                                  CCCGGAAAG AGA   GCGG
                                  |||||||| |||   ||||
                                  GGGCCTTTC TCT   TGCC
                                       G   CC_
GAM3481  SLC13A3  3'  CACTTGGAAAGGAGGTGGAGC  79005    CC       AACCGC
                                  CAC  GGAAAGGAG     GGC
                                  |||  |||||||||     |||
                                  GTG  CCTTTCCTC     TCG
                                    AA       CACC__
GAM3481  SLC25A6  3'  GGAGGAGGCCGCGGCC     79006    AA   AA
                                  GGA  GGAG  CCGCGGCC
                                  |||  ||||  ||||||||
                                  CCT  CCTC  GGCGCCGG
                                    __   C_
GAM3481  SLC7A5   5'  CACCCGGGAGCCGCGGC     79007       AAAG   AA
                                  CACCCGG   GAG  CCGCGGC
                                  |||||||   |||  |||||||
                                  GTGGGCC   CTC  GGCGCCG

                                      ____  __
GAM3481  SLC9A1   5'  CACCCAGAGAGGGGCAG     79008        A   AGAACC
                                  CACCCGGA AGG     GCGG
                                  |||||||| |||     ||||
                                  GTGGGTCT TCC     CGTC
                                       C   C_____
GAM3481  VASP     3'  CGGAAAGGAGAAGCGG      79009          CC
                                  CGGAAAGGAGAA  GCGG
                                  ||||||||||||  ||||
                                  GCCTTTCCTCTT  CGCC

                                       __
GAM3481  WNT3A    3'  CCCGTCCAGGGGGAGCCGCGGC 79010      GAA   A_  A
                C                  CCCG   AGG  GA CCGCGGCC
                                   ||||   |||  || ||||||||
                                   GGGC   TCC  CT GGCGCCGG
                                     AGG   CC  C
GAM3481  C9orf5   3'  CACCTGGAAGGAGAAAACC   79011      C    A    __
                                  CACC GGAA GGAGA  ACC
                                  |||| |||| |||||  |||
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                                GTGG CCTT CCTCT  TGG
                                  A   _    TT
GAM3481  CDH22    5'  CACCCGGACGGGCCCGCGGCC  79012        AA  AGAA
                                CACCCGGA  GG   CCGCGGCC
                                ||||||||  ||   ||||||||
                                GTGGGCCT  CC   GGCGCCGG
                                    GC  G___
GAM3481  CENTB5   3'  CACACGCAGGGCCGCGGC    79013    C  GAA   AGAA
                                CAC CG   AGG   CCGCGGC
                                ||| ||   |||   |||||||
                                GTG GC   TCC   GGCGCCG
                                  T  G__   C___
GAM3481  DPYSL4   3'  CCCTGGGGCCCCCGCGGCC   79014    _  AAA  AGAA
                                CCC GG   GG   CCGCGGCC
                                ||| ||   ||   ||||||||
                                GGG CC   CC   GGCGCCGG
                                  A  ___  GGG_
GAM3481  EIF3S9   5'  ACTCGCAGGGCTCCGCGGCC   79015   C  GAA   AGAA
                                AC CG   AGG   CCGCGGCC
                                || ||   |||   ||||||||
                                TG GC   TCC   GGCGCCGG
                                 A  G__   CGA_
GAM3481  EML4     5'  CCCTGGGGTAGTAAGCCGCGGC 79016    _  AAA  _  _  _
            C                    CCC GG   GG AG AA CCGCGGCC
                                ||| ||   || || || ||||||||
                                GGG CC   CC TC TT GGCGCCGG
                                  A  ___  A  A  C
GAM3481  FLJ20257  5'  CACTGGAGGAGGTGGCCGCGGC 79017    CC   AA   AA__
            C                    CAC  GGA  GGAG   CCGCGGCC
                                |||  |||  ||||   ||||||||
                                GTG  CCT  CCTC   GGCGCCGG
                                  A_  __   CACC
GAM3481  FLJ20793  5'  CCCGGAAAGGGAAACGGAGCC  79018         A   C  C
                                CCCGGAAAGG GAA CG GGCC
                                |||||||||| ||| || ||||
                                GGGCCTTTCC CTT GC TCGG
                                      _  T  C
GAM3481  HRIHFB2436 5'  CCTGGATGGTCTCCGCGGCC   79019    C   AA  AGAA
                                CC GGA  GG   CCGCGGCC
                                || |||  ||   ||||||||
                                GG CCT  CC   GGCGCCGG
                                 A  A_  AGA_
GAM3481  HSU79303  3'  CGGGAAGGGGCCGCGGCC    79020    A   AGAA
                                CGG AAGG   CCGCGGCC
                                ||| ||||   ||||||||
                                GCC TTCC   GGCGCCGG
                                  C   CC__
GAM3481  KIAA0776  3'  GGAAAGAGAACAAACC     79021       G    CGC
                                GGAAAG AGAAC   GGCC
                                |||||| |||||   ||||
```

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                                CCTTTC TCTTG   TTGG
                                   _    T__
GAM3481 KIAA1430 5' CCCTCACCTGAGAGCCGCGGCC 79022    GGAAAG   A
                                CCC     GAGA CCGCGGCC
                                |||     |||| ||||||||
                                GGG     CTCT GGCGCCGG
                                  AGTGGA   C
GAM3481 KIAA1465 3' CCCTCCAGAGAGCCGCGGCC  79023    GGAAA    A
                                CCC    GGAGA CCGCGGCC
                                |||    ||||| ||||||||
                                GGG    TCTCT GGCGCCGG
                                  AGG__    C
GAM3481 KIAA1511 5' CCCGAGTGGGGAACCGCGGCC 79024      AAA  A
                                CCCGG   GG GAACCGCGGCC
                                |||||   || ||||||||||
                                GGGCT   CC CTTGGCGCCGG
                                   CAC  _
GAM3481 KIAA1623 3' GGAAAGGAAAACGGC       79025         ACC
                                GGAAAGGAGA   GCGGC
                                ||||||||||   |||||
                                CCTTTCCTTT   TGCCG
                                      ___
GAM3481 MGC10772 5' CACTCGGGGACCCGCGGC    79026    C   AAA   GAA
                                CAC CGG   GGA   CCGCGGC
                                ||| |||   |||   |||||||
                                GTG GCC   CCT   GGCGCCG
                                  A  ____   G__
GAM3481 MGC16491 3' CACCCTGGAAGGGGCCTGGGC 79027      _   A  AGAA  GC
                                CACCC GGAA GG    CC  GGC
                                ||||| |||| ||    ||  |||
                                GTGGG CCTT CC    GG  CCG
                                   A    C  C___  AC
GAM3481 MGC19570 5' CACCTGGAAAGGAGTCGG    79028     C       AACCG
                                CACC GGAAAGGAG    CGG
                                |||| |||||||||    |||
                                GTGG CCTTTCCTC    GCC
                                  A       A____
GAM3481 NUDT9    5' CCTGGGGAAACCGCGGCC    79029    C  AAA    A
                                CC GG   GGAGA CCGCGGCC
                                || ||   ||||| ||||||||
                                GG CC   CCTTT GGCGCCGG
                                 A  ___    _
GAM3481 PACSIN2  3' ACTCGGAAAGGAGAGACAAAG  79030    C        AC  C
                                AC CGGAAAGGAGA  CG GG
                                || ||||||||||  || ||
                                TG GCCTTTCCTCT  GT TC
                                 A         CT  T
GAM3481 PRDM12   3' CACCCGGACAAGGAGGTCGC   79031        _     AAC
                                CACCCGGA AAGGAG   CGC
                                |||||||| ||||||   |||
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                                GTGGGCCT TTCCTC   GCG
                                    G     CA_
GAM3481  RP4-622L5 3'  CACCTGGAAAGGGCAG      79032      C      AGAACC
                                CACC GGAAAGG     GCGG
                                |||| |||||||     ||||
                                GTGG CCTTTCC     CGTC
                                  A     _______
GAM3481  TFIP11    5'  ACCCGGAAGCACCGTGGC     79033        AAGG  A    C
                                ACCCGGA    AG ACCG GGC
                                |||||||    || |||| |||
                                TGGGCCT    TC TGGC CCG
                                    _____ G    A
GAM3481  TIMM9     5'  GGACAGGAGCCGCGGCC     79034     A     AA
                                GGA AGGAG  CCGCGGCC
                                ||| |||||  ||||||||
                                CCT TCCTC  GGCGCCGG
                                  G    __
GAM3481  TUBGCP3   5'  CACGCGCAGGGACCGCGGC    79035     C  GAA   A  A
                                CAC CG   AGG GA CCGCGGC
                                ||| ||   ||| || |||||||
                                GTG GC   TCC CT GGCGCCG
                                  C  G__   _ _
GAM3481  UXT       5'  CGGTTGGTAGGAACCGCGGC   79036     AAA  A__
                                CGG   GG   GAACCGCGGC
                                |||   ||   ||||||||||
                                GCC   CC   CTTGGCGCCG
                                  AA_  ATC
GAM3481  LOC124930 3'  CCTGGGAAGGTACCCCGCGGCC 79037    C  A    AGAA
                                CC GG AAGG    CCGCGGCC
                                || || ||||    ||||||||
                                GG CC TTCC    GGCGCCGG
                                 A  C    ATGG
GAM3481  LOC126528 5'  CACCTGGCAGGGAAAATGGCC  79038      C  AAA     CCGC
                                CACC GG   GGAGAA    GGCC
                                |||| ||   ||||||    ||||
                                GTGG CC   CCTTTT    CCGG
                                  A  GTC     A___
GAM3481  LOC148697 3'  CACTAGGGGAGGAGAACTGTTG 79039     CC  AA      CGCG
            CC                    CAC  GG  AGGAGAAC    GCC
                                ||| ||  ||||||||   |||
                                GTG  CC  TCCTCTTG    CGG
                                  AT  CC       ACAA
GAM3481  LOC150135 3'  CACCCAGAGGGGAGGGGGACC  79040        AA    AACCGC
                                CACCCGGA  GGAG     GGCC
                                ||||||||  ||||     ||||
                                GTGGGTCT  CCTC     CTGG
                                    CC    CCC___
GAM3481  LOC159766 5'  CACCCGGAACAGGAGGGCAG   79042         _     AACC
                                CACCCGGAA AGGAG    GCGG
                                |||||||| |||||    ||||
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                                GTGGGCCTT TCCTC    CGTC
                                     G    C___
GAM3481  LOC159766 5'  CACCCGGAACAGGGGGACAGC  79041         _  AGAACC
                                CACCCGGAA AGG     GCGGC
                                ||||||||| |||     |||||
                                GTGGGCCTT TCC     TGTCG
                                     G   CCC___
GAM3481  LOC199757 5'  CCGGAAAGGAGGCGG       79043          AACC
                                CCGGAAAGGAG    GCGG
                                ||||||||||    ||||
                                GGCCTTTCCTC    CGCC
                                      ____
GAM3481  LOC202047 5'  CCTGGAGAAGCGGCCGCGGCC  79044    C   AA    AA_
                                CC GGA  GGAG   CCGCGGCC
                                || |||  ||||   ||||||||
                                GG CCT  CTTC   GGCGCCGG
                                 A  __   GCC
GAM3481  LOC221496 3'  CCGCCAAGAGCCGCGGC     79045     GAA     AA
                                CCG   AGGAG  CCGCGGC
                                |||   |||||  |||||||
                                GGC   TTCTC  GGCGCCG
                                  GG_    __
GAM3481  LOC51000  5'  CACCCGGAAGGGTGACGGCAGC 79046         A  A  ACC
           C                     CACCCGGAA GG GA   GCGGCC
                                ||||||||| || ||   ||||||
                                GTGGGCCTT CC CT   CGTCGG
                                     C  A  GC_
GAM3481  LOC51102  3'  CCCTGGGGAAAACCGTGGC    79047     _ AAA       C
                                CCC GG   GGAGAACCG GGC
                                ||| ||   ||||||||| |||
                                GGG CC   CCTTTTGGC CCG
                                  A ___       A
GAM3481  LOC51659  5'  CCCGGAGGAGACGCCGCGGCC  79048       AA    A_
                                CCCGGA  GGAGA  CCGCGGCC
                                ||||||  |||||  ||||||||
                                GGGCCT  CCTCT  GGCGCCGG
                                   __    GC
GAM3481  LOC92299  5'  GGAGGAGCTGCCGCGGCC    79049     AA   AA_
                                GGA  GGAG   CCGCGGCC
                                |||  ||||   ||||||||
                                CCT  CCTC   GGCGCCGG
                                  __   GAC
GAM3482  ARF1     3'  ACACGGTGACCAAACCACGGA  79052      AATAACAAA
                                ACAC        CAGACCGCGGA
                                ||||        ||||||||||||
                                TGTG        GTTTGGTGCCT
                                  CCACTG___
GAM3482  DMXL1    3'  CACAAAACAGACAGAAACAG   79053       T    A    CC
                                CACAA AACA ACAGA  GCGG
                                ||||| |||| |||||  ||||
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                                GTGTT TTGT TGTCT  TGTC
                                  _   C    T_
GAM3482  GRM1     3'  ACACAACAGCAAATAGCAG   79054        A   CAGACC
                                ACACAATA CAAA     GCGG
                                |||||||| ||||     ||||
                                TGTGTTGT GTTT     CGTC
                                    C   AT____
GAM3482  IL13     3'  ACACAATAATAAATAAGACCA  79055        C  C_
                                ACACAATAA AAA  AGACCG
                                ||||||||| |||  ||||||
                                TGTGTTATT TTT  TCTGGT
                                     A  AT
GAM3482  CLDN15   3'  ACACAATACAAACGTGCGG   79056        A    AGACC
                                ACACAATA CAAAC    GCGG
                                |||||||| |||||    ||||
                                TGTGTTAT GTTTG    CGCC
                                    _    CA___
GAM3482  DKFZP434L0117 3'  ACGCAATACAAACAAATGG   79057    A    A      CCGC
                                AC CAATA CAAACAGA    GG
                                || ||||| ||||||||    ||
                                TG GTTAT GTTTGTTT    CC
                                 C    _       A___
GAM3482  FLJ20689  3'  ACAAGGTAACAAATAGAGCAGA 79058     __     C  CC
                                ACAA  TAACAAA AGA  GCGGA
                                ||||  ||||||| |||  |||||
                                TGTT  ATTGTTT TCT  CGTCT
                                  CC      A  __
GAM3482  FLJ20689  3'  ACAAGGTAACAAATAGAGCAGA 79058     __     C  CC
                                ACAA  TAACAAA AGA  GCGGA
                                ||||  ||||||| |||  |||||
                                TGTT  ATTGTTT TCT  CGTCT
                                  CC      A  __
GAM3482  MAGEH1   3'  ACACAACAGCAGACACAAA   79059       ACAAA    C
                                ACACAATA    CAGAC GCGGA
                                ||||||||    ||||| |||||
                                TGTGTTGT    GTCTG TGTTT
                                    C____    _
GAM3482  SLC38A5  5'  CACAGGAACAGACAGACCA   79060     AT   A
                                CACA  AACA ACAGACCG
                                ||||  |||| ||||||||
                                GTGT  TTGT TGTCTGGT
                                  CC   C
GAM3482  TSPEAR   3'  ACACAATAAATAGGTGGCGG  79061        CAAAC  ACC
                                ACACAATAA    AG   GCGG
                                |||||||||    ||  ||||
                                TGTGTTATT    TC   CGCC
                                     TA___  CAC
GAM3482  LOC120534 3'  CACAGGGACAAACCACTGGA  79062     ATAACAA       _
                                CACA      ACAGACCGC GGA
                                ||||      ||||||||| |||
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                                GTGT      TGTTTGGTG CCT
                                  CCC____       A
GAM3482  LOC153222 3'  CACAATAATACATCAATCGGA  79063        CAA   GACCG
                                CACAATAA   ACA    CGGA
                                ||||||||   |||    ||||
                                GTGTTATT   TGT    GCCT
                                    A__   AGTTA
GAM3482  LOC220477 3'  ACACAATAACAAATGGAC    79064           CA
                                ACACAATAACAAA  GAC
                                ||||||||||||  |||
                                TGTGTTATTGTTT  CTG
                                       AC
GAM3483  ABCC2    3'  AGTCCTTTTCTAACCCATGG   79067      G          C
                                AGTC TTTTCTAACCCA GG
                                |||| ||||||||||| ||
                                TCAG AAAAGATTGGGT CC
                                  G          A
GAM3483  GRINL1A   3'  AGTCATTTTCTATGGATG    79068          ACCCAC
                                AGTCGTTTTCTA     GGATG
                                ||||||||||||     |||||
                                TCAGTAAAAGAT     CCTAC
                                       A_____
GAM3483  PAX6     5'  GTTTTCTCCACGGAT       79069        AAC
                                GTTTTCT   CCACGGAT
                                |||||||   ||||||||
                                CAAAAGA   GGTGCCTA
                                   ___
GAM3483  PAX6     5'  GTTTTCTCCACGGAT       79069        AAC
                                GTTTTCT   CCACGGAT
                                |||||||   ||||||||
                                CAAAAGA   GGTGCCTA
                                   ___
GAM3483  RNGTT    3'  AGTCGTTTTTCAATTTCTCGG  79070         C   CCCA_
                                AGTCGTTTT TAA    CGG
                                ||||||||| |||    |||
                                TCAGCAAAA GTT    GCC
                                     A   AAAGA
GAM3483  C20orf103 3'  AGTCGTTTTCTGGTG       79071           AACCCAC  A
                                AGTCGTTTTCT      GG TG
                                ||||||||||       || ||
                                TCAGCAAAAGA      CC AC
                                   ________  _
GAM3483  LOC150174 5'  AGTTGTCTTGACACCACGGATG 79072     C     CTA  _
                                AGT GTTTT   AC CCACGGATG
                                ||| |||||   || |||||||||
                                TCA CAGAA   TG GGTGCCTAC
                                  A    C__  T
GAM3484  SOX11    3'  TGCAGTGAGTTTCAATCA    79075        G    C
                                TGCAGTG AGTT CAATCA
                                ||||||| |||| ||||||
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                                ACGTCAC TCAA GTTAGT
                                   _   A
GAM3484 ARHU     3'  TGCATGGAGTTTCAAAGCTAAG 79076     G     C  TCAAT
              A                  TGCA TGGAGTT CAA    AGA
                                 |||| ||||||| |||    |||
                                 ACGT ACCTCAA GTT    TCT
                                   _     A  TCGAT
GAM3484 CAP      3'  TGCAGTGGAGGTTTCAGTC   79077         _ C  A
                                 TGCAGTGGAG TT CA TC
                                 |||||||||| || || ||
                                 ACGTCACCTC AA GT AG
                                       C  A  C
GAM3484 FLJ21432 3'  GCAGAGCCCGCAATCAGTAGA  79078   TG    _     A
                                 G  GAGTTC CAATCA TAGA
                                 |  |||||| |||||| ||||
                                 C  CTCGGG GTTAGT ATCT
                                  GT     C     C
GAM3484 FLJ22969 3'  TGCAGGGGCATTGATCAGTAGA 79079      T  A  TCCA   A
                                 TGCAG GG GT   ATCA TAGA
                                 ||||| || ||   |||| ||||
                                 ACGTC CC CG   TAGT ATCT
                                   _ _ TAAC   C
GAM3484 LHX9     3'  TGCAGTGGATTTCCGATCA   79080        G   A
                                 TGCAGTGGA TTCC ATCA
                                 ||||||||| |||| ||||
                                 ACGTCACCT AAGG TAGT
                                       A   C
GAM3484 NFAT5    3'  TGCATGGAGTTTCACA      79081      G     CCAA  A
                                 TGCA TGGAGTT   TCA TA
                                 |||| |||||||   ||| ||
                                 ACGT ACCTCAA   AGT GT
                                   _     _____  _
GAM3484 SEPT6    3'  TGGTCACTCACCAATCAATAGA 79082     AGTT___
                                 TGG      CCAATCAATAGA
                                 |||      ||||||||||||
                                 ACC      GGTTAGTTATCT
                                   AGTGAGT
GAM3484 SURB7    3'  CAGTGGAGATTATCAGTAGA   79083       TTCCA   A
                                 CAGTGGAG    ATCA TAGA
                                 ||||||||    |||| ||||
                                 GTCACCTC    TAGT ATCT
                                      TAA__   C
GAM3484 TIMM22   3'  TGCATGGAGTTCCAAGGTAGA  79084     G        TCAA
                                 TGCA TGGAGTTCCAA   TAGA
                                 |||| ||||||||||   ||||
                                 ACGT ACCTCAAGGTT   ATCT
                                   _        CC__
GAM3484 LOC153579 3' TGCAGTGAGTTTCTCTAG    79085       G   CCAA  AA
                                 TGCAGTG AGTT   TC  TAG
                                 ||||||| ||||   ||  |||
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                                ACGTCAC TCAA    AG  ATC
                                   _   _____ AG
GAM3484  LOC199974 3'  TGAGTGGAGTTTTGATCA    79086    C       CCA
                                TG AGTGGAGTT   ATCA
                                || |||||||||   ||||
                                AC TCACCTCAA   TAGT
                                  _        AAC
GAM3485  EIF2C1    3'  AGTTTAGAAACTAAAGT     79089     G       C
                                AGTT TAGAAACTA AGT
                                |||| ||||||||| |||
                                TCAA ATCTTTGAT TCA
                                  _        T
GAM3485  KCNA3     3'  AGTTGTAGAGACACTTAAAAT  79090         AACT   G
                                AGTTGTAGA    ACA TTAAAAT
                                |||||||||    ||| |||||||
                                TCAACATCT    TGT AATTTTA
                                     C___   G
GAM3485  PITPNB    3'  AGTTGTTAGAAAAACATTAAAA 79091       _    CT   G
              T                  AGTTGT AGAAA  ACA TTAAAAT
                                |||||| |||||  ||| |||||||
                                TCAACA TCTTT  TGT AATTTTA
                                   A    T_  _
GAM3485  RAB18     3'  ATTACACAAGCTACAGTTAA   79092       G  A
                                GTTGTA AA CTACAGTTAA
                                |||||| || ||||||||||
                                TAATGT TT GATGTCAATT
                                   G  C
GAM3485  RASGRP1   3'  AGTTGTAAGGCTACAACTA    79093        AAA    GT
                                AGTTGTAG   CTACA  TA
                                ||||||||   |||||  ||
                                TCAACATT   GATGT  AT
                                     CC_    TG
GAM3485  DAMS      5'  GTTGTAGATACTATGTT     79094         A    CA
                                GTTGTAGA ACTA  GTT
                                |||||||| ||||  |||
                                CAACATCT TGAT  CAA
                                     A    A_
GAM3485  FLJ11827  3'  AGTTGTAGAAATAATACAG   79095          C__
                                AGTTGTAGAAA   TACAG
                                ||||||||||   |||||
                                TCAACATCTTT   ATGTC
                                      ATT
GAM3485  FLJ20276  3'  AGTTGTAGAAATACACAGT   79096          C_
                                AGTTGTAGAAA  TACAGT
                                ||||||||||  ||||||
                                TCAACATCTTT  GTGTCA
                                      AT
GAM3485  FLJ20533  3'  AGTTGCAGAAACAAATTAA   79097           TAC
                                AGTTGTAGAAAC   AGTTAA
                                ||||||||||   ||||||
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                                TCAACGTCTTTG  TTAATT
                                      T__
GAM3485 FLJ32919 3' AGTTGTAGAAATAGACAA   79098        CT_
                                AGTTGTAGAAA  ACAG
                                ||||||||||  ||||
                                TCAACATCTTT  TGTT
                                      ATC
GAM3485 GMFB    3' AGTTATAGAAATTAGTCA   79099        CTAC
                                AGTTGTAGAAA   AGTTA
                                ||||||||||   |||||
                                TCAATATCTTT   TCAGT
                                      AA__
GAM3485 KIAA0164 3' AGATGTATACAGTTAAAA   79100   T   GAAAC
                                AG TGTA    TACAGTTAAAA
                                || ||||    ||||||||||
                                TC ACAT    ATGTCAATTTT
                                 T  _____
GAM3485 KIAA1786 3' AGTGGTGGAGACTACAGT   79101    T  A  A
                                AGT GT GA ACTACAGT
                                ||| || || ||||||||
                                TCA CA CT TGATGTCA
                                  C  C  C
GAM3485 SSFA2   3' AGTTGTAGGTAACCTCATAAAA 79102       A_   A  GT
           T                     AGTTGTAG  AACT CA  TAAAAT
                                ||||||||  |||| ||  ||||||
                                TCAACATC  TTGG GT  ATTTTA
                                     CA   A  __
GAM3485 VMP1    3' AGTTGTAAAAATTGATACAG  79103        C___
                                AGTTGTAGAAA   TACAG
                                ||||||||||   |||||
                                TCAACATTTTT   ATGTC
                                      AACT
GAM3485 LOC89919 3' AGTTGTAGAAGCAACAAT   79104        ACT
                                AGTTGTAGAA  ACAGT
                                ||||||||||  |||||
                                TCAACATCTT  TGTTA
                                      CGT
GAM3486 ADAM15  3' CCCGGAGTCTTAAGACACC   79107       A  TT_
                                CCCGGAGT CTT  GCATC
                                |||||||| |||  |||||
                                GGGCCTCA GAA  TGTGG
                                     _  TTC
GAM3486 ARF3    3' CCTGGGTAACACATCAC    79108   C  A  CTTT
                                CC GG GTA   TGCATCAC
                                || || |||   ||||||||
                                GG CC CAT   GTGTAGTG
                                 A  _  T___
GAM3486 BCL2L2  3' CCTGGAGTACCCATCAC    79109   C      TTTG
                                CC GGAGTACT   CATCAC
                                || ||||||||   ||||||
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                                GG CCTCATGG   GTAGTG
                                 A     ____
GAM3486 FMNL    5' CCCGGAGTCGGAGCATCACC  79110       ACTTTT
                                CCCGGAGT    GCATCACC
                                ||||||||    ||||||||
                                GGGCCTCA    CGTAGTGG
                                    GCCT__
GAM3486 NCF2    3' CCTGGGTACTCACATCA    79111   C A    TT
                                CC GG GTACTT  GCATCA
                                || || ||||||  ||||||
                                GG CC CATGAG  TGTAGT
                                 A _    __
GAM3486 PPIF    3' CACTTGGATGGCAACCCATCAC 79112    CC  GT___  TTTG
            C                    CAC  GGA   ACT   CATCACC
                                |||  |||   |||   |||||||
                                GTG  CCT   TGG   GTAGTGG
                                  AA  ACCGT  ____
GAM3486 RGL     5' CCCGGGTGTGCATCAC     79113      A ACTTT
                                CCCGG GT    TGCATCAC
                                ||||| ||    ||||||||
                                GGGCC CA    ACGTAGTG
                                   _ C____
GAM3486 AGS3    5' CCTCGGAGGTGCCCTGCAT   79114   _   TAC
                                CC CGGAG   TTTTGCAT
                                || |||||   ||||||||
                                GG GCCTC   GGGACGTA
                                 A    CAC
GAM3486 CKAP4   3' CCTGGATGCTTTGCATAGTTAC 79115   C  GTAC     C___
            C                    CC GGA   TTTTGCAT   ACC
                                || |||   ||||||||   |||
                                GG CCT   GAAACGTA   TGG
                                 A  AC__      TCAA
GAM3486 GRID1   3' CACCTGGAGTACTGGTCCACC  79116    C      TTTGCA
                                CACC GGAGTACT    TCACC
                                |||| ||||||||    |||||
                                GTGG CCTCATGA    GGTGG
                                  A      CCA___
GAM3486 KIAA0212 3' CACTGGAGTGCTTACCCAC   79117    CC    ACT   A
                                CAC  GGAGT   TTTGC TCAC
                                |||  |||||   ||||| ||||
                                GTG  CCTCA   GAATG GGTG
                                  A_    C__    _
GAM3486 KIAA1952 5' GGGGAACCCTGCATCACC    79118    AGT    T
                                GG   ACTTT GCATCACC
                                ||   ||||| ||||||||
                                CC   TGGGA CGTAGTGG
                                 CCT    _
GAM3486 LYPLA3   3' CCAGAGTACTTTTATTGC    79119          ___
                                CCGGAGTACTTT   TGC
                                ||||||||||||   |||
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                                GGTCTCATGAAA   ACG
                                       ATA
GAM3486  MGC29643  5'  CGGAGCCTGCATCGCC      79120       ACTT      A
                                CGGAGT    TTGCATC CC
                                ||||||    ||||||| ||
                                GCCTCG    GACGTAG GG
                                   ____       C
GAM3486  SPTLC2    3'  CACCAGGAGTGCACATCAC    79121      C     ACTTT
                                CACC GGAGT     TGCATCAC
                                |||| |||||     ||||||||
                                GTGG CCTCA     GTGTAGTG
                                  T    C____
GAM3486  WDR13     5'  CACCCGGGTGTTACCATGGTCA 79122        AG__    TTTG_
              TC                  CACCCGG    TACT     CATC
                                |||||||    ||||     ||||
                                GTGGGCC    ATGG     GTAG
                                    CACA    TACCA
GAM3486  LOC151009 5'  CACCTGAGCAGCTGCGTCACC  79123      CG     CTT    A
                                CACC  GAGTA   TTGC TCACC
                                ||||  |||||   |||| |||||
                                GTGG  CTCGT   GACG AGTGG
                                  A_    C__    C
GAM3487  COL4A3    3'  CAATATAATAAAATAATATTTA 79126             _
                                CAATATAATAAAATA TATTTA
                                |||||||||||||| ||||||
                                GTTATATTATTTTAT ATAAAT
                                         T
GAM3487  COL4A3    3'  CAATATAATAAAATAATATTTA 79126             _
                                CAATATAATAAAATA TATTTA
                                |||||||||||||| ||||||
                                GTTATATTATTTTAT ATAAAT
                                         T
GAM3487  COL4A3    3'  CAATATAATAAAATAATATTTA 79126             _
                                CAATATAATAAAATA TATTTA
                                |||||||||||||| ||||||
                                GTTATATTATTTTAT ATAAAT
                                         T
GAM3487  HSPC047   3'  CAGTATAATAAAATATAT    79127    A
                                CA TATAATAAAATATAT
                                || ||||||||||||||
                                GT ATATTATTTTATATA
                                 C
GAM3487  IRF5      3'  ACAATATAATAAATATATT    79128           A
                                ACAATATAATAAA TATATT
                                |||||||||||| ||||||
                                TGTTATATTATTT ATATAA
                                            _
GAM3487  KIAA0441  3'  TACATATAATAAAATATA     79129      A
                                TACA TATAATAAAATATA
                                |||| ||||||||||||||
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                                ATGT ATATTATTTTATAT
                                   _
GAM3487  RA-GEF-2  3'  AATATATATAAAATATATTTAA 79130       _
                                AATATA ATAAAATATATTTAA
                                |||||| ||||||||||||||||
                                TTATAT TATTTTATATAAATT
                                   A
GAM3487  RDC1      3'  ACAATATTTAAAATATATTTAA 79131        AA
                                ACAATAT  TAAAATATATTTAA
                                |||||||  ||||||||||||||
                                TGTTATA  ATTTTATATAAATT
                                   A_
GAM3488  PCDHB4    3'  TATATGAGATTTTTCTCTT    79134          A_   G
                                TATATGAGATT  TCT TT
                                ||||||||||  ||| ||
                                ATATACTCTAA  AGA AA
                                      AA   G
GAM3488  CNOT7     3'  TATATGAGAATATATATATATT 79135         T   C   _
              TT                  TATATGAGA TAT TGT TATTTT
                                |||||||| ||| ||| ||||||
                                ATATACTCT ATA ATA ATAAAA
                                     T   T   T
GAM3488  FLJ14966  3'  TATATGAGTTATTTGCT     79136         A    C
                                TATATGAG TTAT TGTT
                                |||||||| |||| ||||
                                ATATACTC AATA ACGA
                                   _    A
GAM3488  KLHL4     3'  TATATGAAATTACAGTAATATT 79137            CTGT_
              TTA                   TATATGAGATTAT     TATTTTA
                                ||||||||||||||     |||||||
                                ATATACTTTAATG     ATAAAAT
                                      TCATT
GAM3488  PLAA      3'  TATATGAATTTATAAATTATTT 79138         A    CT
              TA                    TATATGAG TTAT  GTTATTTTA
                                |||||||| ||||  |||||||||
                                ATATACTT AATA  TAATAAAAT
                                   A    TT
GAM3488  LOC115219 3'  GATGATTGTCTGTTATTTTA   79139     _    A
                                GA GATT TCTGTTATTTTA
                                || |||| ||||||||||||
                                CT CTAA AGACAATAAAAT
                                 A    C
GAM3488  LOC92465  5'  TAAGATCCACTGTTATTTTA   79140        AT
                                TGAGATT  CTGTTATTTTA
                                |||||||  ||||||||||||
                                ATTCTAG  GACAATAAAAT
                                   GT
GAM3489  LOC143310 3'  TTTGCTCAGGTCACCA      79143         GACTGA   _
                                TTTGCTC     AGGT ATCA
                                |||||||     |||| ||||
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                                AAACGAG     TCCA TGGT
                                       _____  G
GAM3490  SAH      5'  GCATCAGTCTTGTTGGAAGCTT 79146    CG    C  C
                T                    GC  TAGTC TGT GGAAGCTTT
                                     ||  ||||| ||| |||||||||
                                     CG  GTCAG ACA CCTTCGAAA
                                      TA    A  A
GAM3490  FLJ23588 5'  TGTCGTATCTTGCCCAAAGCTT 79147    C    G  C    G
                T                    TG CGTA TC TGTC GAAGCTTT
                                     || |||| || |||| ||||||||
                                     AC GCAT AG ACGG TTTCGAAA
                                      A   _ A   G
GAM3490  KIAA0638 3'  CCGTAGTCCAAAGGCTT     79148         TGTC  A
                                     CCGTAGTCC    GGA GCTT
                                     |||||||||    ||| ||||
                                     GGCATCAGG    TTT CGAA
                                          ____  C
GAM3490  LOC163682 5'  TGCCGTGGGCCTGTCGGA    79149       AGT
                                     TGCCGT   CCTGTCGGA
                                     ||||||   |||||||||
                                     ACGGCA   GGACAGCCT
                                        CCC
GAM3491  CDH1     3'  CTAACCCCCTTTAGGGCCA    79152      ATCT      AA
                                     CTAAC    CCCCTTTA  GCCA
                                     |||||    ||||||||  ||||
                                     GATTG    GGGGAAAT  CGGT
                                        ____       CC
GAM3491  DMRT2    3'  TCCAACATCTCCCTTTCTTTA  79153           ___
                                     TCTAACATCTCCC   CTTTA
                                     ||||||||||||   |||||
                                     AGGTTGTAGAGGG   GAAAT
                                             AAA
GAM3491  MME      3'  CAACATCTTCTTTTCCCTTT   79154        _ ____
                                     TAACATCT C    CCCTTT
                                     ||||||||  |    ||||||
                                     GTTGTAGA G    GGGAAA
                                          A AAAA
GAM3491  MME      3'  CAACATCTTCTTTTCCCTTT   79154        _ ____
                                     TAACATCT C    CCCTTT
                                     ||||||||  |    ||||||
                                     GTTGTAGA G    GGGAAA
                                          A AAAA
GAM3491  MME      3'  CAACATCTTCTTTTCCCTTT   79154        _ ____
                                     TAACATCT C    CCCTTT
                                     ||||||||  |    ||||||
                                     GTTGTAGA G    GGGAAA
                                          A AAAA
GAM3491  MME      3'  CAACATCTTCTTTTCCCTTT   79154        _ ____
                                     TAACATCT C    CCCTTT
                                     ||||||||  |    ||||||
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                                GTTGTAGA G    GGGAAA
                                    A AAAA
GAM3491  NFE2L1    3'  TCTAAATCTCAAAGC       79155       C     CCCTTT
                                TCTAA ATCTC     AAAGC
                                ||||| |||||     |||||
                                AGATT TAGAG     TTTCG
                                  _    _______
GAM3491  NKX3A     3'  TCTAATGTCTCCCCTCTA     79156       CA
                                TCTAA  TCTCCCCTTTA
                                |||||  ||||||||||
                                AGATT  AGAGGGGAGAT
                                   AC
GAM3491  NME4      3'  TAATGCCTCCCCTTTAGAG    79157     CA          A
                                TAA  TCTCCCCTTTA AG
                                |||  |||||||||| ||
                                ATT  GGAGGGGAAAT TC
                                  AC          C
GAM3491  OGT       3'  TCTATATCTCCCCTCCA      79158      AC
                                TCTA  ATCTCCCCTTTA
                                ||||  ||||||||||||
                                AGAT  TAGAGGGGAGGT
                                  A_
GAM3491  POLA      3'  TCTAAATCTTCCCCCTCAGC   79159       C   _      AA
                                TCTAA ATCT CCCCTTT  AGC
                                ||||| |||| |||||||  |||
                                AGATT TAGA GGGGGAG  TCG
                                   _    A      __
GAM3491  SH2D2A    3'  TCTAACATCTGTTCTCACC    79160          CCC   TAAA
                                TCTAACATCT   CTT    GCC
                                ||||||||||   |||    |||
                                AGATTGTAGA   GAG    TGG
                                     CAA   ____
GAM3491  SLC7A8    3'  CATCTCCCCTCTCCTCCA     79161           AAAG
                                CATCTCCCCTTT    CCA
                                ||||||||||||    |||
                                GTAGAGGGGAGA    GGT
                                      GGA_
GAM3491  SOX4      3'  CAACATCTCCTCCTCCGGC    79162          _    AAA
                                TAACATCTCC CCTTT   GC
                                |||||||||| |||||   ||
                                GTTGTAGAGG GGAGG   CG
                                     A    C__
GAM3491  TFE3      3'  CCTGACATCTCCCTTTCCCA   79163     A       C   AAAG
                                TCT ACATCTCCC TTT    CCA
                                ||| |||||||| |||    |||
                                GGA TGTAGAGGG AAG    GGT
                                  C        A  ____
GAM3491  TLL2      3'  TCCAACATAAATACTCTTTTAA 79164         _____   CCC
              AGC                  TCTAACAT    CTC   TTTAAAGC
                                ||||||||    |||   ||||||||
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                              AGGTTGTA    GAG   AAATTTCG
                                  TTTAT   A__
GAM3491  CASPR3   3'  TCTGGTGACTCCAAGATAAAGC 79165    AACAT    CCTT
            CA                  TCT    CTCC    TAAAGCCA
                              |||    ||||   ||||||||
                              AGA    GAGG    ATTTCGGT
                                CCACT    TTCT
GAM3491  EMILIN-2 3'  CCTGACATCTCCCCAGCC    79166    A       TTTAA
                              TCT ACATCTCCCC    AGCC
                              ||| ||||||||||    ||||
                              GGA TGTAGAGGGG    TCGG
                                C       _____
GAM3491  FLJ13158 3'  TCTAACATCCTCTTTTATAGC  79167        CCCC    A
                              TCTAACATCT    TTTA AGC
                              ||||||||||    |||| |||
                              AGATTGTAGG    AAAT TCG
                                    AGA_    A
GAM3491  FLJ13187 3'  TCTTACATTTCCCCCAAAG   79168    A   C     TT
                              TCT ACAT TCCCCT  AAAG
                              ||| |||| ||||||  ||||
                              AGA TGTA AGGGGG  TTTC
                                A   A     __
GAM3491  FLJ22625 3'  CCTAACATCTCCCTTACC    79169          C  TAAA
                              TCTAACATCTCCC TT    GCC
                              |||||||||||| ||    |||
                              GGATTGTAGAGGG AA    TGG
                                          _ ____
GAM3491  INSM2    3'  TAACATCTTCCTTAAGC     79170        CC    TA
                              TAACATCT  CCTT  AAGC
                              ||||||||  ||||  ||||
                              ATTGTAGA  GGAA  TTCG
                                  A_    __
GAM3491  KIAA0284 3'  CAACTCTTTCCTTTAAAGC   79171     A   CC
                              TAAC TCT  CCTTTAAAGC
                              |||| |||  ||||||||||
                              GTTG AGA  GGAAATTTCG
                                _   AA
GAM3491  KIAA0493 3'  TAACATCTGAGCCAGAAGCCA  79172        CC_  TTTA
                              TAACATCT   CC    AAGCCA
                              ||||||||   ||    ||||||
                              ATTGTAGA   GG    TTCGGT
                                  CTC  TC__
GAM3491  KIAA1024 3'  CAAAATCTTTTTAAAGCCA   79173    C    CCCC
                              TAA ATCT    TTTAAAGCCA
                              ||| ||||    ||||||||||
                              GTT TAGA    AAATTTCGGT
                                T    A___
GAM3491  KIAA1271 3'  TCTGACATCTGCCAAAGCC   79174     A     C  CTTT
                              TCT ACATCT CC    AAAGCC
                              ||| |||||| ||    ||||||
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                                AGA TGTAGA GG    TTTCGG
                                  C     C _____
GAM3491  KIAA1332  3'  ACATCTCCTATGCCCAGGCCA  79175        _____  TTAAA
                                ACATCTCC    CCT    GCCA
                                ||||||||    |||    ||||
                                TGTAGAGG    GGG    CGGT
                                    ATAC   TC___
GAM3491  My015     3'  TCTAAAATCCCTTTAAAGCCA  79176      C  CTC
                                TCTAA AT   CCCTTTAAAGCCA
                                ||||| ||   ||||||||||||
                                AGATT TA   GGGAAATTTCGGT
                                   T ___
GAM3491  PSR       3'  TCTAACATTATCTCCTTCA    79177        C_  C
                                TCTAACAT  TC CCTTTA
                                ||||||||  || ||||||
                                AGATTGTA  AG GGAAGT
                                    AT  A
GAM3491  LOC127540 5'  TCTAGAGAACTCTTTAAAGCCA 79178      ACAT_   CCC
                                TCTA    CTC   TTTAAAGCCA
                                ||||    |||   ||||||||||
                                AGAT    GAG   AAATTTCGGT
                                  CTCTT   ___
GAM3491  LOC145757 5'  TCTAACACTTCCTAACGAGAAA 79179        TC   CCTTT__
           GC                    TCTAACA  TCC      AAAGC
                                ||||||| |||      |||||
                                AGATTGT  AGG      TTTCG
                                    GA   ATTGCTC
GAM3491  LOC149194 3'  TAACATCCCTCCAGCC      79180         C  TTTAA
                                TAACATCTC CC     AGCC
                                ||||||||| ||     ||||
                                ATTGTAGGG GG     TCGG
                                    A  ______
GAM3491  LOC150291 3'  TCTGGCATCTCCCTAACCC    79181     AA       CTTTA  G
                                TCT  CATCTCCC     AA CC
                                |||  ||||||||     || ||
                                AGA  GTAGAGGG     TT GG
                                  CC       A____  G
GAM3491  LOC152048 3'  TCTGGATCTCCCCTTCTCCCA  79182     AAC         AAAG
                                TCT   ATCTCCCCTTT    CCA
                                |||   ||||||||||    |||
                                AGA   TAGAGGGGAAG    GGT
                                  CC_          AG__
GAM3491  LOC197287 3'  TCTAACATATCCCATCAAGGC  79183        C    CT    A
                                TCTAACAT TCCC  TTAA GC
                                |||||||| ||||  |||| ||
                                AGATTGTA AGGG  AGTT CG
                                    T    T_    C
GAM3491  LOC199221 5'  TCTAACACCTCTTCCACT     79184          __  _
                                TCTAACATCTC  CC CT
                                ||||||||||  || ||
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                                AGATTGTGGAG  GG GA
                                      AA  T
GAM3491  LOC221876 5'  TCTAACATTCCCCTCCA     79185        C
                                TCTAACAT TCCCCTTTA
                                |||||||| |||||||||
                                AGATTGTA AGGGGAGGT
                                         _
GAM3491  LOC222134 5'  TCTGTGTCTCTCAGGCAAAGCC 79186     AACA_   CCCTT
           A                     TCT    TCTC    TAAAGCCA
                                |||    ||||    ||||||||
                                AGA    AGAG    GTTTCGGT
                                  CACAG   TCC__
GAM3492  BCL2     3'  AAACAGCCTGCAGCTTTGT   79189        AG   GA
                                AAGCAGCC  TGT  CTTTGT
                                ||||||||  |||  ||||||
                                TTTGTCGG  ACG  GAAACA
                                     __  TC
GAM3492  OCLN     3'  TTAAAGCAACCAAAACTTTGT  79190          TGT
                                TTAAAGCAGCCAG   GACTTTGT
                                ||||||||||||   ||||||||
                                AATTTCGTTGGTT   TTGAAACA
                                         ___
GAM3492  SBBI31   3'  AAGCAGAGAGTGGCTTTGT   79191       CC  T   A
                                AAGCAG  AG GTG CTTTGT
                                ||||||  || ||| ||||||
                                TTCGTC  TC CAC GAAACA
                                   __ T   C
GAM3492  LOC150279 3'  TTAAGGCAGCTGTAACTT    79192     A    CAG
                                TTAA GCAGC   TGTGACTT
                                |||| |||||   ||||||||
                                AATT CGTCG   ACATTGAA
                                  C    ___
GAM3493  TFRC     3'  CAACTAAAACTAAAAG      79195        GAATAC
                                TAACTAA     AACTAAAAG
                                |||||||     |||||||||
                                GTTGATT     TTGATTTTC
                                         _______
GAM3493  KIAA1467  3'  TACTAACACAAGCTAAAAGAT  79196    AG      _
                                TA  AATACAA CTAAAAGAT
                                ||  ||||||| |||||||||
                                AT  TTGTGTT GATTTTCTA
                                 GA      C
GAM3493  PREI3    3'  AACTAAGACTTCTTAAAAGAT  79197        ATACAAC
                                AACTAAGA      TAAAAGAT
                                ||||||||      ||||||||
                                TTGATTCT      ATTTTCTA
                                     GAAGA__
GAM3494  CIS4     3'  TTCTAGTTCCATAGGTTT    79200          CGCTGTG
                                TTCTAGTTTC      AGGTTT
                                ||||||||||      ||||||
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                                AAGATCAAGG      TCCAAA
                                    TA_____
GAM3494  BLP1     3'  TTCTATTTCTGCTGAAGATTTT 79201      G   C   T
                                TTCTA TTTC GCTG GAGGTTTT
                                ||||| |||| |||| ||||||||
                                AAGAT AAAG CGAC TTCTAAAA
                                  _   A   _
GAM3494  BLP1     3'  TTCTATTTCTGCTGAAGATTTT 79201      G   C   T
                                TTCTA TTTC GCTG GAGGTTTT
                                ||||| |||| |||| ||||||||
                                AAGAT AAAG CGAC TTCTAAAA
                                  _   A   _
GAM3494  FLJ10830 3'  TTCCAGTTAGTGAGGTTT    79202        TCCGCT
                                TTCTAGTT     GTGAGGTTT
                                ||||||||     |||||||||
                                AAGGTCAA     CACTCCAAA
                                    T_____
GAM3494  PPFIA2   3'  TTCAGTTTTCACAAAGGTTTT  79203     T    C   TGT
                                TTC AGTTT CGC   GAGGTTTT
                                ||| ||||| |||   ||||||||
                                AAG TCAAA GTG   TTCCAAAA
                                  _    A  T__
GAM3494  LOC202181 5'  TTCTAGCTGTGGGGTT      79204      GTTTCC     A
                                TTCTA     GCTGTG GGTT
                                |||||     |||||| ||||
                                AAGAT     CGACAC CCAA
                                  _______     C
GAM3494  LOC202347 5'  TTCTAGTTTCCAGTGGTTT    79205          CT  GA
                                TTCTAGTTTCCG  GT  GGTTT
                                ||||||||||||  ||  |||||
                                AAGATCAAAGGT  CA  CCAAA
                                      __ __
GAM3494  LOC202460 5'  TTCTAGTTTTAGCTGTGACATT 79206         CC      G
                                TTCTAGTTT  GCTGTGA GTT
                                |||||||||  ||||||| |||
                                AAGATCAAA  CGACACT TAA
                                    AT      G
GAM3495  DMD      3'  TAAATTTTTAAACAACCC    79209           TT
                                TAAATTTTTAAACA  CC
                                ||||||||||||||  ||
                                ATTTAAAAATTTGT  GG
                                      TG
GAM3495  DMD      3'  TAAATTTTTAAACAACCC    79209           TT
                                TAAATTTTTAAACA  CC
                                ||||||||||||||  ||
                                ATTTAAAAATTTGT  GG
                                      TG
GAM3495  DMD      3'  TAAATTTTTAAACAACCC    79209           TT
                                TAAATTTTTAAACA  CC
                                ||||||||||||||  ||
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                                ATTTAAAAATTTGT GG
                                      TG
GAM3495 DMD     3' TAAATTTTTAAACAACCC   79209          TT
                                TAAATTTTTAAACA CC
                                |||||||||||||| ||
                                ATTTAAAAATTTGT GG
                                      TG
GAM3495 DMD     3' TAAATTTTTAAACAACCC   79209          TT
                                TAAATTTTTAAACA CC
                                |||||||||||||| ||
                                ATTTAAAAATTTGT GG
                                      TG
GAM3495 DMD     3' TAAATTTTTAAACAACCC   79209          TT
                                TAAATTTTTAAACA CC
                                |||||||||||||| ||
                                ATTTAAAAATTTGT GG
                                      TG
GAM3495 DMD     3' TAAATTTTTAAACAACCC   79209          TT
                                TAAATTTTTAAACA CC
                                |||||||||||||| ||
                                ATTTAAAAATTTGT GG
                                      TG
GAM3495 DMD     3' TAAATTTTTAAACAACCC   79209          TT
                                TAAATTTTTAAACA CC
                                |||||||||||||| ||
                                ATTTAAAAATTTGT GG
                                      TG
GAM3495 DMD     3' TAAATTTTTAAACAACCC   79209          TT
                                TAAATTTTTAAACA CC
                                |||||||||||||| ||
                                ATTTAAAAATTTGT GG
                                      TG
GAM3495 DMD     3' TAAATTTTTAAACAACCC   79209          TT
                                TAAATTTTTAAACA CC
                                |||||||||||||| ||
                                ATTTAAAAATTTGT GG
                                      TG
GAM3495 DMD     3' TAAATTTTTAAACAACCC   79209          TT
                                TAAATTTTTAAACA CC
                                |||||||||||||| ||
                                ATTTAAAAATTTGT GG
                                      TG
GAM3495 DMD     3' TAAATTTTTAAACAACCC   79209          TT
                                TAAATTTTTAAACA CC
                                |||||||||||||| ||
                                ATTTAAAAATTTGT GG
                                      TG
GAM3495 DMD     3' TAAATTTTTAAACAACCC   79209          TT
                                TAAATTTTTAAACA CC
                                |||||||||||||| ||
                                ATTTAAAAATTTGT GG
                                      TG
GAM3495 DMD     3' TAAATTTTTAAACAACCC   79209          TT
                                TAAATTTTTAAACA CC
                                |||||||||||||| ||
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                                ATTTAAAAATTTGT  GG
                                       TG
GAM3495  PRKWNK3   3'  AATTTTTAAACATTTTTAAA   79210          CC
                                AATTTTTAAACATT  TTAAA
                                |||||||||||||  |||||
                                TTAAAAATTTGTAA  AATTT
                                       A_
GAM3495  PTPRB     3'  TAAAATTTTAAACATTCTCC   79211     T       _
                                TAAA TTTTAAACATTC CT
                                |||| ||||||||||| ||
                                ATTT AAAATTTGTAAG GG
                                  T         A
GAM3495  FLJ10724  3'  TTTTAAACATTTTCCTCAAA   79212         __
                                TTTTAAACAT  TCCTTAAA
                                |||||||||  ||||||||
                                AAAATTTGTA  AGGAGTTT
                                      AA
GAM3495  KIAA1610  3'  AATTTTTAAAATACCCTTAAAA 79213        CAT
                                AATTTTTAAA   TCCTTAAAA
                                ||||||||||   |||||||||
                                TTAAAAATTT   GGGAATTTT
                                      TAT
GAM3495  SSH2      3'  AAATTTTTAAATGCCCTTAAAA 79214         CAT
                                AAATTTTTAAA   TCCTTAAAA
                                ||||||||||   |||||||||
                                TTTAAAAATTT   GGGAATTTT
                                       AC_
GAM3496  ADAM12    3'  GGGTAGTTGGGGGACTGCTTT  79217     CTG   A_
                                GGGT   TGGG  ACTGCTTT
                                ||||   ||||  ||||||||
                                CCCA   ACCC  TGACGAAA
                                  TCA    CC
GAM3496  ATP1B1    3'  GGGTACTGCATTGCTTT     79218     _    GGAAC
                                GGGT CTGTG    TGCTTT
                                |||| |||||    ||||||
                                CCCA GACGT    ACGAAA
                                  T    A____
GAM3496  BSN       3'  CAGGGTATGTGGGGGCCTT   79219      C     AACT
                                CAGGGT TGTGGG   GCTTT
                                |||||| ||||||   |||||
                                GTCCCA ACACCC   CGGAA
                                   T     C___
GAM3496  NDUFA10   3'  TACAGGATGGATTGCT      79220       CTGTG  AC
                                TACAGGGT    GGA  TGCT
                                ||||||||    |||  ||||
                                ATGTCCTA    CCT  ACGA
                                     _____   A_
GAM3496  C17orf31  5'  TACAGGGTCTGTGGGAATTGCC 79221             C
            T                   TACAGGGTCTGTGGGAA TGCTT
                                |||||||||||||||| |||||
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                                ATGTCCCAGACACCCTT ACGGA
                                          A
GAM3496  DKFZP761F241 3'  GGGGGCGCAAAACTGCTTT   79222    TC  TG G
                                GGG  TG  G AACTGCTTT
                                |||  ||  | |||||||||
                                CCC  GC  T TTGACGAAA
                                  CC  GT _
GAM3496  FLJ10898  5'  TACAGAGTCACTGGCTGCTTT  79223        TG   GAA
                                TACAGGGTC  TGG   CTGCTTT
                                |||||||||  |||   |||||||
                                ATGTCTCAG  ACC   GACGAAA
                                     TG  ___
GAM3496  GGA2     3'  AAGGCCTGGGAGCTGCTT    79224       GT   A
                                AGGGTCT  GGGA CTGCTT
                                |||||||  |||| ||||||
                                TTCCGGA  CCCT GACGAA
                                   __   C
GAM3496  GGA2     3'  AAGGCCTGGGAGCTGCTT    79224       GT   A
                                AGGGTCT  GGGA CTGCTT
                                |||||||  |||| ||||||
                                TTCCGGA  CCCT GACGAA
                                   __   C
GAM3496  KIAA0418  3'  GGCACCTGGGAACTGCTTT   79225    _ G
                                GGT CT TGGGAACTGCTTT
                                ||| || ||||||||||||
                                CCG GG ACCCTTGACGAAA
                                  T _
GAM3496  SARM     3'  CAGGTTCTGTCTAGGCTGCTTT 79226     G   __  AA
                                CAGG TCTGT  GGG  CTGCTTT
                                |||| |||||  |||  |||||||
                                GTCC AGACA  TCC  GACGAAA
                                  A    GA  __
GAM3496  ZFP106   3'  GCATGGTGTGGAACTGCTTT   79227    CT_  _
                                GT   GTG GGAACTGCTTT
                                ||   ||| ||||||||||
                                CG   CAC CCTTGACGAAA
                                 TAC   A
GAM3496  LOC147929 5'  GGGTCCCGGGCTGCTTT    79228      G   AA
                                GGGTCT TGGG  CTGCTTT
                                |||||| ||||  |||||||
                                CCCAGG GCCC  GACGAAA
                                   _   __
GAM3496  LOC157624 5'  GGGTTGAAAACTGCTTT    79229     CTG  GG
                                GGGT   TG  AACTGCTTT
                                ||||   ||  |||||||||
                                CCCA   AC  TTGACGAAA
                                  ___ TT
GAM3496  LOC199991 5'  TACAGGGTGTTGTGGGGGCT   79230       C_    AACT
                                TACAGGGT  TGTGGG   GCT
                                ||||||||  ||||||   |||
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                                ATGTCCCA  ACACCC   CGA
                                    CA    C___
GAM3496  LOC201749 5'  CAGGGTTTGGGGGAGCT    79231      C  T   ACT
                                CAGGGT TG GGGA   GCT
                                |||||| || ||||  |||
                                GTCCCA AC CCCT   CGA
                                   A  C   ___
GAM3496  LOC90826  5'  CAGGGTTTAGCTTCACTGCTTT 79232      CT_  GGGA
                                CAGGGT   GT   ACTGCTTT
                                ||||||   ||   ||||||||
                                GTCCCA   CG   TGACGAAA
                                   AAT  AAG_
GAM3497  AK1      3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A   ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  ATM      3'  TCGAACTCCTGACCTTGTGAT  79236      AC   A   _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM3497  ATM      3'  TCGAACTCCTGACCTTGTGAT  79236      AC   A   _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM3497  ATP1A2   3'  TCGAACTCCTGACCTCATGAT  79237      AC   A   _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    T
GAM3497  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 79238      AC   A   ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    GTC
GAM3497  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 79238      AC   A   ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    GTC
GAM3497  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 79238      AC   A   ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    GTC
GAM3497  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 79238      AC   A   ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
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                                AGCTTG  GGA TGGAG   ACTA
                                  A_   C    GTC
GAM3497  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 79238      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                  A_   C    GTC
GAM3497  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 79238      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                  A_   C    GTC
GAM3497  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 79238      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                  A_   C    GTC
GAM3497  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 79238      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                  A_   C    GTC
GAM3497  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 79238      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                  A_   C    GTC
GAM3497  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 79238      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                  A_   C    GTC
GAM3497  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 79238      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                  A_   C    GTC
GAM3497  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 79238      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                  A_   C    GTC
GAM3497  C21orf5  3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                  A_   C    TTC
GAM3497  CASP10   3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                  A_   C    TTC
GAM3497  CASP10   3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
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                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  COG7     3'  TCGAACTCCTGGCTTCATGAT  79240      AC   AA   _
                                TCGAAC  CCT  CTTT TGAT
                                ||||||  |||  |||| ||||
                                AGCTTG  GGA  GAAG ACTA
                                   A_   CC   T
GAM3497  COPA     3'  TCGAACTCCTGGCCTCAGAT   79241      AC   AA   T
                                TCGAAC  CCT  CTTT GAT
                                ||||||  |||  |||| |||
                                AGCTTG  GGA  GGAG CTA
                                   A_   CC   T
GAM3497  CPM      3'  GAACTCCTAACCTCAGGGTGAT 79242      AC       ____
                                GAAC  CCTAACTTT   TGAT
                                ||||  |||||||||   ||||
                                CTTG  GGATTGGAG   ACTA
                                  A_       TCCC
GAM3497  DBT      3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  DNASE2   3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  EGFL5    3'  TCGAACTCCTGACCTTGTGAT  79236      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM3497  FANCD2   3'  GAACTCCTGACCTTGTGAT   79243      AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAA ACTA
                                  A_   C    C
GAM3497  FCMD     3'  TCGAACTCCTGGCCTCAAGTGA 79244      AC   AA   ___
            T                    TCGAAC  CCT  CTTT   TGAT
                                ||||||  |||  ||||   ||||
                                AGCTTG  GGA  GGAG   ACTA
                                   A_   CC   TTC
GAM3497  GGCX     3'  TCGAACTCCTGGCCTCAAGTGA 79244      AC   AA   ___
            T                    TCGAAC  CCT  CTTT   TGAT
                                ||||||  |||  ||||   ||||
                                AGCTTG  GGA  GGAG   ACTA
                                   A_   CC   TTC
GAM3497  GPRK7    3'  GAACCCCTGACCTCATGAT   79245     A   A    _
                                GAAC CCCT ACTTT TGAT
                                |||| |||| ||||| ||||
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                                CTTG GGGA TGGAG ACTA
                                  _   C    T
GAM3497  IAPP     3'  TCGAACTCCTGACCTTGTGAT  79236      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM3497  IL1R1    3'  TCGAACTCCTGACCTCTG    79246      AC   A
                                TCGAAC  CCT ACTTTTG
                                ||||||  ||| |||||||
                                AGCTTG  GGA TGGAGAC
                                   A_   C
GAM3497  JAG1     3'  TCAAACACCTTAATTTTG    79247       C   C
                                TCGAACACC TAA TTTTG
                                ||||||||| ||| |||||
                                AGTTTGTGG ATT AAAAC
                                     A   _
GAM3497  LRRC2    3'  TCGAACTCCTGACCTCATGAT  79237      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    T
GAM3497  LUZP1    3'  GAACTCCTGACCTTGTGAT   79243     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAA ACTA
                                  A_   C    C
GAM3497  MCM4     3'  GAACTCCTGACCTCATGAT   79248     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAG ACTA
                                  A_   C    T
GAM3497  MOG      3'  GAACTCCTGACCTCGTGAT   79249     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAG ACTA
                                  A_   C    C
GAM3497  NPHS1    3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TCC
GAM3497  PDE4C    3'  TCGAACTCCTAACCTCAGGTGA 79250      AC      ___
              T                  TCGAAC  CCTAACTTT   TGAT
                                 ||||||  |||||||||   ||||
                                 AGCTTG  GGATTGGAG   ACTA
                                    A_       TCC
GAM3497  PHKB     3'  GAACTCCTAACCTCAAGTGAT  79251     AC      ___
                                 GAAC  CCTAACTTT   TGAT
                                 ||||  |||||||||   ||||
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                                CTTG  GGATTGGAG   ACTA
                                  A_       TTC
GAM3497  PPP1R12B  3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  RAD1      3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  RAD1      3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  RAD1      3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  RBL1      3'  TCGAACTCCTGACTCCGGTGAT 79253      AC   A    __
                                TCGAAC  CCT ACTTT  TGAT
                                ||||||  ||| |||||  ||||
                                AGCTTG  GGA TGAGG  ACTA
                                   A_   C    CC
GAM3497  RSN       3'  TCGAACACACAGTTGATAA   79254       CCTA  TT
                                TCGAACAC   AC  TTGATAA
                                ||||||||   ||  |||||||
                                AGCTTGTG   TG  AACTATT
                                     ____  TC
GAM3497  SIGLEC11  3'  TCGAACTCCTGACTTGTGAT  79255      AC   A   T
                                TCGAAC  CCT ACTT TGAT
                                ||||||  ||| |||| ||||
                                AGCTTG  GGA TGAA ACTA
                                   A_   C    C
GAM3497  SLC17A5   3'  TCGAACTCCTGATCTCATGAT  79256      A  CTAA   T
                                TCGAAC CC    CTT TGAT
                                |||||| ||    ||| ||||
                                AGCTTG GG    GAG ACTA
                                   A  ACTA   T
GAM3497  TBX6      3'  TCGAACTCCTGGCCTCAGGTGA 79257      AC   AA   ___
           T                     TCGAAC  CCT  CTTT   TGAT
                                ||||||  |||  ||||   ||||
                                AGCTTG  GGA  GGAG   ACTA
                                   A_   CC    TCC
GAM3497  TCTA      3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
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                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  TNFRSF1B  3'  TCGAACTCCTAACCTCAGGTGA 79250      AC       ___
             T                   TCGAAC  CCTAACTTT   TGAT
                                 ||||||  |||||||||   ||||
                                AGCTTG  GGATTGGAG   ACTA
                                   A_       TCC
GAM3497  TNFSF14   3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  TPM4     3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  TRPM8    3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  VHL      3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  ZNF264   3'  TCGAACTCCTGGCCTCAGGTGA 79257      AC   AA   ___
             T                   TCGAAC  CCT  CTTT   TGAT
                                 ||||||  |||  ||||   ||||
                                AGCTTG  GGA  GGAG   ACTA
                                   A_   CC   TCC
GAM3497  BLOV1    3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  C20orf106 3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  C21orf108 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  C6orf29   3'  TCGAACTCCTGACTCAGGTGAT 79258      AC   A    T__
                                TCGAAC  CCT ACTT   TGAT
                                ||||||  ||| ||||   ||||
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                                AGCTTG  GGA TGAG   ACTA
                                   A_   C    TCC
GAM3497  C6orf29   3'  TCGAACTCCTGACTCAGGTGAT 79258       AC   A    T__
                                TCGAAC  CCT ACTT   TGAT
                                ||||||  ||| ||||   ||||
                                AGCTTG  GGA TGAG   ACTA
                                   A_   C    TCC
GAM3497  C8orf2    3'  TCGAACTCCTAACCTCAGGTGA 79250       AC       ___
              T                  TCGAAC  CCTAACTTT   TGAT
                                ||||||  |||||||||   ||||
                                AGCTTG  GGATTGGAG   ACTA
                                   A_       TCC
GAM3497  CBCIP2    3'  TCGAACTCCTGACCTCAAGTGA 79239       AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C     TTC
GAM3497  CFLAR     3'  TCGAACTCCTGACCTGAAGTGA 79259       AC   A    T___
              T                  TCGAAC  CCT ACTT    TGAT
                                ||||||  ||| ||||    ||||
                                AGCTTG  GGA TGGA    ACTA
                                   A_   C    CTTC
GAM3497  CSAD      3'  TCGAACTCCTGACCTCAAGTGA 79239       AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C     TTC
GAM3497  DDX31     3'  AACACCCTAATTCACAA     79260         CTT  G
                                AACACCCTAA   TT ATAA
                                ||||||||||   || ||||
                                TTGTGGGATT   AA TGTT
                                     ___  G
GAM3497  DEGS      3'  TCGAACTCCTGACCTCAGGTGA 79235       AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C     TCC
GAM3497  DKFZP564D0764 3'  GAACATCCAACAGTTTGATAAT 79261       CC     T_
                                GAACA  CTAAC  TTTGATAAT
                                |||||  |||||  |||||||||
                                CTTGT  GGTTG  AAACTATTA
                                   A_     TC
GAM3497  DKFZp564K142 3'  TCGAACTCCTGACCTCGTGAT  79252       AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C     C
GAM3497  DKFZP586D2223 3'  TCGAACTCCTGACCTCAGGTGA 79235       AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
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                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  FLJ10460  3'  TCGAACTCCTGACCTCATGAT  79237      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    T
GAM3497  FLJ11726  3'  TCGAACTCCTGACATCGTGAT  79262      AC   A _  T
                                TCGAAC  CCT AC TT TGAT
                                ||||||  ||| || || ||||
                                AGCTTG  GGA TG AG ACTA
                                   A_   C  T  C
GAM3497  FLJ11996  3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  FLJ12294  3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  FLJ12660  3'  GAACTCCTGACCTCATGAT   79248     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAG ACTA
                                  A_   C    T
GAM3497  FLJ12666  3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  FLJ13456  3'  GAACTCCTGACCTTGTGAT   79243     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAA ACTA
                                  A_   C    C
GAM3497  FLJ13952  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  FLJ14075  3'  AACACCCTAACGATGAT     79263         TTT
                                AACACCCTAAC   TGAT
                                ||||||||||   ||||
                                TTGTGGGATTG   ACTA
                                      CT_
GAM3497  FLJ14251  3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
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                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  FLJ14457  3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  FLJ20004  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  FLJ20034  3'  TCGAACTCCTGACCTCAAATGA 79264      AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTT
GAM3497  FLJ20359  3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  FLJ20686  3'  TCGAACTCCTGGCCTCAAGTGA 79244      AC   AA   ___
           T                     TCGAAC  CCT  CTTT   TGAT
                                ||||||  |||  ||||   ||||
                                AGCTTG  GGA  GGAG   ACTA
                                   A_   CC    TTC
GAM3497  FLJ20695  3'  TCGAACTCCTGACTTCAGGTGA 79265      AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGAAG   ACTA
                                   A_   C    TCC
GAM3497  FLJ20802  3'  GAACTCCTGACTTTGTGAT   79266     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGAAA ACTA
                                  A_   C    C
GAM3497  FLJ20825  3'  TCGAACTCCTGACCTCAGAT   79267      AC   A    T
                                TCGAAC  CCT ACTTT GAT
                                ||||||  ||| ||||| |||
                                AGCTTG  GGA TGGAG CTA
                                   A_   C    T
GAM3497  FLJ20972  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  FLJ20972  3'  GAAACCCTAATTCCCAAT    79268     C      C   TG
                                GAA ACCCTAA TTT  AT
                                ||| ||||||| |||  ||
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                                CTT TGGGATT AGG  TA
                                  _     A  GT
GAM3497  FLJ22167  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
           T                     TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                 AGCTTG  GGA TGGAG  ACTA
                                    A_  C    TCC
GAM3497  FLJ22814  3'  TCGAACTCCTGACCTCAAGTGA 79239      AC  A   ___
           T                     TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                 AGCTTG  GGA TGGAG  ACTA
                                    A_  C    TTC
GAM3497  FLJ23499  3'  TCGAACTCCTGACCTCACGTGA 79269      AC  A   ___
           T                     TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                 AGCTTG  GGA TGGAG  ACTA
                                    A_  C    TGC
GAM3497  FLJ32915  5'  GAACTCCTAACCTCAGGTGAT  79270     AC      ___
                                 GAAC  CCTAACTTT  TGAT
                                 ||||  |||||||||  ||||
                                 CTTG  GGATTGGAG  ACTA
                                   A_       TCC
GAM3497  FUSIP1    3'  TCAGACATCCTAGTTTCCAATA 79271    A  C   AC  TG
           AT                    TCG ACA CCTA  TTT  ATAAT
                                 |||  ||| ||||  |||  |||||
                                 AGT TGT GGAT  AAG  TATTA
                                   C  A   CA  GT
GAM3497  FUSIP1    3'  TCGAACTCCTGACCTCGTGAT  79252      AC  A   _
                                 TCGAAC  CCT ACTTT TGAT
                                 ||||||  ||| ||||| ||||
                                 AGCTTG  GGA TGGAG ACTA
                                    A_  C    C
GAM3497  HIG2      3'  TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
           T                     TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                 AGCTTG  GGA TGGAG  ACTA
                                    A_  C    TCC
GAM3497  IL-23R    3'  TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
           T                     TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                 AGCTTG  GGA TGGAG  ACTA
                                    A_  C    TCC
GAM3497  KIAA0057  3'  GAACTCCTAACCTCAGGTGAT  79270     AC      ___
                                 GAAC  CCTAACTTT  TGAT
                                 ||||  |||||||||  ||||
                                 CTTG  GGATTGGAG  ACTA
                                   A_       TCC
GAM3497  KIAA0355  3'  TCGAACTCCTGACCTTAGGTGA 79272      AC  A   ___
           T                     TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
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                                AGCTTG  GGA TGGAA   ACTA
                                   A_   C    TCC
GAM3497  KIAA0441  3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  KIAA0447  3'  TCGAACTCCTGGCCTTGTGAT  79273      A  CTAA   T
                                TCGAAC CC    CTT TGAT
                                |||||| ||    ||| ||||
                                AGCTTG GG    GAA ACTA
                                   A  ACCG   C
GAM3497  KIAA0475  3'  TCGAACTCCTGGCCTCAGGTGA 79257      AC   AA   ___
            T                    TCGAAC  CCT  CTTT   TGAT
                                ||||||  |||  ||||   ||||
                                AGCTTG  GGA  GGAG   ACTA
                                   A_   CC    TCC
GAM3497  KIAA0565  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  KIAA0596  3'  TCGAACTCCTAACCTCAGGTGA 79250      AC       ___
            T                    TCGAAC  CCTAACTTT   TGAT
                                ||||||  |||||||||   ||||
                                AGCTTG  GGATTGGAG   ACTA
                                   A_       TCC
GAM3497  KIAA0872  3'  TCGAACTCCTAACCTCGTGAT  79274      AC       _
                                TCGAAC  CCTAACTTT TGAT
                                ||||||  ||||||||| ||||
                                AGCTTG  GGATTGGAG ACTA
                                   A_       C
GAM3497  KIAA0884  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  KIAA0953  3'  GAACTCCTAACCTCAGGTGAT  79270     AC       ___
                                GAAC  CCTAACTTT   TGAT
                                ||||  |||||||||   ||||
                                CTTG  GGATTGGAG   ACTA
                                  A_       TCC
GAM3497  KIAA1130  3'  TCGAACTCCTGACCTCATGAT  79237      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    T
GAM3497  KIAA1164  3'  TCGAACTCCTGGCCTCAGAT   79241      AC   AA   T
                                TCGAAC  CCT  CTTT GAT
                                ||||||  |||  |||| |||
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                                AGCTTG  GGA  GGAG CTA
                                   A_   CC    T
GAM3497  KIAA1404  3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  KIAA1586  5'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TTC
GAM3497  KIAA1614  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TCC
GAM3497  KIAA1630  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TCC
GAM3497  KIAA1715  3'  TCGAACTCCTGACCCCAGAT   79275      AC   A   TT
                                TCGAAC  CCT ACTT  GAT
                                ||||||  ||| ||||  |||
                                AGCTTG  GGA TGGG  CTA
                                   A_   C    GT
GAM3497  KIAA1829  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TCC
GAM3497  KIAA1872  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TCC
GAM3497  LIAS      3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TCC
GAM3497  MAWBP     3'  TCGAACCCCTGACCTCAGGTGA 79276       A   A    ___
             T                   TCGAAC CCCT ACTTT   TGAT
                                 ||||||  |||| |||||   ||||
                                 AGCTTG GGGA TGGAG   ACTA
                                    _    C    TCC
GAM3497  MGC10765  3'  TCGAACTCCTGACCTTGTGAT  79236      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
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                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM3497  MGC14126  3'  TCGAACTCCTGACCTTAGGTGA 79272      AC   A    ___
           T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAA   ACTA
                                   A_   C    TCC
GAM3497  MGC14799  3'  TCGAACTCCTGACCTCATGAT  79237      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    T
GAM3497  MGC16037  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
           T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  MGC16385  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
           T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  MGC29937  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
           T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  MGC39350  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
           T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  MGC4771   3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  MGC5457   3'  TCGAACTCCTGACCTTGTGAT  79236      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM3497  MYO3B     3'  TCGAACTCCTGACTTCATGAT  79277      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGAAG ACTA
                                   A_   C    T
GAM3497  NPTXR     3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
           T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
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                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  NPTXR    3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
              T                    TCGAAC  CCT ACTTT   TGAT
                                   ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  OCLM     5'  TCGAACTCCTGACCTCAGAT   79267      AC   A    T
                                TCGAAC  CCT ACTTT GAT
                                ||||||  ||| ||||| |||
                                AGCTTG  GGA TGGAG CTA
                                   A_   C    T
GAM3497  PB1      3'  TCGAACTCCTGACCTCAGGTAA 79279      AC   A    TGA
              T                    TCGAAC  CCT ACTTT   TAAT
                                   ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ATTA
                                   A_   C    TCC
GAM3497  PB1      3'  TCGAACTCCTGATCTCGTGAT  79278      A  CTAA   T
                                TCGAAC CC    CTT TGAT
                                |||||| ||    ||| ||||
                                AGCTTG GG    GAG ACTA
                                   A  ACTA   C
GAM3497  PRIC285  3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
              T                    TCGAAC  CCT ACTTT   TGAT
                                   ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  PRO2198  5'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
              T                    TCGAAC  CCT ACTTT   TGAT
                                   ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  PRO2893  3'  TCGAACTCCTGACCTCAGAT   79267      AC   A    T
                                TCGAAC  CCT ACTTT GAT
                                ||||||  ||| ||||| |||
                                AGCTTG  GGA TGGAG CTA
                                   A_   C    T
GAM3497  SCYA5    3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
              T                    TCGAAC  CCT ACTTT   TGAT
                                   ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  SPRY4    3'  GAACTCCTGACCTCGTGAT   79249     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAG ACTA
                                  A_   C    C
GAM3497  SPRY4    3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
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                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  SYAP1    3'  TCGAACTCCTGACCTCCG    79280       AC   A
                                TCGAAC  CCT ACTTTTG
                                ||||||  ||| |||||||
                                AGCTTG  GGA TGGAGGC
                                   A_   C
GAM3497  THEA     3'  TCGAACTCCTGACCTCAGGTGA 79235       AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  UBCE7IP5 3'  TCGAACTCCTGACCTCAAGTGA 79239       AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  WBSCR23  3'  TCGAACTCCTGACTTGAGGTGA 79281       AC   A   T___
           T                     TCGAAC  CCT ACTT    TGAT
                                ||||||  ||| ||||    ||||
                                AGCTTG  GGA TGAA    ACTA
                                   A_   C   CTCC
GAM3497  ZAK      3'  TCGAACCCCTGACATCAGGTGA 79282       A   A  TTT___
           T                     TCGAAC CCCT AC     TGAT
                                ||||||| |||| ||     ||||
                                AGCTTG GGGA TG     ACTA
                                   _   C  TAGTCC
GAM3497  ZIM3     3'  TCGAACTCCTGACCTCAGGTGA 79235       AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  ZNF297B  5'  TCGAACTCCTGACCGCATGAT  79283       AC   A  TT_
                                TCGAAC  CCT ACT   TGAT
                                ||||||  ||| |||   ||||
                                AGCTTG  GGA TGG   ACTA
                                   A_   C  CGT
GAM3497  ZNF333   3'  TCGAACTCCTGACCTCAGGTGA 79235       AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  ZNF33A   3'  TCGAACTCCTGACCTTGTGAT  79236       AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM3497  LOC115129 5'  TCGAACTCCTGGCCTCAAGTGA 79244       AC   AA   ___
           T                     TCGAAC  CCT  CTTT   TGAT
                                ||||||  |||  ||||   ||||
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                                AGCTTG  GGA  GGAG   ACTA
                                   A_   CC    TTC
GAM3497  LOC115273 3'  TCGAACCCCTGACCTCAGGTGA 79276      A   A    ___
            T                   TCGAAC CCCT ACTTT   TGAT
                                |||||| |||| |||||   ||||
                                AGCTTG GGGA TGGAG   ACTA
                                   _   C    TCC
GAM3497  LOC121504 3'  TCGGGGCCCTAACTTTCA    79284     AACA
                                TCG   CCCTAACTTTTG
                                |||   ||||||||||||
                                AGC   GGGATTGAAAGT
                                  CCC_
GAM3497  LOC122704 3'  TCGAACTCCTGATCTTGTGAT  79285      A  CTAA   T
                                TCGAAC CC   CTT TGAT
                                |||||| ||   ||| ||||
                                AGCTTG GG   GAA ACTA
                                   A  ACTA   C
GAM3497  LOC124602 3'  TCGAACTCCTGGCCTCAAGTGA 79244      AC   AA   ___
            T                   TCGAAC  CCT  CTTT   TGAT
                                ||||||  |||  ||||   ||||
                                AGCTTG  GGA  GGAG   ACTA
                                   A_   CC    TTC
GAM3497  LOC130951 3'  TCGAACTCCTGGCCTCAAGTGA 79244      AC   AA   ___
            T                   TCGAAC  CCT  CTTT   TGAT
                                ||||||  |||  ||||   ||||
                                AGCTTG  GGA  GGAG   ACTA
                                   A_   CC    TTC
GAM3497  LOC132332 5'  GAACACCCTGACTTTTCAATA  79286       A    _
                                GAACACCCT ACTTTT GATA
                                ||||||||| |||||| ||||
                                CTTGTGGGA TGAAAA TTAT
                                     C     G
GAM3497  LOC138241 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
            T                   TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  LOC144289 3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
            T                   TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  LOC144486 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
            T                   TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  LOC144524 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
            T                   TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
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                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  LOC145216 3'  GAAATCCTAACCCTTAA    79287    CAC
                                GAA   CCTAACTTTTGA
                                |||   ||||||||||||
                                CTT   GGATTGGGAATT
                                  TA_
GAM3497  LOC145231 3'  TCGAACTCCTGACCTCATGAT  79237      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    T
GAM3497  LOC145453 3'  TCGAACTCCTAACCTCAGGTGA 79250      AC       ___
            T                    TCGAAC  CCTAACTTT   TGAT
                                ||||||  |||||||||   ||||
                                AGCTTG  GGATTGGAG   ACTA
                                   A_       TCC
GAM3497  LOC145662 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  LOC146229 3'  GAACTCCTGACCTCGTGAT   79249     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAG ACTA
                                  A_   C    C
GAM3497  LOC146669 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  LOC146923 3'  TCGAACTCCTGACCTTGTGAT  79236      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM3497  LOC146975 5'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  LOC147599 3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
            T                    TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  LOC147727 5'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
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                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  LOC148534 3'  TCGAACTCCTGACCTCAGTGAT 79288      AC   A    __
                                TCGAAC  CCT ACTTT  TGAT
                                ||||||  ||| |||||  ||||
                                AGCTTG  GGA TGGAG  ACTA
                                   A_   C    TC
GAM3497  LOC148758 5'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TCC
GAM3497  LOC148946 3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TTC
GAM3497  LOC149668 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TCC
GAM3497  LOC149710 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TCC
GAM3497  LOC150358 3'  TCGAACTCCTGACCTTGTGAT  79236      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM3497  LOC151196 3'  GAACCCCTGACCTCAGTGAT   79289     A    A    __
                                GAAC CCCT ACTTT  TGAT
                                |||| |||| |||||  ||||
                                CTTG GGGA TGGAG  ACTA
                                  _    C    TC
GAM3497  LOC151602 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TCC
GAM3497  LOC151632 3'  TCGAACTCCTGACCTAAGGTGA 79290      AC   A    T___
              T                  TCGAAC  CCT ACTT    TGAT
                                 ||||||  ||| ||||    ||||
                                 AGCTTG  GGA TGGA    ACTA
                                    A_   C    TTCC
GAM3497  LOC152283 3'  TCGAACTCCTGACCTTCG    79291       AC   A
                                TCGAAC  CCT ACTTTTG
                                ||||||  ||| |||||||
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                                AGCTTG  GGA TGGAAGC
                                   A_   C
GAM3497  LOC152453 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
             T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  LOC153260 3'  TCGAACTCCTGACCTTGTGAT  79236      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM3497  LOC157660 3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  LOC158187 3'  GAACTCCTGACCTCGTGAT   79249     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAG ACTA
                                  A_   C    C
GAM3497  LOC158450 5'  GAACACCCCTGGTCTATGGGAT 79292        AA__  TTT_
             A                  GAACACCCT   CT   GATA
                                |||||||||   ||   ||||
                                CTTGTGGGG   GA   CTAT
                                     ACCA  TACC
GAM3497  LOC158504 5'  GAACACCCCTGGTCTATGGGAT 79292        AA__  TTT_
             A                  GAACACCCT   CT   GATA
                                |||||||||   ||   ||||
                                CTTGTGGGG   GA   CTAT
                                     ACCA  TACC
GAM3497  LOC158677 5'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
             T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  LOC158819 3'  GAACTCCTGACCTCGTGAT   79249     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAG ACTA
                                  A_   C    C
GAM3497  LOC158819 5'  GAACTCCTAACCTCAAGTGAT  79251     AC       ___
                                GAAC  CCTAACTTT   TGAT
                                ||||  |||||||||   ||||
                                CTTG  GGATTGGAG   ACTA
                                  A_       TTC
GAM3497  LOC196761 3'  TCGAACTCCTAACCTCAAGTGA 79293      AC       ___
             T                  TCGAAC  CCTAACTTT   TGAT
                                ||||||  |||||||||   ||||
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                                AGCTTG  GGATTGGAG   ACTA
                                   A_       TTC
GAM3497  LOC197196 3'  TCGAACTCCTAACCTCAGGTGA 79250      AC       ___
             T                  TCGAAC  CCTAACTTT   TGAT
                                ||||||  |||||||||   ||||
                                AGCTTG  GGATTGGAG   ACTA
                                   A_       TCC
GAM3497  LOC200251 5'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
             T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  LOC201810 3'  GAACCCCTGACCTCGTGAT   79294     A   A    _
                                GAAC CCCT ACTTT TGAT
                                |||| |||| ||||| ||||
                                CTTG GGGA TGGAG ACTA
                                  _   C    C
GAM3497  LOC201895 3'  TCGAACTCCTGACCTCAAGTGA 79239      AC   A    ___
             T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM3497  LOC201917 5'  GAACACCCTGACAGGAATGAT  79295        A  TTT__
                                GAACACCCT AC    TGAT
                                |||||||||  ||    ||||
                                CTTGTGGGA TG    ACTA
                                     C  TCCTT
GAM3497  LOC203378 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
             T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  LOC203397 3'  TCGAACTCCTGGCCTCAAGTGA 79244      AC   AA   ___
             T                  TCGAAC  CCT  CTTT   TGAT
                                ||||||  |||  ||||   ||||
                                AGCTTG  GGA  GGAG   ACTA
                                   A_   CC    TTC
GAM3497  LOC220662 3'  TCGAACTCCTGACCTCGTGAT  79252      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM3497  LOC221178 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC   A    ___
             T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM3497  LOC221490 3'  GAACTCCTGACCTTGTGAT   79243     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
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                                CTTG  GGA TGGAA ACTA
                                  A_  C    C
GAM3497  LOC221766 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
             T                   TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                AGCTTG  GGA TGGAG  ACTA
                                   A_  C    TCC
GAM3497  LOC221954 5'  TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
             T                   TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                AGCTTG  GGA TGGAG  ACTA
                                   A_  C    TCC
GAM3497  LOC253639 3'  TCGAACTCCTGACCTCATGAT  79237      AC  A   _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_  C    T
GAM3497  LOC253840 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
             T                   TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                AGCTTG  GGA TGGAG  ACTA
                                   A_  C    TCC
GAM3497  LOC255042 3'  GAACTCCTGACCTCATGAT   79248     AC  A   _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAG ACTA
                                  A_  C    T
GAM3497  LOC255177 3'  TCGAACTCCTGACCTTGTGAT  79236      AC  A   _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_  C    C
GAM3497  LOC255196 3'  TCGAACTCCTGACCTCAAGTGA 79239      AC  A   ___
             T                   TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                AGCTTG  GGA TGGAG  ACTA
                                   A_  C    TTC
GAM3497  LOC255328 3'  GAACTCCTGACCTCGTGAT   79249     AC  A   _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAG ACTA
                                  A_  C    C
GAM3497  LOC256207 3'  TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
             T                   TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                AGCTTG  GGA TGGAG  ACTA
                                   A_  C    TCC
GAM3497  LOC256946 3'  TCAGACATCCTAGTTTCCAATA 79271    A  C   AC  TG
             AT                   TCG ACA CCTA  TTT  ATAAT
                                  ||| ||| ||||  |||  |||||
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                                AGT TGT GGAT  AAG  TATTA
                                  C  A   CA   GT
GAM3497 LOC51333 3' TCGAACTCCTAACCTCAAGTGA 79293      AC      ___
             T                   TCGAAC  CCTAACTTT   TGAT
                                 ||||||  |||||||||   ||||
                                 AGCTTG  GGATTGGAG   ACTA
                                    A_       TTC
GAM3497 LOC90092 3' TCGAACTCCTGACCTTGTGAT  79236      AC  A   _
                                 TCGAAC  CCT ACTTT TGAT
                                 ||||||  ||| ||||| ||||
                                 AGCTTG  GGA TGGAA ACTA
                                    A_  C    C
GAM3497 LOC90155 5' TCGAACTCCTGACCTCAAGTGA 79239      AC  A   ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_  C    TTC
GAM3497 LOC90591 3' TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_  C    TCC
GAM3497 LOC90624 3' TCGAACTCCTGACCTTGTGAT  79236      AC  A   _
                                 TCGAAC  CCT ACTTT TGAT
                                 ||||||  ||| ||||| ||||
                                 AGCTTG  GGA TGGAA ACTA
                                    A_  C    C
GAM3497 LOC91380 3' TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_  C    TCC
GAM3497 LOC91442 3' GAACTCCTGACCTCAGAT    79296     AC  A    T
                                 GAAC  CCT ACTTT GAT
                                 ||||  ||| ||||| |||
                                 CTTG  GGA TGGAG CTA
                                   A_  C    T
GAM3497 LOC91796 5' TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_  C    TCC
GAM3497 LOC92223 3' TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_  C    TCC
GAM3497 LOC92228 3' TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
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                                AGCTTG  GGA TGGAG   ACTA
                                   A_  C    TCC
GAM3497  LOC96597  5'  TCGAACTCCTGACCTCAGGTGA 79235      AC  A   ___
             T                   TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_  C    TCC
GAM3498  RAD52    3'  CCTGTCGTGATCCACAGT    79299    GC_     AT
                                CC   CGTGATCC  GCGGT
                                ||   ||||||||  |||||
                                GG   GCACTAGG  TGTCA
                                 ACA      __
GAM3498  RAD52    3'  CCTGTCGTGATCCACAGT    79299    GC_     AT
                                CC   CGTGATCC  GCGGT
                                ||   ||||||||  |||||
                                GG   GCACTAGG  TGTCA
                                 ACA      __
GAM3498  RAD52    3'  CCTGTCGTGATCCACAGT    79299    GC_     AT
                                CC   CGTGATCC  GCGGT
                                ||   ||||||||  |||||
                                GG   GCACTAGG  TGTCA
                                 ACA      __
GAM3498  RAD52    3'  CCTGTCGTGATCCACAGT    79299    GC_     AT
                                CC   CGTGATCC  GCGGT
                                ||   ||||||||  |||||
                                GG   GCACTAGG  TGTCA
                                 ACA      __
GAM3499  KL       3'  GGTTTATCTTGCCTGATACA   79302       A  AA  A
                                GGTTTATC TT  TT ATACA
                                ||||||||  ||  ||  |||||
                                CCAAATAG AA  GA TATGT
                                     _  CG  C
GAM3499  C6orf5   3'  GGCTTTAATCCATTAATACA   79303      ATC   A
                                GGTTT   ATT ATTAATACA
                                |||||   ||| |||||||||
                                CCGAA   TAG TAATTATGT
                                   AT_   G
GAM3499  LOC148195 3'  GGTTTATCAGTTACATAAGTAC 79304        _   AT   _
             A                   GGTTTATCA TTA  TAA TACA
                                 |||||||||  |||  ||| ||||
                                 CCAAATAGT AAT  ATT ATGT
                                      C   GT   C
GAM3499  LOC151405 5'  CCGGGTGTCATTAATTAATGCA 79305     TTTA        A
                                CCGG    TCATTAATTAAT CA
                                ||||    |||||||||||| ||
                                GGCC    AGTAATTAATTA GT
                                  CAC_          C
GAM3499  LOC152015 3'  GGTTTATCATTCTGAAGTACA  79306          AATTAA
                                GGTTTATCATT     TACA
                                ||||||||||      ||||
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                                CCAAATAGTAA     ATGT
                                      GACTTC
GAM3500  DKFZP434H132 3'  AGGTTGCGTTGTCCCATTTTAC 79309       T  C       C
                                AGGTTG CG TGTCCCAT TTAT
                                |||||| || |||||||| ||||
                                TCCAAC GC ACAGGGTA AATG
                                   _ A       A
GAM3500  DKFZP434H132 3'  AGGTTGCGTTGTCCCATTTTAC 79309       T  C       C
                                AGGTTG CG TGTCCCAT TTAT
                                |||||| || |||||||| ||||
                                TCCAAC GC ACAGGGTA AATG
                                   _ A       A
GAM3500  KIAA1032  3'  GGGTCTGGGTCCCATCTTATG  79310    TT   GCT
                                GG  GTC   GTCCCATCTTATG
                                ||  |||   ||||||||||||||
                                CC  CAG   CAGGGTAGAATAC
                                 __   ACC
GAM3500  MGC20576  3'  GGCTGTCGCTGTTCTT      79311           CCCA
                                GGTTGTCGCTGT    TCTT
                                ||||||||||||    ||||
                                CCGACAGCGACA    AGAA
                                          ____
GAM3501  KIAA1580  5'  AACATACTTTTTTCTTTGTG   79314      CG
                                AATAT  TTTTTTCTTTGTG
                                |||||  ||||||||||||||
                                TTGTA  AAAAAAGAAACAC
                                   TG
GAM3501  LOC138399 5'  TATCGTTTTCTTTATG      79315        TT
                                TATCGTTT  TCTTTGTG
                                ||||||||  ||||||||
                                ATAGCAAA  AGAAATAC
                                          __
GAM3501  LOC144932 3'  TGATCATCCTTCTTTGTG    79316   T       T
                                A ATCGTTTTT CTTTGTG
                                | |||||||||| |||||||
                                A TAGTAGGAA GAAACAC
                                 C       _
GAM3501  LOC167147 5'  CAATGTCGTTACATCTTTGTG  79317     A    TTT
                                TAAT TCGTT   TCTTTGTG
                                |||| |||||   ||||||||
                                GTTA AGCAA   AGAAACAC
                                   C    TGT
GAM3502  BRCA1    3'  CATTATCAACTGGCTT      79320          CATCAA
                                CATTATCAACT     GCTT
                                ||||||||||     ||||
                                GTAATAGTTGA     CGAA
                                      C_____
GAM3502  CLASP2   3'  TACATTATTAACTTTTTCAAG  79321        C   CA_
                                TACATTAT AACT   TCAAG
                                |||||||| ||||   |||||
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                                ATGTAATA TTGA   AGTTC
                                    A    AAA
GAM3502 IL18RAP  3' CATTGTCCATCAAGCTT     79322      A  AACT
                                CATT TC    CATCAAGCTT
                                |||| ||    ||||||||||
                                GTAA AG    GTAGTTCGAA
                                  C _____
GAM3502 NAPB     3' TACATTCATTCTCAAGCTT    79323       TA   AC  A
                                TACAT  TCA  TC TCAAGCTT
                                |||||  |||  || ||||||||
                                ATGTA  AGT  AG AGTTCGAA
                                   __   A_  _
GAM3502 NESCA    3' TACATTATCAATACAGGCAACT 79324           CT  TCA
             T                   TACATTATCAA  CA   AGCTT
                                ||||||||||  ||   |||||
                                ATGTAATAGTT  GT   TTGAA
                                      AT  CCG
GAM3502 LOC222233 5' TTATCAATTCTCAAGCCTA    79325        C  A
                                TTATCAA TC TCAAGCTTA
                                ||||||| || |||||||||
                                AATAGTT AG AGTTCGGAT
                                    A  _
GAM3503 DDX11    3' AATGTGATCTCGGGGTGGG    79328           CT_  C
                                AATGTGATCTTG   TG GG
                                ||||||||||||   || ||
                                TTACACTAGAGC   AC CC
                                      CCC  _
GAM3503 SERPINB13 3' ATGTGATCTTGTTAAAAACTGG 79329           CTT___  _
             AG                   ATGTGATCTTG     GC GGAG
                                ||||||||||      || ||||
                                TACACTAGAAC     TG CCTC
                                      AATTTT  A
GAM3503 DKFZP727C091 3' ATGTGATCATACAGGAG     79330        T   TTGC
                                ATGTGATC TGC    GGAG
                                |||||||| |||    ||||
                                TACACTAG ATG    CCTC
                                    T   T___
GAM3503 FLJ11320  3' ACAATGTGATGTTAGGGACTGG 79331          C   CTT  _
                                ACAATGTGAT TTG   GC GG
                                |||||||||| |||   || ||
                                TGTTACACTA AAT   TG CC
                                     C   CCC  A
GAM3503 HPCAL4   3' ACTATGTGATCTTGCACAAGG  79332    A         TTGC
                                AC ATGTGATCTTGC    GG
                                || ||||||||||||    ||
                                TG TACACTAGAACG    CC
                                 A          TGTT
GAM3503 KIAA1371  3' ATGTAATCTTGCTTTGG     79333            GC
                                ATGTGATCTTGCTT  GG
                                ||||||||||||||  ||
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                                TACATTAGAACGAA  CC
                                       A_
GAM3503  PCDH19   3'  ACAATGTGTTTTGCTCTGG   79334        ATC     GC
                                ACAATGTG   TTGCTT  GG
                                ||||||||   ||||||  ||
                                TGTTACAC   AACGAG  CC
                                     AA_     A_
GAM3503  PRO1855  3'  ACAGTGTGATCCTTGTTTGTGC 79335     A       GCT___
                                ACA TGTGATCTT      TGC
                                ||| |||||||||      |||
                                TGT ACACTAGGA      ACG
                                  C        ACAAAC
GAM3503  LOC151507 3'  AACAATGTGGTTCTTGCT    79336         A_
                                AACAATGTG  TCTTGCT
                                |||||||||  |||||||
                                TTGTTACAC  AGAACGA
                                     CA
GAM3503  LOC80298  5'  AATGTGATCTTGTCAG      79337          CTTG
                                AATGTGATCTTG    CGG
                                ||||||||||||    |||
                                TTACACTAGAAC    GTC
                                       A___
GAM3504  FLJ23153  5'  CGCGCCGCGGGCCGGGCGG    79340          ACAT  A
                                CGCGCCGCGGGC    GG CGG
                                ||||||||||||    || |||
                                GCGCGGCGCCCG    CC GCC
                                       GC__  _
GAM3504  LOC166867 5'  TTCCCGCCGCGGGGGGACG    79341     G       CACAT
                                TTC CGCCGCGGG     GGACG
                                |||  |||||||||     |||||
                                AAG GCGGCGCCC     CCTGC
                                  G        C____
GAM3504  LOC91179  5'  TCCGCGCCGTGGAGTCCGGGCG 79342         C   CACA   A
            G                    TTCGCGCCG GGG    TGG CGG
                                |||||||||  |||    |||  |||
                                AGGCGCGGC CCT    GCC GCC
                                     A   CAG_   C
GAM3505  SCA1     3'  TTTAAGAATTGTAAGTGGGGGT 79345         GAA    A  A
                                TTTAAGAAT   TGAG TG GGGT
                                |||||||||   ||||  ||  ||||
                                AAATTCTTA   ATTC AC CCCA
                                     AC_    _  C
GAM3505  SERPINF2  3'  GAAGAAAGATGAGGG       79346     T  AT
                                GAA GA  GAGATGAGGG
                                |||  ||  ||||||||||
                                CTT CT  TTCTACTCCC
                                  _  ___
GAM3505  CHCR     3'  TTTAAGAAGAGTGAATTAGGG  79347         T  A    ATG
                                TTTAAGAA GA TGAG   AGGG
                                ||||||||  ||  ||||   ||||
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                                AAATTCTT CT ACTT   TCCC
                                    _ C    AA_
GAM3505 HCA127    3' CTTAAGGATGAGATGAGGG    79348       AAT  A
                                TTTAAG   GA TGAGATGAGGG
                                ||||||   || ||||||||||
                                GAATTC   CT ACTCTACTCCC
                                   ___  _
GAM3505 KIAA1030  3' CTTAGGAATGAATGAGAT     79349      A
                                TTTA GAATGAATGAGAT
                                |||| ||||||||||||
                                GAAT CTTACTTACTCTA
                                  C
GAM3505 MGC10067  3' TTTAGGAATGAATCAGTGATAT 79350      A       G  A   GG_
             GT                   TTTA GAATGAAT AG TGA   GT
                                |||| |||||||| || |||   ||
                                AAAT CTTACTTA TC ACT   CA
                                  C       G _   ATA
GAM3505 MGC3180   3' GAATGAATGGGAAAAGGGT    79351         A  T
                                GAATGAATG GA GAGGGT
                                ||||||||| || ||||||
                                CTTACTTAC CT TTCCCA
                                     C  T
GAM3505 NS1-BP    3' TTTAGTAATGAATGAGTG     79352      AG        A
                                TTTA  AATGAATGAG TG
                                ||||  |||||||||| ||
                                AAAT  TTACTTACTC AC
                                  CA         _
GAM3505 STRAIT11499 3' GAGGAATGAGAGAGGG      79353    AT       T
                                GA  GAATGAGA GAGGG
                                ||  |||||||| |||||
                                CT  CTTACTCT CTCCC
                                 C_       _
GAM3505 LOC91650  5' TTTAAAACATTGGATGAGGGT  79354        ATGAA  A
                                TTTAAGA     TG GATGAGGGT
                                |||||||     || |||||||||
                                AAATTTT     AC CTACTCCCA
                                    GTA__  _
GAM3506 GNRH1     5' TTTCATTCCTGAGATAGA     79357     G   A_
                                TTT ATT  TGAGATAGA
                                ||| |||  |||||||||
                                AAA TAA  ACTCTATCT
                                  G   GG
GAM3506 LSS       3' TTCACATCTATGAGATAGAG   79358         TGAT
                                TTCACATT    TATGAGATAGAG
                                ||||||||    ||||||||||||
                                AAGTGTAG    ATACTCTATCTC
                                     _____
GAM3506 MTM1      3' TTCACATTTGGATTCATCTTAG 79359          _   ATGAGA
             AG                   TTCACATTTG ATT      TAGAG
                                |||||||||| |||      |||||
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                                AAGTGTAAAC TAA     ATCTC
                                     C   GTAGA_
GAM3506  SCA1     5'  TCACATTTGATTTCTGTAG   79360          A_ _
                                TCACATTTGATT  TG AG
                                ||||||||||||  || ||
                                AGTGTAAACTAA  AC TC
                                   AG  A
GAM3506  SLC6A8   3'  TTCACCTTTGCTAAGAGATAGA 79361      A   A   T
            G                    TTCAC TTTG TTA GAGATAGAG
                                ||||| |||| ||| |||||||||
                                AAGTG AAAC GAT CTCTATCTC
                                  G   _  T
GAM3506  FLJ11252 3'  CATTTGACTTAGAATCAGAG   79362        AT   A
                                CATTTGATT  GAG TAGAG
                                |||||||||  ||| |||||
                                GTAAACTGA  CTT GTCTC
                                     AT   A
GAM3506  KIAA0907  3'  ATTTATTTATGAGATGGAG   79363      A       A
                                ATTTG TTATGAGAT GAG
                                ||||| |||||||||| |||
                                TAAAT AATACTCTA CTC
                                  A       C
GAM3506  SIPL     3'  TTTAATTACTGAGATAGA    79364        _
                                TTTGATTA TGAGATAGA
                                ||||||||| |||||||||
                                AAATTAAT ACTCTATCT
                                     G
GAM3506  STAG3    3'  TCACATTCTTGAGGTAG     79365        GATTA   A
                                TCACATTT    TGAG TAG
                                ||||||||    |||| |||
                                AGTGTAAG    ACTC ATC
                                     A____   C
GAM3506  LOC144559 3'  ATTTGTGAGATAGAG      79366      ATTA
                                ATTTG   TGAGATAGAG
                                |||||   ||||||||||
                                TAAAC   ACTCTATCTC
                                     ____
GAM3506  LOC146488 3'  TTCACCTTTGCTAAGAGATAGA 79361      A   A   T
            G                    TTCAC TTTG TTA GAGATAGAG
                                ||||| |||| ||| |||||||||
                                AAGTG AAAC GAT CTCTATCTC
                                  G   _  T
GAM3506  LOC90906 3'  TCTCTTTGTGAGATAGAG   79367   ACA   ATTA
                                TC  TTTG   TGAGATAGAG
                                ||  ||||   ||||||||||
                                AG  AAAC   ACTCTATCTC
                                 AG_   ____
GAM3507  CCND3    3'  CTAGACTATTCCCCCTCATA  79370       C   AG
                                TTAGACTA TCT  TTCATA
                                |||||||| |||  ||||||
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                                GATCTGAT AGG  GAGTAT
                                     A   GG
GAM3507  DAZL     3'  AACTGCTCTGCTCATAC     79371      A    A
                                GACT CTCT GTTCATAC
                                |||| |||| ||||||||
                                TTGA GAGA CGAGTATG
                                  C   _
GAM3507  PLS1     3'  TTAGACTACTCATTCAC     79372           TA
                                TTAGACTACTC  GTTCAT
                                ||||||||||  ||||||
                                AATCTGATGAG  TAAGTG
                                          __
GAM3507  B3GNT1   3'  TTAAACTCTAGTAGTTCATAC  79373       ACTC
                                TTAGACT    TAGTTCATAC
                                |||||||    ||||||||||
                                AATTTGA    ATCAAGTATG
                                     GATC
GAM3507  B3GNT1   3'  TTAAACTCTAGTAGTTCATAC  79373       ACTC
                                TTAGACT    TAGTTCATAC
                                |||||||    ||||||||||
                                AATTTGA    ATCAAGTATG
                                     GATC
GAM3507  CST8     5'  TCAGCACTCTTAGTTCAT    79374      AC     _
                                TTAG  TACTCT AGTTCAT
                                ||||  |||||| |||||||
                                AGTC  GTGAGA TCAAGTA
                                  __     A
GAM3507  DKFZP564I0422 3'  TTAGTAACCTGGTTCATAC    79375      ACT  T  A
                                TTAG   AC CT GTTCATAC
                                ||||   || || ||||||||
                                AATC   TG GA CAAGTATG
                                  AT_  _  C
GAM3507  FLJ20340 3'  TTAGACTACTGTGCAC      79376          CTA  T
                                TTAGACTACT   GT CAT
                                ||||||||||   || |||
                                AATCTGATGA   CA GTG
                                       ___  C
GAM3507  KIAA0087 3'  TCAGATTCTCAAGTTCATAC   79377      CTA   T
                                TTAGA   CTC AGTTCATAC
                                |||||   ||| |||||||||
                                AGTCT   GAG TCAAGTATG
                                   AA_   T
GAM3507  KIAA0426 3'  TTAGACTACCCATTCCCCATAC 79378           TAG_
                                TTAGACTACTC    TTCATAC
                                ||||||||||    |||||||
                                AATCTGATGGG    GGGTATG
                                      TAAG
GAM3507  KIAA1463 3'  TCAGACTACCCCTTTCAT    79379           AG
                                TTAGACTACTCT  TTCAT
                                ||||||||||  |||||
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                                AGTCTGATGGGG AAGTA
                                      A_
GAM3507 SERP1    3' TTAGACTAATTGTTCATAC   79380       CTCTA
                                TTAGACTA   GTTCATAC
                                ||||||||   ||||||||
                                AATCTGAT   CAAGTATG
                                     TAA__
GAM3507 SH3BGRL  3' TTAGACTAATACACTCATAC  79381       CTCTA
                                TTAGACTA   GTTCATAC
                                ||||||||   ||||||||
                                AATCTGAT   TGAGTATG
                                     TATG_
GAM3507 LOC90509 5' TTAGACTCTAGTTTATA     79382       TAC     C
                                TTAGAC  TCTAGTT ATA
                                ||||||  ||||||| |||
                                AATCTG  AGATCAA TAT
                                   ___     A
GAM3508 ARHGEF12 3' TAGTGTGTGACGTTAAGAGCAA 79385     C        A  AT_
            AGT                   TAG GTGTGACGTTGA AG   AGT
                                ||| |||||||||||| ||   |||
                                ATC CACACTGCAATT TC   TCA
                                  A         C  GTT
GAM3509 GAS7     3' TTAACTGGGTGTGGTCCTGT  79388       C  TTCG
                                TTGACTGGG GT   TTTGT
                                |||||||| ||   |||||
                                AATTGACCC CA   GGACA
                                     A  CCA_
GAM3509 IL8      3' TTAACTGGGTACCCAATTGTTT 79389       CG  C___
            GT                   TTGACTGGG  TTT   GTTTGT
                                |||||||||  |||   ||||||
                                AATTGACCC  GGG   CAAACA
                                     AT   TTAA
GAM3509 RARB     3' TTGACTGGGTCTTTGC      79390       CGTT  G
                                TTGACTGGG   TC TTTGT
                                |||||||||   || |||||
                                AACTGACCC   AG AAACG
                                    _____  _
GAM3509 RARB     3' TTGACTGGGTCTTTGC      79390       CGTT  G
                                TTGACTGGG   TC TTTGT
                                |||||||||   || |||||
                                AACTGACCC   AG AAACG
                                    _____  _
GAM3509 RPP30    3' TTCACTAGGTTTCGTTTGT   79391    G    CG
                                TT ACTGGG  TTTCGTTTGT
                                || ||||||  ||||||||||
                                AA TGATCC  AAAGCAAACA
                                  G     __
GAM3509 DKFZp586H0623 3' TGATTGGGAGTGTTTGT    79392    C   C  TTC
                                TGA TGGG GT   GTTTGT
                                ||| |||| ||   ||||||
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                                ACT ACCC CA   CAAACA
                                  A   T ___
GAM3509  LOC150935 3'  TTGACTGGGCCTGAGATTTTGT 79393          GTTTCG_
                                TTGACTGGGC      TTTGT
                                ||||||||||      |||||
                                AACTGACCCG      AAACA
                                      GACTCTA
GAM3509  LOC158972 3'  TTGGCTGAGCGTTCACCTGT   79394     A       T  TT
                                TTG CTGGGCGTT CG  TGT
                                ||| ||||||||| ||  |||
                                AAC GACTCGCAA GT  ACA
                                  C        _ GG
GAM3509  LOC200488 5'  TTCACCTGCAGTTTTGTTTGT  79395    G   GG  _   C
                                TT ACT  GC GTTT GTTTGT
                                || |||  || |||| ||||||
                                AA TGG  CG CAAA CAAACA
                                 G   A_  T   A
GAM3510  LHX5     3'  AGCAGCTGCCAGTTGAGTGCG  79398      TCC  A       C
                                AGCG   CT CCAGTTGAG GCG
                                ||||   || |||||||| |||
                                TCGT   GA GGTCAACTC CGC
                                  C__  C        A
GAM3510  KIAA0894  3'  AGTGTCCCTACAAAGAGGCG   79399    C       CAGTT   C
                                AG GTCCCTAC     GAG GCG
                                || ||||||||     ||| |||
                                TC CAGGGATG     CTC CGC
                                 A       TTT__   _
GAM3510  UBE3B    3'  TAGCGTCCCTAGCAGGCG    79400          C   TTGA
                                TAGCGTCCCTA CAG    GCG
                                |||||||||||| |||    |||
                                ATCGCAGGGAT GTC    CGC
                                       C  ____
GAM3510  LOC203523 3'  TAGGTCCCTACCAAGTG     79401     C         T
                                TAG GTCCCTACCAG TG
                                ||| ||||||||||| ||
                                ATC CAGGGATGGTT AC
                                  _         C
GAM3510  LOC220932 3'  GCGTCCCTGTCAGCGCCCGCG  79402         AC    T AG
                                GCGTCCCT  CAGT G  CGCG
                                ||||||||  |||| |  ||||
                                CGCAGGGA  GTCG C  GCGC
                                     CA    _ GG
GAM3511  INS      3'  TCTCTCGGTGCAGGAGGCG    79405          T   CCA A
                                TCTCTCGGTGCG GGA   G CG
                                |||||||||||| |||   | ||
                                AGAGAGCCACGT CCT   C GC
                                       _   ___ C
GAM3511  ITGAM    3'  TCTCTCGGTGGTGCAG      79406          C   GAC
                                TCTCTCGGTG GTG   CAG
                                |||||||||| |||   |||
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                                AGAGAGCCAC CAC   GTC
                                      _  ___
GAM3511 MGC4171  5' CCTCGGTGGGCCCCCAGGCGG 79407       C  GGA   A
                                TCTCGGTG GT   CCAG CGG
                                |||||||| ||   |||| |||
                                GGAGCCAC CG   GGTC GCC
                                     C  GG_   C
GAM3511 SEMA5A   3' TCTGCCGGTGTGGACCAGGTGG 79408    C    GC       AC
                                TCT TCGGT  GTGGACCAG  GG
                                ||| |||||  |||||||||  ||
                                AGA GGCCA  CACCTGGTC  CC
                                  C    __       CA
GAM3512 AGM1     3' TGTATACTTAAGTCCCAG    79411        _  _ A
                                TGTATACT AAG CC AG
                                |||||||| ||| || ||
                                ACATATGA TTC GG TC
                                     A  A  G
GAM3512 DAZL     3' TGACATACAGCCAAGTTTAG  79412   _    TA
                                TG TATAC  AGCCAAGTTTAG
                                || |||||  ||||||||||||
                                AC GTATG  TCGGTTCAAATC
                                 T   __
GAM3512 PTGFRN   3' TATATACTCCAAGTTT     79413        AAG
                                TGTATACT  CCAAGTTT
                                ||||||||  ||||||||
                                ATATATGA  GGTTCAAA
                                     ___
GAM3512 FLJ13105 3' TGTATACTAAGGTTTA     79414         CCAA
                                TGTATACTAAG   GTTTA
                                ||||||||||   |||||
                                ACATATGATTC   CAAAT
                                      ____
GAM3512 HRH4     3' ACTGTATACCAGGTCTATCTAG 79415         AGCCAA
                                ACTGTATACTA     GTTTAG
                                ||||||||||     ||||||
                                TGACATATGGT     TAGATC
                                      CCAGA_
GAM3512 KIAA1615 3' CTGTATACAAGGTTTA     79416        T  CCAA
                                CTGTATAC AAG   GTTTA
                                |||||||| |||   |||||
                                GACATATG TTC   CAAAT
                                     _  ____
GAM3512 PRO2325  5' AACTGTAGTGCCTAAGTTTAG 79417       TACTAA  _
                                AACTGTA     GCC AAGTTTAG
                                |||||||     ||| ||||||||
                                TTGACAT     CGG TTCAAATC
                                    CA____  A
GAM3512 PRO2949  5' AACTGTATGCTGAGCCCTTATC 79418       A  A   AA_
             T                   AACTGTAT CT AGCC   GTTT
                                |||||||| || ||||  ||||
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                                TTGACATA GA TCGG   TAGA
                                    C  C    GAA
GAM3513  ANXA3    3'  TTTAATGGAGTAGAACTA    79421     C       TTT
                                TTT ATGGAGTGG   GCTA
                                ||| |||||||||   ||||
                                AAA TACCTCATC   TGAT
                                  T       T__
GAM3513  C9       3'  TTTCATGAAGCATGTTGCTA   79422           GT
                                TTTCATGGAGTG  TTGCTA
                                ||||||||||||  ||||||
                                AAAGTACTTCGT  AACGAT
                                      AC
GAM3513  CBFA2T3  3'  TTTCAGGGAGGCCTGCT     79423      T   GT
                                TTTCA GGA  GGTTTGCT
                                ||||| |||  ||||||||
                                AAAGT CCT  CCGGACGA
                                   C  __
GAM3513  CEBPA    3'  TCTCATGGGGGTCTGCT     79424        AGT
                                TTTCATGG   GGTTTGCT
                                ||||||||   ||||||||
                                AGAGTACC   CCAGACGA
                                    C__
GAM3513  CELL     3'  CTTCATGGAGCTGCT       79425          GGTT
                                TTTCATGGAGT    TGCT
                                ||||||||||    ||||
                                GAAGTACCTCG    ACGA
                                     ____
GAM3513  CNTN3    3'  TCTCATGGAGATATATTGCTA  79426          TGGT_
                                TTTCATGGAG    TTGCTA
                                ||||||||||    ||||||
                                AGAGTACCTC    AACGAT
                                      TATAT
GAM3513  DSCR3    3'  TTTCATGGGTGAAGCC      79427        A    TTT
                                TTTCATGG GTGG   GCT
                                |||||||| ||||   |||
                                AAAGTACC CACT   CGG
                                    _    T__
GAM3513  EHD2     3'  TTCCATGGGGTCCCCT      79428        AGT    G
                                TTTCATGG   GGTTT CT
                                ||||||||   ||||| ||
                                AAGGTACC   CCAGG GA
                                    ___     G
GAM3513  FLRT2    3'  TTTCATGGGTTGTCCTGCTA  79429        AG  GT
                                TTTCATGG  TG  TTGCTA
                                ||||||||  ||  ||||||
                                AAAGTACC  AC  GACGAT
                                    CA  AG
GAM3513  GNRHR    5'  TTTCATGGTGAGTGCT      79430        AG   TT
                                TTTCATGG  TGG  TGCT
                                ||||||||  |||  ||||
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                                AAAGTACC  ACT  ACGA
                                   __  C_
GAM3513  GOLGA4   5'  TTTCATGGAATAAACT     79431          TTT
                                TTTCATGGAGTGG  GCT
                                ||||||||||||  |||
                                AAAGTACCTTATT  TGA
                                      ___
GAM3513  GPR23    5'  TTTCAGGAGGCCTGCT     79432      T  GT
                                TTTCA GGA  GGTTTGCT
                                ||||| |||  ||||||||
                                AAAGT CCT  CCGGACGA
                                  _  __
GAM3513  ITPR2    3'  TTTCCTGGGGCTTACT     79433     A  AGT
                                TTTC TGG  GGTTTGCT
                                |||| |||  ||||||||
                                AAAG ACC  CCGAATGA
                                  G  ___
GAM3513  LAPTM5   3'  TTTCATGGAATCCACTGCTA  79434         GGT
                                TTTCATGGAGT  TTGCTA
                                ||||||||||  ||||||
                                AAAGTACCTTA  GACGAT
                                     GGT
GAM3513  MAN1A1   3'  TTTCATGGAAGTATATCTA   79435        _  GTTTG
                                TTTCATGGA GTG   CTA
                                |||||||| |||   |||
                                AAAGTACCT CAT   GAT
                                     T  ATA__
GAM3513  PPARGC1  3'  CTTCATGGAACTGCT      79436         TGGT
                                TTTCATGGAG   TTGCT
                                ||||||||||   |||||
                                GAAGTACCTT   GACGA
                                      _____
GAM3513  PPP3CA   3'  TTTCACAAGGTTTGCTA    79437      TG AGT
                                TTTCA  G  GGTTTGCTA
                                |||||  |  |||||||||
                                AAAGT  T  CCAAACGAT
                                   GT ___
GAM3513  PSG3     3'  TTTCATGAAGTATCAGCC    79438          GTTT
                                TTTCATGGAGTG   GCT
                                ||||||||||||   |||
                                AAAGTACTTCAT   CGG
                                      AGT_
GAM3513  SPAG11   5'  TTTGATGGAGTGAGGCT     79439     C       TTT
                                TTT ATGGAGTGG  GCT
                                ||| |||||||||  |||
                                AAA TACCTCACT  CGA
                                  C       C__
GAM3513  SPAG11   5'  TTTGATGGAGTGAGGCT     79439     C       TTT
                                TTT ATGGAGTGG  GCT
                                ||| |||||||||  |||
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                                AAA TACCTCACT   CGA
                                  C       C__
GAM3513  SPAG11   5'  TTTGATGGAGTGAGGCT    79439    C      TTT
                                TTT ATGGAGTGG   GCT
                                ||| |||||||||   |||
                                AAA TACCTCACT   CGA
                                  C       C__
GAM3513  SPAG11   5'  TTTGATGGAGTGAGGCT    79439    C      TTT
                                TTT ATGGAGTGG   GCT
                                ||| |||||||||   |||
                                AAA TACCTCACT   CGA
                                  C       C__
GAM3513  SPAG11   5'  TTTGATGGAGTGAGGCT    79439    C      TTT
                                TTT ATGGAGTGG   GCT
                                ||| |||||||||   |||
                                AAA TACCTCACT   CGA
                                  C       C__
GAM3513  WARS     3'  TTTCTGGAGTGGACT      79440    A      TTT
                                TTTC TGGAGTGG   GCT
                                |||| ||||||||   |||
                                AAAG ACCTCACC   TGA
                                  _      ____
GAM3513  XPR1     3'  TTTCATGAATCTGCT      79441       AGTG
                                TTTCATGG   GTTTGCT
                                ||||||||   |||||||
                                AAAGTACT   TAGACGA
                                     _____
GAM3513  BM046    3'  TTTCATGGTGTCACGATTTG  79442       A ___
                                TTTCATGG GT   GGTTTG
                                |||||||| ||   ||||||
                                AAAGTACC CA   CTAAAC
                                     A  GTG
GAM3513  DKFZp434F2322 3'  TTCCATGGGCCCCACTTGCT  79443       A  GG__
                                TTTCATGG GT    TTTGCT
                                |||||||| ||    ||||||
                                AAGGTACC CG    GAACGA
                                     _  GGGT
GAM3513  DKFZP434L0718 3'  TTTCAGGAACTTGGTGCT    79444      T   __   TT
                                TTTCA GGAG  TGGT  GCT
                                ||||| ||||  ||||  |||
                                AAAGT CCTT  ACCA  CGA
                                   _   GA   __
GAM3513  FLJ13456 3'  TTTCTTGGTGACTTGCTA    79445     A   AG  GT
                                TTTC TGG  TG  TTGCTA
                                |||| |||  ||  ||||||
                                AAAG ACC  AC  AACGAT
                                  A   __  TG
GAM3513  FLJ20085 5'  TTTCATGAGGGCCTCGGTGCTA 79446       G  T   _____
                                TTTCATG AG GGTT    TGCTA
                                ||||||| || ||||    |||||
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                                AAAGTAC TC CCGG   ACGAT
                                   _ _   AGCC
GAM3513  FLJ20297  3'  TTTCCTGGAGTGGAGACT   79447     A      TTT
                                TTTC TGGAGTGG  GCT
                                |||| ||||||||  |||
                                AAAG ACCTCACC  TGA
                                  G      TC_
GAM3513  FLJ20297  3'  TTTCCTGGAGTGGAGACT   79447     A      TTT
                                TTTC TGGAGTGG  GCT
                                |||| ||||||||  |||
                                AAAG ACCTCACC  TGA
                                  G      TC_
GAM3513  HSPC129   3'  TTTCACTGGAGTTGCC     79448     _    GGTT
                                TTTCA TGGAGT   TGCT
                                ||||| ||||||   ||||
                                AAAGT ACCTCA   ACGG
                                  G    _____
GAM3513  KIAA0174  3'  TTTCATGGAGATTCTTTG   79449        _ GG
                                TTTCATGGAG T  TTTG
                                |||||||||| |  ||||
                                AAAGTACCTC A  AAAC
                                     T AG
GAM3513  KIAA0202  3'  TCTCATGGGGTTTTGGTTTG  79450       AG___
                                TTTCATGG    TGGTTTG
                                ||||||||    |||||||
                                AGAGTACC    ACCAAAC
                                     CCAAA
GAM3513  KIAA0295  3'  TTTCATAGGGTGCCCTCT   79451       A  G  G
                                TTTCATGG GTG TTT CT
                                |||||||| ||| ||| ||
                                AAAGTATC CAC GGA GA
                                     C  G  _
GAM3513  KIAA0711  3'  TTTCATGGGTGCAAACC    79452       A  G TT
                                TTTCATGG GTG T  GCT
                                |||||||| ||| |  |||
                                AAAGTACC CAC G  TGG
                                     _  _ TT
GAM3513  KIAA1136  3'  TTTCATGGTGGGATGCT    79453       AG  TT
                                TTTCATGG  TGG  TGCT
                                ||||||||  |||  ||||
                                AAAGTACC  ACC  ACGA
                                     __  CT
GAM3513  KIAA1656  5'  TCTCATGCTTATTTGCTA   79454       GAGTG
                                TTTCATG    GTTTGCTA
                                |||||||    ||||||||
                                AGAGTAC    TAAACGAT
                                     GAA__
GAM3513  KIAA1910  3'  TTTCAAGGAGGGAGCTA    79455      T   T  TTT
                                TTTCA GGAG GG  GCTA
                                ||||| |||| ||  ||||
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                                AAAGT CCTC CC   CGAT
                                  T   _ T__
GAM3513 KIAA1918 3' TTTCATGGCCTCTGCTA    79456       AGTGG
                                TTTCATGG    TTTGCTA
                                ||||||||    |||||||
                                AAAGTACC    AGACGAT
                                    GG___
GAM3513 LAGY    3' CTTCATGGAGTGAAGCT    79457         TTT
                                TTTCATGGAGTGG  GCT
                                ||||||||||||   |||
                                GAAGTACCTCACT  CGA
                                       T__
GAM3513 LAGY    3' CTTCATGGAGTGAAGCT    79457         TTT
                                TTTCATGGAGTGG  GCT
                                ||||||||||||   |||
                                GAAGTACCTCACT  CGA
                                       T__
GAM3513 LAGY    3' CTTCATGGAGTGAAGCT    79457         TTT
                                TTTCATGGAGTGG  GCT
                                ||||||||||||   |||
                                GAAGTACCTCACT  CGA
                                       T__
GAM3513 MGC14376 3' TTTCTGTTATGGTTTGCTA   79458    A  GA
                                TTTC TG  GTGGTTTGCTA
                                |||| ||  ||||||||||
                                AAAG AC  TACCAAACGAT
                                  _ AA
GAM3513 P15-2   3' TCATGAAGATTTGCTA     79459       TG
                                TCATGGAG  GTTTGCTA
                                ||||||||  ||||||||
                                AGTACTTC  TAAACGAT
                                     __
GAM3513 RC3     3' TTTCTGAATCAGGTTTGCTA  79460    A   GT_
                                TTTC TGGA   GGTTTGCTA
                                |||| ||||   |||||||||
                                AAAG ACTT   CCAAACGAT
                                  _   AGT
GAM3513 RILP    3' TTTCATGGATGGGGAAACT   79461       G   TTT_
                                TTTCATGGA TGG   GCT
                                ||||||||| |||   |||
                                AAAGTACCT ACC   TGA
                                    _  CCTT
GAM3513 RNF38   3' TTCATGGAGCGAGAATTTG   79462         ___
                                TTCATGGAGTG  GTTTG
                                ||||||||||   |||||
                                AAGTACCTCGC  TAAAC
                                      TCT
GAM3513 SE57-1  3' TTTCATGGAAGTATGAGCTA  79463       _  GTTT
                                TTTCATGGA GTG   GCTA
                                ||||||||| |||   ||||
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                                AAAGTACCT CAT   CGAT
                                     T  ACT_
GAM3513  Spir-1   3'  TTTCATGAAACGGTGCTA    79464          TT
                                TTTCATGGAGTGGT  GCTA
                                |||||||||||||  ||||
                                AAAGTACTTTGCCA  CGAT
                                                ___
GAM3513  SPR1     3'  TTTCATGGAAGCAGCAGCT   79465       _ TG  TT
                                TTTCATGGA G  GT  GCT
                                |||||||| |  ||  |||
                                AAAGTACCT C  CG  CGA
                                     T GT  T_
GAM3513  TAGAP    3'  TTTCATGATTTTTGCTA     79466       AGTGG
                                TTTCATGG    TTTGCTA
                                ||||||||    |||||||
                                AAAGTACT    AAACGAT
                                    AA___
GAM3513  UST      3'  TTTCATGAAGTACAAACT    79467         GTTT
                                TTTCATGGAGTG   GCT
                                ||||||||||||   |||
                                AAAGTACTTCAT   TGA
                                      GTT_
GAM3513  LOC113386 3'  TTTCATGAGAACAGTTTGCT   79468       _   TG
                                TTTCATG GAG  GTTTGCT
                                ||||||| |||  |||||||
                                AAAGTAC CTT  CAAACGA
                                    T   GT
GAM3513  LOC118851 5'  TTCATGATTTATGTTTGCT   79469       AG  _
                                TTCATGG  TG GTTTGCT
                                |||||||  || |||||||
                                AAGTACT  AT CAAACGA
                                    AA  A
GAM3513  LOC125268 3'  CTTCATGGAGTGACTCACT   79470          GT TG
                                TTTCATGGAGTG  T  CT
                                ||||||||||||  |  ||
                                GAAGTACCTCAC  A  GA
                                      TG GT
GAM3513  LOC144245 5'  TTTCCTGGAGTGACGGGTTTA  79471      A     ____
                                TTTC TGGAGT    GGTTTG
                                |||| ||||||    ||||||
                                AAAG ACCTCA    CCAAAT
                                  G     CTGC
GAM3513  LOC145815 5'  TTTCTGAAGCATTTGCTA    79472      A      G
                                TTTC TGGAGTG TTTGCTA
                                |||| ||||||| |||||||
                                AAAG ACTTCGT AAACGAT
                                  _     _
GAM3513  LOC147639 5'  TTTCATGGTGGCGCT       79473        AG    TT
                                TTTCATGG  TGGT  GCT
                                ||||||||  ||||  |||
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                                AAAGTACC  ACCG  CGA
                                   __   __
GAM3513  LOC148085 5'  TTTCATGAGAGTAGGCTTG   79474       _   _
                                TTTCATG GAGT GGTTTG
                                ||||||| |||| ||||||
                                AAAGTAC CTCA CCGAAC
                                    T   T
GAM3513  LOC148255 5'  TTTGATGGAGTGGTGGTGCT  79475    C       T_
                                TTT ATGGAGTGGT  TGCT
                                ||| |||||||||  ||||
                                AAA TACCTCACCA  ACGA
                                  C        CC
GAM3513  LOC148894 5'  TTTCTGAAAAGTTTGCT    79476     A    T
                                TTTC TGGAG GGTTTGCT
                                |||| ||||| ||||||||
                                AAAG ACTTT TCAAACGA
                                   _    _
GAM3513  LOC149132 5'  TTTCATGGTAGATCCAGCT   79477       AGT    _
                                TTTCATGG   GGTTT GCT
                                ||||||||   ||||| |||
                                AAAGTACC   CTAGG CGA
                                    AT_    T
GAM3513  LOC150776 3'  TTTCCTGGAGTGGAGACT    79447     A      TTT
                                TTTC TGGAGTGG   GCT
                                |||| ||||||||   |||
                                AAAG ACCTCACC   TGA
                                  G       TC_
GAM3513  LOC157556 5'  TCTCATGGGGCTGGCTA    79478       AGT   T
                                TTTCATGG   GGTT GCTA
                                ||||||||   |||| ||||
                                AGAGTACC   CCGA CGAT
                                    ___    C
GAM3513  LOC161003 5'  TTTCATGGGTTTGGAGCTA   79479       AG_   TTT
                                TTTCATGG   TGG   GCTA
                                ||||||||   |||   ||||
                                AAAGTACC   ACC   CGAT
                                    CAA   T__
GAM3513  LOC199678 3'  TTTCAGGAGTGACAGTTG    79480     T     T__
                                TTTCA GGAGTGG   TTG
                                ||||| |||||||   |||
                                AAAGT CCTCACT   AAC
                                   _      GTC
GAM3513  LOC199692 3'  TTTCATGGGGTTTCT      79481       AGT    G
                                TTTCATGG   GGTTT CT
                                ||||||||   ||||| ||
                                AAAGTACC   CCAAA GA
                                   ___    _
GAM3513  LOC200035 3'  TCATGGAGATGGGCTA     79482       _   TTT
                                TCATGGAG TGG   GCTA
                                |||||||| |||   ||||
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                                AGTACCTC ACC   CGAT
                                     T  ___
GAM3513  LOC221583 3'  TTTCATAGGAGAAAGCTGCTA  79483       _   T_   T
                                TTTCAT GGAG  GGTT GCTA
                                ||||||| ||||  |||| ||||
                                AAAGTA CCTC  TCGA CGAT
                                   T   TT   _
GAM3513  LOC222057 5'  TTTCATGGTAGATCCAGCT   79477        AGT   _
                                TTTCATGG   GGTTT GCT
                                ||||||||   ||||| |||
                                AAAGTACC   CTAGG CGA
                                     AT_    T
GAM3513  LOC222865 3'  TTTCATGAGAATGAGCT     79484        _    TTT
                                TTTCATG GAGTGG   GCT
                                ||||||| ||||||   |||
                                AAAGTAC CTTACT   CGA
                                     T    ___
GAM3513  LOC255975 5'  TTTCATGGTAGATCCAGCT   79477        AGT   _
                                TTTCATGG   GGTTT GCT
                                ||||||||   ||||| |||
                                AAAGTACC   CTAGG CGA
                                     AT_    T
GAM3513  LOC256878 5'  TTTCATGGTAGATCCAGCT   79477        AGT   _
                                TTTCATGG   GGTTT GCT
                                ||||||||   ||||| |||
                                AAAGTACC   CTAGG CGA
                                     AT_    T
GAM3513  LOC256950 3'  TTTCATGGGCCAGCTGCT    79485        AG    T
                                TTTCATGG  TGGTT GCT
                                ||||||||  ||||| |||
                                AAAGTACC  GTCGA CGA
                                     CG    _
GAM3513  LOC90346  3'  TTCATGATAAAGTTTGCT    79486        AGT
                                TTCATGG   GGTTTGCT
                                |||||||   ||||||||
                                AAGTACT   TCAAACGA
                                     ATT
GAM3514  ADAT1    3'  GATTACAGGTGTGCGCCAC   79489    A    A   GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CAC  ACGCGGTG
                                 A    _  __
GAM3514  ALDH3B1   3'  GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   _____  T
GAM3514  ANKH     3'  GATTACAGGTATGTGCTAC   79491    A    A_  _
                                GA TACAG  GTG GCTGC
                                || |||||  ||| |||||
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                                CT ATGTC  TAC CGATG
                                 A    CA   A
GAM3514  BCAS1    3'  GACTACAGGTGTGTGCCAC   79492    A    A   GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CAC  AC CGGTG
                                 G    _  __ A
GAM3514  CARKL    3'  GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   _____  T
GAM3514  CEACAM5  3'  GACTACAGGTGCGCGCCAC   79493    A    A   G T
                                GA TACAG GTG C GCGCCAC
                                || ||||| ||| | |||||||
                                CT ATGTC CAC G CGCGGTG
                                 G    _  _ _
GAM3514  CYR61    3'  TAGAGTGCAGATAGCTGC    79494     ATA   G
                                TAGA   CAGA TGGCTGC
                                ||||   |||| |||||||
                                ATCT   GTCT ATCGACG
                                  CAC   _
GAM3514  DHFR     3'  GAATACAGGTGTGCGCCAC   79495        A   GC
                                GAATACAG GTG  TGCGCCAC
                                |||||||| |||  ||||||||
                                CTTATGTC CAC  ACGCGGTG
                                          _  __
GAM3514  DNM2     3'  TAGAATACAGAGTGCAGGCAC  79496            G T_
                                TAGAATACAGAGTG C  GCGC
                                |||||||||||||| |  ||||
                                ATCTTATGTCTCAC G  CGTG
                                        _ TC
GAM3514  GALNT7   3'  GATTACAGGTATGCGCCAC   79497    A    A   GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CAT  ACGCGGTG
                                 A    _  __
GAM3514  GNG2     5'  TAGAATCAGAGTGGTGGC    79498       A      C  C
                                TAGAAT CAGAGTGG TG GC
                                |||||| |||||||| || ||
                                ATCTTA GTCTCACC AC CG
                                          _      _ _
GAM3514  HIP1     3'  GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   _____  T
GAM3514  IL10     3'  GATTACAGGTGCGCGCCAC   79499    A    A   G T
                                GA TACAG GTG C GCGCCAC
                                || ||||| ||| | |||||||
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                                CT ATGTC CAC G CGCGGTG
                                 A    _  _ _
GAM3514  IL13RA1  3'  GATTACAGGCACGCGCCAC   79500    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG GCGCGGTG
                                 A  _____  T
GAM3514  ITGAL    3'  GACTACAGGTGTGTGCCAC   79492    A   A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CAC  AC CGGTG
                                 G   _  __ A
GAM3514  KCNA7    3'  GATCACAGGCATGTGCCAC   79501    A   GAGT  _  C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT GTGT   CCG AC CGGTG
                                 A  _____  T  A
GAM3514  KIF1B    3'  GAATTACAGGCATGTGCCAC  79502     _  GAGT  _  C
                                GAAT ACA   GGC TG GCCAC
                                |||| |||   ||| || |||||
                                CTTA TGT   CCG AC CGGTG
                                  A  _____  T  A
GAM3514  LDLR     3'  GATCACAGGCACGTGCCAC   79503    A   GAGT  _  C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT GTGT   CCG GC CGGTG
                                 A  _____  T  A
GAM3514  MSH3     3'  GACTACAGGTGTGCGCCAC   79504    A   A  GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CAC  ACGCGGTG
                                 G   _  __
GAM3514  NPHS1    3'  GACTACAGGCATGCGCCAC   79505    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 G  _____  T
GAM3514  POLK     3'  GATTACAGGCGTGTGCCAC   79506    A   A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 A   _  __ A
GAM3514  PSD      5'  GACTACAGGCGTGCGCCAC   79507    A   A  GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CGC  ACGCGGTG
                                 G   _  __
GAM3514  PTAFR    3'  GACTACAGGCGTGTGCCAC   79508    A   A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
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                                CT ATGTC CGC  AC CGGTG
                                 G    _  __ A
GAM3514  RPN1     5'  GATTACAGGCATGTGCCAC   79509    A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A   ____  T  A
GAM3514  SLC25A15 3'  GACTACAGGCACGTGCCAC   79510    A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG GC CGGTG
                                 G   ____  T  A
GAM3514  SLC2A6   3'  GAACTACGGGTGTGTGCCAC  79511     _ AGA  GC  C
                                GAAT AC   GTG  TG GCCAC
                                |||| ||   |||  || |||||
                                CTTG TG   CAC  AC CGGTG
                                  A  CC_  __ A
GAM3514  SOX11    3'  TAGAGTAACAGTTGTGCTGC  79512     AT_   AG  _
                                TAGA   ACAG  TG GCTGC
                                ||||   ||||  || |||||
                                ATCT   TGTC  AC CGACG
                                  CAT    A_  A
GAM3514  STK38    5'  GATTACAGCGATGCGCTAC   79513    A    A_  _
                                GA TACAG  GTG GCTGC
                                || |||||  ||| |||||
                                CT ATGTC  TAC CGATG
                                 A    GC   G
GAM3514  SUV39H2  3'  GACTACAGGCGTGTGCCAC   79508    A    A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 G    _  __ A
GAM3514  TPM4     3'  GACTACAGGCAGGCGTCAC   79514    A    A TG CT  C
                                GA TACAG G  G  GCG CAC
                                || ||||| |  |  ||| |||
                                CT ATGTC C  C  CGC GTG
                                 G    _ GT __  A
GAM3514  UC28     3'  GATTACAGGCATGTGCCAC   79509    A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A   ____  T  A
GAM3514  VDR      3'  GATTACAGGCTTGCGCCAC   79515    A   GAGT  _
                                GA TACA   GGCT GCGCCAC
                                || ||||   |||| |||||||
                                CT ATGT   CCGA CGCGGTG
                                 A   ____  A
GAM3514  VHL      3'  GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
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                                CT ATGT   CCG ACGCGGTG
                                 A  ____  T
GAM3514  VHL      3'  GATTACAGATGTGTGCCGC   79516    A    _  _
                                GA TACAGA GTG GCTGC
                                || |||||| ||| |||||
                                CT ATGTCT CAC CGGCG
                                 A     A  A
GAM3514  AF020591 3'  GACTACAGGTATGCGCCAC   79517    A    A  GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CAT  ACGCGGTG
                                 G   _  __
GAM3514  ALTE     3'  GATTACAGGCGGGTGCCAC   79518    A    A   CTGC
                                GA TACAG GTGG   GCCAC
                                || ||||| ||||   |||||
                                CT ATGTC CGCC   CGGTG
                                 A   _   CA__
GAM3514  BFAR     3'  GATTACAGGTATGTGCCA    79519    A    A  GC  C
                                GA TACAG GTG  TG GCCA
                                || ||||| |||  || ||||
                                CT ATGTC CAT  AC CGGT
                                 A   _  __  A
GAM3514  BIRC1    3'  GACTACAGGCATGTGCCAC   79520    A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 G  _____  T  A
GAM3514  BLOV1    3'  GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A  _____  T
GAM3514  BLZF1    3'  GAATACAGAATGCCCTGC    79521          G _
                                GAATACAGAGTG C TGC
                                |||||||||||| | |||
                                CTTATGTCTTAC G ACG
                                       G G
GAM3514  C12orf2  3'  GATTACAGGCGCGTGCCAC   79522    A    A  G T C
                                GA TACAG GTG C G GCCAC
                                || ||||| ||| | | |||||
                                CT ATGTC CGC G C CGGTG
                                 A   _  _ _ A
GAM3514  C20orf108 3'  GACTACAGGCGTGTGCCAC   79508    A    A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 G   _  __  A
GAM3514  C20orf29 3'  GATTACAGGTGGGCGCCA    79523    A    A   CT
                                GA TACAG GTGG  GCGCCA
                                || ||||| ||||  ||||||
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                                  CT ATGTC CACC  CGCGGT
                                   A    _  __
GAM3514  C21orf108 3'  GAATTACAGGTGTGCGCTAC  79524     _   A  GC    C
                                  GAAT ACAG GTG  TGCGC AC
                                  |||| |||| |||  ||||| ||
                                  CTTA TGTC CAC  ACGCG TG
                                    A   _  __    A
GAM3514  CG012    5'  TAGAATATAGGCATATGCCAC  79525       CAGAGT  _ C
                                  TAGAATA     GGC TG GCCAC
                                  |||||||     ||| || |||||
                                  ATCTTAT     CCG AT CGGTG
                                      AT____   T  A
GAM3514  COE2     3'  GATTACAGGCATGTGCCAC   79509    A   GAGT  _ C
                                  GA TACA    GGC TG GCCAC
                                  || ||||    ||| || |||||
                                  CT ATGT    CCG AC CGGTG
                                   A   _____  T  A
GAM3514  D21S2056E 3'  GATTACAGGCATGTGCCAC   79509    A   GAGT  _ C
                                  GA TACA    GGC TG GCCAC
                                  || ||||    ||| || |||||
                                  CT ATGT    CCG AC CGGTG
                                   A   _____  T  A
GAM3514  DKFZP434C1715 3'  GACTACAGGTGTGTGCCA    79526    A    A  GC  C
                                  GA TACAG GTG  TG GCCA
                                  || ||||| |||  || ||||
                                  CT ATGTC CAC  AC CGGT
                                   G    _  __ A
GAM3514  DKFZP434I1735 3'  GATTACAGGTGTGTGCCAC   79527    A    A  GC  C
                                  GA TACAG GTG  TG GCCAC
                                  || ||||| |||  || |||||
                                  CT ATGTC CAC  AC CGGTG
                                   A    _  __ A
GAM3514  DKFZP564B1023 3'  GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                  GA TACA    GGC TGCGCCAC
                                  || ||||    ||| ||||||||
                                  CT ATGT    CCG ACGCGGTG
                                   A   _____  T
GAM3514  DKFZP564I122 3'  GATTACAGGTGAGCGCCAC   79528    A    A   CT
                                  GA TACAG GTGG  GCGCCAC
                                  || ||||| ||||  |||||||
                                  CT ATGTC CACT  CGCGGTG
                                   A    _   __
GAM3514  DKFZP566G1424 5'  TAGAATACAGGTGACCA     79529          A
                                  TAGAATACAG GTGGCTG
                                  |||||||||| |||||||
                                  ATCTTATGTC CACTGGT
                                                _
GAM3514  DKFZp761J139 5'  GATTACAGGCGCGTGCCAC   79522    A    A  G T C
                                  GA TACAG GTG C G GCCAC
                                  || ||||| ||| | | |||||
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                                CT ATGTC CGC G C CGGTG
                                 A    _  _ _ A
GAM3514  FLJ10058  3'  GACTATAGGTGTGTGCCAC   79530    A  C  A   GC  C
                                GA TA AG GTG  TG GCCAC
                                || || || |||  || |||||
                                CT AT TC CAC  AC CGGTG
                                 G  A  _  __  A
GAM3514  FLJ10704  3'  GATTACAGGCATGTGCCAC   79509    A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A  _____  T  A
GAM3514  FLJ10781  3'  GATTACAGGCGCGCGCCAC   79531    A    A   G T
                                GA TACAG GTG C GCGCCAC
                                || ||||| ||| | |||||||
                                CT ATGTC CGC G CGCGGTG
                                 A    _  _ _
GAM3514  FLJ10826  3'  GATTACAGGCATGTGCCAC   79509    A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A  _____  T  A
GAM3514  FLJ11126  3'  GACTACAGGCGTGCGCCAC   79507    A    A   GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CGC  ACGCGGTG
                                 G    _  __
GAM3514  FLJ11301  3'  GATTACAGGTGCGCGCCAC   79499    A    A   G T
                                GA TACAG GTG C GCGCCAC
                                || ||||| ||| | |||||||
                                CT ATGTC CAC G CGCGGTG
                                 A    _  _ _
GAM3514  FLJ12056  3'  GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A  _____  T
GAM3514  FLJ12132  3'  GAACTACAGGCATGCGCCAC  79532     _  GAGT  _
                                GAAT ACA   GGC TGCGCCAC
                                |||| |||   ||| ||||||||
                                CTTG TGT   CCG ACGCGGTG
                                  A  _____  T
GAM3514  FLJ12994  3'  TAGATACAGTGTGCTAC    79533     A    A  G
                                TAGA TACAG GTG CTGC
                                |||| ||||| ||| ||||
                                ATCT ATGTC CAC GATG
                                  _    A  _
GAM3514  FLJ12994  3'  TAGATACAGTGTGCTAC    79533     A    A  G
                                TAGA TACAG GTG CTGC
                                |||| ||||| ||| ||||
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                                ATCT ATGTC CAC GATG
                                  _    A  _
GAM3514  FLJ13162  3'  GATTACAGGCATGTGCCAC   79509   A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A  _____  T  A
GAM3514  FLJ13193  3'  GACTACAGGCATGCGCCAC   79505   A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 G  _____  T
GAM3514  FLJ13448  3'  GATTACAGGTGTGTGCCAC   79527   A   A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CAC  AC CGGTG
                                 A   _  __ A
GAM3514  FLJ14326  3'  GAATTACAGGCATGCGCCAC  79534    _  GAGT  _
                                GAAT ACA   GGC TGCGCCAC
                                |||| |||   ||| ||||||||
                                CTTA TGT   CCG ACGCGGTG
                                  A  _____  T
GAM3514  FLJ14346  3'  GACTACAGATGGGTGCCAC   79535   A    G  CTGC
                                GA TACAGA TGG   GCCAC
                                || |||||| |||   |||||
                                CT ATGTCT ACC   CGGTG
                                 G    _  CA__
GAM3514  FLJ14397  3'  TACAGGCATGCGCCAC     79536     GAGT  _
                                TACA   GGC TGCGCCAC
                                ||||   ||| ||||||||
                                ATGT   CCG ACGCGGTG
                                  _____  T
GAM3514  FLJ14621  3'  GACTACAGGCGCGTGCCAC   79537   A   A  G T C
                                GA TACAG GTG C G GCCAC
                                || ||||| ||| | | |||||
                                CT ATGTC CGC G C CGGTG
                                 G   _  _ _ A
GAM3514  FLJ20004  3'  GATTACAGGCAGGCGCCAC   79538   A   A TG CT
                                GA TACAG G  G  GCGCCAC
                                || ||||| |  |  |||||||
                                CT ATGTC C  C  CGCGGTG
                                 A   _ GT __
GAM3514  FLJ20004  3'  GATTACAGGCATGCGCCAC   79490   A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A  _____  T
GAM3514  FLJ20006  3'  GATTACAGGCGTGCGCTAC   79539   A   A_  _
                                GA TACAG  GTG GCTGC
                                || |||||  ||| |||||
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                                CT ATGTC  CAC CGATG
                                 A    CG   G
GAM3514  FLJ20013  3' GACTACAGGTGTGTGCCAC   79492    A    A   GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CAC  AC CGGTG
                                 G    _  __  A
GAM3514  FLJ20059  3' GATTACAGGCAATGCGCCAC   79540    A    A TG C
                                GA TACAG G  G TGCGCCAC
                                || ||||| |  | ||||||||
                                CT ATGTC C  T ACGCGGTG
                                 A    _ GT _
GAM3514  FLJ20306  3' GATTACAGGTGCGTGCCAC   79541    A    A   G T C
                                GA TACAG GTG C G GCCAC
                                || ||||| ||| | | |||||
                                CT ATGTC CAC G C CGGTG
                                 A    _  _ _ A
GAM3514  FLJ20695  3' GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   _____  T
GAM3514  FLJ20825  3' GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   _____  T
GAM3514  FLJ20898  5' GAAAGCAGAGTGGCTGCTGC   79542     TA        _
                                GAA  CAGAGTGGCTGC GC
                                |||  |||||||||||| ||
                                CTT  GTCTCACCGACG CG
                                  TC          A
GAM3514  FLJ21736  3' TAGATACAGAGTGCCCA     79543     A       G
                                TAGA TACAGAGTG CTG
                                |||| ||||||||| |||
                                ATCT ATGTCTCAC GGT
                                  _       G
GAM3514  FLJ23042  3' GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   _____  T
GAM3514  FLJ23447  3' GACTACAGGCATGTGCCAC   79520    A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 G   _____  T  A
GAM3514  FLJ23878  3' GATTACAGGGGCCCGCCAC   79544    A    AGT   G
                                GA TACAG   GGCT CGCCAC
                                || |||||   |||| ||||||
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                                CT ATGTC   CCGG GCGGTG
                                 A    C__   _
GAM3514  FLJ31455  3'  GACTACAGGTATGCGCCAC   79517    A    A   GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CAT  ACGCGGTG
                                 G    _  __
GAM3514  GCN2      3'  GACTACAGGCATGTGCCAC   79520    A   GAGT  _  C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 G   _____  T  A
GAM3514  GLTP      3'  GAACTACAGGCGTGCGCCAC  79545     _   A   GC
                                GAAT ACAG GTG  TGCGCCAC
                                |||| |||| |||  ||||||||
                                CTTG TGTC CGC  ACGCGGTG
                                  A   _  __
GAM3514  HSH2      3'  GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   _____  T
GAM3514  HSPC043   3'  GATTACAGGCGTGTGCCAC   79506    A    A   GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 A    _  __ A
GAM3514  KIAA0042  3'  GATTACAGGCACGCGCCAC   79500    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG GCGCGGTG
                                 A   _____  T
GAM3514  KIAA0226  3'  GATTACAGGCGTGTGCCAC   79506    A    A   GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 A    _  __ A
GAM3514  KIAA0415  3'  TAGATACAGAGTGTCTA     79546     A       G
                                TAGA TACAGAGTG CTG
                                |||| ||||||||| |||
                                ATCT ATGTCTCAC GAT
                                   _        A
GAM3514  KIAA0451  5'  GATTACAGGCACATGCGCCAC  79547    A    A   GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CGT  ACGCGGTG
                                 A    _  GT
GAM3514  KIAA0470  3'  TAGGACACAGAGTGACTG    79548     A
                                TAG ATACAGAGTGGCTG
                                ||| ||||||||||||||
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                                ATC TGTGTCTCACTGAC
                                  C
GAM3514  KIAA0513  3'  TAGAGGCAGAGGCCACGCCAC  79549     ATA   GT   TG
                                TAGA  CAGA  GGC  CGCCAC
                                ||||  ||||  |||  ||||||
                                ATCT  GTCT  CCG  GCGGTG
                                  CC_   __  GT
GAM3514  KIAA0557  3'  GACTACAGGCACGTGCCAC   79510   A   GAGT  _  C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG GC CGGTG
                                 G   ____  T  A
GAM3514  KIAA0565  3'  GACTACAGGTGTGTGCCAC   79492   A   A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CAC  AC CGGTG
                                 G   _  __ A
GAM3514  KIAA0831  3'  GATTACAGGCGTGCGCCAC   79550   A   A  GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CGC  ACGCGGTG
                                 A   _  __
GAM3514  KIAA0892  3'  GACTACAGGCATGCGCCAC   79505   A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 G   ____  T
GAM3514  KIAA0894  3'  GAATACAGAGGCCTGCCAC   79551       GT   GC
                                GAATACAGA  GGCT  GCCAC
                                |||||||||  ||||  |||||
                                CTTATGTCT  CCGG  CGGTG
                                     __   A_
GAM3514  KIAA1130  3'  GATTACAGACGCGCGCCAC   79552   A    GTG  T
                                GA TACAGA  GC GCGCCAC
                                || ||||||  || |||||||
                                CT ATGTCT  CG CGCGGTG
                                 A    G__  _
GAM3514  KIAA1143  3'  GACTACAGGTGTGTGTCGC   79553   A   A  GC  _
                                GA TACAG GTG  TG CGC
                                || ||||| |||  || |||
                                CT ATGTC CAC  AC GCG
                                 G   _  AC  A
GAM3514  KIAA1456  3'  GATTACAGGCATGCGCCAC   79490   A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   ____  T
GAM3514  KIAA1463  3'  TACGGAGTGGGGAACTGTGTCA 79554    A    ____  CGC
            C                   TAC GAGTGG   CTG  CAC
                                ||| ||||||   |||  |||
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                                ATG CTCACC   GAC  GTG
                                  C     CCTT  ACA
GAM3514 KIAA1473 3' GATTACAGGCATGCGCCAC   79490   A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A  _____  T
GAM3514 KIAA1656 5' GACTACGGGGGCCCGCCAC   79555   A  AGAGT   G
                                GA TAC    GGCT CGCCAC
                                || |||    |||| ||||||
                                CT ATG    CCGG GCGGTG
                                 G  CCC__   _
GAM3514 KIAA1735 3' GACTACAGGTGTGTGCCAC   79492   A   A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CAC  AC CGGTG
                                 G   _  __ A
GAM3514 KIAA1843 3' GAATACAATATAGGCGCCA   79556       A   CT
                                GAATACAG GTGG  GCGCCA
                                |||||||| ||||  ||||||
                                CTTATGTT TATC  CGCGGT
                                     A  __
GAM3514 KIAA1872 3' GACTACAGGTGCGCGCCAC   79493   A   A  G T
                                GA TACAG GTG C GCGCCAC
                                || ||||| ||| | |||||||
                                CT ATGTC CAC G CGCGGTG
                                 G   _  _ _
GAM3514 KIAA1969 3' GAATACAGGCACGTGCCAC   79557      GAGT  _ C
                                GAATACA   GGC TG GCCAC
                                |||||||   ||| || |||||
                                CTTATGT   CCG GC CGGTG
                                    ____  T A
GAM3514 KLHL8    3' GAATTACAGGTATGCGCCAC  79558    _   A  GC
                                GAAT ACAG GTG  TGCGCCAC
                                |||| |||| |||  ||||||||
                                CTTA TGTC CAT  ACGCGGTG
                                  A  _  __
GAM3514 KREMEN   3' GATTACAGGTGTGTGCCAC   79527   A   A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CAC  AC CGGTG
                                 A   _  __ A
GAM3514 LIM      3' GATTACAGGCGCGTGCCAC   79522   A   A  G T C
                                GA TACAG GTG C G GCCAC
                                || ||||| ||| | | |||||
                                CT ATGTC CGC G C CGGTG
                                 A   _  _ _ A
GAM3514 MGC10999 3' GATTACAGGCACGTGCCAC   79559   A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
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                                CT ATGT   CCG GC CGGTG
                                 A  _____  T  A
GAM3514 MGC16037 3' GATTACAGGCTTGCGCCAC   79515   A   GAGT  _
                                GA TACA   GGCT GCGCCAC
                                || ||||   |||| |||||||
                                CT ATGT   CCGA CGCGGTG
                                 A  _____  A
GAM3514 MGC2396  3' GATTACAGGCATGTGCCAC   79509   A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A  _____  T  A
GAM3514 MGC2562  3' GATTACAGGTGCGTGCCAC   79541   A   A   G T C
                                GA TACAG GTG C G GCCAC
                                || ||||| ||| | | |||||
                                CT ATGTC CAC G C CGGTG
                                 A   _  _ _ A
GAM3514 MGC29891 3' GACTACAGGCGTGTGCCAC   79508   A   A   GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 G   _  __ A
GAM3514 MGC29937 3' GATTACAGGCATGCGCCA    79560   A   GAGT  _
                                GA TACA   GGC TGCGCCA
                                || ||||   ||| |||||||
                                CT ATGT   CCG ACGCGGT
                                 A  _____  T
GAM3514 MGC4840  3' GACTACAGGCGGGTGCCAC   79561   A   A   CTGC
                                GA TACAG GTGG   GCCAC
                                || ||||| ||||   |||||
                                CT ATGTC CGCC   CGGTG
                                 G   _   CA__
GAM3514 MOST2    5' GACTACAGGCATGTGCCAC   79520   A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 G  _____  T  A
GAM3514 MR       5' GAAGGGGAGTGGCTGTGCTAC 79562    TACA      C  C
                                GAA   GAGTGGCTG GC AC
                                |||   ||||||||| || ||
                                CTT   CTCACCGAC CG TG
                                  CCC_       A  A
GAM3514 MRPS10   3' GATTACAGGCACGTGCCAC   79559   A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG GC CGGTG
                                 A  _____  T  A
GAM3514 MST4     3' TAGAATACAGGTGAAACTA   79563        A  __
                                TAGAATACAG GTG  GCTG
                                |||||||||| |||  ||||
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                                ATCTTATGTC CAC  TGAT
                                      _  TT
GAM3514  PB1      3'  GAATTACAGGCACGCGCCAC  79564     _  GAGT  _
                                GAAT ACA   GGC TGCGCCAC
                                |||| |||   ||| ||||||||
                                CTTA TGT   CCG GCGCGGTG
                                  A  ____  T
GAM3514  PILR(ALPHA) 3'  GATTACAGGTGTGCGCCAC  79489   A   A  GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CAC  ACGCGGTG
                                 A   _  __
GAM3514  PNPASE   3'  GATTACAGGCATGCGCCAC  79490   A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A  ____  T
GAM3514  POFUT1   3'  GAATACAGGCATGTGCCAC  79565      GAGT  _  C
                                GAATACA   GGC TG GCCAC
                                |||||||   ||| || |||||
                                CTTATGT   CCG AC CGGTG
                                    ____  T  A
GAM3514  PP591    5'  GACTACAGGCGCGTGCCAC  79537   A   A  G T C
                                GA TACAG GTG C G GCCAC
                                || ||||| ||| | | |||||
                                CT ATGTC CGC G C CGGTG
                                 G   _  _ _ A
GAM3514  PRO2198  5'  GATTACAGGCGCGCGCCAC  79531   A   A  G T
                                GA TACAG GTG C GCGCCAC
                                || ||||| ||| | |||||||
                                CT ATGTC CGC G CGCGGTG
                                 A   _  _ _
GAM3514  PRO2893  3'  GAATTACAGGCGTGTGCTAC  79566    _   A_  _
                                GAAT ACAG  GTG GCTGC
                                |||| ||||  ||| |||||
                                CTTA TGTC  CAC CGATG
                                  A   CG  A
GAM3514  PSR      3'  GACTACAGGCATGTGCCAC  79520   A   GAGT  _  C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 G  ____  T  A
GAM3514  RAB4B    5'  GATTACAGGCATGCGCCAC  79490   A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A  ____  T
GAM3514  RHOBTB3  3'  GATTACAGGTGTGCGCCAC  79489   A   A  GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
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                                CT ATGTC CAC  ACGCGGTG
                                 A    _  __
GAM3514  Rpo1-2   3'  GAACTACAGGCATGTGCCAC   79568     _  GAGT  _ C
                                GAAT ACA   GGC TG GCCAC
                                |||| |||   ||| || |||||
                                CTTG TGT   CCG AC CGGTG
                                  A  ____  T  A
GAM3514  Rpo1-2   3'  GACTACAGGGGTGTGCCAC   79567   A   AGT  C  C
                                GA TACAG   GG TG GCCAC
                                || |||||   || || |||||
                                CT ATGTC   CC AC CGGTG
                                 G    ___  C  A
GAM3514  SCAND2   3'  GACTACAGGCTTGCGCCAC   79569   A   GAGT   _
                                GA TACA   GGCT GCGCCAC
                                || ||||   |||| |||||||
                                CT ATGT   CCGA CGCGGTG
                                 G   ____   A
GAM3514  SPRY4    3'  GACTACAGGCGTGCGCCAC   79507   A   A  GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CGC  ACGCGGTG
                                 G   _  __
GAM3514  STARD7   3'  GAAACAGAGTGAAACTCCA   79570    T      CT  G
                                GAA ACAGAGTGG  GC CCA
                                ||| |||||||||  || |||
                                CTT TGTCTCACT  TG GGT
                                  _       T_  A
GAM3514  STARD7   3'  GAAACAGAGTGAAACTCCA   79570    T      CT  G
                                GAA ACAGAGTGG  GC CCA
                                ||| |||||||||  || |||
                                CTT TGTCTCACT  TG GGT
                                  _       T_  A
GAM3514  ZNF297B  3'  GATTACAGGTGTGCGCCAC   79489   A   A  GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CAC  ACGCGGTG
                                 A   _  __
GAM3514  LOC115129 3'  GATTACGGGTGTGTGCCAC   79571   A  AGA  GC  C
                                GA TAC   GTG  TG GCCAC
                                || |||   |||  || |||||
                                CT ATG   CAC  AC CGGTG
                                 A  CC_   __  A
GAM3514  LOC126282 3'  GACTACAGGCATGTGCCAC   79520   A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 G   _____  T  A
GAM3514  LOC130026 3'  GACTACAGGCACGTGCCAC   79510   A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
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                                CT ATGT   CCG GC CGGTG
                                 G  ____  T  A
GAM3514  LOC130535 3'  GATCACAGGCATGCGCCAC   79572   A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT GTGT   CCG ACGCGGTG
                                 A  ____  T
GAM3514  LOC130535 3'  GACTACAGGCGTGTGCCAC   79508   A   A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 G   _  __ A
GAM3514  LOC144481 3'  GATTACAGGCATGTGCCAC   79509   A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A  ____  T  A
GAM3514  LOC144563 5'  GAATGCAGGTGCGCGCCAC   54026    A  A  G T
                                GAAT CAG GTG C GCGCCAC
                                |||| ||| ||| | |||||||
                                CTTA GTC CAC G CGCGGTG
                                  C  _  _ _
GAM3514  LOC145482 3'  GATTACAGGCGTGTGCCAC   79506   A   A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 A   _  __ A
GAM3514  LOC145662 3'  GAACTACAGGCATGTGCCAC   79568    _  GAGT  _ C
                                GAAT ACA   GGC TG GCCAC
                                |||| |||   ||| || |||||
                                CTTG TGT   CCG AC CGGTG
                                  A  ____  T  A
GAM3514  LOC146540 3'  GACTACAGGCATGTGCCAC   79520   A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 G  ____  T  A
GAM3514  LOC146723 3'  GATTACAGGCGTGTGCCAC   79506   A   A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 A   _  __ A
GAM3514  LOC146780 5'  GACTACAGGCCTGTGCCAC   79573   A   A GG  C
                                GA TACAG GT  CTG GCCAC
                                || ||||| ||  ||| |||||
                                CT ATGTC CG  GAC CGGTG
                                 G   _ __  A
GAM3514  LOC147040 5'  GAATATAGTGTGCCCCCCAC   79574    C A  G  GCG
                                GAATA AG GTG CT   CCAC
                                ||||| || ||| ||   ||||
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                                CTTAT TC CAC GG   GGTG
                                  A A   G  G__
GAM3514  LOC147080 3'  GATCACAGGTACGCGTCAC   79575    A    A   GC    C
                                GA TACAG GTG  TGCG CAC
                                || ||||| |||  |||| |||
                                CT GTGTC CAT  GCGC GTG
                                 A    _  __    A
GAM3514  LOC147664 3'  GATTACAGGCATGCGCCAC   79490    A   GAGT   _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   _____  T
GAM3514  LOC147700 3'  GATTACAGGCATGTGCCAC   79509    A   GAGT   _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A   _____  T  A
GAM3514  LOC147837 3'  GATTACAGGCATGTGCCA    79576    A   GAGT   _ C
                                GA TACA   GGC TG GCCA
                                || ||||   ||| || ||||
                                CT ATGT   CCG AC CGGT
                                 A   _____  T  A
GAM3514  LOC148198 3'  GATTACAGGCATGCGCCAC   79490    A   GAGT   _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   _____  T
GAM3514  LOC148397 3'  GATTACAGGCATGCGCCAC   79490    A   GAGT   _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   _____  T
GAM3514  LOC149113 5'  GAATTATAGGGATGTGCCAC   79577     ACAG  T  C  C
                                GAAT   AG GG TG GCCAC
                                ||||   || || || |||||
                                CTTA   TC CC AC CGGTG
                                  ATA_  _  T  A
GAM3514  LOC150319 3'  GATTACAGGCATGTGCCAC   79509    A   GAGT   _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A   _____  T  A
GAM3514  LOC150372 3'  GACTACAGGTGCGTGCCAC   79578    A    A   G T C
                                GA TACAG GTG C G GCCAC
                                || ||||| ||| | | |||||
                                CT ATGTC CAC G C CGGTG
                                 G    _  _ _ A
GAM3514  LOC150481 3'  GACTACAGTTGTGTGCCA    79579    A    AG  GC  C
                                GA TACAG  TG  TG GCCA
                                || |||||  ||  || ||||
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                                CT ATGTC  AC  AC CGGT
                                 G    A_ __  A
GAM3514  LOC151602 3'  GATTACAGGCGCGTGCCAC   79522    A    A   G T C
                                GA TACAG GTG C G GCCAC
                                || ||||| ||| | | |||||
                                CT ATGTC CGC G C CGGTG
                                 A    _  _ _ A
GAM3514  LOC151632 5'  GAATGCAGGTGTGCGCCAC   54036     A   A   GC
                                GAAT CAG GTG  TGCGCCAC
                                |||| ||| |||  ||||||||
                                CTTA GTC CAC  ACGCGGTG
                                  C  _  __
GAM3514  LOC152106 3'  GACTACAGGCAGGCGTCAC   79514    A    A TG CT   C
                                GA TACAG G  G  GCG CAC
                                || ||||| |  |  ||| |||
                                CT ATGTC C  C  CGC GTG
                                 G    _ GT __  A
GAM3514  LOC152271 5'  GAATGCAGGTGTGTGCCAC   79580     A   A   GC  C
                                GAAT CAG GTG  TG GCCAC
                                |||| ||| |||  || |||||
                                CTTA GTC CAC  AC CGGTG
                                  C  _  __ A
GAM3514  LOC152445 3'  GAATTACAGGCACGTGCCAC  79581     _  GAGT  _  C
                                GAAT ACA   GGC TG GCCAC
                                |||| |||   ||| || |||||
                                CTTA TGT   CCG GC CGGTG
                                  A  _____  T  A
GAM3514  LOC152445 3'  GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A  _____  T
GAM3514  LOC152860 3'  GATTACAGACATGCGCCAC   79582    A    GTGGC
                                GA TACAGA    TGCGCCAC
                                || ||||||    ||||||||
                                CT ATGTCT    ACGCGGTG
                                 A    GT___
GAM3514  LOC154403 5'  GAATTATAGGGATGTGCCAC  79577     ACAG  T  C  C
                                GAAT   AG GG TG GCCAC
                                ||||   || || || |||||
                                CTTA   TC CC AC CGGTG
                                  ATA_  _  T  A
GAM3514  LOC154791 3'  GATTACAGGCATGTGCCAC   79509    A   GAGT  _  C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A  _____  T  A
GAM3514  LOC154877 3'  TAGGACACAGAGGTGCCGC   79583    A       TG
                                TAG ATACAGAG  GCTGC
                                ||| ||||||||  |||||
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                                ATC TGTGTCTC  CGGCG
                                  C       CA
GAM3514  LOC154992 5'  GAATTACAGGGATGTGCCAC   79584     _   AGT  C  C
                                GAAT ACAG   GG TG GCCAC
                                |||| ||||   || || |||||
                                CTTA TGTC   CC AC CGGTG
                                  A   ___  T  A
GAM3514  LOC157660 3'  GATTACAGGTGCGCGCCAC    79499    A    A   G T
                                GA TACAG GTG C GCGCCAC
                                || ||||| ||| | |||||||
                                CT ATGTC CAC G CGCGGTG
                                 A    _  _ _
GAM3514  LOC158191 3'  GACTACAGGTGTGTGCCAC    79492    A    A   GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CAC  AC CGGTG
                                 G    _  __ A
GAM3514  LOC167994 5'  TAGGGACAGAGTAAGCTGC    79585     AAT      _
                                TAG   ACAGAGTG GCTGC
                                |||   |||||||| |||||
                                ATC   TGTCTCAT CGACG
                                  CC_       T
GAM3514  LOC200317 3'  GATTACAGGCGTGTGCTAC    79586    A    A_  _
                                GA TACAG  GTG GCTGC
                                || |||||  ||| |||||
                                CT ATGTC  CAC CGATG
                                 A    CG   A
GAM3514  LOC200803 3'  GATTACAGGCATGCGCCAC    79490    A   GAGT  _
                                GA TACA    GGC TGCGCCAC
                                || ||||    ||| ||||||||
                                CT ATGT    CCG ACGCGGTG
                                 A   _____  T
GAM3514  LOC200940 3'  GATTACAGGCATGCGCCAC    79490    A   GAGT  _
                                GA TACA    GGC TGCGCCAC
                                || ||||    ||| ||||||||
                                CT ATGT    CCG ACGCGGTG
                                 A   _____  T
GAM3514  LOC201627 3'  GATTACAGGCGCGTGCCAC    79522    A    A   G T C
                                GA TACAG GTG C G GCCAC
                                || ||||| ||| | | |||||
                                CT ATGTC CGC G C CGGTG
                                 A    _  _ _ A
GAM3514  LOC202052 3'  GACTACAGGCATGTGCCAC    79520    A   GAGT  _ C
                                GA TACA    GGC TG GCCAC
                                || ||||    ||| || |||||
                                CT ATGT    CCG AC CGGTG
                                 G   _____  T A
GAM3514  LOC202781 3'  GACTACAGGCGCGTGCCGC    79587    A    A_  _
                                GA TACAG  GTG GCTGC
                                || |||||  ||| |||||
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                                CT ATGTC  CGC CGGCG
                                 G    CG   A
GAM3514  LOC203083 5'  GAATGCAGGTGCGTGCCAC   79588     A   A   G T C
                                GAAT CAG GTG C G GCCAC
                                |||| ||| ||| | | |||||
                                CTTA GTC CAC G C CGGTG
                                  C  _  _ _ A
GAM3514  LOC219627 3'  GATTACAGGCACGTGCCAC   79559    A   GAGT  _  C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG GC CGGTG
                                 A   _____  T  A
GAM3514  LOC219627 3'  GACTACAGGCACGCGCCAC   79589    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG GCGCGGTG
                                 G   _____  T
GAM3514  LOC219649 3'  GATTACAGGTGTGTGCCAC   79527    A    A   GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CAC  AC CGGTG
                                 A    _  __  A
GAM3514  LOC219914 5'  TAGATACAGAGTGTCCA     79590     A       G
                                TAGA TACAGAGTG CTG
                                |||| ||||||||| |||
                                ATCT ATGTCTCAC GGT
                                  _       A
GAM3514  LOC220662 3'  GATGACAGGTGTGTGCCAC   79591    AT   A   GC  C
                                GA  ACAG GTG  TG GCCAC
                                ||  |||| |||  || |||||
                                CT  TGTC CAC  AC CGGTG
                                 AC   _  __  A
GAM3514  LOC220766 3'  TAGGACACAGAGTGACTG    79548    A
                                TAG ATACAGAGTGGCTG
                                ||| ||||||||||||||
                                ATC TGTGTCTCACTGAC
                                  C
GAM3514  LOC221178 3'  GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   _____  T
GAM3514  LOC221410 3'  GACTACAGGCGTGTGCCAC   79508    A    A   GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 G    _  __  A
GAM3514  LOC221543 5'  GACTACAGGGGCCCGCCAC   79592    A    AGT   G
                                GA TACAG   GGCT CGCCAC
                                || |||||   |||| ||||||
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                                CT ATGTC   CCGG GCGGTG
                                 G    C__   _
GAM3514  LOC221795 5'  GAATGCAGGTGCGTGCCAC   79588     A  A   G T C
                                GAAT CAG GTG C G GCCAC
                                |||| ||| ||| | | |||||
                                CTTA GTC CAC G C CGGTG
                                  C  _  _ _ A
GAM3514  LOC253039 3'  GACTACAGGTGCGTGCCAC   79578    A    A   G T C
                                GA TACAG GTG C G GCCAC
                                || ||||| ||| | | |||||
                                CT ATGTC CAC G C CGGTG
                                 G    _  _ _ A
GAM3514  LOC253612 5'  GATTACAGGCACGCGCCAC   79500    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG GCGCGGTG
                                 A   _____  T
GAM3514  LOC253639 3'  GATTACAGGCATGCGCCAC   79490    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   _____  T
GAM3514  LOC253681 5'  GAATATAGTGTGCCCCCCAC   79574      C  A   G  GCG
                                GAATA AG GTG CT   CCAC
                                ||||| || ||| ||   ||||
                                CTTAT TC CAC GG   GGTG
                                   A  A   G  G__
GAM3514  LOC254045 3'  GATTACAGGCATGTGCCAC   79509    A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A   _____  T  A
GAM3514  LOC254176 5'  GAATGCAGGTGCGTGCCAC   79588     A  A   G T C
                                GAAT CAG GTG C G GCCAC
                                |||| ||| ||| | | |||||
                                CTTA GTC CAC G C CGGTG
                                  C  _  _ _ A
GAM3514  LOC254531 5'  GATTACAGGCATGTGCCAC   79509    A   GAGT  _ C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A   _____  T  A
GAM3514  LOC255671 3'  GATTACAGGCGTGTGTCAC   79593    A    A  GC  _
                                GA TACAG GTG  TG CGC
                                || ||||| |||  || |||
                                CT ATGTC CGC  AC GTG
                                 A    _  AC  A
GAM3514  LOC256207 3'  GACTACAGGTGTGTGCCAC   79492    A    A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
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                                CT ATGTC CAC  AC CGGTG
                                 G    _  __  A
GAM3514  LOC256515 5'  GAATGCAGGGGCGCGCCAC   54054     A  AGT  T
                                GAAT CAG   GGC GCGCCAC
                                |||| |||   ||| |||||||
                                CTTA GTC   CCG CGCGGTG
                                  C  C__   _
GAM3514  LOC256520 3'  GATTACAGAGACCGCCAC    79594    A     TG  TG
                                GA TACAGAG  GC  CGCCAC
                                || |||||||  ||  ||||||
                                CT ATGTCTC  TG  GCGGTG
                                 A      __  __
GAM3514  LOC257465 3'  GAAGACAGAGTGAGACTCCA  79595     T       CT  G
                                GAA ACAGAGTGG  GC CCA
                                ||| |||||||||  || |||
                                CTT TGTCTCACT  TG GGT
                                  C       C_  A
GAM3514  LOC257596 5'  GACTACAGGGGCCCGCCAC   79592    A    AGT   G
                                GA TACAG   GGCT CGCCAC
                                || |||||   |||| ||||||
                                CT ATGTC   CCGG GCGGTG
                                 G    C__   _
GAM3514  LOC51759  3'  GATTACAGGCATGTGCCAC   79509    A   GAGT  _ C
                                GA TACA    GGC TG GCCAC
                                || ||||    ||| || |||||
                                CT ATGT    CCG AC CGGTG
                                 A   _____  T  A
GAM3514  LOC90591  3'  GACTACAGGCACGCGCCAC   79589    A   GAGT  _
                                GA TACA    GGC TGCGCCAC
                                || ||||    ||| ||||||||
                                CT ATGT    CCG GCGCGGTG
                                 G   _____  T
GAM3514  LOC90918  5'  GATTACAGGCATGTGCCAC   79509    A   GAGT  _ C
                                GA TACA    GGC TG GCCAC
                                || ||||    ||| || |||||
                                CT ATGT    CCG AC CGGTG
                                 A   _____  T  A
GAM3514  LOC91250  5'  GATTACAGGCGTGTGCCAC   79506    A    A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 A    _  __  A
GAM3514  LOC91812  5'  AATGCAGAGTGGTCGAGGC   79596     A      C  C_
                                AAT CAGAGTGG TG  GC
                                ||| |||||||| ||  ||
                                TTA GTCTCACC GC  CG
                                  C       A  TC
GAM3514  LOC91813  5'  AATGCAGAGTGGTCGAGGC   79596     A      C  C_
                                AAT CAGAGTGG TG  GC
                                ||| |||||||| ||  ||
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                                TTA GTCTCACC GC  CG
                                  C       A  TC
GAM3514  LOC91963  5'  GATTACAGGCGTGTGCCAC   79506    A    A   GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 A    _  __ A
GAM3514  LOC92148  5'  GAAACAGAGTGAGCCTGC    79597    T      _ _
                                GAA ACAGAGTG GC TGC
                                ||| |||||||| || |||
                                CTT TGTCTCAC CG ACG
                                  _      T  G
GAM3515  KCNF1     3'  AGTCTGTCCAGGGGAGGGTT  79600        AGTTC   A
                                AGTCTGTC    GGAG GTT
                                ||||||||    |||| |||
                                TCAGACAG    CCTC CAA
                                     GTCC_   C
GAM3515  M11S1     3'  TAGTTTGTCAGTTATCATTGA  79601     C     __   GA
                                TAGT TGTCAGT  TCG  GA
                                |||| |||||||  |||  ||
                                ATCA ACAGTCA  AGT  CT
                                  A      AT   AA
GAM3515  MAP3K7IP2 3'  TCTGTCAGTGGGTTA      79602        TC  AGA
                                TCTGTCAGT  GG   GTTA
                                |||||||||  ||   ||||
                                AGACAGTCA  CC   CAAT
                                           __ ___
GAM3515  DKFZP564D0372 3'  TAGTCTGCGGTTTGGGA     79603        CA   C  A
                                TAGTCTGT  GTT GG GA
                                ||||||||  ||| || ||
                                ATCAGACG  CAA CC CT
                                     C_   A  _
GAM3515  FLJ20783  3'  GTCTGTGGTTTGAAAAAGTTAA 79604       CAG  CG
                                GTCTGT   TT  GAGAGTTAA
                                ||||||   ||  ||||||||||
                                CAGACA   AA  TTTTCAATT
                                   CCA  CT
GAM3515  FLJ25193  3'  GTCTGTCAGTACACAGGTT   79605         T  G  A
                                GTCTGTCAGT CG AG GTT
                                |||||||||| || || |||
                                CAGACAGTCA GT TC CAA
                                      T  G  _
GAM3515  STIP-1    3'  GTCTGTCATCCTTAGAGTT   79606        G   GG
                                GTCTGTCA TTC  AGAGTT
                                |||||||| |||  ||||||
                                CAGACAGT AGG  TCTCAA
                                     _  AA
GAM3515  LOC161003 3'  GTGCTGGAAGGTGGAGAGTT  79607    _   TC  TTC
                                GT CTG  AG   GGAGAGTT
                                || |||  ||   ||||||||
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                                CA GAC  TC   CCTCTCAA
                                 C   CT  CA_
GAM3515 LOC56267 3'  TAGTCTGCCAAATGAGAGTTAA 79608          TTCG
                                TAGTCTGTCAG    GAGAGTTAA
                                ||||||||||    |||||||||
                                ATCAGACGGTT    CTCTCAATT
                                      TA__
GAM3515 LOC90557 3'  CAGTTTGTCAGTTTGGAG    79609     C       C
                                TAGT TGTCAGTT GGAG
                                |||| |||||||| ||||
                                GTCA ACAGTCAA CCTC
                                  A       A
GAM3515 LOC91409 3'  CAGTTTGTCAGTTTGGAG    79609     C       C
                                TAGT TGTCAGTT GGAG
                                |||| |||||||| ||||
                                GTCA ACAGTCAA CCTC
                                  A       A
GAM3516 FLJ11004 3'  GTCAGCTGTTGGTTTTTGT   79612    A      TTT      C
                                GT CAGTTGT   TGGTTTT GT
                                || |||||||   ||||||| ||
                                CA GTCGACA   ACCAAAA CA
                                 _     ___      A
GAM3516 GMFB     3'  TGTCAGTTGTTGGTTTT     79613     A      TTT
                                TGT CAGTTGT   TGGTTTT
                                ||| |||||||   |||||||
                                ACA GTCAACA   ACCAAAA
                                 _     ___
GAM3517 SOX12    3'  GAGTAACACGATGGGCAC    79616    A        A
                                GA TAACACGATG GCAT
                                || |||||||||| ||||
                                CT ATTGTGCTAC CGTG
                                 C         C
GAM3517 FLJ10232 3'  TGGACAACACGGTGAAACAT   79617    A       A   _
                                TG ATAACACG TGAG CAT
                                || |||||||| |||| |||
                                AC TGTTGTGC ACTT GTA
                                 C       C    T
GAM3517 KRTAP4-10 3'  TAAATGACACTTTCATATCAT  79618       A   GATGAG
                                TGAAT ACAC     CATATCAT
                                ||||| ||||     ||||||||
                                ATTTA TGTG     GTATAGTA
                                  C    AAA___
GAM3517 MGC26954 3'  TGAATGACACGATATTCACAT  79619       A       AG
                                TGAAT ACACGATG  CATAT
                                ||||| ||||||||  |||||
                                ACTTA TGTGCTAT  GTGTA
                                  C       AA
GAM3518 C21orf33 3'  TAGCTGGGCCCCGTCCATGC   79622     GT_   GA
                                TAGC   GTC  CGTCCATGC
                                ||||   |||  |||||||||
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                                ATCG  CGG  GCAGGTACG
                                  ACC  G_
GAM3518 FACL5   5' GCTTCAGAGCGTCCATGC   79623   G _ _
                                GT TC GA CGTCCATGC
                                || || || |||||||||
                                CG AG CT GCAGGTACG
                                 A  T  C
GAM3518 GALNT2  3' TAGCGTGTGACAGCTGC    79624       C   TCCA
                                TAGCGTGT GACG   TGC
                                |||||||| ||||   |||
                                ATCGCACA CTGT   ACG
                                     _   CG__
GAM3518 LDB2    5' TATCAGTAACGTCCATGC   79625     ___
                                TGTC  GACGTCCATGC
                                ||||  ||||||||||
                                ATAG  TTGCAGGTACG
                                  TCA
GAM3518 FLJ13441 3' GCAAGGGTGACGTCCATGC   79626    T__  C
                                GCG  GT GACGTCCATGC
                                |||  || ||||||||||
                                CGT  CA CTGCAGGTACG
                                 TCC  _
GAM3518 FLJ22596 3' TAGCATGTAAGCCATGC    79627       C  C T
                                TAGCGTGT GA G CCATGC
                                |||||||| || | ||||||
                                ATCGTACA TT C GGTACG
                                     _  _ _
GAM3518 KIAA1155 3' CAGCCCTCAGTGTCCATGC   79628    GTG  AC
                                TAGC  TCG  GTCCATGC
                                ||||  |||  ||||||||
                                GTCG  AGT  CAGGTACG
                                  GG_  CA
GAM3518 KIAA1280 5' GCGTGCGGCCCACGC      79629     T  AC
                                GCGTG CG  GTCCATGC
                                ||||| ||  ||||||||
                                CGCAC GC  CGGGTGCG
                                   _  __
GAM3518 KIAA1536 3' GCCATGATGTCCATGC     79630   G  C  C
                                GC TGT GA GTCCATGC
                                || ||| || ||||||||
                                CG GTA CT CAGGTACG
                                 _  _  A
GAM3518 KIAA1932 5' CAGCGTGTGAGCCCCATG   79631       C  CG
                                TAGCGTGT GA  TCCATG
                                |||||||| ||  ||||||
                                GTCGCACA CT  GGGTAC
                                     _ CG
GAM3518 PGLYRP  3' AGGTGTCAGGGTCCATGC   79632   C    AC
                                AG GTGTCG  GTCCATGC
                                || ||||||  ||||||||
```

```
                                TC CACAGT  CAGGTACG
                                 _     CC
GAM3518  PPP1R1A   3'  AACAAATCCGGTGTCCATGC   79633     TG_  AC
                                AGCG   TCG  GTCCATGC
                                ||||   |||  ||||||||
                                TTGT   GGC  CAGGTACG
                                  TTA   CA
GAM3518  RGS18     3'  TAACTGGGTACGTCCATG    79634     G  TCG
                                TAGC TG   ACGTCCATG
                                |||| ||   |||||||||
                                ATTG AC   TGCAGGTAC
                                  _ CCA
GAM3518  LOC128823 5'  CAGCGTGTGAGGGTCTGTG   79635        C  C_   CA
                                TAGCGTGT GA  GTC  TG
                                |||||||| ||  |||  ||
                                GTCGCACA CT  CAG  AC
                                     _ CC   AC
GAM3518  LOC150622 5'  TAGCATGTGCCCATG      79636        CGAC
                                TAGCGTGT    GTCCATG
                                ||||||||    |||||||
                                ATCGTACA    CGGGTAC
                                      ____
GAM3518  LOC158987 5'  GCGTGCGTTGTCCATGC     79637      T  AC
                                GCGTG CG  GTCCATGC
                                ||||| ||  ||||||||
                                CGCAC GC  CAGGTACG
                                  _ AA
GAM3518  LOC164397 5'  TAGATGTAGCCGTCCATGC    79638     C    CGA
                                TAG GTGT   CGTCCATGC
                                ||| ||||   |||||||||
                                ATC TACA   GCAGGTACG
                                  _    TCG
GAM3518  LOC200812 5'  AGCGTGTCTCTCTTCCATGC   79639        GACG_
                                AGCGTGTC     TCCATGC
                                ||||||||     |||||||
                                TCGCACAG     AGGTACG
                                     AGAGA
GAM3518  LOC219690 3'  AGTGTGTTCTGAGCCCATGC   79640    C    _ _  C
                                AG GTGT C GA GTCCATGC
                                || |||| | || ||||||||
                                TC CACA G CT CGGGTACG
                                 A    A A  _
GAM3518  LOC254806 5'  TAGGTGTCGACTGGATGC     79641     C       GTCC
                                TAG GTGTCGAC    ATGC
                                ||| ||||||||    ||||
                                ATC CACAGCTG    TACG
                                  _       ACC_
GAM3519  KPNA1     3'  TTAATGCAGAAACACAGCC    79644        TT__
                                TTAGTGCA    TGCAGCC
                                ||||||||    |||||||
```

```
                                AATTACGT   GTGTCGG
                                    CTTT
GAM3519 LIMD1   3' TTAATGCAATTAAATTTGCAGC 79645       _______      III
            CG                   TTAGTGCA    TTTGCAGCC  G
                                 ||||||||    |||||||||  |
                                 AATTACGT    AAACGTCGG  C
                                     TAATTT       III
GAM3519 ASTN2   3' TTAATGCATGGACAGGCC   79646       TT  _
                                 TTAGTGCAT  GCAG CC
                                 |||||||||  |||| ||
                                 AATTACGTA  TGTC GG
                                      CC   C
GAM3519 SLC17A6 3' TCAGTACAACTTTGTAGC   79647       __  C
                                 TTAGTGCA  TTTG AGC
                                 ||||||||  |||| |||
                                 AGTCATGT  AAAC TCG
                                     TG   A
GAM3519 USP8    3' TTAGTGCACAAATACAGCC   79648       T__
                                 TTAGTGCAT   TGCAGCC
                                 |||||||||   |||||||
                                 AATCACGTG   ATGTCGG
                                      TTT
GAM3519 ZNF297B 5' TTAGTACAAATTCCAGCC   79649       T_ G
                                 TTAGTGCA  TT CAGCC
                                 ||||||||  || |||||
                                 AATCATGT  AA GTCGG
                                     TT  G
GAM3520 AKAP13  3' TCCTGCGGATCCCCA      79652   G   T  CG
                                 TC CTGCG GAT  CCCCA
                                 || ||||| |||  |||||
                                 AG GACGC CTA  GGGGT
                                  _   _  __
GAM3520 BCR     5' TCGCTTCCGCACCGCCCCAC  79653      G_  G
                                 TCGCT  CGT ATCGCCCCAC
                                 |||||  ||| ||||||||||
                                 AGCGA  GCG TGGCGGGGTG
                                    AG  _
GAM3520 BCR     5' TCGCTTCCGCACCGCCCCAC  79653      G_  G
                                 TCGCT  CGT ATCGCCCCAC
                                 |||||  ||| ||||||||||
                                 AGCGA  GCG TGGCGGGGTG
                                    AG  _
GAM3520 CBLB    5' TCGCTGGACACCCCA       79654       CGT  T
                                 TCGCTG   GA CGCCCCA
                                 ||||||   || |||||||
                                 AGCGAC   CT GTGGGGT
                                   ___  _
GAM3520 CSF1R   3' TCTCCCCGTGTCGCCCCA   79655   G  G   A
                                 TC CT CGTG TCGCCCCA
                                 || || |||| ||||||||
```

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                                AG GG GCAC AGCGGGGT
                                 A  G   _
GAM3520  DBT     3'  ACCTCAGGTGATCGCCCCAC  79656    GC__
                                GCT   GTGATCGCCCCAC
                                |||   ||||||||||||
                                TGG   CACTAGCGGGGTG
                                  AGTC
GAM3520  DLEC1   3'  TCCTGGCTCGCCCCA     79657    G   C  GA
                                TC CTG GT  TCGCCCCA
                                || ||| ||  ||||||||
                                AG GAC CG  AGCGGGGT
                                 _   _  __
GAM3520  DLEC1   3'  TCCTGGCTCGCCCCA     79657    G   C  GA
                                TC CTG GT  TCGCCCCA
                                || ||| ||  ||||||||
                                AG GAC CG  AGCGGGGT
                                 _   _  __
GAM3520  EP300   5'  CCGCTGCTACGCCCCAC    79658       GTGAT
                                TCGCTGC    CGCCCCAC
                                |||||||    ||||||||
                                GGCGACG    GCGGGGTG
                                    AT___
GAM3520  ERBB2   5'  TCACTGCGGCTCCGGCCCCA  79659        TGA __
                                TCGCTGCG   TC  GCCCCA
                                ||||||||   ||  ||||||
                                AGTGACGC   AG  CGGGGT
                                     CG_  GC
GAM3520  HLX1    3'  CGCTGCGTCTCCTGCCCTAC  79660       GA _   C
                                CGCTGCGT  TC GCCC AC
                                ||||||||  || |||| ||
                                GCGACGCA  GG CGGG TG
                                     GA  A    A
GAM3520  ITGA6   5'  CCGCTGCGCCCGGCCCCAC   79661        GATC
                                TCGCTGCGT    GCCCCAC
                                |||||||||    |||||||
                                GGCGACGCG    CGGGGTG
                                     GGC_
GAM3520  JUN     5'  CCGCTGCGCCCTCCTCAC    79662       GA  G  C
                                TCGCTGCGT  TC CC CAC
                                |||||||||  || || |||
                                GGCGACGCG  GG GG GTG
                                     __  A  A
GAM3520  LENG4   3'  CCGCTGCGTGGCGGCAC     79663        ATC  CC
                                TCGCTGCGTG   GC  CAC
                                ||||||||||   ||  |||
                                GGCGACGCAC   CG  GTG
                                      ___  CC
GAM3520  LRRC2   3'  TCACTGCAGAAAGCTCCAC   79664       T  TC  C
                                TCGCTGCG GA  GC CCAC
                                ||||||||  ||  ||  ||||
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                                AGTGACGT CT  CG GGTG
                                    _ TT  A
GAM3520 MKPX     5' GCTGCCGCGCCCCAC      79665      G  AT
                                GCTGC TG  CGCCCCAC
                                ||||| ||  ||||||||
                                CGACG GC  GCGGGGTG
                                  _ __
GAM3520 MTA1L1   5' CCGCAGCTATCGCCTCAC    79666     T  GTG     C
                                TCGC GC   ATCGCC CAC
                                |||| ||   |||||| |||
                                GGCG CG   TAGCGG GTG
                                  T A__     A
GAM3520 NAP1     3' CCGCTGCGCATGCGCTTCAC  79667        GAT   CC
                                TCGCTGCGT   CGC  CAC
                                |||||||||   |||  |||
                                GGCGACGCG   GCG  GTG
                                     TAC   AA
GAM3520 POLR2F   5' CCGCTGCGCCCCGGTCCC    79668        GA  C_
                                TCGCTGCGT  TCG  CCC
                                |||||||||  |||  |||
                                GGCGACGCG  GGC  GGG
                                     G_  CA
GAM3520 PTPN2    5' CGCTGCGCGCCGCGCCCC    79669        AT_
                                CGCTGCGTG   CGCCCC
                                |||||||||   ||||||
                                GCGACGCGC   GCGGGG
                                     GGC
GAM3520 RHEB2    5' TCGCTGCGTCATGACCCTCCCA 79670         ___   GC
           C                     TCGCTGCGT   GATC  CCCAC
                                |||||||||   ||||  |||||
                                AGCGACGCA   CTGG  GGGTG
                                     GTA   GA
GAM3520 SIM2     3' TCGCTGCATGACCCA      79671          TCGC
                                TCGCTGCGTGA   CCCA
                                ||||||||||    ||||
                                AGCGACGTACT   GGGT
                                      ____
GAM3520 C22orf19 3' TCACTGCAACCTCCGCCTCA  79672        TGA_   C
                                TCGCTGCG   TCGCC CA
                                ||||||||   ||||| ||
                                AGTGACGT   GGCGG GT
                                     TGGA   A
GAM3520 CAMTA1   5' CCGCCGCCAATCGCCCC     79673       G
                                TCGCTGC TGATCGCCCC
                                ||||||| ||||||||||
                                GGCGGCG GTTAGCGGGG
                                  _
GAM3520 DCLRE1B  5' TCCTGCGTGAGGCTTCCAC   79674    G      TC  C_
                                TC CTGCGTGA  GC  CCAC
                                || ||||||||  ||  ||||
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                                AG GACGCACT  CG  GGTG
                                 _      C_  AA
GAM3520  DJ159A19.3 5'  CCGCTGCGCCACCCC      79675        GAT
                                TCGCTGCGT   CGCCCC
                                |||||||||   ||||||
                                GGCGACGCG   GTGGGG
                                     ____
GAM3520  DKFZP434B205 5'  CCGCTGCGCCGCCCC      79676        GAT
                                TCGCTGCGT   CGCCCC
                                |||||||||   ||||||
                                GGCGACGCG   GCGGGG
                                     ____
GAM3520  EBNA1BP2  5'  TCGCCGCACGCACGTCCCAC  79677         AT  C
                                TCGCTGCGTG  CG CCCAC
                                ||||||||||  || |||||
                                AGCGGCGTGC  GC GGGTG
                                      GT  A
GAM3520  FLJ00001  3'  TCCTGCACGAGCCCCAC    79678    G      TC
                                TC CTGCGTGA  GCCCCAC
                                || ||||||||  |||||||
                                AG GACGTGCT  CGGGGTG
                                 _      ___
GAM3520  FLJ10008  3'  GCTGATGTCCGCCCCAC    79679     C   A
                                GCTG GTG TCGCCCCAC
                                |||| ||| |||||||||
                                CGAC TAC GGCGGGGTG
                                  _  A
GAM3520  FLJ12484  3'  TCACTGCATCCTGCCCCAC   79680         GATC
                                TCGCTGCGT   GCCCCAC
                                |||||||||   |||||||
                                AGTGACGTA   CGGGGTG
                                     GGA_
GAM3520  FLJ12700  5'  GCTGCGCGCGGCCCCAC    79681        ATC
                                GCTGCGTG   GCCCCAC
                                ||||||||   |||||||
                                CGACGCGC   CGGGGTG
                                    GC_
GAM3520  FLJ13340  5'  TCGCCGCGTTGCCCTAC    79682        GATC   C
                                TCGCTGCGT   GCCC AC
                                |||||||||   |||| ||
                                AGCGGCGCA   CGGG TG
                                     A___   A
GAM3520  FLJ20330  5'  CCGCTGCGTGCGCCCC     79683        AT
                                TCGCTGCGTG  CGCCCC
                                ||||||||||  ||||||
                                GGCGACGCAC  GCGGGG
                                     __
GAM3520  FLJ21736  3'  TCTCTTGTCTCGCCCCAC   79684    G  GC  GA
                                TC CT  GT  TCGCCCCAC
                                || ||  ||  |||||||||
```

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                                AG GA  CA  AGCGGGGTG
                                 A  A_  G_
GAM3520  FLJ22390  5'  CCGCTGCGCAGCCCCA      79685          ATC
                                TCGCTGCGTG   GCCCCA
                                ||||||||||   ||||||
                                GGCGACGCGT   CGGGGT
                                      ___
GAM3520  HGC6.1.1  3'  CGCCCAGCATCGCCCCAC    79686     GC  G
                                CGCT  GT ATCGCCCCAC
                                ||||  || ||||||||||
                                GCGG  CG TAGCGGGGTG
                                  GT  _
GAM3520  KIAA0150  3'  TCGCTGCAGACCTCGGCC    79687        T   ___
                                TCGCTGCG GATC   GCC
                                ||||||||| ||||   |||
                                AGCGACGT CTGG   CGG
                                     _   AGC
GAM3520  KIAA1042  3'  TCGTGGTGTGCCAGCCAC    79688     C  C   ATC  __
                                TCG TG GTG   GCC  CCAC
                                ||| || |||   |||  ||||
                                AGC AC CAC   CGG  GGTG
                                  _ _  A__   TC
GAM3520  KIAA1456  5'  TCACTGCAACCTCTGCCTCAC  79689        TGA  _  C
                                TCGCTGCG   TC GCC CAC
                                ||||||||   || ||| |||
                                AGTGACGT   AG CGG GTG
                                     TGG  A   A
GAM3520  MAPK13    5'  CCGCTGCGCCCGCCCC      79690        GA
                                TCGCTGCGT  TCGCCCC
                                |||||||||  |||||||
                                GGCGACGCG  GGCGGGG
                                      __
GAM3520  MGC2555   5'  CCGCTGCGTGTCCAGCCC    79691         A  _
                                TCGCTGCGTG TC GCCC
                                |||||||||| || ||||
                                GGCGACGCAC GG CGGG
                                     A  T
GAM3520  MGC4607   5'  TCGCCGCGTGCGGCTCCC    79692         ATC  _
                                TCGCTGCGTG   GC CCC
                                ||||||||||   || |||
                                AGCGGCGCAC   CG GGG
                                     GC_  A
GAM3520  PRMT6     3'  TCGCTACGCCTCTCCCAC    79693        GA  GC
                                TCGCTGCGT  TC  CCCAC
                                |||||||||  ||  |||||
                                AGCGATGCG  AG  GGGTG
                                     G_  A_
GAM3520  RNF13     5'  TCGCTGCGGGAGAAGTCCCTAC 79694        T  TCG__   C
                                TCGCTGCG GA    CCC AC
                                |||||||| ||    ||| ||
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                                AGCGACGC CT    GGG TG
                                    C  CTTCA   A
GAM3520  SERPINH1  3'  TCCTTCTCAATCGCCTCAC   79695   G  GCG     C
                                TC CT   TGATCGCC CAC
                                || ||   |||||||| |||
                                AG GA   GTTAGCGG GTG
                                 _ AGA      A
GAM3520  SPRY4     5'  TCACAAGCATCGCCCCAC    79696    T_ GTG
                                TCGC  GC   ATCGCCCCAC
                                ||||  ||   ||||||||||
                                AGTG  CG   TAGCGGGGTG
                                  TT  ___
GAM3520  STK17B    5'  CCGCTGTCCCGCCCCAC     79697      CGTGA
                                TCGCTG    TCGCCCCAC
                                ||||||    |||||||||
                                GGCGAC    GGCGGGGTG
                                   AG___
GAM3520  TBDN100   5'  TCGCCGCGTTGCCCTAC     79682       GATC   C
                                TCGCTGCGT    GCCC AC
                                |||||||||    |||| ||
                                AGCGGCGCA    CGGG TG
                                     A___    A
GAM3520  TSPEAR    3'  TCACATGACTGATTGCTCCA   79698    _ CG   C  C
                                TCGC TG  TGAT GC CCA
                                |||| ||  |||| || |||
                                AGTG AC  ACTA CG GGT
                                  T  TG    A  A
GAM3520  VPS4A     5'  TCCTGGGTCCGCCCCAC     79699    G   C  GA
                                TC CTG GT  TCGCCCCAC
                                || ||| ||  |||||||||
                                AG GAC CA  GGCGGGGTG
                                 _  C  __
GAM3520  LOC115131 3'  GCTGCGCAGCCTCCAC      79700       ATC  _
                                GCTGCGTG   GCC CCAC
                                ||||||||   ||| ||||
                                CGACGCGT   CGG GGTG
                                    ___    A
GAM3520  LOC131583 5'  TCACTGCATCTTCGCTCC    79701       GA   C
                                TCGCTGCGT  TCGC CC
                                |||||||||  |||| ||
                                AGTGACGTA  AGCG GG
                                     GA    A
GAM3520  LOC145581 5'  TCGCTGCAATCGCCCCA     79702      GT
                                TCGCTGC  GATCGCCCCA
                                |||||||  ||||||||||
                                AGCGACG  TTAGCGGGGT
                                          __
GAM3520  LOC146958 3'  TCACTGCAACCTCTGCCTCA  79703       TGA  _  C
                                TCGCTGCG   TC GCC CA
                                ||||||||   || ||| ||
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                                AGTGACGT   AG CGG GT
                                    TGG  A   A
GAM3520  LOC147929 5'  CCGACCGGGATCGCCCC     79704     _   CGT
                                TCG CTG   GATCGCCCC
                                ||| |||   |||||||||
                                GGC GGC   CTAGCGGGG
                                  T   C__
GAM3520  LOC148753 3'  CCGCTGCAGCATCGCCCCAC   79705         TG
                                TCGCTGCG  ATCGCCCCAC
                                ||||||||  ||||||||||
                                GGCGACGT  TAGCGGGGTG
                                    CG
GAM3520  LOC149111 3'  GCTGCGTGATTCCAGCTCCCA  79706          C___  _
                                GCTGCGTGAT    GC CCCA
                                ||||||||||    || ||||
                                CGACGCACTA    CG GGGT
                                     AGGT  A
GAM3520  LOC150279 3'  TCACTGCACCTGCTTCAC    79707        GTG   _  CC
                                TCGCTGC   ATC GC  CAC
                                |||||||   ||| ||  |||
                                AGTGACG   TGG CG  GTG
                                   ___   A  AA
GAM3520  LOC203197 5'  CGCTGCGCCGCCTTCAC     79708         GAT    C_
                                CGCTGCGT   CGCC  CAC
                                ||||||||   ||||  |||
                                GCGACGCG   GCGG  GTG
                                    ___    AA
GAM3520  LOC219654 5'  CCGACGGTGATCGCCCC     79709     C  C
                                TCG TG GTGATCGCCCC
                                ||| || ||||||||||
                                GGC GC CACTAGCGGGG
                                  T  _
GAM3520  LOC255290 3'  CGCTGCGTTCCCCAGCCCCAC  79710         GA_  _
                                CGCTGCGT   TC GCCCCAC
                                ||||||||   || |||||||
                                GCGACGCA   GG CGGGGTG
                                    AGG  T
GAM3520  LOC256997 5'  GCTGTGCTCACCCCAC      79711      C  GA
                                GCTG GT  TCGCCCCAC
                                ||||  ||  |||||||||
                                CGAC CG  AGTGGGGTG
                                  A  __
GAM3521  PTTG1IP   3'  TGACGAGTTCTTGAAGT     79714          T  AC
                                TGACGAGTT CT  GAGGT
                                |||||||||  ||  |||||
                                ACTGCTCAA GA  CTTCA
                                    _  A_
GAM3521  TR2       5'  CGATGAGGCCCACGAGGT    79715     C   TT
                                TGA GAG  TCTACGAGGT
                                ||| |||  ||||||||||
```

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                                GCT CTC  GGGTGCTCCA
                                  A   C_
GAM3521  WHSC1     3'  TGAAGAGTTTCCCCCACAGGT  79716     C       A_  _
                                TGA GAGTTTCT  CG AGGT
                                ||| ||||||||  || ||||
                                ACT CTCAAAGG  GT TCCA
                                  T       GG  G
GAM3521  WHSC1     3'  TGAAGAGTTTCCCCCACAGGT  79716     C       A_  _
                                TGA GAGTTTCT  CG AGGT
                                ||| ||||||||  || ||||
                                ACT CTCAAAGG  GT TCCA
                                  T       GG  G
GAM3521  WHSC1     3'  TGAAGAGTTTCCCCCACAGGT  79716     C       A_  _
                                TGA GAGTTTCT  CG AGGT
                                ||| ||||||||  || ||||
                                ACT CTCAAAGG  GT TCCA
                                  T       GG  G
GAM3521  KIAA1255  3'  GACGGCTGCTACGAGGT     79717      A   T
                                GACG GTT CTACGAGGT
                                |||| ||| |||||||||
                                CTGC CGA GATGCTCCA
                                  _  C
GAM3521  KIAA1557  3'  GACGAGTTCTCAGGT       79718        T  A G
                                GACGAGTT CT C AGGT
                                |||||||| || | ||||
                                CTGCTCAA GA G TCCA
                                    _ _ _
GAM3521  MGC14407  3'  TGATGAGTTCCTGATGAGGTA  79719     C       AC_
                                TGA GAGTTTCT   GAGGTA
                                ||| ||||||||   ||||||
                                ACT CTCAAGGA   CTCCAT
                                  A       CTA
GAM3521  LOC150368 3'  TGAGAGTTCCCAGGT       79720     C       ACG
                                TGA GAGTTTCT   AGGT
                                ||| ||||||||   ||||
                                ACT CTCAAGGG   TCCA
                                  _      ____
GAM3521  LOC159199 5'  TGATGAGCTTCTGAAATA     79721     C       AC
                                TGA GAGTTTCT  GAGGTA
                                ||| ||||||||  ||||||
                                ACT CTCGAAGA  CTTTAT
                                  A       __
GAM3521  LOC163231 5'  TGAAGAGTTTCCCACTGTA    79722     C       A  AG
                                TGA GAGTTTCT CG  GTA
                                ||| ||||||||  ||  |||
                                ACT CTCAAAGG GT  CAT
                                  T       _  GA
GAM3521  LOC222174 3'  TGACAAGTTGGAAAGGTA     79723          TCTAC
                                TGACGAGTT    GAGGTA
                                |||||||||    ||||||
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                                ACTGTTCAA    TTCCAT
                                     CCT__
GAM3522 GLUD1    3' TTGGACTGTATCATAATTA   79726      CATA C
                                TTGGAT   GT ATCATAATTA
                                ||||||   || ||||||||||
                                AACCTG   CA TAGTATTAAT
                                   A___ _
GAM3522 NOV      3' GATCATGAGTTTTCATAATTAT 79727      _  CA
                                GATCAT AGT  TCATAATTAT
                                |||||| |||  ||||||||||
                                CTAGTA TCA  AGTATTAATA
                                   C  AA
GAM3523 DNASE1   5' GACAATTTTCTCCTTTT     79730        T
                                GATAATTTT CTCCTTTT
                                ||||||||| ||||||||
                                CTGTTAAAA GAGGAAAA
                                          _
GAM3523 NDUFS2   3' TTTATTATAATTTCTCCTTTT  79731      CG     TT
                                TTTAT  ATAATT  TCTCCTTTT
                                |||||  ||||||  |||||||||
                                AAATA  TATTAA  AGAGGAAAA
                                   A_     __
GAM3523 PLAG1    3' TCACCAATTTTTTTCCTTTT   79732     A       C
                                TCG TAATTTTT TCCTTTT
                                ||| |||||||| |||||||
                                AGT GTTAAAAA AGGAAAA
                                  G       A
GAM3523 FLJ20281 5' TCTTAATTTTCTCCTTTT    79733    GA      T
                                TC  TAATTTT CTCCTTTT
                                ||  ||||||| ||||||||
                                AG  ATTAAAA GAGGAAAA
                                 A_      _
GAM3523 KIAA1870 3' TCTGTCTTTCCTTTTCTCCTTT 79734     A  GATAA
           T                     TTT TC     TTTTTCTCCTTTT
                                |||  ||     ||||||||||||
                                AGA AG     GAAAAGAGGAAAA
                                  C  AAAG_
GAM3523 MGC4638  3' GATTTTCTTTCTCCTTTT    79735     AA
                                GAT  TTTTTCTCCTTTT
                                |||  ||||||||||||
                                CTA  AGAAAGAGGAAAA
                                  AA
GAM3523 TAF5L    3' TTTATCATAATCTTTCT     79736       G
                                TTTATC ATAATTTTTCT
                                |||||| ||||||||||
                                AAATAG TATTAGAAAGA
                                          _
GAM3523 LOC221395 3' TTCATCTTTCTCTTTTTCTTCT 79737       GATAA_      C
           TTT                    TTTATC     TTTTTCT CTTTT
                                |||||||     ||||||| |||||
```

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                                AAGTAG     AAAAAGA GAAAA
                                   AAAGAG      A
GAM3524  ACT     5'  AGTCACCAGCACCATCTGA   79740        ACC   __
                                AGTCACCA   CACC  CTGA
                                ||||||||   ||||  ||||
                                TCAGTGGT   GTGG  GACT
                                     C__    TA
GAM3524  AOX1    5'  AGTACCAACCCATCCACCCCGA 79741     C       ____
                                AGT ACCAACCC    ACCCTGA
                                ||| ||||||||    |||||||
                                TCA TGGTTGGG    TGGGGCT
                                  _       TAGG
GAM3524  BCL7A   3'  GTCACCACCCTAGAGGAATCG  79742        A   ACCCT
                                GTCACCA CCC     GAATCG
                                ||||||| |||     ||||||
                                CAGTGGT GGG     CTTAGC
                                   _   ATCTC
GAM3524  CAST    3'  AGTCACCATCCACCAGCTGA   79743        AC    __
                                AGTCACCA  CCACC  CTGA
                                ||||||||  |||||  ||||
                                TCAGTGGT  GGTGG  GACT
                                     A_     TC
GAM3524  CTNNB1  3'  AGATACCAGCCCACCCCTCGA  79744    TC    A       GAA
                                AG  ACCA CCCACCCT   TCGA
                                ||  |||| ||||||||   ||||
                                TC  TGGT GGGTGGGG   AGCT
                                 TA    C       ___
GAM3524  GPC1    3'  AGTCCCCAGCCCACCCTG     79745      A   A
                                AGTC CCA CCCACCCTG
                                |||| ||| |||||||||
                                TCAG GGT GGGTGGGAC
                                  G   C
GAM3524  HMGCR   3'  AGTCACCAACCTCCTG      79746          CAC
                                AGTCACCAACC   CCTG
                                ||||||||||   ||||
                                TCAGTGGTTGG   GGAC
                                      A__
GAM3524  IKBKG   5'  AGTAACCTGGGTCCTGAATCG  79747     C   AACCCAC
                                AGT ACC      CCTGAATCG
                                ||| |||      |||||||||
                                TCA TGG      GGACTTAGC
                                  T   ACCCA__
GAM3524  ITPR3   3'  AGTCACCAGGCCACCTG     79748        AC    C
                                AGTCACCA  CCACC TG
                                ||||||||  ||||| ||
                                TCAGTGGT  GGTGG AC
                                     CC    _
GAM3524  MUCDHL  3'  GTCACCAATGTGCCTCCGCTCT 79749        C___  A  ___
            GA                    GTCACCAA    CC CC   CTGA
                                ||||||||    || ||   ||||
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                                CAGTGGTT   GG GG   GACT
                                    ACAC  A  CGA
GAM3524 MUCDHL   3' GTCACCAATGTGCCTCCGCTCT 79749       C___  A  ___
          GA                  GTCACCAA   CC CC   CTGA
                              ||||||||   || ||   ||||
                              CAGTGGTT   GG GG   GACT
                                  ACAC  A  CGA
GAM3524 PROK1    3' AGTCACCAACCTGCTCTCA   79750         CACCC  AA_
                              AGTCACCAACC    TG   TCG
                              ||||||||||    ||   |||
                              TCAGTGGTTGG    AC   AGT
                                    _____ GAG
GAM3524 PRSS8    5' AGTCACCAGCACCGTCTG    79751       ACC   __
                              AGTCACCA   CACC  CTG
                              ||||||||   ||||  |||
                              TCAGTGGT   GTGG  GAC
                                  C__    CA
GAM3524 C20orf4   3' AGTCACCAACCAACTTCTCA   79752         C  CCTGAA
                              AGTCACCAACC AC     TCG
                              |||||||||| ||     |||
                              TCAGTGGTTGG TG     AGT
                                   T  AAG___
GAM3524 DKFZp434C0923 3' AGACACCAGCTCACCCCATCA  79753    T    ACC     GA
                              AG CACCA   CACCCT  ATCG
                              || |||||   ||||||  ||||
                              TC GTGGT   GTGGGG  TAGT
                               T    CGA    __
GAM3524 FLJ11413  3' AGTCACCAGTCCACGCTG    79754       AC   C
                              AGTCACCA  CCAC CTG
                              ||||||||  |||| |||
                              TCAGTGGT  GGTG GAC
                                  CA   C
GAM3524 FLJ12270  5' AGTCACCAATCCATTGCTGA   79755       C   CC_
                              AGTCACCAA CCA   CTGA
                              ||||||||| |||   ||||
                              TCAGTGGTT GGT   GACT
                                   A   AAC
GAM3524 FLJ13391  5' AGTACCAACCCATCTTCTG   79756    C       CC__
                              AGT ACCAACCCA    CTG
                              ||| |||||||||    |||
                              TCA TGGTTGGGT    GAC
                                _       AGAA
GAM3524 FLJ14326  5' AGTCACCAGCCACCACCCTGA  79757       AC__
                              AGTCACCA   CCACCCTGA
                              ||||||||   |||||||||
                              TCAGTGGT   GGTGGGACT
                                  CGGT
GAM3524 HERC3    3' AGTCCCAACCCACTTAGA    79758     A       CCT
                              AGTC CCAACCCAC   GA
                              |||| |||||||||   ||
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                                TCAG GGTTGGGTG   CT
                                  _       AAT
GAM3524  IL18BP   5'  AGCCACCAGCCCCAAGGTCG   79759       ACCCA   TG A_
                                AGTCACCA    CCC  A  TCG
                                ||||||||    |||  |  |||
                                TCGGTGGT    GGG  T  AGC
                                    C_____   GT CC
GAM3524  KIAA0953  3'  AGTTTCCAACCCAGAGCATATC 79760     CA       CCCTGA
           G                     AGT  CCAACCCA     ATCG
                                |||  ||||||||     ||||
                                TCA  GGTTGGGT     TAGC
                                  AA       CTCGTA
GAM3524  MGC14136  3'  AGCCACCAGGGCCTTGAAT   79761       ACCCA  C
                                AGTCACCA    CC TGAAT
                                ||||||||    || |||||
                                TCGGTGGT    GG ACTTA
                                    CCC__  A
GAM3524  OSBPL5   3'  AGTCACCATCCTGCTCCTCG   79762       ACCCAC    AA__
                                AGTCACCA     CCTG    TCG
                                ||||||||     ||||    |||
                                TCAGTGGT     GGAC    AGC
                                    A_____    GAGG
GAM3524  SLC16A8   3'  AGTCACTGGGCCACCCCACCCA 79763      _____  A      T
           GA                     AGTCA     CCA CCCACCC GA
                                |||||     ||| |||||||  ||
                                TCAGT     GGT GGGTGGG CT
                                  GACCC   G      T
GAM3524  TRAF3    5'  AGTCACCCGCCCACCCCTGA   79764       AA      _
                                AGTCACC  CCCACCC TGA
                                |||||||  |||||||  |||
                                TCAGTGG  GGGTGGG ACT
                                    GC      G
GAM3524  TRNT1    5'  AGTCACCAACTACACATCG    79765       C_   CCTGA
                                AGTCACCAAC  CAC     ATCG
                                ||||||||||  |||     ||||
                                TCAGTGGTTG  GTG     TAGC
                                    AT  _____
GAM3524  LOC150933 3'  GTCACCACCCCATTTCCTG    79766       A    C__
                                GTCACCA CCCA   CCTG
                                |||||||  ||||   ||||
                                CAGTGGT GGGT   GGAC
                                    G    AAA
GAM3524  LOC197342 3'  AGTCATCAGCCACCCTG     79767      C  AC
                                AGTCA CA  CCACCCTG
                                |||||  ||  ||||||||
                                TCAGT GT  GGTGGGAC
                                  A  C_
GAM3524  LOC253962 5'  AGCCACCAGCCCATCTG     79768       A    CC
                                AGTCACCA CCCA  CTG
                                ||||||||  ||||  |||
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                                TCGGTGGT GGGT  GAC
                                    C    A_
GAM3524  LOC51134  3'  AGTCACCAACTTCACCTCT   79769          C_   _
                                AGTCACCAAC  CACC CT
                                ||||||||||  |||| ||
                                TCAGTGGTTG  GTGG GA
                                     AA    A
GAM3524  LOC51301  3'  AGTCTCCTCAACCCTGAATTGA 79770      A  AACCC        C
                                AGTC CC     ACCCTGAAT GA
                                |||| ||     ||||||||| ||
                                TCAG GG     TGGGACTTA CT
                                  A  AGT__        A
GAM3525  ABCC12    5'  CCTATGGTGTGGTTTTGGT    79773    _        GG
                                CC ATGGTGTGGT  TGGT
                                || ||||||||||  ||||
                                GG TACCACACCA  ACCA
                                 A         AA
GAM3525  BPGM      3'  TGTCATTGTGGTGGTGGTTG   79774    GT  G
                                TG  GT GTGGTGGTGGTTG
                                ||  || ||||||||||||||
                                AC  TA CACCACCACCAAC
                                 AG  A
GAM3525  CLC       3'  CCTGTGGTGTGGCTATGGT    79775    A_       G
                                CC  TGGTGTGGT GTGGT
                                ||  |||||||||  |||||
                                GG  ACCACACCG TACCA
                                 AC        A
GAM3525  JMJ       5'  TGTTGTTGGTGGTGGTTG     79776     GG_
                                TGT   TGGTGGTGGTTG
                                |||   ||||||||||||
                                ACA   ACCACCACCAAC
                                  ACA
GAM3525  MARK3     5'  TCCGTGGGTGGTGGTGCATG   79777     A   T       _
                                TCC TGG GTGGTGGTG GTG
                                ||| ||| |||||||| |||
                                AGG ACC CACCACCAC TAC
                                  C  _        G
GAM3525  MCL1      3'  TGGTTTTGGTGGTGGTGGTGGT 79778     _____
              TG                  TGGT    GTGGTGGTGGTGGTTG
                                ||||    ||||||||||||||||
                                ACCA    CACCACCACCACCAAC
                                   AAAC
GAM3525  MYH11     3'  TGGTGGTGGTGGTGGTGGTTG  79779      _
                                TGGTG TGGTGGTGGTGGTTG
                                ||||| ||||||||||||||
                                ACCAC ACCACCACCACCAAC
                                   C
GAM3525  MYH11     3'  TGGTGGTGGTGGTGGTGGTTG  79779      _
                                TGGTG TGGTGGTGGTGGTTG
                                ||||| ||||||||||||||
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                                ACCAC ACCACCACCACCAAC
                                   C
GAM3525 PPEF2    3' TCCTGGTGTGGTGGTGCATG  79780    A         _
                                TCC TGGTGTGGTGGTG GTG
                                ||| |||||||||||| |||
                                AGG ACCACACCACCAC TAC
                                  _          G
GAM3525 SMTN     3' TGGCGTCGCAGGTGGTTG    79781      G  GGT
                                TGGTGT GT   GGTGGTTG
                                |||||| ||   ||||||||
                                ACCGCA CG   CCACCAAC
                                   G  T__
GAM3525 BCMP1    3' TGTTGGATGGTGGTGGTTG   79782    G  T
                                TG TG GGTGGTGGTGGTTG
                                || || ||||||||||||||
                                AC AC CTACCACCACCAAC
                                 A  _
GAM3525 CSAGE    3' TGGTGTTGATGGGTGGTTG   79783      _    TG
                                TGGTGT GGTGG  GTGGTTG
                                |||||| |||||  |||||||
                                ACCACA CTACC  CACCAAC
                                   A    __
GAM3525 CSTL1    5' TCCAGGGTGTGGTGGTGCCAG 79784     T         G
                                TCCA GGTGTGGTGGTG TGG
                                |||| |||||||||||| |||
                                AGGT CCACACCACCAC GTC
                                  C          G
GAM3525 KIAA0423 5' GTCAGGTGGTGGTGGTTG    79785    GT
                                GT  GGTGGTGGTGGTTG
                                ||  ||||||||||||||
                                CA  CCACCACCACCAAC
                                 GT
GAM3525 KIAA1577 3' GTGTGGTGTAGTGGTGGTTG  79786        __
                                GTGTGGTG  GTGGTGGTTG
                                ||||||||  ||||||||||
                                CACACCAC  CACCACCAAC
                                     AT
GAM3525 KIAA1853 3' GCTGTCGTGGTGGTGGTT    79787    G  G
                                G TGT GTGGTGGTGGTT
                                | ||| ||||||||||||
                                C ACA CACCACCACCAA
                                 G  G
GAM3525 KIAA1866 3' GGGTGGTGGTGGTGGTTG    79788    T
                                GG GTGGTGGTGGTGGTTG
                                || ||||||||||||||||
                                CC CACCACCACCACCAAC
                                 _
GAM3525 PALM     3' TCTGTGGTGTGGGGTGG     79789    CA       T
                                TC  TGGTGTGG GGTGG
                                ||  |||||||| |||||
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                                AG  ACCACACC CCACC
                                 AC       _
GAM3525 RAI17    3'  TCTGTGGTGGGTGGTGGTGG   79790    CA    T
                                TC  TGGTG GGTGGTGGTGG
                                ||  ||||| ||||||||||
                                AG  ACCAC CCACCACCACC
                                 AC    _
GAM3525 ZD52F10  3'  CGGGGCCTCGGTGGTGGTTG   79791     T  GG
                                TGG GT  TGGTGGTGGTTG
                                ||| ||  ||||||||||||
                                GCC CG  GCCACCACCAAC
                                  C  GA
GAM3525 LOC148638 5'  ATGTTGTGGTTAGTGGTTG    79792      G    _
                                GTGT GTGGT GGTGGTTG
                                |||| ||||| ||||||||
                                TACA CACCA TCACCAAC
                                  A    A
GAM3525 LOC221794 5'  CATGGTGGTGGTGGTGG     79793       GT
                                CATGGT  GGTGGTGGTGG
                                ||||||  ||||||||||
                                GTACCA  CCACCACCACC
                                   __
GAM3526 PKHD1    3'  GAAATGAGTCCATCAATACAGA 79796   C    TAC
                                A AATG   TCATCAATACAGA
                                | ||||   ||||||||||||
                                C TTAC   GGTAGTTATGTCT
                                 T    TCA
GAM3526 PPP3CB   3'  ACAGTGGCAATCAATACAG    79797     A  TACTC
                                ACA TG     ATCAATACAG
                                ||| ||     ||||||||||
                                TGT AC     TAGTTATGTC
                                  C  CGT__
GAM3526 RAB18    3'  AACAACAGTCTTGTCAATACAG 79798       _  A  CA
             A                   GACAAT GT CT  TCAATACAGA
                                ||||||| || ||  ||||||||||
                                TTGTTG CA GA  AGTTATGTCT
                                   T  _  AC
GAM3526 TEC      3'  GACAATGTCTCAGGCCCAGA   79799        A    TCAATA
                                GACAATGT CTCA     CAGA
                                |||||||| ||||     ||||
                                CTGTTACA GAGT     GTCT
                                     _    CCGG__
GAM3526 ESAM     3'  GACAGGTTATATCAATACAG   79800      AT  ACTC
                                GACA  GT    ATCAATACAG
                                ||||  ||    ||||||||||
                                CTGT  CA    TAGTTATGTC
                                  C_  ATA_
GAM3526 FLJ20729 3'  CAACAGCCCATCAATGCAGA   79801      GTA       A
                                CAAT   CTCATCAAT CAGA
                                ||||   ||||||||| ||||
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                                GTTG   GGGTAGTTA GTCT
                                  TC_        C
GAM3526  FLJ30046  3'  GCAATGTATTAAAATACAGA   79802    A      CTCATC
                                G CAATGTA     AATACAGA
                                | |||||||     ||||||||
                                C GTTACAT     TTATGTCT
                                _      AATT__
GAM3526  KIAA0410  3'  GAAAATGTACTCAGAAGCAGA  79803    C         TCAATA
                                GA AATGTACTCA     CAGA
                                || ||||||||||     ||||
                                CT TTACATGAGT     GTCT
                                 T         CTTC__
GAM3526  KIAA0903  3'  GACAGACTTTTTATCAATACAG 79804      ATGTACTC
              A                  GACA       ATCAATACAGA
                                ||||       ||||||||||
                                CTGT       TAGTTATGTCT
                                  CTGAAAAA
GAM3526  KIAA1128  5'  GCAATGTACTTCTTACAGA    79805    A       CA  AA
                                G CAATGTACT  TC  TACAGA
                                | |||||||||  ||  ||||||
                                C GTTACATGA  AG  ATGTCT
                                _        __ A_
GAM3526  LBP-9     3'  GATGATGCACCCATTCTGATGC 79806    CA        _ A_  A
              AG                   GA  ATGTACTCAT C  AT CAG
                                ||  |||||||||| |  || |||
                                CT  TACGTGGGTA G  TA GTC
                                 AC         A AC  C
GAM3526  PP35      5'  CACTCTTCATTAATACAGA    79807      A  ___
                                TACTC TCA   ATACAGA
                                ||||| |||   |||||||
                                GTGAG AGT   TATGTCT
                                   A   AAT
GAM3526  LOC144747 5'  GACAATATATCCAACAG     79808         CT  TCAAT
                                GACAATGTA  CA    ACAG
                                |||||||||  ||    ||||
                                CTGTTATAT  GT    TGTC
                                      AG  _____
GAM3526  LOC149401 5'  GACAATGTACAAAATACAGA   79809          TCATC
                                GACAATGTAC    AATACAGA
                                ||||||||||    ||||||||
                                CTGTTACATG    TTATGTCT
                                      TT___
GAM3526  LOC166793 5'  GACAATGTACTATTACAA     79810          C  CAA
                                GACAATGTACT AT   TACAG
                                |||||||||| ||   |||||
                                CTGTTACATGA TA   ATGTT
                                          _ ___
GAM3526  LOC221035 3'  GACAATGTATGCATTATAC    79811         CT   CA
                                GACAATGTA  CAT  ATAC
                                |||||||||  |||  ||||
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                                CTGTTACAT  GTA  TATG
                                     AC   A_
GAM3527  FLJ22054  3'  ACAGCGAGTTTTTCCCG     79814    _      AGCC
                                AC GCGAGTT    TTTCCCG
                                || |||||||    |||||||
                                TG CGCTCAA    AAAGGGC
                                 T     _____
GAM3528  DIO2      3'  GTTTGCTTTCTATTGG      79817        C   ATAG
                                GTTTGCTT CTAT    TGG
                                |||||||| ||||    |||
                                CAAACGAA GATA    ACC
                                     A   _____
GAM3528  DIO2      3'  GTTTGCTTTCTATTGG      79817        C   ATAG
                                GTTTGCTT CTAT    TGG
                                |||||||| ||||    |||
                                CAAACGAA GATA    ACC
                                     A   _____
GAM3528  ECRG4     3'  ATTTGCTTCTTGTACAGCG   79818         CTA
                                GTTTGCTTC   TATAGTG
                                |||||||||   |||||||
                                TAAACGAAG   ATGTCGC
                                     AAC
GAM3528  MS4A6E    3'  GTTTGCTTTTTTATAATGG   79819        CCTA
                                GTTTGCTT    TATAGTGG
                                ||||||||    ||||||||
                                CAAACGAA    ATATTACC
                                     AAA_
GAM3528  LOC146652 5'  GTCTGCTTCAGGGTGGAG    79820         CTATATA    C
                                GTTTGCTTC      GTGGA G
                                |||||||||      ||||| |
                                CAGACGAAG      CACCT C
                                     TCC_____    A
GAM3528  LOC157570 3'  GTTTGCTTCTGATGTGGCA   79821         CTATATA    A
                                GTTTGCTTC      GTGG CG
                                |||||||||      |||| ||
                                CAAACGAAG      CACC GT
                                     ACTA___   _
GAM3529  CTPS      3'  TCTTAAGTTAGAGTACACATC  79824          T  GT_
                                TCTTAAGTTA AG   ACGTC
                                |||||||||| ||   |||||
                                AGAATTCAAT TC   TGTAG
                                      C  ATG
GAM3529  CUL3      3'  TCTTAAGTTACAGTAGAC     79825          GT_
                                TCTTAAGTTATAG   AC
                                ||||||||||||   ||
                                AGAATTCAATGTC   TG
                                       ATC
GAM3529  C20orf162 5'  CCTTGGGTTATAGGTCCG     79826      AA       A
                                TCTT  GTTATAGGT CG
                                ||||  ||||||||| ||
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                                GGAA  CAATATCCA GC
                                  CC       G
GAM3529  FLJ10853  3'  TTAAGTTATATGCTGTCAA   79827        G  AC
                                TTAAGTTATA GT  GTCAA
                                |||||||||| ||  |||||
                                AATTCAATAT CG  CAGTT
                                     A  A_
GAM3529  HSC3      3'  TTAAGTTATAATGCATCAAA   79828        GTA
                                TTAAGTTATAG   CGTCAAA
                                ||||||||||   |||||||
                                AATTCAATATT   GTAGTTT
                                     AC_
GAM3529  KIAA0042  3'  TCTTGAGGTCAAAAACGTCAAA 79829     AA_   TAGGT
           C                     TCTT   GTTA    ACGTCAAAC
                                ||||   ||||    |||||||||
                                AGAA   CAGT    TGCAGTTTG
                                  CTC    TTT__
GAM3529  LOC199974 3'  TCCTAAGTTATATAATTTGTCA 79830         GGTAC_
           AAC                    TCTTAAGTTATA     GTCAAAC
                                ||||||||||||     |||||||
                                AGGATTCAATAT     CAGTTTG
                                     ATTAAA
GAM3530  HSPC129   3'  TGTATAATAAAAAACTAAAAAT 79833         T   TAT
           TG                    TGTATAATAAA AATT   AATTG
                                |||||||||| ||||   |||||
                                ACATATTATTT TTGA   TTAAC
                                     T   TTT
GAM3530  SLC38A1   3'  TGTATAATAAATAAACATTATT 79834          TT   A
           G                     TGTATAATAAATAA  TAT ATTG
                                |||||||||||||  ||| ||||
                                ACATATTATTTATT  GTA TAAC
                                     T_   A
GAM3530  LOC51077  3'  TGTAAATTGACAATTTATAATT 79835     T   AA
           G                     TGTA AAT  ATAATTTATAATTG
                                |||| |||  ||||||||||||||
                                ACAT TTA  TGTTAAATATTAAC
                                  _   AC
GAM3531  AF1Q      5'  TGCCTCGGGAGCTCCGGGGT   79838          GAA
                                TGCCTCGGGAGCTC   GGGT
                                ||||||||||||   ||||
                                ACGGAGCCCTCGAG   CCCA
                                     GC_
GAM3531  ANK1      5'  GCCTTGGGGGCTTGAGGA    79839     C   A   C  A
                                GCCT GGG GCT GA GGG
                                |||| ||| ||| || |||
                                CGGA CCC CGA CT CCT
                                  A   C   A  _
GAM3531  ANK1      5'  GCCTTGGGGGCTTGAGGA    79839     C   A   C  A
                                GCCT GGG GCT GA GGG
                                |||| ||| ||| || |||
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                                CGGA CCC CGA CT CCT
                                  A  C  A  _
GAM3531 AXIN1    3' TGTCCTCTGCTTGGAGGGTGCT 79840    _   GGGA  CGA
                                TG CCTC   GCT  AGGGTGCT
                                || ||||   |||  ||||||||
                                AC GGAG   CGA  TCCCACGA
                                 A   A___  ACC
GAM3531 BIN3     3' TGCCTGCTGGAGGGTG     79841      CGGGA  C  A
                                TGCCT    GCT GA GGGTG
                                |||||    ||| || |||||
                                ACGGA    CGA CT CCCAC
                                   _____  C  _
GAM3531 BIVM     5' CCTTTGGGACCCAAGGGTGCT  79842    CG  AG  G
                                CCT  GG  CTC AAGGGTGCT
                                |||  ||  ||| |||||||||
                                GGA  CC  GGG TTCCCACGA
                                  AA  CT  _
GAM3531 FLJ10241 3' TGCTTCAGGAGCTGGGTGC   79843    C       CGAA
                                TGC TCGGGAGCT   GGGTGC
                                ||| |||||||||   ||||||
                                ACG AGTCCTCGA   CCCACG
                                  A       _____
GAM3531 FLJ10330 3' TGCTTTGGAAGCTTGAGGC   79844    CTC     CGAA  T
                                TGC   GGGAGCT   GGG GC
                                |||   |||||||   ||| ||
                                ACG   CCTTCGA   CTC CG
                                  AAA     A___  _
GAM3531 HSA277841 3' CTTGGGAAAAGGGTGC     79845    C   GCTC
                                CT GGGA   GAAGGGTGC
                                || ||||   |||||||||
                                GA CCCT   TTTCCCACG
                                 A  _____
GAM3531 MGC4737  5' TGCTTCAGCAGGAAGGGTGCT  79846    C   G  CTC
                                TGC TCGG AG   GAAGGGTGCT
                                ||| |||| ||   ||||||||||
                                ACG AGTC TC   CTTCCCACGA
                                  A   G  ___
GAM3531 YAP      5' GCTGGCGTAGAGCTTGAGGGGT 79847    CT_ _    C  A
             G                   GC   CG GGAGCT GA GGGTG
                                 ||   || |||||| || |||||
                                 CG   GC TCTCGA CT CCCAC
                                  ACC  A     A  C
GAM3531 LOC159199 5' TGCCCGGGAGCTCCCCCTGCT  79848      T       GAAGGG
                                TGCC CGGGAGCTC     TGCT
                                ||||  |||||||||     ||||
                                ACGG GCCCTCGAG     ACGA
                                   _       GGGG__
GAM3531 LOC253841 5' GCCTTGGGGGCTTGAGGA    79839      C   A   C  A
                                GCCT GGG GCT GA GGG
                                ||||  ||| ||| ||  |||
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                                CGGA CCC CGA CT CCT
                                  A  C  A  _
GAM3531  LOC254173 3'  TGCCCGTCCCCGAAGGGTGCT  79849     T  GGAG
                                TGCC CG   CTCGAAGGGTGCT
                                |||| ||   ||||||||||||
                                ACGG GC   GGGCTTCCCACGA
                                  _ AG__
GAM3531  LOC254209 5'  TGCCATGGGGTTCAGGGTGCT  79850     TC  AGCTCGA
                                TGCC  GGG     AGGGTGCT
                                ||||  |||     ||||||||
                                ACGG  CCC     TCCCACGA
                                  TA  CAAG___
GAM3531  LOC257081 3'  TGCCTTGGGAGCCCATGC    79851      C      GAAGG
                                TGCCT GGGAGCTC    GTGC
                                ||||| ||||||||    ||||
                                ACGGA CCCTCGGG    TACG
                                  A      _____
GAM3532  DR1      5'  GGAGAGTGATCCCGGGGGGT  79854    T  __      A
                                GG AGA  GATCCCGGG GGT
                                || |||  ||||||||| |||
                                CC TCT  CTAGGGCCC CCA
                                 _  CA       C
GAM3532  FGR      3'  GATAGGAGAGAAGTGAGGGAGG 79855    C  T    TCCC_
           TA                   GA AGG AGAGA    GGGAGGTA
                                || ||| |||||    ||||||||
                                CT TCC TCTCT    CCCTCCAT
                                 A  _    TCACT
GAM3532  MTCP1    5'  GAGAGGTAGCTGGGAGGT    79856    C    AGATCCC
                                GA AGGTAG      GGGAGGT
                                || ||||||      |||||||
                                CT TCCATC      CCCTCCA
                                 C    GA_____
GAM3532  NT5C     3'  GACAGCCTCTCGGGAGGT    79857      GTAGAGA  C
                                GACAG      TC CGGGAGGT
                                |||||      || ||||||||
                                CTGTC      AG GCCCTCCA
                                  GG_____  A
GAM3532  SCNN1B   3'  GACAGGTAGGGACGAGGGT   79858        A  TCC   A
                                GACAGGTAG GA   CGGG GGT
                                ||||||||| ||   |||| |||
                                CTGTCCATC CT   GCTC CCA
                                     C ___   _
GAM3532  SLC6A1   3'  AGGTTGAGATGGAAGGTA    79859     A    CCC
                                AGGT GAGAT   GGGAGGTA
                                |||| |||||   ||||||||
                                TCCA CTCTA   CCTTCCAT
                                  A    ___
GAM3532  DMWD     3'  AACAGAAACATTTCGGGGGGT  79860      TA  G  CC   A
                                GACAGG  GA AT  CGGG GGT
                                ||||||  || ||  |||| |||
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                                TTGTCT  TT TA  GCCC CCA
                                   __ G  AA   C
GAM3532  FLJ10761  3'  GGTAGAAAGGGAGGT      79861        TCCC
                                GGTAGAGA   GGGAGGT
                                ||||||||   |||||||
                                CCATCTTT   CCCTCCA
                                     ____
GAM3532  FLJ22055  3'  GATGGGTGGAGATGGAATTGAG 79862    CA   A    CCCGG_
              GTA                  GA  GGT GAGAT     GAGGTA
                                ||  ||| |||||     ||||||
                                CT  CCA CTCTA     CTCCAT
                                 AC   C    CCTTAA
GAM3532  KIAA0182  3'  CAGGGGGAGTGGAGGAGGTA  79863     TA   ATCCC
                                CAGG  GAG    GGGAGGTA
                                ||||  |||    ||||||||
                                GTCC  CTC    TCCTCCAT
                                  CC   ACC__
GAM3532  KIAA0367  3'  GACGGGAGGAGACAGAGGT   79864     A  TA    CCCG
                                GAC GG  GAGAT    GGAGGT
                                ||| ||  |||||    ||||||
                                CTG CC  CTCTG    TCTCCA
                                  C  TC    ____
GAM3532  KIAA0544  3'  CAGGTAGATGTCAGCAGGT   79865        GATCC   G
                                CAGGTAGA    CGG AGGT
                                ||||||||    ||| ||||
                                GTCCATCT    GTC TCCA
                                     ACA__   G
GAM3532  KIAA1196  3'  GACAGGGGTCTGTCCTGGGAGG 79866       TAGAGA   C
              TA                   GACAGG     TCC GGGAGGTA
                                ||||||     ||| ||||||||
                                CTGTCC     AGG CCCTCCAT
                                   CCAGAC   A
GAM3532  LHPP     3'  CAGGTGGAGGGGAGGCA     79867      A   ATCCC
                                CAGGT GAG    GGGAGGTA
                                ||||| |||    ||||||||
                                GTCCA CTC    CCCTCCGT
                                   C  _____
GAM3532  MGC15619  3'  GGCAGGAGGGAGGCA      79868      A  TCCC
                                GGTAG GA   GGGAGGTA
                                ||||| ||   ||||||||
                                CCGTC CT   CCCTCCGT
                                     _ ____
GAM3532  ODC-p    3'  GCAGGTGGAGCGCGGGGGT   79869   A    A  ATCC   A
                                G CAGGT GAG   CGGG GGT
                                | ||||| |||   |||| |||
                                C GTCCA CTC   GCCC CCA
                                 _    C   GC__   _
GAM3532  SPR1     3'  CAGGAAGACCGGGTGGGAGGTA 79870     TA     CC__
                                CAGG  GAGATC   GGGAGGTA
                                ||||  ||||||   ||||||||
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                                GTCC  TTCTGG   CCCTCCAT
                                  __     CCCA
GAM3532  LOC127281 3'  CAGGTAGTCTGACCTGGGAGGT 79871       A__  T  C
             A                    CAGGTAG   GA CC GGGAGGTA
                                  |||||||   || || ||||||||
                                  GTCCATC   CT GG CCCTCCAT
                                      AGA  _  A
GAM3532  LOC127534 3'  GGGGGAGGTCCAGGAGGTA   79872    TA   ATC
                                  GG  GAG   CCGGGAGGTA
                                  ||  |||   ||||||||||
                                  CC  CTC   GGTCCTCCAT
                                   CC   CA_
GAM3532  LOC138639 5'  GACAGGGAGAGGAGAGGGAGGT 79873       T    ATCCC
                                  GACAGG AGAG    GGGAGGT
                                  |||||| ||||    |||||||
                                  CTGTCC TCTC    CCCTCCA
                                     C    CTCT_
GAM3532  LOC144147 3'  GATAGGCTAGAGAGGAGGT   79874    C   _    TCCCG
                                  GA AGGT AGAGA    GGAGGT
                                  || |||| |||||    ||||||
                                  CT TCCG TCTCT    CCTCCA
                                   A   A   _____
GAM3532  LOC145371 3'  AGGTAGAGAATGGAGGT     79875         TCCCG
                                  AGGTAGAGA    GGAGGT
                                  |||||||||    ||||||
                                  TCCATCTCT    CCTCCA
                                       TA___
GAM3532  LOC159121 5'  GGAGGTAGGGGATGAAGGAGGT 79876   C     A_   CCC
                                  A AGGTAG  GAT   GGGAGGT
                                  | ||||||  |||   |||||||
                                  C TCCATC  CTA   TCCTCCA
                                   C     CC   CT_
GAM3532  LOC199863 5'  AGGCAGGAGGGAGGT       79877       A  TCCC
                                  AGGTAG GA    GGGAGGT
                                  |||||| ||    |||||||
                                  TCCGTC CT    CCCTCCA
                                     _  ____
GAM3532  LOC202500 5'  AACAGGTAGGGATCTGGG    79878         A   CC
                                  GACAGGTAG GATC  GGG
                                  |||||||| ||||  |||
                                  TTGTCCATC CTAG  CCC
                                       C    A_
GAM3533  ETS2     3'  TGAAAAATGAAATAAAACCTCA 79881           _     AA
             GAT                    TGAAAAATGAAA AAAATT  AGAT
                                    |||||||||||| ||||||  ||||
                                    ACTTTTTACTTT TTTTGG  TCTA
                                           A     AG
GAM3533  FMR2     3'  GAGAAATGAAAAAAAAAAGAT  79882    A         TT
                                  GA AAATGAAAAAAA  AAAGAT
                                  || ||||||||||||  ||||||
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                                CT TTTACTTTTTTT  TTTCTA
                                 C         __
GAM3533  ARHE     3'  TGAAAAGTGAAATAAACCAACA 79883       A    A      _
              GAT                    TGAAAA TGAAA AAATTAA AGAT
                                |||||| ||||| ||||||| ||||
                                ACTTTT ACTTT TTTGGTT TCTA
                                   C    A      G
GAM3533  BIRC4    3'  TGAAAAATCAAGAAATTCAAAG 79884        G  A   A
              AT                     TGAAAAAT AA AAA TTAAAGAT
                                |||||||| || ||| ||||||||
                                ACTTTTTA TT TTT AGTTTCTA
                                    G  C   A
GAM3533  FLJ20275 3'  AAAAATTACCAAAAAATTAAAG 79885       GA__
              AT                     AAAAAT    AAAAAATTAAAGAT
                                ||||||    ||||||||||||||
                                TTTTTA    TTTTTTAATTTCTA
                                   ATGG
GAM3533  FLJ20986 5'  GAAAAATGAAAATGAAAAGAT  79886           AAATT
                                GAAAAATGAAAA     AAAGAT
                                ||||||||||||     ||||||
                                CTTTTTACTTTT     TTTCTA
                                       ACT__
GAM3533  KIAA0776 3'  TGACAAATGAAAAAAATTAA   79887     A
                                TGA AAATGAAAAAAATTAA
                                ||| ||||||||||||||||
                                ACT TTTACTTTTTTTAATT
                                  G
GAM3533  KIAA0924 3'  GAAAAATGAAGAAATTTCAAGA 79888          A   A  A
              T                      GAAAAATGAA AAA TT AAGAT
                                |||||||||| ||| || |||||
                                CTTTTTACTT TTT AA TTCTA
                                       C   A  G
GAM3533  NFAT5    3'  GAAAAATGAAAAATTGTAAGAT 79889           AATTA
                                GAAAAATGAAAAA     AAGAT
                                ||||||||||||     |||||
                                CTTTTTACTTTTT     TTCTA
                                       AACA_
GAM3533  TRIM35   3'  TAAAAAATGAAAAAAATTA   79890
                                TGAAAAATGAAAAAAATTA
                                ||||||||||||||||||
                                ATTTTTTACTTTTTTTAAT

GAM3533  LOC145988 3'  TGAAAAAAGAAAAATGCTAAAG 79891        T     AA
                                TGAAAAA GAAAAA  TTAAAG
                                ||||||| ||||||  ||||||
                                ACTTTTT CTTTTT  GATTTC
                                    T     AC
GAM3533  LOC153525 5'  AAAATGAAAAAAATCAAA    79892
                                AAAATGAAAAAAATTAAA
                                ||||||||||||||||||
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                                TTTTACTTTTTTTAGTTT

GAM3533  LOC158629 5'  TAAAAAATGGAAAAAATTTCAG 79893          A       AA
                AT                    TGAAAAATG AAAAAATT  AGAT
                                      ||||||||| ||||||||  ||||
                                      ATTTTTTAC TTTTTTAA  TCTA
                                           C       AG
GAM3533  LOC221849 3'  TGAAAAATAAAAAAATTAATGA 79894              A   A
                T                     TGAAAAATGAAAAAA TTAA GAT
                                      |||||||||||||||| |||| |||
                                      ACTTTTTATTTTTTT AATT CTA
                                                _   A
GAM3533  LOC221981 3'  TGAAAAATGAATGAAAACGAAA 79895           A_    T
                GAT                     TGAAAAATGAA  AAAAT AAAGAT
                                      ||||||||||  ||||| ||||||
                                      ACTTTTTACTT  TTTTG TTTCTA
                                             AC    C
GAM3534  AP2B1    3'  TGAGATTATAATATGGAAAG   79898     A   GTAT
                                      TGA ATTA    TATGGAAAG
                                      ||| ||||    |||||||||
                                      ACT TAAT    ATACCTTTC
                                        C   ATT_
GAM3534  BRCA1    3'  CTGAAATCAGATATGGAGAGAA 79899          TAT     A
                                      TTGAAATTAG   TATGGA AGAA
                                      ||||||||||   |||||| ||||
                                      GACTTTAGTC   ATACCT TCTT
                                             T__      C
GAM3534  FLT1     3'  TTGAAAAATTTATGGAAGGA   79900       TTAGTA       A
                                      TTGAAA      TTATGGAA GA
                                      ||||||      |||||||| ||
                                      AACTTT      AATACCTT CT
                                         TTA___       C
GAM3534  MOCS2    3'  GAAATTAGTCATGGAAGGA    79901         AT      A
                                      GAAATTAGT  TATGGAA GA
                                      |||||||||  ||||||| ||
                                      CTTTAATCA  GTACCTT CT
                                            __       C
GAM3534  RAB5C    3'  TTGAATTAGTATTTGTACAGAA 79902       A       A  GAA
                                      TTGAA TTAGTATT TG   AGAA
                                      ||||| |||||||| ||   ||||
                                      AACTT AATCATAA AC   TCTT
                                        _       _  ATG
GAM3534  RRM2B    3'  TTAGATTGTTATGGAAAGA    79903      TA__
                                      TTAG    TTATGGAAAGA
                                      ||||    ||||||||||||
                                      AATC    AATACCTTTCT
                                        TAAC
GAM3534  TRIM14   3'  TTGAAACTAGCCTAGGAGAG   79904          ATTAT   A
                                      TTGAAATTAGT     GGA AG
                                      ||||||||||     ||| ||
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                                AACTTTGATCG    CCT TC
                                      GAT__   C
GAM3534  TRPM7    3'  TTAAAATTAGTACCAAGGAA  79905            T
                                TTGAAATTAGTATTA GGAA
                                |||||||||||||| ||||
                                AATTTTAATCATGGT CCTT
                                       T
GAM3534  CGGBP1   3'  TCGAAATTAGTATTCATAGTAA 79906          _    A
           GA                    TTGAAATTAGTAT TATGG AAGA
                                |||||||||||| ||||| ||||
                                AGCTTTAATCATA GTATC TTCT
                                      A    A
GAM3534  FLJ21302 3'  GAAATTAGTATTCTAGAA    79907          A
                                GAAATTAGTATT TGGAA
                                |||||||||||| |||||
                                CTTTAATCATAA ATCTT
                                      G
GAM3534  KIAA0937 3'  TTCAAATTAGTATCCAGAGGA  79908    G        AT__
                                TT AAATTAGTATT   GGA
                                || ||||||||||   |||
                                AA TTTAATCATAG   CCT
                                 G         GTCT
GAM3534  KIAA1275 3'  AAATTAGTACATGTAAAGAA   79909         T  G
                                AAATTAGTAT ATG AAAGAA
                                |||||||||| ||| ||||||
                                TTTAATCATG TAC TTTCTT
                                      _  A
GAM3534  MAP      3'  TTGACATTAGTATCTGTAAAGA 79910     A       A  G
                                TTGA ATTAGTATT TG AAAGA
                                |||| ||||||||| || |||||
                                AACT TAATCATAG AC TTTCT
                                  G       _ A
GAM3534  PRO1768  3'  TTGAGATCAGTGTATGAAAAA  79911     A     AT
                                TTGA ATTAGT  TATGGAAAG
                                |||| ||||||  |||||||||
                                AACT TAGTCA  ATACTTTTT
                                  C     C_
GAM3534  LOC126603 5'  TTGAAACTGGTACACGATGGGG 79912        A   T__   AA
           AG                    TTGAAATT GTAT   ATGG  AG
                                ||||||| ||||   ||||  ||
                                AACTTTGA CATG   TACC  TC
                                    C   TGC   CC
GAM3534  LOC152195 3'  TTGAAATTAGGATCTGGAGAG  79913         T  A   A
                                TTGAAATTAG ATT TGGA AG
                                |||||||||| ||| |||| ||
                                AACTTTAATC TAG ACCT TC
                                      C  _   C
GAM3534  LOC158722 3'  TTGAAATTGGTATCGGCAATTT 79914       A    A_______
           GGAAAG                  TGAAATT GTATT      TGGAAAG
                                |||||||  |||||      |||||||
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                                ACTTTAA CATAG      ACCTTTC
                                    C    CCGTTAA
GAM3534  LOC196385 3'  TTAATTTGTATGGAAAGA    79915      AT_
                                TTAGT   TATGGAAAGA
                                |||||   ||||||||||
                                AATTA   ATACCTTTCT
                                   AAC
GAM3535  PTPRT    3'  TTCATGTATGTATGTTTTCGTT 79918         T  CT  C
                                TTTATGTAT GT  TG TTTCGTT
                                ||||||||| ||  || |||||||
                                AAGTACATA CA  AC AAAGCAA
                                      _ T_  A
GAM3535  LOC146820 5'  TTTATGGATTGTCTTCT     79919       T       G
                                TTTATG ATTGTCTT CT
                                |||||| |||||||| ||
                                AAATAC TAACAGAA GA
                                   C       _
GAM3536  LAMC2    3'  GAAGTTGCTTATATACACCTGT 79922       A  C  TCG TG
             T                   GAAGTT CT AT   G  CTTGTT
                                 |||||| || ||   |  |||||||
                                 CTTCAA GA TA   T  GGACAA
                                    C  A  TA_ GT
GAM3536  BRAG     3'  GAGGTTGCTCATTCTGGCA    79923    A   A      _
                                GA GTT CTCATTC GGTG
                                || ||| ||||||| ||||
                                CT CAA GAGTAAG CCGT
                                 C   C       A
GAM3536  GBP2     3'  GAAGTTGCTCATTCATGTTGTT 79924       A       G  C
                                GAAGTT CTCATTCG TG TTGTT
                                |||||| |||||||| || |||||
                                CTTCAA GAGTAAGT AC AACAA
                                   C       _ _
GAM3536  PABPC5   3'  AGTTATTCATCTTTCTTGTT   79925      C    CGGTG
                                AGTTA TCATT     CTTGTT
                                ||||| |||||     ||||||
                                TCAAT AGTAG     GAACAA
                                   A     AAA__
GAM3536  LOC144438 3'  GGATTACTGTACCGTGCTTGTT 79926    A     CAT   G
                                A GTTACT   TCG TGCTTGTT
                                | ||||||   ||| ||||||||
                                C TAATGA   GGC ACGAACAA
                                 C     CAT   _
GAM3536  LOC153769 3'  GAAGTTGTTCTAATGCTTGTT  79927       ACTCA  CG
                                GAAGTT     TT  GTGCTTGTT
                                ||||||     ||  ||||||||||
                                CTTCAA     AG  TACGAACAA
                                   CA___   AT
GAM3537  IFNW1    5'  TATATATAATATATATTCATAT 79931         _      A
             ATA                   TATATATA TATATAT TATATATA
                                   |||||||| ||||||| ||||||||
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                                ATATATAT ATATATA GTATATAT
                                    T      A
GAM3537  IFNW1    5'  TATATAATATATATTCATATAT 79930       _      A
                ATA                   TATATA TATATAT TATATATATA
                                |||||| ||||||| ||||||||||
                                ATATAT ATATATA GTATATATAT
                                   T      A
GAM3537  IFNW1    5'  TATATAATATATATTCATATAT 79930       _      A
                ATA                   TATATA TATATAT TATATATATA
                                |||||| ||||||| ||||||||||
                                ATATAT ATATATA GTATATATAT
                                   T      A
GAM3537  FLJ12078 5'  TATATATATATATTTATATATA 79932            A
                                TATATATATATAT TATATATA
                                |||||||||||| ||||||||
                                ATATATATATATA ATATATAT
                                        A
GAM3537  KIAA0976 5'  TACATATATATACACATATGTA 79933                  A
                T                    TATATATATATATATATAT TAT
                                |||||||||||||||||| |||
                                ATGTATATATATGTGTATA ATA
                                          C
GAM3537  LOC145868 5'  TATATATATCATATTATATATA 79934         A    A
                                TATATATAT TATAT TATATATA
                                ||||||||| ||||| ||||||||
                                ATATATATA GTATA ATATATAT
                                          _   _
GAM3537  LOC153077 5'  CATATATATATATAAATATA   79935            T
                                TATATATATATATA ATATA
                                |||||||||||||| |||||
                                GTATATATATATAT TATAT
                                        T
GAM3538  C7orf2   3'  ATTATATATATACATAAAC   79938             CG
                                ATTATATATATACA  TAGAC
                                |||||||||||||  |||||
                                TAATATATATATGT  ATTTG
                                          __
GAM3538  CLCA1    5'  CATTATATATATACAGATA   79939             C
                                TATTATATATATACA GTA
                                |||||||||||||| |||
                                GTAATATATATATGT TAT
                                          C
GAM3538  ENPP3    3'  ATTATATATTAAGTAGACA   79940         ATACAC
                                ATTATATAT     GTAGACA
                                |||||||||     |||||||
                                TAATATATA     CATCTGT
                                     ATT____
GAM3538  ENPP3    3'  ATTATATATTAAGTAGACA   79940         ATACAC
                                ATTATATAT     GTAGACA
                                |||||||||     |||||||
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                                TAATATATA     CATCTGT
                                      ATT___
GAM3538 H1F0     3' TATATATACACAAACAC     79941          TA
                                TATATATACACG  GACAC
                                ||||||||||||  |||||
                                ATATATATGTGT  TTGTG
                                          __
GAM3538 IGFBP1   3' TACTATATATATATACAT    79942           C
                                TATTATATATATA ACGT
                                |||||||||||| ||||
                                ATGATATATATAT TGTA
                                      A
GAM3538 IL1F9    3' TATTATATAAATACACAAAG  79943         T      T
                                TATTATATA ATACACG AG
                                ||||||||| ||||||| ||
                                ATAATATAT TATGTGT TC
                                      T      T
GAM3538 ZNF141   3' ATTATATATATACAGTAA    79944           C
                                ATTATATATATACA GTAG
                                |||||||||||||| ||||
                                TAATATATATATGT CATT
                                          _
GAM3538 C1orf24  3' TATTATACATATACTGAGTA  79945           AC_
                                TATTATATATATAC   GTA
                                ||||||||||||||   |||
                                ATAATATGTATATG   CAT
                                      ACT
GAM3538 DNCLI1   3' TATATATATATGTATAGAC   79946         CAC
                                TATATATATA   GTAGAC
                                ||||||||||   ||||||
                                ATATATATAT   TATCTG
                                      ACA
GAM3538 GFR      3' TATTATATATATACACAGAG  79947           T
                                TATTATATATATACACG AG
                                |||||||||||||||| ||
                                ATAATATATATATGTGT TC
                                         C
GAM3538 KIAA0937 3' TATATATATATACGTCAAAC  79948         C   _
                                TATATATATA ACGT AGAC
                                |||||||||| |||| ||||
                                ATATATATAT TGCA TTTG
                                      A   G
GAM3538 KIAA1726 3' TATATATATACTGTAACAC   79949         AC  A
                                TATATATATAC  GT GACAC
                                ||||||||||  || |||||
                                ATATATATATG  CA TTGTG
                                      A_  _
GAM3538 MGC12466 3' TATAAGTATACATGTAGACA  79950     TA     C
                                TATA  TATACA GTAGACA
                                ||||  |||||| |||||||
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                                ATAT  ATATGT CATCTGT
                                  TC     A
GAM3538  MYOZ2    3'  TATTACATATATTACGATAGA  79951          AC  _
                                TATTATATATAT  ACG TAGA
                                ||||||||||||  ||| ||||
                                ATAATGTATATA  TGC ATCT
                                       A_   T
GAM3538  OSBPL8   3'  TATTATACTCATATGTAGACAC 79952        A    CAC
                                TATTATAT TATA   GTAGACAC
                                |||||||| ||||   ||||||||
                                ATAATATG GTAT   CATCTGTG
                                     A   A__
GAM3538  PROL2    3'  CATTGTATATATACAAAACAC  79953      A        CGT
                                TATT TATATATACA   AGACAC
                                |||| ||||||||||   ||||||
                                GTAA ATATATATGT   TTTGTG
                                  C        ___
GAM3538  SPIN     3'  TATTATATATGTATACAC     79954          __
                                TATTATATA  TATACAC
                                |||||||||  |||||||
                                ATAATATAT  ATATGTG
                                     AC
GAM3538  ZF       3'  TATATATATAATTCAGTAGGCA 79955          ___ C    A
            C                    TATATATATA   CA GTAG CAC
                                |||||||||||   || |||| |||
                                ATATATATAT   GT CATC GTG
                                      TAA  _   C
GAM3538  LOC135154 3'  TATATATATATATTTAAACAC  79956          CACG
                                TATATATATA    TAGACAC
                                ||||||||||    |||||||
                                ATATATATAT    ATTTGTG
                                      ATAA
GAM3538  LOC145508 3'  TATATATGCACATCTCCAC    79957        A    AGA
                                TATATAT CACGT   CAC
                                ||||||| |||||   |||
                                ATATATA GTGTA   GTG
                                     C    GAG
GAM3538  LOC145868 5'  TATTATATATAATACATAACA  79959          TAC    A
                                TATTATATATA   ACGT GACA
                                ||||||||||||   |||| ||||
                                ATAATATATAT   TGTA TTGT
                                      TA_   _
GAM3538  LOC145868 5'  TATTATATATAACACAT     79958          T
                                TATTATATATA ACACGT
                                |||||||||||| ||||||
                                ATAATATATAT TGTGTA
                                          _
GAM3538  LOC146909 3'  CTATATATATATGCAGA     79960          CAC
                                TTATATATATA   GTAGA
                                ||||||||||   |||||
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                                GATATATATAT   CGTCT
                                      A__
GAM3538  LOC153222 3'  TATATATATATACATAATAC   79961          C     _
                                TATATATATA ACGTAG AC
                                |||||||||| |||||| ||
                                ATATATATAT TGTATT TG
                                      A     A
GAM3538  LOC50999  3'  TATTATATACATATCAGTA    79962           _ C
                                TATTATATATATA CA GTA
                                |||||||||||| || |||
                                ATAATATATGTAT GT CAT
                                      A  _
GAM3539  AGTR1     3'  ATATACATATATATATAT     79965
                                ATATATATATATATATAT
                                ||||||||||||||||||
                                TATATGTATATATATATA

GAM3539  AGTR1     3'  ATATACATATATATATAT     79965
                                ATATATATATATATATAT
                                ||||||||||||||||||
                                TATATGTATATATATATA

GAM3539  AGTR1     3'  ATATACATATATATATAT     79965
                                ATATATATATATATATAT
                                ||||||||||||||||||
                                TATATGTATATATATATA

GAM3539  AGTR1     3'  ATATACATATATATATAT     79965
                                ATATATATATATATATAT
                                ||||||||||||||||||
                                TATATGTATATATATATA

GAM3539  AGTR1     3'  ATATACATATATATATAT     79965
                                ATATATATATATATATAT
                                ||||||||||||||||||
                                TATATGTATATATATATA

GAM3539  ATP2B2    3'  TATATATATATATATATATAA  79967                 ATIII
                                TATATATATATATATATAT     A
                                ||||||||||||||||||     |
                                ATATATATATATATATATA     T
                                      IIITA
GAM3539  ATP2B2    3'  ATATTTATATATATATATATAT 79966      A             III
            A                    ATAT TATATATATATATATAT   A
                                |||| ||||||||||||||||   |
                                TATA ATATATATATATATATA   T
                                  A             III
GAM3539  ATP2B2    3'  ATATATATATATATATCTAC   79968             A
                                ATATATATATATATAT TAT
                                |||||||||||||| |||
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                                TATATATATATATATA ATG
                                       G
GAM3539 ATP8B2   3' TAATATATATATATATAACTGT 79970            ____
           ATATAT                AATATATATATATATA   TATATAT
                                 ||||||||||||||||   |||||||
                                 TTATATATATATATAT   ATATATA
                                       TGAC
GAM3539 ATP8B2   3' ATATATATATAACTGTATATAT 79969       ____       III
           ATATA                 TATATATA   TATATATATAT  A
                                 ||||||||   ||||||||||  |
                                 ATATATAT   ATATATATATA  T
                                    TGAC        III
GAM3539 BACH2    3' ATATATATATATTTTTTATATA 79972         _____
           TATAT                 ATATATATATA   TATATATATAT
                                 ||||||||||    ||||||||||
                                 TATATATATAT   ATATATATATA
                                       AAAAA
GAM3539 BACH2    3' ATATATATATATATATATAT  79973
                                 ATATATATATATATATATAT
                                 ||||||||||||||||||||
                                 TATATATATATATATATATA

GAM3539 BACH2    3' ATATGGATATATATATATATAT 79971     __
           AT                   ATAT  ATATATATATATATATAT
                                ||||  ||||||||||||||||||
                                TATA  TATATATATATATATATA
                                  CC
GAM3539 BCL11B   3' TAATATATATAATATATAC   79974          T
                                TAATATATATA ATATATAT
                                ||||||||||| ||||||||
                                ATTATATATAT TATATATG

                                      _
GAM3539 BCL6     3' ATATATATATATATTTATATAT 79976           A
                                ATATATATATATAT TATATAT
                                ||||||||||||| |||||||
                                TATATATATATATA ATATATA
                                       A
GAM3539 BCL6     3' TATATATATTTATTTTATATAT 79975    ________        III
           ATATATA               ATA     TATATATATATAT  A
                                 |||     ||||||||||||  |
                                 TAT     ATATATATATATA  T
                                   AAATAAA          III
GAM3539 BCL6     3' TATATATATTTATTTTATATAT 79975    ________        III
           ATATATA               ATA     TATATATATATAT  A
                                 |||     ||||||||||||  |
                                 TAT     ATATATATATATA  T
                                   AAATAAA          III
GAM3539 BCL6     3' ATATATATATATATTTATATAT 79976           A
                                ATATATATATATAT TATATAT
                                ||||||||||||| |||||||
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                                TATATATATATATA ATATATA
                                       A
GAM3539  CACNB2   3'  ATATATATATATATATTATATA 79977                _
                T                   ATATATATATATATAT ATATAT
                                    |||||||||||||||| ||||||
                                    TATATATATATATATA TATATA
                                           A
GAM3539  CBFA2T1  3'  TATATATATATATATATAT    79980
                                    TATATATATATATATATAT
                                    ||||||||||||||||||
                                    ATATATATATATATATATA

GAM3539  CBFA2T1  3'  ATATATATATATATATATATAT 79978
                                    ATATATATATATATATATATAT
                                    |||||||||||||||||||||
                                    TATATATATATATATATATATA

GAM3539  CBFA2T1  3'  ATATATATATATATATATATAT 79978
                                    ATATATATATATATATATATAT
                                    |||||||||||||||||||||
                                    TATATATATATATATATATATA

GAM3539  CBFA2T1  3'  ATATATATATATATATATATAT 79978
                                    ATATATATATATATATATATAT
                                    |||||||||||||||||||||
                                    TATATATATATATATATATATA

GAM3539  CBFA2T1  3'  TATATATATATATATATATAT  79979
                                    TATATATATATATATATATAT
                                    ||||||||||||||||||||
                                    ATATATATATATATATATATA

GAM3539  COL4A5   3'  TATATATATATATATCACAT   79981          A
                                    TATATATATATATAT TATAT
                                    |||||||||||||| |||||
                                    ATATATATATATATA GTGTA
                                          _
GAM3539  COL4A5   3'  TATATATATATATATCACAT   79981          A
                                    TATATATATATATAT TATAT
                                    |||||||||||||| |||||
                                    ATATATATATATATA GTGTA
                                          _
GAM3539  COL4A5   3'  TATATATATATATATCACAT   79981          A
                                    TATATATATATATAT TATAT
                                    |||||||||||||| |||||
                                    ATATATATATATATA GTGTA
                                          _
GAM3539  CRADD    3'  ATATATATGGGATATATATATA 79985          ___
                TAT                   ATATATAT   ATATATATATATAT
                                    ||||||||   ||||||||||||||
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TATATATA TATATATATATATA
CCC
GAM3539 CRADD 3' ATATATATATATATGGATATAT 79982
AT ATATATATATATAT ATATATAT
TATATATATATATA TATATATA
CC
GAM3539 CRADD 3' ATATATATATGGGATATATATA 79984
TATA ATATATAT ATATATATATAT A
TATATATA TATATATATATA T
CCC III
GAM3539 CRADD 3' ATATATATATATATGGATATAT 79983
AT
ATATATATATATAT ATATAT
TATATATATATATA TATATA
CC
GAM3539 CRIM1 3' AATATATATGTATATATATATA 79986
A III
TA AATATATAT TATATATATATAT A
TTATATATA ATATATATATATA T
C III
GAM3539 CTGF 3' TACATATATATATATATAT 79987
TATATATATATATATATAT
ATGTATATATATATATATA
GAM3539 CTLA4 3' ATATATATATATATATATATAT 79978
ATATATATATATATATATATAT
TATATATATATATATATATATA
GAM3539 CTLA4 3' ATATATATATATATATATATAT 79978
ATATATATATATATATATATAT
TATATATATATATATATATATA
GAM3539 CTLA4 3' TAAAATATATATATATATATAT 79988
T III
ATA AA ATATATATATATATATATAT A
TT TATATATATATATATATATA T
T III
GAM3539 CTLA4 3' ATATATATATATATATATATAT 79978
ATATATATATATATATATATAT
TATATATATATATATATATATA
GAM3539 CTLA4 3' ATATATATATATATATATAT 79973
ATATATATATATATATATAT

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                                TATATATATATATATATATA

GAM3539  CTLA4    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CTLA4    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CTLA4    3'  ATATATATATATATGTATATAT 79990          A
                                ATATATATATATAT TATATAT
                                |||||||||||||| |||||||
                                TATATATATATATA ATATATA
                                      C
GAM3539  CTLA4    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CTLA4    3'  ATATATATATATATATGTATAT 79991           A
                                ATATATATATATAT TATAT
                                |||||||||||||| |||||
                                TATATATATATATA ATATA
                                       C
GAM3539  CTLA4    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CTLA4    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CTLA4    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CTLA4    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CTLA4    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
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                                TATATATATATATATATATATA

GAM3539  CTLA4    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CTLA4    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CTLA4    3'  AATATATATATATATATATATA 79989                    III
                TA                    AATATATATATATATATATATAT   A
                                ||||||||||||||||||||||||   |
                                TTATATATATATATATATATATA   T
                                                  III
GAM3539  CTLA4    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CYP1A2   3'  TATATATATATGTATATATATA 79992            A        III
                T                     TATATATATAT TATATATAT   AT
                                ||||||||||| |||||||||   ||
                                ATATATATATA ATATATATA   TA
                                       C        III
GAM3539  DAPK1    3'  TAATATATATGTATATACAT   79993           A
                                TAATATATAT TATATATAT
                                |||||||||| |||||||||
                                ATTATATATA ATATATGTA
                                      C
GAM3539  DAPK1    3'  CATATATATATATACATAT    79994
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                GTATATATATATATGTATA

GAM3539  DDX6     3'  ATATATGTATATATATATATAT 80000        A
                                ATATAT TATATATATATATAT
                                |||||| ||||||||||||||
                                TATATA ATATATATATATATA
                                    C
GAM3539  DDX6     3'  TATATATATATATATATAT    79980
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATATATATATATATATA

GAM3539  DDX6     3'  ATATATATGTATATATATATAT 79999         A
                                ATATATAT TATATATATATAT
                                |||||||| ||||||||||||
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                                TATATATA ATATATATATATA
                                     C
GAM3539  DDX6    3'  ATATATATATGTATATATATAT 79998          A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TATATATATA ATATATATATA
                                     C
GAM3539  DDX6    3'  ATATGTATATATATATATATAT 79996      A
                                ATAT TATATATATATATATAT
                                |||| ||||||||||||||||
                                TATA ATATATATATATATATA
                                   C
GAM3539  DDX6    3'  AATATATATATATGTATATATA 79997            A        III
              TA                   AATATATATATAT TATATATAT   A
                                |||||||||||| |||||||||   |
                                TTATATATATATA ATATATATA   T
                                        C        III
GAM3539  DDX6    3'  AATATATATATATGTATATATA 79995           A      ATIII
                A                    AATATATATATAT TATATAT    A
                                |||||||||||| |||||||    |
                                TTATATATATATA ATATATA    T
                                        C      IIITA
GAM3539  DRIL1   3'  TATATATATATATATATATATA 80003                 III
                                TATATATATATATATATATAT   A
                                |||||||||||||||||||   |
                                ATATATATATATATATATATA   T
                                           III
GAM3539  DRIL1   3'  ATATACGTATATATATATATAT 80001       TA
                                ATATA  TATATATATATATAT
                                |||||  ||||||||||||||
                                TATAT  ATATATATATATATA
                                   GC
GAM3539  DRIL1   3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  DRIL1   3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  DRIL1   3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  DRIL1   3'  ATATATACGTATATATATATAT 80002        TA
                                ATATATA  TATATATATATAT
                                |||||||  ||||||||||||
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                                TATATAT  ATATATATATATA
                                    GC
GAM3539  EDNRA    3'  ATATGTATATACATATATAT   80004      A
                                ATAT TATATATATATATAT
                                |||| ||||||||||||||
                                TATA ATATATGTATATATA
                                  C
GAM3539  EP300    3'  TAATATATATTTATATATAT   80006          A
                                TAATATATAT TATATATAT
                                |||||||||| |||||||||
                                ATTATATATA ATATATATA
                                      A
GAM3539  EP300    3'  TATATATATTTATATATATAT  80005          A
                                TATATATAT TATATATATAT
                                ||||||||| ||||||||||
                                ATATATATA ATATATATATA
                                      A
GAM3539  ETV6     3'  AATATATATATATAATAGATAT 80007              T___
              ATAT                   AATATATATATATA    ATATATAT
                                |||||||||||||    ||||||||
                                TTATATATATATAT    TATATATA
                                       TATC
GAM3539  F9       3'  TATATATATATTATATATAT   80008          A
                                TATATATATAT TATATATAT
                                |||||||||| |||||||||
                                ATATATATATA ATATATATA
                                      _
GAM3539  FACL4    3'  TATATATATGCATATATAT    80009          A
                                TATATATAT TATATATAT
                                ||||||||| |||||||||
                                ATATATATA GTATATATA
                                      C
GAM3539  FACL4    3'  TATATATATGCATATATAT    80009          A
                                TATATATAT TATATATAT
                                ||||||||| |||||||||
                                ATATATATA GTATATATA
                                      C
GAM3539  FGFR3    3'  TATATATATATATGTATATATA 80011              A      III
                                TATATATATATAT TATATAT   A
                                |||||||||||| |||||||   |
                                ATATATATATATA ATATATA   T
                                       C      III
GAM3539  FGFR3    3'  TATATATATAGATATATAT    80010          T
                                TATATATATA ATATATAT
                                |||||||||| ||||||||
                                ATATATATAT TATATATA
                                      C
GAM3539  FGFR3    3'  TATATATATGTATATATAC    80012          A
                                TATATATAT TATATATAT
                                ||||||||| |||||||||
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ATATATATA ATATATATG
C
GAM3539 HDAC4 3' AATATATATTATACATATATAT 80013
AT AATATATAT ATATATATATATAT
TTATATATA TATGTATATATATA
A
GAM3539 HOXC4 3' TATATATATATATATATATATA 80003
TATATATATATATATATATAT A
ATATATATATATATATATATA T
GAM3539 HOXC4 3' ATATATATATATATATATATAT 79978
ATATATATATATATATATATAT
TATATATATATATATATATATA
GAM3539 HOXC4 3' ATATATATATATATATATATAT 79978
ATATATATATATATATATATAT
TATATATATATATATATATATA
GAM3539 HS2ST1 3' AATATATATATATGTATATA 80014
TAT ATATATATATATAT TATATAT AT
TATATATATATATA ATATATA TA
C
GAM3539 HS2ST1 3' ATATATATATATGTATATATAT 80015
ATATATATATAT TATATATAT
TATATATATATA ATATATATA
C
GAM3539 IFNW1 5' TAATATATATTCATATATATAT 80016
TAATATATAT TATATATATAT
ATTATATATA GTATATATATA
A
GAM3539 IGF1 3' TAAGATATATATATATATATAT 80017
TAA ATATATATATATATATAT
ATT TATATATATATATATATA
C
GAM3539 INPP5A 3' TATATATATTTATATATATAT 80005
TATATATAT TATATATATAT
ATATATATA ATATATATATA
A
GAM3539 KCNH5 3' TAACAAATATATATGTATATAT 80018
ATAT ATA ATATATAT TATATAT AT

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                                TGT TATATATA ATATATA     TA
                                  T       C       IIITA
GAM3539  KCNH5    3'  TATATACACACATATGTATAT  80019              A
                                TATATATATATATAT TATAT
                                |||||||||||||| |||||
                                ATATATGTGTGTATA ATATA
                                          C
GAM3539  KIF3C    3'  TATATATATATTTATATAT    80020           A
                                TATATATATAT TATATAT
                                |||||||||| |||||||
                                ATATATATATA ATATATA
                                       A
GAM3539  KPNA4    3'  ATATATATGTATATATATATAT 79999          A
                                ATATATAT TATATATATATAT
                                |||||||| ||||||||||||
                                TATATATA ATATATATATATA
                                     C
GAM3539  KPNA4    3'  ACACACATATATATATATATAT 80022
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TGTGTGTATATATATATATATA

GAM3539  KPNA4    3'  ATATATGTATATATATATATAT 80000        A
                                ATATAT TATATATATATATAT
                                |||||| ||||||||||||||
                                TATATA ATATATATATATATA
                                    C
GAM3539  KPNA4    3'  TATATATATGTATATATATATA 80021          A          III
                                TATATATAT TATATATATAT   A
                                ||||||||| ||||||||||   |
                                ATATATATA ATATATATATA   T
                                      C          III
GAM3539  KPNA4    3'  ATATGTATATATATATATATAT 79996      A
                                ATAT TATATATATATATATAT
                                |||| ||||||||||||||||
                                TATA ATATATATATATATATA
                                  C
GAM3539  LMCD1    3'  TATATATATCTCATATATATAT 80023          A_
                                TATATATAT  TATATATATAT
                                |||||||||  ||||||||||
                                ATATATATA  GTATATATATA
                                     GA
GAM3539  MAN1A1   3'  ACATAAATATATATGTATATAT 80024       T       A
                                ATATA ATATATAT TATATAT
                                ||||| |||||||| |||||||
                                TGTAT TATATATA ATATATA
                                  T       C
GAM3539  MAP3K12  3'  ATATATATATATATATGTATAT 80025              A    III
            AT                    ATATATATATATATAT TATAT   AT
                                ||||||||||||||| |||||   ||
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                                TATATATATATATATA ATATA   TA
                                                 C     III
GAM3539  MAP3K12   3'  ATATATATATGTATATATATAT 79998          A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TATATATATA ATATATATATA
                                     C
GAM3539  MAP3K12   3'  ATATATATATATGTATATATAT 80015           A
                                ATATATATATAT TATATATAT
                                |||||||||||| |||||||||
                                TATATATATATA ATATATATA
                                     C
GAM3539  MAP3K12   3'  ATATATATATATATGTATATAT 79990             A
                                ATATATATATATAT TATATAT
                                |||||||||||||| |||||||
                                TATATATATATATA ATATATA
                                     C
GAM3539  MASP1     3'  TAATATATATATATATAT     80026
                                TAATATATATATATATAT
                                ||||||||||||||||||
                                ATTATATATATATATATA

GAM3539  MBNL      3'  ATATATATCTATTATATATATA 80027         ATA_
           T                     ATATATAT    TATATATATAT
                                |||||||||    ||||||||||
                                TATATATA    ATATATATATA
                                     GATA
GAM3539  MEN1      3'  ATATATATATACATATATATAT 80031
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATGTATATATATA

GAM3539  MEN1      3'  ATATATATACATATATATATAT 80029
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATGTATATATATATA

GAM3539  MEN1      3'  TATATATATATGTATATAT    80034          A
                                TATATATATAT TATATAT
                                |||||||||| |||||||
                                ATATATATATA ATATATA
                                     C
GAM3539  MEN1      3'  ATATATATATGTATATATATAT 79998          A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TATATATATA ATATATATATA
                                     C
GAM3539  MEN1      3'  ATATATATATATACATATATAT 80035
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
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                                TATATATATATATGTATATATA

GAM3539  MEN1     3'  ATATGTATATATATATGTATAT 80033      A          A
                                ATAT TATATATATAT TATAT
                                |||| |||||||||| |||||
                                TATA ATATATATATA ATATA
                                   C          C
GAM3539  MEN1     3'  ATATATATATACATATATATAT 80031
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATGTATATATATA

GAM3539  MEN1     3'  ATATATATGTATATATATATAT 79999          A
                                ATATATAT TATATATATATAT
                                |||||||| ||||||||||||
                                TATATATA ATATATATATATA
                                      C
GAM3539  MEN1     3'  ATATATACATATATATATATAT 80032
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATGTATATATATATATA

GAM3539  MEN1     3'  ATATATATATGTATATATATAT 79998           A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TATATATATA ATATATATATA
                                      C
GAM3539  MEN1     3'  ATATATATGTATATATATAT   80030          A
                                ATATATAT TATATATATAT
                                |||||||| ||||||||||
                                TATATATA ATATATATATA
                                      C
GAM3539  MEN1     3'  ATATATATATATATACATATAT 80028
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATGTATATA

GAM3539  MEN1     3'  ATATATATATGTATATATATAT 79998           A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TATATATATA ATATATATATA
                                      C
GAM3539  MEN1     3'  ATATATATATATACATATATAT 80035
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATGTATATATA

GAM3539  MEN1     3'  TATATATATATGTATATATAT  80036           A
                                TATATATATAT TATATATAT
                                |||||||||| |||||||||
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                                ATATATATATA ATATATATA
                                      C
GAM3539  MEN1    3'  ATATATGTATATATATATATAT 80000       A
                                ATATAT TATATATATATATAT
                                |||||| ||||||||||||||||
                                TATATA ATATATATATATATA
                                   C
GAM3539  MOX2    3'  TATATATATATATAAATAT   80037            T
                                TATATATATATATA ATAT
                                |||||||||||||| ||||
                                ATATATATATATAT TATA
                                         T
GAM3539  MYBL1   3'  ATATATAAATATATATATATAT 80041        T
                                ATATATA ATATATATATATAT
                                ||||||| ||||||||||||||
                                TATATAT TATATATATATATA
                                    T
GAM3539  MYBL1   3'  AATATATATATATATAAAATAT 80040              TAT
                                AATATATATATATATA   ATAT
                                |||||||||||||||   ||||
                                TTATATATATATATAT   TATA
                                         TT_
GAM3539  MYBL1   3'  ATATATATATAAATATATATAT 80039           T
                                ATATATATATA ATATATATAT
                                |||||||||| |||||||||
                                TATATATATAT TATATATATA
                                      T
GAM3539  MYBL1   3'  ATATATATAAATATATATATAT 80038          T
                                ATATATATA ATATATATATAT
                                ||||||||| ||||||||||||
                                TATATATAT TATATATATATA
                                     T
GAM3539  MYCL2   3'  TAATATATACATATATACAT   80042
                                TAATATATATATATATATAT
                                ||||||||||||||||||||
                                ATTATATATGTATATATGTA

GAM3539  MYCL2   3'  TACATATATATATACATATAT  80044
                                TATATATATATATATATATAT
                                ||||||||||||||||||||
                                ATGTATATATATATGTATATA

GAM3539  MYCL2   3'  ATATATACATACATATATATAT 80043
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATGTATGTATATATATA

GAM3539  MYCL2   3'  ACATATATATATACATATAT   80045
                                ATATATATATATATATATAT
                                ||||||||||||||||||||
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                                TGTATATATATATGTATATA

GAM3539  MYCL2    3'  ATATATACATACATATATATAT 80043
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATGTATGTATATATATA

GAM3539  MYCL2    3'  ATATATACATACATATATATAT 80043
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATGTATGTATATATATA

GAM3539  MYCL2    3'  TACATATATATATACATATAT  80044
                                TATATATATATATATATATAT
                                ||||||||||||||||||||
                                ATGTATATATATATGTATATA

GAM3539  MYCL2    3'  TACATATATATATACATATAT  80044
                                TATATATATATATATATATAT
                                ||||||||||||||||||||
                                ATGTATATATATATGTATATA

GAM3539  MYCL2    3'  ATATATACATACATATATATAT 80043
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATGTATGTATATATATA

GAM3539  MYF5     3'  TAATATATATATATGTATATAT 80046          A      ATIII
              AA                  AATATATATATAT TATATAT    A
                                ||||||||||||| |||||||    |
                                TTATATATATATA ATATATA    T
                                      C      IIITA
GAM3539  MYF5     3'  TAATATATATATATGTATATAT 80046          A    ATATIII
              AA                  AATATATATATAT TATAT      A
                                ||||||||||||| |||||      |
                                TTATATATATATA ATATA      T
                                      C    IIITATA
GAM3539  NOV      3'  ACATGTATGTATACACATATAT 80047      A  A
                                ATAT TAT TATATATATATAT
                                |||| ||| ||||||||||||
                                TGTA ATA ATATGTGTATATA
                                  C  C
GAM3539  NRF1     3'  ATACATATATATATATATATAT 80049
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATGTATATATATATATATATA

GAM3539  NRF1     3'  TATATATATACTTTATATATAT 80048          A_
                                TATATATATAT  TATATATAT
                                ||||||||||  |||||||||
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                                ATATATATATG  ATATATATA
                                      AA
GAM3539  NRF1     3'  ATATATATATATATATGTATAT 79991              A
                                ATATATATATATATAT TATAT
                                |||||||||||||||| |||||
                                TATATATATATATATA ATATA
                                      C
GAM3539  NRF1     3'  TATATATGTATATATATAC    80050        A
                                TATATAT TATATATATAT
                                ||||||| ||||||||||
                                ATATATA ATATATATATG
                                    C
GAM3539  NRF1     3'  ATATATATATATATGTATATAT 79990             A
                                ATATATATATATAT TATATAT
                                ||||||||||||| |||||||
                                TATATATATATATA ATATATA
                                      C
GAM3539  NRF1     3'  ATATATATATATGTATATATAT 80015            A
                                ATATATATATAT TATATATAT
                                |||||||||||| |||||||||
                                TATATATATATA ATATATATA
                                      C
GAM3539  NRIP1    3'  TATATATATATATATATAT    79980
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATATATATATATATATA

GAM3539  NRIP1    3'  ATATACATATTATATATATATA 80054          _
            T                    ATATATATAT ATATATATATAT
                                ||||||||||| ||||||||||||
                                TATATGTATA TATATATATATA
                                      A
GAM3539  NRIP1    3'  TATATATATATATATATATATA 80003                 III
                                TATATATATATATATATATAT   A
                                ||||||||||||||||||||   |
                                ATATATATATATATATATATA   T
                                         III
GAM3539  NRIP1    3'  CAATATATATATATATACATAT 80055
                                TAATATATATATATATATATAT
                                ||||||||||||||||||||||
                                GTTATATATATATATATGTATA

GAM3539  NRIP1    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  NRIP1    3'  ATATATACATATTATATATATA 80056          _
            T                    ATATATATATAT ATATATATAT
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                                TATATATGTATA TATATATATA
                                       A
GAM3539  NRIP1    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  NRIP1    3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  NRIP1    3'  TATATATATATATATATA    80053
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATAT

GAM3539  NRIP1    3'  ACATATTATATATATATATATA 80057      _
                T                ATATAT ATATATATATATATAT
                                 ||||||| ||||||||||||||||
                                 TGTATA TATATATATATATATA
                                      A
GAM3539  NRIP1    3'  ATACATATTATATATATATATA 80051       _
                T                ATATATAT ATATATATATATAT
                                 |||||||| ||||||||||||||
                                 TATGTATA TATATATATATATA
                                      A
GAM3539  NRIP1    3'  ATATATATATATATAAAATATA 80052            T_
                T                ATATATATATATATA  ATATAT
                                 ||||||||||||||  ||||||
                                 TATATATATATATAT  TATATA
                                        TT
GAM3539  OTX1     3'  ATATATATATGTATATATATAT 79998          A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TATATATATA ATATATATATA
                                      C
GAM3539  OTX1     3'  ATATATGTATATATATATATAT 80000       A
                                ATATAT TATATATATATATAT
                                |||||| ||||||||||||||
                                TATATA ATATATATATATATA
                                     C
GAM3539  OTX1     3'  ATATATGTATATATATATATAT 80000       A
                                ATATAT TATATATATATATAT
                                |||||| ||||||||||||||
                                TATATA ATATATATATATATA
                                     C
GAM3539  OTX1     3'  ATATATATGTATATATATATAT 79999        A
                                ATATATAT TATATATATATAT
                                |||||||| ||||||||||||
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                                TATATATA ATATATATATATA
                                     C
GAM3539  OTX1     3'  TATATATATATGTATATAT    80034          A
                                TATATATATAT TATATAT
                                |||||||||||| |||||||
                                ATATATATATA ATATATA
                                     C
GAM3539  OTX1     3'  TATATATATATGTATATATAT  80036          A
                                TATATATATAT TATATATAT
                                |||||||||||| |||||||||
                                ATATATATATA ATATATATA
                                     C
GAM3539  PCSK2    3'  TATATATATAGCACTATATATA 80059          TA__
                T                TATATATATA    TATATATAT
                                |||||||||    |||||||||
                                ATATATATAT    ATATATATA
                                     CGTG
GAM3539  PCSK2    3'  TATGTATATATACACATATAT  80058     A
                                TAT TATATATATATATATAT
                                ||| ||||||||||||||||
                                ATA ATATATATGTGTATATA
                                  C
GAM3539  PEA15    3'  TAATATACATATATGTAGAATA 80060          _____
                TATAT                TAATATATATATAT     ATATATAT
                                |||||||||||||    ||||||||
                                ATTATATGTATATA     TATATATA
                                     CATCT
GAM3539  PEX3     3'  TATATATATATATATGTATATA 80061          A    III
                                TATATATATATATAT TATAT   A
                                |||||||||||||| |||||   |
                                ATATATATATATATA ATATA   T
                                     C    III
GAM3539  PKIA     3'  TAAAATATATATATATATATAT 79988    T          III
                ATA                  AA ATATATATATATATATATAT   A
                                || ||||||||||||||||||   |
                                TT TATATATATATATATATATA   T
                                  T              III
GAM3539  PLXNA1   3'  TATATATATATGCATATATAT  80062          A
                                TATATATATAT TATATATAT
                                |||||||||| |||||||||
                                ATATATATATA GTATATATA
                                     C
GAM3539  PMX1     3'  TATATATATATATATATA    80053
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATAT

GAM3539  PMX1     3'  TATATATATATATGAAATATAT 80065          AT_
                                TATATATATATAT   ATATAT
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                              ATATATATATATA  TATATA
                                     CTT
GAM3539  PMX1    3' ATATATATATATATATATATAT 79978
                              ATATATATATATATATATATAT
                              ||||||||||||||||||||
                              TATATATATATATATATATATA

GAM3539  PMX1    3' TATATATATATATATATA    80053
                              TATATATATATATATATA
                              ||||||||||||||||||
                              ATATATATATATATATAT

GAM3539  PMX1    3' ATATATATATATATATATATAA 80063              ATIII
                              ATATATATATATATATATAT    A
                              ||||||||||||||||||||    |
                              TATATATATATATATATATA    T
                                    IIITA
GAM3539  PMX1    3' TATATATATATATGAAATATAT 80065          AT_
                              TATATATATATAT  ATATAT
                              ||||||||||||  ||||||
                              ATATATATATATA  TATATA
                                     CTT
GAM3539  PMX1    3' ATATATATATATGAAATATATA 80068          ___
           TAT                  ATATATATATAT  ATATATATAT
                              ||||||||||||  |||||||||
                              TATATATATATA  TATATATATA
                                     CTT
GAM3539  PMX1    3' ATATATATATATATATATATAA 80063              ATIII
                              ATATATATATATATATATAT    A
                              ||||||||||||||||||||    |
                              TATATATATATATATATATA    T
                                    IIITA
GAM3539  PMX1    3' AATATATACAGTATATATAT  80066         _
                              AATATATATA TATATATAT
                              |||||||||| |||||||||
                              TTATATATGT ATATATATA
                                    C
GAM3539  PMX1    3' ATATATATATATATATATATAT 79978
                              ATATATATATATATATATATAT
                              ||||||||||||||||||||||
                              TATATATATATATATATATATA

GAM3539  PMX1    3' ATATATATATATATATATATAT 79978
                              ATATATATATATATATATATAT
                              ||||||||||||||||||||||
                              TATATATATATATATATATATA

GAM3539  PMX1    3' ATATATATATATATATATATAT 80064               III
           A                   ATATATATATATATATATATAT  A
                              ||||||||||||||||||||||  |
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                                TATATATATATATATATATATA   T
                                                    III
GAM3539  PMX1     3'  AATATATATATAAATATAT    80067          T
                                AATATATATATA ATATAT
                                |||||||||||| ||||||
                                TTATATATATAT TATATA
                                       T
GAM3539  PMX1     3'  AATATATACAGTATATATAT   80066          _
                                AATATATATA TATATATAT
                                |||||||||| |||||||||
                                TTATATATGT ATATATATA
                                      C
GAM3539  PMX1     3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  PMX1     3'  ATATATATATATGAAATATATA 80068          ___
              TAT                  ATATATATATAT   ATATATATAT
                                |||||||||||   ||||||||||
                                TATATATATATA   TATATATATA
                                      CTT
GAM3539  PMX1     3'  AATATATATATAAATATAT    80067          T
                                AATATATATATA ATATAT
                                |||||||||||| ||||||
                                TTATATATATAT TATATA
                                       T
GAM3539  PMX1     3'  ATATATATATATATATATATAT 80064                III
              A                   ATATATATATATATATATATAT   A
                                |||||||||||||||||||||||  |
                                TATATATATATATATATATATA   T
                                                    III
GAM3539  PPARGC1  3'  TATATATATATATATATATATA 80003                  III
                                TATATATATATATATATATAT   A
                                |||||||||||||||||||||  |
                                ATATATATATATATATATATA   T
                                                    III
GAM3539  PPARGC1  3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  PPARGC1  3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  PRKCN    3'  TATATATATATATATATATAA  79967                 ATIII
                                TATATATATATATATATAT    A
                                ||||||||||||||||||    |
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                                ATATATATATATATATATA    T
                                        IIITA
GAM3539  PUM1     3'  TATATATATATATATATATATA 80003                 III
                                TATATATATATATATATATAT   A
                                ||||||||||||||||||||   |
                                ATATATATATATATATATATA   T
                                        III
GAM3539  PUM1     3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  PUM1     3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  RBL1     3'  TATTTATATATATATATATAT  80069     A
                                TAT TATATATATATATATAT
                                ||| ||||||||||||||||
                                ATA ATATATATATATATATA
                                  A
GAM3539  RBP3     3'  TATATATATACATATATAT    80070
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATATATATGTATATATA

GAM3539  RNTRE    3'  TATATATATATATATATA    80053
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATAT

GAM3539  RNTRE    3'  CATATATATATATATATATATA 80071                  III
                                TATATATATATATATATATAT   A
                                ||||||||||||||||||||   |
                                GTATATATATATATATATATA   T
                                        III
GAM3539  ROCK2    3'  TATATATATATATATATATAA  79967                ATIII
                                TATATATATATATATATAT    A
                                ||||||||||||||||||    |
                                ATATATATATATATATATA    T
                                        IIITA
GAM3539  ROCK2    3'  ATATATATATATATATAT    80072
                                ATATATATATATATATAT
                                ||||||||||||||||||
                                TATATATATATATATATA

GAM3539  ROCK2    3'  TATATATATATATATATAT   79980
                                TATATATATATATATATAT
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                                ATATATATATATATATATA

GAM3539  ROCK2    3'  TATATATATATATATATAT   79980
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATATATATATATATATA

GAM3539  RP42     3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  RP42     3'  AATATATATATATATATATATA 80074                  ATIII
           A                     AATATATATATATATATATAT    A
                                 ||||||||||||||||||||    |
                                 TTATATATATATATATATATA    T
                                       IIITA
GAM3539  RP42     3'  AATATATATATATATATATATA 79989                   III
           TA                     AATATATATATATATATATAT   A
                                  ||||||||||||||||||||||  |
                                  TTATATATATATATATATATATA  T
                                        III
GAM3539  RP42     3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  RP42     3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  RP42     3'  ATATATATATATATACACACAT 80073
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATGTGTGTA

GAM3539  RPL23A   3'  ATATATATATATATATATATAA 80063                 ATATIII
                                ATATATATATATATATAT      A
                                ||||||||||||||||      |
                                TATATATATATATATATA      T
                                      IIITATA
GAM3539  SEMA3F   3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  SEMA3F   3'  TAATATATATATATATATATAT 80076                   ATIII
           AA                     AATATATATATATATATATAT    A
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                                TTATATATATATATATATATA    T
                                                  IIITA
GAM3539  SEMA3F   3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  SEMA3F   3'  TAATATATATATATATATATAT 80075                    III
              ATA                 AATATATATATATATATATAT   A
                                |||||||||||||||||||||||  |
                                TTATATATATATATATATATATA   T
                                                  III
GAM3539  SGCD     3'  ATATATATTTATTTATATATAT 80077         A   A
                                ATATATAT TAT TATATATAT
                                |||||||| ||| |||||||||
                                TATATATA ATA ATATATATA
                                     A   A
GAM3539  SGCD     3'  TATATATATTTATATATAT    80078         A
                                TATATATAT TATATATAT
                                ||||||||| |||||||||
                                ATATATATA ATATATATA
                                      A
GAM3539  SLC1A1   3'  AATATATACATATATATATAT  80079
                                AATATATATATATATATATAT
                                ||||||||||||||||||||
                                TTATATATGTATATATATATA

GAM3539  SLC1A1   3'  ATATACATATATATATATATAT 80080
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATGTATATATATATATATA

GAM3539  SLC8A1   3'  TATATATATGTATATATAT    80081         A
                                TATATATAT TATATATAT
                                ||||||||| |||||||||
                                ATATATATA ATATATATA
                                      C
GAM3539  SON      3'  ATACAGATATATATATATAT   80082       T
                                ATATA ATATATATATATAT
                                ||||| ||||||||||||||
                                TATGT TATATATATATATA
                                   C
GAM3539  SON      3'  ATATATATATTTACATATATAT 80083          A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TATATATATA ATGTATATATA
                                      A
GAM3539  SRGAP1   5'  AATATATATATATATATATAT  80084
                                AATATATATATATATATATAT
                                |||||||||||||||||||||
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TTATATATATATATATATATA

GAM3539 SRGAP1 5' ATATATATATATATATATATAT 79978
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TATATATATATATATATATATA

GAM3539 SRGAP1 5' ATATATATATATATATATATAT 79978
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TATATATATATATATATATATA

GAM3539 SRGAP1 5' ATATATATATATATATATATAT 79978
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TATATATATATATATATATATA

GAM3539 SRGAP1 5' ATATATATATATATATATATAT 79978
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TATATATATATATATATATATA

GAM3539 SRGAP1 5' ATATATATATATATATATATAT 79978
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TATATATATATATATATATATA

GAM3539 SRGAP1 5' ATATATATATATATATATATAT 79978
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TATATATATATATATATATATA

GAM3539 SRGAP1 5' ATATATATATATATATATATAT 79978
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TATATATATATATATATATATA

GAM3539 SRGAP1 5' ATATATATATATATATATATAT 79978
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TATATATATATATATATATATA

GAM3539 SRGAP1 5' ATATATATATATATATATATAT 79978
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TATATATATATATATATATATA

GAM3539 SRGAP1 5' ATATATATATATATATATATAT 79978
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                                TATATATATATATATATATATA

GAM3539  SRGAP1   5'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
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                                TATATATATATATATATATATA

GAM3539  SRGAP1   5'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
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                                TATATATATATATATATATATA

GAM3539  SRGAP1   5'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  SRGAP1   5'  AATATATATATATATATATATA 79989                    III
                TA                AATATATATATATATATATATAT   A
                                  ||||||||||||||||||||||   |
                                  TTATATATATATATATATATATA   T
                                                 III
GAM3539  SRGAP1   5'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  SRGAP1   5'  ATAAATATATATATATATATAT 80085     T             III
                A                  ATA ATATATATATATATATAT   A
                                   ||| ||||||||||||||||||   |
                                   TAT TATATATATATATATATA   T
                                     T             III
GAM3539  SRGAP1   5'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  SRGAP1   5'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  SRGAP1   5'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
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                                TATATATATATATATATATATA

GAM3539  SRGAP1   5'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
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                                TATATATATATATATATATATA

GAM3539  STK4     3'  TAATTTATATATATATATGCAT 80086      A          A
                AT                    TAAT TATATATATATAT TATAT
                                      |||| |||||||||||| |||||
                                      ATTA ATATATATATATA GTATA
                                        A           C
GAM3539  SVIL     3'  TATATAAATATATATATAT    80087       T
                                      TATATA ATATATATATAT
                                      |||||| ||||||||||||
                                      ATATAT TATATATATATA
                                          T
GAM3539  SVIL     3'  TATATAAATATATATATAT    80087       T
                                      TATATA ATATATATATAT
                                      |||||| ||||||||||||
                                      ATATAT TATATATATATA
                                          T
GAM3539  TAGLN2   3'  AATATATATCTACATATATAT  80088         A
                                      AATATATAT TATATATATAT
                                      ||||||||| ||||||||||
                                      TTATATATA ATGTATATATA
                                            G
GAM3539  TGFBR2   3'  TATATATATATATATATA    80053
                                      TATATATATATATATATA
                                      ||||||||||||||||||
                                      ATATATATATATATATAT

GAM3539  TGFBR2   3'  ATAGATATATATATATATATAT 80089     T
                                      ATA ATATATATATATATATAT
                                      ||| ||||||||||||||||||
                                      TAT TATATATATATATATATA
                                        C
GAM3539  TMEPAI   3'  TATATATATTTATATATAT    80078         A
                                      TATATATAT TATATATAT
                                      ||||||||| |||||||||
                                      ATATATATA ATATATATA
                                            A
GAM3539  TNFSF9   3'  ATATATATATATATAATATATA 80090                _
                T                      ATATATATATATATA TATATAT
                                       |||||||||||||| |||||||
                                       TATATATATATATAT ATATATA
                                                 T
GAM3539  TRAM     3'  ATACAAATATATATATATATAT 80091       T
                                      ATATA ATATATATATATATAT
                                      ||||| ||||||||||||||||
                                      TATGT TATATATATATATATA
                                         T
GAM3539  TRPM6    3'  TAATATACATATTCCATATATA 80093           A_
                T                      TAATATATATAT  TATATATAT
                                       ||||||||||||  |||||||||
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                                ATTATATGTATA  GTATATATA
                                      AG
GAM3539  TRPM6    3'  TAATATATATATTCCATATATA 80092          A_
                T                  TAATATATATAT  TATATATAT
                                   ||||||||||||  |||||||||
                                   ATTATATATATA  GTATATATA
                                         AG
GAM3539  TRPM6    3'  AATAAAAATATATATATATATA 80094     TAT
                T                  AATA   ATATATATATATATAT
                                   ||||   ||||||||||||||||
                                   TTAT   TATATATATATATATA
                                     TTT
GAM3539  TRPM6    3'  TATATATATAATATATATAT   80095         T
                                   TATATATATA ATATATATAT
                                   |||||||||| ||||||||||
                                   ATATATATAT TATATATATA
                                              _
GAM3539  TRPM6    3'  TATATATATAAAAATATATAT  80096         TAT
                                   TATATATATA   ATATATAT
                                   ||||||||||   ||||||||
                                   ATATATATAT   TATATATA
                                         TTT
GAM3539  TRPM6    3'  ATATATATATAAAATATATATA 80097          T_
                T                  ATATATATATA  ATATATATAT
                                   ||||||||||||  |||||||||
                                   TATATATATAT  TATATATATA
                                         TT
GAM3539  UBE2H    3'  ATATATAATATATATATAT    80098       T
                                   ATATATA ATATATATATAT
                                   |||||||| ||||||||||||
                                   TATATAT TATATATATATA
                                           _
GAM3539  VEGF     3'  ATATATATAATATATATATATA 80099         _
                T                  ATATATATA TATATATATATAT
                                   |||||||||| ||||||||||||
                                   TATATATAT ATATATATATATA
                                         T
GAM3539  VEGF     3'  AATATATATATTTTATATATAT 80100          A_
                                   AATATATATAT  TATATATAT
                                   ||||||||||||  |||||||||
                                   TTATATATATA  ATATATATA
                                         AA
GAM3539  VEGF     3'  ATAAACATATATATATATATAT 80101     T
                                   ATA ATATATATATATATATAT
                                   ||| ||||||||||||||||||
                                   TAT TGTATATATATATATATA
                                     T
GAM3539  VENTX2   3'  ACATATATATATTTATATATAT 80103          A
                                   ATATATATATAT TATATATAT
                                   |||||||||||| |||||||||
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                                TGTATATATATA ATATATATA
                                      A
GAM3539  VENTX2   3'  AATATATATATATATATATATA 80074                  ATIII
              A                  AATATATATATATATATATAT     A
                                 ||||||||||||||||||||     |
                                 TTATATATATATATATATATA     T
                                       IIITA
GAM3539  VENTX2   3'  ACACATATATGTATATATATAT 80102          A
                                 ATATATATAT TATATATATAT
                                 |||||||||| ||||||||||
                                 TGTGTATATA ATATATATATA
                                       C
GAM3539  VENTX2   3'  TATATATATATTTATATAT    80020          A
                                 TATATATATAT TATATAT
                                 |||||||||| |||||||
                                 ATATATATATA ATATATA
                                       A
GAM3539  VENTX2   3'  ATATATACGTACATATATATAT 80104        TA
                                 ATATATA  TATATATATATAT
                                 |||||||  |||||||||||||
                                 TATATAT  ATGTATATATATA
                                      GC
GAM3539  WNT11    3'  TACATATATATTTATATATAT  80105          A
                                 TATATATATAT TATATATAT
                                 |||||||||| |||||||||
                                 ATGTATATATA ATATATATA
                                       A
GAM3539  WNT11    3'  TATATATATACATATATAT    80070
                                 TATATATATATATATATAT
                                 ||||||||||||||||||
                                 ATATATATATGTATATATA

GAM3539  WNT5A    3'  ATATATGTATATATATATATAT 80000        A
                                 ATATAT TATATATATATATAT
                                 |||||| ||||||||||||||
                                 TATATA ATATATATATATATA
                                     C
GAM3539  WNT5A    3'  ATATATGTATATATATATATAT 80000        A
                                 ATATAT TATATATATATATAT
                                 |||||| ||||||||||||||
                                 TATATA ATATATATATATATA
                                     C
GAM3539  WNT5A    3'  TATATATATGTATATATATATA 80021          A          III
                                 TATATATAT TATATATATAT   A
                                 ||||||||| ||||||||||   |
                                 ATATATATA ATATATATATA   T
                                       C          III
GAM3539  WNT5A    3'  TATATATATGTATATATATAA  80106          A        ATIII
                                 TATATATAT TATATATAT     A
                                 ||||||||| |||||||||     |
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                                ATATATATA ATATATATA    T
                                      C       IIITA
GAM3539  WNT5A    3'  ATATATATGTATATATATATAT 79999        A
                                ATATATAT TATATATATATAT
                                |||||||| ||||||||||||
                                TATATATA ATATATATATATA
                                     C
GAM3539  AKAP8    3'  ATATATATATATATATTACA  80107            A
                                ATATATATATATATAT TATA
                                |||||||||||||||| ||||
                                TATATATATATATATA ATGT
                                                 _
GAM3539  AKT3     3'  TATATATATATATATATAT   79980
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATATATATATATATATA

GAM3539  ARFD1    3'  TATATATATATATATATATATA 80003                 III
                                TATATATATATATATATATAT  A
                                ||||||||||||||||||||  |
                                ATATATATATATATATATATA  T
                                          III
GAM3539  ARHGAP10 3'  AATATATATATATATATATATA 80074               ATATIII
           A                     AATATATATATATATATAT     A
                                ||||||||||||||||||     |
                                TTATATATATATATATATA     T
                                      IIITATA
GAM3539  ARHGAP10 3'  AATATATATATATATATAT   80108
                                AATATATATATATATATAT
                                ||||||||||||||||||
                                TTATATATATATATATATA

GAM3539  BHLHB2   3'  TAATATATTTATATAATATATA 80109        A     T
           T                     TAATATAT TATATA ATATATAT
                                |||||||| |||||| ||||||||
                                ATTATATA ATATAT TATATATA
                                     A    _
GAM3539  BLOV1    3'  TATATATATACACATGTATAT  80115            A
                                TATATATATATATAT TATAT
                                |||||||||||||| |||||
                                ATATATATATGTGTA ATATA
                                          C
GAM3539  BLOV1    3'  CATATATATATATATATAT   80114
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                GTATATATATATATATATA

GAM3539  BLOV1    3'  TATATATACACATGTATAT   80112            A
                                TATATATATATAT TATAT
                                |||||||||||| |||||
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                                ATATATATGTGTA ATATA
                                      C
GAM3539  BLOV1    3'  ATATATATACACATGTATAT   80113            A
                                ATATATATATATAT TATAT
                                |||||||||||||| |||||
                                TATATATATGTGTA ATATA
                                      C
GAM3539  BLOV1    3'  ATATATATATCCCACATATATA 80111          A_         III
           TA                    ATATATATAT  TATATATATAT   A
                                |||||||||| ||||||||||  |
                                TATATATATA  GTGTATATATA   T
                                     GG         III
GAM3539  BLOV1    3'  CATATATATATATATATATAT  80110
                                TATATATATATATATATATAT
                                ||||||||||||||||||||
                                GTATATATATATATATATATA

GAM3539  BLZF1    3'  TAATATATATTACATAGTATAT 80116          A    _
           AT                    TAATATATAT TATATA TATATAT
                                |||||||||| |||||| |||||||
                                ATTATATATA ATGTAT ATATATA
                                     _    C
GAM3539  BPESC1   3'  TATATATTTATATATATATAT  80117        A
                                TATATAT TATATATATATAT
                                ||||||| ||||||||||||
                                ATATATA ATATATATATATA
                                    A
GAM3539  CACNA1I  3'  ACATATATATATATATATATAT 80128                 III
           A                     ATATATATATATATATATATAT   A
                                ||||||||||||||||||||  |
                                TGTATATATATATATATATATA   T
                                          III
GAM3539  CACNA1I  3'  ACACATATATATATATATATAT 80120                 III
           A                     ATATATATATATATATATATAT   A
                                ||||||||||||||||||||  |
                                TGTGTATATATATATATATATA   T
                                          III
GAM3539  CACNA1I  3'  TATACACATATATATATATAA  80121              ATIII
                                TATATATATATATATATAT    A
                                |||||||||||||||||    |
                                ATATGTGTATATATATATA    T
                                          IIITA
GAM3539  CACNA1I  3'  ATATATATATATGCATATATAT 80131          A
                                ATATATATATAT TATATATAT
                                |||||||||||| |||||||||
                                TATATATATATA GTATATATA
                                      C
GAM3539  CACNA1I  3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
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                                TATATATATATATATATATATA

GAM3539  CACNA1I  3'  ATATATATATATATGCATATAT 80123            A
                                ATATATATATATAT TATATAT
                                |||||||||||||| |||||||
                                TATATATATATATA GTATATA
                                          C
GAM3539  CACNA1I  3'  ATATATATATGCATATATATAT 80118          A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TATATATATA GTATATATATA
                                      C
GAM3539  CACNA1I  3'  ATATATATATATATATATATAT 80064                  III
              A                  ATATATATATATATATATATAT   A
                                ||||||||||||||||||||||   |
                                TATATATATATATATATATATA   T
                                              III
GAM3539  CACNA1I  3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CACNA1I  3'  AATAAATATATATATATAT    80119      T
                                AATA ATATATATATAT
                                |||| |||||||||||||
                                TTAT TATATATATATATA
                                   T
GAM3539  CACNA1I  3'  ATATATGCATATATATATATAT 80122        A
                                ATATAT TATATATATATAT
                                |||||| ||||||||||||||
                                TATATA GTATATATATATATA
                                    C
GAM3539  CACNA1I  3'  ATATATATATATGTATGTATAT 80125           A   A
                                ATATATATATAT TAT TATAT
                                |||||||||||| ||| |||||
                                TATATATATATA ATA ATATA
                                         C   C
GAM3539  CACNA1I  3'  ATATGCATATATATATATATAT 80126      A
                                ATAT TATATATATATATAT
                                |||| ||||||||||||||||
                                TATA GTATATATATATATA
                                   C
GAM3539  CACNA1I  3'  ATATGCATATATATATATATAT 80126      A
                                ATAT TATATATATATATAT
                                |||| ||||||||||||||||
                                TATA GTATATATATATATA
                                   C
GAM3539  CACNA1I  3'  ATATATATATATATATGTAT   80130            A
                                ATATATATATATAT TAT
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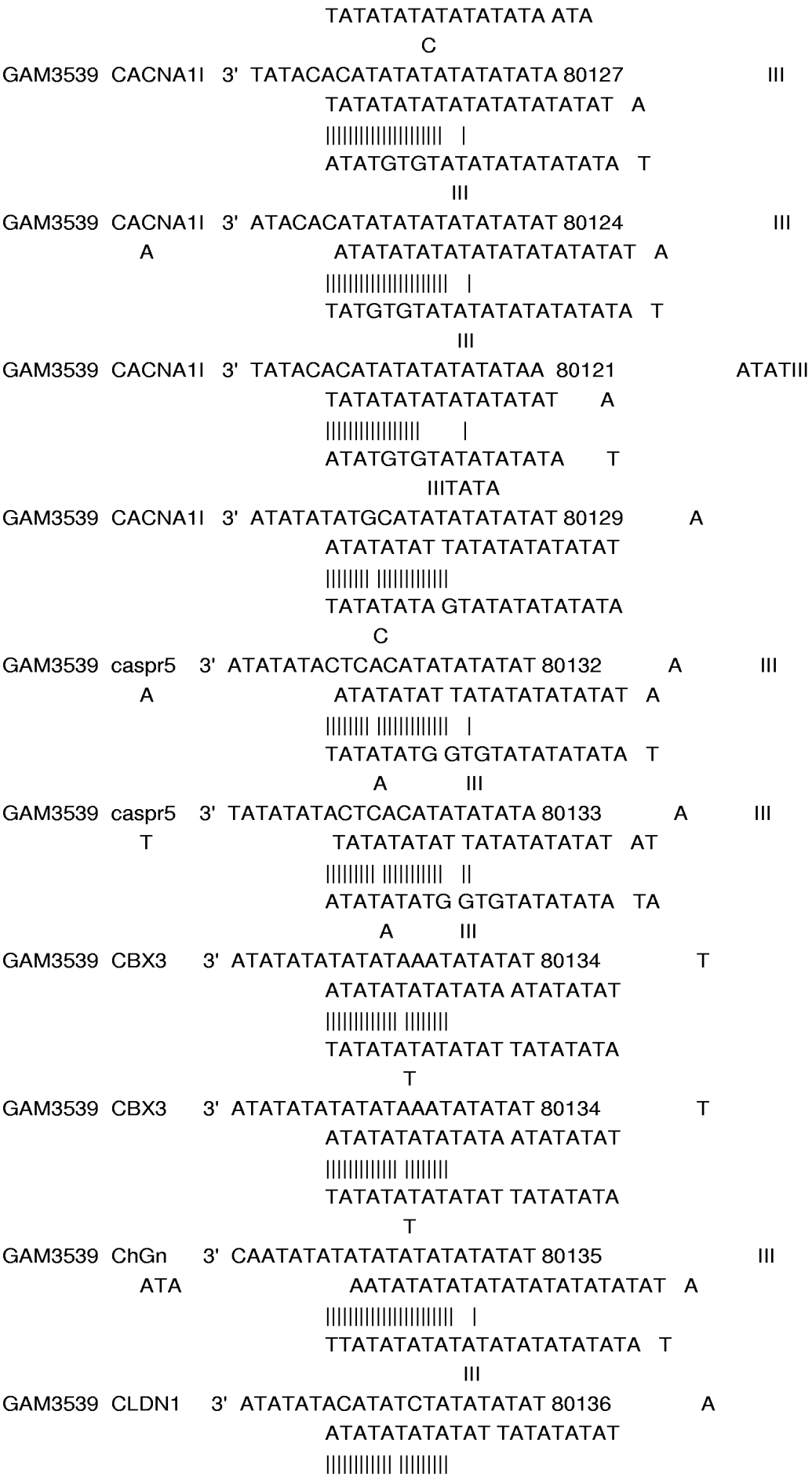
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C
GAM3539 CACNA1I 3' TATACACATATATATATATATA 80127 III
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ATATGTGTATATATATATATA T
III
GAM3539 CACNA1I 3' ATACACATATATATATATATAT 80124 III
A ATATATATATATATATATAT A
TATGTGTATATATATATATA T
III
GAM3539 CACNA1I 3' TATACACATATATATATATAA 80121 ATATIII
TATATATATATATATAT A
ATATGTGTATATATATA T
IIITATA
GAM3539 CACNA1I 3' ATATATATGCATATATATATAT 80129 A
ATATATAT TATATATATATAT
TATATATA GTATATATATATA
C
GAM3539 caspr5 3' ATATATACTCACATATATATAT 80132 A III
A ATATATAT TATATATATATAT A
TATATATG GTGTATATATATA T
A III
GAM3539 caspr5 3' TATATATACTCACATATATATA 80133 A III
T TATATATAT TATATATATAT AT
ATATATATG GTGTATATATA TA
A III
GAM3539 CBX3 3' ATATATATATATAAATATATAT 80134 T
ATATATATATATA ATATATAT
TATATATATATAT TATATATA
T
GAM3539 CBX3 3' ATATATATATATAAATATATAT 80134 T
ATATATATATATA ATATATAT
TATATATATATAT TATATATA
T
GAM3539 ChGn 3' CAATATATATATATATATAT 80135 III
ATA AATATATATATATATATATAT A
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III
GAM3539 CLDN1 3' ATATATACATATCTATATATAT 80136 A
ATATATATATAT TATATATAT

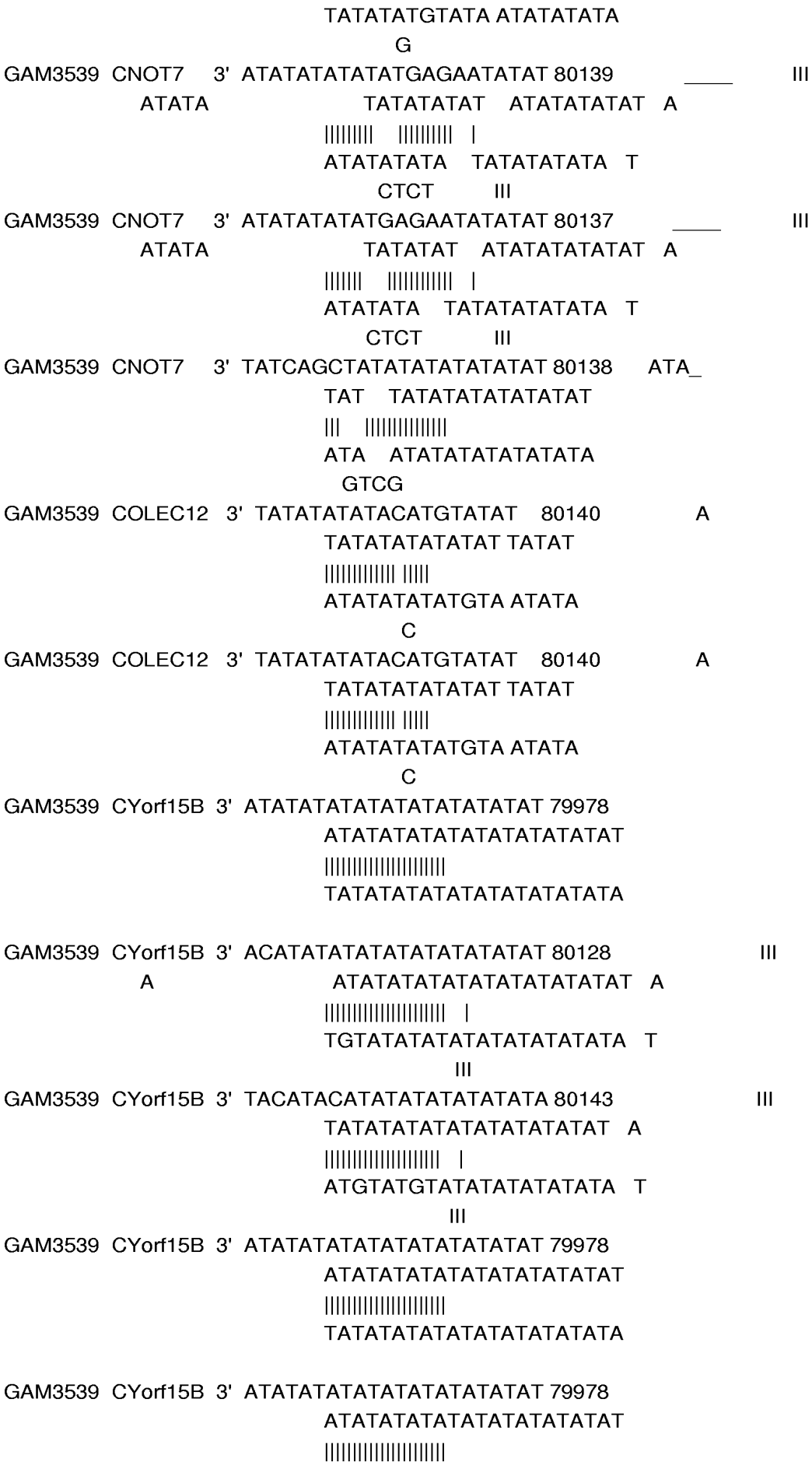
TATATATGTATA ATATATATA
G
GAM3539 CNOT7 3' ATATATATATATGAGAATATAT 80139 ____ III
ATATA TATATATAT ATATATATAT A
ATATATATA TATATATATA T
CTCT III
GAM3539 CNOT7 3' ATATATATATGAGAATATATAT 80137 ____ III
ATATA TATATAT ATATATATATAT A
ATATATA TATATATATATA T
CTCT III
GAM3539 CNOT7 3' TATCAGCTATATATATATATAT 80138 ATA_
TAT TATATATATATATAT
ATA ATATATATATATATA
GTCG
GAM3539 COLEC12 3' TATATATATACATGTATAT 80140 A
TATATATATATAT TATAT
ATATATATATGTA ATATA
C
GAM3539 COLEC12 3' TATATATATACATGTATAT 80140 A
TATATATATATAT TATAT
ATATATATATGTA ATATA
C
GAM3539 CYorf15B 3' ATATATATATATATATATATAT 79978
ATATATATATATATATATATAT
TATATATATATATATATATATA
GAM3539 CYorf15B 3' ACATATATATATATATATATAT 80128 III
A ATATATATATATATATATATAT A
TGTATATATATATATATATA T
III
GAM3539 CYorf15B 3' TACATACATATATATATATATA 80143 III
TATATATATATATATATATAT A
ATGTATGTATATATATATATA T
III
GAM3539 CYorf15B 3' ATATATATATATATATATATAT 79978
ATATATATATATATATATATAT
TATATATATATATATATATATA
GAM3539 CYorf15B 3' ATATATATATATATATATATAT 79978
ATATATATATATATATATATAT

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                                TATATATATATATATATATATA

GAM3539  CYorf15B  3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CYorf15B  3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CYorf15B  3'  ATACATATATATATATATATAT 80144                    III
                  A                  ATATATATATATATATATATAT   A
                                     ||||||||||||||||||||||   |
                                     TATGTATATATATATATATATA   T
                                                    III
GAM3539  CYorf15B  3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CYorf15B  3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CYorf15B  3'  ATATATATATATATATATATAT 80064                    III
                  A                  ATATATATATATATATATATAT   A
                                     ||||||||||||||||||||||   |
                                     TATATATATATATATATATATA   T
                                                    III
GAM3539  CYorf15B  3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CYorf15B  3'  ACATACATATATATATATATAT 80142                    III
                  A                  ATATATATATATATATATATAT   A
                                     ||||||||||||||||||||||   |
                                     TGTATGTATATATATATATATA   T
                                                    III
GAM3539  CYorf15B  3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CYorf15B  3'  TACATACATATATATATATAA  80141                   ATIII
                                TATATATATATATATATAT    A
                                ||||||||||||||||||     |
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                                ATGTATGTATATATATATA    T
                                      IIITA
GAM3539  CYorf15B  3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  CYorf15B  3'  ATATATATATATATATATATAT 79978
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM3539  DDX17     3'  TATATATATATATATATAT   79980
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GAM3539  DDX36     3'  TATATATATATATATATATATA 80003                  III
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                                      III
GAM3539  DDX36     3'  TATATATATATATATATATAA  79967                ATIII
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GAM3539  DIS3      3'  TATATATATCTATATATATAT  80145          A
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GAM3539  DKFZP434E2135 3'  CATATATATATATAATATATAT 80146             _
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GAM3539  DKFZP434P0721 3'  TATATATATATATATAAACAT  80147               T
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GAM3539  DKFZP434P0721 3'  AATAAATATATATATATATAT  80148      T
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GAM3539  DKFZP564B1162 3'  CATATATTTATATATATAT    80149        A
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